

SUPPLEMENTARY MATERIALS

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Contents

Supplementary Table S1. – Quantitative data for the liver and the HepG2 cells from several datasets, obtained in 2013 and 2020 with SOLiD, Illumina GII/HiSeq, qPCR and Oxford Nanopore (MinION), and mapped to the Chr18-encoded proteins

Supplementary Table S2. The top most expressed (“Stakhanov”) genes of Chr18.

Supplementary Table S3. Human Chr18-centric dendrogram-coupled correlation matrix for different biosample types/years, sample preparation methods, transcriptome analytical platforms and bioinformatics pipelines.

Fig. S1. Venn’s diagram for transcripts with TMP/FPKM values ≥ 0.1 obtained by qPCR and RNA-seq technologies.

Fig. S2.1. Correlations between transcripts’ abundances for 235 transcripts encoded on Chr18 and detected in both HepG2 cells and each of three liver samples (donors #1, #3, and #5) by qPCR analysis.

Fig. S2.2. Correlations between transcripts’ abundances for 121 transcripts encoded on Chr18 and detected in both HepG2 cells and each of three liver samples (donors #1, #3, and #5) by Illumina HiSeq sequencing.

Fig. S3. Splicing structure (Sashimi plots) of the observed at protein level but functionally uncharacterized (uPE1) gene C18orf21 derived by the Illumina/HiSeq (a) and Oxford Nanopore Technology, MinION (b) for the liver sample from donor #1.

