

Wissenschaftszentrum Weihenstephan für Ernährung, Landnutzung und Umwelt

Qualitative and quantitative analysis of molecular markers as a tool for classification, risk assessment and monitoring of acute myeloid leukemia

Simone Silvia Weber

Vollständiger Abdruck der von der Fakultät Wissenschaftszentrum Weihenstephan für Ernährung, Landnutzung und Umwelt der Technischen Universität München zur Erlangung des akademischen Grades eines

Doktors der Naturwissenschaften

genehmigten Dissertation.

Vorsitzender:

Prof. Dr. W. Windisch

Prüfende der Dissertation:

1. apl. Prof. Dr. M.W. Pfaffl

2. apl. Prof. Dr. S. Schnittger

3. Prof. Dr. H.R. Fries

Die Dissertation wurde am 21.12.2016 bei der Technischen Universität München eingereicht und durch die Fakultät Wissenschaftszentrum Weihenstephan für Ernährung, Landnutzung und Umwelt am 17.05.2017 angenommen.

## Table of content

Ab	Abbreviationsiii				
Zu	Zusammenfassungv				
Ał	ostra	ctvi			
1		Introduction1			
	1.1	AML1			
		1.1.1 Background, epidemiology and etiology1			
		1.1.2 Classification			
		1.1.3 Genetics of CN-AML			
		1.1.4 Therapy of AML13			
		1.1.5 Monitoring of AML during therapy15			
	1.2	Aim of the dissertation16			
2		Materials and methods17			
	2.1	Sample preparation and nucleic acid isolation17			
	2.2	BAALC and ERG assessment17			
	2.3	Brief overview of methods used to detect molecular alterations, other than BAALC and ERG expression			
	2.4	Patient samples21			
	2.5	Statistical analysis			
3		Results and discussion			
	3.1	BAALC and ERG gene expression in CN-AML			
		3.1.1 BAALC and ERG in CN-AML: range of expression and cut-off definition 23			
		3.1.2 Correlation of diagnostic BAALC and ERG gene expression to clinical and molecular parameters			
		3.1.3 Prognostic value of BAALC and ERG expression as single marker27			
		3.1.4 Prognostic value of <i>BAALC</i> and <i>ERG</i> in the context of other molecular alterations			
	3.2	Analysis of BAALC gene expression for detection of MRD			
		3.2.1 Fundamental validation of the feasibility of <i>BAALC</i> expression for MRD detection			
		3.2.2 Prognostic value of BAALC expression levels during therapy			
	3.3	<i>ERG</i> gene expression in patients with AML and acquired gain of chromosome 21			

	3.3.1 Characterization of patients with cytogenetically visible structural aberrations of chromosome 21	37
	3.3.2 Determination of ERG gene expression and ERG DNA copy number	38
	3.3.3 Correlation of <i>ERG</i> expression with molecular alterations in AML with ga of chromosome 21	in 41
4	Conclusions	43
5	Perspectives	45
6	References	46
Ackno	wledgements	60
List of	scientific communications	61
Curric	ulum vitae	64
Appen	ndix I - VI	65

# Abbreviations

АК	Non-complex aberrant karyotype
AK-AML	Non-complex aberrant karyotype AML
AML	Acute myeloid leukemia
ATRA	All-trans retinoic acid
BAALC	Brain and acute leukemia gene
BM	Bone marrow
cDNA	Complementary DNA
Chr	Chromosome
CI	Confidence interval
СК	Complex aberrant karyotype
CK-AML	Complex aberrant karyotype AML
СМР	Common myeloid progenitor
CN	Cytogenetically normal
Cq	Quantification cycles
CR	Complete remission
DFS	Disease-free survival
DOM	Difference of the mean
DS	Down syndrome
DS-AMKL	Down syndrome acute megakaryoblastic leukemia
EFS	Event-free survival
ERG	E26 transforming sequence-related gene
ETP	Early T-cell precursor
ETS	E26 transforming sequence
FAB	French-American-British
FISH	Fluorescence in situ hybridization
<i>FLT3</i> -ITD≥0.5	<i>FLT3</i> -ITD to <i>FLT3</i> wildtype ratios $\geq 0.5$
GMP	Granulocyte/macrophage progenitor
GOI	Gene of interest
HR	Hazard ratio
HSC	Hematopoietic stem cell
HSCs	Hematopoietic stem cells
ITD	Internal tandem duplication
LT	Long-term
MDS	Myelodysplastic syndrome

MEP	Megakaryocytic/erythroid progenitors
MLP	Multilymphoid progenitors
MPN	Myeloproliferative disease
MPP	Multipotent progenitor
MRD	Minimal residual disease
mRNA	Messenger RNA
mut	Mutation
n.s.	Not significant
NADP <sup>+</sup> /H	Nicotinamide adenine dinucleotide phosphate
NK	Natural killer
NOS	Not otherwise specified
OR	Odds ratio
OS	Overall survival
РВ	Peripheral blood
PCR	Polymerase chain reaction
qPCR	Quantitative real-time polymerase chain reaction
RIN	RNA integrity number
s-AML	Secondary AML
SEM	Standard error of the mean
ST	Short-term
t-AML	Therapy-related AML
TKD	Tyrosine kinase domains
WHO	World Health Organization

## Zusammenfassung

Die Akute Myeloische Leukämie (AML) repräsentiert eine klinisch sehr heterogene Erkrankung. In den letzten Jahren ermöglichte die Entwicklung neuer Technologien die Identifizierung von genetischen Veränderungen, darunter Genmutationen und veränderte Genexpressionen, welche zu einem besseren Verständnis der molekularen Pathogenese, einer detaillierteren Klassifizierung und einer verbesserten Risikostratifikation führten. Dennoch stellt die AML weiterhin eine sehr aggressive Erkrankung mit hohen Rezidivraten dar. Speziell bei einer Subgruppe der AML, der AML mit normalem Karyotyp, fehlen weiterhin molekulare Marker, welche die Grundlage für eine verbesserte Risikostratifikation bei Diagnose, aber auch im Verlauf der Erkrankung bilden könnten. Aus diesem Grund sollte in der hier vorliegenden Arbeit die prognostische und biologische Bedeutung der Genexpressionmarker *BAALC* und *ERG* analysiert werden. Beide Marker wurden schon in früheren Studien analysiert, jedoch mit unterschiedlichen Ergebnissen.

In unseren Studien konnten verschieden Assoziationen der *BAALC* und *ERG* Expression zu klinischen und molekularen Parametern dargestellt werden. So war eine hohe Expression beider Gene mit jüngerem Alter und den prognostisch bedeutsamen molekularen Markern *NPM1* und *FLT3* assoziiert. Weiterhin konnten spezifische Assoziationen einer hohen *BAALC* Expression mit Veränderungen in verschiedenen Signalwegen und den kürzlich identifizierten Klassifikationsmarkern *IDH2*R172- und *RUNX1*-Mutationen gezeigt werden.

Bezüglich der Risikostratifikation, konnte beiden Genen eine prognostische Bedeutung zugewiesen werden, wobei der Einfluss der *ERG* Expression auf das Überleben nicht unabhängig von bereits bekannten Markern war. Im Gegensatz dazu war eine aberrante *BAALC* Expression mit einer schlechten Prognose assoziiert, auch unter Berücksichtigung weiterer prognostisch relevanter Marker. Neben der prognostischen Wertigkeit von *BAALC* bei Diagnose konnte gezeigt werden, dass die *BAALC* Expression den klinischen Verlauf wiederspiegelt und dass eine erhöhte *BAALC* Expression an definierten Therapiezeitpunkten mit einem schlechteren Überleben assoziiert ist. Dies lässt vermuten, dass durch die Analyse der *BAALC* Expression, sowohl bei Diagnose als auch im Therapieverlauf, bereits bestehende Risikostratifikationen noch verfeinert werden können.

Neben der prognostischen Bedeutung, wurden auch pathogene Mechanismen der AML untersucht. So konnte gezeigt werden, dass ein Zugewinn von Chromosom 21 mit einer zunehmenden *ERG* Expression einhergeht. Diese Ergebnisse lassen eine aktive Rolle von ERG in der Leukämogenese der AML mit Zugewinn von Chromosom 21 vermuten.

v

# Abstract

Acute myeloid leukemia (AML) is a heterogeneous disease with respect to the clinical picture and therapeutic outcome. Continuous improvements in genomics technology have enabled the identification of several genetic alterations, including gene mutations and deregulated gene expression, which have contributed to a better understanding of the molecular pathogenesis, refined classification and improved prognostication. However, AML still represents an aggressive disease with poor long-term survival rates, demonstrating that we are just at the beginning of unravelling the enormous molecular complexity of AML. Especially in cytogenetically normal AML (CN-AML), there is a tremendous need to specify molecular alterations which enable improved prognostication at diagnosis and over the course of the disease. Furthermore, it becomes increasingly important to consider the clonal complexity of AML. In this context, the prognostic and biological role of *BAALC* and *ERG* gene expression has been evaluated in previous studies with varying results, either focusing on these markers alone or analyzing in the context of concomitant molecular alterations.

In CN-AML, several specific associations were identified in the present study. High *BAALC* and *ERG* expression correlated with younger ages and with the clinically adverse-risk group defined by the mutational status of *NPM1* and *FLT3*. Furthermore, *BAALC* expression was shown to strongly correlate with mutations in transcription factors, in genes that induce proliferation, and with the previously identified markers *IDH2*R172 and *RUNX1* mutations. In terms of *ERG*, no such associations were revealed.

Regarding the prognostic value of *BAALC* and *ERG*, aberrantly high expression levels of both genes were shown to have an impact on survival. Although for *ERG*, this impact was found to be surrogate only for independent markers. *BAALC* strongly impacted on outcome, conveying an independent and additive effect in the context of other adverse prognostic alterations. This suggests that delineation of genetically defined subtypes could improve prognostication in CN-AML. Furthermore, it was evaluated that *BAALC* expression represents a stable marker during follow-up, reflecting the course of the disease. Moreover, high *BAALC* expression at certain clinically defined follow-up time points was strongly correlated to adverse clinical outcome, predisposing *BAALC* assessment as an applicable strategy to detect residual disease.

Finally, it was shown that a gain of chromosome 21 resulted in increased expression of the *ERG* gene, suggesting that altered *ERG* expression represents a causative mechanism contributing to the pathogenesis of AML with a gain of chromosome 21.

These results indicate that a comprehensive screening of molecular alterations provides new biological insight and broadens the information available for risk assessment in AML.

# 1 Introduction

## 1.1 AML

#### 1.1.1 Background, epidemiology and etiology

Acute myeloid leukemia (AML) is a heterogeneous malignancy in which genetic alterations lead to inhibition of differentiation and enhanced proliferation of myeloid precursor cells (termed blasts) resulting in the accumulation of these blasts at various stages of maturation (Figure 1). AML is the most common type of acute leukemia in adults. The number of new cases between 2008 and 2012 in the U.S. population was 4.0 per 100,000 per year.<sup>1</sup> Although AML can occur at all ages is it most common in older patients, with a median age at diagnosis of 67 years. Thus, the number of new cases is expected to increase as the population ages. In fact, the rates of new AML cases have been rising on average by 2.2% each year over the last 10 years.<sup>1</sup>



Figure 1: Schematic representation of the current hematopoietic model, also depicting the relation of the different AML subtypes (M0 to M7, cytomophologically defined based on maturational stage accoding to FAB classification<sup>2</sup>) to the different progenies of the myeloid lineages. Modified by Doulatov et al.<sup>3</sup>; edited by Elke Roos; Abbreviations: HSC, Hematopoietic stem cell; LT, Long-term; ST, Short-term; MPP, Multipotent progenitor; ETP, Early T-cell precursor; NK, Natural killer; MLP,

Multilymphoid progenitors; GMP, Granulocyte/macrophage progenitor; CMP, Common myeloid progenitor; MEP, Megakaryocytic/erythroid progenitors; FAB, French-American-British.

The etiology of AML remains largely unknown. However, there are some factors that increase the risk of AML. These include exposure to ionizing radiation, chemical benzene and chemotherapy-related drugs that damage DNA as well as having a history of a blood disorder such as myelodysplastic syndrome (MDS) or myeloproliferative disease (MPN). Further, inherited conditions such as Faconi anemia, Down syndrome (DS) as well as predisposing germline mutation, e.g. in *RUNX1* or *CEBPA*, can increase the risk for development of AML.<sup>4,5</sup> For a diagnosis of AML, a blast count (including myeloblasts, monoblasts, and/or megakaryoblasts) of 20% or more is required according to the WHO classification, except for AML with t(15;17), t(8;21), inv(16) or t(16;16) and some cases of erythroleukemia, where the diagnosis of AML can also be made when the blast percentage is less than 20%.<sup>6</sup> AML, which evolves without a prior history of chemo/radiotherapy or myeloid stem cell disorders is termed "*de novo* AML". On the other hand AML which arises from a pre-existing MDS or other myeloid stem cell disorders such as MPN is defined by the term "secondary AML" (s-AML). AML arising after chemotherapy applied for another previous malignancy is described by "therapy-related AML" (t-AML).

#### 1.1.2 Classification

Two staging systems have been commonly used for the classification of AML. The original classification scheme, proposed by the French-American-British (FAB) Cooperative Group in 1976,<sup>2</sup> is solely based on morphologic and cytochemical features and divides AML into eight subtypes (M0 to M7) reflecting the different stages of maturity of the AML blast cells. (Figure 1; Table 1, lower part).

The modern and now commonly used World Health Organization (WHO) classification system introduced in 2001 and updated in 2008 considered new scientific and clinical findings as it incorporated cytogenetic and molecular genetic characteristics in addition to morphologic and cytochemical criteria for the classification of AML. Table 1 gives an overview of the WHO classification scheme of 2008, where two molecular alteration have been incorporated as provisional entities.<sup>6</sup> For the classification of the category "AML, not otherwise specified (NOS)" criteria similar to original FAB classification system have been maintained. Just lately, a revision of the WHO classification system has been released. Changes proposed to the section of AML also comprise the adjustment of "AML with *NPM1* mutation" and "AML with

*CEBPA* mutation" from provisional to definite entities as well as the introduction of "AML with *RUNX1* mutation" as a provisional entity.<sup>7</sup>

Table 1: WHO classification of AML<sup>6</sup>

Categories			
Acute myeloid leukemia with recurrent genetic abnormalities			
AML with t(8;21)(q22;q22); <i>RUNX1-RUNX1T1</i>			
AML with inv(16)(p13.1q22) or t(16;16)(p13.1;q22); CBFB-MYH11			
APL with t(15;17)(q22;q12); <i>PML-RARA</i>			
AML with t(9;11)(p22;q23); <i>MLLT3-MLL</i>			
AML with t(6;9)(p23;q34); <i>DEK-NUP214</i>			
AML with inv(3)(q21q26.2) or t(3;3)(q21;q26.2); RPN1-EVI1			
AML (megakaryoblastic) with t(1;22)(p13;q13); RBM15-MKL1			
Provisional entity: AML with mutated NPM1			
Provisional entity: AML with mutated CEBPA			
Acute myeloid leukemia with myelodysplasia-related changes			
Therapy-related myeloid neoplasms			
Acute myeloid leukemia, not otherwise specified (NOS)	FAB		
Acute myeloid leukemia with minimal differentiation	M0		
Acute myeloid leukemia without maturation	M1		
Acute myeloid leukemia with maturation	M2		
Acute myelomonocytic leukemia	M4		
Acute monoblastic/monocytic leukemia	M5		
Acute erythroid leukemia	M6		
Acute megakaryoblastic leukemia	M7		
Acute basophilic leukemia			
Acute panmyelosis with myelofibrosis (syn.: acute myelofibrosis; acute myelosclerosis)			
For a diagnosis of AML, a blast count of $\geq$ 20% is required, except for AML with the recu abnormalities t(15;17), t(8;21), inv(16) or t(16;16) and some cases of erythroleukemia.	rrent genetic		

## 1.1.3 Genetics of CN-AML

AML represents a heterogeneous group of leukemia not only clinically but also at the molecular level, reflecting various underlying genetic abnormalities. Non-random clonal chromosome aberrations, such as translocations, inversions, deletions, and numerical abnormalities (e.g. trisomies and monosomies), are detectable in approximately 55% of adults with AML.<sup>8</sup> These chromosomal changes have not only contributed to the classification of the

disease, but have also been recognized as the strongest prognostic factors for survival, and moreover, provide a basis for treatment decisions (Table 2).<sup>9-11</sup>

Particularly in terms of allogeneic stem-cell transplantation it has been shown, that patients with adverse risk diseases (Table 2) would profit from stem-cell transplantation, while those with favorable risk disease would not.

Table 2: Current stratificatio	n of molecular	genetic and	cytogenetic	alterations,	according to	ELN
recommendations; revised by	Döhner et al. <sup>11</sup>					

Risk Profile	Subsets				
Favorable	t(8;21)(q22;q22);				
	inv(16)(p13.1q22) or t(16;16)(p13.1;q22); CBFB-MYH11				
	Mutated NPM1 without FLT3-ITD (normal karyotype)				
	Biallelic mutated CEBPA (normal karyotype)				
Intermediate-I <sup>+</sup>	Mutated NPM1 and FLT3-ITD (normal karyotype)				
	Wildtype NPM1 and FLT3-ITD (normal karyotype)				
	Wildtype NPM1 without FLT3-ITD (normal karyotype)				
Intermediate-II	t(9;11)(p22;q23); MLLT3-MLL (KMT2A)				
	Cytogenetic abnormalities not classified as favorable or				
	adverse‡				
Adverse	inv(3)(q21q26.2) or t(3;3)(q21;q26.2); <i>GATA2–MECOM</i>				
	t(6;9)(p23;q34); <i>DEK-NUP214</i>				
	t(v;11)(v;q23); MLL (KMT2A) rearranged				
	-5 or del(5q); -7; abnl(17p); complex karyotype§				
+ This category include	<sup>+</sup> This category includes all cases of AML with a normal karyotype except for those included in the				
favorable subgroup; most of these cases are associated with a poor prognosis, but they should be					
reported separately be	reported separately because of the potential different response to treatment.				
‡ Adequate numbers of most abnormalities have not been studied to draw firm conclusions					
regarding their prognostic significance.					
§ A complex karyotype is defined as three or more chromosomal abnormalities in the absence of					
one of the World Health Organization-designated recurring translocations or inversions - t(8;21),					
inv(16) or t(16;16), t(9;11), t(v;11) (v;q23), t(6;9), and inv(3)/t(3;3). About two thirds of patients					
with AML with a complex karyotype have a mutation of <i>TP53</i> , a deletion of <i>TP53</i> , or both. <i>TP53</i>					
alterations in AML rarely occur outside a complex karyotype.					

However, a large subset of AML, which illustrates enormous heterogeneity with respect to clinical picture and therapeutic outcome, presents with a cytogenetically normal (CN) karyotype - meaning that this subset of AML lacks informative cytogenetic alterations which could allocate the prognostic heterogeneity and moreover which could function as a guide for treatment decisions.<sup>8</sup> But, in recent years, a vast number of gene mutations as well as deregulated gene expression have been identified, which allowed to partly decipher the genetic diversity and differential prognosis of CN-AML. By now, the most useful markers

implicated in risk stratification are mutations in *NPM1*, *FLT3* internal tandem duplication (*FLT3*-ITD), and biallelic *CEBPA* mutations (Table 2).<sup>11</sup> However, the list of newly identified genetic alterations adding more and more prognostic and biological information is continuously growing. Therefore, Table 3 provides an overview of the most commonly mutated genes in CN-AML, also outlining the potential role in hematopoiesis, leukemogenesis, and the clinical significance, if known.

The characterization of these gene mutations has also provided insights into the biology of AML and several lines of evidence have come up showing that different genetic changes cooperate in leukemogenesis. Also from a clinical perspective, data emerge that pretreatment genetic signatures rather than single alterations will become an important tool for risk stratification in therapeutic decision-making processes.<sup>12</sup> For instance, it has been shown that CN-AML patients with mutated *NPM1* in the absence of *FLT3*-ITD (low-risk) have a comparatively better outcome than those with mutated *NPM1* and coexisting *FLT3*-ITD and would therefore no longer benefit from allogeneic stem cell transplantation.<sup>10;13</sup>

Analogically to gene mutations, deregulated expression of genes involved in cell proliferation, survival and differentiation e.g. *BAALC*,<sup>14;15</sup> *ERG*,<sup>16</sup> *MN1*,<sup>16</sup> *WT1*<sup>17</sup> and *EVI1*,<sup>18</sup> have been proposed as prognostic markers especially in CN-AML. More detailed information on *BAALC* and *ERG* gene is given below, since both genes represent the subject of this study.

Mutated Gene; Localization	Frequency in CN-AML	Type of alteration	Impact on hematopoiesis and leukemogenesis; Clinical significance
<i>NPM1</i> 5q35	46-53%	Frameshift mutation; net insertion of 4 nucleotides results in generation of a new C-terminus, with: (i) additional nuclear export signal motif (ii) loss of tryptophan residues	<ul> <li>NPM1 wildtype constantly shuttling between nucleolus and cytoplasm<sup>19</sup></li> <li>various functions: regulation of cell growth and proliferation (e.g. via interaction with ARF/TP53), control of centrosome duplication and mitosis, involved in ribosome biogenesis (nuclear export)<sup>20</sup></li> <li>role in hematopoiesis remains elusive: mutant protein localize aberrantly in the cytoplasm, thereby perturbing some NPM1 functions (e.g. stabilization of ARF), while activating (e.g. shuttle) or gaining (e.g. cytoplasmic interactions) others<sup>21;22</sup></li> <li>significantly associated with better outcome in the absence of <i>FLT3</i>-ITD<sup>23-26</sup></li> </ul>
<i>FLT3-</i> ITD 13q12	28-35%	Internal tandem duplications (ITD) within the cytoplasmic juxtamembrane domain; lead to constitutive activation of the tyrosine kinase domains (TKD)	<ul> <li><i>FLT3</i> encodes a class III receptor tyrosine kinase, which activates PI3K/protein kinase B and mitogen activated protein kinase pathways</li> <li><i>FLT3</i>-ITD and <i>FLT3</i>-TKD lead to constitutive activation of downstream signaling pathways</li> </ul>
<i>FLT3-</i> TKD 13q12	6-14%	Missense mutations in the activation loop, lead to constitutive activation of the TKD	<ul> <li>FLT3-ITD, but not FLT3-TKD or FLT3 wildtype, induces aberrant signaling including strong activation of signal transducer and activator of transcription 5 and repression of CEBPA and PU1.<sup>27</sup></li> <li><i>FLT3</i>-ITD: associated with unfavorable outcome, particularly in patients with a high mutant(ITD) to wildtype ratio or absence of the wildtype allele<sup>28-30</sup></li> <li><i>FLT3</i>-TKD, in contrast to <i>FLT3</i>-ITD, seems not associated with unfavorable outcome<sup>29;31</sup></li> </ul>

Table 3: Overview of molecular alterations in CN-AML

<i>ASXL1</i> 20q11	5-16%	Mainly frameshift and stop mutations in exon 12; predicted to lead to loss of the C-terminal plant homeodomain finger	<ul> <li>member of the enhancer of trithorax and polycomb family, that enlists proteins required for maintenance of activation and silencing of gene expression by modifying chromatin configuration</li> <li>ASXL1 can interact with retinoic acid receptor in the presence of retinoic acid and enhance the transcription of some genes while repressing that of others; dependent on the cell context<sup>32</sup></li> <li>ASXL1 mutations predicted to lead to loss of the C-terminal plant homeodomain finger, which binds specific epigenetic marks on histone tail, recruiting various other factors<sup>33</sup></li> <li>associated with higher age and s-AML<sup>34-36</sup></li> <li>associated with inferior outcome<sup>34-36</sup></li> </ul>
<i>CEBPA</i> 19q13.1	9-13% (of this ~60% biallelic mutated)	Two main hot spots: N-terminal frameshift mutations and C- terminal in-frame insertions/deletions	<ul> <li>belongs to the basic leucin zipper family of transcription factors</li> <li>CEBPA mediates the transition between CMPs and GMPs<sup>37</sup></li> <li>CEBPA essential for long-term HSC function (control of HSC numbers and functions)<sup>38</sup></li> <li>N-terminal frameshift mutations lead to a premature stop of translation of the p42 CEBPA protein, while conserving short p30 isoform</li> <li>C-terminal in-frame insertions/deletions disrupt binding to DNA or dimerization<sup>39;40</sup></li> <li>double-mutated (also termed biallelic) <i>CEBPA</i> preferentially combine an N-terminal mutation on one allele (sustaining the expression of p30 only) with a C-terminal mutation on the other allele (deficient in dimerization/DNA binding)<sup>41</sup></li> <li>double-mutated (biallelic) <i>CEBPA</i> associated with favorable outcome<sup>7;41-43</sup></li> <li>mutations in <i>CEBPA</i> have been associated with familial AML<sup>7;42</sup></li> </ul>
<i>DNMT3A</i> 2p23.3	27-35%	Mainly missense mutations; with ~60% resulting in substitution of Arg882 in the catalytic domain	<ul> <li><i>de novo</i> DNA methyltransferase; catalyzing CpG methylation</li> <li>HSCs lacking <i>DNMT3A</i> have a competitive growth advantage<sup>44</sup></li> <li>mutations also found in non-leukemic HSCs and in healthy individuals; related to age-related increase of clonal hematopoiesis<sup>44-46</sup></li> <li>murine R878 (equivalent to human R882) showed to abrogate catalytic activity and reduced DNA binding<sup>47</sup> and is suggested to have a dominant negative effect in embryonic stem cells<sup>48</sup></li> <li>clinical significance remains elusive: some report significant associations to inferior survival others only moderate effects on outcome, depending on genetic groups<sup>49-52</sup></li> </ul>

<i>IDH1</i> 2q33.3	<i>IDH1</i> and <i>IDH2</i> R140	Missense mutations at 3 specific arginine residues	<ul> <li>IDH1/2 are homodimeric NADP<sup>+</sup>-dependent enzymes that catalyze oxidative decarboxylation of isocitrate to produce the α-ketoglutarate, NADP, and CO2 required for the Krebs cycle</li> <li>mutated enzymes acquire a neomorphic activity that converts α-ketoglutarate to d-2-</li> </ul>
<i>IDH2</i> 15q26.1	~15% <i>IDH2</i> R172 ~1-4%		<ul> <li>hydroxyglutarate in a reaction consuming NADPH<sup>33</sup></li> <li><i>IDH1</i>R132, <i>IDH2</i>R140, <i>IDH2</i>R172 characterize clinical distinct subsets in CN-AML</li> <li>clinical significance of <i>IDH</i> mutations remains elusive, mainly associated with adverse outcome, though only in <i>NPM1</i> mutated/<i>FLT3</i>-ITD negative CN-AML for <i>IDH1</i> and <i>IDH2</i>R140<sup>54-56</sup></li> </ul>
<i>MLL(KMT2A)-</i> PTD 11q23	7-10%	Partial tandem duplication (PTD) of select exons; producing an in- frame, elongated protein. Mutant protein contains a duplicated N- terminus including AT-hooks and CXXC-domain	<ul> <li>MLL maintains normal function of HSC as a positive regulator of gene expression e.g. regulation HOX gene expression in hematopoietic systems<sup>57</sup></li> <li><i>Mll<sup>PTD/wildtype</sup></i> hematopoietic stem and progenitor cells exhibited a proliferative advantage and reduced myeloid differentiation<sup>58</sup></li> <li>clinical significance remains controversial, some report significant associations to risk of relapse or to shorter complete remission duration,<sup>25;59;60</sup> some reveal no impact<sup>61;62</sup></li> </ul>
NRAS 1p13.2	9-13%	Missense mutations exclusively located at codons 12, 13 and 61, resulting in loss of intrinsic GTPase activity and constitutive activation of the RAS protein	<ul> <li>mutant NRAS increases HSC proliferation and self-renewal capability and myeloid differentiation bias<sup>63</sup></li> <li>no significant impact on outcome<sup>25;64</sup></li> </ul>

<i>RUNX1</i> 21q22	6-26%	Missense, nonsense and frameshift mutations; mostly resulting in loss or destruction of the transactivation domain and the Runt homology domain in some cases	<ul> <li>transcription factor: regulates the expression of hematopoiesis specific genes, such as growth factors (GM-CSF, MPO, IL3), surface receptors (TCRA, TCRB, M-CSF receptor, FLT3), signaling molecules (CDKN1A, BLK, BCL2), and transcription activators (STAT3, MYB)<sup>65</sup></li> <li>RUNX1 essential for the maturation of T-, B-lymphocytes and megakaryocytes/platelets; negatively regulates proliferation of HSCs and myeloid progenitors<sup>66;67</sup></li> <li><i>RUNX1</i> mutations found in pedigrees of a rare inherited human disease familial platelet disorder with propensity to develop AML<sup>7</sup></li> <li>associated with higher age and s-AML<sup>68</sup></li> <li>associated with inferior outcome<sup>68-71</sup></li> </ul>
<i>TET2</i> 4q24	6-23%	Missense, nonsense and frameshift mutations; abrogating TET2 enzymatic function	<ul> <li>TET enzymes catalyze the Fe(II)- and α-ketoglutarate-dependent hydroxylation of 5-methylcytosine residues in DNA to form 5-hydroxymethylcytosine, which is involved in epigenetic regulation of gene expression.<sup>72</sup></li> <li>short hairpin RNA-mediated depletion of TET2 in HSCs resulted in skewing toward myeloid differentiation<sup>73</sup></li> <li>Loss of Tet2 resulted in expansion of the HSC compartment in a cell-intrinsic manner and enhanced HSC self-renewal<sup>74</sup></li> <li>associated with higher age and s-AML<sup>75-78</sup></li> <li>mutations also found in non-leukemic HSCs and in healthy individuals; related to agerelated increase of clonal hematopoiesis<sup>44-46</sup></li> <li>clinical significance remains controversial: some report significant associations to inferior survival; others report no impact or only an effect in specific genetic groups (e.g. favorable-risk group (Table 2) or in consumption with IDH)<sup>77-80</sup></li> </ul>
WT1 11p13	6-11%	Mostly frameshift mutations in exon 7 and substitutions in exon 9	<ul> <li>transcription factor: either enhance or repress the expression of specific targets, highly context specific</li> <li>loss of WT1 was associated with decreased growth of leukemic cells and rapid induction of apoptosis<sup>81</sup></li> <li>enforced WT1 expression inhibits differentiation<sup>81</sup></li> <li>elevated expression can be found in high proportion of AML, used for detection of residual disease<sup>82</sup></li> <li>associated with unfavorable outcome, particularly in younger patients<sup>83-86</sup></li> </ul>

#### 1.1.3.1 The BAALC gene

The brain and acute leukemia cytoplasmic (BAALC) gene expression has originally been described in neuroectoderm-derived tissues and was later, in a search for leukemia associated genes, also found in undifferentiated hematopoietic cells.<sup>87</sup> The BAALC gene localizes on human chromosome band 8q22.3. It consists of eight exons, of which exon 2 comprises an alternative termination codon. Up to now, at least 8 differentially spliced transcripts have been described in AML, with the transcript variant 1-8 and 1-6-8 being the most abundant ones.<sup>87</sup> The DNA sequence as well as the expression pattern of *BAALC* is highly conserved among mammals, whereas lower vertebrates lack comparable orthologs. Translation of the different splice variants result in six different protein isoforms, which show a cytoplasmic localization in morphologically immature CD34+ cells. These isoforms only share the Nterminal domain of the first 53 amino acid residues, while the remaining sequence is diverse.<sup>87</sup> The protein sequence of BAALC exhibits no homology to any known protein and does not contain any recognizable motifs or functional domains. A fact, through which the clarification of the functional role of BAALC in biological processes is additionally impeded. In normal hematopoiesis the expression of BAALC is restricted to CD34+ hematopoietic progenitor cells including uncommitted CD34+/CD38- cells as well as more committed CD34+ lymphoid, erythroid and myeloid progenitor cells. In vitro studies revealed that BAALC expression is down regulated during hematopoietic cell differentiation.<sup>88</sup> Based on this restriction of BAALC expression to undifferentiated progenitors in normal hematopoiesis as well as on the association of high BAALC expression to the expression of stem cell markers and more immature subtypes of AML it has been suggested that BAALC functions as a marker of early hematopoietic cells.<sup>87;89</sup> However, since aberrant expression is also found in other tumors like glioblastoma<sup>87</sup> and malignant melanoma<sup>90</sup> a comprehensive role of BAALC in general pathways has been suggested. In a first attempt to unravel the function of BAALC in the hematopoietic system it has been shown that constitutive activation BAALC did not promote proliferation or survival of hematopoietic cells, but did contribute to myeloid differentiation block in Hoxa9-immortalized cell lines.<sup>91</sup> A more recent study provided the molecular basis for a dual function of BAALC in regulating cell differentiation as well as proliferation. In this study Morita et al.92 identified two proteins with substantial roles in the ERK pathway, namely MEKK1 and KLF4, as potential interacting partners of BAALC. Subsequent in vitro assays on leukemic cells implied that BAALC on one hand induced cell cycle progression by sustained ERK activation, and on the other hand blocks ERK-mediated differentiation.

Besides the functional role of BAALC in hematopoiesis and leukemogenesis the mechanisms regulating *BAALC* expression in normal and abnormal hematopoiesis are also under investigation. In search for putative activation sides in the upstream regulatory machinery of *BAALC*, different transcription start sides with potential binding signatures for the transcription factors ARID3A, MFZ1, RUNX1 and the SP1/NFkB transactivation complex have been identified.<sup>93;94</sup> Further, Franzoni et al.<sup>94</sup> hypothesized from a cell line based model, that the *BAALC* promoter exhibits a bivalent mark of active and inactive post-translational-histone modifications, suggesting that *BAALC* represents a so called paused gene which can be specifically activated or repressed during differentiation.

Regarding the clinical significance of *BAALC*, collective data suggest *BAALC* as an important risk factor in CN-AML, where *BAALC* gene expression as a single marker is associated with treatment resistance and poor outcome.<sup>15;89;95-99</sup> Further, an association of *BAALC* expression to other molecular prognostic markers, and to a distinct gene-expression signature in CN-AML has been shown. For instance, high *BAALC* expression has been demonstrated to correlate with the mutational status of *FLT3*-ITD, *CEBPA*, *MLL*-PTD and with an unmuted *NPM1* as well as with elevated expression levels of the ETS-related gene *ERG*, the multi-drug resistance gene 1 and the stem cell markers CD133, CD34 and KIT. <sup>14-16;95</sup> Besides its associated with lower complete remission (CR) rates,<sup>15;95</sup> shorter disease-free survival (DFS)<sup>95</sup> and shorter overall survival (OS),<sup>14;15;95</sup> in some studies, while other studies could not confirm this independent prognostic effect of *BAALC* expression on survival.<sup>16;100</sup>

#### 1.1.3.2 The ERG gene

The E26 transforming sequence (ETS)-related gene (*ERG*) is located on human chromosome band 21q22 and encodes a member of the ETS family of transcription factors. Like all members of this family, ERG possesses an evolutionary-conserved ETS domain of about 85 amino acid residues that mediate binding to purine-rich DNA sequences with a central GGAA/T core consensus and additional flanking nucleotides. This ETS DNA-binding motive is located in the C-terminal region, while the N-terminal region shows a so called pointed domain, a helix-loophelix structure, which confers protein-protein interactions. Further two transcriptional activation domains have been described on either terminal sites. At least five isoforms of the ERG protein are generated by alternative splicing and translation initiation sites, of which isoform 3 represents the major isoform of normal and malignant hematopoietic cells.<sup>101;102</sup> Expression of *ERG* has been shown in several cell lines, including endothelial cells as well as in normal premature (CD34+) and malignant hematopoietic cells, but not in mature lymphoid or

myeloid cells.<sup>102</sup> Regarding the role of ERG in normal hematopoiesis it has been shown that homozygous mice harboring missense mutation in *erg* die at the embryonic stage as they fail to sustain definitive hematopoiesis.<sup>103;104</sup> Mice heterozygous for the same mutation represented with functionally impaired LT-HSCs, significantly lower numbers of committed hematopoietic progenitors and lower platelet numbers.<sup>103</sup> Thus, these data suggest that ERG function is essential to the production and maintenance of the hematopoietic stem cell pool.

Addressing the leukemic potential of ERG, ectopic expression of ERG was shown to induce megakaryocytic differentiation in the erythroleukemia cell line K562 as well as megakaryoblastic leukemia in mice.<sup>102;105</sup> Further, forced expression of ERG has been shown to promote the development and also the maintenance of leukemia in a mouse adult bone marrow (BM) transplantation model<sup>106</sup> and in-vitro assays revealed a growth-promoting effect of ERG on various human leukemia cells of erythroid, myeloid, megakaryocytic, T-, and B-cell lineages.<sup>107</sup> In addition, it has been suggested that ERG, like all ETS family members act in concert with other cellular proteins not only under physiological conditions, but also in the pathogenesis of leukemia. For instance, cooperating effects of elevated ERG expression and specific mutations in the onset of Down syndrome acute megakaryoblastic leukemia (DS-AMKL) have been described.<sup>106-108</sup> Besides, population-based studies show that the incidence of leukemia is 10 to 20 fold higher in individuals with DS compared with the overall population, with a particularly striking increase of AMKL, suggesting a general dosage-sensitive effect of genes located on chromosome 21 within leukemogenesis.<sup>109</sup> In an attempt to identify the respective genes on chromosome 21 a common Down syndrome critical region on chromosome 21g22 has been defined, which narrowed the number of candidate genes potentially involved in DS-associated leukemogenesis.<sup>110;111</sup> Amongst these genes ERG represented one of the most extensively studied, but the results remain controversial.<sup>112;113</sup>

Besides the potential role of an increase in DNA content to elevated *ERG* expression the exact mechanisms regulating *ERG* expression in normal and abnormal hematopoiesis are still under investigation. The human *ERG* locus has at least two recognized promoters and a specific enhancer +85kb downstream of the translation start site.<sup>107</sup> Recently, it has been shown that *ERG* expression is regulated by complexes of HSC transcription factors, namely SCL, LYL1, LMO2, GATA2 or GATA3, RUNX1, FLI1 and ERG itself, binding its promoters and +85 stem cell enhancer. Especially for T-ALL it has been shown, that abnormal *ERG* expression is probably caused by aberrant activation of the +85 enhancer. Even though these findings provide precious insights into transcriptional regulation of *ERG* they still do not explain the mechanisms leading to altered promoter and enhancer activity and therefore to abnormal *ERG* expression.

Finally, it should be mentioned that beside dysregulated expression of *ERG*, the involvement of *ERG* in chromosomal translocations has been implicated in rare cases of leukemia and more commonly in various types of other neoplasms. Therefore, the *ERG* locus can be rearranged and fused with *FUS/TLS* in AML<sup>114</sup>, with *EWS* in Ewing sarcoma<sup>115</sup> and with *TMPRSS2*<sup>116;117</sup> in prostate cancer. Especially in prostate cancer the fusion has been shown to result in *ERG* overexpression and has been associated with poor outcome.<sup>117</sup>

Regarding the clinical significance of deregulated expression of *ERG*, the impact on clinical outcome remains controversial. Especially in CN-AML, high *ERG* expression has been allocated to lower CR rates, shorter DFS, event-free survival (EFS) and OS in some studies,<sup>16;95;118</sup> while other studies only reported an adverse effect of high *ERG* expression on the achievement of CR and on EFS.<sup>119</sup> Besides the prognostic significance it has been published recently that cell based *ERG* overexpression results in resistance to kinase inhibitors such as sorafenib and dovitinib.<sup>120</sup> This finding is of special therapeutic interest since sorafenib currently is being tested in different clinical AML trials.

#### 1.1.4 Therapy of AML

The prognosis of AML is determined by AML-associated factors such as cytogenetic and molecular genetic aberrations as well as patient-related characteristics such as age, comorbidity and the performance status in general. While the latter predict treatment-related mortality the former factors provide a prediction of resistance to therapy.<sup>11</sup>

The treatment of AML is usually performed within randomized clinical trials and typically involves induction therapy, consolidation therapy and in some cases maintenance.

The goal of induction therapy is to bring about a CR, which means to reduce the amount of all leukemic cells to levels below morphological sensitivity (BM blasts < 5%, absolute neutrophil count >  $1.0 \times 10^9$ /L and platelet count >  $100 \times 10^9$ /L).<sup>10</sup> Standard induction therapy of younger adults (aged 18-60) usually consists of one or two cycles of two cytotoxic drugs: cytarabine (also called Ara-C) given as continuous infusion for seven days and an anthracycline (daunorubicin, idarubicin or mitoxantrone) given intravenously for three days, therefore termed the "7+3" regimen. With the 7+3 induction scheme complete response rates of 60-85% can be achieved in younger adults and until recently no other induction regime has been shown to be superior.<sup>11</sup> For older patients (ages >60 years) with favorable-risk and intermediate-risk cytogenetics and no coexisting conditions, the standard induction is the same as in younger adults, while dose reduction, investigational therapy or best supportive care may be considered in some of these patients, who are not eligible to receive standard

intensive chemotherapy.<sup>11</sup> Complete response rates in older patients are 40-60% after induction chemotherapy.

Standard post remission therapy (termed consolidation therapy) aims at the full eradication of the leukemic cell compartment and includes conventional chemotherapy as well as hematopoietic cell transplantation. The decision for hematopoietic cell transplantation depends on the leukemic genetic risk profile (Table 2), the risk of treatment-related death, and specific patient transplantation associated factors (e.g. age, comorbidity). Presently, a predicted risk of relapse of more than 35% is widely considered to warrant hematopoietic cell transplantation during the first remission.<sup>121</sup> Patients with favorable risk genetics (Table 2) and no coexisting conditions, should receive 2-4 cycles of intermediate-dose cytarabine. For patients 16 to 60-65 years with intermediate- or adverse-risk genetics, persistent disease or other high-risk clinical features such as s-AML or t-AML, the aggressive treatment of allogeneic hematopoietic-cell transplantation should be considered. Though the decision for allogeneic hematopoietic-cell transplantation in intermediate-risk patients seems not as clear as most of these patients represent with normal cytogenetics and molecular lesions might provide further prognostic information. For patients 60-65 to 75 years with unfavorable genetic risk allogeneic hematopoietic-cell transplantation can be considered, if they are physically able to undergo this procedure, while for those above 75 years investigational therapy should be considered.<sup>11</sup>

An exception of these recommendations has to be made for the M3 subtype of AML, termed acute promyelocytic leukemia (APL) with a translocation between chromosomes 15 and 17 according to the WHO, where treatment includes the non-chemotherapy drug all-trans retinoic acid (ATRA). ATRA, a derivative of retinoic acid, targets the *RARA* and reverses the differentiation block of promyelocytic blasts induced by the *PML-RARA* chimeric gene, thereby representing the first molecular target-based cancer therapy in AML.

Currently, new compounds targeting different AML specific cellular processes or the mutant proteins directly are under investigation. These compounds include tyrosine kinase inhibitors targeting FLT3 (e.g. midostaurin, quizartinib), inhibitors targeting the mutant metabolic enzymes IDH1 (AG-120) and IDH2 (AG-221), demethylating agents (e.g. azacytidine, decitabine) as well as antibodies, which specifically target antigens on leukemic cells, such as gemtuzumab ozogamicin, a humanized anti-CD33 monoclonal antibody conjugated with the cytotoxic agent calicheamicin. Besides the promising results provided by some of these new compounds in combination with conventional cytotoxic therapies none of them can be used as single agents to cure the disease.<sup>11</sup>

#### **1.1.5** Monitoring of AML during therapy

As described in section "1.1.4 Therapy of AML" antileukemic therapy in AML aims at the eradication of all leukemic cells to achieve cure from the disease. Achieving a morphologically leukemia-free state (termed complete remission) is the aim of the induction chemotherapy and it has consistently been shown that failure of early blast clearance by remission induction therapy is a major independent prognostic factor for prognosis.<sup>122</sup> Despite the relatively high rates of 40-80% of AML patients achieving complete remission, the majority of these patients experience relapse within three years after diagnosis.<sup>10;123-125</sup> The prognosis of patients in relapse is very poor with a five year survival probability of 4 to 46% of the patients (aged 16-60 years), whereby the duration of remission before relapse represents a major prognostic factor as an early relapse (duration of CR <6 month) contributes to a more adverse prognosis.<sup>10</sup> The source of these relapses has been shown to stem from persistent leukemia cells in the majority of cases, existing at levels below morphological sensitivity.<sup>126;127</sup> By now, several studies have shown that it is possible to detect this so called minimal residual disease (MRD) of AML before hematologic manifestation by multiparameter flow cytometry identifying leukemia associated aberrant phenotypes and moreover by quantitative real-time polymerase chain reaction (qPCR) based methods, digital PCR or (ultra) deep sequencing detecting residual leukemia specific targets. Due to the high sensitivity of qPCR-based methods, molecular markers have become key targets for the assessment of treatment response in individual patients to detect early relapse and to allow direct therapeutic intervention.<sup>10;128;129</sup> These targets include fusion genes (e.g. PML-RARA,<sup>130;131</sup> CBFB-MYH11,<sup>131;132</sup> RUNX1-RUNX1T1 (formerly AML1-ETO),<sup>131;133;134</sup>) and gene mutations, of which mutations in NPM1<sup>129;135</sup> and MLL-PTD<sup>136;137</sup> represent the best validated targets amongst the gene mutations. Further, genes highly expressed in some types of leukemia have also been described to represent a suitable MRD target, with the Wilms tumor (WT1) gene representing one of the best evaluated target in CN-AML.<sup>17</sup> The prognostic feasibility of the sensitive detection of leukemia specific targets has been validated just recently in a large clinical trial, where the persistence of NPM1 mutated transcripts after the induction chemotherapy not only provided information of residual disease and predicted risk of relapse, but also was the only independent prognostic factor for death in multivariate analysis. Moreover, this revealed that among patients with a high-risk genotype (FLT3-ITD, mutated DNMT3A, or both), negative results on qPCR after the second chemotherapy cycle distinguished a group of patients (79%) with a relatively favorable outcome. This result has strong implications for clinical/therapeutic decision making, as this group would have been originally suggested for stem-cell transplantation (Table 2).

## **1.2** Aim of the dissertation

The general aim of this doctoral thesis was a molecular characterization of AML to delineate the complex inter-relationships between genetic alterations and the expression of selected genes, in order to get further insight into the disease biology and to improve the risk assessment and clinical decision making.

For this purpose, different approaches were applied. First, a large diagnostic cohort of CN-AML was comprehensively investigated for molecular genetic alterations, essentially focusing on *BAALC* and *ERG* gene expression, as the prognostic value of these genes has been investigated in previous studies with varying results. Putative associations of altered *BAALC* and *ERG* gene expression with recently described molecular alterations and with functional biological pathways needed to be revealed, in order to delineate or define new subgroups of CN-AML.

Furthermore, in an attempt to improve prognostication in CN-AML, the impact of deregulated *BAALC* and *ERG* expression on the clinical outcome was examined - thereby focusing on the prognostic impact of these alterations alone, and moreover in the context of concomitant molecular alterations.

The second approach was to address the applicability of *BAALC* assessment during the course of the disease, as the prognostic information of residual disease becomes increasingly important in clinical decision-making. Therefore, *BAALC* expression was analyzed in a considerable number of CN-AML patients at distinct follow-up time points in order to assess the stability and the prognostic value of *BAALC* gene expression during therapy.

In a third approach, further insights into the functional involvement of altered *ERG* gene expression in the pathogenesis of AML needed to be gained. To concern this approach, *ERG* gene expression was analyzed in a group of patients with AML and an acquired gain of chromosome 21, thereby investigating a possible relationship between a gain of *ERG* DNA copy numbers and *ERG* gene expression levels. Besides this, concomitant molecular alterations were analyzed to reveal putative interacting partners of *ERG* in this subtype of AML.

## 2 Materials and methods

### 2.1 Sample preparation and nucleic acid isolation

Anticoagulated (heparin, EDTA, citrate) BM and peripheral blood (PB) samples were referred to the MLL Munich Leukemia Laboratory for diagnostic or follow-up assessment. Mononuclear cells were separated by Ficoll density gradient at 1204 g for 20 min using Ficoll (PAA Laboratories GmbH, Pasching, Austria) or Pancoll (PAN Biotech GmbH, Aidenbach, Germany) with a density of 1.077 g/ml. Cell pellets of 2.5–5x10<sup>6</sup> cells, depending on yield, were resuspended in PBS or water (only for DNA) and stored at -80°C if not directly processed. Either mRNA or total RNA was extracted with the MagnaPureLC mRNA Kit I (Roche Applied Science, Mannheim, Germany) or with the MagNA Pure 96 Cellular RNA Large Volume Kit (Roche Applied Science) according to the manufacturer's protocol. Genomic DNA was isolated with QIAamp DNA Mini kit or with QIAsymphony DSP DNA Midi Kit (Qiagen, Hilden, Germany) following the manufacturer's protocol. The cDNA synthesis was performed from mRNA or total RNA (from an equivalent of 2.5–5x10<sup>6</sup> cells) using 300 U Superscript II (Life Technologies, Darmstadt, Germany) and random hexamer primers (Roche Applied Science) in a 50 µl reaction. The cDNA and genomic DNA was stored at -20°C and -4°C, respectively.

## 2.2 BAALC and ERG assessment

Quantitative assessments of *BAALC* and *ERG* gene expression, *ERG* genomic DNA as well as *ABL1* expression (reference gene) were performed by the use of the Applied Biosystems 7500 Fast Real Time PCR System (Life Technologies). Each sample was analyzed at least in duplicate. *BAALC* and *ABL1* expression was determined as described before (Appendix I).<sup>96</sup> *ERG* expression and *ERG* DNA copy numbers were assessed as outlined in Weber et al.<sup>138</sup> (Appendix II). To calculate *BAALC, ERG* and *ABL1* copy numbers, standard curves for the respective assays were generated in every run by 10-fold dilution series of five different plasmid concentrations. *BAALC* and *ERG* gene expression was normalized against the expression of the reference gene in hematology. The use of *ABL1* has been proposed by a collaborative initiation within the Europe Against Cancer program, including 26 laboratories in 10 member countries, where 14 potential reference genes have been evaluated on normal and diagnostic leukemic samples.<sup>139</sup> These results of the EAC trial was confirmed by our group, analyzing different reference genes in AML with fusion genes.<sup>140</sup> The use of *ABL1* as reference gene for the assessment of *BAALC* and *ERG* gene expression was further validated for this work in a core-set of patients. The

result on this validation is given in the Appendix V. *ERG* DNA copy numbers were calculated using the comparative Ct method.<sup>141</sup> For quantification of DNA copy numbers, the albumin gene was used for normalization. To calibrate the comparative DNA copy numbers, a mixture of DNA of ten healthy individuals was used. Thus, a relative quantity of 1 corresponds to 2 DNA copies of the *ERG* gene.

# 2.3 Brief overview of methods used to detect molecular alterations, other than *BAALC* and *ERG* expression

Screening of *FLT3*-TKD,<sup>31</sup> *IDH*,<sup>142</sup> *NRAS*,<sup>64;143</sup> and *NPM1*<sup>23</sup> gene mutations was performed using a melting curve based LightCycler assay (Roche Diagnostics, Mannheim, Germany) with hybridization probes. After 40 cycles of amplification the melting-curve analysis was started at 28°C/40°C and continued to 70°C/95°C with slope of 0.2°C per second and continuous detection with channel F2/F1. LightCycler data were analyzed using LightCycler software (Roche Diagnostics). All cases that revealed an aberrant melting curve as compared to wildtype control were subjected to nucleotide sequence analyses (see below).

To quantify the mutation ratio of *NPM1* qPCR was performed by the use of either the LightCycler 1.5 System (Roche Diagnostics) with the application of hybridization probes as the detection format or by digital PCR using a hydrolysis probe-based assay on 12.765 Digital Arrays (Fluidigm, San Francisco, CA, USA), that separates each PCR reaction into 765 reaction chambers. Digital PCR data analysis was done by EP1 Data Collection v.3.1.2 software (Fluidigm). Positive signals were counted with DIGITAL PCR ANALYSIS v.3.1.3 software (Fluidigm) and transformed to a value of estimated targets. Expression levels were calculated as % *NPM1*mut/*ABL1*. Comprehensive information on these methods are provided in the respective publications.<sup>135;144</sup>

Screening of *MLL*-PTD was performed by qPCR using the LightCycler System (Roche Diagnostics) applying hybridization probes as the detection format. The expression levels are given as % *MLL*-PTD/*ABL1*. Detailed information on primer, probes and the reaction conditions are given in Weisser et al.<sup>136</sup>

Determination of the length of the *FLT3*-ITD and quantification of the *FLT3*-ITD mutation/FLT3 wildtype ratio were realized by genescan analysis, where the forward primer was labeled with 6-FAM. PCR products were analyzed using 3130, 3130*xl* and 3730*xl* Genetic Analysers (ABI, Darmstadt, Germany). The *FLT3*-ITD was quantified as the ratio of the mutation compared to the wildtype allele. Detailed information is given elsewhere.<sup>145;146</sup>

The remaining molecular alterations in *ASXL1, CEBPA, DNMT3A, RUNX1, TET2, TP53* and *WT1* were analyzed by either Sanger sequencing or by next-generation sequencing. Sanger sequencing was performed using BigDye chemistry (Applied Biosystems, Weiterstadt, Germany) and the 3130, 3130xl and 3730xl Genetic Analyzers (ABI).

Regarding next generation sequencing, different library preparation and sequencing approaches have been performed in our laboratory. In short:

### Library preparation ThunderStorm (Targeted enrichment by droplet-based multiplex PCR)

Sheared genomic DNA (Covaris S220 instrument; Covaris, Woburn, MA) was combined with a PCR reaction mix excluding the oligonucleotide primer molecules. This reaction mastermix and the primer library were loaded separately into the ThunderStorm instrument (RainDance Technologies, Billerica, MA, USA) and picoliter-size droplets containing one primer library per droplet were generated. After amplification, emulsion PCR droplets were broken, purified and quantified. Barcode indices and suitable MiSeq adaptor sequences were added using a second-round PCR step. Equal amounts of each purified, tagged library were then pooled for cluster generation and sequencing. PhiX control libraries (final concentration 1.5%) (Illumina, San Diego, CA, USA) were added to the pooled library for quality control. Detailed information is given in Delic et al.<sup>147</sup>

#### Library preparation Assay-on-Demand for 454 Pyrosequencing

Target specific regions of interest were amplified using the FastStart High Fidelity PCR System and GC-RICH PCR System kits (Roche Applied Science, Penzberg, Germany) in preconfigured 96-well primer plates containing primer pairs as well as sample specific distinct Multiplexing Identifier. Each PCR product was individually purified using Agencourt AMPure XP beads (Beckman Coulter, Krefeld, Germany) and quantified using the Quant-iT PicoGreen dsDNA kit (Invitrogen, Carlsbad, CA, USA). Detailed information is given in Kohlmann et al.<sup>148</sup>

### Library preparation Fluidigm AccessArray

Amplicon generation on the Fluidgm AccessArray System (Fluidigm) reduces the time required for enrichment of targeted sequences by combining amplicon generation with library preparation. The Access Array System workflow consists of three major phases: 1) designing and validating target-specific primers for targeted re-sequencing, 2) running an Access Array Integrated Fluidic Circuit (IFC), and 3) qualifying and quantifying harvested PCR products for sequencing. Input requirements are DNA 50 - 80ng. Detailed information is given elsewhere.<sup>149</sup>

#### 454 Pyrosequencing

The multiplexed amplicon pool was processed according to the manufacturer's recommendations using GS FLX Titanium small volume emPCR Kit (Lib-A) (Roche Applied Science, Penzberg, Germany). Following the emPCR amplification, clonally amplified beads were enriched for 454 next-generation sequencing. Forward (A) and reverse (B) beads were processed separately until combining them at the step of loading the respective PicoTiterPlate (PTP) lanes.

All data were generated using the GS FLX Sequencer Instrument software version 2.3. Image processing and amplicon pipeline analysis was performed using default settings of the GS RunBrowser software version 2.3 (Roche Applied Science). Sequence alignment and variant detection was performed using the GS Amplicon Variant Analyzer software version 2.3 (Roche Applied Science). The results were further processed and visualized in R/Bioconductor using the package R453Plus1Toolbox (version 1.0.1) and the Sequence Pilot software version 4.0.0 (JSI medical systems, Kippenheim, Germany). For the detection of variants, filters were set to display sequence variances occurring in more than 2% of bidirectional reads per amplicon in at least one patient. Amplicons were considered as dropout and excluded from analysis if the coverage at any analyzed position in any of the two paired-end sequences (minimal coverage) was <80 reads.

#### **MiSeq Sequencing**

Amplified targets were sequenced on the MiSeq sequencing-by-synthesis benchtop sequencer according to the manufacturer's protocol (Illumina). The sequencing runs were set for 'Resequencing' workflow on the Illumina MiSeq Reporter v2.2.29 software (Illumina) and 500-cycle MiSeq v2 reagent cartridges (Illumina) were used to sequence libraries with paired-end, dual-indexing 251 cycles per read (2 x 251). The quality of the sequence run was monitored by the Sequencing Analysis Viewer (Illumina). Data was automatically demultiplexed by the MiSeq Reporter and corresponding zipped FASTQ files were generated for each barcode index.

#### Variant interpretation

Validity of the somatic mutations was checked against the publicly accessible COSMIC database,<sup>150</sup> ClinVar (www.ncbi.nlm.nih.gov/clinvar/) and ExAC database (exac.broadinstitute.org/). Functional interpretation was performed using SIFT 1.03 (sift.jcvi.org), PolyPhen 2.0 (Adzhubei et al, Nat Methods, 2010). Additionally, TP53 variants were verified using the IARC repository (Petitjean A et al, Hum Mutat, 2007). Single-nucleotide

polymorphisms according to NCBI dbSNP database (ncbi.nlm.nih.gov/snp), synonymous variants and alterations within introns with the exception of splice-site mutations at position +/- 1 or 2 were not scored.

### 2.4 Patient samples

All patient samples included in the respective studies were referred to our laboratory for diagnostic or follow-up assessment of AML between September 2005 and July 2015. All patients gave their written informed consent for scientific evaluations. The study was approved by the Internal Review Board and adhered to the tenets of the Declaration of Helsinki. Addressing different scientific aspects following samples were analyzed:

1) BAALC and ERG gene expression in CN-AML (Appendix I; Appendix IV) 96;151

To asses *BAALC* gene expression in CN-AML, a total of 326 younger (<65 years, range: 18-65) CN-AML patients were investigated. Of these, 325 patients have also been investigated for *ERG* gene expression. All these patients had, to the best of our knowledge, *de novo* AML without any preceding malignancy or MDS.

2) BAALC gene expression for detection of MRD (Appendix I; Appendix III) 96;152

To address *BAALC* gene expression as a target for MRD monitoring, in total 632 diagnostic and follow-up samples of 142 *de novo* CN-AML patients with high *BAALC* expression at initial diagnosis for whom at least one follow-up sample was available were investigated. Of these, 57 diagnostic and 301 follow-up samples had been published in both studies (Appendix I; Appendix III).<sup>96;152</sup> The median number of follow-up samples per patient was 2 (range: 1-21) with a median follow-up time of 63 months (range: 1-101 months). If multiple samples per patient were available within the time interval of three to six month after induction chemotherapy, only the first evaluation was included in the respective calculations. Further, 18 samples of 9 *de novo* CN-AML patients with low *BAALC* expression at initial diagnosis, for whom a follow-up sample showing complete molecular remission defined by *NPM1* mutation status was available, were analyzed.

2) *ERG* gene expression in patients with AML and acquired gain of chromosome 21 (Appendix II) <sup>138</sup>

In total 479 AML cases, including 25 secondary AML (s-AML) following MDS (n=16) or myeloproliferative neoplasms (n=9) and 22 therapy-related AML (t-AML), were analyzed. The total cohort was subdivided based on karyotype and fluorescence in situ hybridization (FISH) data into 3 subgroups according to the *ERG* copy number state.

Cohort A (further referred to as "Cases with amplification of *ERG*") included 33 cases with structural aberrations involving the long arm of chromosome 21 and amplification of *ERG* (defined as more than 6 copies) as demonstrated by interphase FISH with probes encompassing the *ERG* gene. Of these, 32 cases showed a complex karyotype (CK) characterized by more than or equal to four chromosomal aberrations.

Cohort B included 95 cases with 3 to 6 *ERG* copies. Of the 95 cases, 41 had a non-complex aberrant karyotype with gain of one (n=40) or two (n=1) chromosomes 21 (further referred as to AK-AML with gain of chr21). The remaining 54 cases had a complex aberrant karyotype with gain of one (n=43), two (n=9), or three (n=2) chromosomes 21. Seven of the latter 54 cases had additional structural aberration involving chromosome arm 21q. *ERG* copy number state of these seven cases were validated by interphase FISH, all of them demonstrating less than or equal to 6 copies. This group is further referred to as to CK-AML with gain of chr21/chr21q.

For comparison, two control cohorts were analyzed. One cohort included the 325 patients with CN-AML, which had been characterized for *BAALC* and *ERG* gene expression.<sup>96</sup> The other cohort included 26 AML patients with a CK but without cytogenetically visible gain of chromosome 21.

## 2.5 Statistical analysis

The definition of OS was the time from diagnosis to death or last follow-up. EFS was defined as the time from diagnosis to treatment failure, relapse, death, or last follow-up. Survival curves were calculated for OS and EFS according to Kaplan-Meier and compared using the two-sided log rank test. Cox regression analysis was performed for OS and EFS with different parameters as covariates. Median follow-up was calculated taking the respective last observations in surviving cases into account and censoring non-surviving cases at the time of death. Results were considered significant at p<0.05 for univariate analyses and at p<0.1 for multivariate analyses. Parameters which were significant in univariate analyses were included into multivariate analyses. Dichotomous variables were compared between different groups using the Fisher's exact test and continuous variables by Student's t-test. Correlation coefficient was specified as Spearman's rank correlation. All reported p-values are two-sided. No adjustments for multiple comparisons were performed. SPSS software version 19.0.0 (IBM corporation, Armonk, NY) was used for statistical analysis.

## 3 Results and discussion

#### 3.1 BAALC and ERG gene expression in CN-AML

#### 3.1.1 BAALC and ERG in CN-AML: range of expression and cut-off definition

In diagnostic CN-AML samples, the normalized levels of % *BAALC/ABL1* and % *ERG/ABL1* varied within a wide range of at least 4 logs (range *BAALC/ABL1*: 0.1% to 8019.9%; range *ERG/ABL1*: 0.1%-1007.5%; Appendix I; Appendix IV).<sup>96;151</sup> Even though, the expression levels of *ERG* seems more evenly distributed, these results indicate that the genes are differentially expressed in some CN-AML samples (Figure 2).



Figure 2: Quantitative analysis of *BAALC* and *ERG* gene expression in CN-AML. Grey circles indicate single cases. The yaxis depicts the % gene of interest (GOI)/*ABL1* on a logarithmic scale.

The translation of gene expression into clinical decision making requires the definition of a cut-off level. Using a survival based method, the level of 33.1% *BAALC/ABL1*, accounting for median *BAALC* expression of the total CN-AML cohort, was found to separate high-risk from low-risk patients (Figure 3, Appendix I).<sup>96</sup> This threshold was further validated in Weber et al.<sup>152</sup> where a high proportion (87%, 13/15) of patients with *BAALC* expression levels above 33.1% *BAALC/ABL1* during therapy experienced relapse (Appendix III). These results partly reflect the literature, where despite differences in the quantification methods, mean expression levels were used to separate low from high *BAALC* expressers.<sup>14-16;95</sup> However, different cut-off levels have also been suggested by other groups using distinctive approaches to define them.<sup>97-99</sup> Using the survival based approach to define a threshold for *ERG* expression the results were less persuasive (Figure 3). Addressing these result as well as the fact that dichotomization on survival based methods represents a data driven classification,



BAALC and ERG expression levels were additionally analyzed as continuous variables, if feasible.

Figure 3: Patients analyzed for *BAALC* and *ERG* expression were initially divided into quartiles (Q1-Q4) according to the levels of expression. (A) Kaplan-Meier curve for *BAALC* expression. Median was chosen for the *BAALC* expression cut-off because the subgroup of Q3 and Q4 showed a clinically distinct outcome with an inferior OS compared with the remaining quartiles (Q1 and Q2). Patients were defined as low *BAALC* with expression levels in Q1 and Q2 and as high *BAALC* with expression levels in Q3 and Q4. (B) Kaplan-Meier curve for *ERG* expression.

# **3.1.2** Correlation of diagnostic *BAALC* and *ERG* gene expression to clinical and molecular parameters

In terms of patients characteristics at the time of diagnosis, for both, *BAALC* and *ERG*, a negative correlation of gene expression levels to age was revealed, meaning that patients with high *BAALC* and/or *ERG* expression tended to be younger than the respective patients with low *BAALC* and/or *ERG* expression (Appendix I; Appendix IV).<sup>96;151</sup>

With regard to molecular alterations, substantial associations of altered *BAALC* and *ERG* expression to specific molecular aberrations were observed. Figure 4 provides an overview of the analyzed associations between the expression of *BAALC* and *ERG* and the remaining molecular parameters, which have been reported by our group (Appendix I; Appendix IV).<sup>96;151</sup> Analysis of *BAALC* as a categorical variable revealed a strong correlation of high *BAALC* expression to the following molecular alteration: *FLT3*-ITD, especially when *FLT3*-ITD to *FLT3* wildtype ratios were high ( $\geq 0.5$ ; further termed *FLT3*-ITD $\geq 0.5$ ), *MLL*-PTD, *IDH2*R172 and to

mutations in *RUNX1*, *CEBPA* and *WT1*. Further, a negative correlation of high *BAALC* expression to mutations in *NPM1* was observed. These correlations were confirmed in terms of *NPM1*, *RUNX1* and WT1 when analyzing *BAALC* expression as a continuous variable. Analyzing *ERG* as a continuous variable, higher *ERG* expression levels were significantly associated with high *BAALC*, *FLT3*-ITD $\geq$ 0.5 and mutations in *WT1* as well as with the absence of mutations in *IDH1* and *NPM1*. These results corroborate the literature as high *BAALC* expression has been demonstrated to correlate with the mutational status of *FLT3*-ITD, *CEBPA*, *MLL*-PTD, *RUNX1* and *WT1* as well as with *NPM1* wildtype.<sup>14-16;84;95;153</sup> Also for *ERG*, these results were consistent with the literature in terms of *BAALC* and *FLT3*-ITD, though *ERG* has been analyzed as a categorical parameter in these previous studies.<sup>16;95;119</sup>



Figure 4: Schematic representation of associations between *BAALC* and *ERG* gene expression and the remaining molecular parameters as reported in Weber et al., 2014<sup>96</sup> and Weber et al., 2016<sup>151</sup> (Appendix I; Appendix IV); edited by Dennis Haupt. Statistical significance was assessed using the Fisher's exact test for categorical variables and the Student's t-test for continuous variables. The difference of the mean (DOM) as well as the binary logarithm of the odds ratio (Log2(OR)) of the association is color coded, and the p-value is given in each field. Green colors indicate a positive association (i.e., 2 characteristics that frequently occurred together in the same patient, or for the association to *BAALC* and *ERG* as continuous variable, a higher value in those carrying the respective molecular alteration). Red colors indicate a negative association. White color indicates no significant association between the tested variables. (A) Pairwise associations between *BAALC* and *ERG* and other

molecular alterations, including the molecular risk group of *NPM1* wildtype or *FLT3*-ITD $\geq$ 0.5. (B) Pairwise associations between *BAALC* and *ERG* and the functional biological categories.

Despite some shared associations individual correlations of altered BAALC and ERG expression were observed, presuming that both genes are associated to distinct functional biological categories or, addressing FLT3-ITD and NPM1, to clinically defined subgroups. Regarding the molecular risk group of NPM1 wildtype or FLT3-ITD≥0.5, both mean BAALC and mean ERG expression levels were significantly higher as compared to the low-risk group (Figure 4A). Grouping the molecular alterations into functional biological categories, BAALC expression revealed distinct associations. For instance, higher BAALC expression levels were significantly related to a mutated status in the myeloid transcription factor group (CEBPA and RUNX1), while substantially lower BAALC expression levels were observed in patients harboring mutations in genes involved in DNA methylation, including DNMT3A, TET2, IDH1 and IDH2 (Figure 4B). On the other hand, the association of ERG expression to functional biological pathways appeared less pronounced, as only slightly higher ERG expression levels were found in patients harboring mutations in one of the myeloid transcription factors, CEBPA and RUNX1 (Figure 4B). Interestingly, aside from the strong correlation to *FLT3*-ITD neither *ERG* expression levels nor BAALC expression levels revealed a significant correlation to the activated signaling/proliferation group (Figure 4B; Appendix I; Appendix IV).<sup>96;151</sup>

Taken together, ERG expression seems to be associated to the clinically defined subgroup and to age-associated single alterations, but not to specific biological pathways. Contrary to high BAALC expression, which seems to gather with certain subgroups of CN-AML, as strong correlations with mutations in transcription factors and genes that induce proliferation, but no or a negative correlation with mutations in epigenetic modifiers were found. An exception represents the epigenetic modifier IDH2R172, which is strongly correlated with high BAALC expression. This association is of special interest as IDH2R172 forms a clinically and molecularly distinct subset in CN-AML as compared to IDH1R132 and IDH2R140.54;154 Unlike IDH1R132 and IDH2R140, which show several co-mutations (mainly with NPM1, FLT3, and RAS), IDH2R172 are nearly mutually exclusive of other common molecular alterations in CN-AML. Thus, high BAALC expression could represent a co-operating event synergizing in the onset of leukemia further defining the subgroup of IDH2R172 mutated AML. Another association with suspected biological consequences is the strong correlation of high BAALC expression to mutations in the transcription factor *RUNX1* (Appendix I).<sup>96</sup> Previously, a search for putative activations sides identified binding signatures for RUNX1 in the upstream regulatory machinery of BAALC and subsequent in vitro assays revealed an direct effect of overexpression or knockdown of RUNX1 on the expression of BAALC in leukemia derived cell

lines.<sup>93;94</sup> However, so far, it remains elusive, if mutated *RUNX1* could also account for elevated *BAALC* expression, since at least some mutations in *RUNX1* have been reported to lead to a loss of protein function by disruption of its DNA binding ability and by now, no correlation of high *BAALC* expression to a distinct *RUNX1* mutation was described (Appendix I).<sup>96;155</sup> Functional studies, which investigate the suspected biological synergisms between *BAALC* expression and *RUNX1* or *IDH2*R172 could provide precious insights in the biology and leukemogenesis of AML.

#### 3.1.3 Prognostic value of BAALC and ERG expression as single marker

Survival analyses revealed an adverse prognostic impact of high *BAALC* on OS and EFS either as categorical variable (Figure 5) and moreover also as continuous variable (OS: HR 1.27, p=0.009; EFS: HR 1.32, p<0.001; Appendix IV).<sup>151</sup> These results corroborate the literature.<sup>15;89;95;97-99</sup>



Figure 5: Outcome of 290 intensively treated CN-AML patients aged younger than 65 years with respect to *BAALC* expression as published in Weber et al.<sup>96</sup> (Appendix I). The median expression level was used to dichotomize the total patient cohort into low (black) and high (gray) *BAALC* expressers. (A) EFS at 3 years: 31.2% vs. 47.4%, p=0.006. (B) OS at 3 years: 46.2% vs. 71.1%, p=0.002.

*ERG* expression levels as a continuous parameter did neither affect OS nor EFS. However, when dichotomizing *ERG* expression at distinct cut-off levels (25th percentile, median, 75th percentile) a significant correlation to shorter EFS and a trend towards inferior OS was observed for *ERG* expression levels above the median (Figure 6; Appendix IV).<sup>151</sup> This is in line

with the literature, as one study analyzing *ERG* expression as a continuous parameter did not reveal an impact of *ERG* expression levels on survival,<sup>156</sup> while other studies where *ERG* expression has been dichotomized at certain cut-off levels (median or 75th percentile) showed an association of high *ERG* expression with inferior outcome.<sup>16;95;118;119</sup>



Figure 6: Outcome of 295 intensively treated CN-AML patients aged younger than 65 years with respect to *ERG* expression. The median expression level was used to dichotomize the total patient cohort into low (black) and high (gray) *ERG* expressers. (A) EFS at 3 years: Low *ERG*: 44.0% vs. high *ERG*: 34.6%, p=0.028, (B) OS at 3 years: Low *ERG*: 64.5% vs. high *ERG*: 50.6%, p=0.089 (Appendix IV).<sup>151</sup>

### 3.1.4 Prognostic value of BAALC and ERG in the context of other molecular alterations

# 3.1.4.1 Prognostic value of *BAALC* and *ERG* within the ELN genetic low- and intermediaterisk group defined by mutational status of *NPM1* and *FLT3*-ITD

As *BAALC* and *ERG* expression have been shown to strongly correlate with *NPM1* wildtype and *FLT3*-ITD,<sup>96;151</sup> the prognostic value in the respective low- and intermediate-risk groups was assessed. Regarding *ERG* expression dichotomized at the median, no differences in EFS and OS was observed neither for the low-risk nor for the intermediate-risk group (Appendix IV).<sup>151</sup> This contrasts the study of Metzeler et al.<sup>16</sup>, where *ERG* expression dichotomized at the 75th percentile provided additional prognostic information in the intermediate-risk group (*NPM1* wildtype and/or *FLT3*-ITD). This discrepancy most probably results from differences in the analyzed cohorts, as in the study of our group younger AML patients (age 18-65) were investigated, while Metzeler et al.<sup>16</sup> analyzed patients aged 17-83 years. Besides differences in treatment protocols of younger and older AML patients, which itself could account for
varied outcome several studies have shown that the mutational profile as well as its prognostic information differs between younger and older AML patients.<sup>34;36;68;86</sup>

Addressing the impact of *BAALC* expression on the intermediate-risk group, *BAALC* expression (dichotomized at the median) provided additional prognostic information on EFS and OS in the intermediate-risk group of *NPM1* wildtype or *FLT3*-ITD (Figure 7; Appendix IV).<sup>151</sup> An impact of *BAALC* expression on the intermediate-risk group has previously been suggested in a preliminary cohort of 29 AML patients with intermediate-risk chromosomal/molecular abnormalities.<sup>157</sup> Based on these findings a refined algorithm for risk stratification in CN-AML can be proposed, as patients with *NPM1* wildtype or *FLT3*-ITD and high *BAALC* expression rather reflect OS of the ELN intermediate II-risk group (Table 2), while the respective low *BAALC* expressers resemble outcome of the favorable-risk group.<sup>158</sup> Therefore future clinical trials should further evaluate if these patients can benefit from reclassification.



Figure 7: Outcome in the intermediate-risk group of patients with *NPM1* wildtype or *FLT3*-ITD with respect to *BAALC* expression (n=186). The median expression level was used to dichotomize the total patient cohort into low (black) and high (gray) *BAALC* expressers. (A) EFS at 3 years: Low *BAALC*: 51.4% vs. high *BAALC*: 25.7%, p=0.009. (B) OS at 3 years: Low *BAALC*: 67.7% vs. high *BAALC*: 40.2%, p=0.019 (Appendix IV).<sup>151</sup>

#### 3.1.4.2 Multivariate analysis to identify independent prognostic factors in CN-AML

Facing the number of correlations observed between various molecular risk markers, Cox regression analysis was performed to identify those factors that independently predicted prognosis in CN-AML.

In multivariate analysis, high *BAALC* expression, but not *ERG* expression, revealed an independent prognostic impact on EFS and OS. Additional independent factors, besides high *BAALC* expression, were *FLT3*-ITD $\geq$ 0.5, *MLL*-PTD and *WT1* mutations for EFS (Table 4) as well as *ASXL1* mutations, *FLT3*-ITD $\geq$ 0.5, *MLL*-PTD and *WT1* mutations for OS (Table 5; Appendix IV).<sup>151</sup>

	Univariate			Multivariate			
	HR	<i>p</i> -value	95% CI	HR	<i>p</i> -value	95% CI	
Age	1.26*	< 0.001	1.12-1.40	1.39*	< 0.001	1.24-1.55	
ASXL1mut	1.86	0.046	1.01-3.43	-	n.s.	-	
Log BAALC expression	1.32	< 0.001	1.13-1.53				
High BAALC (median)	1.68	< 0.001	1.27-2.24	1.44	0.024	1.05-1.97	
<b>CEBPA</b> biallelic	-	n.s.	-				
DNMT3Amut	1.28	0.083	0.97-1.71				
Log ERG expression	-	n.s.	-				
High ERG (median)	1.34	0.030	1.03-1.82	-	n.s.	-	
High ERG (75th percentile)	-	n.s.	-				
FLT3-ITD	-	n.s.	-				
<i>FLT3</i> -ITD(≥0.5)	1.69	0.002	1.22-2.34	1.57	0.012	1.11-2.23	
NPM1wildtype or FLT3-ITD	1.41	0.021	1.05-1.90				
<i>NPM1</i> wildtype or FLT3- ITD(≥0.5)	1.60	0.001	1.20-2.13				
FLT3-TKD	-	n.s.	-				
IDH1R132mut	-	n.s.	-				
IDH2R140mut	-	n.s.	-				
IDH2R172mut	-	n.s.	-				
MLL-PTD	1.70	0.043	1.02-2.84	1.67	0.057	0.99-2.84	
NPM1mut	0.77	0.078	0.58-1.03				
NRASmut	-	n.s.	-				
RUNX1mut	-	n.s.	-				
TET2mut	-	n.s.	-				
WT1mut	2.18	0.000	1.41-3.38	2.47	< 0.001	1.54-3.98	

Table 4: Cox regression analyses for event-free survival in CN-AML

\*Per 10 years of increase. Abbreviations: ITD, internal tandem duplication; TKD, tyrosine kinase domain; PTD, partial tandem duplication; mut, mutation; HR, Hazard ratio; CI, Confidence interval; n.s., not significant.

	Univariate			Multivariate			
	HR	<i>p</i> -value	95% CI	HR	<i>p</i> -value	95% CI	
Age	1.38*	< 0.001	1.21-1.56	1.53*	< 0.001	1.34-1.73	
ASXL1mut	2.39	0.012	1.21-4.72	2.47	0.012	1.22-4.98	
Log BAALC expression	1.27	0.009	1.06-1.52				
High BAALC (median)	1.59	0.007	1.14-2.22	1.36	0.099	0.95-1.95	
<b>CEBPA</b> biallelic	-	n.s.	-				
DNMT3Amut	-	n.s.	-				
Log ERG expression	-	n.s.	-				
High ERG (median)	1.33	0.090	0.96-1.85				
High ERG (75th percentile)	-	n.s.	-				
FLT3-ITD	1.65	0.003	1.18-2.30				
<i>FLT3</i> -ITD(≥0.5)	2.15	< 0.001	1.50-3.08	2.28	< 0.001	1.55-3.36	
<i>NPM1</i> wildtype or <i>FLT3</i> -ITD	1.79	0.002	1.25-2.56				
NPM1wildtype or FLT3-	1.79	0.001	1.28-2.52				
$\frac{110}{20.3}$		nc					
IDH1P122mut	-	n.s.	-				
IDH1R132Indt	-	n.s.	-				
IDH2R172mut	_	n.s.	_				
	2.46	0.001	1 16-1 15	2 5 3	0.001	1 17-1 31	
NPM1mut	2.40	0.001	-	2.55	0.001	1.47-4.34	
NPASmut	_	n.s.					
PLINY1mut	_	n.s.	_				
TET2mut	-	n.s.	-				
WT1mut	- 1 05	0.010	- 1 18_2 25	2 5 7	0.001	1 16-1 52	
IDH2R140mut IDH2R172mut MLL-PTD NPM1mut NRASmut RUNX1mut TET2mut WT1mut	- - 2.46 - - - - 1.95	n.s. n.s. 0.001 n.s. n.s. n.s. n.s. 0.010	- - 1.46-4.15 - - - - 1.18-3.25	2.53	0.001	1.47-4.34	

Table 5: Cox regression analyses for overall survival in CN-AML

\*Per 10 years of increase. Abbreviations: ITD, internal tandem duplication; TKD, tyrosine kinase domain; PTD, partial tandem duplication; mut, mutation; HR, Hazard ratio; CI, Confidence interval; n.s., not significant.

To clarify whether these adverse prognostic markers exhibit an additive effect on survival, the number of independent adverse prognostic parameters for each patient were determined. This resulted in the formation of four subgroups according to the number of the adverse prognostic factors. Included were high *BAALC*, *FLT3*-ITD $\geq$ 0.5, *MLL*-PTD and *WT1*mut for EFS as well as *ASXL1*mut, high *BAALC*, *FLT3*-ITD $\geq$ 0.5, *MLL*-PTD and *WT1*mut for OS; with group A: no adverse marker, group B: 1 adverse marker, group C: 2 adverse markers, group D: 3 or 4 adverse markers. None of the patients harbored concomitant alterations in all 5 adverse prognostic factors (Appendix IV).<sup>151</sup>

Kaplan-Meier analysis revealed that the sole accumulation of these adverse prognostic markers stepwise worsened the prognosis (Figure 8; Appendix IV).<sup>151</sup>

Therefore, despite the frequent co-occurrence of some of these adverse markers, they correlated independently and additively with survival (Appendix IV).<sup>151</sup> Similar results have

been shown just previously, were the number of driver mutations, including fusion genes, aneuploidies, gene mutations and small insertions or deletions, correlated with overall survival.<sup>154</sup> These results indicate that, beside the genetic context which defines functional biological and moreover prognostic categories, the sole accumulation of some molecular aberrations influence clinical outcome. This, in part, reflects the situation of cytogenetic aberrations, where specific alterations as well as the accumulation of  $\geq$ 3 cytogenetic alterations can be allocated to clinical outcome.<sup>11</sup> Therefore, prospective studies are needed to clarify to what extent the described markers influence each other or a given genetic context and which of the markers are beneficial compared to others in terms of prognostic allocation in AML.

Conclusively, these results suggest that a comprehensive screening of molecular genetic alterations provide additional information for risk assessment in CN-AML.



Figure 8: Outcome of 295 intensively treated CN-AML (younger 65 years) at 3 years in the four subgroups allocated according to the number of adverse prognostic markers: group A (no adverse marker), group B (1 adverse marker), group C (2 adverse markers), group D ( $\geq$ 3 adverse markers) (Appendix IV).<sup>151</sup>

### 3.2 Analysis of BAALC gene expression for detection of MRD

Detection of residual leukemia cells during intensified therapies using qPCR-based systems has been found to provide a high prognostic value in AML.<sup>10;128;129</sup> Besides our studies (Appendix I; Appendix III),<sup>96;152</sup> only one prior study has addressed the molecular analysis of *BAALC* expression as a marker to detect MRD.<sup>98</sup> This study indicated the applicability of *BAALC* as an MRD target in a cohort of 34 AML and 11 ALL patients.

### 3.2.1 Fundamental validation of the feasibility of BAALC expression for MRD detection

Since there was no fundamental work establishing the utility of *BAALC* expression for monitoring MRD in CN-AML, these analyses were performed in a first step.

The analysis of serial follow-up PB and BM samples taken from nine patients, in whom diagnostic samples exhibited low *BAALC* gene expression levels, revealed no significant difference of the normalized % *BAALC/ABL1* levels during treatment (mean± standard error of the mean (SEM) % *BAALC/ABL1* at diagnosis vs. mean±SEM % *BAALC/ABL1* at 1st complete molecular remission: 6.2±2.2% vs. 13.8±3.0%, p=0.082). These levels remained below the clinically defined threshold of 33.1% *BAALC/ABL1*, indicating that *BAALC* gene expression is not in general modulated by the treatment regimen or within hematopoietic recovery (Appendix I).<sup>96</sup>

In order to confirm the stability of *BAALC* gene expression during follow-up, parallel assessment of diagnostic and relapse samples of 35 CN-AML patients was performed. Despite a high proportion of clonal evolution found in 49% of paired diagnostic and relapse samples as determined by either karyotype instability or the instability of concomitant molecular alterations, a stable high *BAALC* expression was revealed in 31 of these 35 patients at relapse. Mean *BAALC* expression levels did not differ in paired samples between diagnosis and relapse in these cases (mean±SEM % *BAALC/ABL1* at diagnosis vs. relapse: 602±209% vs. 312±64%, p=0.157; Appendix III).<sup>152</sup> Therefore, irrespective of the high level of clonal evolution detected in AML shown by us as well as in several other studies,<sup>159-161</sup> *BAALC* expression showed stable expression in 89% of the patients analyzed. This is in good consistency with the literature, where the stability of the commonly used MRD marker has been described to range between 78%-93%.<sup>135;137;162-164</sup>

To further evaluate the utility of *BAALC* expression to monitor therapy response, *BAALC* expression levels of diagnostic and follow-up samples were correlated to either the mutational status or the expression levels of accompanying, well-known MRD markers: *FLT3*-ITD, *MLL*-PTD, *NPM1*mut and *RUNX1*mut. A strong correlation of % *RUNX1*mut and % *MLL*-PTD/*ABL1* 

with % *BAALC/ABL1* levels (n=42, r=0.824, p<0.001; n=64, r=0.750, p<0.001, respectively) was found. For % *NPM1*mut/*ABL1* and *FLT3*-ITD expression with % *BAALC/ABL1* levels (n=257, r=0.500, p<0.001 and n=181; r=0.568, p<0.001, respectively) the correlation was less consistent (Appendix III).<sup>152</sup> The conflicting results on *NPM1*mut and *FLT3*-ITD can be explained by the relatively low level *BAALC* expression found in *NPM1*mut patients (Appendix I),<sup>96</sup> which restricts *BAALC* expression assessment to one log range, as well as on the semi-quantitative approach used to detect *FLT3*-ITD, which does not precisely detect very high *FLT3*-ITD expression levels.

More detailed information on these results are given in the respective publications (Appendix I; Appendix III).<sup>96;152</sup>

### 3.2.2 Prognostic value of BAALC expression levels during therapy

To evaluate the prognostic impact of *BAALC* expression levels during therapy, survival analyses were performed at two clinically defined time points: after the second cycle of induction chemotherapy (before start of consolidation chemotherapy) as well as between 3 and 6 months after completion of induction therapy in 46 and 33 patients, respectively. It is of note that patients with early relapse or persistent disease were excluded from this analysis, as these patients are already detected by the routine cytomorphologic assessment and would therefore not profit from more sensitive assessments.

First, Kaplan-Meier analysis was performed using the previously defined threshold of 33.1% *BAALC/ABL1* to separate low from high *BAALC* expression. At both time points analyzed, high *BAALC* expression was found to be associated with shorter EFS. The estimated 1-year EFS for high vs. low *BAALC* expressers was 47% vs. 70% (p=0.026) after second induction and 40% vs. 82% (p=0.021) within 3 to 6 months after completion of induction therapy (Figure 9; Appendix III).<sup>152</sup>



Figure 9: EFS in patients during treatment according to *BAALC* expression as published in Weber et al. <sup>152</sup> (Appendix III). The threshold of 33.1% *BAALC/ABL1* was used to dichotomize patients into low (black) and high (grey) *BAALC* expressers. (A) *BAALC* expression levels were assessed in 46 patients after second cycle of induction chemotherapy. EFS at 1 year: Low *BAALC*: 70% vs. high *BAALC*: 47%, p=0.026. (B) *BAALC* expression levels were assessed in 33 patients in whom samples within 3 to 6 months after completion of induction therapy were available. EFS at 1 year: Low *BAALC*: 82% vs. high *BAALC*: 40%, p=0.021.

Subsequently, Cox regression analysis was performed considering *BAALC* expression as continuous variable. After the second cycle of induction chemotherapy, an increase of *BAALC/ABL1* levels revealed a significant negative impact on EFS and OS (Table 6). Besides *BAALC*, the prognostic value of age, BM blast count, WBC count and *NPM1*mut transcript level (n=18) were analyzed. Interestingly, *NPM1*mut transcript level was the only factor besides *BAALC* expression level revealing a trend towards inferior OS. In multivariate analysis adjusting for *BAALC* and *NPM1*mut, *NPM1*mut retained its prognostic value on OS (Table 6; Appendix III).<sup>152</sup>

Addressing the prognostic value of continues *BAALC* expression within 3 to 6 months after completion of induction chemotherapy, an increase of 10% *BAALC/ABL1* levels as well as higher *NPM1*mut transcript level were again significantly associated with shorter EFS (Table 6). For OS none of the molecular parameters revealed a significant impact, while for higher age a significant association towards inferior OS was found. In multivariate analysis on EFS adjusting for *BAALC* and *NPM1*mut, *NPM1*mut transcript level retained its prognostic value on EFS (Table 6; Appendix III).<sup>152</sup>

Taken together, this data depicts a strong correlation of high *BAALC* expression levels at certain clinically defined time points to adverse clinical outcome as published in *Weber et al.*<sup>152</sup> (Appendix III).

6 1					0			
	Event-free survival				Overall survival			
	univa	riate	multiv	variate	univa	ariate	multiv	variate
Variable	HR	р	HR	р	HR	р	HR	р
after 2nd cycle of induction chemotherapy (before consolidation)								
BAALC expression (n=46)	1.14 <sup>b</sup>	0.002	-	-	1.12 <sup>b</sup>	0.045	1.14	0.289
<i>NPM1</i> mut (n=18)	1.88	0.129	-	-	2.64	0.057	2.82	0.049
within 3 to 6 months after completion of induction therapy								
Age (n=33)	-	n.s.	-	-	1.63ª	0.030	-	-
BAALC expression (n=33)	1.11 <sup>b</sup>	0.004	1.21 <sup>b</sup>	0.434	-	n.s.	-	-
<i>NPM1</i> mut (n=14)	1.26	0.046	1.28	0.039	-	n.s.	-	-

Table 6: Cox regression analyses for event-free and overall survival during therapy

<sup>a</sup>Per 10 years of increase; <sup>b</sup>10% *BAALC/ABL1* increase; Abbreviations: HR, hazard ratio; mut, mutation.

Focusing more closely on the patients who experience relapse, in fact, eight of ten patients revealing high *BAALC* expression levels after completion of induction therapy experienced relapse with a median of 7 months from sampling to relapse. This was confirmed when analyzing *BAALC* expression levels within 3 to 6 months after completion of induction therapy where all five patients with high *BAALC* expression levels relapsed within a median of 3 months from sampling. Interestingly, five of the 13 patients with high risk of relapse according to elevated *BAALC* expression at either analysis time point, revealed an MRD negative status according to the accompanying molecular alterations detected at diagnosis in *CEBPA*mut or *FLT3*-ITD at sensitivities of 1% to 5%.

However, in 24 relapsed cases *BAALC* expression assessment failed to predict relapse. The analysis of accompanying molecular alterations revealed that only *NPM1*mut (n=9) and *MLL*-PTD (n=1), but not *CEBPA*mut (n=4), *FLT3*-ITD (n=6) and *RUNX1*mut (n=3) provided additional information by disclosing an MRD positive status (Appendix III).<sup>152</sup>

These results on one hand confirm the literature, since it has been shown that quantitation of *NPM1*mut transcripts represents a highly sensitive method of MRD determination,<sup>135;163</sup> which retains its prognostic information independently of other risk factors.<sup>129</sup> On the other hand, these results suggest that the sensitivity of *BAALC* expression during follow-up is,

besides its expression in PB and BM of healthy individuals, at least comparable to that of *FLT3*-ITD, *RUNX1*mut and *CEBPA*mut detection assays, when analyzed by gene scan or sequencing approaches (Appendix I; Appendix III).<sup>96;152</sup>

Further, addressing the high clonal heterogeneity of AML shown by our group<sup>152;162</sup> (Appendix III), but also by several other studies,<sup>44;45;160;165</sup> it can be postulated that the analysis of several alterations characterizing one specific AML could provide a more accurate assessment of residual leukemic burden.

Conclusively, these results predispose *BAALC*-based residual disease monitoring during therapy as an applicable strategy to detect patients at high risk of relapse, especially in *NPM1* wildtype cases.

# 3.3 *ERG* gene expression in patients with AML and acquired gain of chromosome 21

Addressing the recently described effects of *ERG* overexpression in the onset of DS-AMKL and other leukemia<sup>107;108</sup> and the high incidence of leukemia in individuals with DS,<sup>109</sup> we reasoned that altered *ERG* expression might be the causative mechanism contributing to the pathogenesis of AML with gain of chromosome 21. To address this hypotheses different AML subtypes with amplification or gain of chromosome 21 were analyzed. All of the data presented in this section has already been published in Weber *et al.*<sup>138</sup> (Appendix II).

