

SANGER SEQUENCING FOR VALIDATION OF VARIANTS

	Primer sense 5'to 3'	Primer size (bp)	Tm	%GC	Amplicon size	Sequence
KNOWN VARIANT Chr19:7122658, c.C3485T, p.A1162V						
1VRsnap	CACCAACCCCGTGTTTCTG	19	58	58	230	A
2VRsnap	CCTGGCCTGGGTCGTTATG	19	59	63		
NOVEL VARIANT Chr19:7267665, c.G332T, p.G111V						
5VNRSNAP	ACGAGGCCCGAAGATTTC	19	59	58	224	C
6VNRSNAP	CCCCGGGTGATGTTTCATCAG	19	59	60		

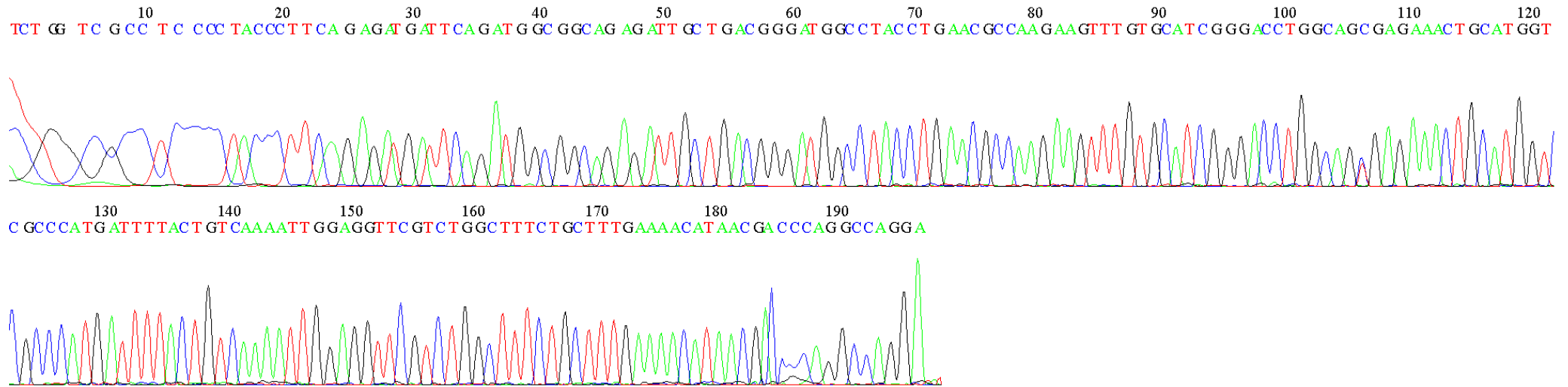
SEQUENCE OF KNOWN VARIANT (A)

CACCAACCCCGTGTTTCTGTTTGTAGAATAATCCTGGCCGCCCTCCCCCTACCCTTCAAGAGATGATTTCAG
ATGGCGGCAGAGATTGCTGACGGGATGGCCTACCTGAACGCCAAGAAGTTTGTGCATCGGGACCTGG
CAGCGAGAACTGCATGGTCGCCCATGATTTTACTGTCAAATTGGAGGTTTCGTCTGGCTTTCTGCTTT
GAAAACATAACGACCCAGGCCAGG

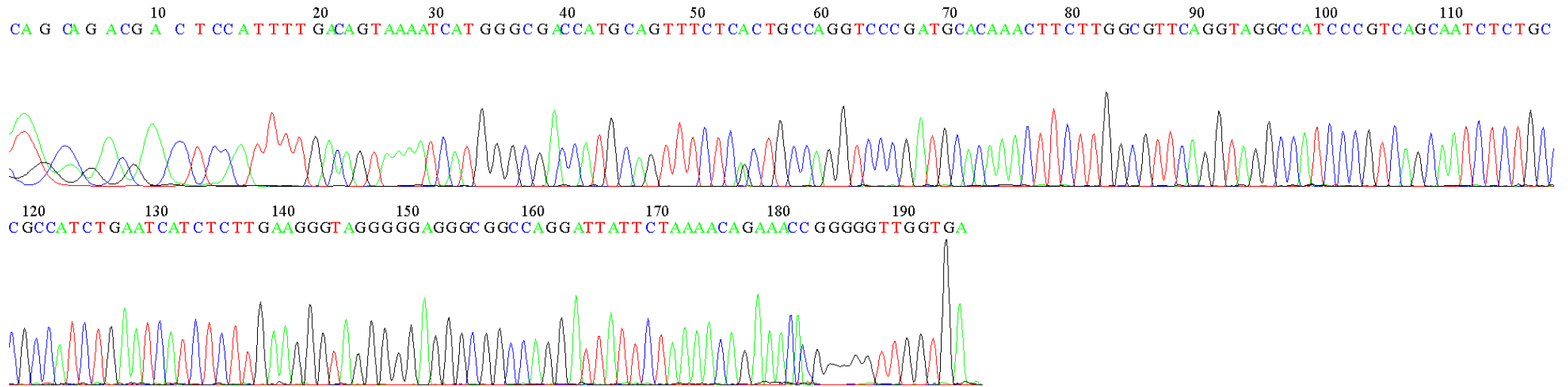
SEQUENCE OF NOVEL VARIANT (C)

