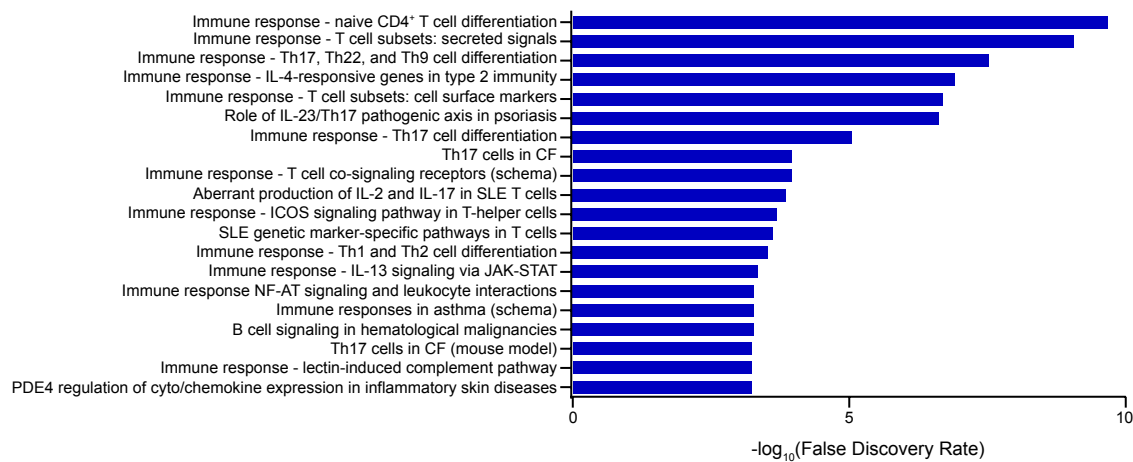
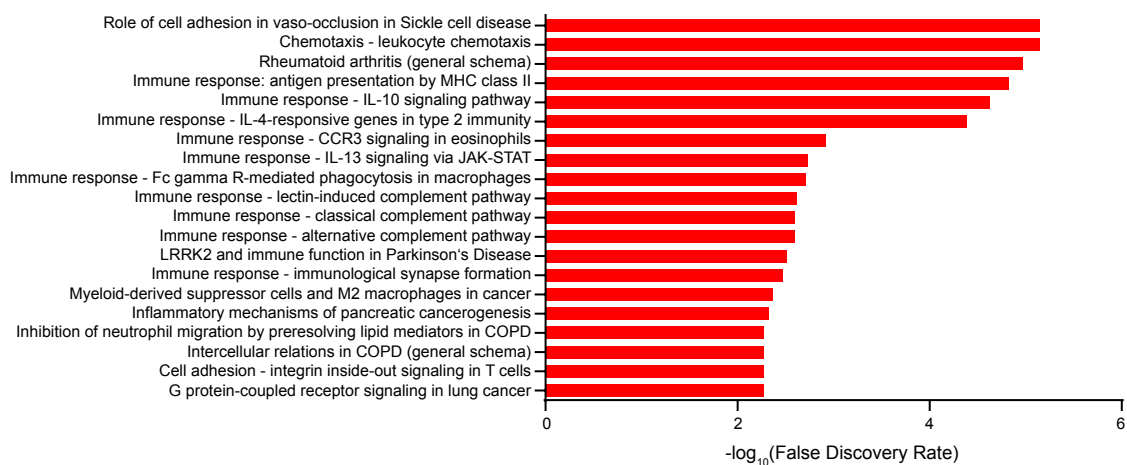


A Downregulated pathways



B Upregulated pathways



Supplementary Figure S7.

Metacore pathway analysis of Nanostring gene expression data. EMT-6 tumor-bearing mice were treated with isotype control, NHS-muIL12 (2 or 10 μg), or avelumab (200 μg), as defined in the Figure 5 legend. Genes that were differentially expressed after combination treatment with NHS-muIL12 (10 μg) and avelumab relative to isotype control treatment were analyzed using Metacore's significant pathways analysis. Plots were generated for the $-\log_{10}$ of the false discovery rate (FDR) for (A) downregulated and (B) upregulated pathways. The analysis was run twice: the first analysis was limited to the set of genes with adjusted p-value < 0.05 and \log_2 fold change > 1 ; the second analysis was limited to the set of genes with adjusted p-value < 0.05 and \log_2 fold change < -1 .