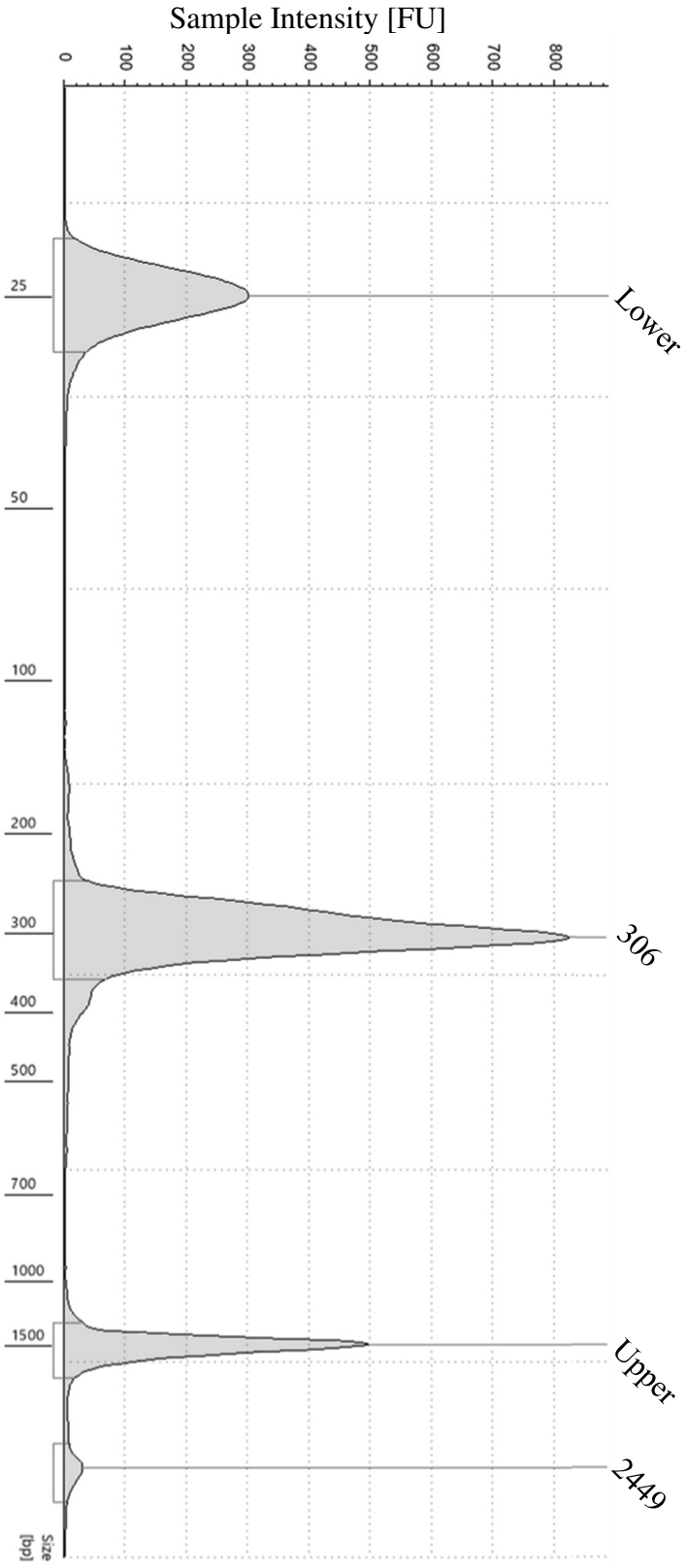
Sample Intensity [FU]
0
100
200
300
400
500
600
700
800
25
50
100
200
300
400
500
700
1000
1500
Size [bp]
Lower
306
Upper
2449

