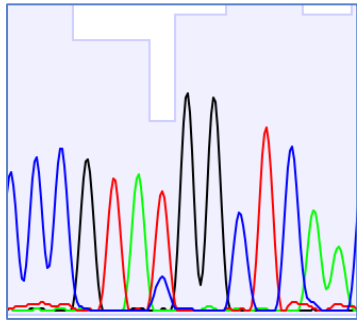
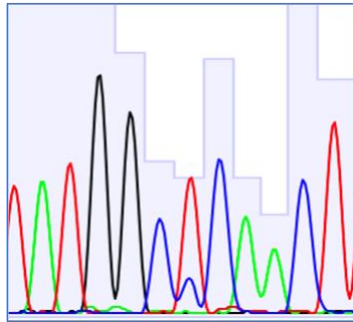


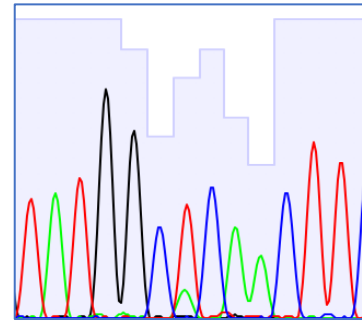
VHL validation by Sanger sequencing



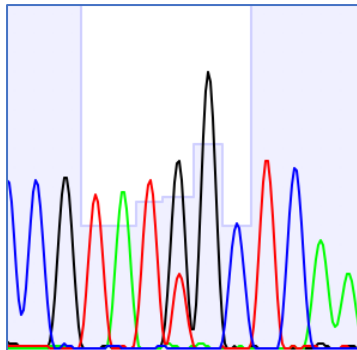
K079 VHL_3:10183793:T:C



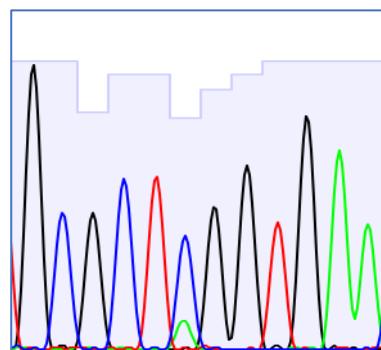
K119 VHL_3:10183797:T:C



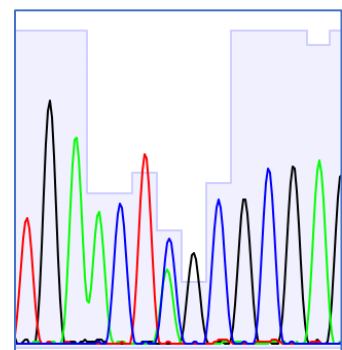
K165 VHL_3:10183797:T:A



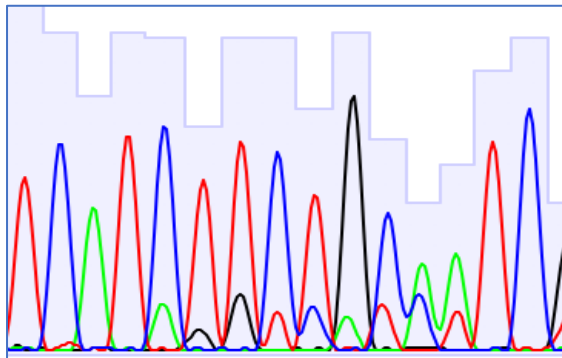
K180 VHL_3:10183794:G:T



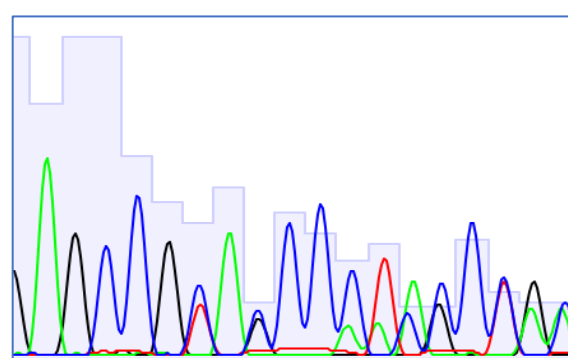
K191 VHL_3:10183725:C:A



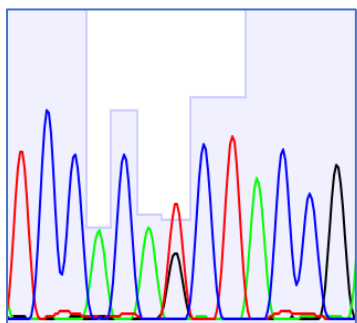
K229 VHL_3:10183734:C:A



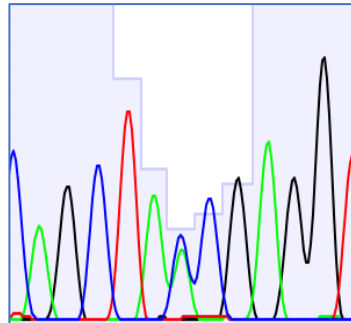
K220 VHL_3:10183748:10183748:-:AGGTC



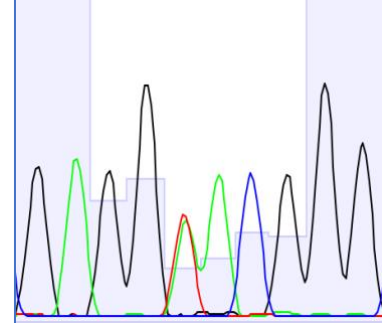
K182 VHL_3:10183846:10183846:-:GGCCG



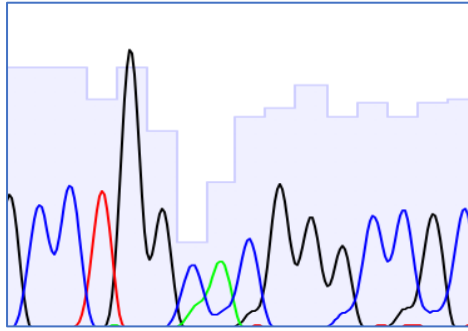
K237 VHL_3:10183863:G:T



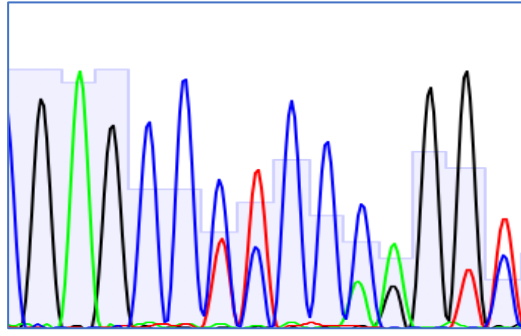
K249 VHL_3:10183867:C:A



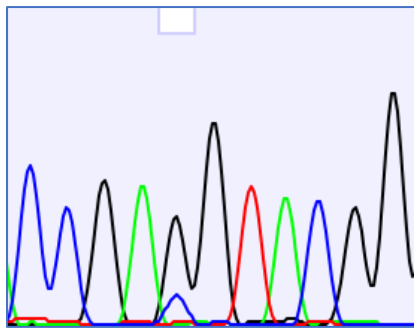
K272 VHL_3:10183873:T:A



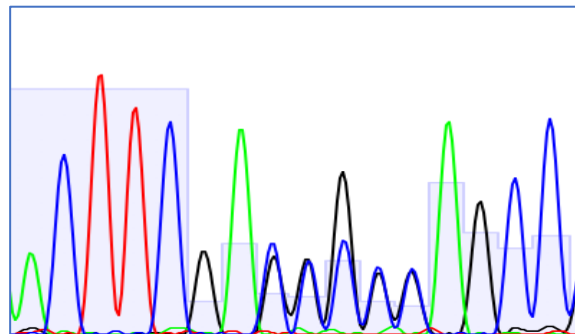
K250 VHL_3:10183843:10183843:C:-



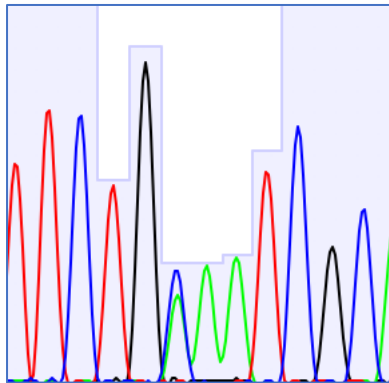
K334_L VHL_3:10183742:10183742:C:-



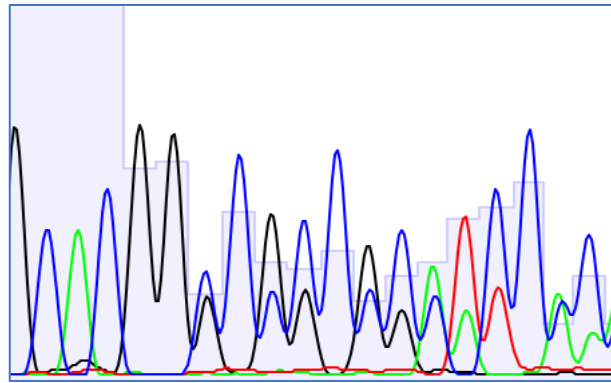
K276 VHL_3:10183873:T:A



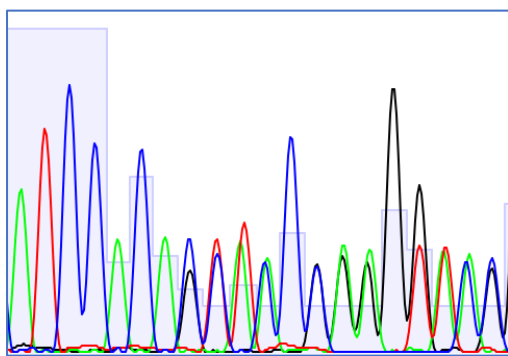
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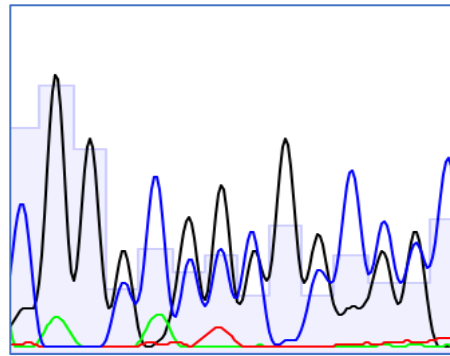
K448 VHL_3:10183762:C:A



