Additional File 1

CHIP whitelist mutations identified and confirmed in the discovery cohort. Listed are 746 CHIP whitelist mutations identified in 600 persons of the POG13K cohort (N = 13,445). CHIP mutations identified as per the criteria used in Jaiswal et al.[1] Each CHIP variant has been manually reviewed independently by two researchers, by Integrative Genomics Viewer with reads support (related to **Table S4**).

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42.1. chr17_1659994_T/A 496
42.2. chr17_1684583_C/A 497
43. *RAD21* 498
43.1. chr8_116856229_C/- 498
43.2. chr8_116856754_TACTAATAAG/- 499
43.3. chr8_116857385_GTTAGAAGTA/- 500
43.4. chr8_116857444_TTATC/- 501
44. *RUNX1* 502
44.1. chr21_34792342_GCCGGCCGAGGCGCCGTAGTACAGGTGGTAGGAG/- 502
44.2. chr21_34859546_T/- 503
44.3. chr21_34886956_C/A 504
45. *SETD2* 505
45.1. chr3_47042637_T/- 505
45.2. chr3_47057173_T/- 506
45.3. chr3_47057449_TCTTTAA/- 507
45.4. chr3_47083905_C/A 508
45.5. chr3_47086278_CC/AA 509
45.6. chr3_47098056_C/A 510
45.7. chr3_47098066_T/- 511

45.8. chr3_47120503_T/- ... 512
45.9. chr3_47120985_C/T ... 513
45.10. chr3_47121349_TGTC/- ... 514
45.11. chr3_47121994_G/T/A ... 515
45.12. chr3_47123182_G/- ... 516
45.13. chr3_47123227_GA/- ... 517
45.14. chr3_47123229_G/T ... 518
45.15. chr3_47123438_G/A ... 519
45.16. chr3_47124301_G/T ... 520
46. *SETDB1* ... 521
46.1. chr1_150950798_A/- ... 521
46.2. chr1_150951452_C/A ... 522
47. *SF1* ... 523
47.1. chr11_64765838_GTGGGGGAGCTGGA/- ... 523
47.2. chr11_64765923_AGGCGGAGGAGGA/- ... 524
47.3. chr11_64765945_GCATA/- ... 525
47.4. chr11_64766106_C/T ... 526
47.5. chr11_64767723_A/- ... 527
47.6. chr11_64770384_G/T ... 528
48. *SF3A1* ... 529
48.1. chr22_30340295_G/A ... 529
49. *SF3B1* ... 530
49.1. chr2_197402110_T/C ... 530
50. *SMC1A* ... 531
50.1. chrX_53405323_CTTCAGGTCACTGGCCCCACCAGAGATCA/- ... 531
51. *SMC3* ... 533
51.1. chr10_110578676_C/- ... 533
51.2. chr10_110580992_AAGA/- ... 534
51.3. chr10_110583874_G/T ... 535
51.4. chr10_110583883_G/T ... 536
51.5. chr10_110589614_C/T ... 537
51.6. chr10_110591080_TTCTG/- ... 538
51.7. chr10_110598264_C/T ... 539
51.8. chr10_110602579_G/T ... 540
51.9. chr10_110602602_GAGGGGTT/- ... 541
52. *STAG1* ... 542
52.1. chr3_136422956_G/T ... 542
52.2. chr3_136472435_G/A ... 543
52.3. chr3_136477399_C/A ... 544
52.4. chr3_136542196_C/A ... 545
52.5. chr3_136630982_C/A ... 546

53. *STAG2* 547
53.1. chrX_124042617_TTCG/- 547
53.2. chrX_124045230_G/T 548
53.3. chrX_124045296_AC/- 549
53.4. chrX_124047455_G/T 550
53.5. chrX_124077972_G/T 551
53.6. chrX_124095433_C/A 552
54. *SUZ12* 553
54.1. chr17_31937376_G/- 553
54.2. chr17_31973167_-/A 554
54.3. chr17_31983082_G/- 555
54.4. chr17_31988474_C/A 556
55. *TET2* 557
55.1. chr4_105234156_-/A 557
55.2. chr4_105234484_T/- 558
55.3. chr4_105234566_T/- 559
55.4. chr4_105234622_-/A 560
55.5. chr4_105234731_G/- 561
55.6. chr4_105234764_C/- 562
55.7. chr4_105235004_AGGTTCCAGCAGCAAT/- 563
55.8. chr4_105235052_T/G 564
55.9. chr4_105235149_C/T 565
55.10. chr4_105235260_C/T 566
55.11. chr4_105235342_C/- 567
55.12. chr4_105235366_-/T 568
55.13. chr4_105235435_T/- 569
55.14. chr4_105235437_C/- 570
55.15. chr4_105235459_A/G 571
55.16. chr4_105235459_G/- 572
55.17. chr4_105235578_A/T 573
55.18. chr4_105235901_C/- 574
55.19. chr4_105235913_-/A 575
55.20. chr4_105235923_CACTTCTCCAAAACAGA/- 576
55.21. chr4_105236130_AC/- 577
55.22. chr4_105236318_-/A 578
55.23. chr4_105236341_AT/- 579
55.24. chr4_105236391_TCCCC/- 580
55.25. chr4_105236493_C/- 581
55.26. chr4_105236598_C/T 582
55.27. chr4_105236599_AGGAGCAG/- 583
55.28. chr4_105236611_C/A 584

55.29. chr4_105236656_-/AT 585
55.30. chr4_105236815_A/AA/- 586
55.31. chr4_105236829_C/T 587
55.32. chr4_105236952_A/- 588
55.33. chr4_105237000_C/T 589
55.34. chr4_105237190_AGCAA/- 590
55.35. chr4_105237262_C/A 591
55.36. chr4_105237292_AAAAT/- 592
55.37. chr4_105237322_AA/- 593
55.38. chr4_105237346_G/T 594
55.39. chr4_105237352_G/T 595
55.40. chr4_105242863_T/A 596
55.41. chr4_105242907_G/T 597
55.42. chr4_105242911_G/A 598
55.43. chr4_105242913_C/G 599
55.44. chr4_105243577_G/C 600
55.45. chr4_105243608_T/A 601
55.46. chr4_105243612_G/T 602
55.47. chr4_105243634_C/A 603
55.48. chr4_105243664_-/T 604
55.49. chr4_105243673_G/A 605
55.50. chr4_105243693_CTGG/- 606
55.51. chr4_105243721_C/A 607
55.52. chr4_105243753_A/- 608
55.53. chr4_105243756_C/T 609
55.54. chr4_105243757_G/A 610
55.55. chr4_105243772_A/T 611
55.56. chr4_105259617_AGG/- 612
55.57. chr4_105259626_T/A 613
55.58. chr4_105259629_G/C 614
55.59. chr4_105259633_G/C 615
55.60. chr4_105259665_T/C 616
55.61. chr4_105259678_G/T 617
55.62. chr4_105259713_T/C 618
55.63. chr4_105259719_A/T 619
55.64. chr4_105259743_A/G 620
55.65. chr4_105259770_G/A 621
55.66. chr4_105261757_A/C 622
55.67. chr4_105261807_C/T 623
55.68. chr4_105269659_G/T 624
55.69. chr4_105269661_C/T 625

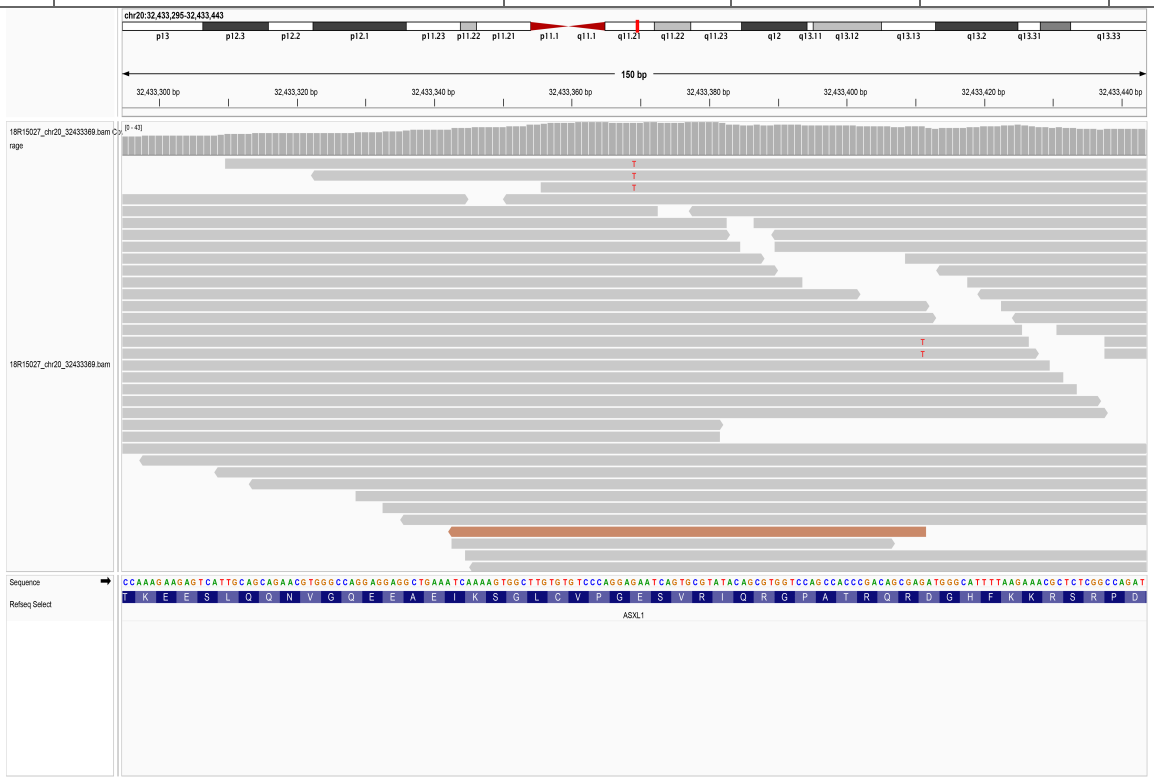
55.70. chr4_105269665_C/T ... 626
55.71. chr4_105269667_TTCTCAGGGGT/- ... 627
55.72. chr4_105269675_GGTC/- ... 628
55.73. chr4_105269691_G/C ... 629
55.74. chr4_105272591_C/T ... 630
55.75. chr4_105272623_G/T ... 632
55.76. chr4_105272700_G/A ... 633
55.77. chr4_105272717_G/A ... 634
55.78. chr4_105272774_C/T ... 635
55.79. chr4_105272902_G/- ... 636
55.80. chr4_105275214_AT/- ... 637
55.81. chr4_105275292_T/- ... 638
55.82. chr4_105275358_C/- ... 639
55.83. chr4_105275365_-/AA ... 640
55.84. chr4_105275377_A/- ... 641
55.85. chr4_105275447_TG/- ... 642
55.86. chr4_105275766_AAATG/- ... 643
55.87. chr4_105275957_T/A ... 644
55.88. chr4_105276031_G/T ... 645
55.89. chr4_105276113_A/- ... 646
55.90. chr4_105276126_C/- ... 647
55.91. chr4_105276128_T/C ... 648
55.92. chr4_105276129_TGAG/- ... 649
55.93. chr4_105276131_A/- ... 650
55.94. chr4_105276133_T/G ... 651
55.95. chr4_105276183_G/T ... 652
55.96. chr4_105276215_A/G ... 653
55.97. chr4_105276487_C/T ... 654
56. *TP53* ... 655
56.1. chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/- ... 655
56.2. chr17_7673704_G/A ... 661
56.3. chr17_7674262_T/C ... 662
56.4. chr17_7674945_G/A ... 663
56.5. chr17_7675066_G/T ... 664
56.6. chr17_7675088_C/T ... 665
56.7. chr17_7675158_G/A ... 666
56.8. chr17_7675161_G/A ... 667
56.9. chr17_7675208_C/A ... 668
56.10. chr17_7675993_C/T ... 669
57. *WT1* ... 670
57.1. chr11_32434804_C/- ... 670

58. *ZRSR2* 671
58.1. chrX_15790496_A/G 671

1. *ASXL1*

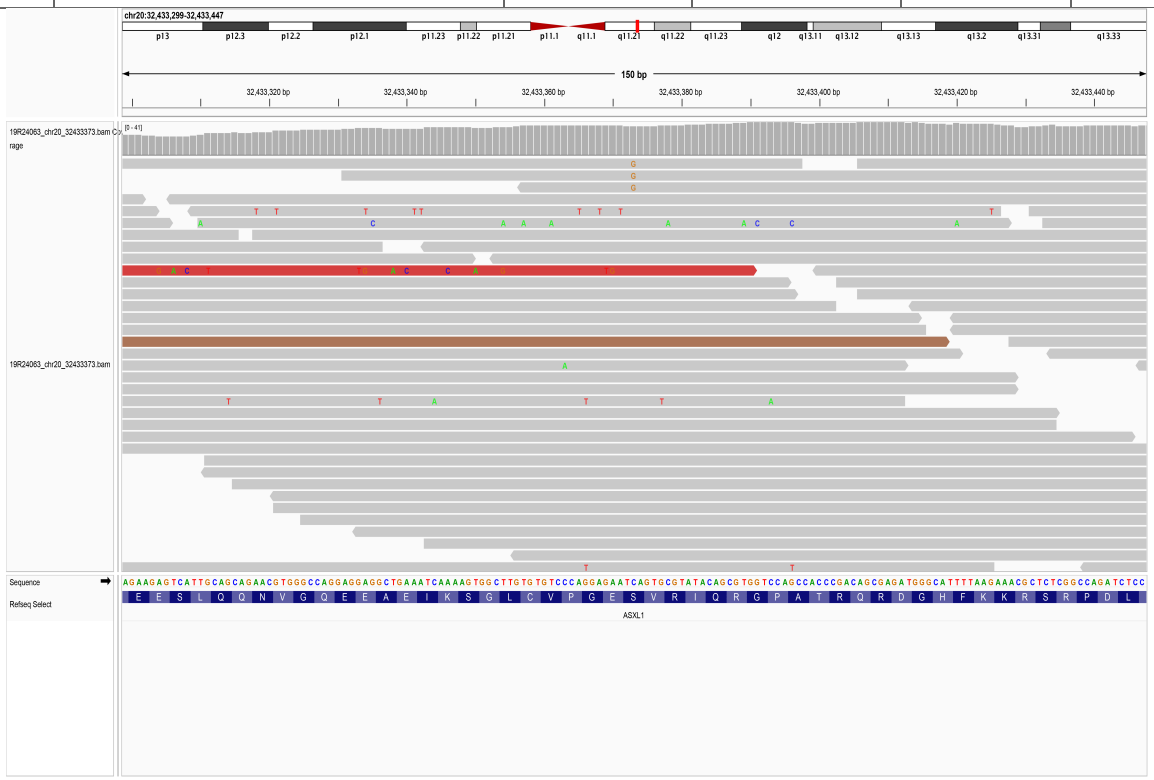
1.1. chr20_32433369_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15027	chr20_32433369_G/T	37	3	*ASXL1*	stop_gained



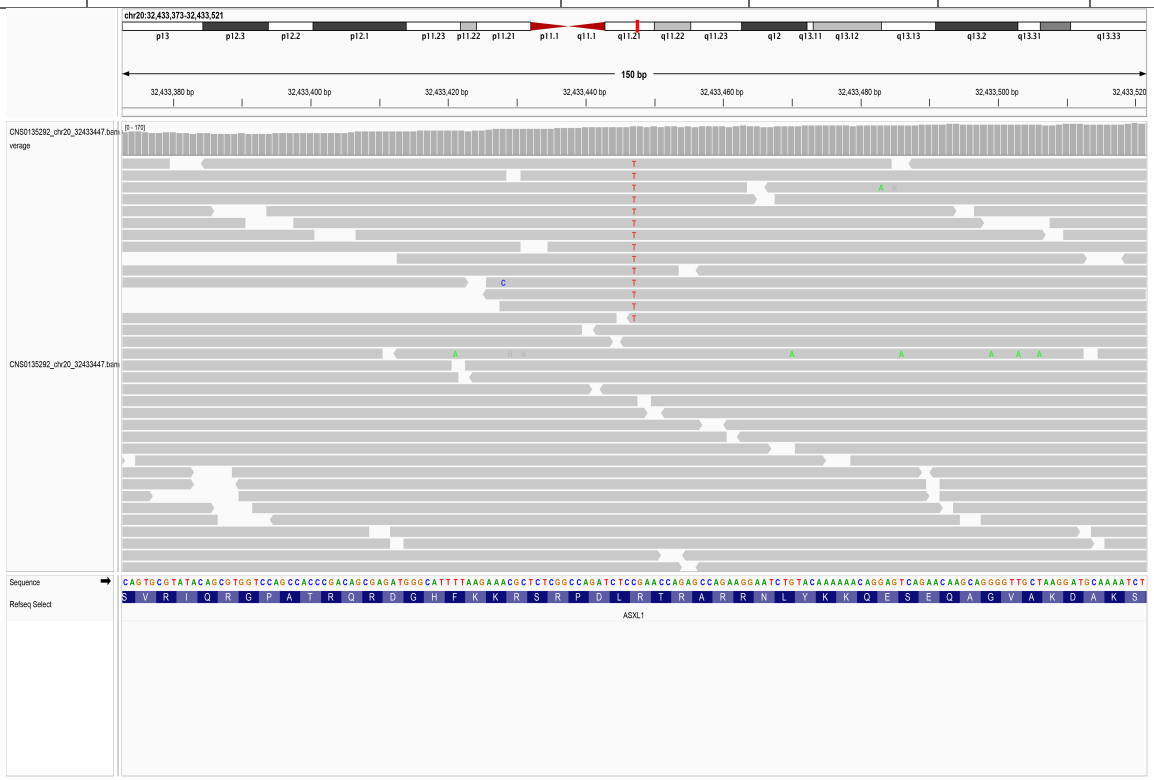
1.2. chr20_32433373_C/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R24063	chr20_32433373_C/G	28	3	*ASXL1*	stop_gained



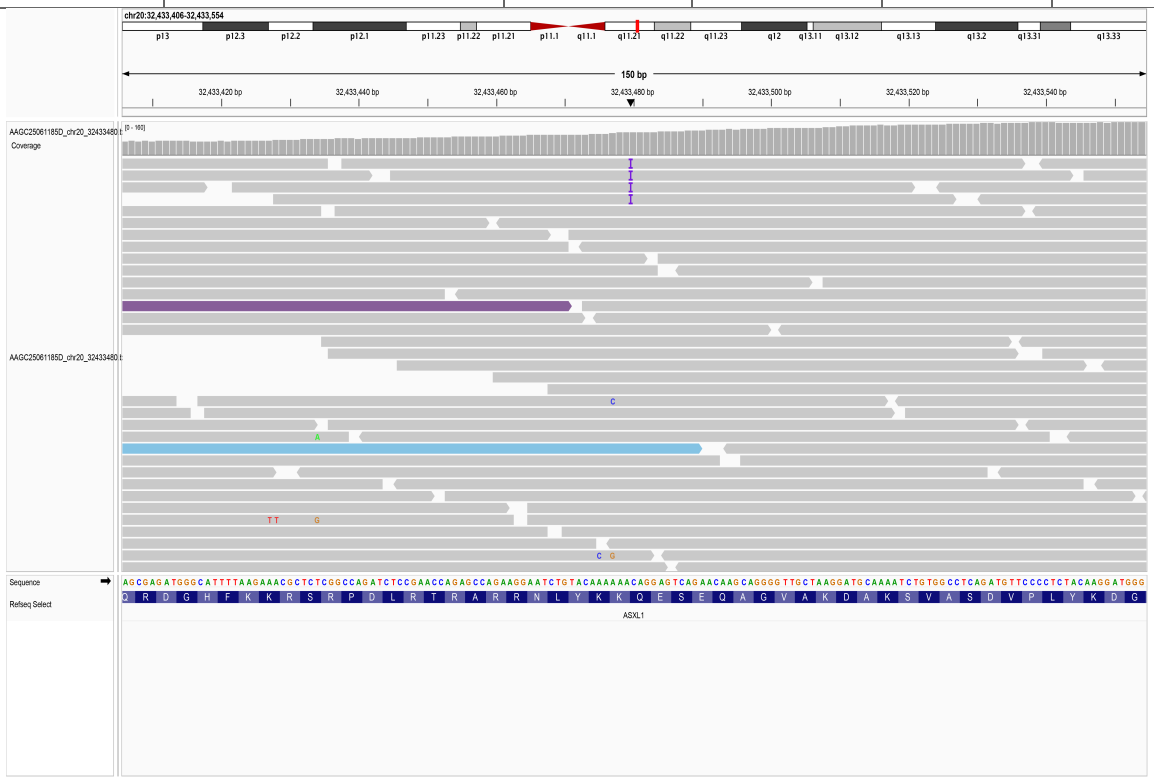
1.3. chr20_32433447_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135292	chr20_32433447_C/T	127	14	*ASXL1*	stop_gained



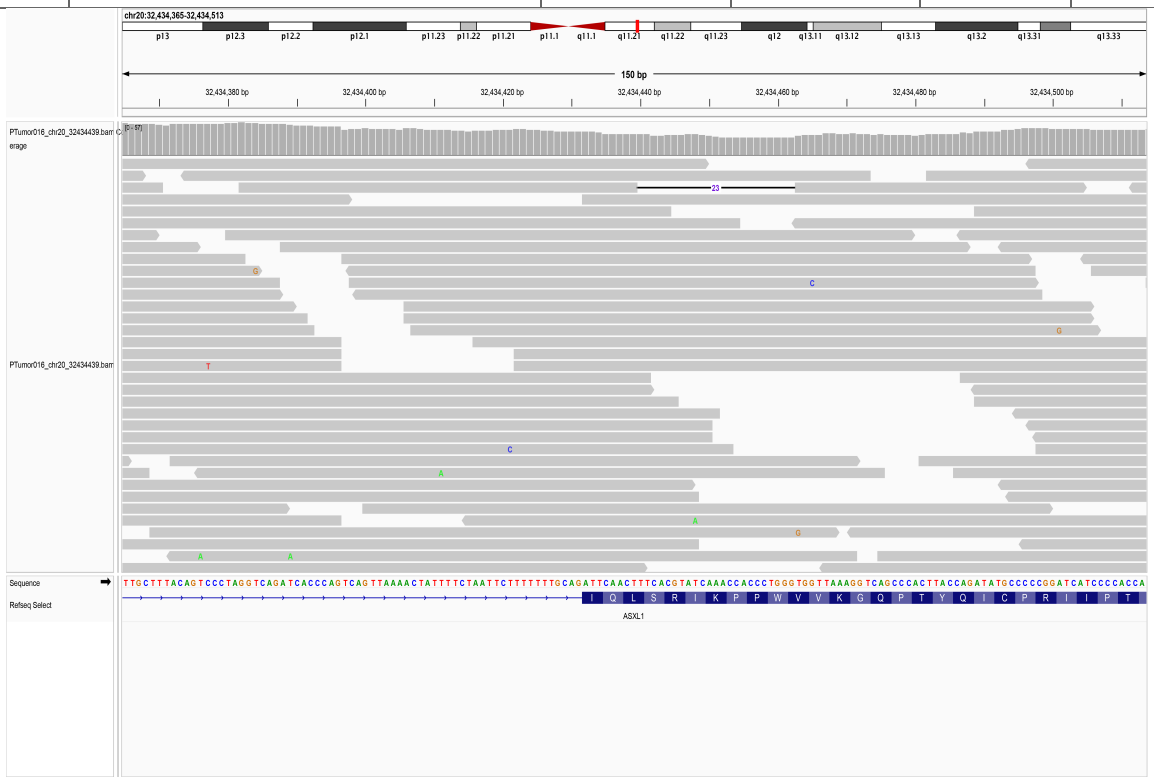
1.4. chr20_32433480_-/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061185D	chr20_32433480_-/G	102	4	*ASXL1*	frameshift_variant



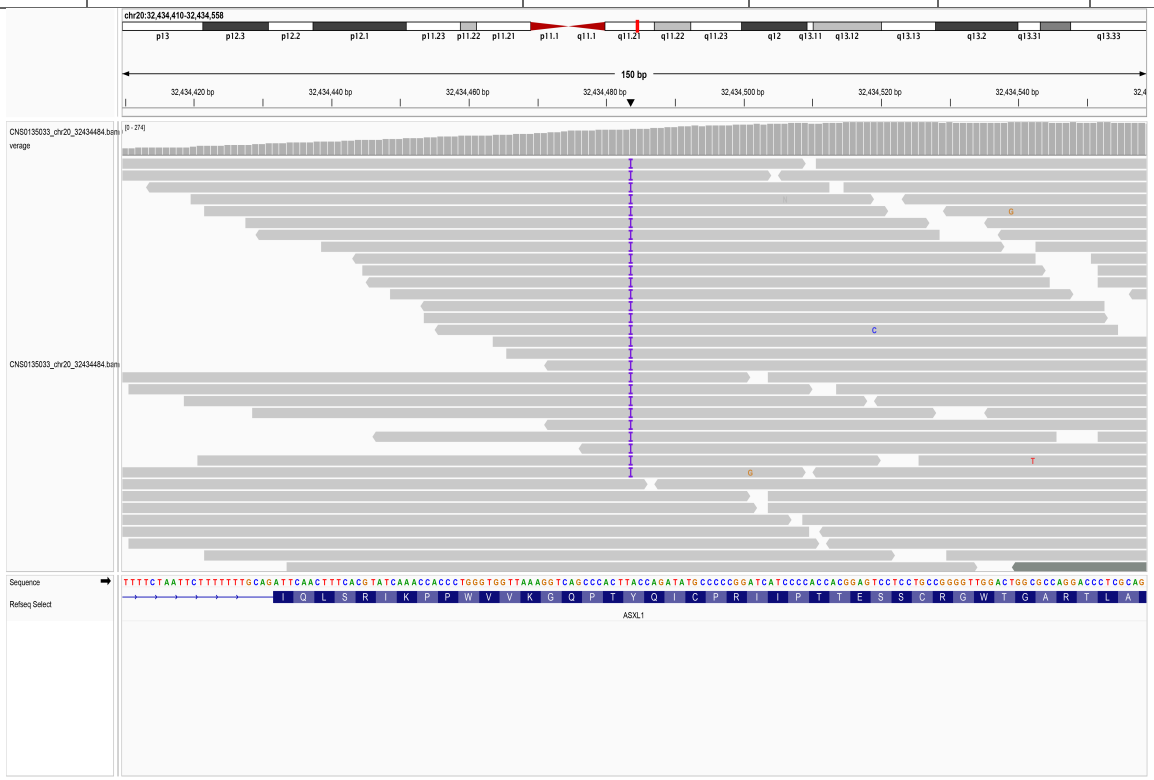
1.5. chr20_32434440_TTCACGTATCAAACCACCCTGGG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
PTumor016	chr20_32434440_TTCACGTATCAAACCACCCTGGG/-	43	3	*ASXL1*	frameshift_variant



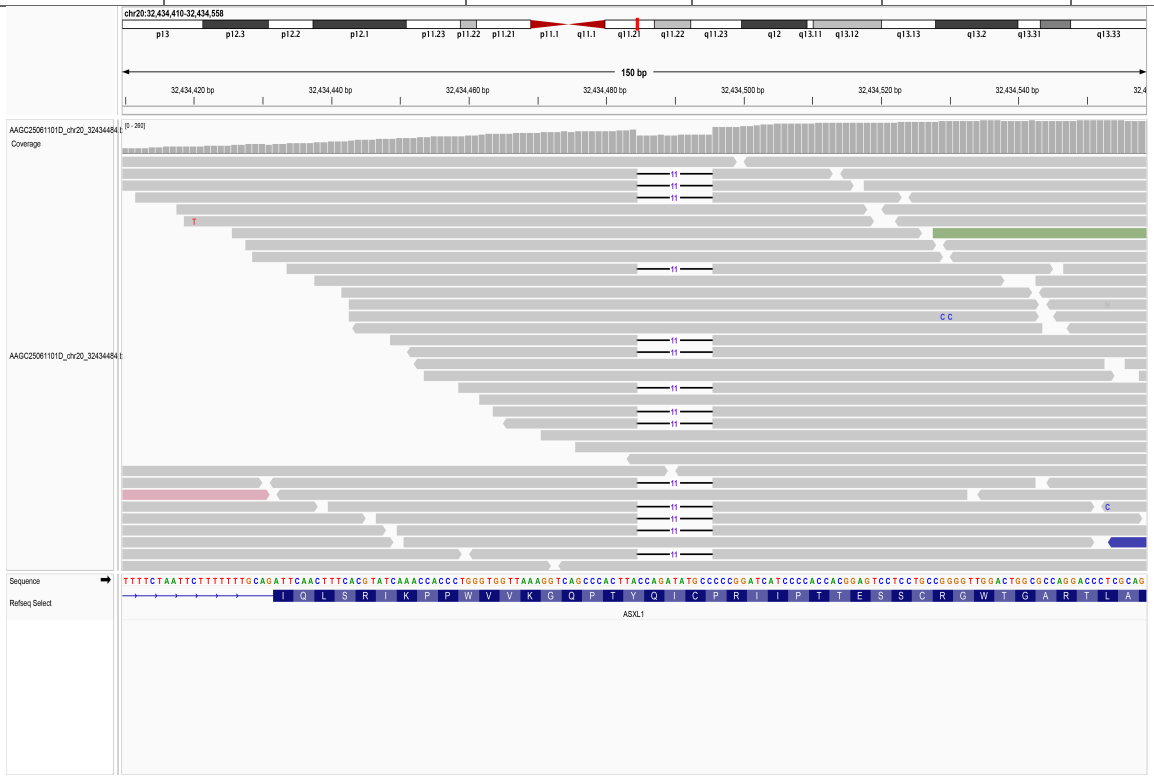
1.6. chr20_32434484_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135033	chr20_32434484_-/A	181	28	*ASXL1*	stop_gained



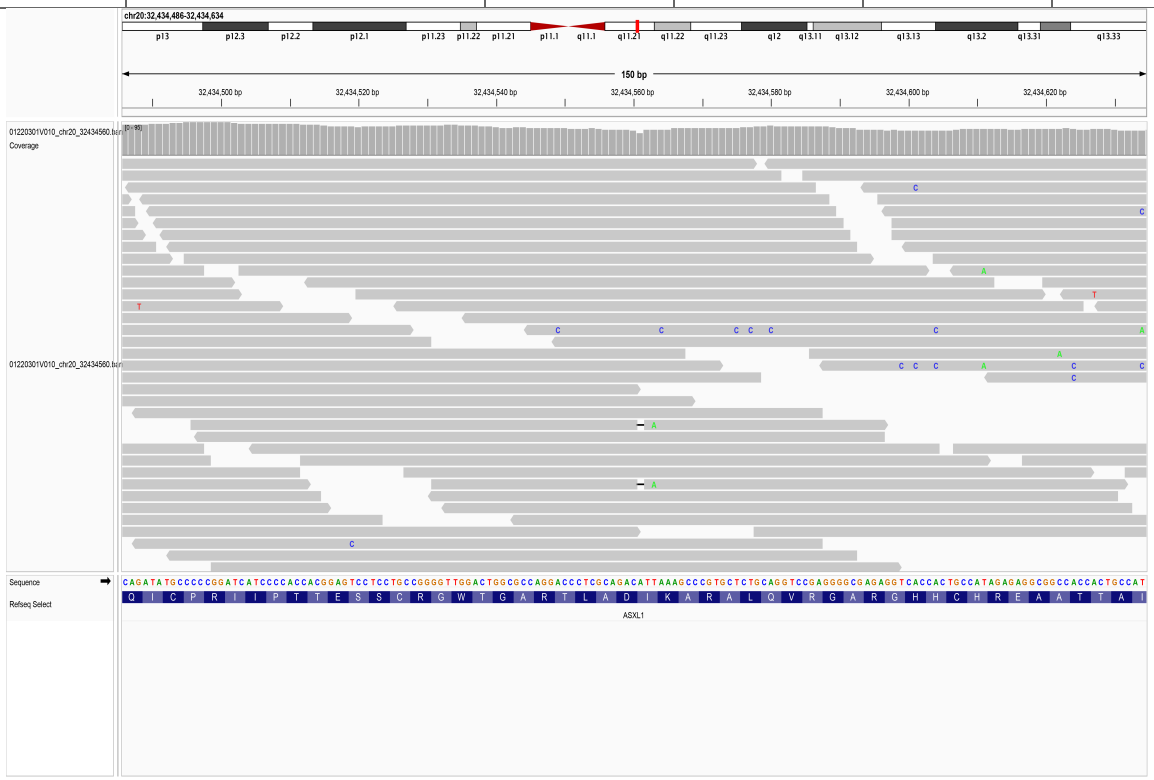
1.7. chr20_32434485_CCAGATATGCC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061101D	chr20_32434485_CCAGATATGCC/-	149	56	*ASXL1*	frameshift_variant



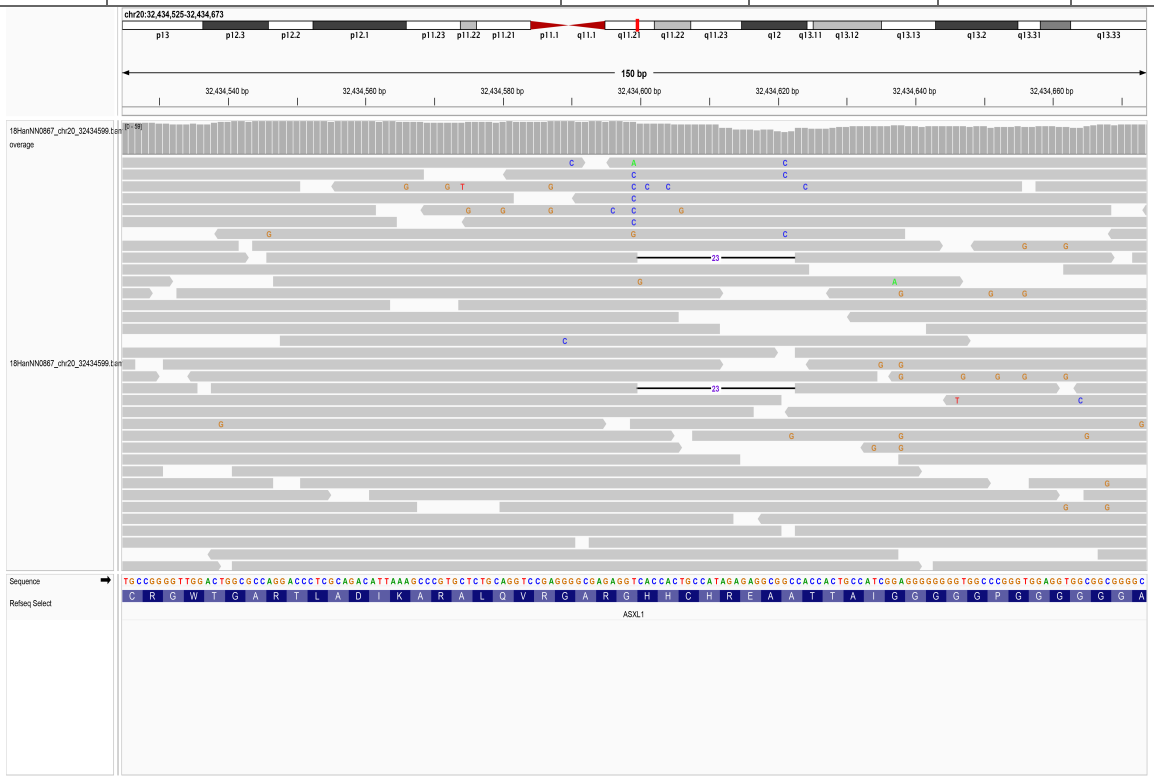
1.8. chr20_32434561_A/-

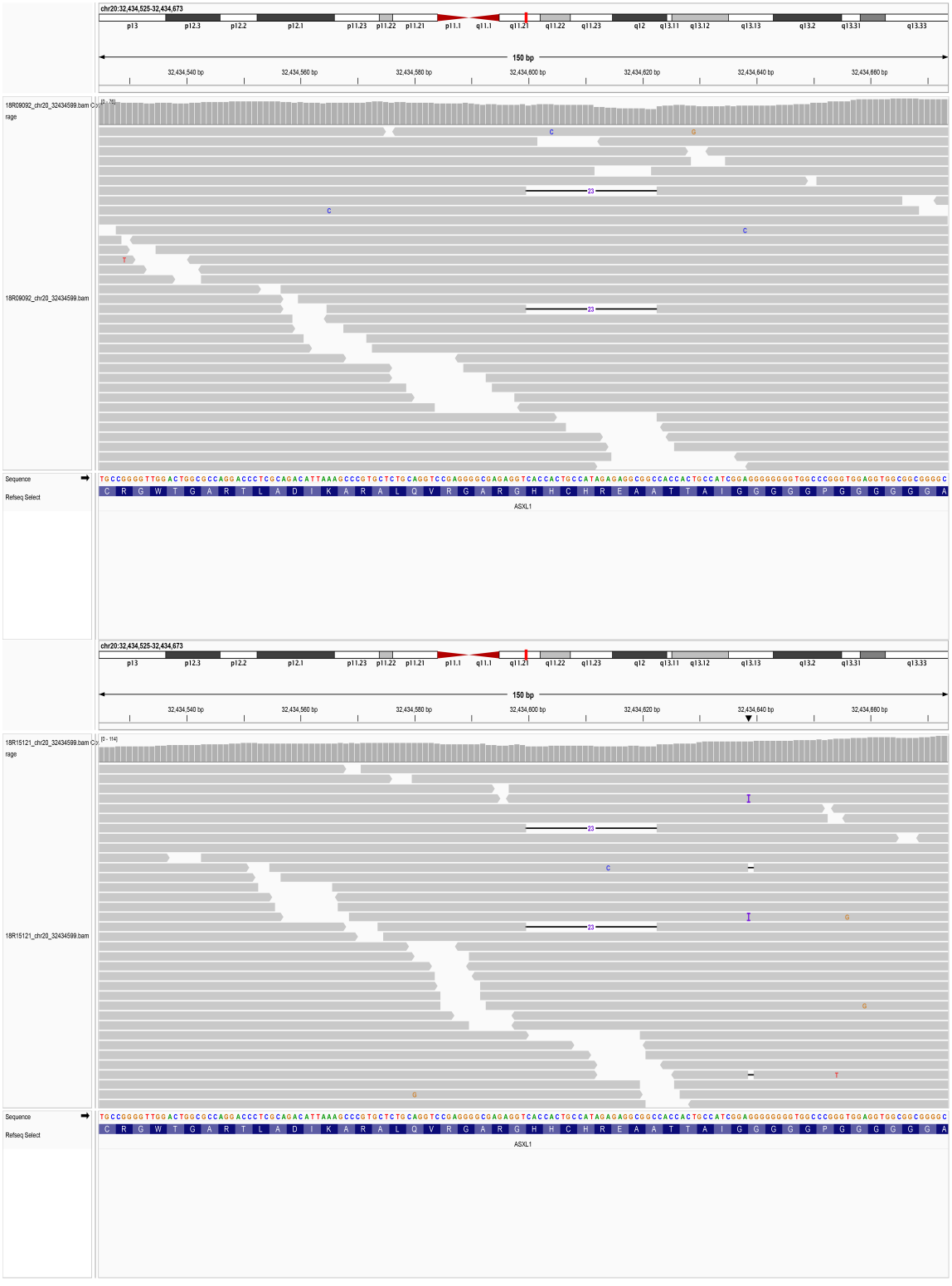
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
01220301V010	chr20_32434561_A/-	64	7	*ASXL1*	frameshift_variant



1.9. chr20_32434600_CACCACTGCCATAGAGAGGCGGC/-

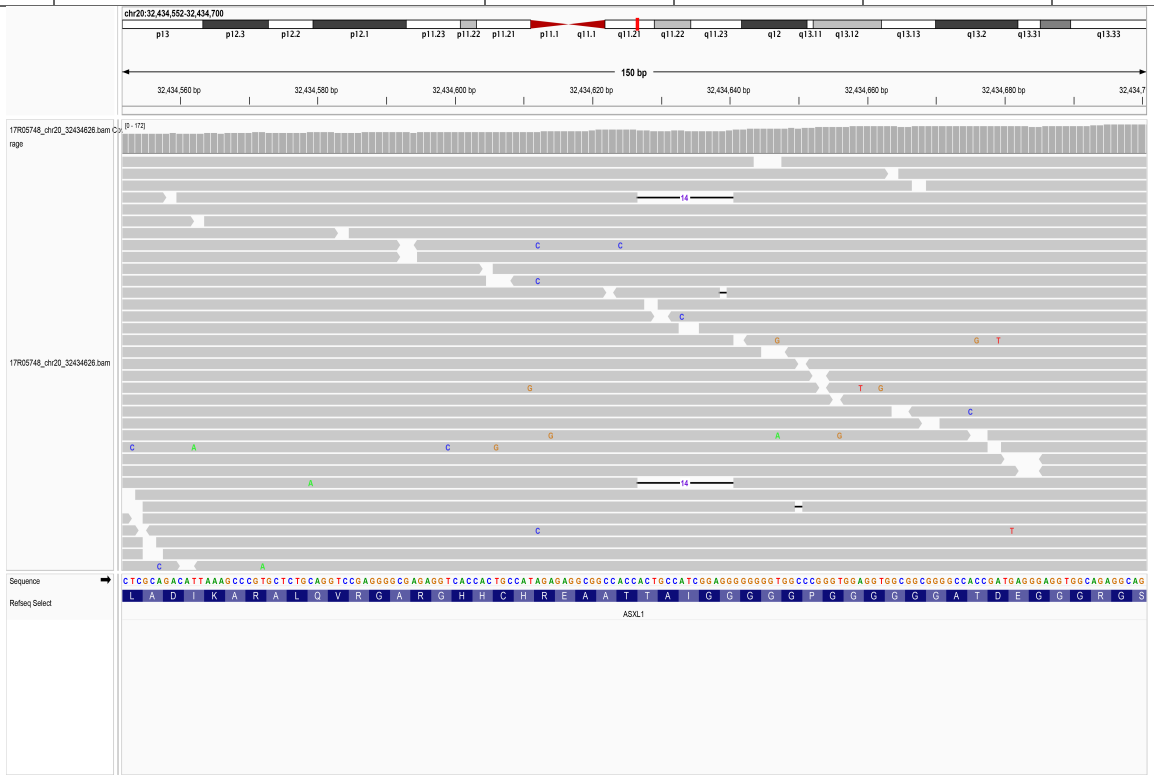
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0867	chr20_32434600_CACCACTGCCATAGAGAGGCGGC/-	45	11	*ASXL1*	frameshift_variant
18R09092	chr20_32434600_CACCACTGCCATAGAGAGGCGGC/-	50	13	*ASXL1*	frameshift_variant
18R15121	chr20_32434600_CACCACTGCCATAGAGAGGCGGC/-	68	9	*ASXL1*	frameshift_variant




chr20:32,434,525-32,434,673
150 bp
18R09092_chr20_32434599.bam Coverage
18R09092_chr20_32434599.bam
Sequence
Refseq Select
ASXL1
18R15121_chr20_32434599.bam Coverage
18R15121_chr20_32434599.bam

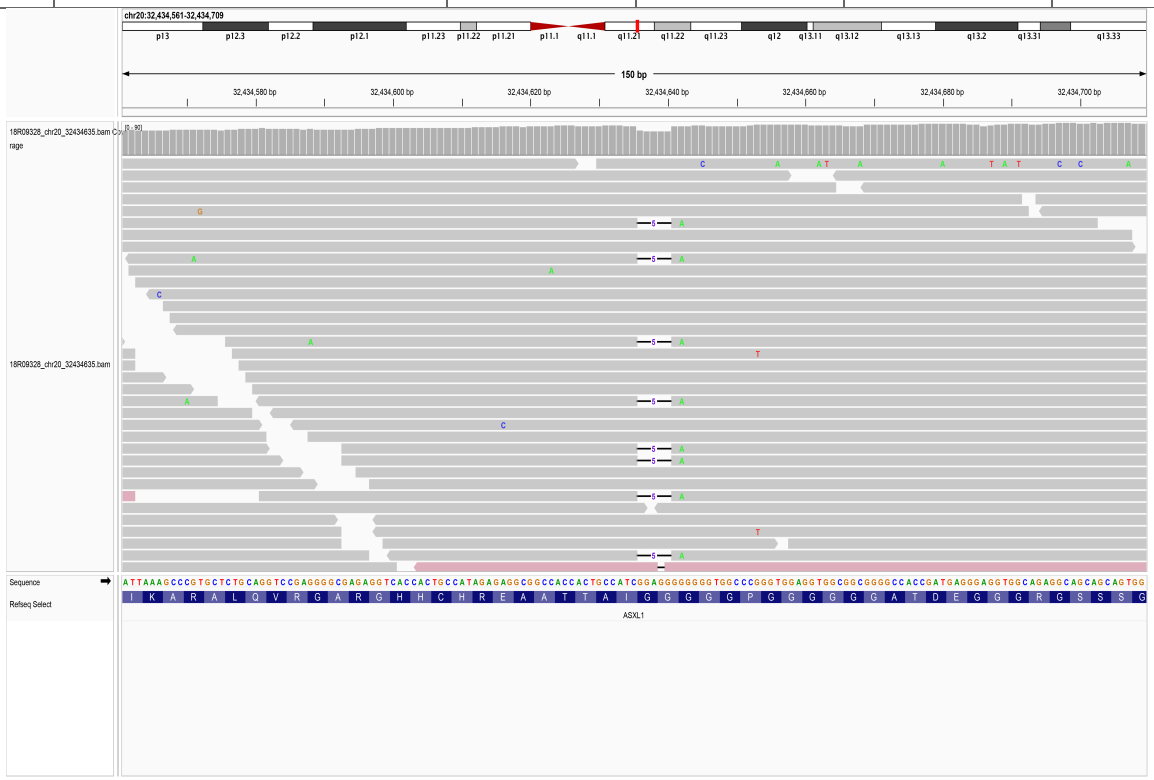
1.10. chr20_32434627_ACTGCCATCGGAGG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05748	chr20_32434627_ACTGCCATCGGAGG/-	122	5	*ASXL1*	frameshift_variant



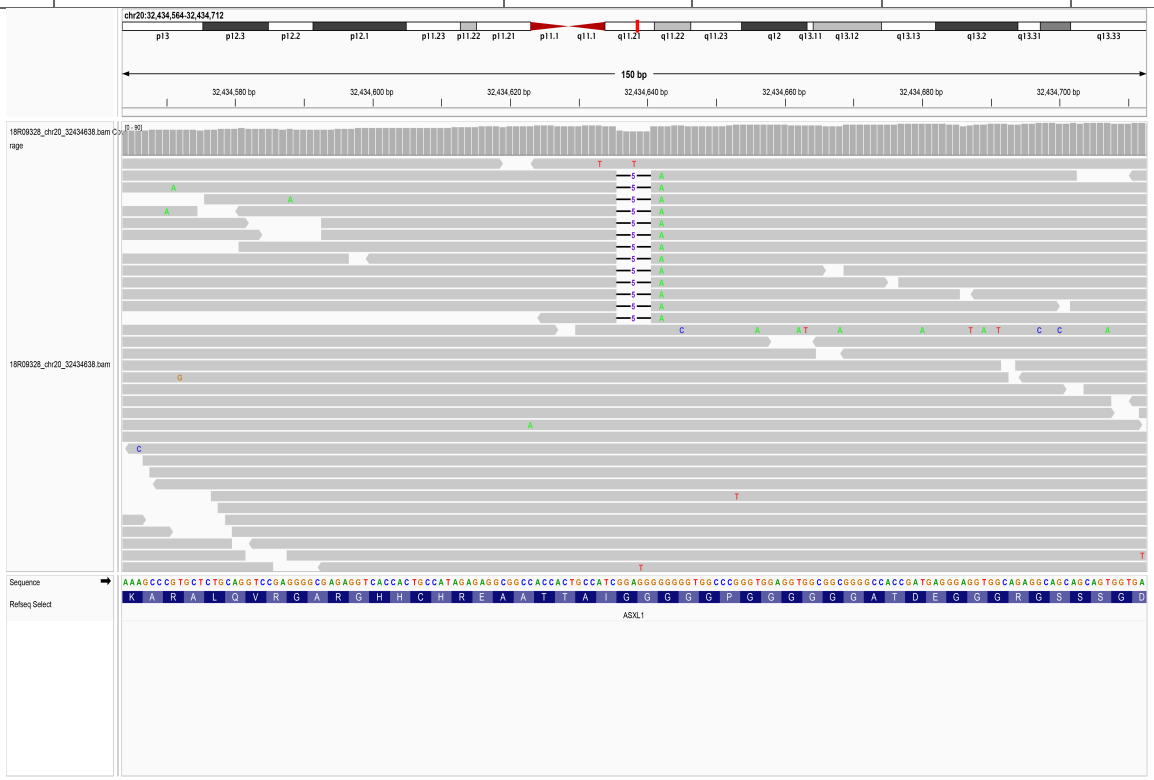
1.11. chr20_32434636_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09328	chr20_32434636_G/-	61	14	*ASXL1*	frameshift_variant



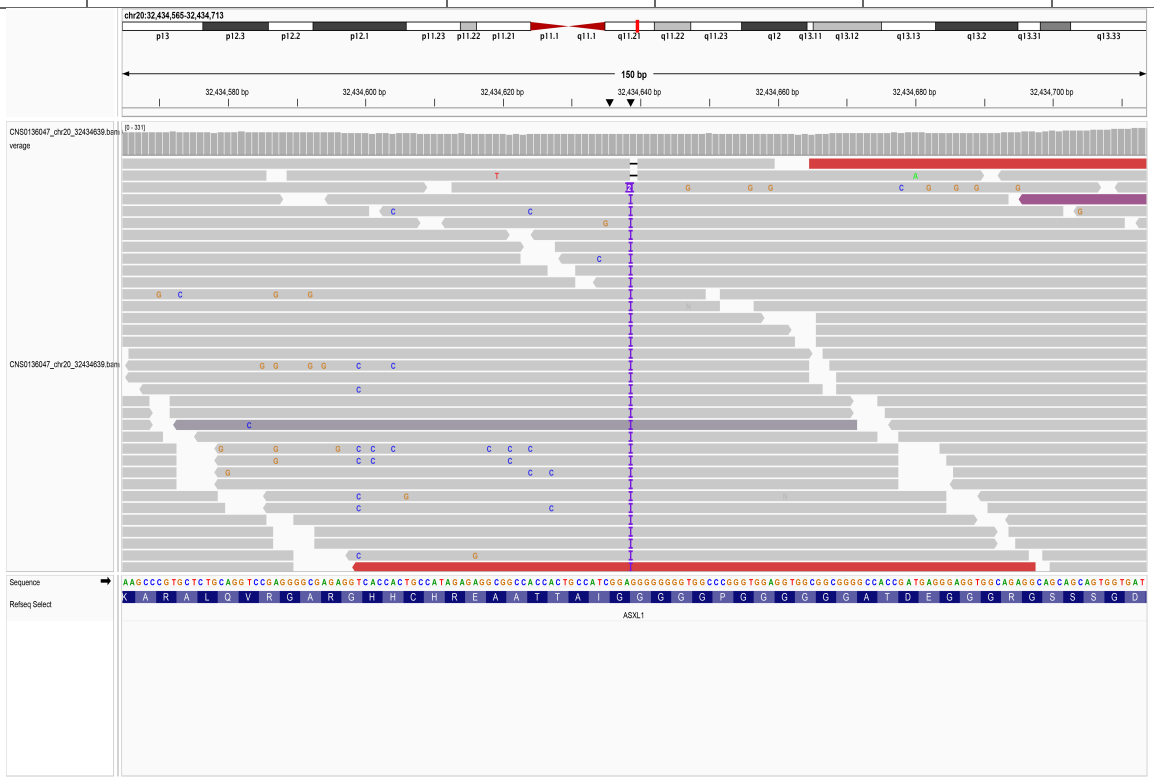
1.12. chr20_32434639_GGGG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09328	chr20_32434639_GGGG/-	64	14	*ASXL1*	frameshift_variant



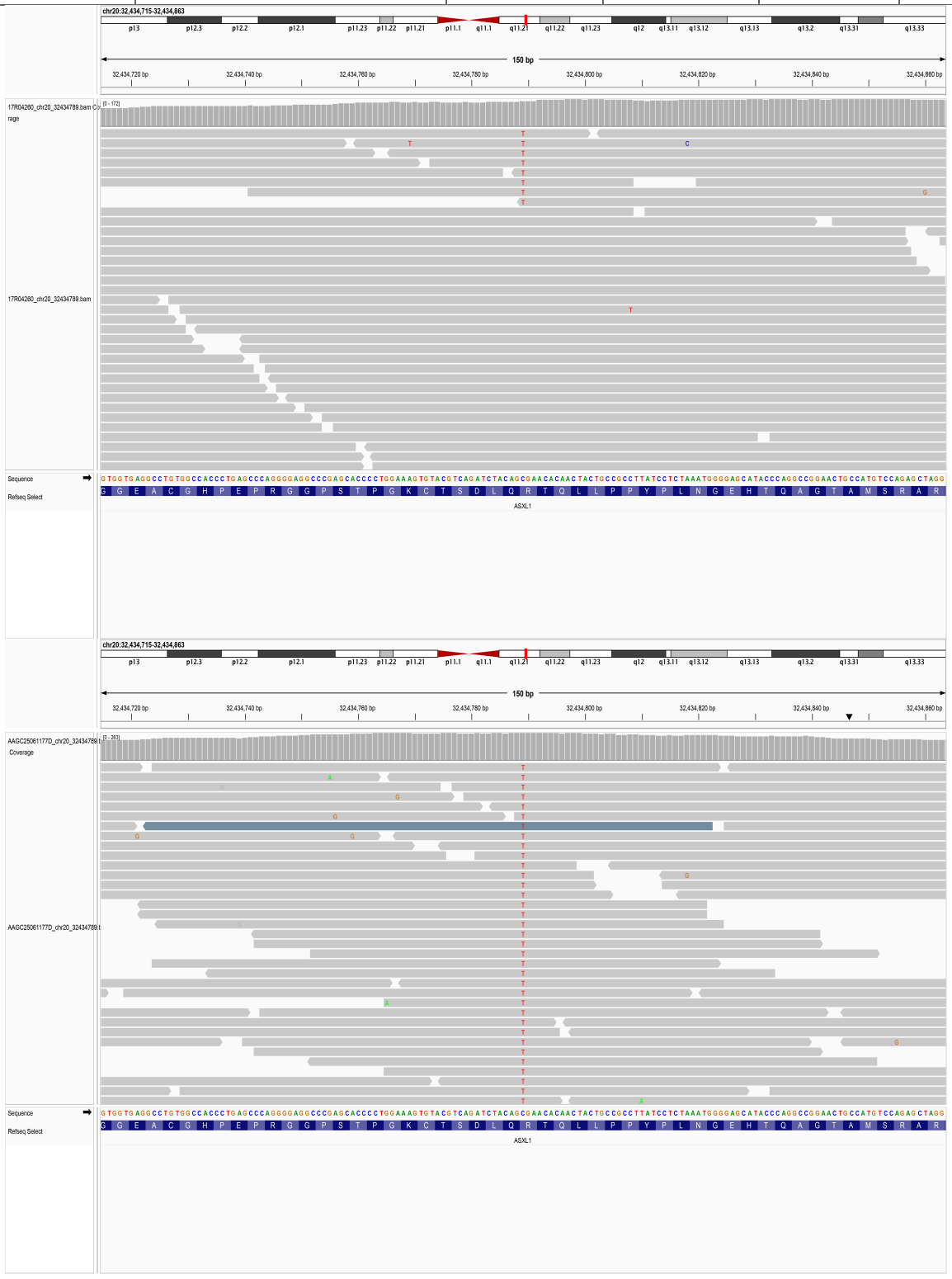
1.13. chr20_32434639_-/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136047	chr20_32434639_-/G	111	51	*ASXL1*	frameshift_variant



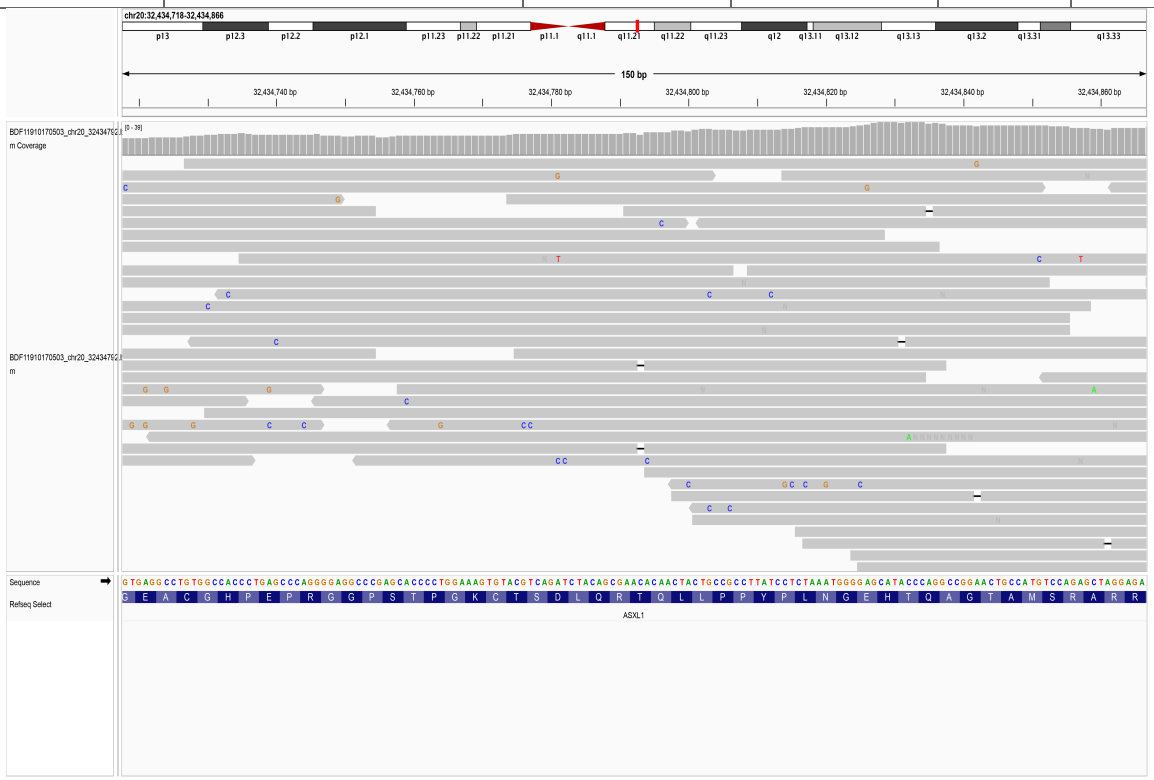
1.14. chr20_32434789_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R04260	chr20_32434789_C/T	146	7	*ASXL1*	stop_gained
AAGC25061177D	chr20_32434789_C/T	223	35	*ASXL1*	stop_gained



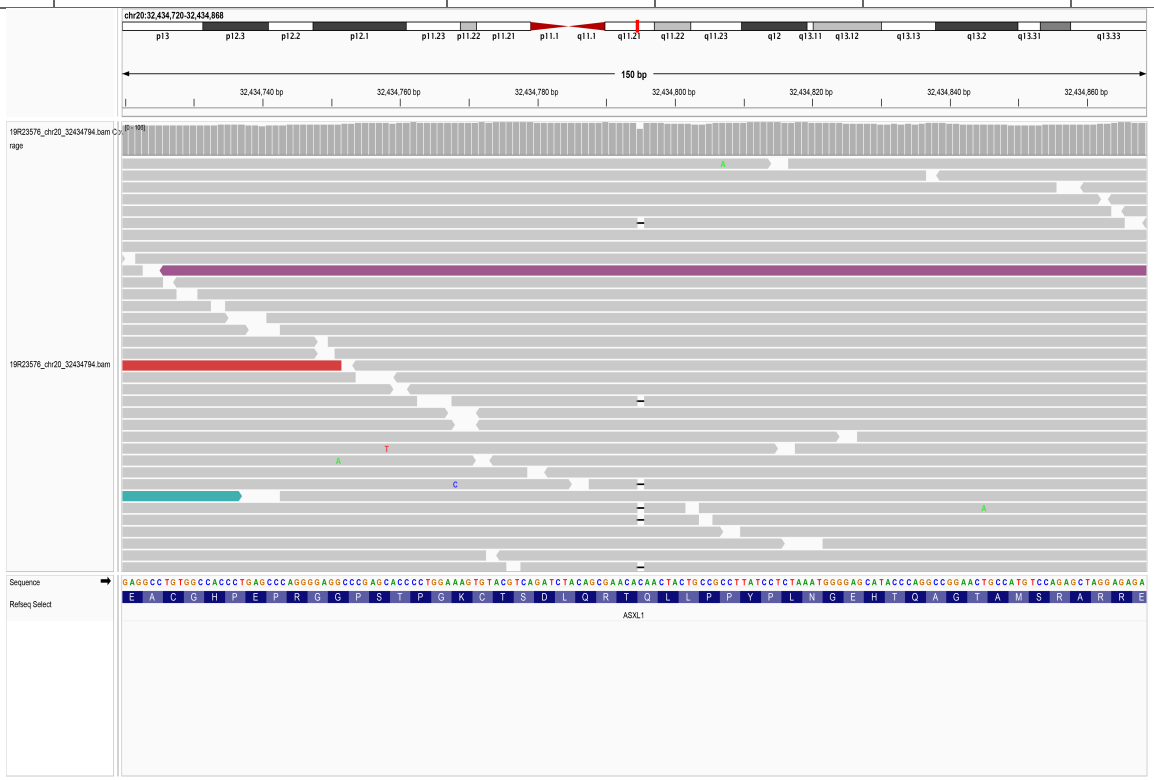
1.15. chr20_32434793_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr20_32434793_C/-	20	2	*ASXL1*	frameshift_variant



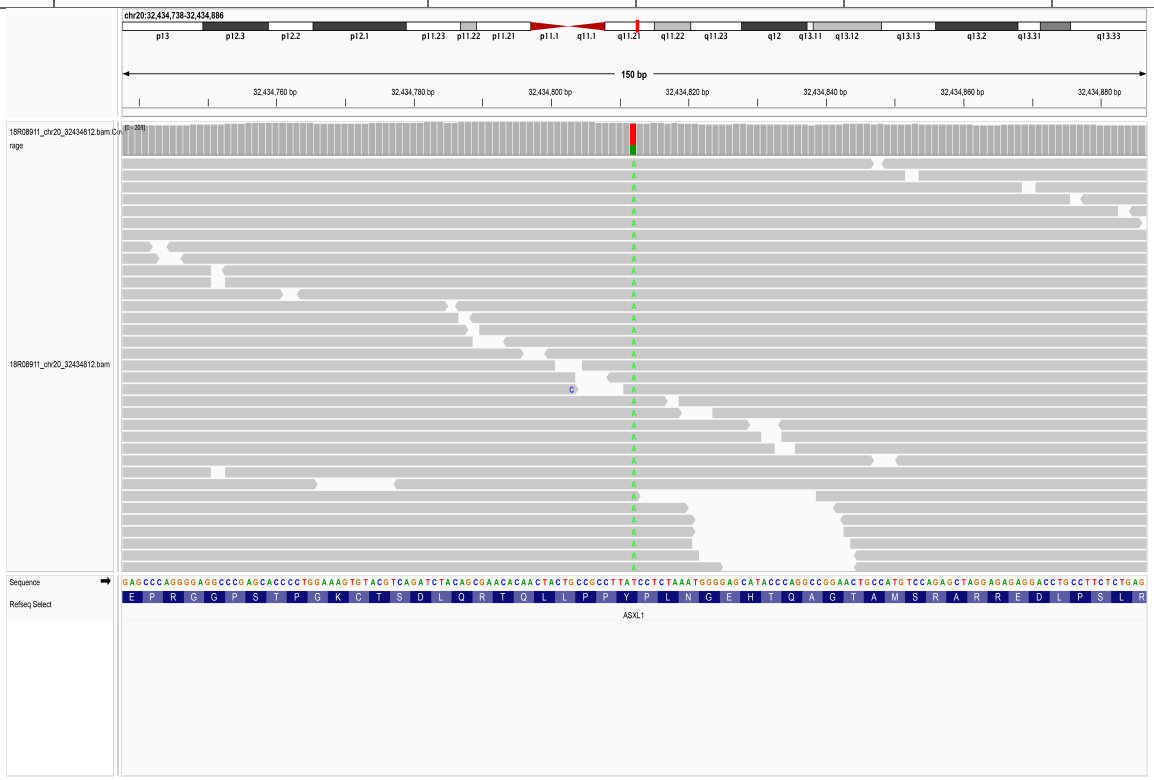
1.16. chr20_32434795_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23576	chr20_32434795_C/-	81	18	*ASXL1*	frameshift_variant



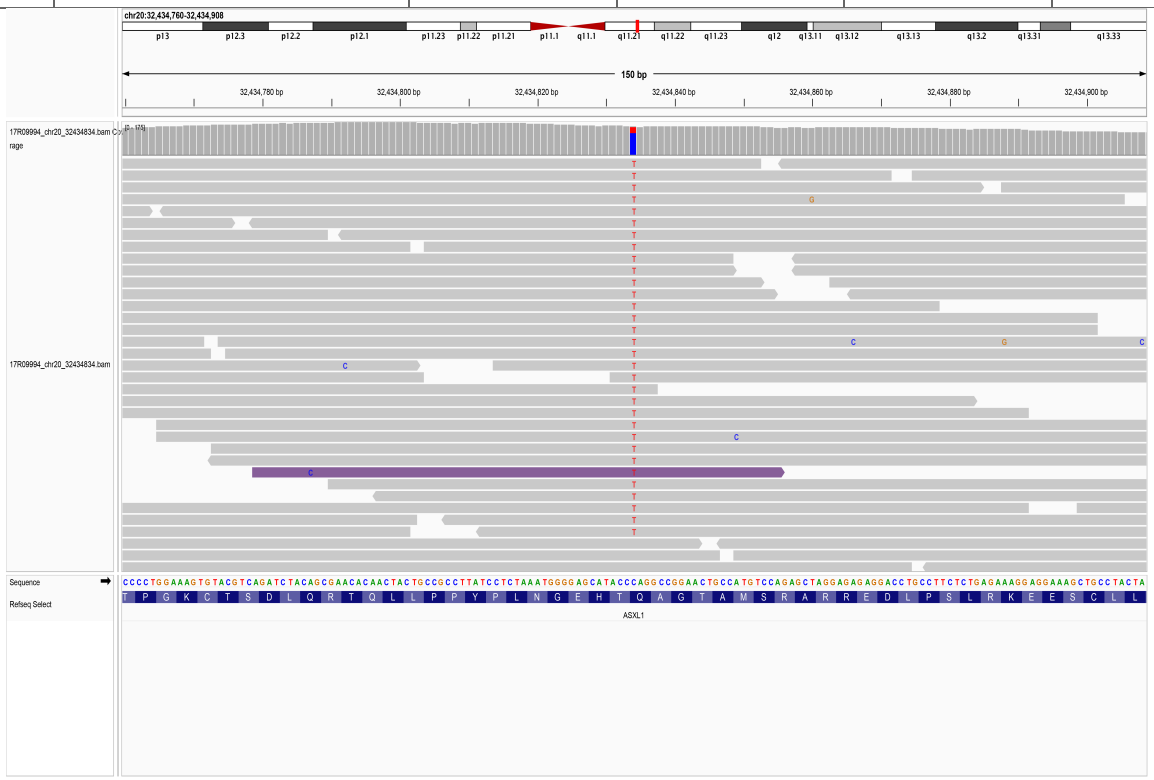
1.17. chr20_32434812_T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08911	chr20_32434812_T/A	128	66	*ASXL1*	stop_gained



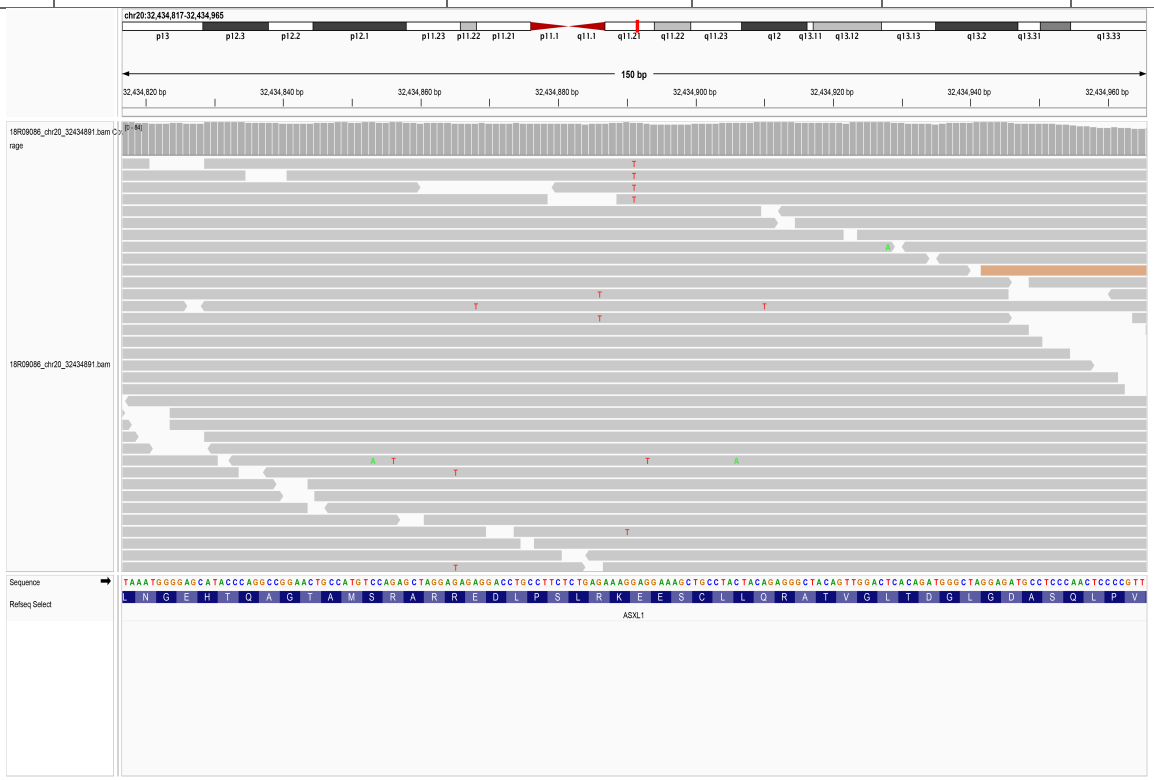
1.18. chr20_32434834_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09994	chr20_32434834_C/T	117	31	*ASXL1*	stop_gained



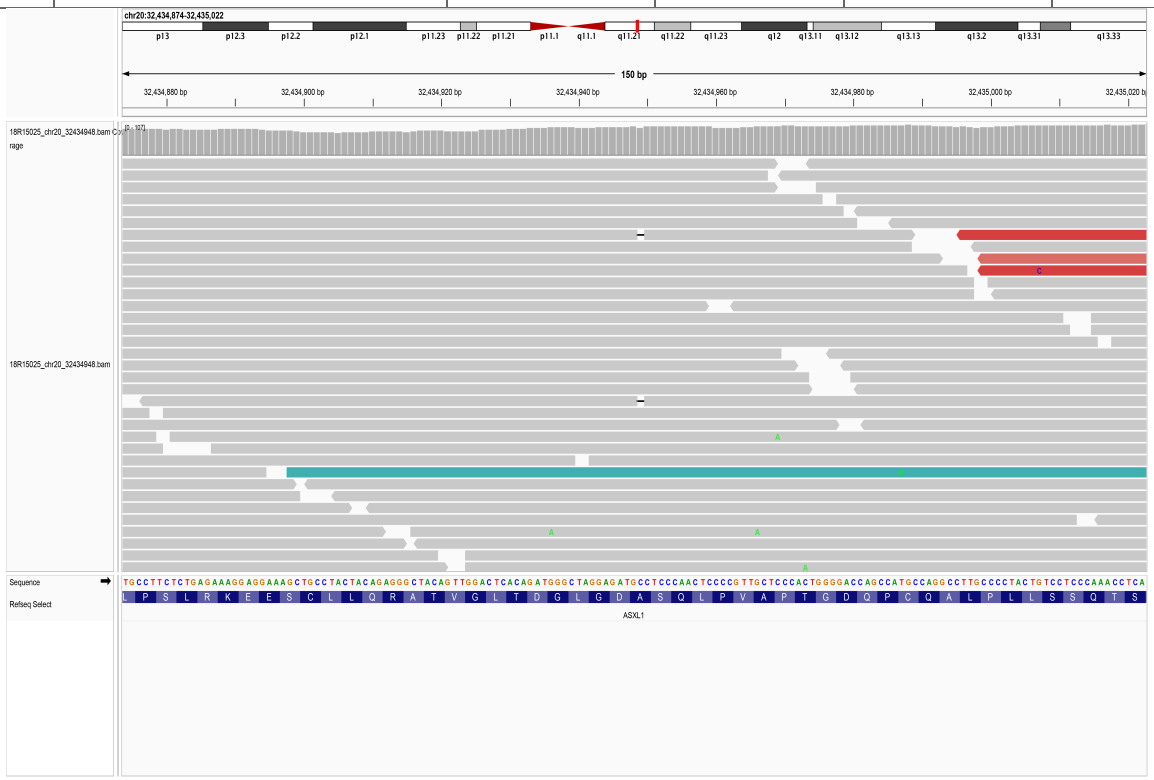
1.19. chr20_32434891_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09086	chr20_32434891_G/T	73	4	*ASXL1*	stop_gained



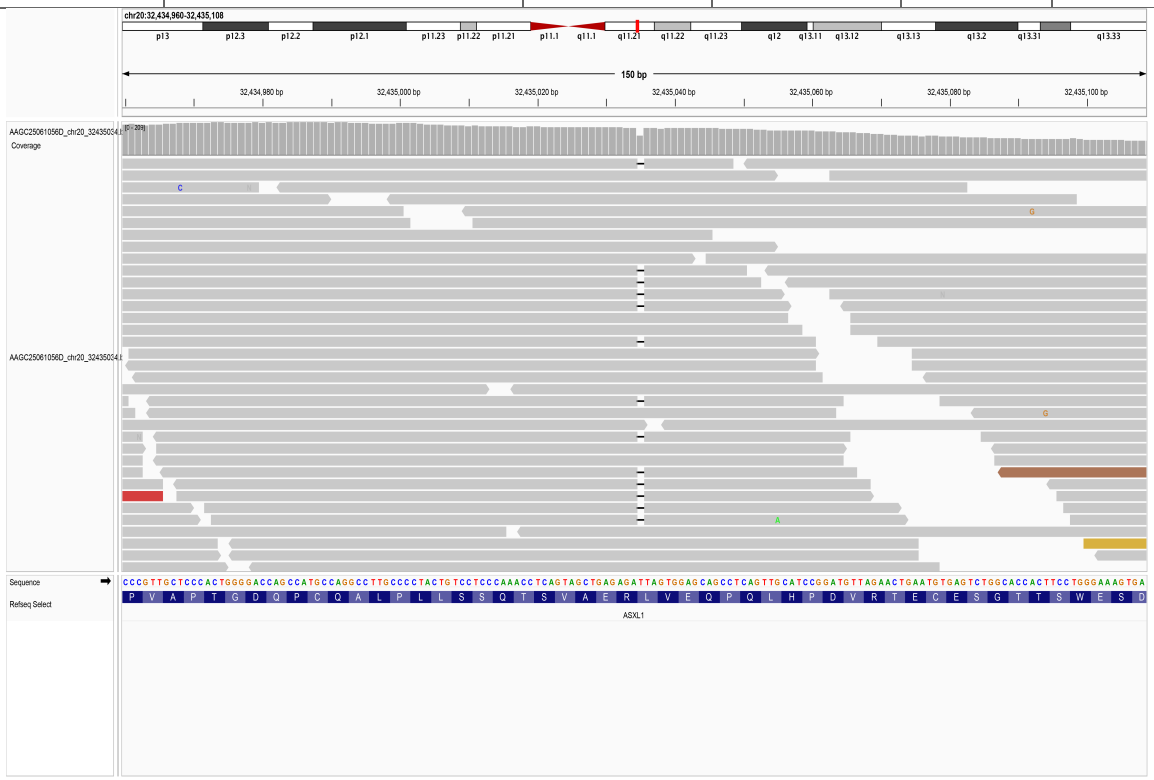
1.20. chr20_32434949_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15025	chr20_32434949_C/-	81	5	*ASXL1*	frameshift_variant



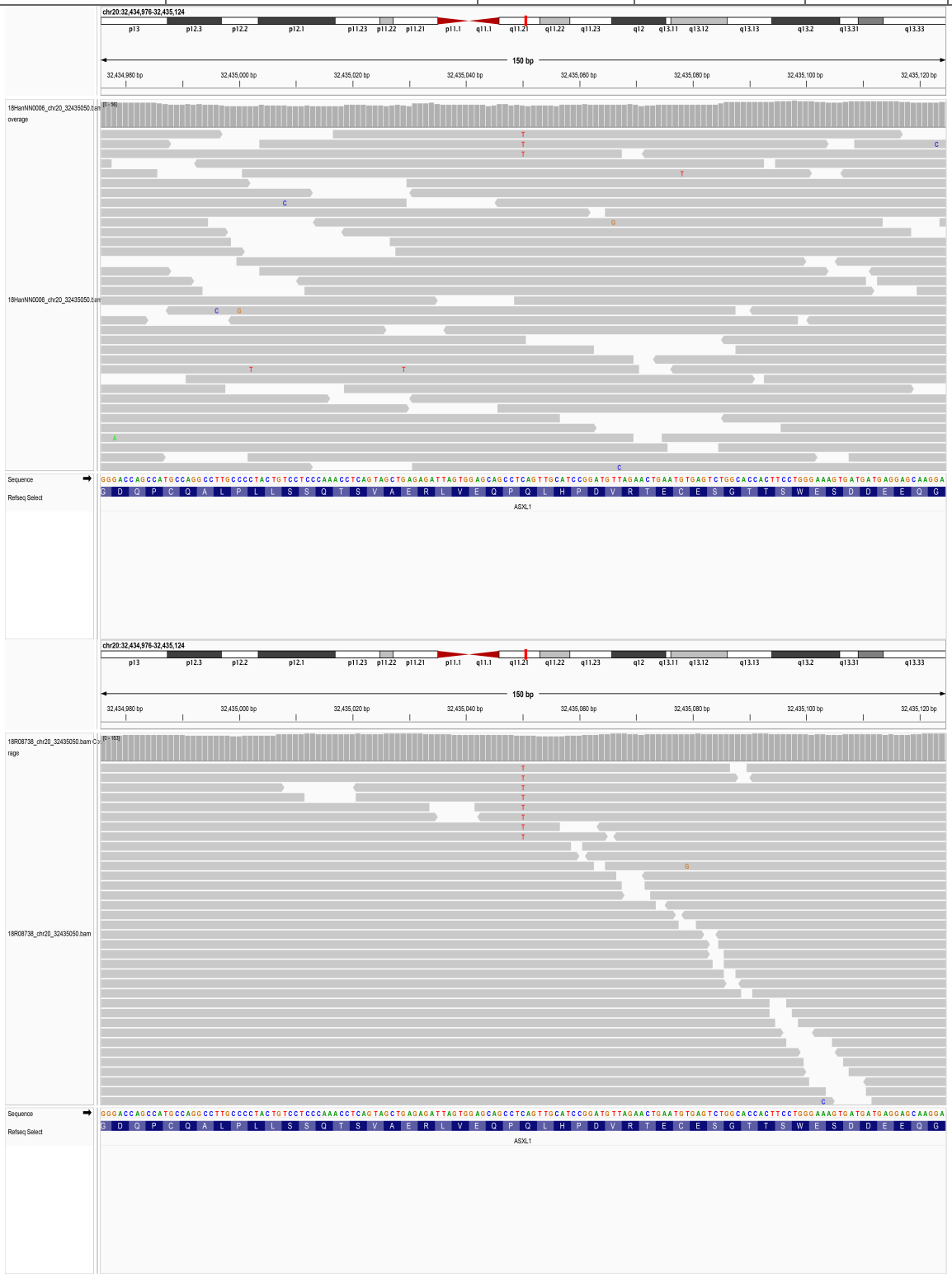
1.21. chr20_32435035_T/-

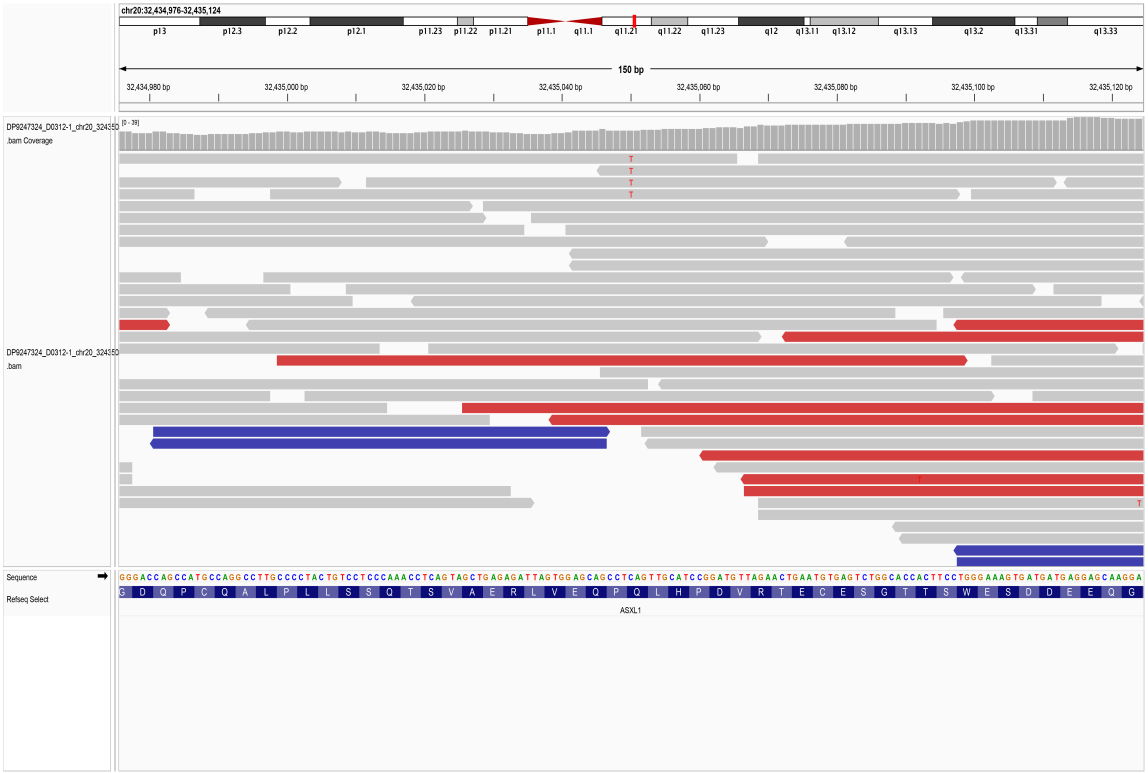
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061056D	chr20_32435035_T/-	117	49	*ASXL1*	frameshift_variant



1.22. chr20_32435050_C/T

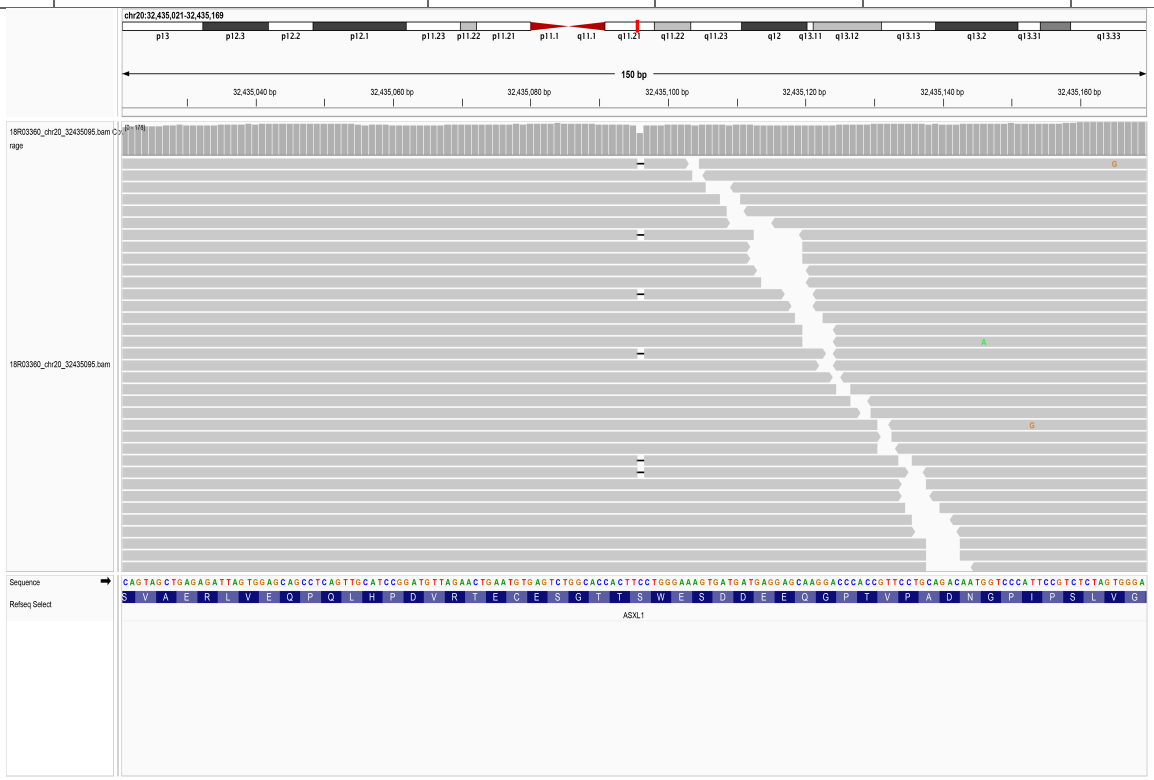
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0006	chr20_32435050_C/T	41	3	*ASXL1*	stop_gained
18R08738	chr20_32435050_C/T	130	8	*ASXL1*	stop_gained
DP9247324_D0312-1	chr20_32435050_C/T	19	4	*ASXL1*	stop_gained




chr20:32,434,976-32,435,124
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
150 bp
32,434,980 bp
32,435,000 bp
32,435,020 bp
32,435,040 bp
32,435,060 bp
32,435,080 bp
32,435,100 bp
32,435,120 bp
DP9247324_D0312-1_chr20_32435D
.bam Coverage
[0 - 39]
DP9247324_D0312-1_chr20_32435D
.bam
Sequence
Refseq Select
GGGACCAGCCATGCCAGGCCTTGCCCCTACTGTCCTCCCAAACCTCAGTAGCTGAGAGATTAGTGGAGCAGCCTCAGTTGCATCCGGATGTTAGAACTGAATGTGAGTCTGGCACCCACTTCCTGGGAAAGTGATGAGGAGCAAGGA
G D Q P C Q A L P L L S S Q T S V A E R L V E Q P Q L H P D V R T E C E S G T T S W E S D D E E Q G
ASXL1

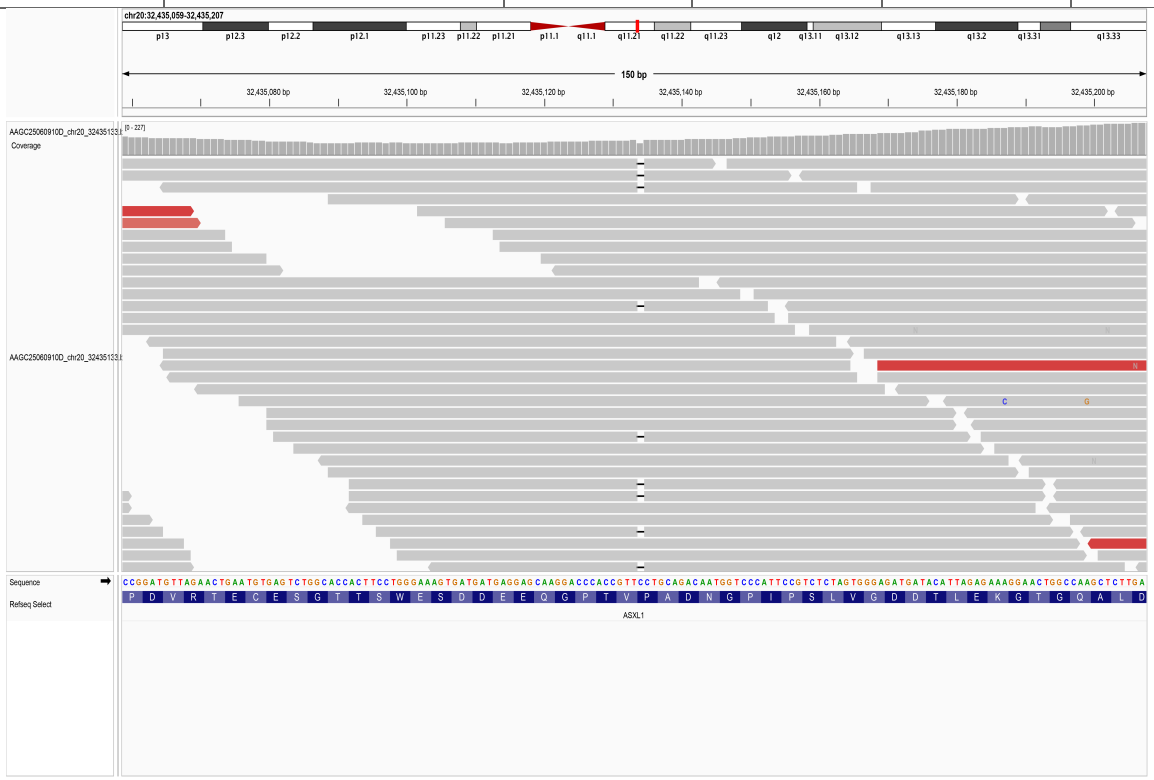
1.23. chr20_32435096_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03360	chr20_32435096_C/-	117	43	*ASXL1*	frameshift_variant



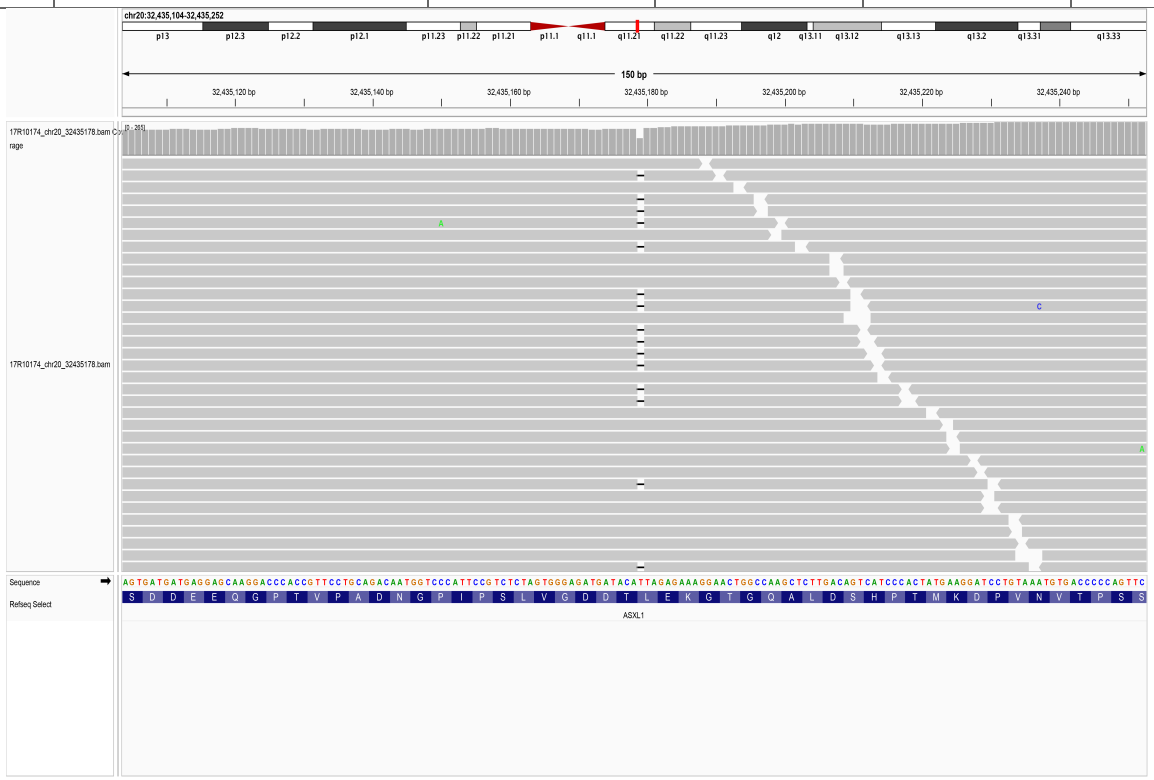
1.24. chr20_32435134_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060910D	chr20_32435134_C/-	80	25	*ASXL1*	frameshift_variant



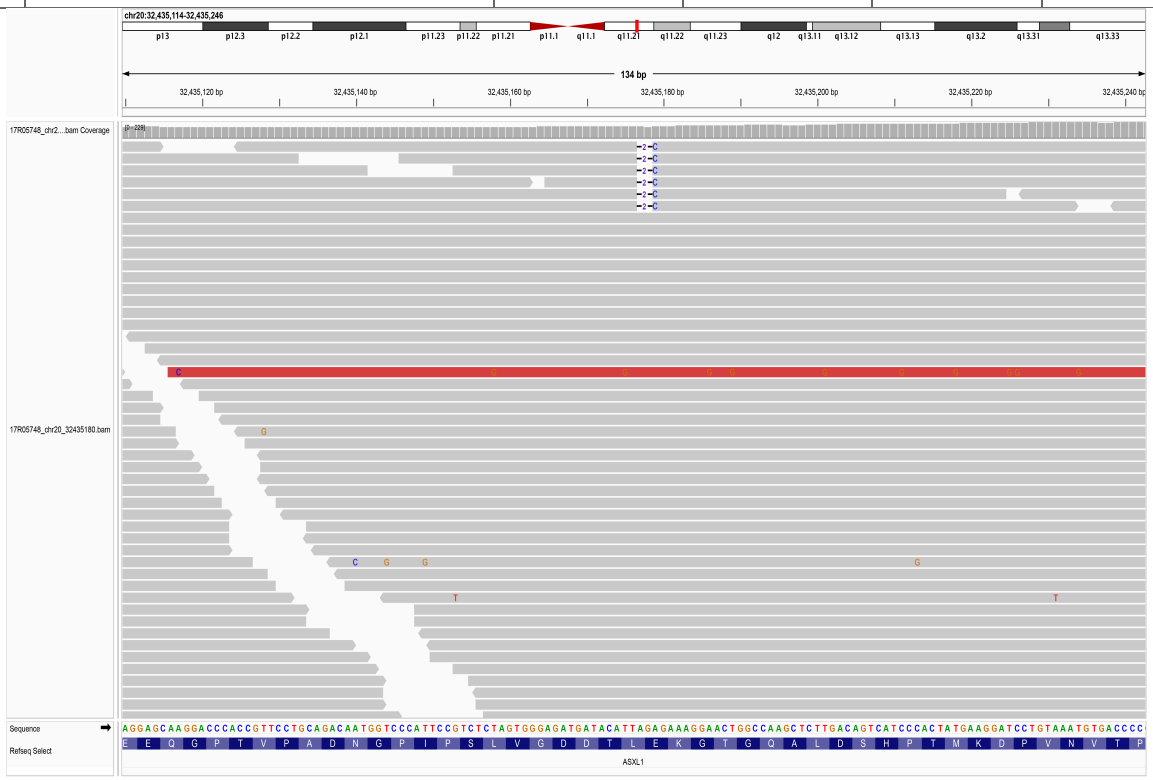
1.25. chr20_32435179_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R10174	chr20_32435179_T/-	130	81	*ASXL1*	frameshift_variant



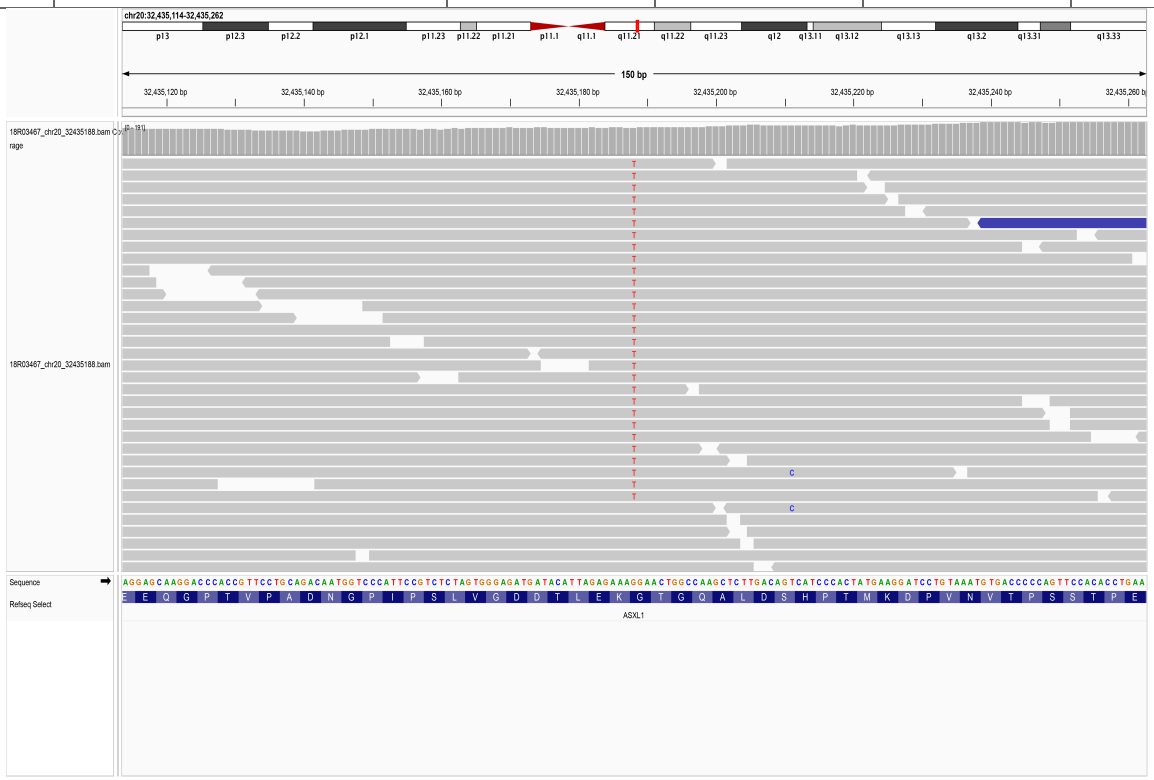
1.26. chr20_32435181_AG/-/AGAG

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05748	chr20_32435181_AG/-/AGAG	152	9	*ASXL1*	frameshift_variant



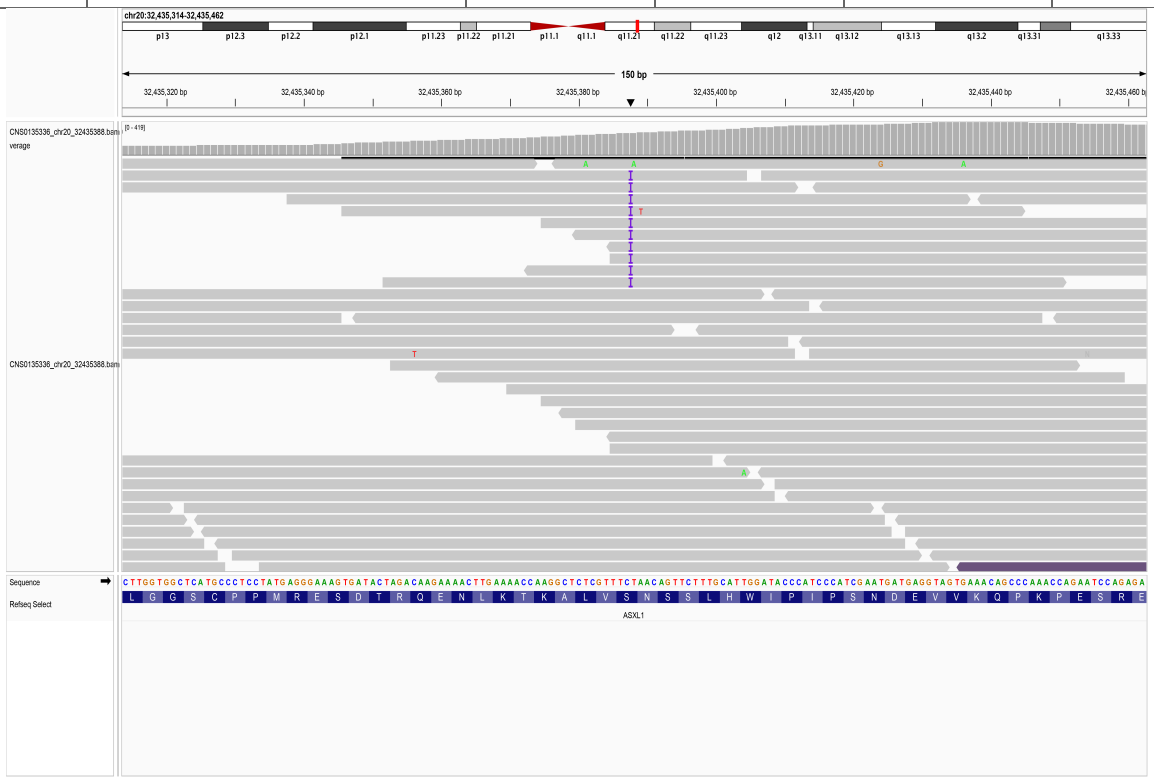
1.27. chr20_32435188_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03467	chr20_32435188_G/T	127	29	*ASXL1*	stop_gained



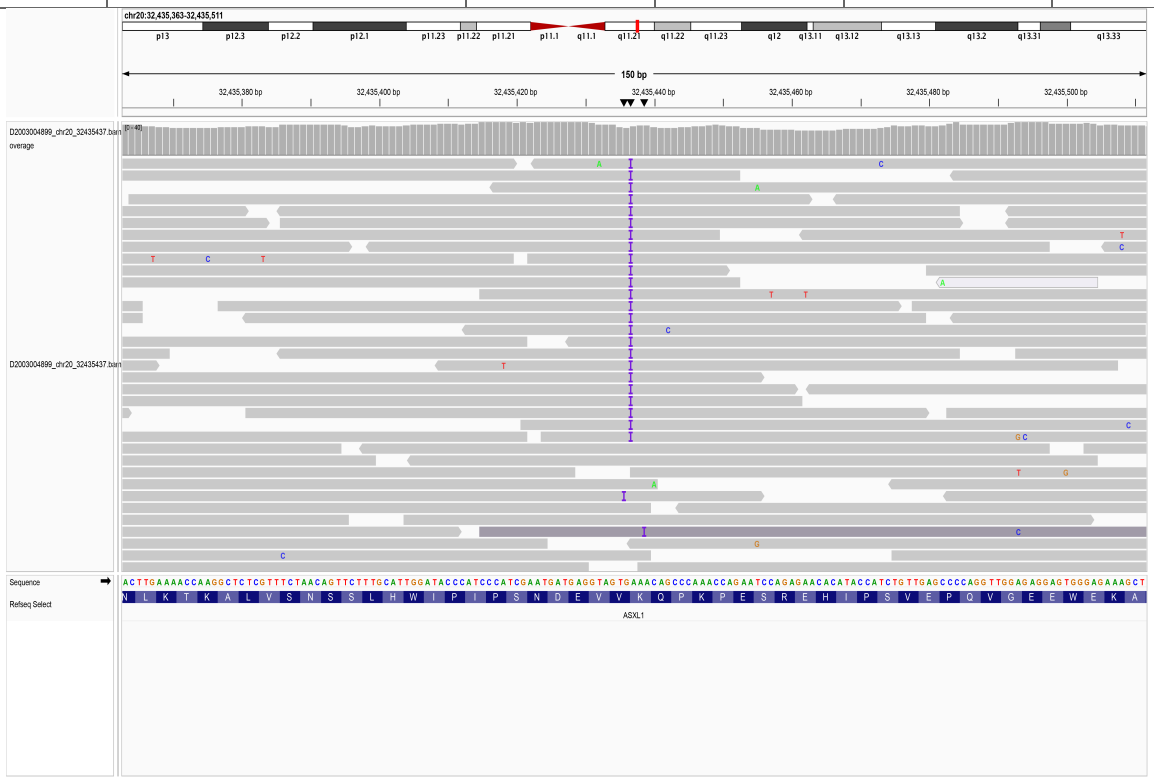
1.28. chr20_32435388_-/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135336	chr20_32435388_-/T	255	16	*ASXL1*	frameshift_variant



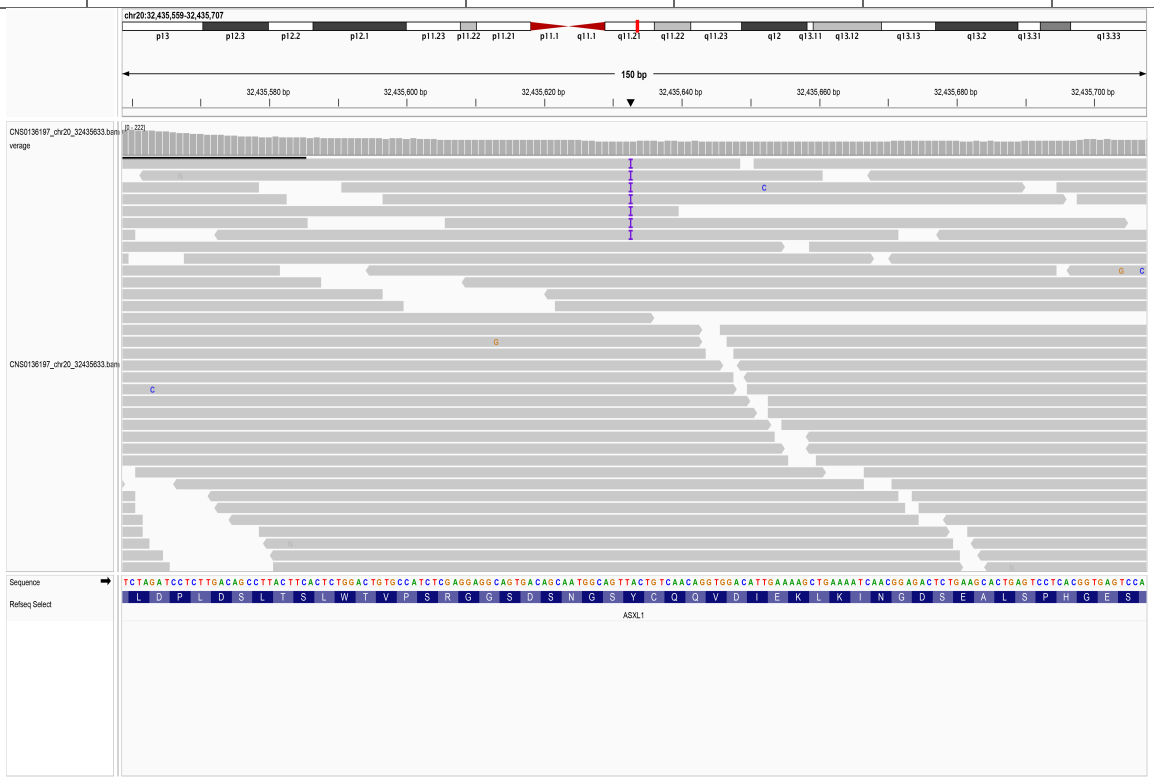
1.29. chr20_32435437_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2003004899	chr20_32435437_-/A	3	29	*ASXL1*	frameshift_variant



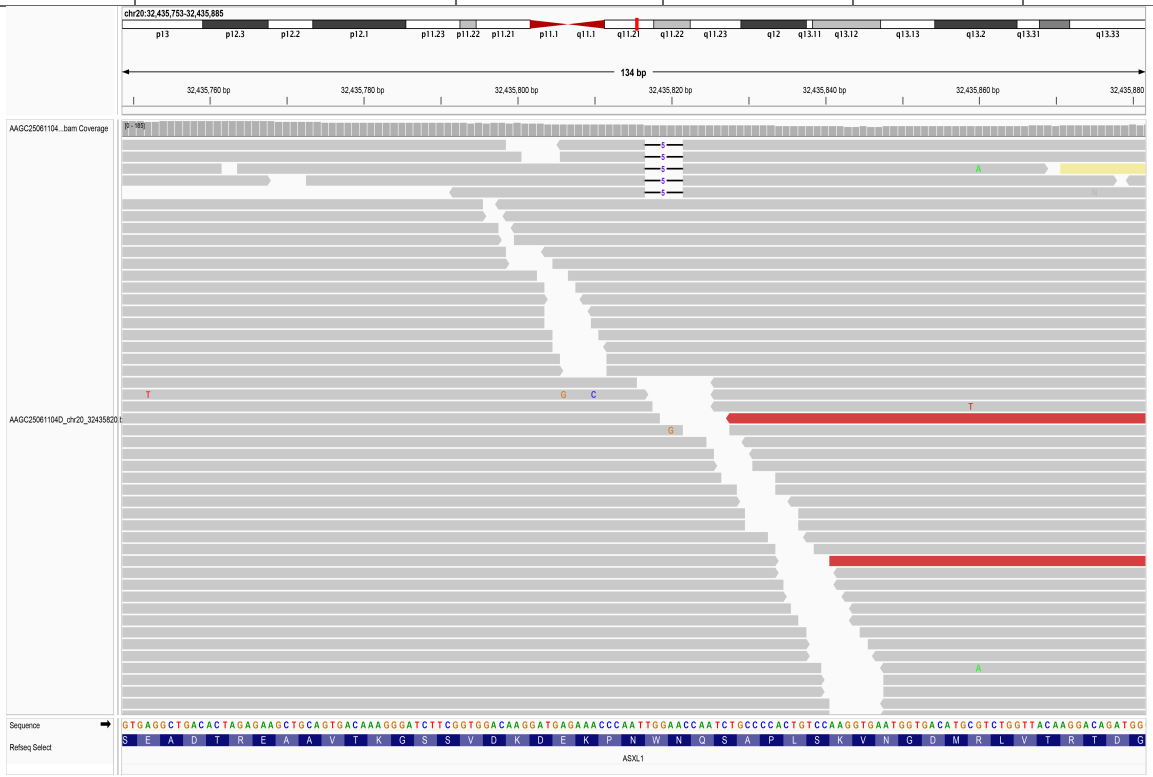
1.30. chr20_32435633_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136197	chr20_32435633_-/A	85	7	*ASXL1*	stop_gained



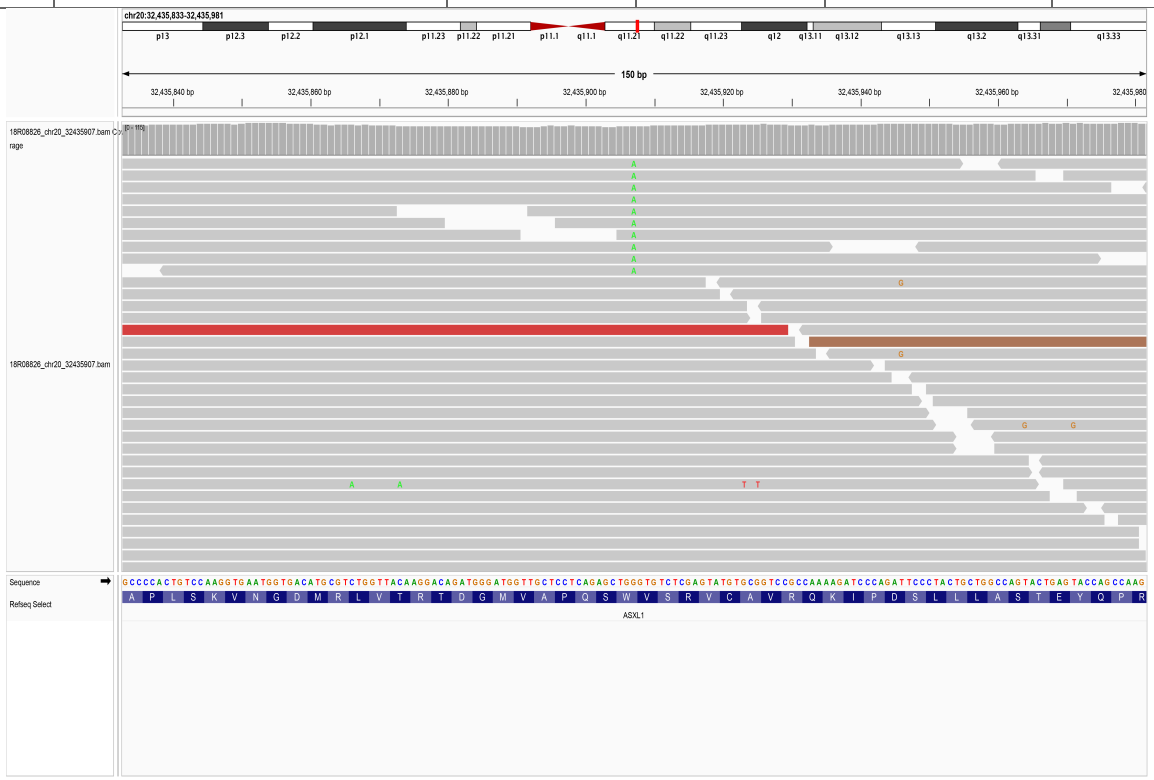
1.31. chr20_32435821_TGGAA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061104D	chr20_32435821_TGGAA/-	128	5	*ASXL1*	frameshift_variant



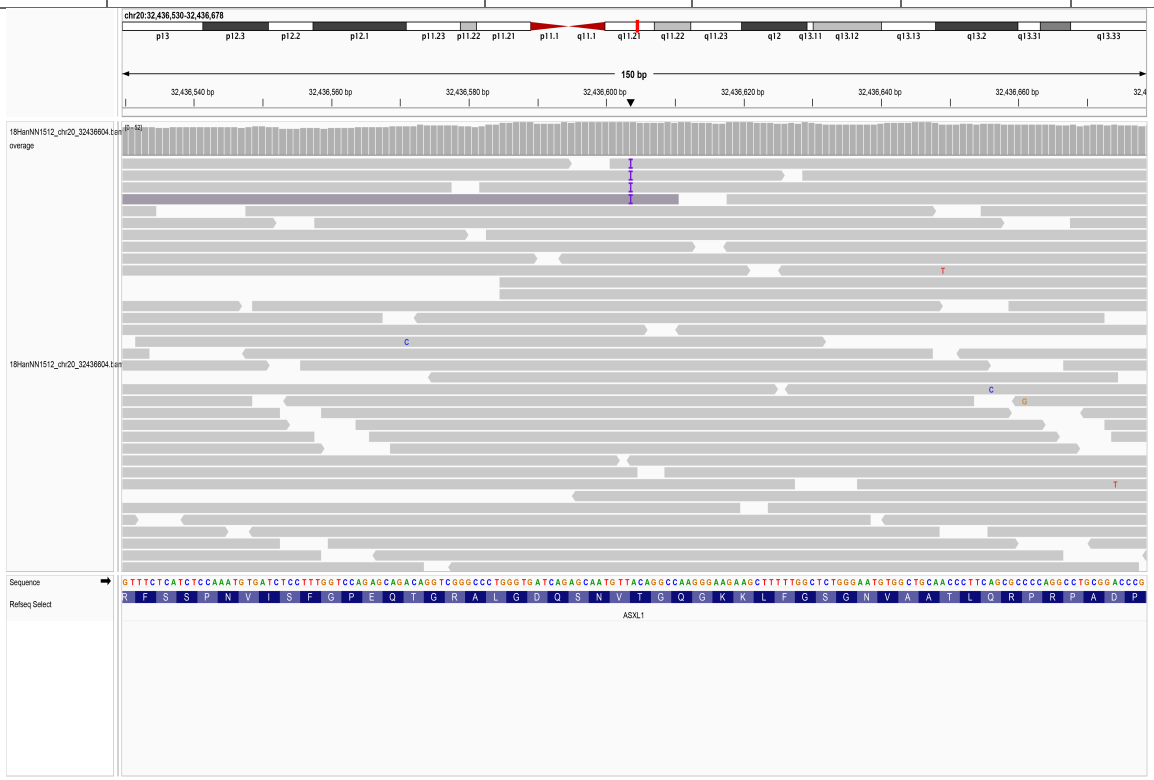
1.32. chr20_32435907_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08826	chr20_32435907_G/A	88	10	*ASXL1*	stop_gained



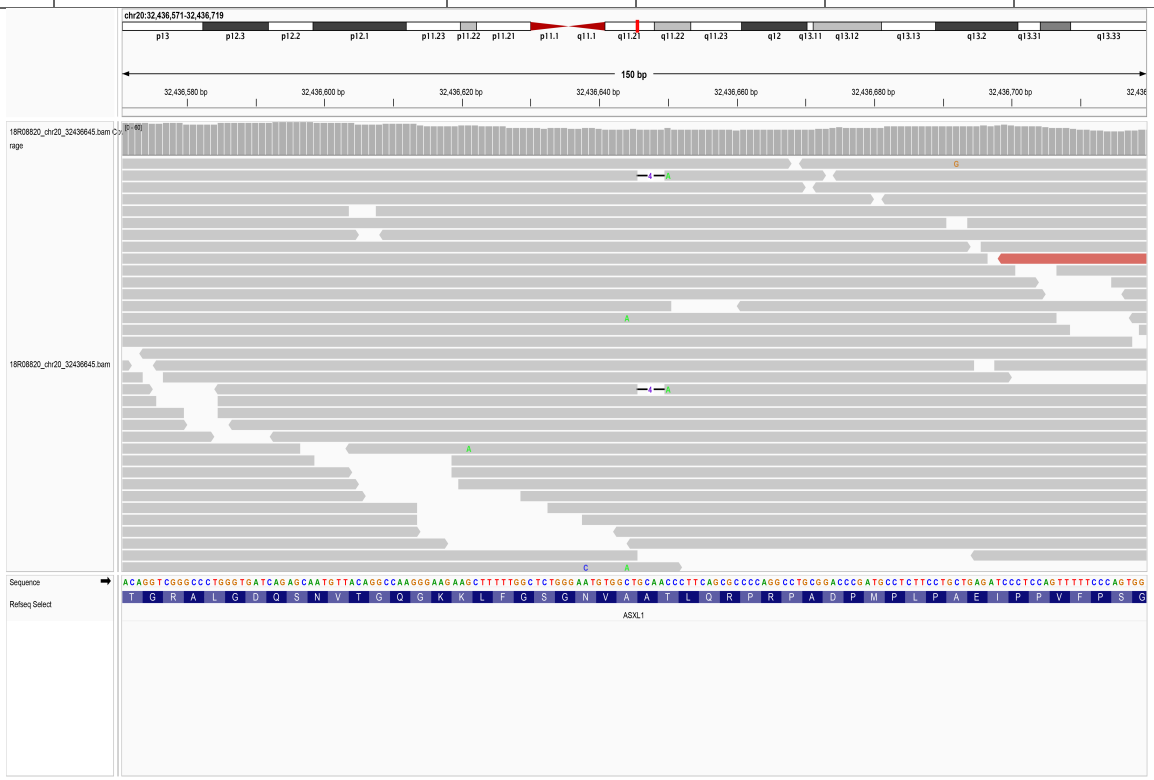
1.33. chr20_32436604_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN1512	chr20_32436604_-/A	45	4	*ASXL1*	frameshift_variant



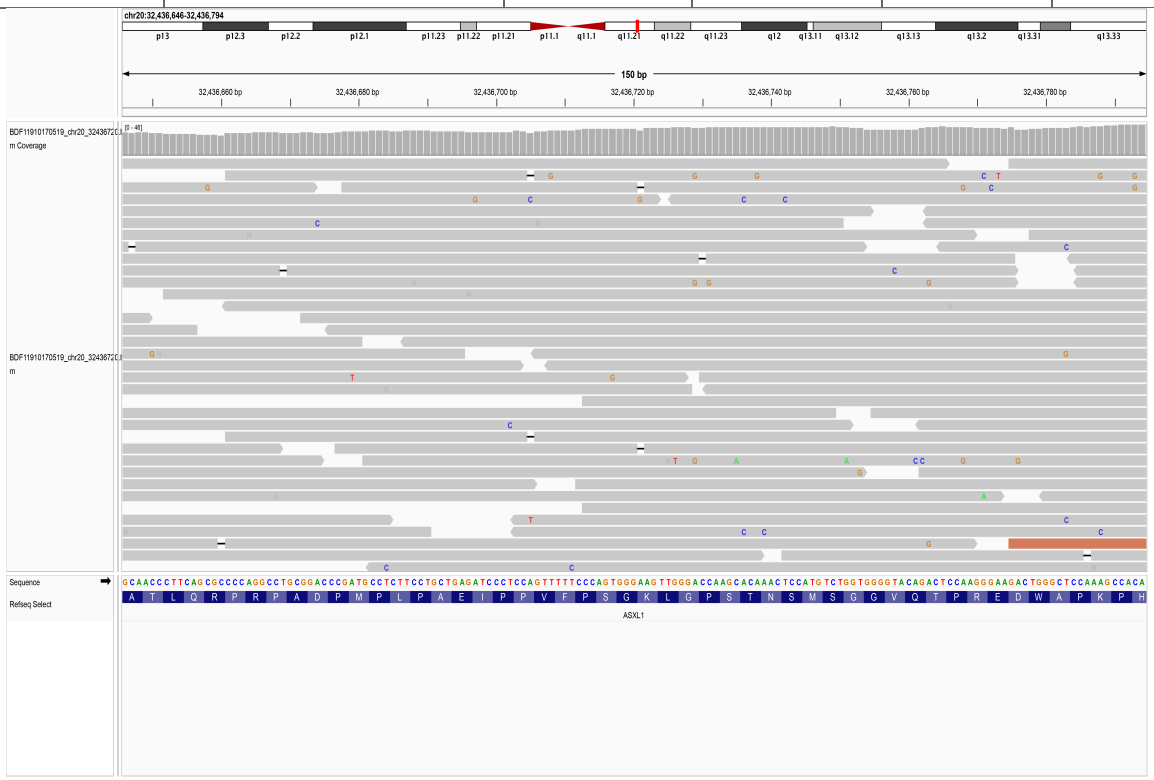
1.34. chr20_32436646_GC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08820	chr20_32436646_GC/-	45	2	*ASXL1*	frameshift_variant



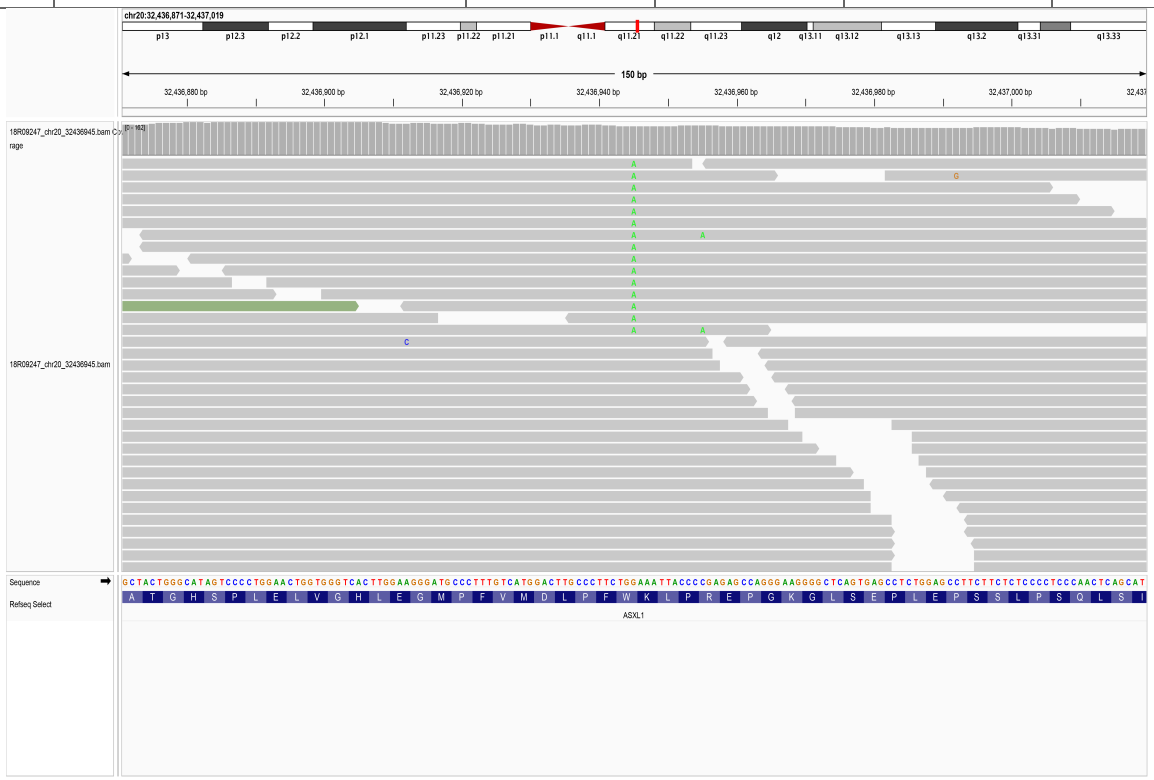
1.35. chr20_32436721_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chr20_32436721_A/-	25	2	*ASXL1*	frameshift_variant



1.36. chr20_32436945_G/A

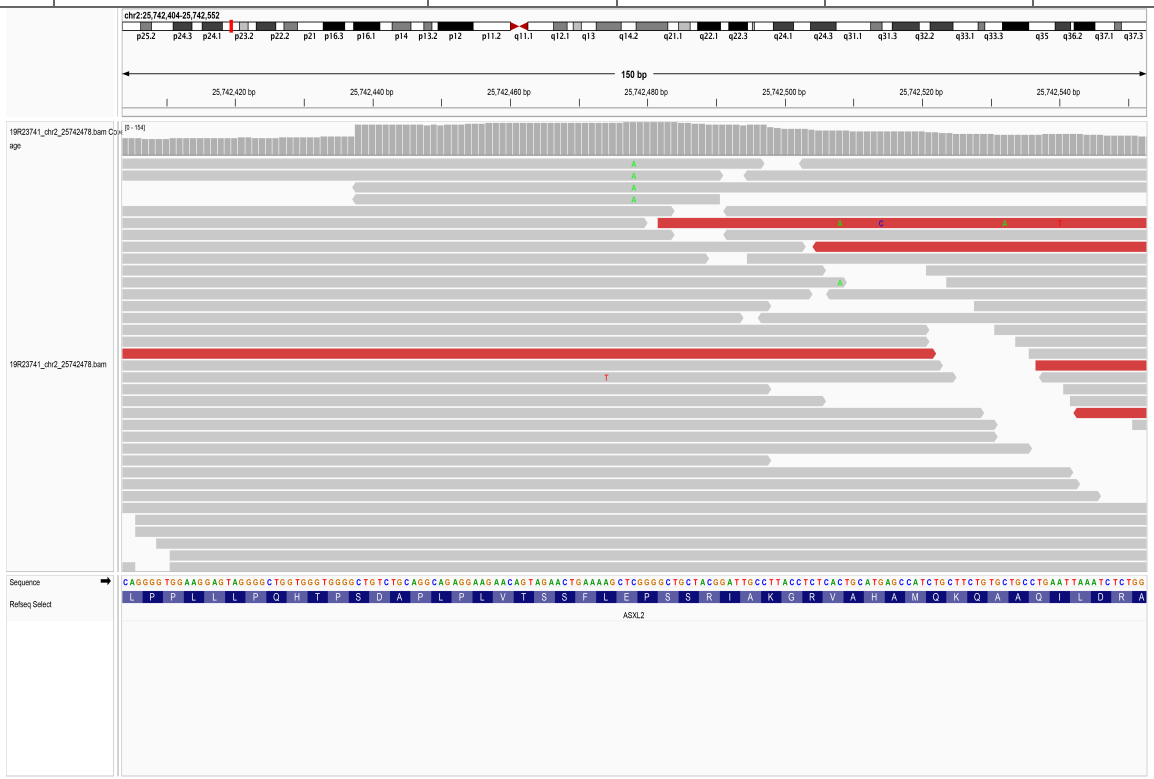
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09247	chr20_32436945_G/A	123	15	*ASXL1*	stop_gained



2. *ASXL2*

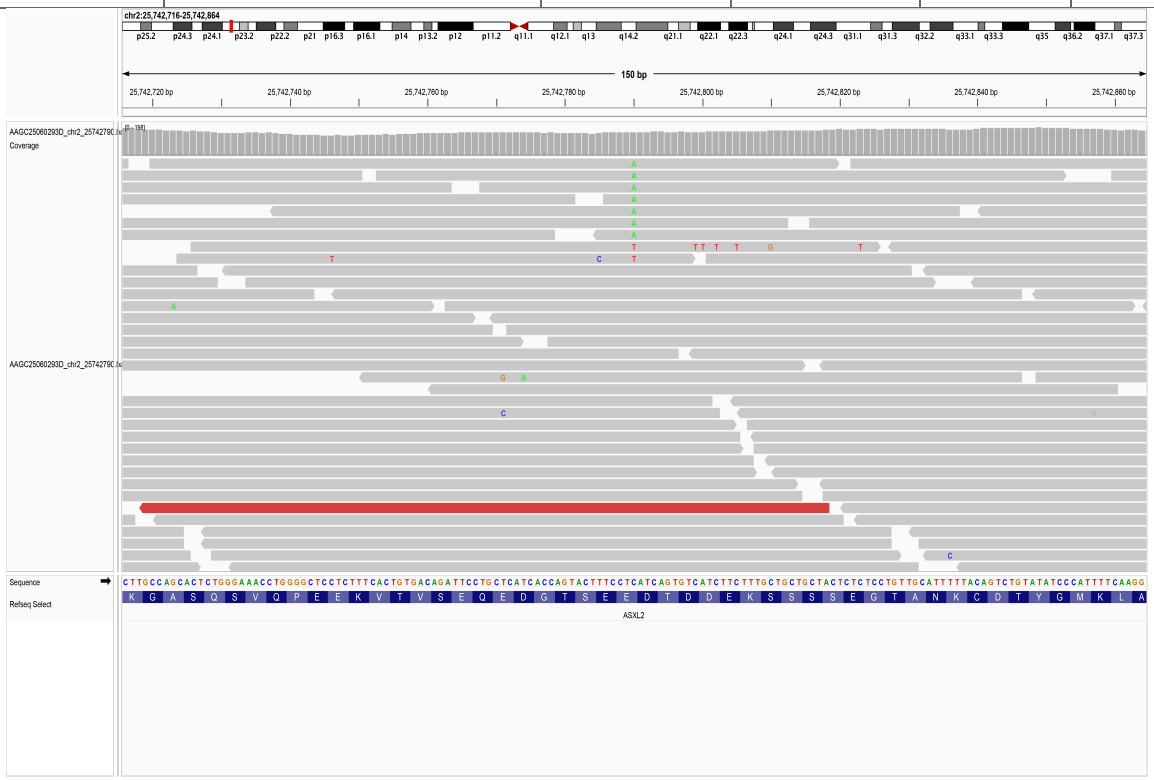
2.1. chr2_25742478_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23741	chr2_25742478_C/A	145	4	*ASXL2*	stop_gained



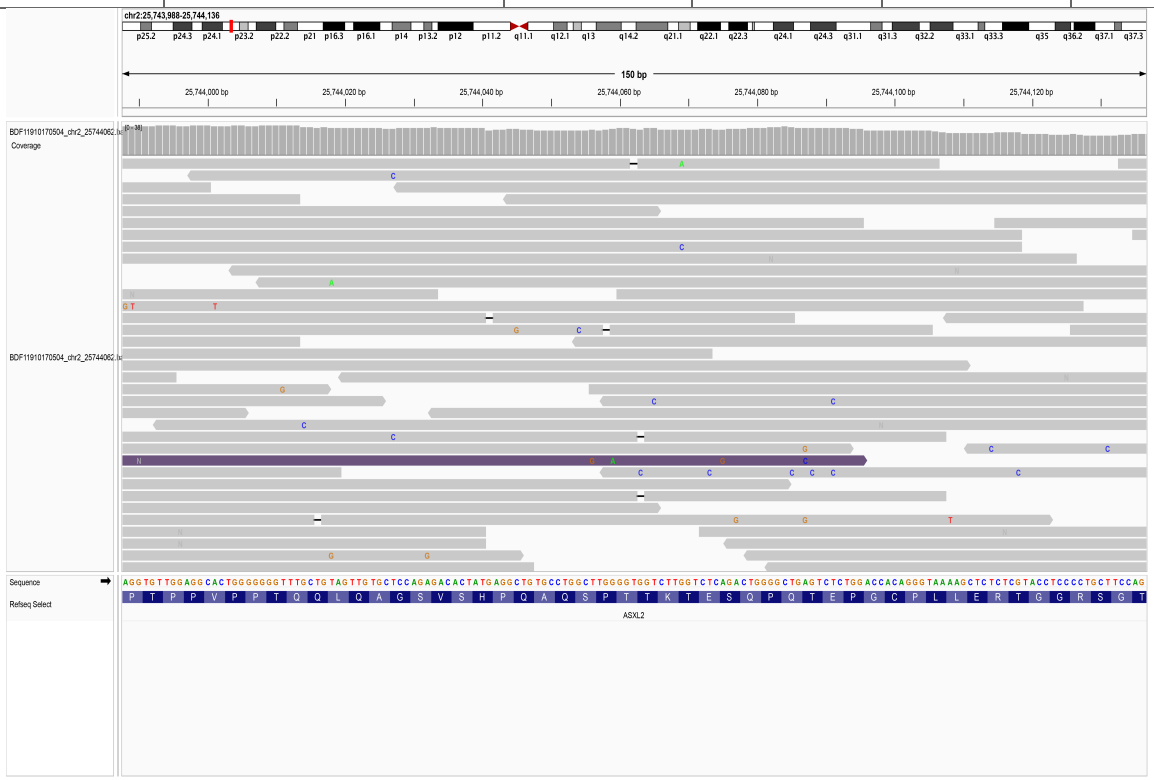
2.2. chr2_25742790_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060293D	chr2_25742790_C/A	125	7	*ASXL2*	stop_gained



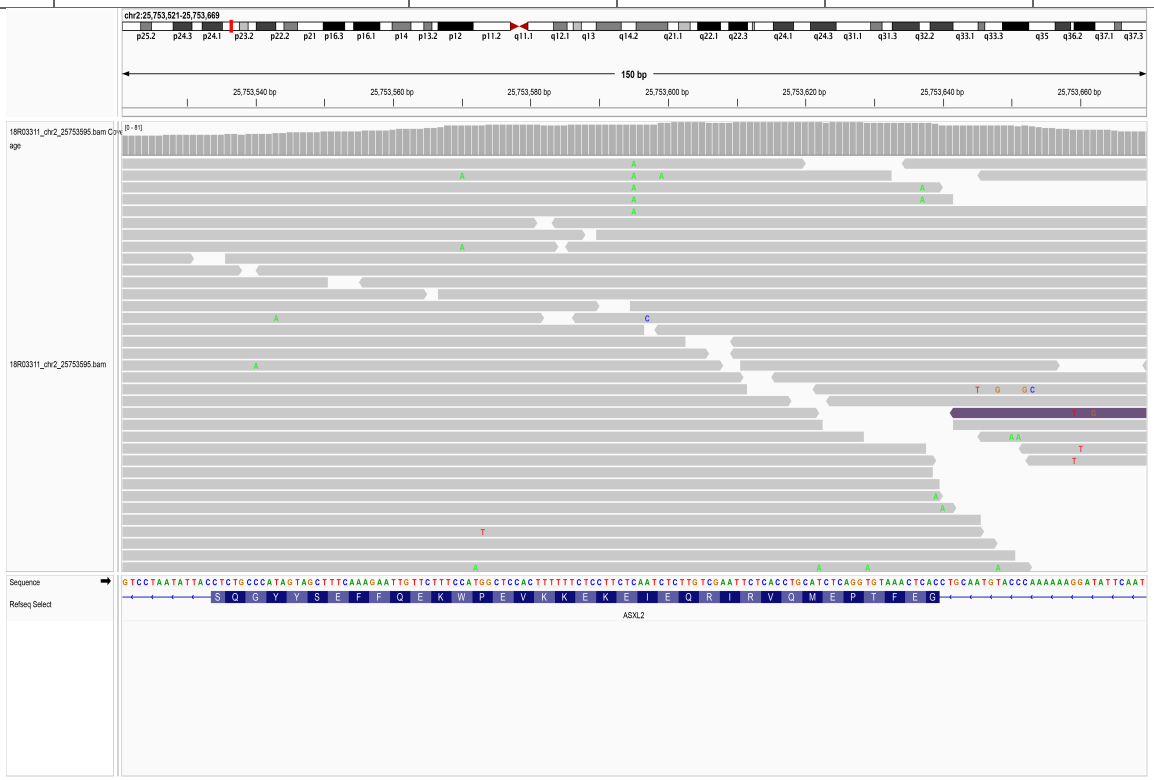
2.3. chr2_25744063_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chr2_25744063_G/-	23	2	*ASXL2*	frameshift_variant



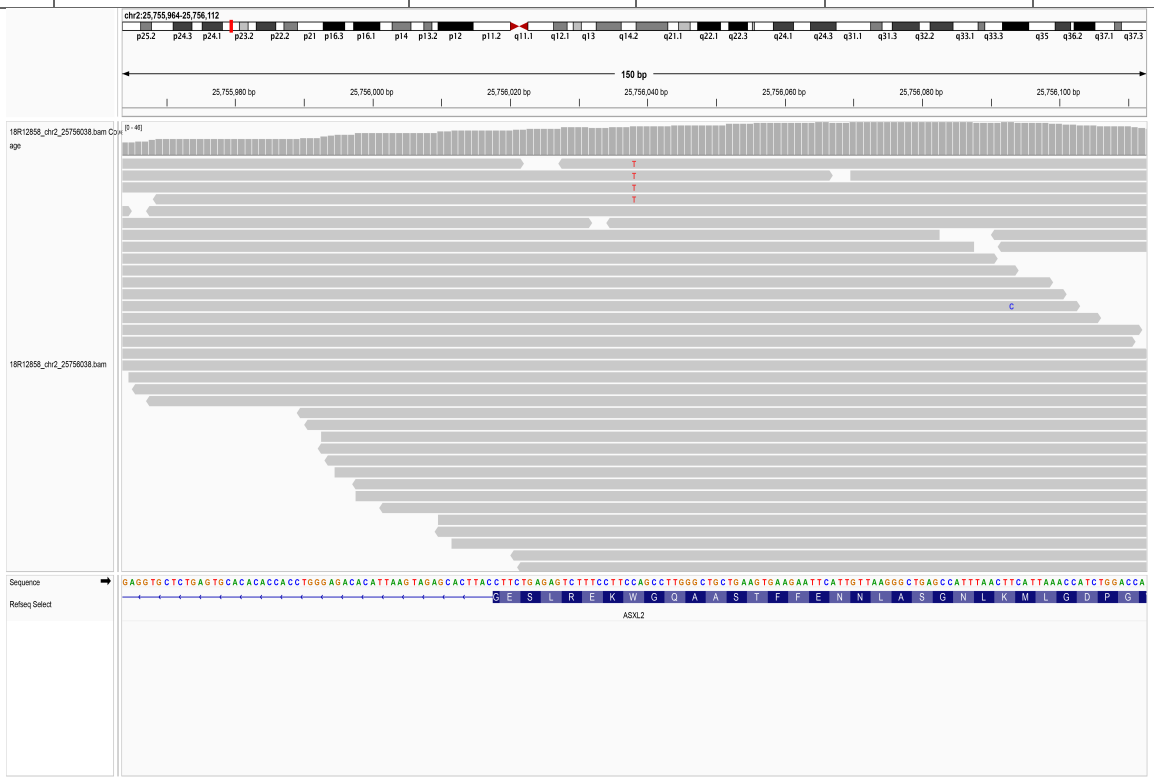
2.4. chr2_25753595_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr2_25753595_C/A	69	5	*ASXL2*	stop_gained



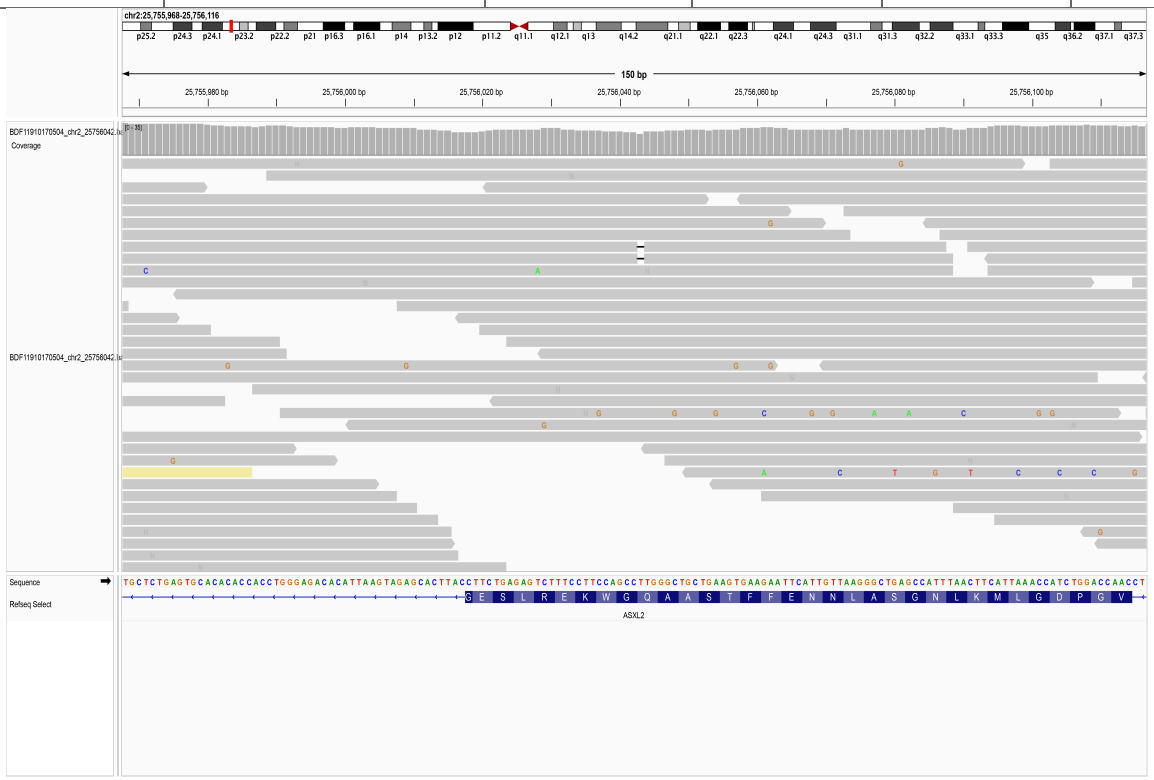
2.5. chr2_25756038_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12858	chr2_25756038_C/T	36	4	*ASXL2*	stop_gained



2.6. chr2_25756043_T/-

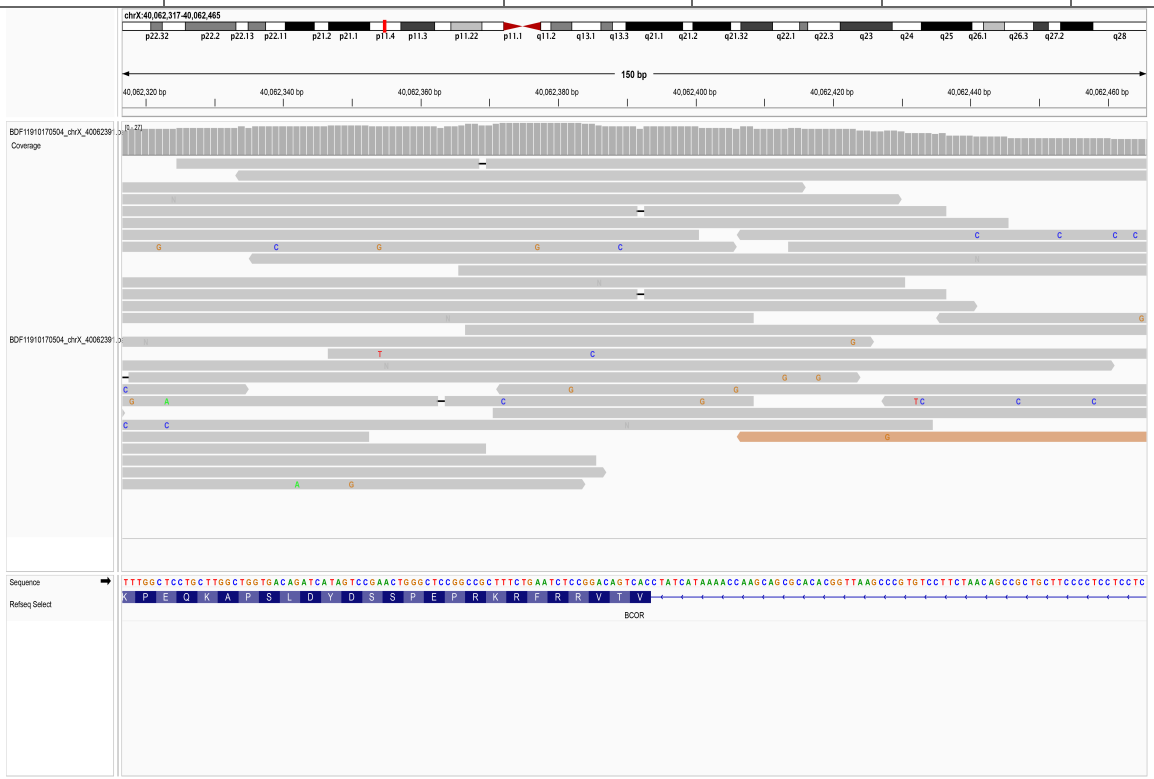
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chr2_25756043_T/-	21	2	*ASXL2*	frameshift_variant



3. *BCOR*

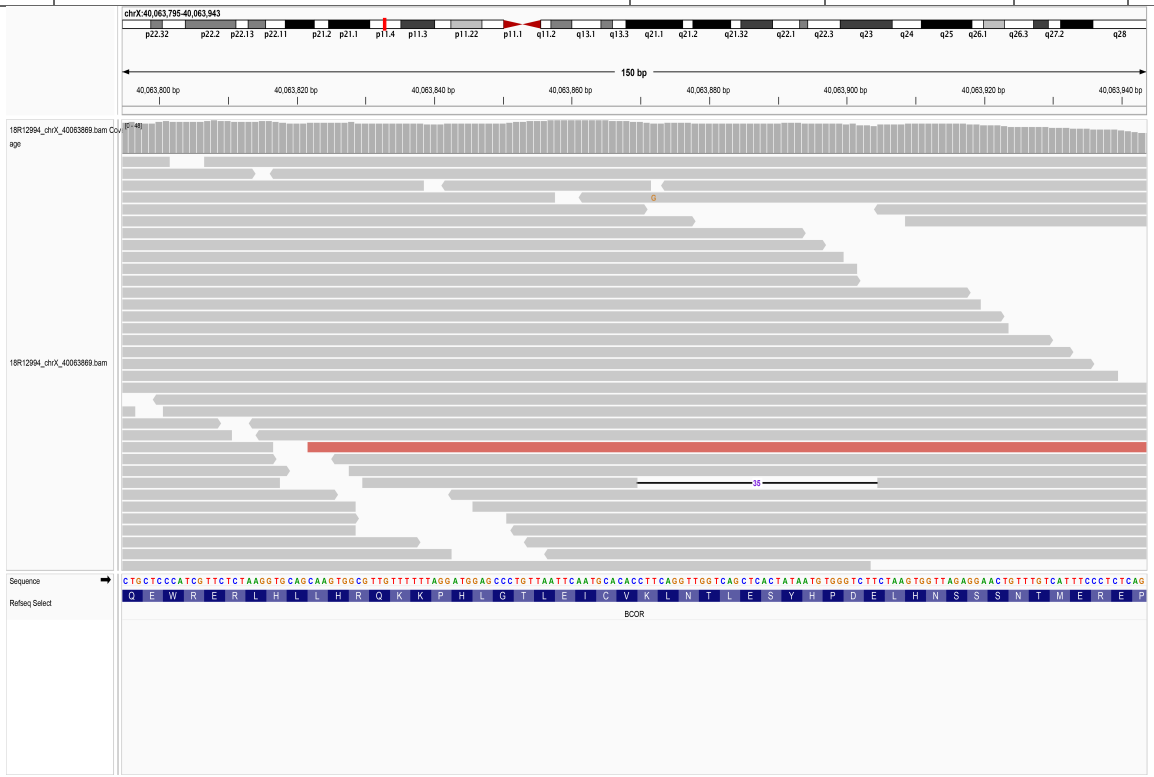
3.1. chrX_40062392_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chrX_40062392_A/-	18	2	*BCOR*	frameshift_variant



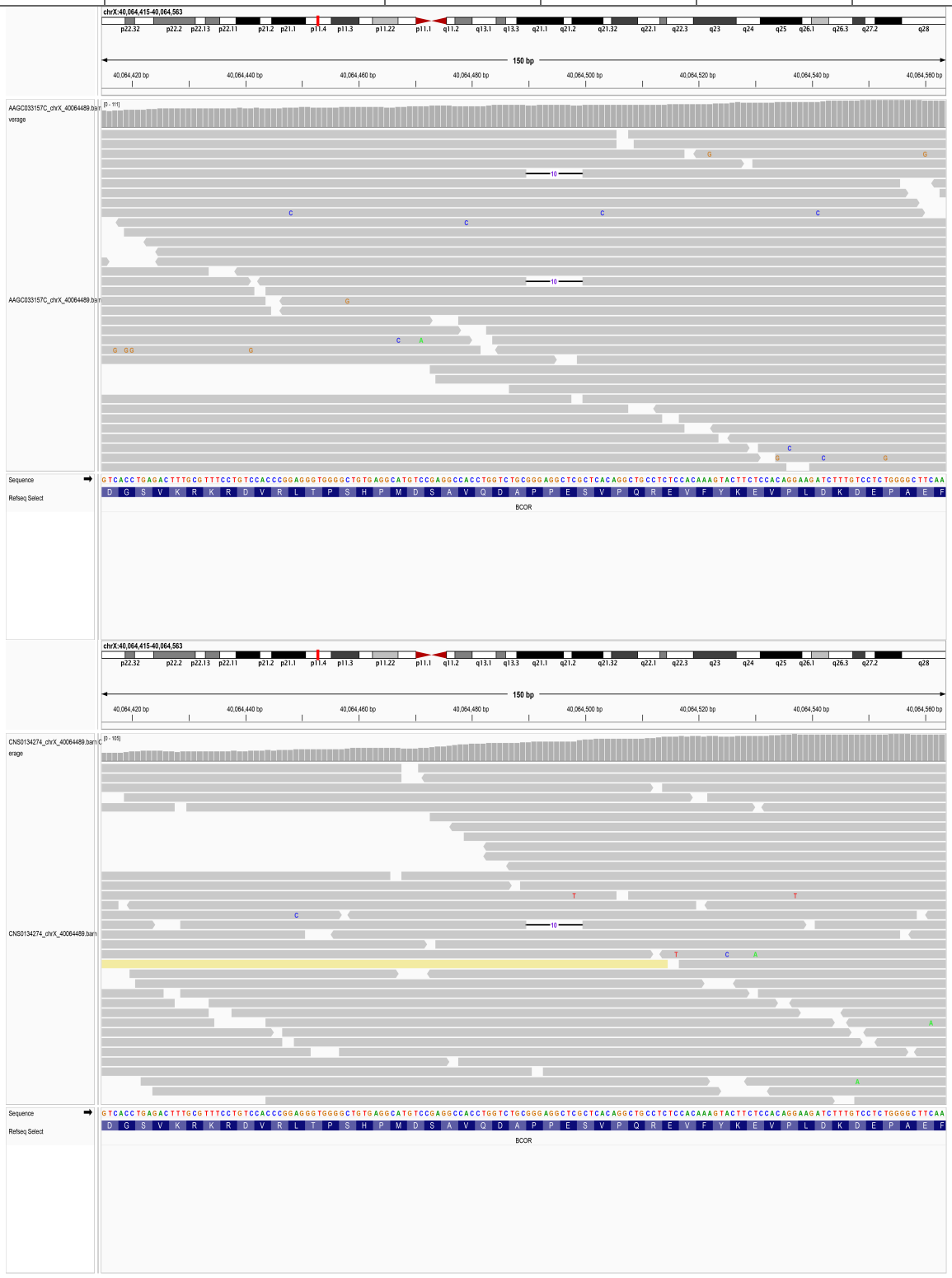
3.2. chrX_40063870_CTTCAGGTTGGTCAGCTCACTATAATGTGGGTCTT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12994	chrX_40063870_CTTCAGGTTGGTCAGCTCACTATAATGTGGGTCTT/-	44	2	*BCOR*	frameshift_variant



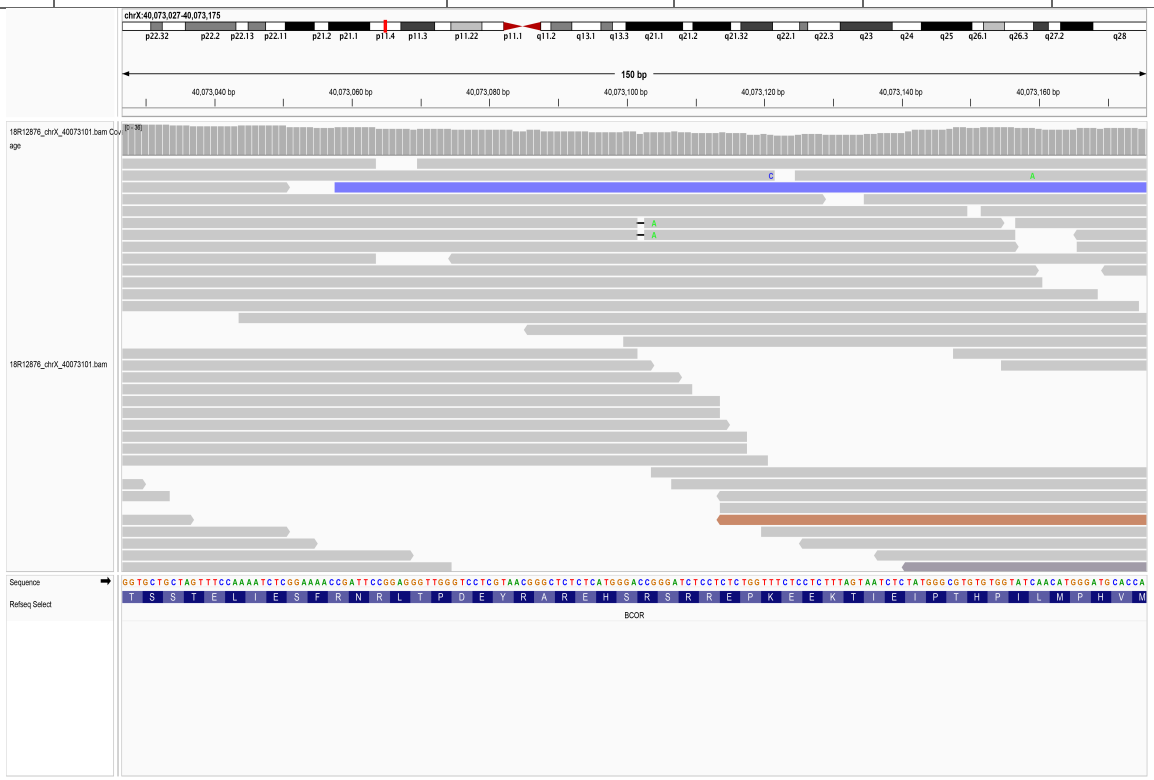
3.3. chrX_40064490_GGGAGGCTCG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033157C	chrX_40064490_GGGAGGCTCG/-	90	3	*BCOR*	frameshift_variant
CNS0134274	chrX_40064490_GGGAGGCTCG/-	79	2	*BCOR*	frameshift_variant



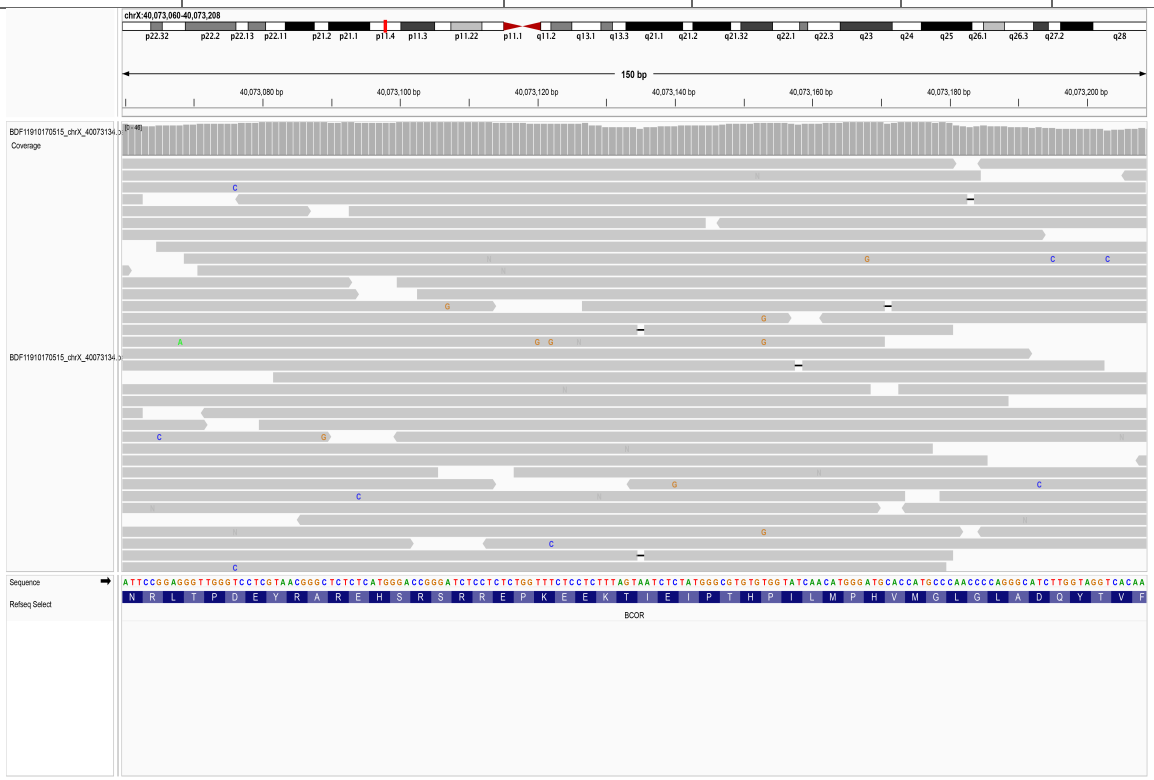
3.4. chrX_40073102_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12876	chrX_40073102_C/-	24	2	*BCOR*	frameshift_variant



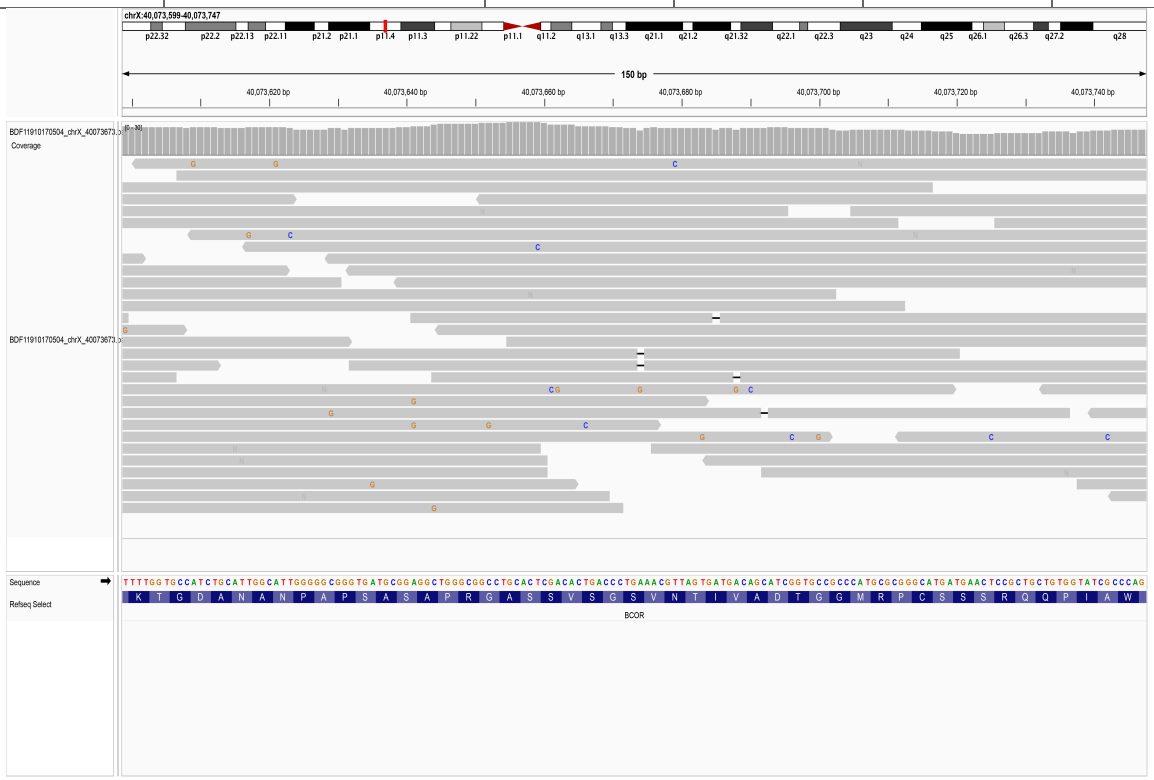
3.5. chrX_40073135_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170515	chrX_40073135_A/-	35	3	*BCOR*	frameshift_variant



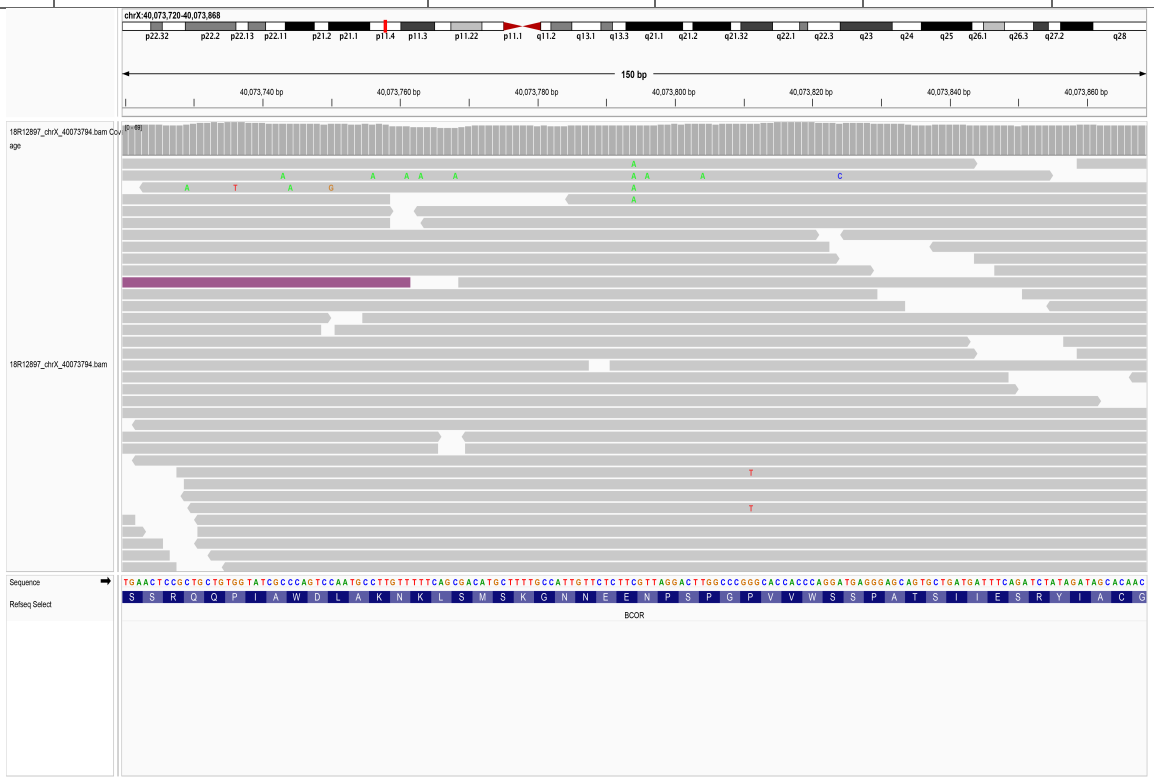
3.6. chrX_40073674_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chrX_40073674_A/-	20	2	*BCOR*	frameshift_variant



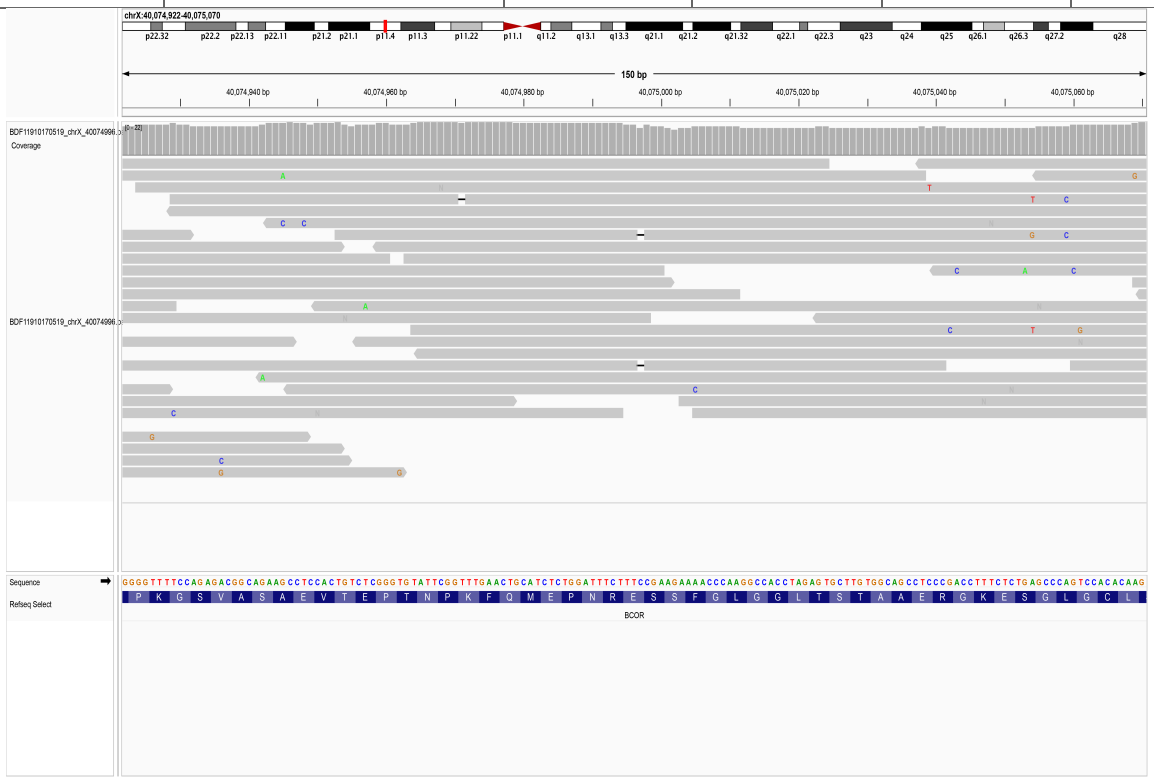
3.7. chrX_40073794_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12897	chrX_40073794_C/A	58	4	*BCOR*	stop_gained



3.8. chrX_40074997_C/-

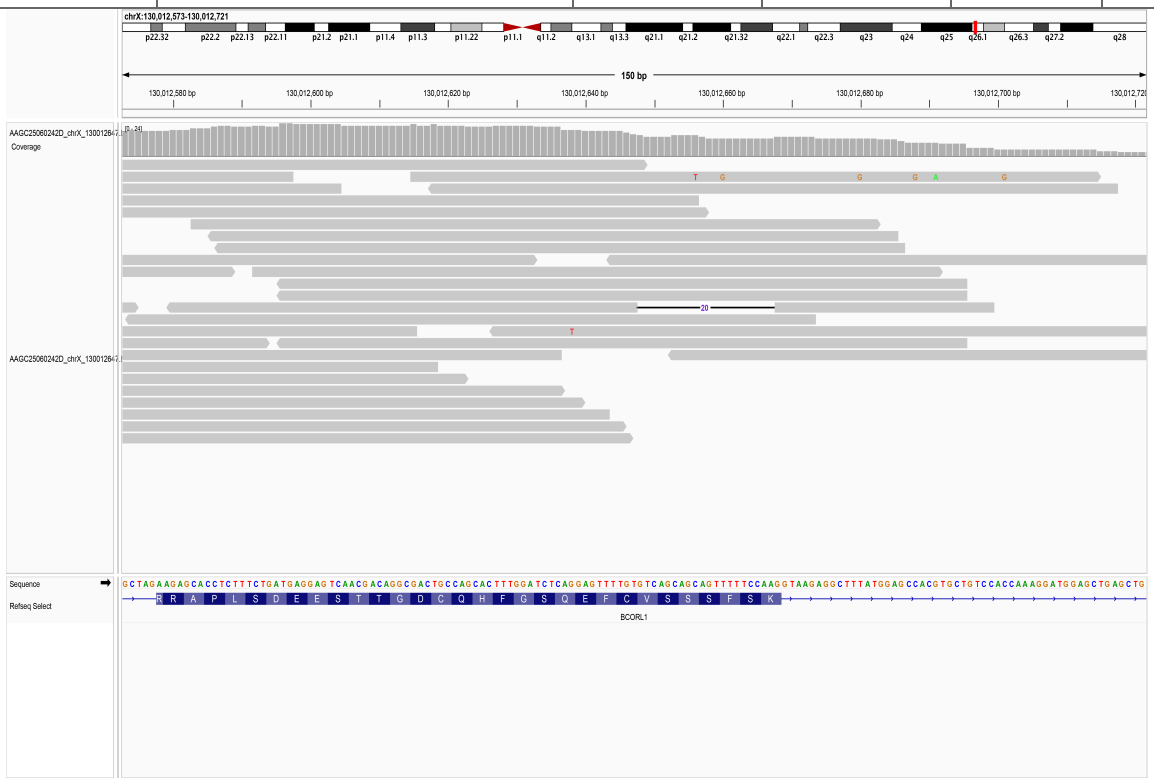
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chrX_40074997_C/-	17	2	*BCOR*	frameshift_variant



4. *BCORL1*

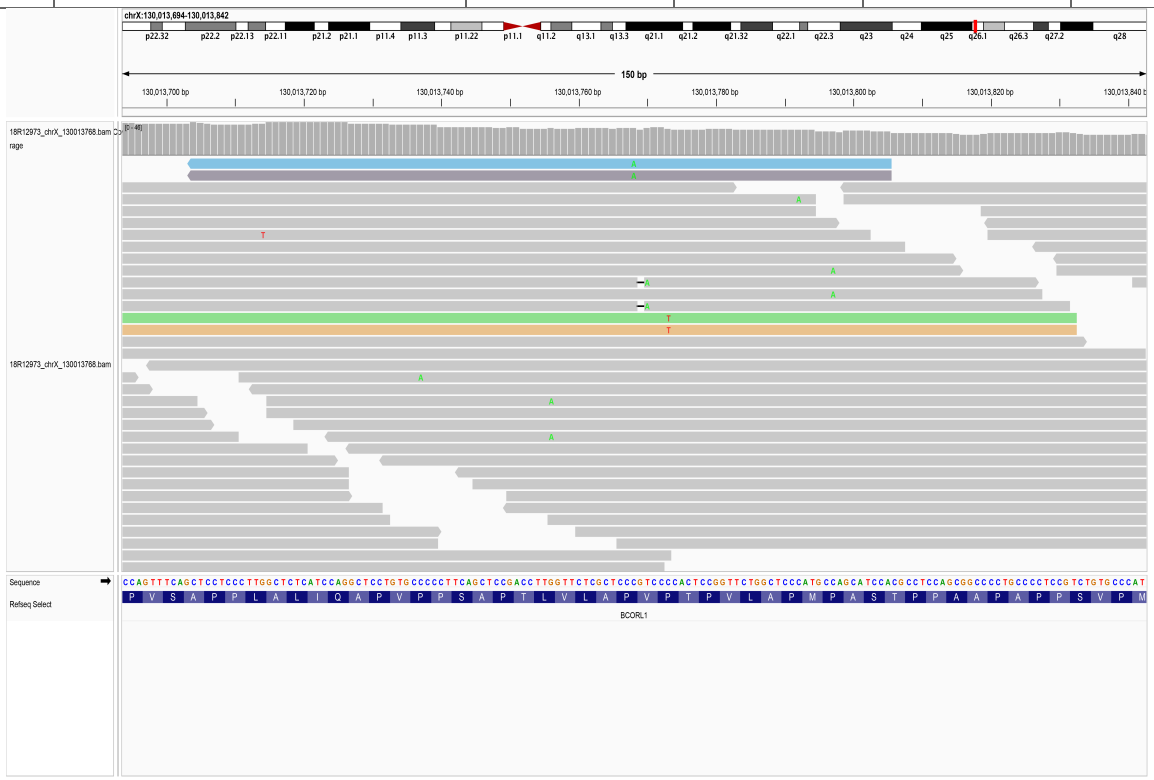
4.1. chrX_130012648_GTCAGCAGCAGTTTTTCCAA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060242D	chrX_130012648_GTCAGCAGCAGTTTTTCCAA/-	14	2	*BCORL1*	frameshift_variant



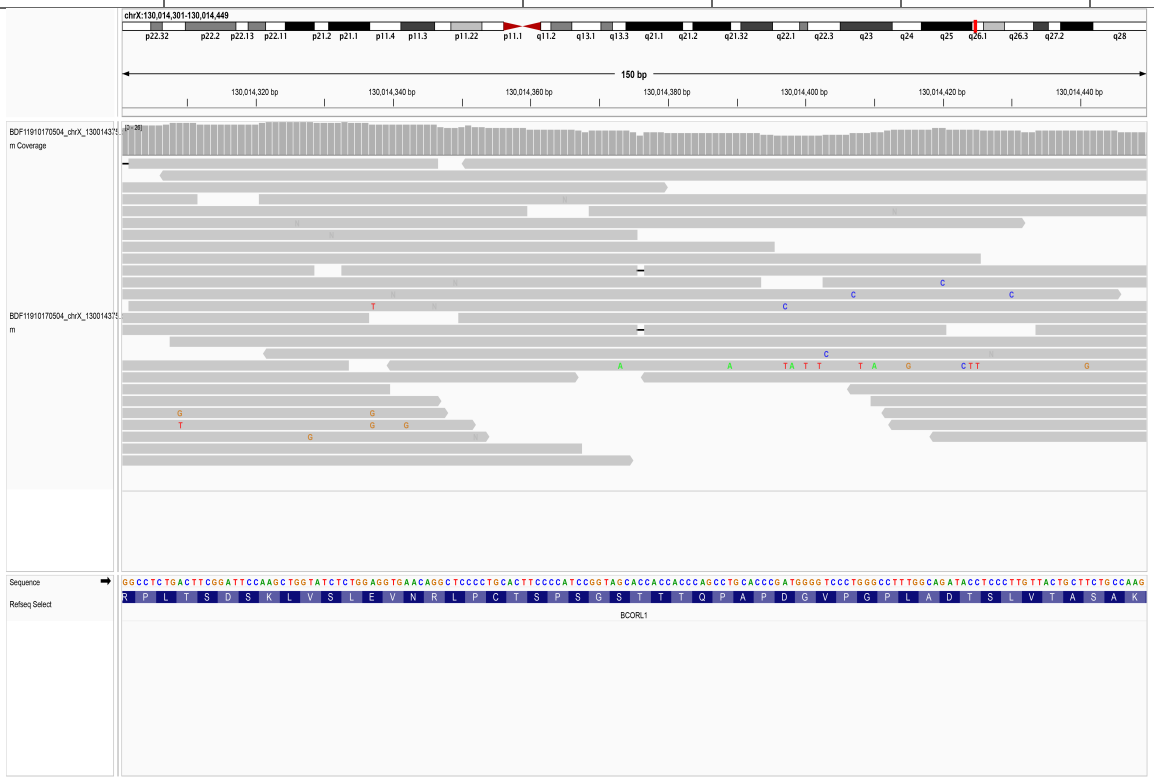
4.2. chrX_130013769_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12973	chrX_130013769_G/-	31	2	*BCORL1*	frameshift_variant



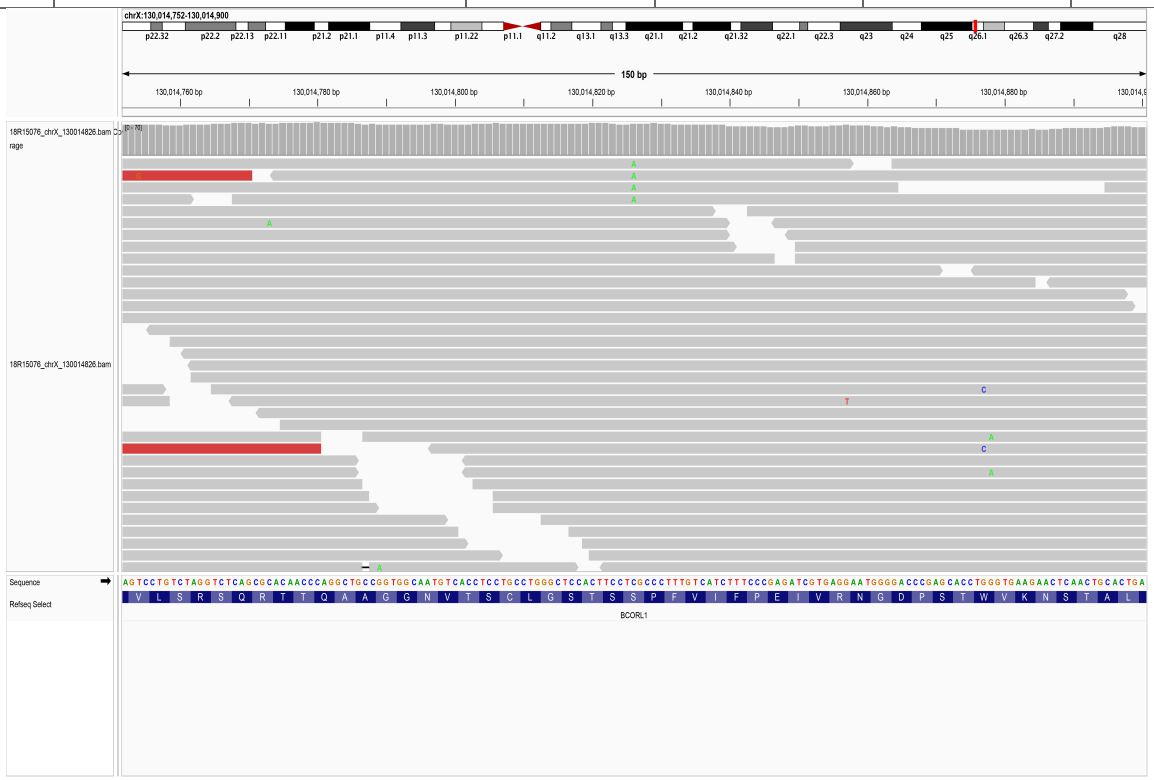
4.3. chrX_130014376_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chrX_130014376_C/-	14	2	*BCORL1*	frameshift_variant



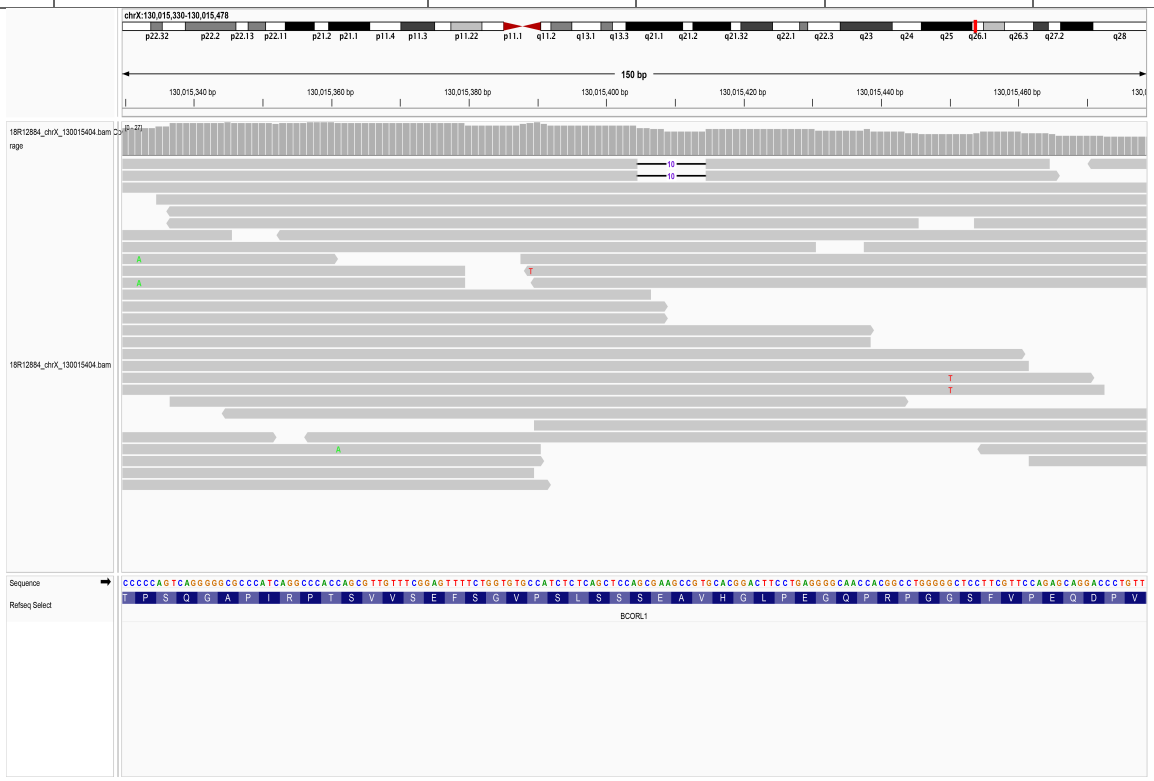
4.4. chrX_130014826_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15076	chrX_130014826_C/A	61	4	*BCORL1*	stop_gained



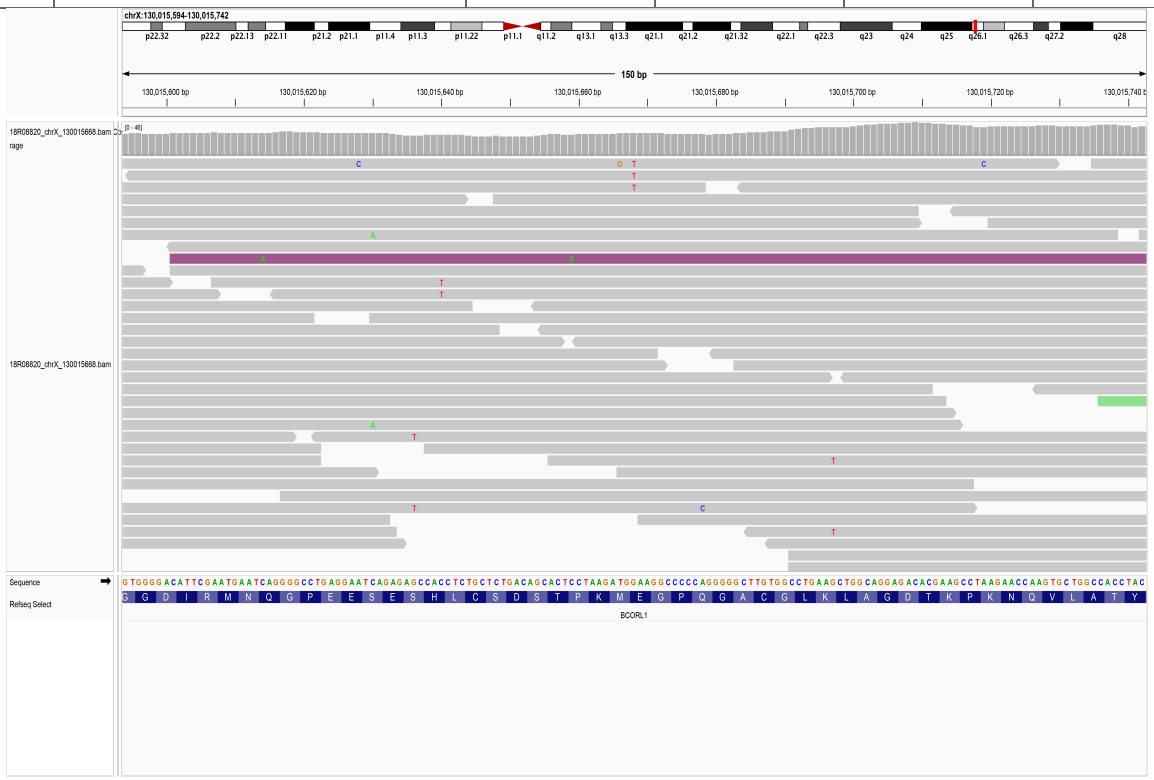
4.5. chrX_130015405_GCGAAGCCGT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12884	chrX_130015405_GCGAAGCCGT/-	20	2	*BCORL1*	frameshift_variant