# 3.3.1 Characterization of patients with cytogenetically visible structural aberrations of chromosome 21

First, the characterization of 40 patients with cytogenetically visible structural aberrations of chromosome 21 by FISH encompassing the *ERG* and *RUNX1* loci revealed amplification (>6 copies/cell) of *ERG* in 33 (83%) patients and a gain (3-6 copies) of *ERG* in the remaining 7 patients. Array CGH was used to determine the exact length of the respective amplified chromosome region in the 33 cases with *ERG* amplification. Though the pattern of amplification on chromosome arm 21q was heterogeneous (range of length: 501 kbp to 16336 kbp; range of location: 31,793,799 bp and 48,129,895 bp from the 21pter) it disclosed a minimal amplified region at the position 39.6 to 40.0 Mbp from *pter* that harbors *ERG* as the only gene (Figure 10; Appendix II).<sup>138</sup>



Figure 10: Diagrammatic representation of amplifications on chromosome arm 21q as assessed by array CGH analysis. Array CGH data showing segments of chromosome arm 21q with amplifications (blue horizontal bars) in 33 cases with AML and cytogenetically visible structural aberrations of chromosome 21q and *ERG* amplification. Orange lines represent the minimally amplified region including all 33 cases. Red lines indicate the extended minimally amplified region when excluding case 30. Grey boxes represent the locations of genes within the amplified regions. The *ERG* gene (labeled in green) was the only gene covered by the minimally amplified region. These results have been published in Weber at al.<sup>138</sup> (Appendix II).

#### 3.3.2 Determination of ERG gene expression and ERG DNA copy number

To assess *ERG* gene expression levels in the 33 patients showing amplifications of *ERG* quantitative real-time reverse transcriptase PCR was performed. Further, *ERG* expression was analyzed in 95 AML cases with gain of chromosome 21. Of these cases 41 had a non-complex aberrant karyotype (AK-AML with gain of chr21) and the remaining 54 cases had a complex aberrant karyotype (CK-AML with gain of chr21/chr21q). In addition, 325 cases with CN-AML and in 26 AML cases with a complex karyotype but without cytogenetically visible gain of chromosome 21 (CK-AML) were analyzed. Detailed information on the cohorts is given in the

material and methods section ("2.4 Patient samples") and in the respective publication (Appendix II).<sup>138</sup>

Although the general expression levels overlapped between the different genetic subgroups, significantly higher mean ERG expression levels were found in the 33 patients with amplification of ERG (mean±SEM: 618±83% ERG/ABL1; range: 11-2324% ERG/ABL1) as well as in 95 patients with gain of chromosome 21 (mean±SEM: 338±30% ERG/ABL1; range: 3-1214% ERG/ABL1) compared to the respective controls (mean±SEM: 222±9% ERG/ABL1; range: 0.1-1007.5% ERG/ABL1; P<0.001; Figure 11). Furthermore, mean ERG expression was also significantly higher in 33 patients with ERG amplification compared with the patients with gain of chromosome 21/chromosome 21q (p=0.003; Figure 11), suggesting a marked correlation between ERG genomic DNA copy number and ERG gene expression. Indeed, the increment of ERG gene expression was significantly correlated to the copy number of ERG DNA as assessed by qPCR. Pearson product-moment correlation revealed a linear correlation of mean ERG expression and mean ERG DNA values of the different genetic subgroups (r=0.956, P=0.011; Appendix II).<sup>138</sup> Regarding ERG gene expression, this data corroborates the literature since amplification and associated elevated expression of ERG has been already described in AML patients with complex karyotypes and abnormal chromosome 21.<sup>166</sup> However, in contrast to the study of Baldus et al.<sup>166</sup> a significant correlation between *ERG* genomic DNA copy numbers and gene expression of ERG was observed. This discrepancy might result from different numbers of patients analyzed as well as from different methods used, as in the previous study BAC array CGH and oligonucleotide expression array analyses were used to compare the DNA and mRNA amount of six patients, respectively.<sup>166</sup>



Figure 11: Quantitative analysis showing *ERG* gene expression and *ERG* DNA values of the different subgroups (Appendix II).<sup>138</sup> (A) *ERG* gene expression in patients with CN-AML, complex karyotype AML (CK-AML), non-complex aberrant karyotype AML (AK-AML) with gain of chromosome 21 (chr21), and CK-AML with gain of chr21 as well as cases with amplification of *ERG*. Grey dots indicate single cases; black lines indicate mean expression. The y-axis depicts the % *ERG/ABL1* on a logarithmic scale; the x-axis depicts the different genetic subgroups. (B) *ERG* copy numbers in patients with CN-AML, CK-AML, AK-AML with gain of chr21, and CK-AML with gain of chr21, and CK-AML with gain of chr21, and CK-AML with gain of chr21, as well as cases; black lines indicate mean DNA values. The y-axis depicts the relative copy number of the *ERG* gene on a logarithmic scale. As a mixture of DNA of ten healthy individuals was used to calibrate the comparative DNA copy numbers a relative quantity of 1 corresponds to 2 DNA copies of the ERG gene. The x-axis depicts the different genetic subgroups.

Besides the linear correlation of the mean *ERG* RNA and mean DNA values, a significant but not linear correlation of *ERG* gene expression and *ERG* DNA values was observed, when correlating the values for individual patient data (r=0.405, P<0.001), which implies that *ERG* expression is additionally influenced (Appendix II).<sup>138</sup> This hypothesis is supported by the fact, that increased *ERG* expression has been observed in some CN-AML cases, in which cryptic gain or amplification of 21q22 has not been described.<sup>16;119;167</sup> In addition, as expression levels did not increase in a linear fashion with an increase in the amount of *ERG* gene amplification. *ERG* expression could also be affected by some kind of negative feedback regulation. This was supported by the fact that *ERG* expression is regulated by complexes of HSC transcription

factors, including ERG itself, binding its promoters and the +85 stem cell enhancer, as recently shown.<sup>156</sup>

# **3.3.3** Correlation of *ERG* expression with molecular alterations in AML with gain of chromosome 21

Mutations in *RUNX1* are frequently found in AML with trisomy 21.<sup>168</sup> Therefore, a possible relationship between high *ERG* expression and *RUNX1* mutations was investigated. In agreement with the literature,<sup>168</sup> mutations in *RUNX1* were found in 25% (10 of 40) of AML patients with a non-complex aberrant karyotype and gain of one or two chromosome 21 (Appendix II).<sup>138</sup> In these 40 patients, higher mean *ERG* expression levels were observed in cases with *RUNX1* mutation compared with those with *RUNX1* wildtype (mean±SEM: 559±128 vs. 304±40, p=0.084; Figure 12), pointing to a cooperative role of *RUNX1* inactivation and elevated *ERG* expression in the onset of leukemia (Appendix II).<sup>138</sup>



Figure 12: Box plot of *ERG* gene expression in patients with noncomplex aberrant karyotype and gain of chromosome 21. Depicted are *ERG* expression levels on a logarithmic scale in *RUNX1* wildtype (n=30) and mutated (n=10) cases. Mean % *ERG/ABL1* expression levels were compared using Student's t-test (Appendix II).<sup>138</sup>

However, this correlation seems exclusive for the subtype of AML with gain of chromosome 21 as no association of altered *ERG* expression and mutations in *RUNX1* was observed in CN-AML (Appendix IV).<sup>151</sup> Cooperating effects of elevated *ERG* expression with specific mutations have been suggested before. In mouse models of T-ALL it has been shown that constitutive overexpression of *ERG* in hematopoietic cells drives the development of T-ALL and cooperates with activating *NOTCH1* mutations in leukemogenesis.<sup>106;107</sup> Mutations of *GATA1* are frequent in childhood DS-AMKL, but rarely detected in other DS and non-DS leukemias.<sup>169;170</sup> Studies focusing on the relationship between *GATA1* mutations and trisomy 21 in DS-AMKL revealed a specific synergy between loss of full-length *GATA1* and overexpression of the ETS family members *ERG* and *ETS2* in leukemogenesis.<sup>108;171</sup> Based on these findings it is conceivable that

inactivation of the *RUNX1* gene in combination with altered *ERG* expression could be another cooperative event in leukemogenesis of AML with gain of chromosome 21, which should be further explored.

## 4 Conclusions

*BAALC* and *ERG* gene expression levels varied within a wide range in CN-AML. They were allocated to clinical outcome, even though the results on *ERG* expression were less persuasive than those of *BAALC* gene expression. Regarding the inter-relationships between altered *BAALC* and *ERG* gene expression, patients' characteristics and concomitant genetic alterations, several specific associations were identified. High expression levels of both genes correlated with a younger age and both genes were specifically associated with the clinically adverse-risk group of *NPM1* wildtype and *FLT3*-ITD. Beside these shared associations, *BAALC* expression was shown to gather with certain subgroups of CN-AML. For instance, strong correlations with mutations in transcription factors and genes that induce proliferation, as well as no or a negative correlate most specifically with single molecular alterations, namely *IDH2*R172 and mutations in *RUNX1*, both of which represent clinical and molecular distinct classifiers in CN-AML. In terms of *ERG*, no such associations could be revealed in CN-AML until now.

Regarding the prognostic value, both altered *BAALC* and *ERG* expression, were shown to impact on survival. Although for *ERG* gene expression this impact was shown to depend on other molecular alterations. *BAALC* expression was strongly associated with clinical outcome even in the context of other adverse prognostic alterations. Therefore, *BAALC* expression has been shown to provide additional prognostic information on survival in the intermediate-risk group of *NPM1* wildtype or *FLT3*-ITD, suggesting that the delineation of genetically defined subtypes could improve prognostication in CN-AML. Opposed to the genetic categories, defined by functional biological characteristics or prognostic parameters, it was shown that the sole accumulation of some molecular aberrations, including *BAALC* gene expression and alterations in *ASXL1*, *FLT3*, *MLL* and *WT1* influence clinical outcome in an additive manner. These results suggest that a comprehensive screening of molecular genetic alterations can provide additional information for risk assessment in CN-AML.

Based on the strong correlation of *BAALC* expression to clinical outcome at diagnosis, the role of *BAALC* as a marker for detection of MRD was analyzed. *BAALC* was validated to be a stable marker, the expression course of which correlated substantially with the course of the disease and furthermore, with the mutational load or expression levels of well-known and already used MRD markers. Moreover, a strong prognostic value of *BAALC* assessment during therapy was observed, as high *BAALC* expression at certain clinically defined follow-up time points was shown to strongly correlate to adverse clinical outcome. These results predispose *BAALC*-

based residual disease monitoring during therapy as an applicable strategy for detecting patients at high risk of relapse, especially in *NPM1* wildtype cases.

Finally, it was shown that a gain of chromosome 21 resulted in an increased expression of the *ERG* gene, suggesting that an altered *ERG* expression represents a causative mechanism, contributing to the pathogenesis in AML with a gain of chromosome 21. However, the correlation of chromosomal gain and elevated *ERG* gene expression was not linear, which strengthens the assumption that *ERG* expression is influenced by additional parameters or alterations. Though the cooperating event could not be entirely defined - neither in CN-AML nor in AML with a gain of chromosome 21 - a strong correlation of *ERG* expression and mutations in *RUNX1* was observed in AML with a gain of chromosome 21. This correlation seemed to be subtype specific as, besides an appropriately high number of *RUNX1* mutated patients in CN-AML, no such association could be revealed.

## 5 Perspectives

Within the presented studies it was possible to identify several specific clusters of genetic alterations, which in some cases could even be allocated to clinical outcome. However, these results need to be validated in independent and extended patient cohorts. It should be strongly suggested to integrate this validation into clinical trials, as these would not only be applicable for data validation, but could also investigate several additional approaches. For instance, it has previously been shown that *ERG* expression results in resistance to kinase inhibitors such as sorafenib, a drug currently tested for treatment of AML. Furthermore, it has been suggested that *BAALC* mediated treatment resistance might be reversed by the use of MEK inhibitors. Clinical trials would be most appropriate to simultaneously address these previously described effects and their consequences in large and uniformly treated patient cohorts. Moreover, as clinical trials conform to stringent sampling intervals, these studies would also provide the conditions to study the relapse kinetics of high *BAALC* expressing leukemic clones. This would allow optimal sampling intervals for high *BAALC* expressing AML subtype to be revealed and therefore most probably even strengthen the information which can be gained from *BAALC* assessment during therapy.

In addition, it has to be pointed out that the results presented here, though representing a comprehensive analysis and providing precious prognostic and biologic information, still represent a snapshot of the enormous heterogeneity of AML. Nowadays it is clear that the outcomes of AML patients depend on a complex interplay of factors, including specific combinations of genetic lesions, patient conditions, the therapeutic approaches used and the magnitude of treatment response. After the great improvements in genomics technology, there is now a tremendous need for developing or adapting analysis tools, which allow the translation of the massively accumulating genetic information into clinically useful and valuable information. For instance, adjusted multivariate projection methodologies could provide the potential to generate discriminative models, favoring the delineation of new subtypes in AML, as multivariate projection methodologies were originally invented to uncover relevant information from huge data sets. Subsequently, these AML subtypes could be studied further to evaluate clinically applicable risk stratification algorithms and individual therapies. However, addressing the dilemma that subclassification by definition accompanies declining sample size, it would be desirable that these studies and subsequent integration of genetic risk factors into clinically applicable algorithms occurs through collaborations of multiple study groups, in order to increase the sample size and therefore the study validity.

## 6 References

- 1. U.S.National Institutes of Health, National Cancer Institute. SEER: Surveillance Epidemiology and End Results. http://seer cancer gov/. 2012.
- Bennett JM, Catovsky D, Daniel MT, et al. Proposals for the classification of the acute leukaemias. French-American-British (FAB) co-operative group. Br J Haematol. 1976;33(4):451-458.
- 3. Doulatov S, Notta F, Laurenti E, Dick JE. Hematopoiesis: a human perspective. Cell Stem Cell. 2012;10(2):120-136.
- 4. West AH, Godley LA, Churpek JE. Familial myelodysplastic syndrome/acute leukemia syndromes: a review and utility for translational investigations. Ann N Y Acad Sci. 2014;1310:111-118.
- 5. Churpek JE, Pyrtel K, Kanchi KL, et al. Genomic analysis of germ line and somatic variants in familial myelodysplasia/acute myeloid leukemia. Blood. 2015;126(22):2484-2490.
- Arber DA, Brunning RD, Le Beau MM, Falini B, Vardiman J, Porwit A et al. Acute myeloid leukemia with recurrent genetic abnormalities. In: Swerdlow SH, Campo E, Harris NL, Jaffe ES, Pileri SA, Stein H et al. WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues, vol. 4th. Lyon: International Agency for Research on Cancer (IARC), 2008:110-23.
- Arber DA, Orazi A, Hasserjian R, et al. The 2016 revision to the World Health Organization (WHO) classification of myeloid neoplasms and acute leukemia. Blood. 2016;127(20):2391-2405.
- 8. Mrozek K, Heerema NA, Bloomfield CD. Cytogenetics in acute leukemia. Blood Rev. 2004;18(2):115-136.
- 9. Grimwade D, Hills RK, Moorman AV, et al. Refinement of cytogenetic classification in acute myeloid leukemia: determination of prognostic significance of rare recurring chromosomal abnormalities among 5876 younger adult patients treated in the United Kingdom Medical Research Council trials. Blood. 2010;116(3):354-365.
- 10. Dohner H, Estey EH, Amadori S, et al. Diagnosis and management of acute myeloid leukemia in adults: recommendations from an international expert panel, on behalf of the European LeukemiaNet. Blood. 2010;115(3):453-474.
- 11. Dohner H, Weisdorf DJ, Bloomfield CD. Acute Myeloid Leukemia. N Engl J Med. 2015;373(12):1136-1152.
- 12. Patel JP, Gonen M, Figueroa ME, et al. Prognostic relevance of integrated genetic profiling in acute myeloid leukemia. N Engl J Med. 2012;366(12):1079-1089.

- 13. Koreth J, Schlenk R, Kopecky KJ, et al. Allogeneic stem cell transplantation for acute myeloid leukemia in first complete remission: systematic review and meta-analysis of prospective clinical trials. JAMA. 2009;301(22):2349-2361.
- 14. Baldus CD, Thiede C, Soucek S, et al. BAALC expression and FLT3 internal tandem duplication mutations in acute myeloid leukemia patients with normal cytogenetics: prognostic implications. J Clin Oncol. 2006;24(5):790-797.
- 15. Langer C, Radmacher MD, Ruppert AS, et al. High BAALC expression associates with other molecular prognostic markers, poor outcome, and a distinct gene-expression signature in cytogenetically normal patients younger than 60 years with acute myeloid leukemia: a Cancer and Leukemia Group B (CALGB) study. Blood. 2008;111(11):5371-5379.
- Metzeler KH, Dufour A, Benthaus T, et al. ERG expression is an independent prognostic factor and allows refined risk stratification in cytogenetically normal acute myeloid leukemia: a comprehensive analysis of ERG, MN1, and BAALC transcript levels using oligonucleotide microarrays. J Clin Oncol. 2009;27(30):5031-5038.
- 17. Cilloni D, Renneville A, Hermitte F, et al. Real-time quantitative polymerase chain reaction detection of minimal residual disease by standardized WT1 assay to enhance risk stratification in acute myeloid leukemia: a European LeukemiaNet study. J Clin Oncol. 2009;27(31):5195-5201.
- 18. Barjesteh van Waalwijk van Doorn-Khosrovani S, Erpelinck C, van Putten WL, et al. High EVI1 expression predicts poor survival in acute myeloid leukemia: a study of 319 de novo AML patients. Blood. 2003;101(3):837-845.
- 19. Borer RA, Lehner CF, Eppenberger HM, Nigg EA. Major nucleolar proteins shuttle between nucleus and cytoplasm. Cell. 1989;56(3):379-390.
- 20. Grisendi S, Mecucci C, Falini B, Pandolfi PP. Nucleophosmin and cancer. Nat Rev Cancer. 2006;6(7):493-505.
- 21. Falini B, Mecucci C, Tiacci E, et al. Cytoplasmic nucleophosmin in acute myelogenous leukemia with a normal karyotype. N Engl J Med. 2005;352(3):254-266.
- 22. Falini B, Nicoletti I, Martelli MF, Mecucci C. Acute myeloid leukemia carrying cytoplasmic/mutated nucleophosmin (NPMc+ AML): biologic and clinical features. Blood. 2007;109(3):874-885.
- 23. Schnittger S, Schoch C, Kern W, et al. Nucleophosmin gene mutations are predictors of favorable prognosis in acute myelogenous leukemia with a normal karyotype. Blood. 2005;106(12):3733-3739.
- 24. Thiede C, Koch S, Creutzig E, et al. Prevalence and prognostic impact of NPM1 mutations in 1485 adult patients with acute myeloid leukemia (AML). Blood. 2006;107(10):4011-4020.

- 25. Schlenk RF, Dohner K, Krauter J, et al. Mutations and treatment outcome in cytogenetically normal acute myeloid leukemia. N Engl J Med. 2008;358(18):1909-1918.
- 26. Becker H, Marcucci G, Maharry K, et al. Favorable prognostic impact of NPM1 mutations in older patients with cytogenetically normal de novo acute myeloid leukemia and associated gene- and microRNA-expression signatures: a Cancer and Leukemia Group B study. J Clin Oncol. 2010;28(4):596-604.
- 27. Choudhary C, Schwable J, Brandts C, et al. AML-associated Flt3 kinase domain mutations show signal transduction differences compared with Flt3 ITD mutations. Blood. 2005;106(1):265-273.
- 28. Whitman SP, Archer KJ, Feng L, et al. Absence of the wild-type allele predicts poor prognosis in adult de novo acute myeloid leukemia with normal cytogenetics and the internal tandem duplication of FLT3: a cancer and leukemia group B study. Cancer Res. 2001;61(19):7233-7239.
- 29. Frohling S, Schlenk RF, Breitruck J, et al. Prognostic significance of activating FLT3 mutations in younger adults (16 to 60 years) with acute myeloid leukemia and normal cytogenetics: a study of the AML Study Group Ulm. Blood. 2002;100(13):4372-4380.
- 30. Schnittger S, Bacher U, Haferlach C, et al. Diversity of the juxtamembrane and TKD1 mutations (Exons 13-15) in the FLT3 gene with regards to mutant load, sequence, length, localization, and correlation with biological data. Genes Chromosomes Cancer. 2012;51(10):910-924.
- Bacher U, Haferlach C, Kern W, Haferlach T, Schnittger S. Prognostic relevance of FLT3-TKD mutations in AML: the combination matters--an analysis of 3082 patients. Blood. 2008;111(5):2527-2537.
- 32. Cho YS, Kim EJ, Park UH, Sin HS, Um SJ. Additional sex comb-like 1 (ASXL1), in cooperation with SRC-1, acts as a ligand-dependent coactivator for retinoic acid receptor. J Biol Chem. 2006;281(26):17588-17598.
- 33. Vainchenker W, Delhommeau F, Constantinescu SN, Bernard OA. New mutations and pathogenesis of myeloproliferative neoplasms. Blood. 2011;118(7):1723-1735.
- 34. Metzeler KH, Becker H, Maharry K, et al. ASXL1 mutations identify a high-risk subgroup of older patients with primary cytogenetically normal AML within the ELN Favorable genetic category. Blood. 2011;118(26):6920-6929.
- 35. Paschka P, Schlenk RF, Gaidzik VI, et al. ASXL1 mutations in younger adult patients with acute myeloid leukemia: a study by the German-Austrian Acute Myeloid Leukemia Study Group. Haematologica. 2015;100(3):324-330.
- 36. Schnittger S, Eder C, Jeromin S, et al. ASXL1 exon 12 mutations are frequent in AML with intermediate risk karyotype and are independently associated with an adverse outcome. Leukemia. 2013;27(1):82-91.

- 37. Zhang P, Iwasaki-Arai J, Iwasaki H, et al. Enhancement of hematopoietic stem cell repopulating capacity and self-renewal in the absence of the transcription factor C/EBP alpha. Immunity. 2004;21(6):853-863.
- 38. Ye M, Zhang H, Amabile G, et al. C/EBPa controls acquisition and maintenance of adult haematopoietic stem cell quiescence. Nat Cell Biol. 2013;15(4):385-394.
- 39. Pabst T, Mueller BU, Zhang P, et al. Dominant-negative mutations of CEBPA, encoding CCAAT/enhancer binding protein-alpha (C/EBPalpha), in acute myeloid leukemia. Nat Genet. 2001;27(3):263-270.
- 40. Nerlov C. C/EBPalpha mutations in acute myeloid leukaemias. Nat Rev Cancer. 2004;4(5):394-400.
- 41. Wouters BJ, Lowenberg B, Erpelinck-Verschueren CA, et al. Double CEBPA mutations, but not single CEBPA mutations, define a subgroup of acute myeloid leukemia with a distinctive gene expression profile that is uniquely associated with a favorable outcome. Blood. 2009;113(13):3088-3091.
- 42. Taskesen E, Bullinger L, Corbacioglu A, et al. Prognostic impact, concurrent genetic mutations, and gene expression features of AML with CEBPA mutations in a cohort of 1182 cytogenetically normal AML patients: further evidence for CEBPA double mutant AML as a distinctive disease entity. Blood. 2011;117(8):2469-2475.
- 43. Dufour A, Schneider F, Hoster E, et al. Monoallelic CEBPA mutations in normal karyotype acute myeloid leukemia: independent favorable prognostic factor within NPM1 mutated patients. Ann Hematol. 2012;91(7):1051-1063.
- 44. Shlush LI, Zandi S, Mitchell A, et al. Identification of pre-leukaemic haematopoietic stem cells in acute leukaemia
  2. Nature. 2014;506(7488):328-333.
- 45. Corces-Zimmerman MR, Hong WJ, Weissman IL, Medeiros BC, Majeti R. Preleukemic mutations in human acute myeloid leukemia affect epigenetic regulators and persist in remission. Proc Natl Acad Sci U S A. 2014;111(7):2548-2553.
- 46. Genovese G, Kahler AK, Handsaker RE, et al. Clonal hematopoiesis and blood-cancer risk inferred from blood DNA sequence. N Engl J Med. 2014;371(26):2477-2487.
- 47. Gowher H, Loutchanwoot P, Vorobjeva O, et al. Mutational analysis of the catalytic domain of the murine Dnmt3a DNA-(cytosine C5)-methyltransferase. J Mol Biol. 2006;357(3):928-941.
- 48. Kim SJ, Zhao H, Hardikar S, et al. A DNMT3A mutation common in AML exhibits dominant-negative effects in murine ES cells. Blood. 2013;122(25):4086-4089.

- 49. Gaidzik VI, Schlenk RF, Paschka P, et al. Clinical impact of DNMT3A mutations in younger adult patients with acute myeloid leukemia: results of the AML Study Group (AMLSG). Blood. 2013;121(23):4769-4777.
- 50. Marcucci G, Metzeler KH, Schwind S, et al. Age-Related Prognostic Impact of Different Types of DNMT3A Mutations in Adults With Primary Cytogenetically Normal Acute Myeloid Leukemia. J Clin Oncol. 2012;30(7):742-750.
- 51. Renneville A, Boissel N, Nibourel O, et al. Prognostic significance of DNA methyltransferase 3A mutations in cytogenetically normal acute myeloid leukemia: a study by the Acute Leukemia French Association. Leukemia. 2012;26(6):1247-1254.
- 52. Thol F, Damm F, Ludeking A, et al. Incidence and prognostic influence of DNMT3A mutations in acute myeloid leukemia. J Clin Oncol. 2011;29(21):2889-2896.
- 53. Dang L, White DW, Gross S, et al. Cancer-associated IDH1 mutations produce 2hydroxyglutarate. Nature. 2009;462(7274):739-744.
- 54. Marcucci G, Maharry K, Wu YZ, et al. IDH1 and IDH2 gene mutations identify novel molecular subsets within de novo cytogenetically normal acute myeloid leukemia: a Cancer and Leukemia Group B study. J Clin Oncol. 2010;28(14):2348-2355.
- 55. Thol F, Damm F, Wagner K, et al. Prognostic impact of IDH2 mutations in cytogenetically normal acute myeloid leukemia. Blood. 2010;116(4):614-616.
- 56. Paschka P, Schlenk RF, Gaidzik VI, et al. IDH1 and IDH2 mutations are frequent genetic alterations in acute myeloid leukemia and confer adverse prognosis in cytogenetically normal acute myeloid leukemia with NPM1 mutation without FLT3 internal tandem duplication. J Clin Oncol. 2010;28(22):3636-3643.
- 57. Krivtsov AV, Armstrong SA. MLL translocations, histone modifications and leukaemia stem-cell development. Nat Rev Cancer. 2007;7(11):823-833.
- 58. Zhang Y, Yan X, Sashida G, et al. Stress hematopoiesis reveals abnormal control of selfrenewal, lineage bias, and myeloid differentiation in Mll partial tandem duplication (Mll-PTD) hematopoietic stem/progenitor cells. Blood. 2012;120(5):1118-1129.
- 59. Schnittger S, Kinkelin U, Schoch C, et al. Screening for MLL tandem duplication in 387 unselected patients with AML identify a prognostically unfavorable subset of AML. Leukemia. 2000;14(5):796-804.
- 60. Dohner K, Tobis K, Ulrich R, et al. Prognostic significance of partial tandem duplications of the MLL gene in adult patients 16 to 60 years old with acute myeloid leukemia and normal cytogenetics: a study of the Acute Myeloid Leukemia Study Group Ulm. J Clin Oncol. 2002;20(15):3254-3261.

- 61. Whitman SP, Ruppert AS, Marcucci G, et al. Long-term disease-free survivors with cytogenetically normal acute myeloid leukemia and MLL partial tandem duplication: a Cancer and Leukemia Group B study. Blood. 2007;109(12):5164-5167.
- 62. Whitman SP, Caligiuri MA, Maharry K, et al. The MLL partial tandem duplication in adults aged 60 years and older with de novo cytogenetically normal acute myeloid leukemia. Leukemia. 2012;26(7):1713-1717.
- 63. Wang J, Kong G, Liu Y, et al. Nras(G12D/+) promotes leukemogenesis by aberrantly regulating hematopoietic stem cell functions. Blood. 2013;121(26):5203-5207.
- 64. Bacher U, Haferlach T, Schoch C, Kern W, Schnittger S. Implications of NRAS mutations in AML: a study of 2502 patients. Blood. 2006;107(10):3847-3853.
- 65. Michaud J, Scott HS, Escher R. AML1 interconnected pathways of leukemogenesis. Cancer Invest. 2003;21(1):105-136.
- 66. Tsuzuki S, Hong D, Gupta R, et al. Isoform-specific potentiation of stem and progenitor cell engraftment by AML1/RUNX1. PLoS Med. 2007;4(5):e172.
- 67. Ichikawa M, Asai T, Saito T, et al. AML-1 is required for megakaryocytic maturation and lymphocytic differentiation, but not for maintenance of hematopoietic stem cells in adult hematopoiesis. Nat Med. 2004;10(3):299-304.
- 68. Mendler JH, Maharry K, Radmacher MD, et al. RUNX1 Mutations Are Associated With Poor Outcome in Younger and Older Patients With Cytogenetically Normal Acute Myeloid Leukemia and With Distinct Gene and MicroRNA Expression Signatures. J Clin Oncol. 2012;30(25):3109-3118.
- 69. Tang JL, Hou HA, Chen CY, et al. AML1/RUNX1 mutations in 470 adult patients with de novo acute myeloid leukemia: prognostic implication and interaction with other gene alterations. Blood. 2009;114(26):5352-5361.
- 70. Schnittger S, Dicker F, Kern W, et al. RUNX1 mutations are frequent in de novo AML with noncomplex karyotype and confer an unfavorable prognosis. Blood. 2011;117(8):2348-2357.
- 71. Gaidzik VI, Bullinger L, Schlenk RF, et al. RUNX1 Mutations in Acute Myeloid Leukemia: Results From a Comprehensive Genetic and Clinical Analysis From the AML Study Group. J Clin Oncol. 2011;29(10):1364-1372.
- 72. Ito S, Shen L, Dai Q, et al. Tet proteins can convert 5-methylcytosine to 5-formylcytosine and 5-carboxylcytosine. Science. 2011;333(6047):1300-1303.
- 73. Ko M, Huang Y, Jankowska AM, et al. Impaired hydroxylation of 5-methylcytosine in myeloid cancers with mutant TET2. Nature. 2010;468(7325):839-843.

- 74. Moran-Crusio K, Reavie L, Shih A, et al. Tet2 loss leads to increased hematopoietic stem cell self-renewal and myeloid transformation. Cancer Cell. 2011;20(1):11-24.
- 75. Saint-Martin C, Leroy G, Delhommeau F, et al. Analysis of the ten-eleven translocation 2 (TET2) gene in familial myeloproliferative neoplasms. Blood. 2009;114(8):1628-1632.
- 76. Abdel-Wahab O, Manshouri T, Patel J, et al. Genetic analysis of transforming events that convert chronic myeloproliferative neoplasms to leukemias. Cancer Res. 2010;70(2):447-452.
- 77. Metzeler KH, Maharry K, Radmacher MD, et al. TET2 Mutations Improve the New European LeukemiaNet Risk Classification of Acute Myeloid Leukemia: A Cancer and Leukemia Group B Study. J Clin Oncol. 2011;29(10):1373-1381.
- 78. Weissmann S, Alpermann T, Grossmann V, et al. Landscape of TET2 mutations in acute myeloid leukemia. Leukemia. 2012;26(5):934-942.
- 79. Gaidzik VI, Paschka P, Spath D, et al. TET2 Mutations in Acute Myeloid Leukemia (AML): Results From a Comprehensive Genetic and Clinical Analysis of the AML Study Group. J Clin Oncol. 2012;30(12):1350-1357.
- Damm F, Markus B, Thol F, et al. TET2 mutations in cytogenetically normal acute myeloid leukemia: clinical implications and evolutionary patterns. Genes Chromosomes Cancer. 2014;53(10):824-832.
- 81. Yang L, Han Y, Suarez SF, Minden MD. A tumor suppressor and oncogene: the WT1 story. Leukemia. 2007;21(5):868-876.
- 82. Cilloni D, Gottardi E, De Micheli D, et al. Quantitative assessment of WT1 expression by real time quantitative PCR may be a useful tool for monitoring minimal residual disease in acute leukemia patients. Leukemia. 2002;16(10):2115-2121.
- 83. Virappane P, Gale R, Hills R, et al. Mutation of the Wilms' tumor 1 gene is a poor prognostic factor associated with chemotherapy resistance in normal karyotype acute myeloid leukemia: the United Kingdom Medical Research Council Adult Leukaemia Working Party. J Clin Oncol. 2008;26(33):5429-5435.
- 84. Paschka P, Marcucci G, Ruppert AS, et al. Wilms Tumor 1 Gene Mutations Independently Predict Poor Outcome in Adults With Cytogenetically Normal Acute Myeloid Leukemia: A Cancer and Leukemia Group B Study. J Clin Oncol. 2008;26(28):4595-4602.
- 85. Renneville A, Boissel N, Zurawski V, et al. Wilms tumor 1 gene mutations are associated with a higher risk of recurrence in young adults with acute myeloid leukemia: a study from the Acute Leukemia French Association. Cancer. 2009;115(16):3719-3727.
- 86. Krauth MT, Alpermann T, Bacher U, et al. WT1 mutations are secondary events in AML, show varying frequencies and impact on prognosis between genetic subgroups. Leukemia. 2015;29(3):660-667.

- 87. Tanner SM, Austin JL, Leone G, et al. BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia. Proc Natl Acad Sci U S A. 2001;98(24):13901-13906.
- 88. Baldus CD, Tanner SM, Kusewitt DF, et al. BAALC, a novel marker of human hematopoietic progenitor cells. Exp Hematol. 2003;31(11):1051-1056.
- 89. Baldus CD, Tanner SM, Ruppert AS, et al. BAALC expression predicts clinical outcome of de novo acute myeloid leukemia patients with normal cytogenetics: a Cancer and Leukemia Group B Study. Blood. 2003;102(5):1613-1618.
- 90. Schrama D, Keller G, Houben R, et al. BRAFV600E mutations in malignant melanoma are associated with increased expressions of BAALC. J Carcinog. 2008;7:1.
- 91. Heuser M, Berg T, Kuchenbauer F, et al. Functional role of BAALC in leukemogenesis. Leukemia. 2012;26(3):532-536.
- 92. Morita K, Masamoto Y, Kataoka K, et al. BAALC potentiates oncogenic ERK pathway through interactions with MEKK1 and KLF4. Leukemia. 2015;29(11):2248-2256.
- 93. Eisfeld AK, Schwind S, Patel R, et al. Intronic miR-3151 within BAALC drives leukemogenesis by deregulating the TP53 pathway. Sci Signal. 2014;7(321):ra36.
- 94. Franzoni A, Passon N, Fabbro D, et al. Histone post-translational modifications associated to BAALC expression in leukemic cells. Biochem Biophys Res Commun. 2012;417(2):721-725.
- 95. Schwind S, Marcucci G, Maharry K, et al. BAALC and ERG expression levels are associated with outcome and distinct gene and microRNA expression profiles in older patients with de novo cytogenetically normal acute myeloid leukemia: a Cancer and Leukemia Group B study. Blood. 2010;116(25):5660-5669.
- 96. Weber S, Alpermann T, Dicker F, et al. BAALC expression: a suitable marker for prognostic risk stratification and detection of residual disease in cytogenetically normal acute myeloid leukemia. Blood Cancer J. 2014;4:e173.
- 97. Bienz M, Ludwig M, Mueller BU, et al. Risk assessment in patients with acute myeloid leukemia and a normal karyotype. Clin Cancer Res. 2005;11(4):1416-1424.
- 98. Najima Y, Ohashi K, Kawamura M, et al. Molecular monitoring of BAALC expression in patients with CD34-positive acute leukemia. Int J Hematol. 2010;91(4):636-645.
- 99. Diaz-Beya M, Brunet S, Nomdedeu J, et al. The expression level of BAALC-associated microRNA miR-3151 is an independent prognostic factor in younger patients with cytogenetic intermediate-risk acute myeloid leukemia. Blood Cancer J. 2015;5:e352.
- 100. Haferlach C, Kern W, Schindela S, et al. Gene expression of BAALC, CDKN1B, ERG, and MN1 adds independent prognostic information to cytogenetics and molecular

mutations in adult acute myeloid leukemia. Genes Chromosomes Cancer. 2012;51(3):257-265.

- 101. Duterque-Coquillaud M, Niel C, Plaza S, Stehelin D. New human erg isoforms generated by alternative splicing are transcriptional activators. Oncogene. 1993;8(7):1865-1873.
- 102. Rainis L, Toki T, Pimanda JE, et al. The proto-oncogene ERG in megakaryoblastic leukemias. Cancer Res. 2005;65(17):7596-7602.
- 103. Loughran SJ, Kruse EA, Hacking DF, et al. The transcription factor Erg is essential for definitive hematopoiesis and the function of adult hematopoietic stem cells. Nat Immunol. 2008;9(7):810-819.
- 104. Taoudi S, Bee T, Hilton A, et al. ERG dependence distinguishes developmental control of hematopoietic stem cell maintenance from hematopoietic specification. Genes Dev. 2011;25(3):251-262.
- 105. Salek-Ardakani S, Smooha G, de Boer J, et al. ERG is a megakaryocytic oncogene. Cancer Res. 2009;69(11):4665-4673.
- 106. Tsuzuki S, Taguchi O, Seto M. Promotion and maintenance of leukemia by ERG. Blood. 2011;117(14):3858-3868.
- 107. Thoms JA, Birger Y, Foster S, et al. ERG promotes T-acute lymphoblastic leukemia and is transcriptionally regulated in leukemic cells by a stem cell enhancer. Blood. 2011;117(26):7079-7089.
- 108. Stankiewicz MJ, Crispino JD. ETS2 and ERG promote megakaryopoiesis and synergize with alterations in GATA-1 to immortalize hematopoietic progenitor cells. Blood. 2009;113(14):3337-3347.
- 109. Khan I, Malinge S, Crispino J. Myeloid leukemia in Down syndrome. Crit Rev Oncog. 2011;16(1-2):25-36.
- 110. Ronan A, Fagan K, Christie L, et al. Familial 4.3 Mb duplication of 21q22 sheds new light on the Down syndrome critical region. J Med Genet. 2007;44(7):448-451.
- 111. Delabar JM, Theophile D, Rahmani Z, et al. Molecular mapping of twenty-four features of Down syndrome on chromosome 21. Eur J Hum Genet. 1993;1(2):114-124.
- 112. Malinge S, Izraeli S, Crispino JD. Insights into the manifestations, outcomes, and mechanisms of leukemogenesis in Down syndrome. Blood. 2009;113(12):2619-2628.
- 113. Canzonetta C, Hoischen A, Giarin E, et al. Amplified segment in the 'Down syndrome critical region' on HSA21 shared between Down syndrome and euploid AML-MO excludes RUNX1, ERG and ETS2. Br J Haematol. 2012;157(2):197-200.

- 114. Ichikawa H, Shimizu K, Hayashi Y, Ohki M. An RNA-binding protein gene, TLS/FUS, is fused to ERG in human myeloid leukemia with t(16;21) chromosomal translocation. Cancer Res. 1994;54(11):2865-2868.
- 115. Giovannini M, Biegel JA, Serra M, et al. EWS-erg and EWS-Fli1 fusion transcripts in Ewing's sarcoma and primitive neuroectodermal tumors with variant translocations. J Clin Invest. 1994;94(2):489-496.
- 116. Soller MJ, Isaksson M, Elfving P, et al. Confirmation of the high frequency of the TMPRSS2/ERG fusion gene in prostate cancer. Genes Chromosomes Cancer. 2006;45(7):717-719.
- 117. Petrovics G, Liu A, Shaheduzzaman S, et al. Frequent overexpression of ETS-related gene-1 (ERG1) in prostate cancer transcriptome. Oncogene. 2005;24(23):3847-3852.
- 118. Marcucci G, Baldus CD, Ruppert AS, et al. Overexpression of the ETS-related gene, ERG, predicts a worse outcome in acute myeloid leukemia with normal karyotype: a Cancer and Leukemia Group B study. J Clin Oncol. 2005;23(36):9234-9242.
- 119. Marcucci G, Maharry K, Whitman SP, et al. High expression levels of the ETS-related gene, ERG, predict adverse outcome and improve molecular risk-based classification of cytogenetically normal acute myeloid leukemia: a Cancer and Leukemia Group B Study. J Clin Oncol. 2007;25(22):3337-3343.
- 120. Bock J, Mochmann LH, Schlee C, et al. ERG transcriptional networks in primary acute leukemia cells implicate a role for ERG in deregulated kinase signaling. PLoS ONE. 2013;8(1):e52872.
- 121. Cornelissen JJ, Gratwohl A, Schlenk RF, et al. The European LeukemiaNet AML Working Party consensus statement on allogeneic HSCT for patients with AML in remission: an integrated-risk adapted approach. Nat Rev Clin Oncol. 2012;9(10):579-590.
- 122. Kern W, Haferlach T, Schoch C, et al. Early blast clearance by remission induction therapy is a major independent prognostic factor for both achievement of complete remission and long-term outcome in acute myeloid leukemia: data from the German AML Cooperative Group (AMLCG) 1992 Trial. Blood. 2003;101(1):64-70.
- 123. Lowenberg B, van Putten W, Theobald M, et al. Effect of priming with granulocyte colony-stimulating factor on the outcome of chemotherapy for acute myeloid leukemia. N Engl J Med. 2003;349(8):743-752.
- 124. Büchner T, Hiddemann W, Wormann B, et al. Double induction strategy for acute myeloid leukemia: the effect of high-dose cytarabine with mitoxantrone instead of standard-dose cytarabine with daunorubicin and 6-thioguanine: a randomized trial by the German AML Cooperative Group. Blood. 1999;93(12):4116-4124.

- 125. Burnett AK, Hills RK, Milligan D, et al. Identification of patients with acute myeloblastic leukemia who benefit from the addition of gemtuzumab ozogamicin: results of the MRC AML15 trial. J Clin Oncol. 2011;29(4):369-377.
- 126. Hokland P, Ommen HB. Towards individualized follow-up in adult acute myeloid leukemia in remission. Blood. 2011;117(9):2577-2584.
- 127. Ommen HB, Schnittger S, Jovanovic JV, et al. Strikingly different molecular relapse kinetics in NPM1c, PML-RARA, RUNX1-RUNX1T1, and CBFB-MYH11 acute myeloid leukemias. Blood. 2010;115(2):198-205.
- 128. Freeman SD, Jovanovic JV, Grimwade D. Development of minimal residual diseasedirected therapy in acute myeloid leukemia. Semin Oncol. 2008;35(4):388-400.
- 129. Ivey A, Hills RK, Simpson MA, et al. Assessment of Minimal Residual Disease in Standard-Risk AML. N Engl J Med. 2016;374(5):422-433.
- 130. Sanz MA, Grimwade D, Tallman MS, et al. Management of acute promyelocytic leukemia: recommendations from an expert panel on behalf of the European LeukemiaNet. Blood. 2009;113(9):1875-1891.
- 131. Schnittger S, Weisser M, Schoch C, et al. New score predicting for prognosis in PML-RARA+, AML1-ETO+, or CBFBMYH11+ acute myeloid leukemia based on quantification of fusion transcripts. Blood. 2003;102(8):2746-2755.
- 132. Corbacioglu A, Scholl C, Schlenk RF, et al. Prognostic impact of minimal residual disease inCBFB-MYH11-positive acute myeloid leukemia. J Clin Oncol. 2010;28(23):3724-3729.
- Viehmann S, Teigler-Schlegel A, Bruch J, et al. Monitoring of minimal residual disease (MRD) by real-time quantitative reverse transcription PCR (RQ-RT-PCR) in childhood acute myeloid leukemia with AML1/ETO rearrangement. Leukemia. 2003;17(6):1130-1136.
- 134. Weisser M, Haferlach C, Hiddemann W, Schnittger S. The quality of molecular response to chemotherapy is predictive for the outcome of AML1-ETO-positive AML and is independent of pretreatment risk factors. Leukemia. 2007;21(6):1177-1182.
- 135. Schnittger S, Kern W, Tschulik C, et al. Minimal residual disease levels assessed by NPM1 mutation-specific RQ-PCR provide important prognostic information in AML. Blood. 2009;114(11):2220-2231.
- 136. Weisser M, Kern W, Schoch C, et al. Risk assessment by monitoring expression levels of partial tandem duplications in the MLL gene in acute myeloid leukemia during therapy. Haematologica. 2005;90(7):881-889.
- 137. Ommen HB, Hokland P, Haferlach T, et al. Relapse kinetics in acute myeloid leukaemias with MLL translocations or partial tandem duplications within the MLL gene. Br J Haematol. 2014;165(5):618-628.

- 138. Weber S, Haferlach C, Jeromin S, et al. Gain of chromosome 21 or amplification of chromosome arm 21q is one mechanism for increased ERG expression in acute myeloid leukemia. Genes Chromosomes Cancer. 2016;55(2):148-157.
- 139. Beillard E, Pallisgaard N, van der Velden VHJ, et al. Evaluation of candidate control genes for diagnosis and residual disease detection in leukemic patients using 'real-time' quantitative reverse-transcriptase polymerase chain reaction (RQ-PCR) - a Europe against cancer program. Leukemia. 2003;17(12):2474-2486.
- 140. Weisser M, Haferlach T, Schoch C, Hiddemann W, Schnittger S. The use of housekeeping genes for real-time PCR-based quantification of fusion gene transcripts in acute myeloid leukemia. Leukemia. 2004;18(9):1551-1553.
- 141. Schmittgen TD, Livak KJ. Analyzing real-time PCR data by the comparative C(T) method. Nat Protoc. 2008;3(6):1101-1108.
- 142. Schnittger S, Haferlach C, Ulke M, et al. IDH1 mutations are detected in 6.6% of 1414 AML patients and are associated with intermediate risk karyotype and unfavorable prognosis in adults younger than 60 years and unmutated NPM1 status. Blood. 2010;116(25):5486-5496.
- 143. Nakao M, Janssen JW, Seriu T, Bartram CR. Rapid and reliable detection of N-ras mutations in acute lymphoblastic leukemia by melting curve analysis using LightCycler technology. Leukemia. 2000;14(2):312-315.
- 144. Bacher U, Dicker F, Haferlach C, et al. Quantification of rare NPM1 mutation subtypes by digital PCR. Br J Haematol. 2014;167(5):710-714.
- 145. Schnittger S, Schoch C, Dugas M, et al. Analysis of FLT3 length mutations in 1003 patients with acute myeloid leukemia: correlation to cytogenetics, FAB subtype, and prognosis in the AMLCG study and usefulness as a marker for the detection of minimal residual disease. Blood. 2002;100(1):59-66.
- 146. Thiede C, Steudel C, Mohr B, et al. Analysis of FLT3-activating mutations in 979 patients with acute myelogenous leukemia: association with FAB subtypes and identification of subgroups with poor prognosis. Blood. 2002;99(12):4326-4335.
- 147. Delic S, Rose D, Kern W, et al. Application of an NGS-based 28-gene panel in myeloproliferative neoplasms reveals distinct mutation patterns in essential thrombocythaemia, primary myelofibrosis and polycythaemia vera. Br J Haematol. 2016.
- 148. Kohlmann A, Klein HU, Weissmann S, et al. The Interlaboratory RObustness of Nextgeneration sequencing (IRON) study: a deep sequencing investigation of TET2, CBL and KRAS mutations by an international consortium involving 10 laboratories. Leukemia. 2011;25(12):1840-1848.

- 149. Lange V, Bohme I, Hofmann J, et al. Cost-efficient high-throughput HLA typing by MiSeq amplicon sequencing. BMC Genomics. 2014;15(1):63.
- 150. Forbes SA, Beare D, Gunasekaran P, et al. COSMIC: exploring the world's knowledge of somatic mutations in human cancer. Nucleic Acids Res. 2015;43(Database issue):D805-D811.
- 151. Weber S, Haferlach T, Haferlach C, et al. Comprehensive study on ERG gene expression in normal karyotype acute myeloid leukemia: ERG expression is of limited prognostic value, whereas the accumulation of adverse prognostic markers stepwise worsens the prognosis. Blood Cancer J. 2016;6(12):e507.
- 152. Weber S, Haferlach T, Alpermann T, et al. Feasibility of BAALC gene expression for detection of minimal residual disease and risk stratification in normal karyotype acute myeloid leukaemia. Br J Haematol. 2016;175(5):904-916.
- 153. Greif PA, Konstandin NP, Metzeler KH, et al. RUNX1 mutations in cytogenetically normal acute myeloid leukemia are associated with a poor prognosis and up-regulation of lymphoid genes. Haematologica. 2012;97(12):1909-1915.
- 154. Papaemmanuil E, Gerstung M, Bullinger L, et al. Genomic Classification and Prognosis in Acute Myeloid Leukemia. N Engl J Med. 2016;374(23):2209-2221.
- 155. Harada Y, Harada H. Molecular pathways mediating MDS/AML with focus on AML1/RUNX1 point mutations. J Cell Physiol. 2009;220(1):16-20.
- 156. Diffner E, Beck D, Gudgin EJ, et al. Activity of a heptad of transcription factors is associated with stem cell programs and clinical outcome in acute myeloid leukemia. Blood. 2013;121(12):2289-2300.
- 157. Santamaria C, Chillon MC, Garcia-Sanz R, et al. BAALC is an important predictor of refractoriness to chemotherapy and poor survival in intermediate-risk acute myeloid leukemia (AML). Ann Hematol. 2010;89(5):453-458.
- 158. Mrozek K, Marcucci G, Nicolet D, et al. Prognostic Significance of the European LeukemiaNet Standardized System for Reporting Cytogenetic and Molecular Alterations in Adults With Acute Myeloid Leukemia. J Clin Oncol. 2012;30(36):4515-4523.
- 159. Kern W, Haferlach T, Schnittger S, et al. Karyotype instability between diagnosis and relapse in 117 patients with acute myeloid leukemia: implications for resistance against therapy. Leukemia. 2002;16(10):2084-2091.
- 160. Ding L, Ley TJ, Larson DE, et al. Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature. 2012;481(7382):506-510.
- 161. Krönke J, Bullinger L, Teleanu V, et al. Clonal evolution in relapsed NPM1-mutated acute myeloid leukemia. Blood. 2013;122(1):100-108.

- 162. Kohlmann A, Nadarajah N, Alpermann T, et al. Monitoring of residual disease by nextgeneration deep-sequencing of RUNX1 mutations can identify acute myeloid leukemia patients with resistant disease. Leukemia. 2014;28(1):129-137.
- 163. Krönke J, Schlenk RF, Jensen KO, et al. Monitoring of minimal residual disease in NPM1mutated acute myeloid leukemia: a study from the German-Austrian acute myeloid leukemia study group. J Clin Oncol. 2011;29(19):2709-2716.
- 164. McCormick SR, McCormick MJ, Grutkoski PS, et al. FLT3 mutations at diagnosis and relapse in acute myeloid leukemia: cytogenetic and pathologic correlations, including cuplike blast morphology. Arch Pathol Lab Med. 2010;134(8):1143-1151.
- 165. Welch JS, Ley TJ, Link DC, et al. The origin and evolution of mutations in acute myeloid leukemia. Cell. 2012;150(2):264-278.
- 166. Baldus CD, Liyanarachchi S, Mrozek K, et al. Acute myeloid leukemia with complex karyotypes and abnormal chromosome 21: Amplification discloses overexpression of APP, ETS2, and ERG genes. Proc Natl Acad Sci U S A. 2004;101(11):3915-3920.
- Baldus CD, Burmeister T, Martus P, et al. High expression of the ETS transcription factor ERG predicts adverse outcome in acute T-lymphoblastic leukemia in adults. J Clin Oncol. 2006;24(29):4714-4720.
- 168. Preudhomme C, Warot-Loze D, Roumier C, et al. High incidence of biallelic point mutations in the Runt domain of the AML1/PEBP2 alpha B gene in Mo acute myeloid leukemia and in myeloid malignancies with acquired trisomy 21. Blood. 2000;96(8):2862-2869.
- 169. Rainis L, Bercovich D, Strehl S, et al. Mutations in exon 2 of GATA1 are early events in megakaryocytic malignancies associated with trisomy 21. Blood. 2003;102(3):981-986.
- 170. Wechsler J, Greene M, McDevitt MA, et al. Acquired mutations in GATA1 in the megakaryoblastic leukemia of Down syndrome. Nat Genet. 2002;32(1):148-152.
- Hollanda LM, Lima CS, Cunha AF, et al. An inherited mutation leading to production of only the short isoform of GATA-1 is associated with impaired erythropoiesis. Nat Genet. 2006;38(7):807-812.

## Acknowledgements

I would like to thank my advisor Prof. Dr. Susanne Schnittger for her continuous support with my PhD study, for her encouragement and supervision during the research and writing of this thesis. Thank you for your constant understanding and open attitude and for the scientific inspiration.

I want to sincerely thank Prof. Dr. Michael W. Pfaffl, who gave me the opportunity to do my PhD thesis at the Chair of Physiology, thereby supporting my work. Thank you for your straightforwardness and for always providing help whenever I needed it.

Additionally, my thanks go to Prof. Dr. Wolfgang Kern, Prof. Dr. Dr. Torsten Haferlach and Prof. Dr. Claudia Haferlach not only for giving me the possibility to do my PhD thesis at the Munich Leukemia Laboratory, but also for sharing their truthful and illuminating views on my PhD-related research.

Many thanks go to all my colleagues from MLL, especially to those from the molecular department. I was always able to count on helping hands and a friendly working atmosphere. I would also like to thank Elke Roos and Niroshan Nadarajah for their creative help with the figure design. A special acknowledgement goes to my office colleague, Sabine Jeromin. You have been a true friend and supportive in every way.

I particularly want to thank my family, my relatives and also my partner's family. Their support has been unconditional throughout the writing of this thesis and my life in general. Thank you for your caring support.

My sincere thanks to my partner, Harald Müller, for supporting me in everything. I can't thank you enough for encouraging me throughout this experience, for always cheering me up in hard times and cherishing every great moment with me.

Last but not least, special thanks go to my friends, who have always been on my side, sharing all the good and bad times. Your friendship is irreplaceable.

## List of scientific communications

### **Research Papers**

Simone Weber, Torsten Haferlach, Claudia Haferlach, Wolfgang Kern

Comprehensive study on *ERG* gene expression in normal karyotype acute myeloid leukemia: *ERG* expression is of limited prognostic value, whereas the accumulation of adverse prognostic markers stepwise worsens the prognosis

Blood Cancer J. 2016 Dec 09; 4:e173. doi:10.1038/bcj.2016.120.

Simone Weber, Torsten Haferlach, Tamara Alpermann, Karolína Perglerová, Susanne Schnittger, Claudia Haferlach, Wolfgang Kern

Feasibility of *BAALC* gene expression for detection of minimal residual disease and risk stratification in normal karyotype acute myeloid leukaemia

British Journal of Haematology. 2016 Dec;175(5):904-916. doi: 10.1111/bjh.14343. Epub 2016 Sep 23.

Torsten Haferlach, Simone Weber, Rabea Konietschke, Niroshan Nadarajah, Anna Stengel, Wolfgang Kern, Claudia Haferlach, Manja Meggendorfer

# Robustness of comprehensive DNA and RNA based assays at diagnosis of acute myeloid leukemia using blood and bone marrow stored on filter cards

Leukemia. 2016 Jun 10. doi: 10.1038/leu.2016.156.

Simone Weber, Claudia Haferlach, Sabine Jeromin, Niroshan Nadarajah, Frank Dicker, Louisa Noël, Melanie Zenger, Tamara Alpermann, Wolfgang Kern, Torsten Haferlach, Susanne Schnittger

Gain of chromosome 21 or amplification of chromosome arm 21q is one mechanism for increased *ERG* expression in acute myeloid leukemia

Genes Chromosomes Cancer. 2016 Feb;55(2):148-57. doi: 10.1002/gcc.22321. Epub 2015 Nov 6.

Simone Weber, Tamara Alpermann, Frank Dicker, Sabine Jeromin, Niroshan Nadarajah, Christiane Eder, Annette Fasan, Alexander Kohlmann, Manja Meggendorfer, Claudia Haferlach, Wolfgang Kern, Torsten Haferlach, Susanne Schnittger

**BAALC** expression: a suitable marker for prognostic risk stratification and detection of residual disease in cytogenetically normal acute myeloid leukemia

Blood Cancer J. 2014 Jan 10; 4:e173. doi: 10.1038/bcj.2013.71.

#### Poster presentations

Simone Weber, Tamara Alpermann, Karolína Perglerová, Susanne Schnittger, Torsten Haferlach, MD, Claudia Haferlach Wolfgang Kern

# **BAALC** Expression Is a Feasible Marker for Risk Stratification and Detection of Minimal Residual Disease in Cytogenetically Normal Acute Myeloid Leukemia

57th ASH Annual Meeting and Exposition; December 5-8, 2015; San Diego, CA

Simone Weber, Manja Meggendorfer, Niroshan Nadarajah, Karolína Perglerová, Susanne Schnittger

#### Molecular Characterization of Philadelphia Chromosome Positive Acute Myeloid

#### Leukemia - New Provisional Entity?

57th ASH Annual Meeting and Exposition; December 5-8, 2015; San Diego, CA

Annette Fasan, Wolfgang Kern, Niroshan Nadarajah, Simone Weber, Sonja Schindela, Nicole Schlenther, Susanne Schnittger, Torsten Haferlach, Claudia Haferlach

#### Three Steps to the Diagnosis of Adult Ph-like ALL

57th ASH Annual Meeting and Exposition; December 5-8, 2015; San Diego, CA

Andreas Roller, Simone Weber, Alexander Kohlmann, Melanie Zenger, Marita Staller, Wolfgang Kern, Susanne Schnittger, Torsten Haferlach, Claudia Haferlach

Gene amplifications in 84 patients with acute myeloid leukemia and 31 patients with myelodysplastic syndrome investigated by array CGH

55th ASH Annual Meeting and Exposition; December 7-10, 2013; New Orleans, LA

Simone Weber, Claudia Haferlach, Louisa Noel, Tamara Alpermann, Niroshan Nadarahja, Wolfgang Kern, Torsten Haferlach, Susanne Schnittger

# *ERG* Overexpression is Highly Associated with *ERG* Gene Amplifications in Patients with Myeloid Malignancies

55th ASH Annual Meeting and Exposition; December 7-10, 2013; New Orleans, LA

Simone Weber, Tamara Alpermann, Christiane Eder, Frank Dicker, Sabine Jeromin, Alexander Kohlmann, Annette Fasan, Claudia Haferlach, Wolfgang Kern, Torsten Haferlach, Susanne Schnittger

High *BAALC* Expression in Cytogenetically Normal Acute Myeloid Leukemia Strongly Correlates with Adverse Markers Such As *RUNX1*mut, *MLL*-PTD and *FLT3*-ITD and Is Useful for Disease Monitoring

54th ASH Annual Meeting and Exposition; December 8-11, 2012; Atlanta, GA

### Scientific talks

Simone Weber

# Amplification of chromosome 21 as a mechanism for *ERG* overexpression in patients with myeloid malignancies

18th Congress of the European Hematology Association; June 13–16, 2013; Stockholm, Sweden

#### Simone Weber

In acute myeloid leukemia high *BAALC* expression levels strongly correlate with adverse outcome but also with established adverse markers such as *RUNX1*mut, *MLL*-PTD and *FLT3*mut/wt ratio>0.5

Gemeinsame Jahrestagung 2012 der DGHO, ÖGHO, SGMO und SGH+SSH; October 19-23, 2012; Stuttgart, Germany

# Curriculum vitae

## Simone Weber

Date of birth	June, 12 <sup>th</sup> 1984			
Place of birth	Freiburg im Breisgau, Germany			
Nationality	German			
Since 12/2012	Scientific Associate and PhD student Münchner Leukämielabor GmbH and Technical University Munich, Germany			
10/2010 – 12/2012	Scientific Associate Münchner Leukämielabor GmbH, Munich, Germany Department of Molecular Genetics			
05/2010 – 10/2010	Scientific Associate Institute for molecular Microbiology and Hygiene, Freiburg, Germany Department of Virology			
09/2006 – 05/2010	Advanced studies in Biology (Diploma) Albert-Ludwigs-University Freiburg, Germany Degree: Diploma in Biology			
09/2004 – 09/2006	Basic studies in Biology Albert-Ludwigs-University Freiburg, Germany Degree: Intermediate diploma			
07/1990 – 07/2003	Primary and Secondary School, Freiburg, Germany Graduation: Abitur (A-levels)			
Appendix I - VI

# Appendix I

Simone Weber et al.

**BAALC** expression: a suitable marker for prognostic risk stratification and detection of residual disease in cytogenetically normal acute myeloid leukemia

Blood Cancer Journal. 2014 Jan 10; 4:e173. doi: 10.1038/bcj.2013.71.

# Appendix II

Simone Weber et al.

Gain of chromosome 21 or amplification of chromosome arm 21q is one mechanism for increased *ERG* expression in acute myeloid leukemia

Genes Chromosomes Cancer. 2016 Feb;55(2):148-57. doi: 10.1002/gcc.22321. Epub 2015 Nov 6.

## Appendix III

Simone Weber et al.

Feasibility of *BAALC* gene expression for detection of minimal residual disease and risk stratification in normal karyotype acute myeloid leukaemia

British Journal of Haematology. 2016 Dec;175(5):904-916. doi: 10.1111/bjh.14343. Epub 2016 Sep 23.

#### **Appendix IV**

Simone Weber et al.

Comprehensive study on *ERG* gene expression in normal karyotype acute myeloid leukemia: *ERG* expression is of limited prognostic value, whereas the accumulation of adverse prognostic markers stepwise worsens the prognosis

Blood Cancer J. 2016 Dec 09; 4:e173. doi:10.1038/bcj.2016.120.

#### **Appendix V**

#### Validation of ABL1 for the assessment of BAALC and ERG gene expression

The use of ABL1 as a reference gene has been proposed by a collaborative initiation within the Europe Against Cancer (EAC) program, including 26 laboratories in 10 member countries, where 14 potential reference genes have been evaluated on normal and diagnostic leukemic samples.<sup>139</sup> Therefore, ABL1 represents the most commonly used reference gene in hematology. However, when testing BAALC and ERG expression the magnitude of quantification cycles (Cq) of ABL1 represented a quite broad range from 23 to 34 cycles, which is beyond the expected range of common reference genes. The differential Cq values are most probably caused by differences in yield (cell numbers) and variations in RNA and cDNA synthesis. But, other factors such as differences in RNA quality or correlated regulation of ABL1 and BAALC or ERG gene expression, could also cause the differential expression of ABL1. To exclude these parameters as source of differential expression we performed additional analysis. Since all analysis were performed on primary patient samples we had to deal with limited amount of material. Therefore, we defined a core-set of 10 primary AML samples with sufficient material, reflecting the full magnitude of Cq. In this core-set the RNA quality and stability of ABL1 was re-evaluated. RNA integrity and concentration was assessed using the RNA 6000 Pico Kit (Agilent Technologies, Inc., Santa Clara, CA). Afterwards, 0.1µg of total RNA and 0.01µg of mRNA of each sample was reverse transcribed and the quantity of ABL1 was analyzed as outlined above. The newly defined Cq values were compared with the originally measured Cq values.

The estimation of the integrity of RNA resulted in a median RIN value (RNA integrity number) of 8.4 demonstrating intact RNA in these cases (range: 6.3 – 9.2). Quantifying *ABL1*, the magnitude of Cq ranged from 27.3 to 29.3 when analyzing cDNA processed from total RNA and from 24.6 to 27.9 when analyzing cDNA processed from mRNA. Conclusively these results suggest that differential Cq values are most probably caused by differences in yield (cell numbers) and variations in RNA and cDNA synthesis, as the quality of the RNA was acceptable and moreover since the broad magnitude of Cq value narrowed down when analyzing cDNA processed from defined amounts of RNA.

# Appendix VI

Gene-Identifier	Material	Sequence: Forward-Primer(5'-3')	Sequence: Reverse-Primer(5'-3')
ASXL1-F13.01	gDNA	GGTCAGATCACCCAGTCAGTT	CCTCACCACCATCACCACT
ASXI 1-F13 02	σΩΝΔ	ATGAGGGAGGTGGCAGAG	
ASXET E13.02	SDNA SDNA		TETTETECACECANTCACTC
ASXL1-E13.03			
ASALI-E13.04	gDNA DNIA		
ASXL1-E13.05	gDNA	GAGAACACATACCATCTGTTGAGC	
ASXL1-E13.06	gDNA	AGTCCACGGATACAGCCTCT	AGCAACTGCATCACAAGTGG
ASXL1-E13.07	gDNA	ATGCCTGGGTCCTCAGTG	GGACTGCCTTGCAATTCTTT
ASXL1-E13.08	gDNA	ACTGGTCTTGCCAGGATTG	GGCCTGTAACATTGCTCTGA
ASXL1-E13.09	gDNA	CACCTCGTTTCTCATCTCCA	GGCATTTGCCTTAAGAGGAC
ASXL1-E13.10	gDNA	CCAAGCACAAACTCCATGTC	CTGGTGGAACTCAGTTGGAG
ASXL1-E13.11	gDNA	CAGCATCAAGCAGGCATTT	CAATGTTTCCCATGGCCATA
CEBPA-E01.01	gDNA	GCCATGCCGGGAGAACT	CCCGGGTAGTCAAAGTCG
CEBPA-E01 02	gDNA	CCTTCAACGACGAGTTCCTG	CGGCTGGTAAGGGAAGAGG
CERDA E01.02	gDNA	CARCARCOACOACOACO	
CERRA E01.03	gDNA gDNA		
CEBPA-E01.04			CCAGGGCGGTCCCACA
CEBPA-E01.XL	gDNA		
DNMT3A-E02	gDNA	GCCTCCAAAGACCACGATAA	TGCTCCATCACCAGAATTGA
DNMT3A-E03	gDNA	ACAGGCCTGGAATGCTACAC	GTGAGGGTGGGATTTGAAGA
DNMT3A-E04	gDNA	AAACAGGCTAAGCCCACTGA	AAGAGGCTGCCCTGGT
DNMT3A-E05	gDNA	GGTGGGCCATCATATTTAACA	CACTTCCTCTCCCACA
DNMT3A-E06	gDNA	CCACCCTAATGCCCTAATGTC	GCTGAAGGAGCAGATGAACC
DNMT3A-E07	gDNA	TTCCTGGAGAGGTCAAGGTG	TGGAGAGAGGAGAGCAGGAC
DNMT3A-E08	gDNA	GCCTCGTGACCACTGTGTAA	ACCCACCACAGGCAGAGTAG
DNMT3A-F09	gDNA	CTCCTCTTTGCATCGGGTAA	ACCTGCACTCCAACTTCCAG
DNMT34-E10	gDNA	Τστοιοιατιστάτοι	TCCCTAAGCATGGCTTTCC
DNMT2A E11 12			
DINIVITOR-E11-12	SDINA		
DINMITSA-E13	gDNA		
DNMT3A-E14	gDNA	CACAGGCAGATGAGGTTTCC	CCCAGCTAAGGAGACCACTG
DNMT3A-E15	gDNA	CCCTAGCCATGCTCCAGAC	CCCACAACCAAGGCTCAG
DNMT3A-E16	gDNA	CAGGGTGTGTGGGTCTAGGA	TGCATACGTTTCCACTTCACA
DNMT3A-E17	gDNA	AAAGATAGGACTTGGGCCTACA	CTGCCTCCAGGTGCTGAG
DNMT3A-E18	gDNA	TGGTCCCGTTCTTGTTTAGG	CAAGGAGGAAGCCTATGTGC
DNMT3A-E19	gDNA	GACAGCTATTCCCGATGACC	GCTCCACAATGCAGATGAGA
DNMT3A-F20	gDNA	TGTGTGGCTCCTGAGAGAGA	CATGGCAGAGCAGCTAGTCA
DNMT3A-F21	gDNA	TGGTGGATTTGTGTCTTTGC	
	SDNA SDNA		
DINIVITSA-EZZ	gDNA DNIA		
DNM13A-E23	gDNA		AAAGCCCTCCGGTATTTCC
DNMT3A-FE06-08	cDNA	GGGGGACCCCTACTACATCA	CCTGGCCACCAGGAGAAG
DNMT3A-FE07-09	cDNA	GTGCAGCAGCCCACTGAC	GGGCTGCTTGTTGTACGTG
DNMT3A-FE08-11	cDNA	GTTCGGAGACGGCAAATTCT	AGGTTCCACCCACATGTCC
DNMT3A-FE10-14	cDNA	GGAGCCACCAGAAGAAGAGA	CAGCAGATGGTGCAGTAGGA
DNMT3A-FE14-16	cDNA	TTCTGGAGTGTGCGTACCAG	GATGGGCTTCCTCTTCTCAG
DNMT3A-FE15-19	cDNA	GGAATTTGACCCTCCAAAGG	AAAGAAGAGCCGGCCAGT
DNMT3A-FF18-22	cDNA	CAATGACCTCTCCATCGTCA	TGCTGAACTTGGCTATCCTG
DNMT3A-FF21-23	CDNA	CCACTGTGAATGATAAGCTGGA	TIGIGICGCTACCTCAGTTIG
FIT3-F13	σDNA	TCTGTTTCATCGCTGAGTGAC	ΤΟΤΤΟΓΟΔΑΔΑΓΤΟΟΓΑΤΤΤΟΔ
FLT3 E14	aDNA		CCAACETCCATTCACACTCC
FLT3-E14	gDNA -DNA		
FLI3-EI5	gDNA		
FLT3-E20	gDNA	GGCACAGCCCAGTAAAGATAAG	CACCACAGTGAGTGCAGTTG
IDH1-E04	gDNA	AAACTTTGCTTCTAATTTTTCTCTTTC	GCAAAATCACATTATTGCCAAC
IDH2-E04	gDNA	TGCAGTGGGACCACTATTATCTC	CACCACTGCCATCTTTTGG
NPM1-E06	gDNA	TGAAGAGGAGGAGGATGTGAAA	CATAGGATGGCTTTTTGTAAATGACT
NPM1-E07	gDNA	TCGATAAACATGGGTGCACAA	GAAAACAGACCATTCCCCACT
NPM1-E11	gDNA	TTTTCCAGGCTATTCAAGAT	ATATTTTTGTCTCCCCACCA
NRAS-E02	gDNA	GGCCGATATTAATCCGGTGT	TCCGACAAGTGAGAGACAGG
NRAS-E03	gDNA	CCCTCCCTGCCCCCTTAC	СААТGTCAAACAACCTAAAACCA
NRAS-E04	gDNA	TGTTGCCCAGGCTAATCTCA	GCAAACTCTTGCACAAATGC
RUNX1-F01	gDNA	GCTGTTTGCAGGGTCCTAAC	
	SDINA		
RUNX1-E03	gDNA	AAATICCGGGAGTGTGTCA	GAAAGGIIGAACCCAAGGAA
KUNX1-E04	gDNA	IGAICICITCCCTCCCT	CAGTIGGTCTGGGAAGGTGT
RUNX1-E05	gDNA	ATTTGAACAAGGGCCACTCA	AATGTTCTGCCAACTCCTTCA
RUNX1-E06.01	gDNA	CTCCGCAACCTCCTACTCAC	CCCACCATGGAGAACTGGTA
RUNX1-E06.02	gDNA	CCCGTTCCAAGCCAGCTC	GCTTGTCGCGAACAGGAG
RUNX1-FE01-03	cDNA	AGCATGGTGGAGGTGCTG	TGATGGCTCTGTGGTAGGTG
RUNX1-FE02-04	cDNA	TGAGCTGAGAAATGCTACCG	AAGGCAGTGGAGTGGTTCAG
RUNX1-FE03-05	cDNA	ACAAACCCACCGCAAGTC	ACAGAAGGAGAGGCAATGGA
RUNX1-FF04-06	cDNA	ATGAGGGTCAGCCCACAC	GTGAAGGCGCCTGGATAGT
TET2-E03.01	gDNA		
TET2 E02 02	4DNA		
TET2 E03.02	SDNA SDNA		
1E12-EU3.U3	gDINA DNIA		
1ET2-E03.04	gDNA	LATUILACATAAATGCCATTAACA	AGUTIGUAAATTGCTGCTG
TET2-E03.05	gDNA	GAAAATAACATCCAGGGAACCA	CCCTCTATTTTCACTTCCCTTAAA
TET2-E03.06	gDNA	GGAGTTTTAGAAGAACACCACCA	TCGACCCTTCAGAATCTCTTG

Table S1: Primer sequences used to analyze the respective genes by 454 Pyrosequencing