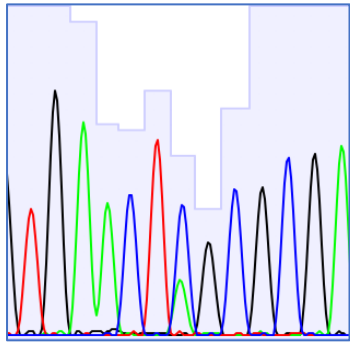
K097_R VHL_3:10183846:10183846:G:-



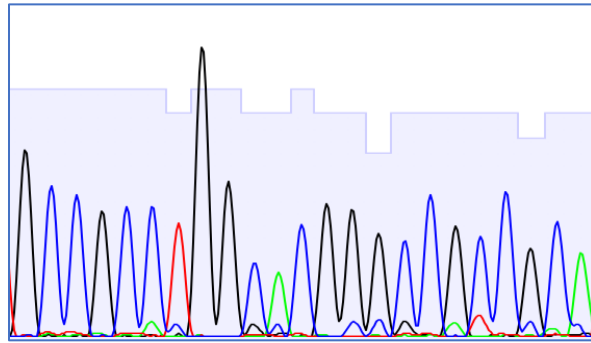
K104 VHL_3:10183863:10183863:G:-



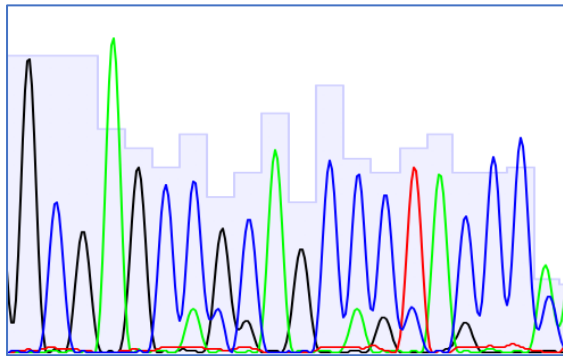
K130 VHL_3:10183712:10183712:C:-



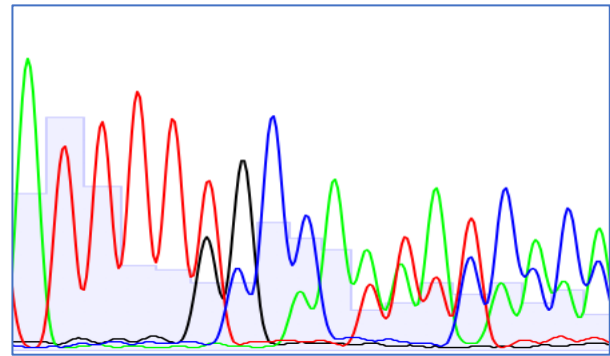
K138 VHL_3:10183734:C:A



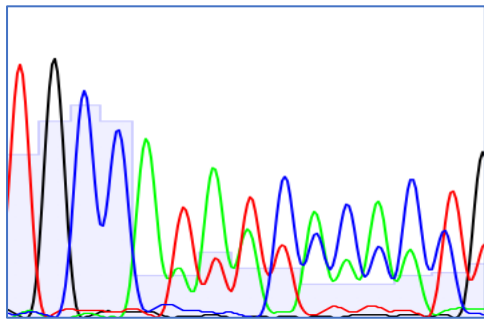
K143 VHL_3:10183837:10183841:GCCTG:-



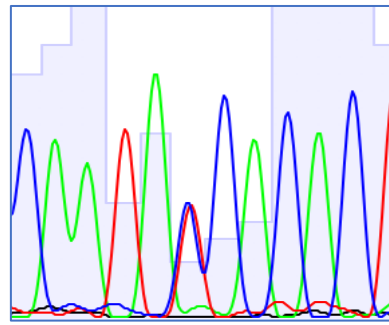
K150 VHL_3:10183809:10183809:-:CGAGC



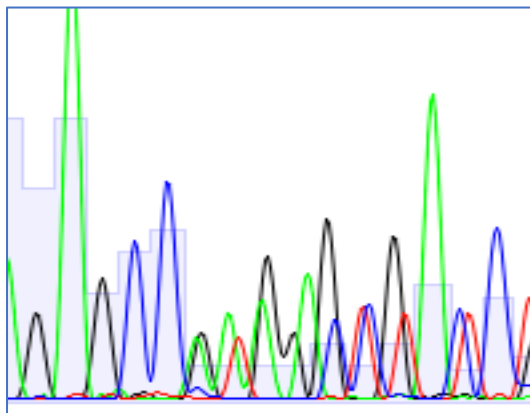
K065 VHL_3:10188297:10188297:T:-



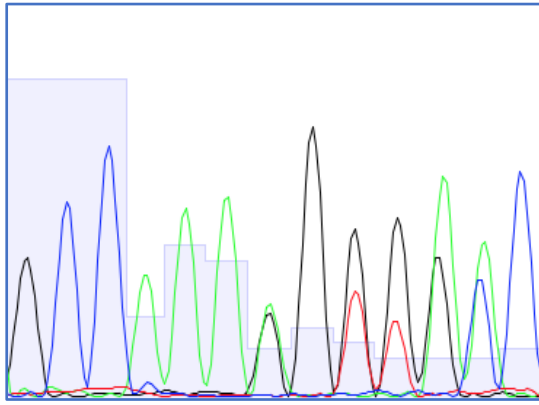
K107 VHL_3:10188305:10188305:A:-



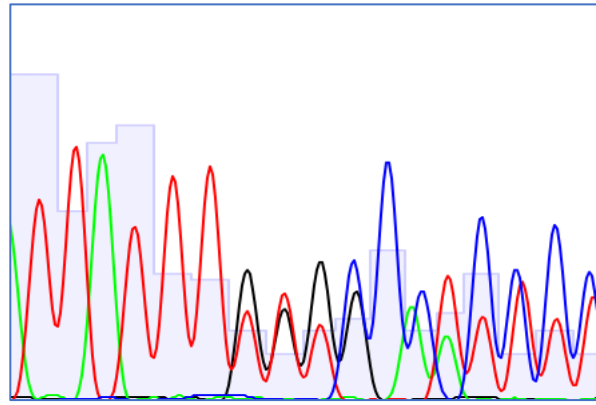
K114 VHL_3:10188309:T:C



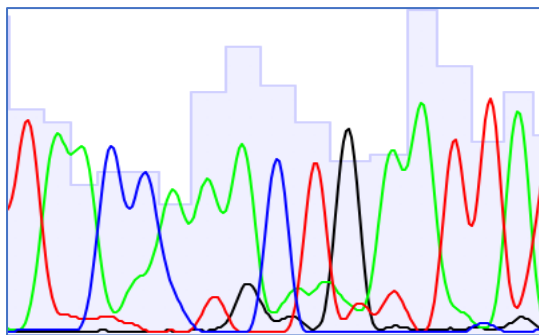
K124 VHL_3:10188203:10188206:CTTT:-



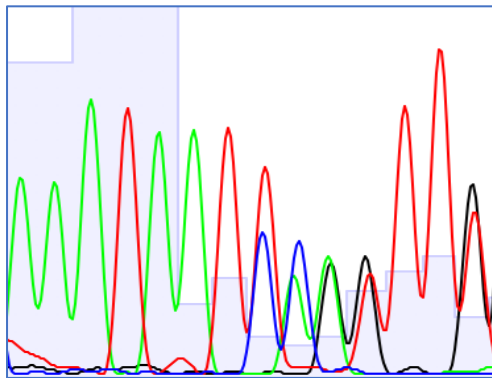
K153 VHL_3:10188203:10188203:-:T



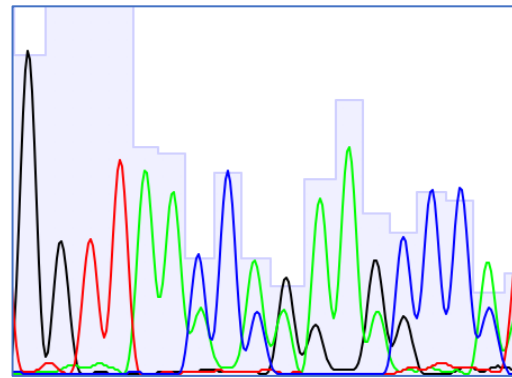
K176 VHL_3:10188252:10188252:A:-



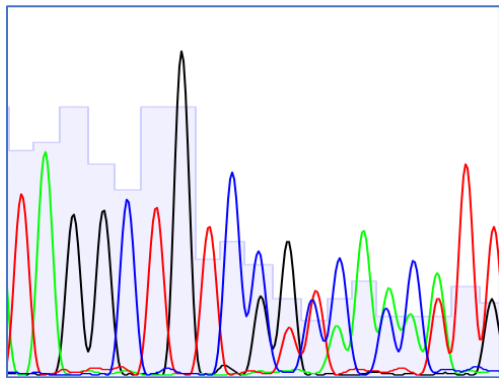
K226 VHL_3:10188251:10188253:CAA:-



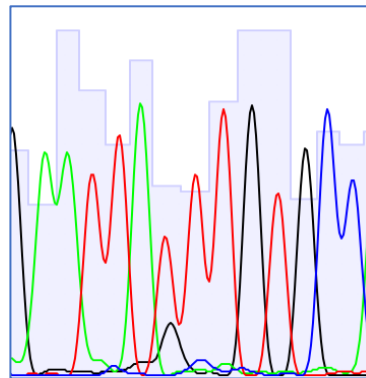
K450 VHL_3:10188258:10188258:A:-



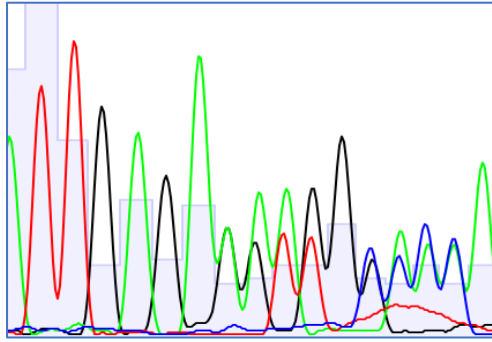
K023 VHL_3:10188245:10188245:-:T



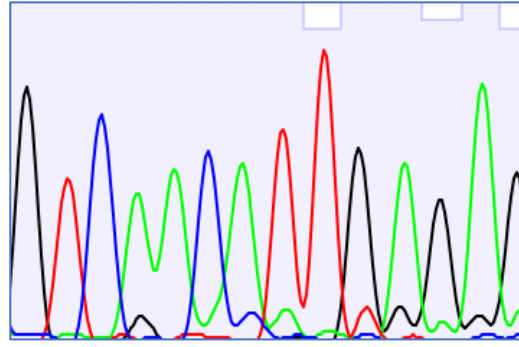
K146 VHL_3:10188287:10188287:G:-



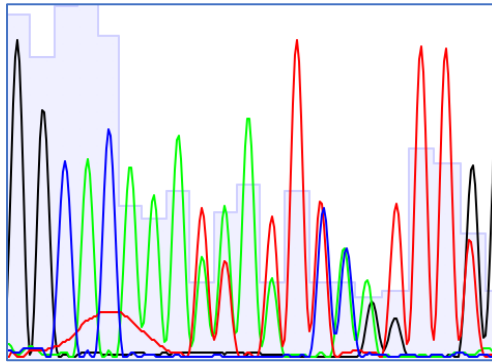
