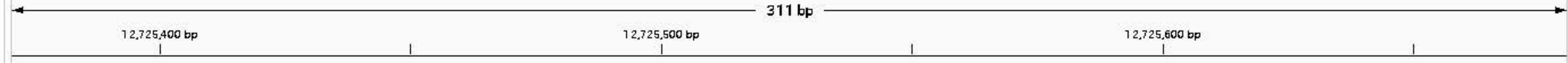
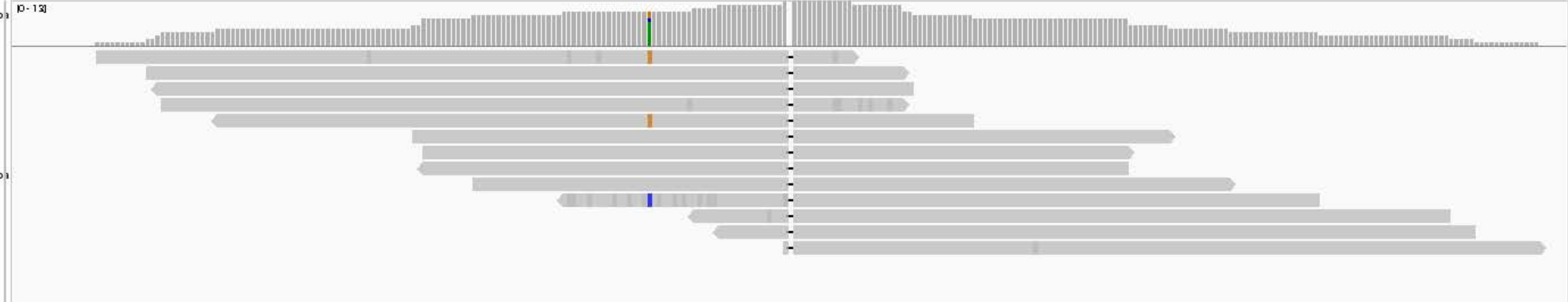


chr1:12,725,371-12,725,680  
p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44



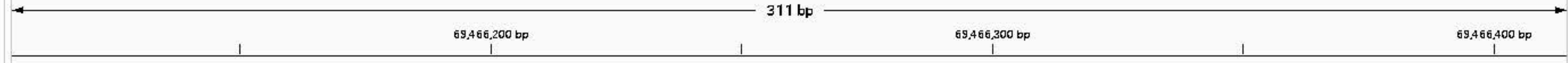
SL\_0015\_LN\_44\_WES\_uniq\_mut. ba  
overage  
SL\_0015\_LN\_44\_WES\_uniq\_mut. ba



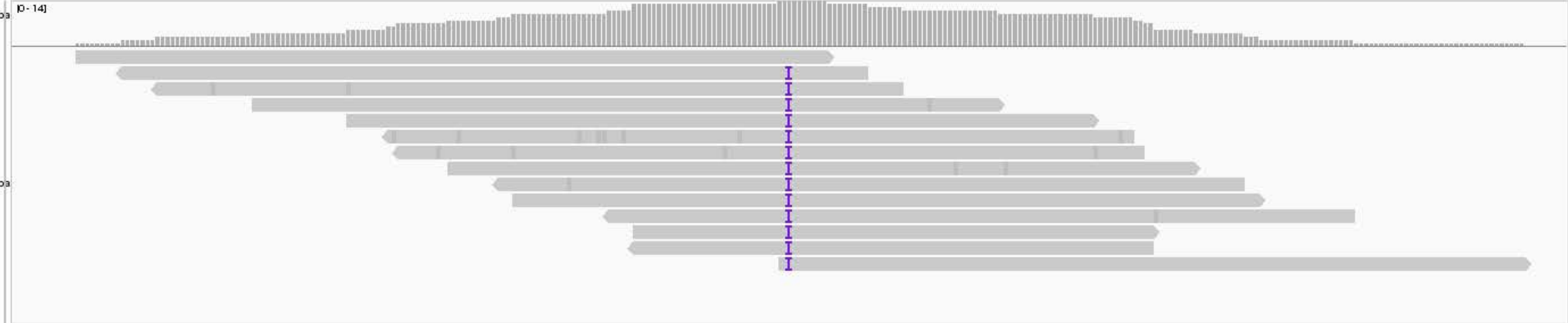
Sequence →  
Refseq Genes



chr2:69,466,105-69,466,414  
p25.2 p24.3 p24.1 p23.2 p22.2 p21 p16.2 p15 p13.3 p12 p11.2 q11.1 q12.1 q13 q14.2 q21.1 q22.1 q22.3 q24.1 q24.3 q31.1 q31.3 q32.2 q33.1 q33.3 q35 q36.2 q37.1 q37.3



SL\_0004\_RN\_61\_WES\_uniq\_mut.ba  
overage



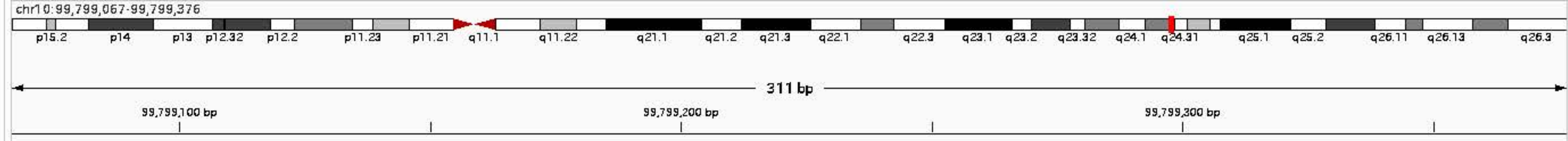
SL\_0004\_RN\_61\_WES\_uniq\_mut.ba

Sequence

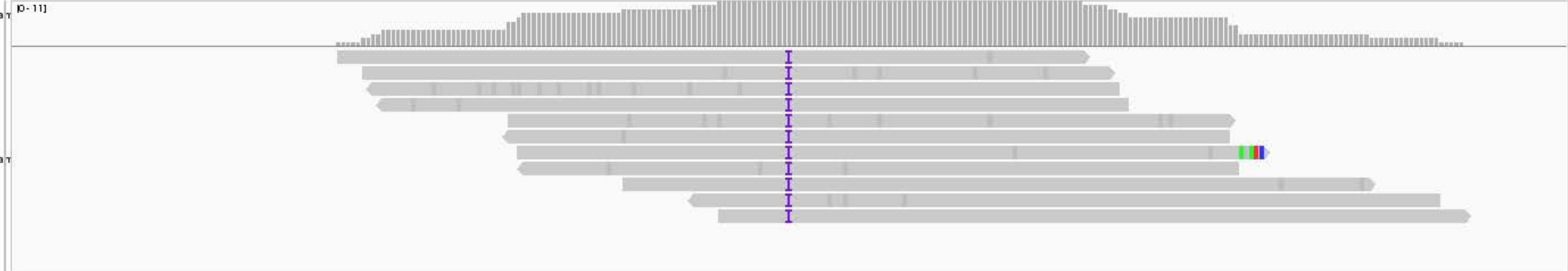
PAIAFVDPESLGDTAPQTF AQFQNKRGGQVTKAQEPSVEPPAFPVAGGLKGPPRCSEDEE ESEM L LPRSGSCDL M

Refseq Genes

AAK1



SL\_0007\_RN\_2\_WES\_uniq\_mut.bar  
verage



SL\_0007\_RN\_2\_WES\_uniq\_mut.bar

Sequence →

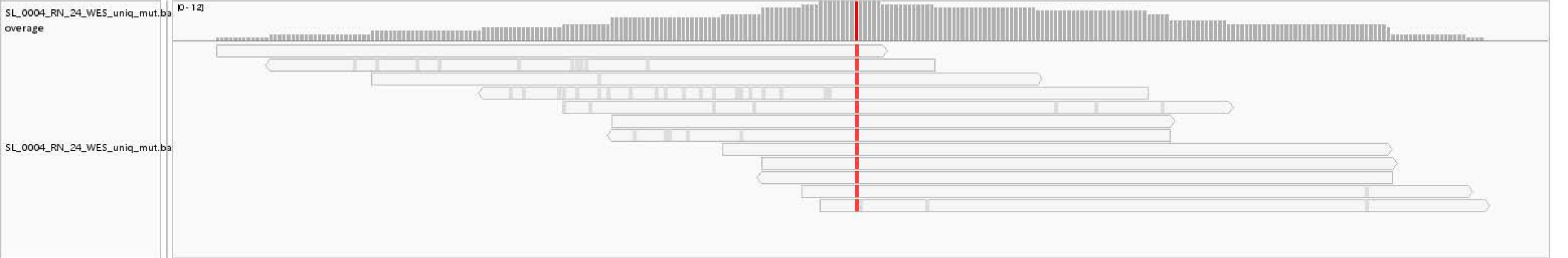
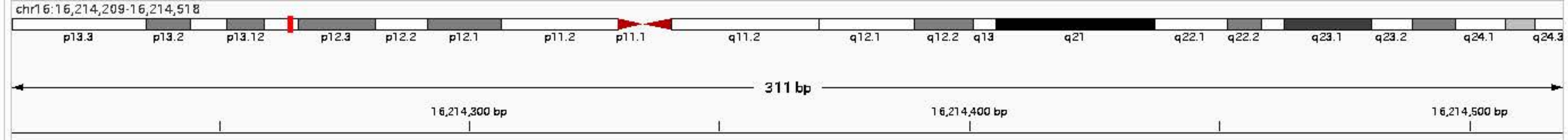


Refseq Genes

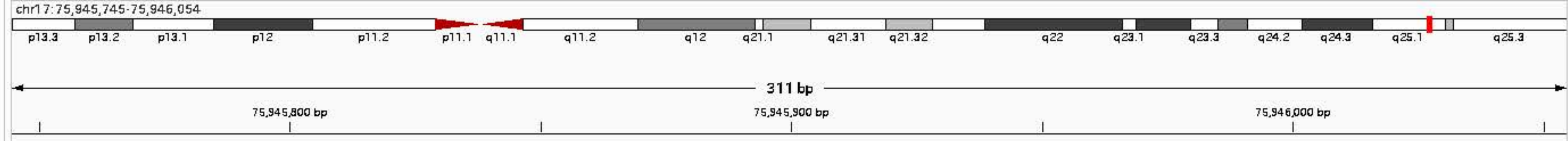
EDVEK K K K K S G T K K D V P K S W L M K A L F K T F Y M V L L K S F L L K L V N D I F T F V S P Q L L K

ABCC2

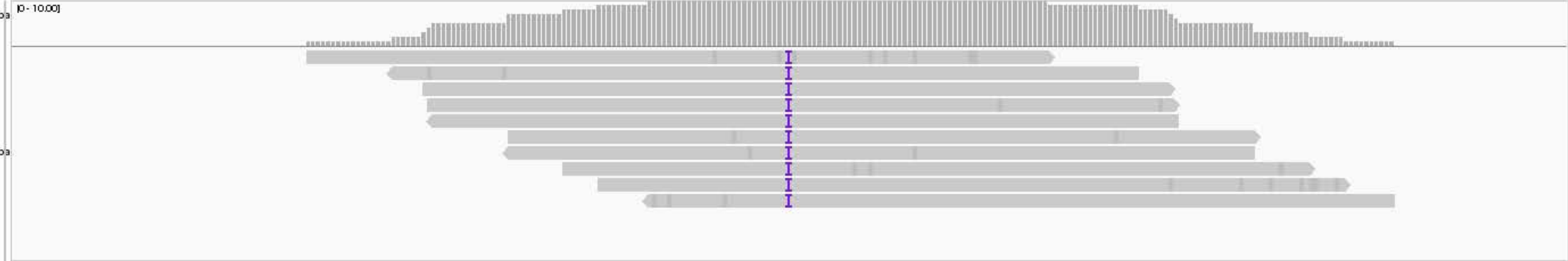




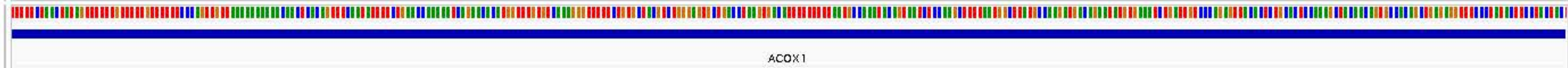


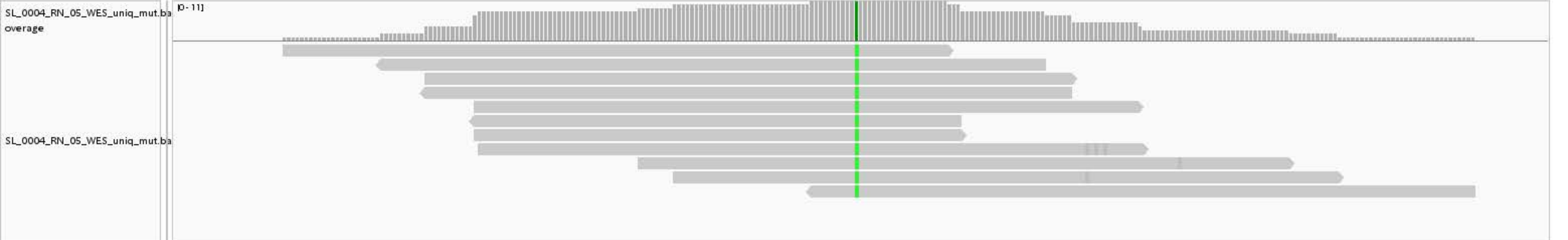
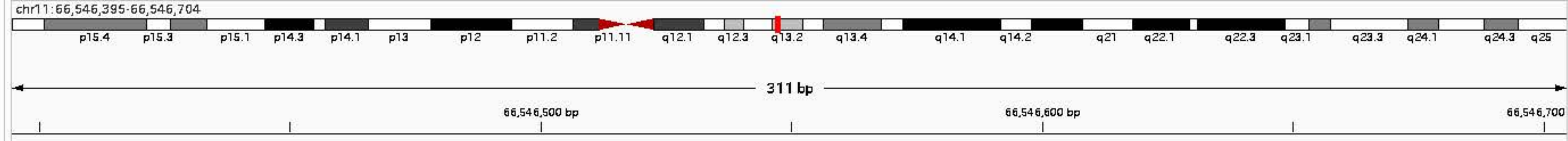


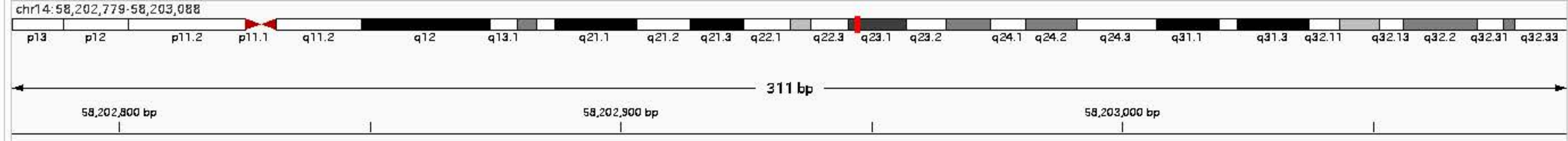
SL\_0004\_RN\_66\_WES\_uniq\_mut.ba  
coverage



Sequence  
Refseq Genes







SL\_0002\_LN\_1\_WES\_uniq\_mut.ba  
verage



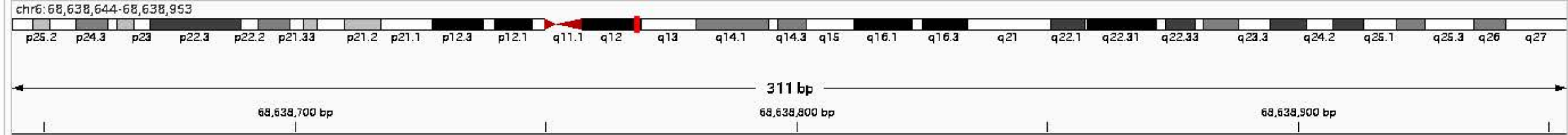
SL\_0002\_LN\_1\_WES\_uniq\_mut.ba r

Sequence →

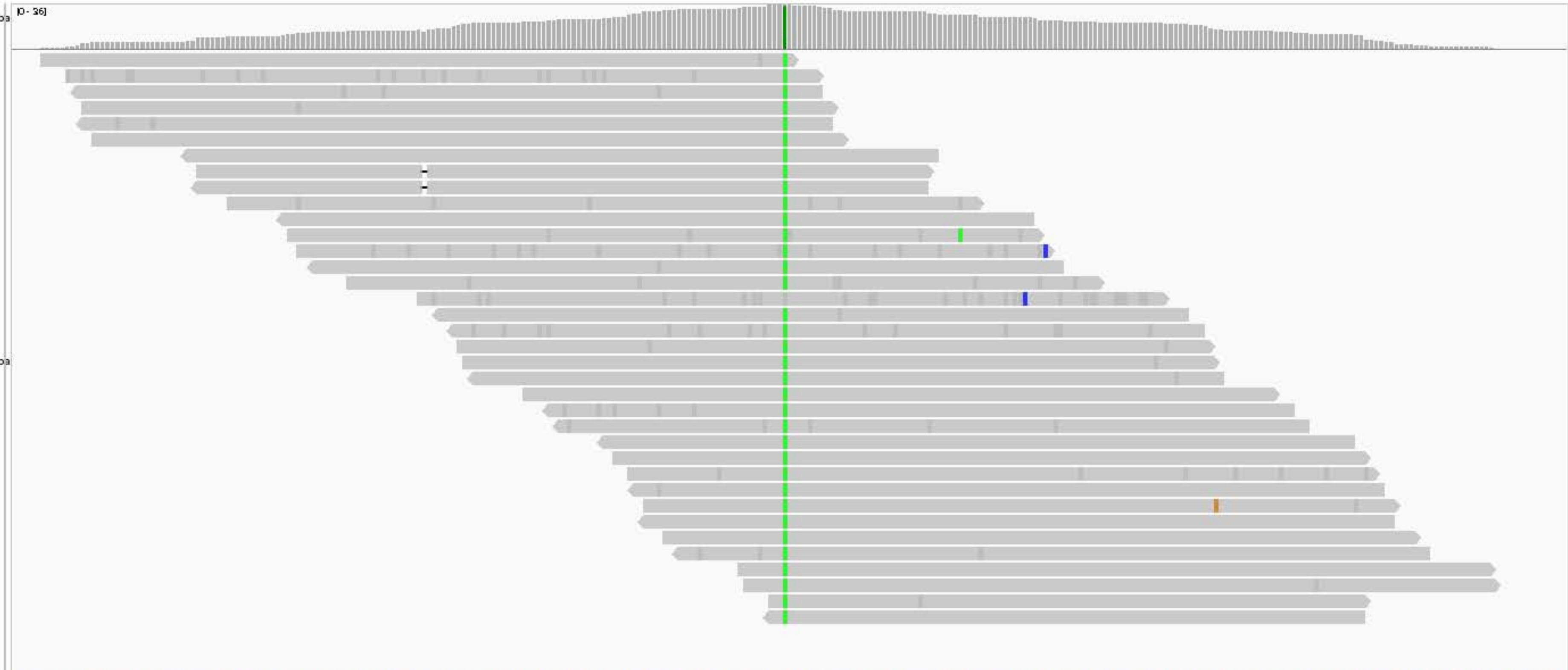


Refseq Genes



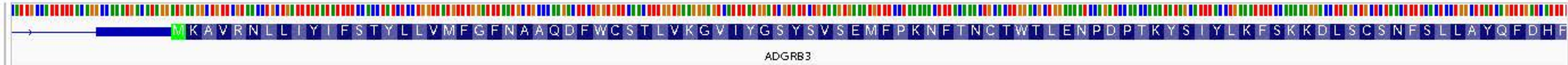


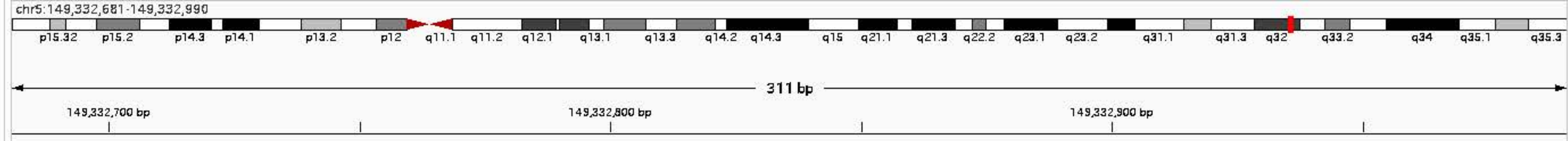
SL\_0004\_RN\_19\_WES\_uniq\_mut.ba  
overage

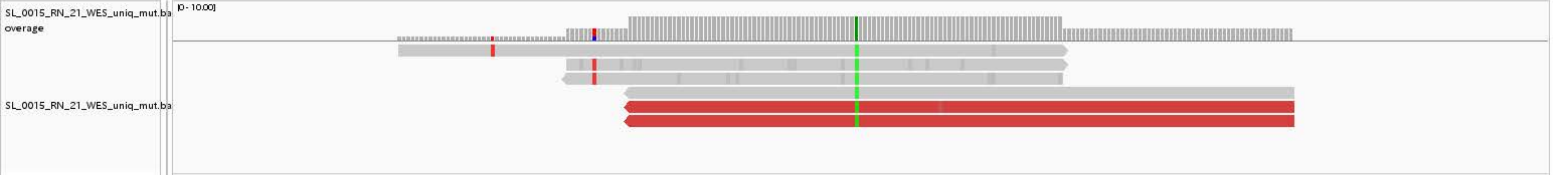
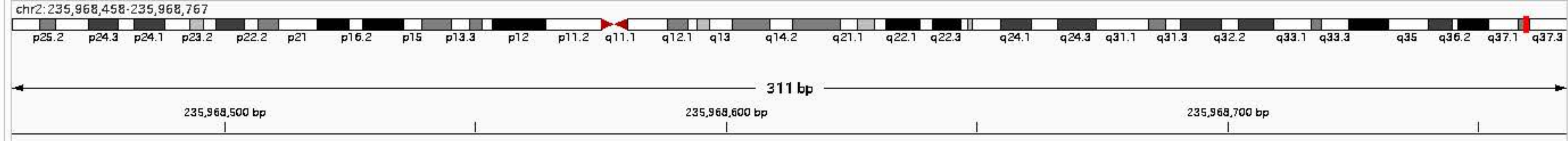


SL\_0004\_RN\_19\_WES\_uniq\_mut.ba

Sequence →  
Refseq Genes



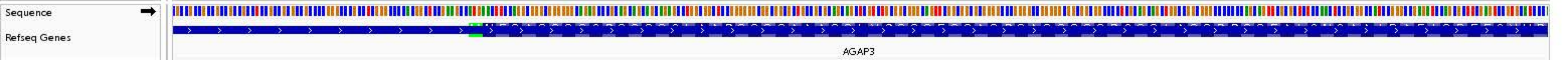
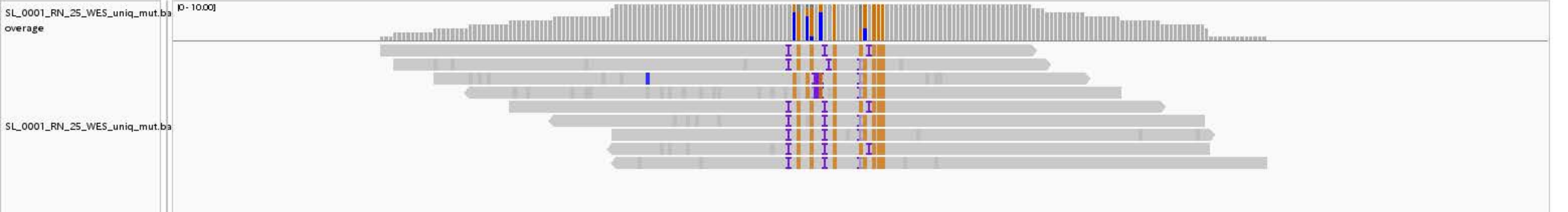
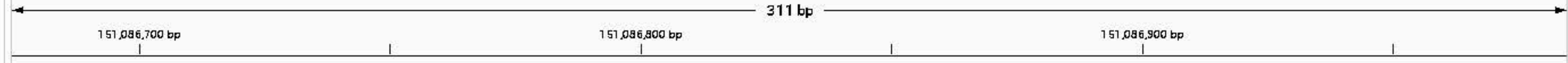




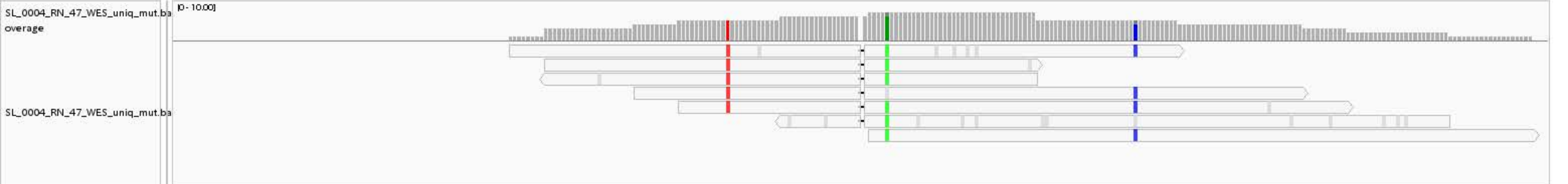
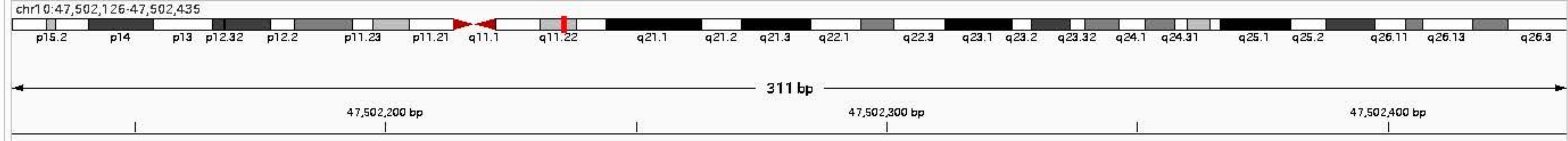


chr7:151,086,675-151,086,984

p22.2 p21.3 p21.2 p15.3 p15.1 p14.2 p13 p12.2 p11.2 q11.1 q11.22 q11.23 q21.11 q21.12 q21.2 q22.1 q22.3 q31.1 q31.2 q31.32 q32.1 q33 q34 q35 q36.1 q36.3



AGAP3

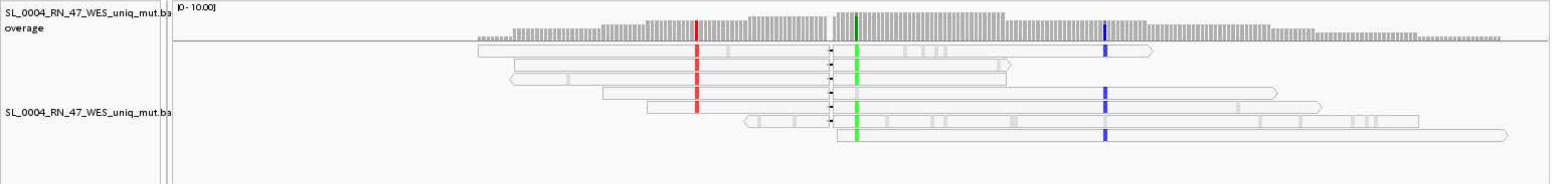
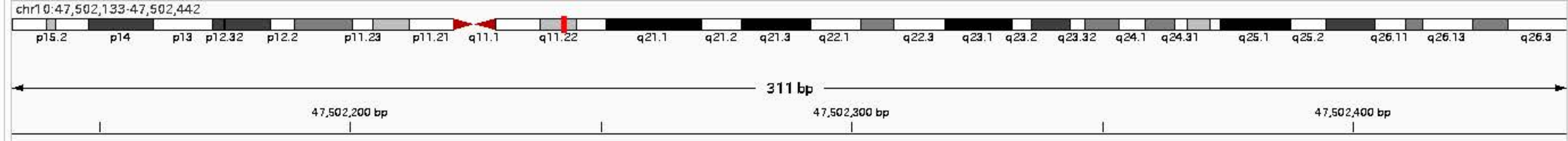


Sequence →

Refseq Genes

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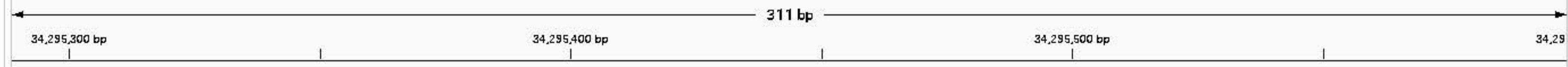
ANXAS



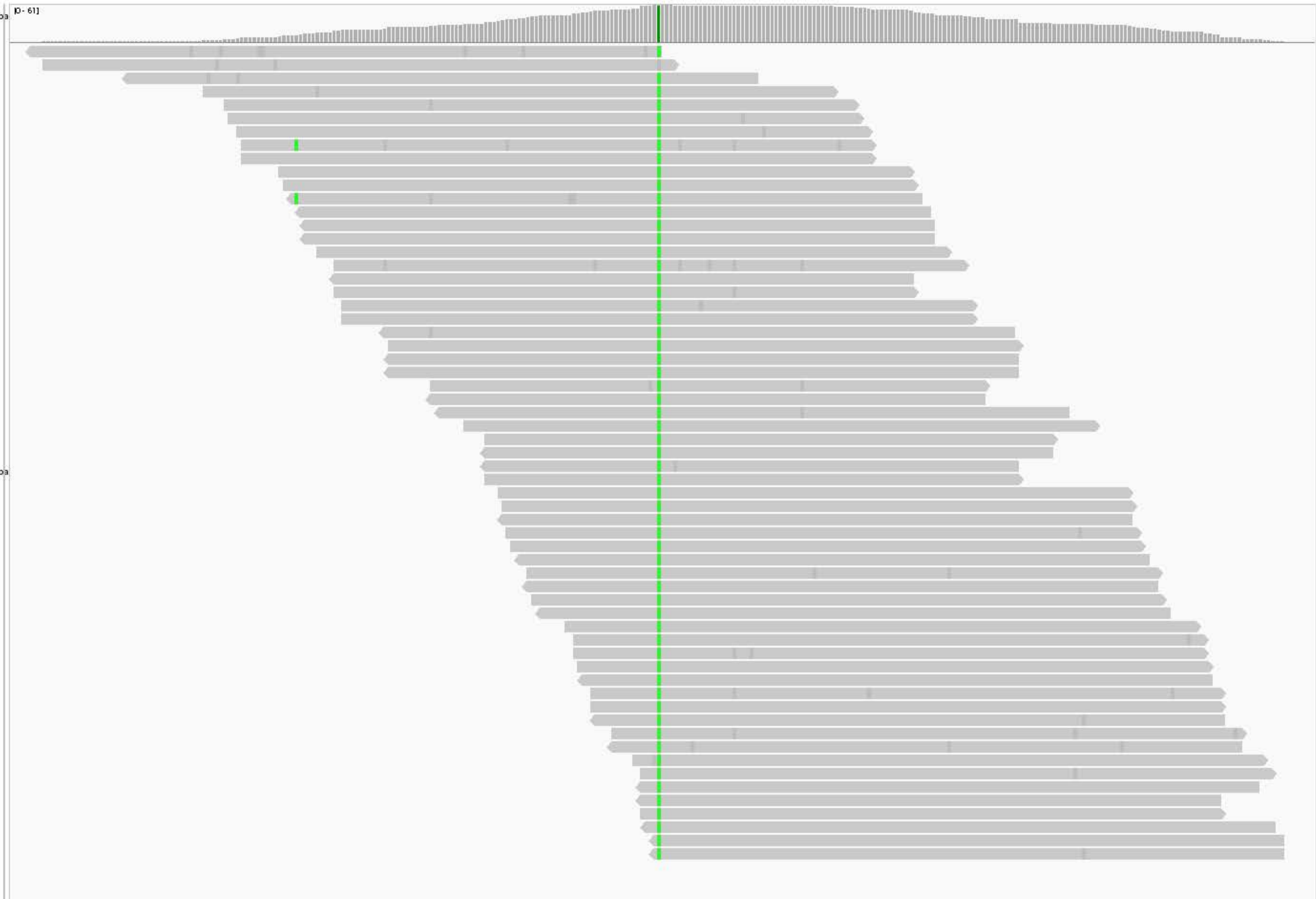


chr20:34,295,289-34,295,598

p13 p12.3 p12.2 p12.1 p11.23 p11.22 p11.21 p11.1 q11.1 q11.21 q11.22 q11.23 q12 q13.11 q13.12 q13.13 q13.2 q13.31 q13.33



SL\_0015\_RN\_21\_WES\_uniq\_mut.ba  
coverage



SL\_0015\_RN\_21\_WES\_uniq\_mut.ba

Sequence

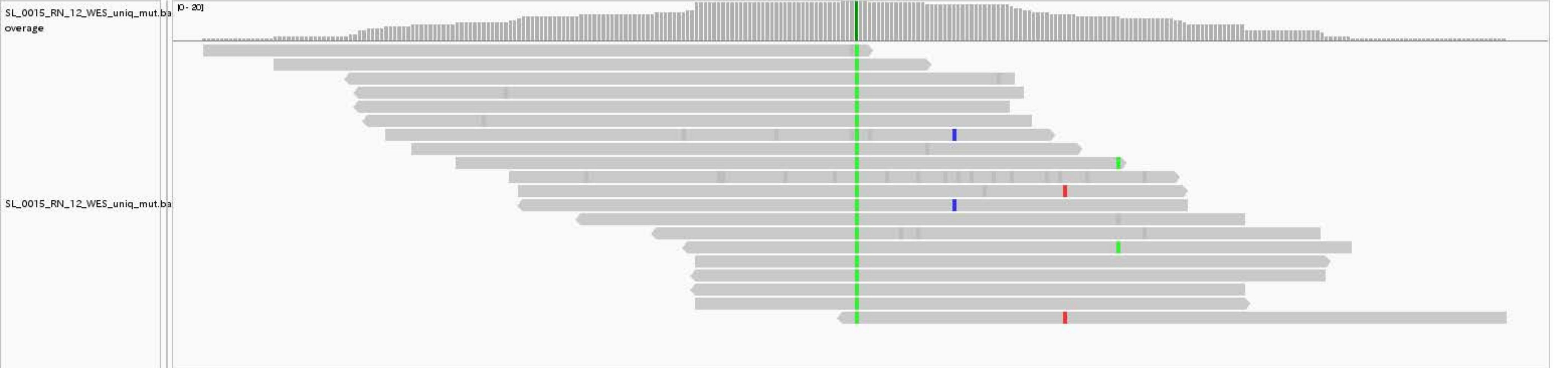
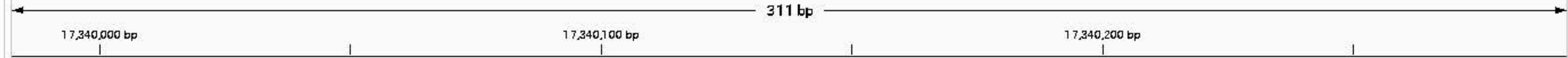
Refseq Genes



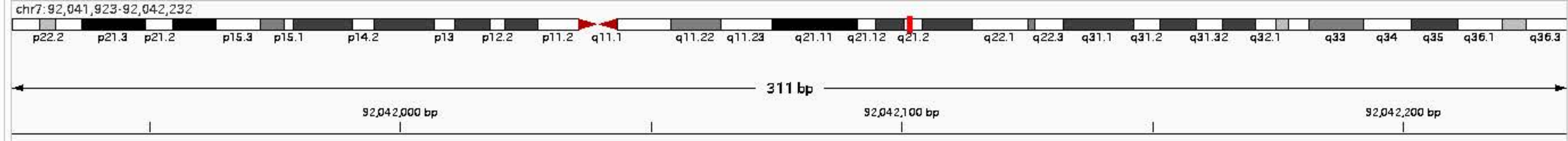
EAGLTVLVEILVATEVVTMHLCCGAI RAGKLPKSASYRERMRLGPM

AHCY

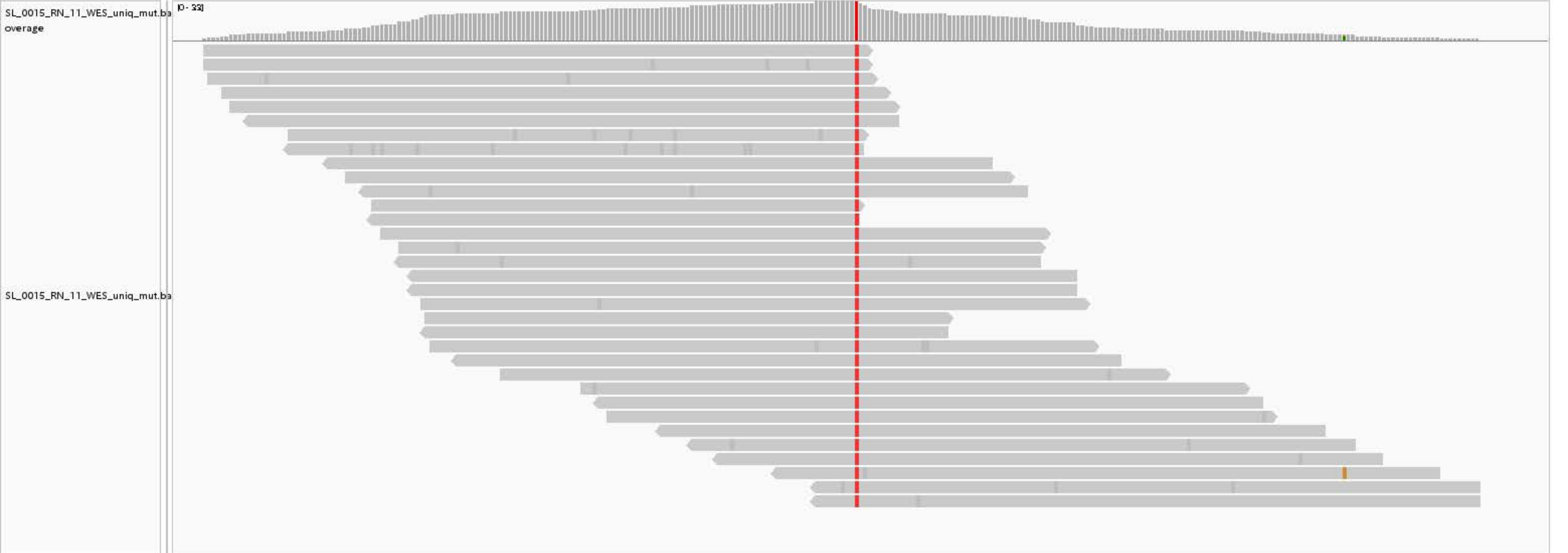
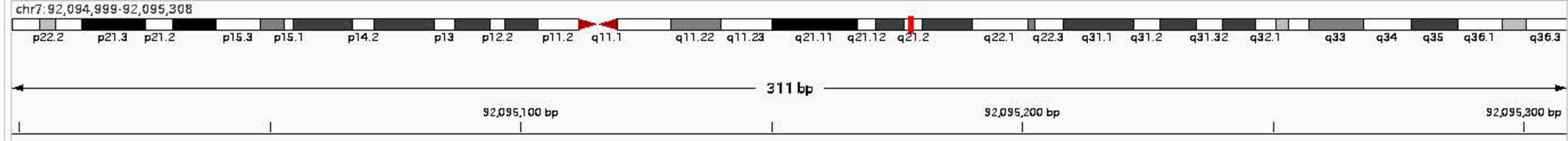
chr7:17,339,983-17,340,292  
p22.2 p21.3 p21.2 p15.3 p15.1 p14.2 p13 p12.2 p11.2 q11.1 q11.22 q11.23 q21.11 q21.12 q21.2 q22.1 q22.3 q31.1 q31.2 q31.32 q32.1 q33 q34 q35 q36.1 q36.3

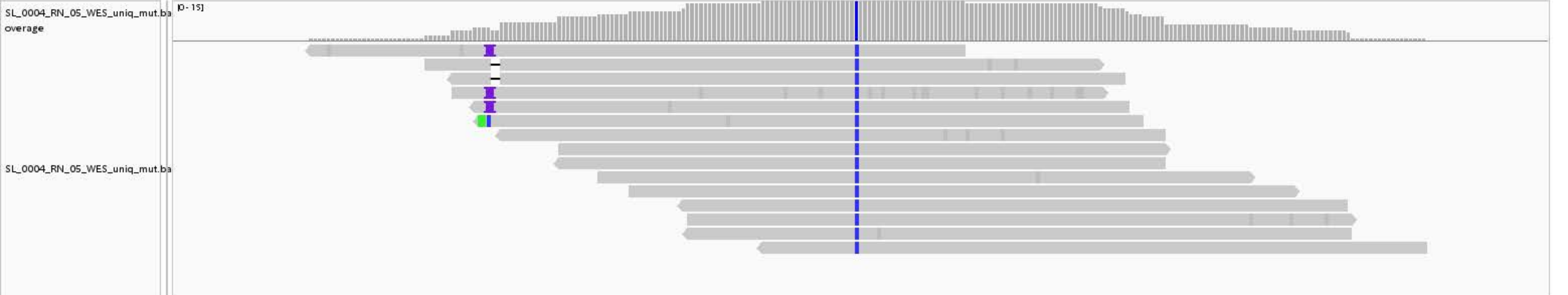
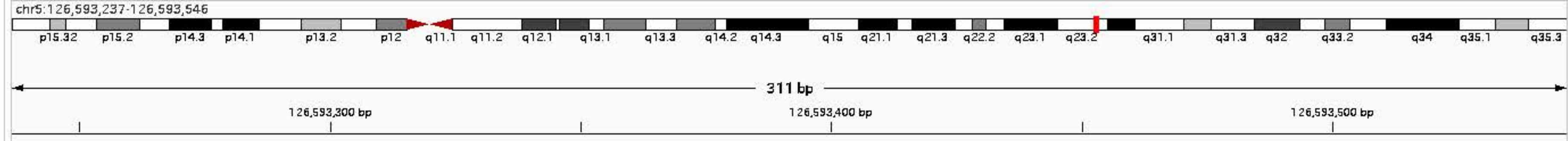


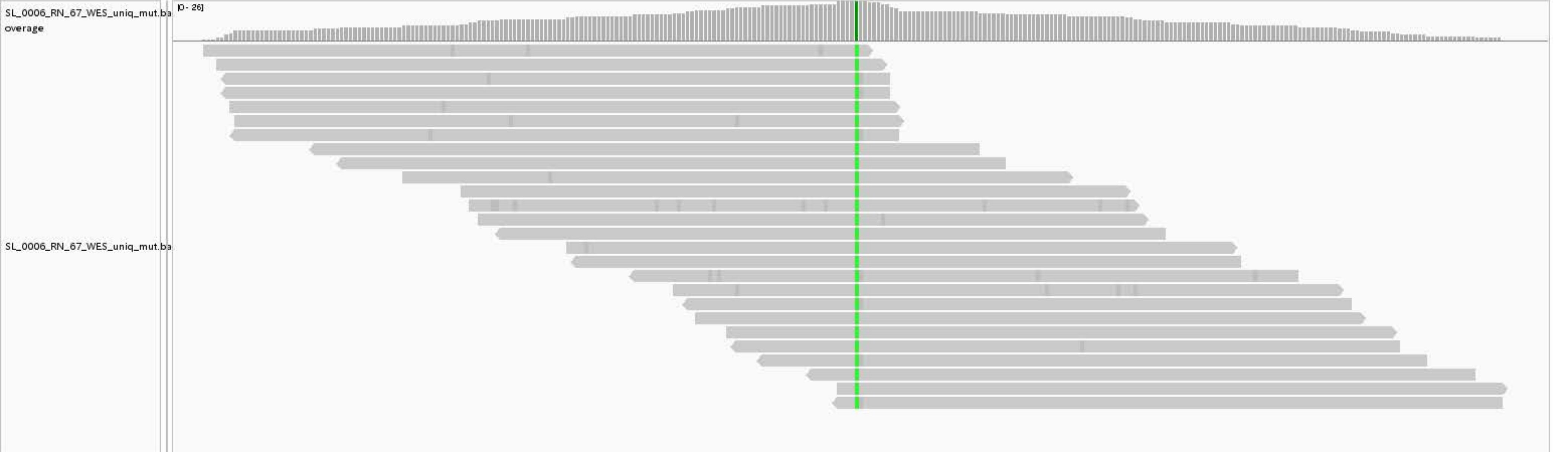
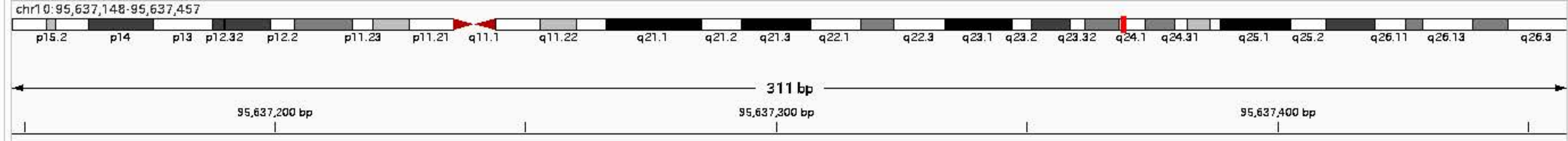
Sequence →  
Refseq Genes  
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AHR



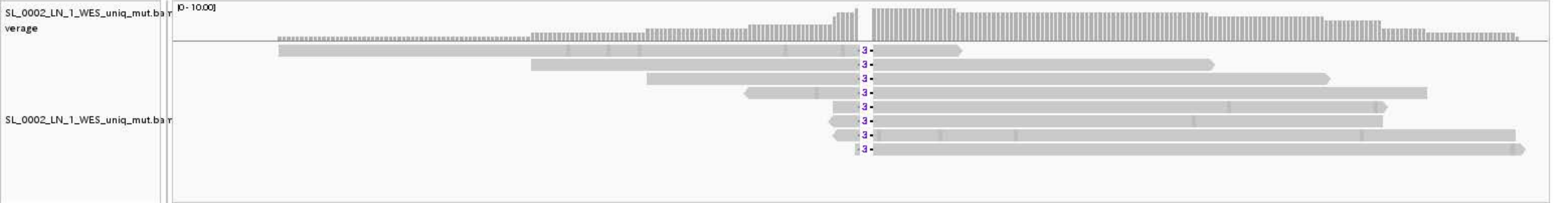
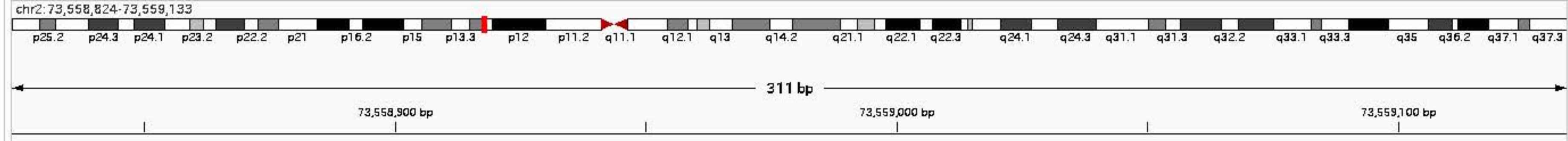


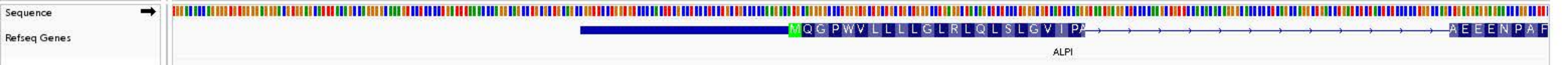
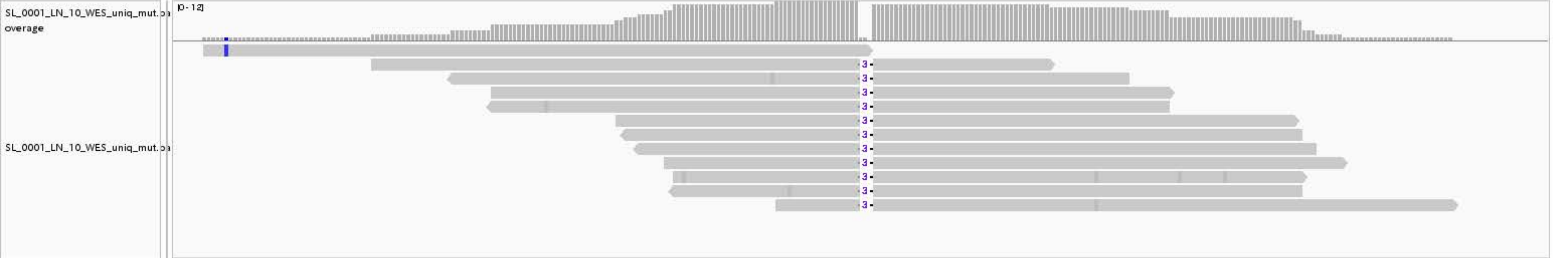
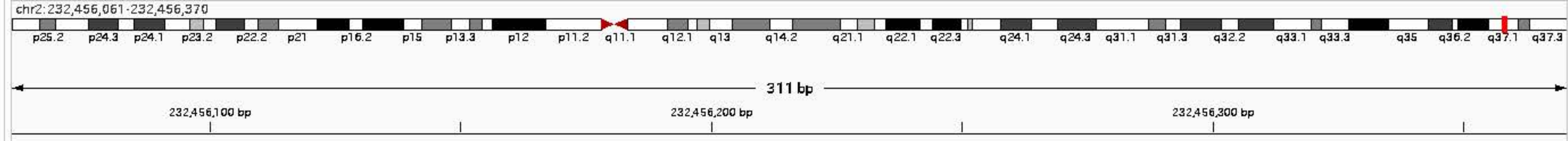


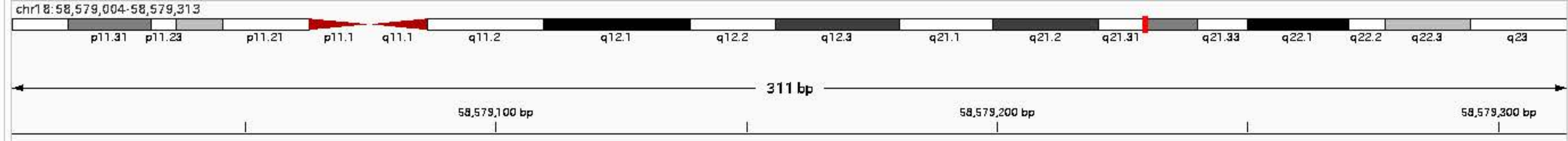




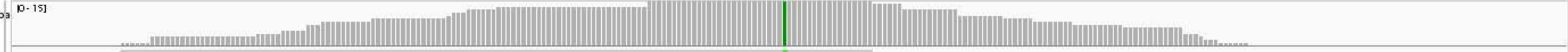




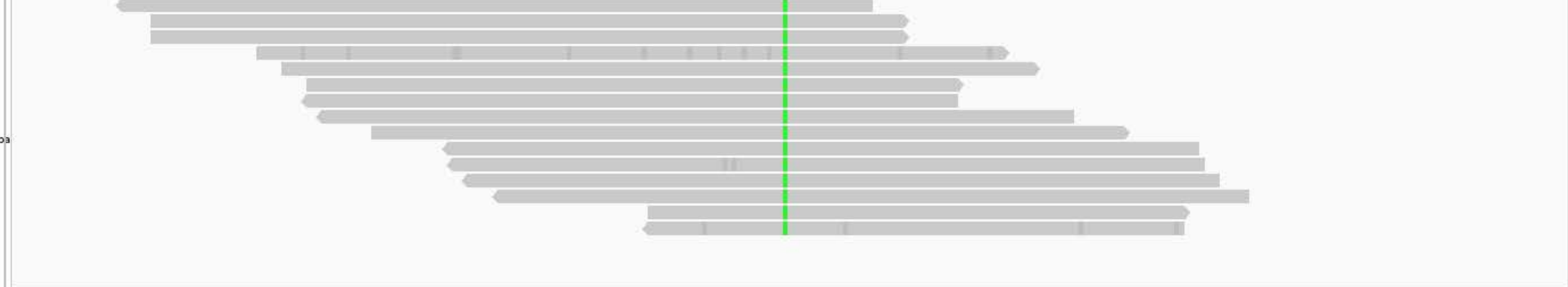




SL\_0015\_RN\_10\_WES\_uniq\_mut.ba  
coverage



SL\_0015\_RN\_10\_WES\_uniq\_mut.ba



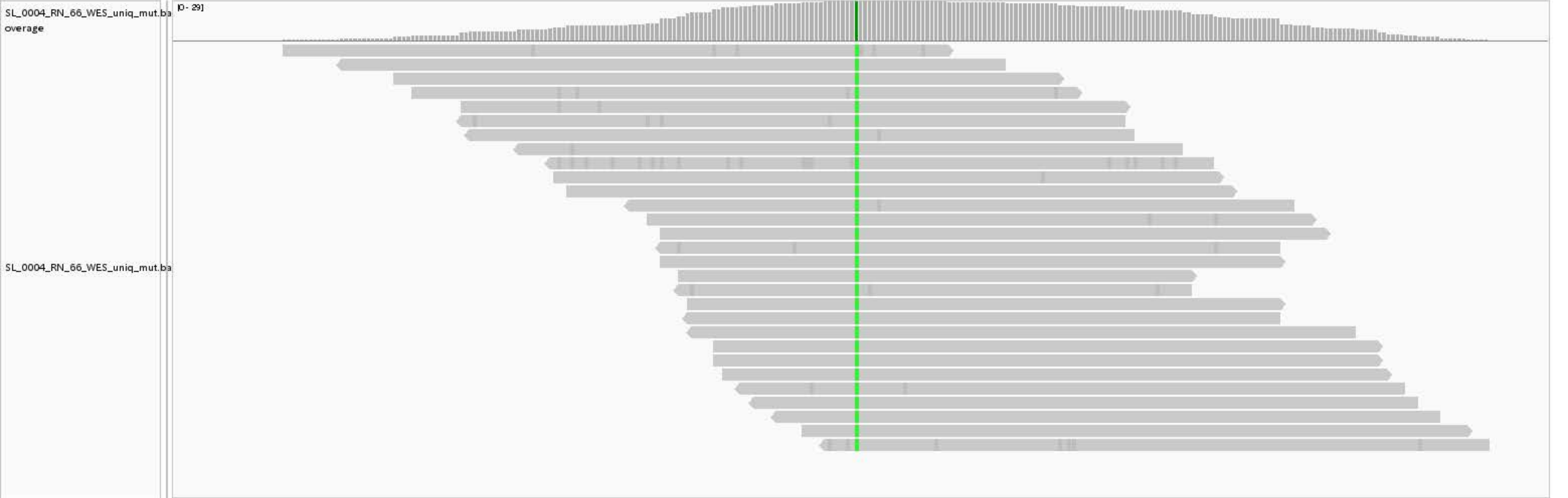
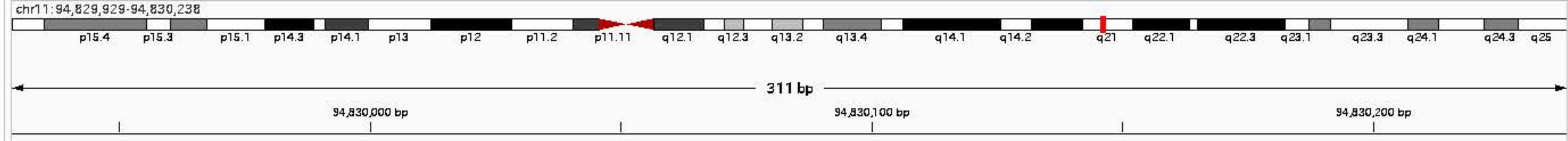
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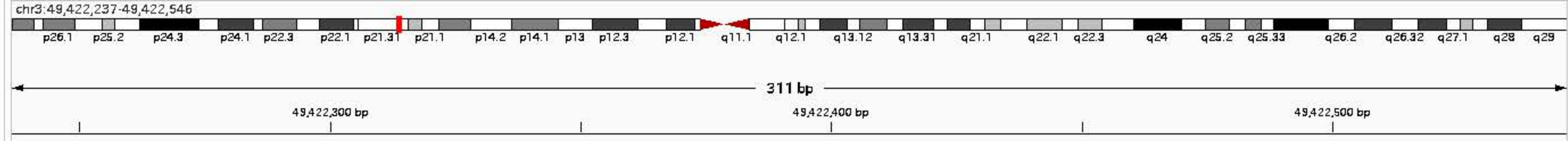
Refseq Genes

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ALPK2







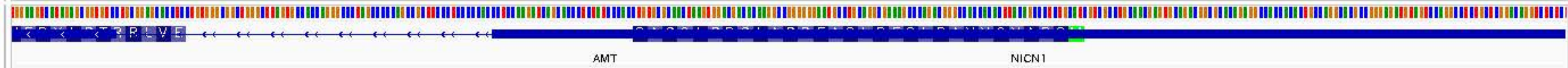
SL\_0006\_RN\_59\_WES\_uniq\_mut.ba  
coverage

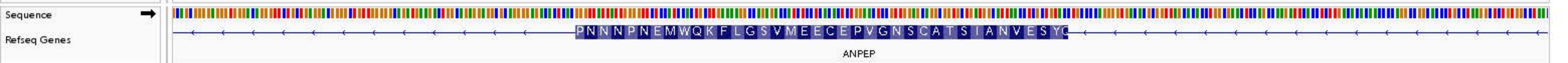
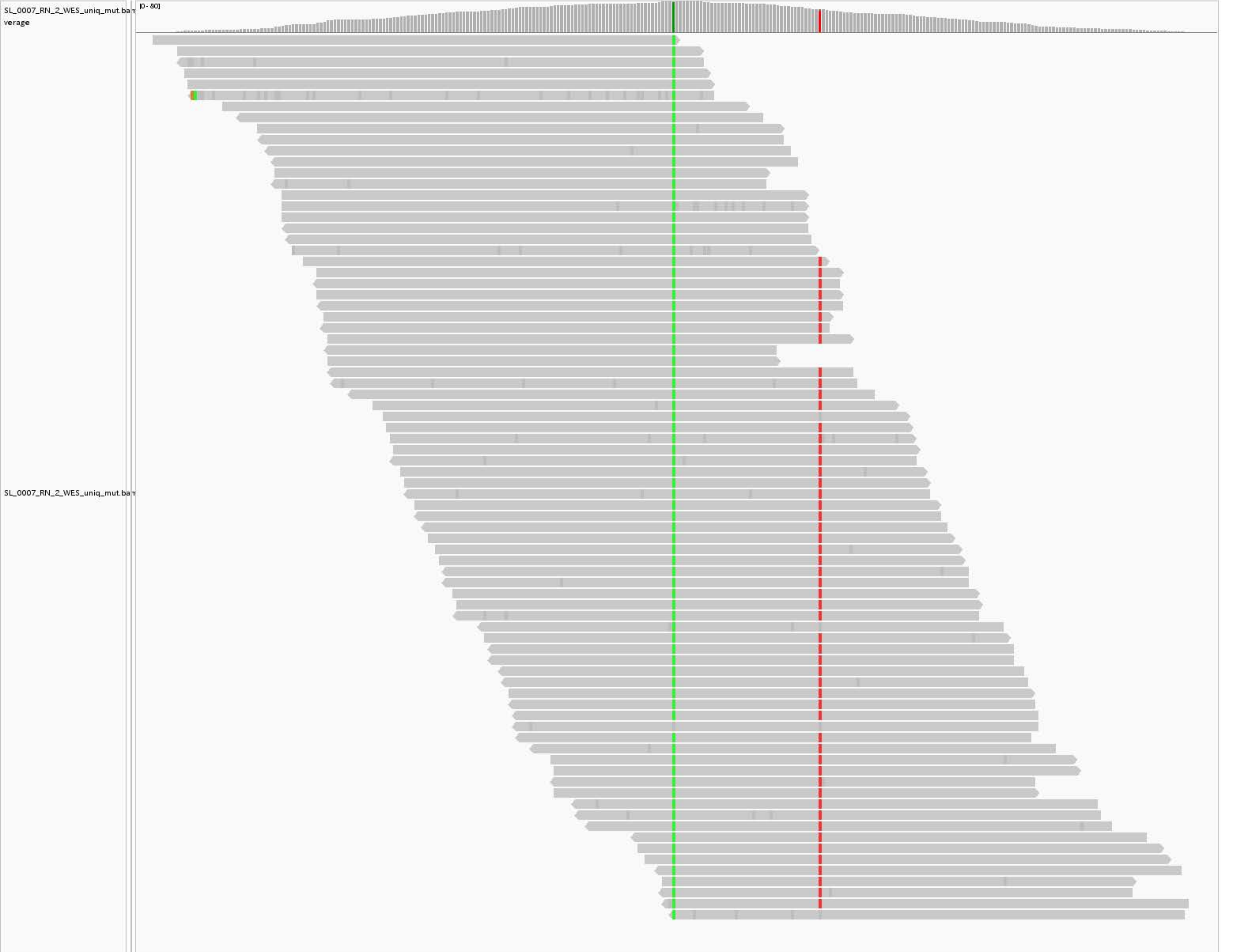
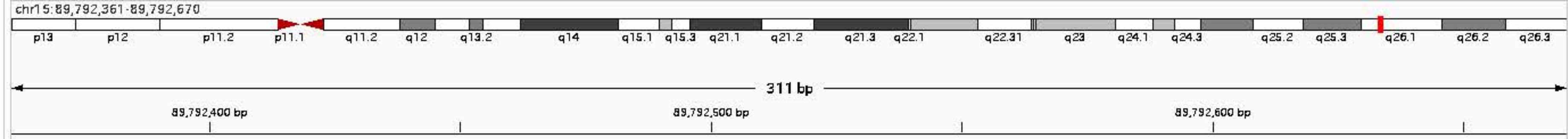


SL\_0006\_RN\_59\_WES\_uniq\_mut.ba

Sequence

Refseq Genes

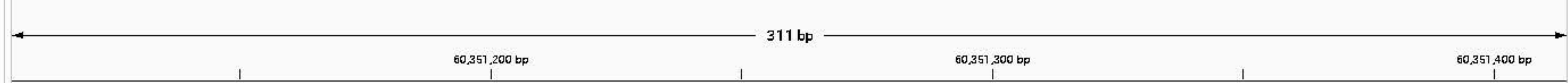




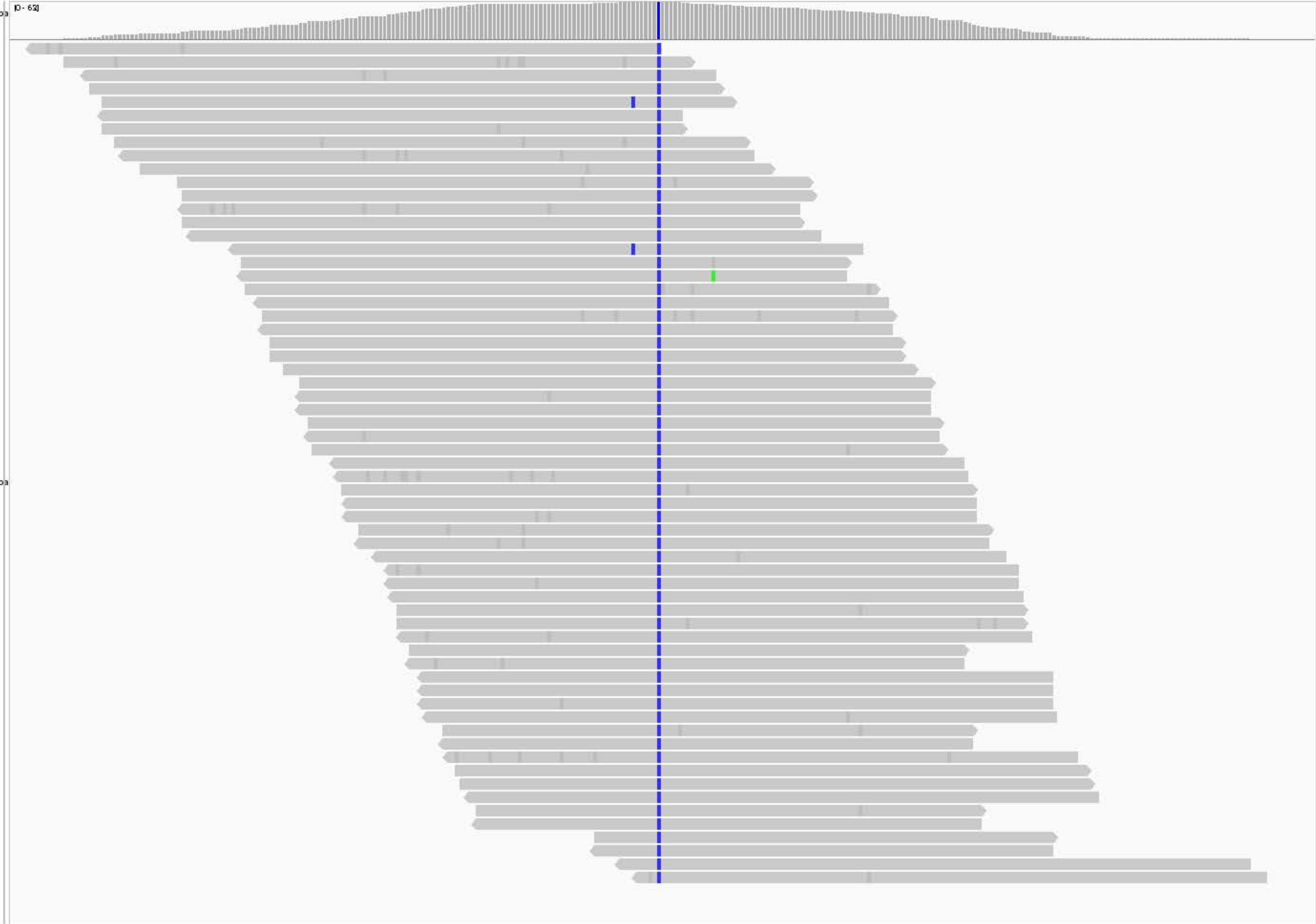


chr15:60,351,105-60,351,414

p13 p12 p11.2 p11.1 q11.2 q12 q13.2 q14 q15.1 q15.3 q21.1 q21.2 q21.3 q22.1 q22.31 q23 q24.1 q24.3 q25.2 q25.3 q26.1 q26.2 q26.3



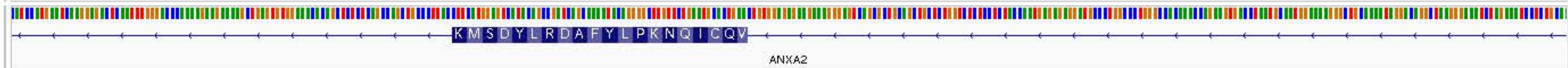
SL\_0010\_RN\_34\_WES\_uniq\_mut.ba  
coverage



SL\_0010\_RN\_34\_WES\_uniq\_mut.ba

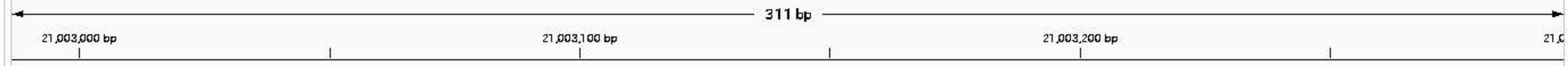
Sequence

Refseq Genes



ANXA2

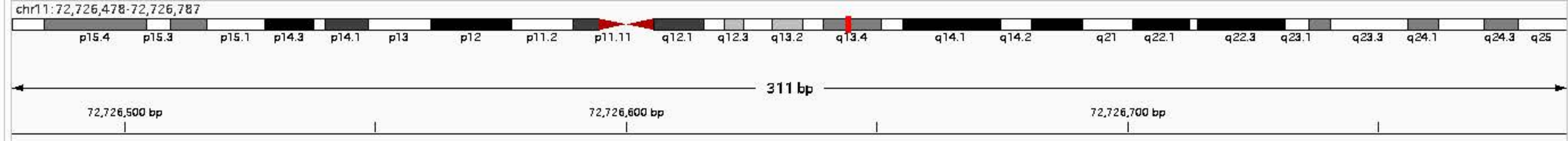
chr2:21,002,987-21,003,296  
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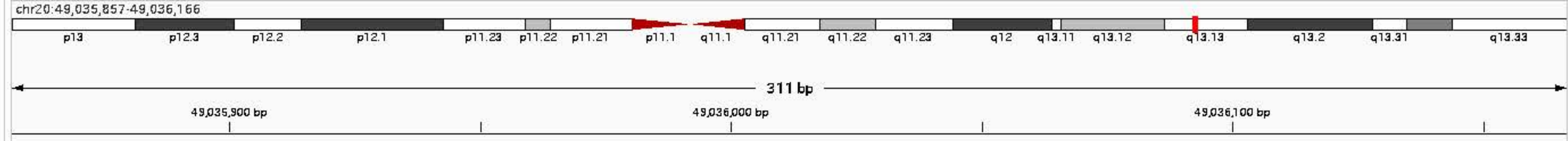
Sequence →  
Refseq Genes

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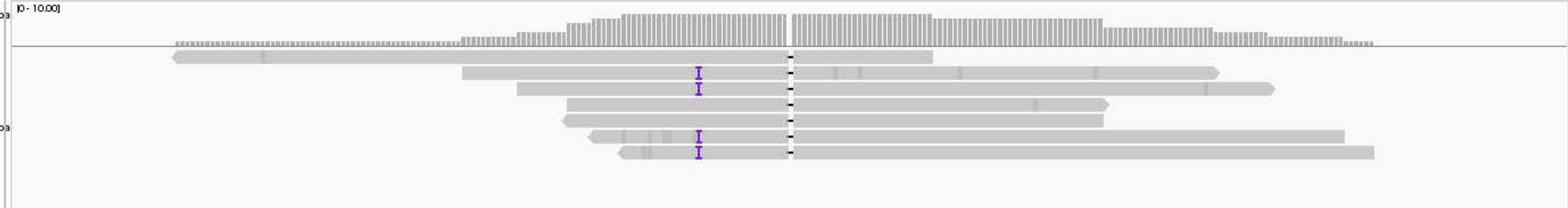
APOB







SL\_0004\_RN\_47\_WES\_uniq\_mut.ba  
coverage

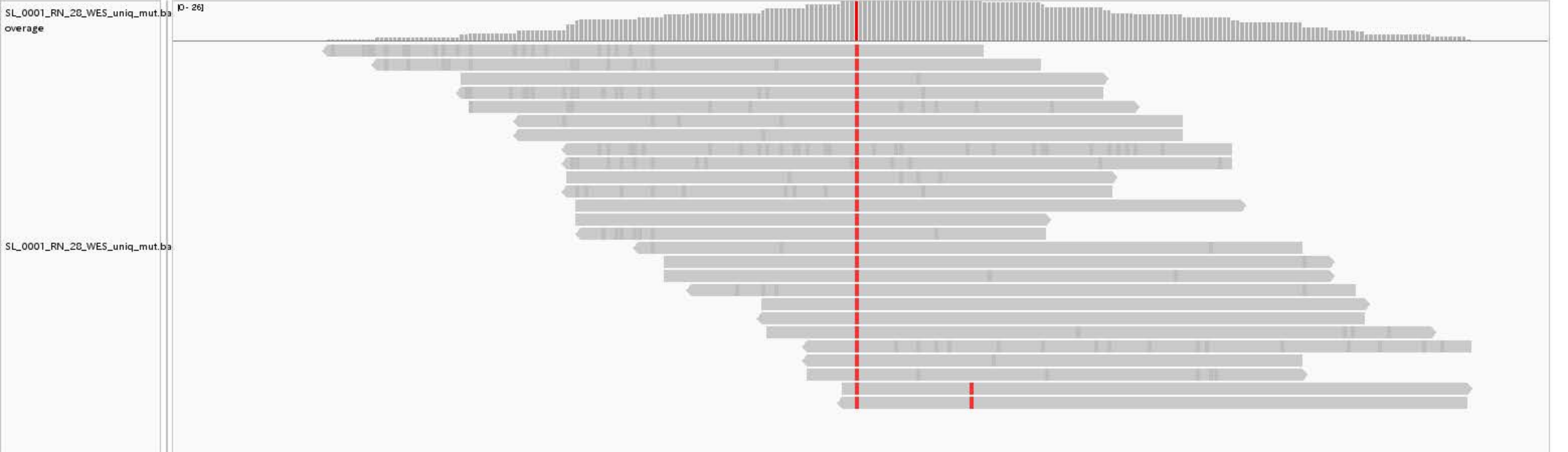
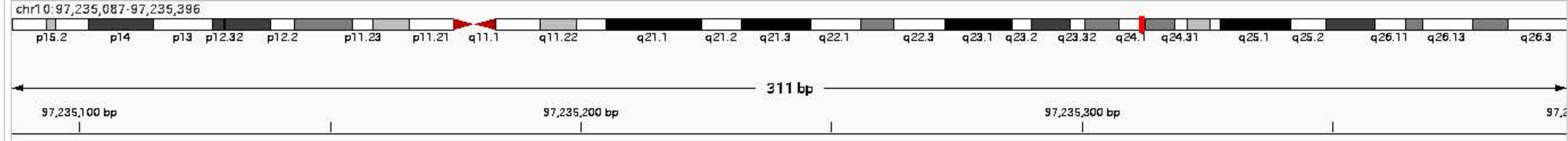


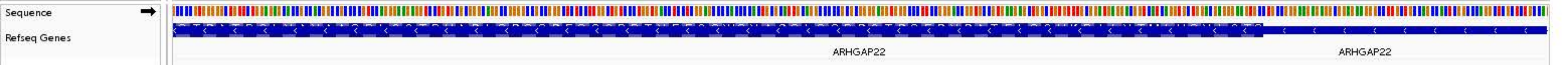
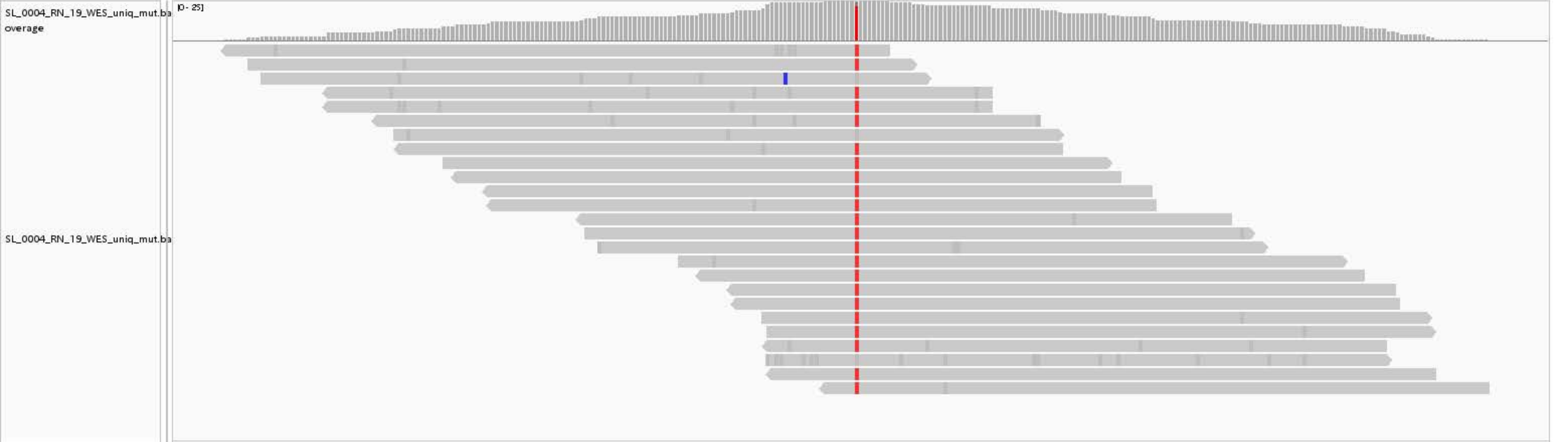
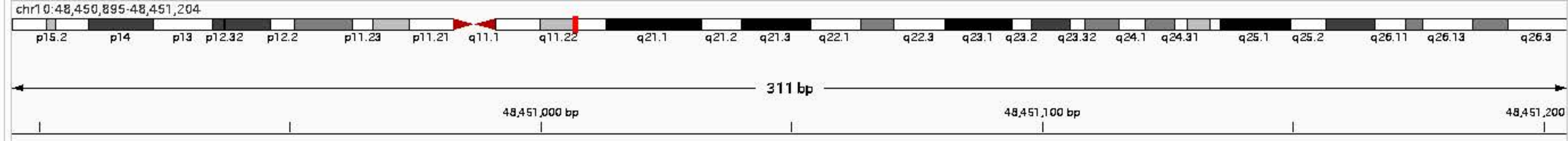
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Sequence

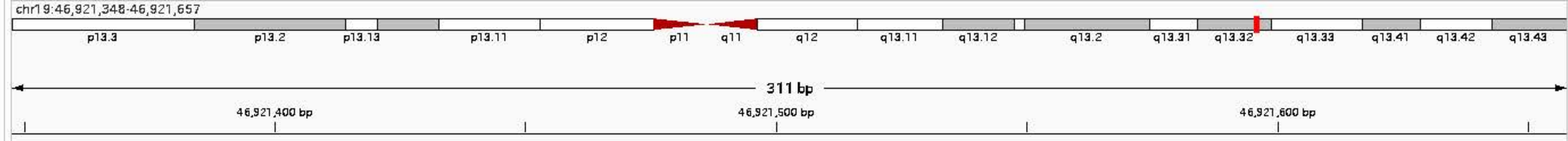
Refseq Genes



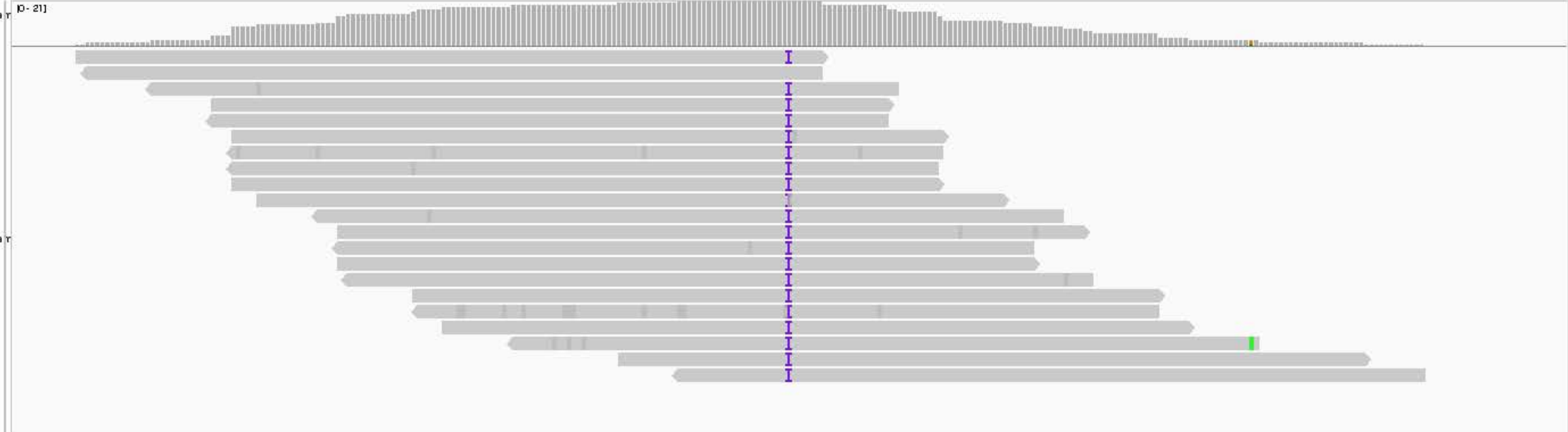






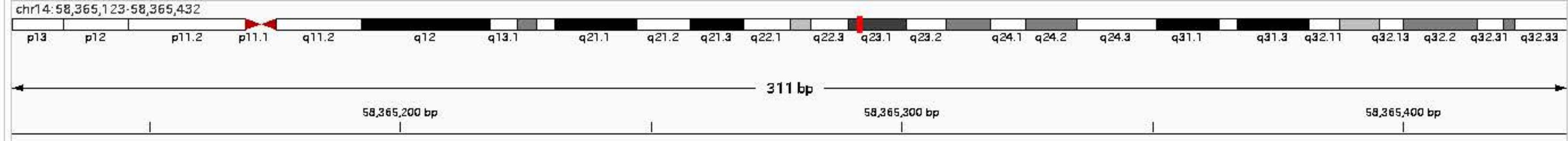


SL\_0002\_LN\_1\_WES\_uniq\_mut.ba  
verage



Sequence →  
Refseq Genes

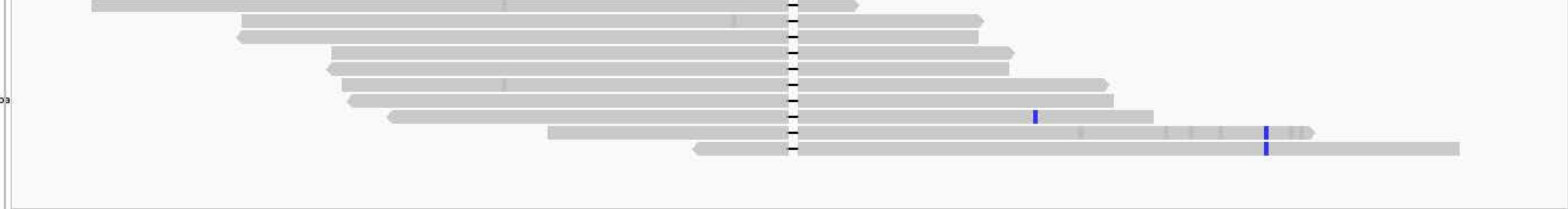




SL\_0015\_RN\_21\_WES\_uniq\_mut.ba  
coverage



SL\_0015\_RN\_21\_WES\_uniq\_mut.ba



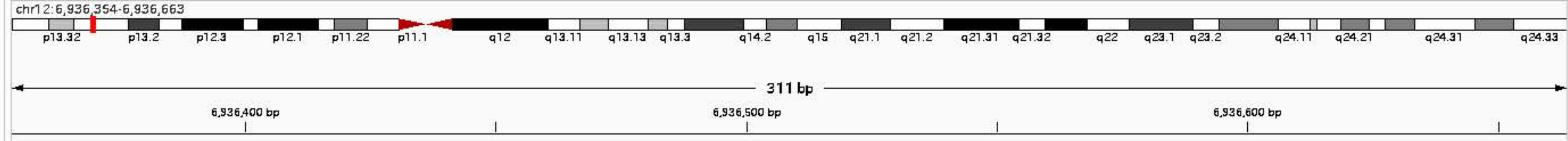
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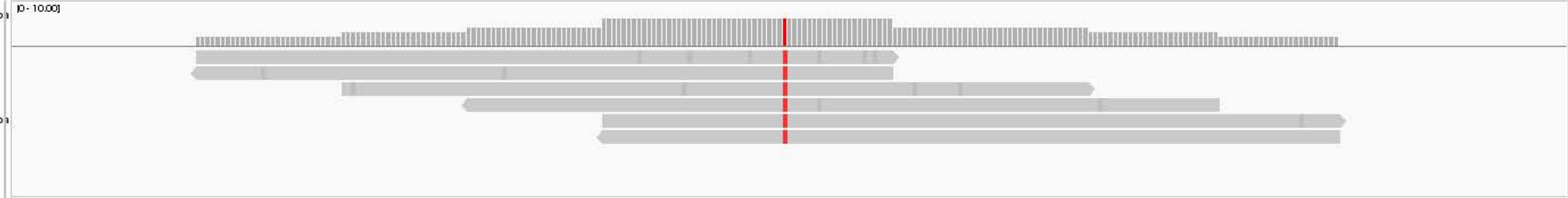
Refseq Genes

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ARID4A



SL\_0003\_LN\_51\_WES\_uniq\_mut.  
coverage



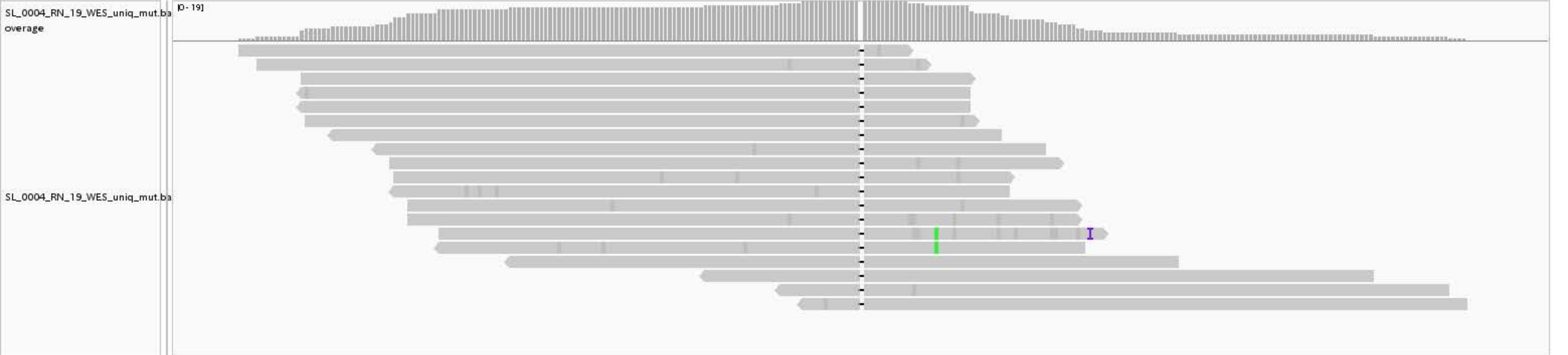
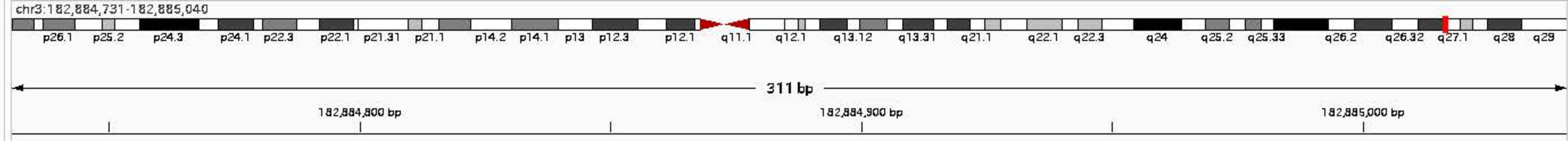
SL\_0003\_LN\_51\_WES\_uniq\_mut.

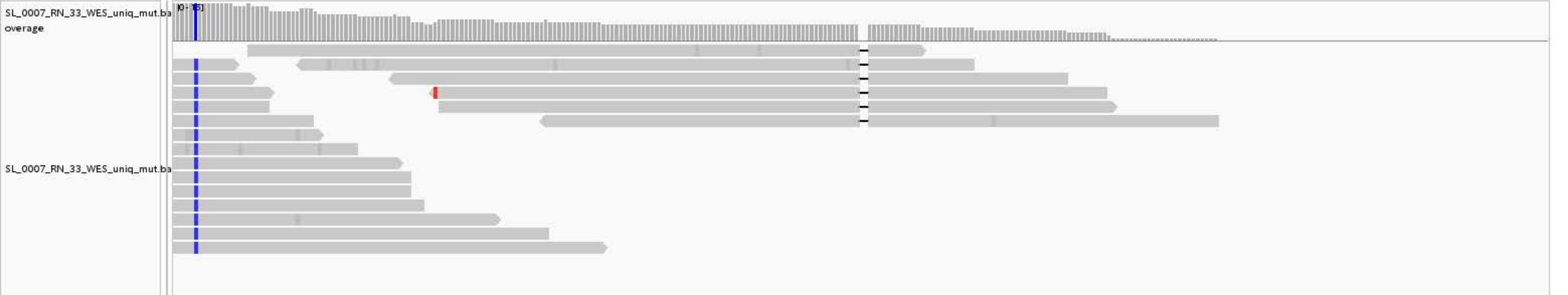
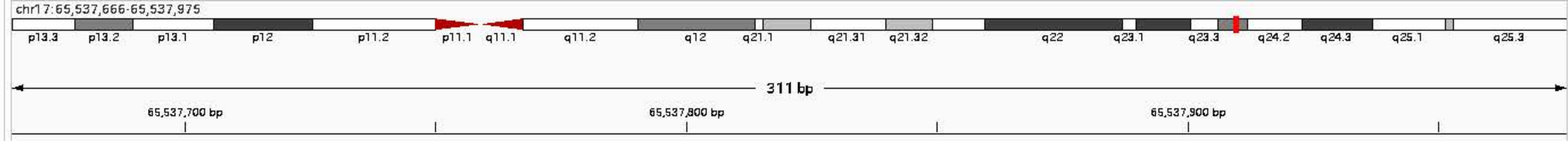
Sequence →  
Refseq Genes

SSSAPAPPMRFPYSSSSSSSAAASSSSSSSSSSASPFPA SQALPSYPHSFPPTSLSVSNQPPKYTQP SLPSQAVWSQGPPPPPYGRL LANSNAHPGPFPS

ATN1

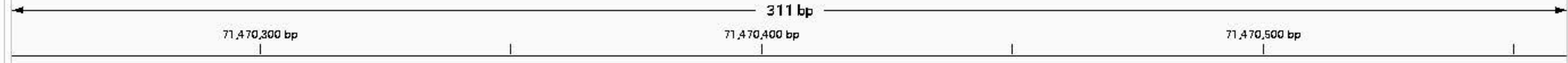






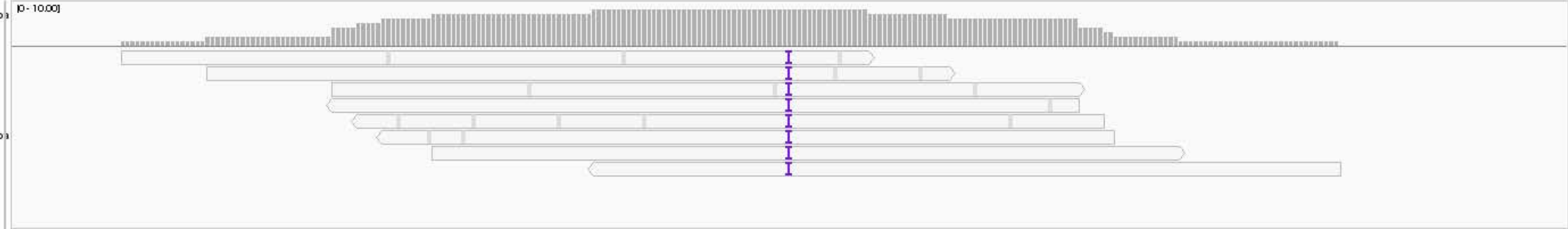
chr5: 71,470,251-71,470,560

p15.32 p15.2 p14.3 p14.1 p13.2 p12 q11.1 q11.2 q12.1 q13.1 q13.3 q14.2 q14.3 q15 q21.1 q21.3 q22.2 q23.1 q23.2 q31.1 q31.3 q32 q33.2 q34 q35.1 q35.3



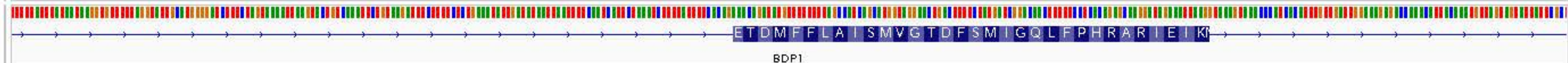
SL\_0015\_LN\_44\_WES\_uniq\_mut. coverage

SL\_0015\_LN\_44\_WES\_uniq\_mut.