Figure 2a

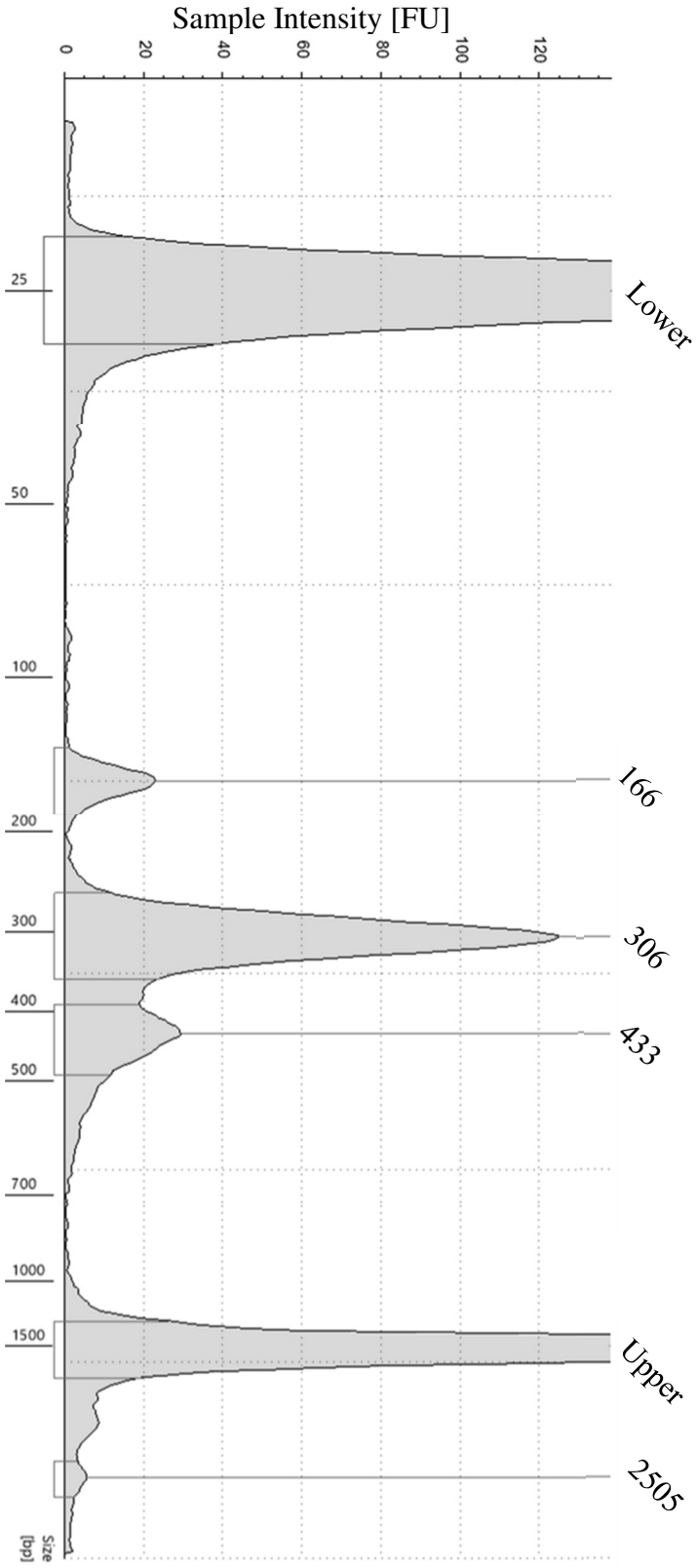
Sample Intensity [FU]
0
20
40
60
80
100
120
25
50
100
200
300
400
500
700
1000
1500
Size [bp]
Lower
166
306
433
Upper
2505

