



Figure S4. Inconsistencies between QC compliant nanopore sequences and Sanger sequences. A, sample 6; B, sample 10; C, sample 24; D, sample 40; E, sample 71. As nanopore sequences, Flongle (f), MinION (m) and combined Flongle + Minion (fm) sequences, based on super high accuracy basecalling, are shown together with the corresponding Sanger sequence (s) on the subtree pruned from the overall tree shown in Figure S1. For each sample, the relevant position of the mis-called base is depicted both in the alignment and the trace files