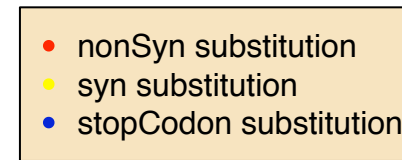
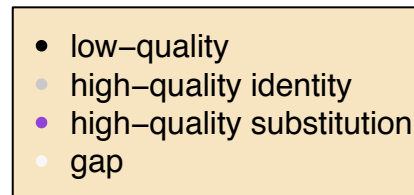
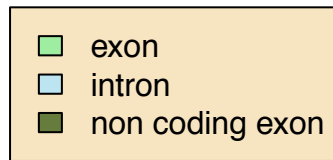
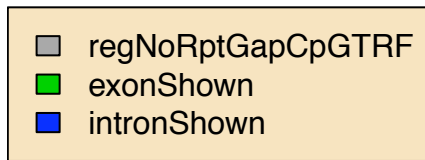
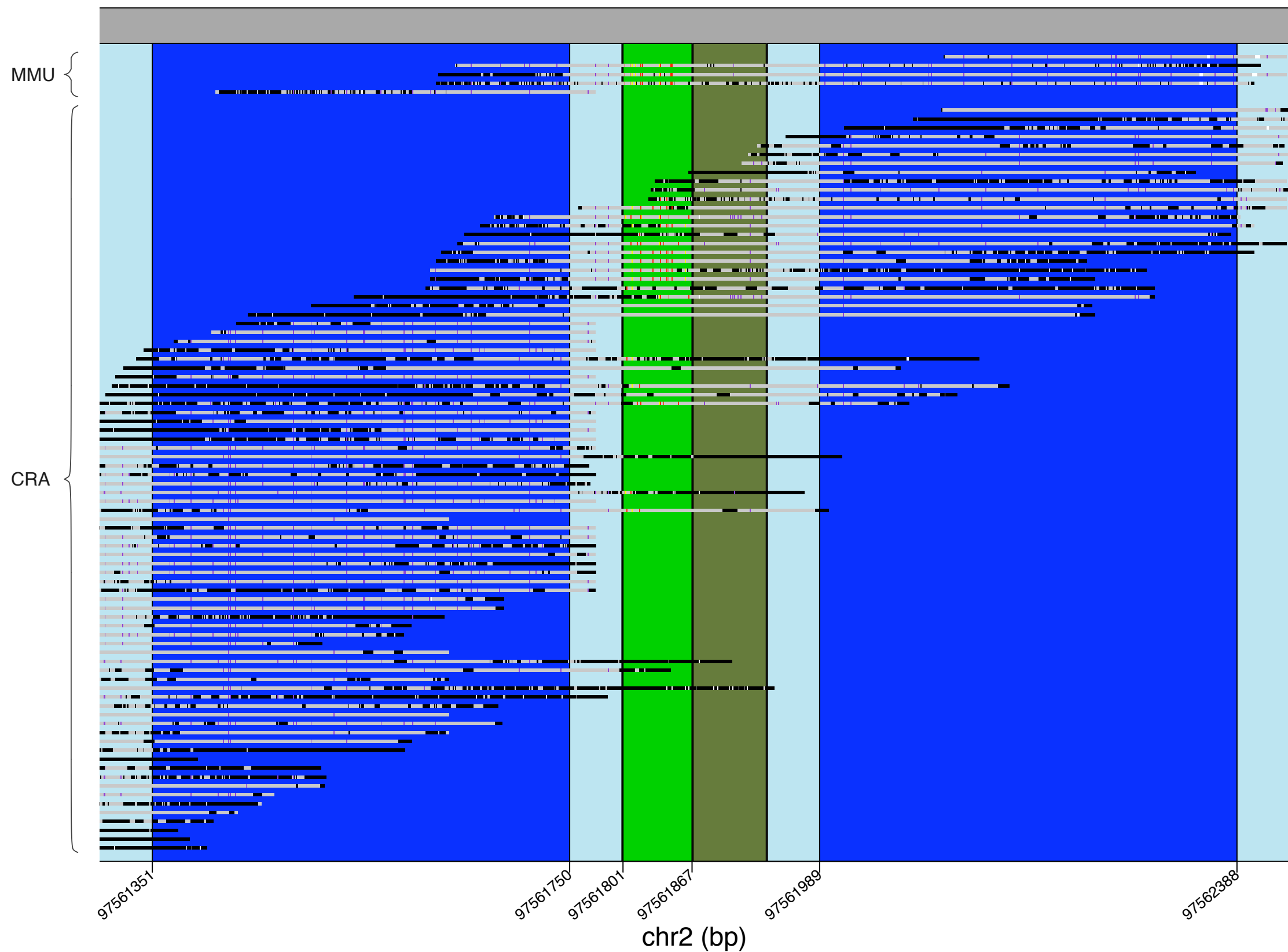


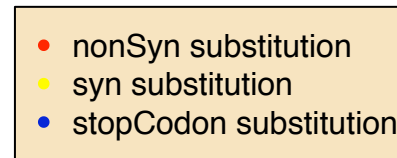
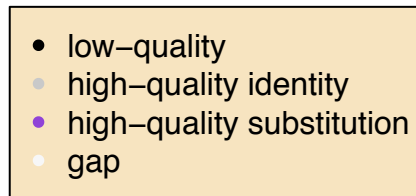
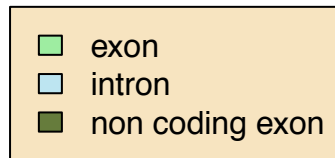
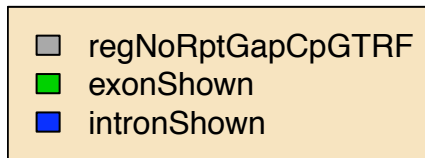
ANKRD36B_NM_025190_97487692-97572761_chr2_exon5



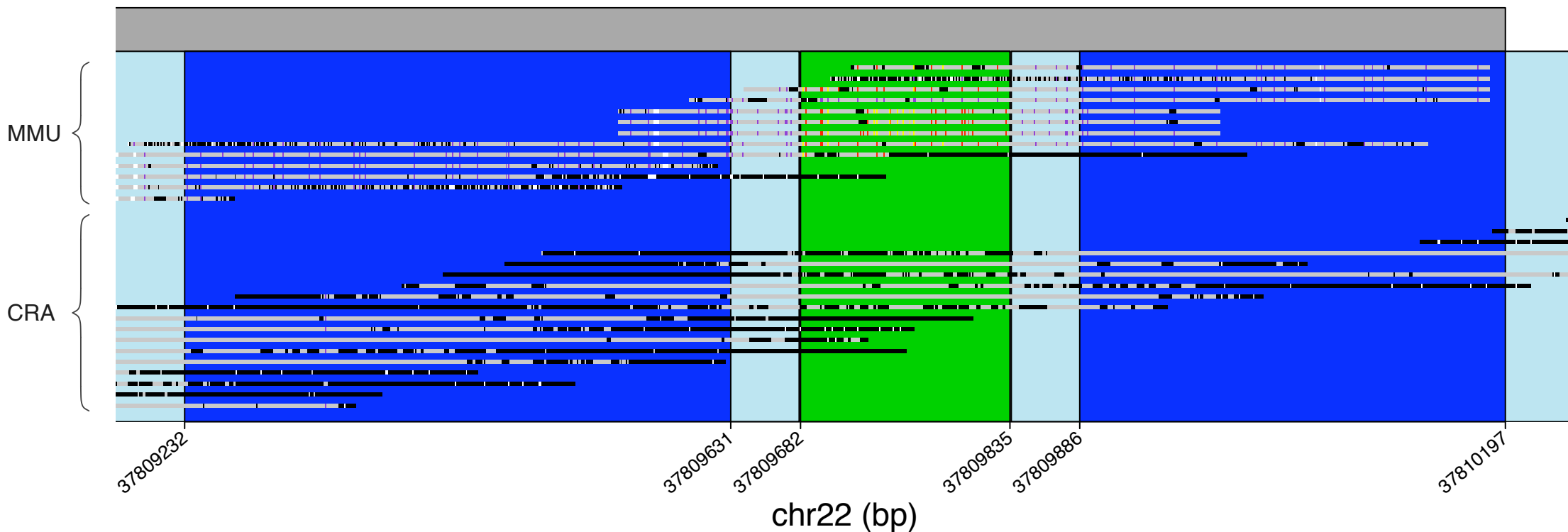
ANKRD36B(NM_025190)



APOBEC3G_NM_021822_37802970-37813693_chr22_exon5



APOBEC3G(NM_021822)



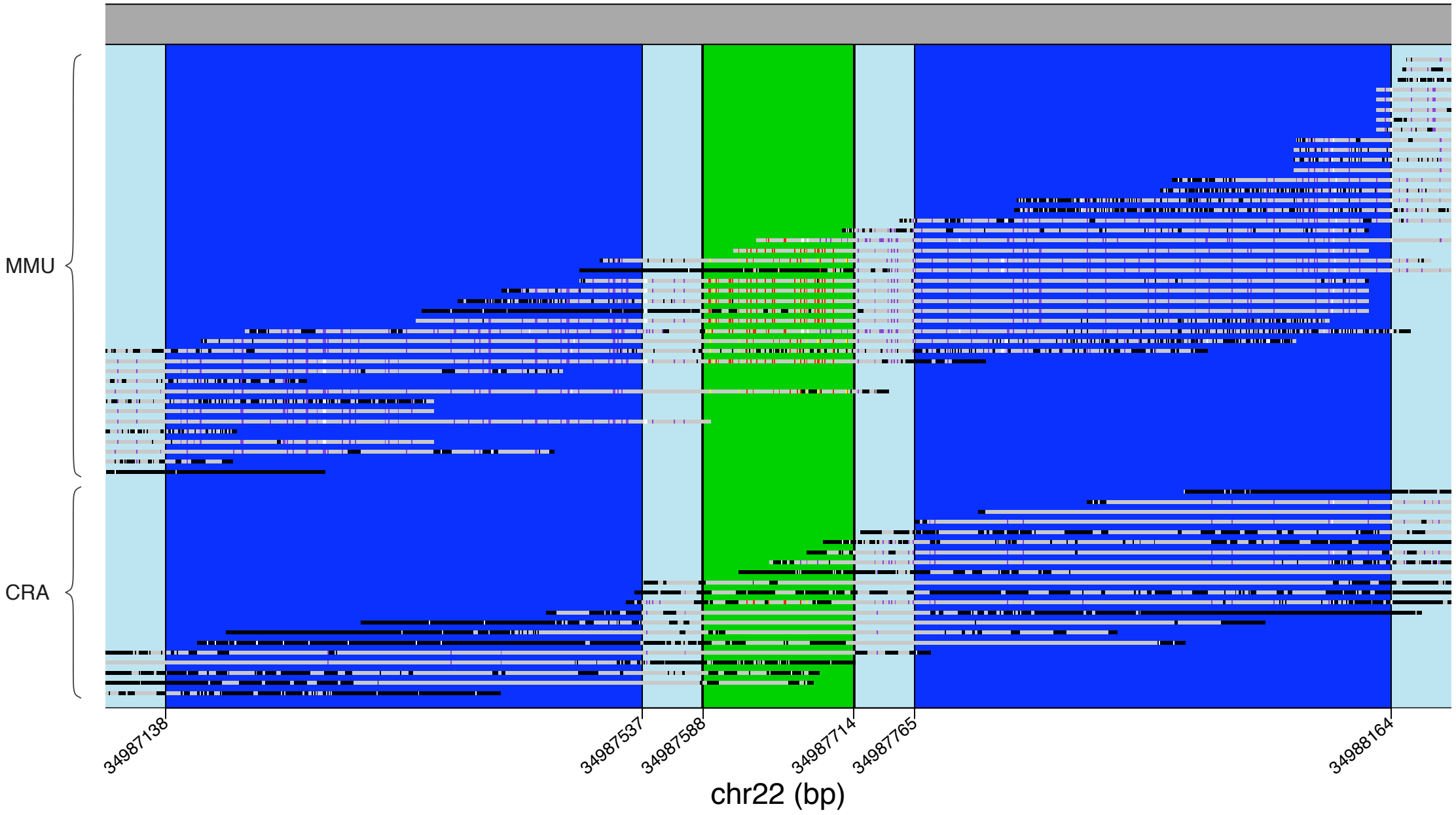
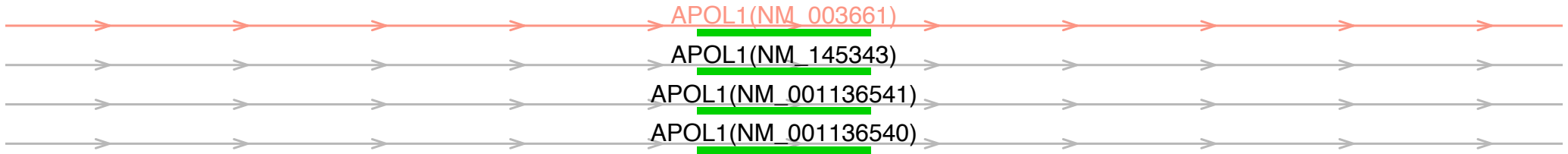
APOL1_NM_003661_34979062-34993522_chr22_exon5

- regNoRptGapCpGTRF
- exonShown
- intronShown

- exon
- intron
- non coding exon

- low-quality
- high-quality identity
- high-quality substitution
- gap

- nonSyn substitution
- syn substitution
- stopCodon substitution



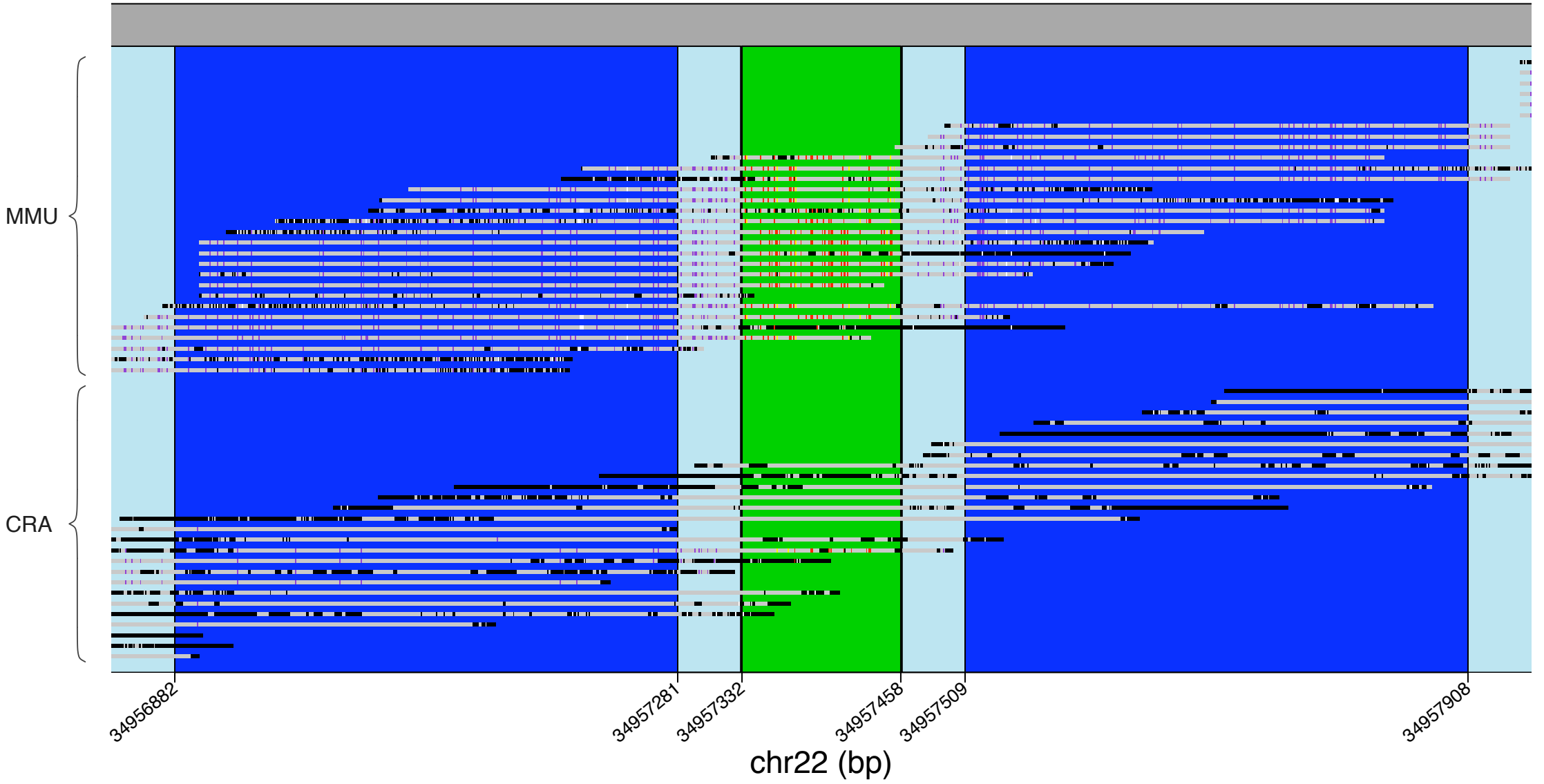
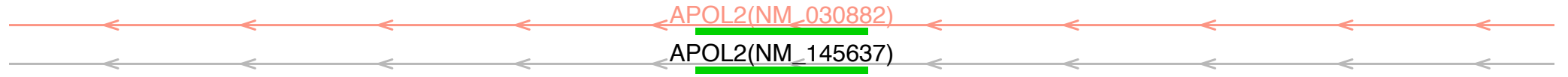
APOL2_NM_030882_34952200-34965635_chr22_exon4

