

# **The glycosyltransferase pathway: an integrated analysis of the cell metabolome**

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## **Supplementary Information:**

Figure S1: Pathway enrichment analysis of metabolic changes common to A) UGT1A1 canonical and alt. proteins and B) UGT2B7 canonical and alt. proteins

Figure S2: Full original uncropped and unadjusted images of Western blots

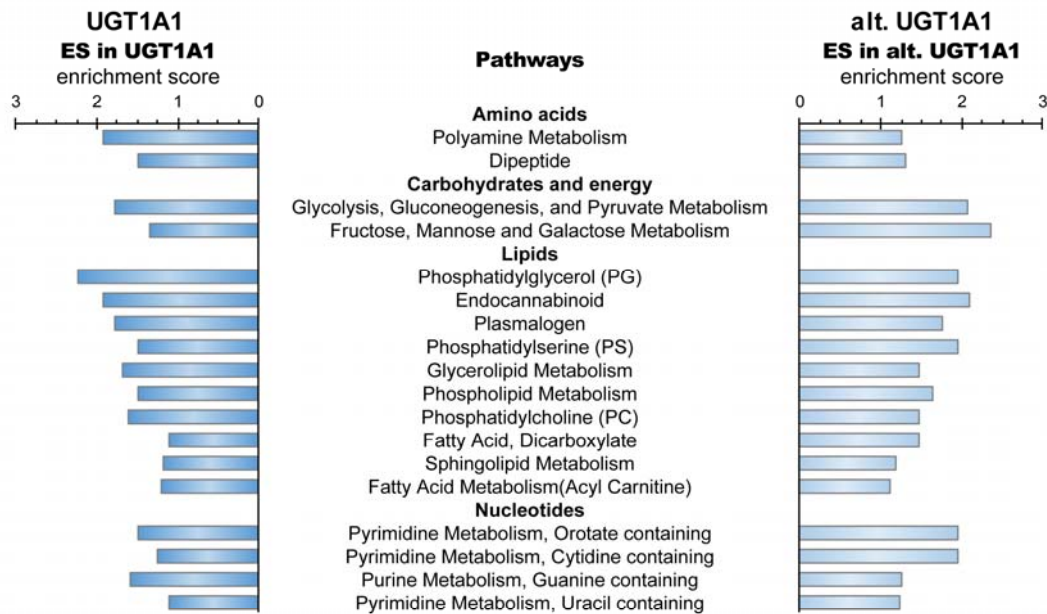
Table S1: Primers and conditions for qPCR analysis

Table S2: Levels of measured metabolites in UGT-expressing cells relative to controls