ACGAGGCCCGAAGATTTCGAGACCTCAGTTTCCCCAACTCATCATGATCACTGATTACTTGCTGCTCT
TCCGGGTCTATGGGCTCGAGAGCCTGAAGGACCTGTTCCCCAACCTCACGGTCATCCGGGGATCACGA
CTGTTCTTTAACTACGCGCTGGTCATCTTCGAGATGGTTCACCTCAAGGAACTCGGCCTCTACAACCTGA
TGAACATCACCCGGGG

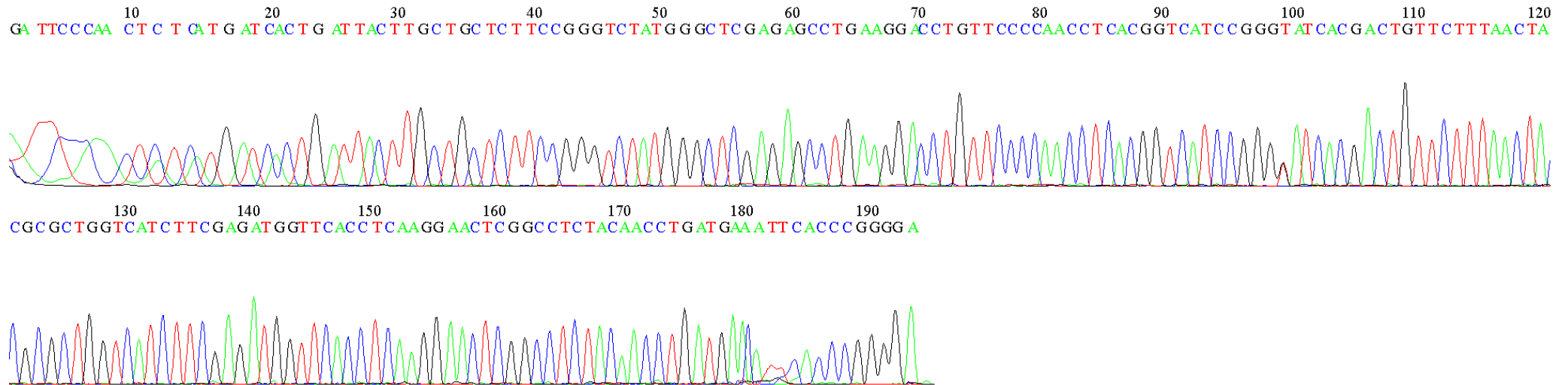
File: A_VRsnap_A_F.ab1 Run Ended: 2022/6/16 22:5:56 Signal G:2927 A:4137 C:7608 T:4516
Sample: A_VRsnap_A_F Lane: 15 Base spacing: 14.198061 197 bases in 2405 scans Page 1 of 1



File: A_VRsnap_A_R.ab1 Run Ended: 2022/6/16 22:5:56 Signal G:4819 A:5543 C:11727 T:7066
Sample: A_VRsnap_A_R Lane: 13 Base spacing: 13.785342 195 bases in 2445 scans Page 1 of 1



File: C_VNRSNAP_C_F.ab1 Run Ended: 2022/6/16 22:5:56 Signal G:4568 A:6757 C:16750 T:9327
 Sample: C_VNRSNAP_C_F Lane: 7 Base spacing: 13.93152 194 bases in 2400 scans Page 1 of 1



File: C_VNRSNAP_C_R.ab1 Run Ended: 2022/6/16 22:5:56 Signal G:2612 A:4202 C:5341 T:3649
Sample: C_VNRSNAP_C_R Lane: 5 Base spacing: 14.131732 196 bases in 2368 scans Page 1 of 1