K158 VHL_3:10188263:T:G



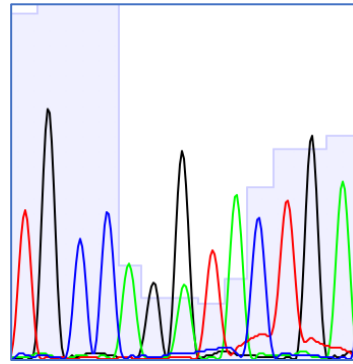
K162 VHL_3:10188273:10188273:-:T



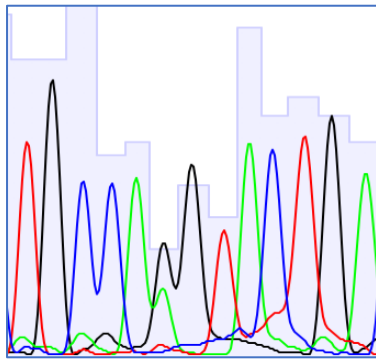
K328 VHL_3:10188283:10188283:-:C



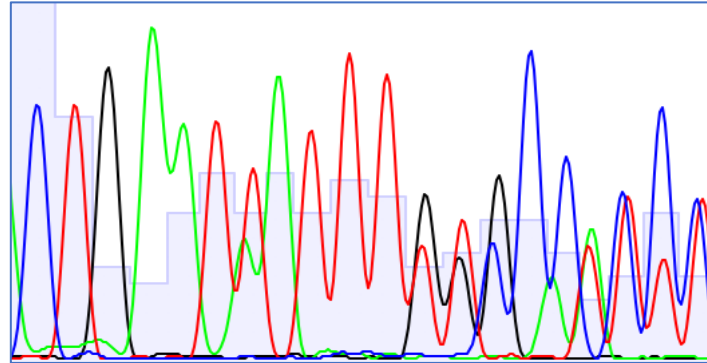
K263 VHL_3:10188262:10188262:-:T



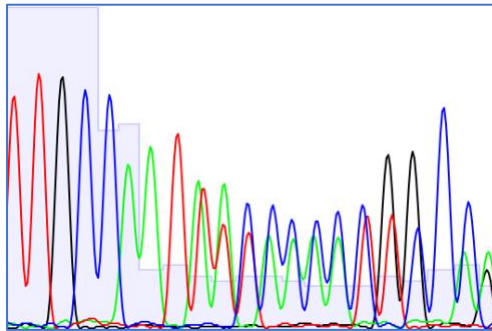
K265 VHL_3:10188321:10188321:-:G:A



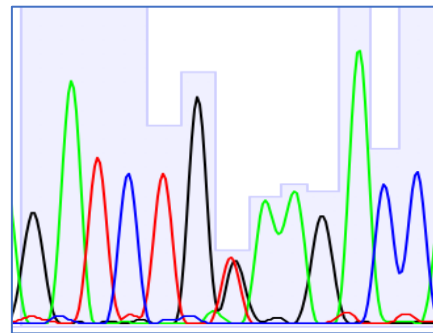
K306 VHL_3:10188320:10188320:-:G:A



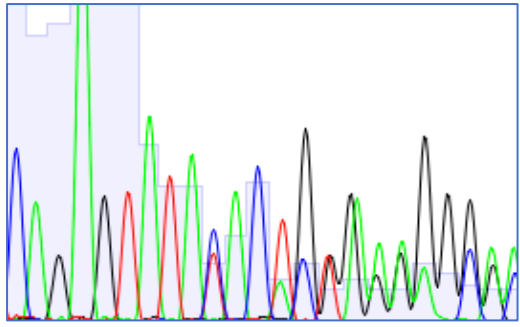
K323 VHL_3:10188266:10188266:-:G:-



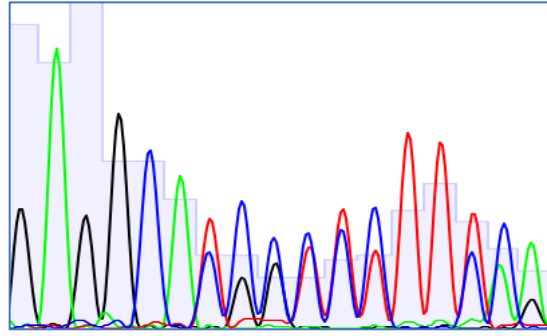
K386 VHL_3:10188306:10188306:-:T



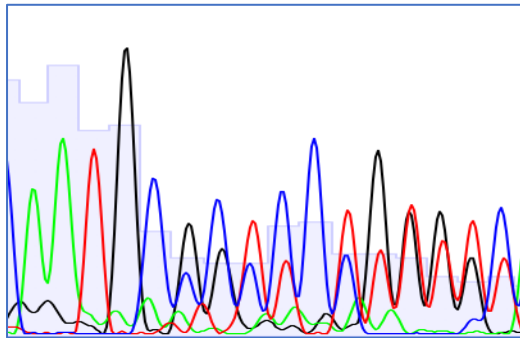
K059 VHL_3:10191572:10191572:-:G:T



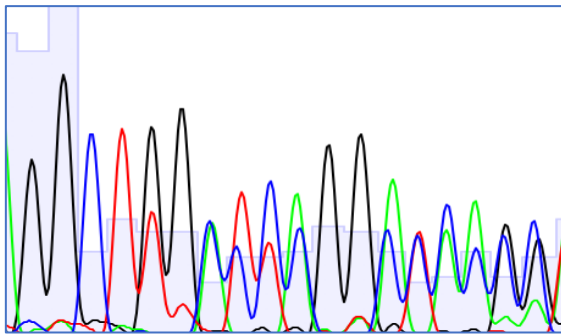
K123 VHL_3:10191472:10191472:-:TA



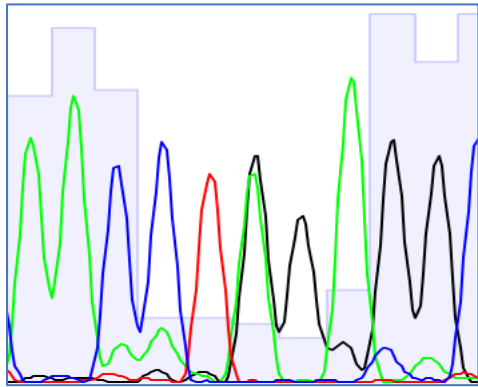
K136 VHL_3:10191490:10191490:A:-



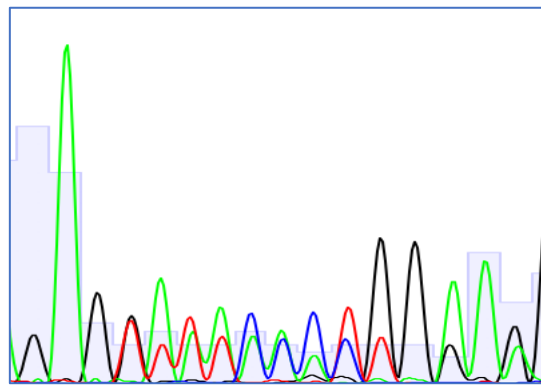
K234 VHL_3:10191620:10191620:-:G



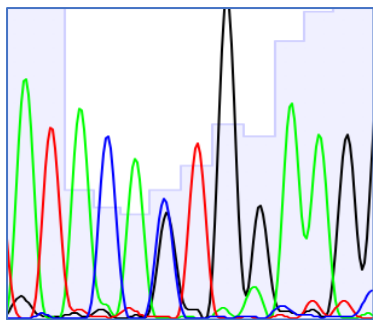
K243 VHL_3:10191513:10191518:TAGTC:-



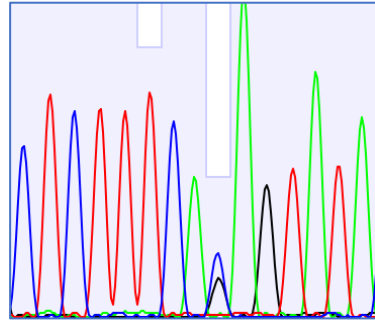
K252 VHL_3:10191497:C:T



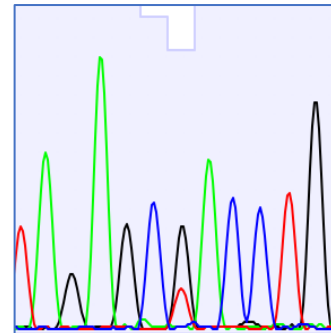
K352 VHL_3:10191476:10191476:-:C



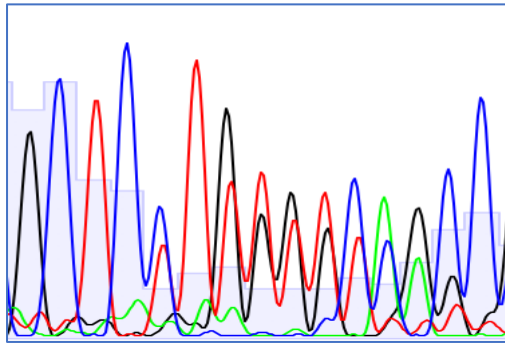
K360 VHL_3:10191470:G:C



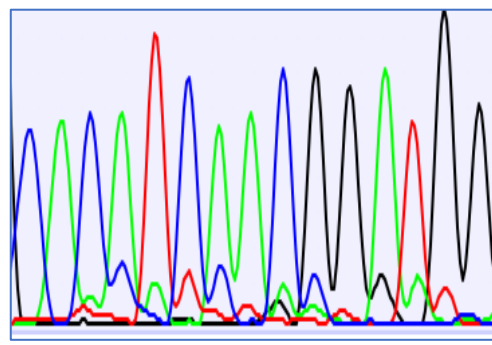
K520 VHL_3:10191479:C:G



