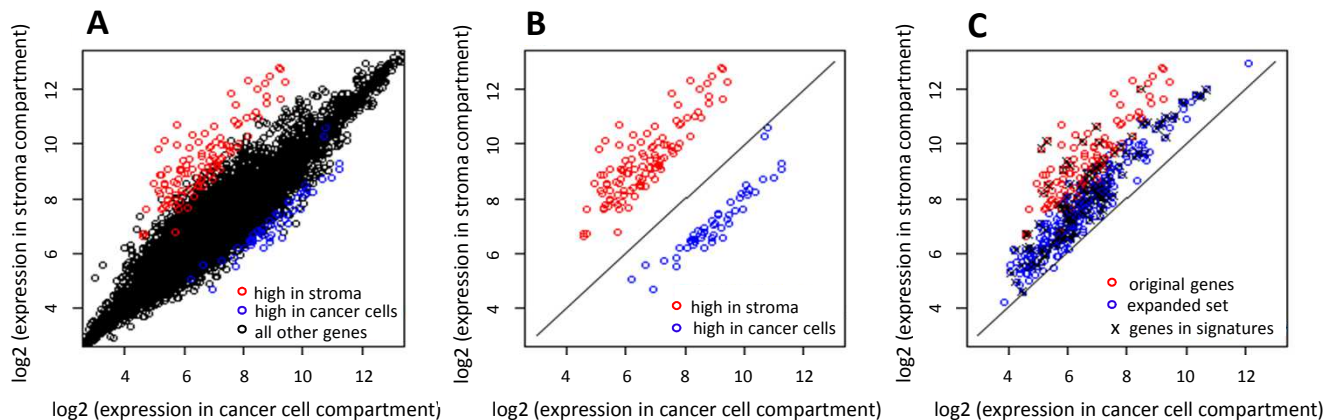


Supplementary Figure S2.



Identification of compartment-enriched genes and stroma gene sets. Using the `lmfit` function in the `limma` package of R, probes that were enriched in either compartment were identified with an adjusted p -value < 0.05 as cutoff. The scatter plots (A and B) show expression values for all probes of genes for which one probe was enriched in stroma (red) or cancer cell (blue) compartment. The black circles in (A) indicate genes for which no probe was significantly enriched in either compartment. In (C) the expanded gene set (361 genes) are shown in red (original genes enriched in stroma) and blue (genes found after expansion with TCGA data); \times denotes the genes in the final signatures.