- regNoRptGapCpGTRF
- exonShown
- intronShown

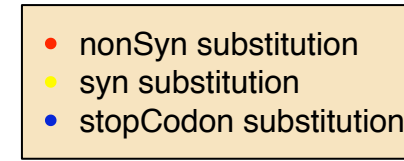
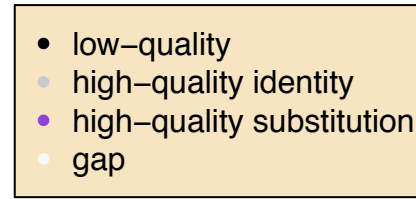
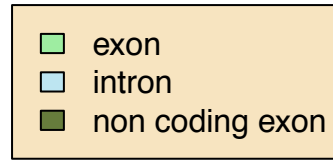
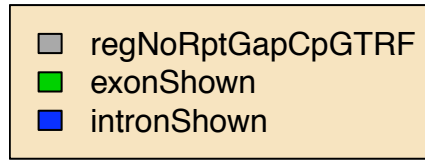
- exon
- intron
- non coding exon

- low-quality
- high-quality identity
- high-quality substitution
- gap

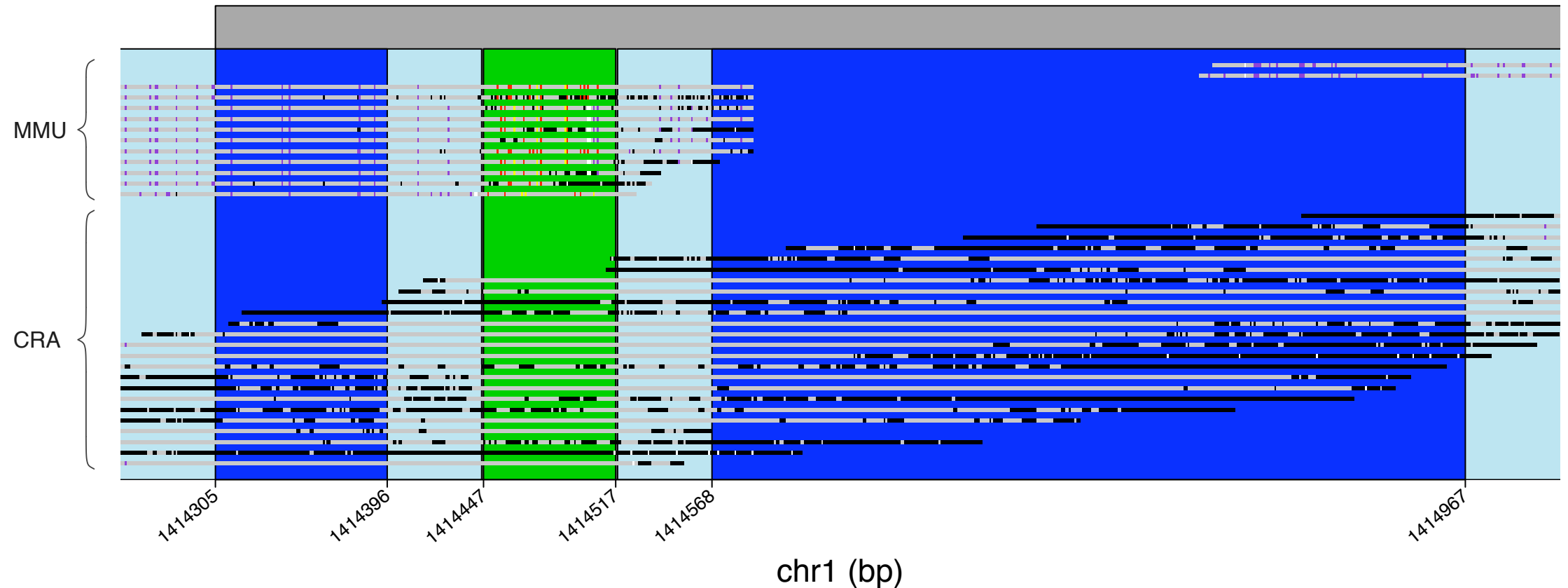
- nonSyn substitution
- syn substitution
- stopCodon substitution



ATAD3B_NM_031921_1397026-1421445_chr1_exon13



ATAD3B(NM_031921)



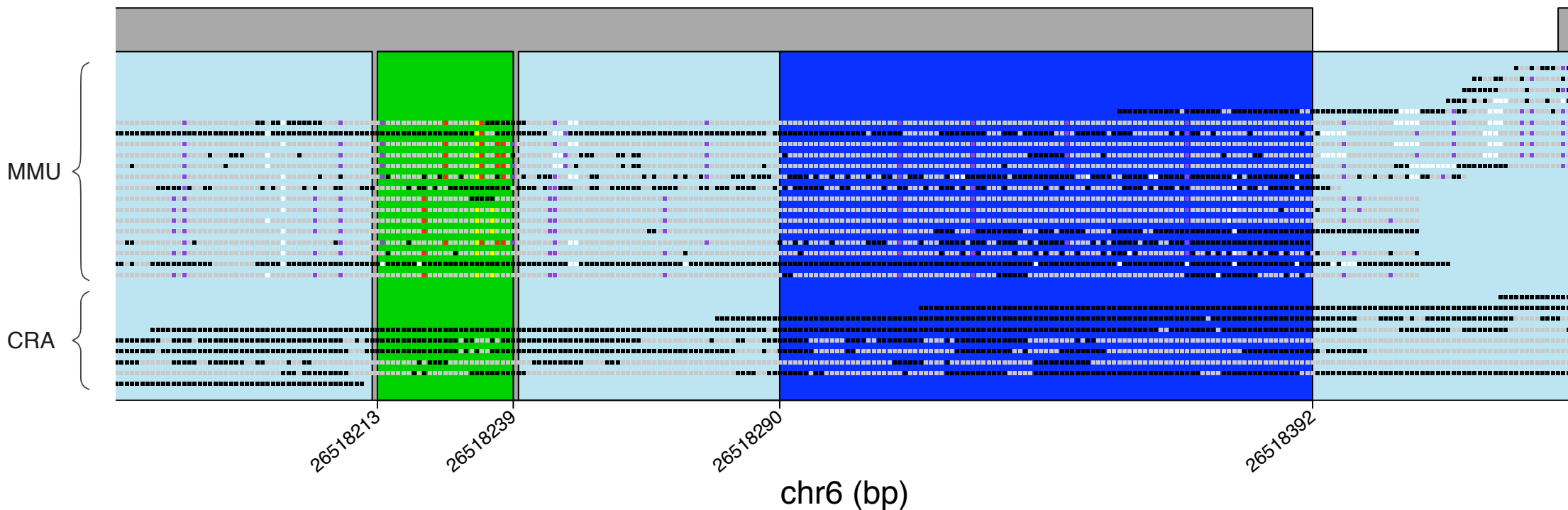
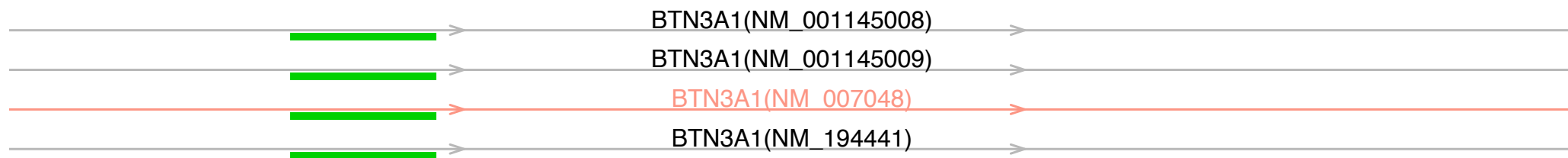
BTN3A1_NM_007048_26510443-26523421_chr6_exon7

- regNoRptGapCpGTRF
- exonShown
- intronShown

- exon
- intron
- non coding exon

- low-quality
- high-quality identity
- high-quality substitution
- gap

- nonSyn substitution
- syn substitution
- stopCodon substitution



BTNL3_NM_197975_180348506-180366333_chr5_exon8

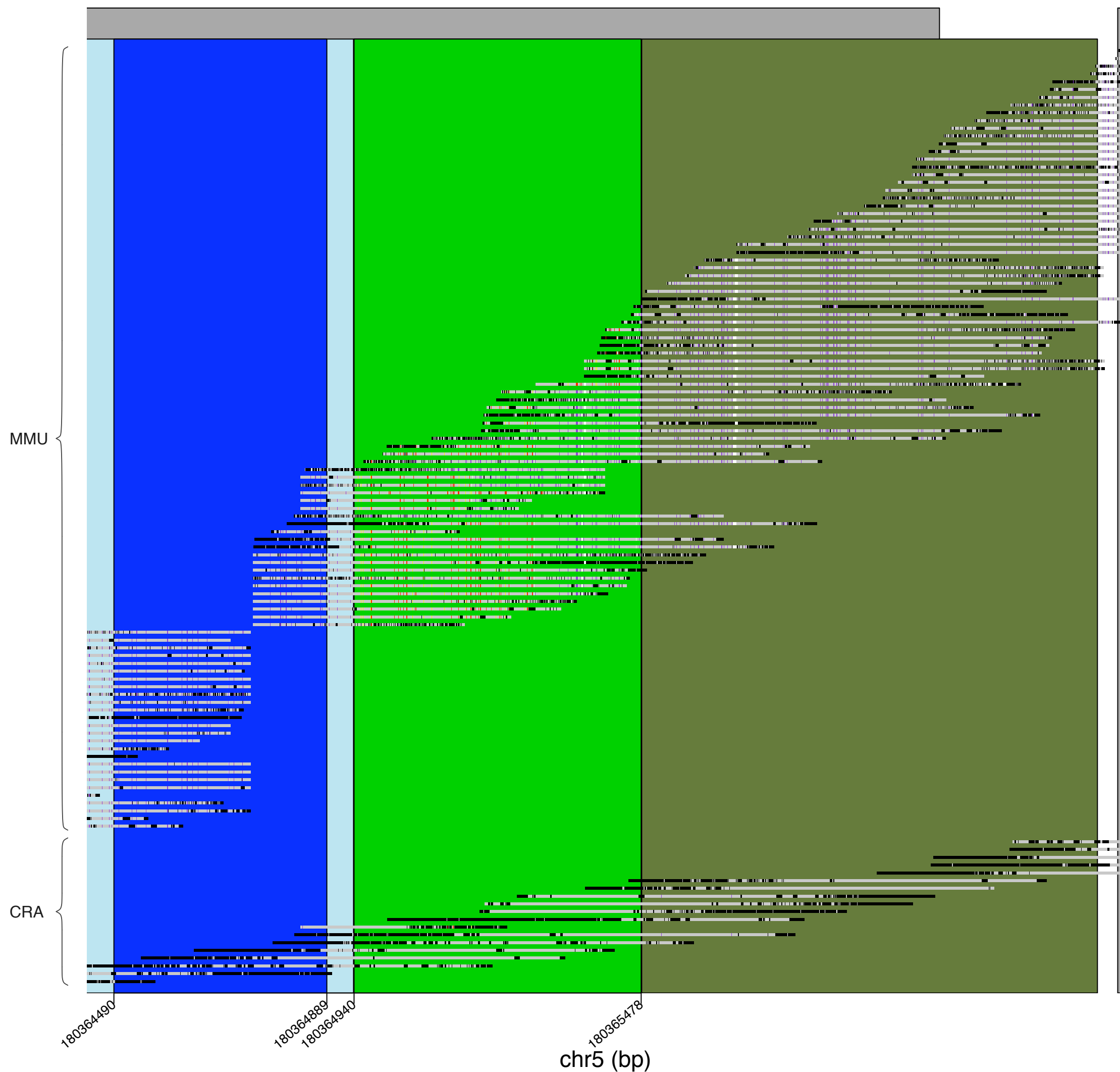
- regNoRptGapCpGTRF
- exonShown
- intronShown

- exon
- intron
- non coding exon

- low-quality
- high-quality identity
- high-quality substitution
- gap

- nonSyn substitution
- syn substitution
- stopCodon substitution

BTNL3(NM_197975)



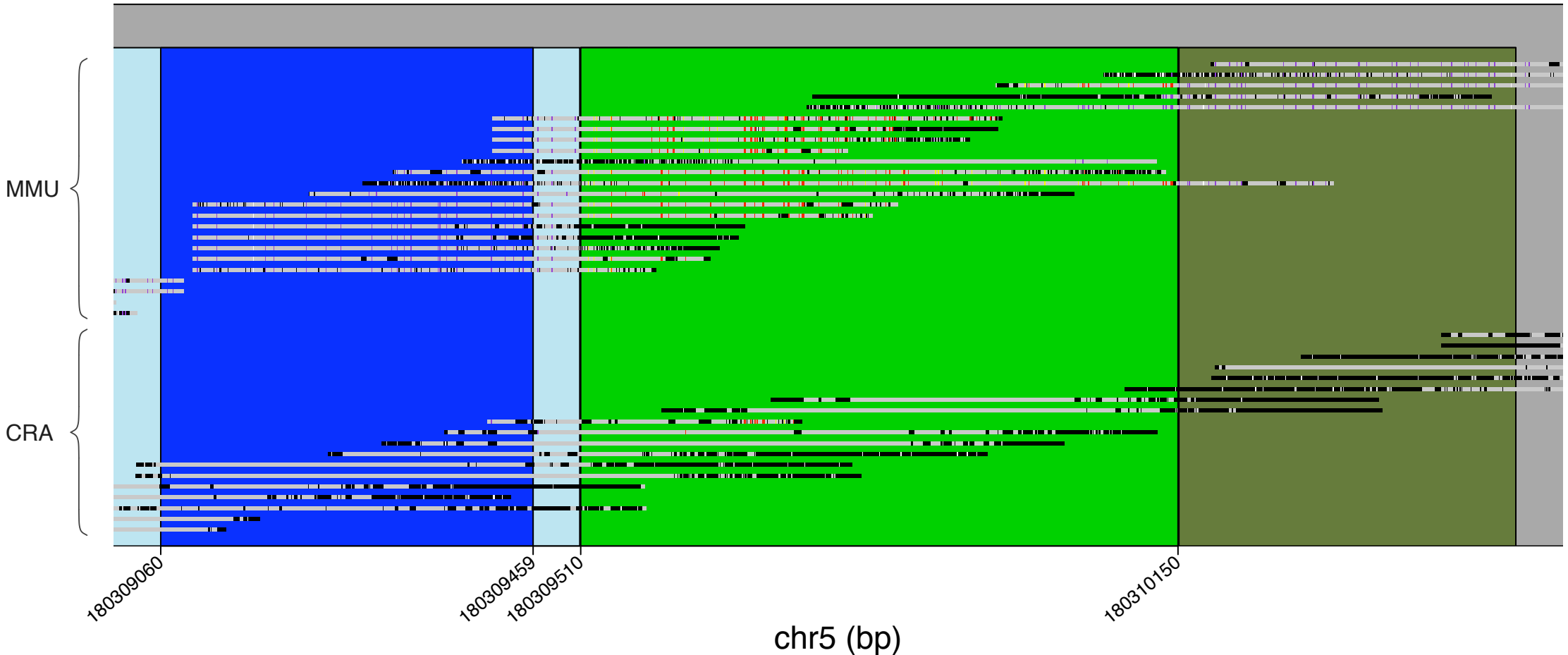
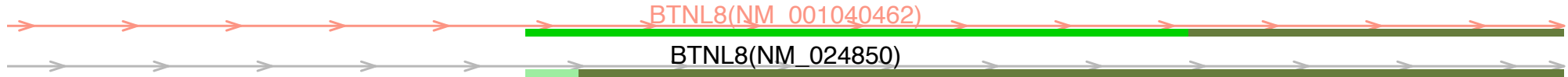
BTNL8_NM_001040462_180258734-180310512_chr5_exon8

- regNoRptGapCpGTRF
- exonShown
- intronShown

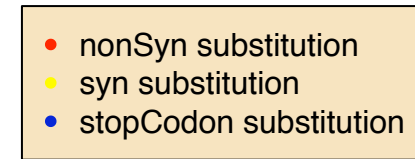
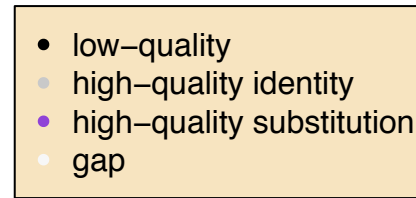
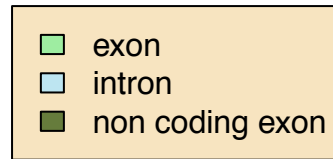
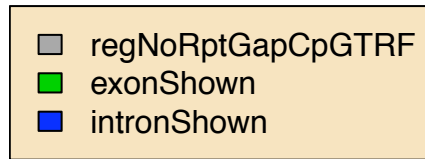
- exon
- intron
- non coding exon

