Dokumenttyp: journal article

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Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis.

By combining genome-wide association data from 8,130 individuals with type 2 diabetes (T2D) and 38,987 controls of European descent and following up previously unidentified meta-analysis signals in a further 34,412 cases and 59,925 controls, we identified 12 new T2D association signals with combined P<5x10^-8. These include a second independent signal at the KCNQ1 locus; the first report, to our knowledge, of an X-chromosomal association (near DUSP9); and a further instance of overlap between loci implicated in monogenic and multifactorial forms of diabetes (at HNF1A). The identified loci affect both beta-cell function and insulin action, and, overall, T2D association signals show evidence of enrichment for genes involved in cell cycle regulation. We also show that a high proportion of T2D susceptibility loci harbor independent association signals influencing apparently unrelated complex traits.