



Supplementary Fig. S5: *SLC25A40-ABCB1* fusion driven transcriptional profiles in HGSOC patient samples

(A) Metascape TRUSST analysis of transcriptional regulatory relationships significantly enriched in AOCs18.5 fusion-positive clones. (B) Unsupervised hierarchical clustering analysis (basal transcriptional profile) of *SLC25A40-ABCB1* fusion-negative (n=21) and fusion-positive (n=6) relapsed HGSOC patient ascites samples. The top 100 significantly differentially expressed genes from RNA-seq analysis are shown as well as *ABCB1* expression. Sample AOCs_120_4_X contains an alternative transcriptional start site in exon 2 of *ABCB1* due to a large insertion in intron 1 of *ABCB1*. (C) Volcano plot showing differentially expressed genes significantly up/down regulated in fusion-positive clones compared to fusion-negative. (D) Metascape pathway analysis of significantly induced genes upregulated by *SLC25A40-ABCB1* fusions in HGSOC patient samples. Cutoff criteria for all analysis was Log2 fold change of 1.5 and p-adj of <0.1.