# Supplementary figures and table

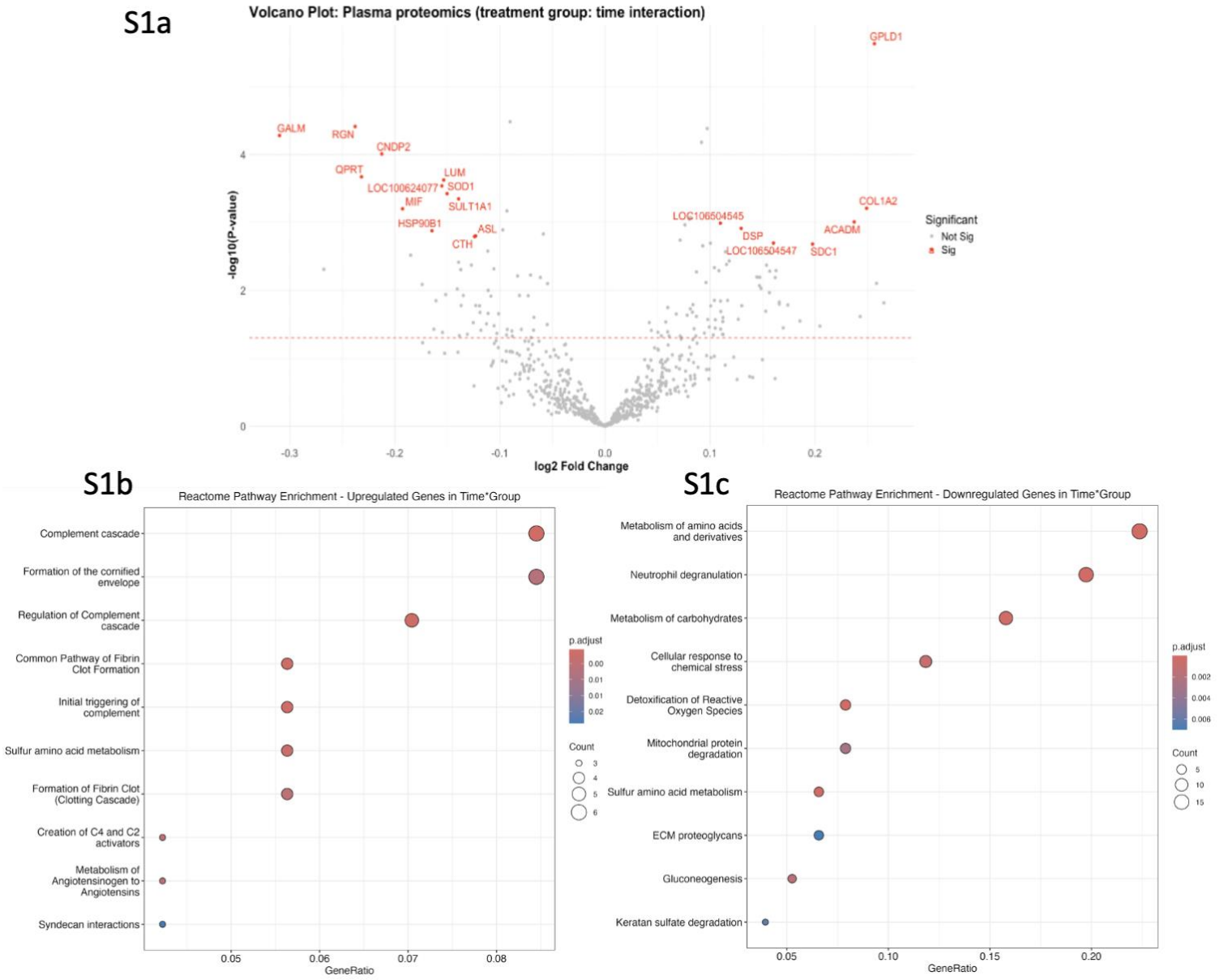


Figure S1: Patient pig plasma proteomics treatment group: time analysis. Differential analyte abundance calculated using empirical bayes moderated t-statistic with false discovery rate determined using Benjamini–Hochberg method. (*n=6* per treatment group per time point). a) Volcano plot: analytes with adjusted p-value < 0.05 and absolute logFC > mean logFC + standard deviation identified as significant. b) Reactome pathway enrichment analysis (upregulated pathways) c) Reactome pathway enrichment analysis (downregulated pathways).


