

SUPPLEMENTARY METHODS

Mutation screening. We designed primers complementary to intronic sequences flanking *PNLIP* exons based on the published nucleotide sequence (ensemble # ENSG00000175535) (*Supplementary Table 1*). After PCR amplification, the entire coding region and the exon-intron boundaries were sequenced. All mutations were confirmed with a second independent PCR reaction. In the German laboratories, we performed PCR using 0.75 U AmpliTaq Gold polymerase (Life Technologies), 400 $\mu\text{mol/L}$ deoxynucleoside triphosphates and 0.1 $\mu\text{mol/L}$ primers in a total volume of 25 μL . Cycle conditions were as follows: initial denaturation for 12 min at 95°C; 48 cycles of 20 s denaturation at 95°C, 40 s annealing at 64°C and 90 s primer extension at 72°C; and a final extension step for 2 min at 72°C. PCR products were digested with antarctic phosphatase and exonuclease I (both New England Biolabs). Cycle sequencing was performed using BigDye terminator mix (Applied Biosystems) with 60°C annealing temperature. The reaction products were purified with ethanol precipitation and loaded onto an ABI 3730 fluorescence sequencer (Applied Biosystems).