Supplemental material

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Supplemental Figure 15. CCL4 expression is associated with a productive tumor immune microenvironment. **A)** High expression of CCL4 is positively associated with the hallmark gene sets of tumor rejection and negatively associated with the hallmarks of tumor promotion. The log2 fold change level of each gene between a high and low group was used as input for the GSEA-preranked. The GSEA was performed using the Molecular Signatures Database (MSigDB). The 50 hallmark gene sets were illustrated by their normalized enrichment score (NES). Red and blue dots show the enrichment and depletion of hallmark gene sets, respectively. **B)** ClueGO analysis of highly significant associated genes with high expression of CCL4 in the tumor microenvironment (R>0.7 and R>0.4, respectively, adj-value <0.05). The bars represent the percentage of highly significantly correlated genes associated with the GO terms (%Genes/term). The number of expressed genes per term is shown as bar label. P-value is indicated by asterisks. **C)** Overview chart with functional groups including specific terms for highly significantly associated genes with high expression of CCL4. * mid-P values of two-sided (enrichment/depletion) tests based on the hyper geometric distribution (Rivals, 2007, PMID. 17182697).