Figure 2b

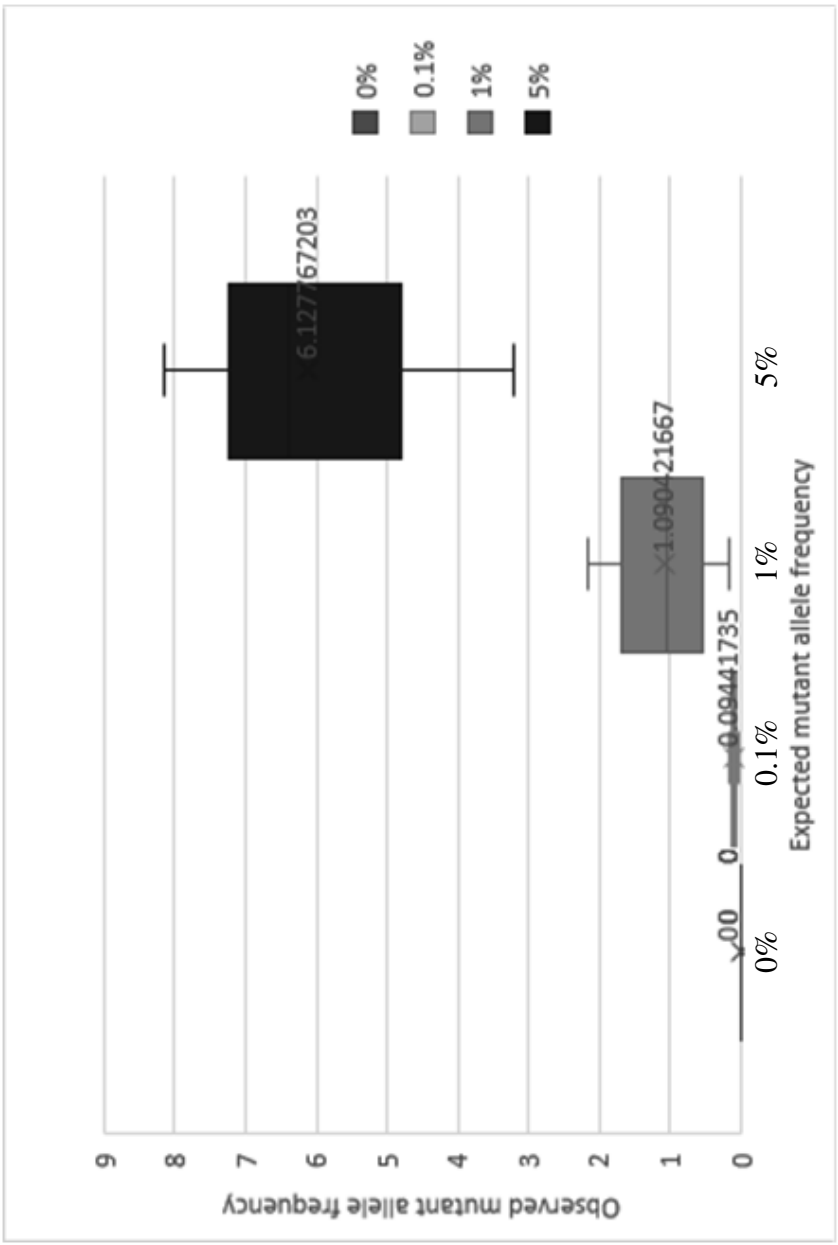
0%
0.1%
1%
5%
6.127767203
1.090421667
0.09441735
0
0
0%
0.1%
1%
5%
Expected mutant allele frequency
Observed mutant allele frequency
0
1
2
3
4
5
6
7
8
9

