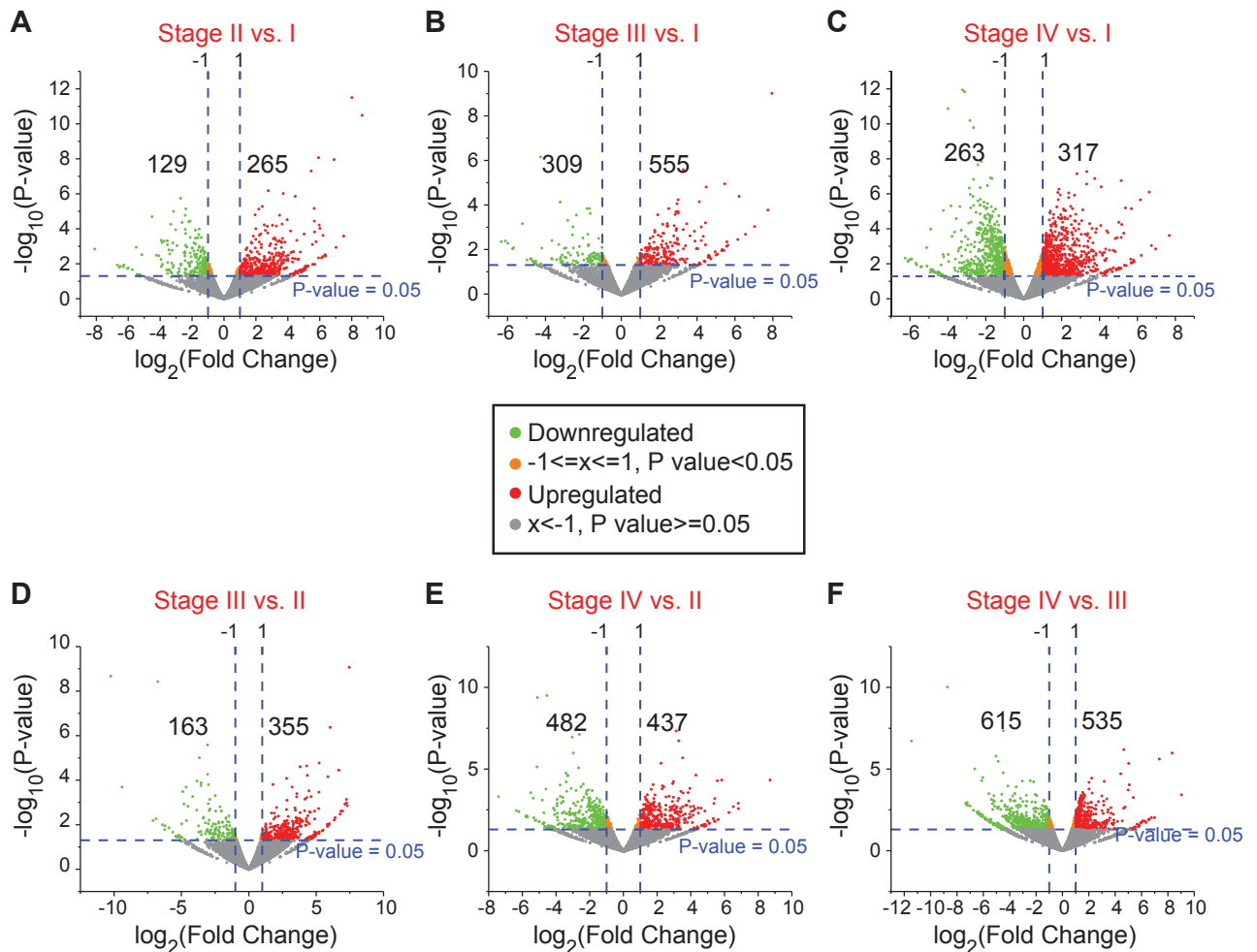
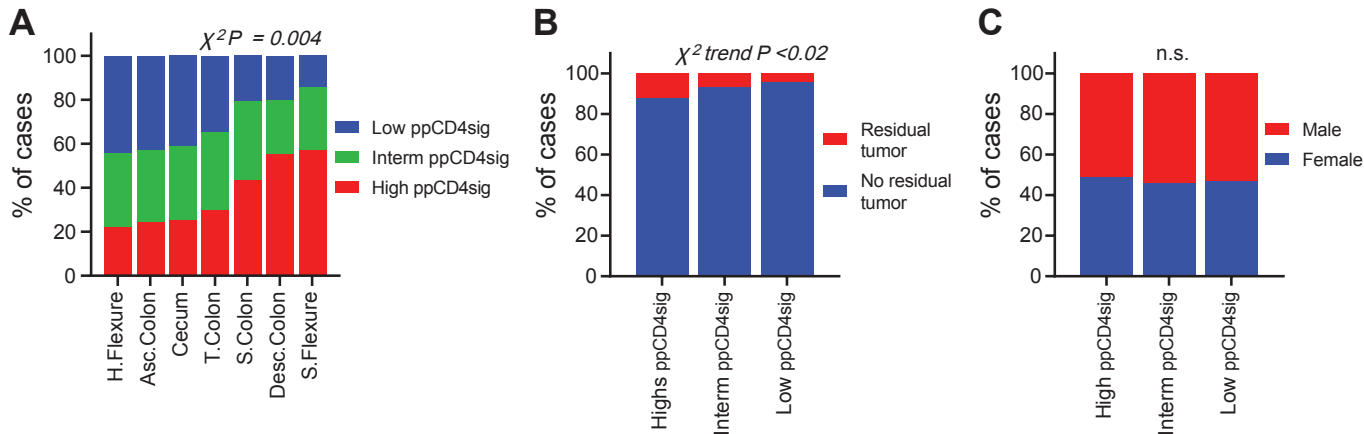