TET2 E02 07	(DNA	CCAATTITICGTACCAGTCCA	CONCILCTENTITICIES
TETZ-E03.07	guna	CCAATTITIGGTAGCAGTGGA	
TET2-E03.08	gDNA	TGACCTCCAAACAATACACTGG	TGAGTTTGAAAATGGCTCAGTC
TET2-E03.09	σDNA	CCCAGTGTTGAAACAGCA	ΔΩΤΤΩΩΤΩΩΔΕΤΩΩΔΕΤΤΙΩ
7572 503.40	BNA		
TET2-E03.10	gDNA	IGGIGAAAAICAGIAIICAAAAICA	CCCIGIAGAACIGAAGCIIGIIG
TET2-E03.11	gDNA	CTTCTTCACAGGTGCTTTCAAG	ATACAGGCATGTGGCTTGC
TET2 E02 12	aDNA	TTECCATAGTCAGATECACAG	CTGAAGAAGTTGTTGCTGCTCT
1112-103.12	gDINA	TIGECATAGICAGATGCACAG	CIGAAGAAGIIGIIIGCIGCICI
TET2-E03.13	gDNA	TTGACTAGACAAACCACTGCTG	TTTATGAGCCTTTACAAATTGCTG
TET2-E04	gDNA	TGGCACATTTTCTAATAGATCAGTC	CTTTGTGTGTGAAGGCTGGA
TETA FOR	-DNA		
TETZ-E05	gDNA	AAACCGITCATTICICAGGATG	GTAATGTTCTTTTTAACTGGCATGA
TET2-E06	gDNA	TGACCCTTGTTTTGTTTTGG	CGCTGAACTCTCTTCCTTTCA
TET2-E07	ØDNA	ATAGACACCTATAATATCAGCTGCAC	CAGTTTGGGAAAAACTTTGATTA
1212 200	SDIA		
TET2-E08	gDNA	CCATATATTGTGTTTGGGATTCAA	GCAGTGGTTTCAACAATTAAGAG
TET2-E09	gDNA	TGCTCTATTTTGTGTCATTCCATT	CAGTGTGAGAACAGACTCAACAG
TET2 E10.01	aDNA	CCCACCTCTACTTCACCCTCT	CCCCTCACTTTTCCTTTTC
1112-110.01	gDINA	GOGACCIGIAGIIGAGGCIGI	GOGGETGAETTTEETTTE
TET2-E10.02	gDNA	GAGTTTGGGAGTGTGGAAGC	GGGGGCAAAACCAAAATAAT
TET2-E11.01	gDNA	GCCTTCATAAAATAATCATCAACA	CTGCAGCTTGAGATGAGGTG
TET2 E11 02	@DNIA	CCANTCCACTTACTCCTTATCCA	
1612-611.02	gDNA	CLAATCLAGTTAGTCCTTATCLA	AAAACTCTGGCTATTTCCAAACC
TET2-E11.03	gDNA	CAAGCCAAGACCCTCTGTCT	GCATGAAGAGAGCTGTTGAA
TET2-E11.04	gDNA	GGTGAACATCATTCACCTTCTC	GAATTGACCCATGAGTTGGAG
TET2 E11 OF		ACACACCACCACCATTIC	AACTITCATCTCCCTCACCA
TET2-E11.05	gDNA	AGACAGCGAGCAGAGCIIIC	AAGTITCATGTGGCTCAGCA
TET2-E11.06	gDNA	AGCCCGTGAGAAAGAGGAAG	ACTGTGACCTTTCCCCACTG
TET2-EE03-04	cDNA	CACGCCAAGTCGTTATTTGA	GGACCTGCTCCTAGATGGGTA
7572 5502 06			
1E12-FE03-06	CDNA	AACAGCIGCIICIGIICICAAIAA	CCCGCACCAAACACAGTAG
TET2-FE03.07	cDNA	CCAATTTTTGGTAGCAGTGGA	CCAGCTGTGTTGTTTCTGG
TET2_EE05_07	CDNA	ΤΟΑΤΟΤΑΤΑΟΤΘΟΤΑΑΑΘΟΛΟΘΟΑΑ	ΔΟΔΤΩΟΤΟΟΔΤΩΔΔΟΟΔ
TETZ-FE03-07	CDINA		ACATOCICCATOAACAACCA
1E12-FE06-08	CUNA	GIGAGGLTGCAGTGATTGTG	TGGTGLLATAAGAGTGGACA
TET2-FE07-10	cDNA	TGGAGCATGTACTACAATGGATG	GGTTTTCCTCCAAATTCTCG
TET2_EE00_10	CDNA	ΔΤΤΟΤΟΔΘΘΘΕΤΟΔΟΤΘΟΛΤ	TGTTCTCCAGGGAGGAAAGC
1212-1203-10			
TET2-FE10-11	CDNA	AGACTTGCCGACAAAGGAAA	GGCCGTCTCATGTATGGATT
TP53-E04	gDNA	ACCTGGTCCTCTGACTGCTC	CAGGCATTGAAGTCTCATGG
	(DNA)	CACTTGTGCCCTGACTTTCA	CACTOGGATAAGATGCTGACC
TP53-E05	gdna	CACITGIGEEEIGAETTIEA	CACICGGATAAGATGCTGAGG
TP53-E06	gDNA	CAGATAGCGATGGTGAGCAG	TTGCACATCTCATGGGGTTA
TP53-E07	σΩΝΔ	GCACTGGCCTCATCTTGG	AAGAGGTCCCAAAGCCAGAG
11 55 207	SDIA		
TP53-E08	gDNA	GGACAGGTAGGACCTGATTTC	TCTCCATCCAGTGGTTTCTTC
TP53-E09	gDNA	AAAGGGGAGCCTCACCAC	TGTCTTTGAGGCATCACTGC
TDE2 E10	aDNA	CCTCTATACCTACTCAACTCCAC	CTCCCTTTCACCATCAACC
1P53-E10	gDNA	GETGTATAGGTAETIGAAGTGEAG	CIGCUITIGACCATGAAGG
TP53-E11	gDNA	AGGGAAAAGGGGCACAG	CCCCACAACAAACACCAGT
WT1-F01 01	ØDNA	TCCTCGCCGCGATCCTG	GGCGCAAAGTCCAGCAC
WT1 501 02	-DNA		
W11-E01.02	gDNA	CAGCGCIGAACGICICCA	GUILAGGLALIGUILUIL
WT1-E01.03	gDNA	GCCTCACTCCTTCATCAAAC	GGGTAAGAGCTGCGGTCA
W/T1 E02	aDNA	CONTRACTORECTICITO	TACTTOCOATCOACCOACAC
WT1-EUZ	guna	COCTOACACTOTOCITCTCT	TACTIGGGATGGAGGGAGAC
WT1-E03	gDNA	CAGGCTCAGGATCTCGTGTC	GTCTCGTGCCTCCAAGACC
WT1-E04	gDNA	TCACATCCCTTCTGCTGTGT	CTTTGAAATGGTTCAAACAGG
	0		
W/T1_E05	σDNA	ΔΤΓΤGΔΤΤΓΓΔΔΔGCCCΔΔG	TCAGTCCTAACTCCTGCATTG
WT1-E05	gDNA	ATCTGATTCCAAAGCCCAAG	TCAGTCCTAACTCCTGCATTG
WT1-E05 WT1-E06	gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA
WT1-E05 WT1-E06 WT1-E07	gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACTCTCCCTCAAGACC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC
WT1-E05 WT1-E06 WT1-E07	gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACTCTCCCTCAAGACC CGATCATCCTCTCAAGACC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC
WT1-E05 WT1-E06 WT1-E07 WT1-E08	gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACTCTCCCTCAAGACC GGATCATCCTACCTAACAAGC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC
WT1-E05 WT1-E06 WT1-E07 WT1-E08 WT1-E09	gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACTCTCCCTCAAGACC GGATCATCCTACCAAGACC CAGCATGGCAGGAAATG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAAACACATGGCTGACTCTC GCCACGCACTATTCCTTCTC
WT1-E05 WT1-E06 WT1-E07 WT1-E08 WT1-E09 WT1-F10	gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACTCTCCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E06 WT1-E07 WT1-E08 WT1-E09 WT1-E10 WT1-E10	gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCCTCCAAGACC GGATCATCCTACCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTTGATA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCC GCCACGGCACTATTCCTTCC CACCGGTATCTTGTCTGGA CACCGGACACTCCTCCCCCCCCCC
WT1-E05 WT1-E06 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01	gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTCCAAGACC GGATCATCCTACCAAGACC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACTCTCCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E06 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTCACAAGACC GGATCATCCTACCAAGACC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCGTGGTGGTGGGGGGG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAAACACATGGCTGACTCC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACTCTCCCTCAAGAGC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACAATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGATGGTGGTGGAGG CACCTGACGACATGGTTCTACAAGTGGTGATGGTGGTGGAGG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCTTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCAAGACC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAACTCTCTGAGAAAGGAGGAAAGCT	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACTCTCCTCAAGACC GGATCATCCTAACCAGAC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACAACCCTGACGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGGTGGGG ACACTGACGACATGGTTCTACAAGTGGTGGTGAGGCT ACACTGACGACATGGTTCTACAACTGAATGGTGAGTGAGCT	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACGCATATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E06 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.05 ASXL1-E13.05	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAAGTGGATGGATGTGAGTCTGGCA ACACTGACGACATGGTTCTACAAGACTGAATGTGATCTGGCA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCC GCCACGGCACTATTCCTTCC CACCGGTATCTTGTCTGGA TACGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGGCAGTAGTGTGTTCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGGACCTCGCTCCTCAT TACGGTAGCAGAGACTTGGTTCTATGAGCCACCAGCCCTCAAT TACGGTAGCAGAGACTTGGTTCTATGACCTGCGGCTCCAACA
WT1-E05 WT1-E06 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCTTAAAGTGG GCTCACTCTCCTCAAGACC GGATCATCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGGTGGTGAGG ACACTGACGACATGGTTCTACAAGTGGTGGTGGTGGGG ACACTGACGACATGGTTCTACAGACTGAATGTGAGGCAGAAAAGCT ACACTGACGACATGGTTCTACAGAACTGAATGTGAGGTCGGCA ACACTGACGACATGGTTCTACAGCAGTCCACACCTGAATCCT	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.07	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTGCTTACAGTCCC ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACACACCGTTCCACACCTGAATGCAGCA ACACTGACGACATGGTTCTACATCAGATCGAGTGGTGGGCA ACACTGACGACATGGTTCTACACCCGTCACATCGAGGTAGTCGACA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCC GCCACGGACTATTCCTTCC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.08	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCTCTAAAGTGG GCTCACCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGGTGATGGTGAGG ACACTGACGACATGGTTCTACAACTGGTGTGTGGTGAGG ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACACACTGAATGTGAGTGGAGGA ACACTGACGACATGGTTCTACACCACTGAATGTGAGTGGAACG ACACTGACGACATGGTTCTACACCACTGAATGGTGAAGGAAAAGC ACACTGACGACATGGTTCTACACCACTGAATGGTGAAGGAAAAGG ACACTGACGACATGGTTCTACACCACTGAATGGTGAAGGAAAACG ACACTGACGACATGGTTCTACACCACTGAATGATGAGGTAGTGAAACGG ACACTGACGACATGGTTCTACACACTGACTGATGGAGGTAGTGAAACGG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.08 ASXL1-E13.08	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCCTCAAGACC GGATCATCCTACCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAATCCTGAGAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAATCTCTCGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACAATCTCAAATGTGAGTCTGGCA ACACTGACGACATGGTTCTACACACCATTCACAATGTGAGTCTGGCA ACACTGACGACATGGTTCTACACGACTTCACACCGAATGCTAGGCA ACACTGACGACATGGTTCTACACGACTGCACTCCGAGGAG ACACTGACGACATGGTTCTACAACGACTGTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAAGCACTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAAGCACTGCCATCTCGAGGAG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCC GCCACGGCACTATTCCTTCC GCCACGGCACTATTCCTTCC CACCGGTAGCAGAACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAACTTGGTCTGGCAGTAGTTGTTCGC TACGGTAGCAGAAACTTGGTCTGGGGAGTTGGGAAGGCATC TACGGTAGCAGAAACTTGGTCTGTGGGCACTCGCCCTCAT TACGGTAGCAGAAACTTGGTCTGTGGGCCCCCCAAT TACGGTAGCAGAAACTTGGTCTGTCGCCCCCAAT TACGGTAGCAGAAACTTGGTCTGTCGCCCCCAACT TACGGTAGCAGAAACTTGGTCTTCAACCTGGGCCCCAACA TACGGTAGCAGAAACTTGGTCTTCAACCTGGGCCCAACA TACGGTAGCAGAAACTTGGTCTTCAATCCACCTGGACCACACGGG TACGGTAGCAGAAACTTGGTCTCTCATCACCTTGGACAGTGGG
WT1-E05 WT1-E06 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.07 ASXL1-E13.08	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCTCGCGAGACATTAAAGC ACACTGACGACATGGTTCTACAACCTCGCGAGAACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAAGTGGTGATGGAGGAAAGCT ACACTGACGACATGGTTCTACAAGTGATGTGAGTGGTGAGG ACACTGACGACATGGTTCTACAACTGAATGTGAGTGGTGAAGC ACACTGACGACATGGTTCTACAACTGAATGTGAGTGTGAAACAG ACACTGACGACATGGTTCTACAAGCGATCGCAATCCT ACACTGACGACATGGTTCTACAAGCAGTGGCAATCCT ACACTGACGACATGGTTCTACAAGCAATGGCCATCCGAGGAG ACACTGACGACATGGTTCTACAAGCGACTGTGCCAATCCT ACACTGACGACATGGTTCTACAAGCGACTGTGCCAACCGGAGG ACACTGACGACATGGTTCTACAAGCGACTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGCGATCTTCGGTGGACAAG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AACGTAACAACATGGCTGACTCTC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.08 ASXL1-E13.09 ASXL1-E13.10	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAAGACC GGATCATCCTAACCAGACC GGATCATCCTACCAAGACC CAGGCATGGCAGGACAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGGTGGTGGGGG ACACTGACGACATGGTTCTACAAGTGGTGGTGGTGGTGGGG ACACTGACGACATGGTTCTACAACTGAATGTGAAGGAGAAAAGCT ACACTGACGACATGGTTCTACACACTGAATGTGAAGGAGAAAAGCT ACACTGACGACATGGTTCTACACCACGATCCACACCTGAATCCT ACACTGACGACATGGTTCTACACGAGTCCACACCTGAATCCT ACACTGACGACATGGTTCTACATCGAATGAAGATGTAGAGTAGTGAAACAG ACACTGACGACATGGTTCTACATCGAATGATGAGGTGTGGTGAGG ACACTGACGACATGGTTCTACAACGGATCTTCGGCAGAGA ACACTGACGACATGGTTCTACAACGACTGTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAACGATCTTCGGTGGTGGTGACAAG ACACTGACGACATGGTTCTACAACGATCCTCACGTGGCACAAG ACACTGACGACATGGTTCTACAAGCATGCCTACTCGCGGGGACAAG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.11	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACAACCCTCGCAGACGTAGGG ACACTGACGACATGGTTCTACAGCACTGAATGGTGGTGAGG ACACTGACGACATGGTTCTACAGCAGTTCACACCCTGACAATGAGGCA ACACTGACGACATGGTTCTACAGCAGTTCCACACCTGAATGCAGCA ACACTGACGACATGGTTCTACAGACTGAGTGGAGGAAGCCT ACACTGACGACATGGTTCTACAGCAGTGCCACCTGAGGAGA ACACTGACGACATGGTTCTACAGCACTGGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGCACTGGCCATCTCGGGACAAG ACACTGACGACATGGTTCTACAGCACTGGCCATCTCGGGACAAG ACACTGACGACATGGTTCTACAGCATTCCTCAGTGGCCA ACACTGACGACATGGTTCTACAGCATTCCTCGGTGGACAAG ACACTGACGACATGGTTCTACAGCATTCCTACTGGTGGACAAG ACACTGACGACATGGTTCTACAGCATCCTACTGCTGGCCA ACACTGACGACATGGTTCTACAGCATTCCTACGCTGCCACGCA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGCACTAACTGCCCCCCCCCC
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.09 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCACAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGACATGACAAGG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGGTGAGGGACATTAAAGC ACACTGACGACATGGTTCTACAACTGGTGTGTGGTGAGG ACACTGACGACATGGTTCTACAACTGGTGTGAGGGAAAGGC ACACTGACGACATGGTTCTACAACTGAATGTGAGTGTGAGGGAAAGCT ACACTGACGACATGGTTCTACACCCCGAGACATGAATGTGAGTCTGGCA ACACTGACGACATGGTTCTACACGCTGCACACTGAATGTGAGTGGAAACG ACACTGACGACATGGTTCTACACGACTGCACACCTGAATCCT ACACTGACGACATGGTTCTACACGAATGGTGCAACGGTAGGGAAACGG ACACTGACGACATGGTTCTACAGCAGTTCCCACGTGGGACAAG ACACTGACGACATGGTTCTACAGAACTGACTGCGGGGACAAG ACACTGACGACATGGTTCTACAGAACTGCCCTCGGGGACAAG ACACTGACGACATGGTTCTACAGAATCCCTGCTGGGCA ACACTGACGACATGGTTCTACAGAATCCCTGGTGGACAAG ACACTGACGACATGGTTCTACAGAATTCCCTACGCTGGCCA ACACTGACGACATGGTTCTACACAGTCCCCGCTGCCCCA ACACTGACGACATGGTTCTACACAGTGCCCGCTCCCAGGCCA ACACTGACGACATGGTTCTACACAGCAGTCCCCACGTAGCCAG ACACTGACGACATGGTTCTACACAGCAGTCCCACGTAGCCACGAGGCCAAG ACACTGACGACATGGTTCTACACGACTGCCCACGCTACGCAGGCCA ACACTGACGACATGGTTCTACACAGCGCAGTCCCACGCTACGCAGGCCA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTCTAACTTCCTGCC AAACTAAACACATGGCTGACTCC GCCACGACTATTCCTTCC CACCGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGCAGTGGTGGTGGTCGCC TACGGTAGCAGAGACTTGGTCTGGCGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGGCCTTGCTCCAT TACGGTAGCAGAGACTTGGTCTGTGGGCCCTCAACA TACGGTAGCAGAGACTTGGTCTTCCACCTGGCCCAACA TACGGTAGCAGAGACTTGGTCTTCAGCTTTCAACGTTGCCCCTAT TACGGTAGCAGAGACTTGGTCTCCATCCTTCCACCTGCCCCTAT TACGGTAGCAGAGACTTGGTCTCCACCTGGGCCTAACA TACGGTAGCAGAGACTTGGTCTCCACCTGCTCCACCT TACGGTAGCAGAGACTTGGTCTCCACCTGGGCTCAACA TACGGTAGCAGAGACTTGGTCTCCACCACGGGCTAGCCT TACGGTAGCAGAGACTTGGTCTCCACCACGGGCTAGCGG TACGGTAGCAGAGACTTGGTCTCCATCACCTGGCCCACGG TACGGTAGCAGAGACTTGGTCTCCATCACCATGCCACTGTT TACGGTAGCAGAGACTTGGTCTCCATCCACTGCACCATGCCACTGTT TACGGTAGCAGAGACTTGGTCTCCATCACCATGCCACTGTT TACGGTAGCAGAGACTTGGTCTCCATCACCATGCCACTGTT TACGGTAGCAGAGACTTGGTCTCCATTCCACTTCCAGTTCCAGGG TACGGTAGCAGAGACTTGGTCTCCATTCCCATGCCCAGAGG TACGGTAGCAGAGACTTGGTCTCCATCCACTGCACGGTTAGTGGC
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGAGTAGTGGTGGTGAGG ACACTGACGACATGGTTCTACAATCCTCGCGAGACATTAAAGC ACACTGACGACATGGTTCTACAATCCTCGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAATGGAGGTAGTGGGA ACACTGACGACATGGTTCTACATCCGAATGATGGAGGTAGTGGAA ACACTGACGACATGGTTCTACACACGATTGCACTCTGAGGAGA ACACTGACGACATGGTTCTACAGACTGGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGGCCATCTCGAGGAGA ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGACA ACACTGACGACATGGTTCTACAGACTGCCCACTCTGCGGGACAAG ACACTGACGACATGGTTCTACAGAGTCCCTACTGCTGGCCA ACACTGACGACATGGTTCTACACAGTGCCCGCTACGCAGCA ACACTGACGACATGGTTCTACACAGGCATCCCTACTGCTAGCACT ACACTGACGACATGGTTCTACACAGGCATCCCTACGCAGCATG ACACTGACGACATGGTTCTACACAGGCATCCCTACGCAGCATG ACACTGACGACATGGTTCTACAGGCATCCCTACTGCTAGCCA ACACTGACGACATGGTTCTACACACTGCCTACCGCAGCTACCCAAGTTTGCACACT ACACTGACGACATGGTTCTACACACTGCCTACCGCAAGCTTCGCACAGCACTGCCAACTGCTACCGCACTGCCACACTGCTACCGCACTGCCACGCACTGCCACACTGGCCACCTGCCACGCACTGCCCACGCACG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGGAACTAAAGGGCCGGTA AGCAGACTAAAGGCCGGCTA AGCAGACACTGGCTGACTCC GCCACGGCACTATTCCTTCC CACCGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTTCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGCACTCGCCCTAAT TACGGTAGCAGAGACTTGGTCTGTGGGCCCCCAAT TACGGTAGCAGAGACTTGGTCTGTCGCCCCCAACT TACGGTAGCAGAGACTTGGTCTCATCCACCTGGGGCCCCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGGGCCCCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGACCACAGCCCCTAAT TACGGTAGCAGAGACTTGGTCTCATCACCTGGAGCCCCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGAGCACAGTGGG TACGGTAGCAGAGACTTGGTCCCCATCACCACCGCCCTAT TACGGTAGCAGAGACTTGGTCCCATCACCACCGGGGTTAGTGGC TACGGTAGCAGAGACTTGGTCCCCATCACCACCACCCTGCTCCCATTT TACGGTAGCAGAGACTTGGTCTCCATTCCCCATTCCCCAGGGG TACGGTAGCAGAGACTTGGTCTCCATTCCCCACCAGCCACAGGGG TACGGTAGCAGAGACTTGGTCTCCATTCCCCACCAGCCACAGGGG TACGGTAGCAGAGACTTGGTCTCCATTCCCACCAGCCACTGGTC TACGGTAGCAGAGACTTGGTCTCCATTCCCCACCAGCCACAGGGG TACGGTAGCAGAGACTTGGTCTCCCATTCCCCACCAGCCACTGGG TACGGTAGCAGAGACTTGGTCTCCCATTCCCCACCAGCCACAGGGG TACGGTAGCAGAGACTTGGTCTCCCATTCCCCACCAGCCACAGGGG TACGGTAGCAGAGACTTGGTCTCCCATTCCCCACCAGCCACAGGGG TACGGTAGCAGAGACTTGGTCTCCCATTCCCCACCAGCCACTGGC TACGGTAGCAGAGACTTGGTCTCCCATTCCCCACCAGCCACAGGGG TACGGTAGCAGAGACTTGGTCCCCCATTCCCCACCAGCCACTGGGC TACGGTAGCCAGAGACTTGGTCCCCCCCCACACGCACTGGC
WT1-E05 WT1-E06 WT1-E07 WT1-E07 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.08 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.12 ASXL1-E13.13	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCTCGCGAGACATTAAAGC ACACTGACGACATGGTTCTACAACGTGGTGATGGTGAGG ACACTGACGACATGGTTCTACAACTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAACTGCATGATGTGATGGTGAGG ACACTGACGACATGGTTCTACAACTGCATGATGTGATGGTGAGG ACACTGACGACATGGTTCTACAACTGCATGAATGTGAGTCTGGCA ACACTGACGACATGGTTCTACAGACTGAATGTGAGTGTGAAACAG ACACTGACGACATGGTTCTACAGACTGAATGCAGTGTGAAACAG ACACTGACGACATGGTTCTACAGCAGTTCCCCACTCGAGGAG ACACTGACGACATGGTTCTACAGGACTGTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGGACTGTCGCCATCTCGAGGAC ACACTGACGACATGGTTCTACAGGACTCTCCGATGGACAAG ACACTGACGACATGGTTCTACAGACTGCCCCTCCCGAGGAC ACACTGACGACATGGTTCTACAGGACTCTCCCGATGGACAAG ACACTGACGACATGGTTCTACAGGACTCTCCCAGTGCCA ACACTGACGACATGGTTCTACAGGCCAGTCCCCAGTG ACACTGACGACATGGTTCTACAGGCCAGTCCCCAGTTTGGACT ACACTGACGACATGGTTCTACAGCCCAGGAGATCTTACTACCT	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AACCTAAACAATGGCTGACTCTC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.04 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGAGAAGGTGAGG ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAATGTGAGTCTGGCA ACACTGACGACATGGTTCTACAGCGTTCCACACCTGAAGGAGAAACG ACACTGACGACATGGTTCTACAGACTGACTGAGGTAGTGAAACG ACACTGACGACATGGTTCTACAGACTGACGACTGCAGGACAACG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTGCTGCCGCA ACACTGACGACATGGTTCTACAGGCATCGCTACGCAGCA ACACTGACGACATGGTTCTACAGGCATCGCCTACGCAGC ACACTGACGACATGGTTCTACAGGCATCGCCTAGCAAG ACACTGACGACATGGTTCTACAGGCATCGCCAAGTTTTGACT ACACTGACGACATGGTTCTACAGCCCCGGAGAGCTCTACTACCAC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTGCTTACTTTCCATCC AACGTAAACACATGGCTGACTCTC GCCACGGCACTATTCCTTCC GCCACGGACATATCCTTCTC CACCGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCGTGGTGGTGGCCCTCAT TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGCAGTAGTTGGTCCCCCAT TACGGTAGCAGAGACTTGGTCTGTGGGCACCCCCAAT TACGGTAGCAGAGACTTGGTCTGTGGCCCCCAAT TACGGTAGCAGAGACTTGGTCTTCATCACCTGGGCCCCAACA TACGGTAGCAGAGACTTGGTCTTCATCACCTGGGCGCCAACA TACGGTAGCAGAGACTTGGTCTCATCACACTGGCGCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCATGGCGCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGACCAAGGCGC TACGGTAGCAGAGACTTGGTCTCCATCACCAGCGCCCTAAT TACGGTAGCAGAGACTTGGTCTCCATCACCAGCGGGTTAGTGGC TACGGTAGCAGAGACTTGGTCTCCATCACCAAGCGAGTTGGTGCC TACGGTAGCAGAGACTTGGTCTCCCATTCTCCCAGTTCCTAGAGG TACGGTAGCAGAGACTTGGTCTCCCATTCTCCCAGTTCCTAGAGG TACGGTAGCAGAGACTTGGTCTCCCATTCTCCCAGTTGCTCGG TACGGTAGCAGAGACTTGGTCTCCATTCCCCGTGGACCAAAGGAG TACGGTAGCAGAGACTTGGTCTCAGCCAGGGTTGGC TACGGTAGCAGAGACTTGGTCTCAGCCAGGGTTGGGC TACGGTAGCAGAGACTTGGTCTAGCCAGGGTTGGCTGGC TACGGTAGCAGAGACTTGGTCTACGCCACTGGACCTAAAGGGTTGGCGC TACGGTAGCAGAGACTTGGTCTACCCAGGGTTGGGCTTGGC TACGGTAGCAGAGACTTGGTCTACCCCAGGAGTTGGTCTGG TACGGTAGCAGAGACTTGGTCTACCCCAGGAGTTGGCTTGGC TACGGTAGCAGAGACTTGGTCTACCCAGGAGTTGGCTTGGCTTGGC
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.08 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.14 ASXL1-E13.14	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCTCGCAGAAGGGAAAGCT ACACTGACGACATGGTTCTACAACTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAACTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAACTCGAATGATGTGATG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAACTAAAGGGCCGGTA AGCAACTAAACGACACATGGCTGACTCC GCCACGCACTATTCCTTCC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.08 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.11 ASXL1-E13.13 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGGCAGACATTAAAGC ACACTGACGACATGGTTCTACAATCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAATCCTCGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACACACGTTCCACACCTGAATGCTGGCA ACACTGACGACATGGTTCTACAGCAGTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGCAGTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGCGCGCTCCCAAGTTTGACT ACACTGACGACATGGTTCTACAGCCGCCGAGGCACTCCAAGTTTGCCT ACACTGACGACATGGTTCTACAGCCGCCGAGGCCCAAGTTTACTACCT ACACTGACGACATGGTTCTACAGCCCGCGAGGACTTTACTACCT ACACTGACGACATGGTTCTACAGCTTGGCCAGGGAATGTGG ACACTGACGACATGGTTCTACAGCTCGCCGAGGGAATGTGG ACACTGACGACATGGTTCTACAGCCCCGGAGGCCCAAGTTTACTACCT ACACTGACGACATGGTTCTACAGCCCCGGAGCCCCAAGCTCAAGAA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTACTAAAGGGCCGGTA AGCAGTACTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACCGACTATTCCTTCTC CACCGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGCAGCGAGTGGTGACCTCACA TACGGTAGCAGAGACTTGGTCTGTGGGCCCTCACA TACGGTAGCAGAGACTTGGTCTTCACCACTGGGCCCACAC TACGGTAGCAGAGACTTGGTCTCCACCTGGGCCCACAC TACGGTAGCAGAGACTTGGTCTCCACCTGGGCCCACAC TACGGTAGCAGAGACTTGGTCTCCACCTGGGCCCACAC TACGGTAGCAGAGACTTGGTCTCCACCTGGGCCCACCA TACGGTAGCAGAGACTTGGTCTCCACCTGGGCCCACCT TACGGTAGCAGAGACTTGGTCTCCACCTGCACCATGGCC TACGGTAGCAGAGACTTGGTCTCCATCACCATGCCACCTGTT TACGGTAGCAGAGACTTGGTCTCCATCACCATGCCACCTGTT TACGGTAGCAGAGACTTGGTCTCCATCTGGACCATGGC TACGGTAGCAGAGACTTGGTCTCACCACGGGCCACAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCACGGACCAAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCCGGCACAAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCCGGACCAAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCCGAGAGCTTGGCCTGGACCATGGCCTTGGCCTGGGCTAGCAGGAGCACTGGTCTCAGCCACGAGGACTTGGTCTCGGGCCACAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCACGTAGCTTGGCTTGGC TACGGTAGCAGAGACTTGGTCTAGCCCCAGTAGCACTTGGCTTGGCCACAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCACGAGACTTGGCTTAGCCCCGC TACGGTAGCAGAGACTTGGTCTAGCCCCAGTAGCTTCCGG TACGGTAGCAGAGACTTGGTCTAGCCCCAGTAGCTTCCGG TACGGTAGCAGAGACTTGGTCTAGCCCCCCATAAAAGGCG TACGGTAGCAGAGACTTGGTCTAGCCCCCCCTTGGACAATGCCTGGC TACGGTAGCAGAGACTTGGTCTAGCCCCCCCCTTGGACAATGCCTGG TACGGTAGCAGAGACTTGGTCTAGCCCCCGC
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.09 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.11 ASXL1-E13.13 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTGGTGATGGTGGAGG ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAAGTGGTGATGGAGGCA ACACTGACGACATGGTTCTACAGCAGTTCCACACCTGAATGCAGC ACACTGACGACATGGTTCTACAGACTGAGTGGGAGCA ACACTGACGACATGGTTCTACAGACTGAGTGGGACAACG ACACTGACGACATGGTTCTACAGACTGAGTGGGACAAG ACACTGACGACATGGTTCTACAGCAGTGCCCACCTGAGGAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTCGCTGCCCA ACACTGACGACATGGTTCTACAAGGATCTCGCTGCCACGCT ACACTGACGACATGGTTCTACAGCCCAGGAGCTCTACGCATG ACACTGACGACATGGTTCTACAGCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGCCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAAGCCCCGGAGAGTCTTACTACCT ACACTGACGACATGGTTCTACAGCCCCGGAGAGTCTTACTACCT ACACTGACGACATGGTTCTACAAGCCCCGGAGCTCCAAGGG ACACTGACGACATGGTTCTACAAGCCCCGGAGCTCAGGAACTGG ACACTGACGACATGGTTCTACAGCCCCGGAGGGCTCAAGAA ACACTGACGACATGGTTCTACAGCTCTGCTGGGAACAAG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGCACTAACGGCCGGTA AGCAGCACATGCTCCC GCCACGCACTATTCCTTCC CACCGGTATCTTGTCTGGA TACGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTGGTGGCGCAGTC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCCTCAT TACGGTAGCAGAGACTTGGTCTGTGGGCAGTCGGCGCACACA TACGGTAGCAGAGACTTGGTCTGCGCAGTAGTGGCAGCCCTAAT TACGGTAGCAGAGACTTGGTCTATCAGCCACCAAGCCCTAAT TACGGTAGCAGAGACTTGGTCTCATCACCATGGCACACA TACGGTAGCAGAGACTTGGTCTCATCACCATGGCCCTCAT TACGGTAGCAGAGACTTGGTCTCATCACCATGGACCACCACCT TACGGTAGCAGAGACTTGGTCTCATCACCATGGCCCTCGT TACGGTAGCAGAGACTTGGTCTCATCACCATGCCACTGGT TACGGTAGCAGAGACTTGGTCTCATCACCATGCCACTGGT TACGGTAGCAGAGACTTGGTCTCATCACCATGCACCTGGT TACGGTAGCAGAGACTTGGTCTCAGCACTGGACCAAAGGGG TACGGTAGCAGAGACTTGGTCTTCGCTCTGGACCAAAGGAG TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGGC TACGGTAGCAGAGACTTGGTCTAGCACAGGAGTTGTGCTGG TACGGTAGCAGAGACTTGGTCTAGCACAGGAGTTGTGCTGG TACGGTAGCAGAGACTTGGTCTAGCCACAGGAGTTGTGCTGG TACGGTAGCAGAGACTTGGTCTAGCCACAGGAGTTGTGCTGG TACGGTAGCAGAGACTTGGTCTAGCCACAGGAGTTGTGCTGG TACGGTAGCAGAGACTTGGTCTAGCCAGAGCTTGGCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.17	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGGTGTGTGGTGAGG ACACTGACGACATGGTTCTACAACTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAACTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAACTGGATGATGGTGGTGAGG ACACTGACGACATGGTTCTACAACTGGATGATGGTGGTGAGG ACACTGACGACATGGTTCTACAACTGCAGAATGGAGAGAGA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTCTAACTCGCGGTA AGCAGTGCTTACTTTCCATCC AAACTAAACACATGGCTGACTCTC GCCACCGACTATTCCTTCTC CACCGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGCGCAGTAGTTGGTGTCGC TACGGTAGCAGAGACTTGGTCTGGCGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGGCCTTGCTCCAT TACGGTAGCAGAGACTTGGTCTGTGGGGCCTTGCTCAT TACGGTAGCAGAGACTTGGTCTGTGGGCCACCAAGCCCTAAT TACGGTAGCAGAGACTTGGTCTGTGGGCTTTCCAACCTGGCCACACA TACGGTAGCAGAGACTTGGTCTCACCACGGGGCTAACA TACGGTAGCAGAGACTTGGTCTCCATCCACCTGGCCCACCA TACGGTAGCAGAGACTTGGTCTCCATCCACCTGGCCCACCA TACGGTAGCAGAGACTTGGTCTCCATCACCTGGGCTCACCA TACGGTAGCAGAGACTTGGTCTCCATCACCTGGGCTAACA TACGGTAGCAGAGACTTGGTCTCCATCACCTGGCCACGGG TACGGTAGCAGAGACTTGGTCTCCATCACCATGCCACTGTT TACGGTAGCAGAGACTTGGTCTCCATCACCATGCCACTGTT TACGGTAGCAGAGACTTGGTCTCCATACACATGGACTTGGTCTGCGC TACGGTAGCAGAGACTTGGTCTAGCCCCAGTAGCTTGCTT
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.17 DNMT2a.E02	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGATTGTGGTGGAGG ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAATCCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAGCAGTTCACACCGATGCAGGA ACACTGACGACATGGTTCTACAGCAGTTCCACACCTGAAGGAGAAACAG ACACTGACGACATGGTTCTACAGCAGTGCCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGCAGTGCCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGGTCCCACCTGAGGAG ACACTGACGACATGGTTCTACAGACTGGCCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGGCCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCCACGCTGCCAAG ACACTGACGACATGGTTCTACAGCTGCCCCACGCAG ACACTGACGACATGGTTCTACAGCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGCCCAGGAGGCTCAGGGG ACACTGACGACATGGTTCTACAGCTAGGCTGCTGGGAAACAG ACACTGACGACATGGTTCTACAGCCAGGAGGCTCAGTGGG ACACTGACGACATGGTTCTACAGCAAAGGCTCTGGGAAACAG ACACTGACGACATGGTTCTACAGGCAGGCTCAGGAGA ACACTGACGACATGGTTCTACAGGCAAGGGCTCAGTGGG ACACTGACGACATGGTTCTACAGCAAACTTTGGTGCGAGCCC ACACTGACGACATGGTTCTACAGCAAACTTTGGTGCGAGCCC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACACATGGCTGACTCC GCCACGGCACTATTCCTTCC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.08 ASXL1-E13.08 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.11 ASXL1-E13.11 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCTCGCAGAACATTAAAGC ACACTGACGACATGGTTCTACAACCTCGCAGAACATTAAAGC ACACTGACGACATGGTTCTACAACGTGGTGATGGTGAGG ACACTGACGACATGGTTCTACAACTGGTGATGGAGGAAAGCT ACACTGACGACATGGTTCTACAAGCTGATGTGAGTGGTGAGG ACACTGACGACATGGTTCTACAAGCTGATGTGAGTGGAAACAG ACACTGACGACATGGTTCTACAAGCAGTGCCAATCCT ACACTGACGACATGGTTCTACAAGCAGTGCCAATCCT ACACTGACGACATGGTTCTACAAGGACTGTGCAATCCT ACACTGACGACATGGTTCTACAAGGATCTTGGGTGACAAG ACACTGACGACATGGTTCTACAAGGATCTTGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTCGCTGCCAA ACACTGACGACATGGTTCTACAAGGCAGTCCCAAGCAT ACACTGACGACATGGTTCTACAGCCAGGCCAAGCATG ACACTGACGACATGGTTCTACAGCCAGGCCAAGCATGGTACTACGCT ACACTGACGACATGGTTCTACAGCCAGGCCAAGCATGGT ACACTGACGACATGGTTCTACAATTGGCCGCGCAAGAA ACACTGACGACATGGTTCTACAATTGGCCGGCGCAAGGA ACACTGACGACATGGTTCTACAATTGGCCAGGCCCAAGAA ACACTGACGACATGGTTCTACAGCCCAGGAGGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGCCAGGAAGGGCCCAAGAA ACACTGACGACATGGTTCTACAGCACACTGGTGCAAGAA ACACTGACGACATGGTTCTACAGCCAGGAAGGGCCCACGTGAG ACACTGACGACATGGTTCTACAGCCAAGGAGCCCCAGTGAG ACACTGACGACATGGTTCTACAGCCACGCACAGGGCCCAGTGAG ACACTGACGACATGGTTCTACAGCCACGCACAGGGCCCACTGGAGAACGCC ACACTGACGACATGGTTCTACACCCCACGAACTTTGGTGCAGCC ACACTGACGACATGGTTCTACAGCCACGCACGCCAGTGAG ACACTGACGACATGGTTCTACAGCCACGCCAGGCCCAGTGAG ACACTGACGACATGGTTCTACAGCCACGCACGCCCAGTGAG ACACTGACGACATGGTTCTACACCCCCCACTGAGCCCAGTGAG ACACTGACGACATGGTTCTACACCCCCCCCCCCCCCCCC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGCACACATGGCTGACTCC GCCACGCACTATTCCTTCC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.04 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E03	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTGGTGTGAGG ACACTGACGACATGGTTCTACAATCCTCGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACACACCGTTCCACACCTGAAGGAGAAAGCT ACACTGACGACATGGTTCTACAGCGATGTGCAGTCTGGCA ACACTGACGACATGGTTCTACAGCGATGCCACCTGAGGAGAACAG ACACTGACGACATGGTTCTACAGACTGACGTGCACATCCTAGAGGAGAACAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGGCATCCCTACTGCTGCCA ACACTGACGACATGGTTCTACAGGCATCCCCAAGTTTTGACT ACACTGACGACATGGTTCTACAGGCATCCCCAGGAGTCTTACTACCT ACACTGACGACATGGTTCTACAGGCATGCCCAGGGATGTGGG ACACTGACGACATGGTTCTACAGGCAAGCCCCAGGGATGTGGG ACACTGACGACATGGTTCTACAGGCAAGCCCCGGAGGGCTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCCCGGGGCTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCCCAGGGCTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCCCGGGCTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCTCTGCGGAGGCC ACACTGACGACATGGTTCTACAGGCAAACTTTGGTGCGAGCC ACACTGACGACATGGTTCTACAGGCAAACTTTGGTGCGAGCC ACACTGACGACATGGTTCTACAGCAAACTTTGGTGCGAGCC ACACTGACGACATGGTTCTACAGCAAACTTTGGTGCGAGCC ACACTGACGACATGGTTCTACAGCAAACTTTGGTGCGAGCC ACACTGACGACATGGTTCTACAGCAAACTTTGGTCGCAGCC ACACTGACGACATGGTTCTACAGCAAACTTTGGTCGCAGCC ACACTGACGACATGGTTCTACACACACGCAAGCGCCCACTGATGTGCTACCACCACTGACGACATGGTTCTACACACGACATGGTCTACACCACTGACTCTTCTCCC ACACTGACGACATGGTTCTACACACACGCACGACTCTTCTCTCCC ACACTGACGACATGGTTCTACACACACGACGCCGGAATGCTACAC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTCTAACGGCCGGTA AGCAGTGCTTACTTTCCATCC AACCTAAACACATGGCTGACTCC GCCACGGCACTATTCCTTCC CACCGGAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCAGTAGTGGTGTCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGCACTAGTGTGTCGC TACGGTAGCAGAGACTTGGTCTGTGGGCCACCAGAGCCCTAAT TACGGTAGCAGAGACTTGGTCTGTGGGCCCCCAAT TACGGTAGCAGAGACTTGGTCTCATCACCTGGGGCTCAACA TACGGTAGCAGAGACTTGGTCTCTATCACCTTGGACCAAGCCCTAAT TACGGTAGCAGAGACTTGGTCTCTATCACCTTGGACCAGGGG TACGGTAGCAGAGACTTGGTCTCATCACCAGGGGTTAGTGGC TACGGTAGCAGAGACTTGGTCTCCATTCATCCACTGGACCATGGGG TACGGTAGCAGAGACTTGGTCTCCATTCACCCTGGACCAAGGGG TACGGTAGCAGAGACTTGGTCTCCATTCCCCGTGCCACAGGGG TACGGTAGCAGAGACTTGGTCTCCCATTCTCCCAGTTCCTAGAGG TACGGTAGCAGAGACTTGGTCTCAGCATGGACTAAGGGGTTGGC TACGGTAGCAGAGACTTGGTCTAGCCACGAGGAGTTGGTCTGG TACGGTAGCAGAGACTTGGTCTAGCCACGACAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCACTAAAATGCCTGC TACGGTAGCAGAGACTTGGTCTAGCCCACTAAAATGCCTGC TACGGTAGCAGAGACTTGGTCTAGCTCCCCATAAAATGCCTGC TACGGTAGCAGAGACTTGGTCTAGCTCCCCATAAAATGCCTGC TACGGTAGCAGAGACTTGGTCTAGCTCCCCATAAAATGCCACG TACGGTAGCAGAGACTTGGTCTAGCTCCACTTATCAAAATACCAACA TACGGTAGCAGAGACTTGGTCTAGCTCACTCACTATACAAAATACCAACA TACGGTAGCAGAGACTTGGTCTAGCTCACTCACATAGGG TACGGTAGCAGAGACTTGGTCTAGCTCACTCACATAGGG TACGGTAGCAGAGACTTGGTCTAGCTCACTCACTATACAAAATACCAACA
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E09 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.05 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.08 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E03 DNMT3A-E04	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAACTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAAGCTGATGTGAGTGGTGAGG ACACTGACGACATGGTTCTACAAGACTGAATGTGAGTGTGAAACAG ACACTGACGACATGGTTCTACAAGCAGTGTGCAATCCTT ACACTGACGACATGGTTCTACAAGGACTGTGCCAATCCTGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGCCATCCGAGGAG ACACTGACGACATGGTTCTACAAGGATGTTGGCCATCCTGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGCCAATCCTGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGCTGCTGCCA ACACTGACGACATGGTTCTACAAGGCATCTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGCAGTCCCAAGCTT ACACTGACGACATGGTTCTACAAGGCAGTCCCAAGCTT ACACTGACGACATGGTTCTACAAGGCAGCCCCAAGTTTACTACCT ACACTGACGACATGGTTCTACATGGCCCCGGCAAGAA ACACTGACGACATGGTTCTACAGCCCAGGAGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGCCCAGGAGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGCCAGGAGGGCCCAAGAA ACACTGACGACATGGTTCTACAGCCACGACAGGGCCCAAGGAA ACACTGACGACATGGTTCTACAGCCAAGGGCCCAGTGAG ACACTGACGACATGGTTCTACAGCCACGACAGGGCCCAGGGAA ACACTGACGACATGGTTCTACAGCCACGCAGGGCCCAGTGAG ACACTGACGACATGGTTCTACAGCCACGCAGGGCCCAGTGAG ACACTGACGACATGGTTCTACACCCACCGACGAAGGCCCCACGCA ACACTGACGACATGGTTCTACACCCACCACGAACTTTGGTGCAAGCC ACACTGACGACATGGTTCTACAACACGCCAGGAACGCTCACGAAGCCACCACGACATGGTTCTACACGCCACGACGCCAACGACCTGGTCTACACAGGCCTGGAAGGCCCACGCAACGCTAGGACGACACGCACATGGTTCTACAAGGCCAGGCTGAACGCAACGCAACGCTCAACGAA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAACTAAAGGGCCGGTA AGCAACTAAACACATGGCTGACTCC GCCACGCACTATTCCTTCC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E03 DNMT3A-E04 DNMT3A-E04	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGAGAAGGTGAGG ACACTGACGACATGGTTCTACAATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAGCATTCCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACAGCATTGCCATCTGAGGAGAACGA ACACTGACGACATGGTTCTACAGACTGTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGGCATCGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGGCATCCCTACTGCTGCCCA ACACTGACGACATGGTTCTACAGGCATCCCTACGCTGCCAAG ACACTGACGACATGGTTCTACAGGCATCCCCAAGTTTTGACT ACACTGACGACATGGTTCTACAGGCATCCCCAGGAGCTCTACAGCA ACACTGACGACATGGTTCTACAGGCATCCCGAGGCTCAAGAA ACACTGACGACATGGTTCTACAGGCATCCCTGGGAGCTAAGAA ACACTGACGACATGGTTCTACAGGGAAGGCCCCAGGAAGA ACACTGACGACATGGTTCTACAGGCAAGCCCGGGAGCTCAAGAA ACACTGACGACATGGTTCTACAGGCAACTTTGGCTCGCGAGG ACACTGACGACATGGTTCTACAGGCAAGCCTCAGGAGAACTGGG ACACTGACGACATGGTTCTACAGGCAAGCGCCCAGGAGCTCAGGAA ACACTGACGACATGGTTCTACAGGCAAACTTTGGTCCTGGGAGGCC ACACTGACGACATGGTTCTACAGGCAAACTTTGGTGCGAGCC ACACTGACGACATGGTTCTACAGCAAACTTGGGCCAAGCC ACACTGACGACATGGTTCTACAACAGGCCCGGAATGCTCACA ACACTGACGACATGGTTCTACAACAGGCCCGGAATGCTCACA ACACTGACGACATGGTTCTACAACAGGCCCGGAATGCTCACAC ACACTGACGACATGGTTCTACAACAGGCCCGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCCTGGAATGCTACAC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGCTA AGCAGACTACCTCC GCCACGGCACTATTCCTTCC GCCCGGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E100 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.03 ASXL1-E13.05 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.15 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E03 DNMT3A-E03 DNMT3A-E05 DNMT3A-E05	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTGGCTGAGG ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAAGTGGTGATGGAGGCA ACACTGACGACATGGTTCTACAGACTGAATGAGGTAGTGGAGA ACACTGACGACATGGTTCTACAGACTGAATGAGGTAGTGAAACAG ACACTGACGACATGGTTCTACAGACTGAGTGGCCATCTCGAGGAGA ACACTGACGACATGGTTCTACAGACTGGACCTCTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGCATCTCGGTGGACAAG ACACTGACGACATGGTTCTACAGGCAGTCCCAACGCTG ACACTGACGACATGGTTCTACAGGCAGTCCCAGCATGG ACACTGACGACATGGTTCTACAGGCAGTCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGCCCAGGAGACTCTTACTACCT ACACTGACGACATGGTTCTACAGGCAGCCCCAAGGATGTGG ACACTGACGACATGGTTCTACAGGCAGCTCCGGACAGGG ACACTGACGACATGGTTCTACAGGCAGGCCCAAGTGGG ACACTGACGACATGGTTCTACAGGCAGGGCCTCAGTGGA ACACTGACGACATGGTTCTACAGCAAACTTGGTGCGAGCC ACACTGACGACATGGTTCTACAGCAAACTTGGTGCGAGCC ACACTGACGACATGGTTCTACAGGCAAGGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGGCAAGGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGGCAAGGGCCTCAGTGAA ACACTGACGACATGGTTCTACAGGCAAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAGGCCAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAAGGCCAGGCCTGAATGCTACAC ACACTGACGACATGGTTCTACAAGGCCAGCTGAATGCTACAC ACACTGACGACATGGTTCTACAAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAAGGCCAGGCCTGGAATGCTACAC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACATGGCTGACTCC GCCACGGCACTATTCCTTCC CACCGGTATCTTGTCTGGGA TACGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTGGTGGCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCCTCAT TACGGTAGCAGAGACTTGGTCTGTGGGGTCTGGCGCCTAAT TACGGTAGCAGAGACTTGGTCTGCACTGGGCGCCAACA TACGGTAGCAGAGACTTGGTCTATCAGCCTTGCACCAACCA
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E03 DNMT3A-E05 DNMT3A-E05 DNMT3A-E06	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTITGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGGCAGACATTAAAGC ACACTGACGACATGGTTCTACAATCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAATCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACACACGTTCCACACCTGAATCTGAGGACA ACACTGACGACATGGTTCTACAGCATTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGCATTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCAACTTGCAGCTGCCA ACACTGACGACATGGTTCTACAGCAGCGCTCCCAAGTTTTGACT ACACTGACGACATGGTTCTACAGCAGCCCCGAGGCTCATGG ACACTGACGACATGGTTCTACAGCCAGCGAGCCTCAGAGA ACACTGACGACATGGTTCTACAGCATTGGCCAGGGCTCATGG ACACTGACGACATGGTTCTACAGCCAGGGACTCCTAGGAA ACACTGACGACATGGTTCTACAGCCCAGGAGCTCATGG ACACTGACGACATGGTTCTACAGCCAGGGACTCCTAGGAA ACACTGACGACATGGTTCTACAGCCAGGGACTCCTAGGA ACACTGACGACATGGTTCTACAGCCAACTTGGCGAAGCGTCAGGAA ACACTGACGACATGGTTCTACAGCCAACTTGGTGCGAAGCC ACACTGACGACATGGTTCTACAGCCAACTTGGTGCGAAGCC ACACTGACGACATGGTTCTACAGCCAACTTGGTGCGAAGCC ACACTGACGACATGGTTCTACAGCCAACTTGGTGCGAAGCC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAACAGGCCTAGTGAA ACACTGACGACATGGTTCTACAACAACAGGCCTAGTGAACACA ACACTGACGACATGGTTCTACAACAACAGGCCTAGTGAACACA ACACTGACGACATGGTTCTACAACAACAGGCCTAAGCCACACACA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGTCTAACTCGCGGTA AGCAGTGCTTACTTTCCATCC GCCACGATATTCCTTCC GCCACGACTATTCCTTCTC CACCGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGGCTCTGCTCCAT TACGGTAGCAGAGACTTGGTCTGTGGGGCCTTGCTCCAT TACGGTAGCAGAGACTTGGTCTGTGGGCCACCAAGCCCTAACA TACGGTAGCAGAGACTTGGTCTCATCACCAGGGGCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCATGGCCTACCA TACGGTAGCAGAGACTTGGTCTCATCACCATGGGCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTTGCACCTGGGC TACGGTAGCAGAGACTTGGTCTCATCACCATGGCCTACCA TACGGTAGCAGAGACTTGGTCTCATCACCATGGGGTTAGTGGC TACGGTAGCAGAGACTTGGTCTCATCACCATGCACATGGG TACGGTAGCAGAGACTTGGTCTCATCACCATGCACATGGG TACGGTAGCAGAGACTTGGTCTCATCACCATGCACATGGG TACGGTAGCAGAGACTTGGTCTAGCACATGGAGTTTGTCCAGGG TACGGTAGCAGAGACTTGGTCTAGCCCAGAGACTTGGTCTGGCCTGGACCAAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCAGTAGCTTCCTGT TACGGTAGCAGAGACTTGGTCTAGCCCAGTAGCTTCCTGG TACGGTAGCAGAGACTTGGTCTAGCCCAGTAGCTTCCTGT TACGGTAGCAGAGACTTGGTCTAGCCCAGTAGCTTCCTGCT TACGGTAGCAGAGACTTGGTCTAGCCCAGTAGCTTCCTGCTGCATACAATACACACA TACGGTAGCAGAGACTTGGTCTGGCTGCATAAAATCCCCGCTGCA TACGGTAGCAGAGACTTGGTCTGGGCTGCATCACAATAGGG TACGGTAGCAGAGACTTGGTCTGGGCTGCATCACAATAGGG TACGGTAGCAGAGACTTGGTCTGGGCTGCATCACAAAGAGA TACGGTAGCAGAGACTTGGTCTGGGCTGCATCACAAAGAGG TACGGTAGCAGAGACTTGGTCTGGGCTGCATCACAATAGGG TACGGTAGCAGAGACTTGGTCTGGGCTGCATCACAATAGGG TACGGTAGCAGAGACTTGGTCTAGGCTGCCCTGCGTCAACAAGAAGA TACGGTAGCAGAGACTTGGTCTAGGCTGCCCCTGGT TACGGTAGCAGAGACTTGGTCTAGGCTGCCCCCGGT TACGGTAGCAGAGACTTGGTCTAGGCTGCCCCCCGGT TACGGTAGCAGAGACTTGGTCTAGGCTGCCCCCCGGT TACGGTAGCAGAGACTTGGTCTAGCACAAGGAGCAGGGATTGGAAGA TACGGTAGCAGAGACTTGGTCTAGCGCTGCCCCCGGT TACGGTAGCAGAGACTTGGTCTAGCTGCAGGGACTTGCCCCCCCGGT TACGGTAGCAGAGACTTGGTCTAGCTGCCCCCCGGT TACGGTAGCAGAGACTTGGTCTAGCTGCCCCCCGGT TACGGTAGCAGAGACTTGGTCTAGCTGCCCCCCCGGT TACGGTAGCAGAGACTTGGTCTAGCTGCCCCCCCCGGT TACGGTAGCAGAGACTTGGTCTGCCCCCCCCCGGT TACGGTAGCAGAGACTTGGTCTAGCTGCCCCCCCCCC
WT1-E05           WT1-E06           WT1-E07           WT1-E08           WT1-E09           WT1-E10           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.09           ASXL1-E13.10           ASXL1-E13.10           ASXL1-E13.11           ASXL1-E13.12           ASXL1-E13.13           ASXL1-E13.14           ASXL1-E13.15           ASXL1-E13.16           ASXL1-E13.17           DNMT3A-E02           DNMT3A-E03           DNMT3A-E04           DNMT3A-E05           DNMT3A-E06           DNMT3A-E07	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACG GGATCATCCTACCTAACAAGC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTGGTGGGGAGG ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAATCCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAGCAGTTGCACACTGAAGGCA ACACTGACGACATGGTTCTACAGCAGTGCCACCTGAGAGG ACACTGACGACATGGTTCTACAGACTGACTGAGGTGGTGAGG ACACTGACGACATGGTTCTACAGACTGGCCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGGCCCACTGGCGCA ACACTGACGACATGGTTCTACAGATTCCTACGGCGGCAAG ACACTGACGACATGGTTCTACAGATTCCTACGGCGAGCAG ACACTGACGACATGGTTCTACAGATCGCTCGCTACGCAG ACACTGACGACATGGTTCTACAGATCGCTCGCTACGCAAG ACACTGACGACATGGTTCTACAGATCGCTCGGCAAG ACACTGACGACATGGTTCTACAGCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGCCCAGGAAGCTCAAGAA ACACTGACGACATGGTTCTACAGGCAGTCCCAAGATGGG ACACTGACGACATGGTTCTACAGGCAGGCCCAAGGAGCTCAAGAA ACACTGACGACATGGTTCTACAGCCAGGAGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGCCAAGGAGCCTCAGTGAG ACACTGACGACATGGTTCTACAGCCAAGGACTCTTACTACCT ACACTGACGACATGGTTCTACAGCCAAGGAGCCTCAGTGAG ACACTGACGACATGGTTCTACAGCCAACGAACCTTGGTGGAGCC ACACTGACGACATGGTTCTACAAGCCAAGGCCTGAGTGAG	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACACATGGCTGACTCC GCCACGGCACTATTCCTTCTC GCCCGGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGGAGGCCTCAT TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGGAGCCCTAAT TACGGTAGCAGAGACTTGGTCTACACCTGGGGGCCCAACA TACGGTAGCAGAGACTTGGTCTACACCTGGGGGCCCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGGACCTAGGG TACGGTAGCAGAGACTTGGTCTCATCACCTGGGACCTAGGG TACGGTAGCAGAGACTTGGTCTCATCACCATGCACCTGGT TACGGTAGCAGAGACTTGGTCTCATCACCATGCACCTGGT TACGGTAGCAGAGACTTGGTCTCATCACCATGCACCTGGT TACGGTAGCAGAGACTTGGTCTCATCACCATGCCACTGGT TACGGTAGCAGAGACTTGGTCTCAGCACTGGCCTGGC
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E03 DNMT3A-E05 DNMT3A-E05 DNMT3A-E06 DNMT3A-E07	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACGTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAACGTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAAGCTGATGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAAGCTGATGTGAGTGGTGAGG ACACTGACGACATGGTTCTACAGCTGAATGATGGAGTGGTGAAGA ACACTGACGACATGGTTCTACAAGCGAATGCAACCTGAATCCT ACACTGACGACATGGTTCTACAGACTGAATGCAGTGGTGAAACAG ACACTGACGACATGGTTCTACAAGGACTGTGCCATCCGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGCCATCCGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGCCACCTGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGCCACCTGCAGCAAG ACACTGACGACATGGTTCTACAGCAGTCCCGCTACGCATG ACACTGACGACATGGTTCTACAGCCAGGCCCAGCAAG ACACTGACGACATGGTTCTACAGCCAGGCCCAGCAAG ACACTGACGACATGGTTCTACAGCCAGGCCCAGGCAAGAACCT ACACTGACGACATGGTTCTACAATTGGCCGCGCAAGAATGTGG ACACTGACGACATGGTTCTACAATTGGCAGGGCCCAAGAA ACACTGACGACATGGTTCTACAGCCAGGGCCCAAGGAA ACACTGACGACATGGTTCTACAGCCAGGGCCCAGTGAG ACACTGACGACATGGTTCTACAGCCAGGGCCCAGGCC ACACTGACGACATGGTTCTACAACAGGCCCGGCCAAGAA ACACTGACGACATGGTTCTACAACAGGCCCGCGAAGGCC ACACTGACGACATGGTTCTACAACAGGCCCAGGCCAAGCAA ACACTGACGACATGGTTCTACAACAGGCCCAGGAAGCCCACCCA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACACATGGCTGACTCC GCCACGCACTATTCCTTCC CACCGGTATCTTGTCTTG
WT1-E05           WT1-E06           WT1-E07           WT1-E07           WT1-E08           WT1-E10           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.09           ASXL1-E13.10           ASXL1-E13.10           ASXL1-E13.11           ASXL1-E13.12           ASXL1-E13.13           ASXL1-E13.14           ASXL1-E13.15           ASXL1-E13.16           ASXL1-E13.17           DNMT3A-E02           DNMT3A-E03           DNMT3A-E04           DNMT3A-E05           DNMT3A-E06           DNMT3A-E07           DNMT3A-E08	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGAGAAGGAGGAAGGGA ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAATCCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCCGAATGATGGAGGTAGTGAGCT ACACTGACGACATGGTTCTACAGCACTGCACTCTCAGAGGA ACACTGACGACATGGTTCTACAGACTGCCACTCTGAGGAG ACACTGACGACATGGTTCTACAGACTGGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGAGCTCTCCTCACGCTGGCCA ACACTGACGACATGGTTCTACAGGCAGCCCCAGGATCTTACTACCT ACACTGACGACATGGTTCTACAGGCAGCCCCAGGACTCTACTACCT ACACTGACGACATGGTTCTACAGGCAGGCCCAAGGAATGTGG ACACTGACGACATGGTTCTACAGGCAGGGCCCAAGAA ACACTGACGACATGGTTCTACAGGCAGAGGCCCAAGGAA ACACTGACGACATGGTTCTACAGGCCAGGACGCCAAGAA ACACTGACGACATGGTTCTACAGGCAAGGGCCCAAGGAA ACACTGACGACATGGTTCTACAGGCCAGGCCCAAGGACGCC ACACTGACGACATGGTTCTACAGGCCAGGCCCACGGAATGCTACC ACACTGACGACATGGTTCTACAGGCCAGGCCAAGGACGCCACGACATGGTTCTACACGCCACTGGAATGCTACAC ACACTGACGACATGGTTCTACAGGCCAGGCCAAGGCCAAGGAC ACACTGACGACATGGTTCTACAGGCCAGGCCAAGGCCAAGGAC ACACTGACGACATGGTTCTACAGGCCAGGCCAAGGCCACACGACATGGTTCTACAAGGCCAAGGCCAAGGCCAAGGCCACACGACATGGTTCTACAAGGCCAAGGCCAAGGCCACACGACATGGTTCTACACACCCACC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGCCGGCTGACTCC GCCACGGCACTATTCCTTCC GCCACGGCACTATTCCTTCC CACCGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGCCCTCACT TACGGTAGCAGAGACTTGGTCTGTGGGCCCTCACA TACGGTAGCAGAGACTTGGTCTGCCCCTAT TACGGTAGCAGAGACTTGGTCTGCCCCCCAAT TACGGTAGCAGAGACTTGGTCTCATCACCTGGGGCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGGCCCCCAAC TACGGTAGCAGAGACTTGGTCTCATCACCTGGACCAAGCGGTTAGTGGC TACGGTAGCAGAGACTTGGTCTCCATTCTCCAGTTGCCACCTGGG TACGGTAGCAGAGACTTGGTCTCCATTCTCCAGTTGCCACTGGT TACGGTAGCAGAGACTTGGTCTCCATTCTCCAGTTCCTAGACGGG TACGGTAGCAGAGACTTGGTCTCCATTCCCCAGTAGCCACAGGGG TACGGTAGCAGAGACTTGGTCTCCATTCCCAGTTGGCCACAAGGAG TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGGCTTGG TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGGCTGCC TACGGTAGCAGAGACTTGGTCTCCATTCCCAGTAGCCTGCC TACGGTAGCAGAGACTTGGTCTCCAGTCCAG
WT1-E05           WT1-E06           WT1-E07           WT1-E07           WT1-E08           WT1-E10           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.09           ASXL1-E13.10           ASXL1-E13.11           ASXL1-E13.12           ASXL1-E13.13           ASXL1-E13.14           ASXL1-E13.15           ASXL1-E13.16           ASXL1-E13.17           DNMT3A-E03           DNMT3A-E04           DNMT3A-E05           DNMT3A-E05           DNMT3A-E06           DNMT3A-E07           DNMT3A-E08           DNMT3A-E07           DNMT3A-E08           DNMT3A-E07	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACCTCTACAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAAGTGGTGATGGAGGAAAGCT ACACTGACGACATGGTTCTACAAGCTGAATGAAGGTAGTGGAGC ACACTGACGACATGGTTCTACAGCACGATCCAGATCGAAGCAAAGCA ACACTGACGACATGGTTCTACAGCAGTTCCCACACCTGAATGCAT ACACTGACGACATGGTTCTACAAGGACTGTGCCAATCCT ACACTGACGACATGGTTCTACAAGGACTGTGCCAATCCTGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGGCCAATCCTGAGGAG ACACTGACGACATGGTTCTACAAGGCATCTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGCATCTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGCAGTCCTCGGTGGCAA ACACTGACGACATGGTTCTACAAGGCAGTCCCAGCATG ACACTGACGACATGGTTCTACAAGGCAGTCCCGACAGCAT ACACTGACGACATGGTTCTACAGCCAGGACGCCCAAGCAT ACACTGACGACATGGTTCTACAATGGCTCGCTCGGGACAAGA ACACTGACGACATGGTTCTACAGCCCAGGAGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGCCAGGAAGGGCCCAGTGAG ACACTGACGACATGGTTCTACAGCCAGGAAGGGCCCAGTGAG ACACTGACGACATGGTTCTACAGCCAGGACGGCCAGTGAG ACACTGACGACATGGTTCTACAGCCACGCTGGAAGGCC ACACTGACGACATGGTTCTACAGCCACGCTGGAAGGCCCAGTGAG ACACTGACGACATGGTTCTACAACAGGCCTGGAAGCCCACTGA ACACTGACGACATGGTTCTACAAGGGCCAGGCTAAGCAA ACACTGACGACATGGTTCTACAAGGGCCAGGCCAACGAAC ACACTGACGACATGGTTCTACAAGGGCCAGGCCAACCATGGA ACACTGACGACATGGTTCTACAAGGCCTGGGCCAACCATGGT ACACTGACGACATGGTTCTACAAGGGCCACGCTAATGTTAACA ACACTGACGACATGGTTCTACACCCCCCTAATGCCCTAATGTC ACACTGACGACATGGTTCTACACCCCCCTGATGCCTAATGTC ACACTGACGACATGGTTCTACACCCCCCTAATGCCCTAATGTC ACACTGACGACATGGTTCTACACCCCCCTGATGCCTAATGTC ACACTGACGACATGGTTCTACACCCCCCTGATGCCCTAATGTC ACACTGACGACATGGTTCTACACCCCCCTGATGCCCTAATGTC ACACTGACGACATGGTTCTACACCCCCCTGATGCCCTAATGTC ACACTGACGACATGGTTCTACACCCCCCTGTGTACCACCTGTGTAAA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACACATGGCTGACTCC GCCACGCACTATTCCTTCTC CACCGGTATCTTGTCTTG
WT1-E05           WT1-E06           WT1-E07           WT1-E07           WT1-E08           WT1-E10           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.09           ASXL1-E13.10           ASXL1-E13.10           ASXL1-E13.11           ASXL1-E13.12           ASXL1-E13.14           ASXL1-E13.15           ASXL1-E13.16           ASXL1-E13.17           DNMT3A-E02           DNMT3A-E05           DNMT3A-E06           DNMT3A-E07           DNMT3A-E07           DNMT3A-E07           DNMT3A-E08           DNMT3A-E09           DNMT3A-E09           DNMT3A-E09           DNMT3A-E09           DNMT3A-E09           DNMT3A-E09           DNMT3A-E09           DNMT3A-E09           DNMT3A-E09	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCACTCTCCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGAGAAGGTGAGGG ACACTGACGACATGGTTCTACAATCCTCGAGACATTAAAGC ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAGCGTTCCACACCTGAATGTGAGCTGGCA ACACTGACGACATGGTTCTACAGACTGACTGAGGTAGTGAAACAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCCACGCTGCCAAG ACACTGACGACATGGTTCTACAGGCATCCCCACGCTACGCATG ACACTGACGACATGGTTCTACAGGCATCCCCAGGTTTTGACT ACACTGACGACATGGTTCTACAGGCATCCCCAGGTCTACGAGA ACACTGACGACATGGTTCTACAGGCATCCCTGGGGATGTGG ACACTGACGACATGGTTCTACAGGCAGCCCCAGGGTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCCCGGAGGGTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCCCAGGGCTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCTGCCAAGCATGGG ACACTGACGACATGGTTCTACAGGCAAGCCTCTGCTGCCC ACACTGACGACATGGTTCTACAGGCAAGCCTCTACTTCTCCC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTGAG ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACACGGCCTGAAAGCCCACTGA ACACTGACGACATGGTTCTACAACACGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACACGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACCCCCTAATGCTCACAAGGCCAAGGTG ACACTGACGACATGGTTCTACAACCCCCCTAATGCTCACAAGGTC ACACTGACGACATGGTTCTACACCCCCCTGTGACACCCCTGTGTACA ACACTGACGACATGGTTCTACACCCCCCTGTGACACCGCCTGTGTAA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGCTA CAACTAAACACACTGGCCTGCC GCCACGGCACTATTCCTTCC GCCCGGCACTATTCCTTCC GCCCGGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTGCC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGCCCCCAAT TACGGTAGCAGAGACTTGGTCTGTGGGCCCCCAAT TACGGTAGCAGAGACTTGGTCTGCCCTTGCTCCTCAT TACGGTAGCAGAGACTTGGTCTCATCACCTGGGCCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGGCCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGACCAGGGGTTAGTGGC TACGGTAGCAGAGACTTGGTCTCATCACCTTGGACCAAGCGGGTTAGTGGC TACGGTAGCAGAGACTTGGTCTCATCACCTTGGACCAAGGGGT TACGGTAGCAGAGACTTGGTCTCCATTCTCCAGCTTCCTGCACCTGGG TACGGTAGCAGAGACTTGGTCTCATCACCATGGACCTAAGGG TACGGTAGCAGAGACTTGGTCTAGCACCAGGAGTTTGTGCCTGGC TACGGTAGCAGAGACTTGGTCTAGCCACCAGGAGGTTGGTCTGG TACGGTAGCAGAGACTTGGTCTAGCCACCATGACAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCACCATGACAATGCACTGG TACGGTAGCAGAGACTTGGTCTAGCCACCATAAAATGCCACG TACGGTAGCAGAGACTTGGTCTAGCCCACTAAAAATGCCTGC TACGGTAGCAGAGACTTGGTCTAGCTCCACTTATCACATTAGGG TACGGTAGCAGAGACTTGGTCTAGCTCCCACTAAAAATGCCTGC TACGGTAGCAGAGACTTGGTCTAGCCACCGTGCTGTCA TACGGTAGCAGAGACTTGGTCTGGAGGAGGGGGATTTGAAGAA TACGGTAGCAGAGACTTGGTCTGGAGGAGGGGGGATTTGAAGAA TACGGTAGCAGAGACTTGGTCTGGCACAAGGAG TACGGTAGCAGAGACTTGGTCTGGTC
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E09 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.16 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E03 DNMT3A-E03 DNMT3A-E05 DNMT3A-E06 DNMT3A-E08 DNMT3A-E09 DNMT3A-E10 DNMT3A-E11 DNMT3A-E11	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAAGTGGTGATGGAGGAGAAAGCT ACACTGACGACATGGTTCTACAGACTGAATGAGGTAGTGGAAACAG ACACTGACGACATGGTTCTACAACAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGACTGTGCCATCTCGAGGAA ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTCGCTGCCCA ACACTGACGACATGGTTCTACAAGGCAGTCCTGGTAGCAA ACACTGACGACATGGTTCTACAAGGCAGTCCTGGTACGATG ACACTGACGACATGGTTCTACAAGCCAGGAGCTCTACGACTG ACACTGACGACATGGTTCTACAGCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGCCCAGGAGACTCTTACTACCT ACACTGACGACATGGTTCTACAGCCCAGGAGGCCCAAGGAA ACACTGACGACATGGTTCTACAAGGCCCGGGACAGGG ACACTGACGACATGGTTCTACAAGGCCTGGGAACAGA ACACTGACGACATGGTTCTACAAGGCCTGGGACCAGGA ACACTGACGACATGGTTCTACAAGGCCTGGAATGCTGACAC ACACTGACGACATGGTTCTACAAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAAGGCCTGGAATGCCACCGA ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCCACCGA ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCCACCGA ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCCACCGA ACACTGACGACATGGTTCTACAACGGCTGAGGTCAAAGGT ACACTGACGACATGGTTCTACAACGGCCGGGACCATCATATTTAACA ACACTGACGACATGGTTCTACAACGGCCGGGCCATCATATTTAACA ACACTGACGACATGGTTCTACAACCCCCCCTGATAGCCCACTGGTAAA ACACTGACGACATGGTTCTACAACCGCCCGTGAACACCTGGTAAA ACACTGACGACATGGTTCTACAACCCCCCCTGATGCCTACTGTGACACCTGGGACAACGGGACATGGTTCTACAACGCCCCCCCC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAACGGCGGGCGGTA AGCAGACACATGGCTGCCTCC GCCCGGCACTATTCCTTCC CACCGGTACCAGAGACTTGGTCTGCAGTGGTGGCGCCTCTGCC CACCGGTAGCAGAGACTTGGTCTGGCGGCGTGGGGAGCCTCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCCTC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCCTCC TACGGTAGCAGAGACTTGGTCTGTGGGGAGTTGGGAGGCCTCAT TACGGTAGCAGAGACTTGGTCTGTGGGGCCTTGCTCCCTAT TACGGTAGCAGAGACTTGGTCTATCAGCCACCAAGCCCTAAT TACGGTAGCAGAGACTTGGTCTCATCACCATGGGCGCCAACA TACGGTAGCAGAGACTTGGTCTCATCACCATGGGCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCATGGGCTCAACCA TACGGTAGCAGAGACTTGGTCTCATCACCATGGACCATGGC TACGGTAGCAGAGACTTGGTCTCATCACCAGTGGGC TACGGTAGCAGAGACTTGGTCTCATCACCAGTGGCCCAAGGG TACGGTAGCAGAGACTTGGTCTCATCACAATGCACTGGTCTGCATCACCAGGG TACGGTAGCAGAGACTTGGTCTCAGCACTGGACCAAAGGAG TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGGTCTGG TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGGCTTGG TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGGCTGGC
WT1-E05           WT1-E06           WT1-E07           WT1-E07           WT1-E08           WT1-E10           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.09           ASXL1-E13.10           ASXL1-E13.10           ASXL1-E13.11           ASXL1-E13.12           ASXL1-E13.13           ASXL1-E13.14           ASXL1-E13.15           ASXL1-E13.16           ASXL1-E13.17           DNMT3A-E02           DNMT3A-E03           DNMT3A-E04           DNMT3A-E05           DNMT3A-E06           DNMT3A-E07           DNMT3A-E08           DNMT3A-E09           DNMT3A-E100           DNMT3A-E100	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGAGAAGGTGAGG ACACTGACGACATGGTTCTACAATCCTCGAGAACATTAAAGC ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAGCACTTCCCTGAGAAAGGAGAAAGCT ACACTGACGACATGGTTCTACAGCACTGCACTCTCAGAGGA ACACTGACGACATGGTTCTACAGACTGACGTGCACATCCT ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCCACGCTCCCAGGACAAG ACACTGACGACATGGTTCTACAGGCATCGCCACGCTACGCATG ACACTGACGACATGGTTCTACAGGCATCCCACGTGCCAAGCATG ACACTGACGACATGGTTCTACAGGCATCCCCAGGAGTCTTACTACCT ACACTGACGACATGGTTCTACAGGCATGCCCAGGGATGTGGG ACACTGACGACATGGTTCTACAGGCAAGCCCCAGGGCTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCCCGGAATGGTGG ACACTGACGACATGGTTCTACAGGCAACTTTGGTCGGGAGG ACACTGACGACATGGTTCTACAGGCAACTTTGGTCCTGGGGAG ACACTGACGACATGGTTCTACAGGCAACCTTGATGTGG ACACTGACGACATGGTTCTACAGGCAACGGCCTCAGGAG ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACACACGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACACACGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACACACCCCCTAATGCTCACACTGACACACTGGTTCACACCCCCCTAATGCTACAAGGCACATGGTTCTACACGCCCCTGTGAAGCCCACTGGTTCACACGCCCCTGTGAAGGTCAAGGTG ACACTGACGACATGGTTCTACACACCCCCTTATGCCCCCTATGTCC ACACTGACGACATGGTTCTACACACGCCCCTGGAAGGGTCAAGGTG ACACTGACGACATGGTTCTACACACCCCCTGTGACGCCCCCTGTGTAA ACACTGACGACATGGTTCTACACGCCCCGTGACGCGCCACGTGTTAA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGCTACCC AACCTAAACACACATGGCCTGCCC GCCACGGCACTATTCCTTCC GCCCGGCACTATTCCTTCC CACCGGATACTTGTTCTGGAG TACGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTGCC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTCGC TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGCCCCCAAT TACGGTAGCAGAGACTTGGTCTGTGGGCCCCCAAT TACGGTAGCAGAGACTTGGTCTGCCCTTGCTCCTCAT TACGGTAGCAGAGACTTGGTCTCATCACCTGGGCCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGGCCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGAGCCACAAGCACTGGT TACGGTAGCAGAGACTTGGTCTCATCACCTGGACCAAGGGGTTAGTGGC TACGGTAGCAGAGACTTGGTCTCCATCACCAGCGCCCTCAT TACGGTAGCAGAGACTTGGTCTCCATCACCAGCGCCCTGGT TACGGTAGCAGAGACTTGGTCTCCATCACCATGGACCTAGGG TACGGTAGCAGAGACTTGGTCTCCCATCACCATGCACCTGGC TACGGTAGCAGAGACTTGGTCTAGCCACGAGGGTTTGGCTTAGCACAGGGG TACGGTAGCAGAGACTTGGTCTAGCCACGAGCAGTGGC TACGGTAGCAGAGACTTGGTCTAGCCACGAGCTGGCTGCCACAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCACGAGCTGGCTGCCACAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCACTAAAATGCCTGC TACGGTAGCAGAGACTTGGTCTAGCCCCGCTGCCACAAGGAG TACGGTAGCAGAGACTTGGTCTGGCCTGCCACAAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCACCGTGCTGTGCA TACGGTAGCAGAGACTTGGTCTAGCACACGCCCTGGC TACGGTAGCAGAGACTTGGTCTGGCACAAGGAGCTGGCTTATACAAAATACACACA TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGGATTTGAAGAA TACGGTAGCAGAGACTTGGTCTGGAGAGGGGGGGATTGAAGAA TACGGTAGCAGAGACTTGGTCTGGAGAGGGGGGAGCAGGACAGACTGGTCTGCACACACA
WT1-E05 WT1-E07 WT1-E07 WT1-E08 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.03 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E03 DNMT3A-E05 DNMT3A-E07 DNMT3A-E07 DNMT3A-E08 DNMT3A-E10 DNMT3A-E10 DNMT3A-E11-12 DNMT3A-E13	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTGGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTGGCGAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTGGCGAGAGGAAAGGCA ACACTGACGACATGGTTCTACAACCTGAGATGGTGGTGAGG ACACTGACGACATGGTTCTACAACAGTGCTGAGGTGGTGAGG ACACTGACGACATGGTTCTACAGCAGTTCCACACCTGAATGCAGC ACACTGACGACATGGTTCTACAGCAGTTCCCCACACCTGAATGCT ACACTGACGACATGGTTCTACAGCAGTGCGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGCCATCTGGGGACAAG ACACTGACGACATGGTTCTACAAGGACTGTGCCATCTGGGGACAAG ACACTGACGACATGGTTCTACAAGGACTGTGCCATCTGGGGACAAG ACACTGACGACATGGTTCTACAAGGCAGTCCTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGCAGTCCTGGTGGACAAG ACACTGACGACATGGTTCTACAAGGCAGTCCTGGTGGCAA ACACTGACGACATGGTTCTACAAGGCAGTCCTGGTAGCAAG ACACTGACGACATGGTTCTACAGGCAGCCCAAGGATCTTACTACCT ACACTGACGACATGGTTCTACAGGCAGGCCCAAGGTAGTGG ACACTGACGACATGGTTCTACAGGCAGGCCCAAGGAG ACACTGACGACATGGTTCTACAGGCAGGCCCAAGGAGGGCCAAGGA ACACTGACGACATGGTTCTACAGGCAGGCCTCAGTGGG ACACTGACGACATGGTTCTACAGGCAGGCCTCAGTGGA ACACTGACGACATGGTTCTACAGGCAGGCCTCAGTGGA ACACTGACGACATGGTTCTACAGGCCAGGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGGCCAGGCCTGAATGGTACAC ACACTGACGACATGGTTCTACAGGCCAGGCCAACGTAGGAG ACACTGACGACATGGTTCTACAGGCCAGGCCACTGATAGCAC ACACTGACGACATGGTTCTACAGGCCGGCCACTCATATTTAACA ACACTGACGACATGGTTCTACAGGCCGGGCCACTCATATTTAACA ACACTGACGACATGGTTCTACAGCCCCACTGGACACCTGGTAA ACACTGACGACATGGTTCTACAGCCCCCCTGAAGGCCAACGGG ACACTGACGACATGGTTCTACAGCCCCCCCTAATGCCAACGGA ACACTGACGACATGGTTCTACAGCCCCCCCCTAATGCCAACGGG ACACTGACGACATGGTTCTACAGCCCCCCCCTAATGCCAACGGG ACACTGACGACATGGTTCTACAGCCCCCCCCCCAATGGTCAAGGG ACACTGACGACATGGTTCTACAGCCCCCCCCCCACTGGTAA ACACTGACGACATGGTTCTACAGCCCCGCCCCCCCCCCC	TCAGTCCTAACTCCTGCATTG         AAGGAACTAAAGGGCCGGTA         AGCAGTGCTTACTTTCCTCC         GCCACGGACTACTTGCTTCCTC         GCCACGGACTATTCCTTCTC         CACCCAGCACTATTCCTTCC         CACCGGACACTTGCTCTGCAGTGGTGACCTCTGCC         TACGGTAGCAGAGACTTGGTCTGCAGTGGTGGACCTCTGCC         TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC         TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC         TACGGTAGCAGAGACTTGGTCTGTGGGGACTCGCCCCAT         TACGGTAGCAGAGACTTGGTCTATGAGCCACCAGCCCTAAT         TACGGTAGCAGAGACTTGGTCTATCAGCCTGGGGCCCAACA         TACGGTAGCAGAGACTTGGTCTCATCACCATGGGGCTAACA         TACGGTAGCAGAGACTTGGTCTCATCACCATGGGGCTAACA         TACGGTAGCAGAGACTTGGTCTCATCACCACAGGGGTTAGTGGC         TACGGTAGCAGAGACTTGGTCTCATCACCACAGCAGTGGGG         TACGGTAGCAGAGACTTGGTCTCACTCACACACTGGACCAAAGGAG         TACGGTAGCAGAGACTTGGTCTAGACATGGACTTAGCCACAGGGG         TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGTCTGG         TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGCTGCTGC         TACGGTAGCAGAGACTTGGTCTAGACCACGTGCACACAAAATGCCTGC         TACGGTAGCAGAGACTTGGTCTAGACCACGTGCTGCAAAAATACACACA         TACGGTAGCAGAGACTTGGTCTAGAGCAGGTGGCGCCTGGCT         TACGGTAGCAGAGACTTGGTCTAAGAGGCTGCCCCTGGT         TACGGTAGCAGAGACTTGGTCTAAGAGGCTGCCCCTGGT         TACGGTAGCAGAGACTTGGTCTAAGAGGGCGCCCCCGGGT         TACGGTAGCAGAGACTTGGTCTAAGAGGAGGAGAGAGAGA
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E07 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.05 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.07 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E09 DNMT3A-E10 DNMT3A-E11 DNMT3A-E114	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAATCCTGCGAGACATTAAAGC ACACTGACGACATGGTTCTACAATCCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAGCAGTTCCACACCTGAATGCTGGCA ACACTGACGACATGGTTCTACAGACTGACTGCACTCTGAGGAG ACACTGACGACATGGTTCTACAGACTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGGCATCCCTACGCTGCCCA ACACTGACGACATGGTTCTACAGGCATCCCCAAGTTTTGACT ACACTGACGACATGGTTCTACAGGCATCCCCAGGAGTCTTACTACCT ACACTGACGACATGGTTCTACAGGCATCCCCAGGCGATGTGG ACACTGACGACATGGTTCTACAGGCATCCCGAGCGTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCTCAGGCGTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCTCAGTGAG ACACTGACGACATGGTTCTACAGGCAAGCGCTCAGTGAG ACACTGACGACATGGTTCTACAGGCAACTTTGGCTGCGCA ACACTGACGACATGGTTCTACAGGCAAGCGTCAAGAA ACACTGACGACATGGTTCTACAACAGGCCTGGAATGTGG ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGAAAGCCACCGGA ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACCAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACACACCCCTGATGTGCAACCCCCCAAGGTG ACACTGACGACATGGTTCTACACACCCCCTGATGCTACAC ACACTGACGACATGGTTCTACACACCCCCTGAAGCCCACTGGTAA ACACTGACGACATGGTTCTACACACCCCCTGTGAAAGCCACTGGTAA ACACTGACGACATGGTTCTACACGCCCTGGAAGGGTCAAGGTG ACACTGACGACATGGTTCTACAGCCTCGTGGACCCCCTGATGTAA ACACTGACGACATGGTTCTACAGCCTCGTGACACCGTGGTAAGGCACACGGTAAGGCCACCGGTAAGGTCAACGGTTCACAGGCTGACGCTCTGACTGGTTACA ACACTGACGACATGGTTCTACACTCCTCTTGGCACCCTGACTGGTAA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGCTACC AACCTAAACACACTGGCCGCGCCCCC GCCACGCACTATTCCTTCC GCCCGGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTGCC CACCGGTAGCAGAGACTTGGTCTGCAGTGGTGGGAGCTCCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTCGC TACGGTAGCAGAGACTTGGTCTGTGGGGAGTTGGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGTGGGCCTTGCTCCTCAT TACGGTAGCAGAGACTTGGTCTGTGGGCCTTGGCCCTAAT TACGGTAGCAGAGACTTGGTCTCATCACCTGGGGCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGGGCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGACCAGAGCCCTAAT TACGGTAGCAGAGACTTGGTCTCCATCACCAGGGGTTAGTGGC TACGGTAGCAGAGACTTGGTCTCCATCACCAGCGGGTTAGTGGC TACGGTAGCAGAGACTTGGTCTCCATCACCATGGCCACTGGG TACGGTAGCAGAGACTTGGTCTCCATCACCATGGCCACTGGG TACGGTAGCAGAGACTTGGTCTCCATCACCATGGACCTAGGGG TACGGTAGCAGAGACTTGGTCTAGCACGAGGGTTGGTCTGG TACGGTAGCAGAGACTTGGTCTAGCCACGAGGAGGC TACGGTAGCAGAGACTTGGTCTAGCCACGAGGGTTGGCTTACCACTGGCCTGCC TACGGTAGCAGAGACTTGGTCTAGCCACGAGGGTTGGCTTACCACAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCACTAAAAATGCCTGC TACGGTAGCAGAGACTTGGTCTAGCCACGTGCTGTCA TACGGTAGCAGAGACTTGGTCTAGCTCCCACTAAAAATGCCTGC TACGGTAGCAGAGACTTGGTCTAGCCCCGCTGTCACAAAGAGG TACGGTAGCAGAGACTTGGTCTGGGCTGCCCCTGGC TACGGTAGCAGAGACTTGGTCTGGGCTGCCCCCGGC TACGGTAGCAGAGACTTGGTCTGGGCTGCCCCCTGGT TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGATTTGAAGA TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGGGATTTGAAGA TACGGTAGCAGAGACTTGGTCTGGAGAGGGGGGGATTGAAGAG TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGGATTGAAGA TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGGATTGAAGA TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGGAGCCCCCGGT TACGGTAGCAGAGACTTGGTCTGGCAGAGGAGAGAGGAGAGCAGGAC TACGGTAGCAGAGACTTGGTCTGGCAGAGGAGGAGGAGGAGGAGGAGGAGAGCC TACGGTAGCAGAGACTTGGTCTGGCACACCCACCACAGGCAGG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.14 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.14 ASXL1-E13.16 DNMT3A-E02 DNMT3A-E03 DNMT3A-E03 DNMT3A-E06 DNMT3A-E07 DNMT3A-E10 DNMT3A-E11 DNMT3A-E13 DNMT3A-E13 DNMT3A-E13 DNMT3A-E14 DNMT3A-E13 DNMT3A-E14 DNMT3A-E13 DNMT3A-E13 DNMT3A-E14 DNMT3A-E14 DNMT3A-E14 DNMT3A-E13 DNMT3A-E13 DNMT3A-E14 DNMT3A-E13 DNMT3A-E14 DNMT3A-E14 DNMT3A-E14 DNMT3A-E14 DNMT3A-E13 DNMT3A-E13 DNMT3A-E14 DNMT3A-	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTGGTGGAGG ACACTGACGACATGGTTCTACATCCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAGCAGTTGCACACTGAATGCTGGCCA ACACTGACGACATGGTTCTACAGCAGTGCCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGCAGTGCCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGGCCCATCTCGAGGAGA ACACTGACGACATGGTTCTACAGACTGGCCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCCACGCTACGCAG ACACTGACGACATGGTTCTACAGACTGCCCACGCTACGCAG ACACTGACGACATGGTTCTACAGACTGCCCACGCAGCAAG ACACTGACGACATGGTTCTACAGCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGCCCAGGAGGCCTACGCAGG ACACTGACGACATGGTTCTACAGCCCAGGAGGCCTACGCAGG ACACTGACGACATGGTTCTACAGCCAGGAGGCCTACGCAGG ACACTGACGACATGGTTCTACAGCCAGGAGGGCCTAGTGGG ACACTGACGACATGGTTCTACAGCCACGAAGGGCCTAGTGAG ACACTGACGACATGGTTCTACAGCCACGAAGGGCCTAGTGAG ACACTGACGACATGGTTCTACAGCCAAGGCCTGAGGAGCC ACACTGACGACATGGTTCTACAGCCACGCAAGGCCTAAGAA ACACTGACGACATGGTTCTACAGCCACGCAAGGCCTAAGGA ACACTGACGACATGGTTCTACAGGCCACGCTGAAGCCCACTGA ACACTGACGACATGGTTCTACAGGCCAAGGCCTAAGCCCACTGA ACACTGACGACATGGTTCTACAGGCCACCGCTGAAGCCCACTGA ACACTGACGACATGGTTCTACAGGCCCACCGCAAGGCCAACGGC ACACTGACGACATGGTTCTACAGGCCCACCGCAAGGCCAAGGGT ACACTGACGACATGGTTCTACAGCCCCCCTGAGACGCCACTGGAA ACACTGACGACATGGTTCTACAGCCCCCCCTAAGGCCAACGGC ACACTGACGACATGGTTCTACAGCCCCCCCTAATGCCACCTGGAAGG ACACTGACGACATGGTTCTACAGCCCCCCTGAGACCCCCCCTGGAAA ACACTGACGACATGGTTCTACAGCCCCCCTGAGACCCTGGGTAA ACACTGACGACATGGTTCTACAGCCCCCCTGAGACGCTGCCTGC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACACATGGCTGCCCC GCCACGCACTATTCCTTCC GCCCGGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTGC CACCGGTAGCAGAGACTTGGTCTGGCGTGGTGGCGCCTCTGCC TACGGTAGCAGAGACTTGGTCTGGGGGAGTTGGGAGGCATC TACGGTAGCAGAGACTTGGTCTGGGGGAGTTGGGAGGCCTAAT TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGCGCCATAT TACGGTAGCAGAGACTTGGTCTGTGGGCCTTACCTCCTAT TACGGTAGCAGAGACTTGGTCTACCACCTGGGGGCTCAACA TACGGTAGCAGAGACTTGGTCTACACCTGGGGGCCCAACA TACGGTAGCAGAGACTTGGTCTACACCTGGGGGCCCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGGACCTAGGG TACGGTAGCAGAGACTTGGTCTCATCACCACGGGGCTCAACC TACGGTAGCAGAGACTTGGTCTCATCACCATGCCACTGGC TACGGTAGCAGAGACTTGGTCTCATCACCATGCCACTGGC TACGGTAGCAGAGACTTGGTCTCACCACGACGGG TACGGTAGCAGAGACTTGGTCTCACCACGACGTGGC TACGGTAGCAGAGACTTGGTCTAGACATGGACTTAGCCAGGG TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGGCCTGGC TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGGCTGGC
WT1-E05           WT1-E06           WT1-E07           WT1-E07           WT1-E08           WT1-E10           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.10           ASXL1-E13.10           ASXL1-E13.11           ASXL1-E13.12           ASXL1-E13.13           ASXL1-E13.14           ASXL1-E13.15           ASXL1-E13.16           ASXL1-E13.17           DNMT3A-E02           DNMT3A-E05           DNMT3A-E06           DNMT3A-E07           DNMT3A-E08           DNMT3A-E09           DNMT3A-E10           DNMT3A-E11-12           DNMT3A-E14           DNMT3A-E14	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACAAGCTGGTGTGAGG ACACTGACGACATGGTTCTACAGCTCGAGACATGAATGCAGC ACACTGACGACATGGTTCTACAACTCGAATGAGGTAGTGGAGA ACACTGACGACATGGTTCTACAAGCAGTGGCCAATCCTGAGAGA ACACTGACGACATGGTTCTACAAGGACTGTGCCATCCGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGCCATCCGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGCCGATCGCAGGAG ACACTGACGACATGGTTCTACAAGGCATCTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGGACTCTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGCAGTCCCAAGCATG ACACTGACGACATGGTTCTACAAGGCAGTCCCAAGCATG ACACTGACGACATGGTTCTACAAGGCAGTCCCAAGCATG ACACTGACGACATGGTTCTACAAGGCAGTCCCAAGCATG ACACTGACGACATGGTTCTACAATGGCCCGCTCCAGGAAG ACACTGACGACATGGTTCTACAATTGGCAGGCGCCAAGAA ACACTGACGACATGGTTCTACAATTGTGGCAGCGCCAAGAA ACACTGACGACATGGTTCTACAACCCCACGAGGCCCAAGGAA ACACTGACGACATGGTTCTACAACCCCACGAGGCCCAAGGAA ACACTGACGACATGGTTCTACAACAGGCCTGGAAGGCC ACACTGACGACATGGTTCTACAACAGGCCTGGAAGCCCACTGA ACACTGACGACATGGTTCTACAACAGGCCTGGAAGCCCACTGA ACACTGACGACATGGTTCTACAACAGGCCTGGTACACAAC ACACTGACGACATGGTTCTACAACAGGCCTGGAAGCCCACTGA ACACTGACGACATGGTTCTACAACAGGCCAGGTCAAGCA ACACTGACGACATGGTTCTACACCCCCTGATGCCACACTGGTAA ACACTGACGACATGGTTCTACACTCCGGAGAGGCCAACCTGGTAA ACACTGACGACATGGTTCTACACTCCTGGGACCCACTGTGTAA ACACTGACGACATGGTTCTACACTCCTGGGACCACTGGTGAA ACACTGACGACATGGTTCTACACTCCTGGGACCCCCTAATGTC ACACTGACGACATGGTTCTACACTGCGCCCCCCACGTGAA ACACTGACGACATGGTTCTACACTGCGCACCTGCTACTGCAACGGC ACACTGACGACATGGTTCTACACTGCCACCCCCCTCACTGCAACGG ACACTGACGACATGGTTCTACACTGGCCACCTGCTTGCAAGGG ACACTGACGACATGGTTCTACACACCCCCTGGCACCTGCTTCC ACACTGACGACATGGTTCTACACACCCCAGGCCCACCTGCTTCC ACACTGACGACATGGTTCTACACACCCCAGGCCACCTGCTCACACGGACTGGG ACACTGACGACATGGTTCTACACCCCAGGCCACGTGCTCCACACGCTCACGACATGGTTCTA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACACATGGCTGACTCC GCCACGCACTATTCCTTCC CACCGGTATCTTGTCTTG
WT1-E05           WT1-E06           WT1-E07           WT1-E07           WT1-E08           WT1-E10           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.09           ASXL1-E13.10           ASXL1-E13.10           ASXL1-E13.10           ASXL1-E13.11           ASXL1-E13.12           ASXL1-E13.13           ASXL1-E13.14           ASXL1-E13.15           ASXL1-E13.16           ASXL1-E13.17           DNMT3A-E02           DNMT3A-E03           DNMT3A-E04           DNMT3A-E05           DNMT3A-E06           DNMT3A-E07           DNMT3A-E10           DNMT3A-E10           DNMT3A-E10           DNMT3A-E10           DNMT3A-E11           DNMT3A-E13           DNMT3A-E14           DNMT3A-E15           DNMT3A-E15           DNMT3A-E16	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAATCCTAGATTGTGGTGGAGG ACACTGACGACATGGTTCTACAATCCTCGAGAAAGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCCTGAGAATGAGGGAGTGGGA ACACTGACGACATGGTTCTACAGCACTGCACTCTGAGGAG ACACTGACGACATGGTTCTACAGCAGTGCCACTCTGAGGAG ACACTGACGACATGGTTCTACAGACTGGCCACTCTGAGGAG ACACTGACGACATGGTTCTACAGACTGGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCCACTGCTGCCAA ACACTGACGACATGGTTCTACAGAGTGCCGCTACGCAG ACACTGACGACATGGTTCTACAGGCAGCCCCAGGAGATCTTACTGCG ACACTGACGACATGGTTCTACAGGCAGCCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGGCAGCCCGAGGAGTCTTACTACCT ACACTGACGACATGGTTCTACAGGCAGGCCCAAGGAA ACACTGACGACATGGTTCTACAGGCAGGGCCCAAGGAA ACACTGACGACATGGTTCTACAGGCCAGGAGCCCAAGAA ACACTGACGACATGGTTCTACAGGCCAGGCCCAAGAA ACACTGACGACATGGTTCTACAGGCCGGCCATAGGCC ACACTGACGACATGGTTCTACAGGCGGCCACAGTGAA ACACTGACGACATGGTTCTACAGGCCGGCCACAGAAG ACACTGACGACATGGTTCTACAGGCCGGCCACAGTGAG ACACTGACGACATGGTTCTACAGGCCGGCCACAGTGAAG ACACTGACGACATGGTTCTACAGGCCGGCCACATGATGCCA ACACTGACGACATGGTTCTACAGGCCGGCCACATGATGCTACAC ACACTGACGACATGGTTCTACAGGCCGGCCACATGATGTCA ACACTGACGACATGGTTCTACAGCCCCCACTGAAGCCCACTGAA ACACTGACGACATGGTTCTACAGCCCCCCTGAGCCACTGATAGCCCACTGAA ACACTGACGACATGGTTCTACAGCCCCCCACTGATGCCAAGGTG ACACTGACGACATGGTTCTACAGCCCCCCCTGAGCCACTGTGTAA ACACTGACGACATGGTTCTACAGCCCCCGCACCCCCACTGATAA ACACTGACGACATGGTTCTACAGCCCCCCTGACCCCTGACACCTGCTACA ACACTGACGACATGGTTCTACAGCCCCCGCCACTGACTACTCA ACACTGACGACATGGTTCTACAGCCCCTGGCCCACTGCTTTC ACACTGACGACATGGTTCTACAGCCCCTGCTCTGAGATGGTG ACACTGACGACATGGTTCTACACACCGCCACCCTGCTTCC ACACTGACGACATGGTTCTACACACCGCCACCCTGCTTCC ACACTGACGACATGGTTCTACACACCGCCACCTGCTTCC ACACTGACGACATGGTTCTACACCCACCTGACGCCCACGACTGGTTCCAGGAC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACACATGGCTGCCC GCCACGCACTATTCCTTCC GCCCGGCACTATTCCTTCC CACCGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTTGGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTGTG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E03 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E03 DNMT3A-E10 DNMT3A-E11-12 DNMT3A-E13 DNMT3A-E13 DNMT3A-E15 DNMT3A-E15 DNMT3A-E15 DNMT3A-E16 DNMT3A-E15	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAAGTGGTGATGGATGGTGGAGG ACACTGACGACATGGTTCTACAAGCGTGATGGAGGAAAGCT ACACTGACGACATGGTTCTACAGCAGTGCAATGAATGGAGTGGAAAGCT ACACTGACGACATGGTTCTACAGCAGATGCAATGAGTGGAGAAACAG ACACTGACGACATGGTTCTACAAGGACTGTGCCAATCCT ACACTGACGACATGGTTCTACAAGGACTGTGCCAATCCTGAGGAG ACACTGACGACATGGTTCTACAAGGACTGTGGCCAATCCTGAGGAAG ACACTGACGACATGGTTCTACAAGGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGGATCTTGGGGACAAG ACACTGACGACATGGTTCTACAAGGCAGTCCTGGTGGCAA ACACTGACGACATGGTTCTACAAGGCAGTCCTGGTAGCAAG ACACTGACGACATGGTTCTACAAGGCAGTCCTGGGGACAAG ACACTGACGACATGGTTCTACAAGGCAGTCCTAGGAATGGTG ACACTGACGACATGGTTCTACAAGCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGCCAGGAAGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGCCAGGAAGGCCTCAGTGAG ACACTGACGACATGGTTCTACAAGCCCAGGAAGCCTCAGTGAG ACACTGACGACATGGTTCTACAAGCCCAGGAAGGCCTCAGTGAG ACACTGACGACATGGTTCTACAACCAGCCTGGAATGCTGACAC ACACTGACGACATGGTTCTACAACCGCCTGGAAGCCCACTGA ACACTGACGACATGGTTCTACAACCCACCTGATGGCCAACC ACACTGACGACATGGTTCTACAACGGCCTGGAAAGCCCACTGA ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACCAGCCCTGGATGCTACAC ACACTGACGACATGGTTCTACAACCACCCCCTAATGTCCAAGGA ACACTGACGACATGGTTCTACAACCACCCCCTGATGCCTAATGTC ACACTGACGACATGGTTCTACAACCACCCCCTAATGCCTAAGAA ACACTGACGACATGGTTCTACAACCACCCCCTGATGCGAAAGGT ACACTGACGACATGGTTCTACAACCTCCTCTTGCACCACCTGGTAAA ACACTGACGACATGGTTCTACAACCACCCCCTCACTGGTAAA ACACTGACGACATGGTTCTACAACCAGGCCTGACACCTGGTTACA ACACTGACGACATGGTTCTACAACCAGGCCTGCTGAGAGGGACACCAGGA ACACTGACGACATGGTTCTACAACAGGCCTGGGCCTACA	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAACGGCGGGCGGCACCTCC GCCACGCACTATTCCTTCC CACCGGTATCTTGTCTTG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.14 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E03 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E10 DNMT3A-E10 DNMT3A-E11 DNMT3A-E11 DNMT3A-E15 DNMT3A-E15 DNMT3A-E15 DNMT3A-E16 DNMT3A-E16 DNMT3A-E16 DNMT3A-E16 DNMT3A-E16 DNMT3A-E17 DNMT3A-E16 DNMT3A-E16 DNMT3A-E16 DNMT3A-E17 DNM	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGAGTAGTGGTGGTGAGG ACACTGACGACATGGTTCTACATCCTCGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAATGAAGGGAAGTCAGCC ACACTGACGACATGGTTCTACATCCGAATGGTGGAGGCA ACACTGACGACATGGTTCTACAGCACTGCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGACTGAGGTAGTGAAACAG ACACTGACGACATGGTTCTACAGACTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCCACGCTACGCAG ACACTGACGACATGGTTCTACAGACTGCCCACGCTACGCAG ACACTGACGACATGGTTCTACAGGCATCCCCACGCATG ACACTGACGACATGGTTCTACAGGCATCCCCAGGTCTACGACAG ACACTGACGACATGGTTCTACAGGCATCCCCAGGATGTTGC ACACTGACGACATGGTTCTACAGGCATCCCCAGGATGTGG ACACTGACGACATGGTTCTACAGGCAGCCCCAGGGATCTTACTACCT ACACTGACGACATGGTTCTACAGGCAAGCCCCAGGGATCTACAGGA ACACTGACGACATGGTTCTACAGGCAAGCCCCAGGGACAGGG ACACTGACGACATGGTTCTACAGGCAAGCCTCAGTGAG ACACTGACGACATGGTTCTACAGGCAAGCCTCAGTGAG ACACTGACGACATGGTTCTACAGCCACGCTGAGGATGCTACAC ACACTGACGACATGGTTCTACAGCGCAAGCTTGAGGAAGGCC ACACTGACGACATGGTTCTACAGCCACTGATCTTCTCCC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACACGGCCGCACACTGATATTAACA ACACTGACGACATGGTTCTACAACCCCCTGTGACAGGGTCAAGGT ACACTGACGACATGGTTCTACAACACGCCCTGGAAGGGCAAGGGT ACACTGACGACATGGTTCTACAACACGCCCTGGAAGGGCAAGGGT ACACTGACGACATGGTTCTACACACCCCTGGACCCCCTACTGTCA ACACTGACGACATGGTTCTACAACAGGCCTGGCCACCGCTCACTGCACACGGT ACACTGACGACATGGTTCTACACACGCCTGGCCTACACTGGTCCACACGGTCTACACACGGGTCTACGACACGGGTCTACACACGGGTCTACGGGCCTACAC	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACACATGGCTGCCC GCCACGGCACTATTCCTTCC GCCCACGGCACTATTCCTTCC CACCGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTGGTGTCGCC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTGGTGTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTGGGGAGGCCTC TACGGTAGCAGAGACTTGGTCTGTGGGCCTTGGCCCTCAT TACGGTAGCAGAGACTTGGTCTGTGGGCCCTCAAC TACGGTAGCAGAGACTTGGTCTGTGGCGCCCCAAC TACGGTAGCAGAGACTTGGTCTCATCACCTGGGCCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGGCGCTCAACA TACGGTAGCAGAGACTTGGTCTCATCACCTGGACCAAGGCGC TACGGTAGCAGAGACTTGGTCTCATCACCAGCGCCCTAAT TACGGTAGCAGAGACTTGGTCTCATCACCTGGACCAAAGGGG TACGGTAGCAGAGACTTGGTCTCATCACCATGGCCACTAGGGG TACGGTAGCAGAGACTTGGTCTCCATTCTCCCAGTTCCTAGAGGG TACGGTAGCAGAGACTTGGTCTCATCACCATGGACCTAAGGGG TACGGTAGCAGAGACTTGGTCTAGCCACGAGGAGTTGTGCTGG TACGGTAGCAGAGACTTGGTCTAGCCACGAGGAGTTGGTCTGG TACGGTAGCAGAGACTTGGTCTAGCCACGAGGGTTGGCTGCA TACGGTAGCAGAGACTTGGTCTAGCCACGAGGAGTTGGCTGCA TACGGTAGCAGAGACTTGGTCTAGCCACCATGAGCTTGCCGCTGTCA TACGGTAGCAGAGACTTGGTCTGGCTCACATCAGTATCACATAGAGC TACGGTAGCAGAGACTTGGTCTGGCAGCAATGGGCTTGCCCCGCTGTCA TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGGGATTTGAAGCAGCGCGCCGCGT TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGGGGGG
WT1-E05           WT1-E06           WT1-E07           WT1-E08           WT1-E09           WT1-E10           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.09           ASXL1-E13.10           ASXL1-E13.10           ASXL1-E13.11           ASXL1-E13.12           ASXL1-E13.13           ASXL1-E13.14           ASXL1-E13.15           ASXL1-E13.16           ASXL1-E13.17           DNMT3A-E03           DNMT3A-E04           DNMT3A-E05           DNMT3A-E07           DNMT3A-E08           DNMT3A-E10           DNMT3A-E11-12           DNMT3A-E11-12           DNMT3A-E14           DNMT3A-E15           DNMT3A-E16           DNMT3A-E16           DNMT3A-E17           DNMT3A-E16           DNMT3A-E16           DNMT3A-E16           DNMT3A-E16           DNMT3A-E17	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAAGTGGTGATGGTGGTGAGG ACACTGACGACATGGTTCTACAAGTGGTGATGGAGGCA ACACTGACGACATGGTTCTACAGACTGAATGTAGGTGTGAAACAG ACACTGACGACATGGTTCTACAGACTGAATGAGGTAGTGAAACAG ACACTGACGACATGGTTCTACAGACTGACTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGACTGTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGGATCTTCGGTGGACAAG ACACTGACGACATGGTTCTACAAGGCATCTCGCTGGCCA ACACTGACGACATGGTTCTACAAGGCAGTCCCAGCATGG ACACTGACGACATGGTTCTACAGGCAGTCCCAGCATGG ACACTGACGACATGGTTCTACAGGCAGCCCAAGGATCTTACTACCT ACACTGACGACATGGTTCTACAGGCAGCTCCGGTACGAGG ACACTGACGACATGGTTCTACAGGCAGGCCCAAGTGTGG ACACTGACGACATGGTTCTACAGGCAGGCCCAAGGAG ACACTGACGACATGGTTCTACAGGCAGGCCCAGTGAGA ACACTGACGACATGGTTCTACAGGCAGGCCCAGTGAGA ACACTGACGACATGGTTCTACAGGCAGGGCCCAGTGAG ACACTGACGACATGGTTCTACAGGCAGGGCCCAGTGAG ACACTGACGACATGGTTCTACAGGCCAGGGCCCACGGAA ACACTGACGACATGGTTCTACAGGCCAGGGCCCACCGAA ACACTGACGACATGGTTCTACAGGCCAGGGCCAACGATGGC ACACTGACGACATGGTTCTACAGGCCGGGCCATCATATTTAACA ACACTGACGACATGGTTCTACAGCCCCCTGATGGCCAACGT ACACTGACGACATGGTTCTACAGCCCCCTGATGGCCAACGT ACACTGACGACATGGTTCTACAGCCCCCTGATGGCCAACGT ACACTGACGACATGGTTCTACAGCCCCCTGATGGCCTAAGGC ACACTGACGACATGGTTCTACAGCCCCCTGGACACCTGGTAA ACACTGACGACATGGTTCTACAGCCCCCTGACGGGCCACCAGGGG ACACTGACGACATGGTTCTACAGCCCCCTGGCCCACCTGGTAA ACACTGACGACATGGTTCTACAACCGCGGGCCTACCATGGGACACAGGG ACACTGACGACATGGTTCTACAACCGGGGCCTACCACGGGACAGGGG ACACTGACGACATGGTTCTACAACAGGGTGTGCCACCCTGCTGGAGCAGGG ACACTGACGACATGGTTCTACAACAGGGTGTGCCACCCTGCTCAGGAC ACACTGACGACATGGTTCTACAACAGGGTGTGGGGCCTACA ACACTGACGACATGGTTCTACAACAGGGTGTGGGGGCTACGACACAGGACATGGTTCTACAACAGGGTGTAGGGGCCTACA	TCAGTCCTAACTCCTGCATTG         AAGGAACTAAAGGGCCGGTA         AGCAGTGCTTACTTTCCTCC         GCCACGGCACTATTCCTTCTC         GCCACGGCACTATTCCTTCTC         CACCGGAACTAGCTGGCTGCACTCTC         GCCACGGACACTTGCTTCTGCGCAGTGGTGGCACCTCTGCC         TACGGTAGCAGAGACTTGGTCTGGCGGCAGTAGTTGTGTCGC         TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC         TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCCTCAT         TACGGTAGCAGAGACTTGGTCTGTGGGGACCCTGCTCCAT         TACGGTAGCAGAGACTTGGTCTATGAGCCACCAACCCAACC         TACGGTAGCAGAGACTTGGTCTCATCACCACTGGGGCTCAACA         TACGGTAGCAGAGACTTGGTCTCATCACCACTGGGGCTAACA         TACGGTAGCAGAGACTTGGTCTCATCACCACTGGGCACCAGTGGG         TACGGTAGCAGAGACTTGGTCTCATCACACAGTGGGCTTAGTGGC         TACGGTAGCAGAGACTTGGTCTCATCACACAGGGGTTAGTGGC         TACGGTAGCAGAGACTTGGTCTTAGACATGGACTTAGCCACAAGGGG         TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGCTGCTGGC         TACGGTAGCAGAGACTTGGTCTAGACATGGACTGCTGCTGC         TACGGTAGCAGAGACTTGGTCTAGACCAGTGGCTGCTGC         TACGGTAGCAGAGACTTGGTCTAGATCACTACATAGGG         TACGGTAGCAGAGACTTGGTCTGCCTCACATAAATGCCTGC         TACGGTAGCAGAGACTTGGTCTAGACCAGGTGGGTGGGATTTGAAGA         TACGGTAGCAGAGACTTGGTCTGCAGCCCCTGGT         TACGGTAGCAGAGACTTGGTCTGCACTCACCACAGGGGGGGG
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E09 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.04 ASXL1-E13.05 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E03 DNMT3A-E03 DNMT3A-E05 DNMT3A-E05 DNMT3A-E10 DNMT3A-E110 DNMT3A-E110 DNMT3A-E13 DNMT3A-E14 DNMT3A-E15 DNMT3A-E15 DNMT3A-E16 DNMT3A-E16 DNMT3A-E17 DNMT3A-E16 DNMT3A-E17 DNMT3A-E16 DNMT3A-E17 DNMT3A-E17 DNMT3A-E18 DNMT3A-E18 DNMT3A-E18 DNMT3A-E18 DNMT3A-E19	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCATCCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGAGAAGGTGAGG ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAATGTAGAGTCTGGCA ACACTGACGACATGGTTCTACAGCACTTCCCACACCTGAATGCT ACACTGACGACATGGTTCTACAGACTGACTGAGGTAGTGAAACAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTCGAGGAG ACACTGACGACATGGTTCTACAGGCATCGCCACGCTACGCAC ACACTGACGACATGGTTCTACAGGCATCCCACGTGCCAC ACACTGACGACATGGTTCTACAGGCATCCCACGGAGTCTTACTACCT ACACTGACGACATGGTTCTACAGGCATCCCCAGGAGTCTTACTACCT ACACTGACGACATGGTTCTACAGGCATCCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGGCAGCCCAGGGCTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCCTGGGAATGTGG ACACTGACGACATGGTTCTACAGGCAACTTTGGTCGGGAGG ACACTGACGACATGGTTCTACAGGCAACTTTGGTGCGAGGC ACACTGACGACATGGTTCTACAGGCAAGCCTCAGTGAG ACACTGACGACATGGTTCTACAGCCACGGCCTCAGGAG ACACTGACGACATGGTTCTACAGCCCCCTGAATGCTACAC ACACTGACGACATGGTTCTACACACGCCTGAATGCTACAC ACACTGACGACATGGTTCTACACACGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACACACGCCTGAATGCTACAC ACACTGACGACATGGTTCTACACACGCCCTGGAATGCTACAC ACACTGACGACATGGTTCTACACACGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACACACGCCCTGAAGCCCACTGTATA ACACTGACGACATGGTTCTACACACGCCCCTGAAGGCCACAGGTG ACACTGACGACATGGTTCTACACACGCCCCTGACACGCTCACAGGT ACACTGACGACATGGTTCTACACACGCCCCTGGACCACCGTGATGG ACACTGACGACATGGTTCTACACACGCCCTGGACGACGACGGGACAGGG ACACTGACGACATGGTTCTACACACGCCCGTGCACGGGGTCCAGGA ACACTGACGACATGGTTCTACACACGCCCTGGCACCGCCTCCACA ACACTGACGACATGGTTCTACACACGGCGGGGGCTCAGGG ACACTGACGACATGGTTCTACACACGGGGGGGGCCCACGACCTCCACA ACACTGACGACATGGTTCTACACACGGCGGGGTCCAGGACTGGGGCTCAGGA ACACTGACGACATGGTTCTACACACGGGTGTGGGGCTCAGGA ACACTGACGACATGGTTCTACACACGGGTCTAGGGCCTCACACA ACACTGACGACAT	TCAGTCCTAACTCCTGCATTG AAGGAACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGTA AGCAGACTAAAGGGCCGGCTA CAGCAGGCCTACTCC GCCACGGCACTATTCCTTCC GCCACGGCACTATTCCTTCC GCCCGGCACTATTCCTTCTC GCCCGGGTACCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTCGC TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGGTCTGCCCTAT TACGGTAGCAGAGACTTGGTCTGTGGGCCTCTGGCCCTAAT TACGGTAGCAGAGACTTGGTCTGTGGGCCCCCAAC TACGGTAGCAGAGACTTGGTCTCATCACCTGGGCCTCAAC TACGGTAGCAGAGACTTGGTCTCTCATCACCTGGGCCTCAAC TACGGTAGCAGAGACTTGGTCTCTCATCACCTGGACCAGGGGTTAGTGGC TACGGTAGCAGAGACTTGGTCTCATCACCTGGACCAAGGCGC TACGGTAGCAGAGACTTGGTCTCCATCACCAGCGCCCTGGT TACGGTAGCAGAGACTTGGTCTCCATCACCAGCGCCCTGGT TACGGTAGCAGAGACTTGGTCTCCATCACCAGCGCCCTGGG TACGGTAGCAGAGACTTGGTCTCCCATCACCACGCCCCTGTT TACGGTAGCAGAGACTTGGTCTCCCCTGCACCAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCCGCTGTCA TACGGTAGCAGAGACTTGGTCTAGCCCCGCTGTCA TACGGTAGCAGAGACTTGGTCTAGCCACGAGGGTTGGCTTACCACTAGGAGG TACGGTAGCAGAGACTTGGTCTAGCCCCGCTGTCACAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCCCGCTGTCACAAAGGAG TACGGTAGCAGAGACTTGGTCTAGCTCCCCTTCACAAAGGGG TACGGTAGCAGAGACTTGGTCTAGCCCCGCTGTCACAAAGGAG TACGGTAGCAGAGACTTGGTCTAGCCACCGTGCTGTCA TACGGTAGCAGAGACTTGGTCTGGCTACACAAGGGG TACGGTAGCAGAGACTTGGTCTGGCCGCCTGTCACAAAGGG TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGGATTTGAAGAA TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGGGATTGAAGA TACGGTAGCAGAGACTTGGTCTGGCAGAGGGGGGAGCAGACAGA
WT1-E05           WT1-E06           WT1-E07           WT1-E08           WT1-E09           WT1-E10           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.09           ASXL1-E13.10           ASXL1-E13.10           ASXL1-E13.11           ASXL1-E13.12           ASXL1-E13.13           ASXL1-E13.14           ASXL1-E13.15           ASXL1-E13.16           ASXL1-E13.17           DNMT3A-E02           DNMT3A-E03           DNMT3A-E04           DNMT3A-E05           DNMT3A-E06           DNMT3A-E07           DNMT3A-E08           DNMT3A-E10           DNMT3A-E10           DNMT3A-E10           DNMT3A-E11           DNMT3A-E13           DNMT3A-E14           DNMT3A-E15           DNMT3A-E16           DNMT3A-E16           DNMT3A-E16           DNMT3A-E17           DNMT3A-E18      <	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTACAGTCCC ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC ACACTGACGACATGGTTCTACAACCCTGGCAGAGGAAAGGGA ACACTGACGACATGGTTCTACAACTCGAGATGGTGGTGAGG ACACTGACGACATGGTTCTACAACTGAATGGAGGTAGTGAGCA ACACTGACGACATGGTTCTACAGCAGTTCCACACCTGAATGCTGGCA ACACTGACGACATGGTTCTACAGCAGTTGCCACACCTGAATGCT ACACTGACGACATGGTTCTACAGACTGAGTGGTGAGGAACAG ACACTGACGACATGGTTCTACAGACTGGTCCTCGGTGGACAAG ACACTGACGACATGGTTCTACAGACTGGCCATCTCGGGGACAAG ACACTGACGACATGGTTCTACAGGCTGTGCCATCTCGGGACAAG ACACTGACGACATGGTTCTACAGGCTGTCCCACCGCAG ACACTGACGACATGGTTCTACAGGCAGCTCTCGGTGGACAAG ACACTGACGACATGGTTCTACAGGCAGCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGGCAGCCCGAGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGGCAGCTCGGGCACAGGA ACACTGACGACATGGTTCTACAGGCAGGCCCAAGGTAGTGGG ACACTGACGACATGGTTCTACAGGCAGGCCCAAGGAG ACACTGACGACATGGTTCTACAGGCAGGCCCAGTGAGA ACACTGACGACATGGTTCTACAGGCAGGCCTCAGTGGG ACACTGACGACATGGTTCTACAGGCAGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGGCAGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGGCCAGGGCCTCAGTGAG ACACTGACGACATGGTTCTACAGGCCAGGGCCAAGGGG ACACTGACGACATGGTTCTACAGGCCAGGGCCAACGCACCGA ACACTGACGACATGGTTCTACAGGCCGCGCCACTGAATGCTACAC ACACTGACGACATGGTTCTACAGGCCGGGCCACTGAATGCTACAC ACACTGACGACATGGTTCTACAGGCCGGGCCACACTGTAAGCC ACACTGACGACATGGTTCTACAGCCCCCCTGAGACCCACTGGA ACACTGACGACATGGTTCTACAGCCCCCCTGAGACCCACTGGAA ACACTGACGACATGGTTCTACAGCCTCGTGACCACCTGGTAA ACACTGACGACATGGTTCTACAGCCTCGTGACCACCTGGTAA ACACTGACGACATGGTTCTACAGCCTCGTGACCACCTGCTACAA ACACTGACGACATGGTTCTACAGCCTGGTGCCTACCACCACCACCACCACACAGGG ACACTGACGACATGGTTCTACAGGCCTCTGGACGACGGGTCAAGGA ACACTGACGACATGGTTCTACAAGGCCTGCTGCTACGACGACATGGGTCTACAA ACACTGACGACATGGTTCTACAAGGCCTGCTGCTCAGGAC ACACTGACGACATGGTTCTACAAGGGCCTCTGGTCTAGGA ACACTGACGACATGGTTCTACAAGGCCTGCTCCAACCCACCACACACA	TCAGTCCTAACTCCTGCATTG         AAGGAACTAAAGGGCCGGTA         AGCAGTGCTTACTTTCCTCC         GCCACGGCACTATTCCTTCTC         GCCACGGACTATTCCTTCTC         CACCGGACACTATCCTTCTC         CACCGGACACTATCCTTCTC         CACCGGACACATGCTCGGCTGCAGTGGTGGACCTCTGCC         TACGGTAGCAGAGACTTGGTCTGGCGAGTAGTGTGTGTGCC         TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC         TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCCCAAT         TACGGTAGCAGAGACTTGGTCTATGAGCCACCAAGCCCTAAT         TACGGTAGCAGAGACTTGGTCTATCAGCCTTGGCACTAACA         TACGGTAGCAGAGACTTGGTCTCATCACCACGGGGCTCAACA         TACGGTAGCAGAGACTTGGTCTCATCACCACGGGGCTAACA         TACGGTAGCAGAGACTTGGTCTCATCACCACGTGGC         TACGGTAGCAGAGACTTGGTCTCATCACCACGTGGCACCACAAGGGG         TACGGTAGCAGAGACTTGGTCTCACTCACCACGTGCCACAAAGGGG         TACGGTAGCAGAGACTTGGTCTAGACATGGACTTGGCTGGC
WT1-E05 WT1-E07 WT1-E07 WT1-E07 WT1-E08 WT1-E10 ASXL1-E13.01 ASXL1-E13.02 ASXL1-E13.02 ASXL1-E13.03 ASXL1-E13.05 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.06 ASXL1-E13.07 ASXL1-E13.09 ASXL1-E13.09 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.10 ASXL1-E13.11 ASXL1-E13.12 ASXL1-E13.13 ASXL1-E13.14 ASXL1-E13.15 ASXL1-E13.16 ASXL1-E13.16 ASXL1-E13.17 DNMT3A-E02 DNMT3A-E03 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E05 DNMT3A-E10 DNMT3A-E10 DNMT3A-E10 DNMT3A-E13 DNMT3A-E13 DNMT3A-E13 DNMT3A-E13 DNMT3A-E14 DNMT3A-E15 DNMT3A-E15 DNMT3A-E15 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E18 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E18 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E17 DNMT3A-E18 DNMT3A-E17 DNMT3A-	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAGAATG ACTTCATCGGGCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTGAGTAGTGGTGAGG ACACTGACGACATGGTTCTACAATCCTCGAGAAAGAAGGAGAAAGC ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCCGAATGTGAGTGAGGA ACACTGACGACATGGTTCTACAGCATTCCCGAGAGGAGAAACG ACACTGACGACATGGTTCTACAGACTGCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGGCATCCCACTGCGCCA ACACTGACGACATGGTTCTACAGGCATCCCACTGCGCAGG ACACTGACGACATGGTTCTACAGGCATCCCACGTGGCCA ACACTGACGACATGGTTCTACAGGCATCCCACGTGGCCA ACACTGACGACATGGTTCTACAGGCATCCCACGCATGG ACACTGACGACATGGTTCTACAGGCATCCCACGTGACGCAG ACACTGACGACATGGTTCTACAGGCAGCCCAGGAGCTCAAGAA ACACTGACGACATGGTTCTACAGGCAAGCCCCGGAATGTGG ACACTGACGACATGGTTCTACAGGCAAGCCTCGCTGGGAGG ACACTGACGACATGGTTCTACAGGCAAGCGTCCAGTGAG ACACTGACGACATGGTTCTACAGGCAAGCGTCCAGTGAG ACACTGACGACATGGTTCTACAACCGGCAAGCGTCAAGAA ACACTGACGACATGGTTCTACAACCAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACAACAGGCCTGGAATGCTACAC ACACTGACGACATGGTTCTACACACCCCTGATGCTACAC ACACTGACGACATGGTTCTACACACCCCTGATGCTACAC ACACTGACGACATGGTTCTACACACCCCTGATGCTACAC ACACTGACGACATGGTTCTACACACCCCTGATGCACCCTGA ACACTGACGACATGGTTCTACACACCCCTGGAAGGGTCAAGGTG ACACTGACGACATGGTTCTACACACGCCTGGGACTCAGGT ACACTGACGACATGGTTCTACACACGCCTGGGACTCAGGTAA ACACTGACGACATGGTTCTACACACGCTGGGCCACCTGCTTTC ACACTGACGACATGGTTCTACACACGCTGGGCCACCGCTCACAA ACACTGACGACATGGTTCTACACACGGCGTGGGGCTCAGGA ACACTGACGACATGGTTCTACACACGGGCGTGGGGCTCAGGA ACACTGACGACATGGTTCTACACACGGGCGTGGGGCTCAGGA ACACTGACGACATGGTTCTACACACGGGCCTGGGGCTCAGGA ACACTGACGACATGGTTCTACACACGGGCCTGGGGCTCAGGA ACACTGACGACATGGTTCTACACACGGGTCTGGGCTCAGGA ACACTGACGACATGGTTCTACAGGTCCTACGACCGCGCTCGAGAGAC	TCAGTCCTAACTCCTGCATTG         AAGGAACTAAAGGGCCGGTA         AGCAGTGCTTACTTTCCTCC         GCCACGGACTATTCCTTCCTC         GCCACGGACTATTCCTTCCTC         GCCACGGACTATTCCTTCTGCAGTGGTGACCTCTCGC         TACGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC         TACGGTAGCAGAGACTTGGTCTGGCGAGTAGTGTGTCGC         TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTCGC         TACGGTAGCAGAGACTTGGTCTGTGGGGAGTTGGGAGCATC         TACGGTAGCAGAGACTTGGTCTGTGGGCCTTGCTCCTCAT         TACGGTAGCAGAGACTTGGTCTGTGGCGCCACAAGCAGGGGCTCAACA         TACGGTAGCAGAGACTTGGTCTCATCACCTGGGGCTCAACA         TACGGTAGCAGAGACTTGGTCTCATCACCTGGGGGTAGCAGGGGG         TACGGTAGCAGAGACTTGGTCTCATCACACCTGGCGCCCCTAAT         TACGGTAGCAGAGACTTGGTCTCCATCACACCAGGGGGTAGGGG         TACGGTAGCAGAGACTTGGTCTCCATCAACCATGCACCTGGG         TACGGTAGCAGAGACTTGGTCTCCATTACACCATGGCCACTGGG         TACGGTAGCAGAGACTTGGTCTACCATCAGGAGTTGGTCTGGC         TACGGTAGCAGAGACTTGGTCTAGCTCCCATAAAATGCCACGGG         TACGGTAGCAGAGACTTGGTCTAGCTTCCCACTAAAAATGCCTGC         TACGGTAGCAGAGACTTGGTCTGGCCTGTCACCACAAAGGAG         TACGGTAGCAGAGACTTGGTCTGGCCTGTCACCACAAAGAGA         TACGGTAGCAGAGACTTGGTCTGCCACATAGGGGAGATTGAAGA         TACGGTAGCAGAGACTTGGTCTGCCCACATAACAATACACACAA         TACGGTAGCAGAGACTTGGTCTGCCCCACATAGGGGAGAGCAGGCCGCCGGG         TACGGTAGCAGAGACTTGGTCTGCCACACCACGGGAAGACAGGACAGGACACCCGCGAAGACAGGCACACTGGCCCCCGGT
WT1-E05           WT1-E06           WT1-E07           WT1-E07           WT1-E07           WT1-E08           WT1-E10           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.09           ASXL1-E13.10           ASXL1-E13.10           ASXL1-E13.11           ASXL1-E13.12           ASXL1-E13.13           ASXL1-E13.14           ASXL1-E13.15           ASXL1-E13.16           ASXL1-E13.17           DNMT3A-E02           DNMT3A-E03           DNMT3A-E04           DNMT3A-E05           DNMT3A-E06           DNMT3A-E07           DNMT3A-E10           DNMT3A-E110           DNMT3A-E13           DNMT3A-E14           DNMT3A-E15           DNMT3A-E16           DNMT3A-E17           DNMT3A-E18           DNMT3A-E20           DNMT3A-E20           DNMT3A-E20	gDNA           gDNA	ATCTGATTCCAAAGCCCAAG AGAACCCTGCATCTAAAGTGG GCTCATCCTCCTCAAAGTGG GCTCATCCTCCTCAAGACC GGATCATCCTACCCTAACAAGC CAGGCATGGCAGGAAATG ACTTCACTCGGGCCCTTGATA ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC ACACTGACGACATGGTTCTACATCCTAGTTTGCGTGGAGG ACACTGACGACATGGTTCTACAATCCTCGCGACACATTAAAGC ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCTCGAGAAAGGAGGAAAGCT ACACTGACGACATGGTTCTACATCCTGAGAATGGAGGTAGTGAGCA ACACTGACGACATGGTTCTACAGCAGTTGCCATCTCGAGGAG ACACTGACGACATGGTTCTACAGACTGACTGAGGTGATGGAGAACAG ACACTGACGACATGGTTCTACAGACTGCCACTCTGAGGAG ACACTGACGACATGGTTCTACAGACTGCCACTCTGAGGAGA ACACTGACGACATGGTTCTACAGAGCTGTGCCATCTCAGAGGAG ACACTGACGACATGGTTCTACAGAGTCTCCCTACTGCTGGCCA ACACTGACGACATGGTTCTACAGGCAGCCCGCAAGCTCTACTGAGGA ACACTGACGACATGGTTCTACAGGCAGCCCGGAGACTTTACTACCT ACACTGACGACATGGTTCTACAGGCAGGCCCAGGAGATCTTACTACCT ACACTGACGACATGGTTCTACAGGCAGGCCCAGGGAATGTGG ACACTGACGACATGGTTCTACAGGCAGGGCCCAGGAGA ACACTGACGACATGGTTCTACAGGCAGGGCCCAGTGAG ACACTGACGACATGGTTCTACAGGCCAGGAGGCCCAGTGAG ACACTGACGACATGGTTCTACAGGCCAGGCCACGGAAG ACACTGACGACATGGTTCTACAGGCCAGGCCCACGGAAG ACACTGACGACATGGTTCTACAGGCCAGGCCCACGAGAG ACACTGACGACATGGTTCTACAGGCCAGGCCACATGATGCT ACACTGACGACATGGTTCTACAGGCCAGGCCACATGATGCT ACACTGACGACATGGTTCTACAGGCCCACCCCTGATGCCA ACACTGACGACATGGTTCTACAGGCCCACCCCCACTGATGCC ACACTGACGACATGGTTCTACAGCCCCCCCCTGAGACGCC ACACTGACGACATGGTTCTACAGCCCCCCCCACTGATGCCA ACACTGACGACATGGTTCTACAGCCCCCCCCACTGATGCC ACACTGACGACATGGTTCTACAGCCCCCCCCACTGACGCCC ACACTGACGACATGGTTCTACAGCCCCCCCACTGACTACTCA ACACTGACGACATGGTTCTACAGCCCCCCCCCCCCCCCC	TCAGTCCTAACTCCTGCATTG         AAGGAACTAAAGGGCCGGTA         AGCAGTGCTTACTTTCCTCC         GCCACGGACTATTCCTTCTC         GCCACGGACTATTCCTTCTC         CACCGGACACTATCCTTCTC         CACGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC         TACGGTAGCAGAGACTTGGTCTGGCGAGTAGTGTGTGTGCGC         TACGGTAGCAGAGACTTGGTCTGGCGCAGTAGTTGTGTGTG