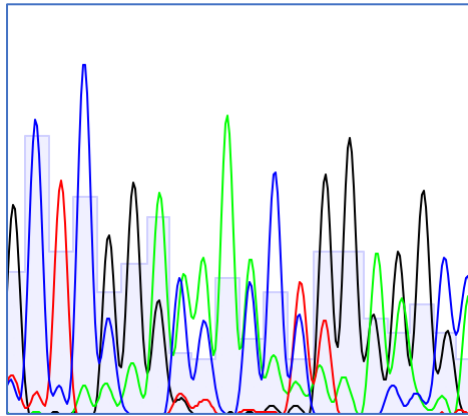
K523 VHL_3:10191555:C:A



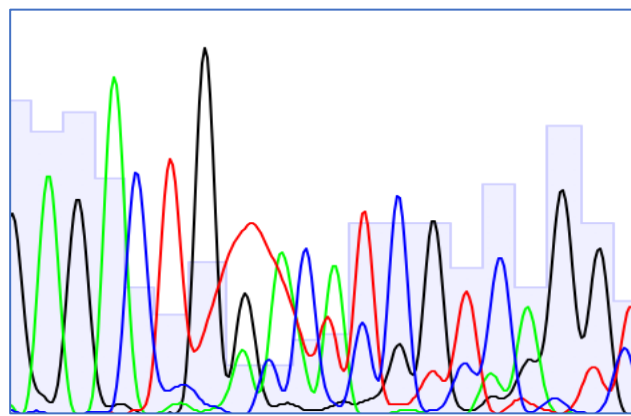
K027 VHL_3:10191614:10191614:-:A



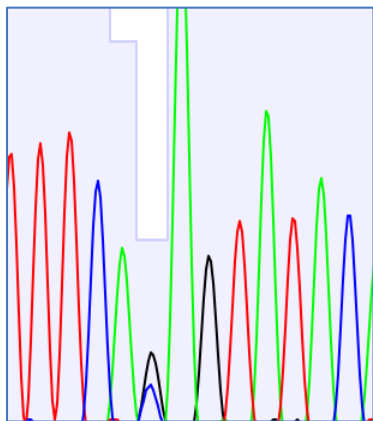
K032 VHL_3:10191627:10191627:-:A



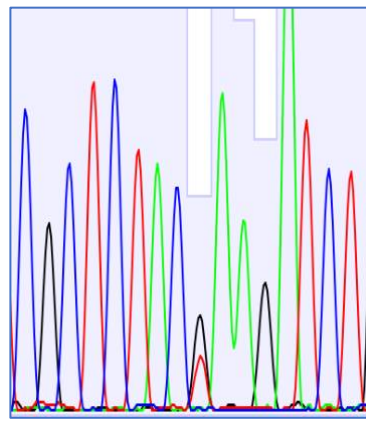
K099 VHL_3:10191507:10191507:G:-



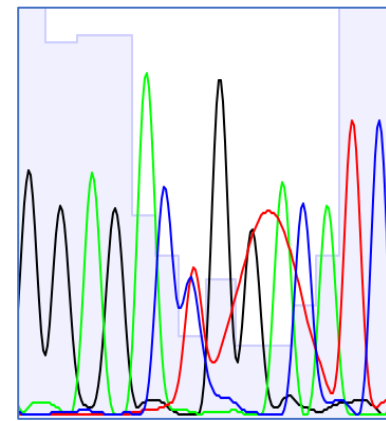
K128 VHL_3:10191541:10191541:G:-



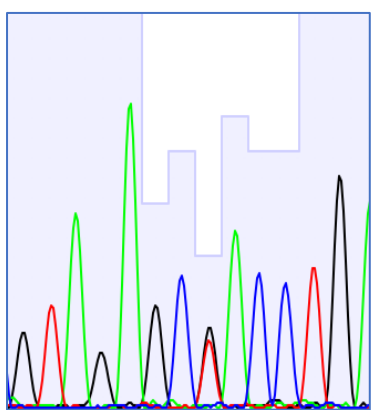
K167 VHL_3:10191479:C:G



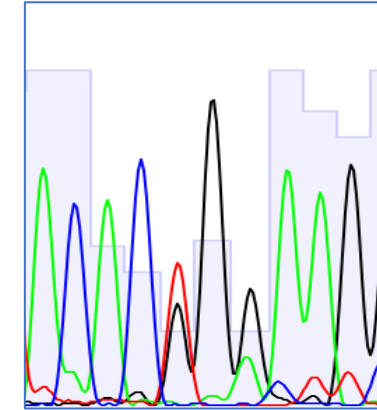
K207 VHL_3:10191563:G:T



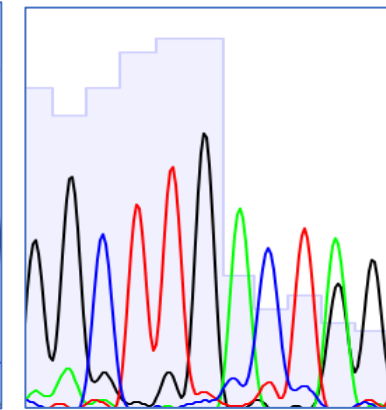
K208 VHL_3:10191540:T:C



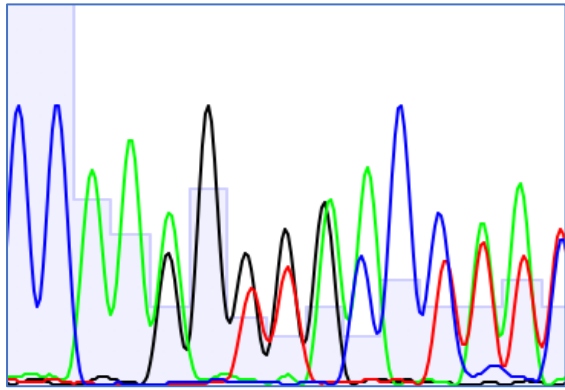
K242 VHL_3:10191555:C:A



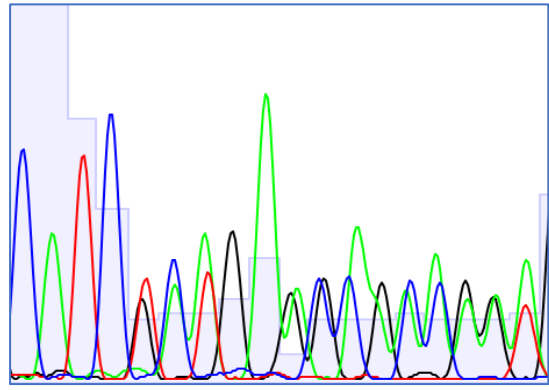
K245 VHL_3:10191469:A:C



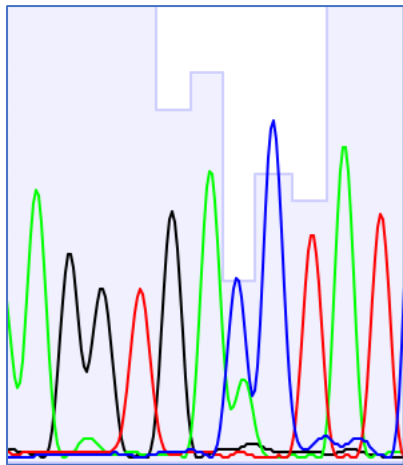
K265 VHL_3:10191513:T:C



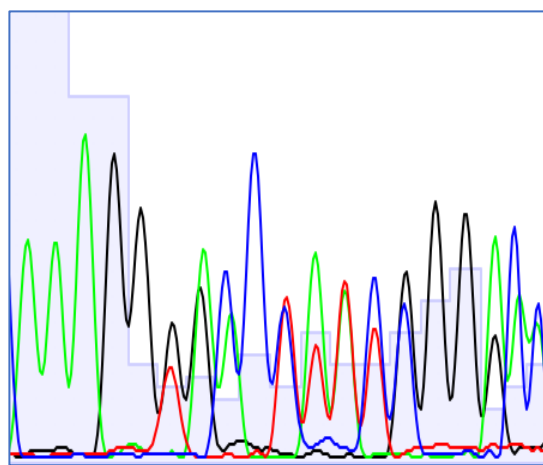
K256 VHL_3:10188204:10188204:T:-



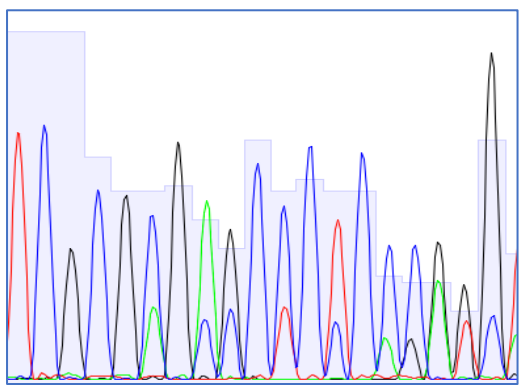
K334 VHL_3:10188215:10188217:AGA:-



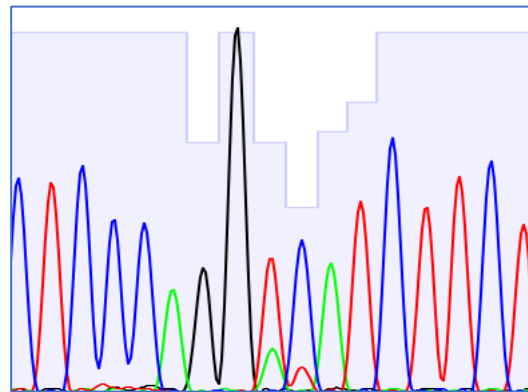
K352 VHL_3:10188198:G:T



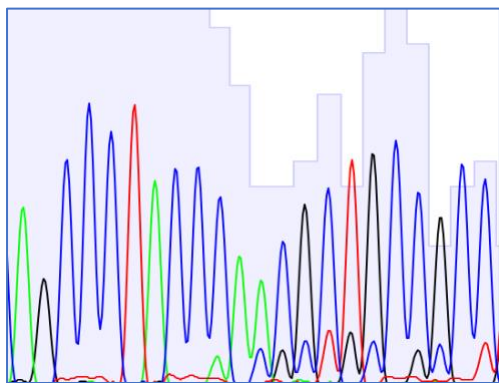
K375 VHL_3:10188201:10188201:A:-



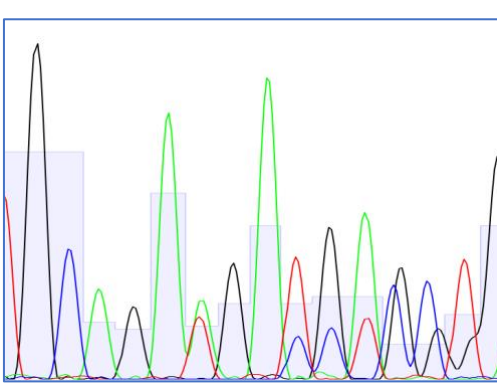
K039 VHL_3:10183734:10183735:CG:-



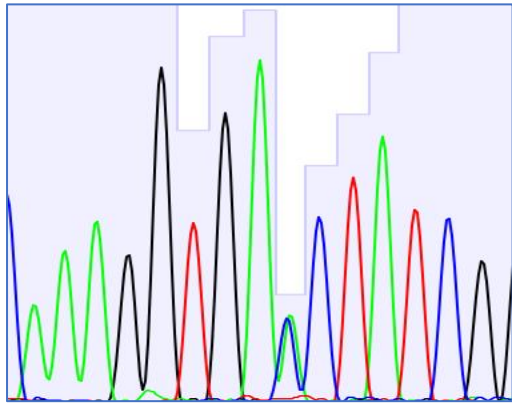
K156 VHL_3:10183752:10183753:TC:AT