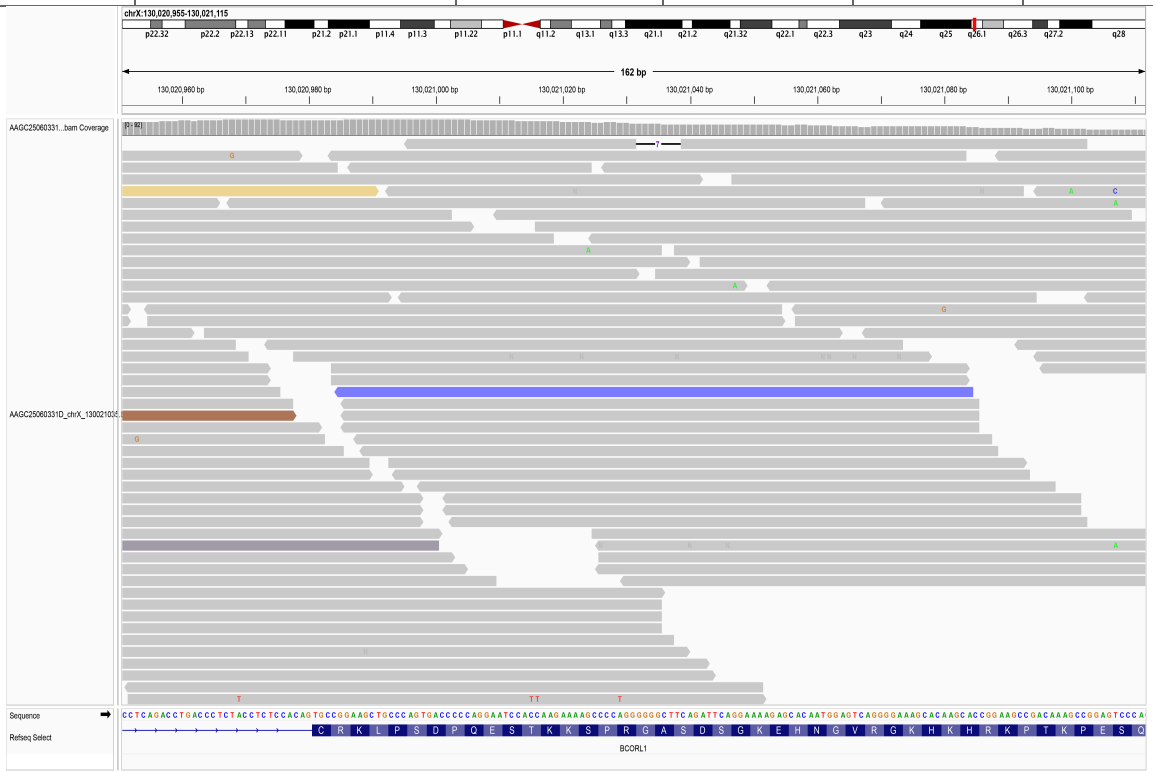
4.6. chrX_130015668_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08820	chrX_130015668_G/T	27	3	*BCORL1*	stop_gained



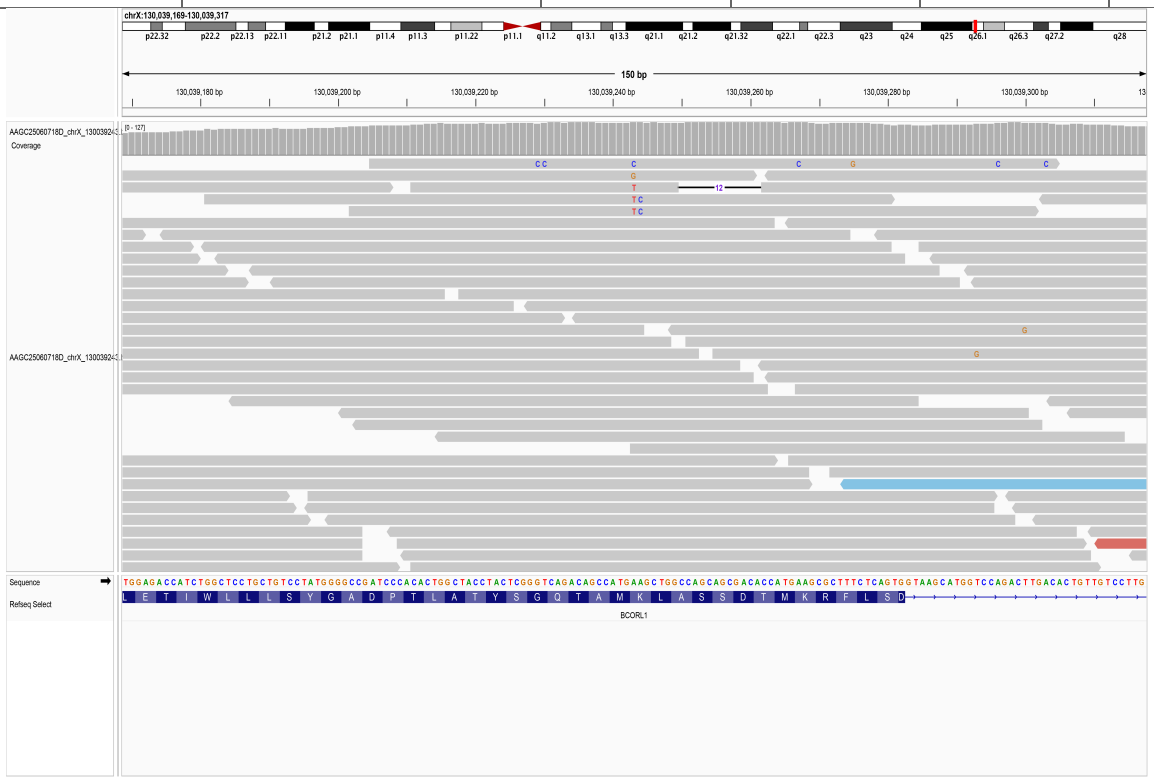
4.7. chrX_130021036_GGGGCTT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060331D	chrX_130021036_GGGGCTT/-	68	2	*BCORL1*	frameshift_variant



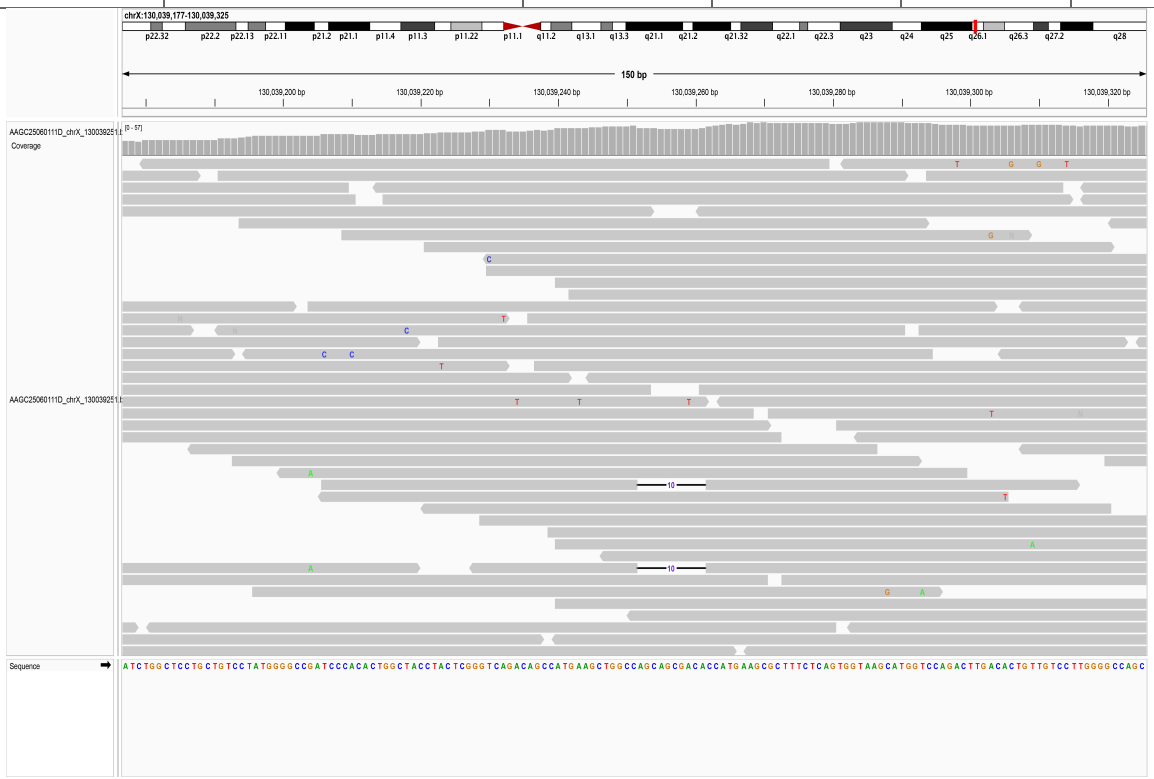
4.8. chrX_130039243_A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060718D	chrX_130039243_A/T	124	2	*BCORL1*	stop_gained



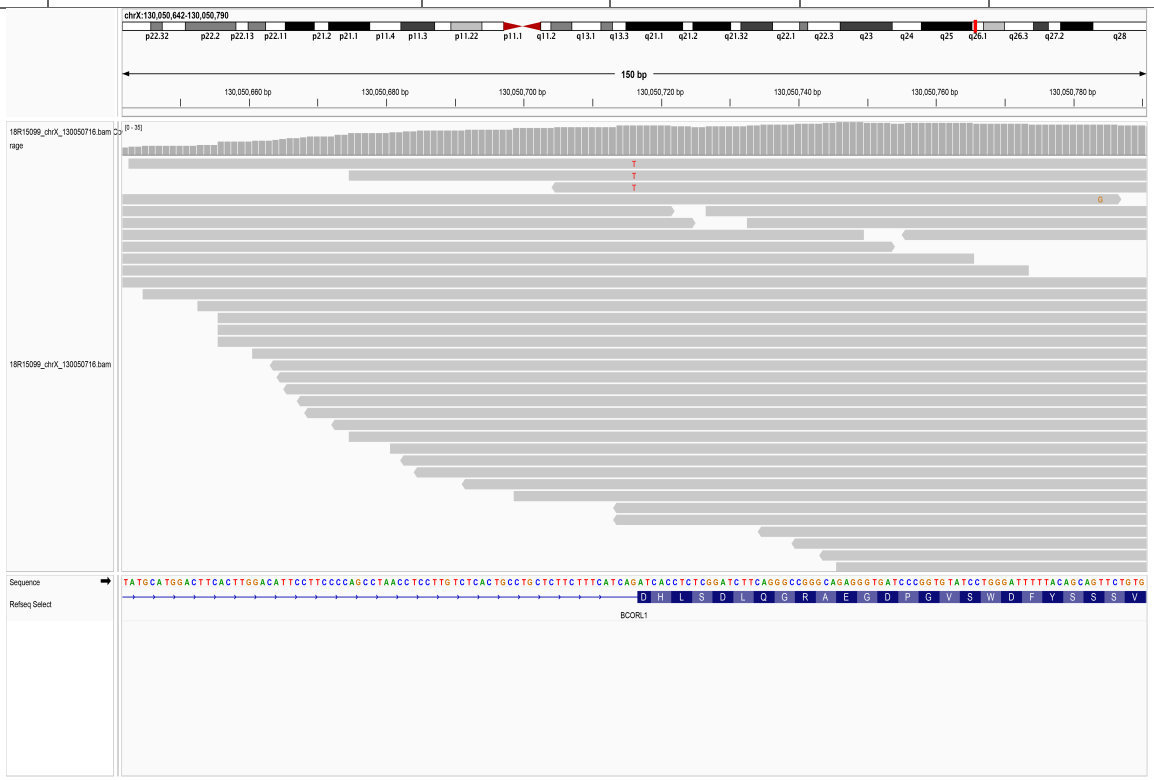
4.9. chrX_130039252_AGCAGCGACA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060111D	chrX_130039252_AGCAGCGACA/-	51	2	*BCORL1*	frameshift_variant



4.10. chrX_130050716_G/T

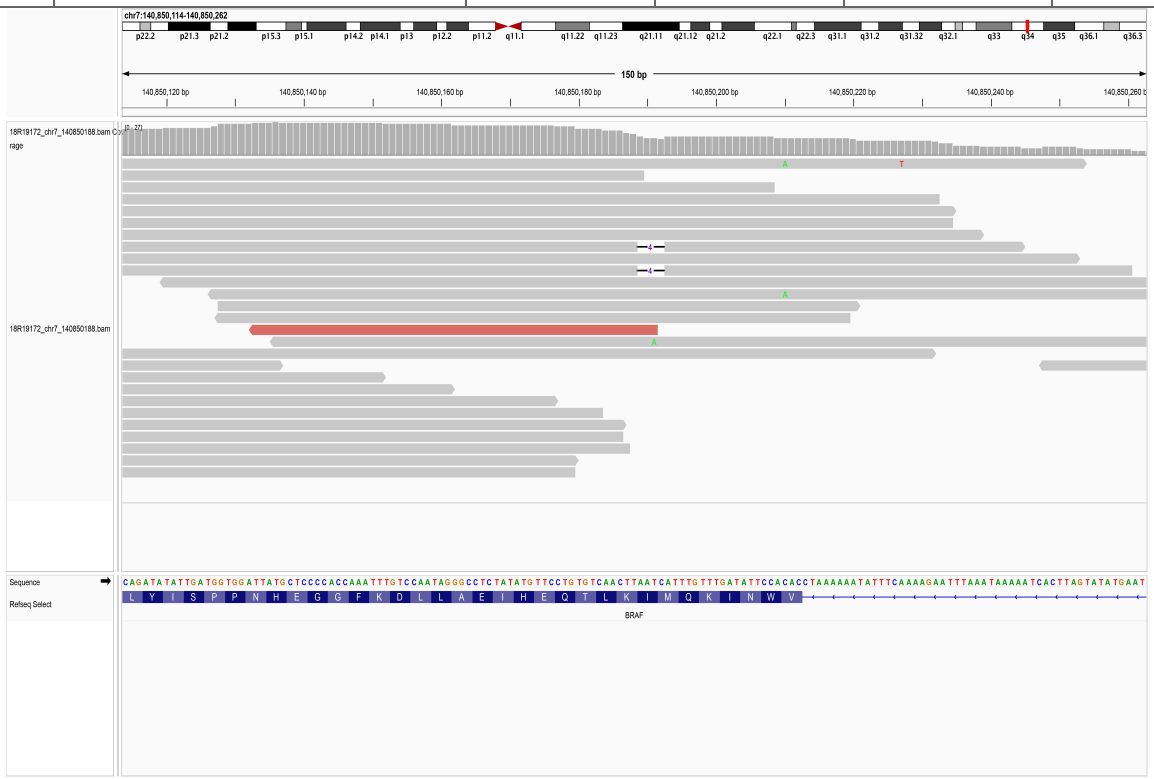
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15099	chrX_130050716_G/T	28	3	*BCORL1*	splice_acceptor_variant



5. *BRAF*

5.1. chr7_140850189_AATC/-

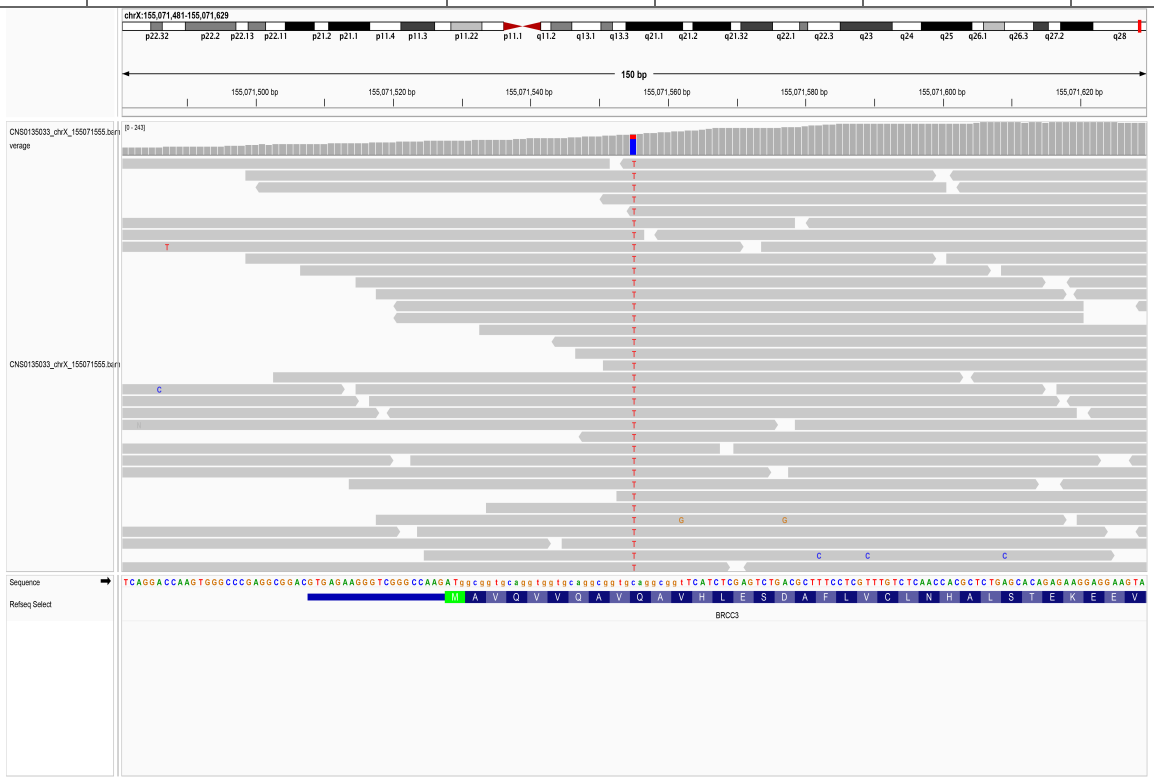
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19172	chr7_140850189_AATC/-	14	2	*BRAF*	frameshift_variant



6. *BRCC3*

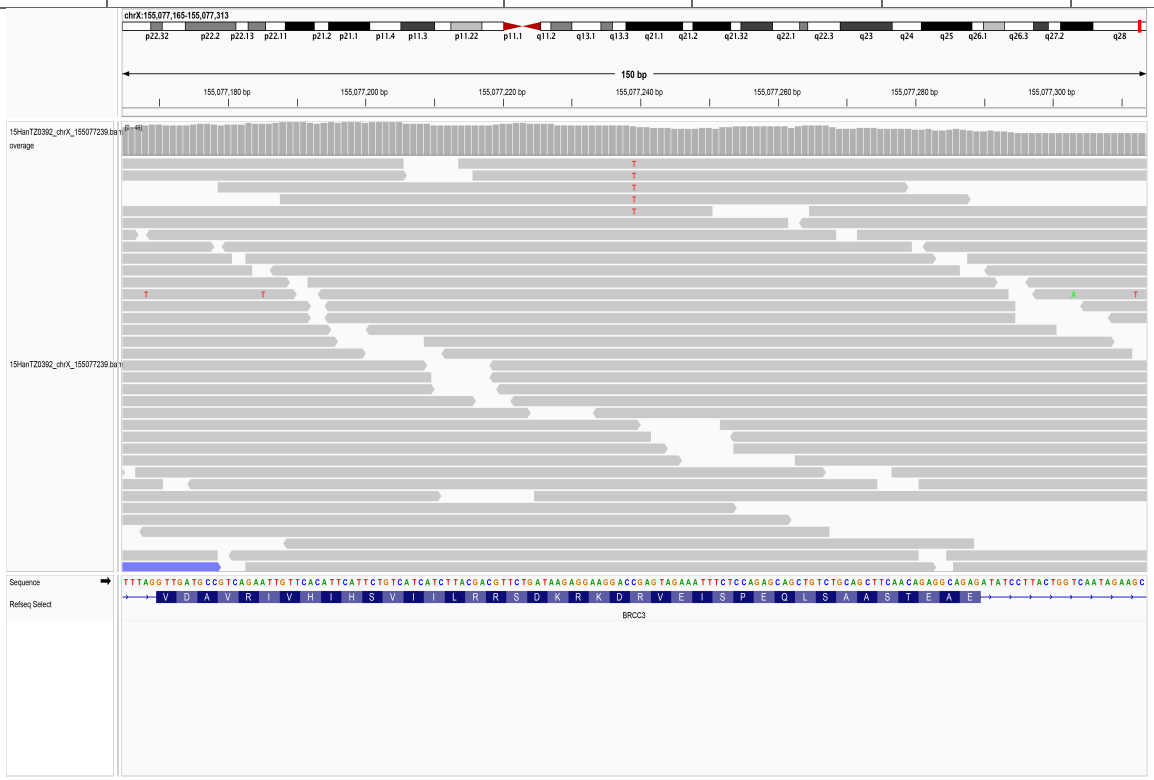
6.1. chrX_155071555_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135033	chrX_155071555_C/T	117	35	*BRCC3*	stop_gained



6.2. chrX_155077239_C/T

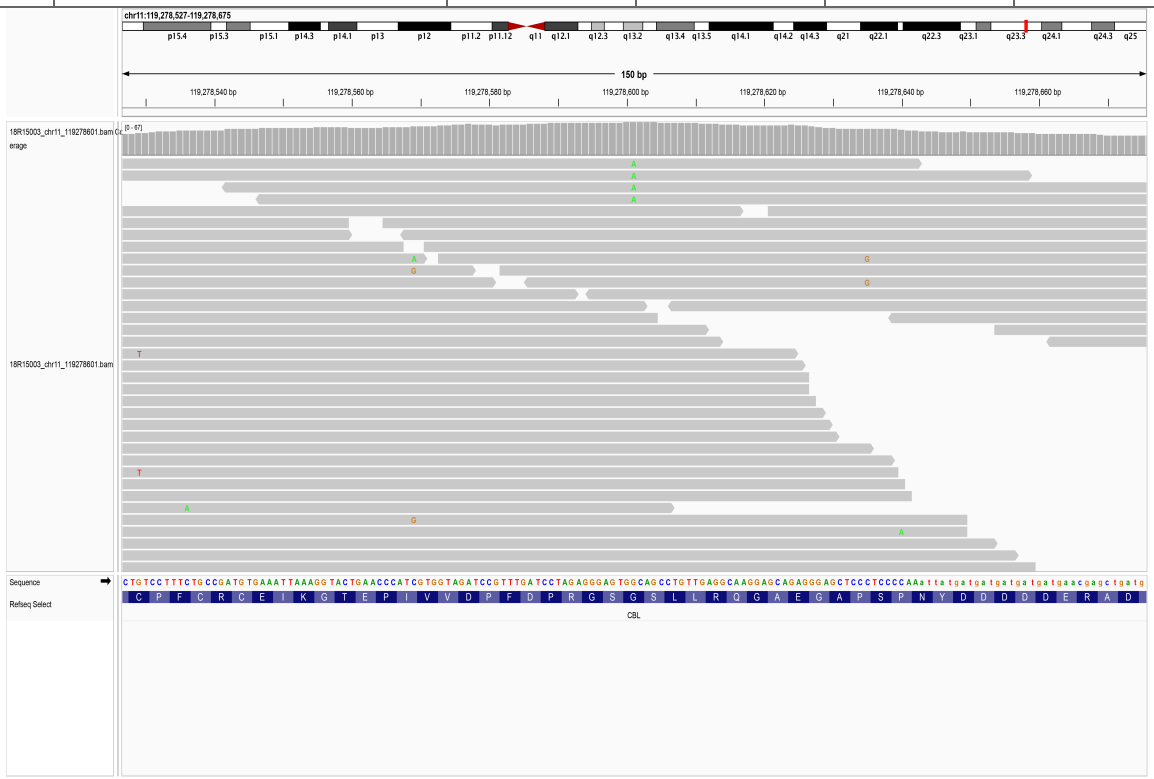
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0392	chrX_155077239_C/T	37	5	*BRCC3*	stop_gained



7. *CBL*

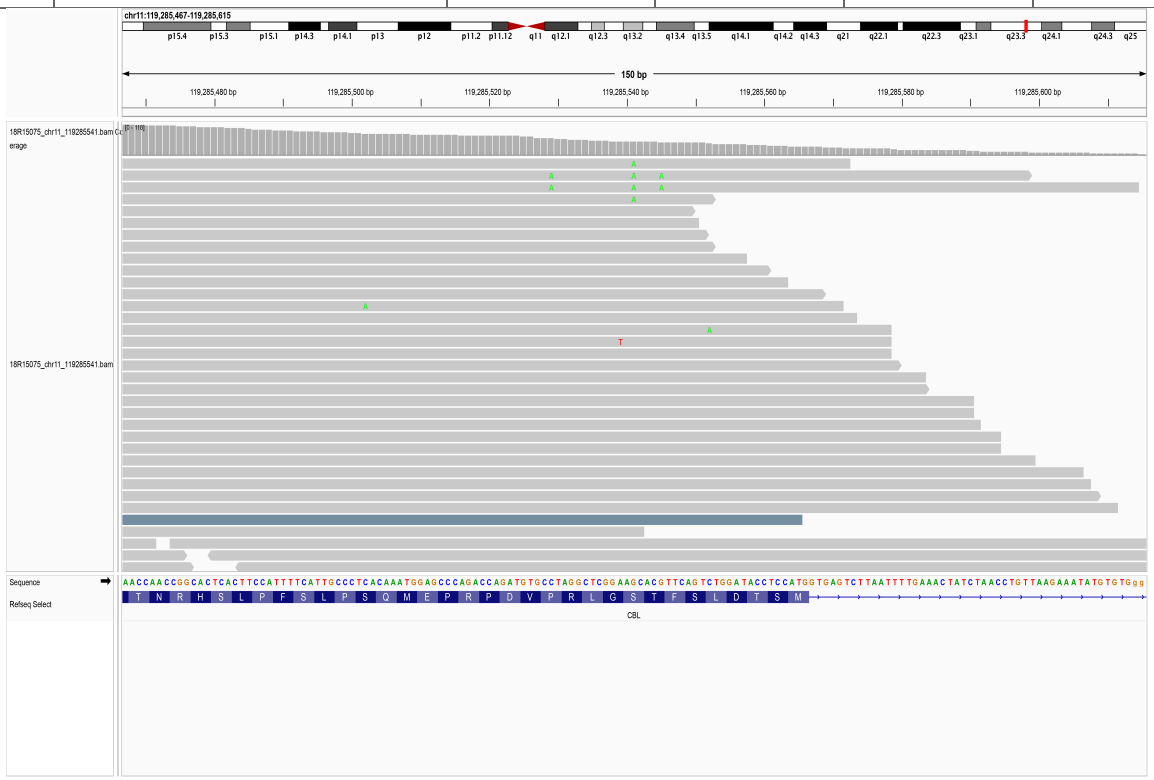
7.1. chr11_119278601_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15003	chr11_119278601_G/A	63	4	*CBL*	missense_variant



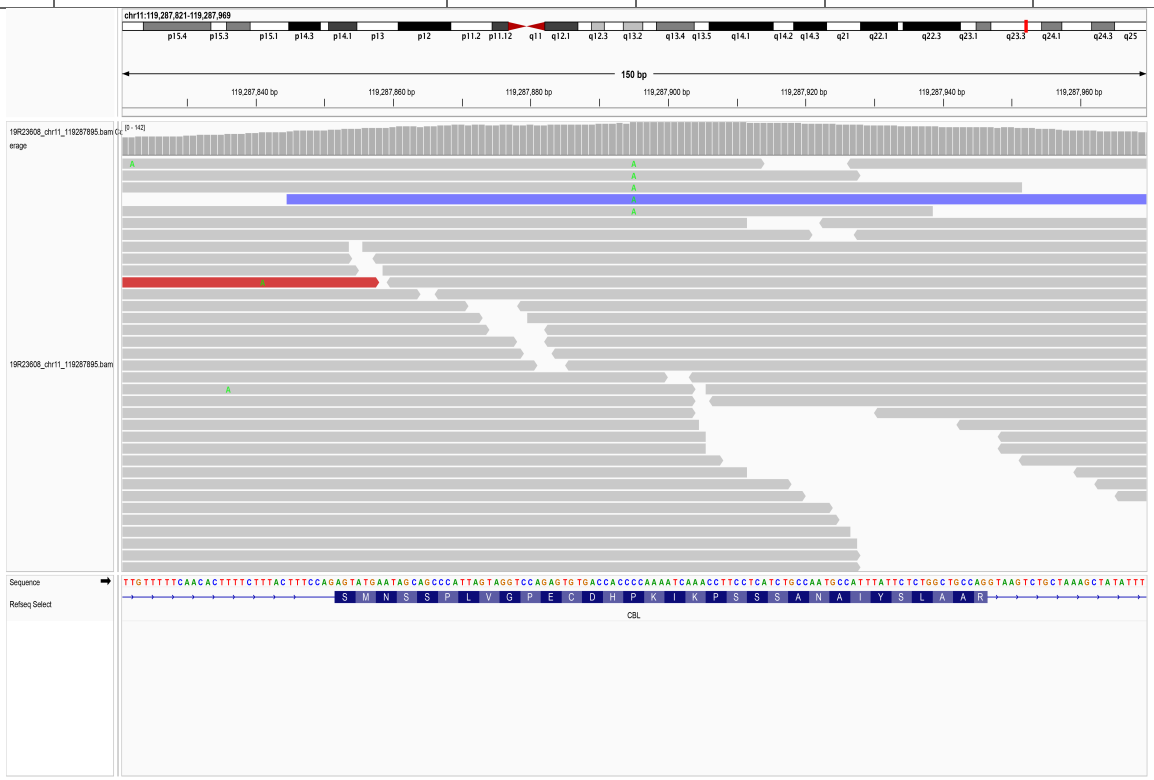
7.2. chr11_119285541_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15075	chr11_119285541_G/A	45	4	*CBL*	missense_variant



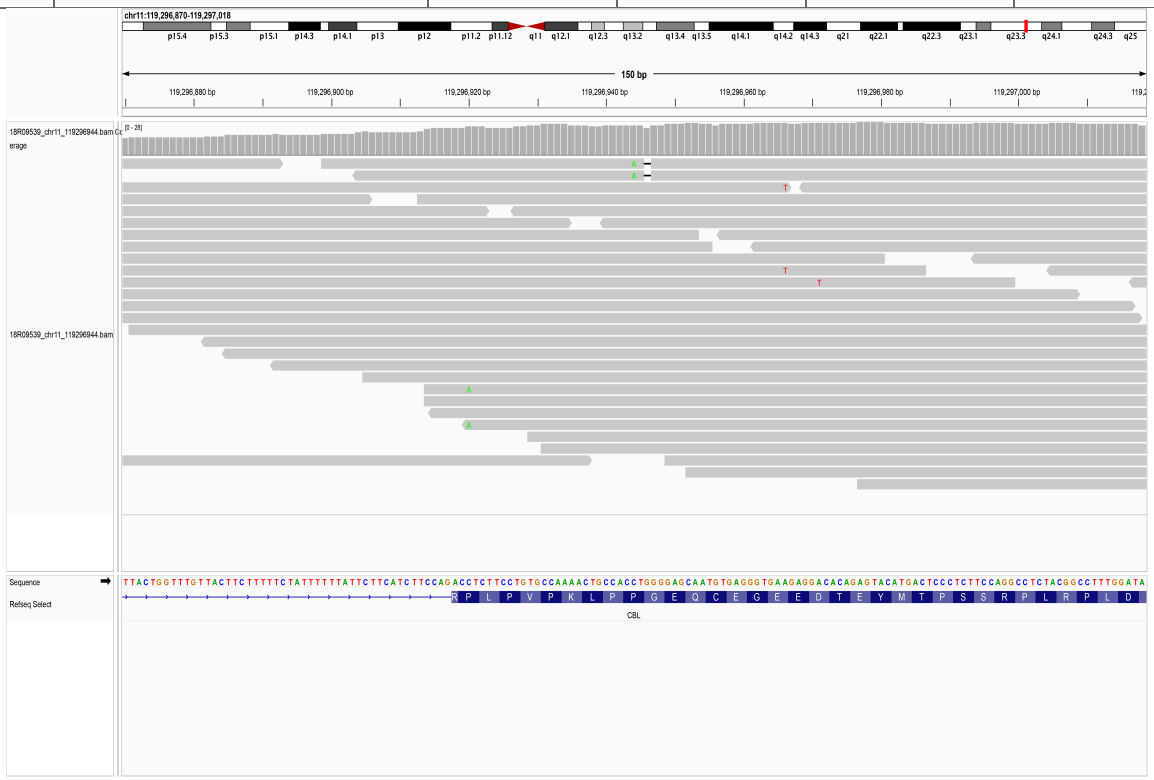
7.3. chr11_119287895_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23608	chr11_119287895_C/A	135	5	*CBL*	missense_variant



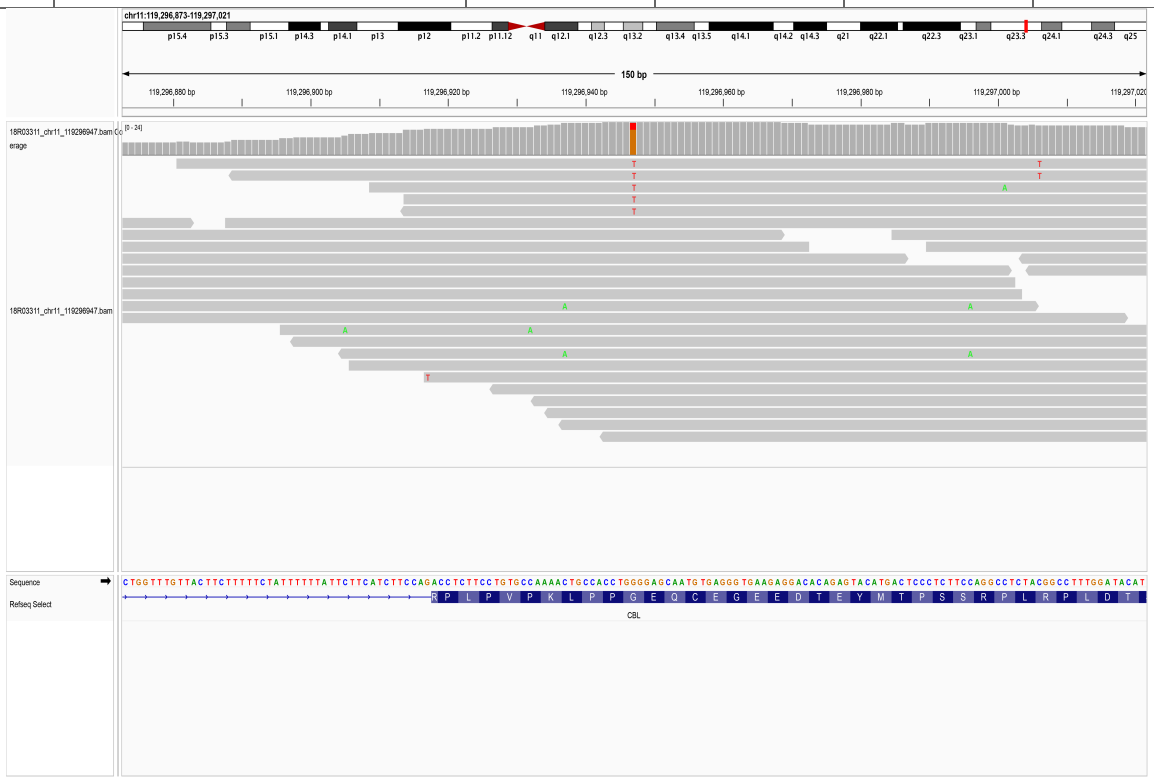
7.4. chr11_119296944_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09539	chr11_119296944_C/A	23	2	*CBL*	missense_variant



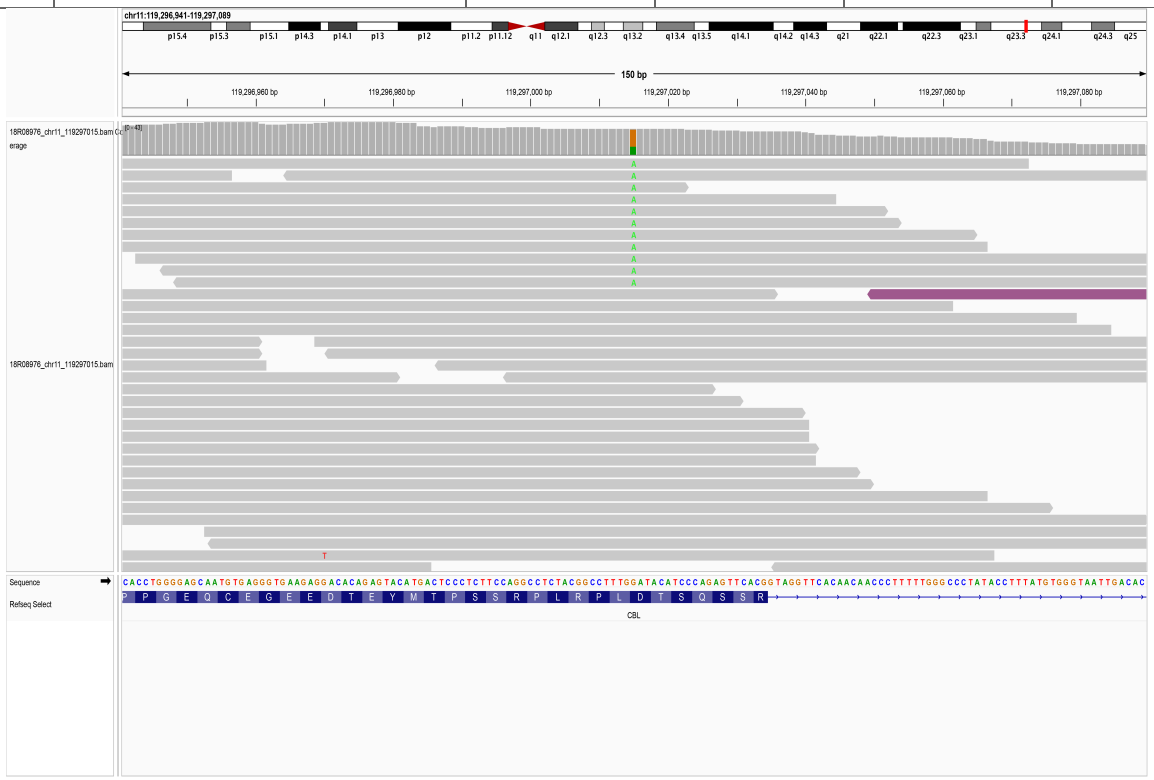
7.5. chr11_119296947_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr11_119296947_G/T	19	5	*CBL*	missense_variant



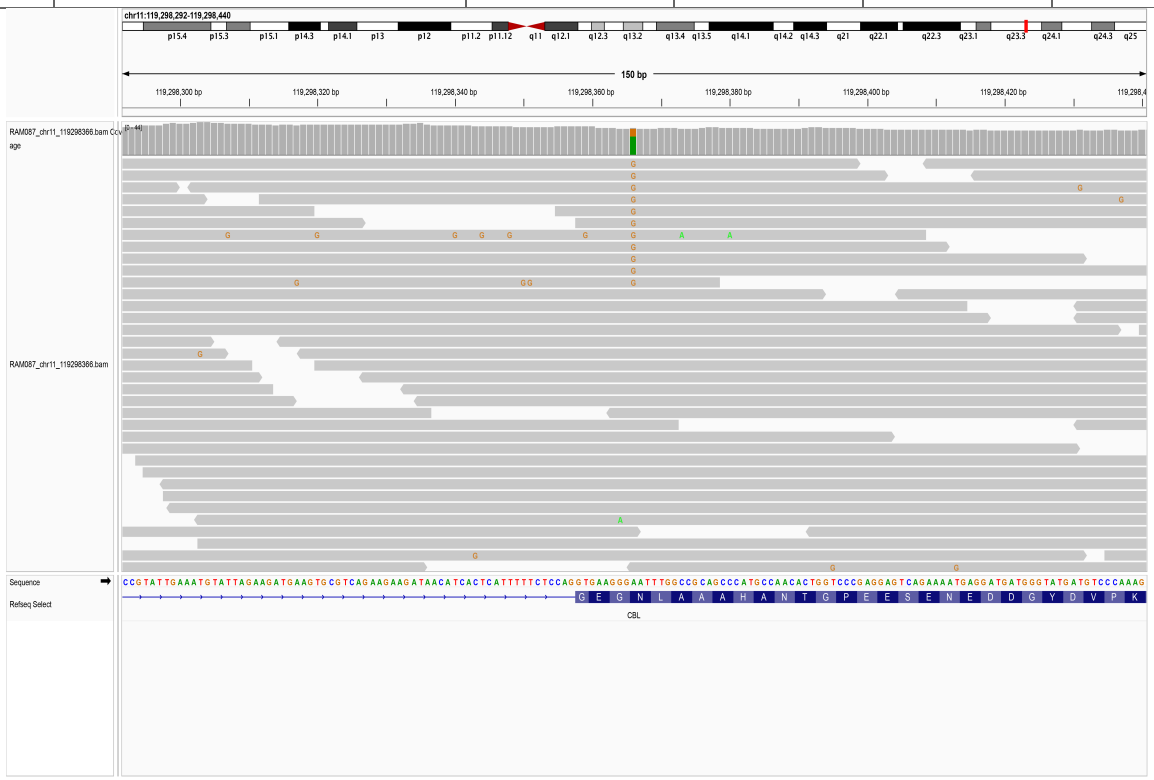
7.6. chr11_119297015_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08976	chr11_119297015_G/A	23	11	*CBL*	missense_variant



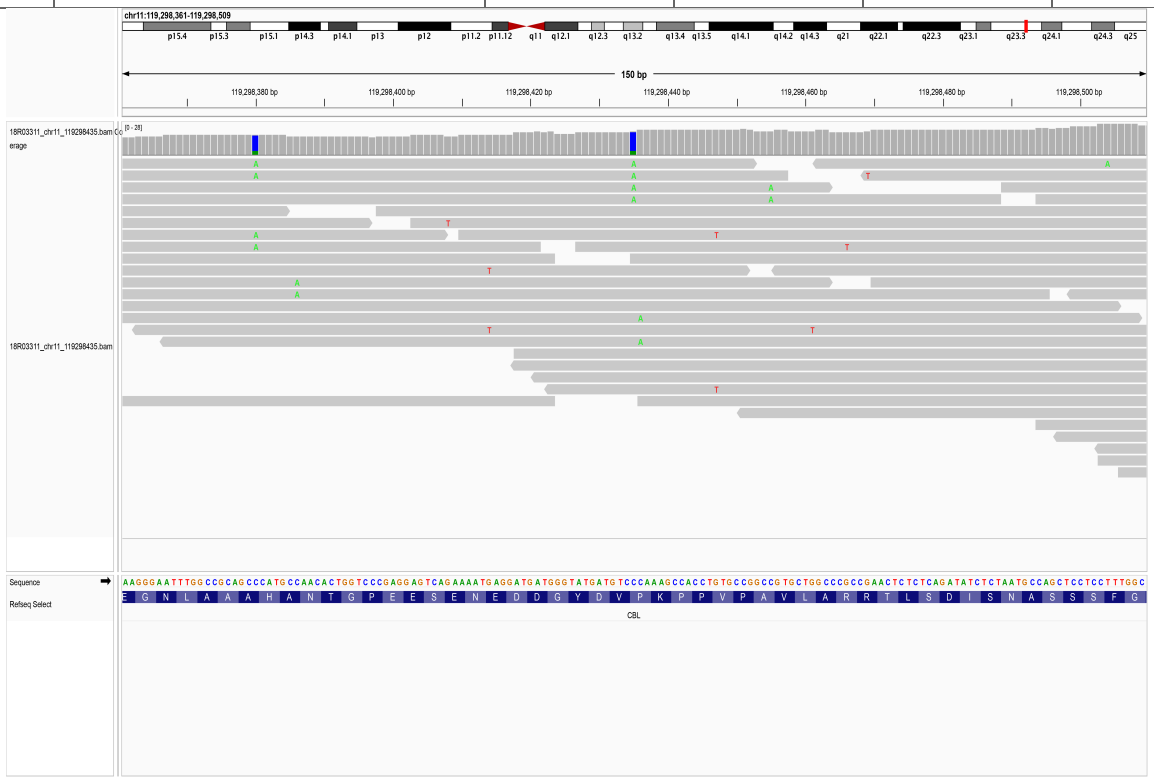
7.7. chr11_119298366_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
RAM087	chr11_119298366_A/G	24	9	*CBL*	missense_variant



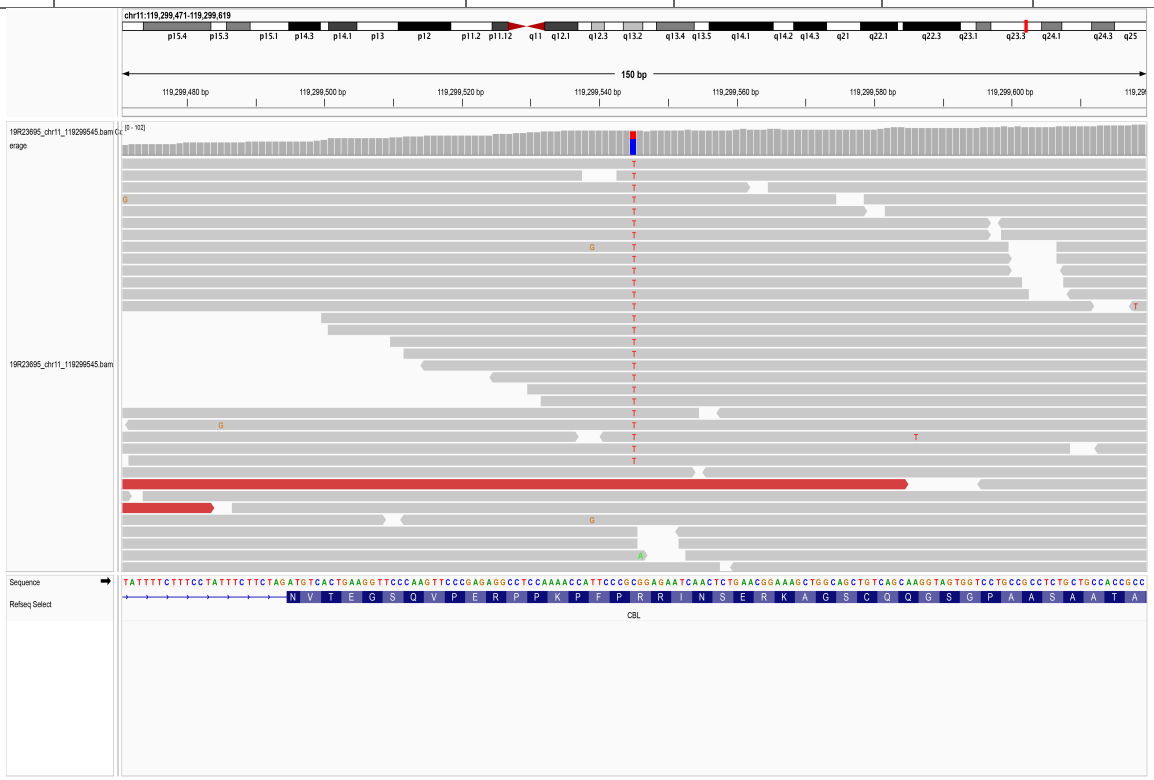
7.8. chr11_119298435_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr11_119298435_C/A	15	4	*CBL*	missense_variant



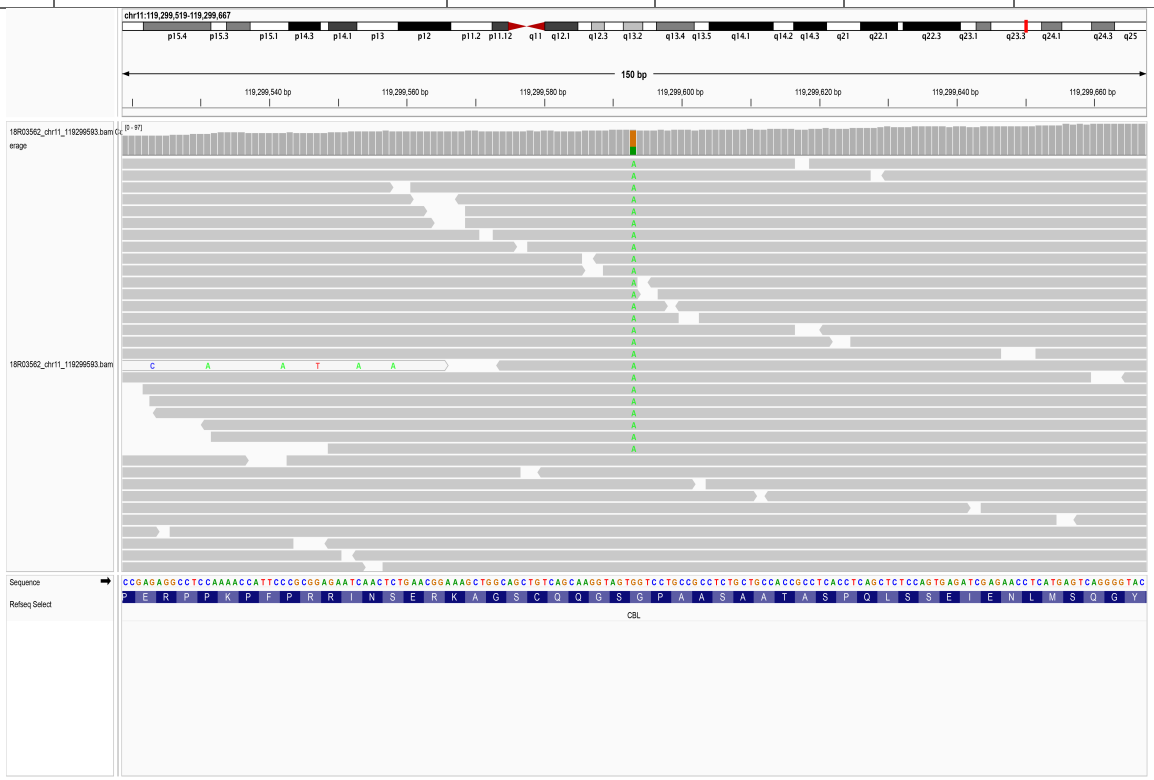
7.9. chr11_119299545_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23695	chr11_119299545_C/T	49	26	*CBL*	missense_variant



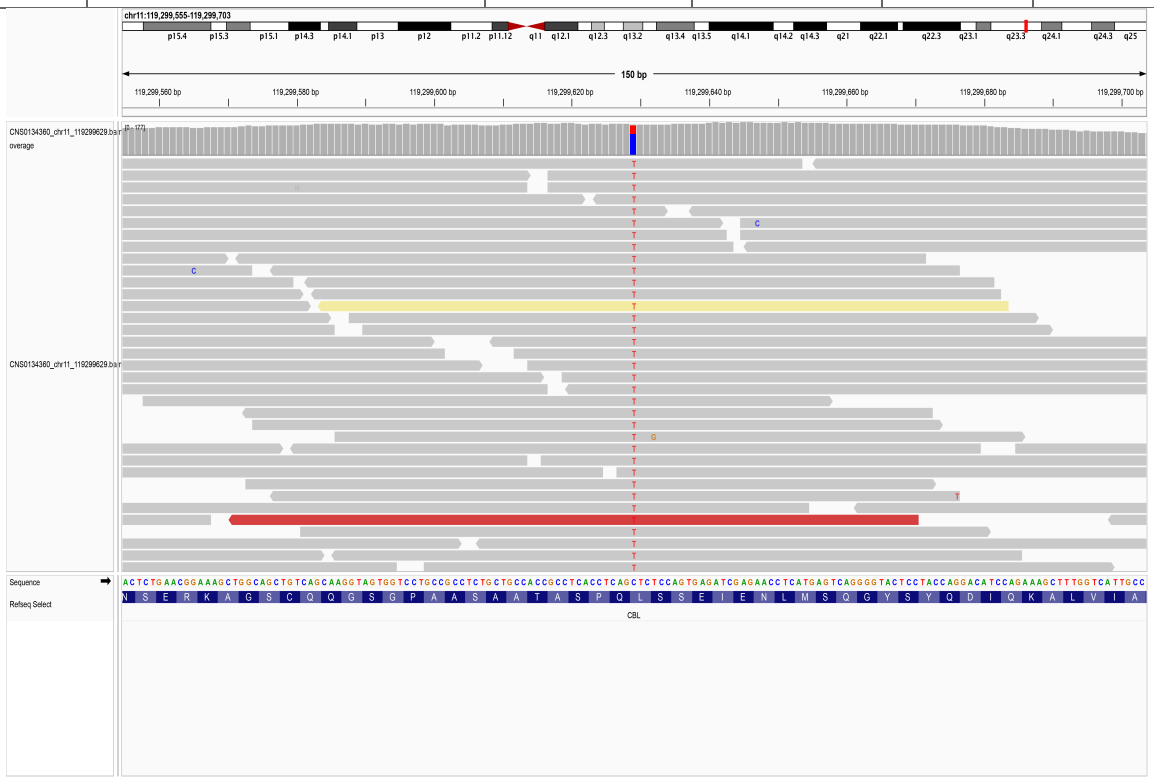
7.10. chr11_119299593_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03562	chr11_119299593_G/A	48	25	*CBL*	missense_variant



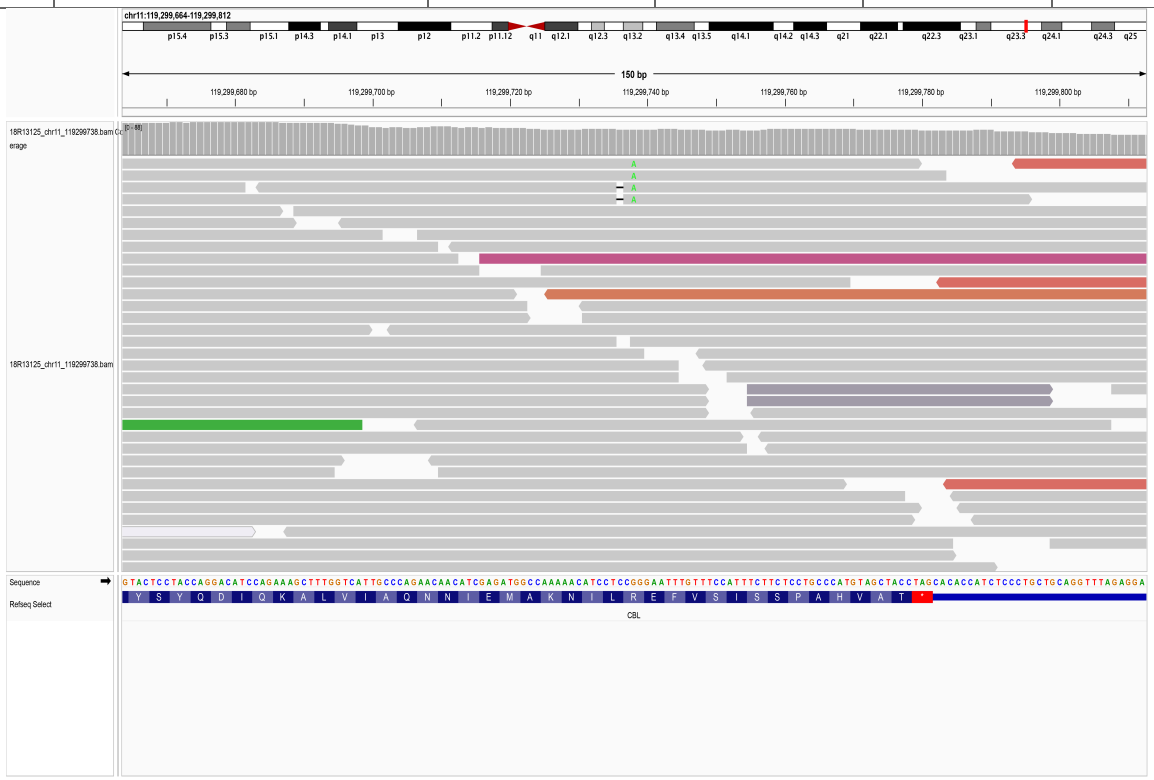
7.11. chr11_119299629_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134360	chr11_119299629_C/T	113	48	*CBL*	missense_variant



7.12. chr11_119299738_G/A

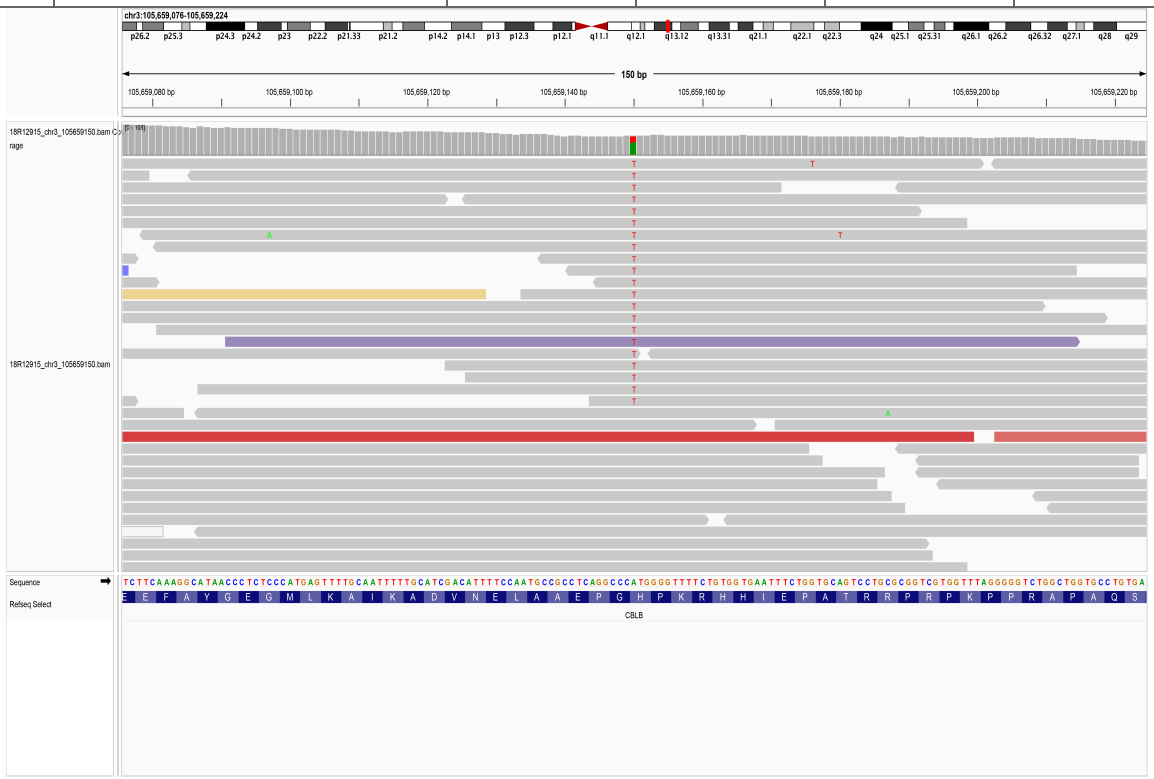
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13125	chr11_119299738_G/A	61	4	*CBL*	missense_variant



8. *CBLB*

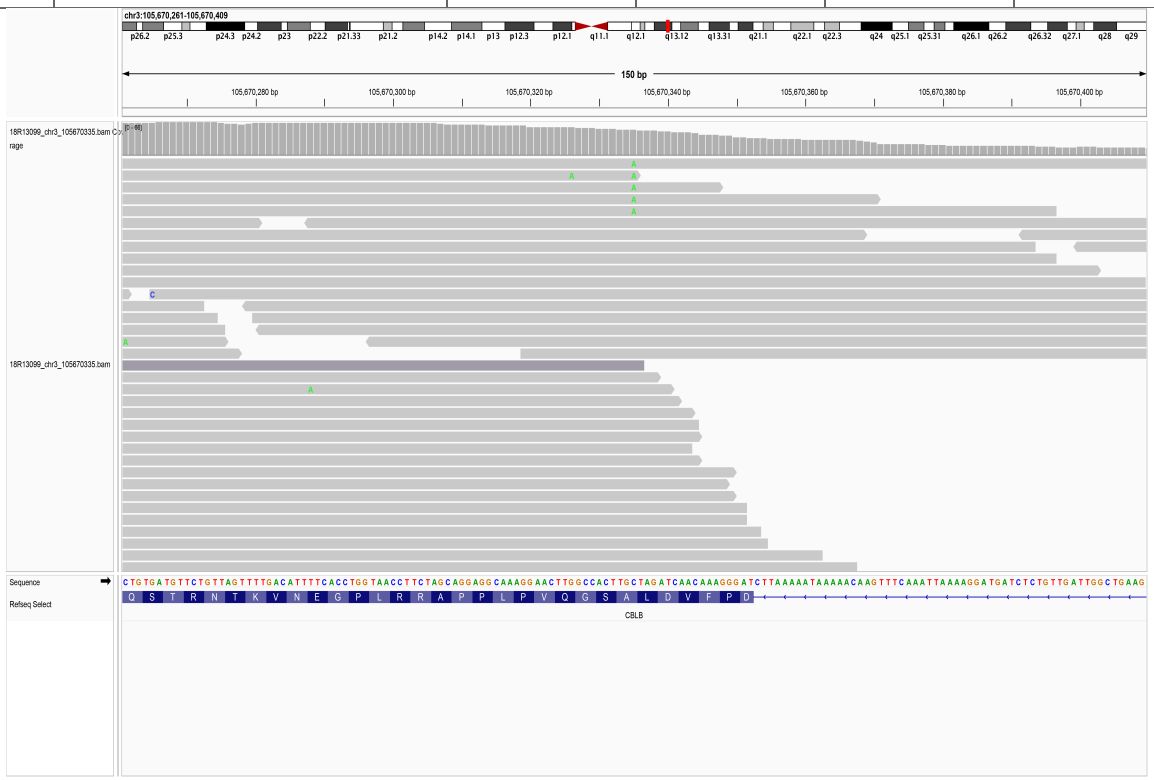
8.1. chr3_105659150_A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12915	chr3_105659150_A/T	41	20	*CBLB*	missense_variant



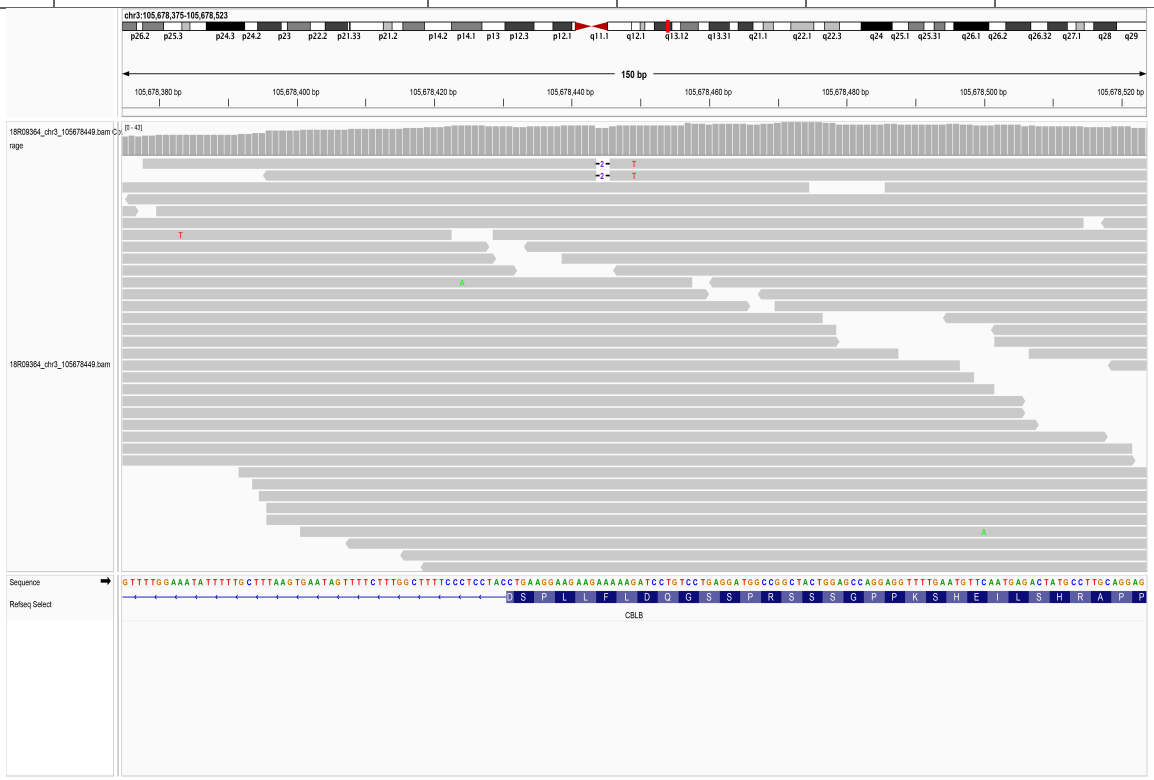
8.2. chr3_105670335_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13099	chr3_105670335_C/A	45	4	*CBLB*	missense_variant



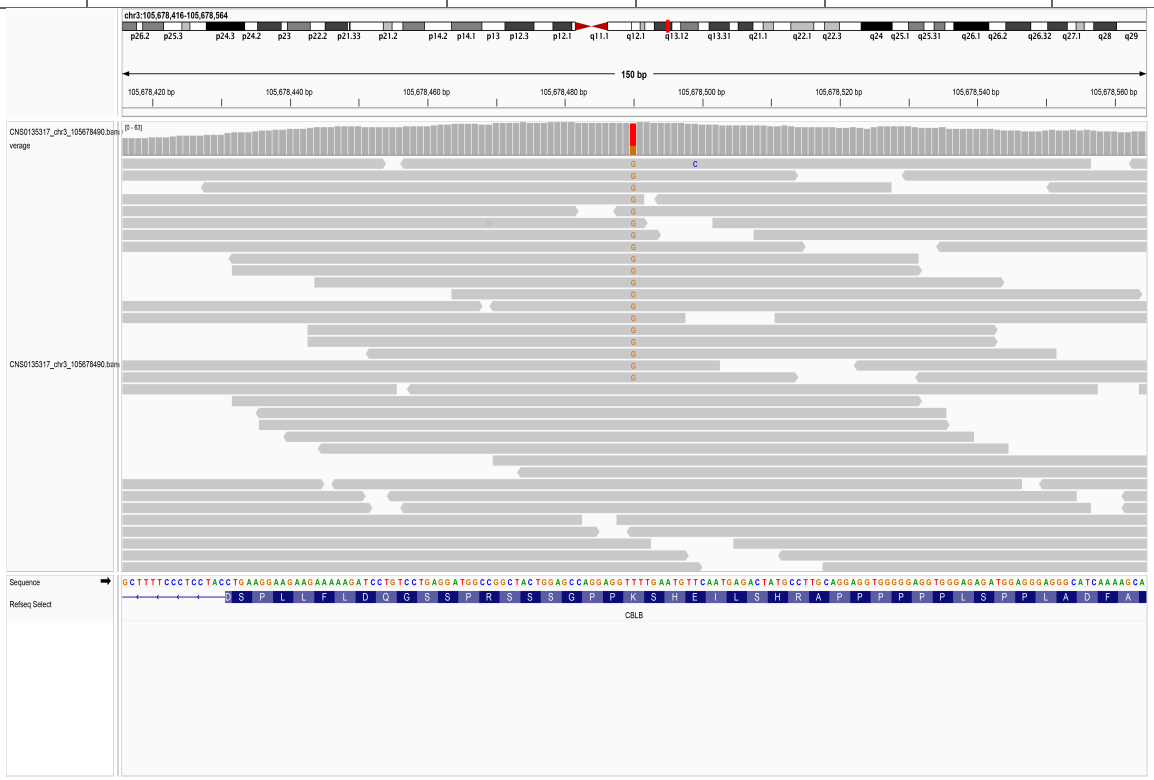
8.3. chr3_105678449_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09364	chr3_105678449_G/T	36	2	*CBLB*	missense_variant



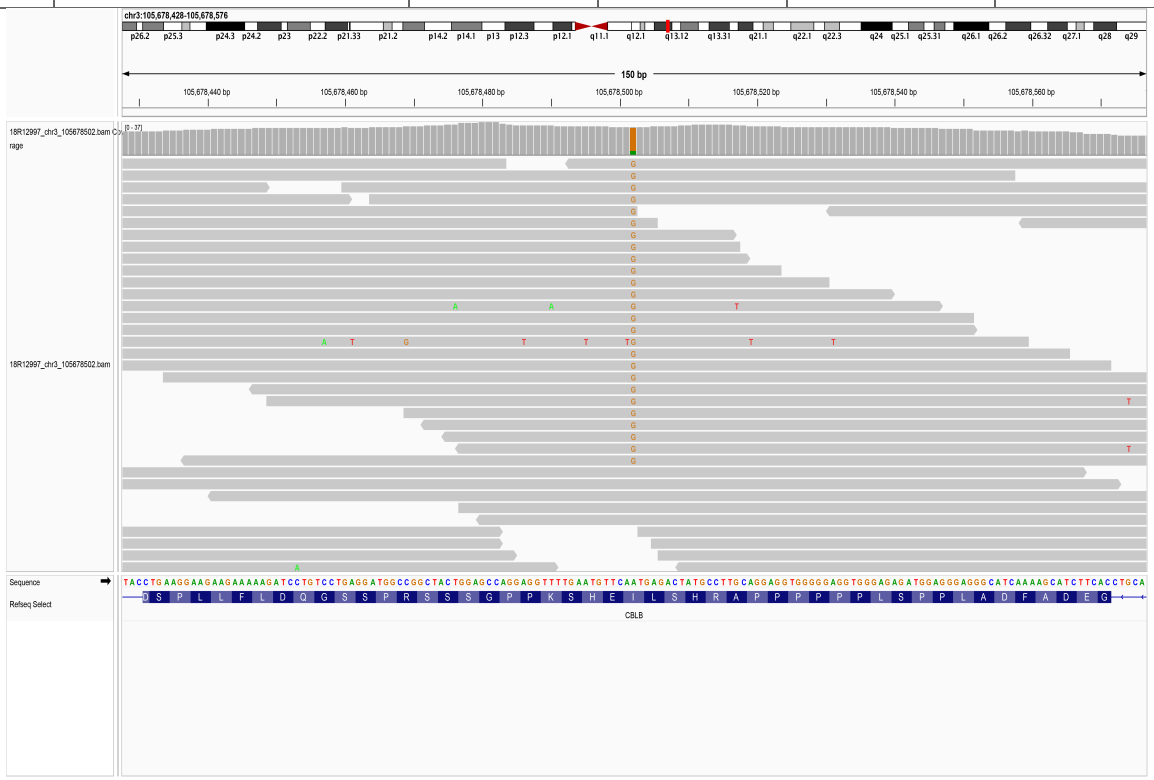
8.4. chr3_105678490_T/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135317	chr3_105678490_T/G	42	19	*CBLB*	missense_variant



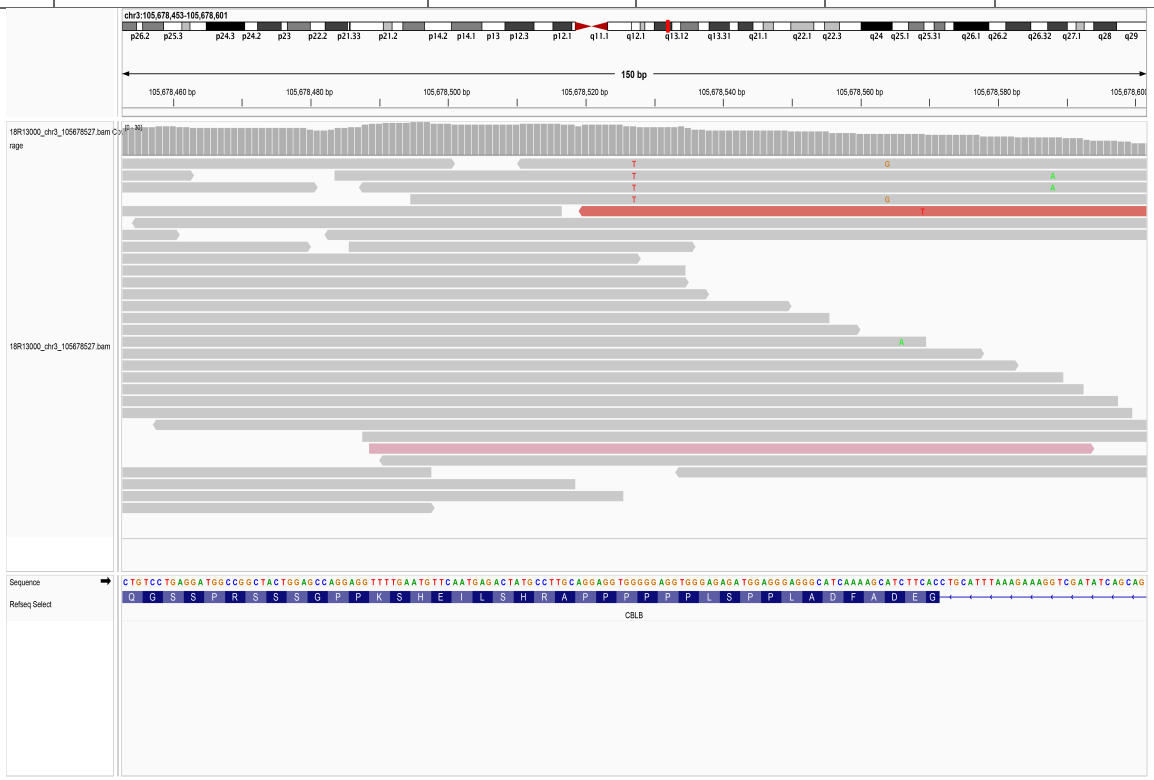
8.5. chr3_105678502_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12997	chr3_105678502_A/G	5	24	*CBLB*	missense_variant



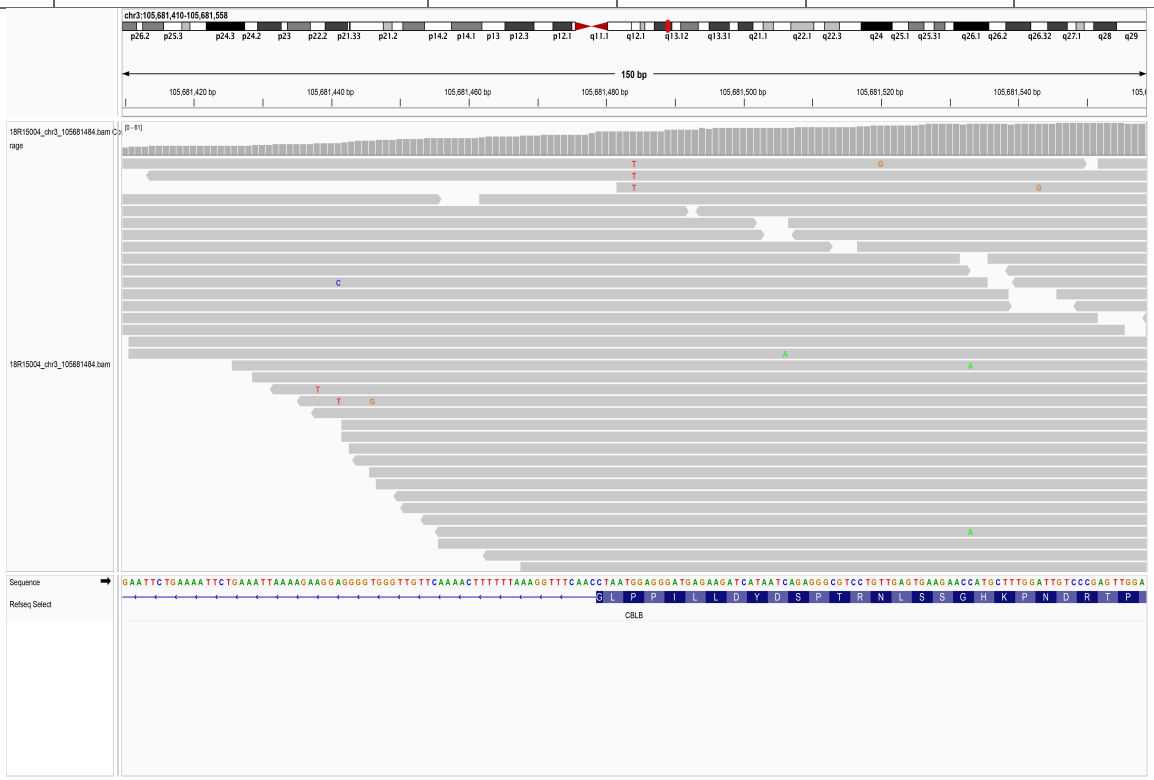
8.6. chr3_105678527_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13000	chr3_105678527_G/T	21	4	*CBLB*	missense_variant



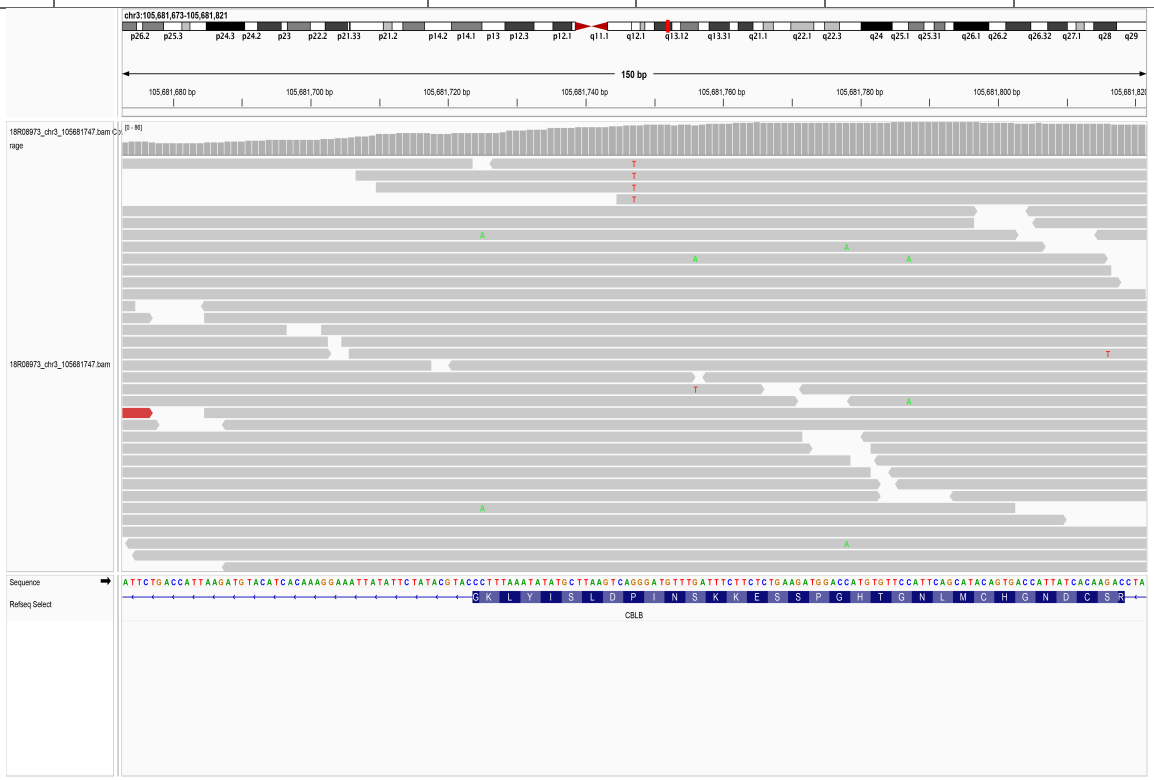
8.7. chr3_105681484_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15004	chr3_105681484_G/T	39	3	*CBLB*	missense_variant



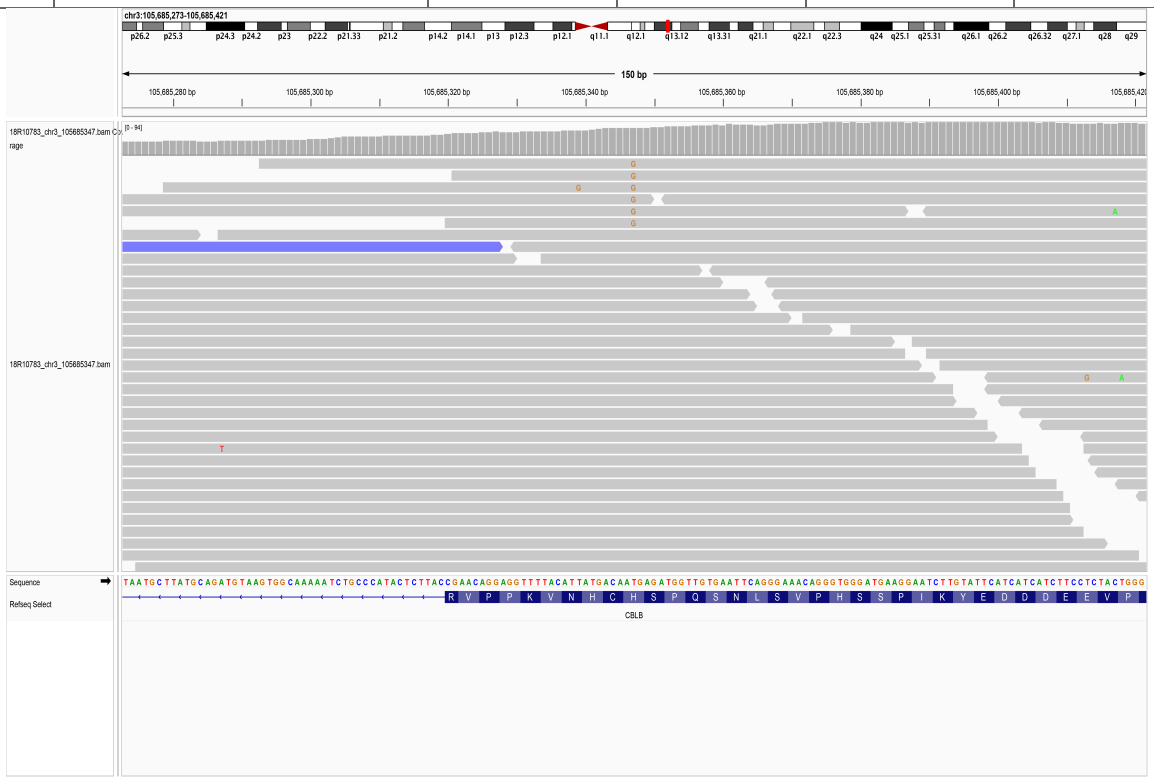
8.8. chr3_105681747_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08973	chr3_105681747_G/T	73	4	*CBLB*	missense_variant



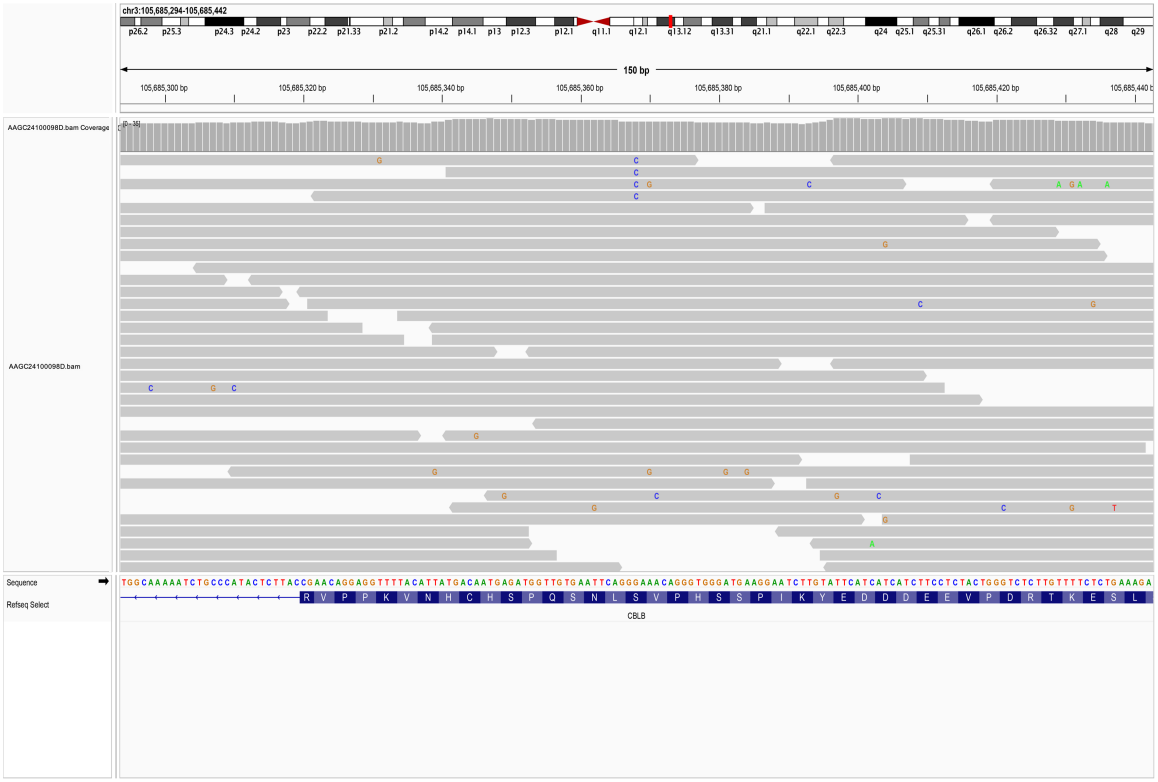
8.9. chr3_105685347_T/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10783	chr3_105685347_T/G	69	6	*CBLB*	missense_variant



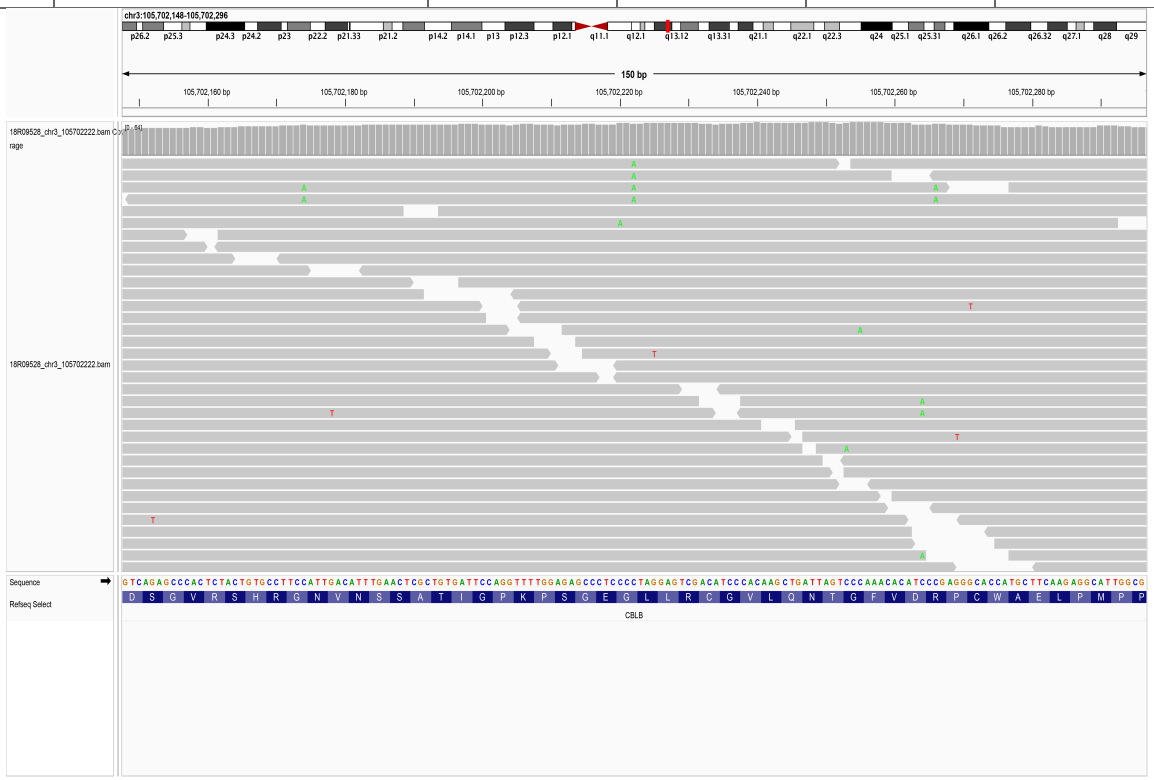
8.10. chr3_105685368_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC24100098D	chr3_105685368_G/C	24	4	*CBLB*	missense_variant



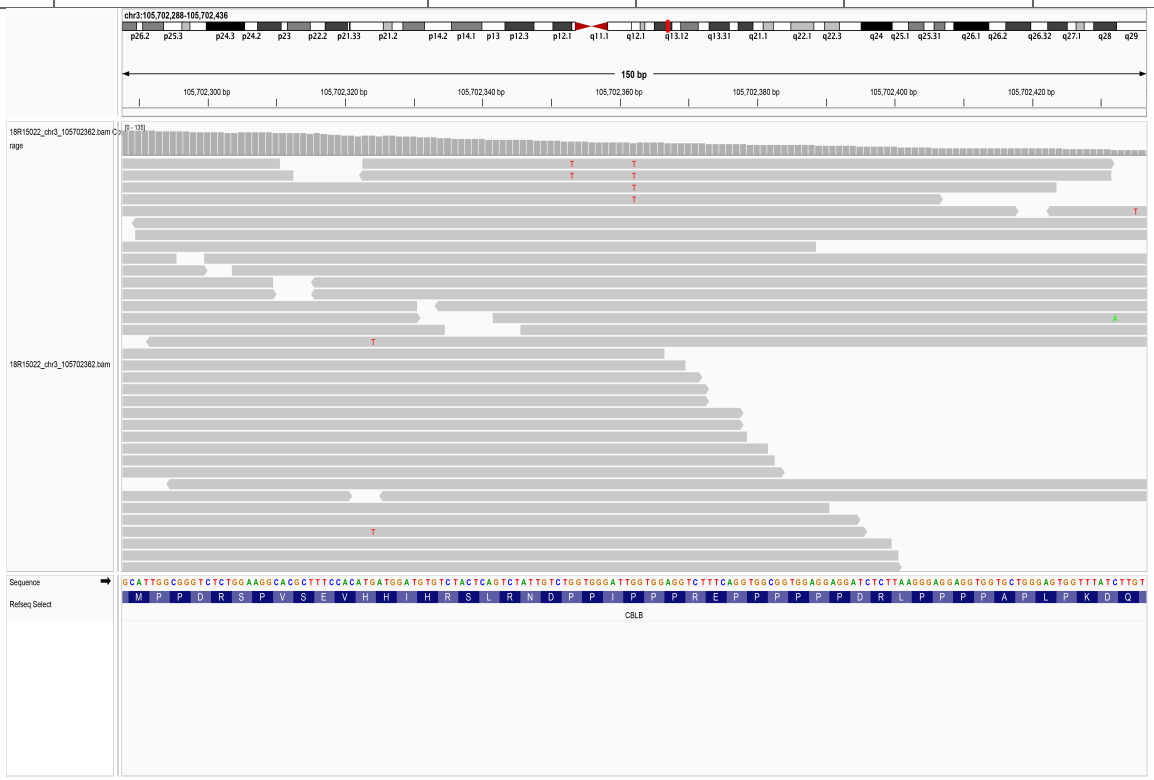
8.11. chr3_105702222_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09528	chr3_105702222_C/A	55	4	*CBLB*	missense_variant



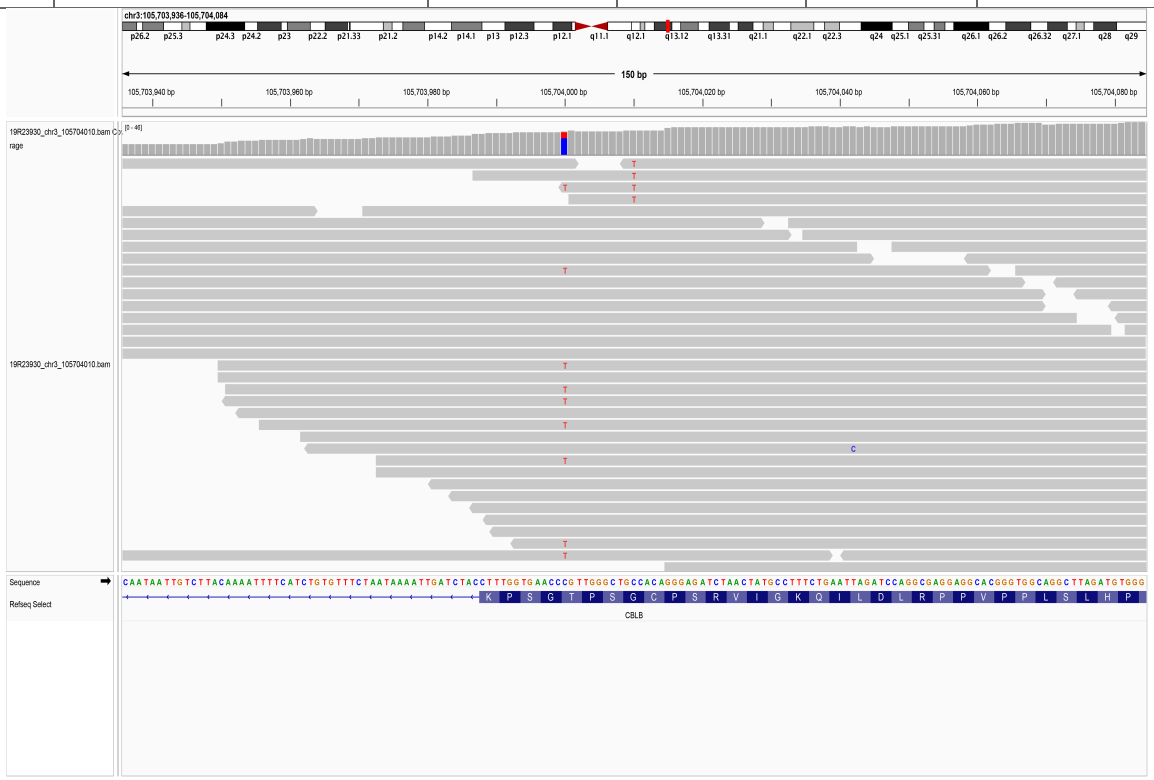
8.12. chr3_105702362_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15022	chr3_105702362_G/T	46	4	*CBLB*	missense_variant



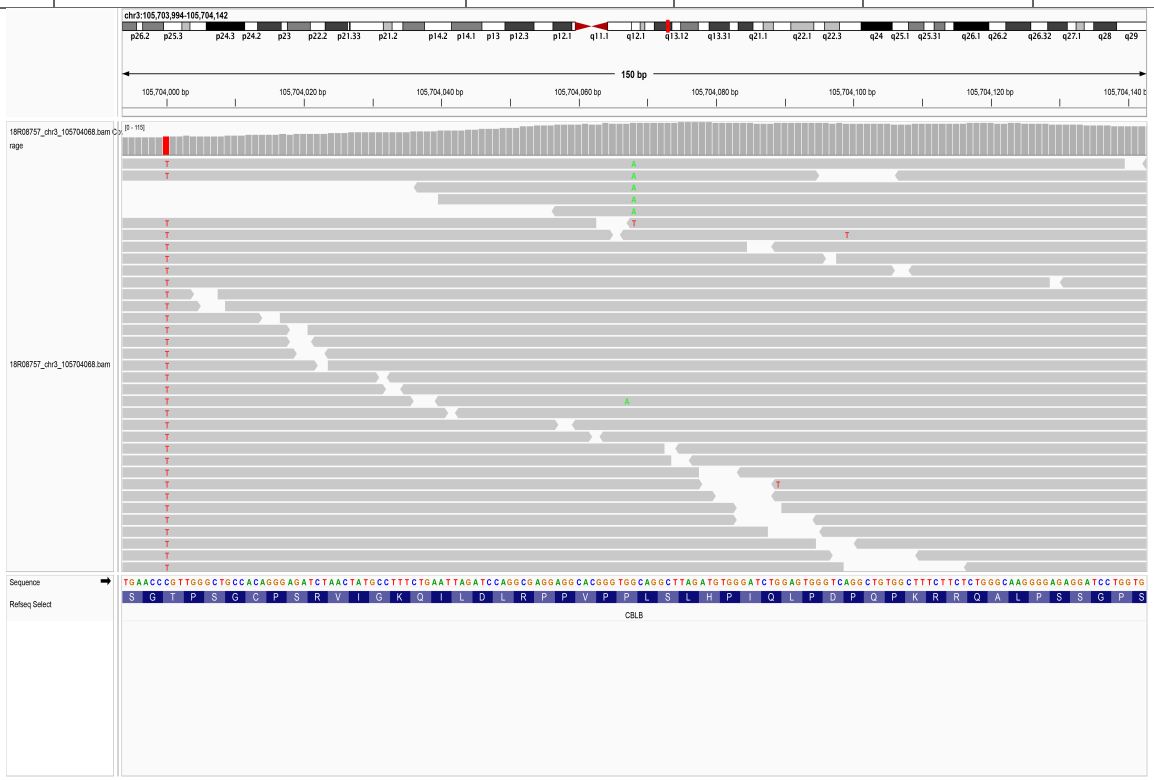
8.13. chr3_105704010_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23930	chr3_105704010_C/T	30	4	*CBLB*	missense_variant



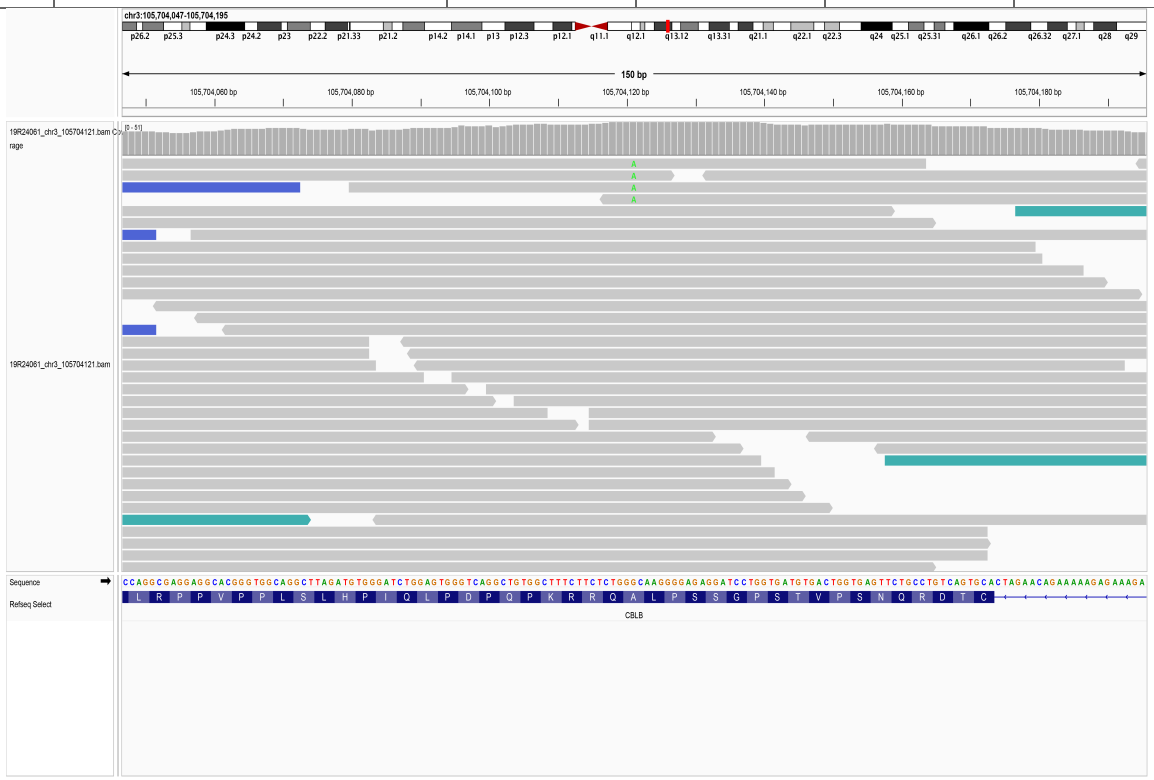
8.14. chr3_105704068_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08757	chr3_105704068_G/A	104	5	*CBLB*	missense_variant



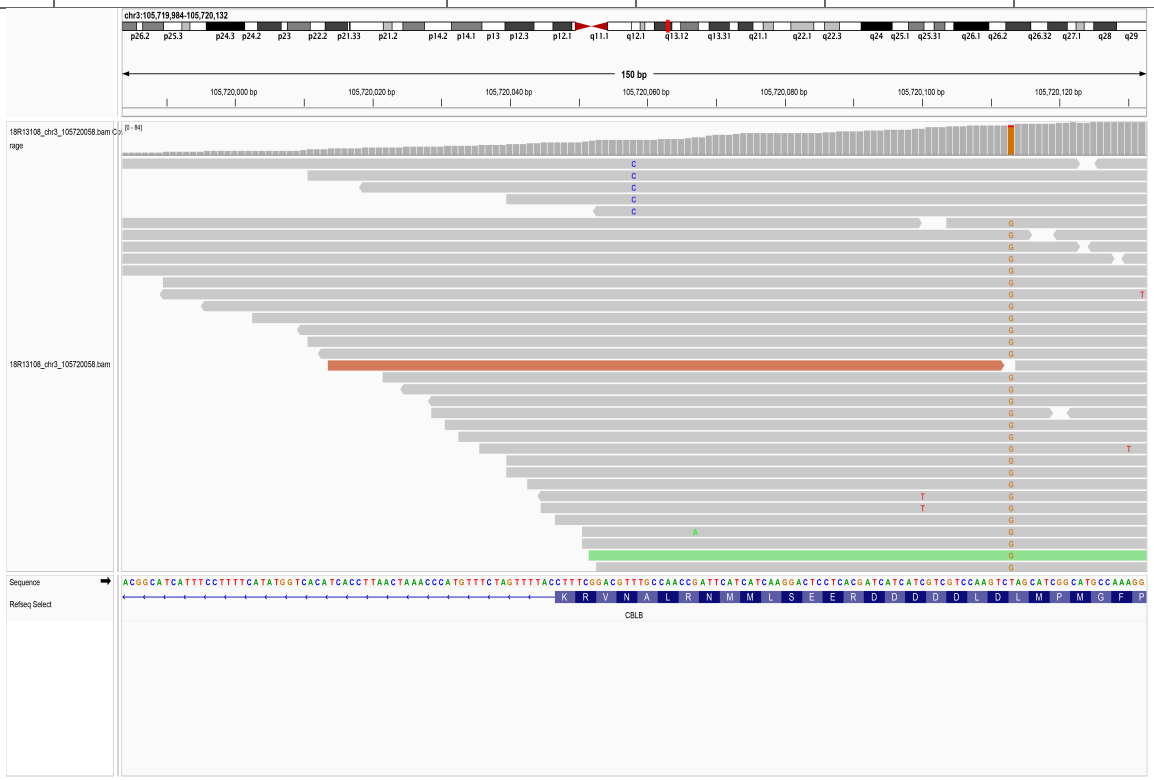
8.15. chr3_105704121_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R24061	chr3_105704121_G/A	46	4	*CBLB*	missense_variant



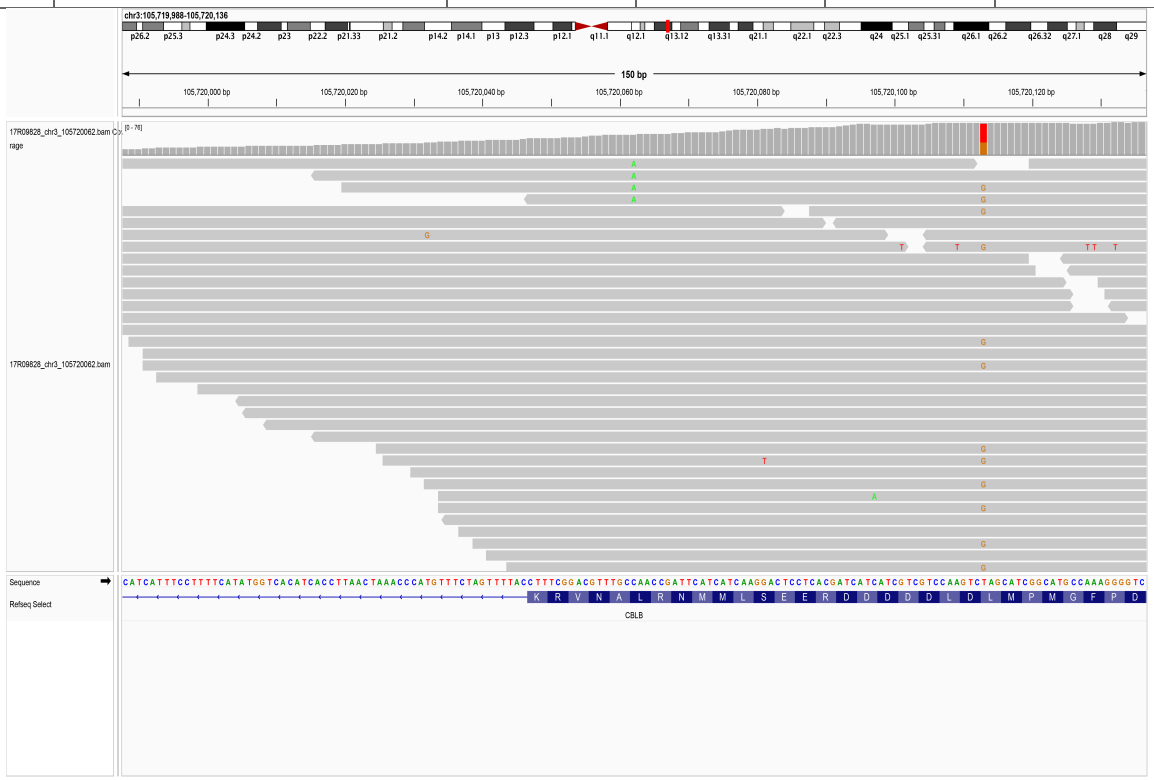
8.16. chr3_105720058_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13108	chr3_105720058_T/C	31	5	*CBLB*	missense_variant



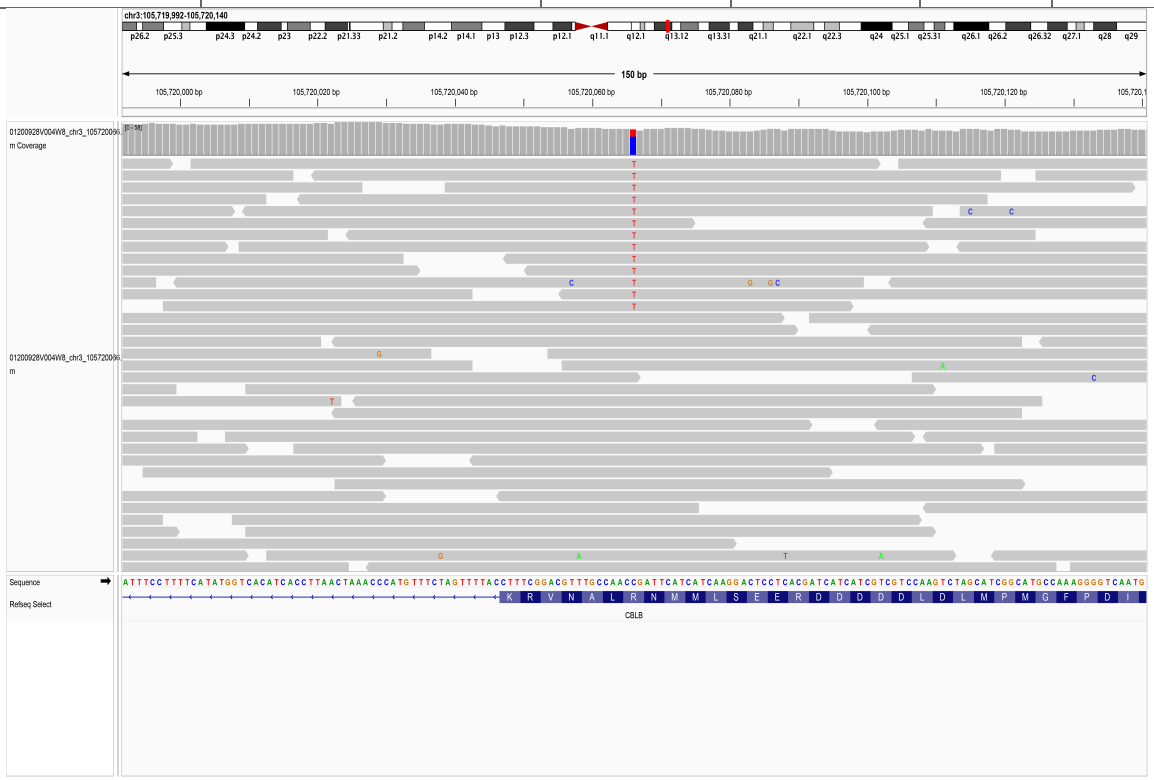
8.17. chr3_105720062_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09828	chr3_105720062_C/A	43	4	*CBLB*	missense_variant



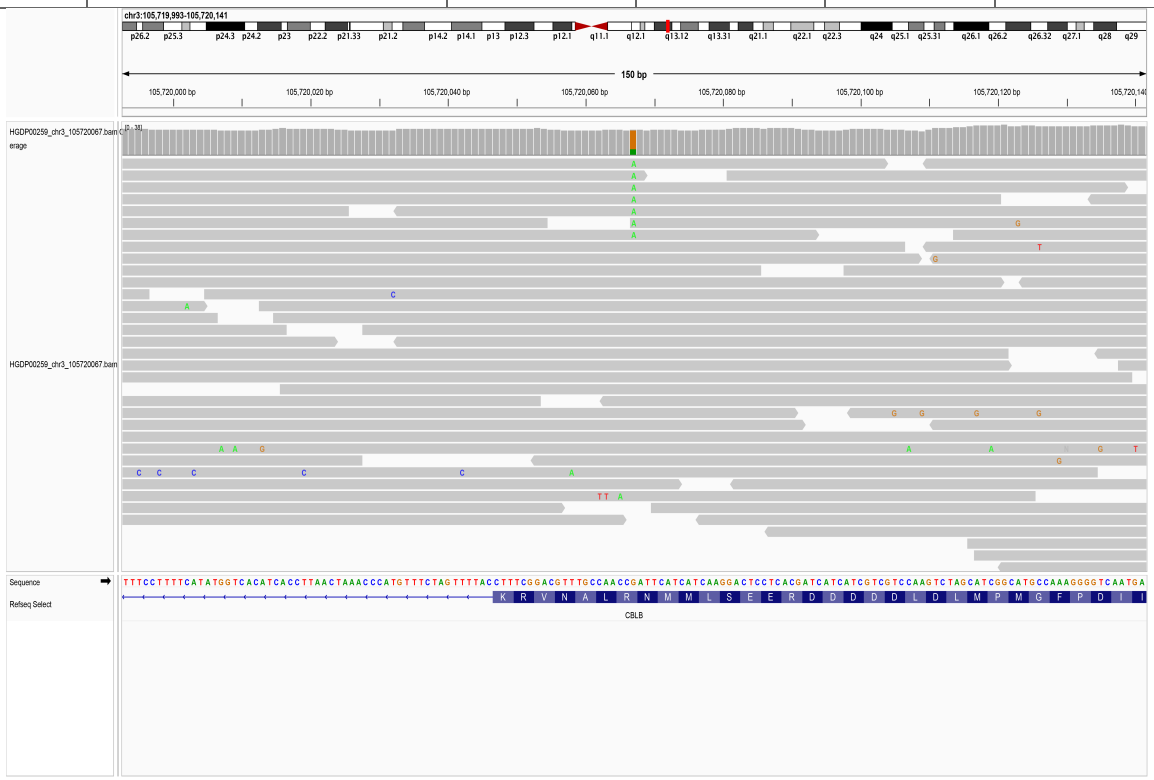
8.18. chr3_105720066_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
01200928V004W8	chr3_105720066_C/T	32	12	*CBLB*	missense_variant



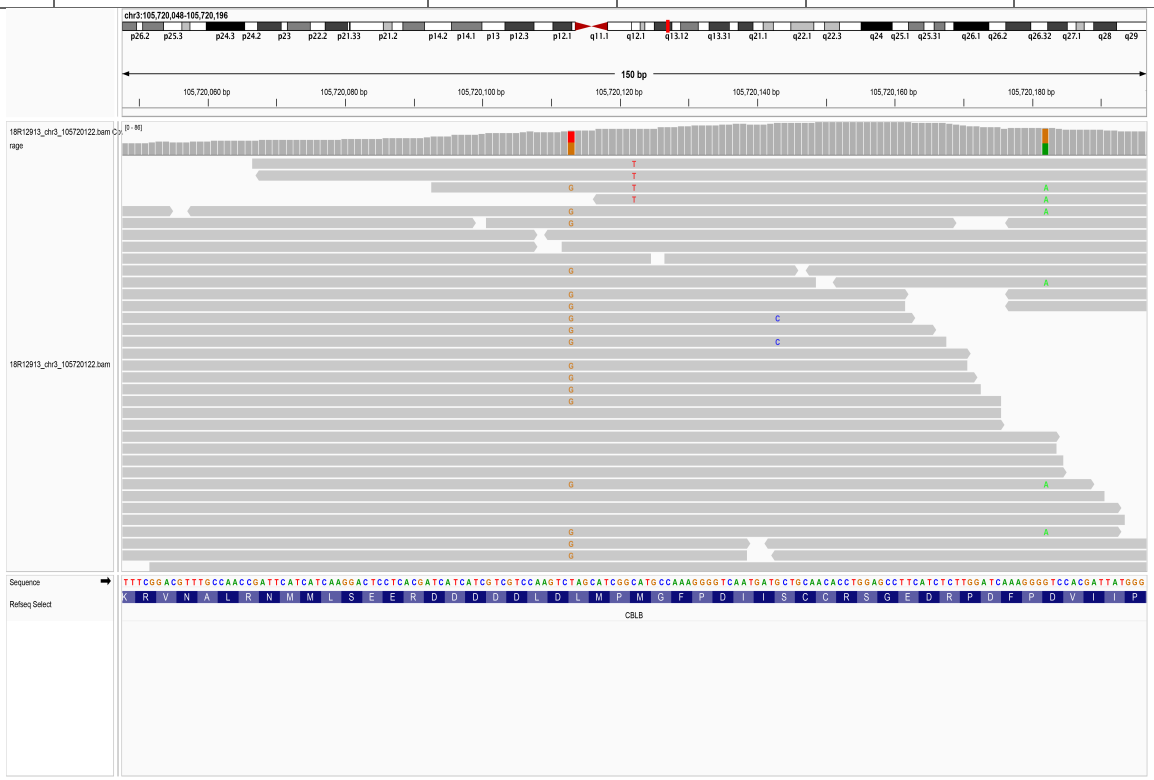
8.19. chr3_105720067_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HGDP00259	chr3_105720067_G/A	21	7	*CBLB*	missense_variant



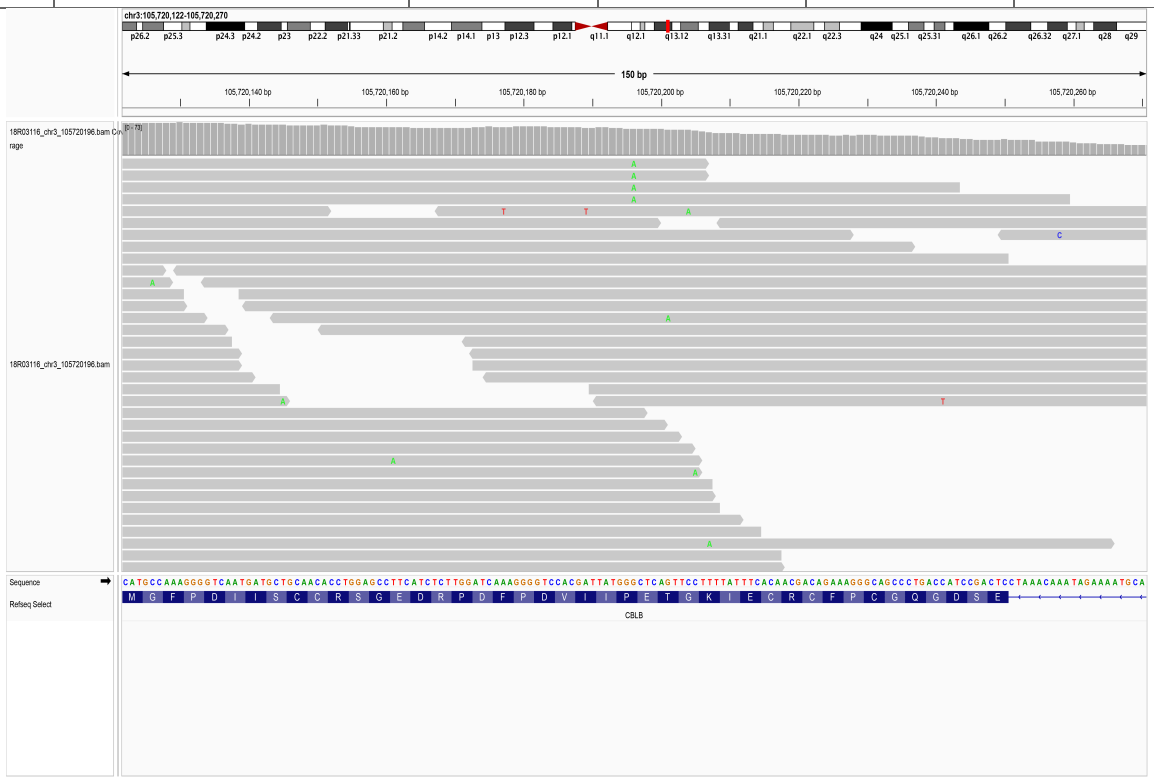
8.20. chr3_105720122_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12913	chr3_105720122_C/T	61	4	*CBLB*	missense_variant



8.21. chr3_105720196_G/A

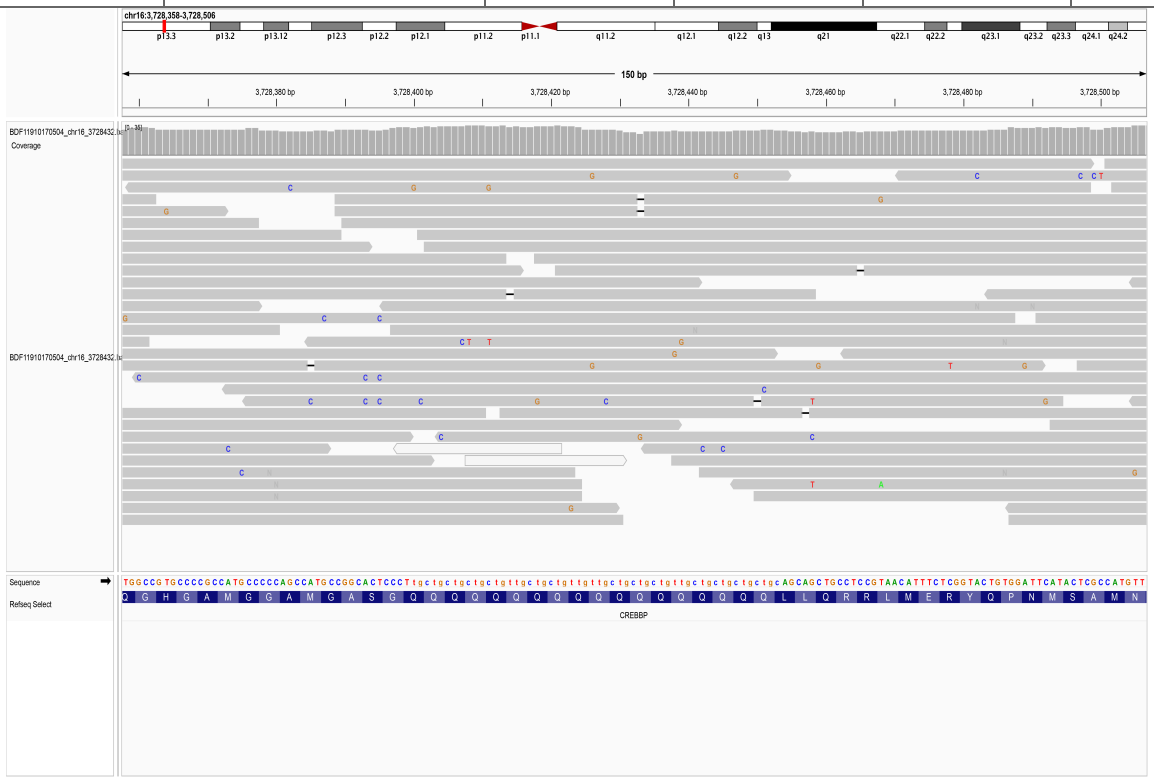
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03116	chr3_105720196_G/A	51	4	*CBLB*	missense_variant



9. *CREBBP*

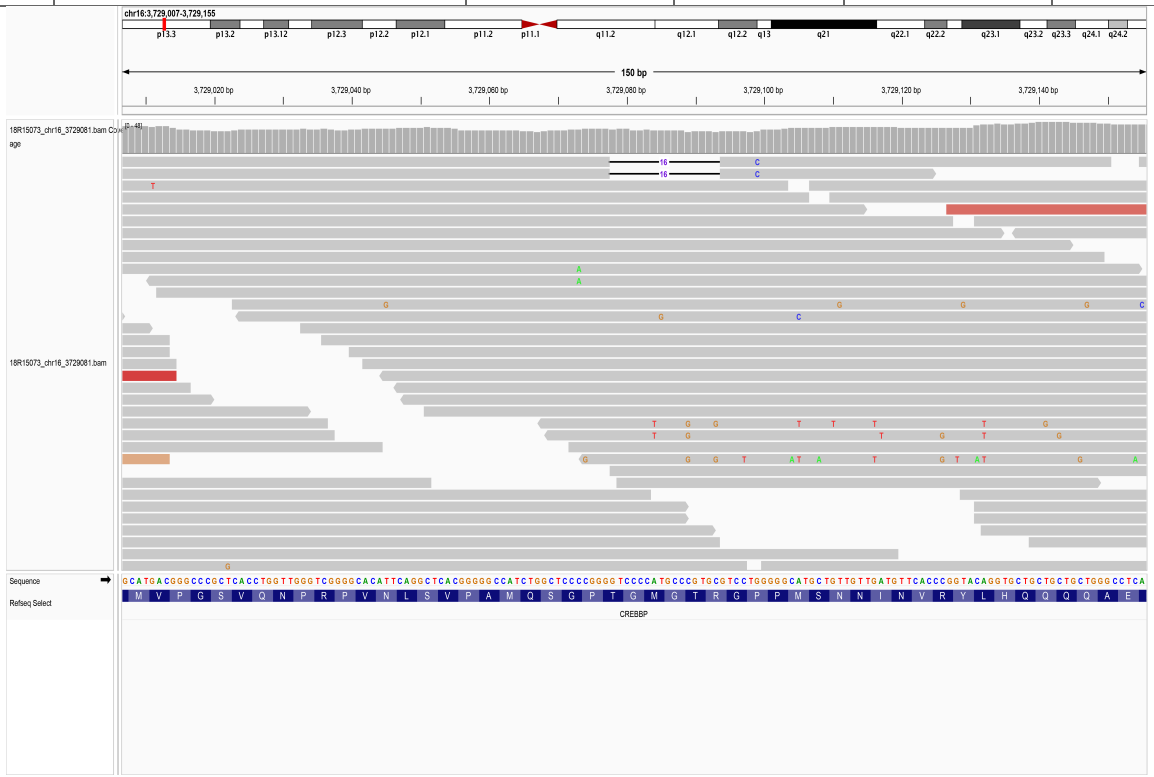
9.1. chr16_3728433_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chr16_3728433_T/-	17	2	*CREBBP*	frameshift_variant



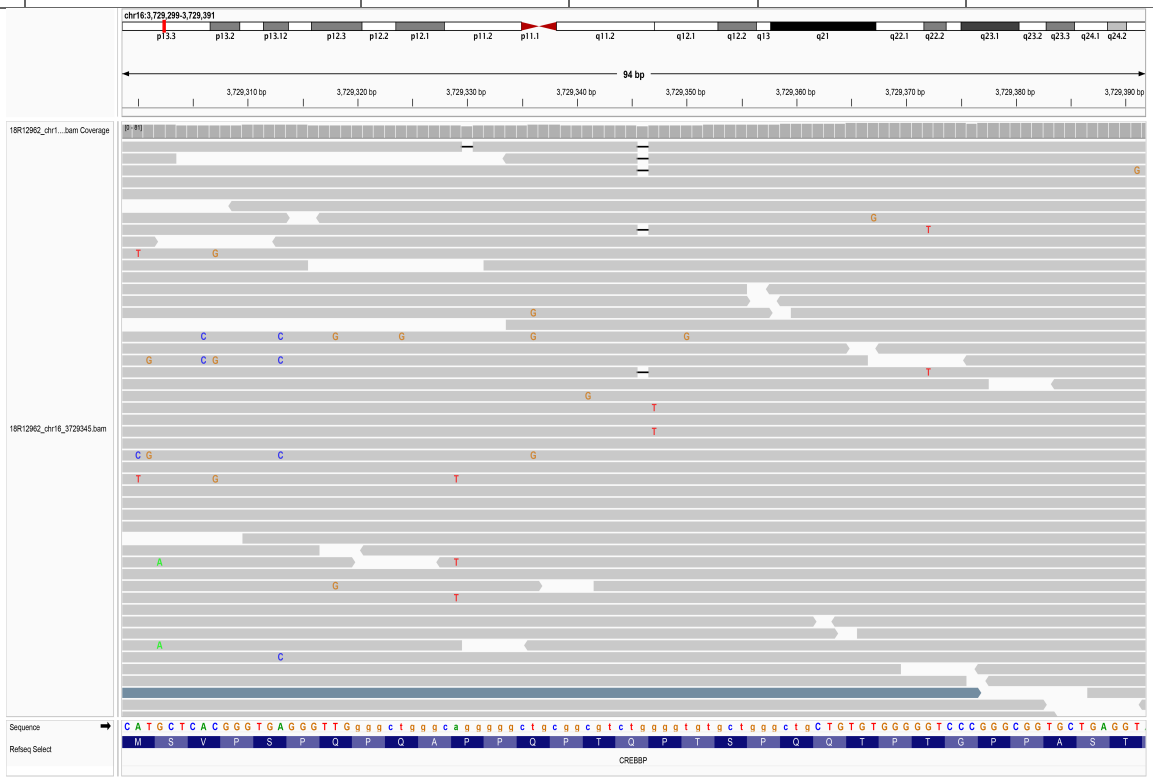
9.2. chr16_3729082_CCATGCCCGTGCG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15073	chr16_3729082_CCATGCCCGTGCG/-	30	2	*CREBBP*	frameshift_variant



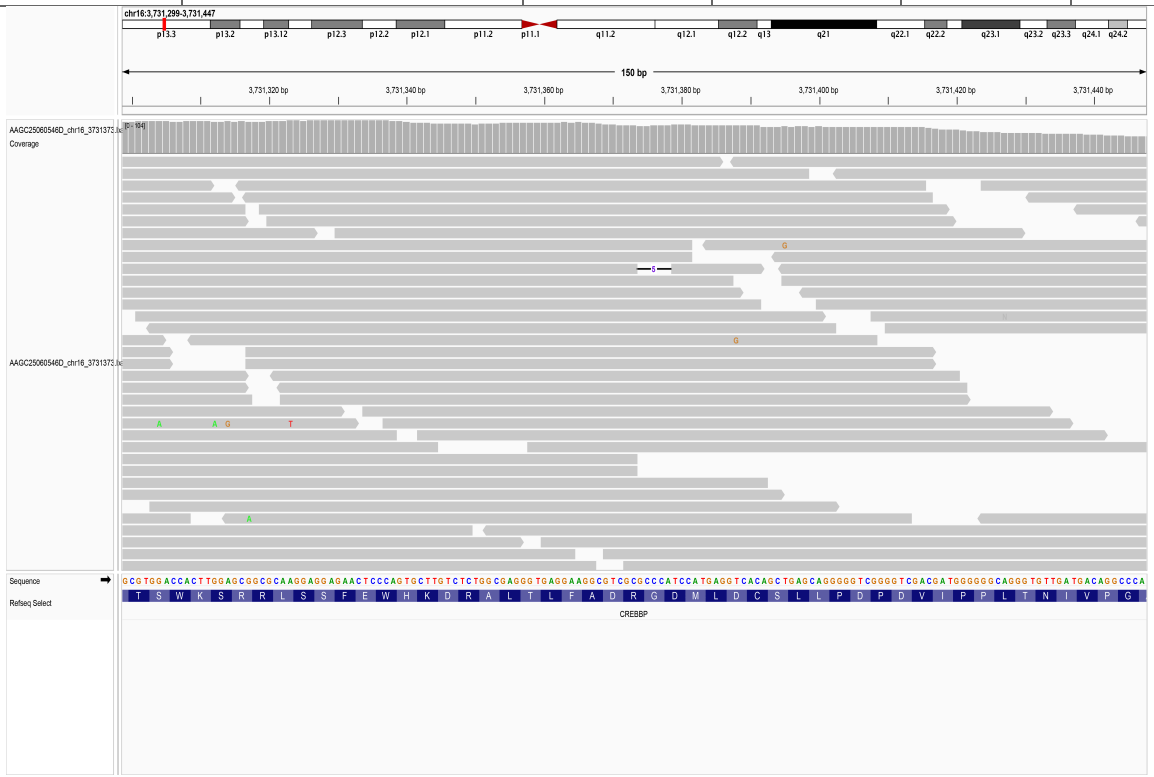
9.3. chr16_3729346_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12962	chr16_3729346_G/-	46	7	*CREBBP*	frameshift_variant



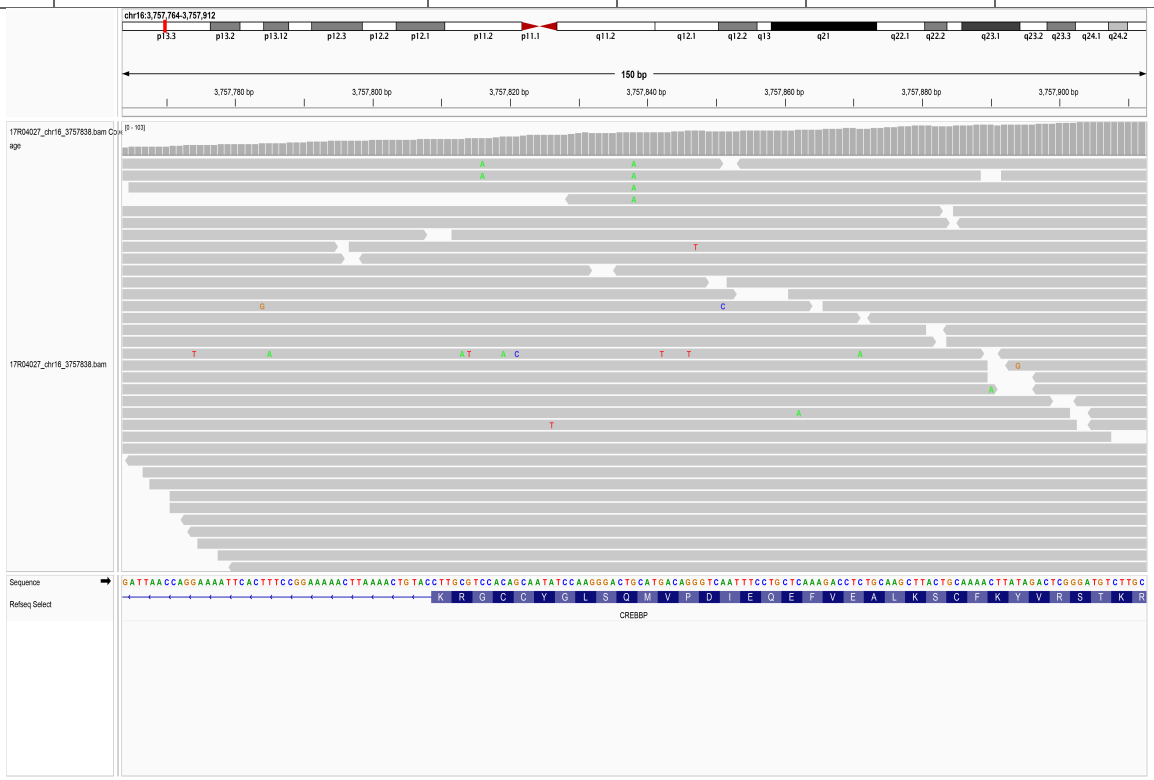
9.4. chr16_3731374_GCCCA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060546D	chr16_3731374_GCCCA/-	86	2	*CREBBP*	frameshift_variant



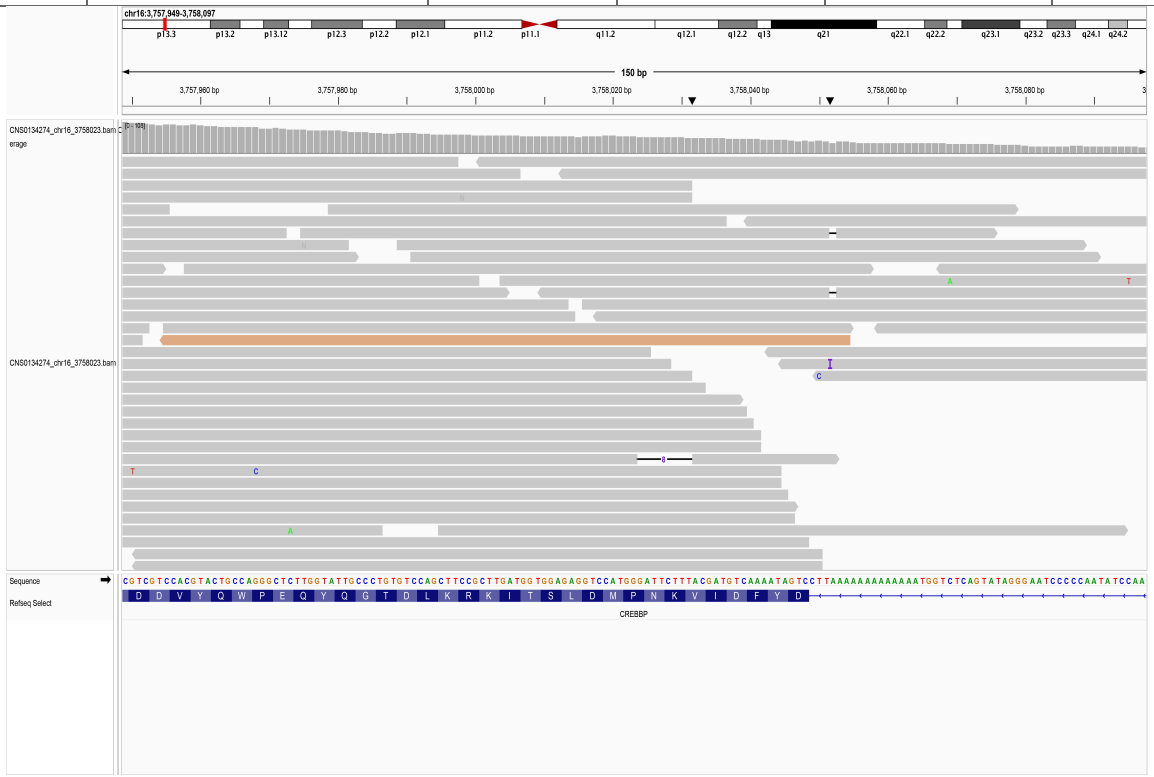
9.5. chr16_3757838_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R04027	chr16_3757838_G/A	65	4	*CREBBP*	stop_gained



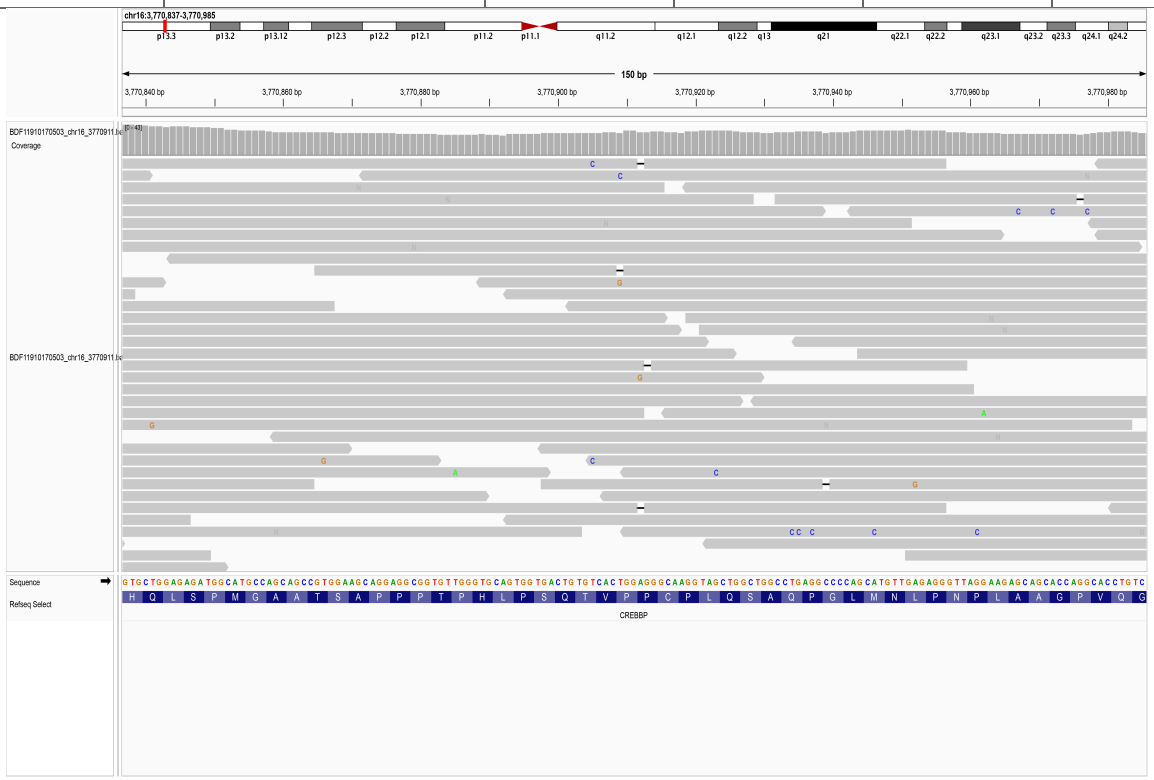
9.6. chr16_3758024_GATTCTTT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134274	chr16_3758024_GATTCTTT/-	52	2	*CREBBP*	frameshift_variant



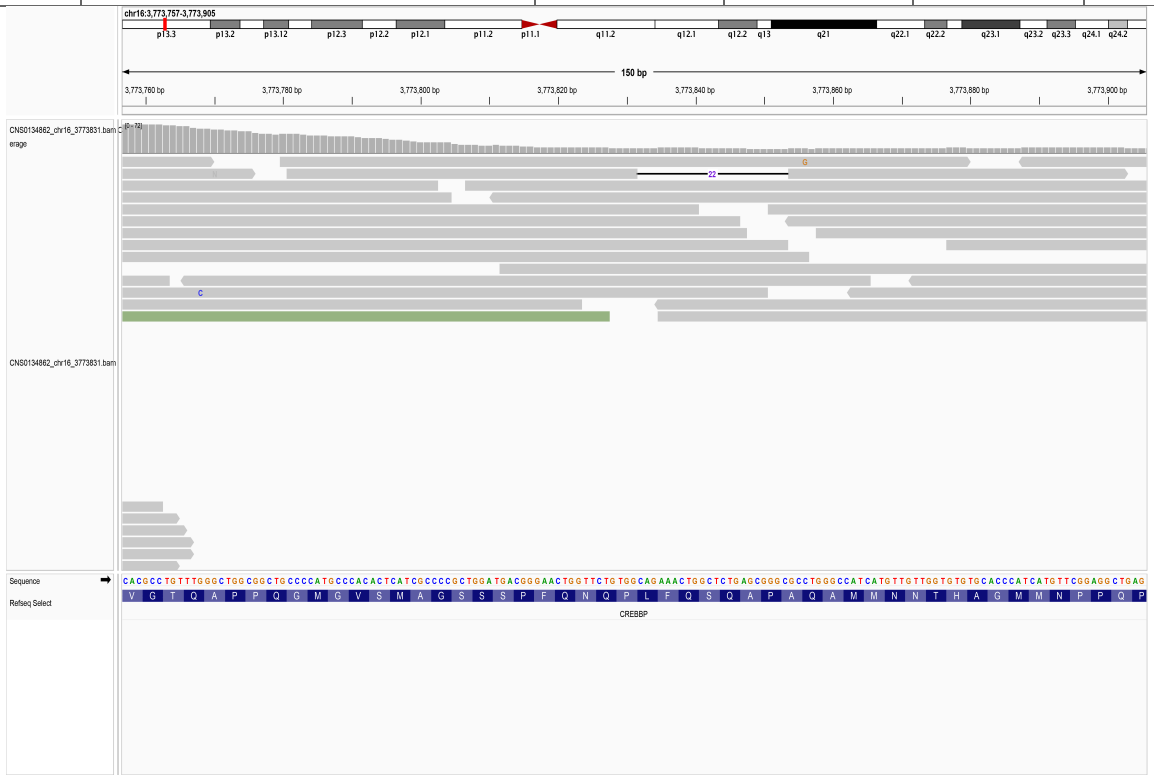
9.7. chr16_3770912_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr16_3770912_A/-	29	2	*CREBBP*	frameshift_variant



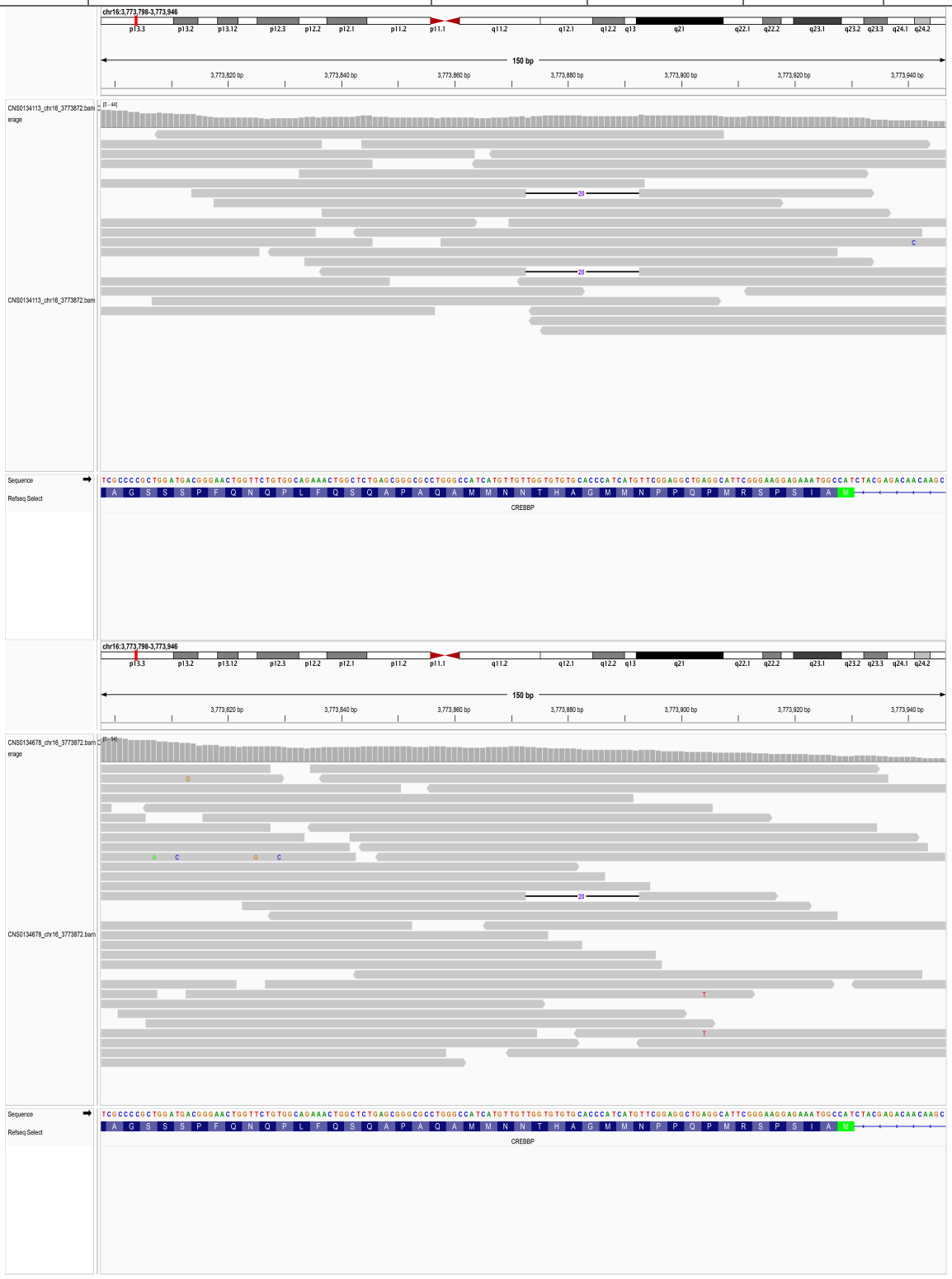
9.8. chr16_3773832_CAGAAACTGGCTCTGAGCGGGC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134862	chr16_3773832_CAGAAACTGG CTCTGAGCGGGC/-	14	2	*CREBBP*	frameshift_variant



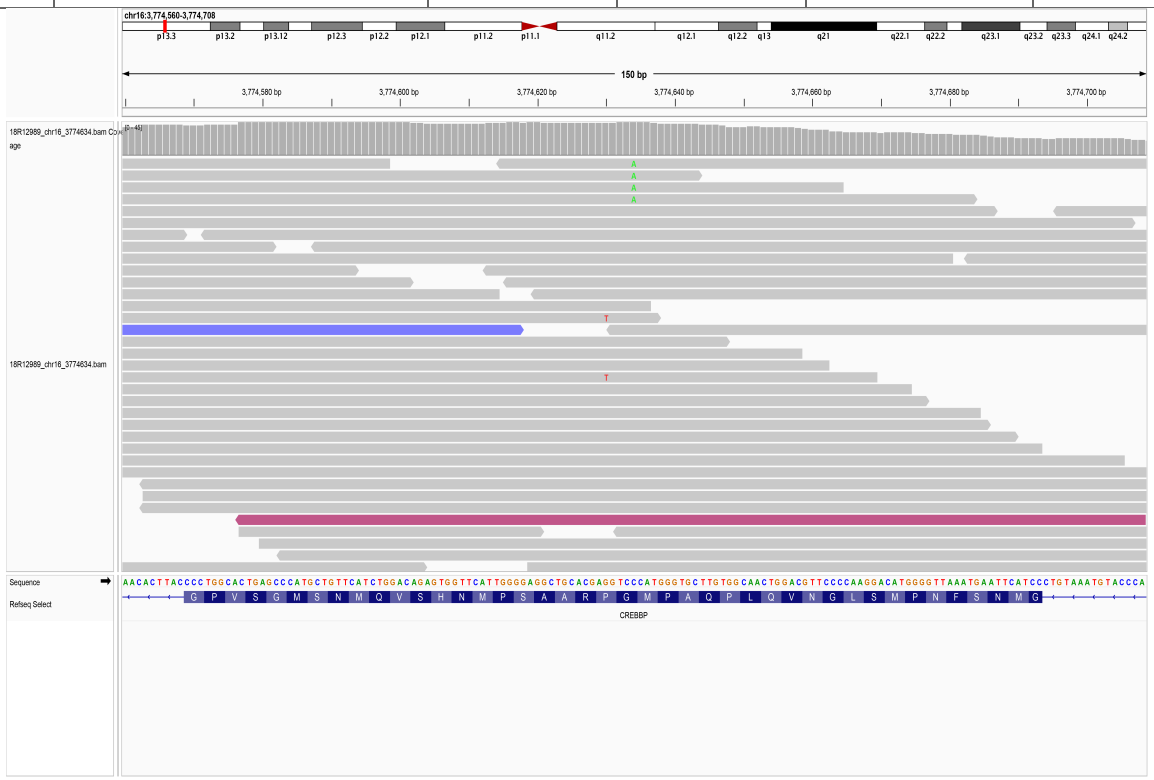
9.9. chr16_3773873_TGGTGTGTGCACCCATCATG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134113	chr16_3773873_TGGTGTGTGCACCCATCATG/-	19	2	*CREBBP*	frameshift_variant
CNS0134678	chr16_3773873_TGGTGTGTGCACCCATCATG/-	30	2	*CREBBP*	frameshift_variant



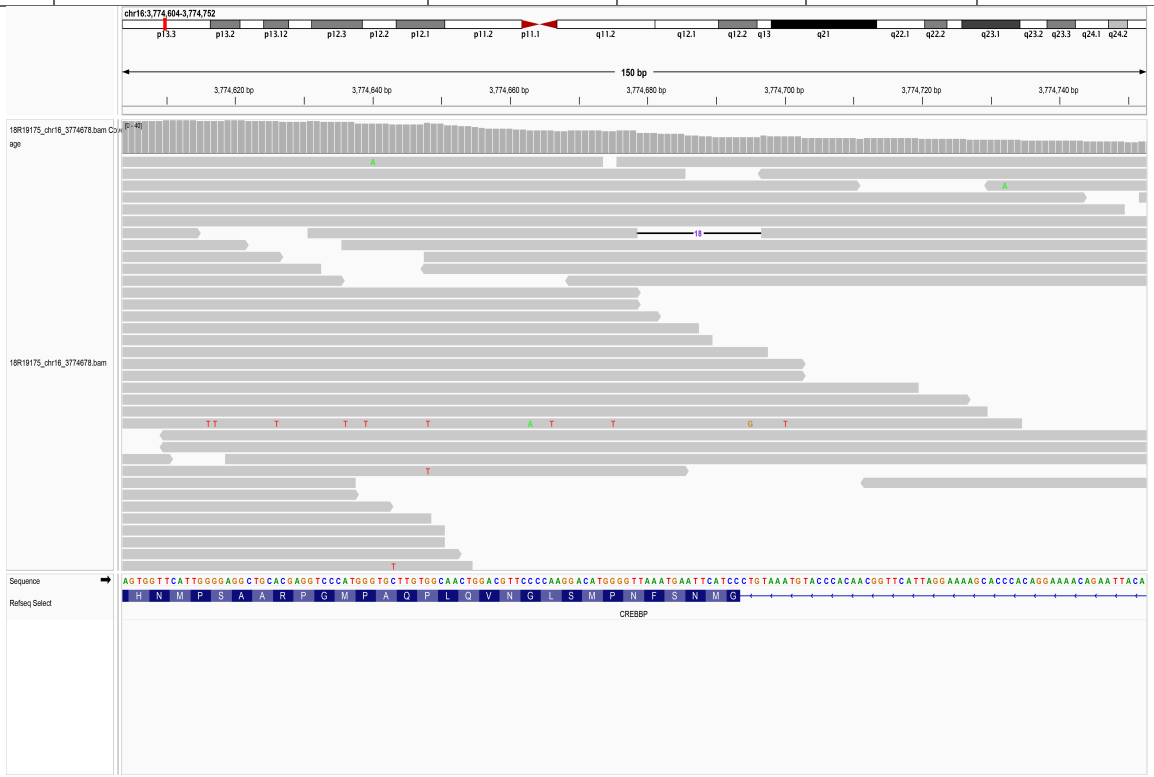
9.10. chr16_3774634_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12989	chr16_3774634_C/A	38	4	*CREBBP*	stop_gained



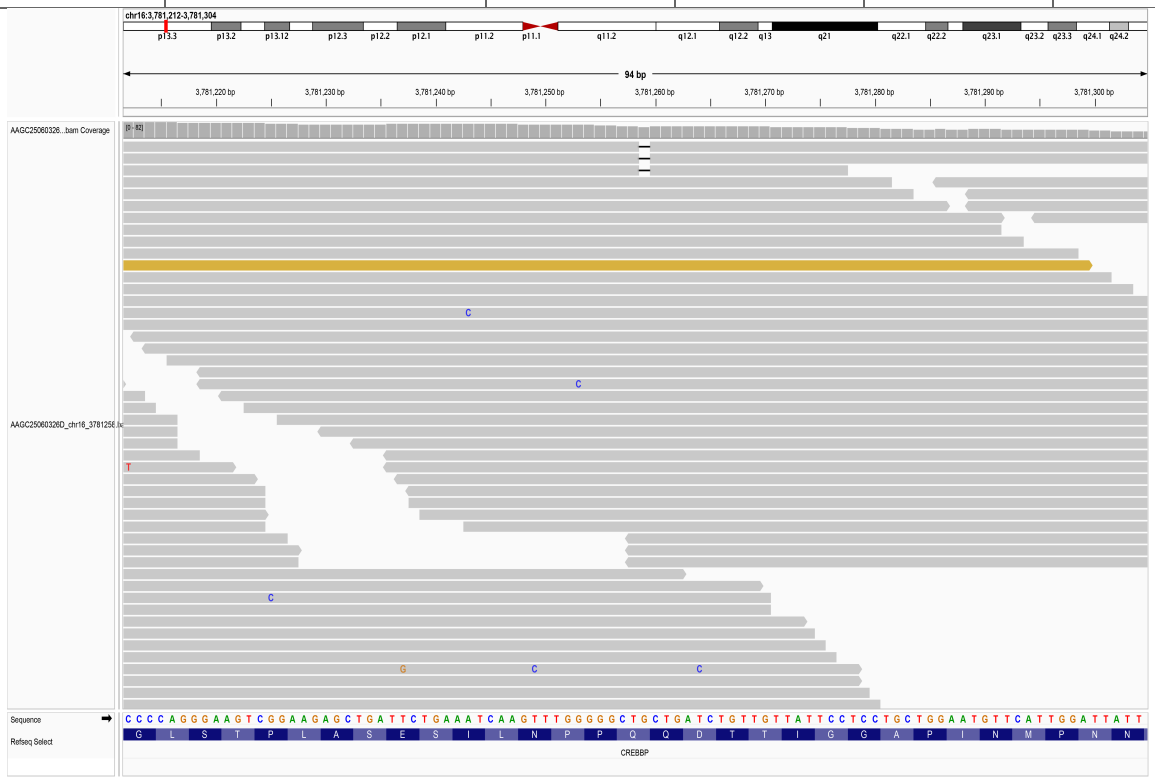
9.11. chr16_3774679_TAAATGAATTCATCCCTG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19175	chr16_3774679_TAAATGAATTCATCCCTG/-	22	2	*CREBBP*	splice_acceptor_variant



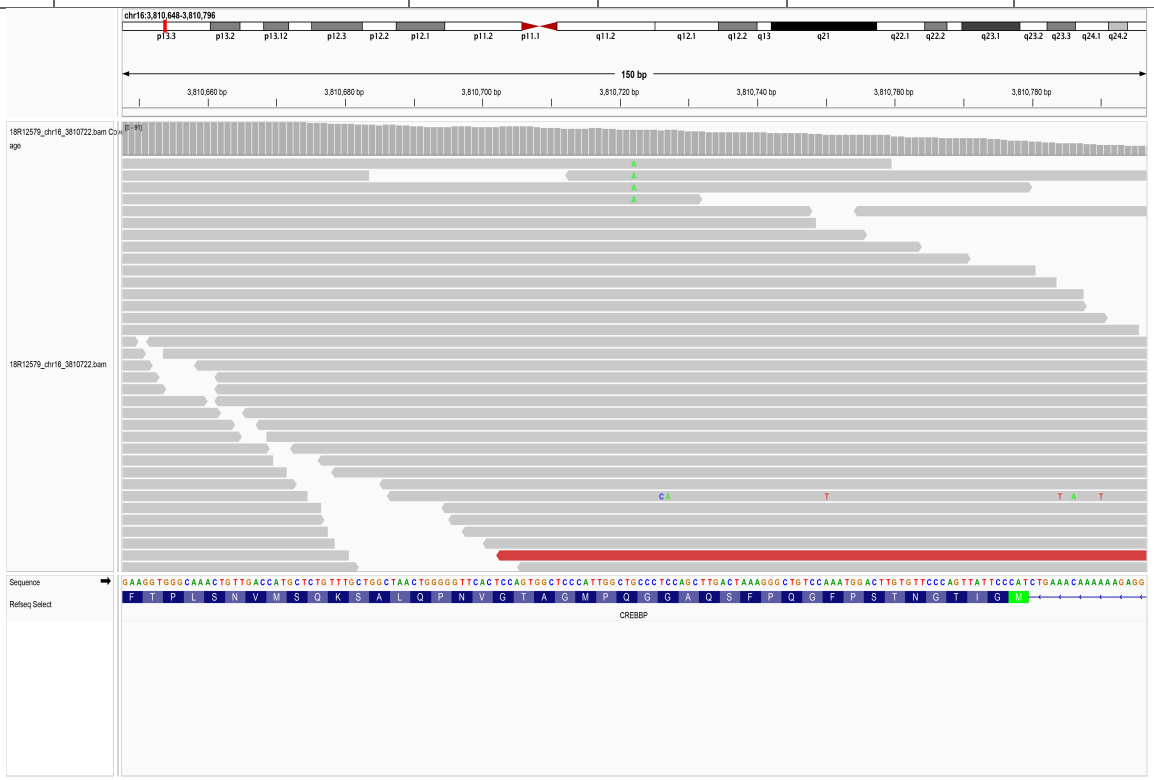
9.12. chr16_3781259_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060326D	chr16_3781259_G/-	52	3	*CREBBP*	frameshift_variant



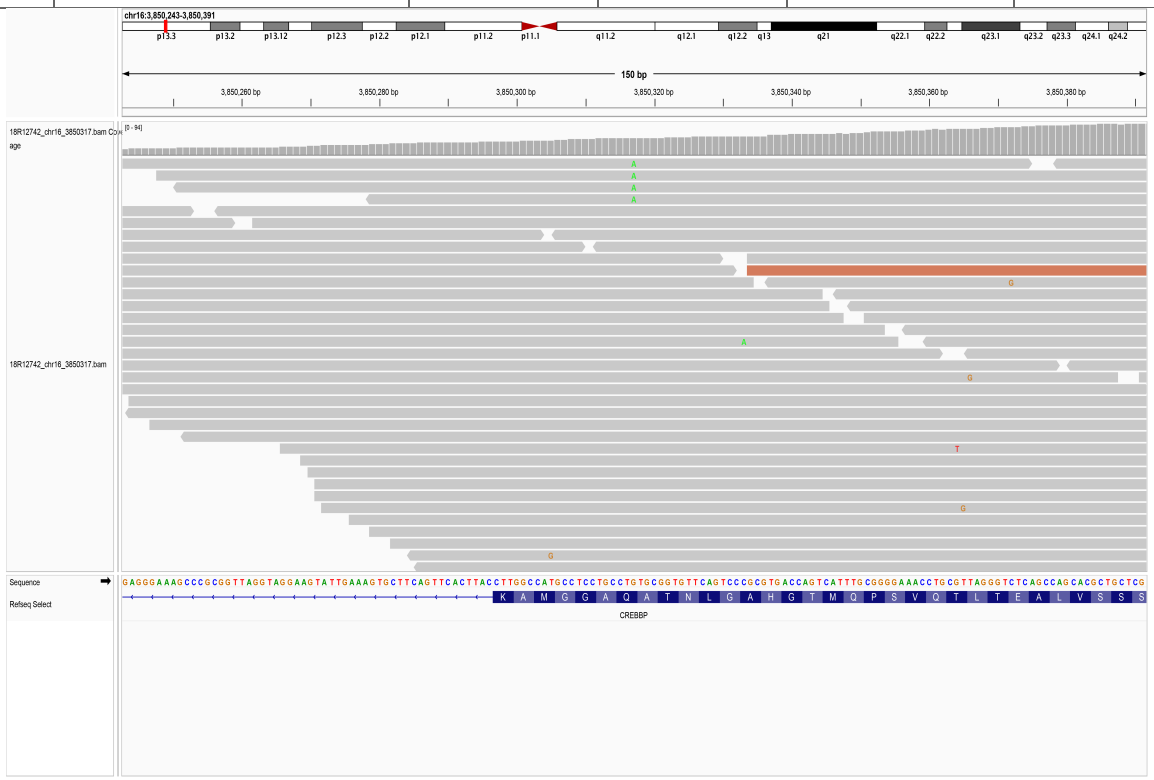
9.13. chr16_3810722_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12579	chr16_3810722_G/A	65	4	*CREBBP*	stop_gained



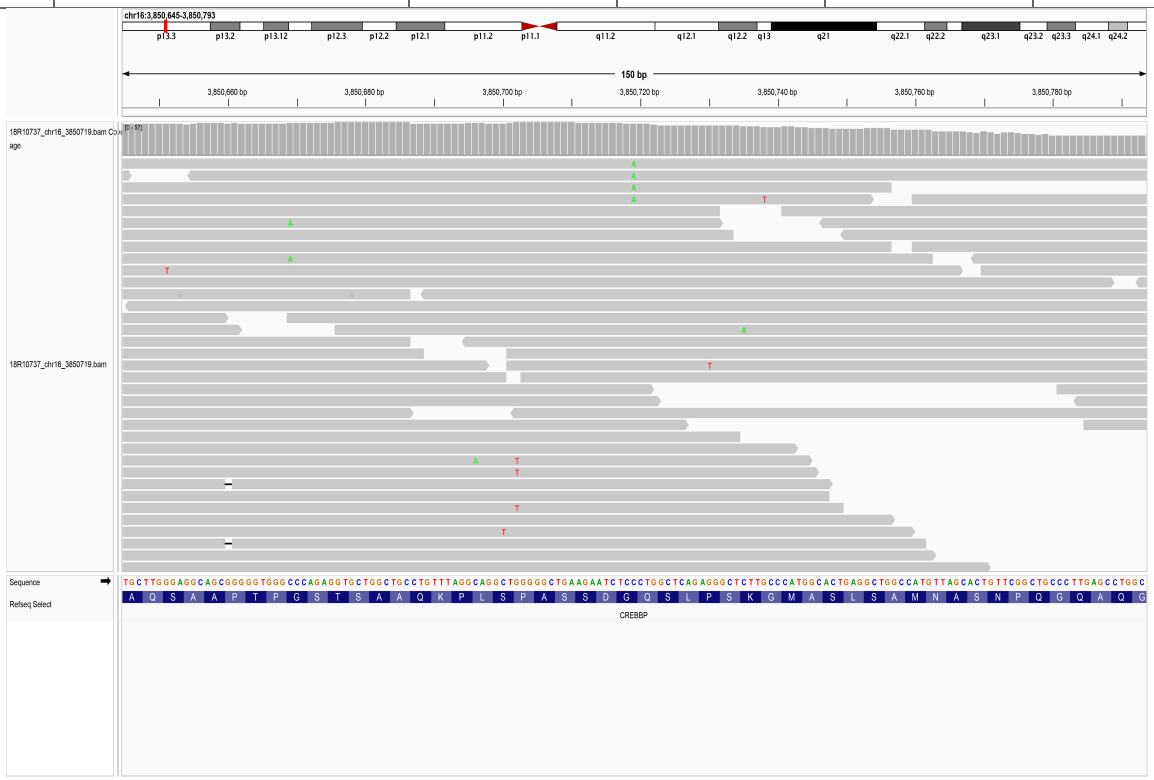
9.14. chr16_3850317_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12742	chr16_3850317_G/A	41	4	*CREBBP*	stop_gained



9.15. chr16_3850719_C/A

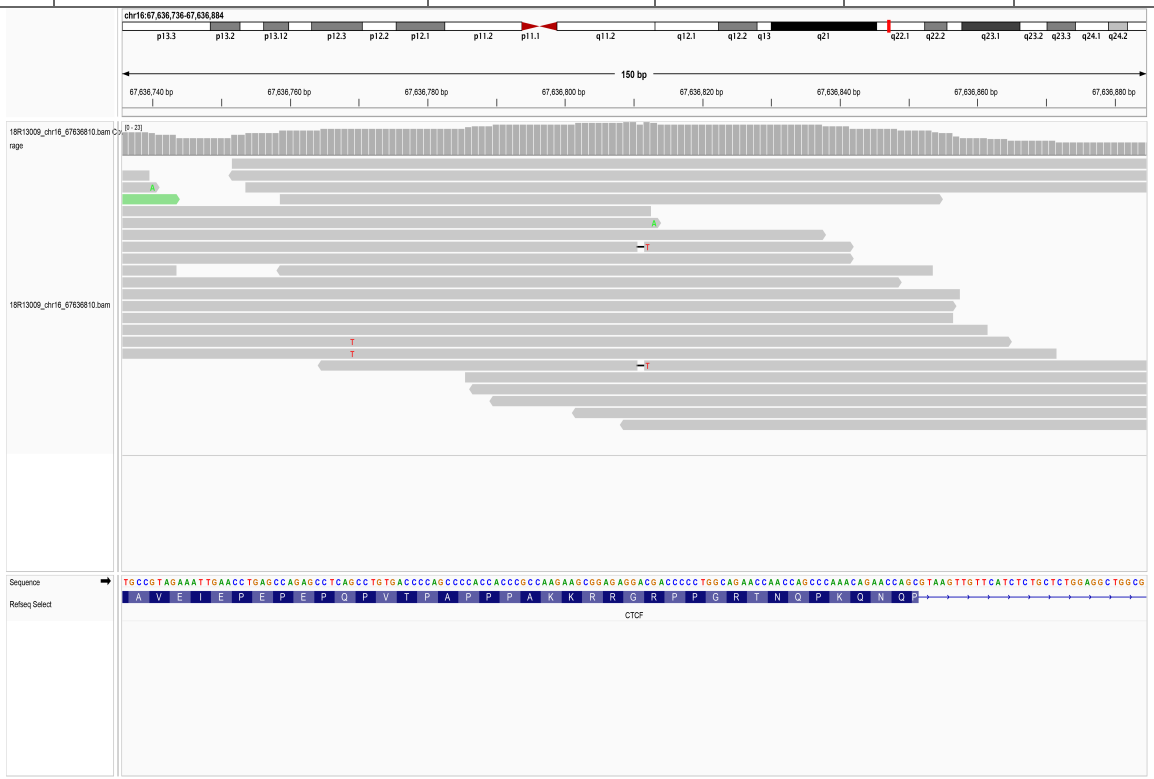
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10737	chr16_3850719_C/A	47	4	*CREBBP*	stop_gained



10. *CTCF*

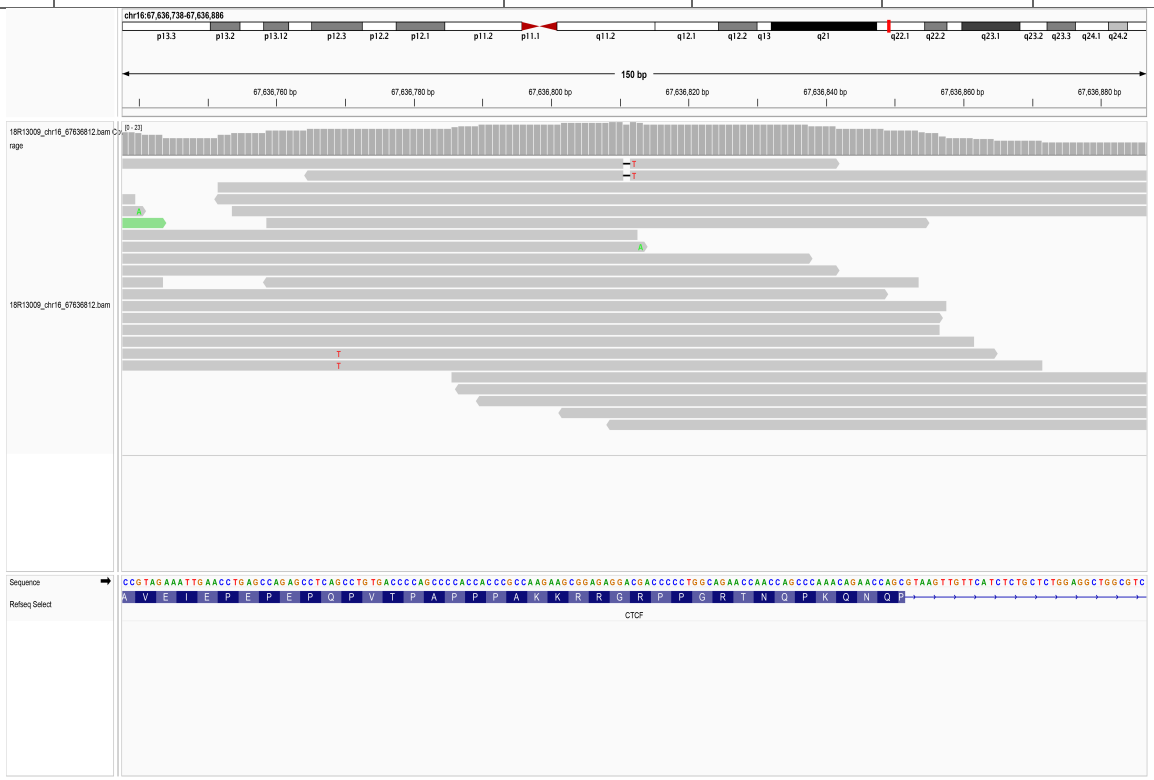
10.1. chr16_67636811_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13009	chr16_67636811_A/-	21	2	*CTCF*	frameshift_variant



10.2. chr16_67636812_C/T

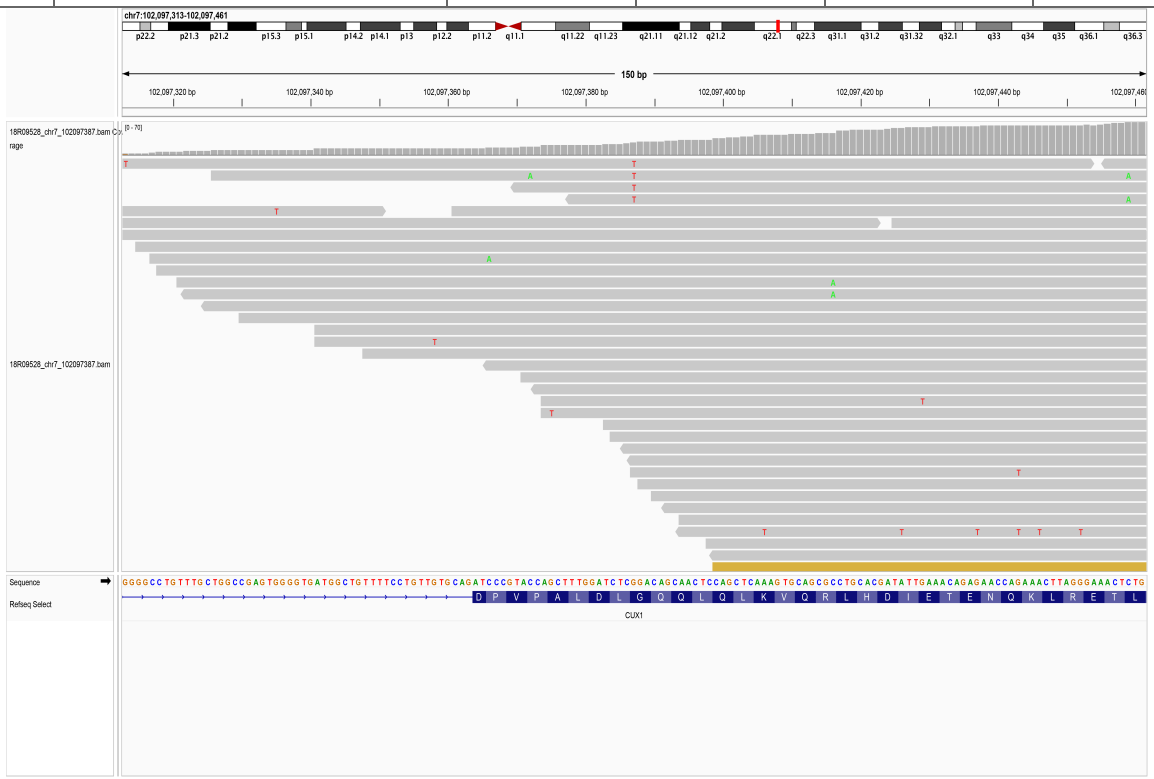
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13009	chr16_67636812_C/T	21	2	*CTCF*	stop_gained



11. *CUX1*

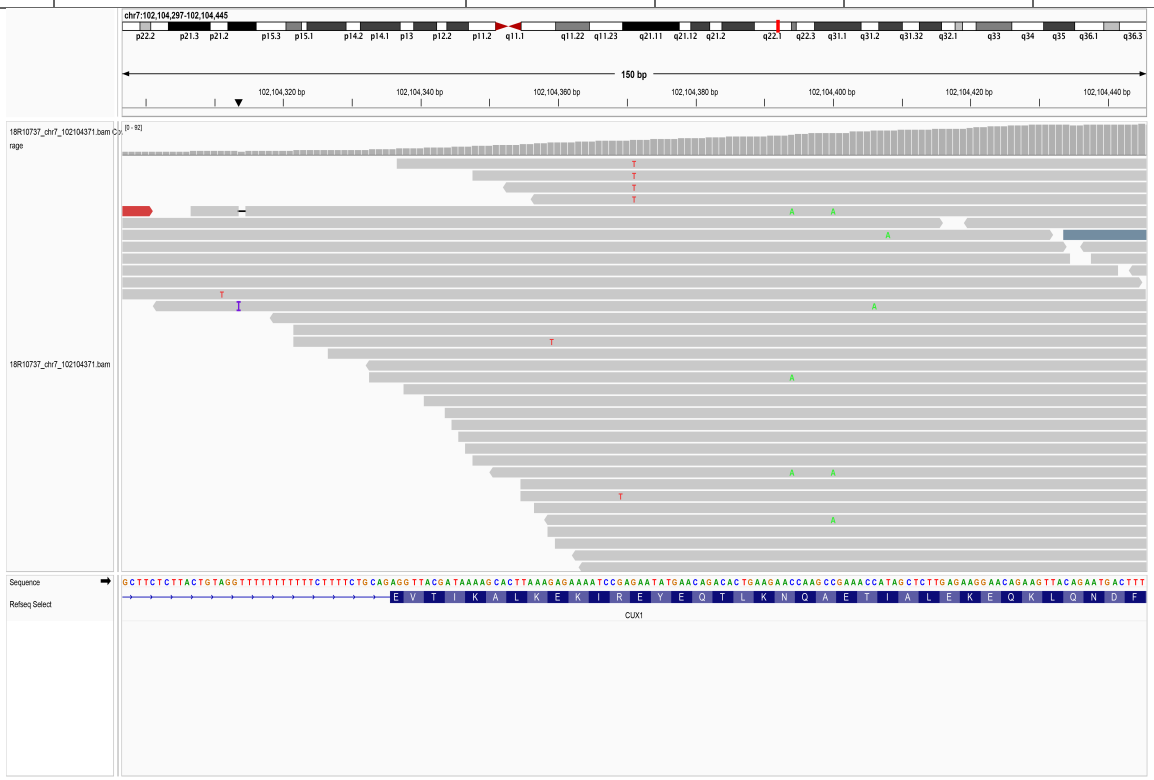
11.1. chr7_102097387_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09528	chr7_102097387_G/T	23	4	*CUX1*	stop_gained



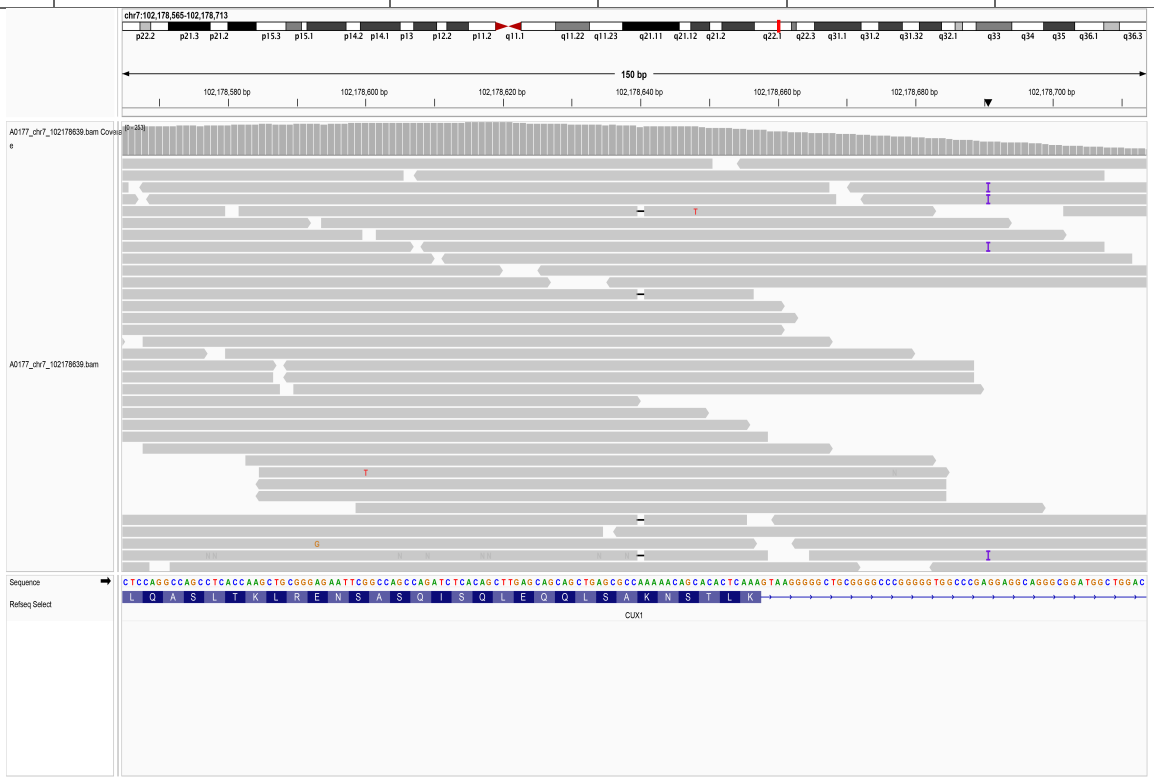
11.2. chr7_102104371_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10737	chr7_102104371_G/T	38	4	*CUX1*	stop_gained



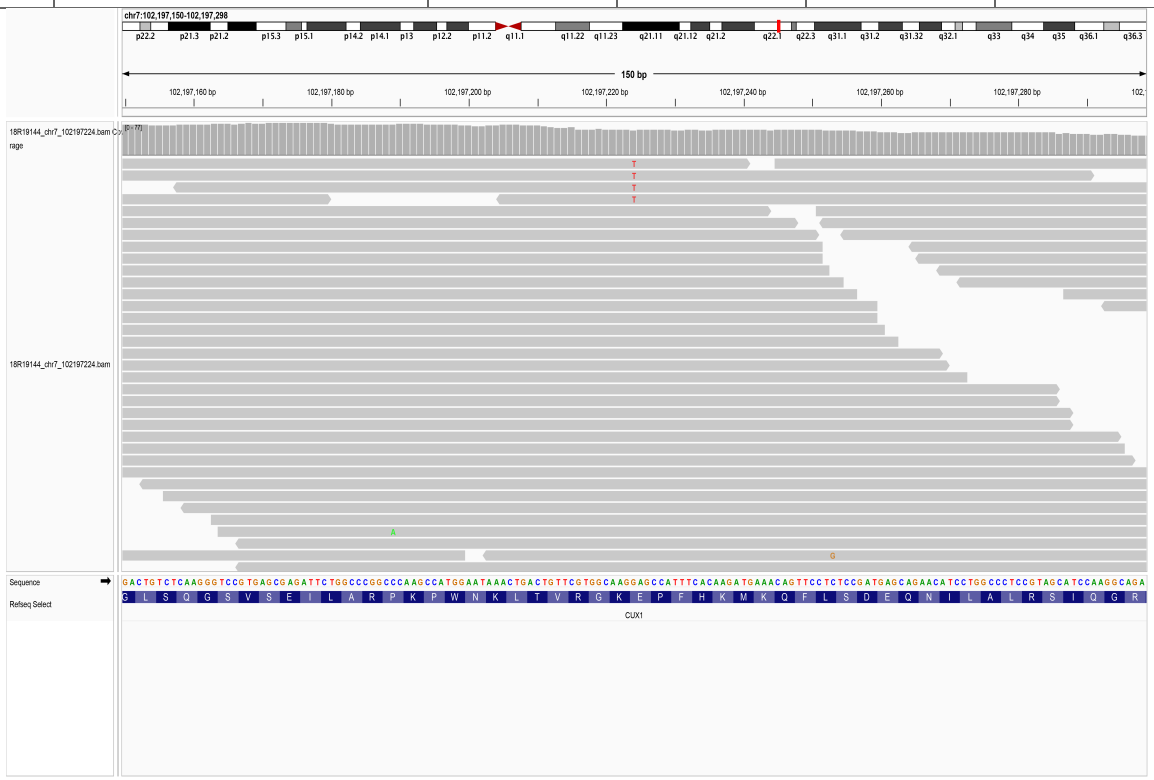
11.3. chr7_102178640_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0177	chr7_102178640_A/-	208	5	*CUX1*	frameshift_variant



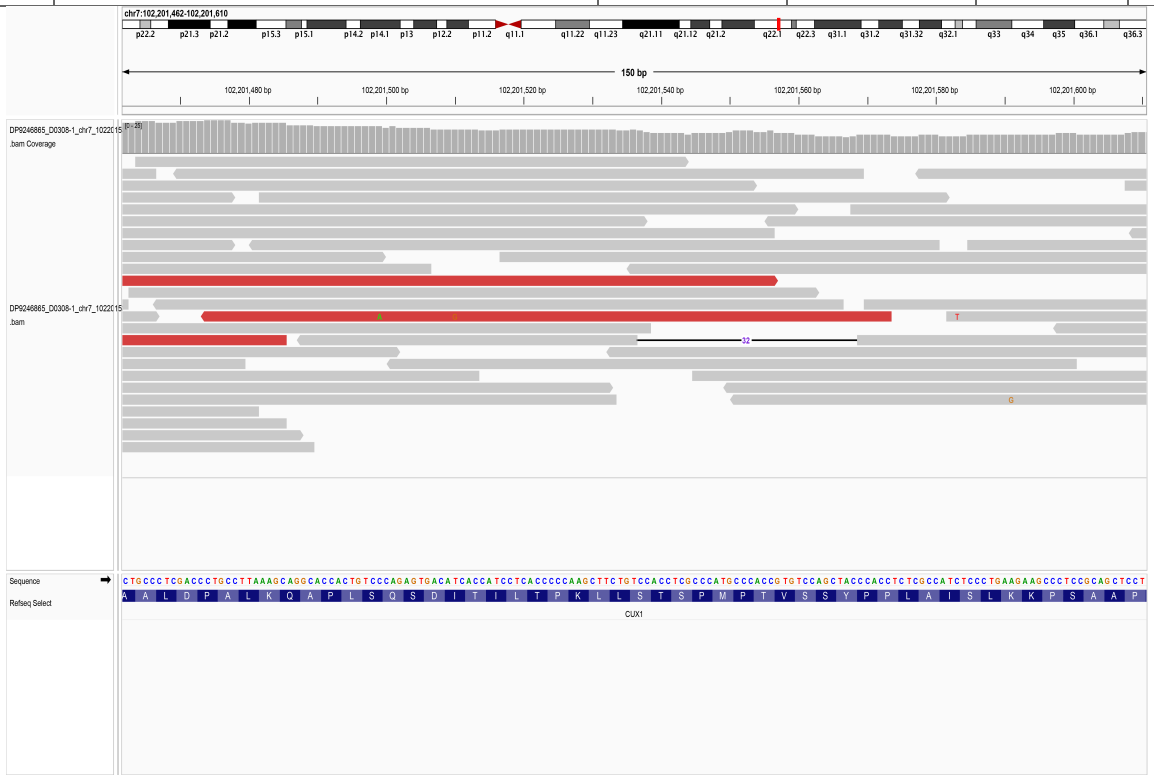
11.4. chr7_102197224_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19144	chr7_102197224_G/T	53	4	*CUX1*	stop_gained



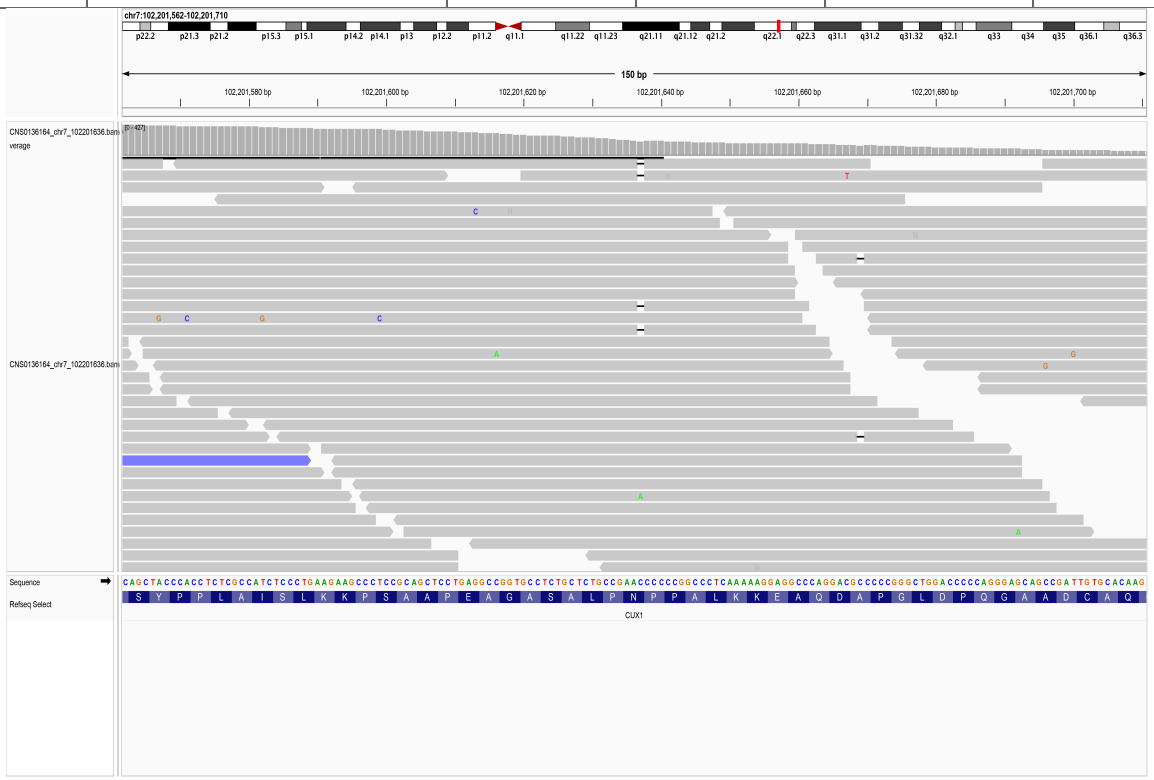
11.5. chr7_102201537_CCACCTCGCCCATGCCCACCGTGTCCAGCTAC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
DP9246865_D0308-1	chr7_102201537_CCACCTCGCCCATGCCCACCGTGTCCAGCTAC/-	19	2	*CUX1*	frameshift_variant