Figure S2: Patient pig plasma proteomics controls time effect analysis. Differential analyte abundance calculated using empirical bayes moderated t-statistic with false discovery rate determined using Benjamini–Hochberg method. (*n=6* per time point). a) Volcano plot: analytes with adjusted p-value < 0.05 and absolute logFC > mean logFC + standard deviation identified as significant. b) Reactome pathway enrichment analysis (upregulated pathways) c) Reactome pathway enrichment analysis (downregulated pathways).

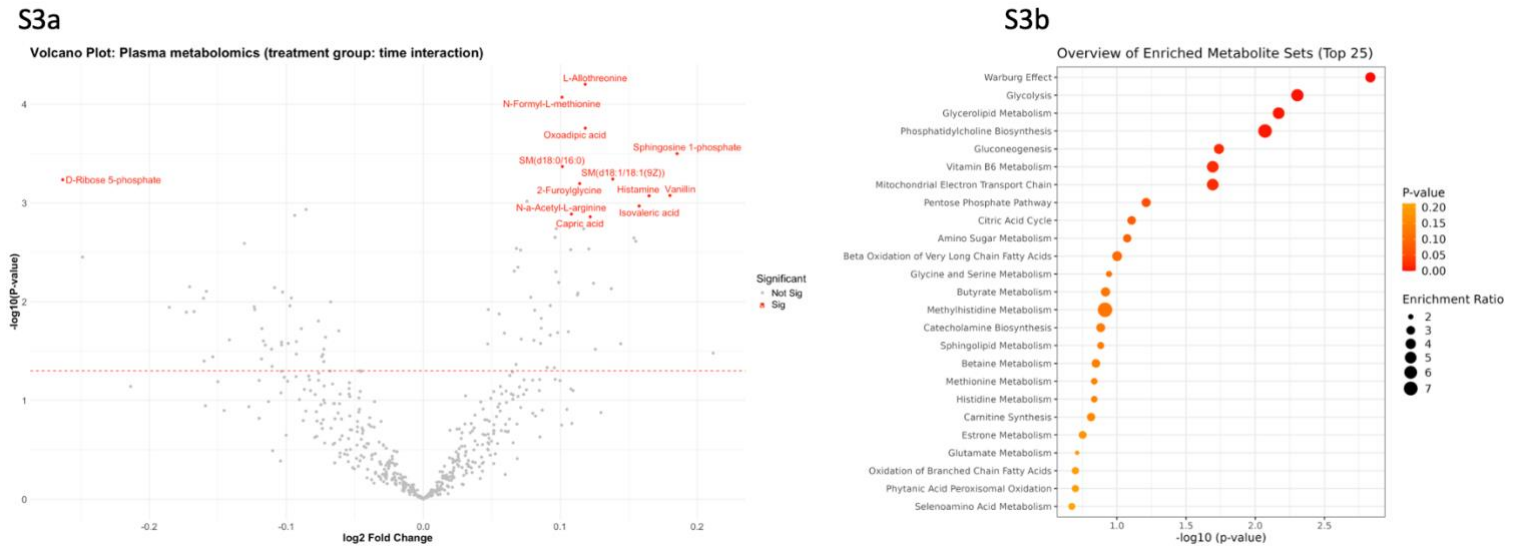


Figure S3: Patient pig plasma metabolomics treatment group: time analysis. Differential analyte abundance calculated using empirical bayes moderated t-statistic with false discovery rate determined using Benjamini–Hochberg method. (*n=6* per treatment group per time point). a) Volcano plot: analytes with adjusted p-value < 0.05 and absolute logFC > mean logFC + standard deviation identified as significant. b) SMPDB pathway enrichment analysis.

