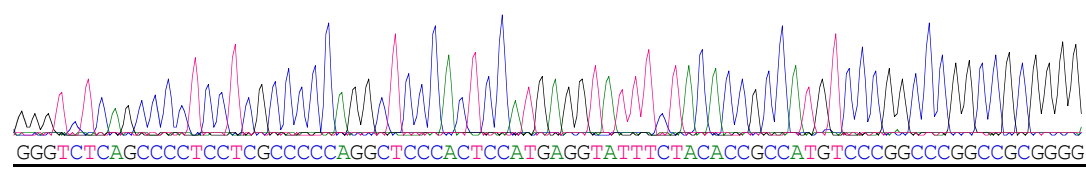


10 20 30 40 50 60 70 80
AGGGAAATGGCCTCTGTGGGGAGGAGCGAGGGGACCGCAGGCGGGGGCGCAGGACC**YGR**GGAGCCGCGCCGGGAGGAGGGTCCG
HLA-B 1502.SEQ (1>989) → AGGGAAATGGCCTCTGTGGGGAGGAGCGAGGGGACCGCAGGCGGGGGCGCAGGACC**c**GGGAGCCGCGCCGGGAGGAGGGTCCG
HLA-B 5801.SEQ (1>962) → AGGAGCGAGGGGACCGCAGGCGGGGGCGCAGGACCT**Ga**GGAGCCGCGCCGGGAGGAGGGTCCG

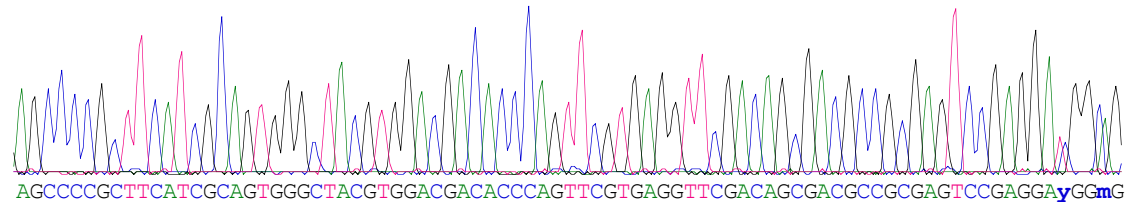
90 100 110 120 130 140 150 160
GGCGGGTCTCAGCCCCTCCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCGCCATGTCCCGGCCGCGCGGGG

HLA-B 1502.SEQ (1>989) → GGCGGGTCTCAGCCCCTCCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCGCCATGTCCCGGCCGCGCGGGG
HLA-B 5801.SEQ (1>962) → GGCGGGTCTCAGCCCCTCCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCGCCATGTCCCGGCCGCGCGGGG
Sample-R1.ab1 (1>310) ←



170 180 190 200 210 220 230 240
AGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACCCAGTTCTGAGGTTTCGACAGCGACGCCGCGAGTCCGAGGAY**YGGMG**

HLA-B 1502.SEQ (1>989) → AGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACCCAGTTCTGAGGTTTCGACAGCGACGCCGCGAGTCCGAGGATGGCG
HLA-B 5801.SEQ (1>962) → AGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACCCAGTTCTGAGGTTTCGACAGCGACGCCGCGAGTCCGAGGAY**cGgaG**
Sample-R1.ab1 (1>310) ←



250 260 270 280 290 300 310 320 330
CCCCGGGCGCCATGGATAGAGCAGGAGGGGCCGGAGTATTGGGAC**SGGRAS**ACACRGAW**WYSA**AGR**RC**W**MR**CR**C**AGACTTA

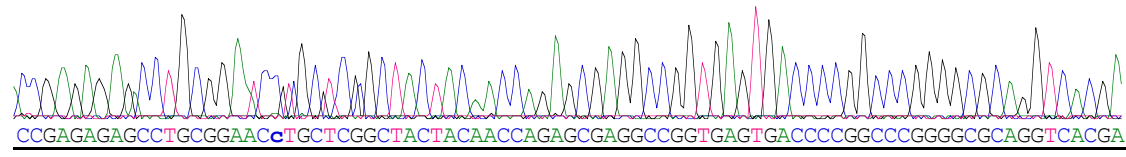
HLA-B 1502.SEQ (1>989) → CCCC GG GCGCCATGGATAGAGCAGGAGGGGCCGGAGTATTGGGAC**ga**ACACACAGATCTCCAAGACC**a**ACACACAGACTTA
HLA-B 5801.SEQ (1>962) → CCCC GG GCGCCATGGATAGAGCAGGAGGGGCCGGAGTATTGGGAC**g**GGG**g**ACAC**g**GA**a**at**g**AAG**g**CCT**c**g**g**CAGACTTA
Sample-F1.ab1 (190>356) →