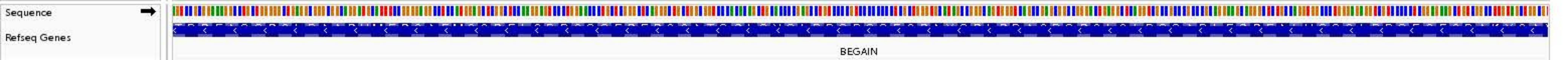
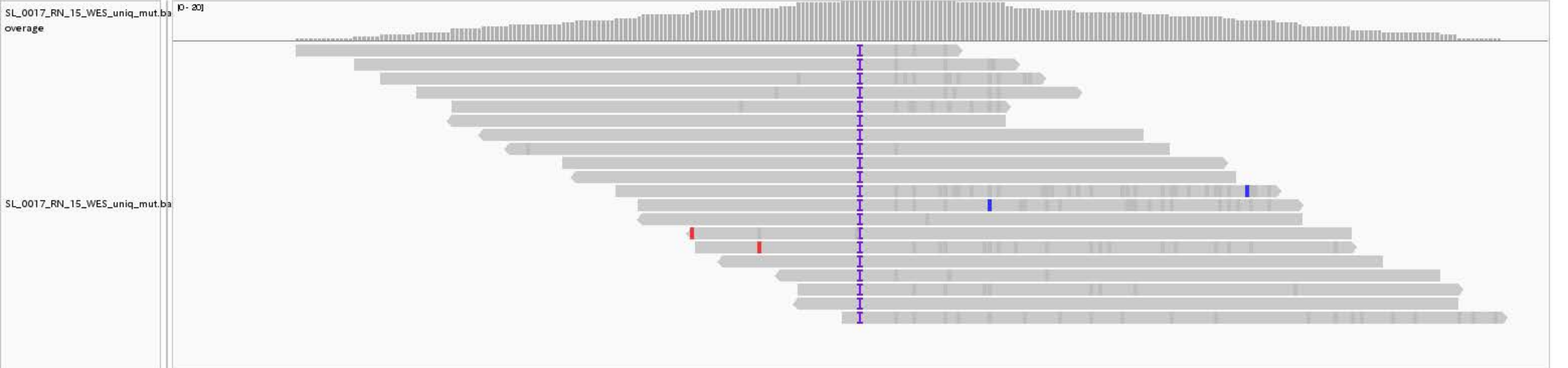
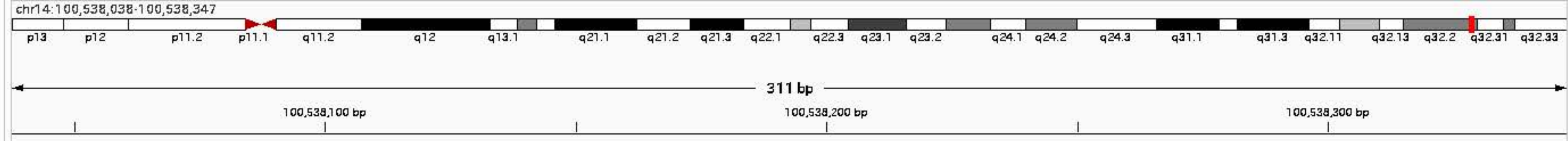


Sequence

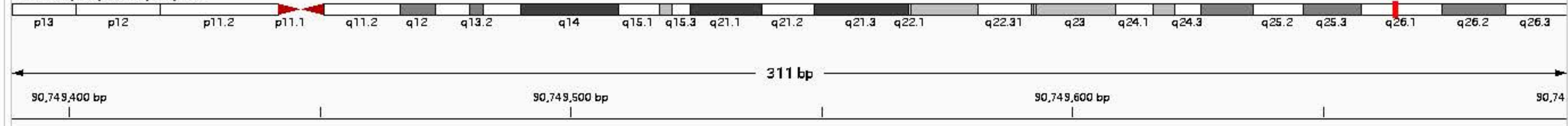
Refseq Genes



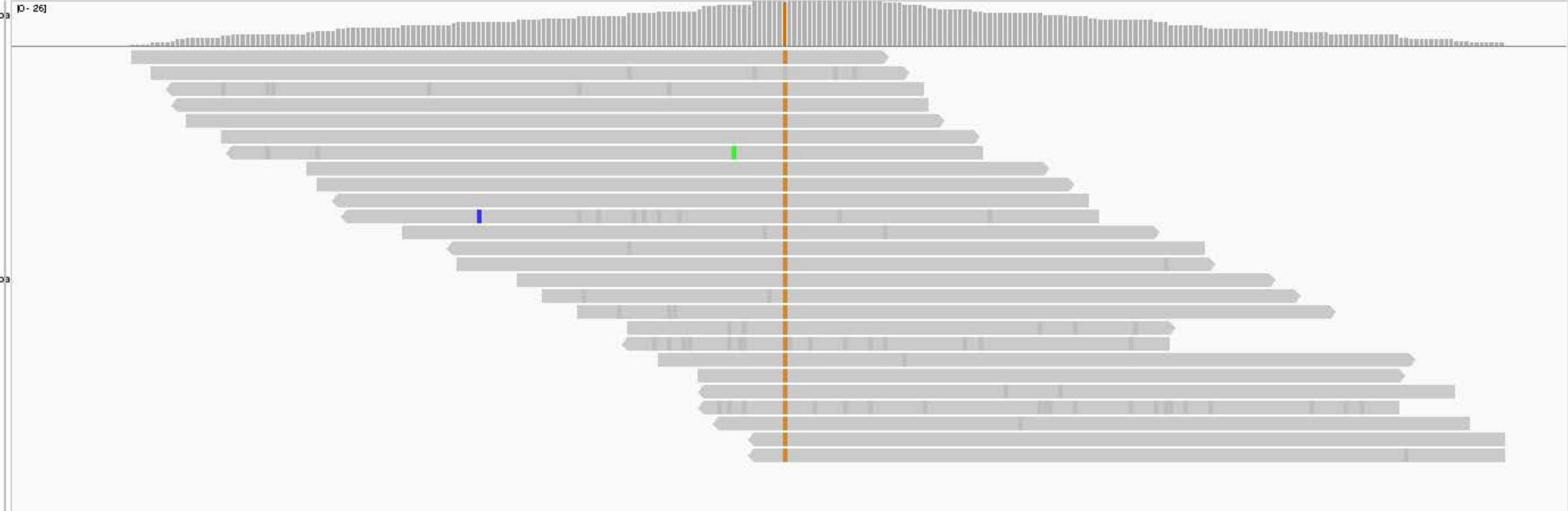




chr15:90,749,389-90,749,698



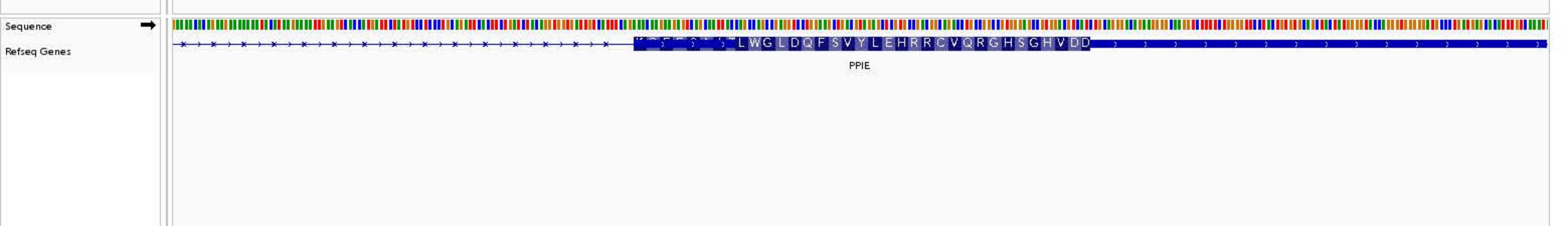
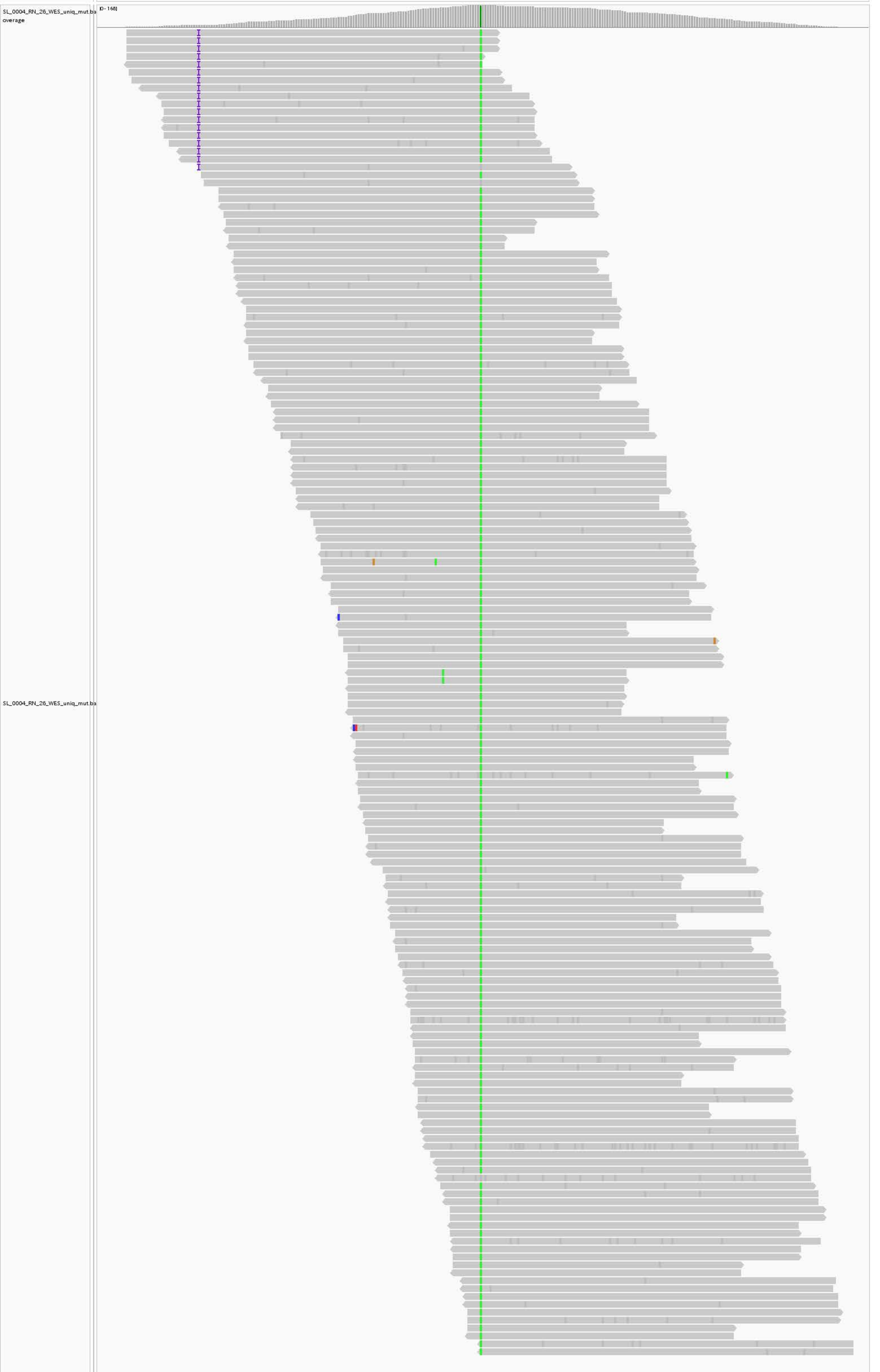
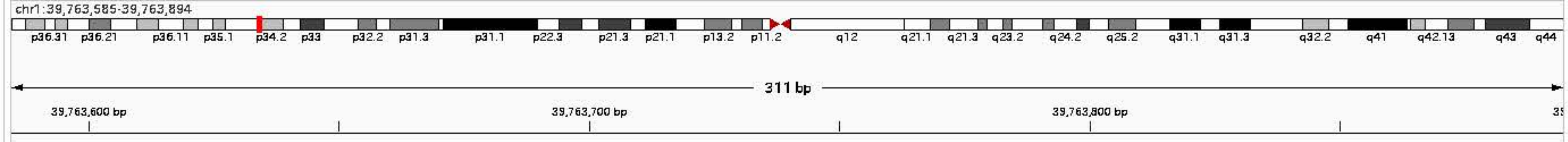
SL\_0001\_RN\_25\_WES\_uniq\_mut.ba  
coverage



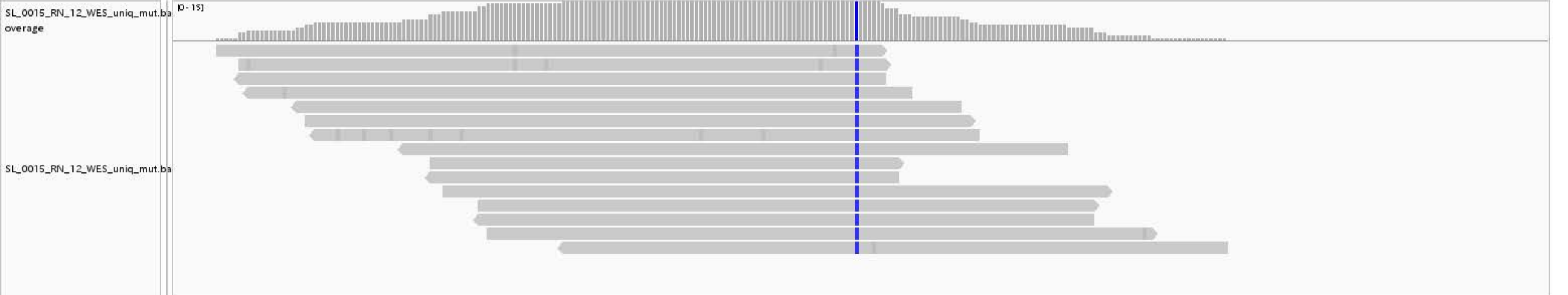
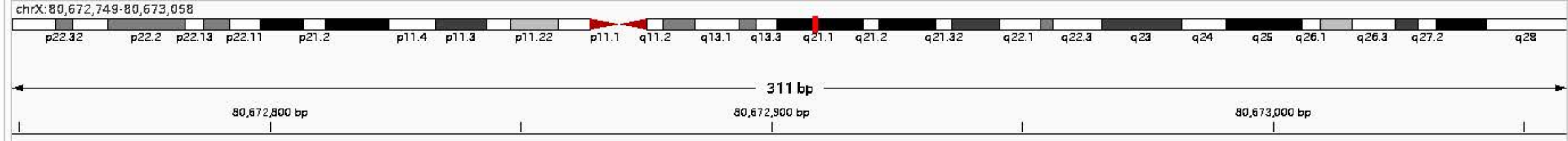
Sequence →  
Refseq Genes

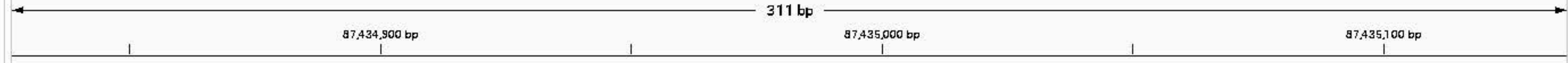
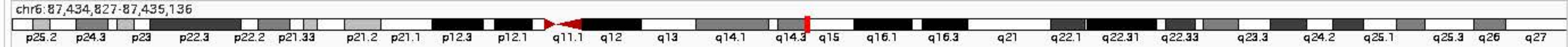
TSSDNNVSVTNVSVAKTPVLRNKDYNVTEDFSFSEPLPNTTNQQRVKDFFKNAPAGQETQRGGSKSLLPDFLQTPKEVVCTTQNTPTVKKSRDTALKKLEFSS  
BLM

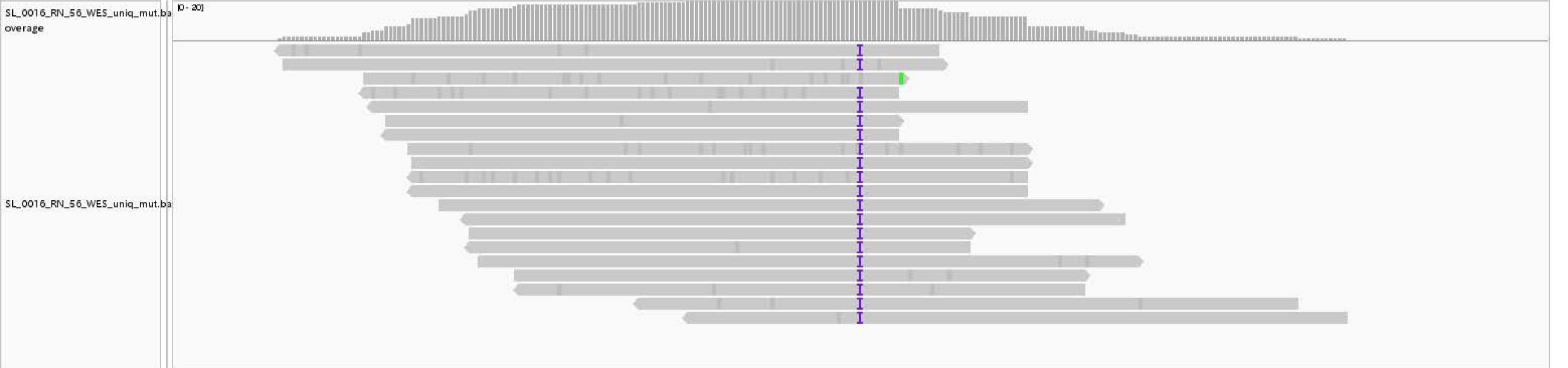
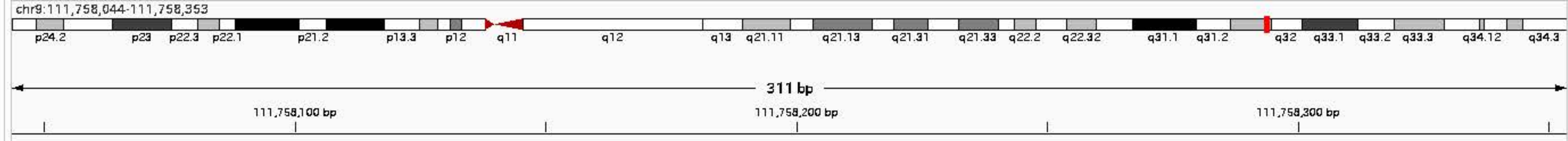




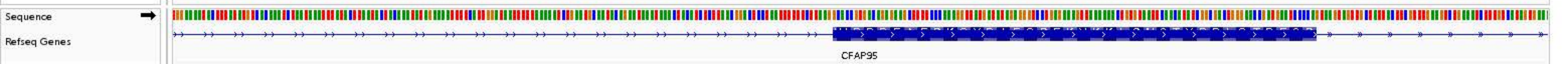
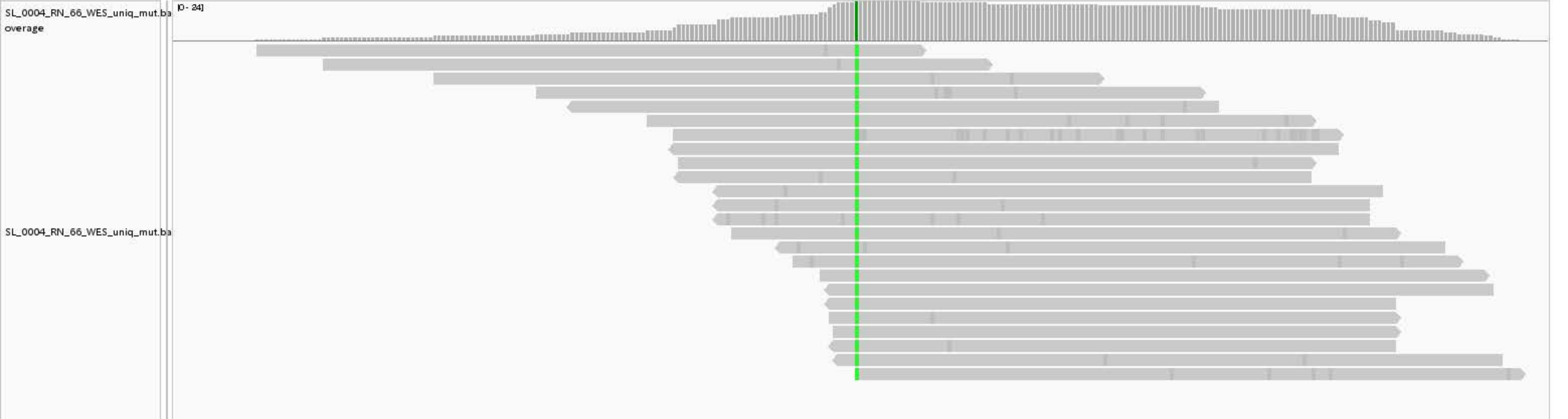
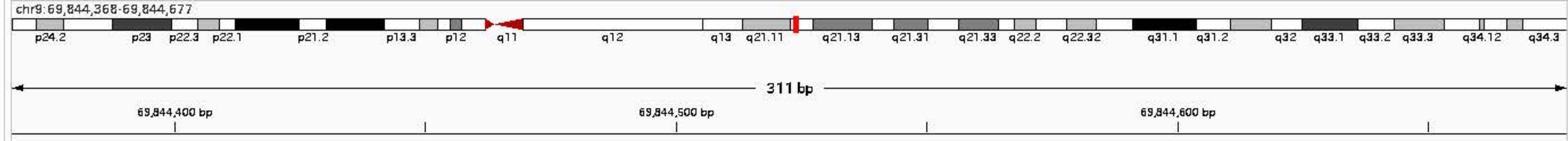


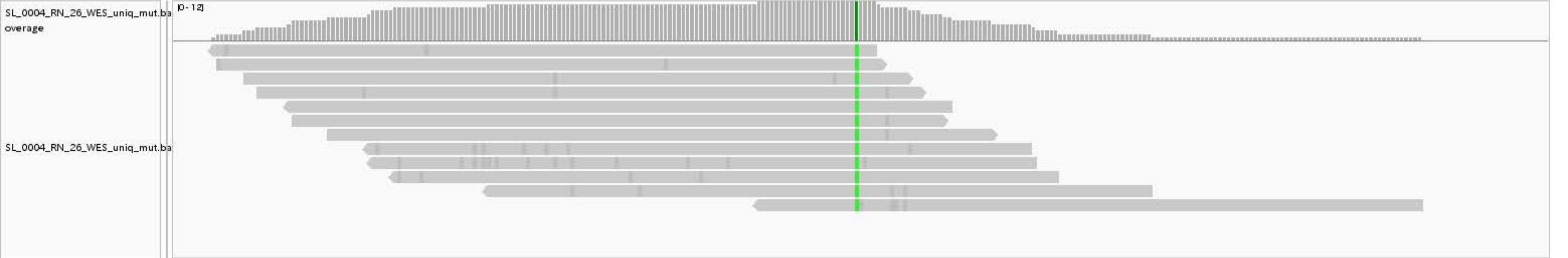
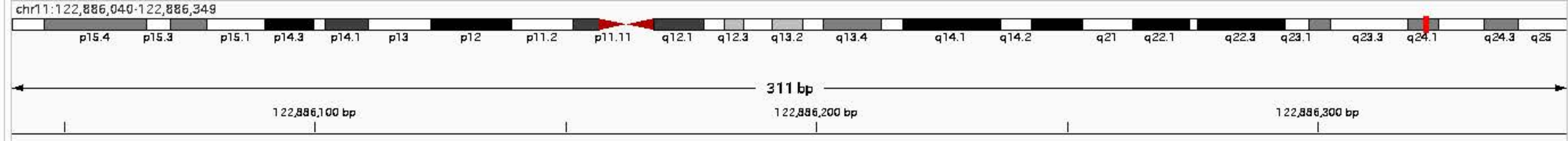


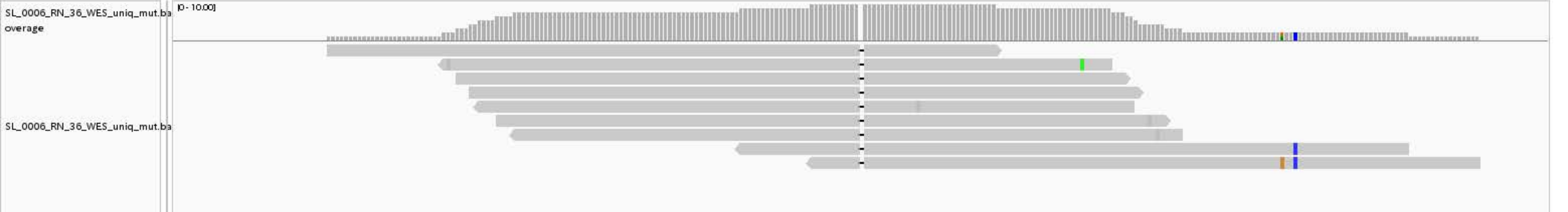
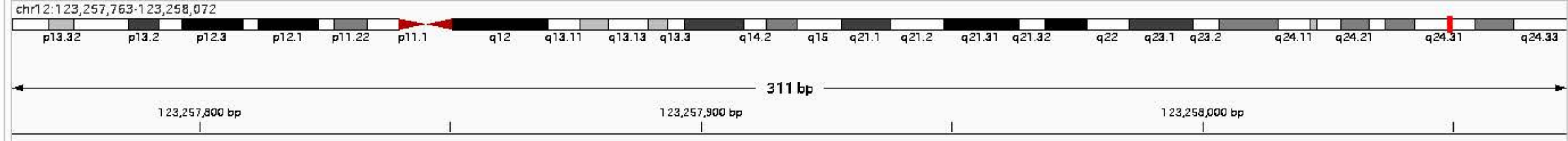




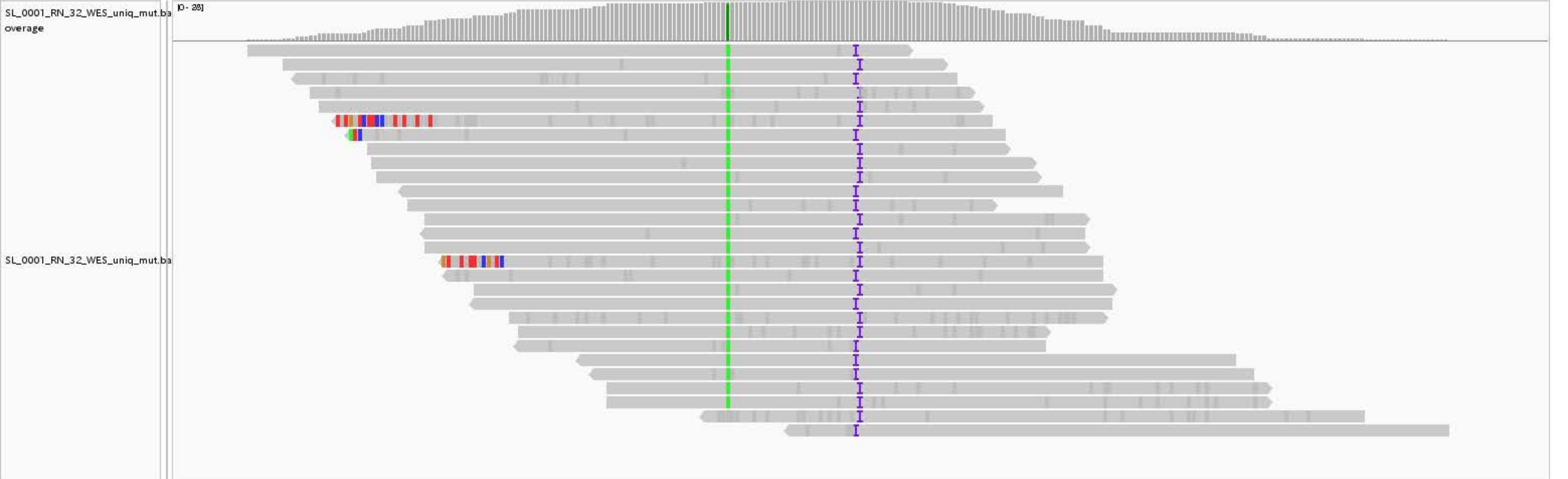
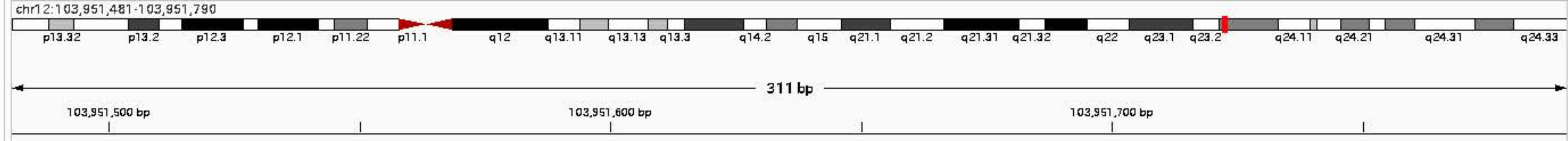


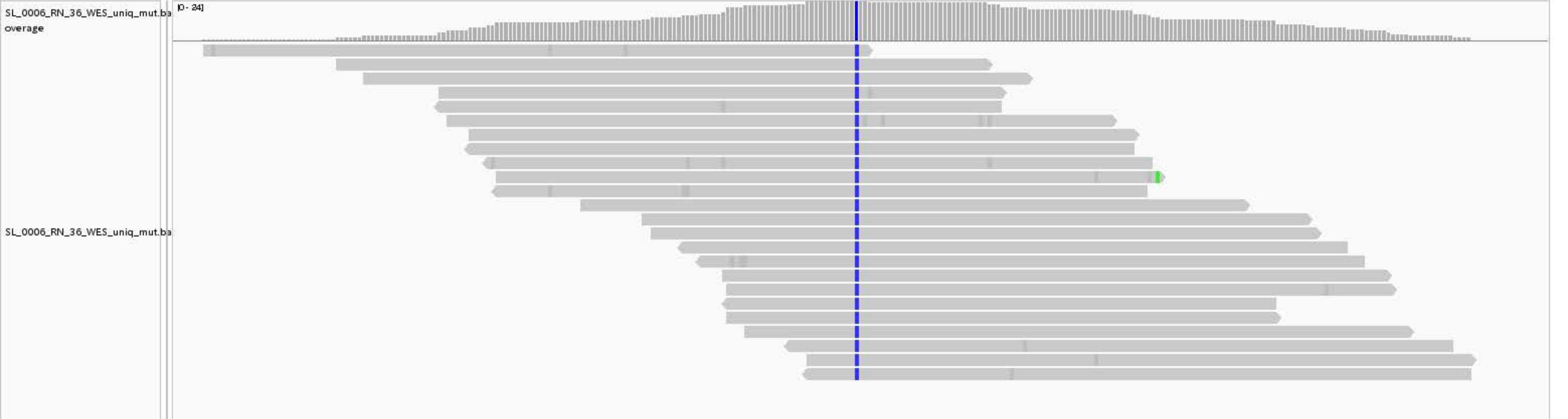
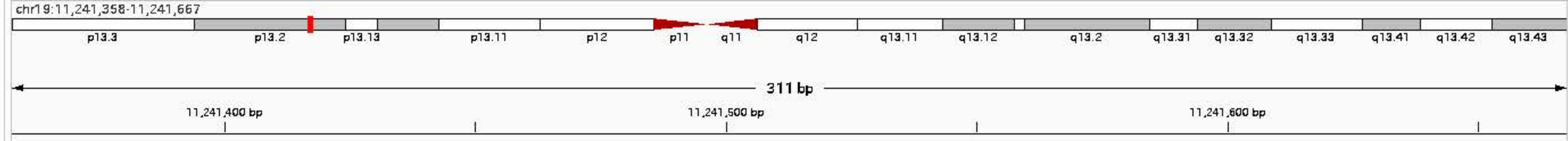


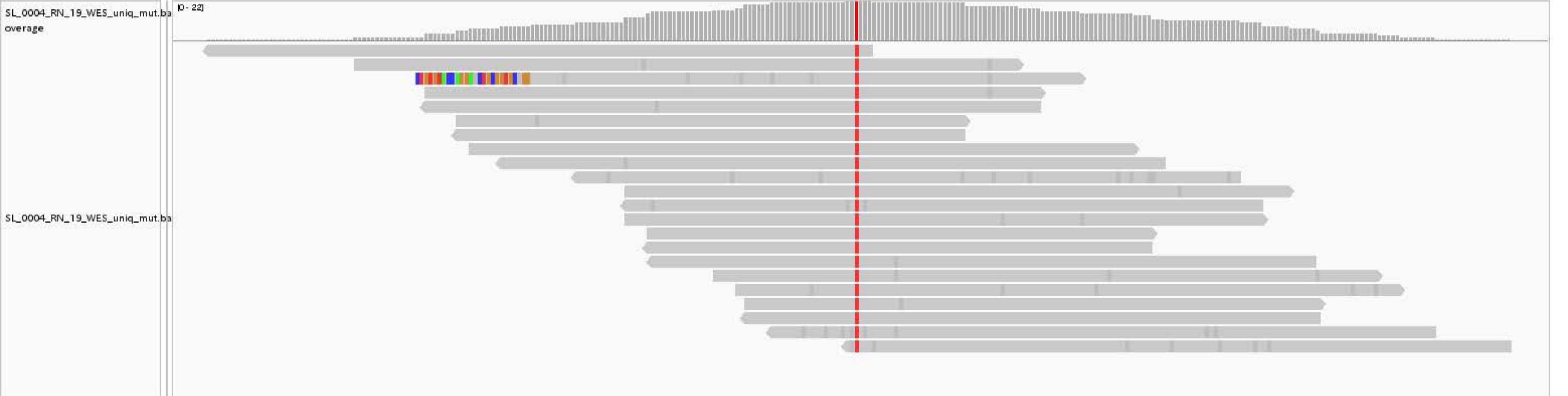
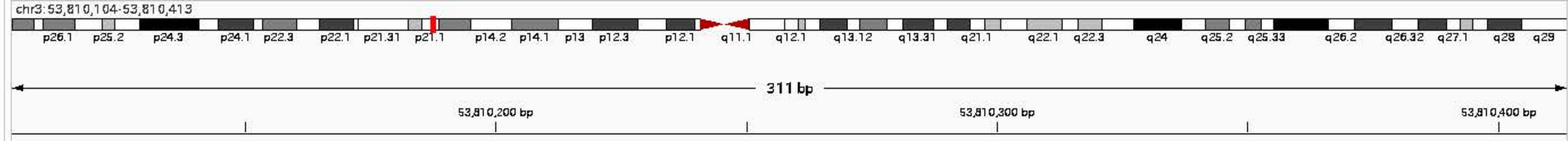






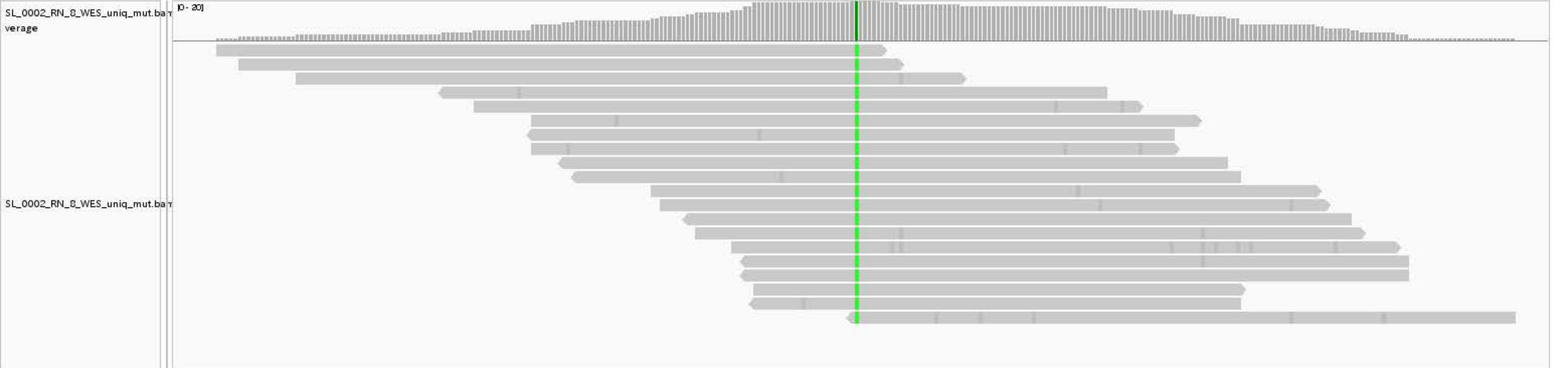
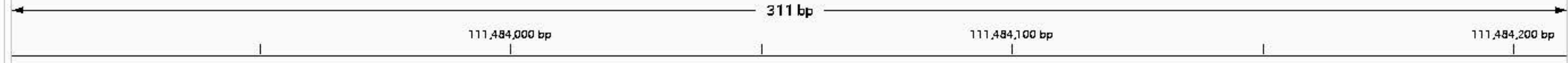
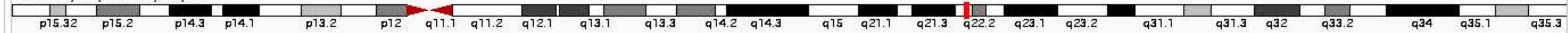






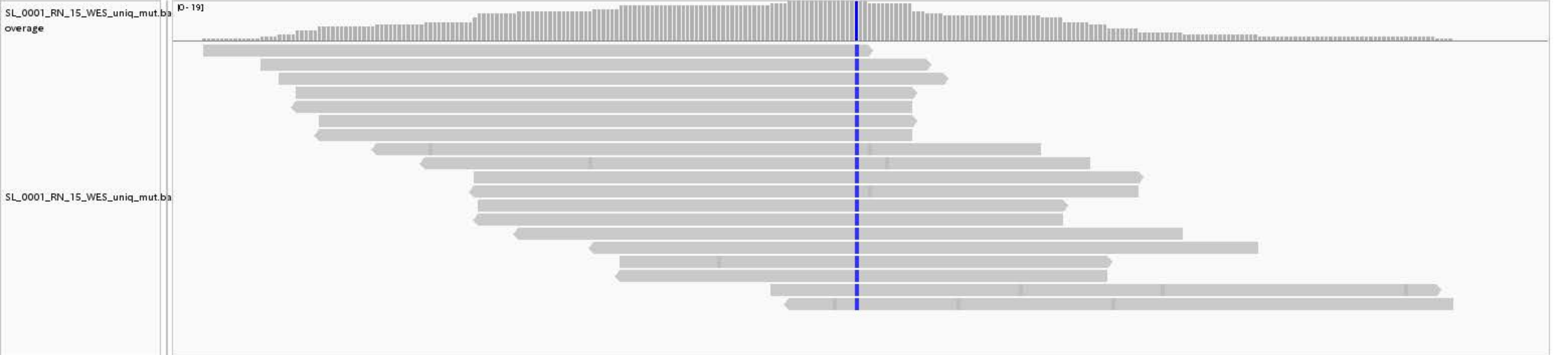
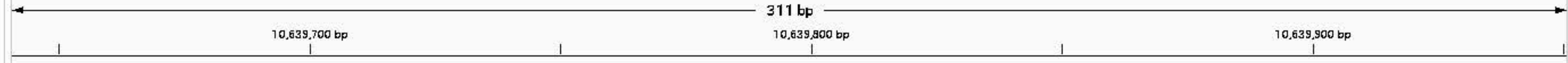


chr5:111,483,901-111,484,210



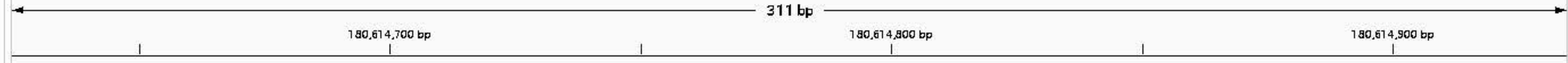
CAMK4

chr1:10,639,641-10,639,950  
p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44

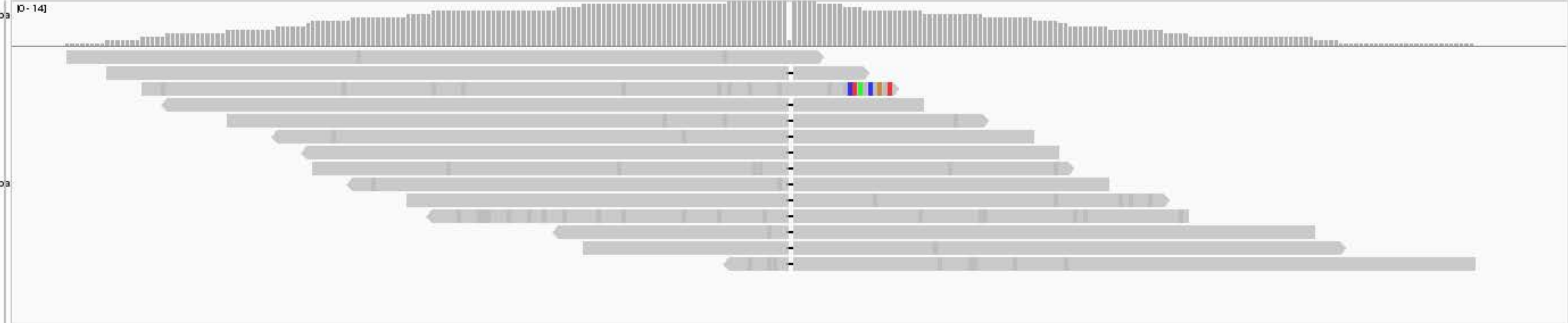


Sequence →  
Refseq Genes  
SDTCRFRRCRLCHFHTSTGSPFCDAFHCSLSAKFRKFDDLVLNDVRDHHQAHKYMHTRGCFKYGCNERTCHYHTVKLSFQCAADKCD EYLD FRRRFGELMMGEDL  
CASZ1

chr3:180,614,625-180,614,934  
p26.1 p25.2 p24.3 p24.1 p22.3 p22.1 p21.31 p21.1 p14.2 p14.1 p13 p12.3 p12.1 q11.1 q12.1 q13.12 q13.31 q21.1 q22.1 q22.3 q24 q25.2 q25.33 q26.2 q26.32 q27.1 q28 q29



SL\_0017\_RN\_15\_WES\_uniq\_mut.ba  
overage



SL\_0017\_RN\_15\_WES\_uniq\_mut.ba

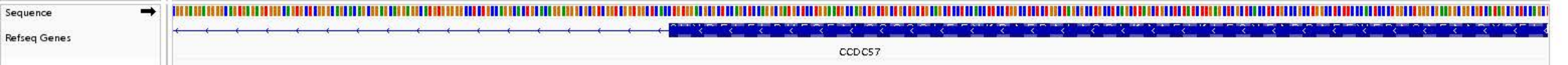
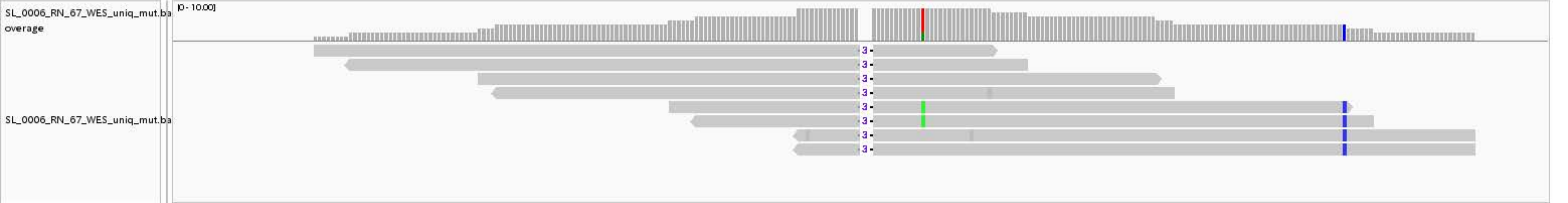
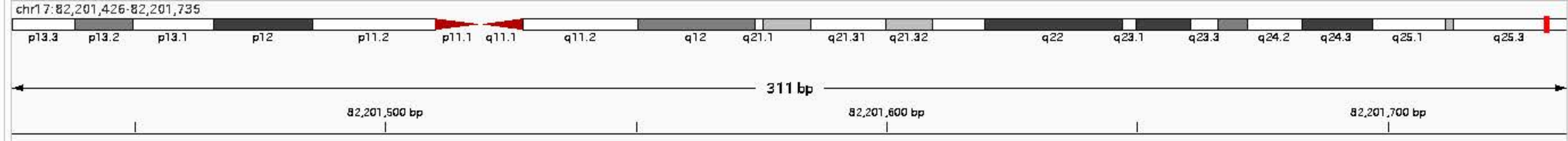
Sequence

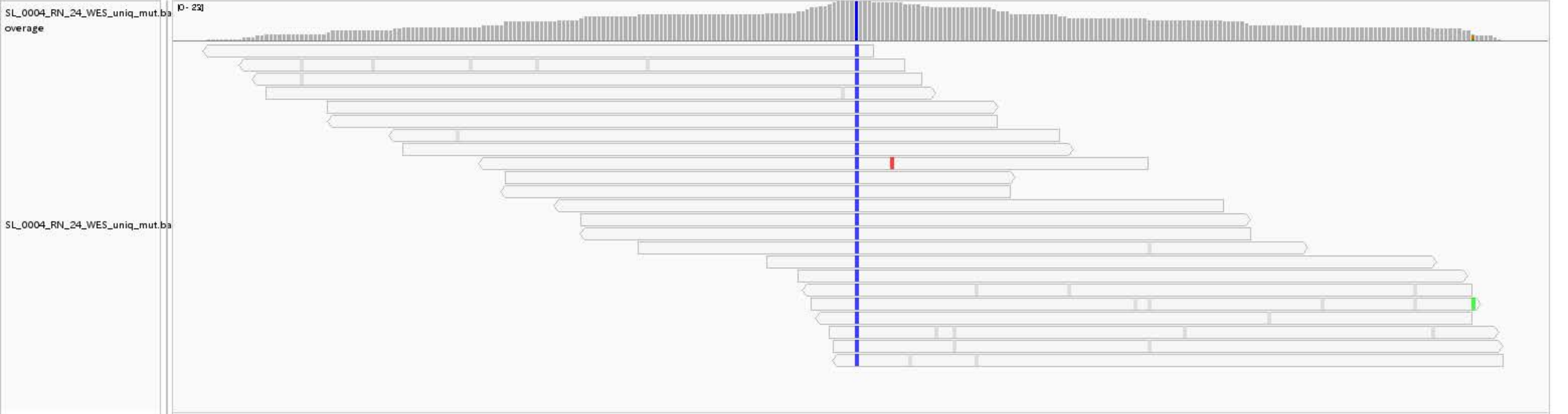
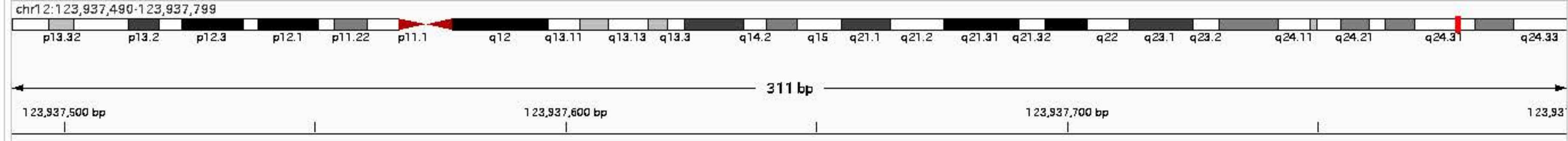
Refseq Genes



TTC14





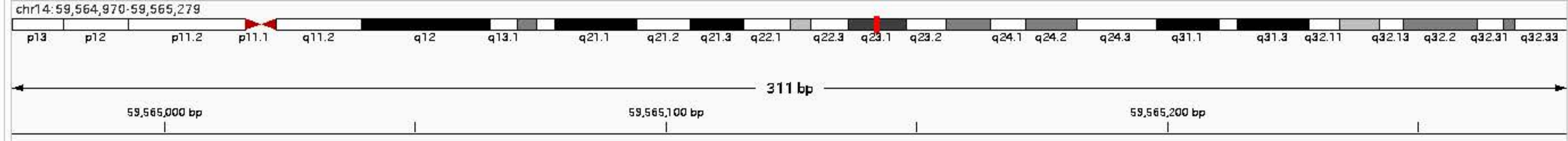


Sequence →

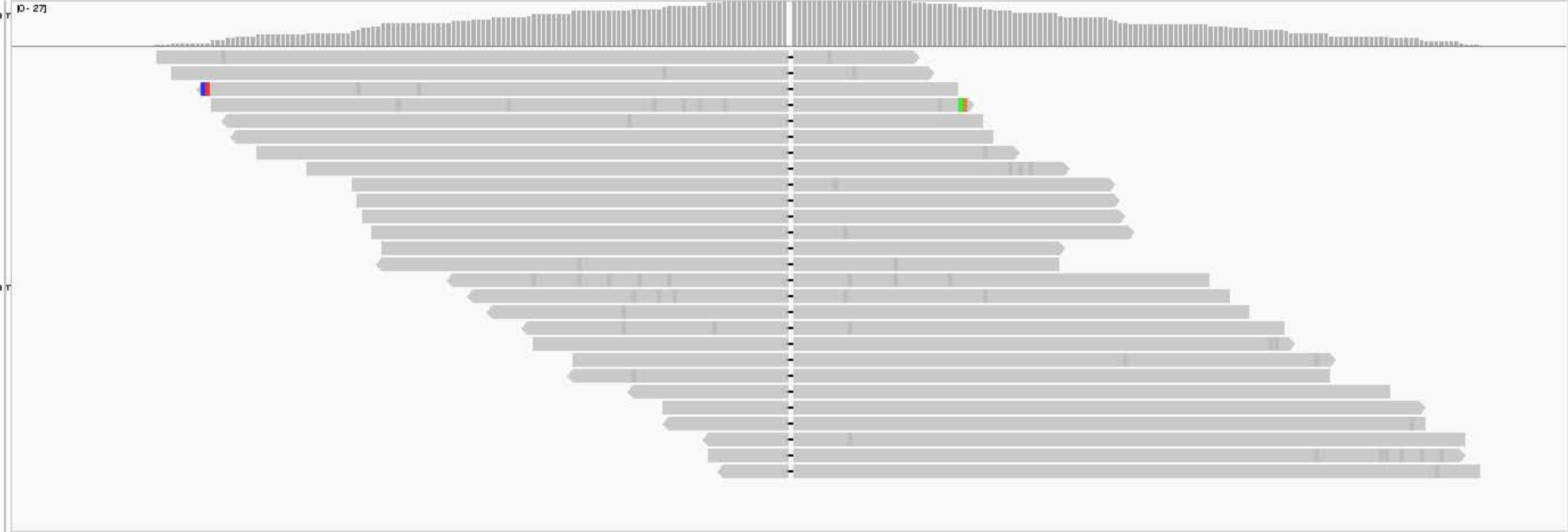
Refseq Genes

SALVPSGSPSADSTGSSSMLKKKAHLQSTLYAITSARQELESSLLTLKHSKAKLEELYKKEREKITNELVTIMANKQELEKLLLEANENEKVKLQAELEECRK

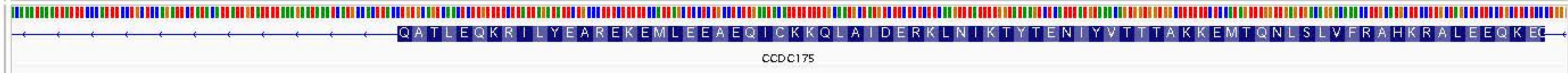
CCDC92



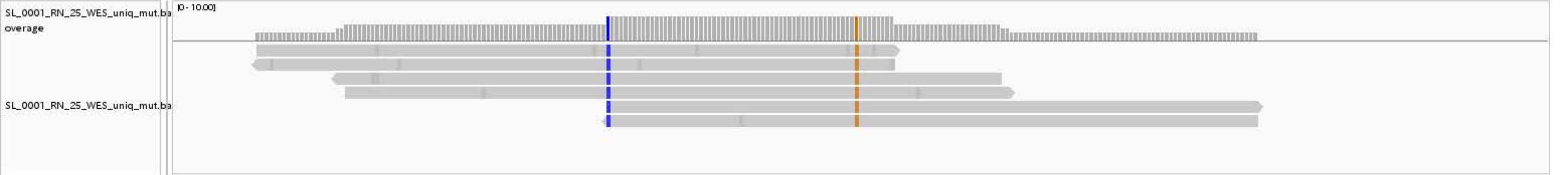
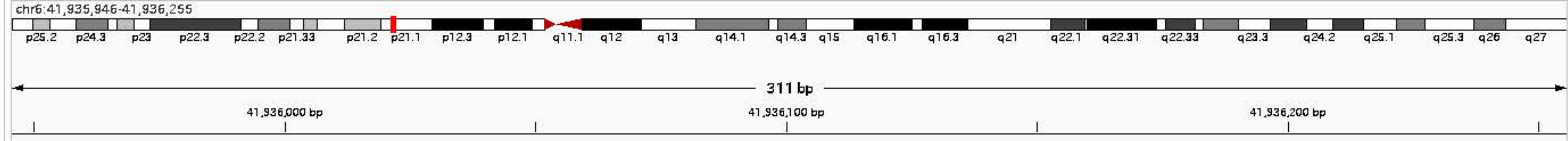
SL\_0001\_LN\_4\_WES\_uniq\_mut.ba  
verage



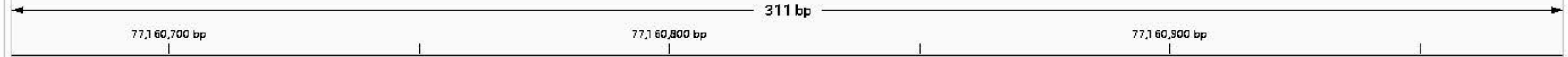
Sequence →  
Refseq Genes



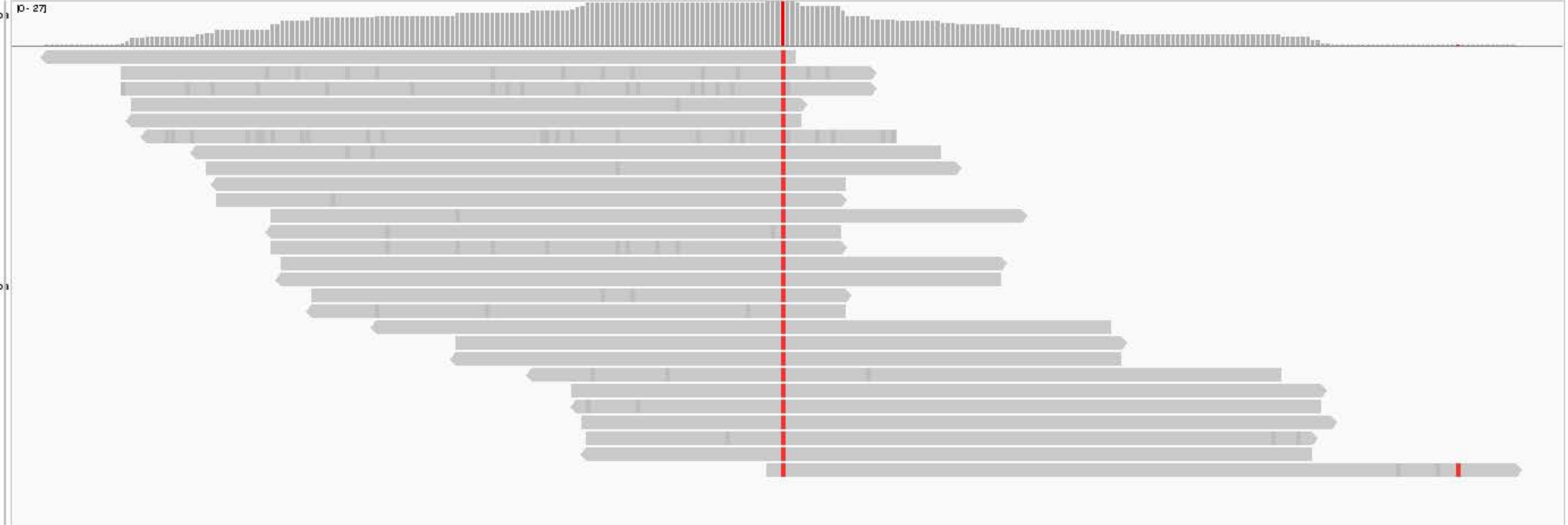




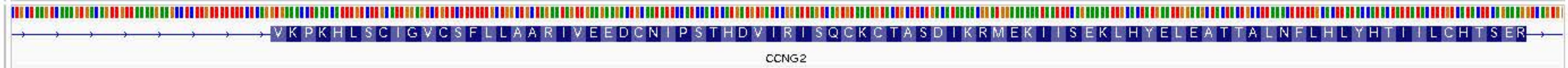
chr4: 77,160,669-77,160,978  
p16.2 p15.33 p15.31 p15.1 p14 p13 p11 q12 q13.1 q13.2 q21.1 q21.22 q22.1 q22.3 q24 q25 q26 q27 q28.2 q28.3 q31.1 q31.22 q32.1 q32.3 q34.1 q34.3 q35.2

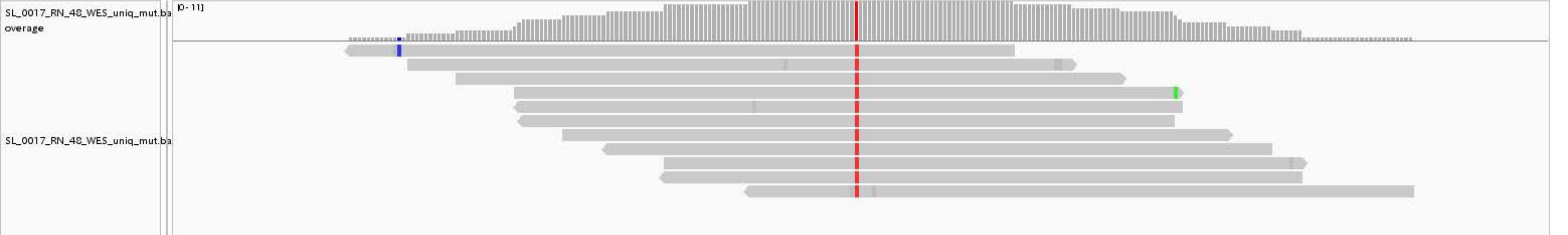
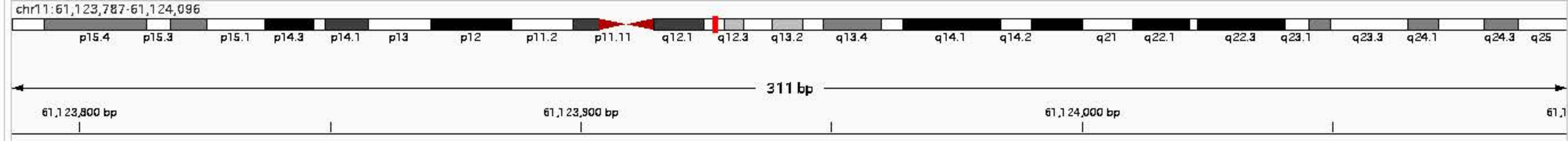


SL\_0003\_LN\_27\_WES\_uniq\_mut. coverage



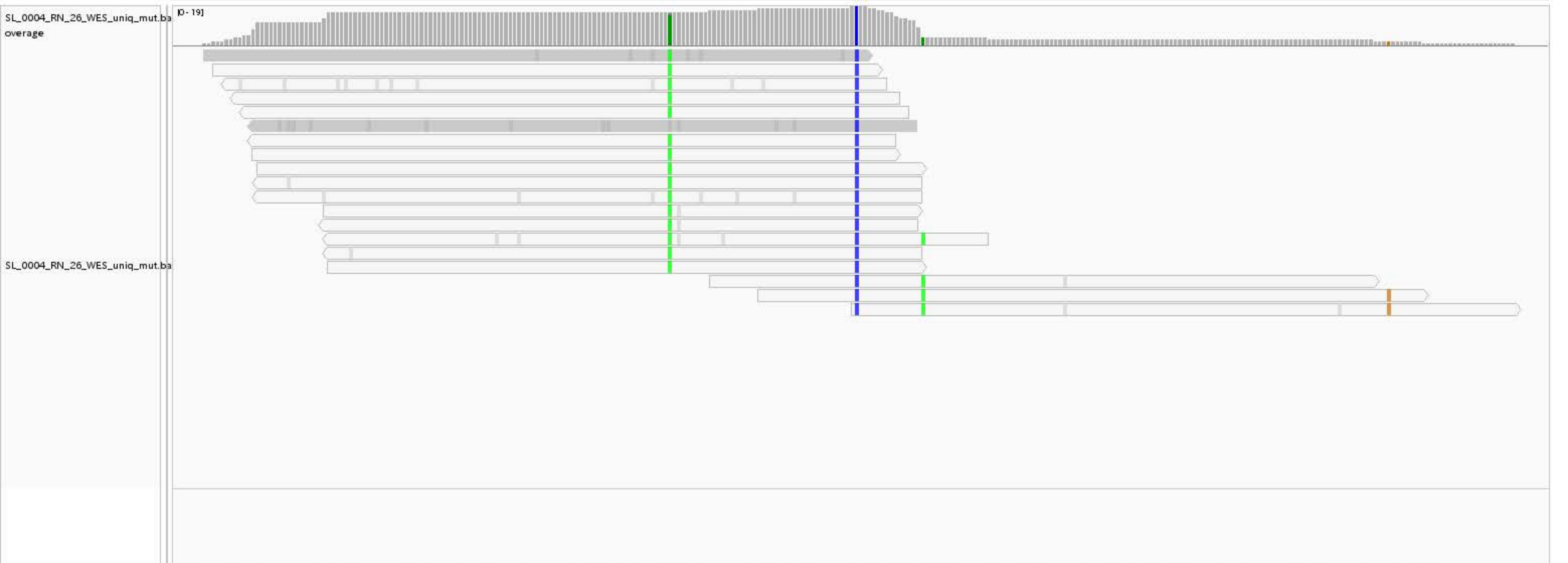
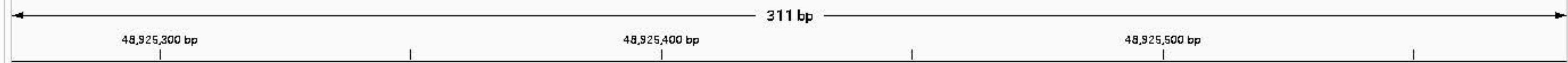
Sequence Refseq Genes



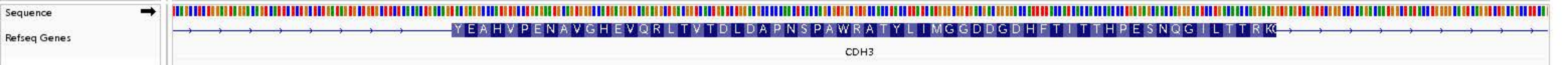
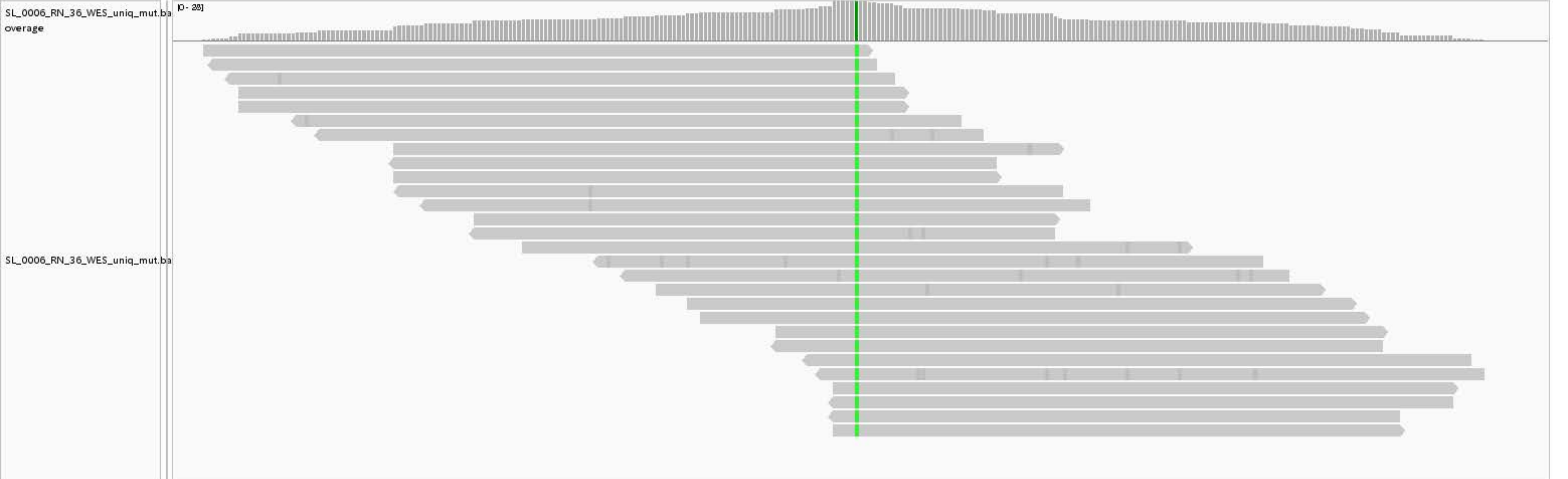
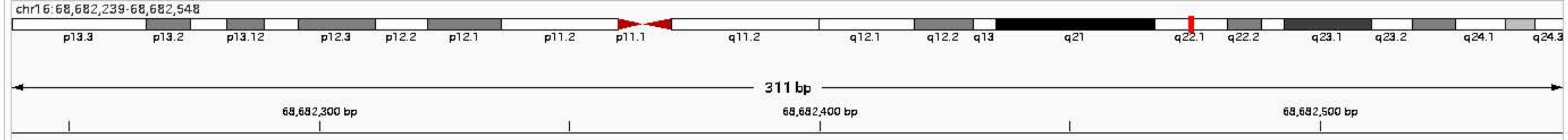




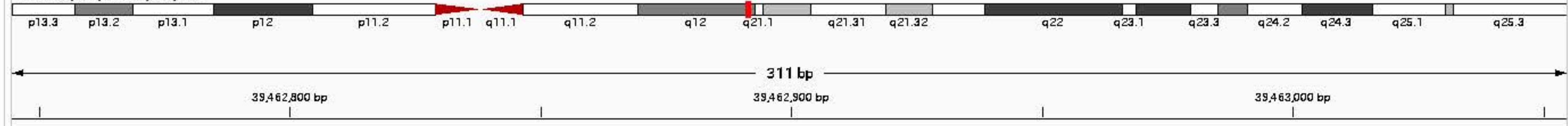
chr7:48,925,271-48,925,580  
p22.2 p21.3 p21.2 p15.3 p15.1 p14.2 p13 p12.2 p11.2 q11.1 q11.22 q11.23 q21.11 q21.12 q21.2 q22.1 q22.3 q31.1 q31.2 q31.32 q32.1 q33 q34 q35 q36.1 q36.3



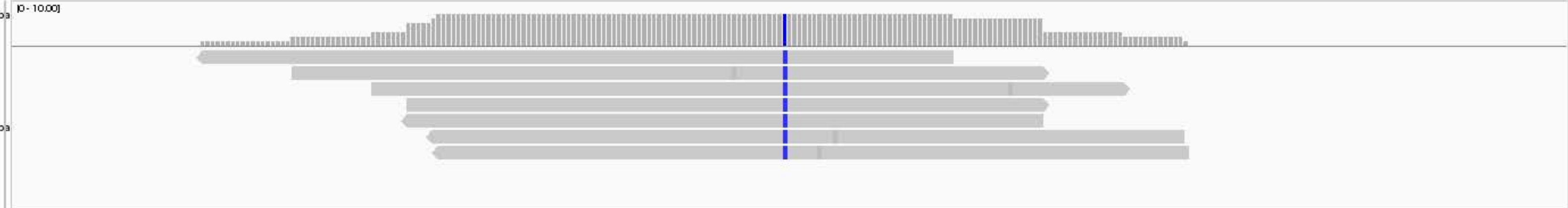
Sequence →  
Refseq Genes  
PHSRARLESGYHQHSPETYIQYFKNHNVTTIIRLNKRMYDAKRFTDAGFDHDLFFADGSTPTDAIVKRFLDICENAEGAIAVHCKAGLGRGTGLIACYIMKHY  
CDC14C



chr17:39,462,745-39,463,054



SL\_0006\_RN\_67\_WES\_uniq\_mut.ba  
coverage



SL\_0006\_RN\_67\_WES\_uniq\_mut.ba

Sequence

Refseq Genes

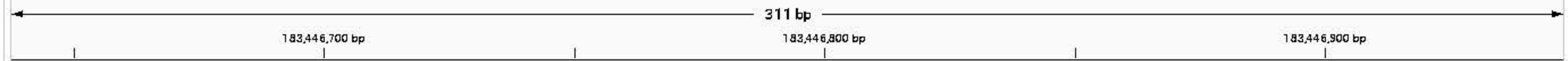
Sequence: RKWSDSSKQDDSPSGASYGQDYDLSPSRSHHTSSNYDSYKKSPGSTSRRQSVSPPYKEPSAYQSSTRSPSPYSRRQRSVSPYSRRRSSSYERSGSYSGRSPSPYC

CDK12

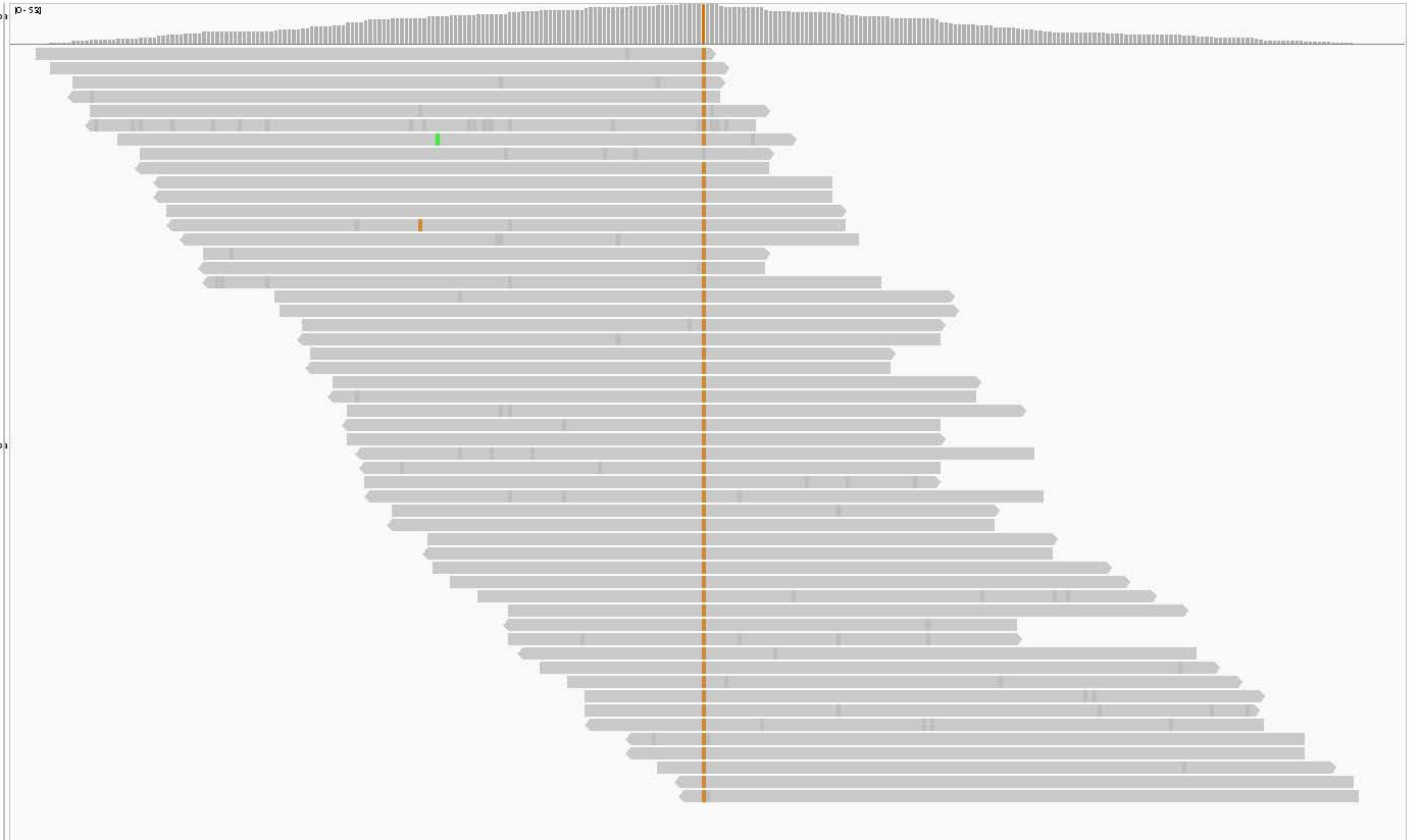


chr4:183,446,638-183,446,947

p16.2 p15.33 p15.31 p15.1 p14 p13 p11 q12 q13.1 q13.2 q21.1 q21.22 q22.1 q22.3 q24 q25 q26 q27 q28.2 q28.3 q31.1 q31.22 q32.1 q32.3 q34.1 q34.3 q35.2



SL\_0015\_LN\_39\_WES\_uniq\_mut. coverage

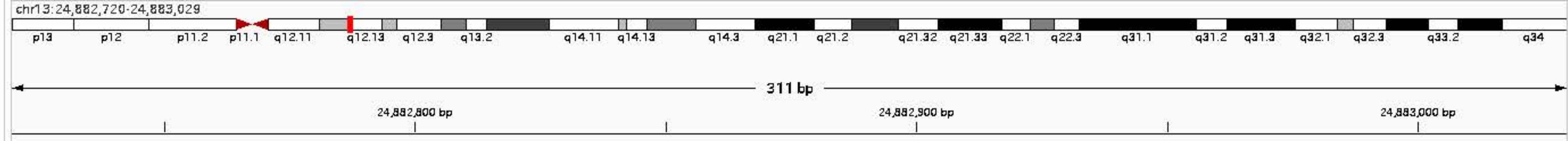


SL\_0015\_LN\_39\_WES\_uniq\_mut.

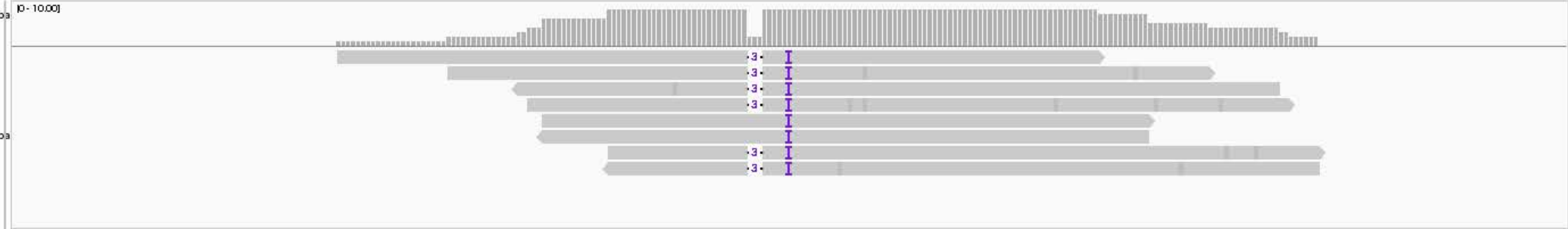
Sequence Refseq Genes

L T S K T S S E A S V S S S V A K N S S S S G T S L L T P K S S S S T N T S L L T S K S T S Q V A A S L L A S K S S S Q T S G S L V S K S T S L A S V S Q L A S K S S S Q T S T S Q L P S K S T S Q S S E S S

CDKN2AIP



SL\_0006\_RN\_36\_WES\_uniq\_mut.ba  
coverage



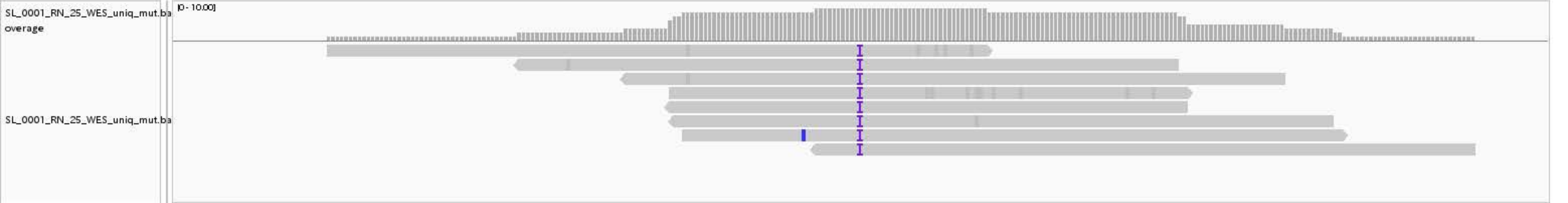
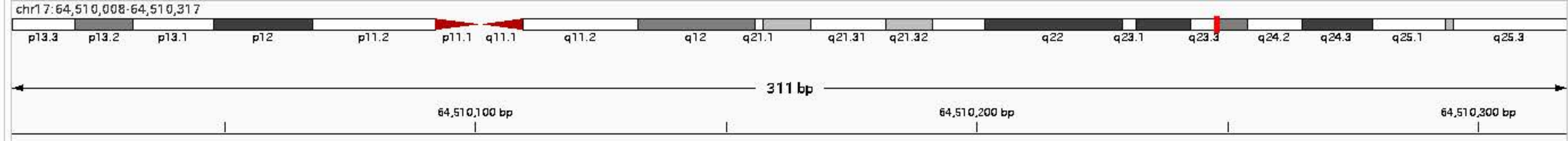
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Sequence →

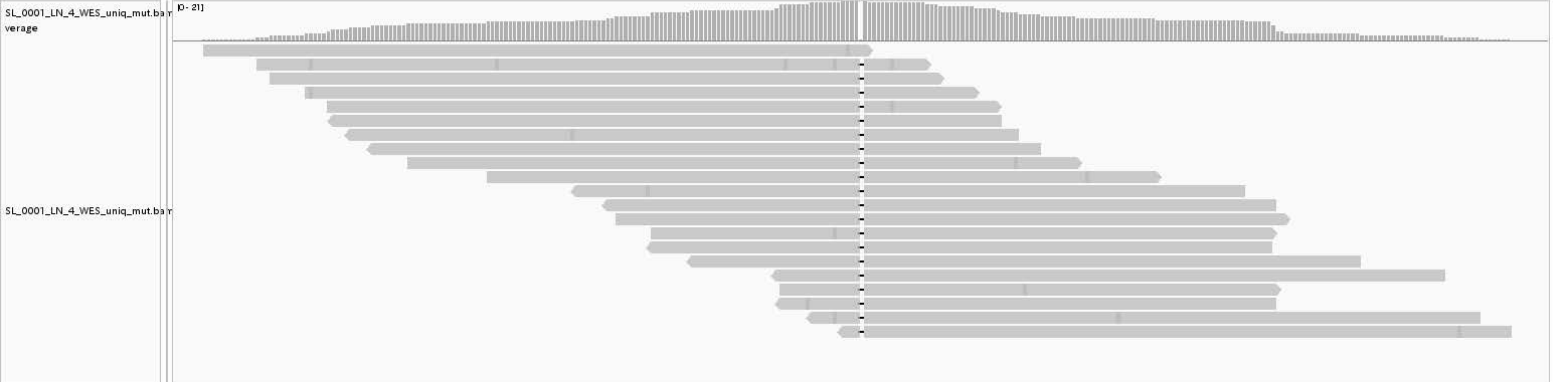
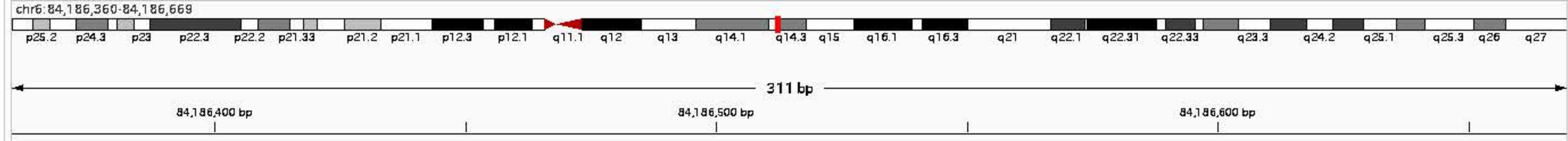


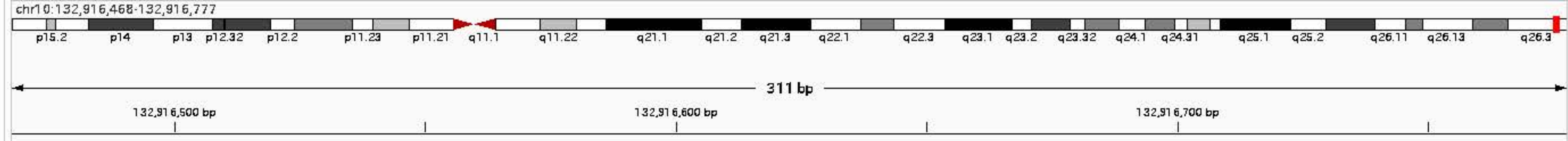
Refseq Genes

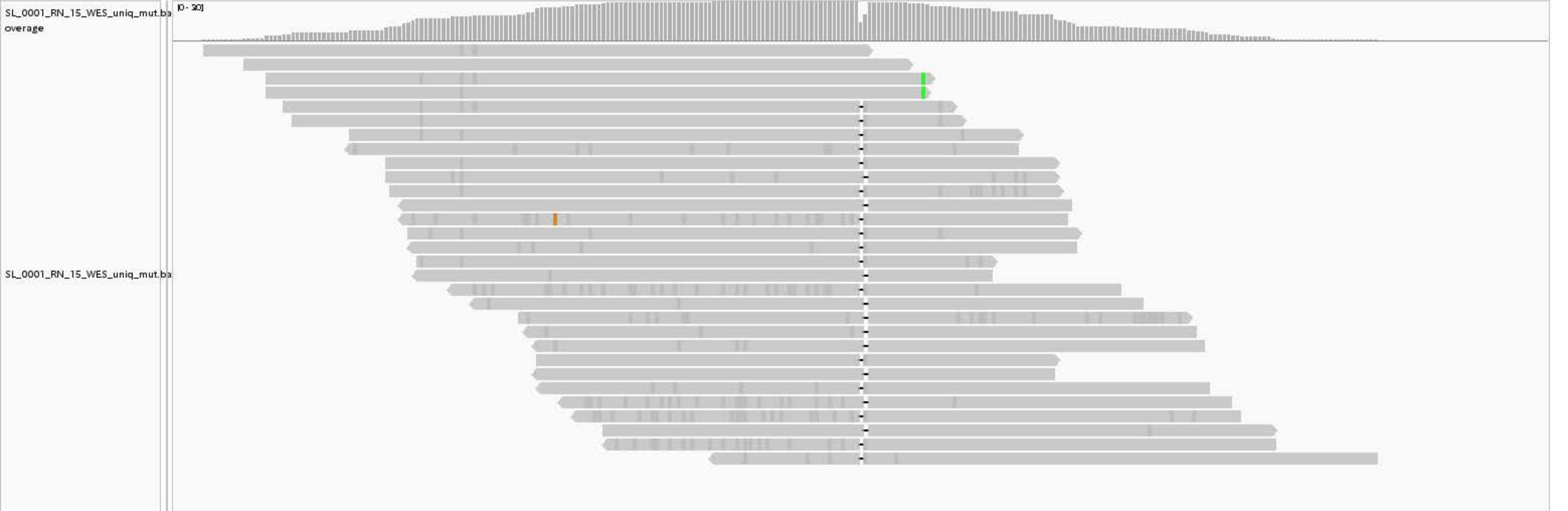
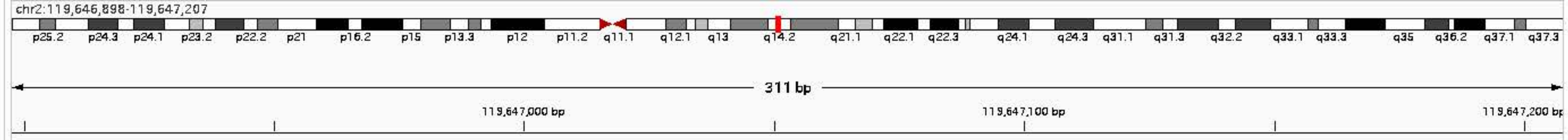
RNF17





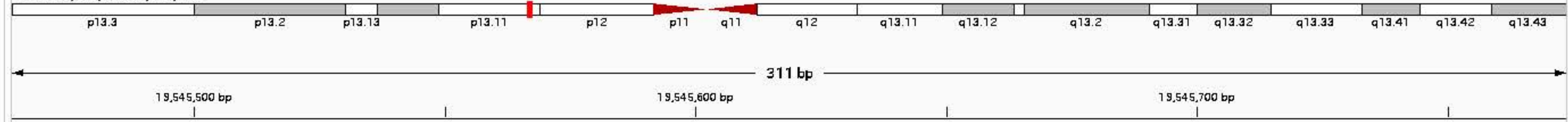




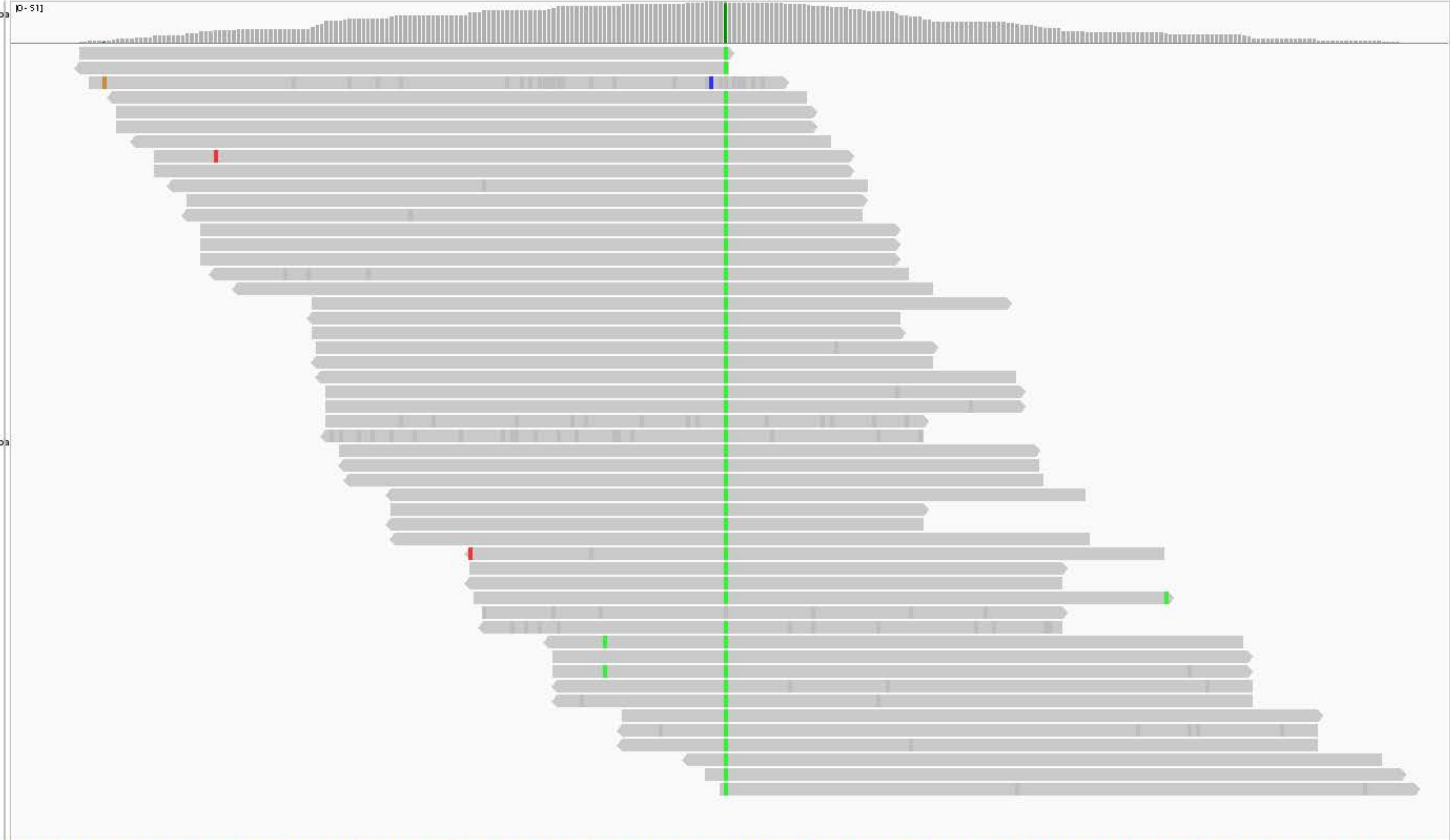




chr19:19,545,464-19,545,773



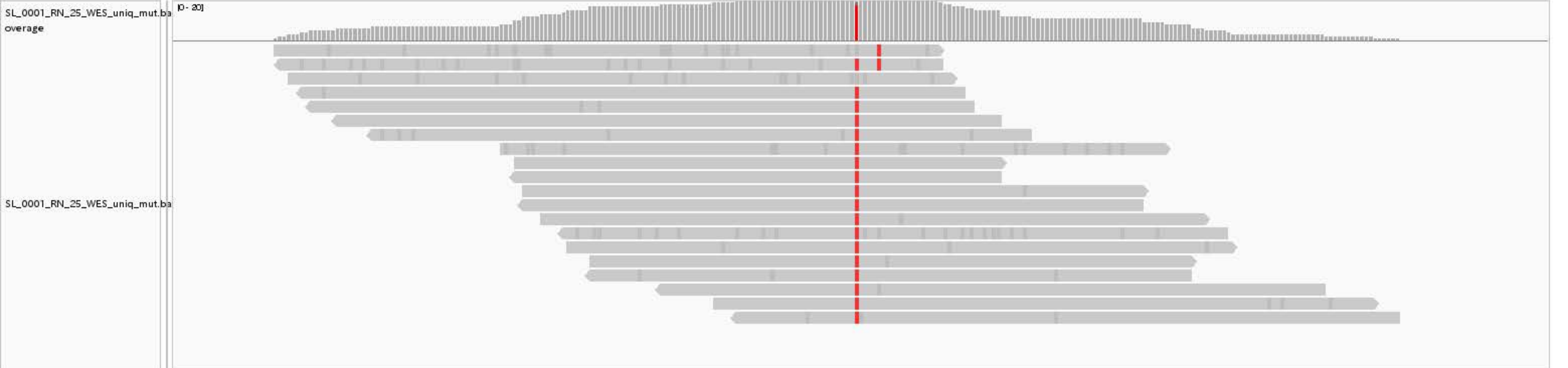
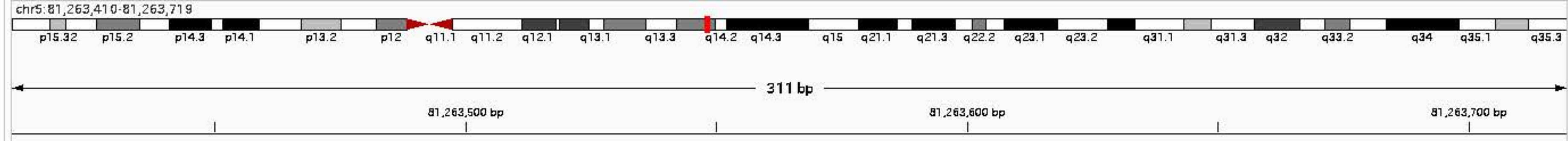
SL\_0001\_RN\_37\_WES\_uniq\_mut.ba  
coverage

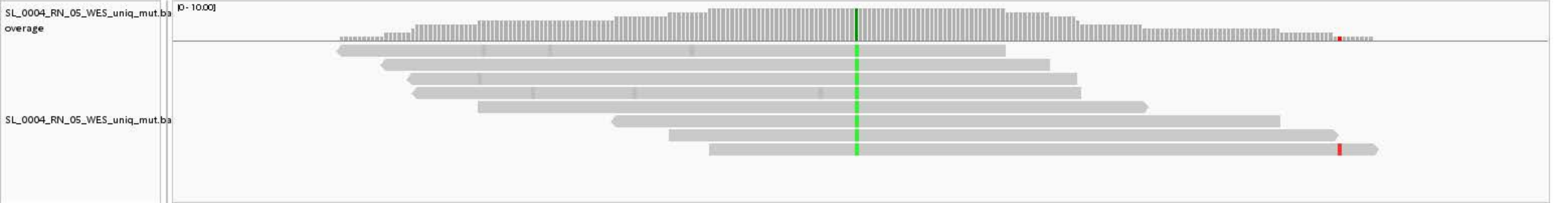
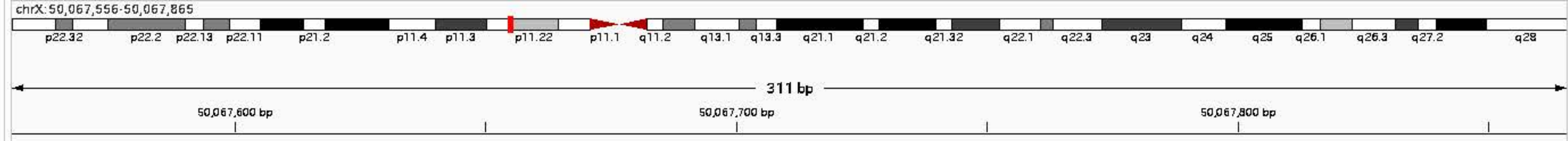


SL\_0001\_RN\_37\_WES\_uniq\_mut.ba

Sequence →  
Refseq Genes

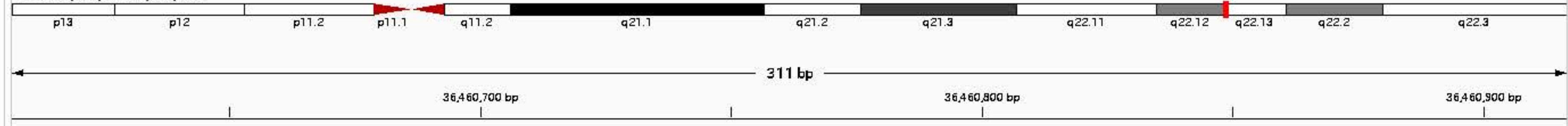
DARSVRDPERPGTSAACVEFKCSGMLFDQRQVDRTLVTIMPQGSCRRVAVNGLLRDYLTRHPPPVAEDPAAFMSMLAPLDPLGHNYGVYTVTQDSPRLAKEIA  
CILP2



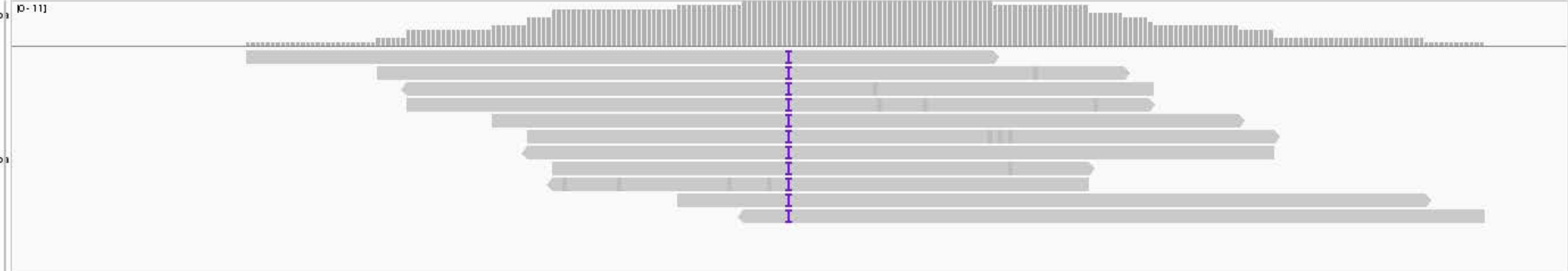




chr21:36,460,607-36,460,916



SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage



SL\_0015\_LN\_46\_WES\_uniq\_mut.

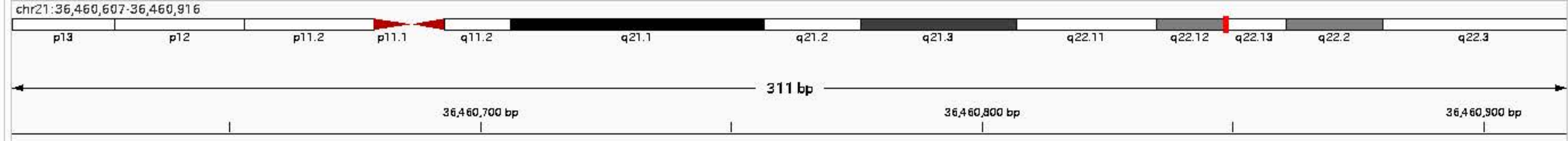
Sequence



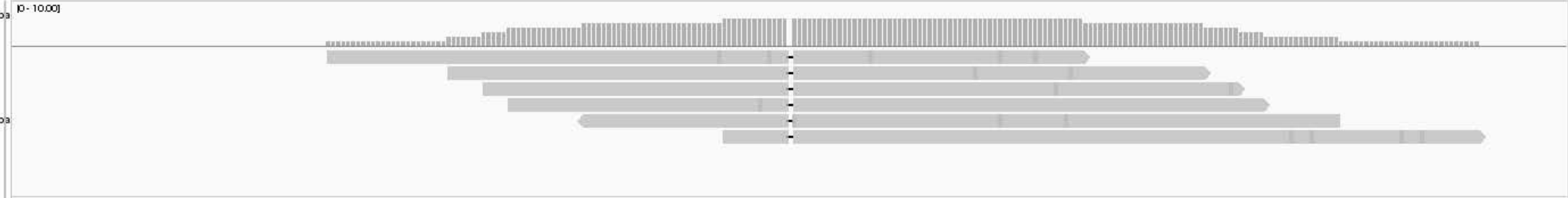
Refseq Genes



CLDN14-AS1



SL\_0015\_RN\_21\_WES\_uniq\_mut.ba  
coverage



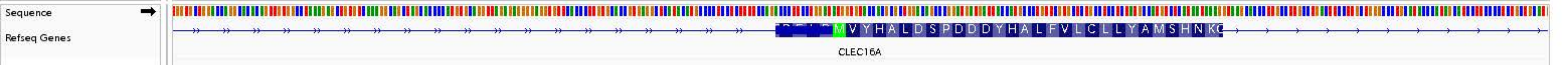
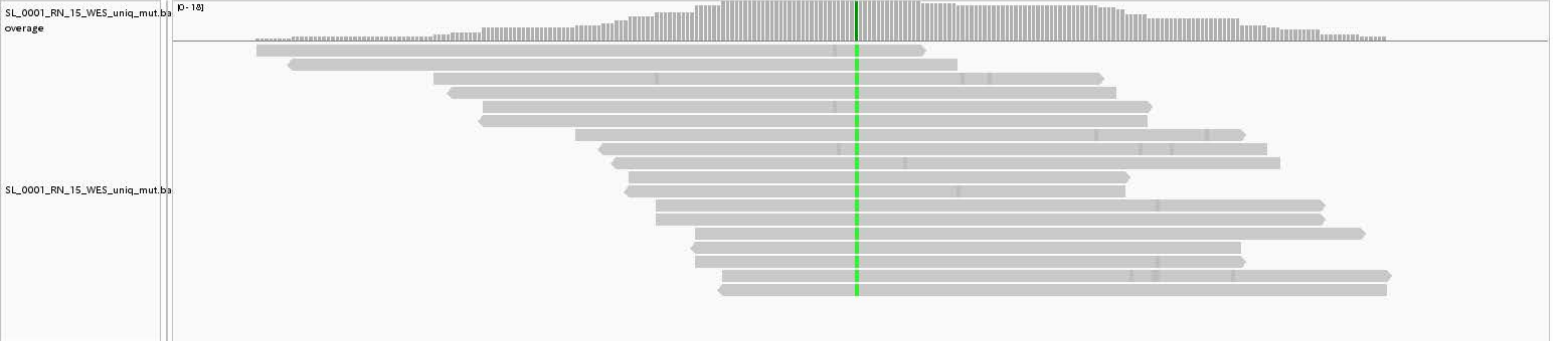
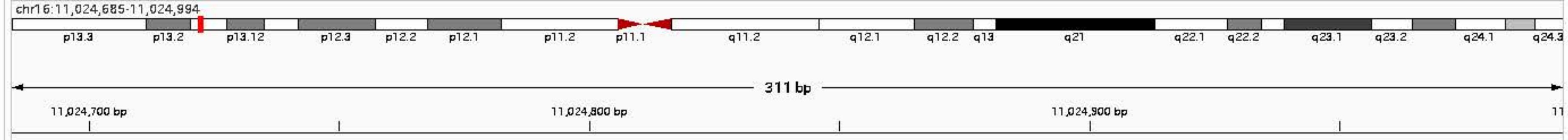
SL\_0015\_RN\_21\_WES\_uniq\_mut.ba

Sequence →

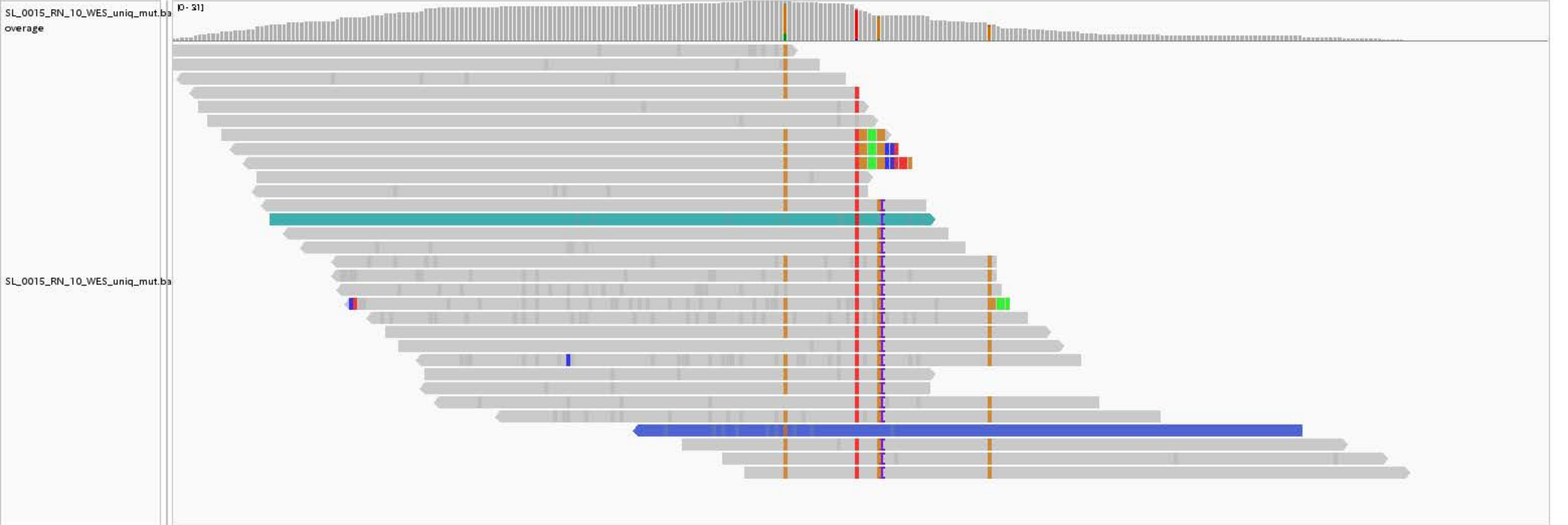
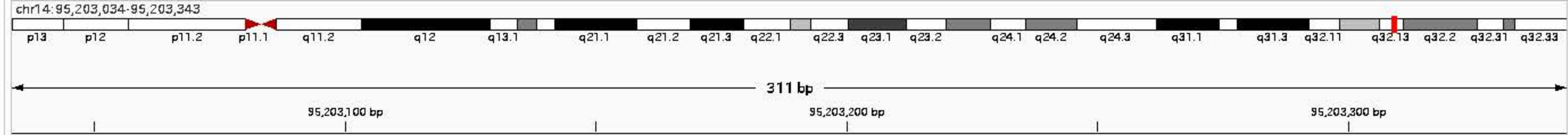


Refseq Genes









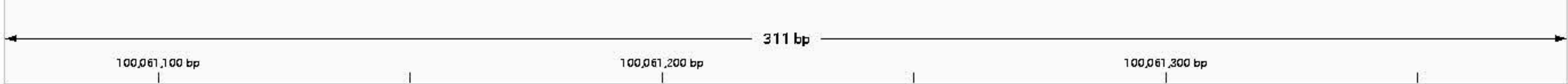
Sequence →

Refseq Genes

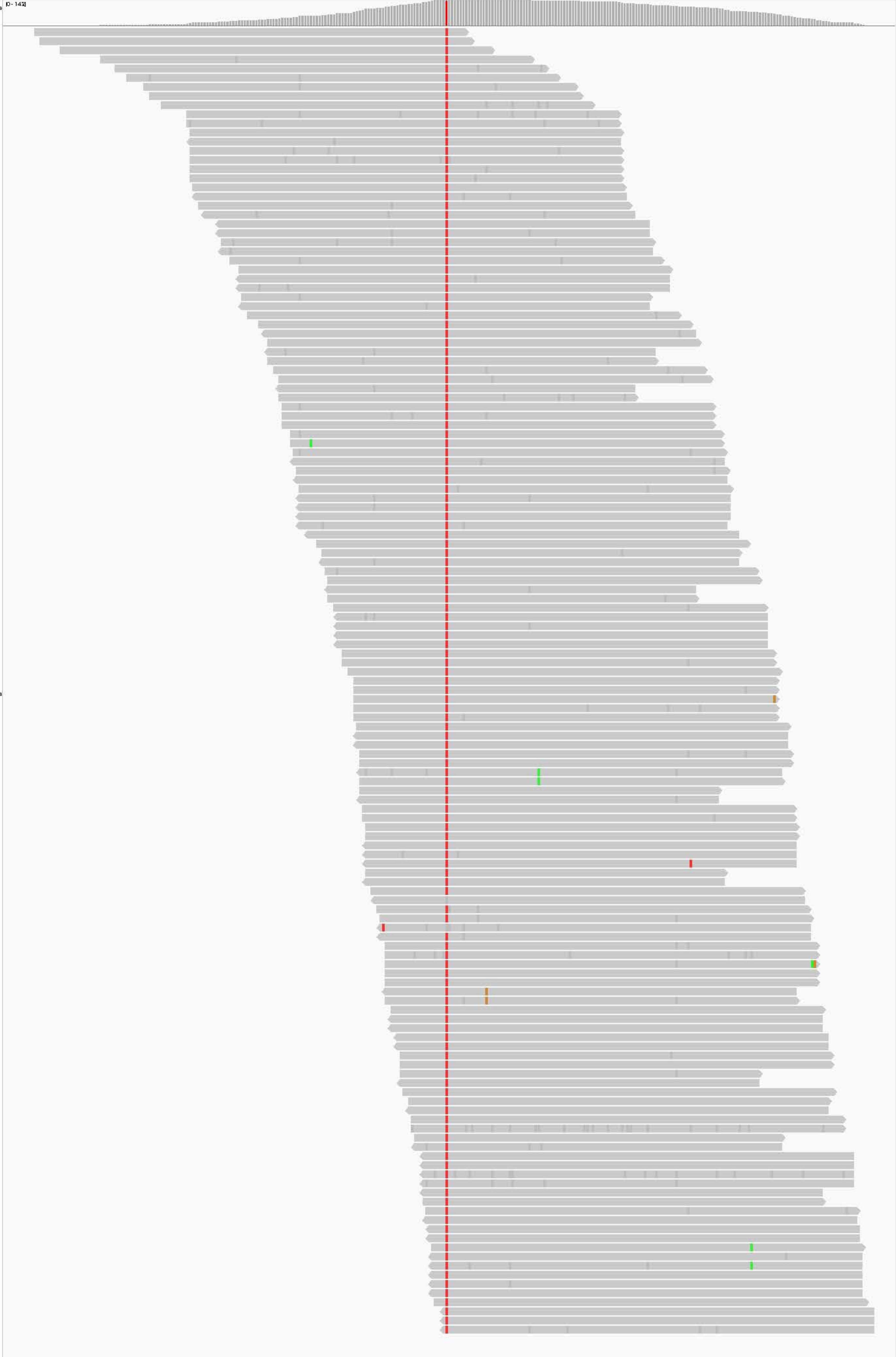
E E R S D L D P M Y G E P E E L D M E E N K L D E P D E V Y A E L V A A L P V E Y H P F Y F L D H P I V S V K S L P P S P K F D L G E E S H S G L T E L S V C S S P P S S S L E E G V G Q L D D D E G E E E Y H

CLMN

chr11:100,061,070-100,061,379



SL\_0004\_RN\_26\_WES\_uniq\_mut.ba  
coverage

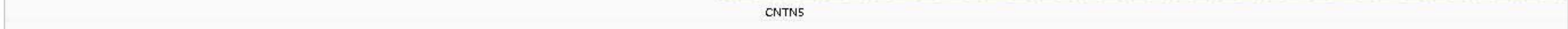


SL\_0004\_RN\_26\_WES\_uniq\_mut.ba

Sequence →

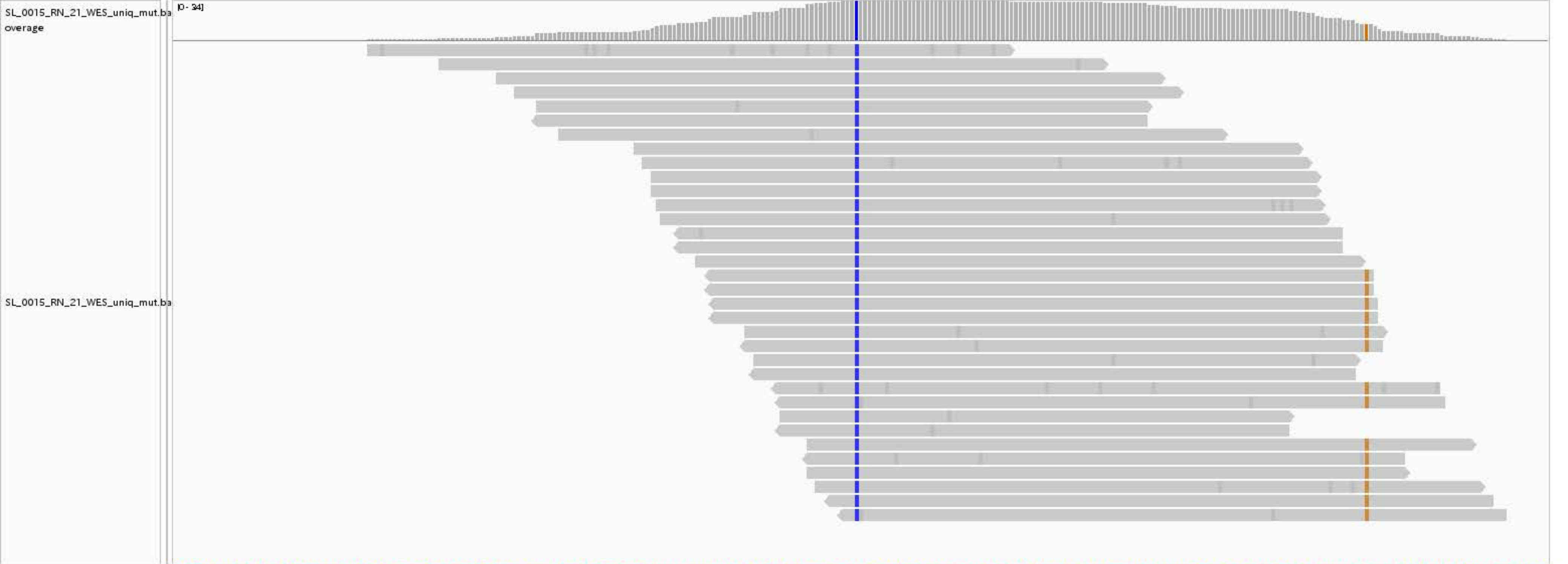
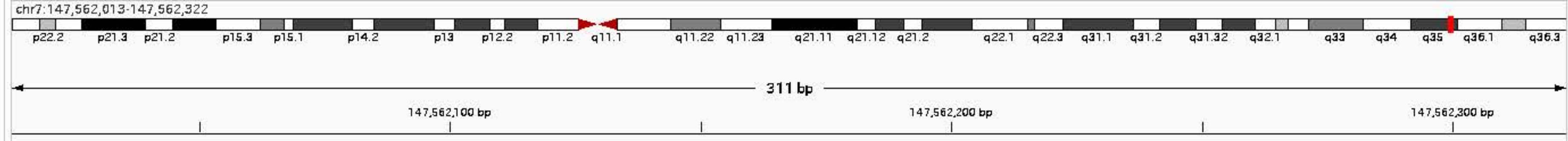


Refseq Genes

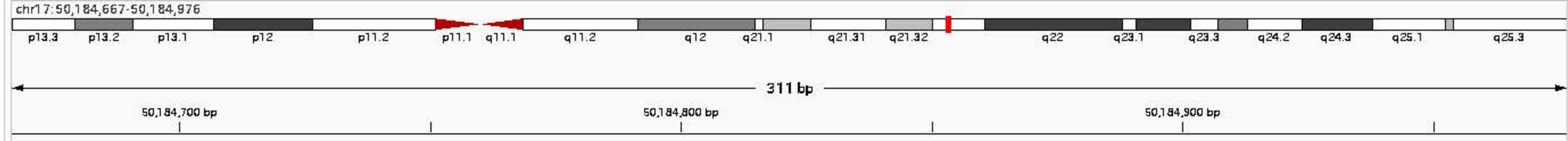


CNTNS

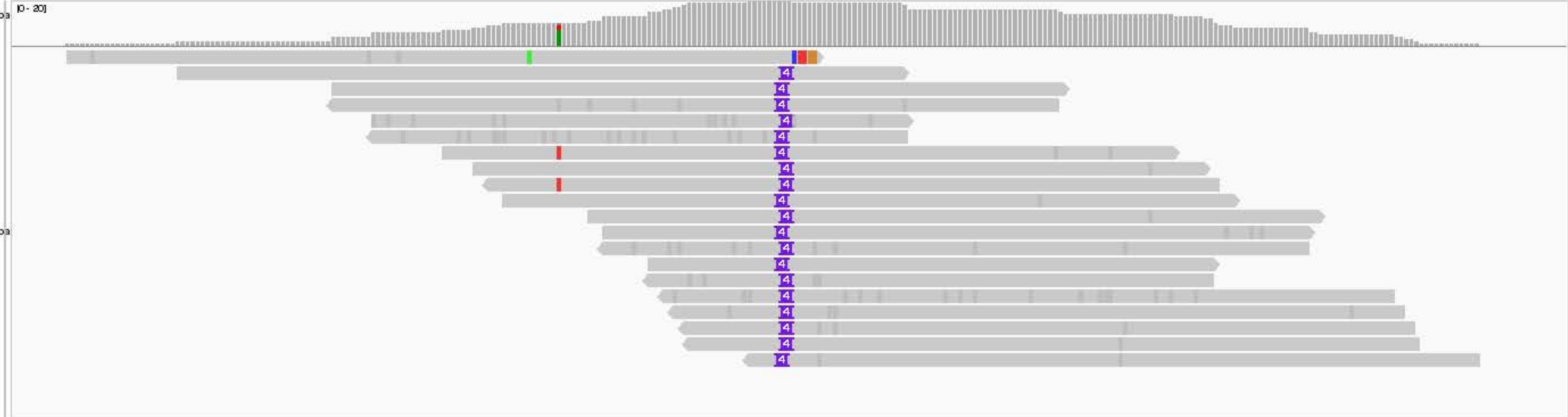








SL\_0010\_RN\_34\_WES\_uniq\_mut.ba  
overage



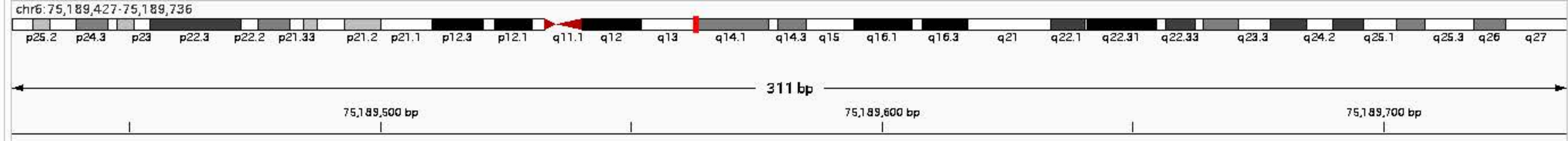
SL\_0010\_RN\_34\_WES\_uniq\_mut.ba

Sequence →



Refseq Genes

COL1A1



SL\_0015\_LN\_44\_WES\_uniq\_mut. coverage



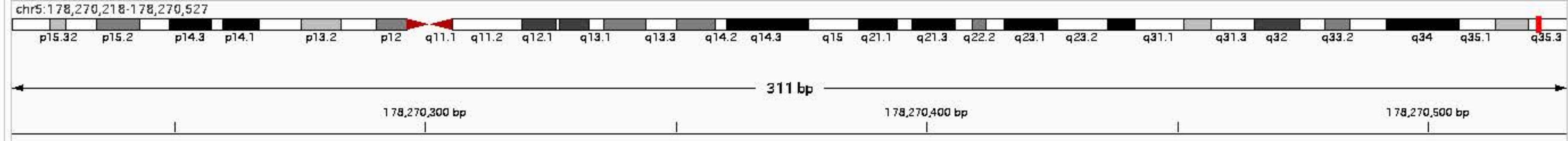
SL\_0015\_LN\_44\_WES\_uniq\_mut.

