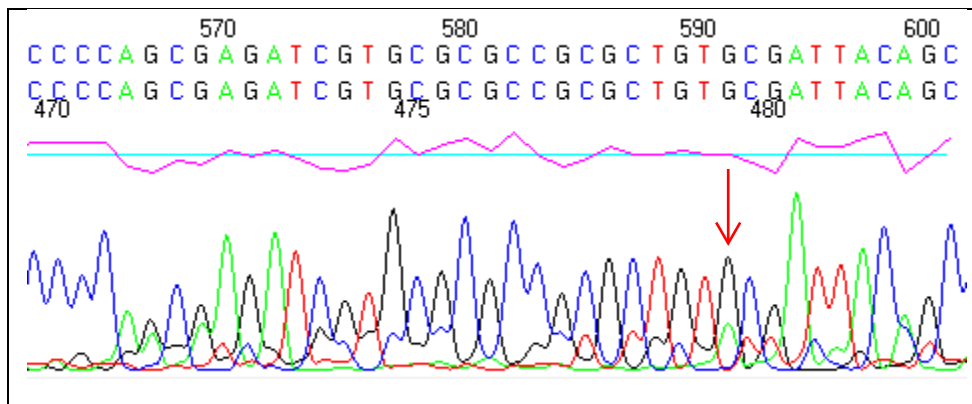
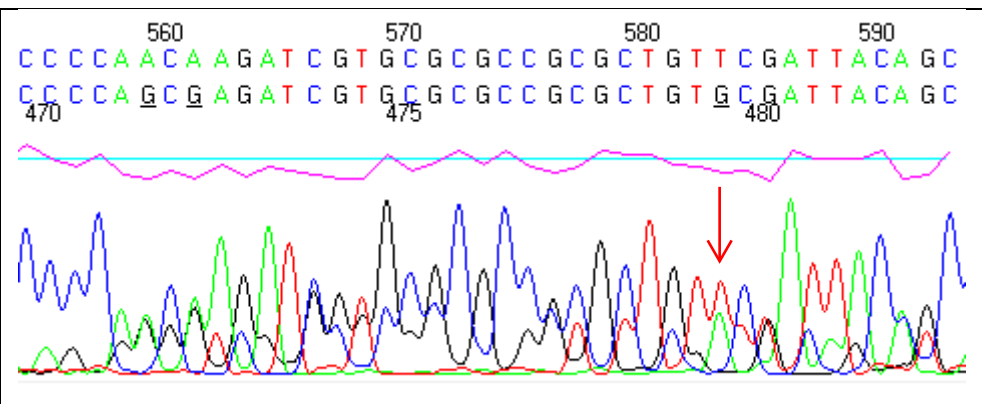


Supplementary Figure 1. UL97 region forward sequencing chromatograms for baseline and follow-up samples showing C480F change in 11 cases