DNMT3A-E23	gDNA	ACACTGACGACATGGTTCTACACACTCACCCTGCCCTCTCT	TACGGTAGCAGAGACTTGGTCTAAAGCCCTCCGGTATTTCC
FLT3-E20X	gDNA	ACACTGACGACATGGTTCTACAGCACTCCAGGATAATACACATCA	TACGGTAGCAGAGACTTGGTCTACAGTGAGTGCAGTTGTTTACC
IDH1-E04	gDNA	ACACTGACGACATGGTTCTACAAAACTTTGCTTCTAATTTTTCTCTTTC	TACGGTAGCAGAGACTTGGTCTGCAAAATCACATTATTGCCAAC
IDH2-E04	gDNA	ACACTGACGACATGGTTCTACATGCAGTGGGACCACTATTATCTC	TACGGTAGCAGAGACTTGGTCTCACCACTGCCATCTTTTGG
NPM1-E11	gDNA	ACACTGACGACATGGTTCTACAAGATGTTGAACTATGCAAAGAGACA	TACGGTAGCAGAGACTTGGTCTACCAAGCAAAGGGTGGAGTT
NRAS-E02	gDNA	ACACTGACGACATGGTTCTACATACTGTAGATGTGGCTCGCC	TACGGTAGCAGAGACTTGGTCTTGATCCGACAAGTGAGAGACA
NRAS-E03	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT
TET2-E03.01	gDNA	ACACTGACGACATGGTTCTACAATTCAACTAGAGGGCAGCCTTG	TACGGTAGCAGAGACTTGGTCTACTGTGCGTTTTATTCCTCCAT
TET2-E03.02	gDNA	ACACTGACGACATGGTTCTACAGAATACCCTGTATGAAGGGAAGC	TACGGTAGCAGAGACTTGGTCTCCCACTGCAGTTATGTGTTGAA
TET2-E03.03	gDNA	ACACTGACGACATGGTTCTACATGTAGCCCAAGAAAATGCAG	TACGGTAGCAGAGACTTGGTCTTGGGTGAGTGATCTCACAGG
TET2-E03.04	gDNA	ACACTGACGACATGGTTCTACACATCTCACATAAATGCCATTAACA	TACGGTAGCAGAGACTTGGTCTAGCTTGCAAATTGCTGCTG
TET2-E03.05	gDNA	ACACTGACGACATGGTTCTACAGAAAATAACATCCAGGGAACCA	TACGGTAGCAGAGACTTGGTCTCCCTCTATTTTCACTTCCCTTAAA
TET2-E03.06	gDNA	ACACTGACGACATGGTTCTACAGGAGTTTTAGAAGAACACCACCA	TACGGTAGCAGAGACTTGGTCTTCGACCCTTCAGAATCTCTTG
TET2-E03.07	gDNA	ACACTGACGACATGGTTCTACACCAATTTTTGGTAGCAGTGGA	TACGGTAGCAGAGACTTGGTCTCCAGCTGTGTTGTTTTCTGG
TET2-E03.08	gDNA	ACACTGACGACATGGTTCTACATGACCTCCAAACAATACACTGG	TACGGTAGCAGAGACTTGGTCTTGAGTTTGAAAATGGCTCAGTC
TET2-E03.09	gDNA	ACACTGACGACATGGTTCTACACCCAGTGTTGAAACAGCA	TACGGTAGCAGAGACTTGGTCTACTTCCTCCAGTCCCATTTG
TET2-E03.10	gDNA	ACACTGACGACATGGTTCTACATGGTGAAAATCAGTATTCAAAATCA	TACGGTAGCAGAGACTTGGTCTTTGACCAGACATATCTTGGTTTC
TET2-E03.11	gDNA	ACACTGACGACATGGTTCTACACTTCTTCACAGGTGCTTTCAAG	TACGGTAGCAGAGACTTGGTCTATACAGGCATGTGGCTTGC
TET2-E03.12	gDNA	ACACTGACGACATGGTTCTACATTGCCATAGTCAGATGCACAG	TACGGTAGCAGAGACTTGGTCTCTGAAGAAGTTGTTTGCTGCTCT
TET2-E03.13	gDNA	ACACTGACGACATGGTTCTACATTGACTAGACAAACCACTGCTG	TACGGTAGCAGAGACTTGGTCTTTTATGAGCCTTTACAAATTGCTG
TET2-E04	gDNA	ACACTGACGACATGGTTCTACATGGCACATTTTCTAATAGATCAGTC	TACGGTAGCAGAGACTTGGTCTCTTTGTGTGTGAAGGCTGGA
TET2-E05	gDNA	ACACTGACGACATGGTTCTACAAAACCGTTCATTTCTCAGGATG	TACGGTAGCAGAGACTTGGTCTGTAATGTTCTTTTTAACTGGCATGA
TET2-E06	gDNA	ACACTGACGACATGGTTCTACAGCCCTTATCTGCTGCAAGTG	TACGGTAGCAGAGACTTGGTCTTTGGGCTTTCCTATCAGTGG
TET2-E07	gDNA	ACACTGACGACATGGTTCTACAATAGACACCTATAATATCAGCTGCAC	TACGGTAGCAGAGACTTGGTCTCAGTTTGGGAAAAACTTTGATTA
TET2-E08	gDNA	ACACTGACGACATGGTTCTACACCATATATTGTGTTTGGGATTCAA	TACGGTAGCAGAGACTTGGTCTGCAGTGGTTTCAACAATTAAGAG
TET2-E09	gDNA	ACACTGACGACATGGTTCTACATGCTCTATTTTGTGTCATTCCATT	TACGGTAGCAGAGACTTGGTCTCAGTGTGAGAACAGACTCAACAG
TET2-E10.01	gDNA	ACACTGACGACATGGTTCTACAGGGACCTGTAGTTGAGGCTGT	TACGGTAGCAGAGACTTGGTCTGGGGCTGACTTTTCCTTTTC
TET2-E10.02	gDNA	ACACTGACGACATGGTTCTACAGAGTTTGGGAGTGTGGAAGC	TACGGTAGCAGAGACTTGGTCTGGGGGGCAAAACCAAAATAAT
TET2-E11.01	gDNA	ACACTGACGACATGGTTCTACAGCCTTCATAAAATAATCATCAACA	TACGGTAGCAGAGACTTGGTCTCTGCAGCTTGAGATGAGGTG
TET2-E11.02	gDNA	ACACTGACGACATGGTTCTACACCAATCCAGTTAGTCCTTATCCA	TACGGTAGCAGAGACTTGGTCTAAAACTCTGGCTATTTCCAAACC
TET2-E11.03	gDNA	ACACTGACGACATGGTTCTACACAAGCCAAGACCCTCTGTCT	TACGGTAGCAGAGACTTGGTCTGCATGAAGAGAGCTGTTGAA
TET2-E11.04	gDNA	ACACTGACGACATGGTTCTACAGGTGAACATCATTCACCTTCTC	TACGGTAGCAGAGACTTGGTCTGAATTGACCCATGAGTTGGAG
TET2-E11.05	gDNA	ACACTGACGACATGGTTCTACAAGACAGCGAGCAGAGCTTTC	TACGGTAGCAGAGACTTGGTCTAAGTTTCATGTGGCTCAGCA
TET2-E11.06	gDNA	ACACTGACGACATGGTTCTACAAGCCCGTGAGAAAGAGGAAG	TACGGTAGCAGAGACTTGGTCTACTGTGACCTTTCCCCACTG
TP53-E04	gDNA	ACACTGACGACATGGTTCTACAACCTGGTCCTCTGACTGCTC	TACGGTAGCAGAGACTTGGTCTCAGGCATTGAAGTCTCATGG
TP53-E05	gDNA	ACACTGACGACATGGTTCTACACACTTGTGCCCTGACTTTCA	TACGGTAGCAGAGACTTGGTCTCACTCGGATAAGATGCTGAGG
TP53-E06	gDNA	ACACTGACGACATGGTTCTACACAGATAGCGATGGTGAGCAG	TACGGTAGCAGAGACTTGGTCTTTGCACATCTCATGGGGTTA
TP53-E07	gDNA	ACACTGACGACATGGTTCTACAGCACTGGCCTCATCTTGG	TACGGTAGCAGAGACTTGGTCTAAGAGGTCCCAAAGCCAGAG
TP53-E08	gDNA	ACACTGACGACATGGTTCTACAGGACAGGTAGGACCTGATTTC	TACGGTAGCAGAGACTTGGTCTTCTCCATCCAGTGGTTTCTTC
TP53-E09	gDNA	ACACTGACGACATGGTTCTACAAAAGGGGAGCCTCACCAC	TACGGTAGCAGAGACTTGGTCTTGTCTTTGAGGCATCACTGC
TP53-E10	gDNA	ACACTGACGACATGGTTCTACAGCTGTATAGGTACTTGAAGTGCAG	TACGGTAGCAGAGACTTGGTCTCTGCCTTTGACCATGAAGG
TP53-E11	gDNA	ACACTGACGACATGGTTCTACAAGGGAAAAGGGGGCACAG	TACGGTAGCAGAGACTTGGTCTCCCCACAACAAAACACCAGT
WT1-E01.01	gDNA	ACACTGACGACATGGTTCTACATCCTCGCCGCGATCCTG	TACGGTAGCAGAGACTTGGTCTGGCGCAAAGTCCAGCAC
WT1-E01.02	gDNA	ACACTGACGACATGGTTCTACACAGCGCTGAACGTCTCCA	TACGGTAGCAGAGACTTGGTCTGCTCAGGCACTGCTCCTC
WT1-E01.03	gDNA	ACACTGACGACATGGTTCTACAGCCTCACTCCTTCATCAAAC	TACGGTAGCAGAGACTTGGTCTGGGTAAGAGCTGCGGTCA
WT1-E02	gDNA	ACACTGACGACATGGTTCTACACGCTGACACTGTGCTTCTCT	TACGGTAGCAGAGACTTGGTCTTACTTGGGATGGAGGGAG
WT1-E03	gDNA	ACACTGACGACATGGTTCTACACAGGCTCAGGATCTCGTGTC	TACGGTAGCAGAGACTTGGTCTGTCTCGTGCCTCCAAGACC
WT1-E04	gDNA	ACACTGACGACATGGTTCTACATCACATCCCTTCTGCTGTGT	TACGGTAGCAGAGACTTGGTCTCTTTGAAATGGTTCAAACAGG
WT1-E05	gDNA	ACACTGACGACATGGTTCTACAATCTGATTCCAAAGCCCAAG	TACGGTAGCAGAGACTTGGTCTTCAGTCCTAACTCCTGCATTG
WT1-E06	gDNA	ACACTGACGACATGGTTCTACAAGAACCCTGCATCTAAAGTGG	TACGGTAGCAGAGACTTGGTCTAAGGAACTAAAGGGCCGGTA
WT1-E07	gDNA	ACACTGACGACATGGTTCTACAGCTCACTCTCCCTCAAGACC	TACGGTAGCAGAGACTTGGTCTAGCAGTGCTTACTTTCCATCC
WT1-E08	gDNA	ACACTGACGACATGGTTCTACAGGATCATCCTACCCTAACAAGC	TACGGTAGCAGAGACTTGGTCTAAACTAAACACATGGCTGACTCTC
WT1-E09	gDNA	ACACTGACGACATGGTTCTACACAGGCATGGCAGGAAATG	TACGGTAGCAGAGACTTGGTCTGCCACGCACTATTCCTTCTC
WT1-E10	gDNA	ACACTGACGACATGGTTCTACAACTTCACTCGGGCCTTGATA	TACGGTAGCAGAGACTTGGTCTCACCGGTATCTTGTCTTGGA

### Table S2: Primer sequences used to analyze the respective genes by MiSeq Sequencing

Gene-Identifier	Material	Sequence: Forward-Primer(5'-3')	Sequence: Reverse-Primer(5'-3')
ASXL1-E13.01	gDNA	ACACTGACGACATGGTTCTACATCCTAGTTTTGCTTTACAGTCCC	TACGGTAGCAGAGACTTGGTCTGCAGTGGTGACCTCTCGC
ASXL1-E13.03	gDNA	ACACTGACGACATGGTTCTACAACCCTCGCAGACATTAAAGC	TACGGTAGCAGAGACTTGGTCTCGGCAGTAGTTGTGTTCGC
ASXL1-E13.04	gDNA	ACACTGACGACATGGTTCTACAAGTGGTGATGGTGGTGAGG	TACGGTAGCAGAGACTTGGTCTGGGGAGTTGGGAGGCATC
ASXL1-E13.05	gDNA	ACACTGACGACATGGTTCTACATCTCTGAGAAAGGAGGAAAGCT	TACGGTAGCAGAGACTTGGTCTGTGGGTCCTTGCTCCTCAT
ASXL1-E13.06	gDNA	ACACTGACGACATGGTTCTACAGAACTGAATGTGAGTCTGGCA	TACGGTAGCAGAGACTTGGTCTATGAGCCACCAAGCCCTAAT
ASXL1-E13.07	gDNA	ACACTGACGACATGGTTCTACACCAGTTCCACACCTGAATCCT	TACGGTAGCAGAGACTTGGTCTCCAACCTGGGGCTCAACA
ASXL1-E13.08	gDNA	ACACTGACGACATGGTTCTACATCGAATGATGAGGTAGTGAAACAG	TACGGTAGCAGAGACTTGGTCTTTCAGCTTTTCAATGTCCACCT
ASXL1-E13.09	gDNA	ACACTGACGACATGGTTCTACAGACTGTGCCATCTCGAGGAG	TACGGTAGCAGAGACTTGGTCTCATTCACCTTGGACAGTGGG
ASXL1-E13.10	gDNA	ACACTGACGACATGGTTCTACAAGGGATCTTCGGTGGACAAG	TACGGTAGCAGAGACTTGGTCTCATCACAAGTGGGTTAGTGGC
ASXL1-E13.11	gDNA	ACACTGACGACATGGTTCTACAGATTCCCTACTGCTGGCCA	TACGGTAGCAGAGACTTGGTCTCCATCAACCATGCCACTGTT
ASXL1-E13.12	gDNA	ACACTGACGACATGGTTCTACACATGGCTCGCTACGCATG	TACGGTAGCAGAGACTTGGTCTCCATTTCTTCCAGTTTCCTAGAGG
ASXL1-E13.13	gDNA	ACACTGACGACATGGTTCTACAGGCAGTCCCAAGTTTTGACT	TACGGTAGCAGAGACTTGGTCTTCTGCTCTGGACCAAAGGAG
ASXL1-E13.14	gDNA	ACACTGACGACATGGTTCTACAGCCCAGGAGATCTTACTACCT	TACGGTAGCAGAGACTTGGTCTAGACATGGAGTTTGTGCTTGG
ASXL1-E13.15	gDNA	ACACTGACGACATGGTTCTACATTTTGGCTCTGGGAATGTGG	TACGGTAGCAGAGACTTGGTCTATGCCCAGTAGCTTTCCTGT
ASXL1-E13.16	gDNA	ACACTGACGACATGGTTCTACATTTGTTGGCAGCGTCAAGAA	TACGGTAGCAGAGACTTGGTCTAGCTTCCCATAAAATGCCTGC
ASXL1-E13.17	gDNA	ACACTGACGACATGGTTCTACAGGGAAGGGGGCTCAGTGAG	TACGGTAGCAGAGACTTGGTCTTCCACCGTGCTGCTGTCA
ASXL1-E13.18	gDNA	ACACTGACGACATGGTTCTACAGCAAACTTTGGTGCGAGCC	TACGGTAGCAGAGACTTGGTCTAGATCAATCATTATCAAAATACACACA
CEBPA-E01.01	gDNA	ACACTGACGACATGGTTCTACACCATGCCGGGAGAACTCTA	TACGGTAGCAGAGACTTGGTCTGTCGTTGAAGGCGGCC
CEBPA-E01.02	gDNA	ACACTGACGACATGGTTCTACAATCTGCGAGCACGAGACG	TACGGTAGCAGAGACTTGGTCTCTCCAGCCTGCCGTCC
CEBPA-E01.03	gDNA	ACACTGACGACATGGTTCTACAGGCGACTTTGACTACCCGG	TACGGTAGCAGAGACTTGGTCTCGGCTGGTAAGGGAAGAGG
CEBPA-E01.04	gDNA	ACACTGACGACATGGTTCTACAGCCGCTGGTGATCAAGC	TACGGTAGCAGAGACTTGGTCTGACCGGGCTGCAGGTG
CEBPA-E01.05	gDNA	ACACTGACGACATGGTTCTACAGCAGTTCCAGATCGCGC	TACGGTAGCAGAGACTTGGTCTCGGTACTCGTTGCTGTTCTT
CEBPA-E01.06	gDNA	ACACTGACGACATGGTTCTACACTCAAGGGGCTGGGCG	TACGGTAGCAGAGACTTGGTCTCAGCTGGCGGAAGATGC
CEBPA-E01.07	gDNA	ACACTGACGACATGGTTCTACAGTGGACAAGAACAGCAACGA	TACGGTAGCAGAGACTTGGTCTCGCAGCGTGTCCAGTTC
CEBPA-E01.08	gDNA	ACACTGACGACATGGTTCTACAGCAAGCGGGTGGAACA	TACGGTAGCAGAGACTTGGTCTAGAGGAAGGGAGGGGACAC
DNMT3A-E07.01	gDNA	ACACTGACGACATGGTTCTACATTCCTGGAGAGGTCAAGGTG	TACGGTAGCAGAGACTTGGTCTTTTGGTGGCATTCTTGTCCC

DNMT3A-E07.02	gDNA	ACACTGACGACATGGTTCTACAGGAAGAAAACCAGGGGCCC	TACGGTAGCAGAGACTTGGTCTGAGGAGCTGGCAGTGGAAG
DNMT3A-F08	ØDNA	ACACTGACGACATGGTTCTACACTCGTGACCACTGTGTGATGAT	TACGGTAGCAGAGACTTGGTCTGCCCTGGGATCAAGAACCTT
	55101		
DNMT3A-E09	gDNA	ACACTGACGACATGGTTCTACAGGTGGGTGCTTGCAAGTG	TACGGTAGCAGAGACTTGGTCTACCTGCACTCCAACTTCCAG
DNMT3A-E10	gDNA	ACACTGACGACATGGTTCTACACTGACAACCCCAACCCTG	TACGGTAGCAGAGACTTGGTCTGCCCTGGTGTGGATCTGC
DNNAT3A F11		ACACTCACCACATCCTTCTACACTCTAACTCACCTTCCCACCT	TACCOTACCACACACTTCCTCTTCCCATCCACCCCTCCT
DNMI3A-EII	guna	ACACIGACGACAIGGIICIACACIGIAACIGACCIIGGCACCI	TALGGTAGLAGAGACTTGGTCTTLGGATGLAGGLCTLLT
DNMT3A-E12	gDNA	ACACTGACGACATGGTTCTACAAGAAGCCCAAGGTCAAGGAG	TACGGTAGCAGAGACTTGGTCTCTCTGCTACTCTGCCCCATG
DNIMT2A E12		ACACTEACEACATECTTCTACATTTTETECCTCCTCCTCC	TACCETACCACACACTTCCTCTACAACCCCTCCACACACTC
DINIVIT3A-E13	BDINA		TACGGTAGCAGAGACTTGGTCTAGAAGCGGTGGACACAGTC
DNMT3A-E14	gDNA	ACACTGACGACATGGTTCTACAGAGCCTCCCTTCGTCCTG	TACGGTAGCAGAGACTTGGTCTGGCCCAGCTAAGGAGACC
DNMT3A-E15.01	σDNA	ΔΓΔΟΤGΔCGΔCΔTGGTTCTΔCΔCCΔGGGCTGΔGΔGTCTCCT	TACGGTAGCAGAGACTTGGTCTGCCCAGCACTCACAAATTCC
DINITISA EIS.01	5011/4		
DNM13A-E15.02	gdna	ACACIGACGACAIGGIICIACAGIGGAGIGIGIGGGACCICII	TALGGTAGLAGAGALTTGGTLTLLLLALAAGLAAGGLTLA
DNMT3A-E16	gDNA	ACACTGACGACATGGTTCTACACTGGGCCTGCATCTGACC	TACGGTAGCAGAGACTTGGTCTGTTTTGCCAGAGTTGCCCAC
DNIMTON 517	-DNA	ACALCER ACATEGOTICE ACATEGOTICE ACTA ACCETE	TACCOTACOACACITECOTOTOTOCACCOACCOACCA
DINIMIT3A-E17	guna	ACACIGACGACAIGGIICIACAGAIGGCICCAAGIAACGGIG	TALGGTAGLAGAGACTTGGTCTGTGLAGGGAGGGGAAGAC
DNMT3A-E18	gDNA	ACACTGACGACATGGTTCTACACTTCCTGTCTGCCTCTGTCC	TACGGTAGCAGAGACTTGGTCTCATCGGGAATAGCTGTCCCA
DNMT3A-F19	σDNA	ΔΟΛΟΤΩΛΟΩΛΟΛΤΩΩΤΤΟΤΛΟΛΩΛΩΟΟΛΟΛΟΛΟΤΩΤΟΤΑΤ	TACGGTAGCAGAGACTTGGTCTCCATTAGTGAGCTGGCCAAAC
DINIVITSA-L15	BDINA	ACACIOACOACAIOGITEIACAOAOCCACACCACIOICEIAI	TACCOTACCACACACITICATICCATTACTCACCTCCCAAAC
DNMT3A-E20	gDNA	ACACTGACGACATGGTTCTACACCTTGGCTCATCTTCAAACCG	TACGGTAGCAGAGACTTGGTCTAGCAGCTAGTCATTCAGCAGA
DNMT3A-F21	gDNA	ACACTGACGACATGGTTCTACAACCCTGTGAACTAGTGGCTG	TACGGTAGCAGAGACTTGGTCTCATCCTGCCCTTCCTTCTCC
DA114 1704 500			
DINIVIT3A-E22	guna		TALGGTAGLAGAGACTTGGTLTLALAGLAATLAGAALAGLLAL
DNMT3A-E23.02	gDNA	ACACTGACGACATGGTTCTACACACTCACCCTGCCCTCTC	TACGGTAGCAGAGACTTGGTCTTGTTTAACTTTGTGTCGCTACCT
ELT3-E06	σDNA	ΔΓΑΓΤΘΑΓΘΑΓΑΤΘΟΤΤΓΤΑΓΑΤΘΓΑΘΓΤΘΤΑΔΑΘΑΔΘΑΔΟΤΓΓ	TACGGTAGCAGAGACTTGGTCTGAACCGGTCACTGAAAATGAA
1213 200	50117	ACACIGACGACATGGITETACATGCAGCIGTAGAGAAGAAGAAGA	TACCOTACACACACITOCICICACICACICACICACICACICACICACICACICAC
FLT3-E20	gDNA	ACACTGACGACATGGTTCTACAGCACTCCAGGATAATACACATCA	TACGGTAGCAGAGACTTGGTCTACAGTGAGTGCAGTTGTTTACC
FLT3-F24	gDNA	ACACTGACGACATGGTTCTACATACTACAGAATTGCCCATTATTGAA	TACGGTAGCAGAGACTTGGTCTTGACAACCATAGCTGCCTACA
5170 104 00	55101		
FL13-101.02	gDNA	ACACIGACGACAIGGIICIACAACCCIGGGIGACAGAGACAG	TACGGTAGCAGAGACTTGGTCTAGCCTCCCGAGTAACTAGGATT
FLT3-I01.03	gDNA	ACACTGACGACATGGTTCTACAGGAGAGAATGGAGGAAAGGAA	TACGGTAGCAGAGACTTGGTCTCAAGAAGTCTGCCAAATGAATG
ELT2 101 06	(DNA		TACGGTAGCAGAGACTTGGTCTGATGCCAATTCCACATTGTCT
FL13-101.00	BDINA	ACACIDACOACAIOUTICIACATTIOCCCAAATTOATCIAOTOA	TACGGTAGCAGAGACTTGGTCTGATGCCAATTCCACATTGTCT
FLT3-I01.07	gDNA	ACACTGACGACATGGTTCTACATTCAGTTAGGAGGGTAAGTTCTGG	TACGGTAGCAGAGACTTGGTCTAGGTGGAGATTGCAGTTGGT
ELT3-I01 09	ØDNA	ACACTGACGACATGGTTCTACAGGAATGGGGTTGGTAGCAG	TACGGTAGCAGAGACTTGGTCTTACTTGGGAGGCTGAAGTGG
5172 104 44	-014		
FLI3-101.11	gDNA	ALALIGALGACATGGTTCTACAAGGCAGCAAGCAAGAGAGAG	TALGGTAGCAGAGACTTGGTCTTTTTCCCCCAAATGACTGACAA
FLT3-I02	gDNA	ACACTGACGACATGGTTCTACATTTGCTCCTGTGTCCTTTCA	TACGGTAGCAGAGACTTGGTCTGGCACACCCAACTCTCAGAT
FI T2 100 01			
FL13-109.01	guna		
FLT3-109.02	gDNA	ACACTGACGACATGGTTCTACACTTGAGGGCAGGAGTTTGAG	TACGGTAGCAGAGACTTGGTCTCCACCACAGCCAGCTAATTT
ELT3-109-04		ACACTGACGACATGGTTCTACATACTGCCACTCCACTCC	TACGGTAGCAGAGACTTGGTCTCCAAGGAGGAGAGAGAAAACCAC
FL13-109.04	gDNA	ACACIGACGACAIGGIICIACAIGGCCACIGCACICCAAC	TACGGTAGCAGAGACTTGGTCTCCAAGGAGGAGACAAAGCAG
FLT3-I11	gDNA	ACACTGACGACATGGTTCTACATGGACCTGGAAGAAGTGTTCA	TACGGTAGCAGAGACTTGGTCTGGATTTCTGCAGCGAGTTCT
ELT2 11E 02			TACCETACCACACACTTCCTCTCCCCCAATCAACCAAAAACA
FL13-113.02	BDINA		TACGOTAGCAGAGACTTGGTCTTGGGGAATGAAGGAAAAACA
FLT3-I15.03	gDNA	ACACTGACGACATGGTTCTACATGGAGAGGGAAGTCCAGAGA	TACGGTAGCAGAGACTTGGTCTAACTGCCAAGCAGGCTAGAA
FLT3-I17	ØDNA	ACACTGACGACATGGTTCTACATTTTAAGTGCAGGCCTCTGG	TACGGTAGCAGAGACTTGGTCTAGGATAGCCCCTCTGTTCCA
	5011/4		
FLT3-I19.02	gDNA	ACACTGACGACATGGTTCTACAACTCCCAACTGGCAGTCAAG	TACGGTAGCAGAGACTTGGTCTTCAAGGGCCTACAGAGGAAA
FLT3-I20	gDNA	ACACTGACGACATGGTTCTACAGGCAGGCACCTAAAATACCA	TACGGTAGCAGAGACTTGGTCTTCCTTGTCCTCCCTGTGAAG
51 70 100			
FLI3-IZZ	guna	ACACIGACGACAIGGIICIACAGCAIICCGGIIGAIGCIAAC	TALGGTAGLAGAGALTTGGTLTLLAALALAGLAAGALLTLAL
FLT3-I23.01	gDNA	ACACTGACGACATGGTTCTACATCAAAAGGCCAGAGGAAATG	TACGGTAGCAGAGACTTGGTCTGATCATTCCACTGCACTCCA
FI T2 122 02		ACACTCACCACATCCTTCTACAACCTACCCTTTCTTCACAATTTC	TACCOLACACACTECETCLACCECTECTCLACTCCA
FL13-123.02	guna	ACACIGACGACATGGITCIACAACCIAGGGITTGITTCACAATTIC	TACGGTAGCAGAGACTTGGTCTAGGCTGGTCTTGCACTCCT
IDH1-E04.X	gDNA	ACACTGACGACATGGTTCTACATCAAGTTGAAACAAATGTGGAAATCA	TACGGTAGCAGAGACTTGGTCTCATACAAGTTGGAAATTTCTGGGC
IDH2-E04	αDNA		TACGGTAGCAGAGACTTGGTCTCAGGTCAGTGGATCCCCTC
IDH2-E04	BDINA	ACACIDACCACATOCITCIACATICIDOTICAAACATOCCOC	TACOUTACCAGAGACTTOUTCTCAGGTCAGTGGATCCCCTC
NPM1-E11	gDNA	ACACTGACGACATGGTTCTACATGTCTATGAAGTGTTGTGGTTCC	TACGGTAGCAGAGACTTGGTCTACAGGCATTTTGGACAACACA
NRAS-E02	gDNA	ACACTGACGACATGGTTCTACATACTGTAGATGTGGCTCGCC	TACGGTAGCAGAGACTTGGTCTTGATCCGACAAGTGAGAGACA
NDAS FOO	0		
	AL 1010	ACACTC ACCATCC TTC TACACCC TCCC TCCC TC	
INITAS E05	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT
RUNX1-E01.01	gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACTGCTTGCTGAAGATCCGC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG
RUNX1-E01.01	gDNA gDNA	ACACTGACGACATGGTTCTACACCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCTGCTGCCGAAGATCCGC ACACTGACGACATGGTTCTACACCGCGCAAGATCAGCGA	TACGGTAGCAGAGACTTGGTCTAGATCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACATG TACGGTAGCAGAGACTTGGTCTCCCCCCTGCCCCCA
RUNX1-E01.01 RUNX1-E01.02	gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACTGCTTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCAGGCAAGATGAGCGA	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTCTCCGCCTGTCCTCCCA
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01	gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTAC ACACTGACGACATGGTTCTACACTGCTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCAGGCAAGATGAGGGG ACACTGACGACATGGTTCTACATCCTCTGCAACCTAAAAAGAAATCA	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTCCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTCCGACTGGTCTTCATGG
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02	gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCCCCCCCCTTAC ACACTGACGACATGGTTCTACACTGCTTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACATCCTCTGCAACCTAAAAAGAAATCA ACACTGACGACATGGTTCTACAGGTGGTTCTACGTGGGTGG	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTCCACCTGGTTCTCATGG TACGGTAGCAGAGACTTGGTCTTGTTTGAAATGTGGGTTTGCTCCC
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02	gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTAC ACACTGACGACATGGTTCTACACTGCTGGTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCCA TACGGTAGCAGAGACTTGGTCTTGCACCTGGTTCTCCATGG TACGGTAGCAGAGACTTGGTCTTGCAACTGGTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTTGTGCC
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02 RUNX1-E03	gDNA gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACTGCTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACATCCTCTGCAACCTAAAAAGAAATCA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAACAGATATGTTCAGGCCACCA	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTCCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTCCGAACTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTTATTTGAAATGTGGGTTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02 RUNX1-E03 RUNX1-E04.01	gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACTGCTGTGTAGAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACCCCTGCAACCTAAAAAGAAATCA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCCC ACACTGACGACATGGTTCTACACGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACACGATCTCTTCCCTCCCTC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTCCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTGCAACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTCTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTTAAACGC TACGGTAGCAGAGACTTGGTCTGACGTCGAGGGCTAAAGGC
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02 RUNX1-E03 RUNX1-E04.01 PUINX1-E04.02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTAC ACACTGACGACATGGTTCTACACTGCTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACTCCTCTGCAACCTAAAAAAGAAATCA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAACAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACAACTGATCTCTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTCCAACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTGATCTGAAATGTGGGTTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTTGACGCTGAGGGTTAAAGGC
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02 RUNX1-E03 RUNX1-E04.01 RUNX1-E04.02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACTGCTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACCCCTGCAACCTAAAAAGAAATCA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCCC ACACTGACGACATGGTTCTACACAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACACGAGCTTGTCCTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTCCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTGCAACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTCTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGAGGTCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGAGGTCTGAGGGTTAAAGGC
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02 RUNX1-E03 RUNX1-E04.01 RUNX1-E04.02 RUNX1-E05	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTAC ACACTGACGACATGGTTCTACACTGCTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAACAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACAACAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACACAGAGCTGTCCTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTGCAACTGGTCTTCTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGAGCTGGGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGTCTGGTCGGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGTCAGTGCAAGAATGTG
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02 RUNX1-E03 RUNX1-E03 RUNX1-E04.01 RUNX1-E04.02 RUNX1-E05 RUNX1-E06.01	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACTGCTGGTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTCTTTCCCTCCCTCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTCCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTGCAACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGAGGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGTCTGGGCTGGGAAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCTCAGGTAGACAGTGTG TACGGTAGCAGAGACTTGGTCTGGCTCAGCTGCAAAGAATGTG
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02 RUNX1-E03 RUNX1-E04.01 RUNX1-E04.02 RUNX1-E05 RUNX1-E05 RUNX1-E05 RUNX1-E05 C2	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCTGCTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTCAGGCGCCCA ACACTGACGACATGGTTCTACACAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACACGGTGTTCTCTCCCCCCC ACACTGACGACATGGTTCTACACGGCTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGGGCAGAGGGAGAGCCTG ACACTGACGACATGGTTCTACAAAATCCCACCCCAC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCCA TACGGTAGCAGAGACTTGGTCTTGCAACTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGAGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGTCGGGGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGTCGGCAGGGTAGGAAGGTGG TACGGTAGCAGAGACTTGGTCTGGCCAGGTAGGAAGGTGG TACGGTAGCAGAGACTTGGTCTGGCCAGGTAGGATGGTG TACGGTAGCAGAGACTTGGTCTGGCCAGGTAGGGTGGTGGTAGC
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02 RUNX1-E03 RUNX1-E04.01 RUNX1-E04.02 RUNX1-E05 RUNX1-E06.01 RUNX1-E06.02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACTGCTGGTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGCGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTCCCTCC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGAGCTGTCCTTTCCCACCCA	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTCCGCCTGTCCTCCAC TACGGTAGCAGAGACTTGGTCTTCCGCCTGTCTTCATGG TACGGTAGCAGAGACTTGGTCTGATCTGACATGGTCCCTGAGTATGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGAAGGTGT TACGGTAGCAGAGACTTGGTCTGACGTCGGCAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGCTGGCAAGGTGTG TACGGTAGCAGAGACTTGGTCGTCAGCTGACAAGAATGGT TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGG TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGG TACGGTAGCAGAGACTTGGTCTGCTCGCAGGTAGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCTCGCAGGAACTGGTAGGAGCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E02.02           RUNX1-E03.01           RUNX1-E04.01           RUNX1-E05           RUNX1-E05.01           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCTGCTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTCAGGCCACCA ACACTGACGACATGGTTCTACAGAGCTGTCCTTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCAC TACGGTAGCAGAGACTTGGTCTTGCACTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTTATGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCAGGTATAACGC TACGGTAGCAGAGACTTGGTCTGACGTCGGCAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGCAGGTCGAAGGATGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGAGAAGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGAGAAGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGAGAAGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGAGCGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCTCAGCAGAACTGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCGCCAGCAGCACTGGTAGGAGCC
RUNX1-E01.01 RUNX1-E01.02 RUNX1-E02.01 RUNX1-E02.02 RUNX1-E03 RUNX1-E04.01 RUNX1-E04.02 RUNX1-E05 RUNX1-E05 RUNX1-E06.01 RUNX1-E06.03 RUNX1-E06.03	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTAC ACACTGACGACATGGTTCTACACCTGCTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCGAGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAACAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACAACAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACAGAGCTGTCCTTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCACCTGTCCTCCAC TACGGTAGCAGAGACTTGGTCTGCAACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACGTGGTCGGGAAGGTGT TACGGTAGCAGAGACTTGGTCTGGTCGGCAGGGTAAAGGC TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGC TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTAGC TACGGTAGCAGAGACTTGGTCTCCACGGAAGGTGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCACGGCACGCTGCCA TACGGTAGCAGAGACTTGGTCTCCCACCGGCCCCCC TACGGTAGCAGAGACTTGGTCTCCCACCGGCCCCCC TACGGTAGCAGAGACTGGTCGCCCCCCCC TACGGTAGCAGAACCTGGTCCTCCCACCGCCCCCC TACCGTAGCAGAACCTGGTCTCCCACCGCCCCCC TACCGTAGCAGAACCTGGTCCTCCCACCGCCCCCCC TACCGTAGCAGAACCTGGTCTCCCACCGCCCCCCC TACCGTAGCAGAACCTGGTCCTCCCCACCGCCCCCCC TACCGTAGCAGACACCCCCCCCCCCCCCCCCCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E02.02           RUNX1-E03.03           RUNX1-E04.01           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTAC ACACTGACGACATGGTTCTACACCCGCTGCTGGAGAGATCGGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTCAGGCCACCA ACACTGACGACATGGTTCTACAGGGCTTGTCCTTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCAC TACGGTAGCAGAGACTTGGTCTTGCACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGCAGGTAGAGATGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGAGGTGG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGAGGTGG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGGCAGGAACTGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTGCCACACGGCACTGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTGCCCACACGGCACTCCTC TACGGTAGCAGAGACTTGGTCTGCCCGGAACAGGAGCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.01	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTAC ACACTGACGACATGGTTCTACACCTGCTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAAGCAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACAACAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACAACAGATATGTTCCTCCCTC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCAC TACGGTAGCAGAGACTTGGTCTGGCACATGGTCCTCCCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGAGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGAGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGCGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCATGAGAGACTGGTAGGC TACGGTAGCAGAGACTTGGTCTCCATGAGAGACTGGTAGGC TACGGTAGCAGAGACTTGGTCTCCCACAGGGCAGGTGAGCC TACGGTAGCAGAGACTTGGTCTCCCACAGGGCCCC TACGGTAGCAGAGACTTGGTCTCCGGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGGCAACAGGAGGCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCTGCTGCTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGCGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAAGAGTCTTTCCCTCCCTC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCAC TACGGTAGCAGAGACTTGGTCTTGCACTGGTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGACGTCGGCAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTGG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGGAGCTGGTAGGCC TACGGTAGCAGAGACTTGGTCTCCACCAGGAACTGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCACAGGAGCCC TACGGTAGCAGAGACTTGGTCTCCCCACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCCACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCCACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACGAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACGAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTTCCTCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTTCCTCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTTCCTCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTTCCTCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTTCCTCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTTCCCCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACCTTCCCCCC TACGGTAGCAGAGCCC TACGGTAGCAGAGCCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCCC TACGTAGCAGAGACTGGTCCCCCCCCCCCCCCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E02.02           RUNX1-E03.03           RUNX1-E04.01           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.02	gDNA	ACACTGACGACATGGTTCTACACCCCTCCCTGCCCCCCTAC ACACTGACGACATGGTTCTACACCCGCTGCTGCAGAGATCGCC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGCGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGCGGTGTTCAGGCCACCA ACACTGACGACATGGTTCTACACGGTGTTCTCCTCCCCCCC ACACTGACGACATGGTTCTACACAGGTGTTCTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCAC TACGGTAGCAGAGACTTGGTCTGGCACTGGTCTTCATGG TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGAGCATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGCTGGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGAAACTGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCTCAGCAGGACTGGTCCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCGCAACTACGTCTTCCC TACGGTAGCAGAGACTTGGTCTCCCCGCAACTACGTCTTCCC TACGGTAGCAGAGACTTGGTCTCCCCGCAACTACGTCTTCCCC TACGGTAGCAGAGACTGGTCTCCCCGCAACTTCGTCCTCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.03	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCCGCTGCTGGTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTTGTTCCCTCCCTCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCAC TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTCTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACGTCGGGCAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGGGTCAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCCAGGGTAGAGATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCACACGGCAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCCACAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACGAGGAGCC TACGGTAGCAGAGACTTGGTCTCCGCAACTACCAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAACTACCAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAACTACCAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAACTACCACGGCTCTCC TACGGTAGCAGAGACTTGGTCTCCGCAACTACCACGGCCCTCC TACGGTAGCAGAGACTTGGTCTCCGCAACTACCACGCCCTCC TACGGTAGCAGAGACTTGGTCTCCGCAACTACCACGCCCTCC TACGGTAGCAGAGACTTGGTCTCCGCAACTACCACGCCCTCC TACGGTAGCAGAGACTTGGTCTCCCGCACTACCACGCCCTCC TACGGTAGCAGAGACTTGGTCTCCCCCACTCCTCCAACAGG
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E02.02           RUNX1-E03.03           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.04	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCCGCTGCTGGAGAGATCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGCAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACAGCAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGAGCTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGAGCTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGGGCAGGG	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCAC TACGGTAGCAGAGACTTGGTCTTGCACACGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGAGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGGCGGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGCGGGAGGGTGAGGGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTGAGGGTGAGGGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGGTGG TACGGTAGCAGAGACTTGGTCTGGCAGGTGCGAAGGTGG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCCCACAGGTACGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCCACAGGCCCCTCCT TACGGTAGCAGAGACTTGGTCTCCCGGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGGAACTGGTCTCCCCTCCTTCATACAGG TACGGTAGCAGAGACTTGGTCTCCCGCAACTTCGCTCTCCCC TACGGTAGCAGAGACTTGGTCTCCCGCAACTTCGCCTTCCCC TACGGTAGCAGAGACTTGGTCTCCCCGCACTAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACTTCGCCTTCCCC TACGGTAGCAGAGACTTGGTCTCCCGCAACTTCGCCTTCCCC TACGGTAGCAGAGACTTGGTCTCCCCGCACTAGGCC TACGGTAGCAGAGACTTGGTCTCCCCGCACTGCCCTTCCCC TACGGTAGCAGAGACTTGGTCTCCCCGCACTTCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCGCTGCTGGTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGCGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTTCTTCCCTCCCTCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCCACCTGGTCTTCCATGG TACGGTAGCAGAGACTTGGTCTTGCACTGGTCTTCATGG TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCGGGATAACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGGGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCCAGGGCAGAGGTGG TACGGTAGCAGAGACTTGGTCTGCCAGCGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCCAGCAGCAGACTGGTAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGCAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGCCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGCCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGCCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGCCC TACGGTAGCAGAGACTTGGTCTCCCGCACCTCCTCCACACGG TACGGTAGCAGAGACTTGGTCTCCCGCACCTCCTCCTCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E02.02           RUNX1-E03.03           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCCGCTGCTGGAGAGATCGC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTCTGCCTCCCTCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTGACATGGTCCCCGAGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGAGGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGCAGGTGAGGGTTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGCGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGCGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGCGTGGAGGC TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCCACACGGCACTCCT TACGGTAGCAGAGACTTGGTCTCCCCACACGGCCCTCCT TACGGTAGCAGAGACTTGGTCTCCCCGACACGGAGCC TACGGTAGCAGAGACTTGGTCTCCCCGACACGGAGCC TACGGTAGCAGAGACTTGGTCTCCCCGACACGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGACACGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGACACGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGACATCGCTCCCCTC TACGGTAGCAGAGACTTGGTCTCCCGACTACGTCTTCCCC TACGGTAGCAGAGACTTGGTCTCCCCGACTACGTCTTCCCC TACGGTAGCAGAGACTTGGTCTCCCCGACTACGTCTTCCCC TACGGTAGCAGAGACTTGGTCTTGCCCTGCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCGACTGAGTTTCCCC TACGGTAGCAGAGACTTGGTCTTGCCCTGCTCATTCCGCA TACGGTAGCAGAGACTTGGTCTTGCCCTGCTCATTCCGCA TACGGTAGCAGAGACTTGGTCTGCCTGCCTGCTCATTCCGC TACGGTAGCAGAGACTTGGTCTTGCCCTGCTCATTCCGCA TACGGTAGCAGAGACTTGGTCTTGCCCTGCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTTGCCCTGCTCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTTGCCCTCCTCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTTGCCCTCCTCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTTGCCCTCCTCCTCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTTGCCCTCCTCCTCATCCAGCACACGCC TACGGTAGCAGAGACTTGGTCTTGCCTGCTCTCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTGCCTCCTCCTCCTCCTCCTCCCTC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03.01           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.01           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCGCTGCTGGTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTCTTTCCCTCCCTCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCCACCACCTCCCA TACGGTAGCAGAGACTTGGTCTTGCAACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGAAGGTGG TACGGTAGCAGAGACTTGGTCTGCTCAGGGTAGAGATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGGTAGAGAGTGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGGCAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTCCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCCAGCAGCAGAGTGGTAGCC TACGGTAGCAGAGACTTGGTCTCCCCACGGCACCAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCCCACGGCACCAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCACCAGGAGCCC TACGGTAGCAGAGACTTGGTCTCCCGCACCAGGAGCCC TACGGTAGCAGAGACTTGGTCTCCCCCCCCTCCTCCACACGG TACGGTAGCAGAGACTTGGTCTCCCCCCCCGCCTCTCC TACGGTAGCAGAGACTTGGTCTCCCCCCCCGCCTCTCC TACGGTAGCAGAGACTTGGTCTCCCCCCCCGCCTCATTCAG TACGGTAGCAGAGACTTGGTCTTGCGAGATTGGTTTTCTCC TACGGTAGCAGAGACTTGGTCTTCGCAACAGCTCCTCCACCAGCACCACCACACAGC TACGGTAGCAGAGACTTGGTCTCCCCCCCCGCCACTCATCCAG TACGGTAGCAGAGACTTGGTCTCCCCCCCCGCCACTCATCAGC TACGGTAGCAGAGACTTGGTCTCCCCCCCCGCCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E02.02           RUNX1-E03.03           RUNX1-E04.01           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCCGCTGCTGAGAGATCCGC ACACTGACGACATGGTTCTACACGCGAGCAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGCTCCG ACACTGACGACATGGTTCTACAGGTGTTCTCCCTCCCCCC ACACTGACGACATGGTTCTACAGGGCTTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGGGCAGGG	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGATATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTCAGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGCAGGTACAACGA TACGGTAGCAGAGACTTGGTCTGGCAGGTACAAGAATGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTACAGCA TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGCGTCCTC TACGGTAGCAGAGACTTGGTCTCGCCAGGTACGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCCACACGGCACTCCTC TACGGTAGCAGAGACTTGGTCTTCTGCCTACCTGCTCATCCAGG TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACGCTCCTC TACGGTAGCAGAGACTTGGTCTTCCGCAACGCTCCTCC TACGGTAGCAGAGACTTGGTCTTCCGCAACGCAGCACCACGCACCACCACCACCACCACCACC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.01           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCGCTGCTGGTGAAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTTTTCTCCCTCCCTC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCAACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCTGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACGTCGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGGGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGCGCAGAGAGTGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGAGGTGG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGAGGTGG TACGGTAGCAGAGACTTGGTCTCCCGCAGCGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGAGCCGTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGCCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGCAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCACTCACACGGG TACGGTAGCAGAGACTTGGTCTCCCGCACTCTCCACACGG TACGGTAGCAGAGACTTGGTCTTCCCGCACTCATCACGG TACGGTAGCAGAGACTTGGTCTTCCCCCTCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTTGCGAGATTACGTTTCTCC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCATCCAG TACGGTAGCAGAGACTTGGTCTTGCGATTACCAGCTCATCACGACTCA TACGGTAGCAGAGACTTGGTCTTGCCATTATCAGCATCATCAGCATCA TACGGTAGCAGAGACTTGGTCTACCGTCAGACTCATCACAGCATCA TACGGTAGCAGAGACTTGGTCTACCGTCAGCATCATCAGCATCA TACGGTAGCAGAGACTTGGTCTACCGTCAGCATCATCAGCATCA TACGGTAGCAGAGACTTGGTCTACCACCACTCACAGAGCTCA TACGGTAGCAGAGACTTGGTCTACCGTCAGCATCATCAGCATCA TACGGTAGCAGAGACTTGGTCTACCACCACTCACTCACAGGCTCAC TACGGTAGCAGAGACTTGGTCTACCGTCACACTCACTCAC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E03           RUNX1-E04.01           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.08	gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCCGCTGCTGAGAGATCCGC ACACTGACGACATGGTTCTACACGCGAGCAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTCTCCCTCCCCCCC ACACTGACGACATGGTTCTACAGGGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGGGCATGCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGGGCAGAGGGAGAGGCTG ACACTGACGACATGGTTCTACAGGCAGAGGGAGAGGCTG ACACTGACGACATGGTTCTACAGGCCAGCGGAGAGGCGCG ACACTGACGACATGGTTCTACAGTGCCTCCCATCTCCGAC ACACTGACGACATGGTTCTACAGTGCCTCCATCTCCGAC ACACTGACGACATGGTTCTACAGTGCCCTCCAACGCCCCC ACACTGACGACATGGTTCTACAGTGCCACGCCTGC ACACTGACGACATGGTTCTACAGTGCCAGCCGGCC ACACTGACGACATGGTTCTACAGTCCAGCCGCTGC ACACTGACGACATGGTTCTACAATTCCAACTGAGGGCAGCCTCG ACACTGACGACATGGTTCTACAATTCCAACTGCGCTGAGAGGC ACACTGACGACATGGTTCTACAATTCCAACTGCGGGGCAGCCTG ACACTGACGACATGGTTCTACAATTCCAACTAGGGCAGCCTG ACACTGACGACATGGTTCTACACTCACACACAACGACGCCCCC ACACTGACGACATGGTTCTACACTCCAACGCCTGGAGAAGC ACACTGACGACATGGTTCTACAGTCCAACGCCTGGAGAAAACACTG ACACTGACGACATGGTTCTACAGTCCAACGCACTGCAAGACGCGG ACACTGACGACATGGTTCTACAGGCCACCCAAGGCCGCG ACACTGACGACATGGTTCTACAGTCCAACGCACTGGAAAAACACTG ACACTGACGACATGGTTCTACAGCTCCAAGGCAGCCGACGCG ACACTGACGACATGGTTCTACAAGCTAGCCTGCTGGGAAAAACACTG ACACTGACGACATGGTTCTACAAGCTGCCCCAAGGCCGGCGAACACCGG ACACTGACGACATGGTTCTACAAGCTAGCCTCCAAGGCAAGCAA	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACTGGTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCGAGGGTATACCA TACGGTAGCAGAGACTTGGTCTGACGTGGGCCCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCCACGTACGTGGTAGCC TACGGTAGCAGAGACTTGGTCTCCCCACAGGAACTGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCCACAGGCACCTCCT TACGGTAGCAGAGACTTGGTCTTCTGCCCACAGGAGCCC TACGGTAGCAGAGACTTGGTCTTCTGCCTCCTTCATACAGG TACGGTAGCAGAGACTTGGTCTTCTGCCTGCTCCTCC TACGGTAGCAGAGACTTGGTCTTCCGCAAAGATGGTGTTTCCC TACGGTAGCAGAGACTTGGTCTCCCCACACGCCCTCC TACGGTAGCAGAGACTTGGTCTTCTGGCTTCCCTTCATACAGG TACGGTAGCAGAGACTTGGTCTTCTGGCAGTTACGTCTTCCC TACGGTAGCAGAGACTTGGTCTTGCCATACAGCATCACAGCATCA TACGGTAGCAGAGACTTGGTCTGCCATTATCAGCATCATCAGCATCA TACGGTAGCAGAGACTTGGTCTGCCATTATCAGCATCATCAGCATCA TACGGTAGCAGAGACTTGGTCTCCCACACTACCAGCACTCA TACGGTAGCAGAGACTTGGTCTCCCACTACCAGCACTCACCAC TACGGTAGCAGAGACTTGGTCTCCCCCCCACTACCAGGATCCCAC TACGGTAGCAGAGACTTGGTCTGCCATTATCAGGACTGCCCCCCCAC TACGGTAGCAGAGACTTGGTCTCCCCACTTATCAGGACTCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.09	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTAC ACACTGACGACATGGTTCTACACCCGCTGCTGAGAGATCCGC ACACTGACGACATGGTTCTACACGCGAGCAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGCAGATATGTTCAGGCCACCA ACACTGACGACATGGTTCTACAGCGATCTCTTCCCTCCC CACACTGACGACATGGTTCTACAGCGGTGTCTCTTTCCGAGC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGAGCTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGAGCTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGAGGCTGCCCCCA ACACTGACGACATGGTTCTACAGGGCAGGG	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGGCACATGGTCTTCATGG TACGGTAGCAGAGACTTGGTCTGGACATGGTCCCTGAGTATACCA TACGGTAGCAGAGACTTGGTCTGGACATGGTCCCGAGGATAAAGGC TACGGTAGCAGAGACTTGGTCTGGGCGGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGGCGGGAGGTGG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGGGAGGC TACGGTAGCAGAGACTTGGTCTGGCAGGAACTGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCCAGCAGCACGGCC TACGGTAGCAGAGACTTGGTCTCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACTGGTCTCCCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAACTGGCTCTCCC TACGGTAGCAGAGACTTGGTCTCCCGCAACTGGCTCTCCCC TACGGTAGCAGAGACTTGGTCTCCCGCAACTGGCTTCCCC TACGGTAGCAGAGACTTGGTCTCCCCGCACTCAGG TACGGTAGCAGAGACTTGGTCTGCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTGCCATTACCGCTCATCAGG TACGGTAGCAGAGACTTGGTCTACCCTCCTCCTCATCAGCATCA TACGGTAGCAGAGACTTGGTCTATCCCGTCAGGCTCATCAGCATCA TACGGTAGCAGAGACTTGGTCTACCCGTCAGGCCTCATCAGCATCA TACGGTAGCAGAGACTTGGTCTATCCCGTCCAGCATCAGCATCA TACGGTAGCAGAGACTTGGTCTATCCCGTCCAGGCCCAC TACGGTAGCAGAGACTTGGTCTATCCCGTCCAGGCCCAC TACGGTAGCAGAGACTTGGTCTACCCGTCAGGCCCAC TACGGTAGCAGAGACTTGGTCTACCCGTCAGGCCCAC TACGGTAGCAGAGACTTGGTCTACCCGTCAGGCCCAC TACGGTAGCAGAGACTTGGTCTACCCGTCAGGCCCAC TACGGTAGCAGAGACTTGGTCTACCCGTCAGGCCCAC TACGGTAGCAGAGACTTGGTCTACCCGTCAGCAGCCCCAC TACGGTAGCAGAGACTTGGTCTACCGTCAGGCTACAGCACGCCAC TACGGTAGCAGAGACTTGGTCTACCCGTCAGGCCCAC TACGGTAGCAGAGACTTGGTCTACCGTCAGCAGCCCCAC TACGGTAGCAGAGACTTGGTCTACCGTCAGCAGCCCCAC TACGGTAGCAGAGACTTGGTCTACCCGTCAGAGCCCGCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.08           TET2-E03.09           TET2-E03.09	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCCGCTGCTGAGAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGCGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGGTGTTTCGCTCCTCCCCCCC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAAGAGCTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAAAATCCCACCCCAC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTCTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAAGGTGG TACGGTAGCAGAGACTTGGTCTGCCAGGGTAGAGGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTCCACCGGCAGGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCACCGGCACGAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGCAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCTGCCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCCAACTTCGTCCTCC TACGGTAGCAGAGACTTGGTCTTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCGCCAACACGCACTCCC TACGGTAGCAGAGACTTGGTCTTCGCCATACCAGCTCCCC TACGGTAGCAGAGACTTGGTCTTGCCATTCAGCTTTCTGCA TACGGTAGCAGAGACTTGGTCTTGCCATTACCAGCATCACACACA
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.09           TET2-E03.10	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCCGCTGCTGAGAGATCCGC ACACTGACGACATGGTTCTACACGCGAGCAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTCAGCCCCCCCC ACACTGACGACATGGTTCTACAGGGTGTCTCTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGGCACTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGGAGGTTGTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCGAGGATAAAGGC TACGGTAGCAGAGACTTGGTCTGGAGGTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGGAGGTGAGGGTTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGGCAGGTAGCGTCTCC TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCCCACACGGCACTGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCCACACGGCCTCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAACTGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCCGACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCGACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGAACTACGTCTTCCC TACGGTAGCAGAGACTTGGTCTCCCCGACTACGTCAGG TACGGTAGCAGAGACTTGGTCTTCCCCGACTCAGCACA TACGGTAGCAGAGACTTGGTCTGCCTGCCTCATACAGG TACGGTAGCAGAGACTTGGTCTGCCATATCAGCACTCAGCACA TACGGTAGCAGAGACTTGGTCTGCCATTATCAGCACTCATCAGCATCA TACGGTAGCAGAGACTTGGTCTGCCGCATCTACAGCACCACC TACGGTAGCAGAGACTTGGTCTGCCGCACCATCAGAGCTCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.01           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCCGCTGCTGAGAGATCCGC ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTTGTTCCCTCCCTCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTCTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAGAGTGG TACGGTAGCAGAGACTTGGTCTGCTCAGGGCACGGGTAAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGGTGGAGGGTGG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGAGGTGG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCACACGGCAGCTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCCACAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCGCAGCTACACAGG TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCTC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCTCCTC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCACCACG TACGGTAGCAGAGACTTGGTCTTCCCCCTCCTCCACACGG TACGGTAGCAGAGACTTGGTCTTCCCCCTCCTCCACACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCCACACAGC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCCGCCATTCAG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCCGCTGCTGAGAGATCCGC ACACTGACGACATGGTTCTACACGCGAGCAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTCAGCCCTCCCTC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCACCTGGTTCTCATGG TACGGTAGCAGAGACTTGGTCTGCACATGGTCCTGGAGGTTGTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGAGGTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGCAGGTGAGGGTTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGGAGGC TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGGGAGGCC TACGGTAGCAGAGACTTGGTCTGCCACGGAACGTGGTAGGCC TACGGTAGCAGAGACTTGGTCTCCCCACACGGCACTGCT TACGGTAGCAGAGACTTGGTCTCCCCACAGGAGCCC TACGGTAGCAGAGACTTGGTCTCCCCACAGGAGCCC TACGGTAGCAGAGACTTGGTCTCCCCACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCACACGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCCACTGCTCTCC TACGGTAGCAGAGACTTGGTCTCCCCGACTGCTTCCCC TACGGTAGCAGAGACTTGGTCTCCCCCACCTGCTCATCCAGG TACGGTAGCAGAGACTTGGTCTGCCCTCCTGCTCATCCCAC TACGGTAGCAGAGACTTGGTCTGCCATTACAGCACTCACGCACCA TACGGTAGCAGAGACTTGGTCTGCCACCATCAGCACTCAC TACGGTAGCAGAGACTTGGTCTGCCACCATCAGACGCCCCCC TACGGTAGCAGAGACTTGGTCTGCCACCATCAGACGCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACCCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTTGTTCCCTCCTCCC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAAGAGCTTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAAGACTTGTCCCACCCCACTTTACATATAA ACACTGACGACATGGTTCTACAAAATCCCACCCCAC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTTGCACTGGTCCTGAGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCCAGGGTAGAGGTGG TACGGTAGCAGAGACTTGGTCTGCCAGGCTGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCACACGGCACCTCC TACGGTAGCAGAGACTTGGTCTCCCCACAGGAGCC TACGGTAGCAGAGACTTGGTCTTCCGCAAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCCACCTCCTCAACAGG TACGGTAGCAGAGACTTGGTCTTCCCCACCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCC TACGGTAGCAGAGACTTGGTCTTGCGAACAGGAGCC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCATCAG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCAACAGCTCA TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCAACAGCTCA TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCAACAGCTCA TACGGTAGCAGAGACTTGGTCTTCCCCCCCCCTCTCAACAGCTCA TACGGTAGCAGAGACTTGGTCTTCCCACCATCACAGCACCA TACGGTAGCAGAGACTTGGTCTTCCCCCCCCCCTCTCATACAGCTCA TACGGTAGCAGAGACTTGGTCTTCCCCACCATCATCAGGCTCA TACGGTAGCAGAGACTTGGTCTTCCCCACCATCATCAGGCTC TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGTTGTGAGGCC TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGTGTTTGTCA TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGTGTTTGTCA TACGGTAGCAGAGACTTGGTCTTGCAACGTCTGTGTTTGTCCT TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGGTGTTGGAGGCA TACGGTAGCAGAGACTTGGTCTTGGAACTGGGACTTGGTCTTGAAGAGGCT TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGGTGTTGGTGGTCC TACGGTAGCAGAGACTTGGTCTTGGAACTGGGACTTGGTCTTGAAGAGGCT TACGGTAGCAGAGACTTGGTCTGGTCTGGAACTGGAGTGGTCC TACGGTAGCAGAGACTTGGTCTGGTCTGGACGTCGGTCGCC TACGGTAGCAGAGACTTGGTCTGGTCTGGACGTGGAGGAGGCC TACGGTAGCAGAGACTTGGTCTGGTCTGGAACTGGGAGAGGCC TACGGTAGCAGAGACTTGGTCTGGTCTGGAGGTCGCC TACGGTAGCAGAGACTTGGTCTGGTCTGGAGGTCGCC TACGGTAGCAGAGACTTGGTCTGGTCTGGTGTGGTCC TACGGTAGCAGAGACTTGGTCTGGTCTGGTGTGG
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.02           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.08           TET2-E03.08           TET2-E03.09           TET2-E03.11           TET2-E03.12           TET2-E03.13	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCGAGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTCTCCTCCCTCC ACACTGACGACATGGTTCTACAGGGCATGTCTCTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTTGTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGATATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTCAGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGGCAGGTACAAGGATGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTACAGGAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTACAGGAGGTGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTACGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCCCACACGGCACTCCTC TACGGTAGCAGAGACTTGGTCTTCTGCCAGCTGCTACTGGTAGCAGGA TACGGTAGCAGAGACTTGGTCTTCTGCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTTCTGCCGACACGGAGGCC TACGGTAGCAGAGACTTGGTCTTCTGCCTGCTCCTTCTCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCTGGCAGGTACGTCTTCCC TACGGTAGCAGAGACTTGGTCTTCTGGCAGTTACGTCTTCCC TACGGTAGCAGAGACTTGGTCTTGCGCATTATCAGGCTTCCC TACGGTAGCAGAGACTTGGTCTGCCACCATTCAGCACTCA TACGGTAGCAGAGACTTGGTCTGCCACCATTCAGAGTGCCC TACGGTAGCAGAGACTTGGTCTGCCACCATTCAGAGTGCCC TACGGTAGCAGAGACTTGGTCTGCCACCATTCAGAGTGCCC TACGGTAGCAGAGACTTGGTCTGCCACCATTCAGAGTGCCC TACGGTAGCAGAGACTTGGTCTTGCCACCATTCAGAGTGCC TACGGTAGCAGAGACTTGGTCTTGCAGATCTCGTGTTGTCCC TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGGTGTTTGCCCT TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGGTGTTTGCCCT TACGGTAGCAGAGACTTGGTCTTGGAACTGGTGTTTGCCCT TACGGTAGCAGAGACTTGGTCTTGGAACTGGTGTTGCCCT TACGGTAGCAGAGACTTGGTCTTGGAGATGTGGTGTTGCCCT TACGGTAGCAGAGACTTGGTCTTGGAGGTCTGTGAGATGTGGTCC TACGGTAGCAGAGACTTGGTCTTGGAGTGGGTGTGAGATGGGCCT TACGGTAGCAGAGACTTGGTCTTGGCAGTGTGAGATGTGGACCC TACGGTAGCAGAGACTTGGTCTTGGAGGTGTGAAGTGGGCCT TACGGTAGCAGAGACTTGGTCTTGGCAGGTGTGGAGGAGTTGGTGGCC TACGGTAGCAGAGACTTGGTCTTGGCAGGTGTGAGATGTGGGCCT TACGGTAGCAGAGACTTGGTCTTGGCCACGGAGATGTGGGCCT TACGGTAGCAGAGACTTGGTCTGGCCAAAGAATGAACCTCTCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCTCCCTGCCCCCCTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTTTTCTCCCTCCCTC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCCACCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGGGTCAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTAGGC TACGGTAGCAGAGACTTGGTCTCCCACAGGAAGCTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCCACGGCAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCGCAGCTACACAGG TACGGTAGCAGAGACTTGGTCTTCCCGCAGCTCCTCTCACACGGG TACGGTAGCAGAGACTTGGTCTTCCCCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTGCTCATTCAG TACGGTAGCAGAGACTTGGTCTTGCCAACAGCTCCCTC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCAACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCAACAGGCTCCC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCACACCAGCACC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCTGCAACAGCTCAC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCTGCAACAGCTCCAC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCCTCTGAGGTCCCACC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCCTCTGATGTCA TACGGTAGCAGAGACTTGGTCTTGGCCAACGTCATCATGGTCT TACGGTAGCAGAGACTTGGTCTTGGCCAACGTCGTTGGTCTCC TACGGTAGCAGAGACTTGGTCTTGGCCAACGGAGTTGGTCTCT TACGGTAGCAGAGACTTGGTCTTGGCCAACGGAACTTGGTCTTGGAGGAGAGACTTGGTCTTGGAGGAGAGCTTGGTCTGGCCAACGGAAGCTTGGTCT TACGGTAGCAGAGACTTGGTCTTGGACGTGGACTGGAGAGGCT TACGGTAGCAGAGACTTGGTCTGGCCAACGGAAGCTTGGTCTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAACGGAAGGACTTGGTCT TACGGTAGCAGAGACTTGGTCTGGCCAACGGAAGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAACGGAAGAGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAACGGAAGAGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAACGGAAGAGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAACGAAGAAGTTGGTCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.12           TET2-E03.12           TET2-E03.12           TET2-E03.12           TET2-E03.12           TET2-E03.12           TET2-E03.12           TET2-E03.12           TET2-E03.14           TET2-E03.15	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCGAGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGAGTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGGGCATGCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGGGCAGGG	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCGCCTGCCTGCCT TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGCACATGGTCGGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGCTGGCAGGGTACAACGA TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCACCGGCACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCACAGGCACCTCCT TACGGTAGCAGAGACTTGGTCTTCTGCCAACGGCCCCTCC TACGGTAGCAGAGACTTGGTCTTCTGCCTACCTGCTATACAGG TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCACACGACGCCCCCCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACACGGCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.14           TET2-E03.15	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTGTTTCACGTGCTCCCCCCC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCCACCACCTCCCA TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGAGAGTGG TACGGTAGCAGAGACTTGGTCTGCTCAGGGCTAAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCACGGCACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCGCACGAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGCAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCGCACTACAGGG TACGGTAGCAGAGACTTGGTCTTCCCGCAGCTACACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCTCTCTCACACGGC TACGGTAGCAGAGACTTGGTCTTCCCCCCCTGCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCGCCTCATTCAG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCACACCAGCACC TACGGTAGCAGAGACTTGGTCTTCCCCCCCTCCTCATACAGC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCACACCACC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCTACAGGCTCC TACGGTAGCAGAGACTTGGTCTTGCTCAAGACTGGCTTCCACCACC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCTATGTCA TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCTTCATGCCACC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCTTGATGTCA TACGGTAGCAGAGACTTGGTCTTGGCAAACGAGCTCCTT TACGGTAGCAGAGACTTGGTCTTGGCAAAGAATGTTGGTCCT TACGGTAGCAGAGACTTGGTCTTGGCCAAAGAATGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGAATGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGAATGATCCTTCCT
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.16	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCGAGCAGGAGGAGGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGGGCAGAGTGCCTTTCCGAGC ACACTGACGACATGGTTCTACAGGGCAGAGGGGAGAGGCTG ACACTGACGACATGGTTCTACAAGTGCCCCCCCCTCC ACACTGACGACATGGTTCTACAAATCCCACCCCAC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACTGGTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCGGAGGGTATACCA TACGGTAGCAGAGACTTGGTCTGACGTGGGCCCAAAGAAGTGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTAGCC TACGGTAGCAGAGACTTGGTCTCCGCAGGAACTGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCCACACGGCACGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCCCACAGGACGCCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCCACACGGCCCCCCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACACGGAGGCC TACGGTAGCAGAGACTTGGTCTTCGCCATCACGCTCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03.01           RUNX1-E04.01           RUNX1-E04.01           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.17	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACCCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTCACGTGCTCCCCCCC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGCCC ACACTGACGACATGGTTCTACAGAGGCTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGAC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAAGACCCCCCCCTTTACATATAA ACACTGACGACATGGTTCTACAAGTCCCCCCCCCTTTCCGAGC ACACTGACGACATGGTTCTACAGTGCCCCCCCACTTCCGAC ACACTGACGACATGGTTCTACAGTGCCCCCCCACTCCGAC ACACTGACGACATGGTTCTACACTGCCCCCACGCCGC ACACTGACGACATGGTTCTACACTGCCCCCACGCCGC ACACTGACGACATGGTTCTACACTGCACCAAGGCGCAGCCTG ACACTGACGACATGGTTCTACACTGCACCAAGCGCCTCCA ACACTGACGACATGGTTCTACACTGCACCAAGGCCAGCCTG ACACTGACGACATGGTTCTACACTCCACTGCCGAGGGCCCTTG ACACTGACGACATGGTTCTACATCCACCCCCCAGCTGC ACACTGACGACATGGTTCTACATCCACCTCCCGAAGAGAC ACACTGACGACATGGTTCTACATCCACACACTAACTGCAGTGGG ACACTGACGACATGGTTCTACATGCCCCCAAGCCCAGCTG ACACTGACGACATGGTTCTACACGCCCCCAAGCCCCGCG ACACTGACGACATGGTTCTACACTGCCCCAAGCGCCGCTG ACACTGACGACATGGTTCTACACGCCCCCCCAAGCGCCGCG ACACTGACGACATGGTTCTACACGTGGGGAACACCTGGGAAGA ACACTGACGACATGGTTCTACACGTGGGGAACCACGGCACGG ACACTGACGACATGGTTCTACACGTGGGGAAGCACACGGGCACAGGAC ACACTGACGACATGGTTCTACACGTGGTGGAGGCAACACGGGA ACACTGACGACATGGTTCTACACGTGGGGAGGCTACAGGAACA ACACTGACGACATGGTTCTACAGCGCCCCGGTTTCCCAAGGCACA ACACTGACGACATGGTTCTACAGCGCCCCGGTTTCACAAGGAACACCTG ACACTGACGACATGGTTCTACAGCGCCCCGGTTTCACAAGGAACACAG ACACTGACGACATGGTTCTACAGCGCCCCGGTTTCACAAGGTACAAGGAA ACACTGACGACATGGTTCTACAAGTGACAACCTGACAAGGACA ACACTGACGACATGGTTCTACAAGCTCACAAGCACAAAACTTGACAAAGTACAA ACACTGACGACATGGTTCTACAAGCTCAAAACTTACAAAGCTGAAGAACACAAAACTGA ACACTGACGACATGGTTCTACAAACTTAGCAACGCCCAAAAATTACAA ACACTGACGACATGGTTCTACAAACGCAACAACCCAAAAACTGAAGACCAAAAACCCAAAAACCCAAAAACCTGACGACAAGGACCAAAAACCCAAAAACCCAAAAACCCAAAAACCCAAAAA	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCCACCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGGTCGGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGCCAGGCTAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAGCAGCAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCACCAGGAGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCACCAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCACCAGGAGCC TACGGTAGCAGAGACTTGGTCTTCCCCCCCTCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCTCATCAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCTCTCATCAGG TACGGTAGCAGAGACTTGGTCTCCCCCCCGCACTACAAGCATCA TACGGTAGCAGAGACTTGGTCTTCCCCCCCTGCATTCAGG TACGGTAGCAGAGACTTGGTCTCCCCCCCCTCTATGCA TACGGTAGCAGAGACTTGGTCTACCACCATTCAGAGCTCCAC TACGGTAGCAGAGACTTGGTCTTCCCCCCCTTCTAGAGCTGCCCAC TACGGTAGCAGAGACTTGGTCTTCCTCCACCATTCAGGCTCCACC TACGGTAGCAGAGACTTGGTCTTGGAACTGGTCTTGATGGCACACC TACGGTAGCAGAGACTTGGTCTTGGAACTGGAGTTGGTTTGTCA TACGGTAGCAGAGACTTGGTCTTGGAACTGGAACTGGAGTTGGTCCT TACGGTAGCAGAGACTTGGTCTTGGAACTGGAACTGGAACTGGGCT TACGGTAGCAGAGACTTGGTCTTGGAACTGGAACTGGAAGAGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGAATGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGAATGATCCTTCT TACGGTAGCAGAGACTTGGTCTGGCCAAAGAATGATCCTTCT TACGGTAGCAGAGACTTGGTCTGGCCAACGAAGATGTTGGTC TACGGTAGCAGAGACTTGGTCTGGCCAACGAAGATGTTGGTC TACGGTAGCAGAGACTTGGTCTGGCCAACGAAGAATGTTCCTCC TACGGTAGCAGAGACTTGGTCTGGCCAACGAATGATCCTCCTC TACGGTAGCAGAGACTTGGTCTGGCCAACGAATGATCCTCCTC TACGGTAGCAGAGACTTGGTCTGGCCAACGAACTTCTCCCTG TACGGTAGCAGAGACTTGGTCTGGCCCTGCCTTGTCTGCACCCCTG TACGGTAGCAGAGACTTGGTCTGGCCAACGAACTTCTCCCTGCACTCCCCCTG TACGGTAGCAGAGACTTGGTCTGGCCCTGCCCTGTCTTGCACCCCCG
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.16	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCGAGGCAGGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGAGTTGTCCTTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGACGTGGTCGGGAAGGTGG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCACCGGCACGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGCAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCGCCATACCAGCTCCCC TACGGTAGCAGAGACTTGGTCTTGCGCATTACCAGCTTCCCC TACGGTAGCAGAGACTTGGTCTTGCCATTACCAGCATCACCAC TACGGTAGCAGAGACTTGGTCTGCCATTCCAGCACTCACCACCAC TACGGTAGCAGAGACTTGGTCTCCCCGCAGTCTGTATGCCACCACC TACGGTAGCAGAGACTTGGTCTGCCCTGCAGGTCTGTATGCCACC TACGGTAGCAGAGACTTGGTCTGCCCGCACCATCAGAGTGCCT TACGGTAGCAGAGACTTGGTCTGCCAACGACTTGGTCGCCCC TACGGTAGCAGAGACTTGGTCTGGCCCAACGACTTGGTCGCCCC TACGGTAGCAGAGACTTGGTCTGGCCCAACGACTTGGTCGCCC TACGGTAGCAGAGACTTGGTCTGGCCGCAACGAGATGTGGTCGCC TACGGTAGCAGAGACTTGGTCTGGCCGAACTGGACTTGGACGTGGACGTGGACTGGGCCCC TACGGTAGCAGAGACTTGGTCTGGCCTGGAACTGGACTGGACTGGACCTGGACCTGGCCT TACGGTAGCAGAGACTTGGTCTGGCCCAAACAACTGGTCTGGACCTGGACCTGGACCTGGACTGGCCCCC TACGGTAGCAGAGACTTGGTCTGCCCGCAACAGATGGTCCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.16           TET2-E03.17           TET2-E03.18	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGGGA ACACTGACGACATGGTTCTACACGCGAGCAAGATGAGGGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTTTTTCCCCCCCCC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGAGCTTGTCCCTTTCCCGAGC ACACTGACGACATGGTTCTACAAGAGCCCCCCCCTTTACATATAA ACACTGACGACATGGTTCTACAGGGCAGAGGGGAAGAGCTG ACACTGACGACATGGTTCTACAGTCCCCCCCCTCCCGAC ACACTGACGACATGGTTCTACACTGCCCCCACTCCGGAC ACACTGACGACATGGTTCTACACTGCCCCCACTCCGGAC ACACTGACGACATGGTTCTACACTGCACCAAGGCGCAGCCTGG ACACTGACGACATGGTTCTACACTGCACCAAGGGCAGAGGCCTGG ACACTGACGACATGGTTCTACACTGCACCACACTAGAGGGGCAGCCTTG ACACTGACGACATGGTTCTACACTGCACCACACTAGAGGGGCAGCCTTG ACACTGACGACATGGTTCTACACTGCACCACATAGTGGGGCCCTCC ACACTGACGACATGGTTCTACACTGCACCACATAACTGCAGTGGG ACACTGACGACATGGTTCTACACTCCCCAAGCCCAGCTG ACACTGACGACATGGTTCTACACGCTACGCT	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGGATAACCA TACGGTAGCAGAGACTTGGTCTGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGCGGCAAGAGATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTAGGCC TACGGTAGCAGAGACTTGGTCTCCTGGCAGGTAGGTAGCC TACGGTAGCAGAGACTTGGTCTCCCGGAACAGGAGCC TACGGTAGCAGAGACTTGGTCTCCGCAAGGAACTGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCGCAAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACTACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCTCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCATCAG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCATCAG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCATCAGG TACGGTAGCAGAGACTTGGTCTACCAGCATCATCAGCATCA TACGGTAGCAGAGACTTGGTCTACCAGCATCATCAGCACCA TACGGTAGCAGAGACTTGGTCTACCACCATCATCAGGCTCA TACGGTAGCAGAGACTTGGTCTTGCCACCATCATCAGGCTCA TACGGTAGCAGAGACTTGGTCTTGGCAGAGACTGGTTTGAACAGGCT TACGGTAGCAGAGACTTGGTCTTGGCAACTGGTCTTGATGGAGAGACTCG TACGGTAGCAGAGACTTGGTCTTGGAACTGGAGATGTGGTCC TACGGTAGCAGAGACTTGGTCTTGGCAACAGAGATGTTGGTCC TACGGTAGCAGAGACTTGGTCTGCCAAAGAATGATCCTTCT TACGGTAGCAGAGACTTGGTCTGGCTGGAGTGAGATGAGTGTGC TACGGTAGCAGAGACTTGGTCTGCCAGACTGGAGTTGAACTGGCT TACGGTAGCAGAGACTTGGTCTGCCTGCAACGAGAGATGTGGTC TACGGTAGCAGAGACTTGGTCTGCCTGCAGCAACGAGATGTGGTC TACGGTAGCAGAGACTTGGTCTGCCTGCAACGAAGAACTGGCT TACGGTAGCAGAGACTTGGTCTGCCTGCAACGAAGAAGAGCCC TACGGTAGCAGAGACTTGGTCTGCCTGCAAAGAATGATCCTTCCT
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.18           TET2-E03.19	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGAGTTGTCCTTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGCTGAGGTCGGGGAAGGTGG TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGCC TACGGTAGCAGAGACTTGGTCTCCCACGGCAGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGCAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCCACACGGCCCCTC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCGCCTTCATCCAG TACGGTAGCAGAGACTTGGTCTTCGCCTTCATCCAG TACGGTAGCAGAGACTTGGTCTTGCGCATTACAGGTCTTCCCC TACGGTAGCAGAGACTTGGTCTGCCATTACAGGTCTTCCCC TACGGTAGCAGAGACTTGGTCTTGCCATTCAGAGTGGCCAC TACGGTAGCAGAGACTTGGTCTTCCCCACACTCAGAGTGCC TACGGTAGCAGAGACTTGGTCTTGCCATCCACCATCAGAGTGCCT TACGGTAGCAGAGACTTGGTCTTGCCAAGACTCGTGTTGGCCAC TACGGTAGCAGAGACTTGGTCTTGGCAACTGGACTTGGTGGTGCC TACGGTAGCAGAGACTTGGTCTTGGCAACTGGACTTGGAACTGGGCCAC TACGGTAGCAGAGACTTGGTCTTGGCAACTGGAACTGGACTTGGTCC TACGGTAGCAGAGACTTGGTCTTGGCACTGGAACTGGACTTGGACGCCAC TACGGTAGCAGAGACTTGGTCTTGGCAACTGGACTTGGAACTGGGTC TACGGTAGCAGAGACTTGGTCTTGGCACTGGAACTGGACTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCTGCAACTGGACTTGGACGTGGACTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCTGCAACGAAGACTTGGTCC TACGGTAGCAGAGACTTGGTCTGCCTGTCTTGCAAACTGGCT TACGGTAGCAGAGACTTGGTCTGGCTGCACTGGACTTGGACTGGCCT TACGGTAGCAGAGACTTGGTCTGGCGTGCACTTGACTGGCCT TACGGTAGCAGAGACTTGGTCTGGCTGCACTGGCCTGGAACTGGCCT TACGGTAGCAGAGACTTGGTCTGGCCTGGCGTGAACTGGCTT TACGGTAGCAGAGACTTGGTCTGGCTGGCGTGAACTGGCCTT TACGGTAGCAGAGACTTGGTCTGGCCTGGCCTGACACTGGCCTTGGCCTGGACTGGCTTTTC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.01           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.17           TET2-E03.18           TET2-E03.19           TET2-E03.19	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGGGA ACACTGACGACATGGTTCTACACCCAGGCAAGATGAGGGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTCTTTTCCCTCCCTC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCGCCTGTCCTCCA TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCCGGGATAACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGGATAACCA TACGGTAGCAGAGACTTGGTCTGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGCGCAAGAGATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGAGGTAGC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCCGCAGCTGCAAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCTACACAGG TACGGTAGCAGAGACTTGGTCTCCCCCCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTCCCCCCCTCCTCCTCC TACGGTAGCAGAGACTTGGTCTCCCCCCCTCCTCATCAG TACGGTAGCAGAGACTTGGTCTCCCTCCACACCACCACC TACGGTAGCAGAGACTTGGTCTCCCTCCACACTCATCAGCATCA TACGGTAGCAGAGACTTGGTCTCCTCCACACTCATCAGCATCA TACGGTAGCAGAGACTTGGTCTTGCCACAGCTCCTCCT TACGGTAGCAGAGACTTGGTCTTGCACAGCTCCCTCCT TACGGTAGCAGAGACTTGGTCTTGGCAACTGCGTTGTATGTCA TACGGTAGCAGAGACTTGGTCTTGGAACTGCGTGTTGATGTCA TACGGTAGCAGAGACTTGGTCTTGGAACTGCGTGTTGATGTCA TACGGTAGCAGAGACTTGGTCTTGGAACTGCGTGTTGATGTCA TACGGTAGCAGAGACTTGGTCTTGGCAACTGCGTGTTGATGTCA TACGGTAGCAGAGACTTGGTCTTGGCAACTGCGTGTTGAATGGCT TACGGTAGCAGAGACTTGGTCTTGGCAACTGGAGTTGGACTTCCCCTG TACGGTAGCAGAGACTTGGTCTTGCCCCTGTGCATGAGAGAGA
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.02           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.19           TET2-E03.19	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTTGTTCCCTCCCTCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT         TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG         TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCCA         TACGGTAGCAGAGACTTGGTCTGCCACCACCTGGTTCTCATGG         TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTGTCC         TACGGTAGCAGAGACTTGGTCTATTTGAAATGTGGGTTATACCA         TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAGGTATACCA         TACGGTAGCAGAGACTTGGTCTGCACATGGTCGGGGAGGTGATACCA         TACGGTAGCAGAGACTTGGTCTGGCTGGGCAGGTAAAGGC         TACGGTAGCAGAGACTTGGTCTGCTCAGGTGCAAAGAATGTG         TACGGTAGCAGAGACTTGGTCTGCCAGGAGACTGGTAGGAGC         TACGGTAGCAGAGACTTGGTCTCCCACACGGCAGCTGGTAGC         TACGGTAGCAGAGACTTGGTCTTCGCAAAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCCGCAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCCGCAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCCGCAACTAGGAGGAGCC         TACGGTAGCAGAGACTTGGTCTTCCCGCAACTACGAGGAGCC         TACGGTAGCAGAGACTTGGTCTTGCCGAACTGGCTCTTCTCCC         TACGGTAGCAGAGACTTGGTCTTGCCATTATCAGCATCATCAGCATCA         TACGGTAGCAGAGACTTGGTCTGCCATTATCACGCACTCATCAGCATCA         TACGGTAGCAGAGACTTGGTCTGCCATTATCAGACTGCT         TACGGTAGCAGAGACTTGGTCTGCCATTACCAGCATCAGAGTGCC         TACGGTAGCAGAGACTTGGTCTGGAACTGGAGCCATTATCAGACTGCT         TACGGTAGCAGAGACTTGGTCTGGCCAAGGCCATTGGTCTGTGAACTGGGTCC         TACGGTAGCAGAGACTTGGTCTGGCCAAGACTCGGTGTATGGAGGCA         TACGGTAGCAGAGACTTGGTCTGGCTGAACTGGAGAGTTGGACTTGGCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.17           TET2-E03.18           TET2-E03.19           TET2-E03.19           TET2-E03.19           TET2-E03.20	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGCGAGGAGCAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGGTTTTCCCTCCCTCC ACACTGACGACATGGTTCTACAGGGCTTGTCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGGGCAGGG	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT         TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG         TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCAC         TACGGTAGCAGAGACTTGGTCTGCCACCACCTGCTCCCA         TACGGTAGCAGAGACTTGGTCTGACATGGTCCTCCGA         TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGCGACGTTATACGG         TACGGTAGCAGAGACTTGGTCTGGTCACATGGTCGGGACGTTAAAGGC         TACGGTAGCAGAGACTTGGTCTGACATGGTCGGAGAGGTGG         TACGGTAGCAGAGACTTGGTCTGGCAGGTCGCAAAGAATGTG         TACGGTAGCAGAGACTTGGTCTGGCAGGTACACGGAAGGTGG         TACGGTAGCAGAGACTTGGTCTGGCAGGAAGGTGGTAGAGC         TACGGTAGCAGAGACTTGGTCTGCCACAGGAAGCTGGTAGGAGC         TACGGTAGCAGAGACTTGGTCTCCGCAAAGGAAGCC         TACGGTAGCAGAGACTTGGTCTTCGGCAAGGAACTGGTAGCAGGAGCC         TACGGTAGCAGAGACTTGGTCTTCCGCAAACGAGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCGCAAACGAGAGCC         TACGGTAGCAGAGACTTGGTCTTCCGCAAACGACGACC         TACGGTAGCAGAGACTTGGTCTTCCGCAAACGATGGCTTTCCC         TACGGTAGCAGAGACTTGGTCTGCTGCAGCTGCACC         TACGGTAGCAGAGACTTGGTCTGGCACCCCCCCCTGCTGATGCAC         TACGGTAGCAGAGACTTGGTCTGGCATCCCCCCCTGCAGCACC         TACGGTAGCAGAGACTTGGTCTTGCACCCACCATTCAGAGTGCCT         TACGGTAGCAGAGACTTGGTCTTGGACGTCGGACCACCA         TACGGTAGCAGAGACTTGGTCTGGCCTGCACCATTGAGAGTGGCT         TACGGTAGCAGAGACTTGGTCTGGCCTGCACCATTGAAGTTGGTCCTAAGCACCA         TACGGTAGCAGAGACTTGGTCTGGCCTGCACCATTGAAGACGCT         TACGGT
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.10           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.18           TET2-E03.19           TET2-E03.19           TET2-E03.19           TET2-E03.19	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGCGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTTGTTCCCTCCCTCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTGCAACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGGAGGTGA TACGGTAGCAGAGACTTGGTCTGCTGAGGTCGGGAAGGTGTG TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCACACGGCAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCCACACGGCCCCTC TACGGTAGCAGAGACTTGGTCTTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCTCC TACGGTAGCAGAGACTTGGTCTTCCCGCAGCTCCTCTCACACGG TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCCCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCCCC TACGGTAGCAGAGACTTGGTCTTCCCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTGCCATTCAG TACGGTAGCAGAGACTTGGTCTTGCAAGATTACCGTCATCACAGCATCA TACGGTAGCAGAGACTTGGTCTTCCCACCATCACAGACTCA TACGGTAGCAGAGACTTGGTCTTCCCACCATCATCAGGCTCC TACGGTAGCAGAGACTTGGTCTTGCAAGATCGTCTTCACAGCACCA TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGTCTTGCA TACGGTAGCAGAGACTTGGTCTTGGAACTGGAACTGGACTCC TACGGTAGCAGAGACTTGGTCTTGGCAAGAGTTGGTCC TACGGTAGCAGAGACTTGGTCTTGGCAAGATTAGATCATCCT TACGGTAGCAGAGACTTGGTCTTGGCAAGATTGATCGTCC TACGGTAGCAGAGACTTGGTCTTGGCAAGATTGATCGTCCT TACGGTAGCAGAGACTTGGTCTTGGCAAGATTGATTGGAGCC TACGGTAGCAGAGACTTGGTCTTGGCAAGAATGACCCCC TACGGTAGCAGAGACTTGGTCTGGCTGGAACTGGAAATGGCT TACGGTAGCAGAGACTTGGTCTGGCTGGAACTGGAACTGGCC TACGGTAGCAGAGACTTGGTCTGGCTGGAACTGGCCT TACGGTAGCAGAGACTTGGTCTGGCTGGAACTGGCCT TACGGTAGCAGAGACTTGGTCTGGCTGGCATGGAAACTGGCT TACGGTAGCAGAGACTTGGTCTTGGCCTGGAACTGGCTTTCCT TACGGTAGCAGAGACTTGGTCTTGCCTGGCGTGAAATGGCT TACGGTAGCAGAGACTTGGTCTTGCTGAAGCCGGAAAATTGCT TACGGTAGCAGAGACTTGGTCTTGCTAAGCCCAACGCCAAGCCCACCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.17           TET2-E03.18           TET2-E03.19           TET2-E03.19           TET2-E03.19           TET2-E03.20	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCGAGCAGGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGAGTTGTCCTTTCCCGAGC ACACTGACGACATGGTTCTACAGGGCTTGCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGGGCAGGG	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT         TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG         TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCAC         TACGGTAGCAGAGACTTGGTCTGCCACCACCTGCTCCCA         TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTTGCC         TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTATACCA         TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAGGTTAAAGGC         TACGGTAGCAGAGACTTGGTCTGACATGGTCGGAGAGTGTG         TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTCGAAAGATGTG         TACGGTAGCAGAGACTTGGTCTGGCAGGTAGGGTGGTAGC         TACGGTAGCAGAGACTTGGTCTGCCACAGGTAGGTGGTAGC         TACGGTAGCAGAGACTTGGTCTCGCCAAGGAAGTGGTAGGAGCC         TACGGTAGCAGAGACTTGGTCTCCCACACGGCCCTCCC         TACGGTAGCAGAGACTTGGTCTTCGCGAAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCGCAACACGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCGCAACACGAGAGCC         TACGGTAGCAGAGACTTGGTCTTCCGCAACACGAGAGCC         TACGGTAGCAGAGACTTGGTCTTGCGCATTATCAGCATCATCAGCATCA         TACGGTAGCAGAGACTTGGTCTAGCCCTGCCTCTCCTATGCAG         TACGGTAGCAGAGACTTGGTCTGGCATATACCGTTCAGAGTGCT         TACGGTAGCAGAGACTTGGTCTGGCCTCCACCATTCAGAGTGCCT         TACGGTAGCAGAGACTTGGTCTTGGCATGCAGACCATCACCATCAGGAGGACTTGGTCTTGGCACAGAGACTGGTCTGGCACCACCATCAGGCTAGCCAGAGACTTGGTCTTGGCCAAGAATGGTCCTTAACGGTAGACGAGACCTGGTCTTGGCCACAGAACTGGTCTTGAACGTGGCCTTGACTGGCTGAAAAATGCCCA         TACGGTAGCAGAGACTTGGTCTGGCCTGCCGTGAAACTGGCT         TACGGTAG
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.18           TET2-E03.19           TET2-E03.10           TET2-E03.11           TET2-E03.14           TET2-E03.15           TET2-E03.16           TET2-E03.17           TET2-E03.18           TET2-E03.19           TET2-E05           TET2-E05           TET2-E05	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCTCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGTTGTTCCCTCCCTCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGGAGATACCA TACGGTAGCAGAGACTTGGTCTGCTGAGGGTCAAAGGC TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCGCAGGTAGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCCACACGGACGCC TACGGTAGCAGAGACTTGGTCTCCCCACAGGACGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCACACGGACCGC TACGGTAGCAGAGACTTGGTCTTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCTC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCTC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCCC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCAACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTGCATTCAG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCCTCCTCACACAGC TACGGTAGCAGAGACTTGGTCTTGCAAGATTGGTCTTCTCCC TACGGTAGCAGAGACTTGGTCTTGCAAGATTACGGTCACAGCACC TACGGTAGCAGAGACTTGGTCTTGCAAGATCACACACCC TACGGTAGCAGAGACTTGGTCTTGCAAGATCATCAGCACCACC TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGTGTTGTGAA TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGGTCTTCCT TACGGTAGCAGAGACTTGGTCTTGGCAAGAGATGGTCC TACGGTAGCAGAGACTTGGTCTTGGCCAAAGAATGGTCC TACGGTAGCAGAGACTTGGTCTGCCAAGAATGGTCTTCTCC TACGGTAGCAGAGACTTGGTCTGCCAAGAATGGCCT TACGGTAGCAGAGACTTGGTCTGCCAAGAATGGCCT TACGGTAGCAGAGACTTGGTCTGCCAAGAATGGCCT TACGGTAGCAGAGACTTGGTCTGGCTGGAACTGGAAACTGGCT TACGGTAGCAGAGACTTGGTCTGGCGTGGAAACTGGCC TACGGTAGCAGAGACTTGGTCTGGCCTGACTGGAAACTGCCT TACGGTAGCAGAGACTTGGTCTGGCCTGACTTGGAAACGCCA TACGGTAGCAGAGACTTGGTCTGGCCTGGC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.16           TET2-E03.17           TET2-E03.19           TET2-E03.19           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.16           TET2-E03.17           TET2-E03.18           TET2-E03.19           TET2-E04           TET2-E05           TET2-E06.01	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCTCCCTGCCCCCTTAC ACACTGACGACATGGTTCTACACCGCAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCGAGGCAGGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGGCTTGCCTTTTCCGAGC ACACTGACGACATGGTTCTACAGGGCAGAGGGGAGAGGCTG ACACTGACGACATGGTTCTACAAGGCAGCTGCCCCCCCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT         TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG         TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCCAC         TACGGTAGCAGAGACTTGGTCTGCCACCACCTGTCTCCCA         TACGGTAGCAGAGACTTGGTCTGACATGGTCCTCCGA         TACGGTAGCAGAGACTTGGTCTATTTTGAAATGTGGGTTGTGTCC         TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAGGTTAAAGGC         TACGGTAGCAGAGACTTGGTCTGACATGGTCGGAGAGGTGG         TACGGTAGCAGAGACTTGGTCTGCCACGGCAAAGAATGTG         TACGGTAGCAGAGACTTGGTCTGCCACGGCAAAGAATGTG         TACGGTAGCAGAGACTTGGTCTGCCACAGGAACTGGTAGGAGC         TACGGTAGCAGAGACTTGGTCTCCCACACGGCACCCCCC         TACGGTAGCAGAGACTTGGTCTCCCACACGGCCCCCCC         TACGGTAGCAGAGACTTGGTCTTCCGCAAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCGCAAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCGCAACACGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCGCGAACACGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCCGCGAACACGAGAGGCC         TACGGTAGCAGAGACTTGGTCTTGCGCAACACGAGAGCTTCCCC         TACGGTAGCAGAGACTTGGTCTGCCCCACCACTACACGCAC         TACGGTAGCAGAGACTTGGTCTGCCTGCATTATCAGGCTGCACCA         TACGGTAGCAGAGACTTGGTCTGGCCTGCAGGACGTGGTGTGACCT         TACGGTAGCAGAGACTTGGTCTGGCACCACCACTCACCACCACCACCACCACCACCACCACCAC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.10           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.18           TET2-E03.18           TET2-E03.20           TET2-E05           TET2-E05           TET2-E05           TET2-E06.01           TET2-E06.02	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACGCGAGACGAGA	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCCACCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTTGCACCGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTGACATGGTCCTCCCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGCTCAGGGCTCAAAGGATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTAGGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTAGGC TACGGTAGCAGAGACTTGGTCTCCCACACGGAAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTTCCCACACGGACGCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGACGCC TACGGTAGCAGAGACTTGGTCTTCCCGCAAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCGCAGCTACACAGG TACGGTAGCAGAGACTTGGTCTTCCCGCAGCTCCTCC TACGGTAGCAGAGACTTGGTCTTCCCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTGCCAAGATTACGTTCACAGCATCA TACGGTAGCAGAGACTTGGTCTTGCCACACTCATCAGGACACC TACGGTAGCAGAGACTTGGTCTTGCCACCACTCATCAGGCTCAC TACGGTAGCAGAGACTTGGTCTTGCCACCATCATCAGGCCACC TACGGTAGCAGAGACTTGGTCTTGCAAGATCTGTGTATGTCA TACGGTAGCAGAGACTTGGTCTTGGCAAAGGCTCCT TACGGTAGCAGAGACTTGGTCTGGCCAAAGGATGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGGATGTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGGATGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGGATGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGGATGGTCCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGGATGGTCCTCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGGATGGTCCTCCC TACGGTAGCAGAGACTTGGTCTGGCCAAGGAAGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCCAAAGGATGACTGCCT TACGGTAGCAGAGACTTGGTCTGGCCAAAGGATGACTGCCT TACGGTAGCAGAGACTTGGTCTGGCCAAGCAGAGAGCCCACC TACGGTAGCAGAGACTTGGTCTGGCCAAGGAGTGGGCTGAAACTGCTT TACGGTAGCAGAGACTTGGTCTGCCAGGCTGAAACTGCTTTCC TACGGTAGCAGAGACTTGGTCTGCCCAGGCTGAAACTGCTTTCC TACGGTAGCAGAGACTTGGTCTGCCCAGGCTGAAACTGCTTTCC TACGGTAGCAGAGACTTGGTCTGCCCAGGCTGAAACTGCTTTCC TACGGTAGCAGAGACTTGGTCTGCCCAGGCTGAAACTGCTTTCC TACGGTAGCAGAGACTTGGTCTGCCCAGGCTGAAACCAAAGG TACGGTAGCAGAGACTTGGTCTGCCCAGGCTTAAGAGCCAAAGG TACGGTAGCA
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.02           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.16           TET2-E03.17           TET2-E03.18           TET2-E03.19           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.16           TET2-E03.17           TET2-E03.18           TET2-E04           TET2-E06.01           TET2-E06.02           TET2-E06.02           TET2-E07.02	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACCCGAGGCAAGATGAGCGA ACACTGACGACATGGTTCTACACGCGAGGCAGGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCCC ACACTGACGACATGGTTCTACAGGAGTTGTCCTTTCCCGCCC C ACACTGACGACATGGTTCTACAGGGCAGAGGGGAGAGGCTG ACACTGACGACATGGTTCTACAAGTGCCCCCCCCTTTCCCATATAA ACACTGACGACATGGTTCTACAAGGCCAGCGCGAGAGGCTG ACACTGACGACATGGTTCTACAAGTGCCCCCCCCCTCCGAC ACACTGACGACATGGTTCTACAAGTGCCCCCACCGCCCC ACACTGACGACATGGTTCTACAATTCAACTGCCCTCCGAC ACACTGACGACATGGTTCTACAATTCAACTGCCGCGCAGCCTTG ACACTGACGACATGGTTCTACAATTCAACTGCCCTGGGGAGAGGCG ACACTGACGACATGGTTCTACAATTCAACTGCCTGGAGAGAGC ACACTGACGACATGGTTCTACAATTCAACTGCCTGGAGAGAGC ACACTGACGACATGGTTCTACAATTCAACTGCCTGGAGAGAGC ACACTGACGACATGGTTCTACAATTCAACTGCCTGGAGAAAACCGTG ACACTGACGACATGGTTCTACAATTCAACTACTGAGGGGCAGCCTTG ACACTGACGACATGGTTCTACAATCACACACATAACTGCAGTGGG ACACTGACGACATGGTTCTACAGCCCCCCTGGTGAAAAAACCACTG ACACTGACGACATGGTTCTACAGCCTCCCCTCTTCCGGAGAAAAACCACTG ACACTGACGACATGGTTCTACAAGCTACGCTCCTGGTGAAGA ACACTGACGACATGGTTCTACACGCTCCCCTCTTCCACAGG ACACTGACGACATGGTTCTACACAGCTACCCTCCTGGTGAAGA ACACTGACGACATGGTTCTACACACCTCCCCCTCTTCCACAAGG ACACTGACGACATGGTTCTACACACCTCCCCCCTCTTCCACAAG ACACTGACGACATGGTTCTACACACGCTACCGGTGGTGAAGA ACACTGACGACATGGTTCTACACAGCTACACGGGCTACAGGACA ACACTGACGACATGGTTCTACACACGTCACAATGGAGCAACAACACCA ACACTGACGACATGGTTCTACAACGCCACAATGGTACCAAGGACA ACACTGACGACATGGTTCTACAACAGCACAAATGGAGCAAACAAC ACACTGACGACATGGTTCTACACACAGGACGACAAACAACGACA ACACTGACGACATGGTTCTACAACACGACACACACACACA	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT         TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG         TACGGTAGCAGAGACTTGGTCTGCCACCACCTGCCCA         TACGGTAGCAGAGACTTGGTCTGCCACCTGGTCTCCCA         TACGGTAGCAGAGACTTGGTCTGCACATGGTCCTCCCA         TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTTATACCA         TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAAGGTGTG         TACGGTAGCAGAGACTTGGTCTGCCACAGGTAGGGTATACCA         TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG         TACGGTAGCAGAGACTTGGTCTGCCAGCGCAAAGAAGGTGG         TACGGTAGCAGAGACTTGGTCTGCCAGCGCAAAGAAGGTGG         TACGGTAGCAGAGACTTGGTCTCCGCAGAGACTGGTAGGCAGGAGCC         TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCGCGAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCGCGAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCGCGAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCGCGAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCGCGAACAGGAGGCC         TACGGTAGCAGAGACTTGGTCTTCGCGAACTGGACTTCCTCC         TACGGTAGCAGAGACTTGGTCTTGCCCACCATCACACACA
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05.01           RUNX1-E06.01           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.18           TET2-E03.20           TET2-E03.18           TET2-E05           TET2-E05           TET2-E05.02           TET2-E06.02           TET2-E06.02           TET2-E07.02	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCCCCCCCCCCCCCC	TACGGTAGCAGAGACTTIGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTIGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTIGGTCTTGCCACCTCGCCA TACGGTAGCAGAGACTTIGGTCTTGCACCTGGTTCTTCATGG TACGGTAGCAGAGACTTIGGTCTATTTTGAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAAGGTGG TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCCCACTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTTCCCCACTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTTCCCCACCGGACGAGGAGCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCTCC TACGGTAGCAGAGACTTGGTCTTCCCGCAAGCAGGAGCC TACGGTAGCAGAGACTTGGTCTTCCCCGCATCATCAGG TACGGTAGCAGAGACTTGGTCTTCCCCCTCCTCC TACGGTAGCAGAGACTTGGTCTTCCCCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTGCTCATTCAG TACGGTAGCAGAGACTTGGTCTTGCCAAGATTACGTCTCACACGCACC TACGGTAGCAGAGACTTGGTCTTGCCACTCATCAGGCTCACACACC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTCTGCATGCCCC TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTTCAAGAGTGCT TACGGTAGCAGAGACTTGGTCTTCCCCCCCCTTCATGCAGCACC TACGGTAGCAGAGACTTGGTCTTGCACACTCATCAGGCTCACCCC TACGGTAGCAGAGACTTGGTCTTGGCAAAGACTGGTCTTGCACCCCCCCC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.02           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.08           TET2-E03.09           TET2-E03.10           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.16           TET2-E03.17           TET2-E03.18           TET2-E03.19           TET2-E03.10           TET2-E03.16           TET2-E03.17           TET2-E03.18           TET2-E03.19           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.16           TET2-E03.17           TET2-E04           TET2-E05           TET2-E06.02           TET2-E06.02           TET2-E06.02           TET2-E08           TET2-E08	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCTCCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACGCGAGGACGAGATGAGCGA ACACTGACGACATGGTTCTACAGCGAGGAGATGAGCGA ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGAGTTGTCCTTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTGCACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCGCGGATATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAGGTATACCA TACGGTAGCAGAGACTTGGTCTGCTGACGTGGGGAGGTG TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCACCGGCACGAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCACCGGCACGAGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGCACGGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGCAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCGCGAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTCCGCAACACGTCACTCAC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.01           RUNX1-E03.01           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E05.01           RUNX1-E06.01           RUNX1-E06.02           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.09           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.18           TET2-E03.19           TET2-E05           TET2-E05           TET2-E06.01           TET2-E06.02           TET2-E06.03           TET2-E06.04           TET2-E06.02           TET2-E06.03           TET2-E06.04           TET2-E06.05           TET2-E06.02           TET2-E08           TET2-E08           TET2-E08           TET2-E09	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCCCCCCCCCCCCCC	TACGGTAGCAGAGACTTIGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTIGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTIGGTCTTGCCACCTCGCCA TACGGTAGCAGAGACTTIGGTCTTGCACCTGGTTCTTCATGG TACGGTAGCAGAGACTTIGGTCTATTTTGAATGTGGGTTGTTGCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGTTAAAGGC TACGGTAGCAGAGACTTGGTCTGACATGGTCCGGGAAGGTGG TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTAGGCC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTCCCGCAGGAGGTGGTAGC TACGGTAGCAGAGACTTGGTCTCCCCGCAGCAAGAGGCC TACGGTAGCAGAGACTTGGTCTCCCCGCAGCAGAGGCC TACGGTAGCAGAGACTTGGTCTCCCGCAGCAGCAGGAGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCGCAACAGGAGGCC TACGGTAGCAGAGACTTGGTCTTCCCGCACCTCCTCATACAGG TACGGTAGCAGAGACTTGGTCTTCCCGCAGCTCATCACGG TACGGTAGCAGAGACTTGGTCTTCCCCCCCTGCTCATTCAG TACGGTAGCAGAGACTTGGTCTTGCGAACAGGAGCC TACGGTAGCAGAGACTTGGTCTTGTGAGAGTGGTTTTCTCC TACGGTAGCAGAGACTTGGTCTTGCAGAGTGGTTTTCTGCA TACGGTAGCAGAGACTTGGTCTTGCACACTCATCAGGCATCA TACGGTAGCAGAGACTTGGTCTTGCACACTCATCAGGCATCA TACGGTAGCAGAGACTTGGTCTTGCACACTCATCAGGCATCA TACGGTAGCAGAGACTTGGTCTTGCACCACTCATCAGGCACC TACGGTAGCAGAGACTTGGTCTTGGCAAAGAGTGTGGTCC TACGGTAGCAGAGACTTGGTCTTGGAACTGGAGAGTGTGGTCC TACGGTAGCAGAGACTTGGTCTGGCAAAGAATGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCAAAGAATGTTGGTCC TACGGTAGCAGAGACTTGGTCTGGCAAAGAATGATCCTTCC TACGGTAGCAGAGACTTGGTCTGGCAAAGAATGTTGGTC TACGGTAGCAGAGACTTGGTCTGGCAAAGAATGTTCGTC TACGGTAGCAGAGACTTGGTCTGGCATGAAGGAACTGGTC TACGGTAGCAGAGACTTGGTCTGGCATGGACTGGAC
RUNX1-E01.01           RUNX1-E01.02           RUNX1-E02.02           RUNX1-E03           RUNX1-E04.01           RUNX1-E04.02           RUNX1-E04.01           RUNX1-E05           RUNX1-E06.01           RUNX1-E06.03           RUNX1-E06.04           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.19           TET2-E03.19           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E03.17           TET2-E03.19           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14           TET2-E03.15           TET2-E04           TET2-E05           TET2-E06.01           TET2-E06.02           TET2-E09           TET2-E09 <td>gDNA           gDNA           gDNA</td> <td>ACACTGACGACATGGTTCTACACCCCTCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACGCGAGACGATGAGCGA ACACTGACGACATGGTTCTACAGCGAGGACGAGATGAGCGA ACACTGACGACATGGTTCTACAGCGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCTCCC</td> <td>TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTGCAACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTGTGTCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGGAGGTG TACGGTAGCAGAGACTTGGTCTGCTGAGGTCGGGAAGGTGG TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTAGGC TACGGTAGCAGAGACTTGGTCTGCGCAGGTAGGTAGGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCACACGGCAGCTGGTAGC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCTC TACGGTAGCAGAGACTTGGTCTTCCGCAAGGAACTGGTAGCA TACGGTAGCAGAGACTTGGTCTTCCGCAAGGAACTGGTAGCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCCCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCCCCC</td>	gDNA           gDNA	ACACTGACGACATGGTTCTACACCCCTCCTGCCCCCCTTAC ACACTGACGACATGGTTCTACACGCGAGACGATGAGCGA ACACTGACGACATGGTTCTACAGCGAGGACGAGATGAGCGA ACACTGACGACATGGTTCTACAGCGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGGTGTTTAGGTGGTGGCCC ACACTGACGACATGGTTCTACAGAGCTTGTCCTTTCCCTCCC	TACGGTAGCAGAGACTTGGTCTAGATTCAGAACACAAAGATCATCCT TACGGTAGCAGAGACTTGGTCTGCCAGCACCTCCACCATG TACGGTAGCAGAGACTTGGTCTGCCGCCTGTCCTCCCA TACGGTAGCAGAGACTTGGTCTTGCAACCTGGTTCTTCATGG TACGGTAGCAGAGACTTGGTCTATTTTGAATGTGGGTTGTGTCC TACGGTAGCAGAGACTTGGTCTGACATGGTCCTGAGGGTATACCA TACGGTAGCAGAGACTTGGTCTGACATGGTCGGGGAGGTG TACGGTAGCAGAGACTTGGTCTGCTGAGGTCGGGAAGGTGG TACGGTAGCAGAGACTTGGTCTGCTCAGCTGCAAAGAATGTG TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGTAGGC TACGGTAGCAGAGACTTGGTCTGCGCAGGTAGGTAGGC TACGGTAGCAGAGACTTGGTCTGCCAGGTAGGAGCC TACGGTAGCAGAGACTTGGTCTCCCACACGGCAGCTGGTAGC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCTC TACGGTAGCAGAGACTTGGTCTTCCGCAAGGAACTGGTAGCA TACGGTAGCAGAGACTTGGTCTTCCGCAAGGAACTGGTAGCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCCCC TACGGTAGCAGAGACTTGGTCTTCCCCACACGGCCCCCCCC