Figure 4b

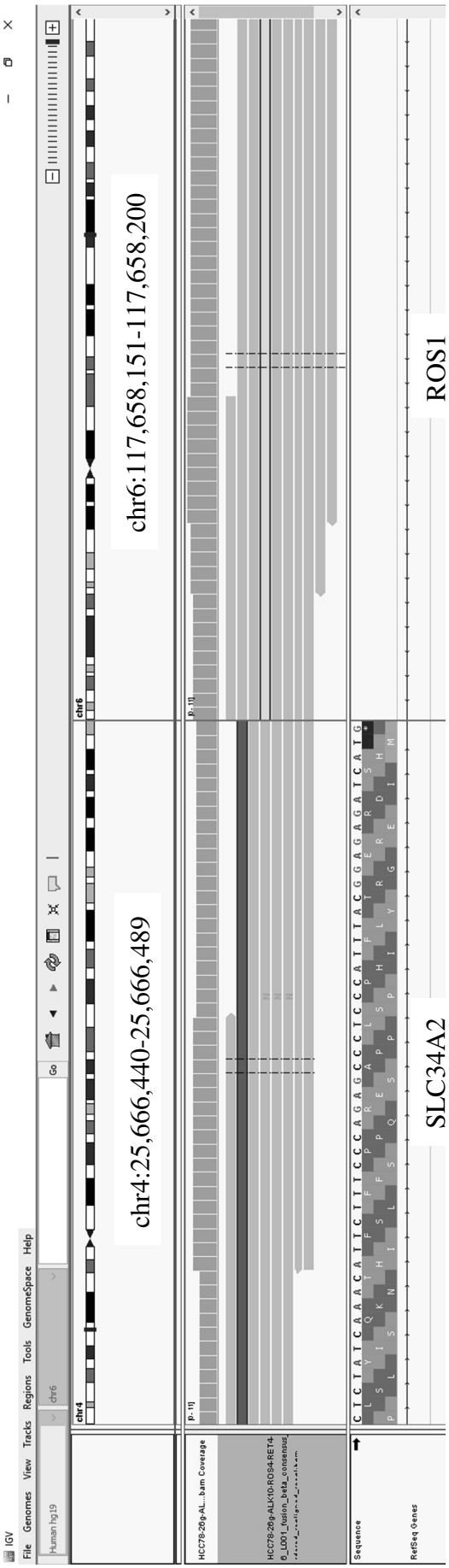
IGV
File Genomes View Tracks Regions Tools GenomeSpace Help
Human hg19
chr6
chr4
chr4:25,666,440-25,666,489
chr6:117,658,151-117,658,200
HCC78-26g-ALK10-ROS4-RET4-6_L001_fusion_beta_consensus
Sequence
RefSeq Genes
SLC34A2
ROS1