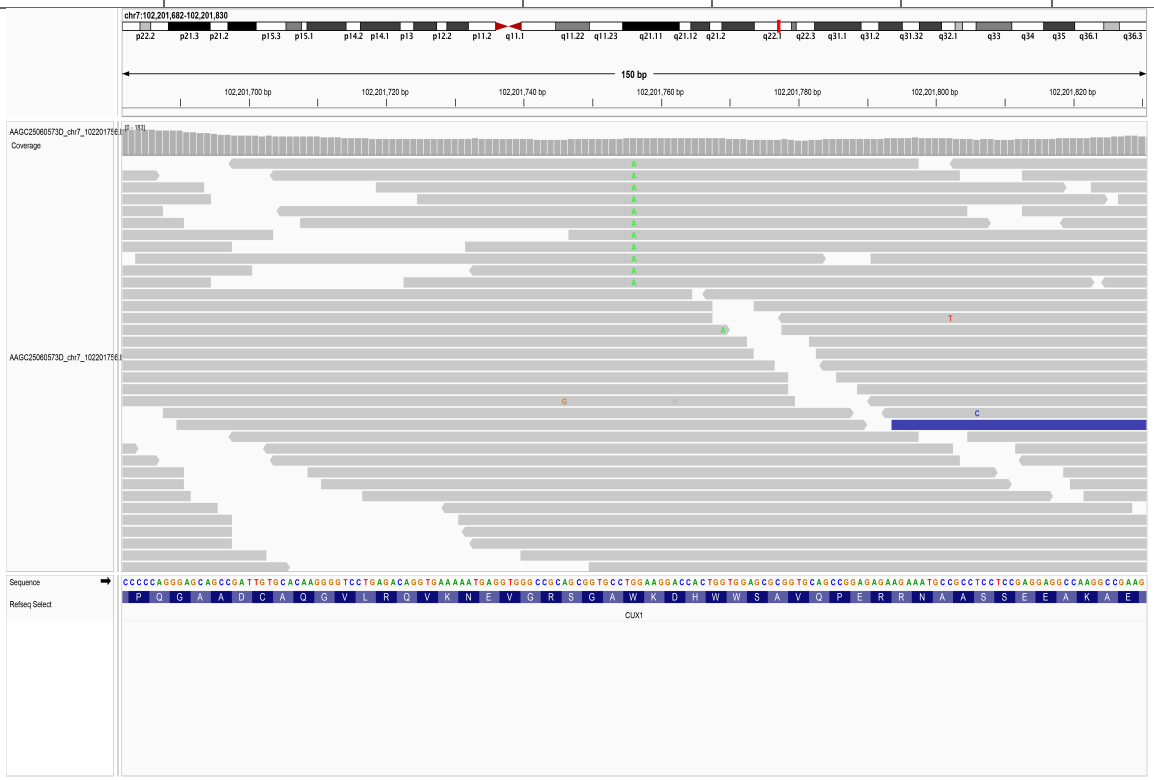
11.6. chr7_102201637_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136164	chr7_102201637_C/-	163	7	*CUX1*	frameshift_variant



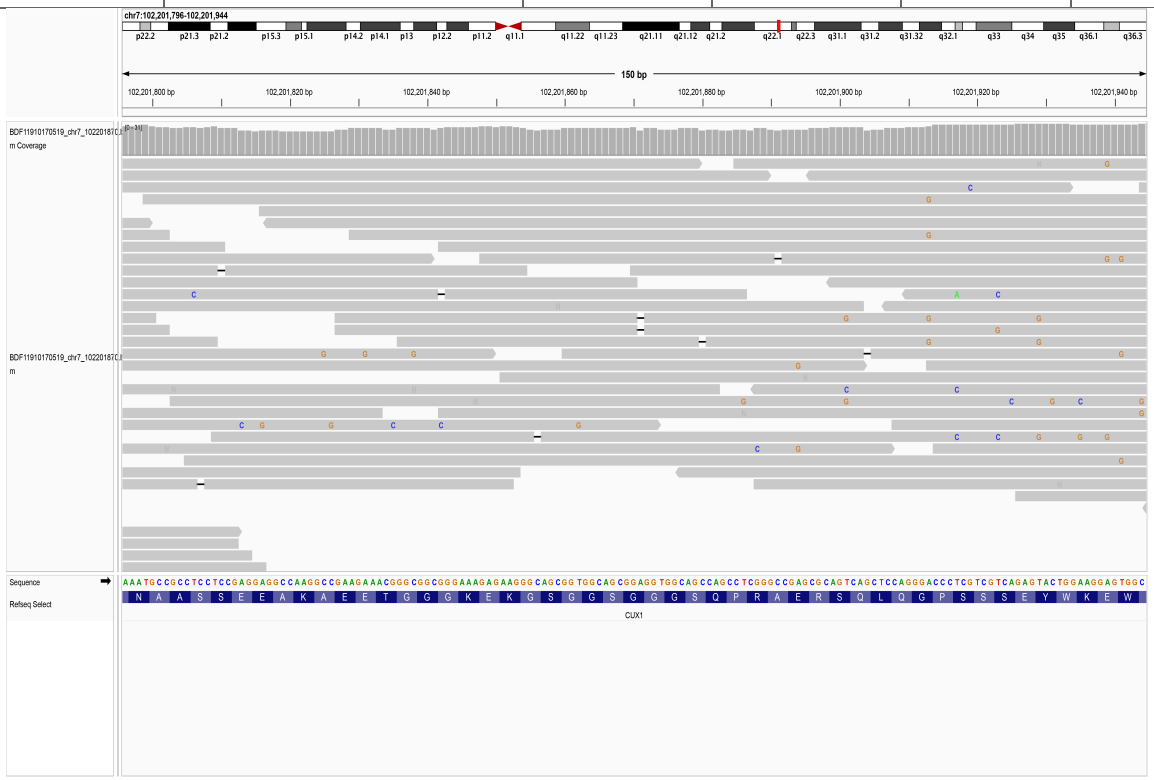
11.7. chr7_102201756_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060573D	chr7_102201756_G/A	81	11	*CUX1*	stop_gained



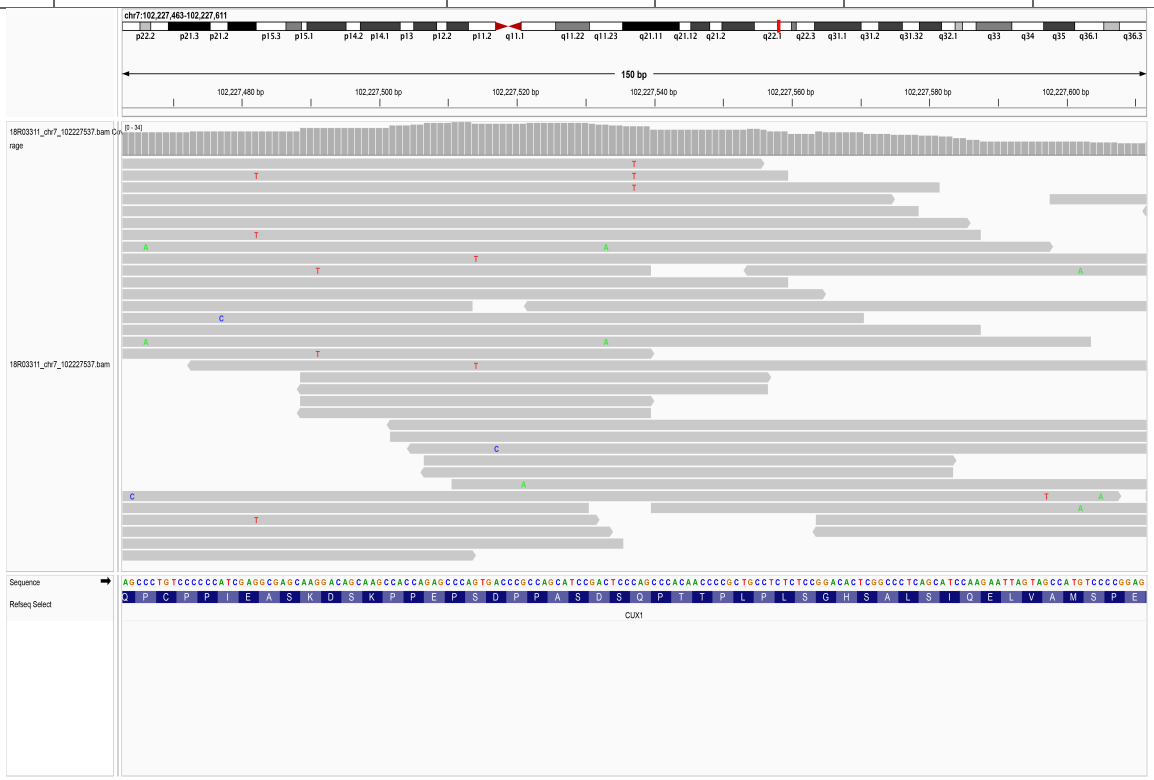
11.8. chr7_102201871_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chr7_102201871_A/-	17	2	*CUX1*	frameshift_variant



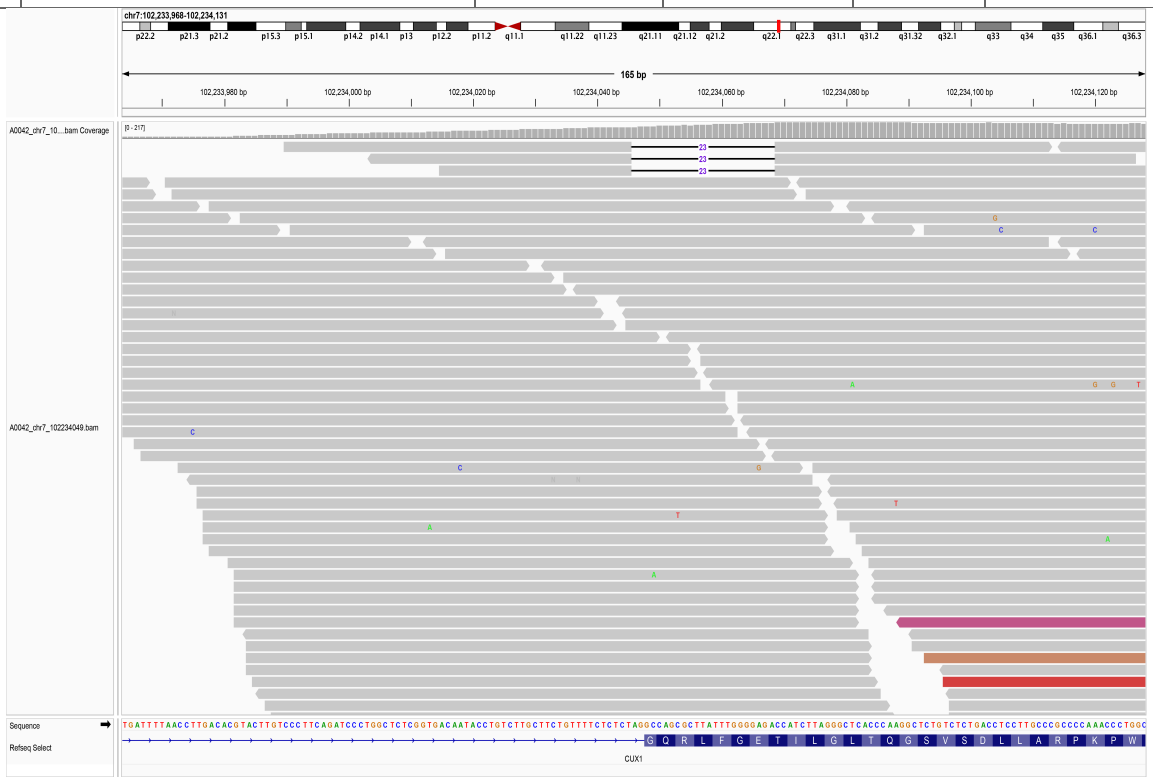
11.9. chr7_102227537_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr7_102227537_C/T	23	3	*CUX1*	stop_gained



11.10. chr7_102234050_AGGCCAGCGCTTATTTGGGGAGA/-

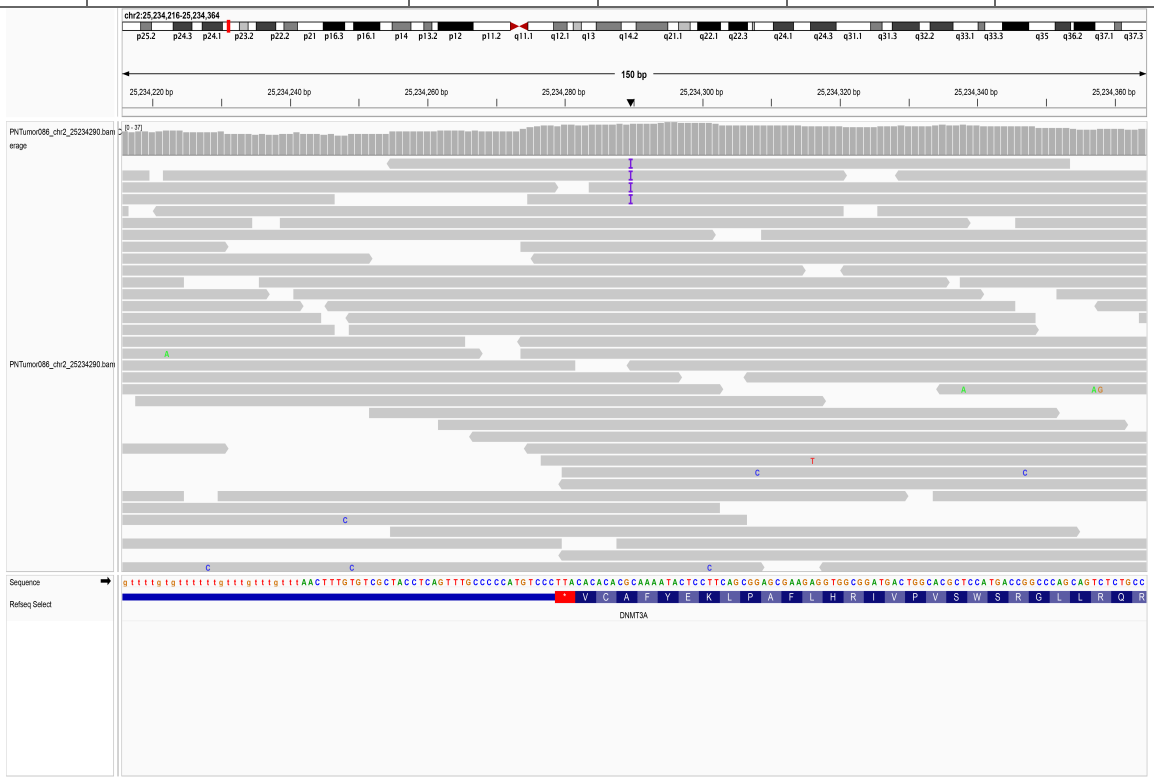
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0042	chr7_102234050_AGGCCAGCG CTTATTTGGGGAGA/-	213	3	*CUX1*	splice_acceptor_variant



12. *DNMT3A*

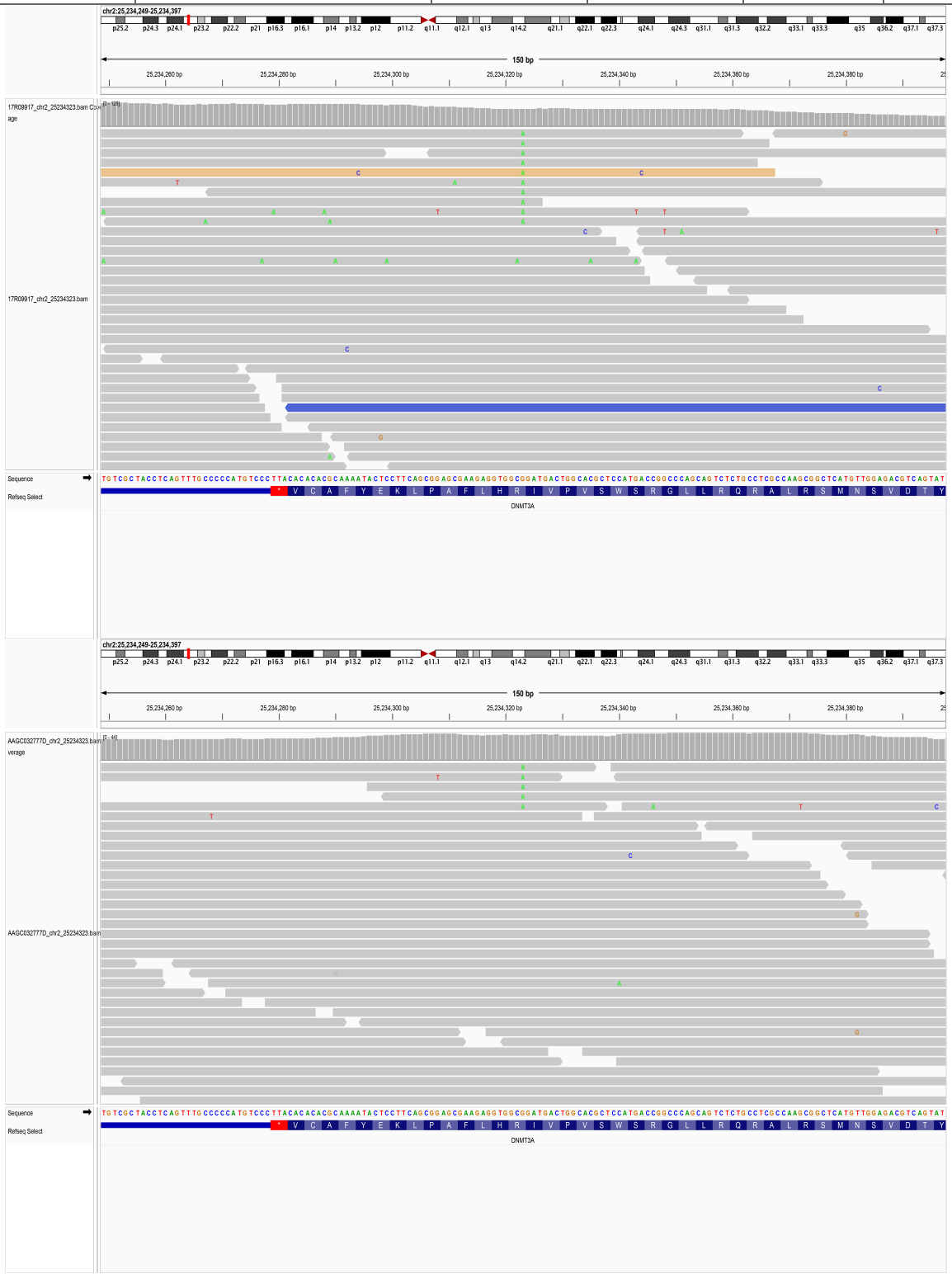
12.1. chr2_25234290_-/C

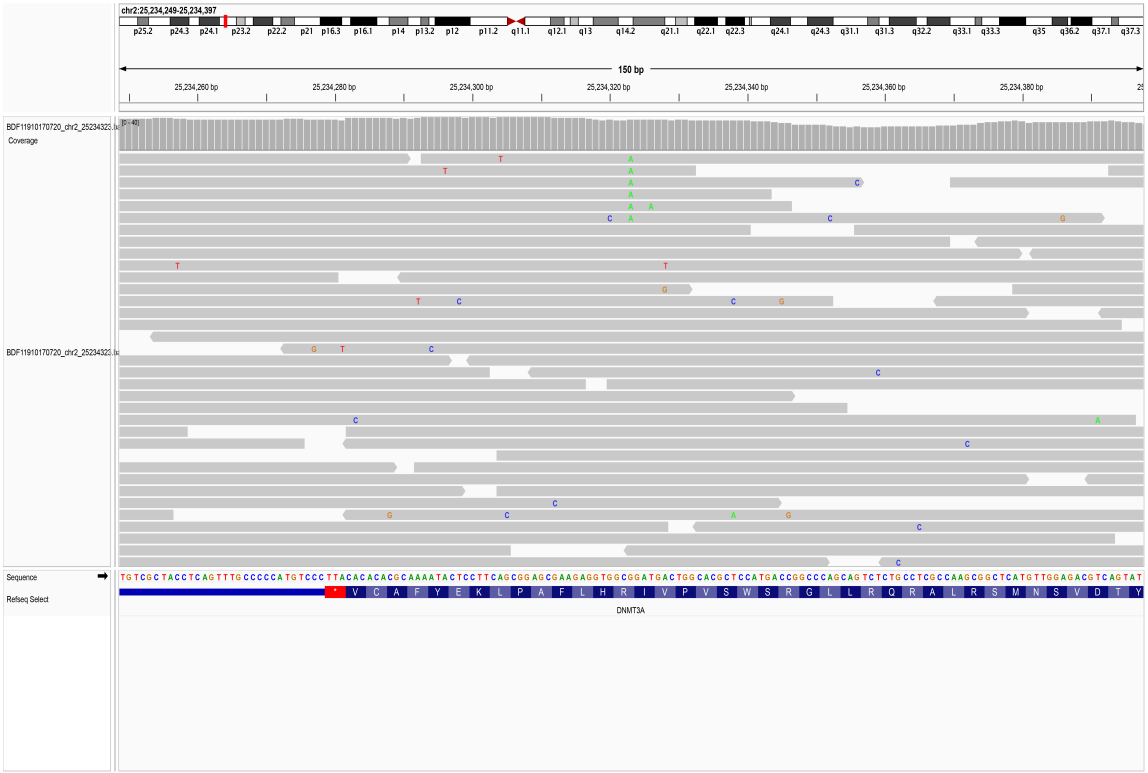
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
PNTumor086	chr2_25234290_-/C	30	4	*DNMT3A*	frameshift_variant



12.2. chr2_25234323_G/A

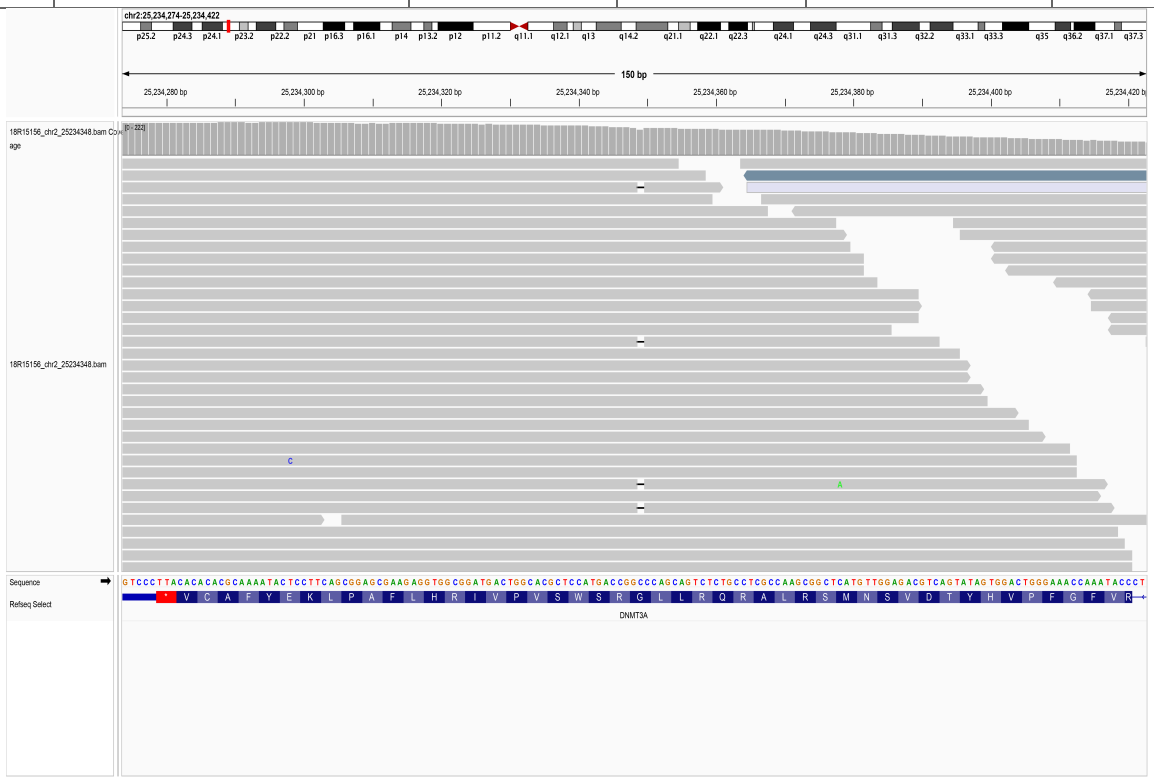
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09917	chr2_25234323_G/A	69	10	*DNMT3A*	missense_variant
AAGC032777D	chr2_25234323_G/A	34	5	*DNMT3A*	missense_variant
BDF11910170720	chr2_25234323_G/A	29	6	*DNMT3A*	missense_variant




chr2:25,234,249-25,234,397
150 bp
25,234,260 bp
25,234,280 bp
25,234,300 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
Coverage
Sequence
Refseq Select
DNMT3A

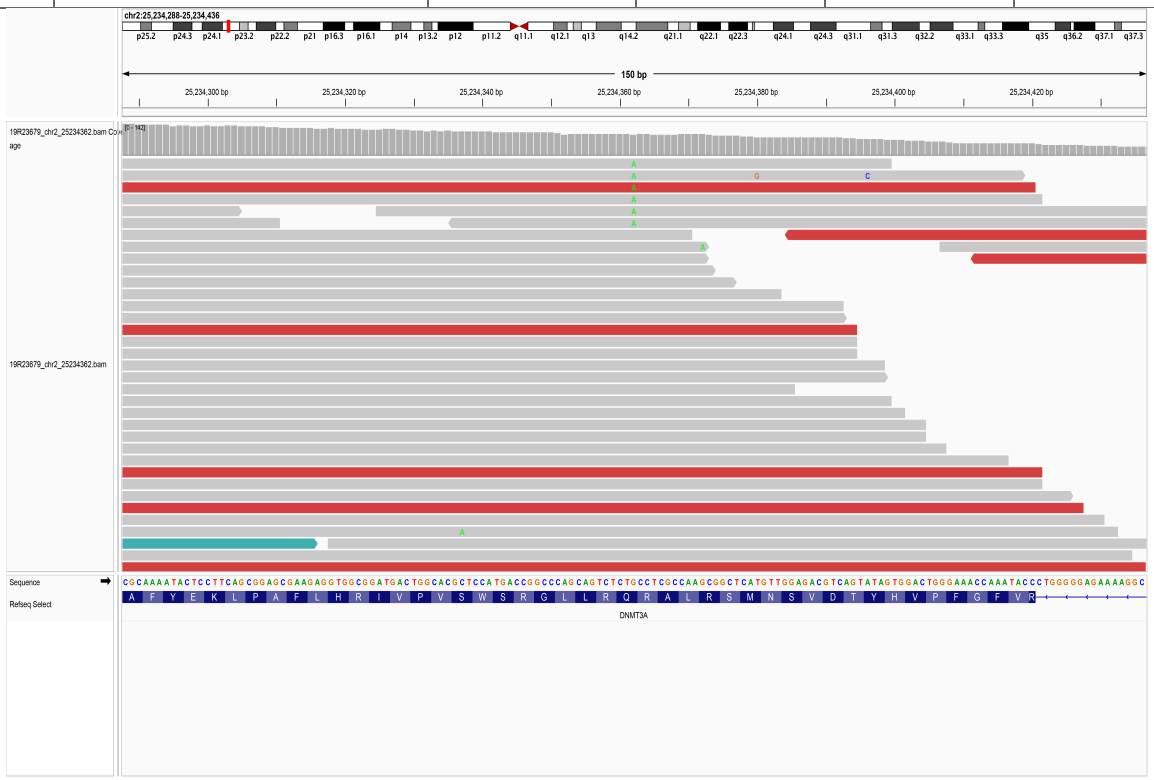
12.3. chr2_25234349_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15156	chr2_25234349_C/-	165	14	*DNMT3A*	frameshift_variant



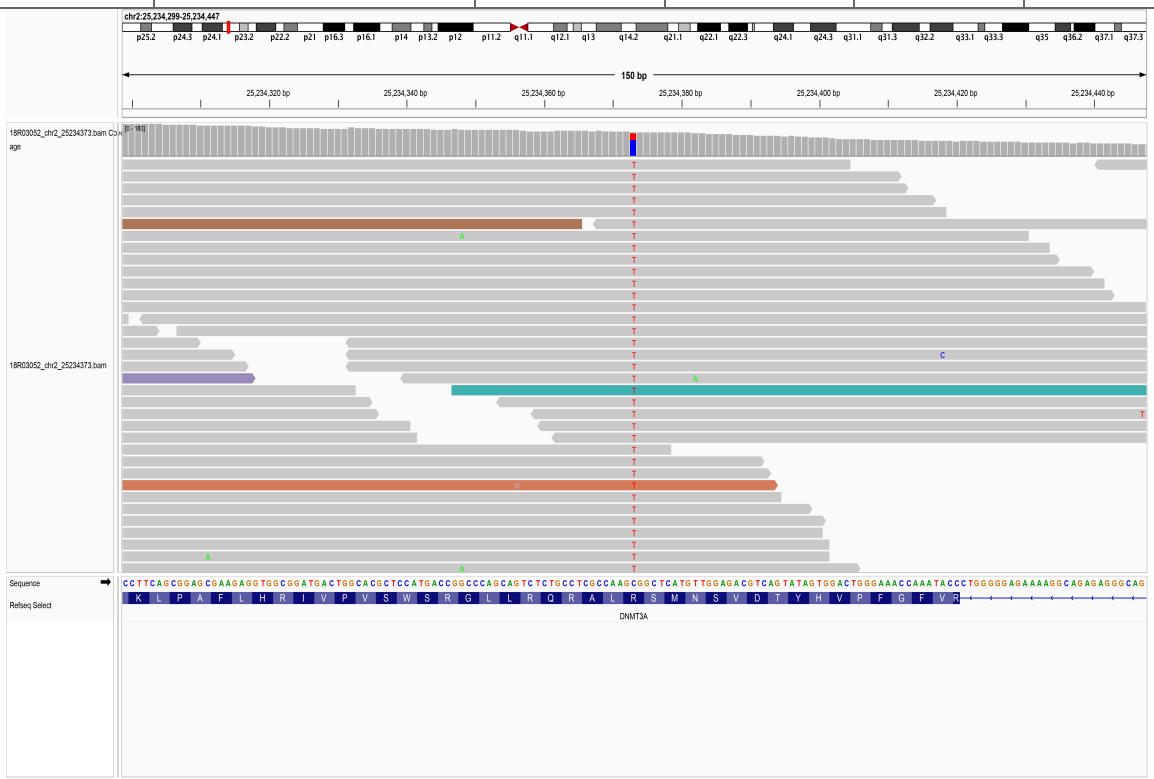
12.4. chr2_25234362_G/A

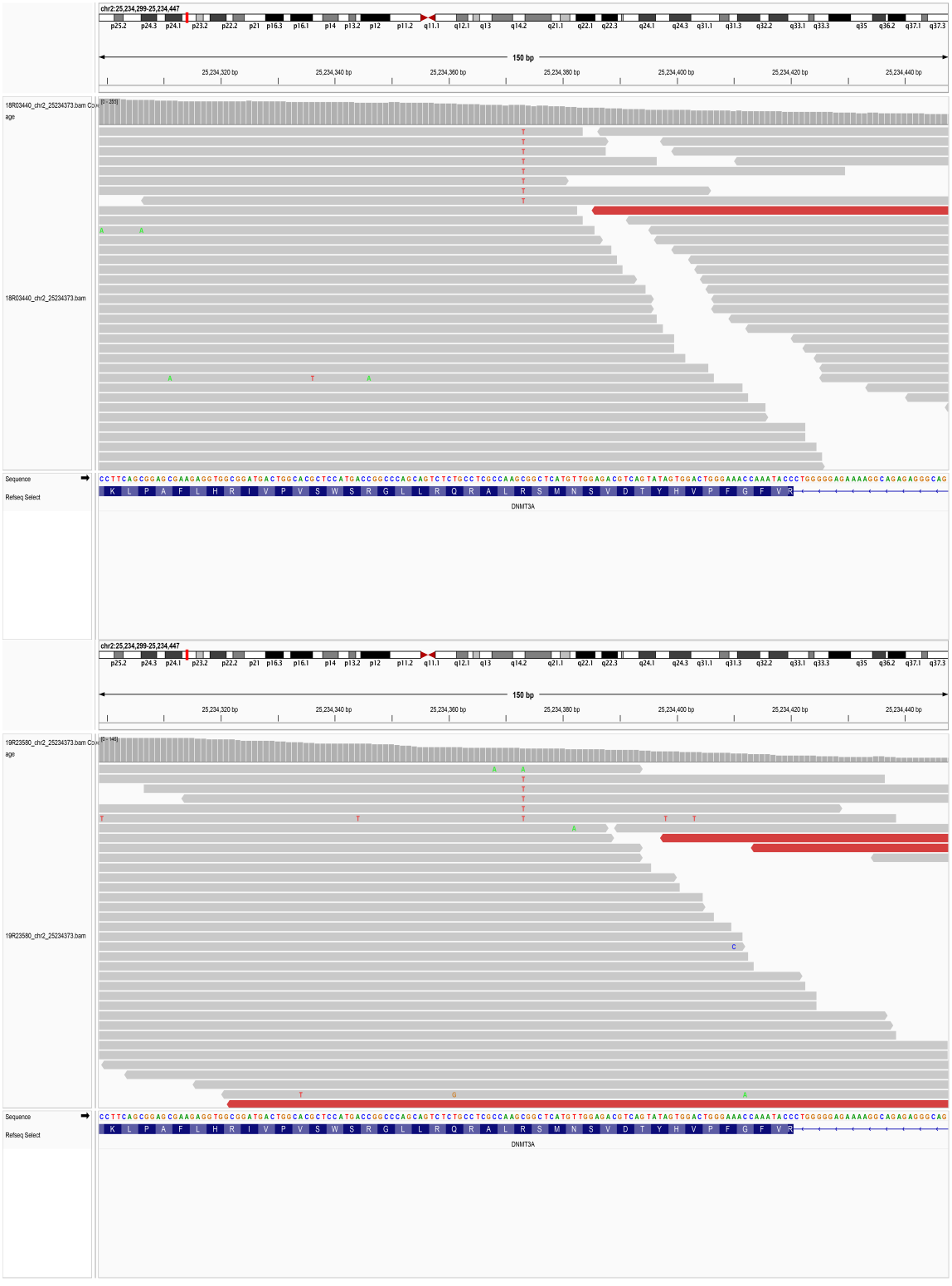
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23679	chr2_25234362_G/A	81	6	*DNMT3A*	stop_gained

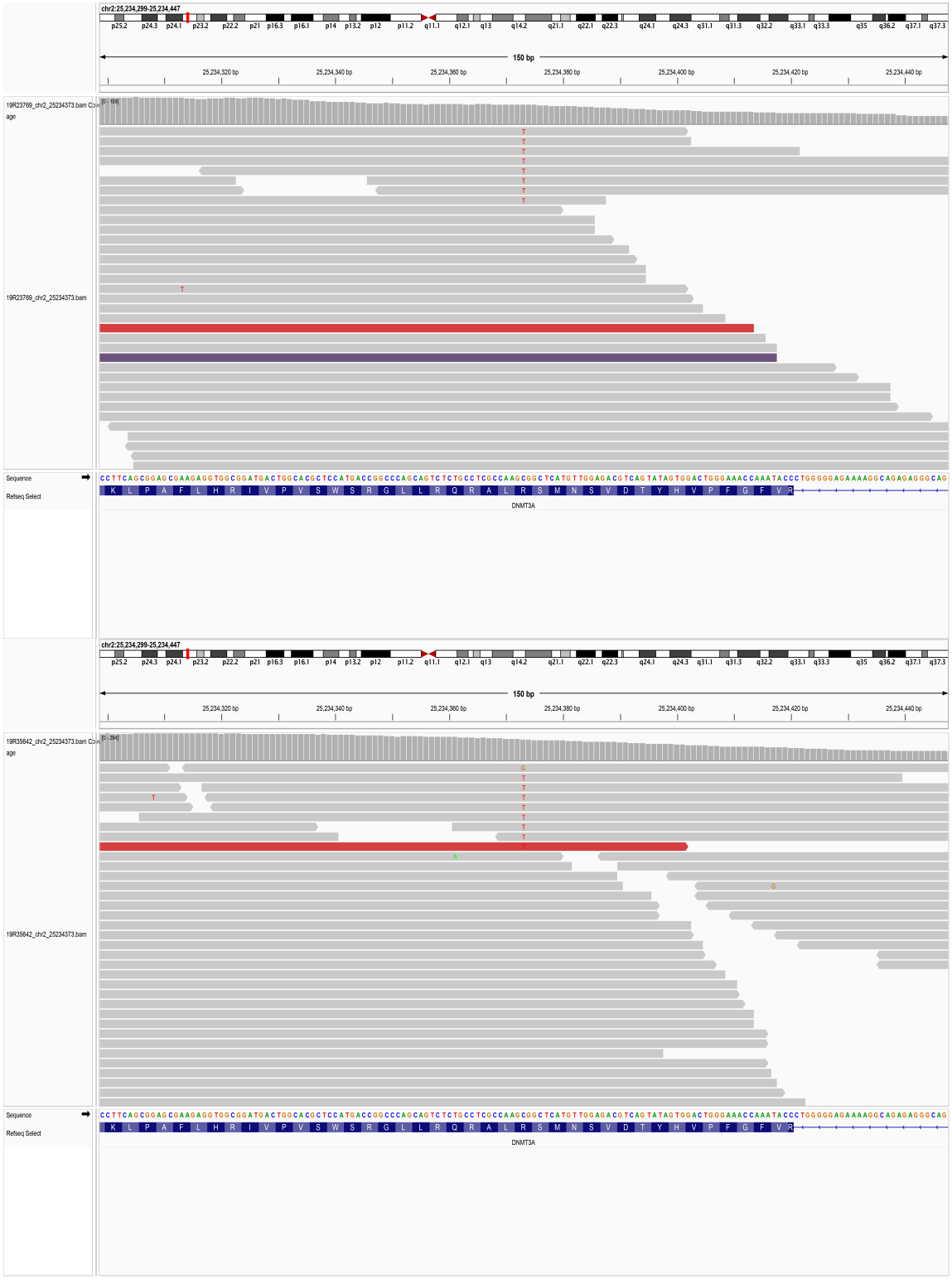


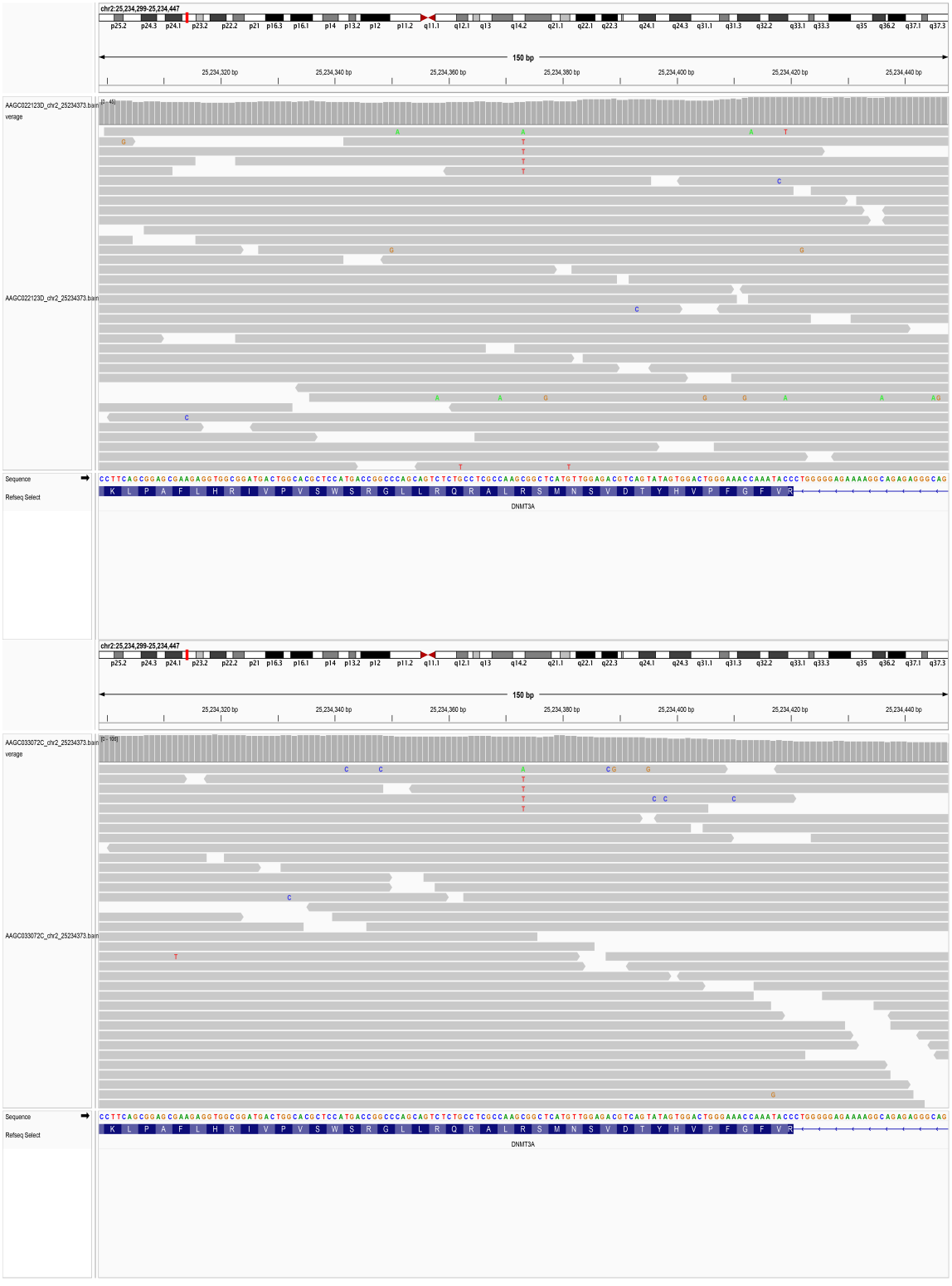
12.5. chr2_25234373_C/T

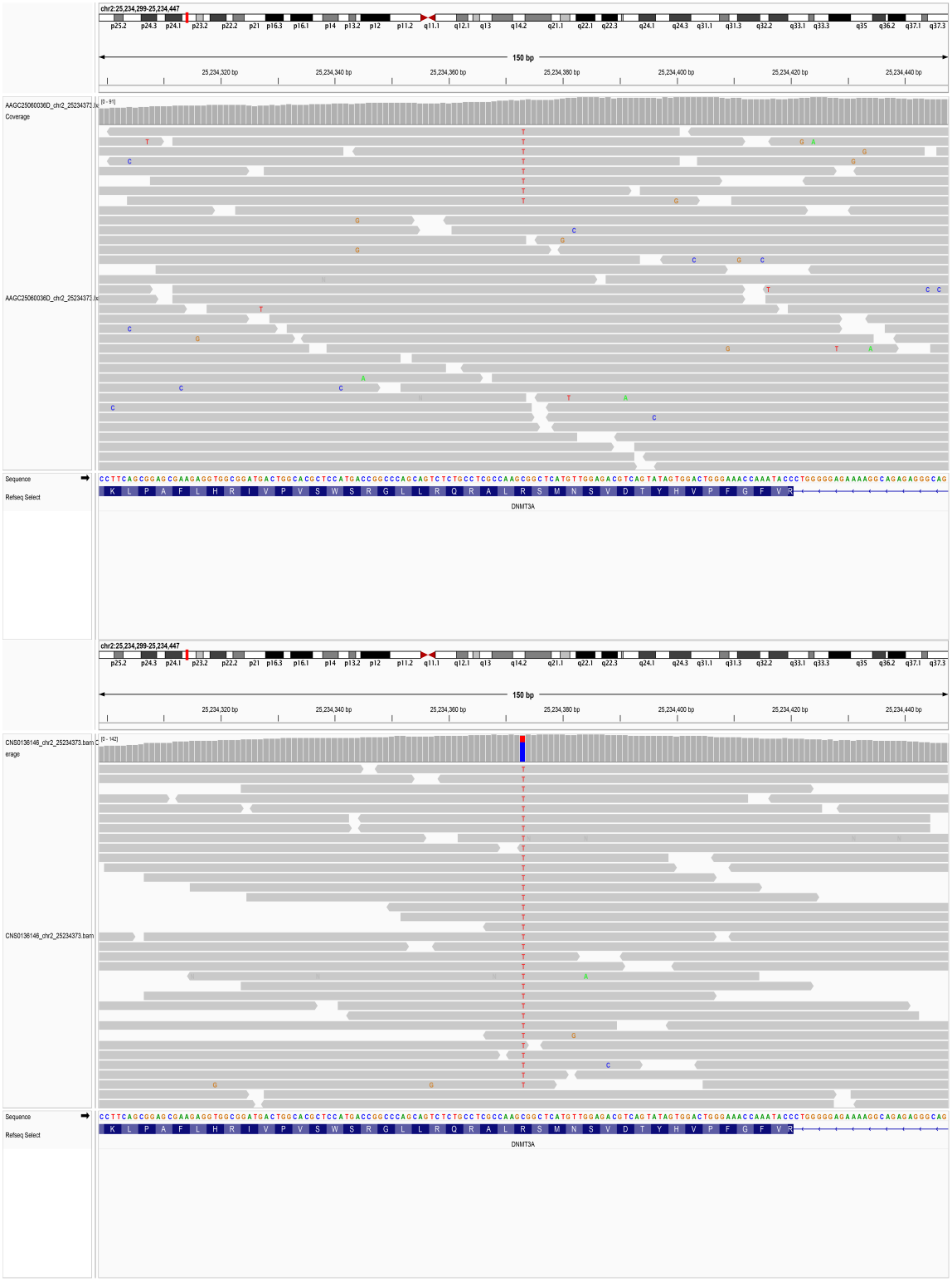
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03052	chr2_25234373_C/T	91	39	*DNMT3A*	missense_variant
18R03440	chr2_25234373_C/T	168	8	*DNMT3A*	missense_variant
19R23580	chr2_25234373_C/T	64	5	*DNMT3A*	missense_variant
19R23769	chr2_25234373_C/T	70	8	*DNMT3A*	missense_variant
19R35642	chr2_25234373_C/T	211	8	*DNMT3A*	missense_variant
AAGC022123D	chr2_25234373_C/T	29	4	*DNMT3A*	missense_variant
AAGC033072C	chr2_25234373_C/T	87	4	*DNMT3A*	missense_variant
AAGC25060036D	chr2_25234373_C/T	65	8	*DNMT3A*	missense_variant
CNS0136146	chr2_25234373_C/T	104	32	*DNMT3A*	missense_variant
HD25_71	chr2_25234373_C/T	43	4	*DNMT3A*	missense_variant
P9248389_D0308-hM	chr2_25234373_C/T	34	3	*DNMT3A*	missense_variant
PNTumor088	chr2_25234373_C/T	31	4	*DNMT3A*	missense_variant

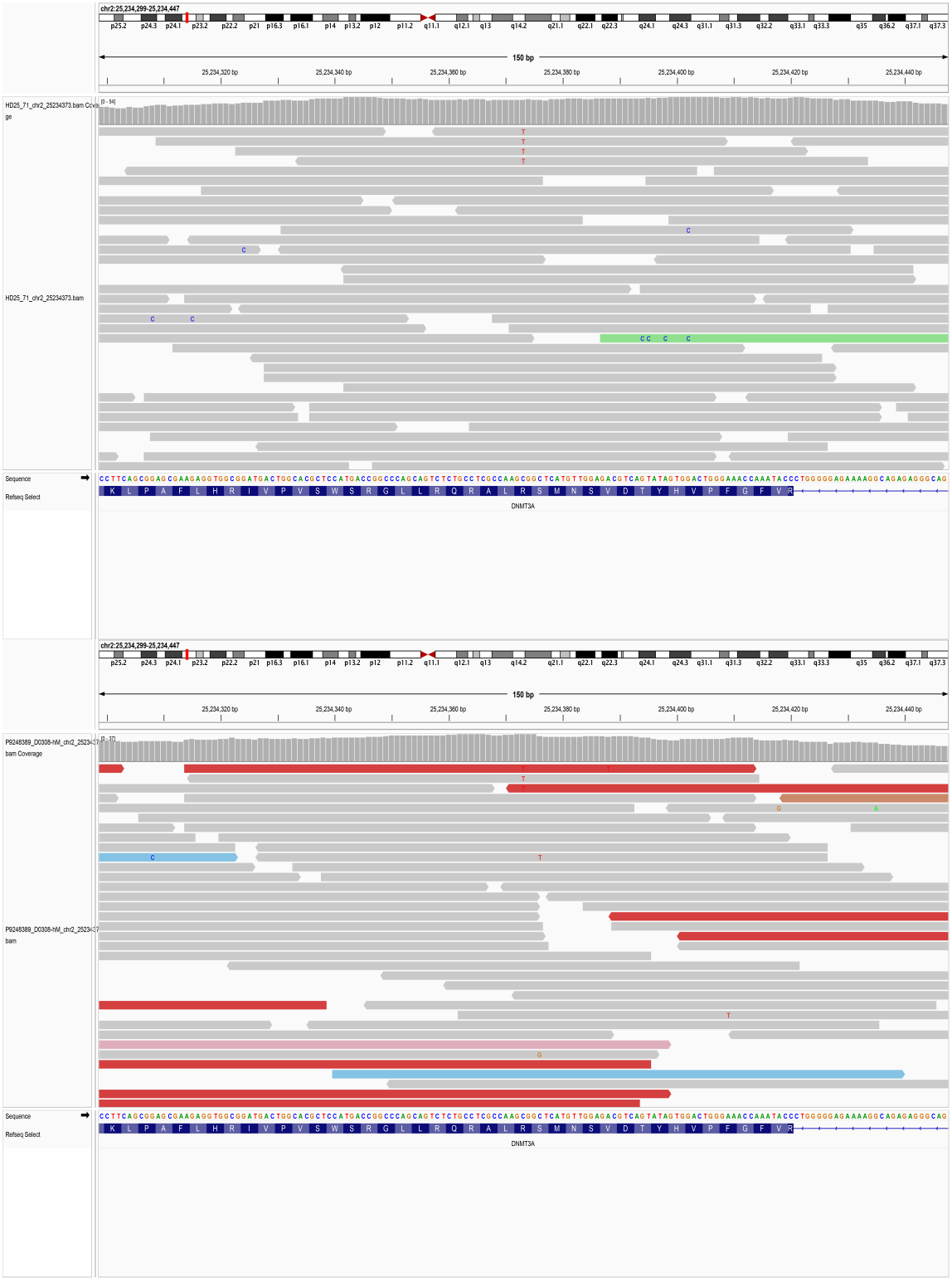


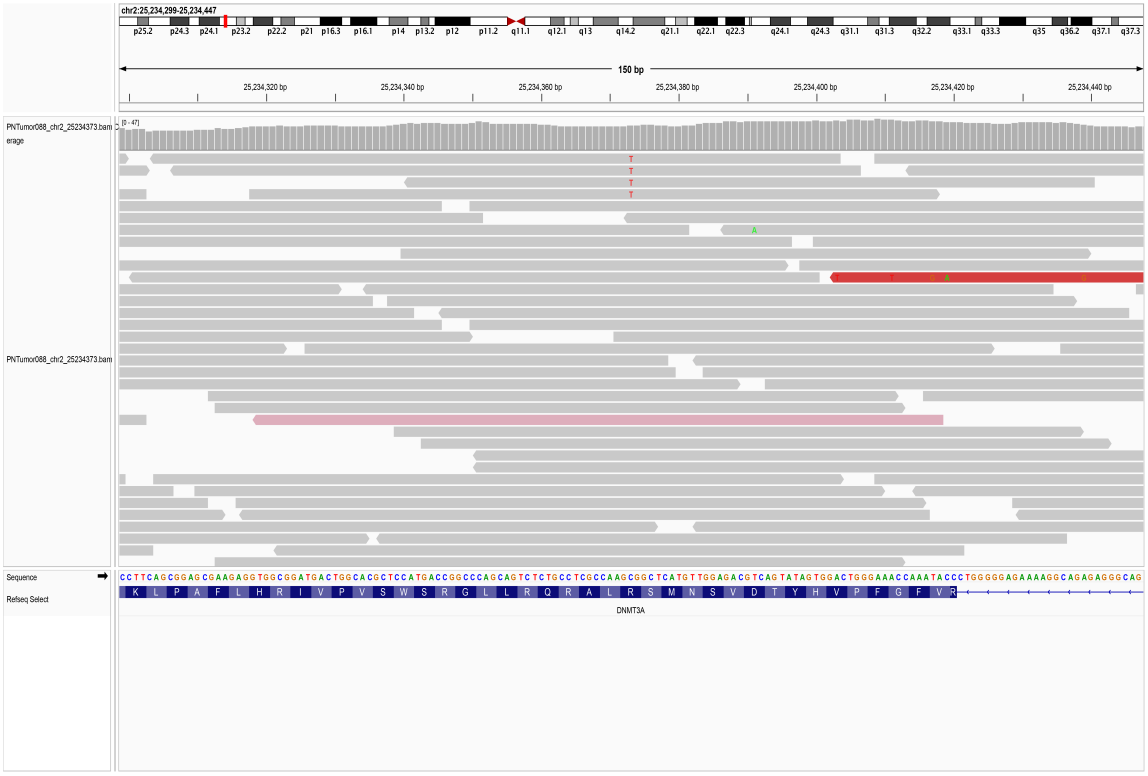

chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
18R03440_chr2_25234373.bam Coverage
18R03440_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A
19R23580_chr2_25234373.bam Coverage
19R23580_chr2_25234373.bam


chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
19R23769_chr2_25234373.bam Coverage
19R23769_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A
chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
19R35642_chr2_25234373.bam Coverage
19R35642_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A


chr2:25,234,299-25,234,447
150 bp
AAGC022123D_chr2_25234373.bam
verage
AAGC022123D_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A
chr2:25,234,299-25,234,447
150 bp
AAGC033072C_chr2_25234373.bam
verage
AAGC033072C_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A

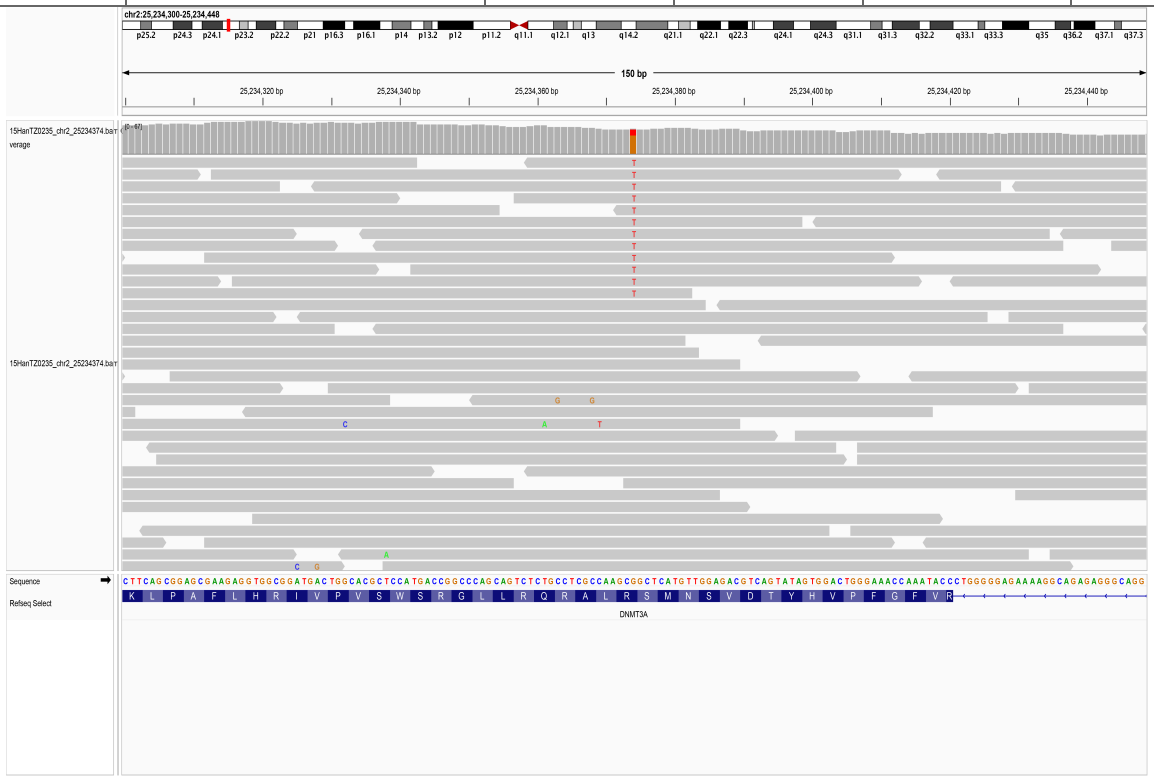

chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
Coverage
Sequence
Refseq Select
DNMT3A
chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
Sequence
Refseq Select
DNMT3A

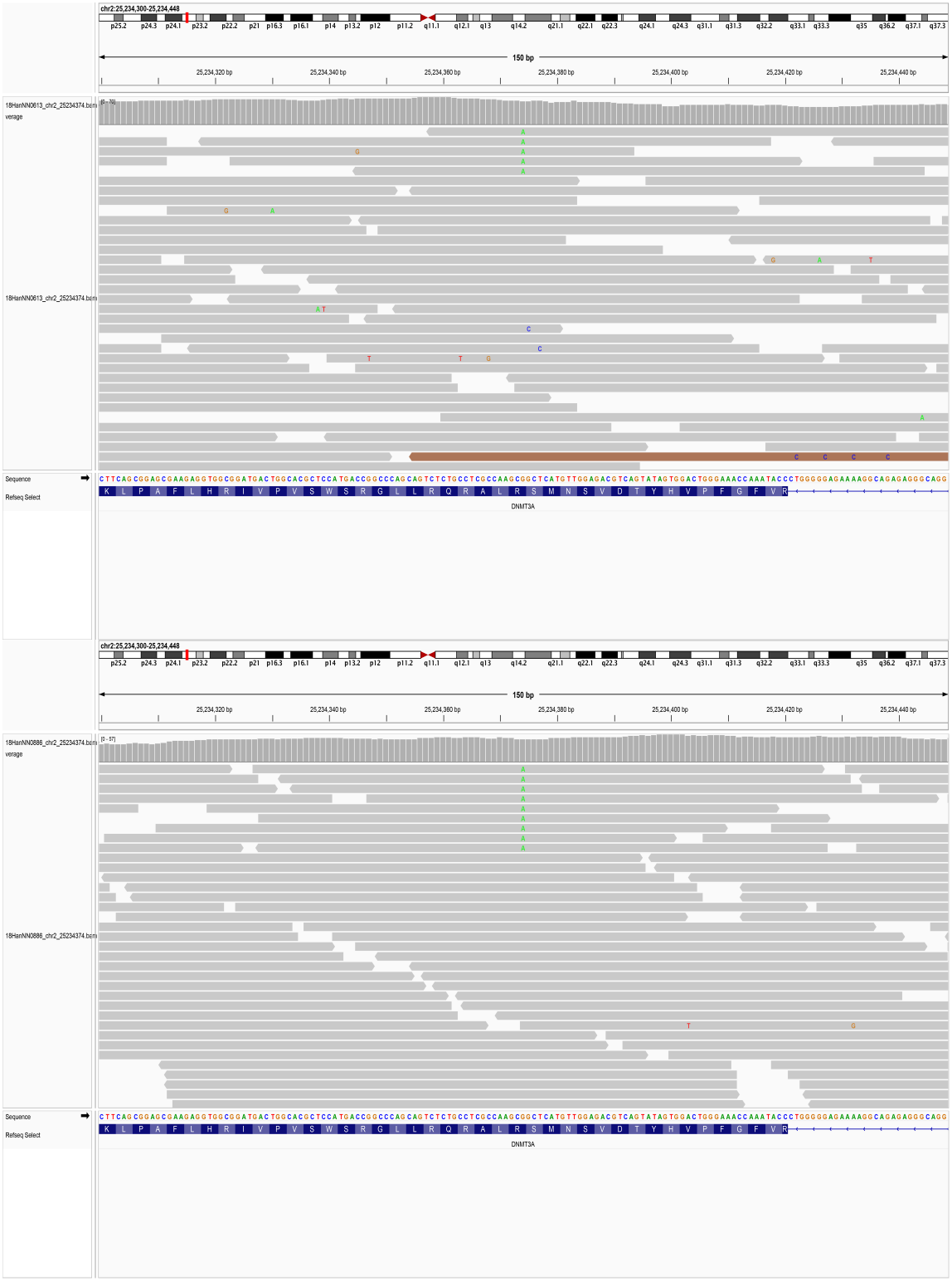

chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
HD25_71_chr2_25234373.bam Coverage
HD25_71_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A
P9248389_D0308-hM_chr2_25234373.bam Coverage
P9248389_D0308-hM_chr2_25234373.bam

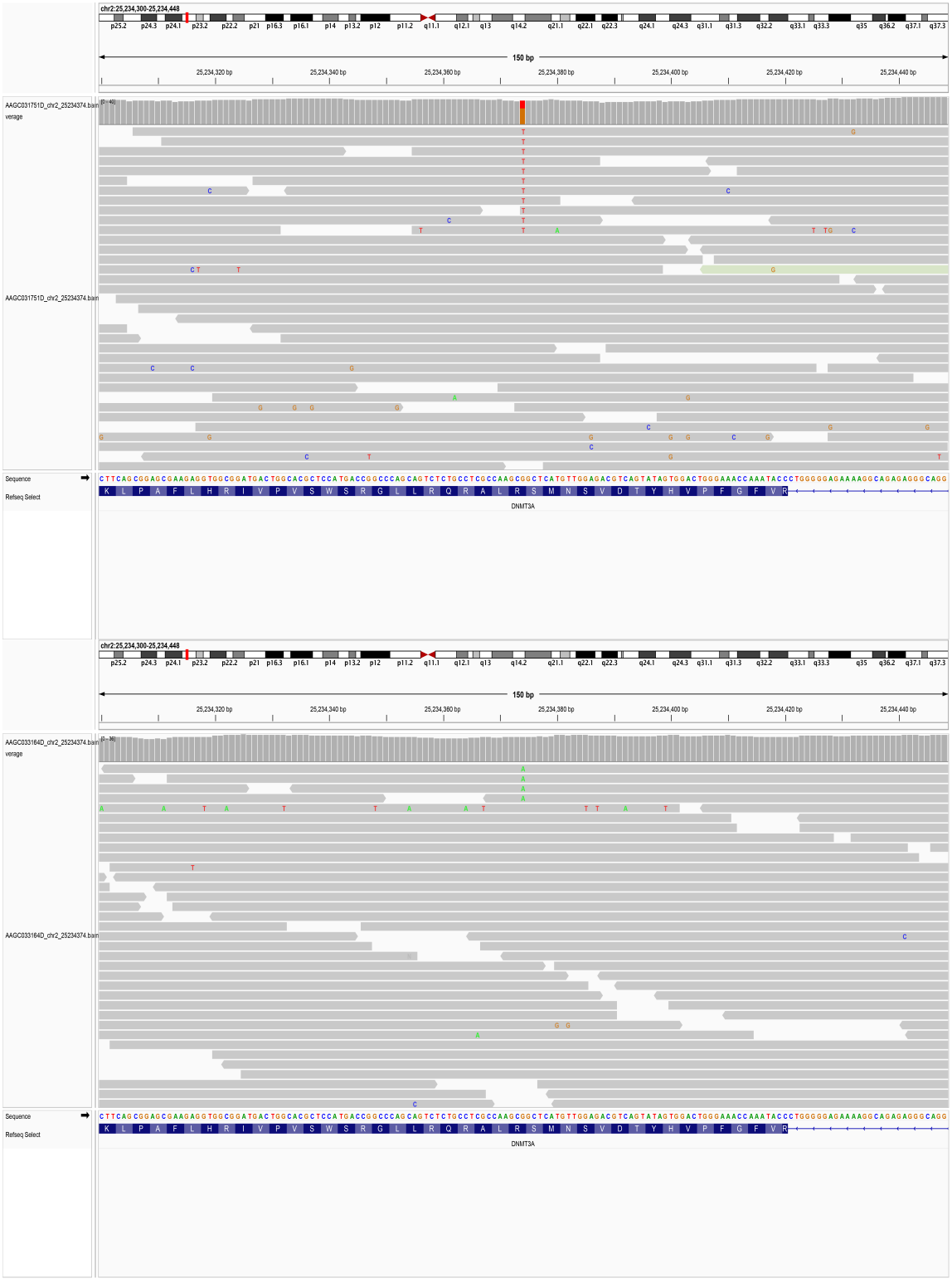

chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
PNTumor088_chr2_25234373.bam
erage
PNTumor088_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A

12.6. chr2_25234374_G/A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0235	chr2_25234374_G/A/T	37	12	*DNMT3A*	missense_variant
18HanNN0613	chr2_25234374_G/A/T	49	5	*DNMT3A*	missense_variant
18HanNN0886	chr2_25234374_G/A/T	38	9	*DNMT3A*	missense_variant
AAGC031751D	chr2_25234374_G/A/T	23	9	*DNMT3A*	missense_variant
AAGC033164D	chr2_25234374_G/A/T	26	4	*DNMT3A*	missense_variant

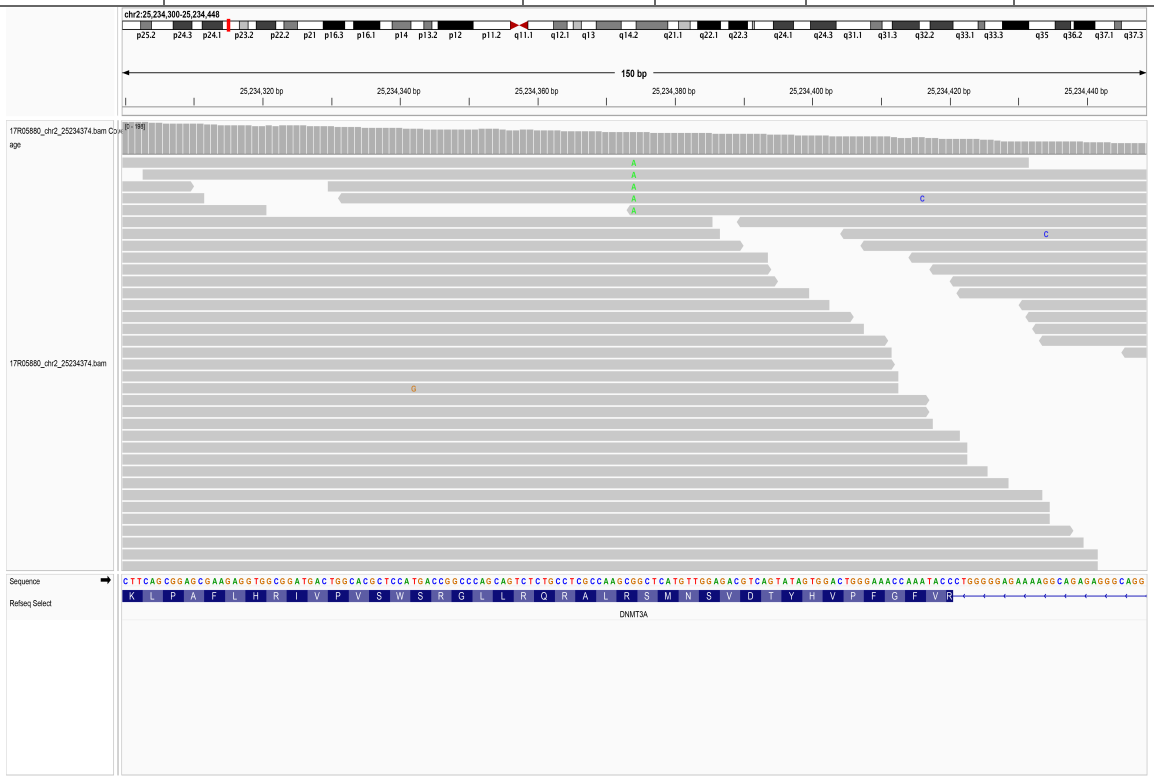


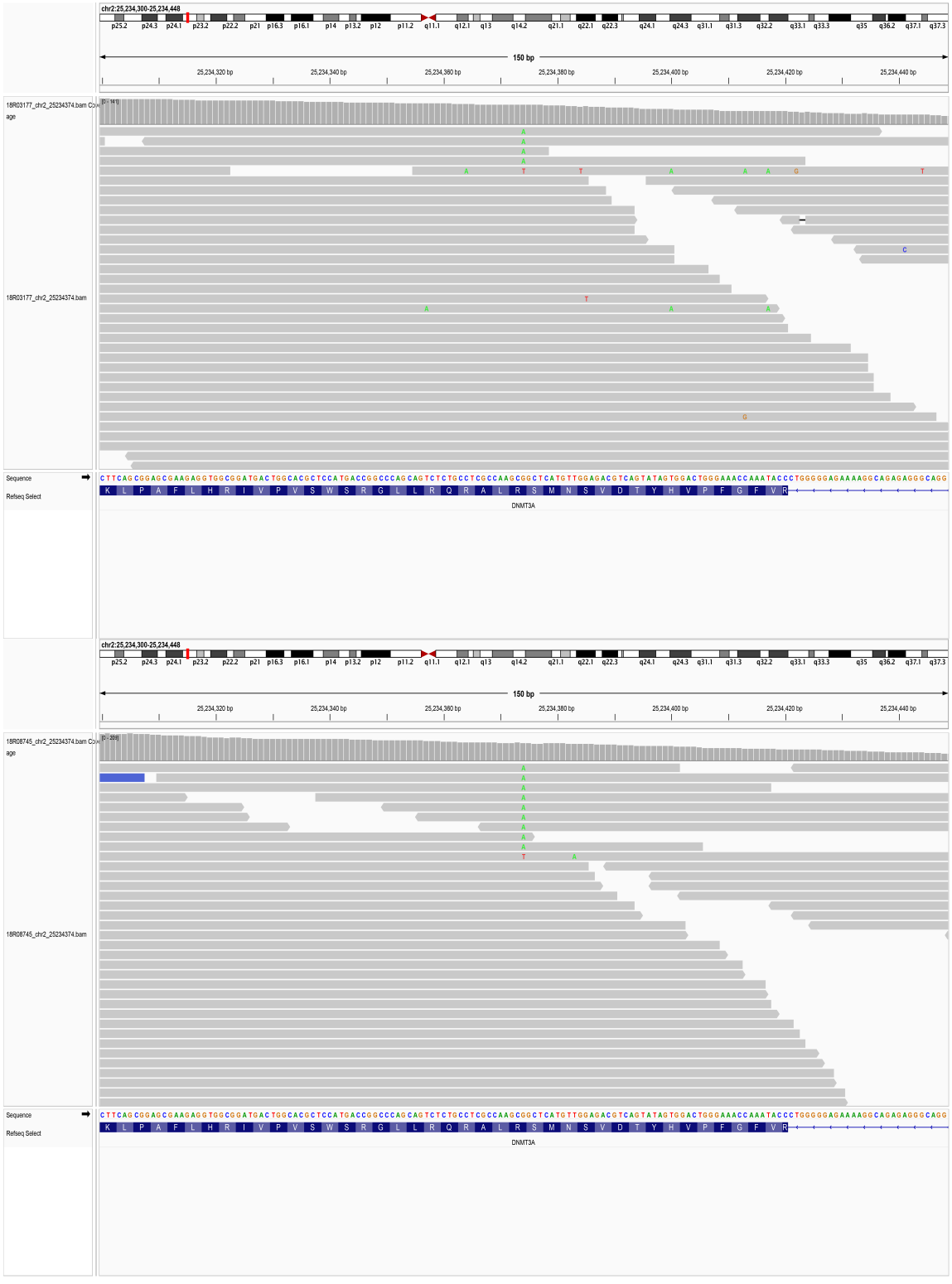

chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
18HanNN0613_chr2_25234374.bam
verage
18HanNN0613_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A
chr2:25,234,300-25,234,448
150 bp
18HanNN0886_chr2_25234374.bam
verage
18HanNN0886_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A

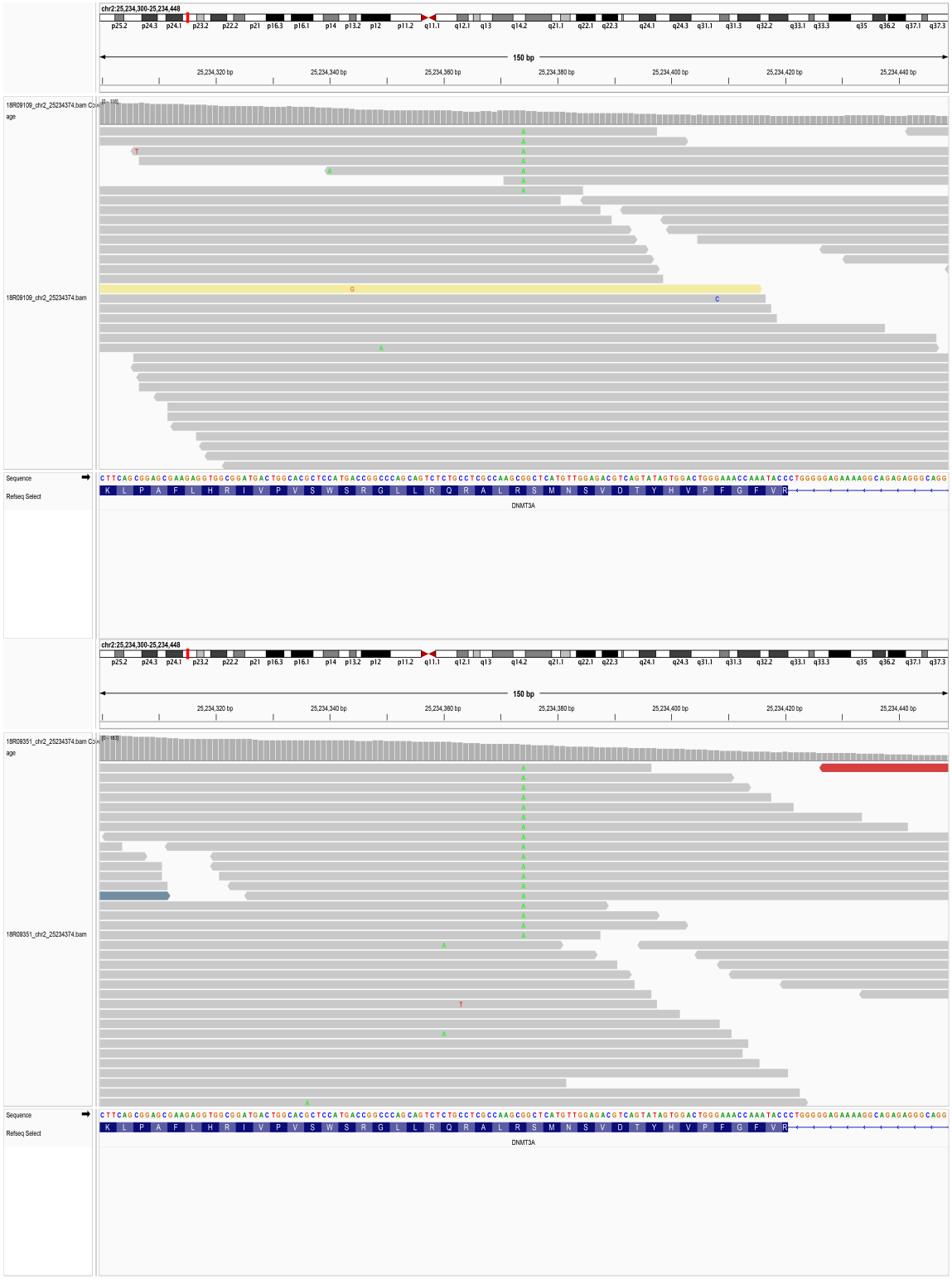

chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
AAGC031751D_chr2_25234374.bam
verage
AAGC031751D_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A
chr2:25,234,300-25,234,448
150 bp
AAGC033164D_chr2_25234374.bam
verage
AAGC033164D_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A

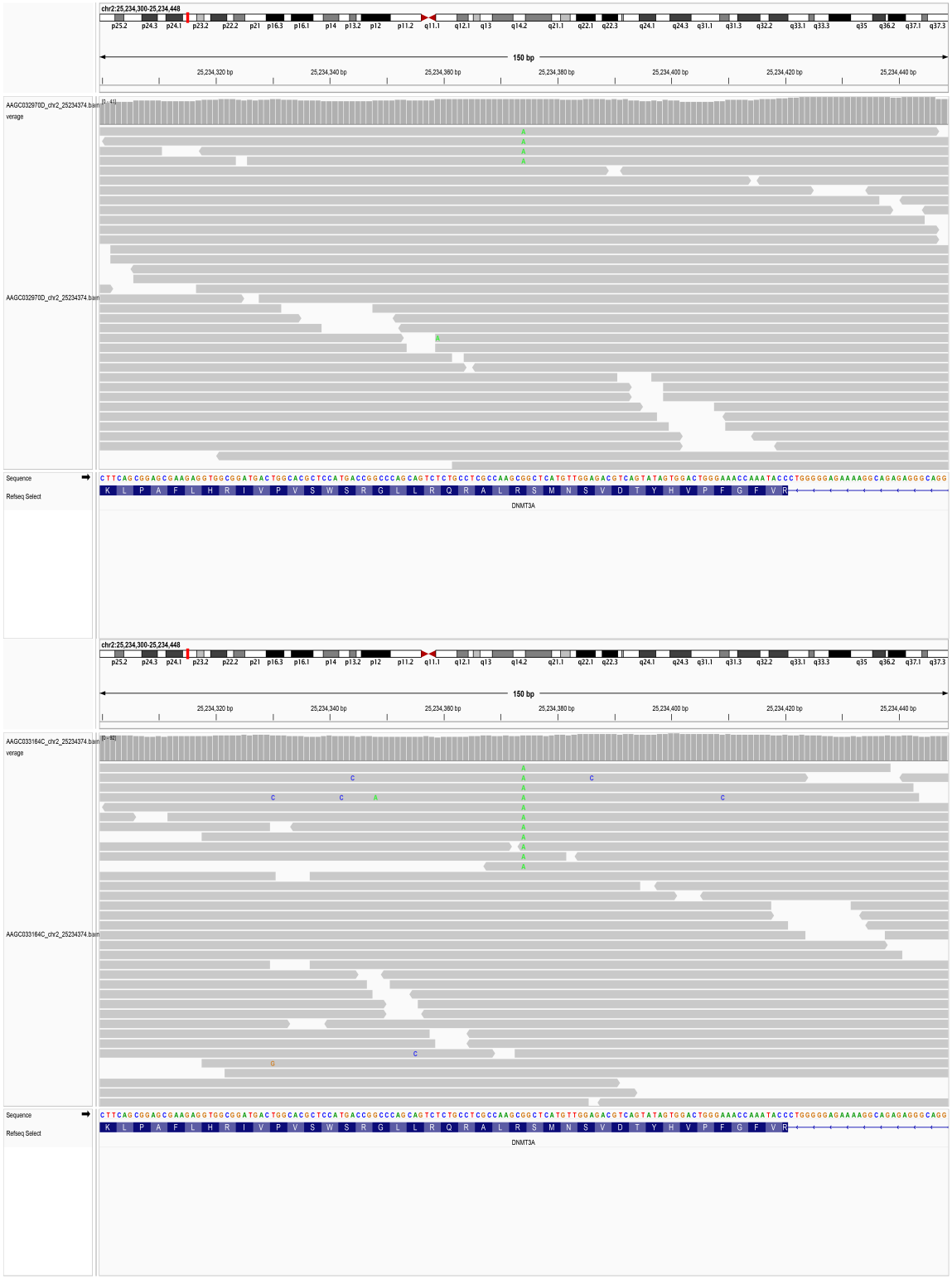
12.7. chr2_25234374_G/A

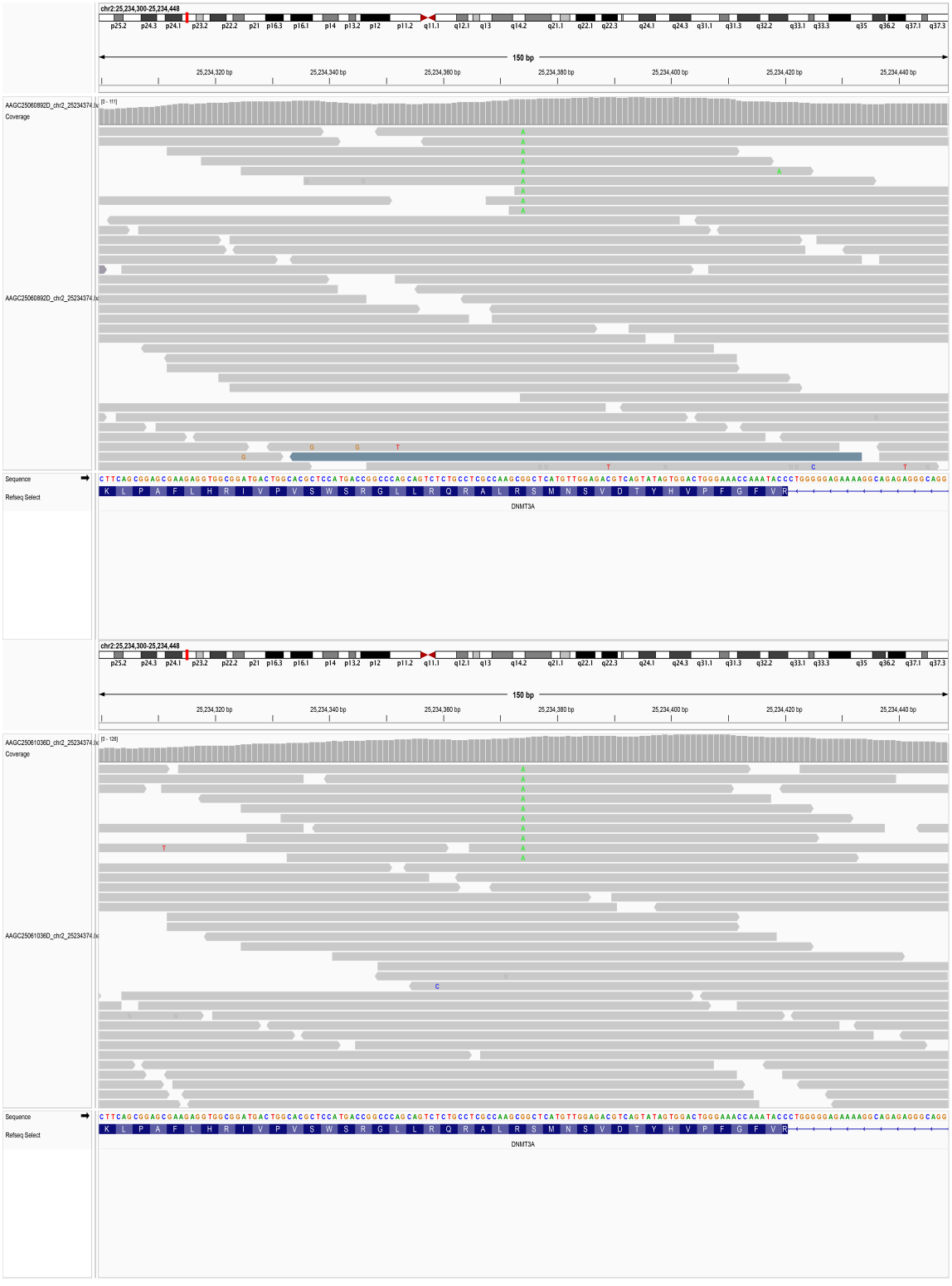
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05880	chr2_25234374_G/A	124	5	*DNMT3A*	missense_variant
18R03177	chr2_25234374_G/A	95	4	*DNMT3A*	missense_variant
18R08745	chr2_25234374_G/A	124	9	*DNMT3A*	missense_variant
18R09109	chr2_25234374_G/A	51	7	*DNMT3A*	missense_variant
18R09351	chr2_25234374_G/A	87	18	*DNMT3A*	missense_variant
AAGC032970D	chr2_25234374_G/A	33	4	*DNMT3A*	missense_variant
AAGC033164C	chr2_25234374_G/A	69	11	*DNMT3A*	missense_variant
AAGC25060892D	chr2_25234374_G/A	93	9	*DNMT3A*	missense_variant
AAGC25061036D	chr2_25234374_G/A	96	10	*DNMT3A*	missense_variant
AAGC25061054D	chr2_25234374_G/A	144	7	*DNMT3A*	missense_variant
BDF11910170409	chr2_25234374_G/A	34	3	*DNMT3A*	missense_variant
D2207136268	chr2_25234374_G/A	85	4	*DNMT3A*	missense_variant
HD25_33	chr2_25234374_G/A	42	5	*DNMT3A*	missense_variant

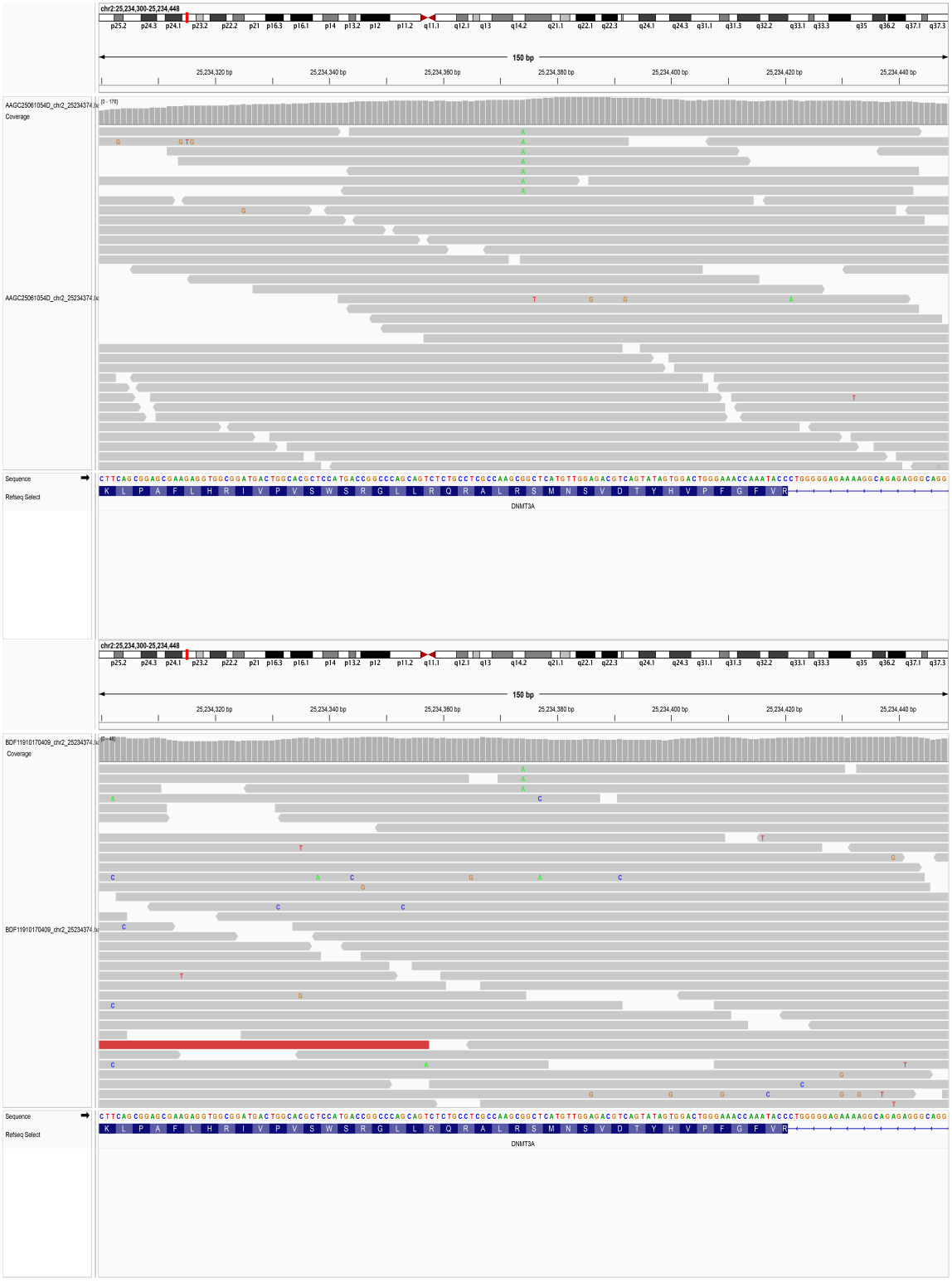


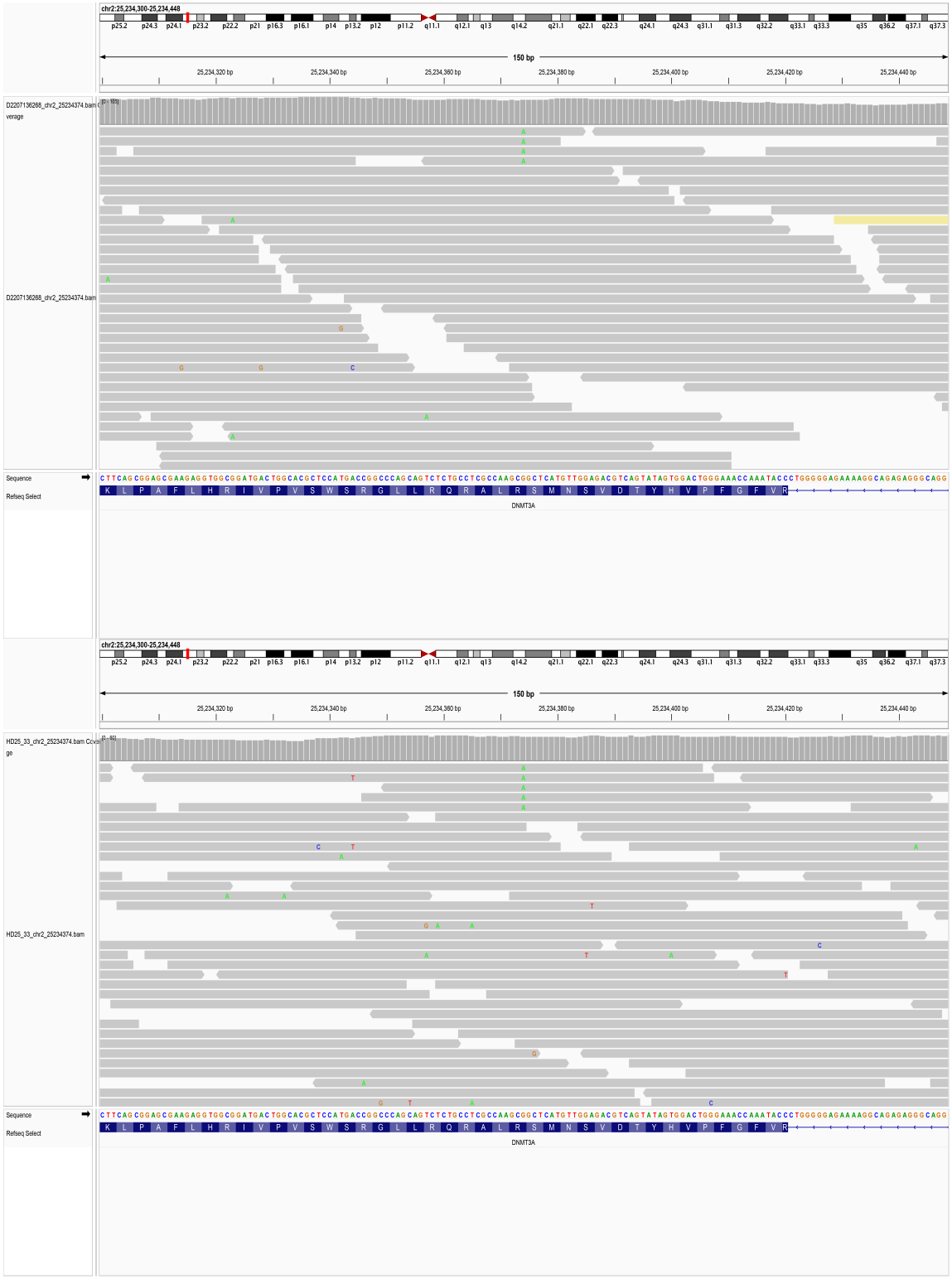

chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
18R03177_chr2_25234374.bam Coverage
18R03177_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A
18R08745_chr2_25234374.bam Coverage
18R08745_chr2_25234374.bam


chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
16R09109_chr2_25234374.bam Coverage
16R09109_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A
chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
16R09351_chr2_25234374.bam Coverage
16R09351_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A


chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
AAGC032970D_chr2_25234374.bam
verage
AAGC032970D_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A
chr2:25,234,300-25,234,448
150 bp
AAGC033164C_chr2_25234374.bam
verage
AAGC033164C_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A

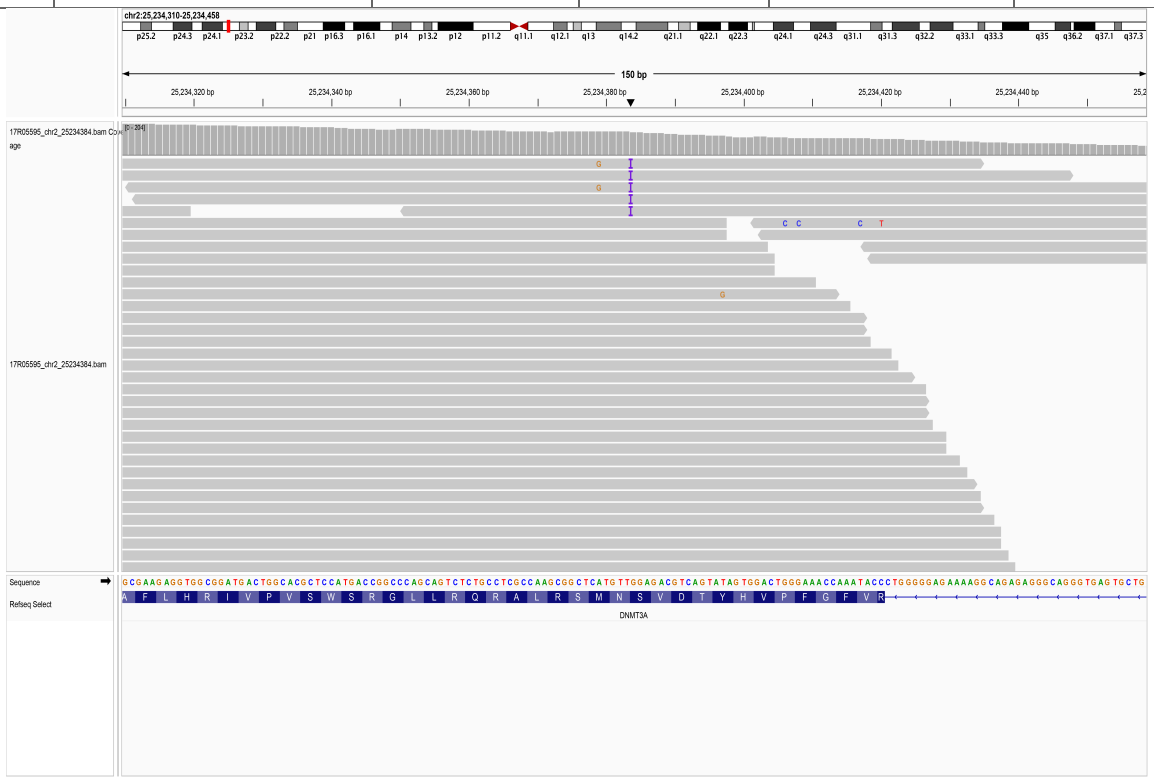

chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
Coverage
Sequence
Refseq Select
DNMT3A
chr2:25,234,300-25,234,448
150 bp
Coverage
Sequence
Refseq Select
DNMT3A


chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
AAGC2506105AD_chr2_25234374.ba
Coverage
AAGC2506105AD_chr2_25234374.ba
Sequence
Refseq Select
DNMT3A
chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
BDF11910170409_chr2_25234374.ba
Coverage
BDF11910170409_chr2_25234374.ba
Sequence
Refseq Select
DNMT3A


chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
D2207136268_chr2_25234374.bam Coverage
D2207136268_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A
HD25_33_chr2_25234374.bam Coverage
HD25_33_chr2_25234374.bam

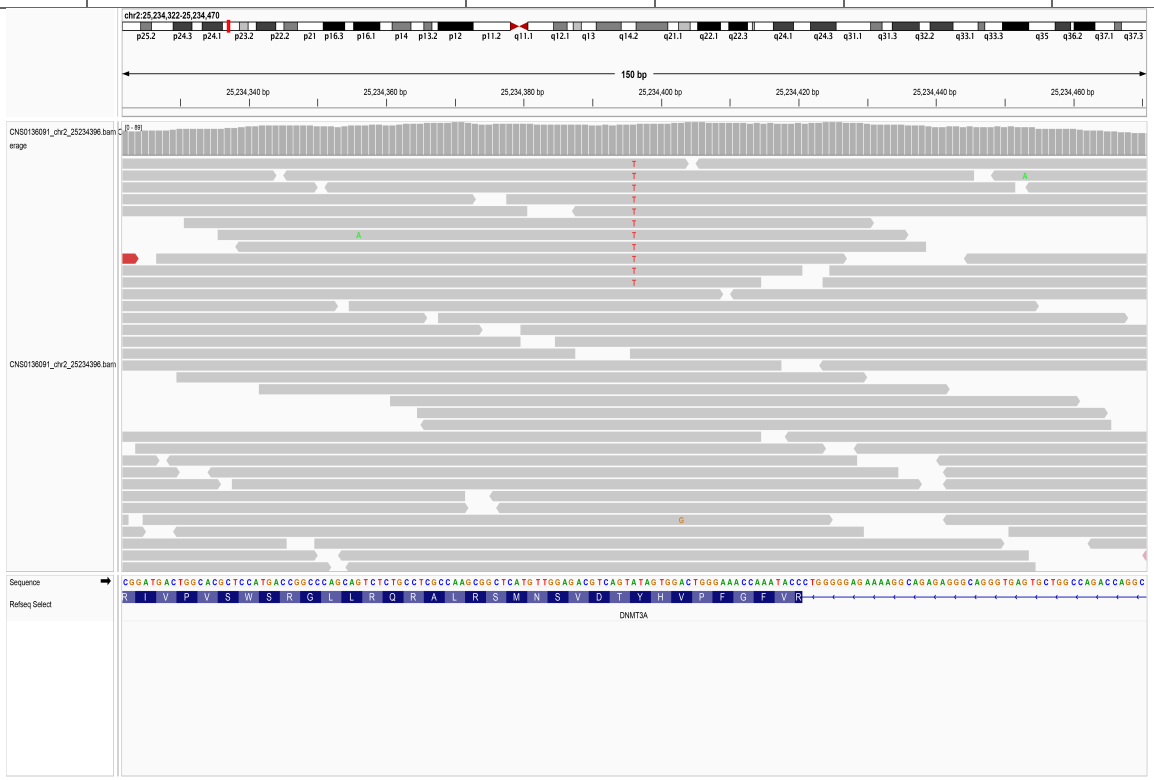
12.8. chr2_25234384_-/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05595	chr2_25234384_-/G	125	5	*DNMT3A*	frameshift_variant



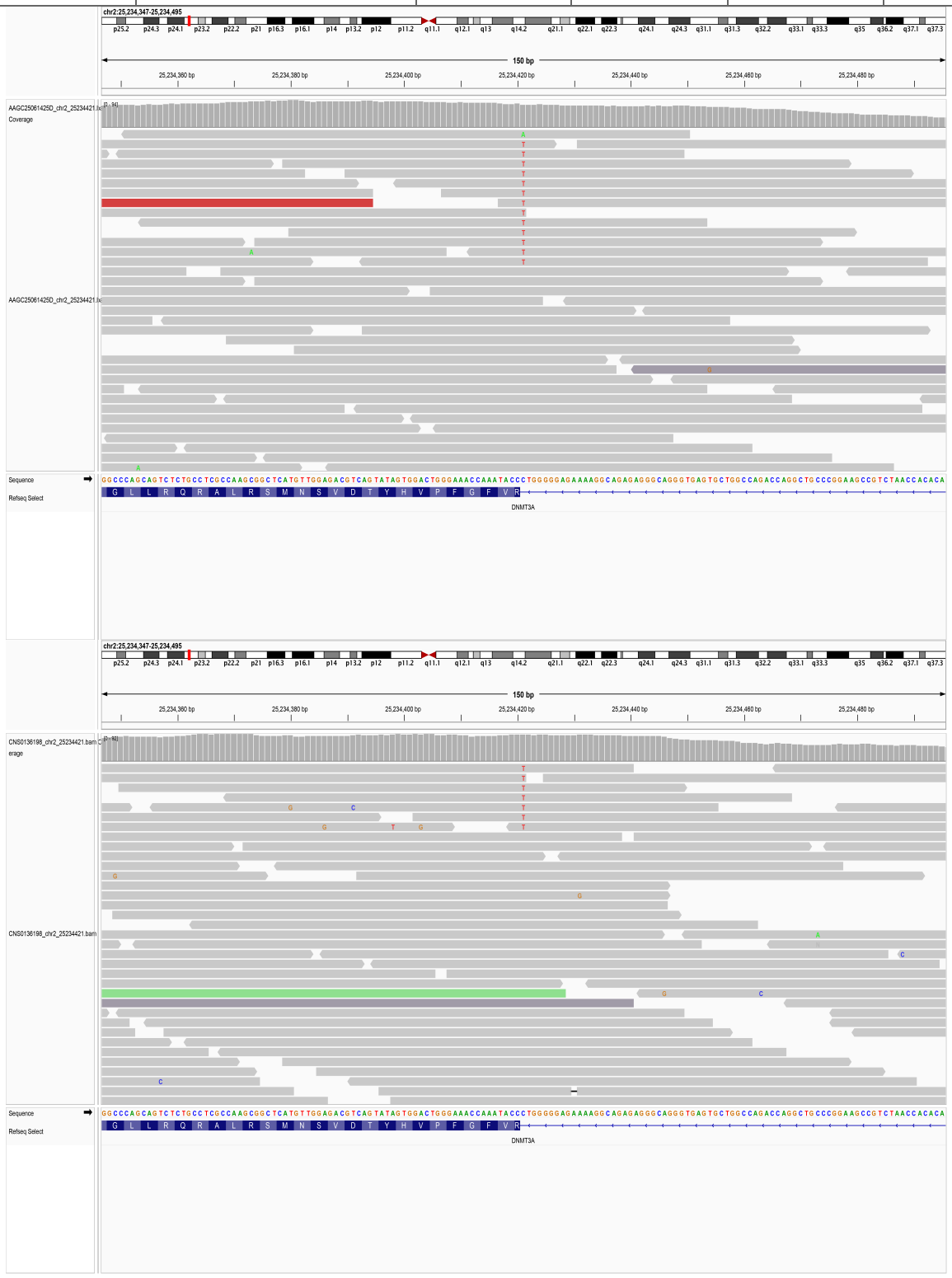
12.9. chr2_25234396_A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136091	chr2_25234396_A/T	70	11	*DNMT3A*	stop_gained



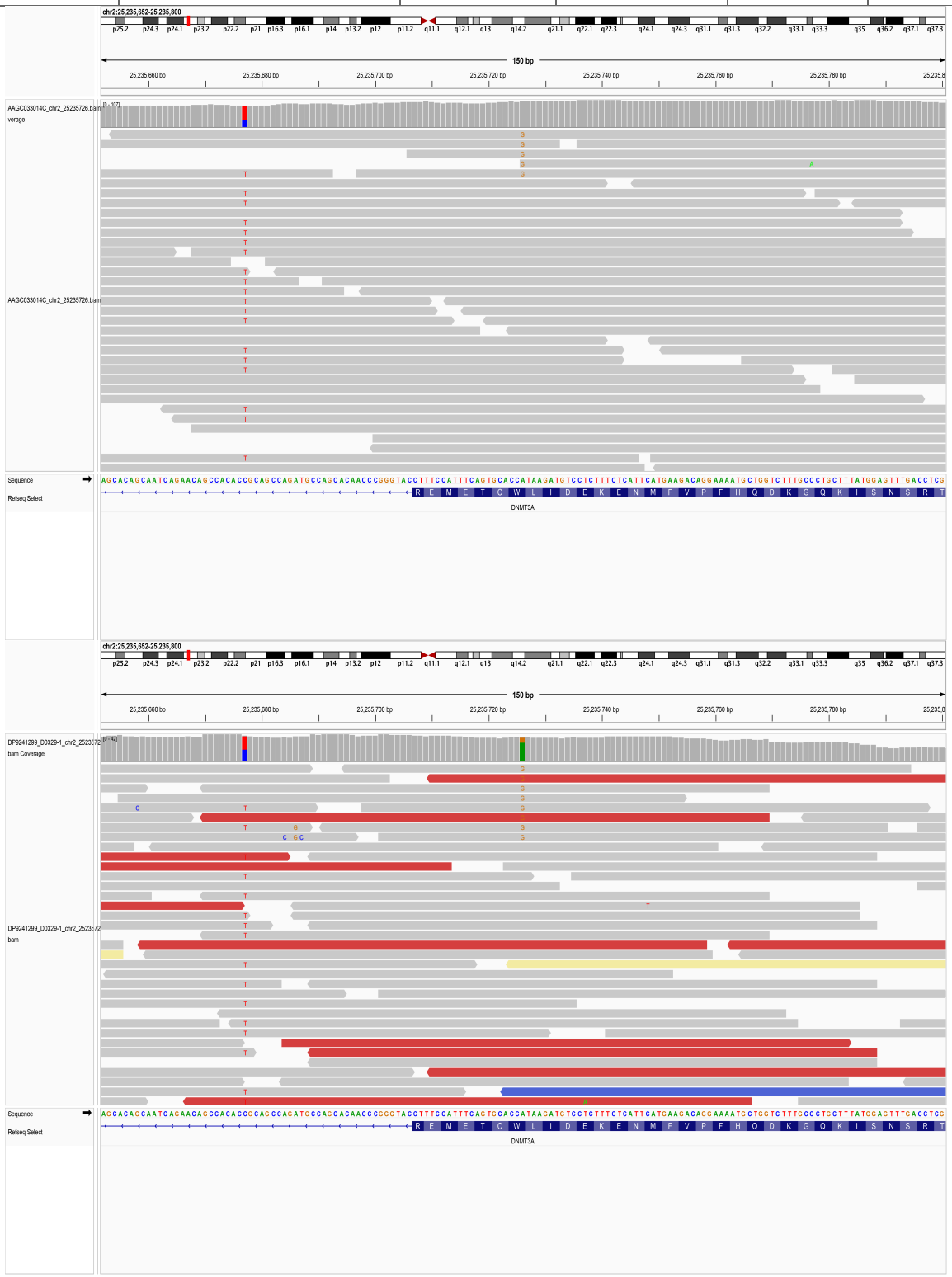
12.10. chr2_25234421_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061425D	chr2_25234421_C/T	63	13	*DNMT3A*	splice_acceptor_variant
CNS0136198	chr2_25234421_C/T	79	7	*DNMT3A*	splice_acceptor_variant



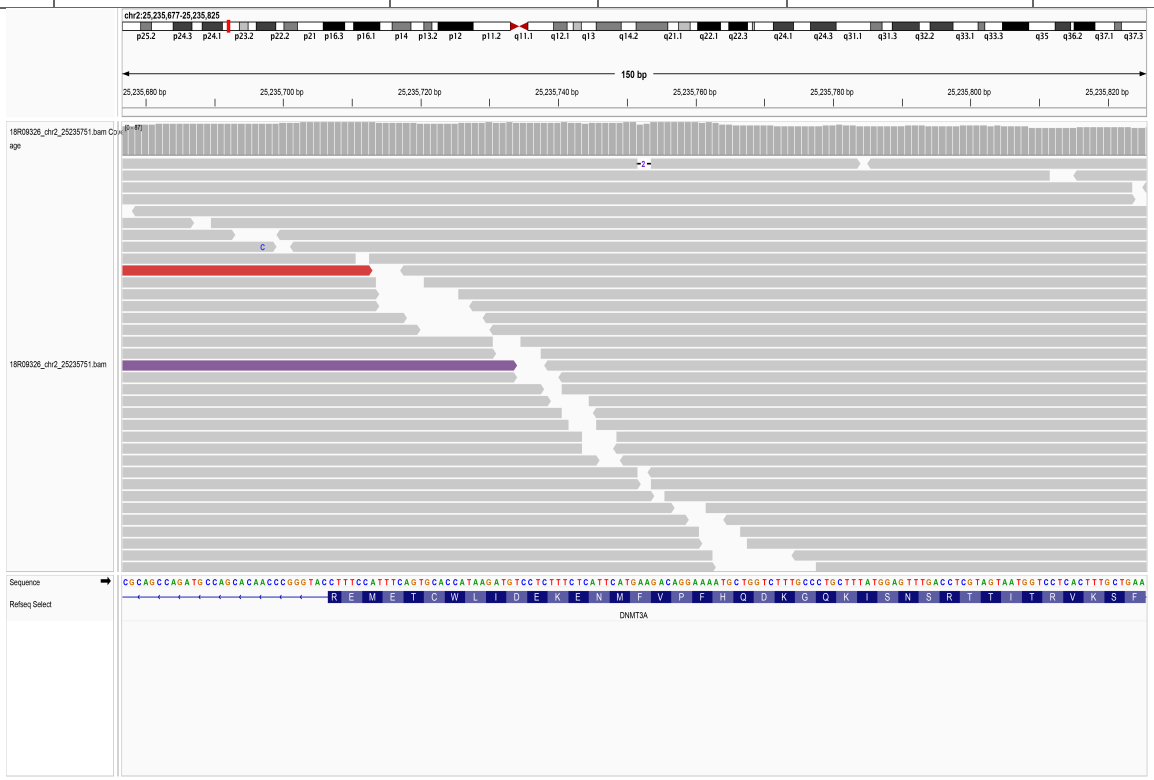
12.11. chr2_25235726_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033014C	chr2_25235726_A/G	93	5	*DNMT3A*	missense_variant
DP9241299_D0329-1	chr2_25235726_A/G	29	8	*DNMT3A*	missense_variant



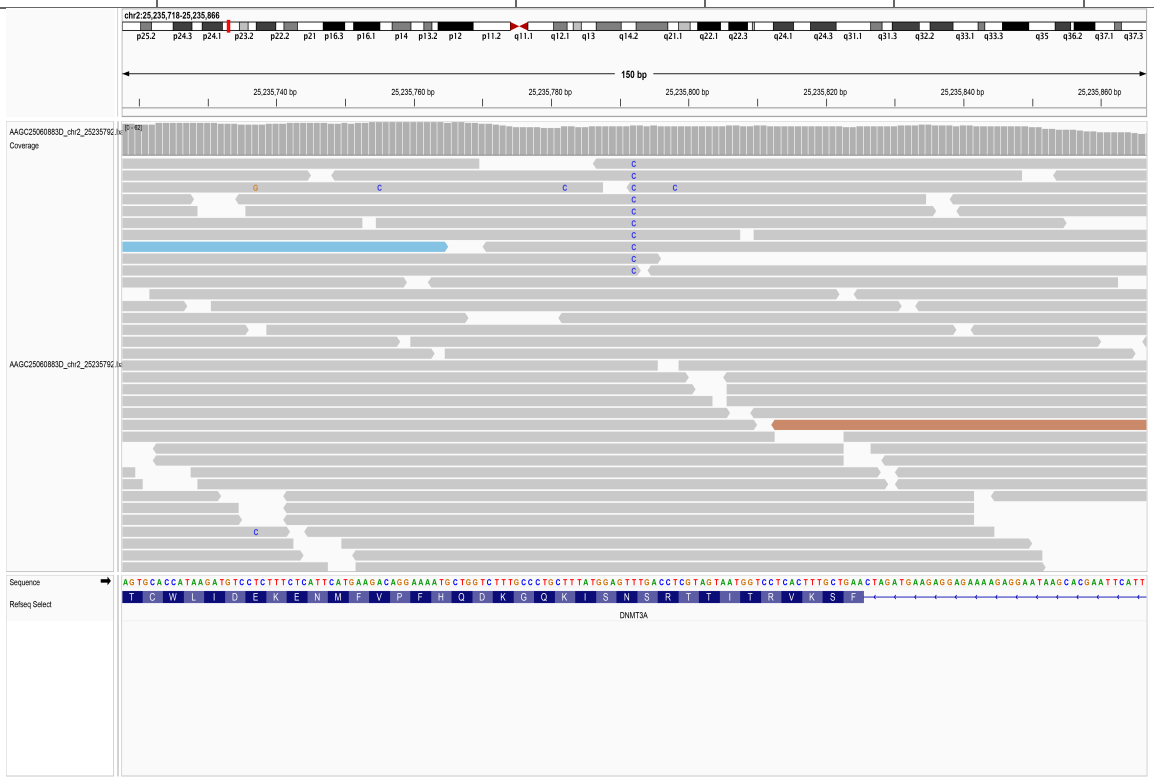
12.12. chr2_25235752_AA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09326	chr2_25235752_AA/-	81	5	*DNMT3A*	frameshift_variant



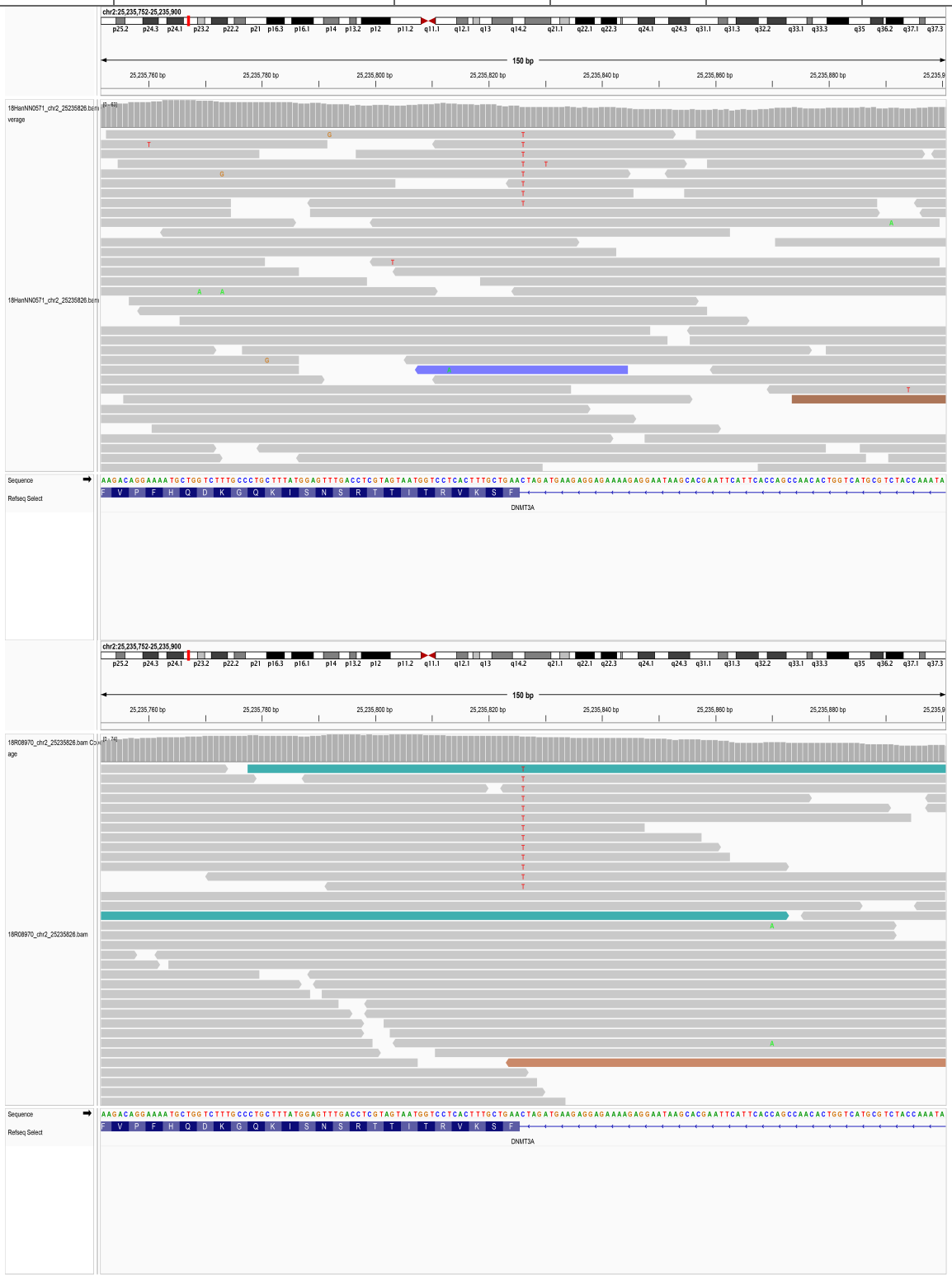
12.13. chr2_25235792_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060883D	chr2_25235792_T/C	45	10	*DNMT3A*	missense_variant



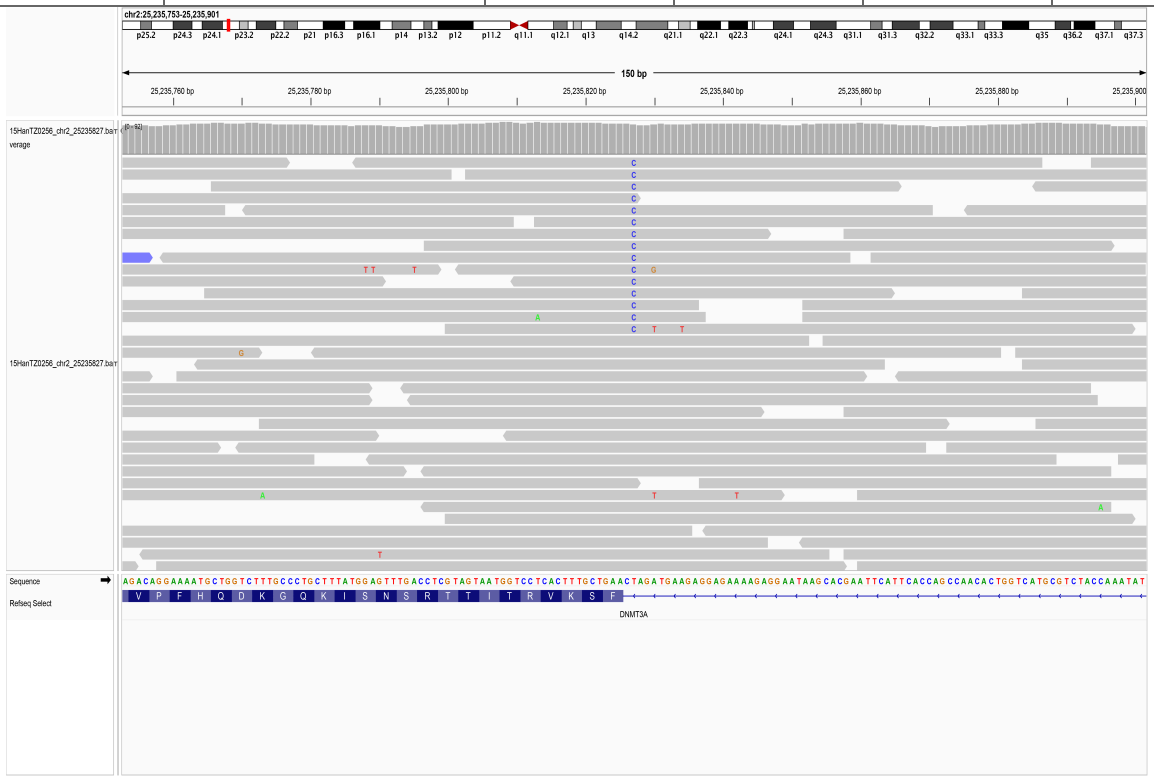
12.14. chr2_25235826_C/T

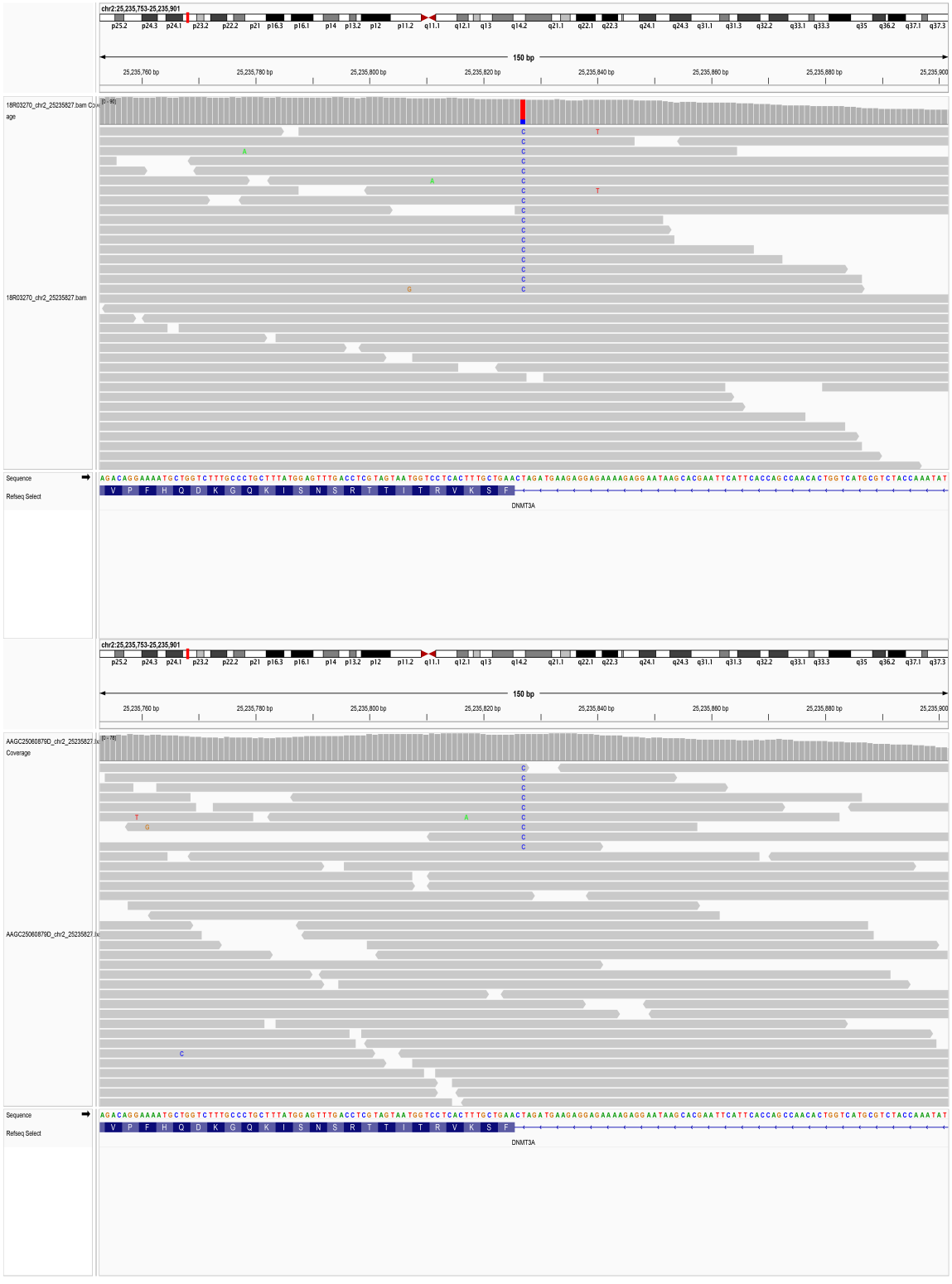
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0571	chr2_25235826_C/T	38	7	*DNMT3A*	splice_acceptor_variant
18R08970	chr2_25235826_C/T	55	13	*DNMT3A*	splice_acceptor_variant



12.15. chr2_25235827_T/C

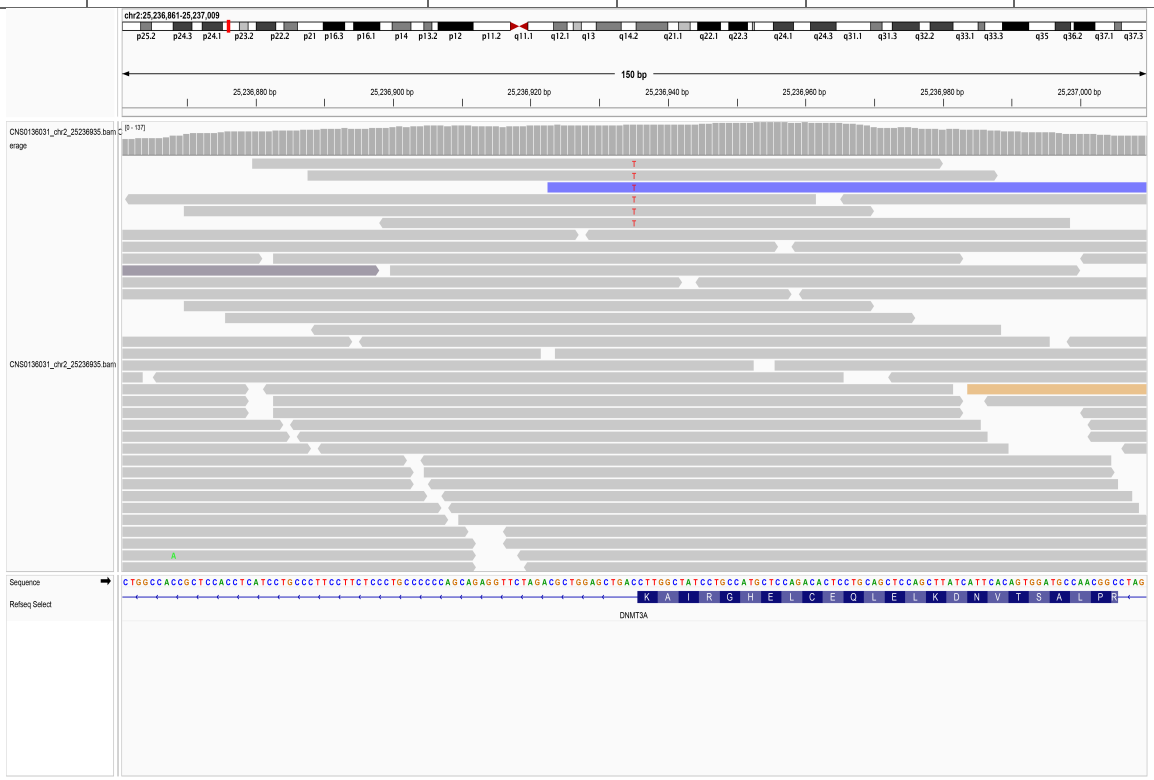
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0256	chr2_25235827_T/C	63	14	*DNMT3A*	splice_acceptor_variant
18R03270	chr2_25235827_T/C	64	17	*DNMT3A*	splice_acceptor_variant
AAGC25060879D	chr2_25235827_T/C	66	9	*DNMT3A*	splice_acceptor_variant




chr2:25,235,753-25,235,901
150 bp
25,235,760 bp
25,235,780 bp
25,235,800 bp
25,235,820 bp
25,235,840 bp
25,235,860 bp
25,235,880 bp
25,235,900
18R03270_chr2_25235827.bam Coverage
18R03270_chr2_25235827.bam
Sequence
Refseq Select
AGACAGGAAAATGCTGGTCTTTGCCCTGCTTTATGGAGTTTGACCTCGTAGTAATGGTCCTCACTTTGCTGAACTAGATGAAGAGGAGAAAAGAGGAATAAGCACGAATTCATTCACCAGCCAACACTGGTCATGCGTCTACCAAATAT
V P F H Q D K G Q K I S N S R T T I T R V K S F
DNMT3A
AAGC25060879D_chr2_25235827.ba
AAGC25060879D_chr2_25235827.ba

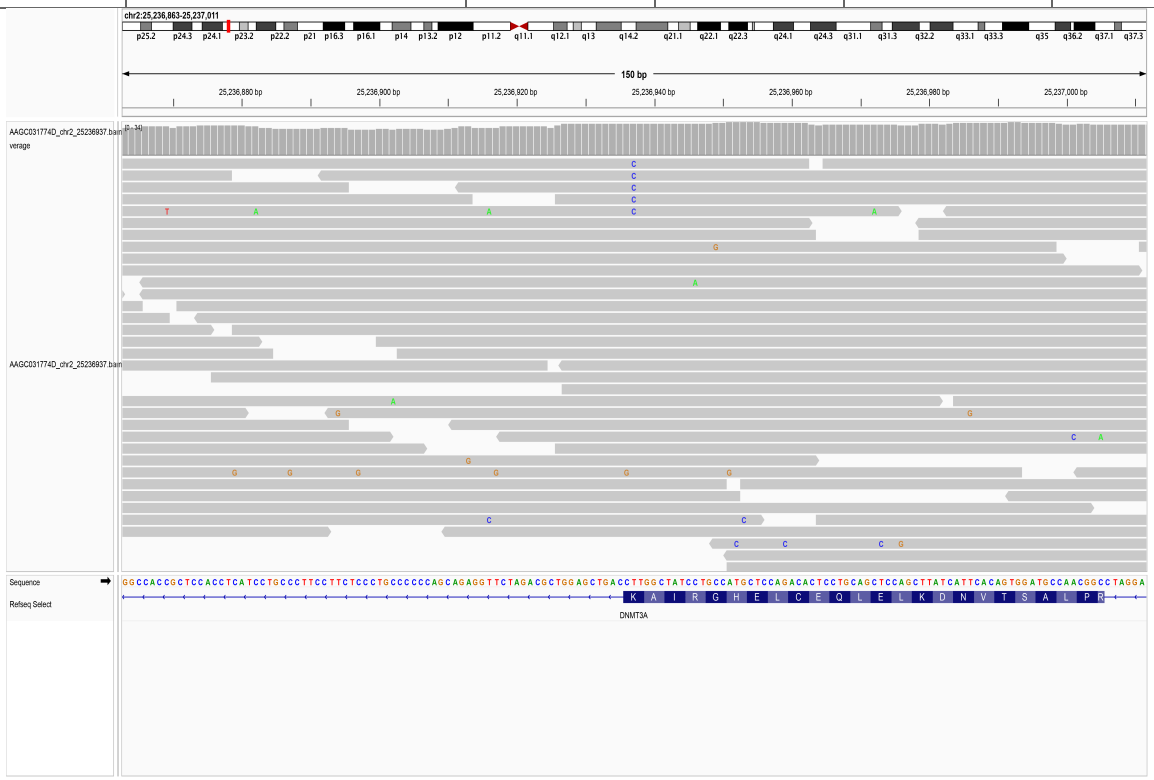
12.16. chr2_25236935_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136031	chr2_25236935_C/T	116	6	*DNMT3A*	splice_donor_variant



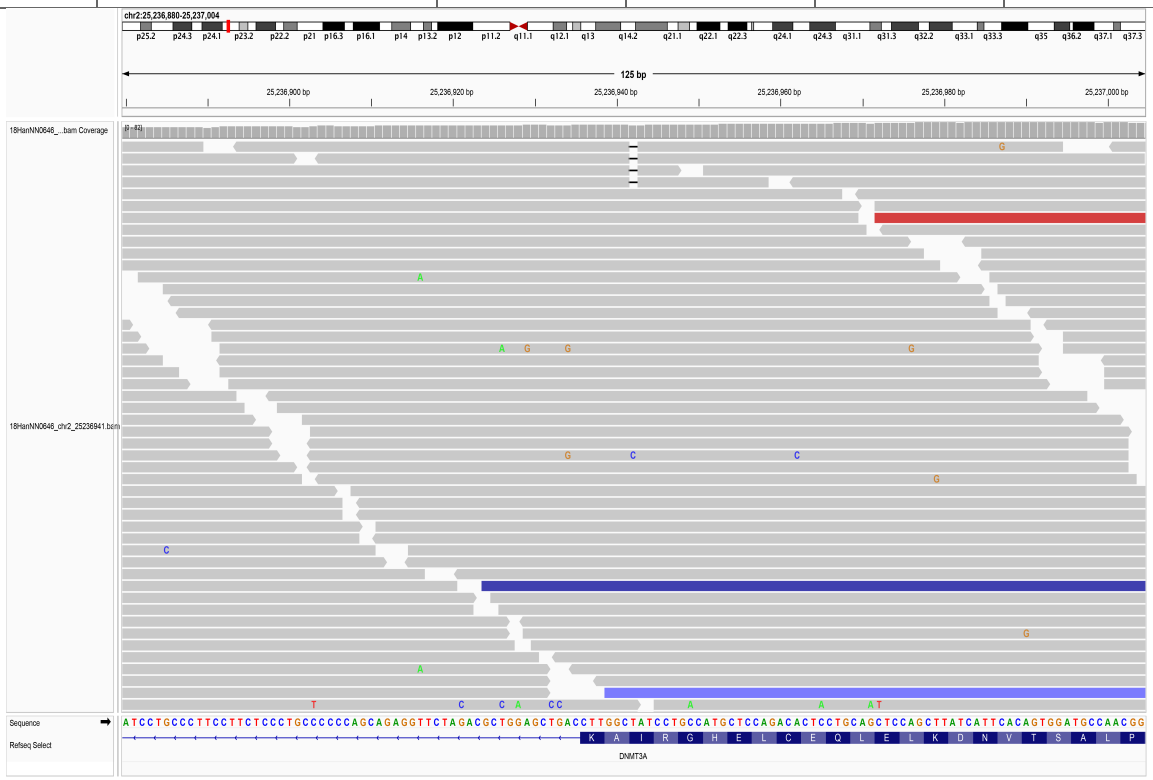
12.17. chr2_25236937_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC031774D	chr2_25236937_T/C	24	5	*DNMT3A*	missense_variant



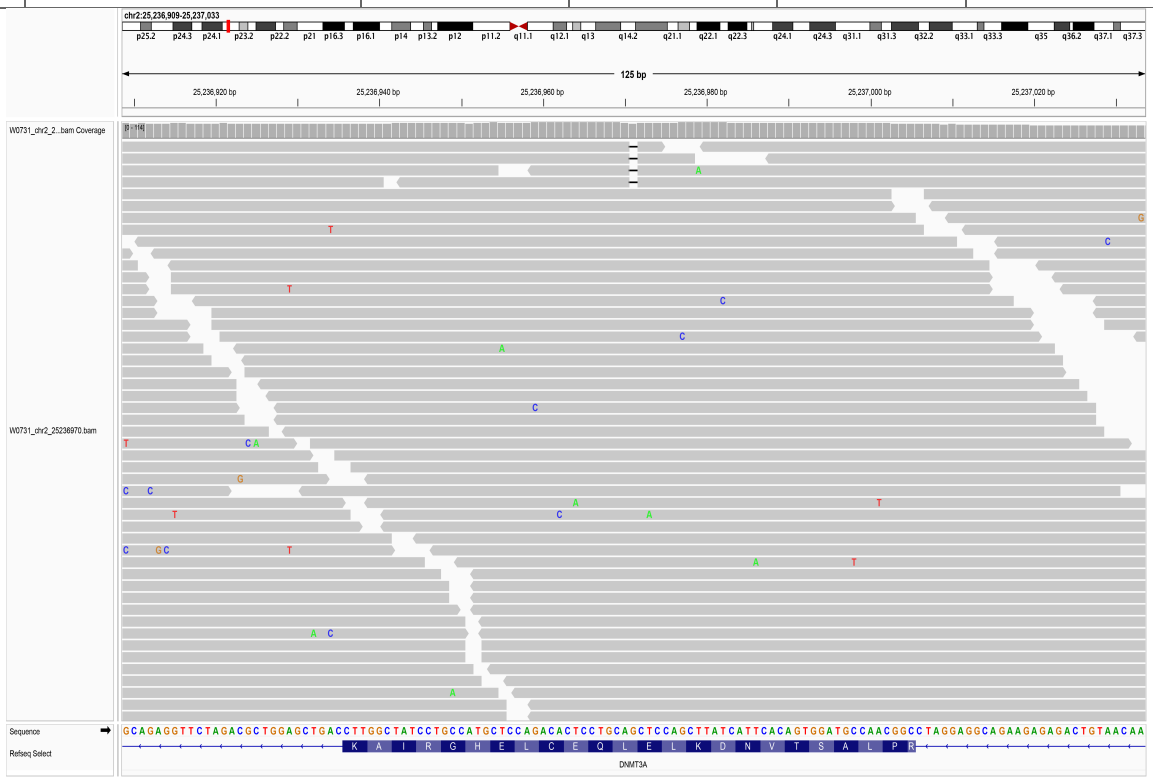
12.18. chr2_25236942_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0646	chr2_25236942_T/-	60	4	*DNMT3A*	frameshift_variant



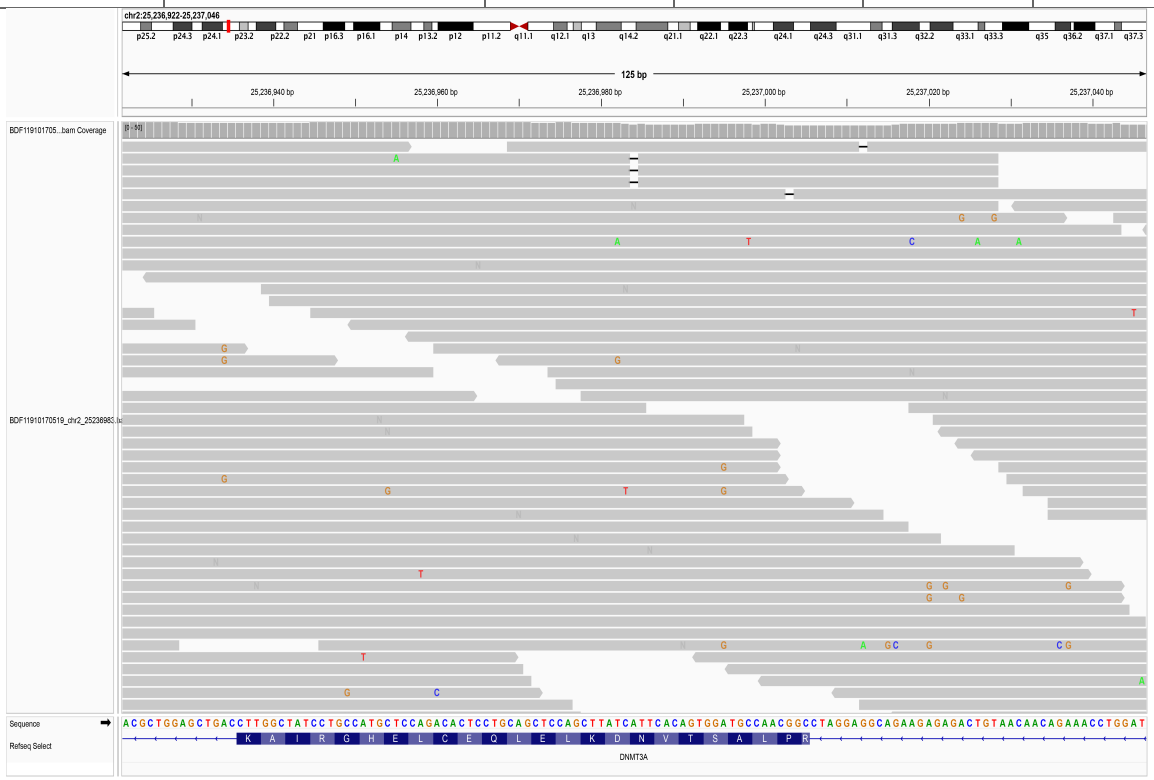
12.19. chr2_25236971_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
W0731	chr2_25236971_G/-	99	4	*DNMT3A*	frameshift_variant



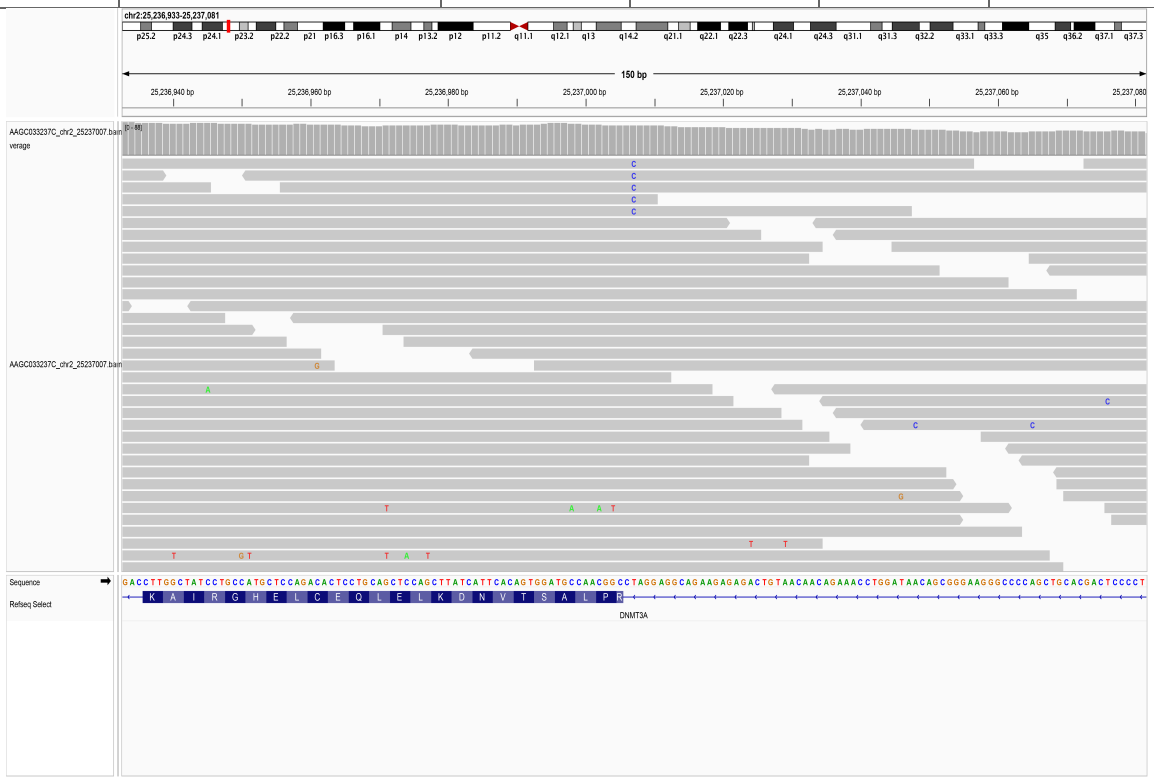
12.20. chr2_25236984_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chr2_25236984_A/-	38	3	*DNMT3A*	frameshift_variant



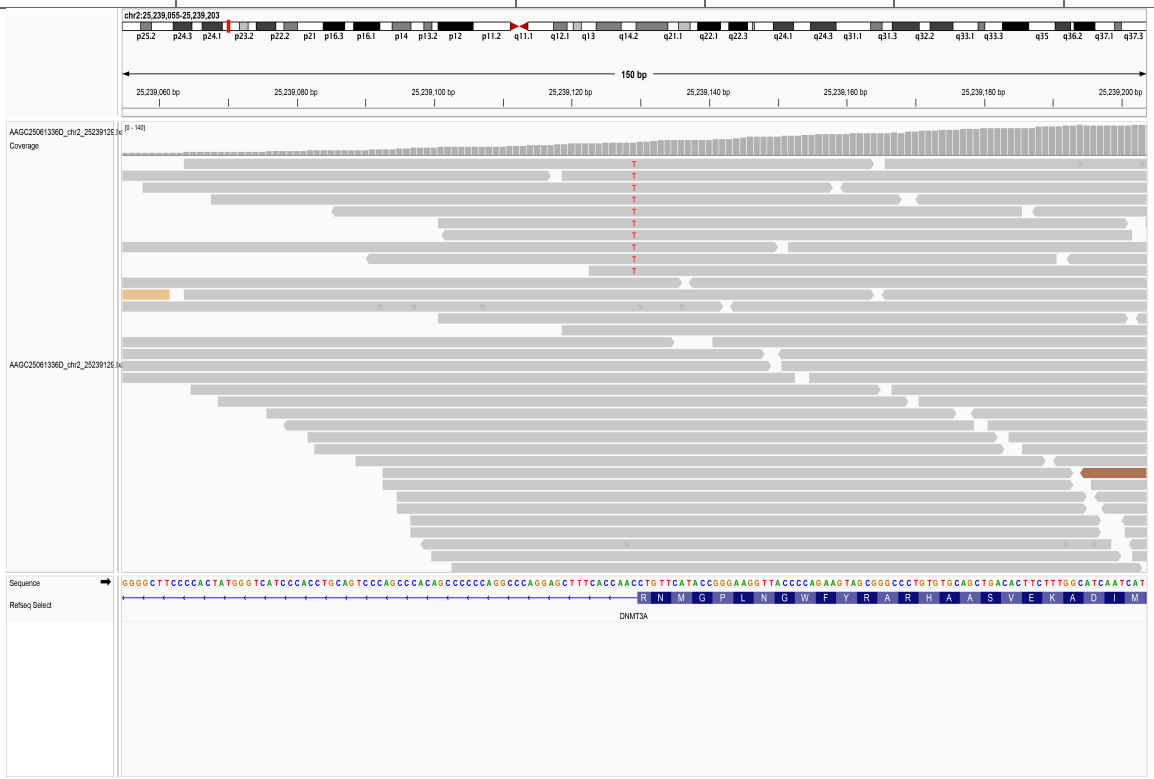
12.21. chr2_25237007_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033237C	chr2_25237007_T/C	68	5	*DNMT3A*	splice_acceptor_variant



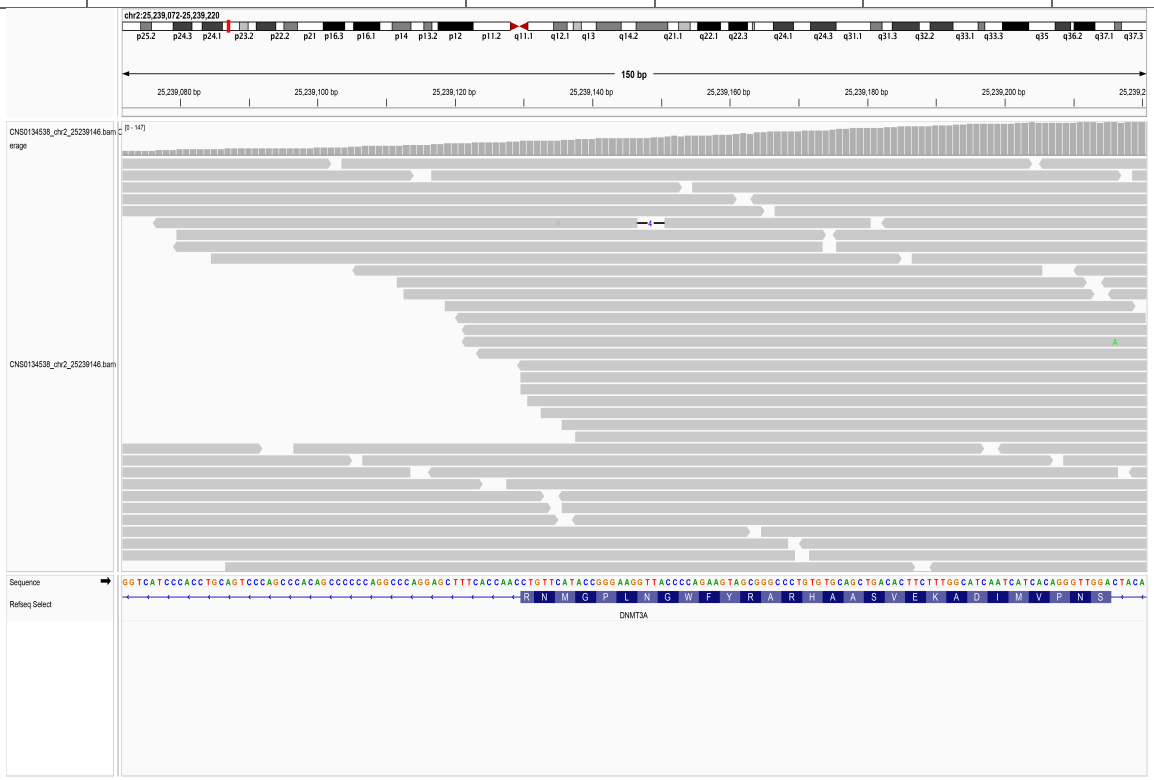
12.22. chr2_25239129_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061336D	chr2_25239129_C/T	44	10	*DNMT3A*	splice_donor_variant



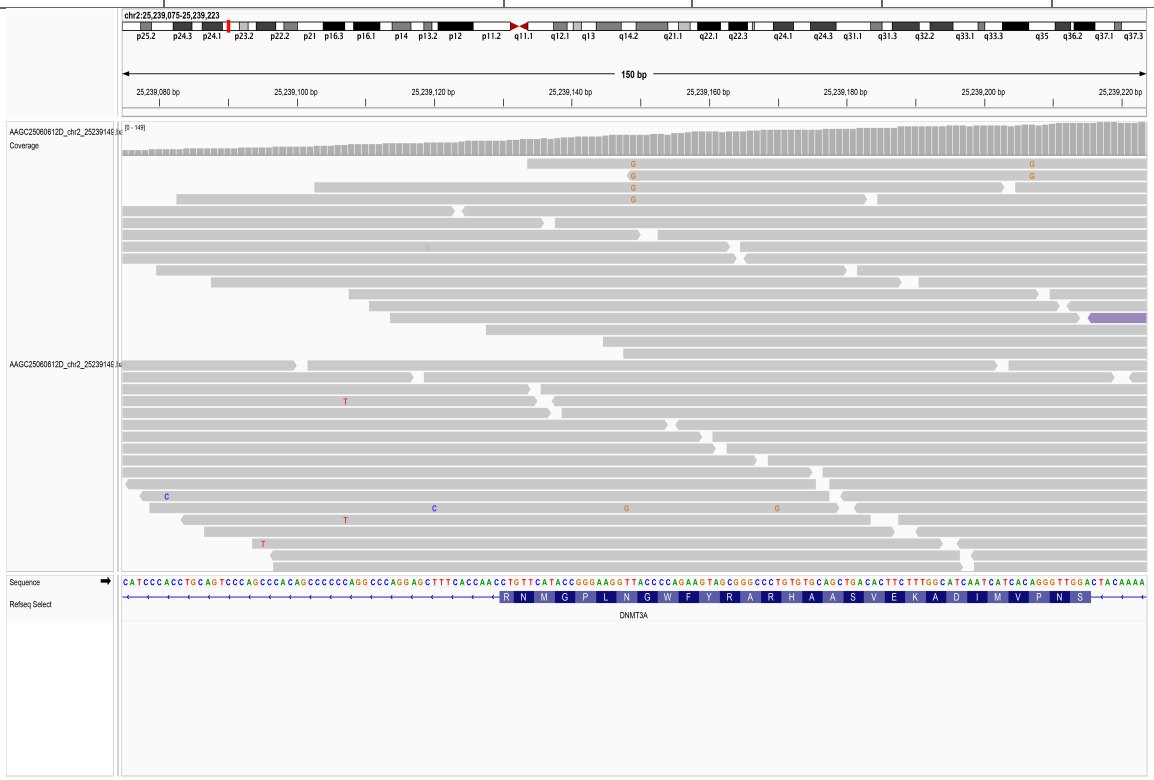
12.23. chr2_25239147_GTTA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134538	chr2_25239147_GTTA/-	77	2	*DNMT3A*	frameshift_variant



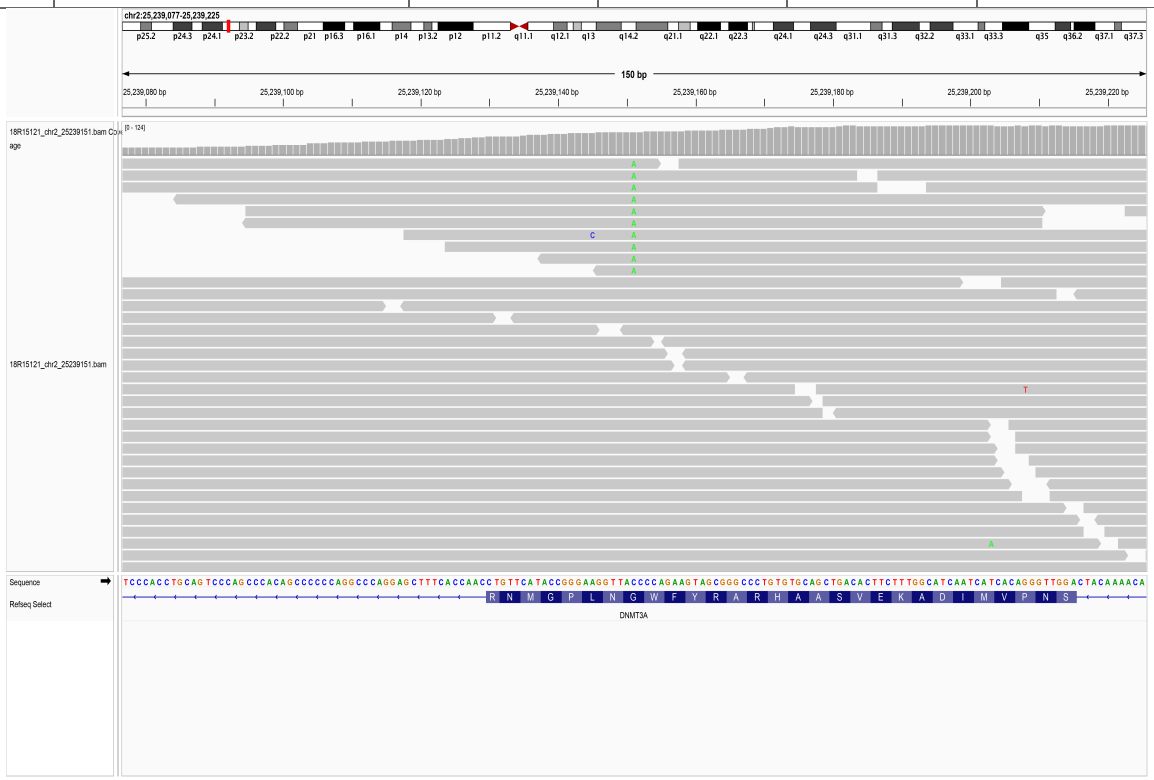
12.24. chr2_25239149_T/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060612D	chr2_25239149_T/G	87	4	*DNMT3A*	missense_variant



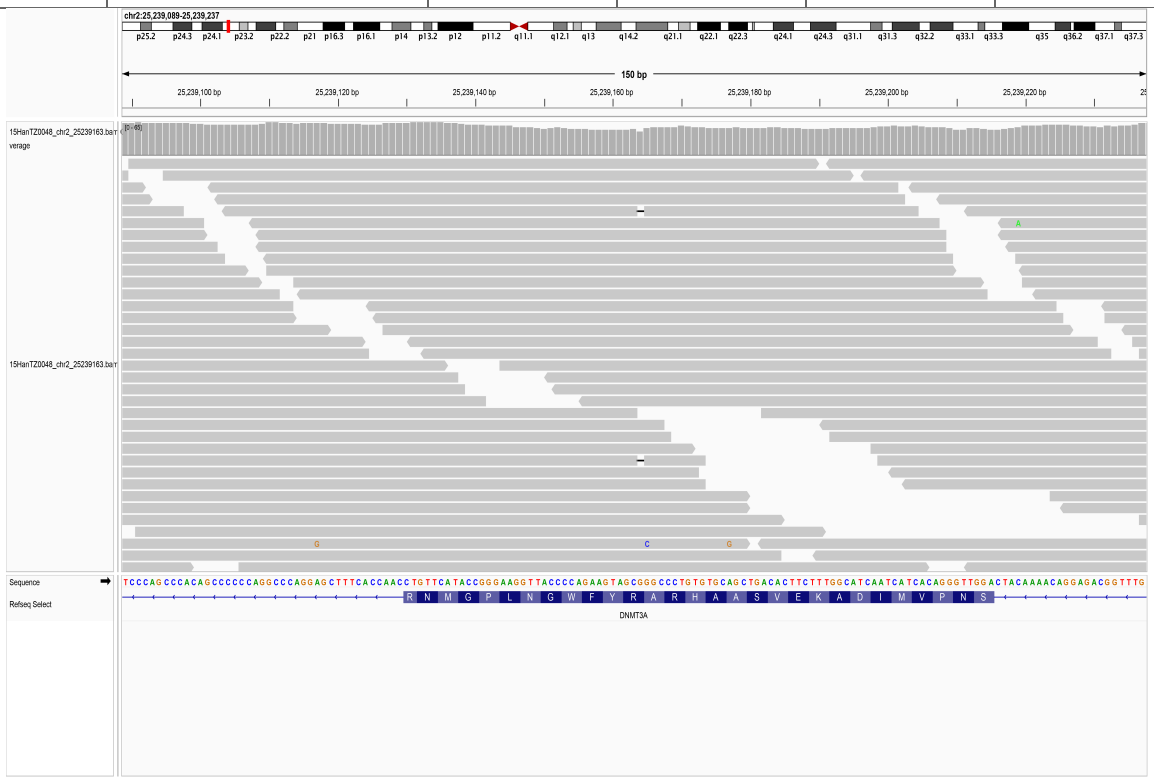
12.25. chr2_25239151_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15121	chr2_25239151_C/A	73	10	*DNMT3A*	missense_variant



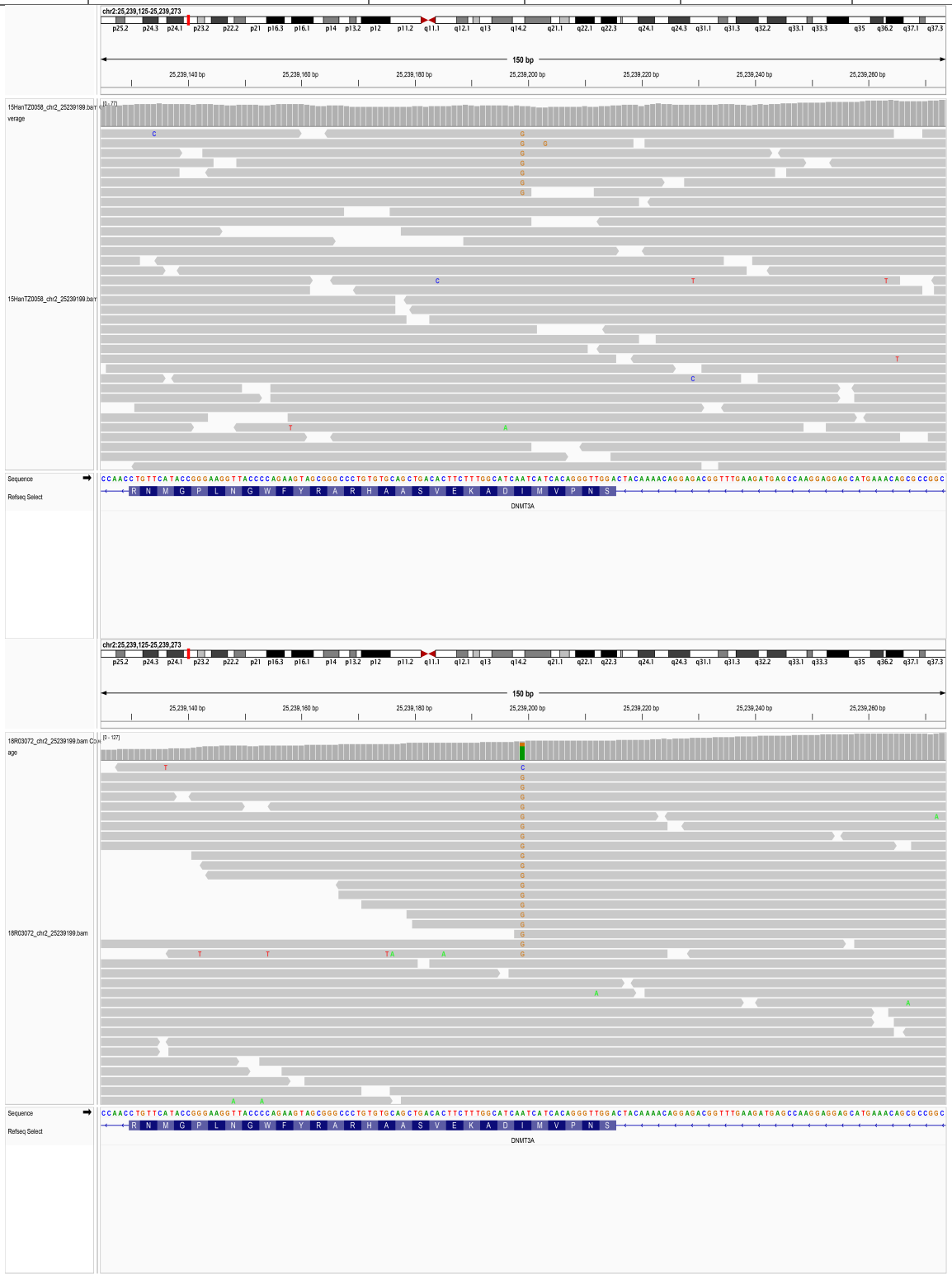
12.26. chr2_25239164_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0048	chr2_25239164_G/-	46	4	*DNMT3A*	frameshift_variant



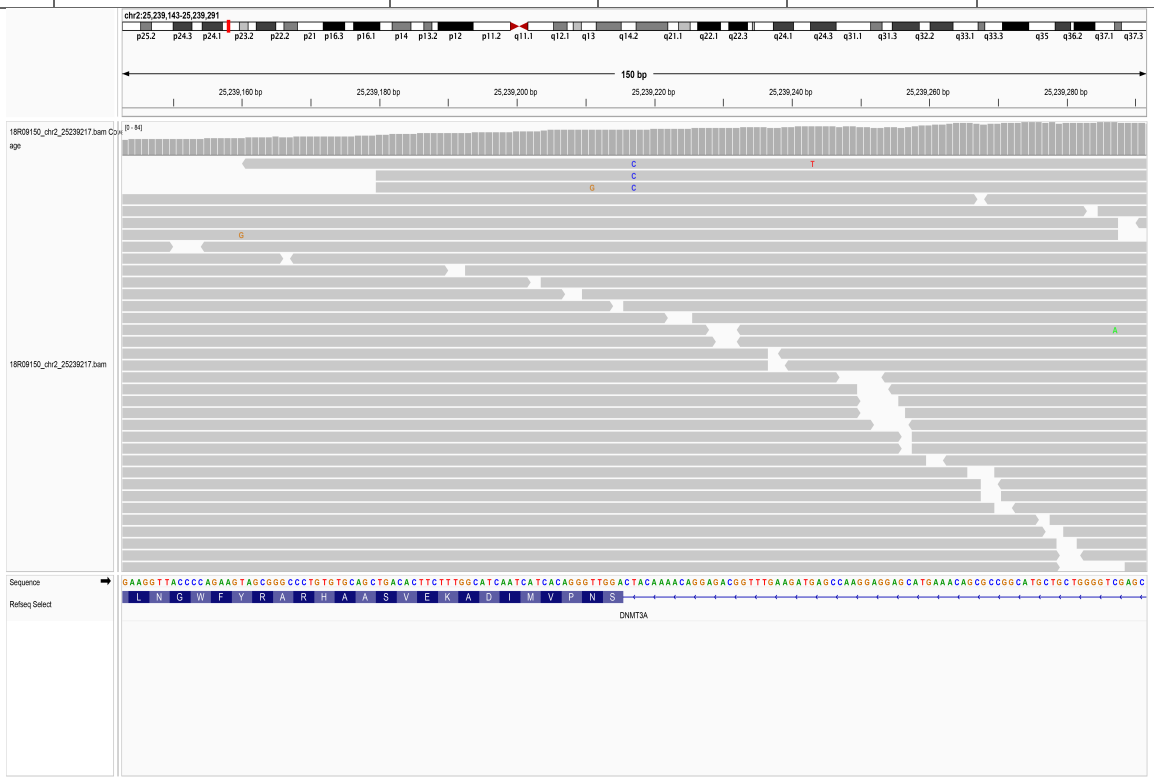
12.27. chr2_25239199_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0058	chr2_25239199_A/G	49	7	*DNMT3A*	missense_variant
18R03072	chr2_25239199_A/G	66	18	*DNMT3A*	missense_variant



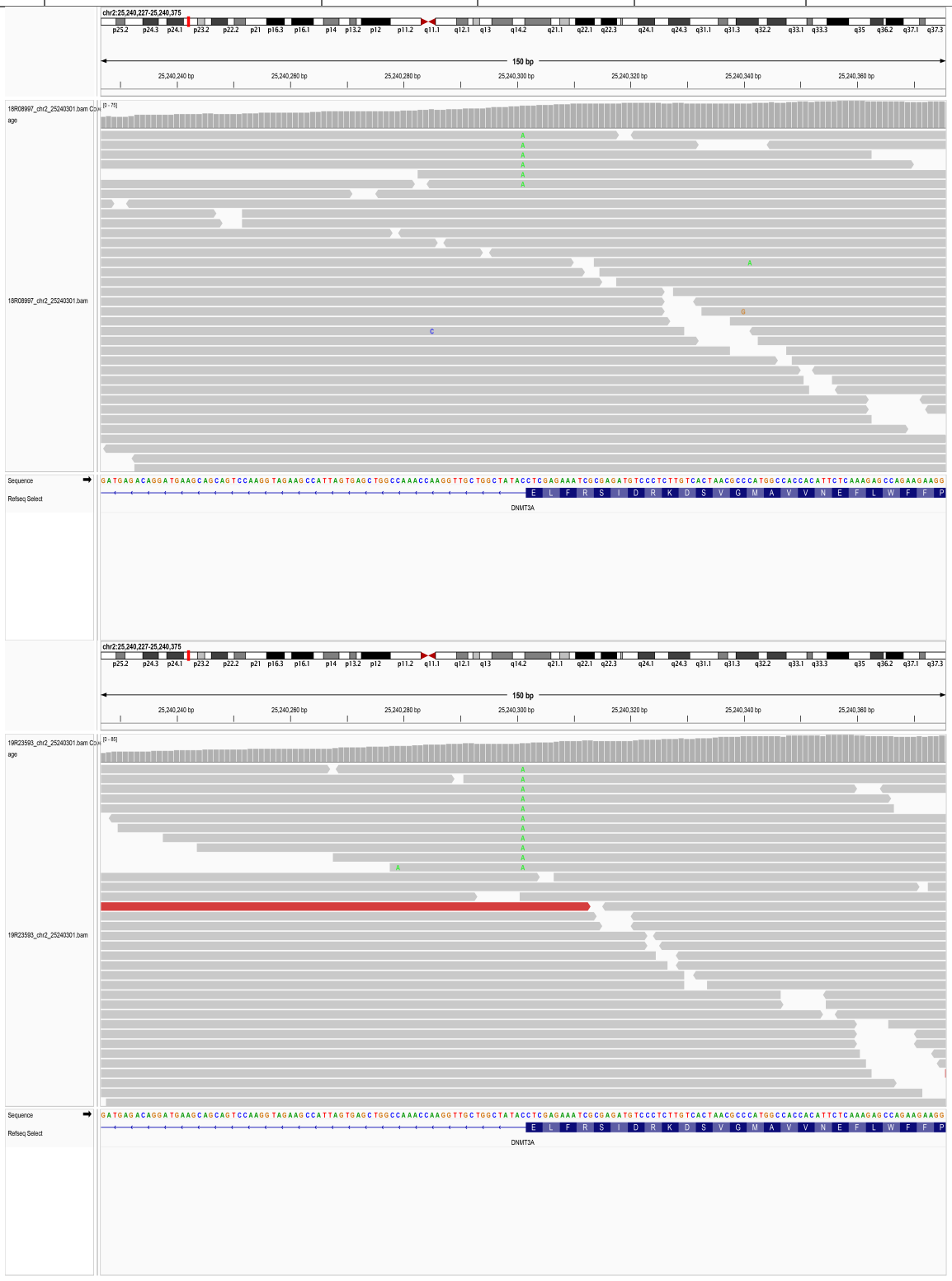
12.28. chr2_25239217_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09150	chr2_25239217_T/C	61	3	*DNMT3A*	splice_acceptor_variant



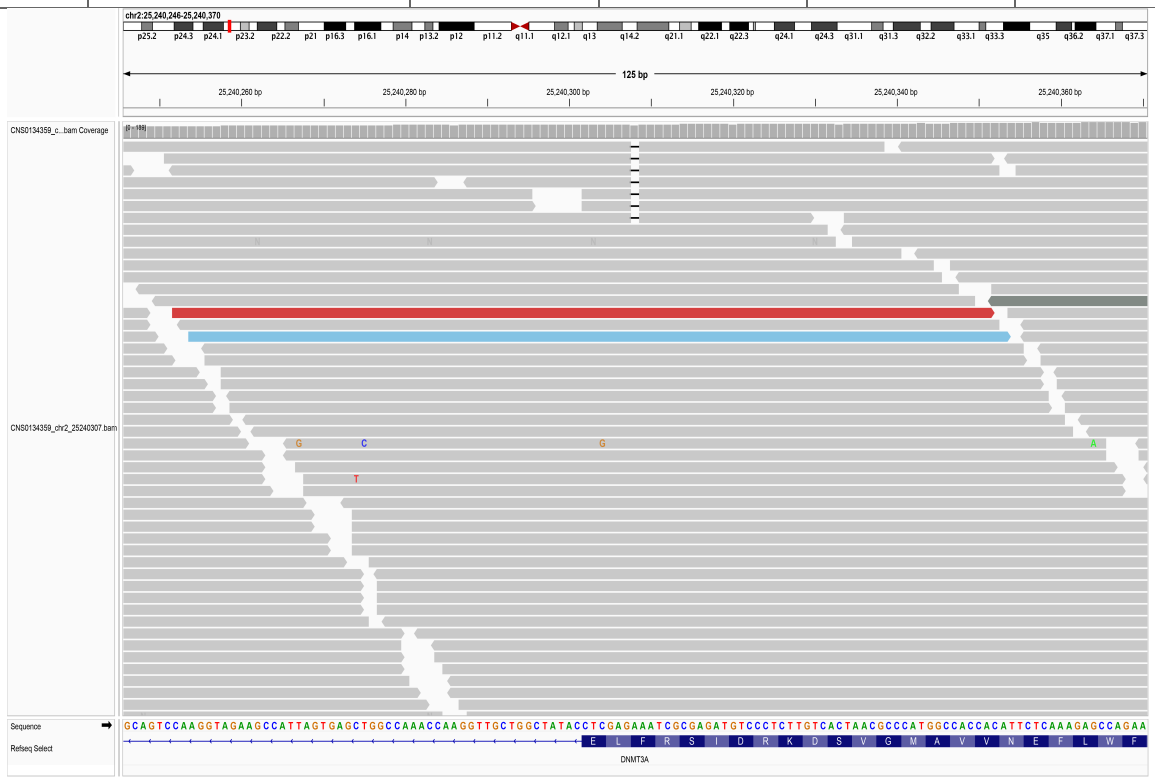
12.29. chr2_25240301_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08997	chr2_25240301_C/A	51	6	*DNMT3A*	splice_donor_variant
19R23593	chr2_25240301_C/A	47	11	*DNMT3A*	splice_donor_variant



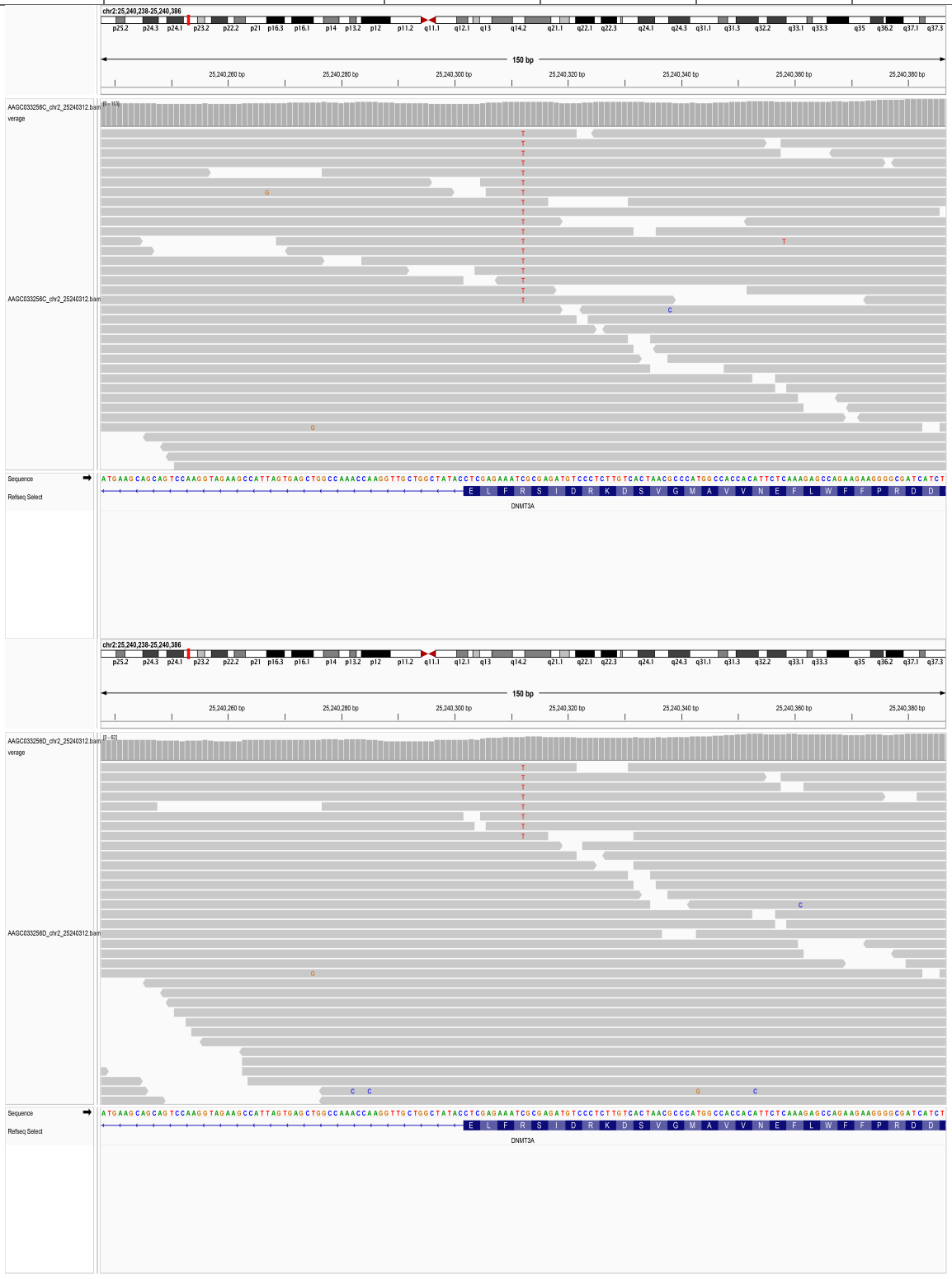
12.30. chr2_25240308_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134359	chr2_25240308_A/-	138	7	*DNMT3A*	frameshift_variant



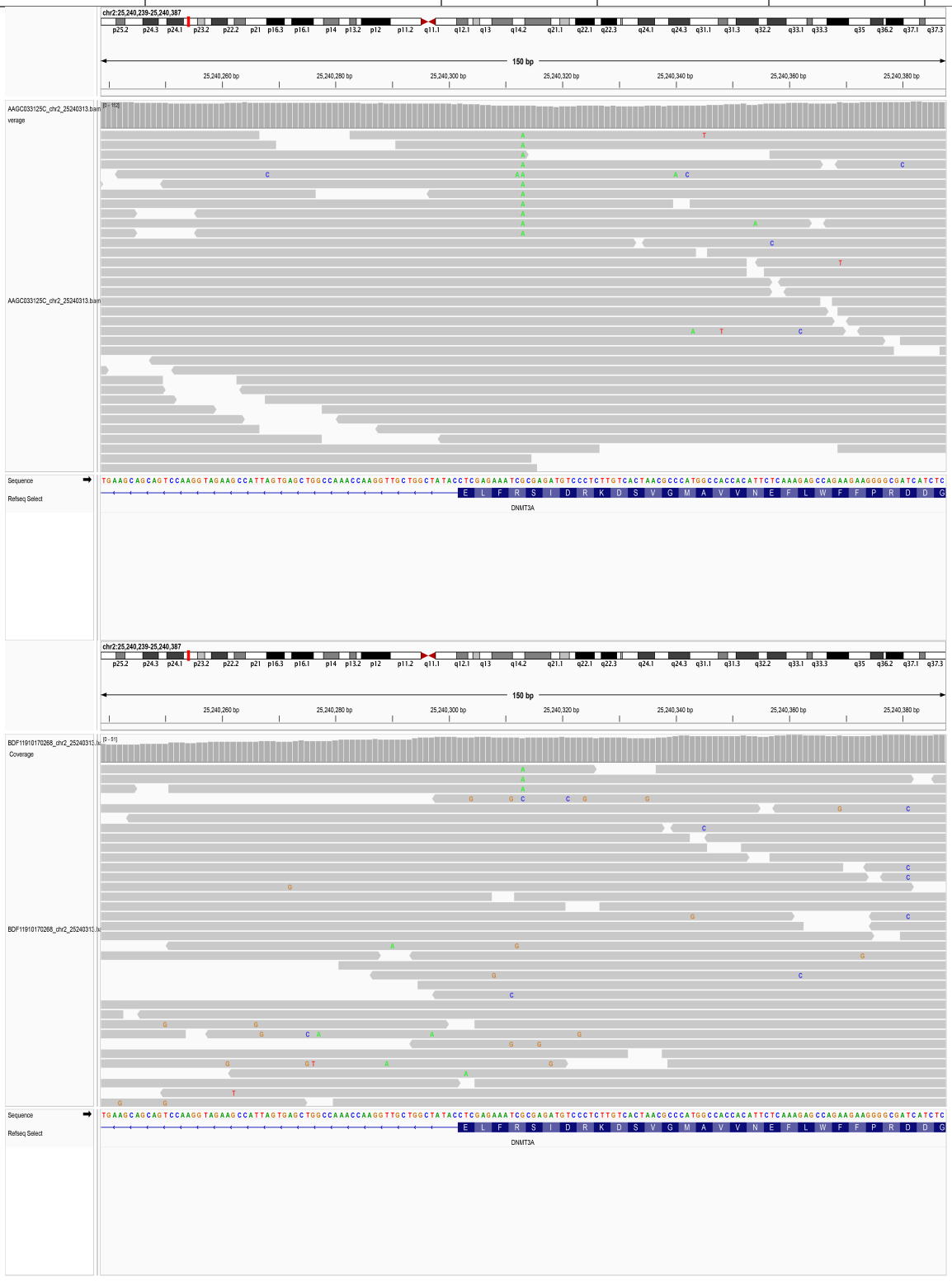
12.31. chr2_25240312_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033256C	chr2_25240312_C/T	79	18	*DNMT3A*	missense_variant
AAGC033256D	chr2_25240312_C/T	44	8	*DNMT3A*	missense_variant



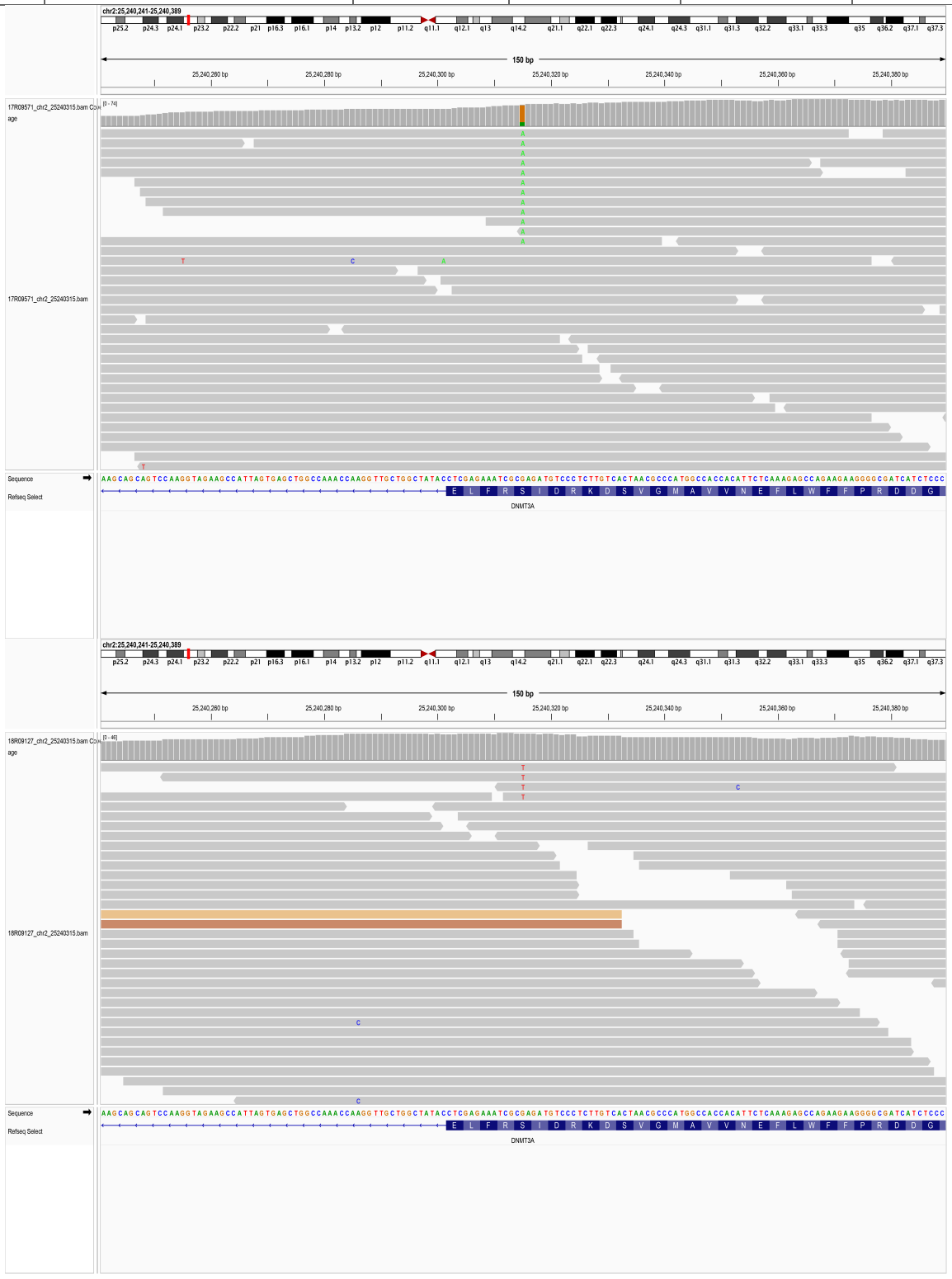
12.32. chr2_25240313_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033125C	chr2_25240313_G/A	78	10	*DNMT3A*	stop_gained
BDF11910170268	chr2_25240313_G/A	37	3	*DNMT3A*	stop_gained



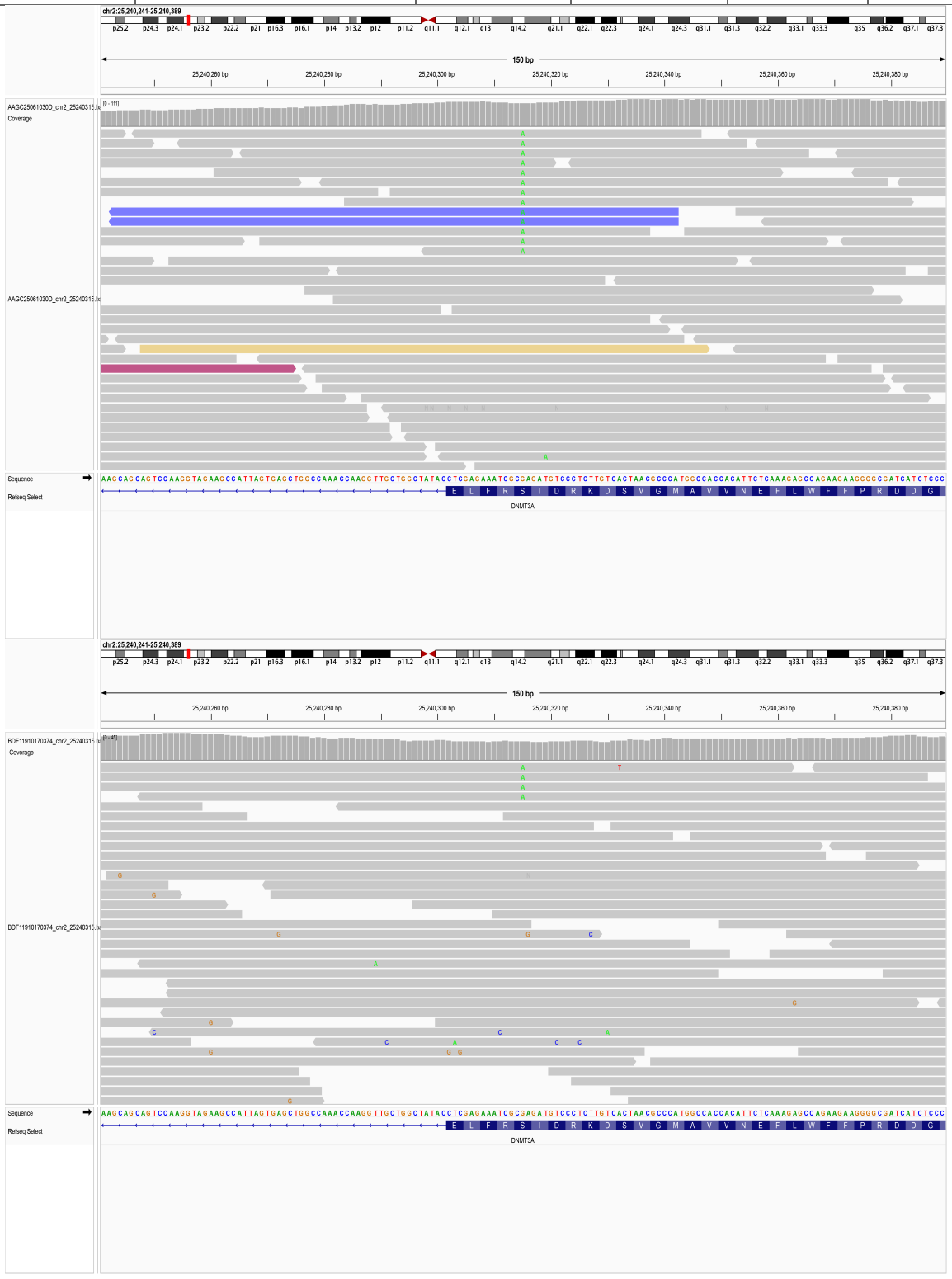
12.33. chr2_25240315_G/A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09571	chr2_25240315_G/A/T	46	12	*DNMT3A*	stop_gained
18R09127	chr2_25240315_G/A/T	38	4	*DNMT3A*	stop_gained



