**Supplementary Figure 1. Flowchart describing microarray analysis.**

Datasets were downloaded from the GEO website and merged (GSE6008 and GSE3149) or analysed as independent dataset (GSE9899). The function geneSetTest from the limma package was used to assess whether each sample had a tendency to be associated with an up or down regulation of members of the CXCR12, TNF or IL6 signaling pathways. The function employs a Wilcoxon t-test to generate p-values. All samples were ranked based a t-statistic for each sample, from the most significant to the least significant. The top and bottom 50 samples were collated to form two groups titled e.g. “highTNF signaling” and “lowTNF signaling” respectively. Differential gene expression was assessed between “highTNF” and “lowTNF” using the empirical Bayes t-test; p-values were adjusted for multiple testing correction using the Benjamini-Hochberg method. Any probesets that exhibited an adjusted p value of 0.05 were called differentially expressed.

**Supplementary Figure 2. Characterization of CXCR4 knockdown in TOV21G ovarian cancer cells.**

A) Real time RT-PCR analysis of CXCR4 expression by TOV21G, TOV21G-Mock and TOV21G-siCXCR4 cells and flow cytometry histograms for cell surface expression of CXCR4: TOV21G (thin line), TOV21G-Mock (dotted line) and siCXCR4 cells (red line). B) Assessment of cytokine mRNA expression of CXCL12, TNF, and IL6 by real time RT-PCR. Data are representative of three independent experiments performed (*, P <0.05 and **, P <0.01).

**Supplementary Figure 3. Effects of CXCR4 knockdown on protein expression levels of members in the TNF network in vivo.**

A) Flow cytometry histograms for cell surface expression of CXCR4 on IGROV-Mock or IGROV-shCXCR4 ovarian cancer cells extracted from primary tumors: IgG2α isotype control (black line), CXCR4 (red line) demonstrating sustained knockdown of CXCR4. B) Cytokine expression measured by ELISA using protein lysates of primary tumors. Data from 5 animals per group, mean values for CXCL12 and TNF (mean ± SEM) are shown.
\* = P<0.05 as compared with IGROV-Mock primary tumors.

C) Representative immunohistochemistry staining for HES1 in sections of the same tumors.

**Supplementary Figure 4 Effects of an anti-TNF antibody on Notch signalling in ovarian cancer xenografts**

HES1 nuclear staining after treatment with anti-TNF antibodies
A) representative immunohistochemistry pictures of nuclear HES1 staining; B) number of tumor cell nuclei showing positive staining for HES1 in 10 randomly selected areas per tumor section (n=3) using a x40 objective with approximately 500 nuclei counted per tumor area (\*, P <0.01).