



Supplementary Figure S2. Functional category analysis of the predictive genes. To identify functional categories within the set of predictive genes we applied a gene ontology (GO) analysis on the predictive genes using the online Expression Profiler software (1, 2). The used GO version was downloaded from <http://www.geneontology.org> on 10 June 2005. Overrepresented functional classes were determined for the three GO categories: cellular component (**A**), biological process (**B**) and molecular function (**C**). Of the 825 predictive genes, 483 were annotated in the GO database, versus 1634 of the 3064 significantly regulated genes across the tumor samples. P-values for overrepresented GO categories in the group of predictive genes are corrected for multiple testing using a stringent simulation correction (3). Significantly ($P < 0.05$) overrepresented categories are colored in grey. The colored bars denote the proportion of upregulation (red) and down-regulation (green).

References:

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