	1		
TET2-E10.03	gDNA	ACACTGACGACATGGTTCTACAGTTAGCAGAGCCAGTCAAGAC	TACGGTAGCAGAGACTTGGTCTTACAAGTTGATGGGGGGCAAAAC
TET2-E11.01	σDNA	ΔΟΔΟΤΘΑΟΘΑΟΑΤΘΟΤΤΟΤΑΟΑΤΟΑΔΟΑΤΟΔΑΘΑΤΑΟΟΤΘΤΤΤΟΤΘΤ	TACGGTAGCAGAGACTTGGTCTGATAAGGACTAACTGGATTGGGC
1012 011.01	50117		TACOGTAGAGAGAGAGAGAGTOGTCTGATAAGGACTAACTGGATTGGGC
TET2-E11.02	gDNA	ACACTGACGACATGGTTCTACATGTCAACTCTTATTCTGCTTCTGG	TACGGTAGCAGAGACTTGGTCTCCACTGATAGGTTTCCATTGCA
TET2-E11 03	ØDNA	ACACTGACGACATGGTTCTACATACCCTGGGCTTTTGAATCAGA	TACGGTAGCAGAGACTTGGTCTTCCCTGCATATTTTGGTTTCCA
	5011/4		
TET2-E11.04	gDNA	ACACTGACGACATGGTTCTACACTCAGTCTACCACCCATCCAT	TACGGTAGCAGAGACTTGGTCTTGTTCACCATTTTTATAGTCCATGTT
TET2-E11.05	ØDNA	ACACTGACGACATGGTTCTACACACTCATGAGATGGATGG	TACGGTAGCAGAGACTTGGTCTGCAGTTCTATCATGGTTAAGAGCT
TET2 511 00	-DNIA		
TET2-E11.06	gDNA	ACACIGACGACAIGGIICIACAAAIGACAIGCIIICCCACACAG	TACGGTAGCAGAGACTTGGTCTCATGAGTTGGAGCCACGG
TET2-E11.07	gDNA	ACACTGACGACATGGTTCTACAGGTCAGACAGCGAGCAGA	TACGGTAGCAGAGACTTGGTCTTCTTTCTCACGGGCTTTTTCAG
TET2 511 00	-DNIA		
TETZ-E11.08	guna	ACACIGACGACAIGGIICIACAGCAIGCCACAACCCCIIIAA	TALGGTAGLAGAGALTIGGTLIGLAGGTAAGIGGGLILIGAA
TET2-E11.09	gDNA	ACACTGACGACATGGTTCTACATATGGCCCAGACTATGTGCC	TACGGTAGCAGAGACTTGGTCTGGTTGGTTGTGGTCTTTTCAAG
TDE 2 E04 01		ACACTCACCACATCCTTCTACATCCTCTCACTCCTCTTTTCAC	TACCCTACCACACACTTCCTCCTACCTTTTCTCCCCAACCCA
TP55-E04.01	guna	ACACIGACGACATGGITCIACATCCICIGACIGCICITITCAC	TACGGTAGCAGAGACTTGGTCTGGTAGGTTTTCTGGGAAGGGA
TP53-E04.02	gDNA	ACACTGACGACATGGTTCTACAGTCCAGATGAAGCTCCCAGA	TACGGTAGCAGAGACTTGGTCTGATACGGCCAGGCATTGAAG
	a DNIA		TACCCTACCACACACTTCCTCTCCCTCTCTCCCACC
TP55-E05	gDNA	ACACIGACGACATGGTTCTACATGTGCCCTGACTTCAACTC	TACGGTAGCAGAGACTIGGTCTCCCTGTCGTCTCTCCAGC
TP53-E06	gDNA	ACACTGACGACATGGTTCTACAGGAGAGACGACAGGGCTG	TACGGTAGCAGAGACTTGGTCTGGAGAAAGCCCCCCTACTG
TDF 2 F07	a DNIA		TACCCTACCACACACTTCCTCTACACCTCCATCCCTACTA
TF33-E07	BDINA	ACACIDACOACAIOUTICIACAOCACIDOCCICAICIIOOO	TACGGTAGCAGAGACTTGGTCTAGAGGTGGATGGGTAGTAGTAGTAG
TP53-E08	gDNA	ACACTGACGACATGGTTCTACAGGGTGGTTGGGAGTAGATGG	TACGGTAGCAGAGACTTGGTCTCTCCACCGCTTCTTGTCCT
	(DNA		TACCCTACCACACACTTCCTCCACCACCCATTCTCTTCA
TP55-E09	gDNA		TACGGTAGCAGAGACTIGGTCTCCAGGAGCCATIGTCTTGA
TP53-E10	gDNA	ACACTGACGACATGGTTCTACAACTTGAACCATCTTTTAACTCAGGT	TACGGTAGCAGAGACTTGGTCTTGAAGGCAGGATGAGAATGGA
ASYL1_E13.02	αDNA	CTTACCAGATATGCCCCCG	
A5AL1-L15.02	SDINA	CHACAGAIAIGCCCCCG	ACCACCATCACCACTOC
ASXL1-E13.03	gDNA	ACTGCCATCGGAGGGG	TCTCCTAGCTCTGGACATGG
RUNY1 E01 01		GTAATAAAGGCCCCTGAACG	ACCCTCCTCATCTTC
NONX1-L01.01	SDINA	GIAAIAAAGGEEEEIGAAEG	Acoccicocicaterio
RUNX1-E01.02	gDNA	TTGTGATGCGTATCCCCG	CAGAGGAAGTTGGGGCTG
RUNY1_E01_03	αDNA	CANGCTEAGEAGCEGEC	CCTGTCCTCCCACCACC
NONX1-L01.05	SDINA	CARGETGAGGAGEGGE	
RUNX1-E02.01	gDNA	ACATCCCTGATGTCTGCATT	GTACCTCTTCCACTTCGACC
BUNX1-E02.02	σDNA	ACTEGTETTAGETEGE	GTTTGTTGCCATGAAACGTG
NONAT-LUZ.UZ	5 DIVA		
RUNX1-E03	gDNA	CCACCAACCTCATTCTGTTTT	GTCCCTGAGTATACCAGCCT
RUNX1-F04 01	gDNA	TCTGATCTCTTCCCTCCCT	GCTGACCCTCATGGCTG
KUNX1-E04.02	gDNA	GAGCITGTCCTTTTCCGAGC	AGGAGAGGCGGGCAGTG
RUNX1-F05-01	gDNA	AATCCCACCCCACTTACAT	GAAAGTTCTGCAGAGAGGGT
	5.000		
KUNX1-E05.02	gDNA	IGGILCTACGATCAGTCCTA	LAIGLACCTCTAGTCTCCTG
RUNX1-F06 01	gDNA	CTACTCACTTCCGCTCCG	GCAGGTAGGTGTGGTAGC
DUDU4 500.01			
RUNX1-E06.02	gDNA	CTTCACCTACTCCCCGAC	CCACCATGGAGAACTGGTAG
RUNX1-E06.03	σDNA	OLOSTICA A CLASSEL	CTCCACCACGTCGCTCTG
NONXI E00:05	50117		
RUNX1-E06.04	gDNA	CCGGCTCCTACCAGTTCTC	CTCCACACGGCCTCCTC
RUNX1-F06.05	ØDNA	CAGCCTCCCGAACCAGAG	GTCGCGAACAGGAGGCC
	55101		
ASXL1-E13.01	gDNA	TCCTAGTTTTGCTTTACAGTCCC	GCAGTGGTGACCTCTCGC
ASXL1-F13.02.A	gDNA	ACTTACCAGATATGCCCCCG	CCTCACCACCATCACCACTG
101111 510 00			
ASXL1-E13.03	gdna	ACCCICGCAGACATIAAAGC	CGGCAGIAGIIGIGIICGC
ASXL1-F13.04	gDNA	AGTGGTGATGGTGGTGAGG	GGGGAGTTGGGAGGCATC
101111 510 05			
ASXL1-E13.05	gdna	ICICIGAGAAAGGAGGAAAGCI	GIGGGILLIIGLILLILAI
ASXL1-F13.06	gDNA	GAACTGAATGTGAGTCTGGCA	ATGAGCCACCAAGCCCTAAT
ACX14 E12 07		CONCTTOCACA COTO A TOOT	
ASXLI-E13.07	guna		LLAALLIGUGULILAALA
ASXL1-E13.08	gDNA	TCGAATGATGAGGTAGTGAAACAG	TTCAGCTTTTCAATGTCCACCT
ASVL1 E13.00		CACTCICCOTCICCOCCAC	CATTCACCTTCCACACTCCC
A3XL1-E13.09	guna	GACTGTGCCATCTCGAGGAG	CATICACCITOGACAGIGGG
ASXL1-E13.10	gDNA	AGGGATCTTCGGTGGACAAG	CATCACAAGTGGGTTAGTGGC
ACVL1 E12 11	a DNIA	CATTOCCTACTCCCCA	CCATCAACCATCCCACTCTT
ASALI-EIS.II	guna	GATTCLCTACTGCTGGCCA	CLATCAACLATGCLACTGTT
ASXL1-E13.12	gDNA	CATGGCTCGCTACGCATG	CCATTTCTTCCAGTTTCCTAGAGG
ACVL1 E12 12	a DNIA	CCCACTCCCAACTTTTCACT	TCTCCTCTCCACCAAACCAC
ASALI-EIS.IS	guna	GGCAGTCCCAAGTTTGACT	TCTGCTCTGGACCAAAGGAG
ASXL1-E13.14	gDNA	GCCCAGGAGATCTTACTACCT	AGACATGGAGTTTGTGCTTGG
ACVI 1 E12 1E		TTTTCCCTCTCCCAATCTCC	ATGCCCAGTAGCTTTCCTGT
A3AL1-E13.13	BDINA	TITIGGCTCTGGGAATGTGG	ATOCCCAOTAOCITICCIOI
ASXL1-E13.16	gDNA	TTTGTTGGCAGCGTCAAGAA	AGCTTCCCATAAAATGCCTGC
ACVI 1 E12 17		CCCAACCCCTCACTCAC	TCCACCETECTECTEA
A3AL1-E13.17	BDINA	GGGAAGGGGCTCAGTGAG	TCCACCOTOCIOCIOTCA
ASXL1-E13.18	gDNA	GCAAACTTTGGTGCGAGCC	AGATCAATCATTATCAAAATACACACA
CEBPA-E01 01	σDNA	CLATECCEEEAEAACTCTA	GTCGTTGAAGGCGGCC
0.0171.01.01	5011A		
CEBPA-E01.02	gDNA	GCACGAGACGTCCATCGA	GTCCAGGTAGCCGGCG
CEBPA-E01 03	ØDNA	GGCGACTTTGACTACCCGG	CGGCTGGTAAGGGAAGAGG
5201 A 101.05	5011A		
CEBPA-E01.04	gDNA	GCCGCTGGTGATCAAGC	GACCGGGCTGCAGGTG
CEBPA-E01.05	ØDNA	GCAGTTCCAGATCGCGC	CGGTACTCGTTGCTGTTCTT
	5510		
CEBPA-E01.06	guna	LILAAGGGGLIGGGGG	LAGEIGGEAAGAIGE
CEBPA-E01.07	gDNA	GTGGACAAGAACAGCAACGA	CGCAGCGTGTCCAGTTC
CERRA FOI CO	«DNIA	CCAACCCCCTCCAACA	
CEBPA-EU1.08	guna	UCAAULUUUIUUAALA	AUAUUAAUUUAUUUALAL
DNMT3A-E07.01	gDNA	TTCCTGGAGAGGTCAAGGTG	TTTGGTGGCATTCTTGTCCC
DNIMT2A FOT 02	«DNIA	CCAACAAAACCACCCCCCC	CACCACCTCCCACC
DINIVIT3A-EU7.02	guna	UUAAUAAAALLAUUUUUL	0400401100440100440
DNMT3A-E08	gDNA	CTCGTGACCACTGTGTAATGAT	GCCCTGGGATCAAGAACCTT
		COTOCOTOCIACIÓ	
UNIVITSA-EU9	BDINA	GOTOGOTOCITOCAAOTO	ACCIOCACICCAACIICCAU
DNMT3A-E10	gDNA	CTGACAACCCCAACCCTG	GCCCTGGTGTGGATCTGC
		CTGTAACTGACCTTGGCACCT	TOCCATCOACCOUNCT
UNIVI JA-EII	BDINA		
DNMT3A-E12	gDNA	AGAAGCCCAAGGTCAAGGAG	CTCTGCTACTCTGCCCCATG
DNMT2A_F12	αDNA	TTTTGTGGCTGGTCTGGTGC	AGAAGCGGTGGACACAGTC
DIVIVITOR-E13	5UNA		
DNMT3A-E14	gDNA	GAGCCTCCCTTCGTCCTG	GGCCCAGCTAAGGAGACC
DNMT24 E1E 01		CLAGGGCTGAGAGTCTCCT	GCCCAGCACTCACAAATTCC
DIMINITOR-E13.01	SUNA		
DNMT3A-E15.02	gDNA	GTGGAGTGTGGGACCTCTT	CCCCACAACCAAGGCTCA
DNMT2A F16		CTEGECCTECATCTEACC	GTTTTGCCAGAGTTGCCCAC
DIVIVITSA-ETD	BDINA		GTTTGLCAGAGTTGLLCAL
DNMT3A-E17	gDNA	AGATGGCTCCAAGTAACGGTG	GTGCAGGGAGGGGAAGAC
DNMT34-F18	σDNA	CTTCCTGTCTGCCTCTGTCC	CATCGGGAATAGCTGTCCCA
DINIVITUR-E10	BUINA		
DNMT3A-E19	gDNA	GAGCCACACCACTGTCCTAT	CCATTAGTGAGCTGGCCAAAC
DNMT3A-F20	σDNA	CCTTGGCTCATCTTCAAACCG	ΔGCΔGCTΔGTCΔTTCΔGCΔGΔ
DINIVITURA=EZU	BUINA		
DNMT3A-E21	gDNA	ACCCTGTGAACTAGTGGCTG	CATCCTGCCCTTCCTCCC
DNMT3A-F22	ØDNA	GCATATTTGGTAGACGCATGACC	CACAGCAATCAGAACAGCCAC
	5.000		
DNMT3A-E23.01.A	gDNA	GGTCCTGCTGTGTGGGTTAGA	GTGTCGCTACCTCAGTTTGC
DNMT3A-F23.02	σDNA		TETTTAACTTTETETETETETET
S.MMI JA-L2J.UZ	D D I I I		
FLT3-E16.01	gDNA	TGCCTGGCTTCTCATAATT	GTGATTTTCGTGGAAGTGGGT
ELT3-E16.02.4	ØDNA	CTGAGCTGAGAAAAATTTTATTTAATGAC	TGTCATCAAGCTACAGTCTTTTGA
5170 500 51 F	50114		
FLI3-E20.01.A	gDNA	GAAGAAGATIGLACICLAGGA	GATAALGALALAALALAAAATAGC
FLT3-E20.02	gDNA	GCACTCCAGGATAATACACATCA	ACAGTGAGTGCAGTTGTTTACC
IIUH1-E04.01.A	gUNA	GAAGCIAIAAAGAAGCAIAATGTTGGC	TGULAALATGALITALITGATCC