- low-quality
- high-quality identity
- high-quality substitution
- gap

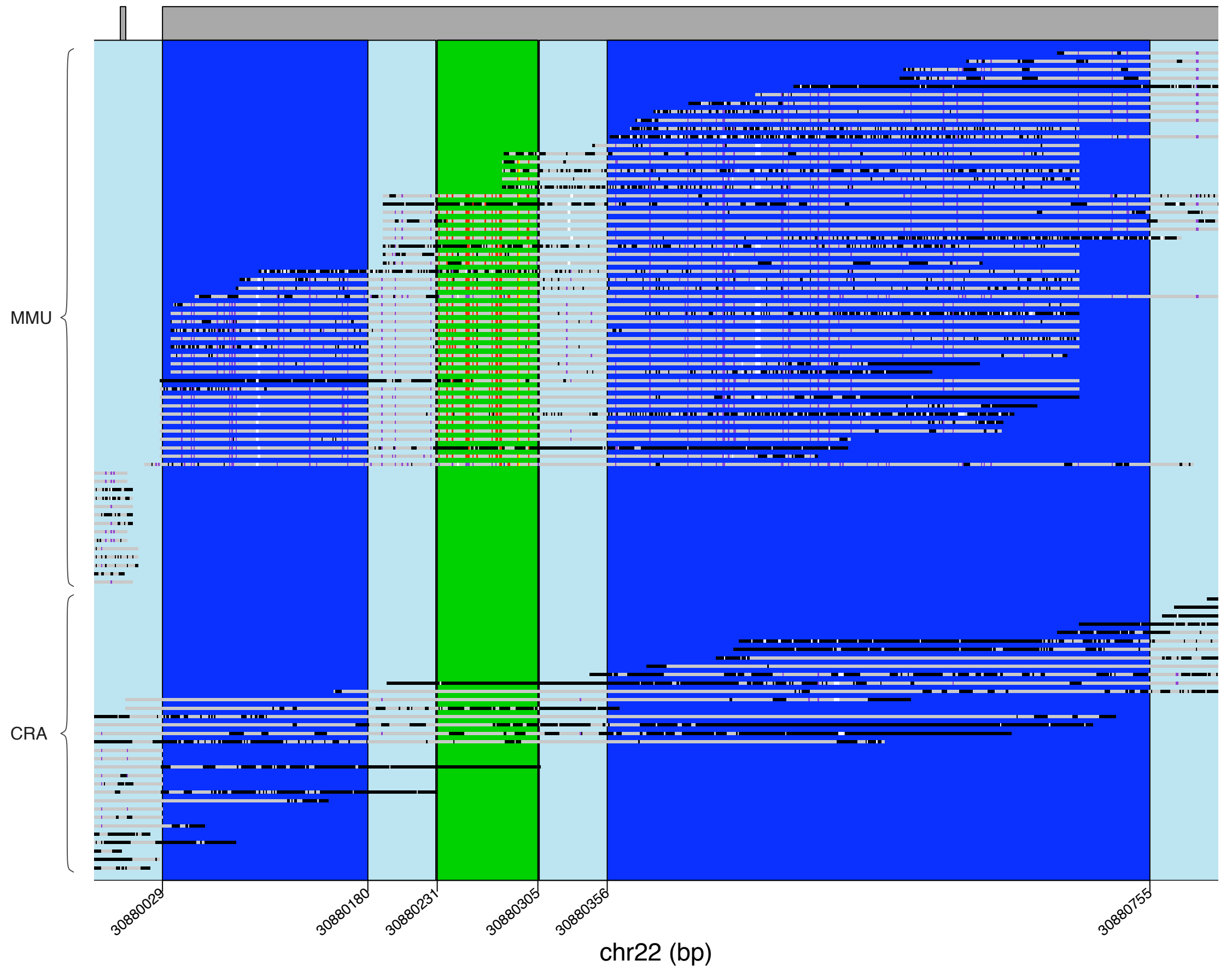
- nonSyn substitution
- syn substitution
- stopCodon substitution



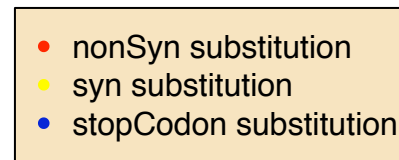
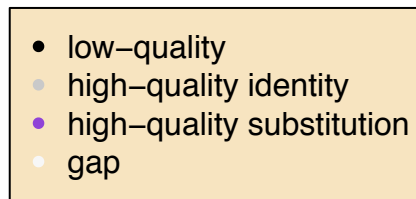
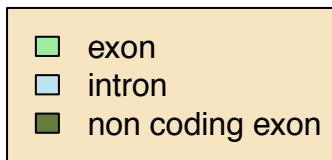
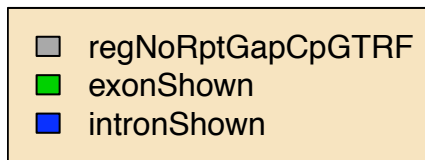
C22orf42_NM_001010859_30875518-30885243_chr22_exon2



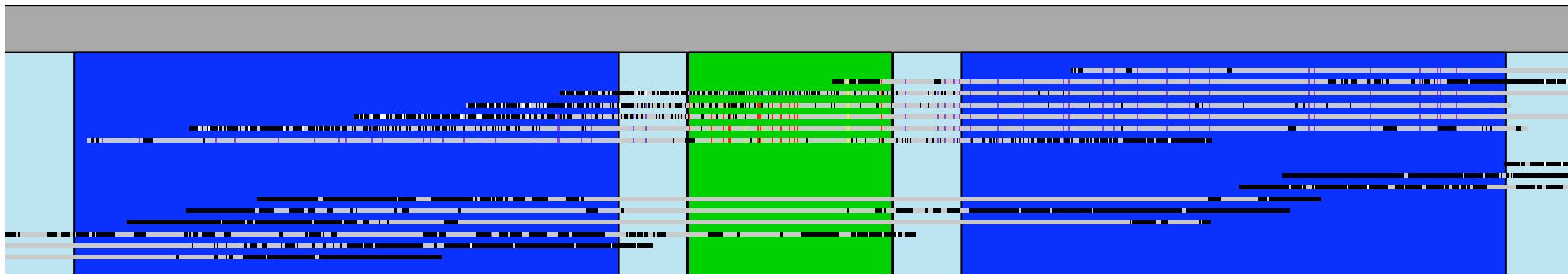
C22orf42(NM_001010859)



CAPN13_NM_144575_30799141-30883815_chr2_exon11



CAPN13(NM_144575)



30827022

30827421

30827472

30827621

30827672

30828071

chr2 (bp)

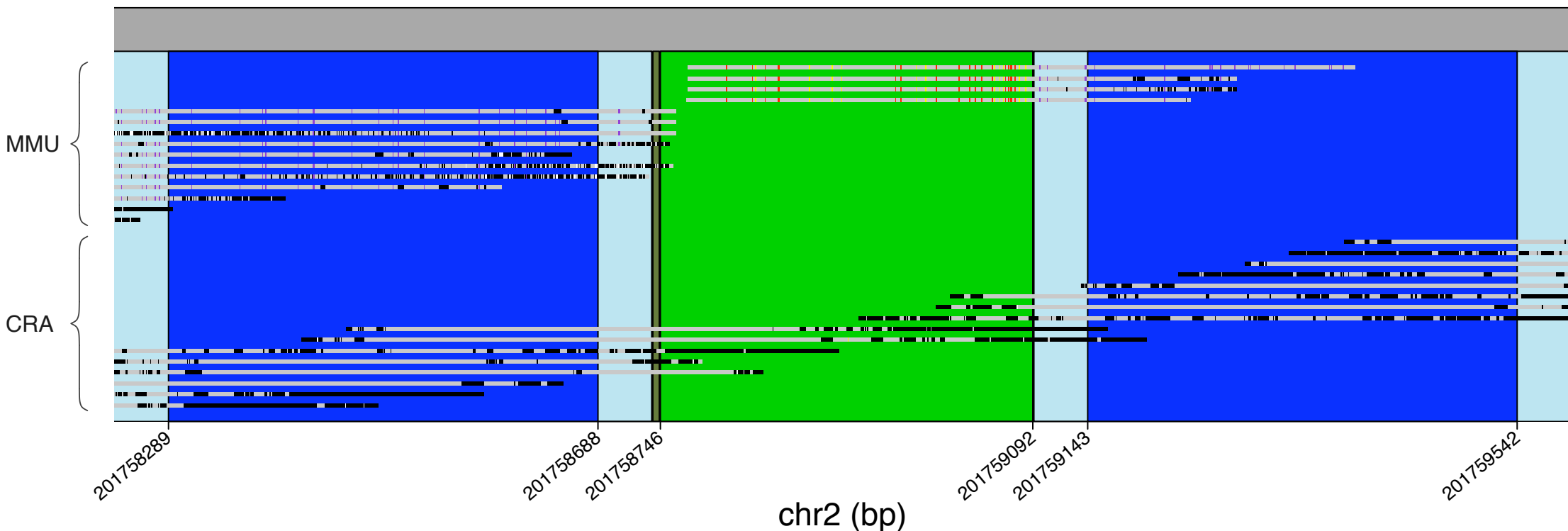
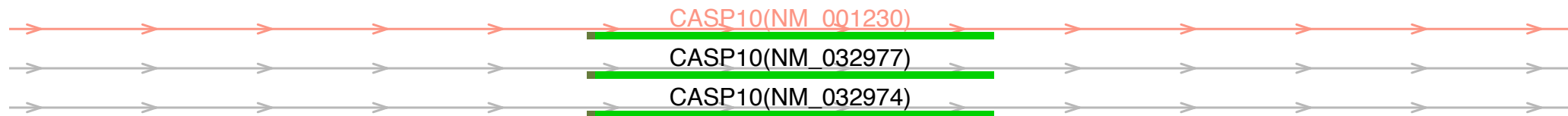
CASP10_NM_001230_201755865–201794628_chr2_exon2

- regNoRptGapCpGTRF
- exonShown
- intronShown

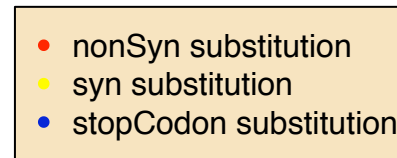
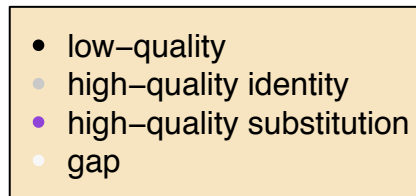
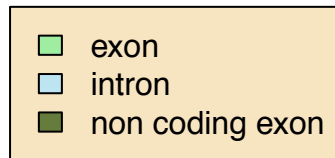
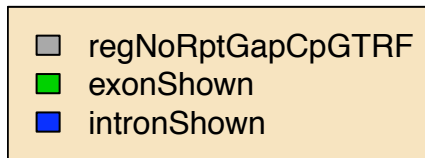
- exon
- intron
- non coding exon

- low-quality
- high-quality identity
- high-quality substitution
- gap

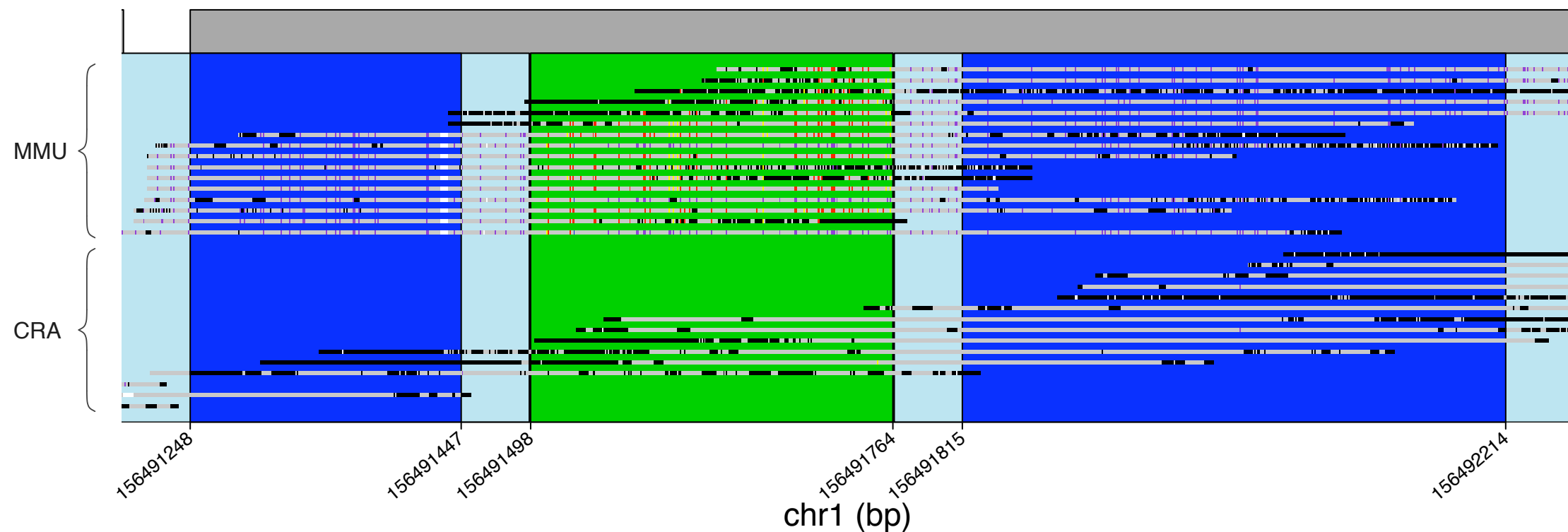
- nonSyn substitution
- syn substitution
- stopCodon substitution



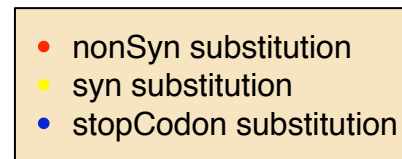
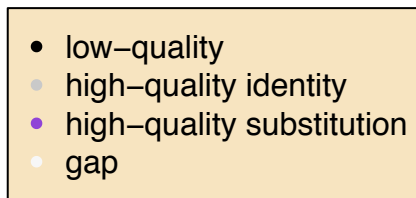
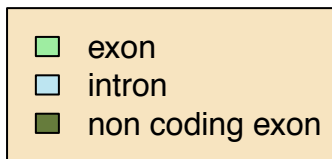
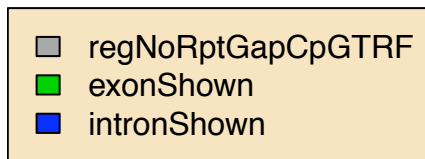
CD1A_NM_001763_156490550-156494682_chr1_exon2



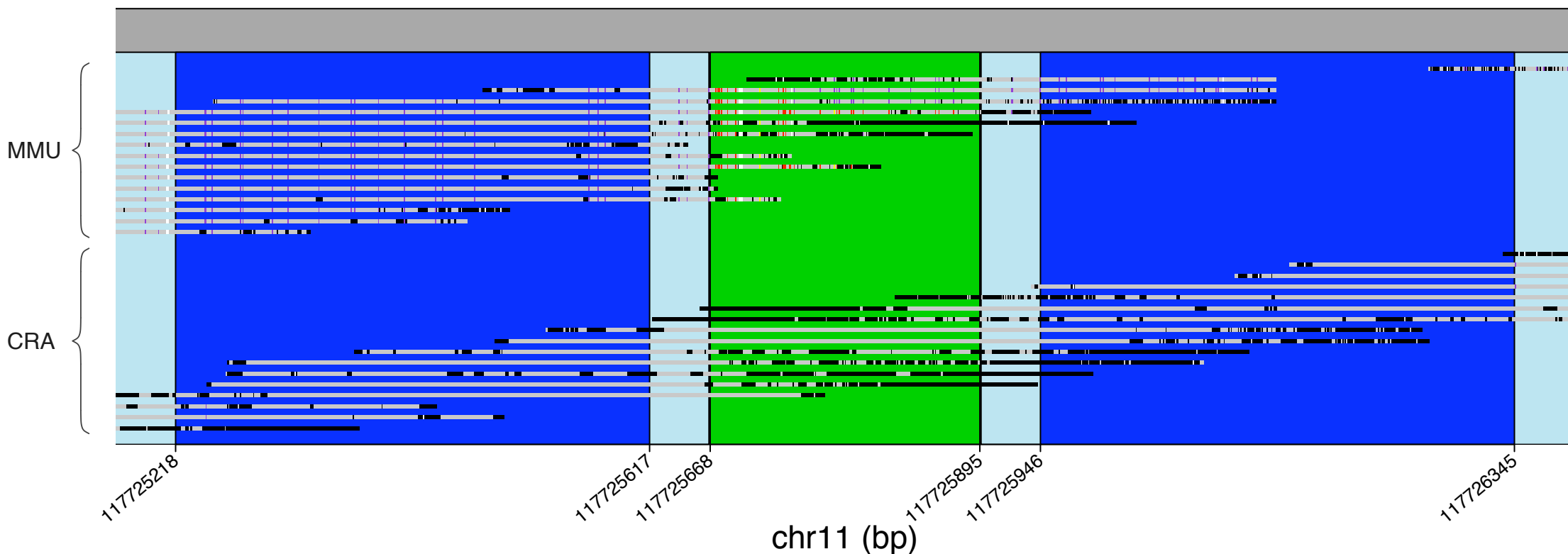
CD1A(NM_001763)