Figure 10a

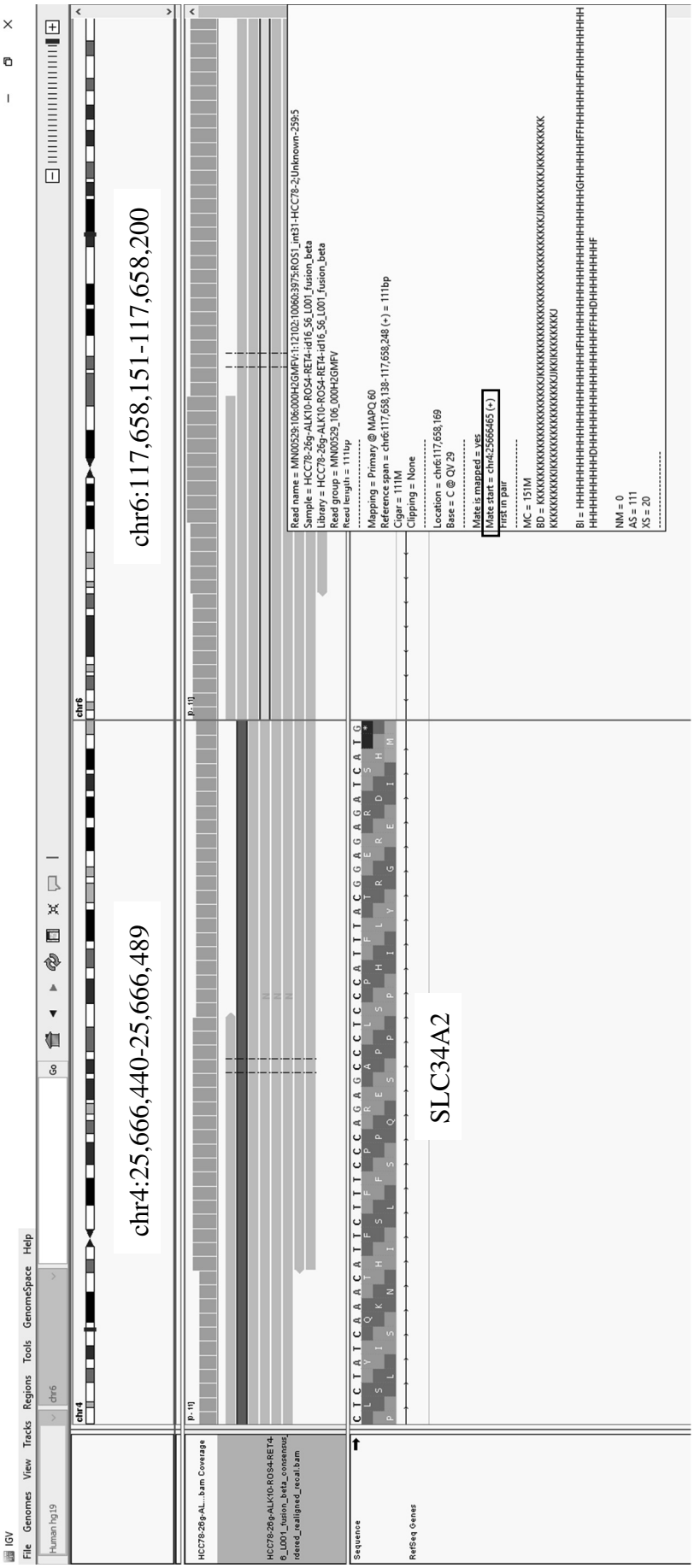
IGV
File Genomes View Tracks Regions Tools GenomeSpace Help
Human hg19
chr6
chr4
chr4:25,666,440-25,666,489
chr6:117,658,151-117,658,200
SLC34A2
HCC78-26g-AL...bam Coverage
HCC78-26g-ALK10-ROS4-RET4-6_L001_fusion_beta_consensus_rdered_realigned_recal.bam
Sequence
RefSeq Genes
Read name = MN00529:106:000H2GMFV:1:12102:10060:3975:ROS1_int31-HCC78-2:Unknown-259:5
Sample = HCC78-26g-ALK10-ROS4-RET4-id16_S6_L001_fusion_beta
Library = HCC78-26g-ALK10-ROS4-RET4-id16_S6_L001_fusion_beta
Read group = MN00529_106_000H2GMFV
Read length = 111bp
Mapping = Primary @ MAPQ 60
Reference span = chr6:117,658,138-117,658,248 (+) = 111bp
Cigar = 111M
Clipping = None
Location = chr6:117,658,169
Base = C @ QV 29
Mate is mapped = yes
Mate start = chr4:25666465 (+)
First in pair
MC = 151M
NM = 0
AS = 111
XS = 20

