



Supplementary Figure S1: Gene-set over-representation analysis of candidate biomarkers.

The biological processes that the 152 candidates were associated with were uncovered by gene-set over-representation analysis (GSOA) using the ConsensusPath database (<http://cpdb.molgen.mpg.de>). The 17 significantly over-represented processes and pathways with greatest statistical power are depicted (P-value < 0.002).