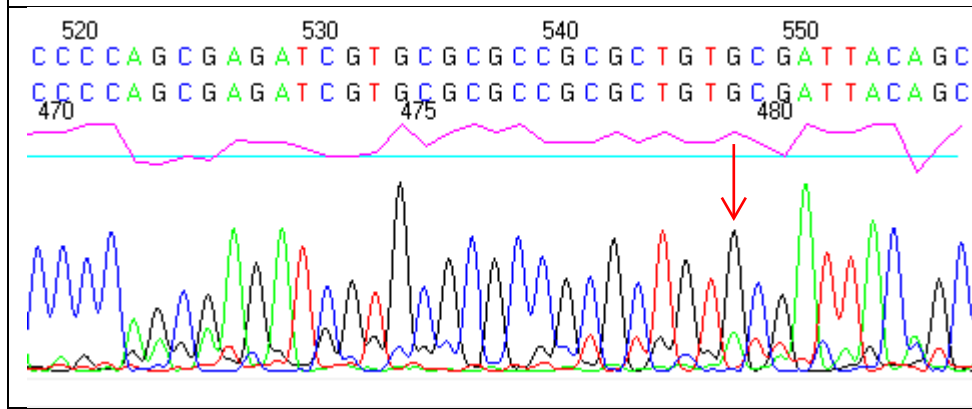




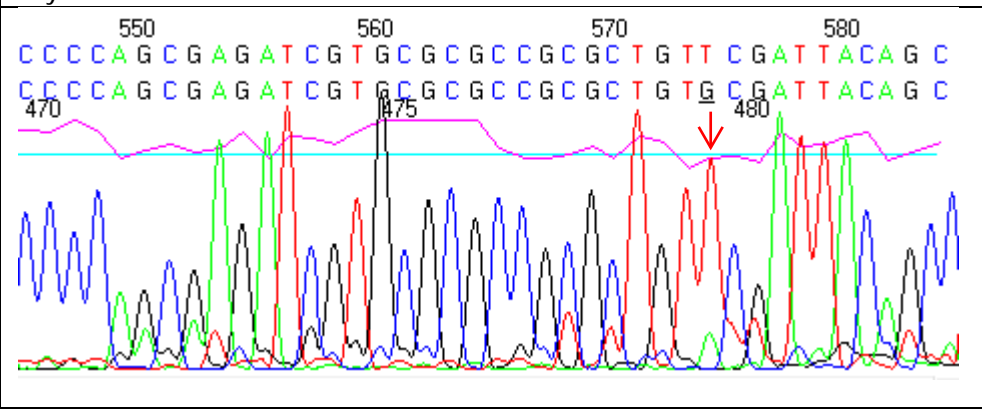
Baseline



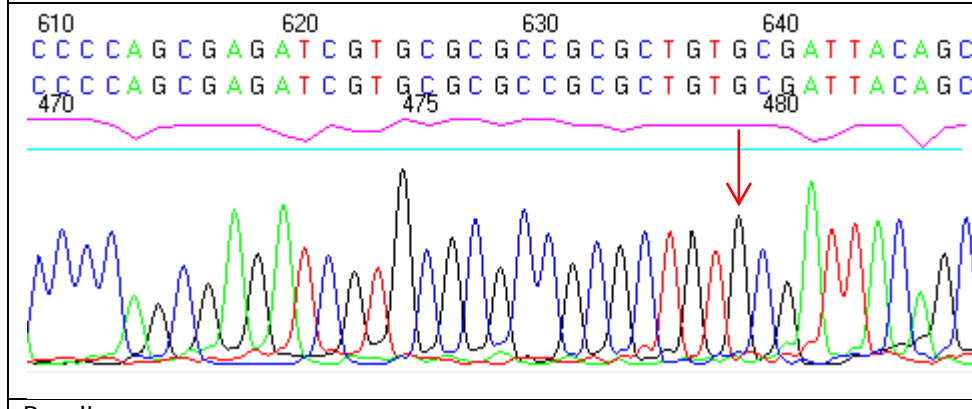
Day 64



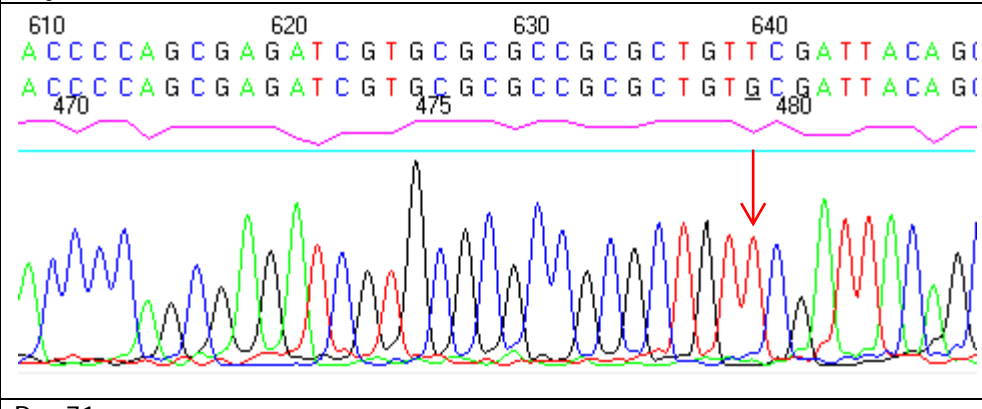
Baseline



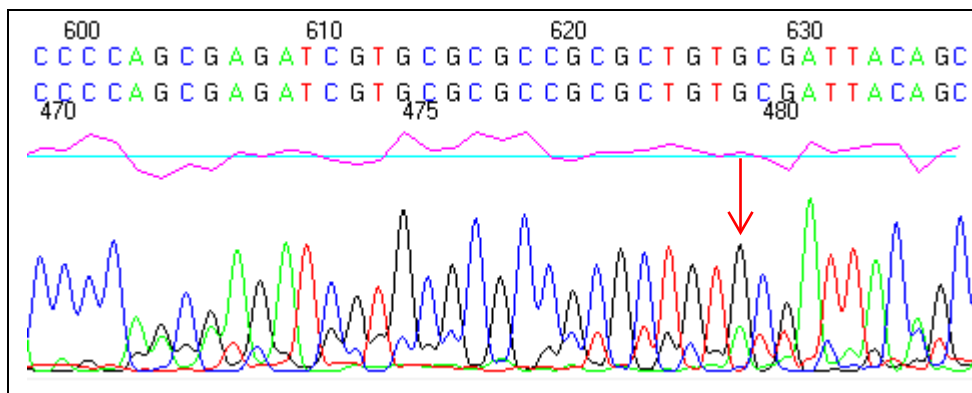
Day 72



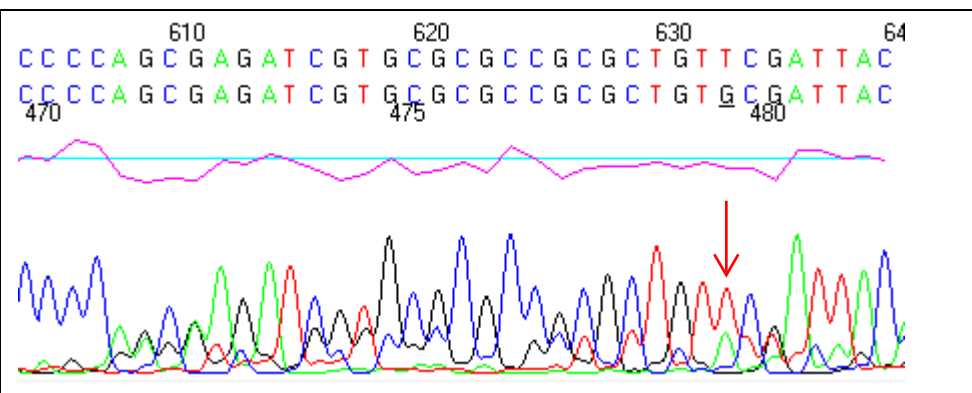
Baseline



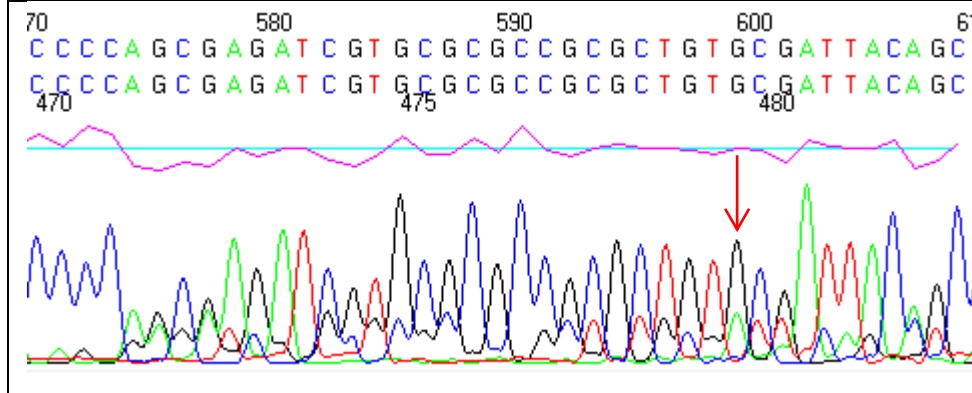
Day 71



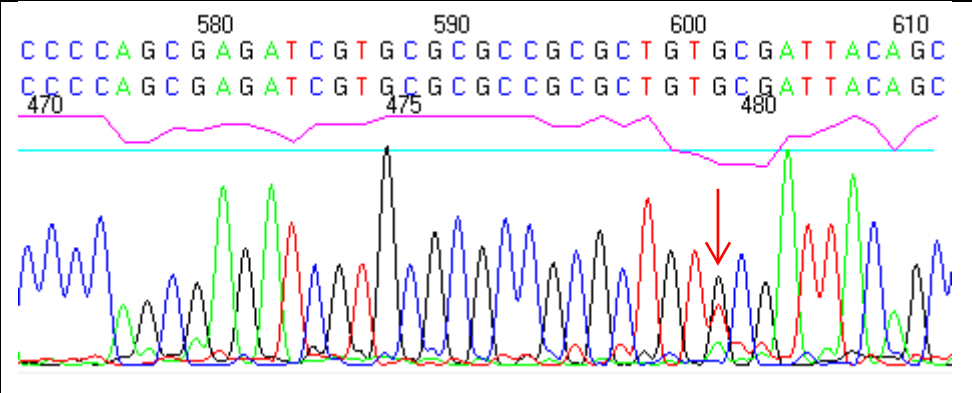
Baseline



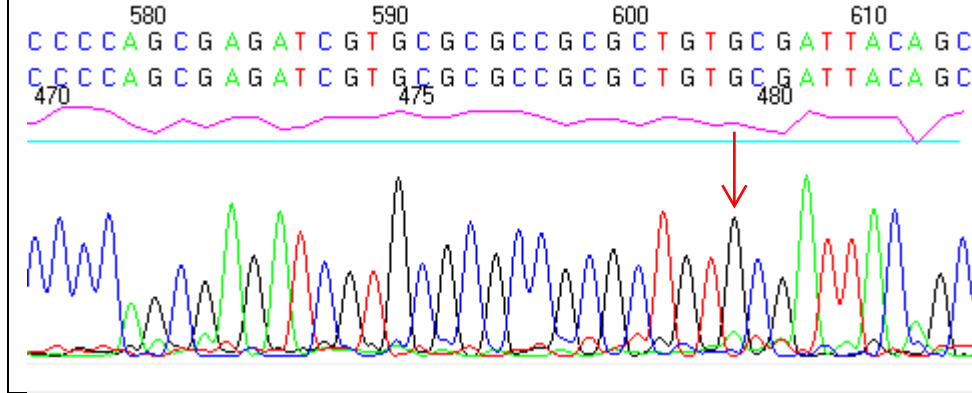
Day 71