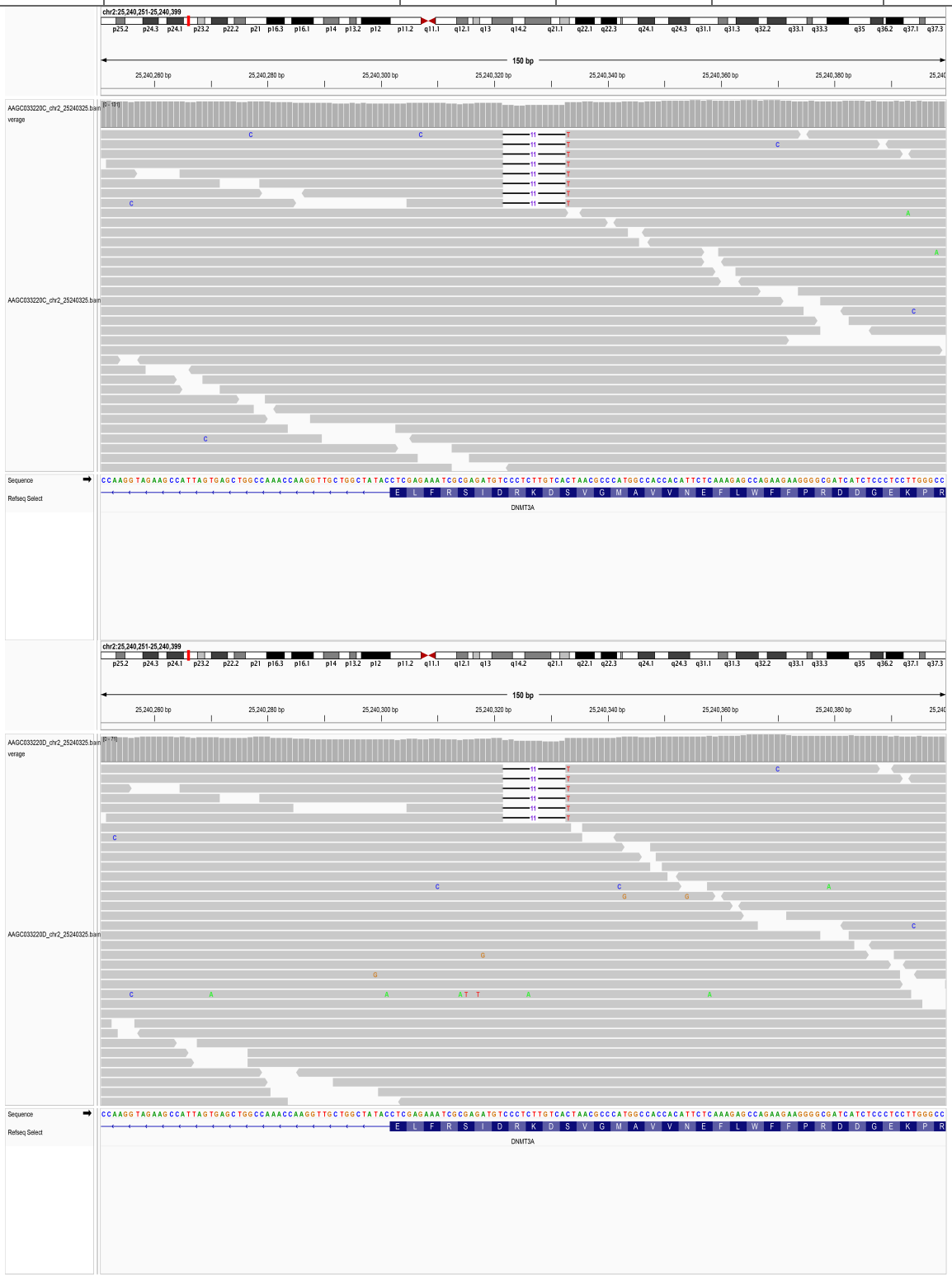
12.34. chr2_25240315_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061030D	chr2_25240315_G/A	79	12	*DNMT3A*	missense_variant
BDF11910170374	chr2_25240315_G/A	24	4	*DNMT3A*	missense_variant



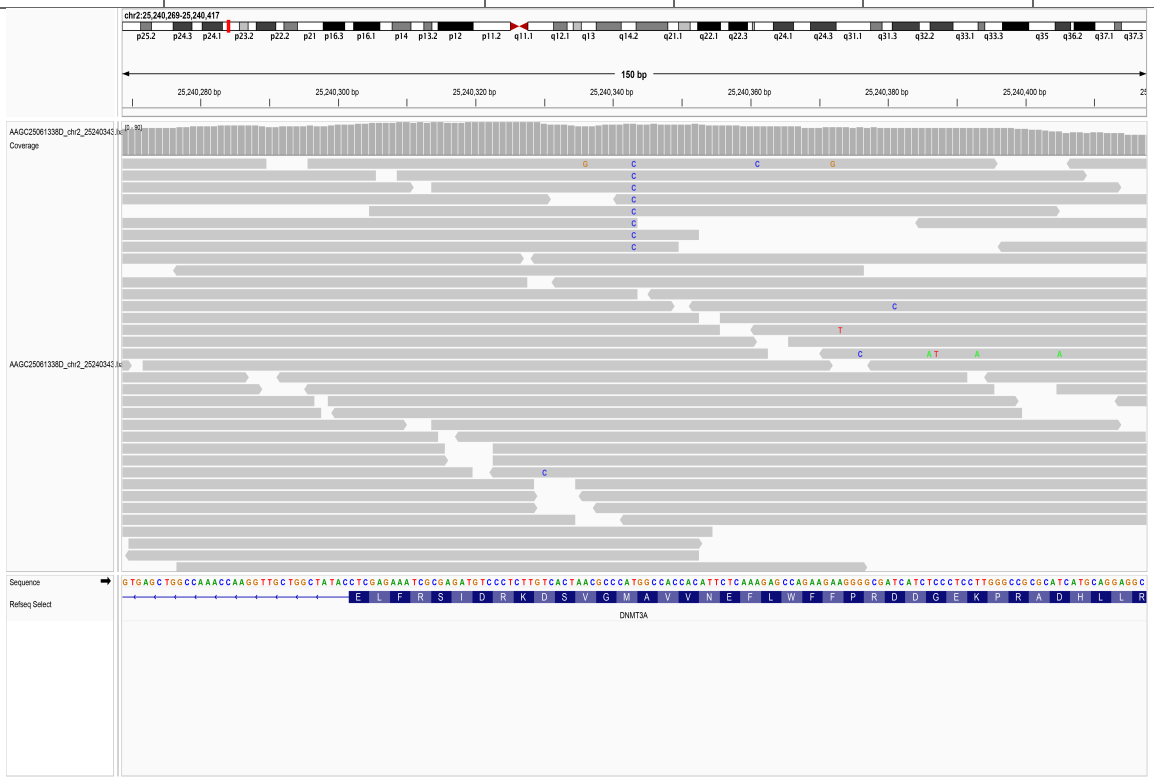
12.35. chr2_25240326_CTTGTCAC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033220C	chr2_25240326_CTTGTCAC/-	116	14	*DNMT3A*	frameshift_variant
AAGC033220D	chr2_25240326_CTTGTCAC/-	59	8	*DNMT3A*	frameshift_variant



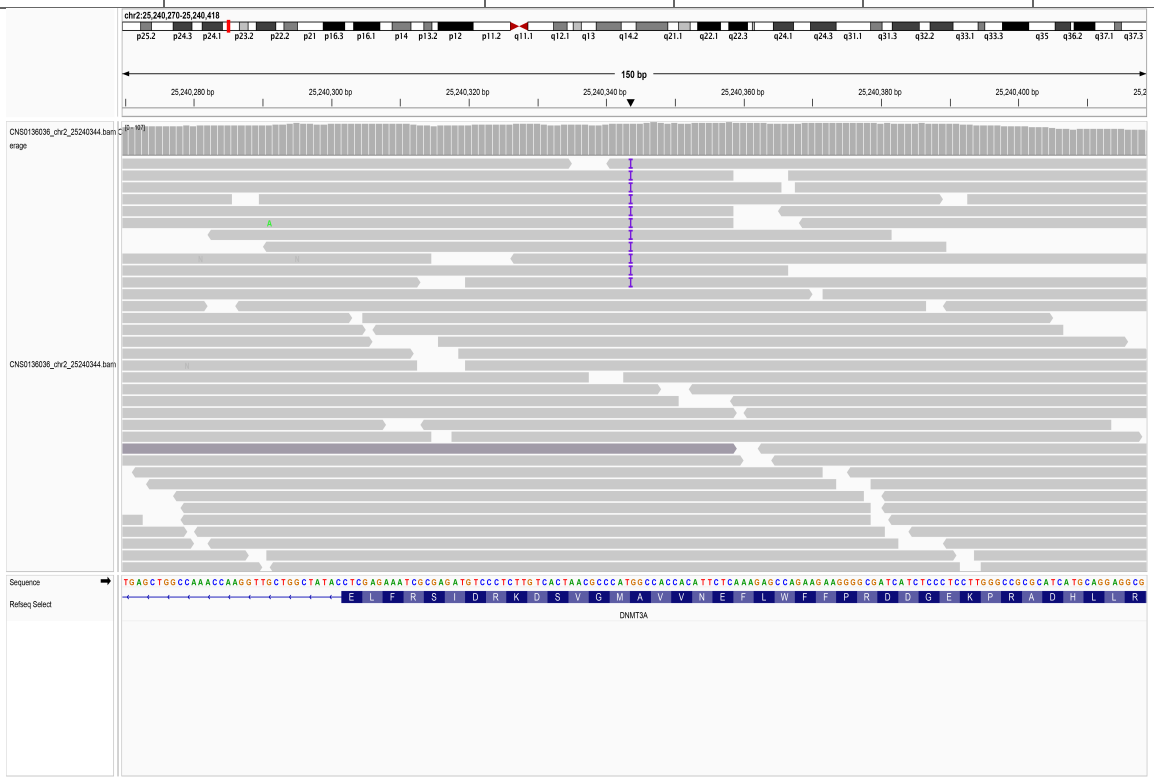
12.36. chr2_25240343_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061338D	chr2_25240343_T/C	72	7	*DNMT3A*	missense_variant



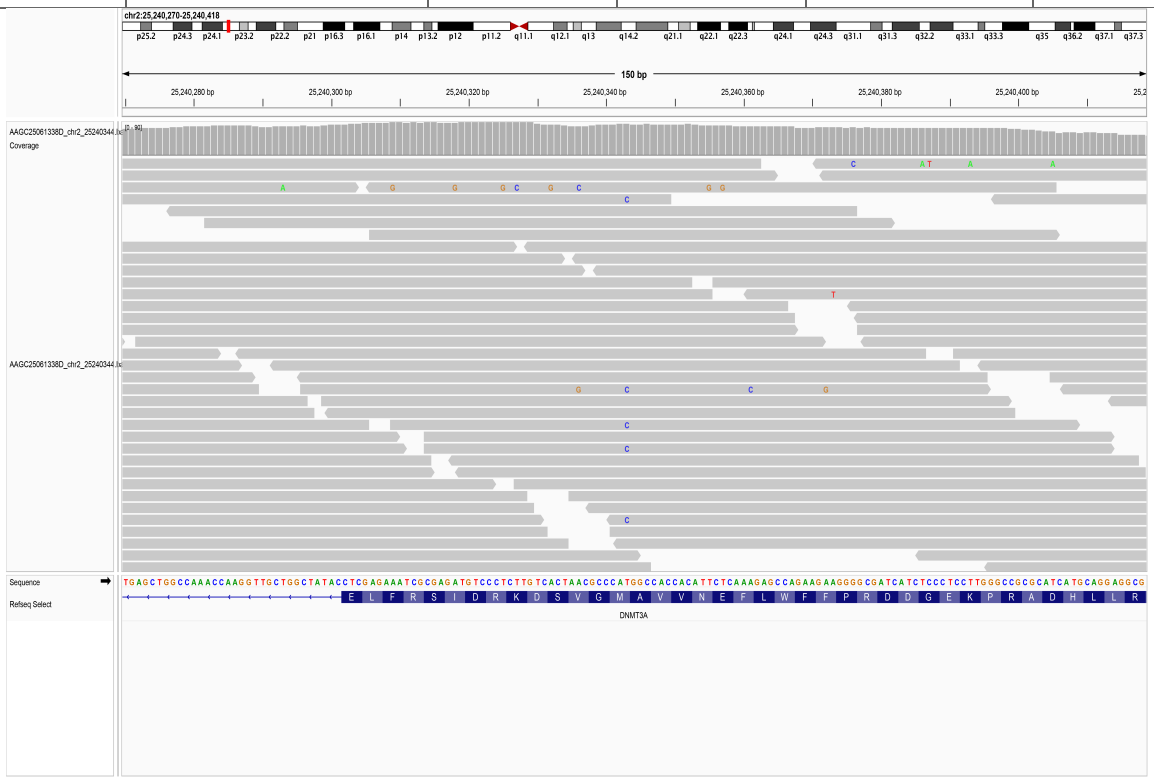
12.37. chr2_25240344_-/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136036	chr2_25240344_-/G	86	11	*DNMT3A*	frameshift_variant



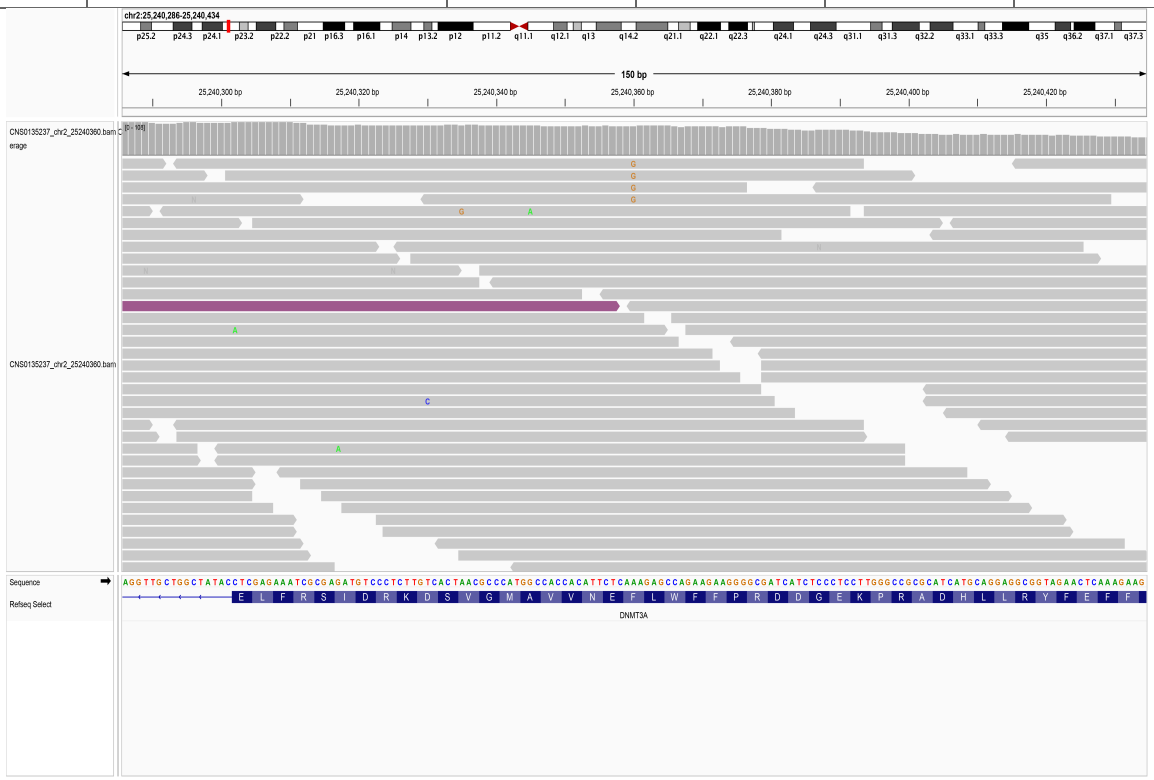
12.38. chr2_25240344_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061338D	chr2_25240344_T/C	72	7	*DNMT3A*	frameshift_variant



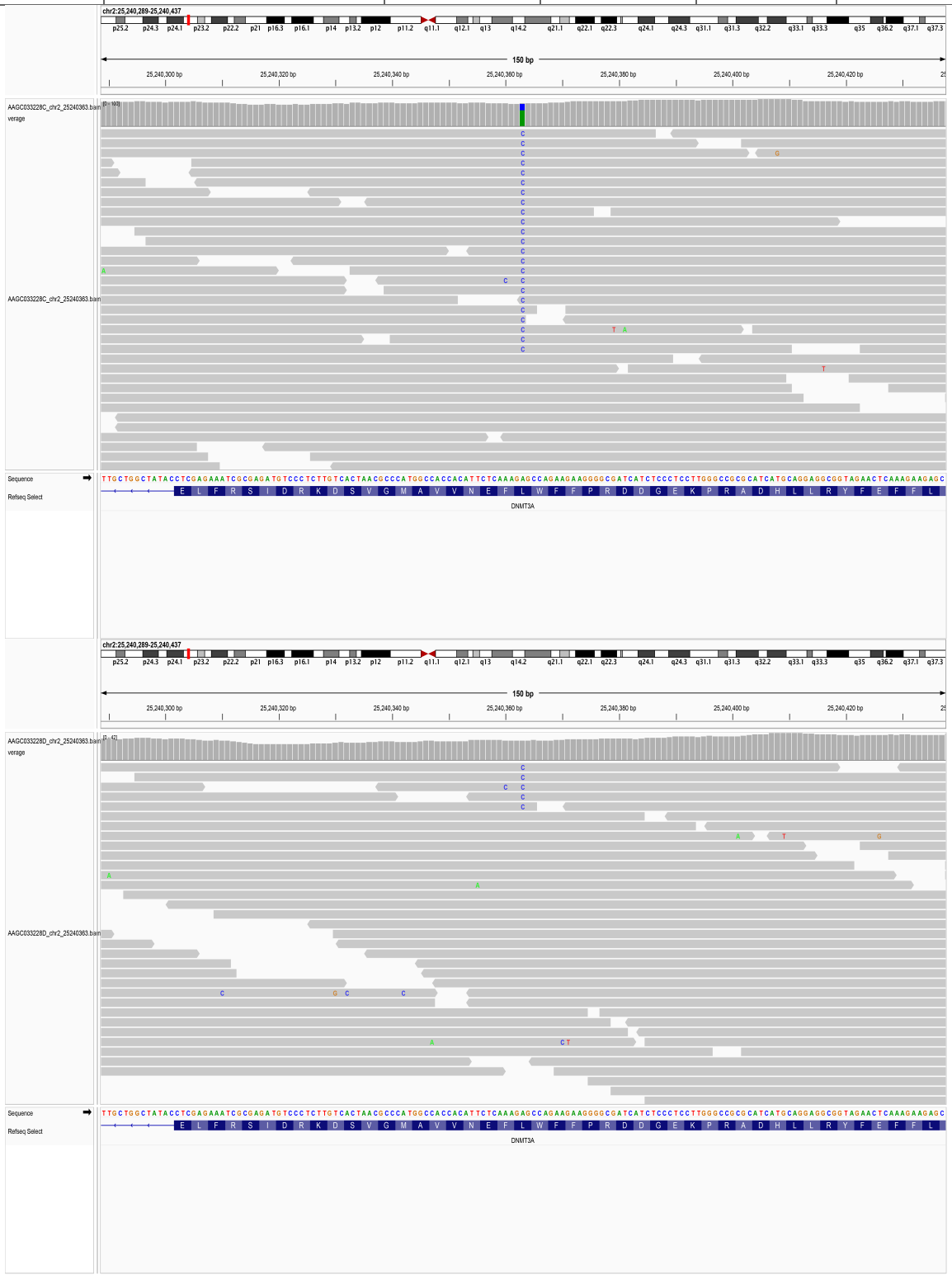
12.39. chr2_25240360_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135237	chr2_25240360_A/G	89	4	*DNMT3A*	missense_variant



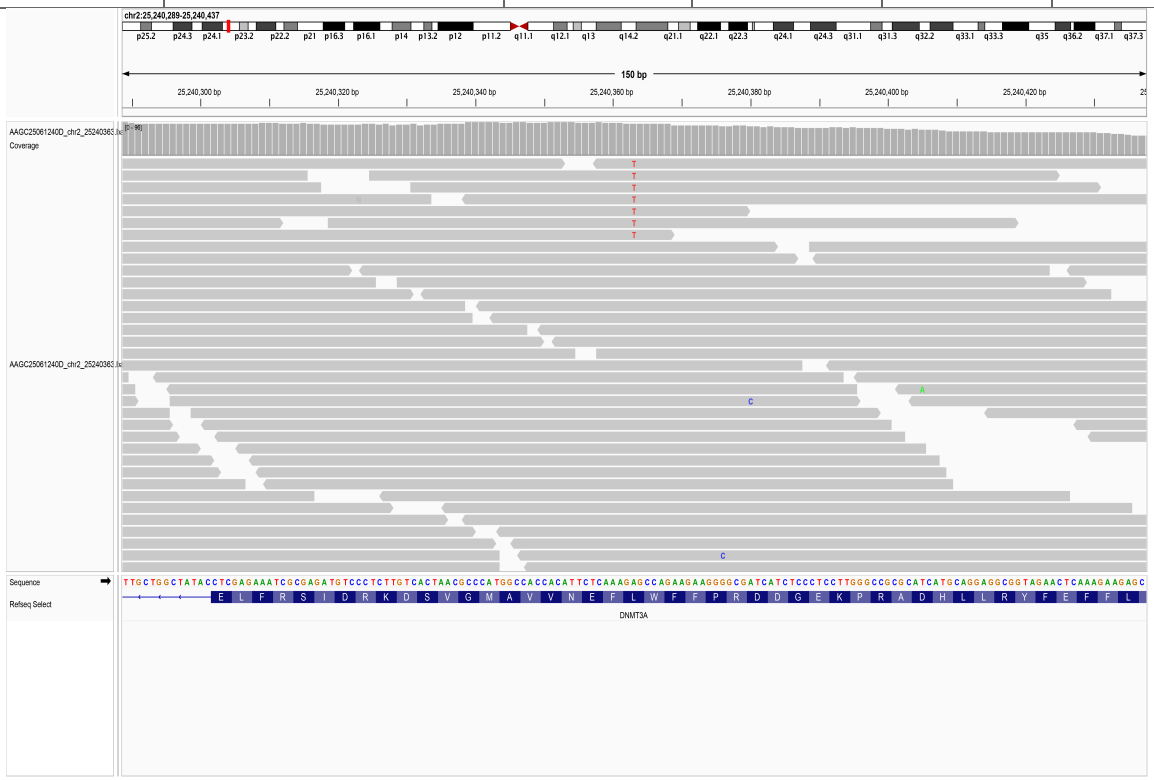
12.40. chr2_25240363_A/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033228C	chr2_25240363_A/C	57	22	*DNMT3A*	missense_variant
AAGC033228D	chr2_25240363_A/C	23	5	*DNMT3A*	missense_variant



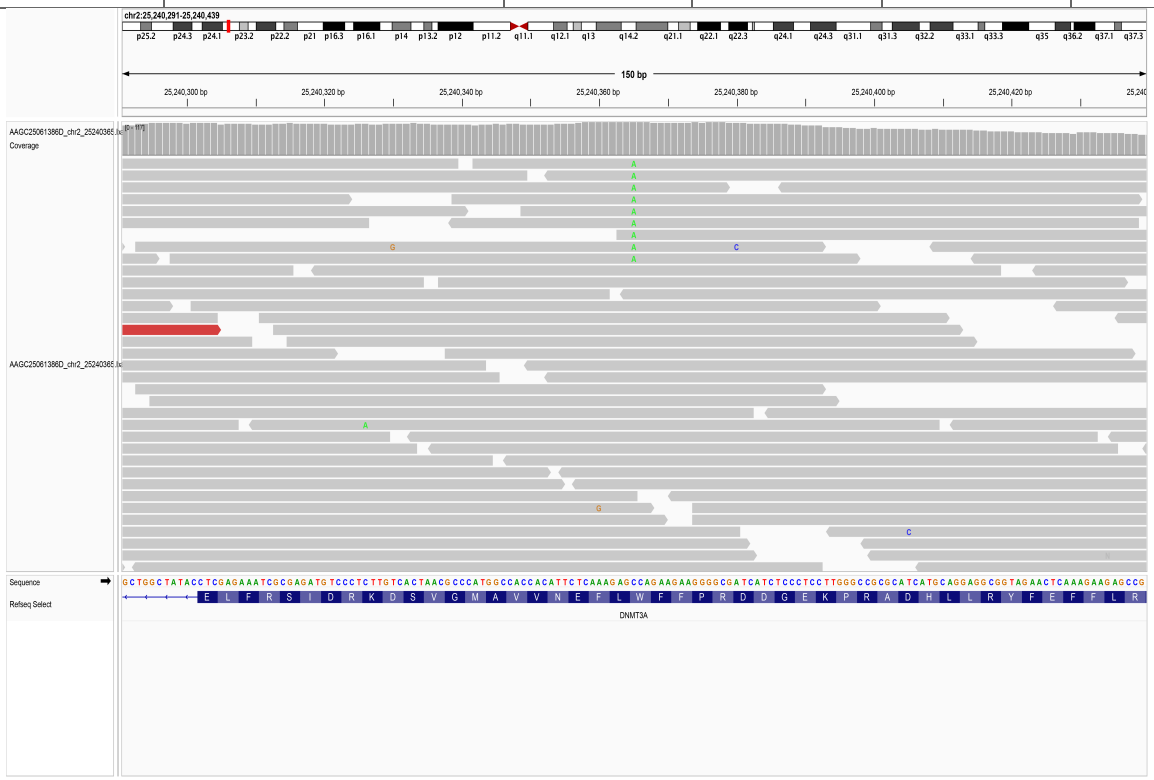
12.41. chr2_25240363_A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061240D	chr2_25240363_A/T	81	7	*DNMT3A*	missense_variant



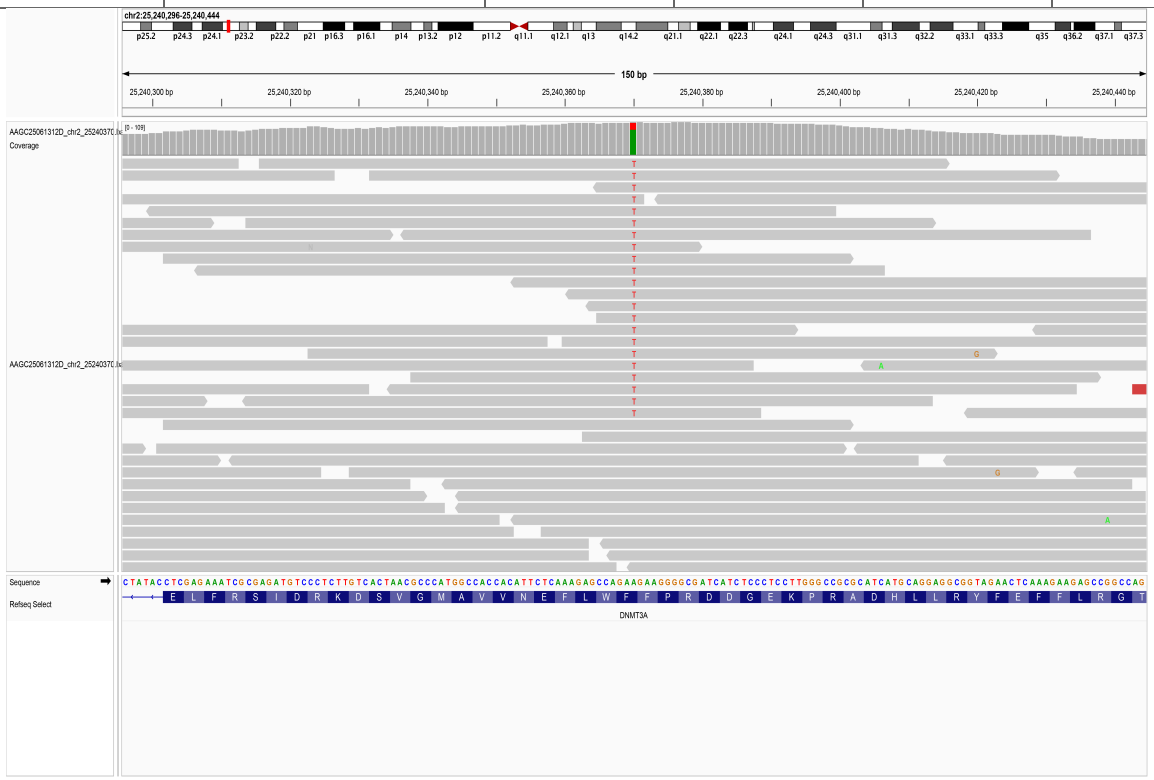
12.42. chr2_25240365_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061386D	chr2_25240365_C/A	106	9	*DNMT3A*	missense_variant



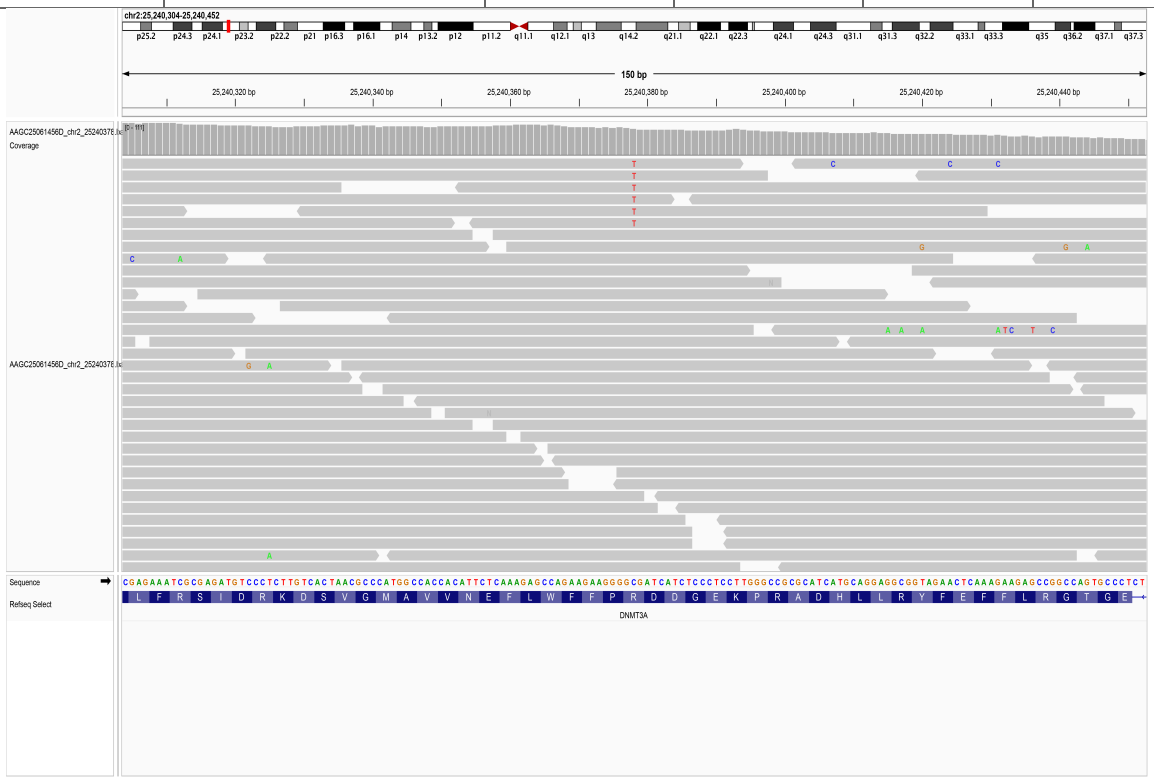
12.43. chr2_25240370_A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061312D	chr2_25240370_A/T	84	21	*DNMT3A*	missense_variant



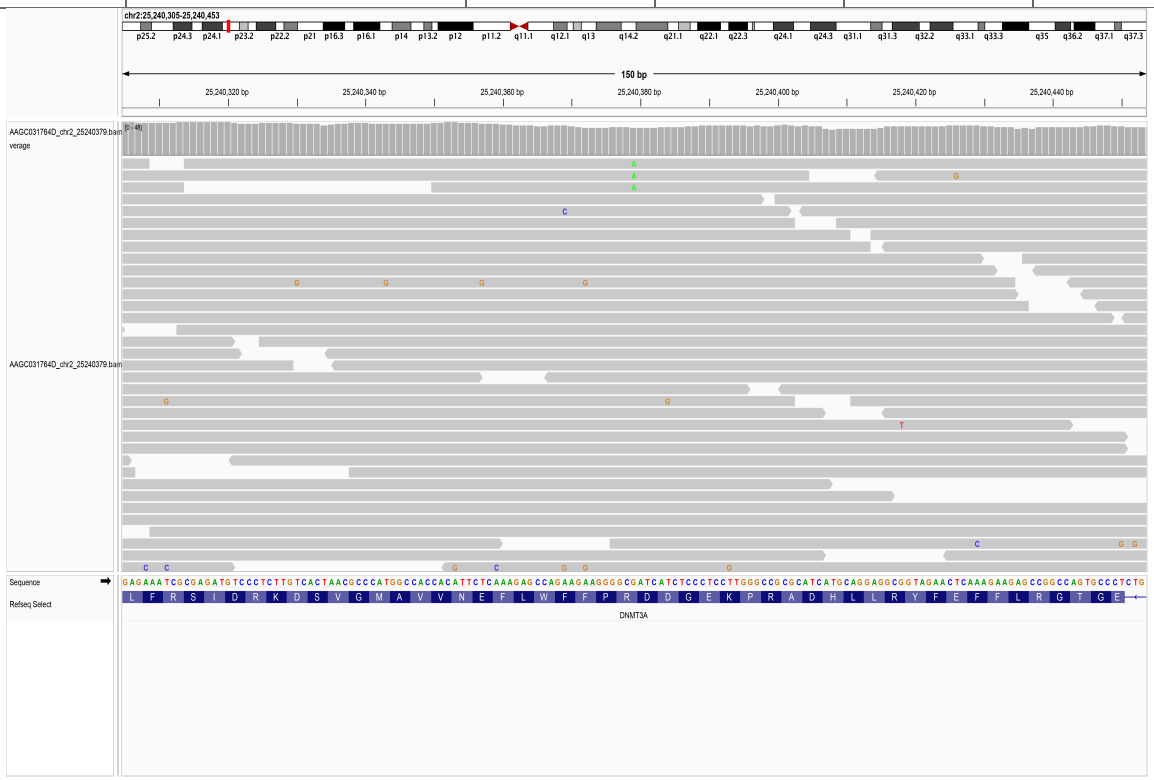
12.44. chr2_25240378_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061456D	chr2_25240378_C/T	77	6	*DNMT3A*	missense_variant



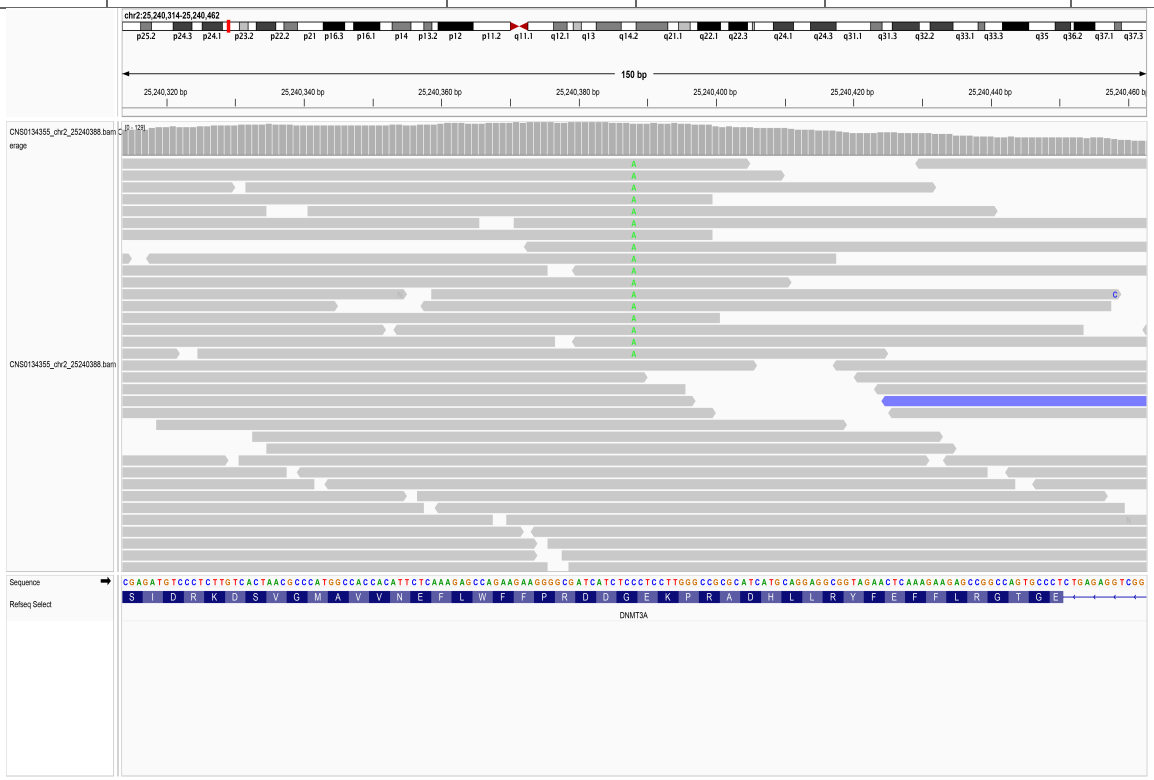
12.45. chr2_25240379_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC031764D	chr2_25240379_G/A	33	3	*DNMT3A*	missense_variant



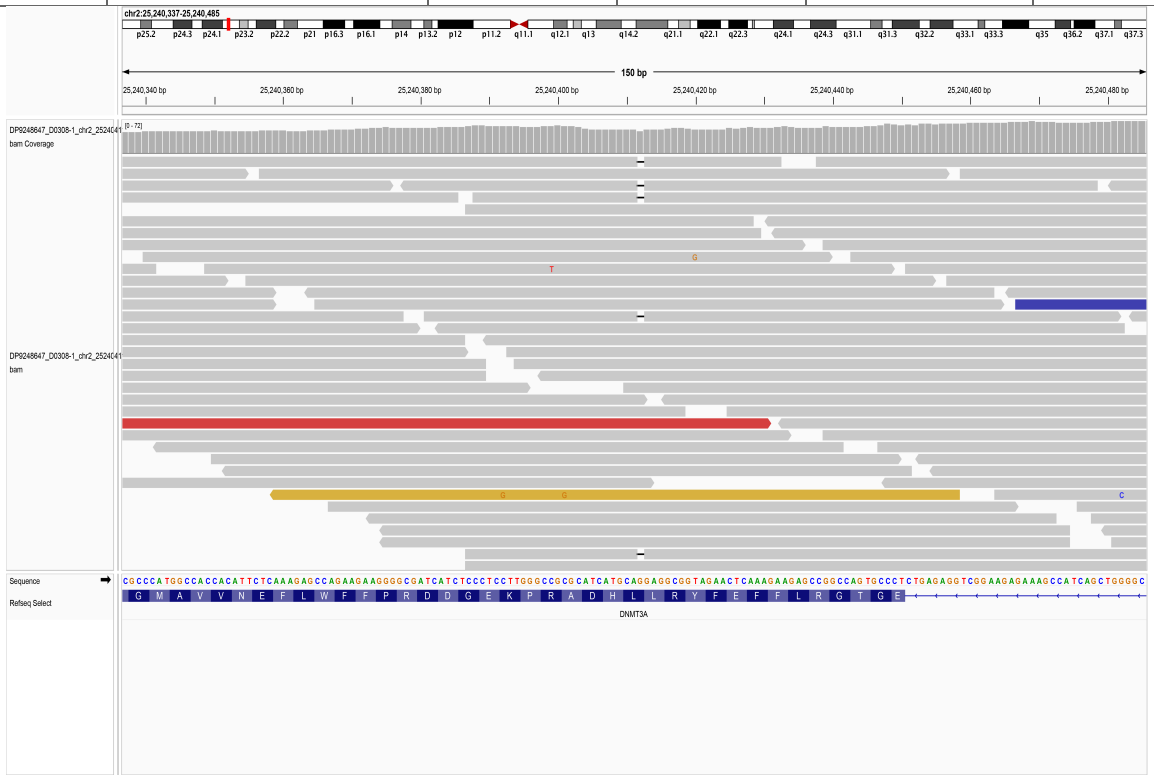
12.46. chr2_25240388_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134355	chr2_25240388_C/A	105	17	*DNMT3A*	stop_gained



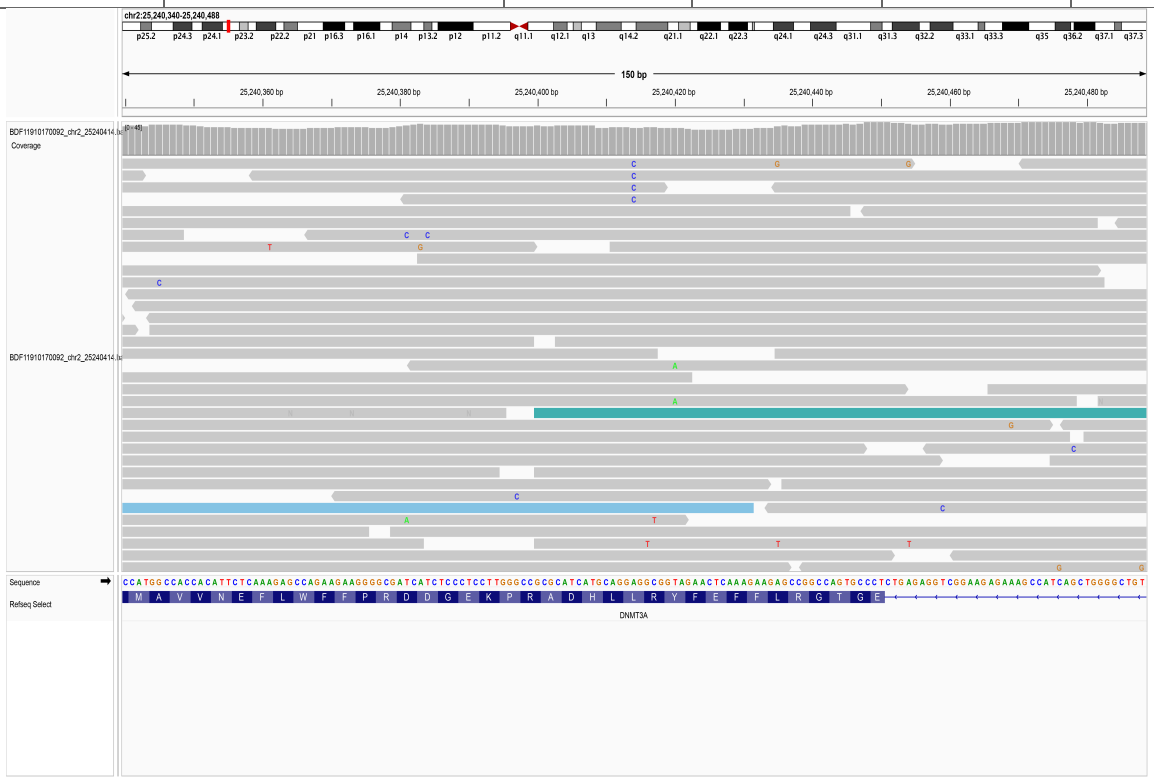
12.47. chr2_25240412_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
DP9248647_D0308-1	chr2_25240412_G/-	46	5	*DNMT3A*	frameshift_variant



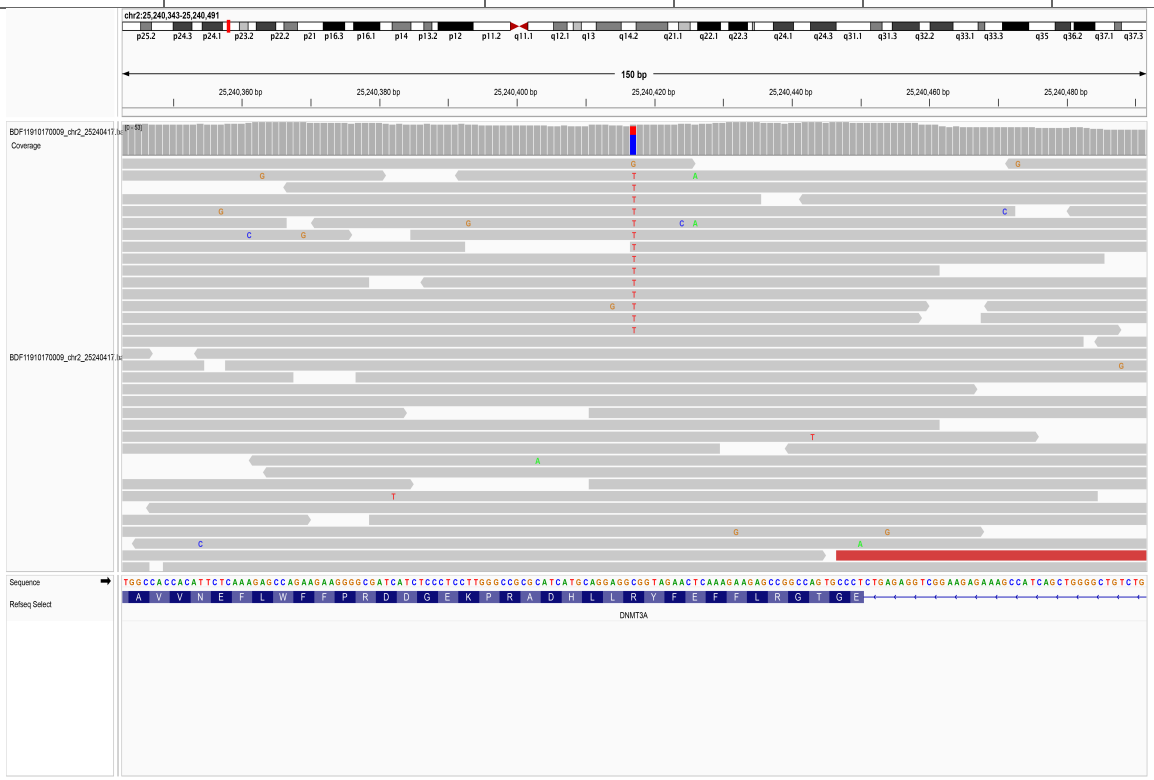
12.48. chr2_25240414_A/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170092	chr2_25240414_A/C	30	4	*DNMT3A*	missense_variant



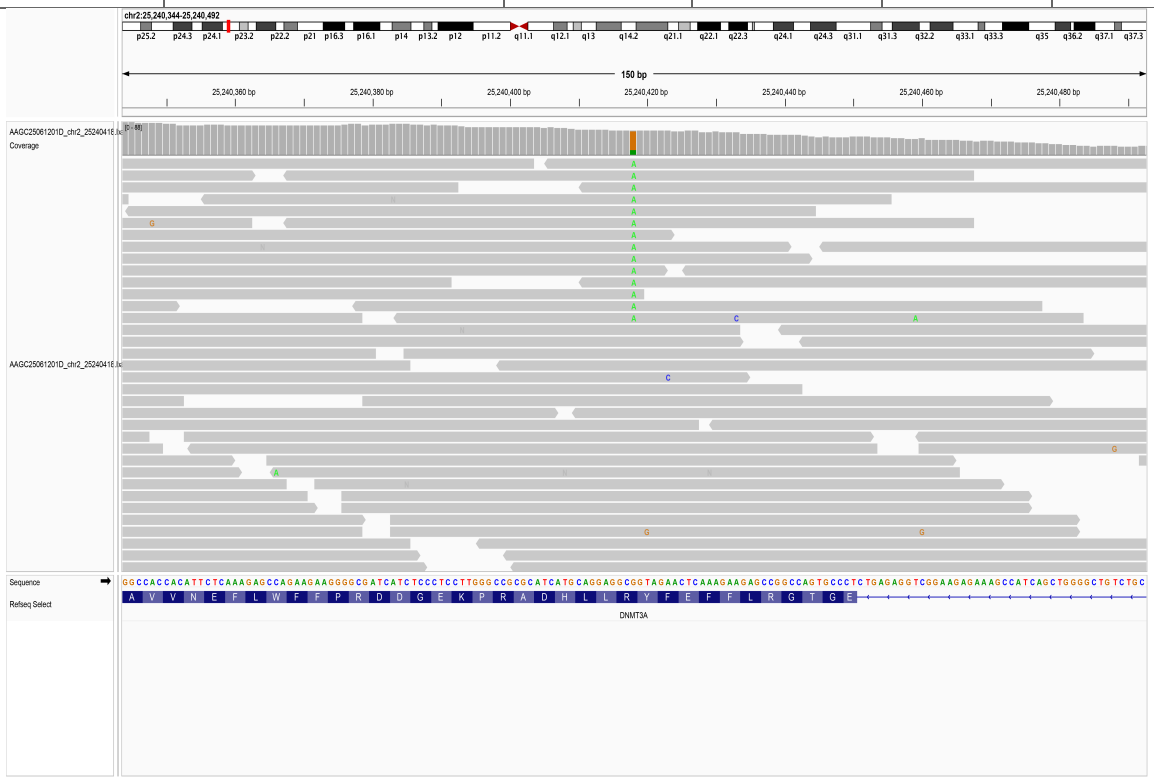
12.49. chr2_25240417_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170009	chr2_25240417_C/T	31	13	*DNMT3A*	missense_variant



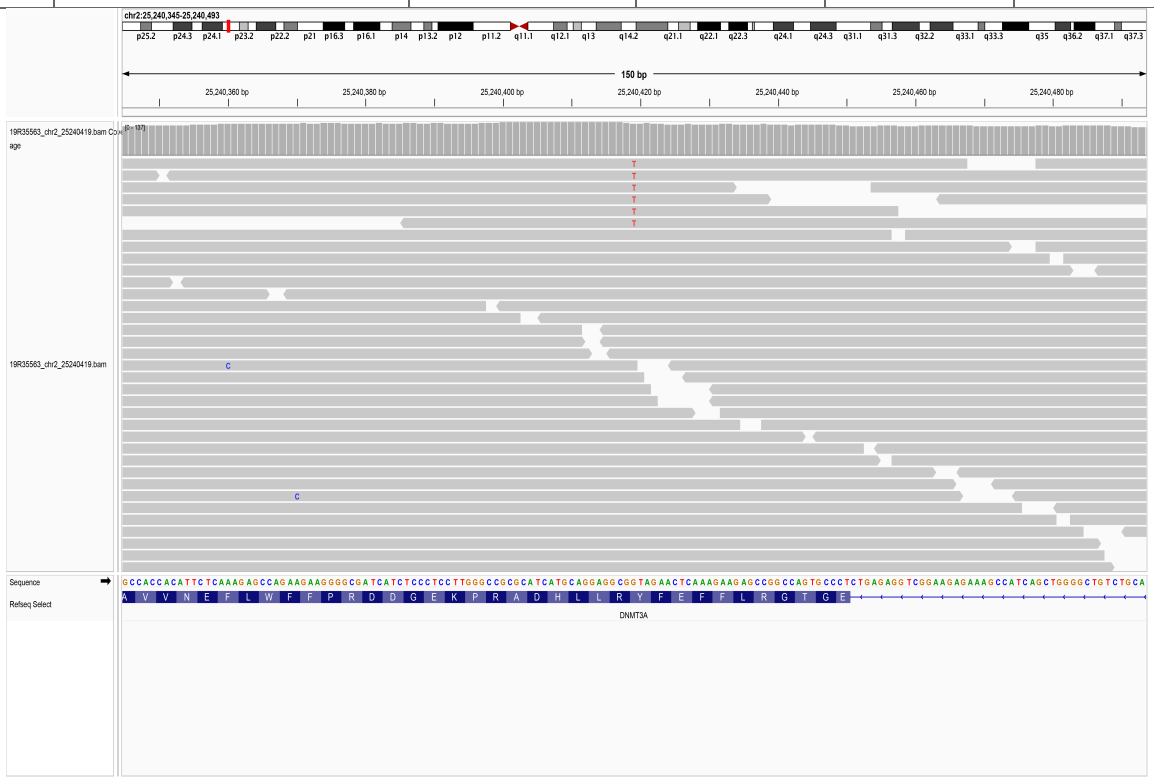
12.50. chr2_25240418_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061201D	chr2_25240418_G/A	49	14	*DNMT3A*	missense_variant



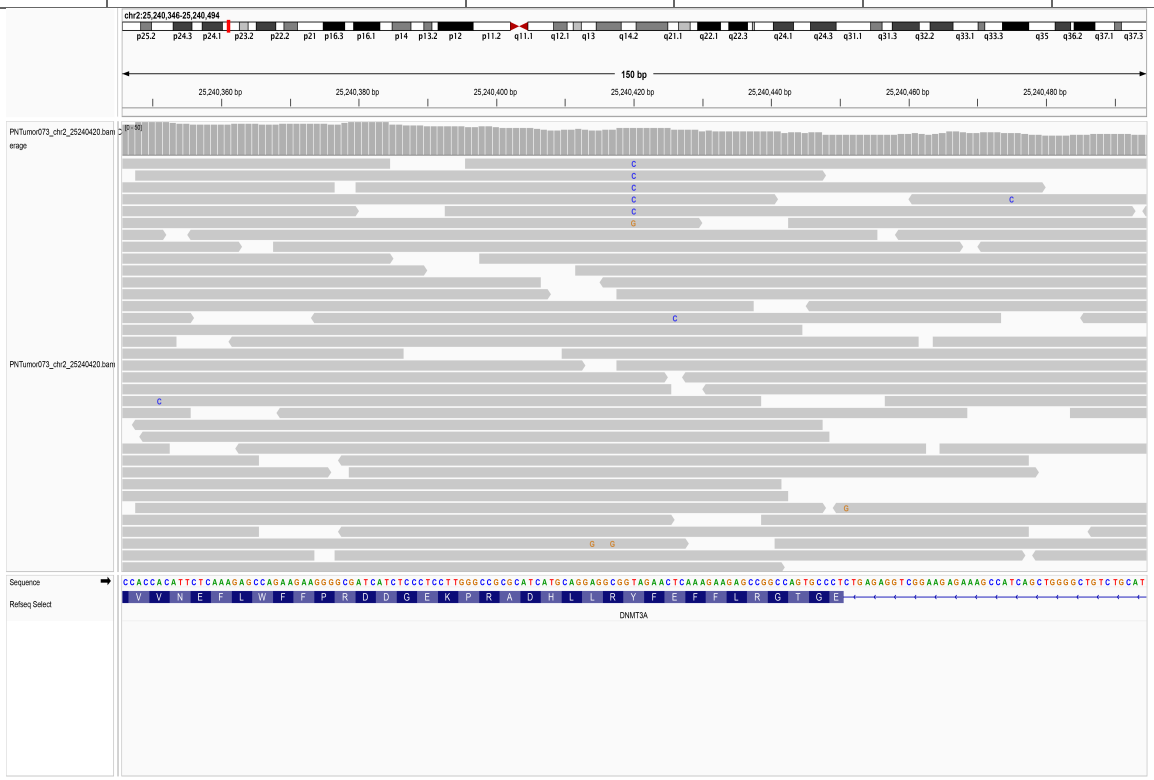
12.51. chr2_25240419_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R35563	chr2_25240419_G/T	122	6	*DNMT3A*	stop_gained



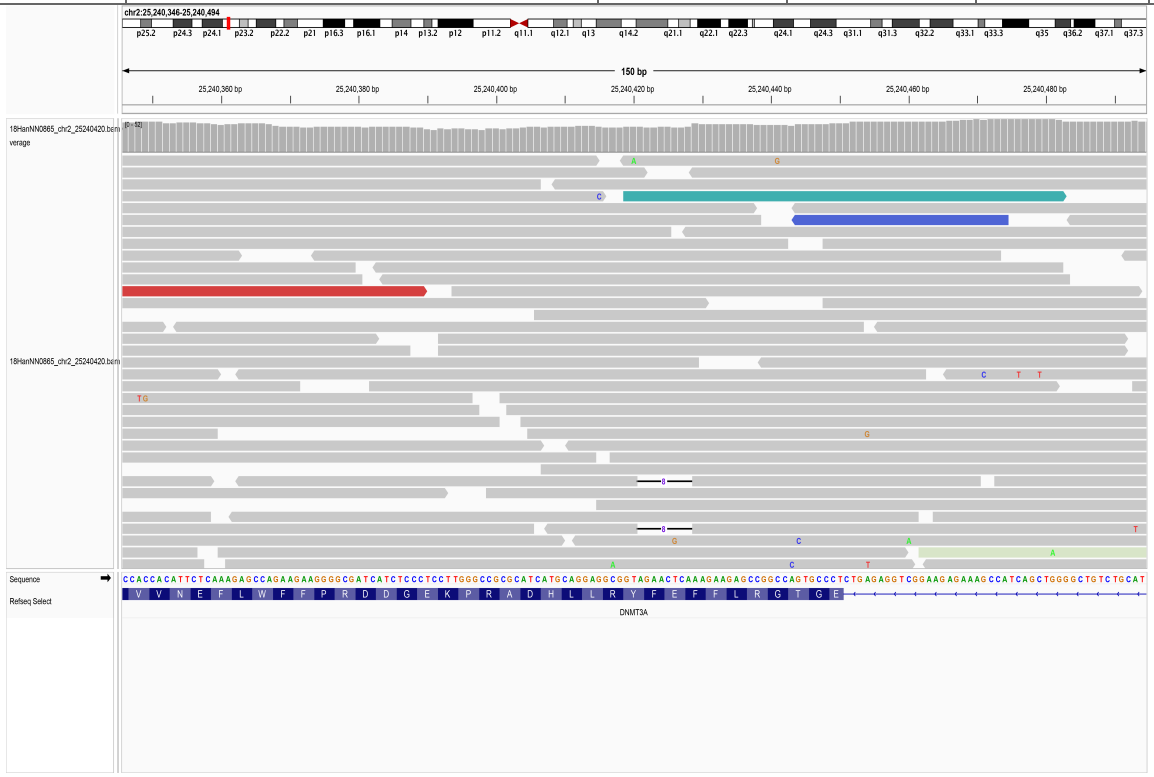
12.52. chr2_25240420_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
PNTumor073	chr2_25240420_T/C	35	5	*DNMT3A*	missense_variant



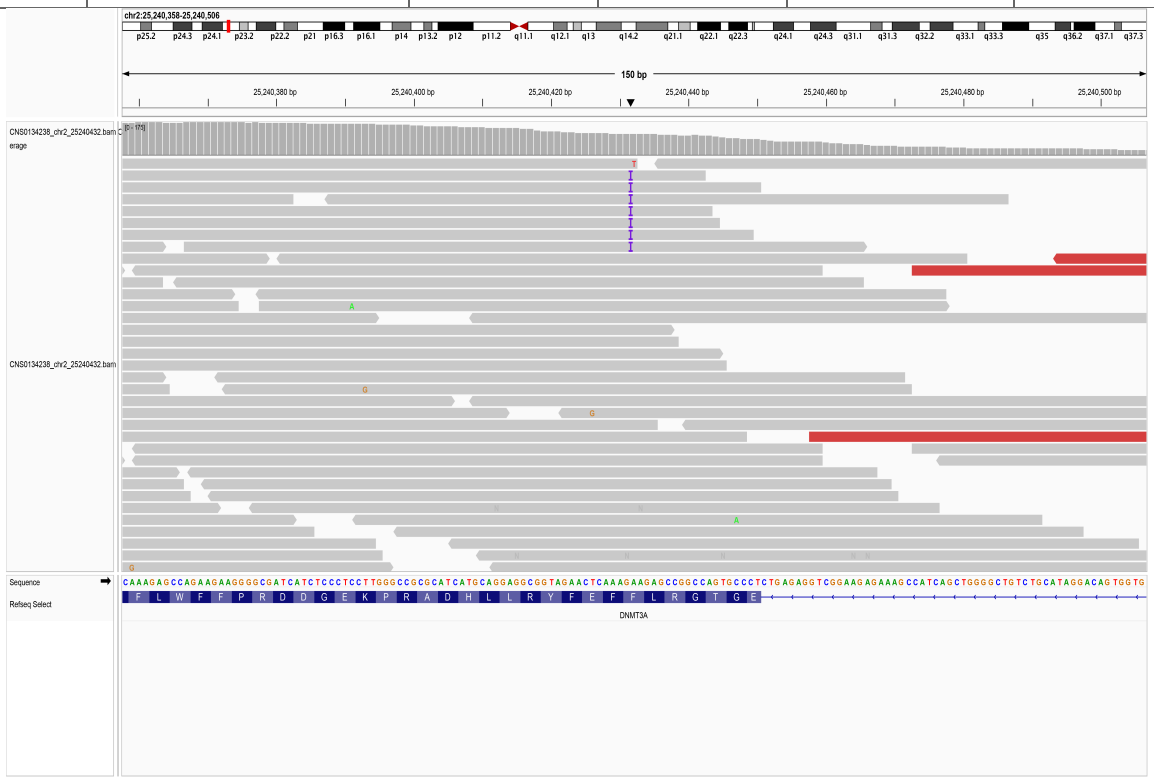
12.53. chr2_25240421_AGAACTCA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0865	chr2_25240421_AGAACTCA/-	39	5	*DNMT3A*	frameshift_variant



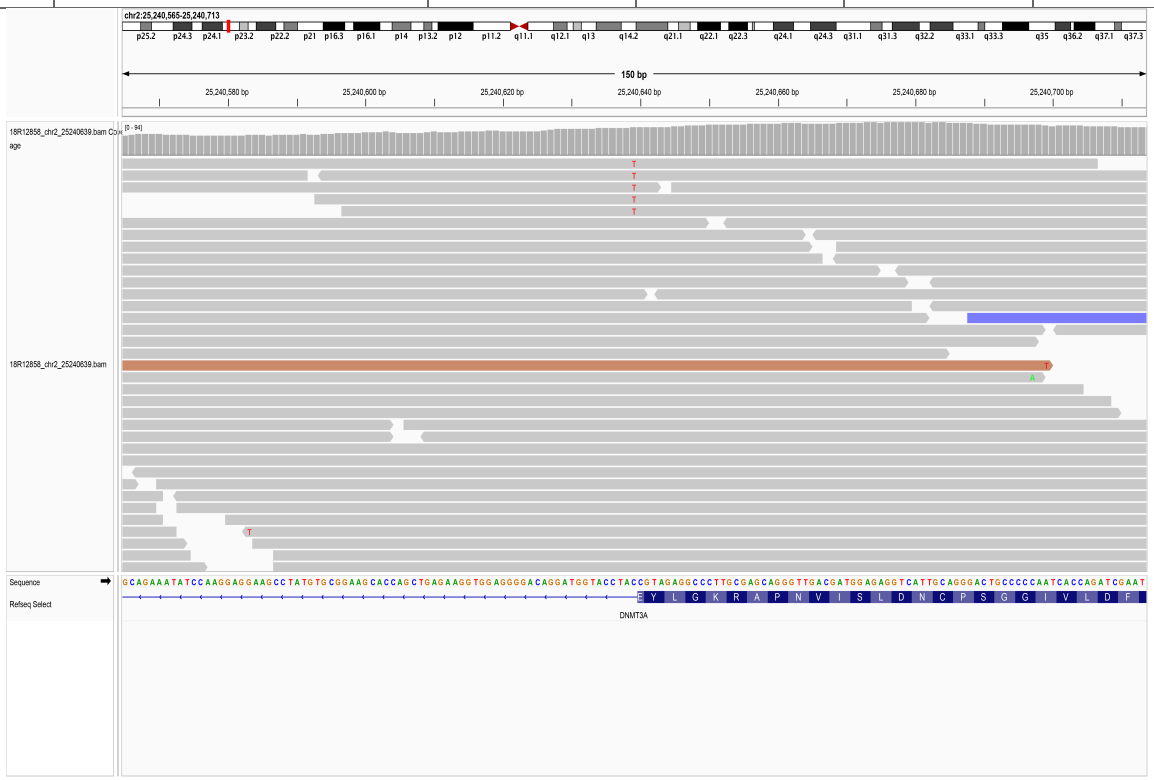
12.54. chr2_25240432_-/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134238	chr2_25240432_-/T	101	8	*DNMT3A*	frameshift_variant



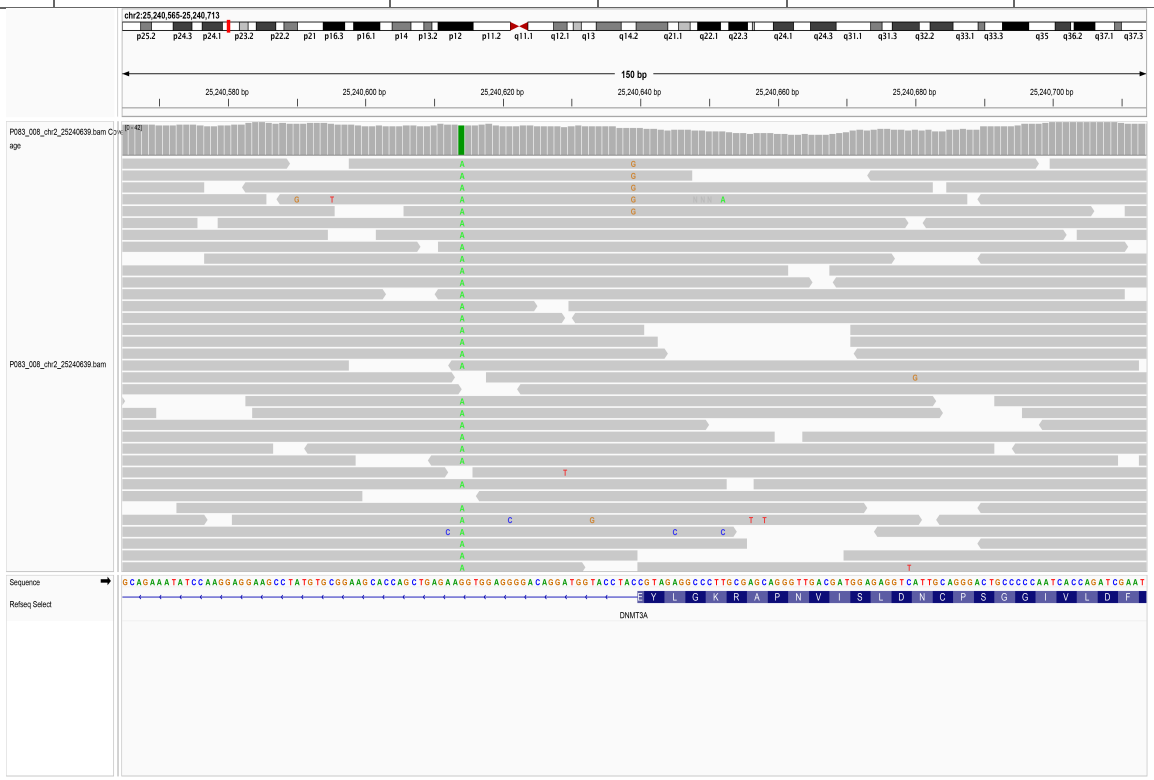
12.55. chr2_25240639_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12858	chr2_25240639_C/T	72	5	*DNMT3A*	splice_donor_variant



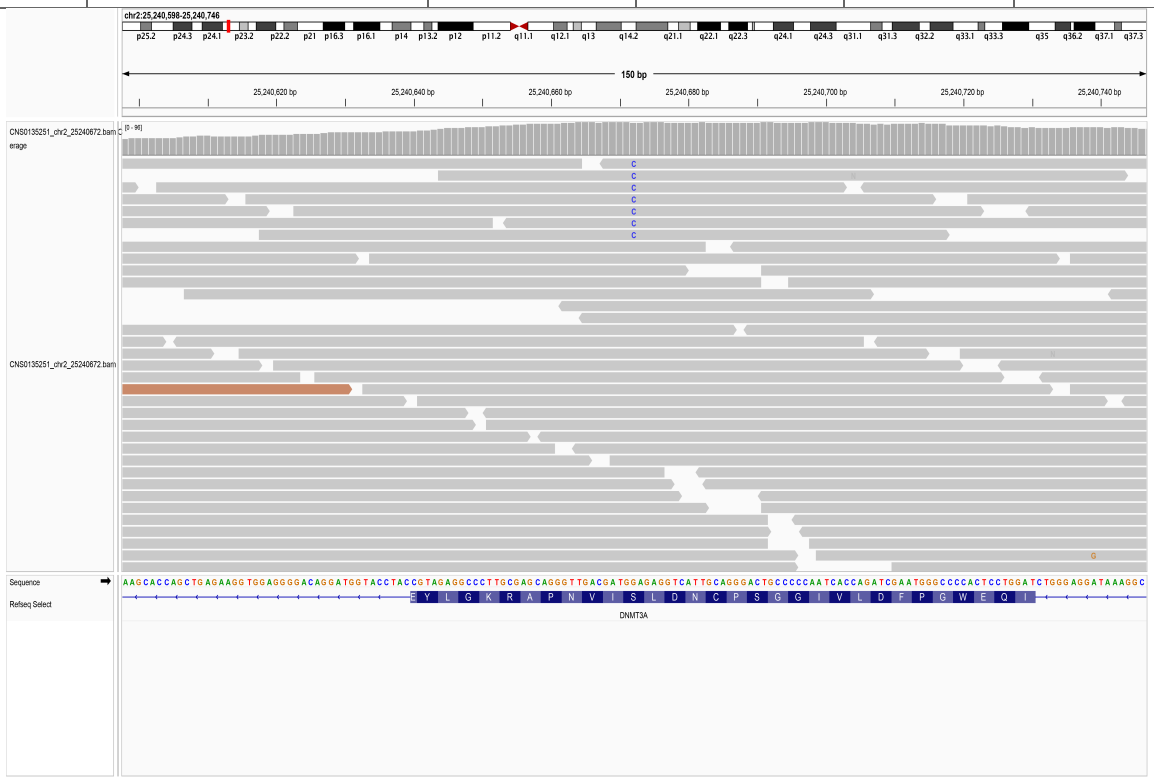
12.56. chr2_25240639_C/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
P083_008	chr2_25240639_C/G	27	5	*DNMT3A*	splice_donor_variant



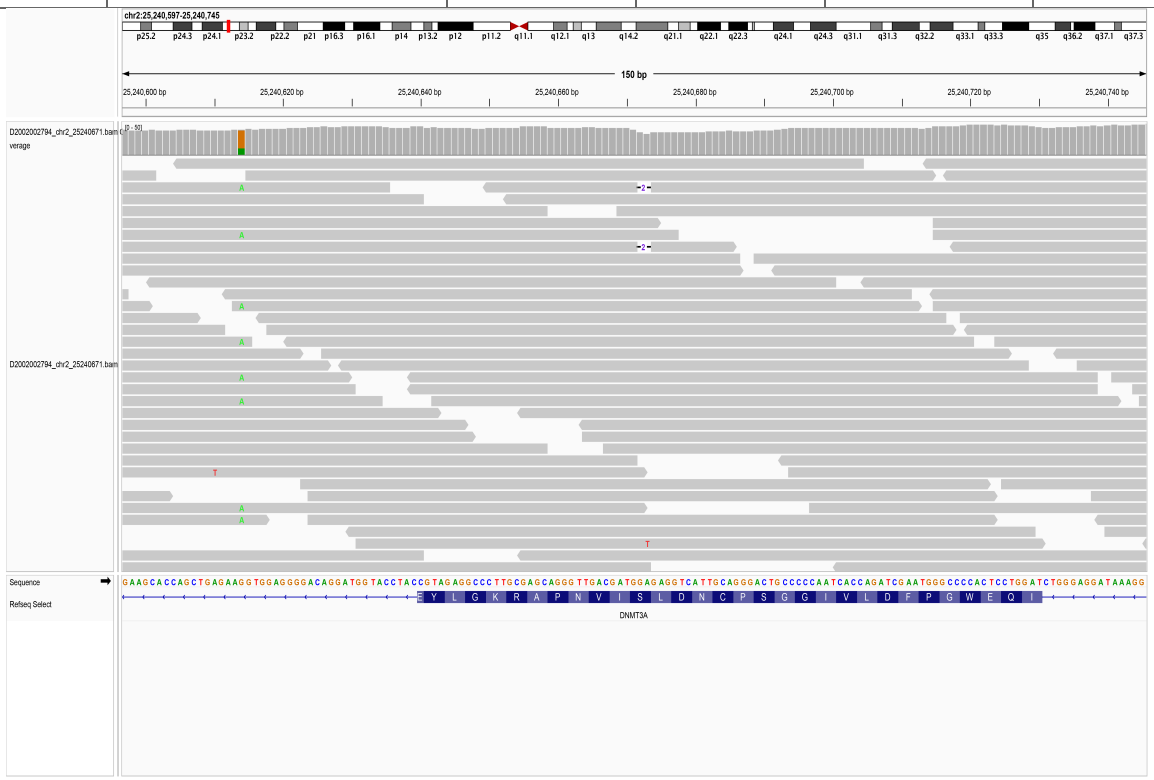
12.57. chr2_25240672_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135251	chr2_25240672_G/C	84	7	*DNMT3A*	missense_variant



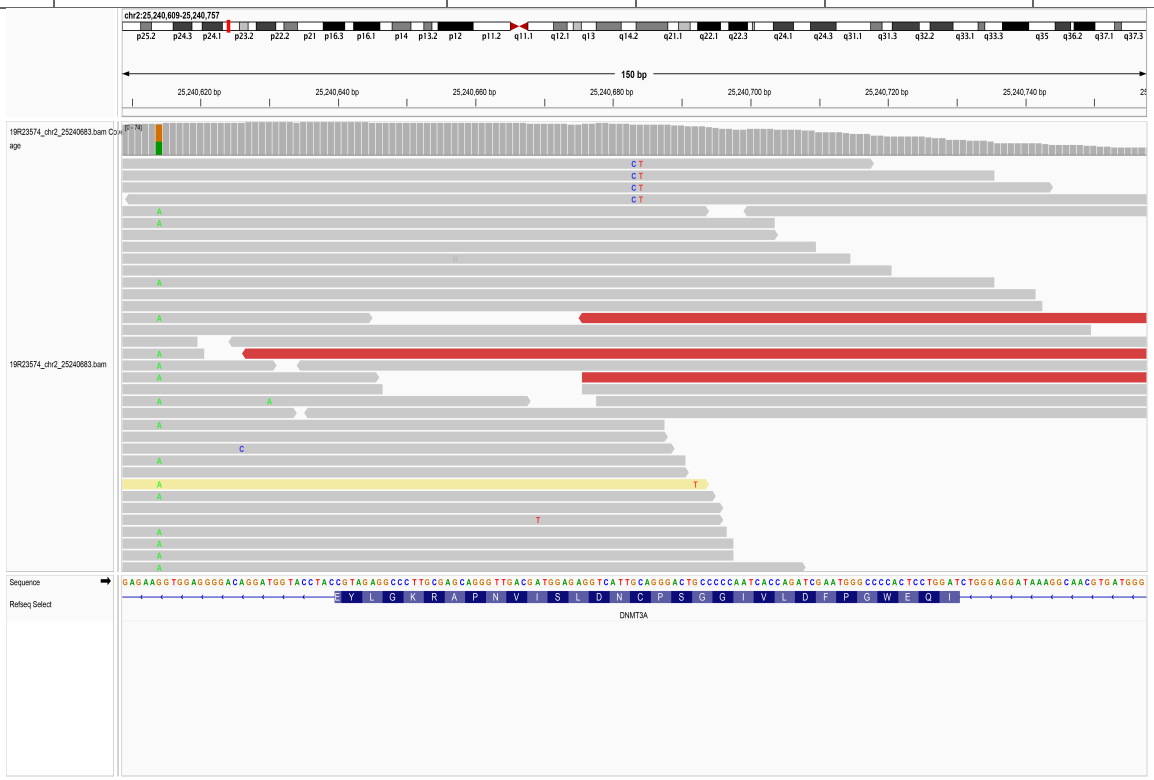
12.58. chr2_25240672_GA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2002002794	chr2_25240672_GA/-	30	3	*DNMT3A*	frameshift_variant



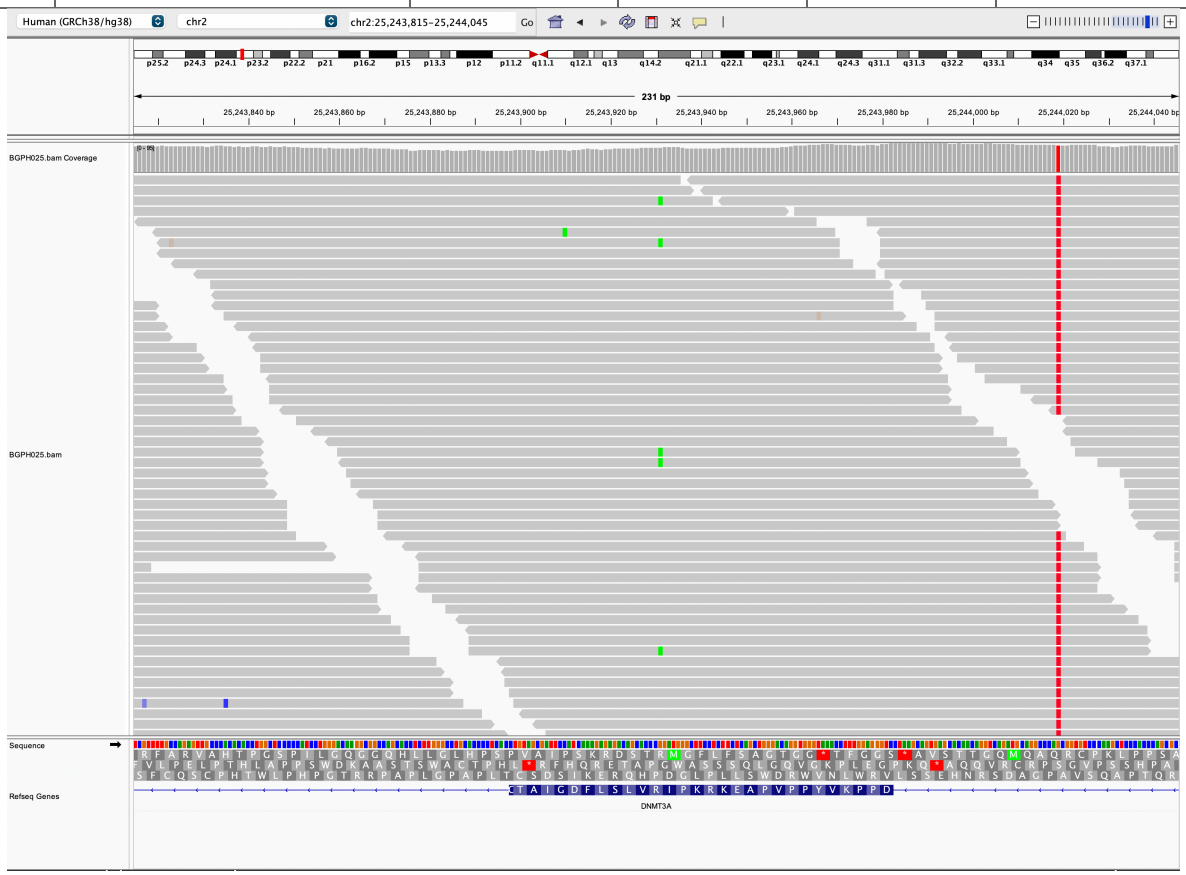
12.59. chr2_25240683_GC/CT

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23574	chr2_25240683_GC/CT	59	4	*DNMT3A*	stop_gained



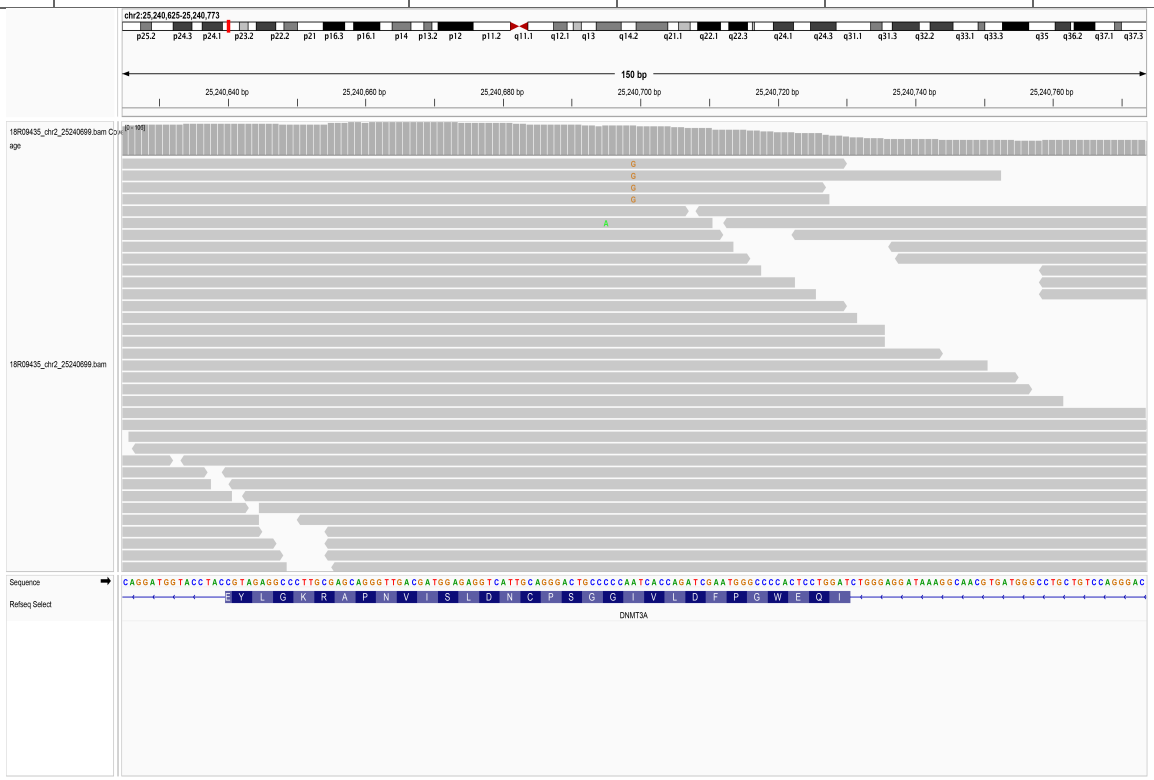
12.60. chr2_25240684_C/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BGPH025	chr2_25243931_G/A	71	8	*DNMT3A*	missense_variant



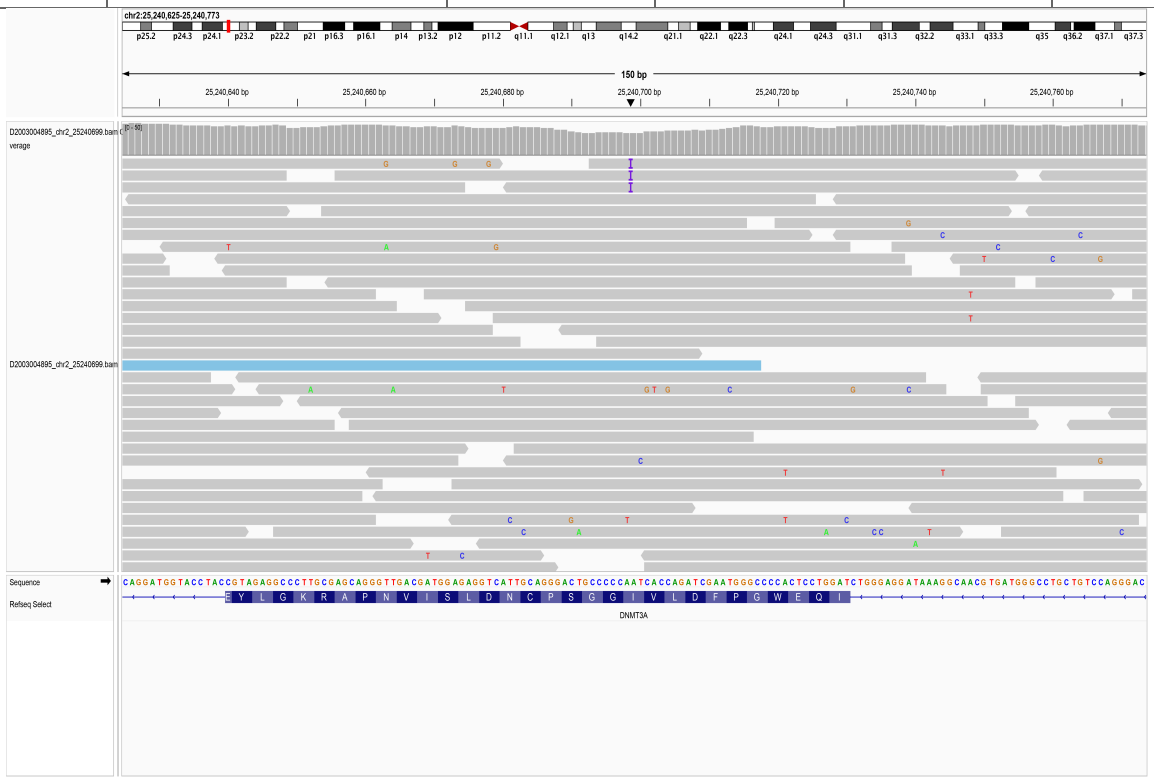
12.61. chr2_25240699_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09435	chr2_25240699_A/G	88	4	*DNMT3A*	missense_variant



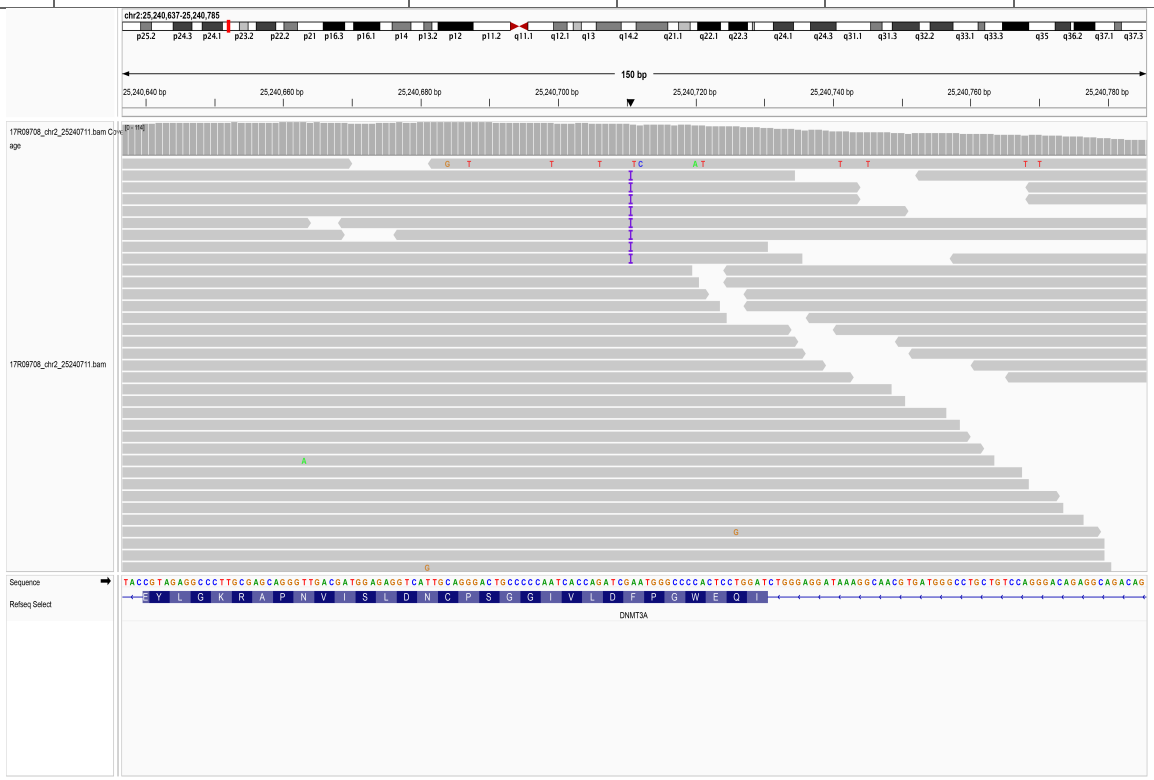
12.62. chr2_25240699_-/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2003004895	chr2_25240699_-/C	27	3	*DNMT3A*	frameshift_variant



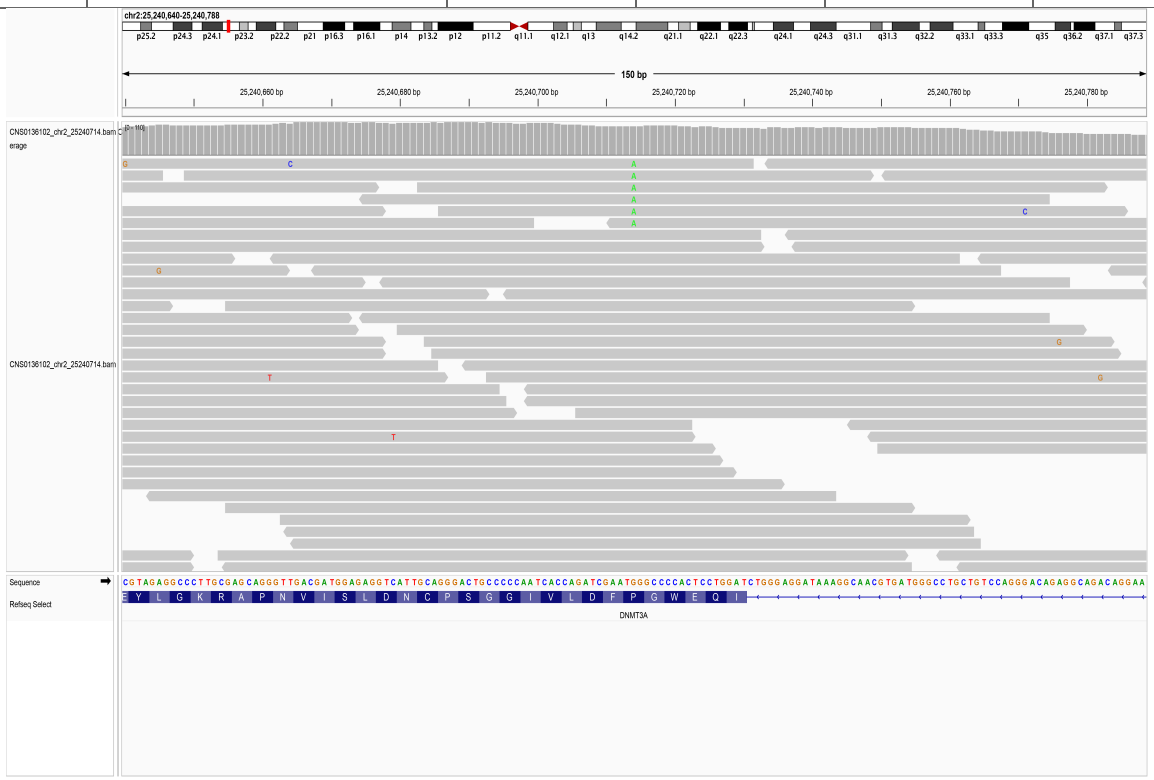
12.63. chr2_25240711_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09708	chr2_25240711_-/A	89	8	*DNMT3A*	frameshift_variant



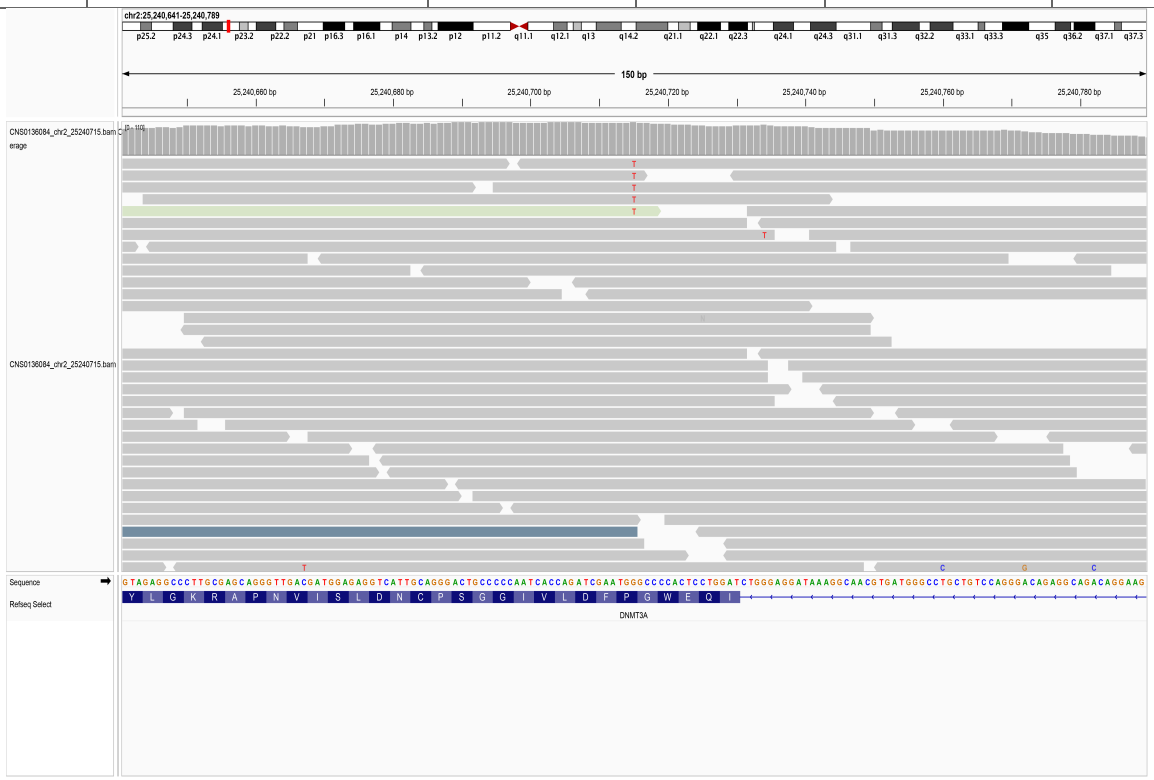
12.64. chr2_25240714_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136102	chr2_25240714_G/A	85	6	*DNMT3A*	missense_variant



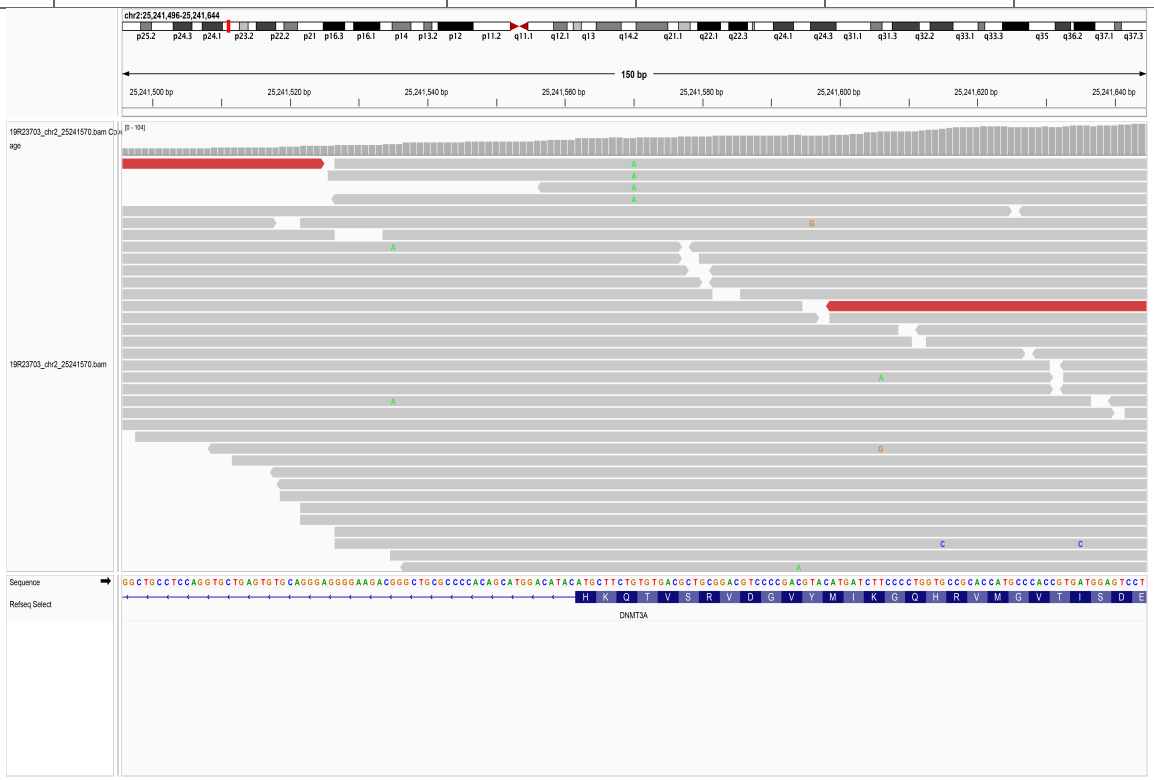
12.65. chr2_25240715_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136084	chr2_25240715_G/T	102	5	*DNMT3A*	missense_variant



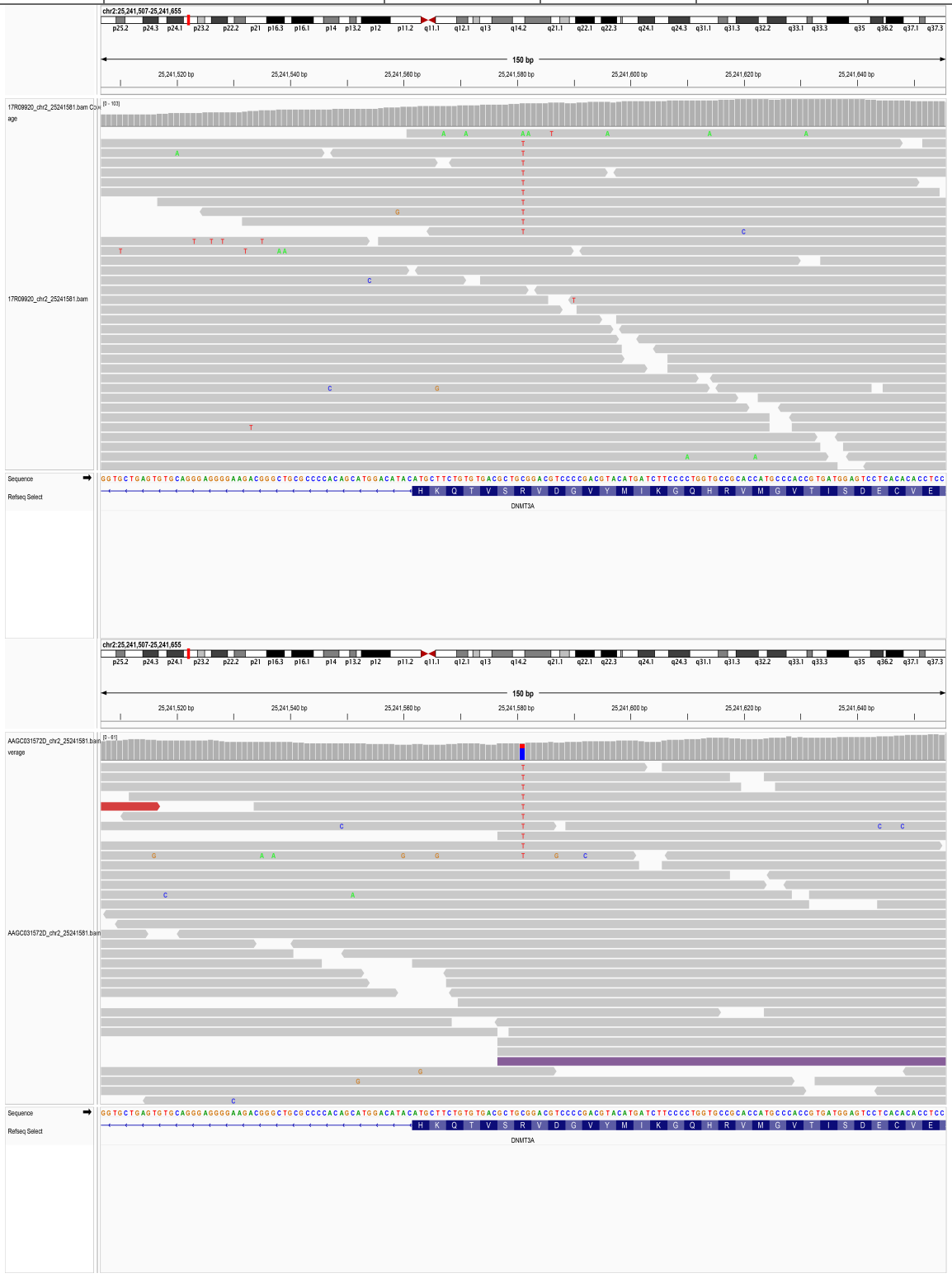
12.66. chr2_25241570_G/A

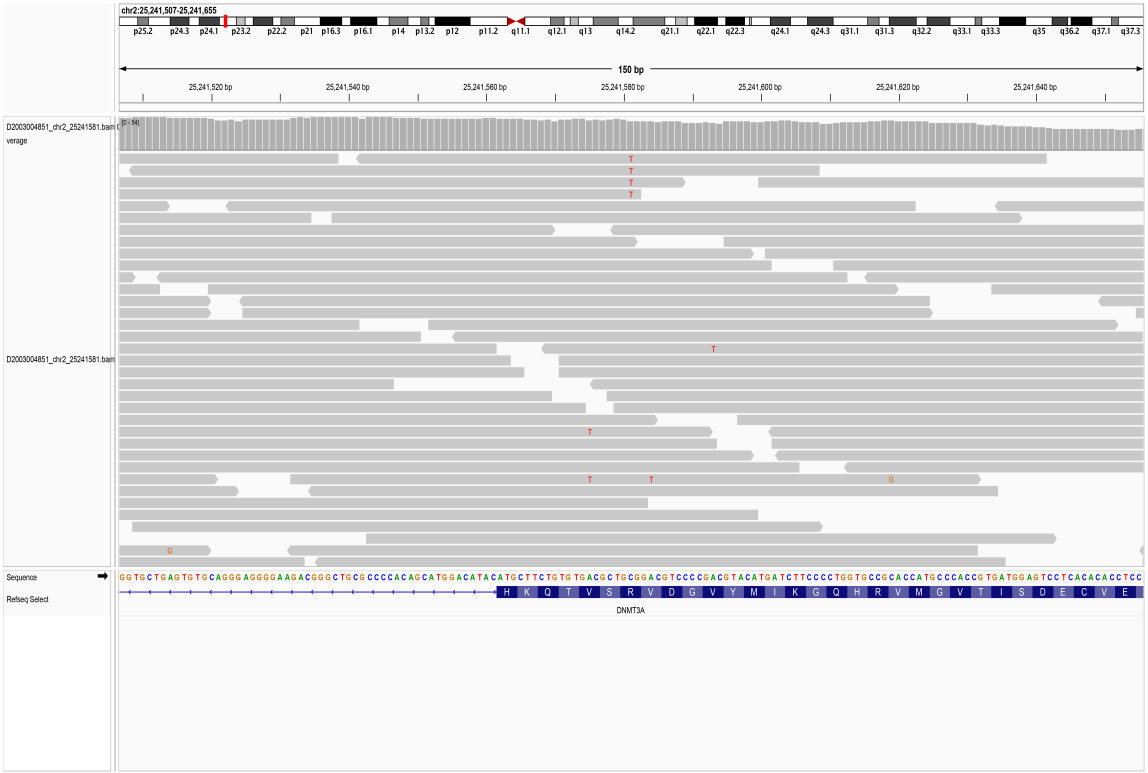
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23703	chr2_25241570_G/A	50	4	*DNMT3A*	stop_gained



12.67. chr2_25241581_C/T

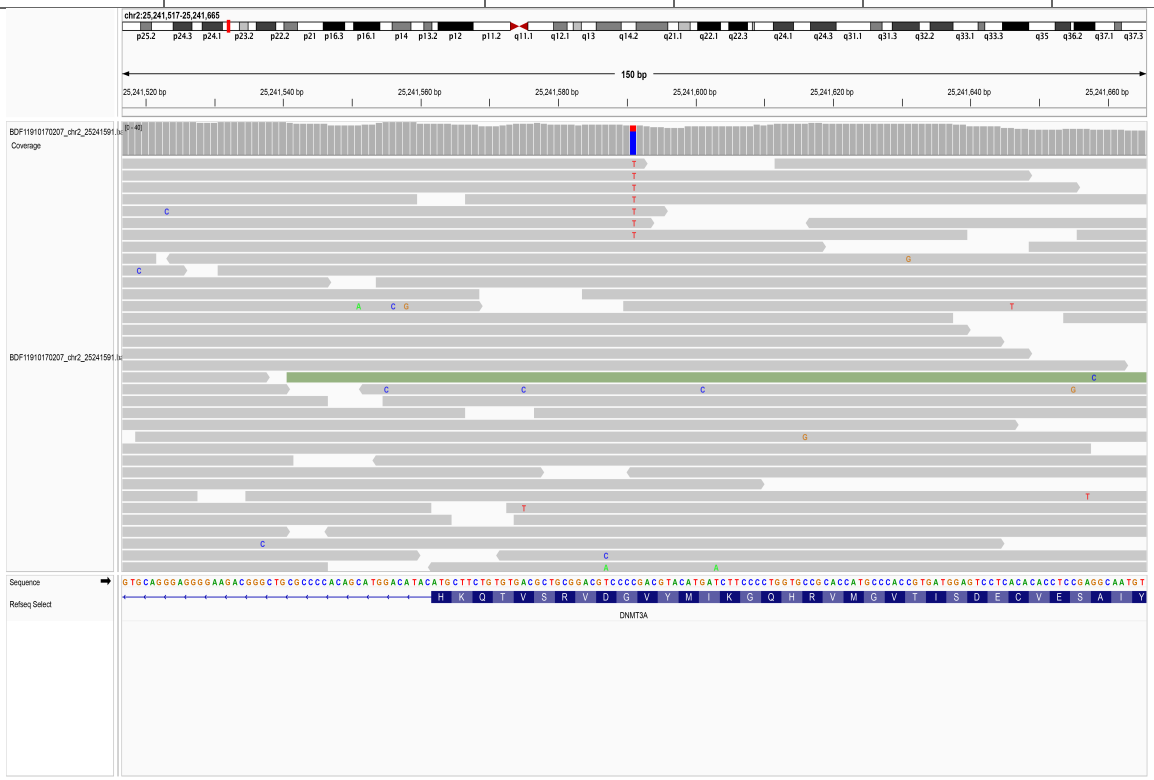
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09920	chr2_25241581_C/T	70	10	*DNMT3A*	missense_variant
AAGC031572D	chr2_25241581_C/T	27	9	*DNMT3A*	missense_variant
D2003004851	chr2_25241581_C/T	42	4	*DNMT3A*	missense_variant




chr2:25,241,507-25,241,655
150 bp
25,241,520 bp
25,241,540 bp
25,241,560 bp
25,241,580 bp
25,241,600 bp
25,241,620 bp
25,241,640 bp
D2003004851_chr2_25241581.bam (
verage
D2003004851_chr2_25241581.bam
Sequence
Refseq Select
DNMT3A

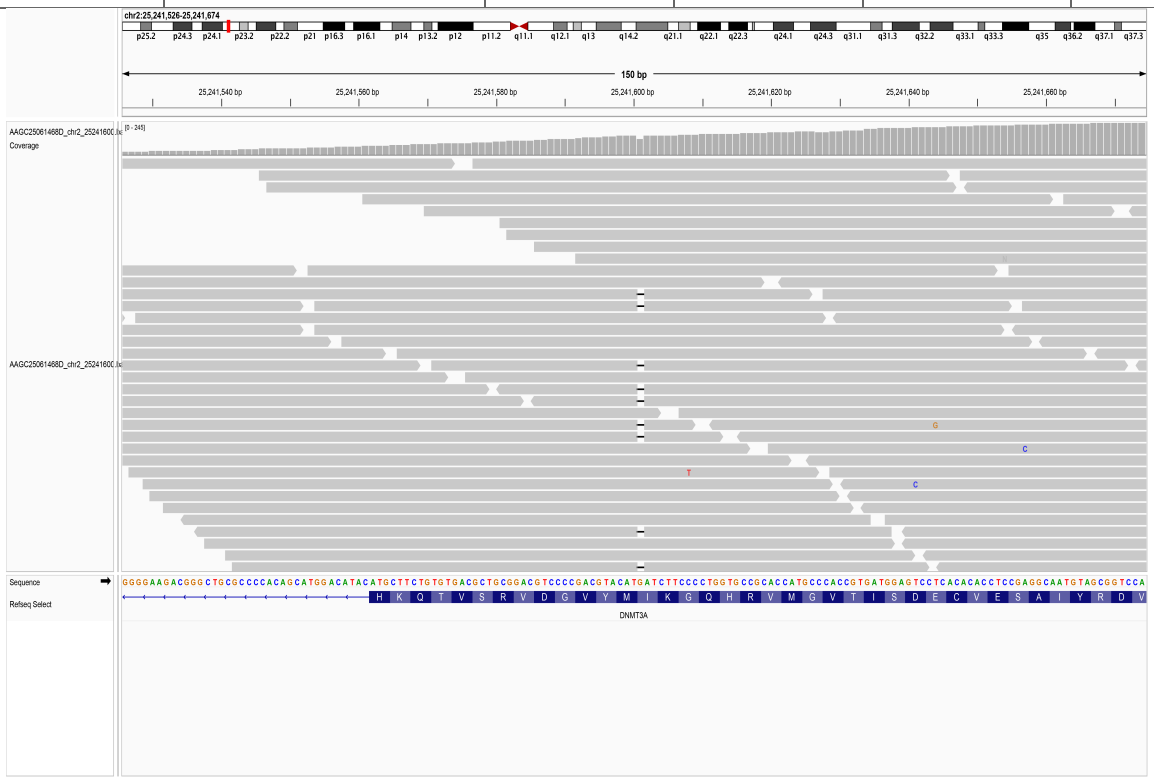
12.68. chr2_25241591_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170207	chr2_25241591_C/T	26	7	*DNMT3A*	missense_variant



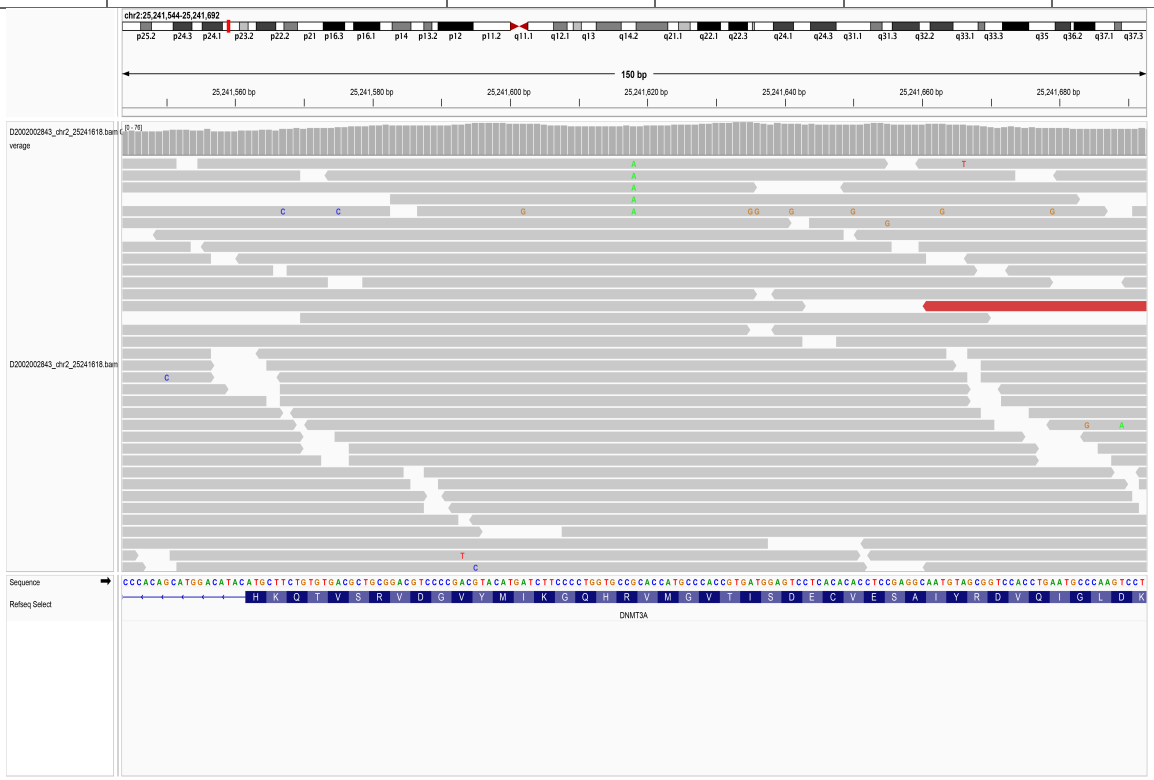
12.69. chr2_25241601_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061468D	chr2_25241601_G/-	119	20	*DNMT3A*	frameshift_variant



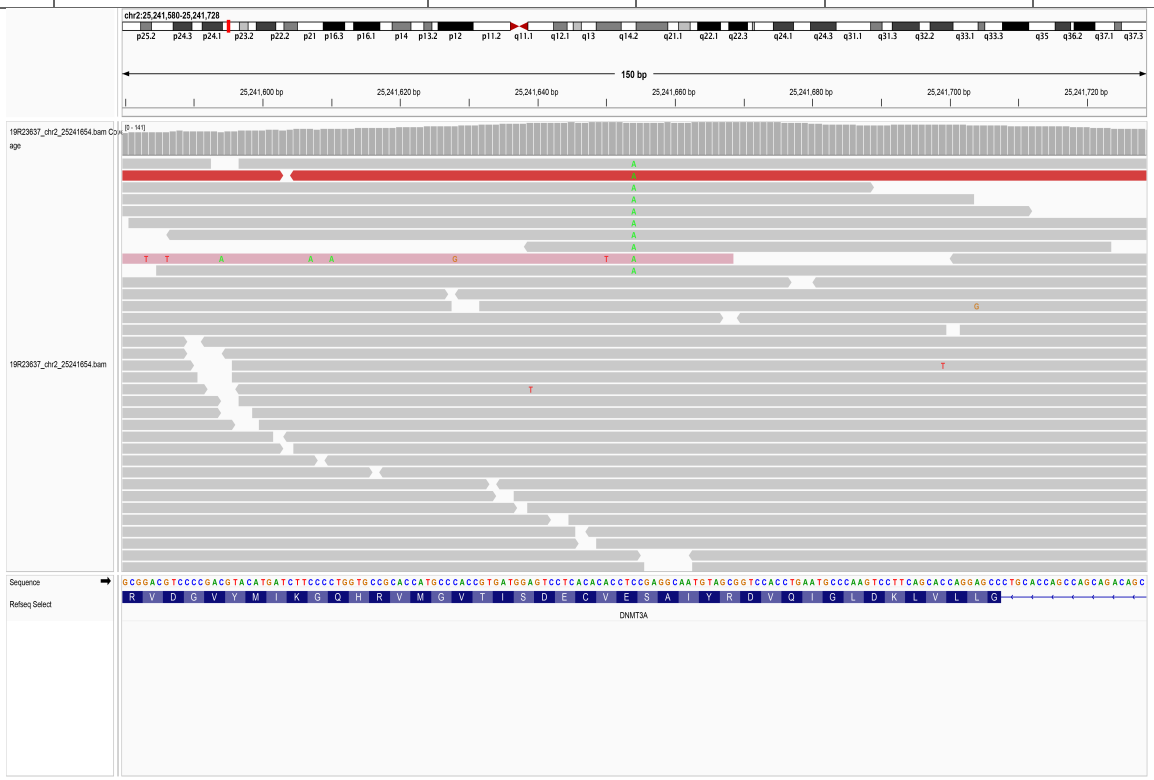
12.70. chr2_25241618_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2002002843	chr2_25241618_G/A	60	4	*DNMT3A*	missense_variant



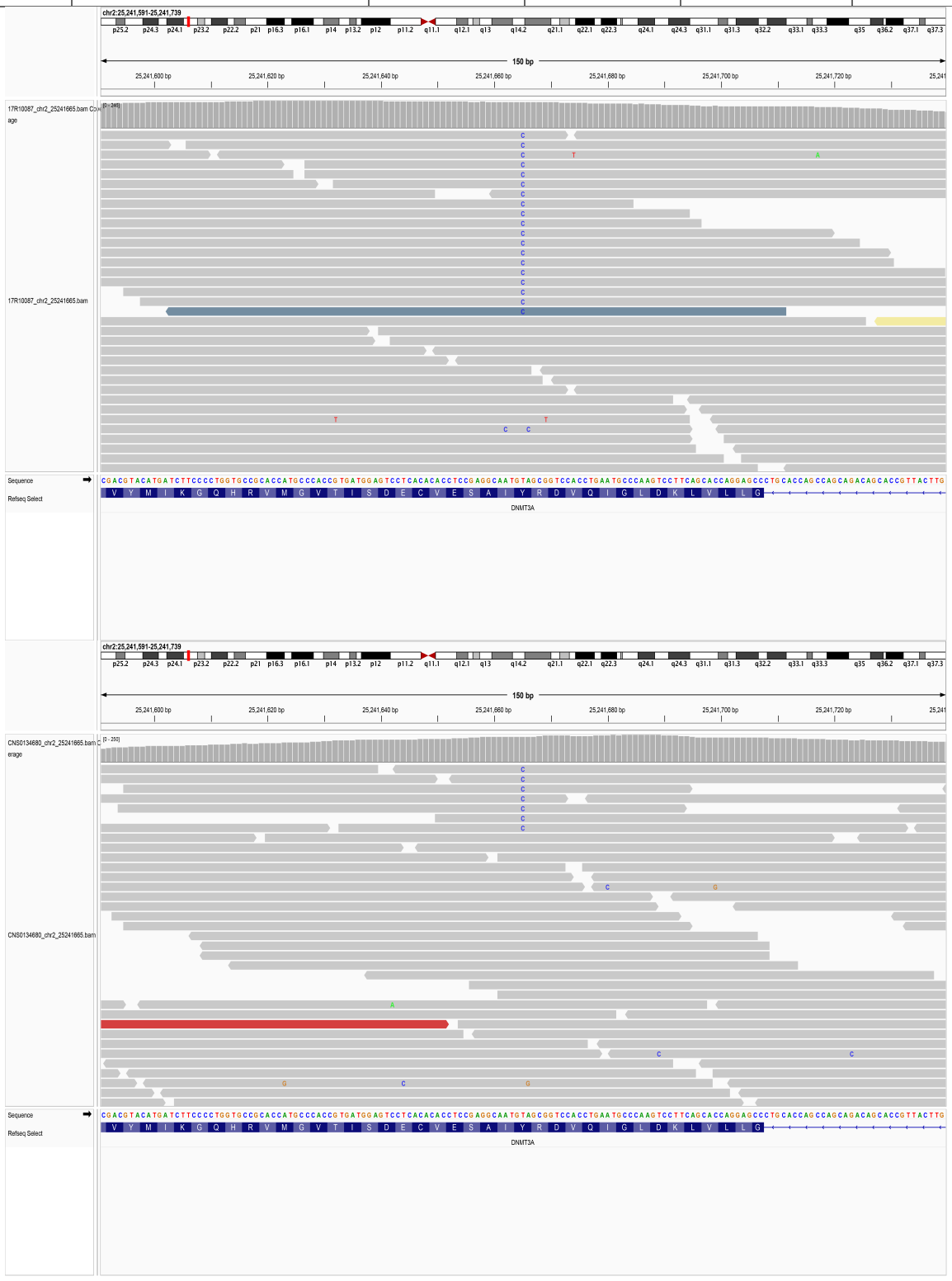
12.71. chr2_25241654_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23637	chr2_25241654_C/A	125	9	*DNMT3A*	stop_gained



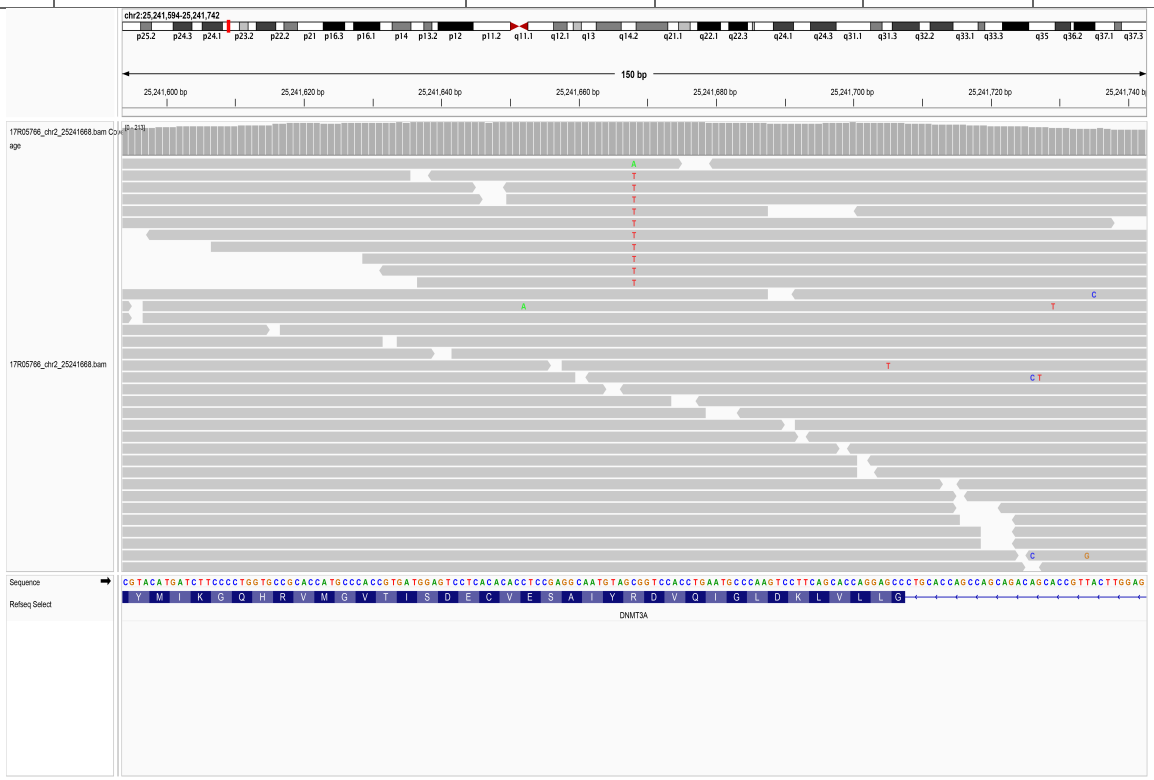
12.72. chr2_25241665_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R10087	chr2_25241665_T/C	204	19	*DNMT3A*	missense_variant
CNS0134680	chr2_25241665_T/C	215	7	*DNMT3A*	missense_variant



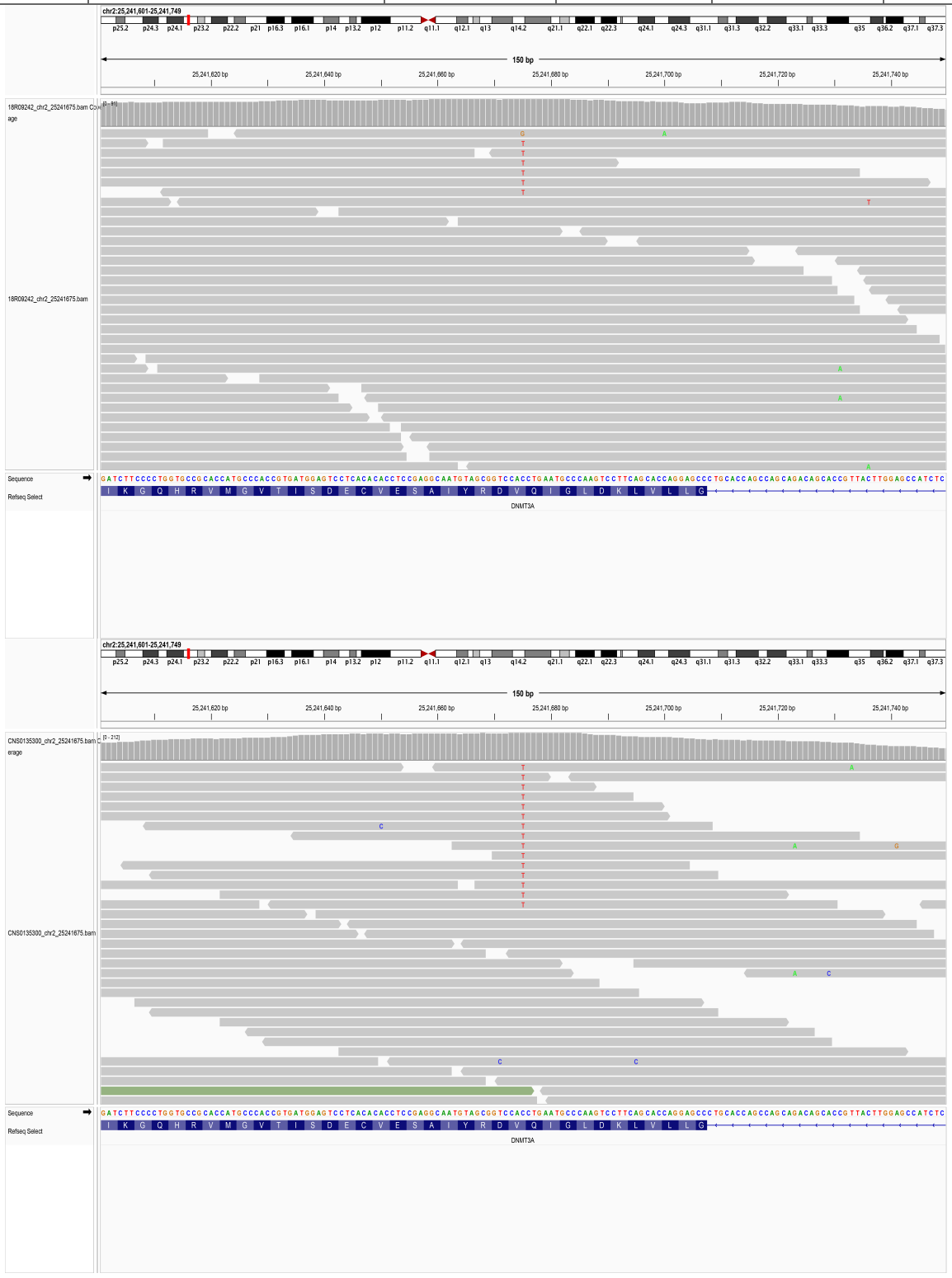
12.73. chr2_25241668_C/T

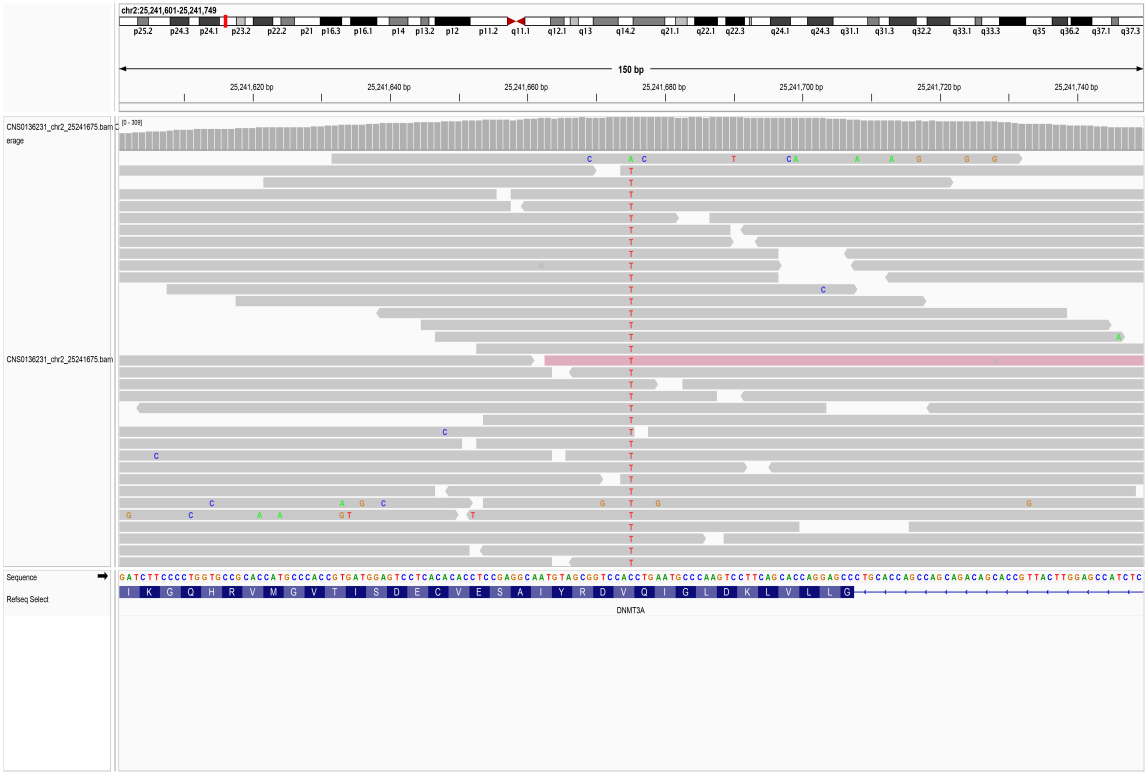
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05766	chr2_25241668_C/T	199	10	*DNMT3A*	missense_variant



12.74. chr2_25241675_C/T

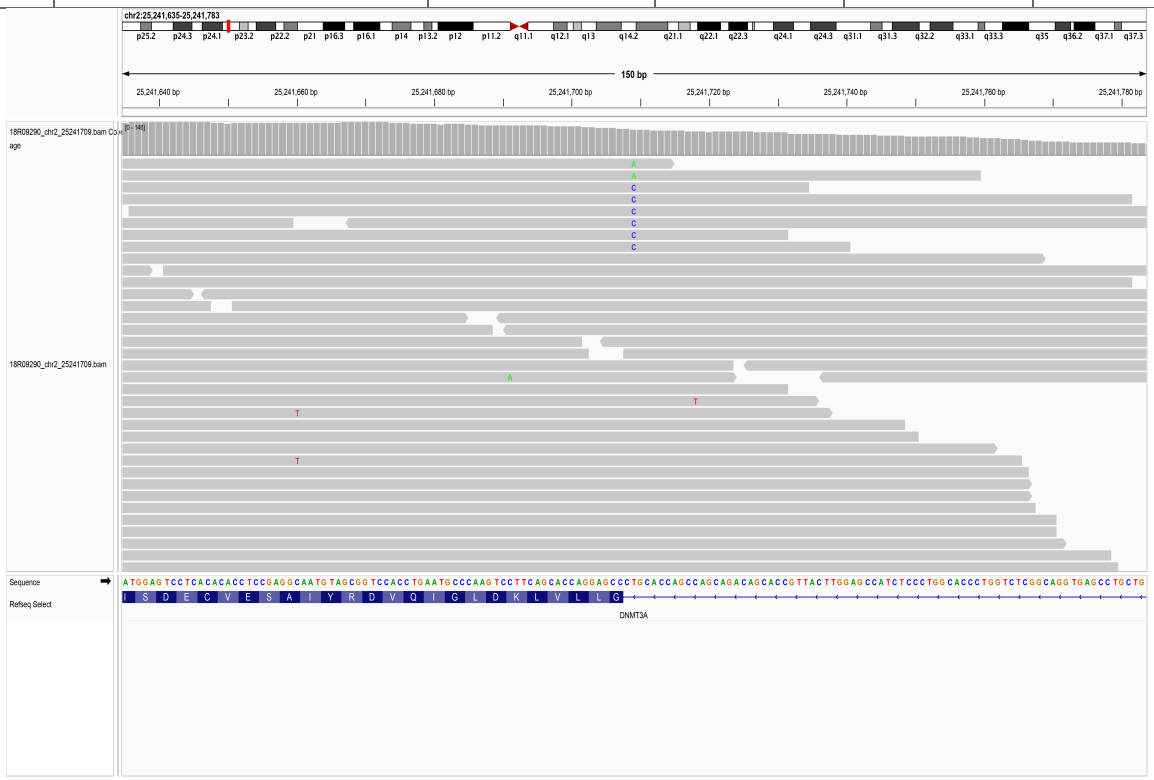
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09242	chr2_25241675_C/T	80	6	*DNMT3A*	missense_variant
CNS0135300	chr2_25241675_C/T	188	15	*DNMT3A*	missense_variant
CNS0136231	chr2_25241675_C/T	251	42	*DNMT3A*	missense_variant




chr2:25,241,601-25,241,749
150 bp
25,241,620 bp
25,241,640 bp
25,241,660 bp
25,241,680 bp
25,241,700 bp
25,241,720 bp
25,241,740 bp
CNS0136231_chr2_25241675.bam C
erage
CNS0136231_chr2_25241675.bam
Sequence
Refseq Select
DNMT3A

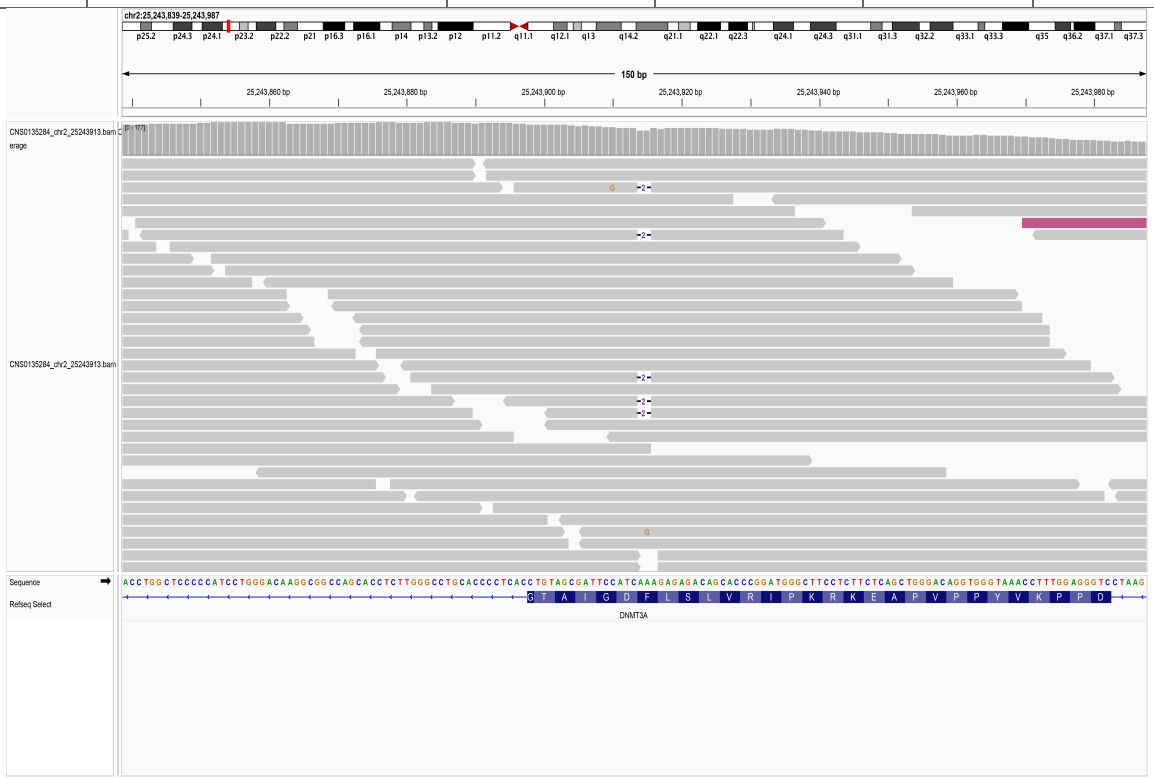
12.75. chr2_25241709_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09290	chr2_25241709_T/C	101	6	*DNMT3A*	splice_acceptor_variant



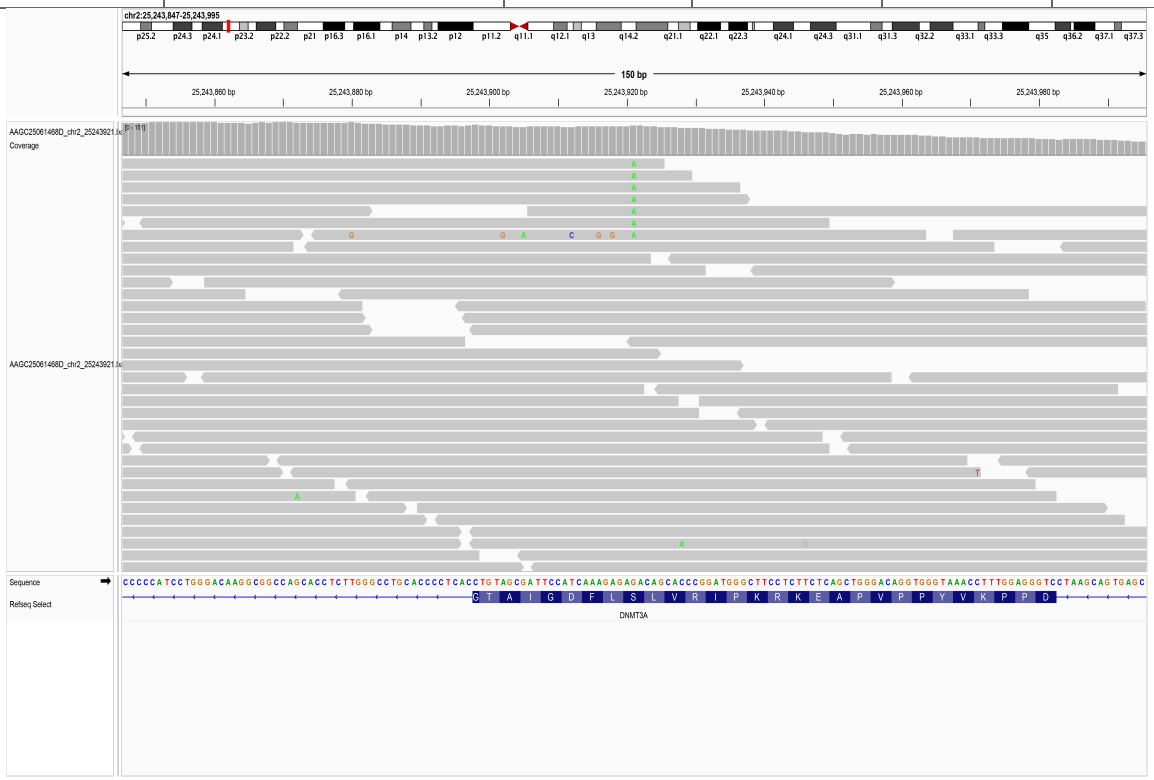
12.76. chr2_25243914_AA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135284	chr2_25243914_AA/-	130	12	*DNMT3A*	frameshift_variant



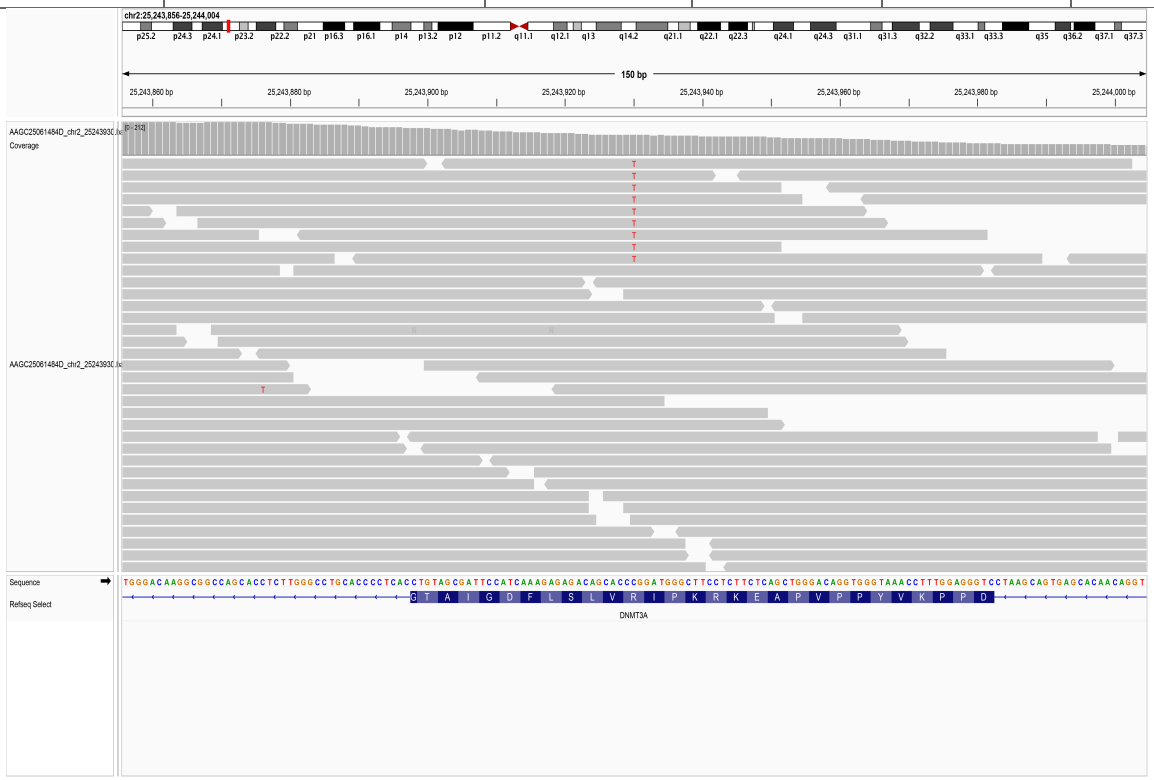
12.77. chr2_25243921_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061468D	chr2_25243921_G/A	122	6	*DNMT3A*	missense_variant



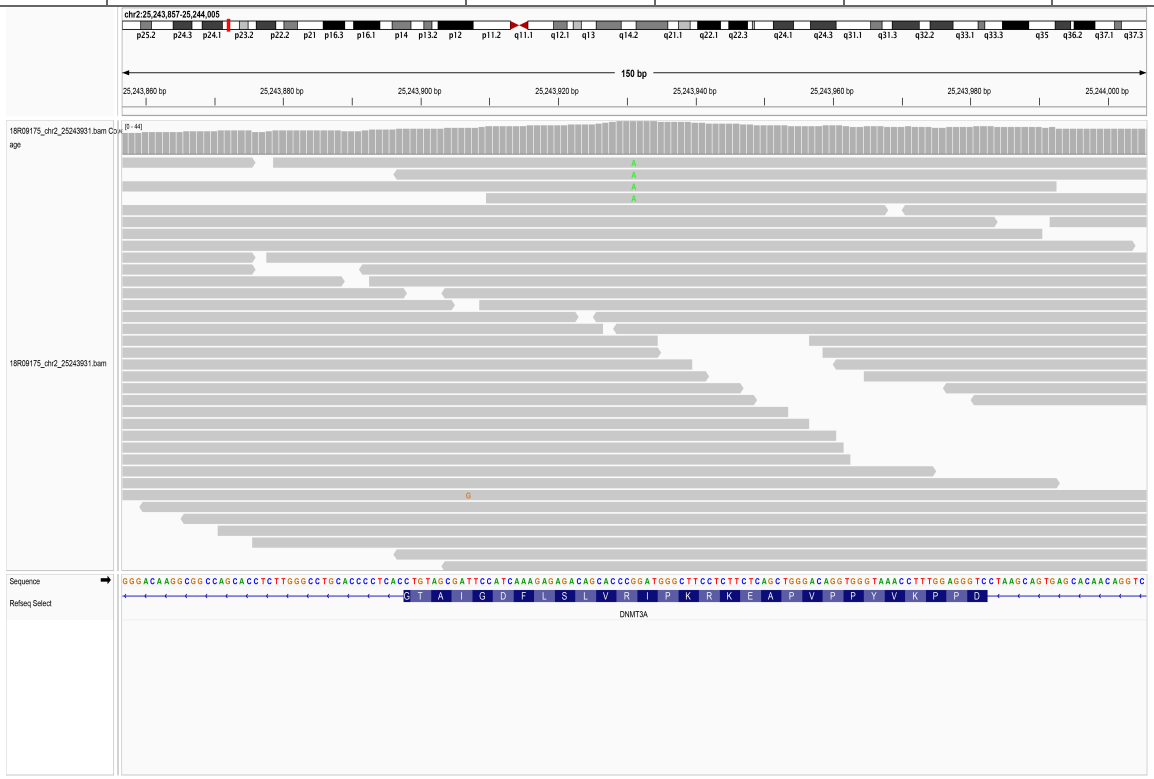
12.78. chr2_25243930_C/T

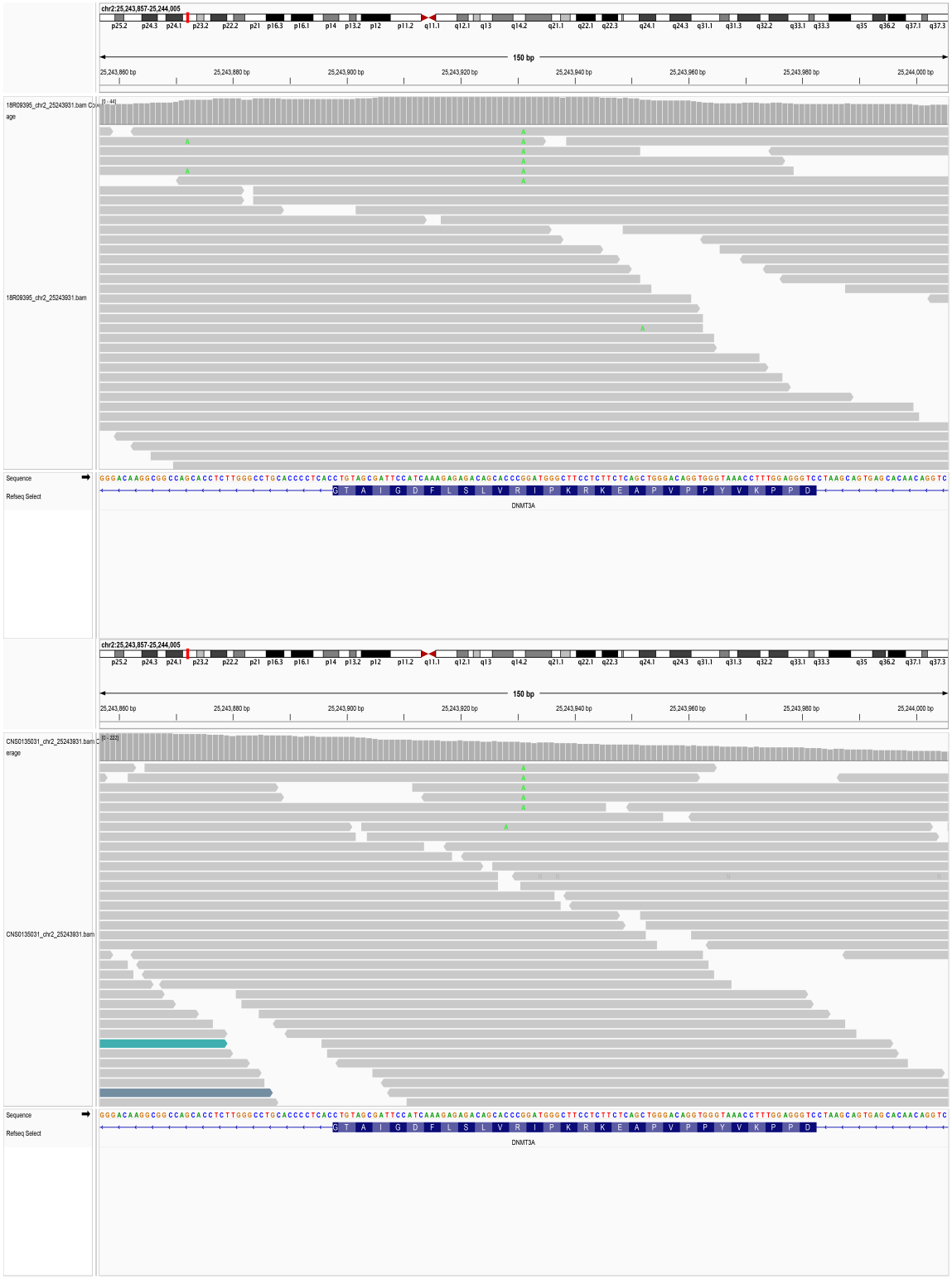
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061484D	chr2_25243930_C/T	118	9	*DNMT3A*	missense_variant

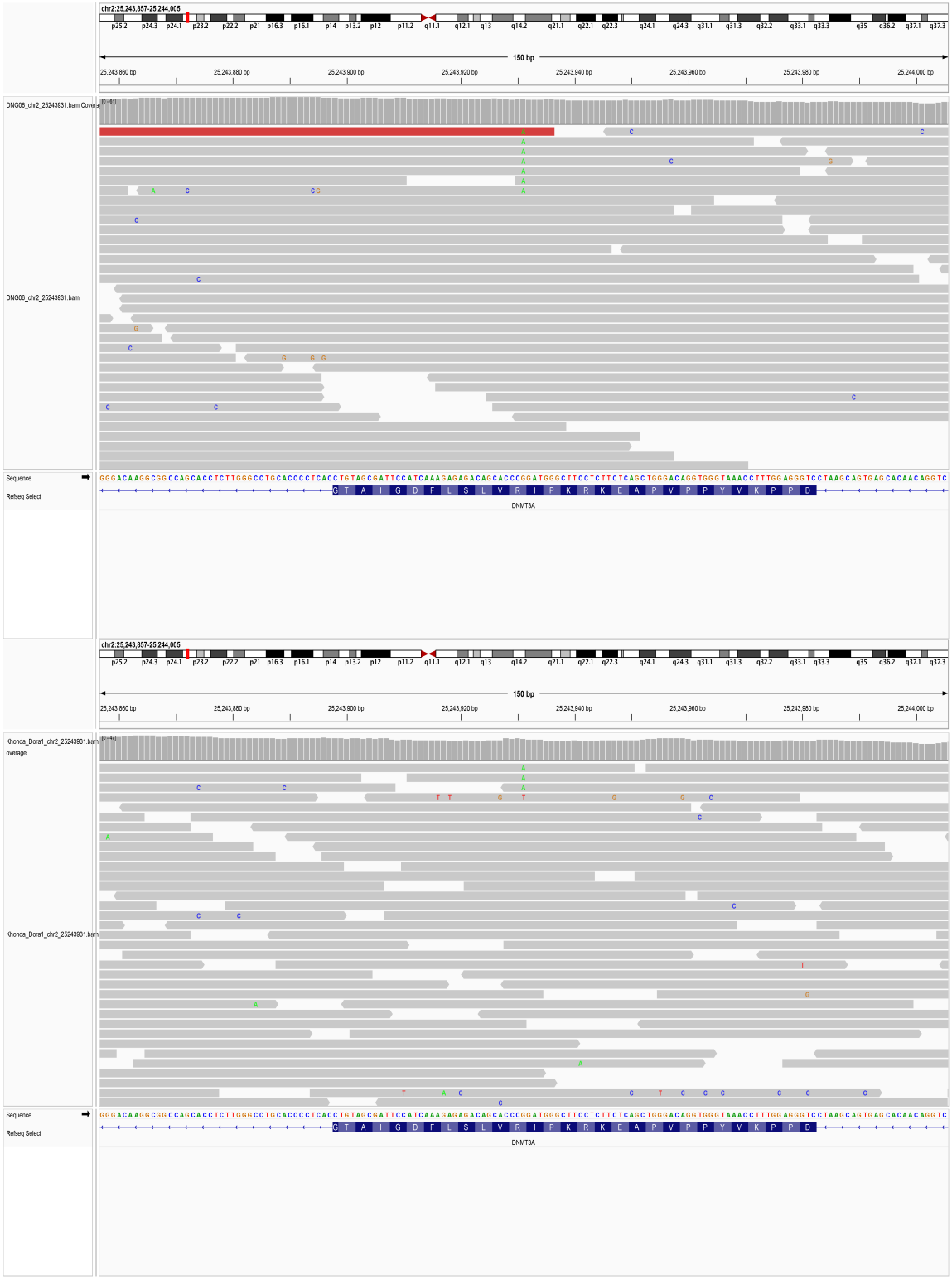


12.79. chr2_25243931_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09175	chr2_25243931_G/A	39	4	*DNMT3A*	missense_variant
18R09395	chr2_25243931_G/A	37	6	*DNMT3A*	missense_variant
CNS0135031	chr2_25243931_G/A	143	5	*DNMT3A*	missense_variant
DNG06	chr2_25243931_G/A	45	7	*DNMT3A*	missense_variant
Khonda_Dora1	chr2_25243931_G/A	29	3	*DNMT3A*	missense_variant

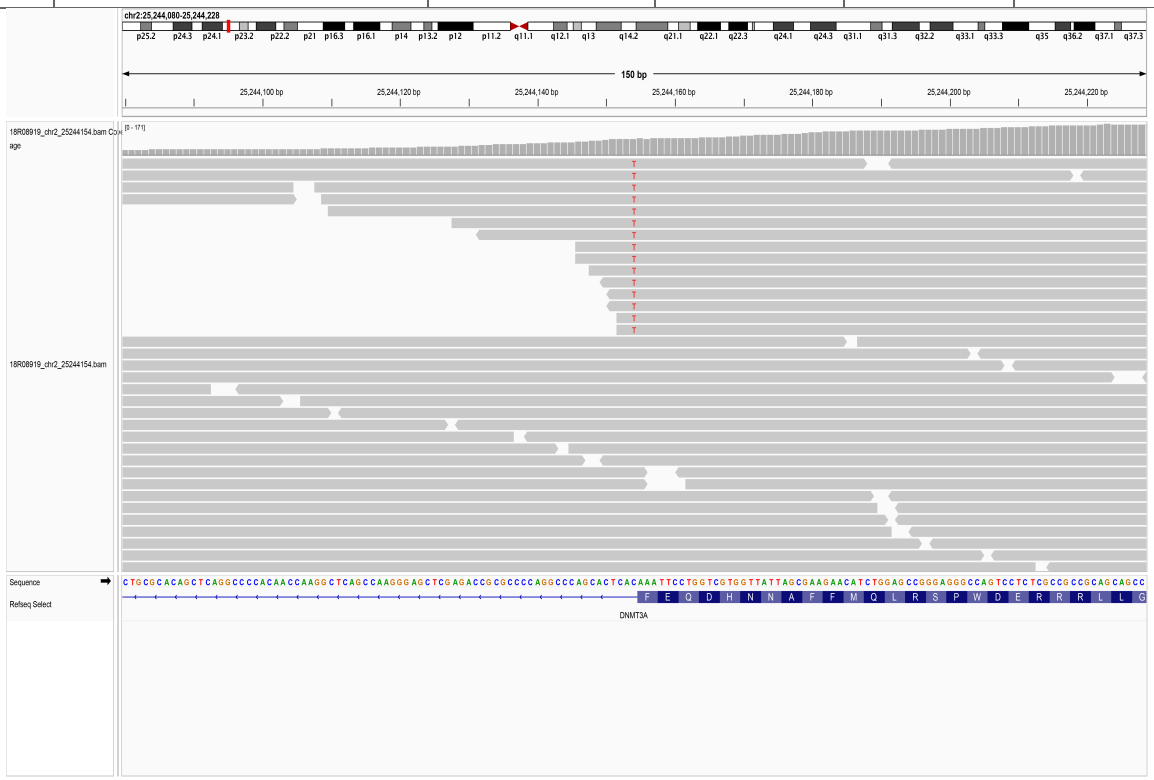



chr2:25,243,857-25,244,005
150 bp
25,243,860 bp
25,243,880 bp
25,243,900 bp
25,243,920 bp
25,243,940 bp
25,243,960 bp
25,243,980 bp
25,244,000 bp
16R09395_chr2_2524393 1.bam Coverage
16R09395_chr2_2524393 1.bam
Sequence
Refseq Select
GTAIGDFLSLVRIPKRKEAPVPPYVKPPD
DNMT3A
CNS0135031_chr2_2524393 1.bam Coverage
CNS0135031_chr2_2524393 1.bam


chr2:25,243,857-25,244,005
150 bp
DNG06_chr2_25243931.bam Coverage
DNG06_chr2_25243931.bam
Sequence
Refseq Select
DNMT3A
Khonda_Dora1_chr2_25243931.bam Coverage
Khonda_Dora1_chr2_25243931.bam

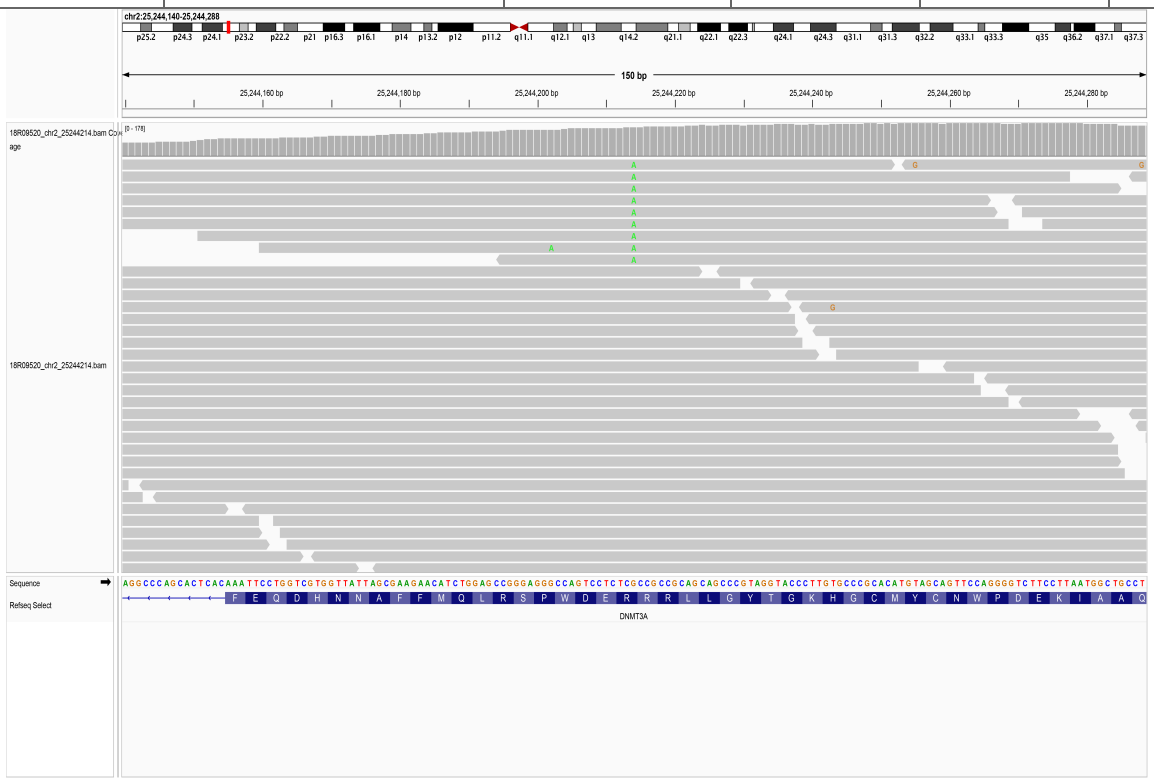
12.80. chr2_25244154_C/T

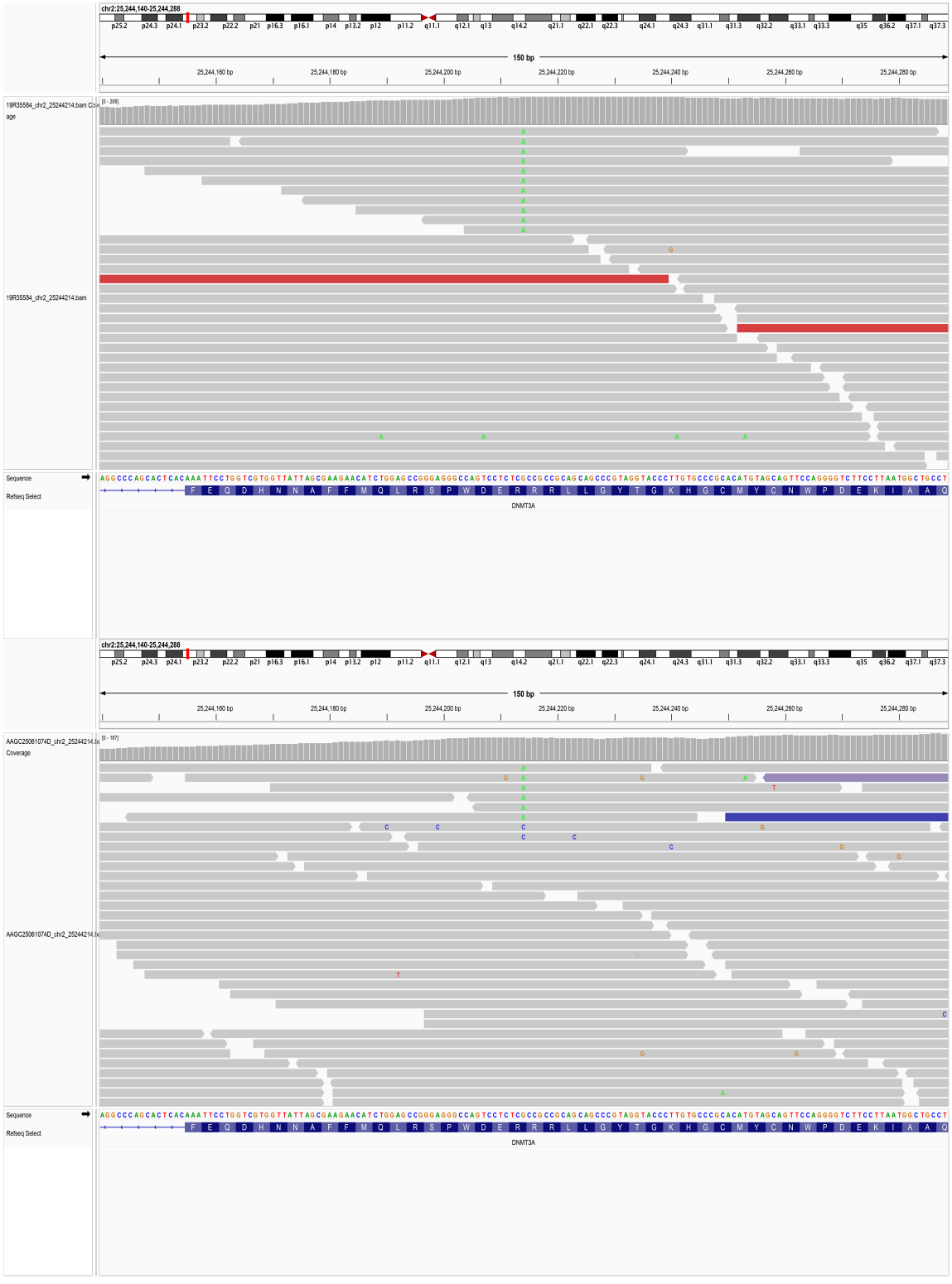
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08919	chr2_25244154_C/T	70	15	*DNMT3A*	splice_donor_variant

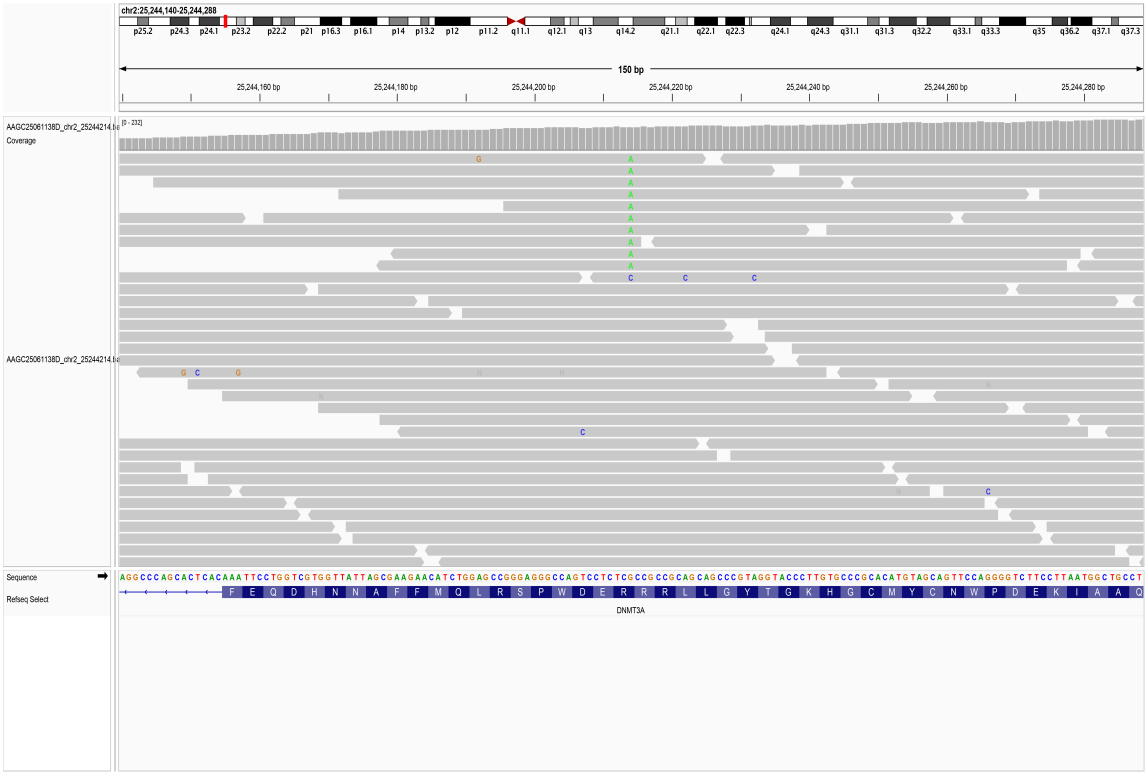


12.81. chr2_25244214_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09520	chr2_25244214_G/A	145	9	*DNMT3A*	stop_gained
19R35584	chr2_25244214_G/A	186	11	*DNMT3A*	stop_gained
AAGC25061074D	chr2_25244214_G/A	135	6	*DNMT3A*	stop_gained
AAGC25061138D	chr2_25244214_G/A	146	10	*DNMT3A*	stop_gained

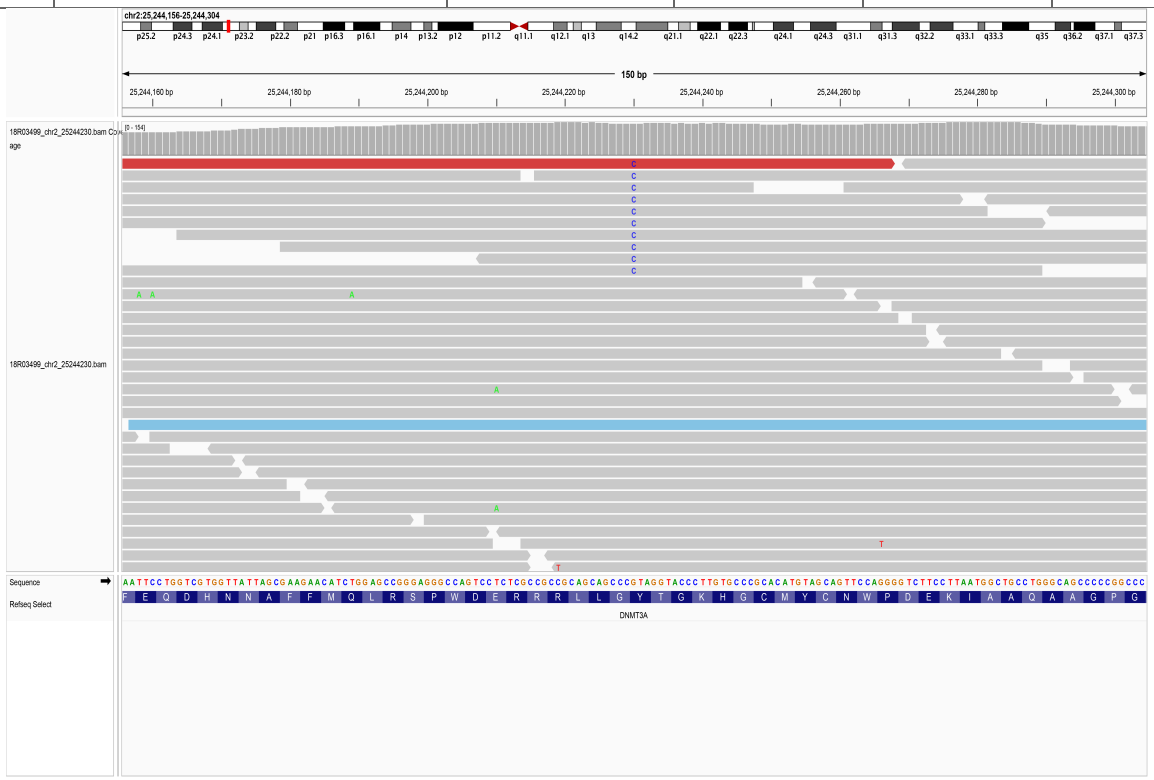



chr2:25,244,140-25,244,288
150 bp
25,244,160 bp
25,244,180 bp
25,244,200 bp
25,244,220 bp
25,244,240 bp
25,244,260 bp
25,244,280 bp
19R35584_chr2_25244214.bam Coverage
19R35584_chr2_25244214.bam
Sequence
Refseq Select
DNMT3A
AAGC25061074D_chr2_25244214.bam Coverage
AAGC25061074D_chr2_25244214.bam


chr2:25,244,140-25,244,288
150 bp
25,244,160 bp
25,244,180 bp
25,244,200 bp
25,244,220 bp
25,244,240 bp
25,244,260 bp
25,244,280 bp
Coverage
Sequence
Refseq Select
DNMT3A

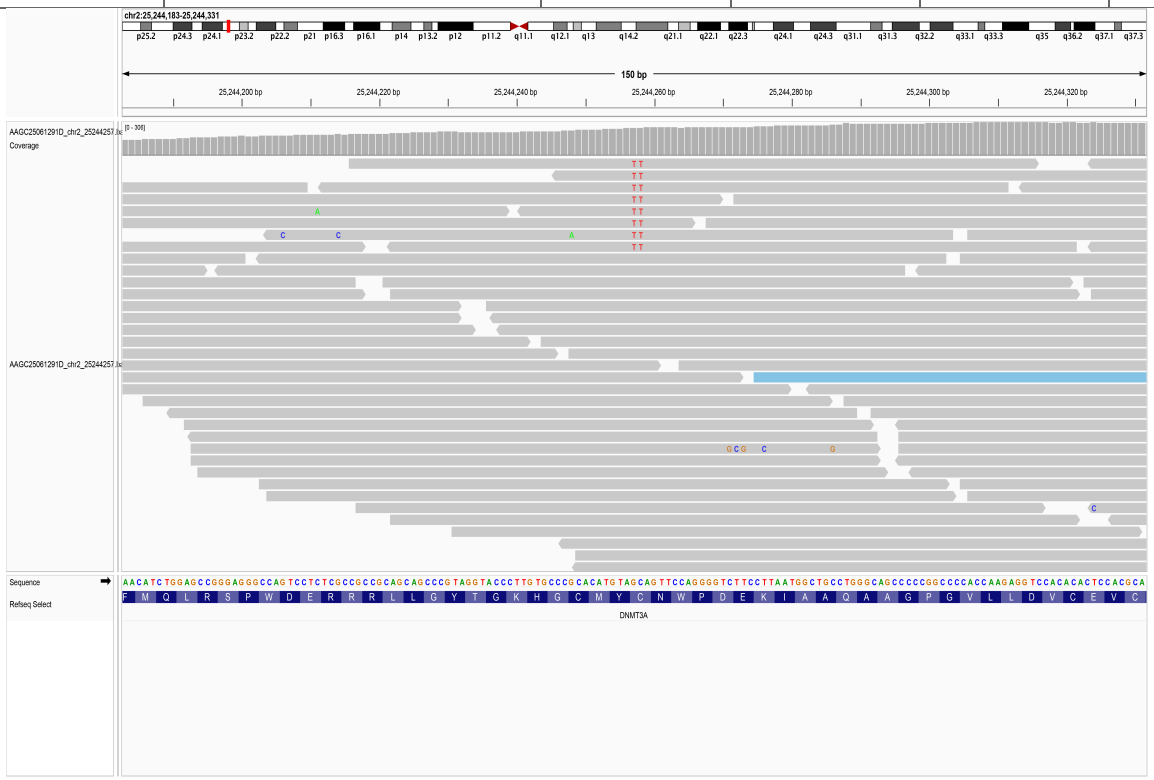
12.82. chr2_25244230_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03499	chr2_25244230_G/C	131	10	*DNMT3A*	stop_gained



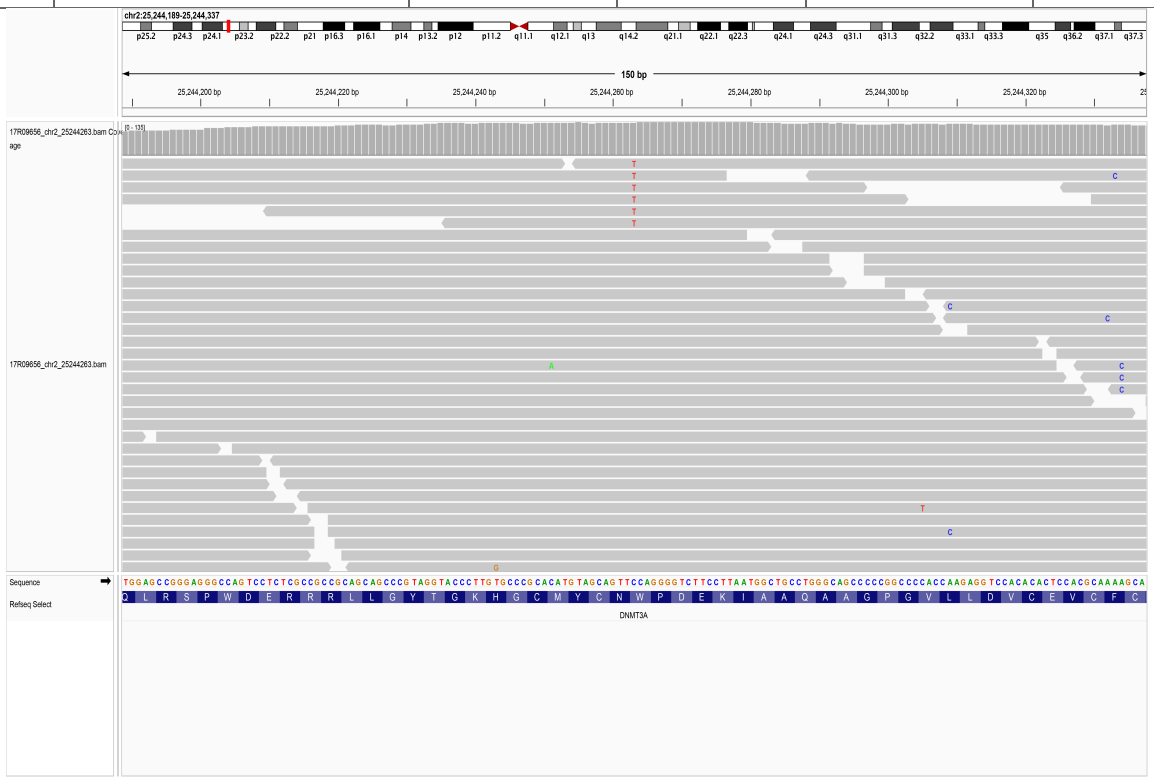
12.83. chr2_25244257_GC/TT

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061291D	chr2_25244257_GC/TT	239	8	*DNMT3A*	stop_gained



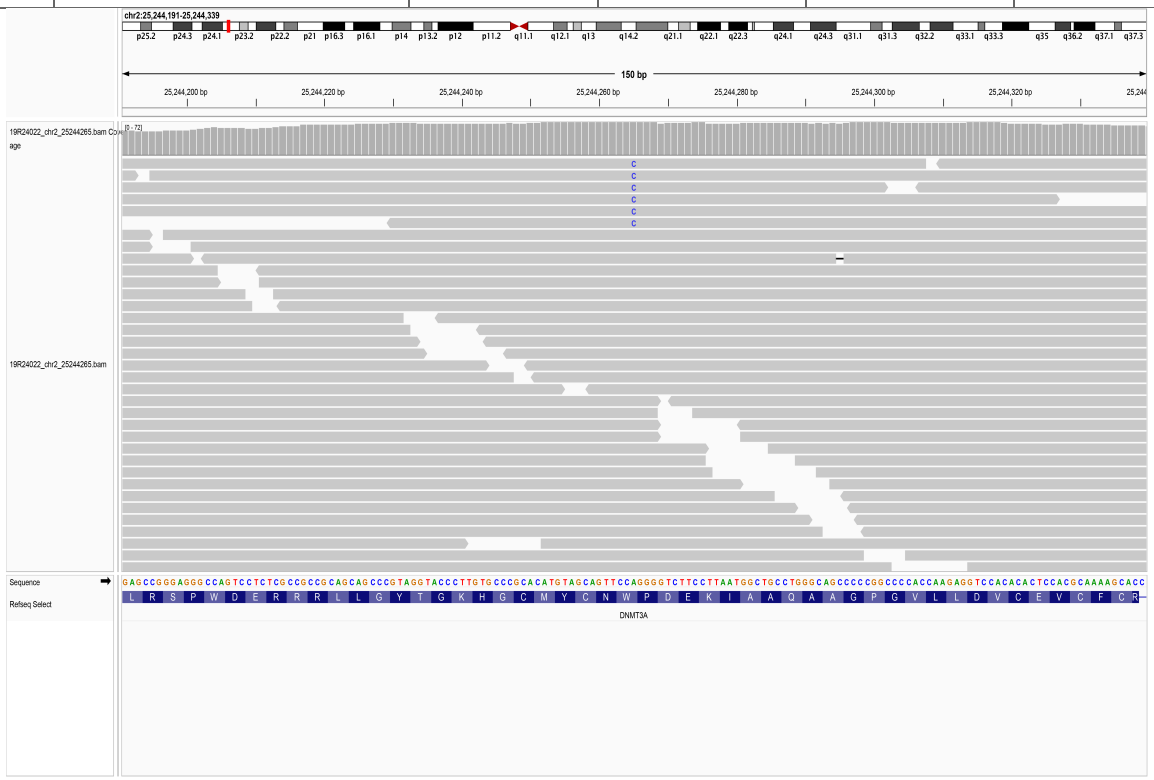
12.84. chr2_25244263_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09656	chr2_25244263_C/T	123	6	*DNMT3A*	stop_gained



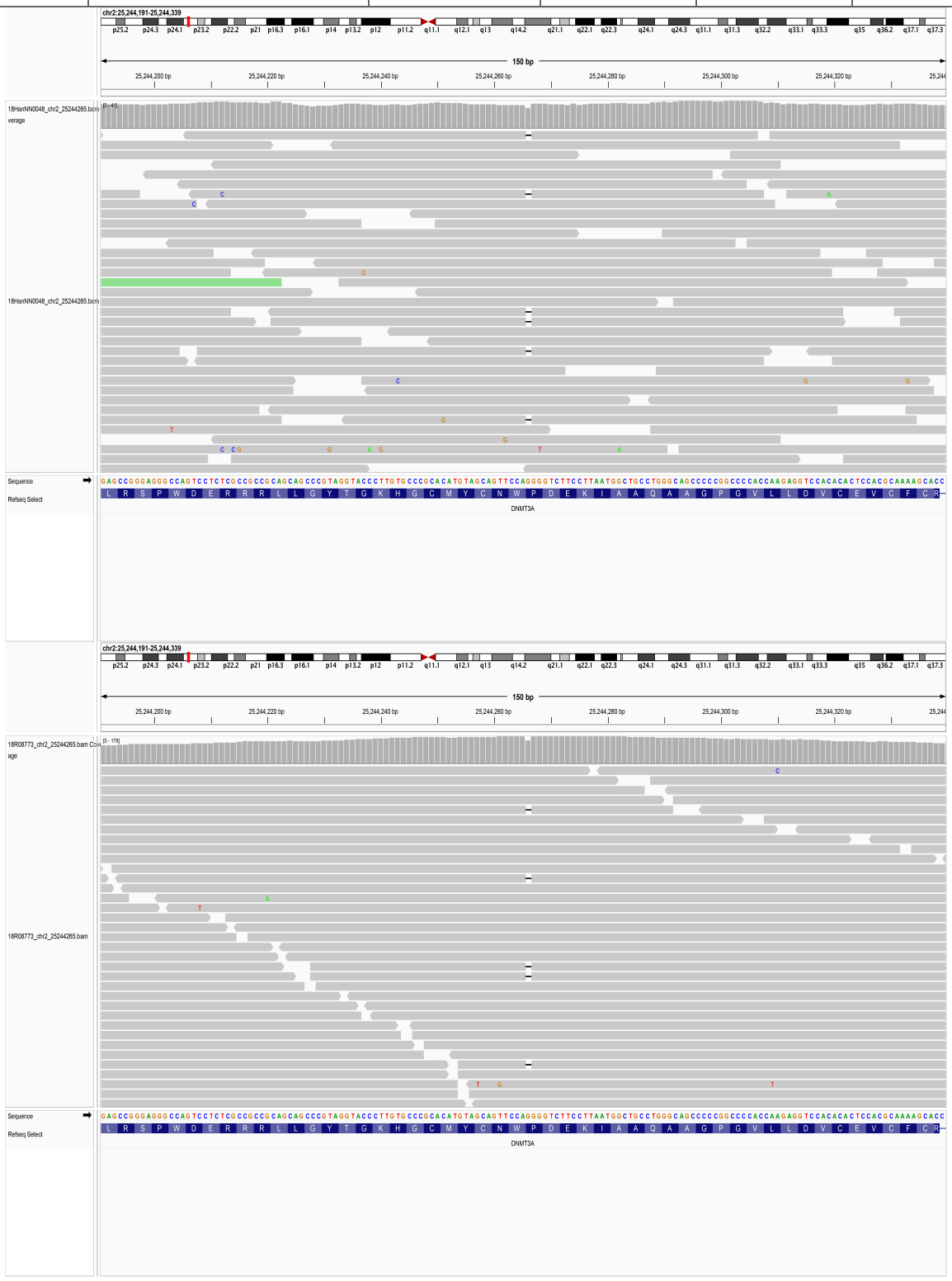
12.85. chr2_25244265_A/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R24022	chr2_25244265_A/C	66	6	*DNMT3A*	missense_variant



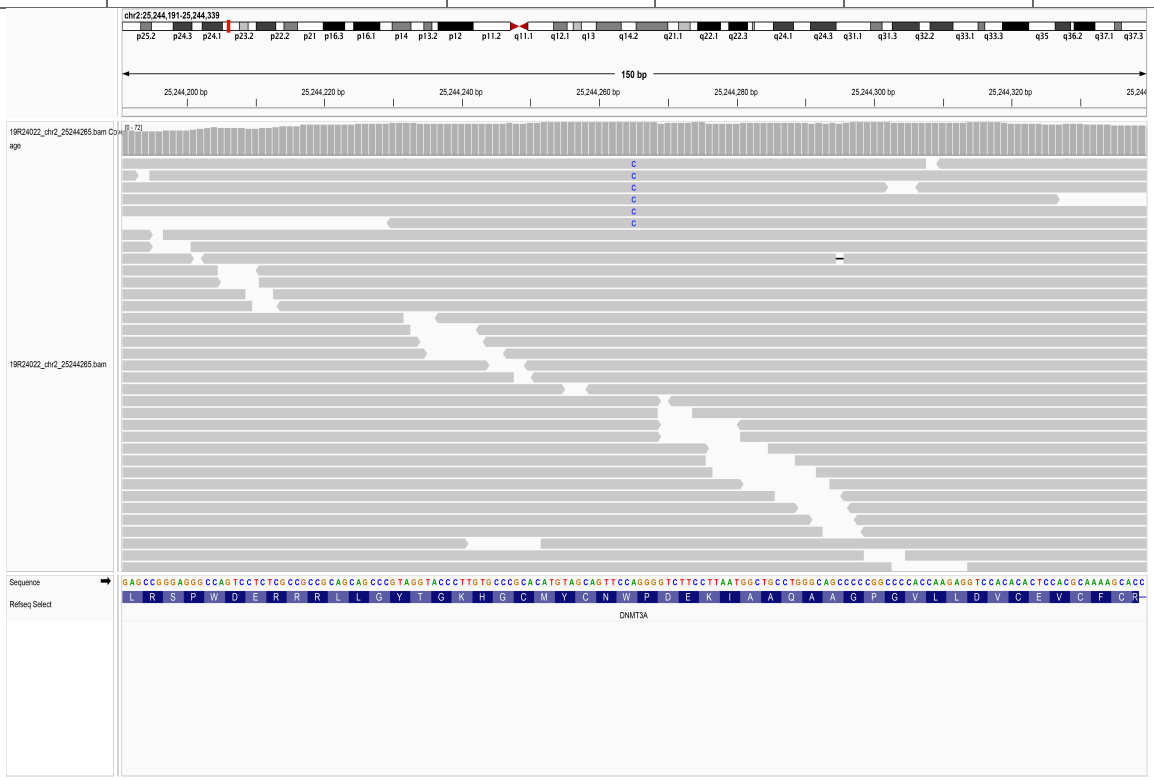
12.86. chr2_25244266_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0048	chr2_25244266_G/-	29	6	*DNMT3A*	frameshift_variant
18R08773	chr2_25244266_G/-	142	27	*DNMT3A*	frameshift_variant