Sequence



Refseq Genes

COL12A1



SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage



SL\_0015\_LN\_46\_WES\_uniq\_mut.

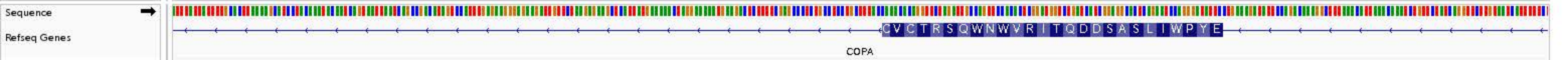
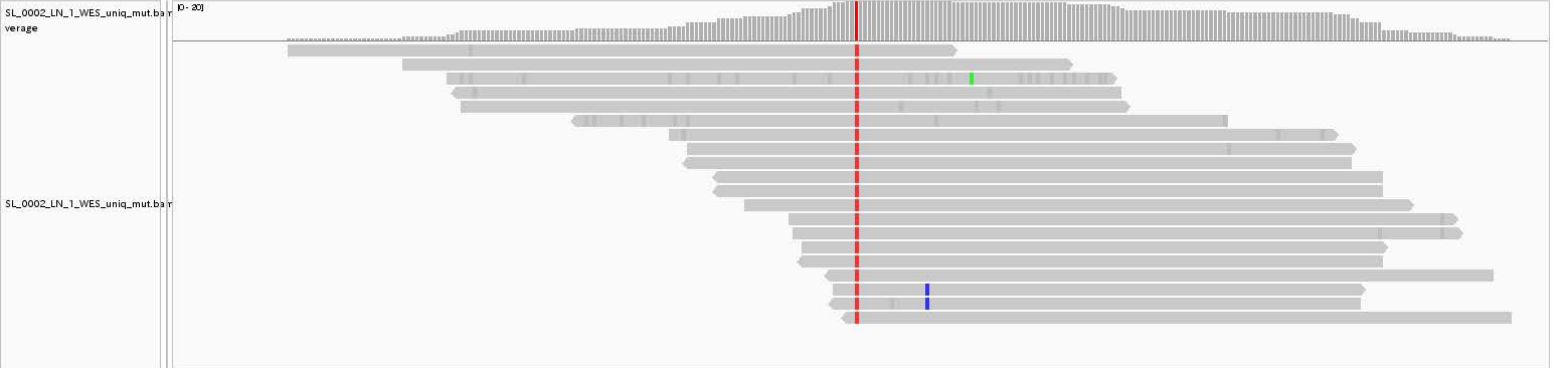
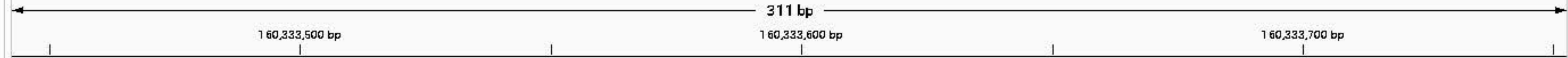
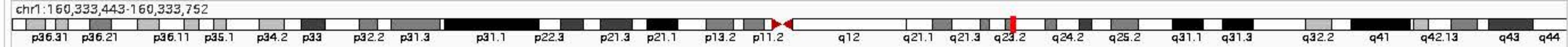
Sequence

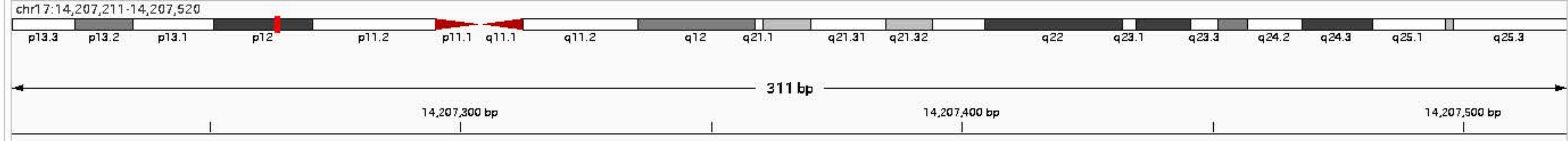


Refseq Genes

PKGDLGLPG  
COL23A1







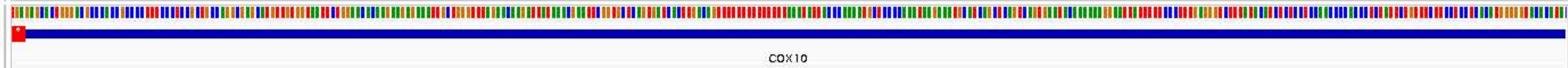
SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage

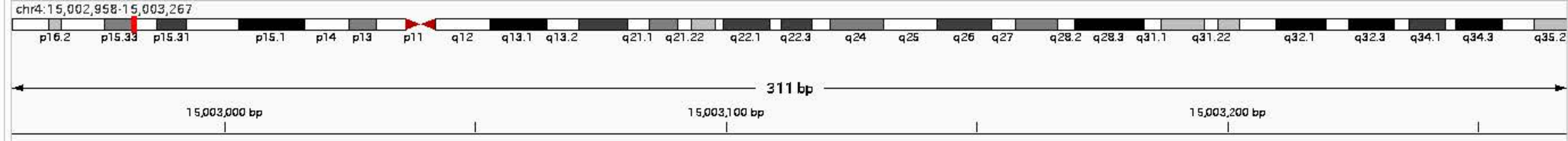


SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage

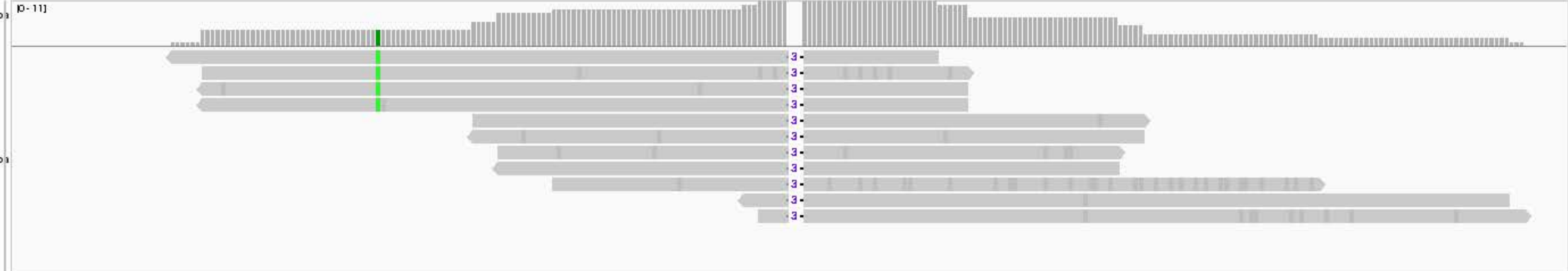
Sequence

Refseq Genes





SL\_0015\_LN\_44\_WES\_uniq\_mut. coverage



SL\_0015\_LN\_44\_WES\_uniq\_mut.

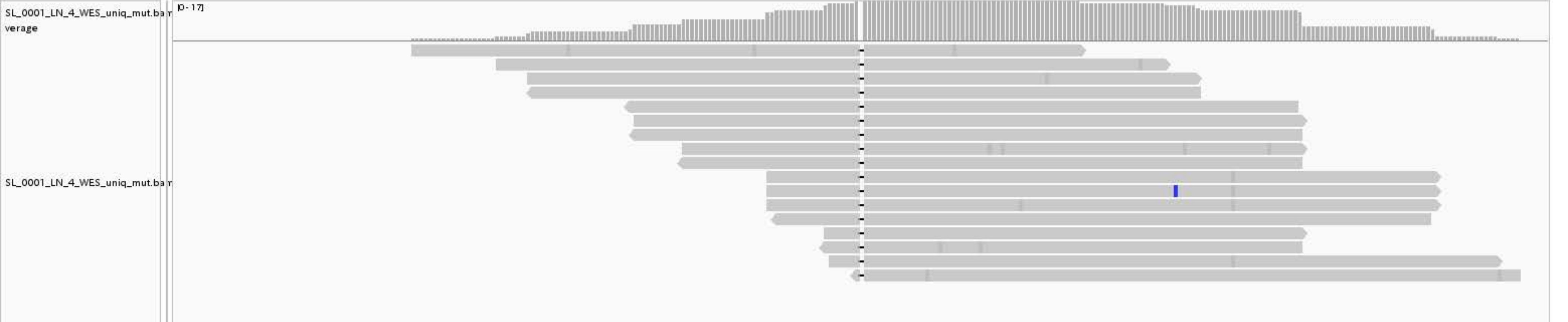
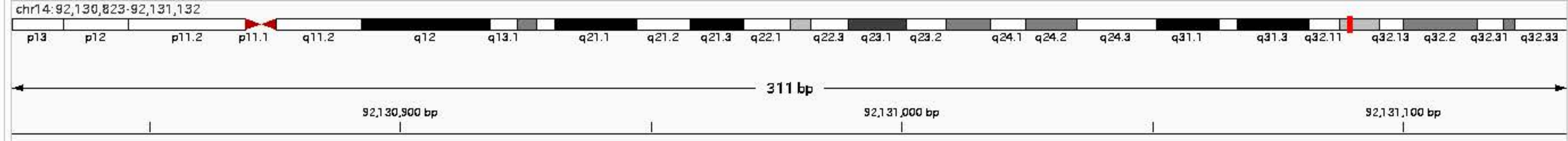
Sequence

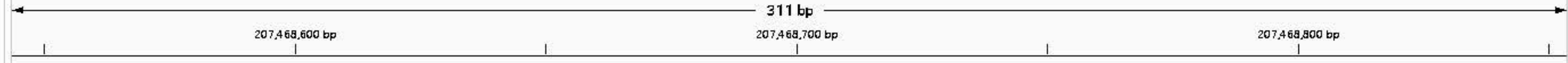
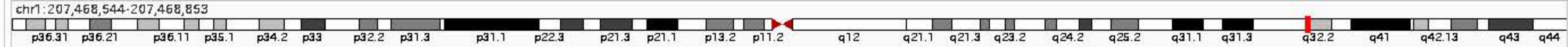
Refseq Genes

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CPEB2







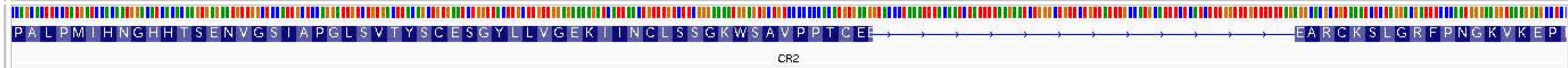
SL\_0003\_LN\_51\_WES\_uniq\_mut. coverage

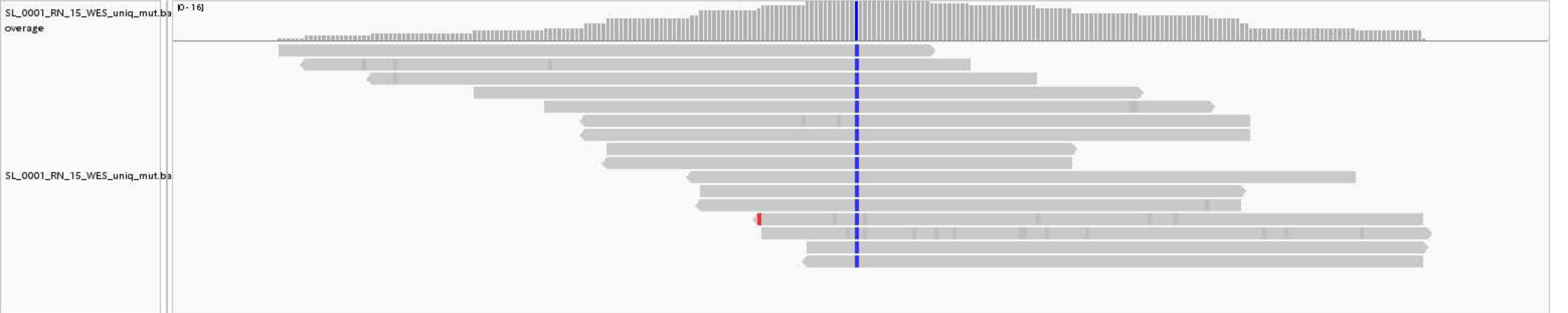
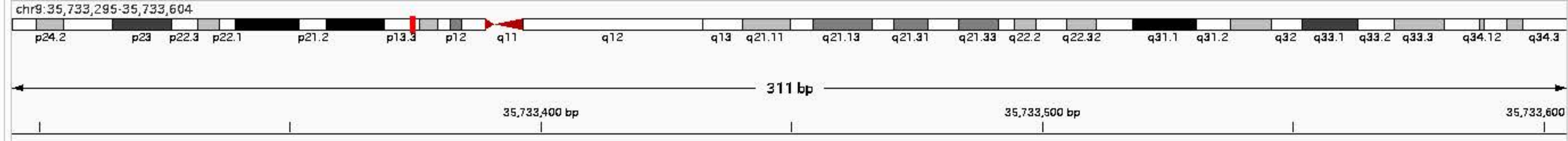
SL\_0003\_LN\_51\_WES\_uniq\_mut. coverage



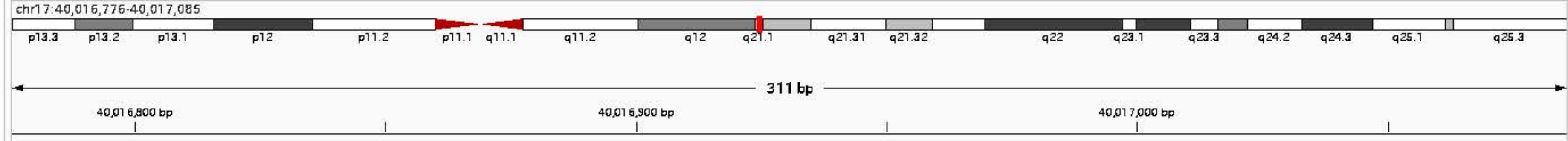
Sequence

Refseq Genes









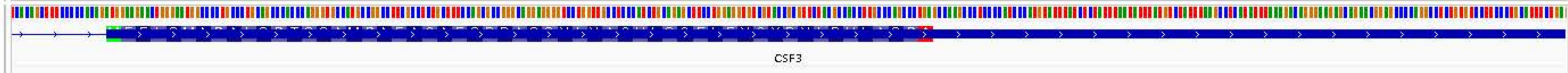
SL\_0007\_RN\_2\_WES\_uniq\_mut.ba  
verage

SL\_0007\_RN\_2\_WES\_uniq\_mut.ba

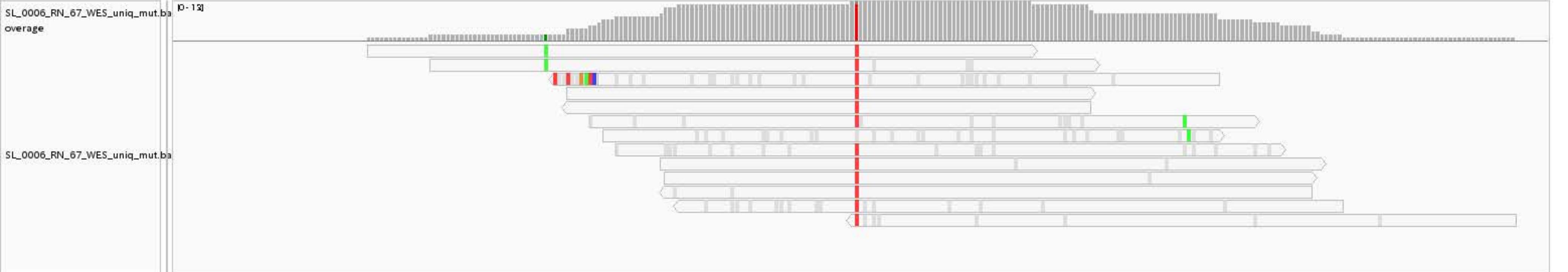
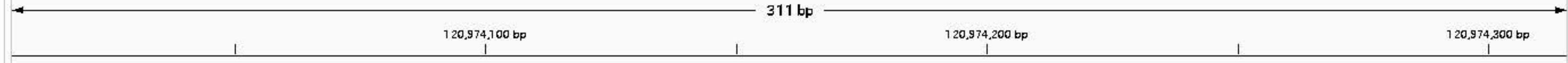


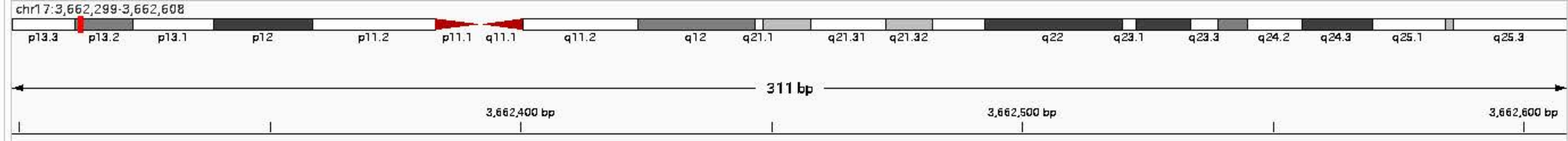
Sequence →

Refseq Genes

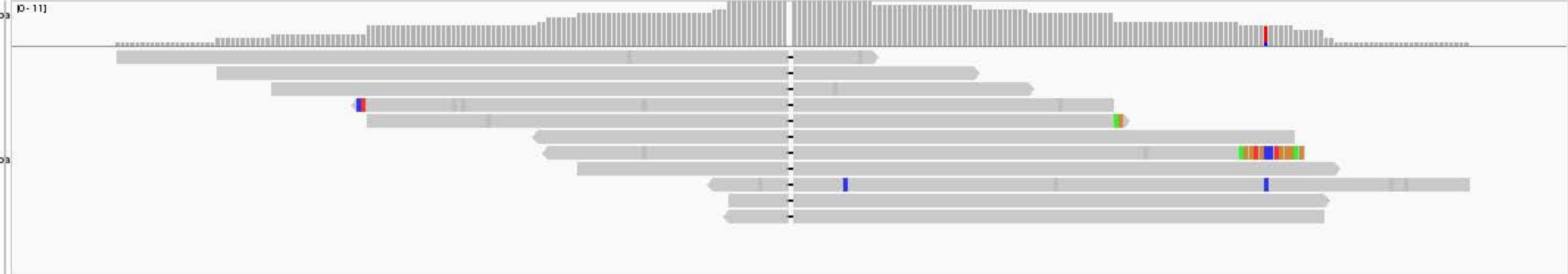


chrX:120,974,006-120,974,315  
p22.32 p22.2 p22.13 p22.11 p21.2 p11.4 p11.3 p11.22 p11.1 q11.2 q13.1 q13.3 q21.1 q21.2 q21.32 q22.1 q22.3 q23 q24 q25 q26.1 q26.3 q27.2 q28





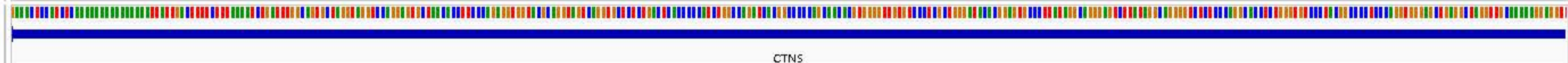
SL\_0006\_RN\_67\_WES\_uniq\_mut.ba  
coverage



SL\_0006\_RN\_67\_WES\_uniq\_mut.ba

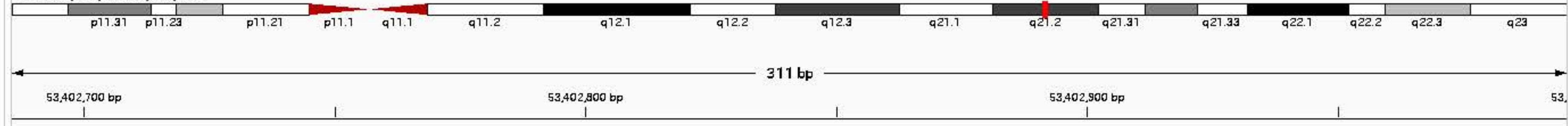
Sequence

Refseq Genes

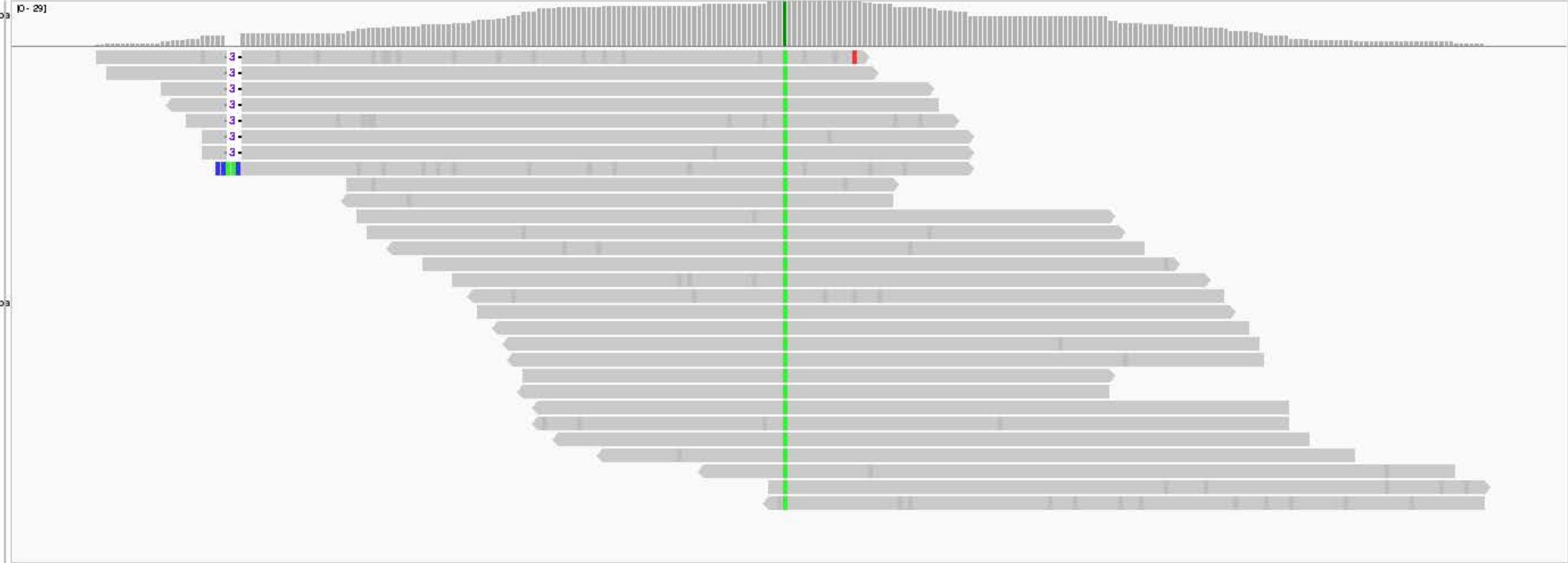




chr18: 53,402,686-53,402,995



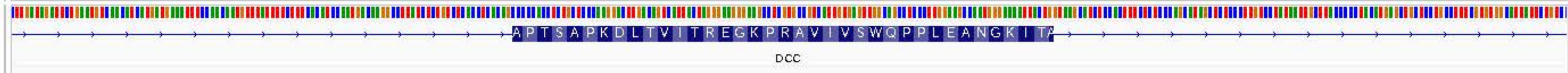
SL\_0001\_RN\_31\_WES\_uniq\_mut.ba  
coverage

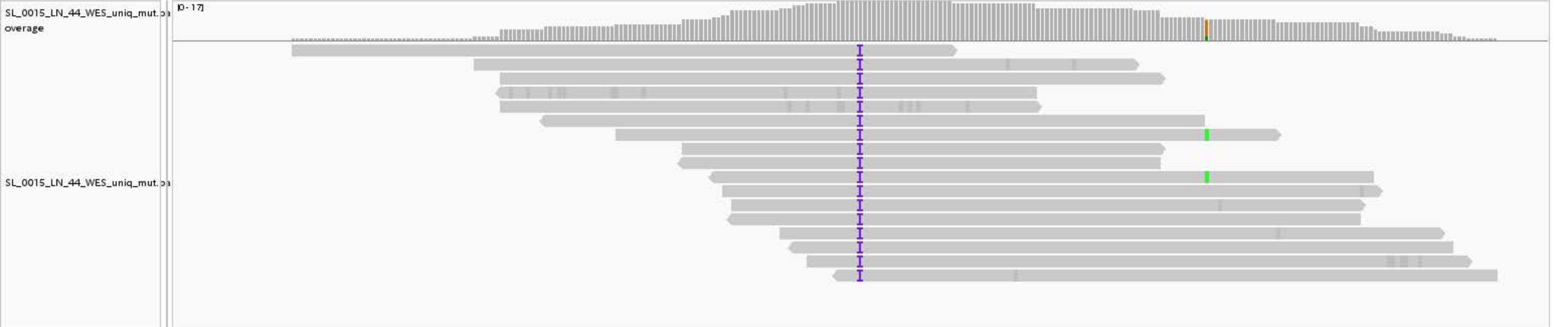
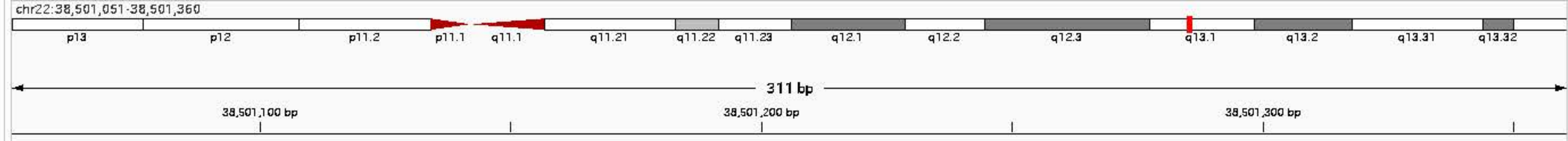


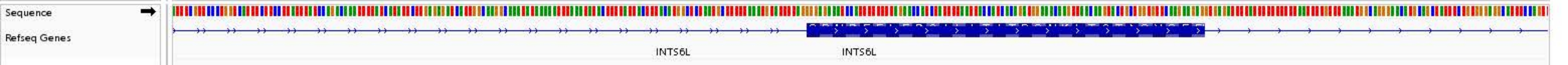
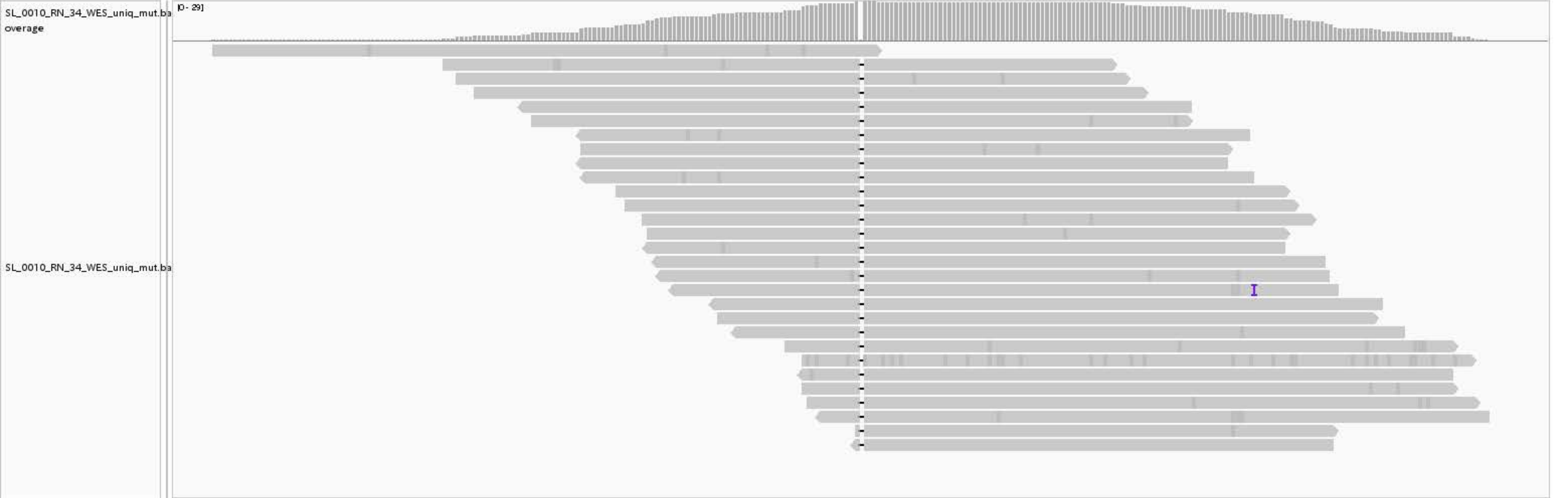
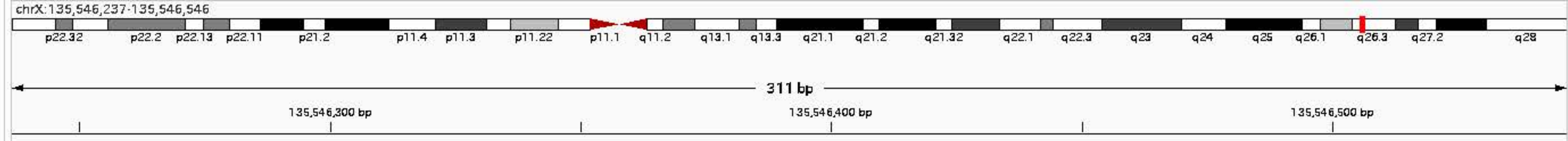
SL\_0001\_RN\_31\_WES\_uniq\_mut.ba

Sequence

Refseq Genes

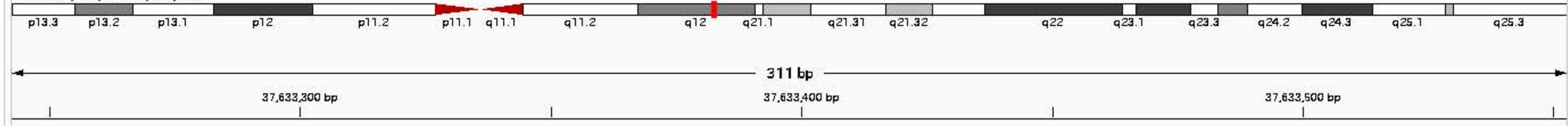




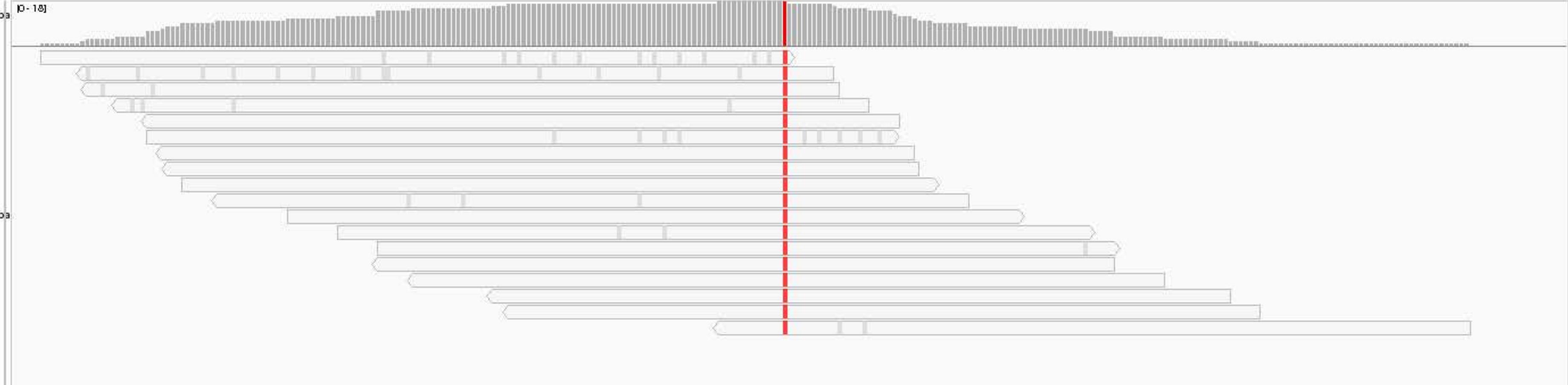




chr17:37,633,243-37,633,552



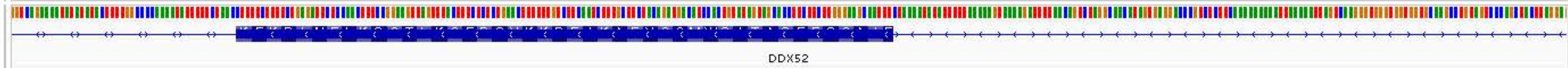
SL\_0004\_RN\_24\_WES\_uniq\_mut.ba  
coverage



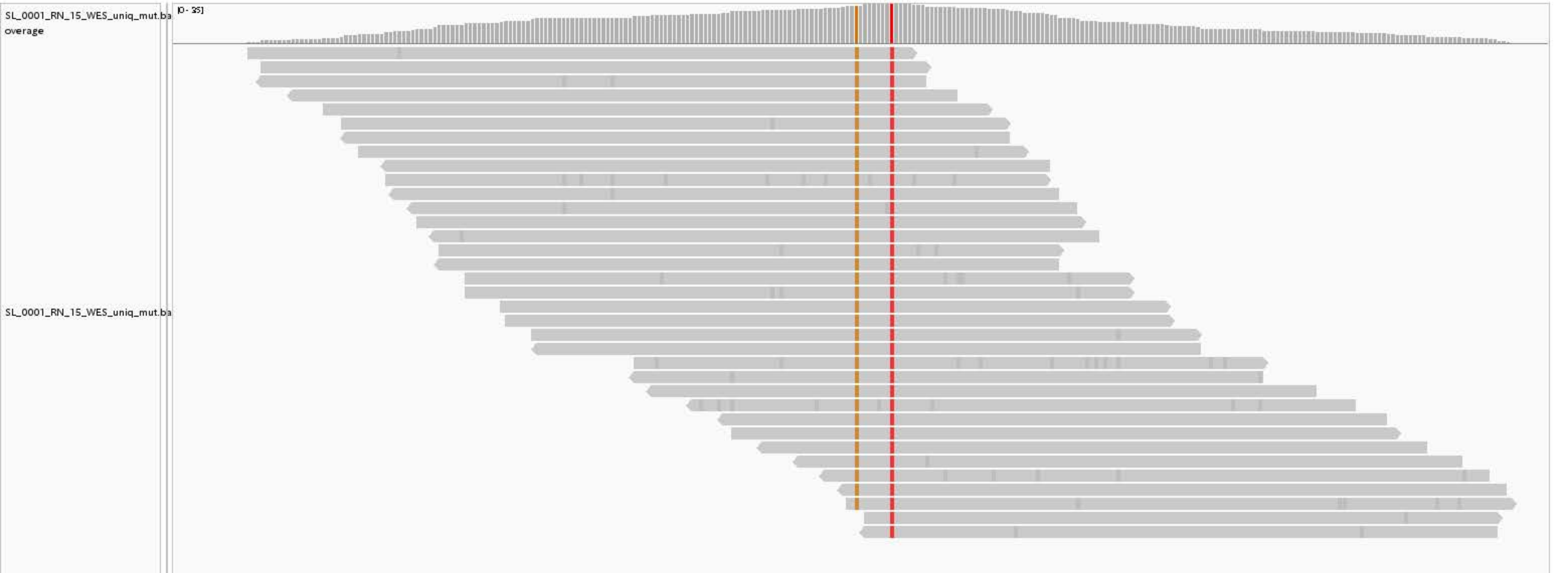
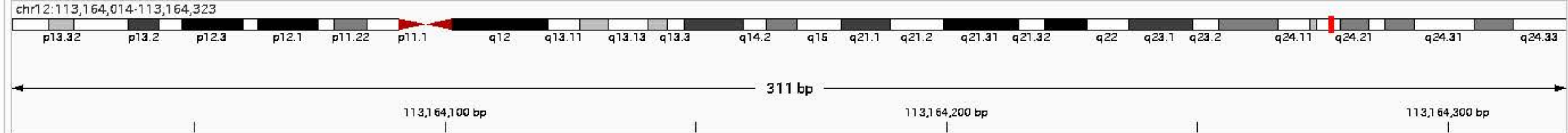
SL\_0004\_RN\_24\_WES\_uniq\_mut.ba

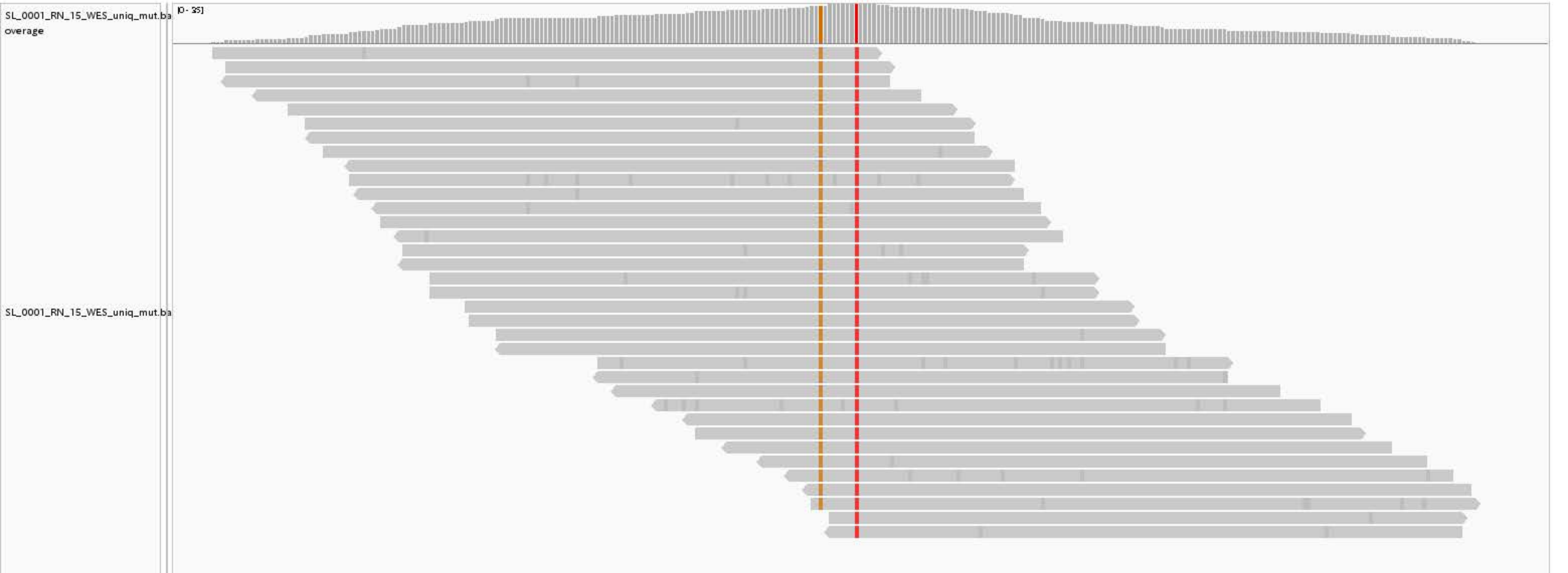
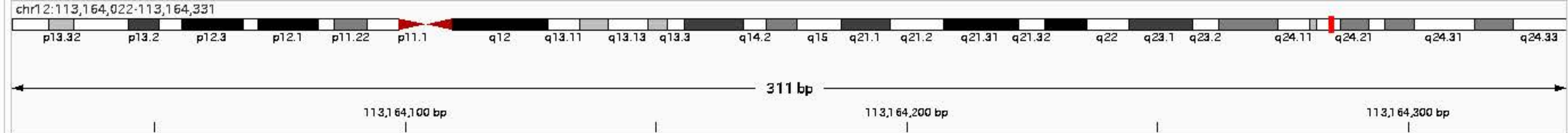
Sequence

Refseq Genes

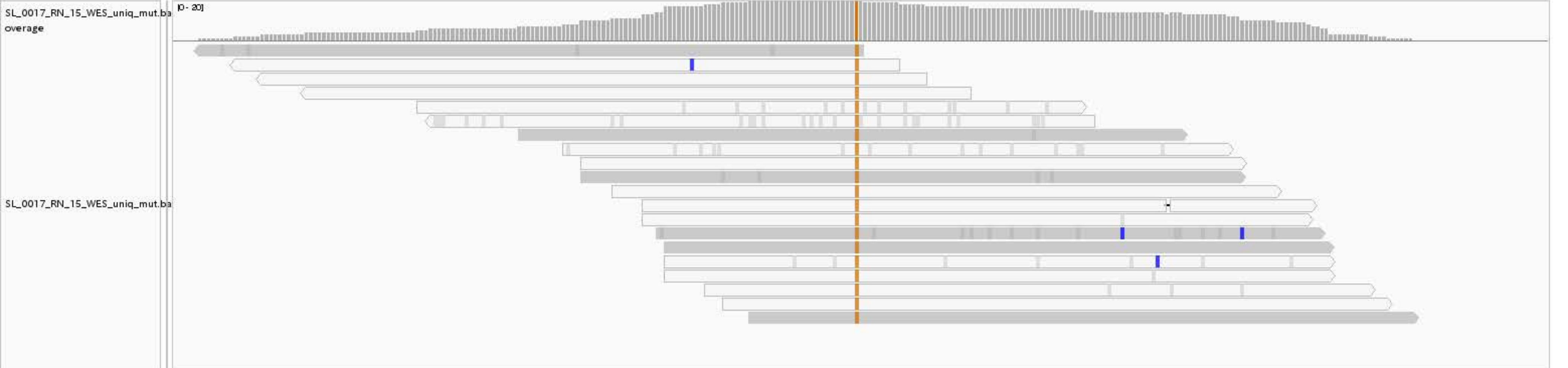
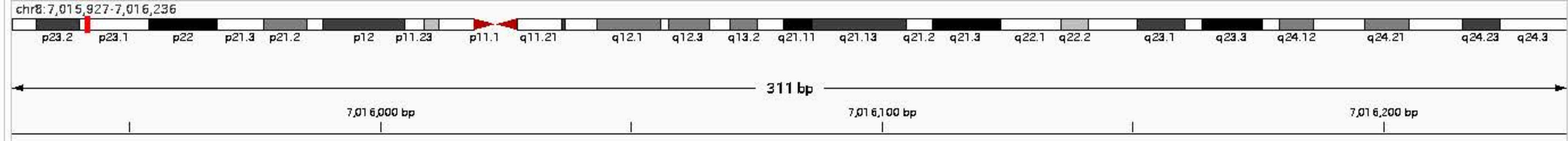


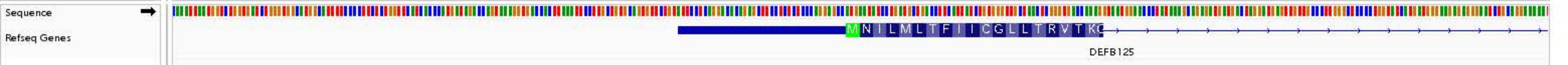
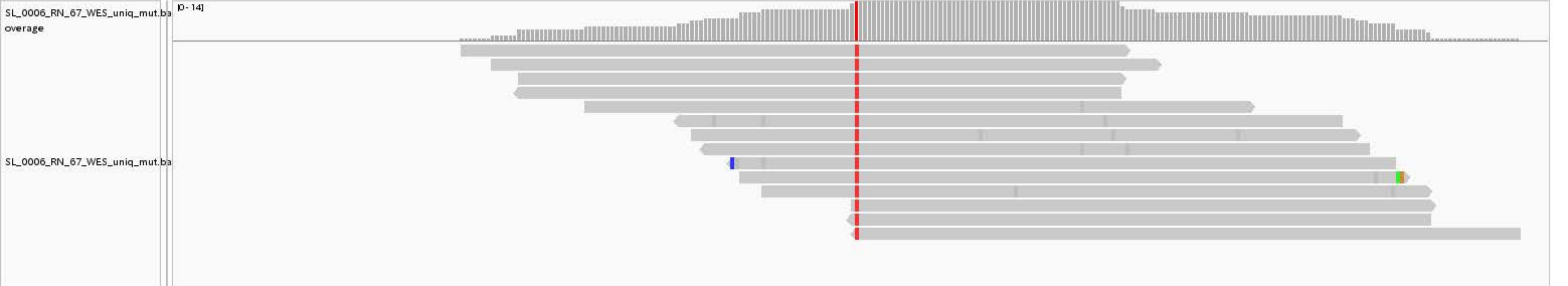
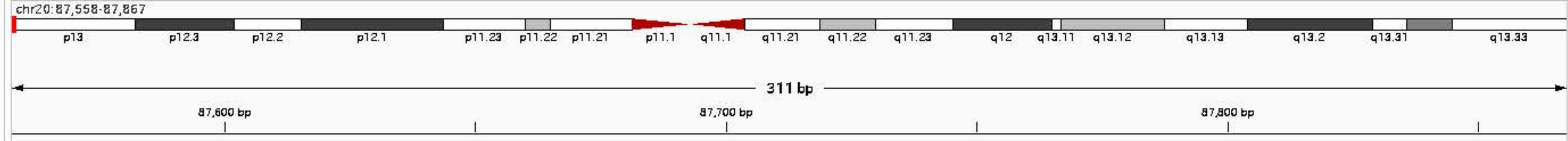
DDX52





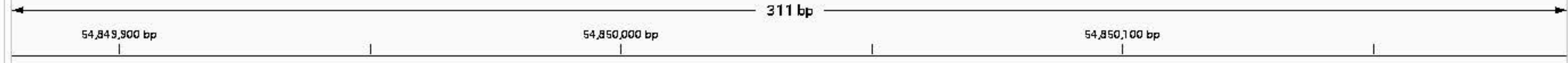




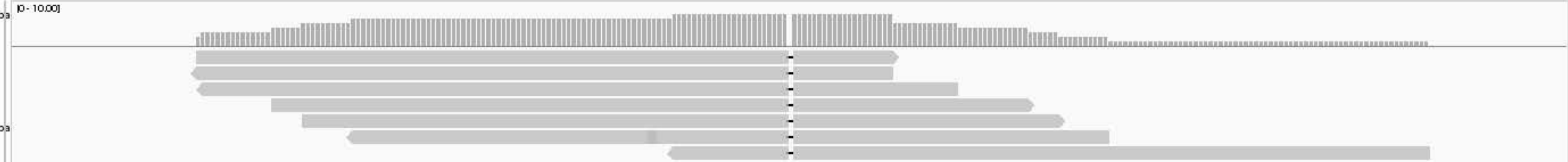


chr1: 54,849,879-54,850,188

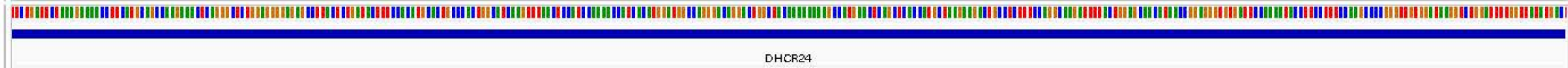
p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44



SL\_0004\_RN\_47\_WES\_uniq\_mut.ba  
coverage

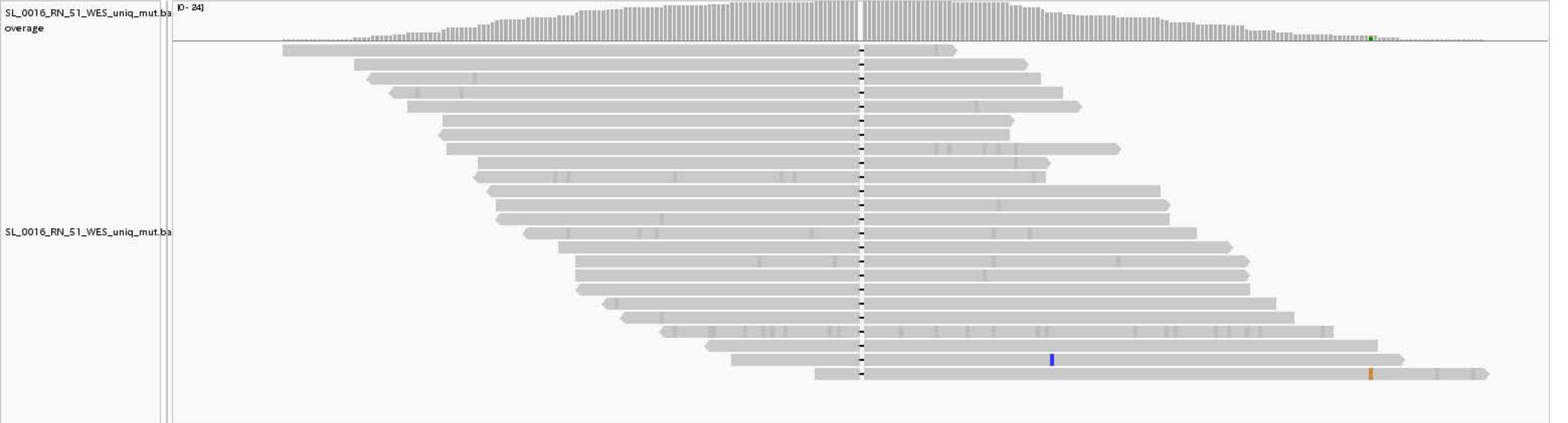
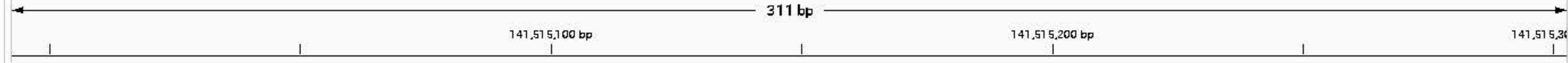
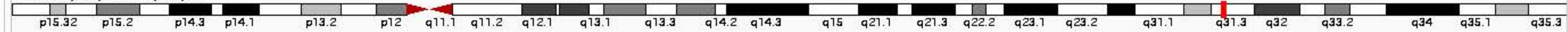


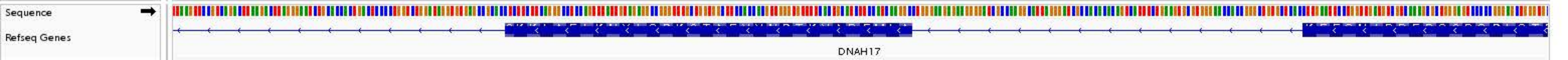
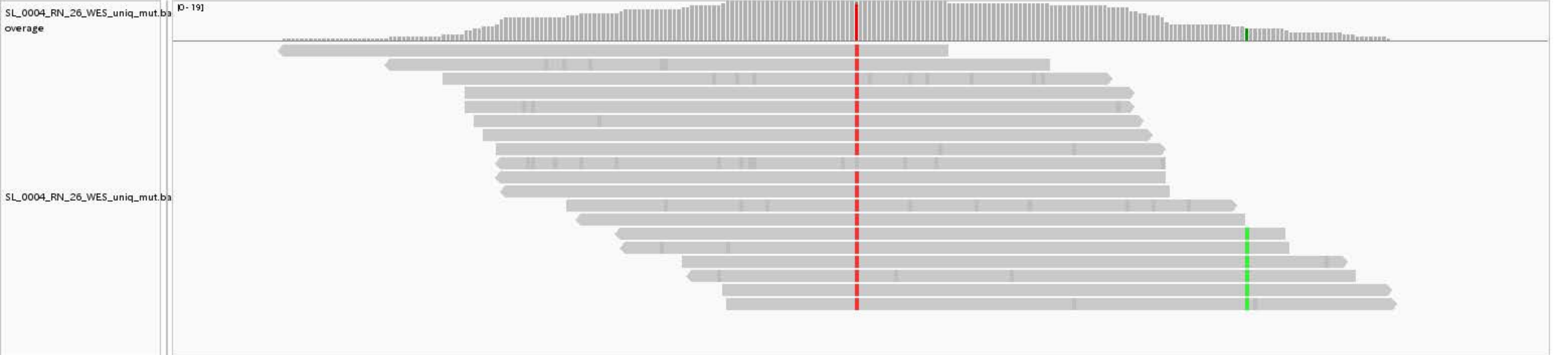
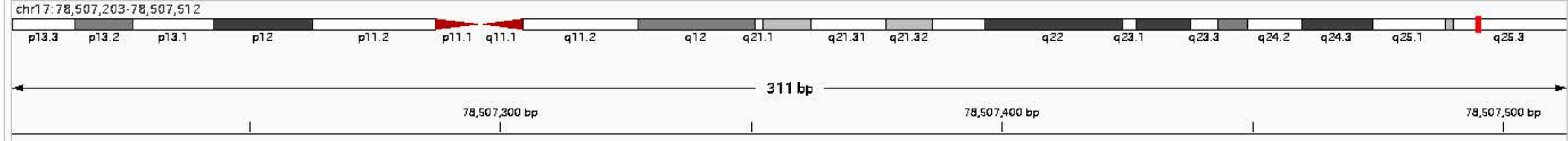
Sequence  
Refseq Genes

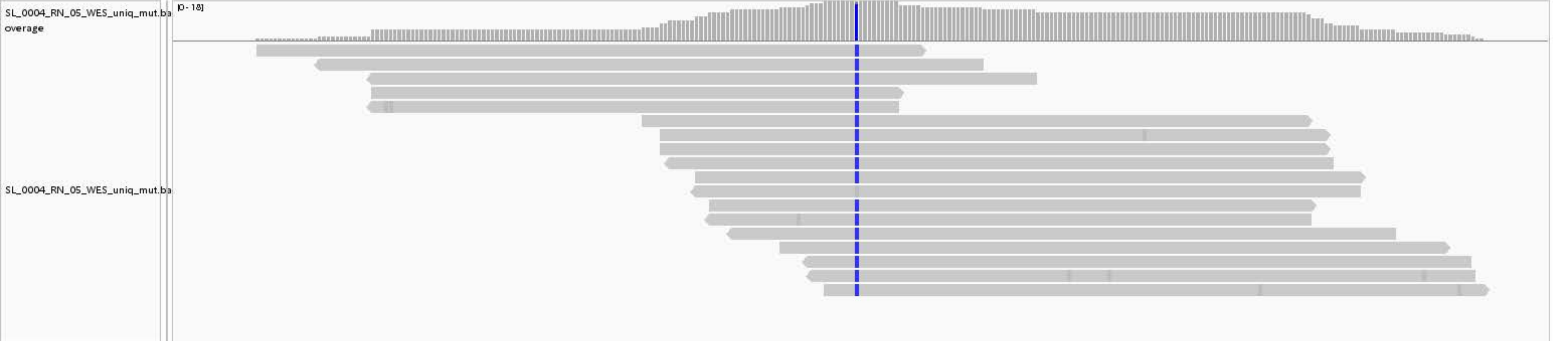
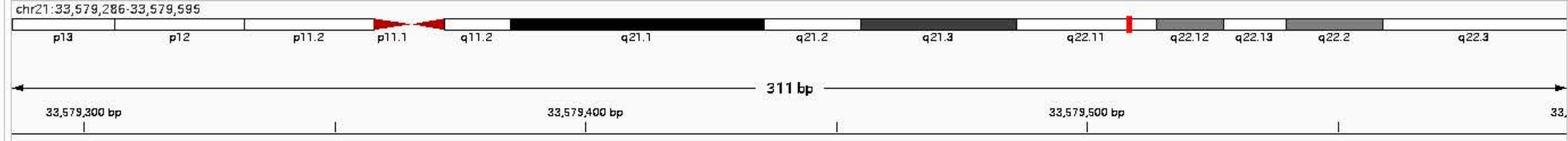




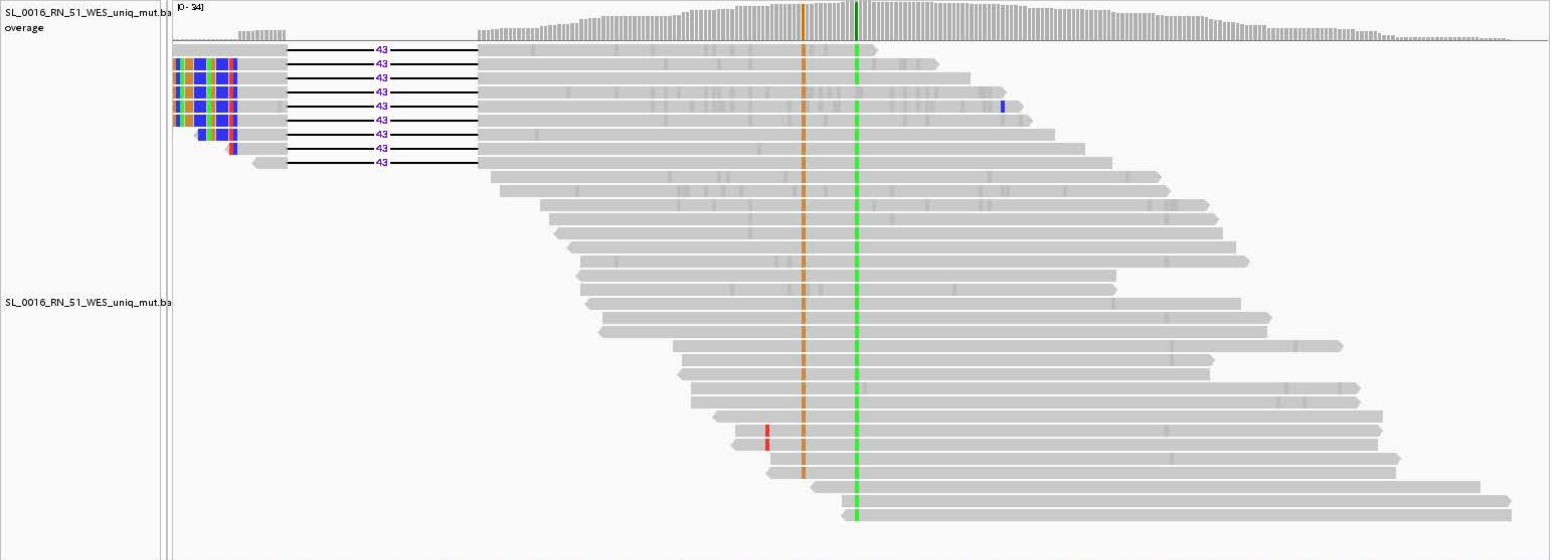
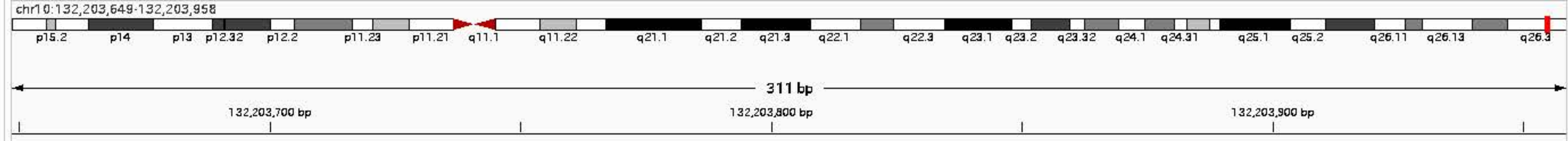
chr5:141,514,993-141,515,302

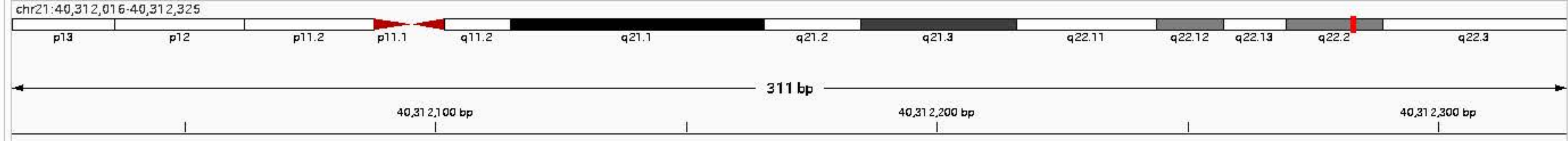




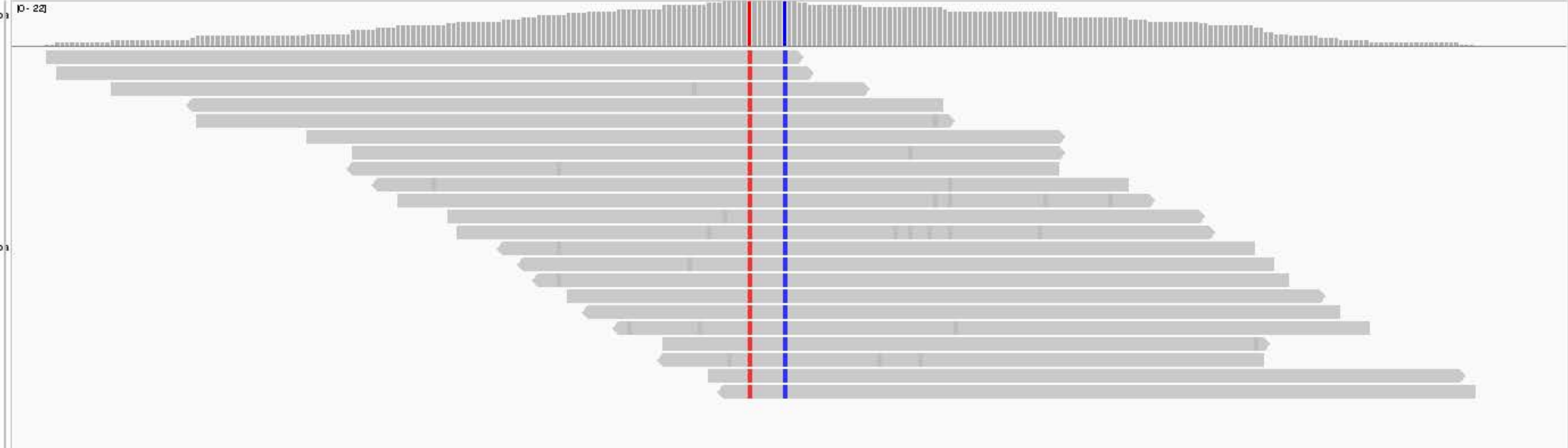








SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage



Sequence



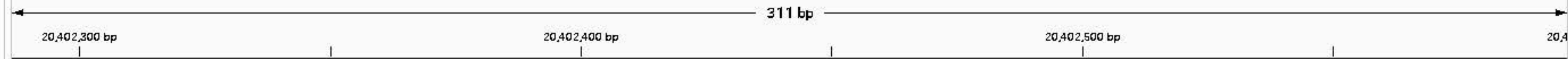
Refseq Genes



DSCAM



chr6:20,402,287-20,402,596  
p25.2 p24.3 p23 p22.3 p22.2 p21.33 p21.2 p21.1 p12.3 p12.1 q11.1 q12 q13 q14.1 q14.3 q15 q16.1 q16.3 q21 q22.1 q22.31 q22.33 q23.3 q24.2 q25.1 q25.3 q26 q27



SL\_0002\_LN\_1\_WES\_uniq\_mut.ba  
verage

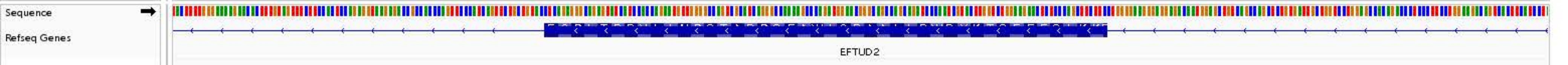
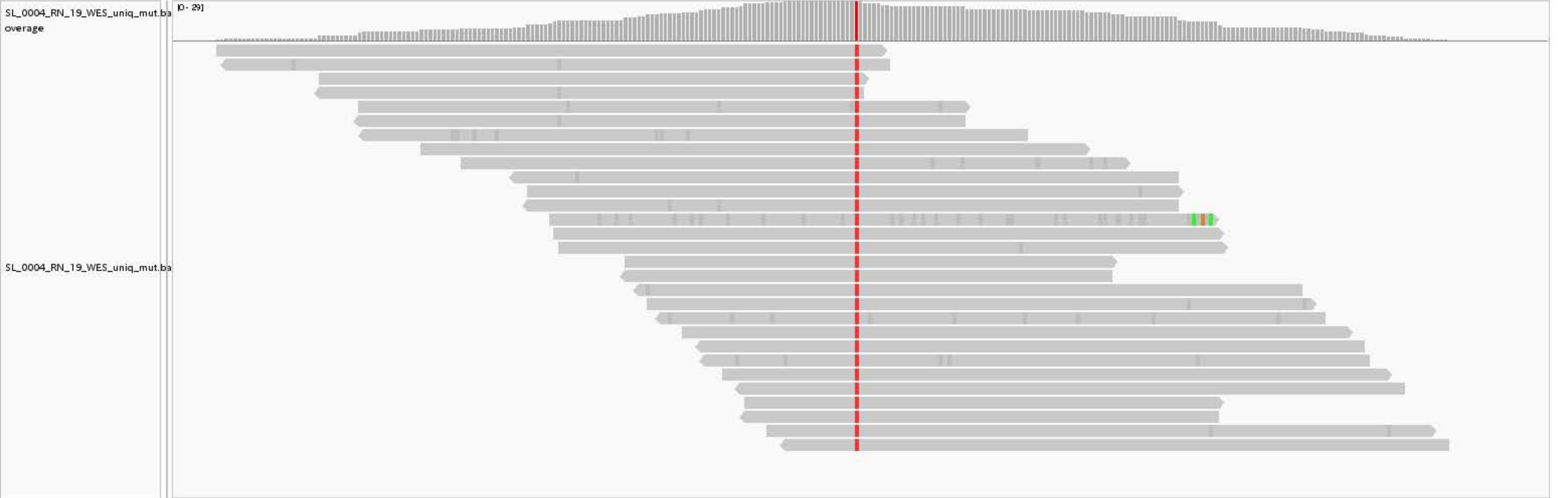
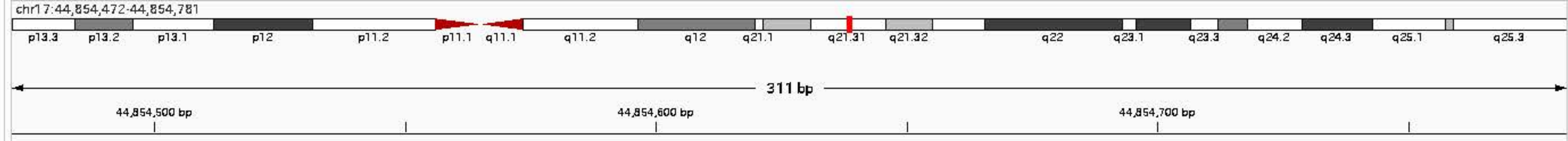


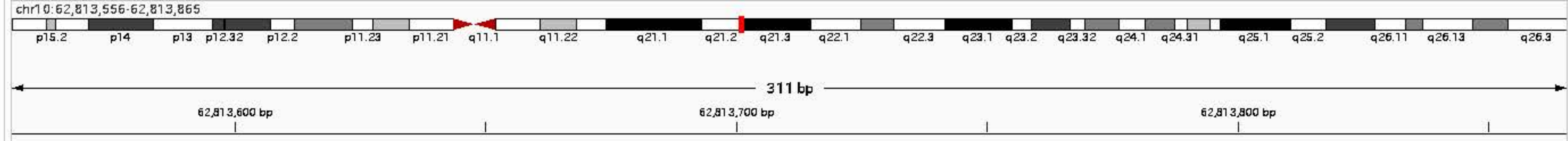
SL\_0002\_LN\_1\_WES\_uniq\_mut.ba

Sequence →  
Refseq Genes

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E2F3





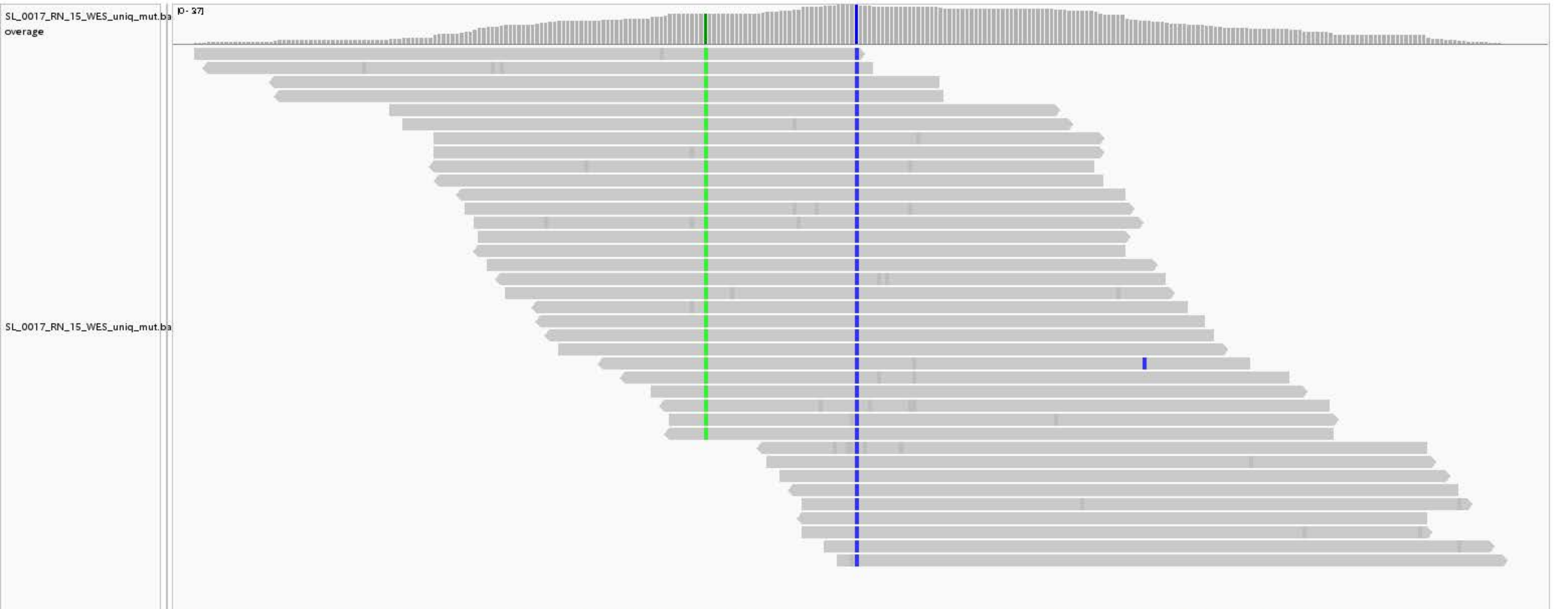
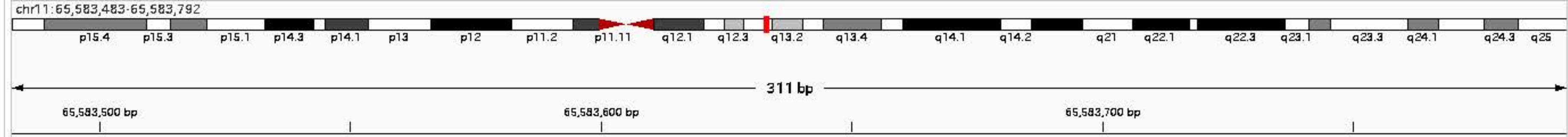


Sequence →

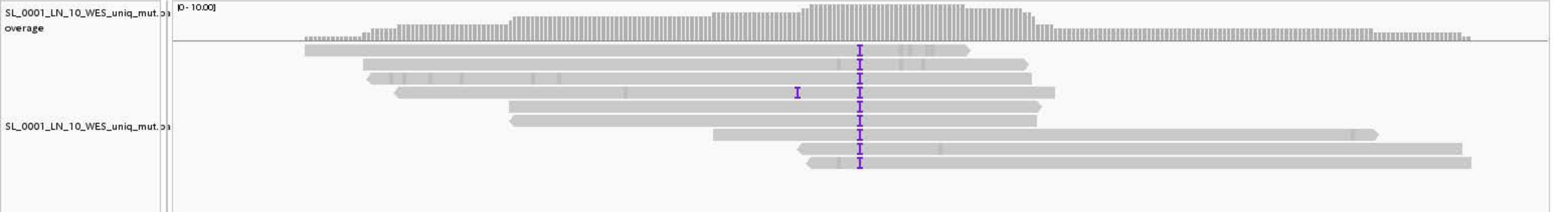
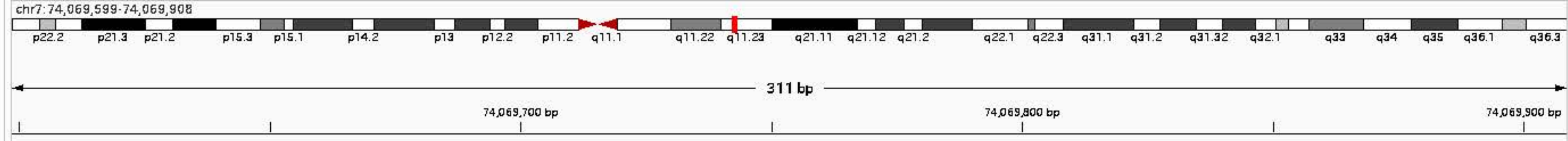
Refseq Genes

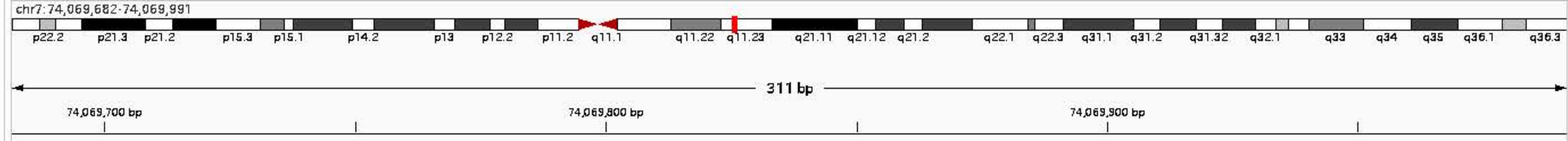
I H R T L E D S R S F R R D C G E A P C P Y P R E H V P T K S P R N P Y K R P R L I P R L P L H H P N Y A A A A A A A A A S S S G P L R P G E S G G S A G P G T V G A S P G G L T F N R I T S L P T L P P P V

EGR2

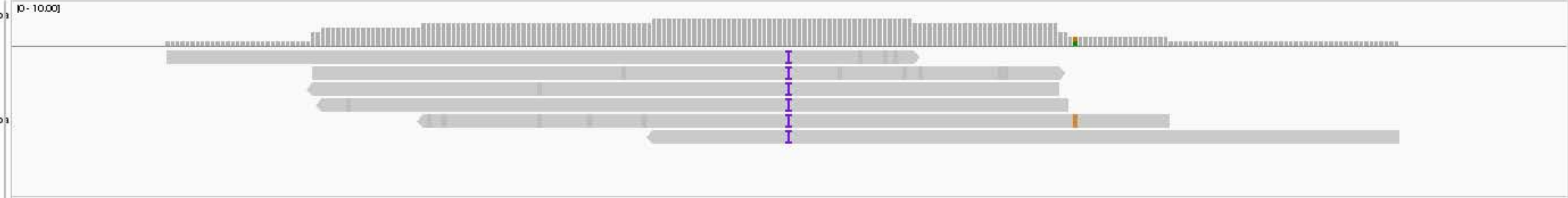






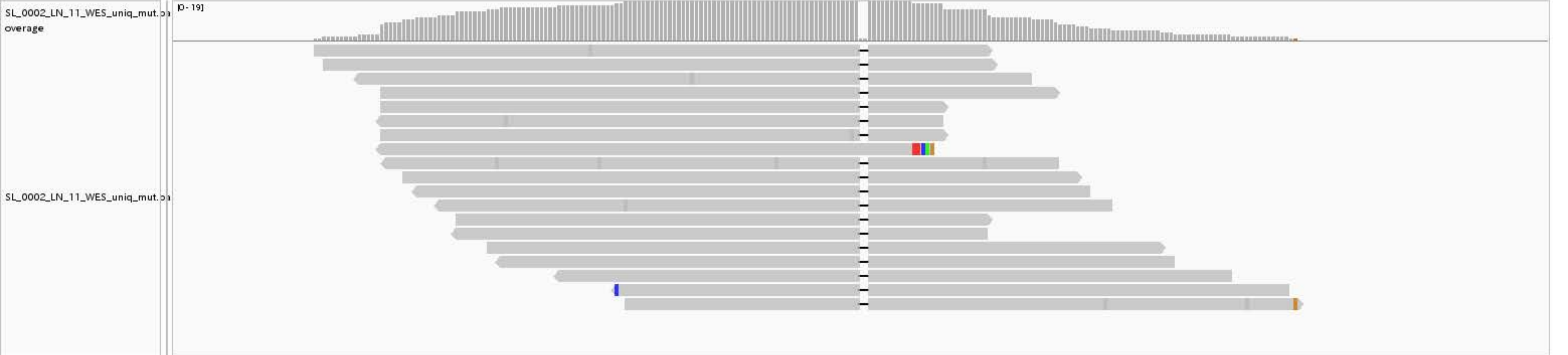
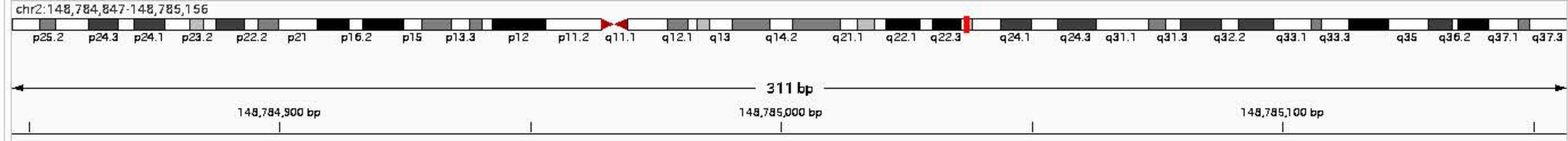


SL\_0015\_LN\_44\_WES\_uniq\_mut.  
coverage

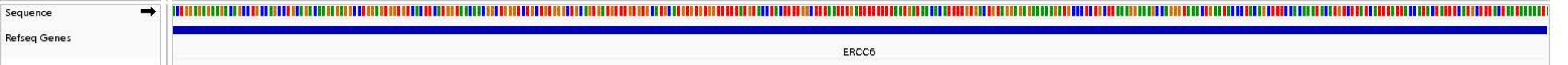
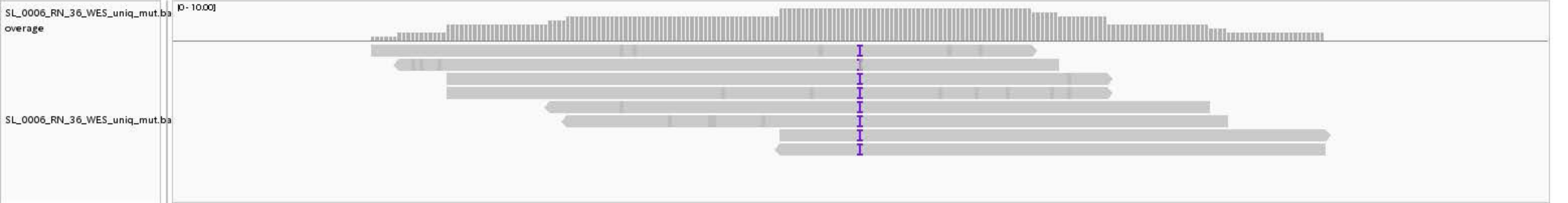
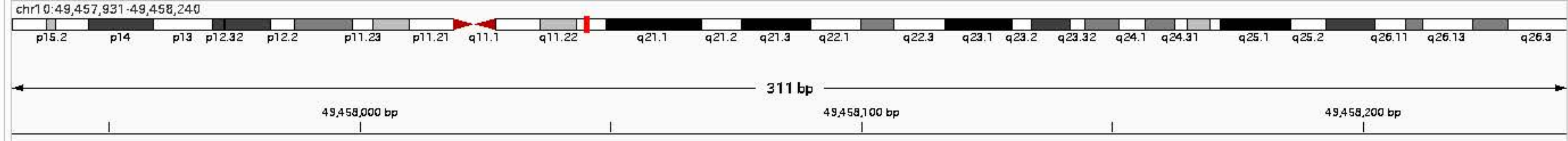


Sequence →  
Refseq Genes

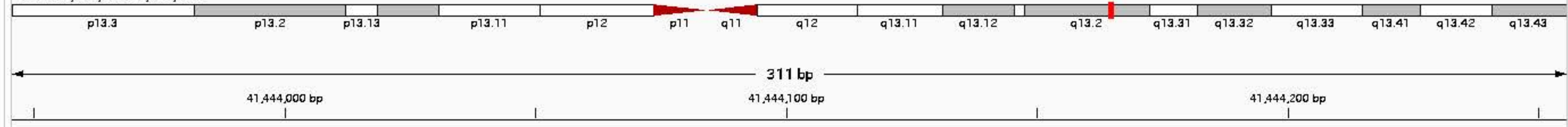




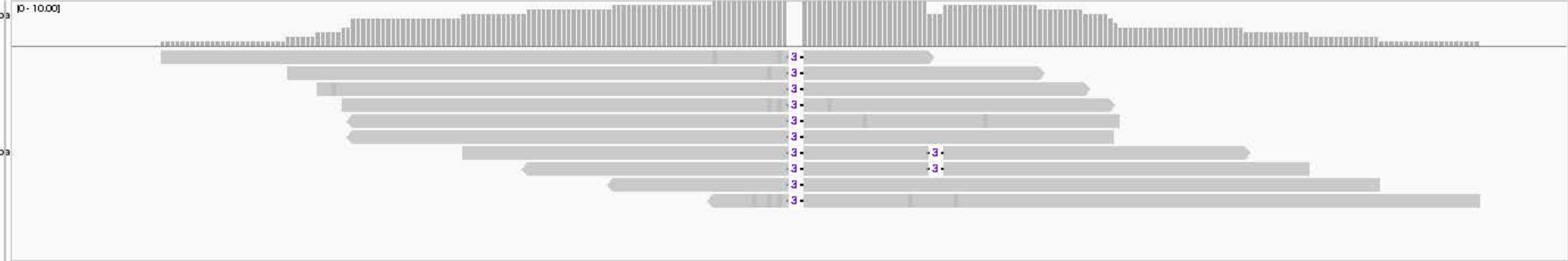




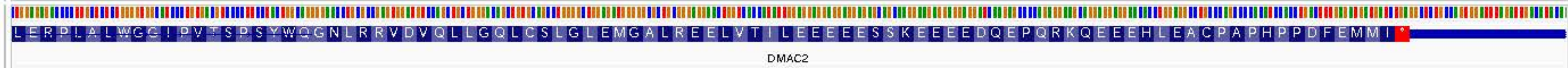
chr19:41,443,946-41,444,255



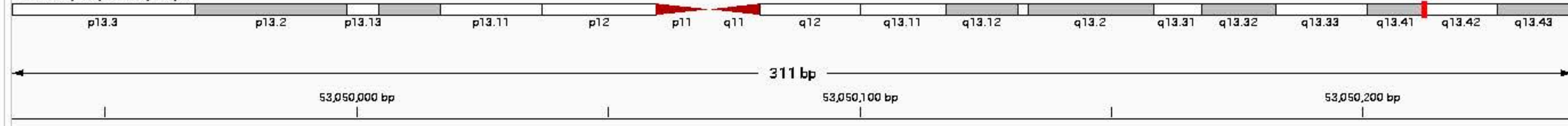
SL\_0007\_RN\_33\_WES\_uniq\_mut.ba  
coverage



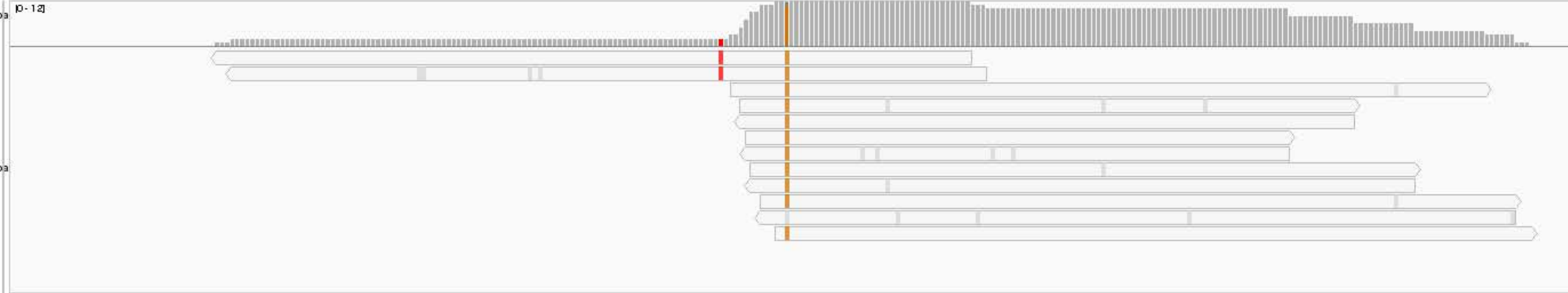
Sequence  
Refseq Genes



chr19:53,049,932-53,050,241



SL\_0004\_RN\_19\_WES\_uniq\_mut.ba  
coverage



SL\_0004\_RN\_19\_WES\_uniq\_mut.ba

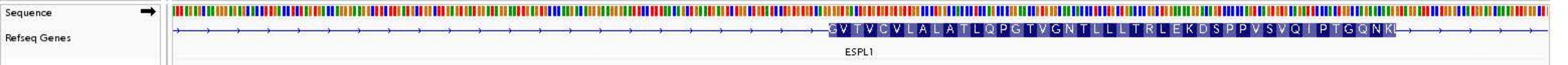
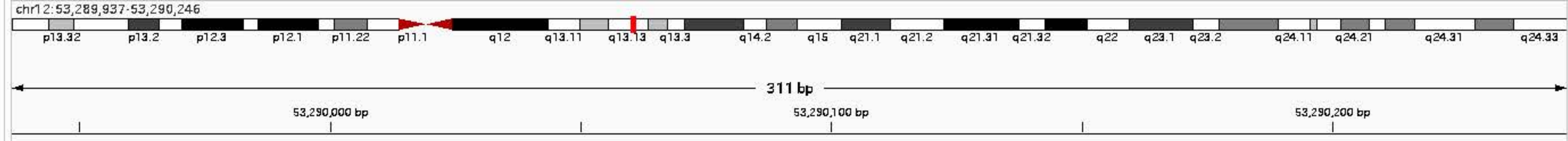
Sequence

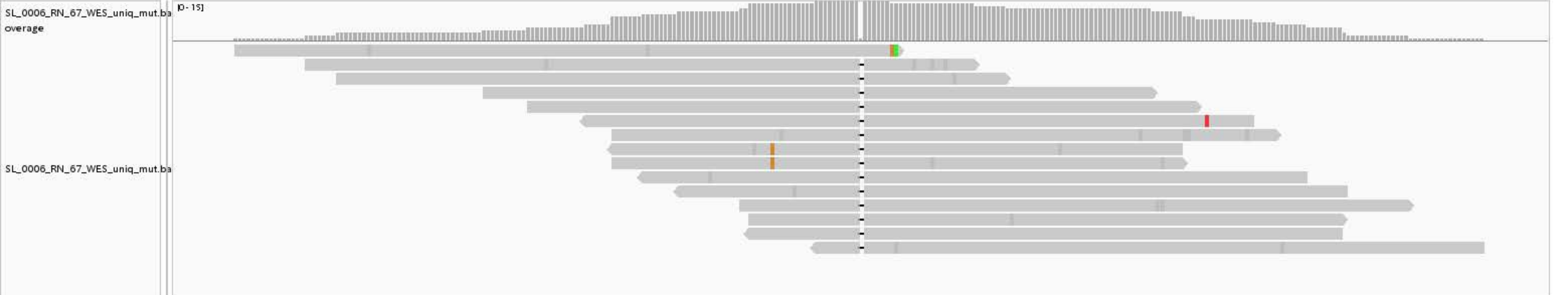
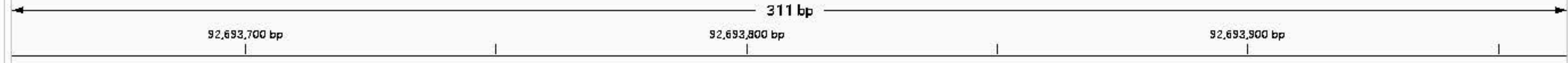
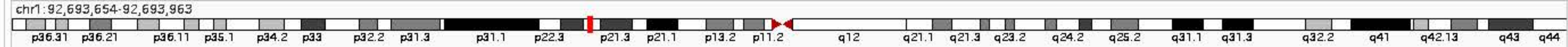
Refseq Genes

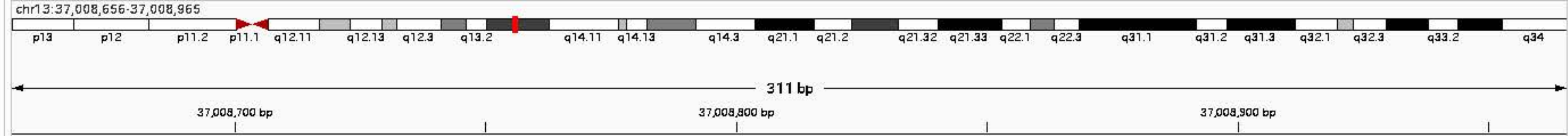
I P A G W K S Q L H K W F D S H I P R W A C T P P G Y V F L C G P Q K N K L P F D G S P K I T Y S T P P V A N L Y T C I N N I Q H T G E C A V G L L G P R G I G V T I Y N T T Q P R Q K R A L G L I L A G M G

ERVV-2

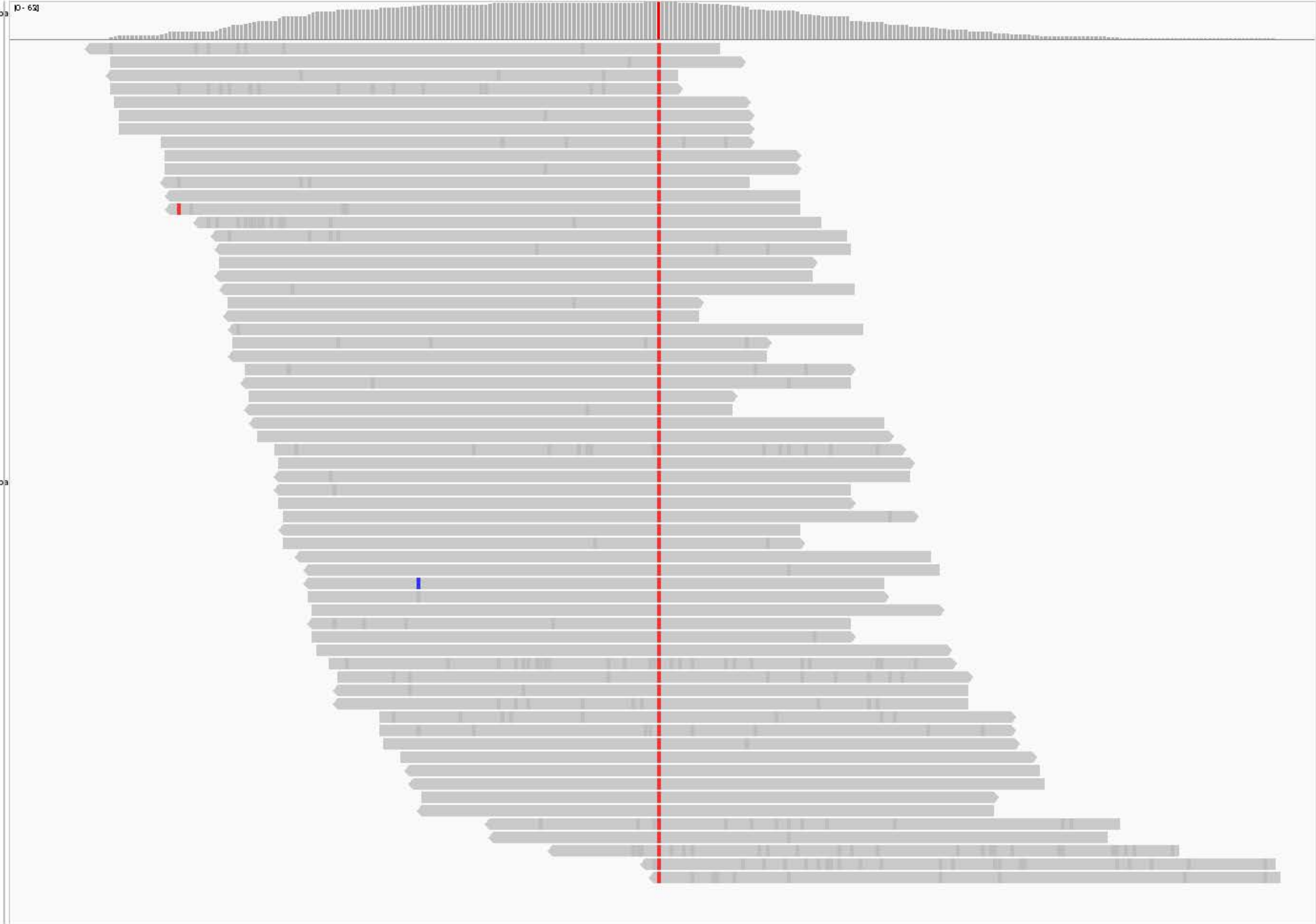






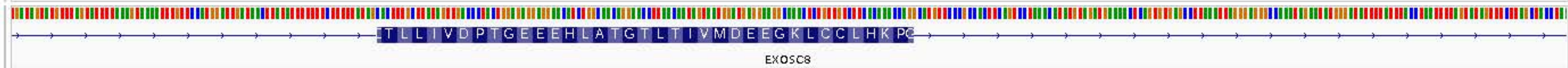


SL\_0015\_RN\_10\_WES\_uniq\_mut.ba  
coverage

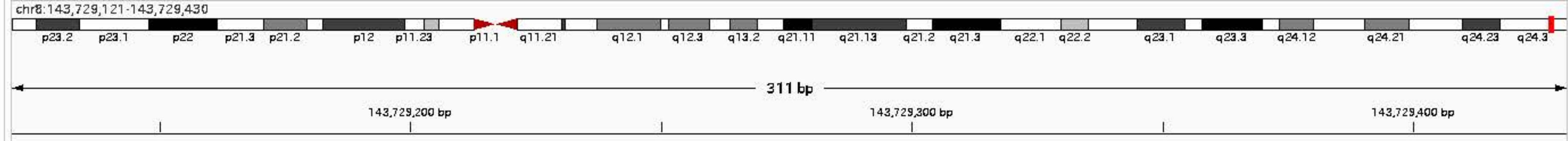


SL\_0015\_RN\_10\_WES\_uniq\_mut.ba

Sequence →  
Refseq Genes

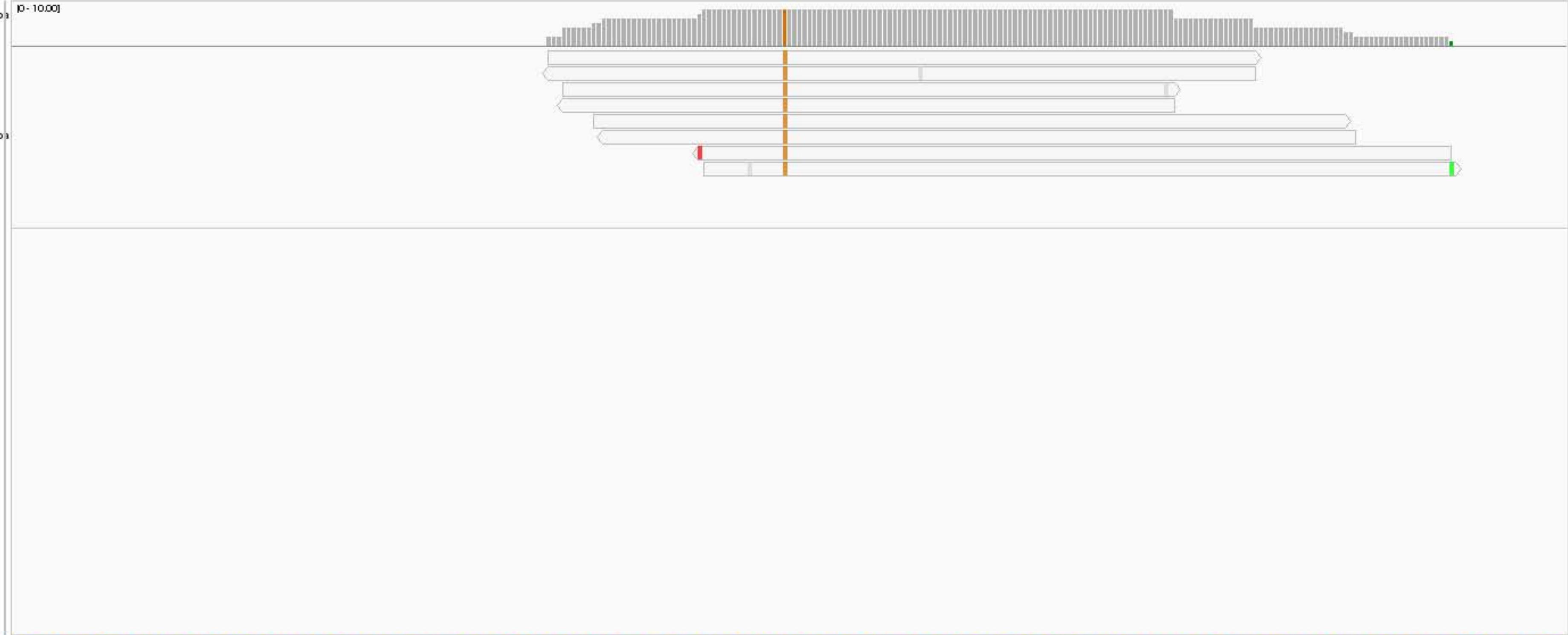






SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage

SL\_0015\_LN\_46\_WES\_uniq\_mut.