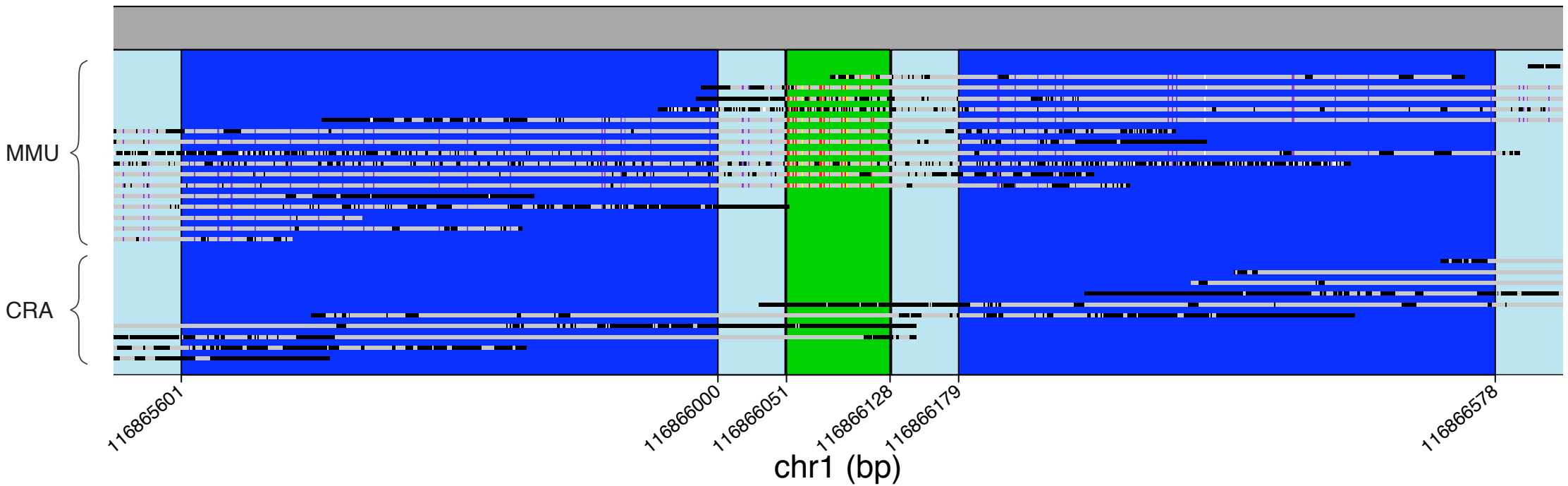
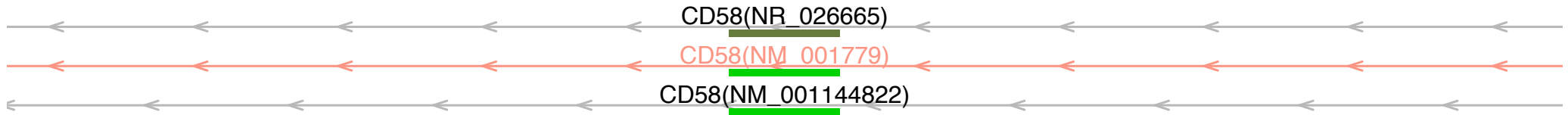
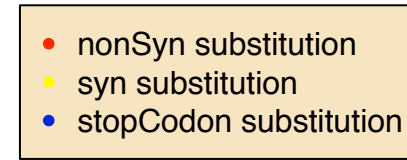
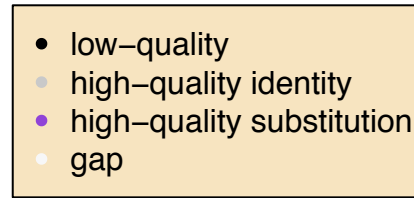
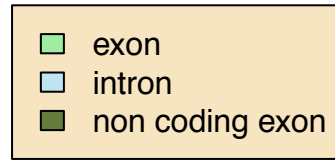
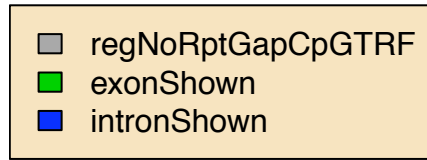
CD3G_NM_000073_117720268-117729707_chr11_exon3



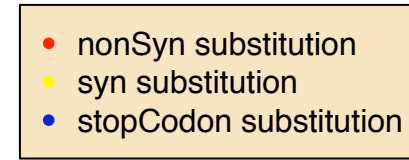
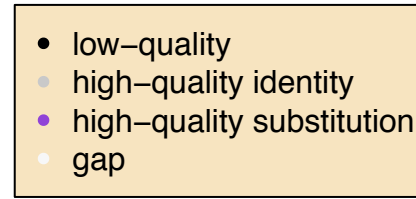
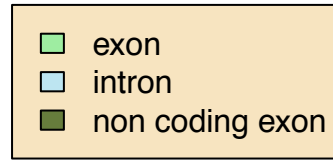
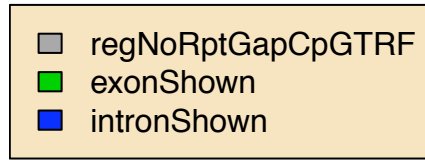
CD3G(NM_000073)



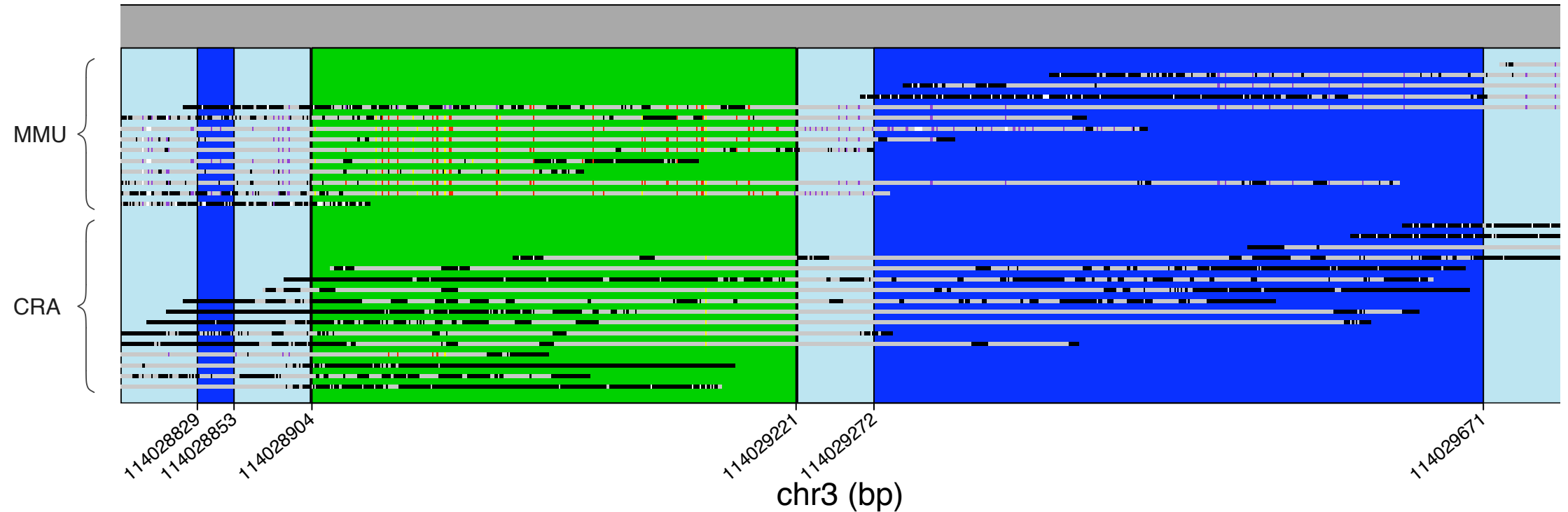
CD58_NM_001779_116858679-116915238_chr1_exon4



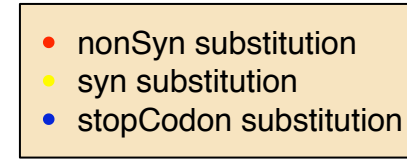
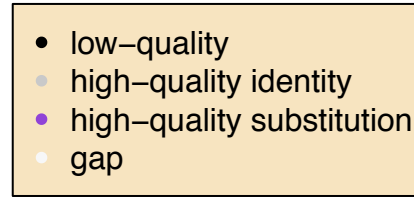
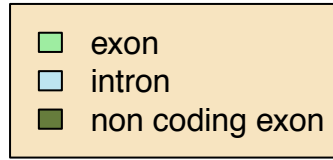
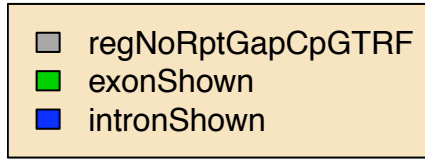
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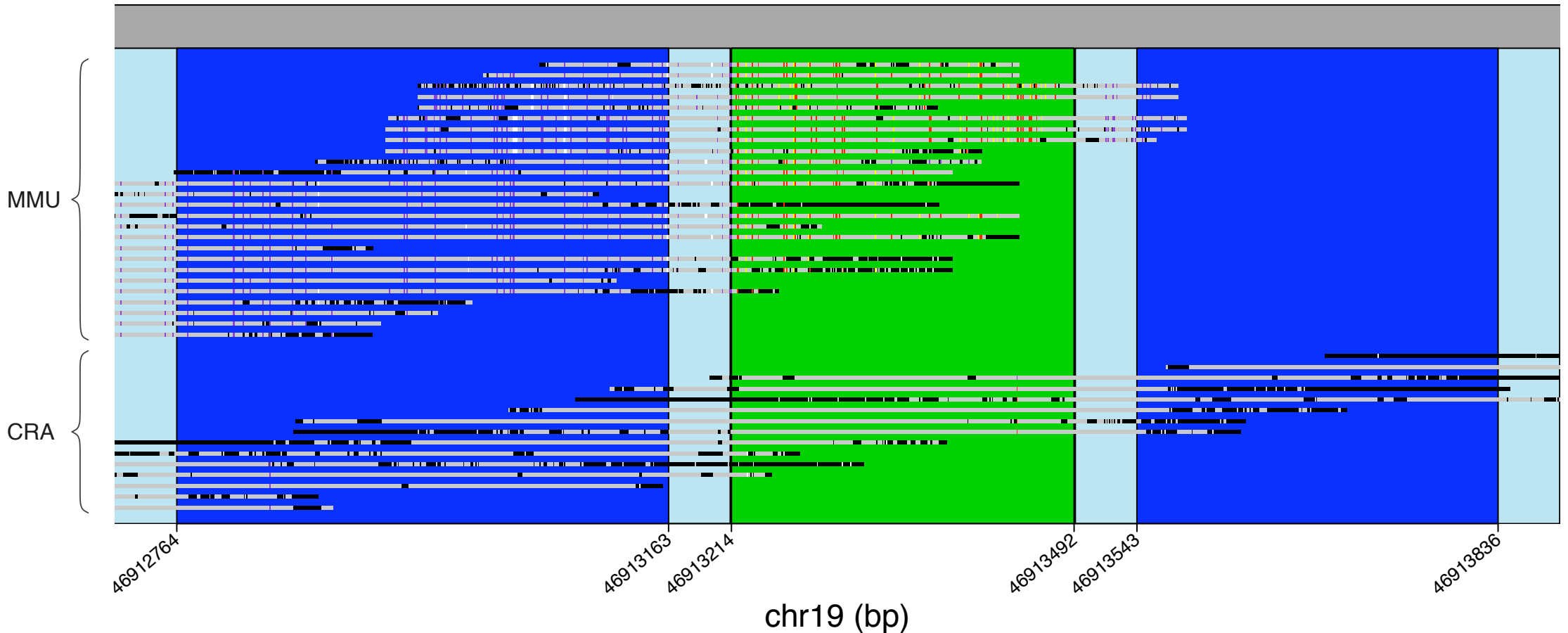
CD200R1L(NM_001008784)



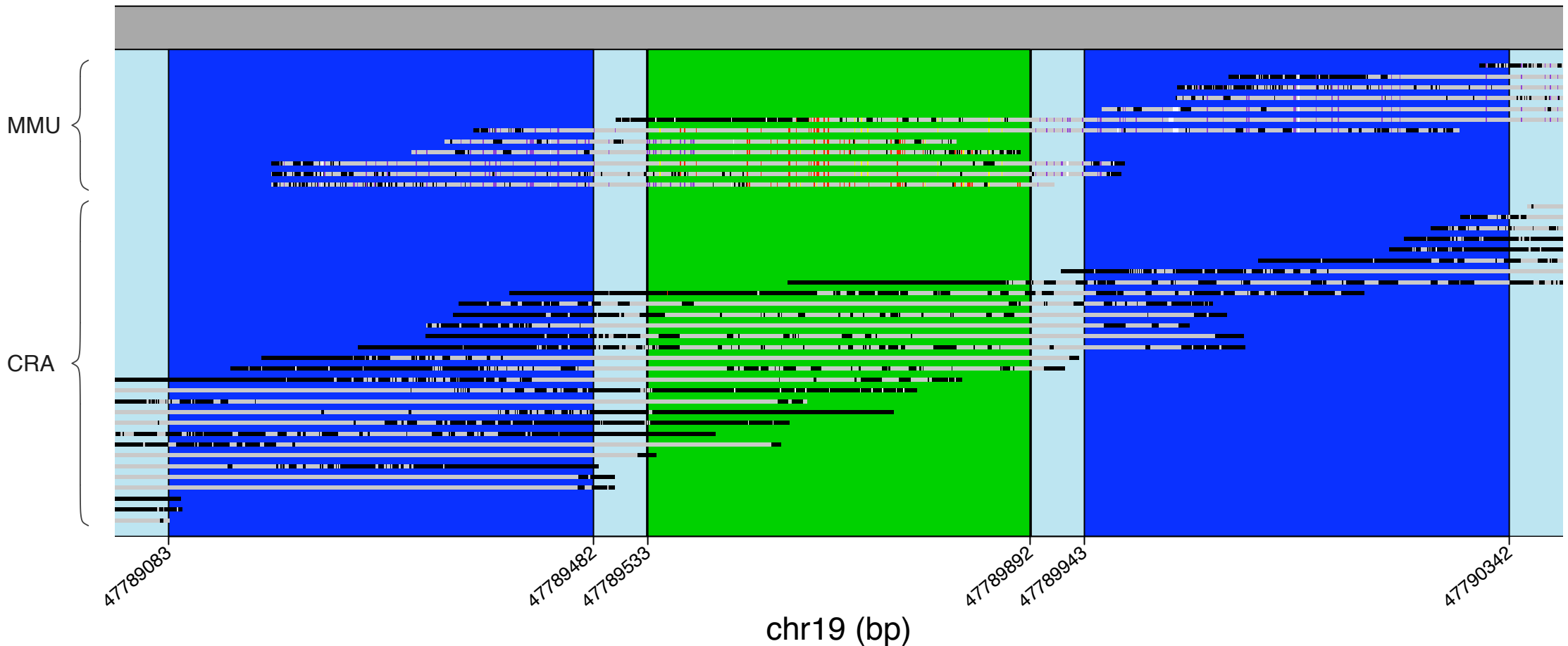
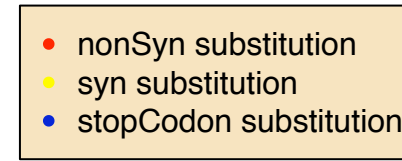
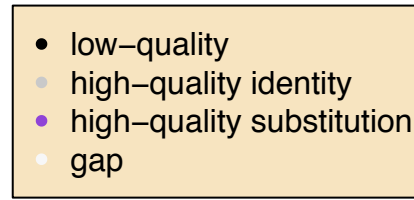
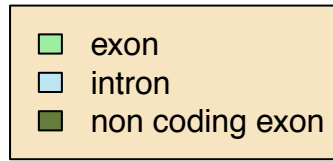
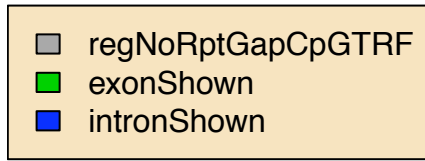
CEACAM5_NM_004363_46904369-46926277_chr19_exon5



