

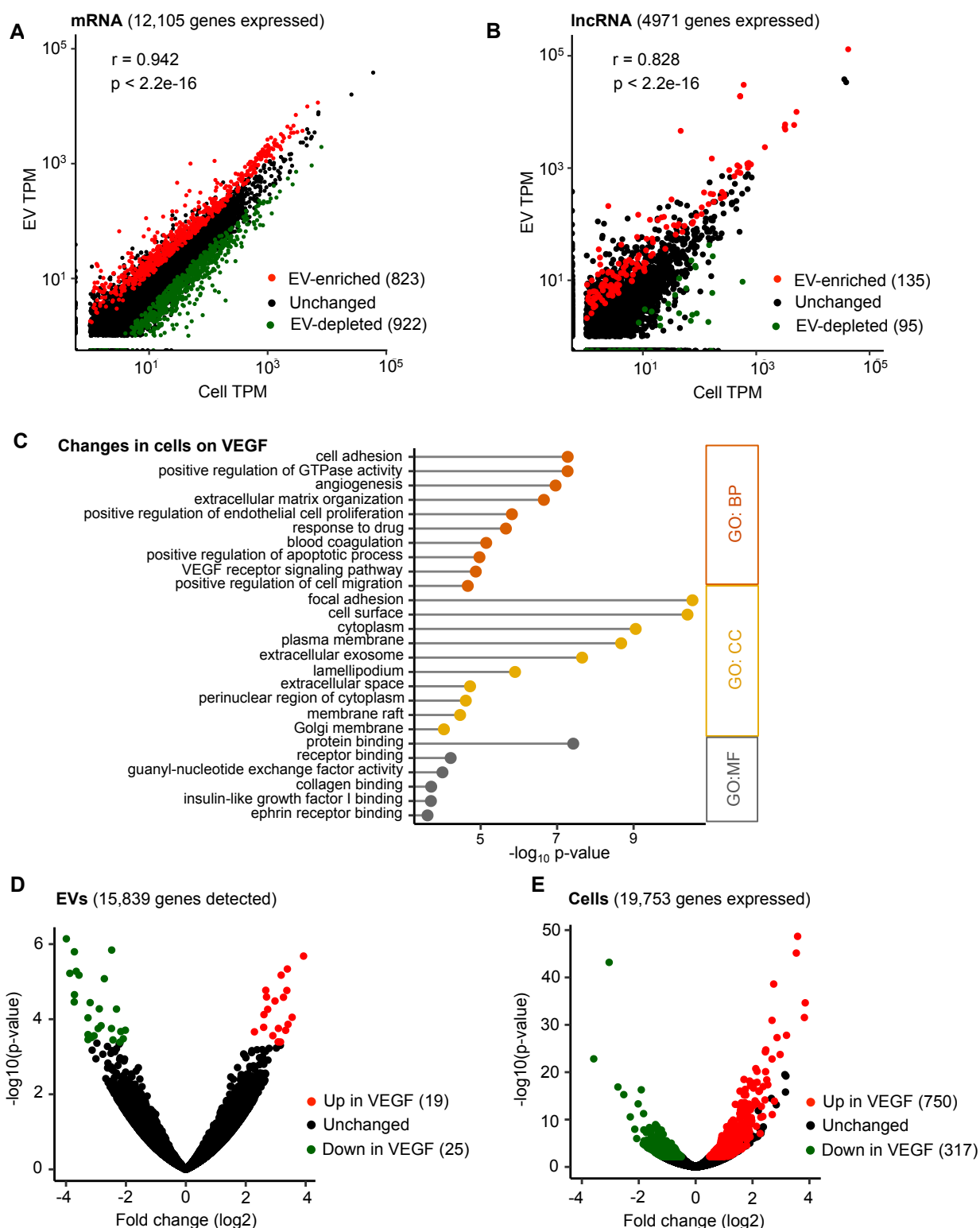


Figure S5: (A) mRNA and (B) lncRNA abundance from RNA-Seq in VEGF-treated cells and their EVs. TPM = transcripts per million. TPM values are averaged across 3 replicates. (C) Gene Ontology analysis of genes altered in cells by VEGF treatment. For each GO category the ten significant (FDR < 0.05) terms with the lowest p-values are displayed. BP = Biological Process, CC = Cellular Component, MF = Molecular Function. Individual values can be found in Additional file 17. (D) Volcano plot of log2 fold changes by RNA-Seq of mRNA and lncRNA genes (combined) in EVs derived from VEGF-treated cells vs. EVs derived from untreated cells. (E) Volcano plot of log2 fold changes by RNA-Seq of mRNA and lncRNA genes in VEGF-treated cells vs. untreated cells. All analyses were performed using 3 EV and 3 cell samples.