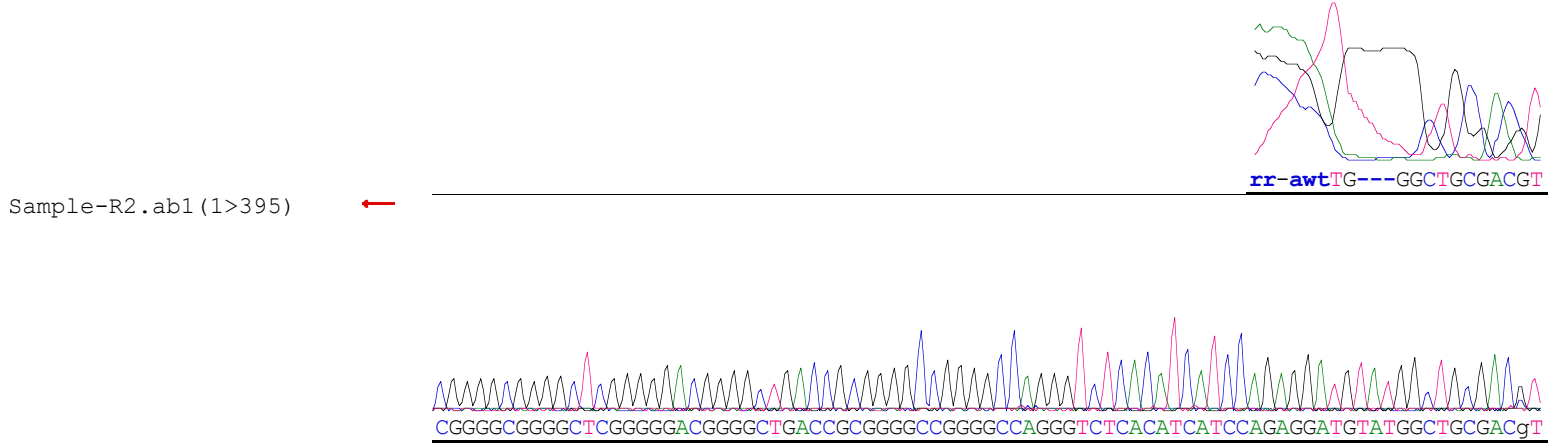
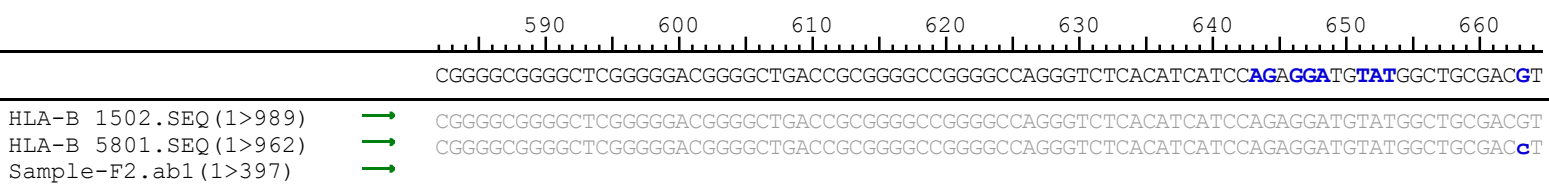
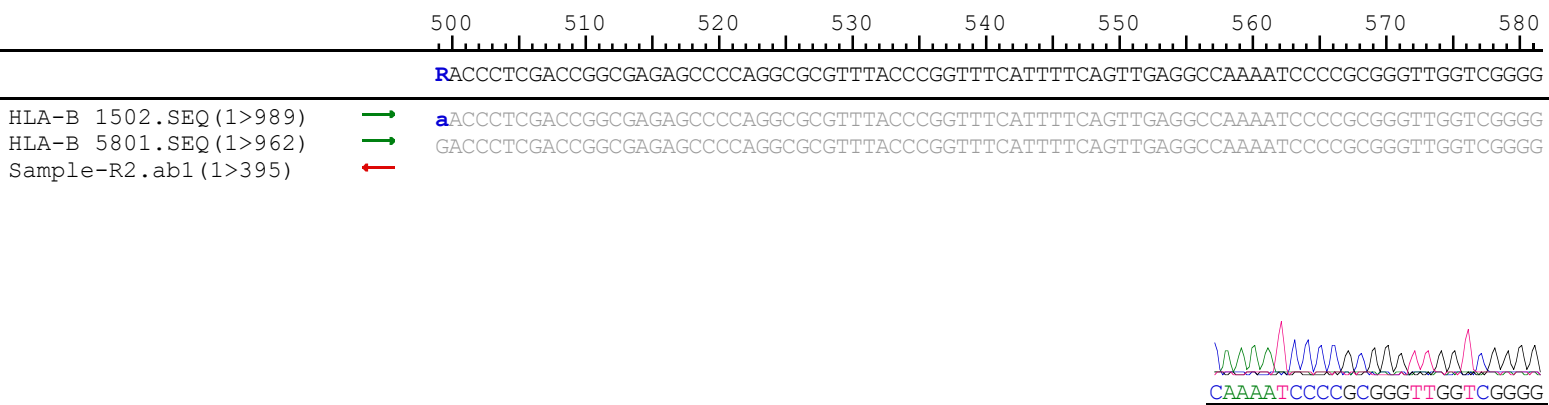
