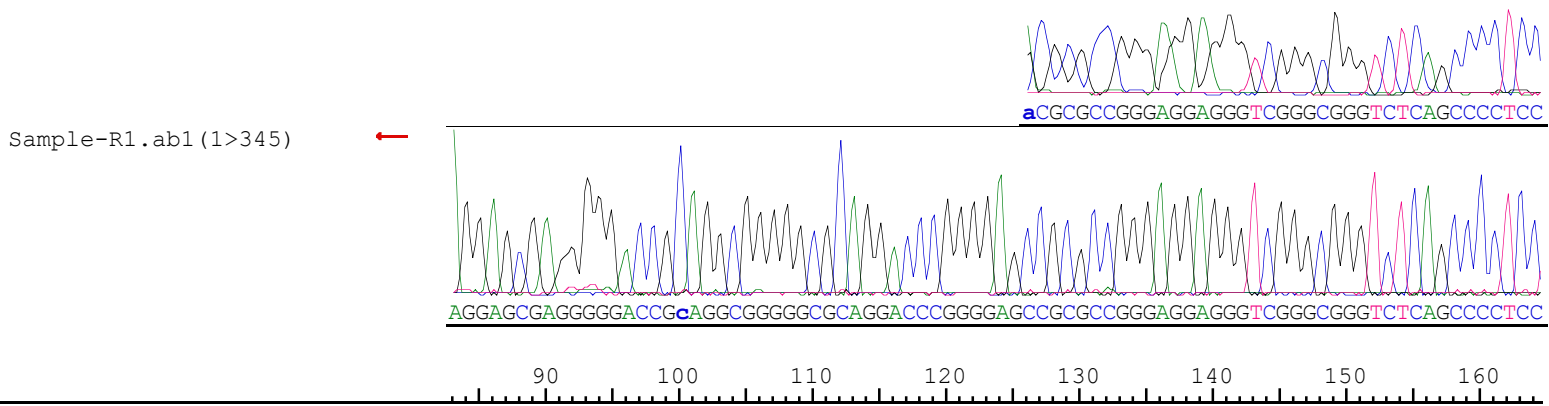
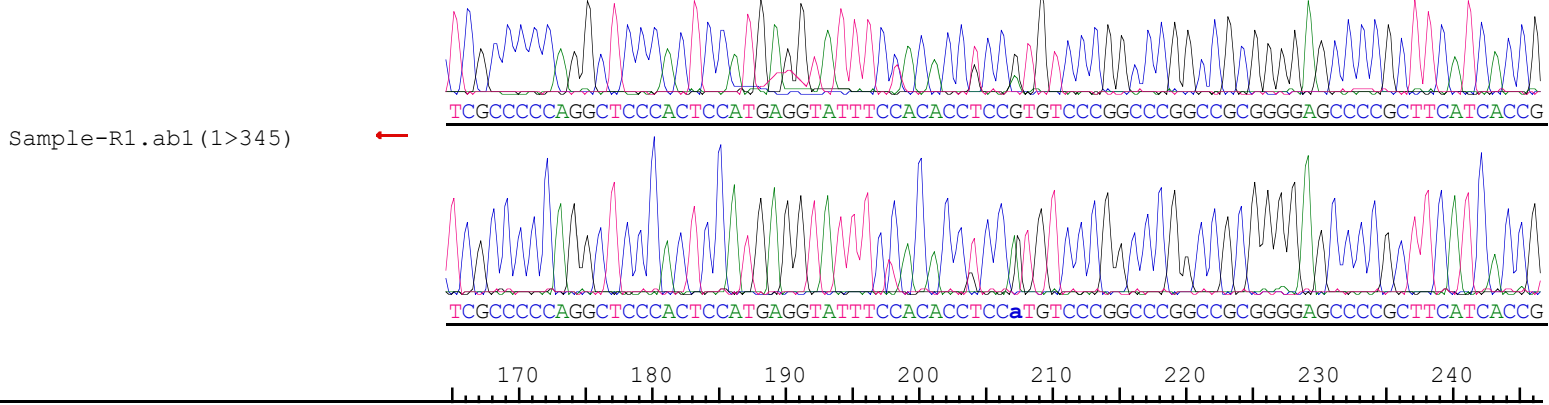