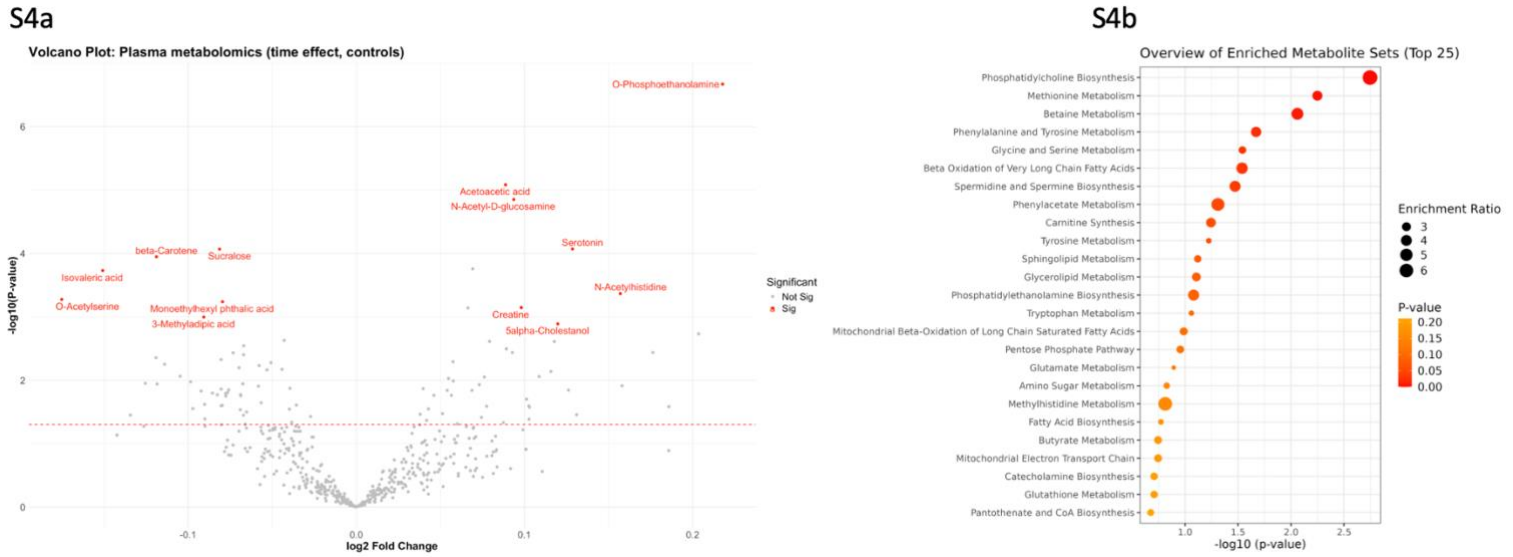


Figure S4: Patient pig plasma metabolomics controls time effect analysis. Differential analyte abundance calculated using empirical bayes moderated t-statistic with false discovery rate determined using Benjamini–Hochberg method. (*n=6* per time point). a) Volcano plot: analytes with adjusted p-value < 0.05 and absolute logFC > mean logFC + standard deviation identified as significant. b) SMPDB pathway enrichment analysis.