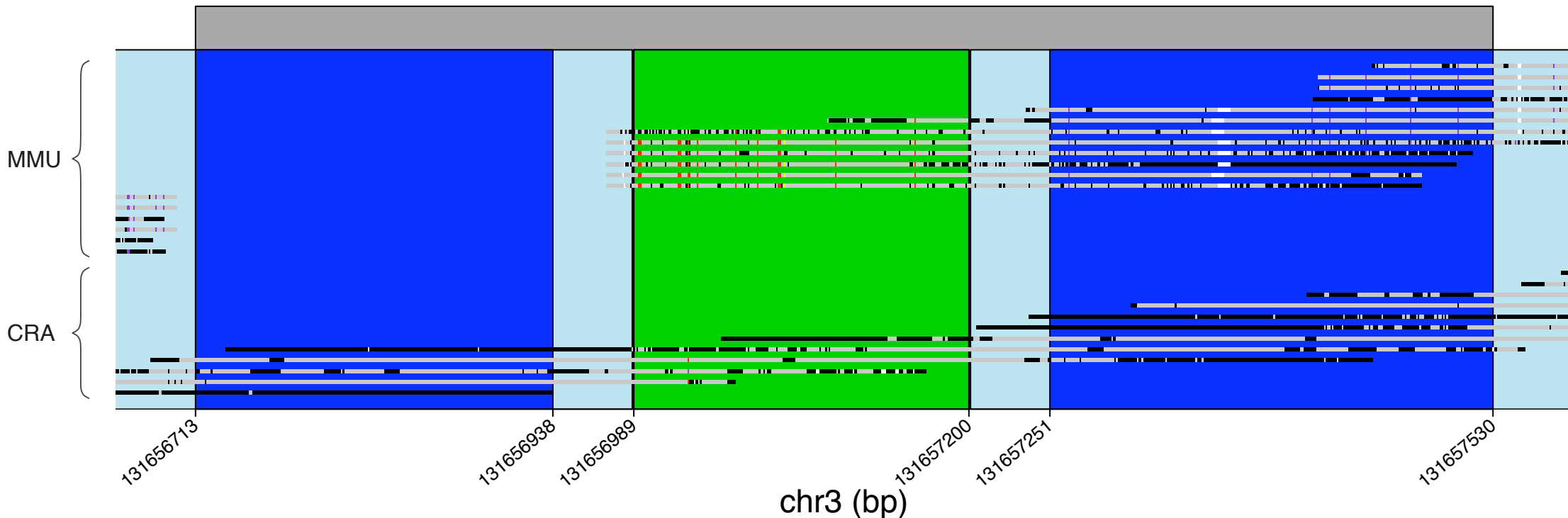
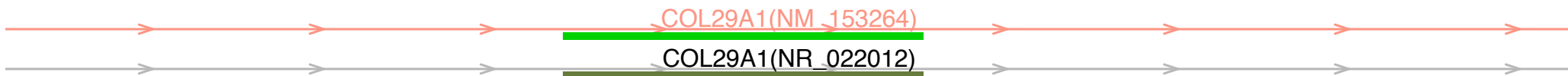
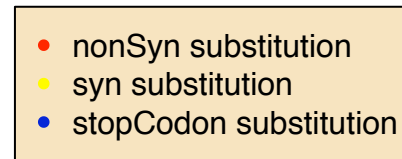
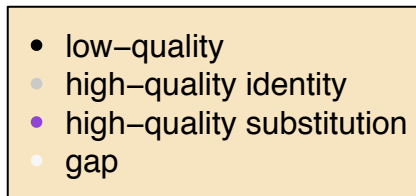
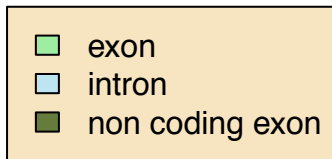
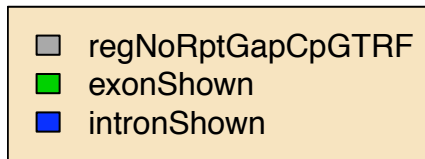
CEACAM5(NM_004363)



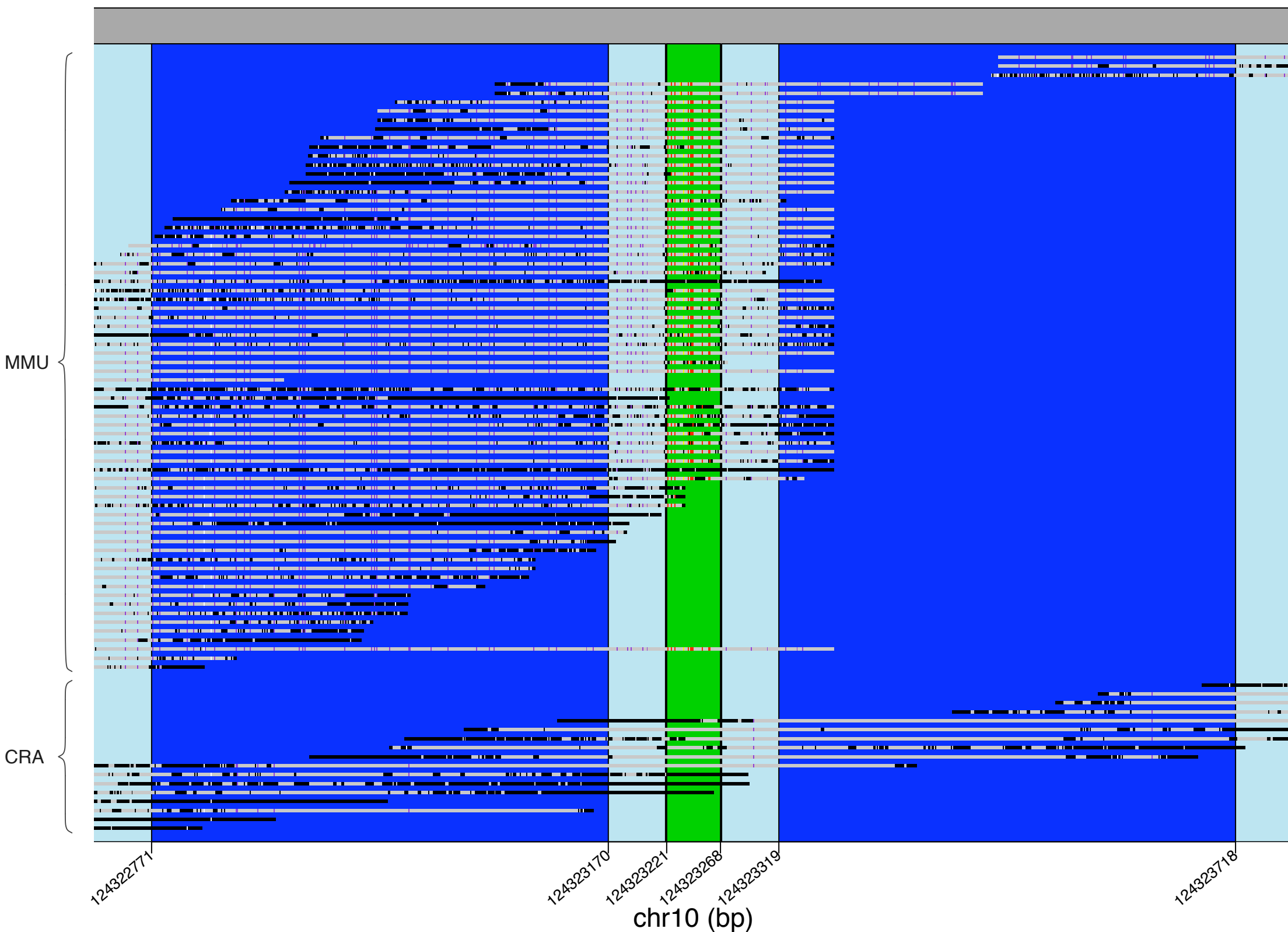
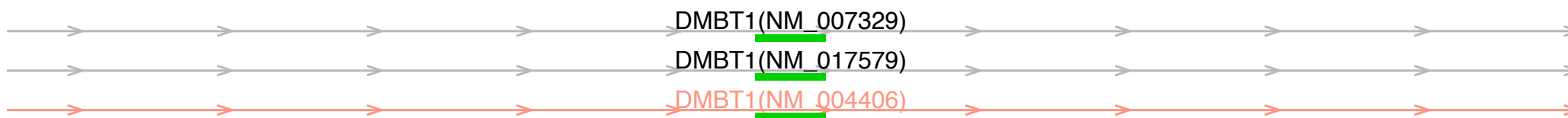
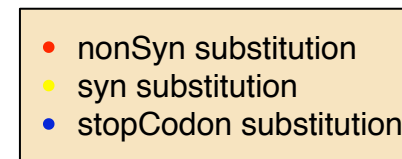
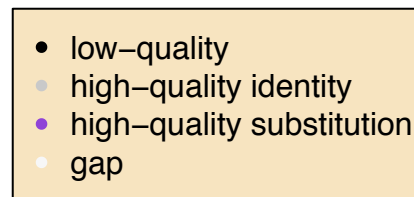
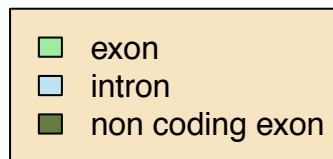
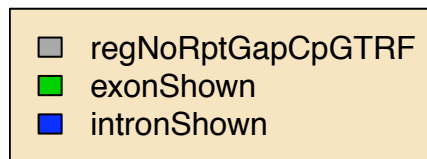
CEACAM8_NM_001816_47776234-47790922_chr19_exon2



COL29A1_NM_153264_131547048-131686378_chr3_exon37



DMBT1_NM_004406_124310170-124393242_chr10_exon6



FAM153B_NM_001079529_175444514-175476063_chr5_exon3

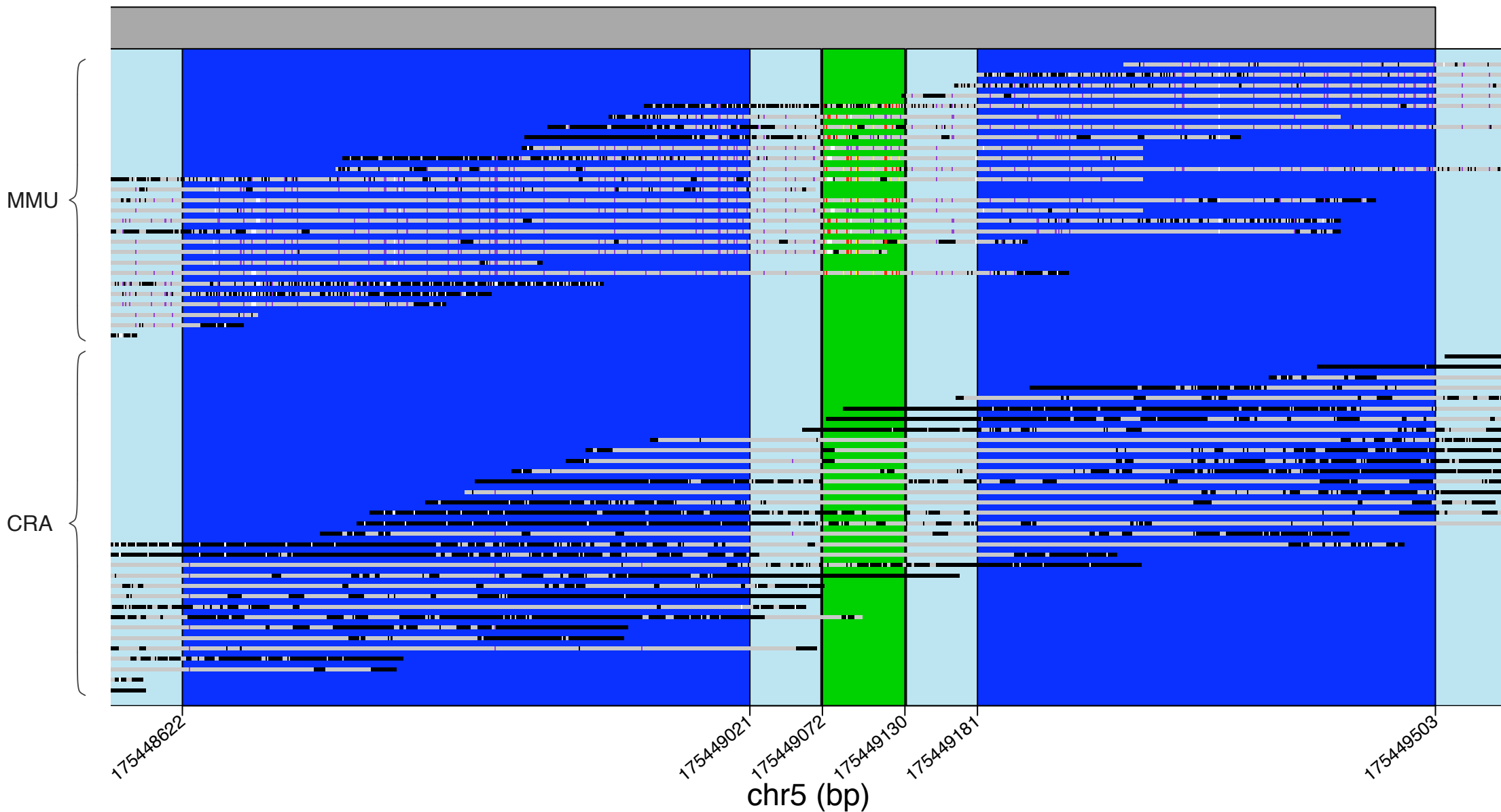
- regNoRptGapCpGTRF
- exonShown
- intronShown

- exon
- intron
- non coding exon

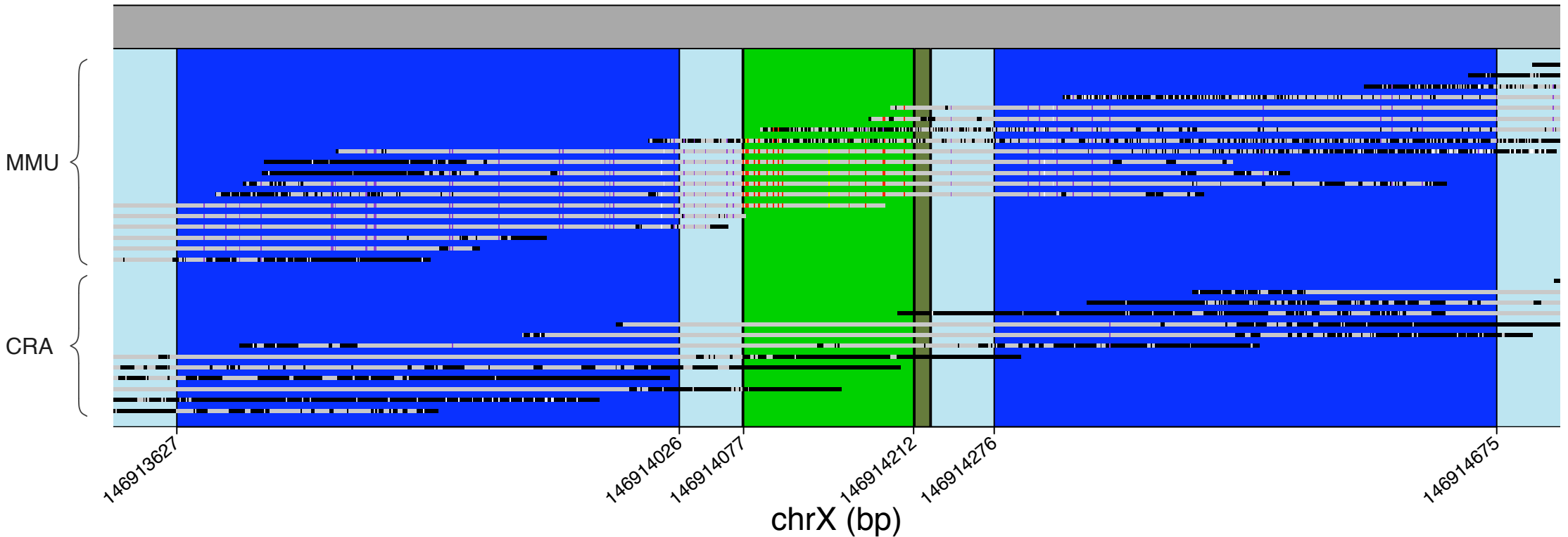
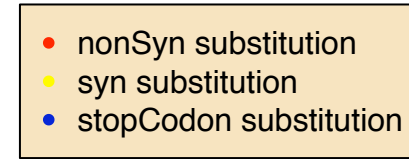
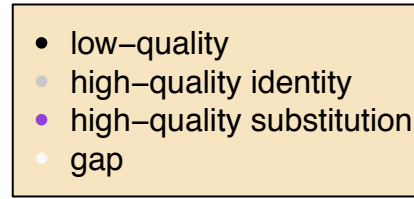
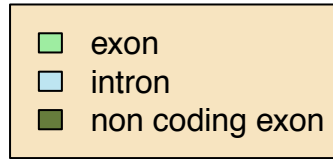
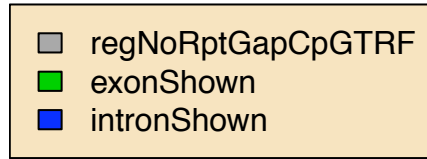
- low-quality
- high-quality identity
- high-quality substitution
- gap