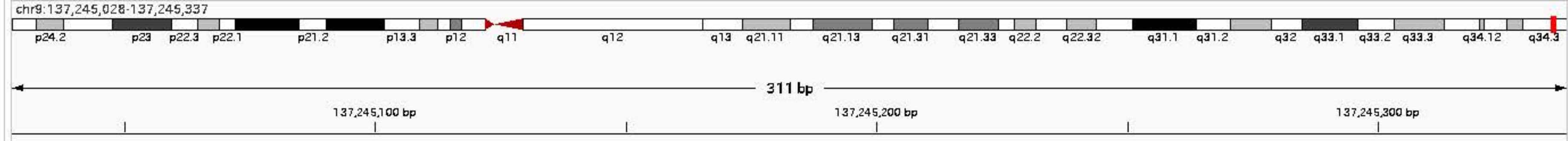


Sequence

Refseq Genes



FAM83H



SL\_0002\_LN\_1\_WES\_uniq\_mut.ba  
verage



SL\_0002\_LN\_1\_WES\_uniq\_mut.ba r

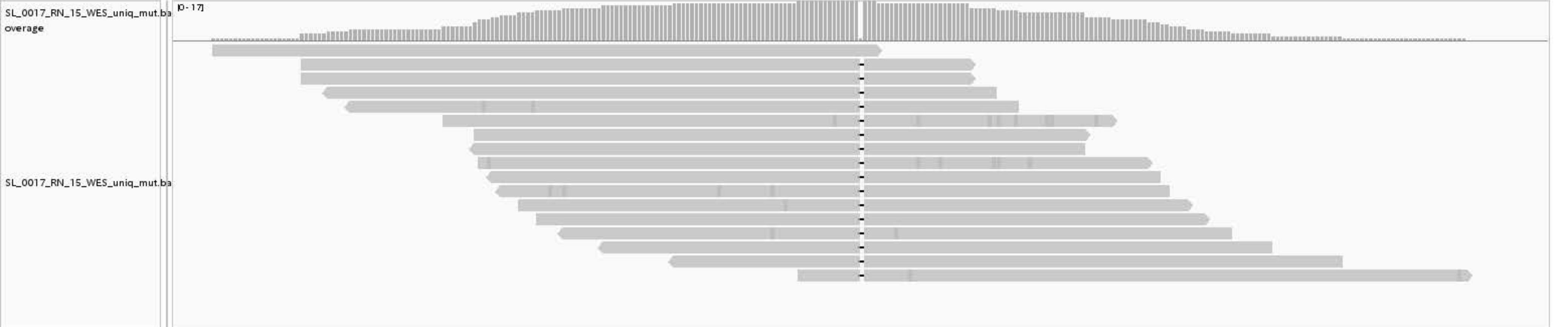
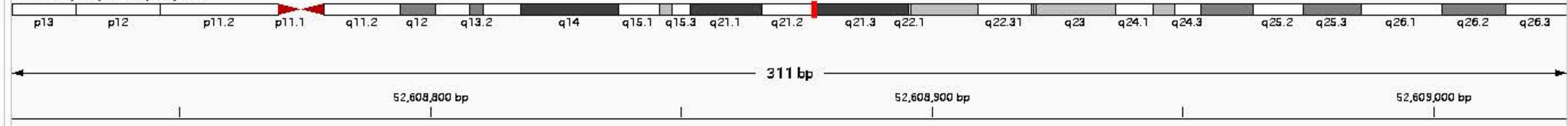


Sequence →



Refseq Genes

chr15:52,608,717-52,609,026



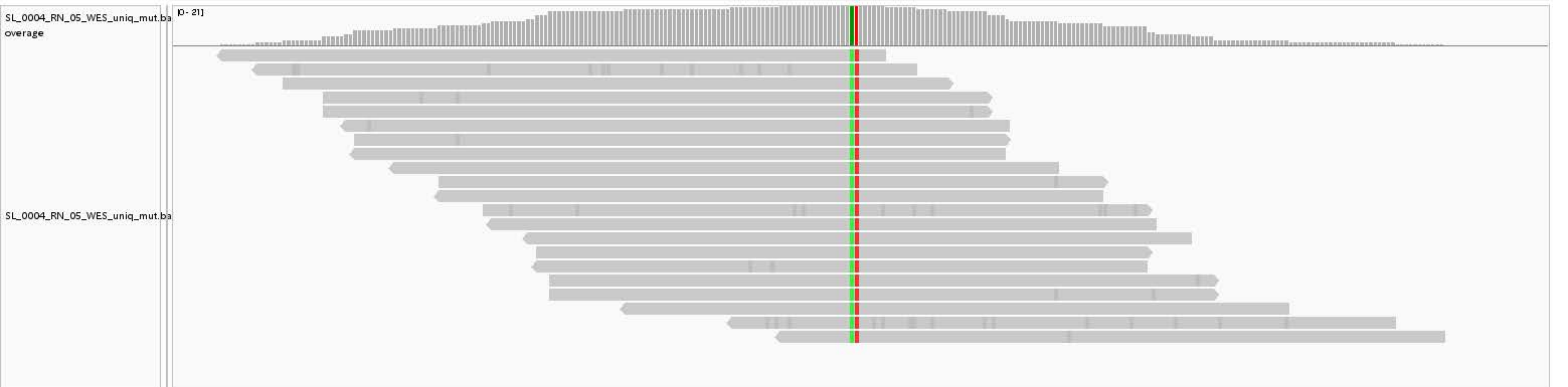
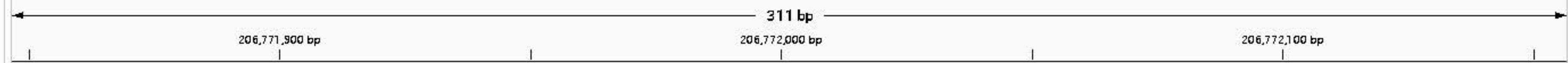
Sequence →  
Refseq Genes

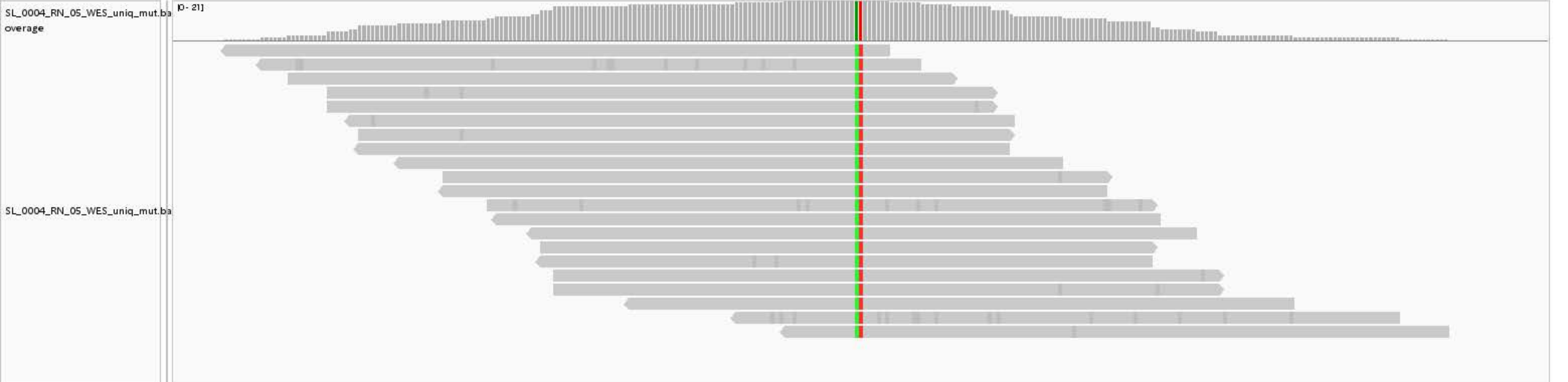
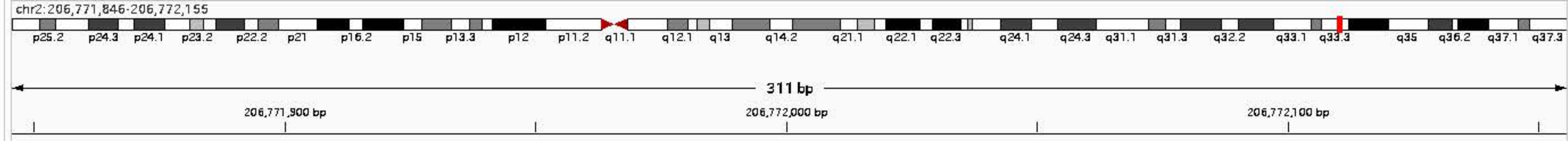
ENDKNLYNEISNLQTNQECTKPRKSDKNSSMSEYKNLYESMELVTVKIKSDNKKSDDSQLNGFFKPNYNENIIEKEYKNTCIQKDITTCNSYQKDIGNSMEQE

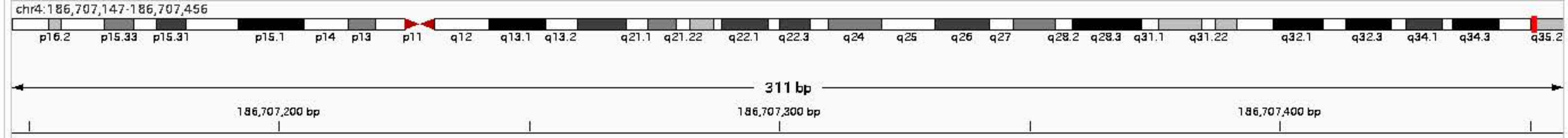
FAM214A



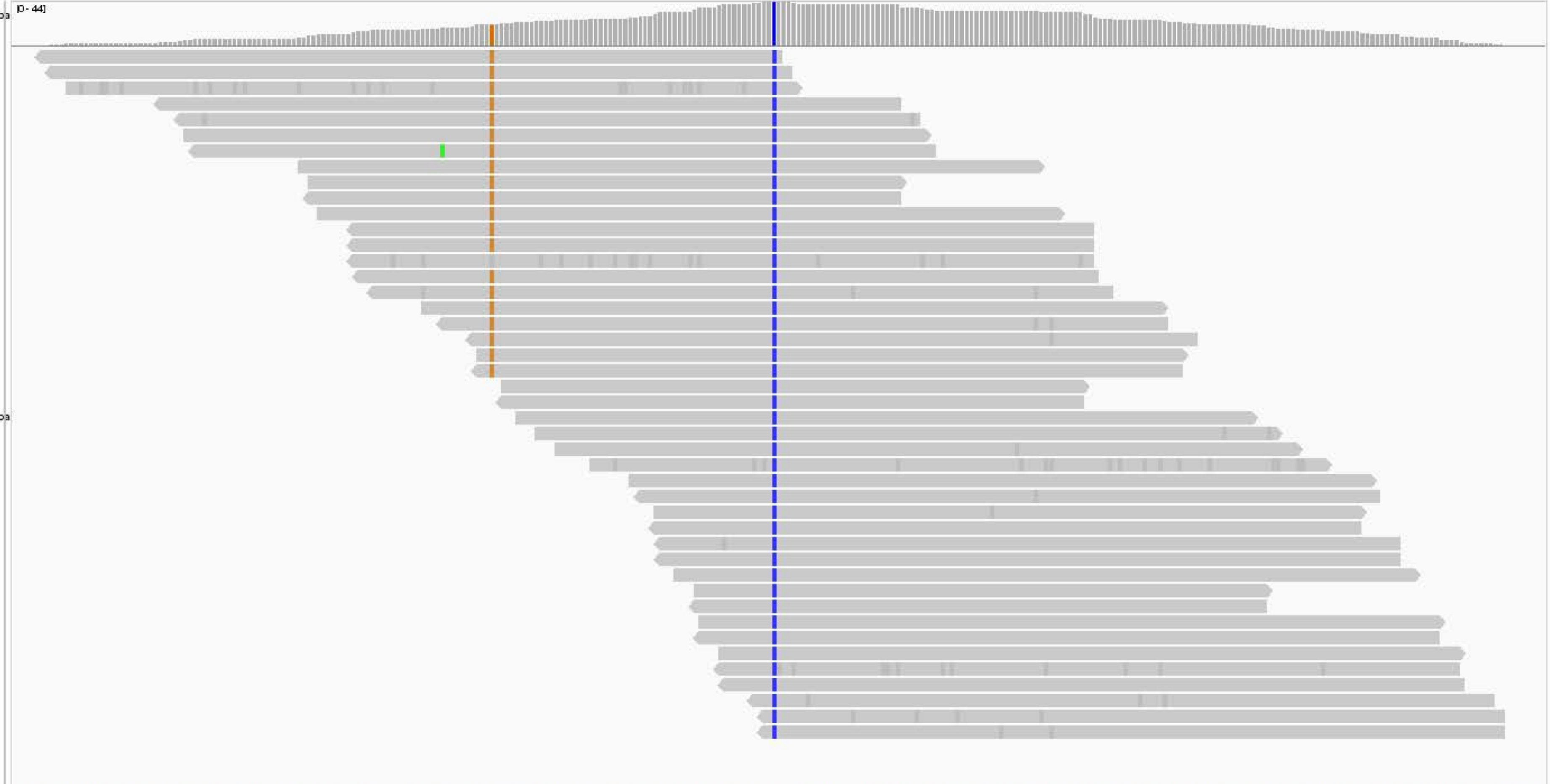
chr2:206,771,847-206,772,156  
p25.2 p24.3 p24.1 p23.2 p22.2 p21 p16.2 p15 p13.3 p12 p11.2 q11.1 q12.1 q13 q14.2 q21.1 q22.1 q22.3 q24.1 q24.3 q31.1 q31.3 q32.2 q33.1 q33.3 q35 q36.2 q37.1 q37.3







SL\_0015\_RN\_10\_WES\_uniq\_mut.ba  
coverage



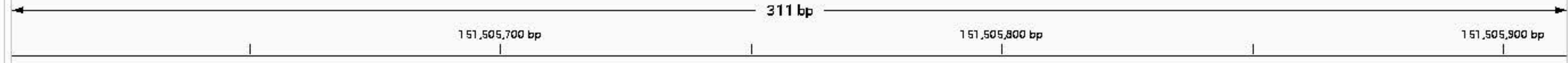
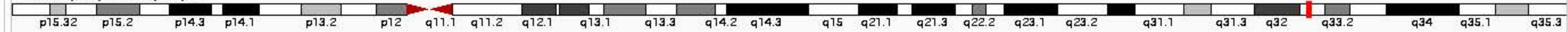
SL\_0015\_RN\_10\_WES\_uniq\_mut.ba

Sequence →  
Refseq Genes

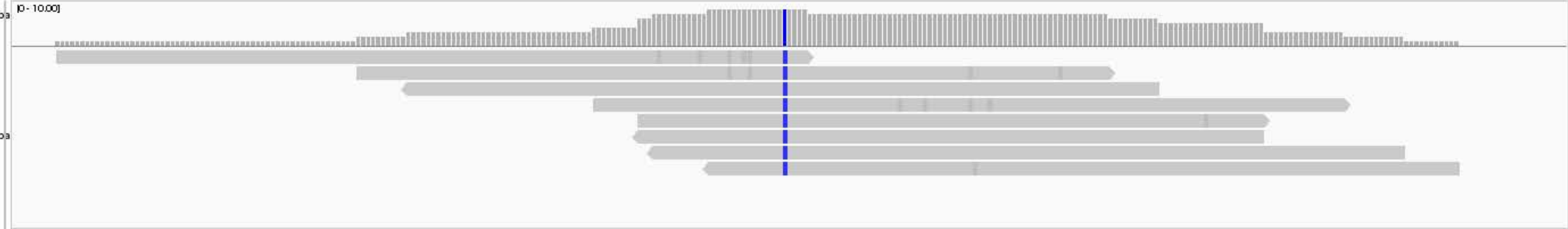
L S H E H Q L E R D L P R A I N V V G T V S D I S F T D T D T V I S Y T V H G N P G L D K D T A E V Q I I E S H V E K D E S V E V F Y S E Q L F E P P N D N A D V V V V H L L R W A A K Q P I G L D Y V T I N  
 FAT1



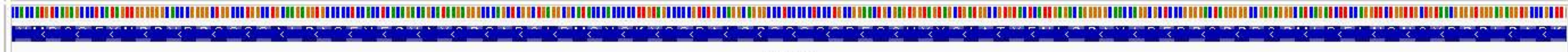
chr5:151,505,603-151,505,912



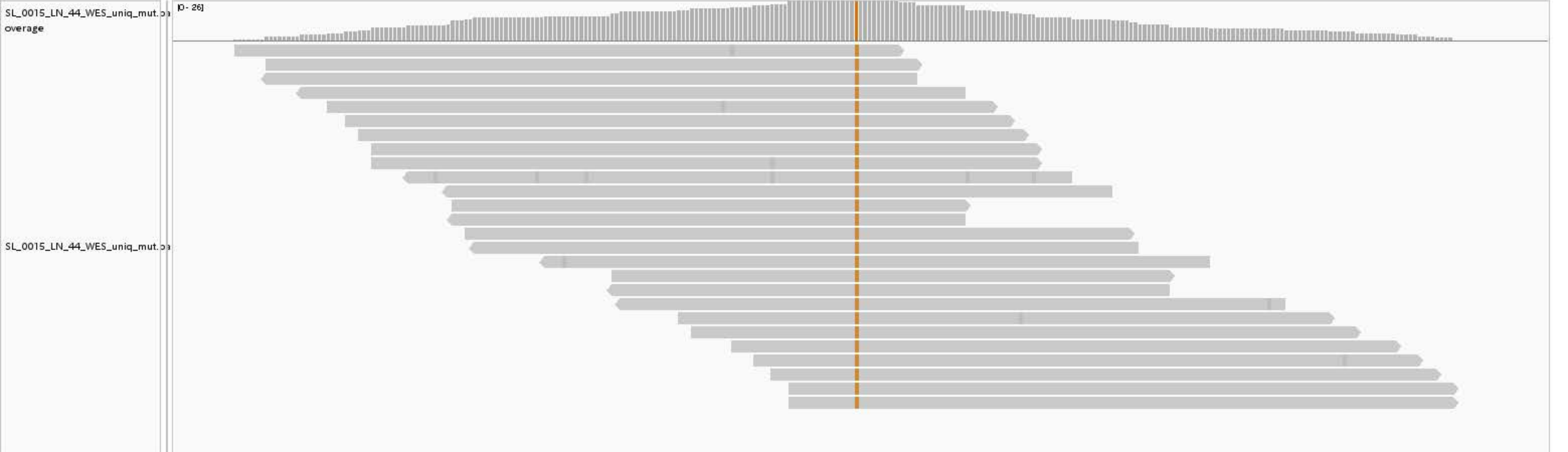
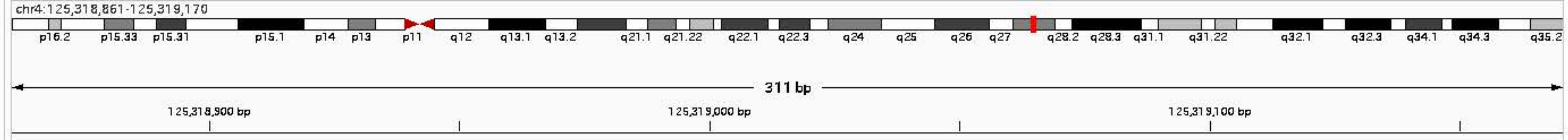
SL\_0006\_RN\_59\_WES\_uniq\_mut.ba  
coverage



Sequence  
Refseq Genes



SLC36A1

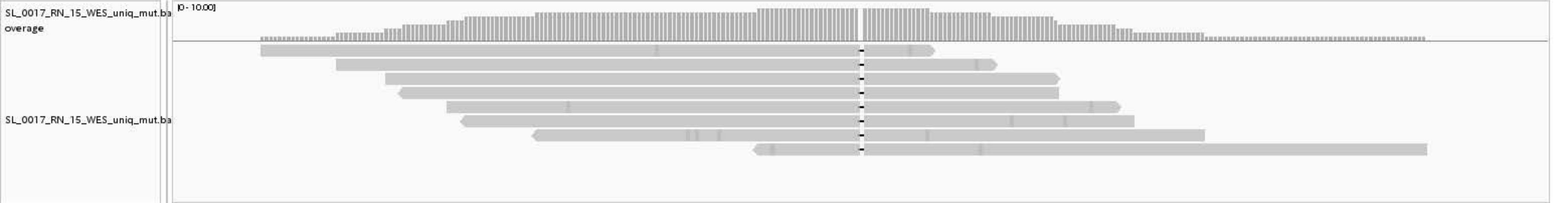
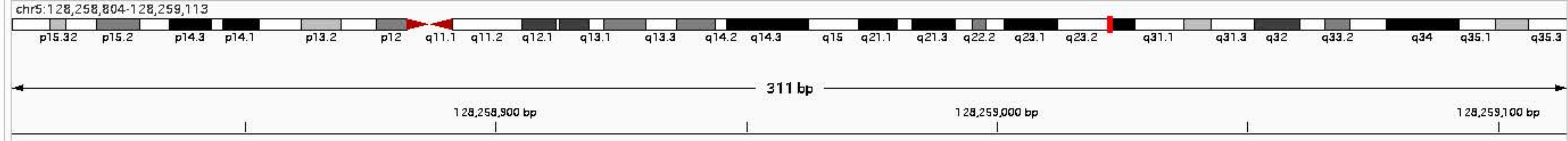


Sequence →

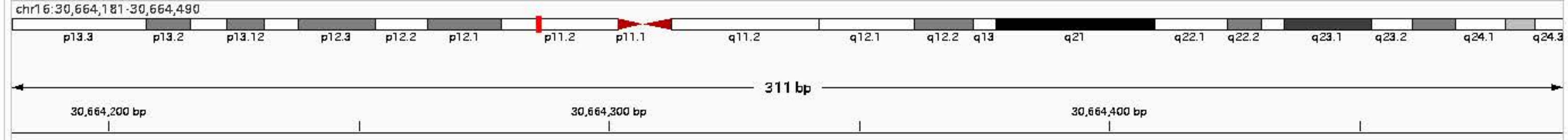
Refseq Genes

ASTMDLNSNISYLITTDGQKGMFAINQVTGQLTTANVIDREEQSFYQLKVVASGGTVTGDTMVNITVKDLNDNSPHFLQAIESVNVVENWQAGHSIFQAKAVDP

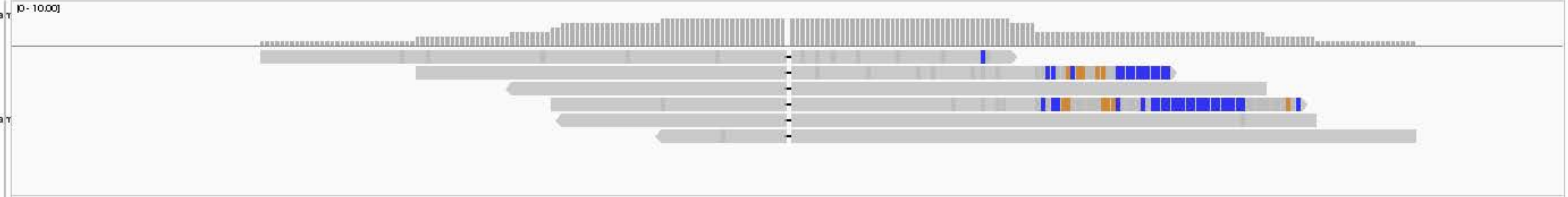
FAT4





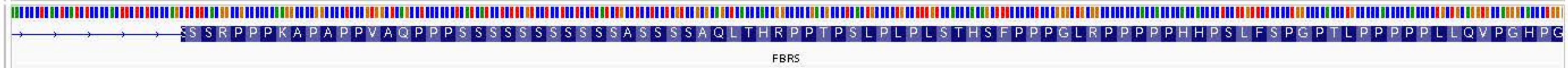


SL\_0007\_RN\_2\_WES\_uniq\_mut.ba  
verage

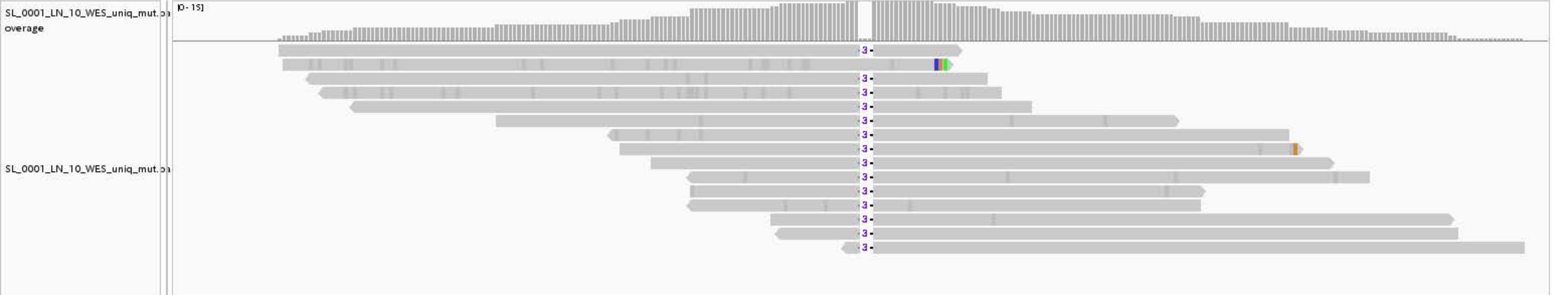
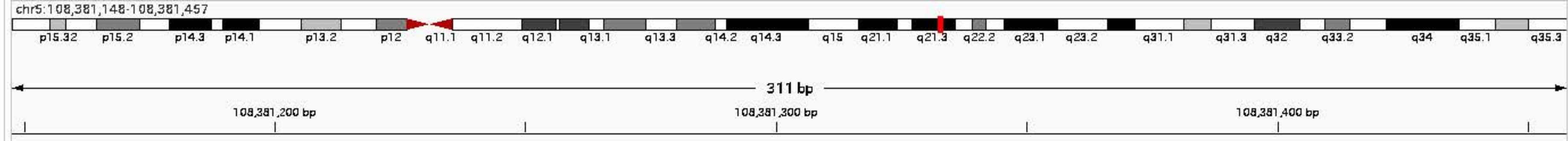


SL\_0007\_RN\_2\_WES\_uniq\_mut.ba

Sequence →



Refseq Genes

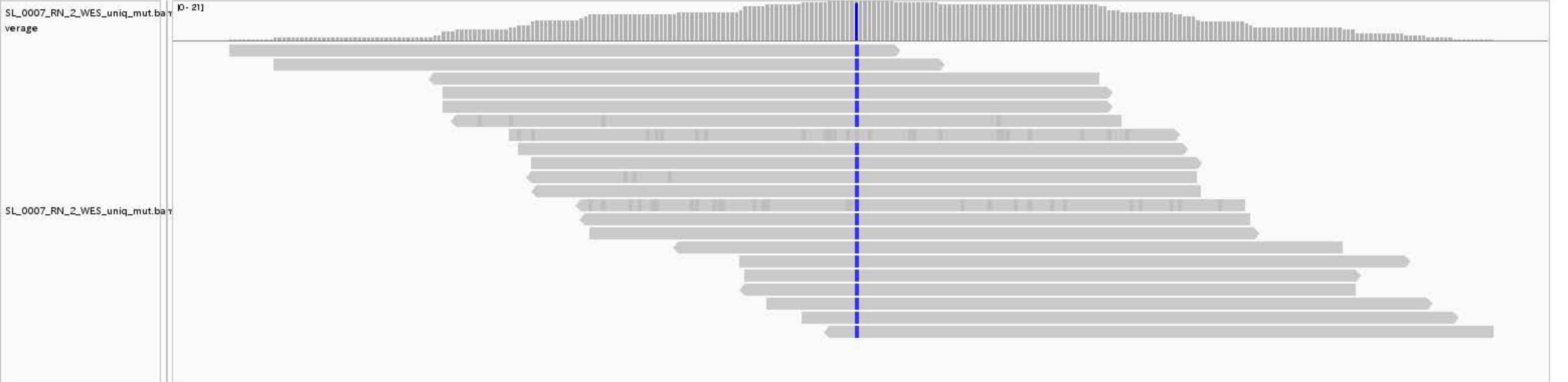
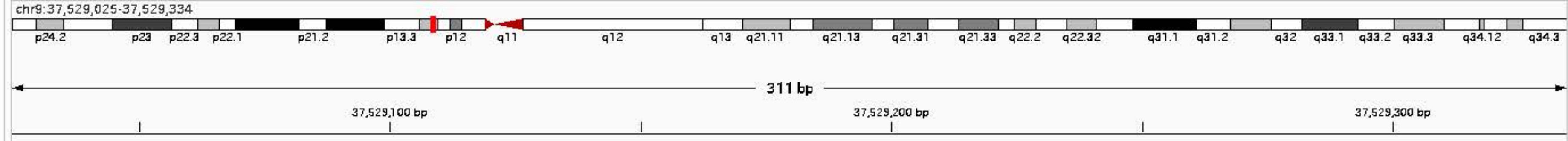


Sequence →

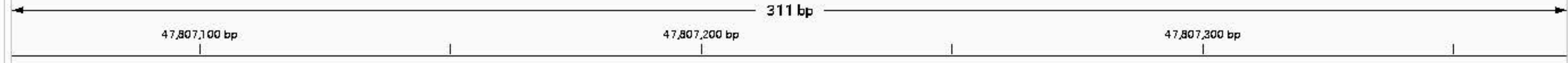
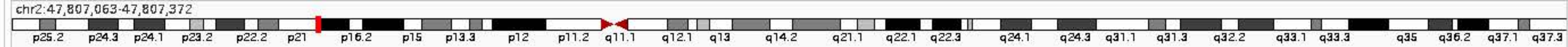
Refseq Genes

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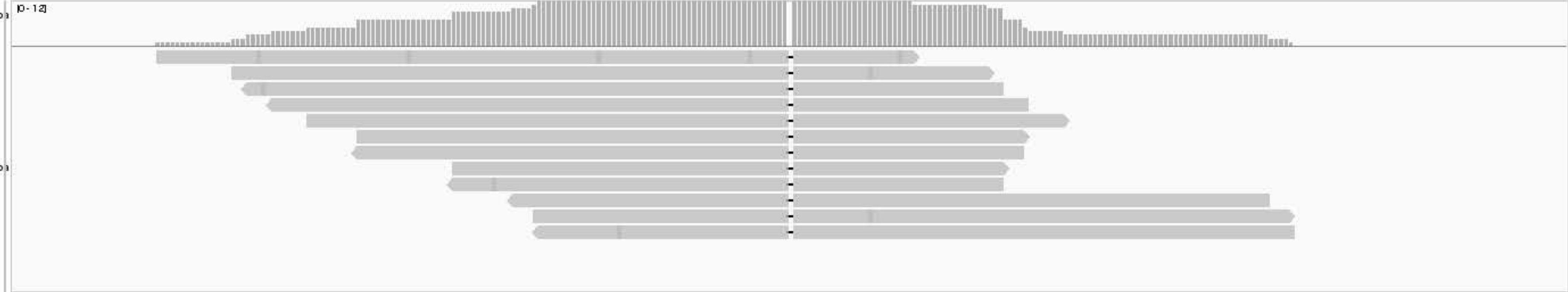
FBXL17







SL\_0001\_LN\_10\_WES\_uniq\_mut. coverage



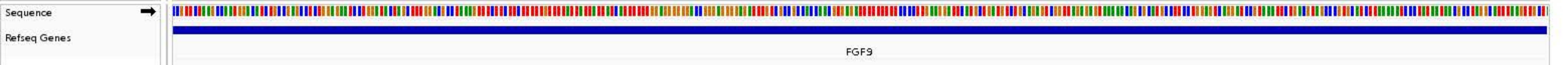
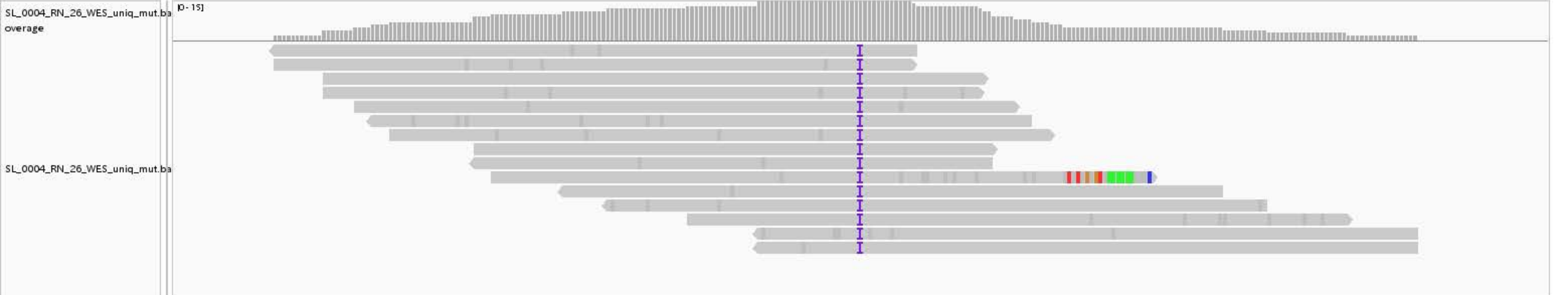
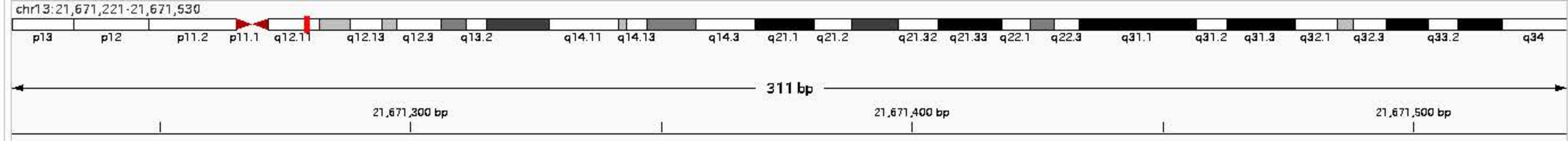
SL\_0001\_LN\_10\_WES\_uniq\_mut. coverage

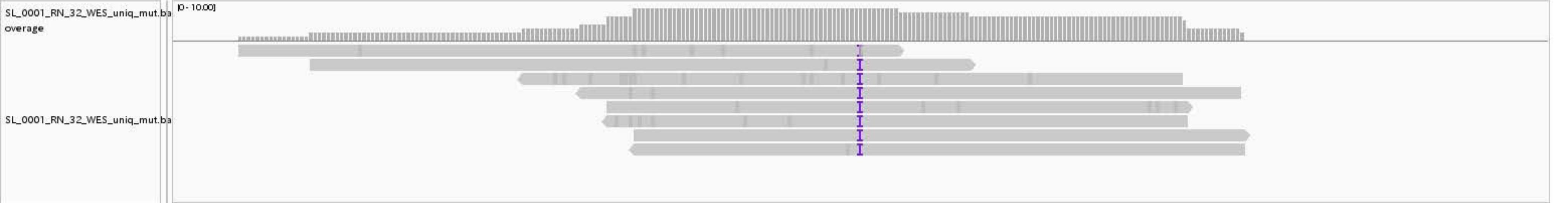
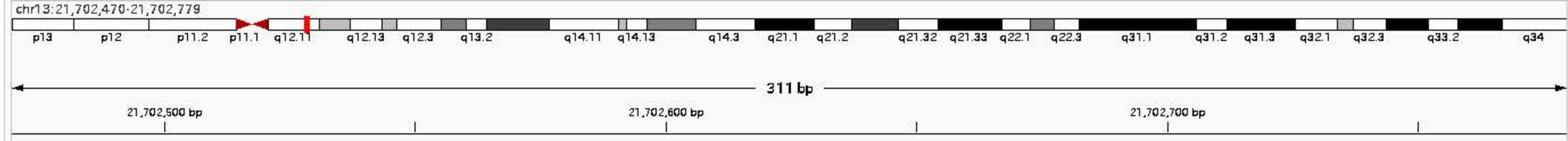
Sequence

Refseq Genes

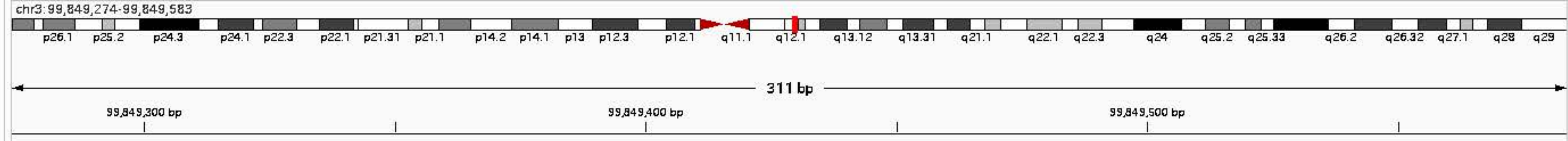


FBXO11

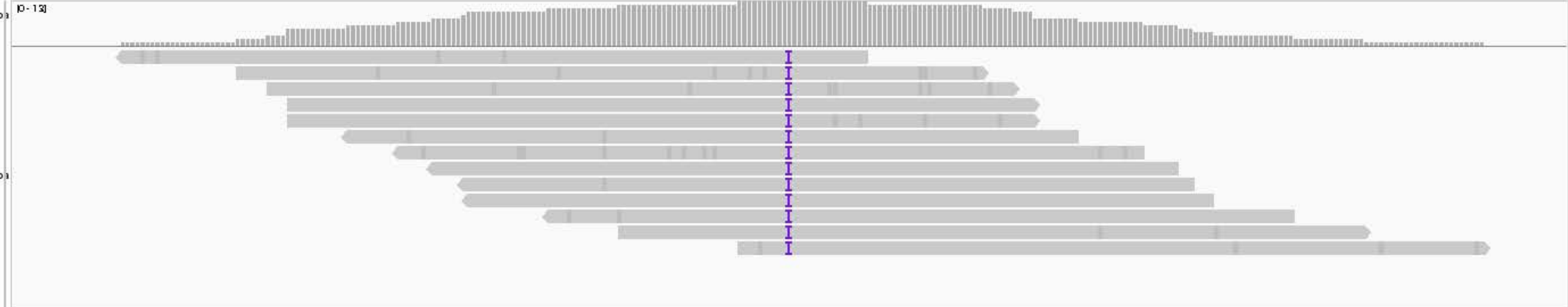








SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage

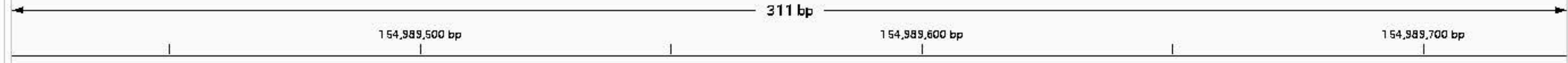


Sequence Refseq Genes

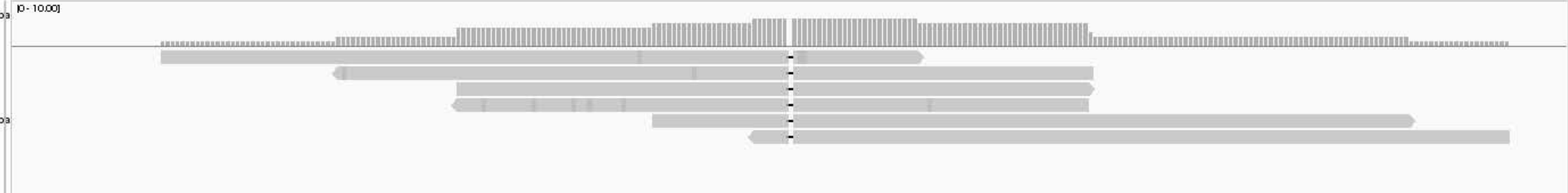
QVEKSFVQPDSIRRGNLS PRLSKSFHRYRELEKTLNEIERGLDRNRNEQQNLKKQLVSHDGQLHCILD ETAMYEH I KEKLADVERS LHGSKAEEEQ L RKFLWQE

CMSS1

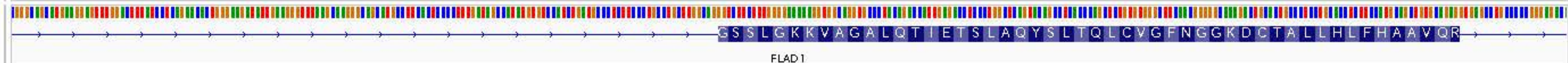
chr1:154,989,419-154,989,728  
p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44



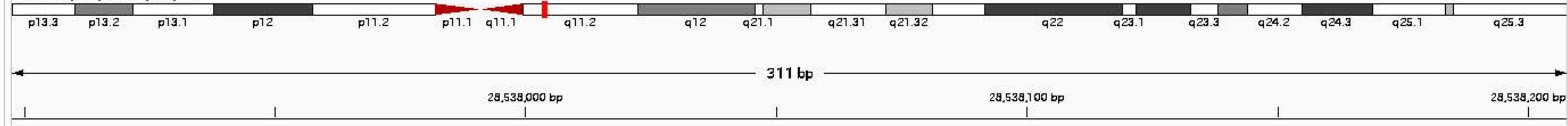
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overage  
SL\_0006\_RN\_67\_WES\_uniq\_mut.ba



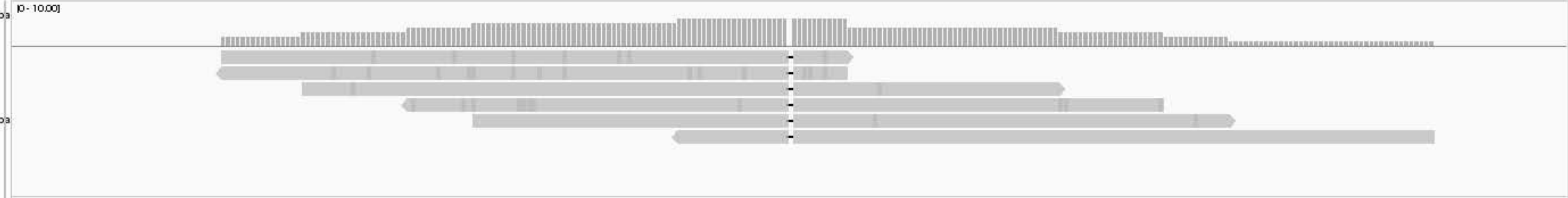
Sequence  
Refseq Genes



chr17:28,537,898-28,538,207



SL\_0017\_RN\_15\_WES\_uniq\_mut.ba  
coverage



SL\_0017\_RN\_15\_WES\_uniq\_mut.ba

Sequence

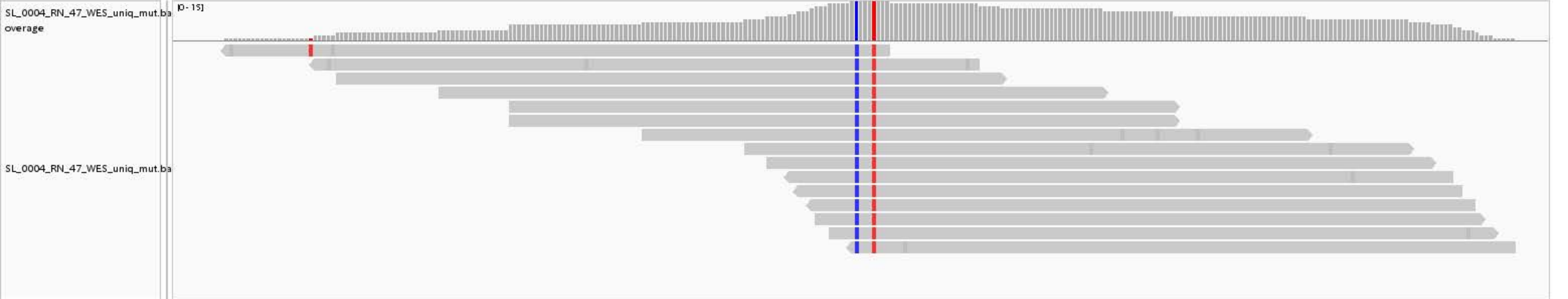
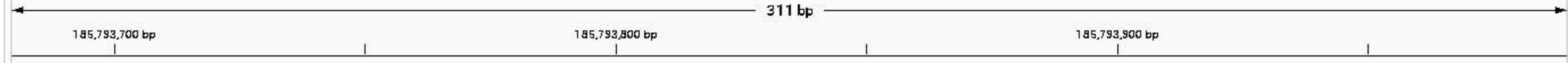


Refseq Genes

FOXN1

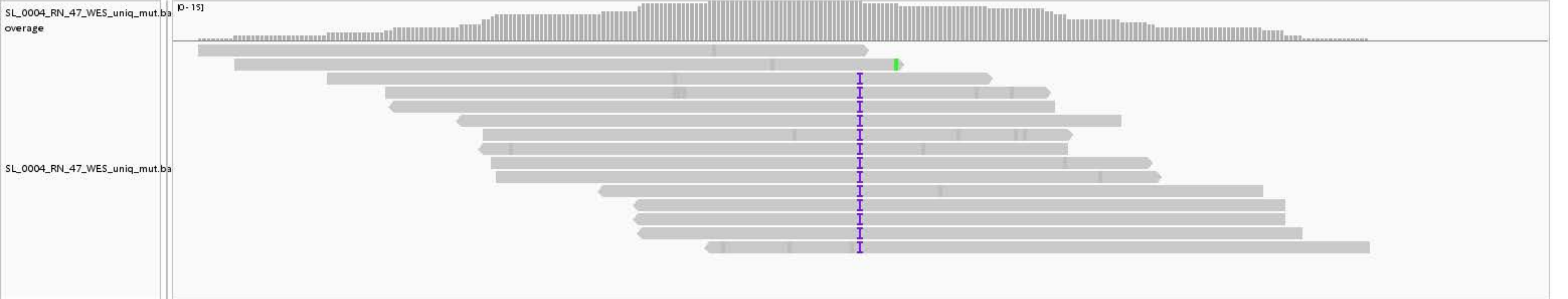
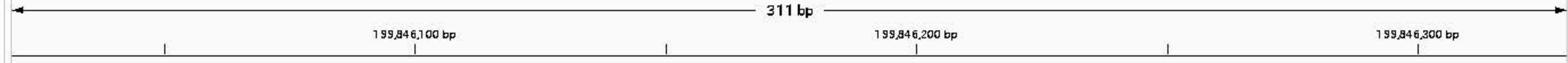


chr2:185,793,680-185,793,989  
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Sequence →  
Refseq Genes  
SARLPLTFCDTFPKIDCQQPLKGSKTERKTERFSYSRNQKSAYADDNQITVVEKEDTQKSATDSC EENANFITKTIKRLLESFATERIDSLITLAFQSKESF  
FSIP2

chr2:199,846,020-199,846,329  
p25.2 p24.3 p24.1 p23.2 p22.2 p21 p16.2 p15 p13.3 p12 p11.2 q11.1 q12.1 q13 q14.2 q21.1 q22.1 q22.3 q24.1 q24.3 q31.1 q31.3 q32.2 q33.1 q33.3 q35 q36.2 q37.1 q37.3



chrX:154,535,140-154,535,449

p22.32 p22.2 p22.13 p22.11 p21.2 p11.4 p11.3 p11.22 p11.1 q11.2 q13.1 q13.3 q21.1 q21.2 q21.32 q22.1 q22.3 q23 q24 q25 q26.1 q26.3 q27.2 q28



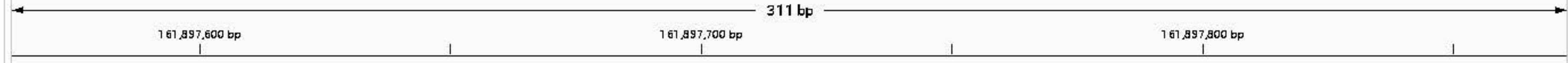
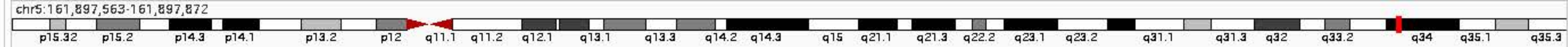
SL\_0001\_RN\_15\_WES\_uniq\_mut.ba  
coverage



Sequence  
Refseq Genes

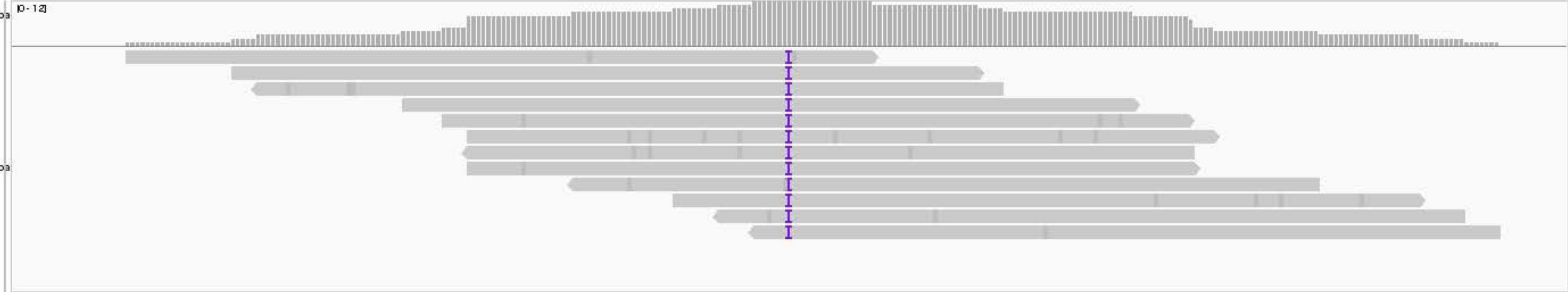






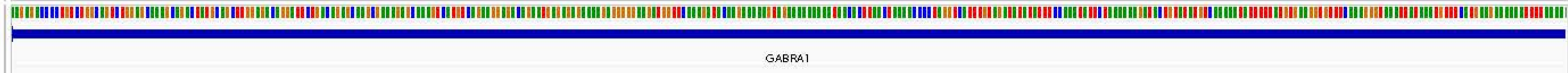
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overage

SL\_0015\_RN\_12\_WES\_uniq\_mut.ba



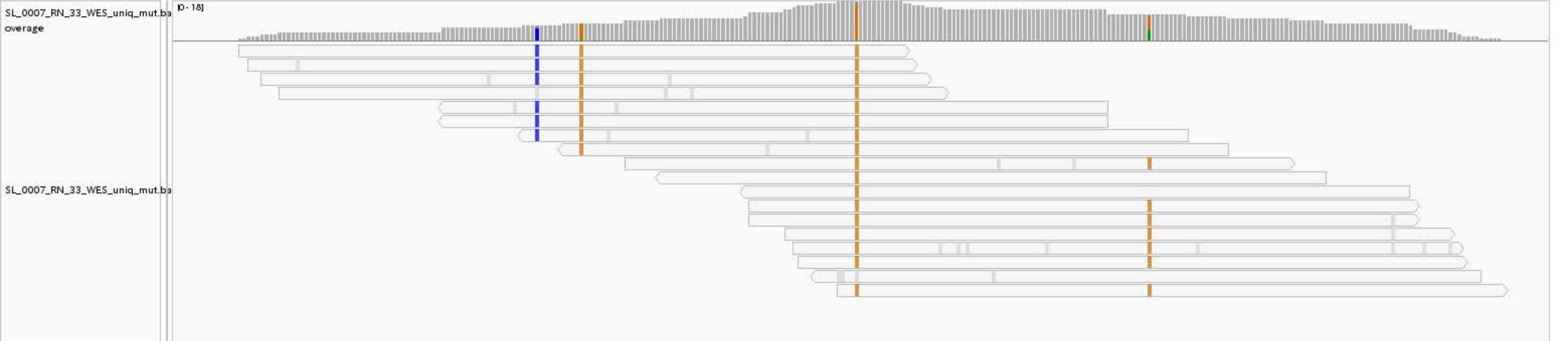
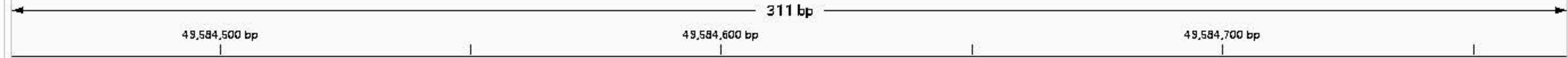
Sequence →

Refseq Genes



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p22.32 p22.2 p22.13 p22.11 p21.2 p11.4 p11.3 p11.22 p11.1 q11.2 q13.1 q13.3 q21.1 q21.2 q21.32 q22.1 q22.3 q23 q24 q25 q26.1 q26.3 q27.2 q28



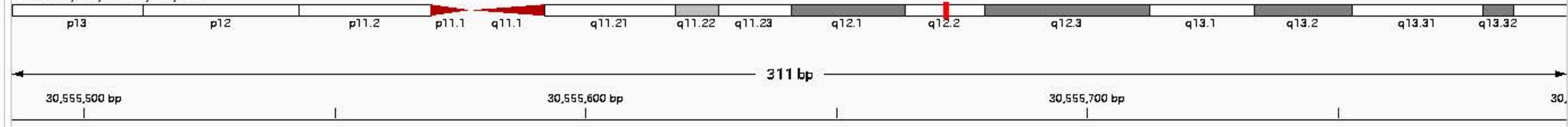
Sequence →

Refseq Genes

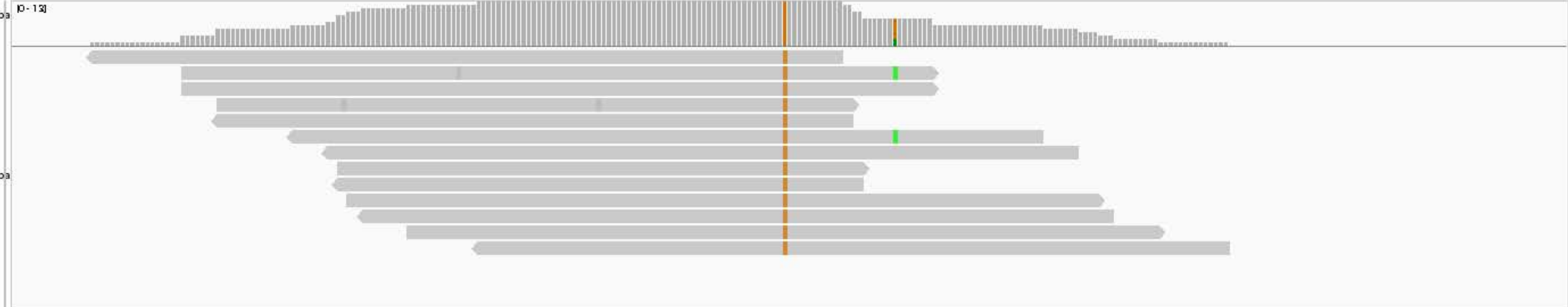
GPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEC

GAGE12H

chr22:30,555,486-30,555,795



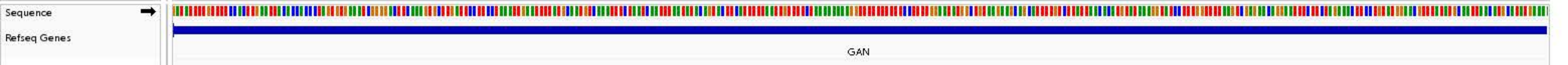
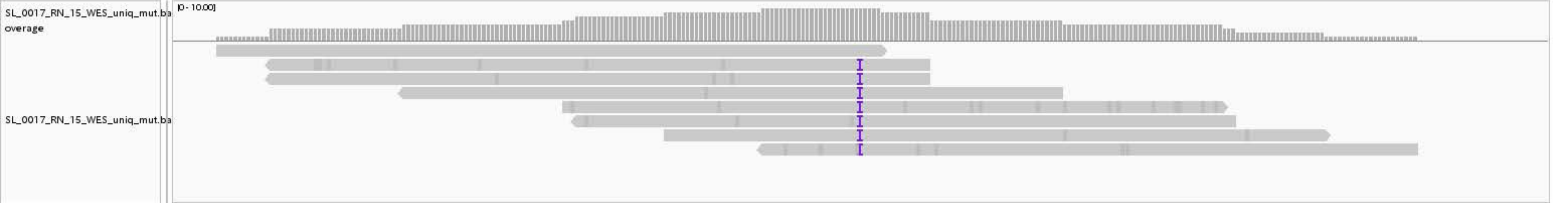
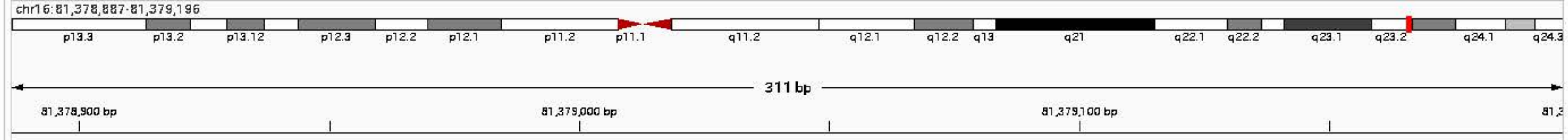
SL\_0007\_RN\_33\_WES\_uniq\_mut.ba  
coverage

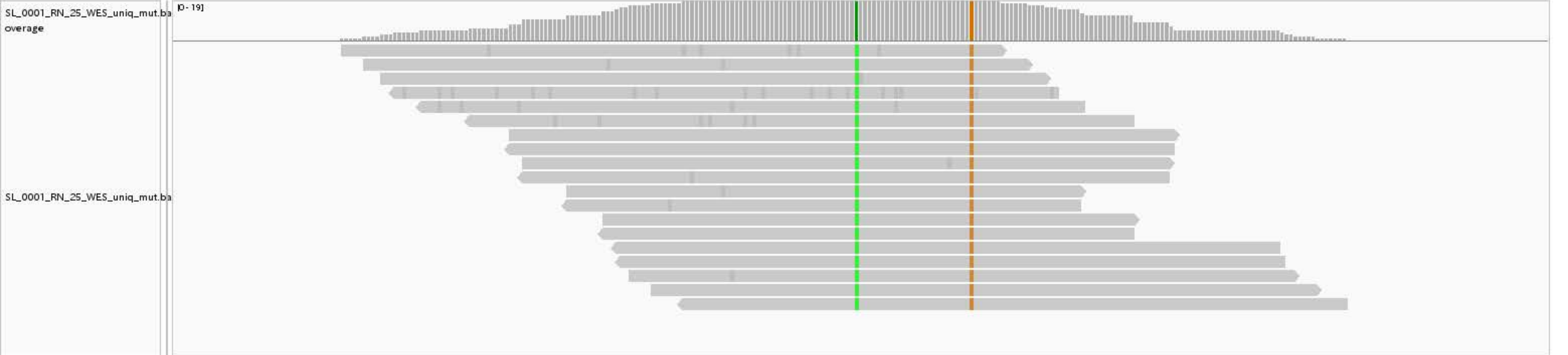
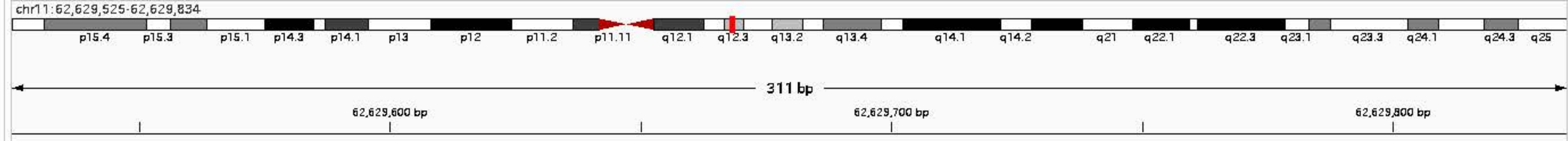


Sequence  
Refseq Genes

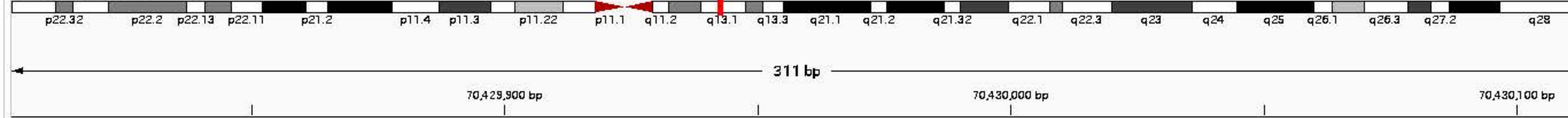
FRREVELIHEQVQPSSPDLNDYGLDFLLNRLYHANFGNPDYRDPDQLFETLKDGLKWTLPVVPGFYHFSSEFLRAPDRLVTIFIANTPVLGRVEDYHF  
GAL3ST1



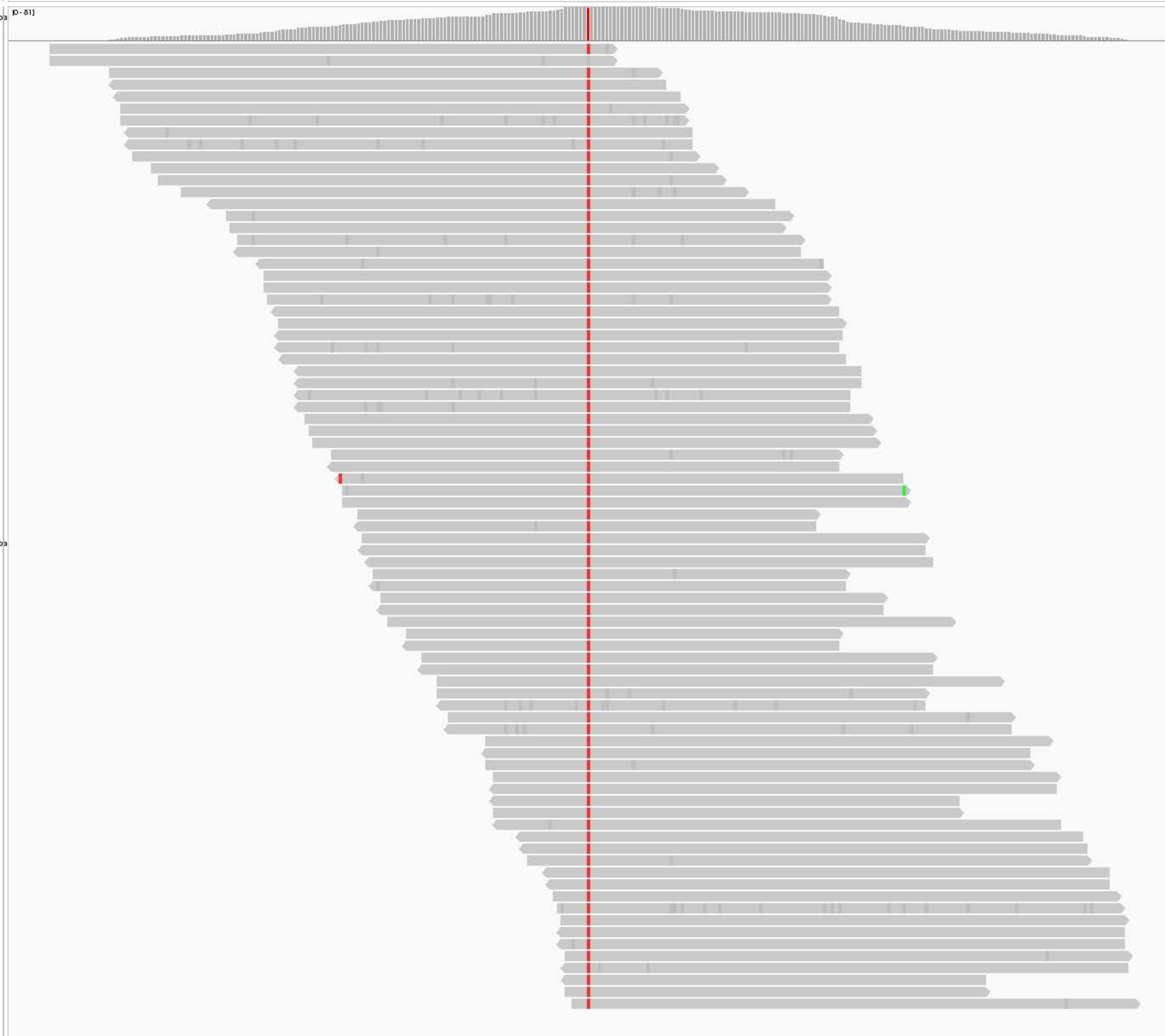




chrX: 70,429,803-70,430,112

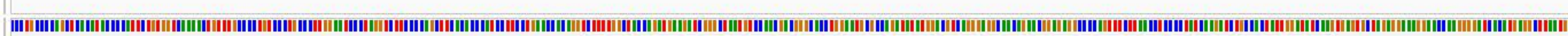


SL\_0004\_RN\_24\_WES\_uniq\_mut.ba  
overage



SL\_0004\_RN\_24\_WES\_uniq\_mut.ba

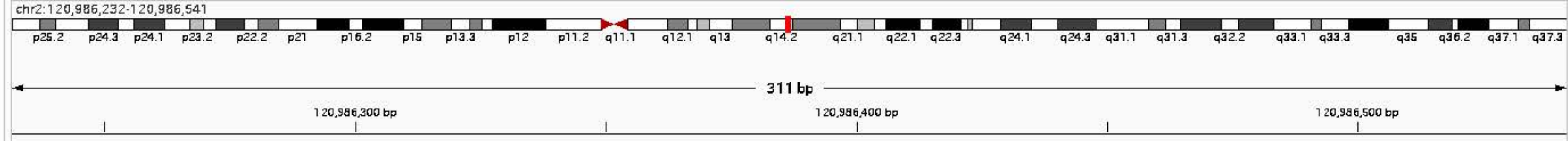
Sequence →



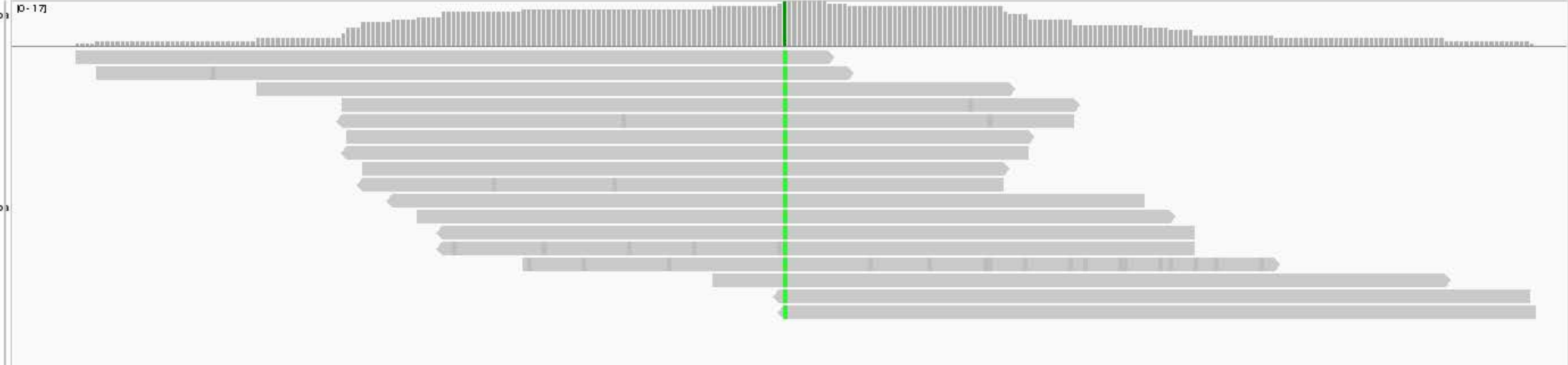
Refseq Genes

GDPD2





SL\_0015\_LN\_44\_WES\_uniq\_mut. coverage



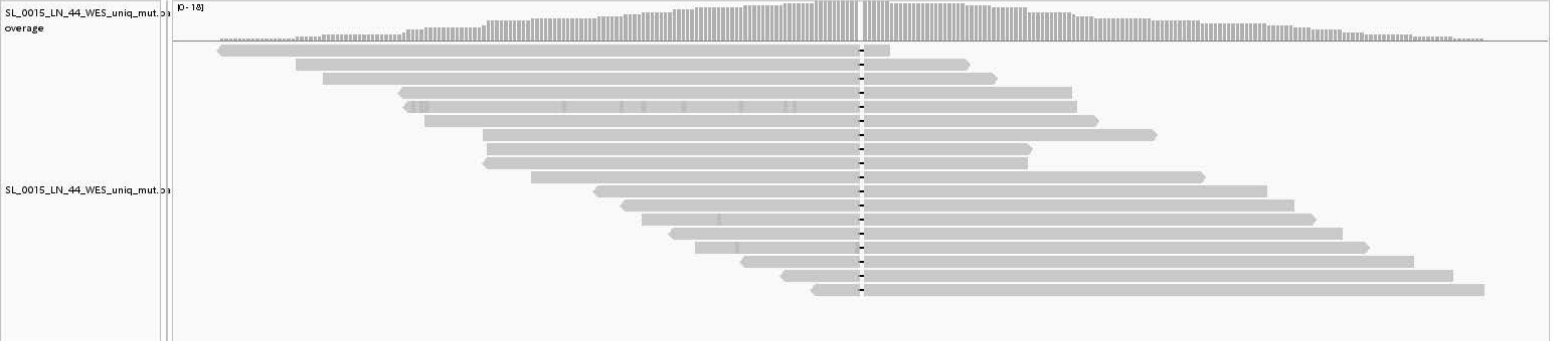
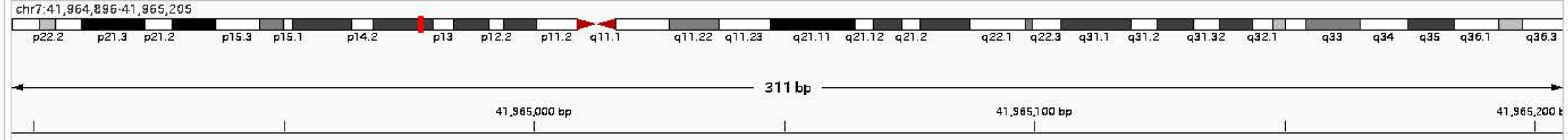
SL\_0015\_LN\_44\_WES\_uniq\_mut.

Sequence



Refseq Genes

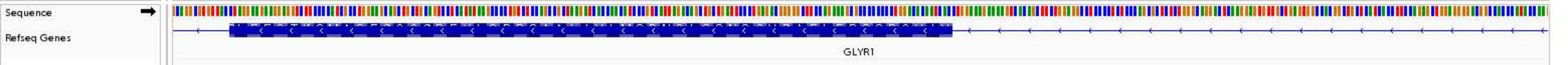
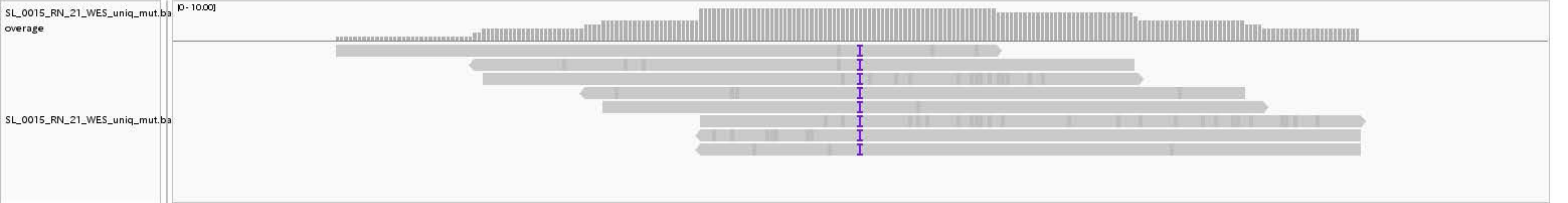
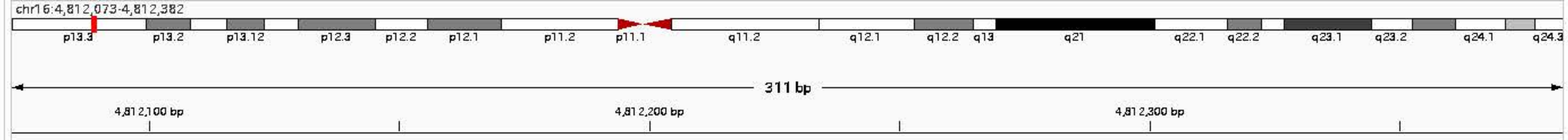
GLI2



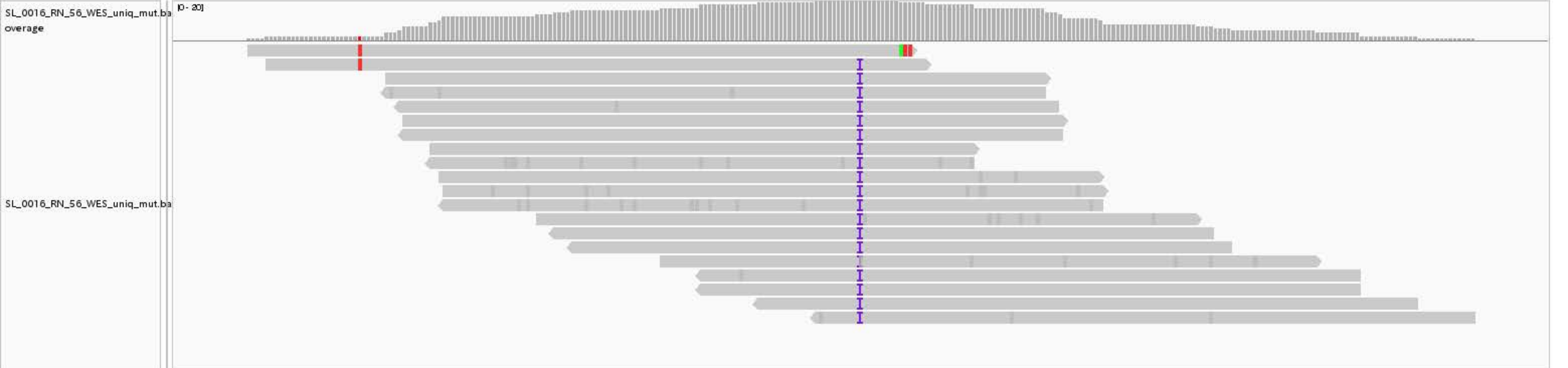
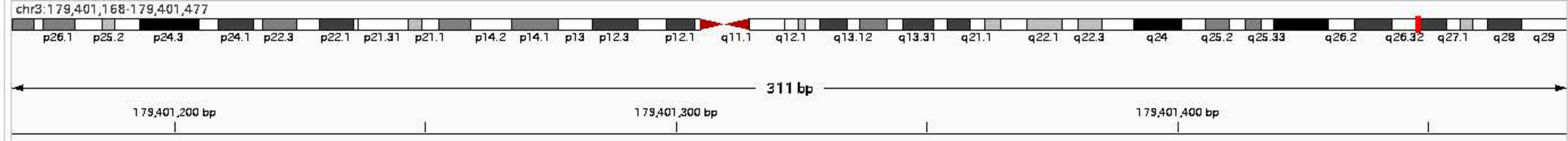
Sequence Refseq Genes

SGGFSACPQYGRVVALSSPQSGMGHAGPLCSEPGQYINIHSTASIQGLMQQGPRGAGPHQMSDGLLQHALYGQGVDPQNMGNVMSGASENPAVPLGFNLQGG

GLI3

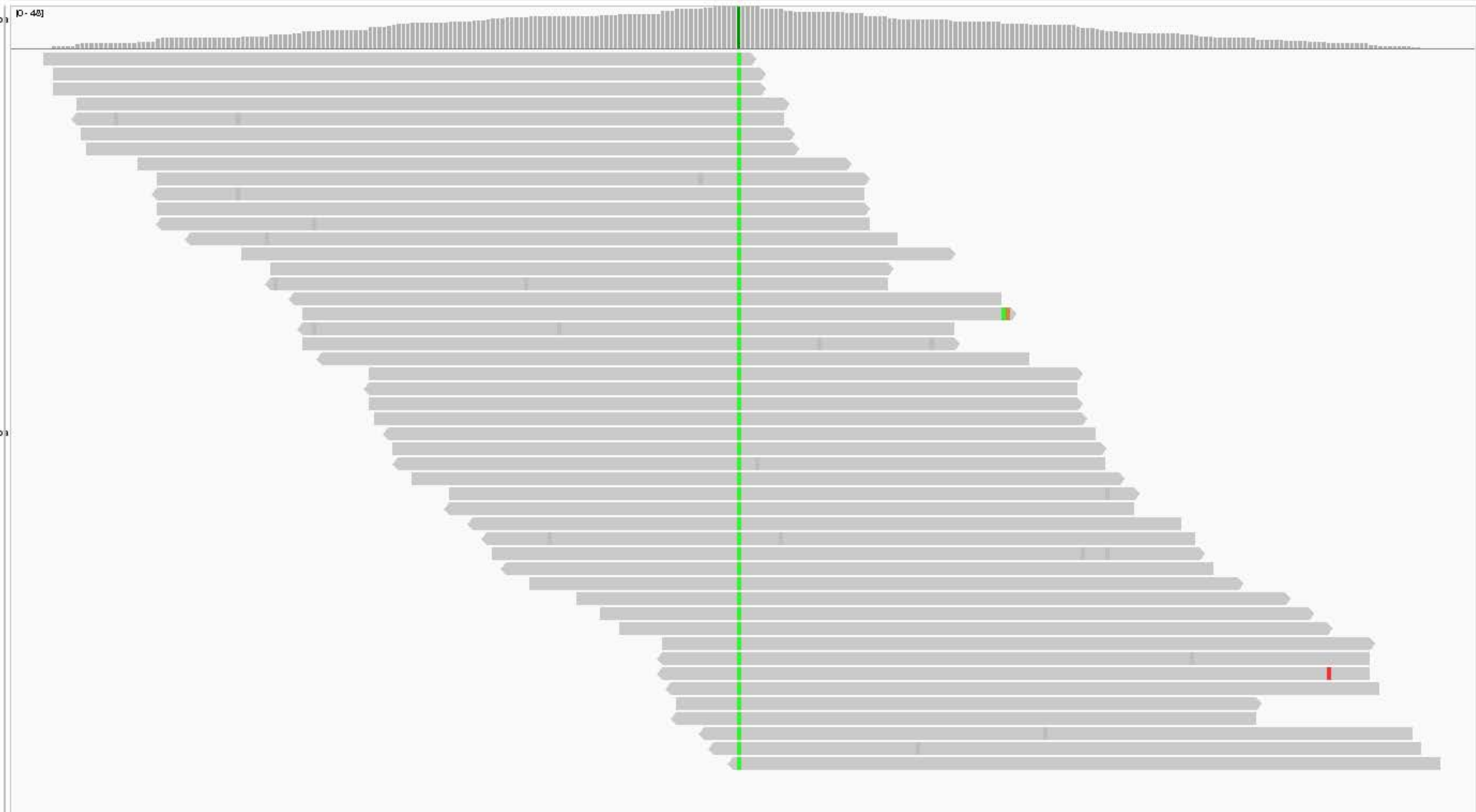








SL\_0015\_LN\_44\_WES\_uniq\_mut. coverage

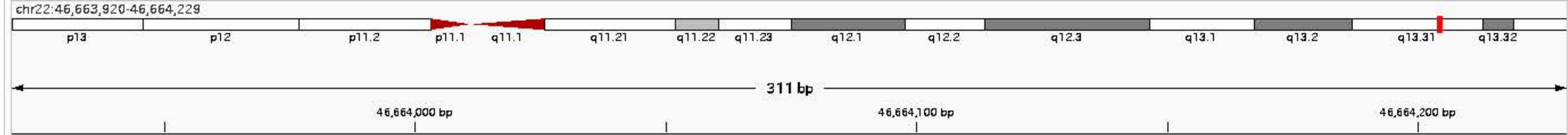


SL\_0015\_LN\_44\_WES\_uniq\_mut.

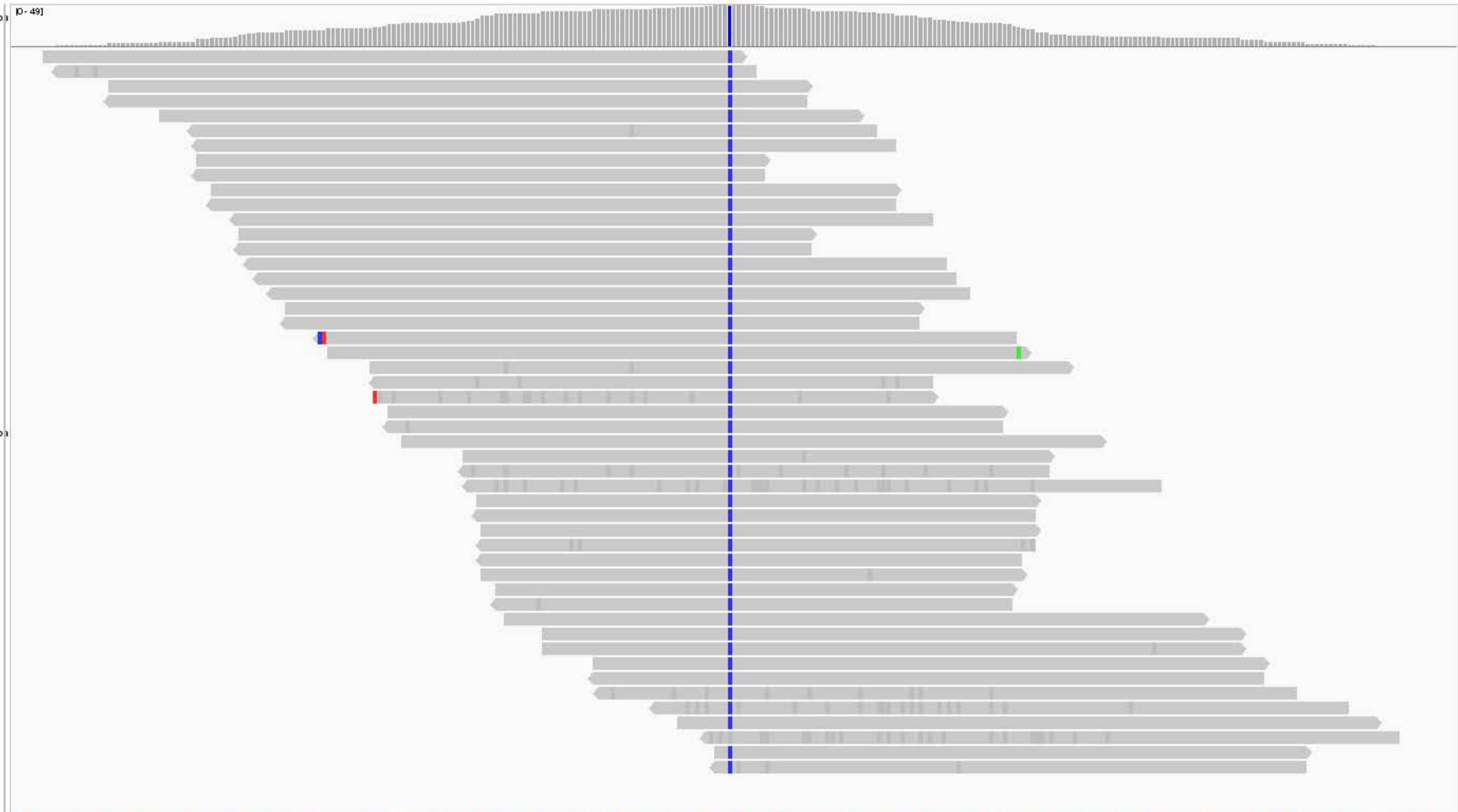
Sequence →

Refseq Genes





SL\_0015\_LN\_44\_WES\_uniq\_mut.  
coverage



SL\_0015\_LN\_44\_WES\_uniq\_mut.

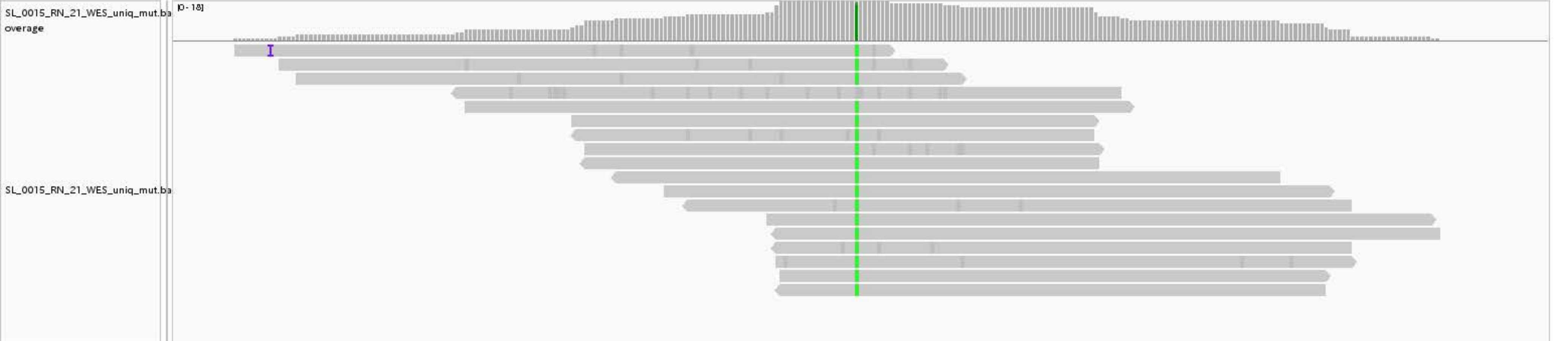
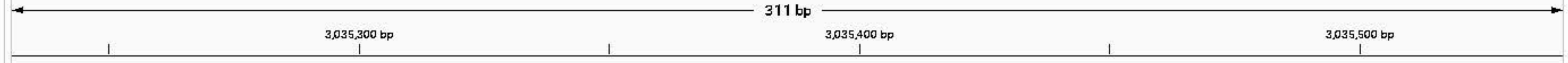
Sequence →  
Refseq Genes



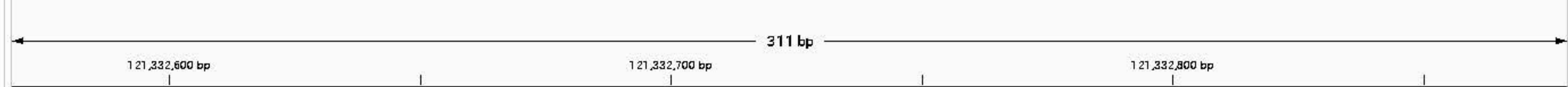


chr4:3,035,231-3,035,540

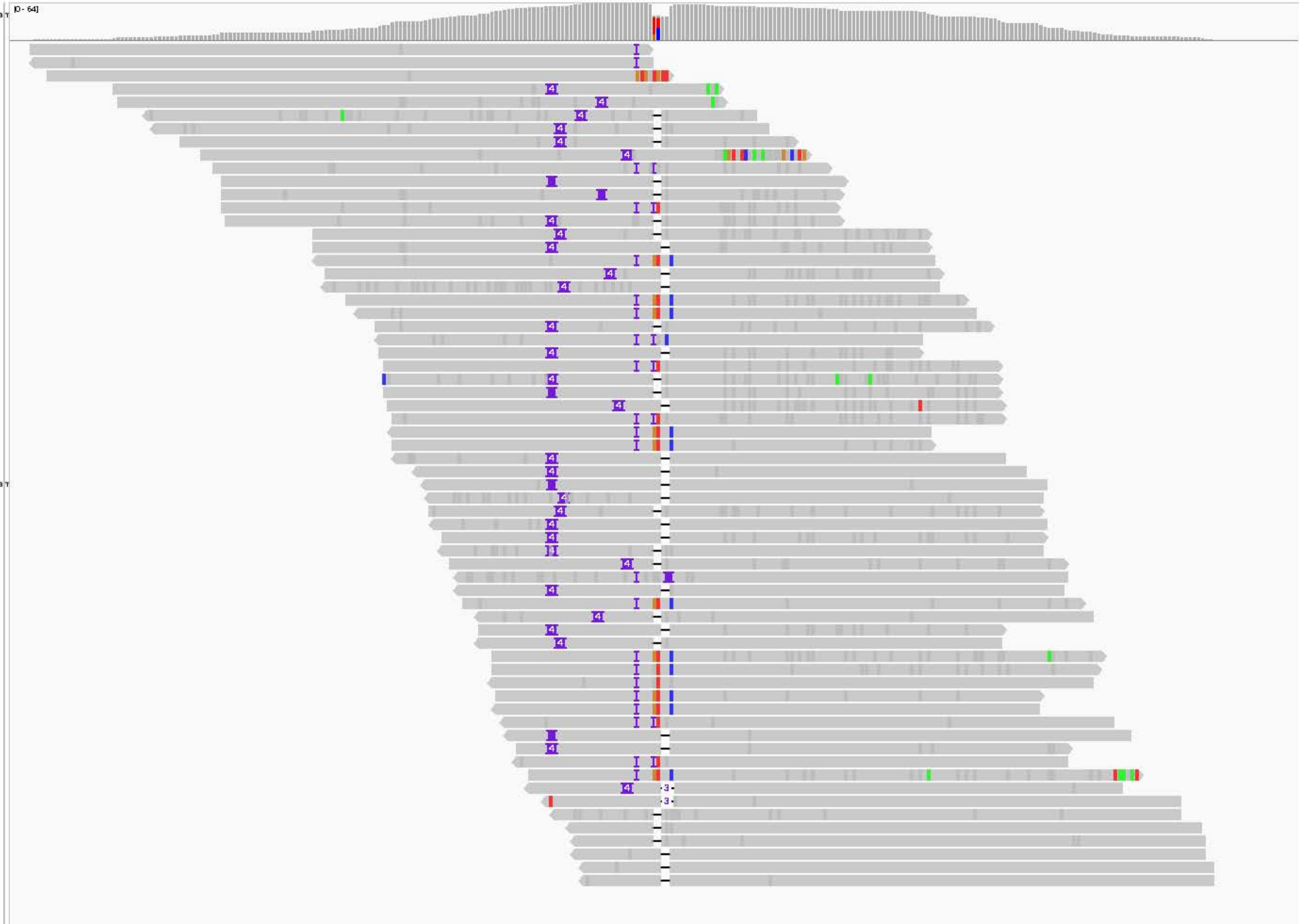
p16.2 p15.33 p15.31 p15.1 p14 p13 p11 q12 q13.1 q13.2 q21.1 q21.22 q22.1 q22.3 q24 q25 q26 q27 q28.2 q28.3 q31.1 q31.22 q32.1 q32.3 q34.1 q34.3 q35.2



chr9:121,332,569-121,332,878



SL\_0002\_RN\_8\_WES\_uniq\_mut\_ba  
verage

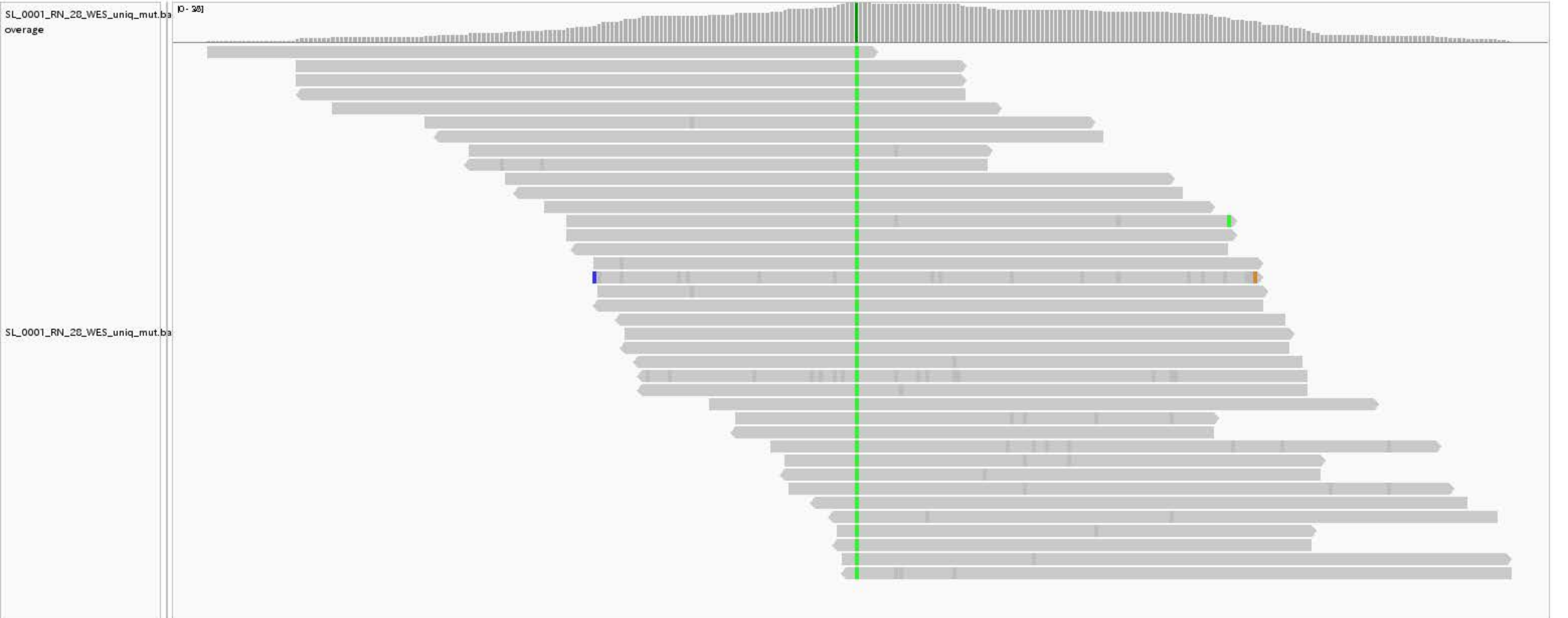
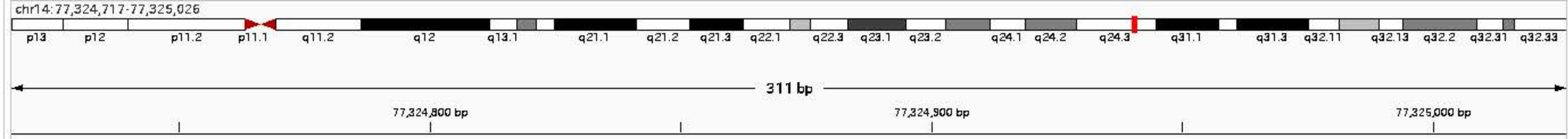


SL\_0002\_RN\_8\_WES\_uniq\_mut\_ba

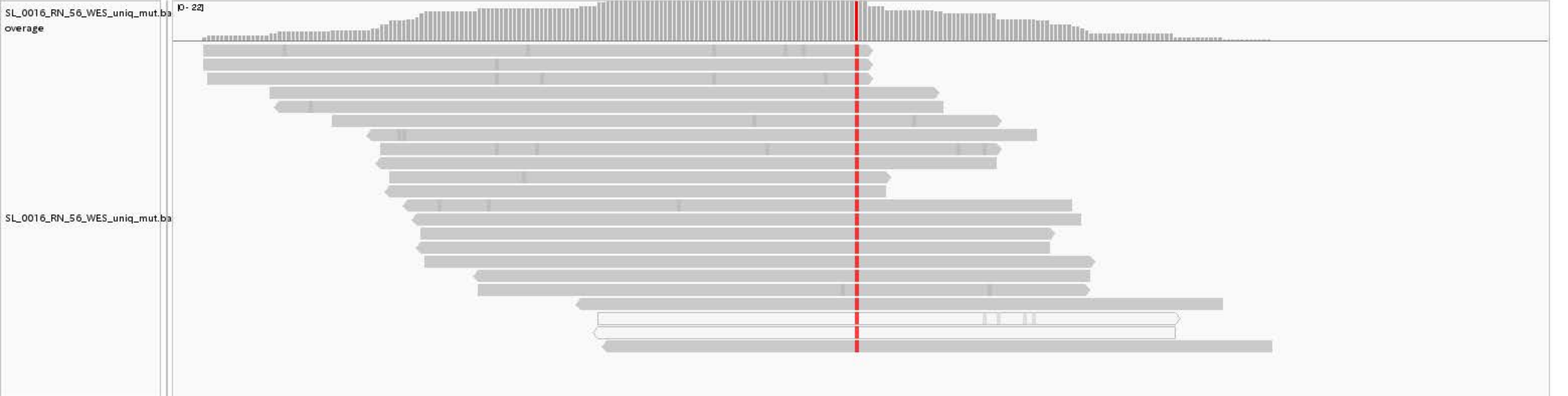
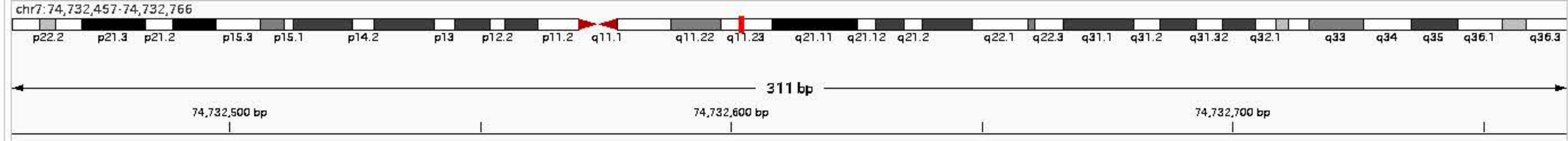
Sequence →  
Refseq Genes

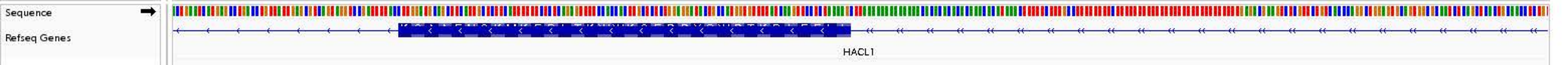
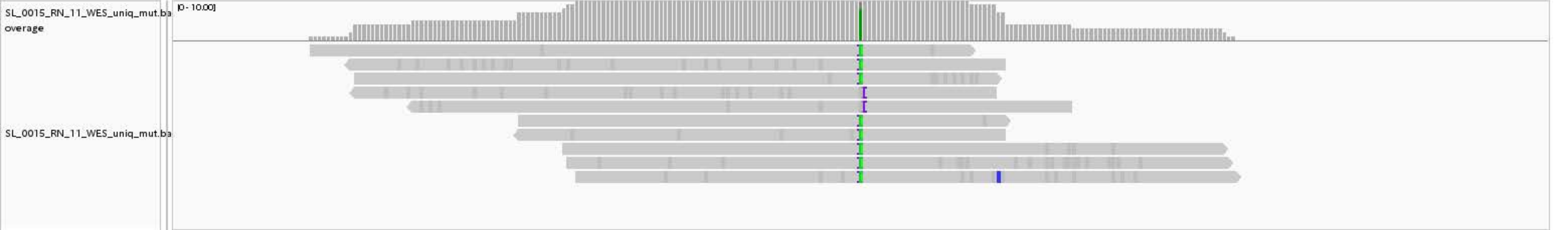
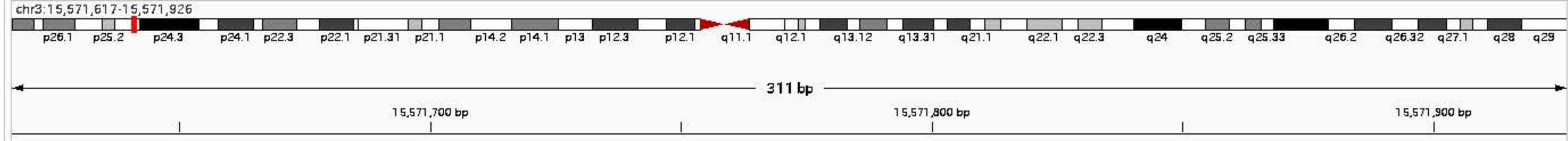


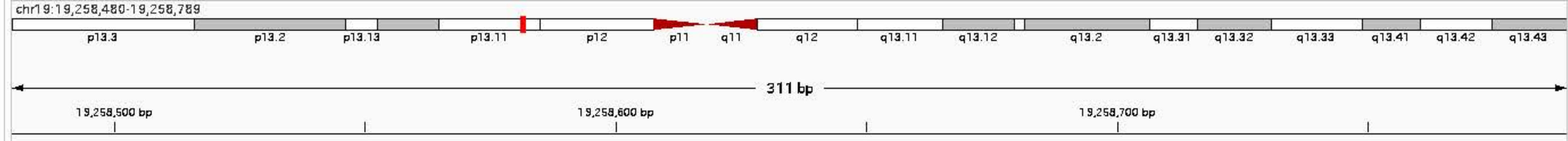
GSN











SL\_0015\_LN\_44\_WES\_uniq\_mut. ba  
coverage



SL\_0015\_LN\_44\_WES\_uniq\_mut. ba

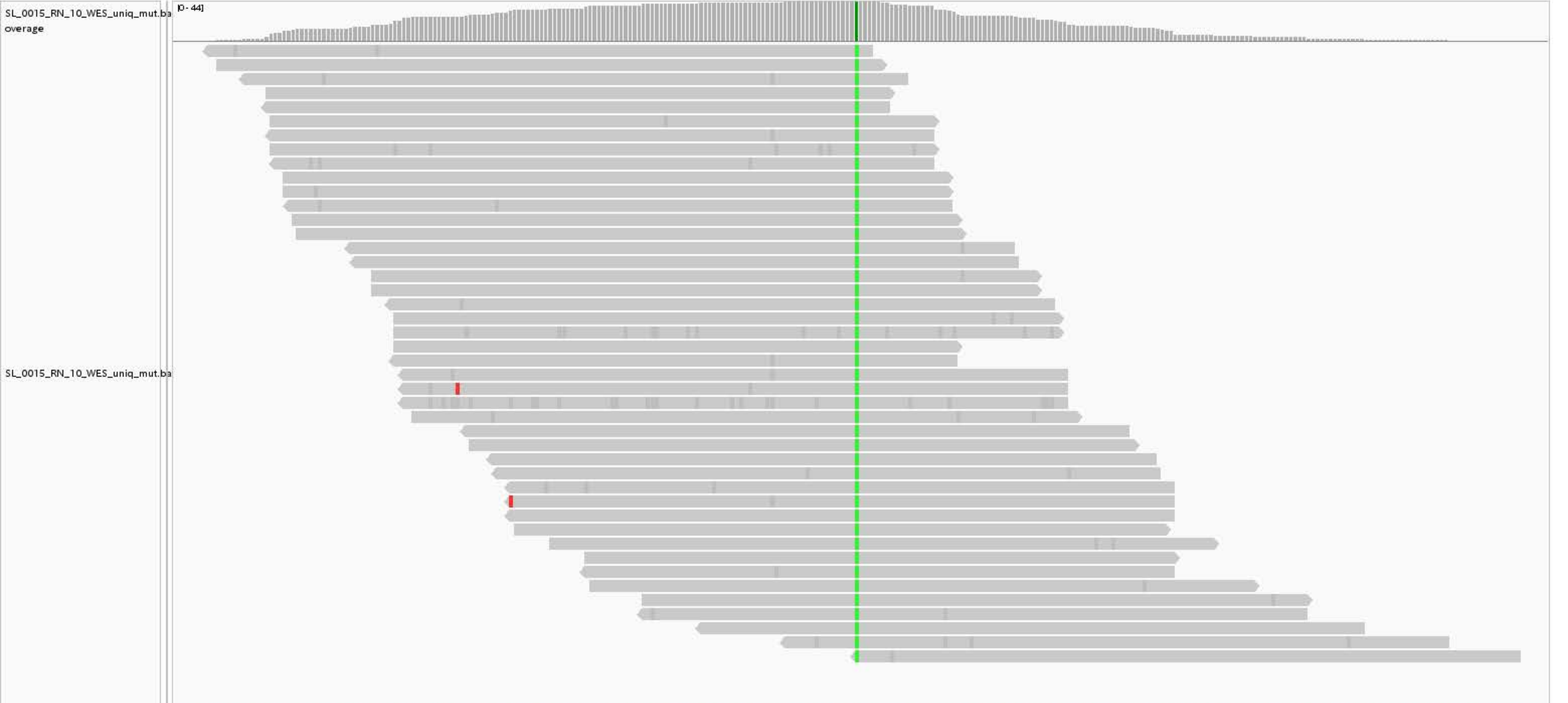
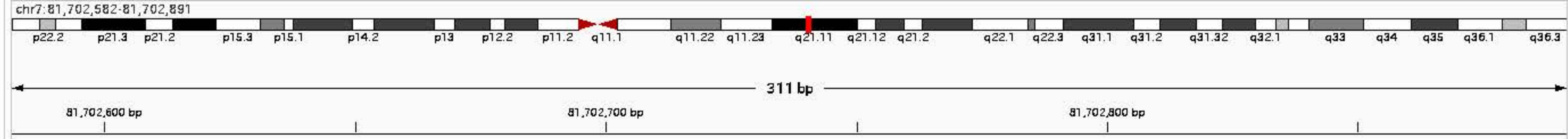
Sequence →

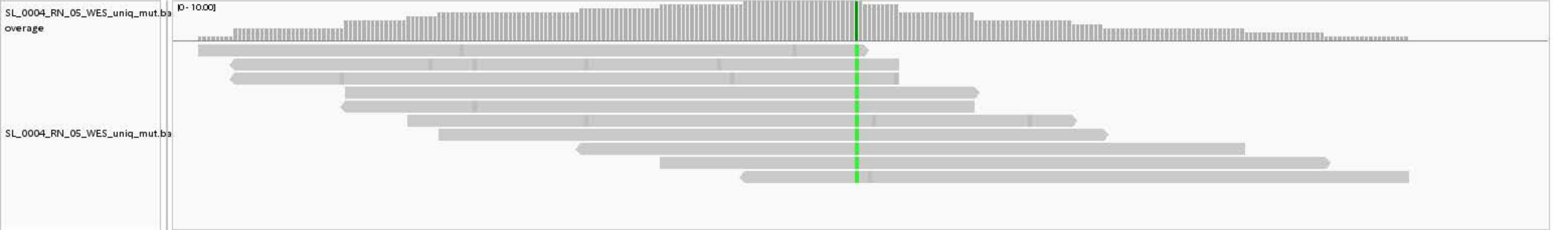
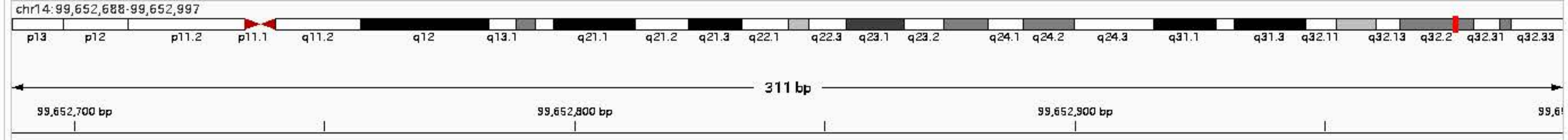


Refseq Genes

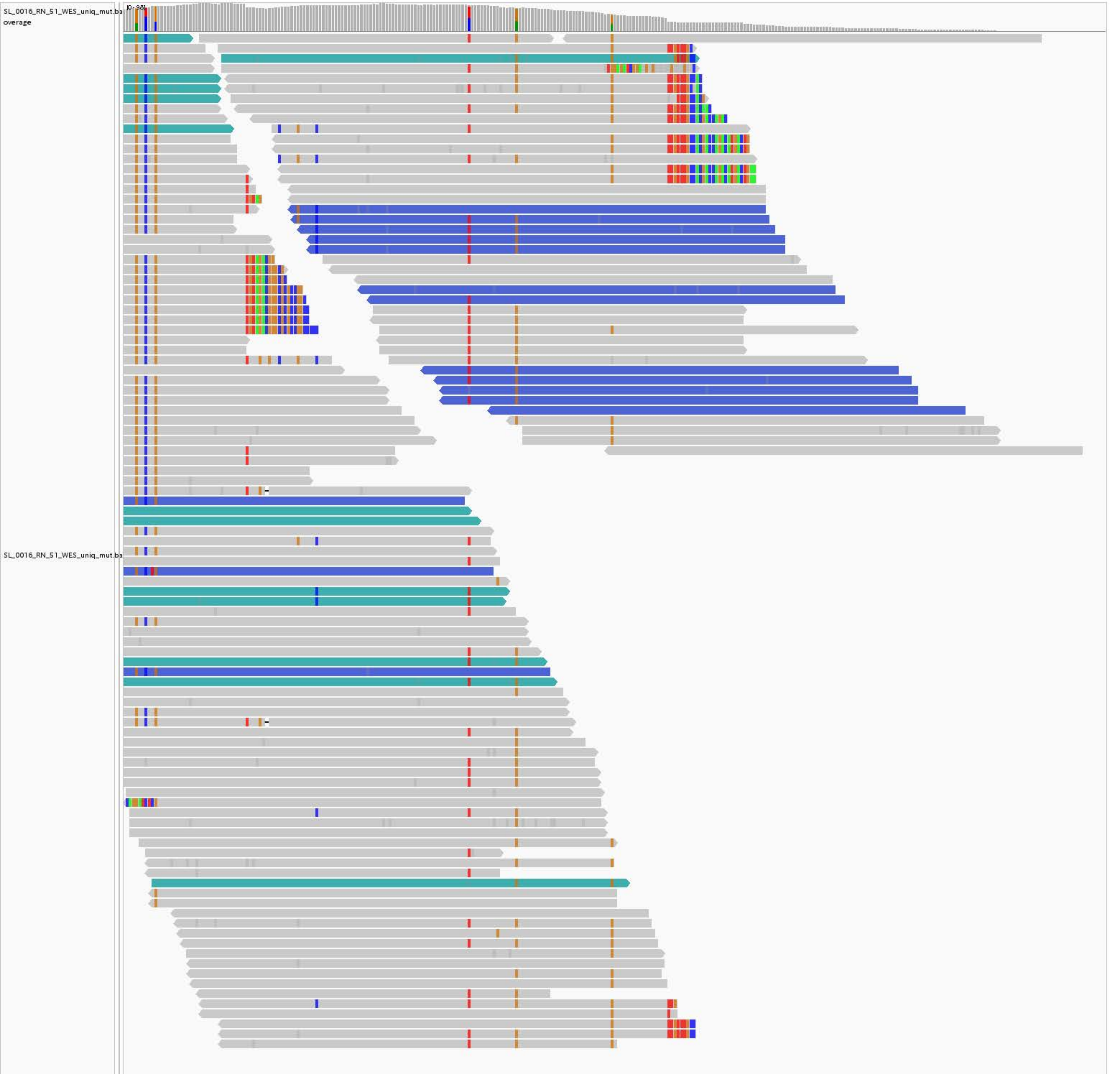
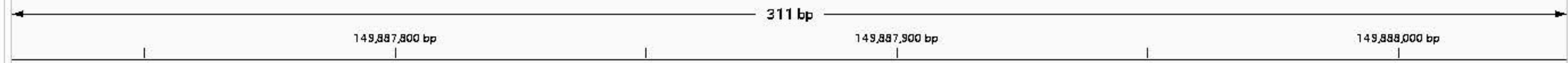
HAPLN4