Figure 10b

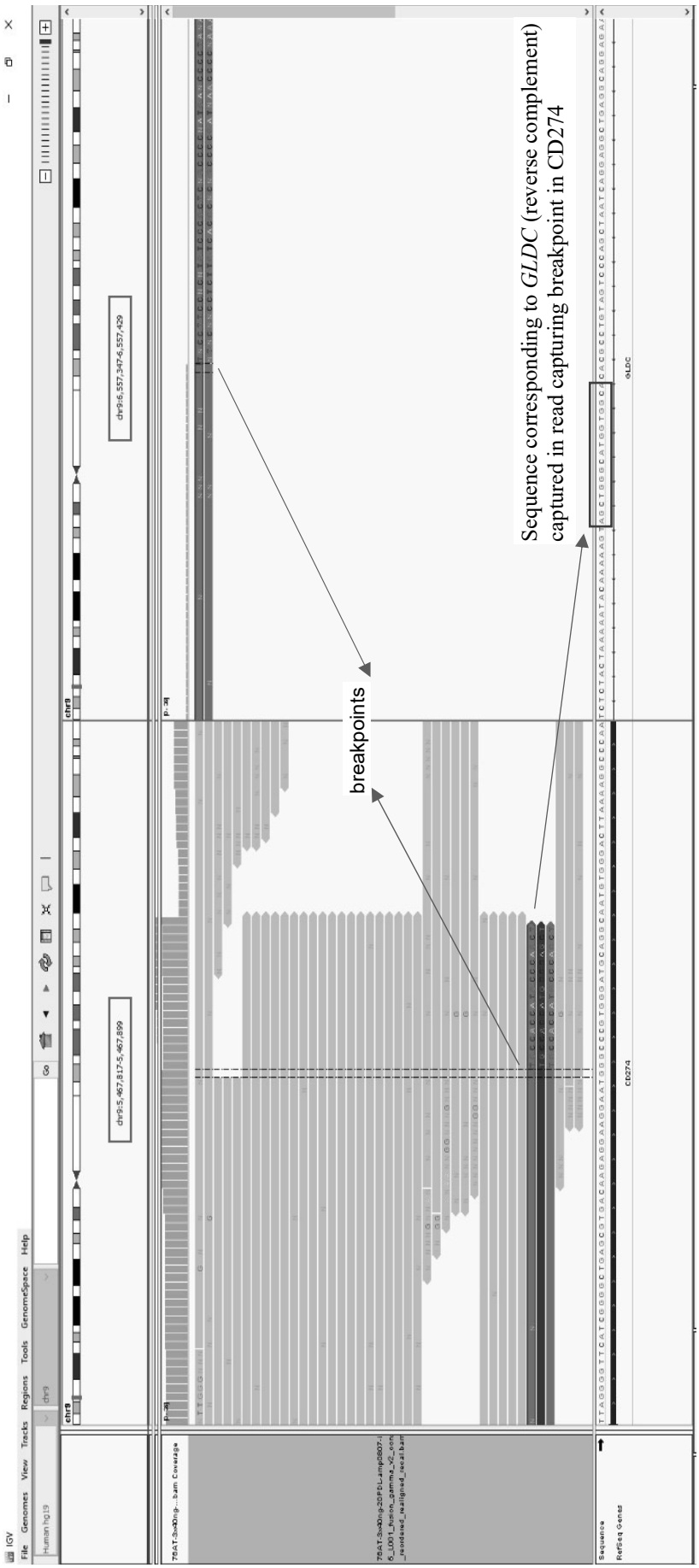
breakpoints
Sequence corresponding to *GLDC* (reverse complement) captured in read capturing breakpoint in CD274

Figure 12

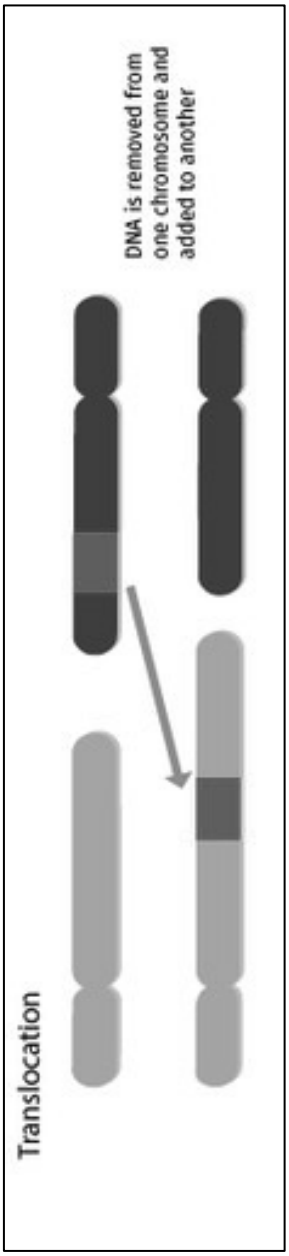
Translocation
DNA is removed from one chromosome and added to another