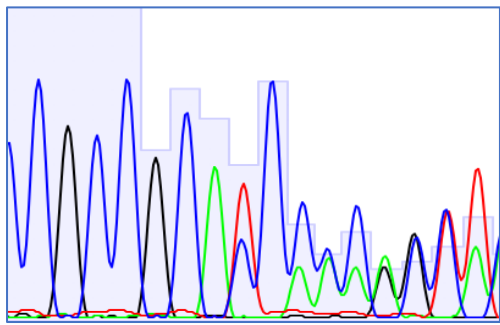
K326 VHL_3:10183825:10183825:C:-



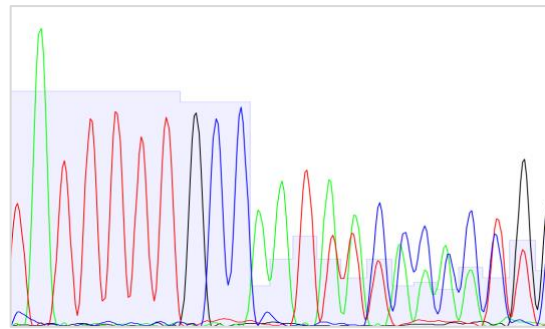
K184 VHL_3:10183755:10183757:TCT:-



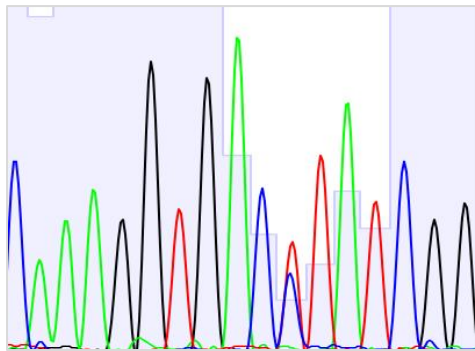
K216 VHL_3:10188198:G:T



K217 VHL_3:10183857:10183857:T:-

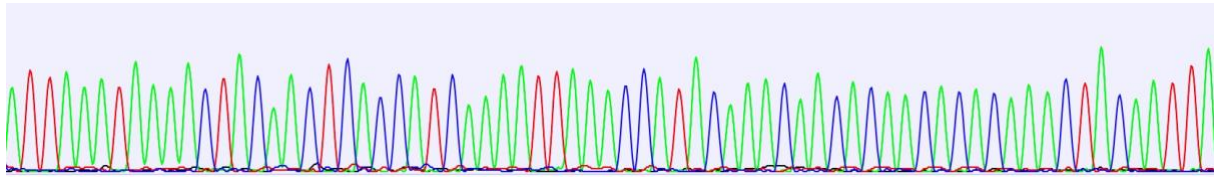


K386 VHL_3:10188306:10188306:-:T

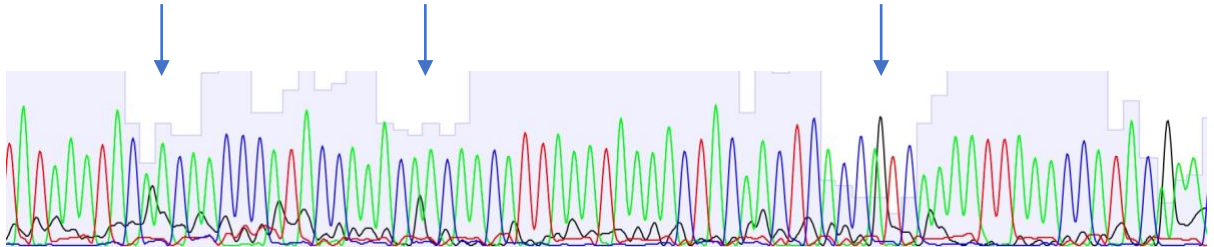


K118 VHL_3:10188197:G:A

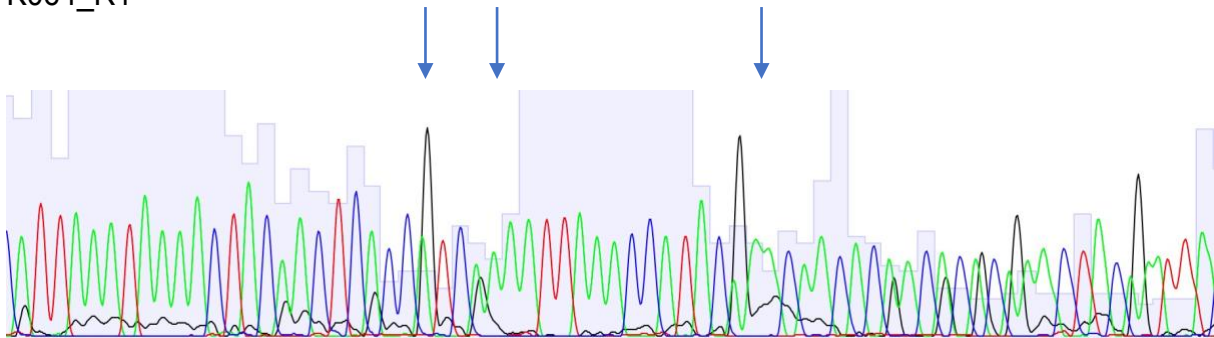
VHL methylation Profiles



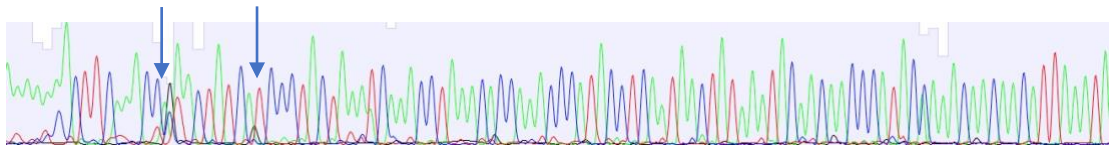
K064_N



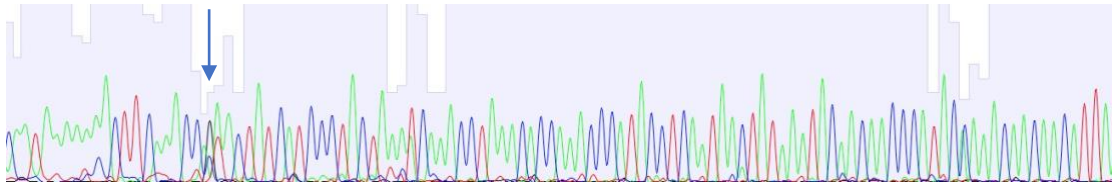
K064_R1



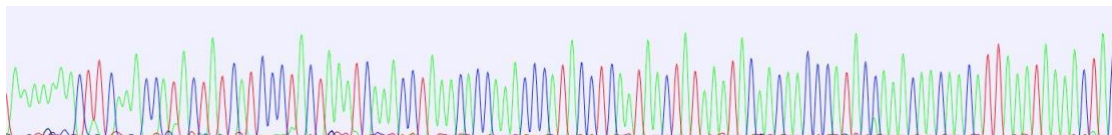
K064_R2



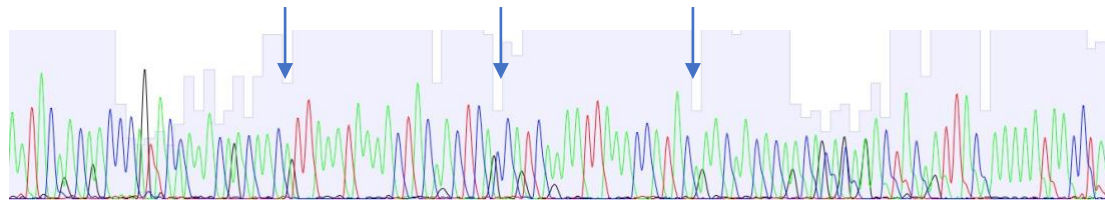
K222_R2



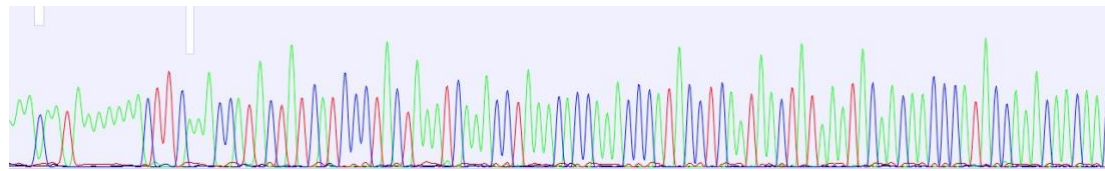
K222_R3



K222_N

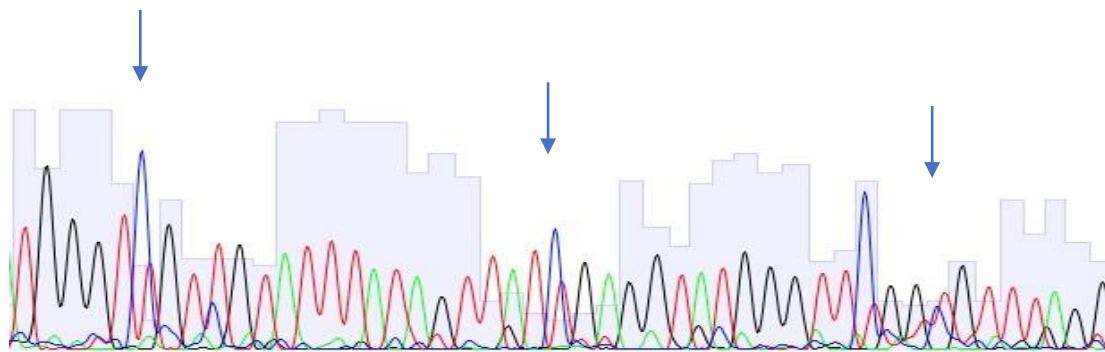


K233_R3



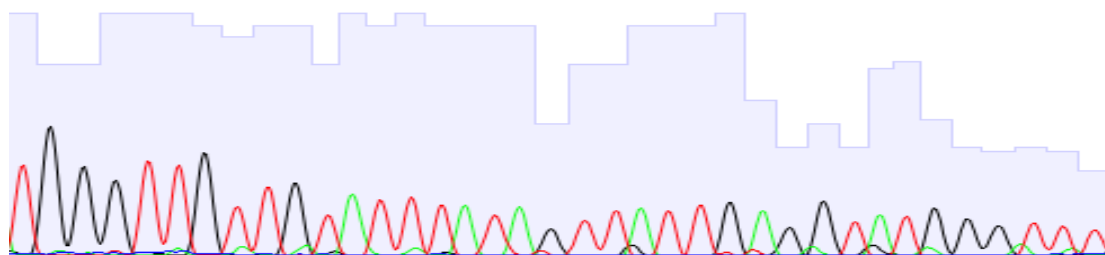
K233_N

90 100 110 120
 T G G G T C G T T G T A T T T A T A G T T A T T G A G G T A T G G G T T C G G C G T T T A G G



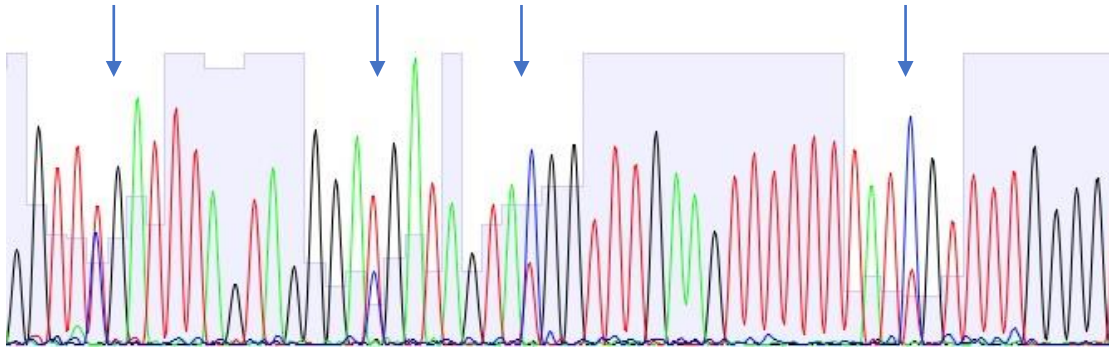
K239_R3

80 90 100 110
 T G G G T T G T T G T A T T T A T A G T T A T T G A G G T A T G G G T T T



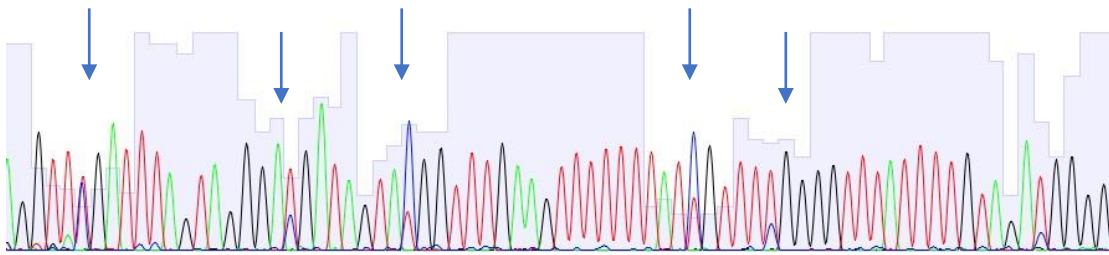
K239_N

130 140 150 160 170
G G T T T G A T T T A G T A G G G A C G A T A G T A C G G T T T G A A G T T T T T T A T T G T T T T G G G G !



