Supplemental materials for: Hose et al

Calculation of the gene expression based proliferation index

The gene expression based proliferation index is calculated as follows. In brief, genes are selected based on genes overexpressed in proliferating cells (malignant: human myeloma cell lines HMCL, benign: polyclonal plasmablastic cells PPC) compared to non-proliferating cells (normal bone marrow plasma cells BMPC and memory B cells MBC). Here, four comparisons between the groups are made (i) HMCL vs. MBC, ii) HMCL vs. BMPC, iii) PPC vs. BMPC and iv) PPC vs. MBC) by a onesided t-test, with the alternative hypothesis being that expression values of HMCL and PPC values are greater compared to BMPC and MBC in each comparison. P-values are permutation-adjusted regarding a family wise error rate with an α level of 0.025. To adjust for comparing each group twice, the α level is halved to 0.0125. Only genes being statistically significant in each of the 4 comparisons are retained for the index. To select biologically (in terms of proliferation) relevant genes, only genes matching with the gene-ontology term "cell proliferation" or "cell cycle" were retained. Thus, 50 genes (57 probesets) represent the final index. For genes with more than one probeset per gene, the probeset with the highest variance within the TG is selected. The index is calculated as follows: as proliferation genes determined as stated above are overexpressed by definition, the individual gene expression based proliferation index for each sample is calculated as the sum of expression values of each of the 50 genes in an individual sample. For genes not expressed as judged by PANP, the expression level of the respective gene is defined as 0.