**Supplementary Figure Legends**

**Supplementary Figure S1** Microarray gene expression across histological subtypes of endometrial cancers. (**A**) Kaplan-Meier analysis with the log-rank test of disease specific survival of 294 patients treated for endometrial cancer during 2004-2012. G1; endometrioid grade 1 (n=148), G2; endometrioid grade 2 (n=55), G3; endometrioid grade 3 (n=53), SPEC; serous papillary endometrial cancer (n=38). SPEC exhibits worse outcome (p<0.0001). (**B**) Unsupervised analysis of genes for which expression in SPEC and some of G3 was differently clustered from G1-G2. Blue bar; G1 (n=22), green bar; G2 (n=18), yellow bar; G3 (n=11), and red bar; SPEC (n=12). (**C**) External validation of the SPEC signature using supervised clustering analysis of TCGA UCEC\_2013 with genes for which expression distinguishes G3 and SPEC from G1-G2. Blue bar; G1, green bar; G2, yellow bar; G3, and red bar; SPEC. SPECs are enriched in a subcluster (in blue rectangle) that highly express *STAT1*. (**D**) A SAM analysis plot of the Kyoto University cohort showing 181 significantly upregulated genes (in red) and 43 significantly downregulated genes (in green) which differentiate serous-like endometrial cancer from endometrioid-like endometrial cancer.

**Supplementary Figure S2** Comparison of *STAT1* mRNA expression among histological subtypes of endometrial cancers. (**A**)The expression of spliced isoforms *STAT1α* and *STAT1β* was measured by quantitative PCR relatively to GAPDH (n=24). *STAT1* mRNA expression is significantly higher in SPEC (\**p*<0.05). (**B**) *STAT1* is highly expressed in SPEC in Kyoto CC microarray data (n=63, \**p*<0.001). (**C**) *STAT1* was highly expressed in SPEC in TCGA UCEC\_2013 microarray data (n=349, \**p*<0.0001). (**D**) *STAT1* was highly expressed in SPEC in GSE17025 microarray data (n=91, \**p*<0.05). (**E**) *STAT1* was highly expressed in SPEC in GSE24537 microarray data (n=33). (**F**) Representative micrographs of immunohistochemical staining of endometrial cancer tissue using an anti-STAT1 antibody and an IgG isotype control antibody (*top*: x4 and *bottom*:x*20*). (**G**) Kaplan-Meier analysis of disease specific survival for 410 patients in the Vancouver cohort between STAT1 expression low ≤1; and high >1. High STAT1 expression exhibits worse prognostic outcome (*p*<0.05).

**Supplementary Figure S3** Activity of STAT1 pathway genes in endometrial cancer cells. (**A**) *STAT1* mRNA expression in SPAC-1L cells was induced by IFNγ in a dose-dependent manner for both isoforms, and this induction was reduced by STAT1-siRNA pretreatment. This dose- dependent induction and reduction was also observed for STAT1-associated genes, *PD-L1* (**B**), and *ICAM1* (**C**). (**D-F**)mRNA expression of *IRF1*, *SMAD7*, and *MCP3* in endometrial cancer cell lines was assessed by quantitative RT-PCR: blue bar; non-treated, red bar; STAT1-suppresed with siRNA, green bar; IFNγ-treated, and purple bar; treated with both STAT1-siRNA and IFNγ. SPAC-1L showed high responsiveness to IFNγ treatment with induction of mRNA expression of *IRF1* (x12), *SMAD7* (x2), and *MCP3* (x3). In contrast, STAT1-siRNA treatment suppressed mRNA expression of *IRF1* and *SMAD7* in HEC50B and SPAC-1L cells.

**Supplementary Figure S4** Stable knockdown of *STAT1* expression. Establishment of SPAC-1L cells with stable knockdown of STAT1 using STAT1-siRNA, a dominant negative STAT1 DNA plasmid (pBOS-STAT1-DN) or STAT1-shRNA. Western blotting showed that STAT1-siRNA-2 (**A**), clone DN5 (**B**), and clone 89-C2 (**C**) exhibited the best suppression and were selected for further experiments. (**D**) Cell proliferation in SPAC-1L was assessed using WST-1 assays. Proliferation significantly decreased for clone DN5 (STAT1-DN5 cells, \**p*<0.0001) to a similar extent as that of STAT1-siRNA cells. (**E**) Colony formation in soft agar of STAT1-DN5 cells significantly decreased as compared to the control (n=5, \**p*<0.0001). (**F-G**) Adhesion and invasion of STAT1-DN5 cells was low, comparable to that of STAT1-siRNA cells (n=10, \**p*<0.0001).

**Supplementary Figure S5** Significance of STAT1-MYC activity in tumorigenesis. (**A**) Xenograft tumor growth did not occur in mice inoculated with STAT1-DN5 cells while tumors grew readily in mice inoculated with SPAC-1L cells (n=7 for each group, \**p*<0.0001). (**B**) Cmap analysis plot of sirolimus, doxorubicin, and paclitaxel for several cell lines based on SPEC’s gene signature. Sirolimus was predicted to be effective against tumors with the SPEC gene signature while doxorubicin and paclitaxel were predicted as not effective. (**C)** Western blotting showed MYC expression is not induced by IFNγ treatment in STAT1-DN5 cells. (**D**) Western blotting showed MYC expression is not influenced by STAT1 manipulation in response to IFNγ treatment in Ishikawa, HEC-1A, and HEC-50B cells. (**E**) Quantification of STAT1 protein expression intensity relative to β-actin: blue bar; mock-treated, red bar; *STAT1*-suppressed with siRNA, green bar; IFNγ-treated, and purple bar; treated with both STAT1-siRNA and IFNγ. (**F**) Quantification of STAT1 protein expression intensity relative to β-actin: blue bar; mock-treated, red bar; *STAT1*-suppressed with siRNA, green bar; IFNγ-treated, and purple bar; treated with both STAT1-siRNA and IFNγ. (**G**) Expression of *MYC* mRNAs in endometrial cancer cell lines was assessed by quantitative real time PCR: blue bar; mock-treated, red bar; *STAT1*-suppressed with siRNA, green bar; IFNγ-treated, and purple bar; treated with both STAT1-siRNA and IFNγ. (**H**) MYC activity was assessed in SPAC-1L cells and cells receiving STAT1-siRNA by binary regression analysis. The MYC signature score was lower in STAT1-siRNA cells (\**p*<0.05). (**I**) MYC signatures were significantly elevated in SPEC in the Kyoto CC microarray data (\**p*<0.05).