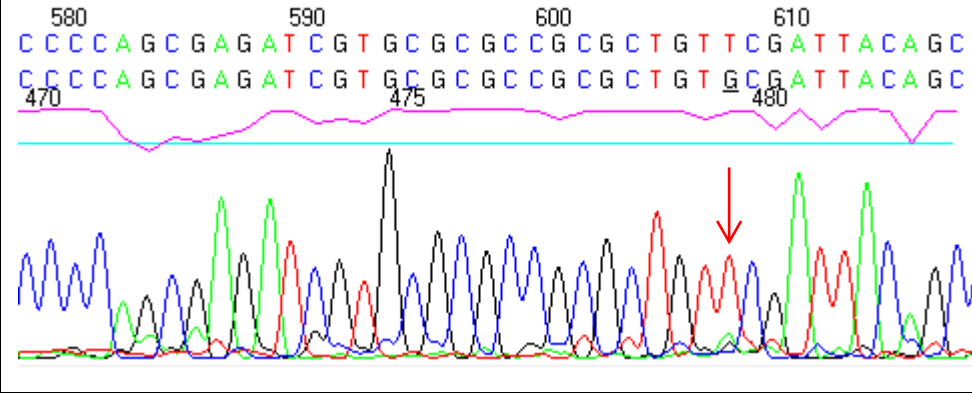
Baseline



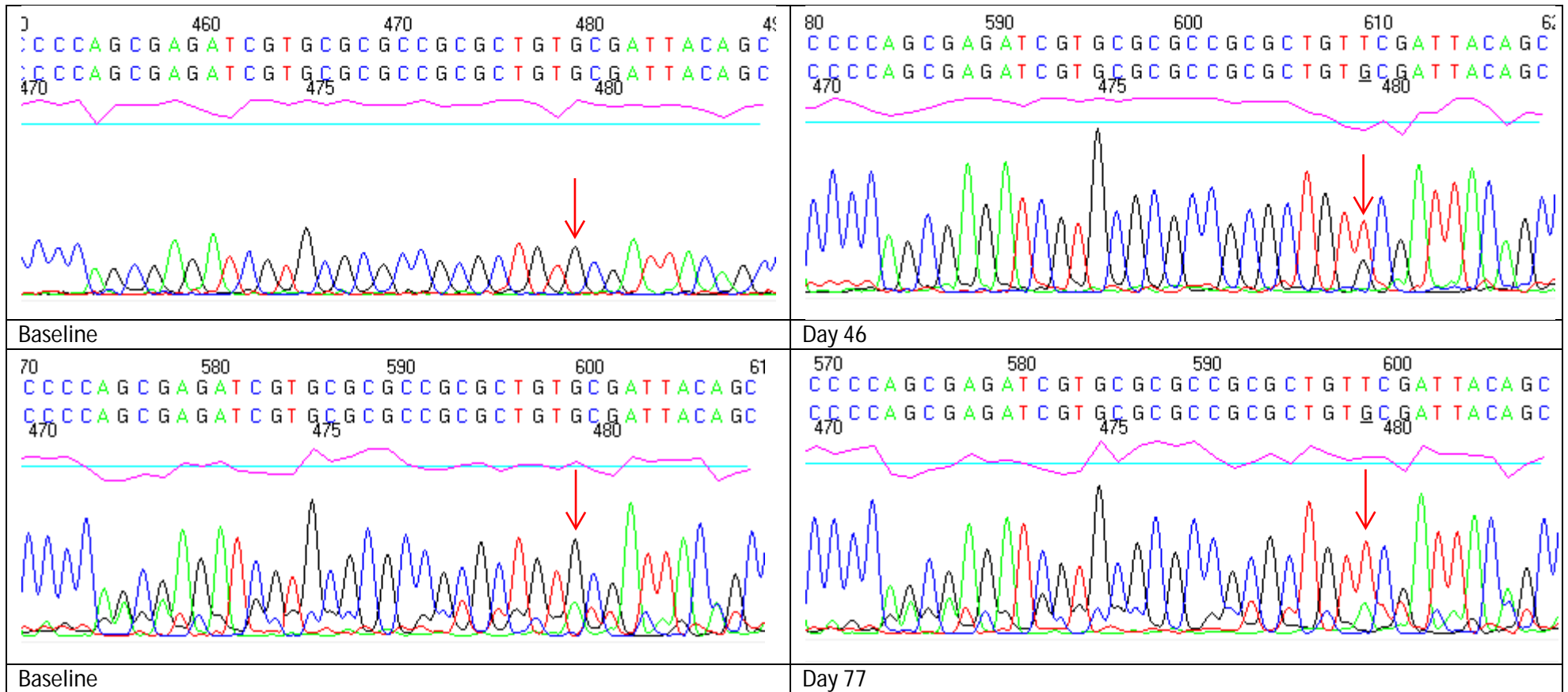
Day 56



Baseline



Day 72



Left and right panels of ABI sequence chromatograms represent the baseline (left) and follow-up (right) samples from 11 study patients (Tables 2 and 3) with evidence of UL97 C480F. Although sequencing was attempted using forward and reverse primers, coverage of UL97 codon 480 was possible only with the forward primer at a read distance of ~630 bases. Despite a noisy baseline reducing the quality value scores in many cases, there is no evidence of any baseline change to T in the middle base of codon 480 (TGC encoding cysteine), whereas in all the follow-up samples there is at least some change from TGC to TTC (encoding phenylalanine). The one follow-up sample (Day 56) that was not called out by the ABI software as having a C480F change was re-sequenced in another laboratory and a partial population of C480F was confirmed. In the panels, the top line sequence is the readout by the ABI software while the second line is the reference AD169 sequence, with the UL97 codon numbering below. The first digit of the codon number is directly below the third base of the corresponding codon. The fluctuating line under the base calls is a plot of the quality value score in relation to the straight horizontal line representing a score of 30.