**Supplementary Figure 1:** Hierarchical clustering and PCA analyses of differentially expressed genes from advanced CRC stages vs. early stages. Hierarchical clustering of deregulated genes, which were significantly (FC >2 and P value <0.05) upregulated or downregulated from advanced stages vs. early stages analyses are represented as heat maps (A). The red colored transcripts are upregulated, while the blue colored are the downregulated transcripts. The PCA plot shows the percentage of variation between the DEGs from advanced stages vs. early stages analyses using first two principal components (B). Bar plots show the validation of RNA-Seq data by qRT-PCR (C). The fold change of 6 deregulated genes from RNA-Seq data (advanced stages vs. early stages) was validated with qRT-PCR. Data obtained are from the differential expression analyses; 8 patients from advanced stages vs. 10 patients from early stages.



**Supplementary Figure 2:** Analyses of deregulated genes from stage-wise comparison. Volcano plots show the deregulated genes obtained from stage II vs. I (**A**), III vs. I (**B**), IV vs. I (**C**), III vs. II (**D**), IV vs. II (**E**) and IV vs. III (**F**). Significantly upregulated transcripts (with  $P < 0.05$ ) are depicted as red circles, downregulated transcripts as green and non-significant transcripts as grey. The number of deregulated genes are stated for each comparison.



**Supplementary Figure 3:** Evaluation of the poor prognosis CD4<sup>+</sup> TIL gene signature in the TCGA CRC dataset. Distribution of patients with high, intermediate, or low ppCD4sig scores across the different anatomical location of their colon cancer. Left-sided colon cancer patients (splenic (S.) flexure, descending (Desc.) and sigmoid (S.) colon) had higher ppCD4sig than patients with transverse colon and right-sided colon cancers (hepatic (H. flexure, ascending (Asc.) colon and the cecum). Stated P value are from Chi-square ( $\chi^2$ ) test (GraphPad Prism) (A). Patients with high ppCD4sig had a trend for presence of residual disease after treatment (Chi-square test for trend) (B). Male and female CRC patients were equally distributed across the three ppCD4sig score groups (C).