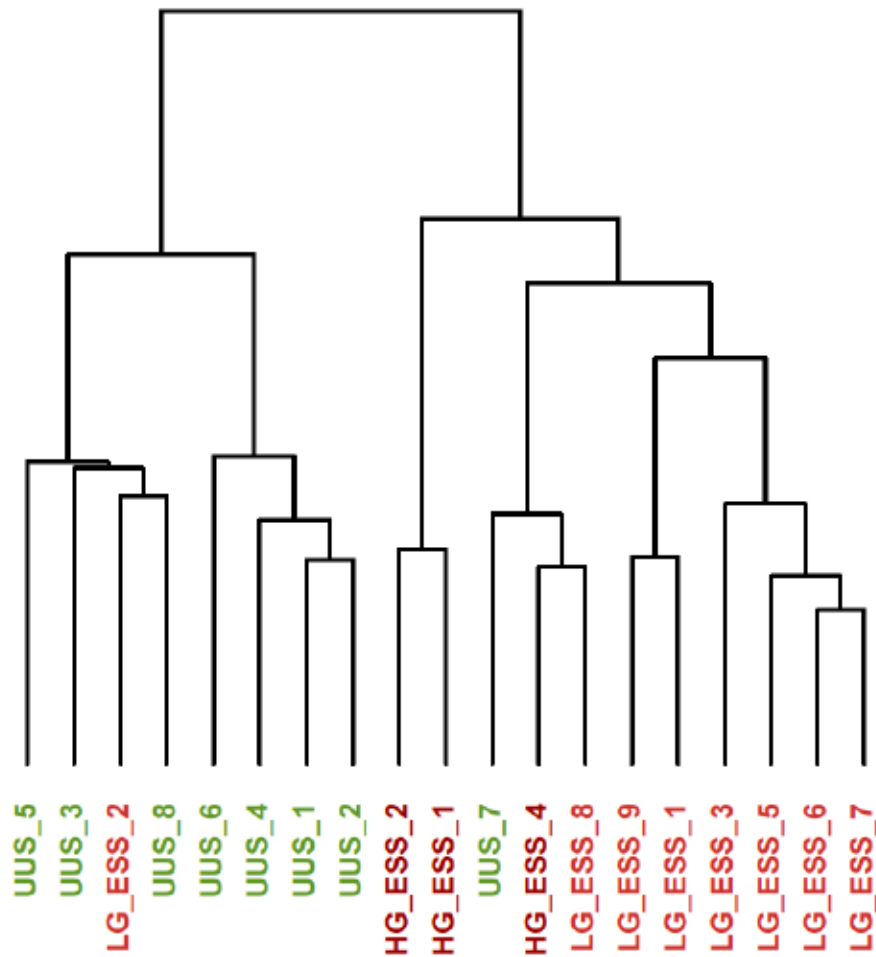


Supplemental Figures

Macrophage infiltration and genetic landscape of undifferentiated uterine sarcomas

