

Expression profiles of most frequently selected informative genes

Figure S5: Expression profiles of most frequently selected signature genes

The heatmap shows the expression profiles of all candidate biomarker genes which are contained in at least 3 of the 8 predicted signatures. These signatures were proposed for 4 different classification tasks (C vs. NC, GC vs. NGC, GC vs. NC, NGC vs. NC). For each classification task two treatment durations (3 days and 14 days) were considered, independently.