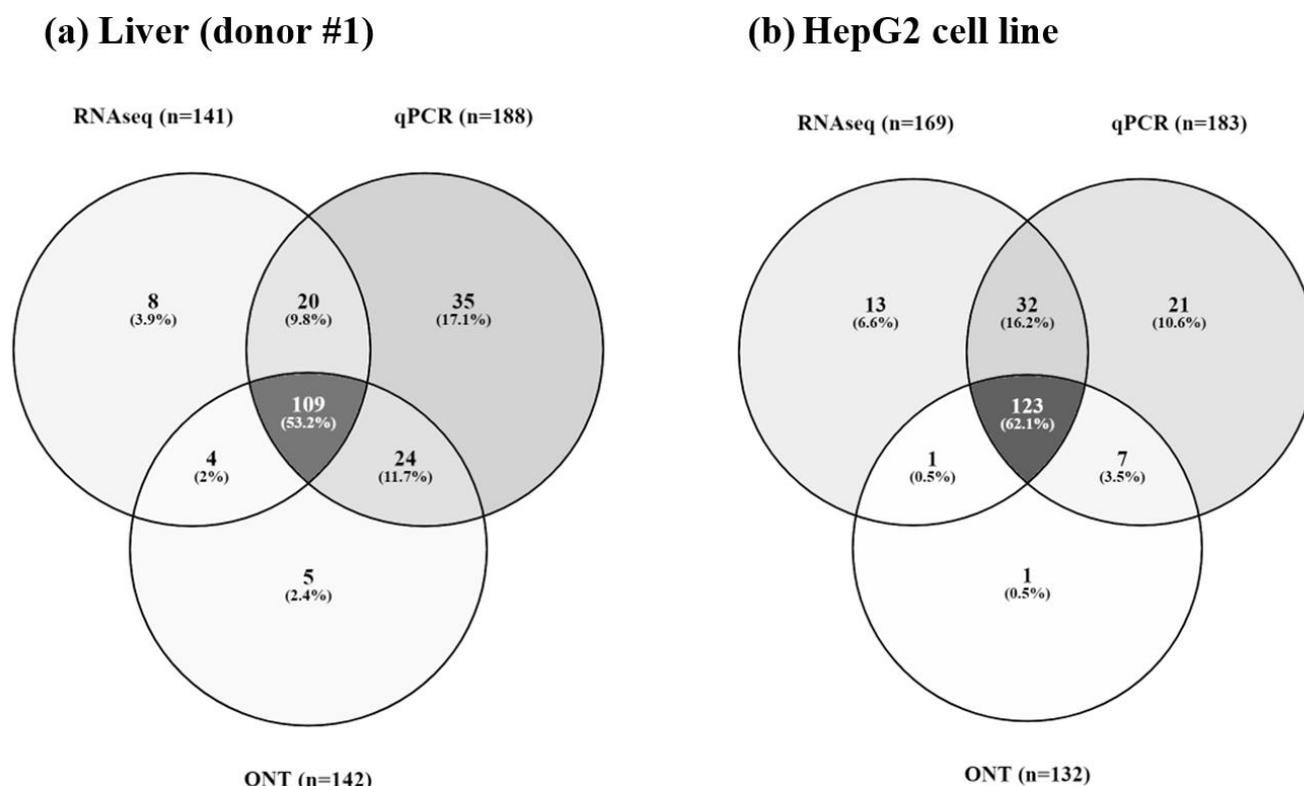


Fig. S1. Venn’s diagram for transcripts with TMP/FPKM values ≥ 0.1 obtained by qPCR and RNA-seq technologies in (a) Liver tissue (number of detected transcripts = 205) and (b) HepG2 cell line (number of detected transcripts = 198). Visualized using Venny 2.1 (<https://bioinfogp.cnb.csic.es/tools/venny/>, Oliveros, J.C. (2007-2015) Venny: An interactive tool for comparing lists with Venn's diagrams.)

