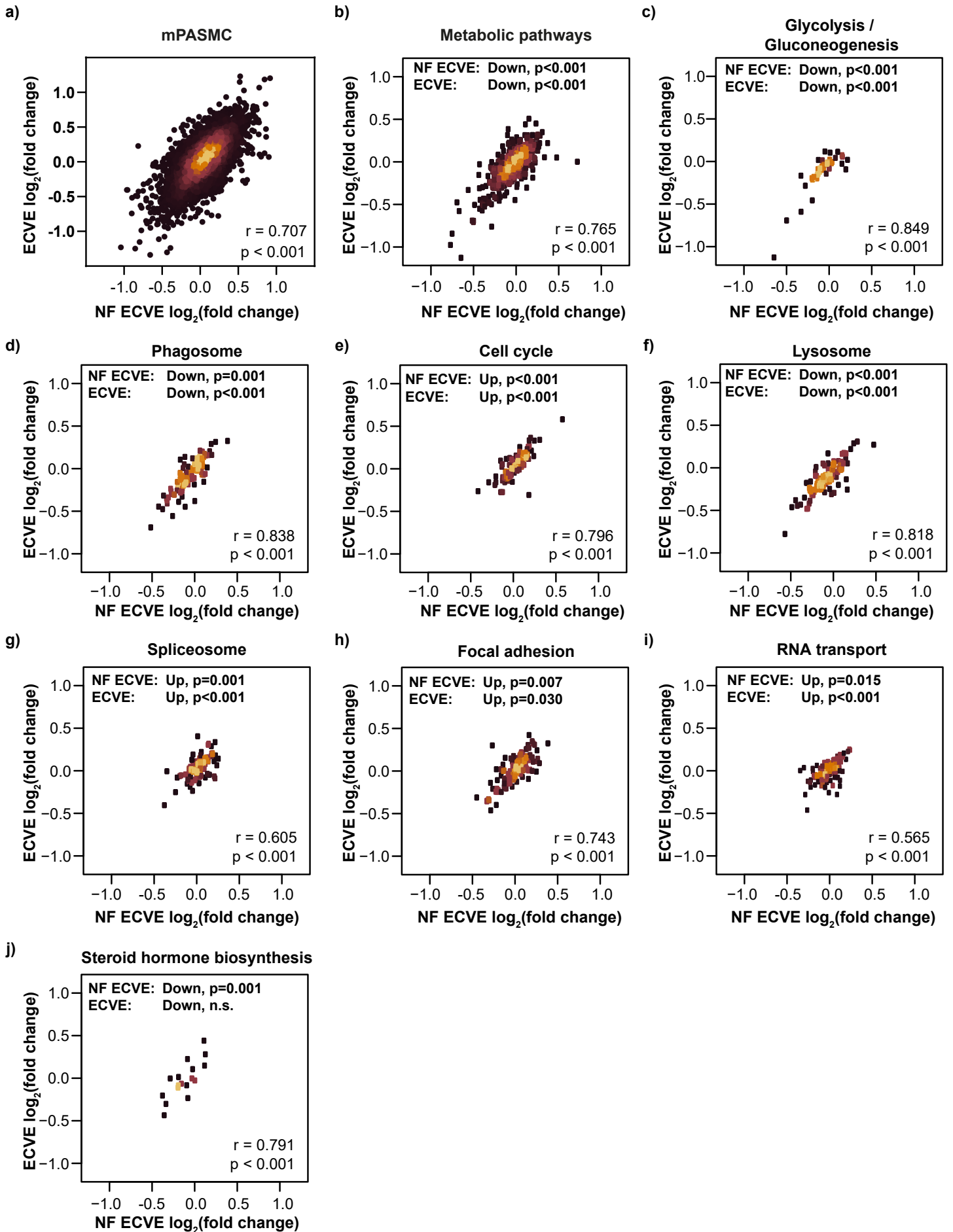




mPASC



**Supplementary figure S5. Comparison of gene expression patterns of mouse pulmonary arterial smooth muscle cells (mPASMC) treated with ECVE or NF ECVE from microarray analyses.**

**a-j)** Correlation of mRNA transcript expression of microarray data between primary mPASMC cells either exposed to 15% nicotine-free e-cigarette vapour extract (NF ECVE) or 15% nicotine-containing e-cigarette vapour extract (ECVE). Controls were treated with medium without ECVE or NF ECVE. Data show measured mRNA transcripts (**a**), or the subsets of the data from genes being annotated to KEGG pathways: “Metabolic pathways”(**b**), “Glycolysis/Gluconeogenesis” (**c**), “Phagosome” (**d**), “Cell cycle” (**e**), “Lysosome” (**f**), “Spliceosome” (**g**) “Focal adhesion” (**h**), “RNA transport” (**i**) and “Steroid hormone biosynthesis” (**j**). The colour of the points indicates the spatial density of the values (lowest density is black, highest density is yellow). The densities were obtained using a 2-dimensional Gaussian kernel estimator. The colouring visualizes the inner structure of dense clouds of overplotted points. “Up” and “Down” indicate up- or downregulation of the majority of respective mRNA transcripts in the specific pathway. n.s., not significant changes. Data are derived from n=8 independent cell isolations per group.