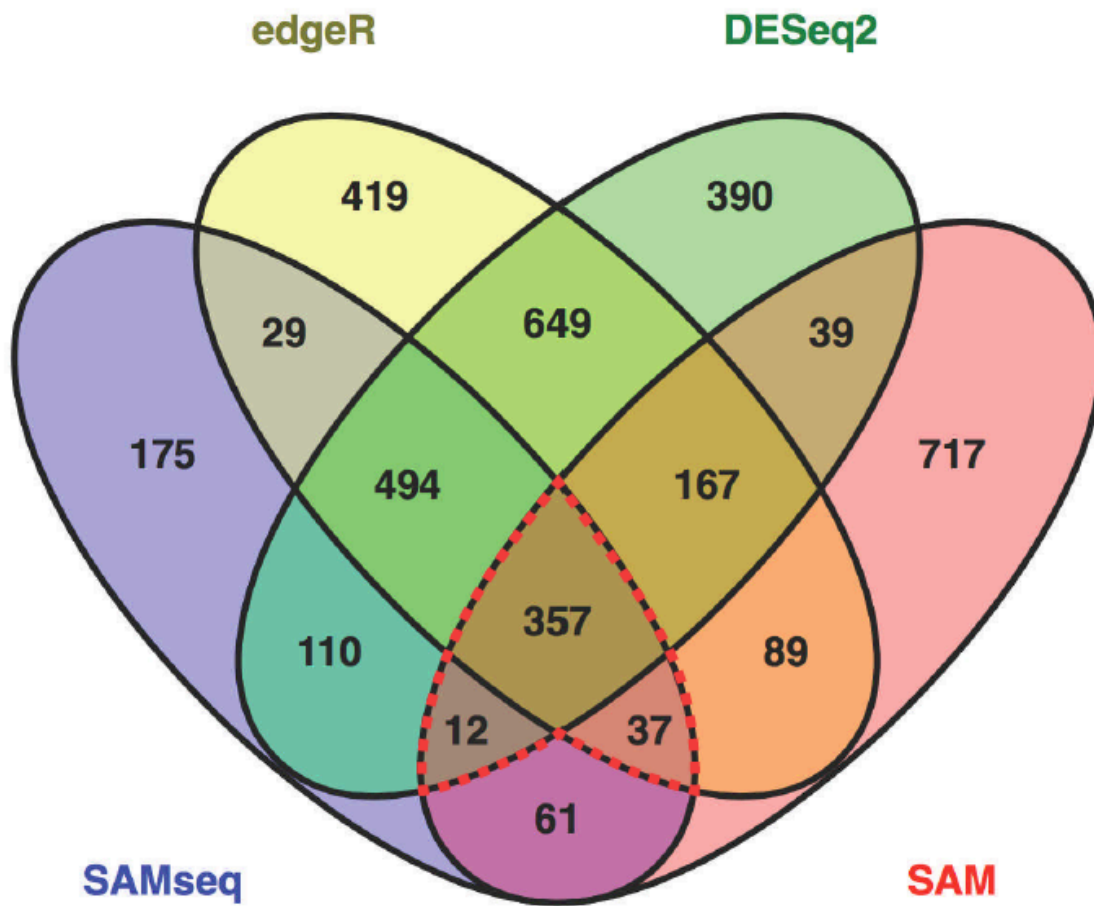
Przybyl et al.