- nonSyn substitution
- syn substitution
- stopCodon substitution

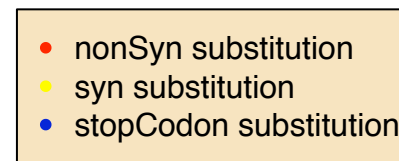
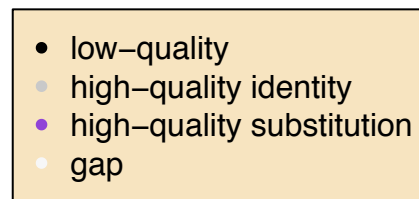
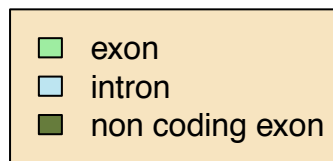
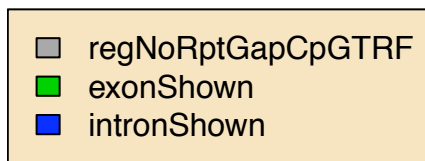
FAM153B(NM_001079529)



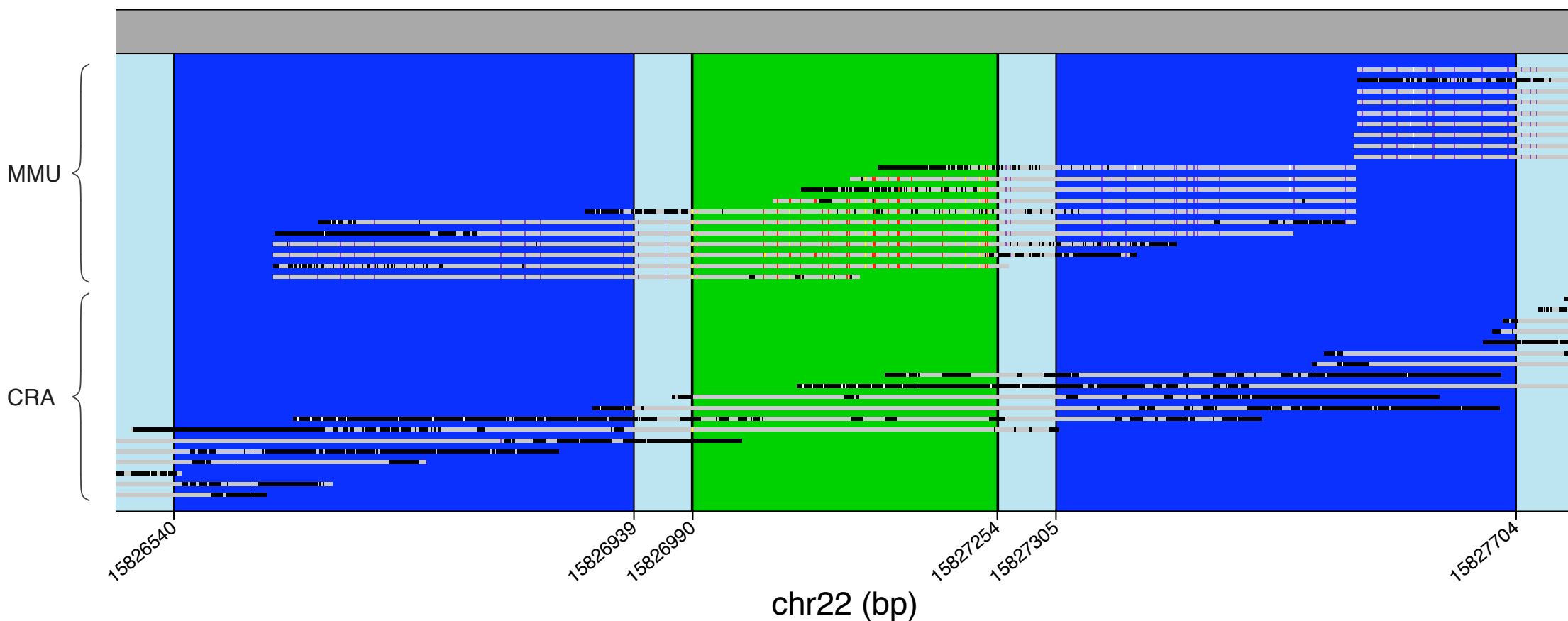
FMR1NB_NM_152578_146870540-146915876_chrX_exon5



GAB4_NM_001037814_15822826-15869112_chr22_exon6



GAB4(NM_001037814)



GOLGA6_NM_001038640_72149250-72161944_chr15_exon10

regNoRptGapCpGTRF
 exonShown
 intronShown

exon
 intron
 non coding exon

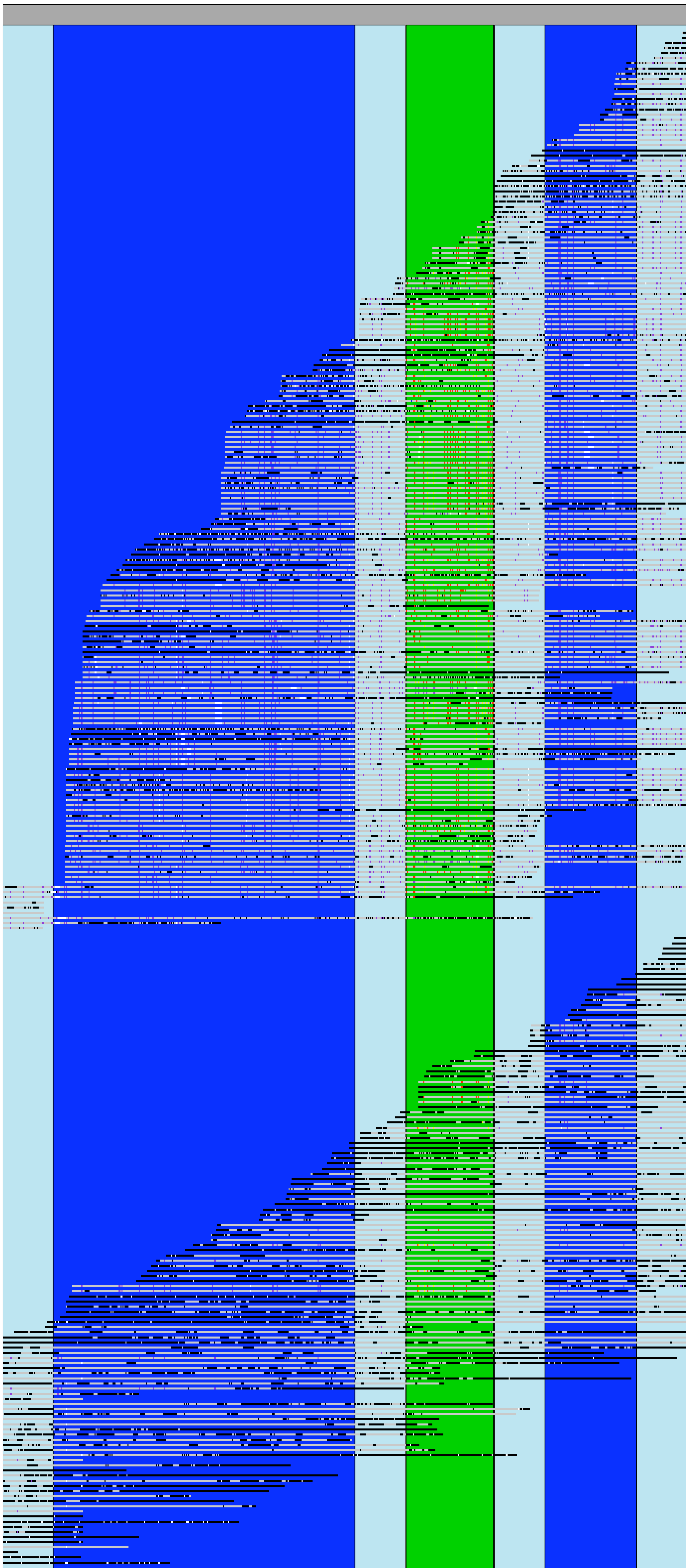
low-quality
 high-quality identity
 high-quality substitution
 gap

nonSyn substitution
 syn substitution
 stopCodon substitution

GOLGA6(NM_001038640)

MMU

CRA



72154448

72154748

72154797

72154884

72154935

72155026

chr15 (bp)

GOLGA6B_NM_018652_70734091-70746791_chr15_exon10

- regNoRptGapCpGTRF
- exonShown
- intronShown

- exon
- intron
- non coding exon

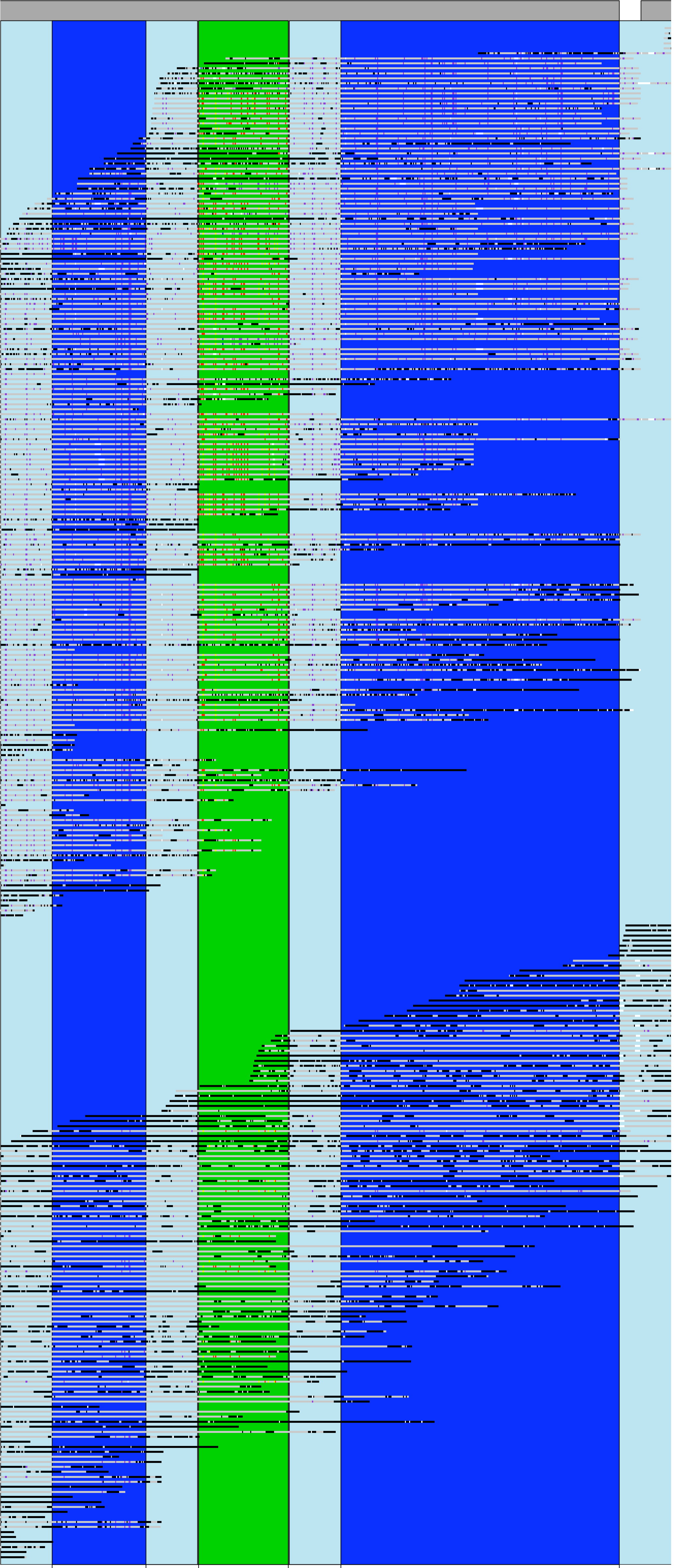
- low-quality
- high-quality identity
- high-quality substitution
- gap

- nonSyn substitution
- syn substitution
- stopCodon substitution

GOLGA6B(NM_018652)

MMU

CRA



70741012 70741103 70741154 70741241 70741292 70741562

chr15 (bp)

GOLGA6D_NM_001145224_73362234-73375199_chr15_exon10

regNoRptGapCpGTRF
exonShown
intronShown

exon
intron
non coding exon

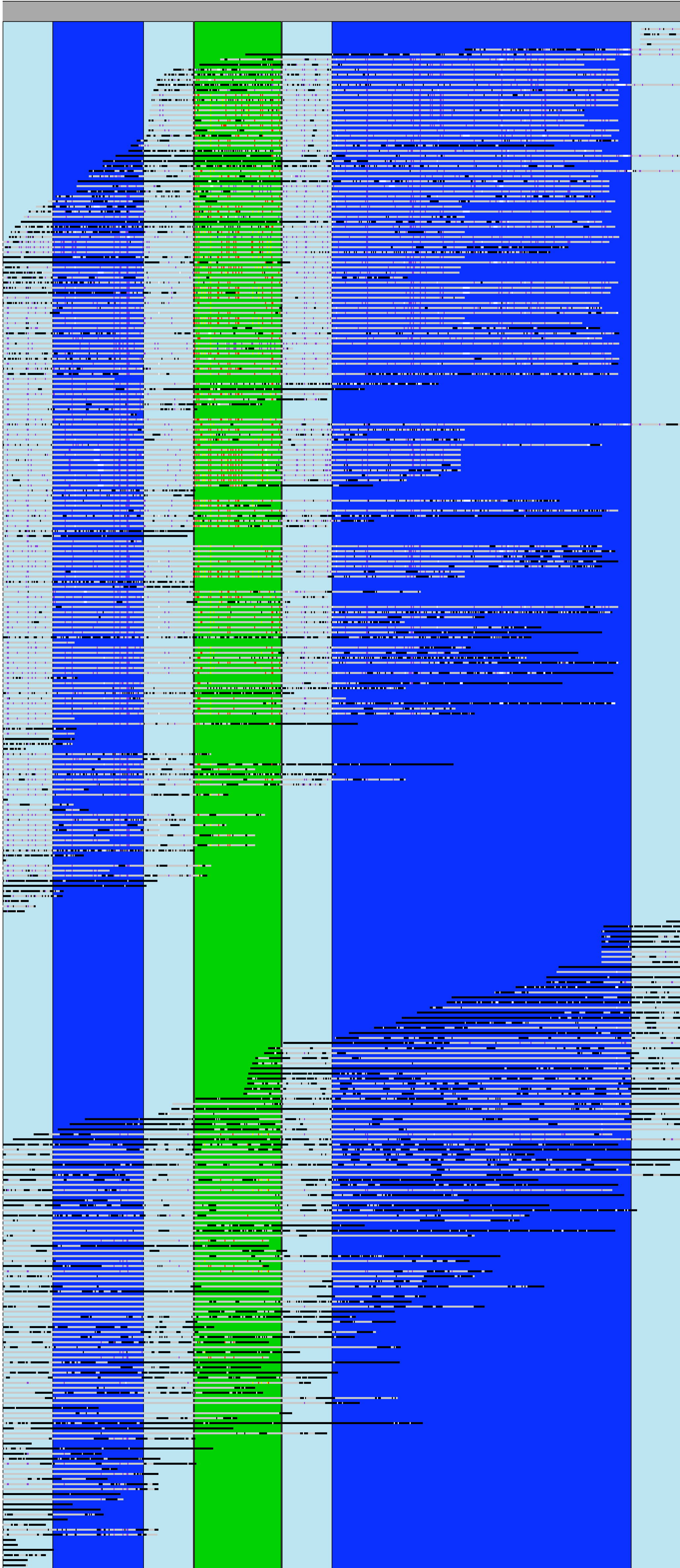
• low-quality
• high-quality identity
• high-quality substitution
• gap

• nonSyn substitution
• syn substitution
• stopCodon substitution

GOLGA6D(NM_001145224)

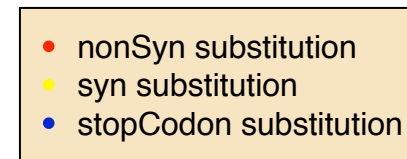
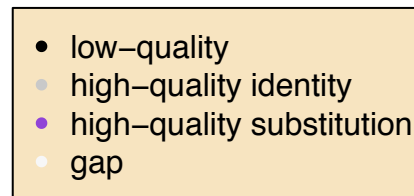
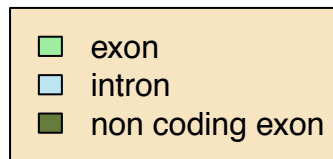
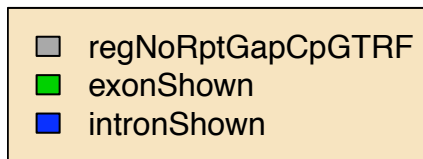
MMU