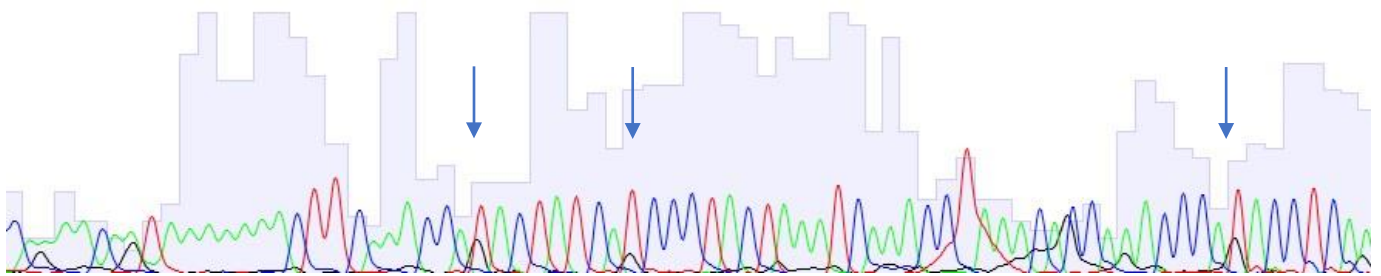
K379_R22

120 130 140 150 160 170 180 190
G C G T T T G A T T T A G T A G G G A T G A T A G T A C G G T T T G A A G T T T T T T A T T G T T T T G G G G T T T A T T T T G T A G A T G G G G



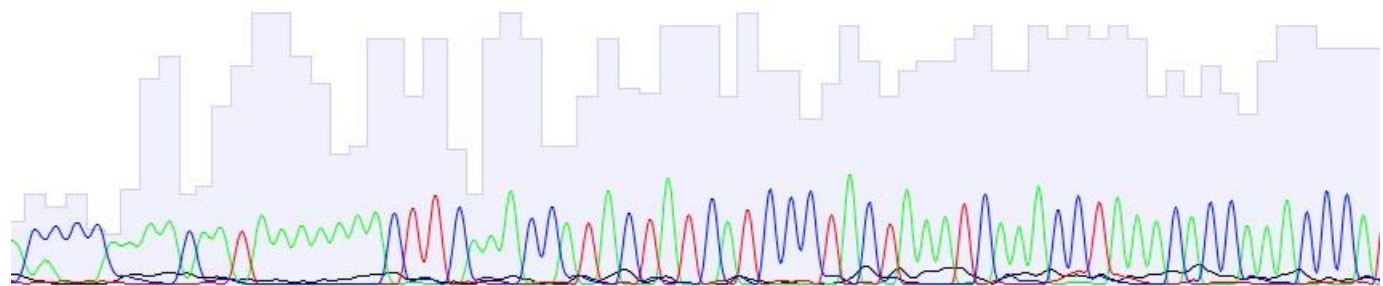
K379_R23

30 40 50 60 70 80 90 100
C A A A A C A G T A A A A A A A C T T C A A A C C A T A C T A T C A T C C C T A C T A A A T C A A A C C T A A A C A C C A A A C C C A T A C C T C A A



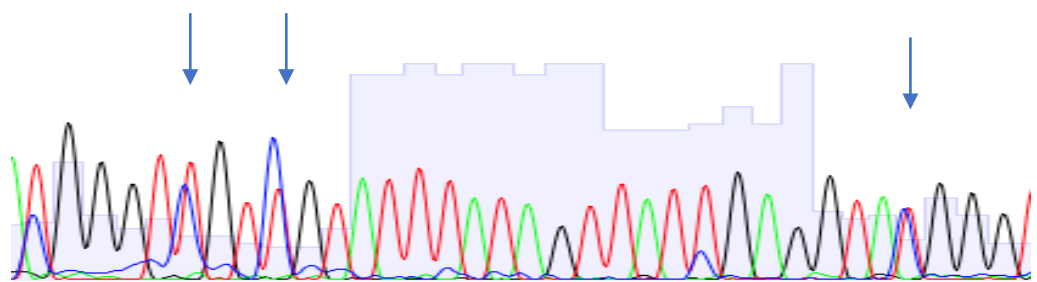
K163_Tumour

30 40 50 60 70 80 90
A C C C C A A A A C A A T A A A A A A A C T T C A A A C C A T A C T A T C A T C C C T A C T A A A T C A A A C C T A A A C A C C A A A C C C A



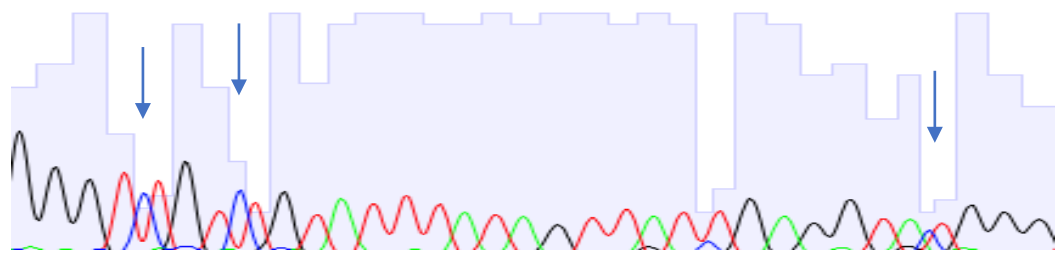
K163_N

80 90 100 110
T G G G T T G T T G T A T T T A T A G T T A T T G A G G T A T T G G G



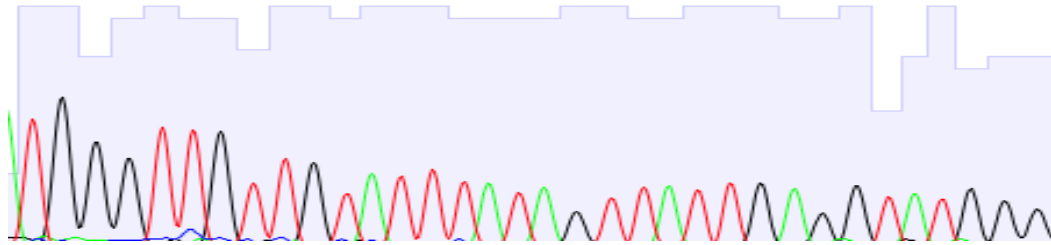
K029_R3

90 100 110 120
G G G T C T G T C T G T A T T T A T A G T T A T C T G A G G T A C T G G G



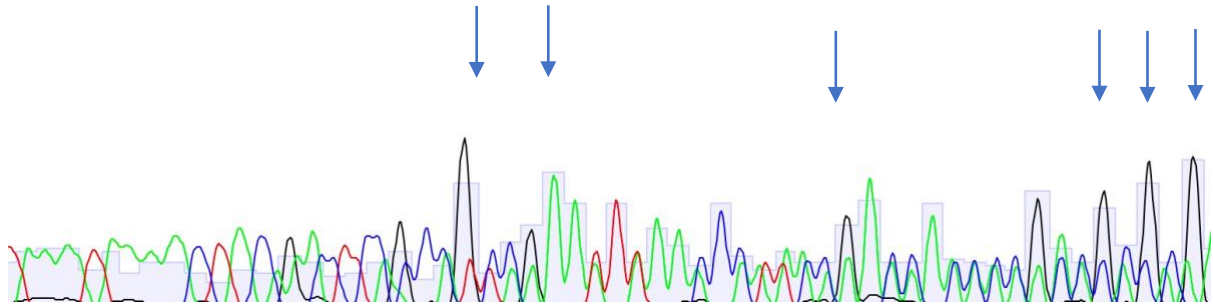
K029_R9

80 90 100 110
T G G G T T G T T G T A T T T A T A G T T A T T G A G G T A T G G G



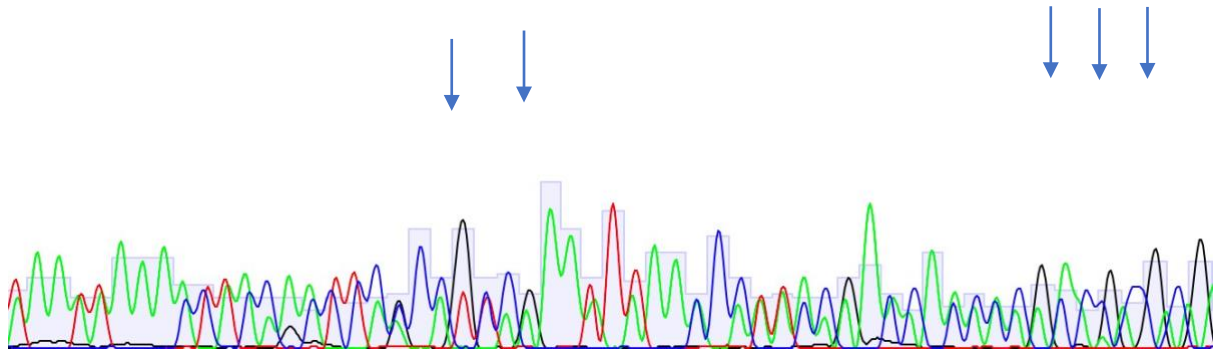
K029_N

140 150 160 170 180 190
A A A T A A A A C T A C G A C T C G C C G C C G A A T T A A A C C C T A A C G A C C A A A C C C G A C G C G C G



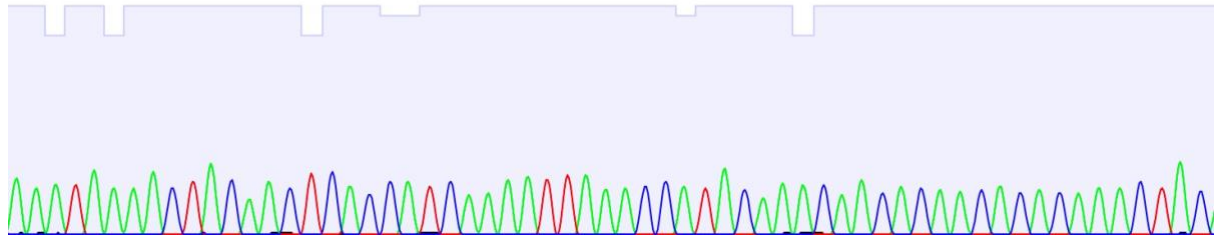
K070_R4

150 160 170 180 190
A A A T A A A A C T A C A C T C C C C C G C C G A A T T T A A C C C T A A C G A C C A A C C C G A C G C G C G



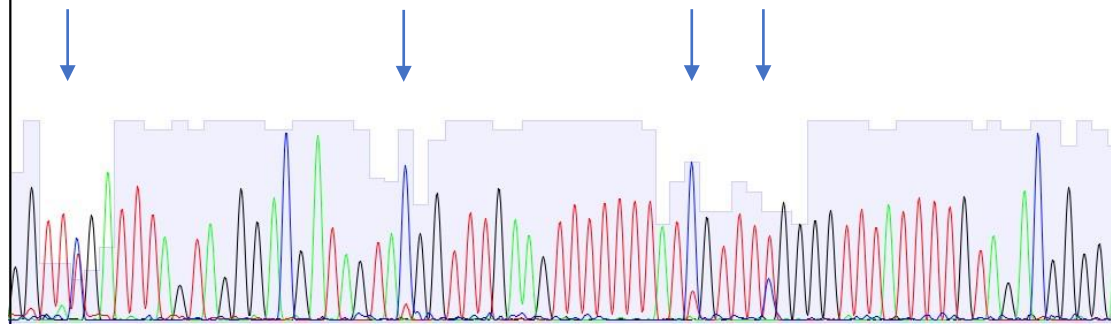
K070_R9

40 150 160 170 180 190 200
A A A T A A A A C T A C A A C T C A C C A T C A A A A T T A A A C C A T A C A A A C A A C A C A A C A C A A A C T A C ;



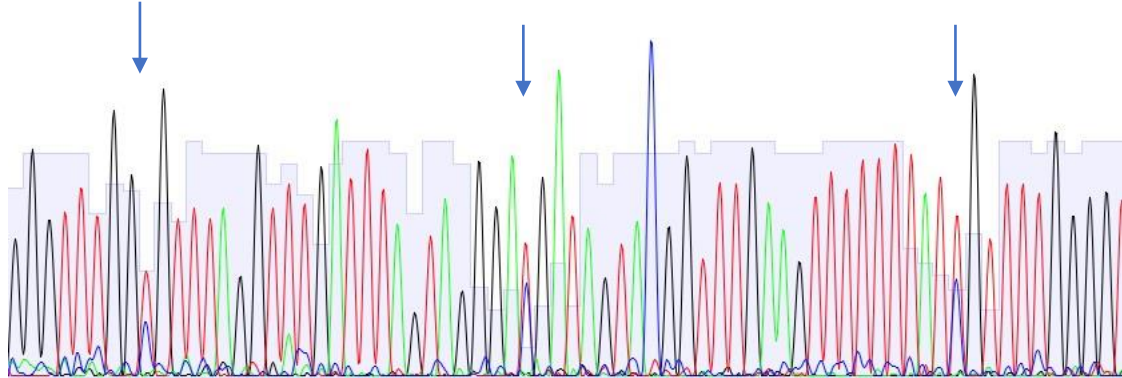
K070_N

140 150 160 170 180 190 200
G G T T T G A T T T A C T A G G G A C G A T A G T A C G G T T T G A A G T T T T T A T C G T T T T G G G T T T A T T T T G T A G A C G G G G .