Supplemental Figure 1



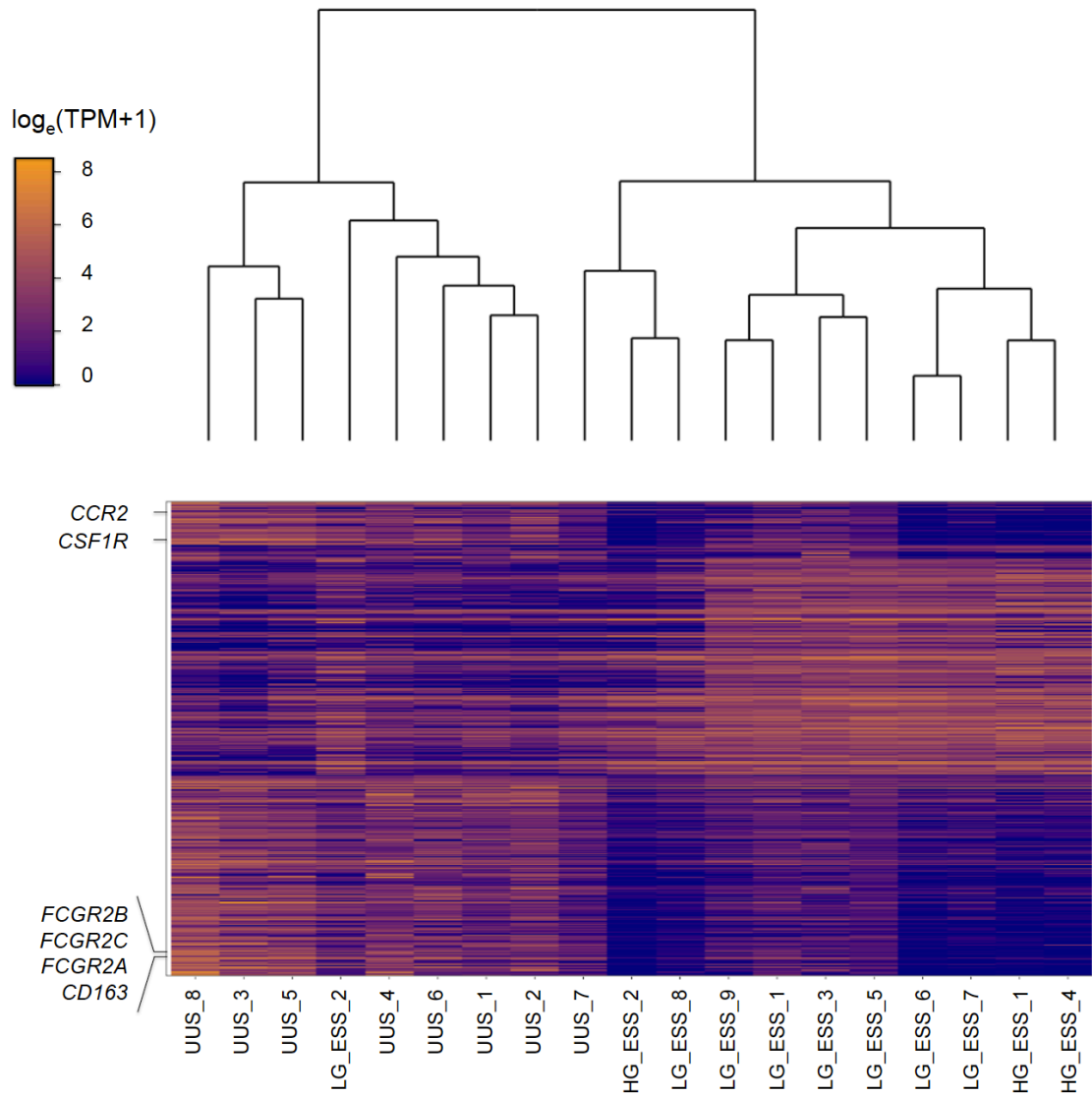
Unsupervised hierarchical clustering of LG ESS (n=8), HG ESS (n=3) and UUS (n=8) specimens based on RNA-seq data. [Note that specimens LG_ESS_2 and UUS_7 belong to the same clusters based on both microarray and RNA-seq data]

Supplemental Figure 2



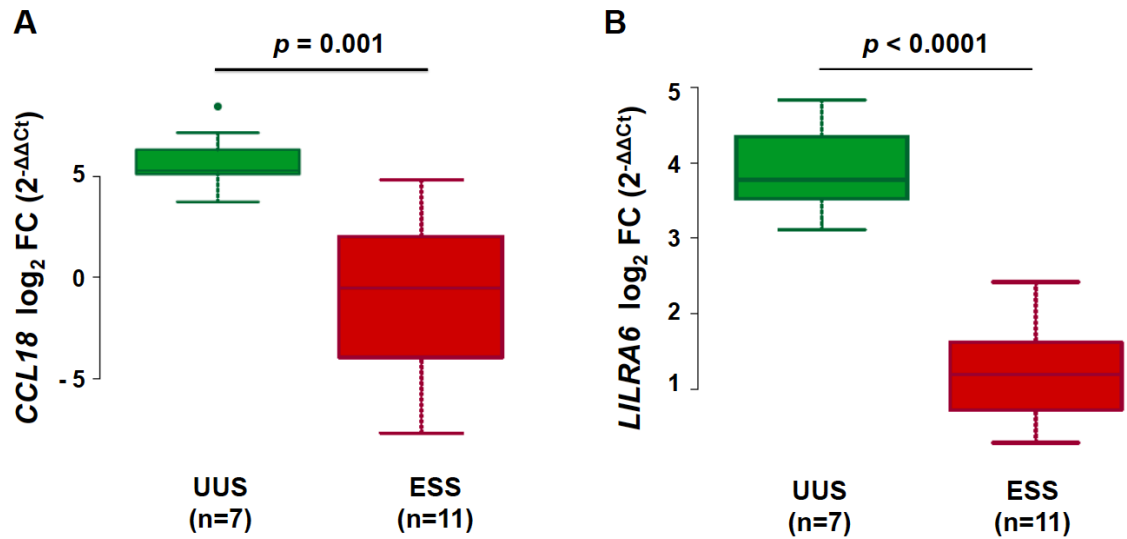
Overlap between significant differentially expressed genes identified in RNA-seq data (by DESeq2, edgeR and SAMseq) and gene microarray data (SAM). 406 genes identified by SAM, SAMseq and edgeR/DESeq2 that were used for the biological significance analyses are marked with dashed red line.

