

Supporting Information for:

**Determining Allele-Specific Protein Expression (ASPE) Using a Novel QconCAT-Based
Proteomics Method**

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Table S1. Sequences, precursor charge, m/z, and retention time of the target peptides. Blue and bold K and R indicated the heavy stable isotope-labeled internal standard peptides from QconCAT.

Peptide Sequence	Precursor Charge	Precursor m/z	Retention Time (min)
NYLEDSLLK	2	547.7900	9.4
NYLEDSLL K	2	550.8001	9.4
NDLEDSLLK	2	523.7719	8.6
NDLEDSLL K	2	526.7819	8.6

Table S2: DNA sequences of the primers for the reverse-transcription PCR and SNaPshot assays

Reverse-transcription PCR	
Forward primer	5'-TCAATGCCAGTAAATCATCTGC-3'
Reverse primer	5'-TCGAGAATTTTCAGAAGAGAATCT-3'
SNaPshot	
Forward primer	5'-TCGGCTTCTACTCTTGTCAATGC-3'
Reverse primer	5'-TTGAAACACCATATATCCATCTATCGAGA-3'
Extension primer	5'-AATTTTCAGAAGAGAATCTTCCAAAT-3'

Figure S1. Preparation of UGT2B15 QconCAT internal standard protein. The QconCAT protein was accumulated in the Elute Fraction 2 during HisTrap affinity column purification.