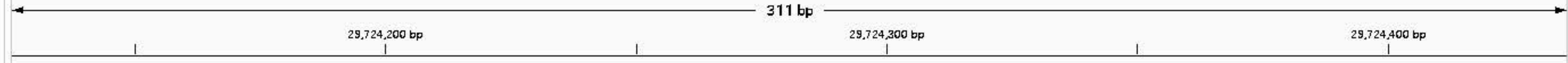




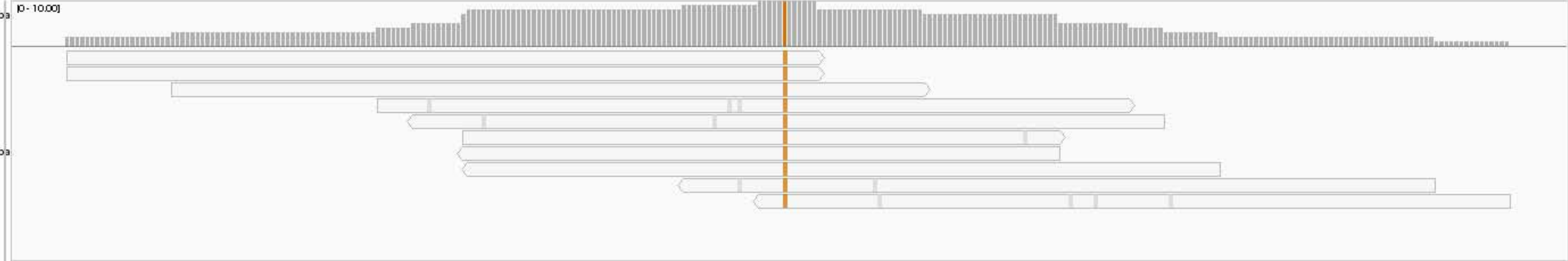
Sequence →  
Refseq Genes  
L I E A T L Y E L V A A L Y V P A G A G V R E A Y N G K R L L R H V R G V P F Q L G A R S S R S K A K A R A K G G Q K G R G S M  
H2AC21



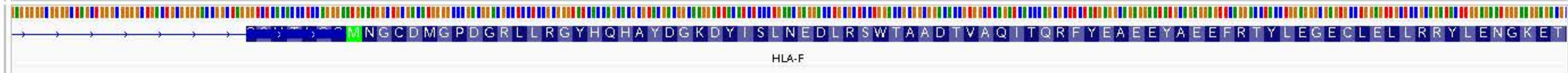
chr6: 29,724,126-29,724,435  
p25.2 p24.3 p23 p22.3 p22.2 p21.33 p21.2 p21.1 p12.3 p12.1 q11.1 q12 q13 q14.1 q14.3 q15 q16.1 q16.3 q21 q22.1 q22.31 q22.33 q23.3 q24.2 q25.1 q25.3 q26 q27

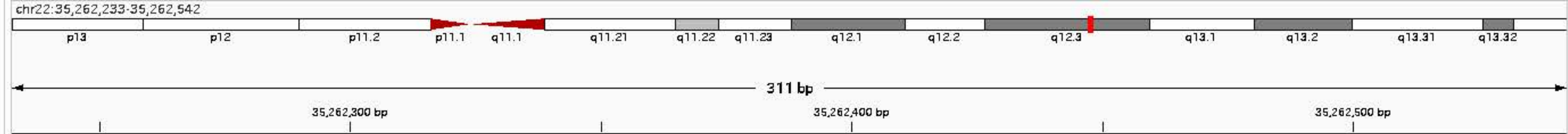


SL\_0016\_RN\_51\_WES\_uniq\_mut.ba  
overage  
SL\_0016\_RN\_51\_WES\_uniq\_mut.ba

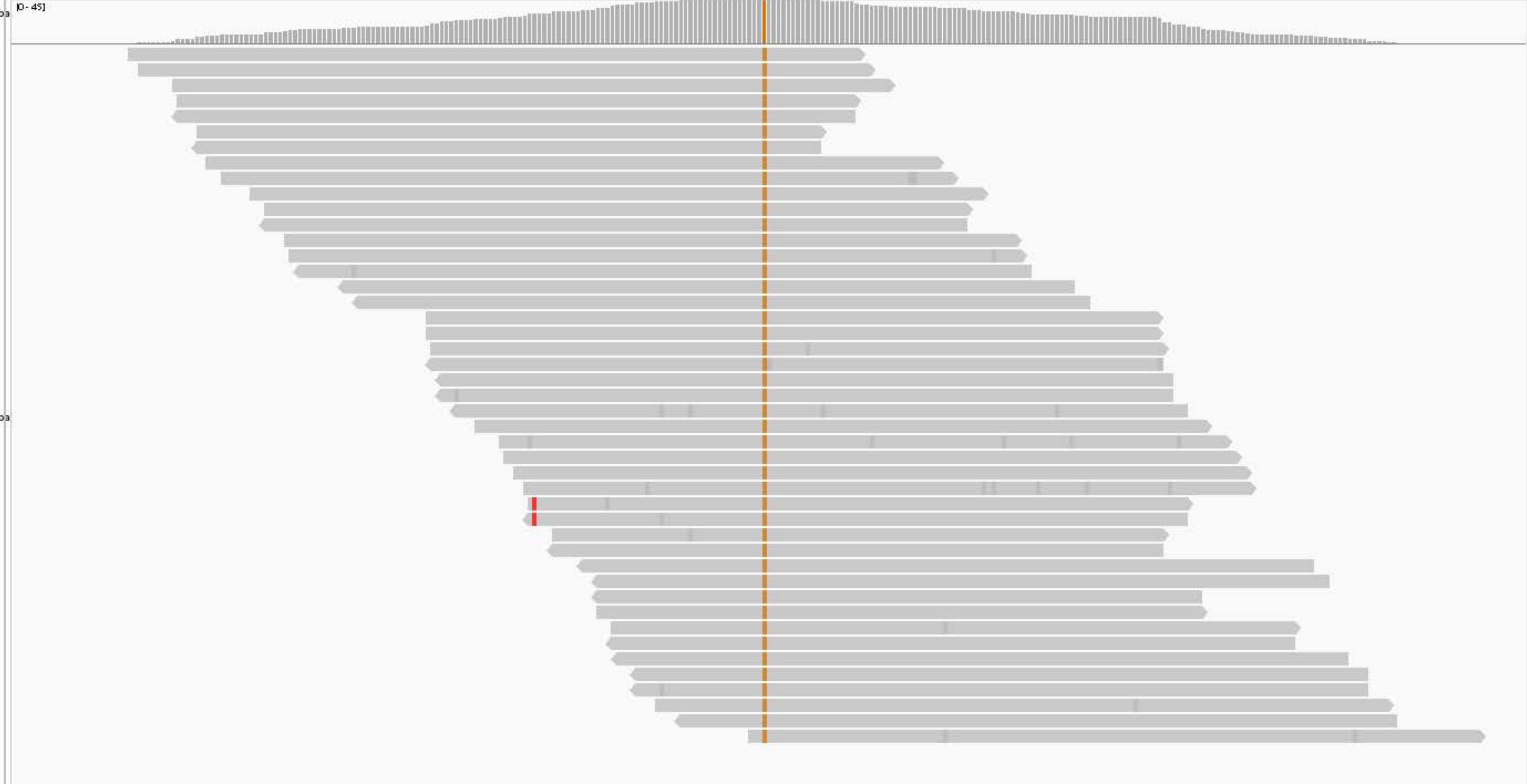


Sequence  
Refseq Genes



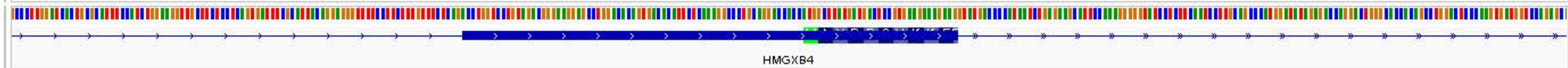


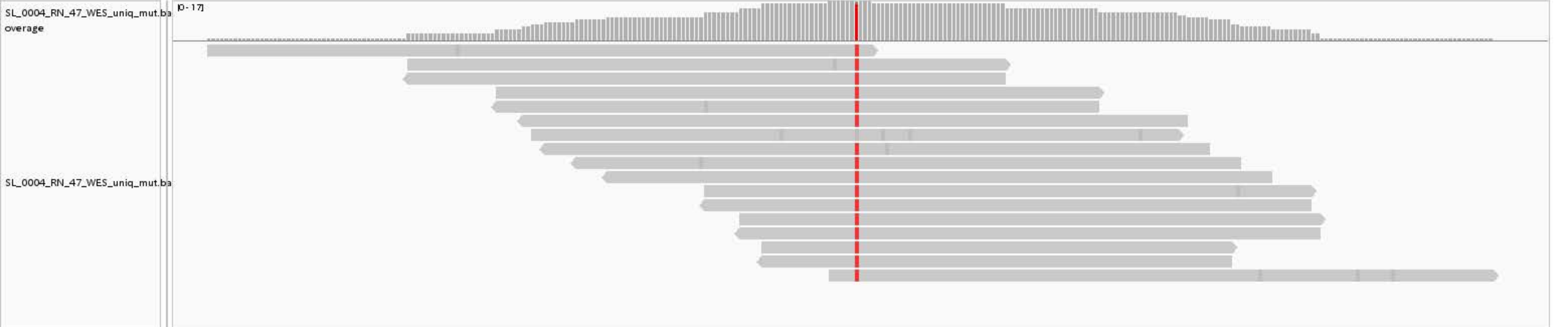
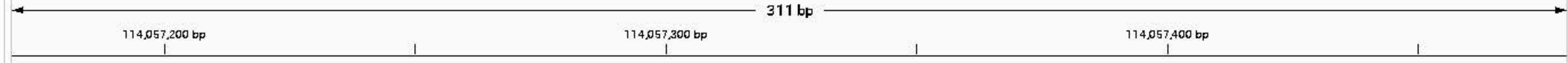
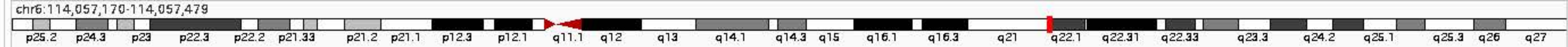
SL\_0015\_RN\_21\_WES\_uniq\_mut.ba  
coverage



SL\_0015\_RN\_21\_WES\_uniq\_mut.ba

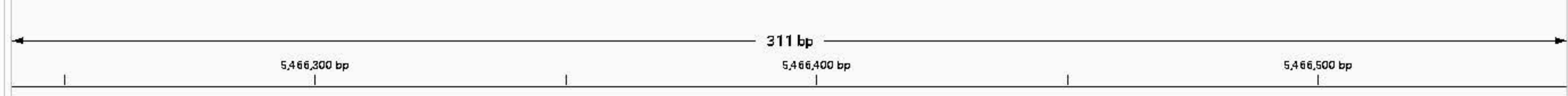
Sequence →  
Refseq Genes





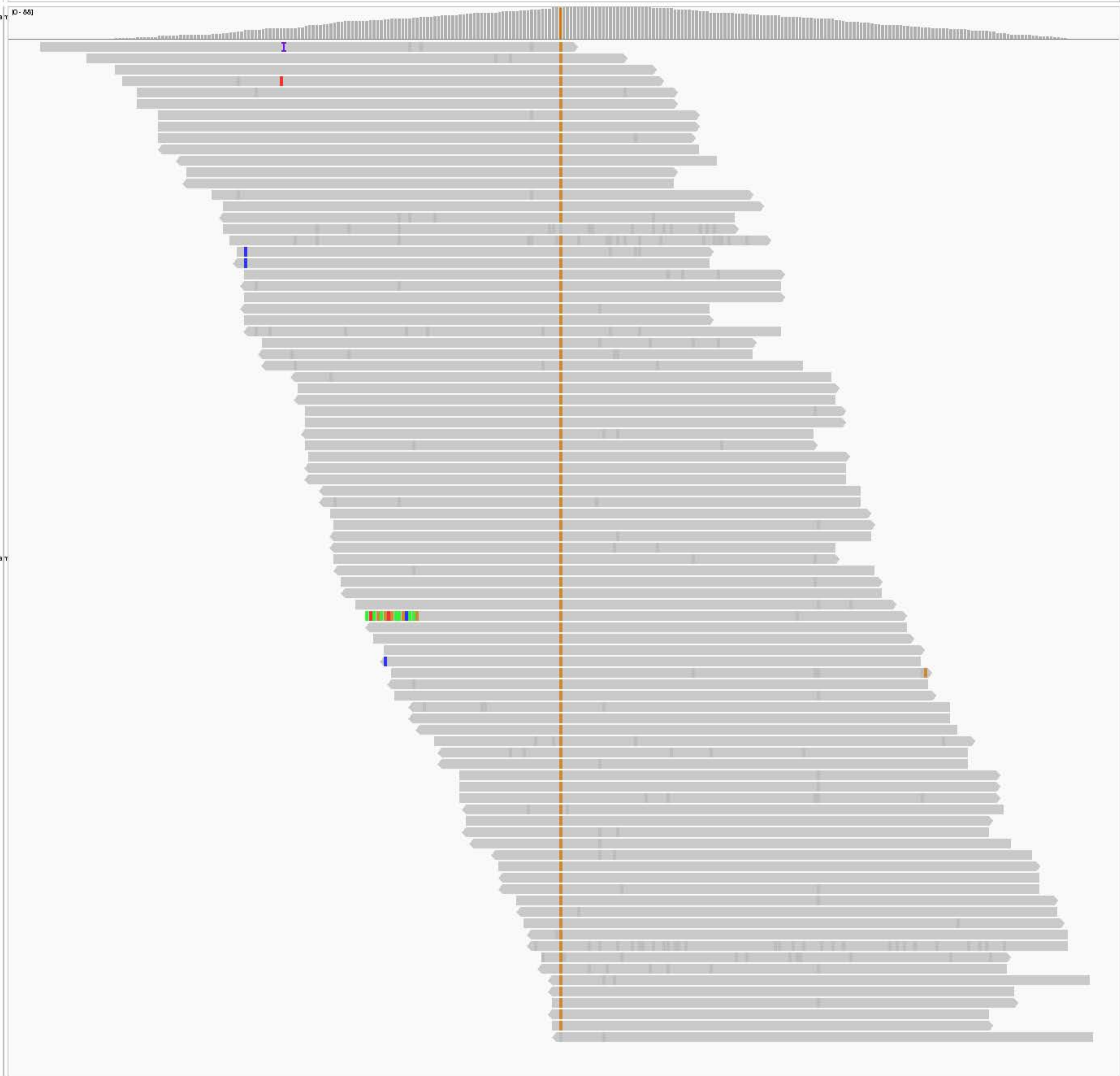


chr5:5,466,240-5,466,549



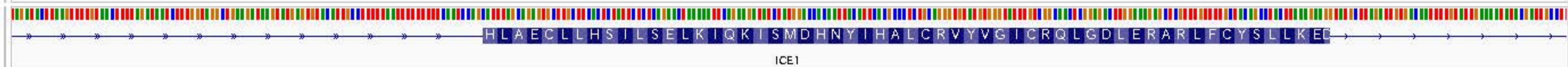
SL\_0007\_RN\_2\_WES\_uniq\_mut.ba  
verage

SL\_0007\_RN\_2\_WES\_uniq\_mut.ba



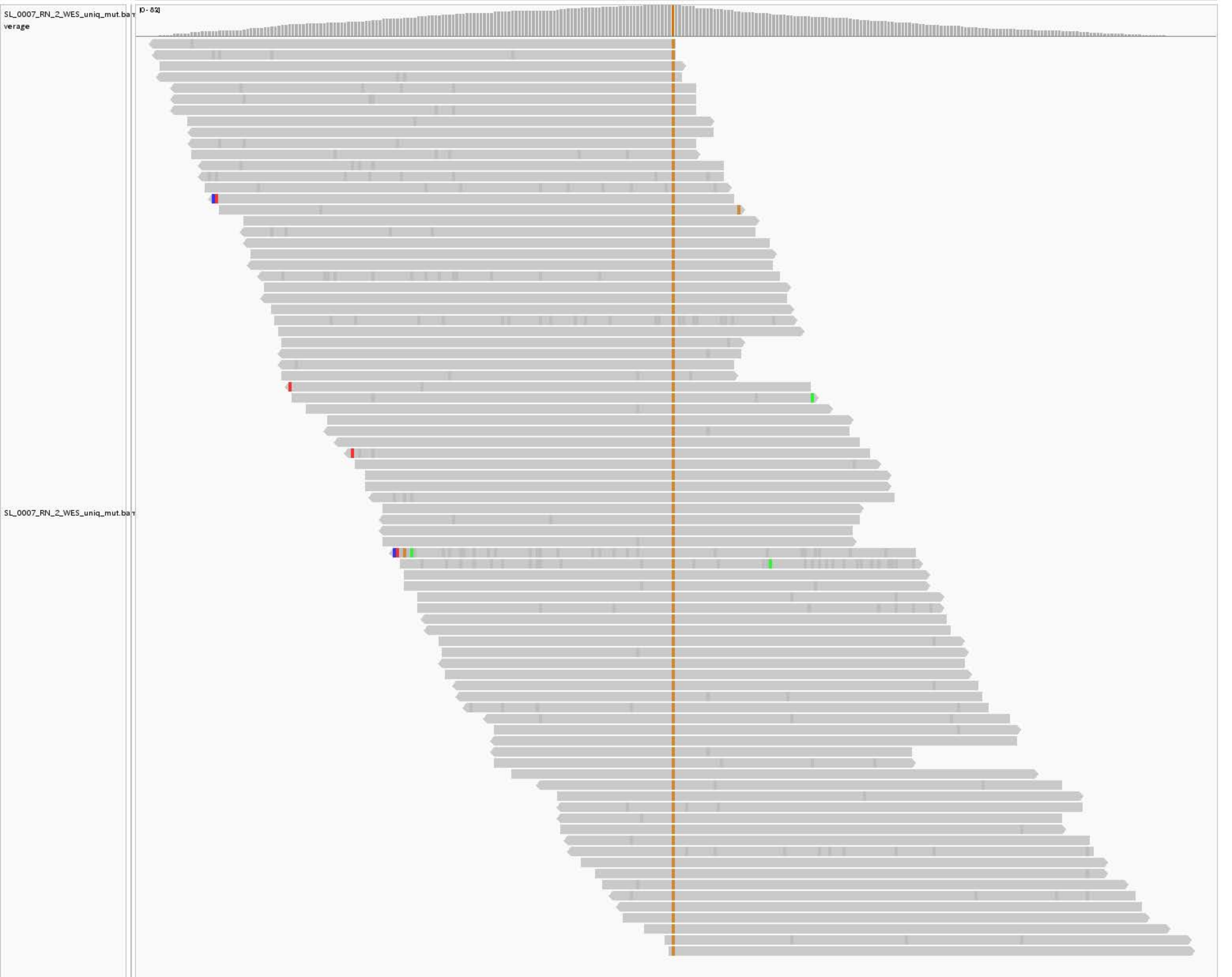
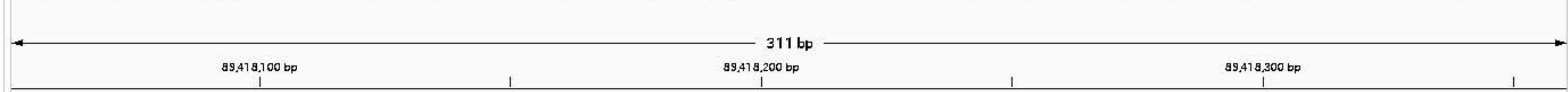
Sequence

Refseq Genes



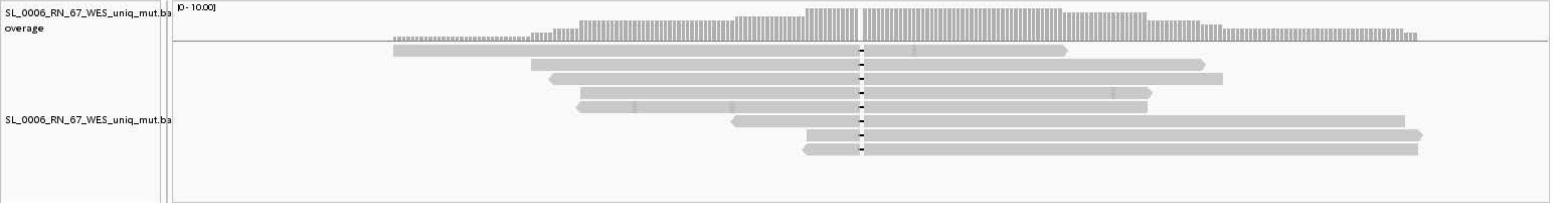
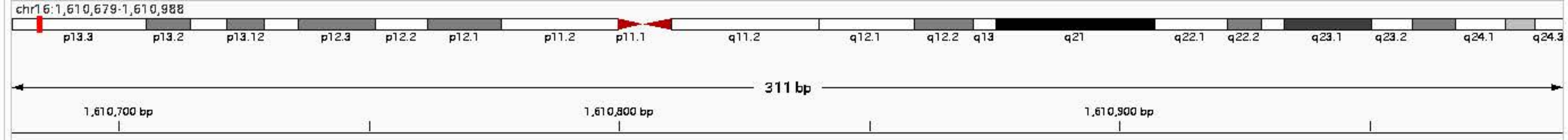
ICE1

chr10:89,418,051-89,418,360

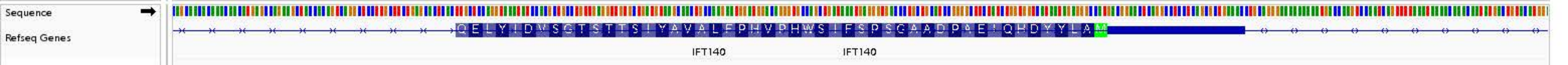
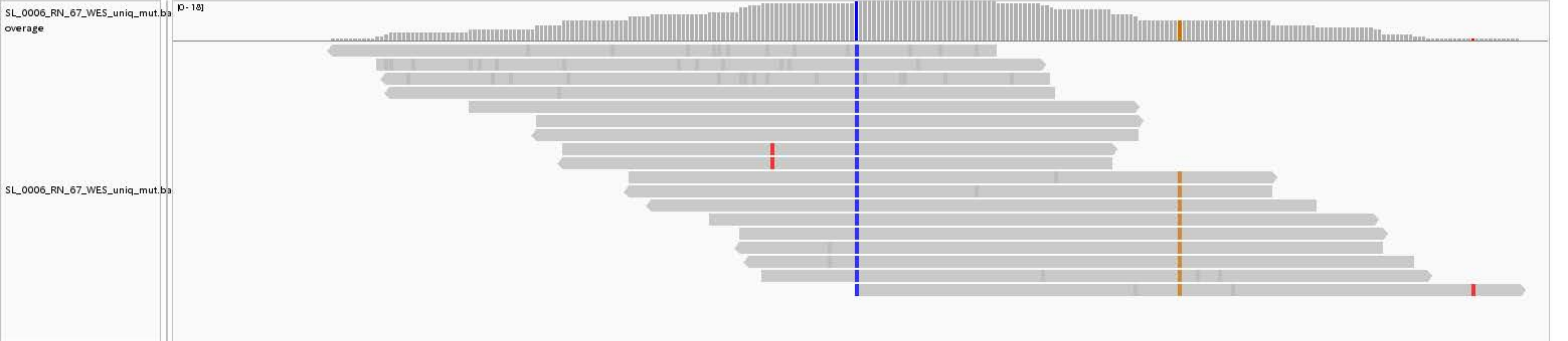
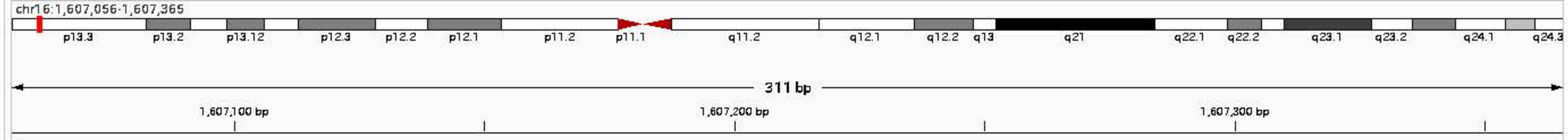


Sequence → LHHQMGLCYRAQMIQIKKATHNRPKGKDKLKVDELISSAIFHFKAAMERDSMFAYTDLANMYAEGGQYSNAEDIFRKALRLENITDDHKHQIHYHYGRFQE

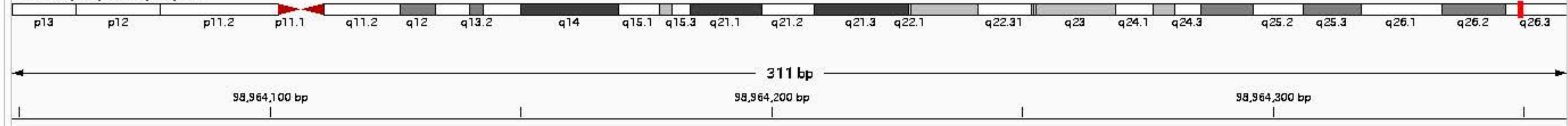
XR\_001747541.1



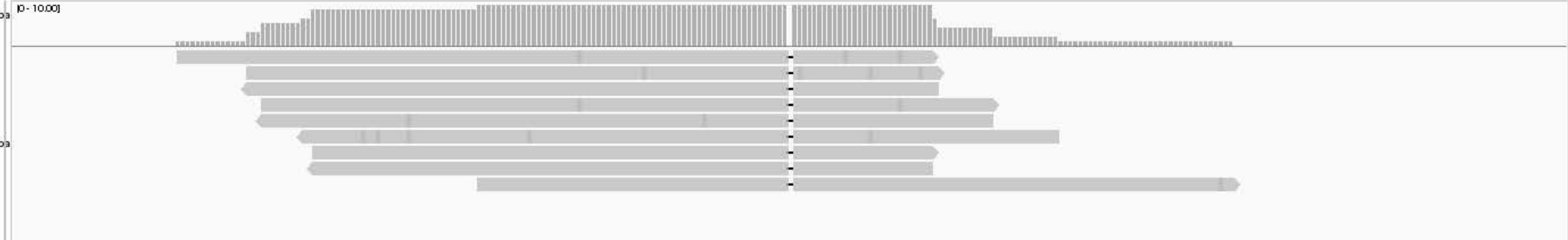




chr15:98,964,049-98,964,358



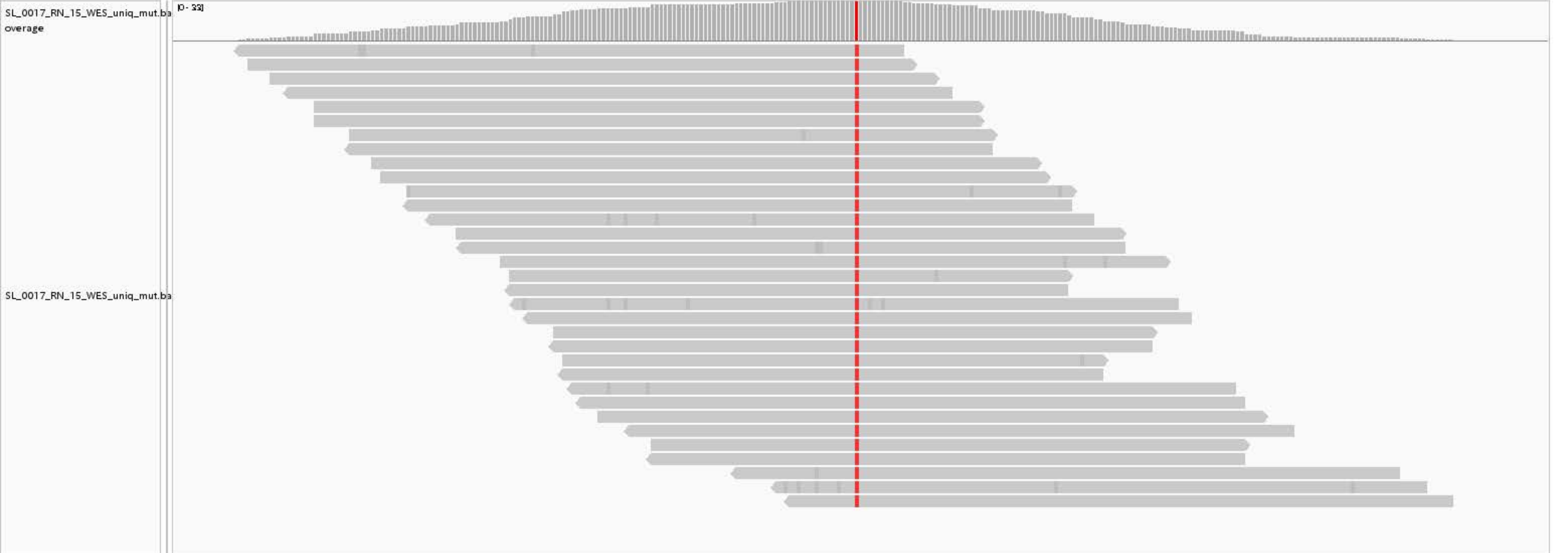
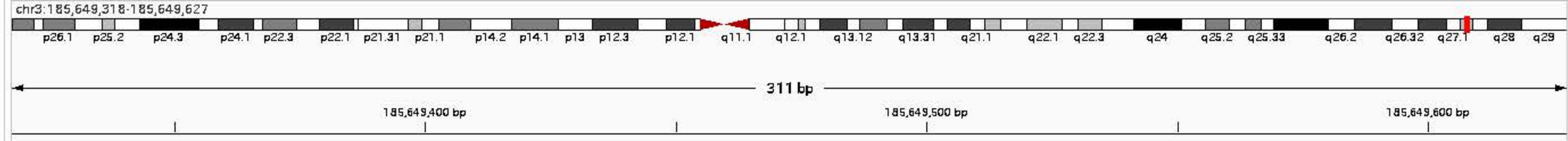
SL\_0017\_RN\_15\_WES\_uniq\_mut.ba  
coverage



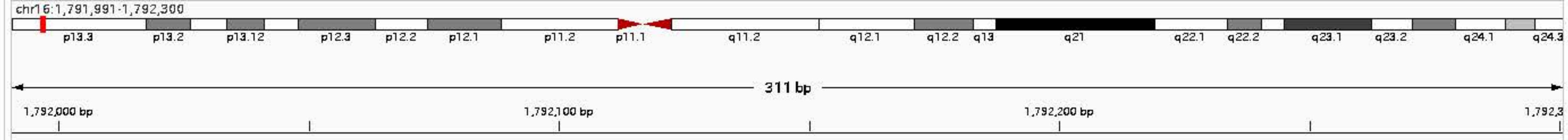
Sequence →  
Refseq Genes



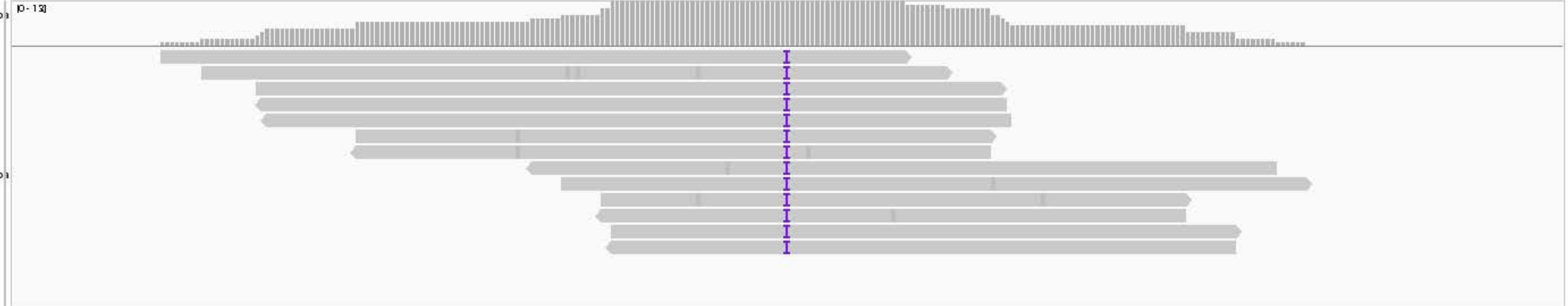
IGF1R





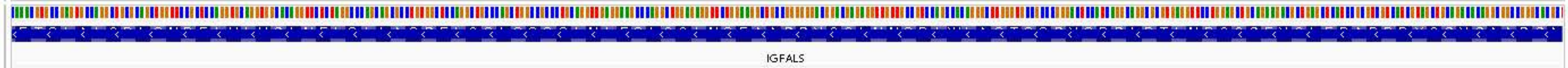


SL\_0015\_LN\_46\_WES\_uniq\_mut. ba  
coverage



SL\_0015\_LN\_46\_WES\_uniq\_mut. ba

Sequence →  
Refseq Genes

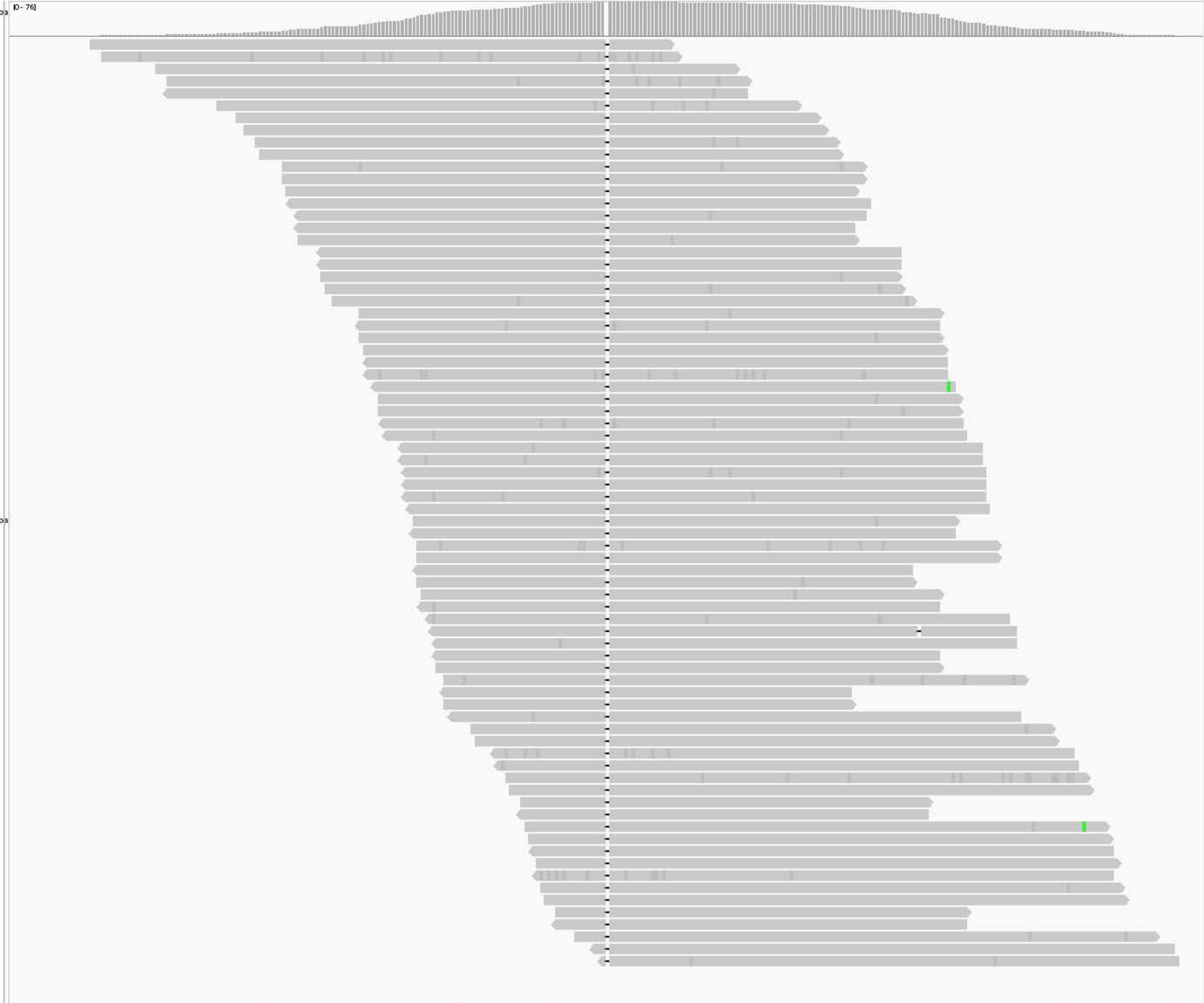


chr3: 57,102,935-57,103,244

p26.1 p25.2 p24.3 p24.1 p22.3 p22.1 p21.31 p21.1 p14.2 p14.1 p13 p12.3 p12.1 q11.1 q12.1 q13.12 q13.31 q21.1 q22.1 q22.3 q24 q25.2 q25.33 q26.2 q26.32 q27.1 q28 q29



SL\_0007\_RN\_33\_WES\_uniq\_mut.ba  
overage



SL\_0007\_RN\_33\_WES\_uniq\_mut.ba

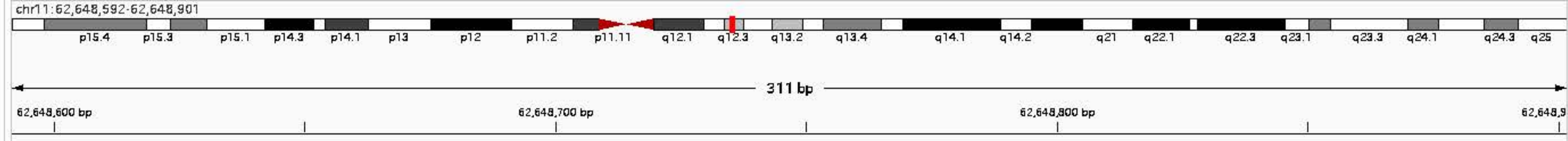
Sequence →

Refseq Genes



VPKLAYHMKRTTNTDDL

IL17RD



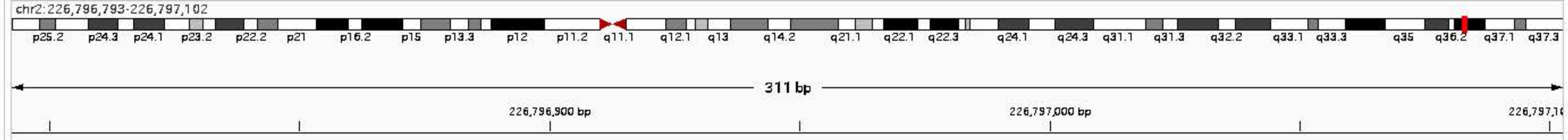
Sequence →

Refseq Genes

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INTS5



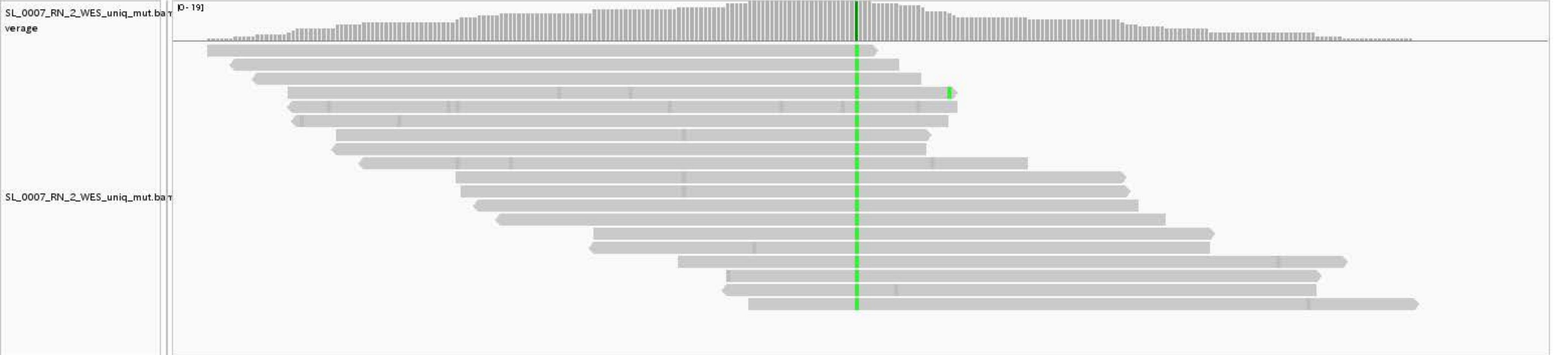
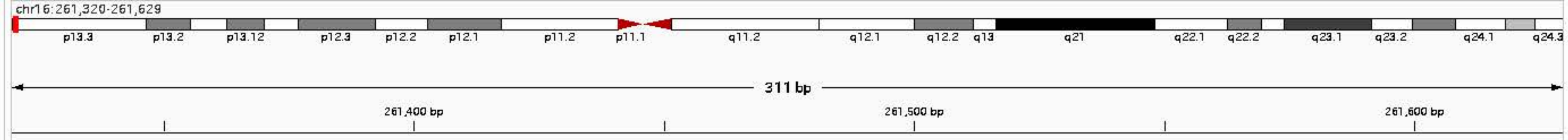


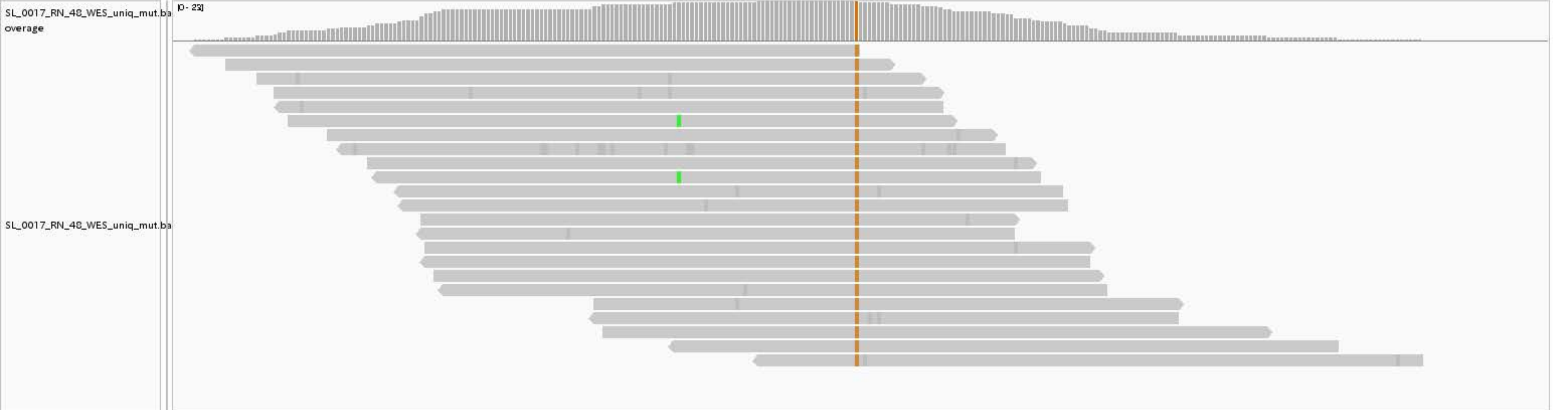
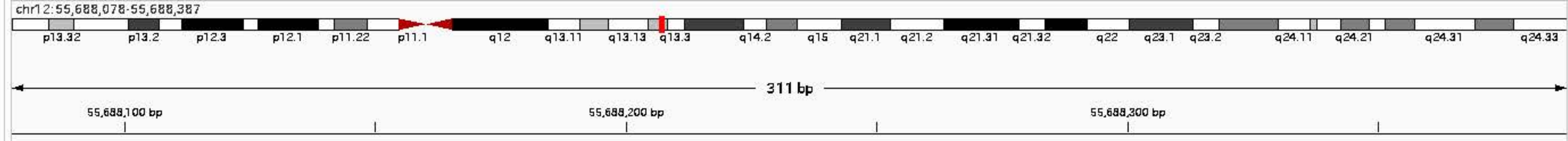
Sequence →

Refseq Genes

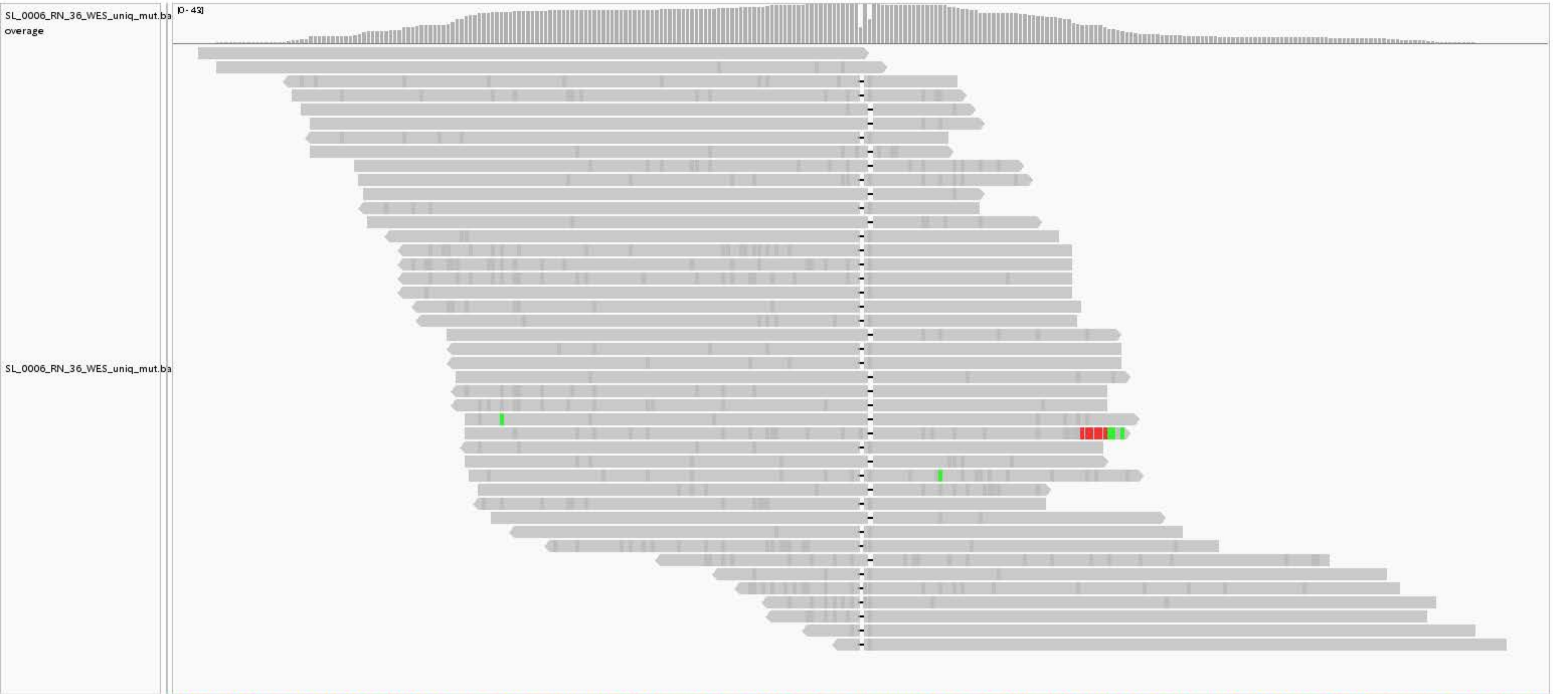
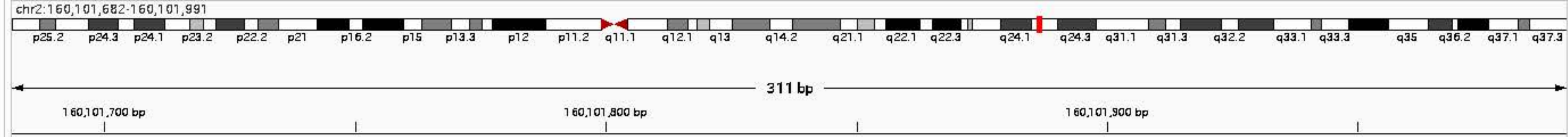
P N I I Q Q P A S V S K P S M P M Y D G S G K R G S P V P A V G P S M P M Y G D D T H L T S S D P R H H G G R R E L P H M E L G E E P Y S R T P V F A S H R H G P L R G G S G G G P P Y A P M M E T Y E E I S A

IRS1

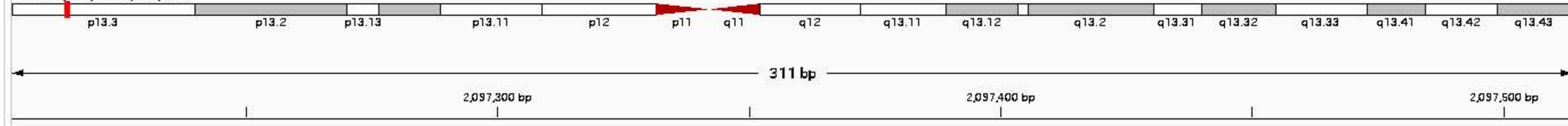




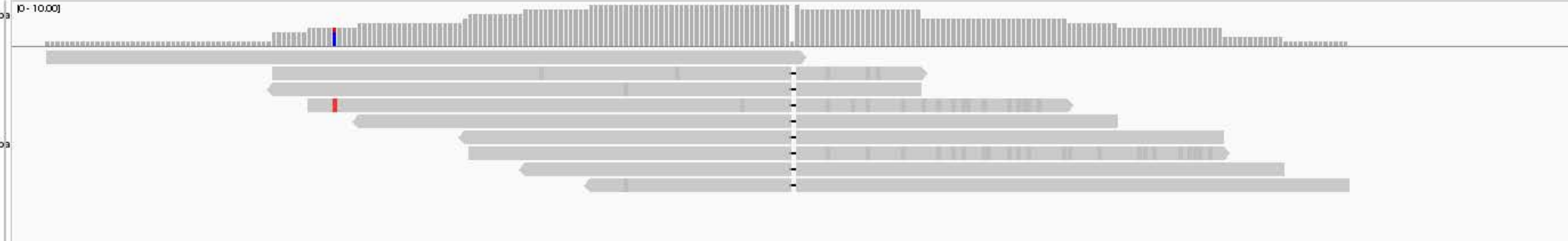




chr19:2,097,204-2,097,513



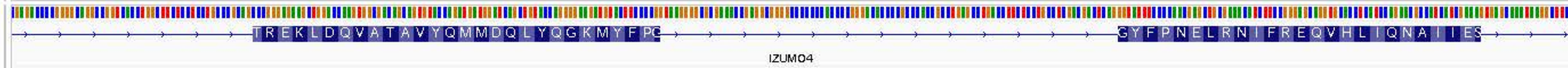
SL\_0017\_RN\_15\_WES\_uniq\_mut.ba  
coverage

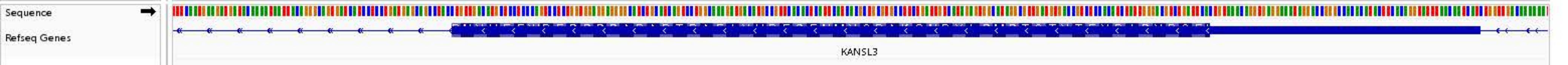
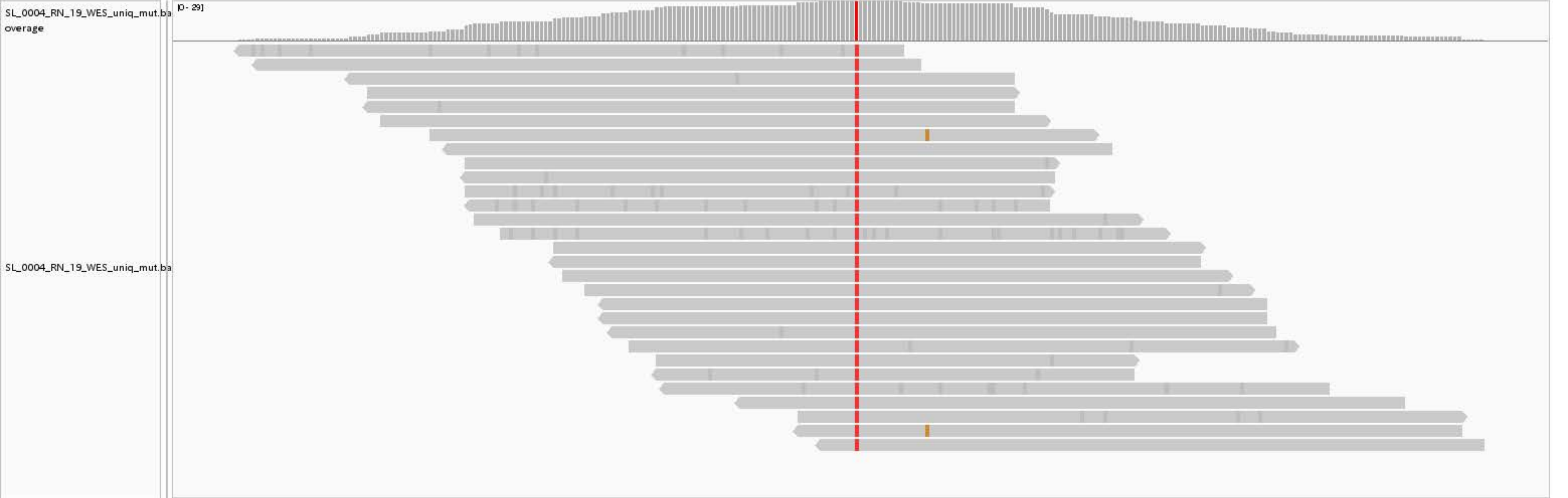
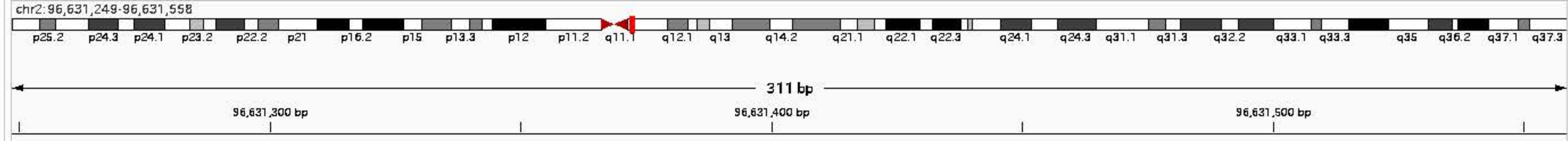


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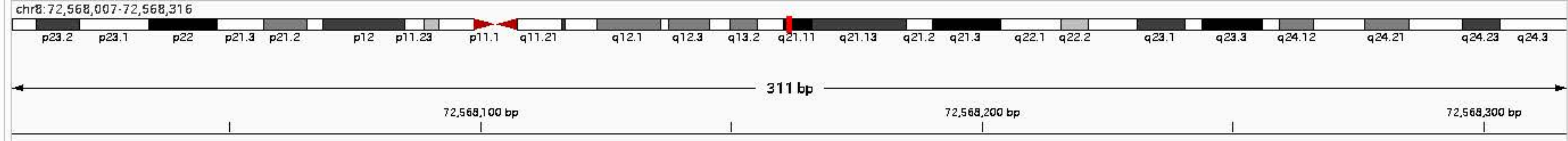
Sequence

Refseq Genes









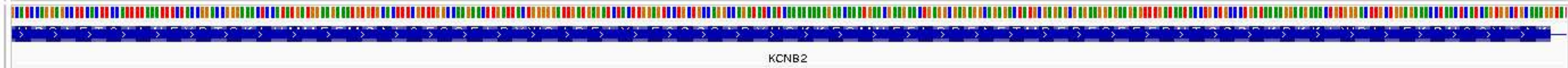
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overage



SL\_0006\_RN\_67\_WES\_uniq\_mut.ba

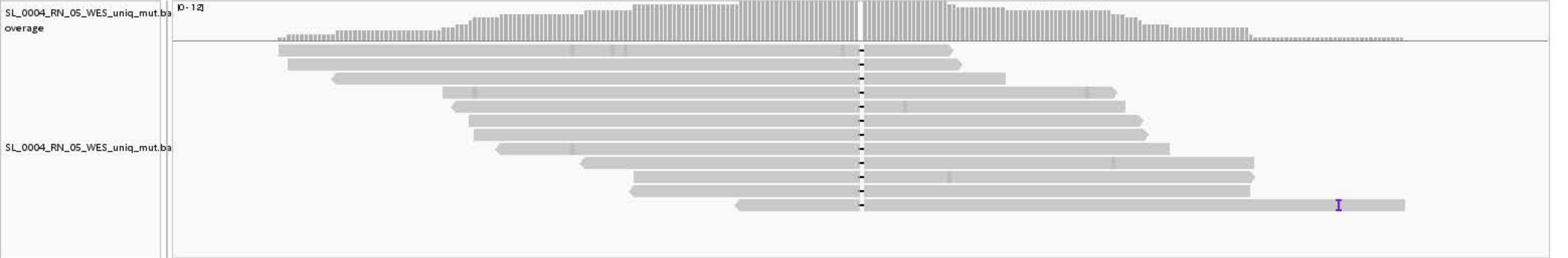
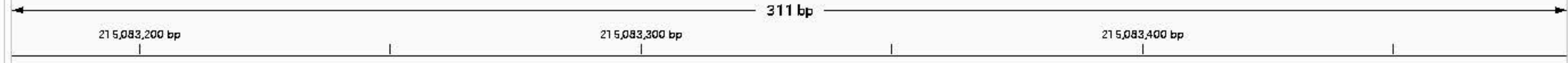
Sequence

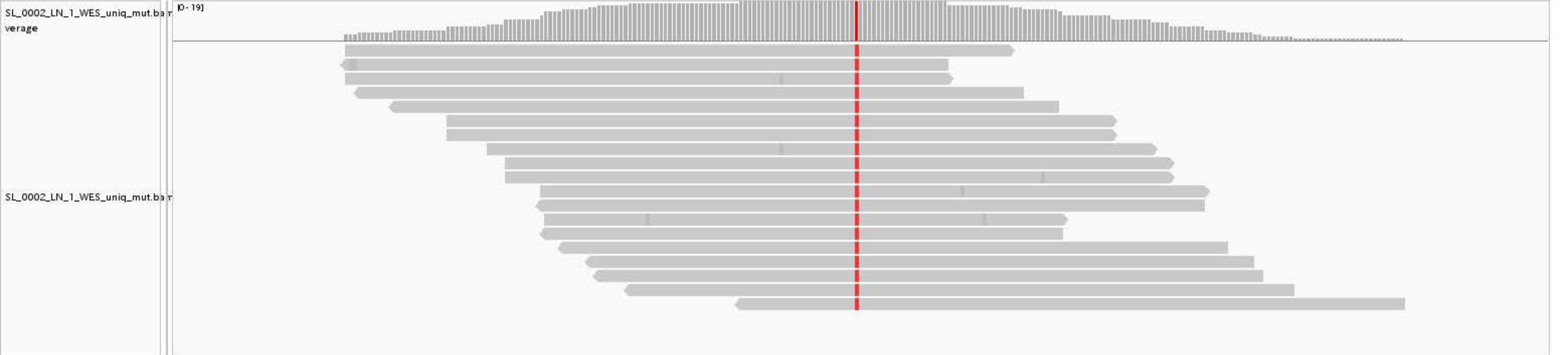
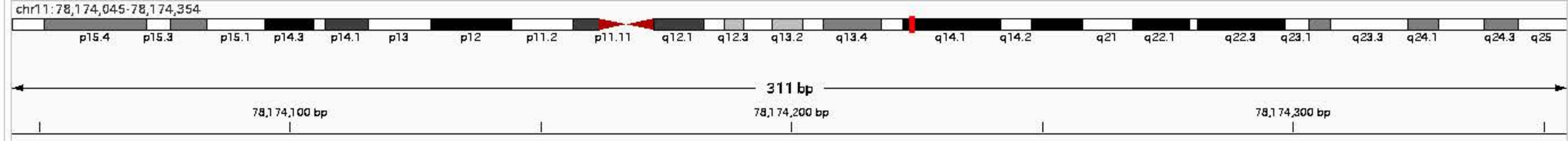
Refseq Genes



chr1:215,083,175-215,083,484

p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44





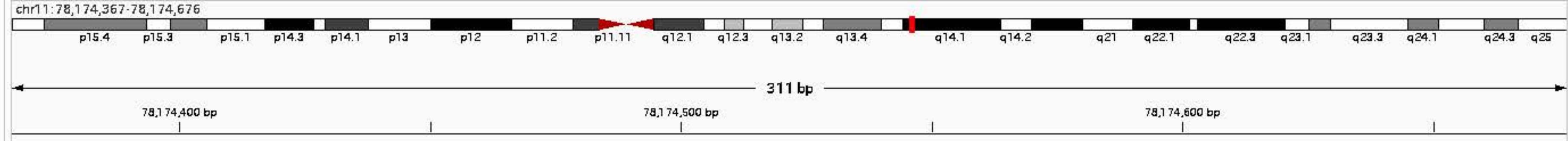
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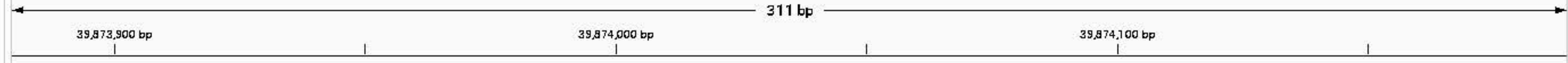
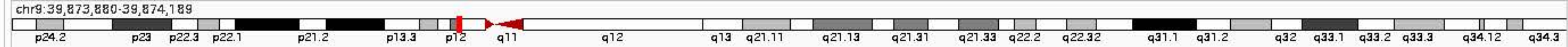
Refseq Genes

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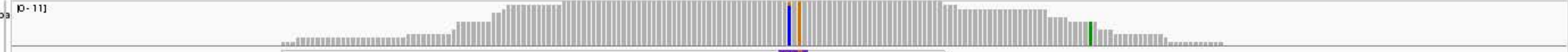
KCTD21



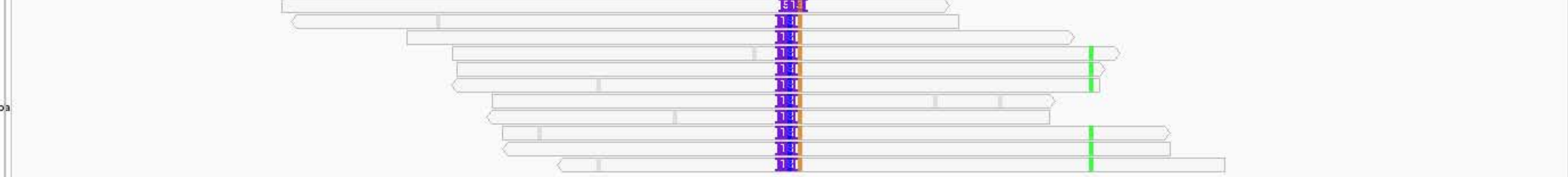




SL\_0004\_RN\_61\_WES\_uniq\_mut.ba  
coverage



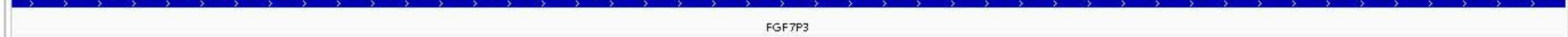
SL\_0004\_RN\_61\_WES\_uniq\_mut.ba



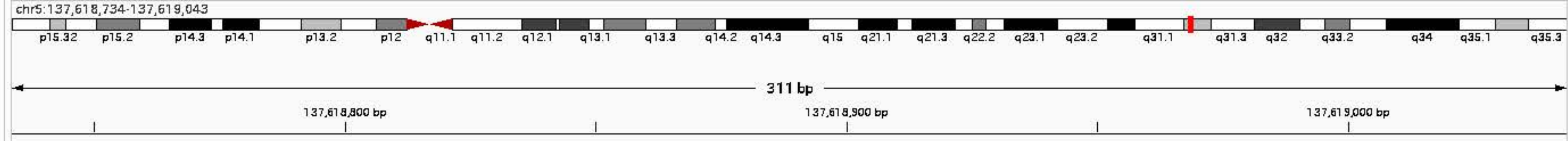
Sequence



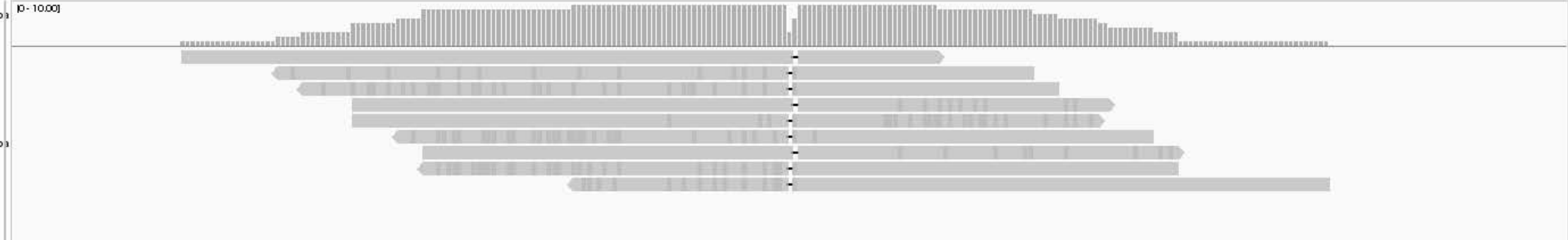
Refseq Genes



FGF7P3



SL\_0015\_LN\_44\_WES\_uniq\_mut. coverage



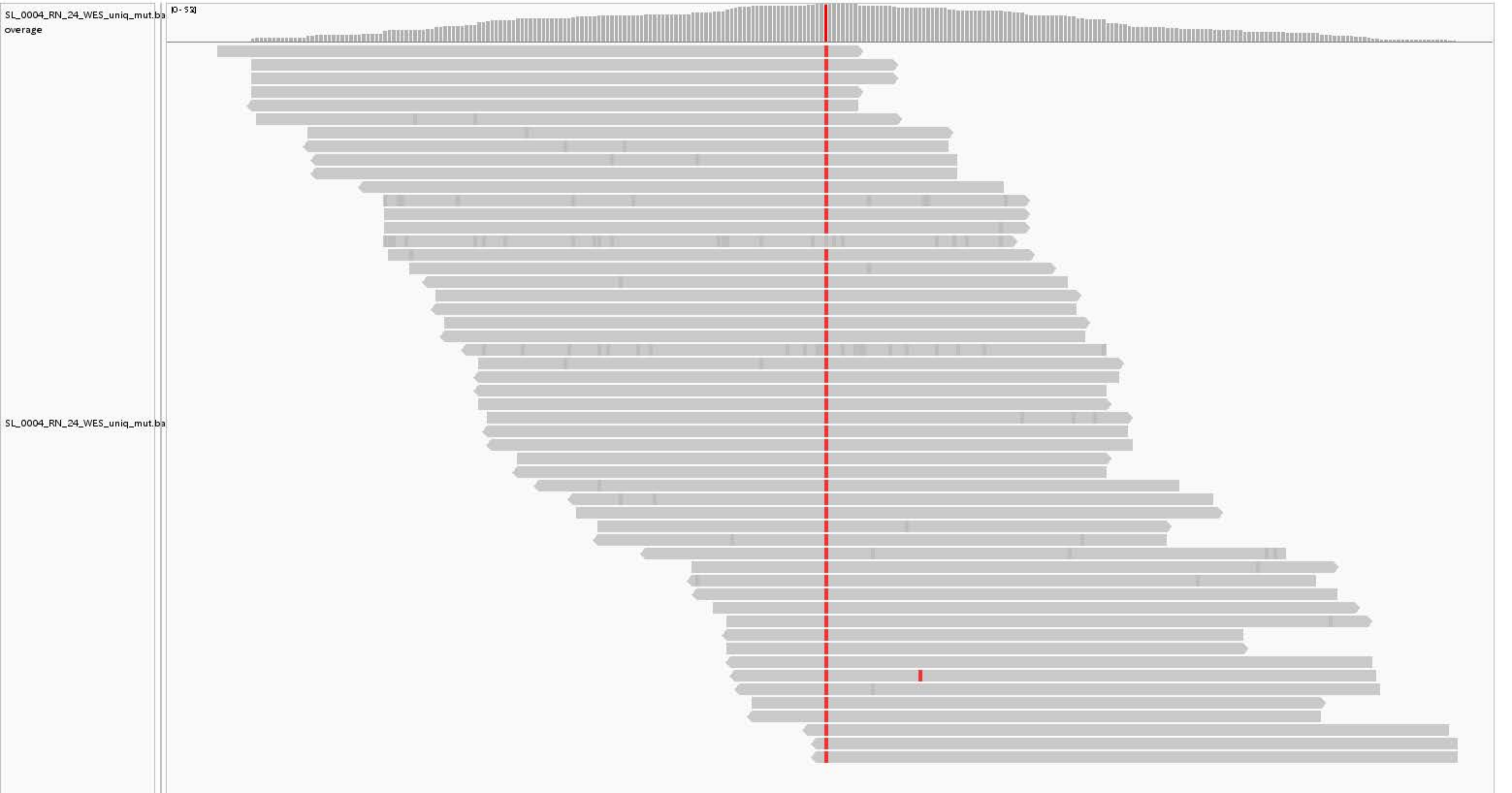
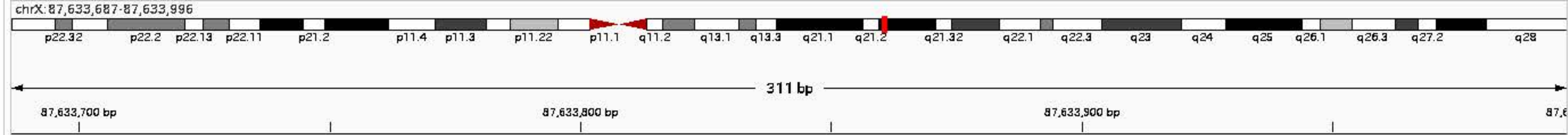
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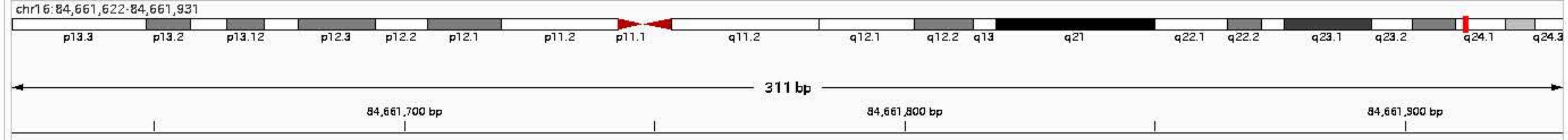
Sequence

Refseq Genes

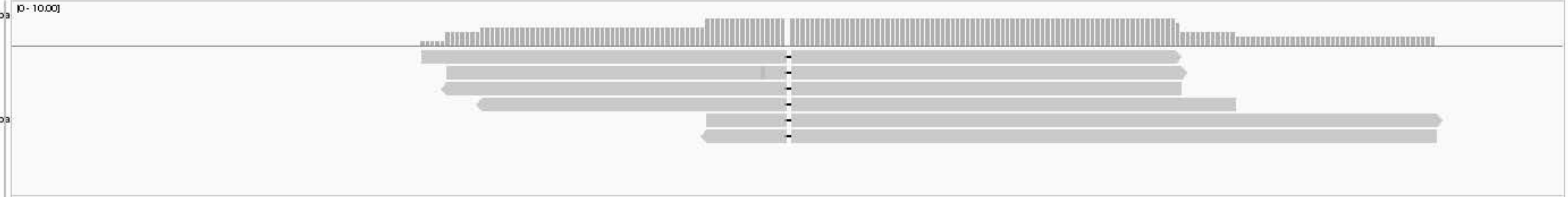








SL\_0007\_RN\_33\_WES\_uniq\_mut.ba  
coverage



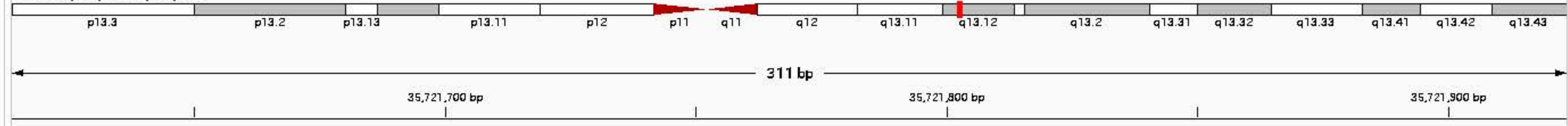
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Sequence →  
Refseq Genes

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KLHL36

chr19:35,721,614-35,721,923



SL\_0004\_RN\_26\_WES\_uniq\_mut.ba  
coverage



SL\_0004\_RN\_26\_WES\_uniq\_mut.ba

Sequence →



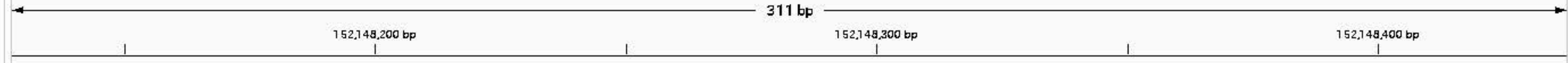
Refseq Genes

KMT2B

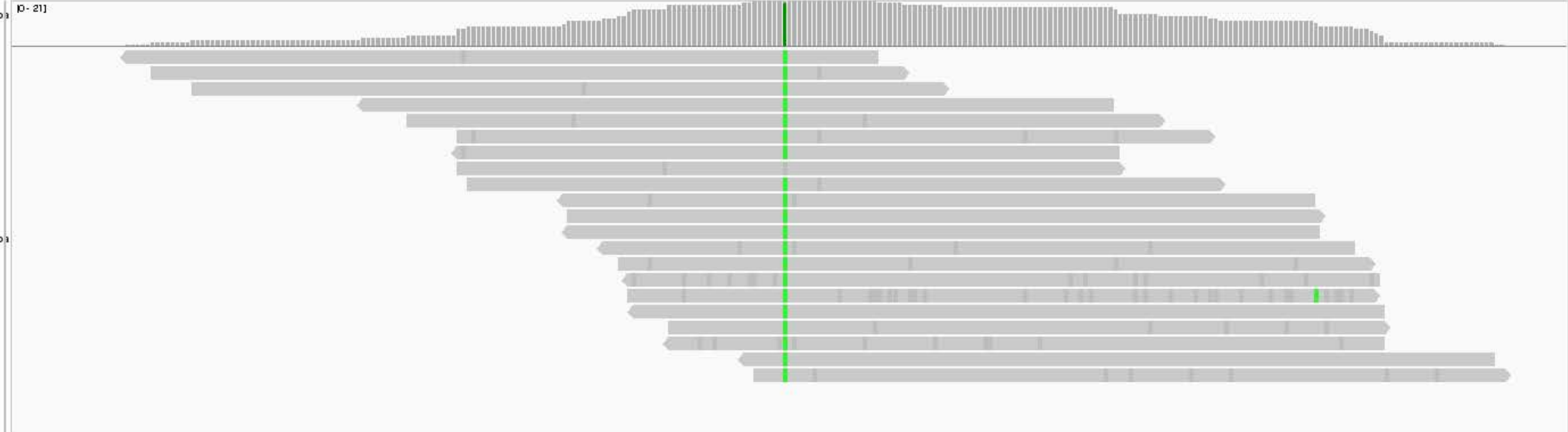


chr7:152,148,128-152,148,437

p22.2 p21.3 p21.2 p15.3 p15.1 p14.2 p13 p12.2 p11.2 q11.1 q11.22 q11.23 q21.11 q21.12 q21.2 q22.1 q22.3 q31.1 q31.2 q31.32 q32.1 q33 q34 q35 q36.1 q36.3



SL\_0001\_LN\_10\_WES\_uniq\_mut.  
coverage



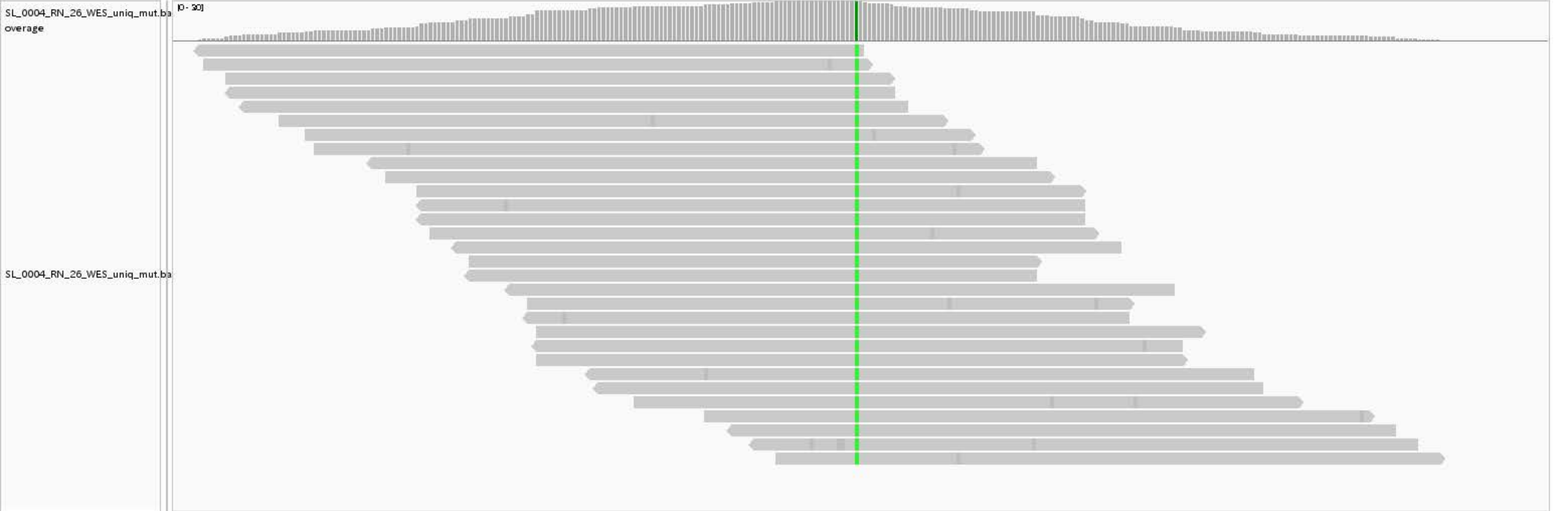
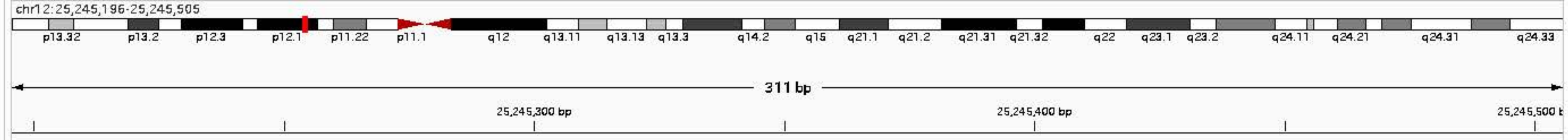
SL\_0001\_LN\_10\_WES\_uniq\_mut.  
aa

Sequence

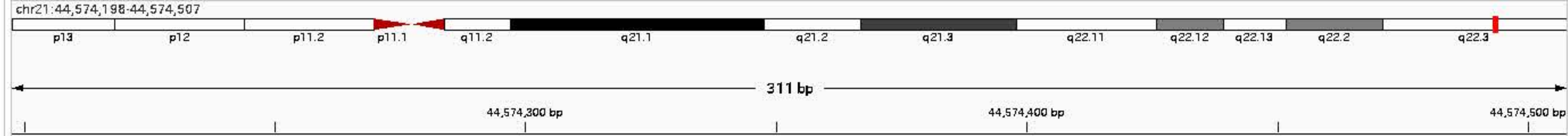
Refseq Genes

CLYRCRRNAYRTSWYLRSAEYGVPLAKPSHFAQMQLLQGITHFILSGVRFTHDREGRQVISAIQRVEDRQVYVRRFVAFYSLEQEHIGKPKHMPCLMTKDK

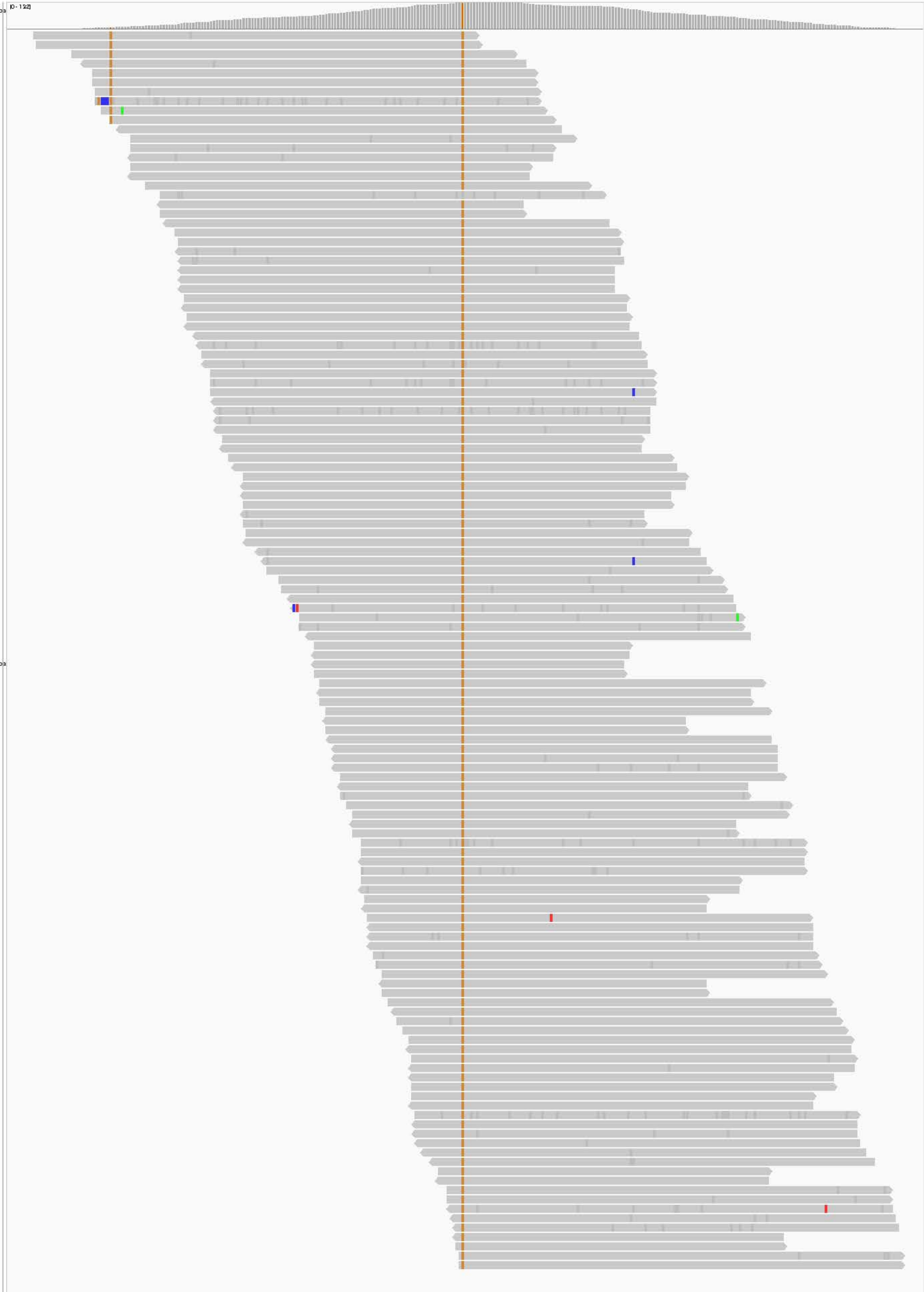
KMT2C







SL\_0007\_RN\_33\_WES\_uniq\_mut.ba  
coverage



SL\_0007\_RN\_33\_WES\_uniq\_mut.ba

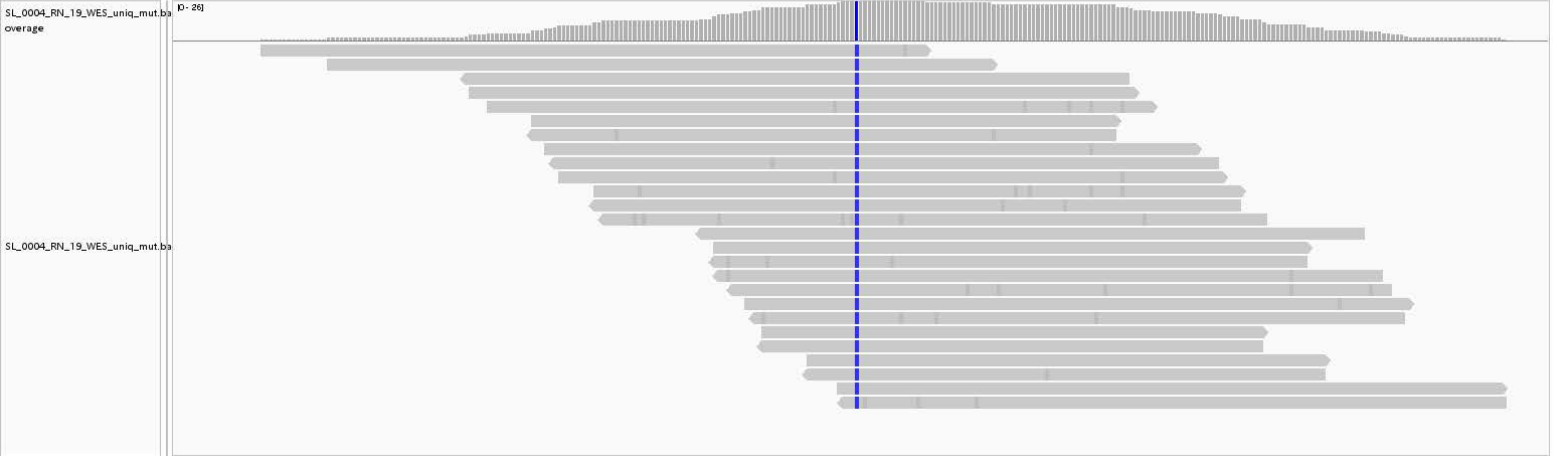
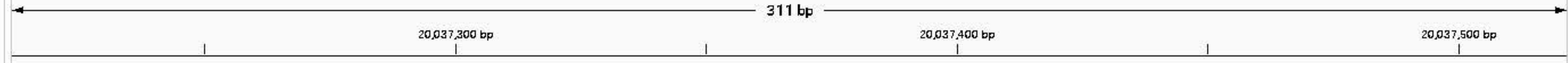
Sequence →  
Refseq Genes

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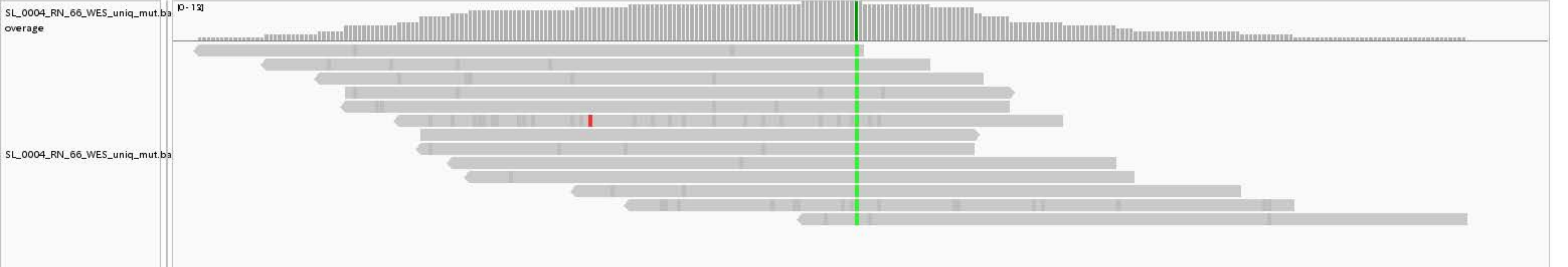
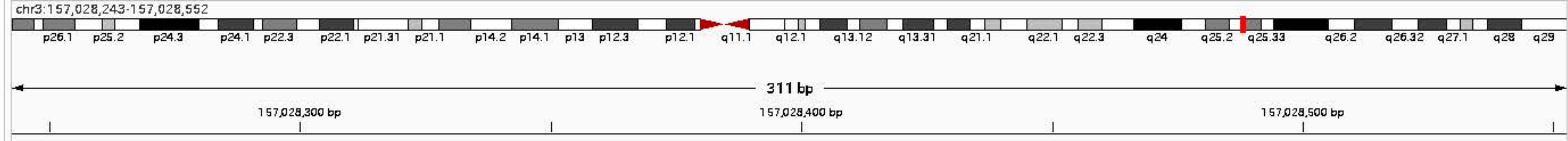
TSPEAR

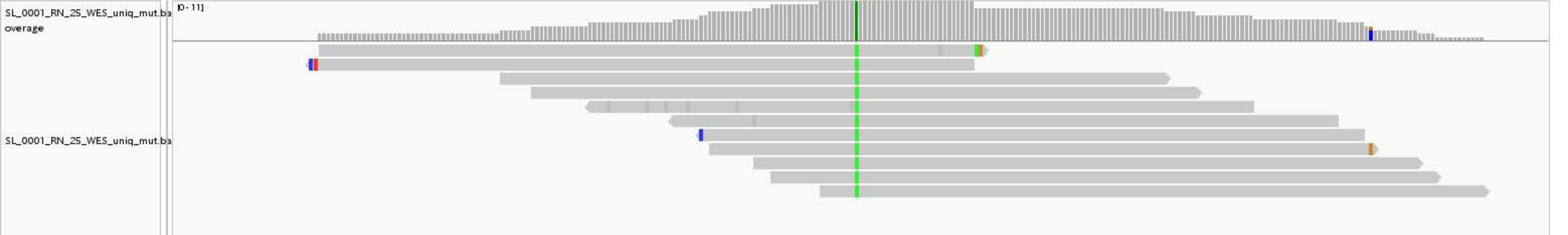
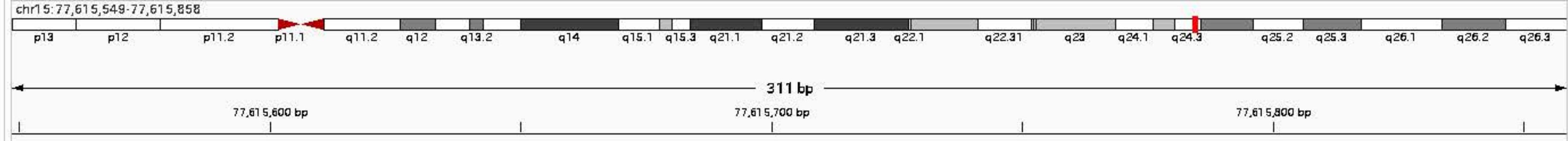


chr2:20,037,212-20,037,521  
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Sequence →  
Refseq Genes  
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LAPTM4A





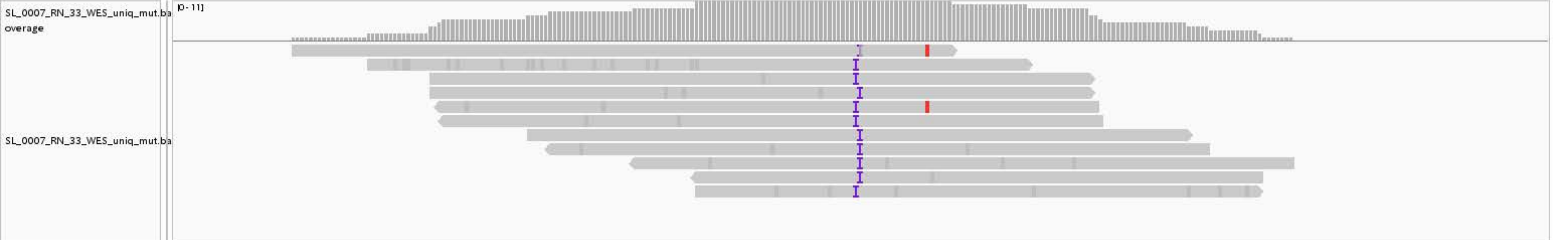
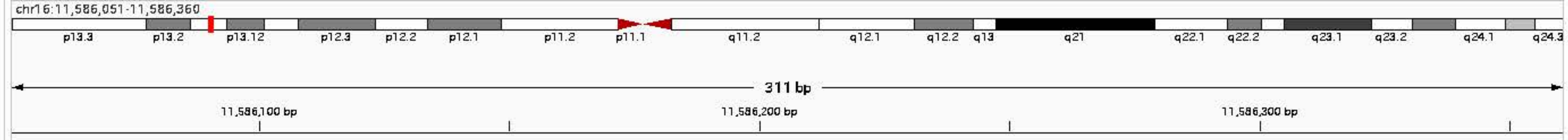
Sequence →

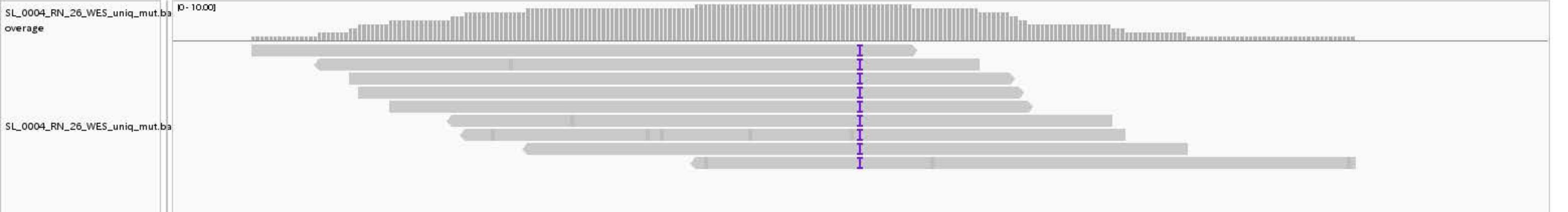
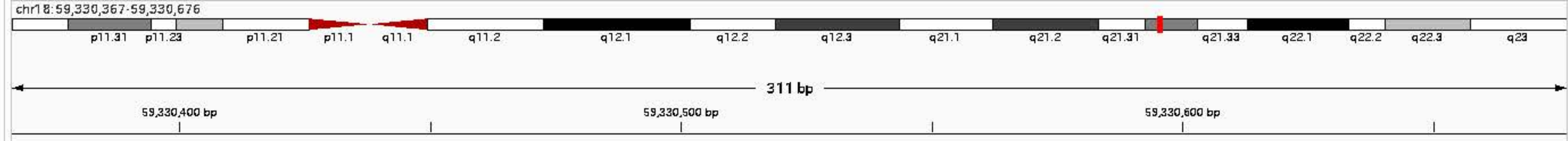
Refseq Genes

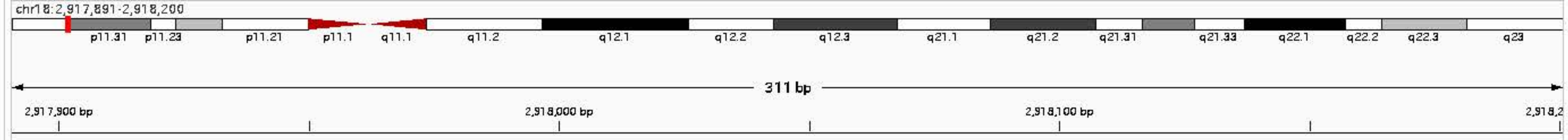
FLNNFAGPEVASVINENLELEELHPFSAFEDQNLTKIRNKGLDLLRTETPIGEPVAVFRKRHCLVARDQASCECRPPCGTASGSLVSGLVLLLI PQWCALLPS

XR\_001751806.1

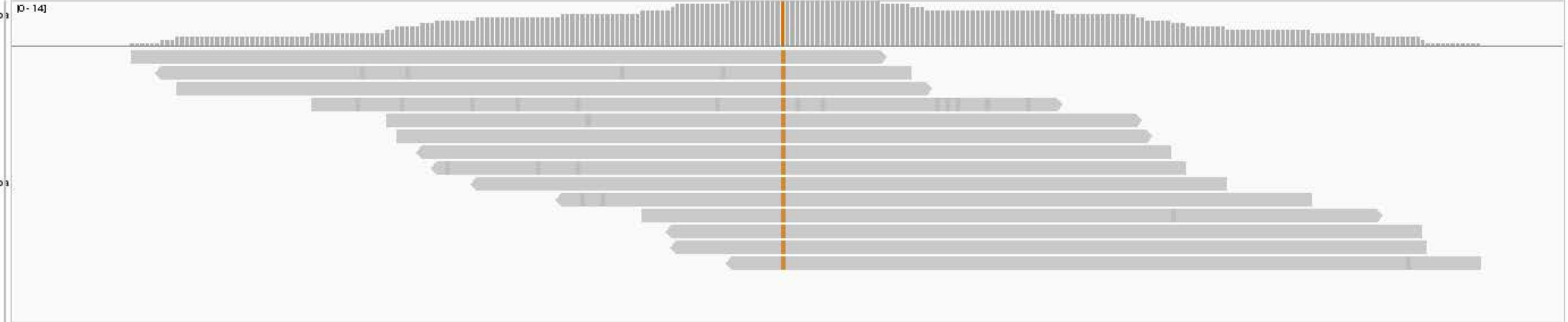








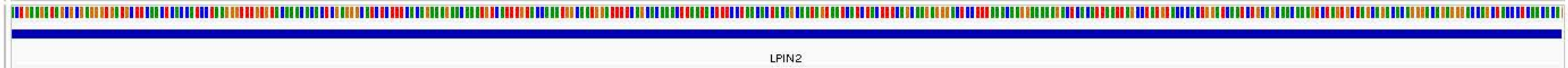
SL\_0001\_LN\_10\_WES\_uniq\_mut.  
coverage



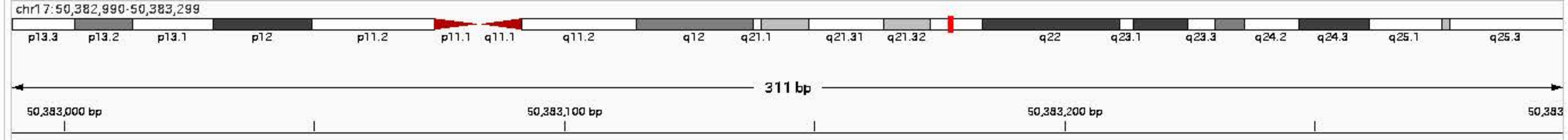
SL\_0001\_LN\_10\_WES\_uniq\_mut.

