**Supplementary Figure S1: Jaccard similarity index between signatures.** Heat map represents the similarity between the different publications for each cell type. Cell types present in two or more publications were only used. For the purpose of this figure, subtype related genes were collated into its parent population, followed by the calculation of Jaccard’s index. A non-collated version of the data is available in Supplementary Table 4.

**Supplementary Figure S2: Correlation between observed and predicted abundance of immune cells.** RNA-Seq data from four melanoma patients (GSE93722) were used in this analysis. X-axis represents the predicted relative abundance of immune cells (*ImSig*), y-axis represents the observed relative abundance of immune cells determined by FACS analysis. The plot shows that the cell types (B cells, T cells and NK cells) from these patients show a high concordance between the observed and predicted values. The blue line represents the regression line.

**Supplementary Figure S3:** **Validation of immuno-subgroups in melanoma. (A)** Expression profile of *ImSig* related genes within the various clusters/grouping defined by MCL clustering a melanoma dataset (GSE65904). Here y-axis is the average expression of the signature genes and x-axis are the patients ordered by the defined groupings. **(B)** Univariate Cox proportional analysis between the patient groups.