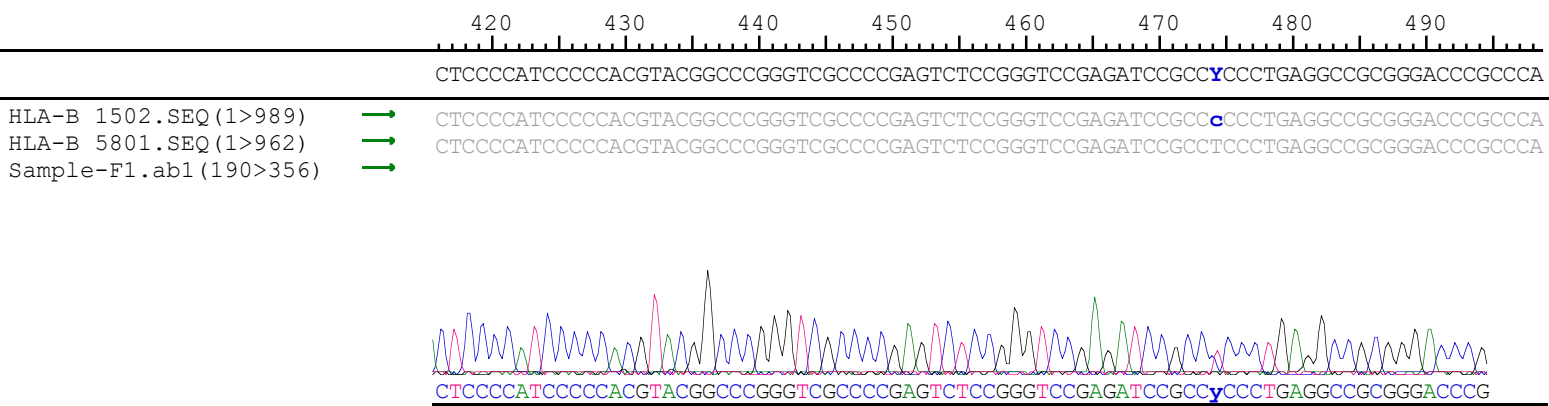
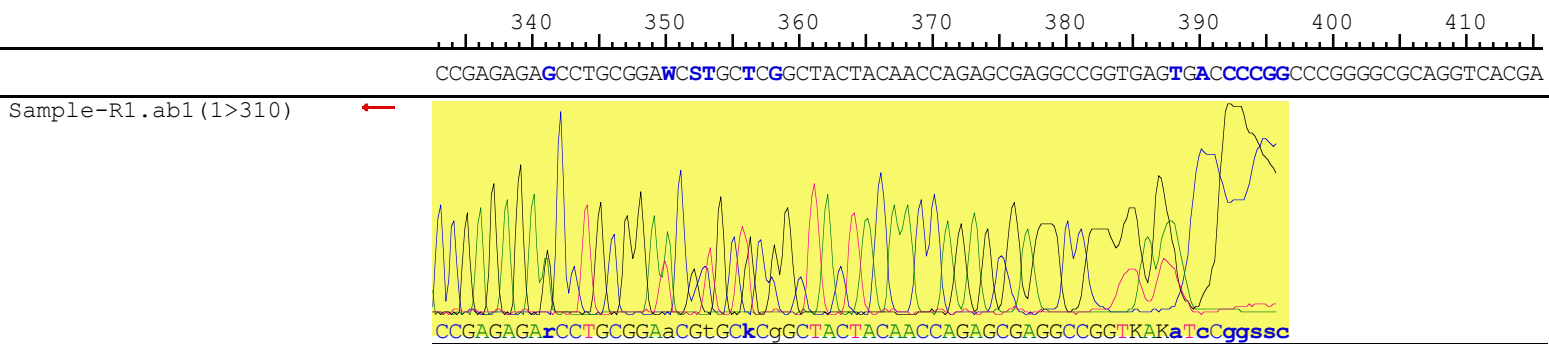
Sample-R1.ab1 (1>310) ←

