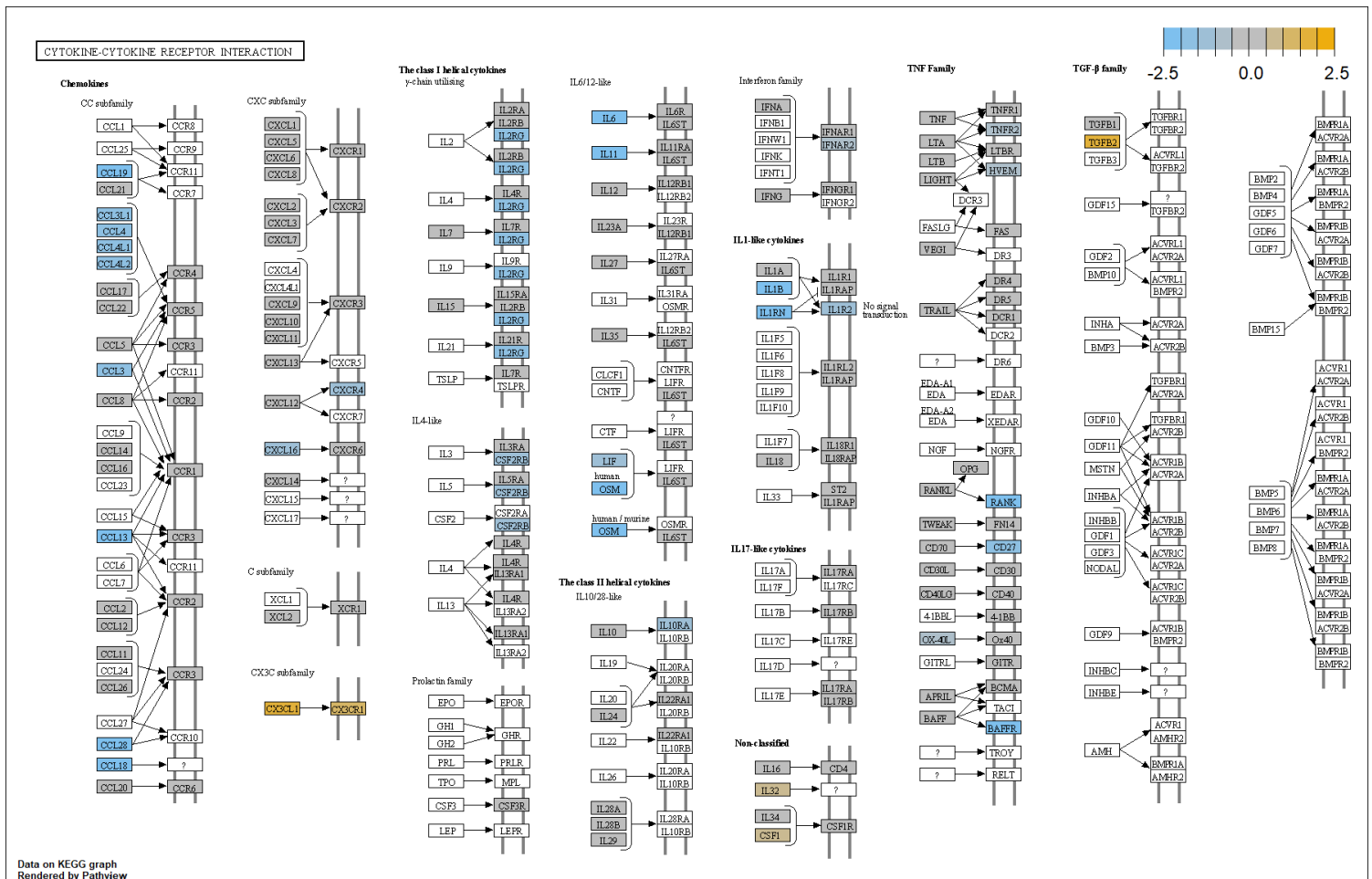
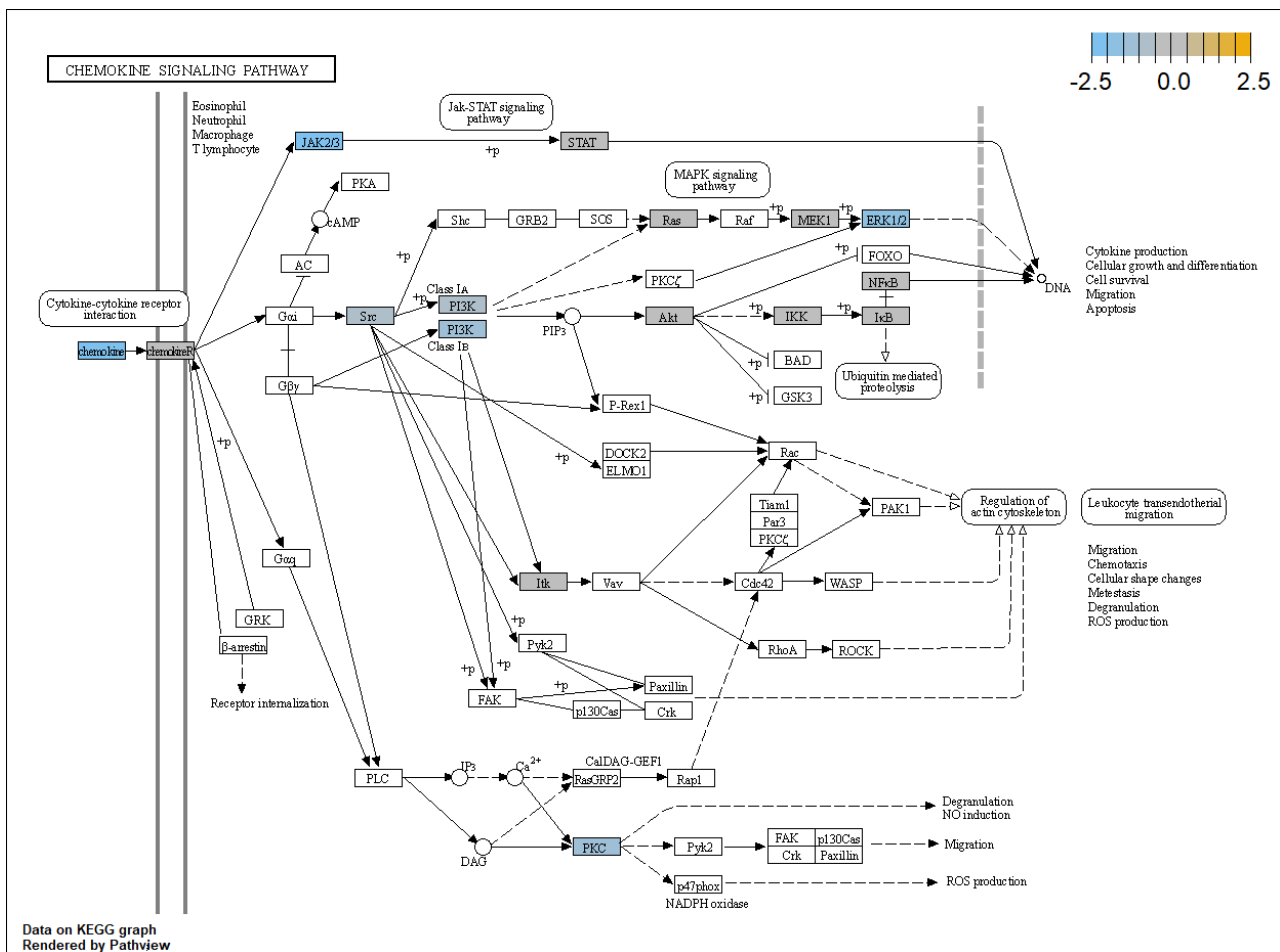


Suppl. Fig. 1 *Pathview: Cytokine-Cytokine Receptor Interaction*



Pathview based on KEGG pathway with overlaid differential expression data. White nodes represent genes which were not represented in the panel. Grey nodes were not significantly differentially expressed. Blue nodes were downregulated and orange nodes were upregulated in SD-iCCA relative to our baseline of LD-iCCA.

Suppl. Fig. 2 Pathview: Chemokine Signaling Pathway



Pathview based on KEGG pathway with overlaid differential expression data. White nodes represent genes which were not represented in the panel. Grey nodes were not significantly differentially expressed. Blue nodes were downregulated and orange nodes were upregulated in SD-iCCA relative to our baseline of LD-iCCA.