Table S3: Levels of measured metabolites per sample

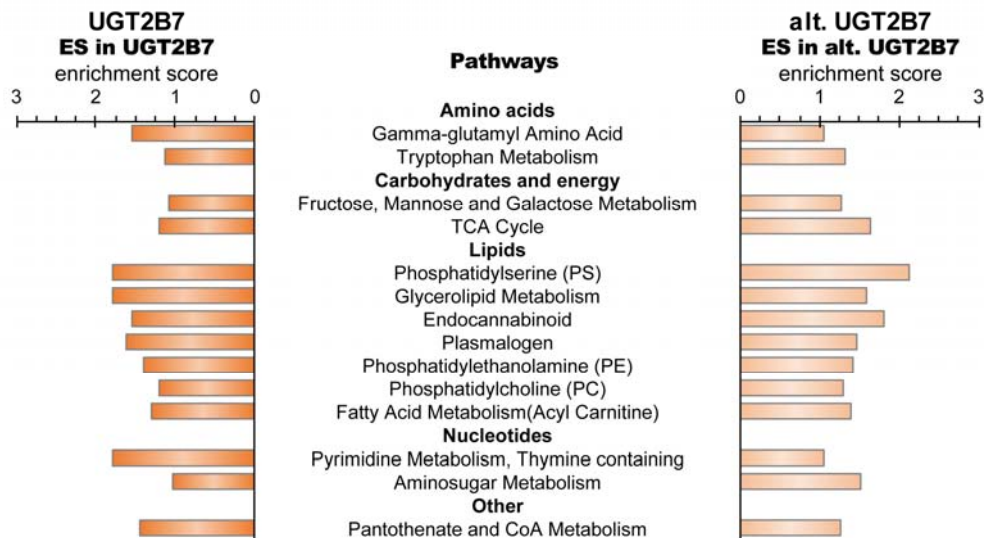
**A**

### Common pathways enriched in cells expressing UGT1A1 proteins



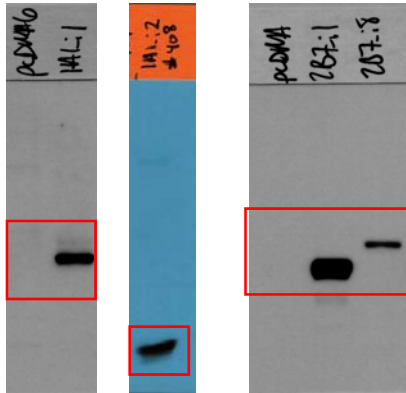
**B**

### Common pathways enriched in cells expressing UGT2B7 proteins

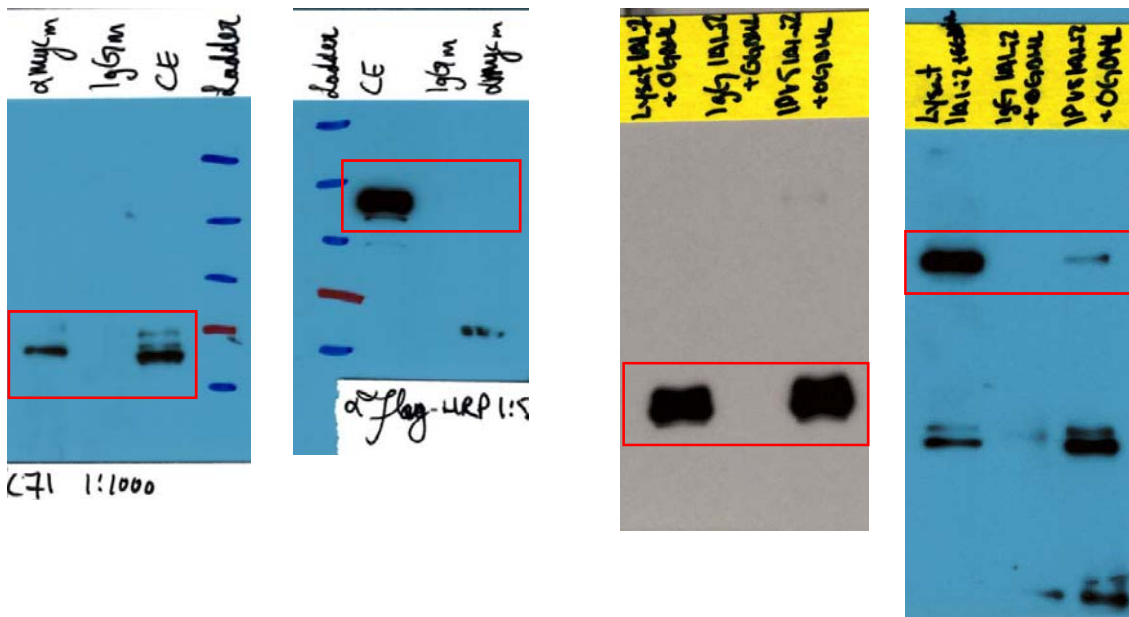


**Figure S1. Pathway enrichment analysis of metabolic changes common to A) UGT1A1 canonical and alt. proteins and B) UGT2B7 canonical and alt. proteins.** Displayed pathways were enriched in both cell models with an enrichment score > 1 and comprised at least 3 metabolites.

**A. Related to Figure 1C-D**



**B. Related to Figure 6D-E**



**Figure S2.** Full original uncropped and unadjusted images of Western blots, related to Fig.1 and Fig.6. Squared regions are shown in A) Figure 1C-D and B) Figure 6D-E.

**Table S1. Primers and conditions for qPCR analysis.**

Gene	Primer Sequences	Primer concentrations (nM)	Temperature (°C)
<i>PLA2G4A</i>	F- ACTGCACAATGCCCTTTACC R- CGGGAGCCATAAAAGTACCA	200 nM	60 °C
<i>DAGLB</i>	F- TGCTTCATCAGCAACAGGAC R- CAGCAGTCACCACCAATCC	300 nM	60 °C
<i>MAGL</i>	F- ATGCAGAAAGACTACCCTGGGC R- TTATTCCGAGAGAGCACGC	200 nM	60 °C
<i>FAAH</i>	F- AAGGTGATTTTCGTGGACCCC R- CCAGCCGAACGAGACTTCAT	200 nM	60 °C
<i>PPARA</i>	F- GCTGGTGTATGACAAGTGCG R- TCTTGGCATTTCGTCCAAAACG	300 nM	60 °C
<i>PPARD</i>	F- CTTCCAGCAGCTACACAGACCTC R- TACTGGCACTTGTTGCGGTT	300 nM	60 °C
<i>PPARG</i>	F- AGATGACAGCGACTTGGAATA R- AGGGCTTGTAGCAGGTTGTCT	200 nM	60 °C
<i>CNR1</i>	F- GATGCGAAGGGATTGCCCC R- GATGGTGCGGAAGGTGGTAT	100 nM	64 °C
<i>TRPV1</i>	F- GGGTACACACCTGATGGCAA R- GCCTGAAACTCTGCTTGACC	300 nM	60 °C
<i>ACAA1</i>	F- GAGATCAATGAGGCCTTTGC R- GATGCACATGGACACCACTC	300 nM	60 °C
<i>ECH1</i>	F- GGGATAGTGGCTTCTCGCAG R- CCAGTGAGGCGAAGGCTAAT	300 nM	60 °C
<i>EHHADH</i>	F- GTGAAGGAGCTTGGTGGTGT R- AAAAGAAGTGGGTGCCAATG	200 nM	60 °C
<i>CPT1a</i>	F- AGATGAGTCGTGCCACCAAG R- CCACCAGTCGCTCACGTAAT	200 nM	60 °C
<i>FASN</i>	F- CTTCAAGGAAGGCGTGA R- ACTGGTACAACGAGCGGATG	300 nM	60 °C
<i>ACAA2</i>	F- GGCTGTTGAGAGGAGTTTGG R- GGCTGTGCTCTGAATGATGA	200 nM	60 °C