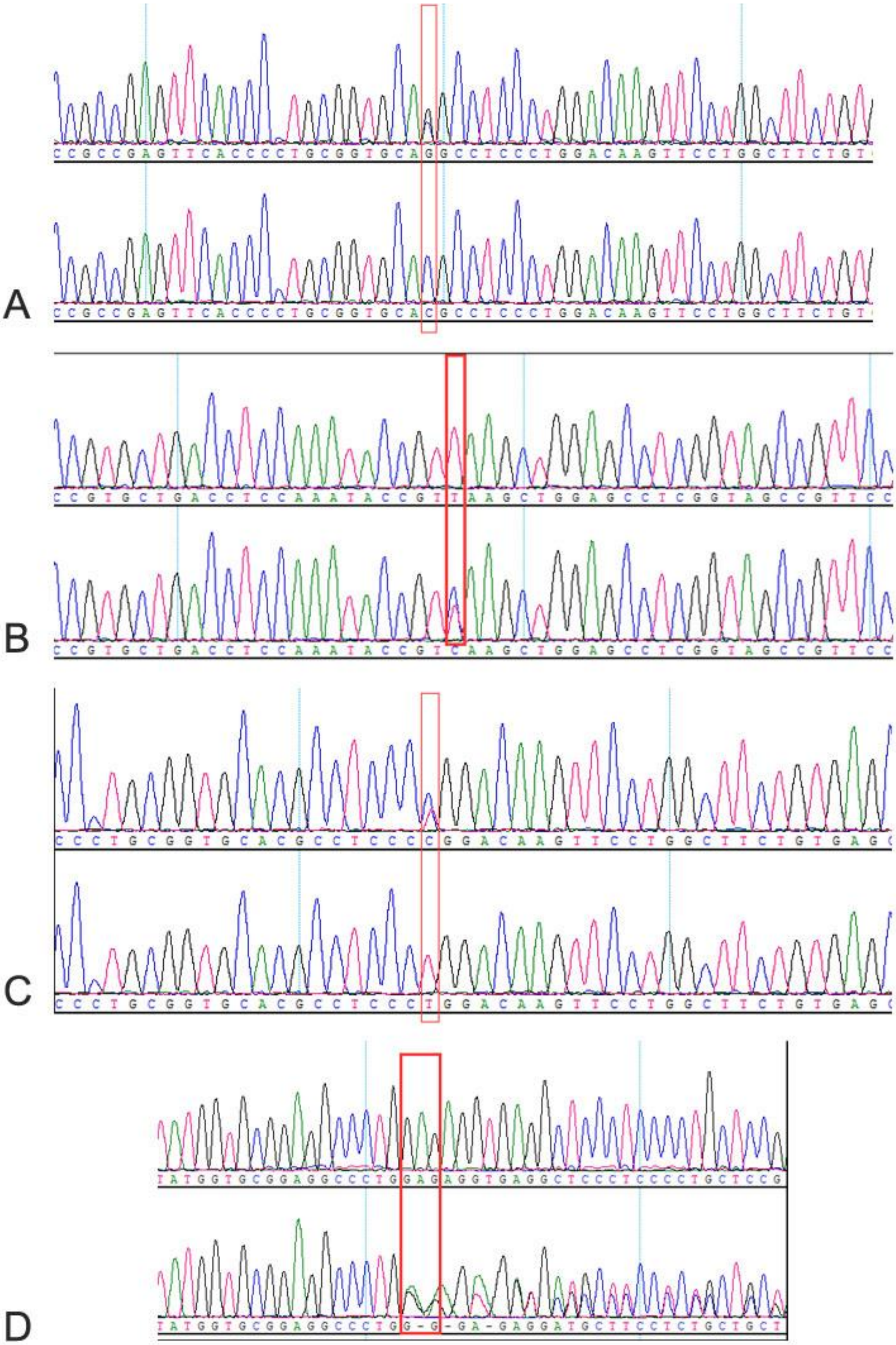
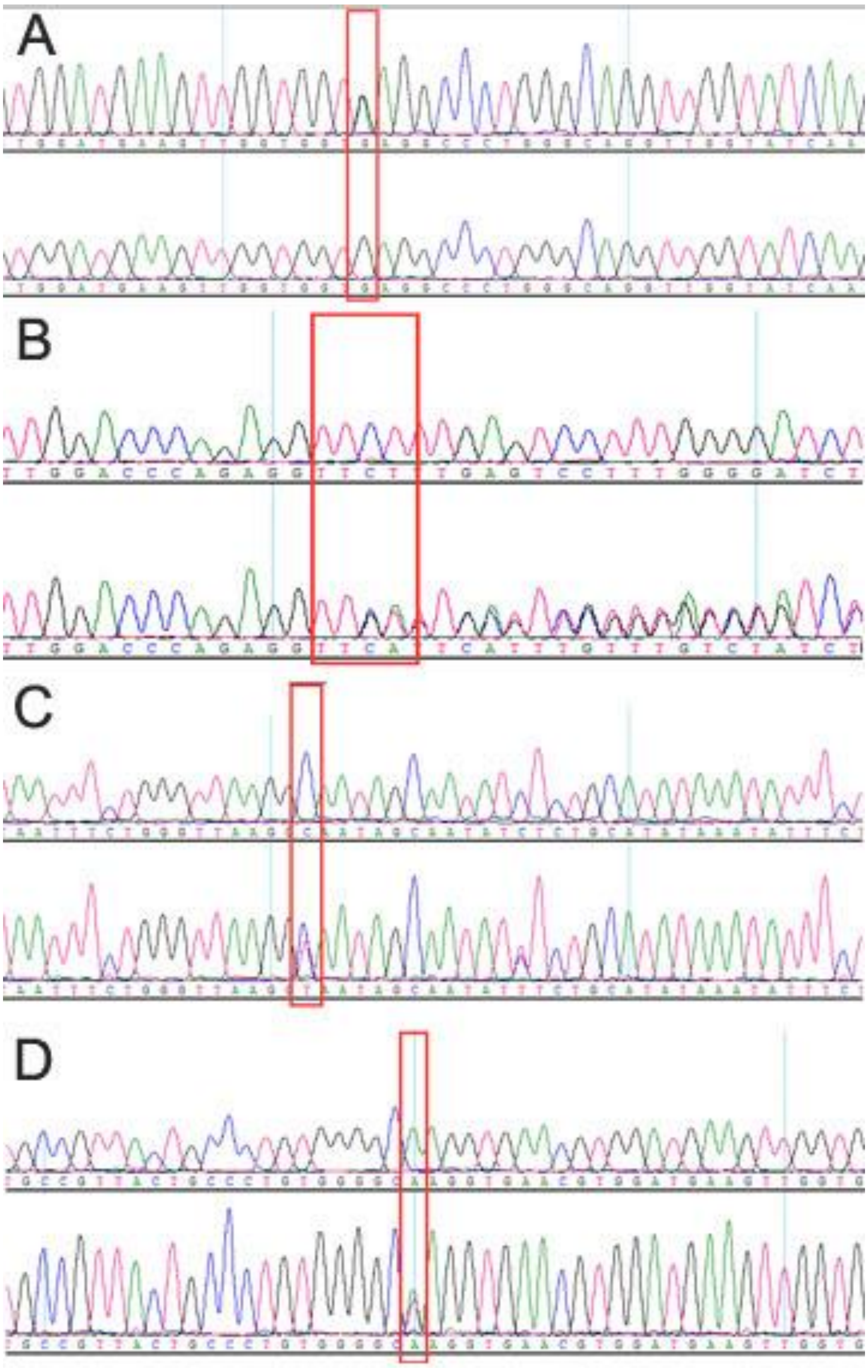
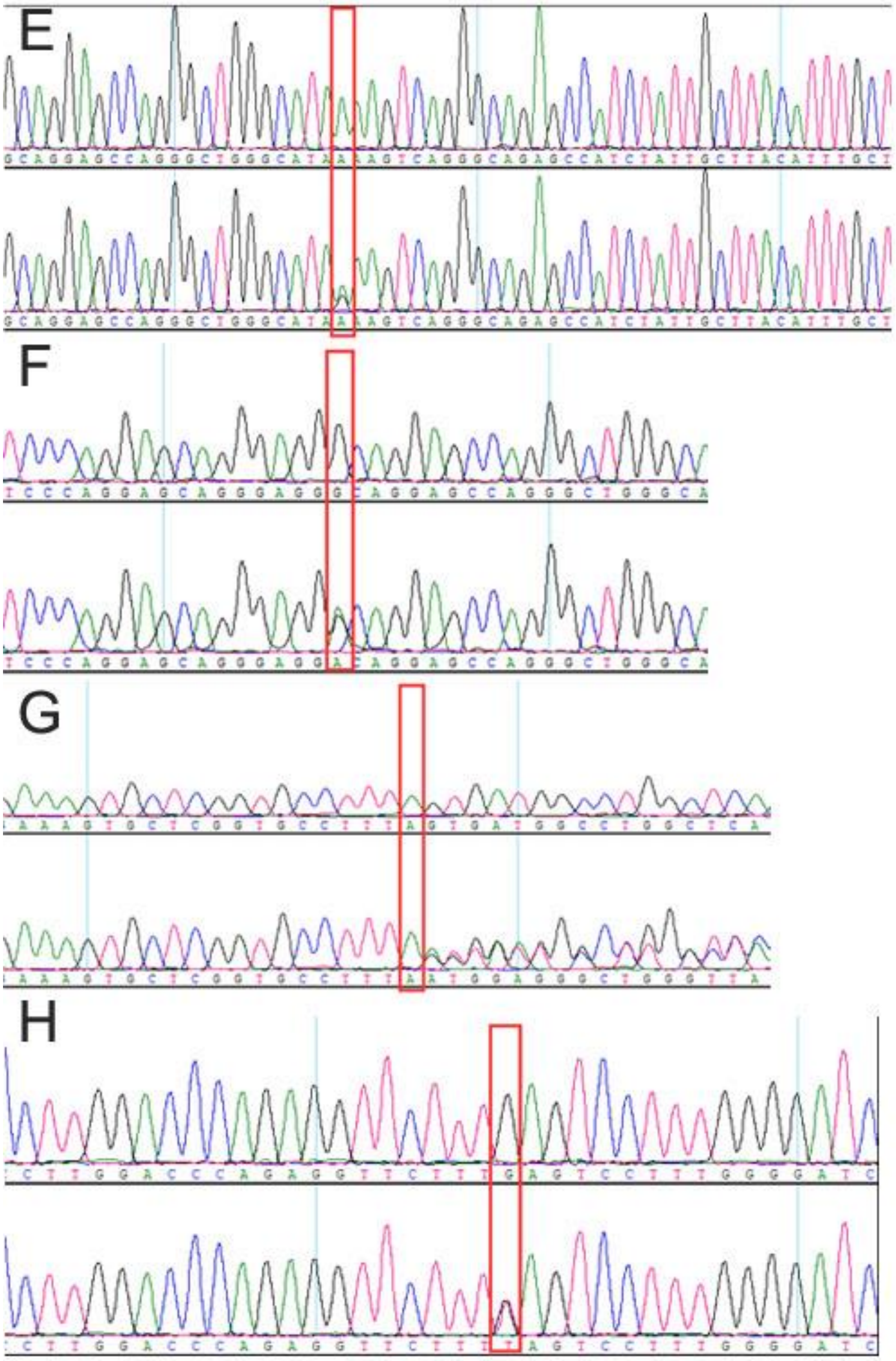


Supplementary Figure1. Validation of NGS method for the α-thalassemia mutations Hb Westmead (A),

Hb Constant Spring (B), Hb Quong Sze (C) and alpha2 Codon 30 del GAG (D). The wildtype (above) and mutant (bottom) of each mutation were shown in the red rectangle.





Supplementary Figure2. Validation of NGS method for the β-thalassemia mutations Hb E(A), Codons 41/42 (-TTCT) (B), IVS-II-654 (C>T) (C), Codon 17 (A>T) (D), -28 (A>G) (E), -50 (G>A) (F), Codons 71/72 (+A) (G) and Codon 43 (G>T) (H). The wildtype (above) and mutant (bottom) of each mutation were shown in the red rectangle.