Sequence

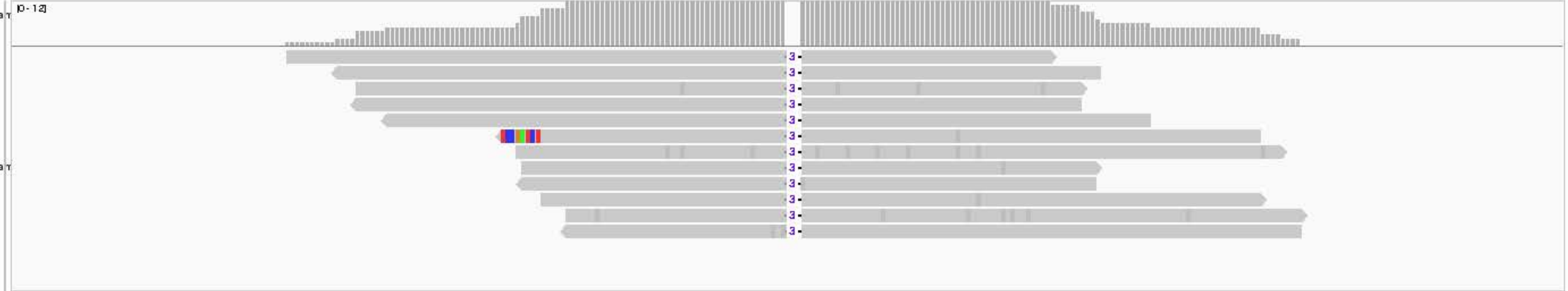
Refseq Genes







SL\_0007\_RN\_2\_WES\_uniq\_mut.ba  
verage



SL\_0007\_RN\_2\_WES\_uniq\_mut.ba

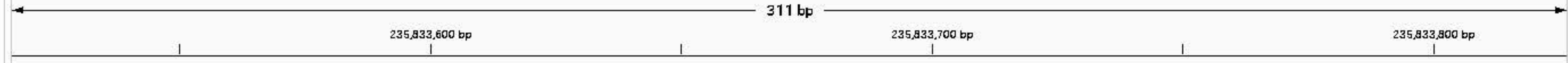
Sequence →

Refseq Genes

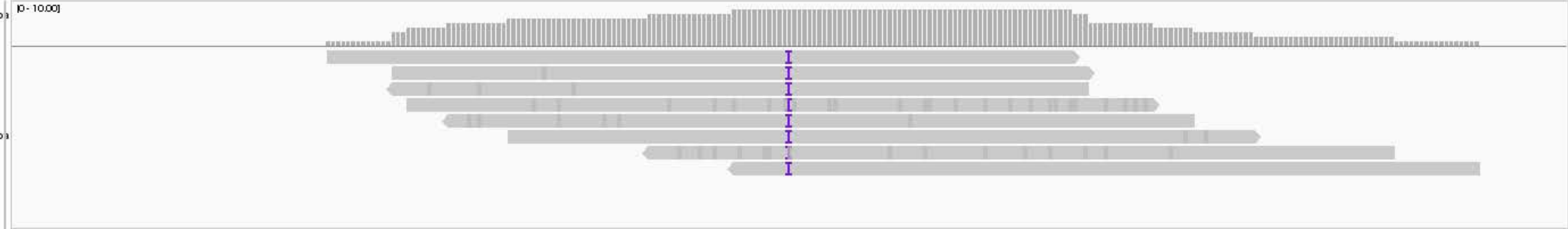


chr1:235,833,517-235,833,826

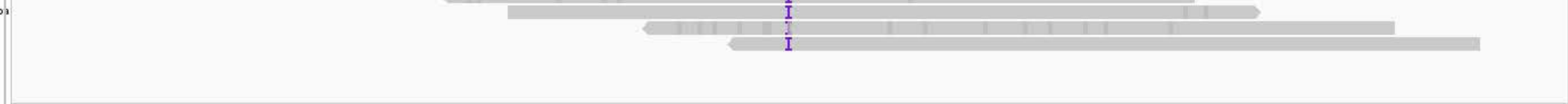
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SL\_0015\_LN\_46\_WES\_uniq\_mut.  
coverage



SL\_0015\_LN\_46\_WES\_uniq\_mut.  
coverage

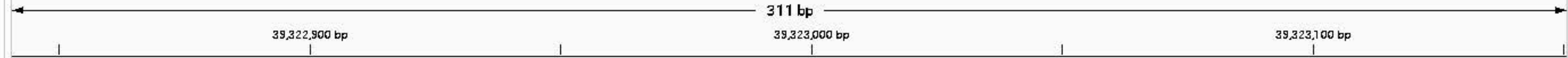
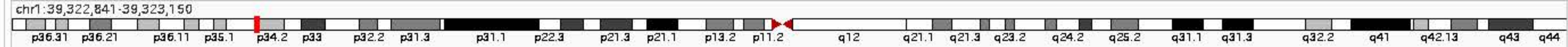


Sequence

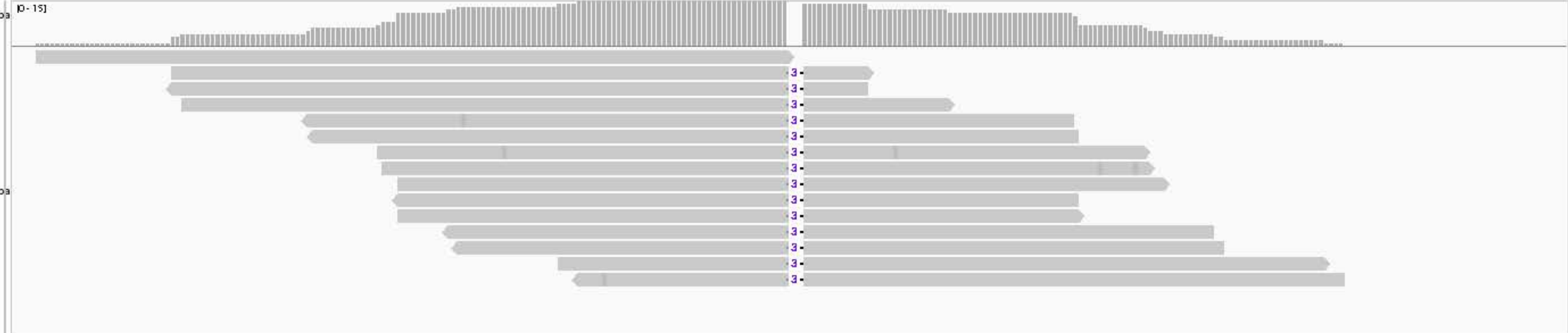


Refseq Genes





SL\_0004\_RN\_47\_WES\_uniq\_mut.ba  
overage



SL\_0004\_RN\_47\_WES\_uniq\_mut.ba

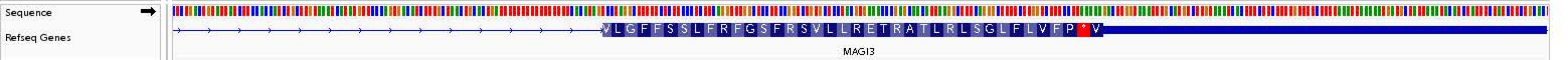
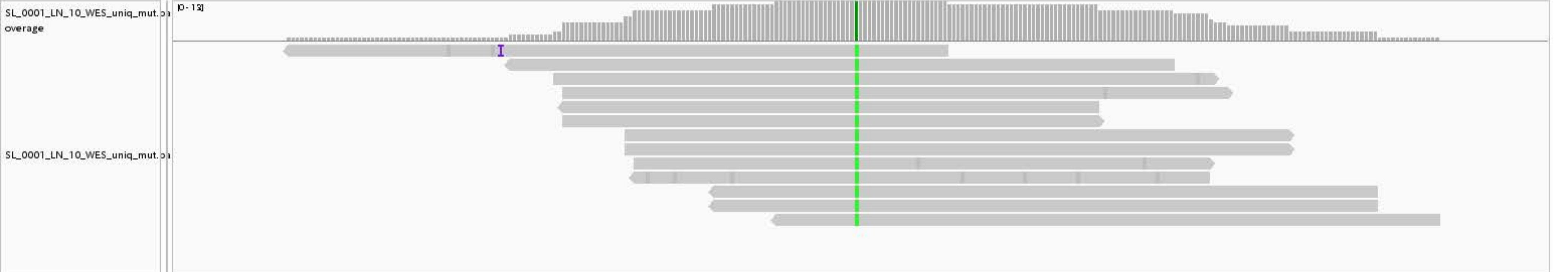
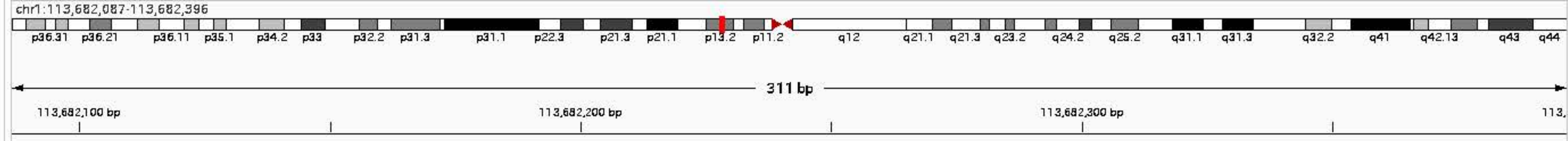
Sequence →

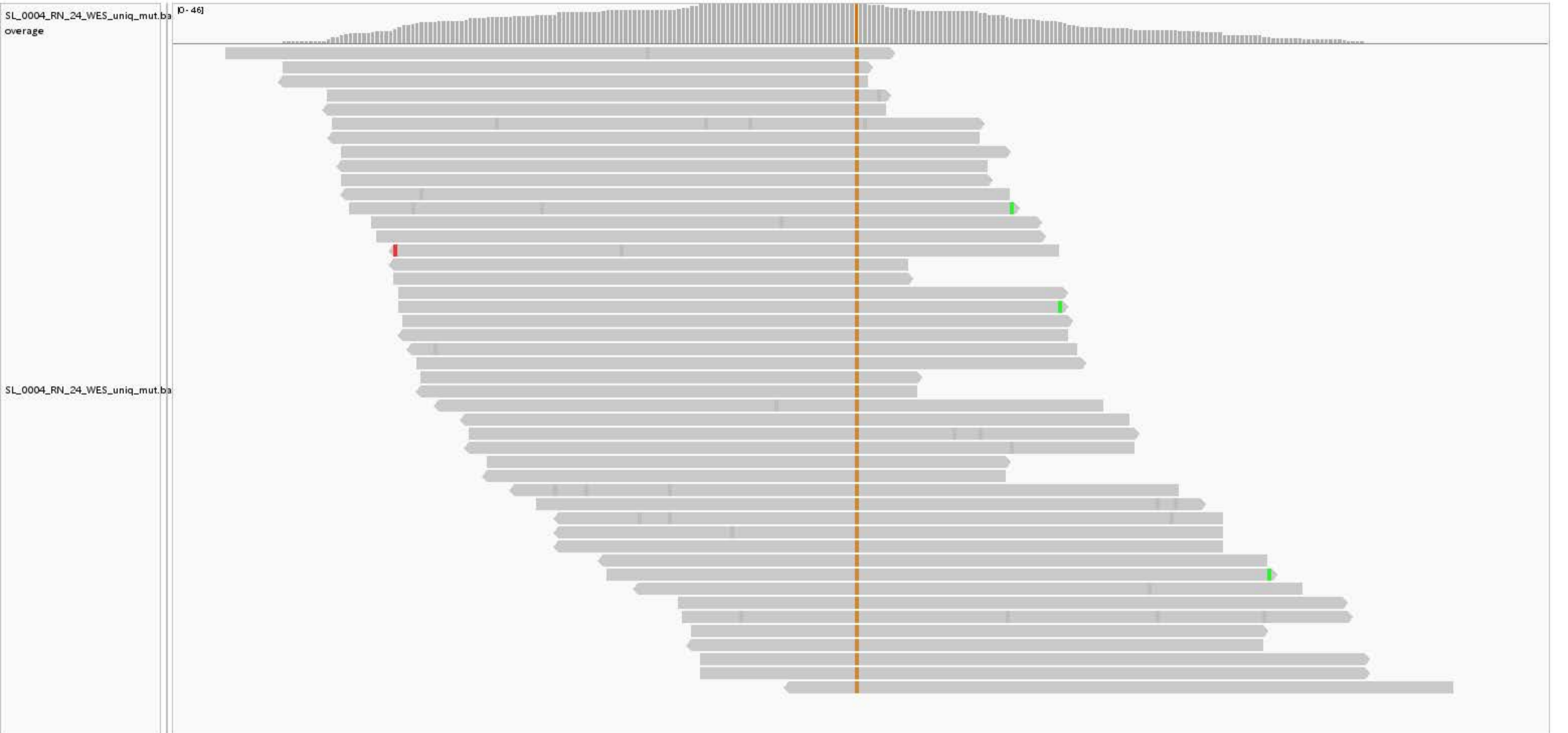
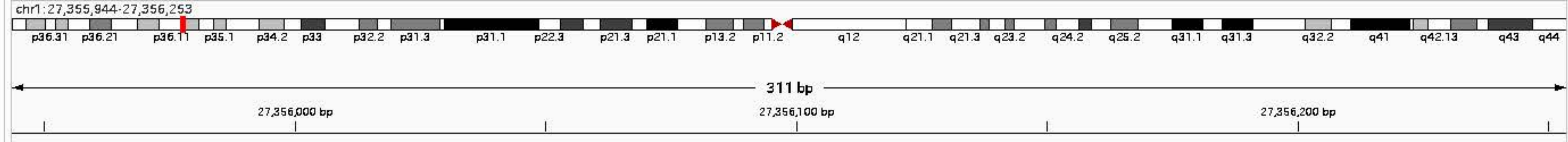


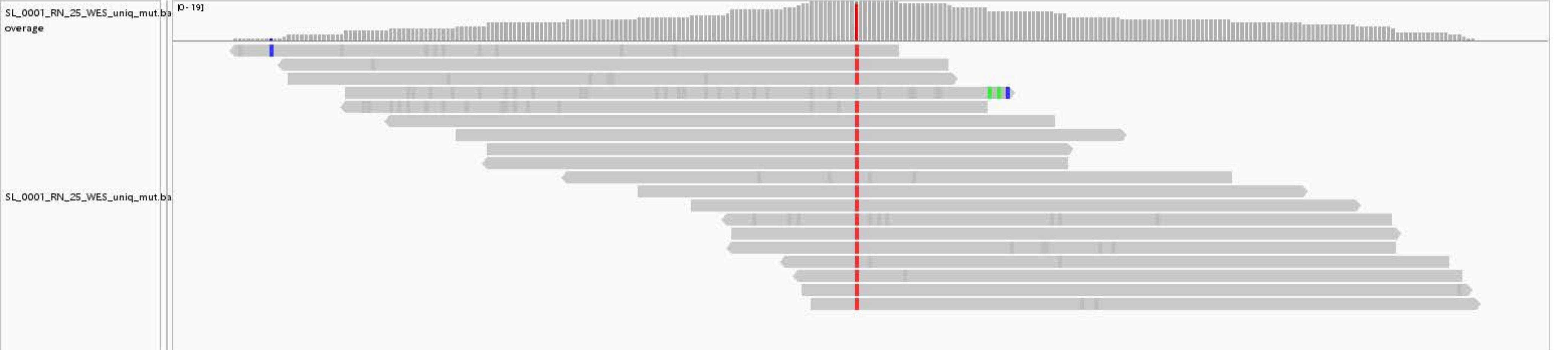
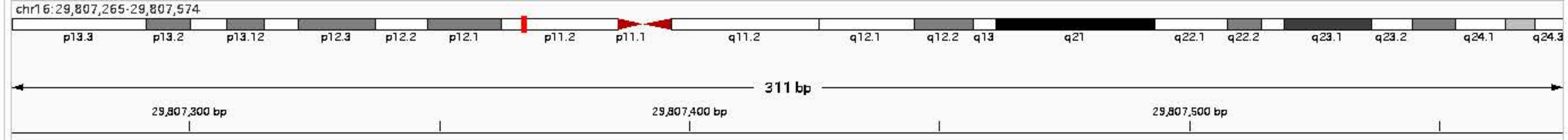
Refseq Genes

MACF1









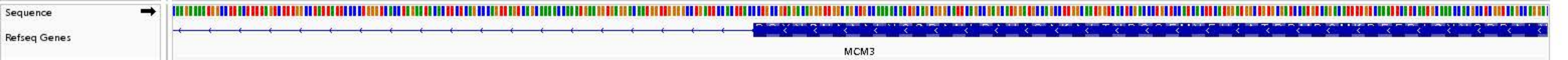
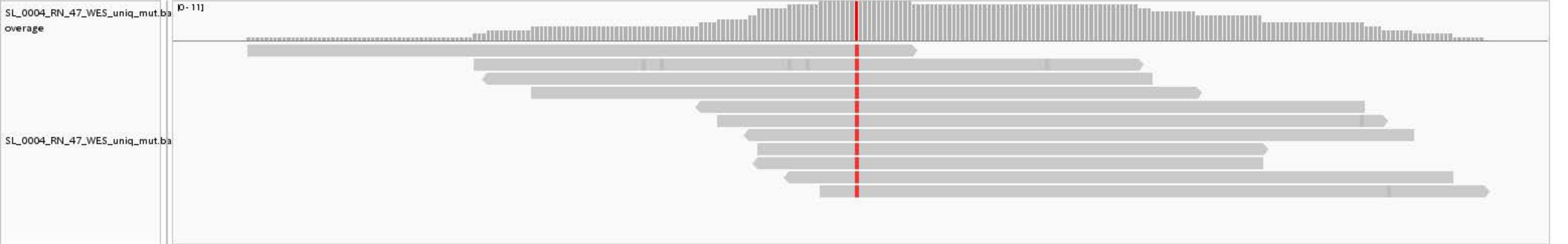
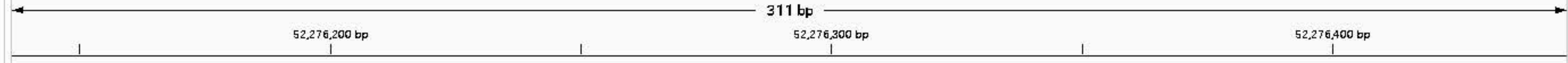
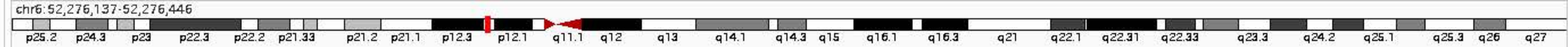
Sequence →

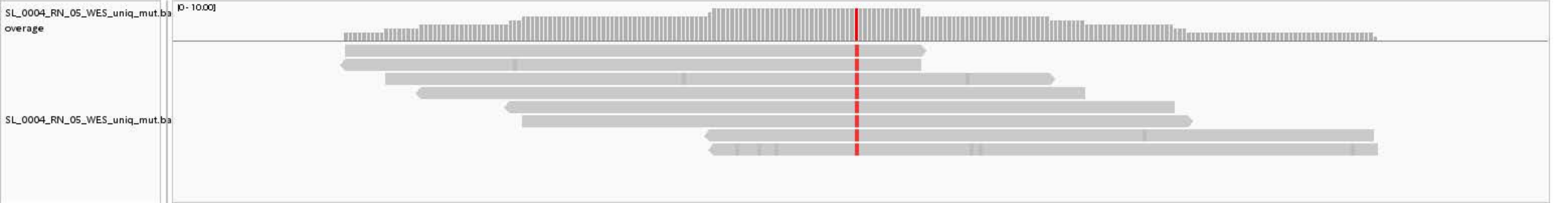
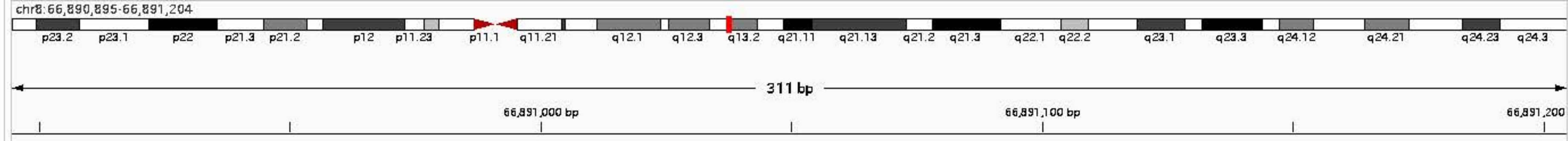
Refseq Genes

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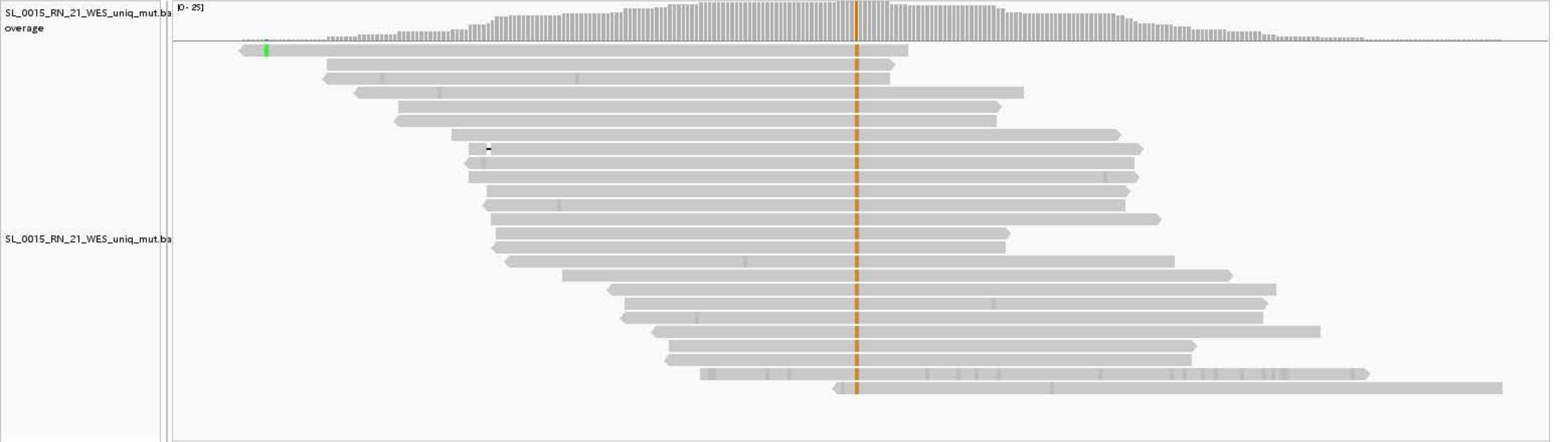
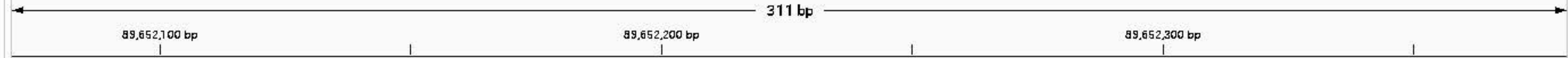
MAZ



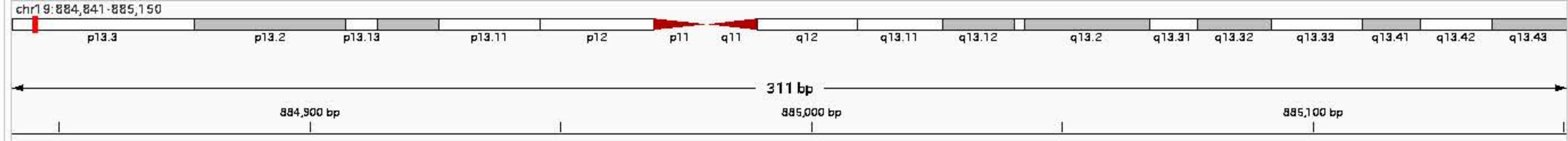




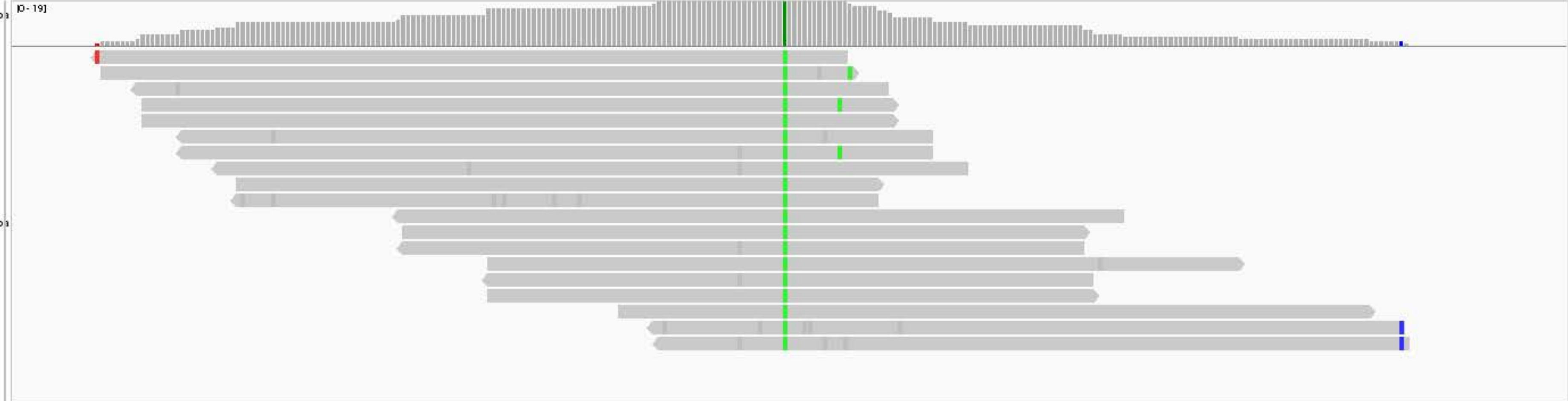
chr6: 89,652,071-89,652,380  
p25.2 p24.3 p23 p22.3 p22.2 p21.33 p21.2 p21.1 p12.3 p12.1 q11.1 q12 q13 q14.1 q14.3 q15 q16.1 q16.3 q21 q22.1 q22.31 q22.33 q23.3 q24.2 q25.1 q25.3 q26 q27





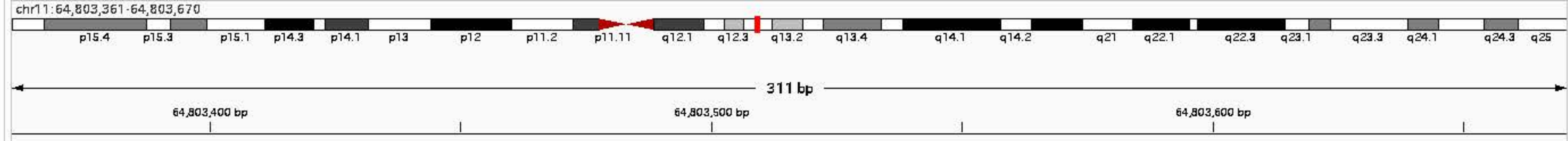


SL\_0001\_LN\_10\_WES\_uniq\_mut. coverage



Sequence Refseq Genes





SL\_0007\_RN\_2\_WES\_uniq\_mut.ba  
verage

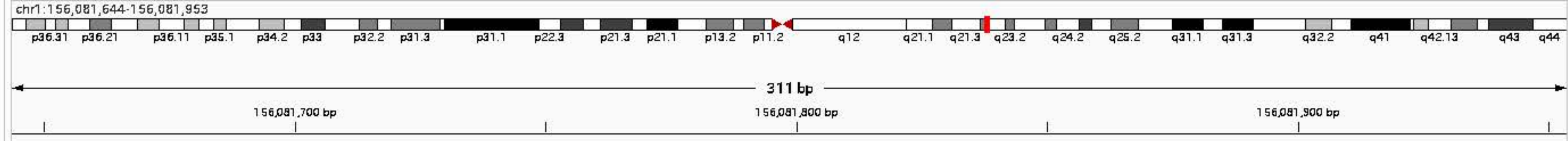


SL\_0007\_RN\_2\_WES\_uniq\_mut.ba

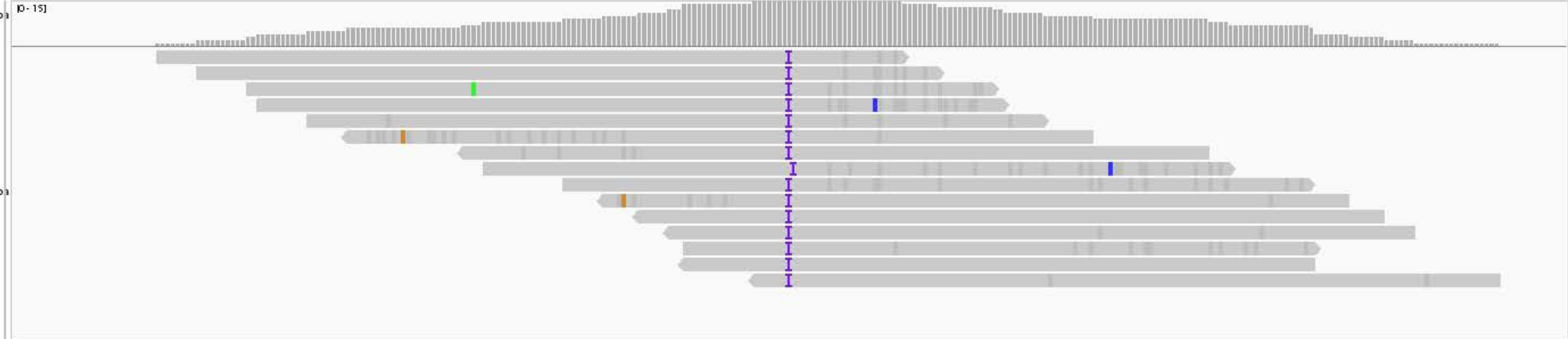
Sequence →  
Refseq Genes



MEN1



SL\_0002\_LN\_62\_WES\_uniq\_mut. coverage



SL\_0002\_LN\_62\_WES\_uniq\_mut.

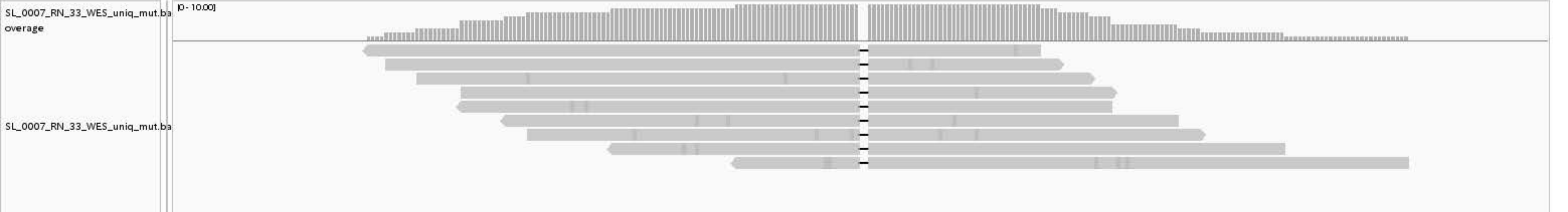
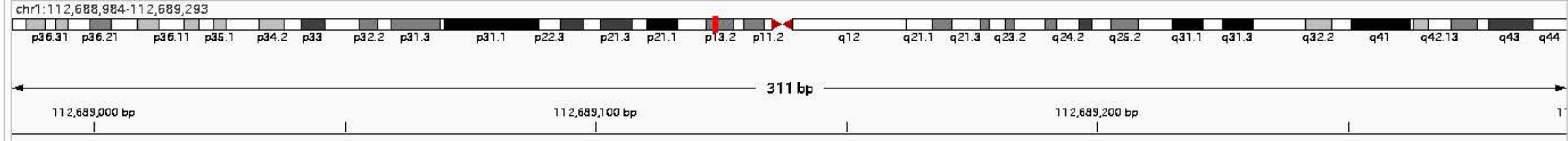
Sequence

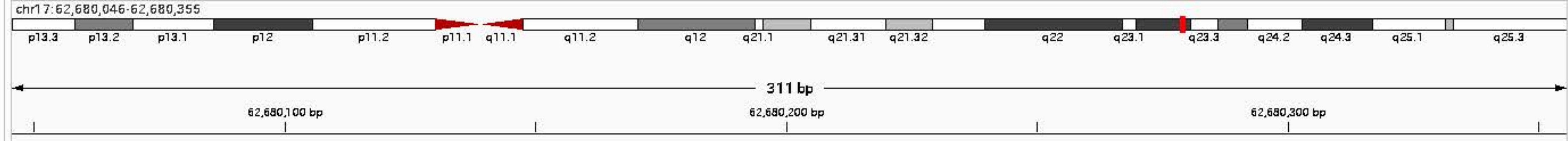
Refseq Genes

L A C L K A D S A G K P A T P P Q P T Q A A P A A T P A A P P A A P P P P A P Q P P A A P Q A P A G G G G G G D E G A T P A P P E G L G L L C L Q D L A L Q L A R E D E L L G R D K A S G G F C G L E G F

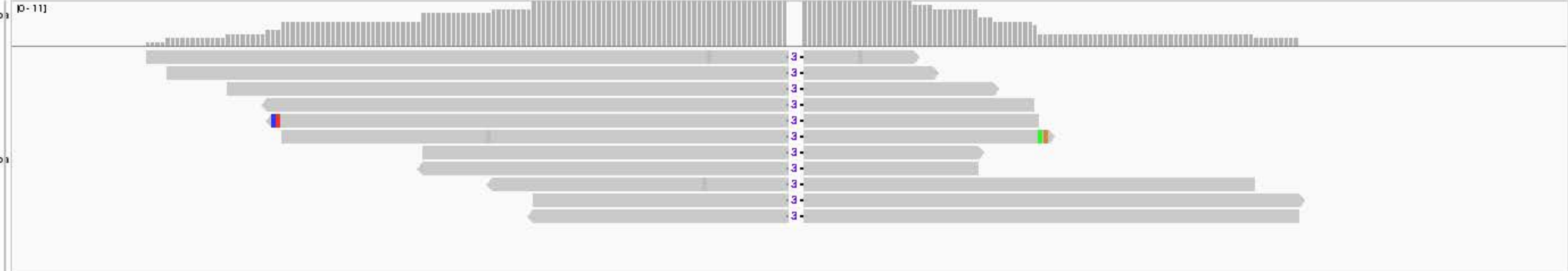
MEX3A



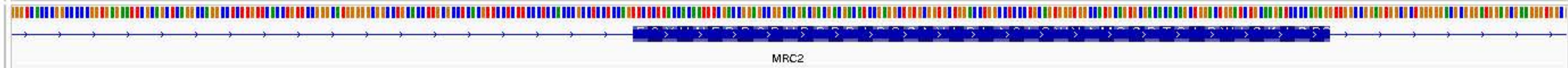


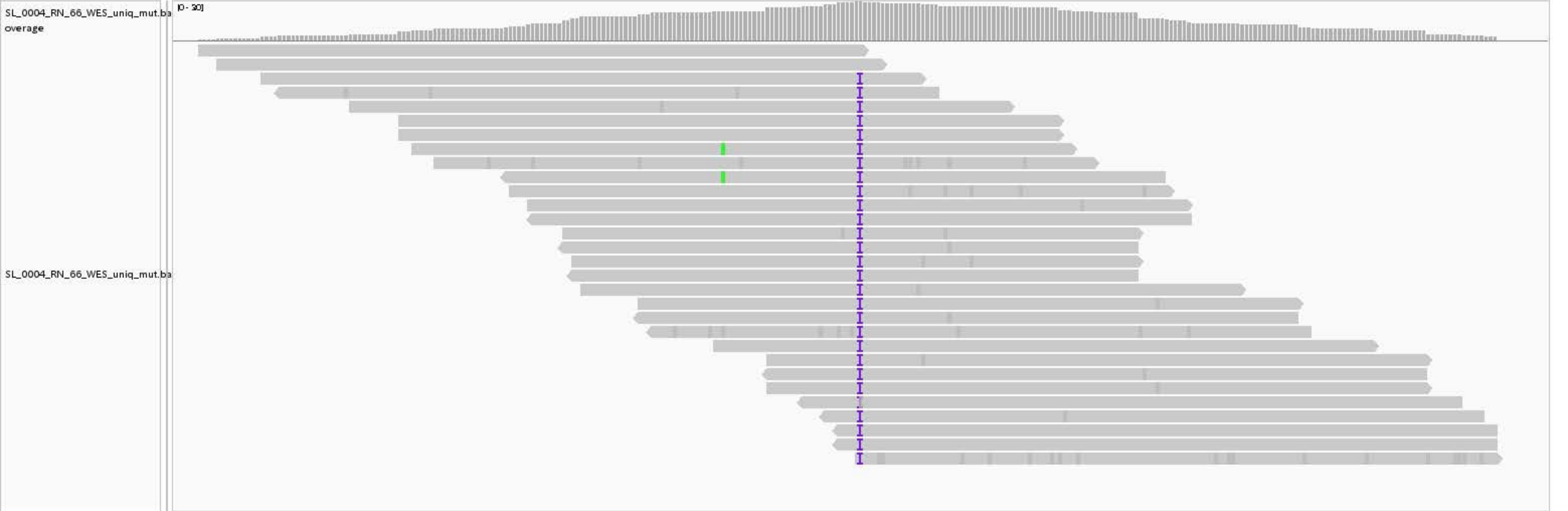
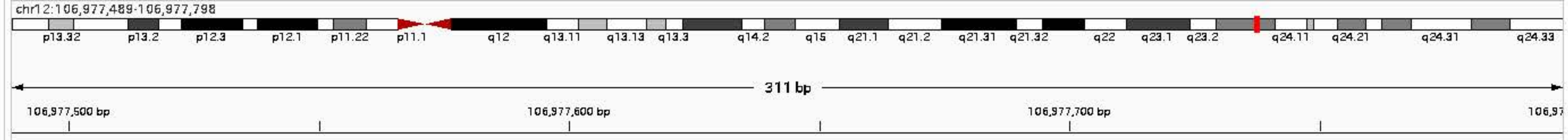


SL\_0001\_LN\_10\_WES\_uniq\_mut.  
coverage

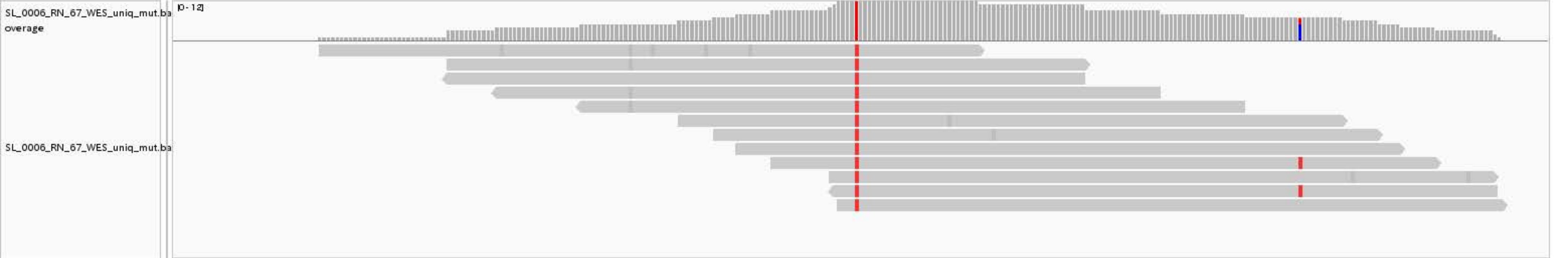
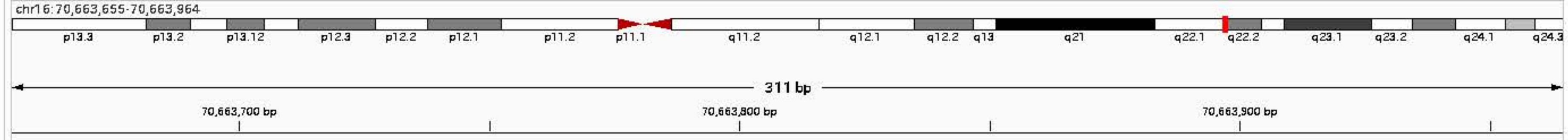


Sequence  
Refseq Genes









Sequence →

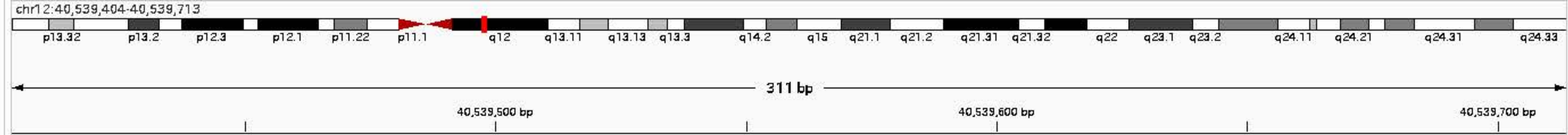
Refseq Genes

L I R P A S R D N T V T R R L R V G R R I A V L M D E A P P D S T A A P P P T P T E E T P T A S L A T P F P F Q G E G L A H A G A V L E G L K E V L S H R N A A L Q Q Q E D E A G A G P Y G A

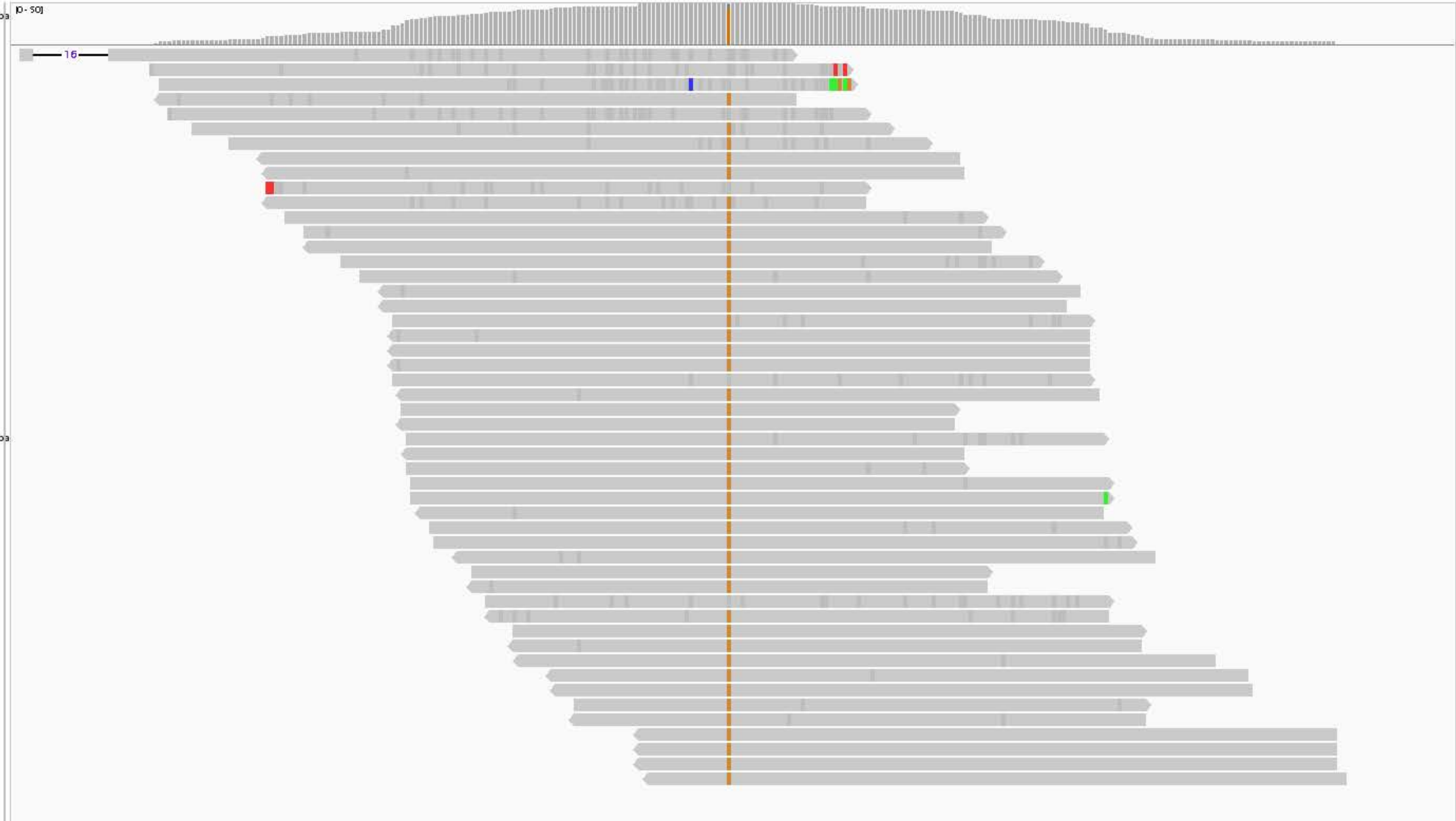
MTSS2





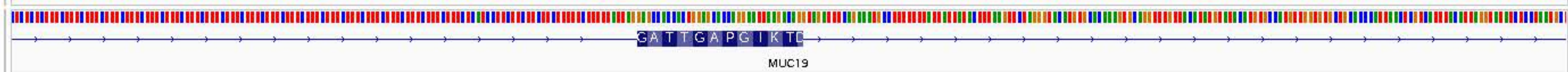


SL\_0007\_RN\_33\_WES\_uniq\_mut.ba  
coverage

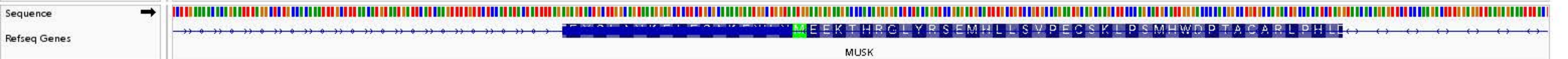
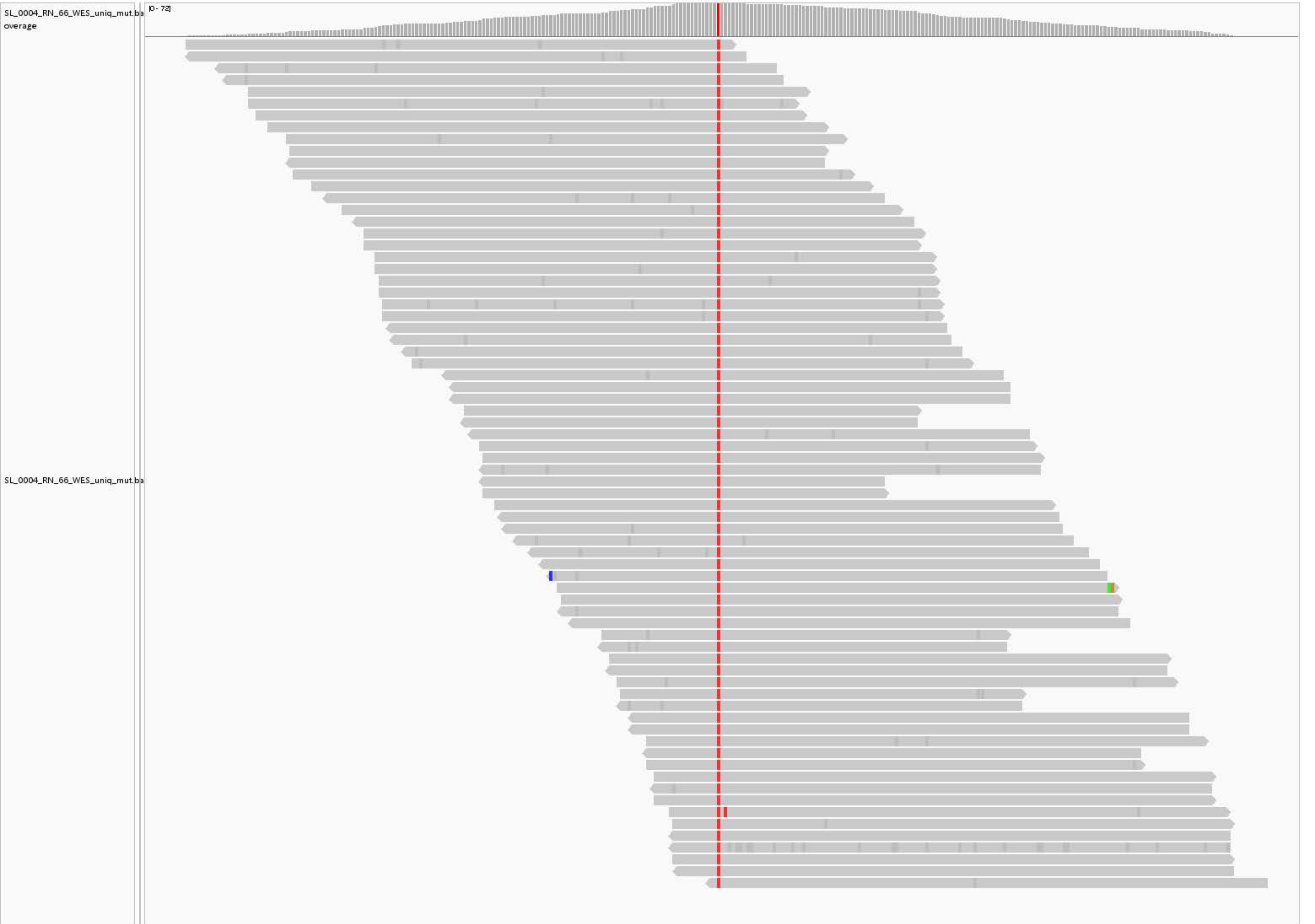
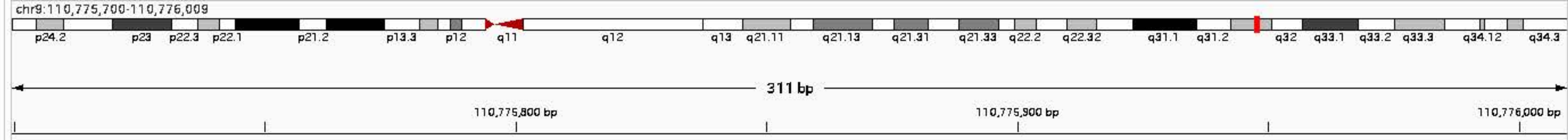


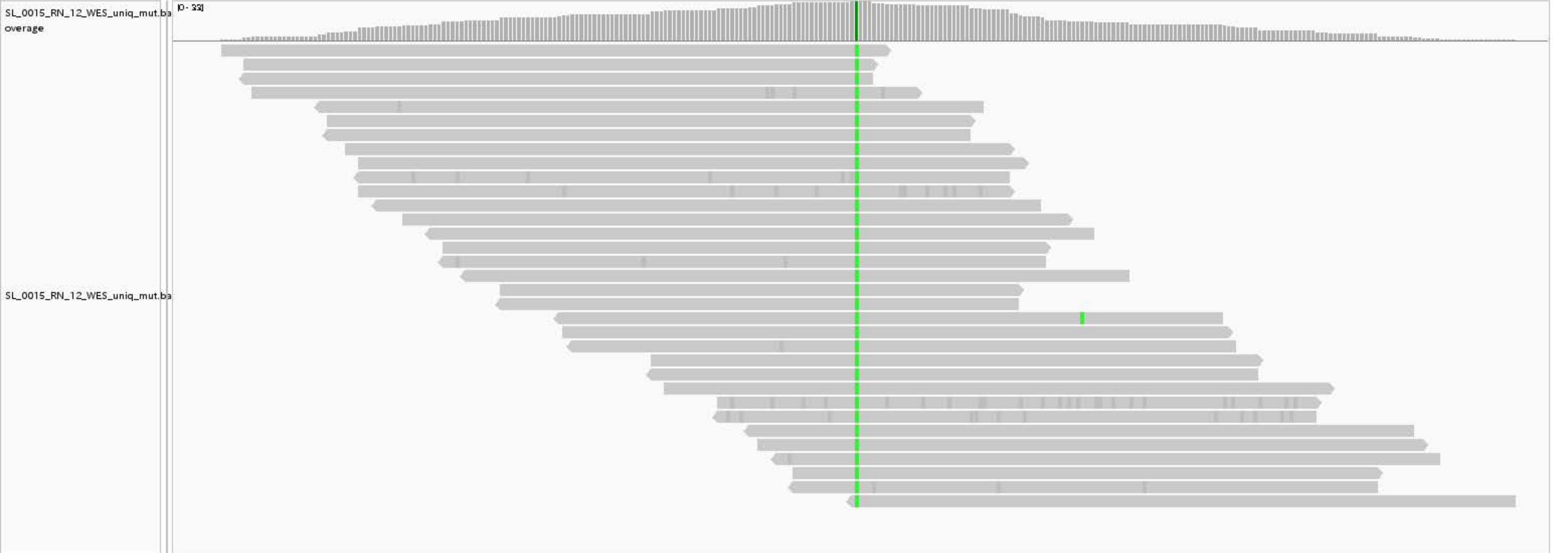
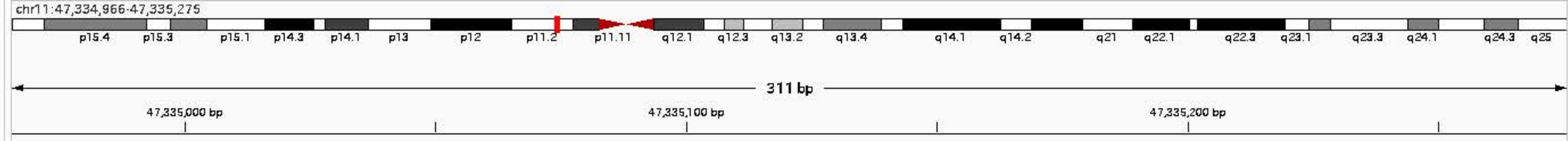
SL\_0007\_RN\_33\_WES\_uniq\_mut.ba

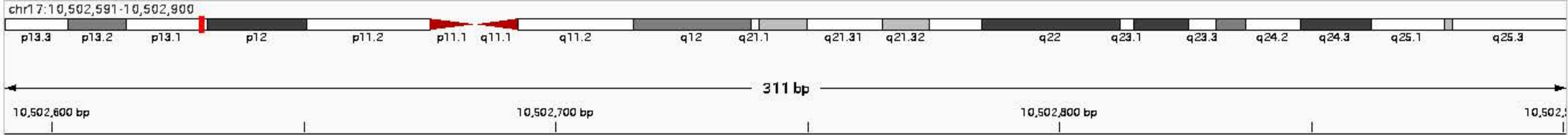
Sequence →  
Refseq Genes



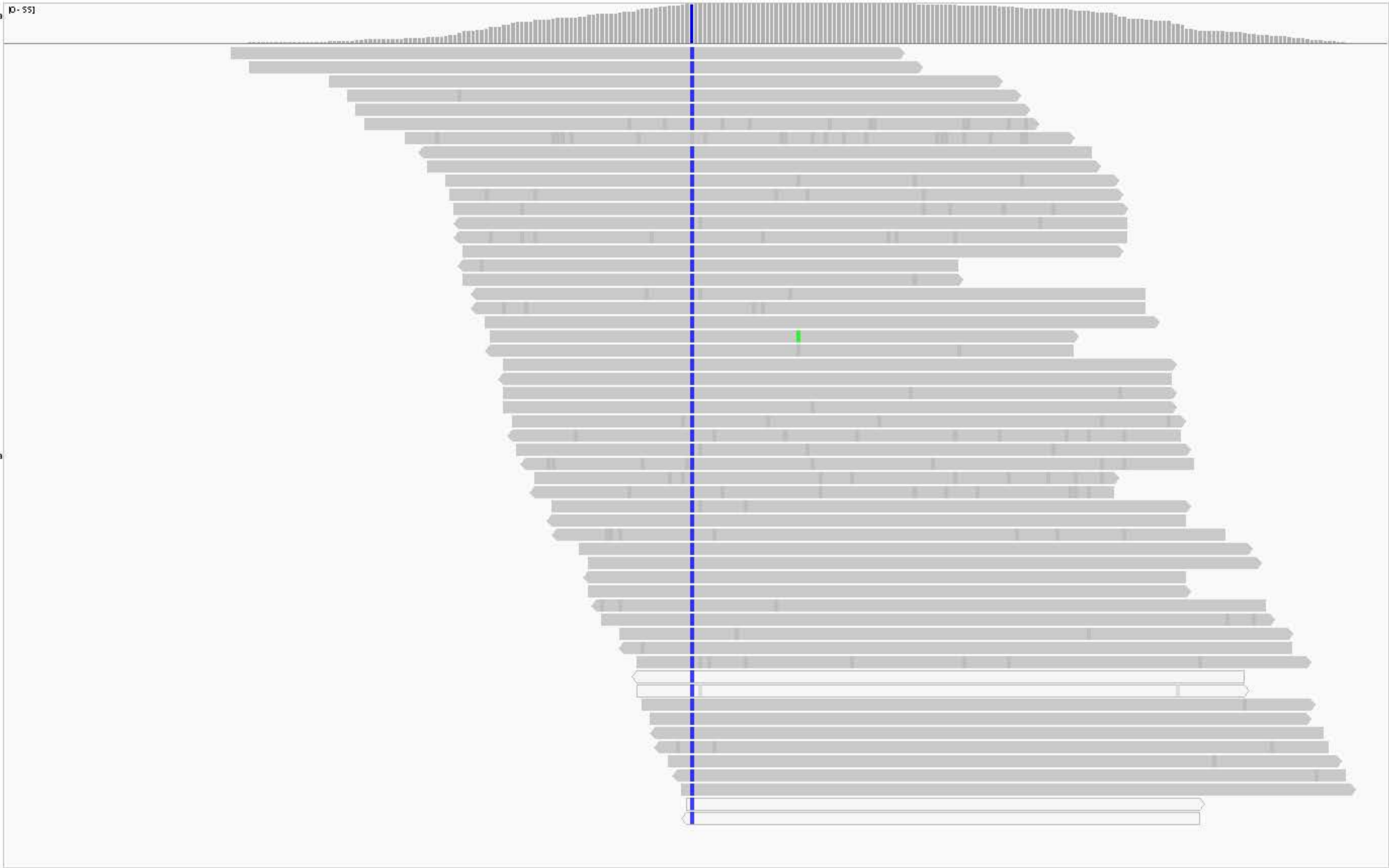








SL\_0007\_RN\_33\_WES\_uniq\_mut.ba  
coverage

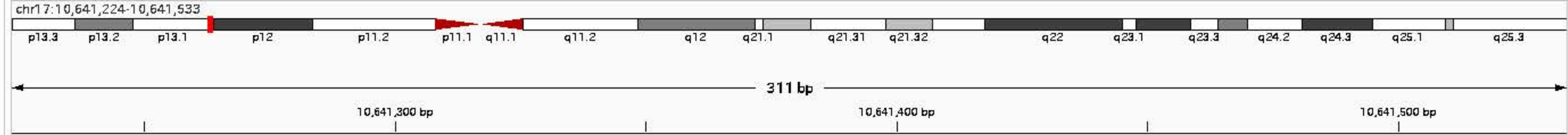


SL\_0007\_RN\_33\_WES\_uniq\_mut.ba

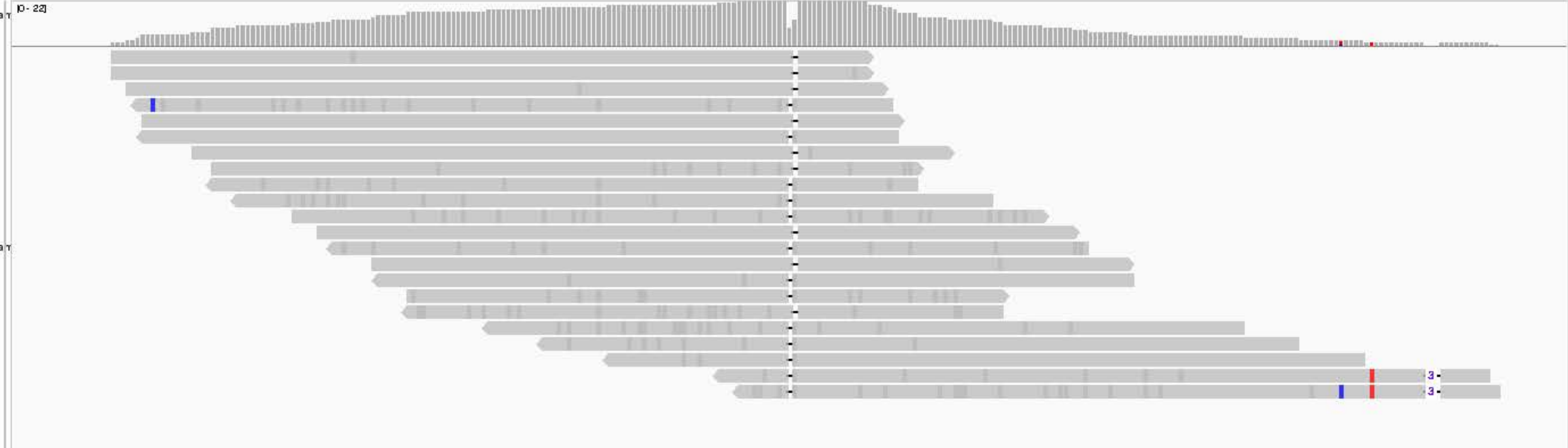
Sequence →  
Refseq Genes



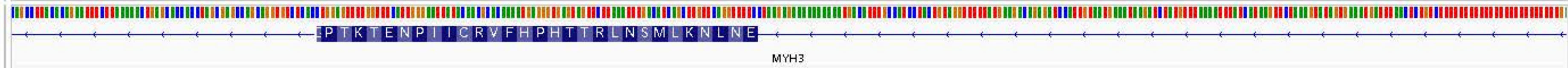


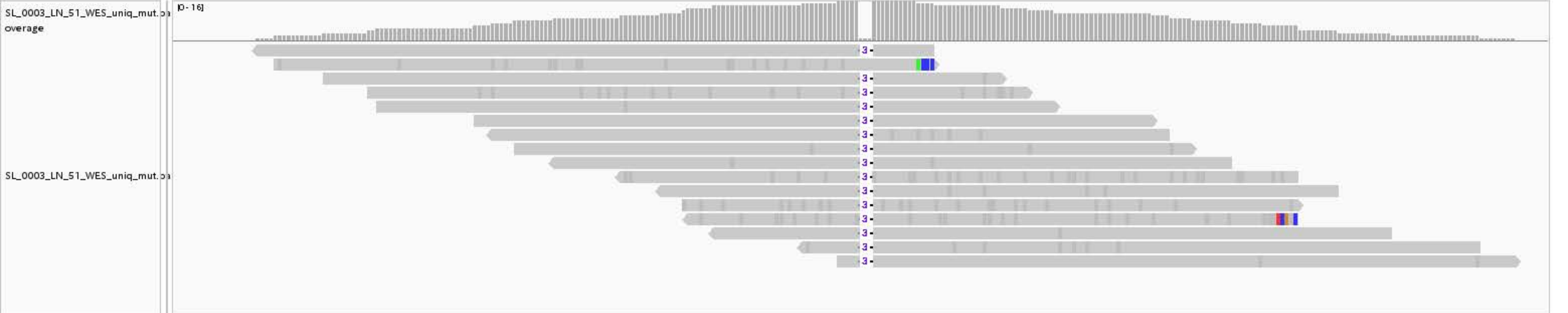
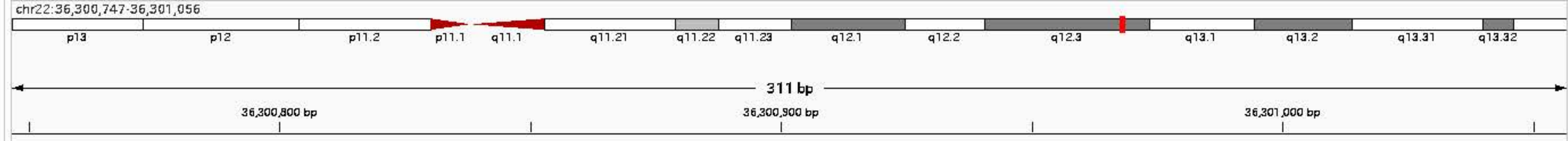


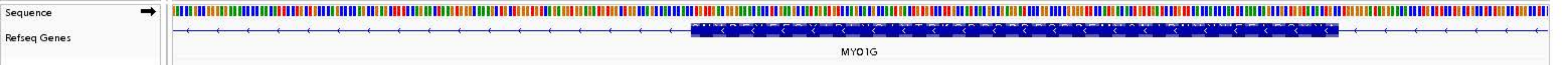
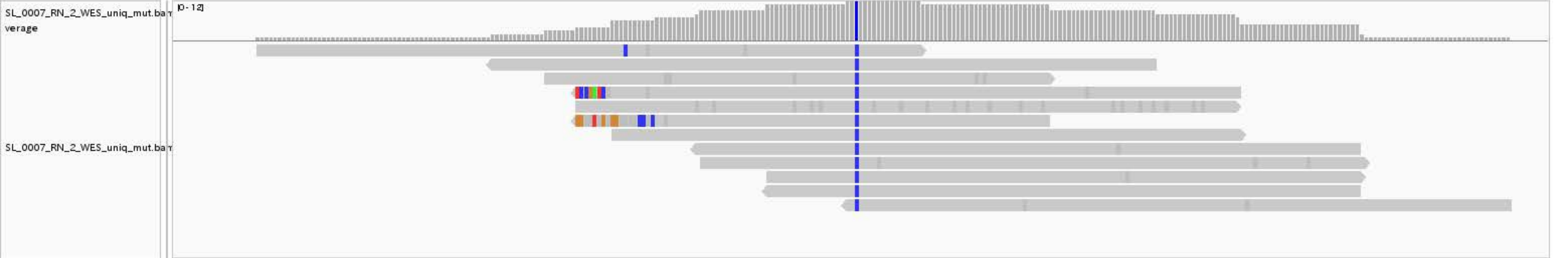
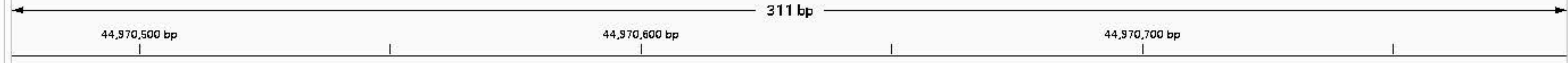
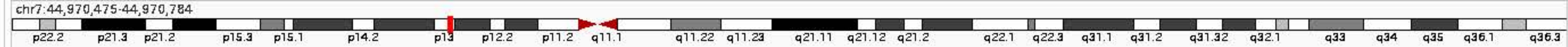
SL\_0002\_RN\_8\_WES\_uniq\_mut.ba  
verage



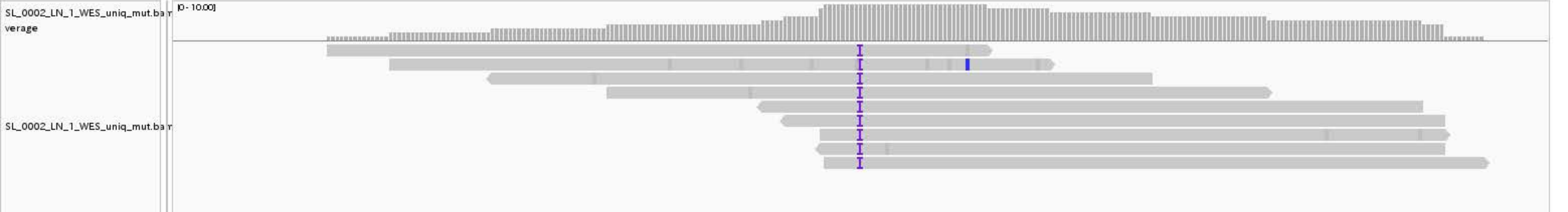
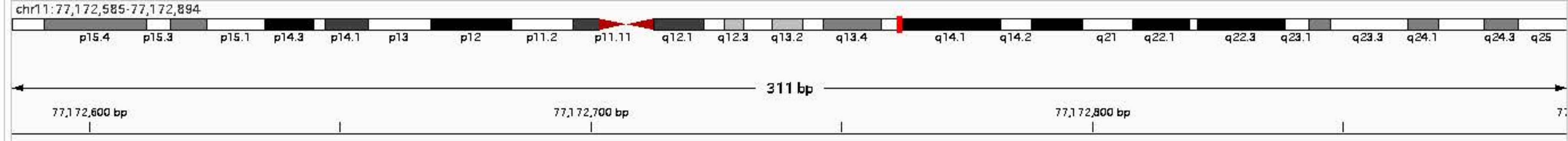
Sequence →  
Refseq Genes

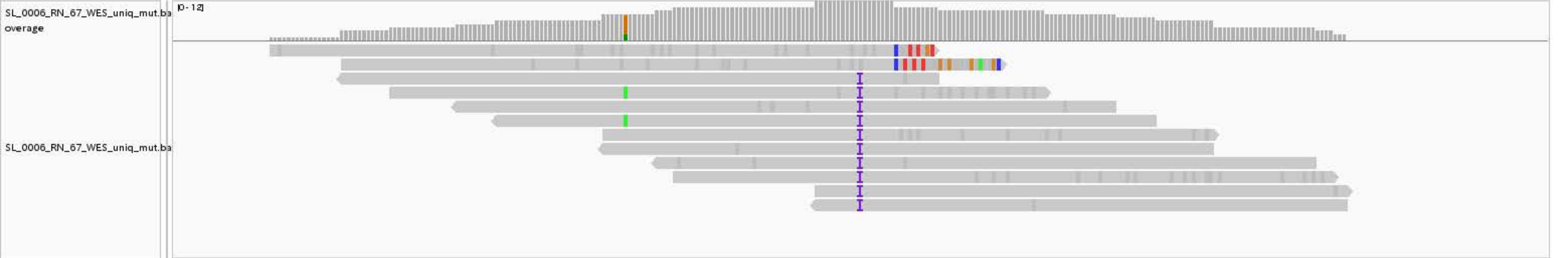
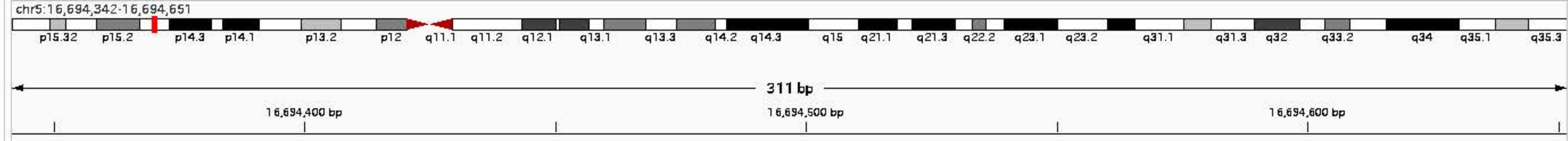


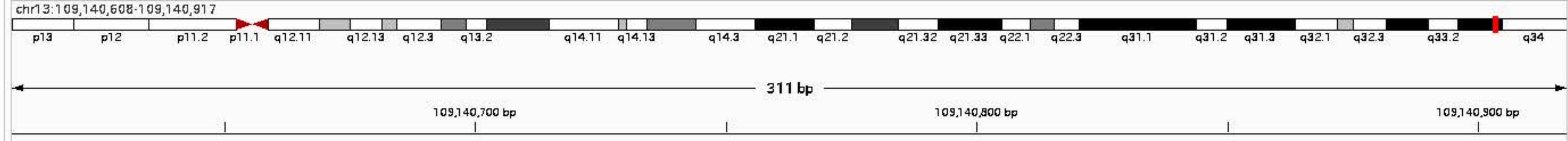












Sequence →

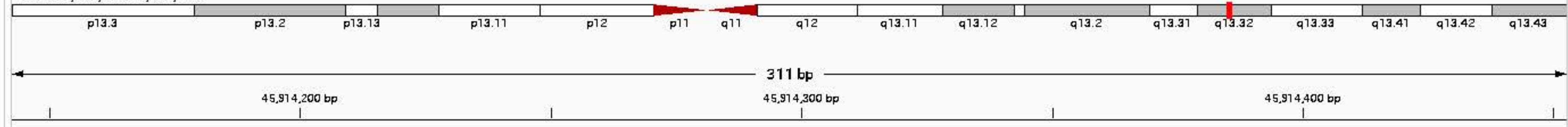
Refseq Genes

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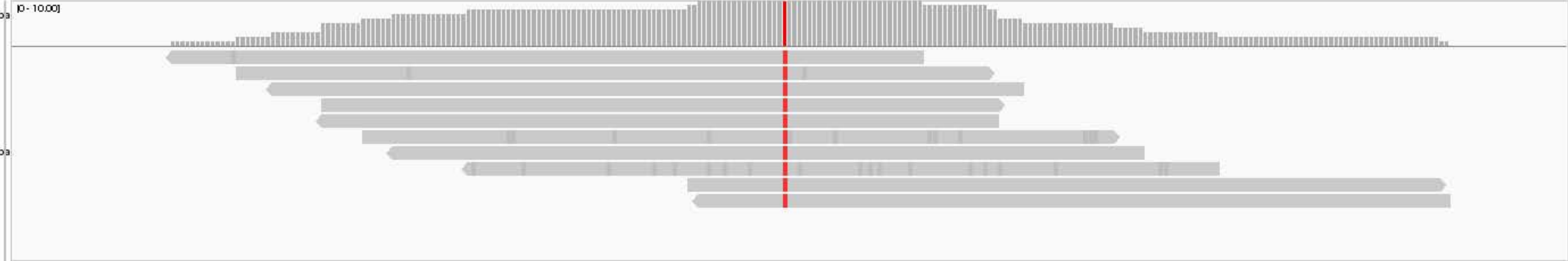
MYO16



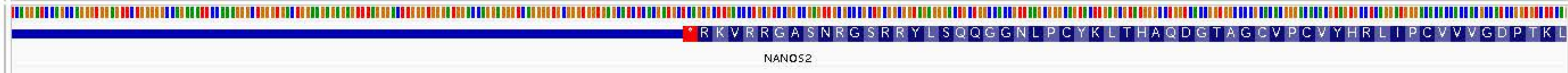
chr19:45,914,143-45,914,452



SL\_0004\_RN\_05\_WES\_uniq\_mut.ba  
coverage

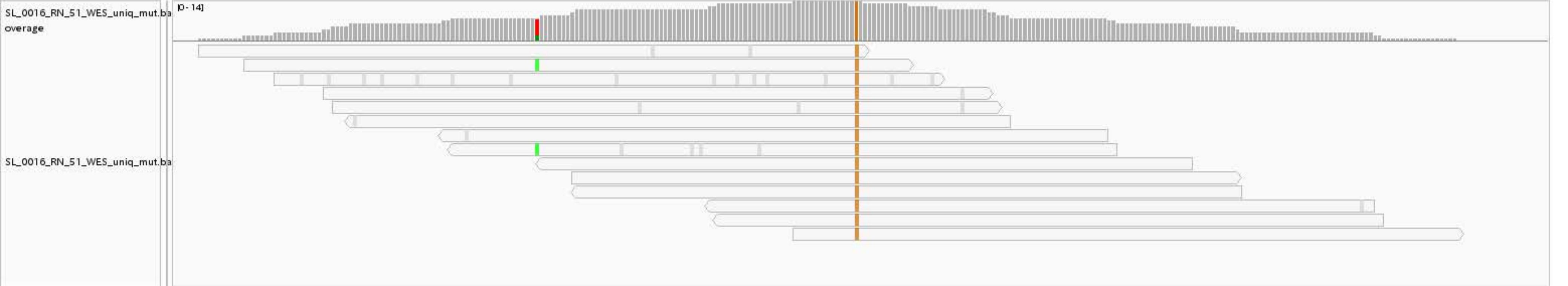
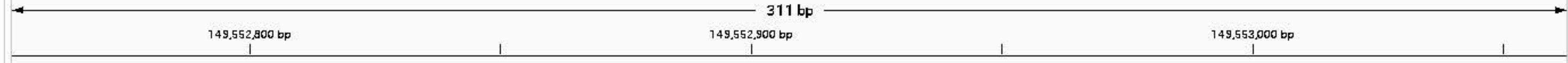


Sequence  
Refseq Genes



chr1:149,552,753-149,553,062

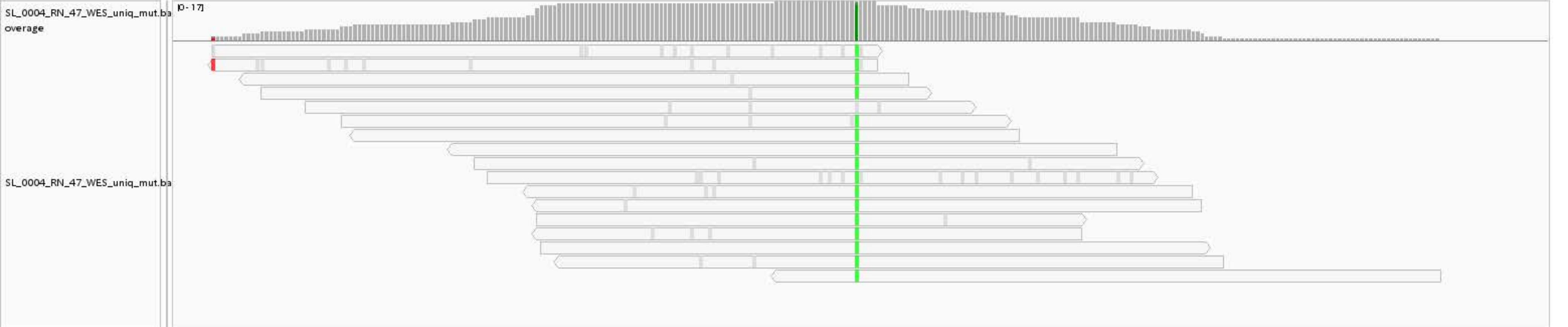
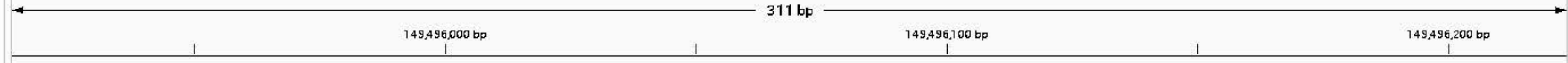
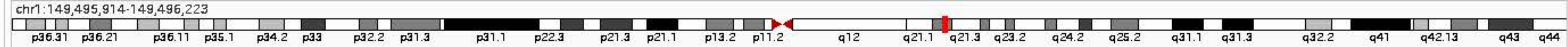
p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44



Sequence Refseq Genes

LSRELLEVVVEPEVLQDSLDRCYSTPSSCLEQPDSQPYGSSFYALEEKHVGFSLDVGE

NBPF19



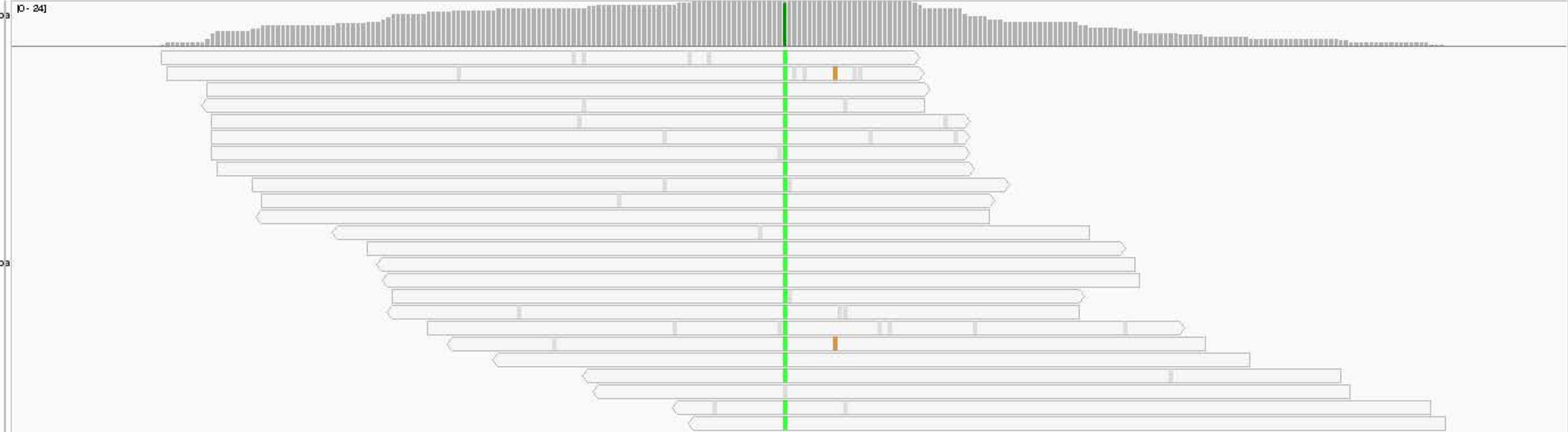


chr1:149,510,191-149,510,500

p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44



SL\_0004\_RN\_26\_WES\_uniq\_mut.ba  
coverage



SL\_0004\_RN\_26\_WES\_uniq\_mut.ba

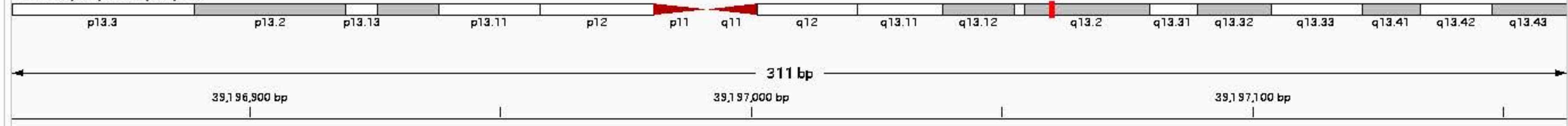
Sequence

Refseq Genes

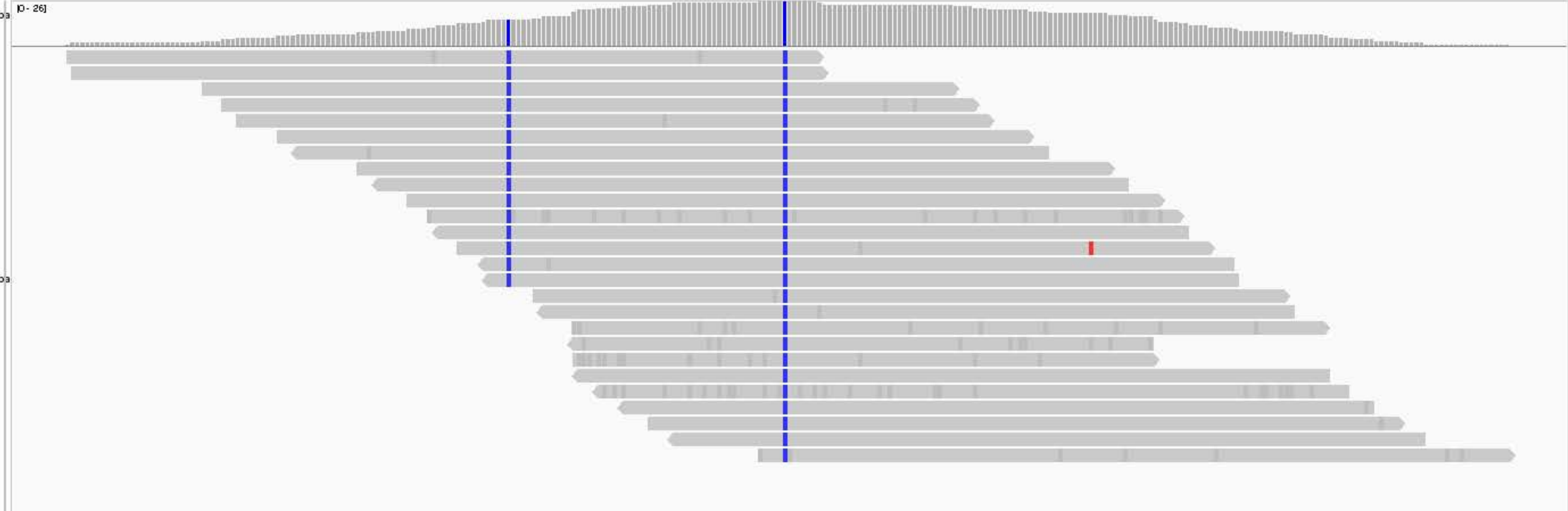
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NBPF19

chr19:39,196,853-39,197,162

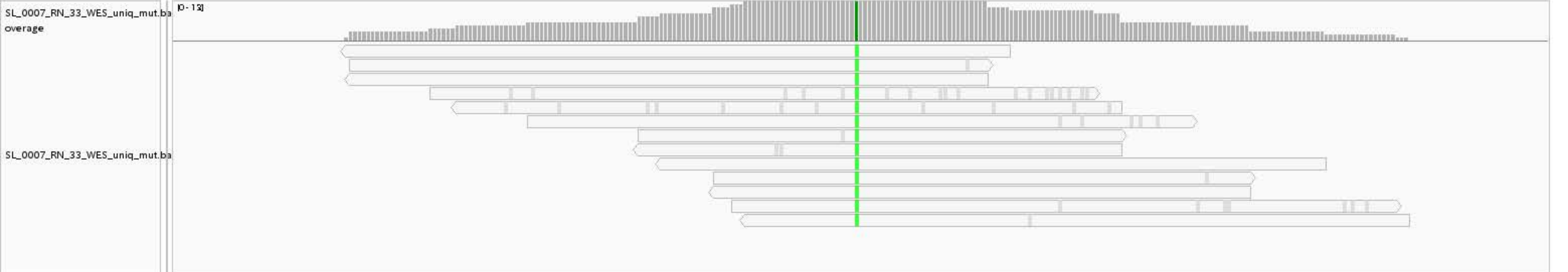
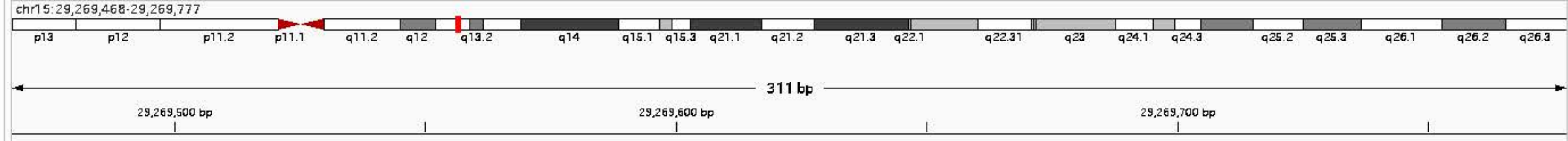


SL\_0006\_RN\_59\_WES\_uniq\_mut.ba  
coverage



Sequence →  
Refseq Genes





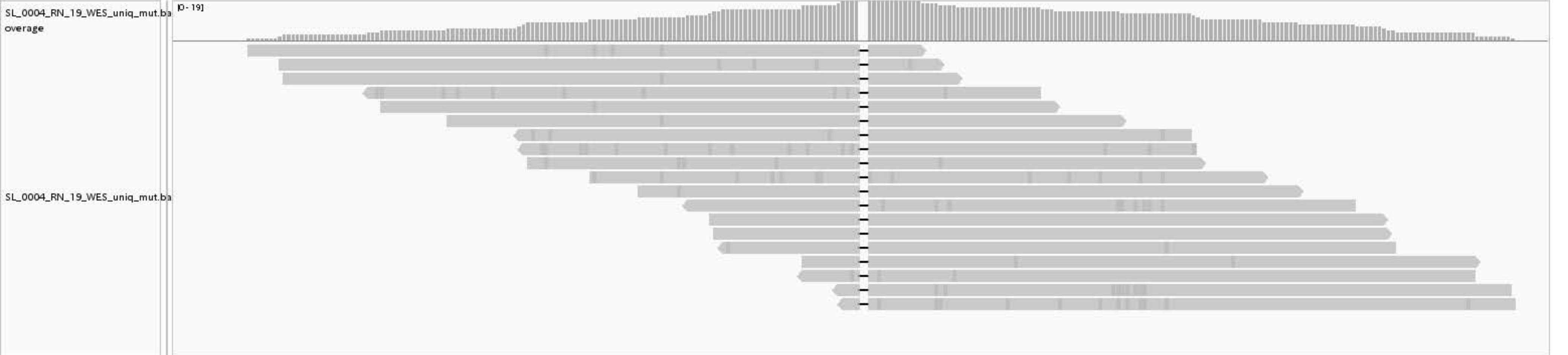
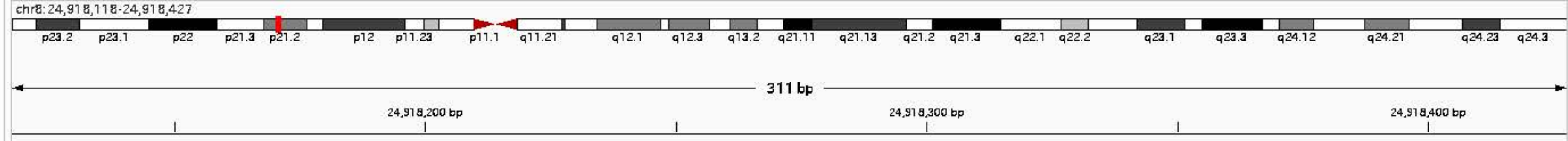
Sequence →

Refseq Genes

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FAM189A1



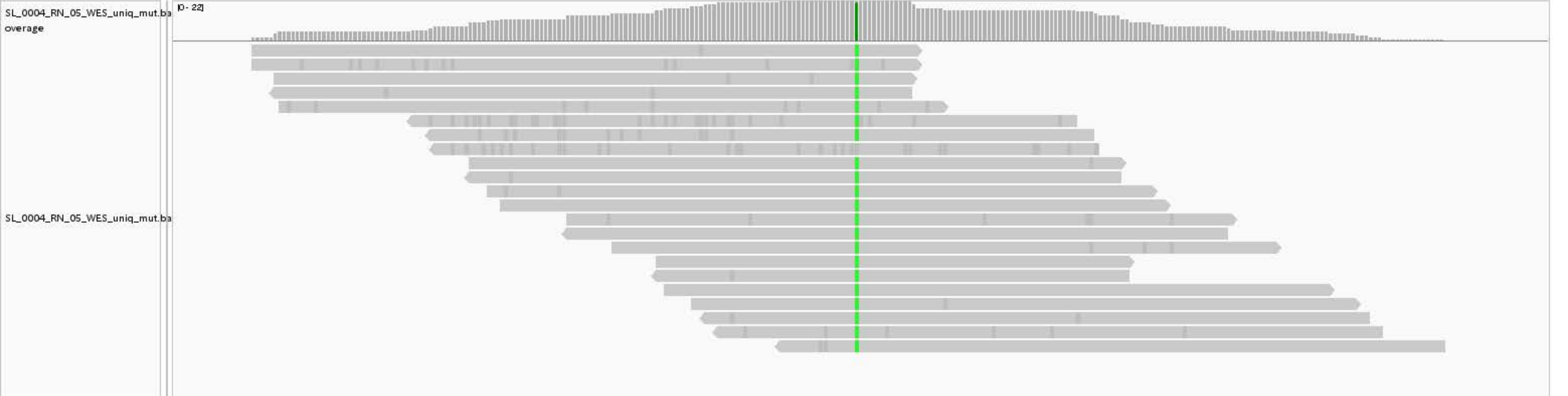
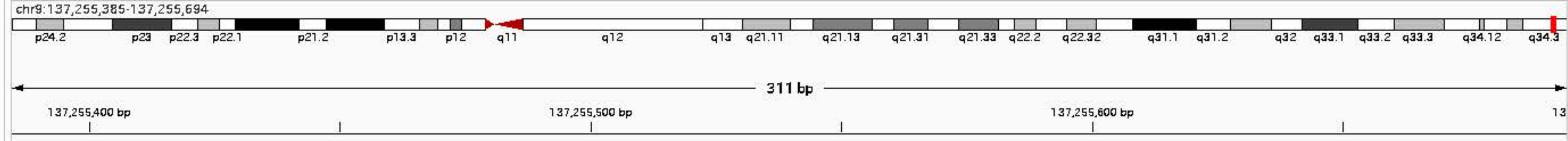


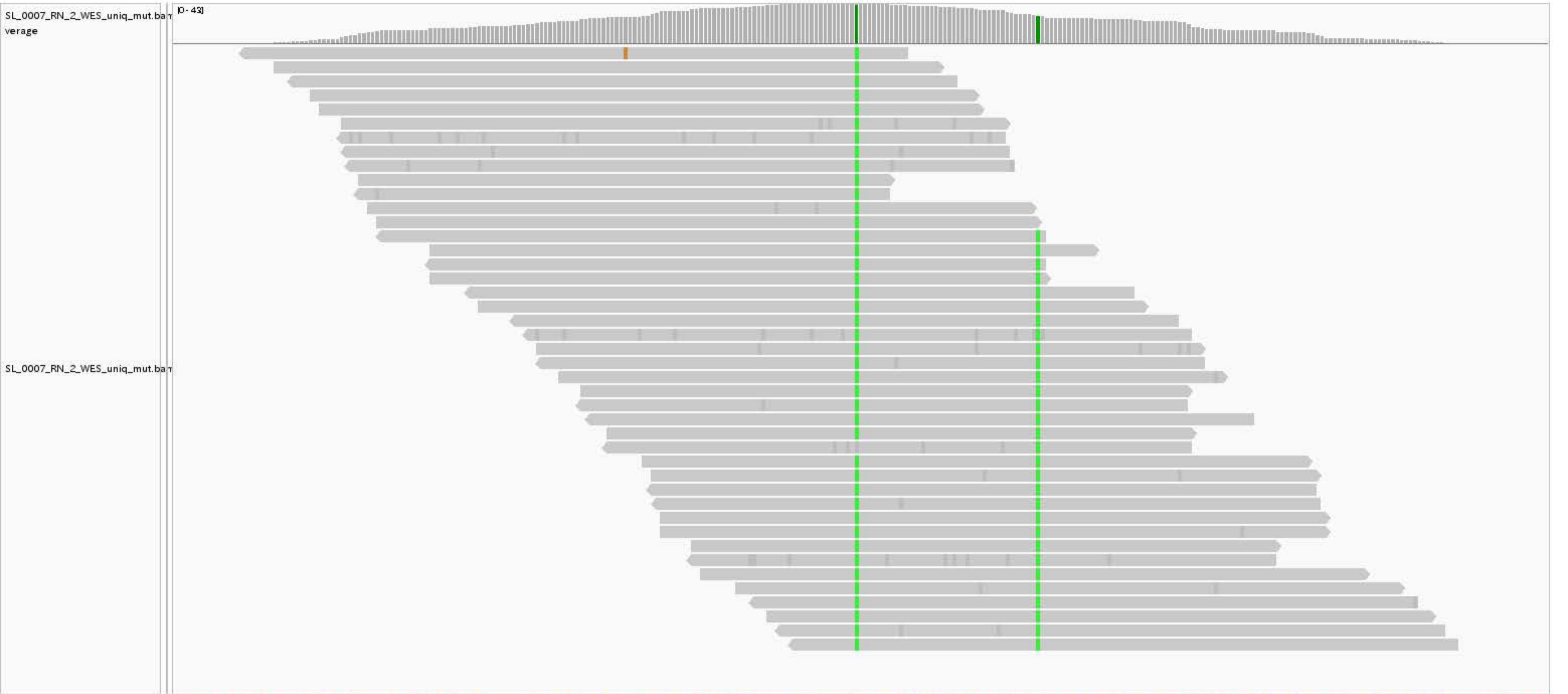
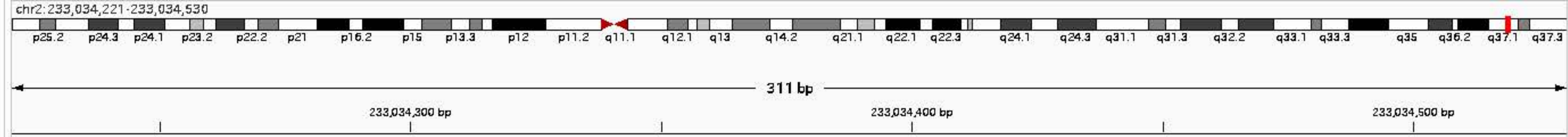
Sequence →

Refseq Genes

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NEFM





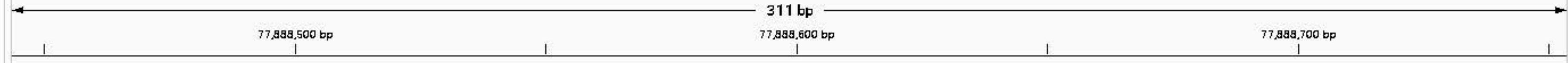
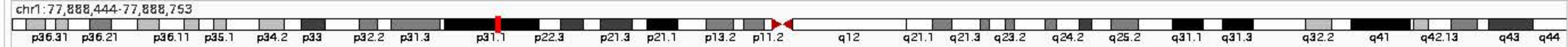
Sequence →

Refseq Genes

IAIPGQVTEQQQLQTRANVTRLCQVTSTDHGRTWSSPRDLTDA AIGPAYREWSTFAVGPGHCLQLHDRARSLVVPAYAYRKLHPIQRPIPSAFCFLSHDHGRTV

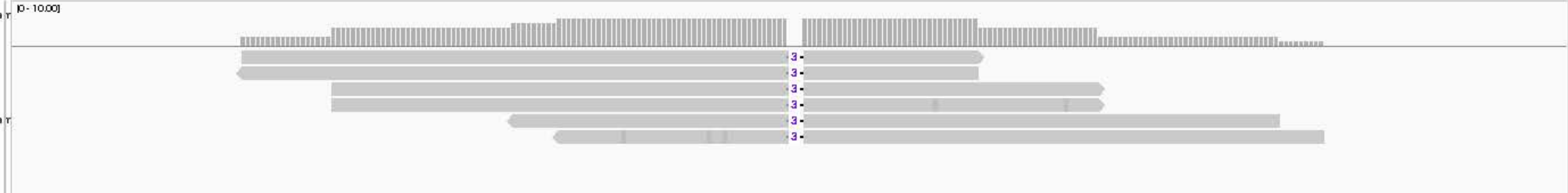
NEU2





SL\_0001\_LN\_4\_WES\_uniq\_mut.ba  
verage

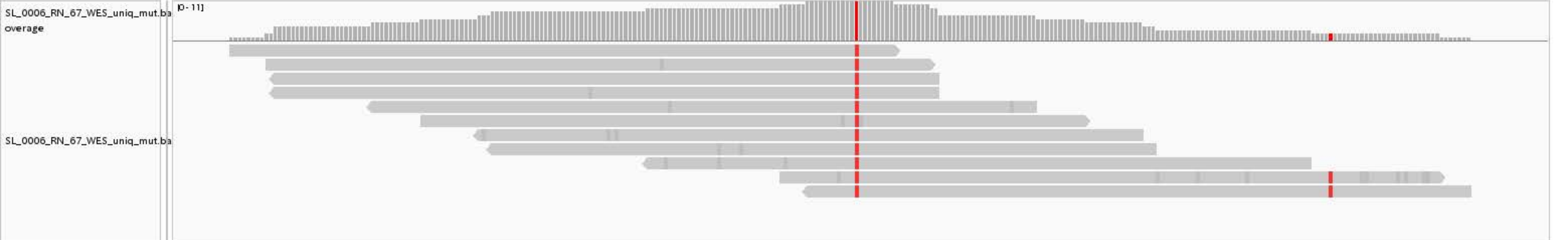
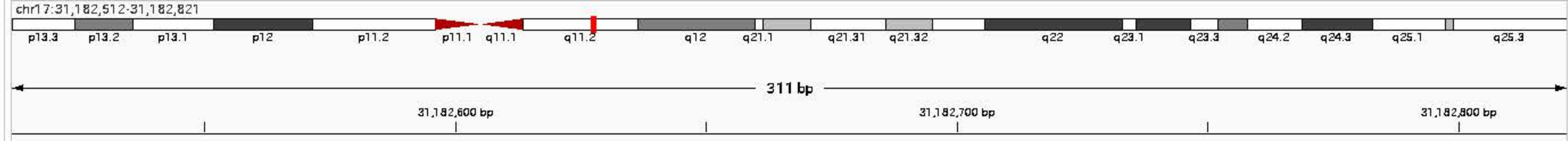
SL\_0001\_LN\_4\_WES\_uniq\_mut.ba r



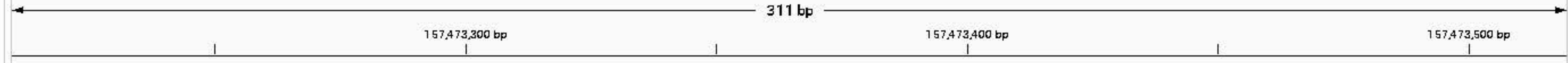
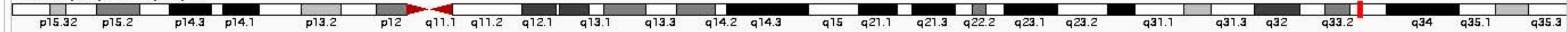
Sequence

Refseq Genes





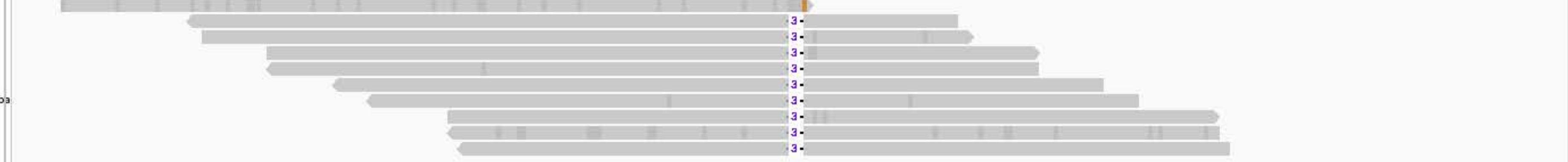
chr5:157,473,210-157,473,519



SL\_0017\_RN\_15\_WES\_uniq\_mut.ba  
coverage



SL\_0017\_RN\_15\_WES\_uniq\_mut.ba



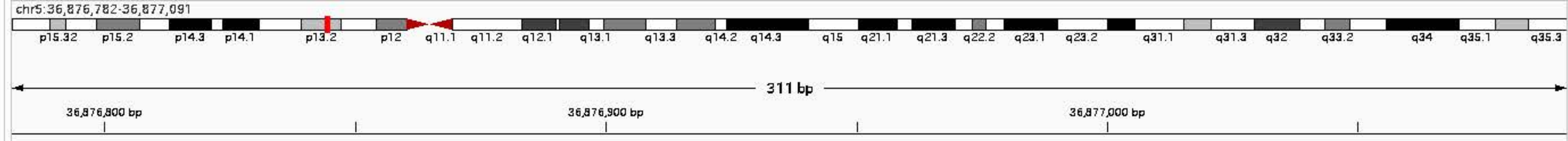
Sequence



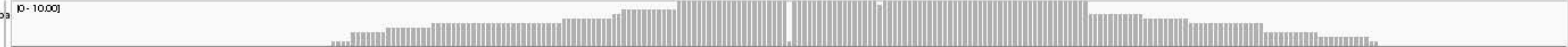
Refseq Genes

NIPAL4

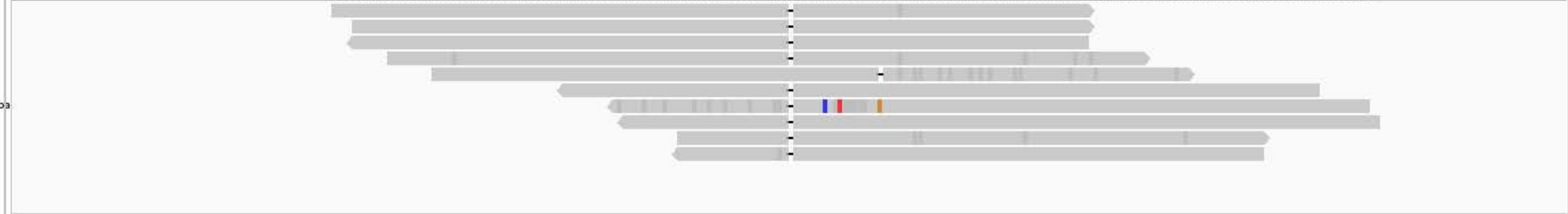




SL\_0001\_RN\_28\_WES\_uniq\_mut.ba  
coverage



SL\_0001\_RN\_28\_WES\_uniq\_mut.ba

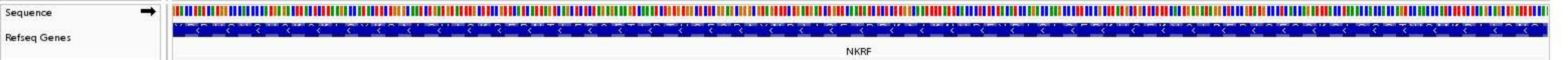
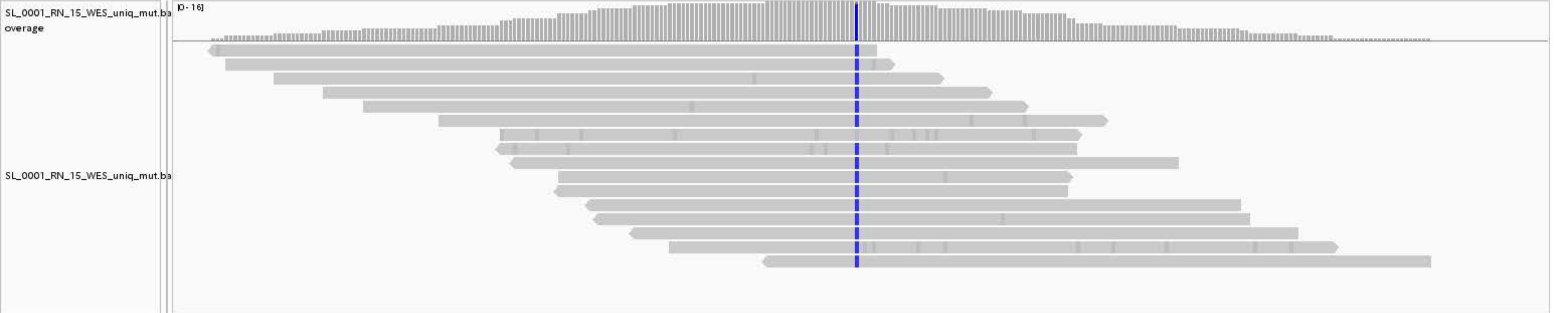
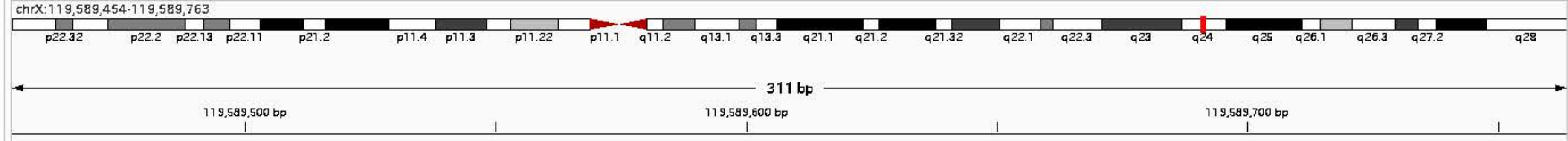


Sequence

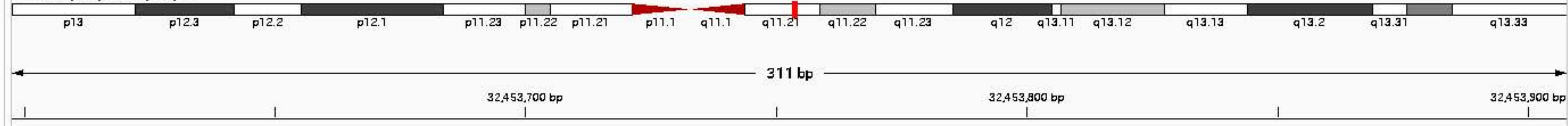


Refseq Genes





chr20:32,453,598-32,453,907



SL\_0001\_LN\_10\_WES\_uniq\_mut. coverage



Sequence



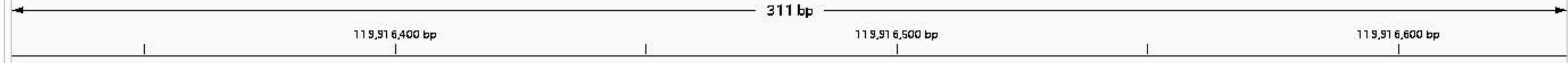
Refseq Genes

NOL4L

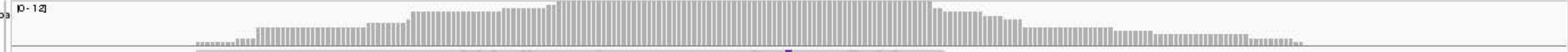


chr1:119,916,324-119,916,633

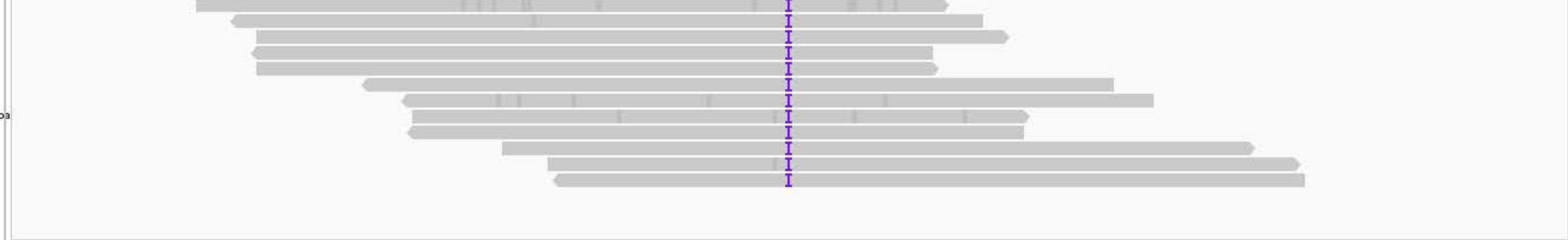
p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44



SL\_0004\_RN\_47\_WES\_uniq\_mut.ba  
coverage



SL\_0004\_RN\_47\_WES\_uniq\_mut.ba



Sequence

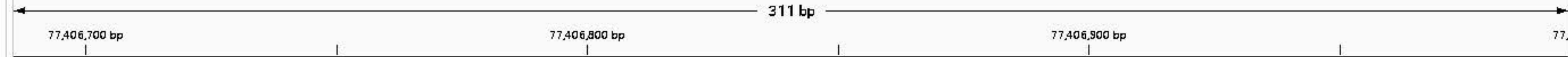


Refseq Genes

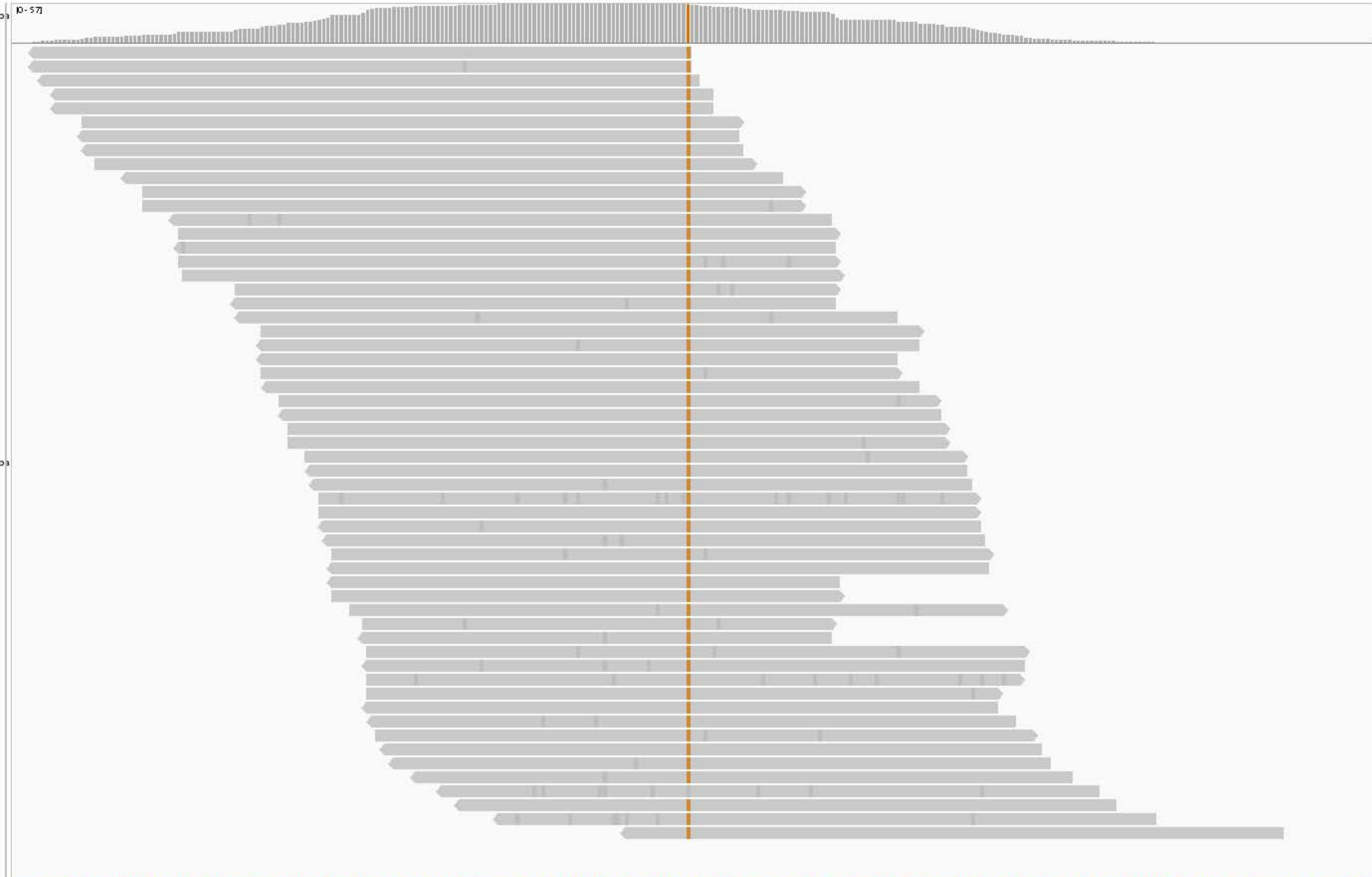
NOTCH2

chr14: 77,406,686-77,406,995

p13 p12 p11.2 p11.1 q11.2 q12 q13.1 q21.1 q21.2 q21.3 q22.1 q22.3 q23.1 q23.2 q24.1 q24.2 q24.3 q31.1 q31.3 q32.11 q32.13 q32.2 q32.31 q32.33



SL\_0015\_LN\_39\_WES\_uniq\_mut.  
coverage



SL\_0015\_LN\_39\_WES\_uniq\_mut.

