

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Extended clinical table.

File Name: Supplementary Data 2

Description: List of differentially expressed genes identified using the R package DESeq2. Differential expression was assessed with the Wald test, and p-values were adjusted for multiple comparisons using the Benjamini–Hochberg (BH) method. Genes with an adjusted p-value < 0.05 were considered significantly differentially expressed.

File Name: Supplementary Data 3

Description: Pathway enrichment analysis was performed on differentially expressed transcripts (DETs) using GO, KEGG, Reactome, and WikiPathways terms for variants P780L, N829S, and E722K. Enrichment was assessed with gprofiler2, which applies a modified Fisher's exact test to evaluate overrepresentation of pathway terms. Results were corrected for multiple testing using the false discovery rate (FDR).

File Name: Supplementary Data 4

Description: List of oligonucleotides used in this study