IDH1-F04 02			
IDTTE EO TIOE	gDNA	TCAAGTTGAAACAAATGTGGAAATCA	CATACAAGTTGGAAATTTCTGGGC
IDH2-E04.01	gDNA	TTCTGGTTGAAAGATGGCGG	CAGGTCAGTGGATCCCCTC
IDH2-F04.02.A	gDNA	TGTCCTCACAGAGTTCAAGCT	AGGATGGCTAGGCGAGGAG
NDM1 E11 01 A	aDNA	TEATETCTATEAACTETTETEET	GECANTAGAACCTEGACAACA
	BUNA		
NPM1-E11.02	gDNA	IGICIAIGAAGIGIIGIGGIICC	ALAGGLATTTGGALAALALA
NPM1-FE10-11	cDNA	TCCCAAAGTGGAAGCC	GGAAAGTTCTCACTCTGC
NRAS-E02.01.A	gDNA	GGAAGGTCACACTAGGGTTTTC	GATCAGGTCAGCGGGCTAC
NRAS-E02 02	gDNA	TACTGTAGATGTGGCTCGCC	TGATCCGACAAGTGAGAGACA
NDAG 502.01 A	-DNA		
NRAS-EU3.UI.A	gDNA	AGTIAGAIGCITATTIAACCITGGCA	AGAGGTTAATATCCGCAAATGACT
NRAS-E03.02	gDNA	CCCTCCCTGCCCCCTTAC	AGATTCAGAACACAAAGATCATCCT
RUNX1-E01.01	gDNA	CTGCTTGCTGAAGATCCGC	GCCAGCACCTCCACCATG
RUNX1-F01 02 A	σDNA	ΤΑΤΓΓΓΓΩΤΑΘΑΤΘΓΓΑΘΓ	CAGGGTCTTGTTGCAGCG
DUNIXA FOL 02	-DNA		
RUNX1-EU1.03	gDNA	LLLAGGLAAGATGAGLGA	
RUNX1-E02.01	gDNA	TCCTCTGCAACCTAAAAAGAAATCA	TGCAACCTGGTTCTTCATGG
RUNX1-E02.02	gDNA	GGTGTTTAGGTGGTGGCCC	ATTTTGAAATGTGGGTTTGTTGCC
RUNX1-E03	gDNA	ACAGATATGTTCAGGCCACCA	GACATGGTCCCTGAGTATACCA
BUNY1 E04 01	#DNIA		
KUNA1-E04.01	gDNA		TGAGGCTGAGGGTTAAAGGC
RUNX1-E04.02	gDNA	GAGCTTGTCCTTTTCCGAGC	AGTTGGTCTGGGAAGGTGTG
RUNX1-E05	gDNA	AAATCCCACCCACTTTACATATAA	GCTCAGCTGCAAAGAATGTG
RUNX1-F06.01	gDNA	GGGCAGAGGGAAGAGCTG	GGCAGGTAGGTGTGGTAGC
BUNY1 EOG 02	gDNA	CTECCCTCCATCTCCEAC	CATEGAGAACTEGTAGGAGCC
RUNA1-E06.02	gDNA	CIGULIULATURUGAL	
RUNX1-E06.03	gDNA	GTTCCAAGCCAGCTCGC	CTCCACACGGCCTCCTC
RUNX1-E06.04	gDNA	CTGCACCAACGCCTCCA	TCGCGAACAGGAGGCC
TFT2-F03.01	gDNA	ATTCAACTAGAGGGCAGCCTTG	TCTGGCTTCCCTTCATACAGG
TET2 503.02	#DNIA	CCACTCCCTCACACC	CCCC A ACTTACCTCTTTCTCC
TE12-E03.02	gDNA	CLLACIGLCIGAGAGAGL	
TET2-E03.03	gDNA	TICICICICTGGGCTCCTTC	TCCCCTCCTGCTCATTCAG
TET2-E03.04	gDNA	TCAACACATAACTGCAGTGGG	TGTGAGATGTGGTTTTCTGCA
TET2-E03.05	gDNA	GGTGAACTCCTGGAAAAAAACACTG	GCATTATCAGCATCAGCATCA
TET2-E03.06	σDNA	ТСССТССАААСССАСТС	ΔΤΔΓΓΩΤΤΓΔΩΔΩΓΤΩΓΓΔΩ
TET2 502.00	BUINA		
TET2-E03.07	gDNA	AAGCTAGCGTCTGGTGAAGA	ALILLALLATTCAGAGTGCT
TET2-E03.08	gDNA	CCTCCTCCTCCACAGG	TCCCTGCAGTCTGTATGTCA
TET2-E03.09	ØDNA	CCCTTCTCCGATGCTTTCTG	CAAGATCTCGTGTTTGCTCCT
TET2 503.40	-DNA		
TET2-E03.10	gDNA	LAGIGGAGAGLIALAGGALA	TGGAGGTCATTIGATIGGAGAGAGA
TET2-E03.11	gDNA	GCCCCTCGTTTTCACCAAG	TGGAACTGGAGATGTTGGTCC
TET2-E03.12	gDNA	GTCACAAATGTACCAAGTTGAAATGA	AGGTGTGAGTTTGAAAATGGCT
TET2-E03 13	gDNA	AAAACTTATGTCCCCAGTGTTGA	TGGCCAAAGAATGATCCTTCTC
TET2 E03.13	-DNA		
TET2-E03.14	gDNA	AGCAACAGCAGCAAAAATTACAA	GCATGCACTIGATTICATGGTC
TET2-E03.15	gDNA	CAAATGGGACTGGAGGAAGTAC	TGCTCCTGTTCTTGAAAGCAC
TET2-E03.16	gDNA	GCAGGAAACAAGACCCAAAAC	TGAGTGTGACTTCCTCCCTG
TET2-E03 17	σDNA	ΔΓΔΔΩΓΤΓΓΔΩΤΤΓΤΔΓΔΩΘΘΔ	CCTGTGCATCTGACTATGGC
TET2 E03.17	-DNA		CACTTOCCCCCCANACTCCCT
TET2-E03.18	gDNA	ALAGAAGLAAGAALAGLAGL	GACITGGCGTGAAACTGCTT
TET2-E03.19	gDNA	GAATCCACCTGCAAGCTGTG	TGTTCTTTTGGTTGGTGTCTTTTC
TET2-E03.20	gDNA	CTAGACAAACCACTGCTGCA	TGCTAATTCTGGATAAACGCCA
TET2-E04	gDNA	AATGTGTAGTTGGGGGTTAAGC	TGTGTGAAGGCTGGAAAAATTCT
TET2_EO5	σDNA	CCGTTCATTTCTCAGGATGTGG	TGCCCAAGATTTAAGACCAAAGG
TET2-E05	BUNA		
TET2-E06.01	gDNA	GCCCTTATCTGCTGCAAGTG	GCCGTATTTCCTCAGCGTCT
TET2-E06.02	gDNA	ACTGTGTTTGGTGCGGGA	GCTGAACTCTCTTCCAACC
TET2-E07.01.A		GACACCTATAATATCAGCTGCACA	ACATCAGGAAGTAAACAAACCTCT
	EDINA		
TET2 E07 02	gDNA gDNA	TCAGCTGCACAGCCTATATAATG	ΤΛΛΤGΛΛΤΤCΤCΤΛΤGΛΛΛΛΛΤΛΛΛCC
TET2-E07.02	gDNA	TCAGCTGCACAGCCTATATAATG	
TET2-E07.02 TET2-E07.03.A	gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT
TET2-E07.02 TET2-E07.03.A TET2-E08	gDNA gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGTGTTTGGG	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09	gDNA gDNA gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGGGTTTGGG AACTACTTTGGCATTCACACACA	TAATGAATITCICTATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09 TET2-E10.01	gDNA gDNA gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGTGTTTGGG AACTACTTTCGCATTCACACACA CACGTTTCTTGGCGACCTGCA	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCCA CTIGACTGGCTCTGCTCAACATC
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09 TET2-E10.01	gDNA gDNA gDNA gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGTGTTTGGG AACTACTTTCGCATTCACACACA CACGTTTTCTTGGGACCTGTA CACGTTTTCTTGGGACCTGTA	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCG CAGCTGCTAAGCTGTCCTCA CTGCACTGGCTCTGCTAACATC CTGCACTGGCTCTGCTAACATC
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09 TET2-E10.01 TET2-E10.02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGGGTTTGGG AACTACTTTCGCATTCACACACA CACGTTTTCTTGGGACCTGTA GTGGATGAGTTTGGGAGTGTG	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCTAACATC CTGGCTTGCGTTTTCAGTTTG
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.03	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGTGTTTGGG AACTACTTTCGCATTCACACACA CACGTTTTCTTGGGACCTGTA GTGGATGAGTTTGGGAGTGTG GTTAGCAGAGCCAGTCAAGAC	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTCGCTAACATC CTGGCTTGCGGTTTCAGTTTG TACAAGTTGATGGGGGGCAAAAC
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.03 TET2-E11.01	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTIGCGCC AGGCACCATATATIGTGTTGGG AACTACTITCGCATTCACACACA CACGTTTTCGTTTGGGACTGTA GTGGATGAGTTTGGGAGTGTG GTTAGCAGAGCCAGTCAAGAC TCACACTCACAAGATACCTGTTTCTGT	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGTCCTCA CTIGACTGGCTCTGCTAACATC CTGGCTTGCGTTTCAGTTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.03 TET2-E11.02 TET2-E11.02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGGTTTGGG AACTACTTTCGCATTCACACACA CACGTTTTCTTGGGACCTGTA GTGGATGAGTTTGGGAGTGTG GTTAGCAGAGCCAGTCAAGAC TCAACATCAAAGATACCTGTTTCTGT TGCAACTCTTTATTCTGCTTCTGG	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCTAACATC CTGGCTTGCGTTTTCAGTTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGGTTGCGGC CCACTGATAGGTTTCCATTGCA
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.02 TET2-E11.01 TET2-E11.01 TET2-E11.02 TET2-E11.02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGTGTTTGGG AACTACTTTCGCATTCACACAACA CACGTTTTCTTTGGGACCTGTA GTGAATGAGTTTGGGAGTGTG GTTAGCAGAGCCAGTCAAGAC TCAACATCAAAGATACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCTGG TAGCCGCCCTTTCAACACCA	TAATGAATITCTCTATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCCTAACATC CTGGCTTGCGTGTCGTCAGTTG TACAAGTTGATGGGGGCCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.03 TET2-E11.03 TET2-E11.02 TET2-E11.02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTIGCGCC AGGCACCATATATTGGTTTGGG AACTACTTTGGCATTCACACACA CACGTTTTCGTTTGGGACCTGTA GTGAGAGAGCCAGTCAAGAC GTTAGCAGAGCCAGTCAAGAC TCAACATCAAAGATACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCTGG TACCCTGGGCTTTTGAATCAGA	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATTGATCATCT TAAGTTGTTACATTIGCTGCCA CAGCTGCTAAGCTGTCCTCA CTIGACTGGCTCTGCTAACATC CTGGCTTGCGTTTTCAGTTTG TACAAGTTGATGGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTTCCA
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.03 TET2-E11.03 TET2-E11.02 TET2-E11.03 TET2-E11.04	EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGGTTTGGG AACTACTTTCGCATTCACACACA CACGTTTTCTTGGGACCTGTA GTGGATGAGTTGGGAGTGTG GTTAGCAGAGCCAGTCAAGAC TCAACATCAAAGATACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCTGG TACCCTGGGCTTTTGAATCAGA CTCAGTCTACCACCCATCCAT	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGATCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCTAACATC CTGGCTTGCGTTTCCAGTTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTTCCA TGTTCACCATTTTTATAGTCCATGTT
TET2-E07.02           TET2-E07.03.A           TET2-E08           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05	gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTIGCGCC AGGCACCATATATGGTTTGGG AACTACTTTGCATTCACACACA CACGTTTTCGCATTCACACACA CACGTTTTCGGAGTGTG GTTAGCAGAGCCAGTCAGGAC TCAACATCACAAGATACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCTGG TACCCTGGCCTTTTGATCAGA CTCAGTCTACCACCACTCCAT CACTCATCAGAGTGGATGGCC	TAATGAATITCTCTATGAAAAATAAAGCC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGTCCTCA CTGGACTGGCGTCTGCGTAACATC CTGGCTTGGGTGCGCTAACATC CTGGCTTGATGGGGGCCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTTCCA TGTCACCATTTTTAGTCCATGTT GCAGTTCTATCATGGTTAAGAGCT
TET2-E07.02 TET2-E07.03.A TET2-E08 TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E11.03 TET2-E11.01 TET2-E11.02 TET2-E11.02 TET2-E11.04 TET2-E11.05 TET2-E11.06	EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTIGCGCC AGGCACCATATATTGTGTTGGG AACTACTTTGGCATTCACACACA CACGTTTTCGTTTGGGACTGTA GTGAGAGAGCCAGTCAGAGA GTTAGCAGAGCCAGTCAGAGAC TCACACTCATAGGATGACTGTTTCTGT TGTCAACTCTTATTCTGCTTCTGG TACCCTGGGCTTTTGAATCAGA CTCAGTCTACCACCCATCCAT CACTCATGGAGTGGATGGCC AATGACATGCTTTCCCCACCAGG	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGAAAAATAAAGC TAAGTTGTTACATTTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCGA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCTAACATC CTGGCTGCGGTTTCAGTTTG TACAAGTTGATGGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTTCCA TGTTCACCATTTTTAGTCCCATGTT GCAGTTCTACAGGTAAGAGCT CCATGAGTTGGAGCCACGG
TET2-E07.02 TET2-E07.03.A TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.03 TET2-E11.02 TET2-E11.02 TET2-E11.02 TET2-E11.03 TET2-E11.03 TET2-E11.04 TET2-E11.05 TET2-E11.07	gDNA	ICAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGGGTTGGG AACTACTTTCGCATTCACACACA CACGTTTTCTTGGGACCTGTA GTGGATGAGTTGGGAGTGTG GTTAGCAGAGCCAGTCAAGAC TCAACATCAAAGATACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCTGG TACCCTGGCTTTTGAATCAGA CTCAGTCTACCACCCATCCAT CACTCATGAGATGGAGGCC AATGACATGCTTTCCCACACAG GGTCAGACAGCGAGCAGAG	TAATGAATITCTCTATGAAAAATAAAGGC AAGGATATGTCATATTGATCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGTCCTCA CTIGACTGGCCTCTGCTCAACATC CTGGCTTGCGTGCGTTTGATGGGC CACTGGATGAGGGCCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTGGTTTCCA TCCCTGCATATTTGATCCATGTT GCAGTTCTATCATGGTTAAGAGCT CATGAGTTGGAGCCACGG CATGGGGCTTTTCAG
TET2-E07.02 TET2-E07.03.A TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.03 TET2-E11.01 TET2-E11.03 TET2-E11.03 TET2-E11.03 TET2-E11.05 TET2-E11.05 TET2-E11.05 TET2-E11.07 TET2-E11.07	gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTIGCGCC AGGCACCATATATIGTGTTGGG AACTACTITCGCATTCACACACA CACGTTTTCGTGATCACACACA CACGTTTTCGGAGTGG GTTAGCAGAGCCAGTCAGGA GTGAGCAGGACCAGTCAGAGA TCACACTCAAAGATACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCGG TACCCTGGCCTTTTGAATCAGA CTCAGGATGGATGGATGGCC AATGACAGCCAGCCAGCAGA GGTCAGCCAGCCAGCAGCAGA	TAATGAATTCTCTATGAAAAATAAAGCC AAGATATGTCATATGATCATCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGTCCTCA CTGGACTGGCGTCTGCGTAACATC CTGGCTTGGGTGCGCTAACATC CTGGCTTGATGGGGGCCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGGA CCCTGCATATTTTGGTTCCAT GTCACCAATTTTTAGTTCCATGTT GCAGTTCATCATGGTTAAGAGCT CATGAGTTGGGAGCCACGG CTTCTCTACGGGGCTTTCGAA
TET2-E07.02 TET2-E07.03.A TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.03 TET2-E11.03 TET2-E11.02 TET2-E11.02 TET2-E11.03 TET2-E11.04 TET2-E11.05 TET2-E11.06 TET2-E11.06 TET2-E11.07	EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA EDINA	ICAGCTGCACAGCCTATATAATG TTCAGGAGAACTIGCGCC AGGCACCATATATTGGTTTGGG AACTACTITGGCATTCACACACA CACGTTTTCGTTTGGGAGCTGTG GTTAGCAGAGCCAGTCAAGAC TCAACATCAAAGATACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCTGG TACCCTGGGCTTTTGAATCAGA CTCAGTCTACCACCCATCCAT CACTCATGGAGTGGAGGGCC AATGACATGCTTTCCCACACAG GGTCAGACAGCGAGCAGA GCATGCCACCCCTTTAA	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGAAAAATAAAGC AAGATATGTCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTIGACTGGCTCTGCTAACATC CTGGCTGCGTTTCCAGTTIG TACAAGTTGATGGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTIGGTTTCCA TGTTCACCATTTTTATGTCCATGTT GCAGTTCTACTGGTAAGAGCT CATGAGTTGGAGCCACGG TCTTTCTCACGGGCTTTTCAG GCAGGTAAGTGGGGCCTCGAA
TET2-E07.02 TET2-E07.03.A TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.03 TET2-E11.03 TET2-E11.03 TET2-E11.03 TET2-E11.04 TET2-E11.05 TET2-E11.05 TET2-E11.06 TET2-E11.08 TET2-E11.08 TET2-E11.09	gDNA	ICAGCTGCACAGCCTATATAATG TTCAGGAGAACTTGCGCC AGGCACCATATATTGGGTTGGG AACTACTTTCGCATTCACACACA CACGTTTTCTTGGGACCTGTA GTGGATGAGTTGGGAGTGTG GTTAGCAGAGCCAGTCAAGAC TCAACATCAAAGATACCTGTTTCTGT TGTCAACTTTTGCTTCTGGT TGTCAACTCTTTGCTTCTGGT TACCCTGGCTTTTGAATCAGA CTCAGTCTACCACCCATCCAT CACTCATGAGATGGATGGCC AATGACATGCTTTCCCACACAG GGTCAGACAGCGAGCAGA CGCAGCCACACCCCTTTAA TATGGCCCAGACTATGTGCC	TAATGAATITCTCTATGAAAAATAAAGGC AAGATATGTCATATGATAAAAGC TAAGTTGATCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGCCTCCA CTGACTGGCTGCGCTCACACTC CTGGCTTGCATGGGGGCCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGGA CCCCTGCATATTTTGGTTTCCA TGTTCACCATTTTTATAGTCCATGTT GCAGTTCATCAGGGTCACAGG TCTTTCCACGGGCTTTTCAA GCCAGTTCATCGGGCCCTCGAA GGTTGGTTGTGGGCCTCTGAA
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TET2-E11.09           TET2-E11.09           TET2-E11.09           TET2-E11.09           TET2-E10.09	gDNA	TCAGGTGCACAGCCTATATAATG TTCAGGAGAACTIGCGCC AGGCACCATATATIGTGTTGGG AACTACTTTGCGATTGCACACACA CACGTTTTCGCATTCACACACA CACGTTTTGGGAGTGG GTTAGCAGAGCCAGTCAGGAC TCACACTCAAAGATACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCTGG TACCCTGGGCTTTTGAATCAGA CTCAGTCTACCACCCATCCAT CACCATCGAGATGGATGGCC CACTCATGAGATGGATGGCC GGTCAGACAGCCAGCAGA GGTAGCCACACCCCTTTAA TATGGCCCAGACTGTGTGCC TCCTCTGACTGCTTTCAC	TAATGAATTCTCTATGAAAAATAAAGCC AAGATATGTCATATGATAAAAGCC TAAGTTGATCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGTCCTCA CTGGCTTGCGTTTTCAGTTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGTTTCCATTGGCA TCCCTGCATATTTTGGTTTCCA GCAGTCTCATCATGGTTAGCAGCT CATGAGTTGGGAGCCACGG TCTTCTCACGGGGCTTTAGAGCT CATGAGTTAGGGGGCCTGGAA GGCAGGTAAGTGGGCCCTGGAA GGTAGGTAGTGGGGCCTGGAA GGTAGGTTGTCGGGGCTTTCCAGG
TET2-E07.02 TET2-E07.03.A TET2-E09 TET2-E10.01 TET2-E10.02 TET2-E10.03 TET2-E11.02 TET2-E11.02 TET2-E11.02 TET2-E11.03 TET2-E11.04 TET2-E11.05 TET2-E11.06 TET2-E11.07 TET2-E11.07 TET2-E11.09 TET2-E11.09 TET2-E11.09 TET3-E04.01 TP53-E04.02	EDINA EDINA	ICAGCTGCACAGCCTATATAATG TTCAGGAGAACTIGCGCC AGGCACCATATATIGGTTTGGG AACTACTITGGCATTCACACACA CACGTTTTCGTTTGGGAGCTGTG GTGAGTGAGGTGAGGCCAGTGA GTGAACATCATAGGAGCCAGTCAAGAC TCAACATCATAGGAACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCTGG TACCCTGGGCTTTTGATCAGA CTCAGTCTACCACCCATCCAT CACTCATGGAGTGGCC AATGACATGCTTTCCCACACAG GGTCAGACAGCGAGCAGA GCATGCCCAACACCGTTTAA TATGGCCCAGACTATGTGCC TCCTCTGACTGCTCTTCAC	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGAAAAATAAAGC AAGATATGTCATATGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTIGACTGGCTCTGCTAACATC CTGGCTGCGGTTTCAGTTTG TACAAGTTGATGGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTACGA CCCTGCATATTTTGGTTACGA TGTCACCATTTTTATAGTCCATGTT GCAGTTCTACTGGTTAGGTCACGG TCTTTCTCACGGGCTTTTCAG GCAGGTAGGTGGGCCTCGAA GGTAGGTTTGGGGCCTGAA GGTAGGTTTGTGGGCCTTGAAG GGTAGGTTTGTGGGCCTTGAAG GGTAGGTTTGTGGGCAGGGAA
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.03           TET2-E11.01           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TET2-E11.09           TET2-E11.09           TET2-E11.09           TP53-E04.02           TP53-E05	gDNA	TCAGCTGCACAGCCTATATAATG TTCAGGAGAACTIGCGCC AGGCACCATATATIGTGTTGGG AACTACTTTGCATTCACACACA CACGTTTTCGCATTCACACACA CACGTTTTCGGATGAGTGG GTTAGCAGAGCCAGTCAGGAC TCACACTCAAAGATACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCGG TACCCTGGCCTTTGAATCAGA CTCAGTCTACCACCACTCCAT CACCATCGAGATGGATGGCC AATGACAGGCAGAGGAG GGTCAGACAGCGAGCAGA GCATGCCACAACCCTTTAA TATGGCCCCAGACTGTGCC TCCCTGGACTGTTCCCCAGA GTCCAGATGAACTCCCAGA	TAATGAATITCTCTATGAAAAATAAAGGC AAGATATGTCATATGATGAAAATAAAGC TAAGTTGATCATATGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGCCTCCA CTGGCTGGCGTTTCCGTAGCATC CTGGCTTGGTGGCGCCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGGA CCCCTGCATATTTTGGTTTCCA TGTCCACCATTTTTATGTCCATGTT GCAGTTCTATCATGGTTAAGAGCT CATGAGTTGGAGCCACGG TCTTCTCCACGGGCTTTTCCAG GCAGGTAGTGGGCCTCGAA GGTTGGTGTGGGCCTCGAA GGTGGTTGTGGGCCTGAA GGTAGGTTGTGGGCCTGAA GGTAGGTTTTGGGAAGGGA GATACGGCCAGGCATTGAAG CCCTGTCGTCTCTCCACC
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E11.03           TET2-E11.01           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E04.02           TP53-E04.02           TP53-E04.02           TP53-E04.02           TP53-E04.02	EDINA EDINA	TCAGGTGCACAGCCTATATAATG TTCAGGAGAACTIGCGCC AGGCACCATATATIGTGTTGGG AACTACTITGCGATTGCACACACA CACGTTTTCGCATTCACACACA CACGTTTTGGCAGTGGG GTTAGCAGAGCCAGTCAGAG GTTAGCAGAGCCAGTCAGAGA TCACACTCTAATCTGCTTCTGG TACCCTGGGCTTTTGGATCAGA CTCAGTCTACCACCCATCCAT CACCATGGAGTGGAGGGCC AATGACATGCTTTCCCACACAG GGTCAGACAGCGAGCAGA GGCAGCCAGCCAGCCAGA GGCAGCCACCCCTTTCAC GTCCAGATGGATGGCC CCCTCGACTGCTCCACCAG GGCCAGACGCCCAGAC CCCCTGGCTTTCCACCC CCCCTGACTTCCACCCGC	TAATGAATTCTCTATGAAAAATAAAGCC AAGATATGTCATATGATAAAAGCC TAAGTTGATGATATGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGTCCTCA CTGACTGGCTGCGCTAACATC CTGGCTTGCGTTTCAGTTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTTCCA TGTTCACCATTTTTATGGTCCATGTT GCAGTTCTATCATGGTTAGAGCT CATGAGTAGGGCACAGG TCTTCTCACGGGCTTTACAGGC CAGAGTAGTGGAGCCACGG CTTTCTCACGGGCTTTTCAG GCAGGTAGTGGAGCCTGCAA GGTAGGTTTCTGGGAAGGGA GATACGGCCAGGCATTGAAG CCCTGTCGTCTCCCAGC
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.07           TET2-E11.08           TET2-E11.07           TET2-E11.08           TET2-E11.07           TET2-E11.08           TET2-E11.07           TET2-E10.08           TET2-E10.07           TET2-E10.07           TET2-E10.07           TET2-E10.08           TET2-E10.07           TET2-E10.07           TET2-E10.08           TET2-E10.09           TP53-E04.01           TP53-E05           TP53-E05           TP53-E06	EDINA EDINA	ICAGCTGCACAGCCTATATAATG ITCAGGAGAACTIGCGCC AGGCACCATATATIGGTTTGGG AACTACTITGCGATTGCACACACA CACGTTTTCGTTTGGGAGTGTG GTGAGAGGAGCCAGTCAAGAC ICAACATCATAAGATACCTGTTTCTGT TGTCAACTCTTATTCTGCTTCTGG TACCCTGGGCTTTIGAATCAGA CTCAGTCTACCACCCATCCAT CACCATGCAGATGGAGGGCC AATGACATGCTATCTCACACAGA GGTCAGACAGCGAGCAGAG GCATGCCCAGACTATGTGCC TCCTCTGACTGCTCTTCAC GTCCAGATGCAAGCTCCCAGA	TAATGAATITCICTATGAAAAATAAAGGC AAGATATGTCATATGATGAAAATAAAGC TAAGTGATTGACATATGTCACTICATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGCCTCA CTIGACTGGCTGCGCTCACACTC CTGGCTTGGTGGGGCCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGGA CCCCTGCATATTTTGGTTTCCA TGTTCACCGATATTTTGGTTCCATGT GCAGTTCATGAGTGCACCACGG TCTTTCCACGGGCTTTTCAG GCAGGTAAGTGGGCCCTGAA GGTTGGTTGGGGCCTGAA GGTAGGTTGTGGGCCTGAA GGTAGGTTTCTGGGAAGGGA GATACGGCCAGGGATTGAAG CCCTGTCCTCCCAGC GGAGAAAGCCCCCCTACTG
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.09           TET2-E11.09           TP53-E04.01           TP53-E06           TP53-E06           TP53-E06           TP53-E07	gDNA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTTTGCGATTGCACACACA         CACGTTTTCGCATTCACACACA         CACGTTTTCGGAGTGG         GTGAGAGAGCCAGTCAGAGA         TCACACACCAACA         CACCACTGAGACCTGTTCTGT         TGCAACACCTGATTCGACCAGAC         TCACACATCCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGGATGAATGGATGGACC         AATGACAGCCAGCCAGCAGA         GGTCAACACCCCTTTAA         TATGGCCCAGACAGCAGCAGA         GCATGCCACAACCCCTTTAA         TATGGCCCAGACCAGCAGCAG         GCATGCCAGACAGCAGCAGCA         GCATGCCAGACCAGCTTTCAC         GTCCAGACTGGATGTGCC         TCTCCGAGTGAGAGCTCCCAGA         GGCAGGACGACAGCAGCTG         GGACAGACGACAGCAGCGCTG         GCACTGGCCTCATCTTGGG	TAATGAATTCTCTATGAAAAATAAAGCC AAGATATGTCATATGATAAAAGCC TAAGTTGATCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGCCTCCA CTGGCTGCGCTTTCCAGTTG TACAAGTTGATGGGGGCCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATGGA GCAGTCTCATCATGGTTAGCAGC CCACTGATATTTTGGTTCCATGTT GTTCACCATTTTTATGTCCATGTT GCAGTCTCATCATGGTTAAGAGCT CATGAGTTGGGGCCCCGG CATGAGTGGGGCCTCTGAA GGTAGGTGGGGCCTCTGAA GGTAGGTTGTGGGGCCTCTGAA GGTAGGTTGTGGGACCAGG GATACGGCCAGGCATTGAAG CCCTGCGTCTCTCCAGC GGAGAAAGCCCCCCTCTG AGAGGTGGGGCCCCGCG GGAGGAAGCCCCCCTGCA
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.03           TET2-E11.03           TET2-E11.00           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E05           TP53-E05           TP53-E08	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTITIGGCATTGCACACACA         CACGTTTICTTIGGGAGCTGTG         GTTAGCAGAGCCAGTCAGAC         TCAACATCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGCTCTACCACCACAC         CACCATGGAGCAGTCAGAC         TCAACATCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGTCTACCACCCATCCAT         CACTCATGGAGTGGCC         AATGACATGCTTTCCCACACAGG         GGTCAGACAGCGAGCAGA         GCATGCCACACCCCTTTAA         TATGGCCCAGACTATGTGCC         TCCCTGGACTGTCCCAGAA         GTCCAGATGAAGCTCCCAGA         GGTCAGACAGCAGCAGGGCTG         GCACTGGCCTCATCTTGGG         GGGTGGCTGGGGCGGGGGGGGGGGGGGGGGGGGGGGGG	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGAAAAATAAAGC AAGATATGTCATATGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGCCTCA CTIGACTGGCTCTGCTAACATC CTGGCTGCGGTTTCCAGTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGTTTCCATTGGCA TCCCTGCATATTITIGGTTCCATGTT GCCAGTTCTATCATGGTTAGAGCT CATGAGTTGGAGCCACGG TCTTTCTACGGGAGGCTAGAGGC GCAGTTGGAGCCACGG GCTGGTTGTGGGCCTTTCAAG GGTAGGTTGGGGCCTTGAA GGTAGGTTTCTGGGACGCAGGG GATACGGCCAGGCATTGAAG CCCTGTCGTCTCCCAGC GGAAAAGCCCCCCTACTG AGAGGTGGGTGGGTGTAGTAGTAG CCCGCTGCTCTCCCAGC
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E11.01           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E06           TP53-E06           TP53-E06           TP53-E08           TP53-E09	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTTTGCATTCACACACA         CACGTTTTCGCATTCACACACA         CAGGTAGAGTTGGGAGTGTG         GTTAGCAGAGCCAGTCAGAGAC         TCACACATCACAAGAC         TCACACATCACAAGAC         CCACCATCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGCCTTTGAATCAGA         CTCAGTCTACACACCACCACCAG         GGTCAGACGCAGCAGAA         GCATGCCAACAGCAGAGAG         GCATGCCAGACAGCAGAGA         GCATGCCAGACAGCAGAGA         GCCAGCCCAGACAGCAGA         GCCATGCCAGACAGCAGAA         GCCAGCCCAGACAGCAGCAG         GCCAGCCCAGACAGCAGCAG         GCCAGCCCAGACTAGTGTGCC         TCCCTGACTGCTCTTTTCAC         GTCCAGACAGCAGCTGCCAGA         GGAGAGACGACAGCAGCGGG         GGAGAGACGACAGCGGCTG         GCACTGGCCTCAACTTGGGG         GGGTGGTGGGGAGAGAGGGCTG         GCACTGGCCTCACATCTGGGG         GGGTGGTGGGAGATAGATGG	TAATGAATITCTCTATGAAAAATAAAGGC AAGATATGTCATATGATGATAAAGC TAAGTTGATCATATTGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGCCTCCA CTGACTGGCTGCGCTCCCACACTC CTGGCTGGCGTTTCAGTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGGA CCCTGCATATTTTGGTTTCCA TGTTCACCATTTTTATAGTCCATGTT GCAGTTCATCATGGTTAAGAGCT CATGAGTTGGAGCCACGG TCTTTCTCACGGGCTTTTCAAG GCAGGTAAGTGGGCCTCGAA GGTTAGGTTGTGGGCCTCGAA GGTAGGTTGTGGGCCTCGAA GGTAGGTTTTGGGGCACGGA GGTAGGTTTTCGAGGGAGGA GGTAGGTTTTCCACGGCAGGA GGTAGGTTCTTCCACGC GGAGAAAGCCCCCCCTACG AGAGGTAGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTG
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E04.02           TP53-E06           TP53-E07           TP53-E08           TP53-E09           TP53-E09           TP53-E07	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTTTGCATTCACACACA         CACGTTTTCGTTTGGGACTGTA         GTGGATGAGTTGGGACTGTG         GTTAGCAGAGCCAGTCAGAGAC         TCACACATCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGGTCAAGCACCCCATCCAT         CACTCATGAGATGGATGGCC         AATGACATGCATGCACACAG         GGTCAGACAGCGAGCAGA         GGCAGCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCTTAA         TATGGCCCCAACCCCTTAA         TATGGCCCCAACCCCTTAA         TATGGCCCCAACCCCCTTAA         TATGGCCCCAACCCCCTTAA         TATGGCCCCAACCCCCTTAA         TATGGCCCCAACCCCCTTAA         TGTCCAAGCAAGGGGCTG         GCACTGGCCCATCTAACTC         GGAGAAGACAAGCGGCTG         GCACTGGCCCAACTTCAACTC         GGAGAAGACAAGCGGGCTG         GCACTGGCCCAACTACTACTGGG         GGGTGGTGGGAGATAGATGG         CAATTATACCCACACTTCACTTTT         CCTCACTGCCACTTCAACTCCCCTT	TAATGAATTCTCTATGAAAAATAAAGGC AAGATATGTCATATGATAAAAGC TAAGTTGATGATATGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGCCTCA CTGACCTGGCTGCGCTCACACTC CTGGCTGCGTTTTCAGTTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGGA TCCCTGCATATTTTGGTTTCCA GCAGTCTCATCATGGTTAGCAGCT CATGAGTTGGGAGCCACGG TCTTCTCACGGGCTTTAGAGCT CATGAGTTGGGAGCCACGG TCTTCTCACGGGCCTTGAA GGCAGGTAGTGGGGCCTGGAA GGTAGGTTGTGGGACGCAGGG GATACGGCCAGGCATTGAAG GGTAGGTTTCTGGGAAGGGA GATACGGCCAGGCATTGAAG CCCTGTCGTCTCTCCAGC GGAGAAAGCCCCCCTACTG AGAGGTGGGTGGGTGGGTAGTAGTATG CTCCACCGCTCTTGTCTCA
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.03           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.02           TP53-E05           TP53-E08           TP53-E08           TP53-E08           TP53-E09           TP53-E10	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTIGGG         AACTACTITIGCATTCACACACA         CACGTTTICTTIGGGAGTGTG         GTGAATGAGCAGCAGTCAAGAC         TCAACATCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTIGAATCAGA         CTCAGGCTAGTGAGAGC         TCACACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGTCTACCACCCATCCAT         CACTGTGTACCACCCATCCAT         CACTGCTGCCACACAGG         GGTCAGACAGCGAGCAGA         GCTAGCCAACCCCTTTAA         TATGGCCCAGACTATGTGCC         TCCTCTGACTGCTCTTTCAC         GTCCAGAATGAAGCTCCCCAGA         GGTCAGACAGCAGAGGGCTG         GCCAGACAGCAGACGGGCTG         GCAGGCAGATGGAGGGG         GGGTGGTGGGGAGTAGATGGG         CAGTTAGCCCAGAGTAGATGGG         CAGTTAGCCCAGAGTAGATGGG	TAATGAATITCICTATGAAAAAAAAGGC AAGATATGTCATATGATGATCATCATCT TAAGTTGTTACAATIGCTGCCA CAGCTGCTAAGCTGTCCTCA CTIGACTGGCTGCCGTAACATC CTGGCTTGCGTGACGTAGGGC CACTGATGGGGGCCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTTCCA TGTTCACCGGTTTTTATAGTCCATGTT GCAGTTCATGGGCCCCCGG TCTTTCTACGGGCTTTTCAG GCAGGTAGTGGGCCTCTGAA GGTTGGTGGGCCTCTGAA GGTGGGTTGTGGGCCTCGAA GGTAGGTTGAGGCCCTCGAA GGTAGGTTGTGGGCCTGGAA GGTAGGTGTGGGCCTGGAA GGTAGGTGTGTGGCCTCGAA GGTAGGTGGTGTGGCATGAAG CCCCTGCTCTCCCAGC GGAGAAAGCCCCCCTACTG AGAGGTGAAGGGCATGTAGTATG CCCGCCCCCTACTG CCAGGGAGGGTGGTAGTAGTATG CTCCACCGCTTTTGA
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.09           TET2-E11.09           TET2-E11.09           TP53-E04.01           TP53-E06           TP53-E06           TP53-E08           TP53-E08           TP53-E10           TP53-E10           TP53-E10	gDNA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTITGCGATTGCACACACA         CACGTTTTCGCATTCACACACA         CACGTTTTCGGAGTGG         GTGAGAGAGCTGGGAGTGG         GTGAGAGAGCCAGTCAGAGAC         TCACACATCAAAGATACCTGTTTCGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGCCTTTGAATCAGA         CTCAGTCACCACCCATCCAT         CACTCATGAGAGGGCC         AATGACAGCAGCAGGCAGA         GGCAAGCCAGCAGCAGA         GGCAAGCCAGCAGCAGA         GGCAAGCCAGCAGCAGA         GGCAAGCCAGCAGCAGA         GGCAGGCAGTGAGCC         AATGACATGCTTTCCCACACAG         GGTCAGACAGCGAGCAGA         GGCAAGCCACAGCCCTTTAA         TATGGCCCAGACCAGTGCCCCAGC         TCTCTGACTGCACACCAGCTTTAA         TATGGCCCAGACATGAGCCC         GGCAAGACGACAGGGCTG         GGCAACGACCAGCAGGGCTG         GGCACGGCTCAGCTTGAGGGCCC         GGGTGGTTGGGGAGTAGAGGG         GGGTGGTGGGGGAGTAGAGGG         GGGTGGTTGGGGAGTAGAGGG         GGGTGGTTGGGGAGTAGAGGG         GGGAGAACCACCAGCTTTTAACTCAGGGT         GGACAGGCCCAAGTTAGATGG         GGGGAGAACGACCAGACGGCTG         GGGGAGTAGGGGCCCAGAGGGCCC	TAATGAATITCICTATGAAAAATAAAGGC AAGATATGTCATATGATGAAAATAAAGC TAAGTTGATGATATGTTCACTICATCT TAAGTTGTTACAATTGCTGCCCA CAGCTGCTAAGCTGCCTCCA CTGACTGGCTGCGCTCAGCT CTGGCTGGCGTTTCAGTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATGGA GCCGCGCATATTTTGGTTTCCA GCAGTTCATCATGGTTAAGAGCT CATGAGTTGGAGCCACGG TCTTCTCACGGGCTTTTCAA GGTAGGTGGGGCCTGGA GGTAGGTAGTGGGCCTCGAA GGTTGGTGTGGGCCTGGA GGTAGGTTGTGGGCCCGG GGTAGGTTGTGGGCCCGG GGTAGGTTGTGGGCTCGAA GGTGGGTGTGGGCTCGAA GGTAGGTTGTGGGCCCGGC CCCTGTCGCCACGG GGAGGAAAGCCCCCCTACTG AGAGGTGGATGGGGTAGTAGGAC CCCCGCGCCTTGTCCT CCAGGCGGGTAGGGAATGGA TGCAAGCAAGGGTCCAAAGGA
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E04.02           TP53-E07           TP53-E07           TP53-E08           TP53-E09           TP53-E10           TP53-E07	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTIGGG         AACTACTTIGGCATTGCACACACA         CACGTTTICTTIGGGACTGTG         GTGAGAGAGTGGGACCTGTA         GTGAGATGAGTCAGGACAGCA         CCACATCAAAGATACCTGTTTGTG         TGCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTGAATCAGA         CTCAGCATCCAAGGACAGCC         CACCATGGGCTTTGAATCAGA         CTCAGTCTACCACCCATCCAT         CACTCATGGAGTGGGCC         AATGACATGGTTTCCCCACACAG         GGTCAGACAGCGAGCAGA         GGCAGGCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         GGCAGGCAGACAGAGGGCG         GCACTGCCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         GCATGCCCCAACCCCCTTAA         GGAGAAGACGACGACGGCTG         GCCACTGGCCCCACACTGGG         GGAGAGACGACAGAGGGCTG         GCACTGGCCTCACACTGGG         GGGTGGTGGGAGATAGATGG         CAGTTAGCCTCAGATTCACTTTT         ACTCACACTCTTTTACCCAGGT         AGGGAAAAGGGGGCACAACA         AGGGAAAAGGGGGCACAGAC </td <td>TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGATAAAAGC AAGATATGTCATATGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGCTCCA CTGACTGGCTGCGCTACACATC CTGGCTGCGTTTCAGTTTG TACAAGTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTCCA GCAGTCTCATCATGGTTAGGAGC CATGAGTTGGAGCCACGG TCTTCTCACGGGCTTTACAGAGCT CATGAGTTGGAGCCACGG CCAGTGAGTGGGAGCCACGG CCAGGTAAGTGGGCCTCGAA GGTAGGTTGCGGCTCTGAA GGTAGGTTTCTGGGAAGGGA GATACGGCCAGGCATTGAAG CCCTGCGCTCTCCCAGC GGAGAAAGCCCCTACTG AGAGGTGGGTGGGTGGTAGTAGTAGC CCCCCCCCCTACTG CAGGGGATGGGTGGGTAGTAGTAGTG CCCCACCGCTTGTCTCCAGC GGAGAAAGCCCCTACTG CCCAGCGATGGGTAGGAATGGA TGCAAGGCAGGGTTCAGAGACGC CCTGCACCAGGTTGAAGAACGCCT</td>	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGATAAAAGC AAGATATGTCATATGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGCTCCA CTGACTGGCTGCGCTACACATC CTGGCTGCGTTTCAGTTTG TACAAGTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTCCA GCAGTCTCATCATGGTTAGGAGC CATGAGTTGGAGCCACGG TCTTCTCACGGGCTTTACAGAGCT CATGAGTTGGAGCCACGG CCAGTGAGTGGGAGCCACGG CCAGGTAAGTGGGCCTCGAA GGTAGGTTGCGGCTCTGAA GGTAGGTTTCTGGGAAGGGA GATACGGCCAGGCATTGAAG CCCTGCGCTCTCCCAGC GGAGAAAGCCCCTACTG AGAGGTGGGTGGGTGGTAGTAGTAGC CCCCCCCCCTACTG CAGGGGATGGGTGGGTAGTAGTAGTG CCCCACCGCTTGTCTCCAGC GGAGAAAGCCCCTACTG CCCAGCGATGGGTAGGAATGGA TGCAAGGCAGGGTTCAGAGACGC CCTGCACCAGGTTGAAGAACGCCT
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E11.01           TET2-E11.01           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E05           TP53-E06           TP53-E09           TP53-E10           TP53-E10           TP53-E10           TP53-E10           TP53-E10	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTTTGCATTCACACACA         CACGTTTTCGCATTCACACACA         GTGAGAGAGTGGGGGCAGTGG         GTTAGCAGAGCCAGTCAGGAC         TCACACATCAAAGATACCTGTTTCTGT         TGCAACATCTAATTGTGCTTCTGG         TACCCTGGCCTTTGAATCAGA         CTCAGGATGAGTGGCC         AATGACAGAGCAGTCAGGAC         CACCATGAGATTGAATGGACC         TAGCCAGAGCAGAGAGCC         AATGACAGCAGCCAGCAGA         GCATGCCAGACGAGAGAG         GCATGCCAGACCAGTCCATA         CACTCATGAGATGGACC         AATGACAGCGCAGTTCACAGA         GGTCAGACAGCGAGCAGA         GCCAGCCCAGACCCCTTTAA         TATGGCCCAGACCAGTCTTTCAC         GTCCAGACTGCTCTTTAA         TATGGCCCAGACTAGTGTCC         GTGCAGCAGACGACAGGGCTG         GGAGAGACGACAGGGGCTAGATGG         GGGGTGGTGGGGATAGATCACTTTGGG         GGGGGTGGGGGATAGATCACTTTTGGG         GAGTGACTCAGAGTAGATCACTTTTGGG         GAGTGGCTCAGATAGATGGC         GGGGAGAGACGACAGGGCAAGGG         GGGGAAAGGGGCACAGAGC         AGGGAAAAGGGGGCACAGAC         AGGGAAAAGGGGGCACAGAC         AGGGAAAAGGGGGCACAGAC	TAATGAATITCICTATGAAAAATAAAGGC AAGATATGTCATATGATGATCATCT TAAGTTGTTACAATIGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCCTAACATC CTGGCTTGCGTTGCG
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E04.01           TP53-E06           TP53-E07           TP53-E07           TP53-E08           TP53-E01           TP53-E01           TP53-E04           TP53-E07           TP53-E07           TP53-E07           TP53-E07           TP53-E07           TP53-E07           TP53-E07           TP53-E07           TP53-E10           TP53-E10           TP53-E11           WT1-E07           WT1-E07	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTITGCATTCACACACA         CACGTTTTCGCATTCACACACA         CACGTTTTCGGAGTGG         GTGAGAGAGCCAGTCAGAGA         TCACACATCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGTCTACACACCATCCAT         CACCATCGAGTGATGGGCC         AATGACATGCATGCACACAGG         GGTCAGACAGCGAGCAGA         GGCAGCCAAGCCAGCAGA         GGCAGCCAAGCCCCTTAA         TATGGCCCAACCCCTTTAA         TATGGCCCAGACCAGCAGA         GGTCAGACAGCGAGCAGA         GCACGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAACCCCCTTAA         TATGGCCCAGACCAGGCAGA         GCACGGCCCAATGTGGCC         CCCTCGACTTCAACTC         GGAAGAAGACGACACAGGGCTG         GCACTGGCCCAACTCACTTT         ACTGACACACCAAGGGCAGAC         AGGACAAAGGGGCACAGAC         AGGCAAAGGGGCACAGAC         AGGCAAAGGGGCACAGAC         AGCCTCCCTCTCTCTATACTC         CCACGGCGCAAGATCAG	TAATGAATTCTCTATGAAAAATAAAGGC AAGATATGTCATATGATGAAAATAAAGC AAGATATGTCATATGTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGCCTCA CTGACTGGCTGCGCTCCA CTGGCTGCGTTTCAGTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATGGA TCCCTGCATATTTTGGTTCCA GTTCACCATTTTTATGGTCCATGTT GCCAGTCATCATGGTTAAGAGCT CATGAGTTGGAGCCACGG TCTTCTCACGGGCCTTTACAGGC CCAGGTAAGTGGGAGCCACGG GCAGGTAGTGGGGCCTGGAA GGTAGGTTGTGGGGCCTGGAA GGTAGGTTGTGGGCCTGGAA GGTAGGTTGTGGGCCTGGAA GGTAGGTTGTGGGCCTGGAA GGTAGGTTGTGGGCCTACTG AGAGGTGGGCCAGCGC CCCCCCCTACTG AGAGGAGGGATGGGAT
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E05           TP53-E08           TP53-E08           TP53-E09           TP53-E10           TP53-E10           TP53-E09           TP53-E10	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTTGCGCC         AGGCACCATATATTGTGTTGGG         AACTACTTTGCGATTCACACACA         CACGTTTTCTTTGGGAGCTGTG         GTTAGCAGAGCCAGTCAAGAC         TCAACATCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGCTCTACCACCATCCAT         CACCATGCAGCAGTCGAGA         CTCAGTCTACCACCCATCCAT         CACTCATGGAGTGGCC         AATGACATGCTTTTCCACCACCAGG         GGTCAGACAGCGAGCAGA         GCATGCCACACACCCCTTTAA         TATGGCCCAGACTATGTGCC         TCCCTGGACTGTCGCCAGAC         GGCAGGAGAGAGGGCTG         GCACTGGCCTCATCTTGAGG         GGGGTGGTTGGGAGTAGATGG         GGGTGGGTGGGGGAGAGAGGG         GGGTGGGTGGGGGAGAGAGGG         GGGTGGGTGGGGGACAGAGC         GGGGGGCTTGGGGACAGAGC         GGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAGGGGCACAGAC         AGGCAAGACGCAGGCTCAG         CAGCTCCCTTCTCTCCCCCAGAC         CAGCTCCCTCTTACTCT         CCAGCTGCCGGAAGTCAG         CAGCTCAGACTCACCCAGTC	TAATGAATITCICTATGAAAAAAAAGGC AAGATATGICATATATGATCATCATCT TAAGTTGATCAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTIGACTGGCCTCCCTAACATC CTGGCTTGGCGTTTCAGTTIG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTTCCA TGTTCACCATTTTTATAGTCCATGTT GCAGTTCATGGGCCCCCGG CCTTCCACGGGCTTTTCAG GCAGGTAAGTGGCCCTCGAA GGTAGGTTGTGGGCCCTGAA GGTAGGTTGTGGGCCTGGAA GGTAGGTGGTGGTGCTTCAAG GGTAGGTGGTGGGCACGGG GATACGGCCAGGGA GGTAGGTGGGCCTCTGAA GGTAGGTGGTGCTCTCAAGC GGAGAAAGCGCCCCCTACTG AGAGGTGATGGGTAGTAGTATG CCCGCTCCTCTCCCAGC GGAGAAAGCCCCCCTACTG AGAGGTAGATGGGTAGTAGTATG CCCAGCAGGCATGAAATGGA TGCAAGCAAGGGATGAAAAGGA CCTAGCAGGGATGAAAAGGA CCTAGCAGGAGGAGGAAATGGA CCTAGCAGGTGGTAGTAGAATGGA CCTAGCAGGGAGGAGGAAGGAA CCTTAGCAGGAGGAGGAACGGA CCTAGCAGGCAGGATGAAAAGGA CCTAGCAGGAGGATGAAAAGGA CCTAGCAGGGATGAAGAACGCA CCTTAGGCAGGGATGAAAAGGA CCTTAGGCAGGGAGGAGGAGGA CCTAGCAGGAGGAGGAGGAA CCTTAGGCAGGGAGGAGGAGCA CCTTAGGCAGGGAGGAGGAGGA CCTTAGGCAGGGAGGAGGAGGA CCTTAGGCAGGGAGGAGGAGGA CCTTAGGCAGGGAGGAGGAGGA CCTTAGGCAGGAGGAGGAGGA CCTTAGGCAGGAGGAGGAGGA CCTTAGGCAGGGAGGAGGAGGA CCTTAGGCAGGGAGGAGGAGGA CCTTAGGCAGGAGGAGGAGGA CCTTAGGCAGGGAGGAGGAGGA CCTTAGGCAGGGAGGAGGGGGGGGGGGGGGGGGGGGGGAGGAGG
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TET2-E11.09           TP53-E04.01           TP53-E06           TP53-E06           TP53-E06           TP53-E09           TP53-E10           TP53-E10           TP53-E10           TP53-E10           TP53-E10           TP53-E10           TP53-E10           TP53-E10           TP53-E10           TP53-E11           WT1-E07           WT1-E09           ASXL1-E13.01           ASXL1-E13.02	EDINA           gDNA	TCAGGTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTITICGCATTCACACACA         CACGTTTTCGGAGTGG         GTGAGAGACTGGGAGTGG         GTGAGAGACTGGGAGTGG         GTGAGAGACTCAGACAC         CACACTCAAAAGATACCTGTTTCGT         TGCAACACCTATTGCACCAGAC         TCACACATCAAAAGATACCTGTTTCGT         TGCAACTCTTATTCTGCTTGAATCAGA         CTCAGGTCAAGCAGCC         AATGACAGCAGCCAGCC         AATGACAGCGAGCAGA         GGTCAAGACAGCAGCAGAA         GGTCAAGACAGCAGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCAGCAGAA         GGTCCAGACTGCCTTTAA         TATGGCCCAGACTATGTGCC         TCCTCTGACTGCACCTCAGGA         GTCCAGACAGACGACGCGA         GGCAGGACGACAGAGGGCTG         GGACTGGGCTGATAGATGAGC         GGAGTAGACGACAGAGGGCTG         GGAGTAGACGACAGAGGAGGAC         GAGTGGTTGGGAGTAGATGAGT         GAGTGGTGGGGGACAGAGG         GGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC	TAATGAATITCICTATGAAAAATAAAGGC AAGATATGTCATATGATGATCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGCCTCA CTTGACTGGCTCTGCTCAACATC CTGGCTTGGCGTTTCAGTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGGA CCCTGCATATTTTGGTTTCCA TGTTCACCACTTTTTAATGCCATGTT GCAGTTCTATCATGGTTAAGAGCT CATGAGTGGACCACGG TCTTTCTCACGGGCTTTTCAA GGTAGGTTGTGGGCCTGAA GGTGGTTGTGGCCTCGAA GGTGGTTGTGGCCTGAA GGTGGTTGTGGGCCTGAA GGTGGTTGTGGGCCCCGA GGAGAAAGGGGCACGGG CCCCTGCTCCCAGC GGAGAAAGCCCCCCTGA GGAGGAAGGCGATGGAGGA GTACGCCCCCTCTCAGC CCCAGGGATGGGGTAGTAGTATG CCCAGGCAGGATGAGAATGGA TGCAAGCAGGGTTCAAAGA CCTTAGCAGGGGTCAAAGA CCTTAGCAGGGGTCAAAGA CCTTGCCTCCCCACCA CCTCTCTCACAGC CCTCTCCCACCGC CCCTCTCCCACGC CCAGGAGCAGGGTAGAATGGA TGCAAGCAGGGTTCAAAGA CCTTAGCAGCGGTGAGAACGCA CCTTCCCAGCCCCCCCCCC
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E06           TP53-E07           TP53-E08           TP53-E07           TP53-E09           TF53-E10           MT1-E07           WT1-E07           ASXL1-E13.01           ASXL1-E13.03	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTIGGG         AACTACTTTGCGATTGCACACACA         CACGTTTTCGCATTCACACACA         CACGTTTTGGGAGTGTG         GTGAGAGAGTCAGGAC         TCACACACCAAAGAC         TCACACTCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCACGTCACCACCCCCTCAT         CACTCATGGAGTGGAGGCG         AATGACATGCATTCCACACAGG         GGTCAGACAGCGAGCAGA         GGCAGGCCAAGCCCCTTTAA         TATGGCCCAGCCCCTTAA         TATGGCCCAGACCCCTTTAA         TATGGCCCAGACCCCTTTAA         TATGGCCCAGACCCCTTTCAC         GGAGAGAAGACGGGCGG         GCACTGCCCCATCCTTGAC         GCACTGGCCCCATCCTTGAC         GTCAGACAGGGGAGAAGAGGC         GGAGAGAACAAGGGGCTG         GCACTGGCCCAACCCAGATCAGG         GGGTGGTTGGGAGTAGATGG         CAGTGCCTGCGCCCAGAC         AGGGTAAAGGGGCACAGAC         AGGGCAAAAGGGGCACAGAC         AGGCTCCCTCTCTTTACTCT         CCACTGCCGGAAGTCAG         CAGCTGCCCGGAAGTCAG         CAGCTGCCCGGAAGTCAG         CAGCTGCCGGAAGCCGG	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGATAAAAGC AAGATATGTCATATGTTCACTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGCCTCA CTTGACTGGCTCTGCGTAACATC CTGGCTTGGCT
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.03           TET2-E11.03           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E05           TP53-E06           TP53-E09           TP53-E09           TP53-E10           TP53-E10           ASXL1-E13.01           ASXL1-E13.03           ASXL1-E13.03           ASXL1-F13.04	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTTTGCATTCACACACA         CACGTTTTCGCATTCACACACA         CACGATTTGGGAGTGTG         GTTAGCAGAGCCAGTCAGAGAC         TCAACATCAAAAGATACCTGTTTCTGT         TGTCAACACCACCATCCAT         CACCATGAGATGAGGCC         AATGACTGTACCACCCATCCAT         CACCATGAGATGAGGCC         AATGACAGGCCAGTCAAGA         CTCAGGCTTTGCAACCAGA         CTCAGGCTTCCCACCCATCCAT         CACTCATGAGATGGATGGCC         AATGACAGCGAGAGAG         GGCAAGCCAGCAGAGA         GCATGCCCAGACCAGTGAGCC         AATGACATGCTTTTCACCAGAG         GGTCAGACAGCAGAGAGA         GCATGCCCAGACCATTTTCAC         GGCAGGCAGACAGCCAGAGA         GCCAGGCCAGACCAGAGCAGA         GTCCAGATGACTCCCAGA         GTGCCCTGACTTTTACC         GGGAGAGACGACAGGGCTG         GGGGTGGTGGGAGGAAGAGC         GGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGGCACAGAC         AGGGAAAAGGGGGCACAGAC         AGGGAAAAGGGGGCACAGACC         AGGGAAAAGGGGGACACGACC         CAGGTCAGATCACCCAGTC         CTAGGTCAGATCACCCAGTC         CTAGGTCAGATCACCCAGGC	TAATGAATITCICTATGAAAAATAAAGGC AAGATATGTCATATGATGATCATCT TAAGTTGTTACAATIGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTCCCTAACATC CTGGCTTGCGTTGCG
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.09           TET2-E11.09           TP53-E04.01           TP53-E06           TP53-E06           TP53-E06           TP53-E06           TP53-E01           TP53-E03           TP53-E04           ASXL1-E13.01           ASXL1-E13.02           ASXL1-E13.04	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTTGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTTTGCATTCACACACA         CACGTTTTCGCATTCACACACA         CACGTTTTCGGAGTGG         GTGAGAGAGCCAGTCAGA         GTGAGAGACTGGGAGTGG         GTTAGCAGAGCCAGTCAGAC         TCACACTCAAAGATACCTGTTTCGT         TGCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGTCACCACCCACTCAT         CACTCATGAGATGGATGGCC         AATGACAGCCAGCAGAAG         GGTAGACAGCAGAGCAGA         GGCAAGCCAGACAGCAGAGA         GGCAGCCCAAACCCCTTTAA         TATGGCCCAGACCCTTTAA         TATGGCCCAGACCCTTTAA         TATGGCCCAGACCCCAGA         GGCAGGCCCAGACCCAGAC         GGACAGGCCAGCTCCCAGA         GGCCCAGACTCCCAGA         TGCCCGAACGCAGGGCTG         GGACAGGCCCAGCTCAGG         GGGTGGTTGGGGAGTAGATGG         CACTGCCTCACTTTGGG         GGGTGGTGGGGCACAGAC         GGGTGGTTGGGGAGTAGATGG         GGGTGGTTGGGGAGTAGATGG         GGGTGGTTGGGGCACAGAC         AGGCTCCCTTTACTTTACCTGGG         GGGTGGTTGGGGCCACAGAC         AGGCAAAGGGGCCACAGAC         AGGCAAGGGGCCACAGAC         AGGCAAGGGGCCACAGAC	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGATGAAAATAAAGC AAGATATGTCATATGTTCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGCCTCA CTGACTGGCTGCGCTCAGCAACC CTGGCTGGCGTTTCAGTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTCCA GCAGTCTATCATGGTTAGGAGC CATGAGTTGGGAGCCACGG TCTTCTATCATGGTTAGAGCT CATGAGTTGGGAGCCACGG CTCTTCTACCATGGTTAGAGCT CATGAGTTGGGAGCCACGG GGTAGGTTGTGGGCCTGGA GGTAGGTTGTGGGCTCTGAA GGTTGGTGTGTGGGCTCTGAA GGTAGGTTGTGGGCCCGG CCCCTGTCTCCAGC GGAGAAAGCCCCCCTACTG AGAGGTGGGTGGTGTGAGAGGA CCCTGTCTCCCAGC GGAGAAAGCCCCCCCTACTG AGAGGTGGATGGGGTGGTAGTATG CTCCACCAGCTGTGAAGGA CCTTGCGCAGGGGTGGAGAGGA CCTTGCGCCCCCTACTG CAGGCAGGGTGGAGAGGA CCTTGCGCCCCCAAG CCTTGCGCCCCCCAGC CCTCTCCCAGC CCTTCCCAGGGGTGGAGAGGA CCTTCCCAGCGGTGGAAAGGA CCTTCCCAGCGGTGGAGAGGA CCTTCCCAGCGGTGGAGAGGA CCTCCCCCCCCCC
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E10.03           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E04.02           TP53-E04.01           TP53-E04.02           TP53-E05           TP53-E08           TP53-E08           TP53-E08           TP53-E08           TP53-E08           TP53-E08           TP53-E08           TP53-E09           TP53-E11           WT1-E07           WT1-E07           WT1-E07           ASXL1-E13.01           ASXL1-E13.03           ASXL1-E13.04           ASXL1-E13.05	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTTGCGCC         AGGCACCATATATTGTGTTTGGG         AACTACTTTGCGATTGCACACACA         CACGTTTTCGTTTGGGAGCTGTG         GTTAGCAGAGCCAGTCAGAC         TCAACATCAAAGATAACTGTTTCGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCACATCCAAAGATACCTGTTTCGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGTCTACCACCCATCCAT         CACTCATGGAGTGGCC         AATGACATGCTTTCCCACACAGG         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCCCCCAGA         TGTGCCCTGACTTTCACT         GGAGGCTGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGG	TAATGAATITCICTATGAAAAAAAAGGC AAGATATGICATATTGITCACTICATCT TAAGTTGITACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTIGACTGGCTCTCCCTAACATC CTGGCTTGGTGTGCTCAGTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTCCAT GCAGTTCATCATGGTTAAGAGCT CATGAGTTGATGCACCACGG TCTTTCCACGGGCTTTTCAG GCAGGTAAGTGGCCCCCGA GGTAGGTTGTGGGCCCTGAA GGTGGTTGTGGGCCTCGAA GGTAGGTTGTGGGCCTCTGAA GGTAGGTTGTGGGCCCTGAA GGTAGGTGGTGCTGCACGG GAAGAAAGCGCCCCCTAGA GGTAGGTGGTGTGGCATGAAG CCCTGTCCTCCCAGC GGAGAAAGCCCCCCTACTG AGAGGTGATGGGTAGTAGTATG CTCCACGGCTTTTGAA GGTAGGCAGGATGAAGAAC CCTGTCGTCCCAGC GGAAGCAAGGGATGAAAAGGA CCTGTCGTCTCCAAC CCTTAGCAGGGATGAAAAGGA CCTTAGCAGGAGAGGAA CCTTAGCAGGAGGAGGAAATGGA TGCAAGCAAGGGATGAAAATGGA CCTTAGCAGGAGGAGGAGA CCTTAGCAGGAGGAGGAGA CCTTAGCAGGAGGAGGAGA CCTTAGCAGGAGGAGGAGA CCTTAGCAGGAGGAGGAGA CCTCTCAAGCCAGGGATGAAAGA CCTTAGCAGGAGGAGGAGAA CCTCTCAGGCCAGGAGGAGA CCTCTCCAAGCAAGGAGCCT CTTTCCAAGCCAGGGATGAAGAA CCTCTCTGGACACGG ACCACCATCACACGC ACTACCATGGCAAGGAGAA CCTCTCTGGACAGGAGCCT CTTCCAAGCCAGGAGGAGGA ACGACCATGGCCAGGACTGA ACGACGAGGACGACTGG ACAGCCATGGGCCCCCAGG GAAGTGGGTGCCCAGACTCA CAGGCGGCCCCCCAGT GAAGGGGGCCCCCCAGT GAAGGGGGCCCCCCAGT
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.07           TET2-E11.08           TET2-E11.09           TET2-E11.09           TET2-E11.09           TET2-E11.09           TP53-E04.01           TP53-E06           TP53-E06           TP53-E09           TP53-E10           TP53-E11           WT1-E09           ASXL1-E13.02           ASXL1-E13.05           ASXL1-E13.06 <td>EDINA EDINA</td> <td>TCAGGTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTIGGG         AACTACTITICGCATTCACACACA         CACGTTTICGGAGTGG         GTGGATGAGTTIGGGAGTGG         GTGAGAGACTGGCAGTCAGAGAC         TCACACATCAAAGATACCTGTTTCGT         TGTCAACACCACACAC         CACCATGAGAGACCTGTTGG         TAGCCAGGCCAGTCAAGAC         TCACACATCCAAAGATACCGGT         CTCAGGTCTAGGAGTGGCC         AATGACAGCGAGCAGCAGA         GCATGCCAACAGCAGCAGAG         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCCAGACCCCTTTAA         TATGCCCCAGACCATTCACACG         GGTCAGACAGCGAGCGC         GGTCAGACACCCCTTTAA         TATGGCCCAGACTATGTGCC         TCCTCTGACTGCACTTTCACC         GGCAGGACGACAGAGGGCTG         GCACTGGCCTGATCTTGGG         GGGTGGTGGGAGGATAGATGG         GGGTGGTGGGAGGACAGAGC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAGGGGCACAGAC         AGGGAAAGGGGCACAGAC         CAGGTCCCCCCCCAGATCACCAGTC         CTTACCAGAATAGCCCCCG         ACTGCCAGATCACCAGGACC         ACGGCAAGGCGCAAGCC</td> <td>TAATGAATITCICTATGAAAAATAAAGC AAGATATGTCATATGATGATCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCTAACATC CTGGCTGGCTTTCAGTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGGA CCCTGCATATTTGGTTTCCA TGTCCACCATTTTTATAGTCCATGTT GCAGTTCATCATGGTTAAGAGCT CATGAGTGGACCACGG TCTTTCCACGGGCTTTTCAA GGTAGGTTGTGGGCCTGAA GGTTGGTTGTGGGCCTGAA GGTTGGTTGTGGGCCTGAA GGTTGGTTGTGGGCCTGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCCTGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGCCTGAA GGTAGGTTGTGGCCTGAA GGTAGGTTGTGGCCTGAA GGTAGGTTGGGCTCGAC CCCGTCCTCCCAGC GGAGAAAGCCCCCCCTCG AGAGAGAGCCCCCCCTG CCAGGAGCAGGATGAGAATGGA TGCAAGCAGGATGAGAATGGA CCTTAGCAGGTGGAAATGGA CCTTAGCAGTGGAGAGGG ACCACCACCACTGC CCCTCCTAGCCCGGC CCCCCCCCCC</td>	EDINA EDINA	TCAGGTGCACAGCCTATATAATG         TTCAGGAGAACTIGCGCC         AGGCACCATATATIGTGTTIGGG         AACTACTITICGCATTCACACACA         CACGTTTICGGAGTGG         GTGGATGAGTTIGGGAGTGG         GTGAGAGACTGGCAGTCAGAGAC         TCACACATCAAAGATACCTGTTTCGT         TGTCAACACCACACAC         CACCATGAGAGACCTGTTGG         TAGCCAGGCCAGTCAAGAC         TCACACATCCAAAGATACCGGT         CTCAGGTCTAGGAGTGGCC         AATGACAGCGAGCAGCAGA         GCATGCCAACAGCAGCAGAG         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCCAGACCCCTTTAA         TATGCCCCAGACCATTCACACG         GGTCAGACAGCGAGCGC         GGTCAGACACCCCTTTAA         TATGGCCCAGACTATGTGCC         TCCTCTGACTGCACTTTCACC         GGCAGGACGACAGAGGGCTG         GCACTGGCCTGATCTTGGG         GGGTGGTGGGAGGATAGATGG         GGGTGGTGGGAGGACAGAGC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAGGGGCACAGAC         AGGGAAAGGGGCACAGAC         CAGGTCCCCCCCCAGATCACCAGTC         CTTACCAGAATAGCCCCCG         ACTGCCAGATCACCAGGACC         ACGGCAAGGCGCAAGCC	TAATGAATITCICTATGAAAAATAAAGC AAGATATGTCATATGATGATCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCTAACATC CTGGCTGGCTTTCAGTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGGA CCCTGCATATTTGGTTTCCA TGTCCACCATTTTTATAGTCCATGTT GCAGTTCATCATGGTTAAGAGCT CATGAGTGGACCACGG TCTTTCCACGGGCTTTTCAA GGTAGGTTGTGGGCCTGAA GGTTGGTTGTGGGCCTGAA GGTTGGTTGTGGGCCTGAA GGTTGGTTGTGGGCCTGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCCTGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGGCTCGAA GGTAGGTTGTGGCCTGAA GGTAGGTTGTGGCCTGAA GGTAGGTTGTGGCCTGAA GGTAGGTTGGGCTCGAC CCCGTCCTCCCAGC GGAGAAAGCCCCCCCTCG AGAGAGAGCCCCCCCTG CCAGGAGCAGGATGAGAATGGA TGCAAGCAGGATGAGAATGGA CCTTAGCAGGTGGAAATGGA CCTTAGCAGTGGAGAGGG ACCACCACCACTGC CCCTCCTAGCCCGGC CCCCCCCCCC
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E04.01           TP53-E06           TP53-E07           TP53-E07           TP53-E07           TP53-E08           TP53-E07           TP53-E01           TP53-E03           TP53-E04           TP53-E07           TP53-E08           TP53-E07           TP53-E07           TP53-E07           TP53-E07           TP53-E07           TP53-E07           TP53-E07           TP53-E01           TP53-E03           TP53-E04           TP53-E05           TP53-E07           TP53-E07           TP53-E08           TP53-E09	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTTGCGCC         AGGCACCATATATTGTGTTTGGG         AACTACTTTGCATTCACACACA         CACGTTTTCGCATTCACACACA         CACGTTTTCGGATGACCGTA         GTGGATGAGTTGGGAGTGTG         GTTAGCAGAGCCAGTCAGAC         TCACACATCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGTCTACACACCACCCATCCAT         CACTCATGAGATGATGGAGGCC         AATGACATGCTTTCCCACACAG         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GGTCAGACAGCGAGCAGA         GCACTGGCCCAATCCCCAGA         TGTCCCGACTTCAACTC         GGAGAGACAAGGGGCAGACGA         GGGTGGTTGGGAGTAGATGG         CAGTGTAGGAGAGAGAGGAGGAGGAGGAGGAGGAG         GGGTGGTTGGGAGTAGATGG         CAGCTCCCTTCCTCTTACCT         CCAGCTGCCGGAAGATCAGG         CAGGTAAGAGGGCACAGAC         AGGCTCCCTTCCTCTTACCTGC         CCAGTGCGCGAAGGCAGAC         AGGCATAGCCCAGGGC         CAGTGCATCACCAGGGG         CTCCCTCGGAAGGCAAC	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGATGATCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTGCGTCACACTC CTGGCTTGGCT
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E11.01           TET2-E11.03           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E05           TP53-E06           TP53-E09           TP53-E09           TP53-E10           TP53-E10           TP53-E10           ASXL1-E13.02           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.07	EDINA ED	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTTGCGCC         AGGCACCATATATGTGTTTGGG         AACTACTTTGCATTCACACACA         CACGTTTTCGCATTCACACACA         CACGATTTGGGAGTGTG         GTTAGCAGAGCCAGTCAGAGAC         TCAACATCAAAGATACCTGTTTCTGT         TGTCAACTCTTATTCTGCTTCTGG         TACCCTGGCCTTTGAATCAGA         CTCAGTCTACACACCACTCCAT         CACCATGAGATGGACGCC         AATGACAGGCCAGTCAGGAC         GGTAGAAGTGACGCC         AATGACAGGCAGTGGCC         AATGACAGGCAGCAGA         GCCAGCCAAGCGAGCAGA         GCATGCCAGACCACTTTAA         TATGGCCCAGACCAGTGGC         GGTCAGACAGCGGCGA         GCCAGGCCAGTGAGCGC         TATGGCCCAGACTTTTCAC         GTCAGCAGACGACAGGCGA         GCCAGGCCTCATCTTTGGG         GGAGAGACGACAGGCGG         GGAGAGACGACAGGGCTG         GGGGTGGTGGGAGATAGATGG         GGGGAAAGGGGCACAGAC         AGGGCAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         GGGCAGAGACAGACCAGGC         AGGCACAGATAGCCCCAGTC         CTAGGCCCCCCGGAAGTAGAGC         CAGGCAGAACGAGCCAGACC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         CAGCTCCCCCCAGATCACA <td< td=""><td>TAATGAATITCTCTATGAAAAATAAAGGC AAGATATGTCATATGTTGATCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCCTAACATC CTGGCTTGGCT</td></td<>	TAATGAATITCTCTATGAAAAATAAAGGC AAGATATGTCATATGTTGATCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCCTAACATC CTGGCTTGGCT
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TET2-E11.09           TP53-E04.01           TP53-E06           TP53-E06           TP53-E06           TP53-E06           TP53-E07           TP53-E08           TP53-E01           TP53-E03           TP53-E10           TP53-E10           TP53-E10           TP53-E10           ASXL1-E13.02           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.04           ASXL1-E13.05           ASXL1-E13.06           ASXL1-E13.07           ASXL1-E13.08           ASXL1-E13.07	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTTGCGCC         AGGCACCATATATIGTGTTGGG         AACTACTTTGCATTCACACACA         CACGTTTTCGCATTCACACACA         CACGTTTTCGGAGTGG         GTGAGAGACTGGGAGTGG         GTGAGAGACTCACAGAC         TCACACATCAAAGATACCTGTTTCGT         TGTCAACACCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCAGTGACAGCCAGCC         AATGACATGCATCCACCAC         CACTCATGAGATGGATGGCC         AATGACAGCCAGCCAGCAG         GGTCAGACAGCAGCAGA         GGCAGCCCAGACAGCAGCAG         GGTCAGACAGCGAGCAGA         GGCAGGCCAGACCCCTTTAA         TATGGCCCAGACCTTTCACC         GGCAGGCCAGACGCCCAGAC         GGCAGGCCCAGACCCAGGC         GGCAGTGGAGTAGAGGCCCAGAC         GGCAGGGCTGGGGGCGG         GGCACTGGCCTCATCTTGGG         GGGTGGTTGGGGAGTAGATGG         GGGTAGAGCCCAGACC         AGGGAAAGGGGCACAGAC         AGGGAAAGGGGCACAGAC         AGGGAAAGGGCCAAGAC         AGCCTCCCTCTCTTTACTCT         CCAGGTCAGGAGAGGGC         CAGCTGCCGGAAGGCAC         AGCACGCCCAGGC         ACTCCCCGGAAGGGG         ACTCCCCGGAAGCGCAAC         AGGGAAAGCTGACCCCAGTC         CTGCCCCCCA	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGATGATCATCT TAAGTTGTTACATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTGCGTACACATC CTGGCTTGGGTTTCAGTTG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTTCCA TGTCACCATTTTTAGTTCCATGTT GCAGTTCTATCATGGTTAAGAGCT CATGAGTTGAGGCCCCGG TCTTCTCCACGGGCTTTTCAG GCAGGTCATGGGCCCTGAA GGTAGGTTGTGGGCCTGGAA GGTAGGTTGTGGGCCTGGAA GGTAGGTTGTGGGCCTGGAA GGTAGGTTGTGGGCCTGGAA GGTAGGTTGTGGGCCTGGAA GGTAGGTTGTGGGCTCTGAA GGGAGAAAGCCCCCGG CCCTGTCTCCCAGC GGAGAAAAGCCCCCCTG CAGGGTAGGGGTGGGTAGTATG CCCCGCCCCTCTGCAC GGAGAAAGCCCCCCTCTG CCAGGAGCAGGGTCGAAATGGA TGCAAGCAGGGTCGAAATGGA CCTTGCCTCTCCACAG CCTGTCTCCCAGC CCTGTCTCCCAGC CCTGTCTCCCAGC CCTGCTCTCCCAGC CCTCTCTCAGCGGTGGTAGTAGGA CCTTAGCAGGTGGAGTGGA
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E10.03           TET2-E11.01           TET2-E11.02           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.06           TET2-E11.07           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E04.01           TP53-E07           TP53-E08           TP53-E07           TP53-E09           TP53-E07           TP53-E08	EDINA EDINA	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTTGCGCC         AGGCACCATATATTGTGTTGGG         AACTACTTTGCATTCACACACA         CACGTTTTCGCATTCACACACA         CACGTTTTCGGAGTCAGGAC         TCACACACACA         GTGAGAGACTGGGACTGTG         GTTAGCAGAGCCAGTCAGAC         TCACACTCACAAGACACCCGTTA         TGCAACTCTTATTCTGCTTCTGG         TACCCTGGGCTTTTGAATCAGA         CTCACATCACAAGATGACCGTCCAT         CACCATGGATGGATGGCC         AATGACATGCTTTCCCACACAGG         GGTCAGACAGCGAGCAGA         GCATGCCACACCCCTTTAA         TATGGCCCAGACCCCTTAA         TATGGCCCAGACCCCTTTAA         TATGGCCCAACCCCCTTTAA         TATGGCCCAACCCCCTTTAA         TATGGCCCAACCCCCTTTAA         TATGGCCCCAACCCCCTTTAA         TGTCAGCTGCTCTTTCACCT         GGAGAGAACACAGGGGCG         GCACTGGCCCCATCTTGGG         GGAGAGACACACAGGGGCG         GGGTGGTTGGGAGTAGATGG         CAGTGACCTCCCGGAACCAGAC         AGGGTAAAGGGGCAACAGAC         AGGGTAGATGCCCCGG         CATGCCTTCCTCTTACTCT         CCACTGGCCAAGCCAAGC         AGGGTAGACTGGCCAACC         AGGGAAAGGGAACTGCCAGGC         CTCAGTCGGAGAGGGCAACGC         ACTGCACCACCCCGGACCCAGC <td>TAATGAATTCTCTATGAAAAATAAAGGC AAGATATGTCATATGTTGATCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTIGACTGGCCTCGCTAACATC CTGGCTGGCGTTTCAGTTIG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTTCCA TGTTCACCGGTTTTTATAGTCCATGTT GCAGTTCATCATGGTTAAGAGCT CATGAGTTGAAGCACAGG TCTTTCTCACGGGCTTTTCAG GCAGGTAAGTGGGCCTCGAA GGTTGGTTGTGGGCCCTGAA GGTAGGTTGTGGGCCTCGAA GGTAGGTTGTGGGCCTCTGAA GGTAGGTGGTGGTGCTTGAG GCAGGTAAGTGGGACTGAAG CCCTGTCCTCCCAGC GGAGAAAGCGCCCCCTACTG AGAGGTGAGTGGTAGTAGTATG CTCCACGGGTTCTAGAG CCCTGTCTCTCCAGC GGAGGAGGAGGAGTGAGAATGGA TGCAAGCAAGGGATGAAGA CCTTTCTGGGAGGGATCTAGAA CCTTTCCATGCCTCCACC GGAGGAGGAGGAGGAGAGGA TGCAAGCAAGGGTCAAAGGA CCTTTCCATGCCCCCCTACTG AGAGGCAGGATGAGAATGGA CCTTTCCAAGCGCATGGAGCT CTTCCACCGCTTCTAACAGC CCTCTCTGGACGCGTGCAAGGA CCTTTCCAAGCGAGGAGGAGAGAA CCTTTCGAAGCAGGATGAAGAAC CCTCTCTGGGACGCATGGAATGGA TGCAAGCAAGGGTGCAAGGA CCTCTCCAGGCACTGGC ACCACCATCCCTCCCACCA CCTCTCGGGCCCCCAGT GAAGGAGGAGGAAGGAGCCT CTTCCAGGCCCCGGACTGA ACGCCTGGGCCCCGACTG ACAGCCATGCCTTCC CAGGAGGCAGGATGGAATGGA CTTCCTGGGCCCCAGT GAAGGCAGGTGCCAGACTGA CTTCCTGGGCCCCAGT GAAGGGTGCCCAGACTCA CTTCCTGGGCCCCAGT GAAGGGTGCCCAGACTCA CTGCTGGGCCCCGATGAA GGATGGGTGCCCAGACTCA CTGCTCCCAGGCCTTCTC CCCACGCCTTCTCC CCCACGCCCTACCACCAC CTCCTCTGGACCCCGATGAA CTCCTCTGGGCCCCAGT GAAGGCGGATGCCAGGCCT CTTCCTCTGGGCCCCAGT GAAGGCACGCCTTCTC CCCCACGCCCTGCCAGC CTCCCCACGCCCTACCACCCCCCCACCC CTCCCCCGCCCCACTG CTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC</td>	TAATGAATTCTCTATGAAAAATAAAGGC AAGATATGTCATATGTTGATCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTIGACTGGCCTCGCTAACATC CTGGCTGGCGTTTCAGTTIG TACAAGTTGATGGGGGCAAAAC GATAAGGACTAACTGGATTGGGC CCACTGATAGGTTTCCATTGCA TCCCTGCATATTTTGGTTTCCA TGTTCACCGGTTTTTATAGTCCATGTT GCAGTTCATCATGGTTAAGAGCT CATGAGTTGAAGCACAGG TCTTTCTCACGGGCTTTTCAG GCAGGTAAGTGGGCCTCGAA GGTTGGTTGTGGGCCCTGAA GGTAGGTTGTGGGCCTCGAA GGTAGGTTGTGGGCCTCTGAA GGTAGGTGGTGGTGCTTGAG GCAGGTAAGTGGGACTGAAG CCCTGTCCTCCCAGC GGAGAAAGCGCCCCCTACTG AGAGGTGAGTGGTAGTAGTATG CTCCACGGGTTCTAGAG CCCTGTCTCTCCAGC GGAGGAGGAGGAGTGAGAATGGA TGCAAGCAAGGGATGAAGA CCTTTCTGGGAGGGATCTAGAA CCTTTCCATGCCTCCACC GGAGGAGGAGGAGGAGAGGA TGCAAGCAAGGGTCAAAGGA CCTTTCCATGCCCCCCTACTG AGAGGCAGGATGAGAATGGA CCTTTCCAAGCGCATGGAGCT CTTCCACCGCTTCTAACAGC CCTCTCTGGACGCGTGCAAGGA CCTTTCCAAGCGAGGAGGAGAGAA CCTTTCGAAGCAGGATGAAGAAC CCTCTCTGGGACGCATGGAATGGA TGCAAGCAAGGGTGCAAGGA CCTCTCCAGGCACTGGC ACCACCATCCCTCCCACCA CCTCTCGGGCCCCCAGT GAAGGAGGAGGAAGGAGCCT CTTCCAGGCCCCGGACTGA ACGCCTGGGCCCCGACTG ACAGCCATGCCTTCC CAGGAGGCAGGATGGAATGGA CTTCCTGGGCCCCAGT GAAGGCAGGTGCCAGACTGA CTTCCTGGGCCCCAGT GAAGGGTGCCCAGACTCA CTTCCTGGGCCCCAGT GAAGGGTGCCCAGACTCA CTGCTGGGCCCCGATGAA GGATGGGTGCCCAGACTCA CTGCTCCCAGGCCTTCTC CCCACGCCTTCTCC CCCACGCCCTACCACCAC CTCCTCTGGACCCCGATGAA CTCCTCTGGGCCCCAGT GAAGGCGGATGCCAGGCCT CTTCCTCTGGGCCCCAGT GAAGGCACGCCTTCTC CCCCACGCCCTGCCAGC CTCCCCACGCCCTACCACCCCCCCACCC CTCCCCCGCCCCACTG CTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
TET2-E07.02           TET2-E07.03.A           TET2-E09           TET2-E10.01           TET2-E10.02           TET2-E10.03           TET2-E11.01           TET2-E11.03           TET2-E11.04           TET2-E11.05           TET2-E11.07           TET2-E11.08           TET2-E11.09           TET2-E11.09           TET2-E11.09           TET2-E11.08           TET2-E11.09           TP53-E04.01           TP53-E06           TP53-E06           TP53-E07           TP53-E08           TP53-E10	EDINA ED	TCAGCTGCACAGCCTATATAATG         TTCAGGAGAACTTGCGCC         AGGCACCATATATGTGTTTGGG         AACTACTTTCGCATTCACACACA         CACGTTTTCTGGAGTGG         GTGGATGACTTGGGAGTGG         GTTAGCAGAGCCAGTCAGAC         TCACACTCAAAGATACCTGTTTCTGT         TGCAACACCTTTTGAATCAGA         CTCACTCACACACCATCCAT         CACCATGAGAGTGGCC         AATGACTTTTCCACCCACCAG         GGTAGAGTGCCAGTCCAT         CACCATGAGATGGACGCC         AATGACAGCGAGCAGA         GCATGCCAGACAGCAGAGA         GCATGCCAGACAGCAGAGA         GCATGCCAGACGCAGCAGA         GCATGCCAGACCCCTTTAA         TATGGCCCAGACTGTGTGCC         TCCTCTGACTGCTCTTTCAC         GTCCAGATGAAGCCCCAGA         GGTGGTGGGGGATAGATGGC         GACAGGCCAGACGAGAGGGCTG         GGGTGGTTGGGAGTAGATGG         GGACAGACGACAGGGCTG         GGGTGGTGGGGGGATAGATGG         GGGTGGTGGGAGGACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         AGGGAAAAGGGGCACAGAC         CAGTGCTCCTCTCTTATCTT         CCAGCGGCAGAGGGA         CTAGGTCCAGAATGCCCCAGTC         CTGAGTCAGAACTGCCCAGC         ACTGCAGATGACCCAGAC	TAATGAATTCTCTATGAAAAATAAAGC AAGATATGTCATATGATGATCATCT TAAGTTGTTACAATTGCTGCCA CAGCTGCTAAGCTGTCCTCA CTTGACTGGCTCTGCTAACATC CTGGCTTGCGTTGCG

ASXI 1-F13 12	ØDNA	GAGAAAGCTGCTCCCACC	GACCTTCAAAGTCAGAGGCT
ASXI 1-E13 13	σDNA	TGTCAACAGGTGGACATTGA	ΤGTAACCAGACGCATGTCA
ASXI 1 512 14	aDNIA		
ASXLI-E13.14	gDNA		
ASXLI-E13.15	gDNA		GTAAGTGGTACTTGTGGGGGA
ASXL1-E13.16	gDNA	ACTTGTGATGCAGTTGCTG	TGGCAGAAGAGGCTCC
ASXL1-E13.17	gDNA	GCATGGGATCTTTACATGGT	GAGGGAGTCAAAACTTGGGA
ASXL1-E13.18	gDNA	AAAACAGTGGCATGGTTGAT	ATTTGTCACTGGATGGAGGG
ASXL1-E13.19	gDNA	TCCTGGAGCACCCCAA	TTTCCTGGAGCAGCATTTGA
ASXL1-E13.20	gDNA	AAAGAATTGCAAGGCAGTCC	GAGATGAGAAACGAGGTGTT
ASXI 1-E13 21	gDNA	AGAGCAGTTCTCTTTAGT	CTTCTTCCCTTGGCCTGTAA
ASXI 1-E13 22	σDNA		
ASVI 1 E12 22	gDNA	ттаслеессалеесалелае	CCAACAAAGGCATGTGGC
ASKEI-E13.23			
ASXLI-E13.24	gDNA		
ASXL1-E13.25	gDNA	CTGGGCTCCAAAGCCAC	GAGTTGGGAGGGGGGGAGAGA
ASXL1-E13.26	gDNA	GGACTTGCCCTTCTGGAAAT	CCTTTGGGAAAGGTGGGAG
ASXL1-E13.27	gDNA	CAAGCAGGCATTTTATGGGA	CGCACACTGGAGCGAG
ASXL1-E13.28	gDNA	CTAGCTCTCCCACCTTTCC	CAGAGCTTTGAGGGTCCAAT
ASXL1-E13.29	gDNA	CCACAGTGCATCACTTTCC	AGATCAATCATTATCAAAATACACACA
DNMT3A-E07.01	gDNA	AAACATGGTCCCCTTGAGTG	TAGCCACAGTGGGGGATG
DNMT3A-F07.02	gDNA	TCAGAAGGTGGAGGAGGC	GAGCTGGCAGTGGAAGG
DNMT3A-F08 01	gDNA	CGTGACCACTGTGTAATGAT	
DNMT3A E08.03	gDNA		
DINIMITSA-E08.02	BUNA		
DNMT3A-E09	gDNA	GTAAGCUTUGGLAAALAAG	ACCIGLACITCC
DNMT3A-E10.01	gDNA	CTACTCAGAGTCTGGCCTTG	CCATTCAATCATGGGCTTGT
DNMT3A-E10.02	gDNA	AAGCTGTTCCCGGTGTG	CCTCCCTAAGCATGGCTTTC
DNMT3A-E11.01	gDNA	AGTTTCCTGTCAGCCTGTAA	CAGGCCAACTACCTCTTGT
DNMT3A-E11.02	gDNA	ACAAAGAAGTGTACACGGAC	AGCTGGCGTCAGAGGA
DNMT3A-E12	gDNA	CACAAGAGGTAGTTGGCCT	CACACTAGGAGTGCCAGAG
DNMT3A-E13	gDNA	GGTGGTACTCACCCCATC	CCTCAACGGCACCTCTC
DNMT3A-E14 01		GGTCATGTCTTCAGGGCTTA	ATGGTGCAGTAGGACTGGTA
DNIMT2A E14.01	d DNA		
DINIVITOR-E14.02	SDINA		
UNMI 3A-E15.01	gDNA		
DNMT3A-E15.02	gDNA	GTCTCCTTCCAGGTGCTTTT	CCCAGCACTCACAAATTCC
DNMT3A-E15.03	gDNA	CCATTAAGGAAGACCCCTGG	TCCTAGACCCACACACCC
DNMT3A-E16	gDNA	GGCCTGCATCTGACCTG	CATCCTGGGACAAGGCG
DNMT3A-E17.01	gDNA	AGATGGCTCCAAGTAACGG	TACATGATCTTCCCCTGGTG
DNMT3A-E17.02	gDNA	AAGGACTTGGGCATTCAGG	GAACAAAATGAAAGGAGGCAA
DNMT3A-F18	σΩΝΔ	GCAGGCCCATCACGTT	GGAAGCCTATGTGCGGAA
DNMT3A E10 01	gDNA		GCCACCACATTCTCAAAGAG
DNMT3A-E19.01	-DNA		
DNM13A-E19.02	gDNA	ILILAGAGGGLALIGGL	AAGLAGLAGILLAAGGIAG
DNMT3A-E20	gDNA	CCTCCTTGGCTCATCTTCAA	CAGTCCCAGCCCACAG
DNMT3A-E21	gDNA	CCAGGTTTCTGTTGTTACAGTC	ССТТССТТСТСССТБСС
DNMT3A-E22.01	gDNA	GTGTTGGCTGGTGAATGAAT	CAGTGCACCATAAGATGTCC
DNMT3A-E22.02	gDNA	CGTGCTTATTCCTCTTTTCTCC	CAGCAAGCACAGCAATCAG
DNMT3A-F23.01	<b>BNN</b>	CCA CCA CTCA CCCTCC	TTECTOTOCOTACCTCACT
DITITION	gDNA	LLAGLALILALLLIGL	IIIGIGICGCIACCICAGII
DNMT3A-E23.02	gDNA gDNA	CCAGCACITACCUIGC	TGTTTGTTTAACTTTGTGTCGC
DNMT3A-E23.02	gDNA gDNA gDNA		TGTTGTCGCTACTCAGT TGTTGTTAACTTGTGTCGC AAATAGCAGCCTCACATTGC
DNMT3A-E23.02 FLT3-E20.01	gDNA gDNA gDNA	CCCTCTCTGCCTTTTCTCCC AAGAAAGATTGCACTCCAGG GACAGTGTGTTCACAGAGA	
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02	gDNA gDNA gDNA gDNA	CCCTCTCTGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGTGTTCACAGAGA	
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X	gDNA gDNA gDNA gDNA gDNA	CCGCTCTGCCTTTTCCC AAGAAAGATTGCACTCCAGG TGACAGTGGTTCACAGAGA TGTGGAAATCACCAAATGGC	TIGTIGGCIACTICAGT GTITGTTTAACTITGTGTCGC AATTAGCAGCCTCACATTGC AGTGAGTGCAGTTGTTTACC CATACAAGTTGGCAAATTTCTGGG
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01	gDNA gDNA gDNA gDNA gDNA gDNA	CCGCCTCTGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TTGTTGCTTGGGGTTCAAAT	TIGTIGGUACITAGTI TGTTIGTTAACTITGTGTCGC AAATAGCAGCCTCACATTGC AGTGAGTGCAGTTGTTACC CATACAAGTTGGAAATTTCTGGG ACTAGGCGTGGGAATGTTTTT CATACAGGCGTGGGAATGTTTTT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	CCGCTCTCGCCTTTTCTCC AAGAAAGATTGCACTCCCAGG TGACAGTGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TIGTTGCTTGGGGTTCAAAT TGTGGAAAAGTCCCAATGGA	TIGTIGICICICAGIT GTITIGTITAACTITIGTGTCGC AAATAGCAGCCTCACATTGC AGTGAGTIGCAGTIGTITACC CATACAAGTIGGAAATITICTGGG ACTAGGCGTGGGGATGTITIT CAAGAGGATGGCTAGGCG
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	CCGCTCTGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TIGTTGCTTGGGGTTCAAATGGC TGTGGAAAAGTCCCCAATGGA TCTATGAAAGTGCTCGAGTGCC	TITGIGGCIACITAGTI TGTTIGTITAACTTIGTGGG AATAGCAGCCTCACATIGC AGTGAGTGCAGTIGTTACC CATACAAGTIGGAAATTICTGGG ACTAGGCGTGGGATGTTITT CAAGAGGATGGCTAGCG GCCAGATATCAACTGTTACAGAA
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	CCGCTCTGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGGTTCACAGAGA TGTGGAAATCACCAAATGGC TTGTTGCTTGGGGTTCAAAT TGTGGAAAAGTCTCAATGGA TCTATGAAAGTGTTGTGGTTCC ACCCTGATTACTGGTTTCCA	TIGTIGICUCICAGT GTITIGTTTAACTITGTGTCGC AATAGCAGCCTCACATTGC AGTGAGTGCAGTTGTTTACC CATACAAGTTGGAAATTTCTGGG ACTAGGCGTGGGATGTTTTT CAAGAGGATGGCTAGGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E02 NRAS-E03.01	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	CCACCACTCACCCTRC CCCTCTCGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGGTTCACAGAGA TGTGGAAATCACCAAATGGC TTGTTGCTTGGGGTTCAAAT TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTTCCA CCTCCCTGCCCCCTTAC	TIGTIGTUGLIACITAGTT TGTTIGTTAACTTIGTGTCGC AAATAGCAGCCTCACATTGC AGTGAGTGCAGTTGTTACC CATACAAGTTGGAAATTTCTGGG ACTAGGCGTGGGATGTTTTT CAAGAGGATGCTAGGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGAGACAG TCCGCAAATGACTTGCTATT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E02 NRAS-E03.01 NRAS-E03.02	gDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	CCATCATCACCURAC CCCTCATCACCCURAC GACAGTGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TIGTTGGAAAGTCACCAAATGGC TIGTTGGAAAGTCCCAATGGA TCTATGAAAGTCCCAATGGA TCTATGAAAGTGTTGTGGTTCC ACCCTGATTACTGGTTTCCA CCTCCCCGCACCCCTTAC AGATGGTGAAACCTGTTTGTT	TITGIGUELACITAGTI TGTTIGTITAACTTIGTGGG AATAGCAGCCTCACATTGC AGTGAGTGCAGTTGTTACC CATACAAGTTGGAAATTICTGGG ACTAGGCGTGGGATGTTITT CAAGAGGATGGCTAGGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG TCCGCAAATGACTTGCTATT CTCATTICCCCATAAAGATTCAGA
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01	gDNA	CCGCTCTGCCTTTGCC AGGAAGATTGCACTCCAGG TGACAGTGGTTCACAGAGA TGTGGAAATCACCAAATGGC TTGTTGGAAAGTCCCAATGGA TGTGGAAAGTCCCAATGGA TCTATGAAAGTCCTAATGGATCC ACCCTGATTACTGGTTCCA CCTCCCTGCCCCTTAC AGATGGTGAAACCTGTTGTG TCAGAGGCCAGCCTTGTGG	TIGITIGICUCICAGTI GITIGITTACTITGIGICGC AATAGCAGCCTCACATIGC AGTGAGTGCAGTIGITTACC CATACAAGTIGGAAATITCIGGG ACTAGGCGTGGGAATGITITT CAGAGGGTGGCTAGGCG GCCAGATATCAACTGITIACAGAA ATCCGACAAGTGAGAGAGACAG TCCGCAAATGACTIGCTATT CTCATTCCCCATAAAGATICAGA AAGAGTGCCACTIGGTGT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.02	gDNA	CCAGCACICACCUIGC CCCTCTGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TTGTTGCTTGGGGTTCAAAT TGTGGAAAAGTCTCAATGGA TCTATGAAAGTGTTGTGGTTCC ACCCTGATTACTGGTTTCCA CCTCCCTGCCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TCCTGATACCATCACCTCC	TIGITIGITUSCIACUTAGTT GITTIGITIGATCACITIGIGTCGC AATAGCAGCCTCACATIGC AGTGAGTGCAGTTGTTTACC CATACAAGTIGGAAATITCTGGG ACTAGGCGTGGGATGTITTT CAAGAGGATGGCTAGGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG TCCGCAAATGACTTGCTATT CTCATTTCCCCATAAGATTCAGA AAGAGTGCCCATGGGGT GCAAACTGGAATACCTT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.02 TET2-E03.02 TET2-E03.02 TET2-E03.02	gDNA	CCACCTCTGCCCCTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCCAATGGA TCTTGGAAAGTCCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCCGCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC	TITGIGUCICICAGTT TGTTIGTTIAACTTIGGTCGC AATAGCAGCCTCACATTGC AGTGAGTGGAAGTTGTTACC CATACAAGTTGGAAATTICTGGG ACTAGGCGTGGGATGTTTTT CAGAGAGGATGGCTAGGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG TCCGCAAATGACTGCTATT CTCATTTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAAACACTTGGAATACCCT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.02 TET2-E03.02 TET2-E03.02 TET2-E03.03 TET2-E03.04	gDNA	CCGCTCTGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCCAATGGA TGTGGAAAGTCCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCGGCCCCTTAC AGATGGTGAAACCTGTTTGT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCACTCTTTCAA AAGCCGGAATAGTCGGTGCA	TITGIGGCIACITAGTI GITTGITTACTTGGTGGGC AATAGCAGCCTCACATTGC AGTGAGTGCAGTTGTTACC CATACAAGTTGGAAATTCTGGG ACTAGGCGTGGGATGTTTT CAAGAGGATGGCTAGGGG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGAGACAG TCCGCAAATGACTGCTATT CTCATTTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTTGGTCTGGTTCA
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.04 TET2-E03.04	gDNA	CCGCCTCTGCCTTTCCC AAGAAAGATTGCACTCCAGG TGACAGTGGTTCACAGAGA TGTGGAAATCACCAAATGGC TTGTTGGAAAGTGTCAAAT TGTGGAAAAGTGTGATGGG TCATGAAAGTGTTGTGGTTCC ACCCTGATTACTGGTTTCCA CCTCCCTGCCCCTTAC AGATGGTGAAACCTGTTGTT TAGAAGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCACTCTTTCAA AAGCCAGAATAGTCGTGTGA	TIGITIGITUSCICACITAGT GITTIGITTIAACITIGIGTCGC AATAGCAGCCTCACATTGC AGTGAGTGCAGTTGTTTACC CATACAAGTTGGAAATTTCTGGG ACTAGGCGTGGGATGTTTT CAGAGGGGTGGGATGTTTT CAGAGGGTGGGAGAGACAG TCCGCAAATGACTTGCTATT CTCATTCCCCATAAGGATCAGA AAGAGTGCCACATAGGTG GCAAACACTTGGAATACCCT AGCCTTTGGCTGTGTTCA
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.05 TET2-E03.05 TET2-E03.05	gDNA	CCARCINACTORIC CCCTCTCTGCCCCTTTCTCC AAGAAAGATTGCACTCCAGG TGGGAAATCACCAAATGGC TTGTGGAAATCACCAAATGGC TTGTGGTGGGGTTCAAAAT TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTGGGGTCC ACCCTGATTACTGGTTTCCA CCTCCCTGGCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCACTCTTCAA AAGCCAGAATAATACGGCAG	TITGIGGCGLACCTAGTT TGTTIGTTIAACTTIGGTGGC AATAGCAGCCTCACATTGC AGTGAGTGCAGTTGGAAATTICTGGG ACTAGCGCGTGGGATGTITTT CAAGAGGATGGCAAGCCG GCCAGATATCAACTGTTACAGAA ATCCGACAATGACTGGTAACAGA ATCCGACAATGACTGCTATT CTCATTTCCCCATAAGATTCAGA AAAGAGTGCCACTTGGAGT GCAAAACACTTGGAATACCCT AGCCTTTTGGTCTGCACTTCC CTTGGCTTACCCCGAAGTTA GGTGAAATCTTTAACTGCATTTCC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.02 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.05 TET2-E03.06	gDNA	CCATCIFICACCTIGC CCCTCTGGCCTTTGCC AAGAAAGATTGCACTCCAGG TGACAGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCGGCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAGTGGCAACTCTTCAA AAGCCAGAATAGTCGTGTGA TGGAGGAATAAAACGCACAG AGAAAGACGTAACTTCGGGG	TITGIGUCICACITAGTI TGTTIGTITAACTTIGTGTGGC AATAGCAGCCTCACATTGC AGTGAGTGCAGTTGTTACC CATACAAGTTGGAAATTICTGGG ACTAGGCGTGGGATGTTTTT CAAGAGGATGGCTAGCGG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG TCCGCACAAGTGAGAGACAG TCCGCCACAGTGGGAGTCAGA AAAGAGTGCCACTTGGTGT GCAAACCTTGGAATACCCT AGCCTTTGGCTTACGCATTTC CTTGGCCTACCCGAAGTTA GGTGAAATCTTTAACTGCATTTC TTTCCCCTCCTGCTCATTC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.07	gDNA	CCGCTCTGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TIGTTGGAAATCACCAAATGGG TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTTCCA CCTCCCTGCCCCTTAC AGATGGTGAAACCTGTTGG TTCCTGATACCATCACCTCC ACCAAGTGGCATCCTTTCAA AAGCCAGAATAGTCGTGTGA TGGAGGAATAAAACGCACAG AGAAAGACGTAACTTCGGGG GCCCAAGAAAATGCAGTTAAAG	TIGITIGICUCICAGTI TGITIGITTIAACTITGIGTCGC AAATAGCAGCCTCACATIGC AGTGAGTGCAGTIGITTACC CATACAAGTIGGAAATITCTGGG ACTAGGCGTGGGATGITITT CAAGAGGATGGCTAGGCG GCCAGATATCAACTGITACAGAA ATCCGACAAGTGAGAGAGACAG TCCGCAAATGACTIGCTATT CTCATTTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTATT GCAAACACTTGGAATACCCT AGCCITITGGTCTTGTTCA CTIGGTCTTCCCGAAGTTA GGTGAAATCTTACGCATTC TTTCCCCCTGCTCATTC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.05 TET2-E03.07 TET2-E03.08	gDNA	CCARCHACTCACCTIC AAGAAAGATTGCACTCCAGG TGACAAGTGCACTCCAGG TGGGAAATCACAAATGGC TTGTGGTTGGGGGTCAAAT TGTGGAAAGTCCCAATGGA TCTATGAAGTGTGGGTTCCA CCTCGATTACTGGTTTCCA CCTCCCTGCCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAACCTGTTGGG TTCCTGGATACCATCACCCC ACCAGATAGGCACTGTGGA TGGAGGGAATAAAACGCACAG AGAAAGACGTAACTTCGGGG GCCCAAGAAAATGCAGTTAAAG AGGAGGGGAAAAGTGCTAAT	TITGIGGCIACITAGTI TGTTIGTTIAACTTIGTGGG AATAGCAGCCTCACATTGC AGTGAGTGCAGTIGGTTACC CATACAAGTTGGAAATTTCTGGG ACTAGCGGTGGGATGTTITT CAAGAGGATGGCAAGGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAGG CCCGCAAATGACTGCTATT CTCATTTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTITGGTCTTGGTATTCC CTTGGCTTACCCCGAAGTTA GGTGACAACTTTGACGATTTCC TTCACCCTGCTGCTGTCCA TGAGATGGGTTTTCCACC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.02 TET2-E03.04 TET2-E03.05 TET2-E03.06 TET2-E03.08 TET2-E03.08 TET2-E03.09	gDNA	CCATCIFIGECTITICTCC AAGAAAGATTGCACTCCAGG TGACAGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAAGTCACCAAATGGC TGTGGAAAGTCCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCGTTCC CCTCCCTGATTACTGGTTTCCA CCTGCCCCCTTAC AGATGGGAAACCTGTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCTACCTCCA ACCAAGTGGCACACTTCGTGA TGGAGAATAAGCCACAG AGAAAGGCGAACTATCTGGGG GCCCAAGAAAATGCCACTTCGGG GCCCAAGAAAATGCCATTCAA	ITIGIGUCICACITAGTI TGTTIGTTIAACTTIGTGGCG AATAGCAGCCTCACATTGC AGTGAGTGGAAATTICTGGG ACTAGGCGTGGGATAGTTITT CAAGAGGATGGCTAGGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG TCCGCAAATGACTTGCTATT CTCATTTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCGTTITGGTCTGGTCA GGTGAAATCTTTAACTGCATTTC TTCACCCCGCAAGTTA GGTGAAATCTTTAACTGCATTTC TTCACCCCGTGGTGTCACCA TCAGGTGGTGTGTCCA TGAGATGTGGTTTCGCAC CAGAGTGGGGTGGCGCG CAGAGTGGGGTGCGGCG CAGAGTGAGGTCGTGCGCG
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.02 TET2-E03.01 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.07 TET2-E03.07 TET2-E03.08 TET2-E03.09 TET2-E03.10	gDNA           gDNA	CCACTCITIGCCTTTTCTCC CCCTCTCTGCCTTTTCCC AAGAAAGATTGCACTCCAGG TGACAGTGTGTTCACAGAGA TGTGGAAAATCACCAAATGGC TGTGGAAAAGTCCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGTGGTTCC ACCCTGGCTCCCTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCACTCTTTCA AAGCCAGAATAGTCGTGGA TGGAGGAATAAAACGCGCACAG AGAAAGACGTAACTTCGGGG GCCCAAGAAAATGCAGTTAAAG AGGAGGGAAAAATGCAGTTAAAG AGGAGGGAAAAATGCAGTTAAAG AGATGGTGTTCCATCCGGG	TITGIGGCIACITAGTI GITTGITTAACTITGIGTGGC AATAGCAGCCTCACATIGC AGTGAGTGCAGTTGITTACC CATACAAGTTGGAAATITCTGGG ACTAGGCGTGGGATGITITT CAAGAGGATGGCTAGGGG GCCAGATATCAACTGITACAGAA ATCCGACAAGTGAGAGAGACAG TCCGCAAATGACTGGTATACAGAA AAGAGTGCCACTTGGTGT GCAAATGACTTGGTATGGAA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTTGGTCTTGTTCA CTTGGCTTACCCGAAGTTA GGTGAAATCTTTAACTGCATTTC TTTCCCCTCCTGCTCATTC TTCACCATGTGTGTGTCCA TGAGATGGGATTGGGCG CAGAGTAGAGGTCTGTGCGG CATCATCAGCATCACAGGC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.05 TET2-E03.07 TET2-E03.07 TET2-E03.08 TET2-E03.09 TET2-E03.10 TET2-E03.11	gDNA           gDNA	CCARCHACTGACCTGC CCCTCTCTGCCTTTCCC AAGAAAGATTGCACTCCAGG TGGGAAATCACAAATGGC TTGTGGCAAATGGGGGTCCAAAT TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTGGGTCCC ACCCTGATTACTGGTTTCCA CCTCCCTGCCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTGTGGG TTCCTGGATACCATCACCCC ACCAGAGGGCAATAGTCGTGTGA AGACAGGAATAAGTCGTGTGA TGGAGGAATAAAACGCACAG AGAAAGACGTAACTTCGGGG GCCCAAGAAAATGCAGTTAAAG AGGAGGGAAAAGTGCTAAT TGCTACAGTTCCACCTCC ACCAGTTCCCCCTTCAA AGGCAGAAAATGCAGTTAAAG AGAAGAGGGAAAAGTGCTAAT TGCTACAGTTCCATGCCGG CCCCAGAATTCCAGTCAACT	TITGIGUGUACITAGTI TGTTIGTTIAACTTIGTGGG AATAGCAGCCTCACATTGC AGTGAGTGCAGTIGGTTACC CATACAAGTTGGAAATTTCTGGG ACTAGCGGTGGGATGTTTTT CAAGAGGATGGCAAGGCG GCCAGATATCAACTGTTACAGAA ATCCGACAATGACTGGTAGCG GCCAGATGACGTGAGAGACAG TCCGCAAATGACTGGTATT CTCATTTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTTIGGTCTTGGTATTC CTTGGCTACCCGAAGTTA GGTGACATCTGGAGTTACGCATTTC TTCACCATGGTGTGTGTCCA TGAGATGGGTTTTCCACT CAGAGTTGGGGTTTCCACCC CAGAGTTAGAGGTCTGTGCG CATCATCAGCAATCACAGC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.06 TET2-E03.08 TET2-E03.09 TET2-E03.10 TET2-E03.12	gDNA           gDNA	CCARCHACIGACUIGE CCCTCTCTGCCTTTCC AAGAAAGATTGCACTCCAGG TGACAGTGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCGGCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCAACCTGTGGA TGGAGGAATAAACGCACAG AGAAGAGCGAACTACTCGGGG GCCCAAGAAAATGCCACTGGA AGGAAGGGAAAATGCCATTA TGCTACAGTTTCTGCTCTT AGGATGGAAACGCACGTAAT TGCTACAGTTTCTGCCCCTT AGGATGGAAACCTCCTT AGGATGGGAACCTTAT TGCTACAGTTCCGCCCTT	ITIGIGUELIACITAGIT GITTIGITIAACITIGIGUEGE AATAGCAGCCTCACATIGC AGTGAGTGGAAATITCIGGG ACTAGGCGIGGGATGITITT CAAGAGGATGGCAAATITCIGGG GCCAGATATCAACIGITACAGAA ACTCCGACAAGTAGAGAGACAG TCCGGCAAATGACTGGTATT CCCATITCCCCATAAAGATICAGA AAAGAGTGCCACTIGGTGT GCAAAACACTIGGAATACCCT AGCCTITIGGTCTGGTA GGGAAATCITTAACIGCATITC TICACCACCGGGGTAACGCAC GGGGAAATCITTACGCATTC TICACCACGTGGGGTCACCC CAGGTTAGCGCGCGC CAGAGTTAGAGGTCGGGC CATCATCACACAGGC TGGGCATATCTCACAAAACTGAGT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.02 TET2-E03.01 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.09 TET2-E03.10 TET2-E03.11 TET2-E03.12 TET2-E03.13	gDNA           gDNA	CCATCIFICECTIFICTCC AAGAAAGATTGCACTCCAGG TGACAGTGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCCAATGGA TCTATGAAGTGTTGTGGTTCCA CCTCCTGATTACTGGTTGCATCACCCCCC ACCAGTGGAACCTGTTGTT TAGAGGGCAGCCTTGTGG TCCTGATACGCGCACCACA AGAAGGCGAAAAGTGCGATAATGC TGGAGAAAAGTCGTTCAA AAGCCAGAATAGCGCTTACA AGGCAGCGTAACTCGGG GCCCAAGAAAAGTGCATAAG AGGAGGGAAAAGTGCTATA	ITIGIGGCIACITAGTI GITIGITIACTITGIGGC AATAGCAGCCICACATIGC AGTGAGTGCAGTIGGTAAC CATACAAGTIGGAAATITCTGGG ACTAGGCGTGGGATATTTTC CAGAGGGTGGCTAGCG GCCAGATATCAACTGTTACAGAA ACTCCGACAAGTGAGAGACAG TCCGCAAATGACTGCTATT CTCATTCCCCATAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTTGGCTTGGTTCA CTTGGCTTACCCGAAGTTA GGTGAAATCTTAACTGCATTTC TTCCCCCTGCTCATTC TTCACCCCCGAAGTTA GGTGAAATCTTTACTGCATTTC TTCCCCCCGTGCTGTTCA CTTGGCTTACCCCGAAGTTA GGTGAAATCTTTACTGCATTTC TTCCCCCCGGCCATTC TCACCCCCGCGCCCATC TGAGATGTGGTTTCCGCG CATCATCAGCATCACAGGC TGGGCATATCTCAAAAACTGATT CTGCGCATCACCGCGG CATCATCACAGCGC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.03 TET2-E03.04 TET2-E03.05 TET2-E03.06 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.10 TET2-E03.11 TET2-E03.13 TET2-E03.14 TET2-E03.14 TET2-E03.14	gDNA           gDNA	CCARCHARCTERE CCCTCTGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGGGTTCC ACCCTGGCTCCCTAC AGATGGTGAAACCTGTTGG TTCCTGATACCATCACCTCC ACCAGATAGCGCATCCTTCAA AAGCCAGAATAGTCGTGGG TTCCTGATACCATCACCTCC ACCAGAGAAAAAGCGCACAG AGAAGGGAATAAAAGCGCACAG AGAAGGGAATAAATGCAGTAAAG AGAAGGGAATAAATGCAGTAAAG AGAAGGGAAAAATGCCACAG AGAAGAGGAAAAATGCCTCAT TGCTACAGTTTCCCATCGGG CCCCAAGAAAATGCCGCTTAT TGCTACAGTTTCCCATCCGGG CTCGAGACCTCACTCCC ACCAAGAAAATGCCCAT CTGTGAGATCACTCACCCAT CTGTGAGATCACTCACCCAT CCTGAGAGCGAACCACAA	TITGITGICGUACITAGTT GITTGITTAACTITGIGTGGC AATAGCAGCCTCACATTGC AGTGAGTGCAGTTGITTACC CATACAAGTTGGAAATTTCTGGG ACTAGGCGTGGGATGITTT CAAGAGGATGGCTAGGGG GCCAGATATCAACTGITACAGAA ATCCGACAAGTGAGAGAGACAG TCCGCAAATGACTGCTATT CTCATTTCCCCATAAAGATTCAGA AAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTTGGCTTGGTGTG GCAAACCTTGGAATACCCT AGCCTTTGGCTGGTGGTGTCA CTTGGCTTACCCCGAAGTTA GGTGAAATCTTTACGCATTC TTCACCCTGCTGCTGTCCA TGACGTTACGGGTGTGGTCCA TGACGTTAGGGTTGCGGC CATCATCAAGCATCAGGCG TGGGCATATCCCAAAAACTGGATT CTTGGCATCACGCGGG CAGGGGAGAAAGAAGCAGC TGGGGGGGGAGAAGAAGCAGC TGGGGGGGGGGAGAAGAAGCAGC TGGGCGTTGTGCGGC CAGGGGGGGAGAAGAAGCAGT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.06 TET2-E03.07 TET2-E03.08 TET2-E03.09 TET2-E03.10 TET2-E03.12 TET2-E03.14 TET2-E0	gDNA           gDNA	CCARCHACUSCUSC CCCTCTGCCTTTCCC AAGAAAGATTGCACTCCAGG TGACAGTGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCCGCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCAACCTGTTGA AGGCAGGAATAATGCGTGTGA TGGAGGAATAATGCGTGTGA TGGAGGAATAATGCGTGTGA GGCCCAAGAAATGCCATTGCTTA TGCTACAGTTTCTGCTCTT AGGATGGGAAACTGCTAAT TGCTACAGTTCCGCCCTTT AGATGTGTTCCATCCCC CTGCTGCCGCCCTCC CTGCTGATACCATCCCCTT AGGATGGAAACTGCTAAT TGCTACAGTTCCGCCACTT CCTGCTGCGCCCTGTGA CGCGAAGAAAGTCGCACAG CTGTGATGATCCTGATAATGC TAACATCCAGGGAACCACAA TCAAGCCAAGC	TITGIGUCICACITAGTI TGTTIGTTIAACTTIGTGGCG AATAGCAGCCTCACATTGC AGTGAGTGGAAATTGTTACC CATACAAGTTGGAAATTTCTGGG ACTAGGCGTGGGATGTTTTT CAGAGGGGGGGGGGGGGG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG TCCGCACAAGTGAGAGACAG TCCGCACAGTGAGAGACAG CCCGCAAATGACTTGGTGT GCAAAACACTTGGAATACCCT AGCCTTTGGTCTGGTGT GCAAACCCTGGAGTACCCT AGCCTTTGGTCTGGTTCA CTTGGCTTACCCCGAAGTTA GGTGAAATCTTTAACTGCATTTC TTCCCCCTGCGTCGTTC TTCACCCCGACAGTTA GGTGAAATCTTTAACTGCATTTC TTCCCCCTGCGTGGTCCA TCGGCACAGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E03.02 TET2-E03.01 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.09 TET2-E03.10 TET2-E03.13 TET2-E03.14 TET2-E03.15 TET2	gDNA           gDNA	CCARCITACCUREC CCCTCTCTGCCTTTTCC AAGAAAGATTGCACTCCAGG TGACAGTGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAAAGTCCCAATGGA TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCGGCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAGTGGACACCTGTTGTA TGGAGGAATAAAACGCACAG AGGAAGGGGAAAAGTGCATTAAAG AGGAGGGGAAAAATGCAGTTAAAG AGGAGGGGAAAAATGCAGTTAAAG AGGAGGGGAAAAATGCAGTTAAAG AGGAGGGGAAAAATGCAGTTAAAG AGGAGGGGAAACCACTTT TGCTAGTACCACCTCTT AGGATGAATCACCTCTT AGGATGAATCACCTCTT AGGATGAGTCCCCTTT AGGATGAAAATGCCGTGTA TGCTACAGTTCCCACCCACA CTGTGAGATCACTCACCCACA CTGTGAGATCACTCACCCACA TCAAGCAAAGCCCACACA TCAAGCAAAGCCCACTACCACCACA	ITIGIGUCICAGIT GITIGITIAACITIGIGUGG AATAGCAGCCTCACATIGC AGTGAGTGCAGTIGITTACC CATACAAGTIGGAAATITCTGGG ACTAGGCAGGGAGAATITCTGGG ACTAGGCATGGGATAGTITT CAGAGGATGGCTAGCG GCCAGATATCAACTGTTACAGAA ACCCGACAAGTGAGAGACAG TCCGCAAATGACTGCTATT CTCATTCCCCATAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAATGCCCCATAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAATGCCCCATAAGATTCAGA AAGAGTGCCACTTGGTGT GCAAATCCCCGAAGTTA GGTGAAATCTTAACTGCATTTC TTCCCCCCTGCTCATTC TTCACCCCCGAGGTA GGTGAAATCTTGACGCATTTC TTCCCCCCGGCCATTC TTCACCCCGGCCATTC TCACCATGGGTTGTCCCA GGGGAAATCTTACGCAGTT CGGCATATCCCAAAACCGATT CTGGCATATCCCAAAAACCGATT CTTGCAAATTGCTGGCG CATCATCAGCATCACGGG GGCCTACTCGCGGG GCCTCAGCGTGGCGG GCCTCAGGTTTCCCATGCGG GCCCCAAGGTTGGCGG GCCCCCCGCTGCCGTC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.02 TET2-E03.03 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.10 TET2-E03.11 TET2-E03.12 TET2-E03.15 TET2-E03.16	gDNA           gDNA	CCARCITACCETERE CCCCTCTGCCCTTTCCC AAGAAAGATTGCACTCCAGG TGACAGTGGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAAAGTCCCAAATGGA TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCGCCCCTAC AGATGGTGAAACCTGTTGG TTCCTGATACCATCACCTCC ACCAAGTGGCACCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCACCTCTTCAA AAGCCAGAATAGTCGTGTGA TGGAGGAATAAAACGCACAG AGAAAGACGTAACTTCGGGG GCCCAAGAAAATGCAGTTAAAG AGGAGGGAAAAATGCAGTTAAAG AGGCAGGGAAAAATGCAGTTAAAG AGGCAGGGAAAAATGCCTAT TGCTAGAGTCCTCTTT AGATGGTGTTCCCATTGCGG CTGTGAGATCACTCACCCAT GCTGAGGACCACCTGGTGC TAACATCCAGGGAACCACAA TCCAAGCCAAG	TITGIGGCIACITAGTT GITTGITTAACTITGIGTGGC AATAGCAGCCTCACATTGC AGTGAGTGCAGTTGITTACC CATACAAGTTGGAAATTCTGGG ACTAGGCGTGGGATGITTT CAAGAGGATGGCTAGGGG GCCAGATATCAACTGITACAGAA ATCCGACAAGTGAGAGAGACAG TCCGCAAATGACTGCTATT CTCATTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTTGGCTGGTGTTCA CTTGGCTTACCCCGAAGTTA GGTGAAATCTTTACGCATTTC TTTCCCCTCGGTCATTC TTCACCATGGTGTGGTCCA TGAGATGGGATTGGCGC CAGAGTTAGAGGTCTGTGCGG CATCATCAAGCATCGCGG GGGGAAATCTTCAAAAACTGGATT CTGGCATATCCAAAAACTGGAT CTGGGCATACTCCAAAAACTGGAT CTGGCAATGCTGGCGG GAGGGGGAAAAAAGCAAT TGGGAACGCTATTGCCCTG GGGAACGTCATGTCCCGG
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.05 TET2-E03.06 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.08 TET2-E03.10 TET2-E03.12 TET2-E03.12 TET2-E03.14 TET2-E03.16 TET2-E03.16 TET2-E03.17	gDNA           gDNA	CCARCHACTGACCTGC CCCTCTCTGCCTTTCC AAGAAAGATTGCACTCCAGG TGACAGTGTGTTCACAAATGC TGTGGAAATCACCAAATGGC TTGTGGAAAGTCACCAATGGA TGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCCAATGGA CCTGGGTGGAACCCGTTGGT CCTCCCTGCCCCCTTAC AGATGGTGAAACCTGTTGTT TAGAGGGCAGCCCTGTGG TTCCTGATACCATCACCTCC ACCAGTGGCAACCTGTTGTA TGGAGGAATAAAACGCACAG AGAAGGGGAAACTGTGTGA TGGAGGAATAAAACGCACAG AGAAGGGGAAAAGTGCTAAT TGCTACAGTTTCTGCCTCTT AGATGGGAAACCTGCTAAT GCCCAAGAATAGTCCTGTGA TGCTGAGGACACCTCTT AGAGGGGAAAAGTGCTAAT TGCTACAGTTTCTGCCTCTT AGAGGAGGAAAAGTGCTAAT TGCTACAGTTCTGCATCCCA CCTGTGAGATCACTCACCCAT GCTGATGCTGATACTGCG TAACATCCAGGGAACCACAA TCAAGCAAAGCTCAATGCC TAACATCCAGGGAACCACAA TCAAGCAAAGCCCAAGCACAA ATAGAAGGGAAAACCCGAGCC	TITGIGUCICAGIT GITTGITTAACTTIGTGGG AAATAGCAGCCTCACATTGC AGTGAGTGGAAATTGTTACC CATACAAGTIGGAAATTTCTGGG ACTAGGCGTGGGATGITTT CAAGAGGATGGCTAGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTAGAGAGACAG TCCGACAAGTAGAGAGACAG CCCGCAAATGACTGGCATT CCCATTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTTGGTCTGGTGT GGAAACCTTGAATACCGCATTTC CTTGCCCTACCCGAAGTA GGTGAAATCTTTAACTGCATTTC TTCCCCCTCGCTCATTC CTTGCCCTACCCGAAGTTA GGTGAAATCTTTAACTGCATTTC TTCCCCCTGCTGCATTC TTCCCCTGCGTGGTGTCCA CAGAGTTAGGGTCTGGCG CATCATCAGCATCACAGGC TGGGCATATCTCAAAACTGAG CAGGGGGAGAAAGAAGCAAT TTGGTACCTCGATGCCG GCCTCAGGTTACCCCTGG GCCCTCAGTTACCCCTGG GCCCTCAGTTACCCCTGG GCCCCAGGTTACCCCCGA
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.04 TET2-E03.06 TET2-E03.07 TET2-E03.08 TET2-E03.10 TET2-E03.11 TET2-E03.12 TET2-E03.13 TET2-E03.14 TET2-E03.15 TET2-E03.17 TET2-E03.17 TET2-E03.18 	gDNA           gDNA	CCARCHARCHARC	ITIGIGUCICICAGT GITIGITIAACTTIGGTCGC AATAGCAGCCTCACATTGC AGTGAGTGGAGATGTGTTAACC CATACAAGTTGGAAATTTCTGGG ACTAGGCGTGGGATAGTTTT CAGAGGGGGGGGAGCG GCCAGATATCAACTGTTACAGAA ACTCCGACAAGTGAGAGACAG TCCGGCAAGTGACTGCTATT CCCATTCCCCATAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCGTTTGGTCTGGTC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.06 TET2-E03.07 TET2-E03.10 TET2-E03.11 TET2-E03.12 TET2-E03.14 TET2-E03.15 TET2-E03.18 TET2-E03.18 TET2-E03.18 TET2-E03.19 TET2-E03.19 TET2-E03.19 TET2-E03.17 TET2-E03.18 TET2-E03.19 TET2-E03.19 TET2-E03.19 TET2-E03.19 TET2-E03.18 TET2-E03.19 TET2	gDNA           gDNA	CCARCITACUERCE CCCTCTEGCCTITICTCC AAGAAAGATTGCACTCCAGG TGACAGTGGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAAATCACCAAATGGC TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCGGCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCACCTCTTCAA AAGCCAGAATAGTCGTGTGA TGGAGGAATAAAACCGCACAG AGAAGGCGAAACTTCGGGG GCCCAAGAAAATGCCGTTAAT GGAGGAAAAATGCGTTAAG AGGAGGGAAAAATGCGTTAAG AGGAGGGGAAAAATGCGTTAAG AGGAGGGGAAAAGTGCTAAT GCTACAGTTCCTGCTCT AGATGTGTTTCCATTGCGG CTGTGAGGCACCCTCTT AGATTGTTTCCATTGCGG CTGTGAGGAACCACAATGCC TCAAGCAAGCCACAAC TCAAGCAAAGCCCAACAC ACCAAGGGGAACCACAACCCCACA ACCAAGGGGAACCACAACCCCACA CTCAAGCAAGCTCACGACACACCCACA CTCAAGCAAGCTCACGACACACCACAC	ITIGIGUCICAGIT GITIGITIACTITGIGUC AATAGCAGCCTCACATIGC AATAGCAGCGCCAGCTGITTACC CATACAAGTIGGAAATITCTGGG ACTAGGCATGGGAAATITCTGGG ACTAGGCATGGGAATITCTGGGG GCCAGATATCAACTGITACAGAA ACTCCGACAAGGAGAGCAG GCCAGATATCAACTGITACAGAA ATCCGACAAGGACTGCTATACAGAA ATCCGACAAGGACTGCTATACAGAA ACTCCGACAAGGACTGCTATACAGAA ACTCCCATACAGCTGCATT CTCATTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTTGGCTTGGTGTTCA CTTGGCTTTGCCCGAAGTTA GGGGAAAACCTTGGCATTC TTCACCCTCGGCTCATTC TTCACCCTGCGGCTATC TTCACCATGGGTGTGTCCA GGGGAAAGTGGGGTTTCGGCG CATCATCAGCATCACAGGC TGGGCATATCTCAAAAACTGATT CTGGCAATGGCTTTGCCGG GAGGGGGGAAAAGAAGCAAT TGGGTAACCTTGAGCTGCCG GCCCAGGTTTACCTGCAC CACAGCTACAGCCCTAT TGGACAGCATCATCGCAT GGGACAGCATTGTCCCAC GGGCAGAAGAAGCAAT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.05 TET2-E03.06 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.08 TET2-E03.10 TET2-E03.11 TET2-E03.12 TET2-E03.13 TET2-E03.15 TET2-E03.16 TET2-E03.18 TET2-E03.19 TET2-E03.20	gDNA           gDNA	CLAGCACITACTIGE CCTCTCTGCCTTTGC AAGAAAGATTGCACTCCAGG TGGGAAATCACACAAATGGC TTGTGGAAATCACCAAATGGC TTGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCAATGGA TGTGGAAAGTGTGGGTGCA ACCCTGGTGGGGTGAACTGTGG TCCTGGATACTGGTTCCA CCTCCCTGCCCCTTAC AGATGGTGAAACCTGTTGTG TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCACACTGTGG AGCAGGGAAAAGCTGCTGGA GGAGGGAAAAGCGCACAG AGAAGAGCGAACAGTTAAAG AGGAGGGAAAAGCGCACAG AGAAGGGAAAAGCGCACAG CCCAACAAATGCAGTTAAAG AGGAGGGAAAAGCGCACAG CCCAAGAAAAGCCACAT TGCTGGAACCCCATGCCC TACCAGGGAACCACCAT CCGGGAGAACCCCCAT CCGGGAGAACCCCCAT CCGGATGATCCGCACCAG TCACGCAAGCACCCCA CCCACACCAAGAAACCCCCA CCCACACCAAGAACCCCCA CCCACACCAAGCACCCCA CCCACACCAAGCACCCCA CCCACACCAAGCACCCCA CCCACACCAAGCACCCCA CCCACACCCAAGCACCCCA CCCCACCCA	THIGHOLE LACHAGTT TGTTIGTTIAACTTIGTIGGC AATAGCAGCCTCACATTGC AGTGAGTGCAGTTGGAAATTCTGGG ACTAGCGCTGGGAATTTTTT CAAGAGGATGGCAAGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG TCCGCAAATGACTGCTATT CTCATTTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTATT CTCATTTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGAATACCCT GCAAACACTTGGAATACCCT AGCCTTTGGTCTGGTGTCCA CTTGGCTTACCCCGAAGTTA GGTGAAATCTTTACTGCATTTCC TTCACCCATGGGGTTCCA TGAGATGGGTTTCCACCC CAGAGTTAGGCGTCGGTCCA TGAGATGGGGTTCGCGC CATCATCAGCATCACAGCG CAGGGGAGAAAAACTGGGG GCGCAAATGCCCTCGG GGGCGAAATGCTCGTGGG GCGCCAGGTTACCCCGAGC TGGGCATATCTCAAAACTGGATT CTTGCACTCGAGTGGGG GCCTCAGGTTGTGCGG GCCTCAGGTTCGCCCCG TGGAAATGCTCCCCGA CAGAGTACTCGACCCCG CATCAGTCCCCGAC CAGGGGGAGAAAAACGCAAT TTGGTACCTCGAACCCCCG GGCCTAGGTTCGCCCCG GGCCTAGGTTCCCCCG TGGCAAATCCCCCGAC CACAGGTCTCCCCCG TGCTGAGGTTCCCCCG TGCCTGAGGTTCCCCCG TGCTGAGGTTCCGACCC CACAAGTCCTCCACC CACAAGTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.06 TET2-E03.07 TET2-E03.08 TET2-E03.10 TET2-E03.12 TET2-E03.13 TET2-E03.14 TET2-E03.15 TET2-E03.17 TET2-E03.17 TET2-E03.19 TET2-E03.19 TET2-E03.19 TET2-E03.17 TET2-E03.19 TET2-E03.19 TET2-E03.19 TET2-E03.17 TET2-E03.19 TET2-E03.17 TET2-E03.19 TET2-E03.20 TET2-E03.21	gDNA           gDNA	CCARCHACTGACCTIGE CCCTCTCTGCCTTTGC AAGAAAGATTGCACTCCAGG TGACAGTGGTTCACAAATGGC TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCGCCCCTTAC AGATGGTGAAACCTGTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCAACCTGTGA TGGAGGAATAGTCGTGAA AGGCAGGCATCATCTGGGG GCCCAAGAATAGTCGTGAA TGGAGGAATAGTCGTGAA TGGAGGAATAGTCGTGAA TGCTACAGTTACTGCGGG GCCCAAGAAATGCCATTAAT TGCTACAGTTCCACCCCT AGGAGGGAAAAGTCCTTAT TGCTACAGTTCCCCCTT AGGATGAGCCCACCAG GCCGAAGAAATGCCAGTAATGC TAACTCCAGGGAACCACAG ACCAAGGCAGCCACGA TCCTGCAGCCCACGCAG CTGTGAGATCACTCACCCAT GCTGAGATCACTCACCCAG ACCAAGGAACCCCACAG TCCCAAGAAAGTCCCCAT CCCAAGCAAAGTCCCCACGA TCAAGCCAAGC	ITIGIGUCICAGIT GITIGITIAACITIGGIGG AATAGCAGCCTCACATIGC AGTGAGTGGAAATITCIGGG ACTAGGCAGGGAAATITCIGGG ACTAGGCGTGGGAATITTIC CAGAGGGATGCTAGGCG GCCAGATATCAACIGTTACAGAA ACCCGACAATGAGAGACAG TCCGGCAAGTGACAGTGCAGA ACTCCGACAAGTGAGAGACAG TCCGCAAATGACTIGGTATT CCCATITCCCCATAAGATICAGA AAAGAGTGCCACTIGGTGT GCAAACCTIGGAATACCCT AGCGTTACCCCGAAGTA GGTGAAATCTTTAACTGCATTTC TTCACCCCCGACAGTA GGTGAAATCTTTAACTGCATTTC TTCACCCCGCAGGTA GGGGAAATCTTTACTGCATTC TTCACCCCGGCGCC CATCATCGGGTGTGCCA CAGAGTGGGGTTCCGACC CAGAGTTAGCGGCG CATCATCAGCAGCGG CATCATCAGCATCACAGGC TGGGCATATCCCAAAACTGATT CTTGGCTTACCCCGCAGC CAGAGTTAGAGGTCGTGGG GAGGGGGAAAAGAAGCAAT TTGTGTTACTTGGTGCGC CATCATCGGGGGGAGAAAGCAAT TTGTGTTACTTGGACAT GGGAACAGTCATGCCCCG CGCCAGGTTTCCCCCGAC CAGAGTTACGCTCCCG CTGGAACAGTCATGCCCCG TGGGACAGTCCCCCGAC CACAGGTTCCCGACAT CTGGAACGTCCCCCCAC ACAAGATCCCGTAGCTCCCCC TAGAGATCCCGTAGCTCCCCC TTGGAACGTCCCCGCC CACGATGTCCGTGCCC CCCCGAGGTTCCCACC CACAGGATCCCCGACACC CACAGGATCCCCCCAC CACAGGTCCCCGCAC CACAGGCTCCCCCAC CACAGGATCCCGCTGCCC CTTGAGATCCCGCTGCG CCCCCGAGGTTCCCCCCCCCC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.06 TET2-E03.07 TET2-E03.10 TET2-E03.11 TET2-E03.12 TET2-E03.13 TET2-E03.14 TET2-E03.15 TET2-E03.15 TET2-E03.17 TET2-E03.18 TET2-E03.19 TET2-E03.20 TET2-E03.21 TET2-E03.21 TET2-E03.21 TET2-E03.22	gDNA           gDNA	CCARCITACCURAC CCCTCTCTGCCTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGTGTTCACAGAGA TGTGGAAATCACCAAATGGC TGTGGAAAACTACCAAATGGC TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCGGCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TCCTGATACCATCACCTCC ACCAGTGGCACCTCTTCA AAGCCAGAATAACCGCACAG AGAAGGCGAACCTACTCACA CGAGGGGAATAAAACGCACAG AGGAAGGGGAAAAGTGCTTAAT TGCTACAGTTCCCGC CCCAGGAATAAAACGCACAG AGGAGGGGAAAAGTGCTAAT GCTACAGTTTCTGCCTCTT AGAGTGGTTCCATTGCGG CTGTGAGATCACTCACCACA CTAGGGGAACCACACA TCAAGGCAAACTCGTGTGC TCCTGTGAGATCACCTCCC TCCTGTGAGATCACTCACCCCT CAACACTCACGGAACCACAA TCAAGGCAAACTCGGGG CTGTGAGATCCCGATCACCCCA CTACACTCACGGGAACCACAA TCAAGGCAAACTCGGGACCACAA TCAAGGCAAACTCGAGGACACACA ATAGAGGGTAAACCGCACA ATAGAGGGTAAACCCGAGGACAA TGCAGACACCCCAAGCACAA	ITIGIGUCICLAGIT GITIGITIACTIGIGUCICAGIT AATAGCAGCCICACATIGC AGTGAGTGCAGTIGITTACC CATACAAGTIGGAAATITCTGGG ACTAGGCAGGGAGAATITCTGGG ACTAGGCAGGGAGGATGITIT CAGAGGGTGGCTAGCGG GCCAGATATCAACTGITACAGAA ACCCGACAAGGAGAGACAG TCCGCAAATGACTGGCAT TCCGCAAAGGACGCCATTGGTAT CCCATTCCCCATAAGATICAGA AAAGAGTGCCACTTGGTGT GCAAACACTIGGAATACCCT AGCCTTTGGCTTGGTGTTCA CTTGGCTTCCCCGAAGTTA GGTGAAATCTTTACTGCATTTC TTCCCCCTGCGCAGTTA GGTGAAATCTTTACTGCATTTC TTCCCCCCGACAGGC CAGGGTAGGGT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.03 TET2-E03.04 TET2-E03.05 TET2-E03.06 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.10 TET2-E03.10 TET2-E03.11 TET2-E03.12 TET2-E03.15 TET2-E03.15 TET2-E03.16 TET2-E03.19 TET2-E03.20 TET2-E03.21 TET2-E03.21 TET2-E03.21 TET2-E03.23 TET2	gDNA           gDNA	CLAGCACIGACIGAC CCCTCTCTGCCTTTCTCC AAGAAAGATTGCACTCCAGG TGGGAAATCACAAATGGC TTGTGGAAATCACCAAATGGC TTGTGGAAAAGTCCCAATGGA TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTGGGGTCC ACCCTGATTACTGGTTTCCA CCTCCCTGCCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTGTGGG TTCCTGATACCATCACCTCC ACCAGTGGCACTGTTGGA TGCAGGAATAAACGCACAG AGAAGAGGGAAAATGCGTGTGA TGGAGGAATAAAACGCACAG AGAAGAGGGAAAATGCGTGTGA TGCTGATACCTACCTCC ACCAGTGGCACTCTTCAA AAGCCAGAATAGTCGTGTGA TGGAGGGAAAATGCGTGATA TGCTGATACTGGGCCACAG AGAAGAGGGAAAATGCAGTTAAAG AGGAGGGGAAAATGCAGTTAAAG AGGAGGGGAAAATGCAGTTAAAG AGGAGGGGAAAAGTCGTAAT TGCTACAGTTTCCTGCCTCTT AGATTGTGTTCCATTGCGG CTGTGAGATCCAGTGACCCAT GCGATGATGCTGATAATGC TAACATCCAGGGAACCACAA TCAAGCAAAGCTCAGTGCC TACCACGTAACTCGAGGC CTACACACAAGACTCAACCA ATCAGGGTAAACCTGAGGC CTACACACAAGACTCAACCA ATGAGGGTAAACCTGAGGC CTACACACCAAAGGACACACA ATAGAGGGTAAACCTGAGGC CTACACACACACACACA TGCAGGAAAACCCCAAGCAT ATTCTGAAGGGTCGAGCACA ATGCAGGGTCGACCACA ATGCAGGGTCGACCACA	InterforceCreater GittrigtThAACTITIGTCGC AATAAGCAGCCTCACATTGC CATACAAGTTGGAAATTTCTGGG ACTAGCGCGTGGAAATTTCTGGG GCCAAGGGTGGGAATTTTT CAAGAGGATGGCAAGGCAG GCCAGATATCAACTGTTACAGAA ATCCGACAATGACTGGTAACAGA CCCGCAAATGACTGGTATACAGAA ATCCGACAATGACTGGTATT CTCATTTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGAATACCCT AGCCTTTGGGCTGGCTGT GCAAACACTTGGAATACCCT AGCCTTTGGTCTGGTTTCA CTTGGCTTACCCCGAAGTTA GGTGAAATCTTTAACTGCATTTCC TTTCCCCTGGTGGTGTTCCA TGAGATGTGGTTTTCTGCAC CAGAGTTACGCGATCCCT AGAGTGGGTTTTCTGCAC CAGAGTTACACCGGG CATCATCACCAGCGC CAGAGTTACCCCGATCC TGGGCATACTCCAATACGGG GGGGGGAGAAAGAAGCAAT TTGGTTACTTGGTGGGG GGCCCAGGTATCTCCACTAC GGGGGGTAACCTCTAT TGGAAATGTTGGCCGC TTGGAAATGCTGCCGG GAGGGGGAGAAAGAAGCAAT TTGGTAACTGGTGTGGGG GGCCCAGGTTACCCCCGAC TGGGGGTTACCCCCTAT TGGAACGTTTGCCCCG TGGGGGTTACCCCCCAC CACAGGGTTACCCCCGAC TTGGAAGTTTGGTCGCG CACCAGTATTGCCCCGG GCCCCAGGTTACCCCCAC CACAGGGTTACCCCCCAC CACAGGTTTGCCCCGG GCCCCAGGTATCTCGACTGGC CACCAGTATTGCCCCGG CCCCCGGGGGGAGAAAGAAGCAAT TTGGGAATCCGCCTGG CCCCGTGTGTTTGCCCCG TTGGGGGTTCGCCCTGG CCACGTGTTGTCCCCGG CCACGTGTTGTCCCCGG CCACGGGGGGGGGCCCCCCCCCC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.06 TET2-E03.06 TET2-E03.07 TET2-E03.08 TET2-E03.10 TET2-E03.12 TET2-E03.12 TET2-E03.12 TET2-E03.14 TET2-E03.15 TET2-E03.16 TET2-E03.17 TET2-E03.19 TET2-E03.20 TET2-E03.21 TET2-E03.21 TET2-E03.24	gDNA           gDNA	CCATCITIGACCITIC CCTCITIGACCITIC AAGAAAGATTGCACTCCAGG TGACAGTGTGTTCACAAATGGC TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCAATGGA TCTATGAAGTGTTGGGTTCC ACCCTGATTACTGGTTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCAACCTGTTGA TGGAGGAATAATGCCGTGTGA TGGAGGAATAATGCCGTGTGA TGGAGGAATAAACGCACAG AGAAGGGGAAAATGCCATT TGCTACAGTTCCGCCCTT AGGAGGGAAAATGCCATT TGCTACAGTTCCGCCCTT AGGAGGGAAAATGCCATTGC TAACATCCAGGGAACCACAA TCAAGCAAGCTAACTCGAGC CTGTGATGATCCTCATGCG CTGTGATGATCCGCACAA TCAAGCAAAGCTCAACTCACCCAT CCTCATAAGGCACACCAA TCAAGCAAAGCTCACTCACCCAT CCTCATACCATGCCCAT CCTCATACCATGCGGGC CTGTGATGCTGATGCTGAT TCCTTTTCTGCCACCTACCCA CTACACCAAGTACACCA ATAGAGGGTAAACCTGAGCC CTACACATGCAGGGACAA TGCAAGACTGCAGGGACAA CTACACCCCAAGCTAACCCA TACACCCCAAGCTAACTGCACA ATTCGAACACCTCAAGCACA ATTCGAACACCTCAAGCCCT CTACACATGCAGGCCC TAACAACCTGCAAGCCCC TAACAACCTGCAAGCCCC TAACAACCTGCAAGCCCC TAACAACCTGCAAGCCCC TAACAACCTGCAAGCCCC TAACAACCTGCAAGCCCC TAACACCTGCAAGCCCC TAACAACCTGCAAGCCCC TAACCAACAATCCCCCA CCCCCAACAACCTCCCCCA CCCCCCAACCAA	ITIGIGUELIACITAGTI GITTIGITIAACTTIGIGIGG AATAGCAGCCTCACATIGC AGTGAGTGGAAATITCIGGG ACTAGGCGIGGGATGITITT CAAGAGGATGGCTAGCG GCCAGATATCAACTGTTACAGAA ACTCCGACAAGTAGAGAGACAG TCCGACAAGTAGAGAGACAG TCCGACAAGTGAGAGACAG CCGCAAATGACTIGGTATT CCATITCCCCATAAAGATICAGA AAAGAGTGCCACTIGGTG GCAAAACACTTGGAATACCCT AGCCTITIGGTCTGGTTCA CTTGCCTTACCCCGAAGTTA GGTGAAATCTTTAACTGCATTTC TTCCCCCTCGCCCGATC TCACCCCGACAGTTA GGTGAAATCTTTAACTGCATTTC TTCCCCCTGCGTGCG CATCACTGGGTGTGTCCA TGAGATGGGTTTCTGCAC CAGAGTTAGAGGTCGTGGG GAGGGGAGAAAGAGCGAT TGGCTACTCCAGGG GGCCAGGTTACCCCGA GGCGAGACAGTCATGGGG GCCCCAGGTTACCCCGA GGCGAGACAGTCGTGCG GCCCCAGGTTACCCCGA GGCCAGGTTACCCCGA CAGAGTTGGCTCGTGGG GCCCCAGGTTACCCCGA CAGAGTCGGTGTCCGAC CACAGTCGTGCTCCAC CAGAGTTACCCCGAGG GCCCCAGGTTACCCCGAC CACAGTCTGGCCCCCGA CACAGTCCGTGTCCCAC CACAGATCCGTGTCCCCG TGGCCAGGTTACCCCCGA CACAGTCCGCGC CACCAGGTTACCCCCGAC CACAGGTCCCCCCCCCC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E02 NRAS-E03.01 TET2-E03.02 TET2-E03.03 TET2-E03.06 TET2-E03.06 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.10 TET2-E03.10 TET2-E03.12 TET2-E03.13 TET2-E03.14 TET2-E03.14 TET2-E03.14 TET2-E03.15 TET2-E03.18 TET2-E03.19 TET2-E03.20 TET2-E03.21 TET2-E03.21 TET2-E03.22 TET2-E03.23 TET2-E03.24 TET2-E0	gDNA           gDNA	CCARCITACUTICS CCCTCTCTGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGGTTCACAAATGGC TGTGGAAATCACCAAATGGC TGTGGAAAAGTCCCAATGGA TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGCTGCTCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTTGTG TTCTGATACCATCACCTCC ACCAAGTGGCACCTCTGTG TGGAGGAATAAAACGCACAG AGGAGGGGAAAAGTGCTTACAA AAGCCAGAATAGTCGTGTGA TGGAGGAATAAAACGCACAG AGGAGGGGAAAAGTGCTATAT TGCTACAGTTCCCCTTT AGGAGGAAAAATGCCGTTGTA TGCTACAGTTCCCCCTT AGGAGGGAAAAATGCGTGTAAT TGCTACAGTTCCCCCCTT AGATGGGTCAACCTCCCTT AGATGGTCACCACCACA CCTGATGCCCCCCCTT AGATGAGTCACTCACCCCA CCTGAGAGATCACTCAGGG CCCCAAGAAAATGCCGTGTC TTCCTTTCGCCCCCCTT AGATGGGTCAACTCGAGGC CTGTGAGAGCCCAGAA TCAAGCCAAGGTAACTCGAGGC CTCACAAGGAAACGCACAA TCAAGCCAAGGTAACCTGAGGC CTCACAGGGAAACCCCACAA TCAAGCCAAGC	THIGHOLE LACHAGTT GITHGITHAACTITGIGTGGC AATAGCAGCCTCACATIGC AGTGAGTGCAGTTGTTACC CATACAAGTTGGAAATITCTGGG ACTAGGCAGGGATAGTTTTTC CAGAGGGTGGCTAGGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGAGCAG TCCGCACAGTGAGCTGCGTT CCGCTATAAGACTTCAGA AAGAGTGCCACTTGGTGT GCAAATGCCCTATAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTTGGTCTCAC GGTGAAATCCTCAGCAGTTA GGTGAAATCTTTACTGCATTTC TTCCCCCTCGCTCATTC TTCACCCCCGAGGTA GGTGAAATCTTTACTGCATTTC TTCCCCCTCGGCTCATTC TTCACCCCGAGGTA GGGGAAATCTTTACTGCATTTC TTCCCCCTCGGCTCATTC TTCACCCCGAGGTA GGGGAGAAGCAGGC CATCATCAGCATCACAGGC CAGCGTTAGAGGTCTGTGCG CATCATCAGCATCACAGGC TGGGCATATCTCAAAAACTGATT CTTGCAAATTGCTGCCG GCCCAAGGTTTACCCTCA TGGGTAGGGGTTCTCGACA CAGAGTTAGGGGTTGCCG GCCCAAGGTTTGCCCTG GGTGAACGTCGTGGGG GCCCAAGGTTTGCCAC CACAGGTTAGGCTCCCCG GGTGCAGGTTGCCCCTG GGTGCGGGGGAAAGGAAGCAAT TTGTGTTACTGAGAGTGCCCCG CCAGGGTATCTCGACAT GGTGGTCCGGGGGGGCCCCCCCCCC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.03 TET2-E03.04 TET2-E03.05 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.10 TET2-E03.10 TET2-E03.11 TET2-E03.12 TET2-E03.13 TET2-E03.14 TET2-E03.15 TET2-E03.15 TET2-E03.16 TET2-E03.19 TET2-E03.20 TET2-E03.21 TET2-E03.23 TET2-E03.24 TET2-E03.24 TET2-E03.25 TET2	gDNA           gDNA	CLAGCAACIGACUGAC CCCTCTCTGCCTTTCTCC AAGAAAGATTGCACTCCAGG TGGGAAATCACCAAATGGC TTGTGGAAATCACCAAATGGC TTGTGGAAAGTCTCAAAT TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTGGGGTCC ACCCTGATTACTGGTTTCCA CCTCCCTGCCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTGTGGG TTCCTGATACCATCACCTCC ACCAGTGGCACCTGTGGA CGCAGGAATAAACGCACGG AGAAGAGGGAAAATGCGTGTGA TGGAGGAATAAAACGCACAG AGAAGAGGGAAAATGCAGTTAAAG AGGAGGGGAAAATGCAGTTAAAG AGGAGGGGAAAATGCAGTTAAAG AGGAGGGGAAAATGCAGTTAAAG AGAAGGCTAACTTCGGG CCCAAGAATAGTCGTGTGA TGGAGGGAAAATGCAGTTAAAG AGGAGGGGAAAATGCAGTTAAAG AGAAGGGGAAAATGCAGTTAAAG AGAAGGCTAACTTCGGGG CCCAAGATCCTGCGG CTGTGAGATCACTACCCAT GCTGATGCTGGATACCCAT CACACTCCAGGGAACCACAA TCAAGCCCAAGCTCAACCCA TCACAGCTCAGCGACCACA ACCCCAACAAGTCAGCCC CTACACAGTGAGCCCC TCAACAGTGCAGCCCA ACCCCACAGGGACAACACACA ATGCAGGGTAAACCTGAGGC CTATCAAGCTCAGCGACCACA TGCAGGGTCAACCCCAT GCTGATGCAGCACCCA CTCCAACAGTGCAGCCCC TAACAAGCGCAGCACCACA TGCAGGGTCAACCCCAT CGATGAAGACCCCAAGCACA ATGCAGGGTCAACCCCAT CGCATGAAGCTCAGGGACAA TGCAGAACCCCCAAGCACA ATGCAGAACCCCCAACACCC CTAACAAGCTCGAGGACCAC CTCCCAACAATGCAGCCCC TAACAAGCTCGAGGACCACA CGCCCAACAATGCAGCCCC TAACAAGCTCGAGGCCCC TAACAAGCTCAAGCACCA ACCCCCAACAATCCACCGCCC CTAACAAGCTCAAGCACCA ACCCCCAACAATCCACCGCCC CTAACAACCTCAAGCACCACA CCCCCAACAATCCACCGCCC CTAACAACCTCAACCCCA CCCCCAACAATCCACCCC CTAACAACCTCAACCCCC CTAACAACCTCAACCCCA CCCCCAACAATCCACCCC CCCAACAACACCCCC CTAACAACCTCAACCCCC CCCAACAACCCCC CCCAACAACCCCCC CCCAACAA	ITIGIGUELACITAGT GITTIGITIAACTTIGIGIGG AATAGCAGCCTCACATIGC AGTGAGTGCAGTIGGTAAC CATACAGCTGGAATTITTGGG GAAAGTGGAAATTICTGGG GCCAGGTGGGATGTITTT CAAGAGGATGGAAGAGACAG GCCAGATATCAACTGTTACAGAA ATCCGACAATGACTGTTACAGAA ATCCGACAATGACTGGTATACAGA ATCCGACAATGACTGGTAGGAG CCCAGCAGTGGAGAGACAG CCCATACGGCATGGAGAGACAG CCCATACGGCATGGAGAGACAG CCCATACGGAATGACCT AGACATTGGGATTGGTG GCAAACACTGGAGATACCCT AGCCTTIGGGCTGGCTGTGC CTGGCTACCCCGAAGTTA GGTGAAATCTTTAACTGCATTTC TTTCCCCTGGTGGTTTCCA TGAGATGGGTTTCCAC CAGAGTTAGAGGTCTGTGCG CATCATCAGCAGTCGCATTC TGGACAATGCTGGTGGGC CATCATCAGCAGTCAGGC TGGGGGAGAAAGAAGCAAT TTGGTAACTGGGTTGCCGG GAGGGGGAGAAAGAAGCAAT TTGGTAACTGGTGTGGGG GGCCCAGGTATCCCCTAT TGGAACGTTTGGTGGGG GGCCTAGGCATTGCCCTG TGGGAGTATCTCGACAT GTGTCCTGTAGCTCCCAC CCACAGTAGCGCTTGGCG CCCCAGGTTACCCCCAC CCACAGTAGCGCTTGGGG GGCCTAGCGCTTGGCG CCCCAGGTTACCCCCAC CCACAGTATCGGGTGGGG GGCCTAGCCTCCAC CCACGTGTTGCTGCGC TTAGATGGGATTCCGCTG TTGGAGGGTTCCGCCTGG CCACGTGTTGCTGGAGGC CCCCGGGGGAGAAAGAGGC CCCCGGGTTTTGGAGAGTC CCACGTGTTTGGAGAGTC CCACGTGTTTGGAGAGTC CCACGTGTTTGGAGAGTC CCACGTGTTTGGAGAGTGC CCACGTGTTTGGAGAGTGC CCACGTGTTTGGAGAGTGC CCACGTGTTTGGAGAGTGC CCACGTGTTTGGAGAGTGC CCACGTGTTTGGAGAGTGC CCACGTGTTTGGAGAGTGC CCACGTGTTTGGAGAGTGC CCACGTGTTTGGAGAGTGC CCACGTGTTGCCGC CCACGTGTTTGGAGAGTGC CCACGTGTTGCCGC CCACGTGTTTGGAGAGTGC
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.04 TET2-E03.06 TET2-E03.06 TET2-E03.07 TET2-E03.08 TET2-E03.10 TET2-E03.10 TET2-E03.12 TET2-E03.12 TET2-E03.14 TET2-E03.15 TET2-E03.16 TET2-E03.16 TET2-E03.17 TET2-E03.18 TET2-E03.19 TET2-E03.20 TET2-E03.21 TET2-E03.21 TET2-E03.22 TET2-E03.23 TET2-E03.24 TET2-E03.26 TET2-E0	gDNA           gDNA	CCARCHACURAC CCCTCTCTGCCTTTCCC AAGAAAGATTGCACTCCAGG TGACAGTGGTTCACAAATGGC TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCAATGGA TCTATGAAGTGTTGAGTTCCA ACCTGATTACTGGTTGCA CCTCCCTGCTCCCTTAC AGATGGTGAAACCTGTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCAACCTGTTGA TGGAGGAATAAACGCACAG AGAAGGGGAAACTCGGTGA TGGAGGAATAATGTCGTGTGA TGGAGGAATAATGCCGTGTGA TGGAGGAATAATGCCGTGTGA TGGAGGAATAAACGCACAG AGAAGGGGAAAAGTGCTAAT TGCTACAGTTTCTGCCTCTT AGATGGGAAACCTCGTTCA CCAAGGAATAGTCGTGTAA TGCTACAGTTTCTGCCTCTT AGATGGGAAACTCGCTAT TGCTACAGGAACACCTCAAT TCCTTTCTGCCACTAGCGC CTGTGAGATCACTCAGGGA CCCAAGAAAGCCGAACCACAA TCAAGCAAAGCTAACTGCGTAAT TCCTTTCTGCCACTAGCGC CTGTGAGATCACTCAGGGACCACAA TCAAGCAAAGCTCAACTCACCAA CCCCAACCAAAGCTCACCAA TCAAGCAAAGCTCAACCAA ATAGAGGGAAAACCTGAGGC CTACACATGTATGCCAGGACCACA ATAGAGGGTCGAGACCACA ATAGAGGGTCGAGACCACA ATAGAGGGTCGAGACCACA ATCCGAACACCTCAAGCAT ATTCTGAAGGCTCGAGGACAA TGCAAGGTCGAAGCCCC TAATGAAGGCTCACCCA CCCCAACCAAAACCCCCA CCCCAACCAAAACCCCCA CCCCAACCAAACCCCCAA CCCCCAACCCAAAGCCCC TAACAACTCCAAGCACAC CTACCCAACCCCCAAGCAC CTACCCAACCCCCAAGCAC CTACCCAACCCCCCAGCAC CTACCCAACCCCCAAGCAC CTACCCAACCCCCCAGCAC CTACCCAACCCCCCAGCAC CTACCCAACCCCCCAGCAC CTACCCAACCCCCCAGCAC CTACCCAACCCCCCAGCAC CCCCAACCAACCCCCCC CTACACCTCCAACCCCC CTACCCAACCACACGCAC CCCCCAACCAACCCCCACACCCC CTACCCAACCACACGCAC CCCCCAACCAACCCCCACCCC CCCCAACCAA	ITIGIGUCICAGIT GITIGITIAACTTIGIGIGG AAATAGCAGCCTCACATIGC AGTGAGTGGAAATITCIGGG ACTAGGCGIGGATGITITACC CAAGAGGATGGCAAATITCIGGG ACTAGGCGIGGGATGITITT CAAGAGGATGCTAGCGG GCCAGATATCAACTGITACAGAA ACCCGACAAGTGAGAGACAG TCCGGCAAATGACTGCTATT CTCATITCCCCATAAAGATICAGA AAAGAGTGCCACTIGGTGT GCAAAACACTTGGAATACCCT AGCCTITIGGTCTGGTA GCGAAATGATCACCGATTA GGTGAAATCTITAACTGCATTTC TITCCCCTCCCCCAAGTA GGTGAAATCTTTAACTGCATTTC TITCCCCTCGCTCCATTC TICACCCCGAGGTTACCCCA AGGGTAACTCTGAGATACCCT AGGCTACCCCGAAGTTA GGTGAAATCTTTACTGCATTTC TITCCCCCTGCGTCGATTC TITCCCCTCGCTCCATTC CAGGATGGGTTTCTGCAC CAGAGTTAGAGGTCTGTGCG CATCATCAGCATCACAGGC TGGGCATATCTCAAAAACTGGAT CTGGCACAATGCTGTGGG GAGGGGGAGAAAGAAGCAAT TTGTTACTTCGACACGG GCCTCAGGTTTACCCCCGA CAGAGTTAGCCTCCTGA GGCCTCAGGTTTCCCAC CAGAGTTCGCACTGGG GCCCCAGGTTACCCCCGA CACAGATCCCGTGTGGG CCCCAGGTTTACCCCTGAT CGGACAGTCCCCTGG CCCCAGGTTTACCCCTGG CCCCAGGTTTCGCAC CAGGGTATCCTCCAC CAGAGATCCCGTGTGGG CCCCCAGGTTTCCCAC CAGAGATCCCGTGGG CCCCCAGGTTTCCCCG TGGCCCAGGTTTCCCCCG CCCCGGGCGAGAAAGAAGCAAT TTGTGCCCTGTGGCCCCCG CCCCCGGGCCCCCG CCCCCGGGCTCCCCAC CAGGGGAGAAAAGAAGCAAT CTGGCTCTGAGGTTCCCCTG CCCCCGTGTTGTTGCCCCG CCCCCGGGCCCCCG CCCCCGGGTTTCCCCCG CCCCCGGGCTTGCCCCCG CCCCCGTGGTTCCCCCG CCCCCGGGCGGAGAAGAAGCAAT CCCCCTTGGCACCCCGAC CAGCGTGTGTTCCCCCG CCCCCGTGCTTGGGC CCCCCGGGCGGG
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 TET2-E03.02 TET2-E03.04 TET2-E03.04 TET2-E03.05 TET2-E03.06 TET2-E03.07 TET2-E03.08 TET2-E03.10 TET2-E03.10 TET2-E03.12 TET2-E03.13 TET2-E03.13 TET2-E03.14 TET2-E03.15 TET2-E03.15 TET2-E03.17 TET2-E03.17 TET2-E03.17 TET2-E03.17 TET2-E03.17 TET2-E03.21 TET2-E03.21 TET2-E03.21 TET2-E03.22 TET2-E03.26 TET2-E03.26 TET2-E03.27	gDNA           gDNA	CCARCITAGECETITEC CCTCTCTGECTITTETCC AAGAAAGATTGCACTCCAGG TGACAGTGGTTCACAAATGGC TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGCA CCTCCCCGCTCCCTAC AGATGGTGAAACCTGTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCACACCTGTGA TGGAGGAATAACGCACG AGGAGGGAAACGTGACACGGG GCCCAAGAATAGTCGTGTGA TGGAGGAAAAGTGCTATAT TGCTACAGTTCCGCCCCTT AGGAGGGAAAAGTGCTAAT TGCTACAGTTCCACCCCCT CTCCCGCCCCTTC AGGAGGGAAAAGTGCTAAT TGCTACAGTTCCGCCCCTT AGGATGATCACTCACGGG CTCTTGGCACCCCCCTT AGATGGTGACCCCCCT CTACAGCAAGATAGTCCGTGTC TCCTTTTCGCCCCCCAT GCCCAAGAAAGCCCACACA TCAAGCAAGGCCAGGAACACCCCACA CCCAAGCAAGCCCACACA TCAAGCAAAGCCCAGGACCACA TCAAGCAAAGCCCACACA CCCCAAGCAAAGCCCACACA TCAAGCAAAGCCCACACA TCAAGCAAAGCCCAGGGACCACA TCAAGCAAAGCCCCACACA TCAAGCAAAGCCCAGGACCACA TCACACCAAGAAACCCCACAC TCACACAAGCTCAGGACCCC CTACACAAGTAGCCCCC CTACACAAGTAGCCCCACACA TGTCAGGACACCCCAGGGC CTCACACAAAGCCCCCAGGACAC TGTCAGAGCCCCCCAGGC CTACACAAGCTCACGCCC TACACACCCCCAAGCACA TGCCCAACACCCCCAGGACCAC TGCCCAACACACCCCCC TACACCCCCCAAGCACACA TGCCCAACACCCCCAAGCCC TACACCCCCCAAGCACACA CCCCCCCCCC	ITIGIGUECIACITAGTI GITIGITIAACTTIGGIGG AAATAGCAGCCTCACATIGC AGTGAGTGCAGTIGGITAACT CAAGAGGAGGGAAATITCIGGG ACTAGGCAGGGAAATITCIGGG ACTAGGCAGGGAGGATGITIT CAAGAGGATGGCTAGGCG GCCAGATATCAACTGITACAGAA ATCCGACAAGTGAGAGACAG TCCGACAAGGACGCTGGTA CCGCAAATGACTTGGTAT CCGCTATAAGACTTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTITIGGTCTGGTCA CTIGGCTTACCCCGAAGTTA GGTGAAATCTTTAACTGCATTTC TTCACCCCCGAGGTA GGGGAAATCCTTAACGCATTTC TTCACCCCCGAGGTA GGGGAAATCTTTACTGCATTTC TTCACCCCGAGGTTACCGCA CAGGGTGGGTTCTGGCG CATCATCAGCATCACGGC CAGGGTGAGCTCGCGG CATCATCAGCATCACAGGC TGGGCATATCCCAAAAACTGATT CTTGGCTTACCCCGAAGCAA TTGTGTTACTGCAGCG GCCCCAGGTTTACCCCGA GGGAGAAGAAGAAGCAAT TTGTGTTACTTGGAGGG GCCCCAGGTTTGCCCCG TGGGACAATGCCCTGAT GGGAACAGTCGTGTCGG GCCCCAGGTTACCCCGAC CACAGGTTACCCCGAGGC CCCCGAGGTTCCGACA CAAGATCCGTGTGCGC CACAGGTTACCCCCGAT GGGACAATCGCCTGAC CGCTGAGGTTCCGACAT GTGGACCGCTGTGGG CCAGGGTTCCGACAT GGGACCATCGTGTGCCG CCAGGGTTTCCGACAT GTGGACCGCCTGTACC CAGCGTGTTCTGACAT GTGGACCGCCTGTACC CAGCGTGTTGTGGAGGTC CCCGTGTGTTGGAGAGTGC CCCGTGTTGTGGAGAAGGAA CAAGGTCCCCGTAACC CAGCGTGTTCTGAAAATGAA CCCGTTGTGTGAAAATGCAT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.03 TET2-E03.03 TET2-E03.04 TET2-E03.04 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.10 TET2-E03.10 TET2-E03.11 TET2-E03.12 TET2-E03.13 TET2-E03.14 TET2-E03.15 TET2-E03.15 TET2-E03.19 TET2-E03.20 TET2-E03.21 TET2-E03.23 TET2-E03.24 TET2-E03.27 TET2-E03.28	gDNA           gDNA	CLAGCAACTGACUTACCAAGA CCCTCTCTGCCTTTCCC AAGAAAGATTGCACTCCAGG TGGGAAATCACCAAATGGC TTGTGGAAATCACCAAATGGC TTGTGGAAAGTCCCAATGGA TCTATGAAGTGTGGGGTCCAAAT TGTGGAAAAGTCCCAATGGA TCTATGAAGTGTGGTGCCA ACCCTGATTACTGGTTTCCA CCTCCCTGCCCCCTTAC AGATGGTGAAACCTGTTTGTT TAGAGGGCAGCCTGTGG TTCCTGGATACCACCTCC ACCAGTGGCACTGTTGCA CCCAGAGGAATAAAACGCACAG AGAAGAGGGAAAAGTGCTAAT TGCTGACAGCATCACTCCG CCCCAGGGAATAGTCGTGTGA AGGAGGGGAAAAGTGCTAAT TGCTACAGTTTCCATCCCC TCCCGGCCCCTT AGATGGTTTCCATTGCGG CCCCAAGAAAATGCAGTTAAAG AGGAGGGGAAAAGTGCTAAT TGCTACAGTTTCCATTGCGG CCCAAGCAAGCTGCAGACCACA TCAAGCAAGCTCAGTGACCCCAT GCTGAGAATGCCGGATAATGC TCAAGCAAGCTCAGTGACCCCAT CCCAACCAAGCTCAGTACCCCA TCCAAGCCAAG	ITIGIGUELIAGIT GITTIGITIAACTITIGIGIGG AATAGCAGCCTCACATIGC AGTGAGTGCAGTIGGTTACC CATACAAGTIGGAAATITICTGGG ACTAGCGGGGGAGATITITT CAAGAGGATGGAAAGTTACGG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGAGACAG CCCGCAAATGACTGGTAGT CCGCAAATGACTGGTAGT CCGCAAATGACTGGTAGT CCGCAAATGACTGGTAGT CCGCAAATGACTGGTAGT CCGCAAATGACTGGTAGT CCGCAAATGACTGGAGTACCCT AGACATTGGGATACCCT AGCCTITIGGTCTGGTGT GCAAACCTTGGAATACCCT AGCCTTIGGTGTGTGTCA CTIGGCTTACCCCGAAGTTA GGTGAAATCTTTAACTGCATTTC TTTCCCCTGCTGCTGTCC CTGGCATATCCCAGCGC CAGAGTTAGGGGTTTCCCA TGAGATGTGGTTTCCAC CGGCAATGGGTTTCCCAC CAGAGTTAGGGGTTTCCCAC CAGAGTTAGCGCGGG GAGGGGAGAAAGAAGCGAT CTIGCAAATGCTGCGG GAGGGGGAGAAAGAAGCAAT TTGTGTTACTTGGTGGGGG GCCCCAGGTTACCCCTAT TGGAACAGTCGTGTGGGGG GGCCTCAGGTTGTCGACT CTGCAGGTTTGCCCCTG TGGCATTGTCGACTGCC CACAGGTCCGTGTGGCC CACGGGGAGAAGAAGCGAT TTGGTTACCTGCTGGG CCCAGGTTACCCCCCAC CCAGGTTACCCCCTAT TGGAACAGTCGTGTGGGG CCCAGGTTTGCCGCTGG CCCAGGTTTGCCCCTGG CCCAGGTTTGCCCCTGG CCCAGGTTTGGCGCCTCGC CCGCTGTGTTGGAGCTCCCG CAGCGGGAAACGCCTTGGG CCAGGTGTTTGGAGGAGCC CCGCTGTGTTTGGAGAAGTGC CCGCTGTGTTTGGAGAAGTGC CCGCTGTGTTTGGAGAAGGC CCGCTGTGTTGGAGAAGGC CCGCTGTGTTGGAGGAGCG CCGCTGTGTTGGAGAAGGC CCGCTGTGTTTGGAGAAGGC CCGCTGTGTTGGAGAAGTGC CCGCTGTGTTGGAGAAGTGC TCTGCCGCTTTGGCGCTGTTA TTGCTGGGTTTGGAGGGGAGAA CCTGTTGAGGGTGCGCT CCGCTGTGTTGAGGGGAGAAT
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.01 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.04 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.07 TET2-E03.08 TET2-E03.07 TET2-E03.10 TET2-E03.10 TET2-E03.12 TET2-E03.12 TET2-E03.14 TET2-E03.15 TET2-E03.16 TET2-E03.16 TET2-E03.20 TET2-E03.20 TET2-E03.21 TET2-E03.22 TET2-E03.24 TET2-E03.28 TET2-E03.28 TET2-E03.29 TET2-E03.28 TET2-E03.29 TET2-E03.29 TET2-E03.29 TET2-E03.28 TET2-E03.29 TET2-E03.29 TET2-E03.29 TET2-E03.28 TET2-E03.29 TET2-E0	gDNA           gDNA	CLAGCACITACUBLE CCTCTCTGCCTTTTCTCC AAGAAAGATTGCACTCCAGG TGACAGTGGTGTTCACAAATGC TGTGGAAATCACCAAATGGC TTGTGGAAAGTCCCAAATGGA TGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCCAATGGA CCTACGAGTGGGGTCCAAC ACCCTGCTGCTCCCTTAC ACCCTGGTGAAACCTGTTGTT TAGAGGGCAGCCCTTGTGG TTCCTGATACCATCACCTCC ACCAGTGGCAACCCTGTGGA TGGAGGAATAAACGCACAG AGAAGGGGAAACTCGTTGA TGGAGGAATAAACGCACAG AGAAGGGGAAACTCGTTGA TGGAGGAATAAAACGCACAG AGAAGGGGAAAAGTGCTAAT TGCTACAGTTTCTGCCTCTT AGATGGGAACCTCATTCGGG CCCAAGAATAGTCGTGTAA TGCTACAGTTTCTGCCTCTT AGATGGGAACCTCATTCGGG CCCAAGAATAGTCGTGTAAT TGCTACAGTTTCTGCCTCTT AGATGGGAACACCTCAATGCC TAACATCCAGGGAACCACAA TCAAGCAAAGCTCAATGCC TAACATCCAGGGAACCACAA TCAAGCAAAGCTCAATGCC TAACATCCAGGGAACCACAA ACCCCCAAGCCAAG	ITIGIGUECIACITAGTI GITTIGITIAACTTIGIGUEGE AAATAGCAGCCTCACATIGC AGTGAGTGGAAATTGTITACC CATACAAGTIGGAAATTTCTGGG ACTAGGCGIGGATGTTGATACGGG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG TCCGCACAAGTGAGAGACAG CCCGCAAATGACTTGGTATT CTCATTTCCCCATAAAGATTCAGA AAAGAGTGCCACTTGGTGT GCAAACACTTGGAATACCCT AGCCTTTGGTCTGGTGT GCAAACACTTGGAATACCCT AGCCTTTGGTCTGCCCCATTC CTTGCCTACCCCGAAGTTA GGTGAAATCTTTAACTGCATTTCC TTCCCCTCGCTCGTCC TTCACCCGTGGTGTGTCCA CAGAGTTAGGGGTTGTGCGC CATCATCAGCATCACAGGC TGGGCATATCTCAAAACTGGAC CAGAGTTAGCCGCGG GAGGGGGAGAAAGAAGCAAT TTGTGTACTCCGAGTTGGCG GCCTCAGGTTTACCCCTG TGGCACATGCTCGCGC GCCTCAGGTTTACCCCTG TGGCACATGCTCCCGAC CAGAGTTCGCCCCGAC CACAGTCATGCCCCGAC CAGAGTTACCCCGAGC CGCCCAGGTTTACCCCTGG GCCTCAGGTTTCCCCGG GCCTCAGGTTTCCCCGG GCCTCAGGTTTCCCCGG GCCCCAGGTTTCCCAC CACAGTCATTGCCCTGG GCCCCAGGTTTCGCACC CAGGGTATCCCCCGAC CACGTGTGTGTGCCCCCG TGGCCATTCGCACCTCAT TGGAACAGTCCTCCAC CACAGTCTTGGCCCTGG CCCCCGGTGTTGTGCCCCG TGCTGTGAGGTTTCGGACAT CTGCTGTGTGTGCCCTGG CCAGTGTTTTGGAGAAGTGC CCAGTGTTTTGGAGAAGTGC TCGCCTCTGTGACCTG TCGCCTGTGTGCCGCTGTACCT GGTCTGTTTGGAGAAGTGC CCGCCCAGGGAGAAGAACGACT TTGCTGTGTTGTGCCGCTGTTA TTGCTGGTTTGAGGGAGTC CCGCCTGTTGTGACATGCC TCGCCCTGTTGAGCCTGTACCT GGTCTGTTTGGAGAAGTGC CCGCCCAGGATTCCCGTGTTA CTGCTGTTGTGCCCGGTTACCCTG CTGCCTCTTGTGAGAGTGC CCGCCGTTGGGCCAAAGAGGGAGTC CCGCCCGCGTGTTTGAGGGAGTC CCGCCCGCGTGTGCCG CCGCCGGTGTTTGAGGGAGTC CCGCCCGTGTTTGAGGGAGGACG CCGCCGCAGGTATCCCCTGTTA CTGCTGTTGTGCCGCGTGTACCTT GGTCGTTTGGAGAAGGCC CCGCCGCGGTGTGTGCC TTGGCCGCTGGGCC CCGCCGGTGTGTGCCG CCGCCGGGGGGGAGAAGTGC CCGCCGGGTGTGTGCCG CCGCCGGGGGGGGGG
DNMT3A-E23.02 FLT3-E20.01 FLT3-E20.02 IDH1-E04.X IDH2-E04.01 IDH2-E04.02 NPM1-E11 NRAS-E03.01 NRAS-E03.01 NRAS-E03.02 TET2-E03.02 TET2-E03.03 TET2-E03.04 TET2-E03.04 TET2-E03.05 TET2-E03.06 TET2-E03.07 TET2-E03.08 TET2-E03.09 TET2-E03.10 TET2-E03.12 TET2-E03.12 TET2-E03.13 TET2-E03.14 TET2-E03.15 TET2-E03.15 TET2-E03.16 TET2-E03.17 TET2-E03.17 TET2-E03.21 TET2-E03.21 TET2-E03.21 TET2-E03.21 TET2-E03.22 TET2-E03.23 TET2-E03.24 TET2-E03.26 TET2-E03.27 TET2-E03.28 TET2-E03.29 TET2-E03.29 TET2-E03.20 TET2-E03.29 TET2-E03.20 TET2-E03.29 TET2-E03.20 TET2-E03.29 TET2-E03.20 TET2-E03.29 TET2-E03.20 TET2-E03.20 TET2-E03.20 TET2-E03.21 TET2-E03.25 TET2-E03.26 TET2-E03.29 TET2-E03.20 TET2-E03.20 TET2-E03.29 TET2-E03.20 TET2-E0	gDNA           gDNA	CCARCHACTARCECTER CCCTCTCTGACCTITIC AAGAAAGATTGCACTCCAGG TGACAGTGGTTCACAAATGGC TGTGGAAATCACCAAATGGC TGTGGAAAGTCCCAATGGA TGTGGAAAGTCCCAATGGA TCTATGAAGTGTTGTGGTTCC ACCCTGATTACTGGTTGGTTCC ACCCTGGCTGCACCCCTTAC AGATGGTGAAACCTGTTGTT TAGAGGGCAGCCTTGTGG TTCCTGATACCATCACCTCC ACCAAGTGGCAACCCTGTGG TGCGAGAATAGTCGTGTGA TGGAGGAATAGTCGTGTGA TGGAGGAATAGTCGTGTGA TGGAGGAATAGTCGTGTGA TGGAGGGAAATGCCGTTAAT TGCTACAGTTACTGCGGG GCCCAAGAAATGCCGTTAAT TGCTACAGTTCCTCCC AGGAGGGAAAAGTCCCTAT TGCTACAGTTCCCCCCTT AGGATGGAACCCCCCT TCCTTGCCACCCCAG CCCAAGAAATGCCAGTAATGC TAACATCCAGGGAACCACAA TCAAGCCAAGTCACTCACCCAG ACCAAGTGACCCCACG CTGTGAGATCACTCACCCAT GCTGACGACCCAGGAACCACAA TCAAGCAAAGCCCAGAACGCCC CTACAAGTAGCCCAGGGACCACAA TCAAGCAAAGCCCAGGAACCACA ACCCCCAAGAAACTCAGCCCT CTACACTTGCAGGGACCACAA TGTCAGGGTCAACCTGAGGC CTACACATGCCCAGGGACAA TGTCAAGGCTCAACTGAGGC CTACACATGCCCCAAGGACCACAA TGTCAAGACTGCAGGGACAA TGTCAAGGCTCAACCGCA CCCCAACCAAAACCCGCA CCCCAACCAAAACCTCAGCCAT ACCCCCAACCAAACCGCCC TACCAAGATGAACCTGAGGC CTACCAAGAACCTCAAGCAT ATCTGAAAGCTCCAGGGACAA TGGATGAATGAACCTGAGGC CCCCAACCAAAACCTGCCAT ACCCCCAACAAAACCTGCCAT ACCCCCAACAAAACCTGCCAT ACCCCCAACAAAACCCGCA CCCCAACCAAAACCCCCACA ACCCCCAACAAAACCCCCC	ITIGIGUECIACITAGTI GITTIGITIAACTTIGIGIGG AAATAGCAGCCTCACATIGC AGTGAGTGGAAGTIGITTACC CATACAAGTIGGAAATITCIGGG ACTAGGCAGGGATGGTITTT CAGAGAGGATGGCTAGGCG GCCAGATATCAACTGTTACAGAA ATCCGACAAGTGAGAGACAG TCCGGACAAGTGACTGGTAT CCGATATCAACTGGTATACAGAA ATCCGACAAGTGAGAGACAG TCCGGACAAGTGACTGGTAT CCCATTCCCCATAAGAGTTCAGA AAAGAGTGCCACTIGGTGT GCAAACCTTGGAATACCCT AGCGTTTGGTCTGGTTCA CTTGGCTTACCCCGAAGTTA GGTGAAATCTTTAACTGCATTTC TTCACCCCGAGAGTA GGTGAAATCTTTAACTGCATTTC TTCACCCCGAGGTA GGGGAAATCCTGGAGTCA CAGGGTGGGTTTCGCAC CAGAGTGGGTTTCGCAC CAGAGTTAGAGGTCTGTGCG CATCATCAGCATCACAGGC TGGGCATATCTCAAAAACTGATT CTTGGCTACGTGG GGGACAATCGTGGG GGCCTAGGTTTCGGCG GGCCAGGTTACGCGG GGCCAGGTTACGCGG GGCCCAGGTTAGGGGG GCCCCAGGTTAGGCGC CAGGGGGAGAAAGAAGCAAT TTGTGTTACTGGAGAGCACT GTGGACAGTCCTGTGCG CACGGGGGAGAAAGAAGCAAT TTGGGTTACGGCTGTGCG CCCCAGGTTTCCGACAT GTGGCCAGGTTCCGACAT GTGGCCAGGTTCCGACAT GTGGGCGAGAAGGAAGGCACT CTGGCCTGTGTTGGCCC CAGCGTGTTCTGACAT GTGTGGCCCCGTAGCT CGGTCGTGGTGCTGCCG CCCCGGTGTTCTGACAT GTGTGGCCACGGTACCC CAGCTGTGTTGTGGAGGTC CCAGGTGTTCTGAAATGAA CCCGTTGGAGAGGAGGC CCCGTGGTTGTGGAGAGTGC CCGGTGTTTGGACGTGG GGTCGTTTGGAGAGTGCTG CCGGTGTTGTGGCCCGTGTTA TTGGGTGGCCACGTGTCG GTGTGTTGGCCCCGTGTTA TTGGGTGGCCAAGGAATGAAC CCGGTGGTTGTGGCCGCTGTTA TTGGGCAAAGGACGCAT CTGGCCTTTGGCCACGTTGG CCCCAGGCCATTGG CCCCAGGCCAAGGAATGACC ACCTCCCCCAGCCCTTGG