CCCCGGGCGCCATGGATAGAGCAGGAGGGGCCGGAGTATTGGGAC**c**GG**r**AcACACaGAtCTCcAAGaCCwaCaCaCAGACTTA

340 350 360 370 380 390 400 410
CCGAGAGAG**GC**CTGCGGA**WCST**GC**TC**GGCTACTACAACCAGAGCGAGGCCGGTGAGT**GAC**CCCCGGCCCCGGGGCGCAGGTACCGA

HLA-B 1502.SEQ (1>989) → CCGAGAGAGCCTGCGGA**c**TG**g**CGGCTACTACAACCAGAGCGAGGCCGGTGAGT**G**ACCCCCGGCCCCGGGGCGCAGGTACCGA
HLA-B 5801.SEQ (1>962) → CCGAGAGAG**a**CTGCGGA**t**CC**g**CGCT**c**GCTACTACAACCAGAGCGAGGCCGGTGAGT**G**ACCCCCGGCCCCGGGGCGCAGGTACCGA
Sample-F1.ab1 (190>356) →



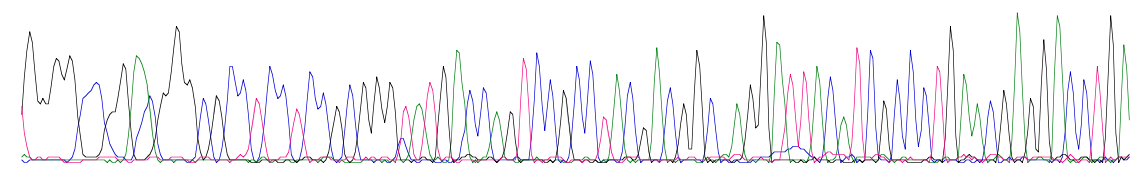


Project: Untitled Contig 1

670 680 690 700 710 720 730 740

GGGGCC**G**GACGGGCGCCTCCTCCGCGGG**T**ATGACCAGTCCGCC**T**ACGACGGC**a**AGGATTACATCGCCCTGAACGAGGACCTGA

Sample-F2.ab1 (1>397) →



Sample-R2.ab1 (1>395) ←

GGGGCC**G**GACGGGCGCCTCCTCCGCGGG**T**ATGACCAGTCCGCC**T**ACGACGGC**a**AGGATTACATCGCCCTGAACGAGGACCTGA

GGGGCC**G**GACGGGCGCCTCCTCCGCGGG**T**ATGACCAGTCCGCC**T**ACGACGGC**a**AGGATTACATCGCCCTGAACGAGGACCTGA

750 760 770 780 790 800 810 820 830

GCTCCTGGACCGCGCGGACAC**G**GCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCGT**G**AGGCGGAGCAGCTGAGAGCC

HLA-B 1502.SEQ (1>989) →

HLA-B 5801.SEQ (1>962) →

Sample-F2.ab1 (1>397) →

GCTCCTGGACCGCGCGGACAC**G**GCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCGT**G**AGGCGGAGCAGCTGAGAGCC

GCTCCTGGACCGCGCGGACAC**G**GCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCGT**G**AGGCGGAGCAGCTGAGAGCC

Sample-R2.ab1 (1>395) ←