Supplemental Figure 3



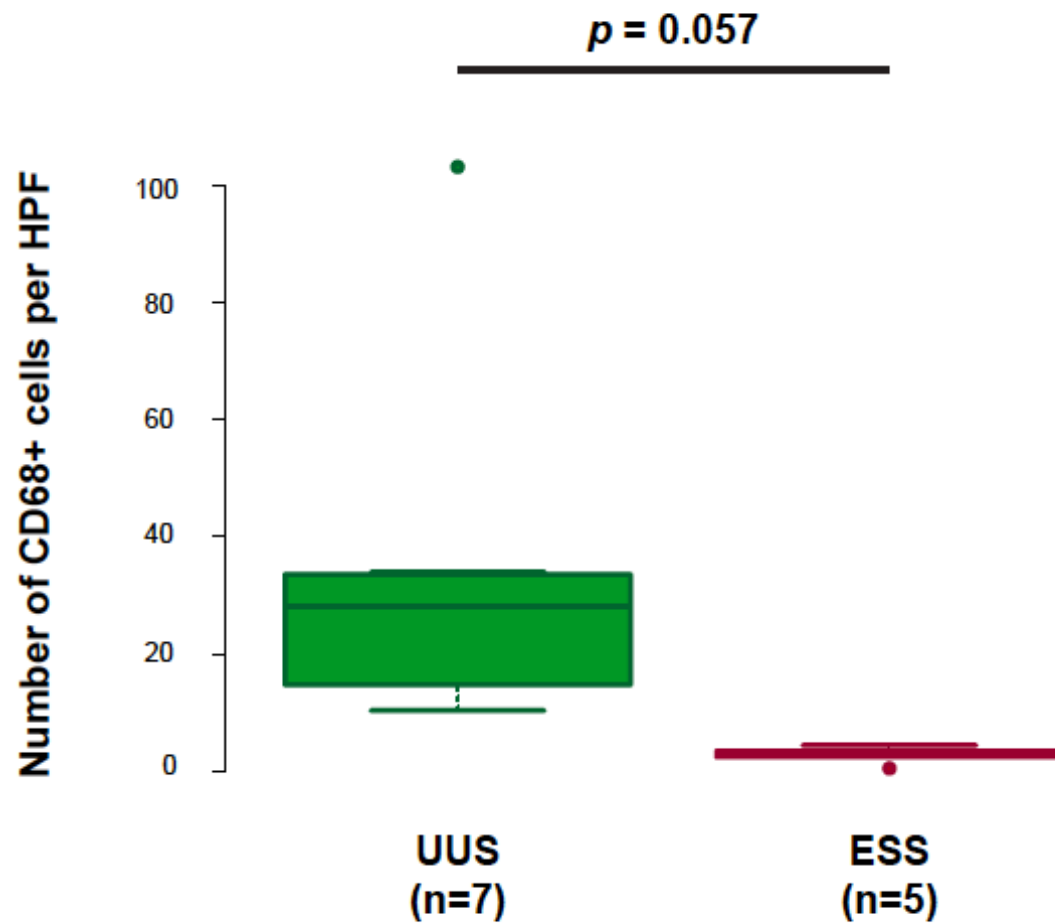
Supervised hierarchical clustering of UUS (n=8) and ESS (n=11) specimens based on $\log_e(\text{TPM}+1)$ expression values from RNA-seq for 406 genes differentially expressed between UUS and ESS.

Supplemental Figure 4



Validation of differential gene expression of selected M2 macrophage related genes (*CCL18* and *LILRA6*) using qRT-PCR. [FC – fold change, Ct – threshold cycle]

Supplemental Figure 5



Numbers of CD68-positive cell counts in UUS (n=7) and ESS (n=5) specimens in the training cohort of patients evaluated by immunohistochemistry.