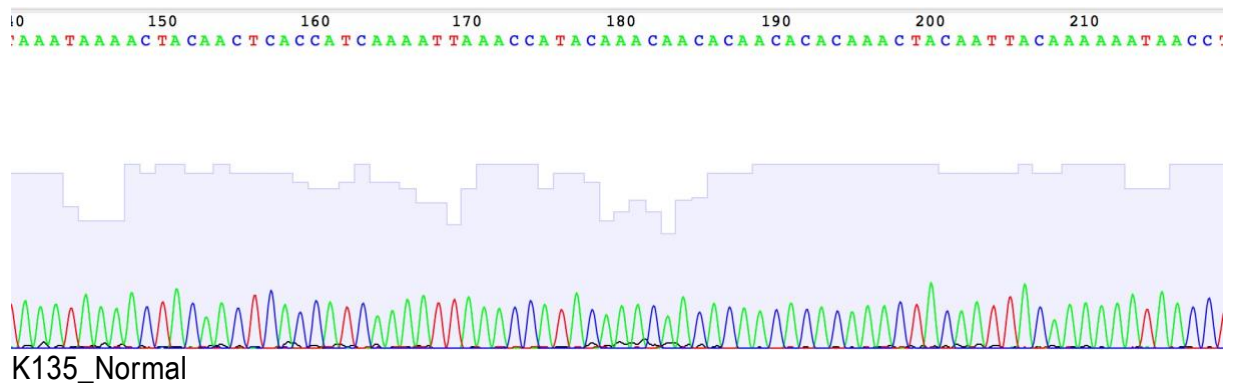
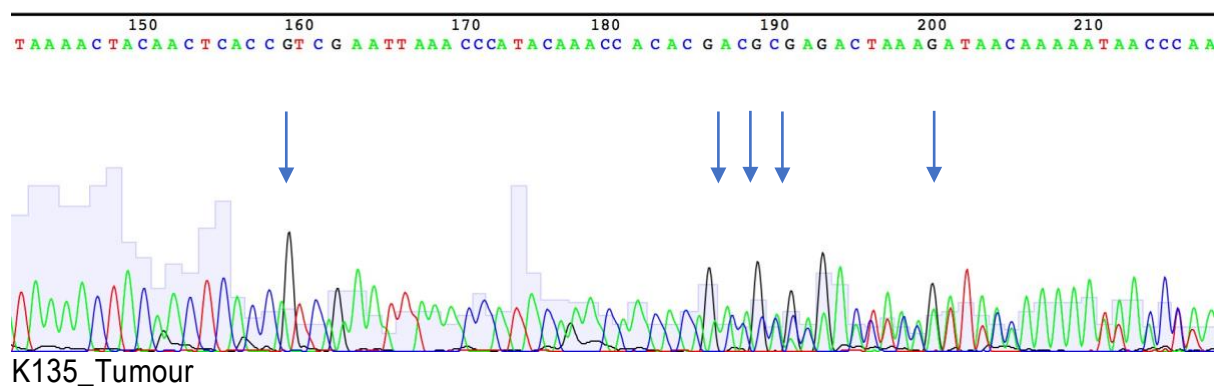
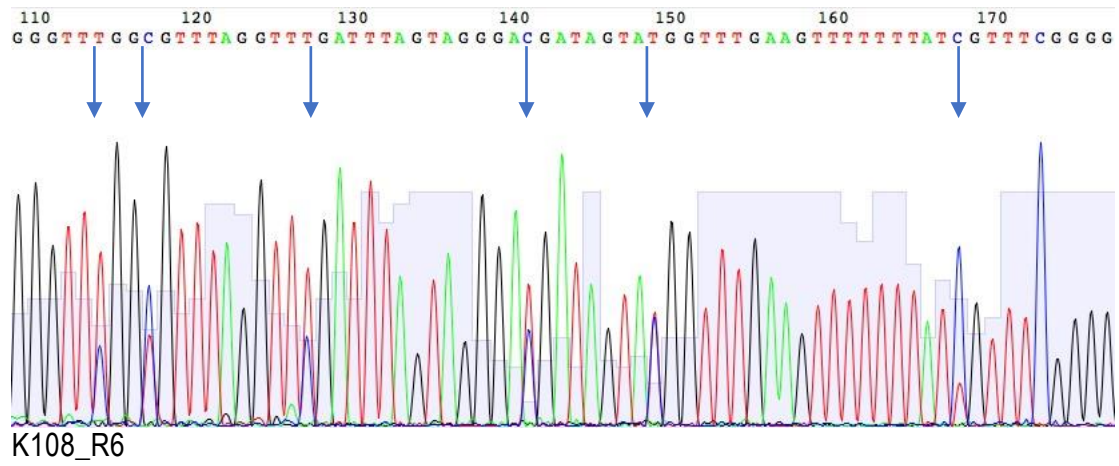


K098_R1

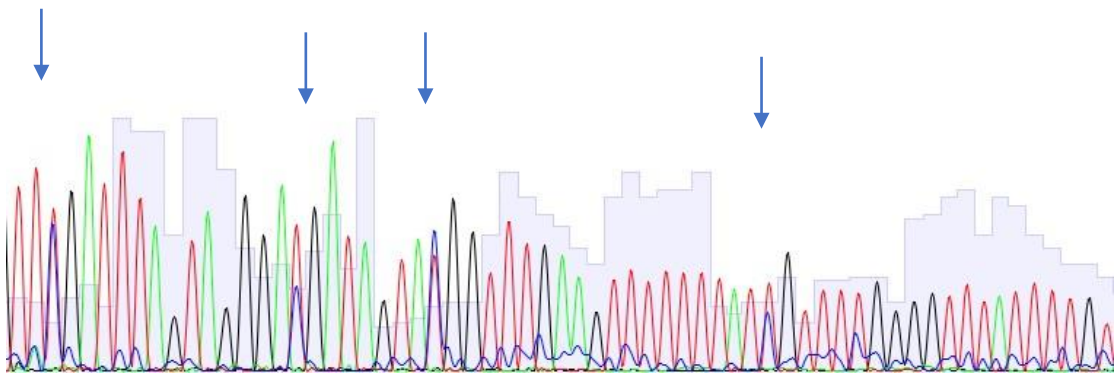
110 120 130 140 150 160 170
G G G T T T G G T G T T A G G T T T G A T T T A G T A G G G A C G A T A G T A C G G T T T G A A G T T T T T T A T T G T T T T G G G G T



K108_R3

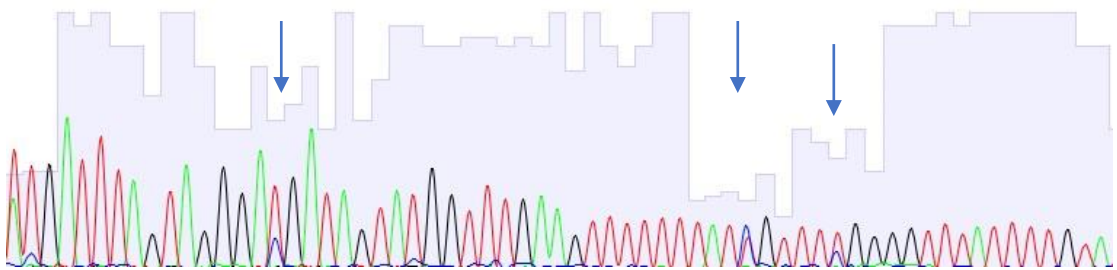


130 140 150 160 170 180
T T G A T T T A G T A G G G A T G A T A G T A C G G T T G A A C T T T T T T A T T C T T T G G G C T T A T T T T G T

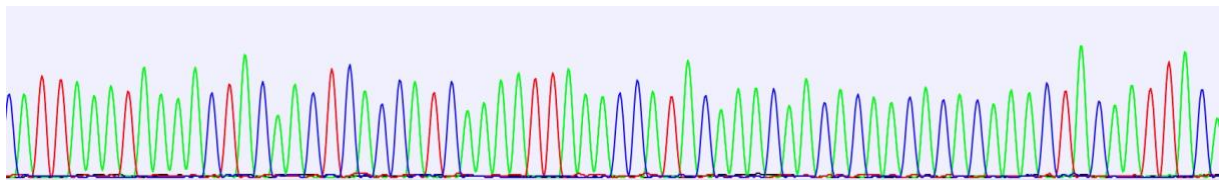


K177_R2

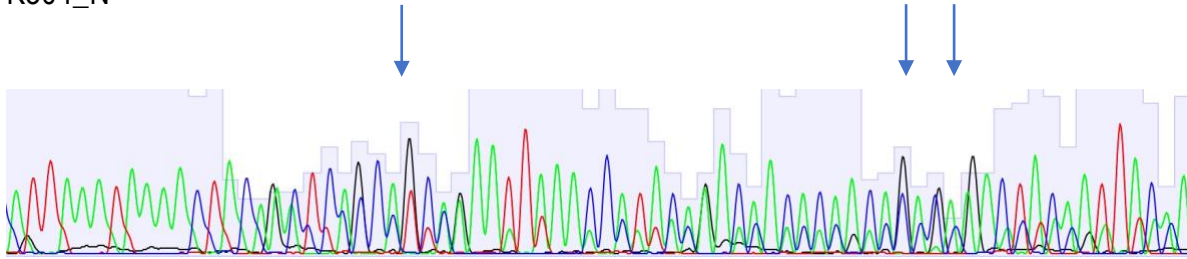
30 140 150 160 170 180 190
T T G A T T T A G T A G G G A T G A T A G T A T G G T T T G A A G T T T T T T A T C G T T T T G G G G T T T A T T T T G T A



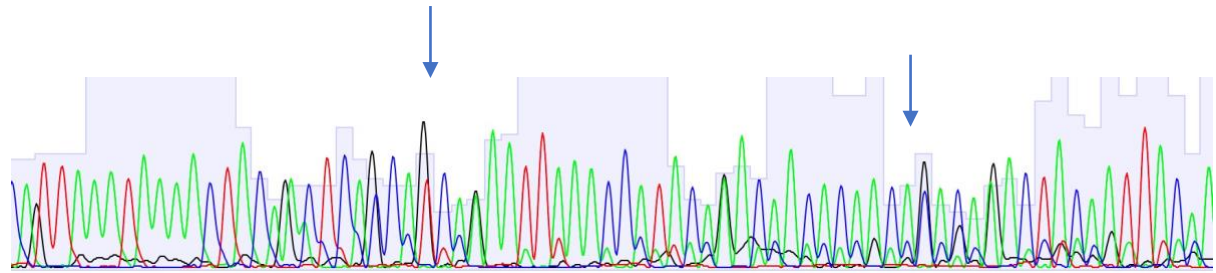
K177_R4



K304_N

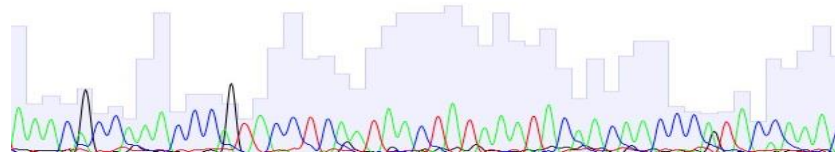


K304_R3



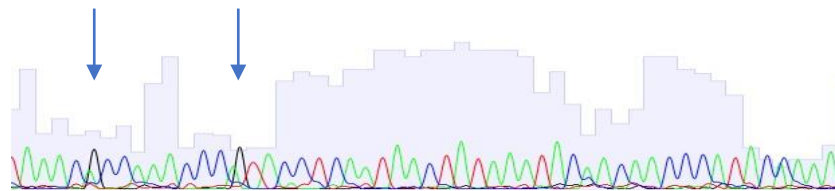
K304_R4

80 90 100 110 120 130
 A A A C G C C A A A C C C C G T A C C T C A A T A A C T A T A A A T A C A A C A C C C A T A C C A A A C



