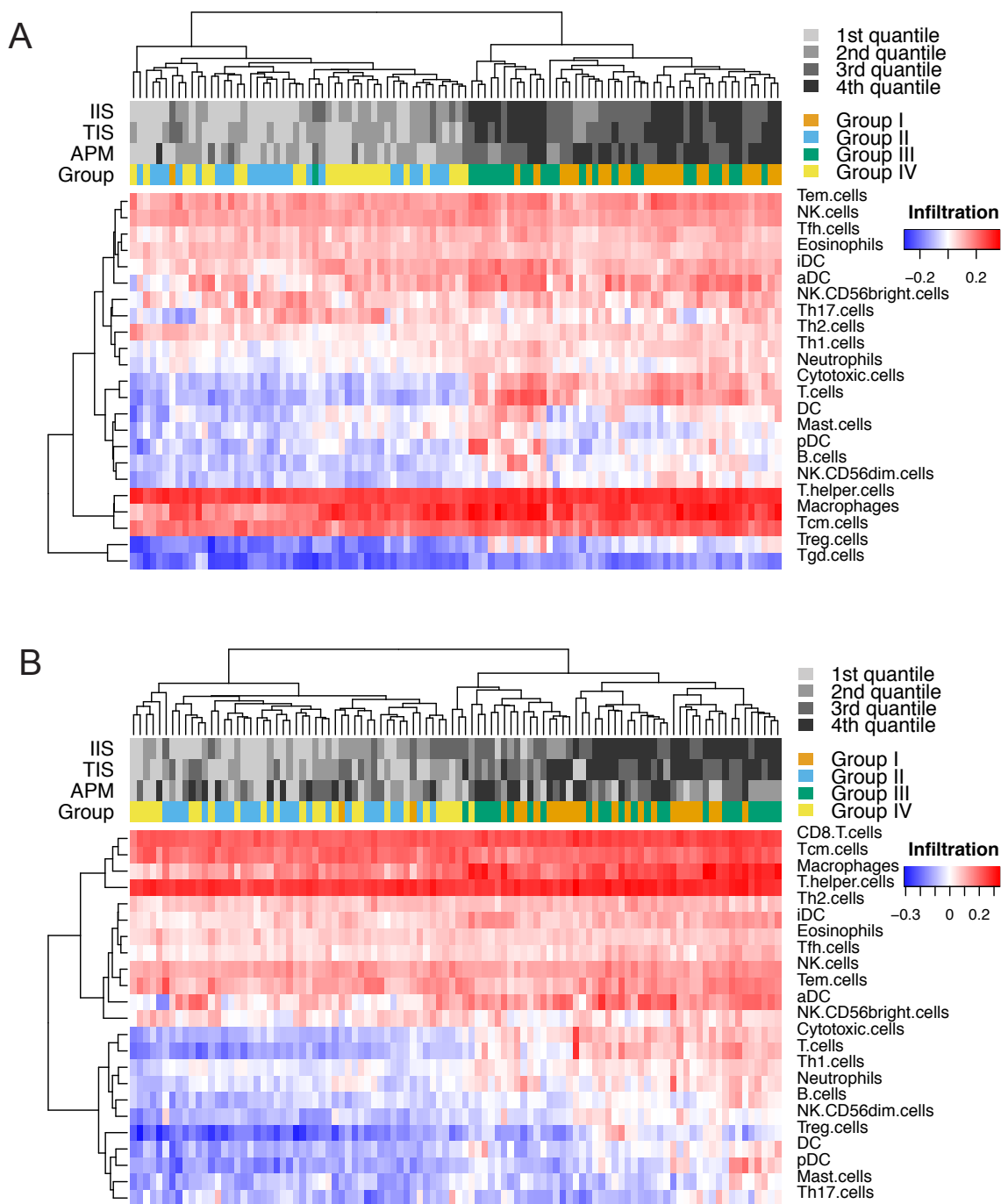
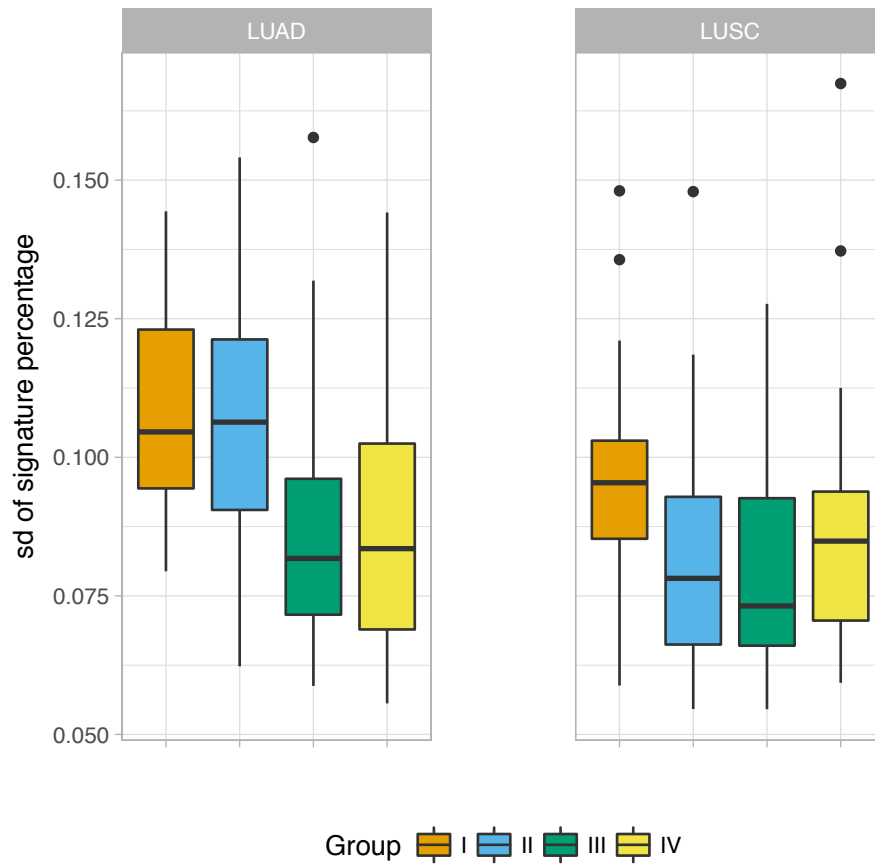


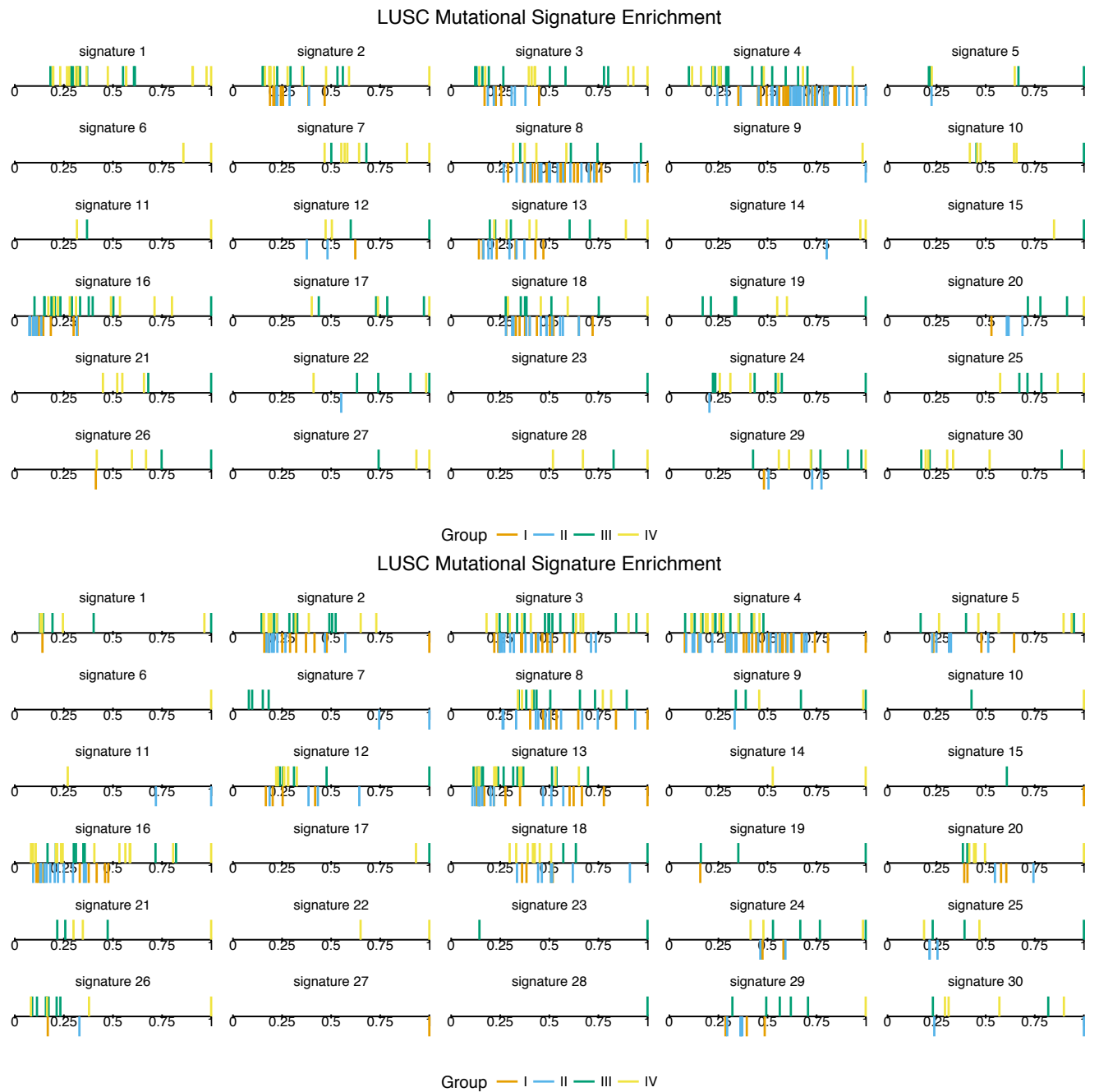
**Supplementary Figure 1. The scatter plots of mutation load and inflammation signature (CYT values) in LUAD (A) and LUSC (B).** The CYT values were calculated as log-average expression of *GZMA* and *PRF1*. (A) LUAD patients with extreme mutational load and CYT values were evenly selected from 4 groups (25 per group): group I with high mutation load (>450) and high CYT (log-average >9); group II with high mutational (>450) load and low CYT (log-average <6.57); group III with low mutational load (<210) and high CYT (log-average >8.95); group IV with low mutational load (<190) and low CYT (log-average <5.98). (B) LUSC patients with extreme mutational load and CYT values were evenly selected from 4 groups (25 per group): I with high mutation load (>450) and high CYT (log-average >8.7); II with high mutational (>450) load and low CYT (log-average <6.85); III with low mutational load (<240) and high CYT (log-average >8.7); IV with low mutational load (<219) and low CYT (log-average <6.3).



