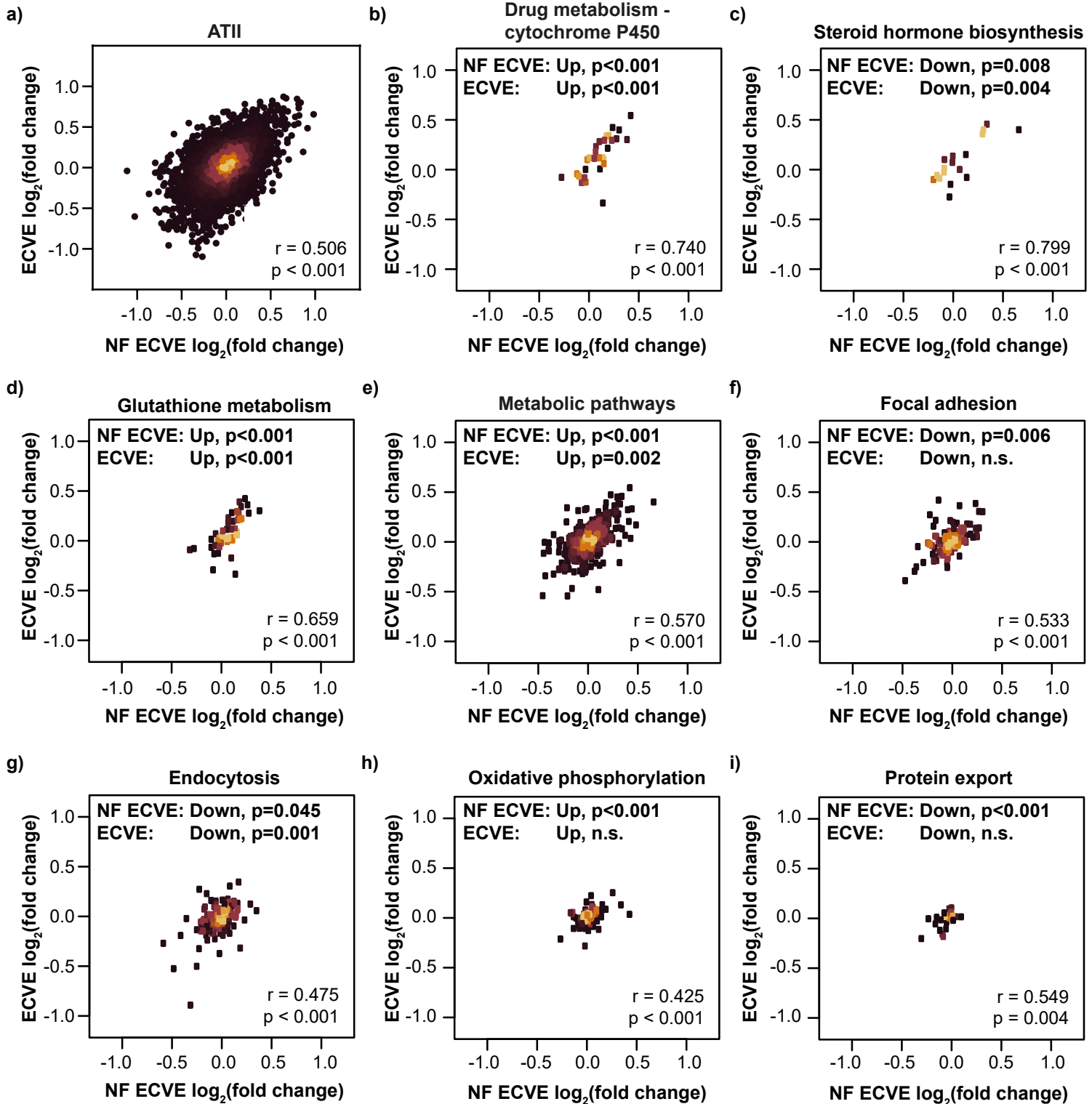


**mATII**


**Supplementary figure S4. Comparison of gene expression patterns of mouse alveolar epithelial type II cells (mATII) exposed to ECVE or NF ECVE from microarray analyses.**

**a-i)** Correlation of mRNA transcript expression of microarray data between primary mATII 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 all measured mRNA transcripts (**a**), or the subsets of the data from genes being annotated to KEGG pathways: “Drug metabolism – cytochrome” p450 (**b**), “Steroid hormone biosynthesis” (**c**), “Glutathione metabolism” (**d**), “Metabolic pathways” (**e**), “Focal adhesion” (**f**), “Endocytosis” (**g**) “Oxidative phosphorylation” (**h**), and “Protein export” (**i**). 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.