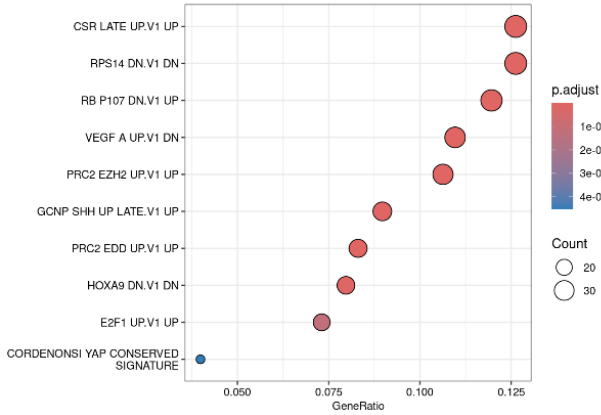


# Figure S7

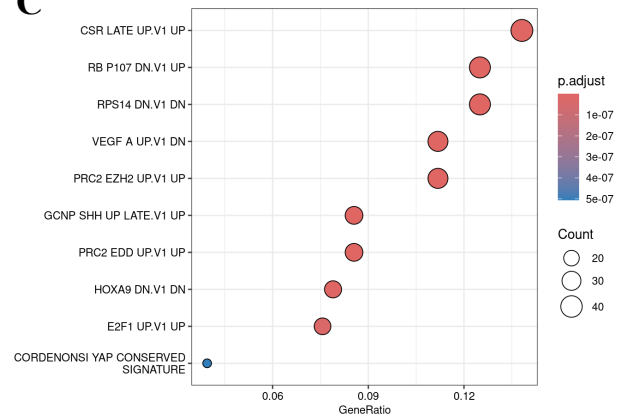
**A**

**2.8K**



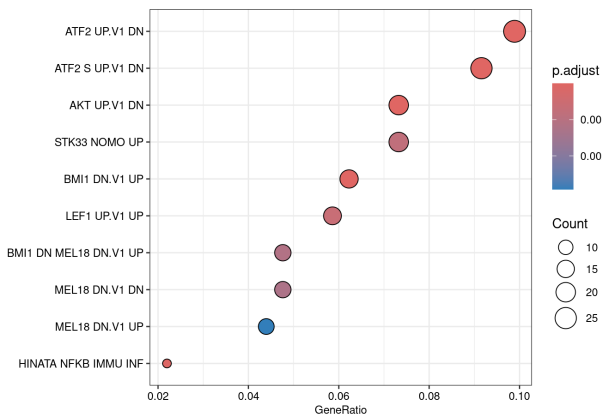
**C**

**10K**



**B**

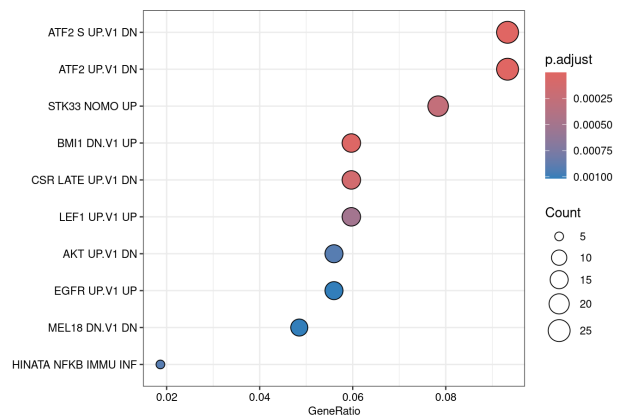
**Upregulated genes**



**Down-regulated genes**

**D**

**Upregulated genes**



**Down-regulated genes**

**Figure S7: Gene set enrichment analysis (GSEA) of fibroblasts (MRC5) treated with Met5A and MSTO-derived EVs for MSigDB\_Oncogenic\_Signatures.** Differential expression results from fibroblasts treated with Met5A and MSTO-derived EVs (2.8k, 10k, 100k) were used for the analysis. The enrichment analysis was performed separately for the up- or downregulated mRNA using the clusterProfiler package (R). Gene sets with  $p \leq 0.05$  were considered significantly enriched.

**A-B)** GSEA for up- and down-regulated mRNA in fibroblasts (MRC5) treated with 2.8k EV fractions.

**C-D)** GSEA for up- and down-regulated mRNA in fibroblasts (MRC5) treated with 10k EV fractions.