GCTCCTGGACCGCGCGGACAC**G**GCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCGT**G**AGGCGGAGCAGCTGAGAGCC

GCTCCTGGACCGCGCGGACAC**G**GCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCGT**G**AGGCGGAGCAGCTGAGAGCC

840 850 860 870 880 890 900 910

TACCTGGAGGGCTGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCGGGTACCAGGGG

HLA-B 1502.SEQ (1>989) →

HLA-B 5801.SEQ (1>962) →

Sample-F2.ab1 (1>397) →

TACCTGGAGGGCTGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCGGGTACCAGGGG

TACCTGGAGGGCTGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCGGGTACCAGGGG

Sample-R2.ab1 (1>395) ←

TACCTGGAGGGCTGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCGGGTACCAGGGG

TACCTGGAGGGCTGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGGAGACGCTGCAGCGCGCGGGTACCAGGGG

920 930 940 950 960 970 980 990

CAGTGGGAGCCT**t**CCCC**A**TCTCCTATAG**G**TCGCC**G**GGG**A**TGGCTCCACGAGAAGAGGAGGAAAATGGGATCAGCGCTAGA

HLA-B 1502.SEQ (1>989) →

HLA-B 5801.SEQ (1>962) →

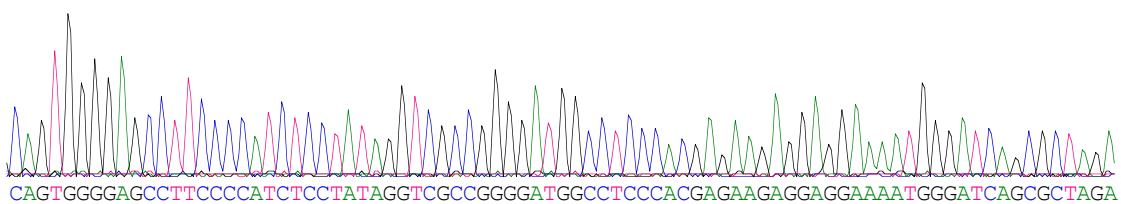
CAGTGGGAGCCT**t**CCCC**A**TCTCCTATAG**G**TCGCC**G**GGG**A**TGGCTCCACGAGAAGAGGAGGAAAATGGGATCAGCGCTAGA

CAGTGGGAGCCT**t**CCCC**A**TCTCCTATAG**G**TCGCC**G**GGG**A**TGGCTCCACGAGAAGAGGAGGAAAATGG

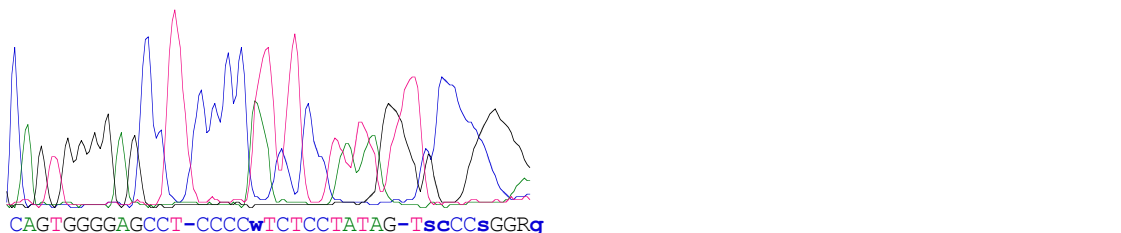
920 930 940 950 960 970 980 990

CAGTGGGGAGCCTtCCCCATCTCCTATAGGTCGCCGGGGATGGCCTCCCACGAGAAGAGGAGGAAAAATGGGATCAGCGCTAGA

Sample-F2.ab1 (1>397)



Sample-R2.ab1 (1>395)



1000 1010 1020 1030 1040

ATGTCGCCCTCCCTTGAATGGAGAATGGCATGAGTTTTCCTGAGTTTC

Sample-F2.ab1 (1>397)