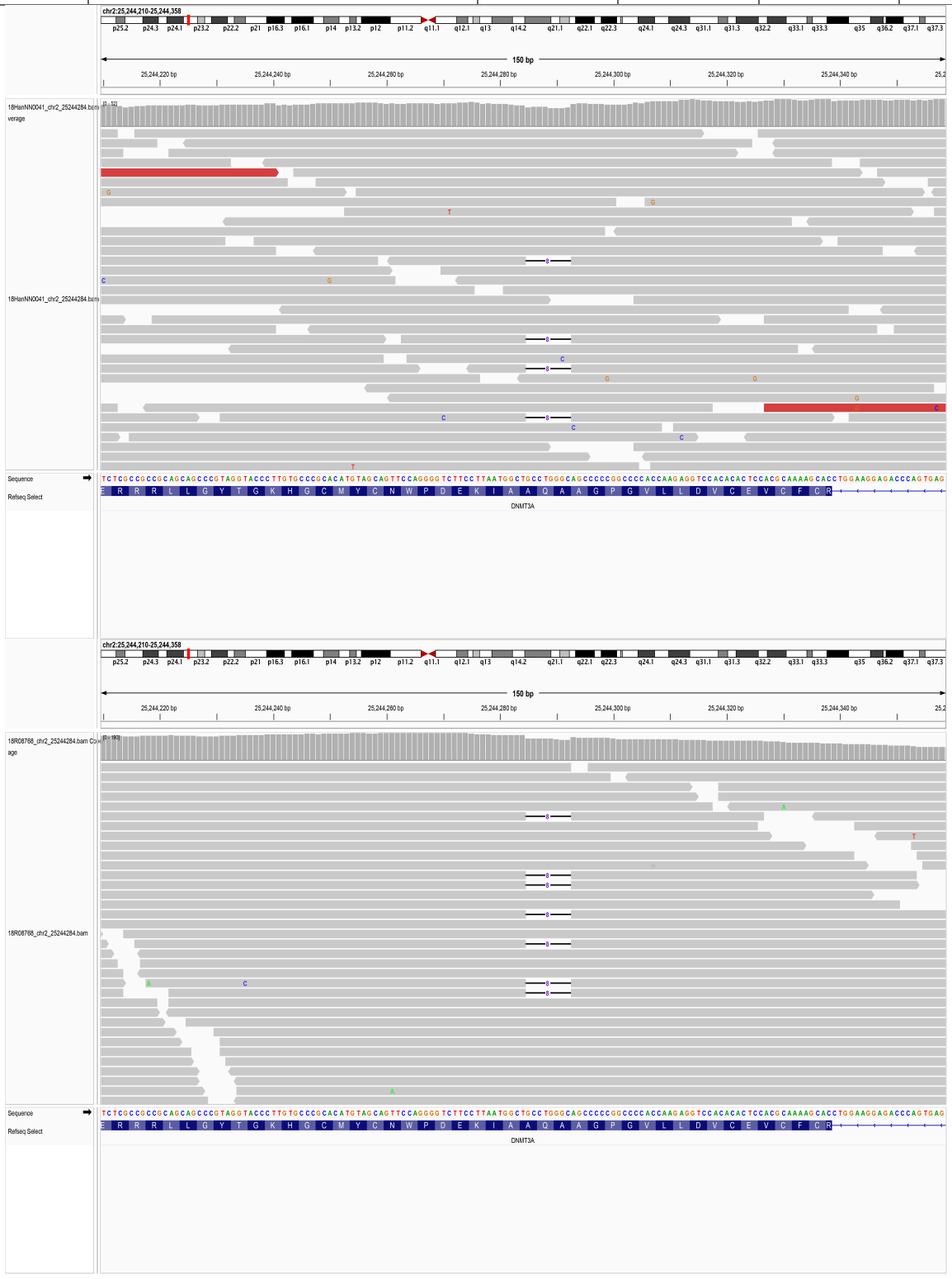
12.87. chr2_25244266_A/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R24022	chr2_25244266_A/C	66	6	*DNMT3A*	frameshift_variant



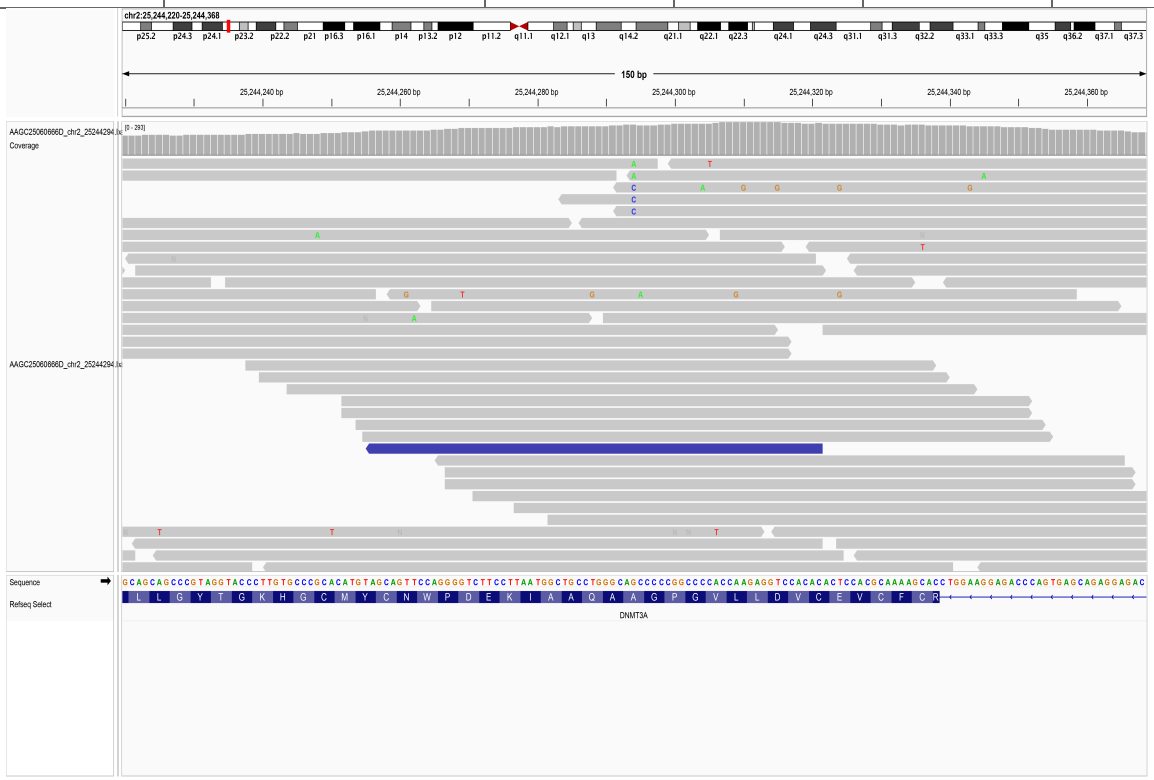
12.88. chr2_25244285_GCCTGGGC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0041	chr2_25244285_GCCTGGGC/-	38	5	*DNMT3A*	frameshift_variant
18R08768	chr2_25244285_GCCTGGGC/-	149	18	*DNMT3A*	frameshift_variant



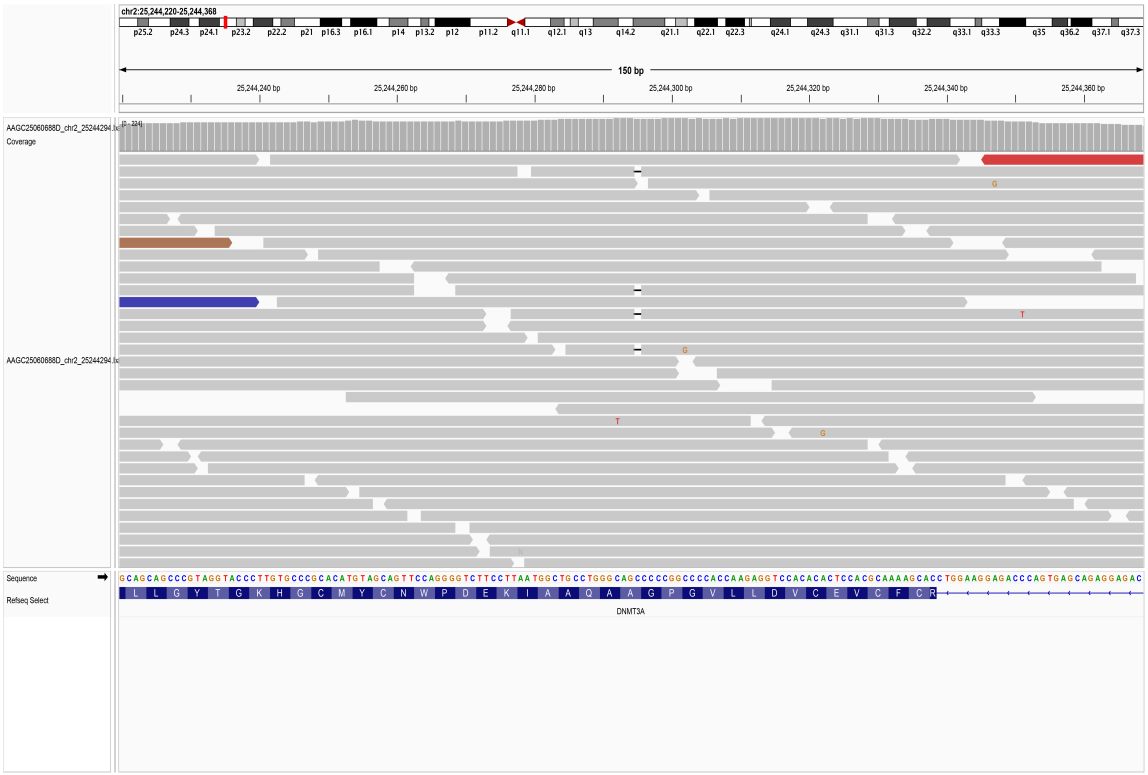
12.89. chr2_25244295_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060666D	chr2_25244295_G/C	242	6	*DNMT3A*	frameshift_variant



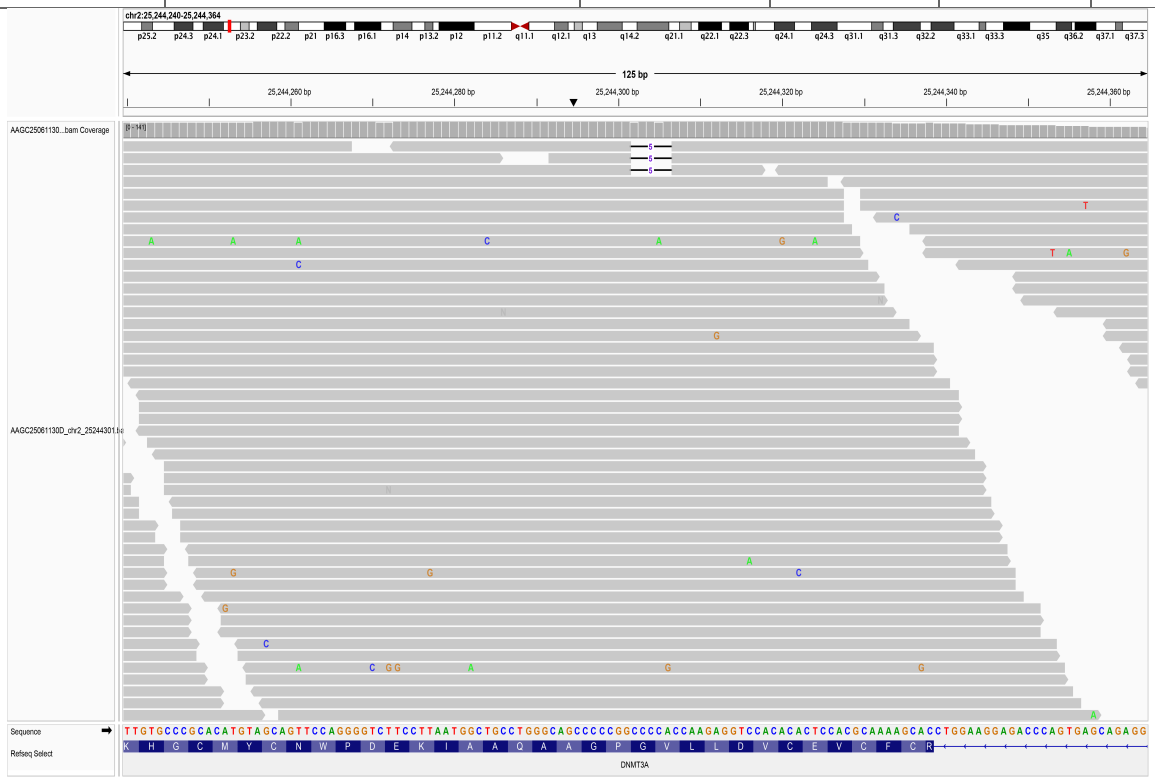
12.90. chr2_25244295_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060688D	chr2_25244295_C/-	204	6	*DNMT3A*	frameshift_variant



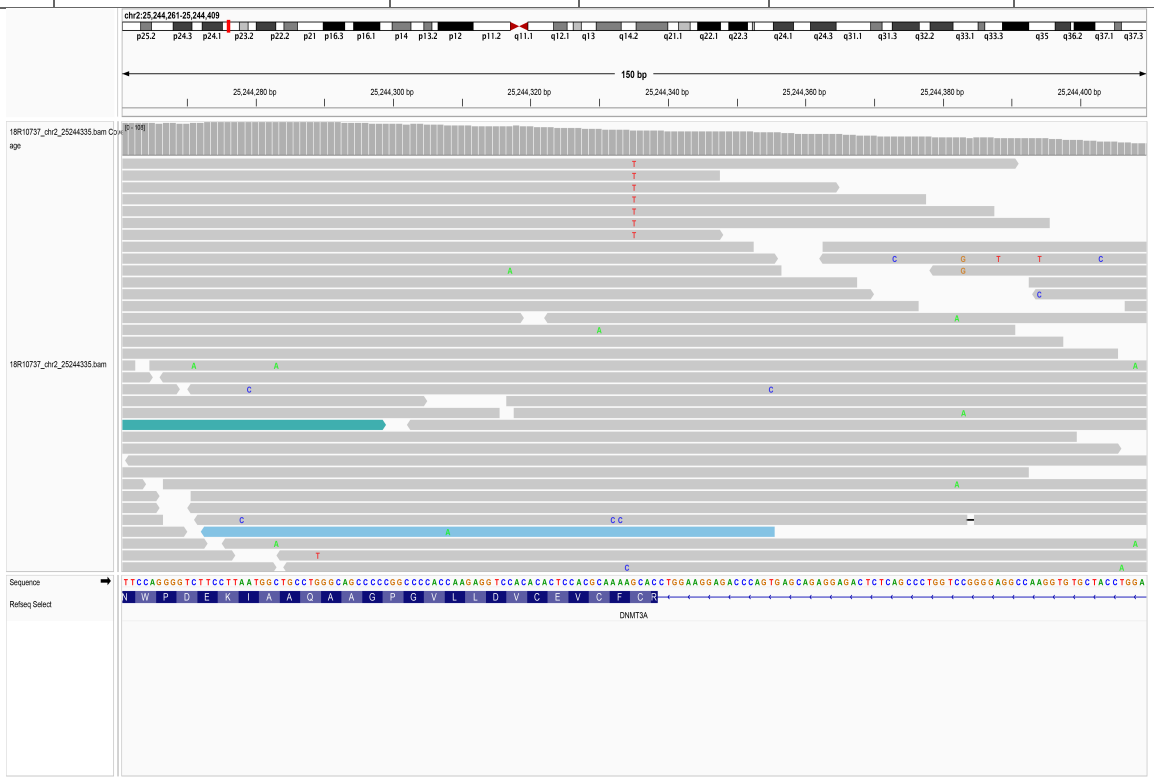
12.91. chr2_25244302_CCCCA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061130D	chr2_25244302_CCCCA/-	127	3	*DNMT3A*	frameshift_variant



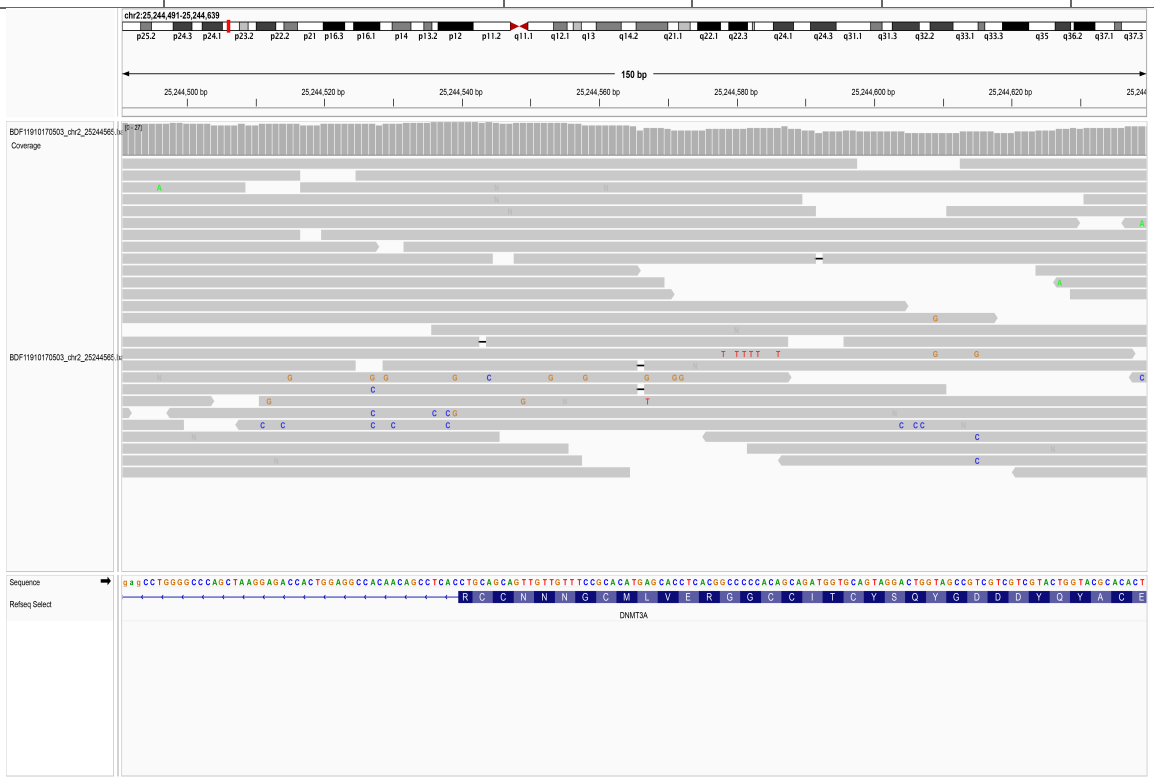
12.92. chr2_25244335_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10737	chr2_25244335_G/T	66	7	*DNMT3A*	stop_gained



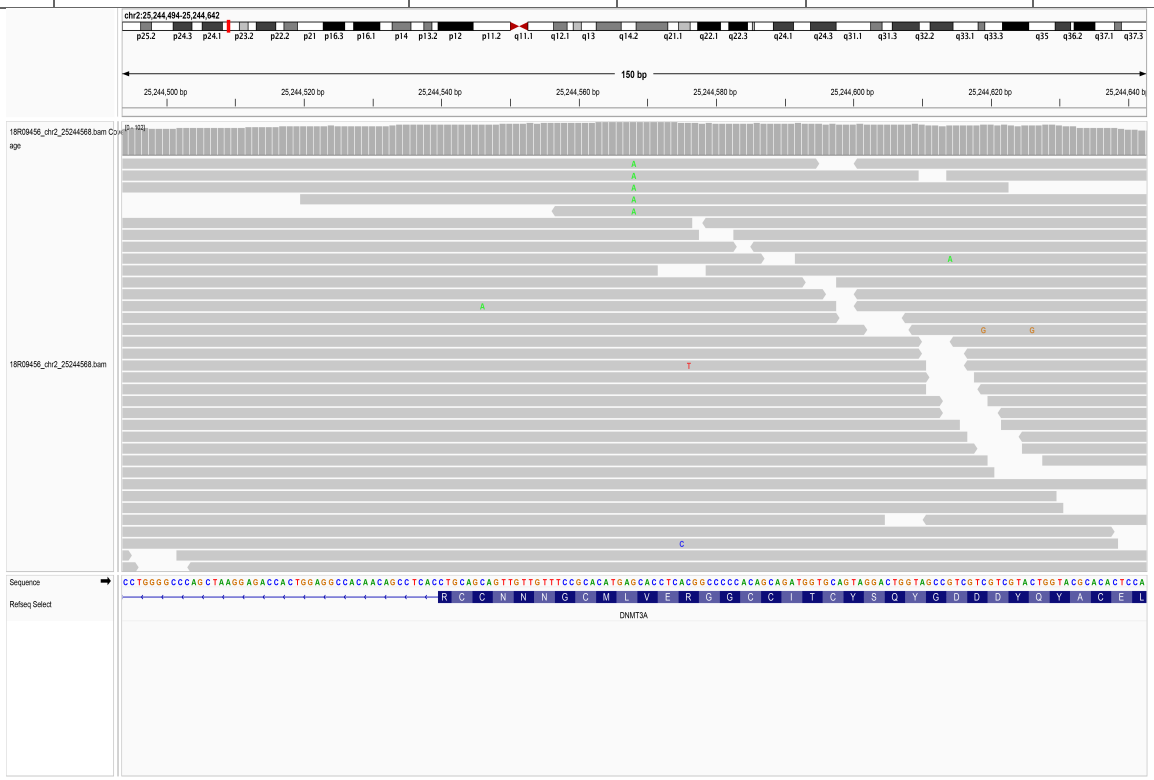
12.93. chr2_25244566_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr2_25244566_G/-	15	2	*DNMT3A*	frameshift_variant



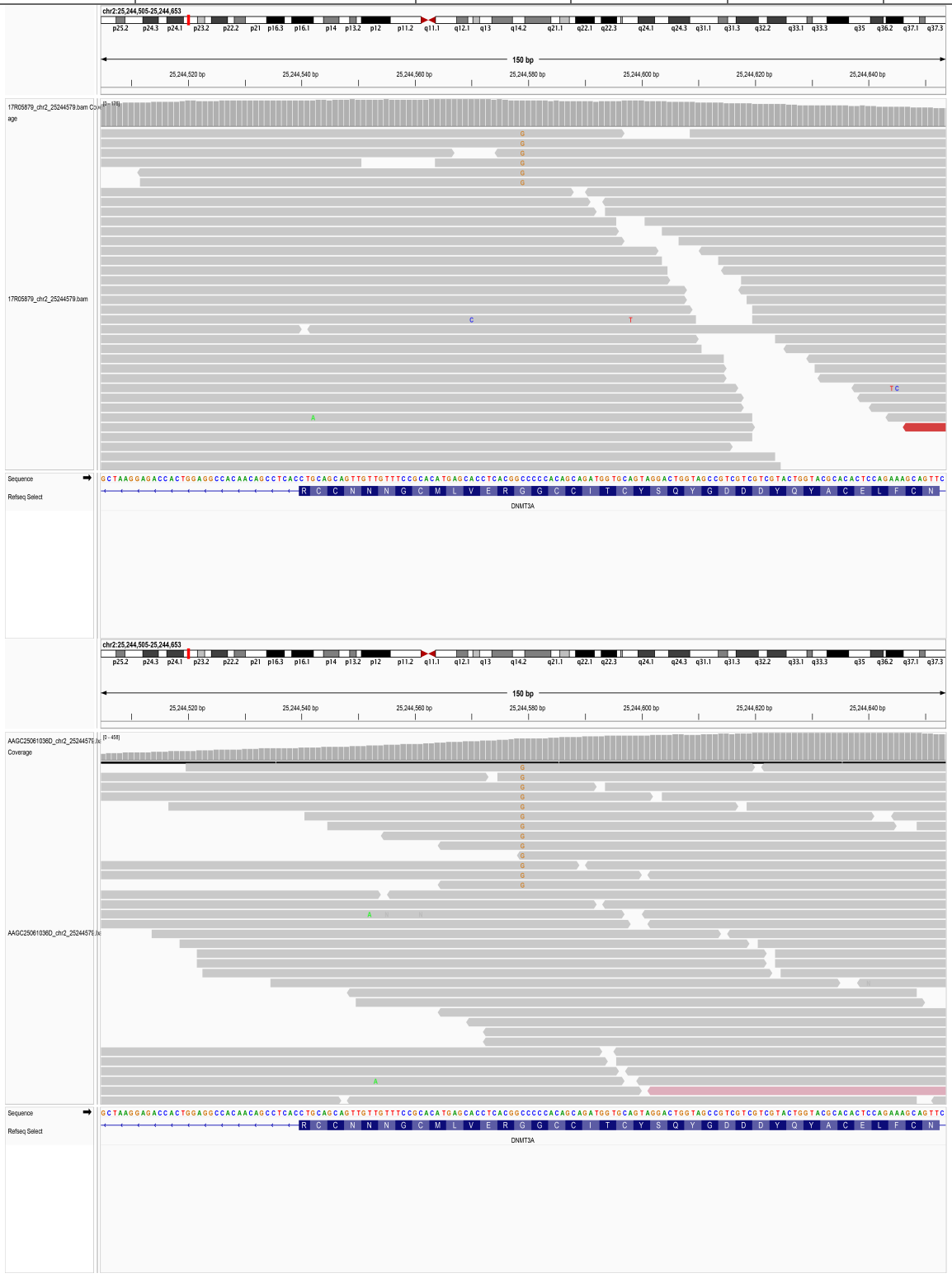
12.94. chr2_25244568_G/A

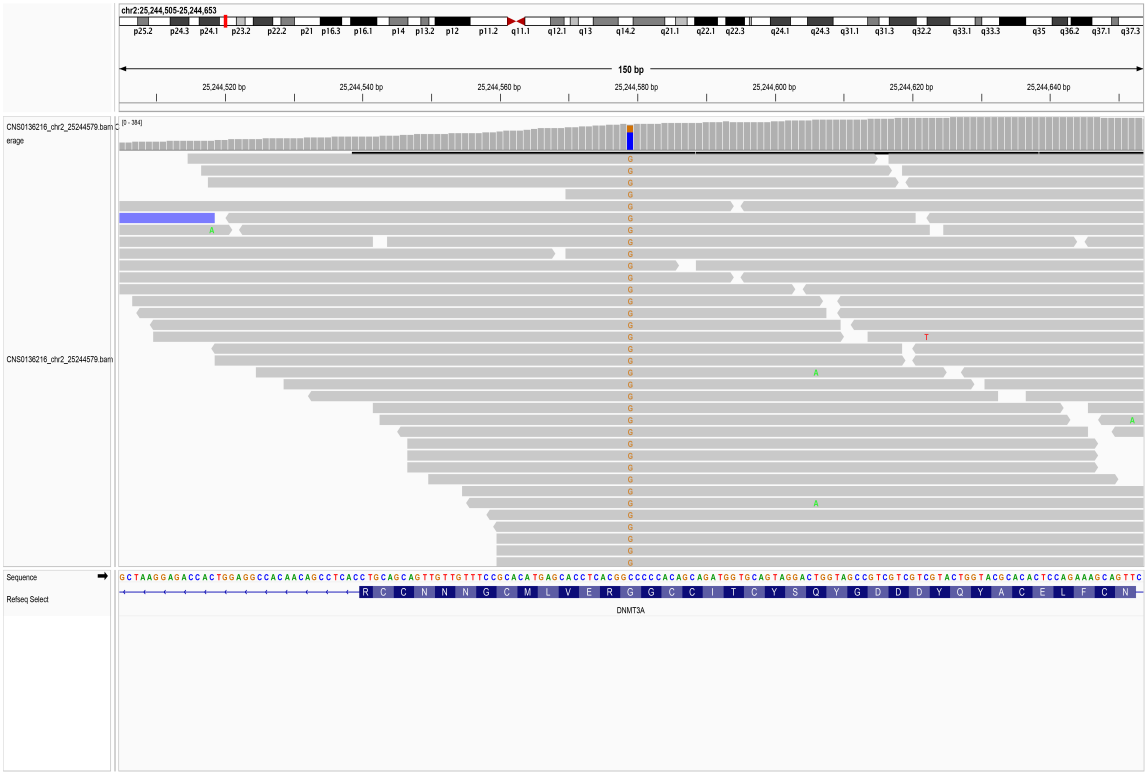
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09456	chr2_25244568_G/A	92	5	*DNMT3A*	missense_variant



12.95. chr2_25244579_C/G

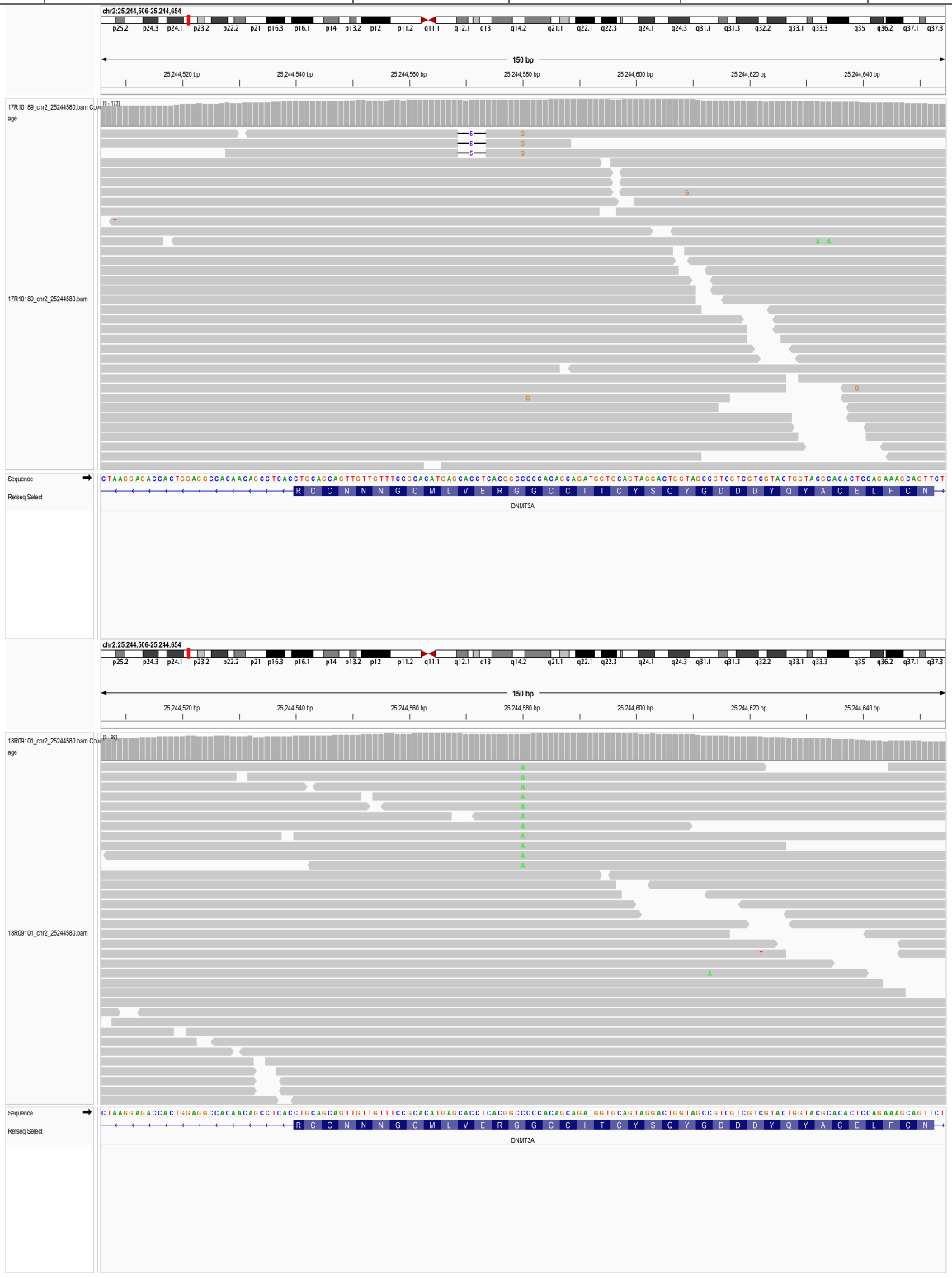
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05879	chr2_25244579_C/G	156	6	*DNMT3A*	missense_variant
AAGC25061036D	chr2_25244579_C/G	336	15	*DNMT3A*	missense_variant
CNS0136216	chr2_25244579_C/G	209	80	*DNMT3A*	missense_variant

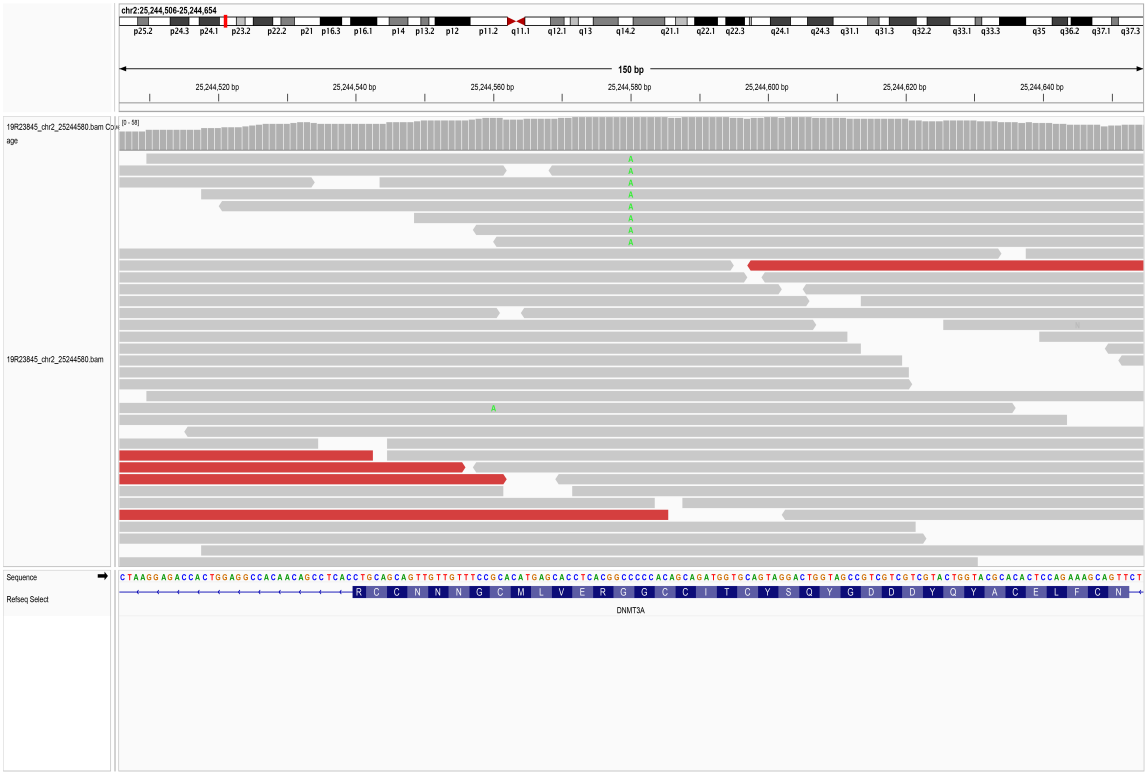



chr2:25,244,505-25,244,653
150 bp
25,244,520 bp
25,244,540 bp
25,244,560 bp
25,244,580 bp
25,244,600 bp
25,244,620 bp
25,244,640 bp
CNS0136216_chr2_25244579.bam
CNS0136216_chr2_25244579.bam
Sequence
Refseq Select
DNMT3A

12.96. chr2_25244580_C/G/A

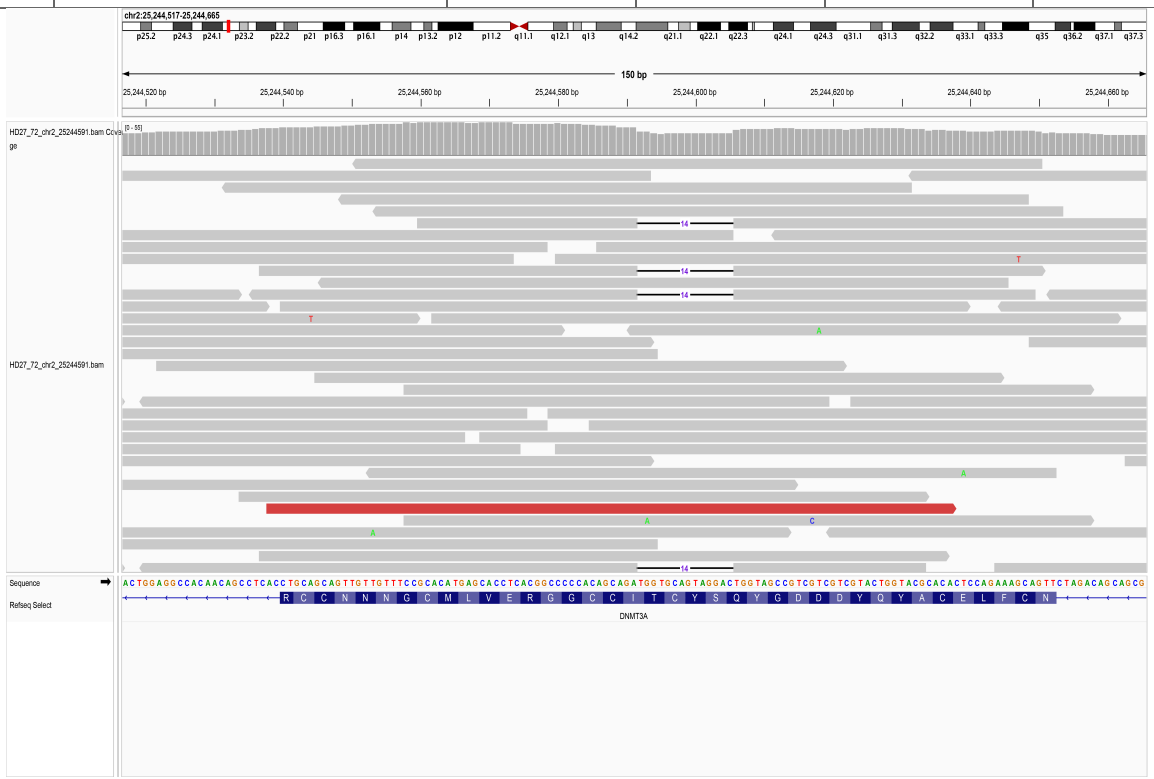
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R10189	chr2_25244580_C/G/A	165	3	*DNMT3A*	missense_variant
18R09101	chr2_25244580_C/G/A	82	11	*DNMT3A*	missense_variant
19R23845	chr2_25244580_C/G/A	49	8	*DNMT3A*	missense_variant




chr2:25,244,506-25,244,654
p25.2 p24.3 p24.1 p23.2 p22.2 p21 p16.3 p16.1 p14 p13.2 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
150 bp
25,244,520 bp
25,244,540 bp
25,244,560 bp
25,244,580 bp
25,244,600 bp
25,244,620 bp
25,244,640 bp
19R23845_chr2_25244580.bam Cov
age
[0 - 58]
19R23845_chr2_25244580.bam
Sequence
Refseq Select
DNMT3A

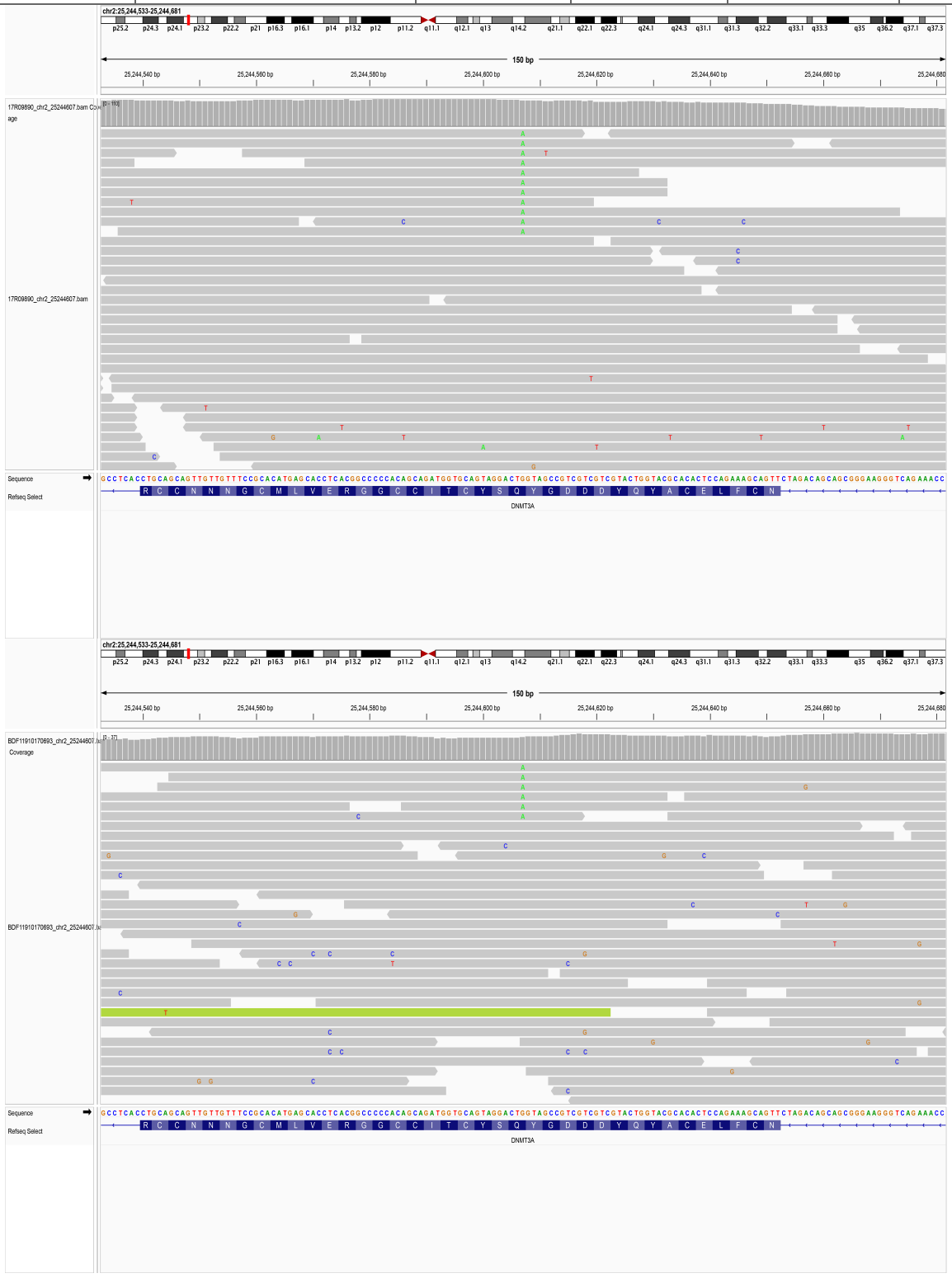
12.97. chr2_25244592_TGGTGCAGTAGGAC/-

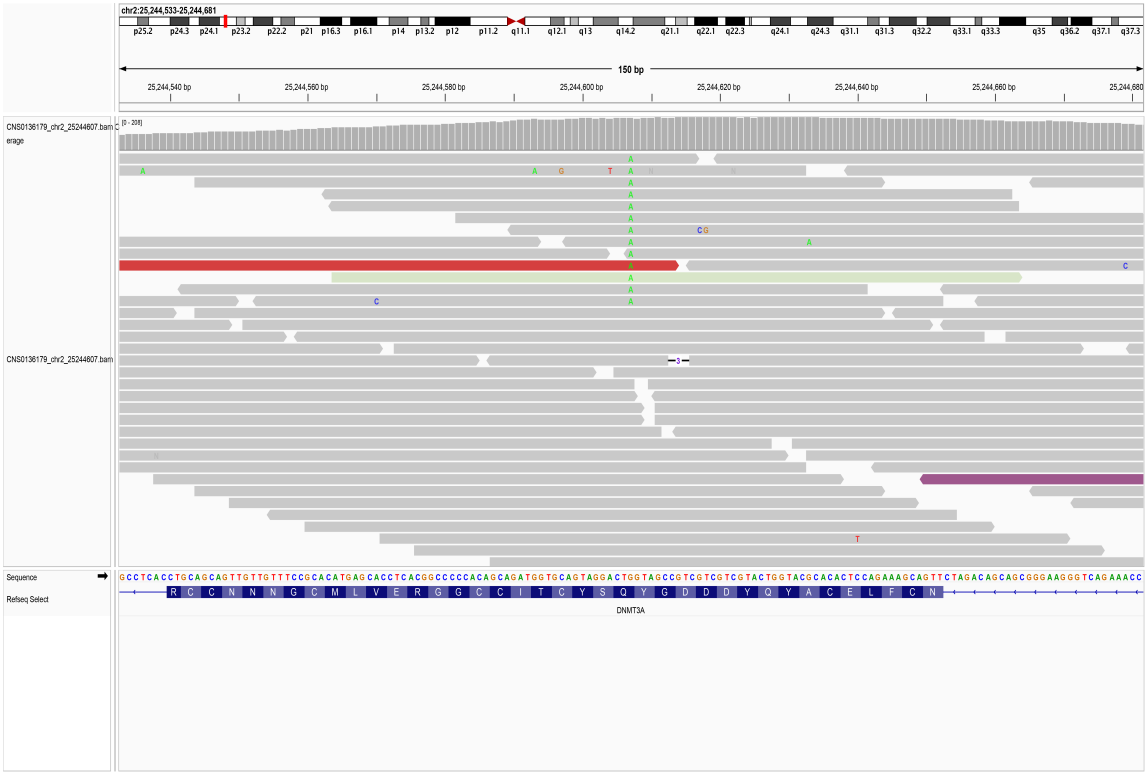
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HD27_72	chr2_25244592_TGGTGCAGTAGGAC/-	36	5	*DNMT3A*	frameshift_variant



12.98. chr2_25244607_G/A

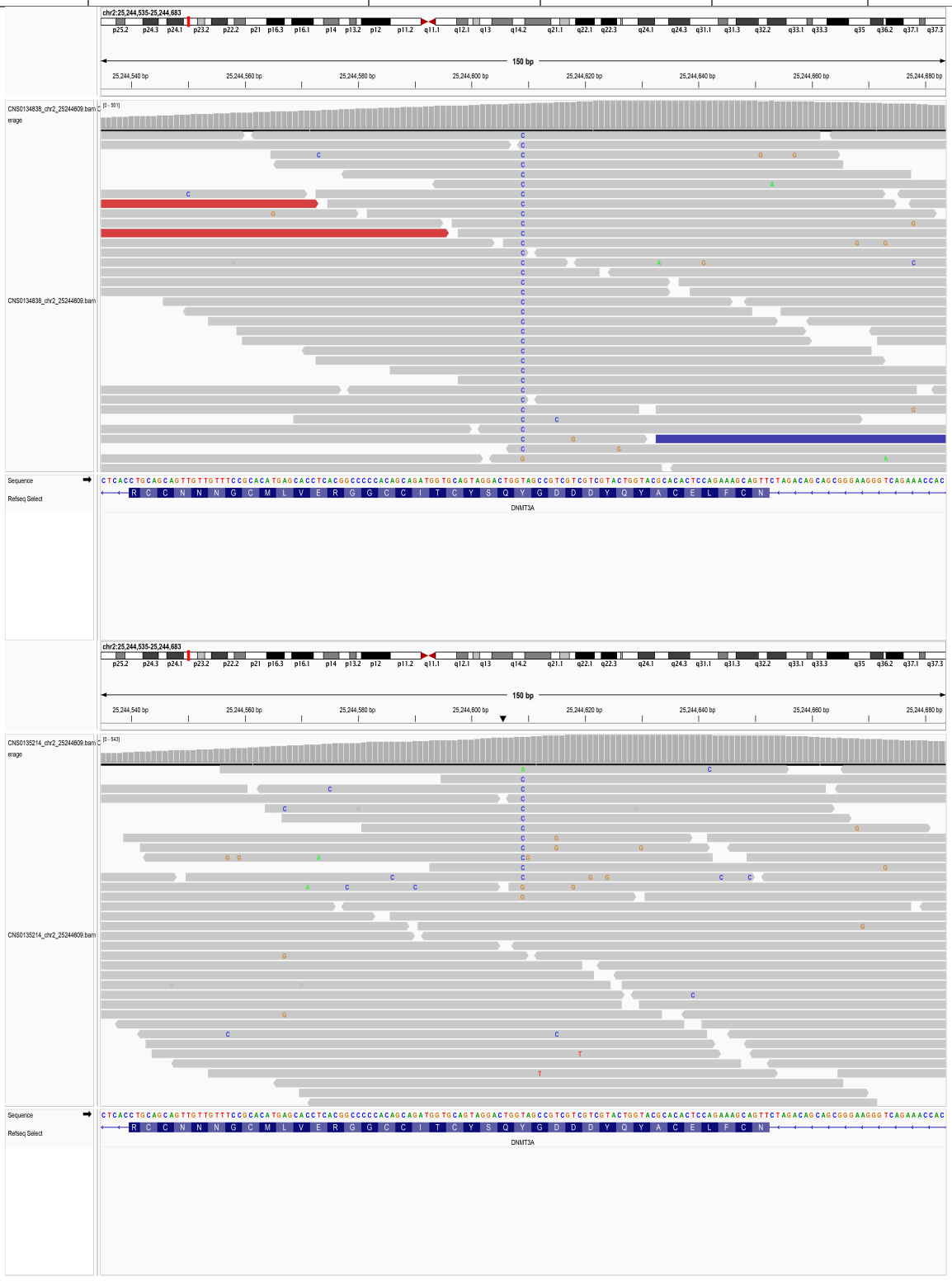
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09890	chr2_25244607_G/A	88	11	*DNMT3A*	stop_gained
BDF11910170693	chr2_25244607_G/A	24	6	*DNMT3A*	stop_gained
CNS0136179	chr2_25244607_G/A	182	11	*DNMT3A*	stop_gained




chr2:25,244,533-25,244,681
150 bp
25,244,540 bp
25,244,560 bp
25,244,580 bp
25,244,600 bp
25,244,620 bp
25,244,640 bp
25,244,660 bp
25,244,680
CNS0136179_chr2_25244607.bam C
erage
CNS0136179_chr2_25244607.bam
Sequence
Refseq Select
DNMT3A

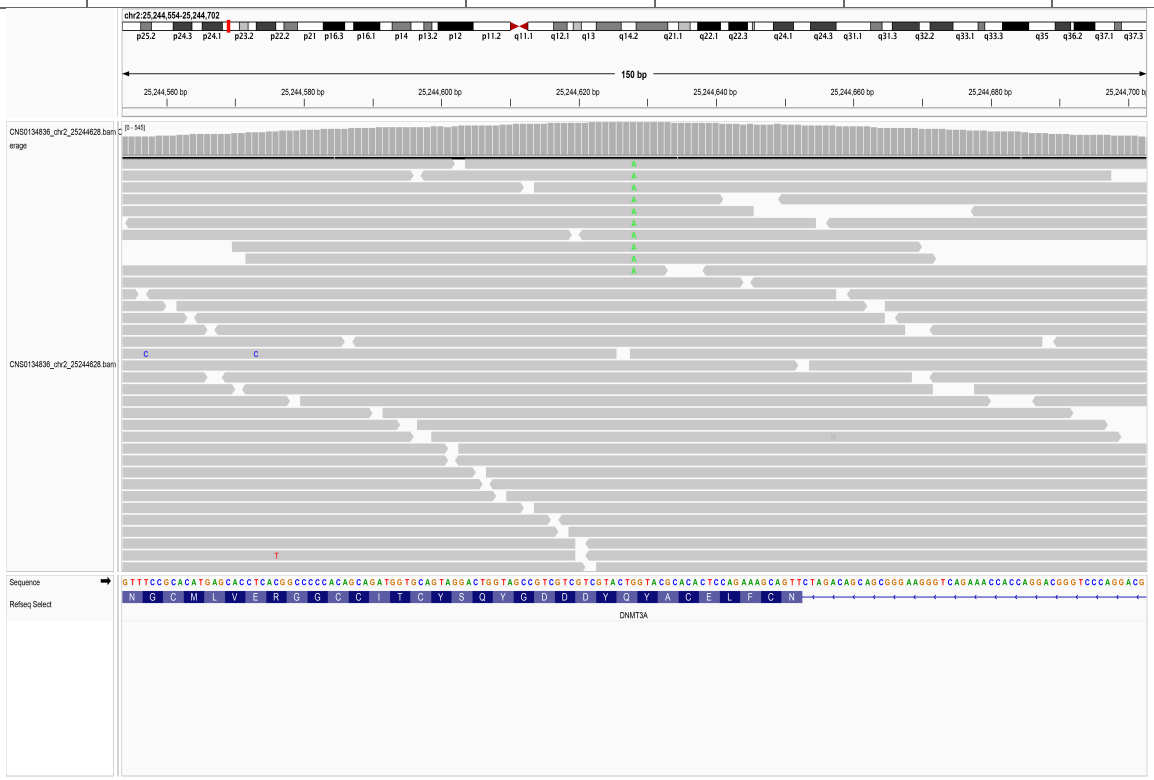
12.99. chr2_25244609_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134838	chr2_25244609_T/C	391	38	*DNMT3A*	missense_variant
CNS0135214	chr2_25244609_T/C	468	12	*DNMT3A*	missense_variant



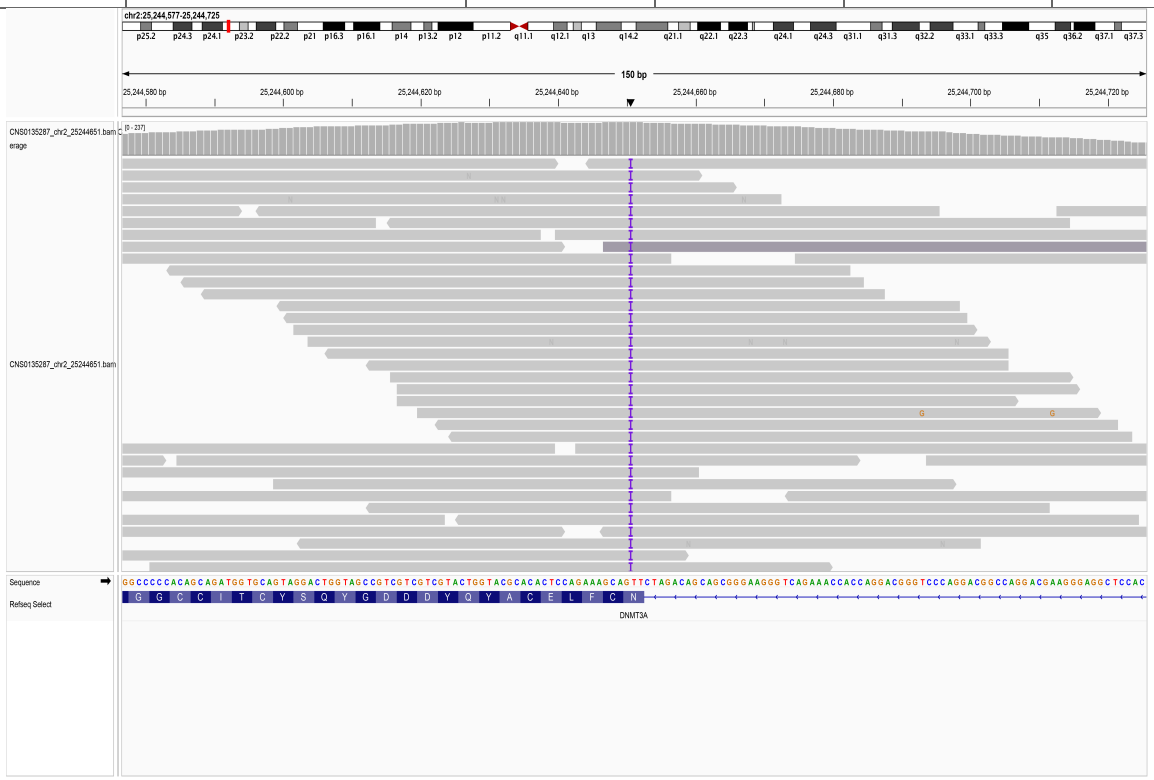
12.100. chr2_25244628_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134836	chr2_25244628_G/A	503	21	*DNMT3A*	stop_gained



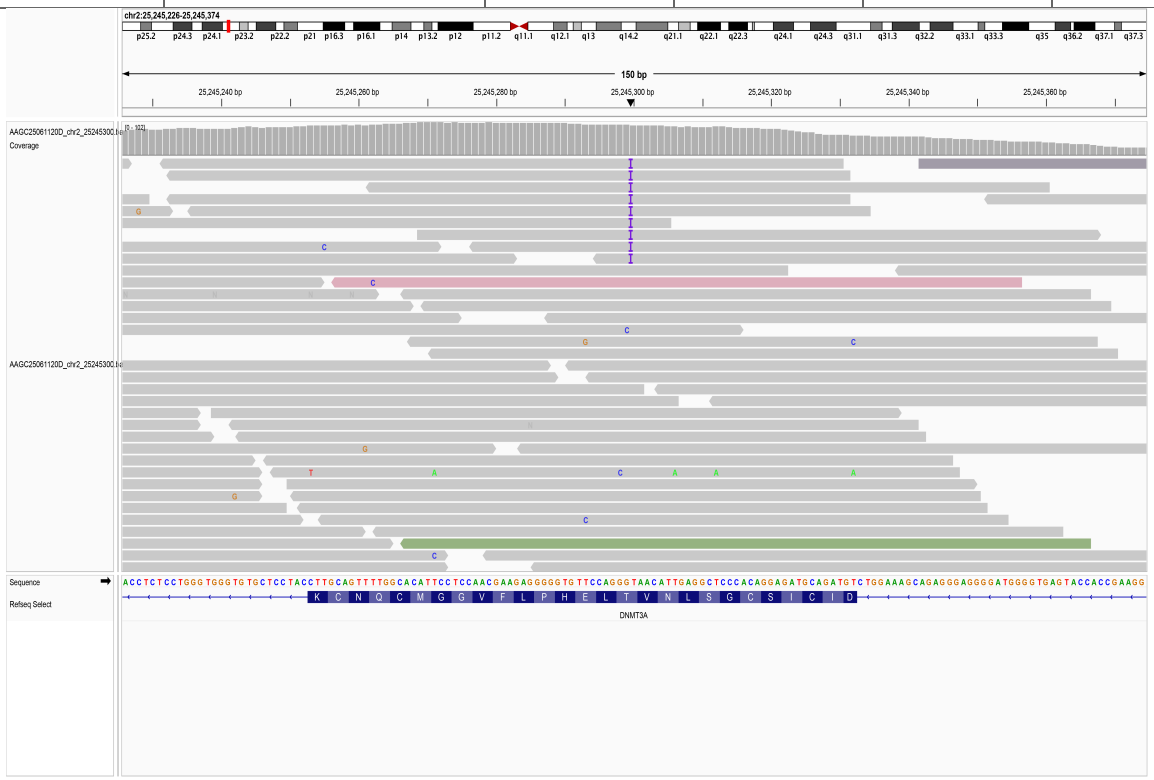
12.101. chr2_25244651_-/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135287	chr2_25244651_-/T	174	43	*DNMT3A*	frameshift_variant



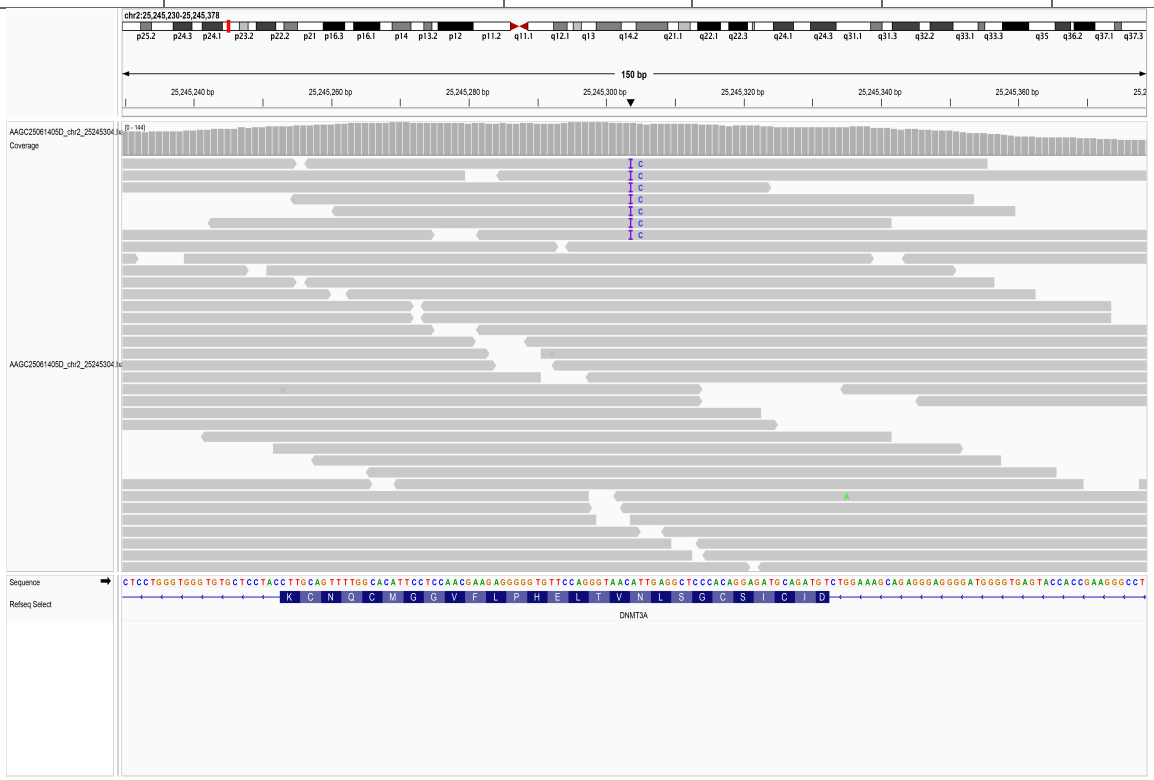
12.102. chr2_25245300_-/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061120D	chr2_25245300_-/T	78	9	*DNMT3A*	frameshift_variant



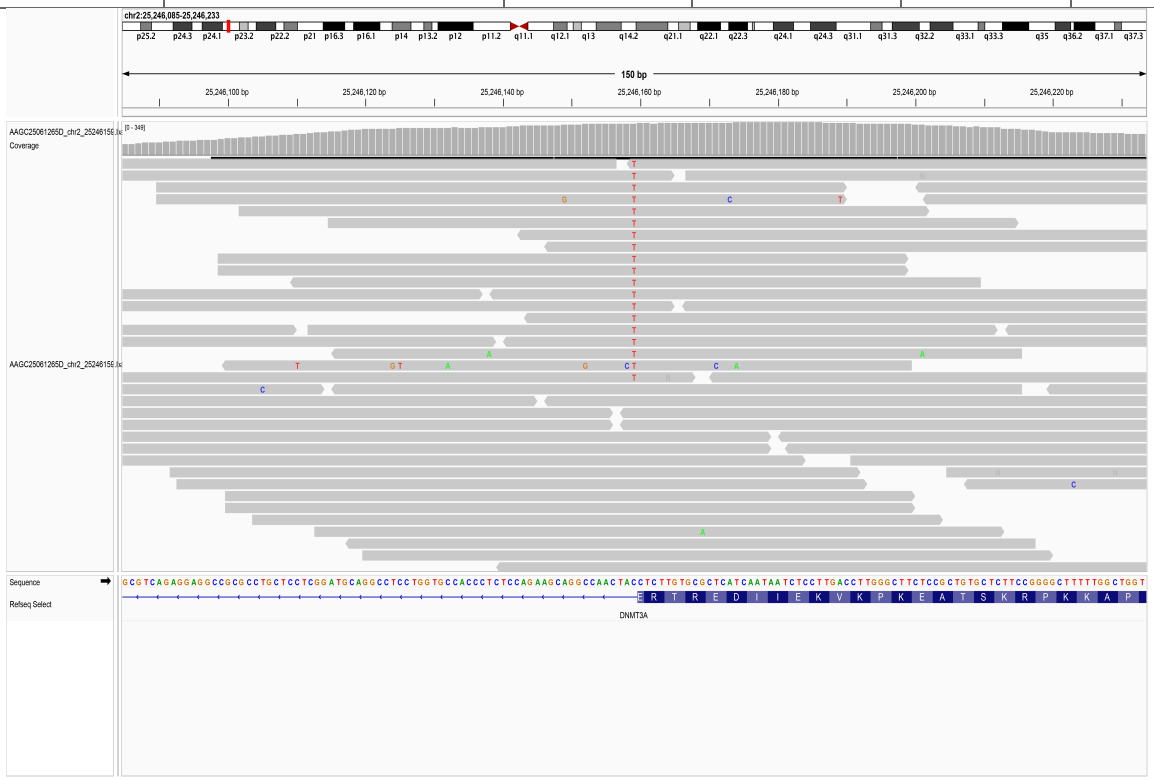
12.103. chr2_25245304_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061405D	chr2_25245304_-/A	127	8	*DNMT3A*	frameshift_variant



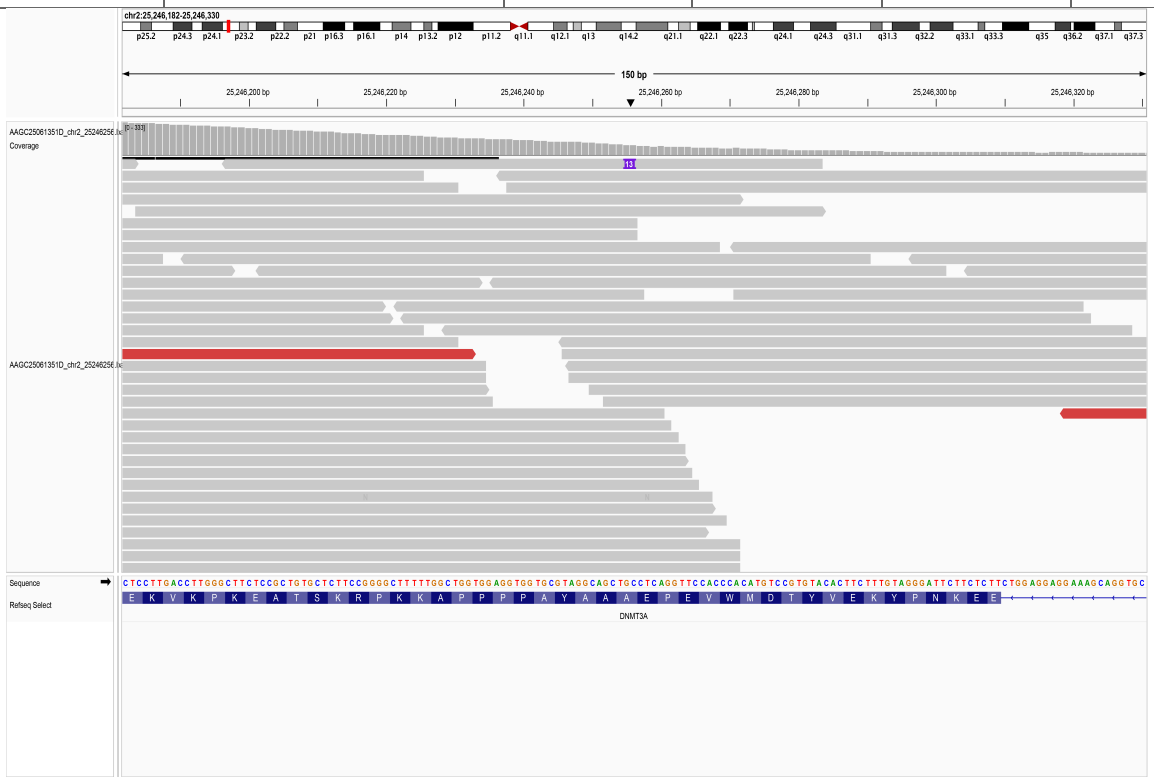
12.104. chr2_25246159_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061265D	chr2_25246159_C/T	304	18	*DNMT3A*	splice_donor_variant



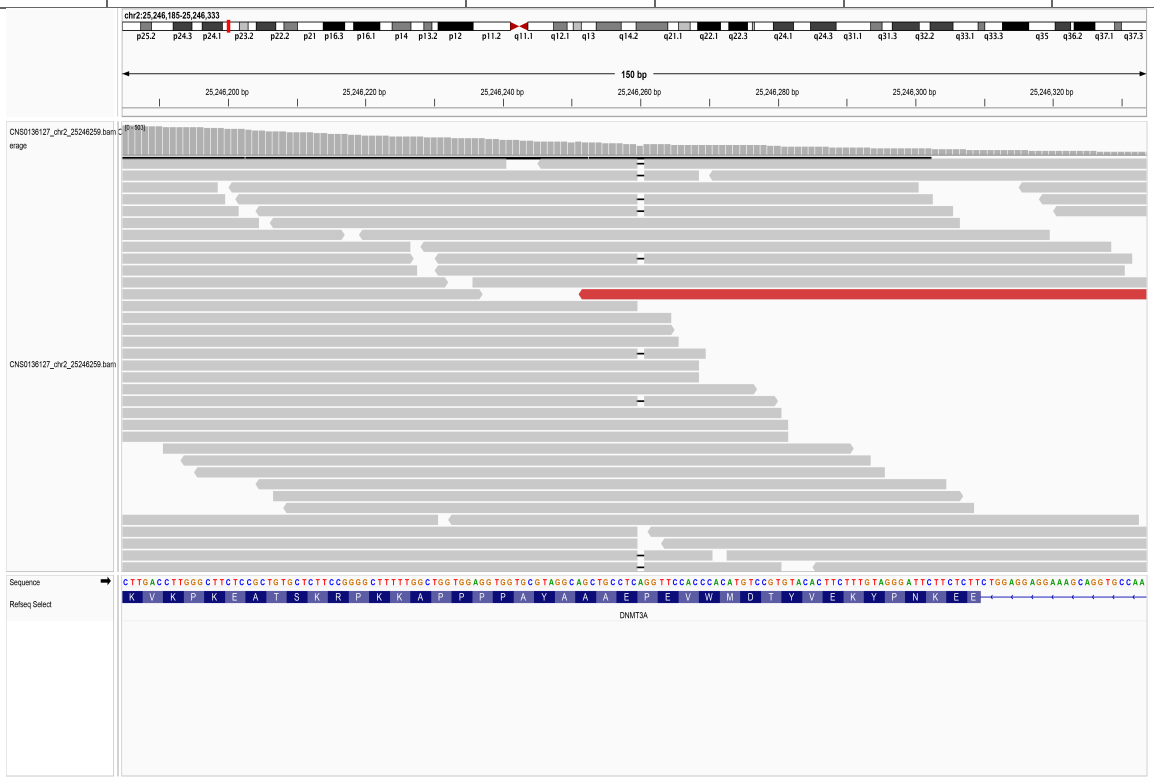
12.105. chr2_25246256_-/CCTCAGGTTCCCT

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061351D	chr2_25246256_-/CCTCAGGTTCCCT	75	3	*DNMT3A*	stop_gained



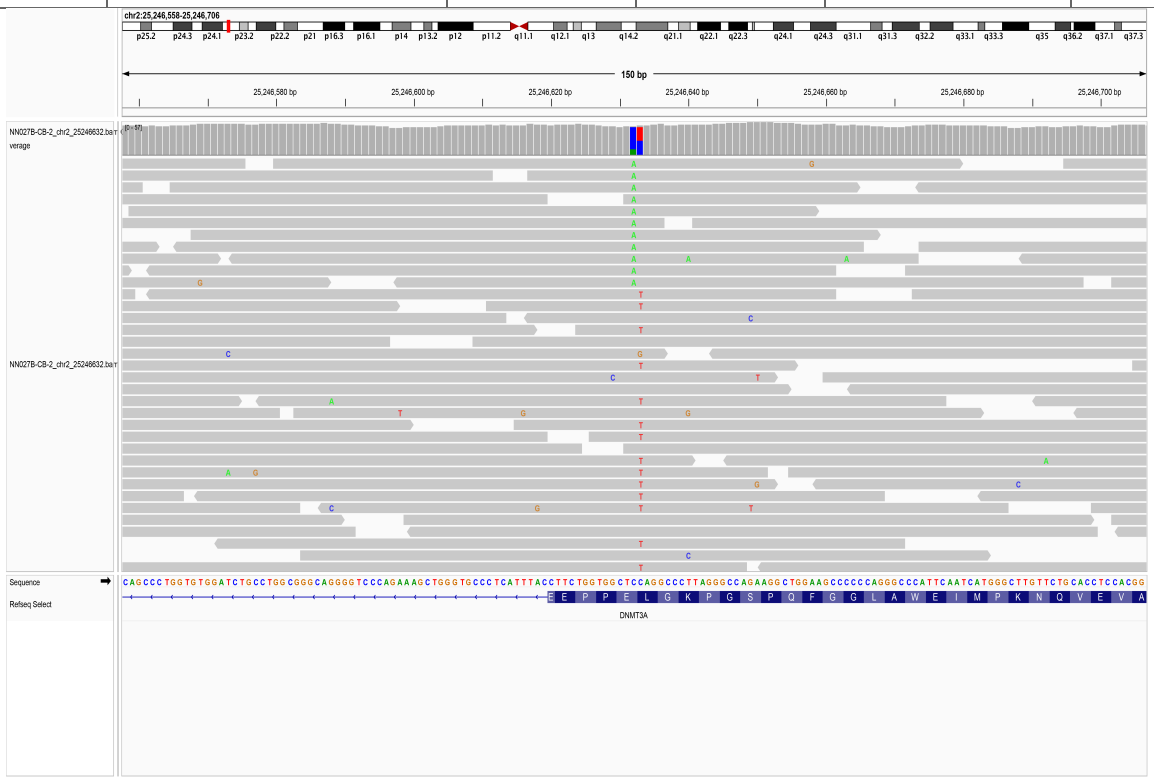
12.106. chr2_25246260_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136127	chr2_25246260_A/-	138	31	*DNMT3A*	frameshift_variant



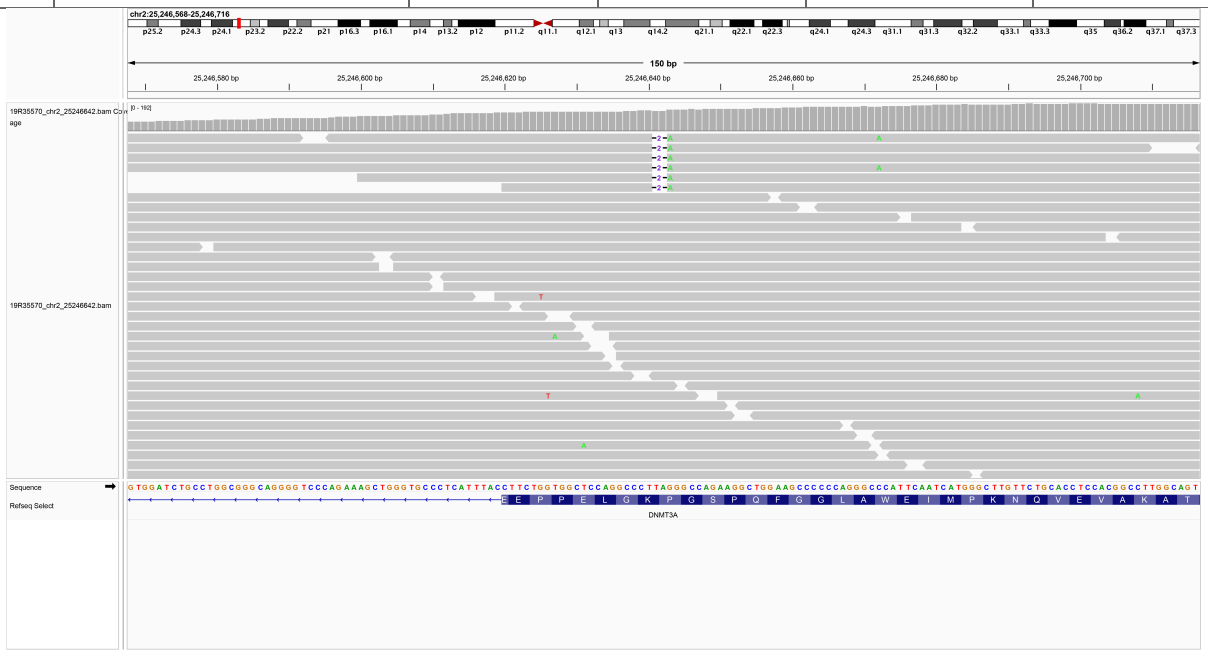
12.107. chr2_25246632_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NN027B-CB-2	chr2_25246632_C/A	38	11	*DNMT3A*	stop_gained



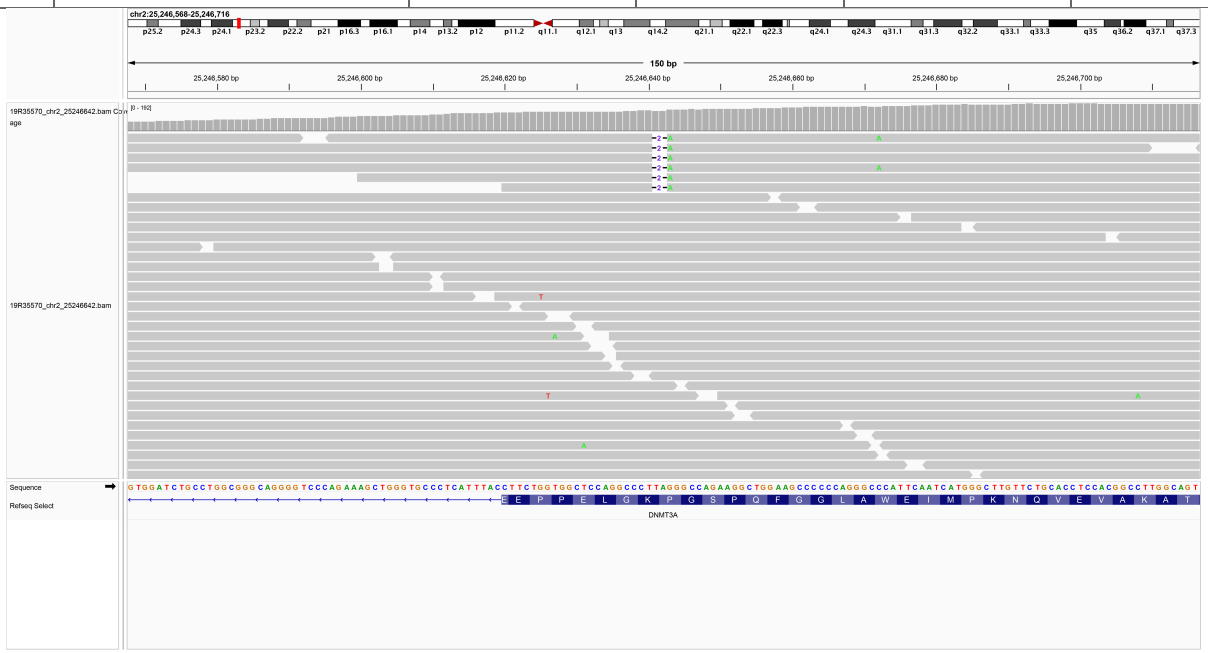
12.108. chr2_25246640_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R35570	chr2_25246640_T/-	137	6	*DNMT3A*	frameshift_variant



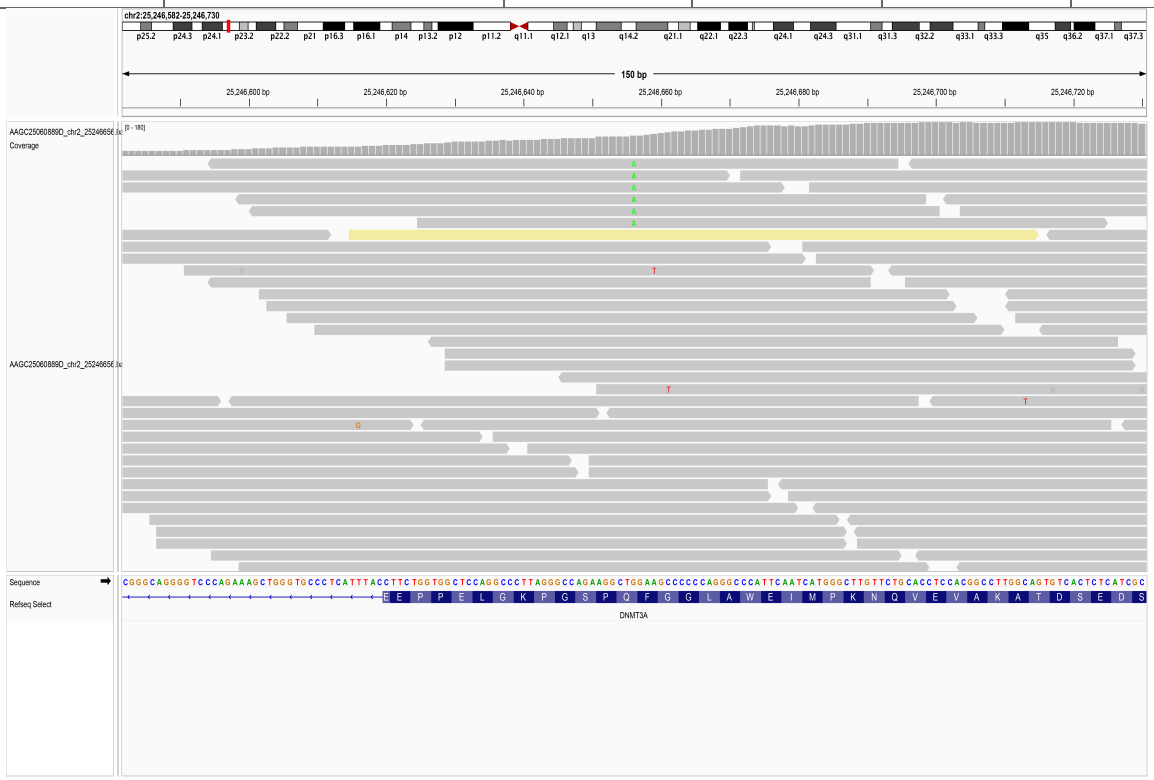
12.109. chr2_25246641_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R35570	chr2_25246641_G/-	139	6	*DNMT3A*	frameshift_variant



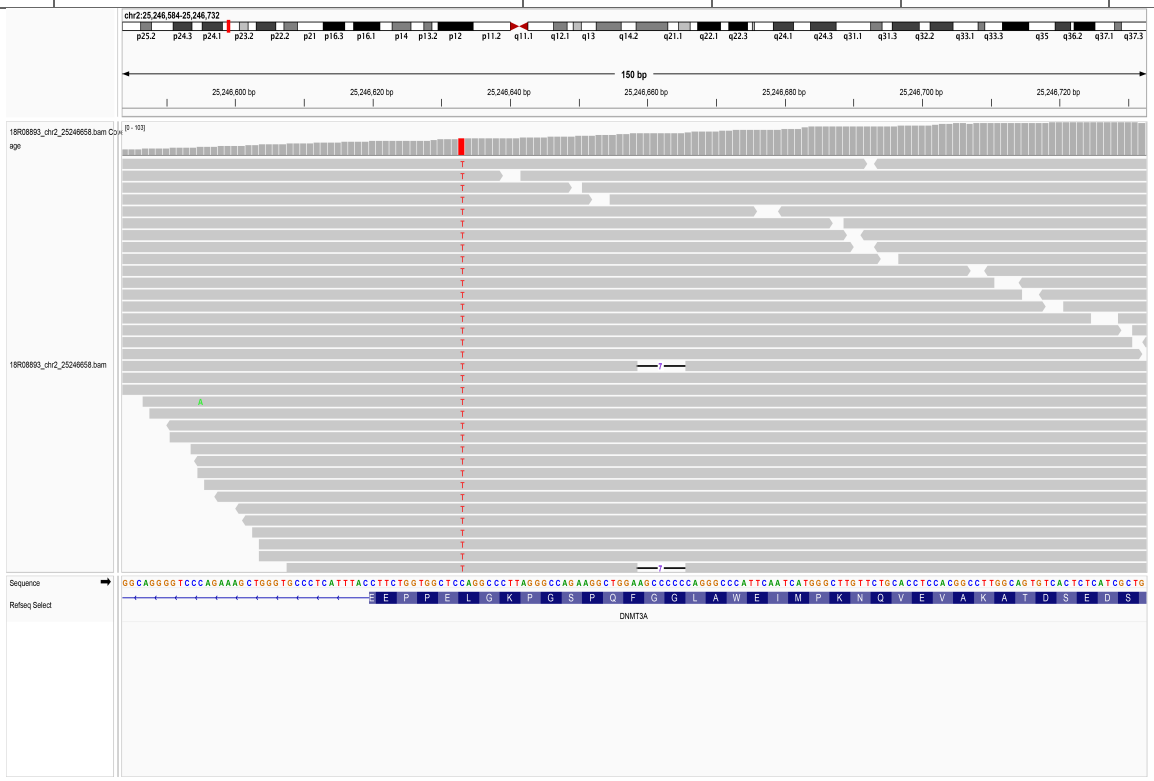
12.110. chr2_25246656_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060889D	chr2_25246656_G/A	96	6	*DNMT3A*	stop_gained



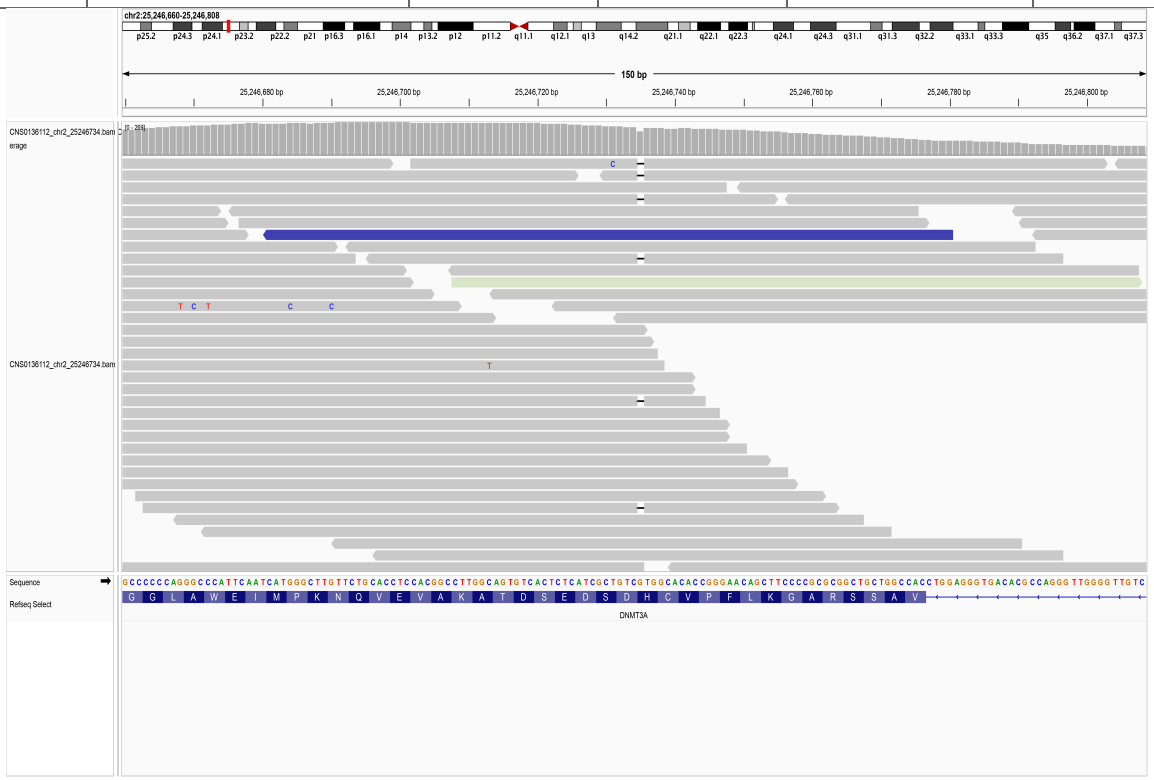
12.111. chr2_25246659_AGCCCCC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08893	chr2_25246659_AGCCCCC/-	68	3	*DNMT3A*	frameshift_variant



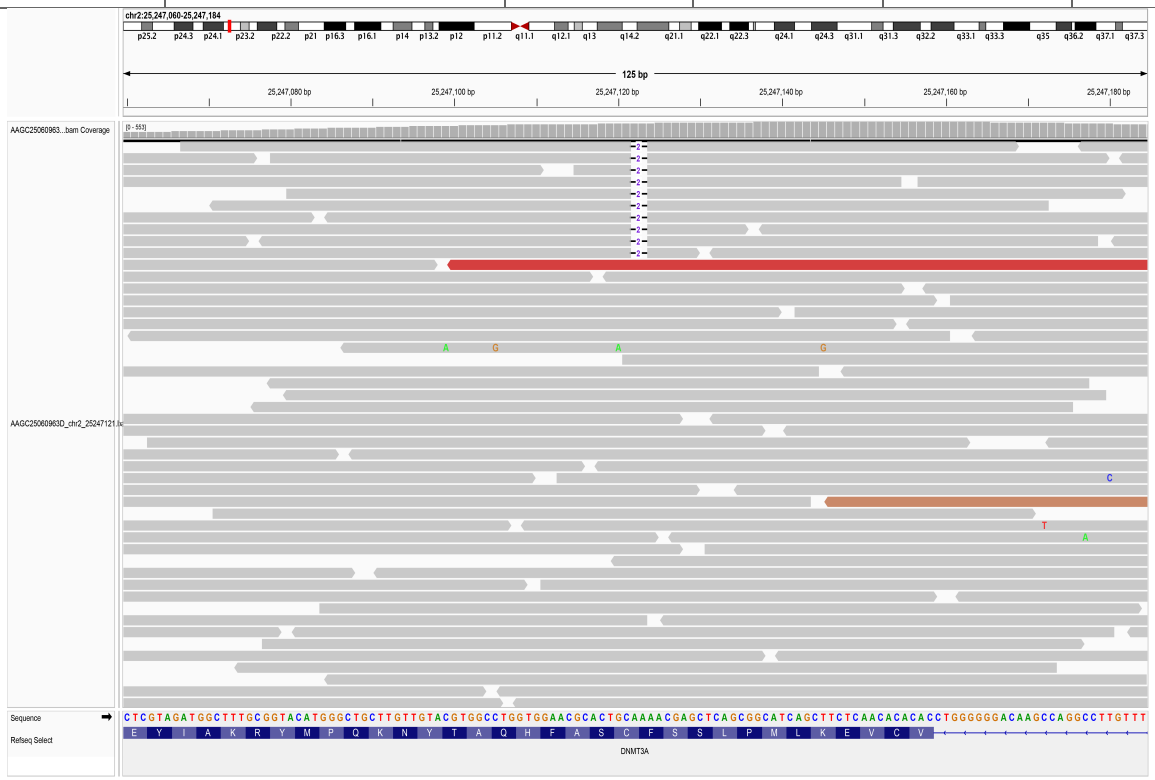
12.112. chr2_25246735_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136112	chr2_25246735_G/-	188	28	*DNMT3A*	frameshift_variant



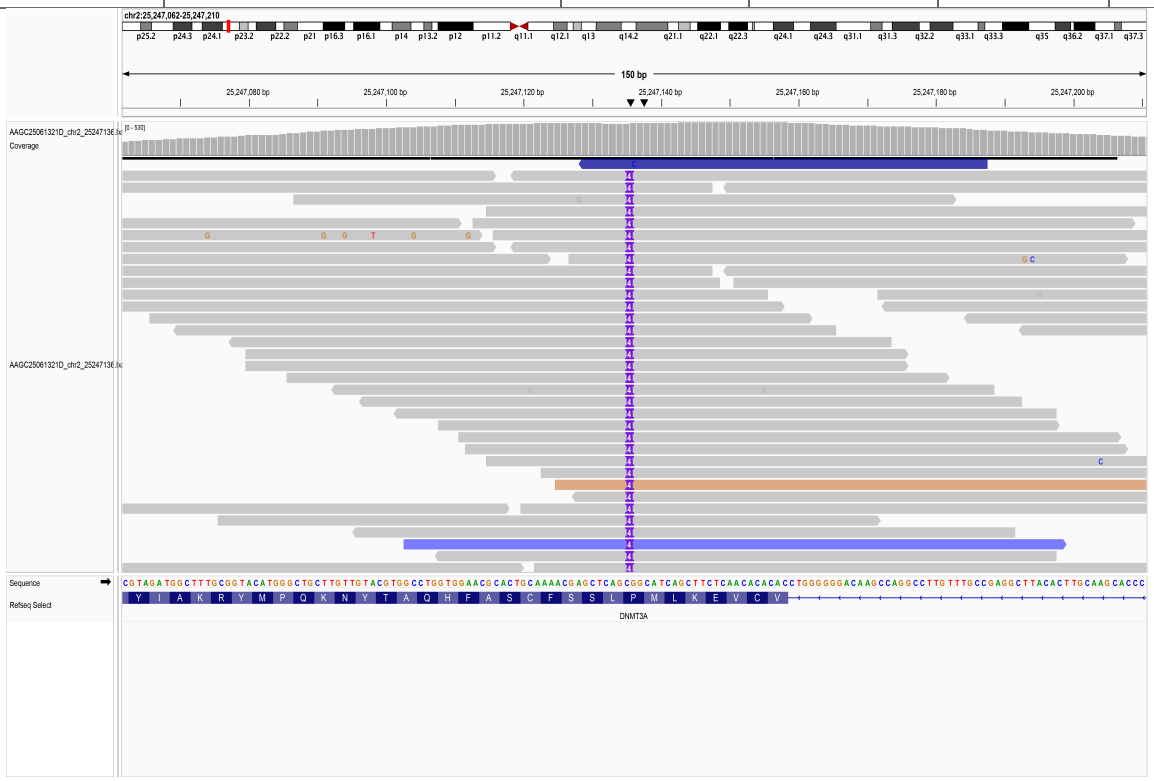
12.113. chr2_25247122_AA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060963D	chr2_25247122_AA/-	473	16	*DNMT3A*	frameshift_variant



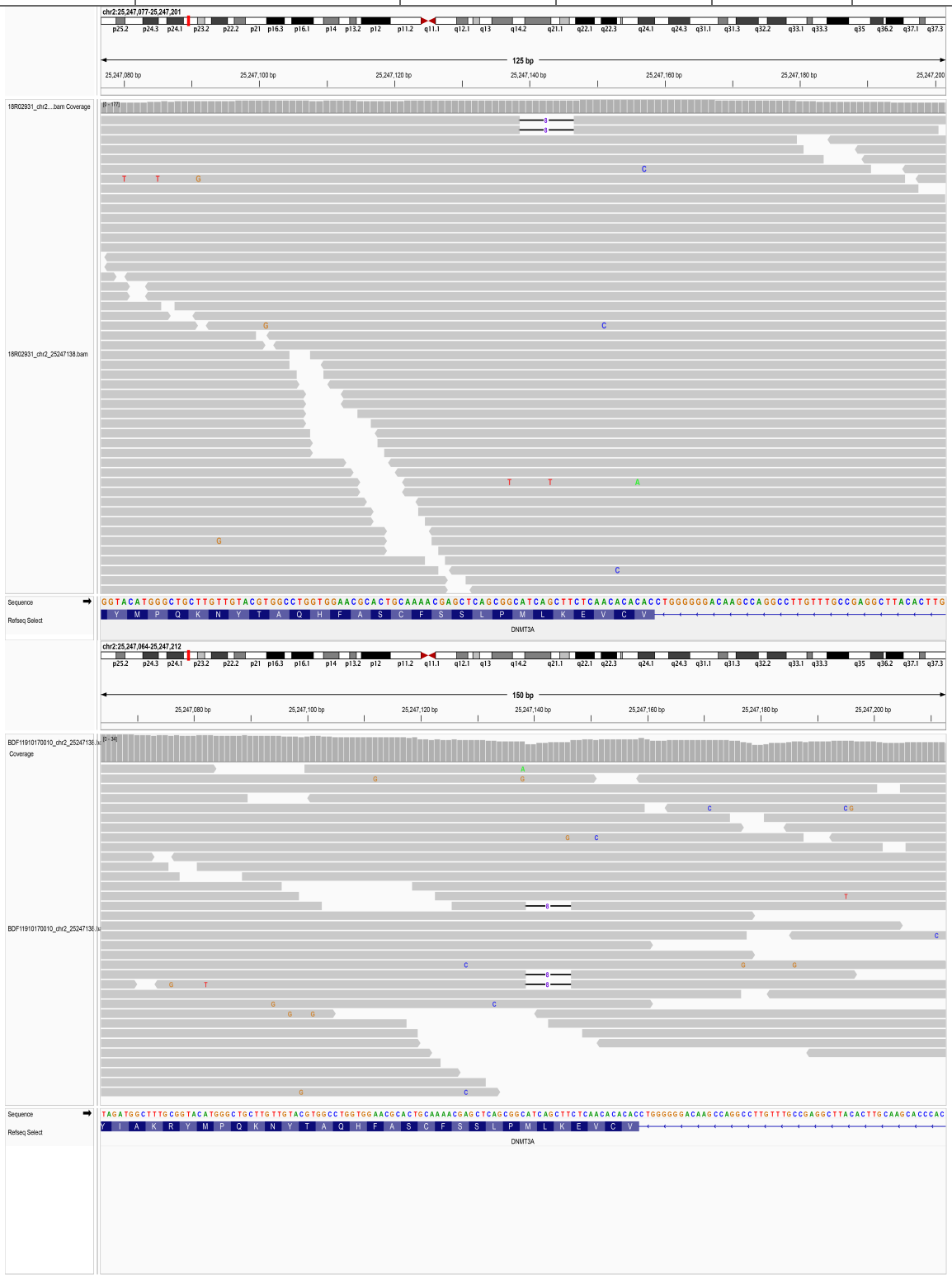
12.114. chr2_25247136_-/GGCA

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061321D	chr2_25247136_-/GGCA	394	68	*DNMT3A*	frameshift_variant



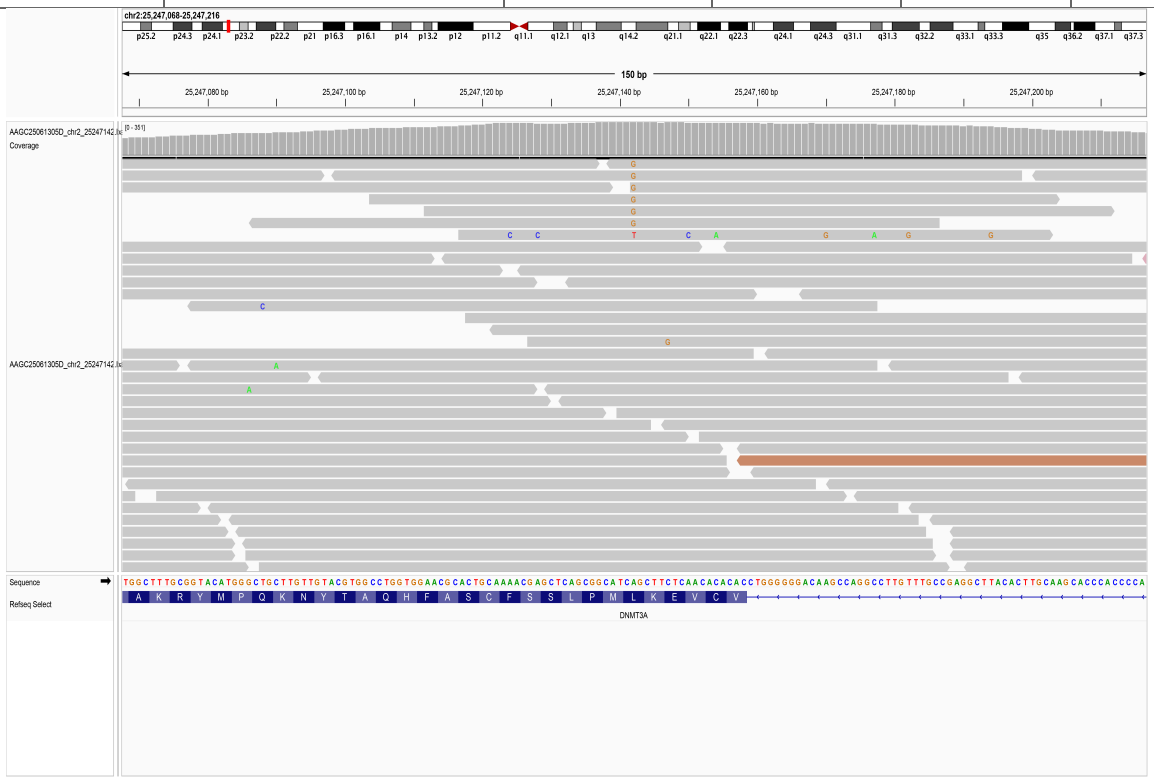
12.115. chr2_25247139_ATCAGCTT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R02931	chr2_25247139_ATCAGCTT/-	168	4	*DNMT3A*	frameshift_variant
BDF11910170010	chr2_25247139_ATCAGCTT/-	24	3	*DNMT3A*	frameshift_variant



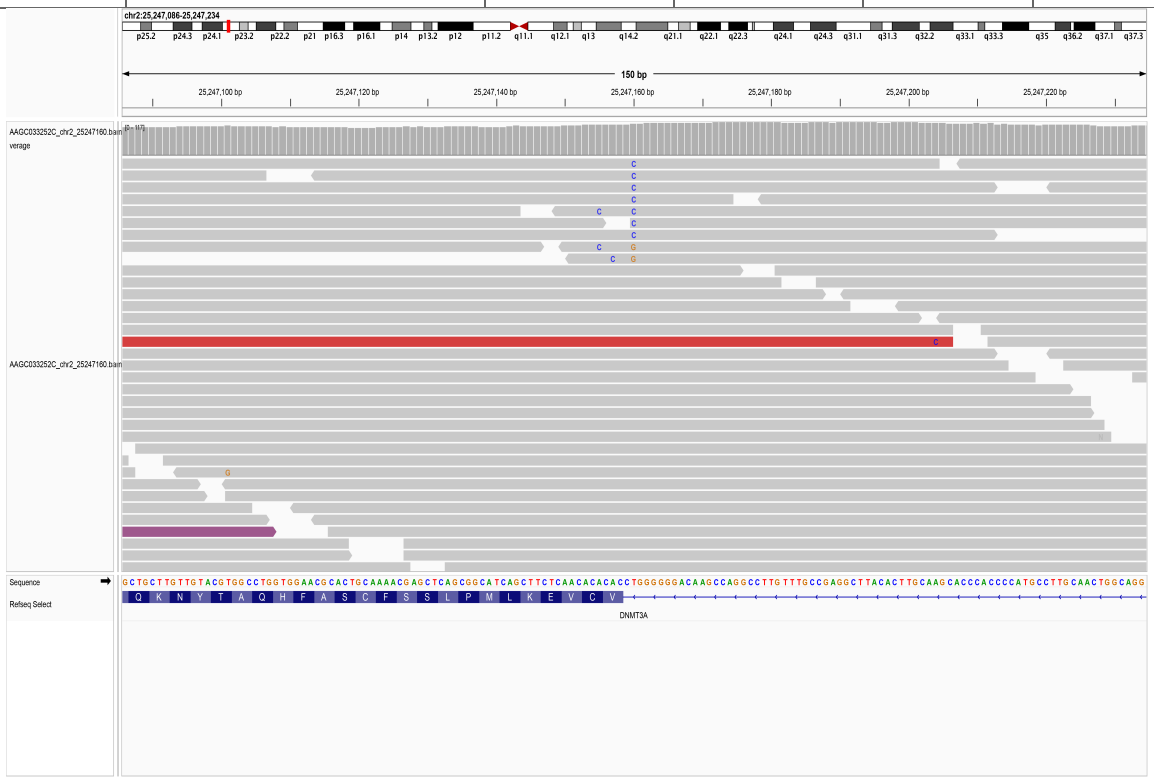
12.116. chr2_25247142_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061305D	chr2_25247142_A/G	328	6	*DNMT3A*	missense_variant



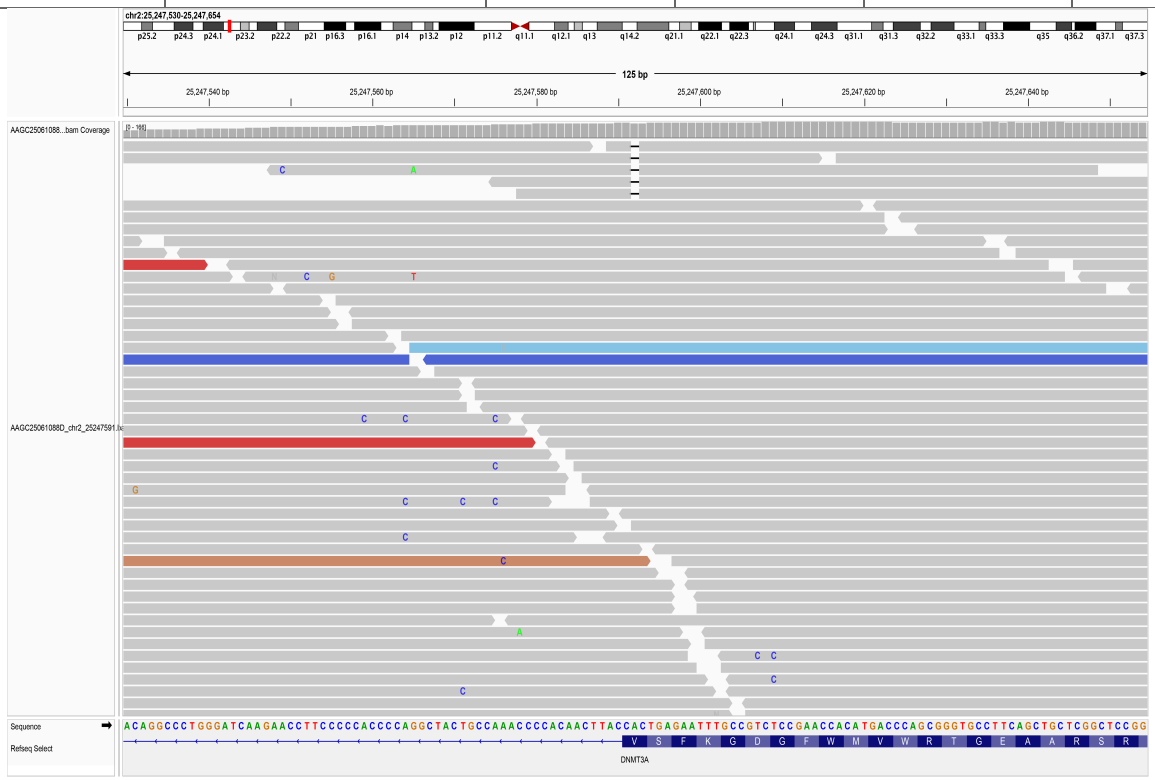
12.117. chr2_25247160_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033252C	chr2_25247160_T/C	98	6	*DNMT3A*	splice_acceptor_variant



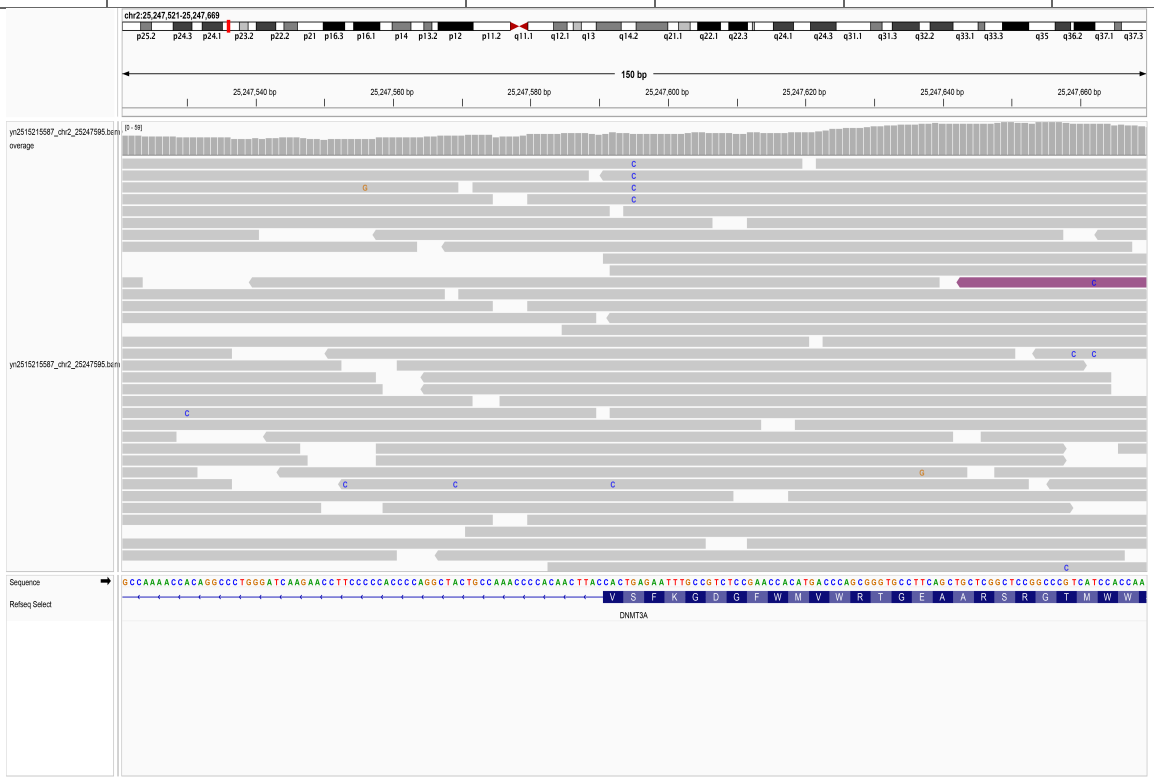
12.118. chr2_25247592_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061088D	chr2_25247592_A/-	142	5	*DNMT3A*	frameshift_variant



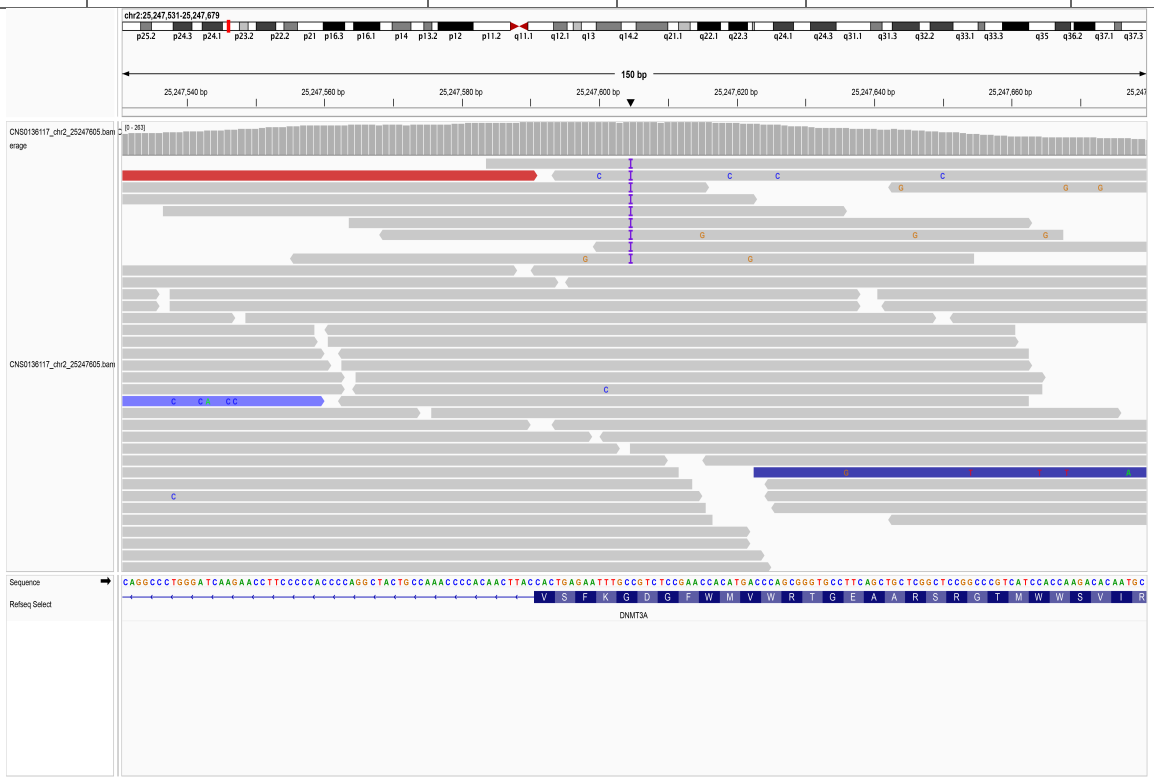
12.119. chr2_25247595_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
yn2515215587	chr2_25247595_G/C	34	4	*DNMT3A*	stop_gained



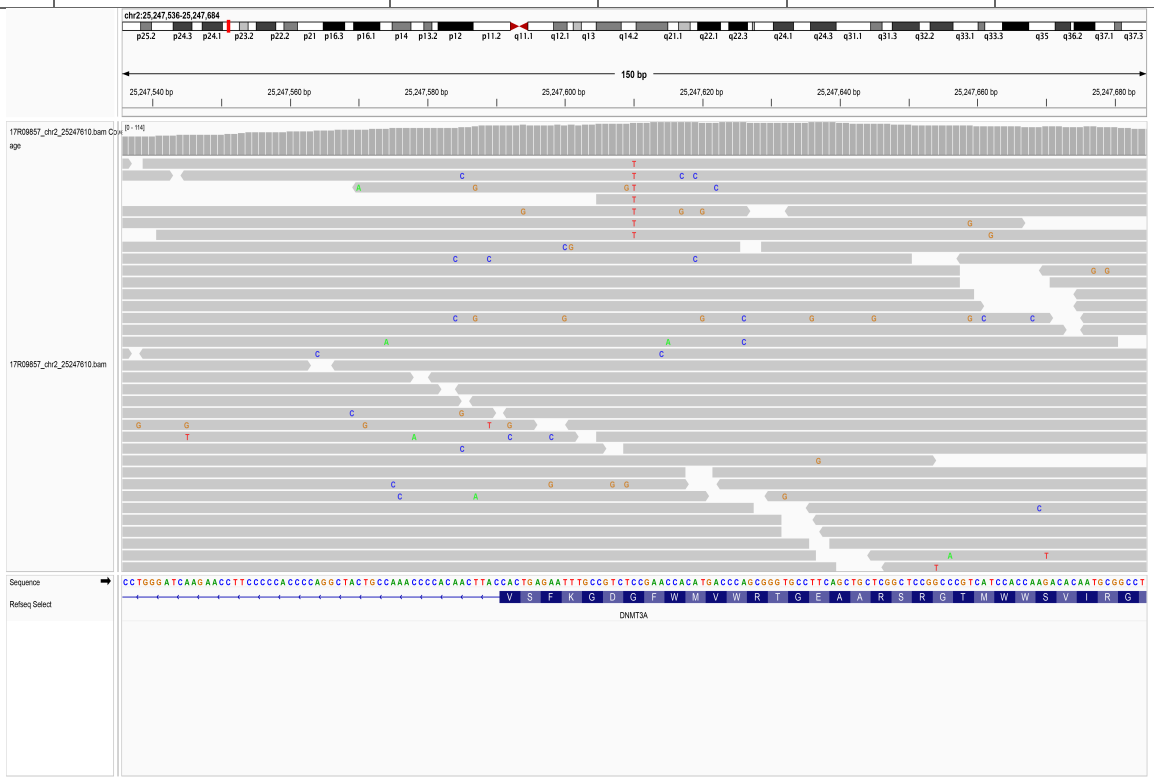
12.120. chr2_25247605_-/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136117	chr2_25247605_-/G	239	10	*DNMT3A*	frameshift_variant



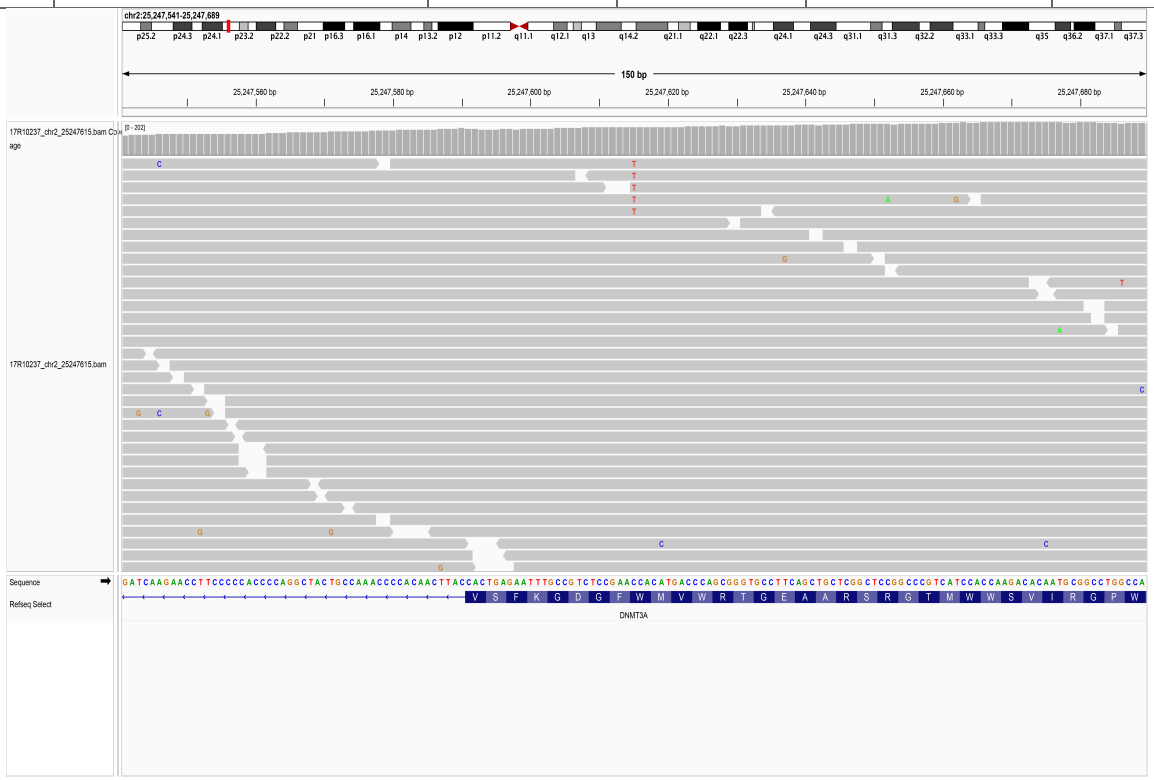
12.121. chr2_25247610_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09857	chr2_25247610_C/T	84	5	*DNMT3A*	missense_variant



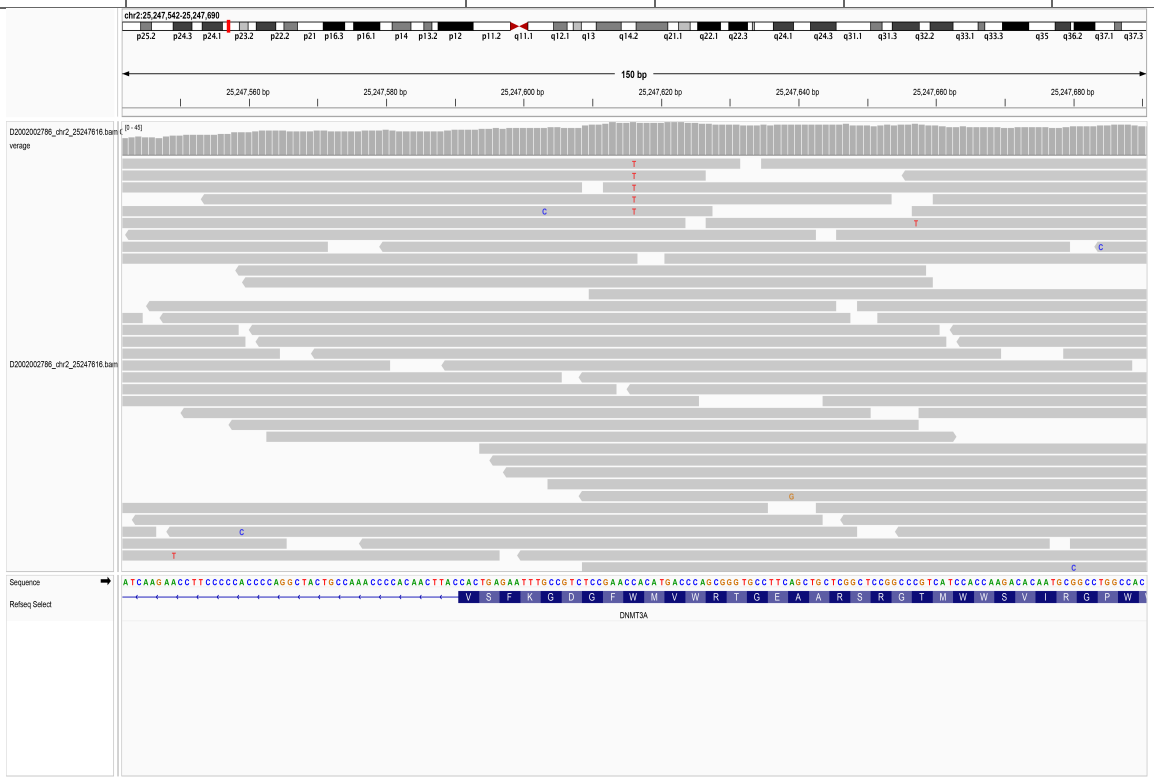
12.122. chr2_25247615_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R10237	chr2_25247615_C/T	156	5	*DNMT3A*	stop_gained



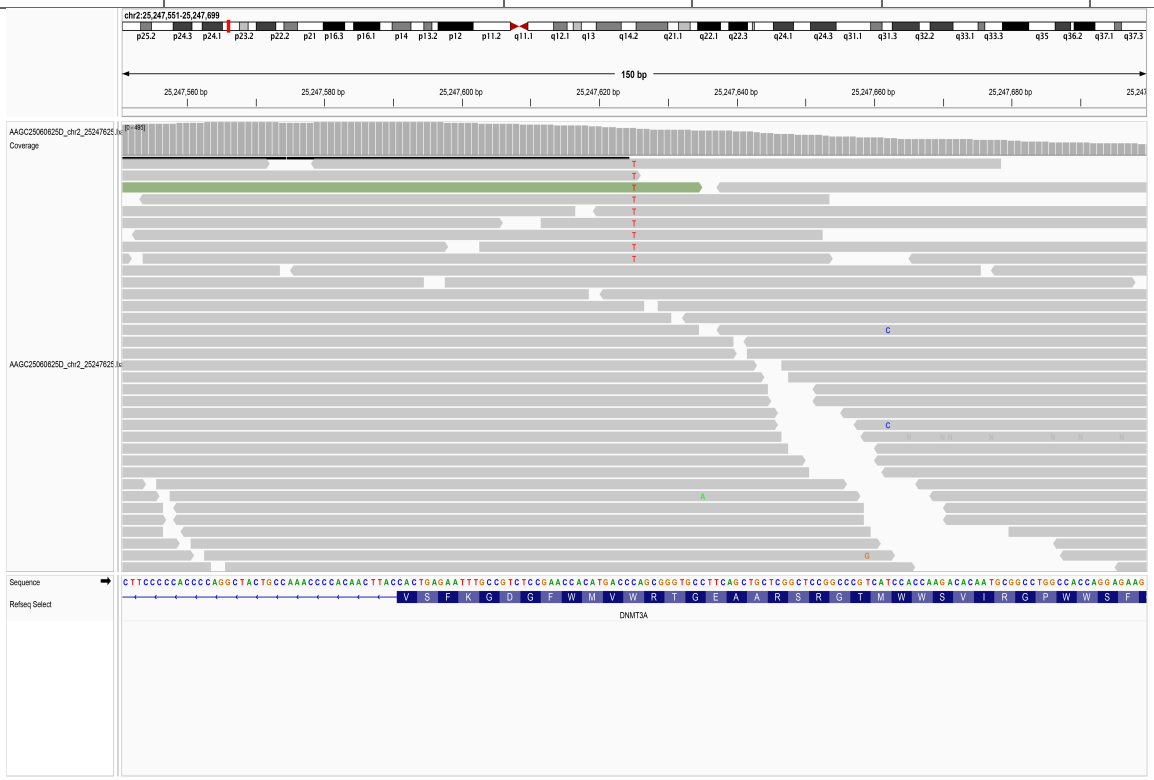
12.123. chr2_25247616_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2002002786	chr2_25247616_C/T	37	5	*DNMT3A*	stop_gained



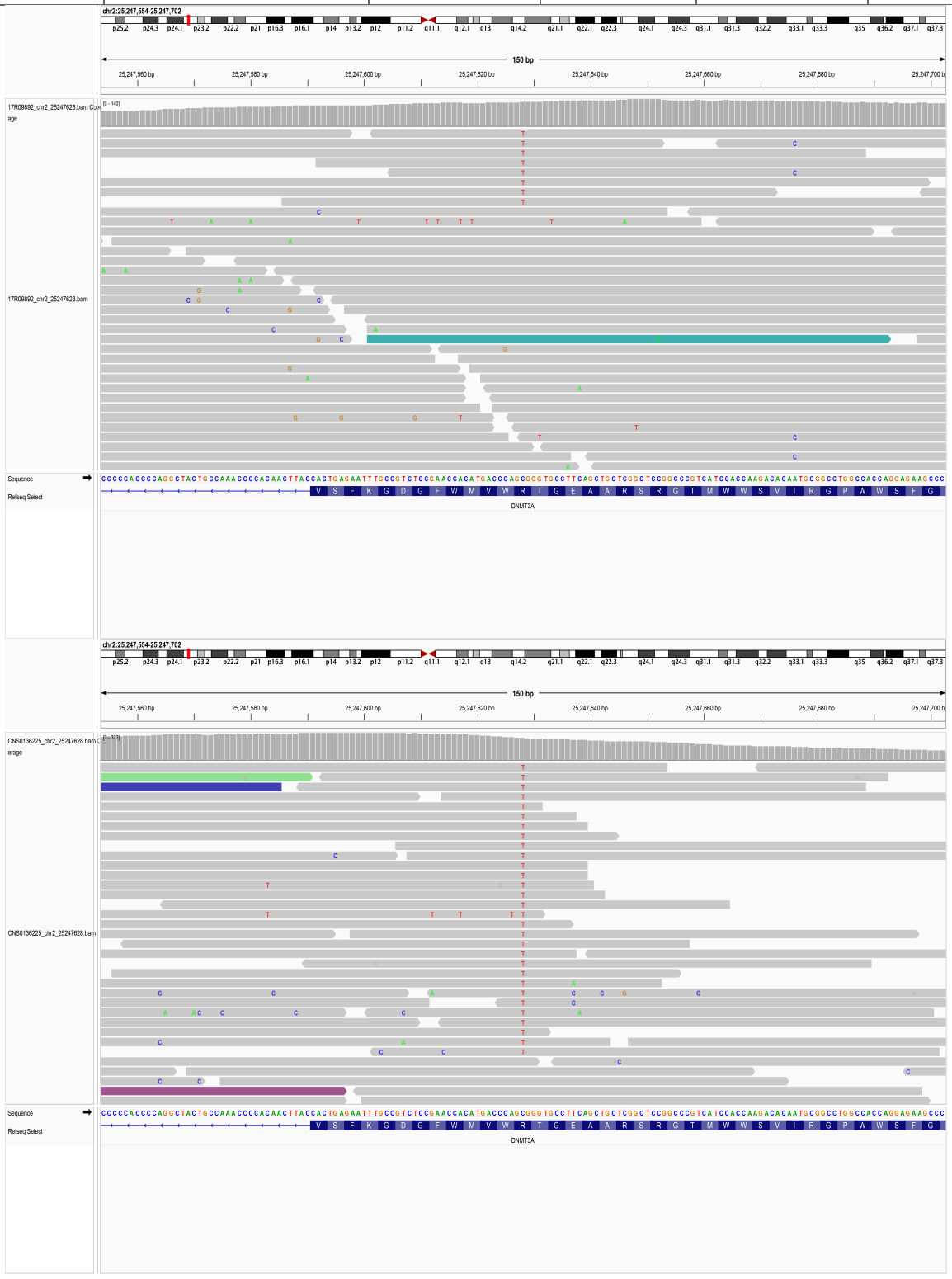
12.124. chr2_25247625_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060625D	chr2_25247625_C/T	381	9	*DNMT3A*	stop_gained



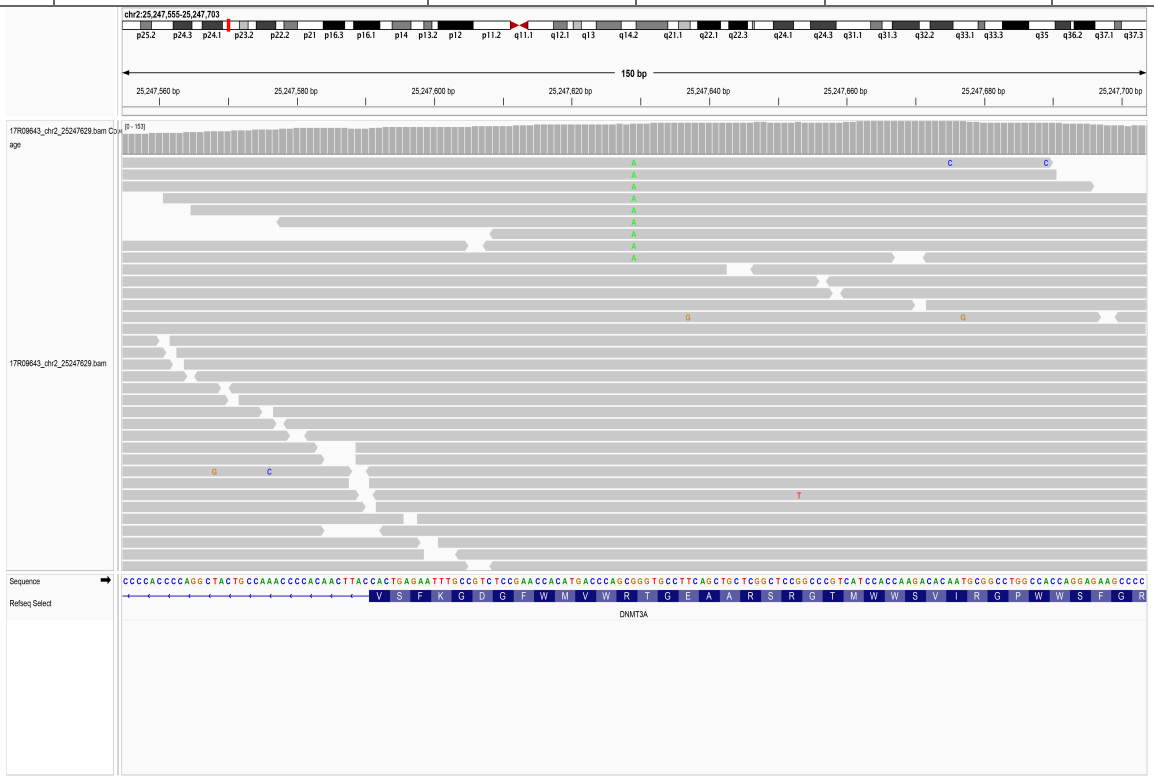
12.125. chr2_25247628_C/T

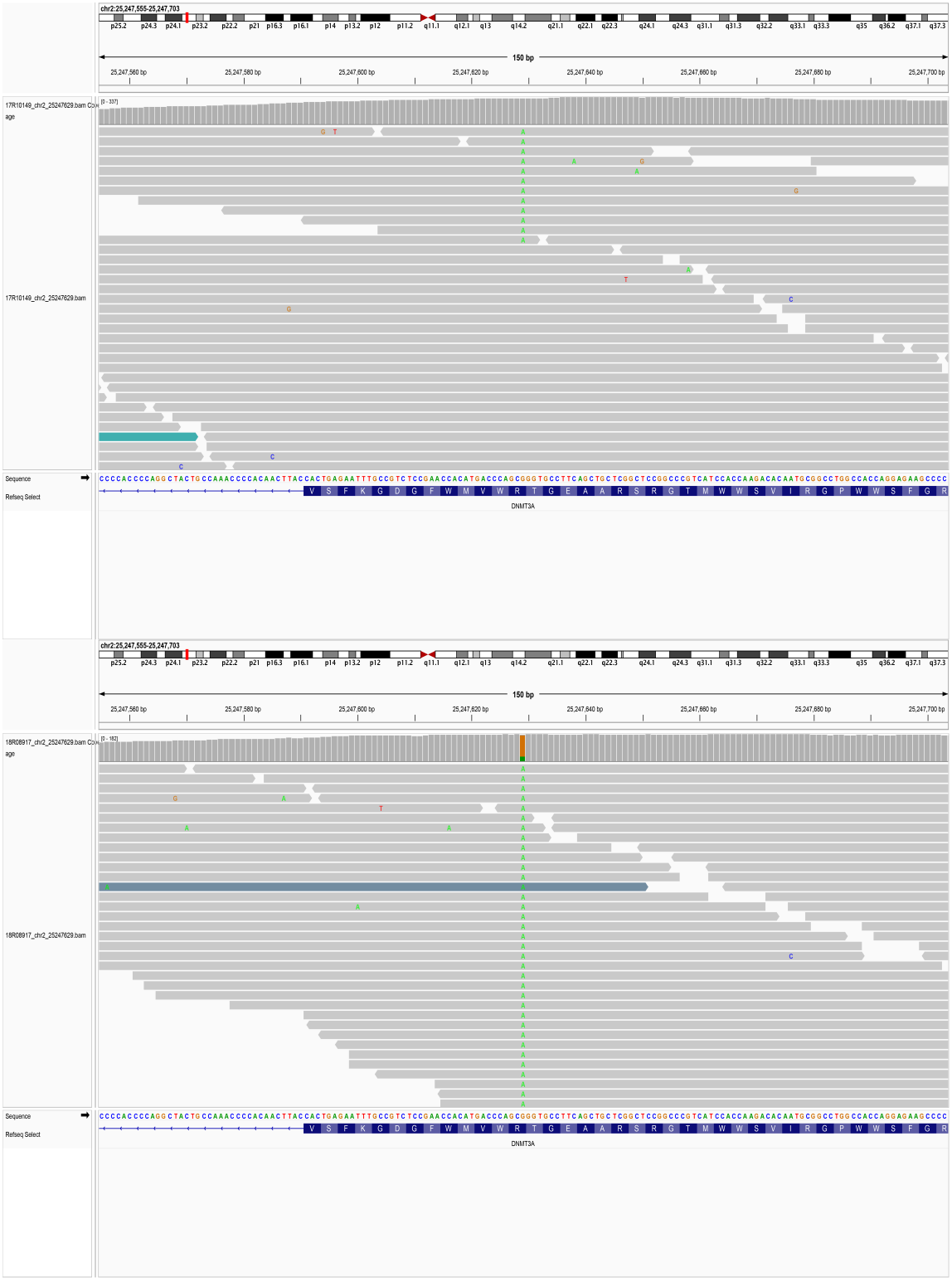
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09892	chr2_25247628_C/T	100	8	*DNMT3A*	missense_variant
CNS0136225	chr2_25247628_C/T	226	27	*DNMT3A*	missense_variant

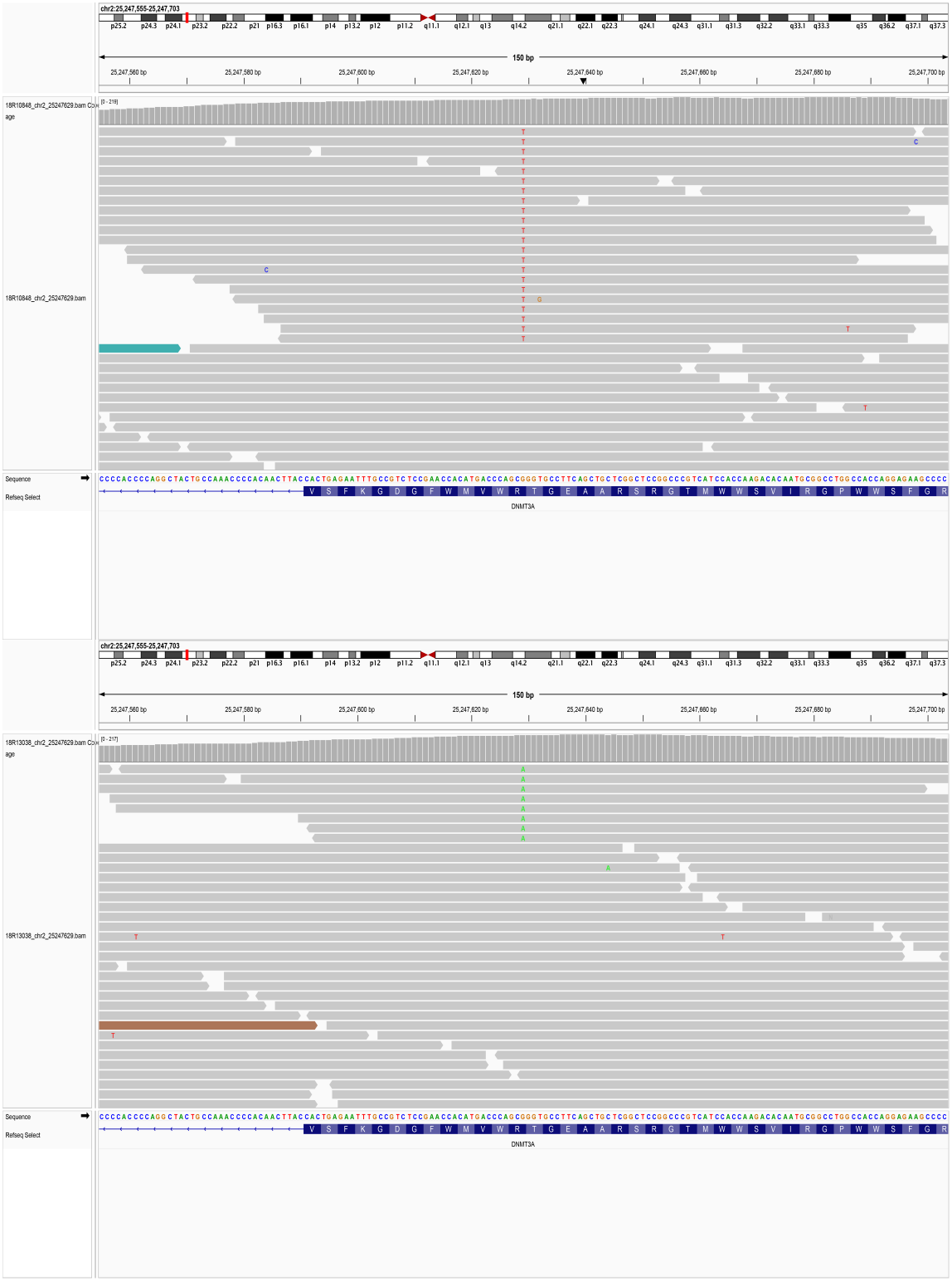


12.126. chr2_25247629_G/A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09643	chr2_25247629_G/A/T	126	9	*DNMT3A*	missense_variant
17R10149	chr2_25247629_G/A/T	298	11	*DNMT3A*	missense_variant
18R08917	chr2_25247629_G/A/T	138	35	*DNMT3A*	missense_variant
18R10848	chr2_25247629_G/A/T	173	22	*DNMT3A*	missense_variant
18R13038	chr2_25247629_G/A/T	199	8	*DNMT3A*	missense_variant

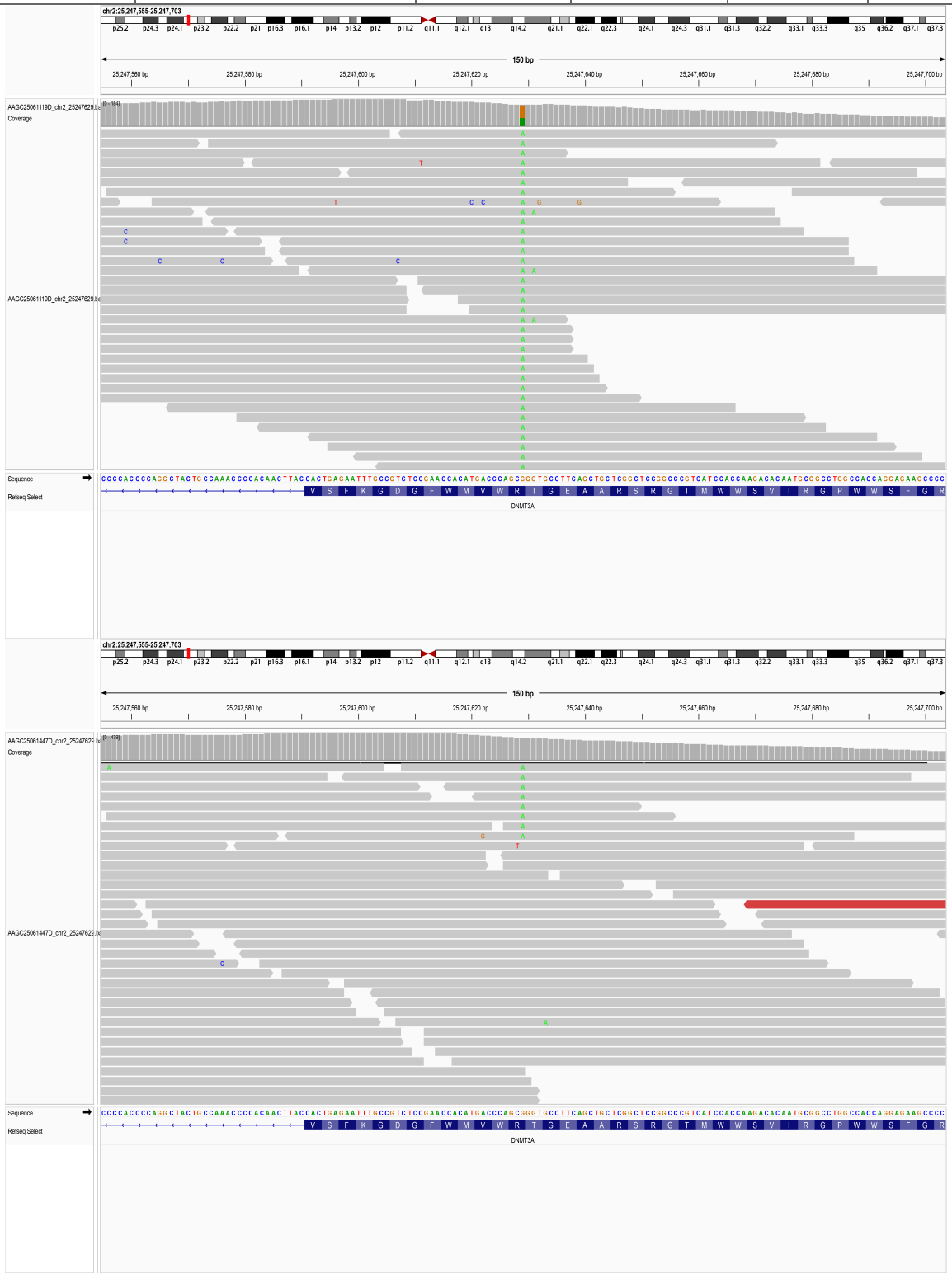


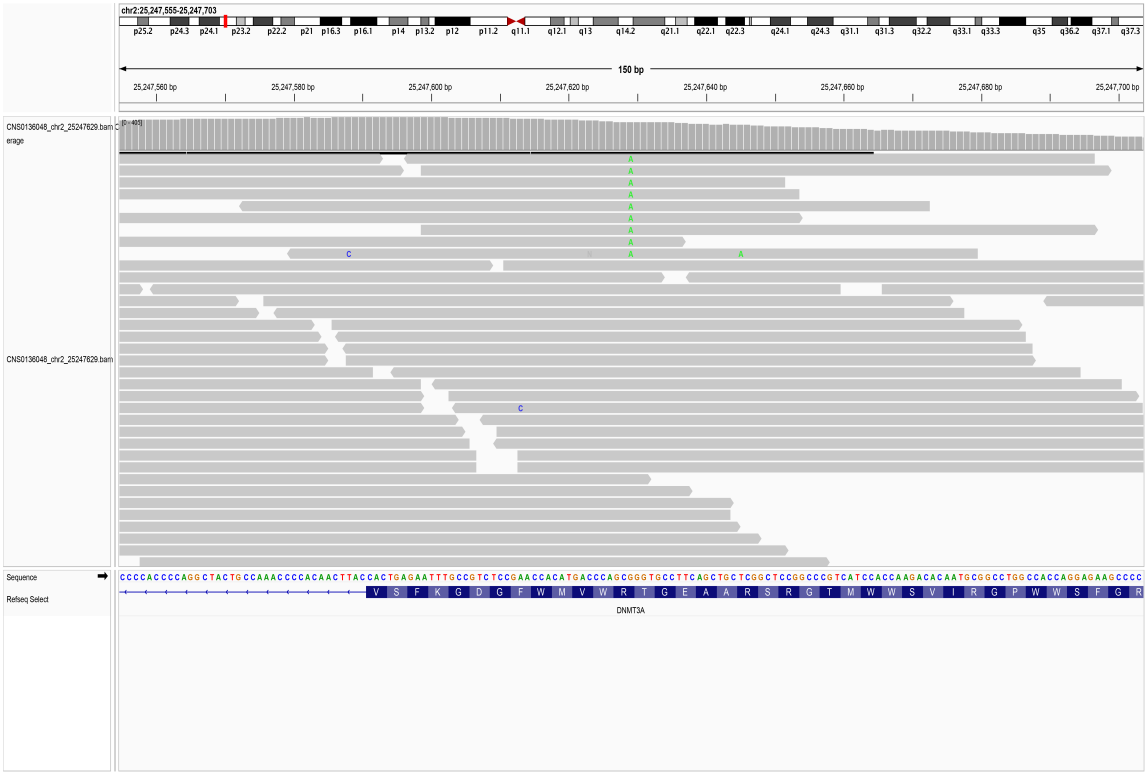

chr2:25,247,555-25,247,703
150 bp
17R10149_chr2_25247629.bam Coverage
17R10149_chr2_25247629.bam
Sequence
Refseq Select
DNMT3A
chr2:25,247,555-25,247,703
150 bp
18R08917_chr2_25247629.bam Coverage
18R08917_chr2_25247629.bam
Sequence
Refseq Select
DNMT3A


chr2:25,247,555-25,247,703
150 bp
25,247,560 bp
25,247,580 bp
25,247,600 bp
25,247,620 bp
25,247,640 bp
25,247,660 bp
25,247,680 bp
25,247,700 bp
18R10848_chr2_25247629.bam Coverage
18R10848_chr2_25247629.bam
Sequence
Refseq Select
DNMT3A
chr2:25,247,555-25,247,703
150 bp
18R13038_chr2_25247629.bam Coverage
18R13038_chr2_25247629.bam
Sequence
Refseq Select
DNMT3A

12.127. chr2_25247629_G/A

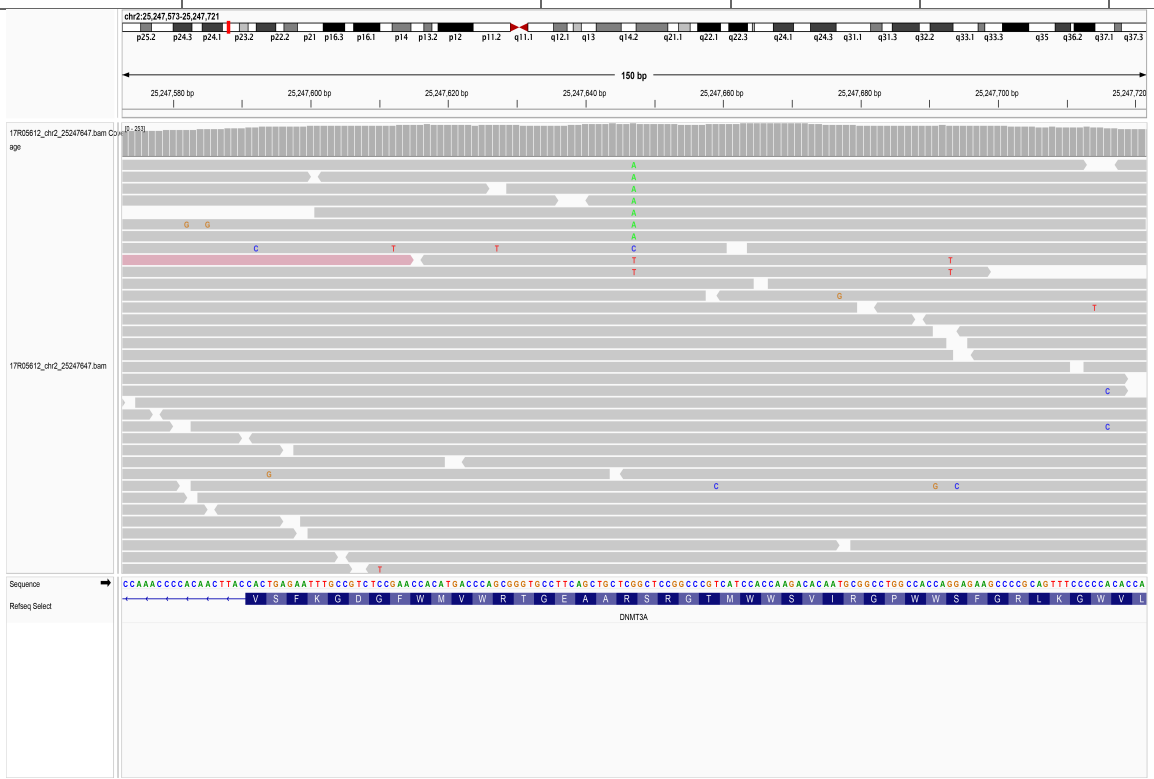
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061119D	chr2_25247629_G/A	83	53	*DNMT3A*	missense_variant
AAGC25061447D	chr2_25247629_G/A	379	10	*DNMT3A*	missense_variant
CNS0136048	chr2_25247629_G/A	327	9	*DNMT3A*	missense_variant

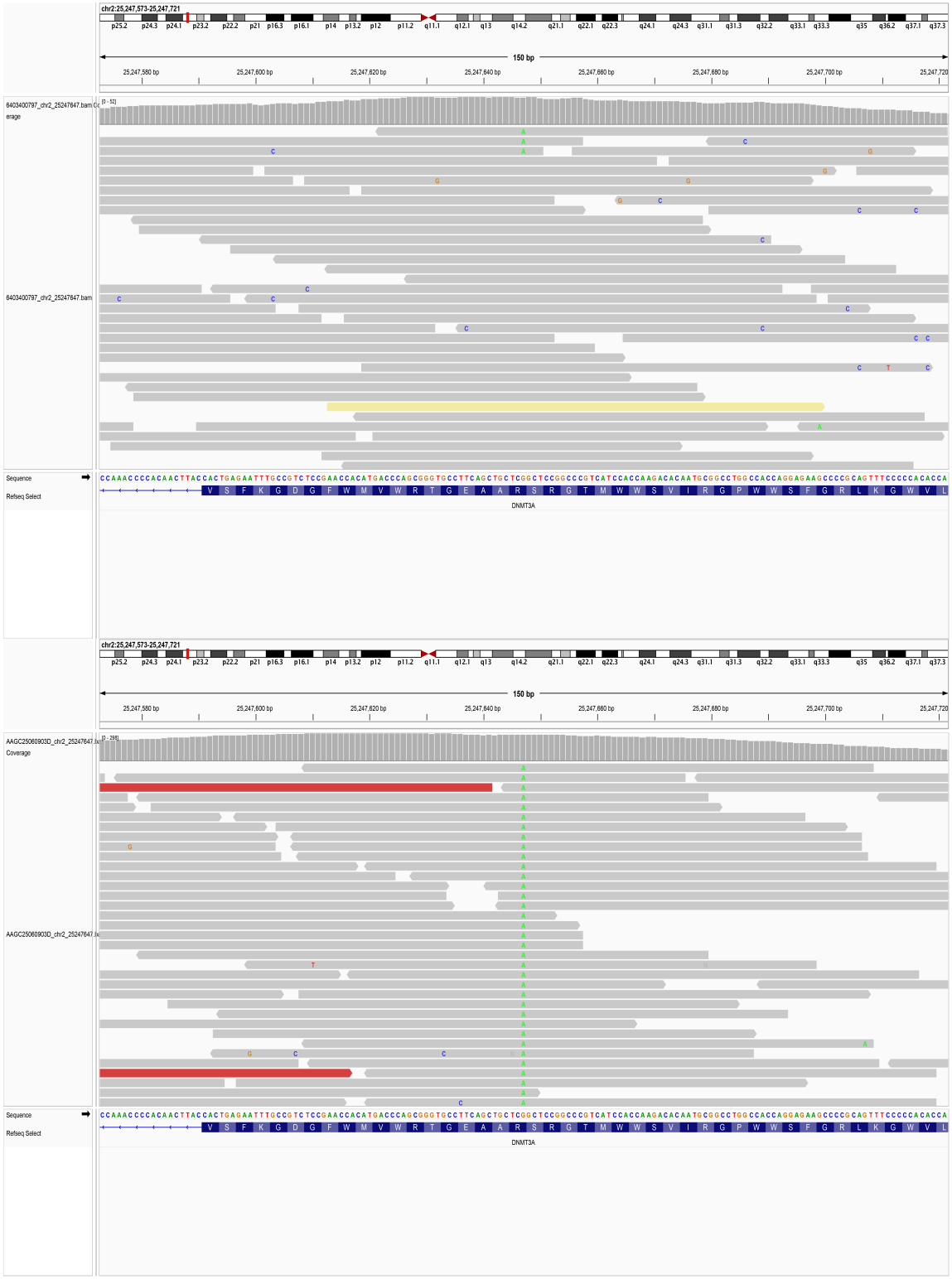


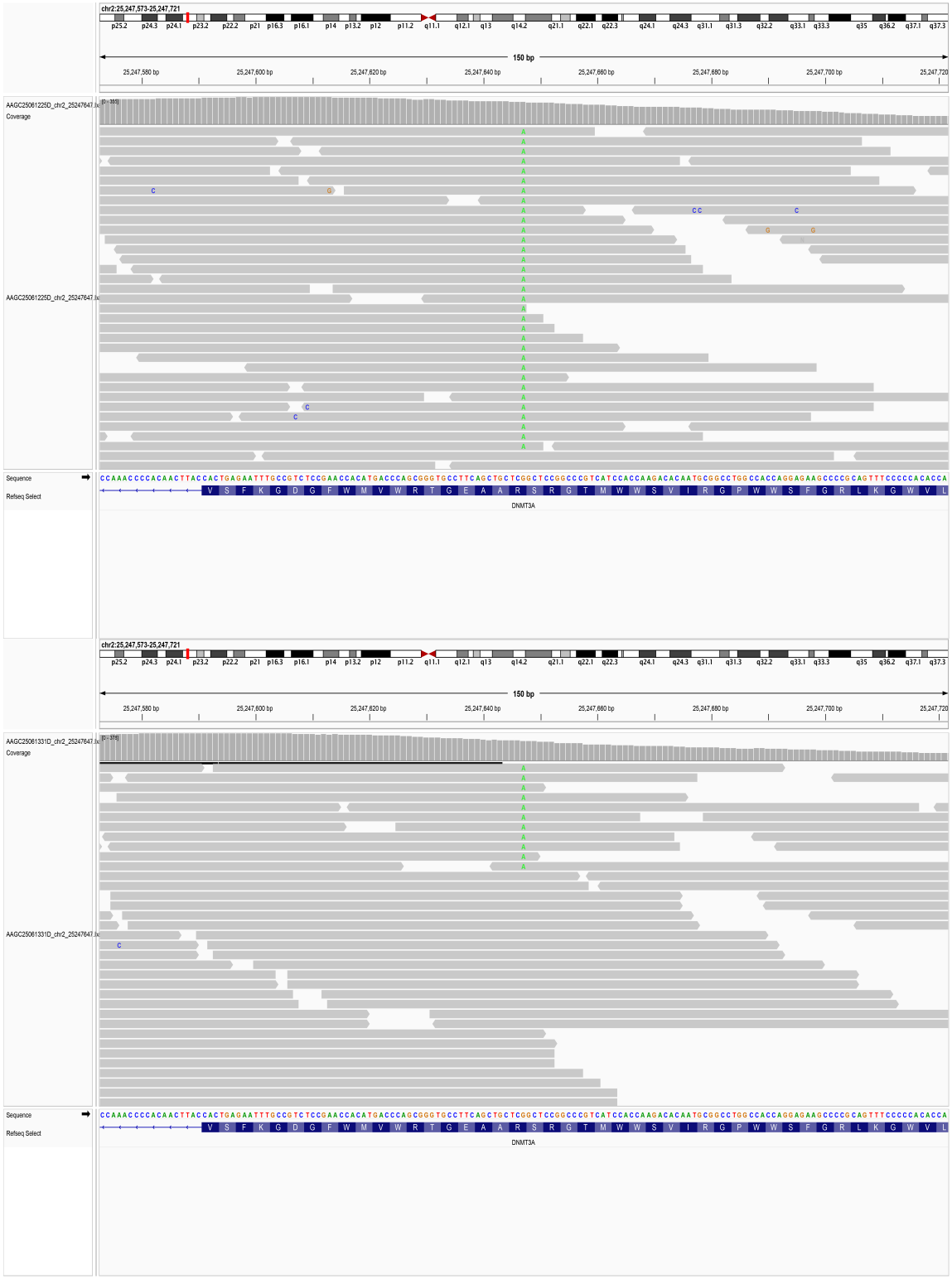

chr2:25,247,555-25,247,703
150 bp
25,247,560 bp
25,247,580 bp
25,247,600 bp
25,247,620 bp
25,247,640 bp
25,247,660 bp
25,247,680 bp
25,247,700 bp
CNS0136048_chr2_25247629.bam C
erage
CNS0136048_chr2_25247629.bam
Sequence
Refseq Select
DNMT3A

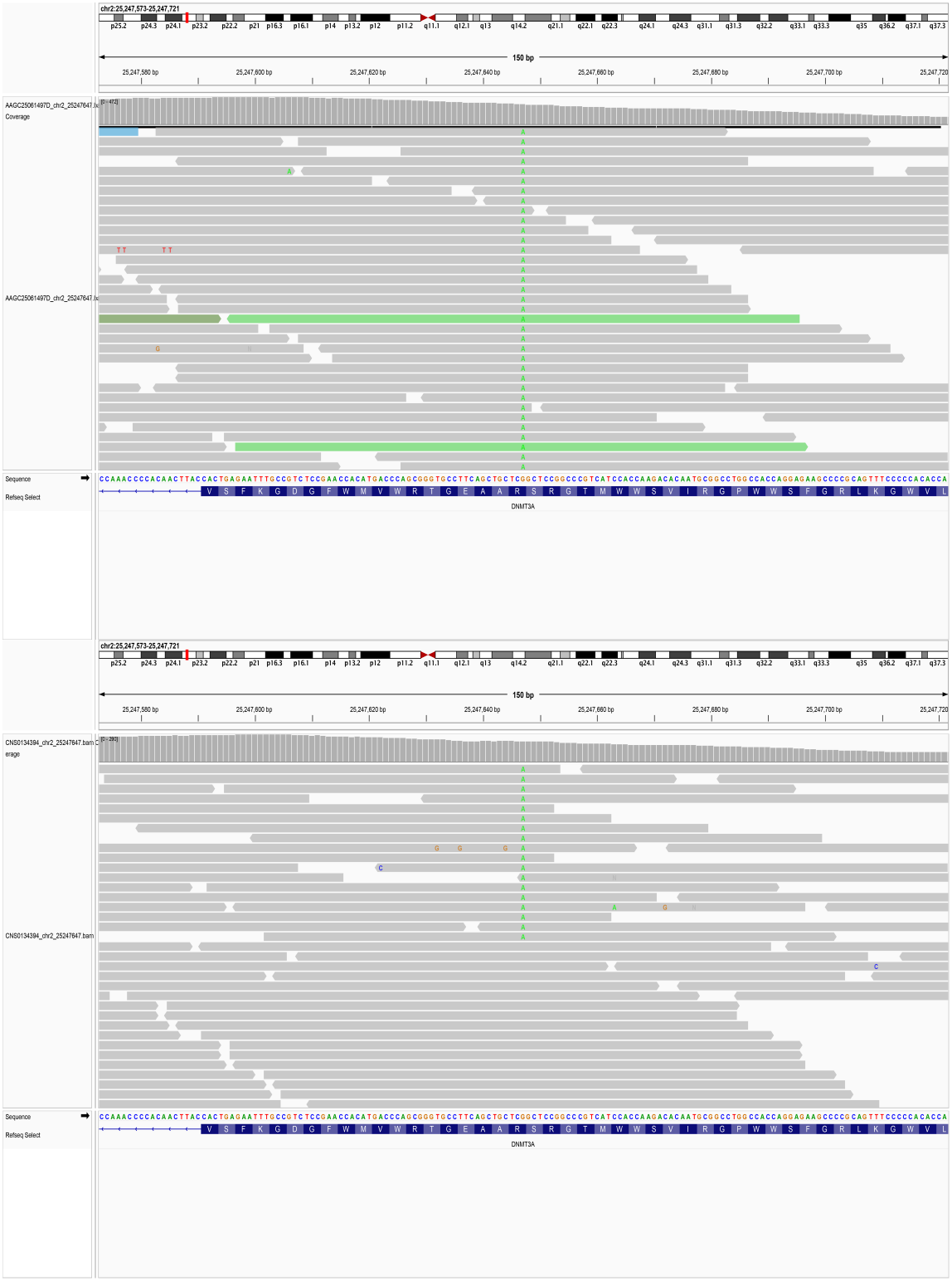
12.128. chr2_25247647_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05612	chr2_25247647_G/A	222	7	*DNMT3A*	stop_gained
6403400797	chr2_25247647_G/A	44	3	*DNMT3A*	stop_gained
AAGC25060903D	chr2_25247647_G/A	228	36	*DNMT3A*	stop_gained
AAGC25061225D	chr2_25247647_G/A	249	33	*DNMT3A*	stop_gained
AAGC25061331D	chr2_25247647_G/A	250	11	*DNMT3A*	stop_gained
AAGC25061497D	chr2_25247647_G/A	297	41	*DNMT3A*	stop_gained
CNS0134394	chr2_25247647_G/A	190	17	*DNMT3A*	stop_gained



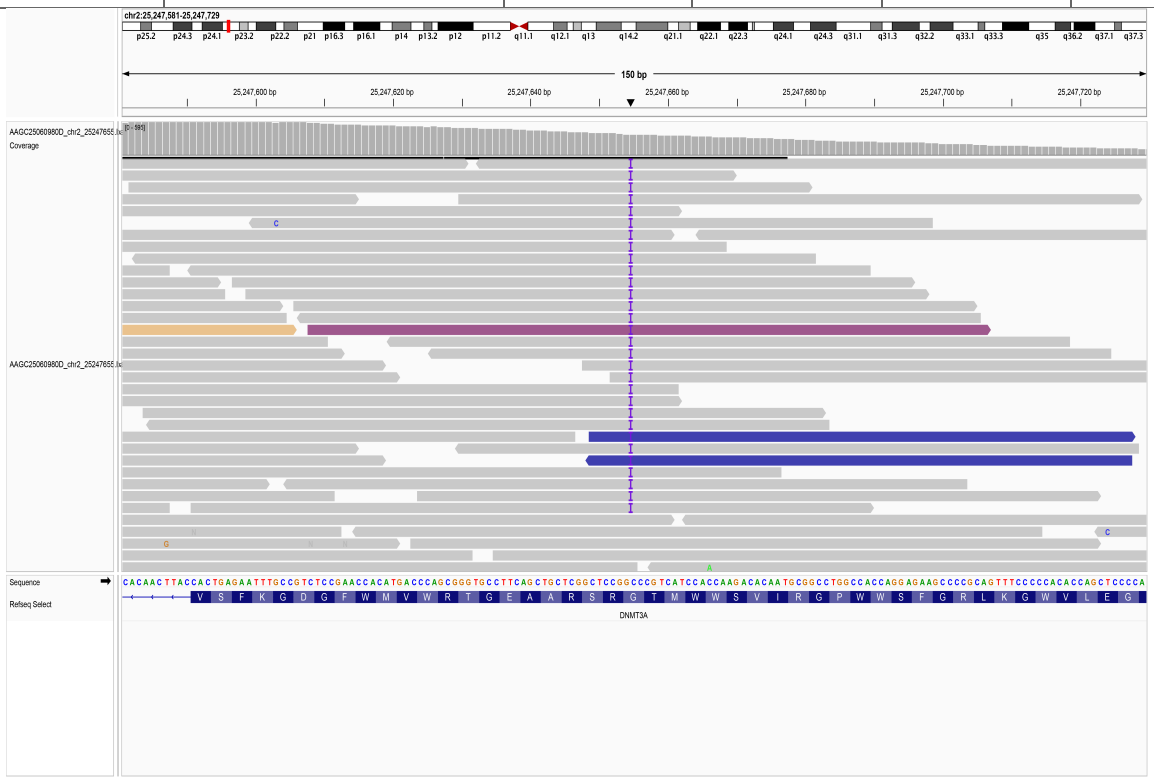

chr2:25,247,573-25,247,721
150 bp
25,247,580 bp
25,247,600 bp
25,247,620 bp
25,247,640 bp
25,247,660 bp
25,247,680 bp
25,247,700 bp
25,247,720
6403400797_chr2_25247647.bam
Coverage
Sequence
Refseq Select
DNMT3A
AAGC25060903D_chr2_25247647.bam


chr2:25,247,573-25,247,721
150 bp
25,247,580 bp
25,247,600 bp
25,247,620 bp
25,247,640 bp
25,247,660 bp
25,247,680 bp
25,247,700 bp
25,247,720
AAGC250612250_chr2_25247647.bc
Coverage
Sequence
Refseq Select
DNMT3A
AAGC250613310_chr2_25247647.bc


chr2:25,247,573-25,247,721
150 bp
25,247,580 bp
25,247,600 bp
25,247,620 bp
25,247,640 bp
25,247,660 bp
25,247,680 bp
25,247,700 bp
25,247,720
AAGC25061497D_chr2_25247647.ba
Coverage
AAGC25061497D_chr2_25247647.ba
Sequence
Refseq Select
DNMT3A
CNS0134394_chr2_25247647.bam
erage
CNS0134394_chr2_25247647.bam
Sequence
Refseq Select
DNMT3A

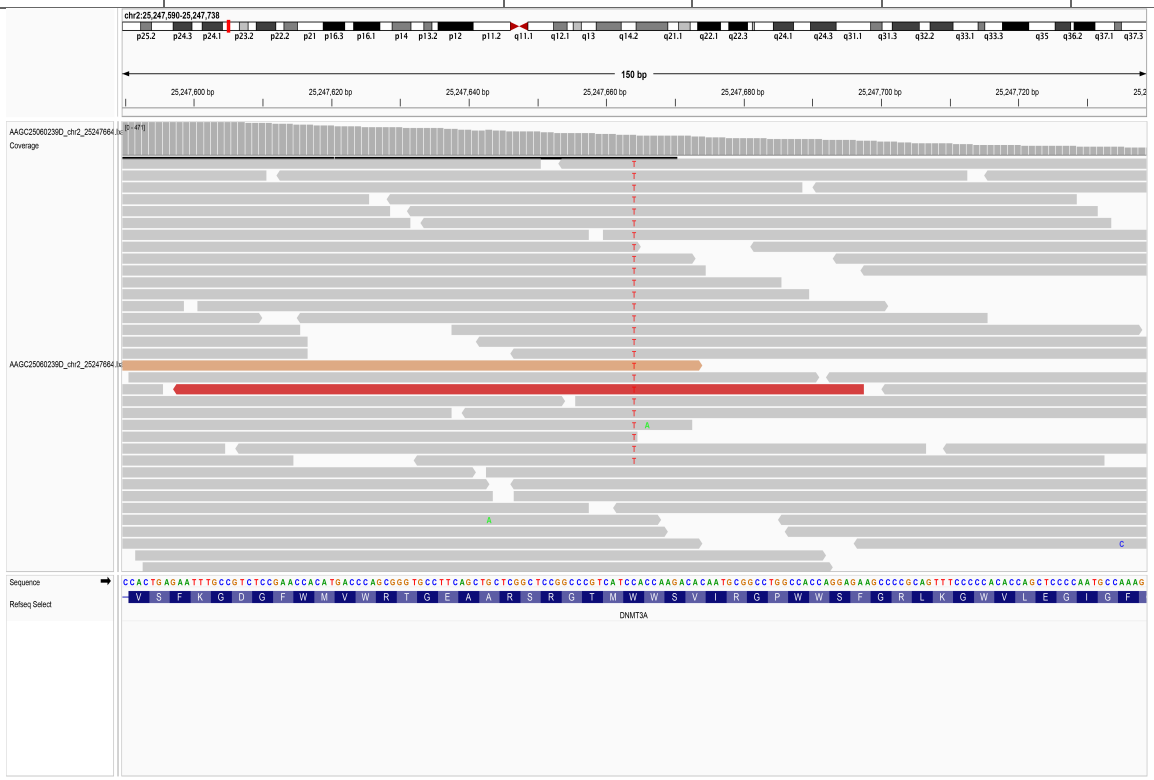
12.129. chr2_25247655_-/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060980D	chr2_25247655_-/C	307	35	*DNMT3A*	frameshift_variant



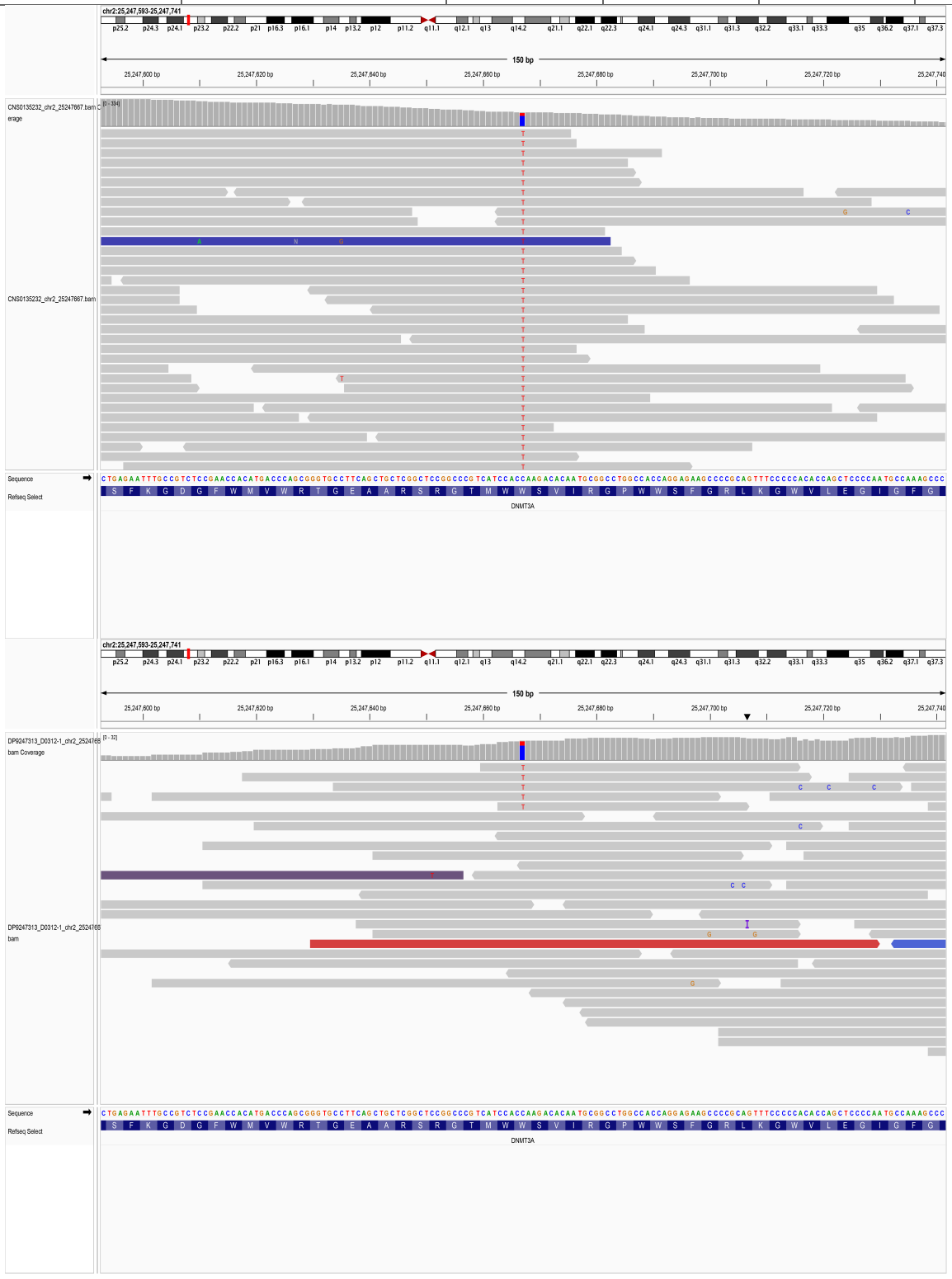
12.130. chr2_25247664_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060239D	chr2_25247664_C/T	254	26	*DNMT3A*	stop_gained



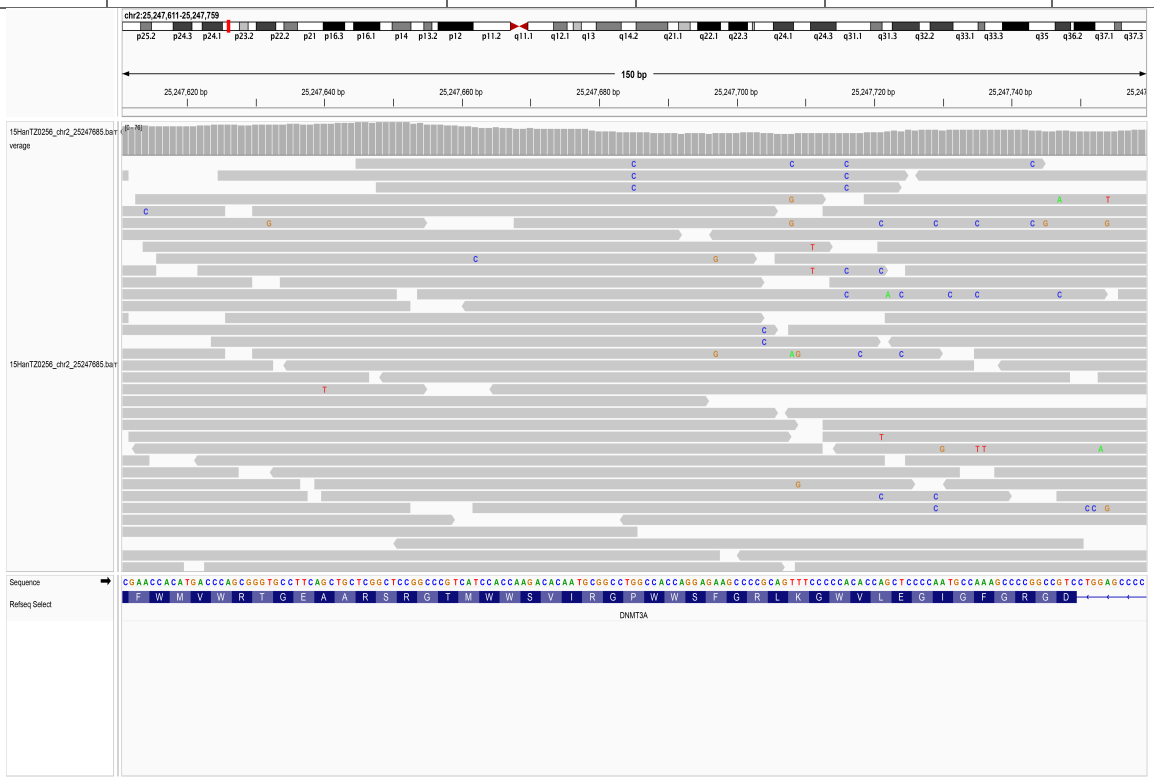
12.131. chr2_25247667_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135232	chr2_25247667_C/T	131	37	*DNMT3A*	stop_gained
DP9247313_D0312-1	chr2_25247667_C/T	18	4	*DNMT3A*	stop_gained



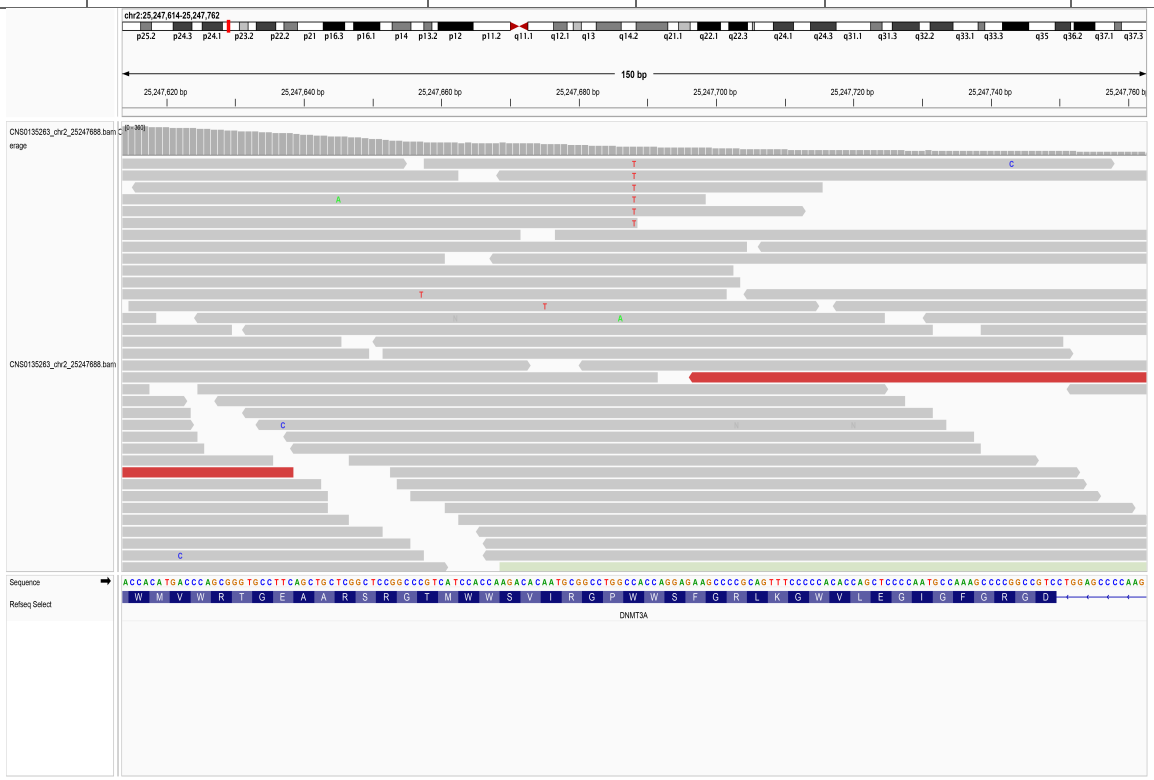
12.132. chr2_25247685_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0256	chr2_25247685_G/C	47	3	*DNMT3A*	missense_variant



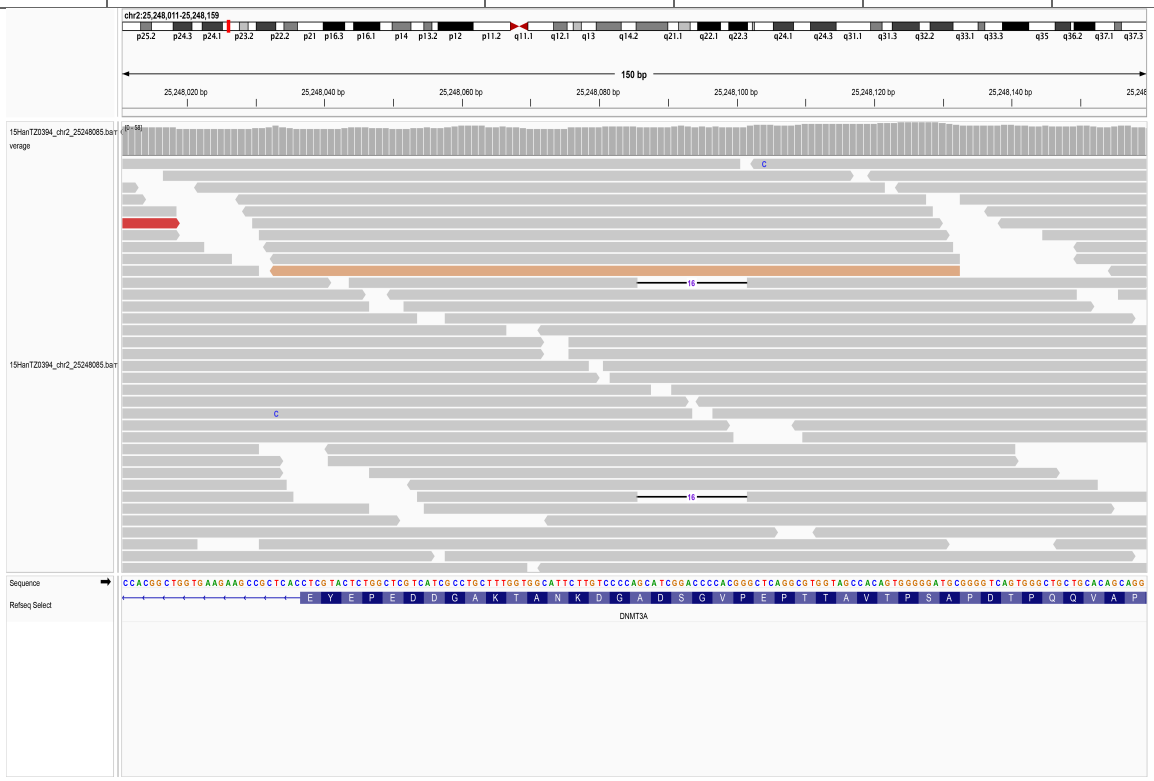
12.133. chr2_25247688_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135263	chr2_25247688_C/T	88	6	*DNMT3A*	stop_gained



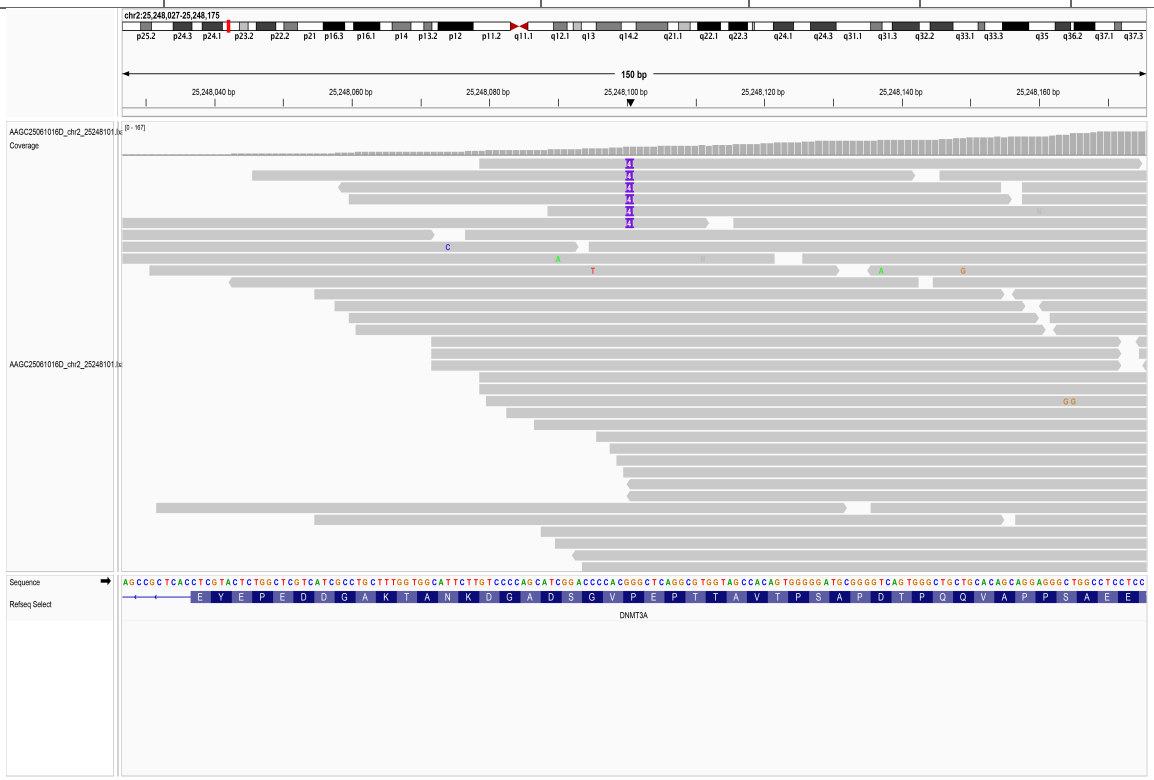
12.134. chr2_25248086_GCATCGGACCCCACGG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0394	chr2_25248086_GCATCGGACCCCACGG/-	56	3	*DNMT3A*	frameshift_variant



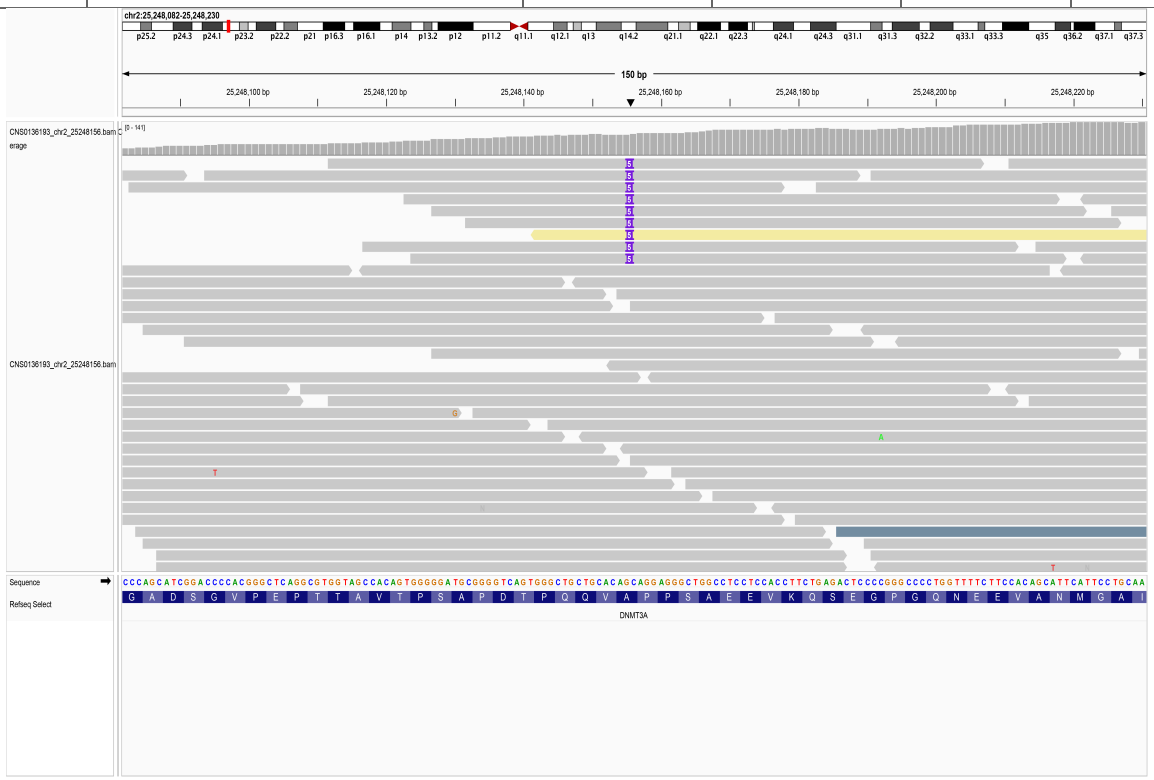
12.135. chr2_25248101_-/GGCC

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061016D	chr2_25248101_-/GGCC	36	7	*DNMT3A*	frameshift_variant