CRA

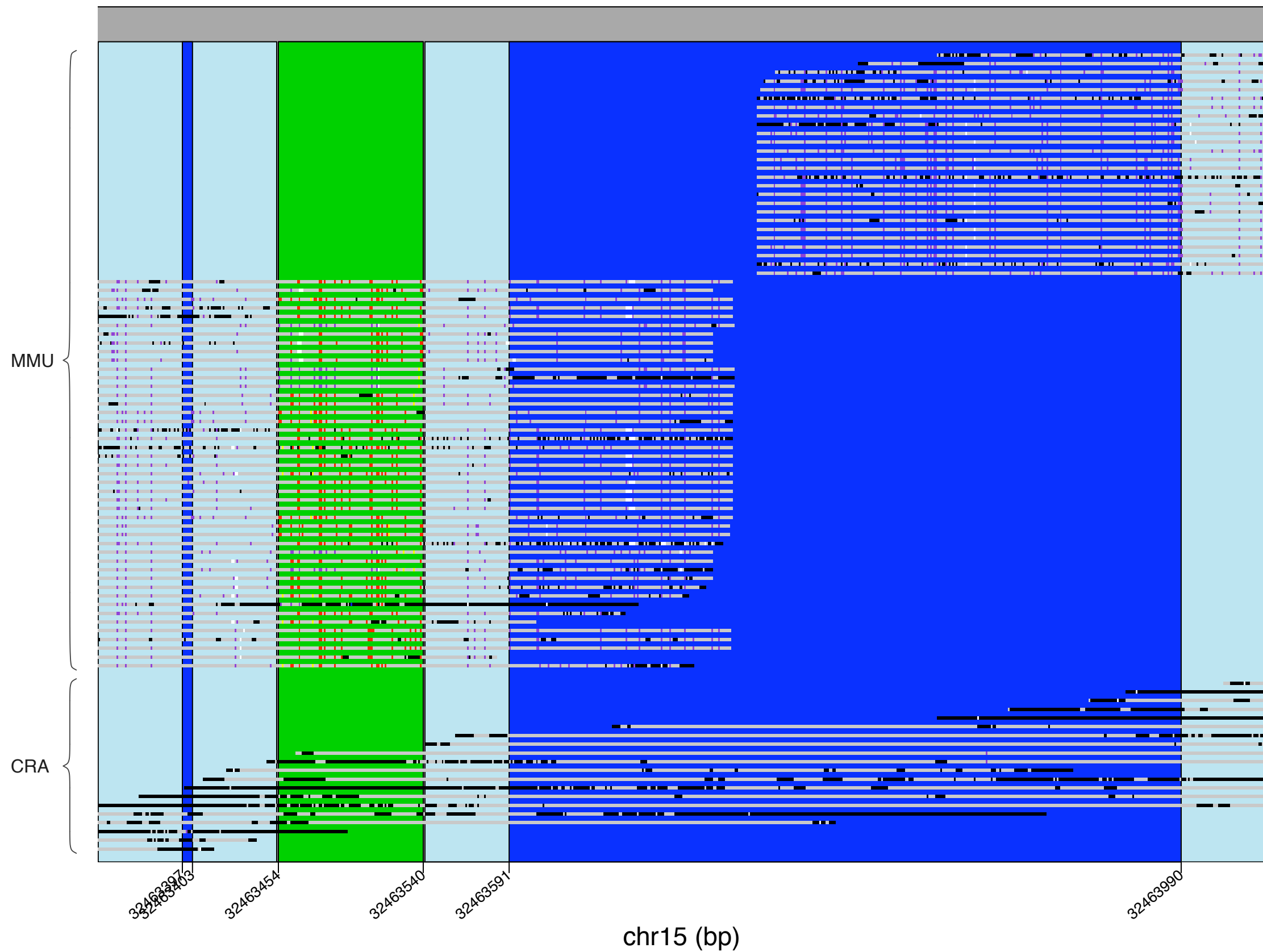


73369144 73369235 73369286 73369373 73369424 73369724
chr15 (bp)

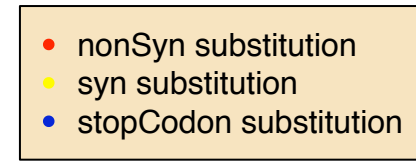
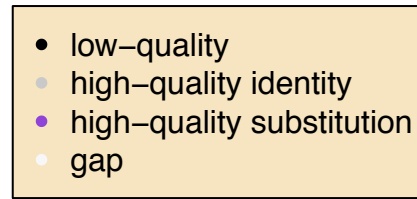
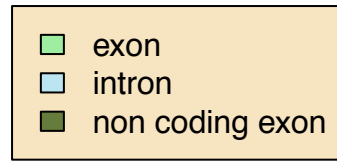
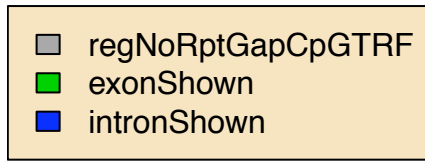
GOLGA8A_NM_181077_32458561-32487180_chr15_exon15



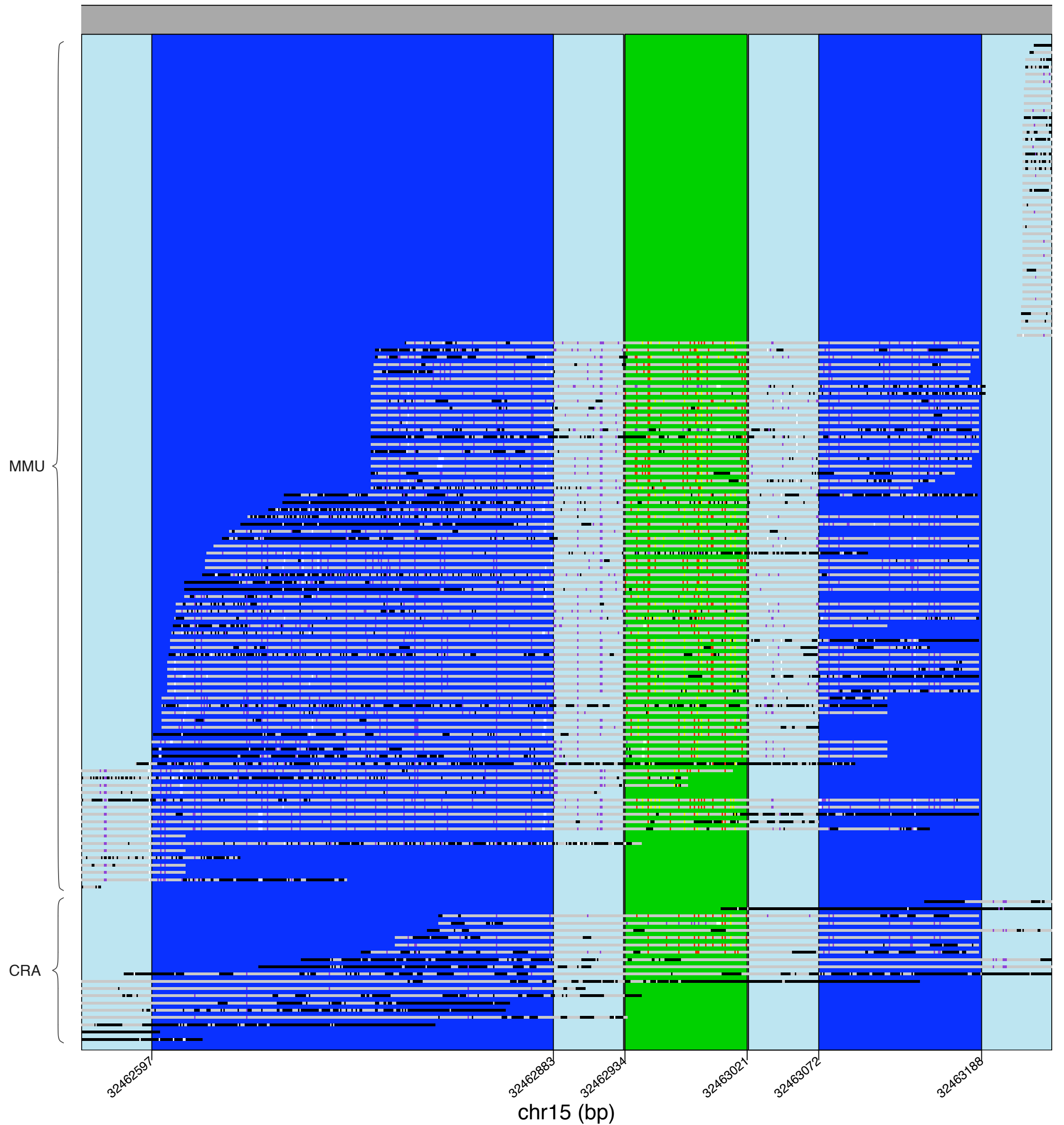
GOLGA8A(NM 181077)



GOLGA8A_NM_181077_32458561-32487180_chr15_exon17

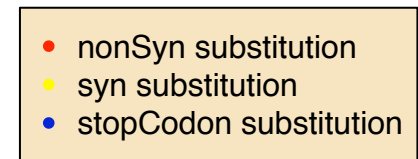
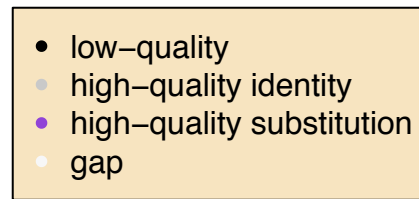
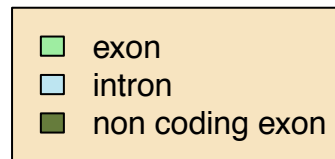
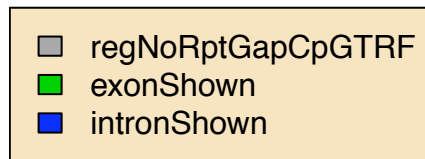


GOLGA8A(NM 181077)

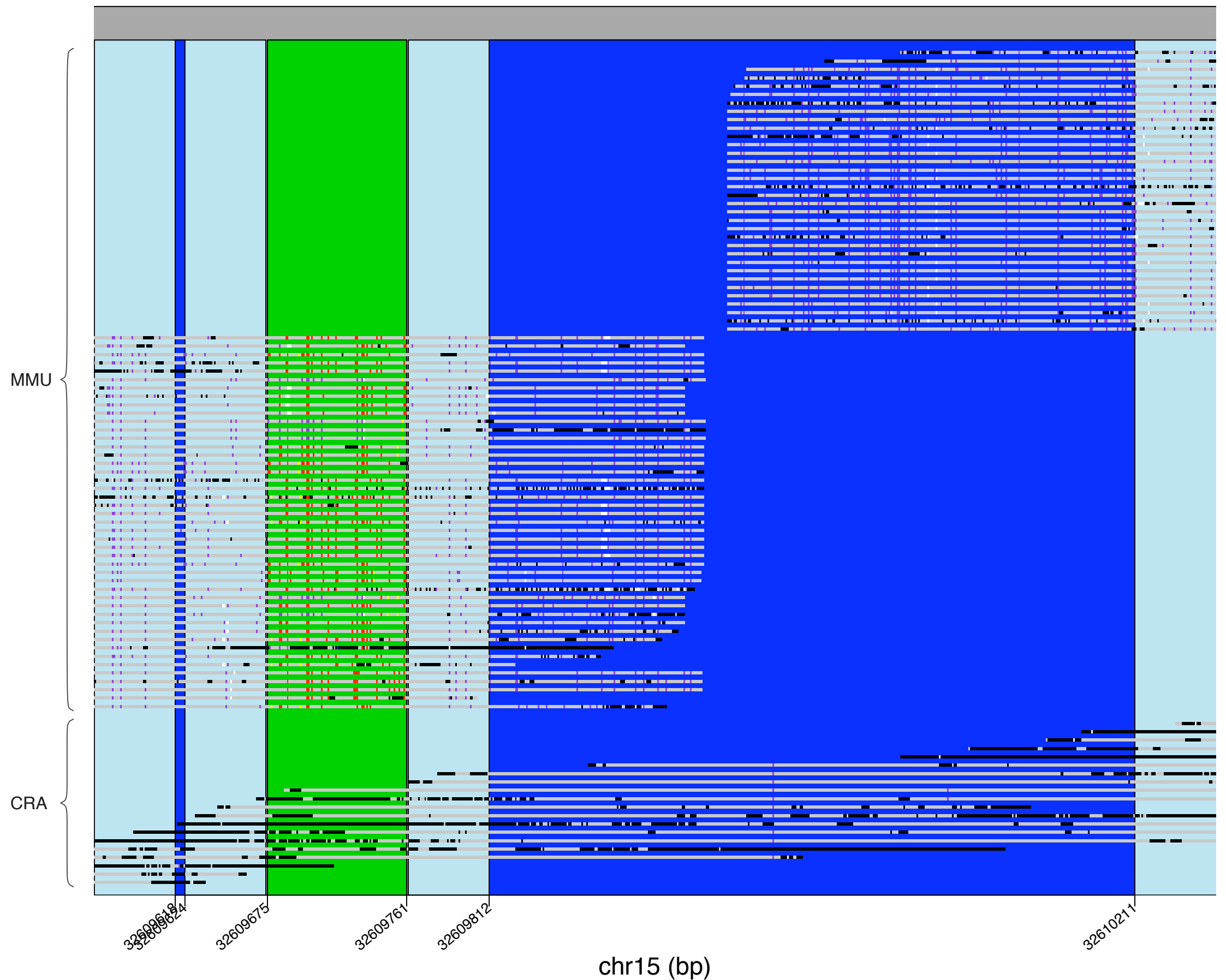


chr15 (bp)

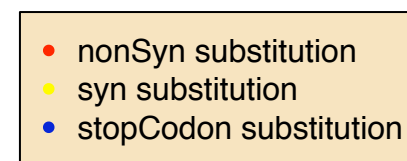
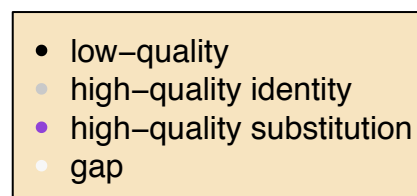
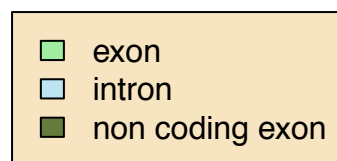
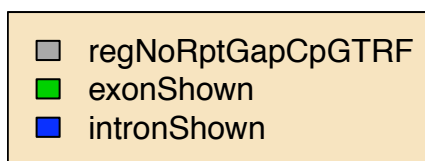
GOLGA8B_NM_001023567_32605149-32662353_chr15_exon16



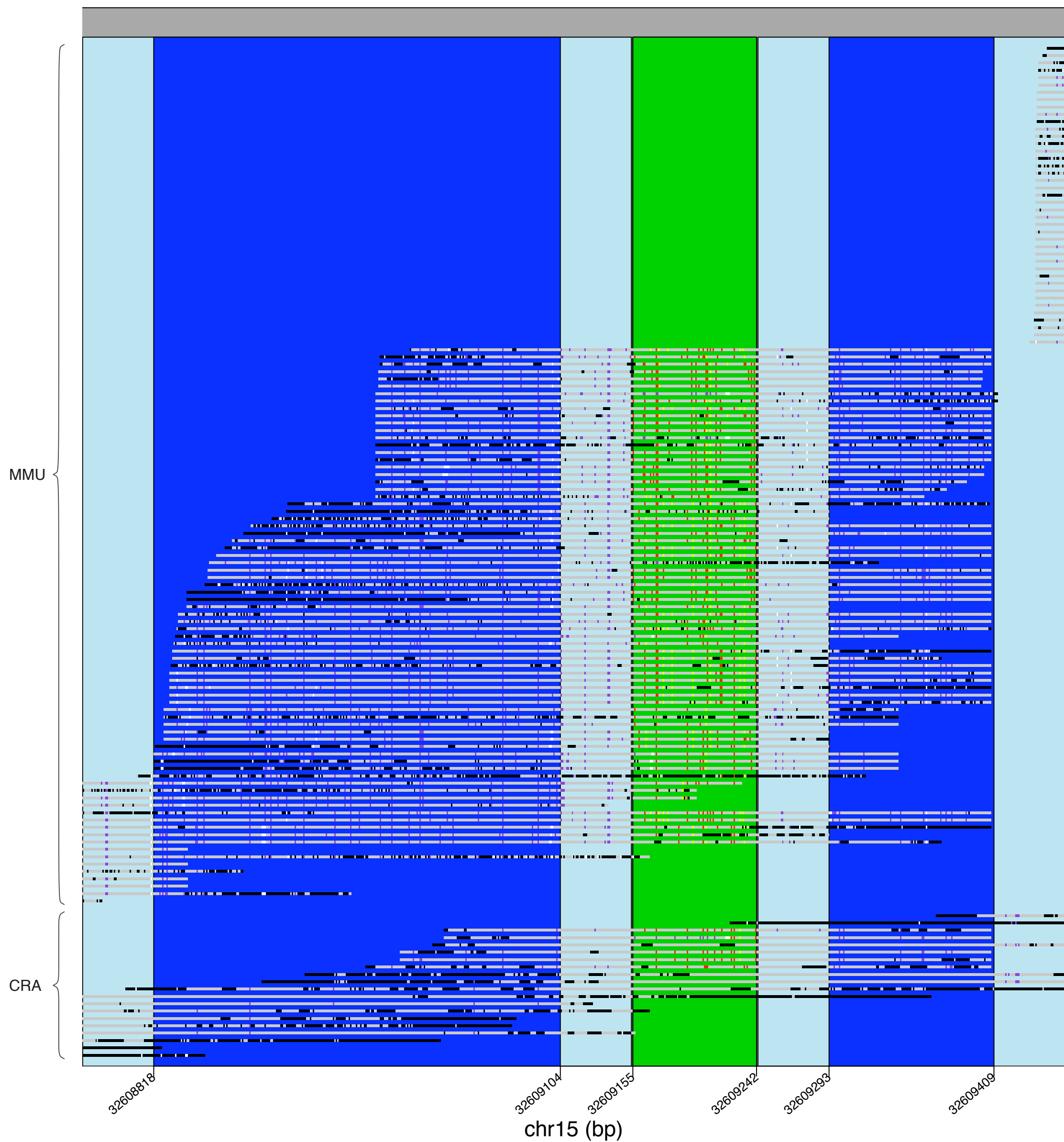
GOLGA8B(NM_001023567)



