

Supplemental Figure 7: Identification of ‘chemokine signaling’ as a key downregulated function in obese subjects based on analysis performed in DAVID software (Database for Annotation, Visualization and Integrated Discovery, <http://david.abcc.ncifcrf.gov/>). A list of 2234 Agilent probes (downregulated at 1.5-fold or greater in the obese compared to lean) was entered as input into DAVID. Functional annotation of the top KEGG pathways identified the ‘chemokine signaling’ pathway as a highly enriched module (Fisher exact $p < 1.2E-7$, Benjamini FDR 6.8E-6). Among all genes in the pathway, the genes marked with a red star satisfied the fold-change threshold criteria for input into DAVID.