TET2-E03.32	gDNA	CAAATGGGACTGGAGGAAGT	TTGGGTCTTGTTTCCTGCAA
TET2-E03 33	gDNA	TGCAAAATACAGGTTTCTTGTT	TTATATCCCTGTAGAACTGAAGC
TET2 E02 24	gDNA	TECREGANACAGACCCANA	TEACCAGACATATETTEETTE
TET2-E03.34	gDNA		
TET2-E03.35	gDNA	ATGTGATCCCAAAGCAAGAT	GGICIGAGIGIGACIICCIC
TET2-E03.36	gDNA	AGCTTCAGTTCTACAGGGAT	GTTTGCTGCTGTTCTTGCTT
TET2-E03.37	gDNA	TGACCAGGGAGGAAGTCA	GTTCCACCTTAATTGGCCTG
TET2-E03.38	gDNA	CCCCAGAAGGACACTCAAA	TGCTTAGTTACCTTTTTCCATGT
TET2-E03.39	gDNA	GAAGCAAGAACAGCAGCAAA	TTGCTGCACATTATCACAGC
TET2-E03 40	gDNA	ACAGGCCAATTAAGGTGGAA	TGTGATTTGAGAGTAAGAGCCT
TET2 E03.10	gDNA		
TET2-E03.41	#DNA		
TET2-E03.42	gDNA		
TET2-E03.43	gDNA	CTGCAGAACTTGATAGCCAC	CATCTGCAAGATGGGAAATCA
TET2-E03.44	gDNA	ACAGCTGCTTCTGTTCTCAA	TCCCATATCTGAAGATAAATTTGC
TET2-E04	gDNA	TGTGGATGTAGCCTTTATATTTAGTA	ATAAACGTTAATCTGCCCTGT
TET2-E05	gDNA	TGCCTCTTGAATTCATTTGC	CAAAATGCCCAAGATTTAAGACC
TET2-E06.01	gDNA	TGTTTTGTTTTGGTTGGGGT	TCCGAGTAGAGTTTGTCAGC
TET2-E06.02	σDNA	GAAGCAGCAGTGAAGAAGA	ΔΟΤΟΤΤΟΔΤΤΟΔΑΘΘΟΔΟΔΟ
TET2 E06.02	gDNA	GECTECASTEATTECATTC	
TET2-E00.03	#DNA	GOCTOCACTOCATIONATIC	
TET2-E07.01	gDNA		
TET2-E07.02	gDNA		
TET2-E08	gDNA	GGAATAATCTAACTGATAGTCTCTTTT	AAGTTGTTACAATTGCTGCC
TET2-E09.01	gDNA	TTTTTAAAGTTCTAAATGGTCTAAATACTA	ATGTGCTGCCATTCTGC
TET2-E09.02	gDNA	TGAACACAGAGCACCAGAG	ACAGCTGCTAAGCTGTCC
TET2-E09.03	gDNA	CTGCATGTTTGGACTTCTGT	CCTCATTTGCCTTCAGCTAT
TET2-E10.01	σDNA	ACACACACGTTTCTTTGGG	TCAGTACCTGAATGGCACC
TET2 E10.01	aDNA	TECHCEANAACCTEACCATE	CTCCACCTTTCTTCCCTT
TET2 E10.02	SDNA SDNA		
TET2-E10.03	BDINA		
TET2-E10.04	gDNA	TGCCGACAAAGGAAACTAGA	ATACCACACACACATTTATCTAC
TET2-E11.01	gDNA	CATCAACATCAAAGATACCTGTTT	GATTGGTGGATCCAGAAGCA
TET2-E11.02	gDNA	ACCCTGTCCACAGAACTTTT	ACTAACTGGATTGGGCCG
TET2-E11.03	gDNA	CCAGCAGCAGAGAGAC	AGCTTGAGATGAGGTGGAAT
TET2-E11 04	gDNA	CAATCCATACATGAGACGGC	CACTGATAGGTTTCCATTGCAT
TET2_E11.05		TCAAGCTGCAGGTTCATATT	ΔΤΔΓΔ6ΔΤΓΓΩΑΤΓ6ΔΓΤΓ6ΔΘ
TET2-E11.05			
TETZ-EII.06	gDNA		
TET2-E11.07	gDNA	TCCCCATATCTGGGTTCCTA	ACAACTGCTGAAACCATCTC
TET2-E11.08	gDNA	GTATCCAAGCCAAGACCCT	GAAGTGGCCATCCATCTCA
TET2-E11.09	gDNA	TACACTTTACCAGCCAAGGT	TTGGATTGCTCAGATTGGGT
TET2-E11.10	gDNA	CAGGGAGATGGTTTCAGC	TGATGTTCACCATTTTTATAGTCCA
TFT2-F11.11	gDNA	ATGGATGGCCACTTCATGG	CATTAGCTGTGTGGGAAAGC
TET2-E11 12	σDNA	ΤΘΘΟΔΟΓΓΑΓΓΤΑΘΑΤΤΑ	CATGGTTAAGAGCTGGAAGC
TET2 E11.12	aDNA	CETCAACATCATTCACCETCE	
TET2-E11.15	gDNA		GACCATTAGCATCACTTAATTIGT
TET2-E11.14	gDNA		GACCAGACCICAICGIIGI
TET2-E11.15	gDNA	AGAACTGCTTGTGTCCAAGG	ATTGACCCATGAGTTGGAGC
TET2-E11.16	gDNA	TGCTAATGGTCAGGAAAAGC	GCTCACGCTTTGCACAC
TET2-E11.17	gDNA	ACAACGATGAGGTCTGGTC	CTGGTAAAAGACGAGGGAGA
TET2-E11.18	gDNA	GATCCTGACATTGGGGGAG	GGGCTTTTTCAGCCATTTTG
TFT2-F11.19	gDNA	CAAAGCGTGAGCTGCAT	CTGGGCCATACTTTCACAC
TET2-E11 20		CCCTCGTCTTTTACCAGCAT	GAGACTTGATGAAACGCAGG
TET2-E11.20	#DNA		
TET2-E11.21	gDNA		
TET2-E11.22	gDNA	CATGAAACTTCAGAGCCCAC	ACCAACAAAAGGGGGTGATA
TET2-E11.23	gDNA	GACCACAGACTCCACAGTAA	CTGGTGAGCTGAGGTTTTTC
TP53-E04.01	gDNA	ACAACGTTCTGGTAAGGACA	GAACCATTGTTCAATATCGTCC
TP53-E04.02	gDNA	CTGACTGCTCTTTTCACCCA	GAAGATGACAGGGGCCAG
TP53-E04.03	gDNA	TGGATGATTTGATGCTGTCC	TAGCTGCCCTGGTAGGTTT
TP53-E04.04	gDNA	CAGCAGCTCCTACACCG	CAAAAGAAATGCAGGGGGAT
TDE2 E0E 01	gDNA		
TP53-E05.01	#DNA	TOTOCCOLORCITICARCI	
TD52 505 02	BDINA		
TP53-E05.03	gDNA	GCAGCTGTGGGTTGATTC	CCTGGGCAACCAGCC
TP53-E06.01	gDNA	CTGGTTGCCCAGGGTC	CCAGAGACCCCAGTTGC
TP53-E06.02	gDNA	CTCCTCAGCATCTTATCCGA	CAGCAGGAGAAAGCCCC
TP53-E07	gDNA	CTGGCCTCATCTTGGGC	CAGGCCAGTGTGCAGG
TP53-E08	gDNA	GGACAGGTAGGACCTGATTT	TCTCCTCCACCGCTTCT
TP53-E09	gDNA	TTATGCCTCAGATTCACTTTTATC	GCATTTTGAGTGTTAGACTGG
TP53-F10.01	gDNA	GGTACTTGAAGTGCAGTTTCT	CTGGCTCCTTCCCAGC
TDE2 E10.01	aDNA		
TD52 544	BDINA		
TP53-E11	gDNA	TGATGTCATCTCTCCCCCT	AGGCTGTCAGTGGGGAA
WT1-E02	gDNA	GCTGACACTGTGCTTCTCT	GAGGAGGATAGCACGGAAG
WT1-E03	gDNA	CTTGGGGCGCACTCG	GTCCCAAGGACCCAGAC
WT1-E04	gDNA	TGTGGTTATGTGTTTCTAACTCTA	ACTGTGGAAAGGCAATGGAA
WT1-E05	gDNA	GGGCTTTTCACTGGATTCTG	GCCTACGCCATTTGCTTTG
WT1-E06	gDNA	CATTTCCAAATGGCGACTGT	GGTAAGTAGGAAGAGGCAGT
WT1-E07 01	gDNA	CTCCCTCAAGACCTACGTG	TGCATCTGTAAGTGGGACAG
WT1_E07.02	aDNA		GAACCATGTTTGCCCAAGA
WT1-EU/.UZ	BUNA		
W11-E08	gDNA	GAGAGGI (GCCTTTAATGAGA	
WT1-E09	gDNA	CACTGTGCCCACATTGTT	CTCTCATCACAATTTCATTCCAC
WT1-E10.01	gDNA	CAGGGACAGAATGATGGGAA	ATGTTGTGATGGCGGACTAA
WT1-E10.02	gDNA	GTCAACAGGTGAAAAGCCC	GGAGTGGAGAGTCAGACTTG
ASXL1-E13.01	gDNA	GGTCAGATCACCCAGTCAGT	GTCCAACTGTAGCCCTCTGT
ASXL1-F13 02	gDNA	GGACCTGCCTTCTCTGAGA	TCTGGATTCTGGTTTGGGCT
ASYL1_E13 02	aDNA	CCAAGGCTCTCGTTTCTAACAG	CATACTICGAGACACCCAGCT
ACVL1 F12 04	aDNA		
ASALI-E13.04	guna .		
ASXL1-E13.05	gDNA	ALAAATCCCATTACATCCTCTAGG	LILGGGGTAATTTCCAGAAGG
ASXL1-E13.06	gDNA	TGCCGAGAACAGGAAAGCTA	TTTTGGGGGAAGGCAAGAGT
ASXL1-FE13.01	cDNA	AAGCCACAGCCCACTAAAGA	GTCCAACTGTAGCCCTCTGT
ASXL1-FE13.02	cDNA	GGACCTGCCTTCTCTGAGA	TCTGGATTCTGGTTTGGGCT
ASXL1-FE13.03	cDNA	CCAAGGCTCTCGTTTCTAACAG	CATACTCGAGACACCCAGCT
0			