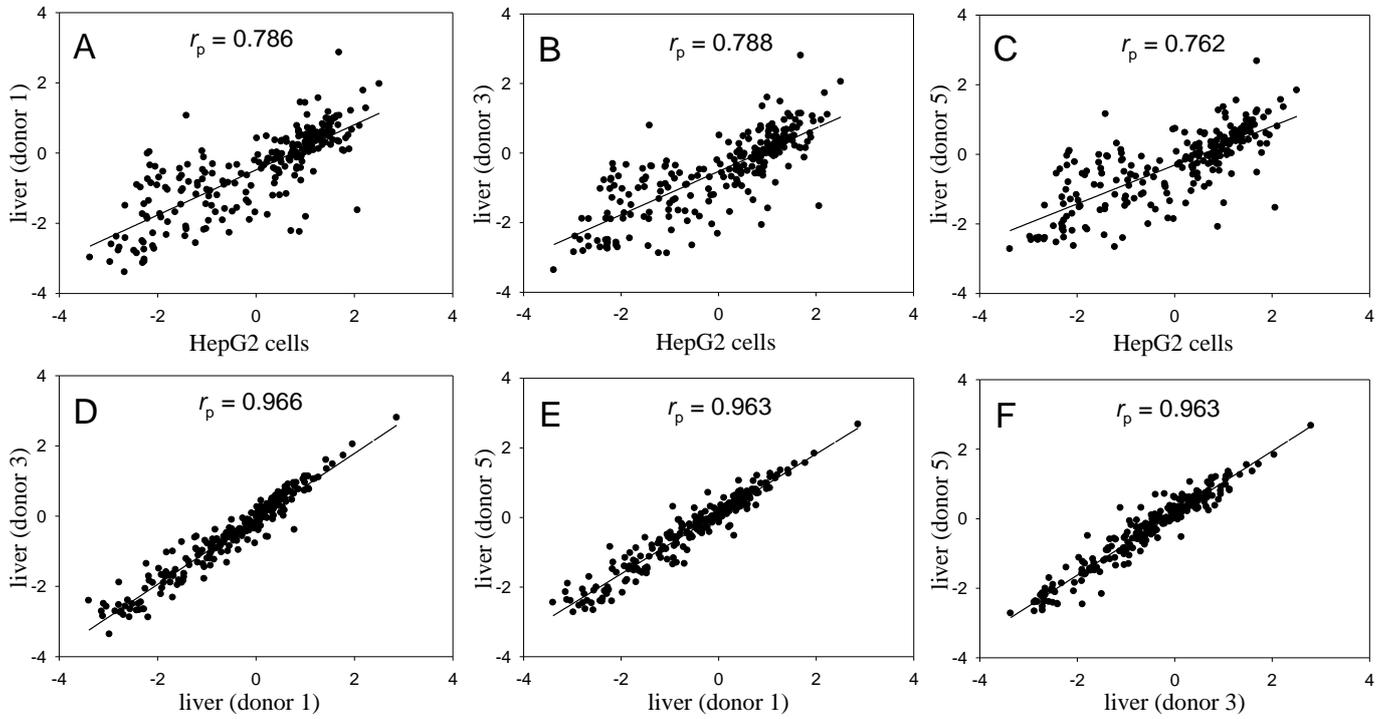


Fig. S2.1. Correlations between transcripts' abundances for 235 transcripts encoded on Chr18 and detected in both HepG2 cells and each of three liver samples (donors #1, #3, and #5) by qPCR analysis. Axis represent decimal logarithms of transcripts abundance. The transcript abundance is estimated as the copy numbers of cDNA per a cell. Values of Pearson's correlation coefficient, r_p , are shown in panels.

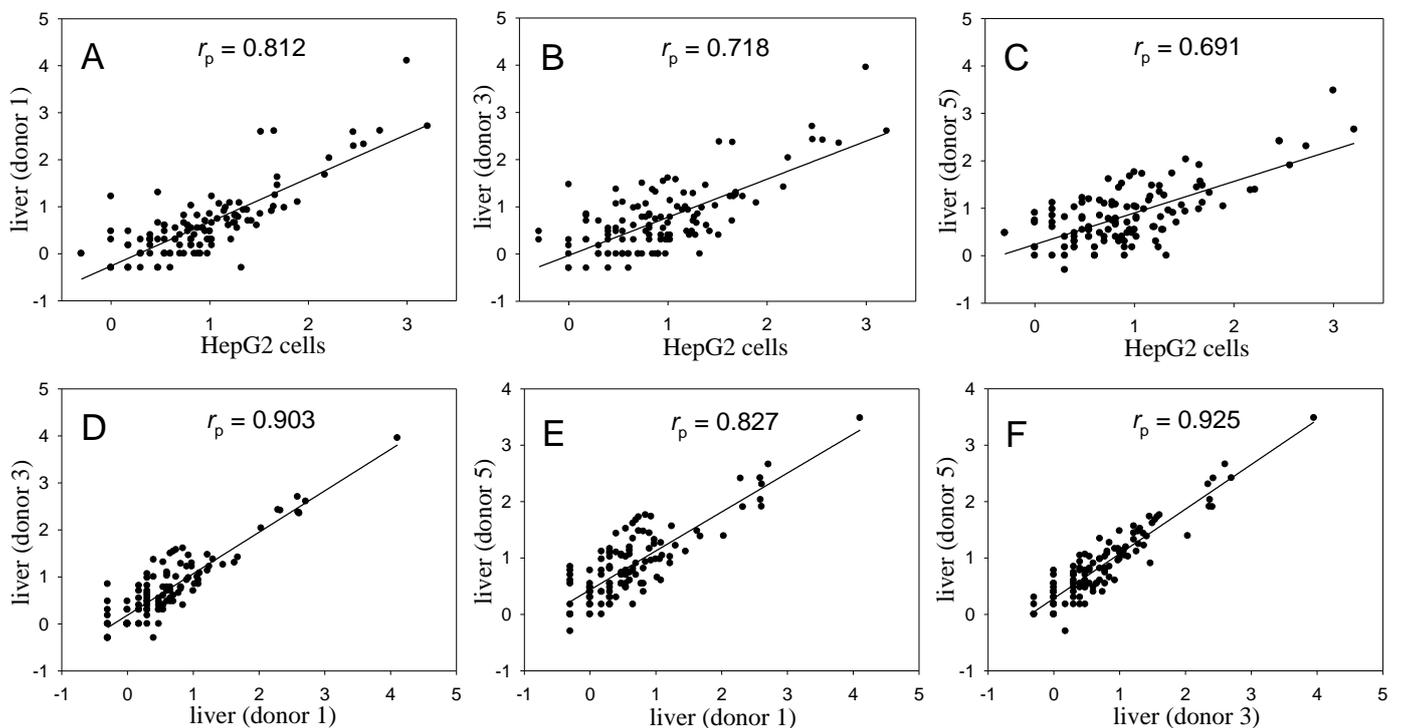


Fig. S2.2. Correlations between transcripts' abundances for 121 transcripts encoded on Chr18 and detected in both HepG2 cells and each of three liver samples (donors #1, #3, and #5) by Illumina HiSeq sequencing. Axes represent decimal logarithms of transcripts abundance. The transcript abundance is estimated as FPKM. Values of Pearson's correlation coefficient, r_p , are shown in panels.