GOLGA8B_NM_001023567_32605149-32662353_chr15_exon18

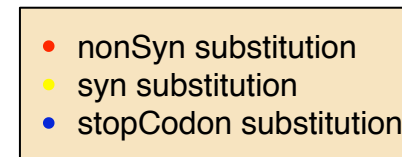
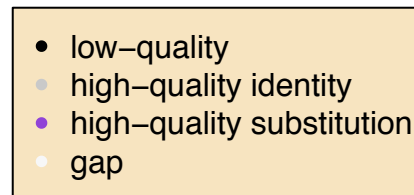
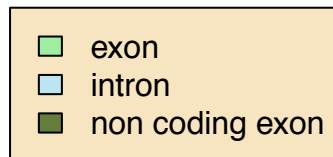
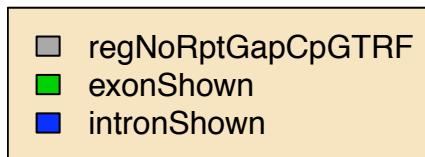


GOLGA8B(NM_001023567)

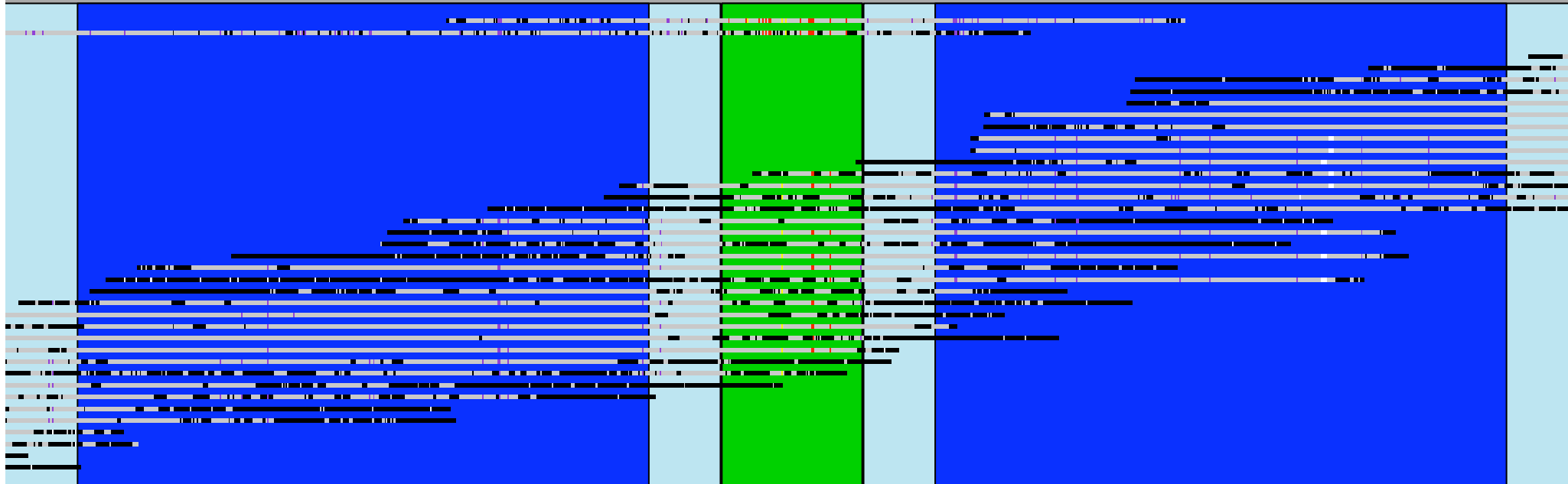


chr15 (bp)

GYPA_NM_002099_145249905-145281354_chr4_exon2



GYPA(NM_002099)



MMU

CRA

145260643

145261042

145261093

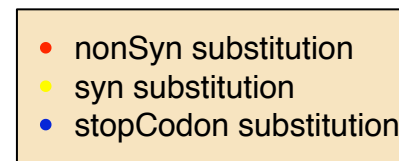
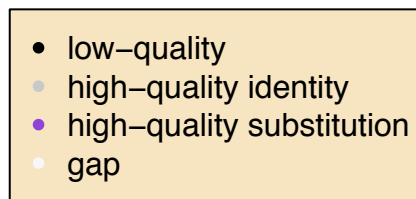
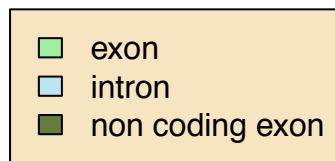
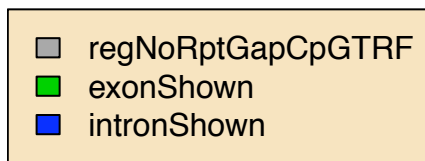
145261191

145261242

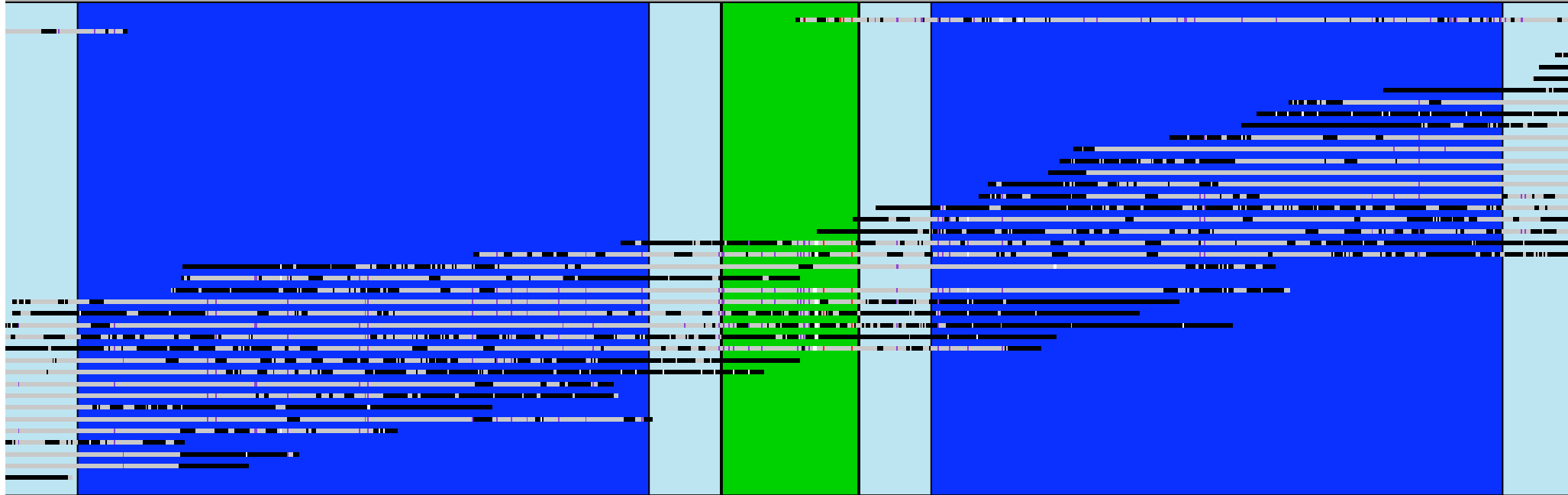
145261641

chr4 (bp)

GYPA_NM_002099_145249905-145281354_chr4_exon3



GYPA(NM_002099)



MMU

CRA

145259839

145260238

145260289

145260384

145260435

145260834

chr4 (bp)

GYPA_NM_002099_145249905-145281354_chr4_exon5

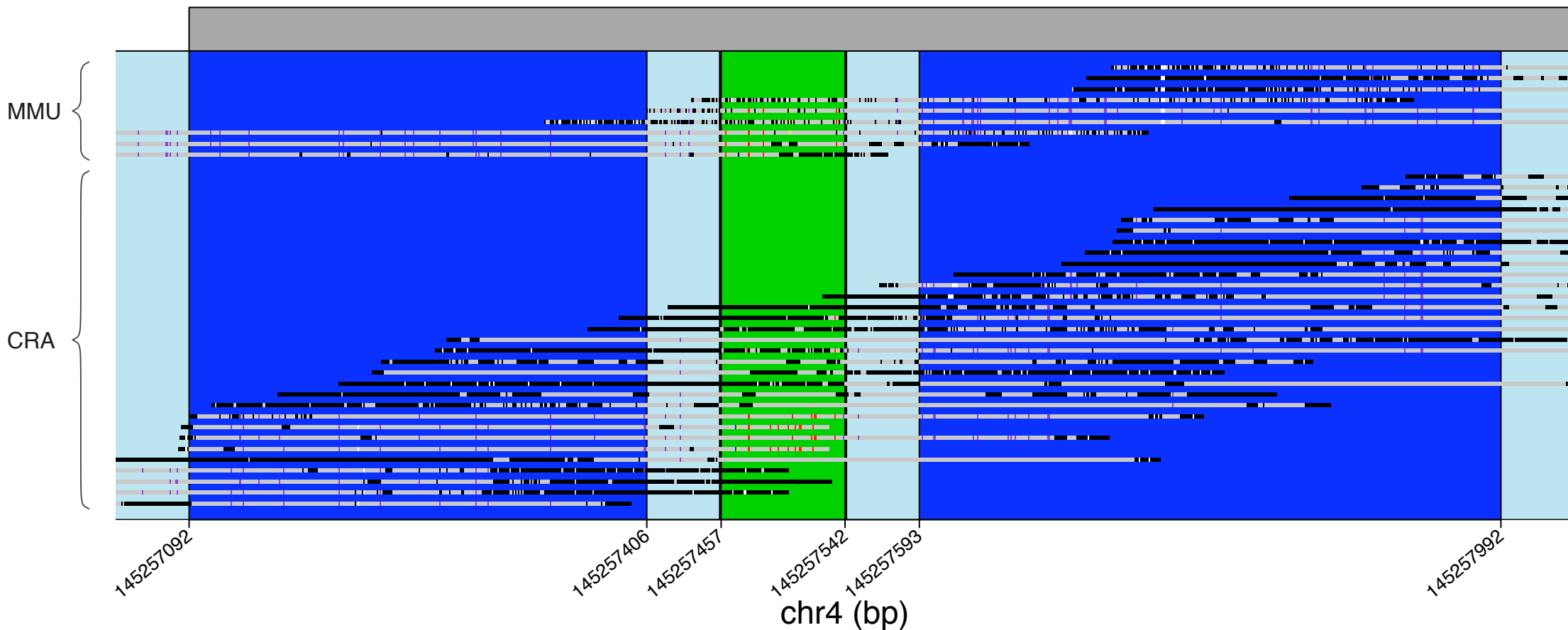
- regNoRptGapCpGTRF
- exonShown
- intronShown

- exon
- intron
- non coding exon

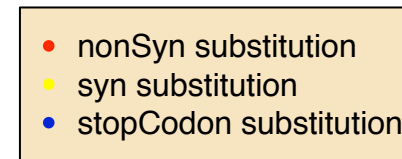
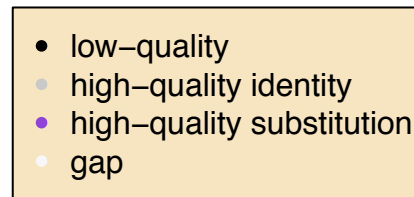
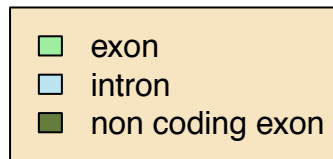
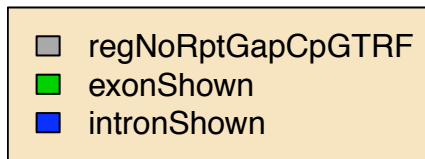
- low-quality
- high-quality identity
- high-quality substitution
- gap

- nonSyn substitution
- syn substitution
- stopCodon substitution

GYPA(NM_002099)

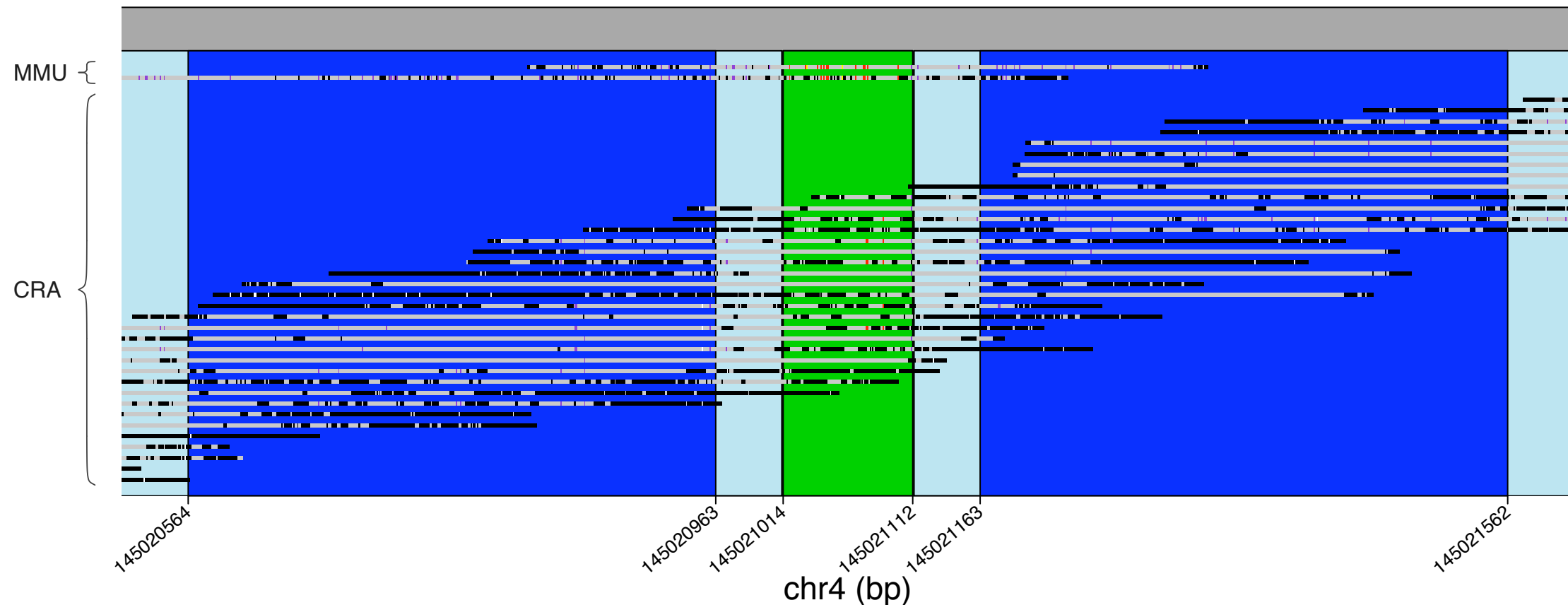


GYPE_NM_002102_145015917-145046166_chr4_exon2

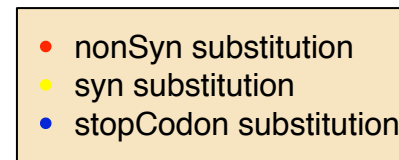
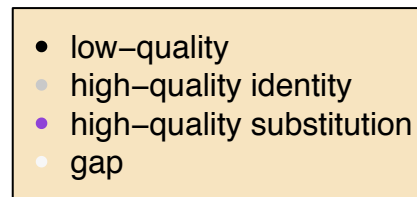
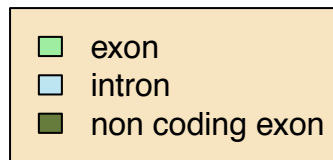
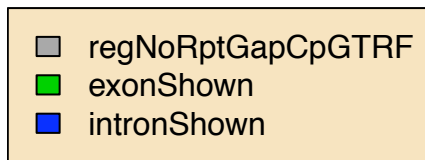


GYPE(NM_198682)

GYPE(NM_002102)



HRASLS2_NM_017878_63076817-63087431_chr11_exon4



HRASLS2(NM 017878)