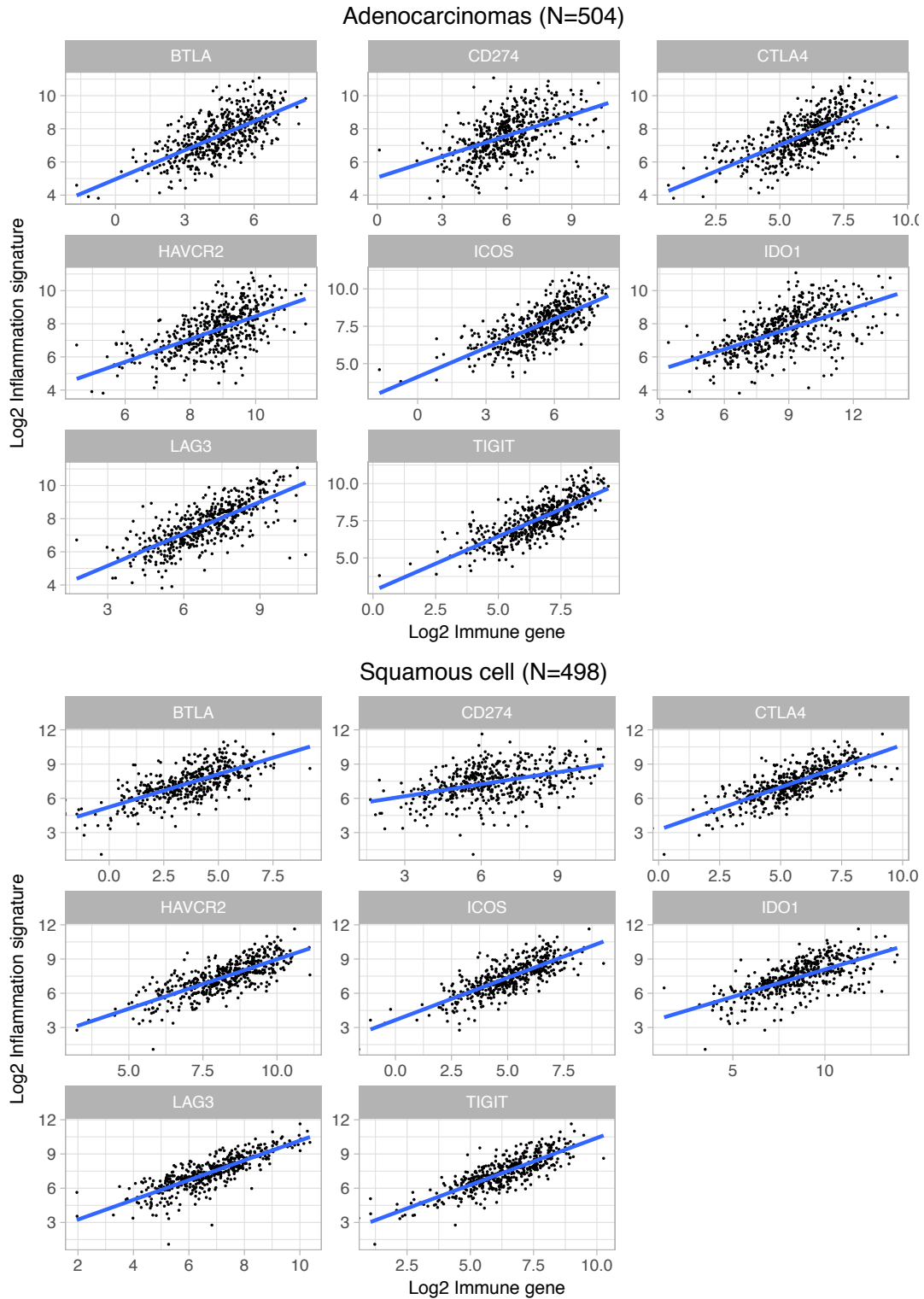
**Supplementary Figure 2. Heatmap and clustering analysis of relative cell infiltrates based on estimates from ssGSEA for LUAD (A) and LUSC (B).**



**Supplementary Figure 3. Standard deviations of mutational signatures (per patient) in four groups.** Larger standard deviations of mutational scores indicate smaller diversity. High-mutation group (I and II) patients showed less diversity of mutational landscape in LUAD, while only group I in LUSC samples show relatively lower diversity.



**Supplementary Figure 4. Enrichment plot of 30 mutational signatures in LUAD and LUSC cohorts.** The X axis are the scaled signature score (divided by the maximum value across all samples). The bars above the axis are patient values from low mutation groups (III and IV) and the bars below the axis are from the high mutation groups (I and II).



**Supplementary Figure 5. Correlation of CYT values and immune checkpoint genes (all TCGA lung cancer samples).**