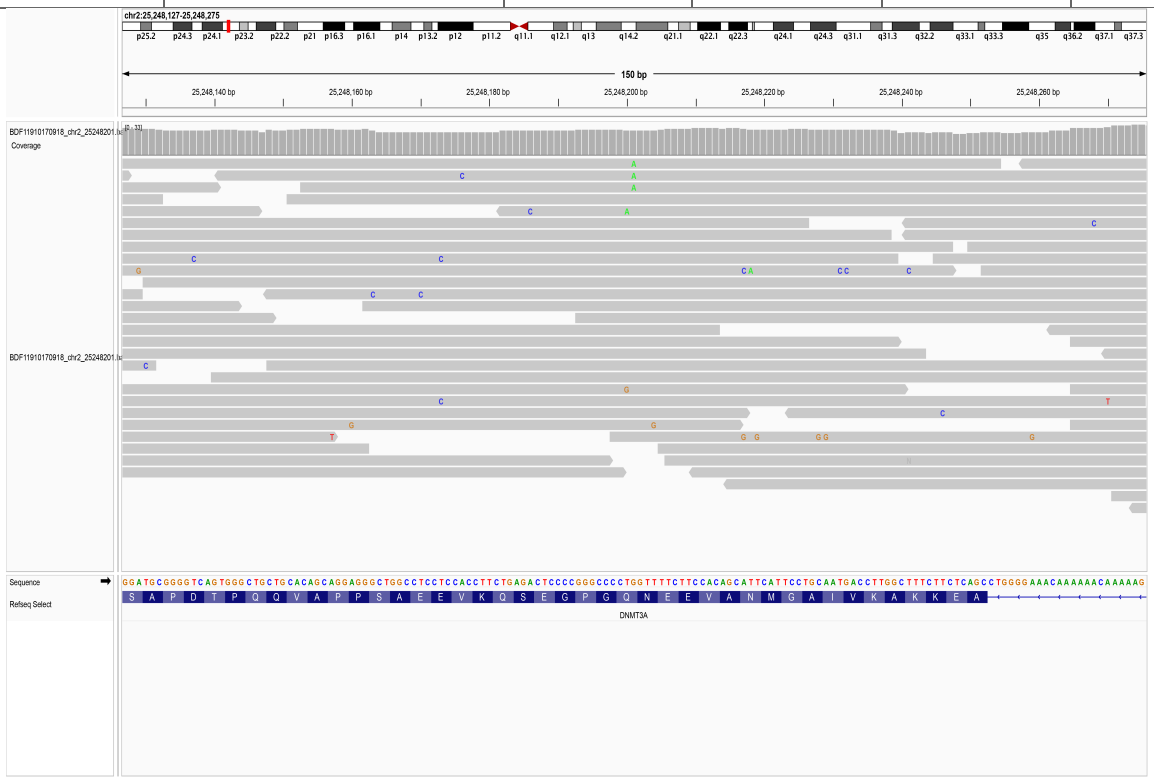
12.136. chr2_25248156_-/GAGGA

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136193	chr2_25248156_-/GAGGA	76	11	*DNMT3A*	frameshift_variant



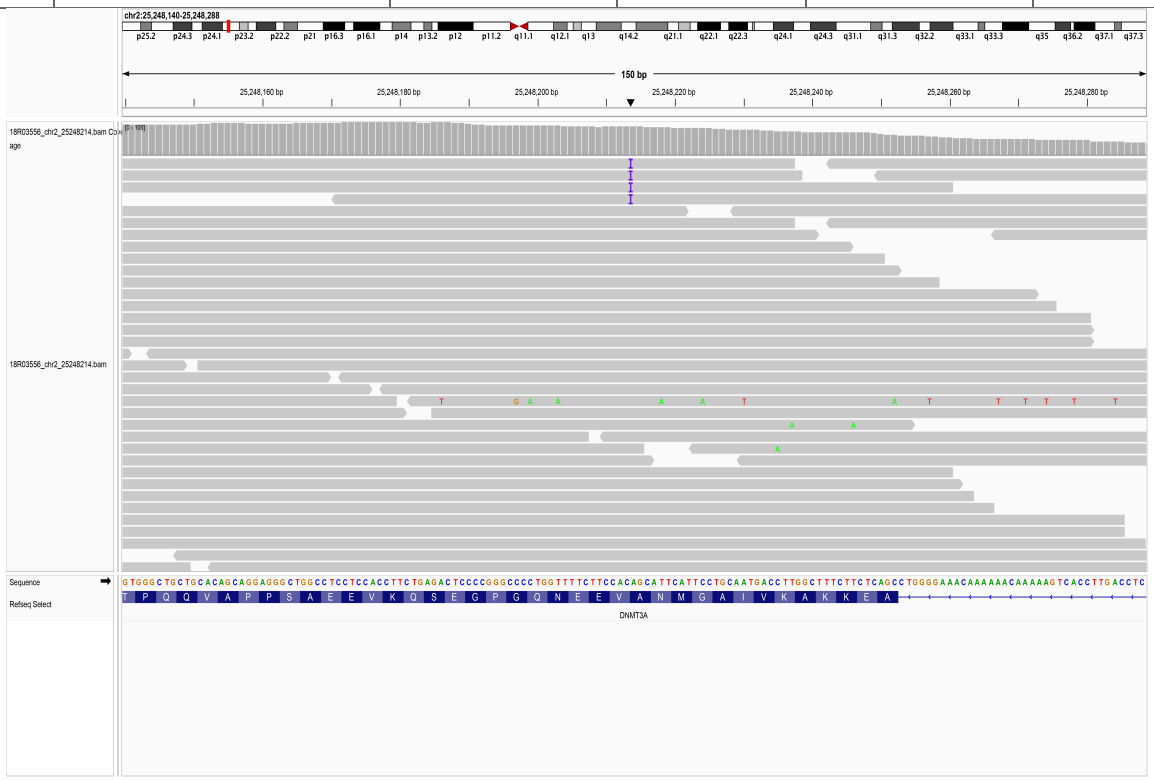
12.137. chr2_25248201_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170918	chr2_25248201_G/A	19	3	*DNMT3A*	stop_gained



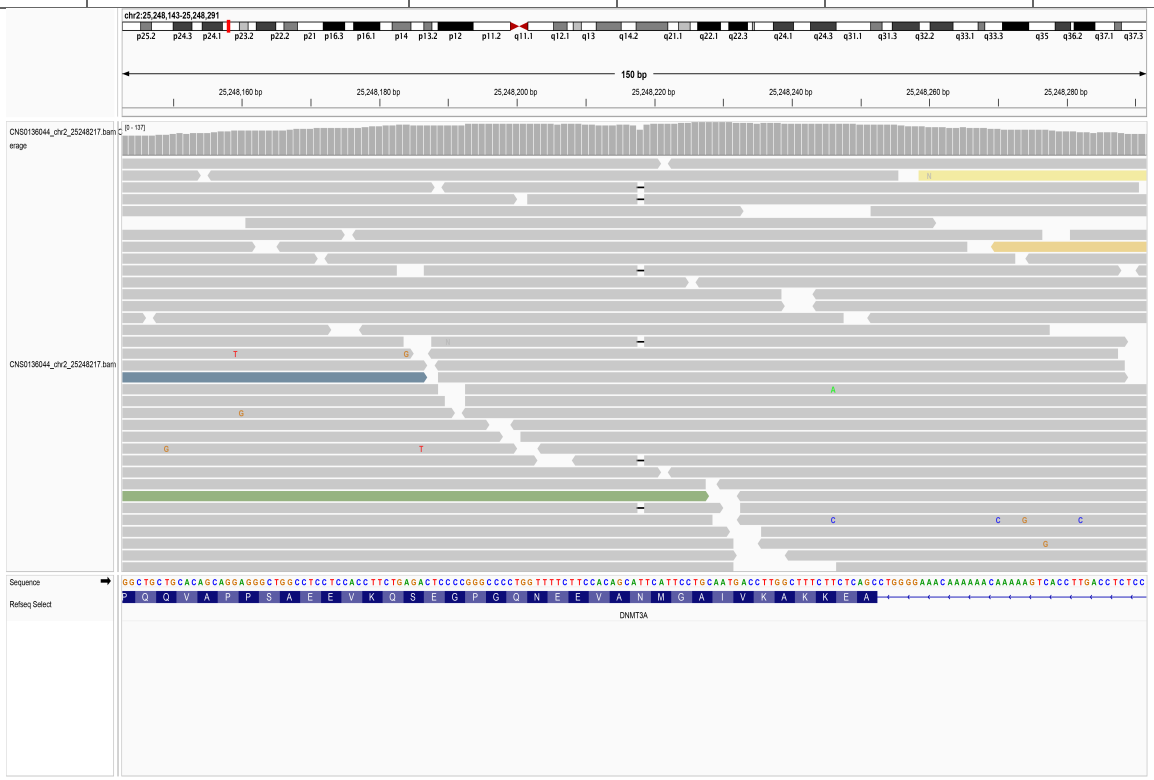
12.138. chr2_25248214_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03556	chr2_25248214_-/A	85	4	*DNMT3A*	frameshift_variant



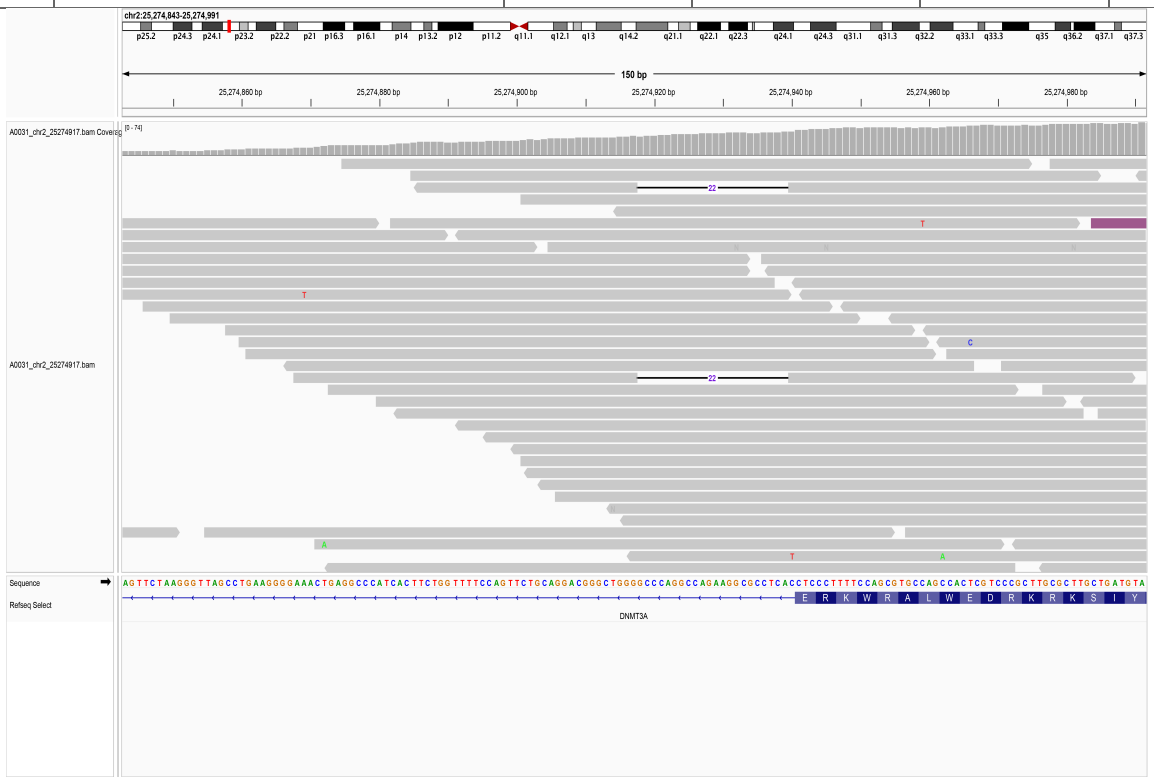
12.139. chr2_25248218_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136044	chr2_25248218_T/-	103	18	*DNMT3A*	frameshift_variant



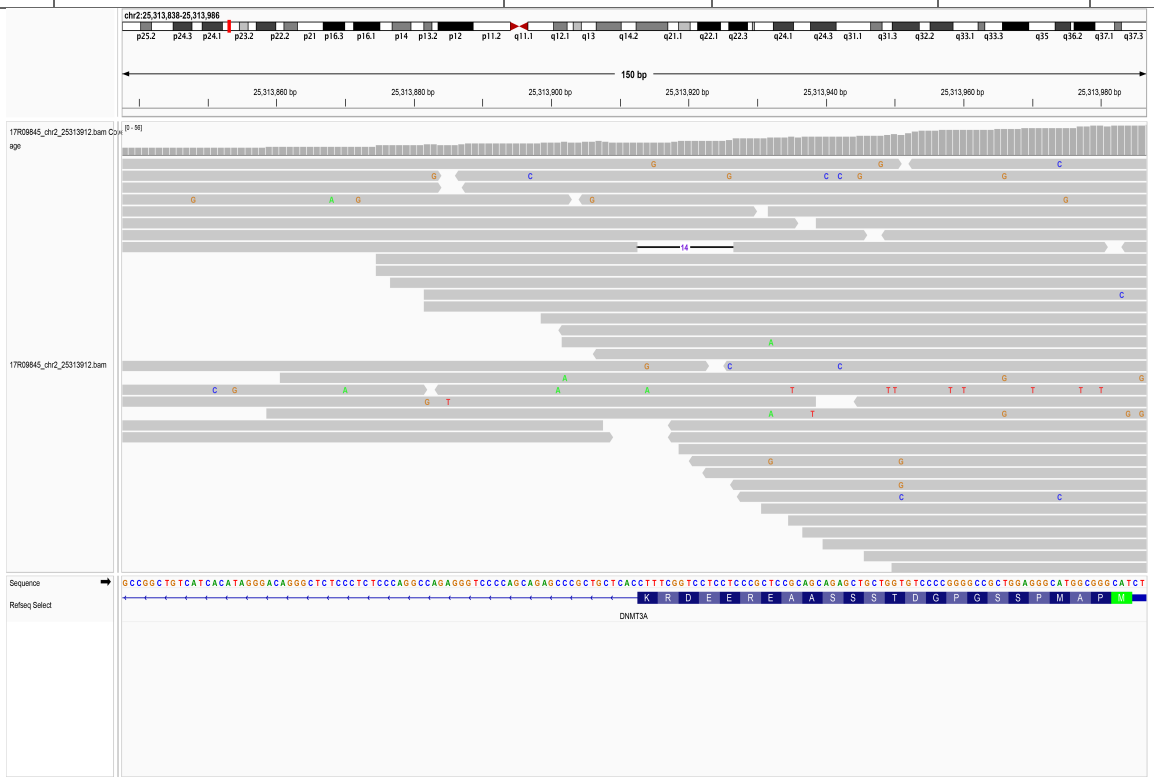
12.140. chr2_25274918_GCCCAGGCCAGAAGGCGCCTCA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0031	chr2_25274918_GCCCAGGCCAGAAGGCGCCTCA/-	54	2	*DNMT3A*	splice_donor_variant



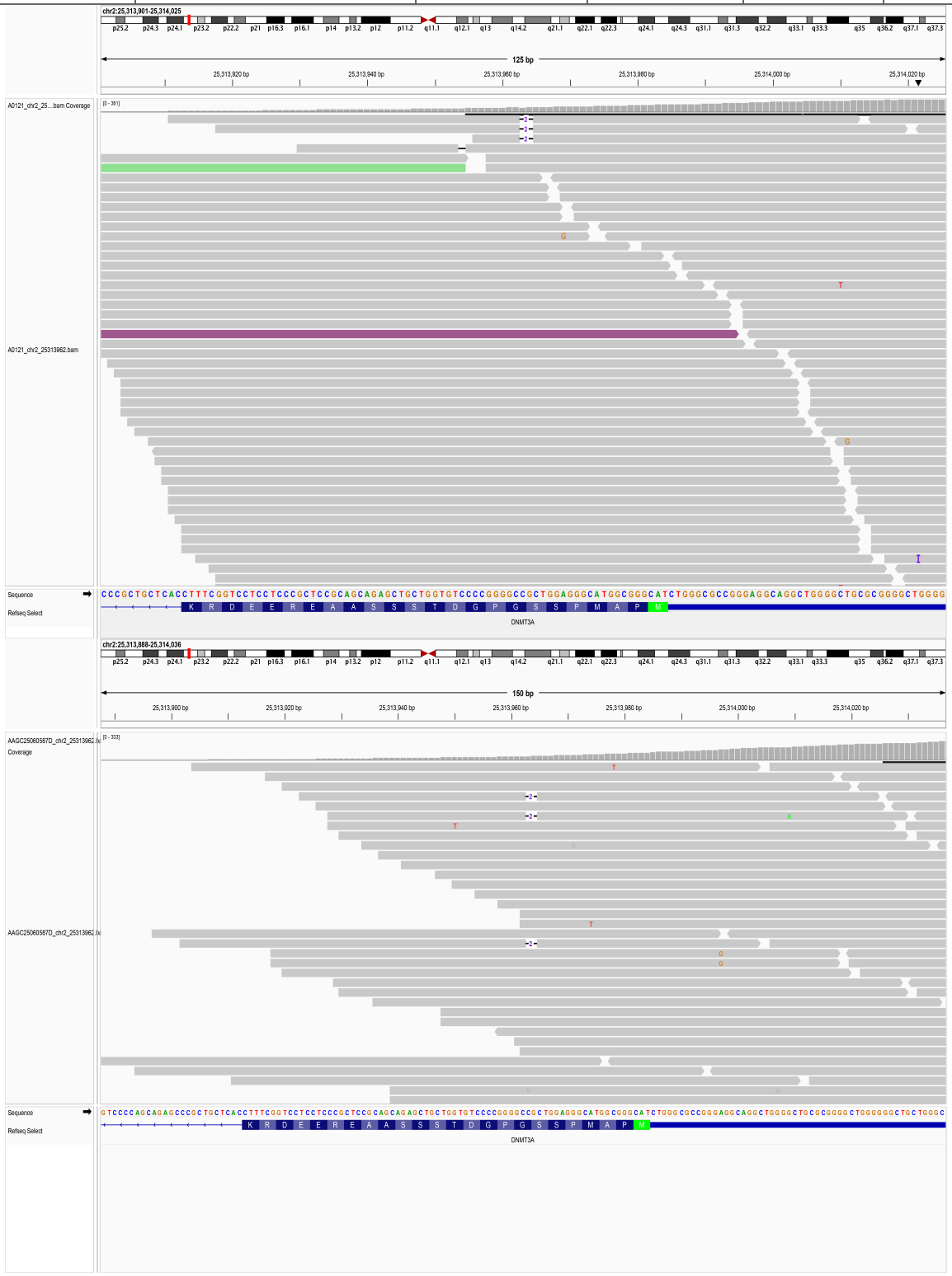
12.141. chr2_25313913_CTTTCGGTCCTCCT/-

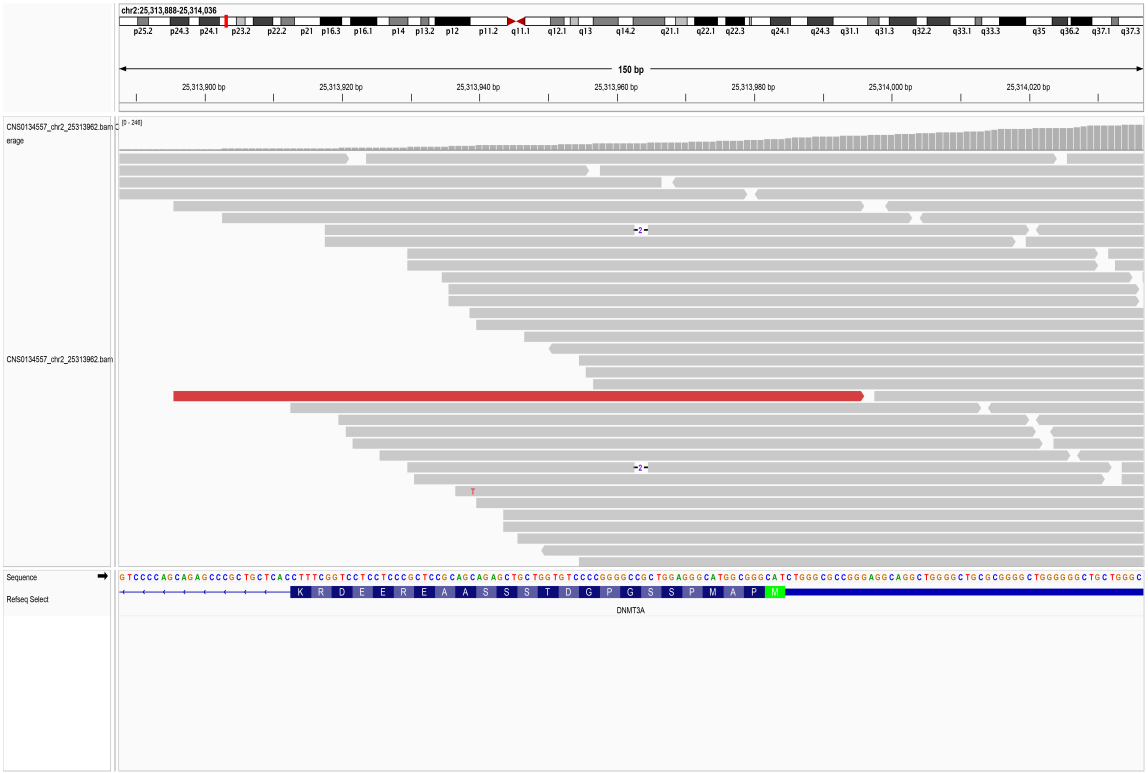
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09845	chr2_25313913_CTTTCGGTCCTCCT/-	20	3	*DNMT3A*	frameshift_variant



12.142. chr2_25313963_CG/-

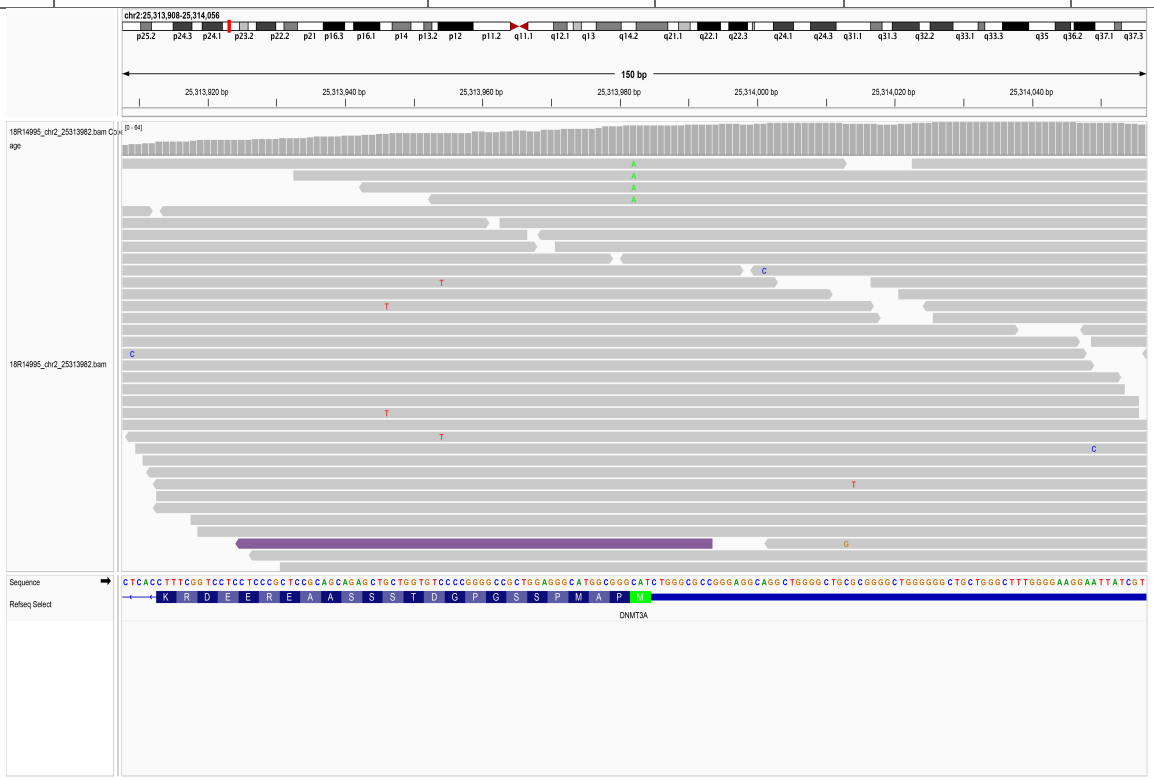
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0121	chr2_25313963_CG/-	132	3	*DNMT3A*	frameshift_variant
AAGC25060587D	chr2_25313963_CG/-	50	3	*DNMT3A*	frameshift_variant
CNS0134557	chr2_25313963_CG/-	51	3	*DNMT3A*	frameshift_variant




chr2:25,313,888-25,314,036
p25.2 p24.3 p24.1 p23.2 p22.2 p21 p16.3 p16.1 p14 p13.2 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
150 bp
25,313,900 bp
25,313,920 bp
25,313,940 bp
25,313,960 bp
25,313,980 bp
25,314,000 bp
25,314,020 bp
CNS0134557_chr2_25313962.bam C
erage
[0 - 245]
CNS0134557_chr2_25313962.bam
Sequence
Refseq Select
K R D E E R E A A S S S T D G P G S S P M A P M
DNMT3A

12.143. chr2_25313982_C/A

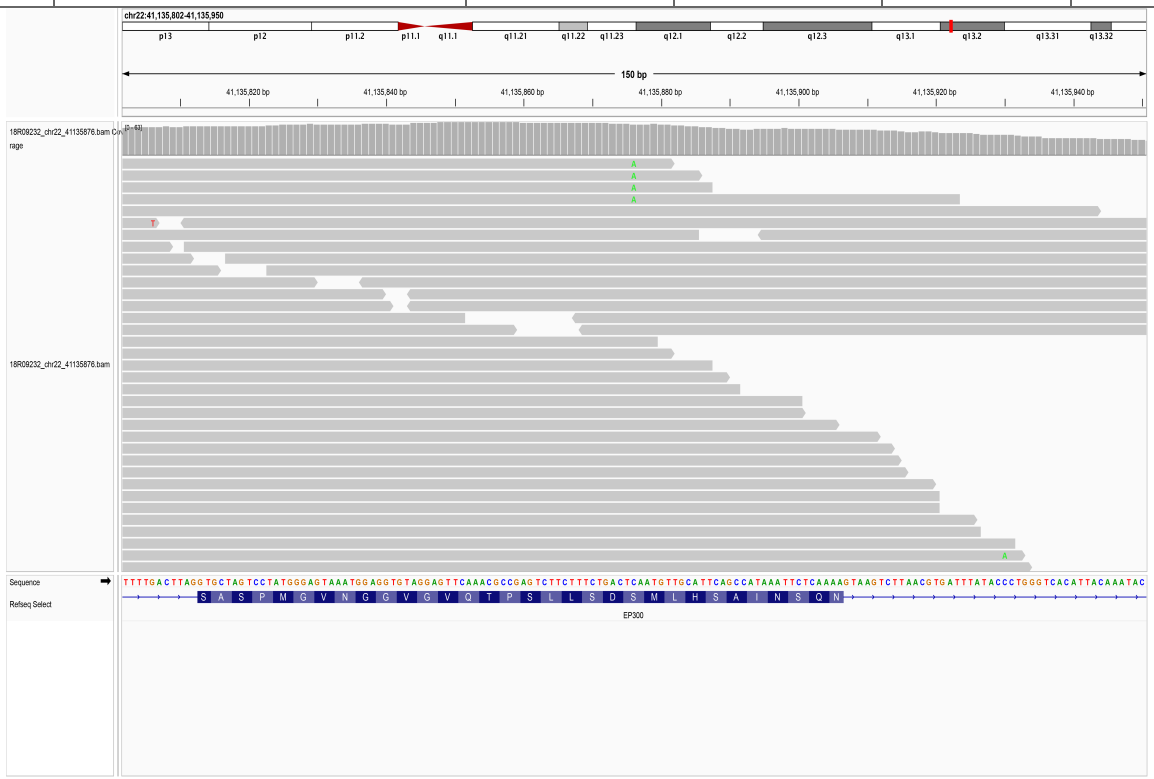
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R14995	chr2_25313982_C/A	52	4	*DNMT3A*	start_lost



13. *EP300*

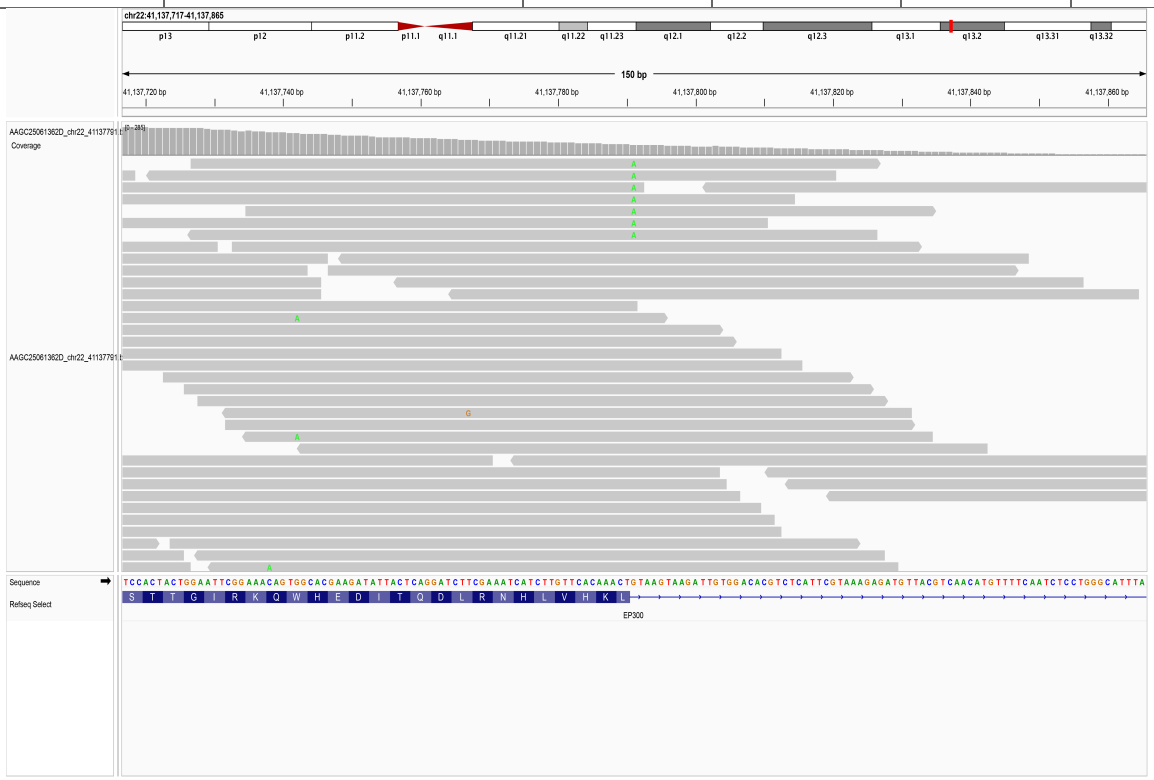
13.1. chr22_41135876_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09232	chr22_41135876_C/A	53	4	*EP300*	stop_gained



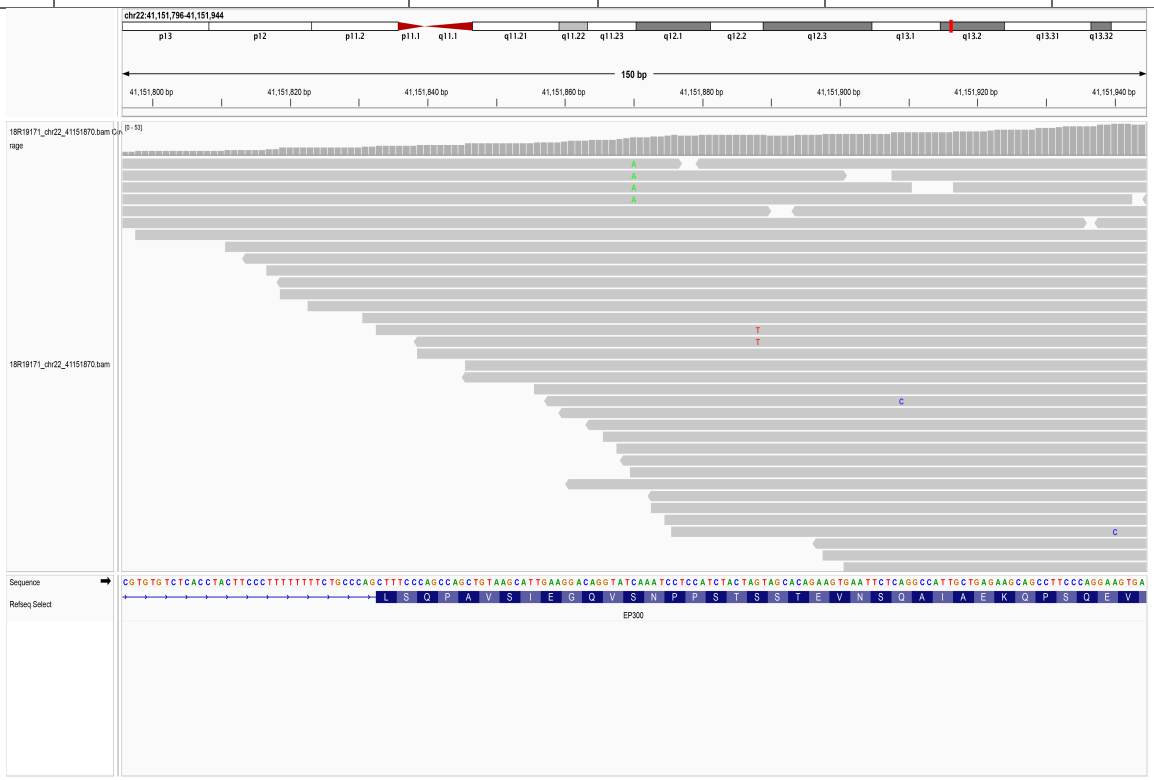
13.2. chr22_41137791_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061362D	chr22_41137791_G/A	84	7	*EP300*	splice_donor_variant



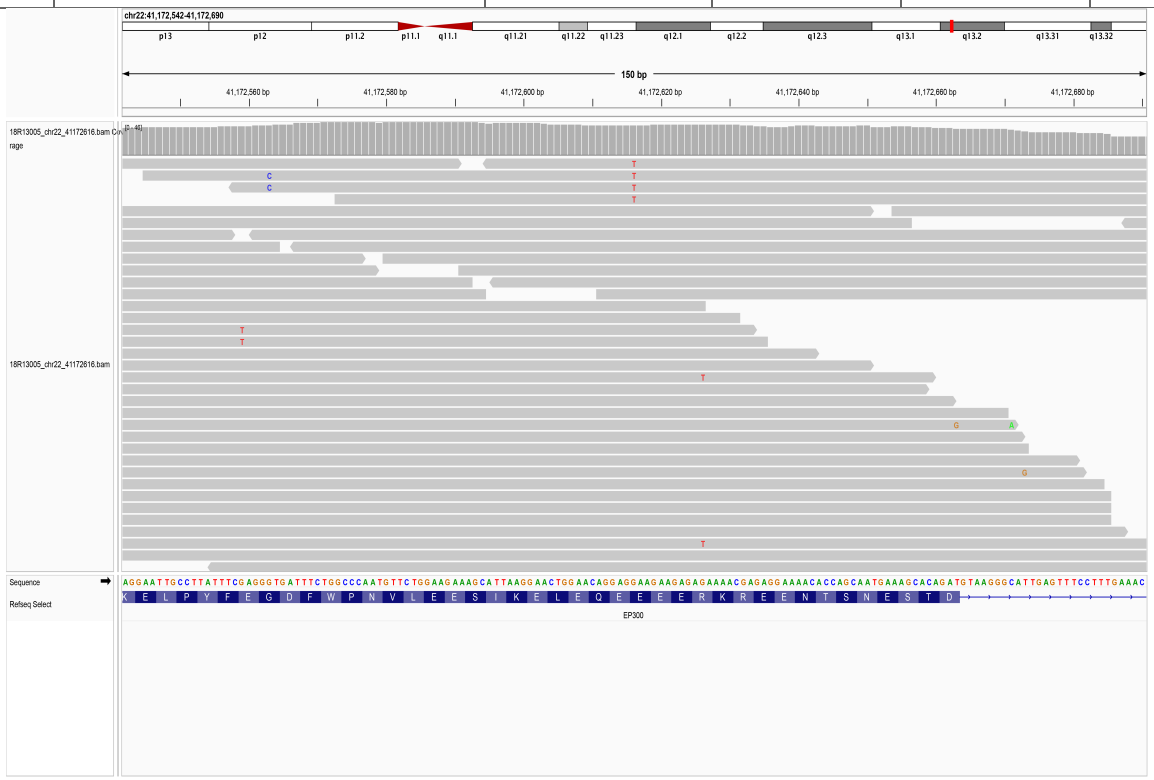
13.3. chr22_41151870_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19171	chr22_41151870_C/A	24	4	*EP300*	stop_gained



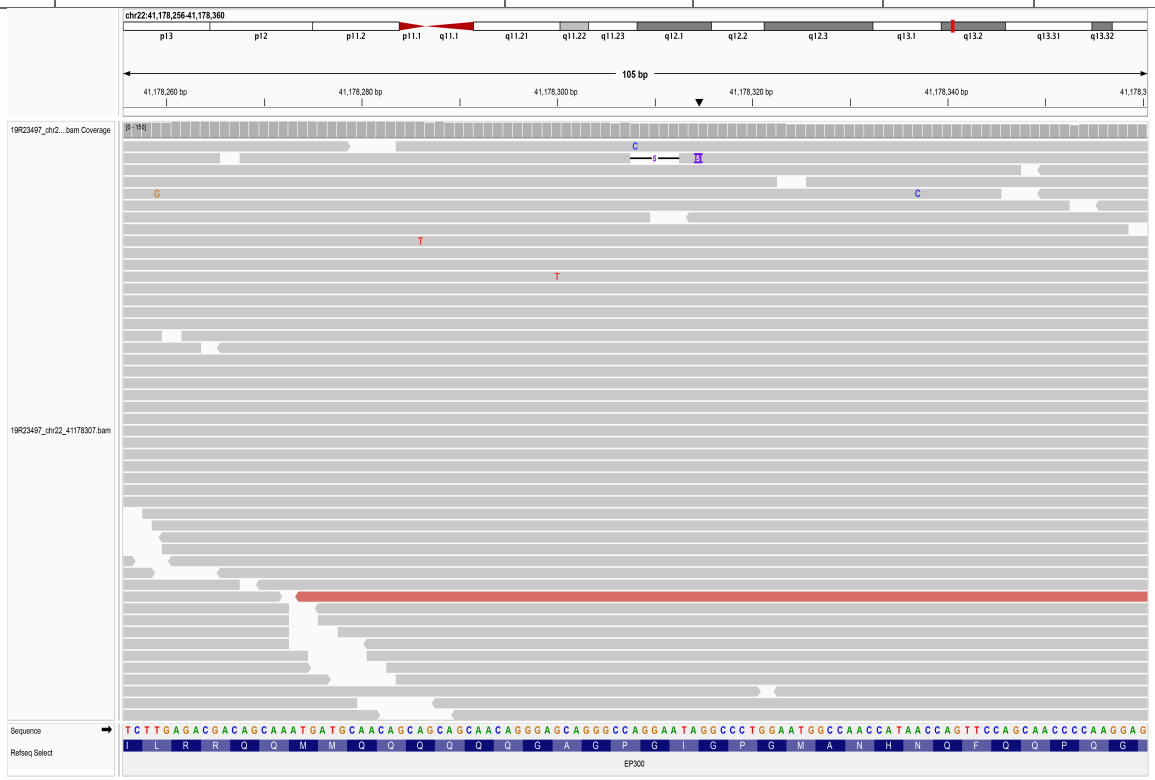
13.4. chr22_41172616_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13005	chr22_41172616_G/T	37	4	*EP300*	stop_gained



13.5. chr22_41178308_AGGAA/-

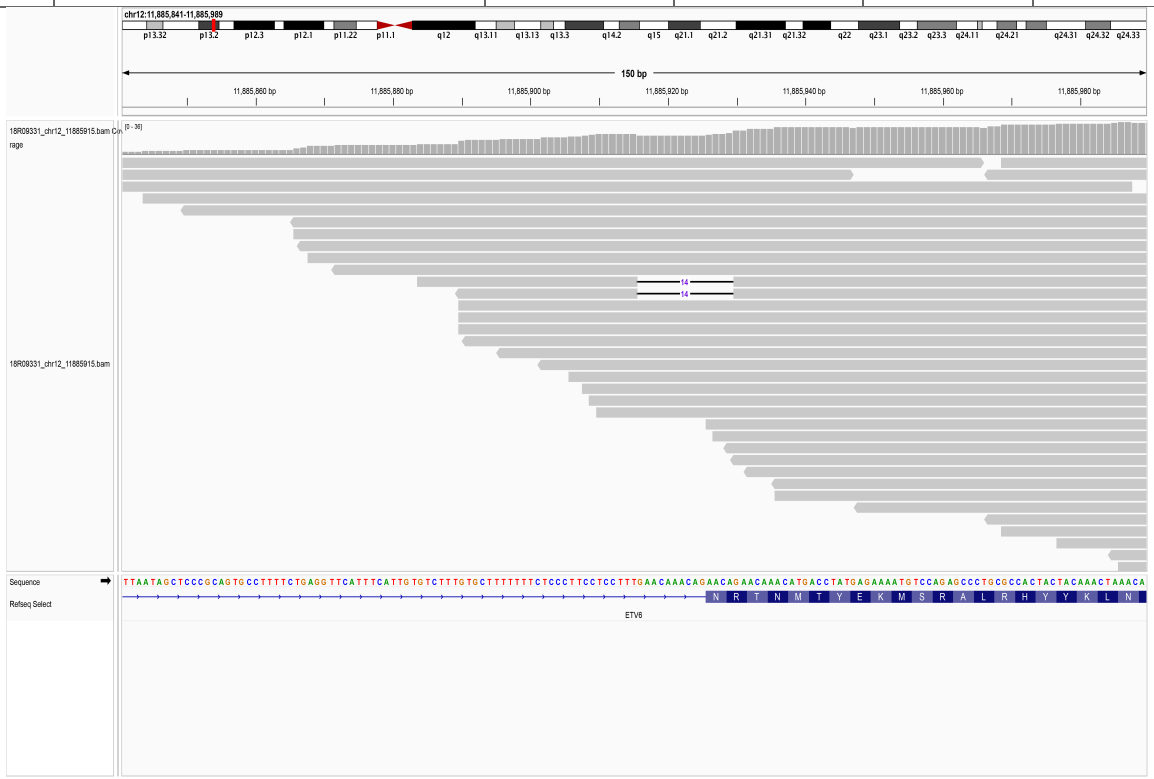
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23497	chr22_41178308_AGGAA/-	127	5	*EP300*	frameshift_variant

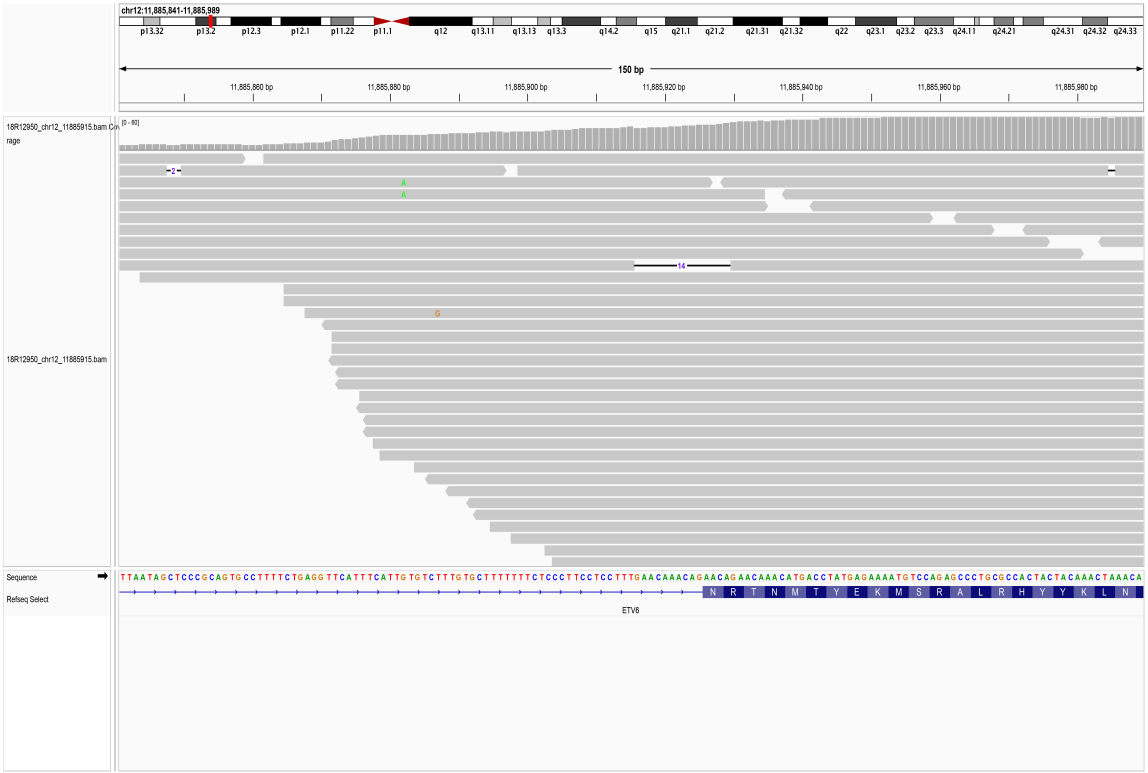


14. *ETV6*

14.1. chr12_11885916_GAACAAACAGAACA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09331	chr12_11885916_GAACAAACAGAACA/-	23	2	*ETV6*	splice_acceptor_variant
18R12950	chr12_11885916_GAACAAACAGAACA/-	49	2	*ETV6*	splice_acceptor_variant

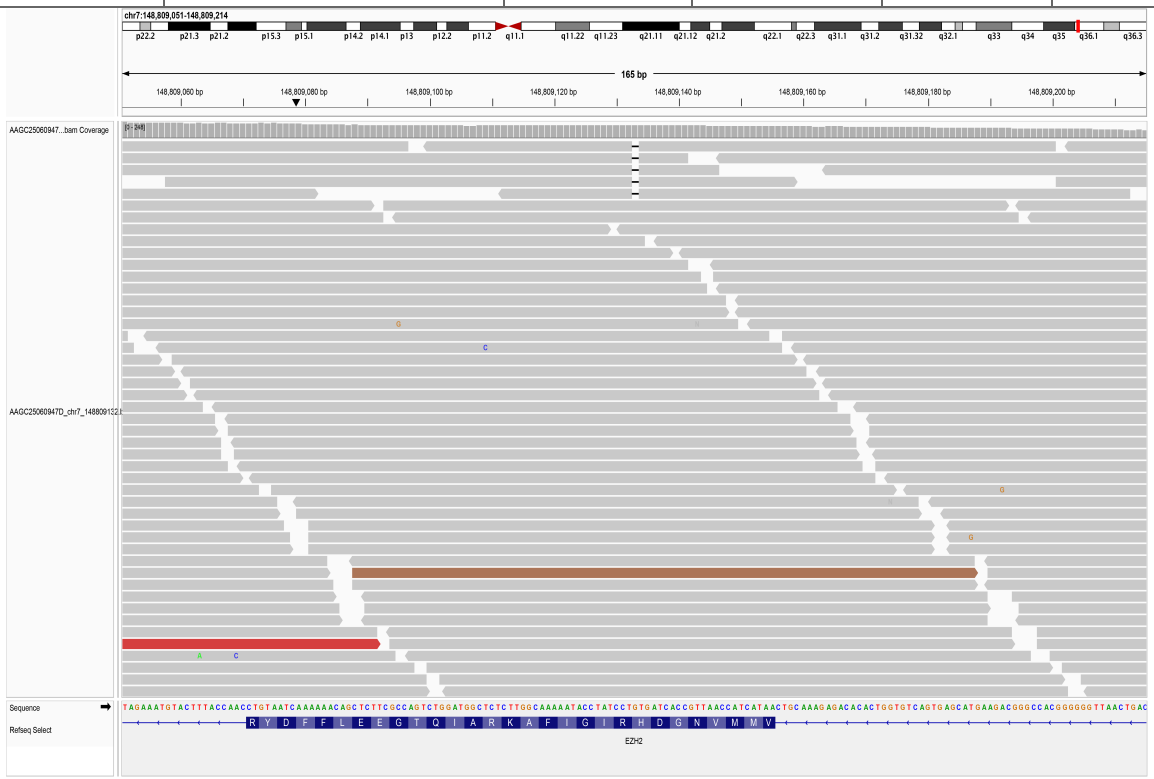



chr12:11,885,841-11,885,989
p13.32 p13.2 p12.3 p12.1 p11.22 p11.1 q12 q13.11 q13.13 q13.3 q14.2 q15 q21.1 q21.2 q21.31 q21.32 q22 q23.1 q23.2 q23.3 q24.11 q24.21 q24.31 q24.32 q24.33
150 bp
11,885,860 bp
11,885,880 bp
11,885,900 bp
11,885,920 bp
11,885,940 bp
11,885,960 bp
11,885,980 bp
18R12950_chr12_11885915.bam Cov
rage
[0 - 60]
18R12950_chr12_11885915.bam
Sequence
Refseq Select
ETV6

15. *EZH2*

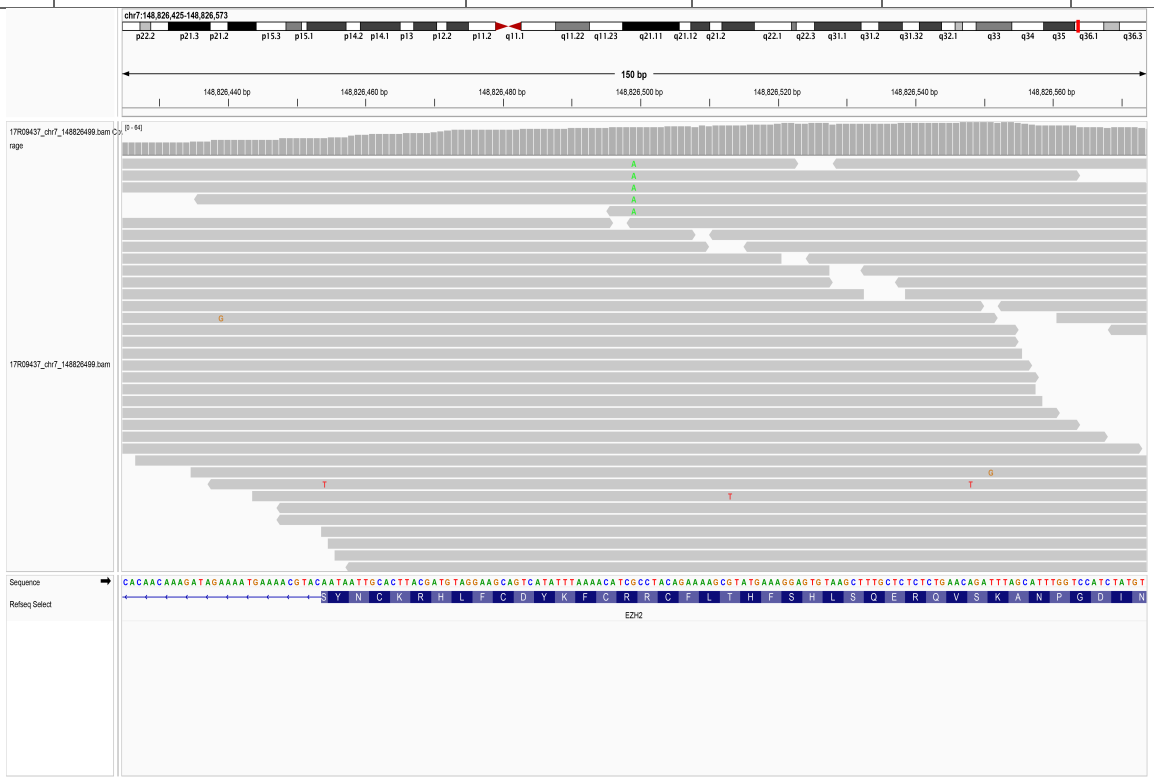
15.1. chr7_148809133_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060947D	chr7_148809133_G/-	187	5	*EZH2*	frameshift_variant



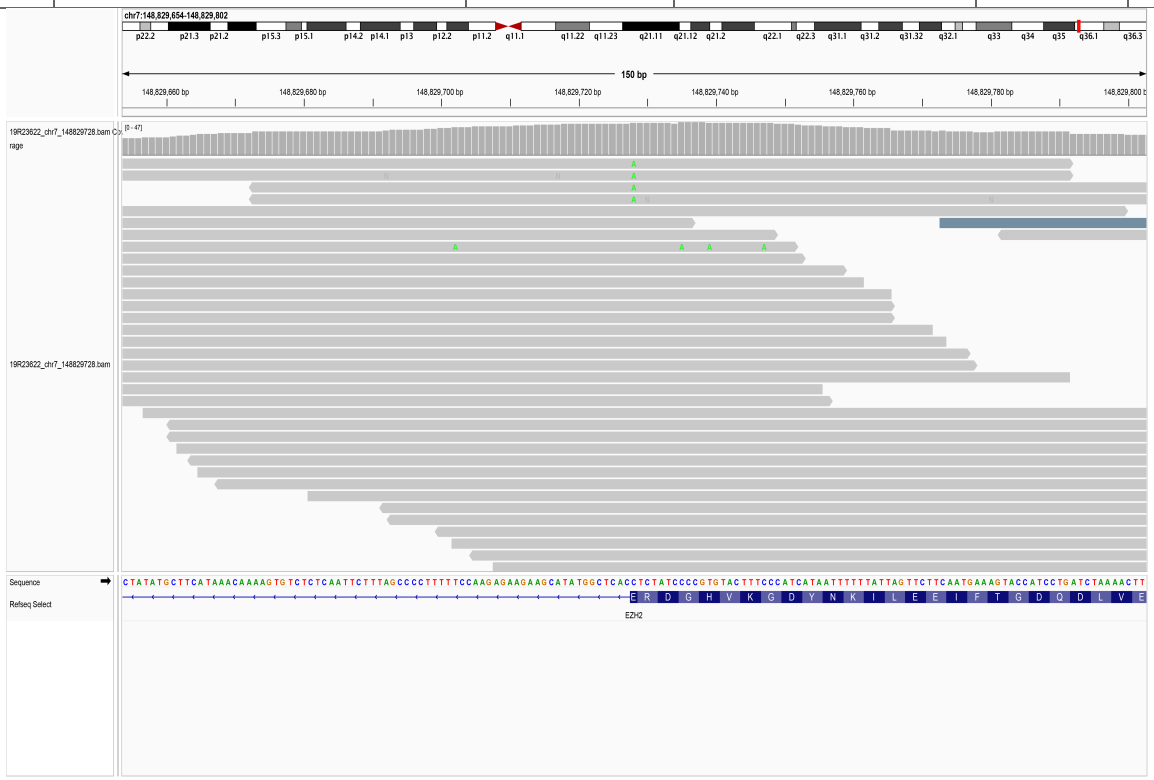
15.2. chr7_148826499_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09437	chr7_148826499_G/A	48	5	*EZH2*	stop_gained



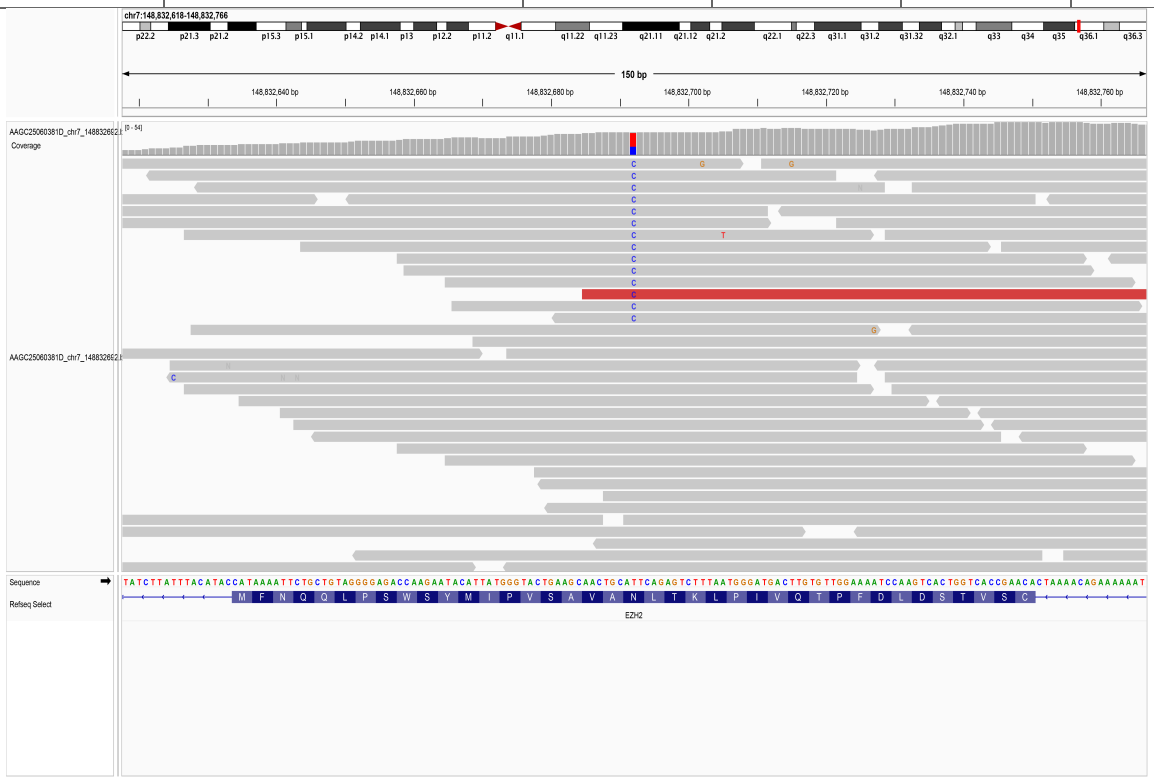
15.3. chr7_148829728_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23622	chr7_148829728_C/A	40	4	*EZH2*	stop_gained



15.4. chr7_148832692_T/C

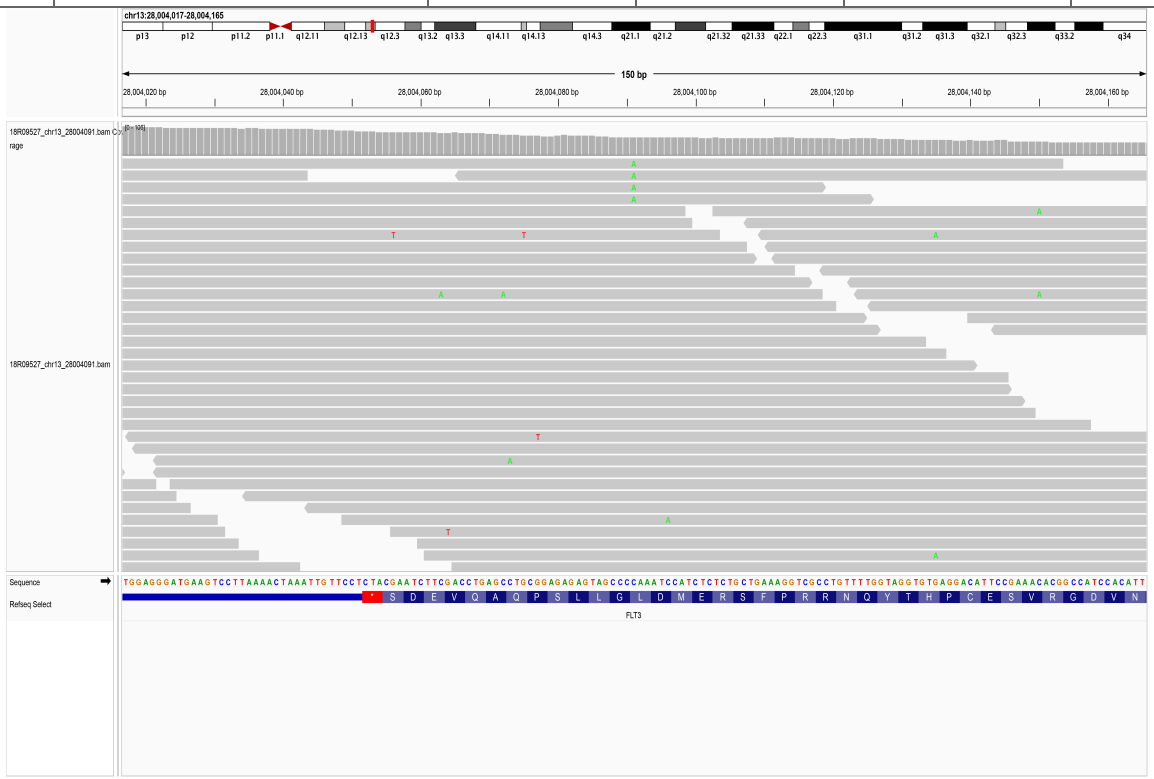
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060381D	chr7_148832692_T/C	23	14	*EZH2*	missense_variant



16. *FLT3*

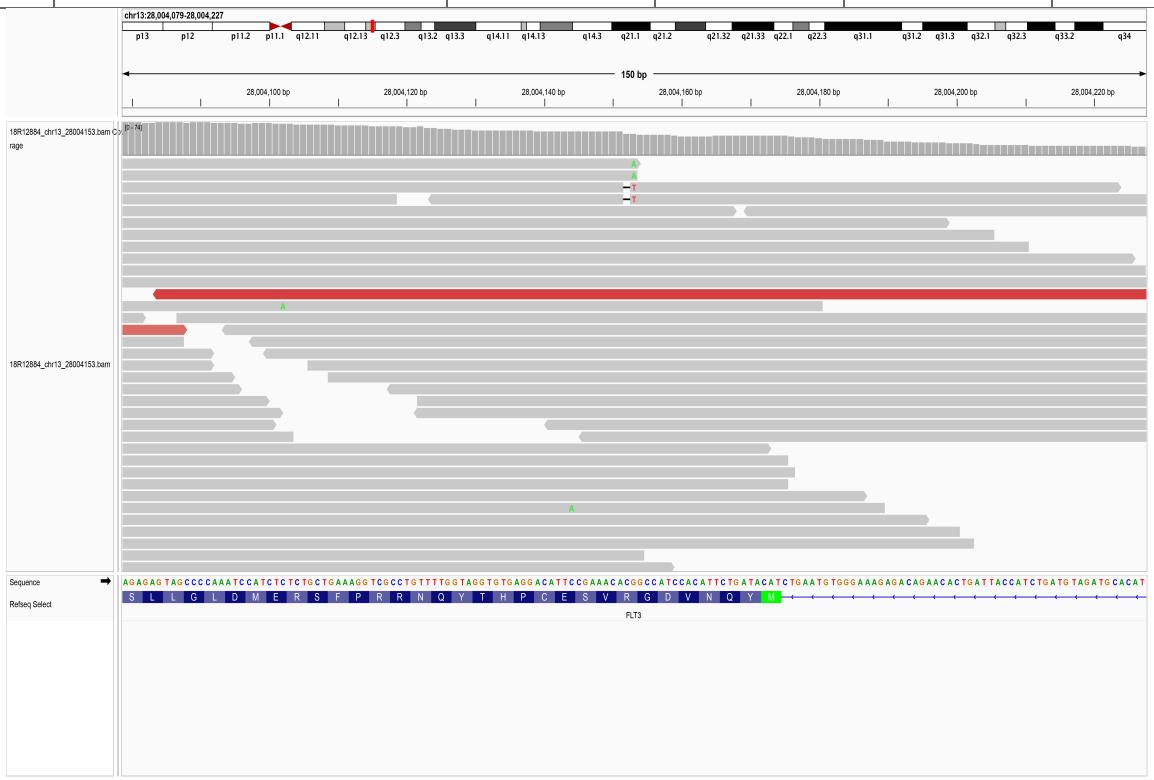
16.1. chr13_28004091_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09527	chr13_28004091_C/A	44	4	*FLT3*	missense_variant



16.2. chr13_28004153_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12884	chr13_28004153_G/T	46	2	*FLT3*	missense_variant



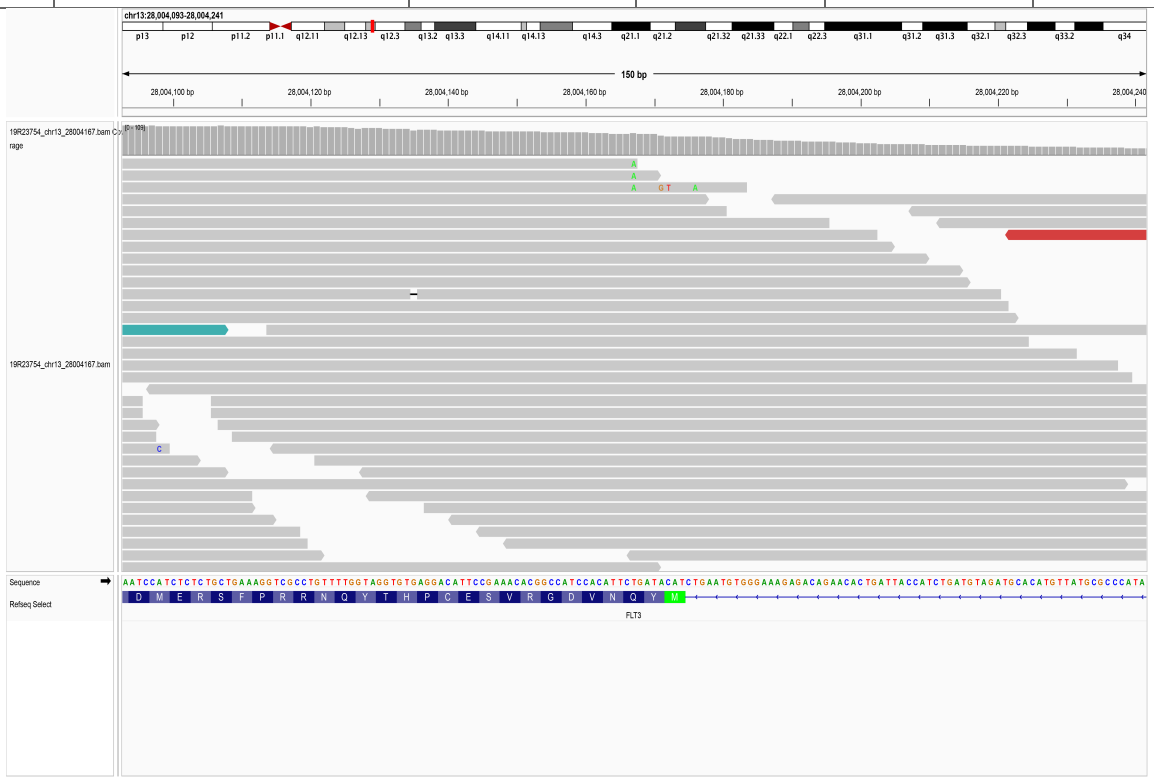
16.3. chr13_28004153_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033129C	chr13_28004153_G/A	63	31	*FLT3*	missense_variant



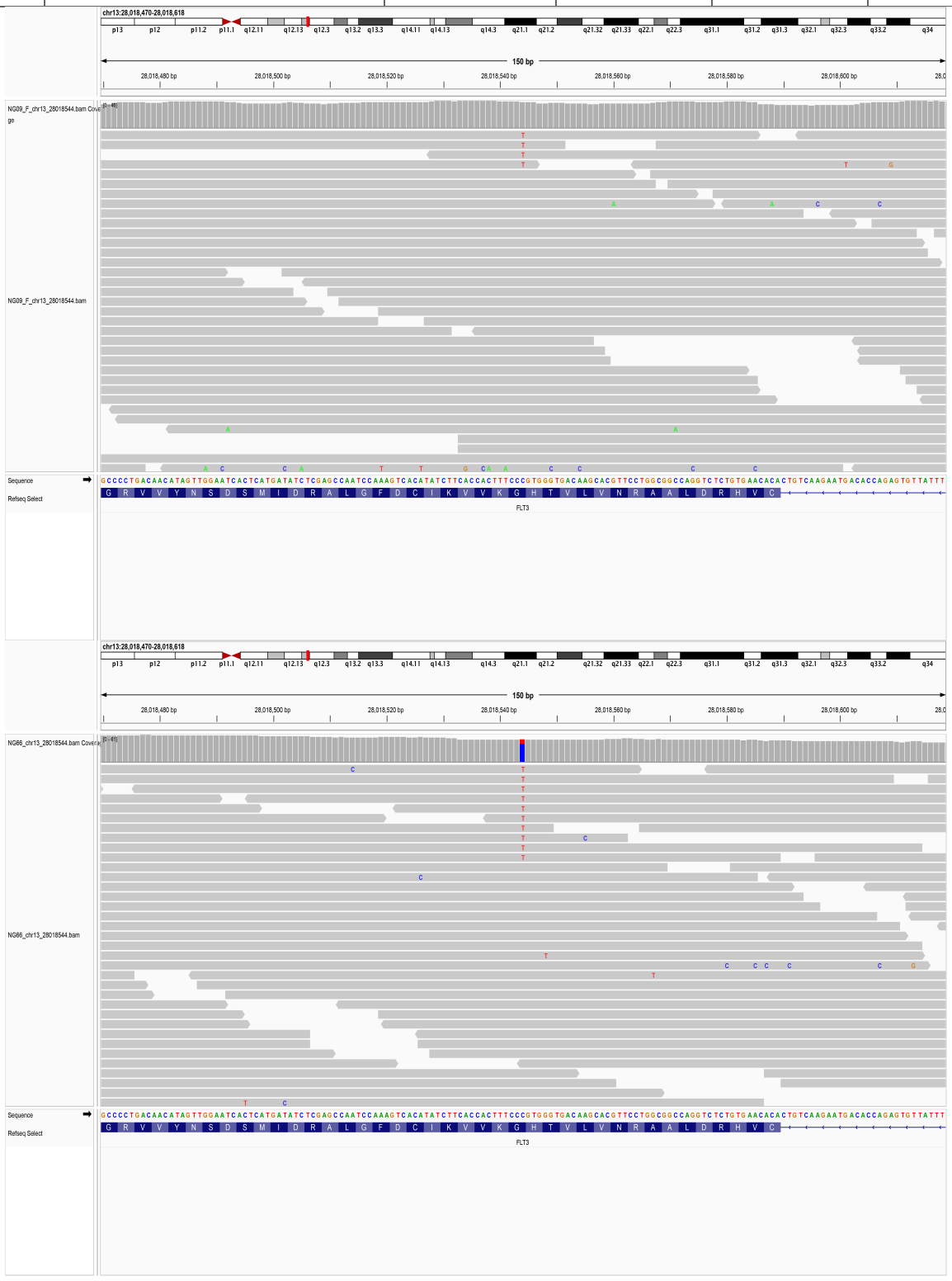
16.4. chr13_28004167_T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23754	chr13_28004167_T/A	67	3	*FLT3*	missense_variant



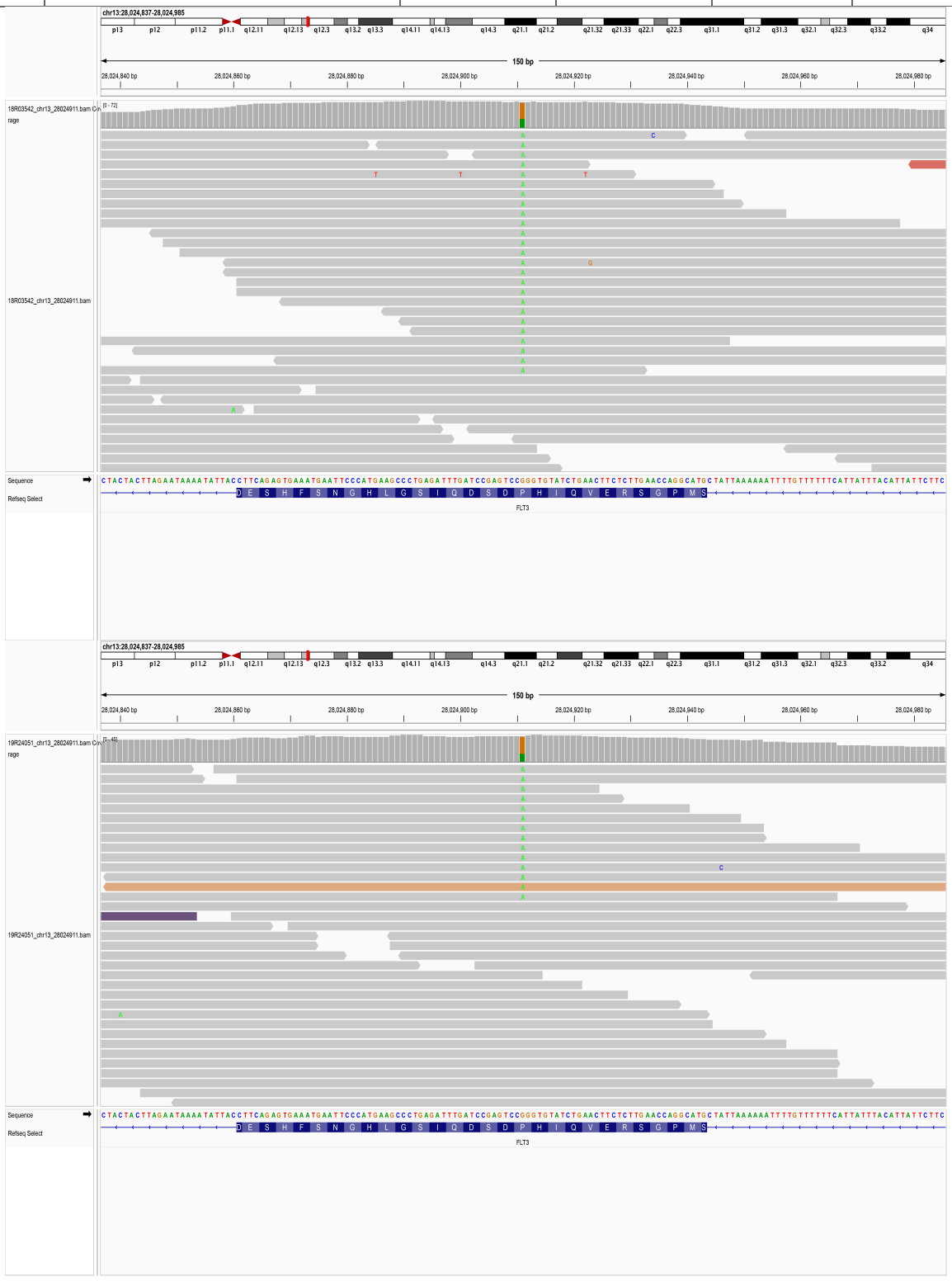
16.5. chr13_28018544_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NG09_F	chr13_28018544_C/T	34	4	*FLT3*	missense_variant
NG66	chr13_28018544_C/T	39	10	*FLT3*	missense_variant



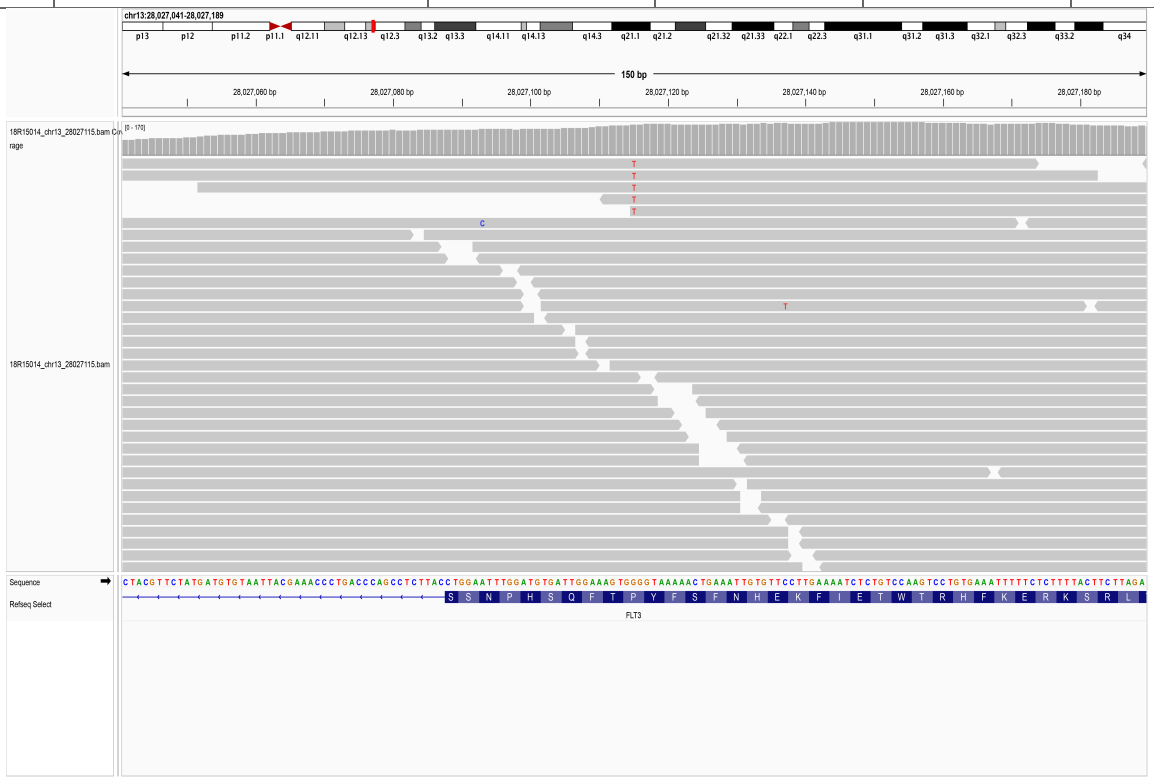
16.6. chr13_28024911_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03542	chr13_28024911_G/A	43	23	*FLT3*	missense_variant
19R24051	chr13_28024911_G/A	28	14	*FLT3*	missense_variant



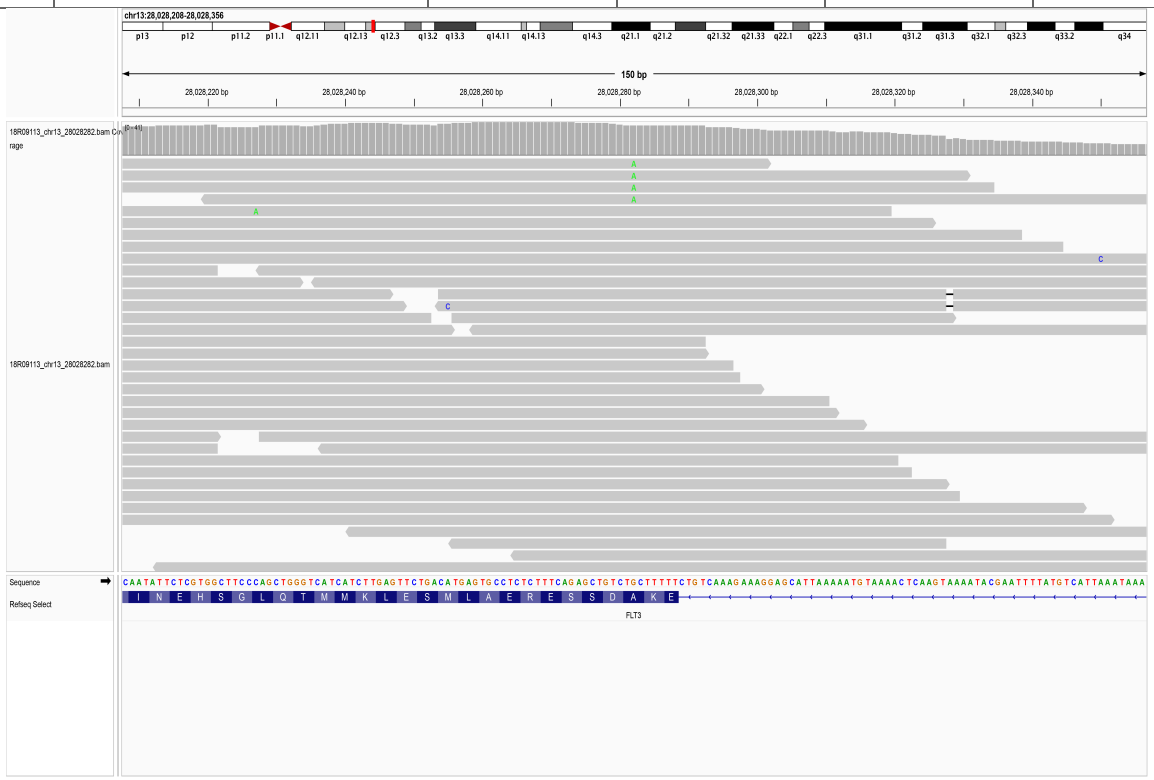
16.7. chr13_28027115_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15014	chr13_28027115_G/T	141	5	*FLT3*	missense_variant



16.8. chr13_28028282_G/A

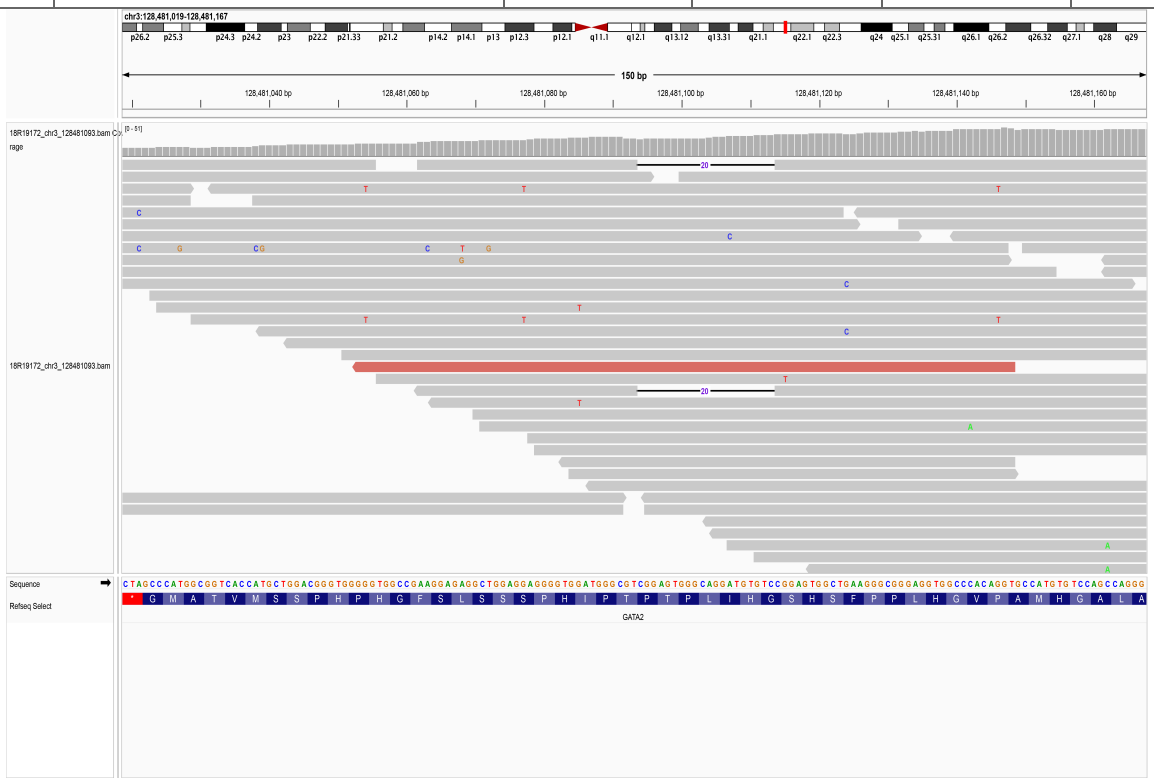
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09113	chr13_28028282_G/A	32	4	*FLT3*	missense_variant



17. *GATA2*

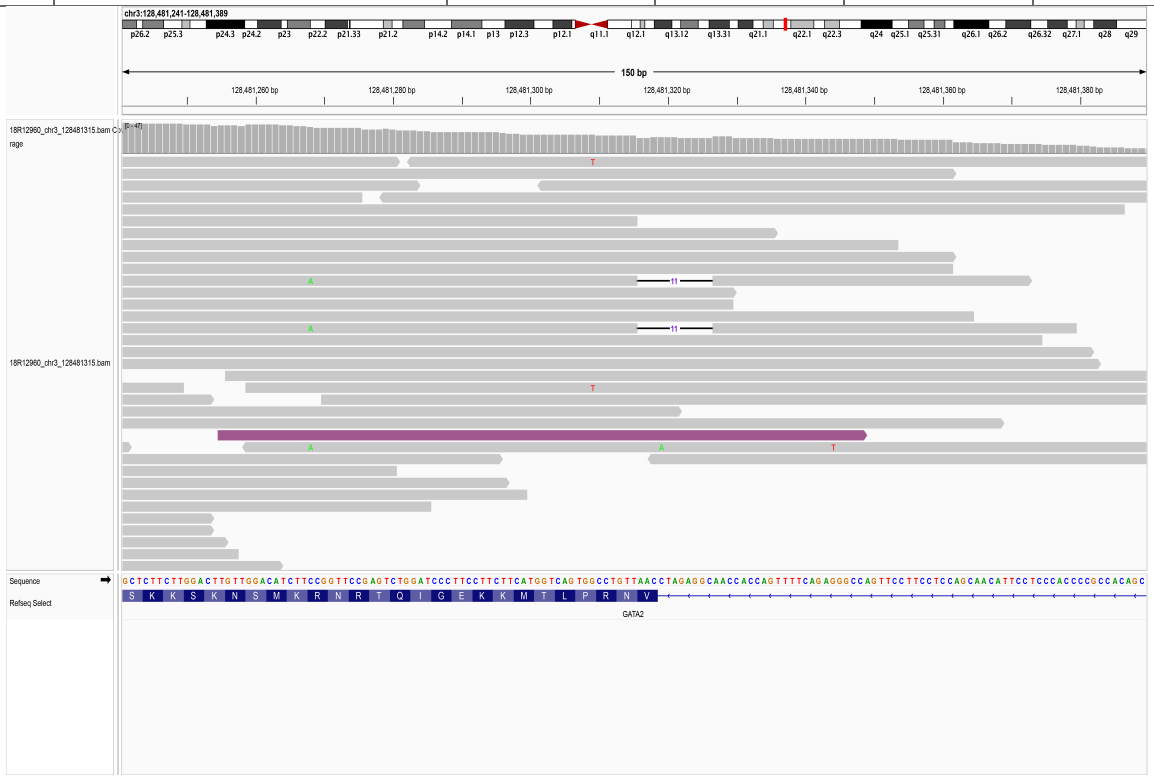
17.1. chr3_128481094_CGGAGTGGGCAGGATGTGTC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19172	chr3_128481094_CGGAGTGGGCAGGATGTGTC/-	30	2	*GATA2*	frameshift_variant



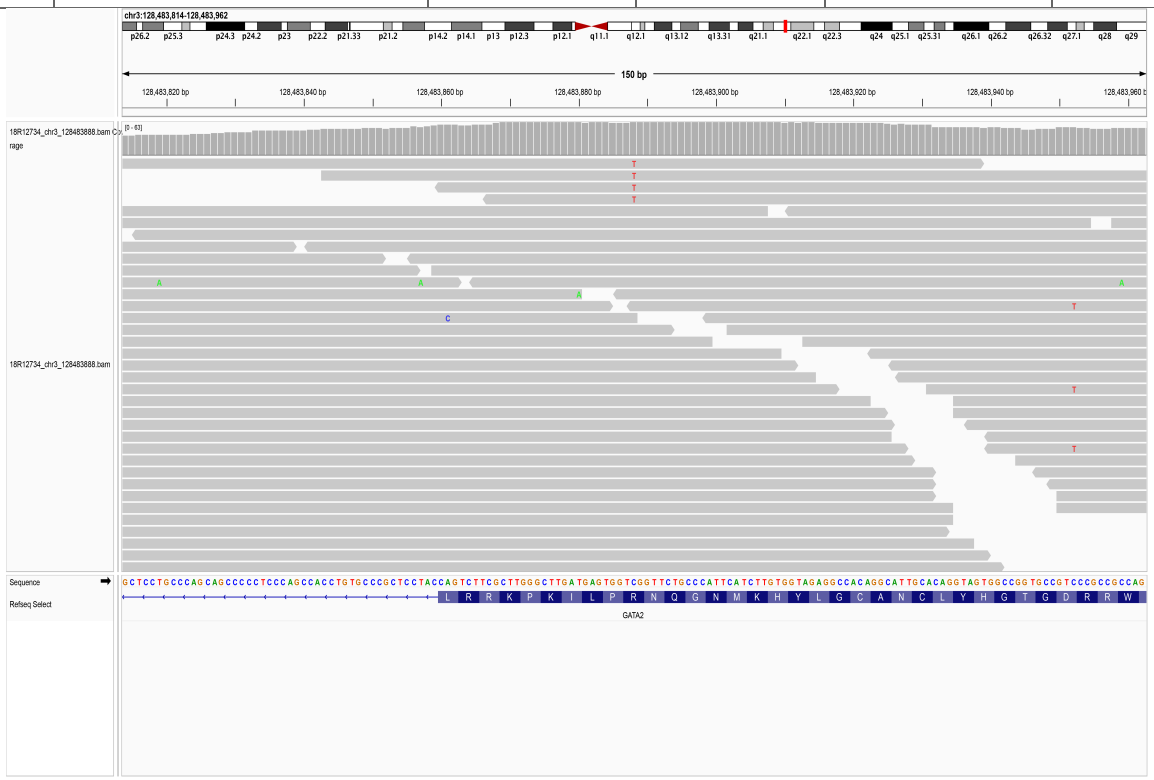
17.2. chr3_128481316_AACCTAGAGGC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12960	chr3_128481316_AACCTAGAGGC/-	22	2	*GATA2*	splice_acceptor_variant



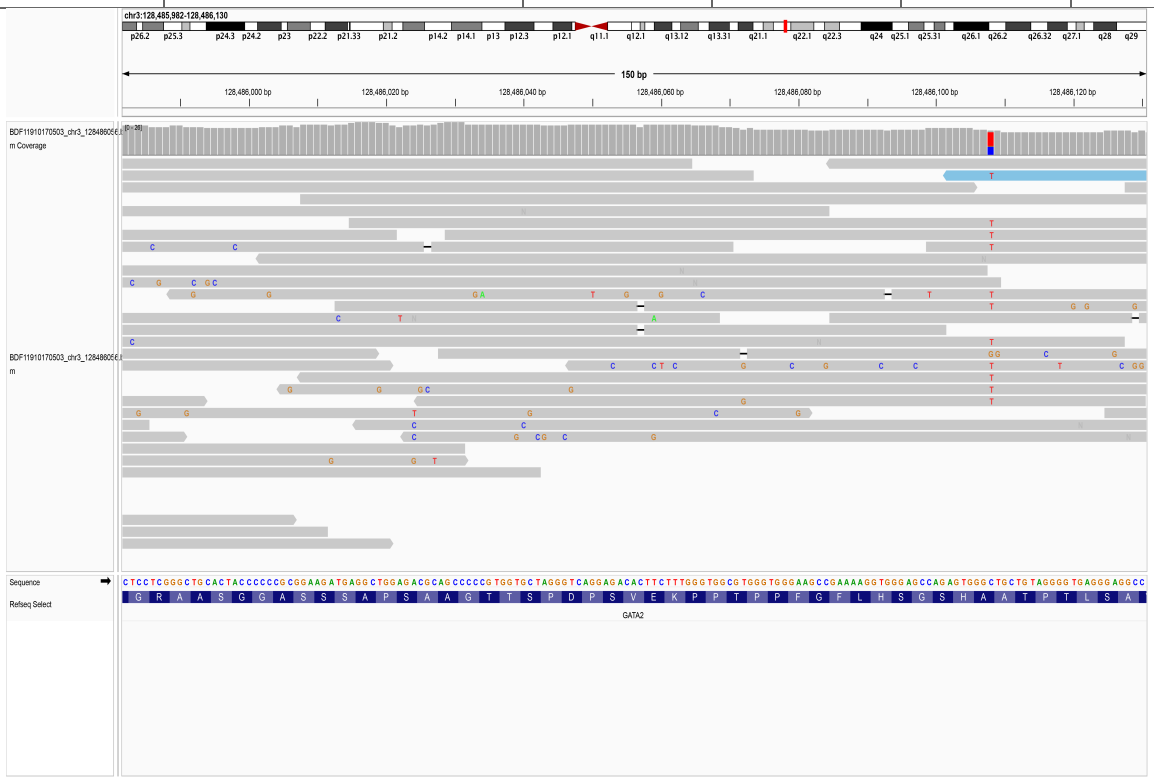
17.3. chr3_128483888_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12734	chr3_128483888_C/T	58	4	*GATA2*	missense_variant



17.4. chr3_128486057_C/-

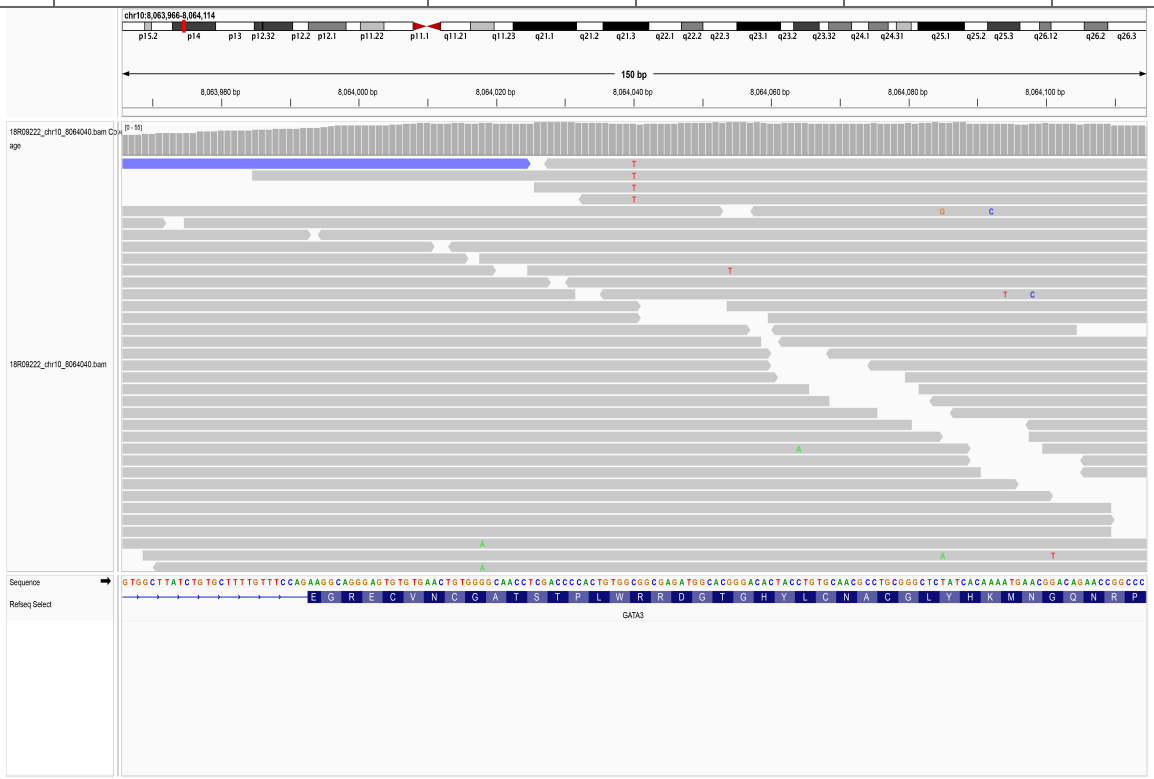
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr3_128486057_C/-	12	2	*GATA2*	frameshift_variant



18. *GATA3*

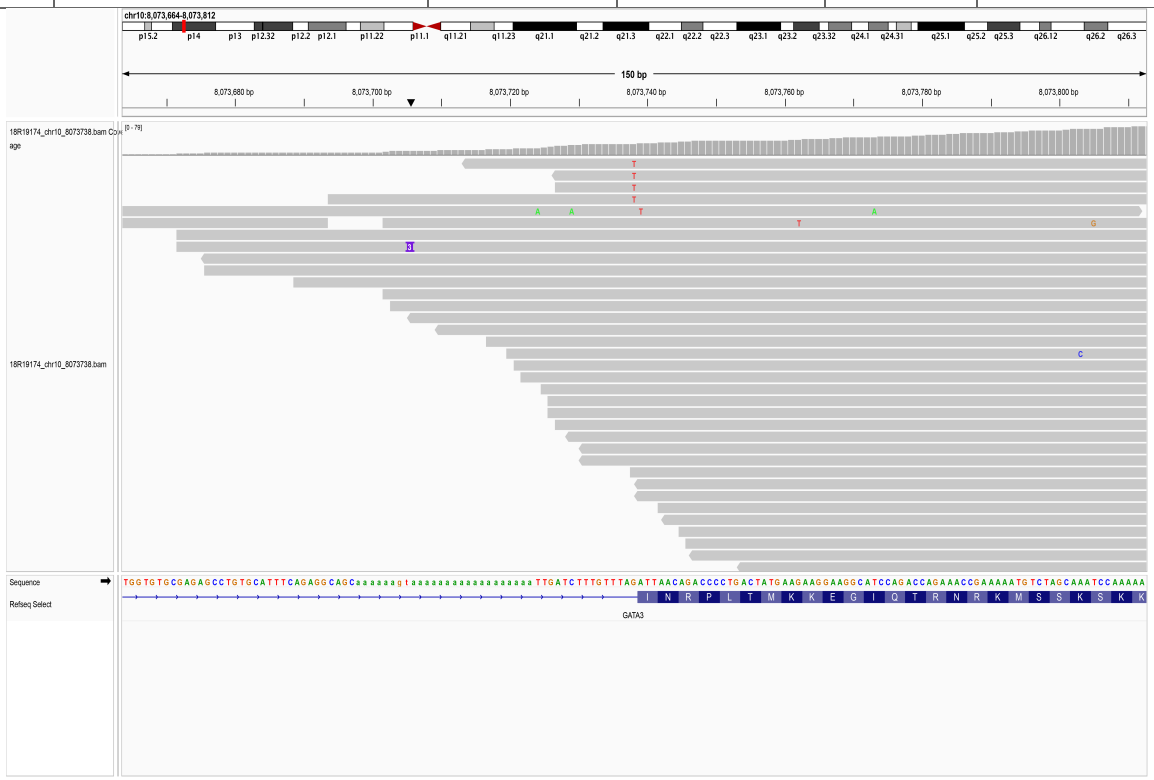
18.1. chr10_8064040_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09222	chr10_8064040_C/T	46	4	*GATA3*	missense_variant



18.2. chr10_8073738_G/T

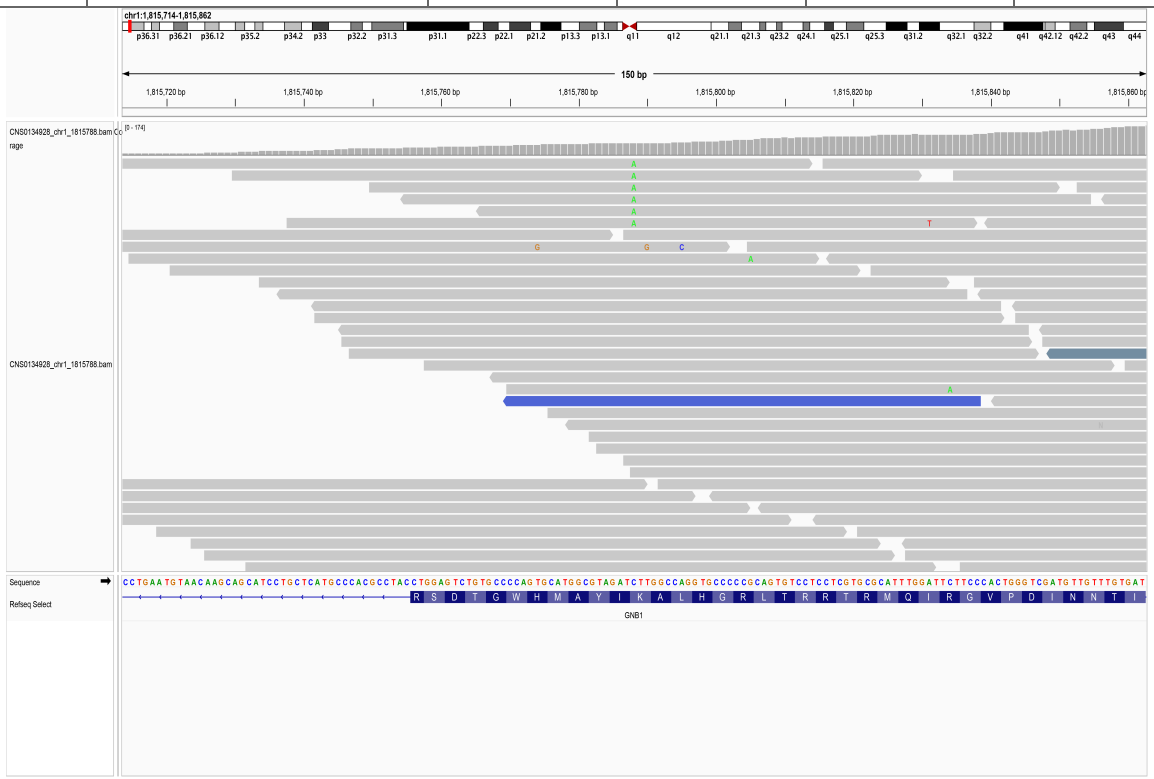
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19174	chr10_8073738_G/T	22	4	*GATA3*	splice_acceptor_variant



19. *GNB1*

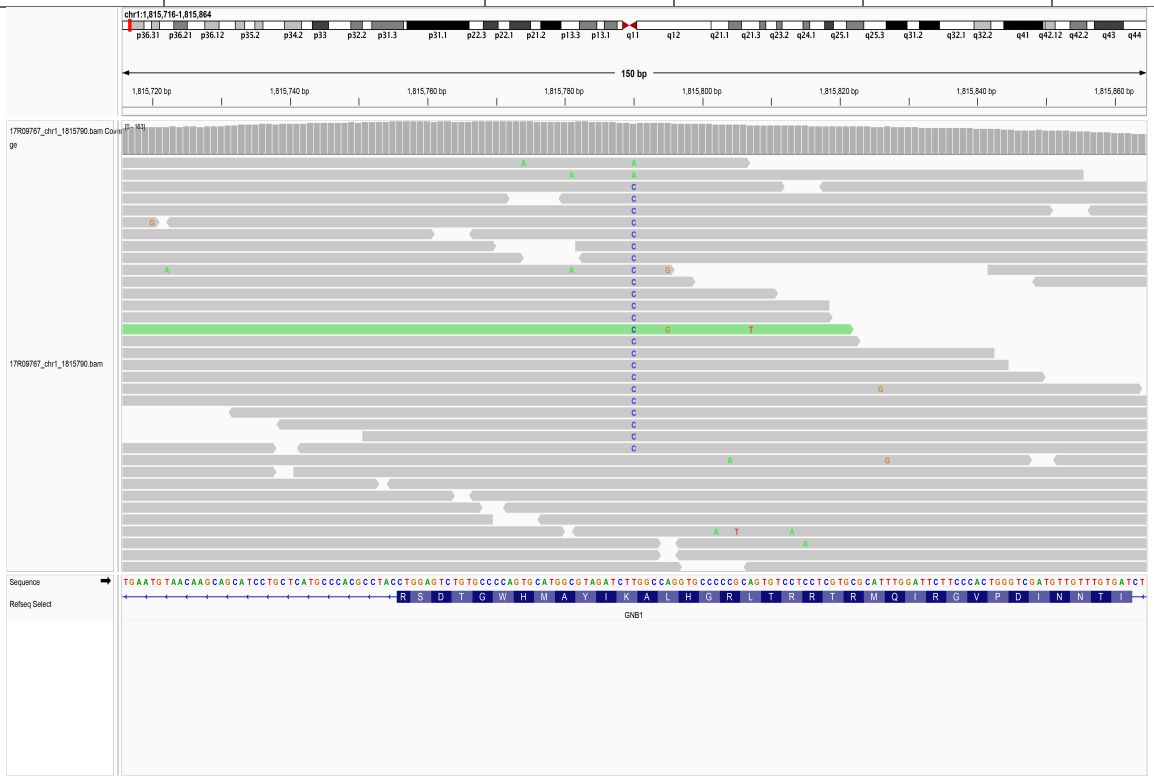
19.1. chr1_1815788_C/A

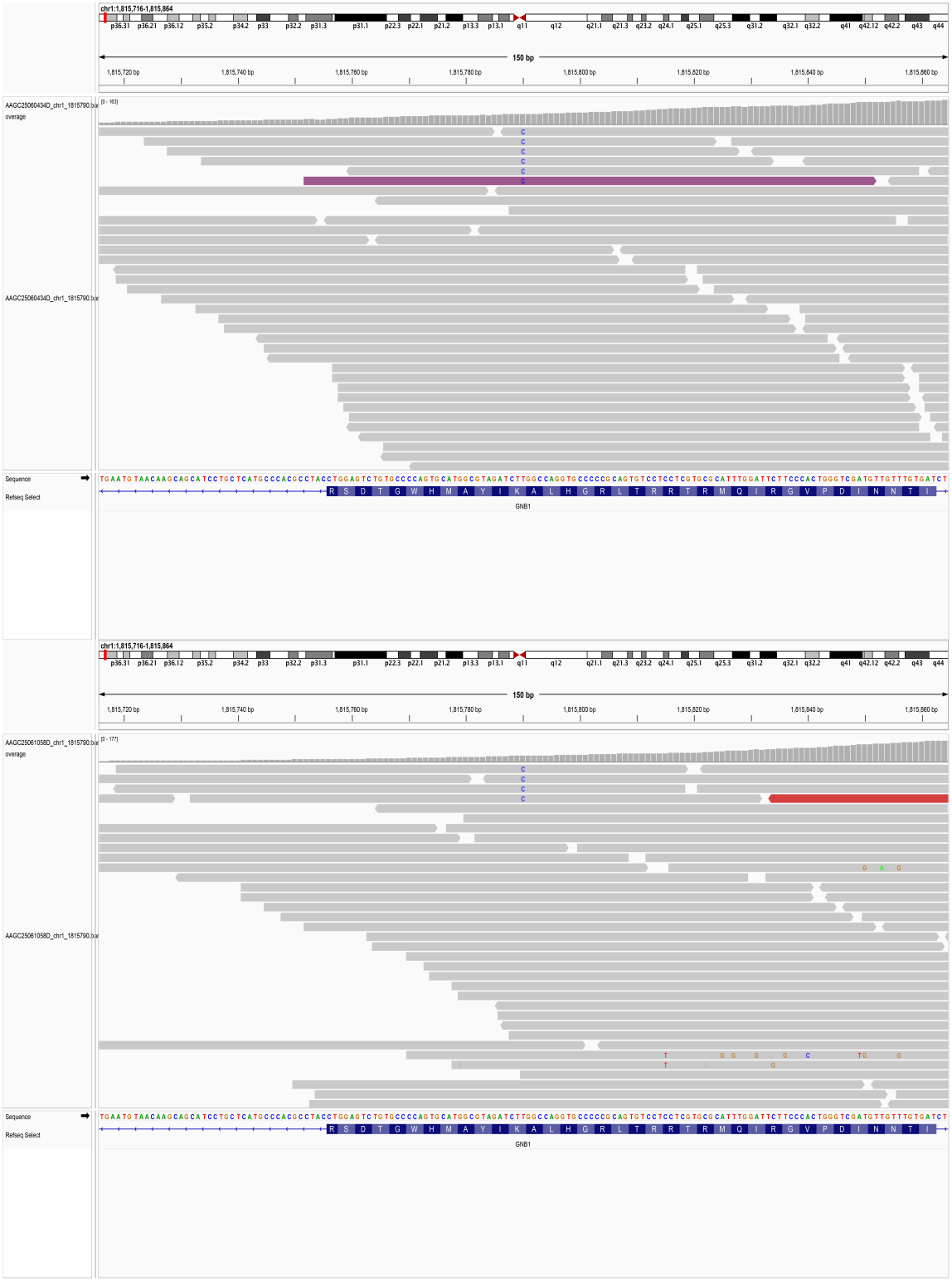
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134928	chr1_1815788_C/A	55	6	*GNB1*	missense_variant

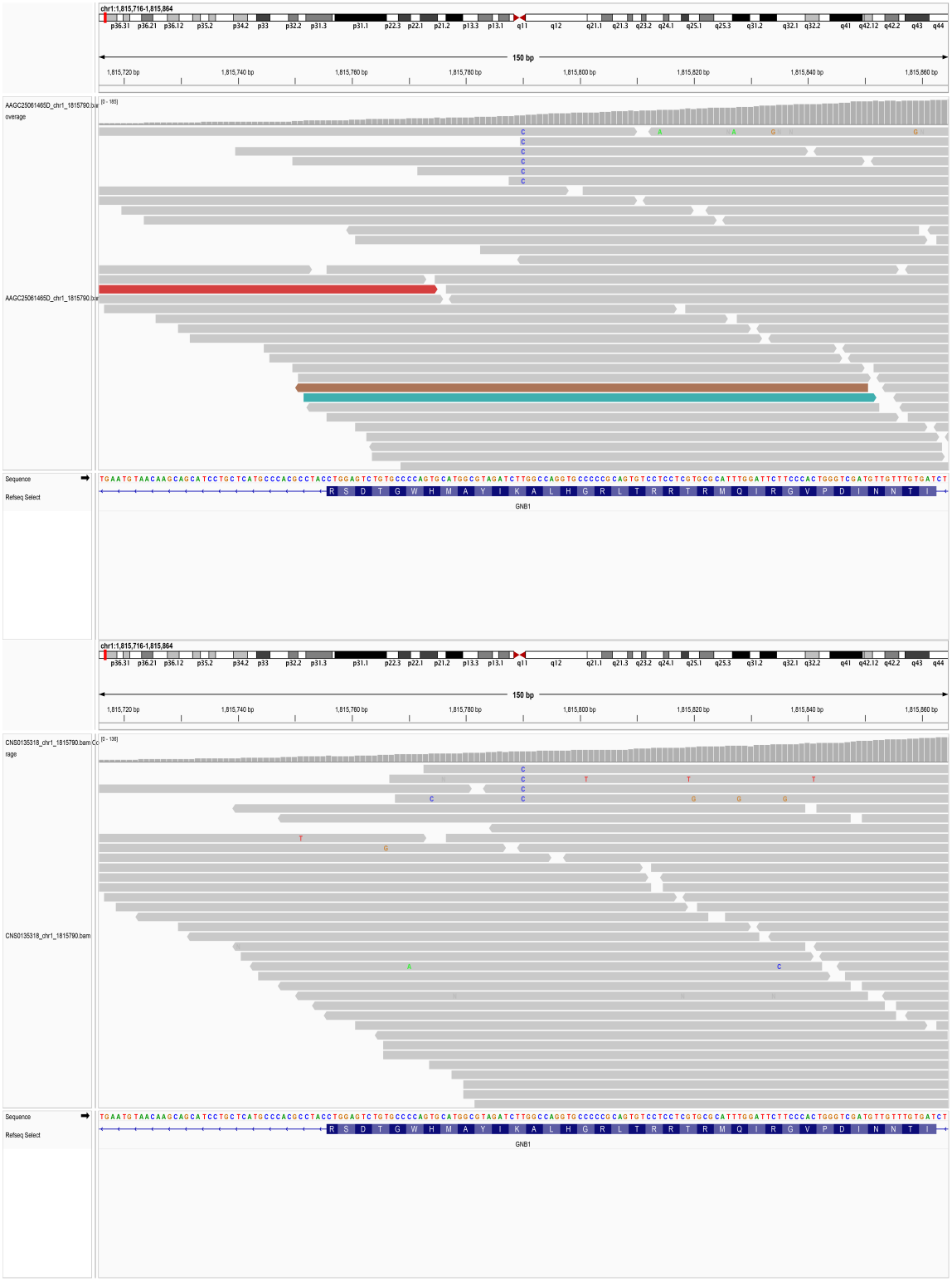


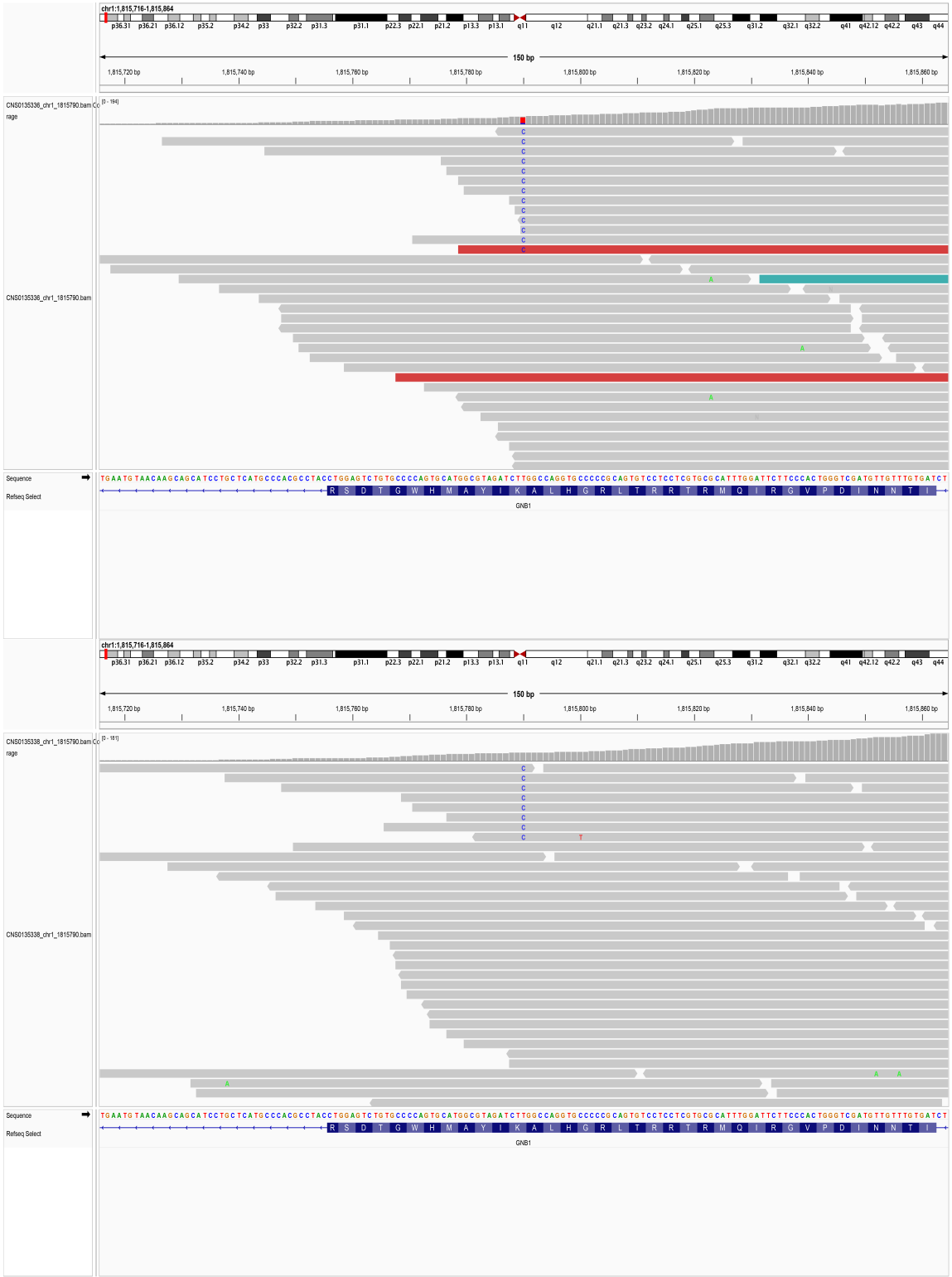
19.2. chr1_1815790_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09767	chr1_1815790_T/C	124	22	*GNB1*	missense_variant
AAGC25060434D	chr1_1815790_T/C	56	6	*GNB1*	missense_variant
AAGC25061058D	chr1_1815790_T/C	36	4	*GNB1*	missense_variant
AAGC25061465D	chr1_1815790_T/C	57	6	*GNB1*	missense_variant
CNS0135318	chr1_1815790_T/C	47	4	*GNB1*	missense_variant
CNS0135336	chr1_1815790_T/C	45	13	*GNB1*	missense_variant
CNS0135338	chr1_1815790_T/C	50	8	*GNB1*	missense_variant




chr1:1,815,716-1,815,864
150 bp
1,815,720 bp
1,815,740 bp
1,815,760 bp
1,815,780 bp
1,815,800 bp
1,815,820 bp
1,815,840 bp
1,815,860 bp
AAGC25060434D_chr1_1815790.bai
overage
AAGC25060434D_chr1_1815790.bai
Sequence
Refseq Select
GNB1
chr1:1,815,716-1,815,864
150 bp
AAGC25061058D_chr1_1815790.bai
overage
AAGC25061058D_chr1_1815790.bai
Sequence
Refseq Select
GNB1

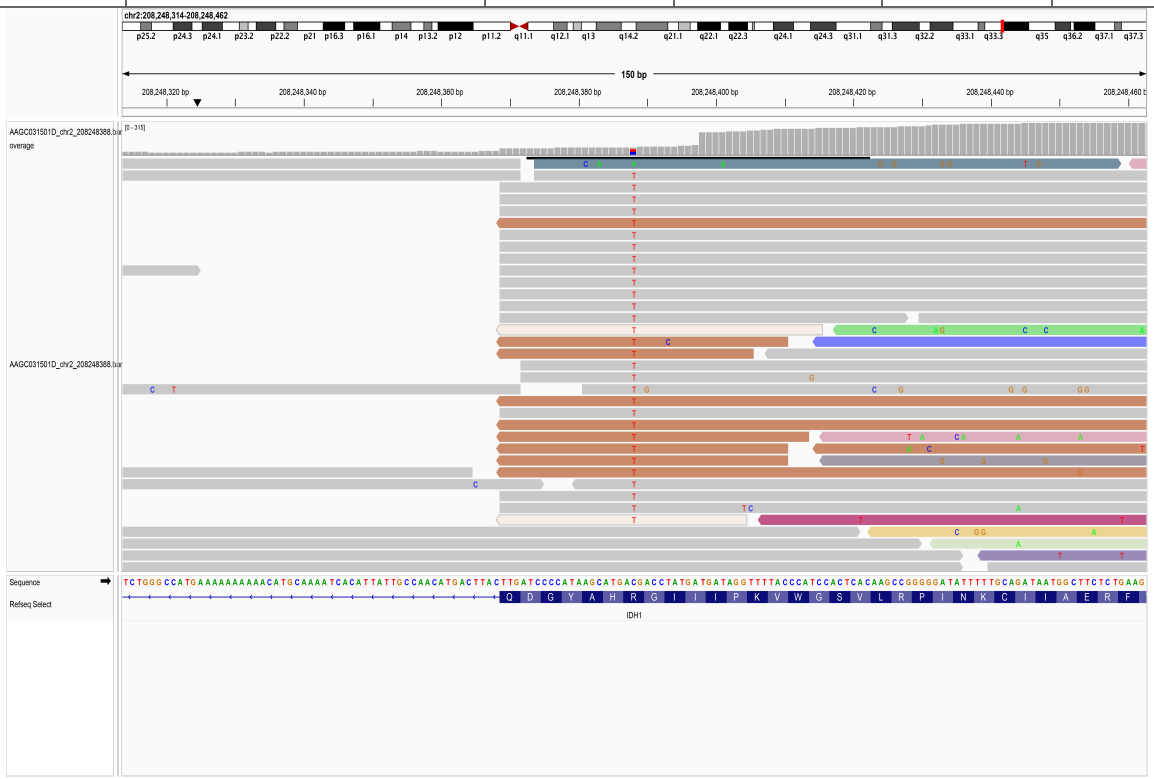

chr1:1,815,716-1,815,864
150 bp
1,815,720 bp
1,815,740 bp
1,815,760 bp
1,815,780 bp
1,815,800 bp
1,815,820 bp
1,815,840 bp
1,815,860 bp
AAGC25061465D_chr1_1815790.bar
overage
AAGC25061465D_chr1_1815790.bar
Sequence
Refseq Select
GNB1
CNS0135318_chr1_1815790.bam
rage
CNS0135318_chr1_1815790.bam


chr1:1,815,716-1,815,864
150 bp
1,815,720 bp
1,815,740 bp
1,815,760 bp
1,815,780 bp
1,815,800 bp
1,815,820 bp
1,815,840 bp
1,815,860 bp
CNS0135336_chr1_1815790.bam Coverage
CNS0135336_chr1_1815790.bam
Sequence
Refseq Select
GNB1
CNS0135338_chr1_1815790.bam Coverage
CNS0135338_chr1_1815790.bam
Sequence
Refseq Select
GNB1

20. *IDH1*

20.1. chr2_208248388_C/T

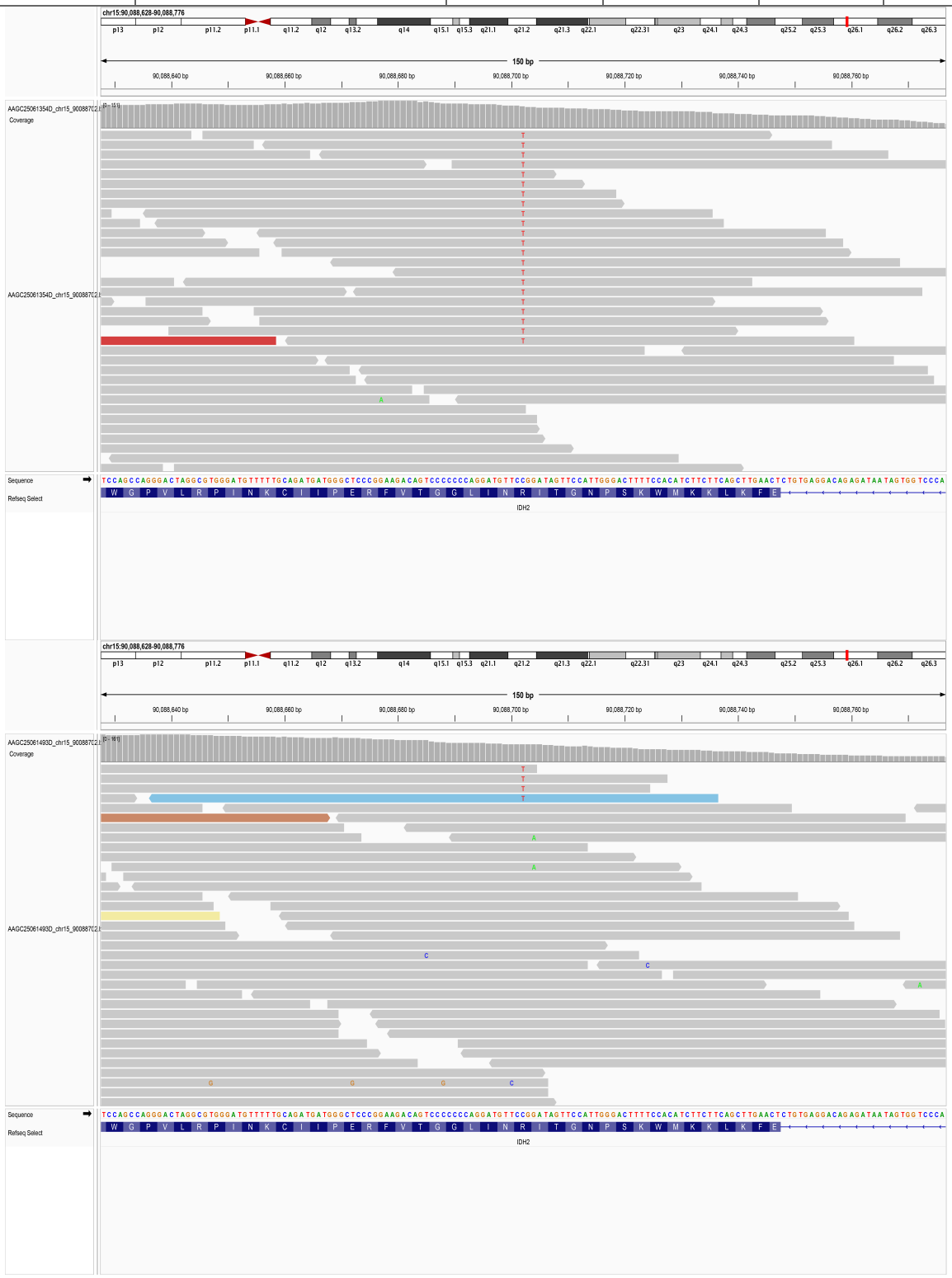
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC031501D	chr2_208248388_C/T	38	6	*IDH1*	missense_variant



21. *IDH2*

21.1. chr15_90088702_C/T

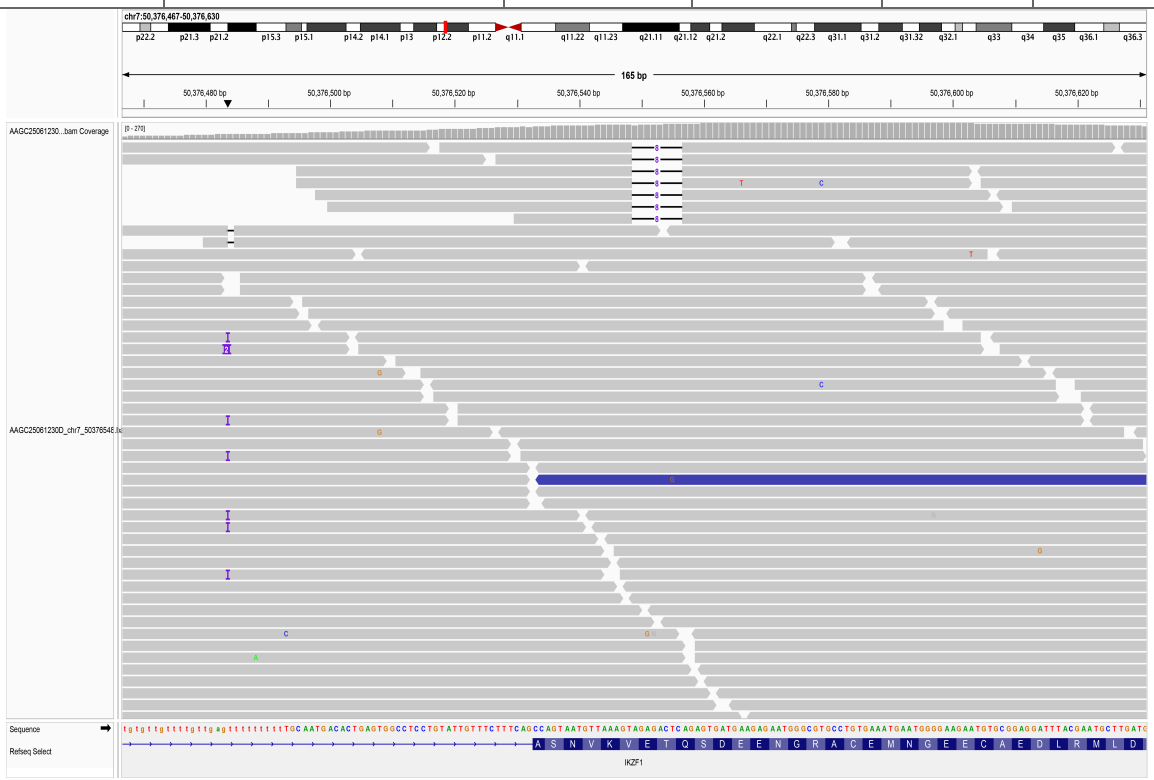
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061354D	chr15_90088702_C/T	96	22	*IDH2*	missense_variant
AAGC25061493D	chr15_90088702_C/T	97	4	*IDH2*	missense_variant



22. *IKZF1*

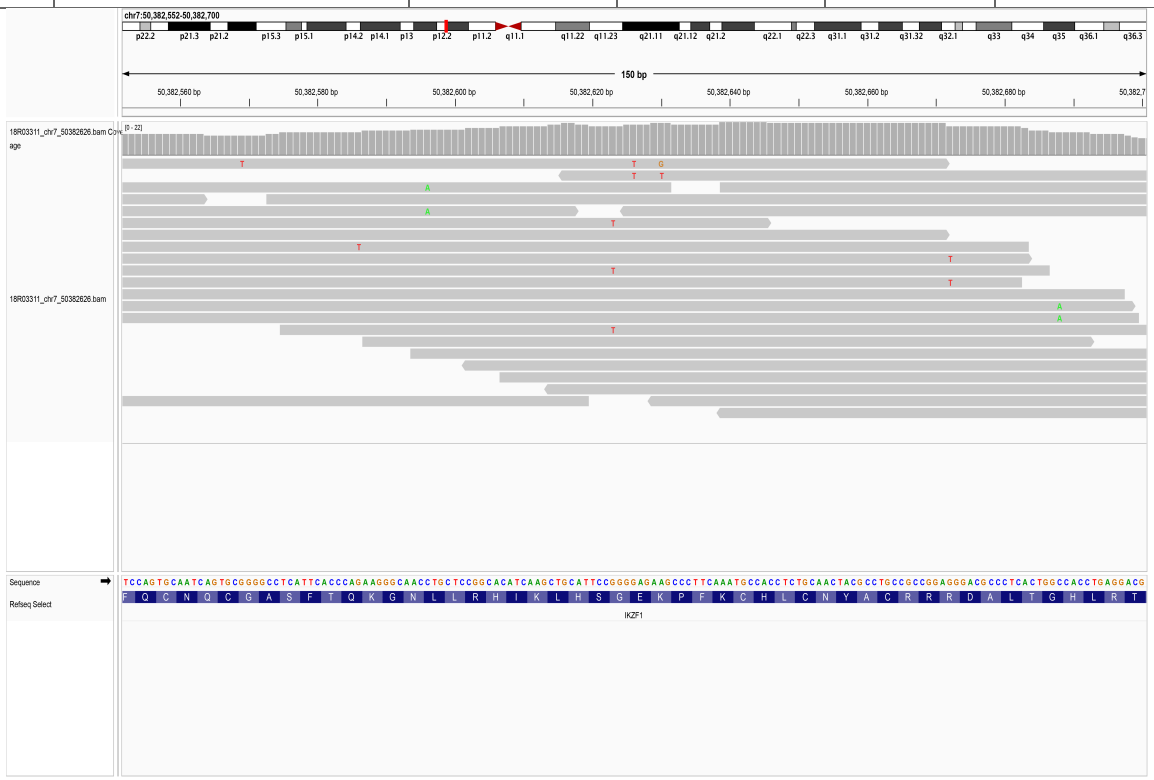
22.1. chr7_50376549_AGAGACTC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061230D	chr7_50376549_AGAGACTC/-	241	8	*IKZF1*	frameshift_variant



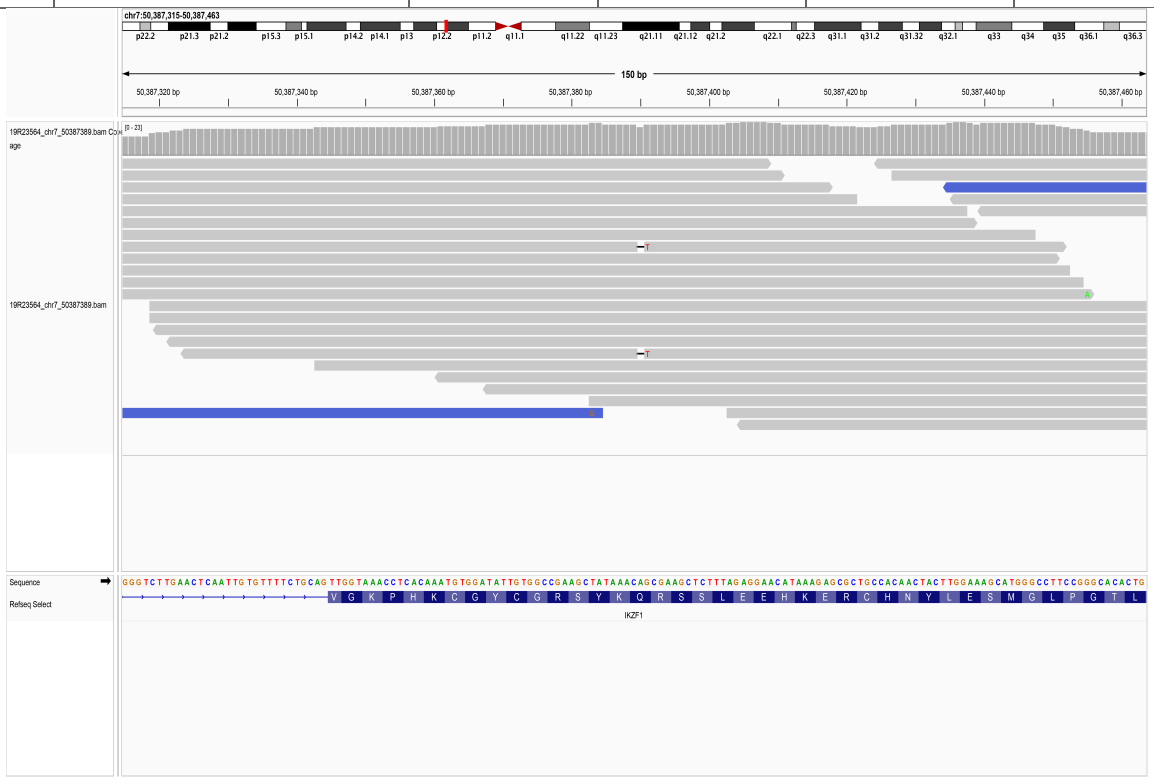
22.2. chr7_50382626_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr7_50382626_G/T	18	2	*IKZF1*	stop_gained



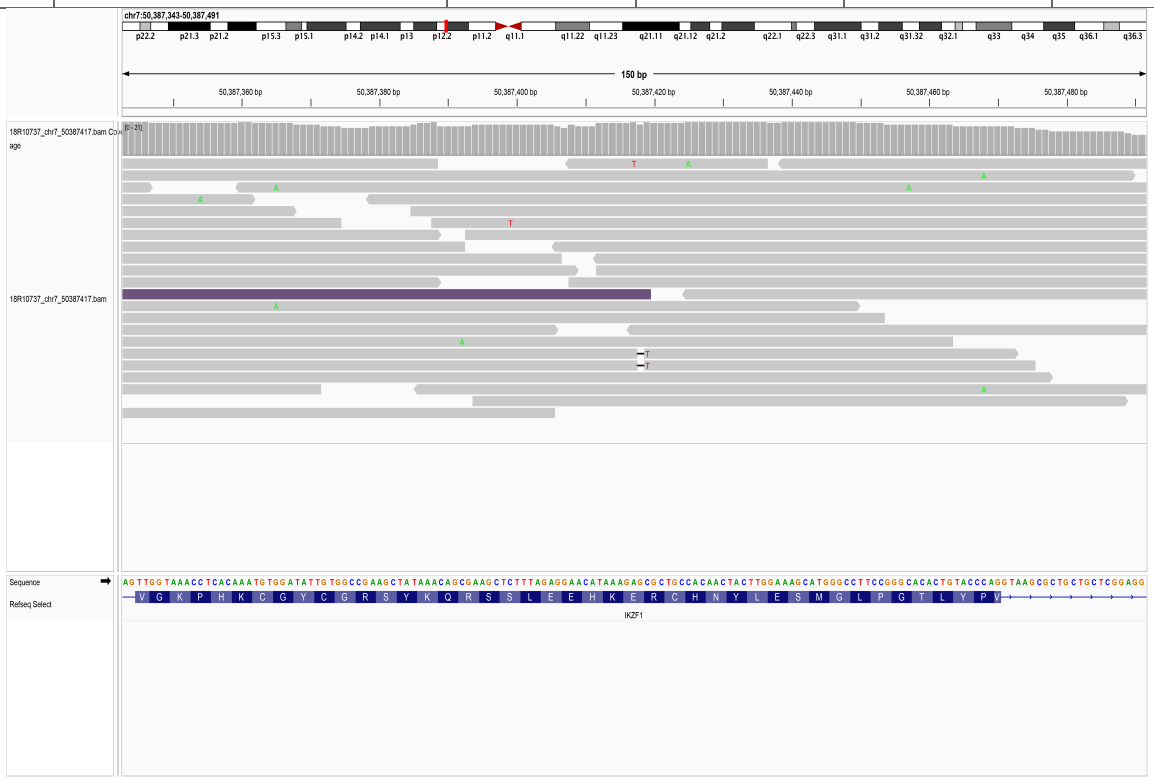
22.3. chr7_50387390_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23564	chr7_50387390_A/-	19	2	*IKZF1*	frameshift_variant



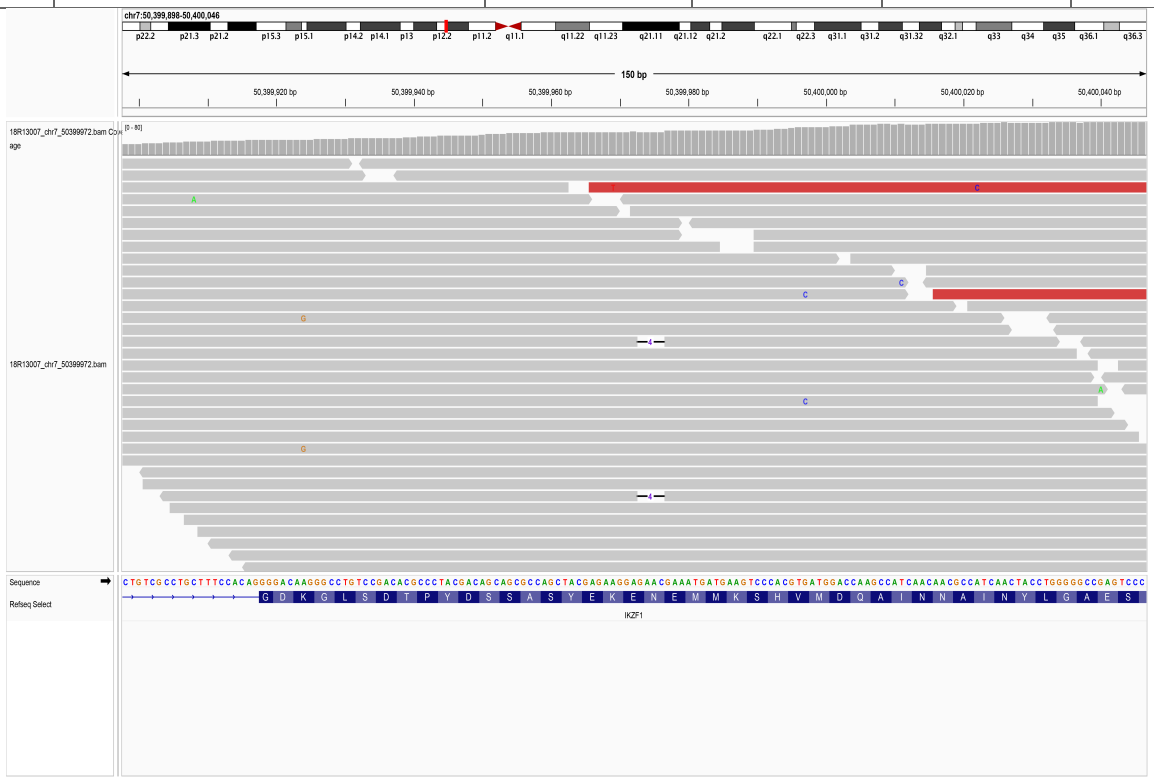
22.4. chr7_50387418_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10737	chr7_50387418_G/-	18	2	*IKZF1*	frameshift_variant



22.5. chr7_50399973_GAAC/-

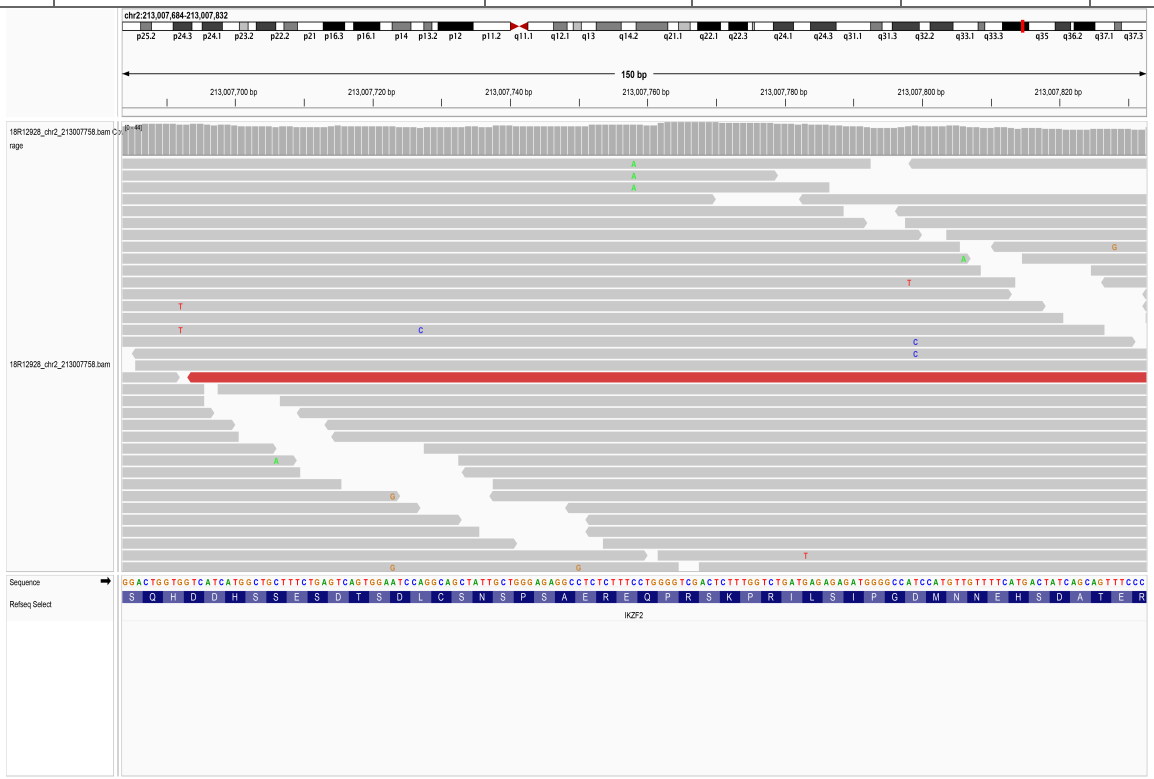
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13007	chr7_50399973_GAAC/-	55	2	*IKZF1*	frameshift_variant



23. *IKZF2*

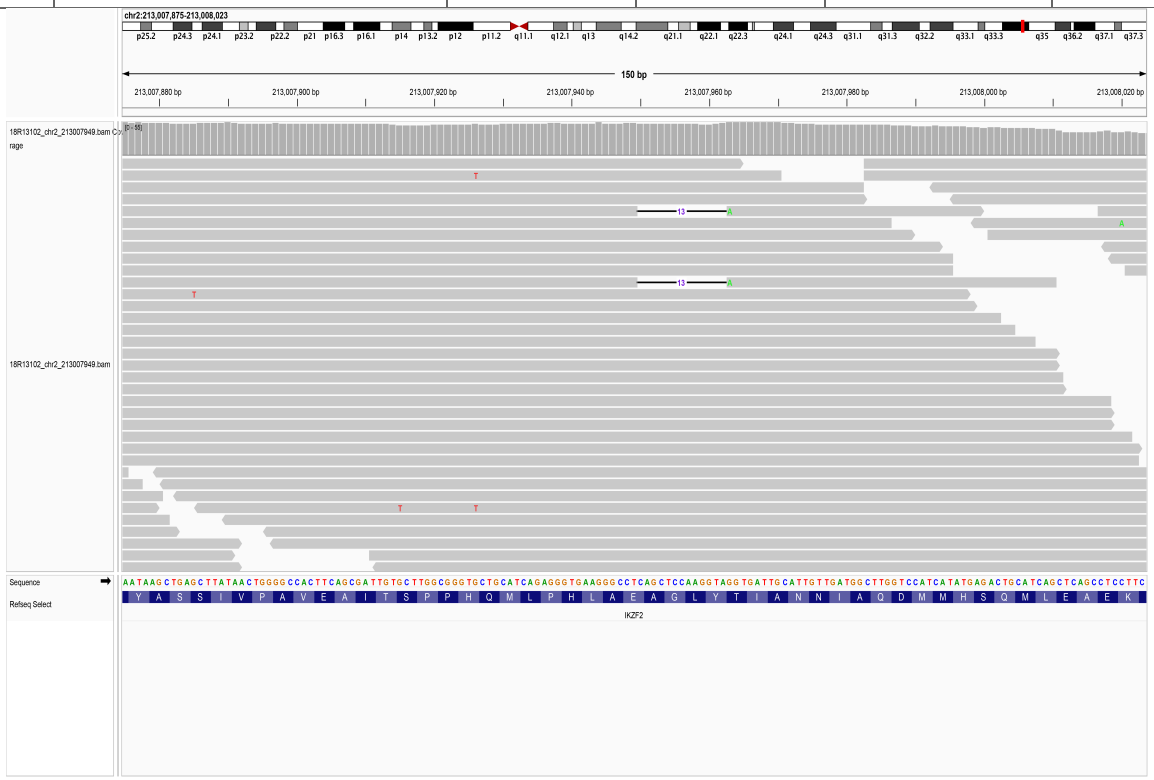
23.1. chr2_213007758_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12928	chr2_213007758_C/A	37	3	*IKZF2*	stop_gained



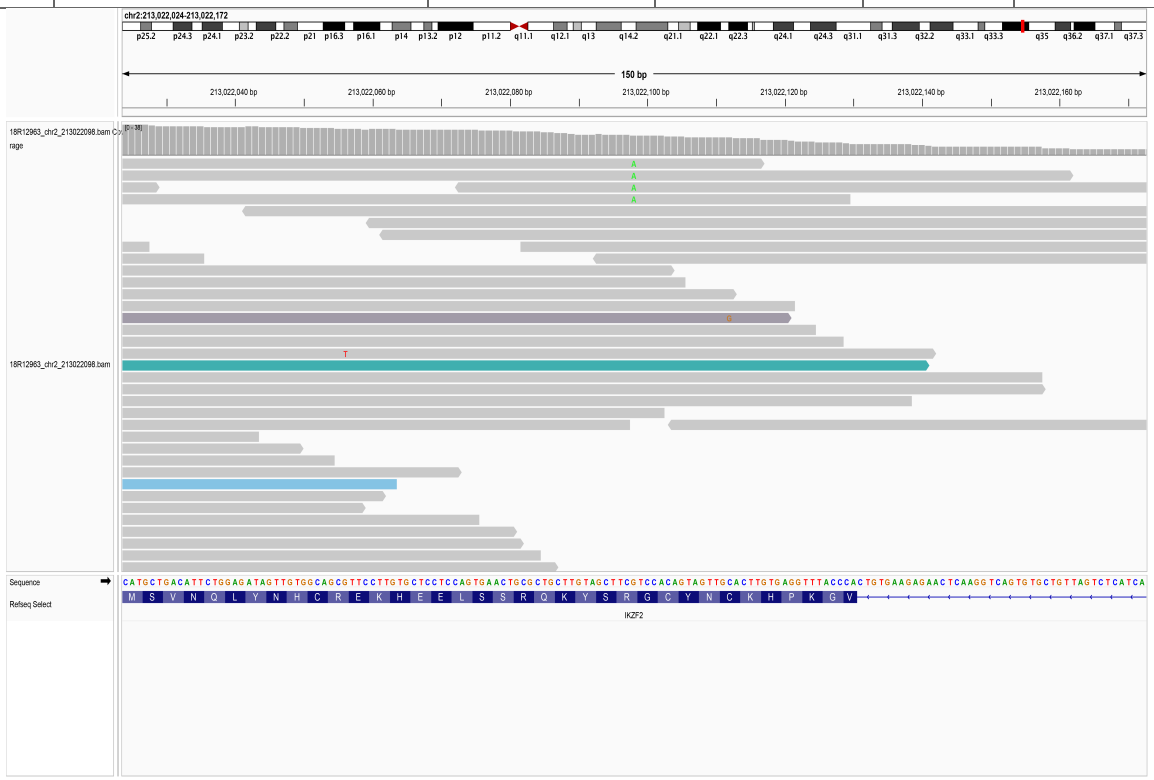
23.2. chr2_213007950_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13102	chr2_213007950_C/-	51	2	*IKZF2*	frameshift_variant



23.3. chr2_213022098_G/A

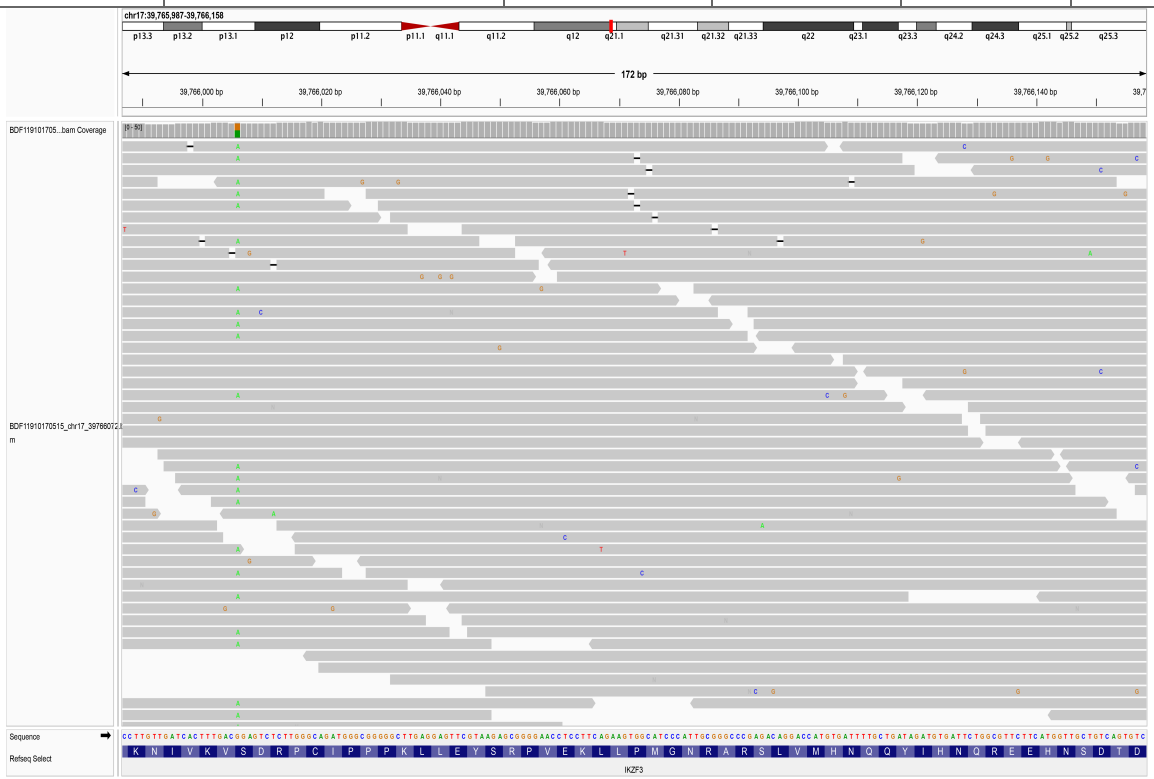
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12963	chr2_213022098_G/A	17	4	*IKZF2*	stop_gained



24. *IKZF3*

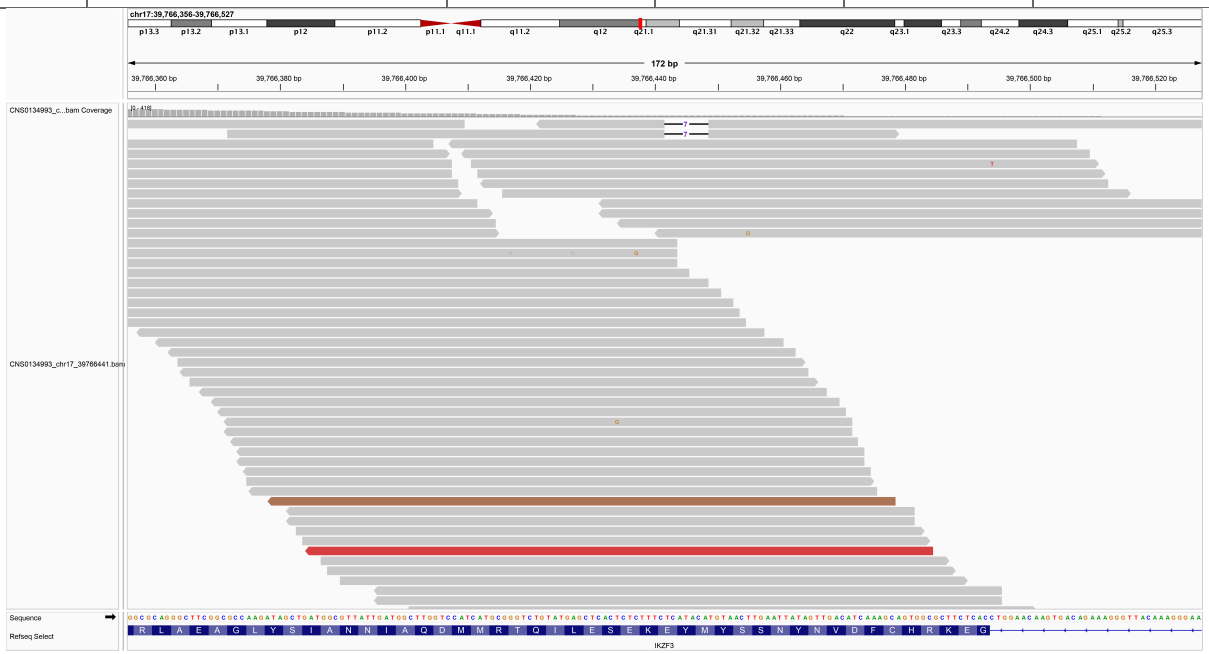
24.1. chr17_39766073_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170515	chr17_39766073_G/-	42	4	*IKZF3*	frameshift_variant



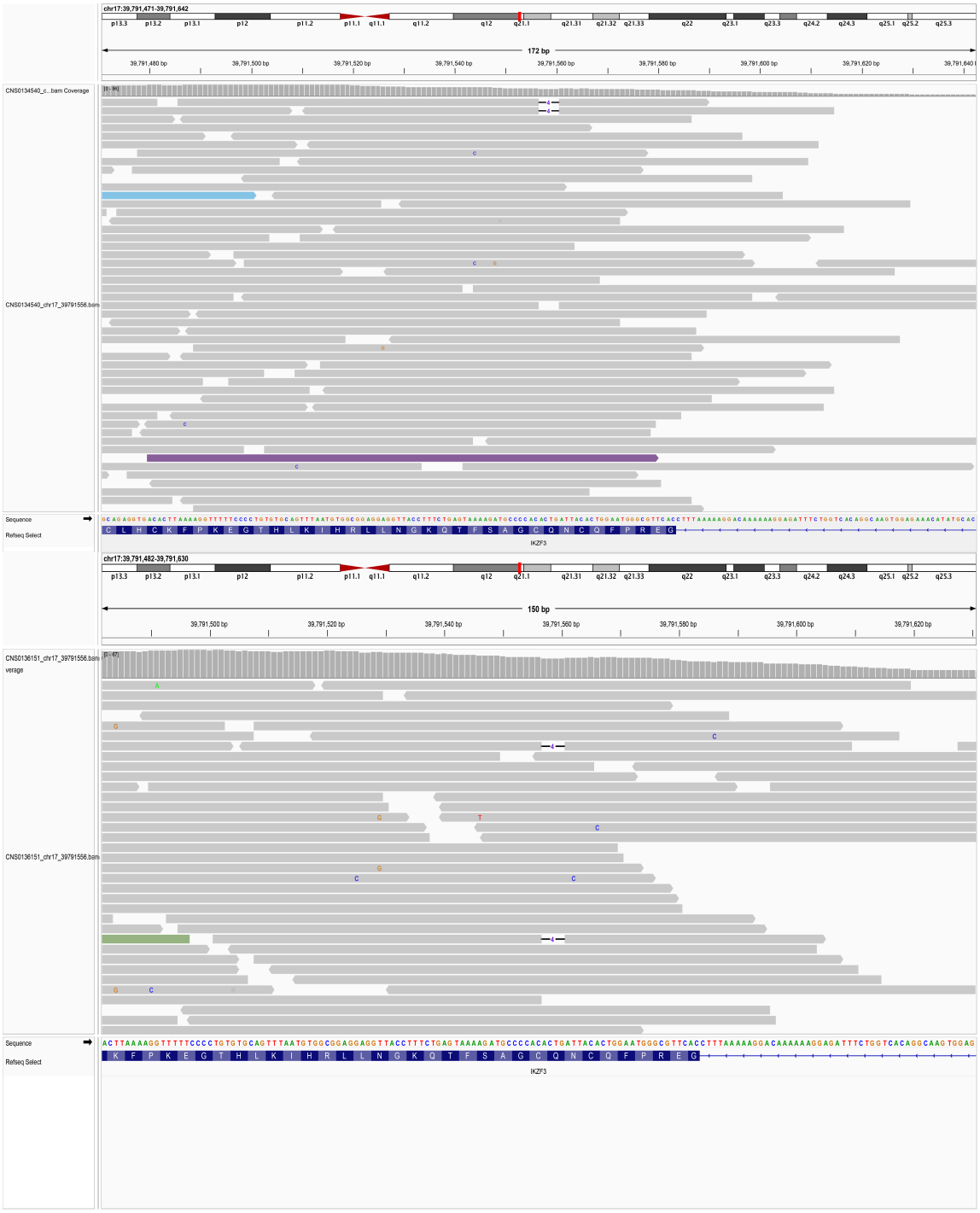
24.2. chr17_39766442_TCATACA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134993	chr17_39766442_TCATACA/-	53	2	*IKZF3*	frameshift_variant



24.3. chr17_39791557_ACTG/-

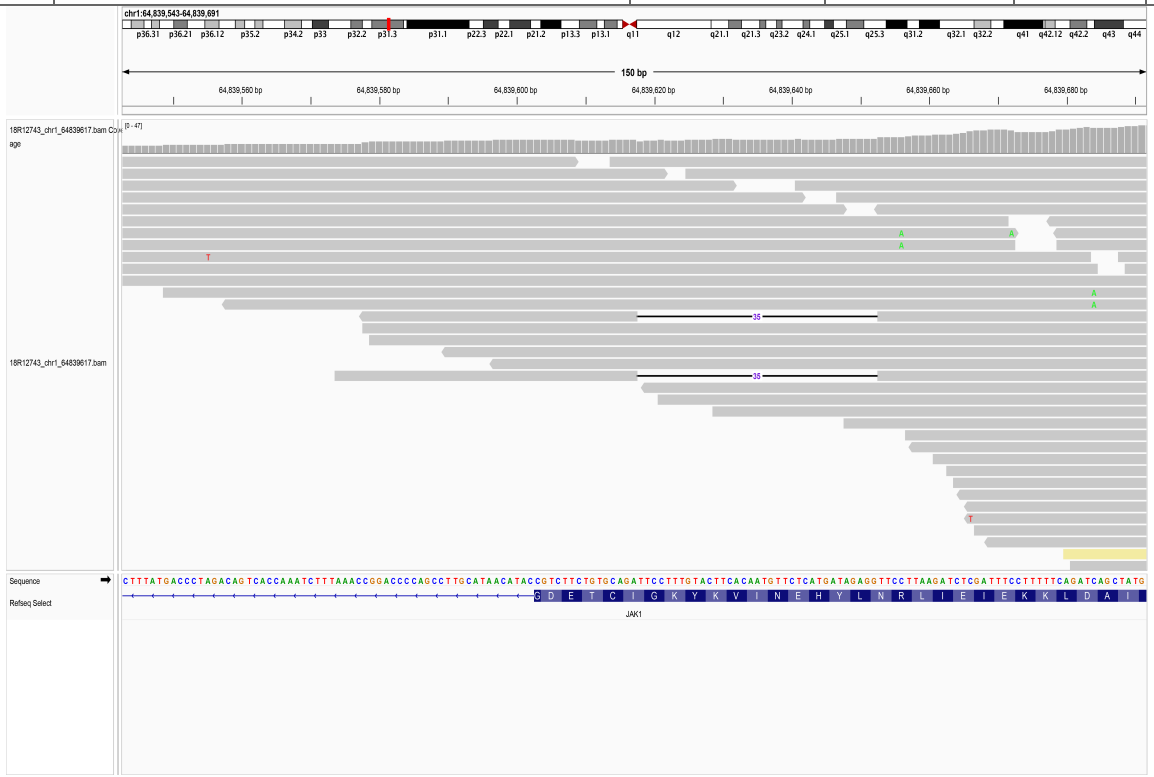
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134540	chr17_39791557_ACTG/-	59	2	*IKZF3*	frameshift_variant
CNS0136151	chr17_39791557_ACTG/-	46	2	*IKZF3*	frameshift_variant



25. *JAK1*

25.1. chr1_64839618_TTCCTTTGTACTTCACAATGTTCTCATGATAGAGG/-

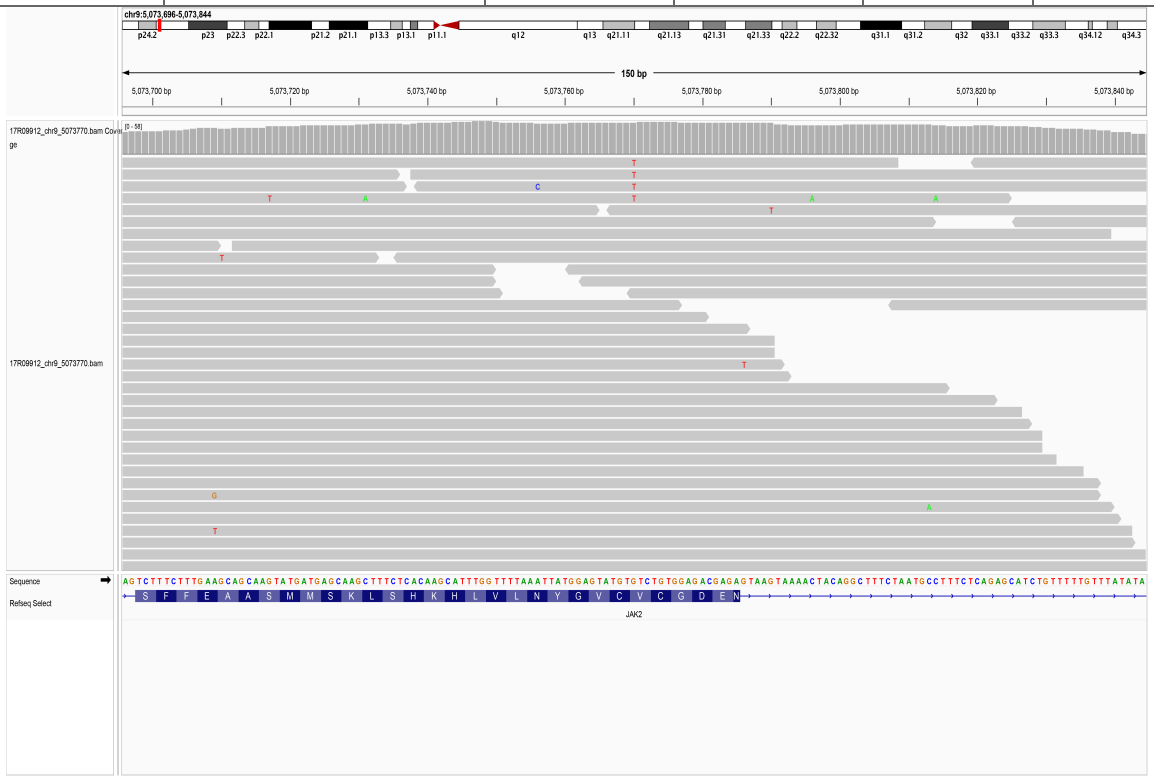
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12743	chr1_64839618_TTCCTTTGTACTTCACAATGTTCTCATGATAGAGG/-	23	2	*JAK1*	frameshift_variant

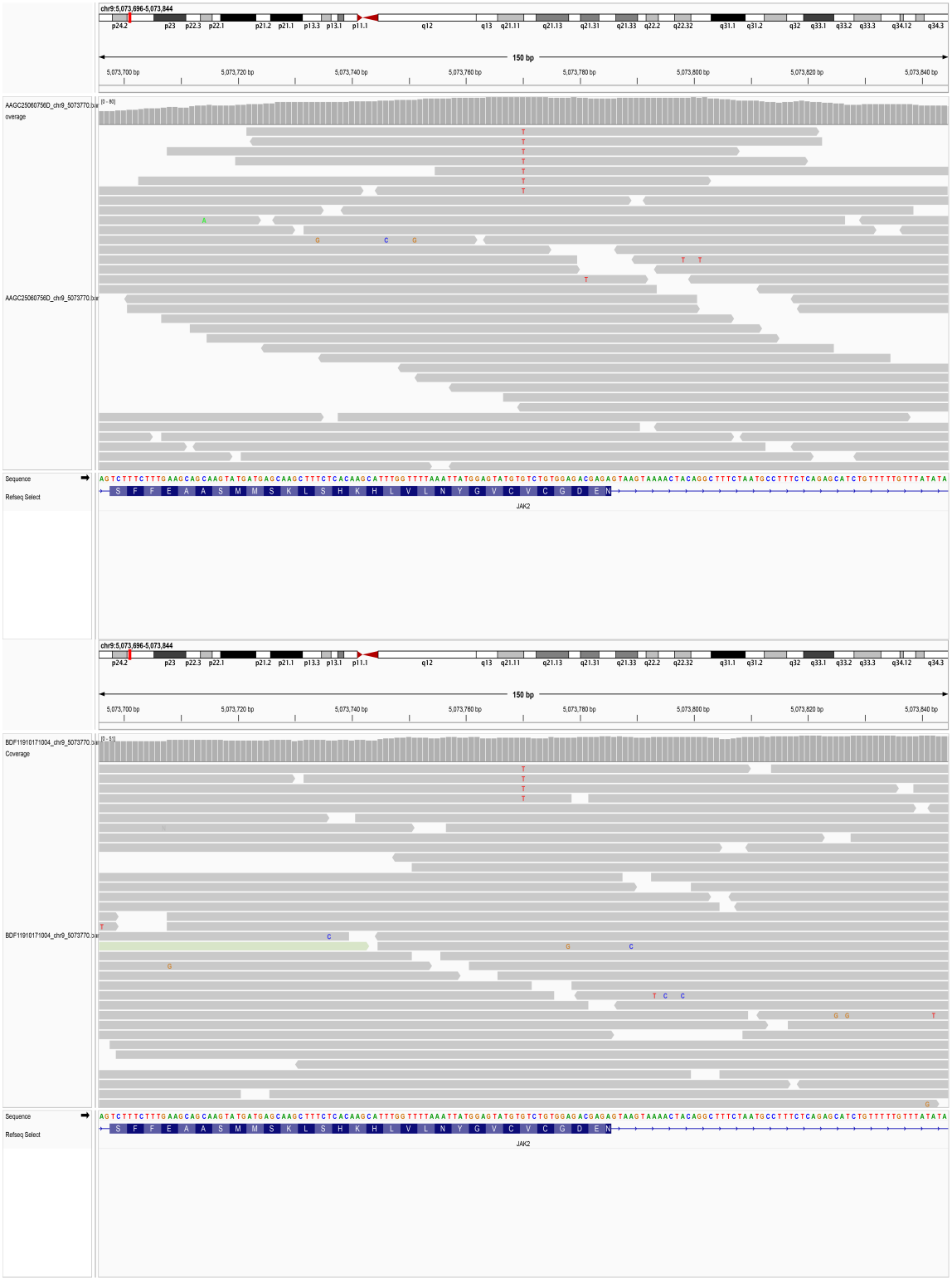


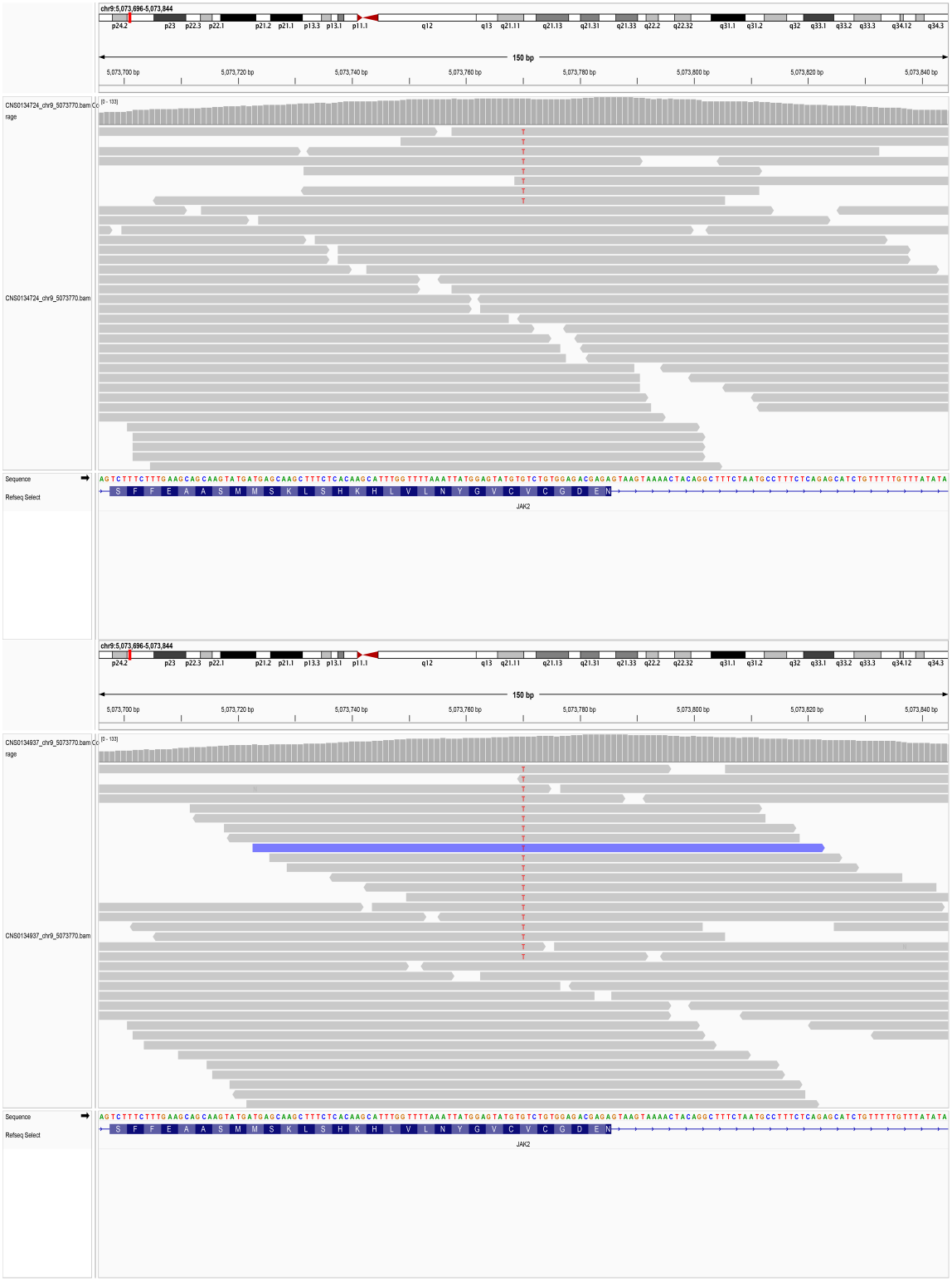
26. *JAK2*

26.1. chr9_5073770_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09912	chr9_5073770_G/T	50	4	*JAK2*	missense_variant
AAGC25060756D	chr9_5073770_G/T	71	7	*JAK2*	missense_variant
BDF11910171004	chr9_5073770_G/T	38	4	*JAK2*	missense_variant
CNS0134724	chr9_5073770_G/T	117	8	*JAK2*	missense_variant
CNS0134937	chr9_5073770_G/T	100	20	*JAK2*	missense_variant



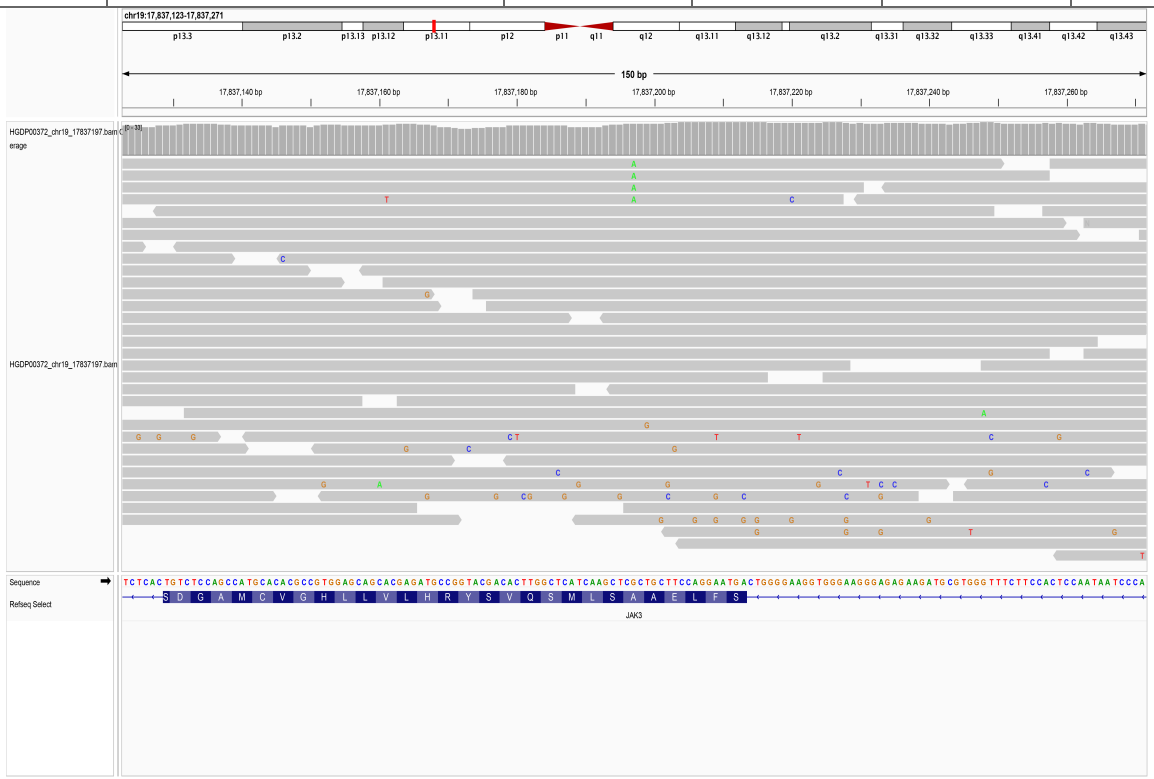

chr9:5,073,696-5,073,844
150 bp
5,073,700 bp
5,073,720 bp
5,073,740 bp
5,073,760 bp
5,073,780 bp
5,073,800 bp
5,073,820 bp
5,073,840 bp
AAGC25060756D_chr9_5073770.bai
overage
AAGC25060756D_chr9_5073770.bai
Sequence
Refseq Select
JAK2
BDF11910171004_chr9_5073770.bai
Coverage
BDF11910171004_chr9_5073770.bai
Sequence
Refseq Select
JAK2


chr9:5,073,696-5,073,844
150 bp
5,073,700 bp
5,073,720 bp
5,073,740 bp
5,073,760 bp
5,073,780 bp
5,073,800 bp
5,073,820 bp
5,073,840 bp
CNS0134724_chr9_5073770.bam Coverage
CNS0134724_chr9_5073770.bam
Sequence
Refseq Select
JAK2
CNS0134937_chr9_5073770.bam Coverage
CNS0134937_chr9_5073770.bam
Sequence
Refseq Select
JAK2

27. *JAK3*

27.1. chr19_17837197_G/A

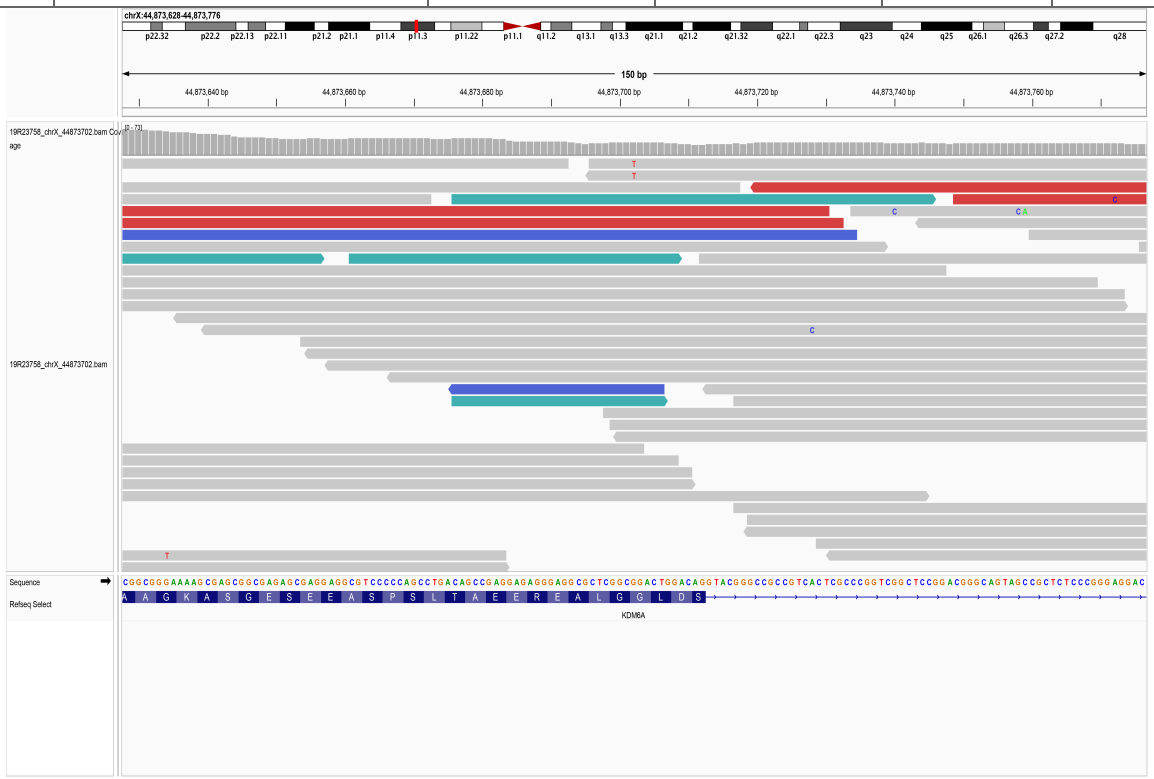
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HGDP00372	chr19_17837197_G/A	23	4	*JAK3*	missense_variant



28. *KDM6A*

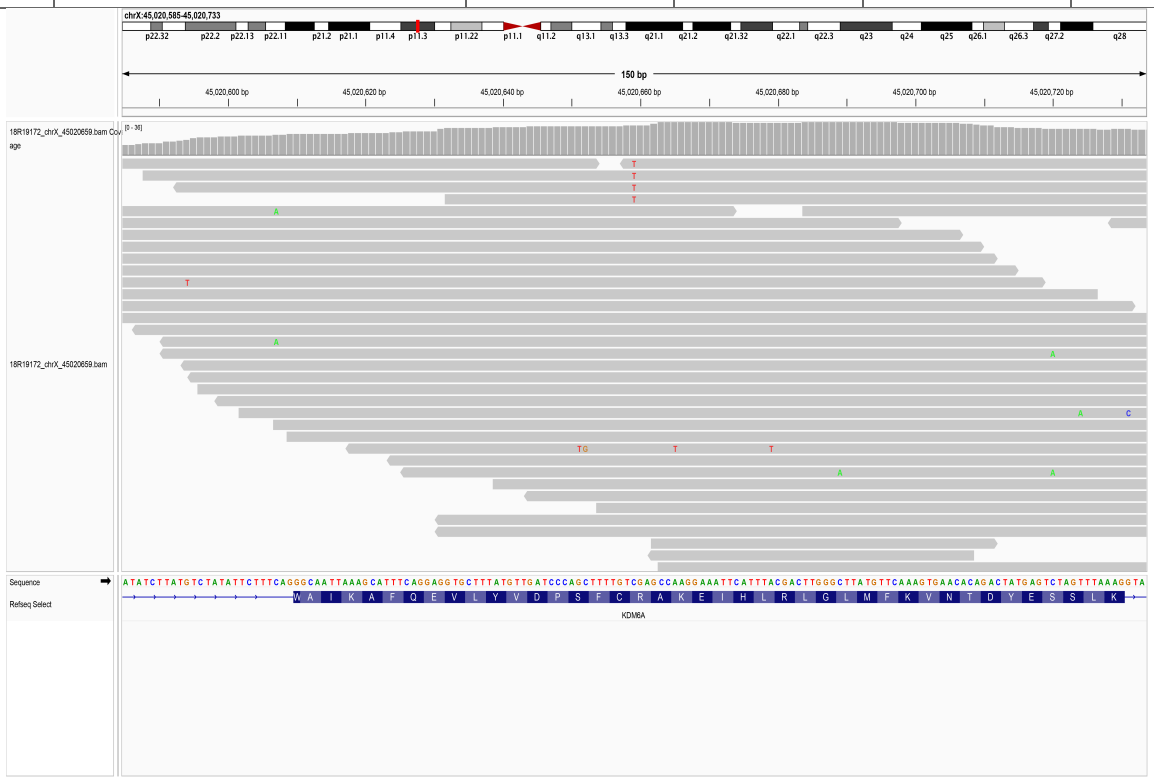
28.1. chrX_44873702_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23758	chrX_44873702_G/T	22	3	*KDM6A*	stop_gained



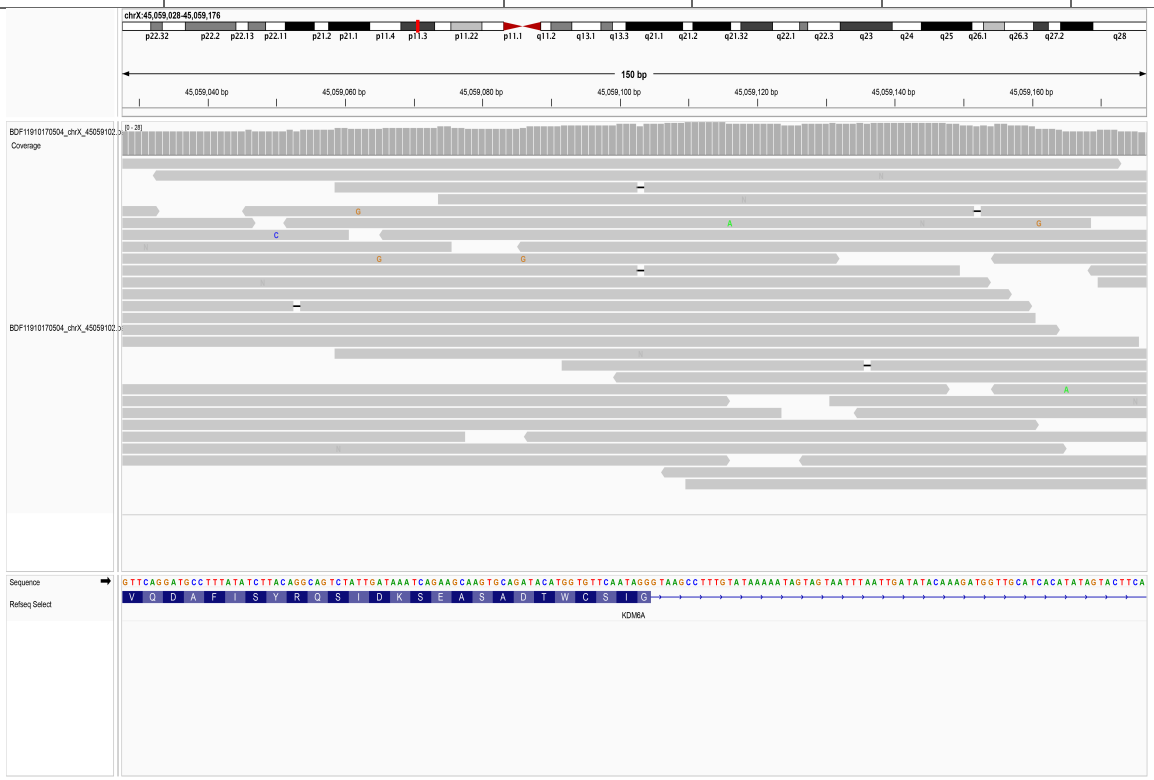
28.2. chrX_45020659_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19172	chrX_45020659_C/T	27	4	*KDM6A*	stop_gained



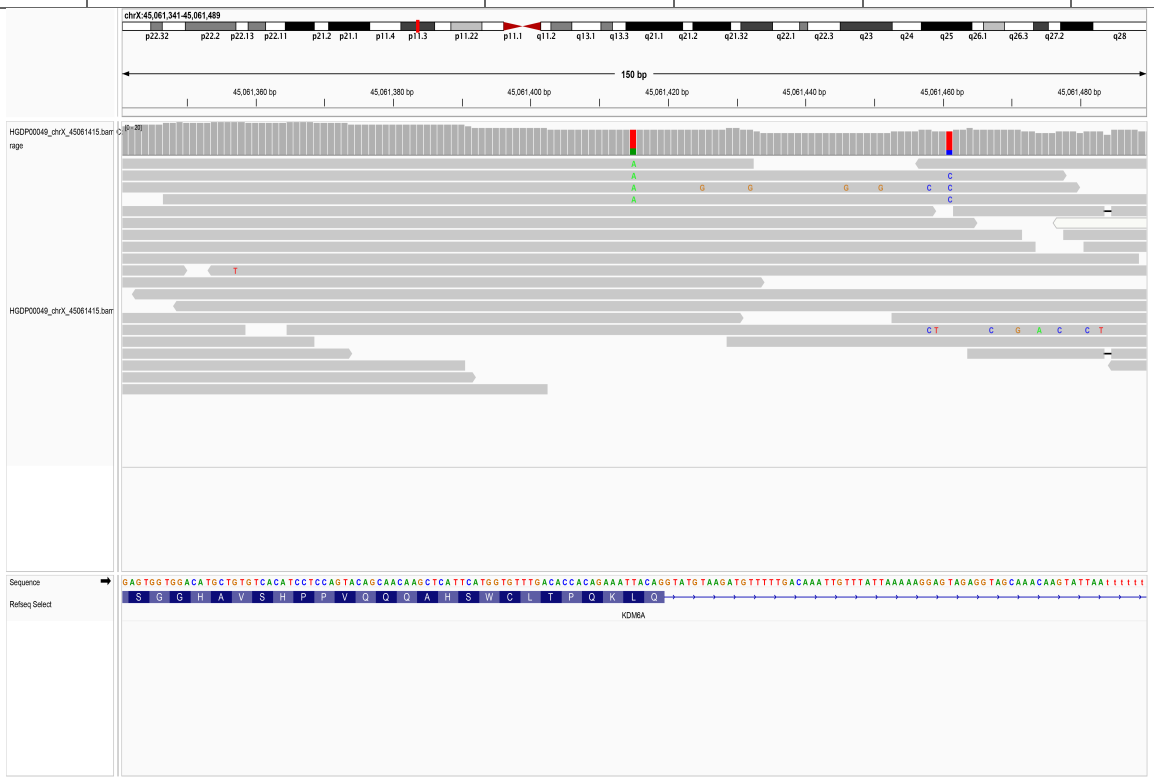
28.3. chrX_45059103_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chrX_45059103_G/-	22	2	*KDM6A*	frameshift_variant