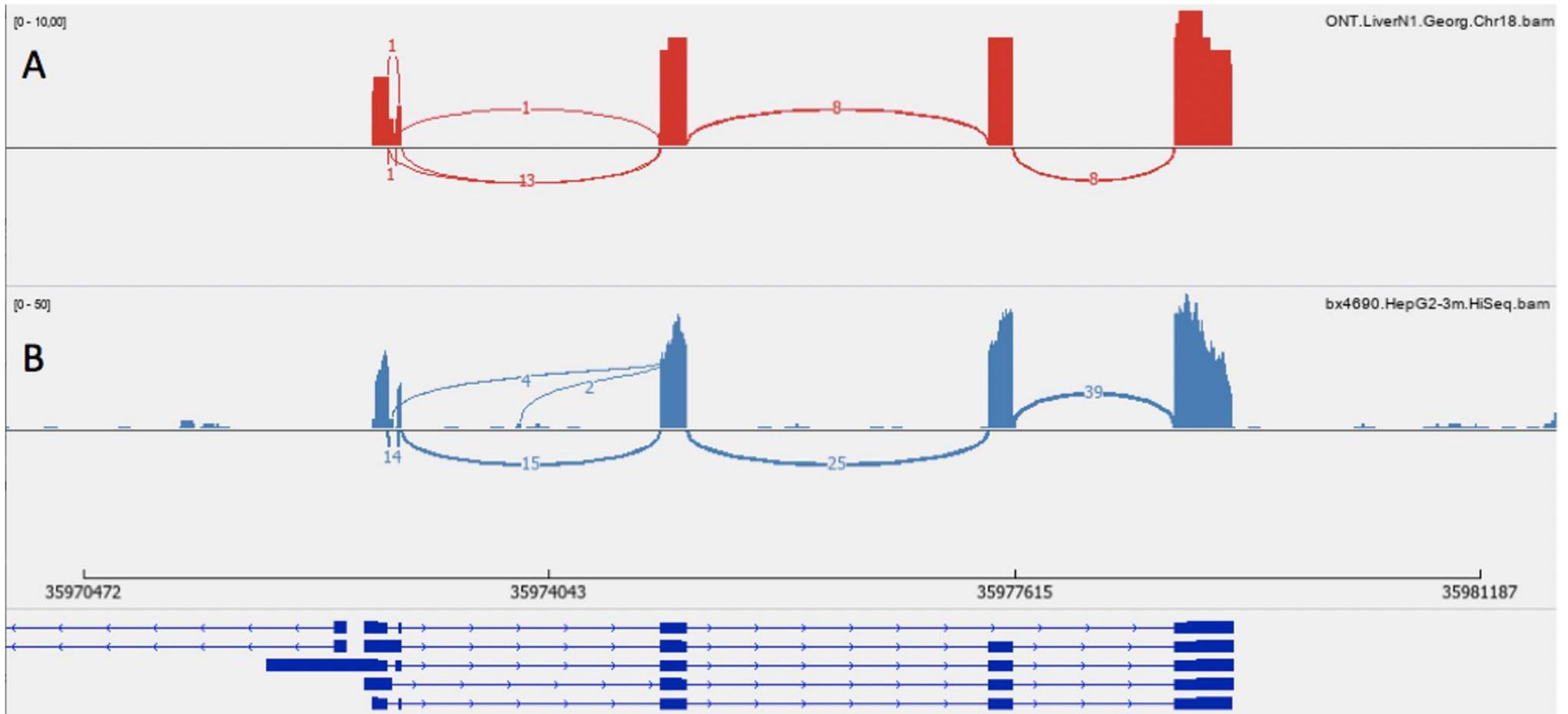


Fig. S3. Splicing sketch (Sashimi plot) of the observed as uPE1 (rarely seen at the protein level and functionally uncharacterized) translated from the C18orf21 gene. Derived by the Illumina/HiSeq (A) and Oxford Nanopore Technology, MinION (B) for the liver sample from donor #1.