An integrative approach for the identification of prognostic and predictive biomarkers in rectal cancer.

Colorectal cancer is the third most common cancer in the world, a small fraction of which is represented by locally advanced rectal cancer (LARC). If not medically contraindicated, preoperative chemoradiotherapy, represent the standard of care for LARC patients. Unfortunately, patients shows a wide range of response rates in which approximately 20% has a complete pathological response, whereas in 20 to 40% the response is poor or absent. The following specific gene signature, able to discriminate responders' patients from non-responders, were founded: AKR1C3, CXCL11, CXCL10, IDO1, CXCL9, MMP12 and HLA-DRA. These genes are mainly involved in immune system pathways and interact with drugs traditionally used in the adjuvant treatment of rectal cancer. The present study suggests that new ideas for therapy could be found not only limited to studying genes differentially expressed between the two groups of patients but deepening the mechanisms, associated to response, in which they are involved. Gene expression studies performed by: Agostini et al., Rimkus et al. and Kim et al. have been merged through a meta-analysis of the
raw data. Gene expression data-sets have been processed using A-MADMAN. Common differentially expressed gene (DEG) were identified through SAM analysis. To further characterize the identified DEG we deeply investigated its biological role using an integrative computational biology approach.