



Supplementary Figure S5: Comparison of signature detection in High Quality and Low Quality Samples

Upper row presents results from AIMS subtyping for 221 *High Quality Samples* (left) and 68 *Low Quality samples* (right). Log₂ count data of the 268 genes shown in the lower (red/green) heatmaps were normalized by median centering across all 289 samples together for the analysis shown here. Gene signatures in the above (yellow/blue) heatmaps were calculated as mean values of the respective gene clusters in the lower panels. The *Low Quality samples* on the right show a larger proportion of samples classified as Her2-enriched and Normal-Like (NL) subtypes (Supplementary Table S8). The heatmaps of the *Low Quality samples* reveal that no effective detection was obtained for most individual genes (green in the lower right panel) and signatures (blue in the upper right panel). (Sample sorting from left to right follows AIMS subtype and subsequently T-cell signature expression).