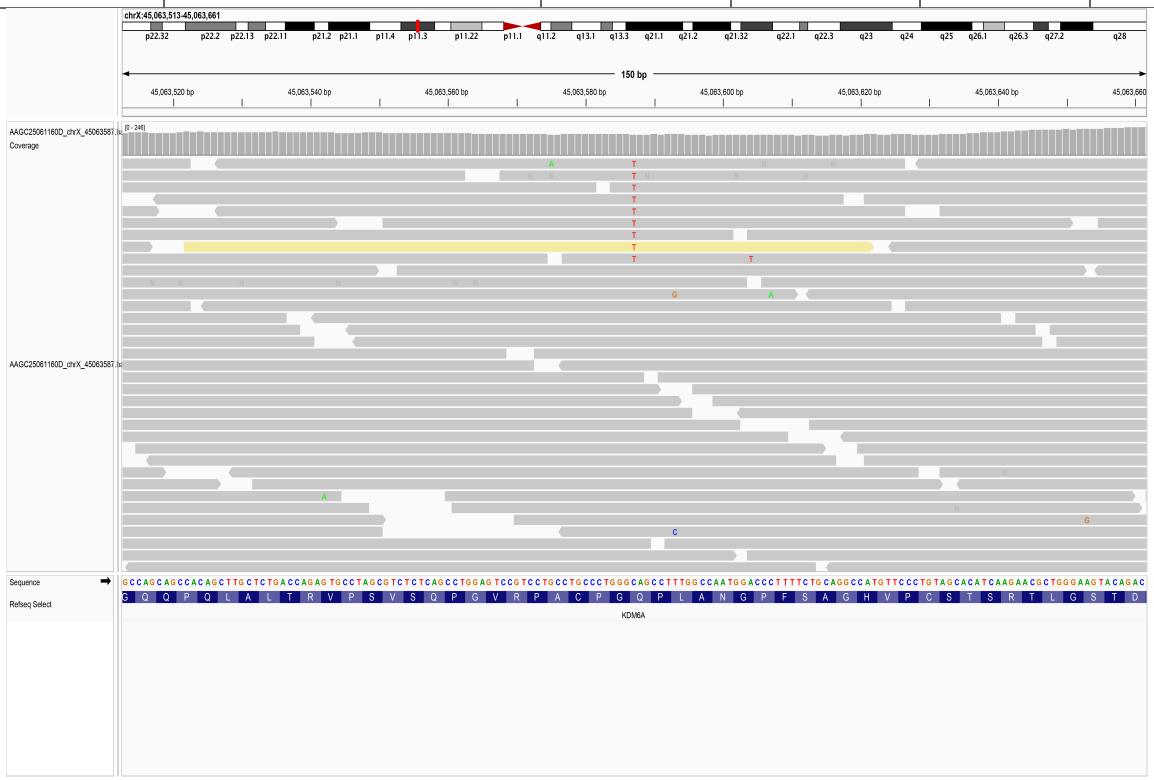
28.4. chrX_45061415_T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HGDP00049	chrX_45061415_T/A	11	3	*KDM6A*	stop_gained



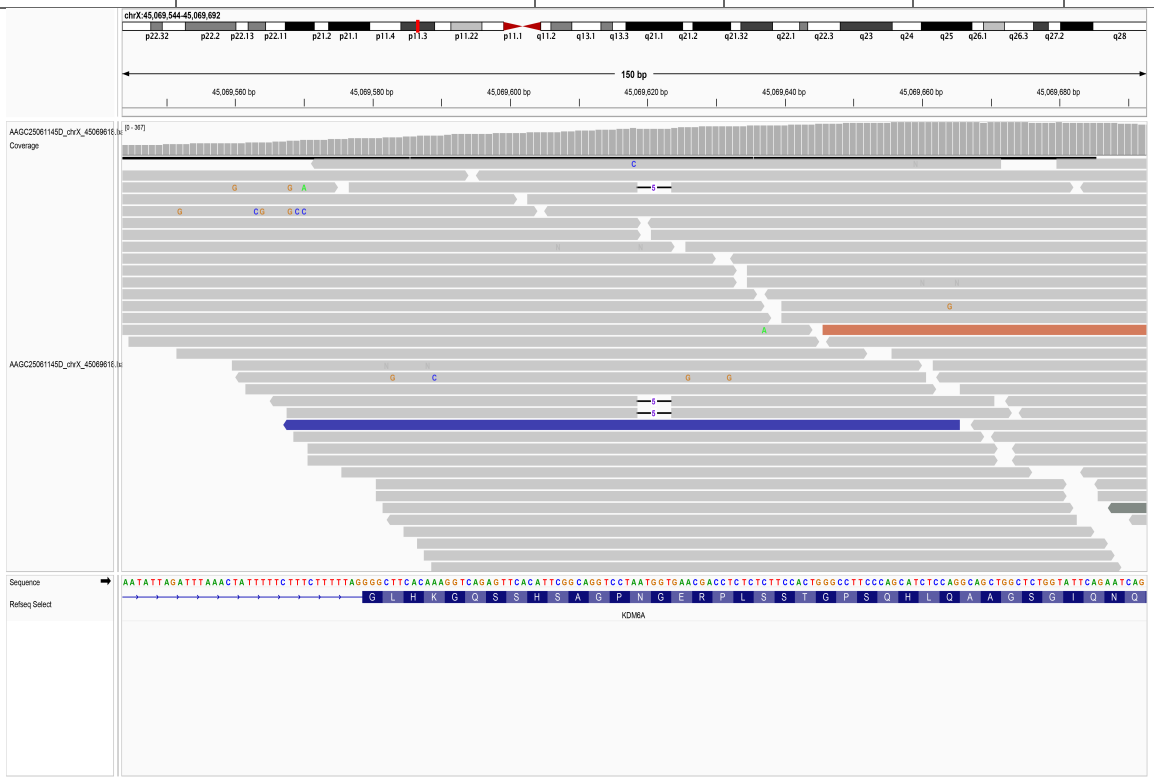
28.5. chrX_45063587_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061160D	chrX_45063587_C/T	139	9	*KDM6A*	stop_gained



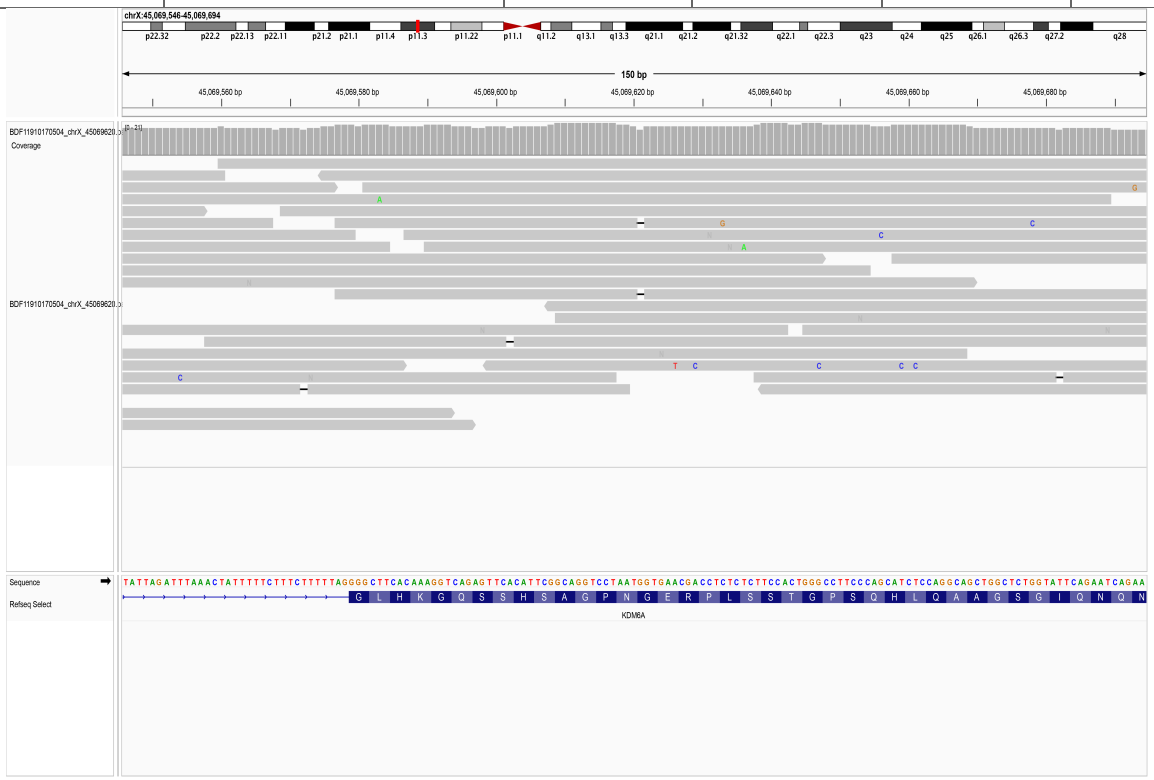
28.6. chrX_45069619_ATGGT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061145D	chrX_45069619_ATGGT/-	298	4	*KDM6A*	frameshift_variant



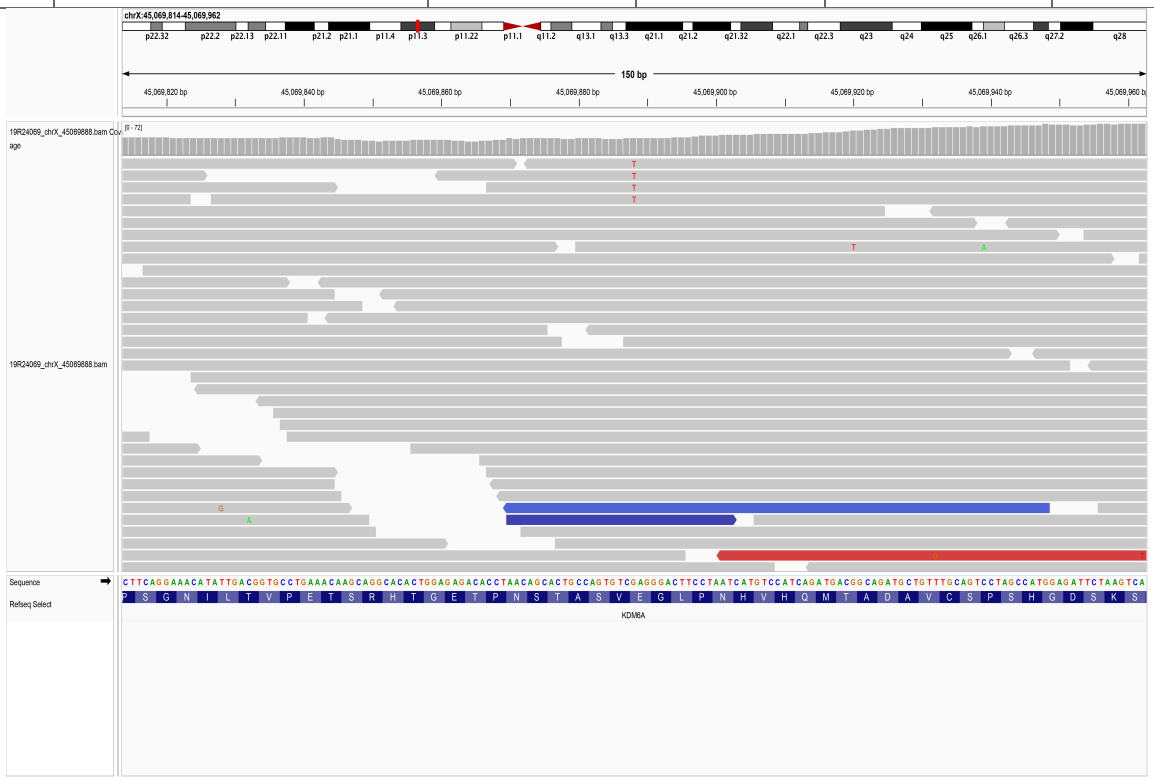
28.7. chrX_45069621_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chrX_45069621_G/-	15	2	*KDM6A*	frameshift_variant



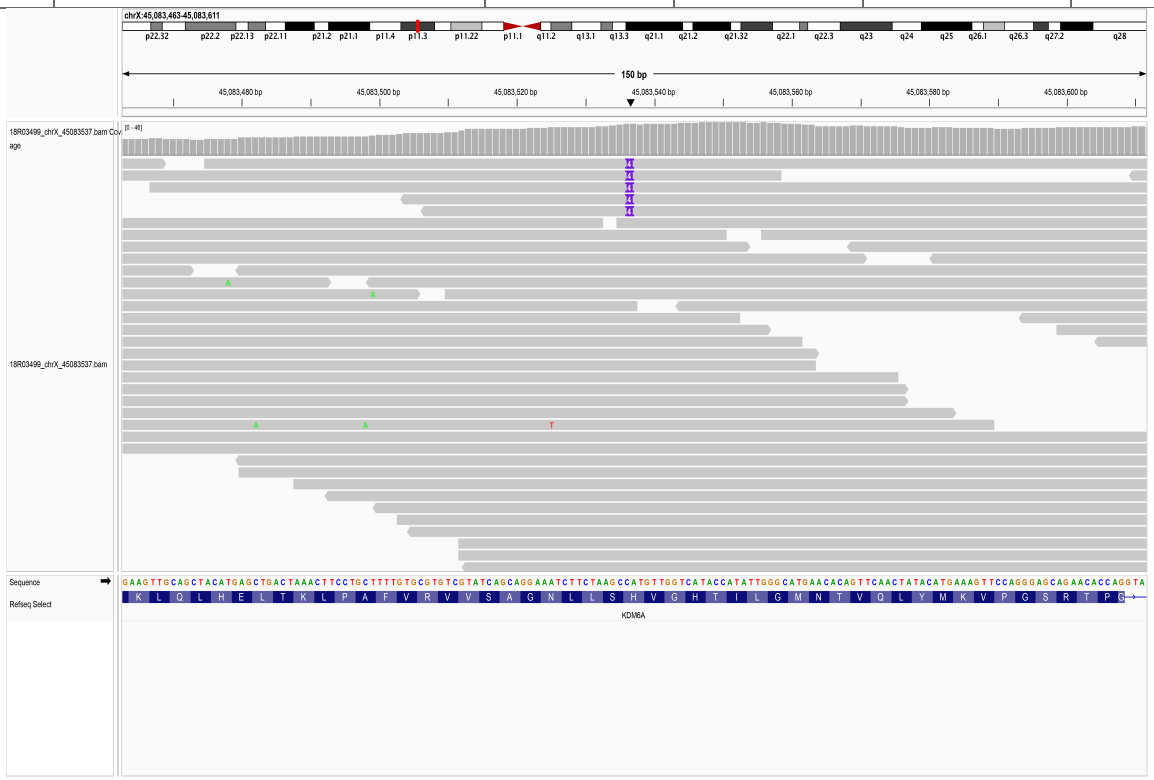
28.8. chrX_45069888_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R24069	chrX_45069888_G/T	31	4	*KDM6A*	stop_gained



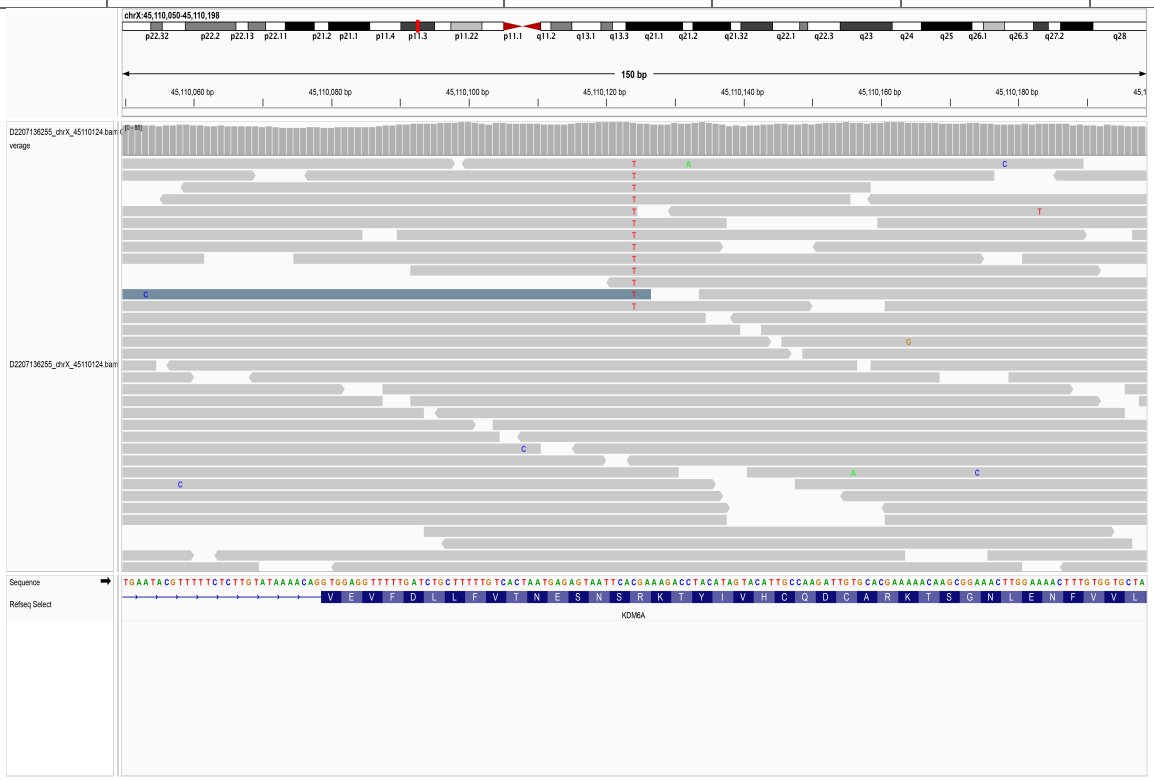
28.9. chrX_45083537_-/ACAT

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03499	chrX_45083537_-/ACAT	37	6	*KDM6A*	frameshift_variant



28.10. chrX_45110124_C/T

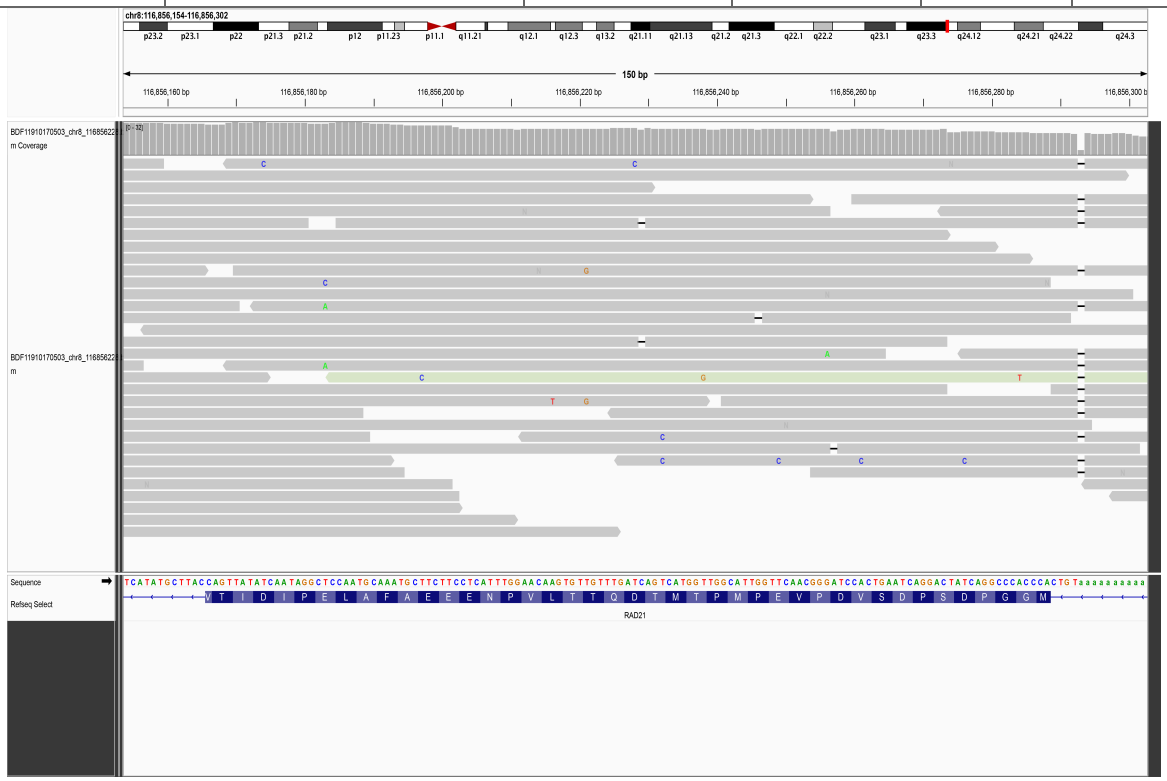
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2207136255	chrX_45110124_C/T	67	13	*KDM6A*	stop_gained



29. *KMT2A*

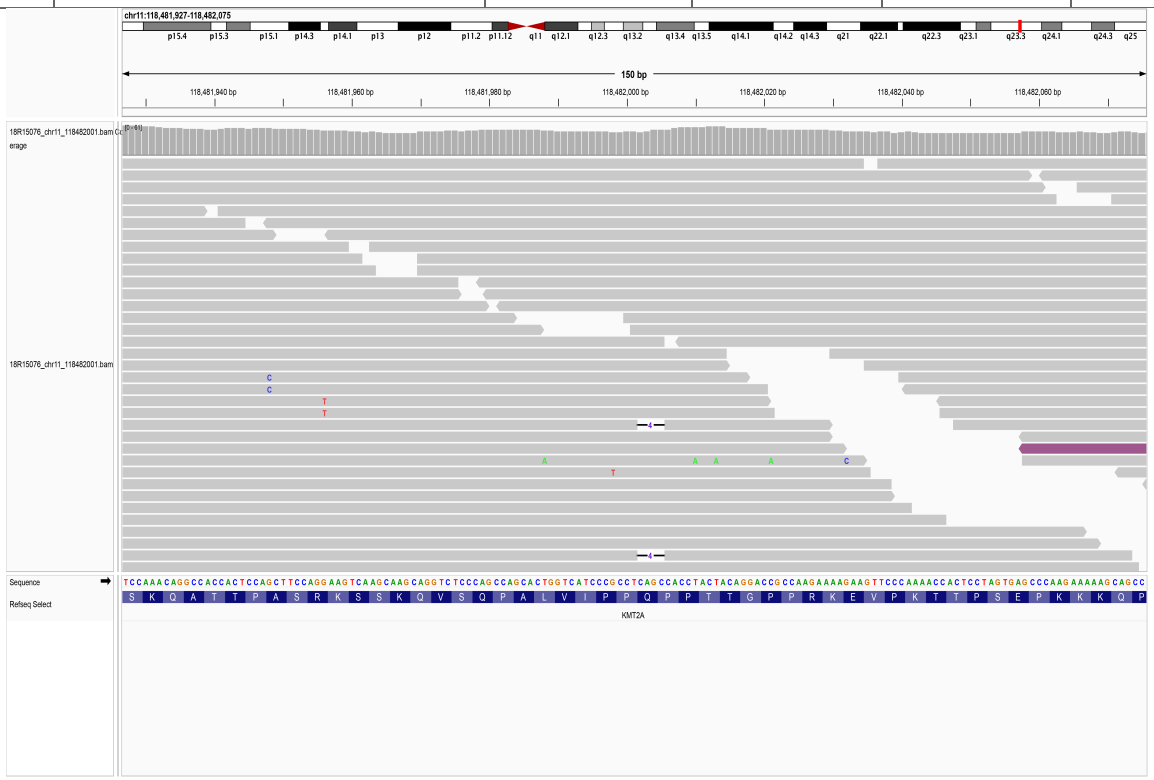
29.1. chr11_118473674_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chr11_118473674_T/-	19	2	*KMT2A*	frameshift_variant



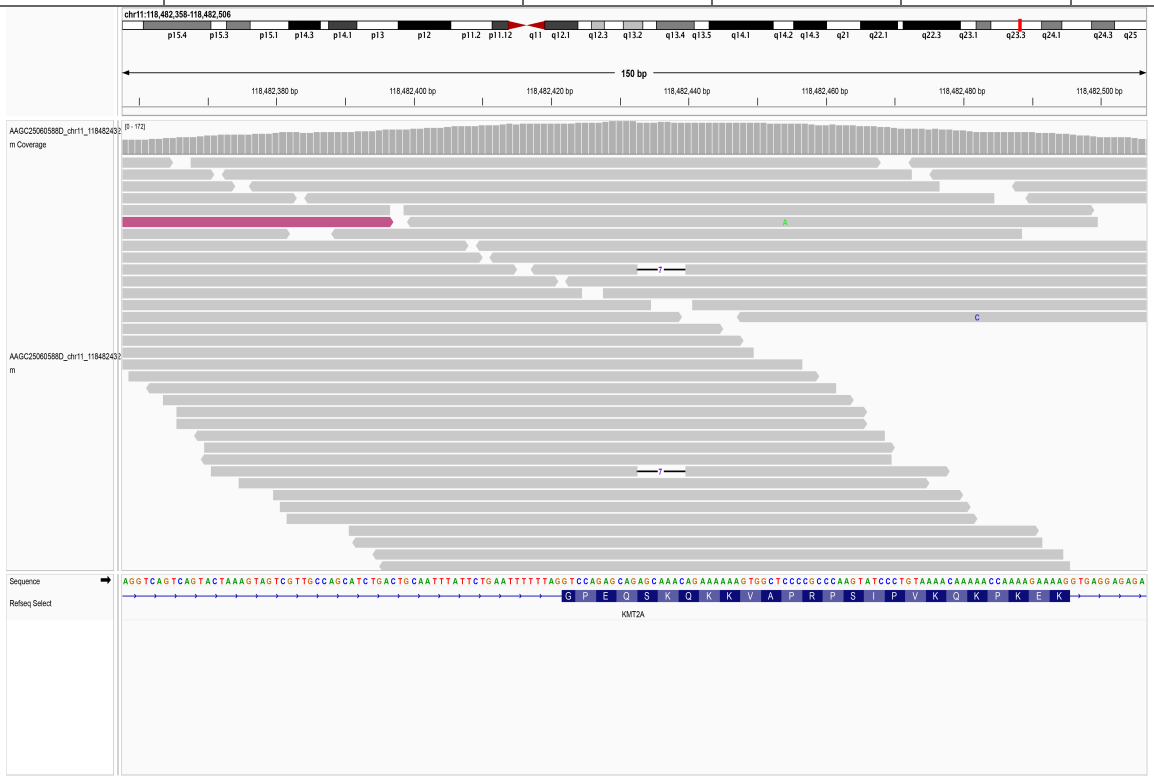
29.2. chr11_118482002_CAGC/-

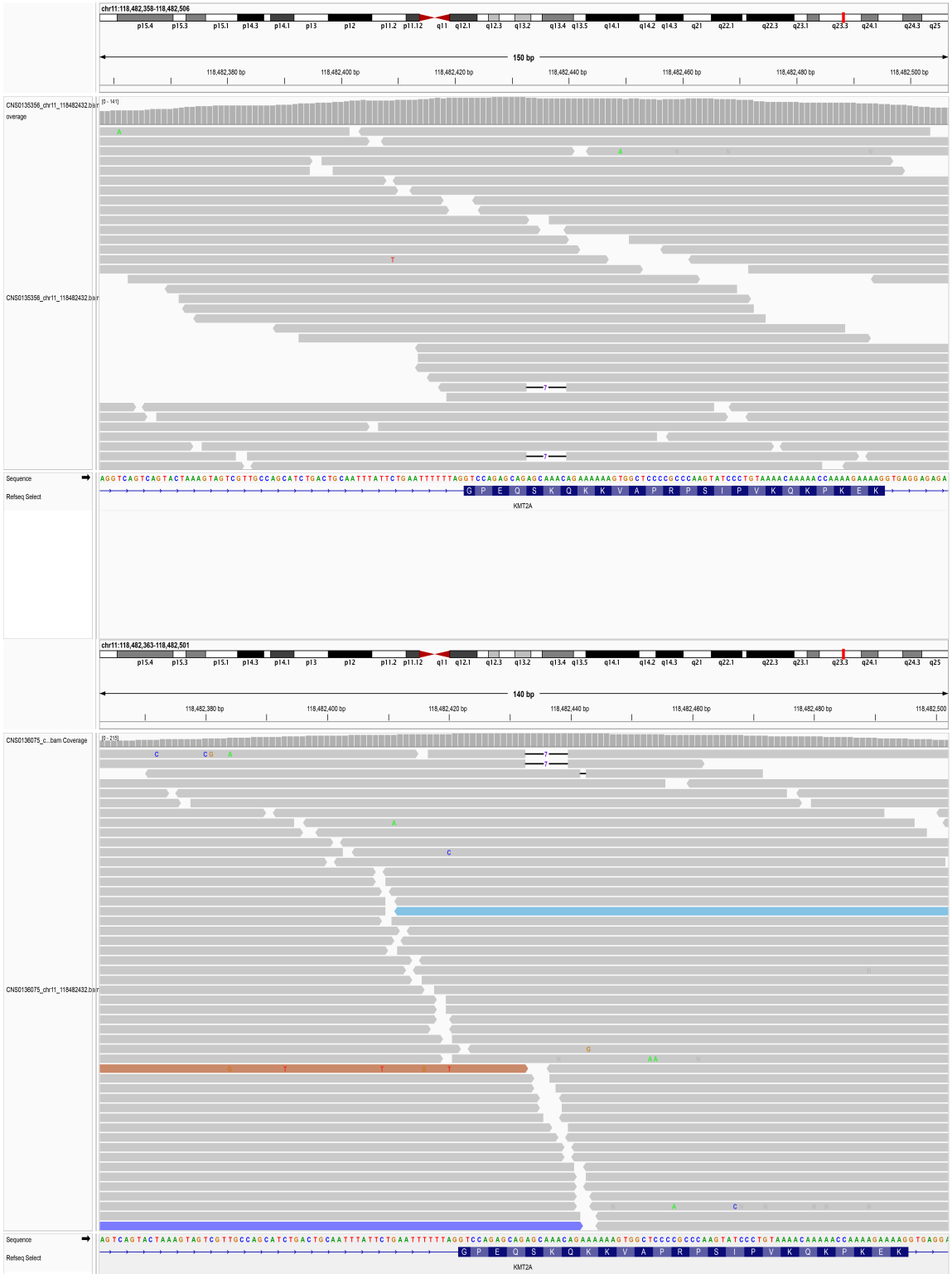
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15076	chr11_118482002_CAGC/-	44	2	*KMT2A*	frameshift_variant



29.3. chr11_118482433_AGCAAAC/-

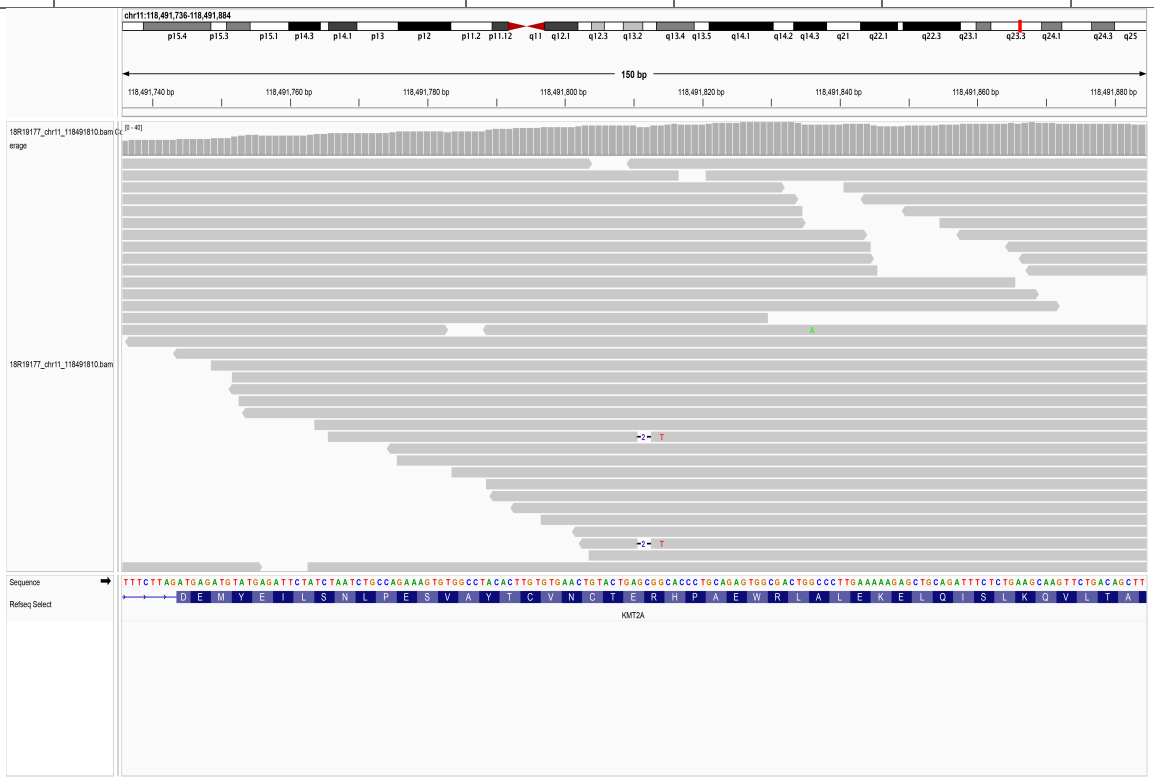
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060588D	chr11_118482433_AGCAAAC/-	166	4	*KMT2A*	frameshift_variant
CNS0135356	chr11_118482433_AGCAAAC/-	136	4	*KMT2A*	frameshift_variant
CNS0136075	chr11_118482433_AGCAAAC/-	206	4	*KMT2A*	frameshift_variant




chr11:118,482,358-118,482,506
150 bp
118,482,380 bp
118,482,400 bp
118,482,420 bp
118,482,440 bp
118,482,460 bp
118,482,480 bp
118,482,500 bp
CNS0135356_chr11_118482432.bam
overage
CNS0135356_chr11_118482432.bam
Sequence
Refseq Select
KMT2A
chr11:118,482,363-118,482,501
140 bp
118,482,380 bp
118,482,400 bp
118,482,420 bp
118,482,440 bp
118,482,460 bp
118,482,480 bp
118,482,500
CNS0136075_c...bam Coverage
CNS0136075_chr11_118482432.bam
Sequence
Refseq Select
KMT2A

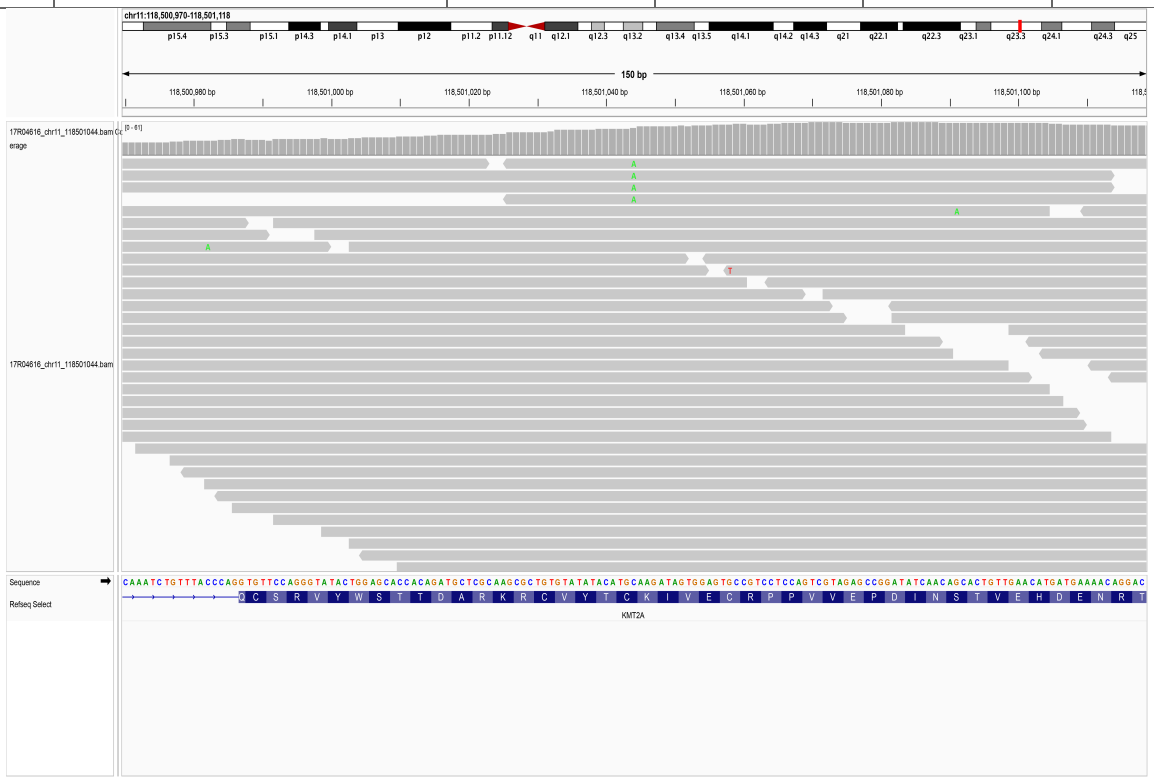
29.4. chr11_118491811_GC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19177	chr11_118491811_GC/-	33	2	*KMT2A*	frameshift_variant



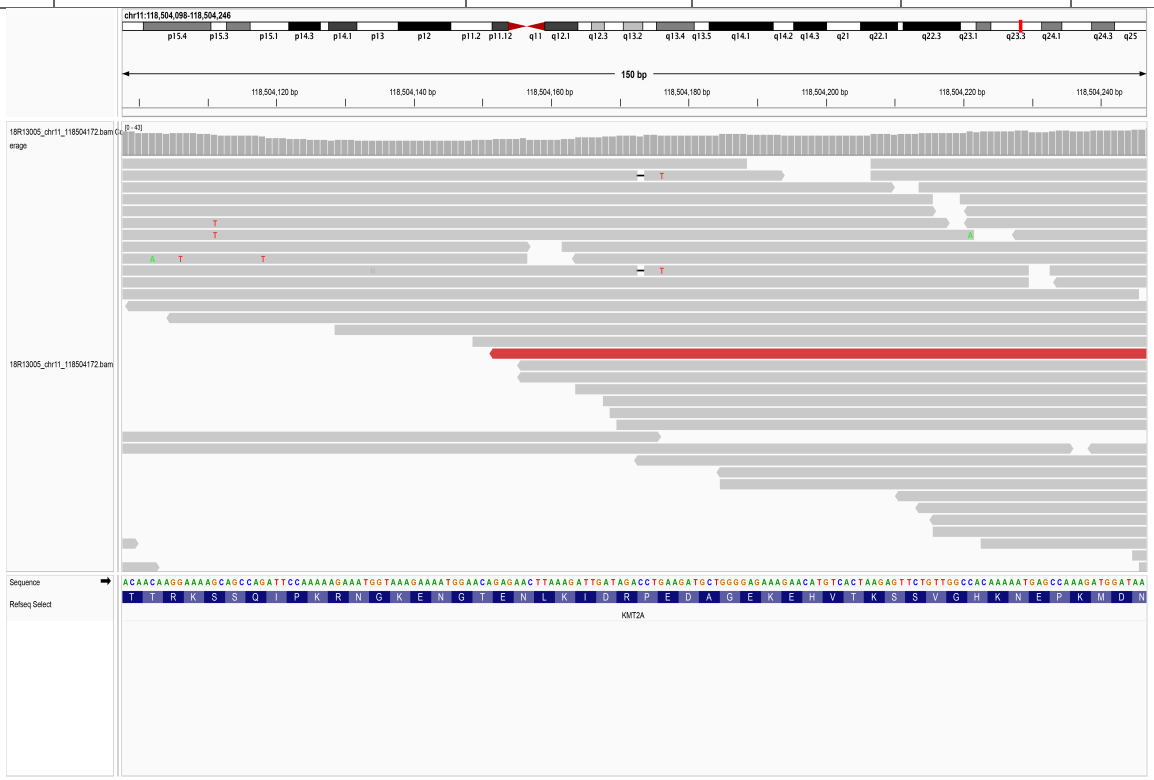
29.5. chr11_118501044_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R04616	chr11_118501044_C/A	46	4	*KMT2A*	stop_gained



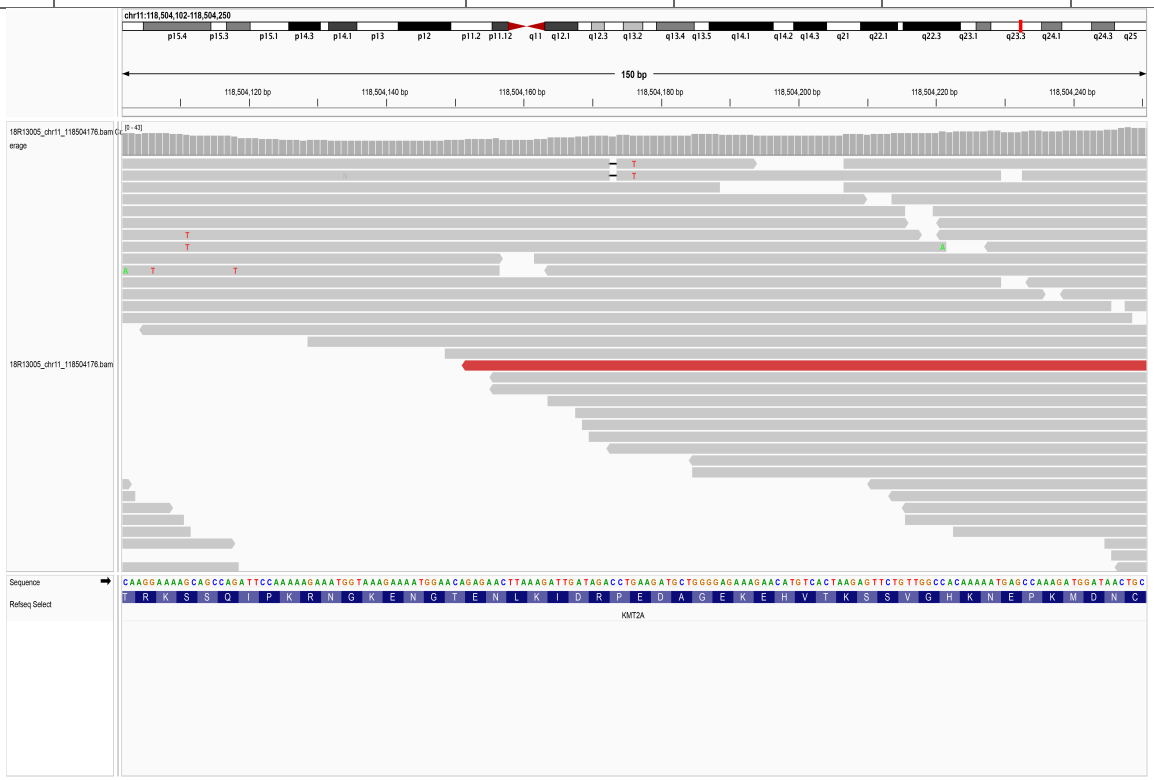
29.6. chr11_118504173_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13005	chr11_118504173_C/-	24	2	*KMT2A*	frameshift_variant



29.7. chr11_118504176_G/T

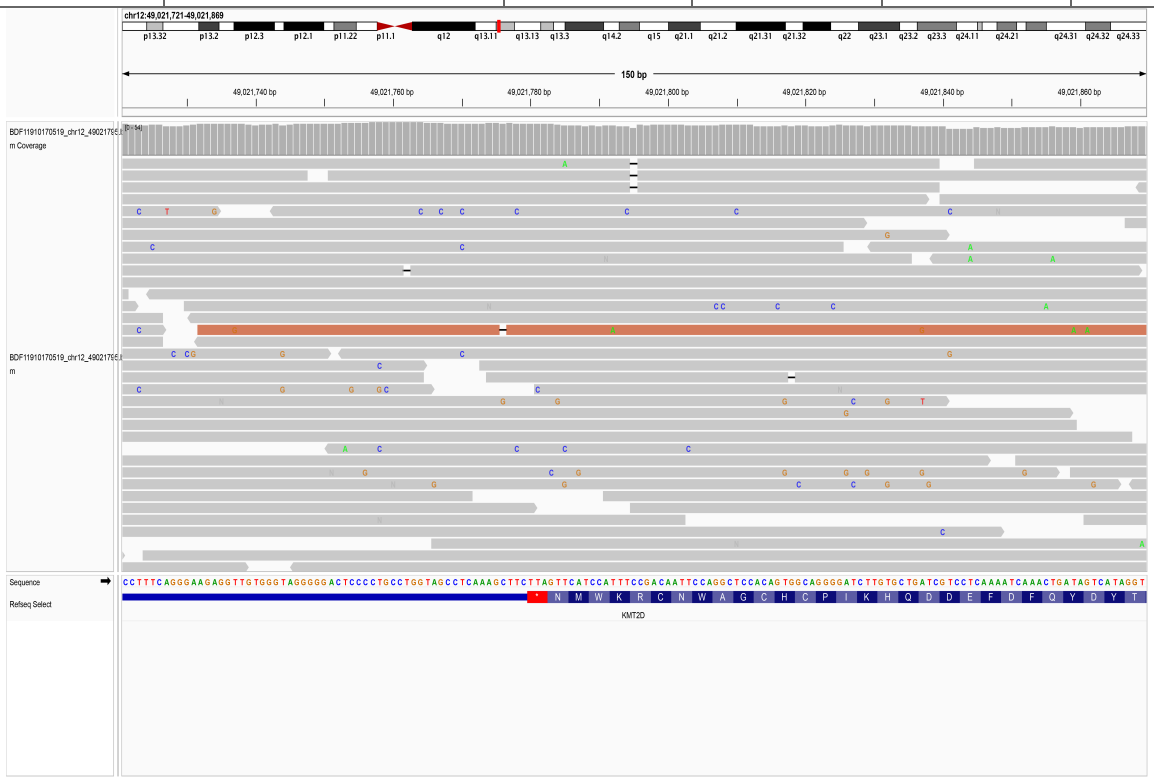
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13005	chr11_118504176_G/T	24	2	*KMT2A*	stop_gained



30. *KMT2D*

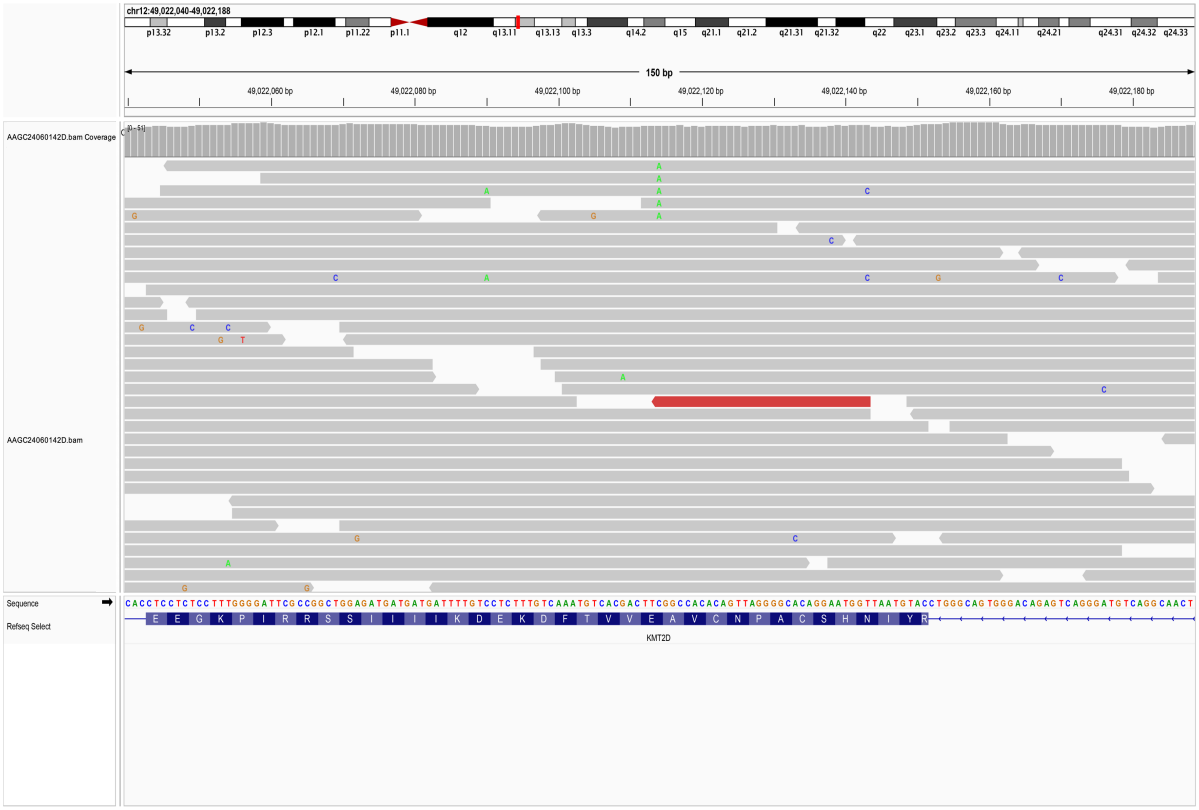
30.1. chr12_49021795_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chr12_49021795_C/-	35	4	*KMT2D*	frameshift_variant



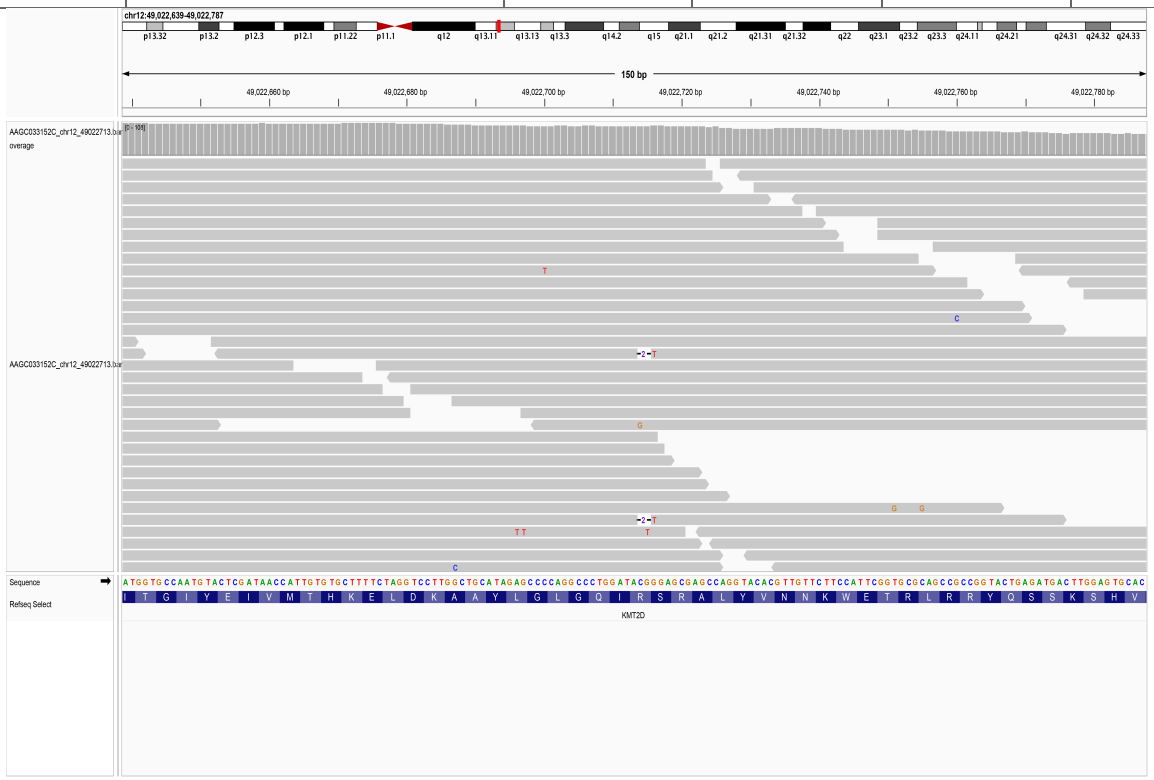
30.2. chr12_49022114_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC24060142D	chr12_49022114_C/A	35	4	*KMT2D*	stop_gained



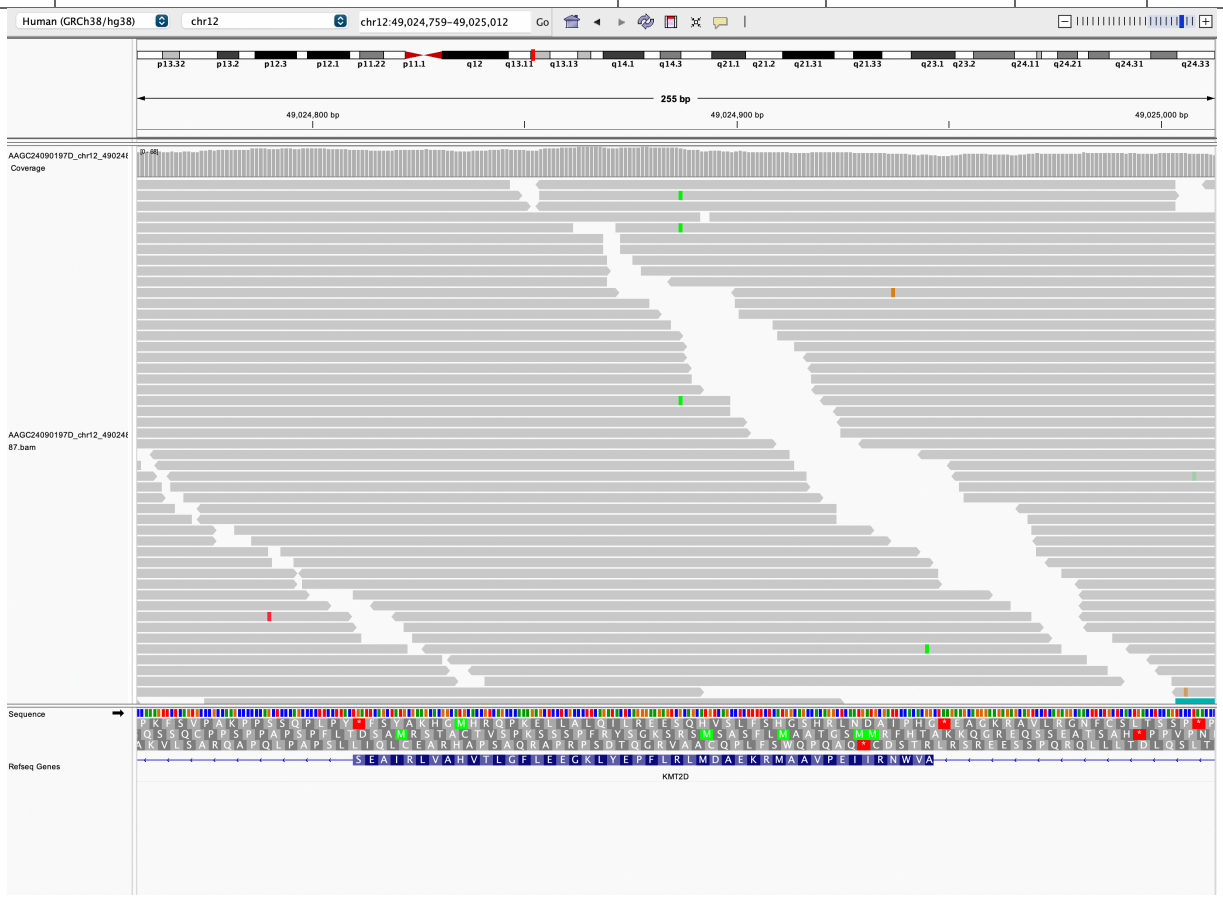
30.3. chr12_49022714_CG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033152C	chr12_49022714_CG/-	93	2	*KMT2D*	frameshift_variant



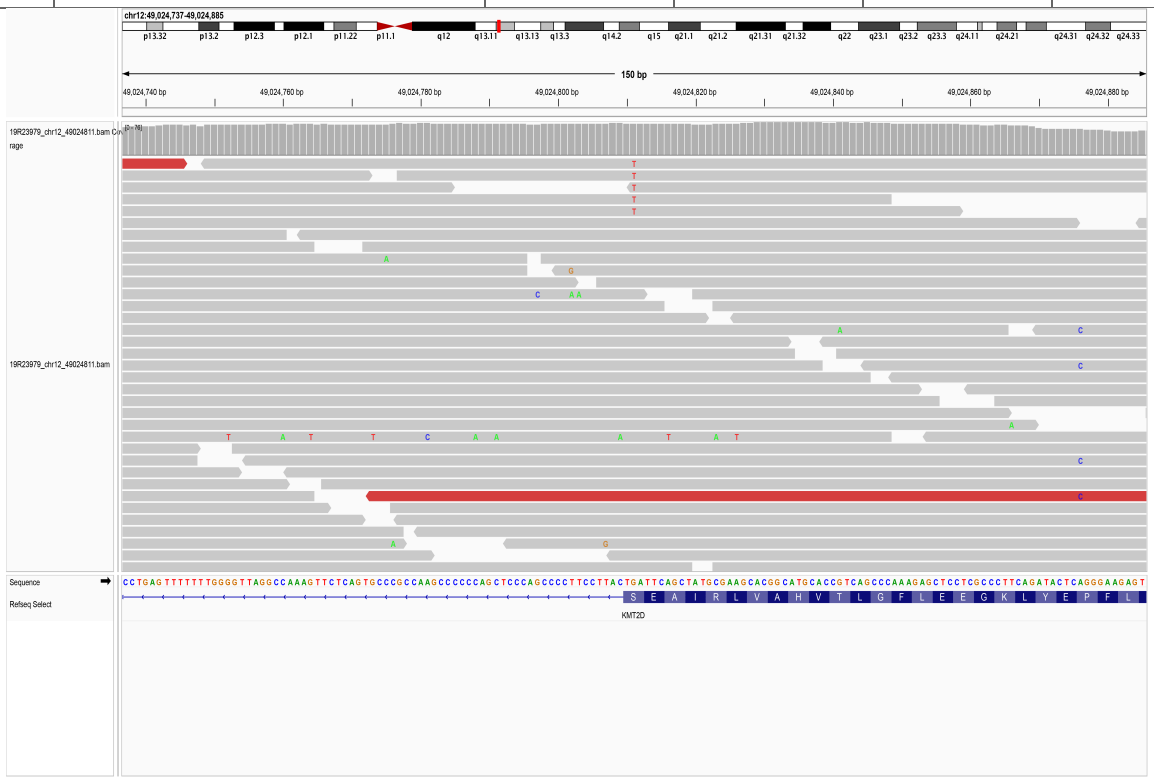
30.4. chr12_49027229_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC24090197D	chr12_49024887_G/A	59	4	*KMT2D*	stop_gained



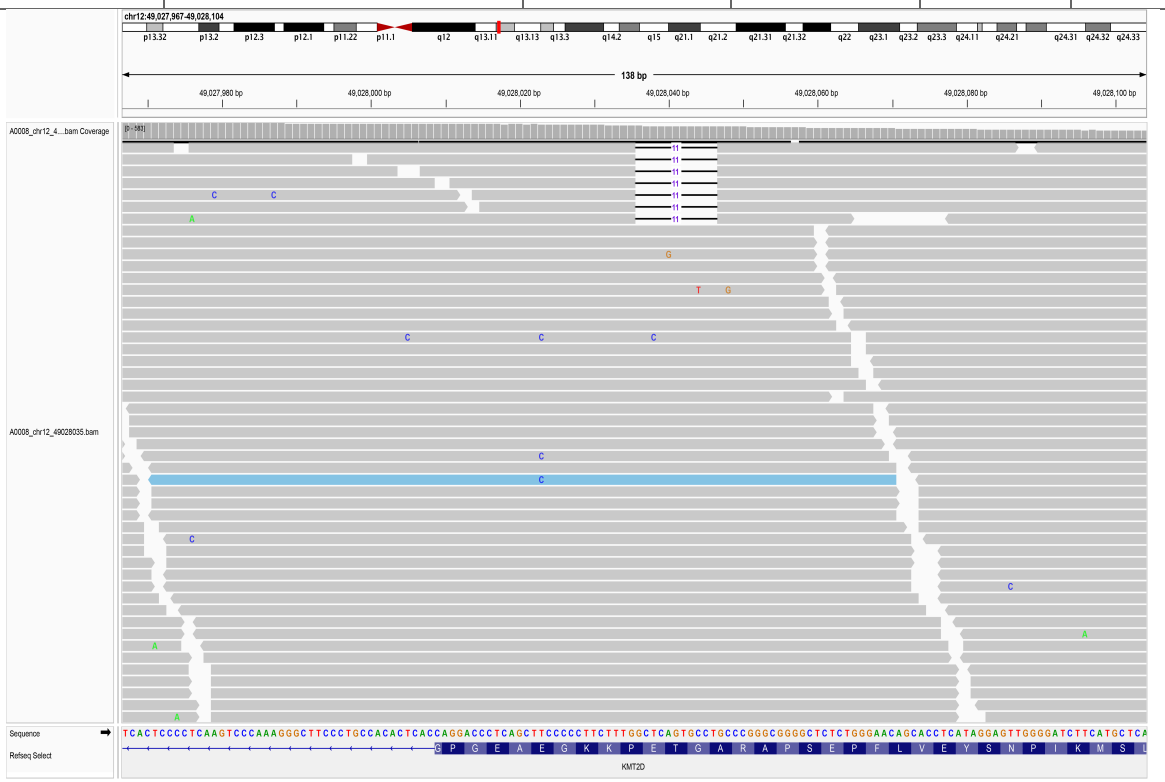
30.5. chr12_49024811_G/T

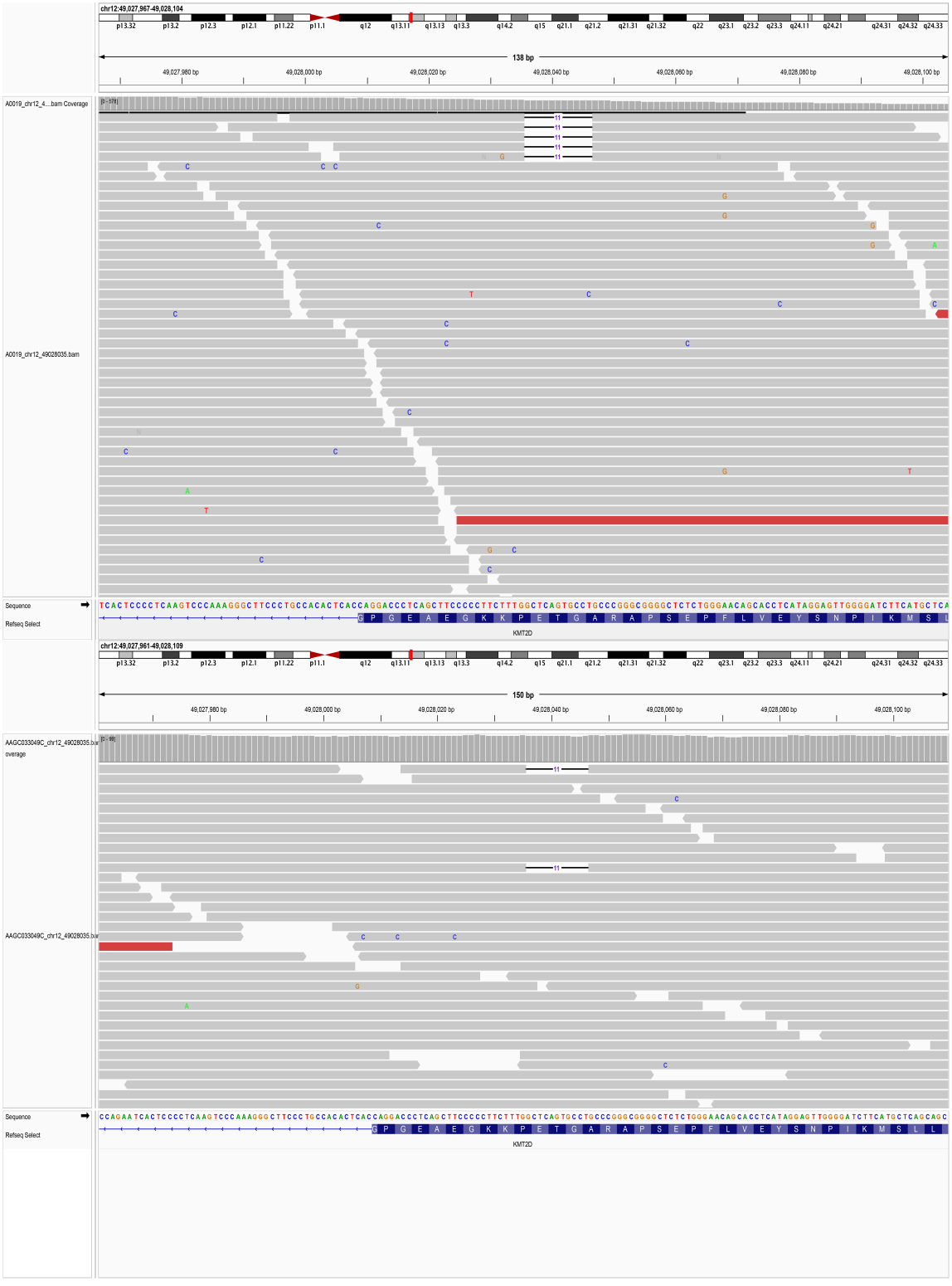
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23979	chr12_49024811_G/T	60	5	*KMT2D*	stop_gained

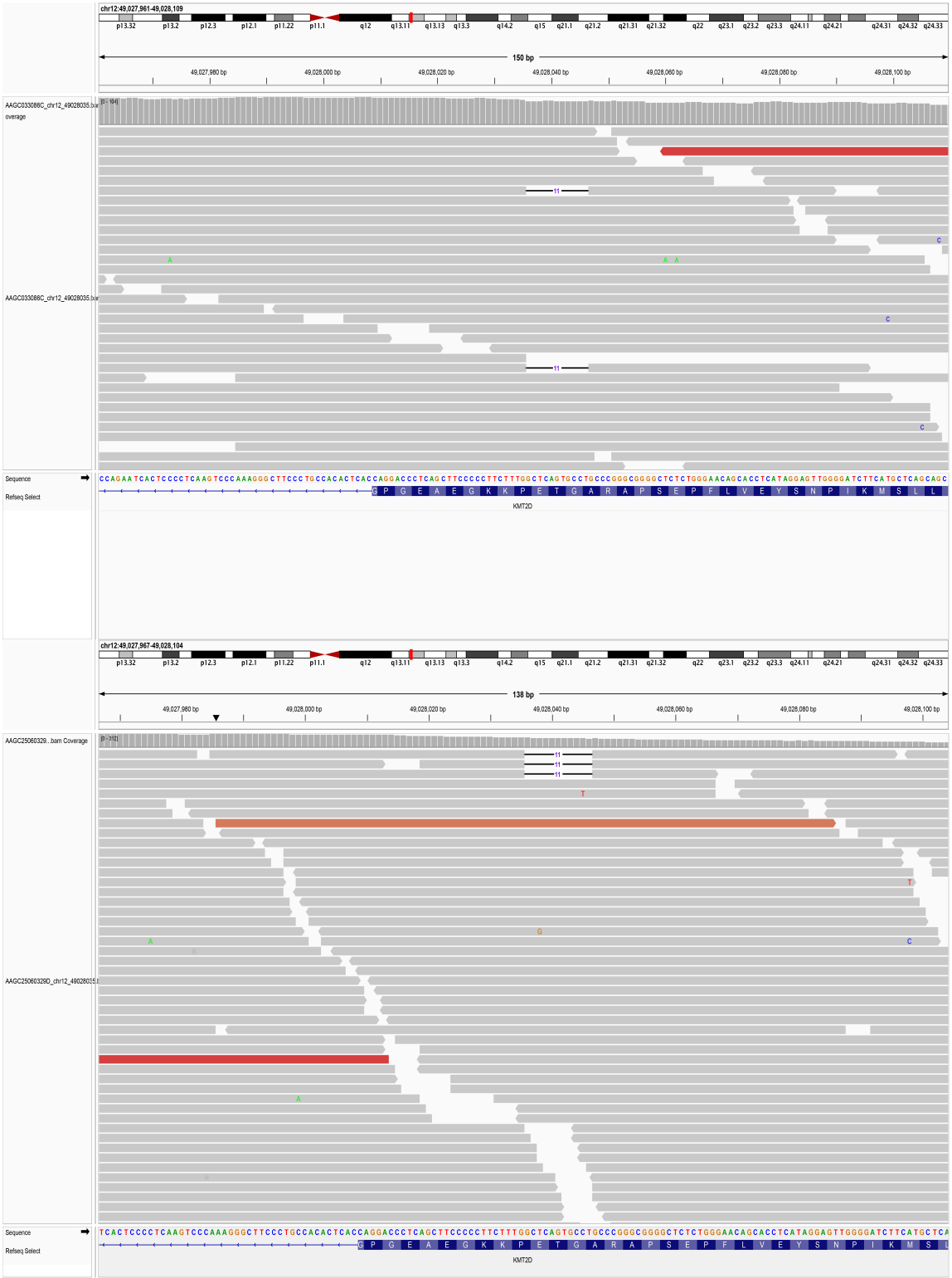


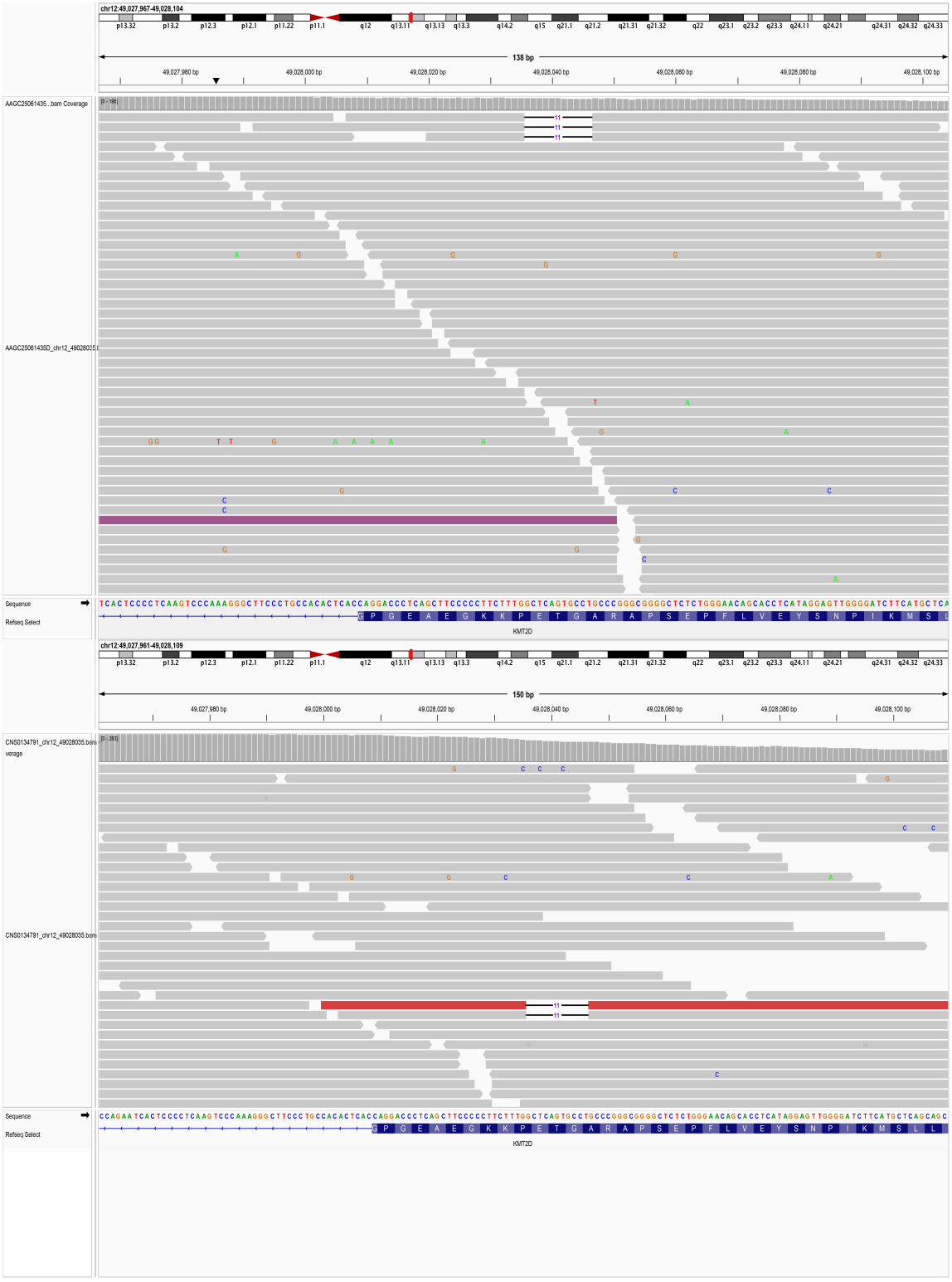
30.6. chr12_49028036_GCTCAGTGCCT/-

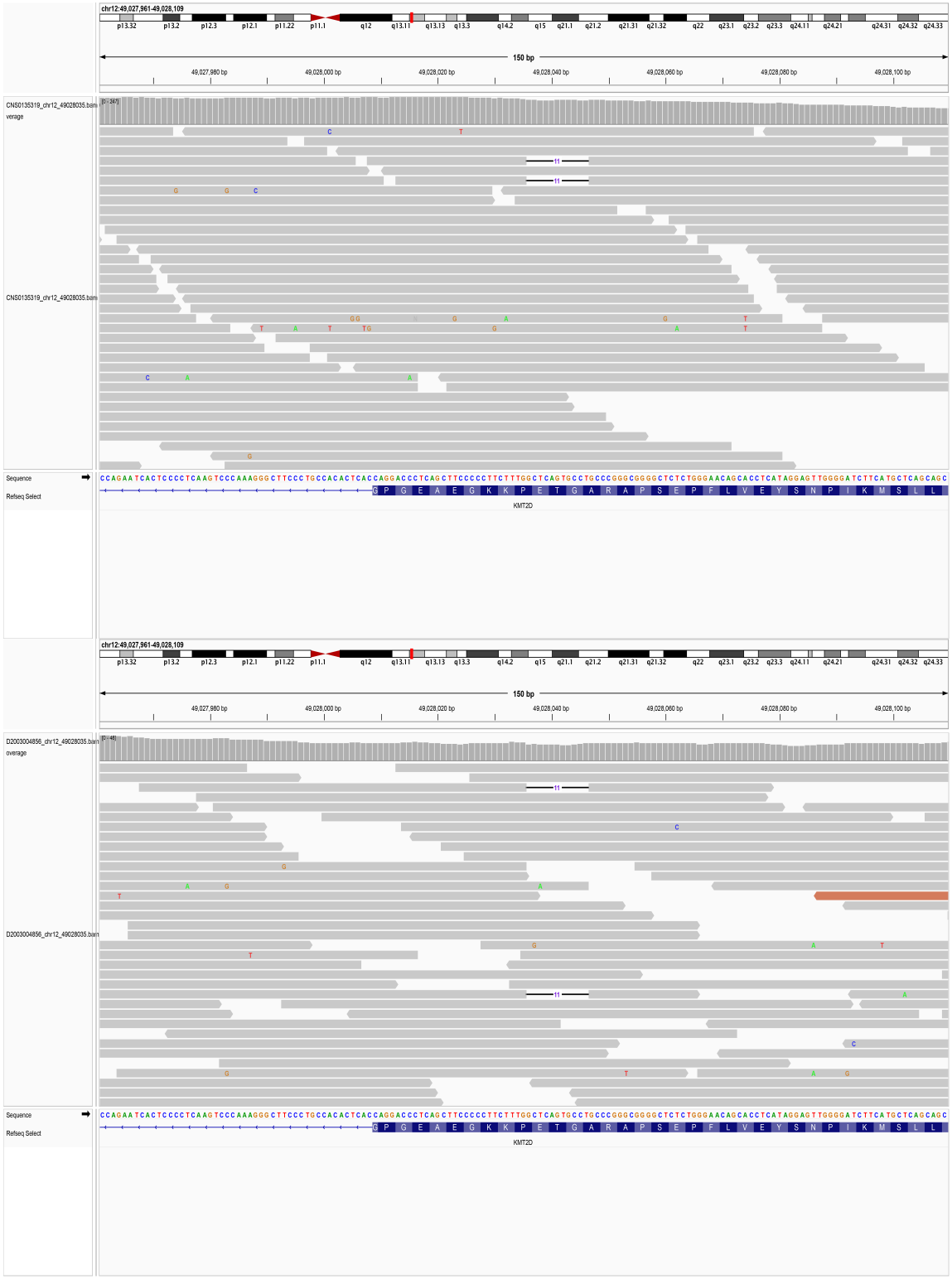
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0008	chr12_49028036_GCTCAGTGCCT/-	471	8	*KMT2D*	frameshift_variant
A0019	chr12_49028036_GCTCAGTGCCT/-	418	6	*KMT2D*	frameshift_variant
AAGC033049C	chr12_49028036_GCTCAGTGCCT/-	91	3	*KMT2D*	frameshift_variant
AAGC033086C	chr12_49028036_GCTCAGTGCCT/-	88	3	*KMT2D*	frameshift_variant
AAGC25060329D	chr12_49028036_GCTCAGTGCCT/-	223	5	*KMT2D*	frameshift_variant
AAGC25061435D	chr12_49028036_GCTCAGTGCCT/-	171	4	*KMT2D*	frameshift_variant
CNS0134791	chr12_49028036_GCTCAGTGCCT/-	220	6	*KMT2D*	frameshift_variant
CNS0135319	chr12_49028036_GCTCAGTGCCT/-	220	4	*KMT2D*	frameshift_variant
D2003004856	chr12_49028036_GCTCAGTGCCT/-	29	3	*KMT2D*	frameshift_variant
D2003004908	chr12_49028036_GCTCAGTGCCT/-	33	3	*KMT2D*	frameshift_variant

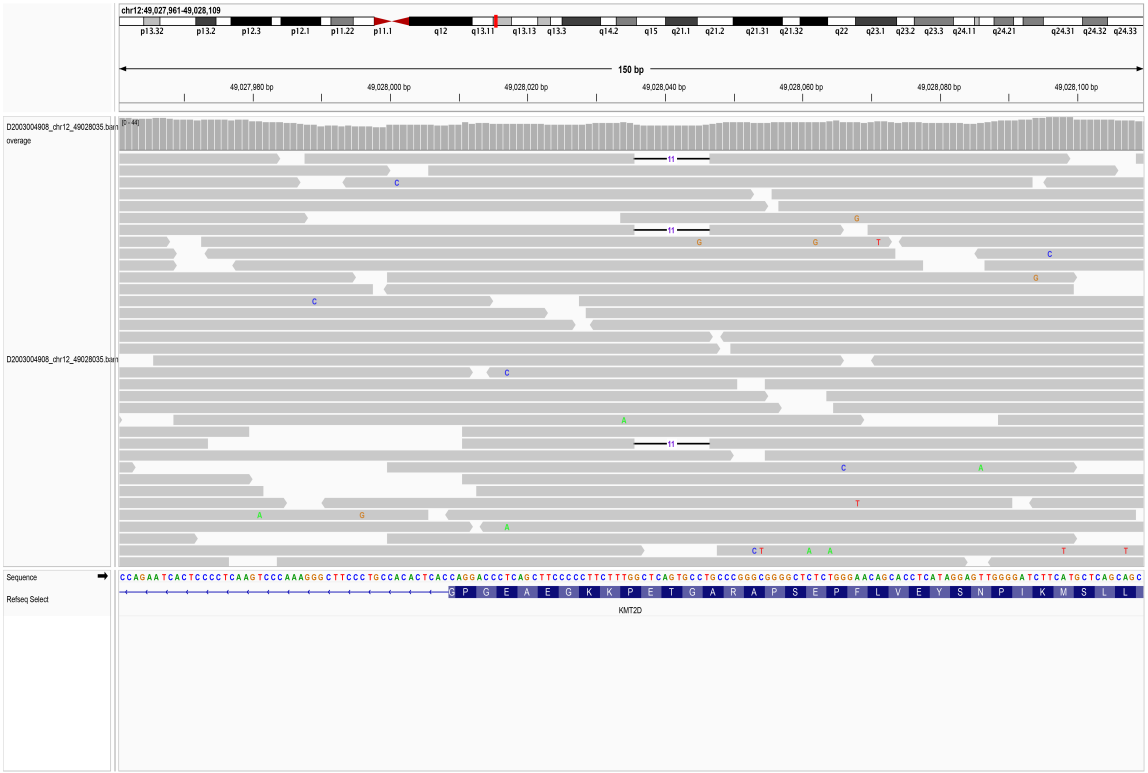



chr12:49,027,967-49,028,104
138 bp
A0019_chr12_4....bam Coverage
A0019_chr12_49028035.bam
Sequence
Refseq Select
KMT2D
chr12:49,027,961-49,028,109
150 bp
AAGC033049C_chr12_49028035.bai overage
AAGC033049C_chr12_49028035.bai
Sequence
Refseq Select
KMT2D


chr12:49,027,961-49,028,109
150 bp
AAGC033086C_chr12_49028035.bai
overage
AAGC033086C_chr12_49028035.bai
Sequence
Refseq Select
KMT2D
chr12:49,027,967-49,028,104
138 bp
AAGC25060329...bam Coverage
AAGC25060329D_chr12_49028055.
Sequence
Refseq Select
KMT2D

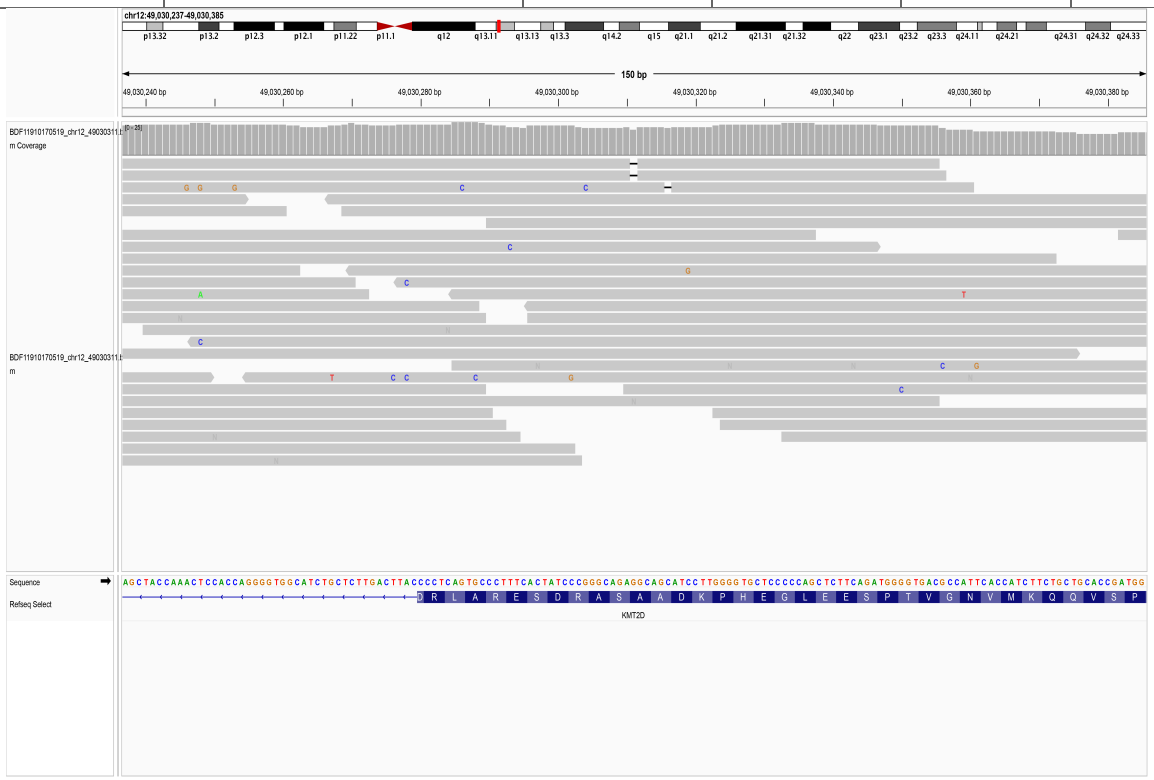

chr12:49,027,967-49,028,104
138 bp
AAGC25061435...bam Coverage
AAGC25061435D_chr12_49028035.b
Sequence
Refseq Select
KMT2D
chr12:49,027,961-49,028,109
150 bp
CNS0134791_chr12_49028035.bam
verage
CNS0134791_chr12_49028035.bam
Sequence
Refseq Select
KMT2D


chr12:49,027,961-49,028,109
150 bp
CNS0135319_chr12_49028035.bam
verage
CNS0135319_chr12_49028035.bam
Sequence
Refseq Select
KMT2D
chr12:49,027,961-49,028,109
150 bp
D2003004856_chr12_49028035.bam
overage
D2003004856_chr12_49028035.bam
Sequence
Refseq Select
KMT2D


chr12:49,027,961-49,028,109
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 q23.3 q24.11 q24.21 q24.31 q24.32 q24.33
150 bp
49,027,980 bp
49,028,000 bp
49,028,020 bp
49,028,040 bp
49,028,060 bp
49,028,080 bp
49,028,100 bp
D2003004908_chr12_49028035.bam
overage
D2003004908_chr12_49028035.bam
Sequence
Refseq Select
KMT2D

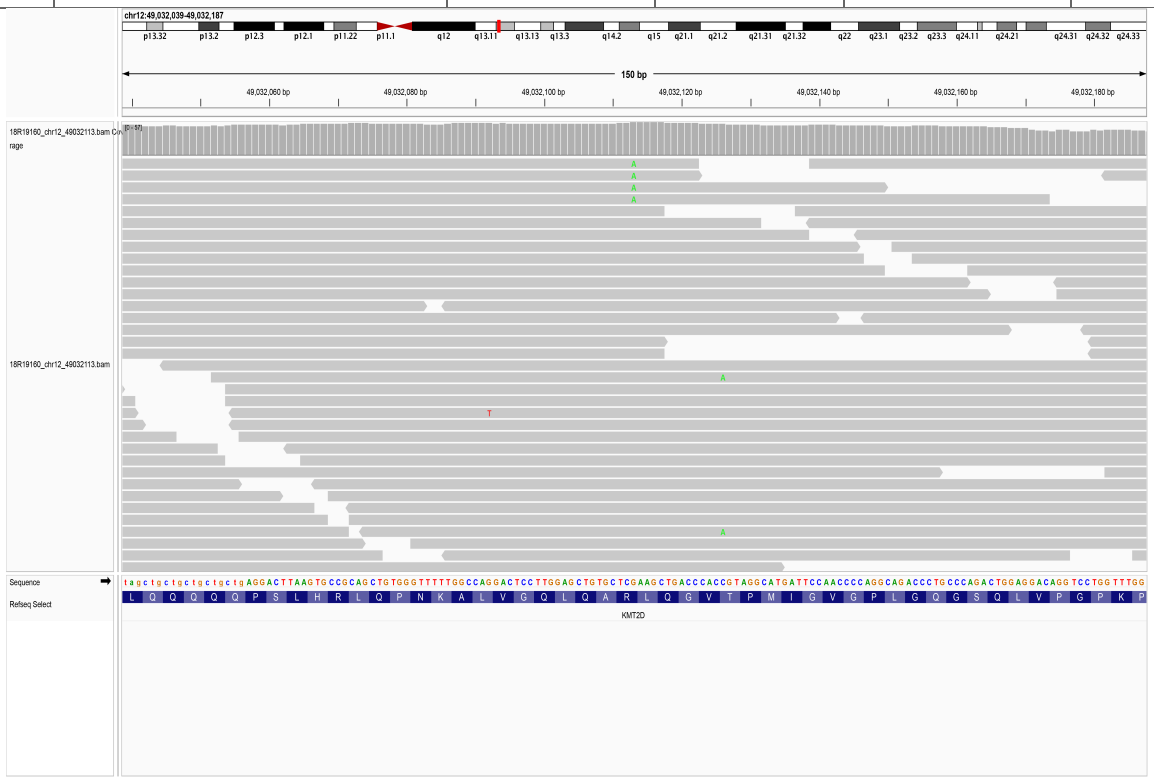
30.7. chr12_49030311_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chr12_49030311_G/-	17	2	*KMT2D*	frameshift_variant



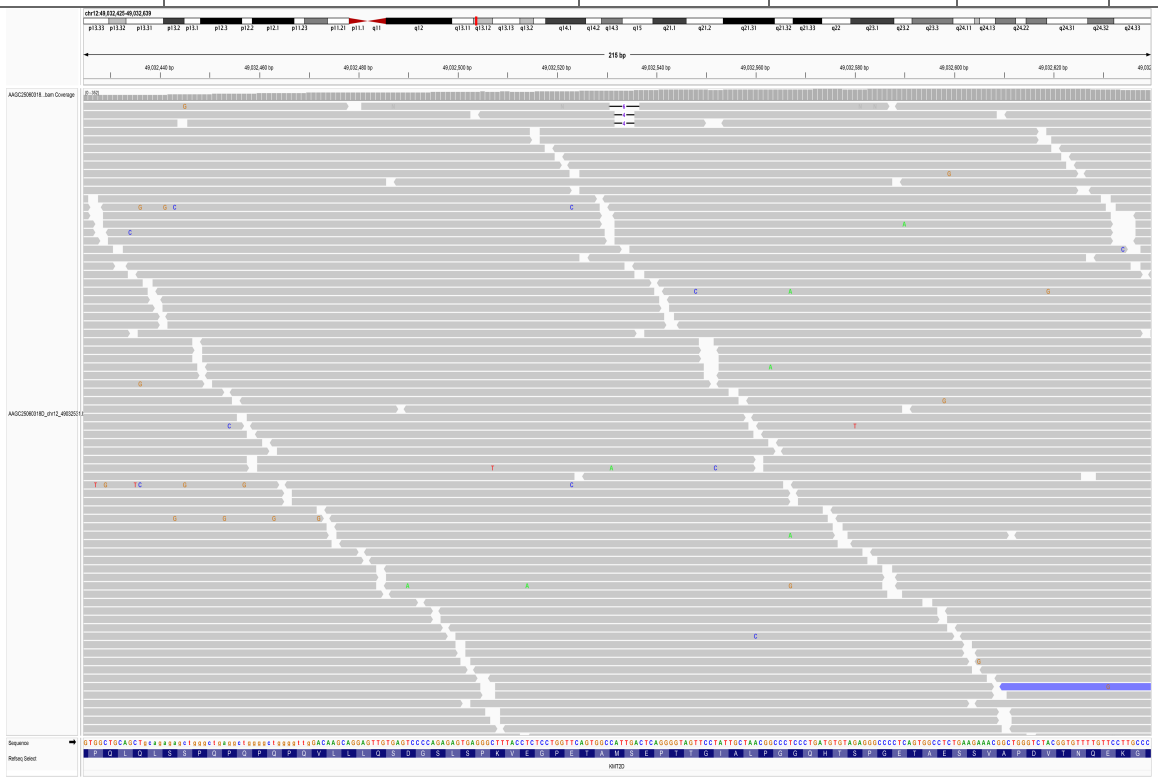
30.8. chr12_49032113_G/A

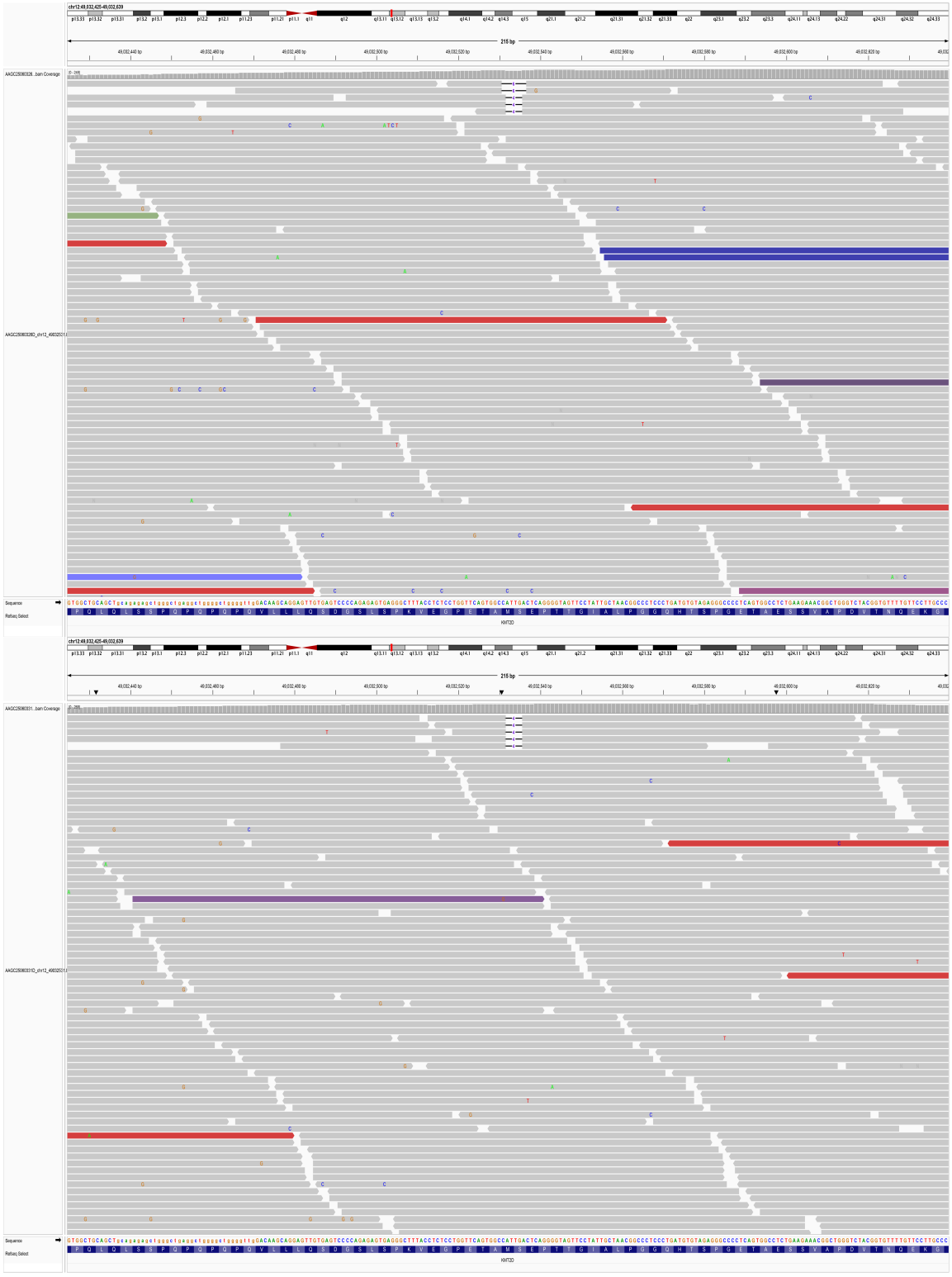
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19160	chr12_49032113_G/A	52	4	*KMT2D*	stop_gained

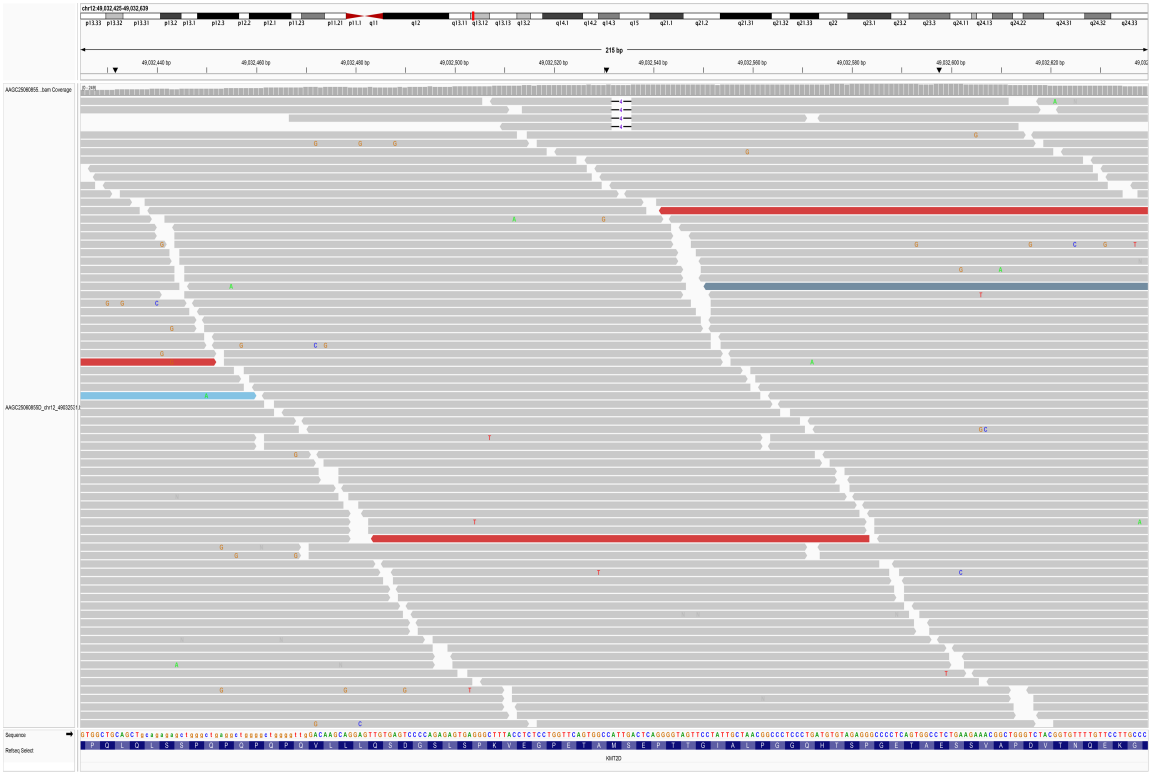


30.9. chr12_49032532_ATTG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060318D	chr12_49032532_ATTG/-	289	5	*KMT2D*	frameshift_variant
AAGC25060326D	chr12_49032532_ATTG/-	206	6	*KMT2D*	frameshift_variant
AAGC25060331D	chr12_49032532_ATTG/-	241	6	*KMT2D*	frameshift_variant
AAGC25060855D	chr12_49032532_ATTG/-	216	4	*KMT2D*	frameshift_variant

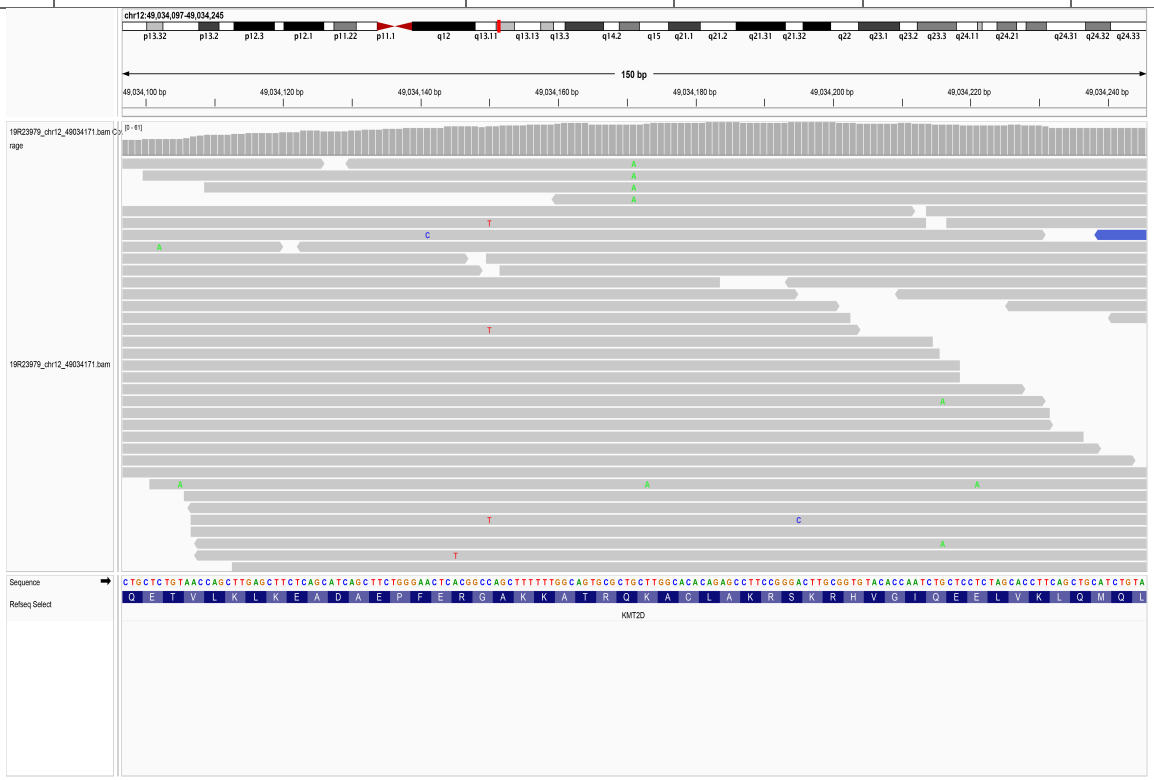






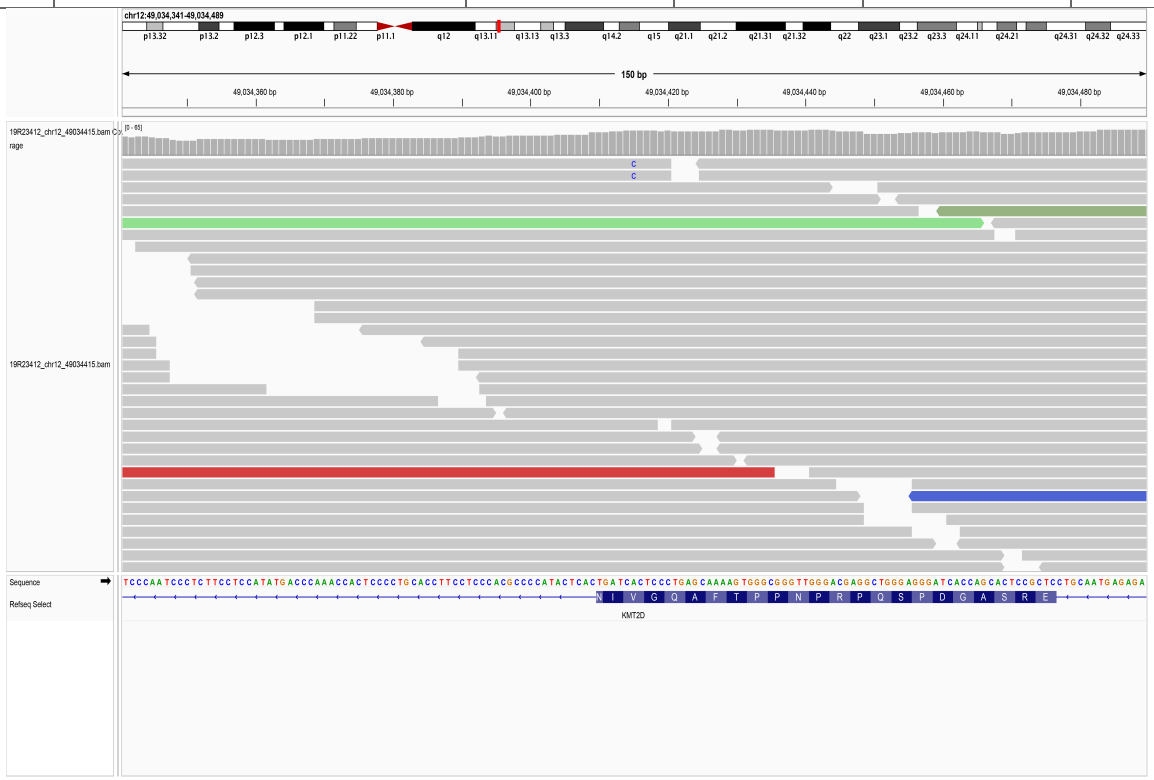
30.10. chr12_49034171_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23979	chr12_49034171_G/A	51	4	*KMT2D*	stop_gained



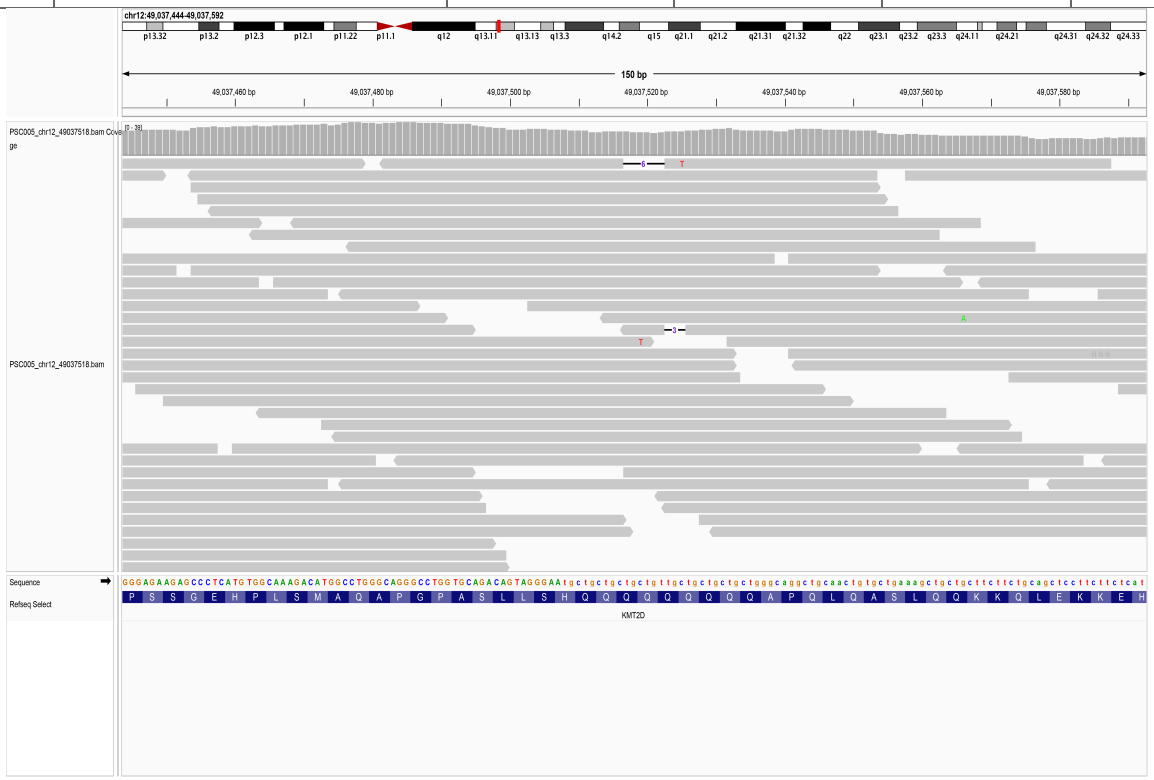
30.11. chr12_49034415_A/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23412	chr12_49034415_A/C	41	2	*KMT2D*	stop_lost



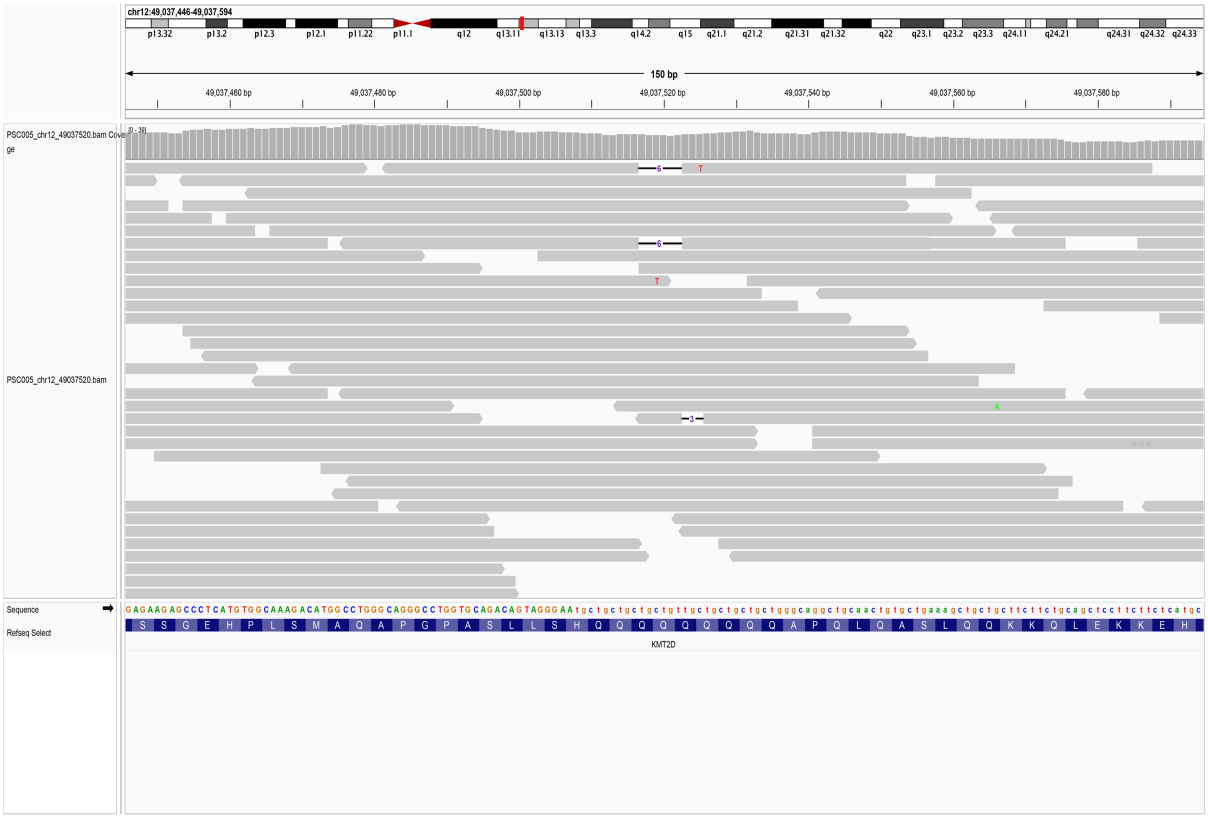
30.12. chr12_49037519_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
PSC005	chr12_49037519_C/-	25	3	*KMT2D*	frameshift_variant



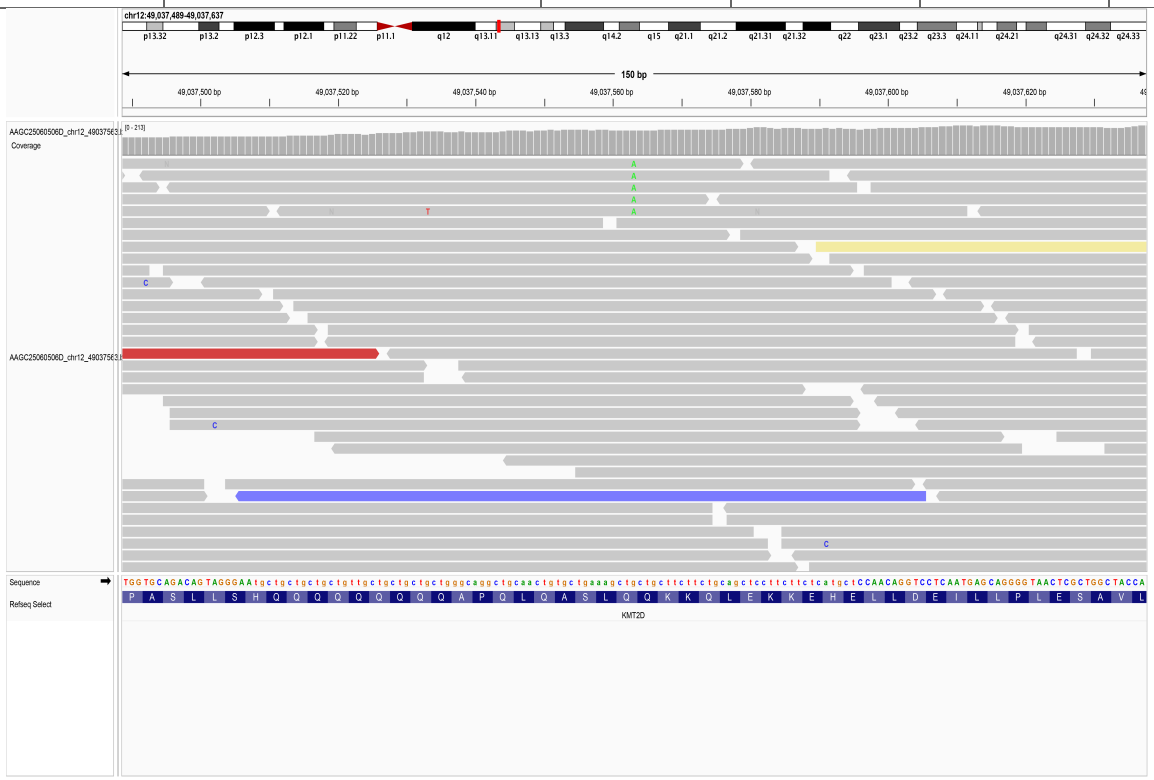
30.13. chr12_49037521_GTTGC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
PSC005	chr12_49037521_GTTGC/-	27	3	*KMT2D*	frameshift_variant



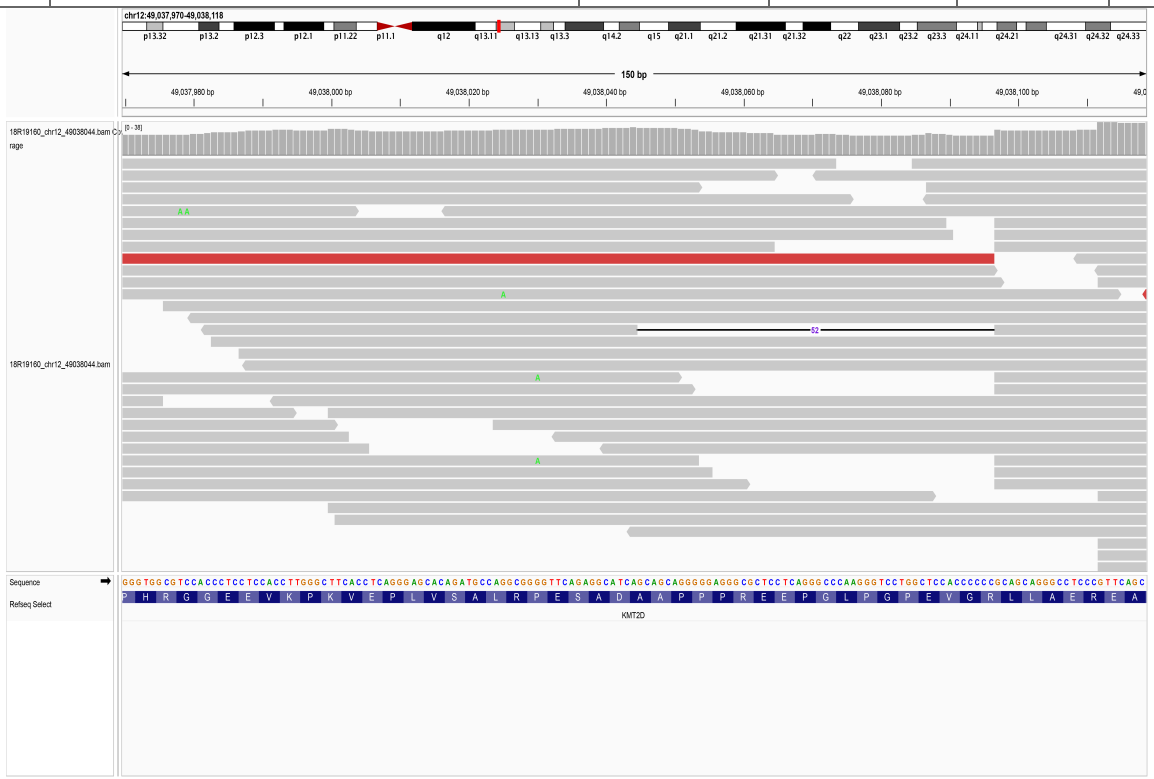
30.14. chr12_49037563_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060506D	chr12_49037563_G/A	147	5	*KMT2D*	stop_gained



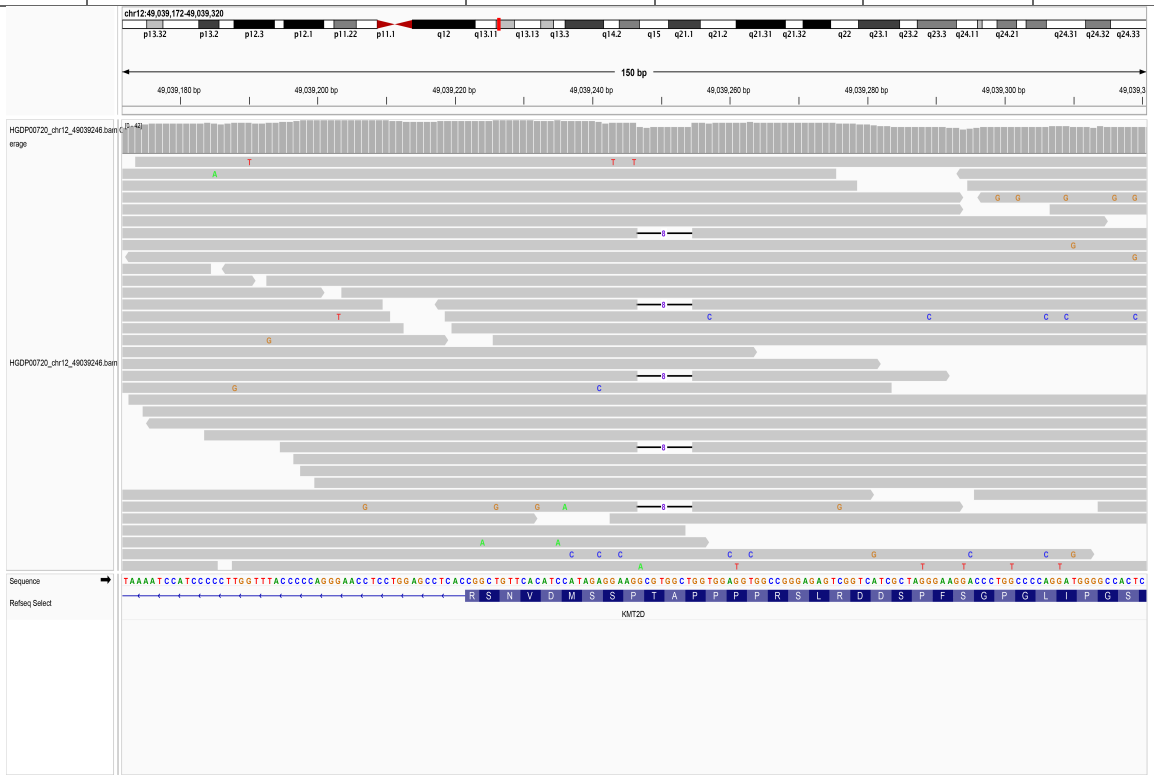
30.15. chr12_49038045_GCAGCAGGGGGAGGGCGCTCCTCAGGGCCCAAGGGTCCTGGCTCCACCCCCC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19160	chr12_49038045_GCAGCAGGGGGAGGGCGCTCCTCAGGGCCCAAGGGTCCTGGCTCCACCCCCC/-	30	2	*KMT2D*	frameshift_variant



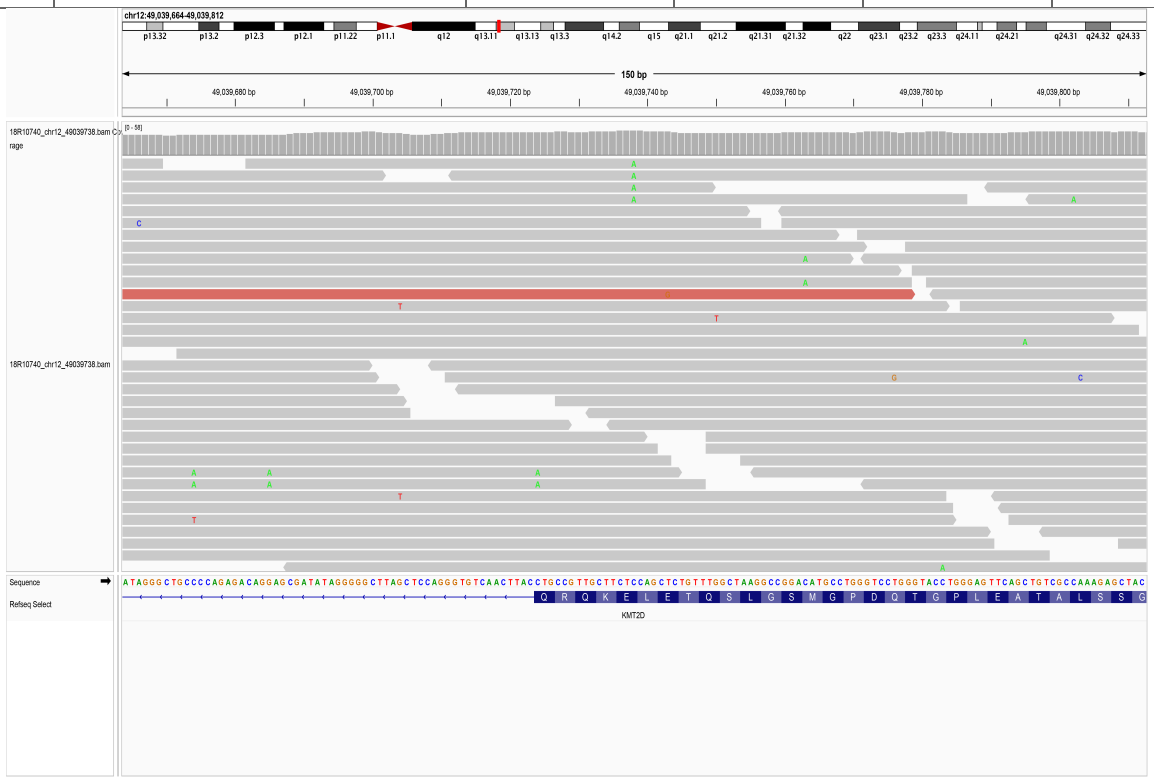
30.16. chr12_49039247_GCGTGGCT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HGDP00720	chr12_49039247_GCGTGGCT/-	29	5	*KMT2D*	frameshift_variant



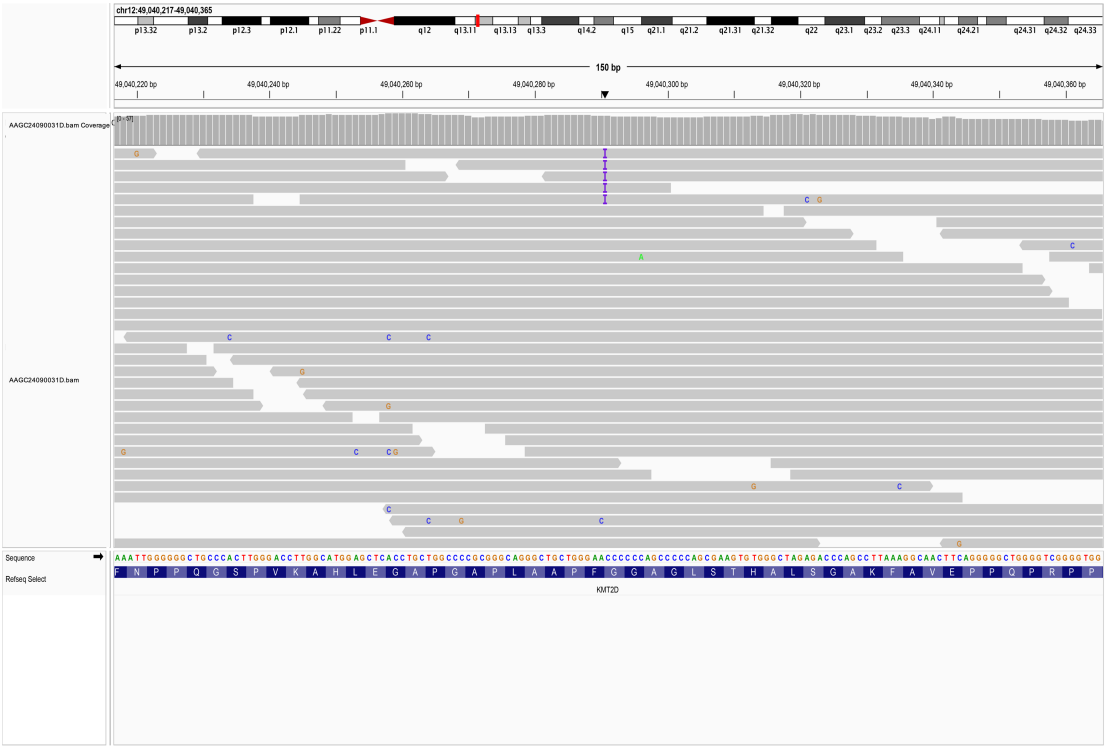
30.17. chr12_49039738_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10740	chr12_49039738_C/A	39	4	*KMT2D*	stop_gained



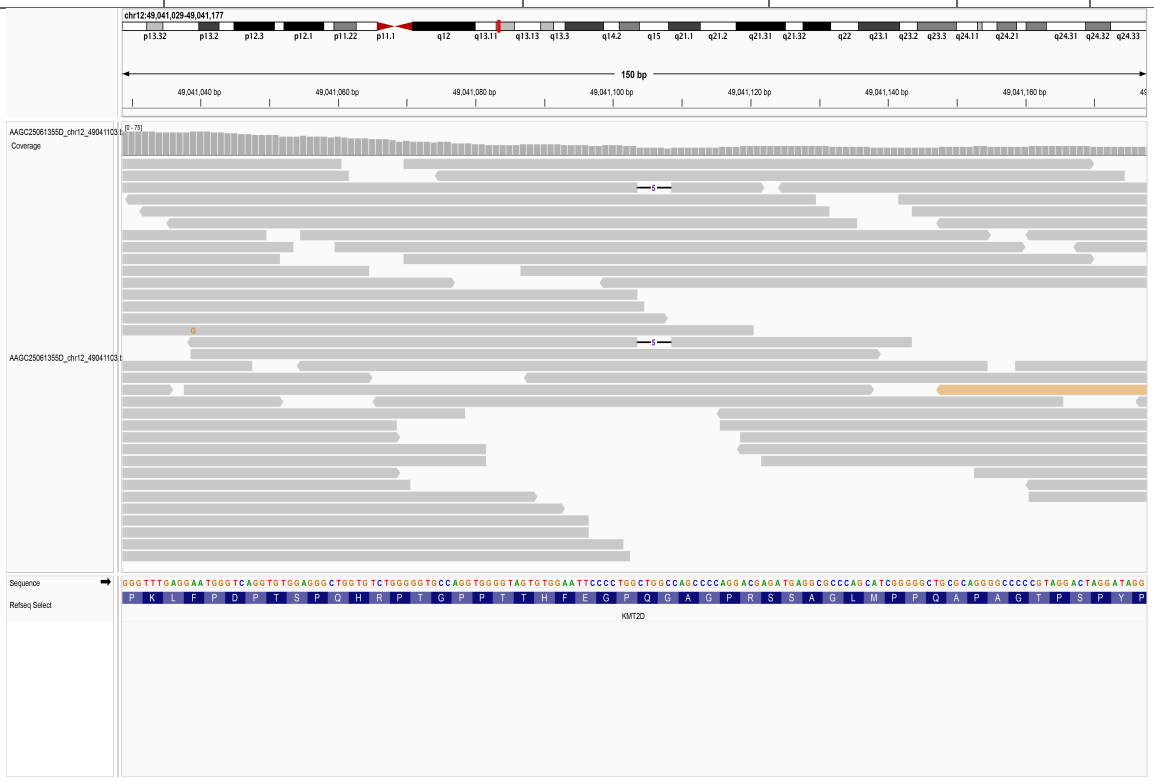
30.18. chr12_49040291_-/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC24090031D	chr12_49040291_-/C	37	5	*KMT2D*	frameshift_variant



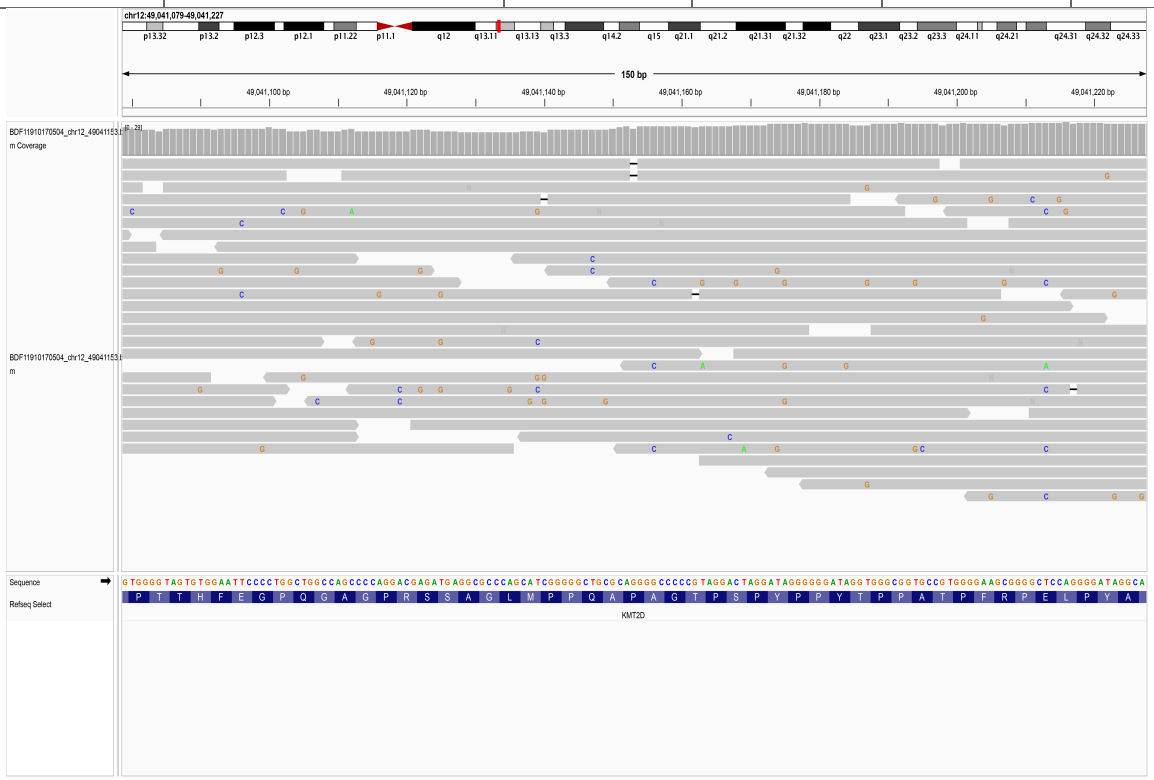
30.19. chr12_49041104_CTGGC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061355D	chr12_49041104_CTGGC/-	17	2	*KMT2D*	frameshift_variant



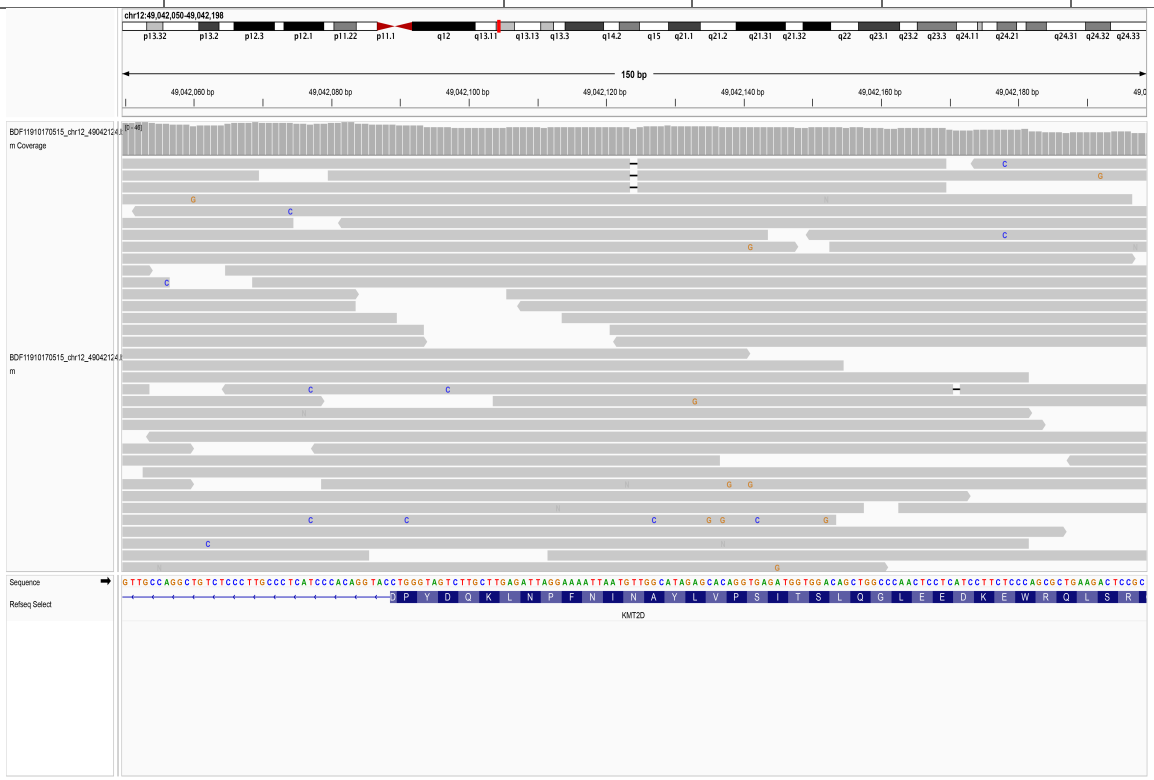
30.20. chr12_49041153_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chr12_49041153_G/-	12	2	*KMT2D*	frameshift_variant



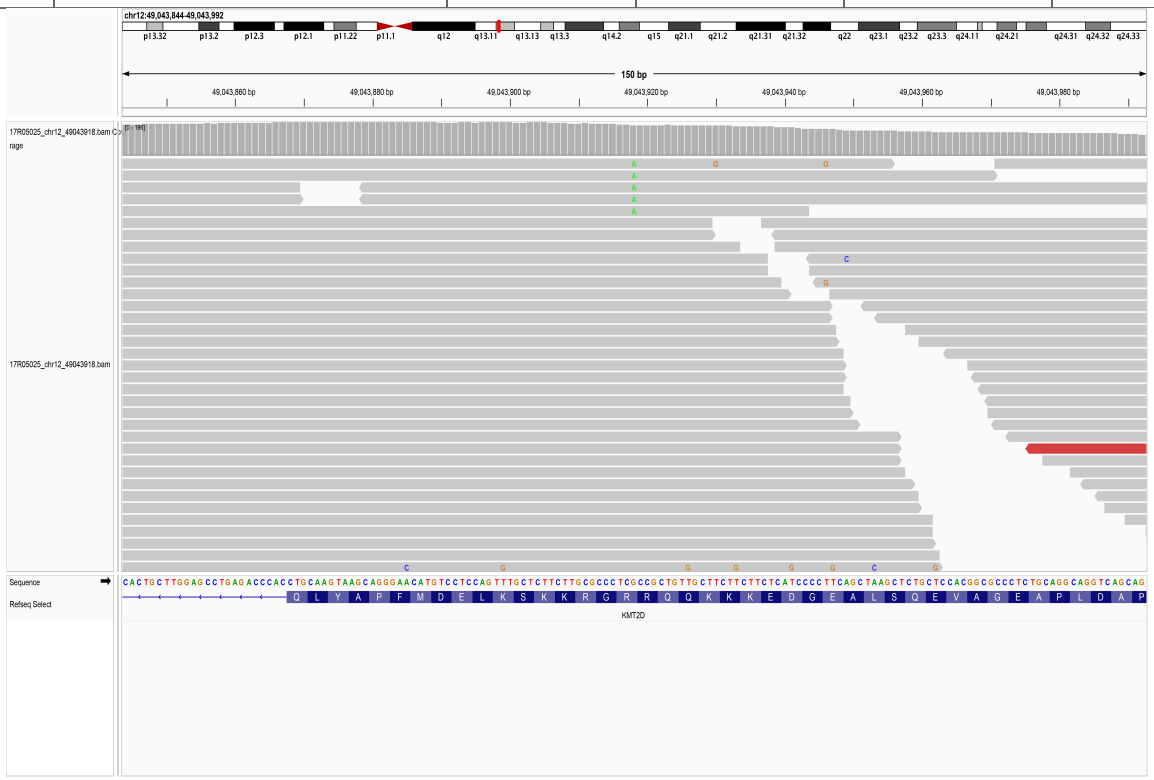
30.21. chr12_49042124_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170515	chr12_49042124_T/-	32	3	*KMT2D*	frameshift_variant



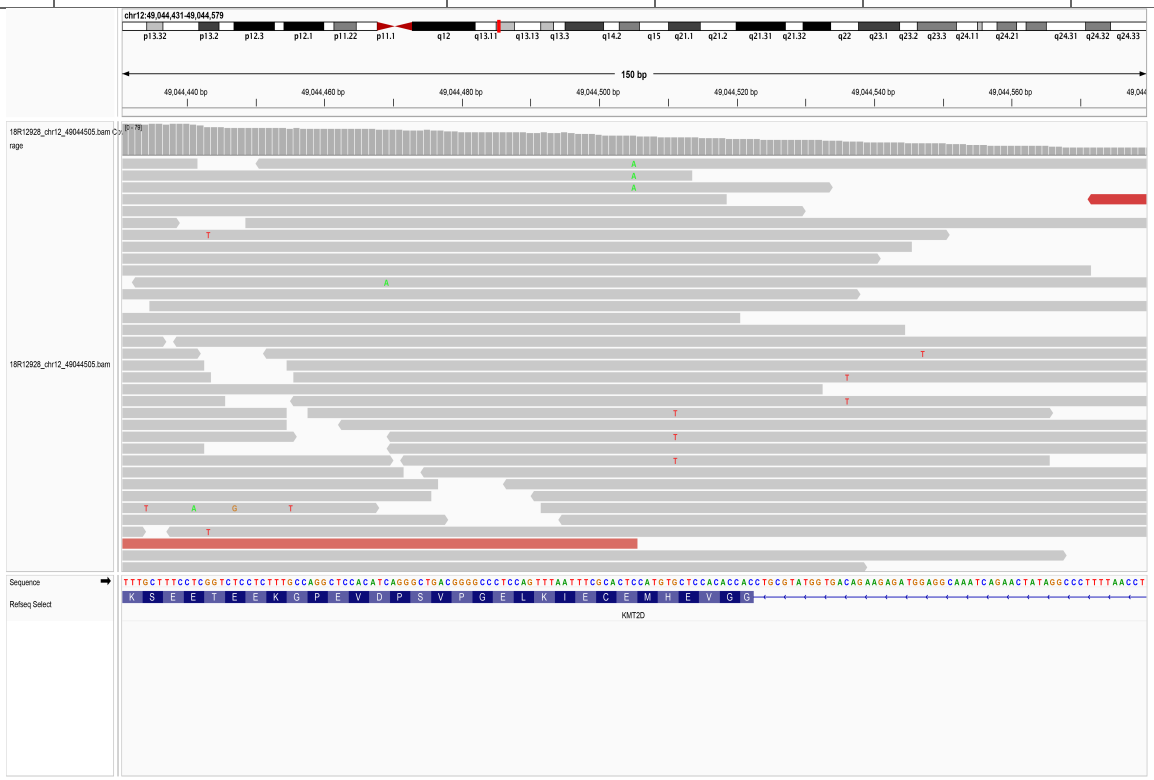
30.22. chr12_49043918_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05025	chr12_49043918_G/A	168	5	*KMT2D*	stop_gained



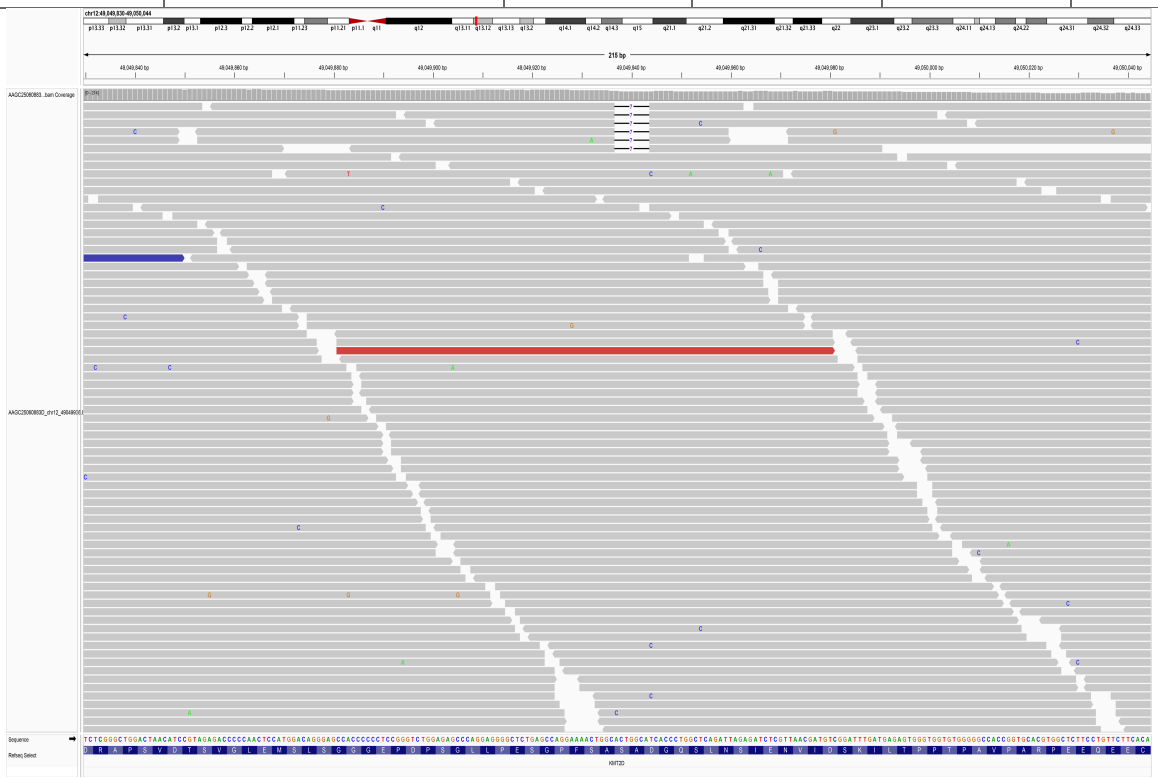
30.23. chr12_49044505_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12928	chr12_49044505_C/A	42	3	*KMT2D*	stop_gained



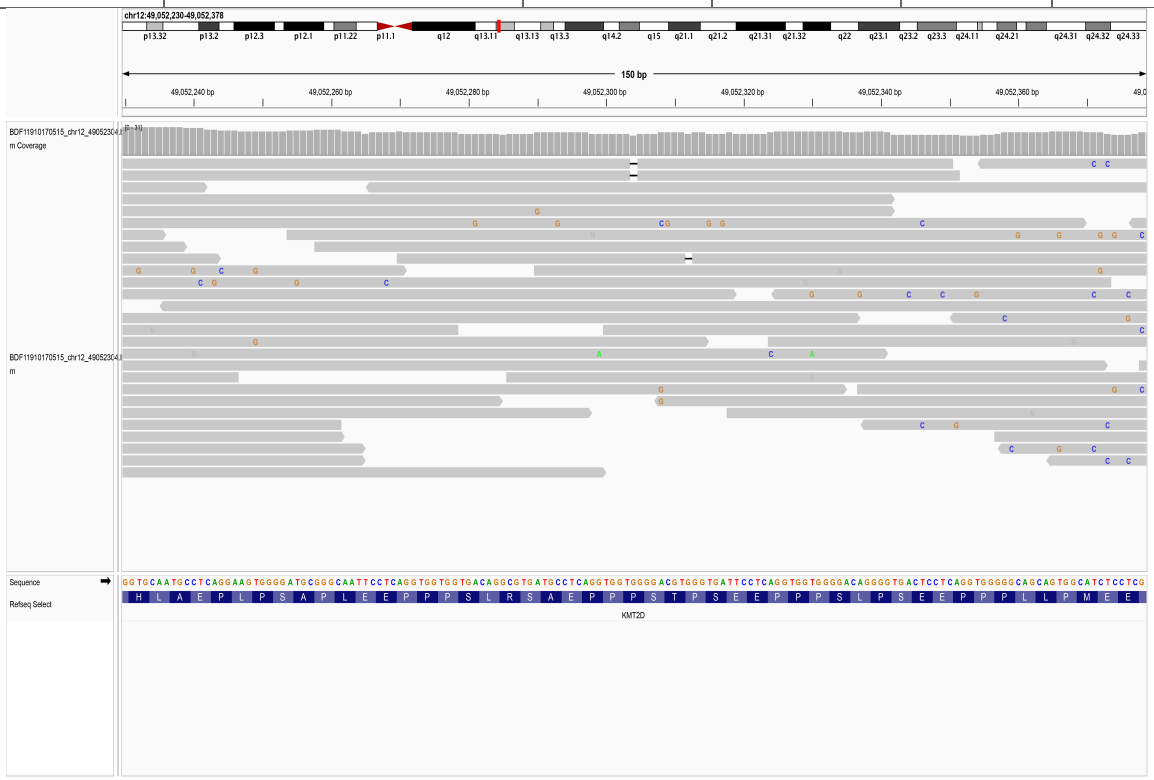
30.24. chr12_49049937_ACTGGCA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060883D	chr12_49049937_ACTGGCA/-	180	6	*KMT2D*	frameshift_variant



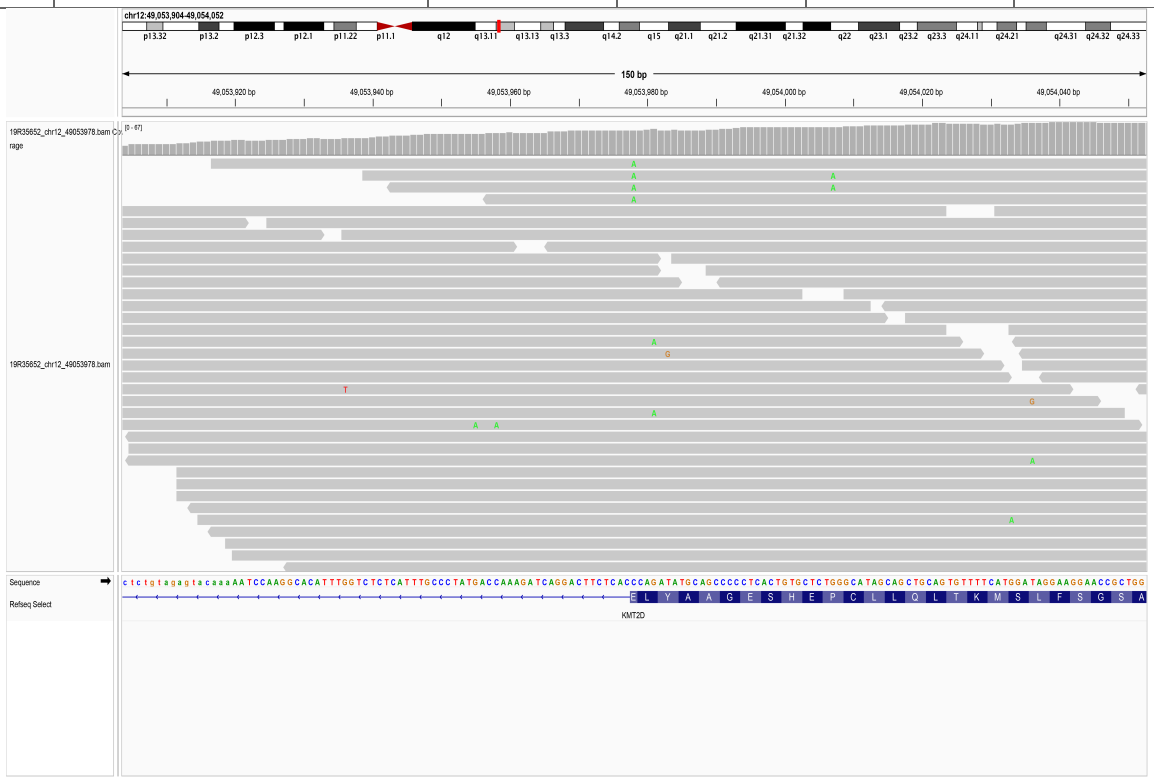
30.25. chr12_49052304_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170515	chr12_49052304_G/-	14	2	*KMT2D*	frameshift_variant



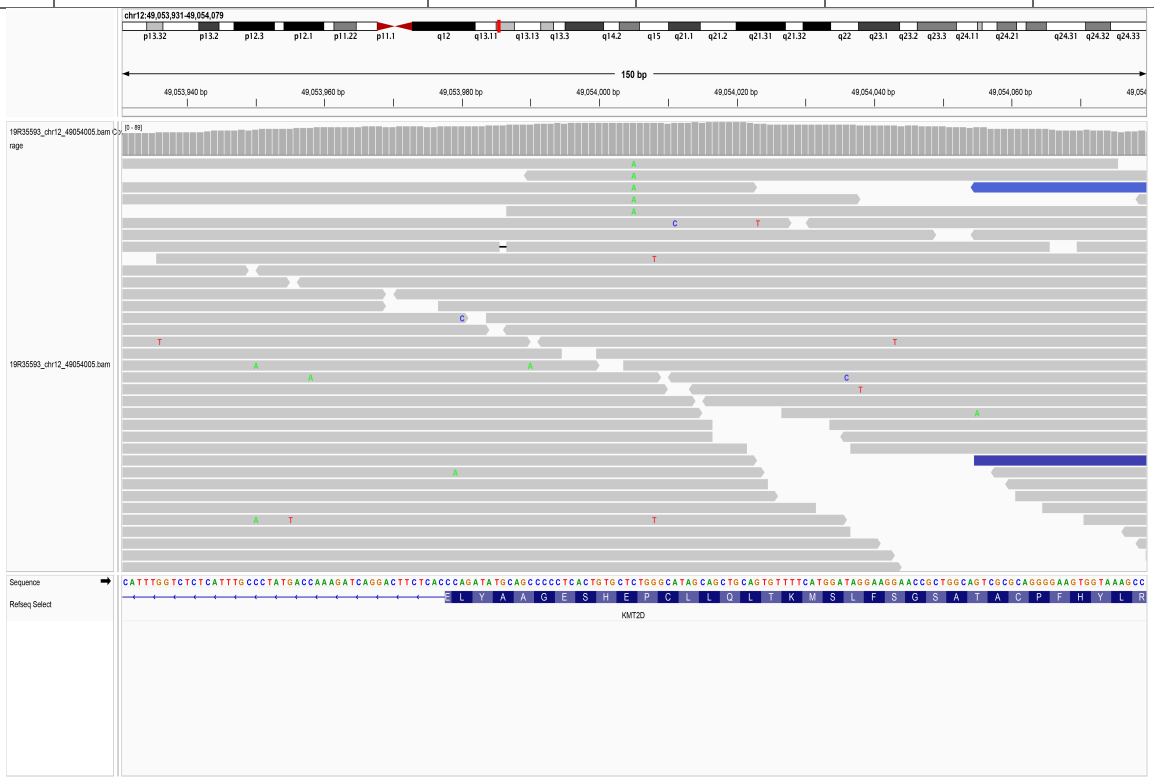
30.26. chr12_49053978_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R35652	chr12_49053978_C/A	45	4	*KMT2D*	stop_gained



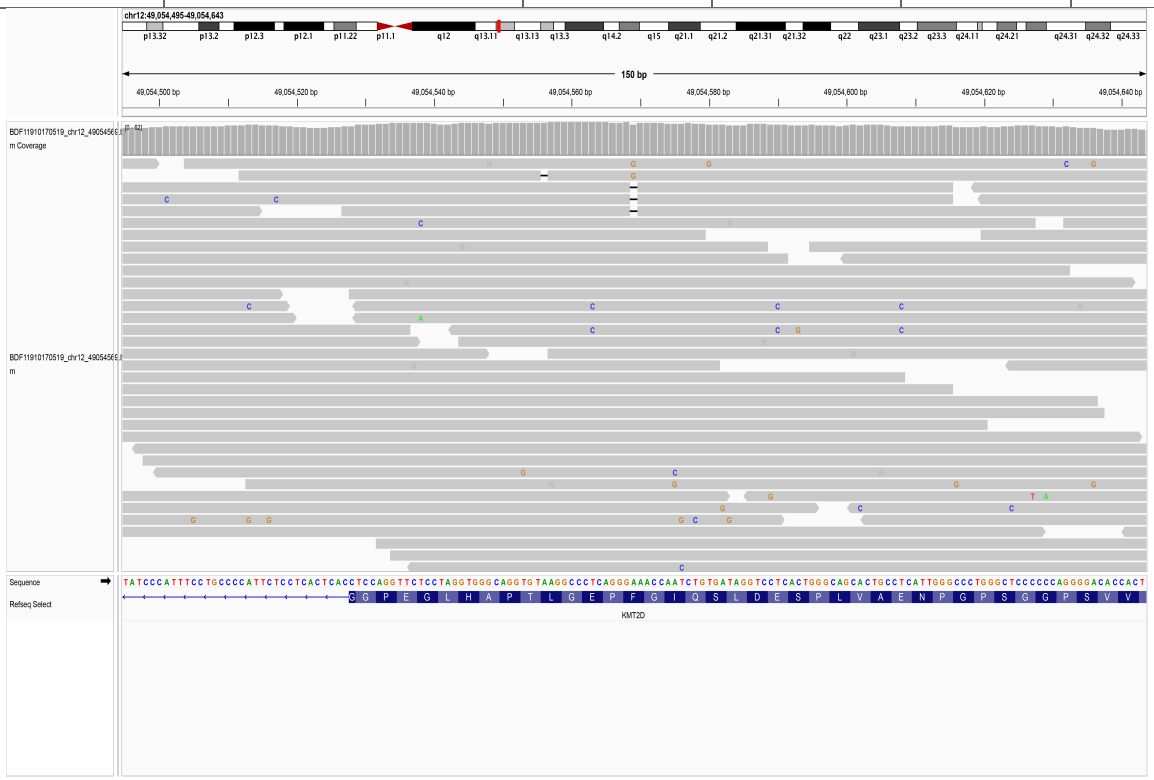
30.27. chr12_49054005_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R35593	chr12_49054005_C/A	80	5	*KMT2D*	stop_gained



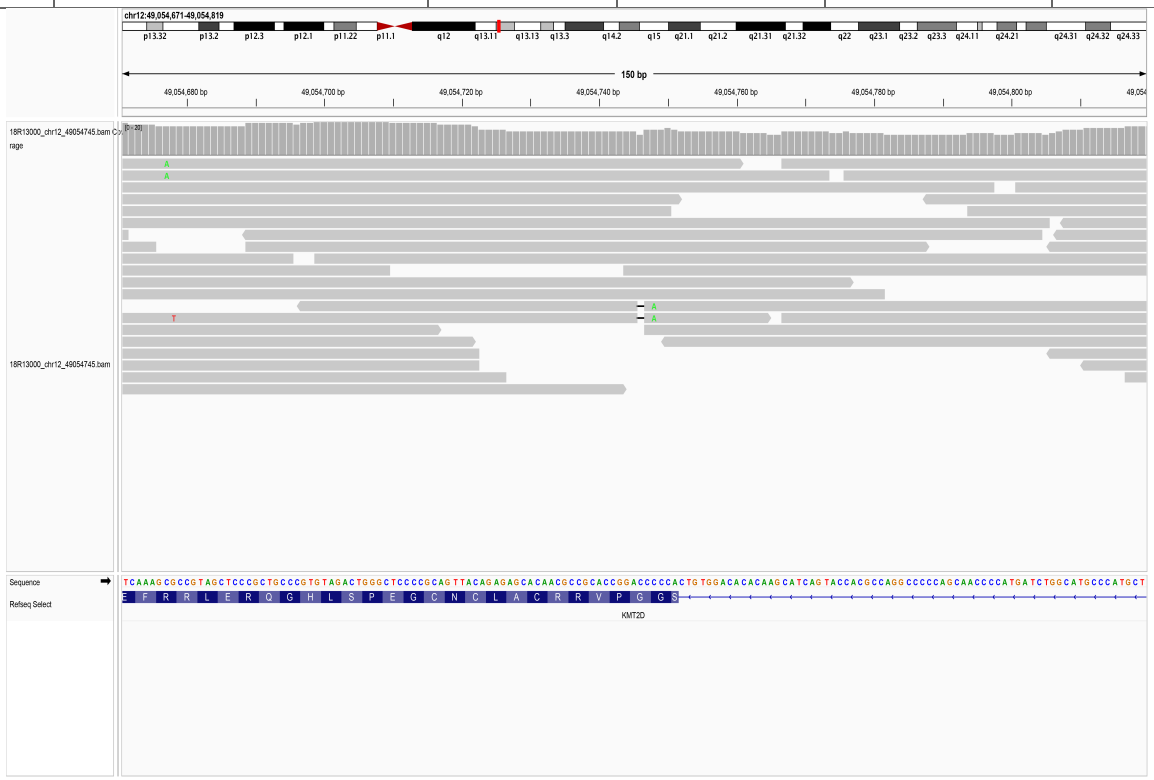
30.28. chr12_49054569_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chr12_49054569_A/-	49	4	*KMT2D*	frameshift_variant



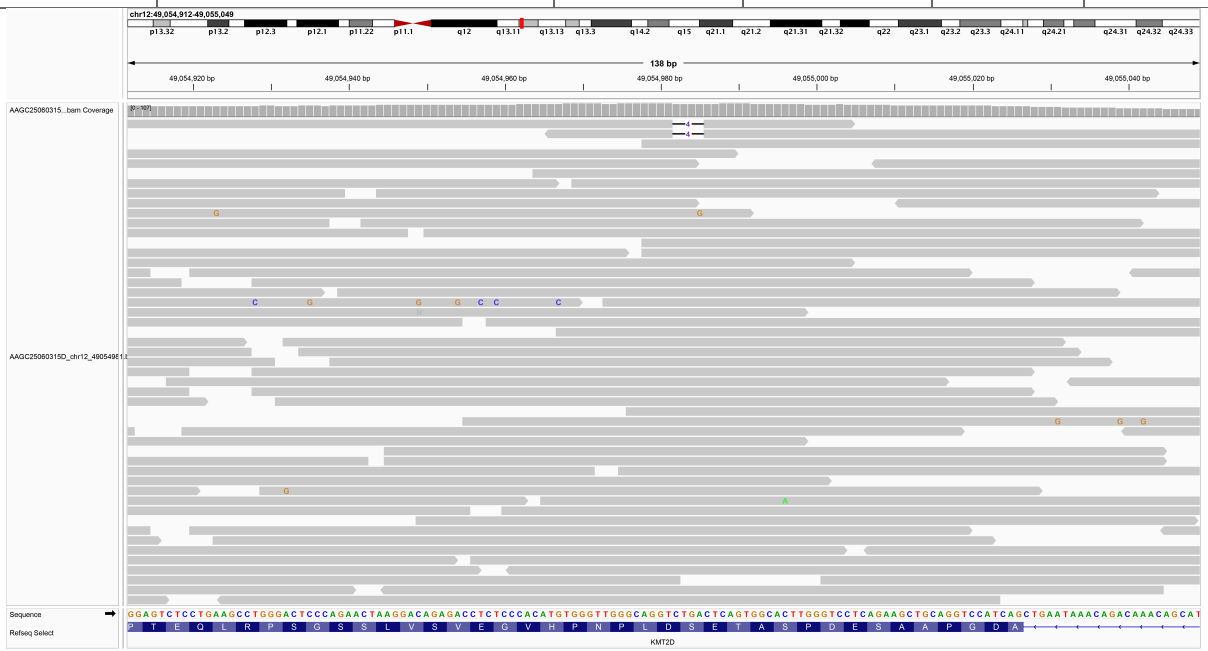
30.29. chr12_49054746_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13000	chr12_49054746_C/-	12	2	*KMT2D*	frameshift_variant



30.30. chr12_49054982_CTGA/-

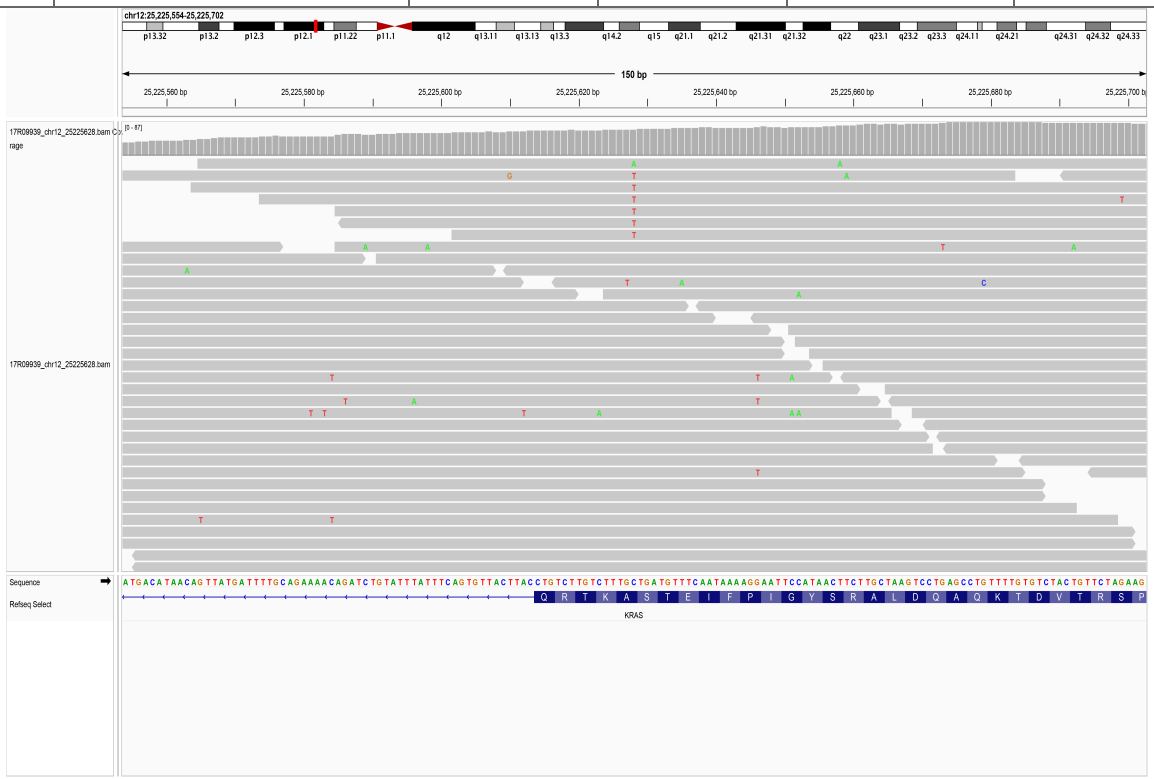
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060315D	chr12_49054982_CTGA/-	99	2	*KMT2D*	frameshift_variant



31. *KRAS*

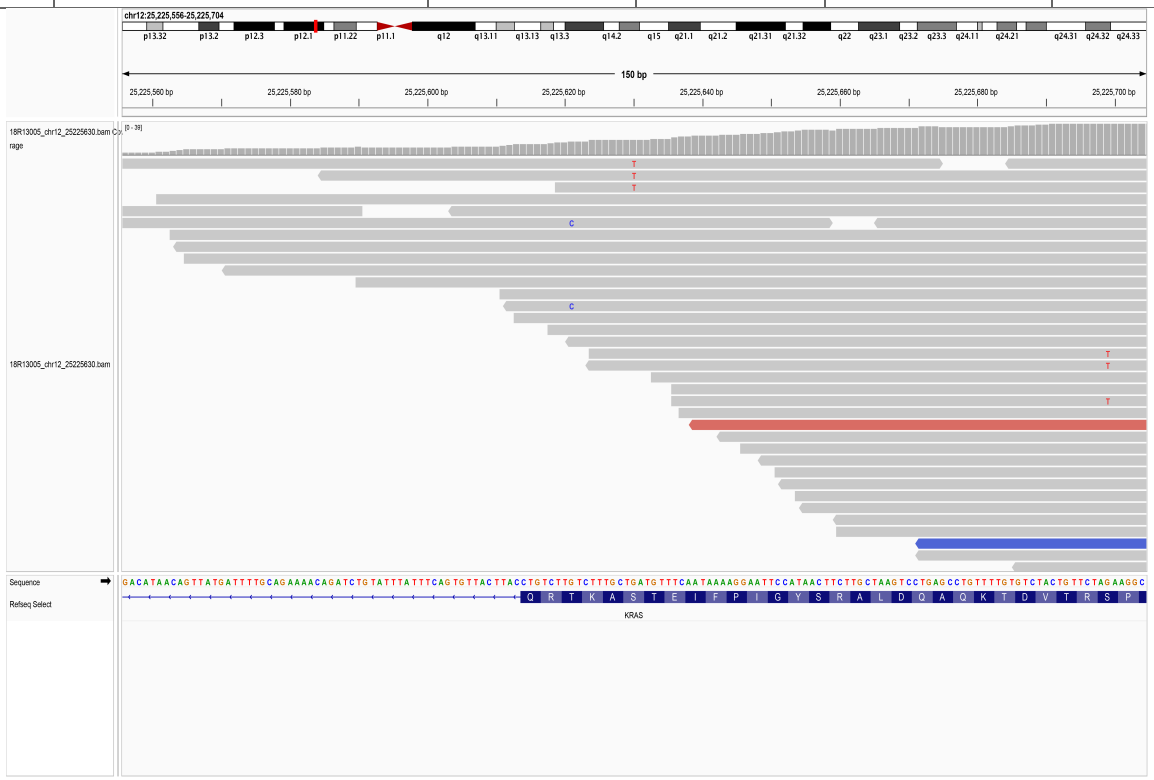
31.1. chr12_25225628_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09939	chr12_25225628_C/T	56	6	*KRAS*	missense_variant



31.2. chr12_25225630_G/T

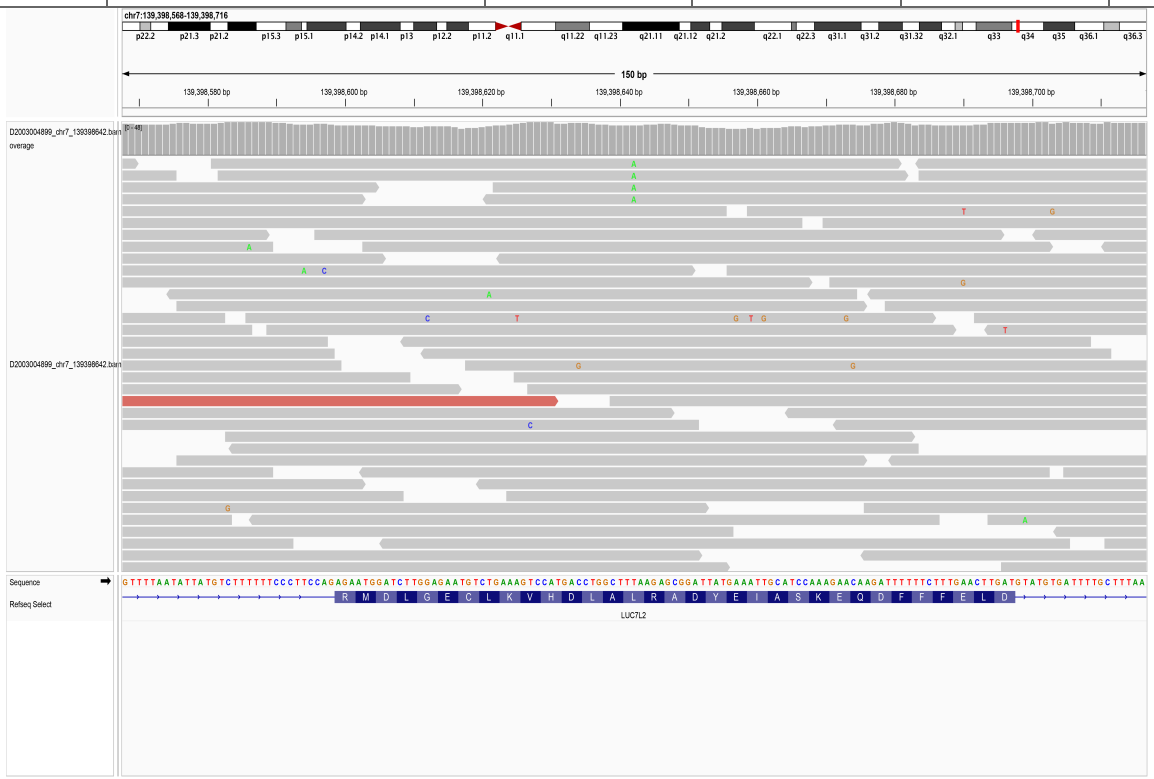
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13005	chr12_25225630_G/T	15	3	*KRAS*	stop_gained



32. *LUC7L2*

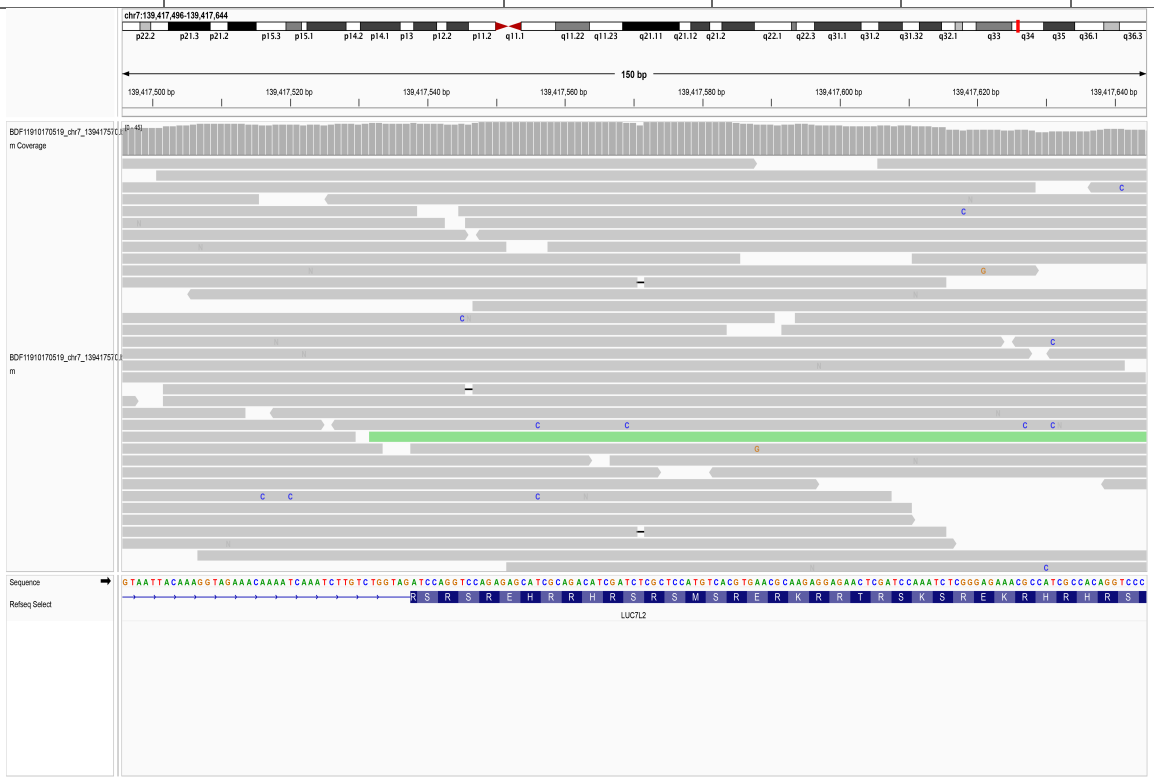
32.1. chr7_139398642_T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2003004899	chr7_139398642_T/A	37	4	*LUC7L2*	stop_gained



32.2. chr7_139417571_T/-

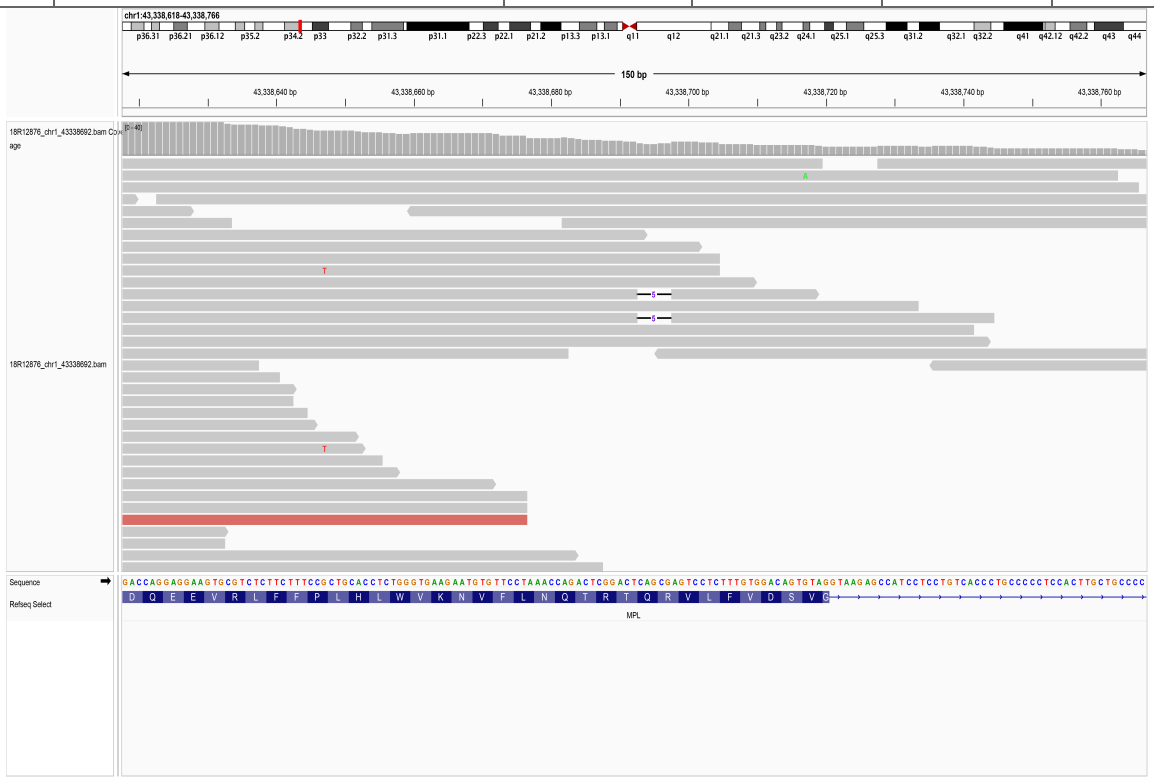
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chr7_139417571_T/-	38	3	*LUC7L2*	frameshift_variant



33. *MPL*

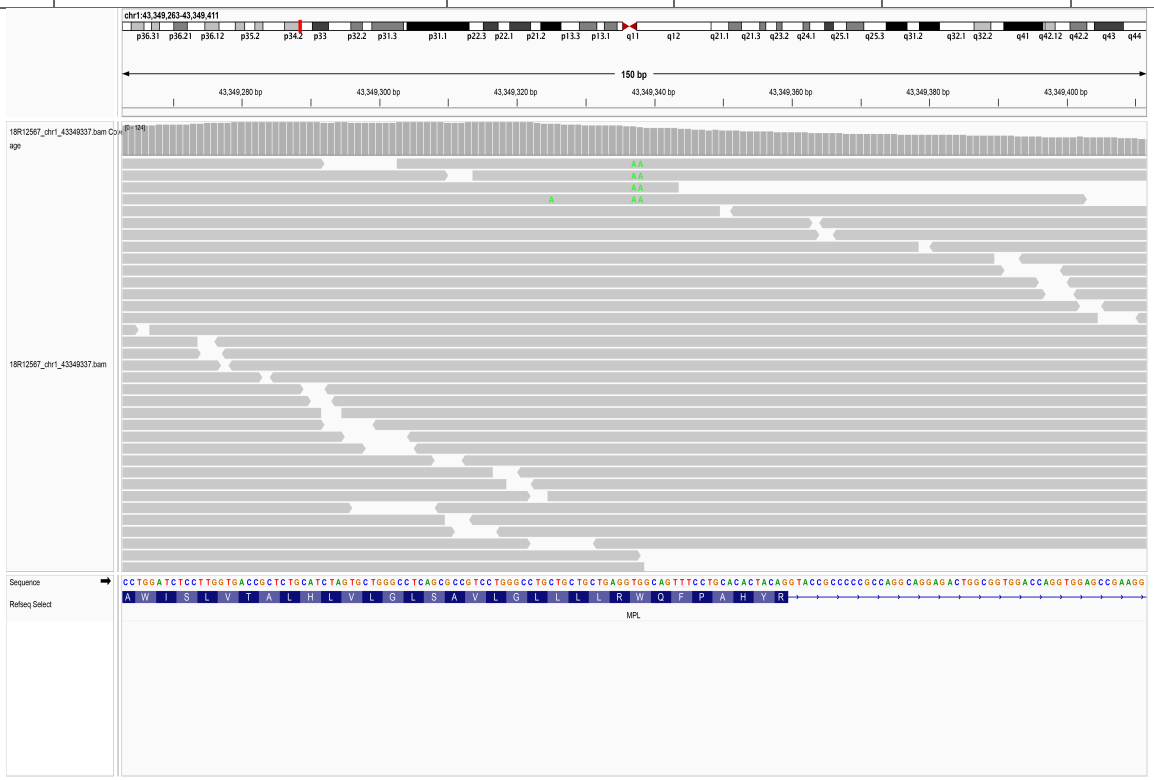
33.1. chr1_43338693_CAGCG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12876	chr1_43338693_CAGCG/-	15	2	*MPL*	frameshift_variant



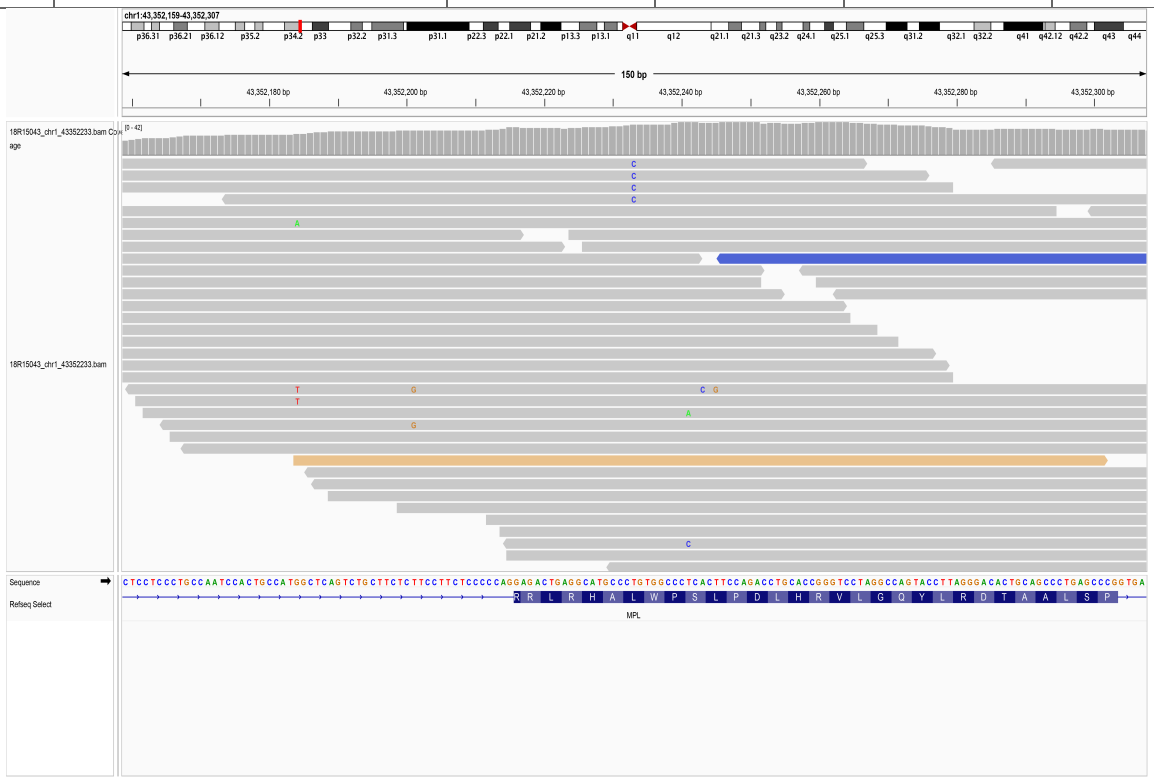
33.2. chr1_43349337_TG/AA

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12567	chr1_43349337_TG/AA	102	4	*MPL*	missense_variant



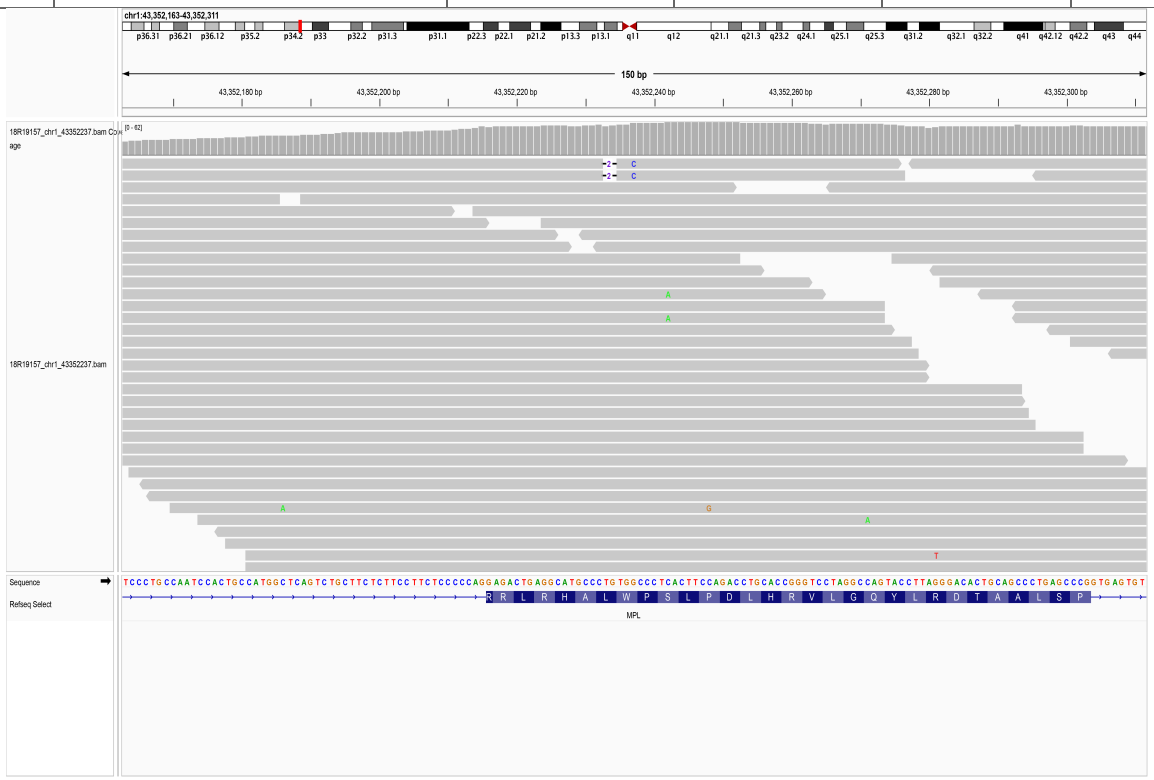
33.3. chr1_43352233_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15043	chr1_43352233_T/C	33	4	*MPL*	missense_variant



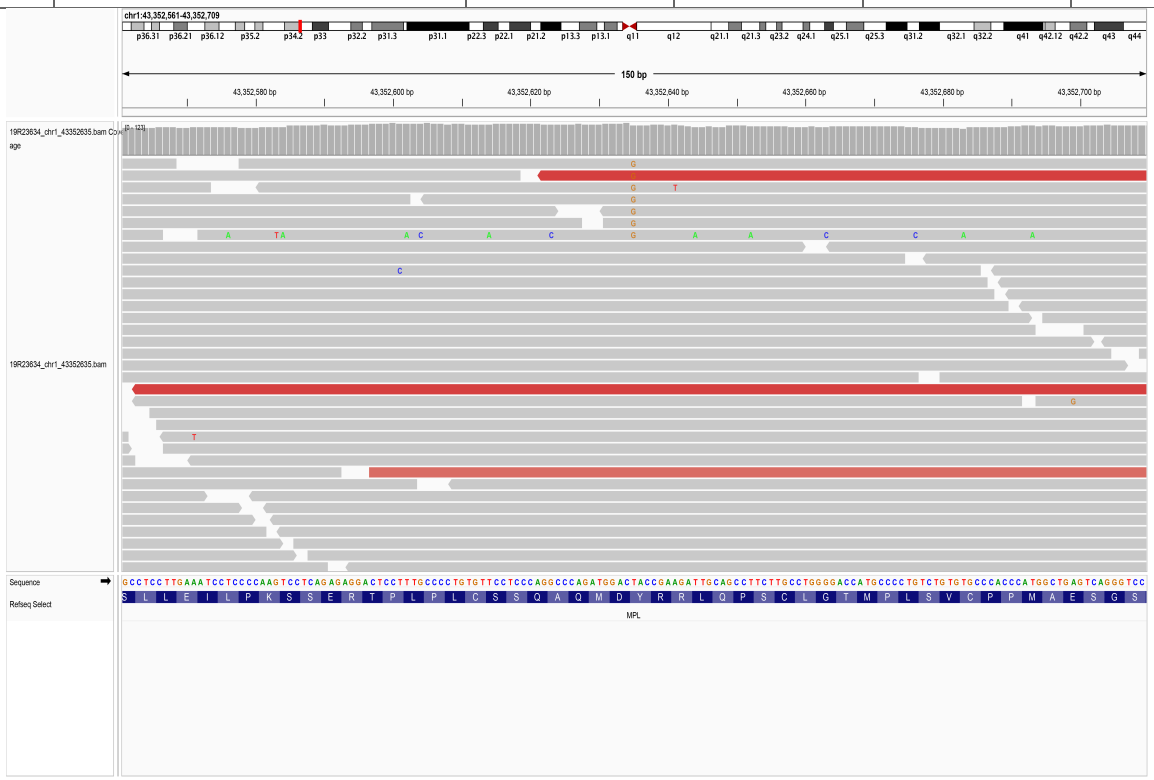
33.4. chr1_43352237_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19157	chr1_43352237_G/C	57	2	*MPL*	missense_variant