Figure 13

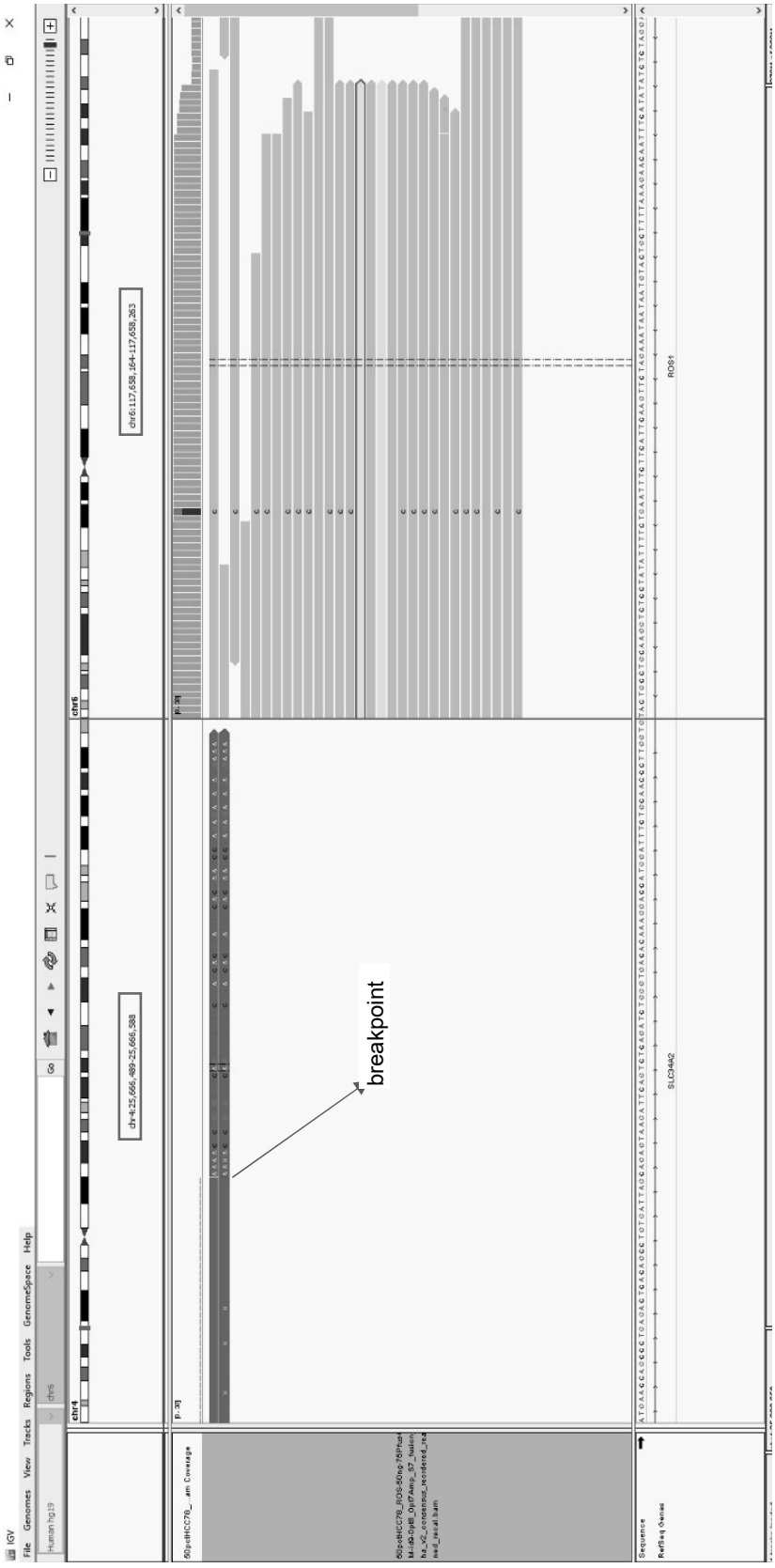

Figure 14