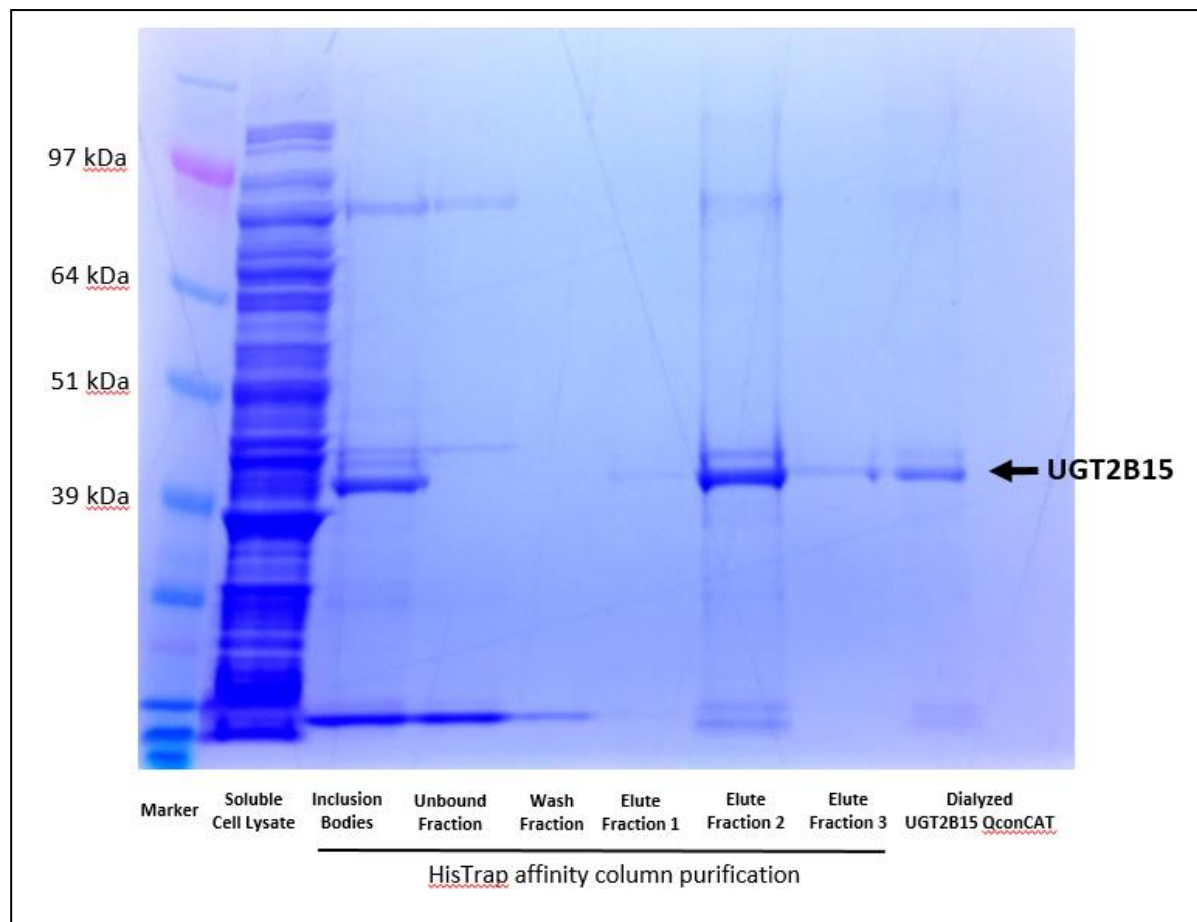
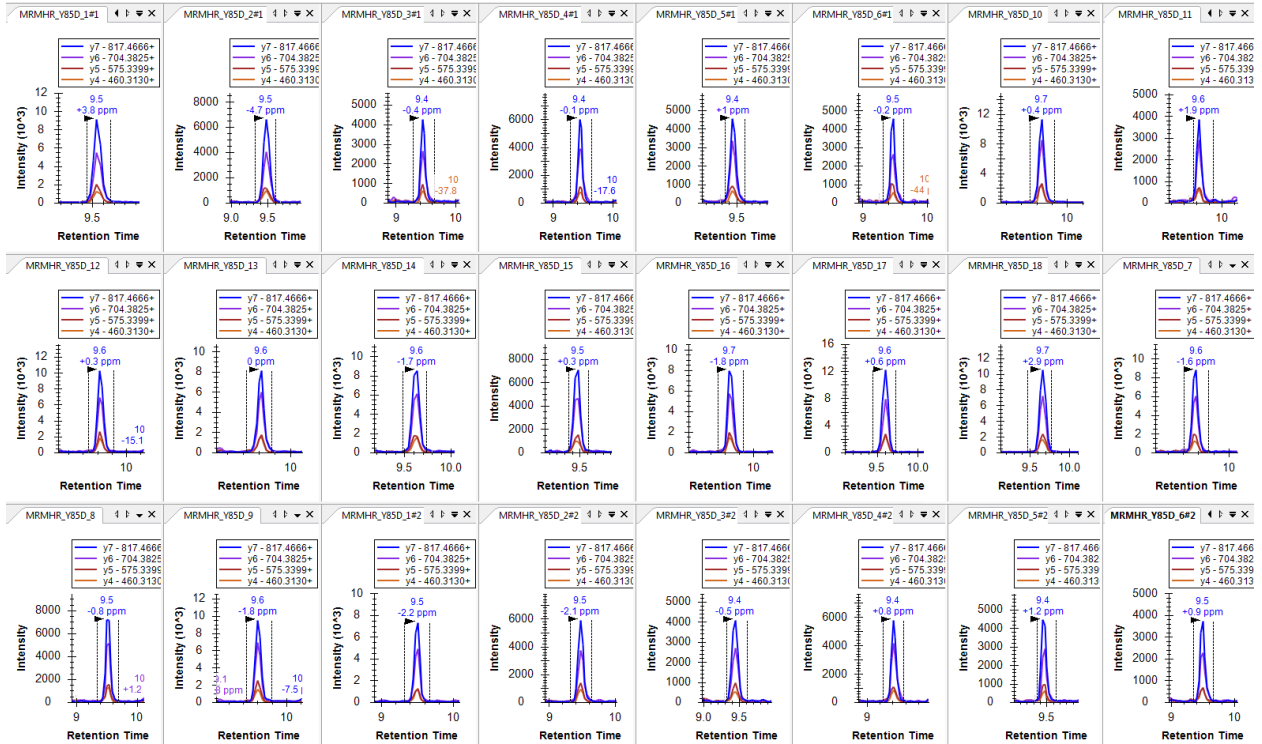
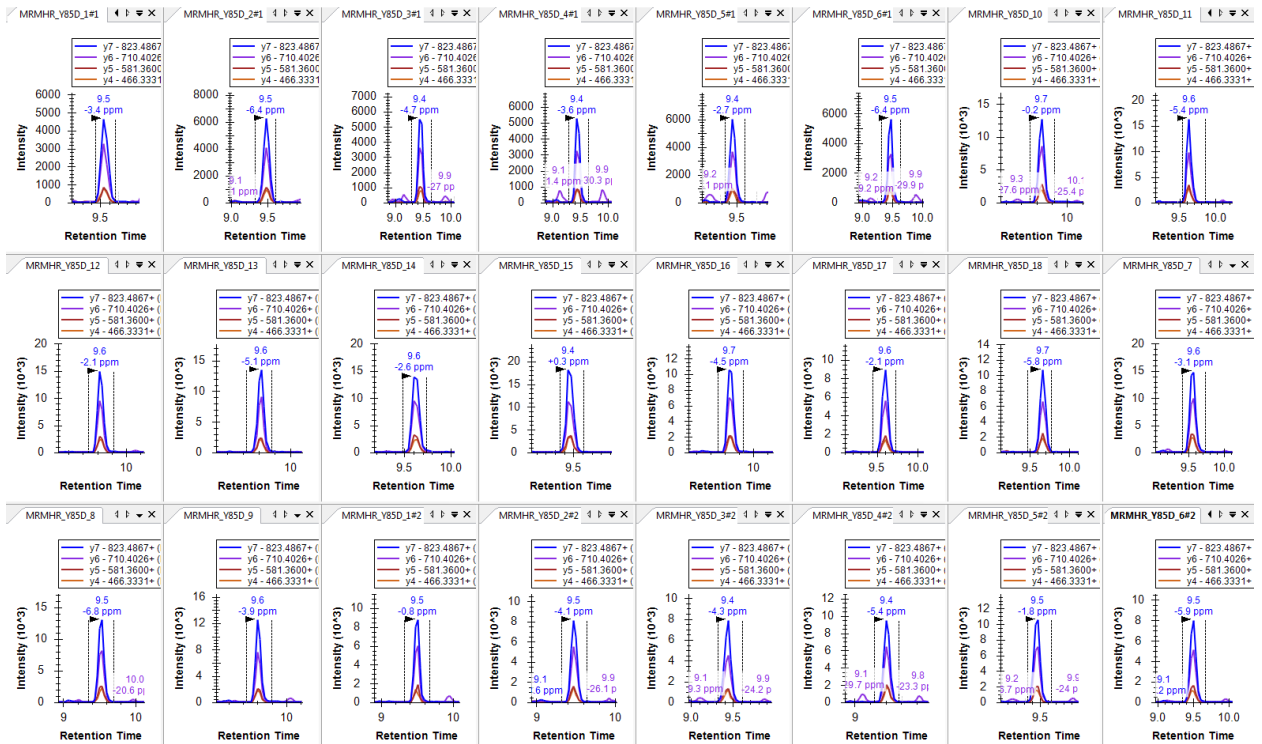


