



Supplementary Figure 2: Metabolomics analysis of HBVP upon TGF-β treatment. (A) Heatmap of all quantified metabolites in VBHP, illustrated as auto scaled concentration values (-2;2), features clustered by Ward clustering algorithm based on Euclidean distance measure. (B) Principal component analysis (PCA) scores plot illustrating the treatment and sample group separation based on different metabolic profile, PC 1 61.8%, PC 2 25.4%. (C) PCA bi-plot indicates specific metabolites that drive the group separation: aspartate and glutamate are more associated to control group, while glutamine, pyroglutamate, glucose, lactate and formate are more associated with the TGF-β treatment group. (D) Bar plots with visualizing individual replicate points and SEM of significant metabolite changes upon TGF-β treatment (black triangles), in addition to Figure 4 C: inosine, pyroglutamate, tyrosine, lysine, alanine and leucine concentrations were increased compared to control (black dots), while NAD⁺ concentration was reduced in TGF-β treatment group based on parametric, unpaired t-test, * p < 0.05, ** p < 0.01. (E) Volcano plot visualizing most significant metabolite increased concentrations (orange dots) and decreased concentrations (purple dots) upon TGF-β treatment compared to control for p<0.05, with fold change (FC) threshold 0.8.