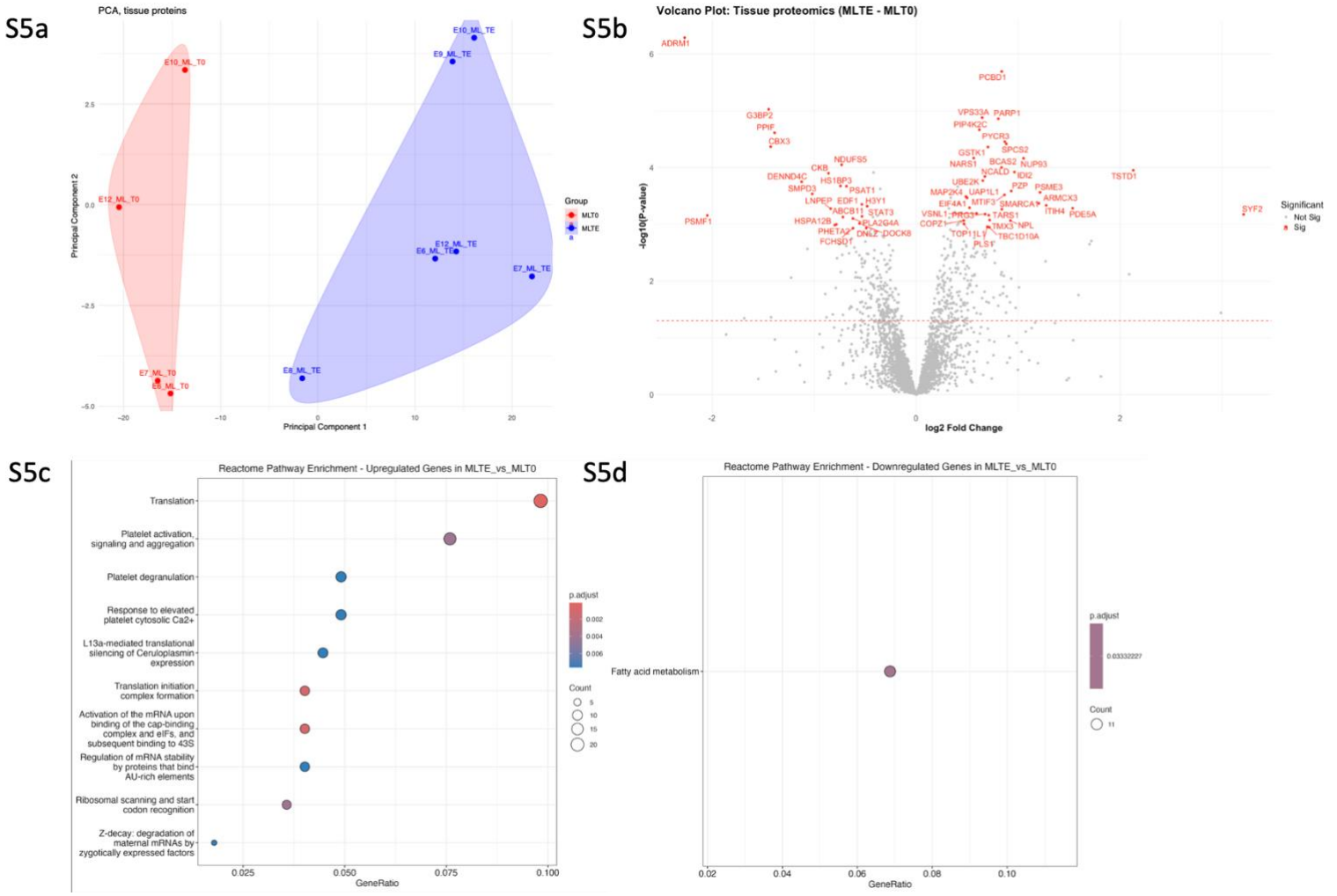


Figure S5: Extra-corporeal liver tissue proteomics analysis of extra-corporeal liver at end-ELC (MLTE, n=6) vs pre-isolated NMP (MLT0, n=4). Differential analyte abundance calculated using empirical bayes moderated t-statistic with false discovery rate determined using Benjamini–Hochberg method. a) Extra-corporeal liver tissue proteome principal component analysis (proteins with p<0.05 in end-ELC (MLTE) vs pre-NMP (MLT0) analysis). b) Volcano plot: analytes with adjusted p-value < 0.05 and absolute logFC > mean logFC + standard deviation identified as significant. c) Reactome pathway enrichment analysis (upregulated pathways) d) Reactome pathway enrichment analysis (downregulated pathways).