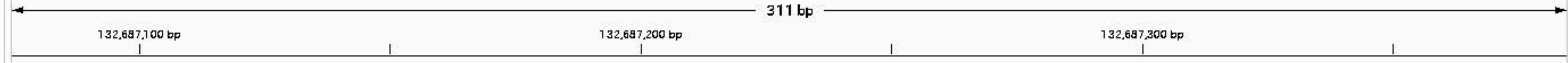
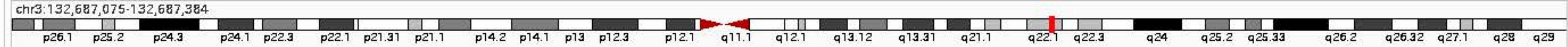
Sequence



Refseq Genes

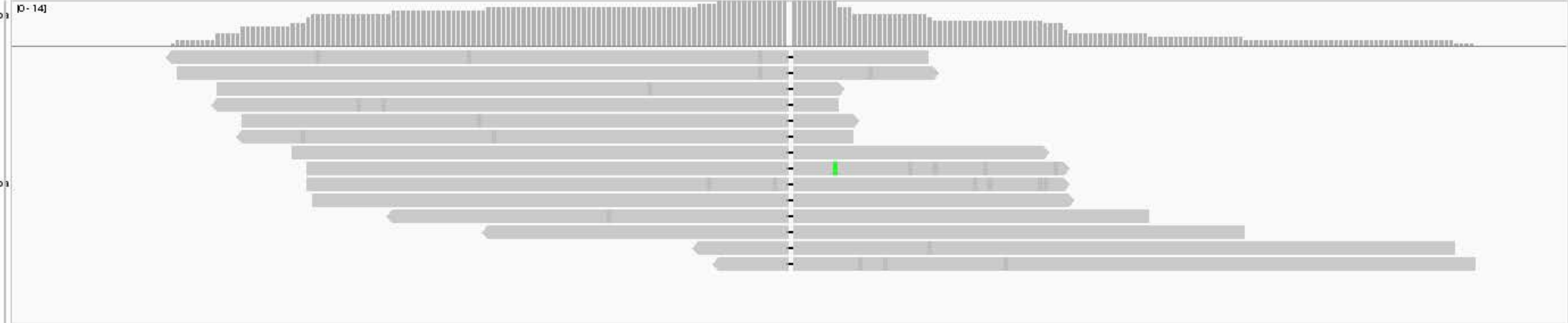
A P S Y P C T A Q L I T P D Q L A A I V G K N A G W V S V S D E D Y Q Y Q P R L I N T H N L L L K L F

NOXRED1



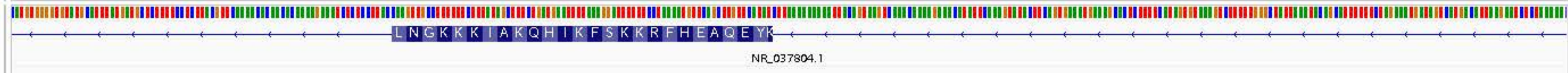
SL\_0003\_LN\_51\_WES\_uniq\_mut. ba  
coverage

SL\_0003\_LN\_51\_WES\_uniq\_mut. ba



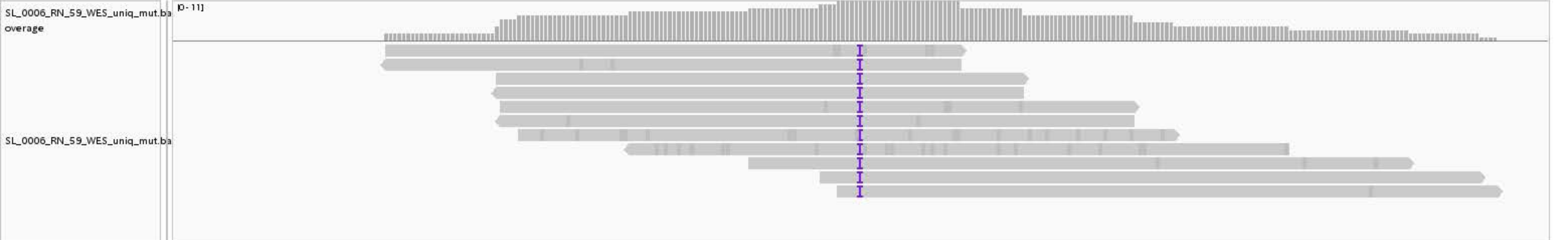
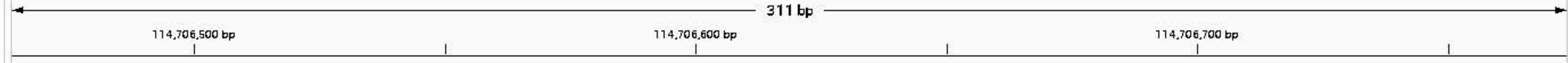
Sequence →

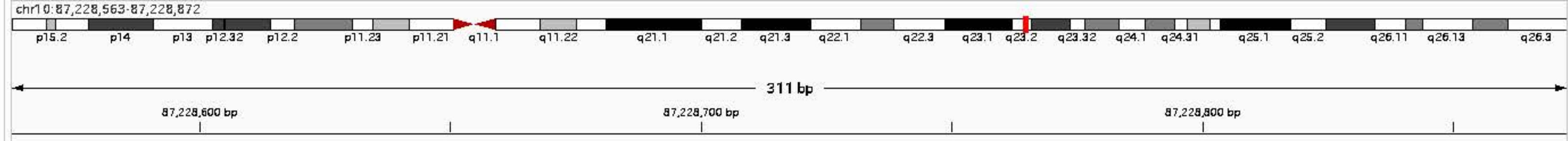
Refseq Genes



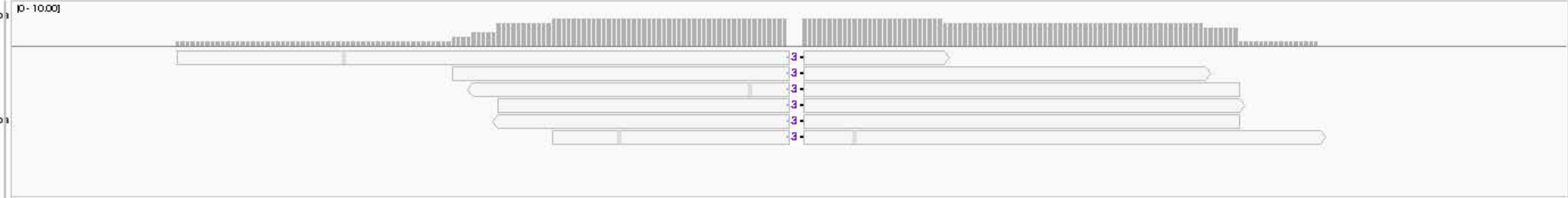


chr1:114,706,464-114,706,773  
p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44





SL\_0001\_LN\_10\_WES\_uniq\_mut.  
coverage



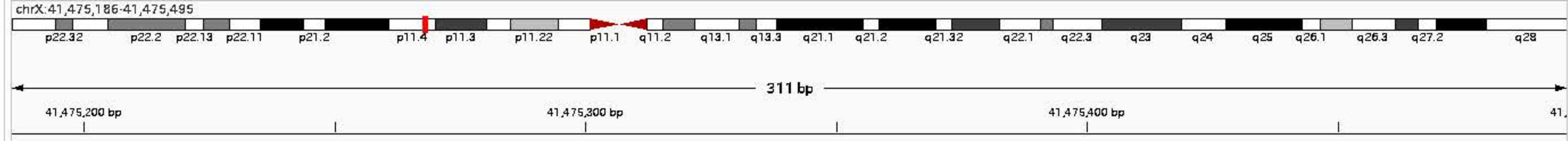
SL\_0001\_LN\_10\_WES\_uniq\_mut.

Sequence

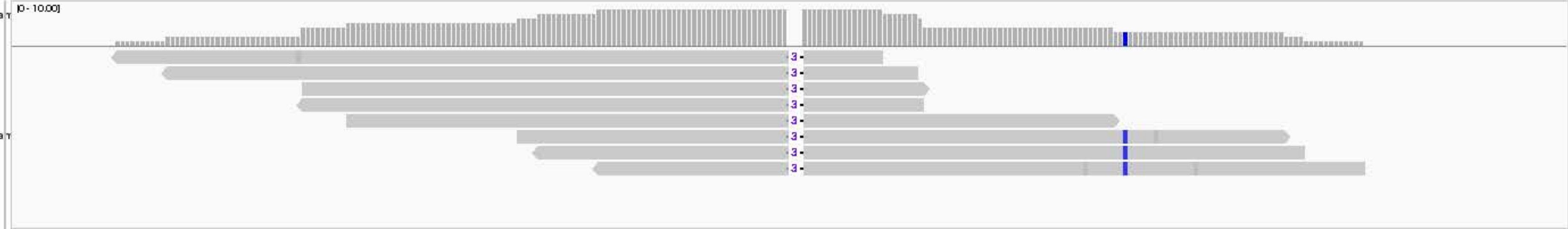


Refseq Genes

NUTM2A



SL\_0007\_RN\_2\_WES\_uniq\_mut.ba  
verage



SL\_0007\_RN\_2\_WES\_uniq\_mut.ba

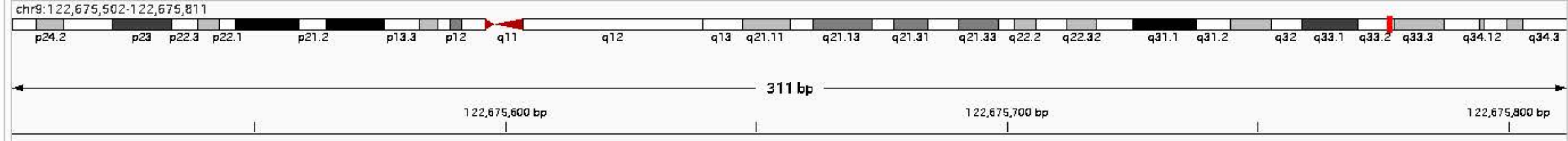
Sequence →



Refseq Genes







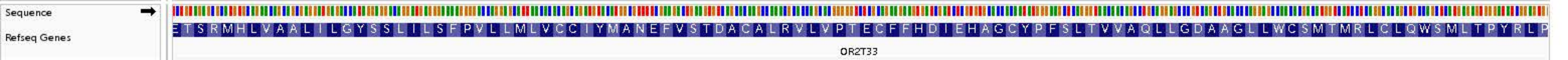
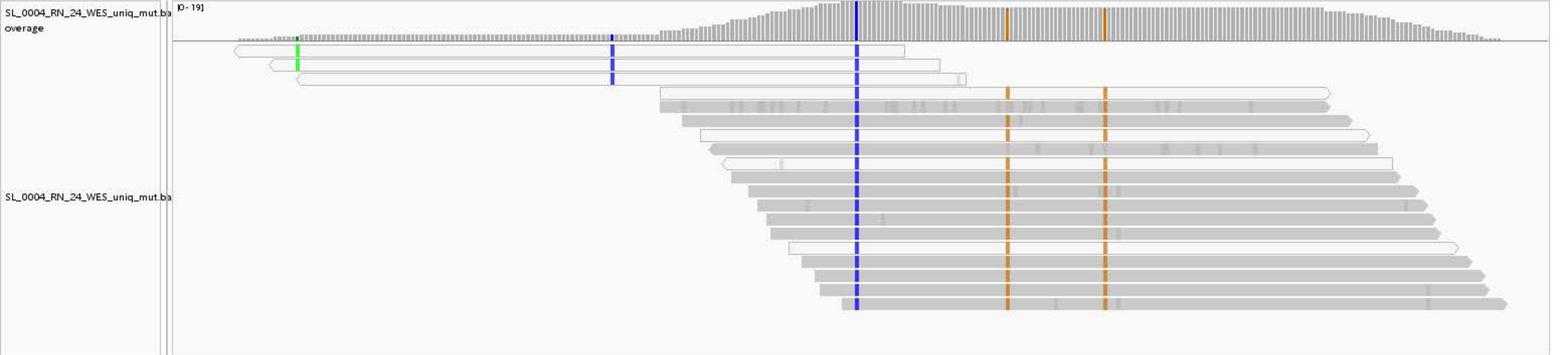
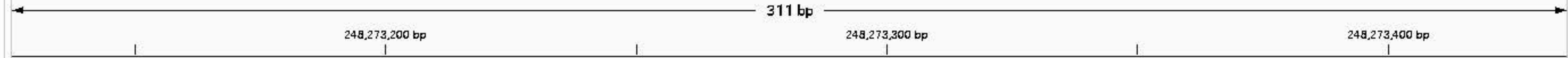
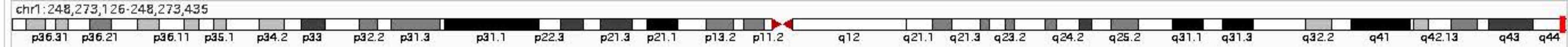
SL\_0003\_LN\_51\_WES\_uniq\_mut. coverage

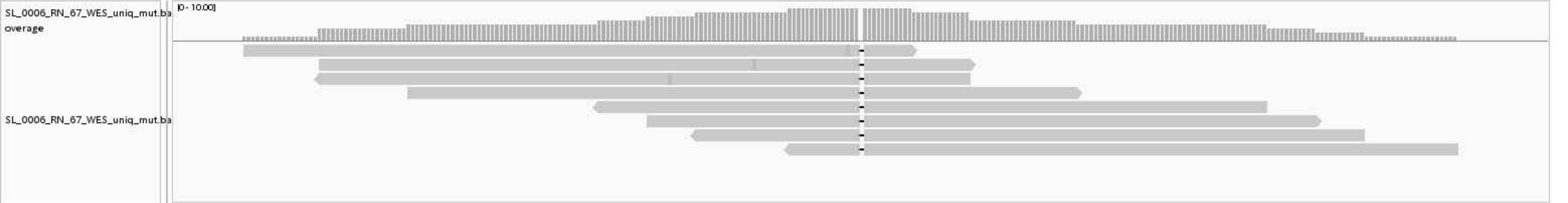
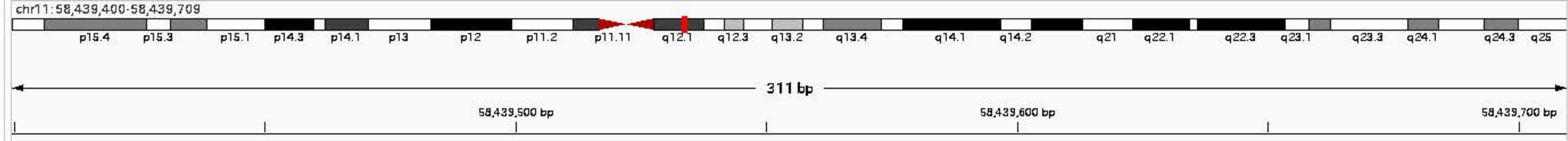


Sequence Refseq Genes

A I C N P F H Y V T V M N R R C C V L L L A F P I T F S Y F H S L L H V L L V N R L T F C T S N V I H H F F C D V N P V L K L S C S S T F V N E I V A M T E G L A S V M A P F V C I I I S Y L R I L I A V L K

OR1L3





Sequence →

Refseq Genes

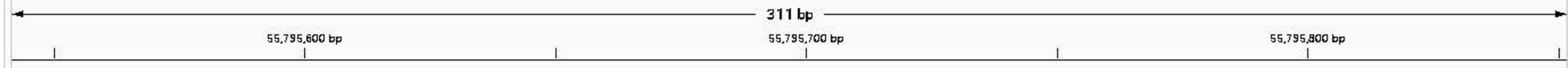
GYFISVATLHSACTSFQKQRGEP SRMKMITIFIFLYSILIVLISFLDNFGVVFFIVMESIYNDSCSLTLLPPADCFFHEVVNSRCFSLRFTNGTHISANLFGCI

OR5B12

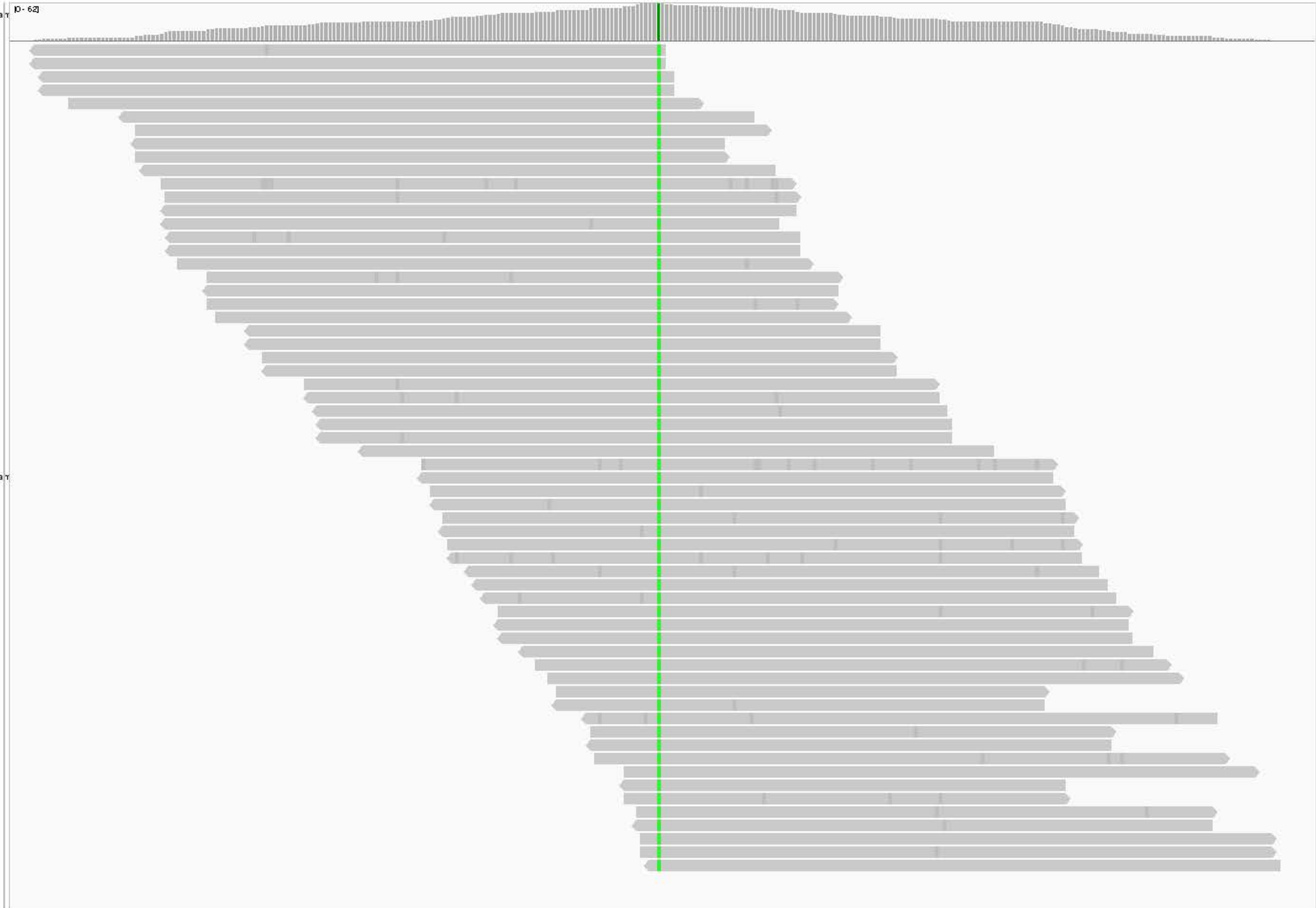


chr11:55,795,542-55,795,851

p15.4 p15.3 p15.1 p14.3 p14.1 p13 p12 p11.2 p11.1 q12.1 q12.3 q13.2 q13.4 q14.1 q14.2 q21 q22.1 q22.3 q23.1 q23.3 q24.1 q24.3 q25



SL\_0007\_RN\_2\_WES\_uniq\_mut.ba  
verage



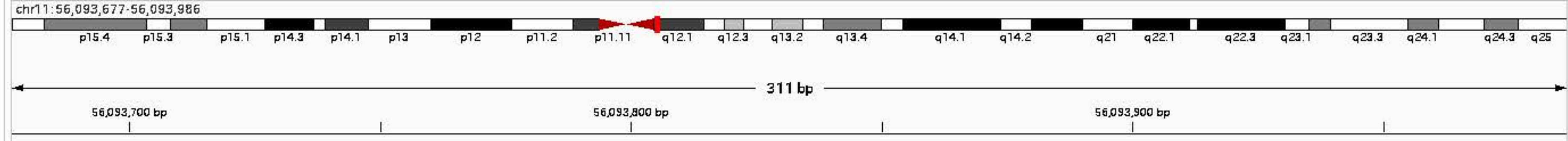
SL\_0007\_RN\_2\_WES\_uniq\_mut.ba

Sequence →

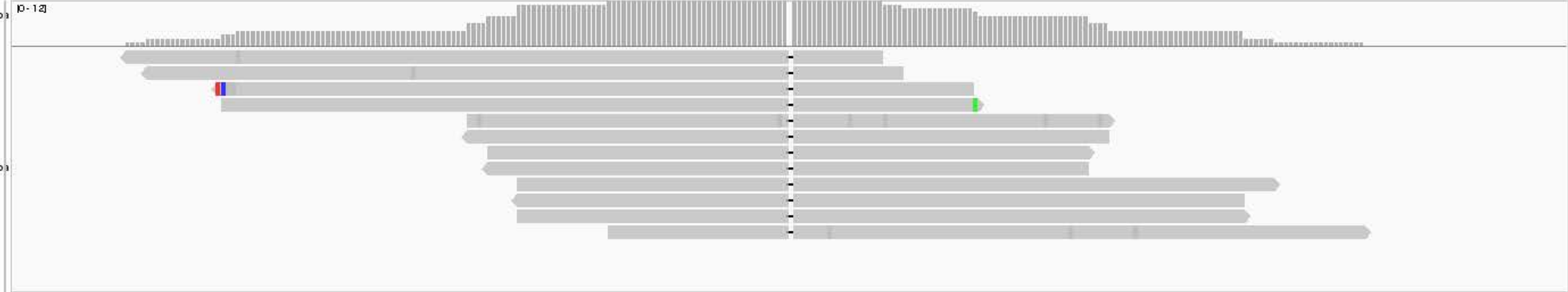
Refseq Genes

MMVLRNLSMEPTFALLGFTDYPKLIPLFLVFLLMYVITVVGNLGMIITIKINPKFHTPMYFFLSHLSFVDFCYSSIVTPKLLLENLVMADKSIIFYFS

OR5D14



SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage



SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage

Sequence

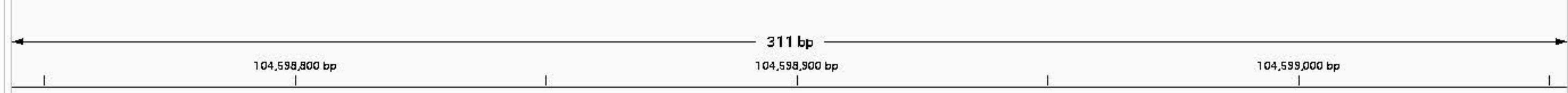
Refseq Genes

I A I C N P L L Y S V V M S Q K V S N W L G V M P Y V I G F T S S L I S V W V I S S L A F C D S S I N H F F C D T T A L L A L S C V D T F G T E M V S F V L A G F T L L S S L L I I T V T Y I I I S A I L R

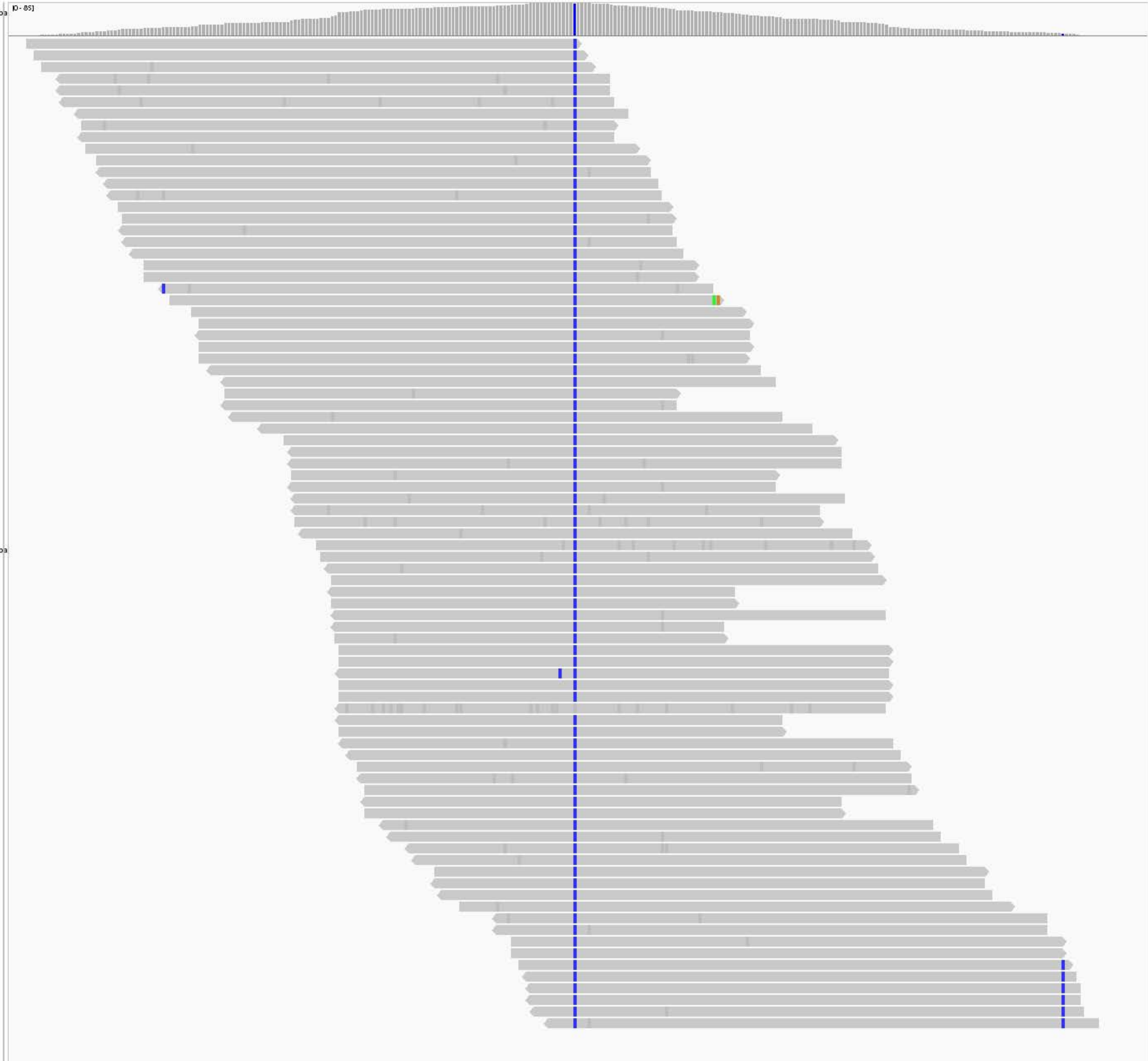
OR812

chr9:104,598,744-104,599,053

p24.2 p23 p22.3 p22.1 p21.2 p13.3 p12 q11 q12 q13 q21.11 q21.13 q21.31 q21.33 q22.2 q22.32 q31.1 q31.2 q32 q33.1 q33.2 q33.3 q34.12 q34.3



SL\_0004\_RN\_26\_WES\_uniq\_mut.ba  
coverage



SL\_0004\_RN\_26\_WES\_uniq\_mut.ba

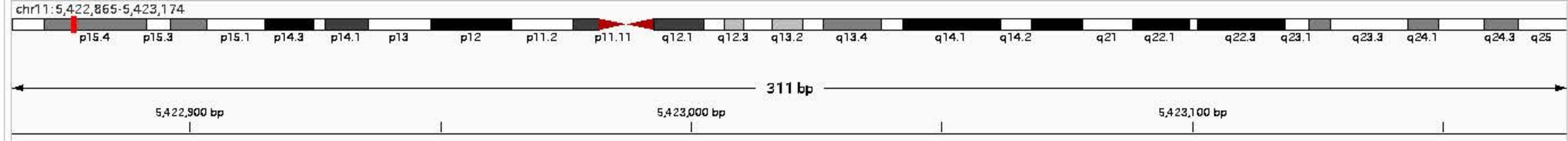
Sequence →

Refseq Genes

L I I L T Y S V I I L L L P T L L F L T T T V L L I F E N G S I D A C A L K M V A L I E C T F H N I I N N R C F P L Q V V F V T Q V A S N V A G I I W S G A A M P V Y A D K S M I I P Y R L P N C I A V Y R D

OR13C5



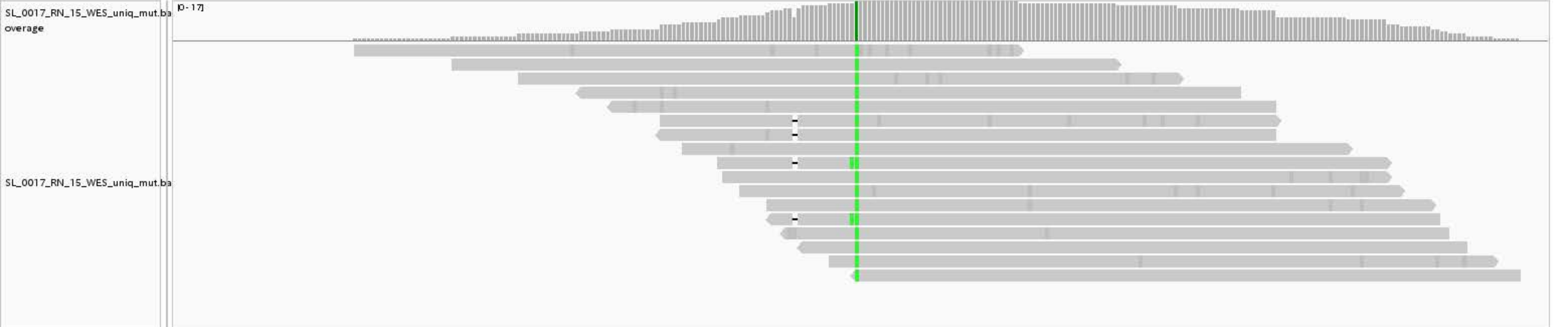
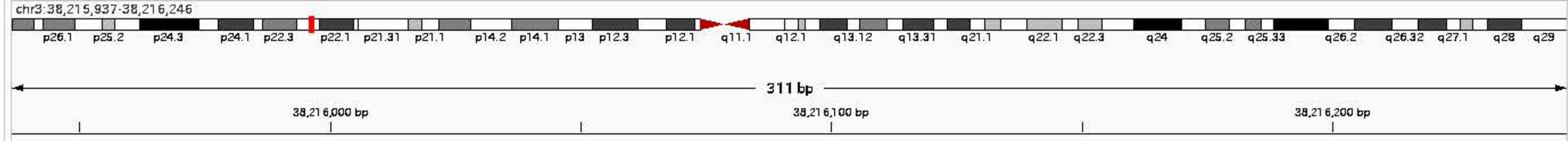


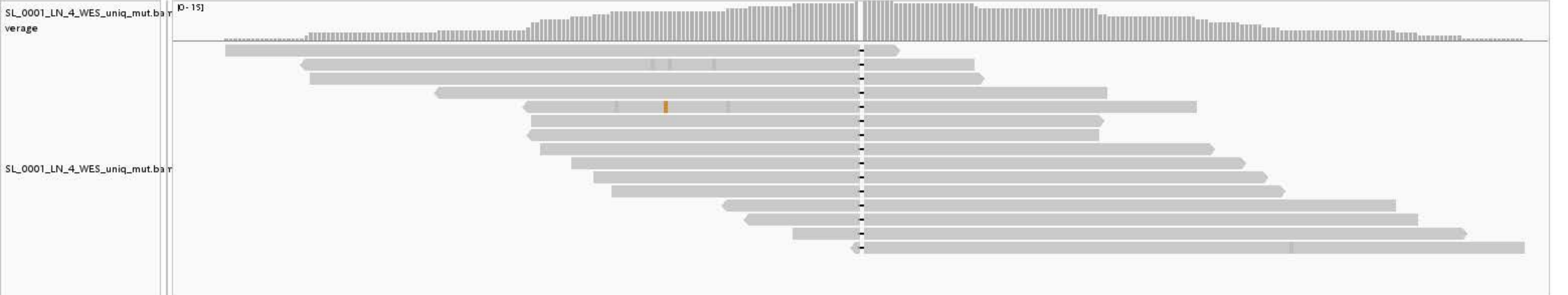
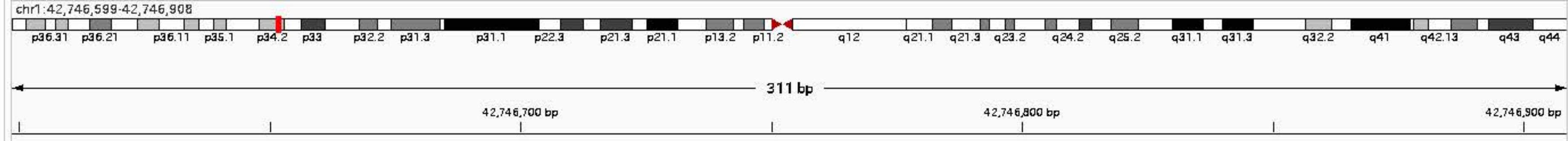
Sequence →

Refseq Genes

L I L K N I L G T A T W A E R L R A L N N C L S H I L A V L V L Y I P M V G V S M T H R F A K H A S P L V H V I M A N I Y L L A P P V M N P I I Y S V K N K Q I Q W G M L N F L S L K N M H S R

OR51B5

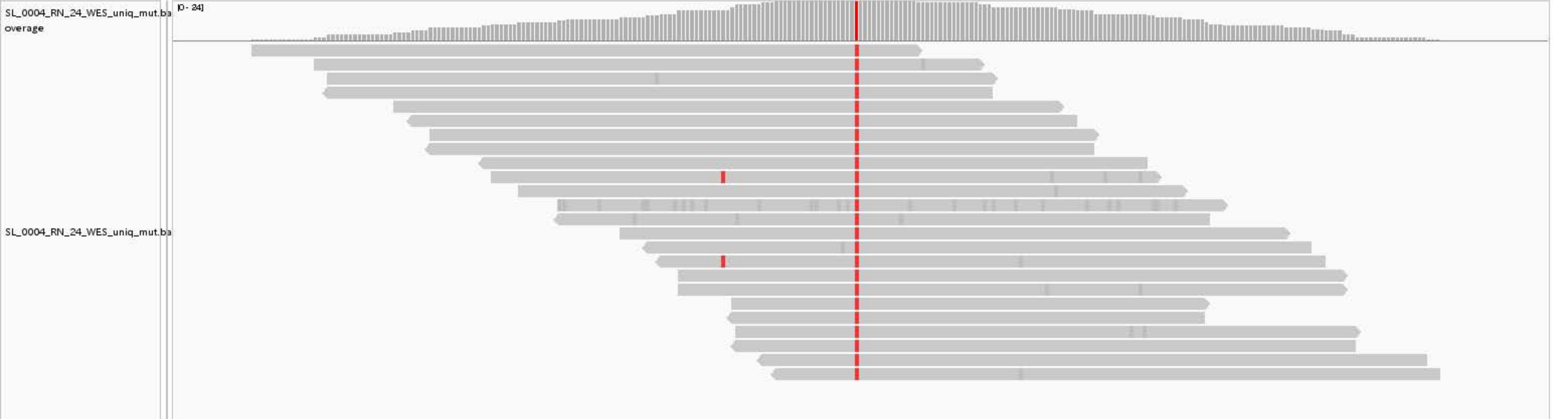
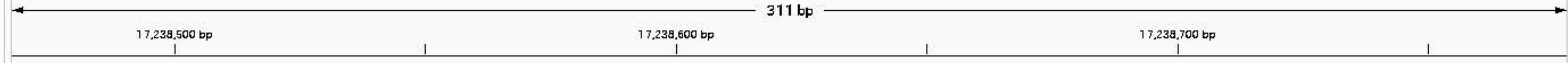






chr1:17,238,468-17,238,777

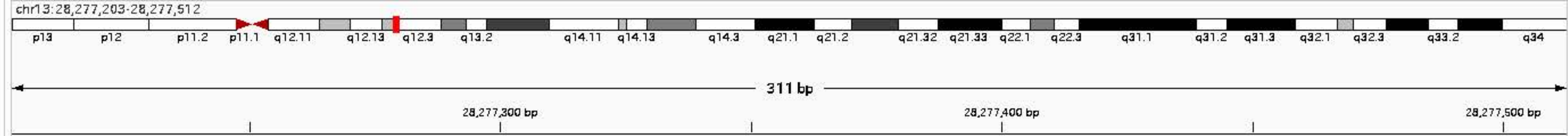
p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44



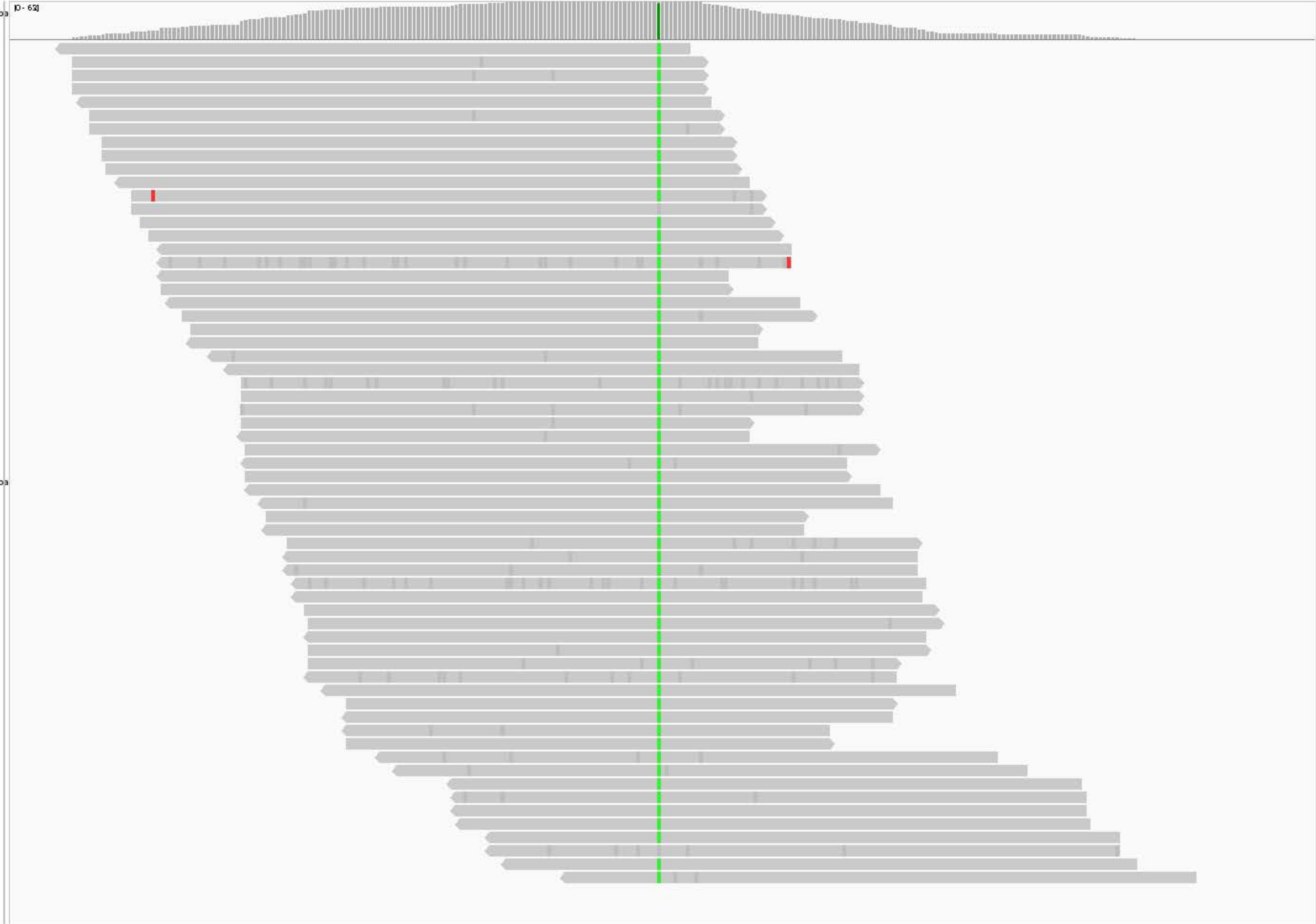
Sequence Refseq Genes

GFRLLASPSACLKLFQEKKEEGYGEEAAQFDC

PADI1

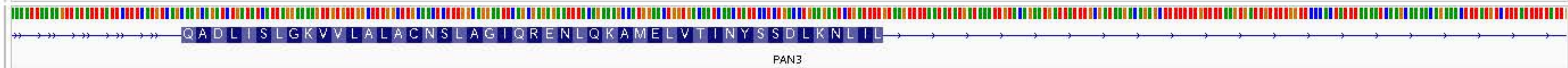


SL\_0004\_RN\_26\_WES\_uniq\_mut.ba  
 overage



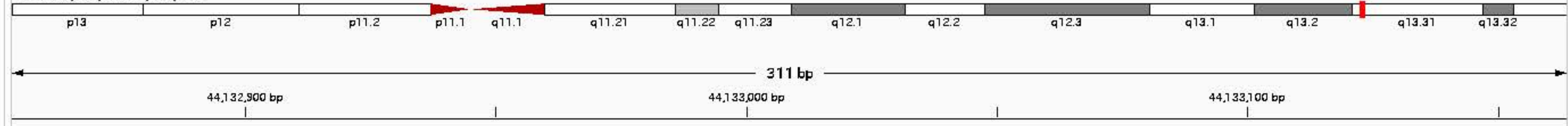
SL\_0004\_RN\_26\_WES\_uniq\_mut.ba

Sequence →  
 Refseq Genes

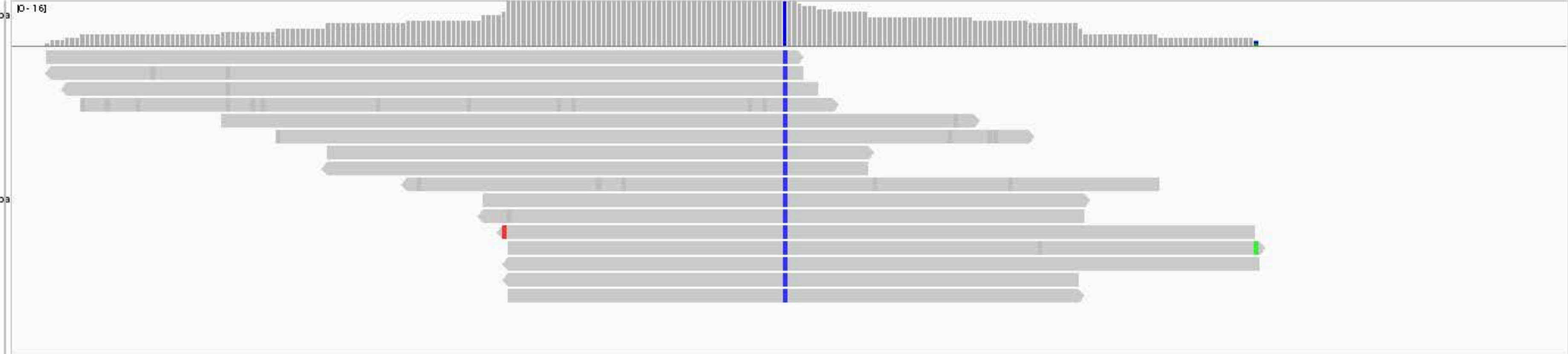


PAN3

chr22:44,132,854-44,133,163



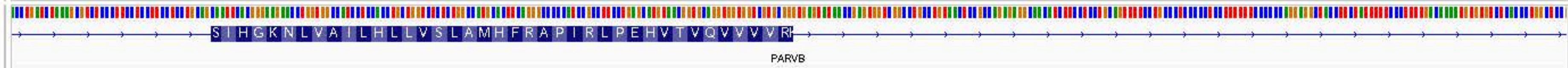
SL\_0006\_RN\_59\_WES\_uniq\_mut.ba  
coverage



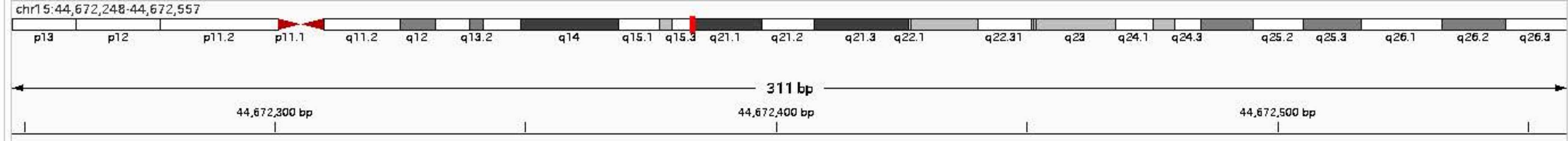
SL\_0006\_RN\_59\_WES\_uniq\_mut.ba

Sequence

Refseq Genes

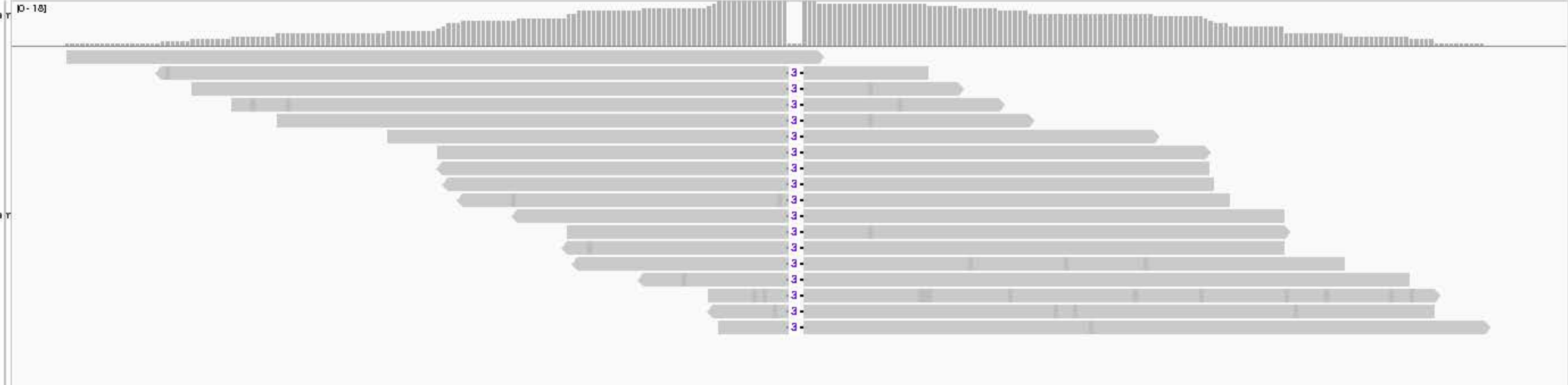






SL\_0002\_LN\_1\_WES\_uniq\_mut.ba  
verage

SL\_0002\_LN\_1\_WES\_uniq\_mut.ba r

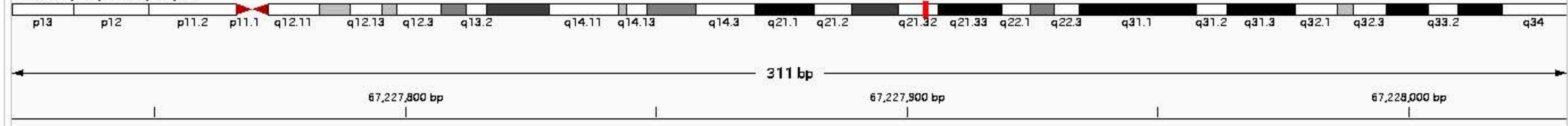


Sequence →

Refseq Genes



chr13:67,227,722-67,228,031



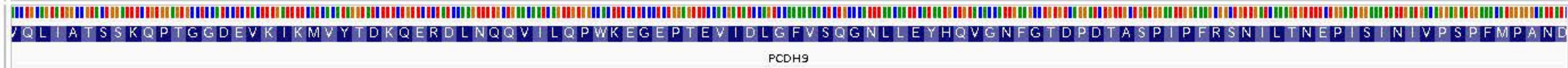
SL\_0007\_RN\_2\_WES\_uniq\_mut.ba  
verage

SL\_0007\_RN\_2\_WES\_uniq\_mut.ba r

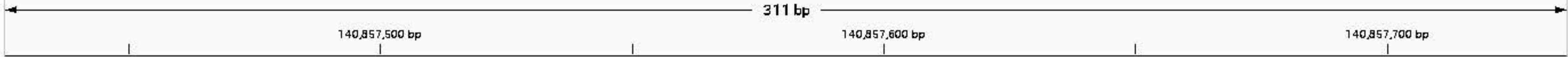


Sequence →

Refseq Genes



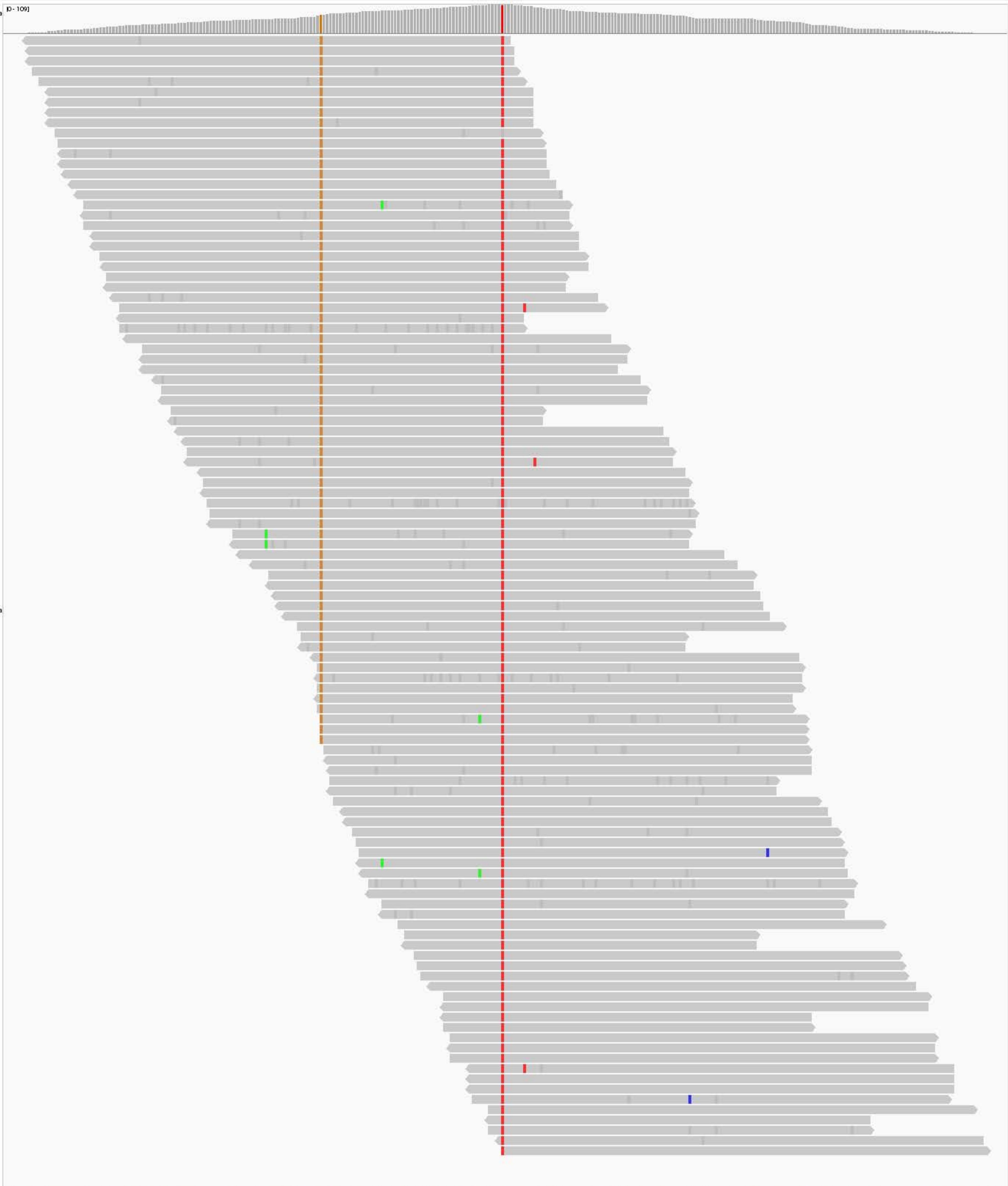




SL\_0007\_RN\_33\_WES\_uniq\_mut.ba  
overage

D-109]

SL\_0007\_RN\_33\_WES\_uniq\_mut.ba



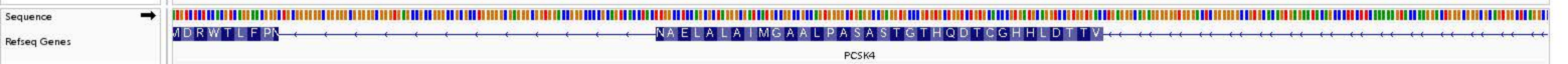
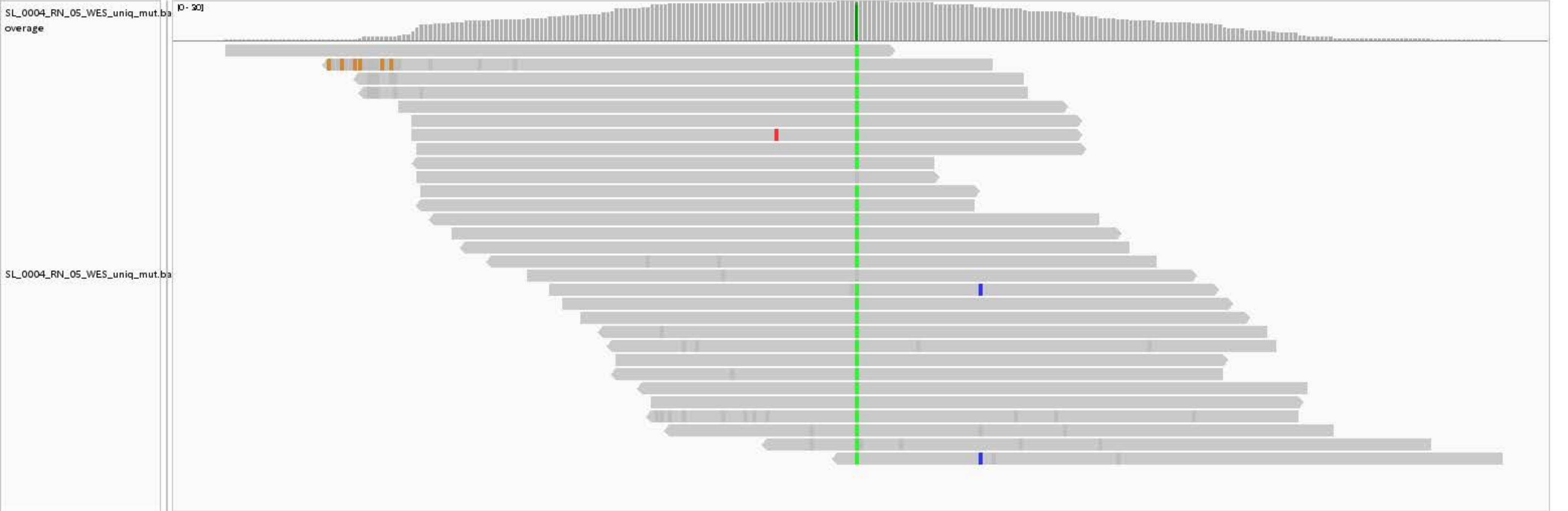
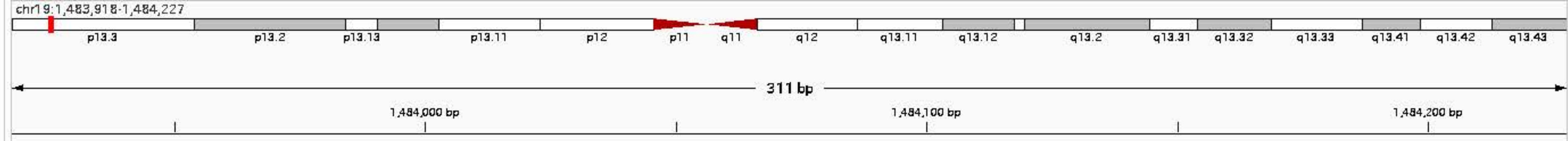
Sequence →

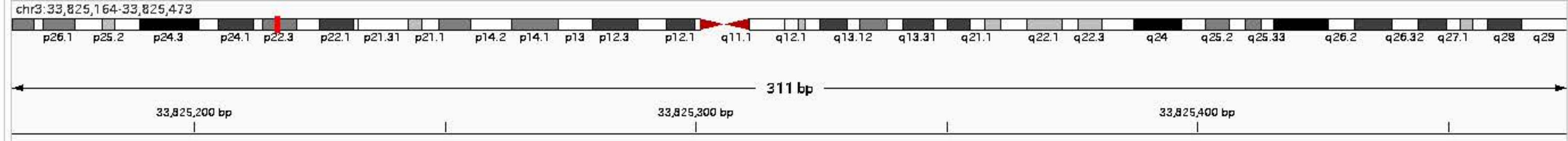
Refseq Genes

TVFVKEKNPPGCHIFTVSAWDADAQENALVSYSLVERRRLGERSLSSYVSVHAESGKVYALQPLDHEELELLQFQVSARDGGVPPLGSNLTLQVFVLDENDNAP

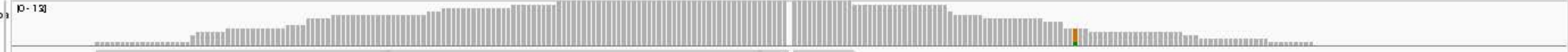
PCDH1



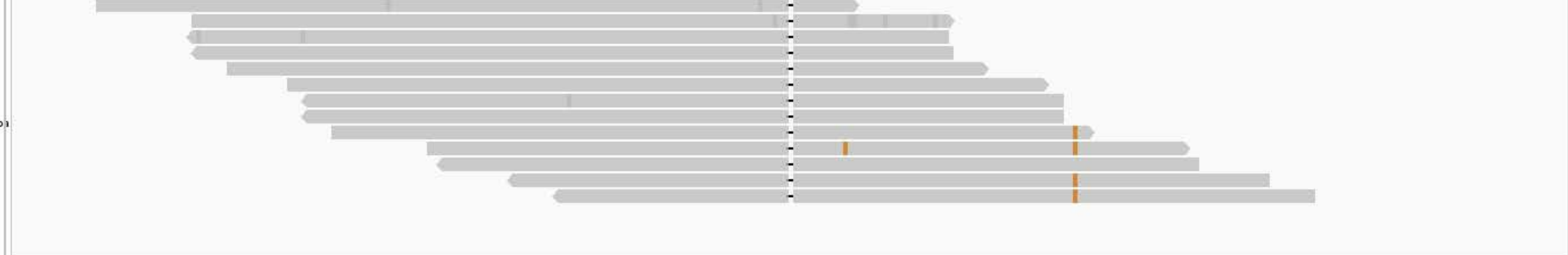




SL\_0015\_LN\_44\_WES\_uniq\_mut. coverage



SL\_0015\_LN\_44\_WES\_uniq\_mut. ba



Sequence

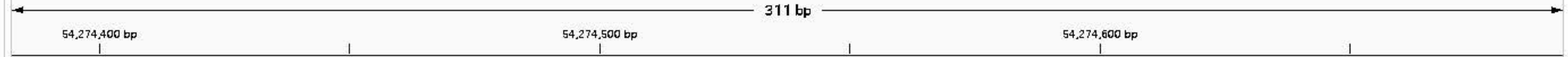


Refseq Genes

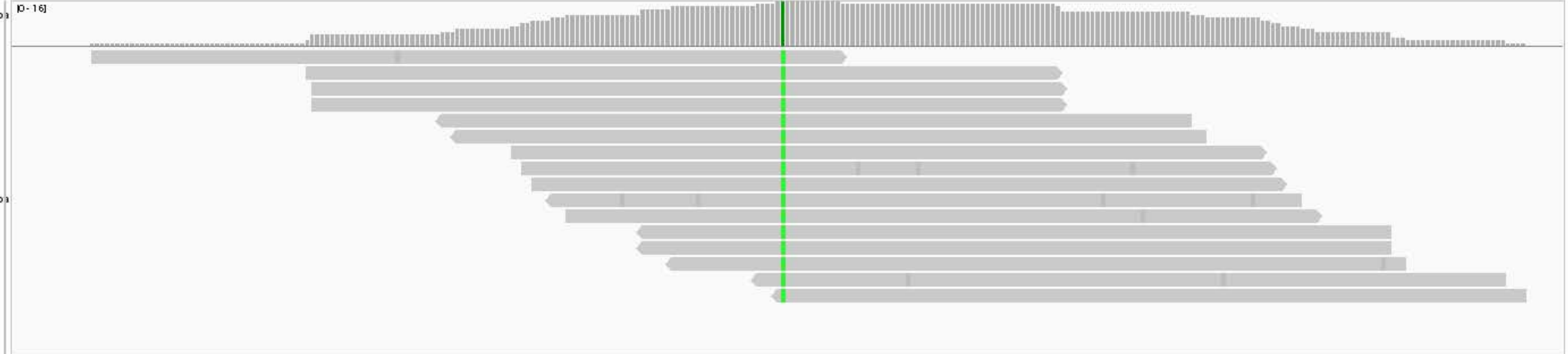


chr4: 54,274,383-54,274,692

p16.2 p15.33 p15.31 p15.1 p14 p13 p11 q12 q13.1 q13.2 q21.1 q21.22 q22.1 q22.3 q24 q25 q26 q27 q28.2 q28.3 q31.1 q31.22 q32.1 q32.3 q34.1 q34.3 q35.2



SL\_0001\_LN\_10\_WES\_uniq\_mut. coverage



SL\_0001\_LN\_10\_WES\_uniq\_mut.

Sequence

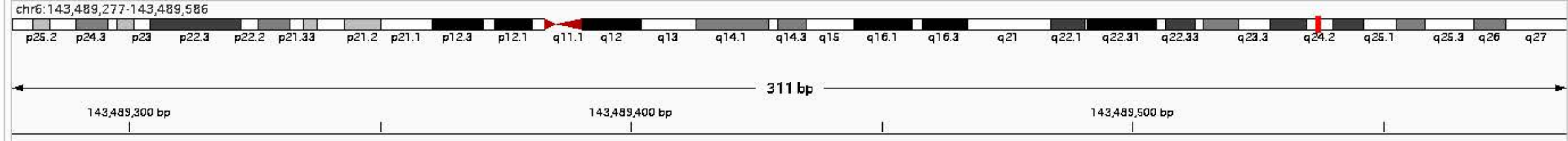


Refseq Genes

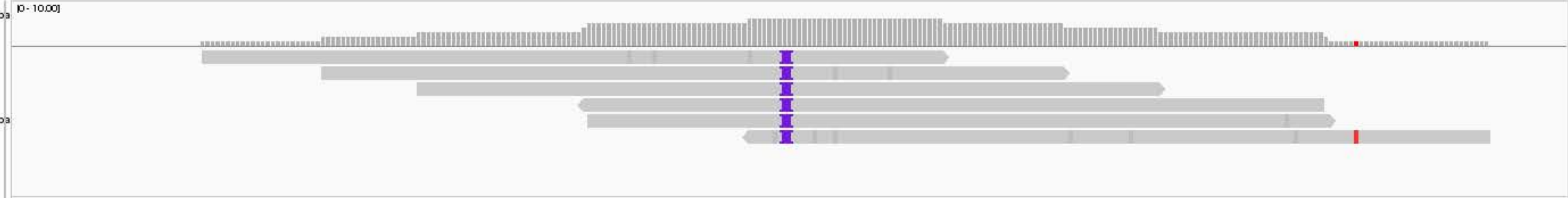
TLRSELTVA AAVLVLLVIVITSLIVLVVIWKQ

PDGFRA





SL\_0006\_RN\_36\_WES\_uniq\_mut.ba  
overage

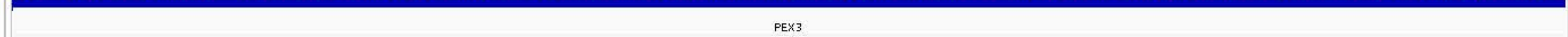


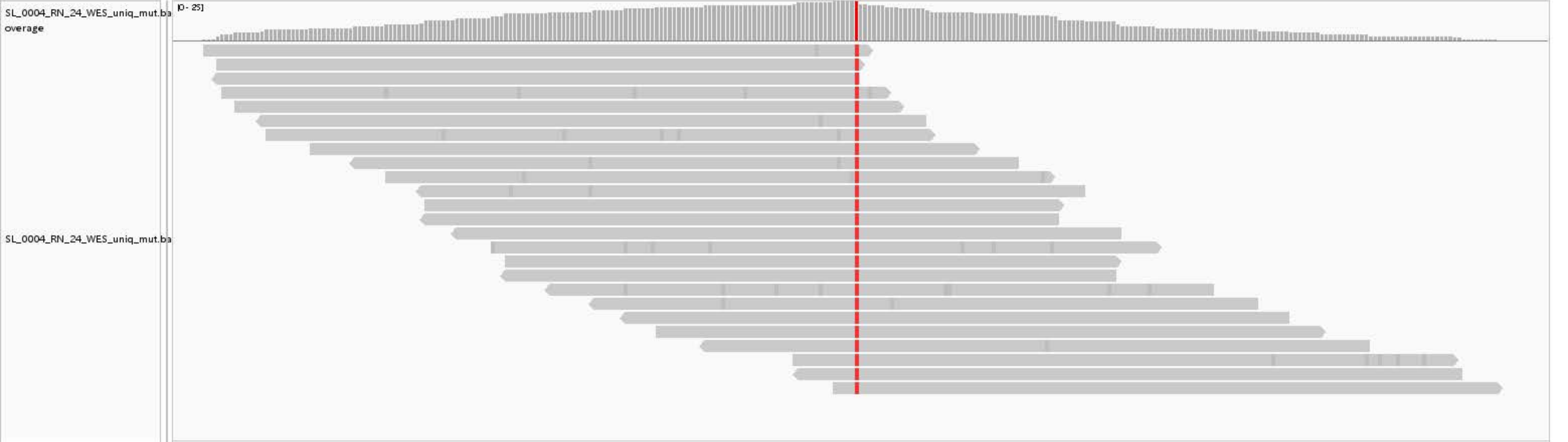
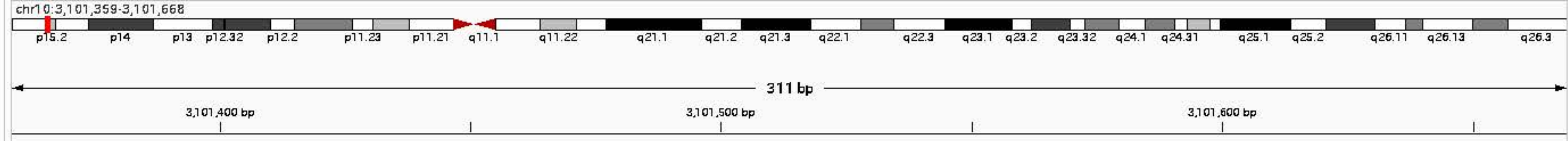
SL\_0006\_RN\_36\_WES\_uniq\_mut.ba

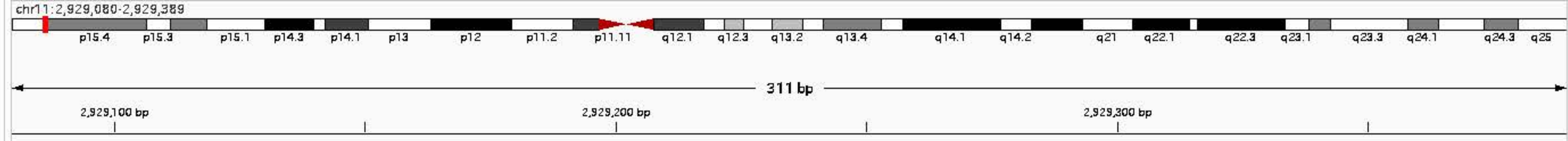
Sequence →



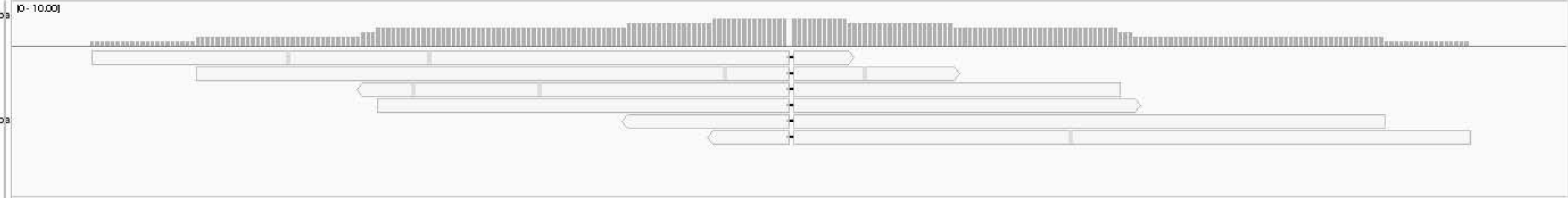
Refseq Genes







SL\_0006\_RN\_36\_WES\_uniq\_mut.ba  
coverage



SL\_0006\_RN\_36\_WES\_uniq\_mut.ba

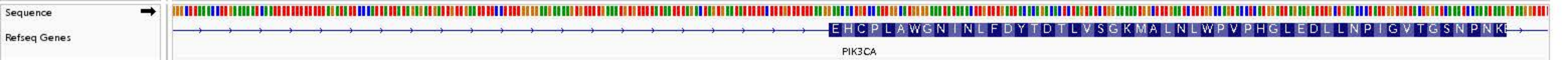
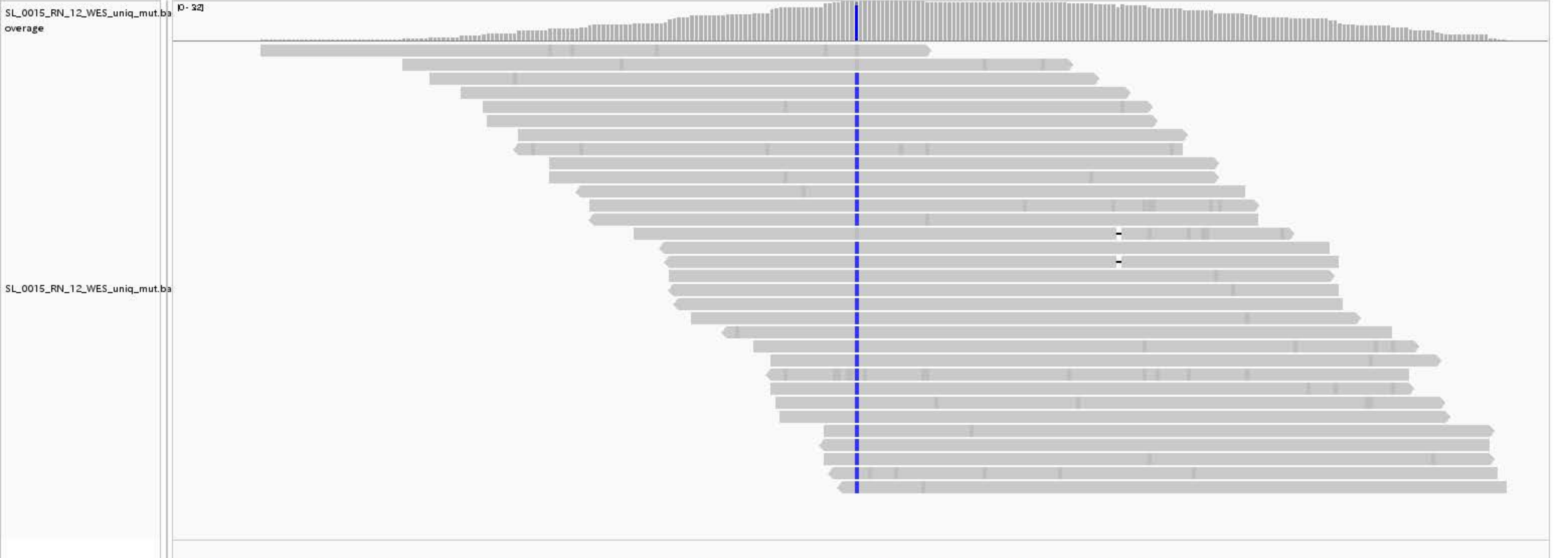
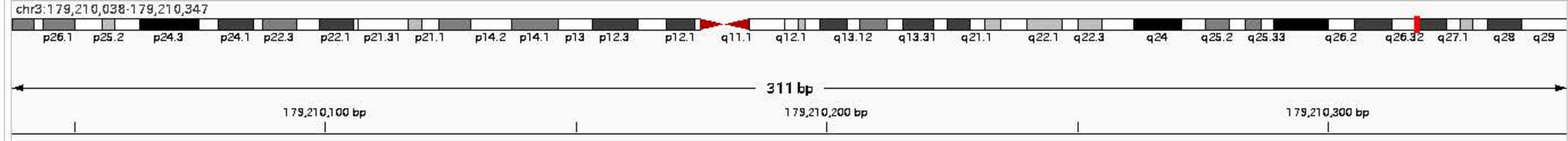
Sequence →

A I A A N W C S E G A C R F D I E K H D T T V I T F Y V Y K G T R E V C D V K L I S H F R L E K P R A R P S A P F L S L R D S T L V G R K K K W L Q F L S D S R K E L E G E R L V E D P S K M

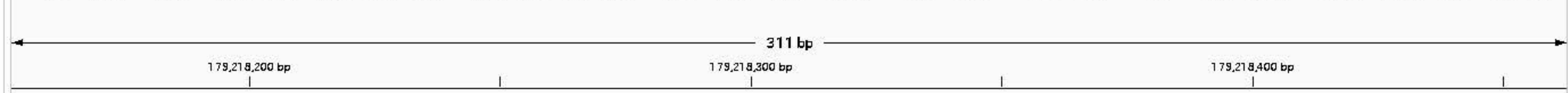
Refseq Genes

PHLDA2

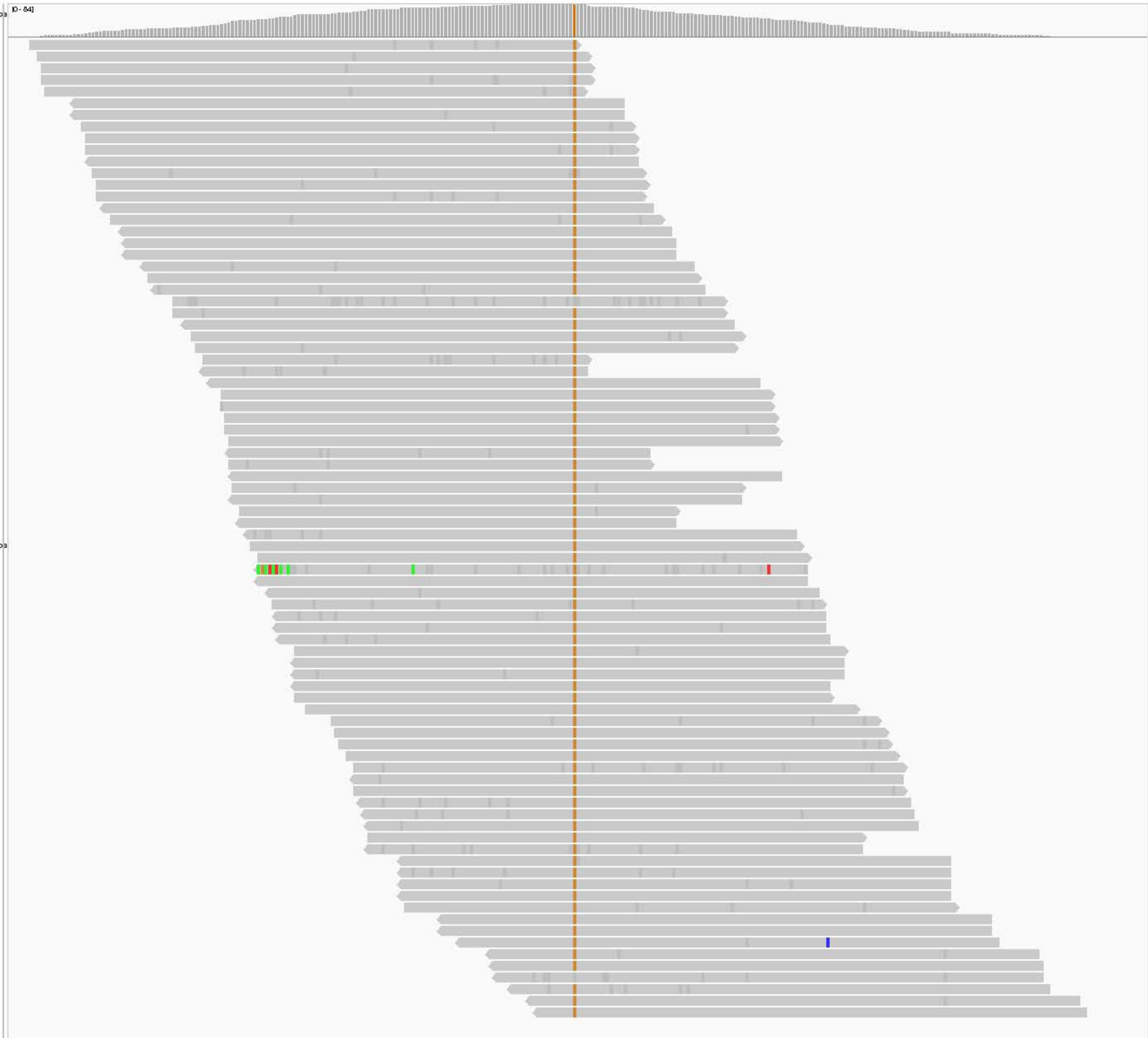




chr3:179,218,153-179,218,462



SL\_0004\_RN\_66\_WES\_uniq\_mut.ba  
verage



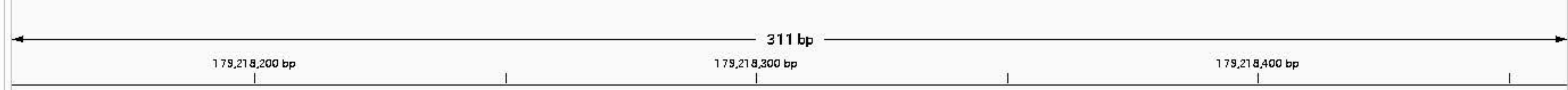
SL\_0004\_RN\_66\_WES\_uniq\_mut.ba

Sequence →  
Refseq Genes

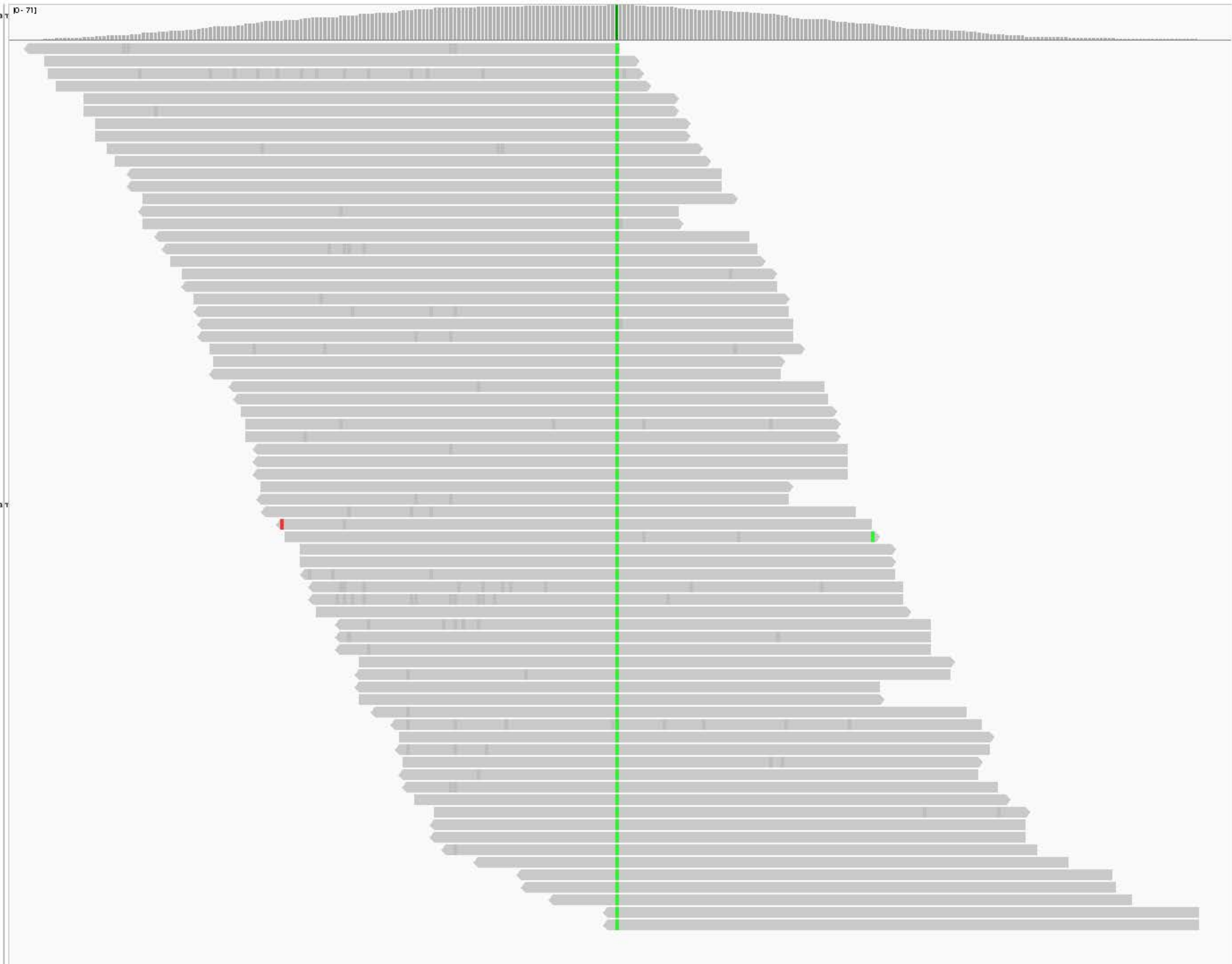


PIK3CA

chr3:179,218,152-179,218,461



SL\_0007\_RN\_2\_WES\_uniq\_mut.ba  
verage



SL\_0007\_RN\_2\_WES\_uniq\_mut.ba

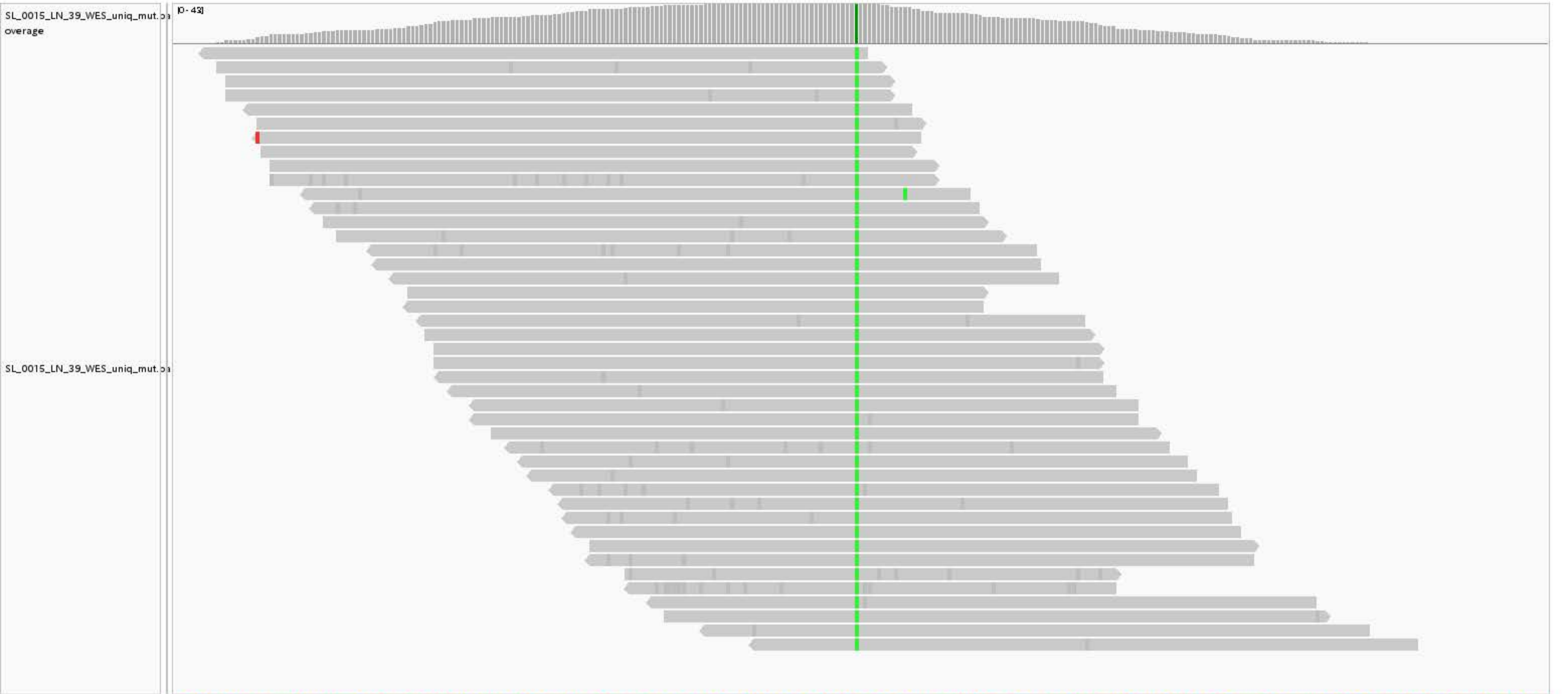
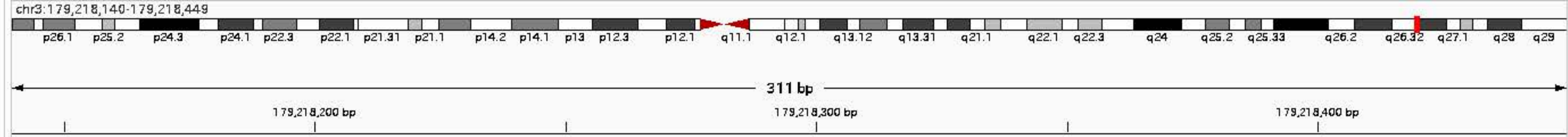
Sequence

Refseq Genes



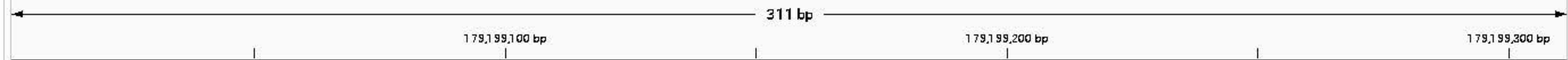
PIK3CA



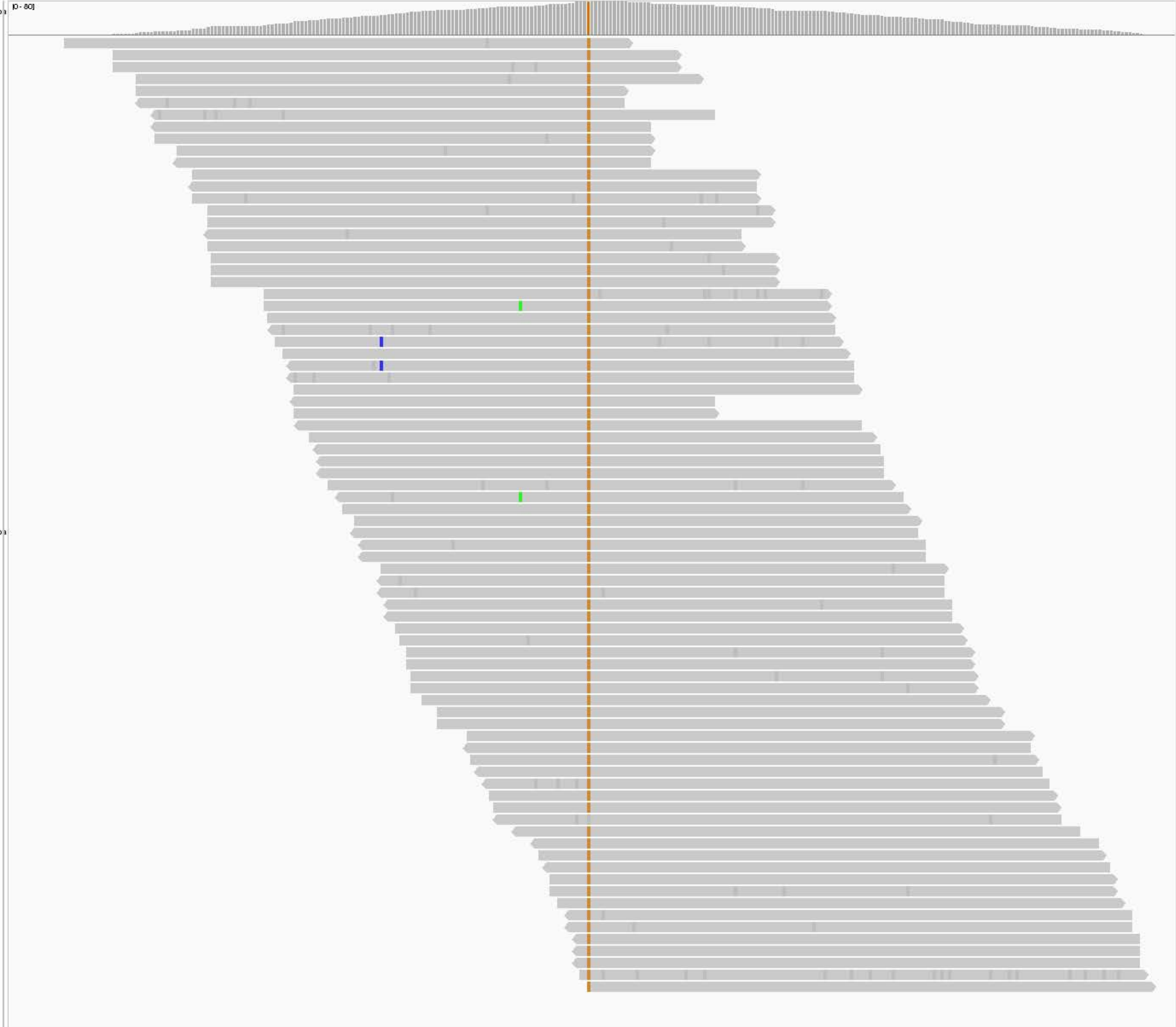


chr3:179,199,002-179,199,311

p26.1 p25.2 p24.3 p24.1 p22.3 p22.1 p21.31 p21.1 p14.2 p14.1 p13 p12.3 p12.1 q11.1 q12.1 q13.12 q13.31 q21.1 q22.1 q22.3 q24 q25.2 q25.33 q26.2 q26.32 q27.1 q28 q29



SL\_0015\_LN\_44\_WES\_uniq\_mut. coverage



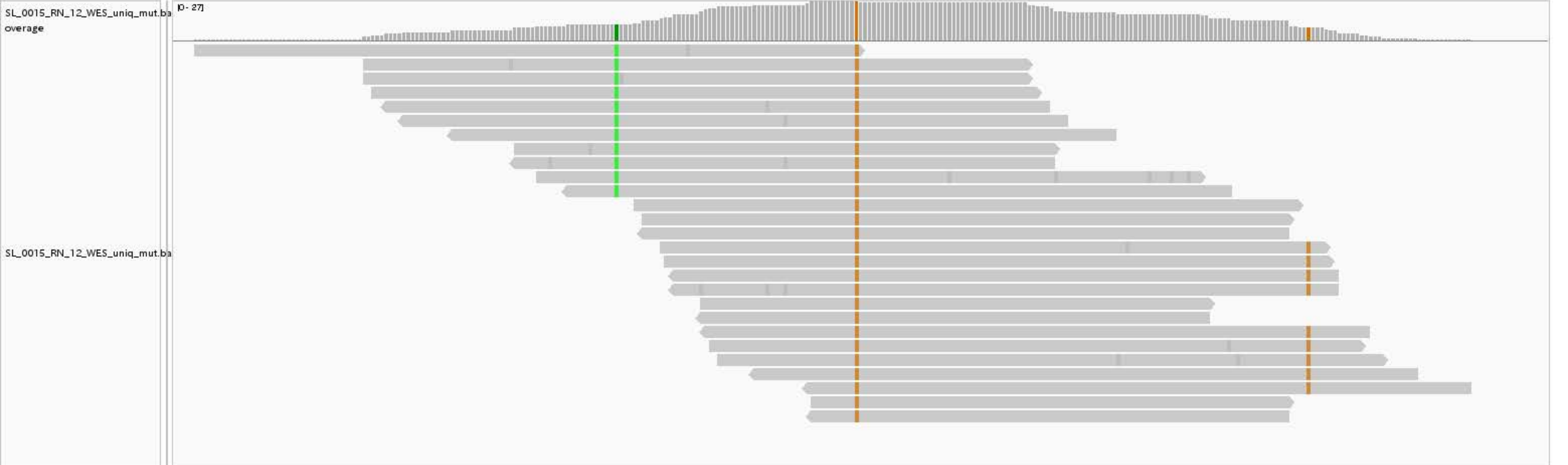
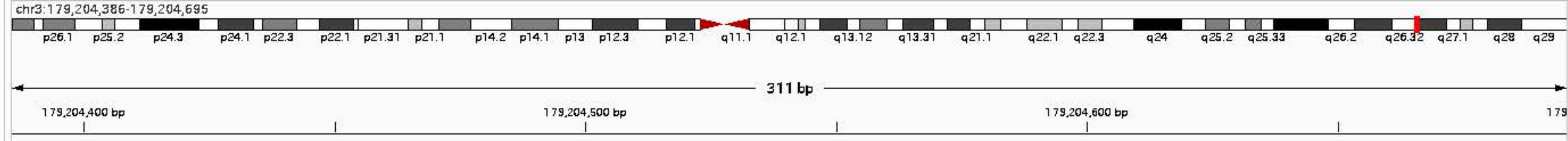
SL\_0015\_LN\_44\_WES\_uniq\_mut.