Figure S2. Chromatograms of the tryptic peptides for the quantification of the ASPE of *UGT2B15*. The peptide NYLED^NSLLK and the Y85D variant peptide NDLED^NSLLK were used for the quantification of the wild type and mutant alleles of *UGT2B15*, respectively. Quantification was based on the peak area ratios of the light peptides to the heavy peptides from the QconCAT standard.

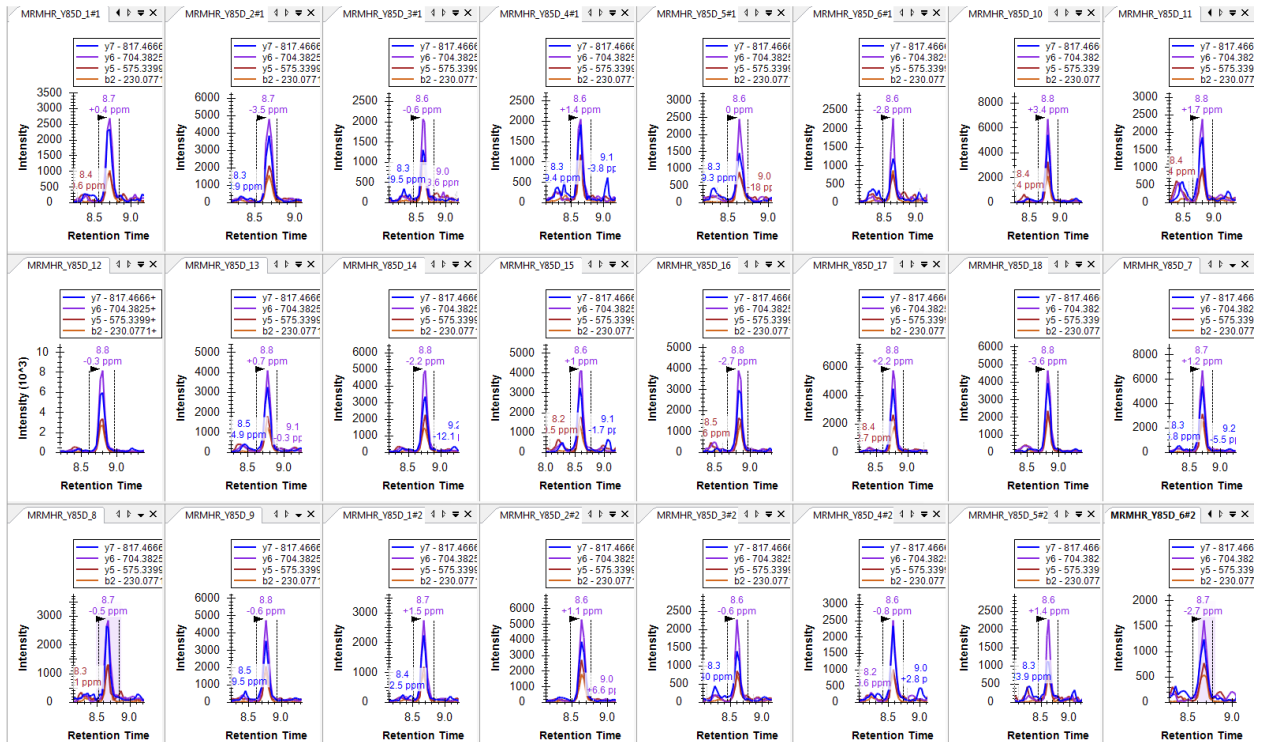
Chromatograms of the UGT2B15 tryptic peptide NYLED^NSLLK (light)



Chromatograms of the UGT2B15 tryptic peptide NYLED^NSLLK (heavy)



Chromatograms of the UGT2B15 Y85D variant peptide NDLEDSLK (light)



Chromatograms of the UGT2B15 Y85D variant peptide NDLEDSLK (heavy)