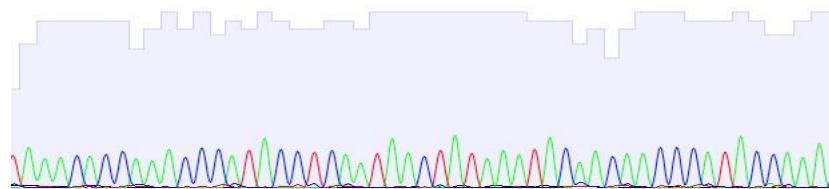
K308_R2

80 90 100 110 120 130
 T A A A C C C C A A A C C C C G T A C C T C A A T A A C T A T A A A T A C A A C A A C C C A T A C A A A A A



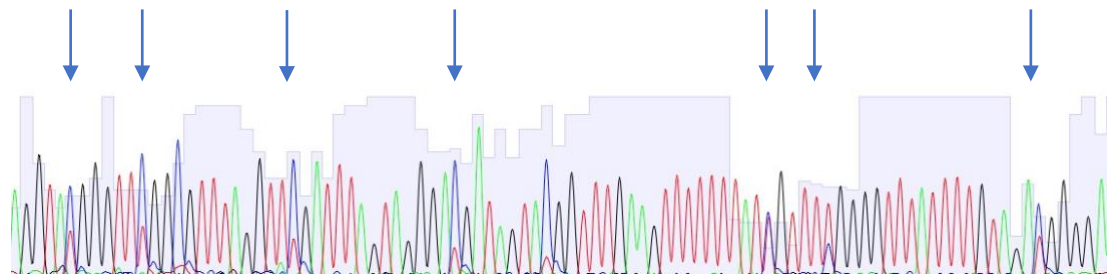
K308_R3

80 90 100 110 120 130
 T A A A C A C C A A A C C C A T A C C T C A A T A A C T A T A A A T A C A A C A A C C C A T A C C A A A A



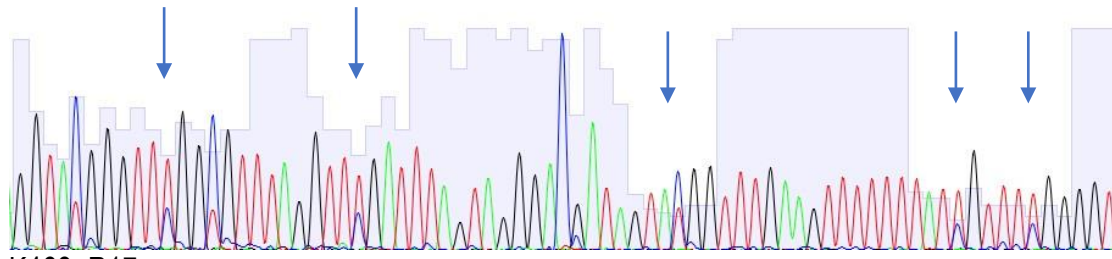
K308_N

110 120 130 140 150 160 170 180 190 200
 A G G T A C G G G T T C G G C C T T T A G G T T C G A T T T A G T A G C G C A C G A T A G T A C G C T T T C A A G T T T T T A T C G T T T C G G G T T T A T T T G T A C A C C G G G A A



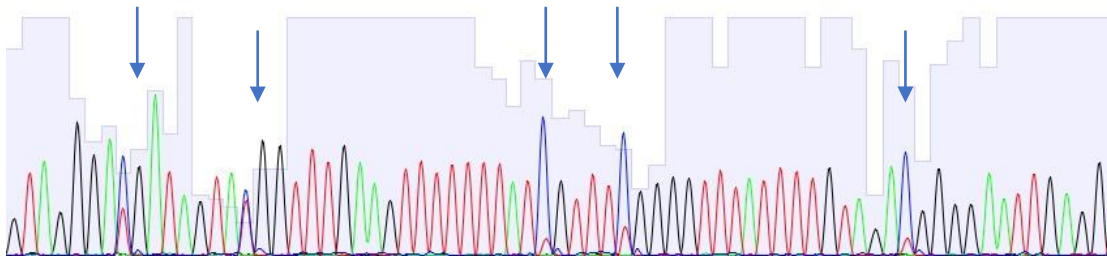
K463_R8

110 120 130 140 150 160 170 180
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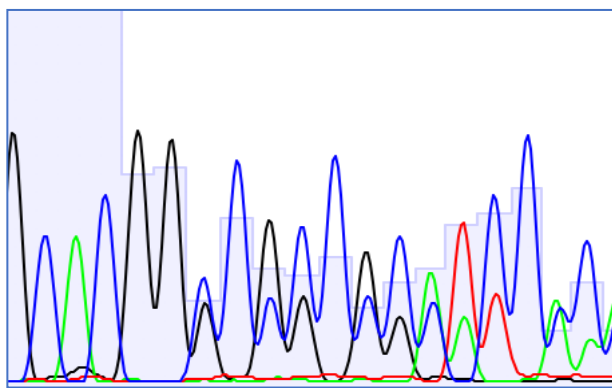
K463_R17

140 150 160 170 180 190 200
 GTAGGGACGATAGTATGGTTTGAAGTTTTTTATTCGTTTCGGGGTTATTTTGTAGACGGGGAAATTGAGG'

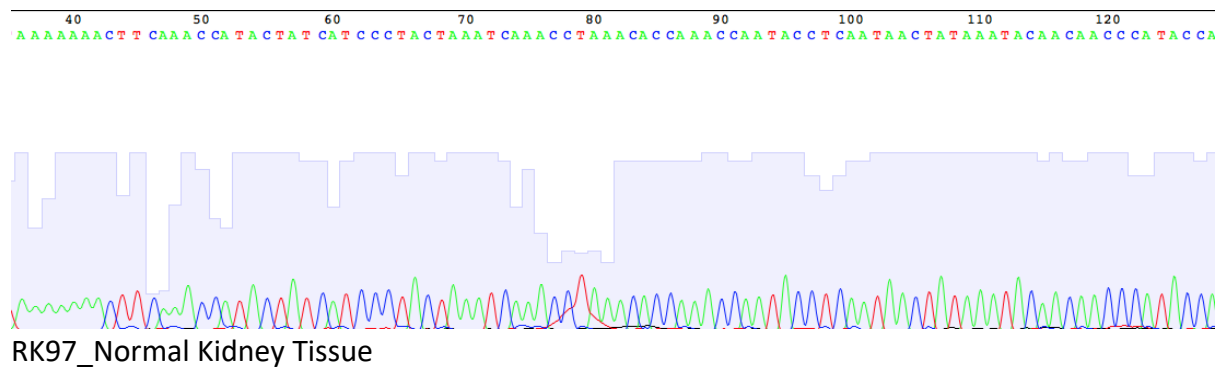
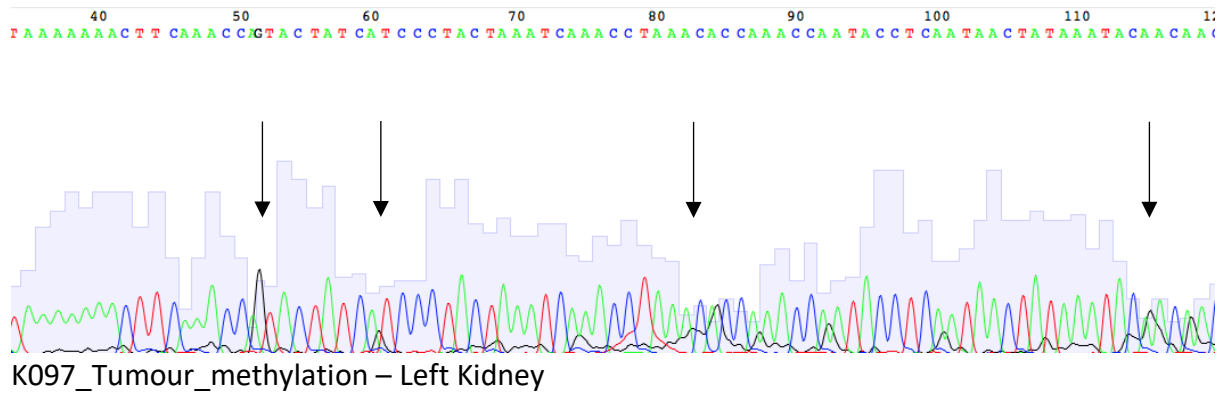


K463_R3

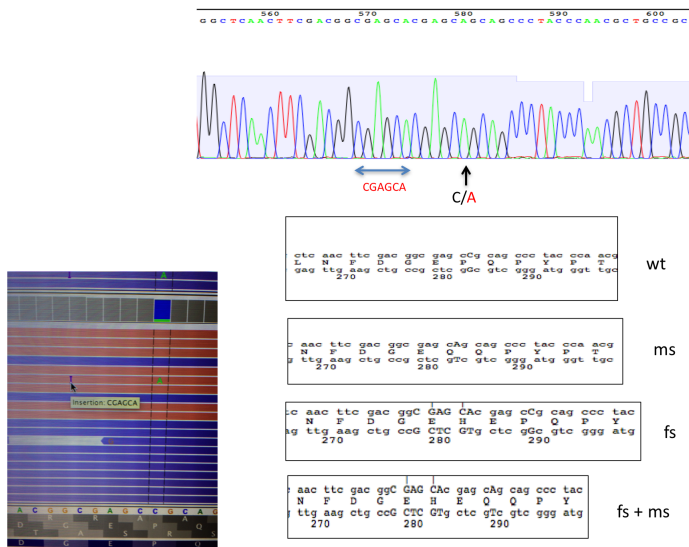
Sanger sequence trace of the VHL INDEL identified in the right kidney tumour of patient K097 and VHL methylation in the left kidney tumour.



K097_Right Kidney VHL_3:10183846:10183846:G:-



VHL mutations in left K150 tumours (historical)



Oligonucleotide sequences for VHL exon amplification and methylation specific PCR

Oligonucleotide name	Oligonucleotide Sequence 5'-3'
VHL_X1_F	gtggaatacacgtaacgagttgg
VHL_X1_R	caggcaaaaattgagaactgg
VHL_X2_F	aaccttggcttgtcccgata
VHL_X2_R	caggcaaaaattgagaactgg
VHL_X3a_F	ctgccactgaggatttggtt
VHL_X3a_R	ccatcaaaagctgagatgaaa
VHL_methylation_1F	gagtttttttaggttatttttgaat
VHL_methylation_1R,	tcacctaaatatatcctacctcaaaa
VHL_methylation_2F	ccctctaaaatttaatatTTTT
VHL_methylation_2R	ggttaaggtttagtgagttaagtt