Sequence

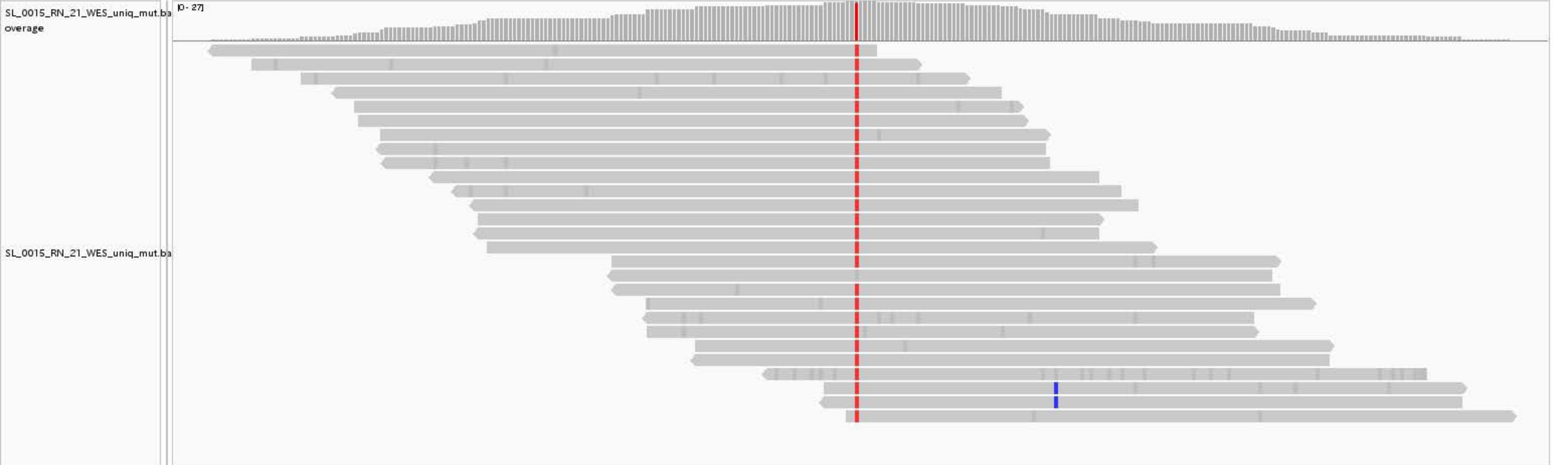
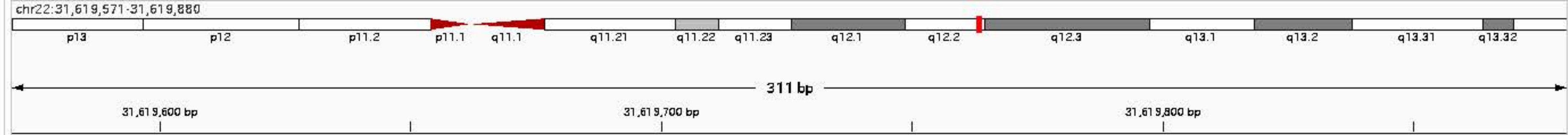
Refseq Genes

QLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPFLLKVIPEVGNREEKLNREIC

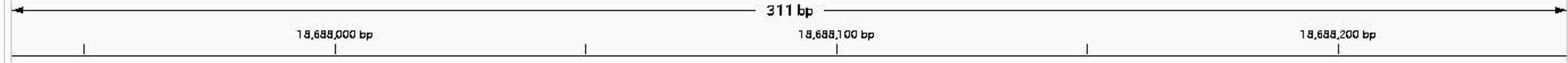
PIK3CA



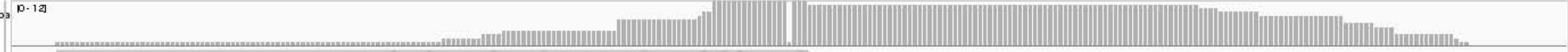




chr12:18,687,936-18,688,245  
p13.32 p13.2 p12.3 p12.1 p11.22 p11.1 q12 q13.11 q13.13 q13.3 q14.2 q15 q21.1 q21.2 q21.31 q21.32 q22 q23.1 q23.2 q24.11 q24.21 q24.31 q24.33



SL\_0017\_RN\_15\_WES\_uniq\_mut.ba  
overage



SL\_0017\_RN\_15\_WES\_uniq\_mut.ba

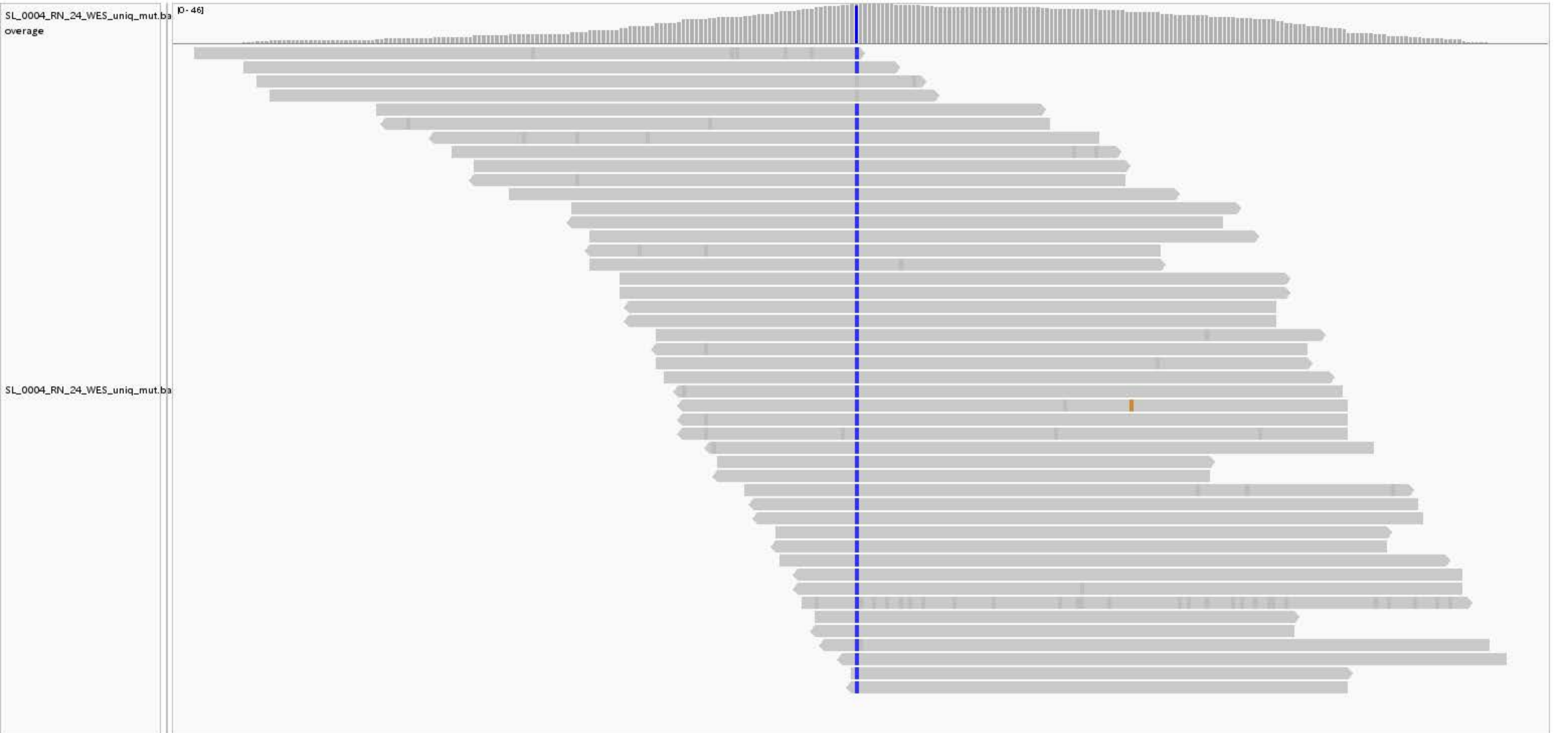
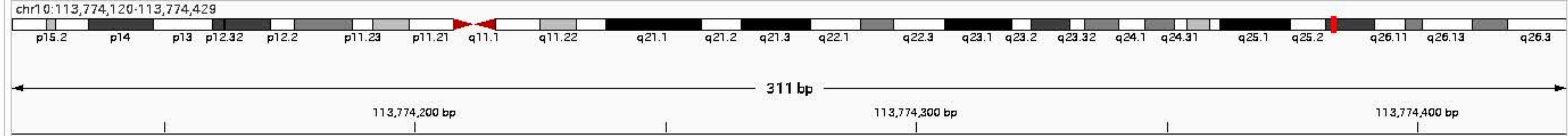


Sequence

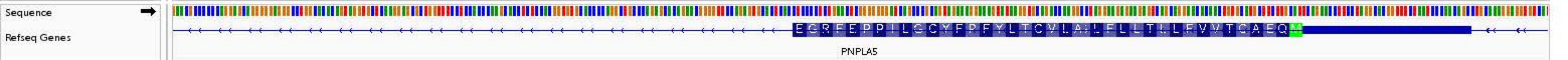
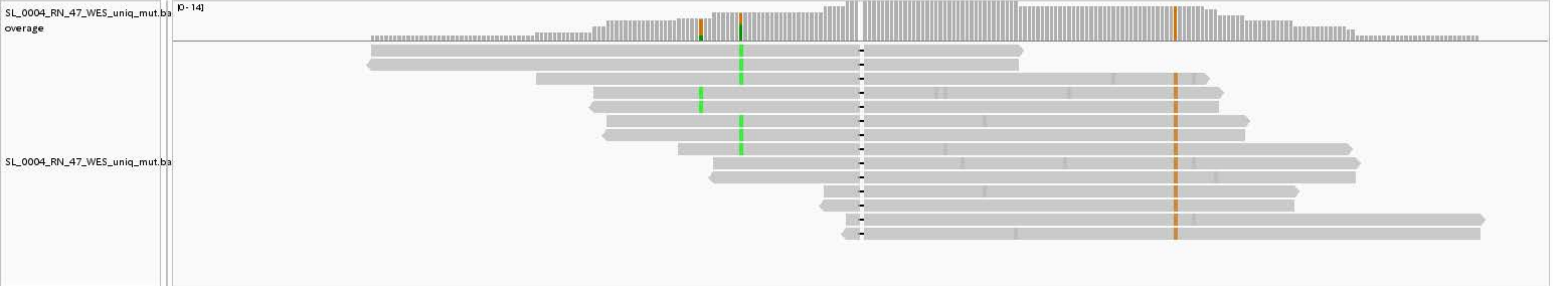
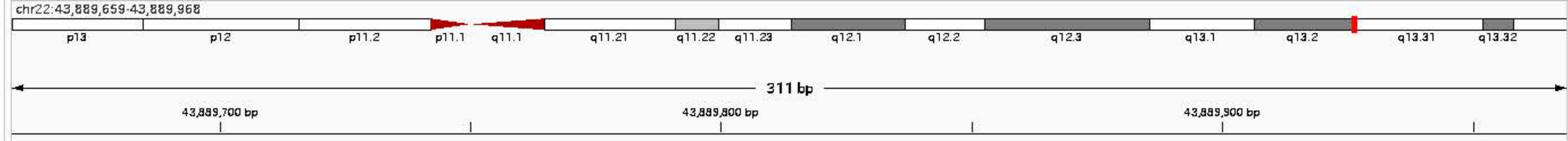


Refseq Genes

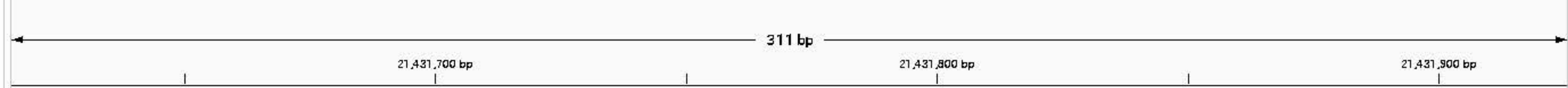
INKKIVRTQQKMQDNPVGFVEIIVLSDGKNSSSHTLPLQICSL  
PIK3C2G



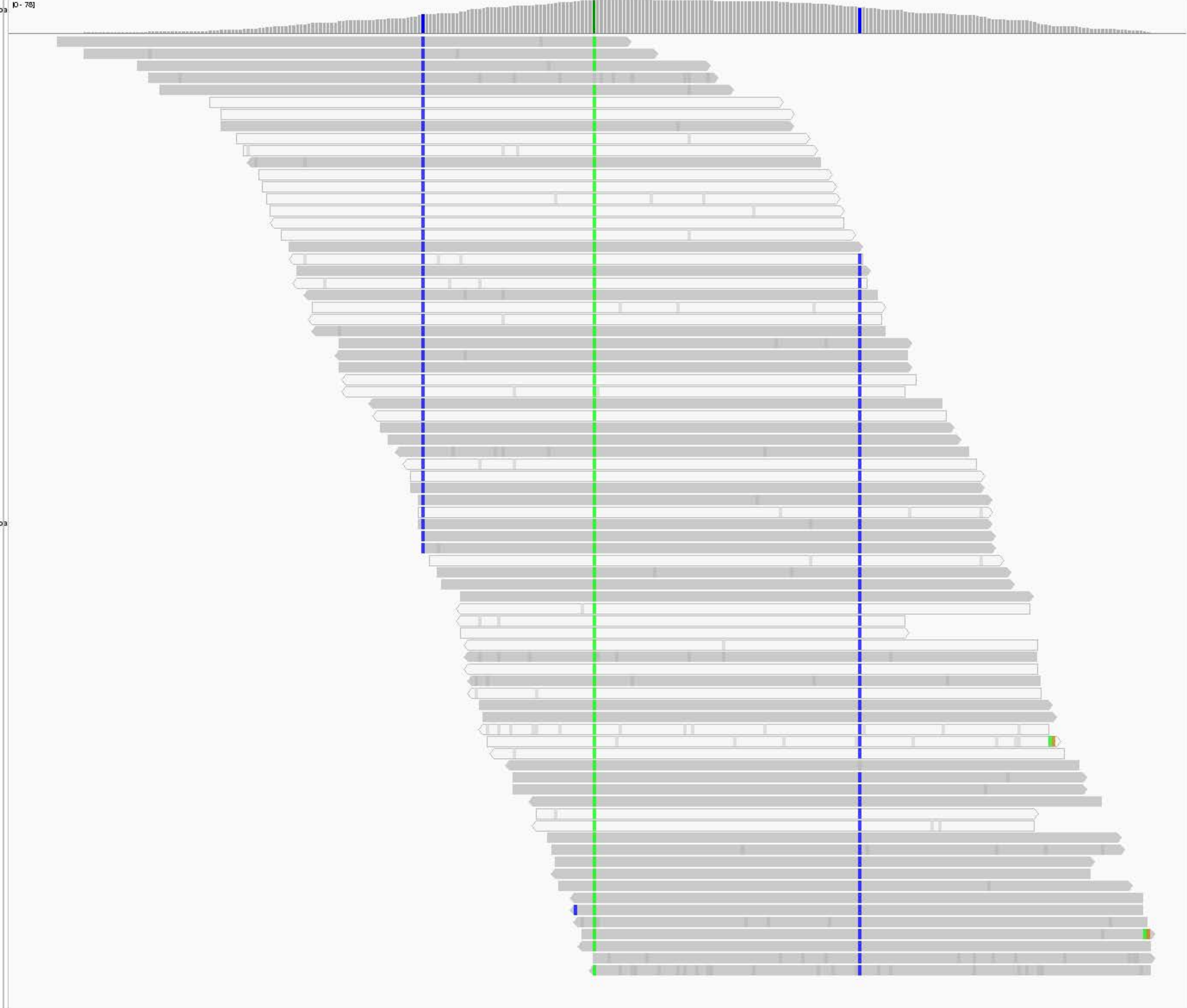




chr15:21,431,616-21,431,925



SL\_0004\_RN\_26\_WES\_uniq\_mut.ba  
coverage

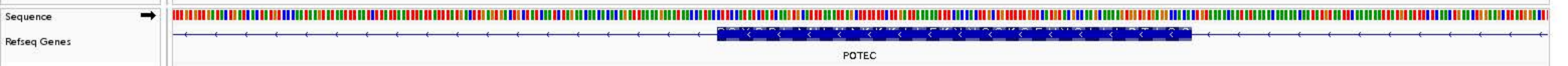
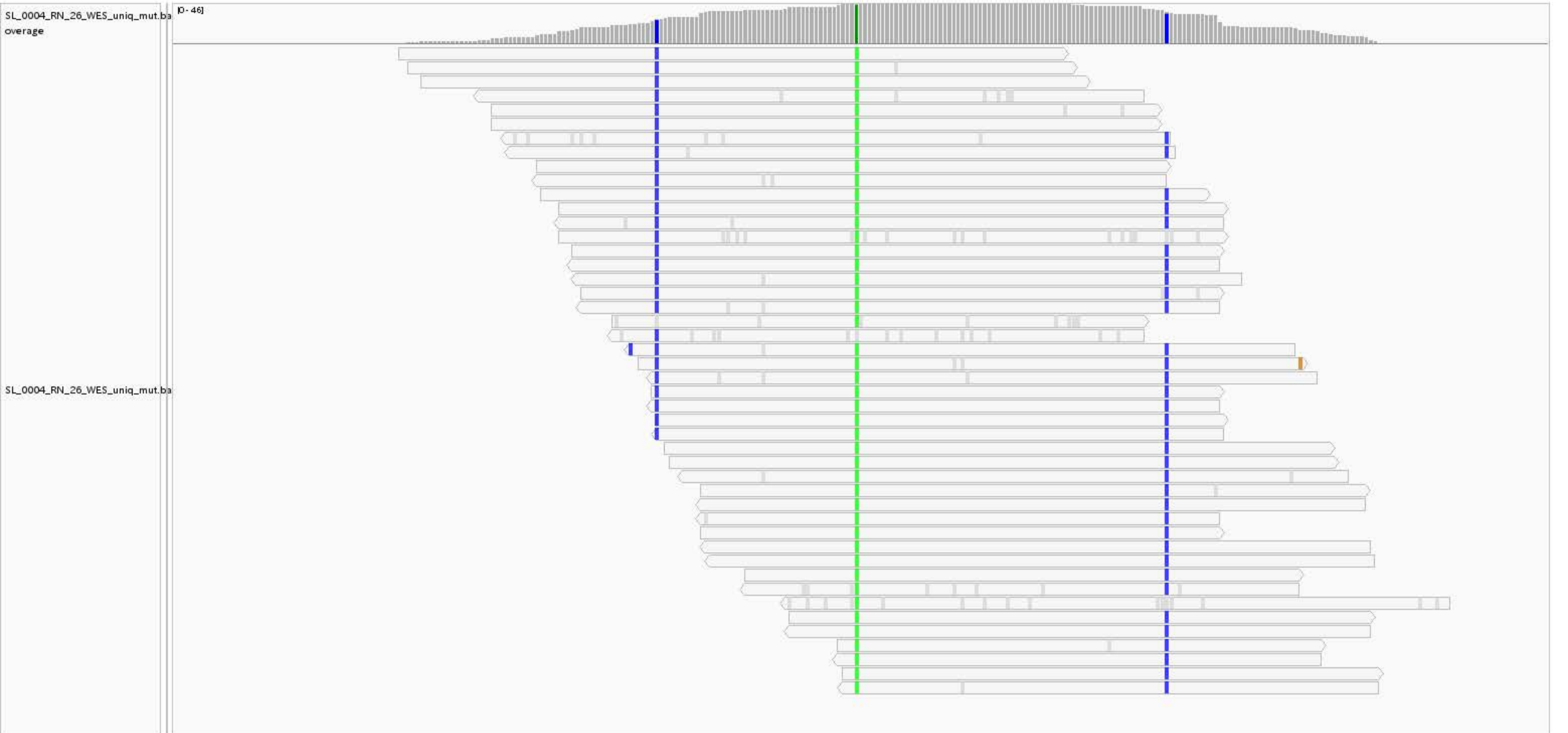
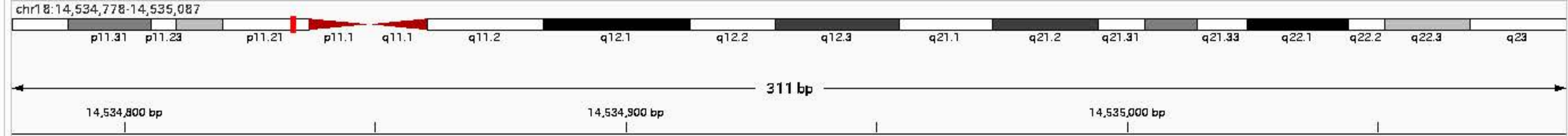


SL\_0004\_RN\_26\_WES\_uniq\_mut.ba

Sequence  
Refseq Genes

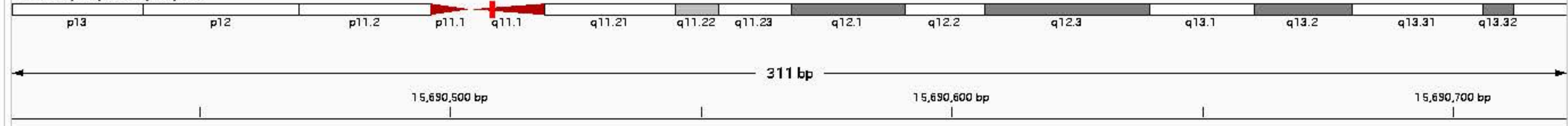


POTEB3

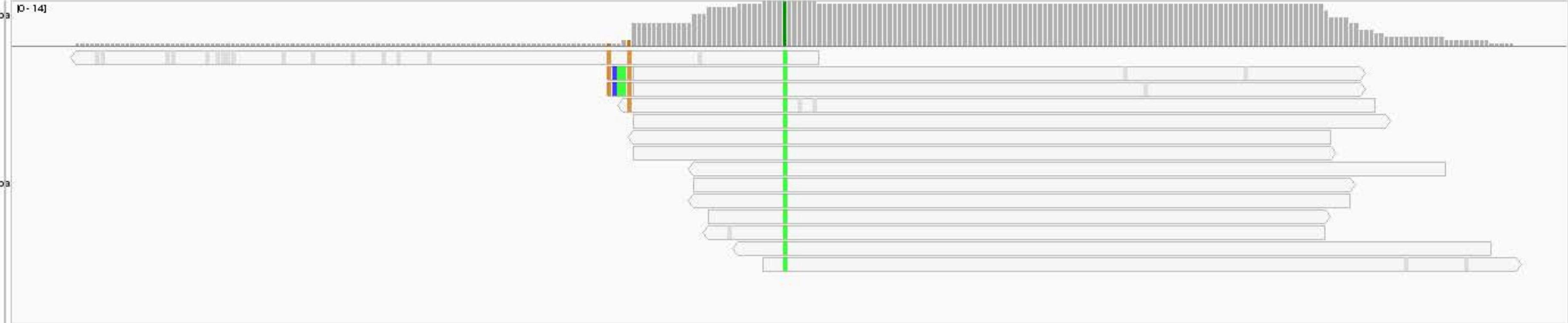




chr22:15,690,413-15,690,722



SL\_0007\_RN\_33\_WES\_uniq\_mut.ba  
coverage



SL\_0007\_RN\_33\_WES\_uniq\_mut.ba

Sequence

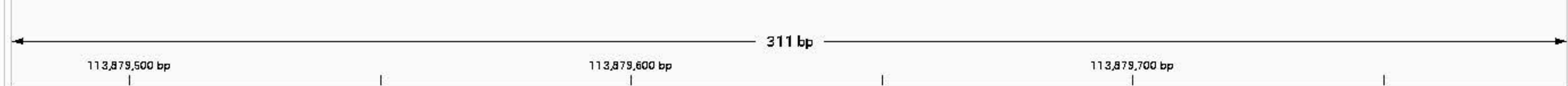


Refseq Genes

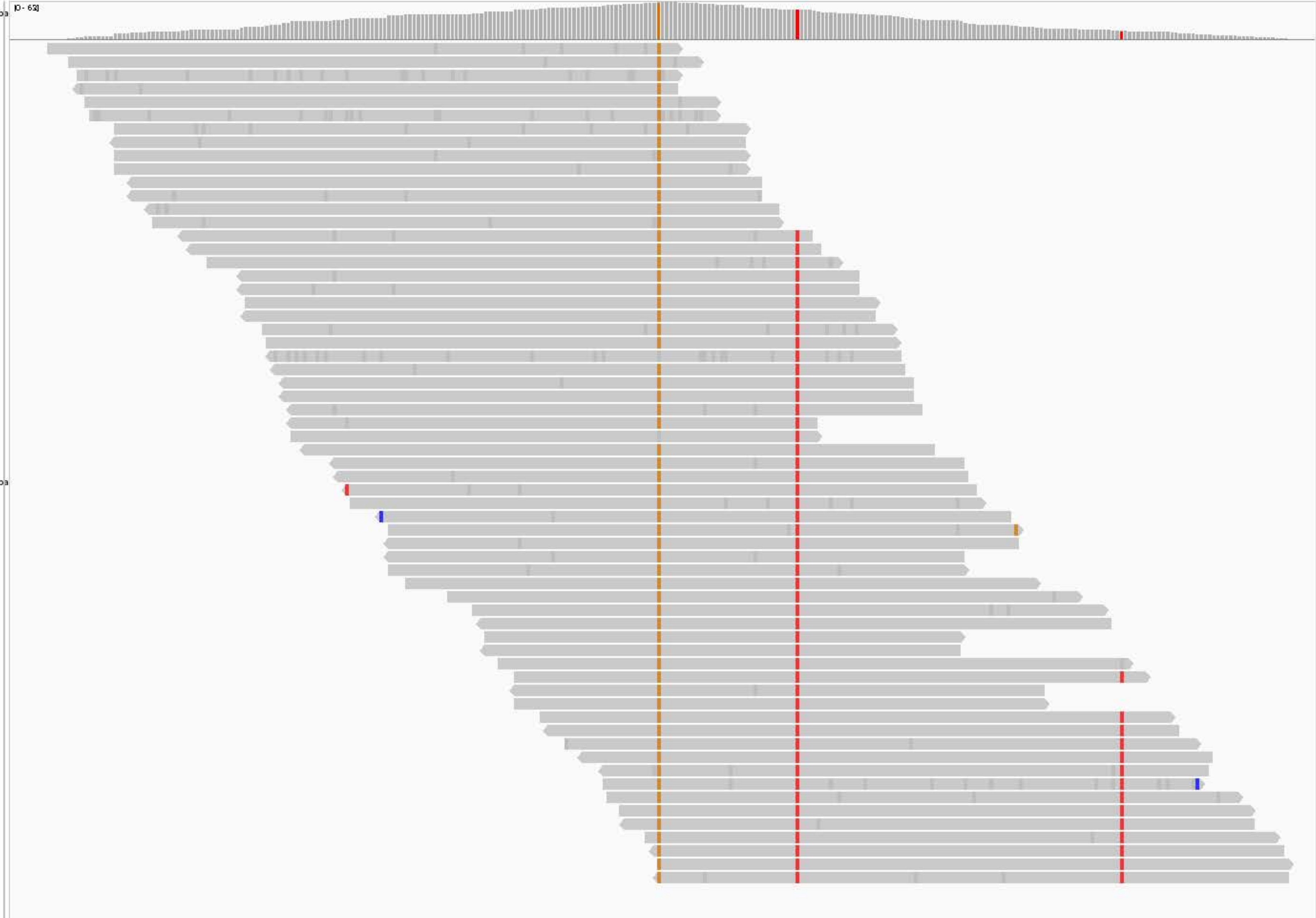
GKSNVGTSGDHDDSAMKTLRSKMGKWCCHCFPCCRGSGKNKVGPGDYDDSAFMEPRYHVRREDLDKLRRAAWWGKVPRKDLIVMLKDTDMNKKDKQKR

POTEH

chr7:113,879,477-113,879,786



SL\_0015\_RN\_10\_WES\_uniq\_mut.ba  
coverage

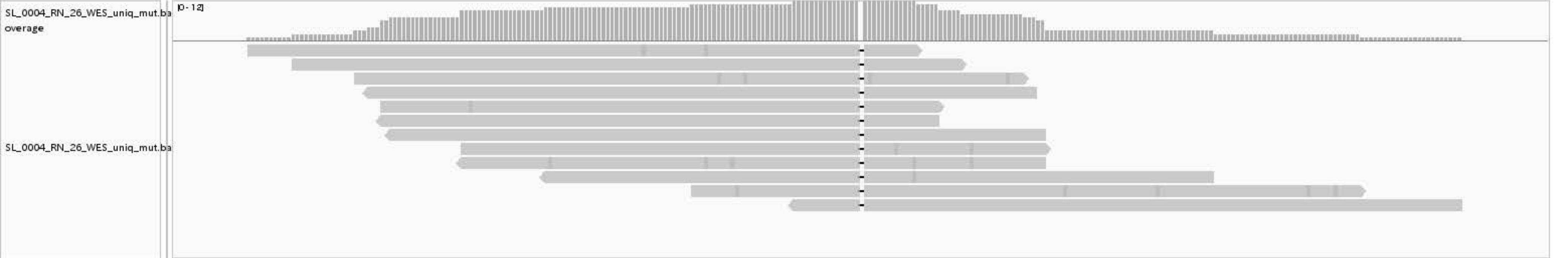
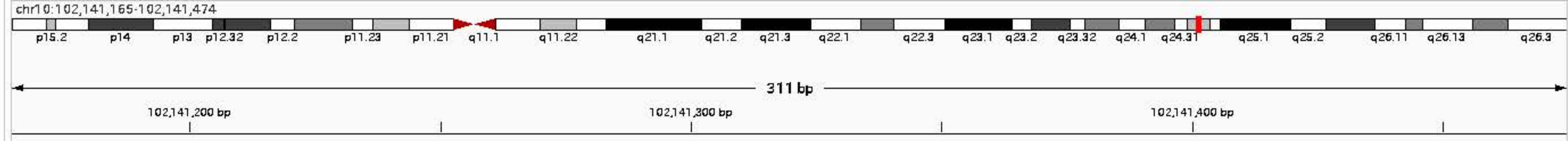


SL\_0015\_RN\_10\_WES\_uniq\_mut.ba

Sequence  
Refseq Genes

L I T Q F N K R Q K E N V G L Y I R Q E E D D K G N G Y D E K S S G E E T S E K L C A S T D S H F D R R L C G L D K V E I N K A G G E H K K N L N G A M L Q D S S P C P I Q V T G N G H A P N A N D D L V E

PPP1R3A



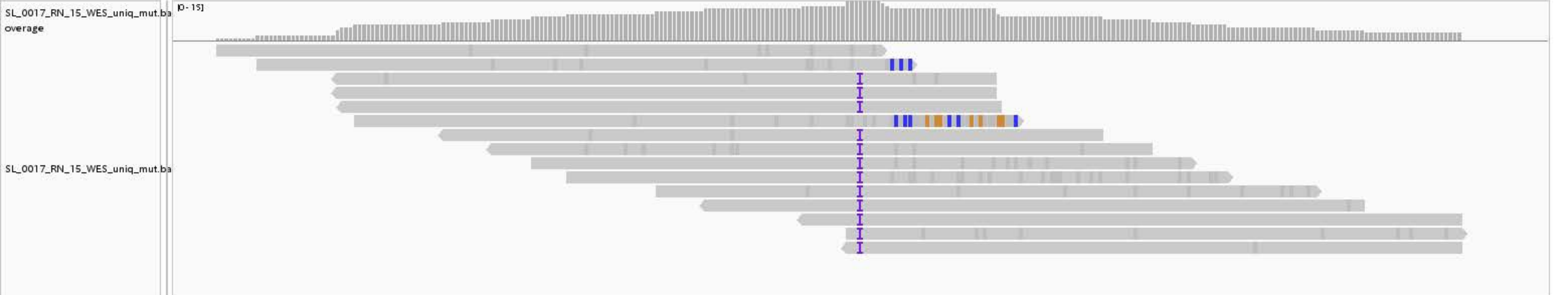
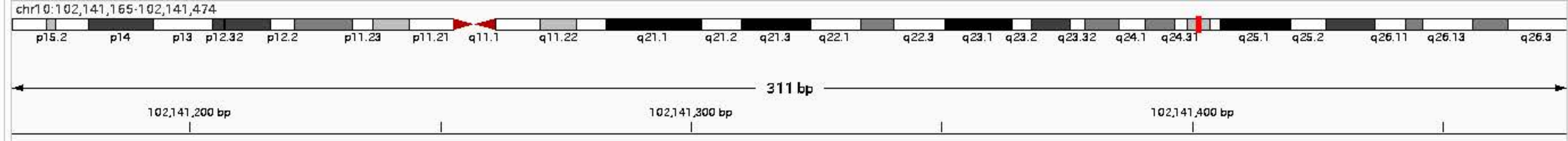
Sequence →

Refseq Genes

LGMPPSLPPPLQPPSLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPSGYPCLPPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPYSSTCTYGPLGWGPGPQ

PPRC1



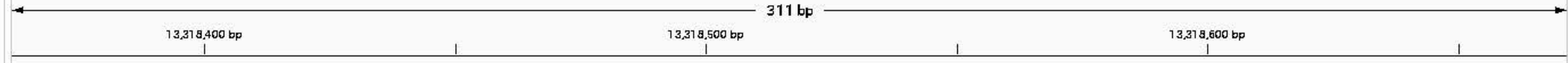
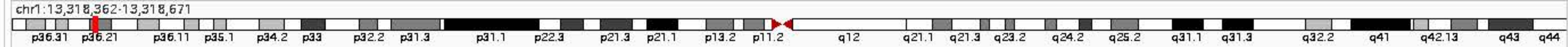


Sequence →

Refseq Genes

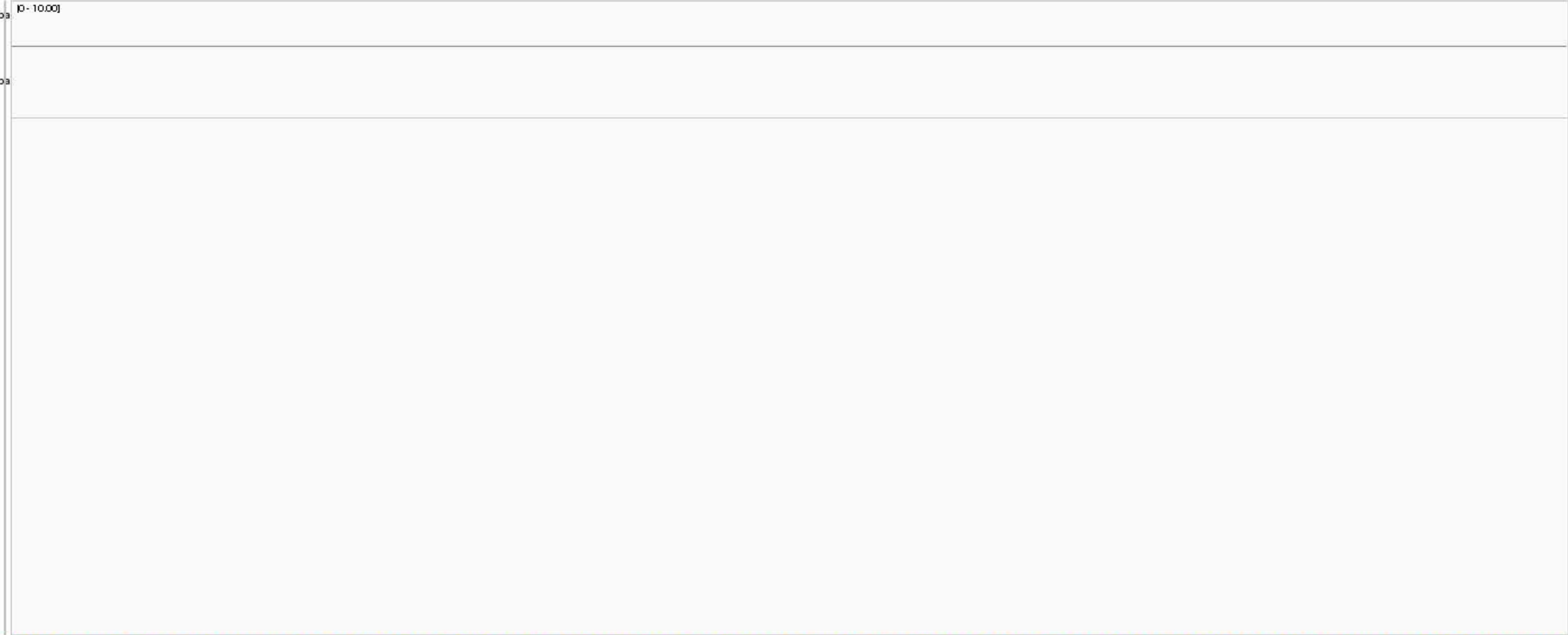
LGMPPSLPPPLQPPSLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPSGYPCLPPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPYSSTCTYGPLGWGPGPQ

PPRC1



SL\_0004\_RN\_26\_WES\_uniq\_mut.ba  
overage

SL\_0004\_RN\_26\_WES\_uniq\_mut.ba

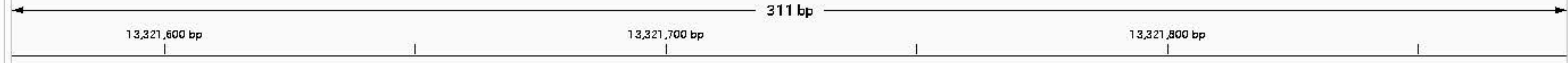


Sequence →

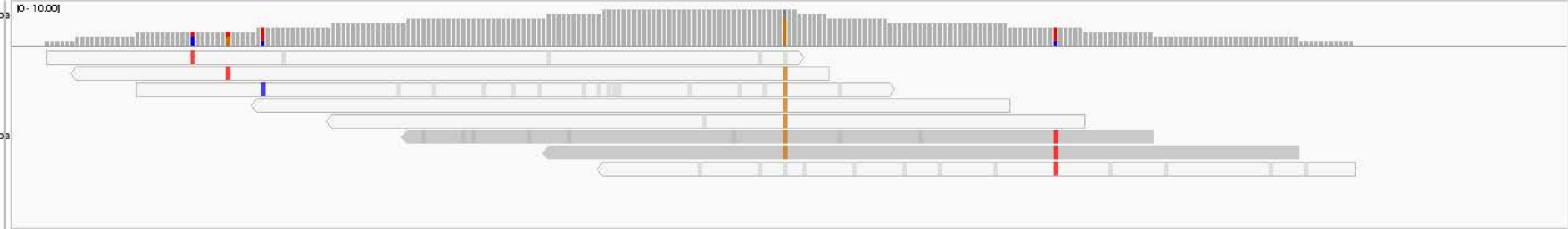
Refseq Genes



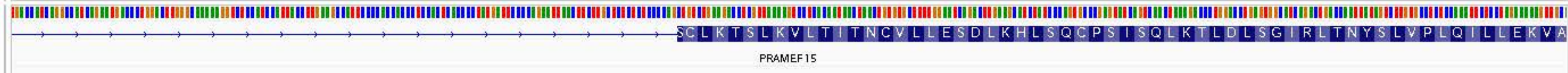
chr1:13,321,570-13,321,879  
p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44



SL\_0004\_RN\_05\_WES\_uniq\_mut.ba  
overage  
SL\_0004\_RN\_05\_WES\_uniq\_mut.ba



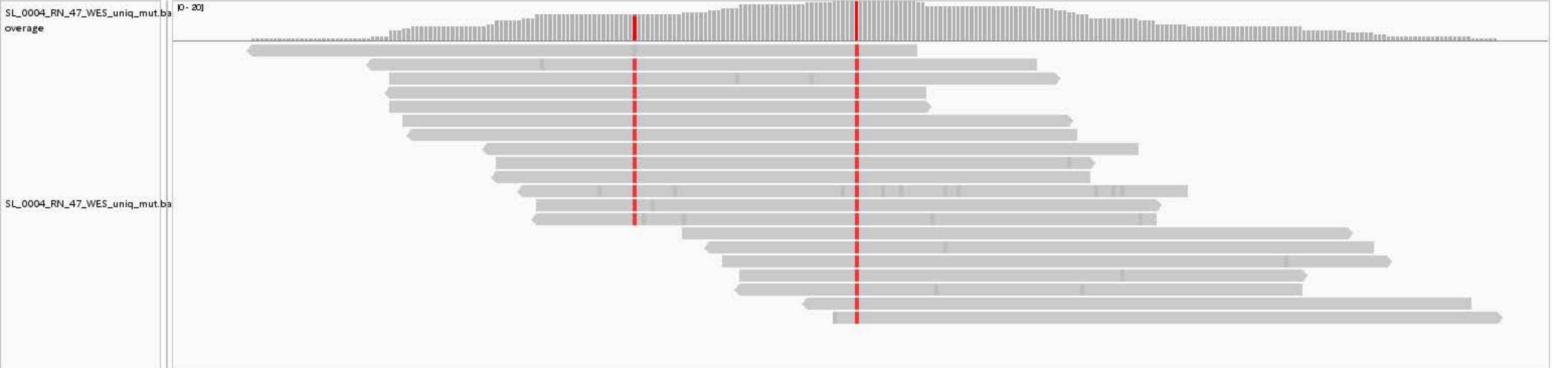
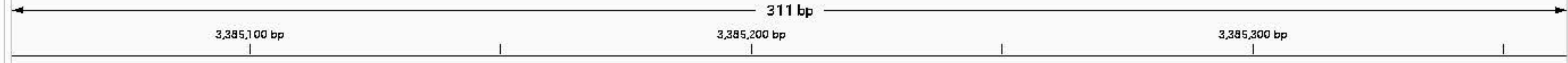
Sequence  
Refseq Genes





chr1:3,385,053-3,385,362

p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44

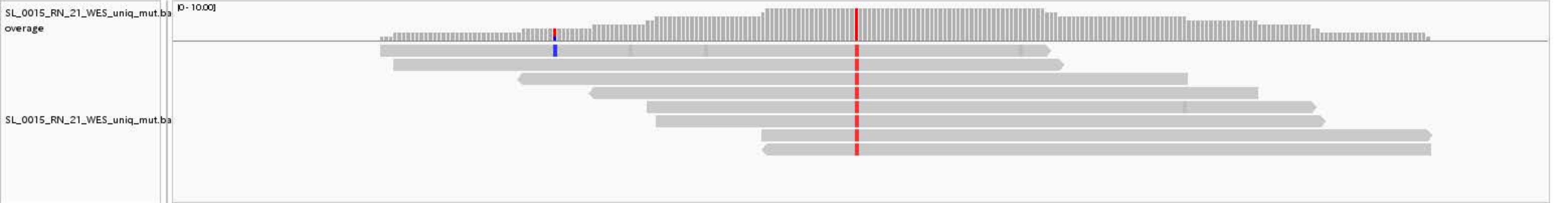
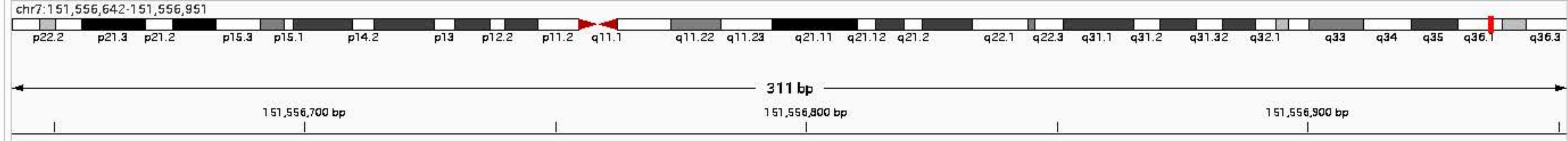


Sequence →

Refseq Genes

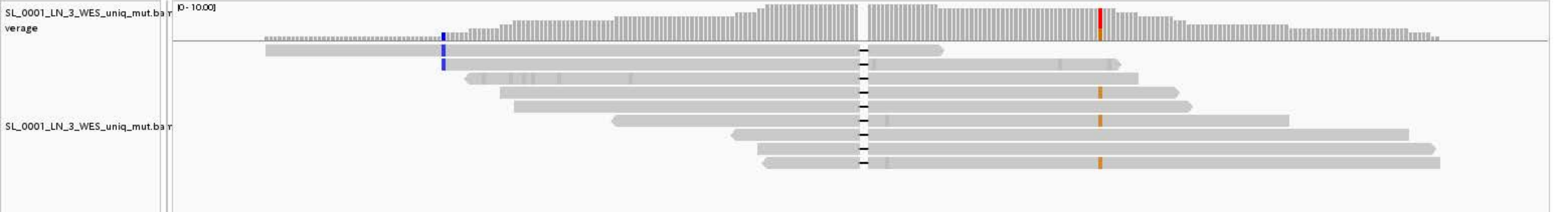
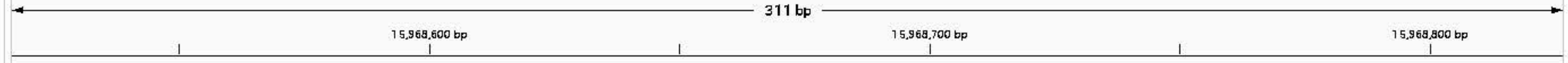
ISEDLGSEKFCVDANQAGAGSWLKYIRVACSCDDQNLTMCISEQ

PRDM16

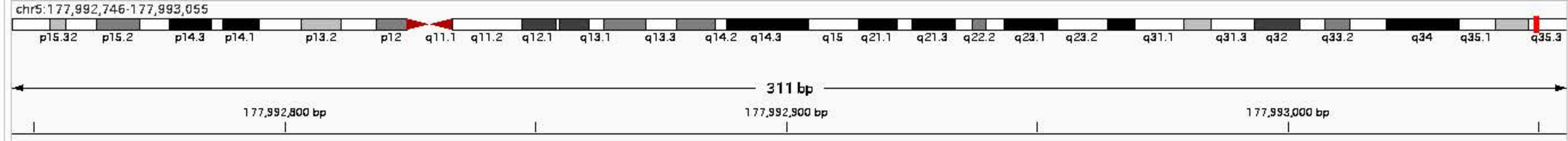


chr4:15,968,517-15,968,826

p16.2 p15.33 p15.31 p15.1 p14 p13 p11 q12 q13.1 q13.2 q21.1 q21.22 q22.1 q22.3 q24 q25 q26 q27 q28.2 q28.3 q31.1 q31.22 q32.1 q32.3 q34.1 q34.3 q35.2

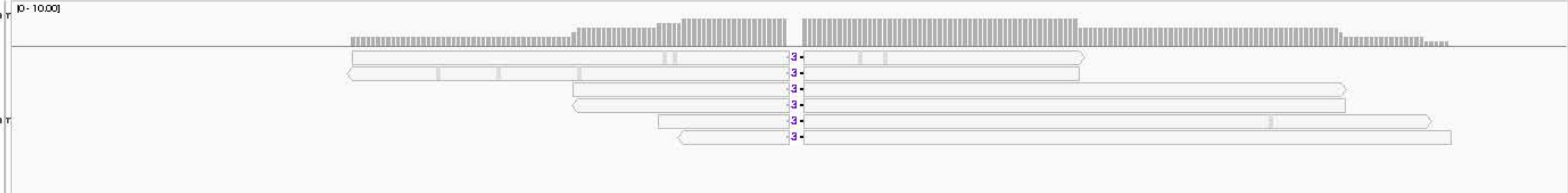






SL\_0001\_LN\_3\_WES\_uniq\_mut.ba  
verage

SL\_0001\_LN\_3\_WES\_uniq\_mut.ba

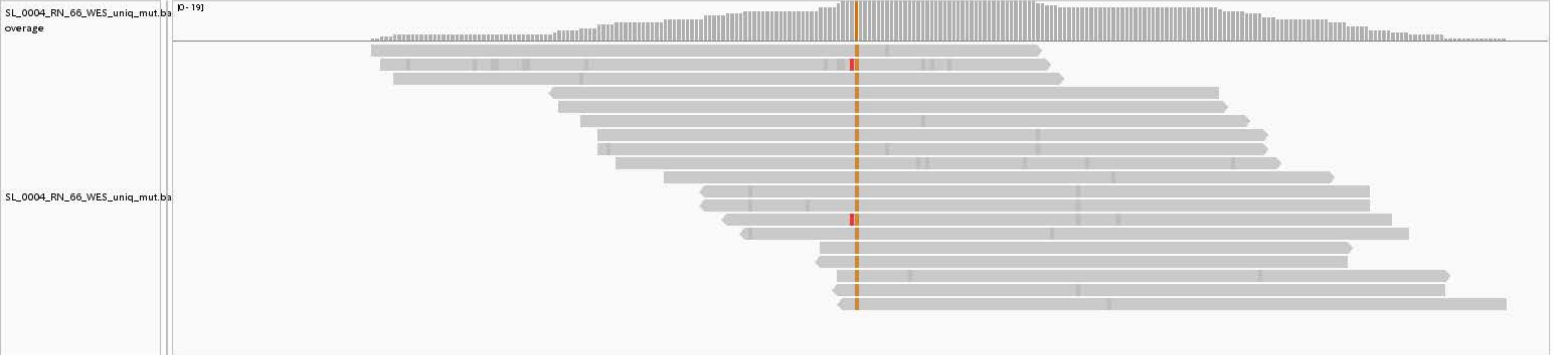
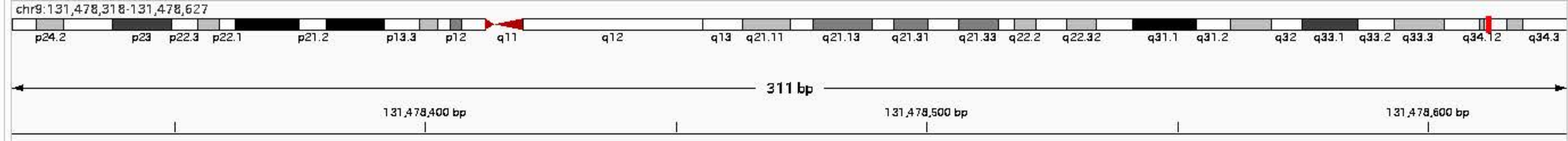


Sequence →

Refseq Genes

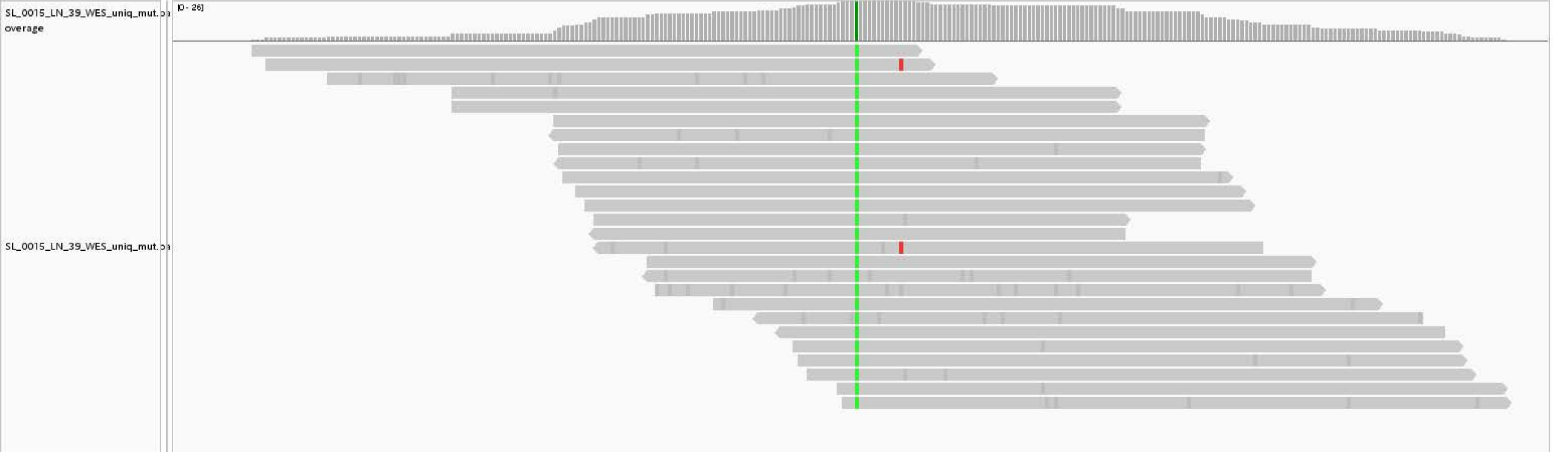
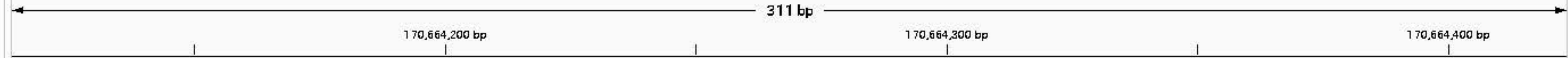
LMPPPPCPLHGAPAPHLTPYWDESQHSLAFAGGTSPQSPLAHSYPHPFCTVPPPPAAYSYPCHATSEPLFSSFAAPSLHALPQLLSREQKRQKARRNQFWV ←

PROP1



chr1:170,664,114-170,664,423

p36.31 p36.21 p36.11 p35.1 p34.2 p33 p32.2 p31.3 p31.1 p22.3 p21.3 p21.1 p13.2 p11.2 q12 q21.1 q21.3 q23.2 q24.2 q25.2 q31.1 q31.3 q32.2 q41 q42.13 q43 q44



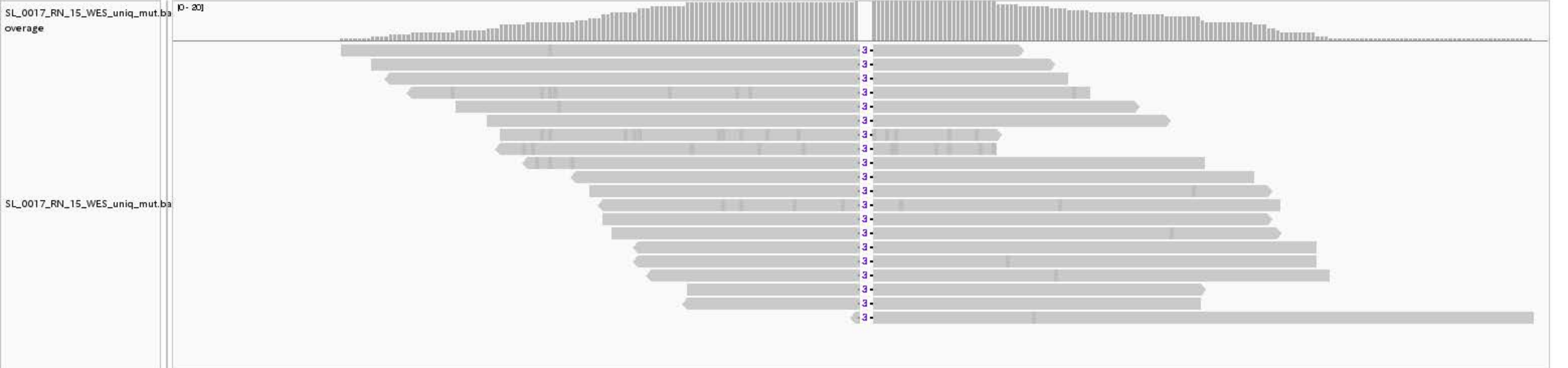
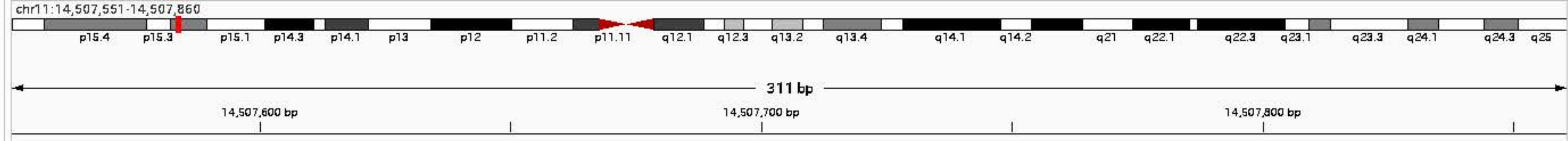
Sequence →

Refseq Genes

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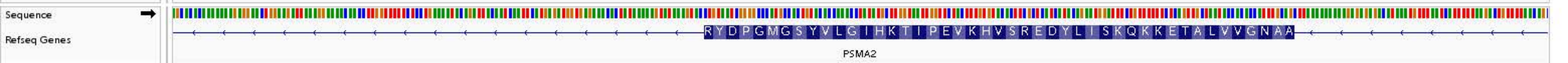
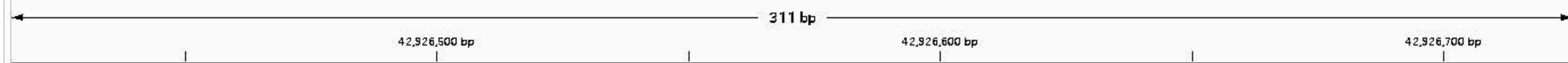
PRRX1



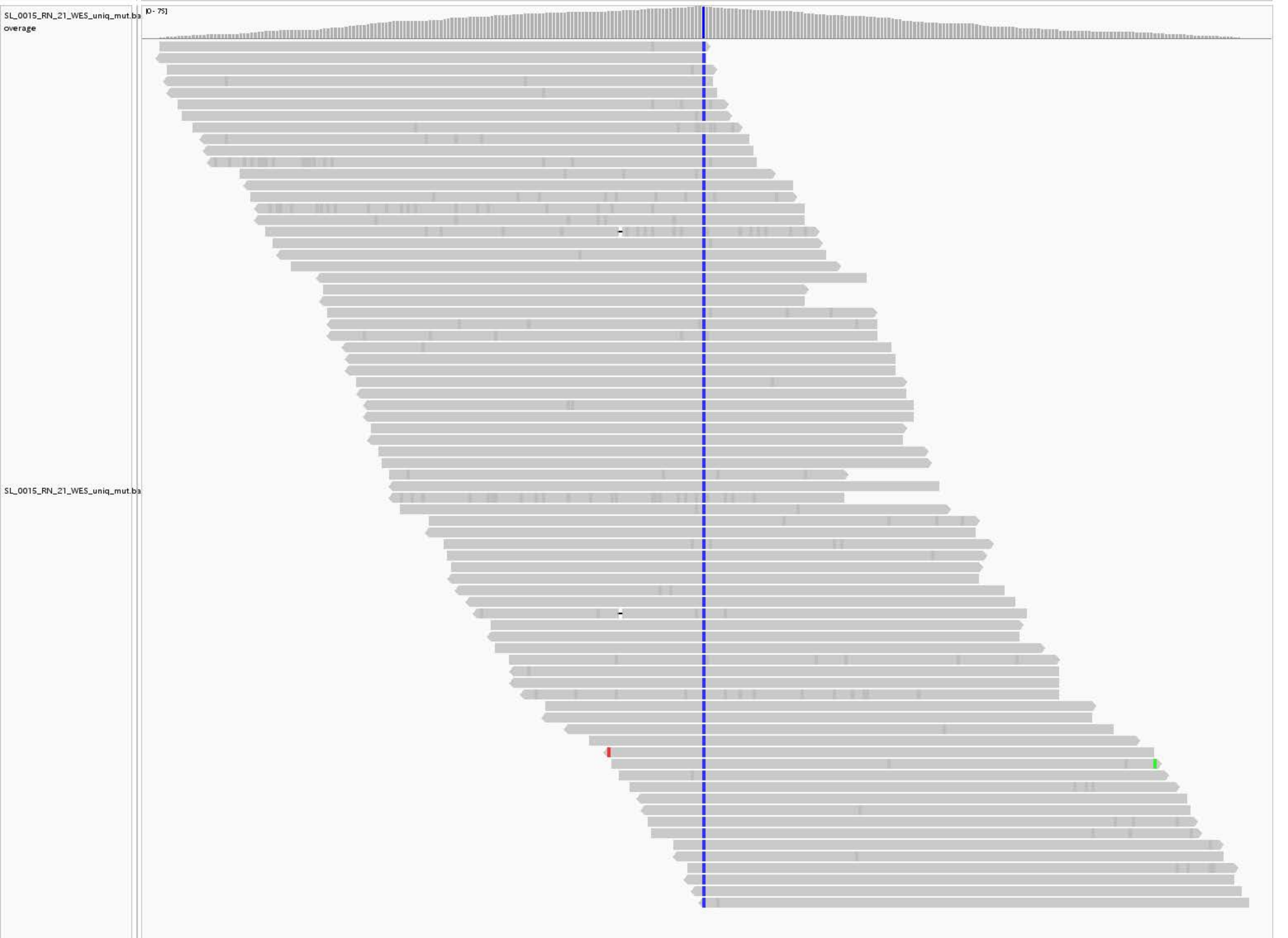
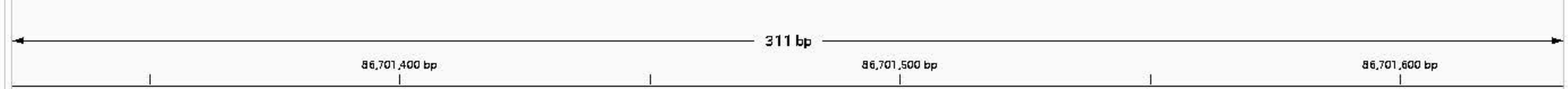


chr7:42,926,416-42,926,725

p22.2 p21.3 p21.2 p15.3 p15.1 p14.2 p13 p12.2 p11.2 q11.1 q11.22 q11.23 q21.11 q21.12 q21.2 q22.1 q22.3 q31.1 q31.2 q31.32 q32.1 q33 q34 q35 q36.1 q36.3



chr4: 86,701,323-86,701,632

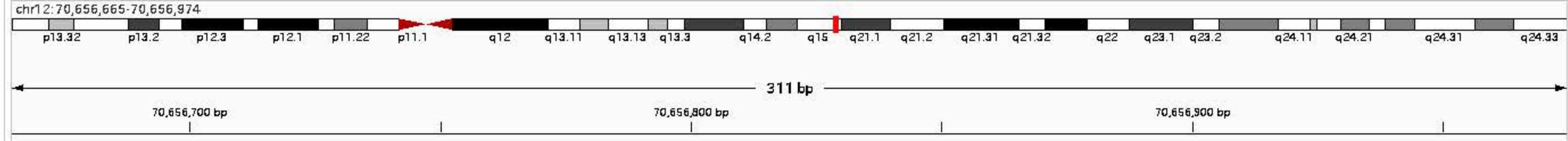


Sequence Refseq Genes

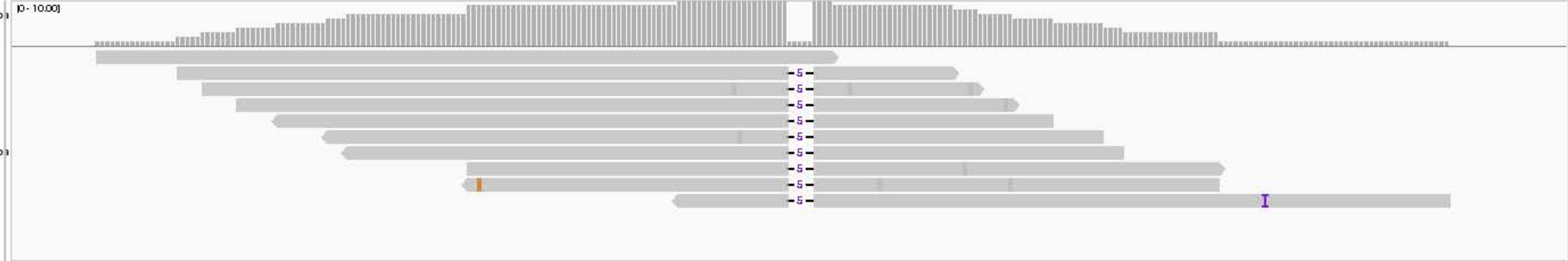
SMGFLSIKDTQDENYFKDILSDNSGREDSSENTFSPYQFKTSGPEKKPIPGIDVLSKKKIWASSMDLLCTADRFSSGETATYRRCHPEAVTVRTSTTPRKKEA

PTPN13





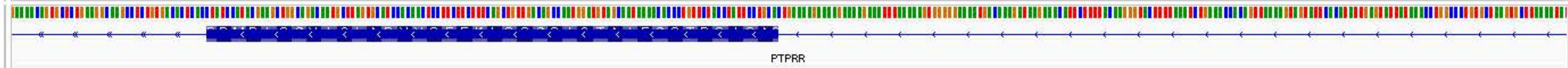
SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage

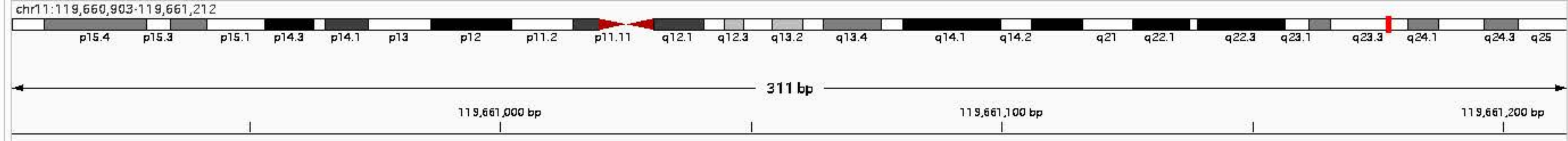


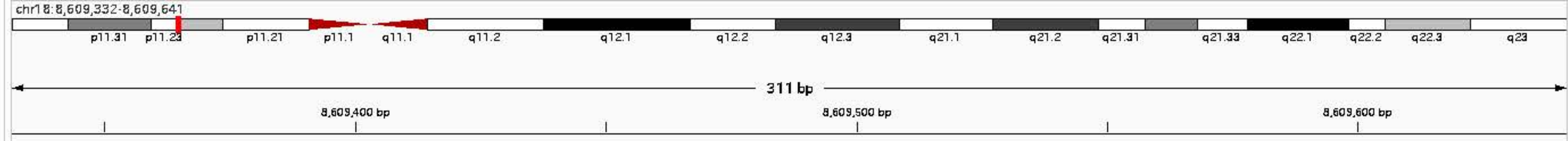
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Sequence

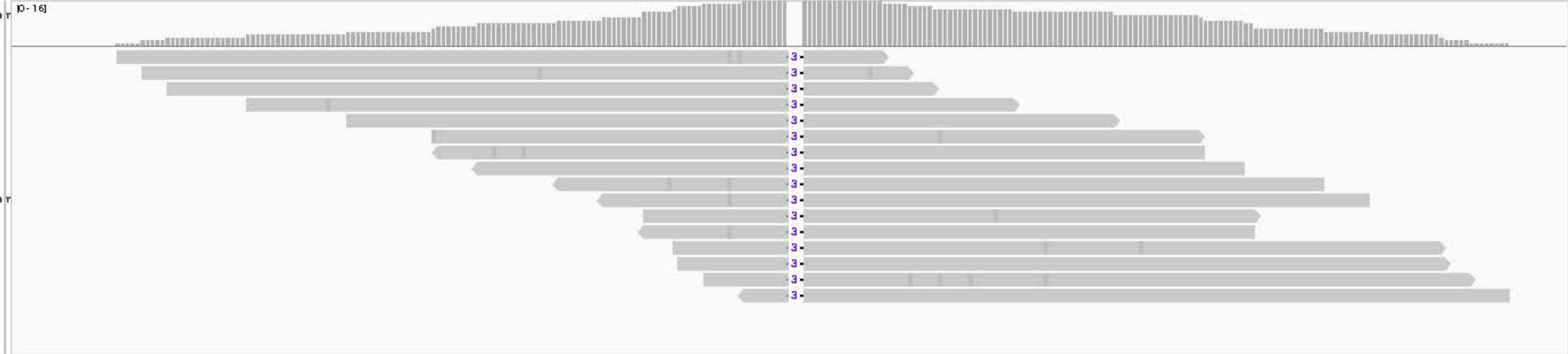
Refseq Genes





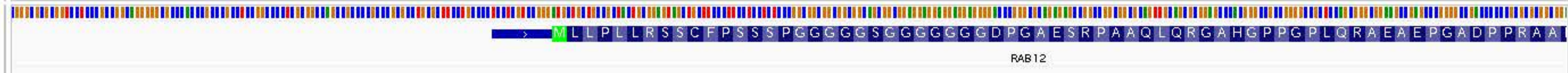


SL\_0001\_LN\_3\_WES\_uniq\_mut.ba  
verage

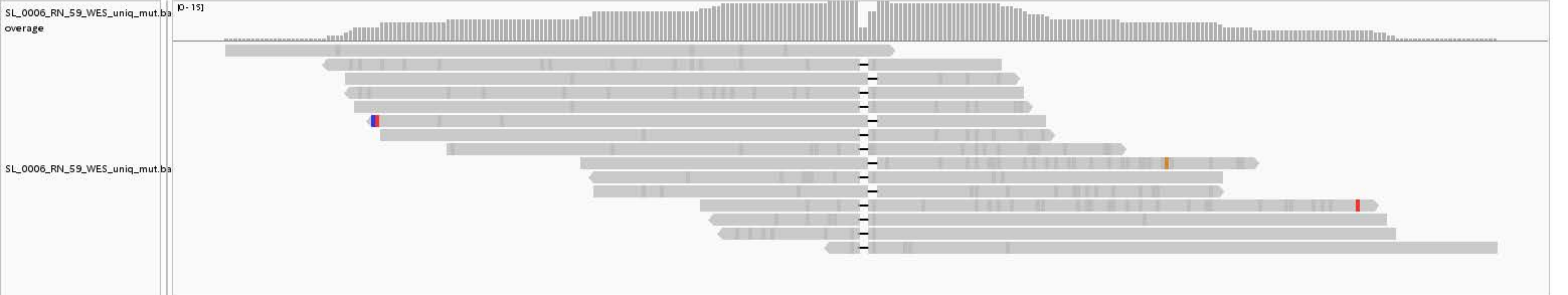
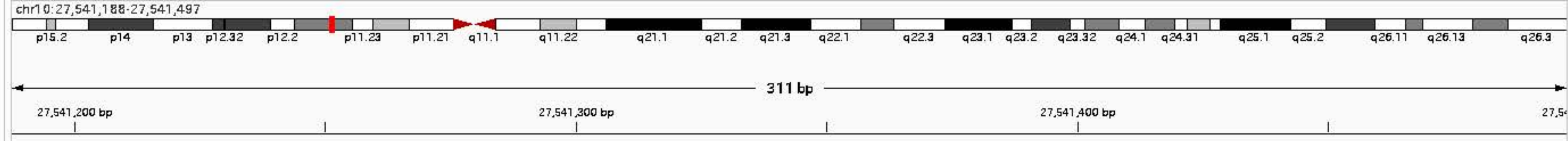


SL\_0001\_LN\_3\_WES\_uniq\_mut.ba r

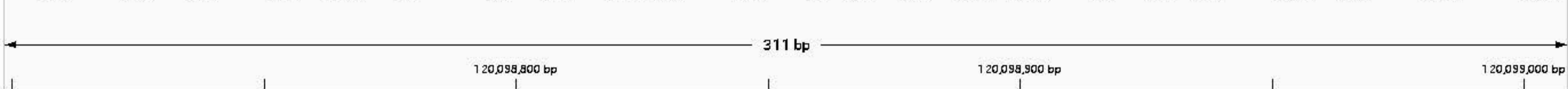
Sequence →  
Refseq Genes



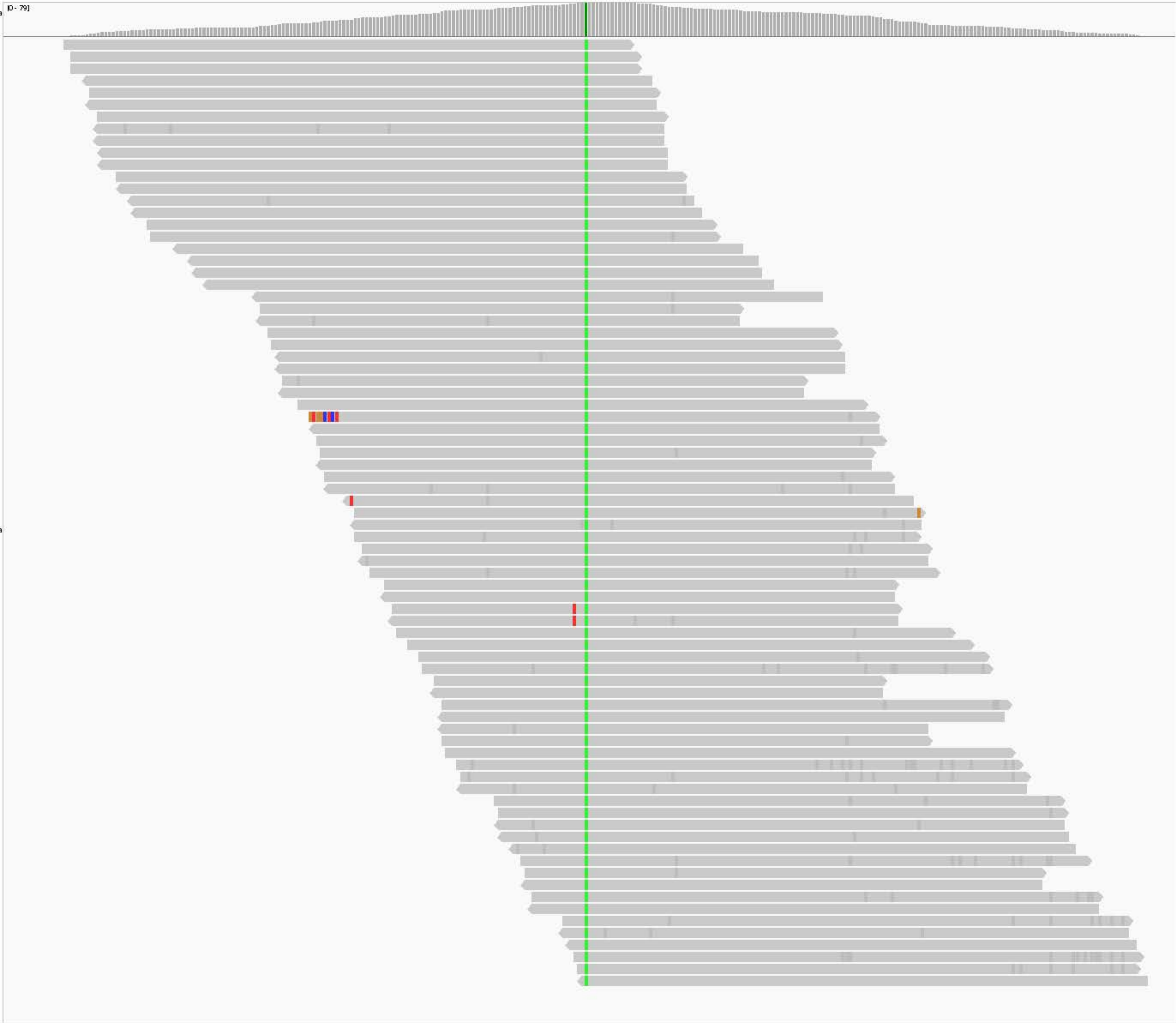




chr12:120,098,699-120,099,008



SL\_0007\_RN\_33\_WES\_uniq\_mut.ba  
overage



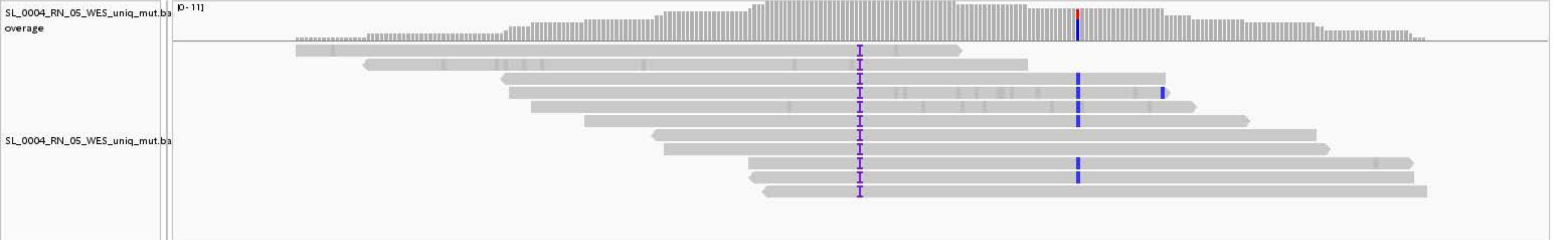
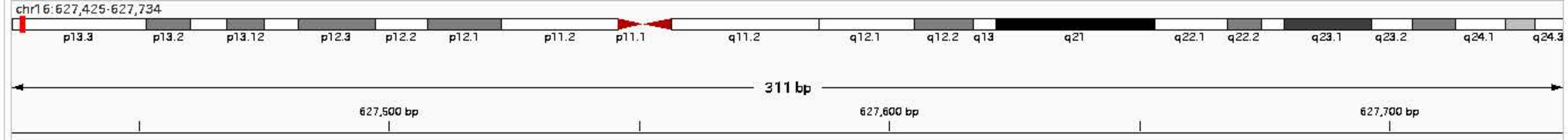
SL\_0007\_RN\_33\_WES\_uniq\_mut.ba

Sequence →

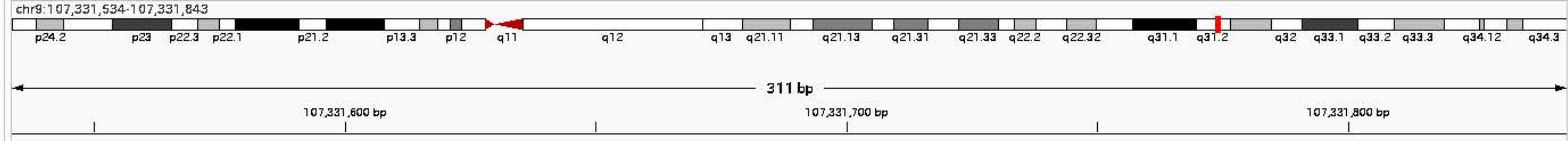
Refseq Genes



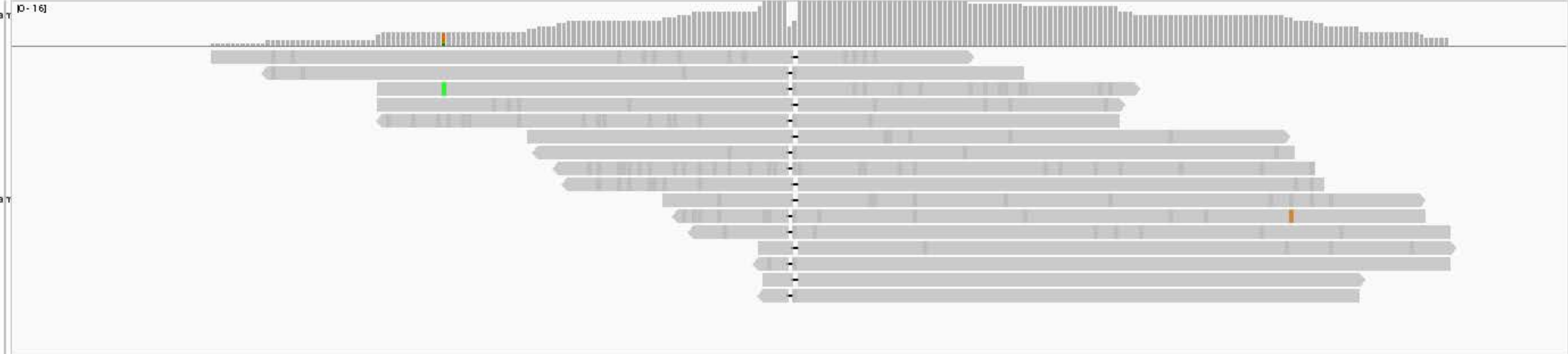
RAB35







SL\_0007\_RN\_2\_WES\_uniq\_mut.ba  
verage



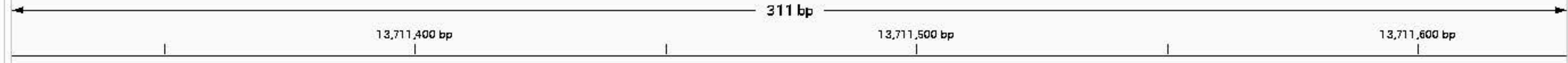
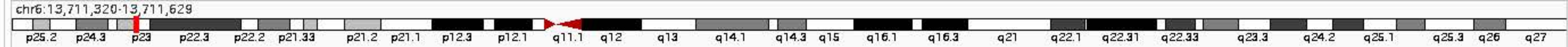
SL\_0007\_RN\_2\_WES\_uniq\_mut.ba

Sequence →



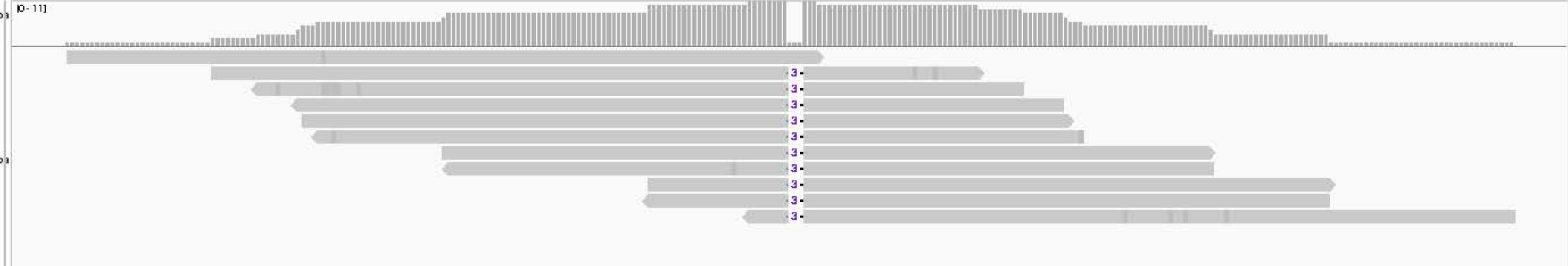
Refseq Genes

RAD23B



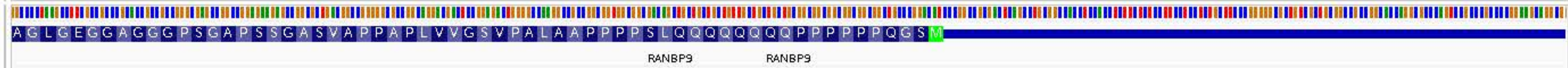
SL\_0015\_LN\_44\_WES\_uniq\_mut. coverage

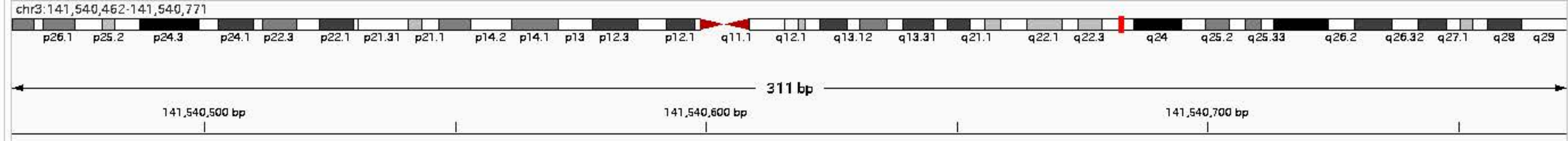
SL\_0015\_LN\_44\_WES\_uniq\_mut.



Sequence

Refseq Genes

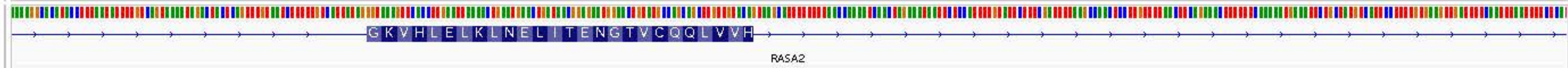




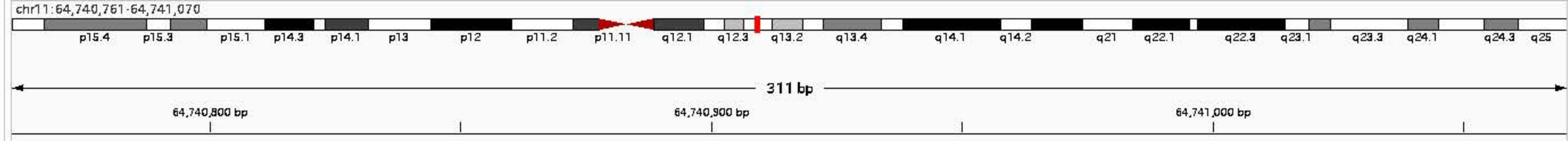
SL\_0015\_LN\_46\_WES\_uniq\_mut. coverage



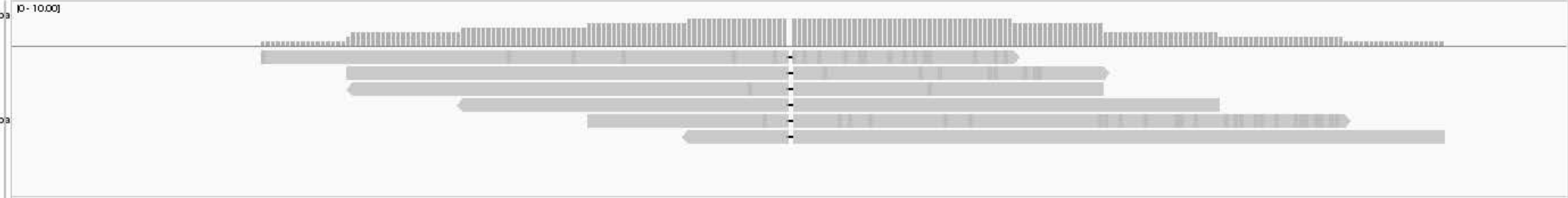
Sequence Refseq Genes





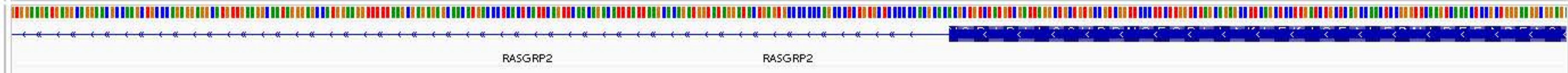


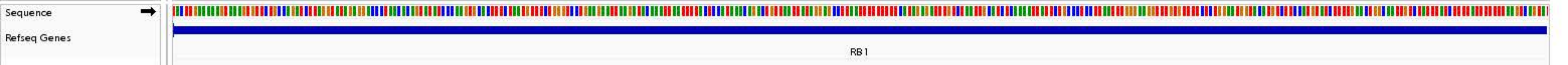
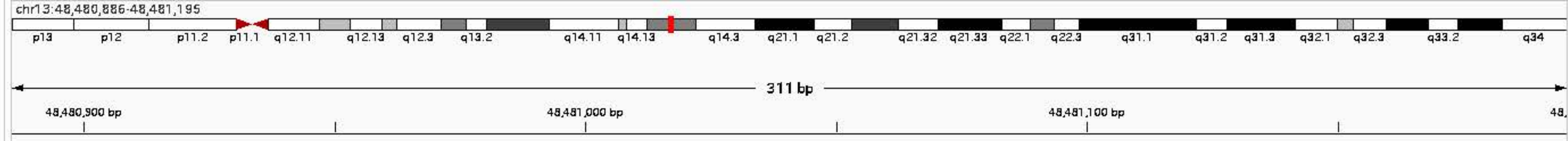
SL\_0006\_RN\_36\_WES\_uniq\_mut.ba  
coverage



SL\_0006\_RN\_36\_WES\_uniq\_mut.ba

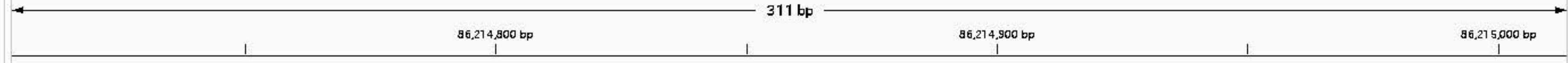
Sequence →  
Refseq Genes



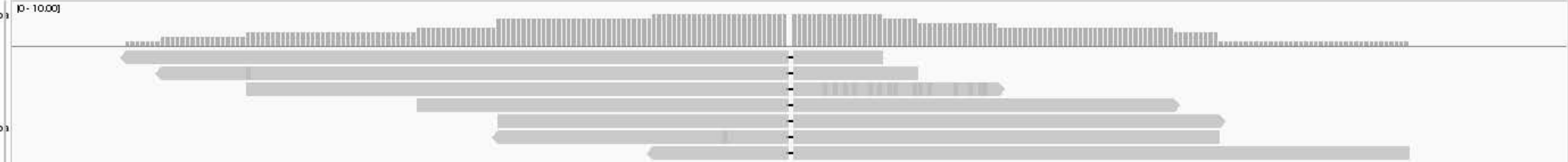


chr2:86,214,704-86,215,013

p25.2 p24.3 p24.1 p23.2 p22.2 p21 p16.2 p15 p13.3 p12 p11.2 q11.1 q12.1 q13 q14.2 q21.1 q22.1 q22.3 q24.1 q24.3 q31.1 q31.3 q32.2 q33.1 q33.3 q35 q36.2 q37.1 q37.3



SL\_0001\_LN\_10\_WES\_uniq\_mut.  
coverage



SL\_0001\_LN\_10\_WES\_uniq\_mut.

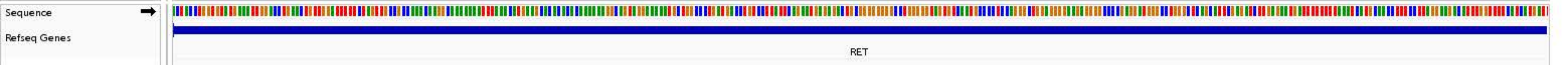
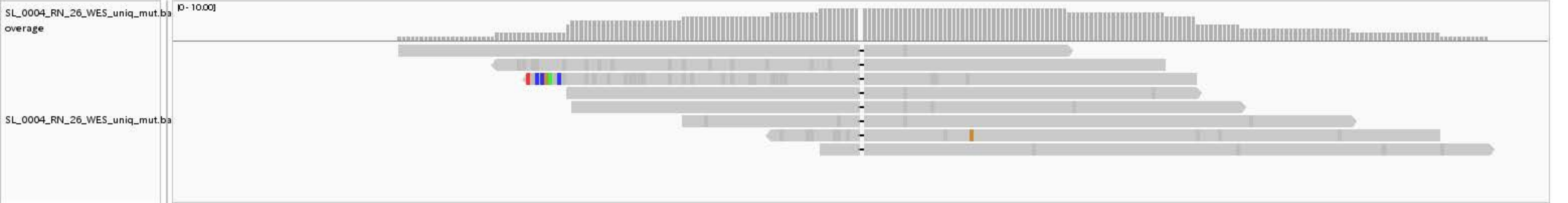
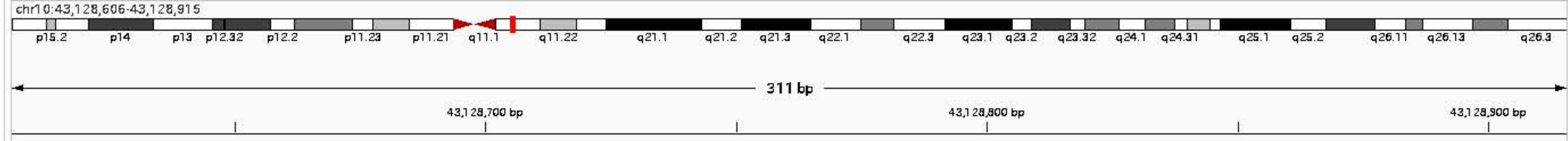
Sequence

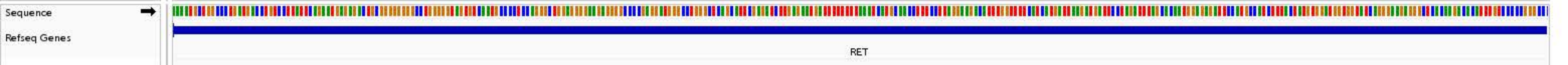
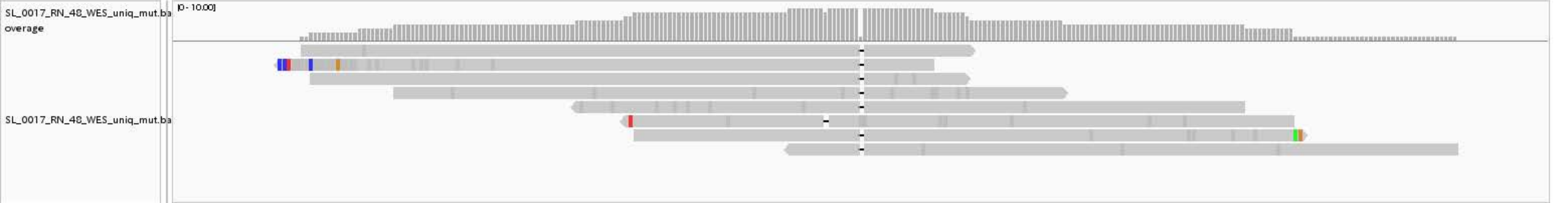
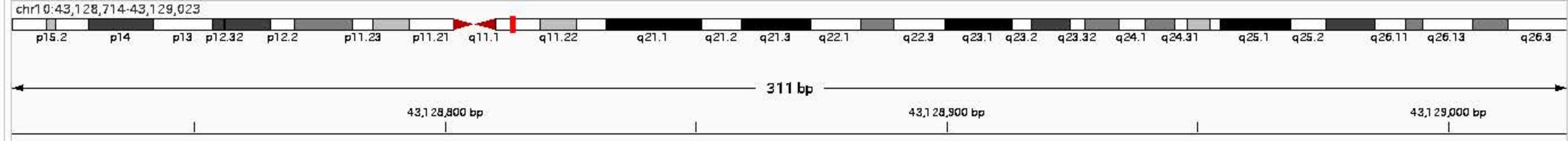
Refseq Genes

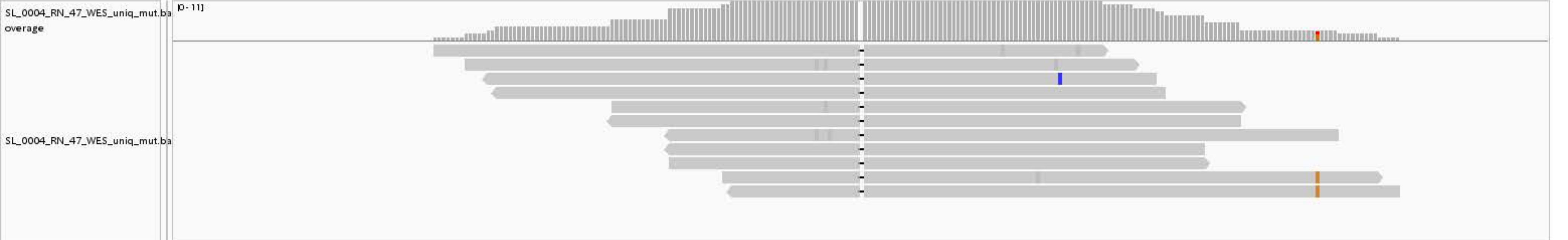
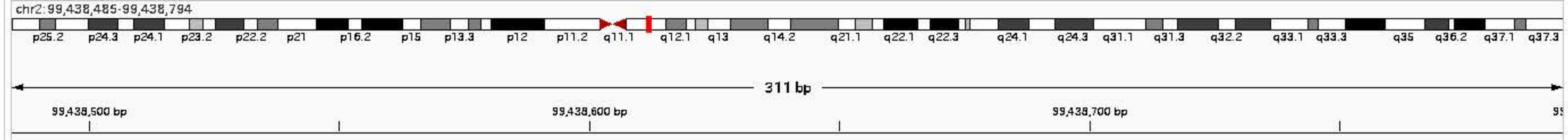


REEP1

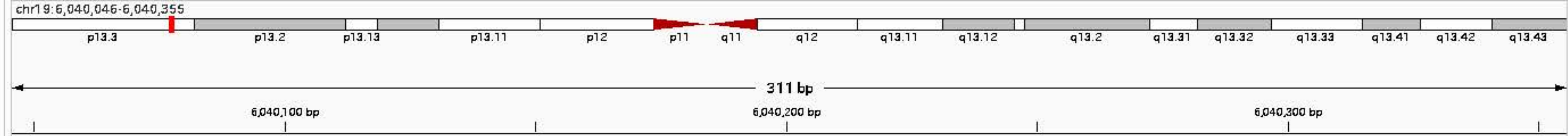




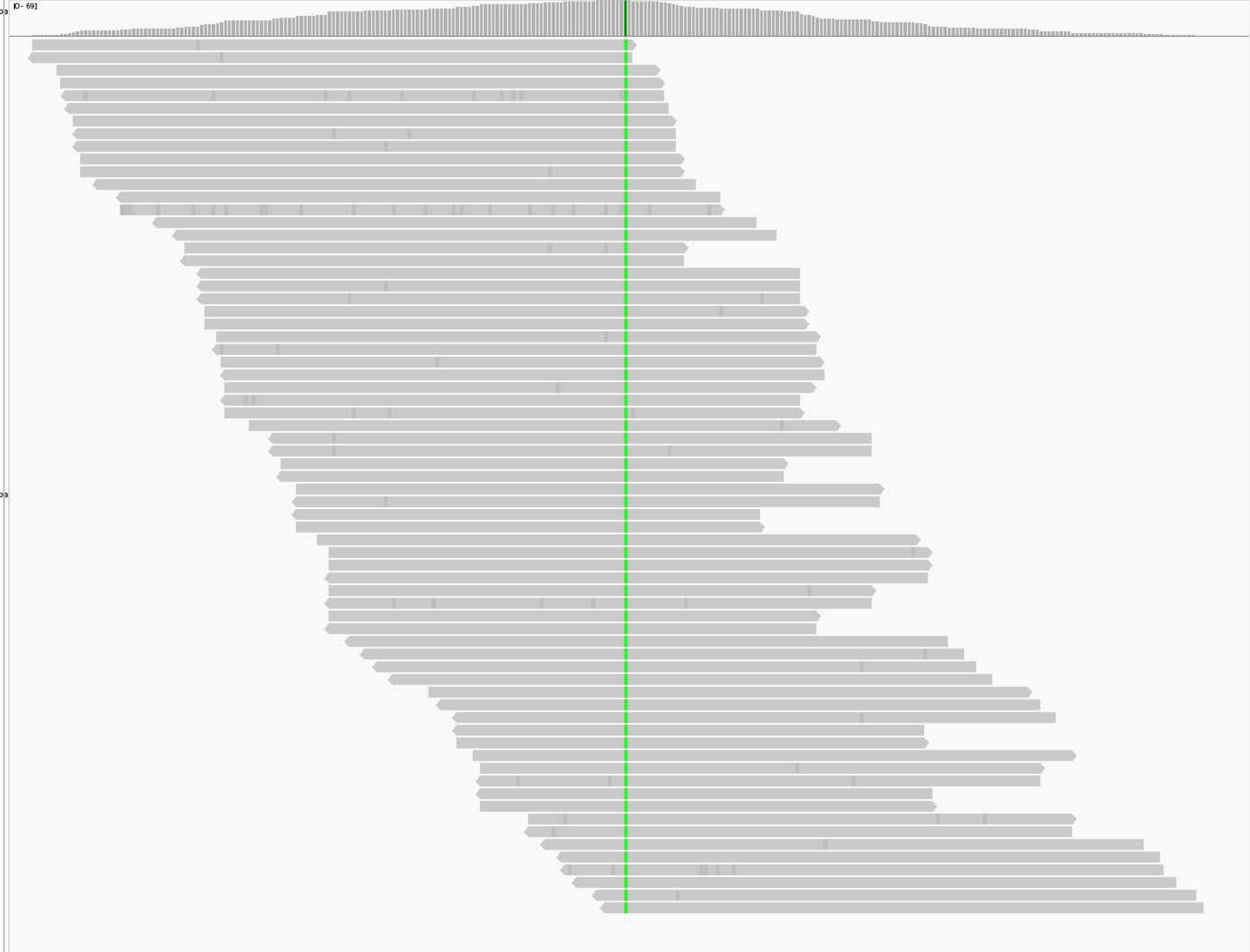








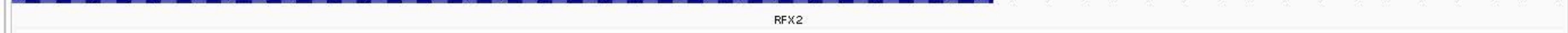
SL\_0004\_RN\_66\_WES\_uniq\_mut.ba  
coverage



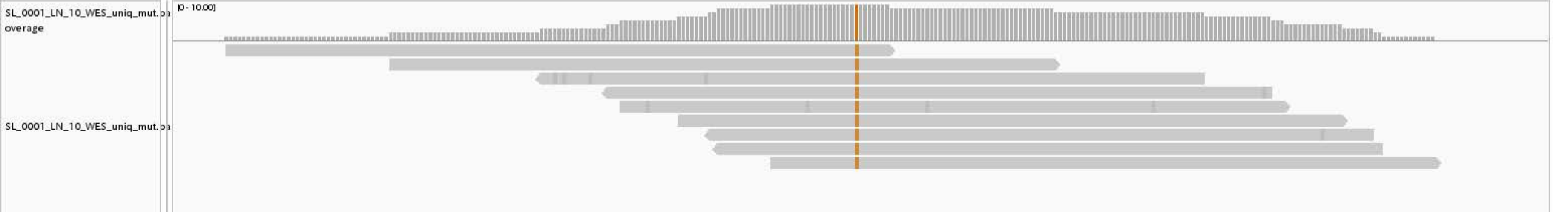
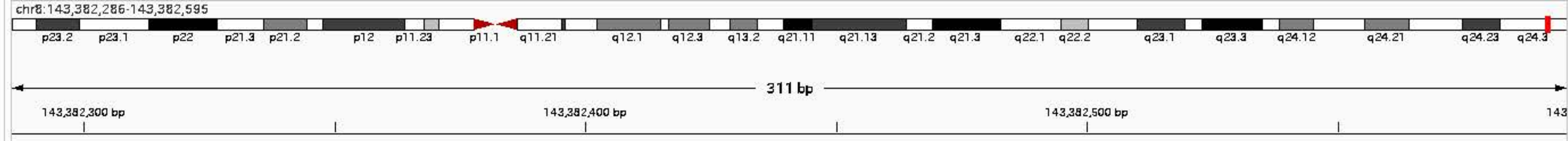
Sequence →



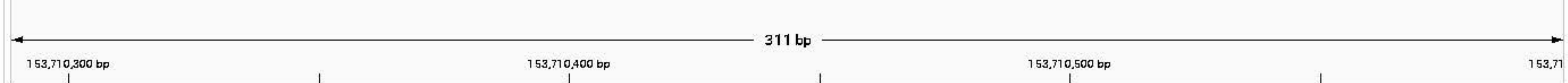
Refseq Genes



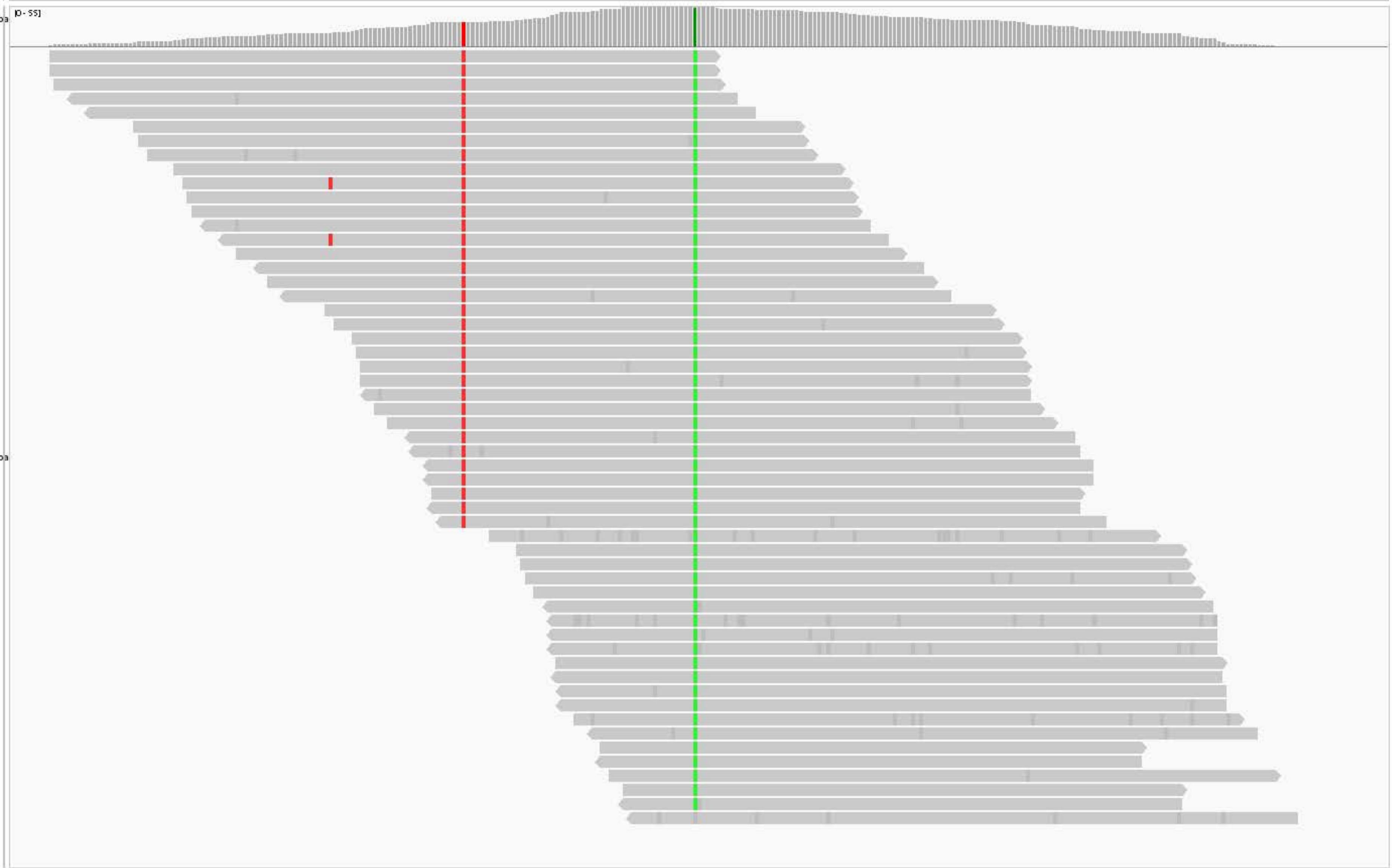
RFX2



chr4:153,710,289-153,710,598



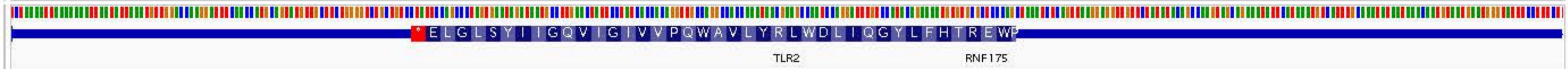
SL\_0004\_RN\_24\_WES\_uniq\_mut.ba  
coverage



SL\_0004\_RN\_24\_WES\_uniq\_mut.ba

Sequence

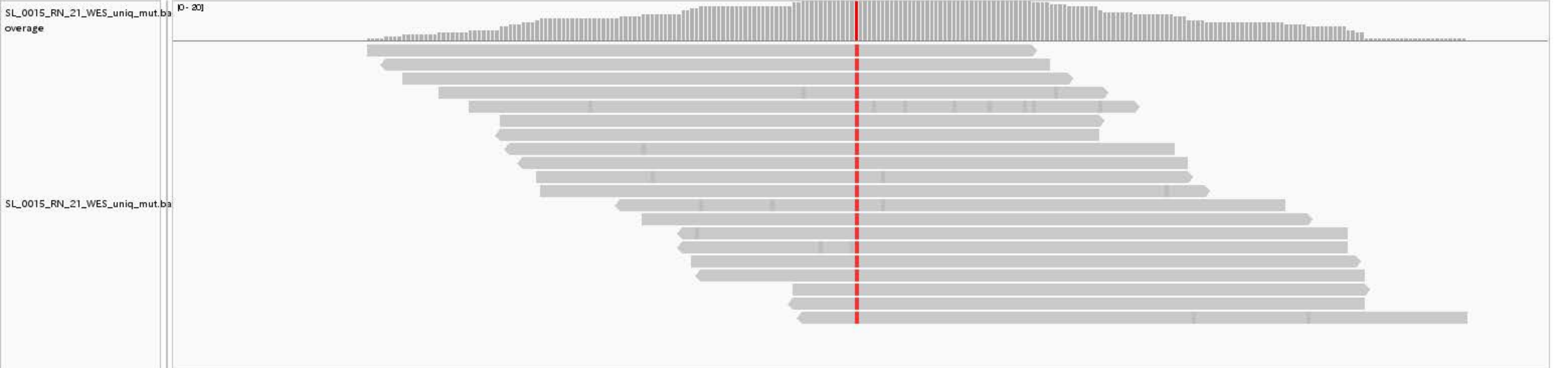
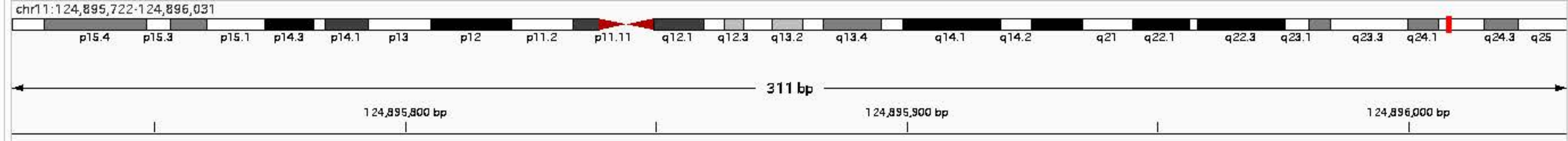
Refseq Genes

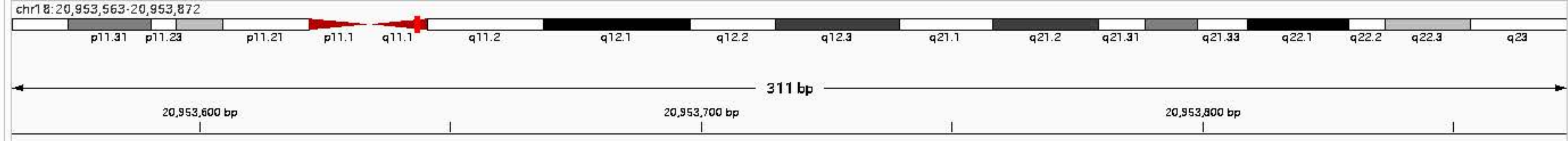


TLR2

RNF175







SL\_0001\_LN\_10\_WES\_uniq\_mut. coverage



SL\_0001\_LN\_10\_WES\_uniq\_mut. coverage

Sequence

Refseq Genes