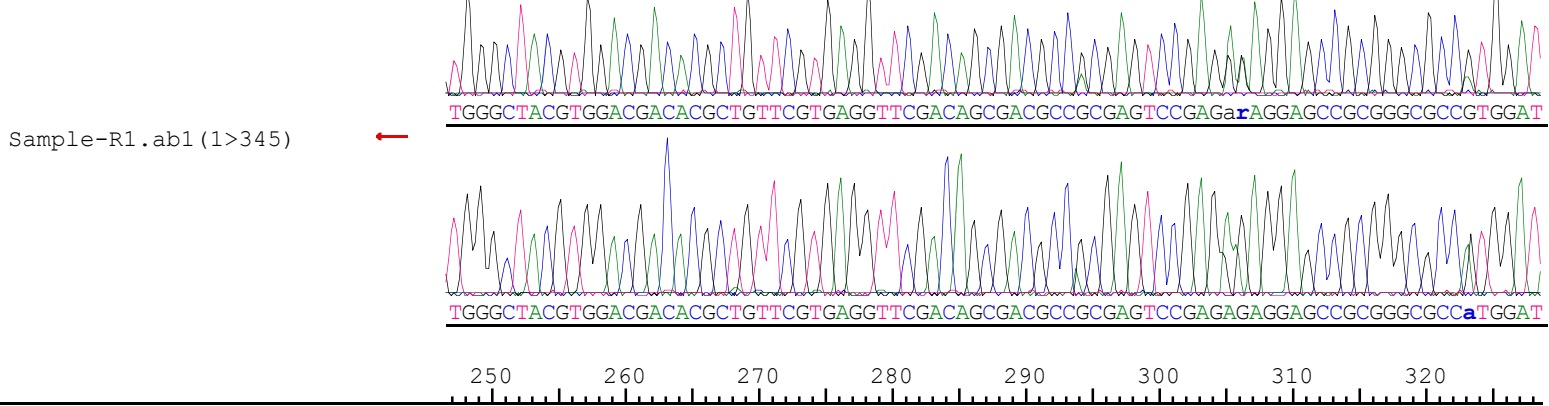
10 20 30 40 50 60 70 80
AGGAGCGAGGGGACCG**Sm**GGCGGGGGCGCAGGACCCGGGGAG**C**CGCGCCGGGAGGAGGGTTCGGGCGGGTCTCAGCCCCCTCC
HLA-B 270701.SEQ(1>649) → GGCGGGGGCGCAGGACCCGGGGAGCCCGCCGGGAGGAGGGTTCGGGCGGGTCTCAGCCCCCTCC
HLA-B 440301.SEQ(1>651) → GC-GGCGGGGGCGCAGGACCCGGGGAG**C**CGCGCCGGGAGGAGGGTTCGGGCGGGTCTCAGCCCCCTCC
Sample-F1.ab1(1>339) →



90 100 110 120 130 140 150 160
TCGCCCCAGGCTCCCACTCCATGAGGTATTT**C**ACACCT**T**CC**R**TGTCCCGGCCCGCCGCGGGGAGCCCCGCTTCATCACCG
HLA-B 270701.SEQ(1>649) → TCGCCCCAGGCTCCCACTCCATGAGGTATTTCCACACCTCCGTGTCCCGGCCCGCCGCGGGGAGCCCCGCTTCATCACCG
HLA-B 440301.SEQ(1>651) → TCGCCCCAGGCTCCCACTCCATGAGGTATTT**t**ACAC**g**CC**a**TGTCCCGGCCCGCCGCGGGGAGCCCCGCTTCATCACCG
Sample-F1.ab1(1>339) →



170 180 190 200 210 220 230 240
TGGGTACGTGGACGACACGCTGTTCGTGAGGTTTCGACAGCGACGCC**C**CGAGTCCGAG**AG**AGGAGCCCGGGCGCC**G**TGGAT
HLA-B 270701.SEQ(1>649) → TGGGTACGTGGACGACACGCTGTTCGTGAGGTTTCGACAGCGACGCCCGCGAGTCCGAGAGAGAGCCCGGGCGCCGTGGAT
HLA-B 440301.SEQ(1>651) → TGGGTACGTGGACGACACGCTGTTCGTGAGGTTTCGACAGCGACGCC**a**CGAGTCCGAG**ga**AGGAGCCCGGGCGCC**a**TGGAT
Sample-F1.ab1(1>339) →



250 260 270 280 290 300 310 320
AGAGCAGGAGGGGCCGGAGTATTGGGACCGGGAGACACAGATCT**G**CAAG**G**CCAA**G**GCACAGACT**G**ACCAGAG**R**ACCT**G**CC**S**
HLA-B 270701.SEQ(1>649) → AGAGCAGGAGGGGCCGGAGTATTGGGACCGGGAGACACAGATCTGCAAGGCCAAAGGCACAGACTGACCAGAGGACCTGCGG
HLA-B 440301.SEQ(1>651) → AGAGCAGGAGGGGCCGGAGTATTGGGACCGGGAGACACAGATCT**c**CAA**a**CCAA**ca**CACAGACT**t**ACCAGAG**ga**ACCT**G**CC**c**
Sample-F1.ab1(1>339) →