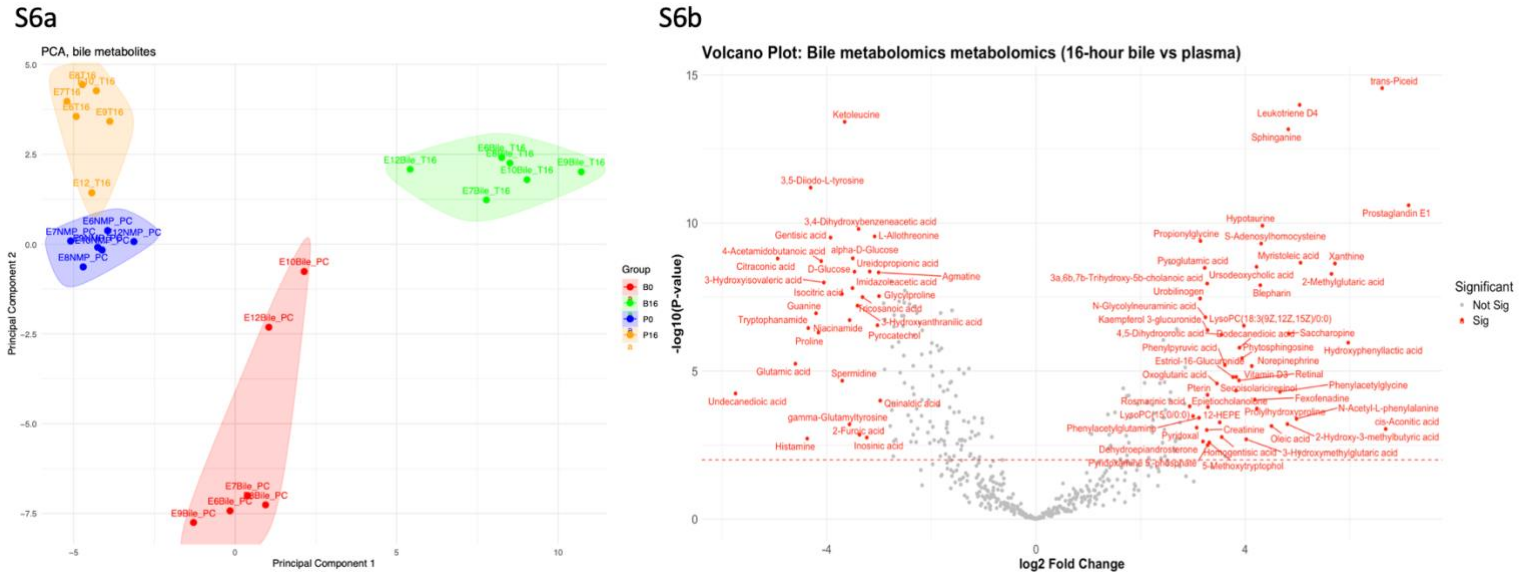


Figure S6: Extra-corporeal liver bile metabolomics analysis comparing bile samples at 16 hours of ELC and end of isolated NMP with corresponding plasma and perfusate samples. Differential analyte abundance calculated using empirical bayes moderated t-statistic with false discovery rate determined using Benjamini–Hochberg method. (*n=6* per sample type per timepoint). a) Extra-corporeal liver bile metabolome principal component analysis (metabolites with p<0.05 in 16-hour bile samples). b) Volcano plot: analytes with adjusted p-value < 0.01 and absolute logFC > mean logFC + standard deviation identified as significant.

| **Liver** | **Patient native liver (*n=12*)** | | **Extra-corporeal liver (*n=6*)** | |
|---|---|---|---|---|
| **Time** | **Pre-devascularisation** | **End of study** | **Pre-NMP** | **End-ELC** |
| Necrosis | 0.2 (0-2) | 2.8 (2-4) | 0.3 (0-1) | 1.3 (0-2) |
| Sinusoidal congestion | 1.0 (0-2) | 3.5 (0-4) | 0.8 (0-1) | 1.7 (1-2) |
| Vacuolisation/ballooning | 1.5 (0-3) | 0.1 (0-1) | 1.5 (0-2) | 0.7 (0-2) |
| Neutrophil infiltration | 1.3 (0-3) | 3.0 (2-4) | 1.3 (0-2) | 3.5 (2-4) |
| Cholestasis | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) |
| Hepatocyte glycogen content | 2.4 (0-3) | 0.4 (0-3) | 2.8 (2-3) | 2.0 (0-3) |
| Perl's stain | 0.3 (0-2) | 0.8 (0-2) | 0.3 (0-1) | 1.0 (0-2) |

Table S1: Histological scoring of patient native liver (*n=12*) at baseline (pre-devascularisation) and end of study, and extra-corporeal liver (*n=6*) pre-NMP and at end of ELC on H&E, PAS and Perl's staining (mean (range)). Key: Necrosis: 0: none; 1: single-cell; 2: <30%; 3: 30-60%; 4: >60%. Remainder of measures: 0: none; 1: minimal; 2: mild; 3: moderate; 4: severe.