**Supplementary Table/Figure legends**

**Supplementary Table 1** Summary of cases, clinical variables and expression of immune signatures.

**Supplementary Table 2** Gene expression signatures for immune and stromal cell populations.

**Supplementary Table 3** Summary of functional signatures.

**Supplementary Table 4** Stratified survival analysis of immune, stromal and functional signatures as well as immune checkpoint molecules.

**Supplemental Figure 1** (a) Graphical illustration of batch correction for the datasets. (b) Box-plots of age distribution of different mutational subgroups.

**Supplemental Figure 2** (a) Immune cluster (1-4) distribution (in %) among age, mutational- and transcriptional subgroups. Immune clusters were defined in Figure 3. (b) Immune cluster (1-4) distribution (total n) among age, mutational- and transcriptional subgroups. (c) Correlation of the gene expression signature of different cellular immune subsets and stromal components.

**Supplemental Figure 3** (a) Progression-free survival of different immune clusters defined in Figure 4. (b) T-SNE representation as illustrated in Figure 4. Neoadjuvant samples are highlighted in orange. (c) Gene expression level of different signature for immune cell subsets. (d) Progression-free survival of immune clusters (immune 1-4) as defined in Figure 3.

**Supplemental Figure 4** (a+b) Box-plots of published gene expression signatures as described in Figure 4. Individual signatures were plotted according to age, histological diagnosis, mutational- or transcriptional subtype.