ASYL1_EE13 04	CDNA	ACATGCGTCTGGTTACAAGG	AGCACGGACTTCCTTCTGAT
ASXL1 FE13.04	-DNA		
ASALI-FEIS.05	CDNA	IGGATICCAAAGAGCAGTICICITC	
ASXL1-FE13.06	cDNA	ACAGGAAAGCTACTGGGCATAGTC	CAAGAGTGCTCCTGCCTAAAGAGT
CEBPA-E01.01	gDNA	GCCATGCCGGGAGAACT	CCCGGGTAGTCAAAGTCG
CEBPA-E01.02	gDNA	CCTTCAACGACGAGTTCCTG	CGGCTGGTAAGGGAAGAGG
CERPA-E01 03		GAGGAGGATGAAGCCAAGC	CTCGTTGCTGTTCTTGTCCA
CEDIA E01.05			
CEBPA-E01.04	gDNA	TGGLAGLGLGLTLAAG	LLAGGGLGGTLLLALA
CEBPA-FE01.01	cDNA	GCCATGCCGGGAGAACT	CCCGGGTAGTCAAAGTCG
CEBPA-FE01.02	cDNA	CCTTCAACGACGAGTTCCTG	CGGCTGGTAAGGGAAGAGG
CEBPA-EE01.03	cDNA	GAGGAGGATGAAGCCAAGC	CTCGTTGCTGTTCTTGTCCA
CEBPA-EE01 04	CDNA	TEECVECECECTCAAE	CLAGGGCGGTCCCACA
CEBFA-TEO1.04	-DNA		
DNM13A-E07	gDNA	IICCIGGAGAGGICAAGGIG	TGGAGAGAGAGAGAGAGAG
DNMT3A-E08	gDNA	GCCTCGTGACCACTGTGTAA	ACCCACCAGGGCAGAGTAG
DNMT3A-E09	gDNA	CTCCTCTTTGCATCGGGTAA	ACCTGCACTCCAACTTCCAG
DNMT3A-E10	gDNA	TGTGCCACCCTCACTACTCA	TCCCTAAGCATGGCTTTCC
DNMT2A_F11F12		GACCTTGGCACCTGCTTTC	CCACACTAGGAGTGCCAGAGTT
DNIVIT3A-E13	gDNA	GGTLALAGTGLLTLLLTTT	ACCUTGTACATGCCCAGAAG
DNMT3A-E14	gDNA	CACAGGCAGATGAGGTTTCC	CCCAGCTAAGGAGACCACTG
DNMT3A-E15	gDNA	CCCTAGCCATGCTCCAGAC	CCCACAACCAAGGCTCAG
DNMT3A-E16	gDNA	CAGGGTGTGTGGGTCTAGGA	TGCATACGTTTCCACTTCACA
DNMT3A-F17	gDNA	AAAGATAGGACTTGGGCCTACA	CTGCCTCCAGGTGCTGAG
DNIMT2A E19	aDNA.		
DINIVITSA-E18	gDNA		
DNMT3A-E19	gDNA	GACAGCTATTCCCGATGACC	GCTCCACAATGCAGATGAGA
DNMT3A-E20	gDNA	TGTGTGGCTCCTGAGAGAGA	CATGGCAGAGCAGCTAGTCA
DNMT3A-E21	gDNA	TGGTGGATTTGTGTCTTTGC	CATCCTGCCCTTCCTTCTC
DNMT3A-F22	σDNA	CTGCGAACTCTGCTCACTCA	ΔΟΓΑΔΟΓΑΓΑΟΓΑΔΤΓΑΘΑΔ
DNMT3A 522	aDNA		
DIVIVITOR-E23	BUINA		
DNMT3A-FE06-08	CUNA	GGGGGACCCCTACTACATCA	LLIGGLLACCAGGAGAAG
DNMT3A-FE07-09	cDNA	GTGGCTACCACGCCTGAG	GACCTCGTAGATGGCTTTGC
DNMT3A-FE08-11	cDNA	GTTCGGAGACGGCAAATTCT	AGGTTCCACCCACATGTCC
DNMT3A-FF10-14	cDNA	GGGGCTTCCAGCCTTCT	CGTCGTCGTCGTACTGGT
DNIMT2A FE12 16	«DNIA		CCCACACCTCCCTAAACCTT
DINIVITSA-FE13-10	CDINA		GGGACAGGTGGGTAAACCTT
DNMT3A-FE15-18	cDNA	GGCACAAGGGTACCTACGG	CCCAATCACCAGATCGAATG
DNMT3A-FE17-20	cDNA	CCAGGGGAAGATCATGTACG	TGCAGCTGACACTTCTTTGG
DNMT3A-FE19-22	cDNA	CCCTTCTTCTGGCTCTTTGA	CTTTCCATTTCAGTGCACCA
DNMT3A-EE21-23	cDNA	CCACTGTGAATGATAAGCTGGA	TIGTGTCGCTACCTCAGTTTG
	«DNIA	CACCTETERANCACACCE	
FLI3-FE10-17	CDNA		
FL13-FE20-22	CDNA	LLGLLAGGAALGIGLIIG	ATGCCAGGGTAAGGATTCACACC
IDH1-E04	gDNA	AAACTTTGCTTCTAATTTTTCTCTTTC	GCAAAATCACATTATTGCCAAC
IDH1-FE04-05	cDNA	GCTTGTGAGTGGATGGGTAA	TATGTACCAGGTATGTCACCTT
IDH2-E04	ØDNA	TGCAGTGGGACCACTATTATCTC	CACCACTGCCATCTTTTGG
	CDNA		
IDH2-FE03-03	CDINA		
NPM1-FE10-11	cDNA	TCCCAAAGTGGAAGCC	IGGAAAGTTCTCACTCTGC
NRAS-E02	gDNA	GGCCGATATTAATCCGGTGT	TCCGACAAGTGAGAGACAGG
NRAS-E02 NRAS-E03	gDNA gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA
NRAS-E02 NRAS-E03 NRAS-FE02-03	gDNA gDNA cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA
NRAS-E02 NRAS-E03 NRAS-FE02-03 NRAS-EE02-03	gDNA gDNA cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC
NRAS-E02 NRAS-E03 NRAS-FE02-03 NRAS-FE02-03	gDNA gDNA cDNA cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCCTGCCTCATGTA AGGTACATCATCCGAGTCTTTTAC
NRAS-E02 NRAS-E03 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01	gDNA gDNA cDNA cDNA gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC
NRAS-E02 NRAS-E03 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E02	gDNA gDNA cDNA cDNA gDNA gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTATTCCTCTGCAACC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG
NRAS-E02 NRAS-F02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E02 RUNX1-E02 RUNX1-E03	gDNA gDNA cDNA cDNA gDNA gDNA gDNA	GGCCGATATTAATCCGGTGT CCCTCCTGCCCCCTTAC GGGAAAAGCGCACTGACCAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTAGGGTCCTAAC CATTGCTATTCCTCTGCCAACC AAATTCCGGGAGTGTTGTCA	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA
NRAS-E02 NRAS-E03 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E02 RUNX1-E03 RUNX1-E04	gDNA gDNA cDNA gDNA gDNA gDNA gDNA gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATTCCTCTGCAAC CATTGCTATTCCTCGGAACC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCCT	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAGGTGT
NRAS-E02 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E02 RUNX1-E03 RUNX1-E05	gDNA gDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTATTCCTCTGCAACC AAATTCCGGGAGTGTTGTCA TGATCTCTCCCCCCCCT ATTGAACAAGGGCCACTCA	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGGGAAGGTGT AATGTTCTGCCAACTCCTTCA
NRAS-E02 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E02 RUNX1-E03 RUNX1-E03 RUNX1-E04 RUNX1-E05 PUINX1-E05 PUINX1-E05 01	gDNA gDNA cDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACCAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTATTCCTCTGCAACC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCCTCA ATTGCAACAGGGCCACTCA CTCGGCAACCTCCTACTCAC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCGGGAAAGGTGT AATGTTCTGCCAAGCATCGGTA
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06_01	gDNA gDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA g	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATTCCTCTGCAAC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CTCCGCAACCTCCTACTCAC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCCAGTCTTITAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA CCCACCATGGAGAACTGGTA
NRAS-E02 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E02 RUNX1-E03 RUNX1-E04 RUNX1-E05 RUNX1-E05 RUNX1-E06.01 RUNX1-E06.02	gDNA gDNA cDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA g	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTATTCCTCTGCAACC AAATTCCGGGAGTGTTGTCA TGATCTCTCCCCCCCT ATTTGAACAAGGGCCACTCA CTCCGGAACCTCCTACTCAC CCCGTTCCAAGCCAGCTC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG
NRAS-E02 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E02 RUNX1-E03 RUNX1-E04 RUNX1-E05 RUNX1-E06.01 RUNX1-E06.02 RUNX1-FE01-02	gDNA gDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA g	GGCCGATATTAATCCGGTGT CCCTCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTATTCCTCTGCAACC AAATTCCGGGAGTGTTGTCA TGATCTCTCCCTCCCT ATTGAACAAGGGCCACTCA CTCCGCAACCGCCATCCA CCCGTTCCAGCCAGCCC TGCAGGGTCCTAACTCAATC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCAGGTCTTTTAC GGCCTCCGCCTGTCCTC GATTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGCAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG CATTGCCAGCAATCACAGTGAC
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-F01-02           RUNX1-F02-02	gDNA gDNA cDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA cDNA cDNA cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAGGGTCCTAAC CATTGCAGGGGGGTGTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CTCCGCAACCTCCTACTCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAACTCAATC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGGAAAGGTGT AATGTTCTGCCAACACTCTCA CCCACCATGAGAAACTGGTA GCTTGTCGCGAACAGGAG CATTGCCAGCACACAGGAG CATTGCCCAGCCATCACAGTGAAC CTGAGGGTTAAAGGCAGTGGAGT
NRAS-E02 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E02 RUNX1-E03 RUNX1-E04 RUNX1-E05 RUNX1-E05 RUNX1-E06.01 RUNX1-E06.02 RUNX1-FE01-02 RUNX1-FE04-06	gDNA gDNA cDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA g	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTATTCCTCTGCAACC AAATTCCGGGAGTGTTGTCA TGATCTTCCCTCCCTCT ATTGAACAAGGGCCACTCA CTCCGCAACCTCATCCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAATCCATC TTTCAAGGTGGTGCCCTA	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCGGGAAGGTGT AATGTTCTGCCAACTGCTA GCTTGTCGCGAACAGGAG CATTGCCGGAACAGGAG CATTGCCGGAACAGGAG CATTGCCAGCATCACAGTGAC CTGAGGGTTAAAGGCAGTGGAAG CGGCAGGTAGGTGTGGTAG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-F06.02           RUNX1-F06-02           RUNX1-F06-04           RUNX1-F07-04           RUNX1-F06-06           RUNX1-FE05-06	gDNA           gDNA           cDNA           cDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTAATTCCTCGCAACC AAATTCCGGGAGTGTTGTCA TGATCTCTCCCTCCCTC ATTTGAACAAGGGCCACTCA CTCCGCAACCTCCTACTCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAACTCAATC TTTCAAGGTGGTGGCCCTA CCCGGAGCTTGTCCTTTCC CAGGGGCCTTCACTCACTC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCAGGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAGGTGT AATGTTCTGCCAGCACACTGGTA GCCTCGCGAACACGGTA GCTTGTCGCGAACAGGAG CATTGCCAGCCATCACAGTGAC CTGAGGGTTAAAGGCAGTGGTAG CGGCCAGGTAGGTGGTAG GGCCTACAGCGAGATCCTG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-F06.02           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE04-06           RUNX1-FE05-06           RUNX1-FE06-06           RUNX1-FE06-06	gDNA           gDNA           cDNA           cDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           cDNA           gDNA           gDNA           gDNA           gDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAGGGTCCTAAC CATTGCAGGGGTGTTGTCA TGATCTCTTCCCTCCCTC ATTTGAACAAGGGCCACTCA CTCCGCAACCTCCTACTCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGAGCTTGACCTACTC CAGGCGCCTTCACCTACTC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGAGGTG AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG CATTGCCAGCCATCACAGGAG CATTGCCAGCCATCACAGGAG CGCTGCAGGTAGGTGGGTAG TGACCTACAGCGAGATCCTG CTCAGGGGCCCCCACACG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-F06.02           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE04-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06	gDNA gDNA cDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA g	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTATTCCTCTGCAACC AAATTCCGGGAGTGTTGTCA TGATCTTCCCTCCCTCCT ATTGAACAAGGGCCACTCA CTCCGCAACCTCCTACTCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAATCATC TTTCAAGGTGGTGCCCTA CCGGGAGCTTGACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGGGAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG CATTGCCGGAACAGGAG CATTGCCAGCCATCACAGTGAC CTGAGGGTTAAAGGCAGTGGAGT CGGCAGGTAGGTGTGAG GCTGATGGGCATCCGCCCCCCCCC
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-F01-02           RUNX1-F00-06           RUNX1-FE04-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06	gDNA           gDNA           cDNA           cDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAGGGTCCTAAC CATTGCAGGGGGTGTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGGTACCAACCAC CCCGTTCCAGCAGCC CCCGTTCCAGCTGACCCATCC CCGGTGGTGGTGGCCCTA CCGGGGCCTTAACTCAATC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACCGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAACAGGTA GCTTGTCGCGAACAGGAG CCTGACGGAACAGGAG CTGAGGGTTAAAGGCAGTGGAG CGGCCAGCAACGGAGATCCTG CTCAGTAGGGCCTCCACACG TGACCTACAGCGAGATCCTG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E02           RUNX1-E04           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE04-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06-01	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAGGGTCCTAAC CATTCCTCGCGGAGTGTGTCA GATCTCTTCCCTCCCTC ATTTGAACAAGGGCCACTCA CTCCGCAACCTCCTACTCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAACTCATC TTCCAAGCGAGCTC CCGGGAGCTTGCCTTTTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGGAG CAGTGGGCAGGAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTGTGCCGGAACAGGAG CATTGCCAGCCATCACAGGAG CATTGCCAGCCATCACAGGAG CTGAGGGTAAAGGCGAGGT CGGCAGGTAGGTGGGAG TGACCTACAGCGAGATCCTG GTCGATCAGCGAGATCCTG GTCGCTCCAGCGAGATCCTG GTCGCTCCAGCGAGATCCTG GTCGCTCGGTTCAGGGAG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE04-06           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06.01           RUNX1-FE06.01           RUNX1-FE06.01           RUNX1-FE06.01           RUNX1-FE06.02	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTAATCCTGCAACC AAATTCCGGGAGTGTTGTCA TGATCTTCCCTCCCTCCT ATTGAACAAGGGCCACTCA CTCCGCAACCTCATCACC CCCGTTCCAAGCCAGCTC TGCAGGTCCTAATCATC TTTCAAGGTGGTGCCCTA CCGGGAGCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCCTCACCCACCTACTC CCCCTCCCCCCCTCCCCCCCC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGGGAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG CATTGCCAGCCAACAGGAG CATTGCCAGCCAACAGGAG CTTGACGGATAAGGCAGTGGAGT CGGCAGGTAGGTGTGAG GTGACCTACAGCGAGATCCTG GTCGCTCAGCAGGAGCCG GTCGCTCGGTTCGGGAG
NRAS-E02 NRAS-E02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E01 RUNX1-E03 RUNX1-E03 RUNX1-E04 RUNX1-E05 RUNX1-E06.01 RUNX1-FE06.02 RUNX1-FE02-04 RUNX1-FE02-04 RUNX1-FE02-06 RUNX1-FE06-06 RUNX1-FE06-06 RUNX1-FE06-06 RUNX1-FE06-01 RUNX1-FE06.01 RUNX1-FE06.02 TET2-E03.01	gDNA           gDNA           cDNA           cDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAGGGTCCTAAC CATTGCAGGGGGTGTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGGTCCAAGCGGCCCTCA CCCGGTCCAAGCCAGCC TTCCAGGGGCCTAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTCACCTACTC CCAGGCGCCTCACCTACTC CCAGGCGCCTCACCTACTC CCAGGCGCCTCACCTACTC CCAGGCGCCTCACCTACTC CCAGGCGCCTCACCTACTC CCCTCACCACTACTC CCCCTCACCTACTC CTCCTACCACCTGTACTACGG ATTCAACTAGAGGGCAGCCTTG	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACCGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGGAG CAGTTGGTCGGGAAAGGTGT AATGTTCTGCGAACAGGTA GCTTGTCGCGAACAGGTA GCTTGTCGCGAACAGGTAG GCTGTCGCGAACAGGTAG CTGAGCGAGCAGGAGCGGGGG TGACCTACAGCGAGGAGCCTG GTCGCTCAGGCGAGGAGCCTG GTCGCTCAGGCGAGGAGCCTG GTCGCTCAGGCGAGGAGCCTG CTGACTAGGGCGAGGAGCCTG CTGACTAGGGCGAGGAGCCTG CTGACTACAGCGAGGAGCCTG CTGACTACAGCGAGGAGCCTG ACCTGACGGCGAGGAGCCTG CTGACTACGGCGAGGAGCCTG CTGACTACAGCGAGGAGCCTG
NRAS-E02 NRAS-E03 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E02 RUNX1-E04 RUNX1-E04 RUNX1-E05 RUNX1-E06.01 RUNX1-FE06.02 RUNX1-FE02-04 RUNX1-FE02-04 RUNX1-FE06-06 RUNX1-FE06-06 RUNX1-FE06-01 RUNX1-FE06.01 RUNX1-FE06.01 RUNX1-FE06.02 TET2-E03.01 TET2-E03.02	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAGGGTCCTAAC CATTGCAGGGAGTGTTGTCA TGATCTCTCCCCCCCTC ATTGCAACAAGGGCCACTCA CTCCGCAACCTCATCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAACTCATC TTCCAAGCGAGCTC CCGGGAGCTTGCCCTACTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCCGTACCACCTACTC CCCCTACCTACCTC CAGGCGCCTTCACCTACTC CCCCTACCACCTACTC CCCCTCCACCTACTC CCCCTACCACCTACTC CCCCTCCACCTACTC CCCCTCCACCTACTC CCCCTCCACCTGTACTACGG ATTCAACTAGAGGGCACCCTG CAATACCTGTATGAAGGCACCCC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAG CAGTTGGTCAGCCAAGAGGTG AAATGTTCTGCCAACTCCTTCA CCCACCATGGAGAGACTGGTA GCTGTCGCGAACAGGAG CATTGCCAGCCATCACAGGAG CATGCCAGCCATCACAGGAG CGCAGGTAGGTGTGGTAG CGCAGGTAGGGTGGTGGTAG CGCAGGTAGGGGTGGGTGG CGCCTCCAGCGAGATCCTG GTCGCTCCAGCGAGATCCTG GTCGCTCCAGCGGAGATCCTG GTCGCTCCAGCGGAGATCCTG CTGACGTCACAGCGAGATCCTG CTCAGTGGGTTTAGTGCGAG
NRAS-E02 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E01 RUNX1-E03 RUNX1-E03 RUNX1-E04 RUNX1-E06-01 RUNX1-E06-02 RUNX1-FE02-04 RUNX1-FE06-06 RUNX1-FE06-06 RUNX1-FE06-06 RUNX1-FE06-01 RUNX1-FE06-01 RUNX1-FE06-01 RUNX1-FE06-01 RUNX1-FE06-02 TET2-E03.01 TET2-E03.02	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTAATCCTGCAACC AAATTCCGGGAGTGTTGTCA TGATCTTCCCTCCCTCCT ATTGAACAAGGGCCACTCA CTCCGCAACCTCCTACTCAC CCCGTTCCAAGCCAGCTC TGCAGGTCCTAACTCAATC TTTCAAGGTGGTGGCCTA CCGGGAGCTTGACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCTCCCCCCCTCTCCCCCCCCCC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCGGGAAGGTGT AATGTTCTGCCAACTCGTA GCTTGTCGCGAACAGGAG CCATCGCGGAACAGGAG CATTGCCAGCCAACAGGAG CATTGCCAGCCAACAGGAG CCTGAGGGTAAAGGCAGTGGAA CGGCAGGTAGGTGTGGTAG TGACCTACAGCGAGATCCTG GTCGCTCAGGGAGATCCTG GTCGCTCAGGCAGATCCTG GTCGCTCAGGCGAGATCCTG GTCGCTCAGCGGAGATCCTG CTGACCTACAGCGAGATCCTG GTCGCTCTGGTTGGGGAG CTGACCTACAGCGAGATCCTG CTGACCTACAGCGAGATCCTG CTCAGTACGCGAGATCCTG CTGACCTACAGCGAGATCCTG CTGACCTACAGCGAGATCCTG ACTGTGCGTTTGTTCGAA
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE04-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06.01           RUNX1-FE06.02           TET2-E03.02           TET2-E03.03	gDNA           gDNA           cDNA           cDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           gDNA           cDNA           gDNA           gDNA           gDNA           cDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTAGCAGGGTCCTAAC CATTGCAGGGGTGTTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CTCCGCAACCTCATCTCAC CCCGTTCCAGCGCAGCTC TGCAGGGGTGGGCCCCTA CCGGGAGCTTGACCTCATCC CAGGCGCCTTCACCTCATCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGCGCCTTCACCTACTC CTCCTACCACCTGTACTACGG ATTCACCTGTATGAAGGGAAGC TGTAGCCCAAGAAAATGCAG	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGGAG CAGTGGTCTGGGAAGGTGT AATGTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG CATTGCCAGCACACGAGGAG CATTGCCAGCCATCACAGTGAG CTGAGGTTAAAGGCAGTGGAGT CGGCAGGTAGAGGTGTGGTAG TGACCTACAGCGAGATCCTG GTCGCTCAGGCAGAGTCCTG GTCGCTCAGGCGAGATCCTG GTCGCTCAGGCGAGATCCTG CTGACGTCACAGCGAGATCCTG CTGACGTCACAGCGAGATCCTG CTGACGTCACAGCGAGATCCTG CTGACCTACAGCGAGATCCTG CTGACCTACAGCGAGATCCTG CTGACCTACAGCGAGATCCTG CTGACCTACAGCGAGATCCTG CTGACCTACAGCGAGATCCTG CTGACCTACAGCGAGATCCTG CCCACTGCAGTTATGTTGAA TGGGTGAGTGAGTGTCACAGG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06.01           RUNX1-FE06.01           RUNX1-FE06.01           RUNX1-FE06.01           RUNX1-FE06.03           TET2-E03.03           TET2-E03.04	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTAATCTGTCA CATTGCAGGGTCTTAAC CATTGCAGGGGCGTGTGTGCA TGATCTCTCCCCCCCT ATTGAACAAGGGCCACTCA CTCCGCAACCTCATCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAACTCATC TTTCAAGGTGGTGGCCCTA CCGGGAGCTTGCCCTTTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCCGTACCACCTACTC CCCGCAGCCTTCACCTACTC CCCGCAGCCTTCACCTACTC CCCGCAGCCTTCACCTACTC CCCGCAGCCTTCACCTACTC CCCCTACCACCTACTC CCCCTACCACCTACTC CCCCTCACCTACTC CCCCCAGGAGCCTTG GAATACCTGTATGAAGGGAAGC CATCTCACATAAATGCCA	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAG CAGTTGGTCAGCCCAAGGAGG CAGTGGGCTGGGAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTGTGCGGAACAGGAG CATTGCCAGCCATCACAGGAG CATTGCCAGCCATCACAGTGGAG CGGCAGGTAAGGTGTGAG CGGCAGGTAGGTGTGGTAG TGACCTACAGCGAGATCCTG GTCGTCGGGAGCTCCGACG CTGACGTACGGCAGCCCG CTGACGTACGGCAGATCCTG GCCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG CCCACCGGGTTATTCCTCCAT CCCACCGGGTTATTCCTCCAT CCCACCGCGGTTATGGTTGGAA TGGGTGAGTTACGGTGGAG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06.01           RUNX1-FE06.02           TET2-E03.01           TET2-E03.03           TET2-E03.04           TET2-E03.05	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCCCTTACA GCTGTGGTCCTAAATCTGTCC GCTGTGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAGGGGTGTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGGTCCAACTCAATCC CCCGTTCCAGCGGCCCTA CCCGGTCCAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGGCCTTAACTCAATC CAGGCGCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CTCCTACCACTGTC CTCCTACCACTGTACTACGG ATTCAACTAGAGGGCAGCCTTG GAATACCCTGTATGAAGGGAAGC TGTAGCCCAAGAAATGCCAG CATCTCCACTAACTGCCATACCA GAAATAACATCCAGGGAACCA	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTGTTGCCATGAAACCGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCGGGAAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAACAGGAG CCTGACGGACAAGGAG CCTGACGGACAGGAG CTGACGAACAGGAG CTGACGCAACCAGGAG CGCCAGCTACAGCGAGATCCTG CTCAGTAGGGCCTCCACACG TGACCTACAGCGAGAGTCCTG GTCGCTCAGCGAGAGTCCTG CTGACCTACAGCGAGGATCCTG GTCGCTCAGCGAGGATCCTG CTGACCTACAGCGAGGATCCTG CTGACCTACAGCGAGGATCCTG CCCACTACAGCGAGGATCCTG CCCACTACGCGAGGATCCTG CCCACTACGGCGAGGATCCTG CCCACTACGCGAGGATCCTG CCCACTGCGCTTCCACAGG ACCTGCCGCTTCCCCAT CCCACTGCAGTTATGTGTGAA TGGGTGAGTATCGCACG CCCCTCTTTTCACTCCCTTAA
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE04-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.02           TET2-E03.04           TET2-E03.05           TET2-E03.06	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCCCTTAC GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAGGGTCCTAAC CATTGCAGGGGTCTTACA GATCTCTTCCCTGCCAC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCT ATTTGAACAAGGGCCACTCA CTCCGCAACCTCATCAC CCCGTTCCAGCGAGCTC TGCAGGGGTGGCCCCTA CCGGGAGCTTGACCTAATC TTTCAAGGTGGTGGCCCTA CCGGGAGCTTGACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CTCCTACCACCTGTCTC CAGGCGCCTTCACCTACTC CTCCTCACCACTACTC CTCCTCACCAAGAAATGCAG CATCTCCCCAAGAAATGCCAG CATCTCACCATACTCACACACCACCA	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGGGAA CAGTTGGTCGGGAAGGTGT AATGTCTGCCAACTCCTTCA CCCACCATGGAGAGACTGGTA GCTTGTCGCGAACAGGAG CATTGCCAGCCATCACAGTGAG CTGAGGTTAAAGGCAGTGGAG CGCTGCAGGTAGAGGTGGGAG CGCACCTACAGCGAGATCCTG CTCAGTAGGGCCTCCACAGG GTCGCTCAGGCGAGATCCTG GTCGCTCAGGCGAGATCCTG GTCGCTCAGGCGAGATCCTG GTCGCTCAGGCGAGATCCTG CTGACGTCACAGCGAGATCCTG CTCAGTGGGTTTATTCCTCCAT CCCCCTCGAGTTATGTTGAA TGGGTGGAGTGATCTCACAGG AGCTTGCAATTGCTGCTG CCCCTTCGCATTCACTCCTG CCCCTTGCAATTGCTGCTG CCCCTTCAGCTGAATTGCTGCTG CCCCTTCAGCTGCAATTGCTGCTG CCCCTTCAGCTGCAATTGCTGCTG CCCCTTCAGCTGCAATTGCTGCTG CCCCTTCAGCTGCAATTGCTGCTG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-02           RUNX1-FE06-03           RUNX1-FE06-04           RUNX1-FE06-05           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.02           TET2-E03.04           TET2-E03.05           TET2-E03.07	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCCCTTAC GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTAATCTGTCC CATTGCTATTCCTCGCAACC AAATTCCGGGAGTGTTGTCA TGATCTTCCCTCCCTCCT ATTGAACAAGGGCCACTCA CTCCGCAACCTCATCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAACTCATC TTTCAAGGTGGTGGCCCTA CCGGGAGCTTGCCTTTTCC CAGGCGCCTTCACCTACTC CCGGGAGCTTGCCTTTTCC CAGGCGCCTTCACCTACTC CCGGGAGCTTCACCTACTC CCGCGACCTCACCTACTC CCGCGCCTCCACCTACTC CCGGGAGCTTCACCTACTC CCGCGCCTCCACCTACTC CCCGCCTCCACCTACTC CCCGCCCTCCCCTACTC CCCGCCTCCACCTACTC CCCCCTCCCTCC CCCCTCACCTACTC CCCCTCACCTACTC CCCCTCCCCTGTATGAAGGGAAGC CTCTCACCTAGCAGCAG CATCTCACCTAATGCCATTAACA GAAAATAACATCCAGGGAACCA GGAGTTTTAGAAGAACACCACCA	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGGTCTTTAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGCCAGCGAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG CATTGCCAGCCACTCACAGTGAA CGGGAGGTAAAGGCAGTGGAAGT CGGCAGGTAGAGTGTGGTAG CGGCAGGTAGGTGTGGTAG TGACCTACAGCGAGAGTCCTG CTCAGTGGGGCTCCCACACG CTGACGCAGGAGATCCTG GTGACCTACAGCGAGATCCTG GCGCAGGTTTATGTCGCAAC CCCACCGGAGATCCTG CCCACCGCAGTTATGGTTGGAA CGGGCAGGTTATGGTTGGAA CGGCAGGTTATGTTGCAA
NRAS-E02 NRAS-E02-03 NRAS-FE02-03 NRAS-FE02-03 RUNX1-E01 RUNX1-E03 RUNX1-E03 RUNX1-E04 RUNX1-E06.01 RUNX1-E06.02 RUNX1-FE01-02 RUNX1-FE02-04 RUNX1-FE06-06 RUNX1-FE06-06 RUNX1-FE06-06 RUNX1-FE06-06 RUNX1-FE06-01 RUNX1-FE06-01 RUNX1-FE06-01 RUNX1-FE06-02 TET2-E03.01 TET2-E03.02 TET2-E03.03 TET2-E03.05 TET2-E03.07 TET2-E03.07 TET2-E03.07	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCCCTTAC GCTGTGGTCCTAAATCTGTCC GCTGTGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAGGGTCGTGTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGGTCCAACGCAGCC CCCGTTCCAGCGAGCCCTCA CCCGGTCCAAGCTGACC TTCCAGGGGTCGTACCTCAATC TTTCAAGGTGGTGGCCCTA CCGGGGCCTTACCTCACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CCAGGCGCCTCACCTACTC CTCCTACCACGACACTCC CAGCGCCTCCACCTACTC CTCCTACCACGAAATGCAG CATCCACGTGAAATGCAG CATCTCCACAAAATGCCAG CATCTCCACAAAATGCCATCC CAAATAACATCCAGGGAACCA CGACTTTCACCACTGCG	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTGTTGCCATGCAAACCGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCGGGAAAGGTGT AATGTTCTGCCAACTCGTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG CCTGACGGACAGGGAG CTGACCAGCCATCACAGTGAG CGCCAGCTACAGCGAGAGTGGGAG TGACCTACAGCGAGAGTGGTAG TGACCTACAGCGAGAGTCCTG CTCAGTAGGGCCTCCACACG TGACCTACAGCGAGAGTCCTG CTGACCTACAGCGAGAGTCCTG CTGACCTACAGCGAGGATCCTG CTGACCTACAGCGAGGATCCTG CTGACCTACAGCGAGGATCCTG CCCACTACGGCGAGATCCTG CCCACTACGGCGAGATCCTG CCCACTACGGCGAGATCCTG CCCACTGCGGTTTATTCCTCCAT CCCACTGCAGTTATGTGTTGAA TGGGTGGGTATGTGGTGA TGGCCCTCCAGGAGTCCTG CCCCTCTATTCCCCTTAA TCGACCCTTCAGAATCCTTG CCCACTTCAGAATCCTCTG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE04-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06.01           RUNX1-FE06.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.07           TET2-E03.08           TET2-E03.09	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCCCTTAC GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTAGGGGTCCTAAC CATTGCAGGGGTCTTACA TGATCTCTTCCCTGCCA ATTTGAACAAGGGCCACTCA CTCCGCAACCTCCTCCT ATTTGAACAAGGGCCACTCA CCCGTTCCAAGCCAGCC CCGTTCCAAGCCAGCCC CCGGGAGCTTGCCTTACTCAC CCGGGAGCTTGCCTTACTCAC CCGGGAGCTTGCCTTACTCAC CCGGGAGCTTGCCCTACTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CCTCCTCACCAGGAGCAGCCTTG GAATACCTGTATGAAGGAAACC TGTAGCCCAGAAAATGCCA GAAAATAACATCCAGGGAACCA GAAAATAACATCCAGGGAACCA CCACTTCCACAATCACACCAGCA CCACTTCGACAATCACATGGC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTITAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGGAG CAGTGGGTCAGGAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTGTGCGGAACAGGAG CATTGCCAACCACTCACAGGAG CATTGCCAGCCAACACGTGAG CTGAGGTTAAAGGCAGTGGAG CGCTCCAGGGTAGAGGGGTG CGGCAGGTAGAGGGGTGGGAG CTGACGTACAGCGAGATCCTG GTCGCTCAGGGAGATCCTG GTCGCTCAGGGAGATCCTG GTCGCTCAGGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGGTTGGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGGTTGGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCTGGTTCGGGAG CTGACCTACAGCGAGATCCTG CCCACTGCAGTTATGTTGAA TGGGTGAGTGATCTCACAGG AGCTTGCAATTGCTGCTG CCCCTTGCAGTTATGTTGAA TGGGTGAGTGATCTCCCTTAAA
NRAS-E02           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-07           R	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCCCTTAC GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTATTCCTCGCAACC AAATTCCGGGAGTGTTGTCA TGATCTTCCCTCCCTCCT ATTTGAACAAGGGCCACTCA CTCCGCAACCTCATCAC CCCGTTCCAAGCCAGCTC TGCAGGGTGTGGCCCTA CCGGGAGCTTGCCTTTTCC CAGGCGCCTTCACCTACTCA CCGGGAGCTGGTGGCCCTA CCGGGAGCTGTCCACTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCGGAACCTGTACTACTC CTCCTACCACCTACTC CCGGGAGCTTGCCTTTCC CAGGCGCCTTCACCTACTC CCGCGACCTCACCTACTC CTCCTACCACCTACTC CCCCTCACCTACTC CCCCTCACCTACTC CTCCTACCACCTACTC CTCCTACCACCTACTC CTCCTACCACCTACTC CTCCTACCACCTACTC CTCCTACCACCTACTC CCCCTGACGAGGCAGCC CATCTCACCTAATGCAG GAATACCCTGTATGAAGGAAGC CACTCTCACCAAATGCAG GAATTTTGGAAGAACACCACCA CCACTTTTAGAAGAACACCACCA CCCCCCACACACTGGG CCCAGTGTGAAACAGCA	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGGTCTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGCCAGGAGAGGTG AAATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG CATTGCCGCACACCCCTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG CATGTCCGCACACGAGGAG CTGAGGGTAAAGGCAGTGGAAG CGGCAGGTAGAGTGTGGTAG TGACCTACAGCGAGATCCTG GCCAGGCAGGTCCGCACACG CTGACGGAGGTTACGGAG CTGACCTACAGCGAGATCCTG GCCACCTCGGTTCGGCAG CTGACCTACAGCGAGATCCTG CCCACCTGCAGTAGGTCGGAG CTGACCTACAGCGAGATCCTG CCCACCGCAGGTTATGGTTGGAA TGGGCGAGGTAGTGTGGGAG CTGACCTACAGCGAGATCCTG CCCACTGCAGTTATGCTTGAA TGGGCGAGTAGTCTGCCG CCCCTCTATTTCCCCATACGCG CCCCTCTATTTCCCCTTAAA TCGACCCTCAGATCCTCG CCCACCTGCGTGTTCTGGC CCCACCTGGTGTTTCTGCG CCACCTGGGTTGTTTCCCCTTAAA
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE06-02           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.01           TET2-E03.02           TET2-E03.05           TET2-E03.07           TET2-E03.08           TET2-E03.09           TET2-E03.10	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCCCTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTCGCAAC AAATTCCGGGAGTGTTGTCA TGATCCTTTCCCTCCCT ATTTGAACAAGGGCCACTCA CTCCGCAACCTCATCAC CCCGTTCCAGCGAGCCACCA CCCGTTCCAGCGGCCCTA CCGGGGCCTTAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGGCCTTCACTCACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CCGCGGCCTCACCTACTC CCCTGCACCAGAAATGCAG CATCCACCTGATGAAGGGAAGC TGTAGCCCAGGAAAATGCAG GAAATAACCTCCGGGAACCA CCAGTTTTAGAAGAACACCACCA CCAGTTTTGGAACAACATCAATCA CCGCGTTGAACAATCCAGGA CCACTCCCAACAATCCATGG CCCAGTGTGAAACACACTACCA	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACCGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAACAGGAG CCTGTCGGCAACAGGAG CCTGACGGAACAGGAG CTGACGAACAGGAG CTGACGACCAGGAGCAGG CTGACCTACAGCGAGAGTGGAGG TGACCTACAGCGAGAGTCGG GTCGCTCAGGCGAGAGTCGG GTCGCTCAGGCGAGATCCTG CTCAGTAGGGGCTCCACAGG GTCGCTCAGGCGAGATCCTG CTGACTACAGCGAGGATCCTG CTGACTACAGCGAGGATCCTG CCCACTACGGCGAGATCCTG CCCACTGGGTTATATGTGTTGAA TGGGGTGAGTGATGCTGG CCCCTCTTTCACTCCCTTAA TCGACCCTCAGAACTGCGG CCGCCTCTGGTGGGGG CGCCCTCAGGAGATCCTG CCCCTCTTTCAGTCCCCTTAAA TCGACCCTCAGAATTGCTGGG CCCCCTTTTTTCCCCTTAAA TCGACCCTCAGAATCCTTG CCCCCCATTGAGCCCCGTC ACTTGCCCCAGTCCATTG CCCCCTCTGTTGGGCCCGC CCCCCTTTCAGAACTGCTCG CCCCCCATTGACGCCCGTC ACTTCCCCCCGTCCCATTG CCCCCCATTGACGCCCAGTC
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE04-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.08           TET2-E03.10           TET2-E03.11	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTCTGCAAC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CTCCGCAACCTCATCTACTCAC CCCGTTCCAAGCCAGCTC TGCAGGGGCCTTACTCAC CCGGGAGCTTGCACTCAATC TTTCAAGGTGGTGGCCCCTA CCGGGAGCTTGCCTTTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCTCTCACCAGGAGCAGCCTTG GAATACCTGTATGAAGGGAAGC TGTAGCCCAGGAAAATGCCAG GAAAATACATCCAGGGAACCA GAAAATACATCCAGGGAACCA CCACTTTTGGAAGACACCACCA CCACTTTTGGAAGACACCACCA CCACTTTGACACACATACACTGG CCCAGTGTTGAAAACACCACCA CCCATGTTGAAAACACCACCA CCCAGTGTTGAAAACACCACCA CCCATGTTGAAAACACCACCA CCCAGTGTTGAAAACACCACCA CCCATGTTGAAAACACCACCA CCCAGTGTTGAAACAGCA TGGTGAAAATCAGTTCCAAAATCA CTTCTCACCAGGGACTTCAAAATCA CTTCTCACAGGTGCTTCAAG	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCCATGTA AGGTACATCATCCGAGTCTTITAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGGAG CAGTGGGCTGGGAAGGTGT AATGTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTGTGCCGAACACGTGA CATTGCCAACCACTCCTCA CCGACGGTAAAGGCAGGGGAG CATTGCCAGCCATCACAGGAG CTGACGTACAGCGGAGT CGGCAGGTAGAGGGTGGTAG TGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACGTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACGTCACGCGAGATCCTG GTCGCTCGGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTGGGAGA CTGACCTACAGCGAGATCCTG GTCGCTCGGGTTGGTGGAG CGCCTCGCAGTTATGTGTGAA TGGGTGAGTGATCTCACAGG AGCTTGCAATTGCTGCTG CCCCTGCGTTGTGTTGAA TGGGTGAGTGATCTCCCCATCC CCCCTGTGTGTTTTTCCTCCTTAAA TCGACCCTTCAGAATTGCTGCTG CCCCCTGGTTGGTTTTTCTGG TGGACTTACAGCAATGGCCCAGTC ACTGTCGCATTGGTTGGTG CCCCTGTGTGTTTTTCGG TGGCTGGAATGAGCTGTGG CCCGTGAGAACTGAACT
NRAS-E02           NRAS-FE02-03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.08           TET2-E03	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTGCAGGGTCCTAAC CATTGCTAATCCTGCAAC AAATCCGGGAGTGTTGTCA TGATCTTCCCTCCCTC ATTTGAACAAGGGCCACTCA CTCCGCAACCTCATCAC CCCGTTCCAAGCCAGCTC CCGGTCCAAGCAGCTC TGCAGGGTCCTACTCAC CCGGGAGCTTGCCTTTTCC CAGGCGCCTTCACCTACTC CCGGGAGCTTGCCTTTTCC CAGGCGCCTTCACCTACTC CCGGGAGCTTGCCTTTCC CAGGCGCCTTCACCTACTC CCGGGAGCTTCACCTACTC CCCGCACCTCACCT	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCCATGTA AGGTACATCATCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTITGTTGCCACGAGACGTG GAAAGGTTGAACCCAAGGAG CAGTTGGTCAGCCCAAGGAG CAGTTGGCCAGCCCACGCCTCA CCCACCATGGAGAACTGGTA GCTGTCGCGAACACGGAG CATTGCCAGCCACTCCCTCA CCCACCATGGAGAACTGGTA GCTGTCGCGAACAGGAG CATTGCCAGCCATCACAGTGGAG CGGCAGGTAAAGGCAGTGGAG CGGCAGGTAGAGTGTGGAG CGGCAGGTAGAGTGTGGTAG CGGCAGGTAGGTGTGGTAG TGACCTACAGCGAGATCCTG CTCAGTGGGGCTCCCACACG GGCGGCTTATGGCGAGACCTG GCGCCTGGTTCGGGAG CTGACCTACAGCGAGATCCTG CCCACTGCGGTAGGTTCGGAG CTGACCTACAGCGAGATCCTG CCCACTGCGGTTATGTGTGAA TGGGCGAGGTTATGGTTGGAA CGGCTGGCTTCGGCTCCCACAGG AGCTTGCAAATGCTGCTG CCCCTCGGTTCGGGAG CCCCTCTAGTTCGGGAG CCCCTCAAATGCTGCGTG CCCCTCGGTTGGTTCGGG CCCCTCTGGTTCGGGCTGG CCCGCTGGTGTGTTTCTGG CCCACTGCGTGTTTTCTGG CCCGCTGGTGGTTGGTTCGG CCCGCTGGTGGTTGGT
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06.01           RUNX1-FE06.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.09           TET2-E03.10           TET2-E03.11           TET2-E03.13	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCCCTTAC GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTAGCGGGGTCTAAC CATTCGCAGGGGTGTTGTCA TGATCCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CTCCGCCACCTCCTCCT ATTTGAACAAGGGCCACTCA CCCGTTCCAGCCAGCTC TTCCAGGCGGCCTACTCAC CCGGTCCAAGCTACTCAC CCGGTCCAAGCTACTC TTTCAAGGTGGTGGCCCTA CCGGGGCCTTCACCTCACTC CAGGCGCCTTCACCTCACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CTCCTACCACGTACTACG ATTCACATGAGGGCAGCCTTG GAATACCCTGTATGAAGGGAAGC TGTAGCCCAAGAAAATGCAG GAAAATACACTCCAGGGAACCA GAAAATACACTCCAGGGAACCA CCAATTTTGGAAGAGCAATCCACGG CCCATGTTGAAAATCACTGG CCCATGTTGAAAATCACTGG CTCCTCACAACAATCCACTGG CCCATGTTGAAAATCAGTGG TGGTGAAAATCAGTATTCAAAATCA CTTCTCACAACCAAGCCATGGC CTCTCACACAGCAGTGCACAG CTCCTCACAGCAAGCCATGCTG	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTTTAC GGCCTCCGCCTGTCCTC GTTTGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTTGTCGCGAACAGGAG CCTACGGCAACAGGAG CTGACGGTTAAAGCCAGTGGAG TGACCTACAGCGAACAGTGGAG TGACCTACAGCGAGCAGTGGGAG TGACCTACAGCGAGATCCTG GTCGCTTGGGAGAGTCTG GTCGCTCGGGTAGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGGTGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGGTTAGTGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGGTTAGTGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGATTATGTTGAA TGGGTGAGTGATCTCACAGG AGCTTGCAAATTGCTGCTG CCCCTTCAGTTGGGAGTCCTG CCCCTTCAGTTGGGAGTCCTG CCCCTTCAGATCGCTCTG CCCCTTCAGATCCTCTG CCCCTTCAGATCCTCTG CCCCCTCAGATCCTCTG CCCCTTCAGAATGCTCG CCCCTTCAGAATGCTCG CCCCTTCAGAATGCTCGG CCCCTTCAGACCGAGCCCAGTC CCCCTTCAGAACTGGACCTGG CCCCTTCAGACCGAGCTCG CCCCTTGAAACTGAGCTGTGG TGACCTCCCAGTGGCTGC CCCGTTGAAACTGAGCTGGCTGC CCCGTTGAAACTGAGCTGGCTCC CCCGTTGAAACTGAGCTGGC CCCGTTGAAACTGAGCTGC CCCGTTGAAACTGAGCTGC CCCGTTGAAACTGAGCTGGC CCCGTTGAAACTGAGCTGC CCCGTTGAAACTGGAGCTGC CCCGTTGAAACTGAGCTGCC CCCGTTGAAACTGAGCTGCC CCCGTTGAAACTGAGCTGCC CCCGTGAGACTGAGCTGCC CCGGCTGGAGTGGCTGC CCGGCTGCAACTGGAGCTGC CCGGCTGCAACTGAGCTGCC CTGAAGAGGCTTGCCCCTCT
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06.01           RUNX1-FE06.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E03.14	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTGCACAC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCTCA ATTGAACAAGGGCCACTCA CTCCGCAACCTCATCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAACTCATC TTCCAAGCGAGCTC CCGGGAGCTTGCCTTTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGCGCCCTCACCTACTC CTCCTACCACAGAGACAGC TGTACCCCAGAAAATGCAG CATCTCACATAAATGCCATTAACA GAAATACACCCAGGGAACCC GGAGTTTTGAAACACCACGG CCCACGTTCACATACACTGG CCCACGTGTGAAACACCACGA CCCCTCCACAACAATACACTGG CCCACGTGTTGAAACACCACGA CCCTCCACAGGAGCATCCAAACCACCA CCCACGTGTTGAAACACCACGA CCCCTCCACAGCACCACG CCCACGTGTTGAAACACCACGA CCCCACGTCTCCACACGCC CCCACGTGTCGAACACCACGA CCCCACGTCTCCACACGCC CCCACGTCTCACCACGCACCA CCCCACGTCTCCACCACGC CCCACGTCTCCACCACGCC CCCACGTCTCACACACCACGC CCCACGTCTCCACCACCCCCCCCCC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCCATGTA AGGTACATCATCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGAGGG AAAGGTTGAACCCAAGGAG CCACCATGGAGAACTGGTA GCTGTCGCGAACACGTCA CCCACCATGGAGAACTGGTA GCTGTGCCGGACACGGAG CATTGCCAGCCATCACAGTGGAG CATTGCCAGCCATCACAGTGGAG CGCAGGTAAAGGCAGTGGAG CGCAGGTAGGTGTGGTAG CGGCAGGTAGGTGGGAG CTGACGTACAGCGAGATCCTG GTCGCTCGGTTCAGGGAGACTCTG GTCGCTCGGTTCAGGGAGATCCTG GTCGCTGCGGTTATGTGTGAA TGGGTGAGGTATGTGTGAA TGGGTGAGTATGTGTGGAG CCCCTTGCGGACACGTGGGAG CCCCTGCGGTTATGTGTGAA TGGGTGAGTATGCTGCG CCCCTTGCAGCCACTCG CCCCTTGCGGTTCGGGGG CCCCTTGCGTTCGGGGG CCCCTTGCGGTTGTGTGGA CCGCCTGCGGTTAGTGTGGA CCGCCTGCGGTTGTGTGGA CCGCCTGCGGTTGCGCCCCT CCAGCTGCGTGTGGTGGTG CCCCTTGCGGTGGCGCGCCCCACACG CCGCCTGGGTGGTGGTGG CCCCTTATTTCCTCCTTAAA TCGACCCTTCAGGAAGCTGGC CCCCGGAGAAGTGGTGGCAGTC ACTGCGCGTTGCGCTGC CCCGGAGAGAGTGTGGCCAGTC CCCGGAGAGAGGTGTGGCCCGC CCGAAGAAGTGGTGGCGCCCC CTGAAGAAGTGTGTGCGCCCC CTGAAGAAGTGTGTGCGCCCC CTGAAGAAGTGTGTGCGCCCC CTGAAGAAGTGTGTGCGCCCCCCCCCC
NRAS-E02           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.01           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.09           TET2-E03.11           TET2-E03.13           TET2-E03.13	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCTTAC GGGAAAAGCGCCCTTAC GCTGTGTCTAAATCTGTCC GCTGTGTCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAGGGTCGTAAC AAATTCCGGGAGGTGTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGGTCCAACTCAC CCCGTTCCAGCAGCTC TCCAGGGGCCTAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGGCCTTACTCACTC CAGGCGCCTTCACTCACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCCTCTACCACACTACTC CCCCTGTAGAGGGCAGCCTTG GAATACCCTGTATGAAGGGAAGC TGTAGCCCAAGAAATGCAG CATCTCCACAAAATGCCATGG CATCTCCACAACAATACCCACCA CCAATTTTGGTAGCAGTGGA TGACCTCCAAGAACACCACCA CCAATTTTGGTAGCAGTGGA CTCCTCCCAACAACAATCCACGG CCCATGTTGAAACAGCA CCAATTTTAGAAGAACCACCACCA CCCATGTTGAAACAGCA TGGCGAAAATCAGTATTCAAAATCA CTTCTTCCACAGGTGCCTTCAGG TTGACTAAGCAGTGCCAGC	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTATGTA AGGTACATCATCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACCGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCGGGAAAGGTGT AATGTTCTGCCAACTCGTCA CCCACCATGGAACAGGAG CCTGGCGAACAGGAG CCTGACGAACAGGAG CCTGACGAACAGGAG CTGACCAGCCATCACAGTGAG CCTGACGGAGATGGTGGTAG TGACCTACAGCGAGAGTCGG CGCCAGGTAGGTGTGGTAG TGACCTACAGCGAGAGTCGG CTGACTACGGCGAGAGTCGG GTGGCCTCAGTGGGAG CTGACCTACAGCGAGATCCTG CCCACTACGGCGAGATCCTG CCCACTACGGCGAGATCCTG CCCACTACGGCGAGATCCTG CCCACTGGCGTTTATTCCTCCAT CCCACTGCAGGTATGGTGGAA TGGGTGAGTATGGTGTGAA TGGGTGAGTATCTCCCAT CCCACTGCAGTTAGGGCTCCCACG TGACCTCCAGGCAGATCCTG ACCTTCCGGCAGATCCTG CCCCTCTAGTGCGGGAG CCCCCTCTGTCGGGCTGC CCCCCTTAGAACTGCGGC CCCCCTTAGAACTGCGCG CCCCCTCAGGCCACTTG CCCCCCTCAGGCCCCTTG CCCCCCTCAGGCCCCTTG CCCCCCTCAGGCCCCTTG CCCCCCTCAGGCCCCCTTG CCCCCCCCCC
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-05           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-05           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           TET2-E03.00           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E04 <td>gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA</td> <td>GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCCCTTAC GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTCTGCAAC AAATTCCGGGAGTGTTGTCA TGATCCTTTCCCTCCCT ATTTGAACAAGGGCCACTCA CTCCGCAACCTCCTACTCAC CCCGTTCCAGCGGCCCTA TTTCAAGGTGGTGGCCCTA CCCGGTCCAAGCTGACTC TTTCAAGGTGGTGGCCCTA CCGGGCCTTCACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CTCCTCACCACCTACTC CTCCTCACCACCTACTC CTCTCACCACCTACTC GAATACCCTGTATGACGGAAGC TGTAGCCCAAGAAAATGCCAG GAATTTTAGAAGGGACACCAG GAAAATACACTCAGGGAACCA CCCATGTTGAAACACACCACCA CCCATGTTGAAACACACCACCA CCCATGTTGAAACACACCACCA CCCATGTTGAAACACACCACCA CCCATGTTGAAAATCAGTGG TTGCCCAAGAAATCCAGGGATCCA CTCTCCCACAACAATCCACTGG CCCAGTGTTGAAACACCACCA CCCATGTGTGAAACACCACCA CCCATGTTGAAACACCACCA CTCTCCCACAACACATCCACGA TTGACTCACGTGCTTTCAAG TTGACCCAAGCAATCCACTGG TTGACCCAAGCAATCCACTGG TTGACCCCAAGCAATCCACCGCA CCCAGTGTTGAAACACCACCA CCCATGTGTGAAACACCACCA CTTCTCCCACAACCATTCCACGA CTTCTCCCACGTGCTTCAAG TTGACCAAACCCACCCA CCCATGTGTGAAACACCCCCCA CCCATGTGTGAAACCCCCCCA CCCATGTGTGAAACCCCCCCA CCCATGTGTGAAACCCCCCG TTGACCCAAGCAATCCACCGTG TTGACCAAACCCACCCG CCAGTTTTCTAATAGATCACGTG TTGACCAAACCCACCCG CCAGTTTTCTAATAGATCAGCA CTGCCCAATTTCTAAGATCAGCG CCAGTTTCCAAACCCCCCCA CCAATTTCCTACCAAGCCACCCA CCAATTTCCTCCCCCCCACCCA CCAATTTCCACCACCCCCA CCAATTCCACGTGCTTCACCACCCA CCAATTCCACCCCCCCCCC</td> <td>TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTITAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAAGGTGT AATGTTCTGCCAACACTCCTCA CCCACCATGAGAACTGGTA GCTGTCGCGAACAGGAG CATTGCCAGCAACACGGAG CATTGCCAGCACACGAGAG CCATCGCCACACACGTGAG CTGCGGTTAAAGGCAGTGGAG TGACCTACAGCGAGATCCTG CTCAGTGGGTAGGTGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG CCCACTGCAGTTATGTTGAA TGGGTGAGTGATCTCACAGG AGCTTGCAATTGCTGCTG CCCCTCTGCAGTTATGTTGAA TGGGTGAGTGATCTCACAGG AGCTTGCAATTGCTGCTG CCCCTCTAGATTGCTGCTG CCCCTCTAGACCGAGACTCTTG CCCCTCTAGACTGAGCTGCAGC CCCCTTCAGATGGCTCGC CCCCTTGCAATTGCTCCTG CCCCTTGCAATTGCTCCTG CCCCTTGCAATTGCTCCTG CCCCTTGCAATTGCTCCTG CCCCTTGCAATTGCTCCTG CCCCTTGCAATTGCTCCTG CCCCTTGCAACTGAGCCTGG CCCCTTGCAACTGAGCTGC ACTTCCCCAGTGGCTTGC CCCGTTGCAACTGAGCTGC CCCCTTGGAACTGAGCTGC CCCGTTGCAAGTGGCTTGC CTGAAGAGTGTTTGCGCCTC TTATGGACCTTTACAATTGCTGC CCTGTTGCAAGTGGCTGC CCTGTGGAAGTGGTTGC CCTGTTGCAAGTGGCTGC CCTGTGGAAGTGGCTGC CCTGTGGAAGTGGCTGC CCTGTGGAAGTGGCTGC CCTGTGGAAGTGGCTGC CTGAAGGCTGTGCCCCT TTATGGACCTTACAAATTGCTG CCTGTGGAAGGCTGGA GTAATGTTCTTTTAACTGGCCTGG</td>	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCCCTTAC GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTCTGCAAC AAATTCCGGGAGTGTTGTCA TGATCCTTTCCCTCCCT ATTTGAACAAGGGCCACTCA CTCCGCAACCTCCTACTCAC CCCGTTCCAGCGGCCCTA TTTCAAGGTGGTGGCCCTA CCCGGTCCAAGCTGACTC TTTCAAGGTGGTGGCCCTA CCGGGCCTTCACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CTCCTCACCACCTACTC CTCCTCACCACCTACTC CTCTCACCACCTACTC GAATACCCTGTATGACGGAAGC TGTAGCCCAAGAAAATGCCAG GAATTTTAGAAGGGACACCAG GAAAATACACTCAGGGAACCA CCCATGTTGAAACACACCACCA CCCATGTTGAAACACACCACCA CCCATGTTGAAACACACCACCA CCCATGTTGAAACACACCACCA CCCATGTTGAAAATCAGTGG TTGCCCAAGAAATCCAGGGATCCA CTCTCCCACAACAATCCACTGG CCCAGTGTTGAAACACCACCA CCCATGTGTGAAACACCACCA CCCATGTTGAAACACCACCA CTCTCCCACAACACATCCACGA TTGACTCACGTGCTTTCAAG TTGACCCAAGCAATCCACTGG TTGACCCAAGCAATCCACTGG TTGACCCCAAGCAATCCACCGCA CCCAGTGTTGAAACACCACCA CCCATGTGTGAAACACCACCA CTTCTCCCACAACCATTCCACGA CTTCTCCCACGTGCTTCAAG TTGACCAAACCCACCCA CCCATGTGTGAAACACCCCCCA CCCATGTGTGAAACCCCCCCA CCCATGTGTGAAACCCCCCCA CCCATGTGTGAAACCCCCCG TTGACCCAAGCAATCCACCGTG TTGACCAAACCCACCCG CCAGTTTTCTAATAGATCACGTG TTGACCAAACCCACCCG CCAGTTTTCTAATAGATCAGCA CTGCCCAATTTCTAAGATCAGCG CCAGTTTCCAAACCCCCCCA CCAATTTCCTACCAAGCCACCCA CCAATTTCCTCCCCCCCACCCA CCAATTTCCACCACCCCCA CCAATTCCACGTGCTTCACCACCCA CCAATTCCACCCCCCCCCC	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTITAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAAGGTGT AATGTTCTGCCAACACTCCTCA CCCACCATGAGAACTGGTA GCTGTCGCGAACAGGAG CATTGCCAGCAACACGGAG CATTGCCAGCACACGAGAG CCATCGCCACACACGTGAG CTGCGGTTAAAGGCAGTGGAG TGACCTACAGCGAGATCCTG CTCAGTGGGTAGGTGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG CCCACTGCAGTTATGTTGAA TGGGTGAGTGATCTCACAGG AGCTTGCAATTGCTGCTG CCCCTCTGCAGTTATGTTGAA TGGGTGAGTGATCTCACAGG AGCTTGCAATTGCTGCTG CCCCTCTAGATTGCTGCTG CCCCTCTAGACCGAGACTCTTG CCCCTCTAGACTGAGCTGCAGC CCCCTTCAGATGGCTCGC CCCCTTGCAATTGCTCCTG CCCCTTGCAATTGCTCCTG CCCCTTGCAATTGCTCCTG CCCCTTGCAATTGCTCCTG CCCCTTGCAATTGCTCCTG CCCCTTGCAATTGCTCCTG CCCCTTGCAACTGAGCCTGG CCCCTTGCAACTGAGCTGC ACTTCCCCAGTGGCTTGC CCCGTTGCAACTGAGCTGC CCCCTTGGAACTGAGCTGC CCCGTTGCAAGTGGCTTGC CTGAAGAGTGTTTGCGCCTC TTATGGACCTTTACAATTGCTGC CCTGTTGCAAGTGGCTGC CCTGTGGAAGTGGTTGC CCTGTTGCAAGTGGCTGC CCTGTGGAAGTGGCTGC CCTGTGGAAGTGGCTGC CCTGTGGAAGTGGCTGC CCTGTGGAAGTGGCTGC CTGAAGGCTGTGCCCCT TTATGGACCTTACAAATTGCTG CCTGTGGAAGGCTGGA GTAATGTTCTTTTAACTGGCCTGG
NRAS-E02           NRAS-FE02-03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE04-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.01           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.12           TET2-E03.12           TET2-E05           TET2-E06	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTCTGCCAAC AAATTCCGGGAGTGTTGTCA GATCTCTTCCCTCCCTC ATTTGAACAAGGGCCACTCA CTCCGCAACCTCATCTACC CCCGTTCCAAGCCAGCTC TGCAGGGTCCTAACTCATC TTTCAAGGTGGTGGCCCTA CCGGGAGCTTGCCTTTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACTC CAGGCGCCTCACCTACC CAGCTGACAAAATGCAG CATCCCCAGAAAATGCAG CATCTCACATAAATGCACTTAACA GAAATACACCCAGGGAACCA GGAGTTTTGAAACACCACGG CCCTCCAAACAATACACTGG CCCAGTGTTGAAACACCACGA CCCATGTTGAAACAGCA TGGCAAATACAGTACACAGG TTGCCCTAGACAACCACGG CCCATGTTGAAACACCACGG CCCATGTTGAAACACCACGG CCCATGTTGAAACACCACGG CCCATGTTGAAACCACCGCG CCCATGTTGAAACCACCGCG CCCATGTTGAAACACCACGCA CCACTTTCCAAAGAGCACGC TGCCATAGCAGAGGACCAGG TTGCCATAGCAGATGCACGC TTGCCATAGCAGATGCACAG TTGCCATAGCAGATGCACAG TTGCCATAGCAGATGCACAGC CCACTTTTCTAATAGATCAGCT TGCCATAGCCAGCACGC CCACTTTTCTAATGAGCACGC CCACTTCCCAGGTGCTTCAGGATG TGCCACTTCCAGGAGGC TGGCCACTTCCAGGAGC CCACTTTCCAGGAGCC CCACTTTCCAGGAGCC CCACTTTCCAGGAGCC CCACTTTCCAGGAGCC CCACTTTCCAGGAGCACCAG CCACTTTCCACAGCACGC CCACTTTCCACAGCACGC CCACTTTCCACAGCACGC CCACTTTCCACAGCACGC CCACTTTCCACAGCACGC CCACTTTCCACAGCACGC CCACTTTCCACAGCACGC CCACTTTCCACAGCACGC CCACTTCCCAGGACCACGC CCACTTCCACACCCCCGC CCACTTCCACACCCCCCCCCC	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCCATGTA AGGTACATCATCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGAGGTG AAAGGTTGACCCAAGAGGAG CCACCGACCACCCCTCA CCCACCATGGAGAACTGGTA GCTGTCGCGAACAGGAG CATTGCCGGAACAGGAG CATTGCCAGCCATCACAGTGGAG CATGCCAGCCATCACAGTGGAG CGCAGGTAGAGGTGTGGTAG CGGCAGGTAGGTGGGTGGTAG CGGCAGGTAGGTGGGTGGTAG CGCACGTACAGCGAGATCCTG CTCAGTGAGGCCTCCACACG GGCCGCCTCAGGCGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCCTGCGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCTGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCTGGTTCGGGAG CCGCTGCGGTTATGTGTGAA TGGGTGAGGTATGCTGCCA CCCCTGCGGTTAGTGTGGAA TCGACCCTCCAGGACGCTG CCCCTGCGTTGTGTTTTCCCCAT CCCACTGCAGTTATGCTGCG CCCCTTATTTCCTCCCTTAAA TCGACCCTTCAGGAAGCTCGG CCCCTGTGTGTGTTTTCCTGG CCCCTGTGTGTG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.01           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.09           TET2-E03.11           TET2-E03.13           TET2-E03.13           TET2-E03           TET2-E05           TET2-E05           TET2-E05           TET2-E05           TET2-E05           TET2-E06	gDNA gDNA cDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA cDNA cDNA cDNA cDNA cDNA cDNA cDNA c	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGAAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTCTGCAAC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGGTCCAACTCACC CCCGTTCCAGCAGCTC TCCAGGGTCCTAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGCCTTACTCACTC CAGGCGCCTTCACTCACTC CAGGCGCCTTCACTCACTC CAGGCGCCTTCACTCACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CTCCTACCACCTGTC CTCCTACCACTGTC GAATACCCTGTATGAAGGGAAGC TGTAGCCCAAGAAATGCAG GAATTTAGAAGAGCACCACCA GGAGTTTTAGAAGGGAACCACCAC GGAGTTTTAGAAGAACACCACCA CCAGTGTGAAAATCCAGG CTCCCCACAAATACACTGG CCCCAGTGTGAAACAGCA CCACTGTTGAAACAGCA CCAGTGTTGAAACAGCA CCACTGTTGAAACAGCA CTCCTCCCACAAACCATCCAGG CCACTGTTGAAACAGCA CCACTGTTGAAACAGCA TGGCGAAAATCAGTATTCAAAATCA CTCCTTCACAGAGTGCCACG CACTTCCCACAAACCACTGCG CCCATGTTGAAACAGCAGC TGGCCAAAGTCAAGCAGCC CACTTTCCCAGGAGCCTTCAGG TTGACCCAAGCAATCCACGG CCCATGTTGAAACAGCA CTCCTCCAAAACCAATCCACGG CCCATGTTGAAACAGCA TGGCACAATCCCAGGCA CTCCTTCCCACAGAAGCCACTGG CCCCGTGTGAAAACGCACTGC CCACTTGTTGAAACAGCA TGGCACAATCCCAGGGCCCTG TGGCCACATTTCCAGGAGCC CAATTTCCCAGGAGCCCACG CACTTCCCACAGAACCCACCGCG CCACTTGTTCAACGAGCCCCACCA CCACTTGTTGAACAACCCACTGCTG TGGCCCAAGTCCACTGCTG TGGCCCAAGTCCATACATCAGGC CACCTTGTTTCCCAGGAGCC CACTTCTTCCCAGGAGCCCACCGCCCCACCCACCCACCCA	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTATGTA AGGTACATCATCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTTGTTGCCATGAAACCGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAACAGGTA GCTTGTCGCGAACAGGTA GCTTGTCGCGAACAGGTA GCTTGTCGCGAACAGGTA CTGAGGGTTAAAGGCAGTGGAG CCTACTACGGCGAGATCCTG CTCAGTAGGGCTCCACAG GTGCTCACGCGAGAGTCGG GTCGCTCAGTCGGGAG CTGACCTACAGCGAGATCCTG CTCAGTAGGGCCTCCACAG GTGGCCTCAGTGGGAG CTGACCTACAGCGAGATCCTG CCCACTACAGCGAGATCCTG CCCACTGGCGTTATGTGTGAA TGGGTGAGTATGTGTGAA TGGGTGAGTATGTGTGAA TGGGTGAGTATCCCCATA CCCCCTCTAGTCGGAGCCTCG ACCTTCAGACTCGGCG CCCCTCTTTCACTCCCAT CCCACTCAGAGCAGTCTG CCCCTCTAGTGCGGG GTGACTTCACAGCGAGCTCTG CCCCCTCTGGTCGGGAG CCGCCTCAGGCAGTCCTG CCCCCTCTGGTGCGGCG CCCCCTTTCACTCCCCTTAA TCGACCCTCCCAGTCCCTTG CCCCCGTGTGGCTGC CCCCGTAGAACTGACGCTGC CCCCGTTGAGACTGAGCTGGTG CCCCGTTGAGACTGAGCTGGTG CCCCGTTTAGAACTGAGCTGGTG CCCCGTTGAGAACTGGCTGC CCCCGTTTAGCTTCCCCTTAC CCCCGTAGAACTGAGCTGGCTCC CCCGAGTGGTGTTGCTCCC TGAAGAAGTGGTTGCTCCC TTAGAGCCTTTACACTCCGCGC CTGAAGAAGTGGTTGCTGCCC CTGAGAGAGTGTTGCTGCTC CTTGTGGGAAAAATGCTGG CCTCTTTACACTCCCTTACA CCCGGTGGGGAGGCTGGA GTAATGTCTTTTCACTCCCTTAC CCCGGTAGGCGGAGCTGGA GTAATGTCTTTTCACTCCCCTTC CCCGGGAACTCTCCCCGCCCC CTGAGACTGTGGCTGC CTTGTGTGGGAACACCTTGCGC CTTGTGGGAACTCTCCTTCCA CCCGTTTACCAACTGGCGAG GTAATGTCTTTTCACTCCCTTCA CCCGTCTGGGAACTCTCCTTCCCCCCCCCC
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-05           RUNX1-FE06-06           RUNX1-FE06-07           TET2-E03.01           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.10           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E04           TET2-E05           TET2-E06           TET2-E07           TET2-E08	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCCCTAAC GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTCTGCAAC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGTTCCAAGGGCCACTCA CCCGTTCCAAGCGCCCC GCGGTCCAAGCGAGCTC TGCAGGGTGGGCCCCTA CCGGGAGCTTGCCTACTCAC CCGGGAGCTTGCCTACTCA CCGGGAGCTTGCCTTTTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCCTCCACCTACTCC CAGGCGCCTTCACCTACTC CTCCTACCACCTACTC CTCCTACCACCTACTC CTCCTCACCACAGGAACCC CTGTAGCCCCAAAAATGCCAG CATCTCCCCAAAAATGCCAG GAAAATAACATCCAGGGAACC CCCATGTTGAAAATGCAGGAACC CCCAGTGTTGAAATCACTGG CCCAGTGTTGAAACACCACCA CCCATTTTGGTAGCAGTGGA CCCCAGGAGTCTCACAAACCCACCA CCCATGTTGCAAACACCACCA CCCATGTGTGAAACACCACCA CCCATGTTGCAAACACCACCA CCCATGTGTGAAACACCACCGCA CCCAGTGTTGAAACACCACCGCG TTGACCCCAAAAATCCAGTGG CCCAGTGTTGAAACACCACCGCA CCCAGTGTTGAAACACCACCGCA CCCAGTGTTGAAACACCACCGCG TTGACCACAAACCCACCGCG CCCAGTGTTGAAACACCACCGCG CCCAGTGTTGAAACACCCACCG CCCAGTGTTGAAACACCACCGCG CCCAGTGTTGAAACACCCACGCG CCCAGTGTTGAAACACCCCGCG CCCAGTGTTGAAACACCCACGCG CCCAGTGTTGAAACCCCGCG CCCAGTGTTGAAACCCCGCG CCCAGTGTTGAAACCCCGCG CCCAGTGTTGAAACCCCGCG CCCAGTGTTGAAACCCCGCG CCCAGTGTTGAAACCCCGCG CCCAGTGTTGAAACCCCGCG CCCAGTGTTGAAACCCCGCG CCCAGTGTTGAAACCCCGCG CCCAGTGTTGAAACCCCCGCG CCCAGTGTTGAAACCCCCCGCG CCCAGTGTGTGAACCCCCGCG CCCAGTGTTGAAACCCCCCGCG CCCAGTGTTGAAACCCCCGCG CCCAGTGTTGAAACCCCGCG CCCAGTGTGTGCCCCCGCG CCCAGTGTGTGAACCCCCGCG CCCAGTGTGTGAACCCCCGCG CCCAGTGTGTGTTGGGGATCCAG CCAGTGTGTTTGGGATCAAGCC CCAGTGTGTGTTGGGATCAAGCC CCAGTGTGTGTGTGGGGATCCAGCC CCAGTGTGTGTGTGGGGATCCAGCCCCCCCCCC	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTITAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CCAGTIGGTCAGGCAAGGTGT AATGTCTGCCAACTCCTTCA CCCACCATGGAGAAGTGGTA GCTGTGCGGAACAGGAG CATTGCCAGCAACACGTGA CTGAGGTTAAAGGCAGTGGAG CTGAGGTTAAAGGCAGTGGAG CTGAGGTAGAGGTGGTAG CGCAGGTAGAGGTGGTAG TGACCTACAGCGAGATCCTG GTCGCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACGTACAGCGAGAGTCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGAGTCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTGCAGTTGGGAG CTGACCTACAGCGAGATCCTG GTCGCTGCAGTTATGTGTGAA TGGGTGGAGTATCTCTCCAT CCCCCTGCAGTTATGTGTGAA TGGGTGGAGTGCTCGCCTG CCCCTCTAGATCGCCTGG CCCCTCTAGACTCGCTG CCCCTCTAGAATGCTCCTG CCCCTCTAGACCTGCCCCACACG TGACCTACAGCGAGATCCTG CCCCTCTGCAGTTATGTGCGCTG CCCCTCTGCAGTTATGTTGAA TGGGTGGAGTGATCTCCTCAAC CCCCTTGCAGTTGCGCTG CCCCTTGCAATGCCCCATTG CCCCTCTGGAACGCCCCGTG CCCCTTAGACCTGACGCCCGC CCCGTTAGAACTGGAGCTGC CCCGTTGGAAAGTGGCTGC CCCGTTGGAAGGCTGGCTGC CCCGTTGGAAGTGGCTGC CCCGTTGGAAGGCTGGCTGC CCCGTTGGAAGTGGCTGC CCCGTTGGAAGTGGCTGC CCGGACCTCTTCCTTCAC TTATGGACCTTACAATTGCGGCAGG GTAATGTTCTTTTCACTGCGCTG CCGGTGGAACTCCTCCTTTCA CAGTGGAACTGCAACTGGAG GTAATGTTCTTTCTCCTCA CGCGTGGACCTCCTCCTTCA CAGTTGGAAAAACTTGATTA CGCCTCGGACCTCCTCCTTCA CAGTTGGAAAACTTGCTTCACACGGC
NRAS-E02           NRAS-FE02-03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06-02           RUNX1-FE06-03           RUNX1-FE06-04           RUNX1-FE06-05           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.08           TET2-E03.10           TET2-E03.12           TET2-E03.13           TET2-E03.12           TET2-E06           TET2-E06           TET2-E06           TET2-E06           TET2-E06           TET2-E06           TET2-E07           TET2-E08           TET2-E09	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCAAGGGTCCTAAC CATTGCAAGGGTCGTACC AAATTCCGGGAGTGTTGTCA GATCTCTTCCCTCCCTC ATTTGAACAAGGGCCCCTCA CTCCGCAACCTCATCTACC CCCGTTCCAAGCCAGCCC TGCAGGGTCCTAACTCATC TTTCAAGGTGGTGGCCCCTA CCGGGAGCTTGCCTTTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCCGTACCACCTACTC CCCGCAAGCAGGCAGCCTTG GAATACCTGAGGGGCAGCCTTG GAATACCCTGATGAAGGGAAGC TGTAGCCCAAGAAAATGCAG GAATTACCTGCAGGAAGCA CGCAGTTTTGAAAGGAAGCA CGCATTTTGGAAGAACACCAGCA CCCATTTTTGAAGGGAAGCA CCCATTTTTGGAAGACACCAGCA CCCATTTTTGAAACACCAGGG CCCCCTTCACCTACTC CCCATTTTTGGAAGACACCAGCA CCCATTTTTGGAAGACGCAGG CCCATGTTGAAACACCACGA CCCATTTTTGGAAAACCACTGG CCCATGTTGAAACACCAGG CCCATGTTGAAACACCACGA CTTCCCCAAGCAATACACTGG CCCATGTTGAAACCCTGG TGCCACAGAAAATCCAGGGACCA CGCCTTCACCTACTCC CCAGTGTTGAAACACCACGA CCCATTTTTGGACAACCACGA CCCATTTTTGGACAACCCCGG CCCAGTGTTGAAACCCCGG CCCAGTGTTGAAACCCCGGC CCCATTTTGGACAACCCCGG CCCAGTGTTGAAACCCCGGC CCCATTTTTGGACAACCCCGG CCCAGTGTTGAAACCCCGCG CCCATTTTTGGACAACCCCGG CCCATTTTTGGACAACCCCGCG CCCATTTTTGGACAACCCCGCG CCCATTTTTGGGCAACACCACGC CCATTTTTGGGCATCAA CCCCATTTTTGGGCATCCAA CCCATTTTTGGTGCTCCCCCCCCCC	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAG CAGTTGGCCAGCAACGCCAAGGAG CAGTTGGCCAGCACCCCTCA CCCACCATGGAGAACTGGTA GCTGTCGCGAACAGGAG CATTGCCGCACACCCCTCA CCCACCATGGAGAACTGGTA GCTGTCGCGAACAGGAG CATTGCCAGCCATCACAGTGGAG CTGAGGTAAAGGCAGGAGAG CTGACGTACAGCGAGATCCTG GTCCAGCGAGAGTCCTG GTCGCTCAGGCGAGATCCTG GTCGCTCAGGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCTGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCTGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCTGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCTGGTTCGGGAG CCGCTCTGGTTCGGGAG CTGACCTACAGCGAGATCCTG CCCACTGCAGTTATGTGTGAA TGGGTGAGTAATGCTGCG CCCACTGCAGTAGTCTCCCAT CCCACTGCAGTTATGCTGCG CCCCTTATTTCCTCCAT CCCACTGCAGTTATGTTGGAA TCGACCCTTCAGGAAGCTTGG CCCCTGTGTGTGTGTGTTCTGG CCCGTGAAATGGCTCGC CTGAAGAAGTGTGTGCCAGTC ACTGTGGGAGTAGGCTGGC CTGAAGAAGTGTGTGCGCCCC CTGAAGAAGTGTGTGCGCCC CTGAAGAAGTGTTTGCTGCC CTGAAGAAGTGTTTGCTGCC CTGAAGAAGTGTTTGCTGCC CTGAAGAAGTGTTTGCTGCC CTGAAGAAGTGTTTGCTGCC CTGAAGAAGTGTTTGCTGCC CTGAAGAAGTGTTTGCTGCC CTGAAGAAGTGTTTGCTGCC CTGAAGAAGTGTTTGCTGCC CTGAAGAAGTGTTTTCACAAGTGA CAGTTGGGAAAAACTTTGATGA CAGTTGGGAAAAACTTTGATA CAGTTGGGAAAAACTTTGATTA
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE02-04           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-02           RUNX1-FE06-03           RUNX1-FE06-04           RUNX1-FE06-05           RUNX1-FE06-06           RUNX1-FE06-07           RET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.05           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.13           TET2-E03.13           TET2-E05           TET2-E06           TET2-E07           TET2-E08           TET2-E08           TET2-E08           TET2-E08           TET2-E08           TET2-E07 <td>gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA</td> <td>GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGAAAAAGCGCCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTGTGCAAC AAATTCCGGGAGTGTTGTCA TGATCCTTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGGTCCTAACTCAC CCCGTTCCAGCGGCCCTAC CCCGTTCCAGCGGCCCTA CCCGGTCCTAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGGCCTTACCTCACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CCCGTCCACCTACTC CCCCTGCACCTACTC CTCCTACCACGTGACTACCG ATTCAACTAGAGGGCAGCC TGTAGCCCGGAAAATGCAG GAATAACCCTGTATGAAGGGAAGC TGTAGCCCAAGAAAATGCAG GAAATACACTCAGGGAACCA CCAGTTTTAGAAGAGCACCACCA CCAATTTTGGTAGCAGTGGA CTCTCCACAAACAATACACTGG CCCCATGTTGAAACAGCA CCAATTTTGGAACAGCA TGGTGAAAATCAGTATCAAGACA CTCTTCACAACAATGCATGCA CAACTCCAGGAGCCTTCAGG TTGACCCAAGTCAAGCACCACCA CCAATTTTGGAACAGCA TGGTGAAAATCAGTTCAAAATCA CTTCTTCACAAGAGTGCCAAG TGGCCAATTCACAAGCACTGCG CAACTTCACAAACCATGCG CAACTTCACAACCACTGCG CCCATGTTGAAACAGTCCAGGC CAATTTCACTAGAGAGCAGCC TGGCCAATTCTCAGAGCAGCC CCAATTTCTCACAAGCCATCCAGCCA CCAATTTCTCACAAGCCACTGCT TGGCCACATTCCACGAGCCAGCC CCAATTTCTCACAGAGCCACCACCA CCAATTTCTCAAGATCACGTGC CAACCTTGTTTGATTAGATCAGCTC AAACCCTTGTTTCTAATAGATCAGCTC AAACCCTTGTTTCTCAGGATCAA CCAATTTTCTAATAGATCAGCTC AAACCCTTGTTTCTAATAGCTCGCAC CCAATTTTCTCTATAGACCAGCGCC CCATTTTTCTAATAGCTCGCACCACCCA CCAATTTTCTCTATAGAACCACTGCT AAACCCTTGTTTCTCCAGGATCAA CCCTTGTTTCCACTATATATCAGCTCCACCACCCACCACCCAC</td> <td>TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCGGGAAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAAAAGGTG CAATGGTCTGGGAAAGGTG GCTGTCGGCAACCAGTGAG CCTGCCGAACAGGAG CCTGCCGCACCACGCAG CTGACGAGCAGGAGCCGGAG CTGACCTACAGCGAGCAGTGGAG TGACCTACAGCGAGGAGCCTG CTCAGTAGGGCTCCACAGG GTCGCTCTGGTCGGGAG CTGACCTACAGCGAGGAGCCTG CCCACTACAGCGAGGAGCCTG GTCGCTCTGGTTGGGGAG CTGACCTACAGCGAGGAGCCTG CCCACTGGGTTATGTGTTGAA TGGGTGAGTGATCTCACAGG AGCTTGCAACTGCGTG CCCCTTCAGTCGGGAG CCGCCTTCGAGTAGCTCTG CCCCCTTCAGTCGGGAG CCGCCTTCGAGTAGCTGTGAA TGGGTGAGTGATCTCCCTTAA TCGACCCTTCAGACACTGG CCCCCTTCAGTCGCTG CCCCCTTCAGTGCGTG CCACTGCAGCTGGCTCC CCACGTCGAGTGGCTGG CCGCCTTCGAGTGGCTGG CCGCCTTCGAGTGGCTGG CCCCCTTCAGACTGAGCTGG CCCCCTTCAGACTGGAGCTCG CCCCCTTCAGACTGGAGCTGG CCGCCTTCGAACTGGGCTGG CCGCCTTCGAACTGGGCTGG CCGCCTTCGAACTGGGCTGG CCGCCTTCGAACTGGGCTGG CCGCCTTCGAACTGGGCTGG CCTGCTAGGGCTGGCCTGC CCGCGTTGCAAATTGGCTGG CCTGCTAGACTGAAGCTGGA GTAAGGCTGGGAGCTGGA GTAAGTGTTCCAAACTTGGGC CCGCTGGAACTCTTTCCCTTCA CCAGGTTGCAAACTGGAGCTGGA CCTTGGGAACACGACTGCAGC CCGCTGGGGAACACTGGAGCTGGA CCTGGGTTCCAACATTAGGCTGGA CCTTGGGGAACACGTGGA CAGTGTGCAACACTGCAACTGGA CAGTGTGGTGAACACGACTCAACAG CAGTGTGCAACACGACTCAACAG CAGTGTGGTGAACACGACTCAACAG CAGTGTGGGAACACGACTCAACAG</td>	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGAAAAAGCGCCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTGTGCAAC AAATTCCGGGAGTGTTGTCA TGATCCTTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGGTCCTAACTCAC CCCGTTCCAGCGGCCCTAC CCCGTTCCAGCGGCCCTA CCCGGTCCTAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGGCCTTACCTCACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CCCGTCCACCTACTC CCCCTGCACCTACTC CTCCTACCACGTGACTACCG ATTCAACTAGAGGGCAGCC TGTAGCCCGGAAAATGCAG GAATAACCCTGTATGAAGGGAAGC TGTAGCCCAAGAAAATGCAG GAAATACACTCAGGGAACCA CCAGTTTTAGAAGAGCACCACCA CCAATTTTGGTAGCAGTGGA CTCTCCACAAACAATACACTGG CCCCATGTTGAAACAGCA CCAATTTTGGAACAGCA TGGTGAAAATCAGTATCAAGACA CTCTTCACAACAATGCATGCA CAACTCCAGGAGCCTTCAGG TTGACCCAAGTCAAGCACCACCA CCAATTTTGGAACAGCA TGGTGAAAATCAGTTCAAAATCA CTTCTTCACAAGAGTGCCAAG TGGCCAATTCACAAGCACTGCG CAACTTCACAAACCATGCG CAACTTCACAACCACTGCG CCCATGTTGAAACAGTCCAGGC CAATTTCACTAGAGAGCAGCC TGGCCAATTCTCAGAGCAGCC CCAATTTCTCACAAGCCATCCAGCCA CCAATTTCTCACAAGCCACTGCT TGGCCACATTCCACGAGCCAGCC CCAATTTCTCACAGAGCCACCACCA CCAATTTCTCAAGATCACGTGC CAACCTTGTTTGATTAGATCAGCTC AAACCCTTGTTTCTAATAGATCAGCTC AAACCCTTGTTTCTCAGGATCAA CCAATTTTCTAATAGATCAGCTC AAACCCTTGTTTCTAATAGCTCGCAC CCAATTTTCTCTATAGACCAGCGCC CCATTTTTCTAATAGCTCGCACCACCCA CCAATTTTCTCTATAGAACCACTGCT AAACCCTTGTTTCTCCAGGATCAA CCCTTGTTTCCACTATATATCAGCTCCACCACCCACCACCCAC	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCGGGAAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAAAAGGTG CAATGGTCTGGGAAAGGTG GCTGTCGGCAACCAGTGAG CCTGCCGAACAGGAG CCTGCCGCACCACGCAG CTGACGAGCAGGAGCCGGAG CTGACCTACAGCGAGCAGTGGAG TGACCTACAGCGAGGAGCCTG CTCAGTAGGGCTCCACAGG GTCGCTCTGGTCGGGAG CTGACCTACAGCGAGGAGCCTG CCCACTACAGCGAGGAGCCTG GTCGCTCTGGTTGGGGAG CTGACCTACAGCGAGGAGCCTG CCCACTGGGTTATGTGTTGAA TGGGTGAGTGATCTCACAGG AGCTTGCAACTGCGTG CCCCTTCAGTCGGGAG CCGCCTTCGAGTAGCTCTG CCCCCTTCAGTCGGGAG CCGCCTTCGAGTAGCTGTGAA TGGGTGAGTGATCTCCCTTAA TCGACCCTTCAGACACTGG CCCCCTTCAGTCGCTG CCCCCTTCAGTGCGTG CCACTGCAGCTGGCTCC CCACGTCGAGTGGCTGG CCGCCTTCGAGTGGCTGG CCGCCTTCGAGTGGCTGG CCCCCTTCAGACTGAGCTGG CCCCCTTCAGACTGGAGCTCG CCCCCTTCAGACTGGAGCTGG CCGCCTTCGAACTGGGCTGG CCGCCTTCGAACTGGGCTGG CCGCCTTCGAACTGGGCTGG CCGCCTTCGAACTGGGCTGG CCGCCTTCGAACTGGGCTGG CCTGCTAGGGCTGGCCTGC CCGCGTTGCAAATTGGCTGG CCTGCTAGACTGAAGCTGGA GTAAGGCTGGGAGCTGGA GTAAGTGTTCCAAACTTGGGC CCGCTGGAACTCTTTCCCTTCA CCAGGTTGCAAACTGGAGCTGGA CCTTGGGAACACGACTGCAGC CCGCTGGGGAACACTGGAGCTGGA CCTGGGTTCCAACATTAGGCTGGA CCTTGGGGAACACGTGGA CAGTGTGCAACACTGCAACTGGA CAGTGTGGTGAACACGACTCAACAG CAGTGTGCAACACGACTCAACAG CAGTGTGGTGAACACGACTCAACAG CAGTGTGGGAACACGACTCAACAG
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06.01           RUNX1-FE06.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E05           TET2-E05           TET2-E05           TET2-E05           TET2-E05           TET2-E05           TET2-E09           TET2-E09           TET2-E01.01	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCCCTAAC GCTGTGGTCCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTCTGCAAC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CTCCGCAACCTCATCTACTCAC CCCGTTCCAAGCCAGCTC TGCAGGGTCGTACCTCATC CCGGGAGCTTGCACTCAATC TTTCAAGGTGGTGGCCCCTA CCGGGAGCTTGCCTTTTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CTCCTACCACCTACTC CTCCTACCACCTACTC CTCCTCACCAGGAGCAGCCTTG GAATACCTGTATGAAGGGAAGC TGTAGCCCAGAAAATGCCAG GAAAATACATCCAGGGAACCA GGAATTTGAACAACACCACCA CCATTTTGGTAGCAGTGGA CCCAGTGTTGAAACACCACCA CCATTTTGGTAGCAGTGGA TGACCTCCAACAATACCATGG CCCAGTGTTGAAACAGCA CCCATGTTGAAACAGCA TGGGACATTCCAAGATGCCAGG CCCAGTGTTGAAACAGCA CCACTTCCACAAGATGCCAGGG CCCAGTGTTGAAACCACCACGG CCCAGTGTTGAAACACCACCG CCCATGTTGAAACCACCACGG CCCAGTGTTGAAACCACCACGG CCCAGTGTTGAAACCACCACGG CCCAGTGTTGAAACCACCACGG CCCAGTGTTGAAACCACCACGG CCCATGTTGAAACCACCACGG CCCAGTGTTGAAACCACCACGG CCCAGTGTTGAAACCACCACGG CCCATATTCCTACAAGTGCAAGCG CCCATATTCCACAGATGCCACGG CCCATATTCCTACAGGATGCACAG CGCACTTTTCTACAGGATGC CCATATTTCTAATAGATCAGCTG CCCATATTTCTCACGGATCA CCATATTTGTGTGGATTCAA	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGGAGG CATGGCCTGGGAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTIGTCGCGAACAGGAG CATTGCCAGCCATCACAGGAG CATTGCCAGCCATCACAGGAG CTGAGGTTAAAGGCAGTGGAGT CGGCAGGTAGAGGTGGTAG TGACCTACAGCGAGATCCTG GTCAGTAGGGCCTCCACACG GTCGCTCGGTTCGGGAG CTGACGTCAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CCGCCTGCGATTATGTGTGAA TGGGTGGAGTGATCTCACAGG AGCTGCCAATTGCTCCTG CCCCTGCGGTTGCTGGTG CCCCTGTGTTTTTTCCTCCAT CCCACTGCAGTTAGGTGCTG CCCCTGTGTGTTTTTCGCG GTGGCTGCAATGGCCCGTC CCCGTGTGGATGGCCGCCCACTG CCCGTGTGGAATGCCCGTC CCCGTGTGGATGGCCCGCCCCCACG CCGCTGGAACTGAGCTGGC CCCGTGTGGAATGCCCGTC CCCGTGTGGATTTGCGCCG CCCGTGTGGAAGGCTGCACCG CCGGACTGAAGGCTGCACCG CCGGACTGGAAGGCTGCC CCGGTGAAGTGGACGCCGGC CTGAAGAAGTGGCTGC CCCGTGTGGAAGGCTGCACCG CTGAAGAAGTGGCTGC CCGTGAAGACGGAGCTGC CCGTGAACTCCTCCTTCA CAGCTGTGGAAAACTTGCGCTG CTGGAGGATCCCCTTCC CCGGAACTCCCCCTTCA CAGGTGGAAACTGCAGCTCGAC CCGTGAACTCCTCCCCTTCA CAGTGGGAAAACTTGCTGCTC CTGAGGGTTCCACAACTGAAGG CGGGGCTGACTTCCCCTTTCC
NRAS-E02           NRAS-FE02-03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-02           RUNX1-FE06-03           RUNX1-FE06-04           RUNX1-FE06-05           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.06           TET2-E03.08           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E06           TET2-E06           TET2-E06           TET2-E08           TET2-E09           TET2-E0.01           TET2-E0.02	gDNA gDNA cDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA cDNA cDNA cDNA cDNA cDNA cDNA cDNA c	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGAAAAGCGCCCTAAC GCTGTGTCTAAATCTGTCC GCTGTGTCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTCTGCAAC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGTTCCAAGGGCCACCA CCCGTTCCAAGCGAGCC CCCGTTCCAAGCGAGCC CCCGTTCCAAGCGAGCC CCCGTTCCACGTCACTCAC CCGGGGCCTTAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCCAGGCGCCTTCACCTACTC CCCAGGCGCCTTCACCTACTC CCCCTGTACCTACTG GAATACCCTGTATGAAGGGAAGC TGTAGCCCAAGAAATGCAG CATCTCACAAATGCCATGGA CATCTCCACAAAATGCAG GAAATAACATCCAGGGAACCA CCATTTTGGTAGCAGTGGA TGACCTCCAAGAACCACCACCA CCAATTTTGGTAGCAGTGGA TGGCCAAGATGCACTGC CCCAGGTGTGAAACAGCA CTCCTCCACAGAATGCCATGG CCCCGTGTGAAACGCACTGG CCCCTTCCCACGACTCCAGG CCCTTCCCACAGAATGCCAGG TGGCACATTTCAGAGAGCA CTCCCCAAGAAATCCACTGG CCCCGGTGTGAAACACCACCAC CCAATTTTGGTAGCCATGCCA CCAGTGTTGAAACAGCA TGGCACAATCCCAGGAGCCTG GGCACCTTTCCAGGAGCC CCATTTTTCCAGGAGTGCCACA CCATTTTTCCAGGAGTGCCACC CCATTTTTGTTGCATTCCAGGATG CCCCTTGTTGAACAACCACCGCC CCATTTTTGTTGGGAGTCCAA CCCATTTTTGTTGGGAGTCCAA CCCATTTTTGTTGGGAGTCCAA CCCATTTTTGTGTGGCAGCC CCATTATTGTGTTGGGAGCCTG GGGACCTTATGTGTTGGGAGCC	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCGGGAAAGGTGT AATGTTCTGCCAACTCGTCA CCCACCATGGAACAGGAG CCTGTCGCGAACAGGAG CCTGACGAACAGGAG CCTGACGAACAGGAG CCTGACGAACAGGAG CCTGACGAACAGGAG CCTGACGAGCAACAGTGAG CTGACCTACAGCGAGATCCTG CTCAGTAGGGCCTCCACACG GTGACCTACAGCGAGATCCTG CTGACCTACAGCGAGATCCTG GTCGCTCGGTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGTCGGGAG CTGACCTACAGCGAGATCCTG CCCACTGGCGAGATCCTG GTCGCTCAGTGGGGAG CCGCCTCAGTGGGGAG CCGCCTCAGTTGGGGAG CCGCCTCAGTAGCGAGATCCTG CCCCCTTTATTCCTCCAT CCCACTGCAGTTATGTGTGAA TGGGTGAGTGATCTCCCAAGG AGCTTGCAAATTGCTCTG CCCCCTTAGAAATCGCTGG CCCCCTTAGAAATCGCTGG CCCCCTTAGAAATCGCTGG CCCCCTTAGAAATCGCAGTC CCCCCTATGAGCCCCCACG TGAGCTGAAATGGCTCAGTC CCAGCTGCCATTG CCAGCGCAGTGGCTCC CCCGTAGAAATGGCTCGG CCCCCTTAGGAACTGAAGCTGGTG CCCCCTTAGAAATGGCTCAGTC ACTGCCAATGACGCAGGC CCCCTTATACACTCCCATG CCCCCTTAGGAACTGAAGCTTGTG CCCCCTATGAGACTGAAGCTTGTG CCCCCTTAGAAATGGCTCAGTC CCCCCTTAGGAAATGGCTGGC CCTGAGAACTGAAGCTTGTTG CCCTGTAGAACTGAAGCTGGC CTTGAGGAAAACTGAAGCTGGA CCTGAGGGTGGCGGA GTAATGTCTTTACACTCCCACG CCCGTGAGACTGTGGCTCC CCTGAGAACTGAAGCTGGAA CGCTGAACTCCTTTCCA CCCGTGTGGGAAAAACTTGATTA CGCGGGGCGACTTTACAAATTAGCG GGGGCGAAAACCAAAATAAT
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-05           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.07           TET2-E03.08           TET2-E03.10           TET2-E03.13           TET2-E03.13           TET2-E05           TET2-E08           TET2-E08           TET2-E08	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGAAAAAGCGCCCTAAC GCTGTGGTCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTGTGCAAC AAATTCCGGGAGTGTTGTCA TGATCTCTTCCCTCCCT ATTTGAACAAGGGCCACTCA CCCGTTCCAGCGCCCTCA CCCGTTCCAGCCAGCTC TTCCAGGGGCCTAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGGCCTTACTCACTC CAGGCGCCTTCACTCACTC CAGGCGCCTTCACTCACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCCTCTCCCCTGTCACCTACTC CTCCTACCACCTGCT CTCCTACCACCTGCT GAATACCCTGTATGAAGGGAAGC TGTAGCCCAAGAAAATGCAG GAATATCACTCAGGGAAACACACCA GAAAATAACATCCAGGGAAACCA GAAAATAACATCCAGGGAACCA GAAAATACATCCAGGGAACCA CCCATGTTTGAAAGAAAACCCACCA CCCATGTTTGAAACAGCA TGCCCAAAAATACAATCCACGG CTCTCTCACAACCATCCACG CCCATGTGTGAAACACCACCA CCCATGTGTGAAACACCACCA CCCATGTTTGAAACAGCA TGCCCAAGAAATCCACGTG TGGCCAATTCCTCACATACCACGA CCCATTGTCTCAAAATCCACGCA CCCATTGTTGAAACACCACCAC CCCATTGTTGAAACAGCACCACCA CCCATTGTTGAAACAGCACCACCA CCCATTGTTGAAACACCACCACCA CCCATTGTTGAAACACCACCACCA CCCATTTTCTAATAGATCAAGCA TGGCCAAATTCCAAGCATGCA CCATTTTCTAATAGATCAGCATC CCATTATTCTAATAGATCACGTG TGGCCCATTGTTTGAGGGCTTCAAG TGCCCCTATTTTGTTTGGGATTCAAA TGCCCTATTTTGTGTTGGGATCAA TGCCCTATTTTGGGATCCACAC	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAAGGTGT AATGTTCTGCCAACACGGTA CCACCATGGAACAGGAG CCACCATGGAACAGGAG CCTACGGAACAGGAG CCTACGGAACAGGAG CCTGCCGGACAGGAG CCTGCCGGCACCAGTGAG TGACCTACAGCGAGACCGG GCCGGTTAAAGCCAGTGGAG TGACCTACAGCGAGACTCG CTCAGTAGGGCTCCACACG GCCGCTCGGGTCGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGGTGGGAG CTGACCTACAGCGAGATCCTG GTCGCTCGGGTGGGAG CTGACCTACAGCGAGATCCTG CCCACTGGGGCTCCACAGG GCGCTCCGGGTGGAGG CCGCTCGGGTTAGTGGAA TGGGTGGAGTGACTCACAGG ACCTTCCAGCGAGAGTCCTG CCCCTCTGGTTCGGGAG CCGCTCCAGCGAGATCCTG CCCCTCTGGTTGCGGAGA CTGACCTACAGCGAGATCCTG CCCCTCTGGTTGCGGAG CCGCTTCCAACTGGGGAG CCGCTTCCAACGCAGGAGCCCG CCCCTTCAGTTGCGGTT CCACTGCAATTGCTGCAA CCCCTCTAGTTGCGCTG CCCCTTCAGATGCCCCG CCCCTTCAGAATGCCCCG CCCCTTCAGACTGGCCCGG CCCCTTGAACTGGAGCTGG CCCCTTGGAACTGGCCTGG CCCCTTGAACTGGGCTGG CCCCTTGAACTGGAGCTGC ACTTCCCCAGTGGCTGG CCCGTTGAAACTGAAGCTGGTG CCCGTTGAAACTGAAGCTGGC CCCGTTGAAACTGAAGCTGGC CCGGGAGCTGCAACTGGA GTAAGGCTGGAACTGCAACTG GCGGGGCCAAACGAACTGAACT
NRAS-E02           NRAS-FE02-03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE01-02           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.08           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E05           TET2-E05           TET2-E09           TET2-E00.01           TET2-E00.02           TET2-E00.01           TET2-E09           TET2-E10.01           TET2-E10.01           TET2-E10.01           TET2-E10.01           TET2-E10.01           TET2-E	gDNA           gDNA           cDNA           cDNA           gDNA           cDNA           cDNA           gDNA           gDNA	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGGAAAAGCGCACTGACAAT GCTGTGGTCTAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTATCCTGCGAACC AAATTCCGGGAGTGTTGTCA TGATCTTTCCTCGCCCCT ATTTGAACAAGGGCCCTCA CTCCGCAACCTCATCTCAC CCCGTTCCAAGCCAGCTC TGCAGGGTGTGGCCCTA CCGGGAGCTTGCACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGAGCTTGCCTTTCC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCCGTACCACCTACTC CCCGTACCACCTACTC CTCCTACCACCTACTC CTCCTACCACCTACTC CTCCTACCACCTACTC CTCCTCACCAGGGAGCCTTG GAATACCTCGAGAGAGAGC TGTAGCCCAAGAAAATGCCAG GAATATACCTCCAGGGAACC CCATTTTGGAAGACACCACCA CCATTTTGGTAGCAGTGGA CCCCTGTTGAAACACCACCA CCCATTTTGGAACACCCCG CCCATGTTGAAACACCACCA CCCATGTTGAAACACCACCA CCCATGTTGAAACACCACCAG CCCATGTTGAAACACCACCG CCCATGTTGAAACACCACCG CCCATGTTGAAACACCACGG CTCTCCCCAAGCAGTGGA TGGCACTACGAGTGCTTCAAG TGGCACAGCTACTACTC CCCCTGTTCACATACTGCG CCCATGTTGAAACACCACCAC CCCATTTTGGAACACCCCG CCCATGTTGAAACCCCTGG GGGCCTTCCTTCCAGGATGCA CCCATGTTGAAACCCCTGG GGGCCTTCATCAATATCACGTGG CCCATCATAATTCCAGGATGCA CCCATTCTTTCTACAGGATGCACACC CCATATTTGTGTGGGATCAA CCCTCTTTTGTGGGATCAA CCCTTCTTTGGGAGTGGAACC CCATATATGGTGGGAGCG GCCTTCATAAAATAACATCACCACCACCACCC CCATATATGGTGGGAGCG CCCATCAGTTGAGGCGCG CCCATCAGTTGAGGCGGCG CCCATCAGTTGAACCACCACCACCC CCATCATAATGGTGGAACCCACCACCCC CCATCATAATGGTGGAACCCACCACCCC CCATATTGGTGGAGCGC CCATCCAGTTGAACCACCACCACCCC CCATCATAATGGTGGAACCCACCACCCC CCATCATAATGGTGGAACCCACCACCCC CCATCATAATGGTGGAGCCG CCCATCCAGTTGAACCACCACCACCCCCCCCCC	TCCGACAAGTGAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTITTAC GGCCTCCGCCTGTCCTC GTITGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCAGCCAAGGAGG CATGGCCAGCCAACTCCTTCA CCCACCATGGAGAACTGGTA GCTGTCGCGAACACGTCA CCCACCATGGAGAACTGGTA GCTGTCGCGAACACGGAG CATTGCCAGCCATCACAGTGGAG CTGACGTACAGCGGAGC CTGAGGGTAAAGGCAGTGGAG TGACCTACAGCGAGATCCTG GTCGCTGGGTCGGGAG CTGACGTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACGTACAGCGAGATCCTG GTCGCTCGGTTCGGGAG CTGACCTACAGCGAGATCCTG GTCGCCTGGGTTGGGGAG CCGCTGGGTTTATTCCTCCAT CCCCCTGCGGTAGGTGGTGGAA TGGGTGAGTGATCTCACAGG AGCTTGCAGTCAGCGAGATCCTG CCCCTGCGGTTATGTTGAA TGGGTGAGTGATCTCACAGG AGCTTGCAGTATGCTGCTG CCCCTGCGGTTGTGTTGAA TGGGCGAGTAGTCTCGCG CCCCTGGTGTGTGTTGTGGA CCGCCTGCGGTTGGTGGGG CCCCTTATTTCCCCAT CCCCCTGGGTGGGTGGCCAGTC CCCCTGGGTGGGTTGGCCAGTC CCCCTGGGTGTGGTTGGCCAGTC ACTGTGCGATTGGCTGGC CCCCTGGGTGGGTTGCCACGC CCCGTGGAGGAGGCTCGC CCCGTGGAGGAGGCTGC CCCGTGGGGTTGGCCCGCCCCCCCCCC
NRAS-E02           NRAS-E03           NRAS-FE02-03           NRAS-FE02-03           RUNX1-E01           RUNX1-E03           RUNX1-E03           RUNX1-E04           RUNX1-E05           RUNX1-E06.01           RUNX1-FE02-04           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-06           RUNX1-FE06-07           RUNX1-FE06-08           RUNX1-FE06-09           RUNX1-FE06-01           RUNX1-FE06-02           TET2-E03.01           TET2-E03.02           TET2-E03.03           TET2-E03.04           TET2-E03.05           TET2-E03.10           TET2-E03.13           TET2-E03.13           TET2-E03.13           TET2-E03           TET2-E03           RUAX1-FE06-05           TET2-E03.10           TET2-E03.11           TET2-E03.12           TET2-E03.13           TET2-E04           TET2-E05           TET2-E06           TET2-E08           TET2-E0.02           TET2-E10.02           TET2-E10.02           TET2-E10.02	gDNA gDNA cDNA cDNA gDNA gDNA gDNA gDNA gDNA gDNA gDNA g	GGCCGATATTAATCCGGTGT CCCTCCCTGCCCCCTTAC GGAAAAAGCGCACTGACAAT GCTGTGGTCCTAAATCTGTCC GCTGTGTCCAAATCTGTCC GCTGTTTGCAGGGTCCTAAC CATTGCTACTCGCGACC AAATTCCGGGAGTGTTGCA TGATCCTTTCCCTCCCTCT ATTTGAACAAGGGCCACTCA CCCGTTCCAAGGCCACTCA CCCGGTCCAACTCAATCC TTCCAAGGTGGTGGCCCTA CCCGGTCCAACTCAATC TTTCAAGGTGGTGGCCCTA CCGGGCCTTACTCACTC CAGGCGCCTTCACTCACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CAGGCGCCTTCACCTACTC CCAGGCGCCTTCACCTACTC CCCGTCCACCTACTC CCCGGGCCTTCACCTACTC CTCCTACCACCTGTC CTCCTACCACCTGCT GAATACCCTGTATGAAGGGAAGC TGTAGCCCAAGAAATGCAG CATCTCCACAAAATGCCAG GAATTAACATCCAGGGAACCA CCATCTCCACAAAAACCACCACA GGAGTTTTAGAAGAGACACCACCA CCATTTTGGTAGCAGTGGA TGACCTCCAAGAAACACACCACCA CCAATTTTGGTAGCAGTGGA TGGCCAAGACAATCCATGG CCCCATGTGTGAAACAGCA CCCCTCCACAAACCATCCAGG CCCCTCCACAAACCATGC CCCATGTGTGAAACAGCA CCCCTTCCCACAAACCACCAC CCAATTTTCCCAGGAACCCACCA CCAATTTTCCCAGGAACCCACCA CCAATTTTCCCCAGGAACCCACCA CCAATTTTCCCAGGAACCCACCA CCAATTTTCCCCAGGAACCCACG CCCATGTTGAAACAGCATTCAAAATCA CTCCTCCAAAACCAATCCACGG CCCCTTCACTATAATACATCAGCA TGGCCAAAGTCCAGGATGCAAGC CCCATGTTGTAAACAGCCATGCT GGCACCTTTCCAGGAGCCTG GGCACCTTTCCAGGAGCCTG GGGACCTTTAGTAGAGCACGC CCATATATTGTGTTTGGGATTCAA TGCCTAATTGTGTTTGGGATCAA CCAATGTCATTTCGCATCCAT CCAATGTCATTTCGCATCCACT CCAATGTTGGGAGTGCCACC CCATATTTGTGTTGGGAGCTGT GGGACCTTTAAAAATCATCACCACCA CCAATGTGGGAGTGCCAAGCC CCATGTAAATAATCATCACCACCA CCAATGTTGGGAGTGCTGAAGC CCATCCAAATCACTGCTT CACCCACGTCATTCCATCCA CCAATGTCAAATCAGTGCCACCACCA CCAATGTTGGGAGTGCTGAAGCC CCATGTAATATCAGCTGCTG CACCTCCAAAATCACCTGCTG CCAATGTTGGGAGTGCTGAAGCC CCAATGTCAAAATCAATCCACCTGCT CCAATGTTGGGAGTGCTGAAGC CCAATGTGCCATAATCATCCACCA CCAATGTGCATAATCAGCTGCT CACCCACGTGCATGCCACCC CCATGTAATATGGCCTTCCAT CACCCACGTGCTGCAAGCC CCAATGTGCCATAACCTGCTT CACCCACGTGCGCGC CCCACTGCAAATCCACTGCTT CACCCACGTGCCTCCACCACCC CCATGTAAATAATCACCCTGCTG CCACCTGCAAATCCACCCCCCCC CCATGTAAAATCAGCCTCCCCC CCATGTAAATCAGTGCTTAACCACCCCCCCCCC	TCCGACAAGTGAAGAGACAGG CAATGTCAAACAACCTAAAACCA CCTTCGCCTGTCCTCATGTA AGGTACATCATCCGAGTCTTITAC GGCCTCCGCCTGTCCTC GTTIGTTGCCATGAAACGTG GAAAGGTTGAACCCAAGGAA CAGTTGGTCTGGGAAAGGTGT AATGTTCTGCCAACTCCTTCA CCCACCATGGAACAGGTG GCTGTCGCGAACAGGTA GCTTGTCGCGAACAGGTA GCTTGTCGCGAACAGGTA CTGAGGGTTAAAGGCAGTGGAG CTGACCAGCGAGAGTGGTAG TGACCTACAGCGAGATCCTG CTCAGTAGGGCCTCCACAG GTGGCTCAGGCGAGATCCTG GTCGCTCAGTGGGAGACCTG GTCGCTCAGTGGGAGACCTG GTCGCTCAGTGGGAGACCTG GTCGCTCAGTGGGAGACCTG GTCGCTCAGGCGAGATCCTG CCCACTGCAGCGAGATCCTG CCCACTGCAGCGAGATCCTG GTCGCTCAGTGGGGAG CTGACCTACAGCGAGATCCTG ACTGTGCGAGTTATGTGTGAA TGGGTGAGTGATGCTGCA CCCACTGCAGTTAGTGTTGAA TGGGTGGAGTGATCTCCCAT CCCACTGCAGTTCCCCTTAA TCGACCCTCCAGTCCCTTG CCCCTCTGTTCGGCAGCCTCG ACTTCCCCATCCCCTTAA TCGACCCTTCAGAACTGCTG CCCCTCTAGTGCGTGC CCCCTCTAGTGCCTCC TGAAGTGCAACTGAGCTGGTG CCCTGTAGAACTGAGCTGGTG CCCTGTTGAACTGAGCTGGTG CCCTGTAGAACTGAGCTGGTG CCCTGTAGAACTGAGCTGGTG CCCTGTTTCACTCCCTTAA TCGACCCTTCAGAACTGGCTG CCCTGTAGAACTGAGCTGGTG CCCTGTAGAACTGAGCTGGTG CCCTGTAGAACTGAAGCTTGTG CCCTGTAGAACTGAAGCTGGTG CTTGAGGGAAGTGTTGCTGCTC TTTATGAGCCTTTAACTGCGGA GTAATGTTCTTTTAACTGCGGAG CAGTGGTGAAGACTGAAGCTGGA CAGTGTGGAAAACGAAATTAGTGG CGGGGCGAACTTTGCTCCCACAGG GGGGCGAACACCAAATTAAGAG CAGTGTGAGAACCAAATTAAGAG CAGTGTGAGAACCAAATTAAT CTGCAGCTGGGAGAGCTGA CAATGTGGGAAAACCAAATTAAT CTGCAGCTGGGAGAGCTGGA CAATCTGGGCAAACCAAATTAACC CCACTGGAGACCAGAGCGGAG

TET2-E11.04	gDNA	GGTGAACATCATTCACCTTCTC	GAATTGACCCATGAGTTGGAG
TET2-E11.05	gDNA	AGACAGCGAGCAGAGCTTTC	AAGTTTCATGTGGCTCAGCA
TET2-E11.06	gDNA	AGCCCGTGAGAAAGAGGAAG	ACTGTGACCTTTCCCCACTG
TP53-E04	gDNA	ACCTGGTCCTCTGACTGCTC	CAGGCATTGAAGTCTCATGG
TP53-E05E06	gDNA	CACTTGTGCCCTGACTTTCA	GCCACTGACAACCACCCTTA
TP53-E07	gDNA	CTTGCCACAGGTCTCCCC	AAGAGGTCCCAAAGCCAGAG
TP53-E08E09	gDNA	GACAAGGGTGGTTGGGAGTA	ACAGTCAAGAAGAAAACGGCA
TP53-E10	gDNA	ACTTGAACCATCTTTTAACTCAGGT	TCTGTGCAGGGCTGGGAC
TP53-FE02-06	cDNA	CAGTCAGATCCTAGCGTCGAG	ACACGCAAATTTCCTTCCAC
TP53-FE03-05	cDNA	TCAGACCTATGGAAACTACTTCCTG	GGCAAAACATCTTGTTGAGG
TP53-FE04-06	cDNA	GGCCCCTGTCATCTTCTGT	ACACGCAAATTTCCTTCCAC
TP53-FE05-08	cDNA	TGGCCATCTACAAGCAGTCA	AGCTGTTCCGTCCCAGTAGA
TP53-FE06-11	cDNA	CTCAGCATCTTATCCGAGTGG	TTATGGCGGGAGGTAGACTG
TP53-FE07-10	cDNA	TGGCTCTGACTGTACCACCA	CCTCATTCAGCTCTCGGAAC
TP53-FE09-11	cDNA	CCAGCCAAAGAAGAAACCAC	TTCTGACGCACACCTATTGC
WT1-E07	gDNA	GACCTACGTGAATGTTCACATG	ACAACACCTGGATCAGACCT
WT1-E09	gDNA	TGCAGACATTGCAGGCATGGCAGG	GCACTATTCCTTCTCAACTGAG

# Table S3: Primer sequences used to analyze the respective genes by Sanger Sequencing

	•		
Gene-Identifier	Material	Sequence: Forward-Primer(5'-3')	Sequence: Reverse-Primer(5'-3')
ASXL1-E13.01	gDNA	GGTCAGATCACCCAGTCAGT	GTCCAACTGTAGCCCTCTGT
ASXL1-E13.02	gDNA	GGACCTGCCTTCTCTGAGA	TCTGGATTCTGGTTTGGGCT
ASXL1-E13.03	gDNA	CCAAGGCTCTCGTTTCTAACAG	CATACTCGAGACACCCAGCT
ASXL1-E13.04	gDNA	ACATGCGTCTGGTTACAAGG	AGCACGGACTTCCTTCTGAT
ASXL1-E13.05	gDNA	ACAAATCCCATTACATCCTCTAGG	CTCGGGGTAATTTCCAGAAGG
ASXL1-E13.06	gDNA	TGCCGAGAACAGGAAAGCTA	TTTTGGGGGAAGGCAAGAGT
ASXL1-FE13.01	cDNA	AAGCCACAGCCCACTAAAGA	GTCCAACTGTAGCCCTCTGT
ASXL1-FE13.02	cDNA	GGACCTGCCTTCTCTGAGA	TCTGGATTCTGGTTTGGGCT
ASXL1-FE13.03	cDNA	CCAAGGCTCTCGTTTCTAACAG	CATACTCGAGACACCCAGCT
ASXL1-FE13.04	cDNA	ACATGCGTCTGGTTACAAGG	AGCACGGACTTCCTTCTGAT
ASXL1-FE13.05	cDNA	TGGATTCCAAAGAGCAGTTCTCTTC	CATGACAAAGGGCATCCCTTCCAA
ASXL1-FE13.06	cDNA	ACAGGAAAGCTACTGGGCATAGTC	CAAGAGTGCTCCTGCCTAAAGAGT
CEBPA-E01.01	gDNA	GCCATGCCGGGAGAACT	CCCGGGTAGTCAAAGTCG
CEBPA-E01.02	gDNA	CCTTCAACGACGAGTTCCTG	CGGCTGGTAAGGGAAGAGG
CEBPA-E01.03	gDNA	GAGGAGGATGAAGCCAAGC	CTCGTTGCTGTTCTTGTCCA
CEBPA-E01.04	gDNA	TGGCAGCGCGCTCAAG	CCAGGGCGGTCCCACA
CEBPA-FE01.01	cDNA	GCCATGCCGGGAGAACT	CCCGGGTAGTCAAAGTCG
CEBPA-FE01.02	cDNA	CCTTCAACGACGAGTTCCTG	CGGCTGGTAAGGGAAGAGG
CEBPA-FE01.03	cDNA	GAGGAGGATGAAGCCAAGC	CTCGTTGCTGTTCTTGTCCA
CEBPA-FE01.04	cDNA	TGGCAGCGCGCTCAAG	CCAGGGCGGTCCCACA
DNMT3A-E07	gDNA	TTCCTGGAGAGGTCAAGGTG	TGGAGAGAGAGAGAGAGAC
DNMT3A-E08	gDNA	GCCTCGTGACCACTGTGTAA	ACCCACCACAGGCAGAGTAG
DNMT3A-F09	gDNA	CTCCTCTTTGCATCGGGTAA	ACCTGCACTCCAACTTCCAG
DNMT3A-F10	gDNA	TGTGCCACCTCACTACTCA	TCCCTAAGCATGGCTTTCC
DNMT3A-E11E12	gDNA	GACCTTGGCACCTGCTTTC	CCACACTAGGAGTGCCAGAGTT
DNMT3A-F13	gDNA	GGTCACAGTGCCTCCCTTT	
DNMT3A-F14	gDNA		
DNMT3A-F15	gDNA		
DNMT3A-E16	gDNA	CAGGGTGTGTGGGTCTAGGA	TGCATACGTTTCCACTTCACA
DNMT3A-F17	σDNΔ		
DNMT3A-F18	gDNA	TGGTCCCGTTCTTGTTTAGG	CAAGGAGGAAGCCTATGTGC
DNMT3A-F19	gDNA	GACAGCTATTCCCGATGACC	GCTCCACAATGCAGATGAGA
DNMT3A-F20	gDNA	TGTGTGGCTCCTGAGAGAGA	
DNMT3A-F21	gDNA	TGGTGGATTIGTGTCTTTGC	
DNMT3A-F22	gDNA		
DNMT3A-F23	gDNA		
DNMT3A-FE06-08	CDNA	GGGGGACCCCTACTACATCA	
DNMT3A-FE07-09	cDNA	GTGGCTACCACGCCTGAG	GACCTCGTAGATGGCTTTGC
DNMT3A-FE08-11	cDNA	GTTCGGAGACGGCAAATTCT	AGGTTCCACCCACATGTCC
DNMT3A-FF10-14	cDNA	GGGGCTTCCAGCCTTCT	CGTCGTCGTCGTACTGGT
DNMT3A-EF13-16	cDNA	CCTCTTCGTTGGAGGAATGT	GGGACAGGTGGGTAAACCTT
DNMT3A-EF15-18	cDNA	GGCACAAGGGTACCTACGG	CCCAATCACCAGATCGAATG
DNMT3A-FF17-20	cDNA	CCAGGGGAAGATCATGTACG	TGCAGCTGACACTTCTTTGG
DNMT3A-FF19-22	cDNA	CCCTTCTTCTGGCTCTTTGA	CTTTCCATTTCAGTGCACCA
DNMT3A-FE21-23	cDNA	CCACTGTGAATGATAAGCTGGA	TTGTGTCGCTACCTCAGTTTG
ELT3-EE16-17	cDNA	CAGCTCTGAAAGAGAGGGC	CTICTTAGATAGTTGAGAAGATCACC
FLT3-FE20-22	cDNA	CCGCCAGGAACGTGCTTG	ATGCCAGGGTAAGGATTCACACC
IDH1-E04	gDNA	AAACTTTGCTTCTAATTTTTCTCTTTC	GCAAAATCACATTATTGCCAAC
IDH1-FE04-05	cDNA	GCTTGTGAGTGGATGGGTAA	TATGTACCAGGTATGTCACCTT
IDH2-E04	gDNA	TGCAGTGGGACCACTATTATCTC	CACCACTGCCATCTTTTGG
IDH2-FE03-05	cDNA	ACTGGCCACCCAGAAGTA	TTGTACACTTCCCACTCC
NPM1-FE10-11	cDNA	TCCCAAAGTGGAAGCC	GGAAAGTTCTCACTCTGC
NRAS-E02	gDNA	GGCCGATATTAATCCGGTGT	TCCGACAAGTGAGAGACAGG
NRAS-E03	gDNA	CCCTCCCTGCCCCCTTAC	СААТGTCAAACAACCTAAAACCA
NRAS-FE02-03	cDNA	GGGAAAAGCGCACTGACAAT	CCTTCGCCTGTCCTCATGTA
NRAS-FE02-03	cDNA	GCTGTGGTCCTAAATCTGTCC	AGGTACATCATCCGAGTCTTTTAC
RUNX1-E01	gDNA	GCTGTTTGCAGGGTCCTAAC	GGCCTCCGCCTGTCCTC
RUNX1-E02	gDNA	CATTGCTATTCCTCTGCAACC	GTTTGTTGCCATGAAACGTG
RUNX1-E03	gDNA	AAATTCCGGGAGTGTTGTCA	GAAAGGTTGAACCCAAGGAA
RUNX1-E04	gDNA	TGATCTCTTCCCTCCTCCT	CAGTTGGTCTGGGAAGGTGT
RUNX1-E05	gDNA	ATTTGAACAAGGGCCACTCA	AATGTTCTGCCAACTCCTTCA
RUNX1-E06.01	gDNA	CTCCGCAACCTCCTACTCAC	CCCACCATGGAGAACTGGTA
RUNX1-E06.02	gDNA	CCCGTTCCAAGCCAGCTC	GCTTGTCGCGAACAGGAG
	1		

RUNX1-FE01-02	cDNA	TGCAGGGTCCTAACTCAATC	CATTGCCAGCCATCACAGTGAC
RUNX1-FE02-04	cDNA	TTTCAAGGTGGTGGCCCTA	CTGAGGGTTAAAGGCAGTGGAGT
RUNX1-FE04-06	cDNA	CCGGGAGCTTGTCCTTTTCC	CGGCAGGTAGGTGTGGTAG
RUNX1-FE06-06	cDNA	CAGGCGCCTTCACCTACTC	TGACCTACAGCGAGATCCTG
RUNX1-FE06-06	cDNA	CAGGCGCCTTCACCTACTC	CTCAGTAGGGCCTCCACACG
RUNX1-FE06.01	cDNA	CAGGCGCCTTCACCTACTC	TGACCTACAGCGAGATCCTG
RUNX1-FE06.01	cDNA	CAGGCGCCTTCACCTACTC	GTCGCTCTGGTTCGGGAG
RUNX1-FE06.02	cDNA	CTCCTACCACCTGTACTACGG	CTGACCTACAGCGAGATCCTG
TET2-E03.01	gDNA	ATTCAACTAGAGGGCAGCCTTG	ACTGTGCGTTTTATTCCTCCAT
TET2-E03.02	gDNA	GAATACCCTGTATGAAGGGAAGC	CCCACTGCAGTTATGTGTTGAA
TET2-E03.03	gDNA	TGTAGCCCAAGAAAATGCAG	TGGGTGAGTGATCTCACAGG
TET2-E03.04	gDNA	CATCTCACATAAATGCCATTAACA	AGCTTGCAAATTGCTGCTG
TET2-E03.05	gDNA	GAAAATAACATCCAGGGAACCA	CCCTCTATTTTCACTTCCCTTAAA
TET2-E03.06	gDNA	GGAGTTTTAGAAGAACACCACCA	TCGACCCTTCAGAATCTCTTG
TET2-E03.07	gDNA	CCAATTTTTGGTAGCAGTGGA	CCAGCTGTGTTGTTTCTGG
TET2-E03.08	gDNA	TGACCTCCAAACAATACACTGG	TGAGTTTGAAAATGGCTCAGTC
TET2-E03.09	gDNA	CCCAGTGTTGAAACAGCA	ACTTCCTCCAGTCCCATTTG
TET2-E03.10	gDNA	TGGTGAAAATCAGTATTCAAAATCA	CCCTGTAGAACTGAAGCTTGTTG
TET2-E03.11	gDNA	CTTCTTCACAGGTGCTTTCAAG	ATACAGGCATGTGGCTTGC
TET2-E03.12	gDNA	TTGCCATAGTCAGATGCACAG	CTGAAGAAGTTGTTTGCTGCTCT
TET2-E03.13	gDNA	TTGACTAGACAAACCACTGCTG	TTTATGAGCCTTTACAAATTGCTG
TET2-E04	gDNA	TGGCACATTTTCTAATAGATCAGTC	CTTTGTGTGTGAAGGCTGGA
TET2-E05	gDNA	AAACCGTTCATTTCTCAGGATG	GTAATGTTCTTTTTAACTGGCATGA
TET2-E06	gDNA	TGACCCTTGTTTTGTTTTGG	CGCTGAACTCTCTTCCA
TET2-E07	gDNA	ATAGACACCTATAATATCAGCTGCAC	CAGTTTGGGAAAAACTTTGATTA
TET2-E08	gDNA	CCATATATTGTGTTTGGGATTCAA	GCAGTGGTTTCAACAATTAAGAG
TET2-E09	gDNA	TGCTCTATTTTGTGTCATTCCATT	CAGTGTGAGAACAGACTCAACAG
TET2-E10.01	gDNA	GGGACCTGTAGTTGAGGCTGT	GGGGCTGACTTTTCCTTTTC
TET2-E10.02	gDNA	GAGTTTGGGAGTGTGGAAGC	GGGGGCAAAACCAAAATAAT
TET2-E11.01	gDNA	GCCTTCATAAAATAATCATCAACA	CTGCAGCTTGAGATGAGGTG
TET2-E11.02	gDNA	CCAATCCAGTTAGTCCTTATCCA	AAAACTCTGGCTATTTCCAAACC
TET2-E11.03	gDNA	CAAGCCAAGACCCTCTGTCT	GCATGAAGAGAGCTGTTGAA
TET2-E11.04	gDNA	GGTGAACATCATTCACCTTCTC	GAATTGACCCATGAGTTGGAG
TET2-E11.05	gDNA	AGACAGCGAGCAGAGCTTTC	AAGTTTCATGTGGCTCAGCA
TET2-E11.06	gDNA	AGCCCGTGAGAAAGAGGAAG	ACTGTGACCTTTCCCCACTG
TP53-E04	gDNA	ACCTGGTCCTCTGACTGCTC	CAGGCATTGAAGTCTCATGG
TP53-E05E06	gDNA	CACTTGTGCCCTGACTTTCA	GCCACTGACAACCACCCTTA
TP53-E07	gDNA	CTTGCCACAGGTCTCCCC	AAGAGGTCCCAAAGCCAGAG
TP53-E08E09	gDNA	GACAAGGGTGGTTGGGAGTA	ACAGTCAAGAAGAAAACGGCA
TP53-E10	gDNA	ACTTGAACCATCTTTTAACTCAGGT	TCTGTGCAGGGCTGGGAC
TP53-FE02-06	cDNA	CAGTCAGATCCTAGCGTCGAG	ACACGCAAATTTCCTTCCAC
TP53-FE03-05	cDNA	TCAGACCTATGGAAACTACTTCCTG	GGCAAAACATCTTGTTGAGG
TP53-FE04-06	cDNA	GGCCCCTGTCATCTTCTGT	ACACGCAAATTTCCTTCCAC
TP53-FE05-08	cDNA	TGGCCATCTACAAGCAGTCA	AGCTGTTCCGTCCCAGTAGA
TP53-FE06-11	cDNA	CTCAGCATCTTATCCGAGTGG	TTATGGCGGGAGGTAGACTG
TP53-FE07-10	cDNA	TGGCTCTGACTGTACCACCA	CCTCATTCAGCTCTCGGAAC
TP53-FE09-11	cDNA	CCAGCCAAAGAAGAAACCAC	TTCTGACGCACACCTATTGC
WT1-E07	gDNA	GACCTACGTGAATGTTCACATG	ACAACACCTGGATCAGACCT
WT1-E09	gDNA	TGCAGACATTGCAGGCATGGCAGG	GCACTATTCCTTCTCAACTGAG