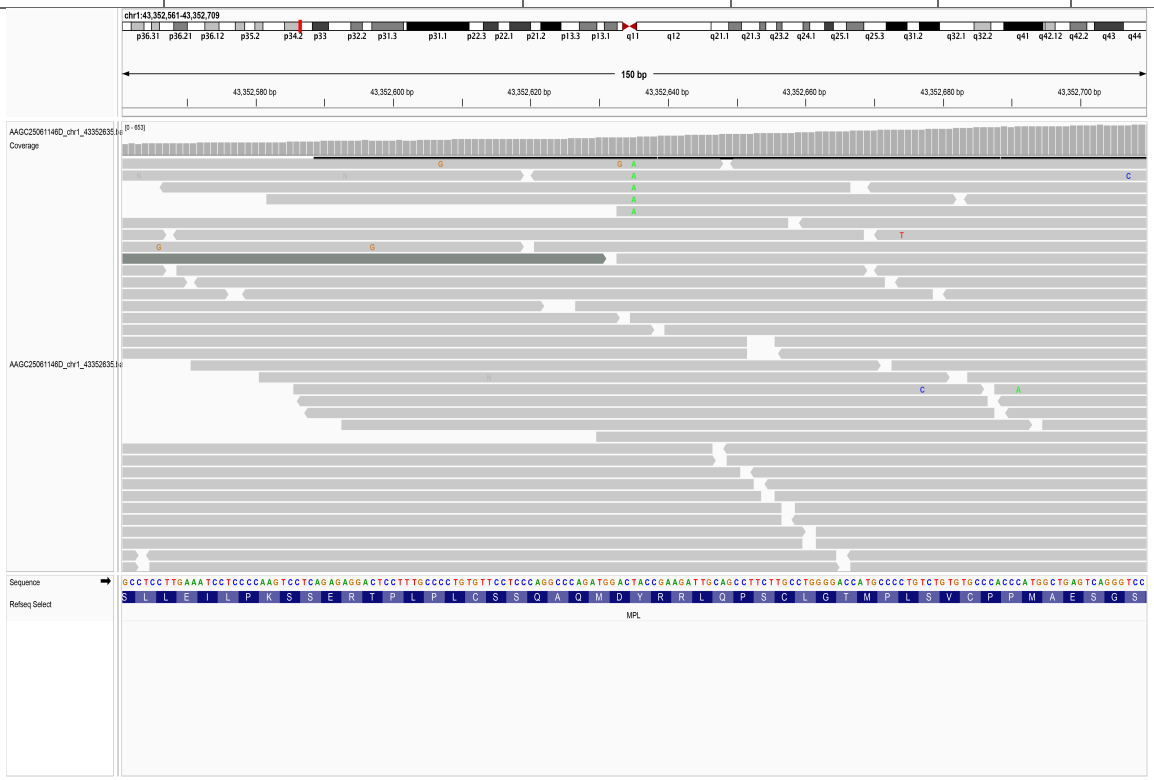
33.5. chr1_43352635_T/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23634	chr1_43352635_T/G	100	5	*MPL*	missense_variant



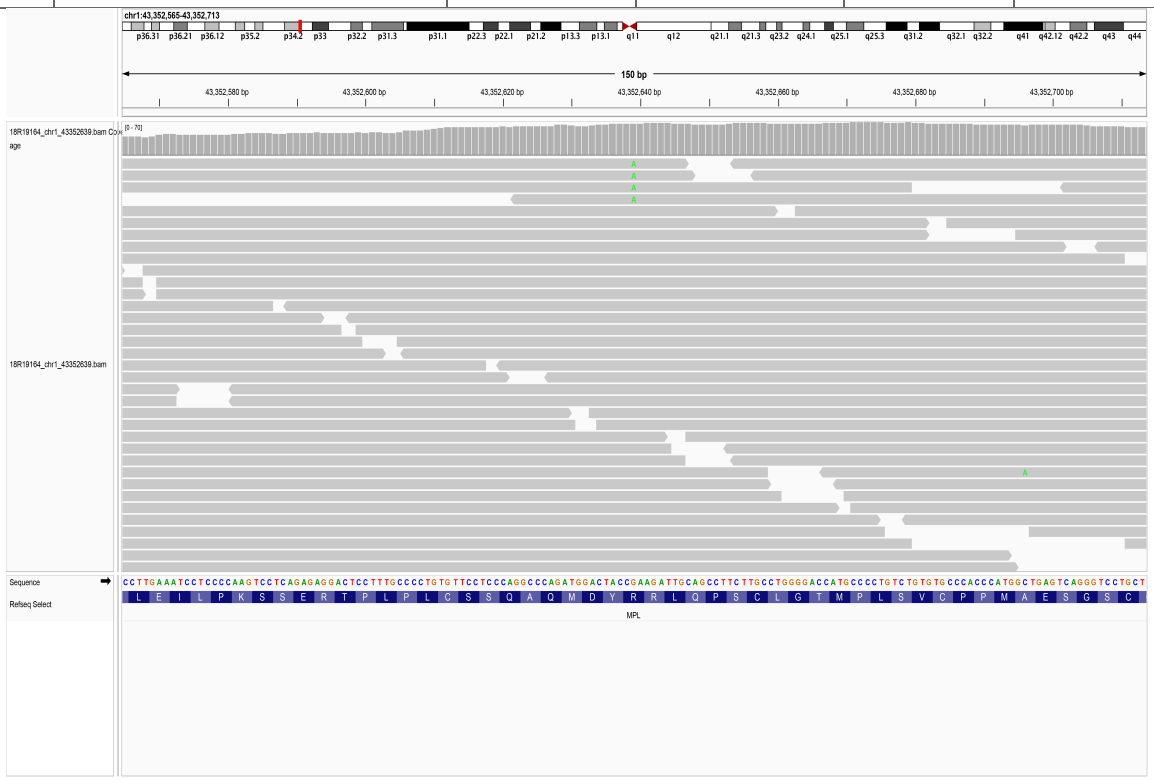
33.6. chr1_43352635_T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061146D	chr1_43352635_T/A	344	7	*MPL*	missense_variant



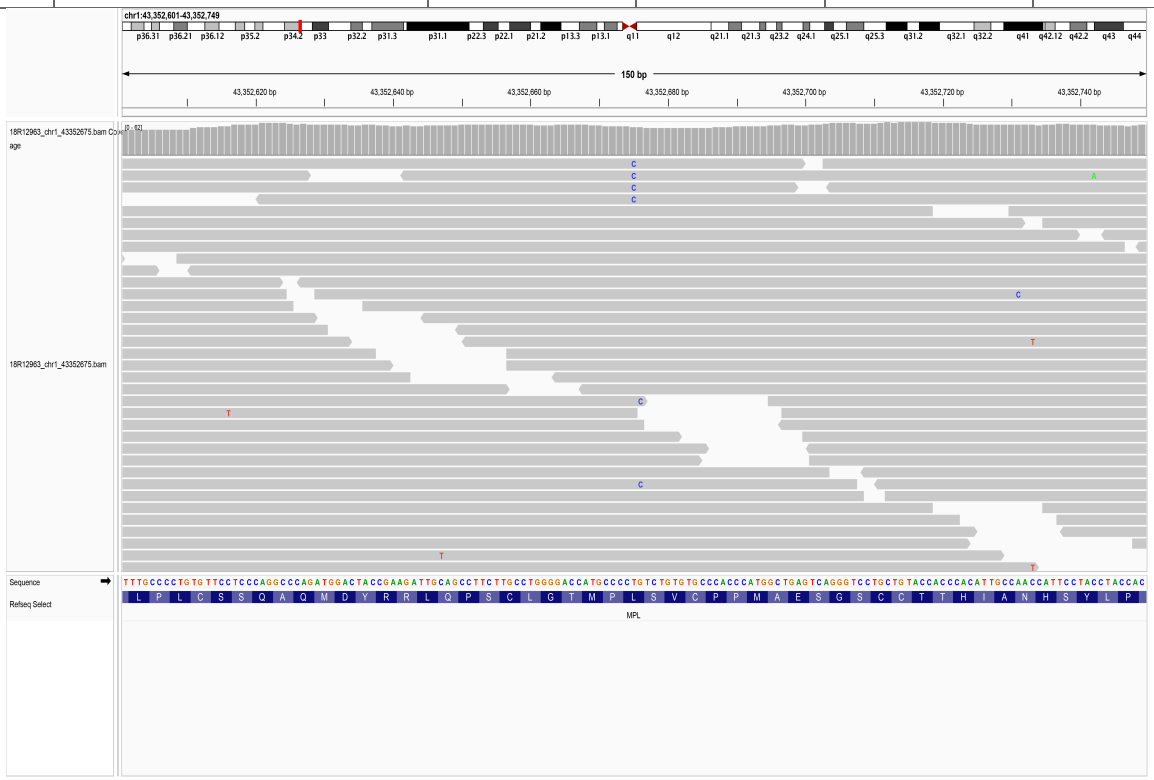
33.7. chr1_43352639_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19164	chr1_43352639_G/A	62	4	*MPL*	missense_variant



33.8. chr1_43352675_T/C

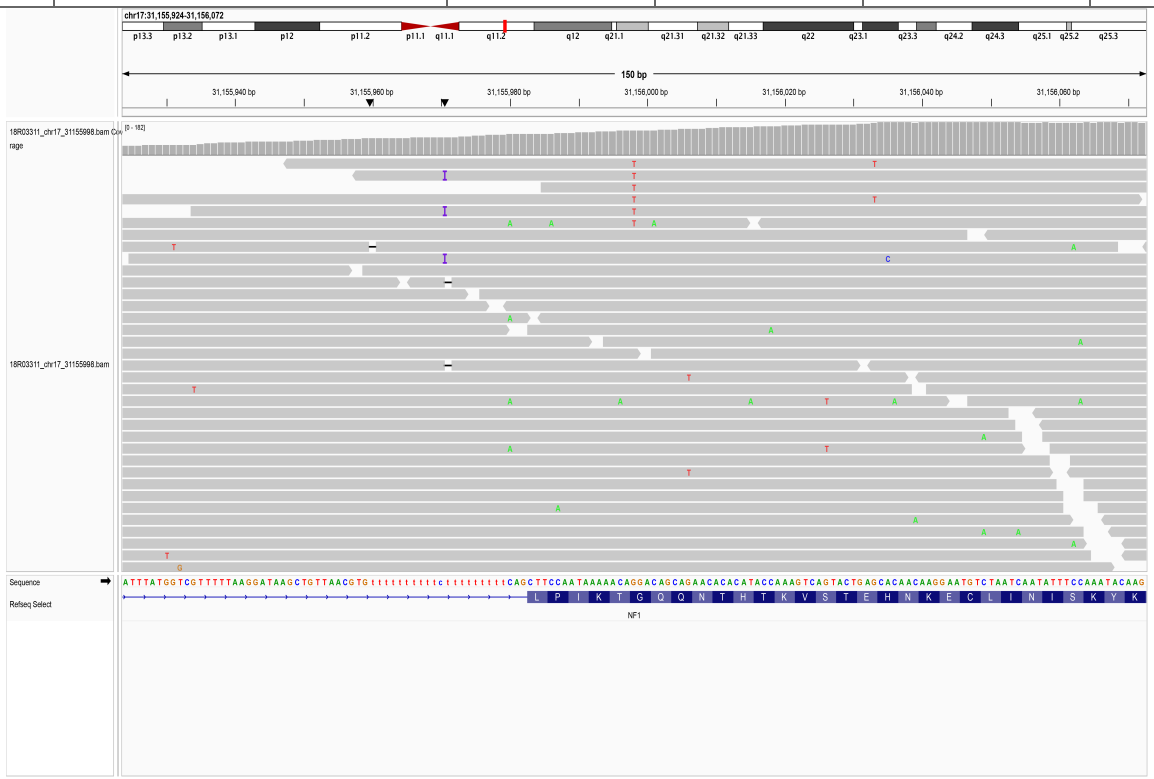
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12963	chr1_43352675_T/C	48	4	*MPL*	missense_variant



34. *NF1*

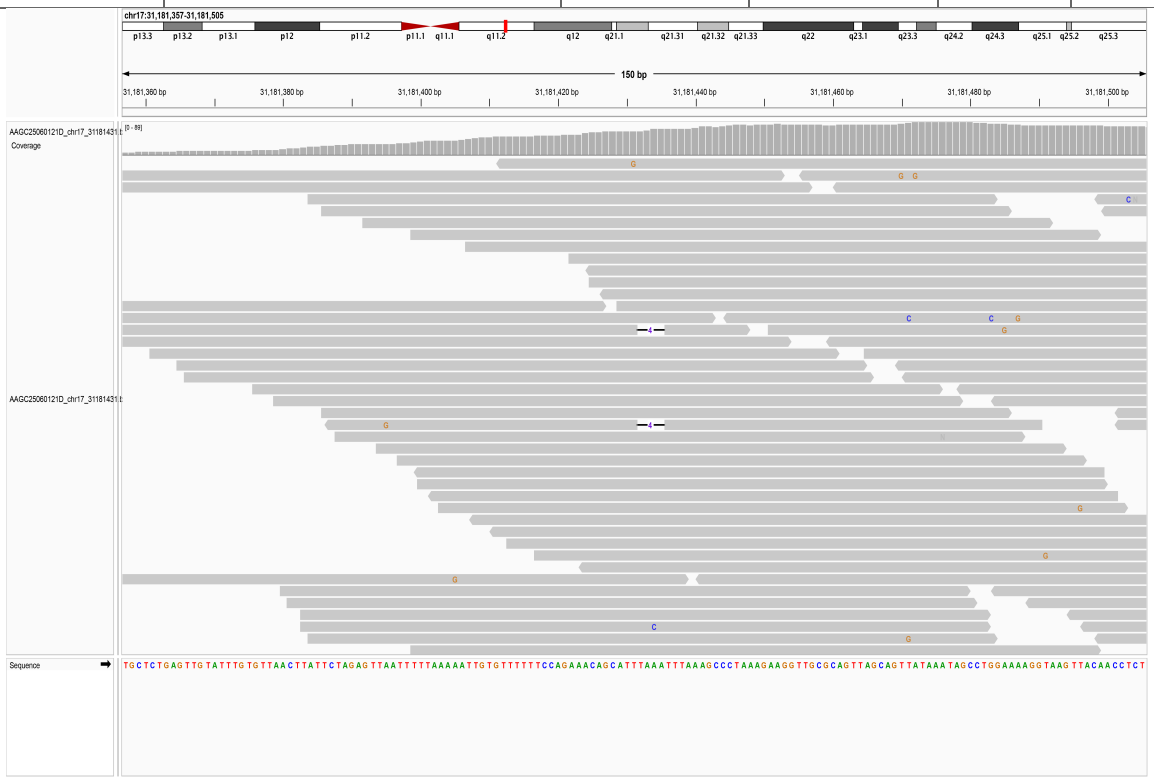
34.1. chr17_31155998_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr17_31155998_G/T	112	5	*NF1*	stop_gained



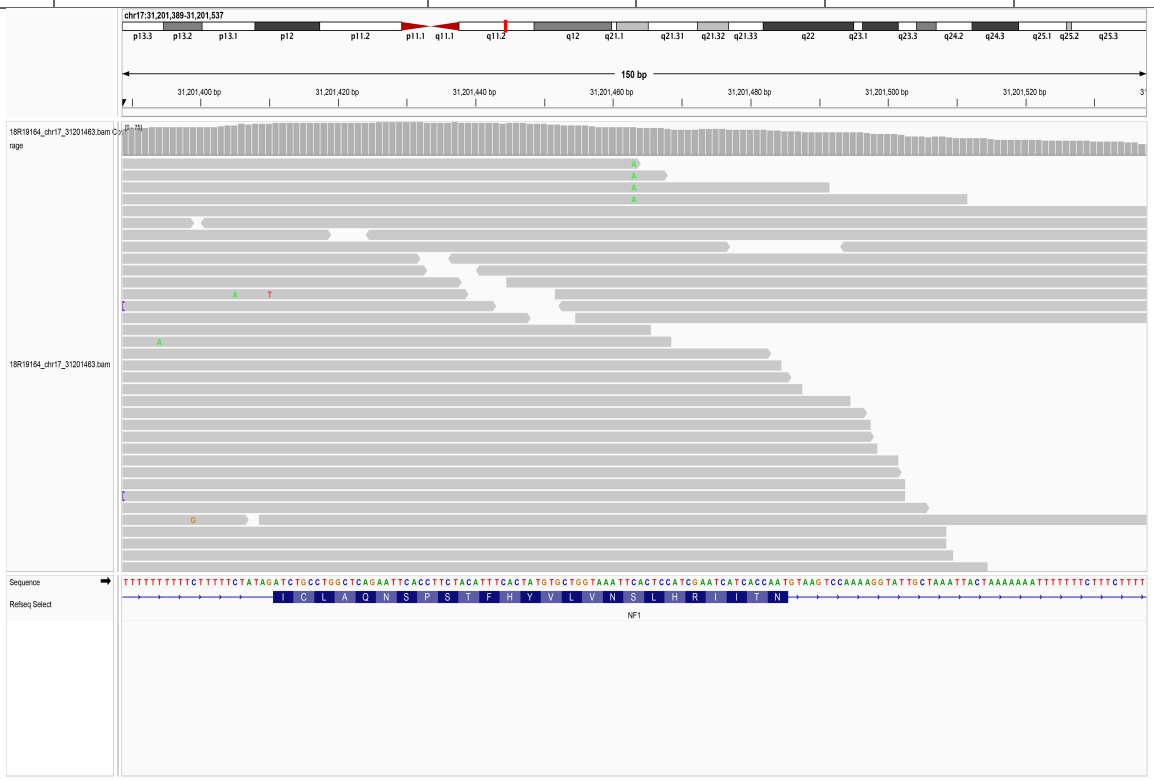
34.2. chr17_31181432_TAAA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060121D	chr17_31181432_TAAA/-	67	2	*NF1*	frameshift_variant



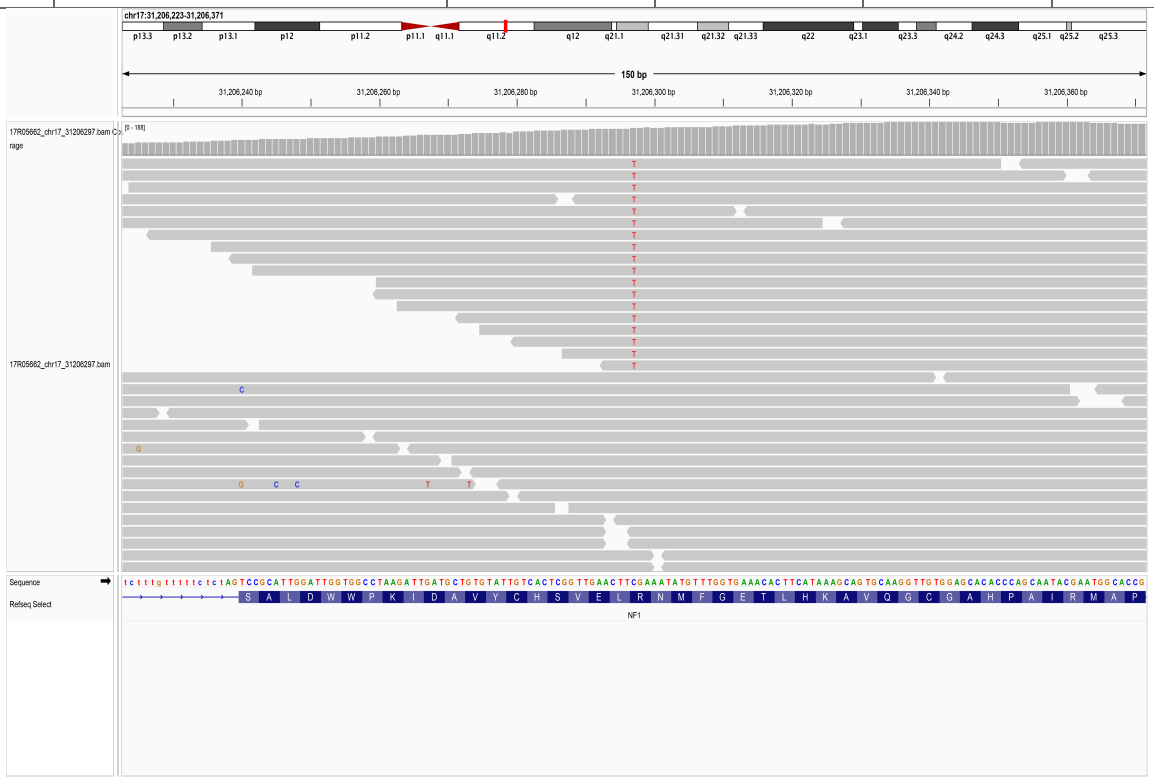
34.3. chr17_31201463_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19164	chr17_31201463_C/A	57	4	*NF1*	stop_gained



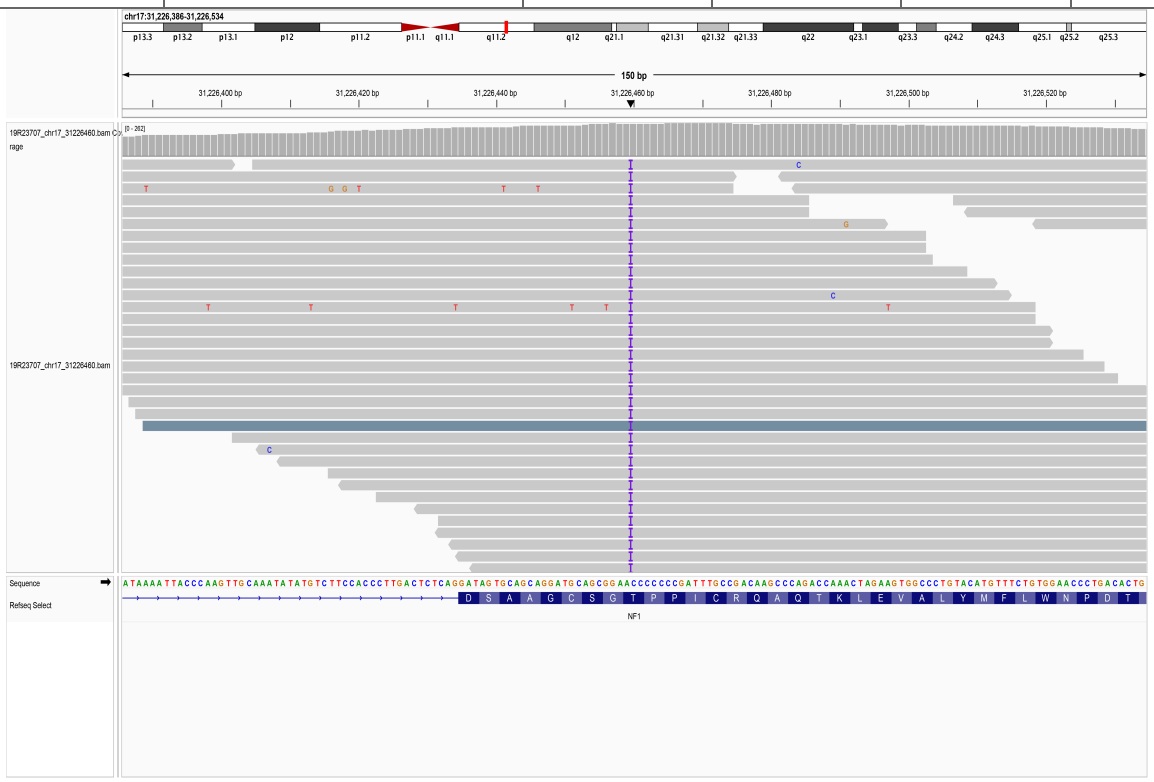
34.4. chr17_31206297_C/T

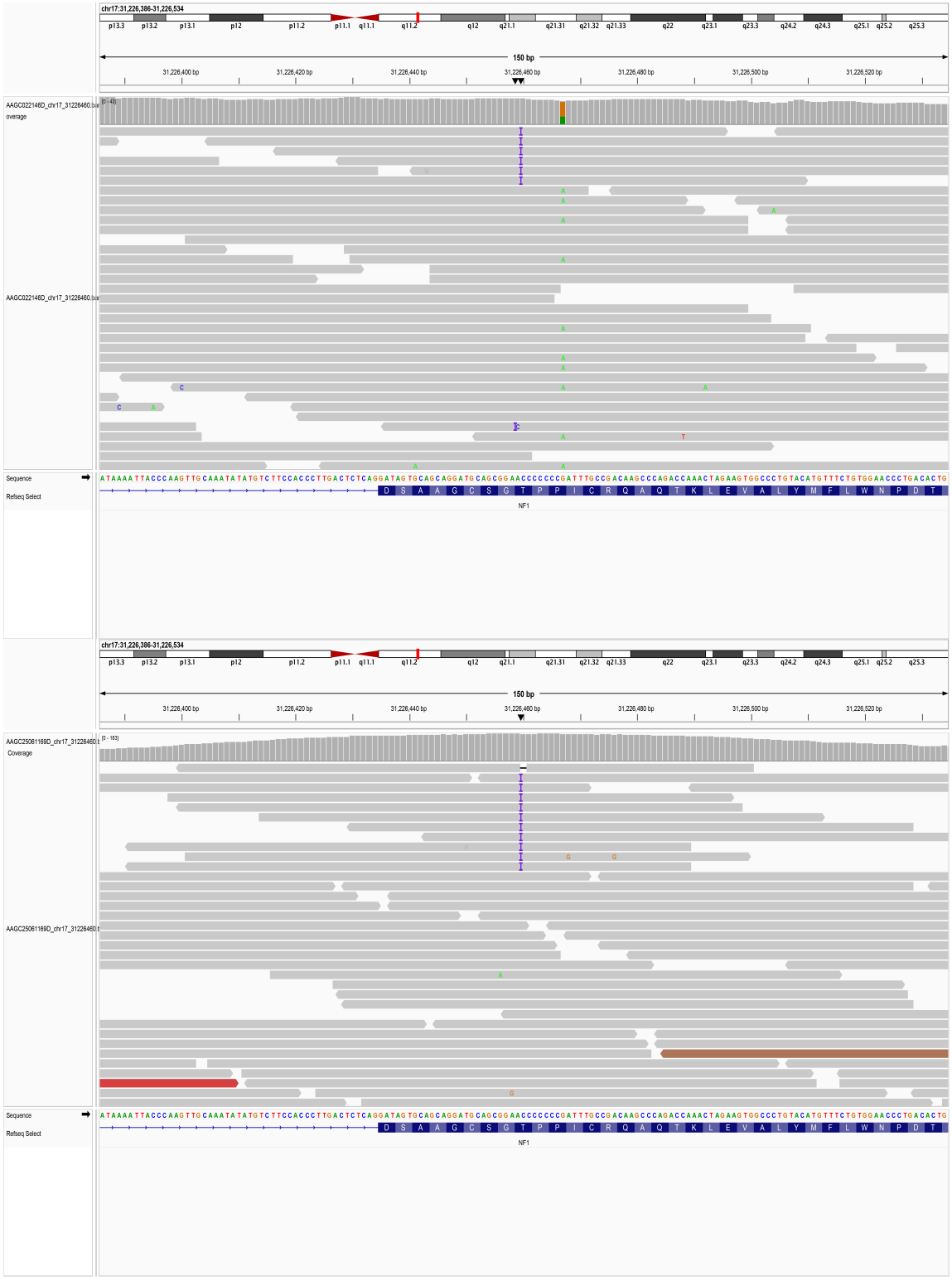
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05662	chr17_31206297_C/T	130	18	*NF1*	stop_gained

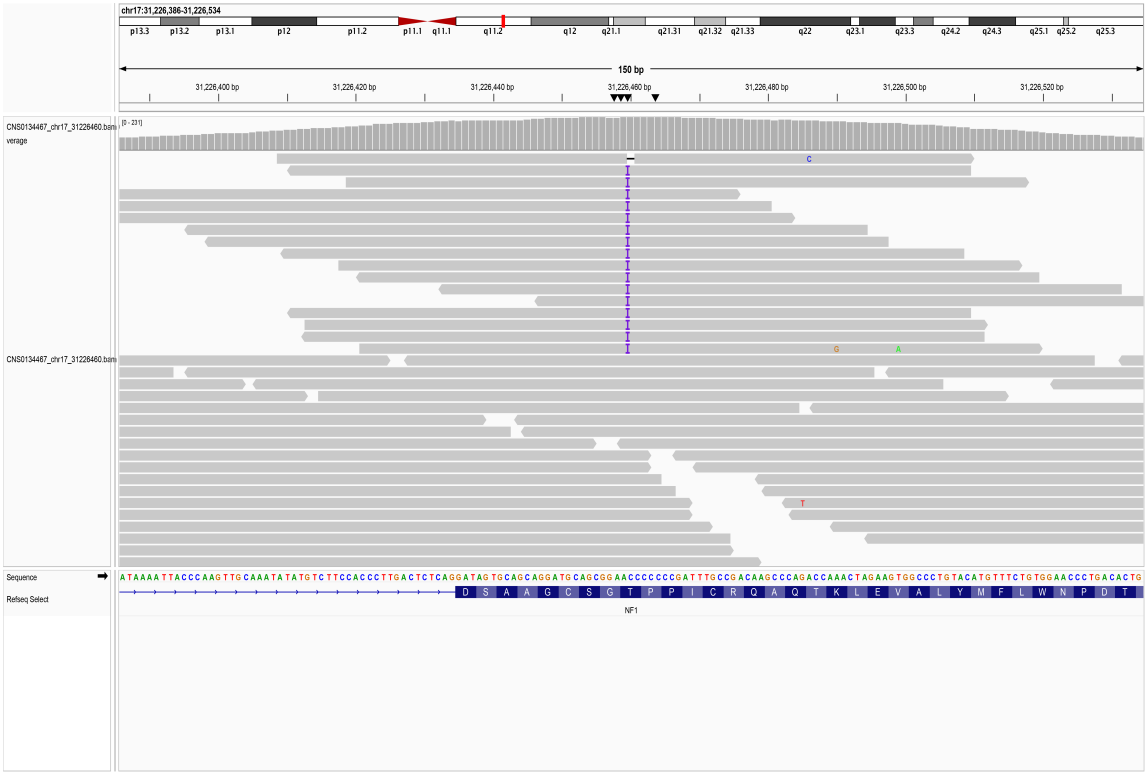


34.5. chr17_31226460_-/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23707	chr17_31226460_-/C	187	42	*NF1*	frameshift_variant
AAGC022146D	chr17_31226460_-/C	29	7	*NF1*	frameshift_variant
AAGC25061169D	chr17_31226460_-/C	153	12	*NF1*	frameshift_variant
CNS0134467	chr17_31226460_-/C	185	21	*NF1*	frameshift_variant

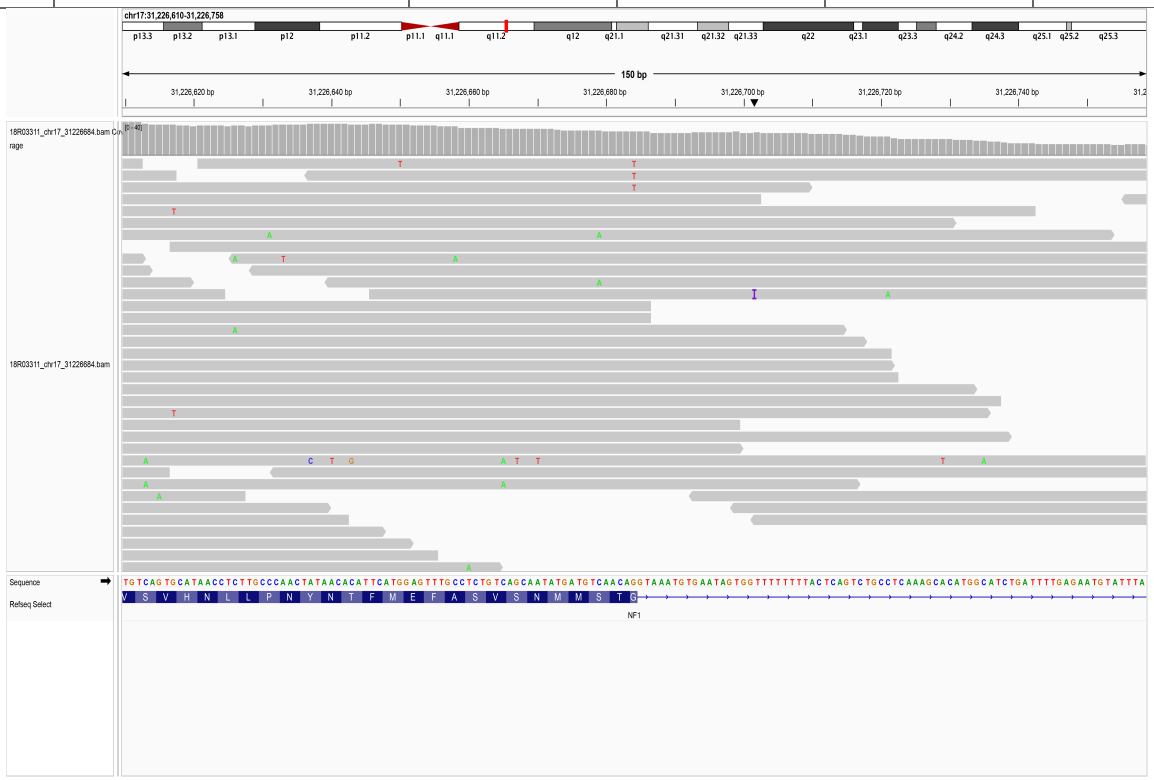



chr17:31,226,386-31,226,534
150 bp
31,226,400 bp
31,226,420 bp
31,226,440 bp
31,226,460 bp
31,226,480 bp
31,226,500 bp
31,226,520 bp
AAGC022146D_chr17_31226460.bai
overage
AAGC022146D_chr17_31226460.bai
Sequence
Refseq Select
NF1
chr17:31,226,386-31,226,534
150 bp
Coverage
Sequence
Refseq Select
NF1


chr17:31,226,386-31,226,534
p13.3 p13.2 p13.1 p12 p11.2 p11.1 q11.1 q11.2 q12 q21.1 q21.31 q21.32 q21.33 q22 q23.1 q23.3 q24.2 q24.3 q25.1 q25.2 q25.3
150 bp
31,226,400 bp
31,226,420 bp
31,226,440 bp
31,226,460 bp
31,226,480 bp
31,226,500 bp
31,226,520 bp
CNS0134467_chr17_31226460.bam
verage
CNS0134467_chr17_31226460.bam
Sequence
Refseq Select
NF1

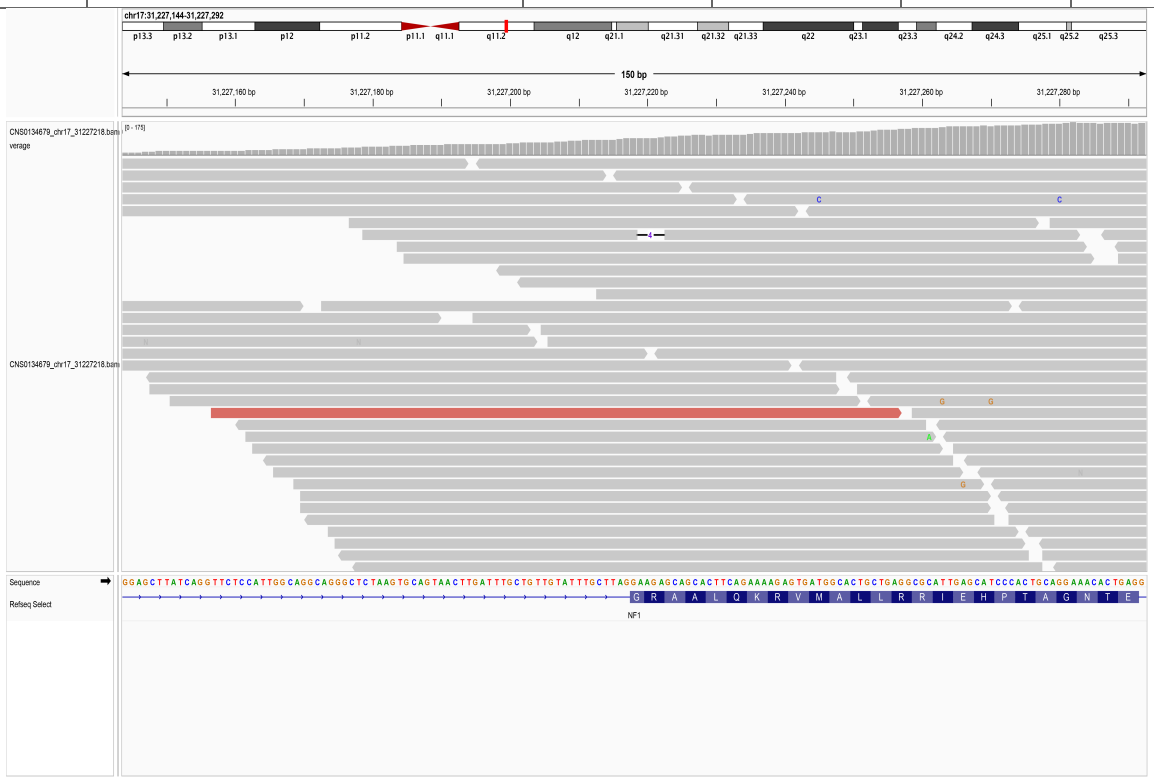
34.6. chr17_31226684_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr17_31226684_G/T	22	3	*NF1*	stop_gained



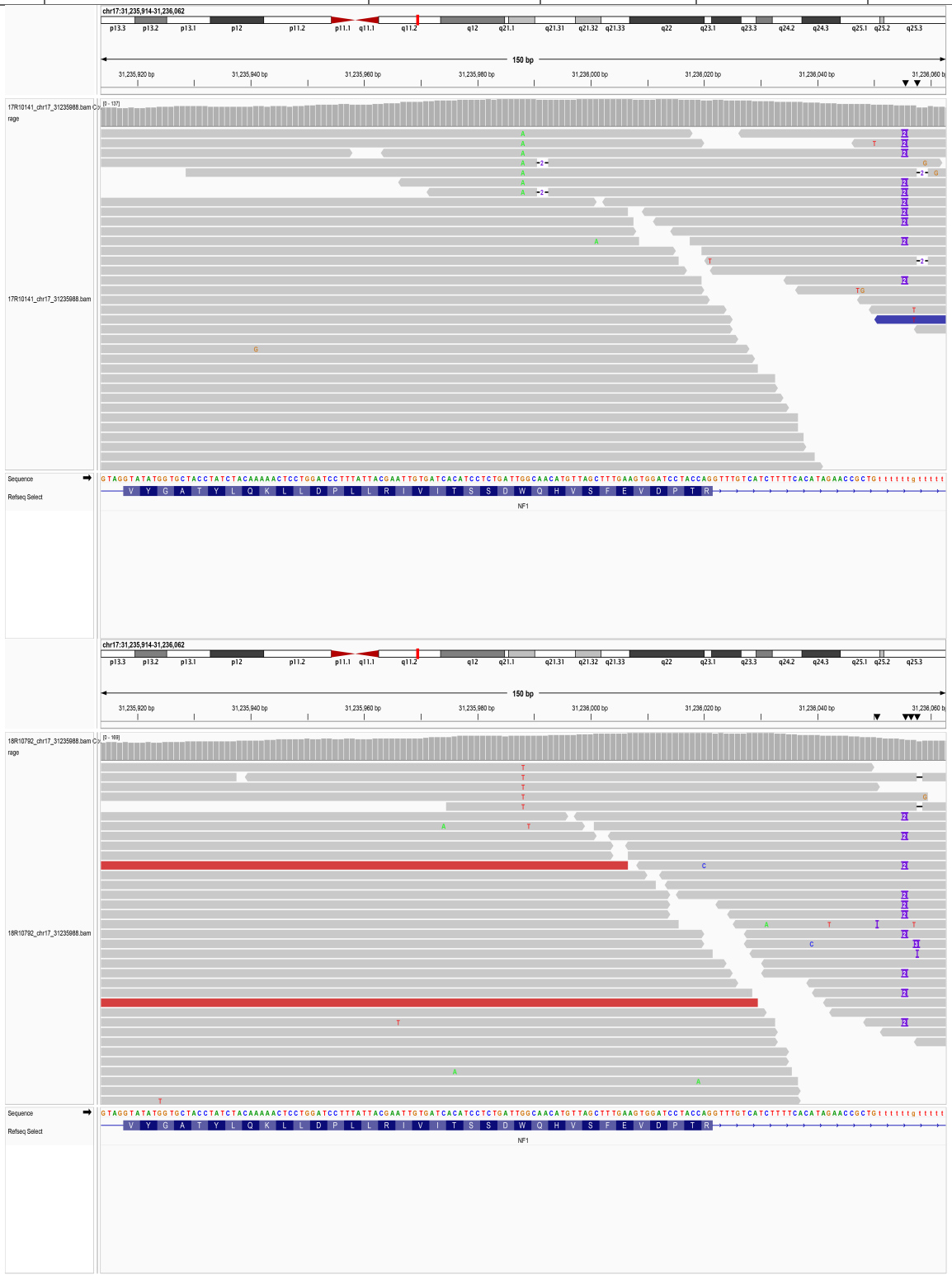
34.7. chr17_31227219_AAGA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134679	chr17_31227219_AAGA/-	95	2	*NF1*	frameshift_variant



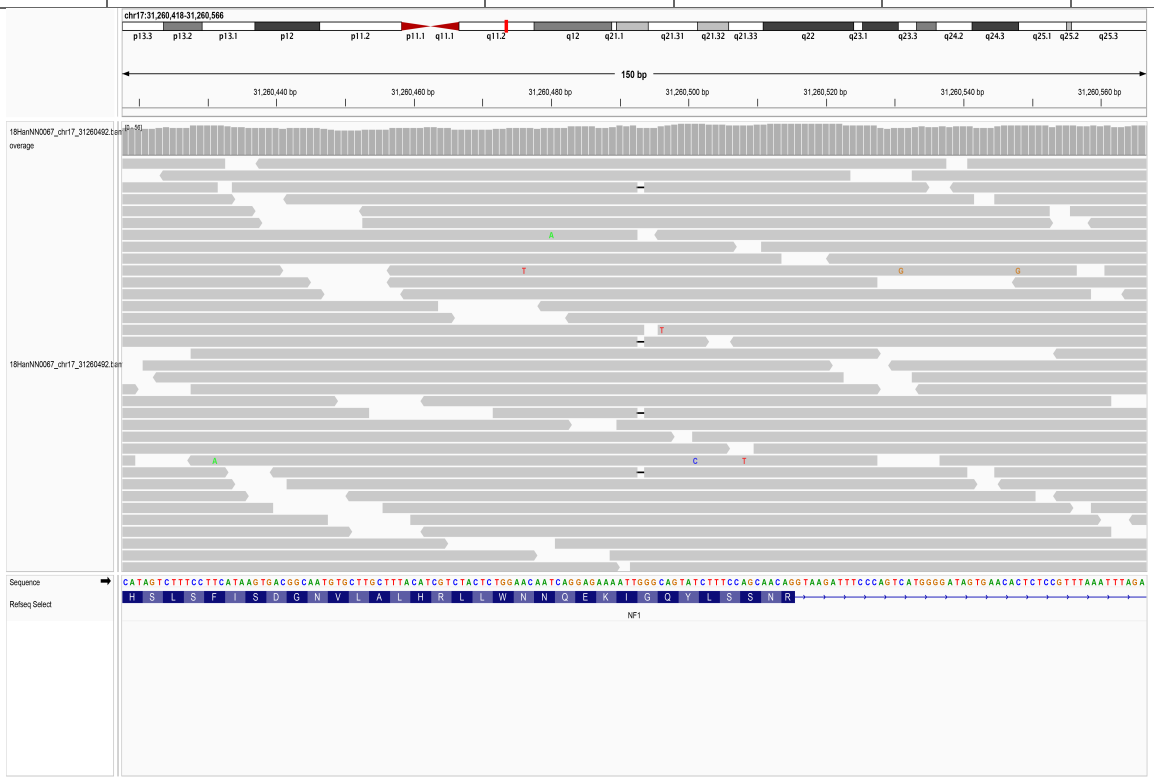
34.8. chr17_31235988_G/A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R10141	chr17_31235988_G/A/T	124	7	*NF1*	stop_gained
18R10792	chr17_31235988_G/A/T	140	5	*NF1*	stop_gained



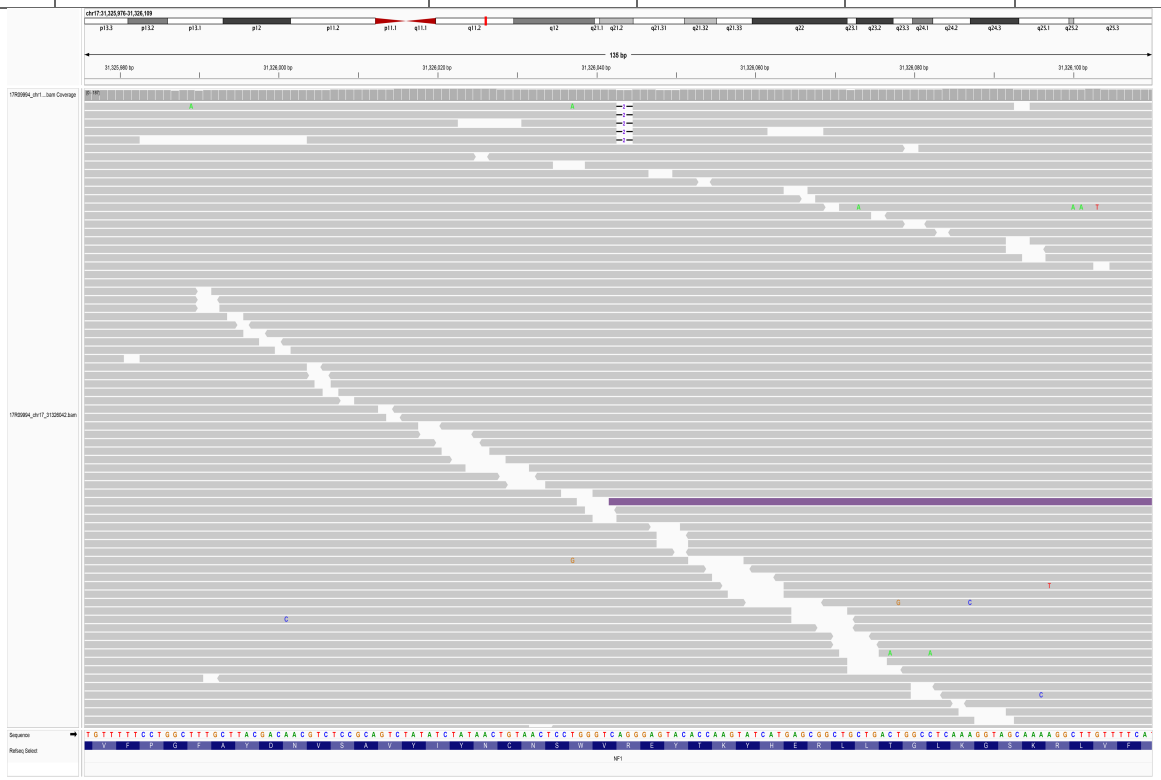
34.9. chr17_31260493_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0067	chr17_31260493_G/-	40	4	*NF1*	frameshift_variant



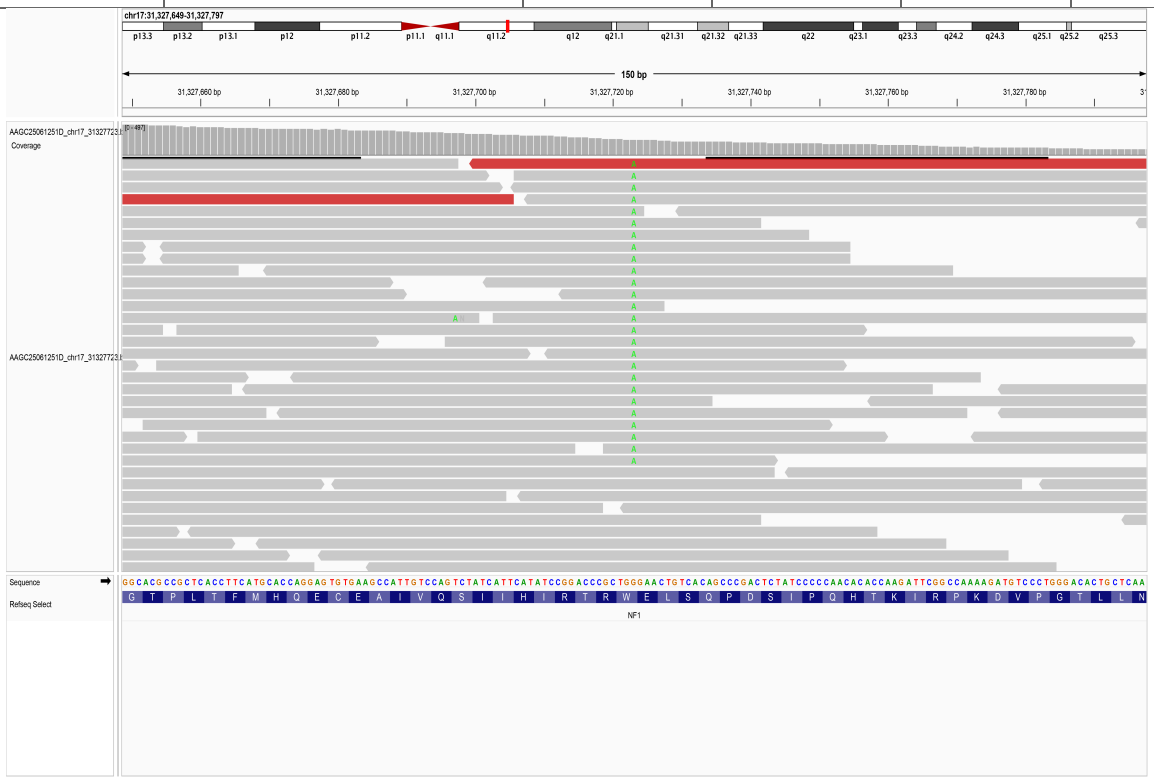
34.10. chr17_31326043_AG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09994	chr17_31326043_AG/-	162	6	*NF1*	frameshift_variant



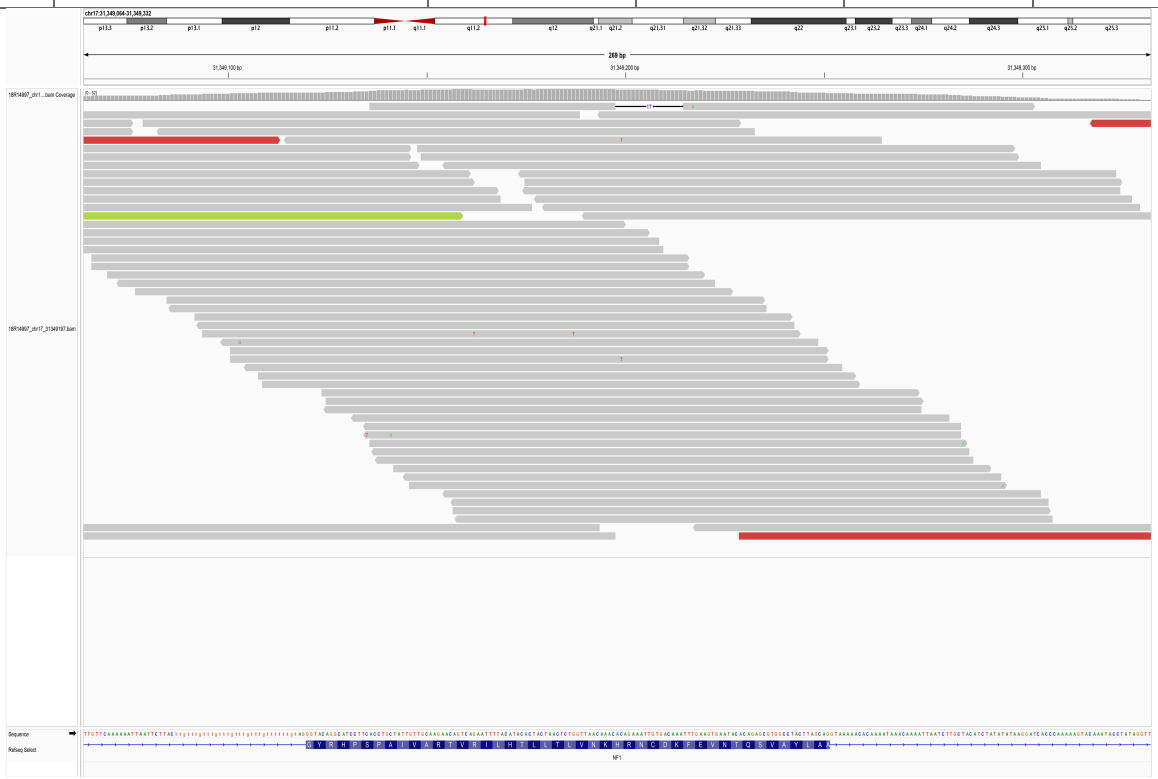
34.11. chr17_31327723_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061251D	chr17_31327723_G/A	198	29	*NF1*	stop_gained



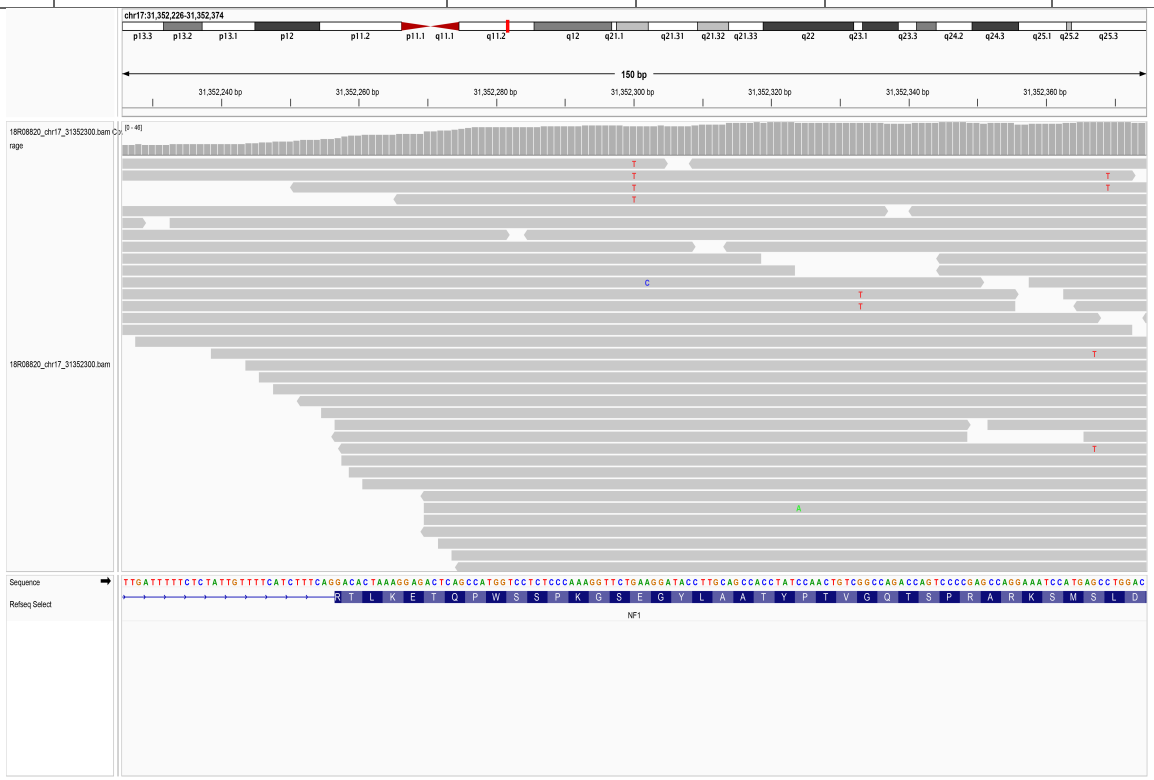
34.12. chr17_31349198_ACAGAAATTGTGACAAA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R14997	chr17_31349198_ACAGAAATTGTGACAAA/-	48	2	*NF1*	frameshift_variant



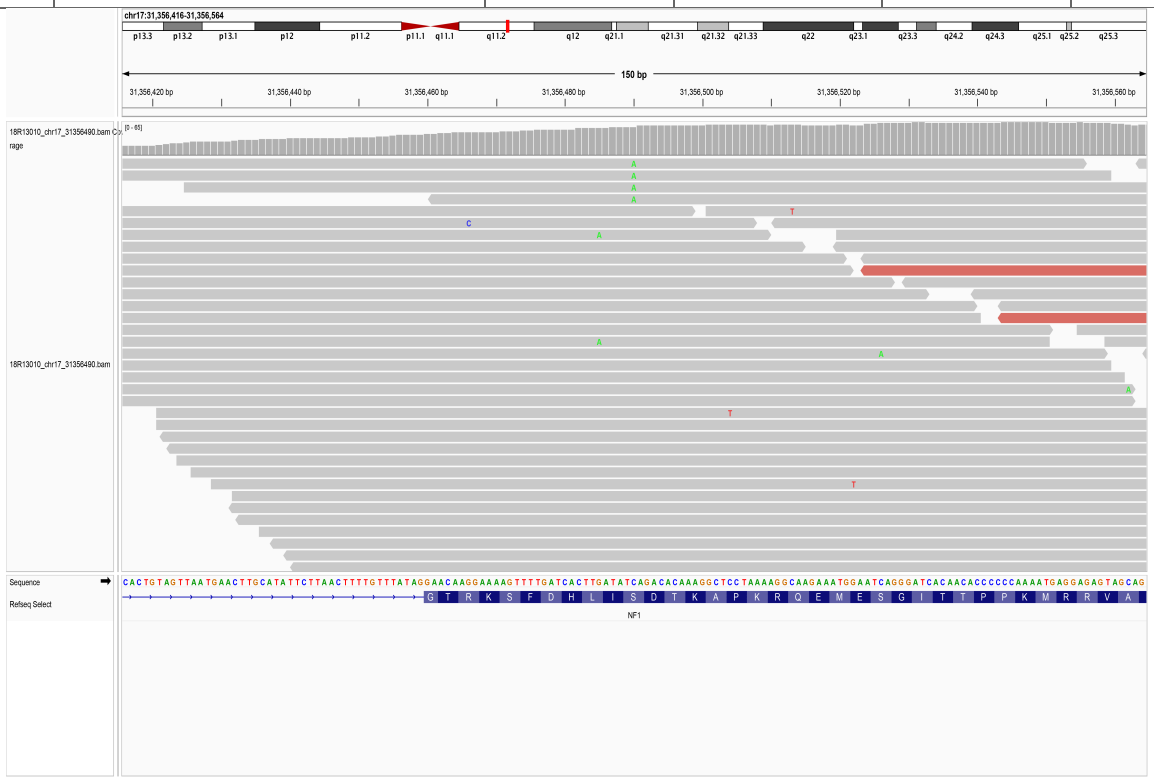
34.13. chr17_31352300_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08820	chr17_31352300_G/T	36	4	*NF1*	stop_gained



34.14. chr17_31356490_C/A

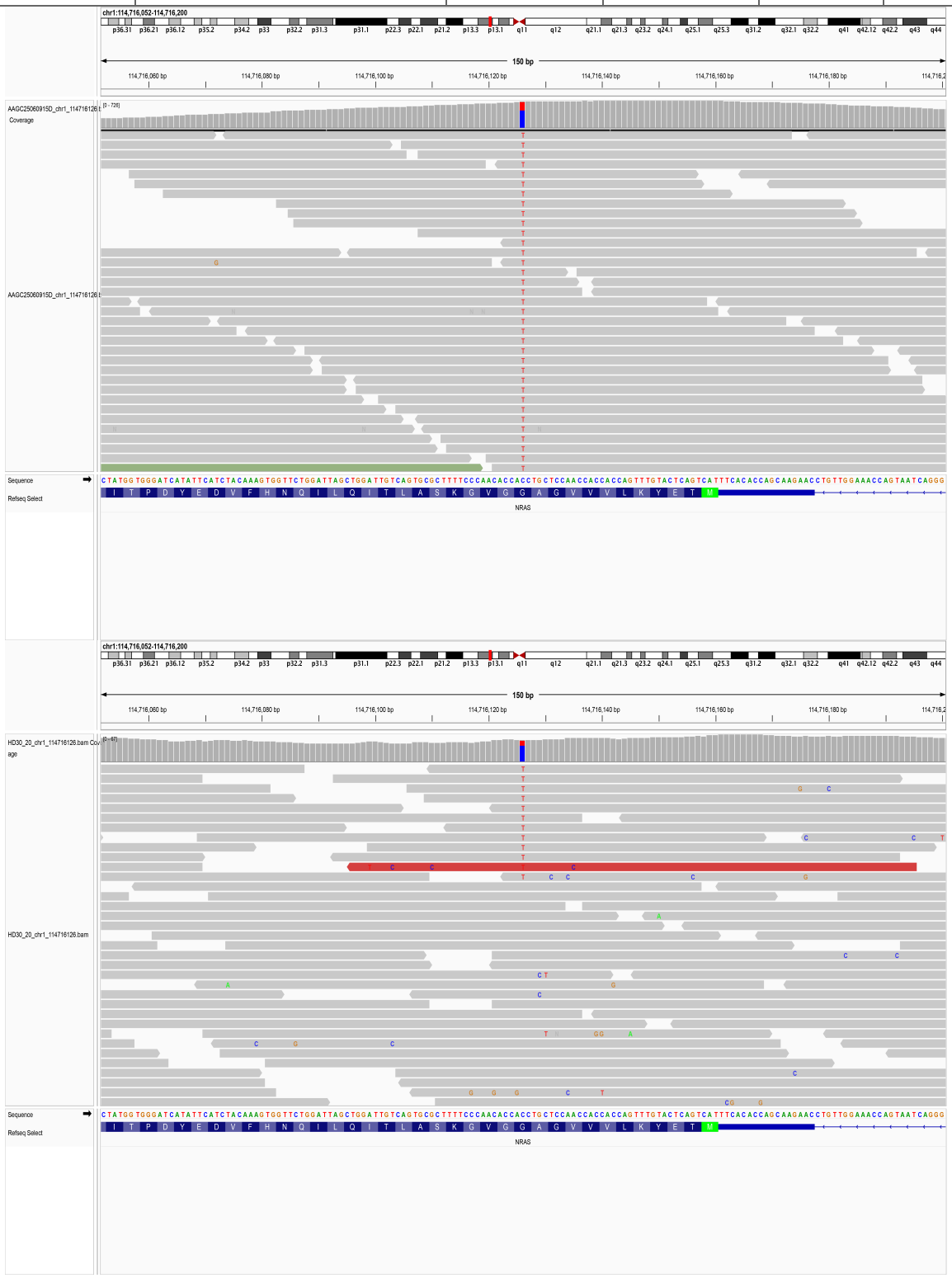
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13010	chr17_31356490_C/A	51	4	*NF1*	stop_gained



35. *NRAS*

35.1. chr1_114716126_C/T

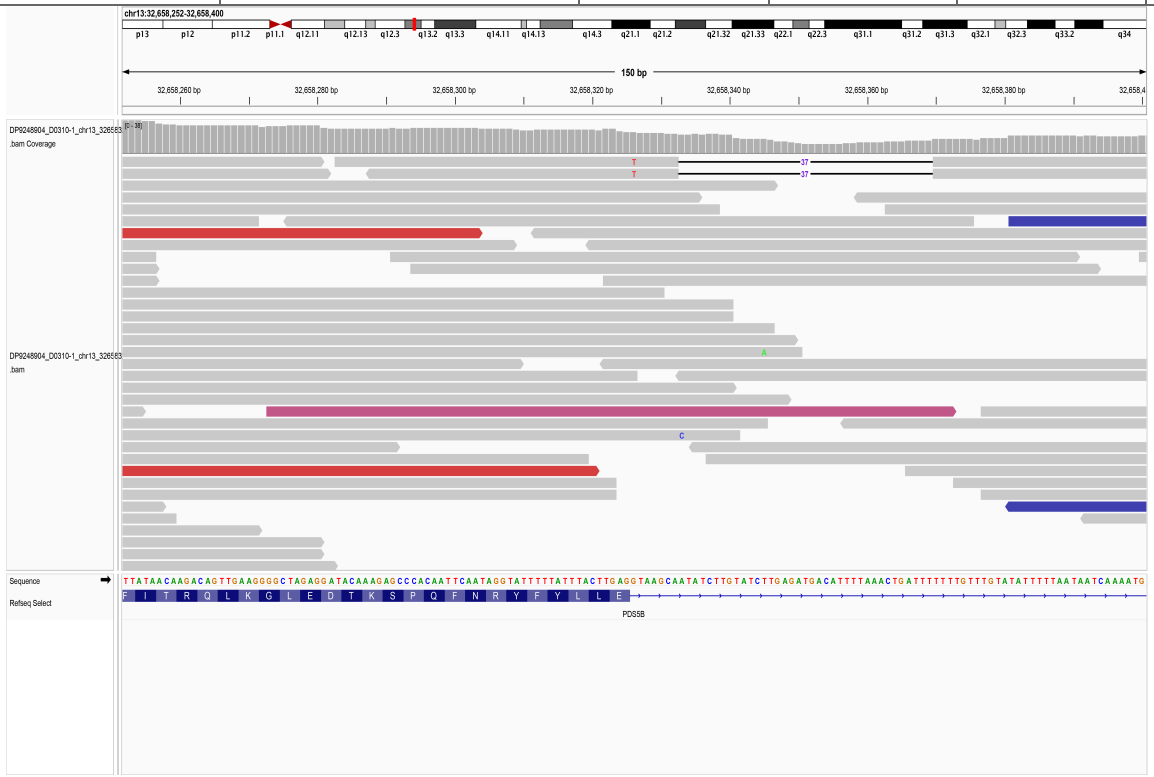
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060915D	chr1_114716126_C/T	457236	457236	*NRAS*	missense_variant
HD30_20	chr1_114716126_C/T	36	11	*NRAS*	missense_variant



36. *PDS5B*

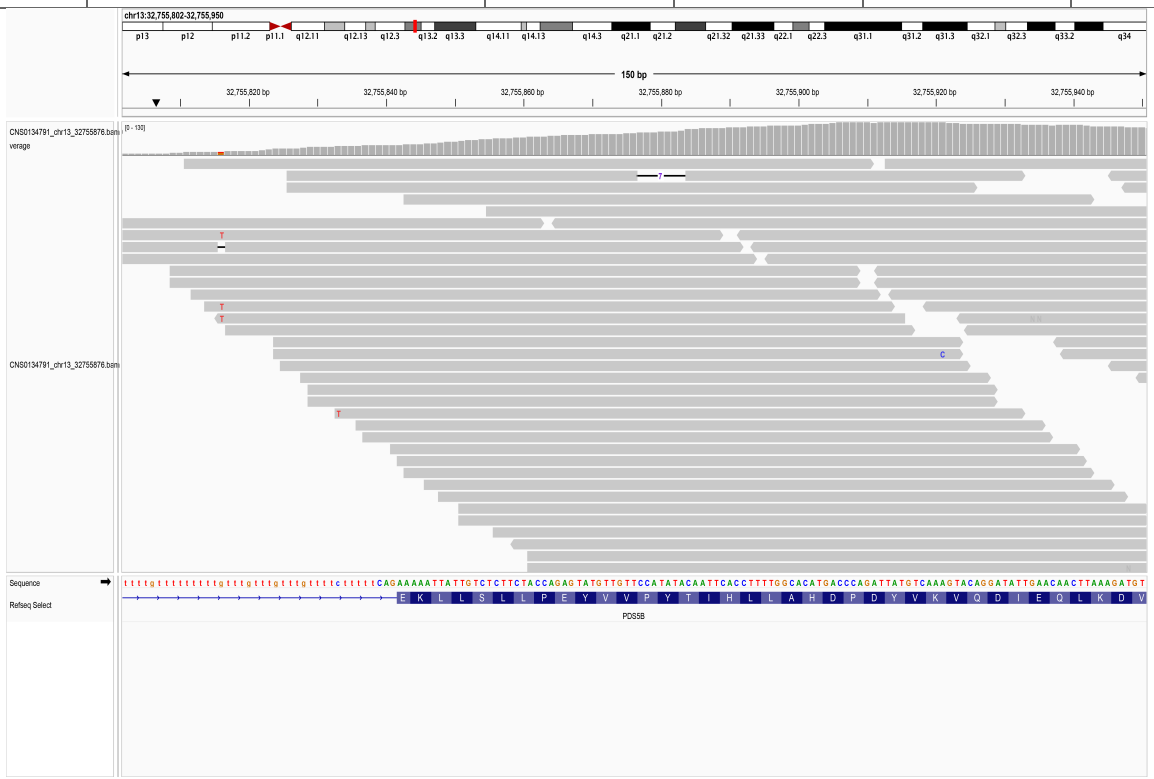
36.1. chr13_32658326_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
DP9248904_D0310-1	chr13_32658326_G/T	22	2	*PDS5B*	splice_donor_variant



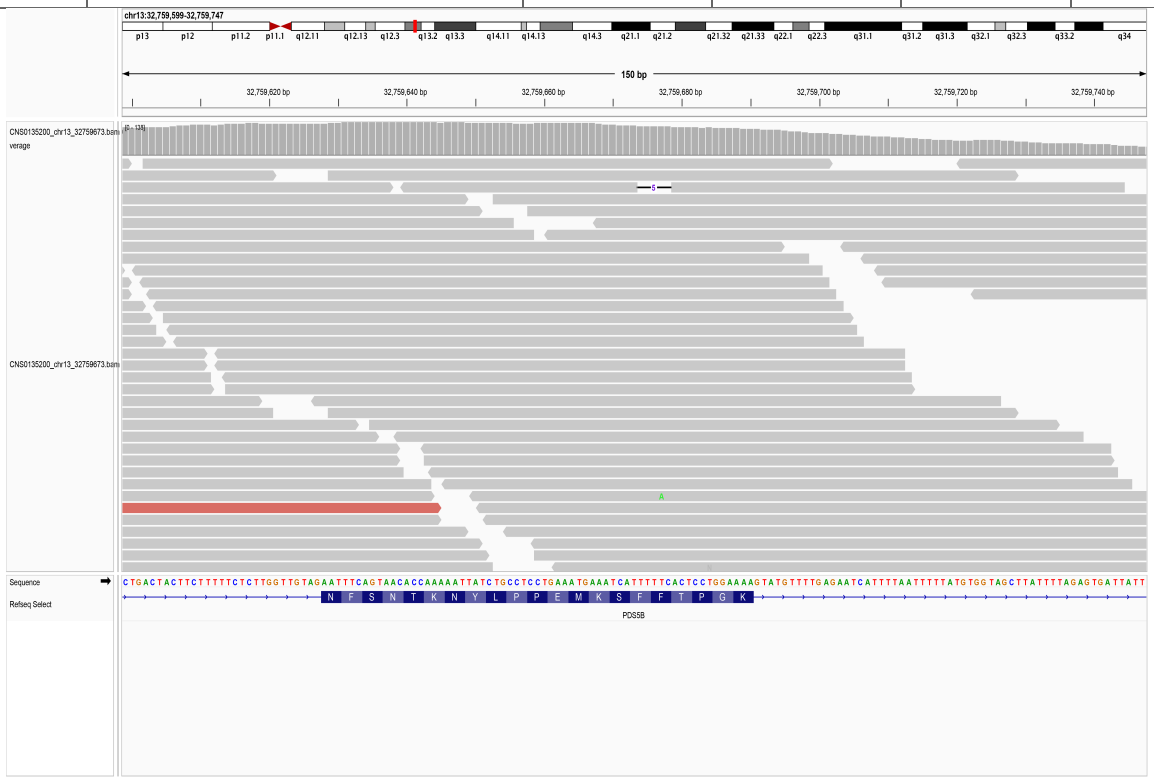
36.2. chr13_32755877_CCATATA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134791	chr13_32755877_CCATATA/-	97	2	*PDS5B*	frameshift_variant



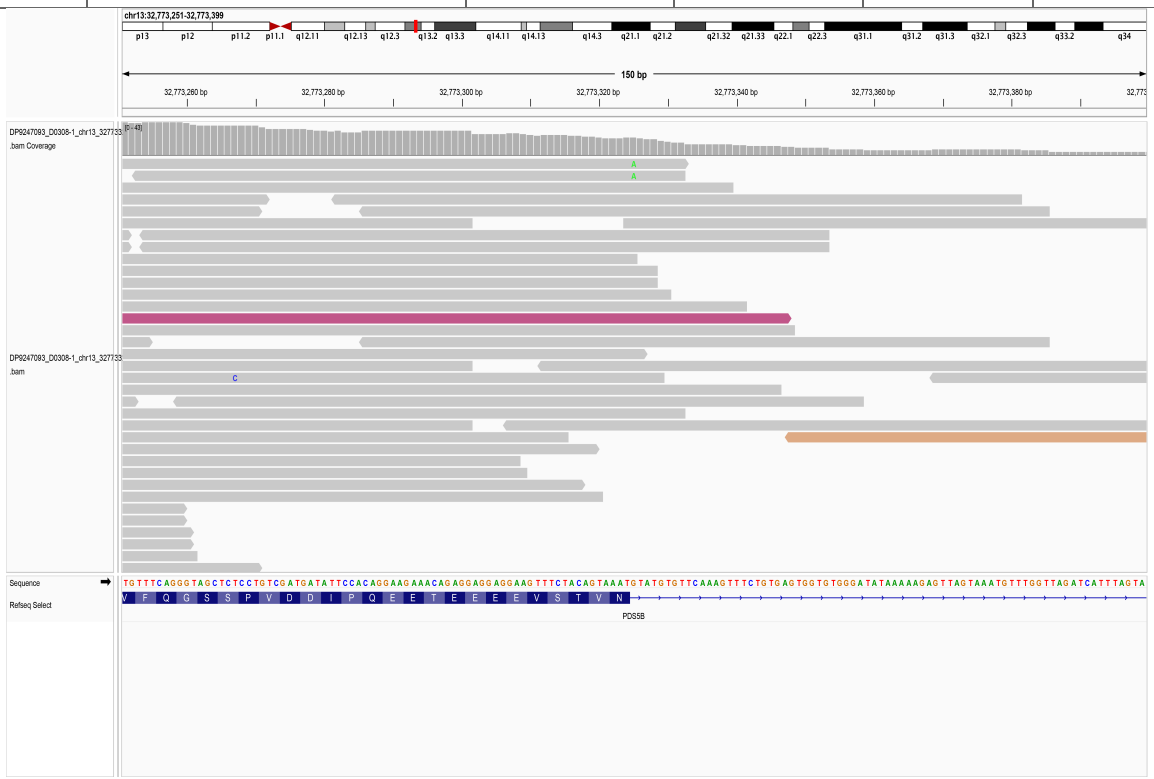
36.3. chr13_32759674_TTTTC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135200	chr13_32759674_TTTTC/-	120	2	*PDS5B*	frameshift_variant



36.4. chr13_32773325_G/A

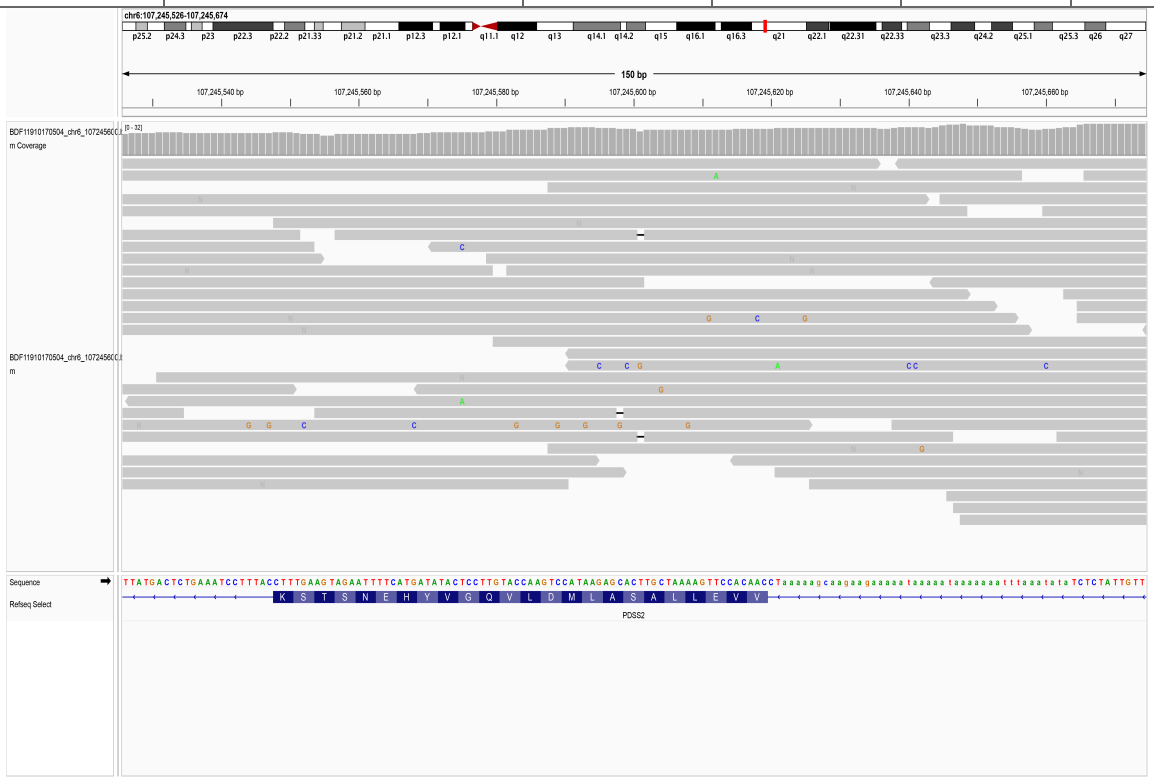
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
DP9247093_D0308-1	chr13_32773325_G/A	21	2	*PDS5B*	splice_donor_variant



37. *PDSS2*

37.1. chr6_107245601_T/-

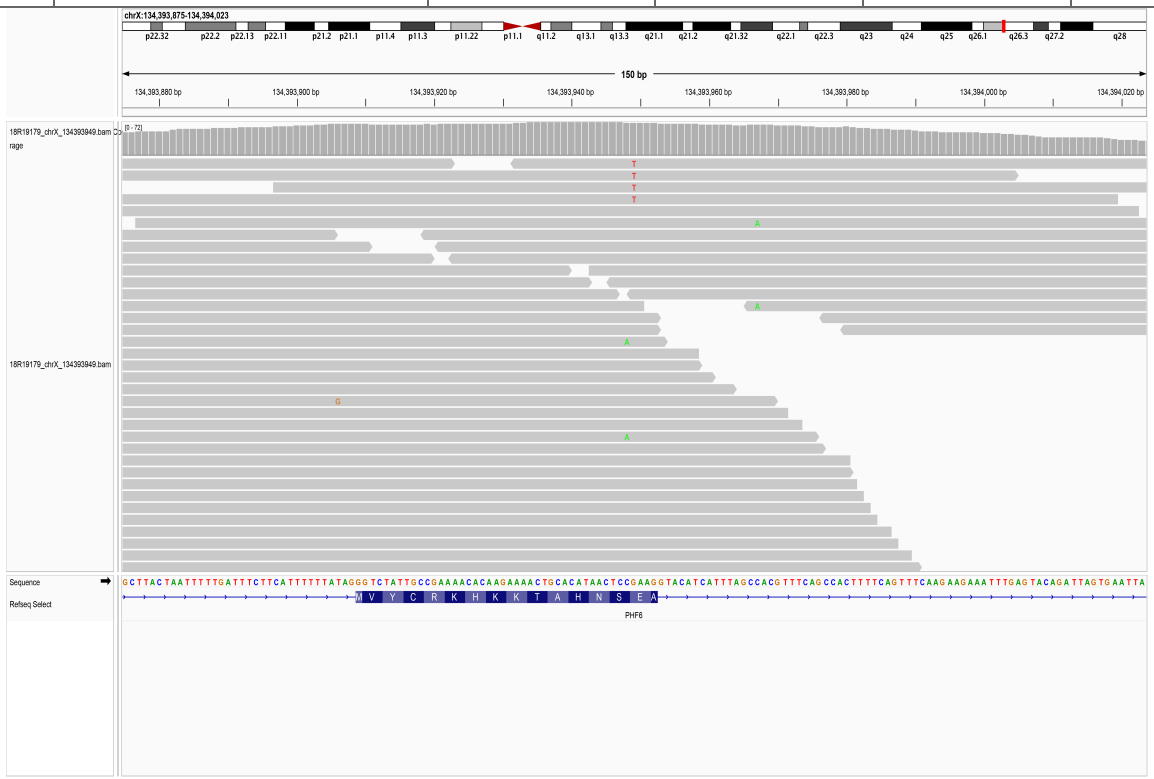
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chr6_107245601_T/-	20	2	*PDSS2*	frameshift_variant



38. *PHF6*

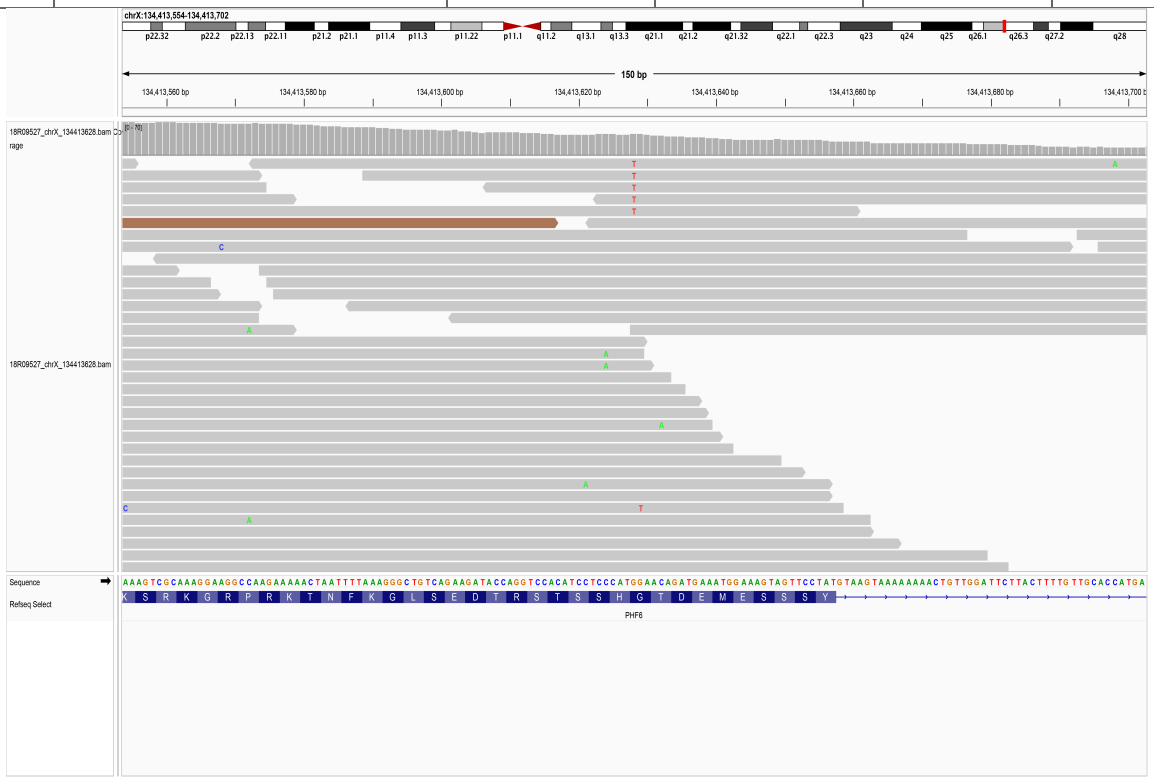
38.1. chrX_134393949_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19179	chrX_134393949_G/T	66	4	*PHF6*	stop_gained



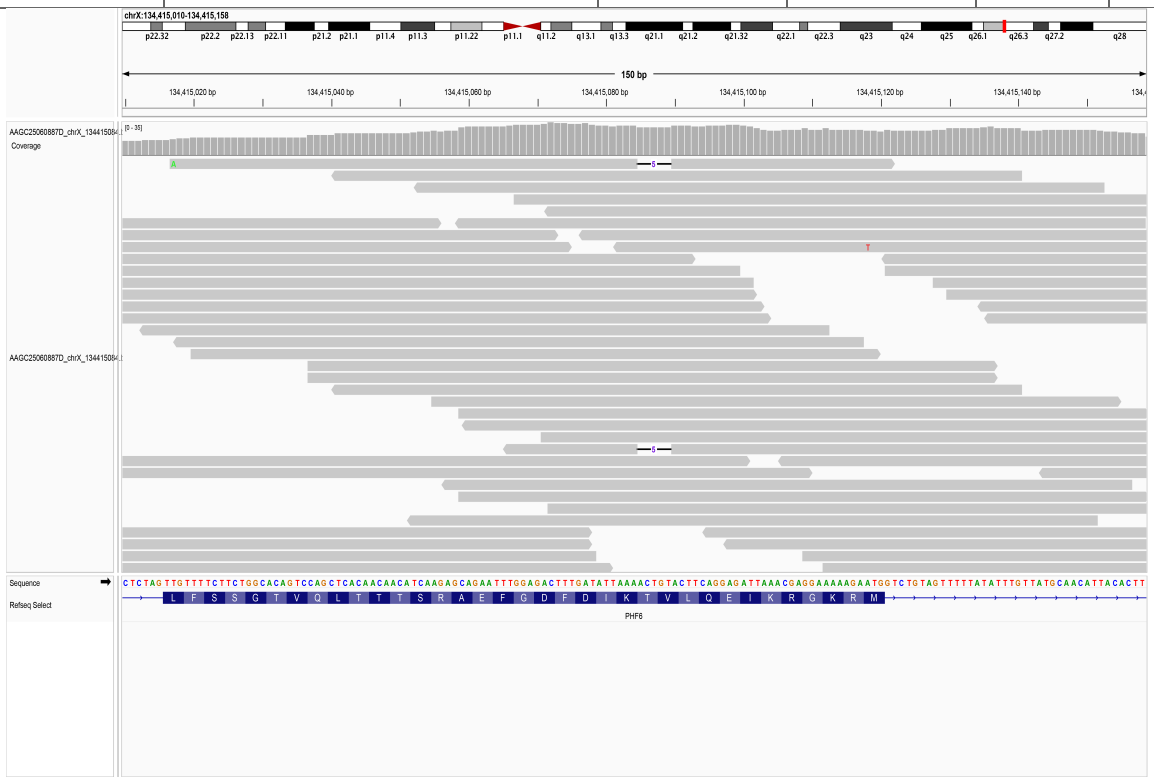
38.2. chrX_134413628_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09527	chrX_134413628_G/T	38	5	*PHF6*	stop_gained



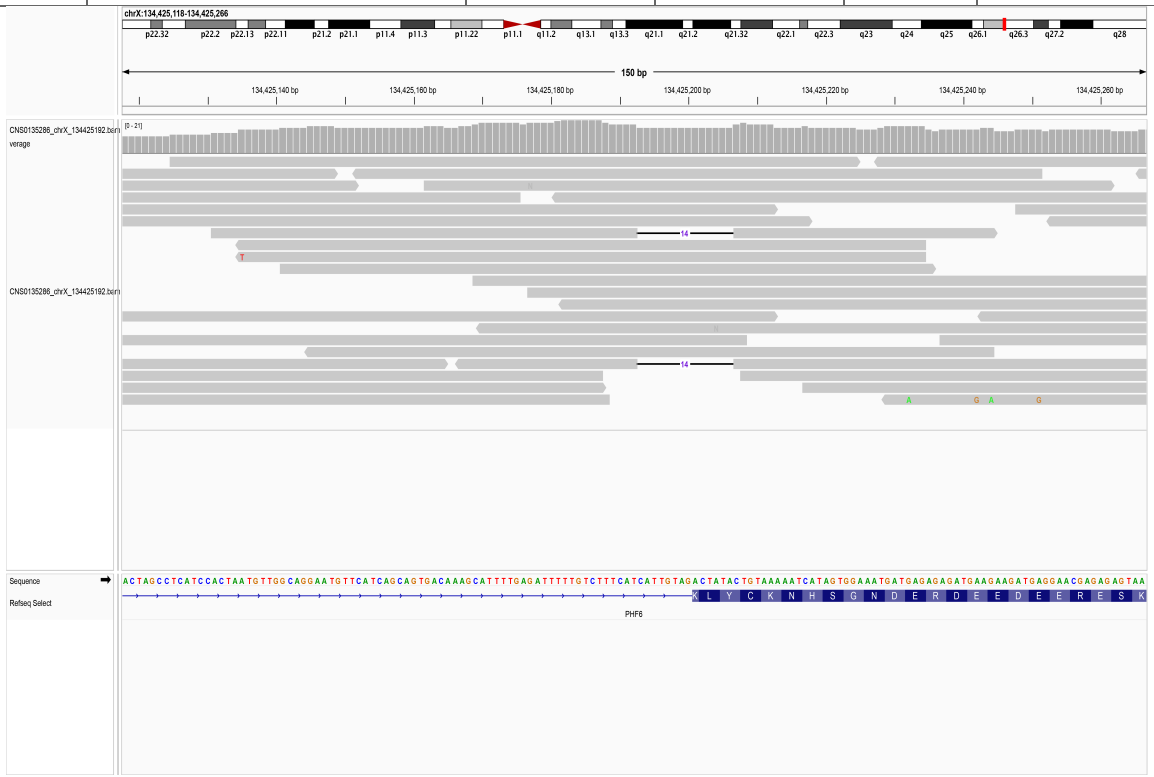
38.3. chrX_134415085_ACTGT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060887D	chrX_134415085_ACTGT/-	29	2	*PHF6*	frameshift_variant



38.4. chrX_134425193_CATTGTAGACTATA/-

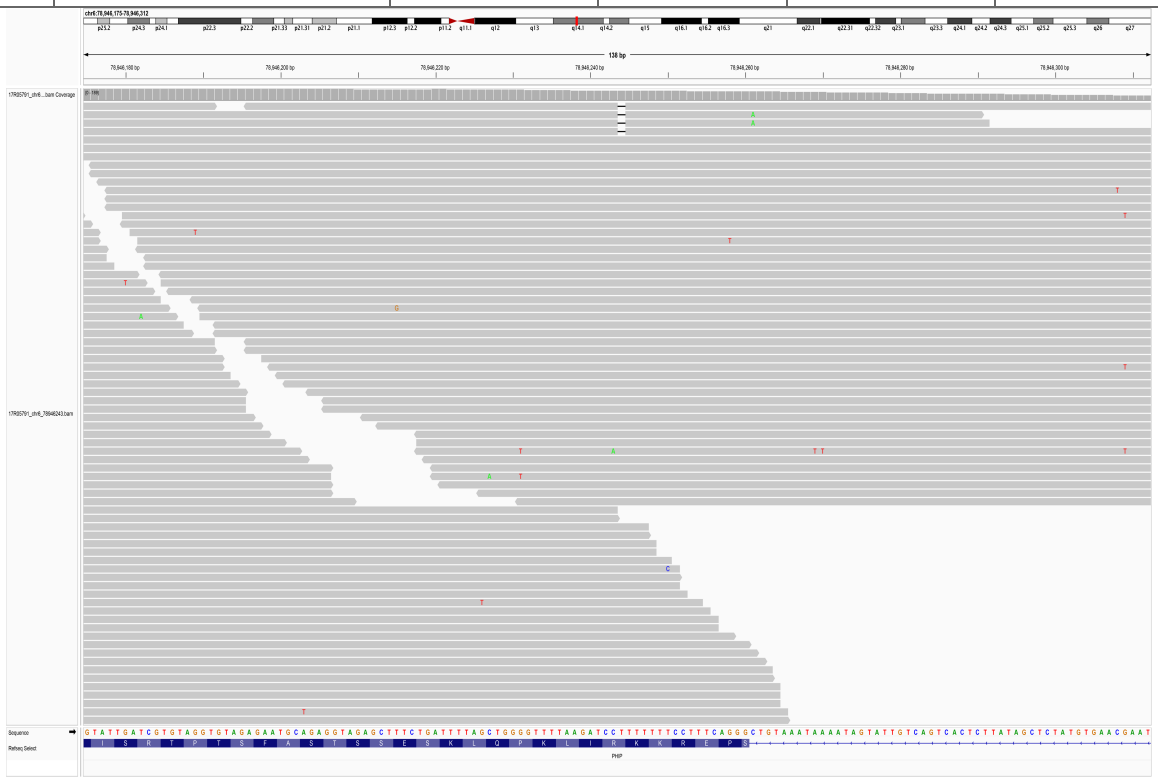
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135286	chrX_134425193_CATTGTAGACTATA/-	15	2	*PHF6*	splice_acceptor_variant



39. *PHIP*

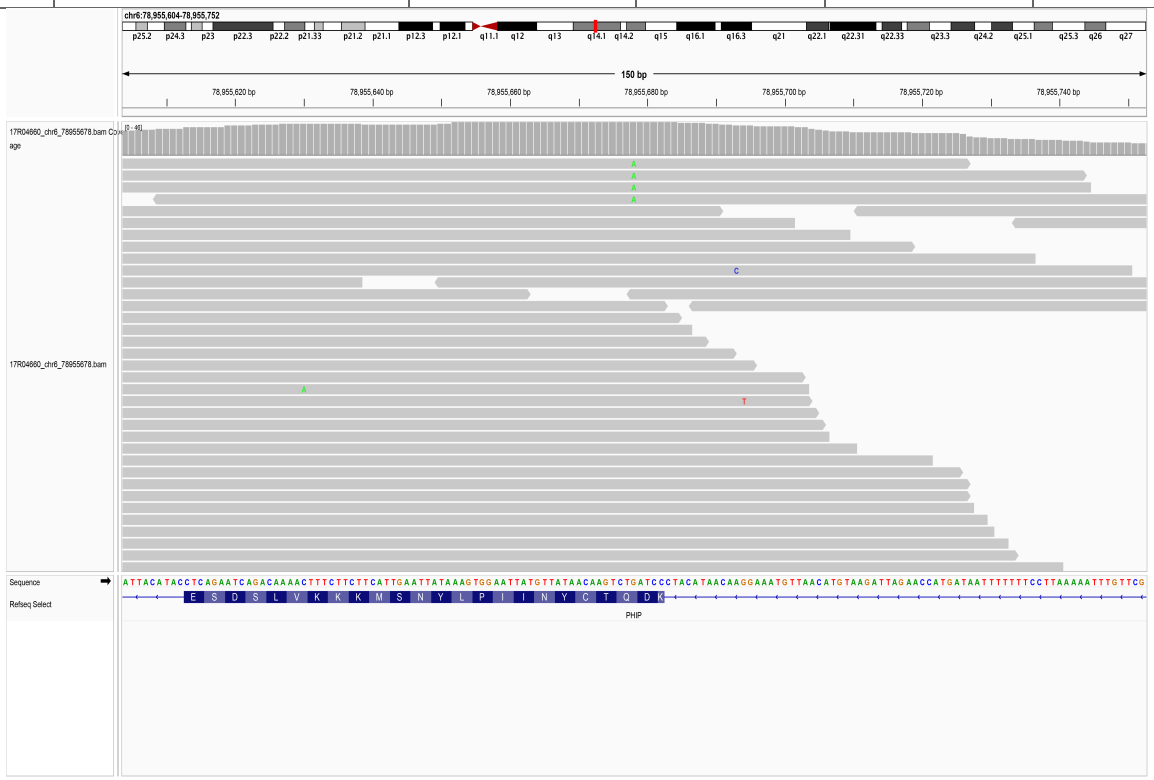
39.1. chr6_78946244_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05791	chr6_78946244_T/-	143	5	*PHIP*	frameshift_variant



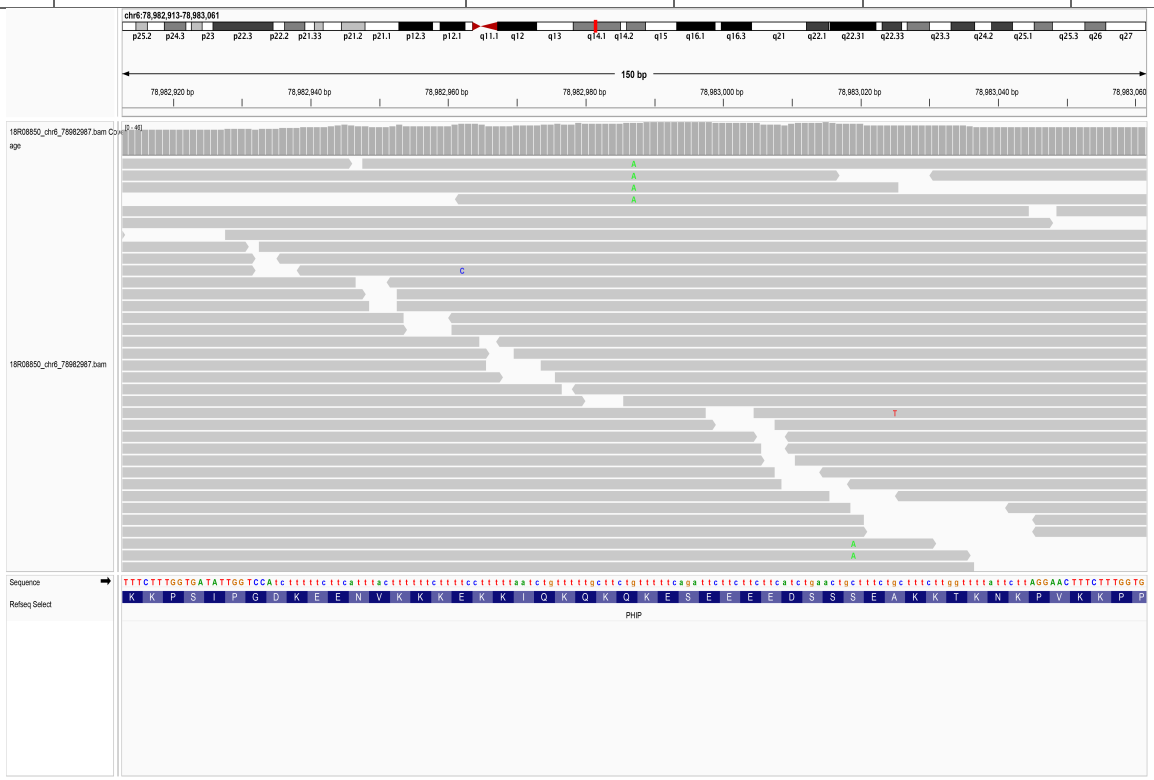
39.2. chr6_78955678_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R04660	chr6_78955678_G/A	42	4	*PHIP*	stop_gained



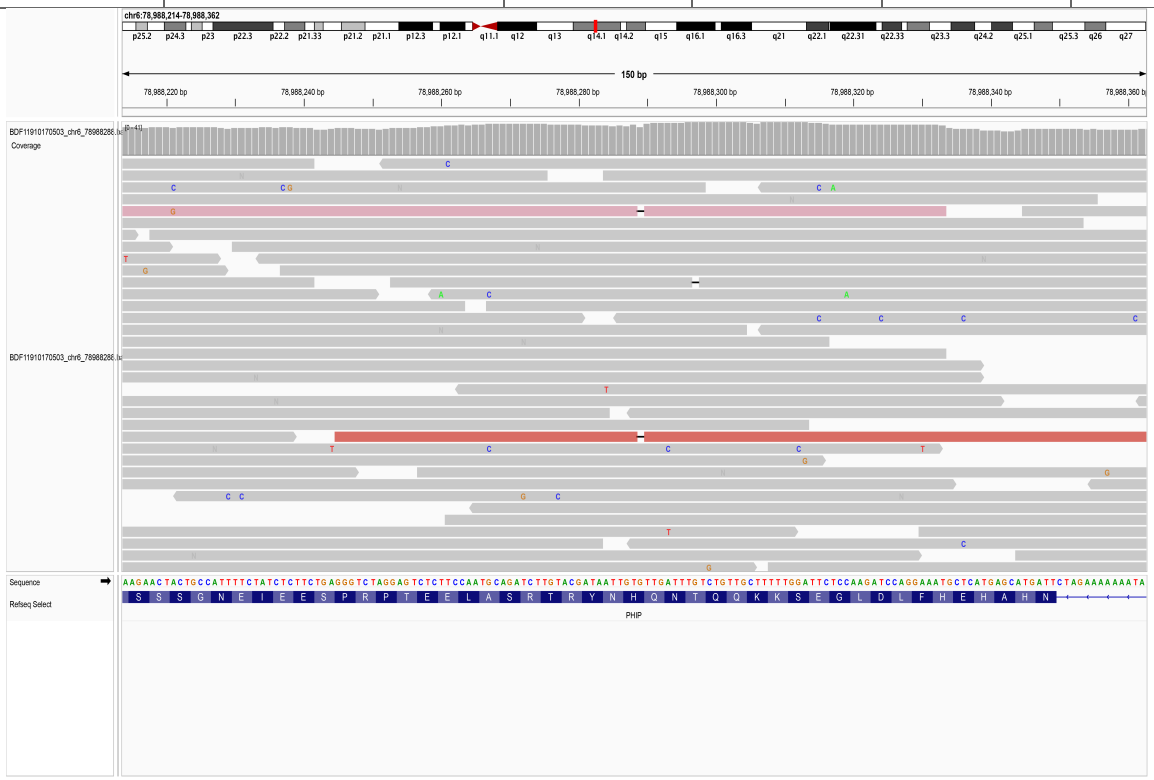
39.3. chr6_78982987_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08850	chr6_78982987_G/A	40	4	*PHIP*	stop_gained



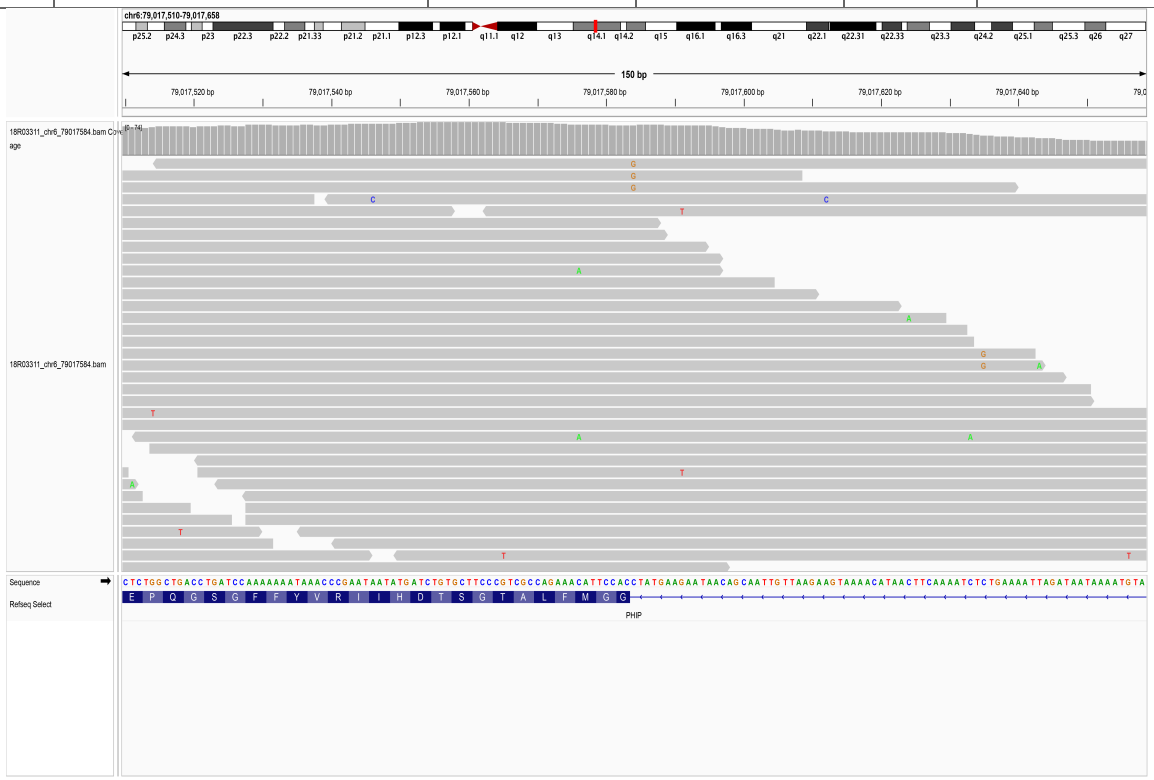
39.4. chr6_78988289_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr6_78988289_G/-	31	3	*PHIP*	frameshift_variant



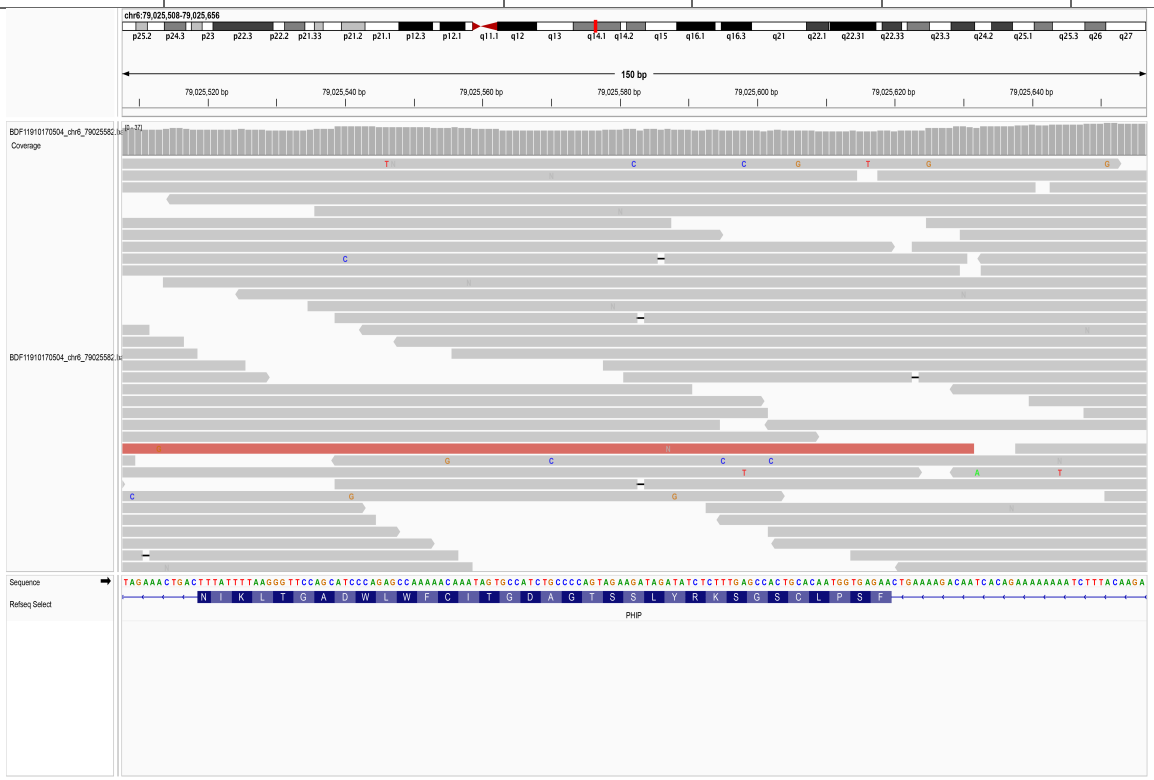
39.5. chr6_79017584_C/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr6_79017584_C/G	62	3	*PHIP*	splice_acceptor_variant



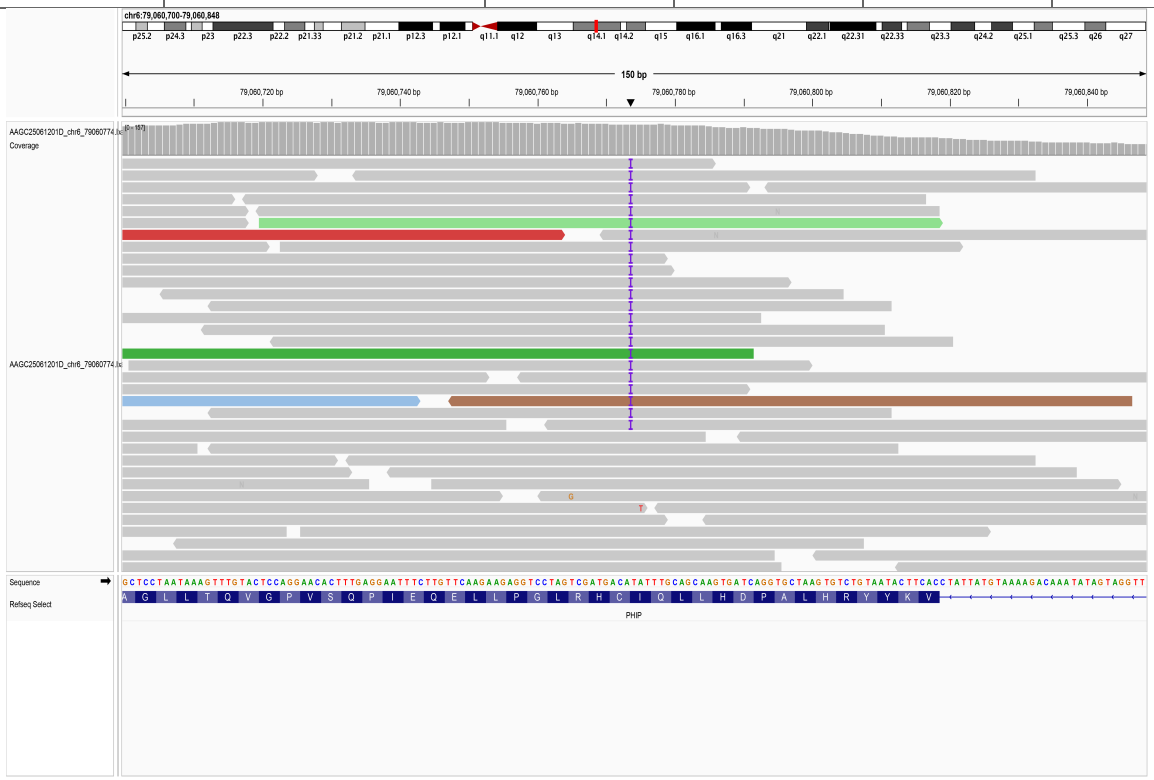
39.6. chr6_79025583_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chr6_79025583_A/-	24	2	*PHIP*	frameshift_variant



39.7. chr6_79060774_-/T

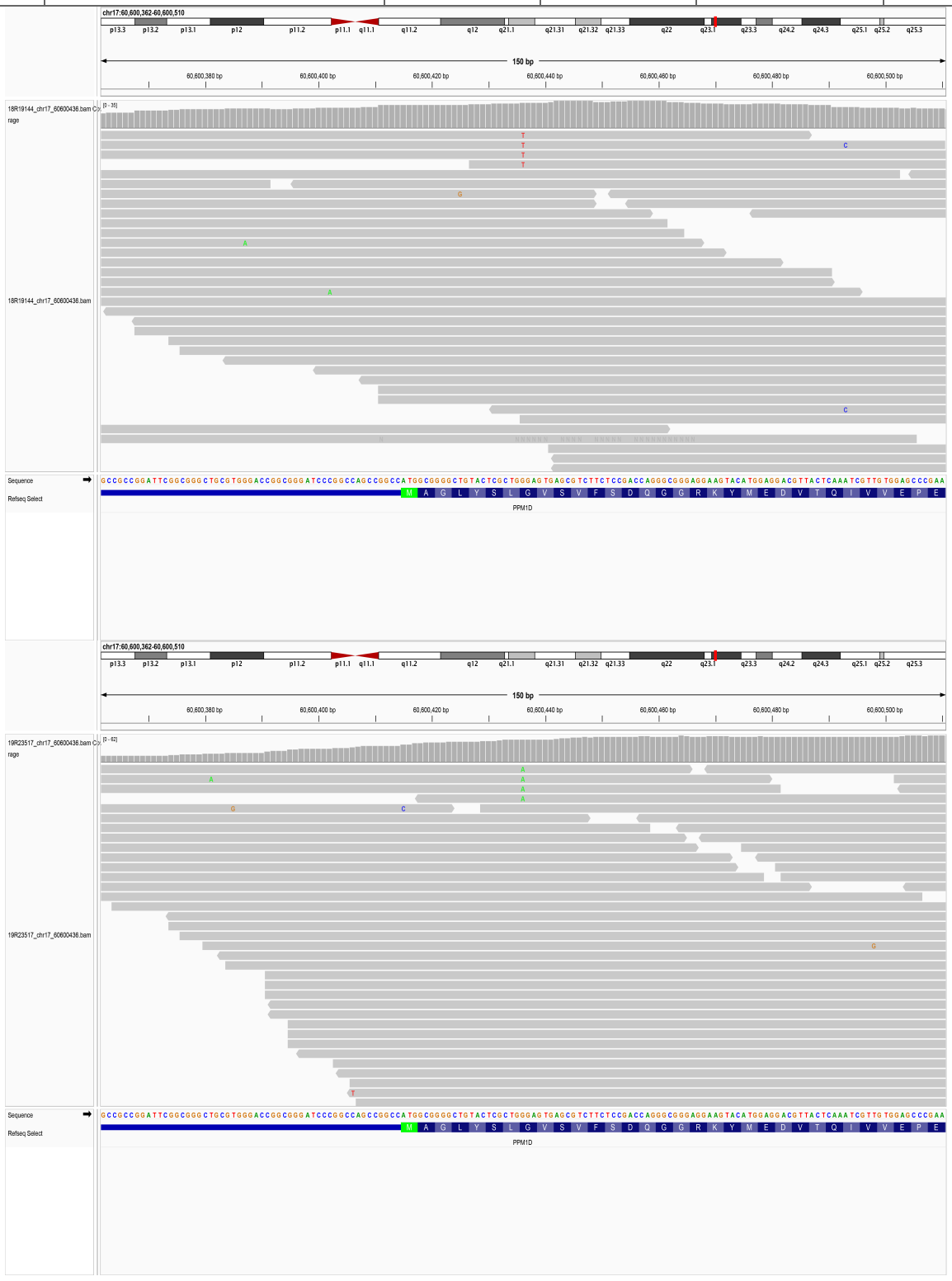
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061201D	chr6_79060774_-/T	116	23	*PHIP*	frameshift_variant



40. *PPM1D*

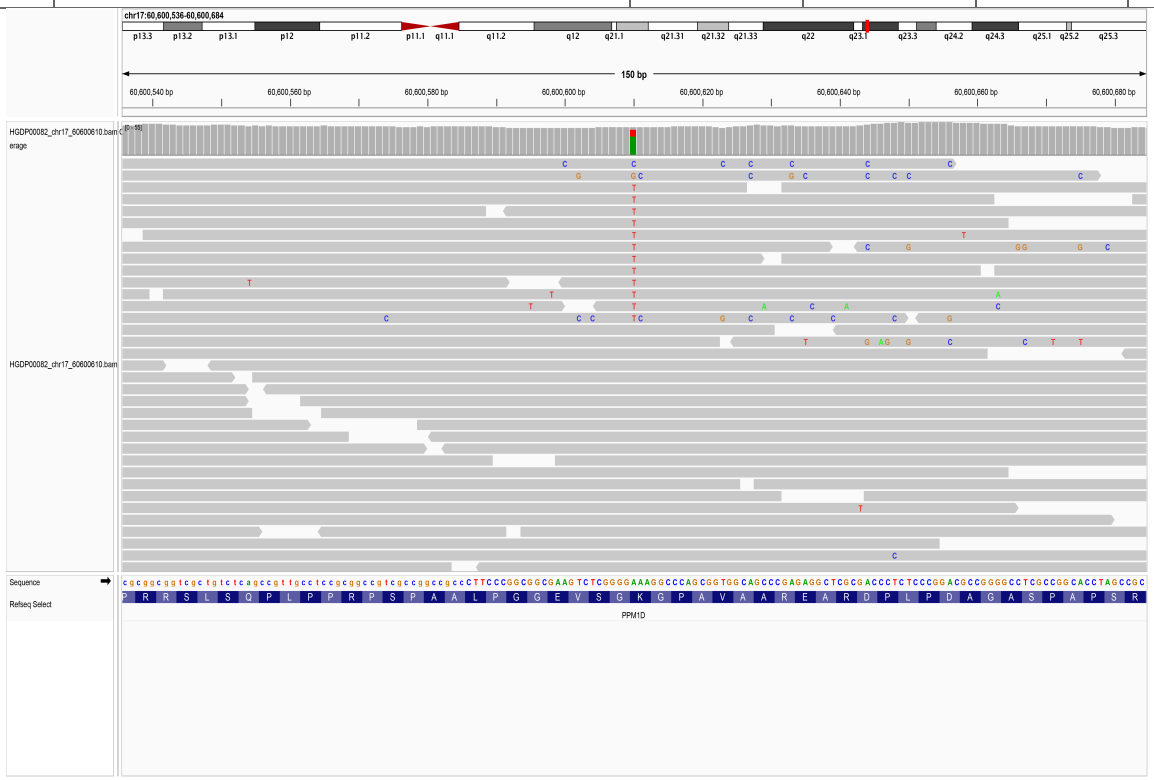
40.1. chr17_60600436_G/T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19144	chr17_60600436_G/T/A	27	4	*PPM1D*	stop_gained
19R23517	chr17_60600436_G/T/A	46	4	*PPM1D*	stop_gained



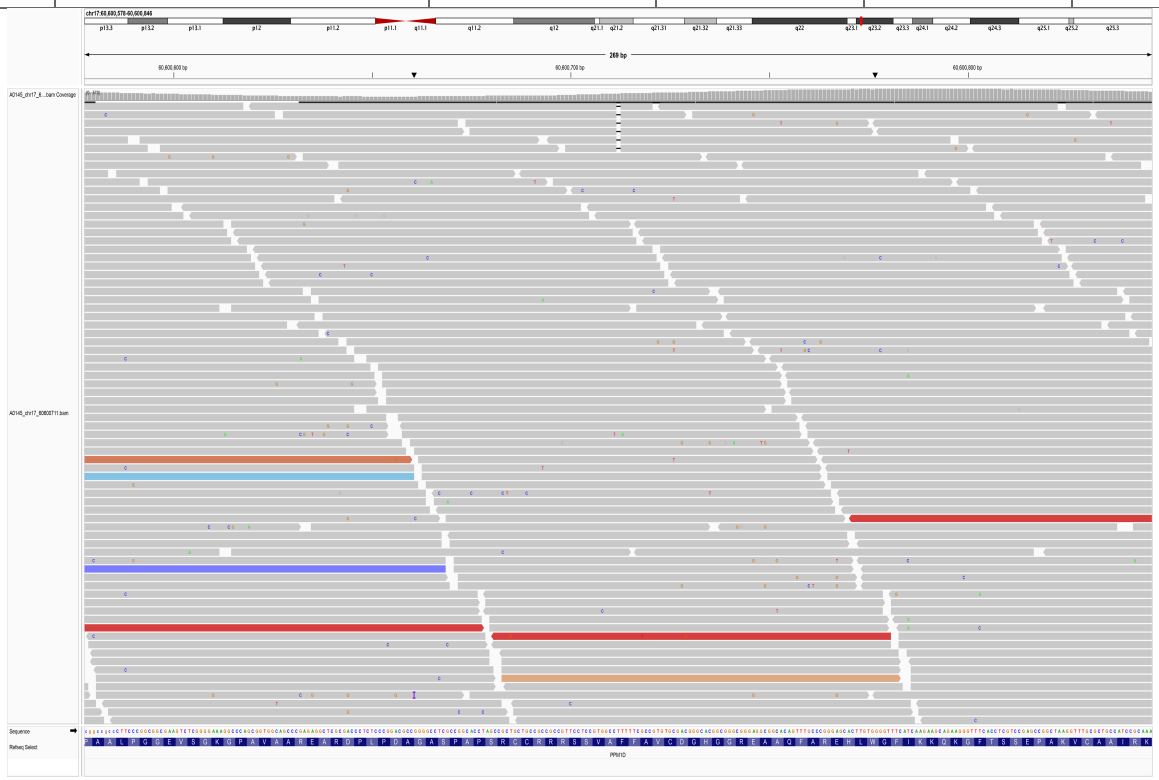
40.2. chr17_60600610_A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HGDP00082	chr17_60600610_A/T	30	10	*PPM1D*	stop_gained



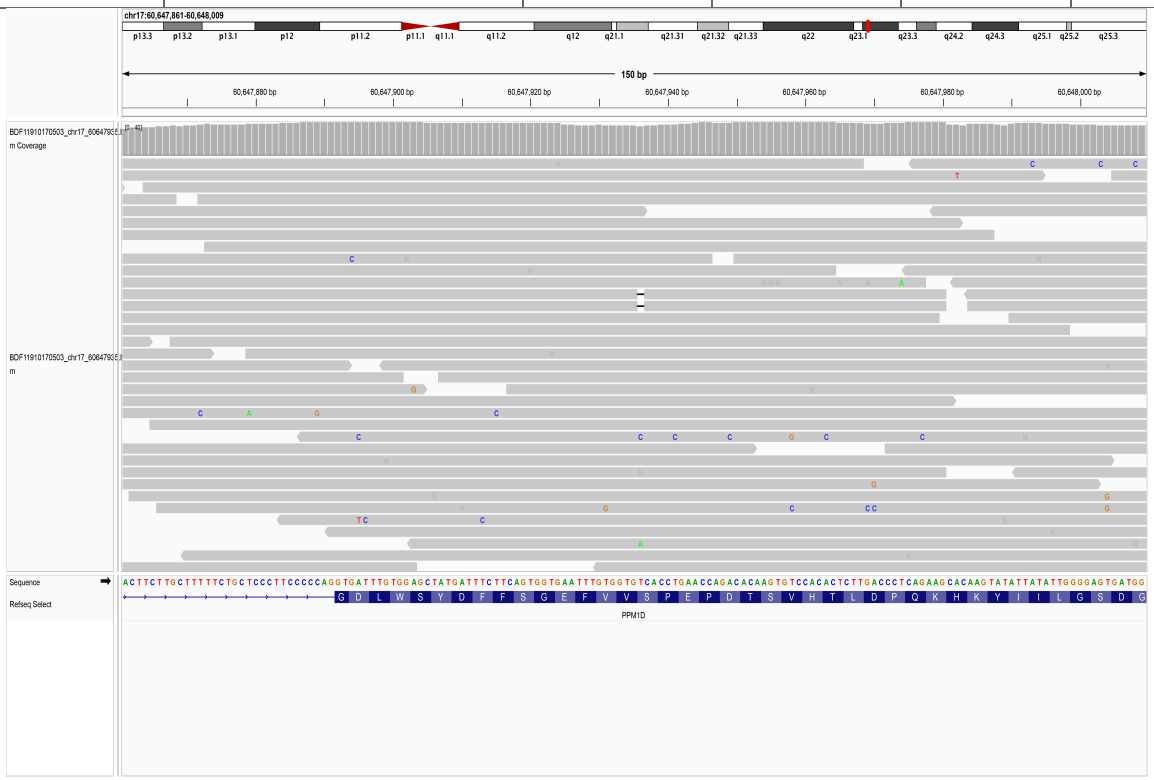
40.3. chr17_60600712_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0145	chr17_60600712_T/-	295	7	*PPM1D*	frameshift_variant



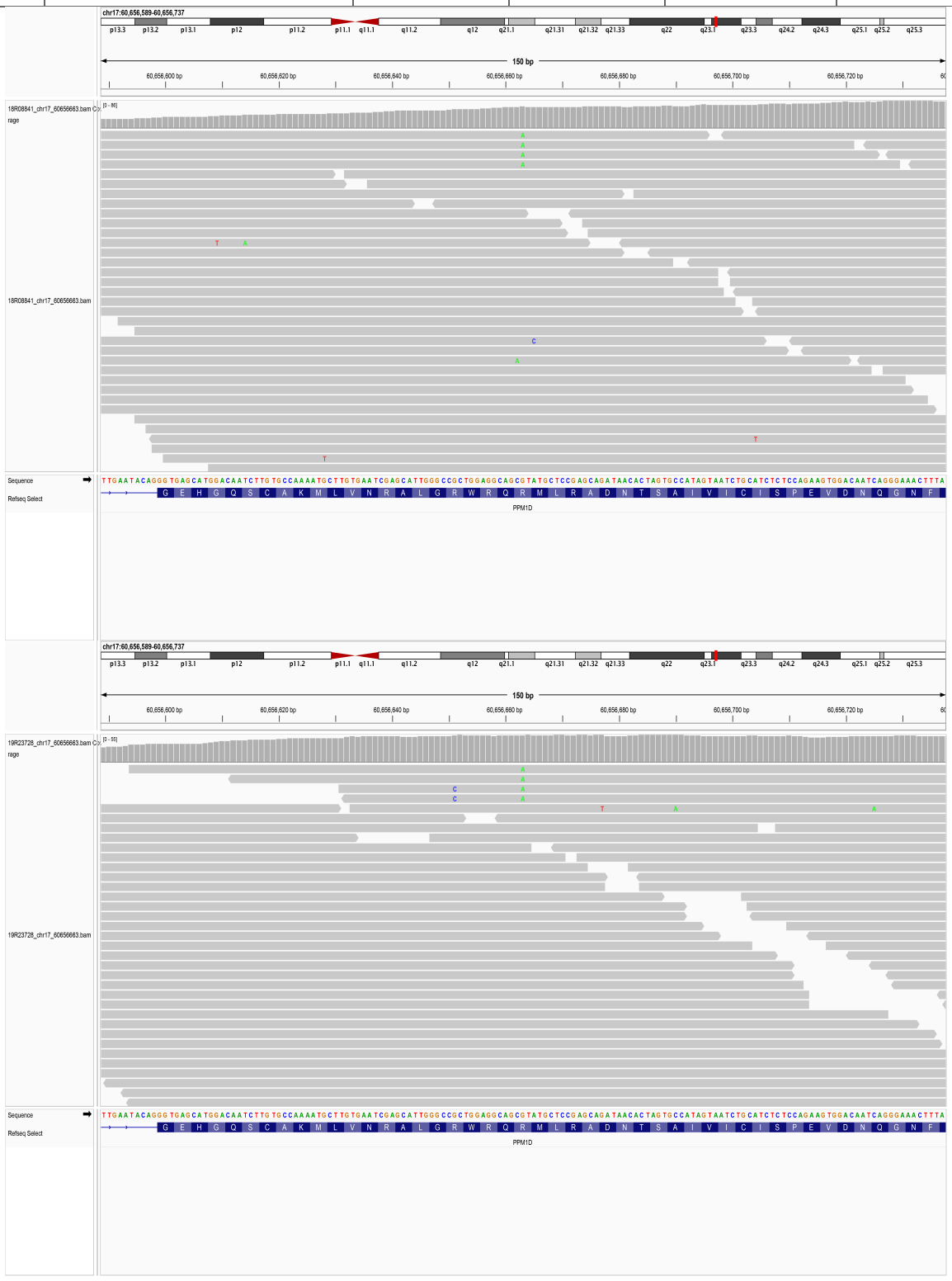
40.4. chr17_60647936_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr17_60647936_T/-	31	2	*PPM1D*	frameshift_variant



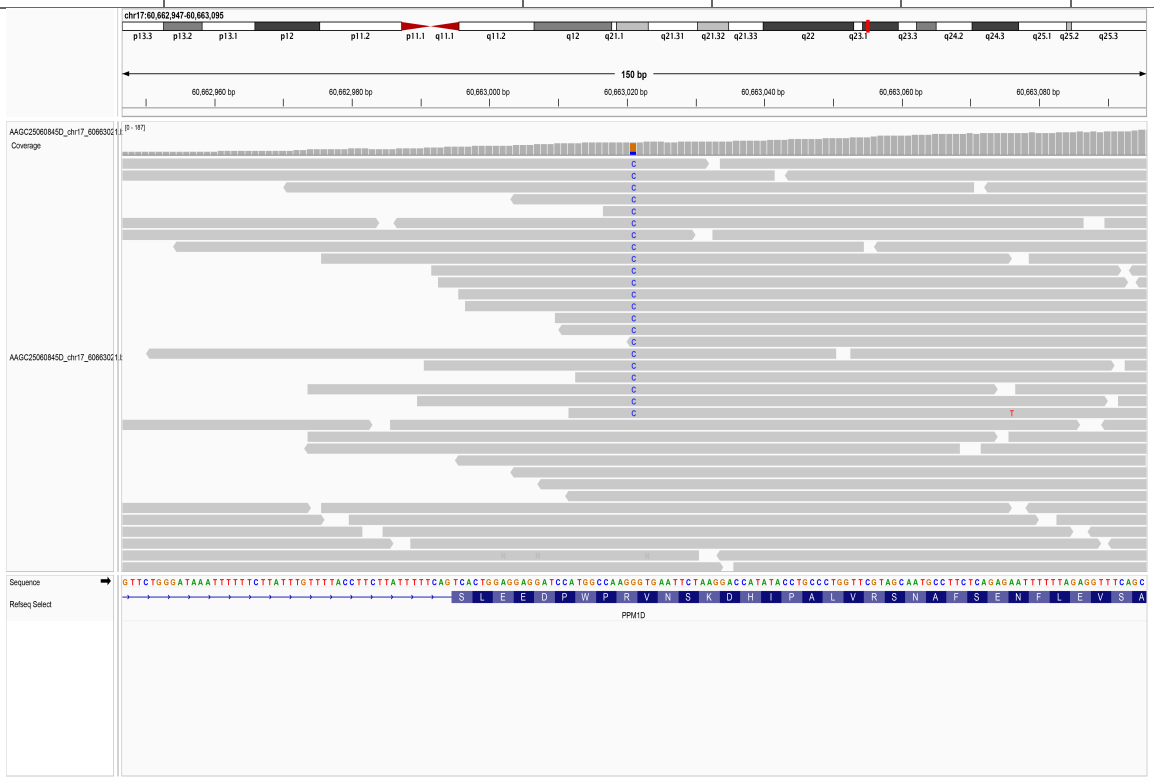
40.5. chr17_60656663_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08841	chr17_60656663_G/A	63	4	*PPM1D*	missense_variant
19R23728	chr17_60656663_G/A	48	4	*PPM1D*	missense_variant



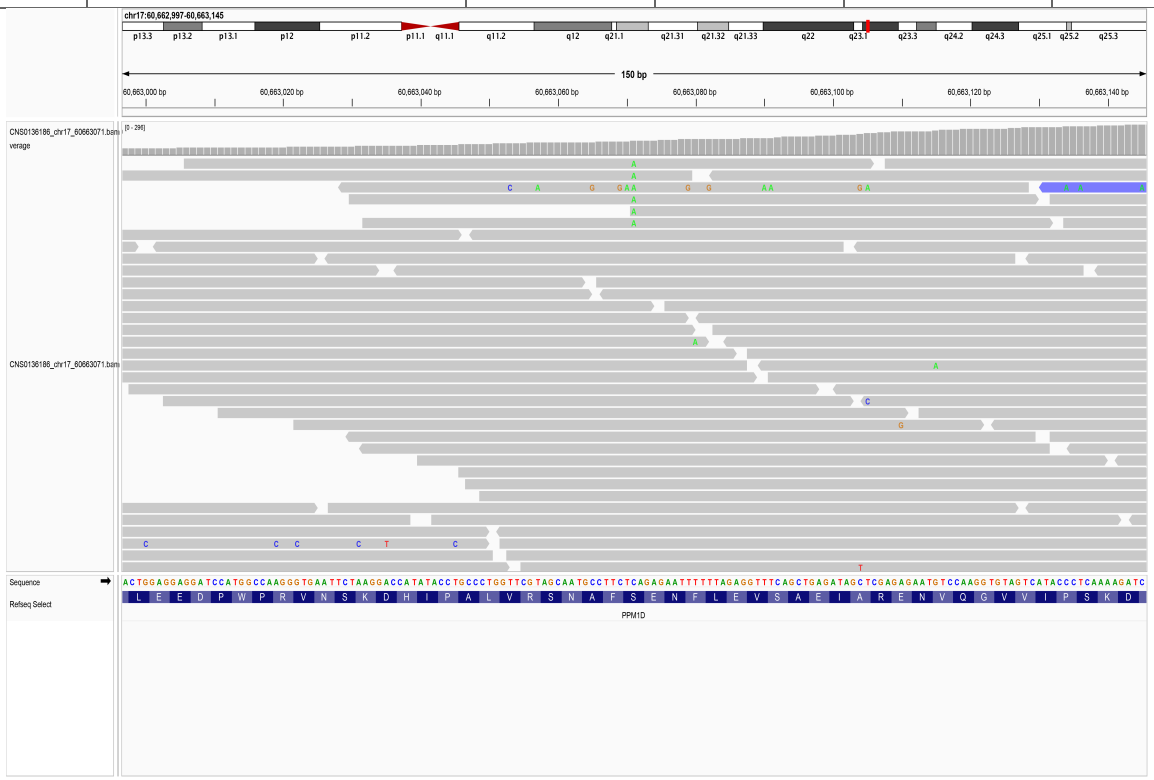
40.6. chr17_60663021_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060845D	chr17_60663021_G/C	51	22	*PPM1D*	missense_variant



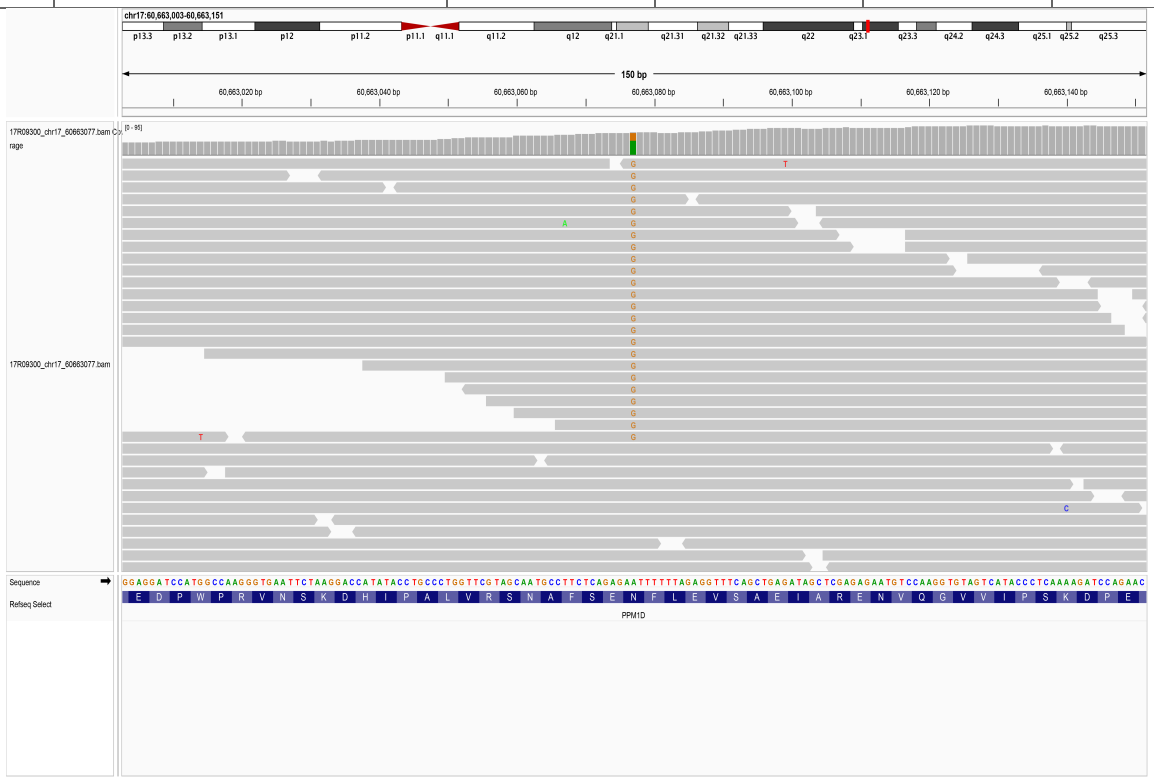
40.7. chr17_60663071_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136186	chr17_60663071_C/A	119	5	*PPM1D*	stop_gained



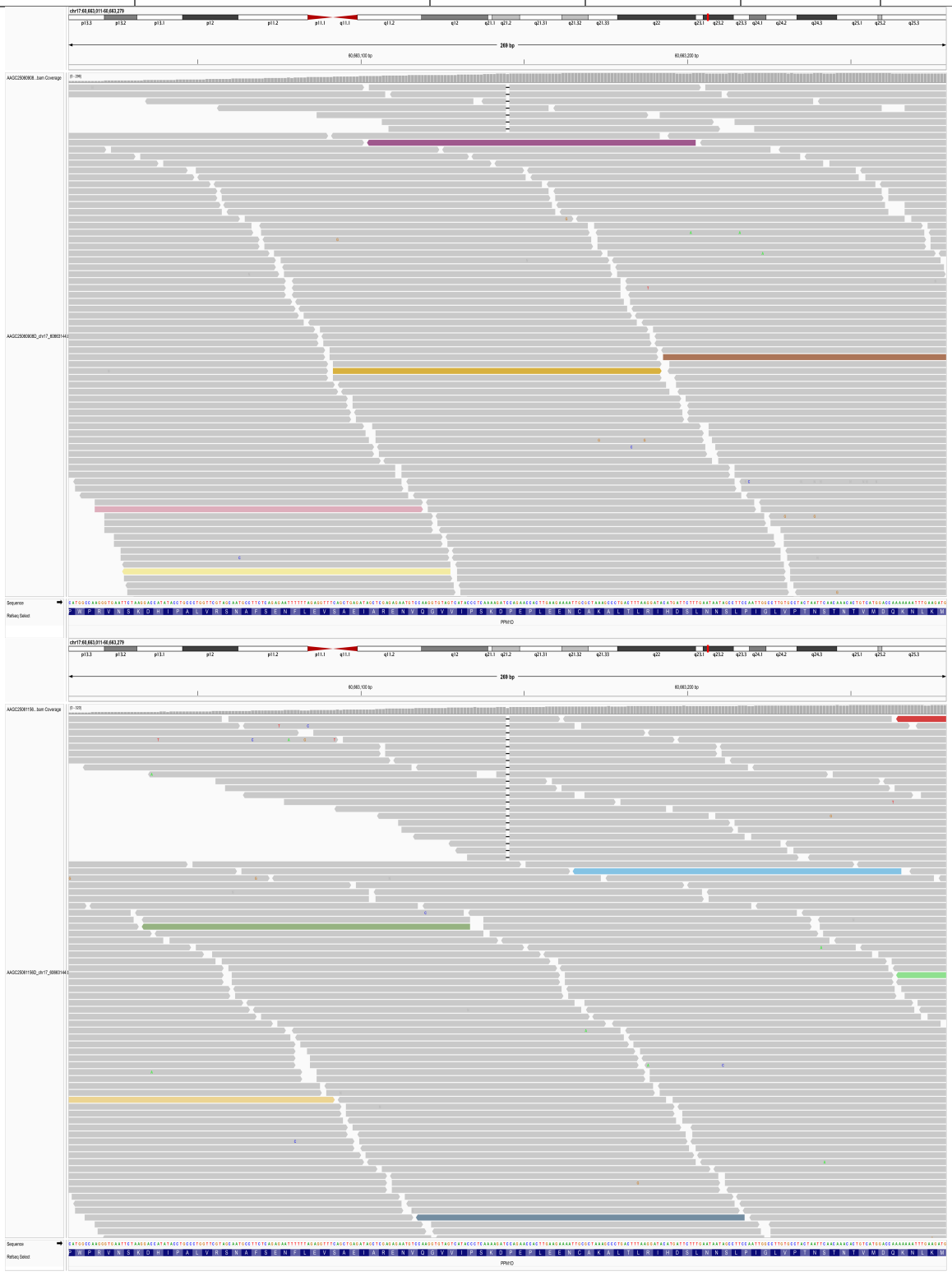
40.8. chr17_60663077_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09300	chr17_60663077_A/G	41	23	*PPM1D*	missense_variant



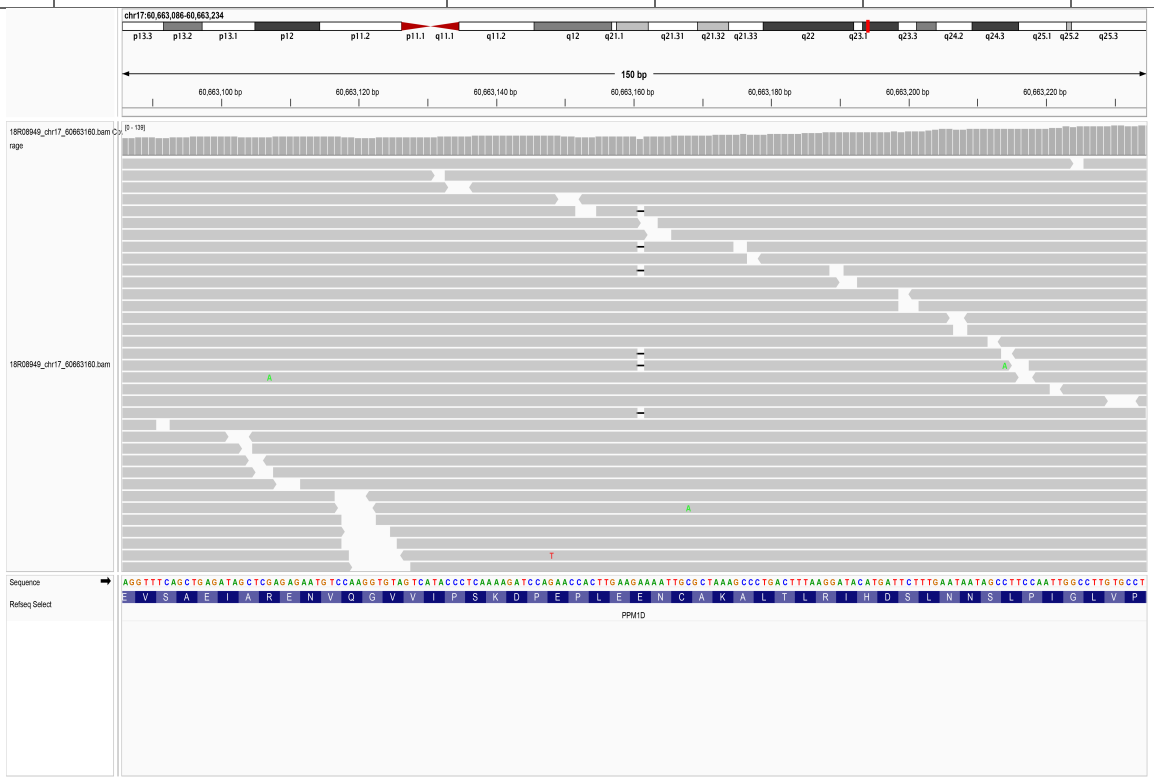
40.9. chr17_60663145_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060908D	chr17_60663145_C/-	255	7	*PPM1D*	frameshift_variant
AAGC25061156D	chr17_60663145_C/-	198	24	*PPM1D*	frameshift_variant



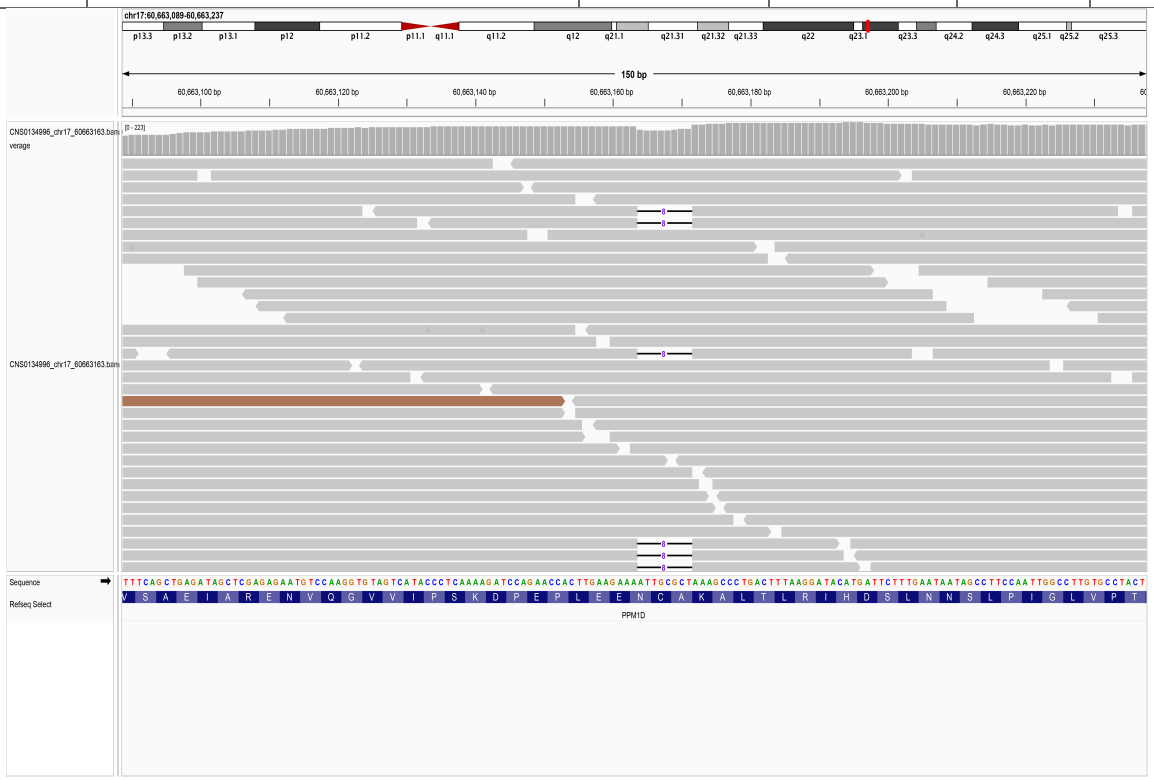
40.10. chr17_60663161_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08949	chr17_60663161_A/-	67	10	*PPM1D*	frameshift_variant



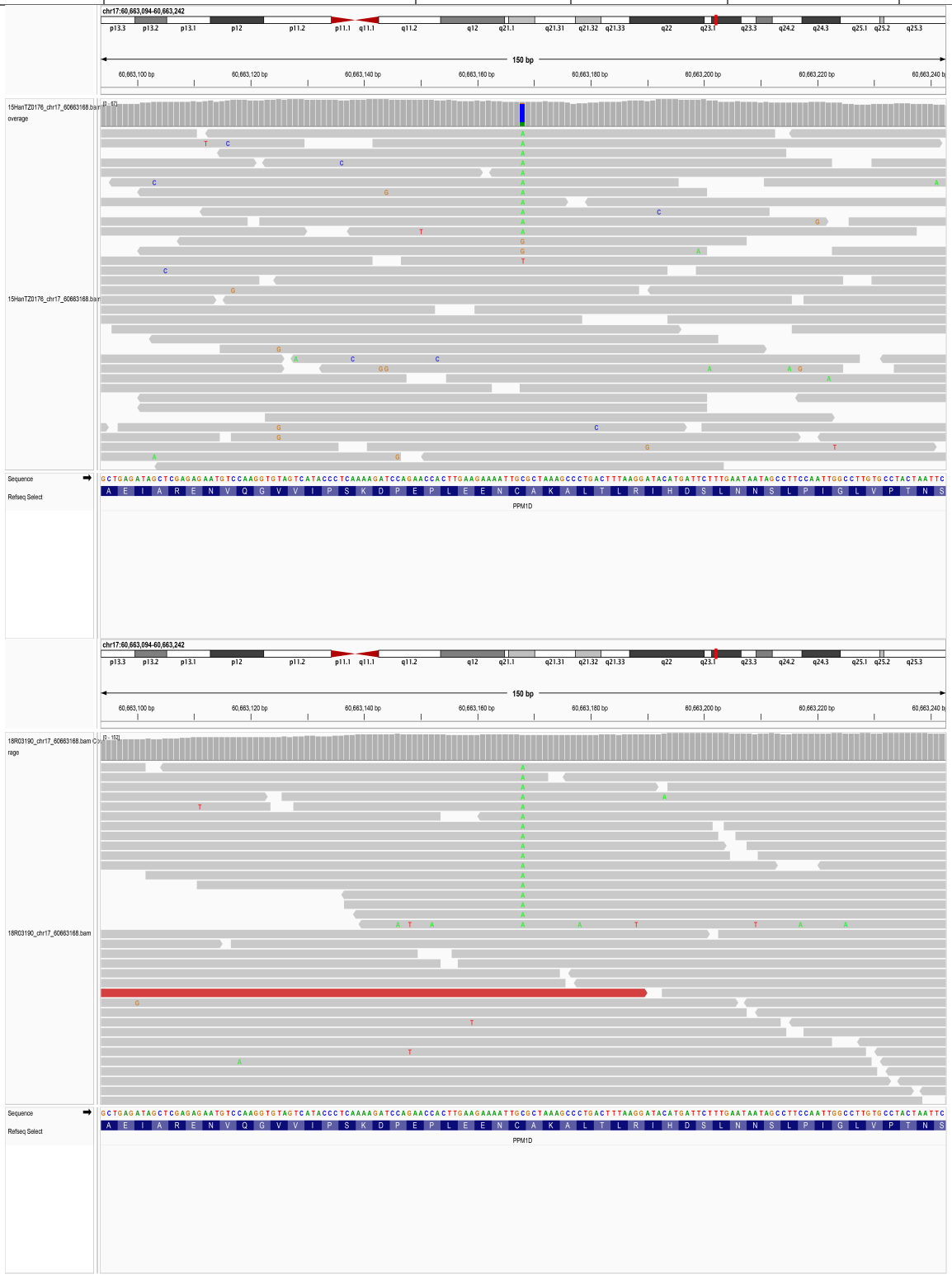
40.11. chr17_60663164_ATTGCGCT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134996	chr17_60663164_ATTGCGCT/-	184	28	*PPM1D*	frameshift_variant



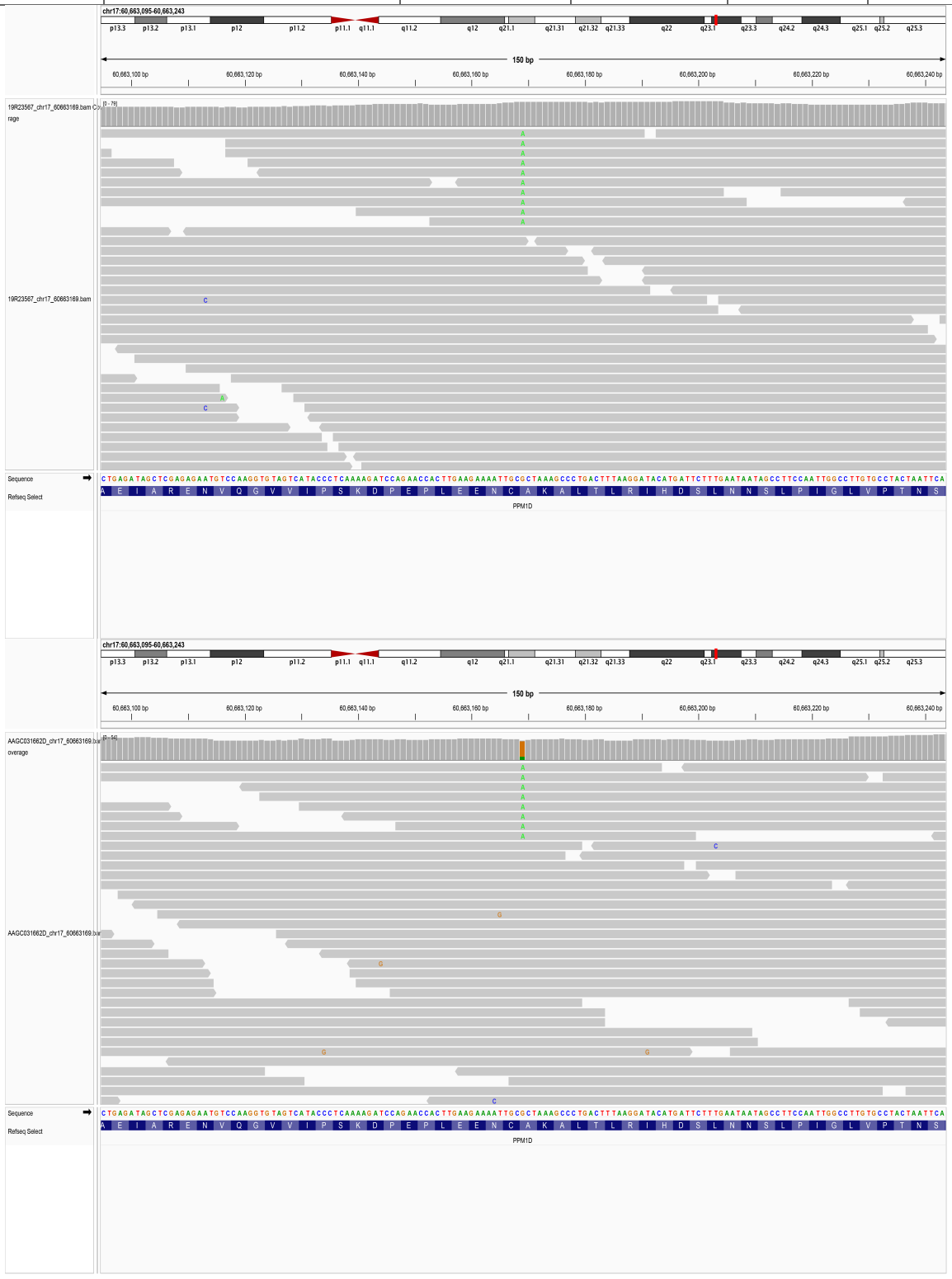
40.12. chr17_60663168_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0176	chr17_60663168_C/A	41	11	*PPM1D*	stop_gained
18R03190	chr17_60663168_C/A	121	16	*PPM1D*	stop_gained



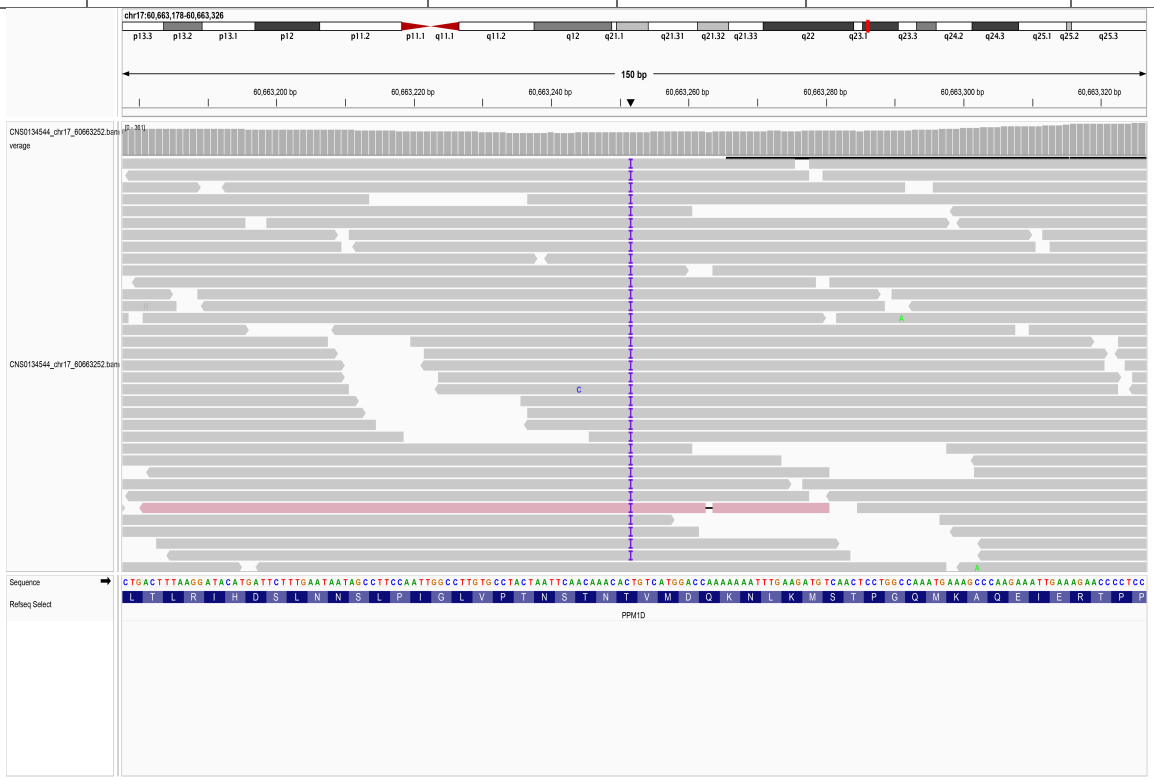
40.13. chr17_60663169_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23567	chr17_60663169_G/A	60	10	*PPM1D*	missense_variant
AAGC031662D	chr17_60663169_G/A	29	8	*PPM1D*	missense_variant



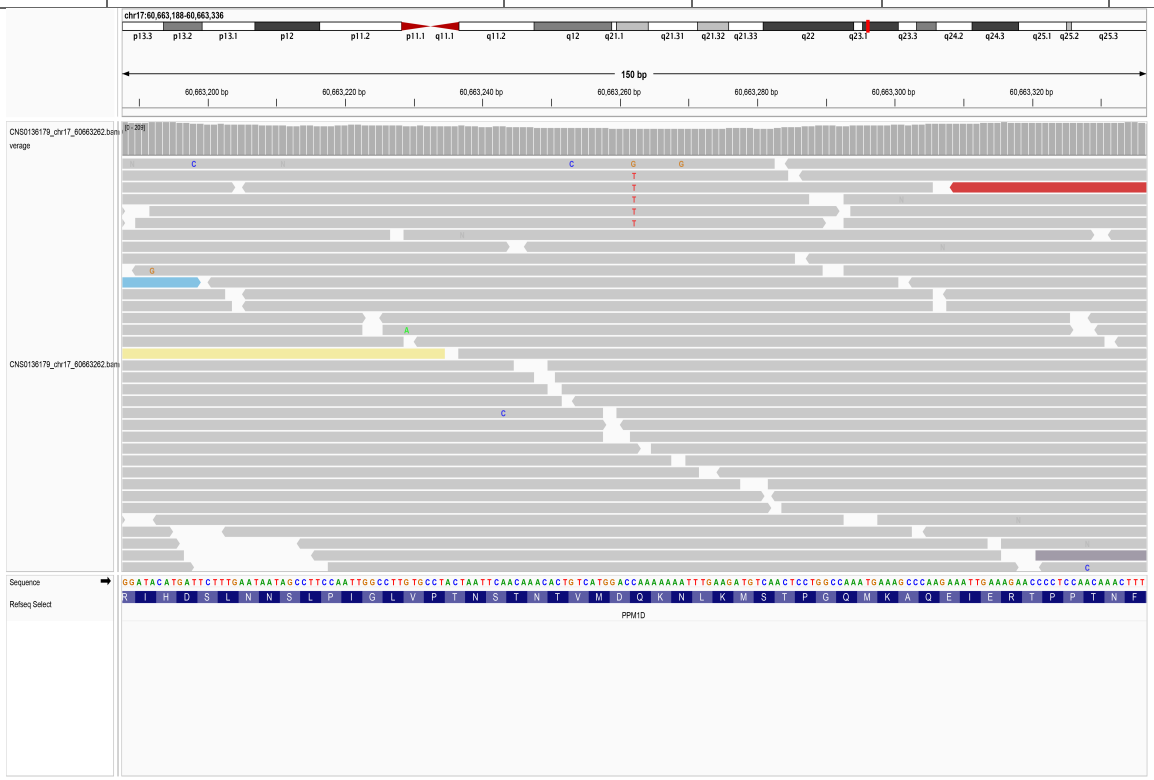
40.14. chr17_60663252_-/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134544	chr17_60663252_-/T	205	36	*PPM1D*	frameshift_variant



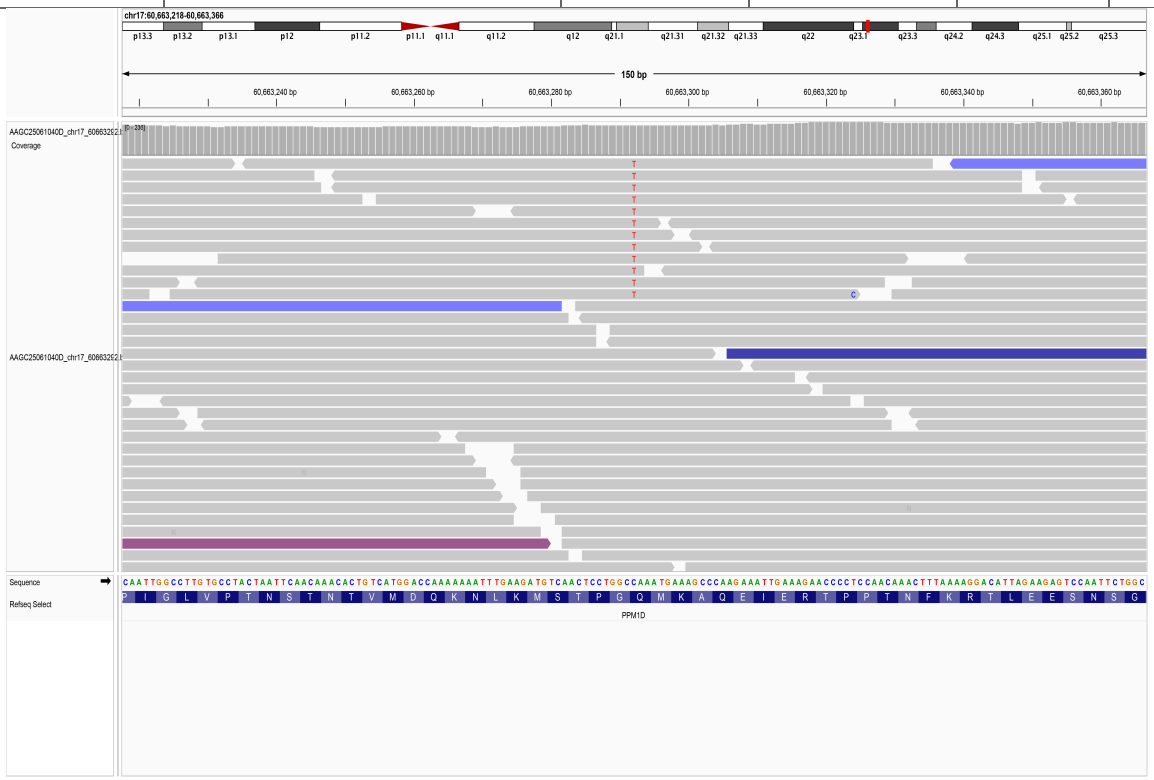
40.15. chr17_60663262_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136179	chr17_60663262_C/T	157	5	*PPM1D*	stop_gained



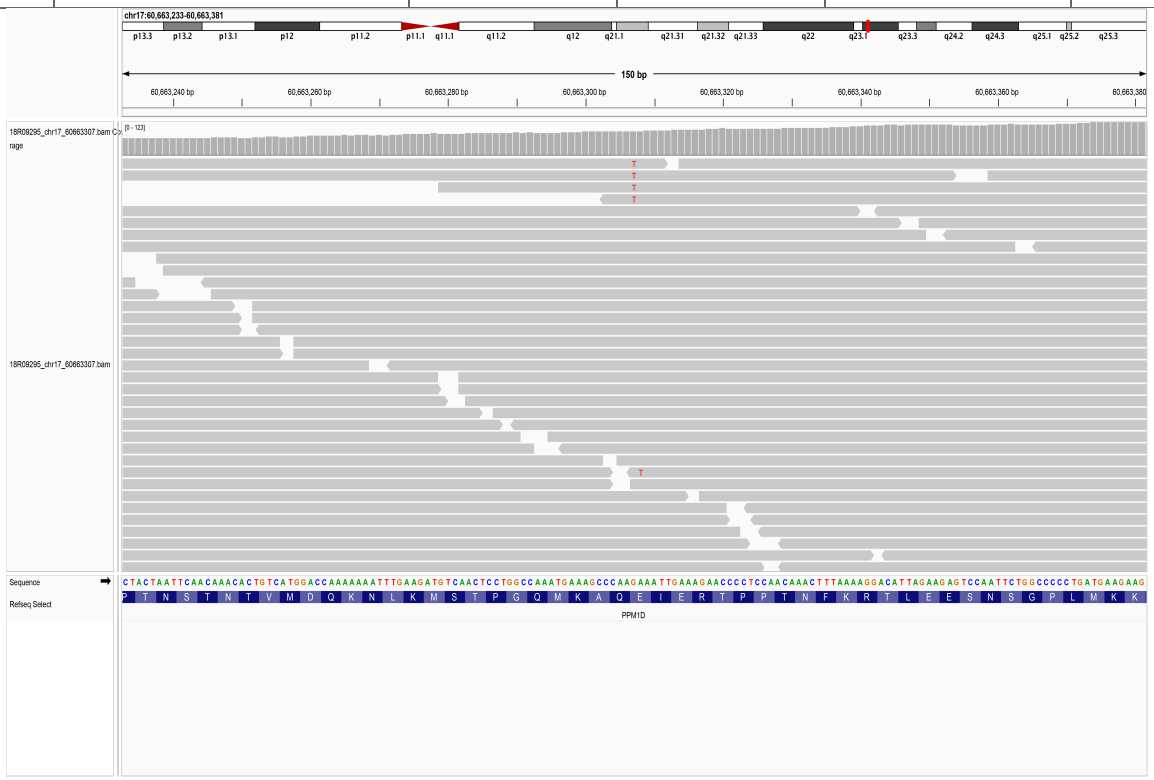
40.16. chr17_60663292_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061040D	chr17_60663292_C/T	196	12	*PPM1D*	stop_gained



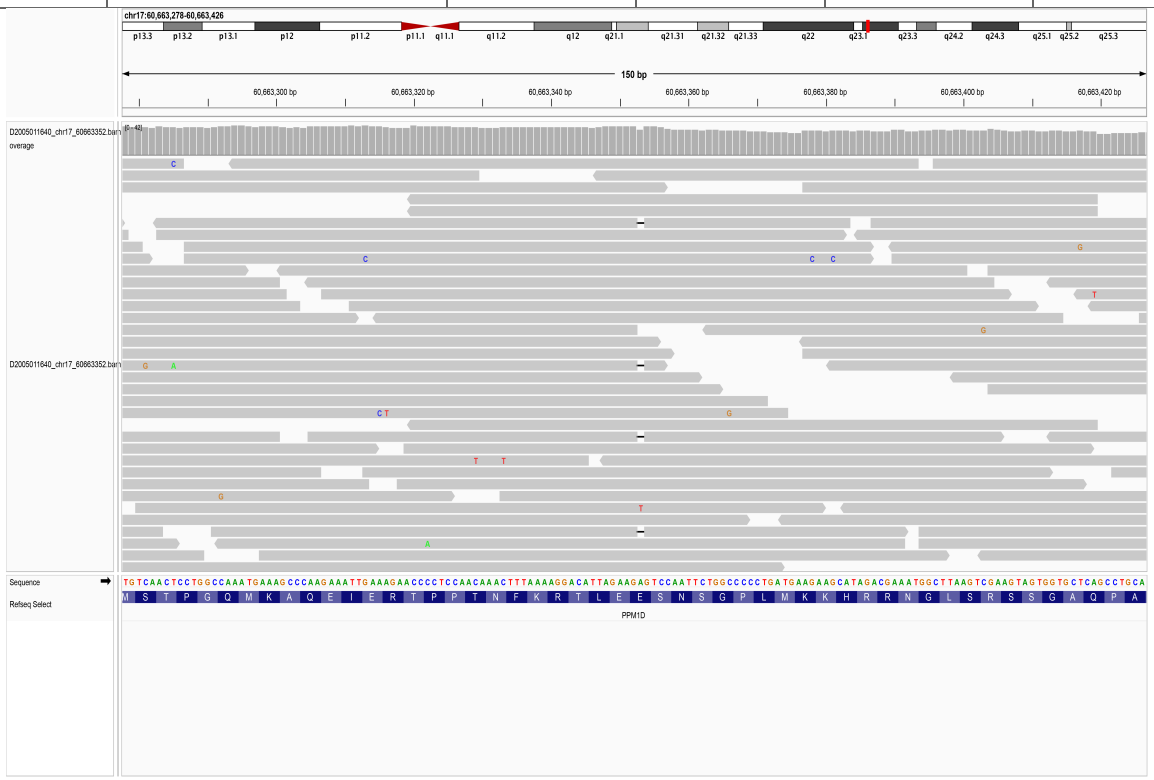
40.17. chr17_60663307_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09295	chr17_60663307_G/T	83	4	*PPM1D*	stop_gained



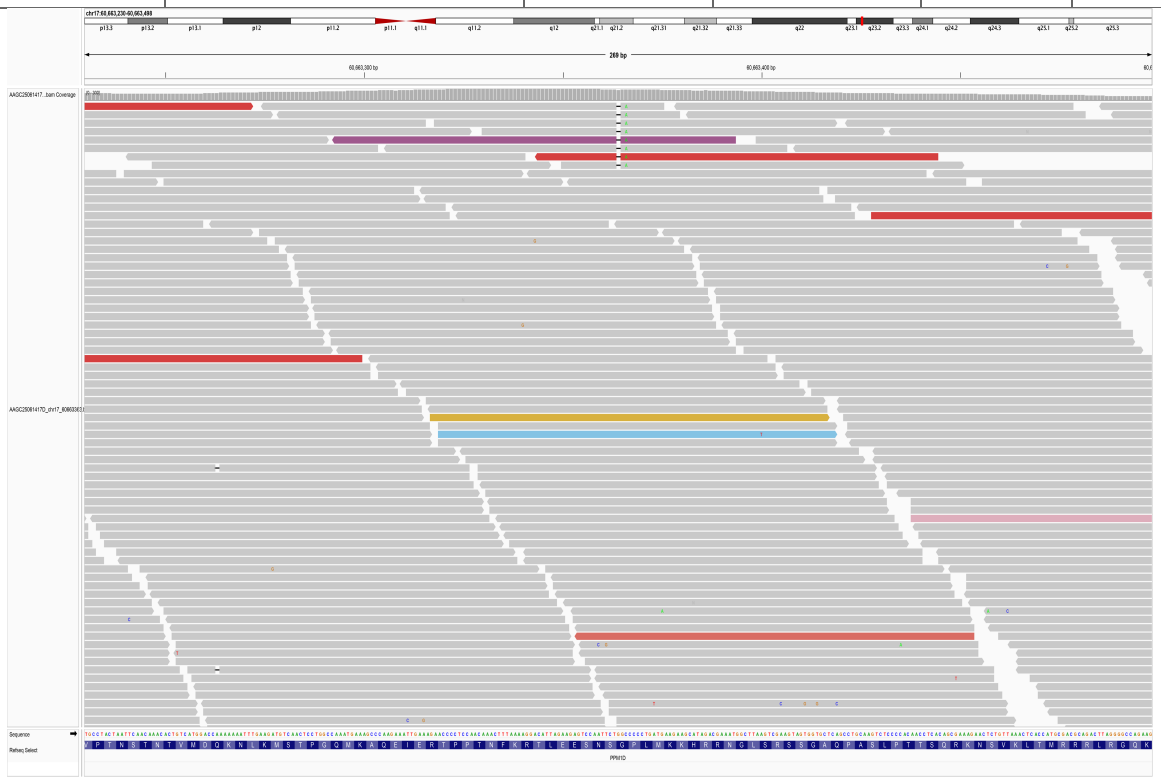
40.18. chr17_60663353_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2005011640	chr17_60663353_A/-	32	4	*PPM1D*	frameshift_variant



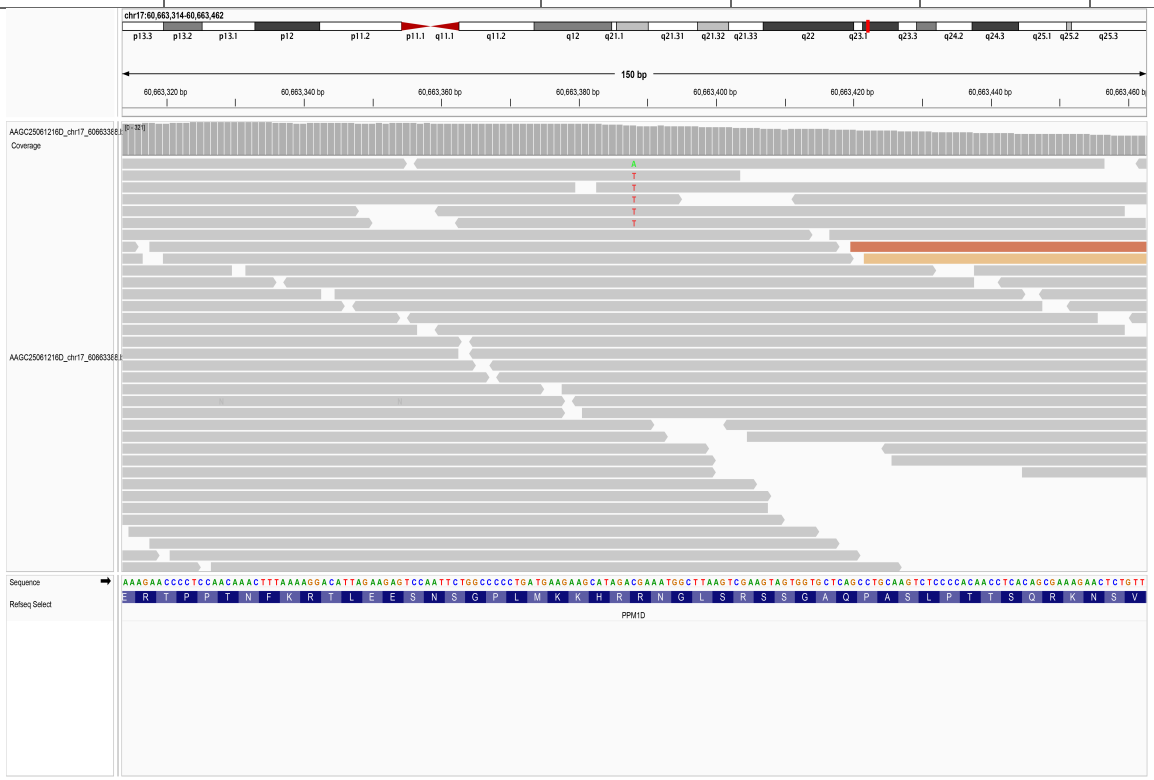
40.19. chr17_60663364_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061417D	chr17_60663364_G/-	265	9	*PPM1D*	frameshift_variant



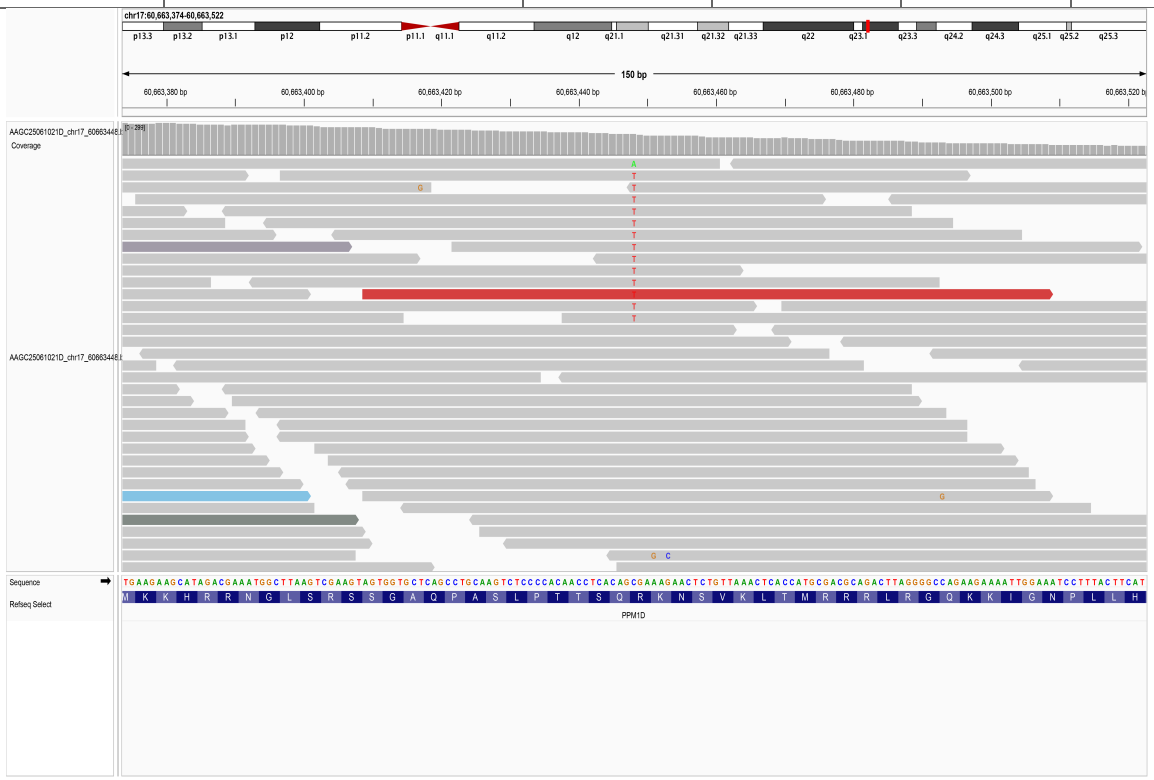
40.20. chr17_60663388_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061216D	chr17_60663388_C/T	274	5	*PPM1D*	stop_gained



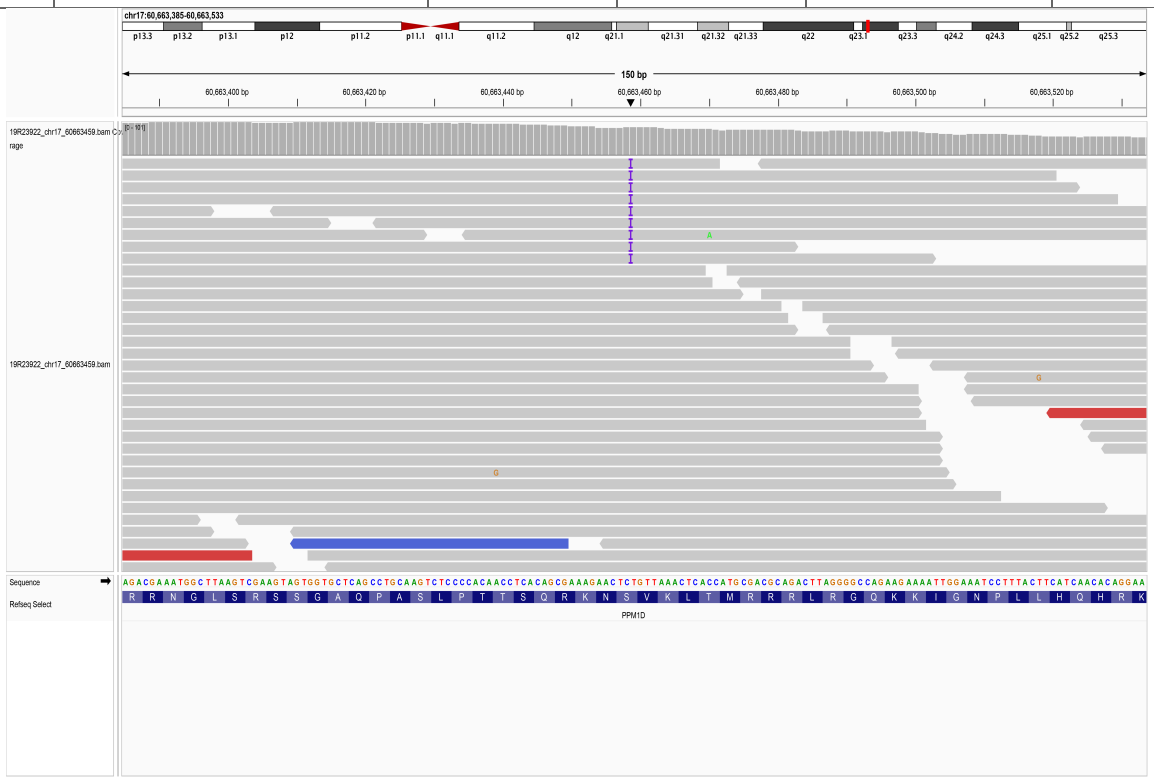
40.21. chr17_60663448_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061021D	chr17_60663448_C/T	166	13	*PPM1D*	stop_gained



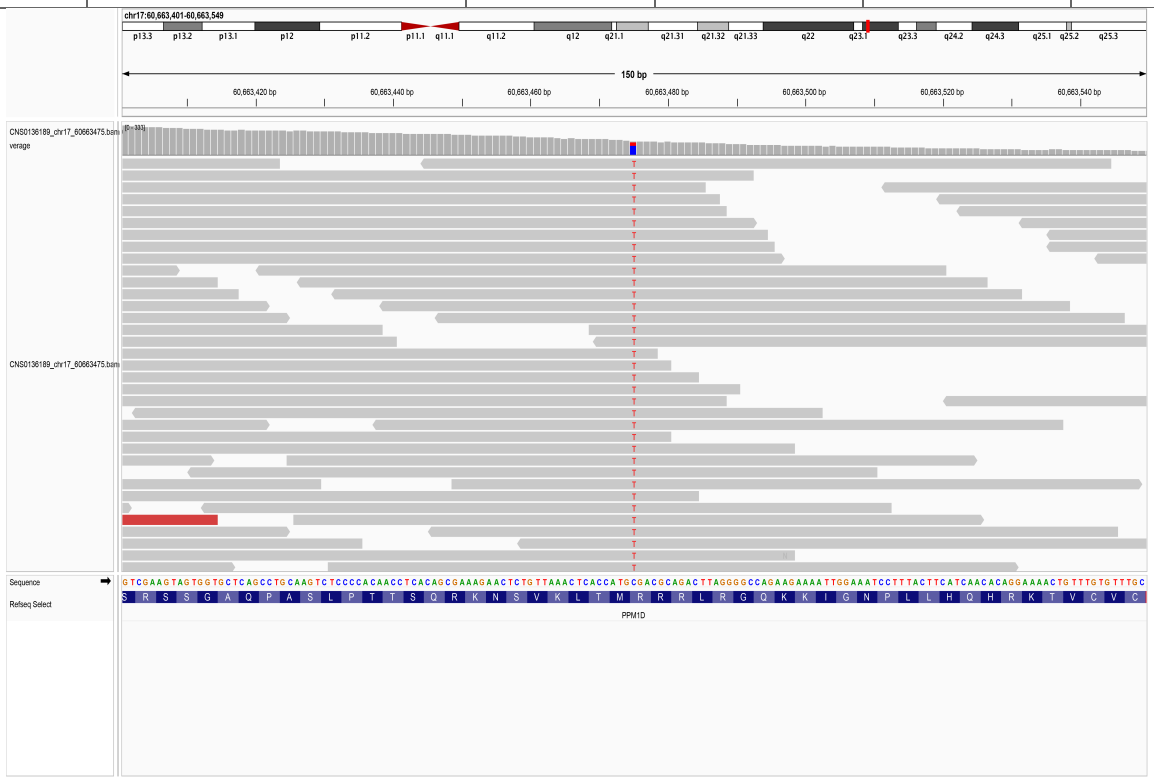
40.22. chr17_60663459_-/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23922	chr17_60663459_-/T	74	9	*PPM1D*	frameshift_variant



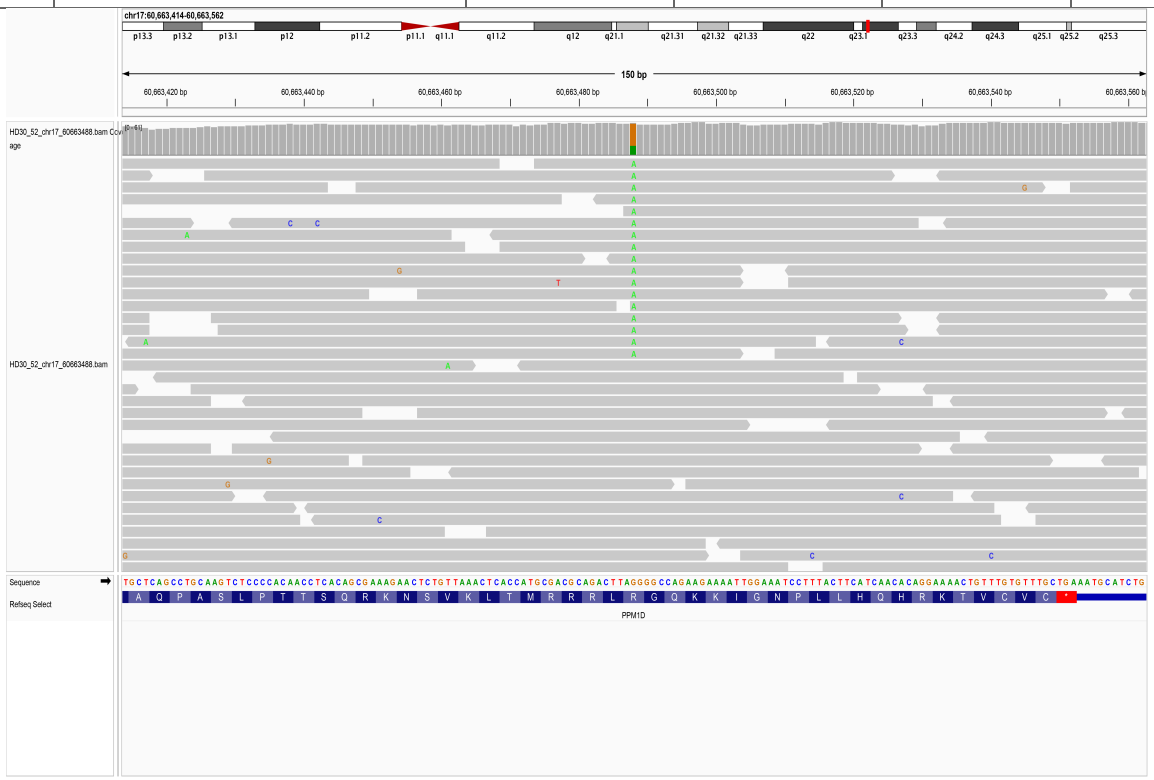
40.23. chr17_60663475_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136189	chr17_60663475_C/T	103	36	*PPM1D*	stop_gained



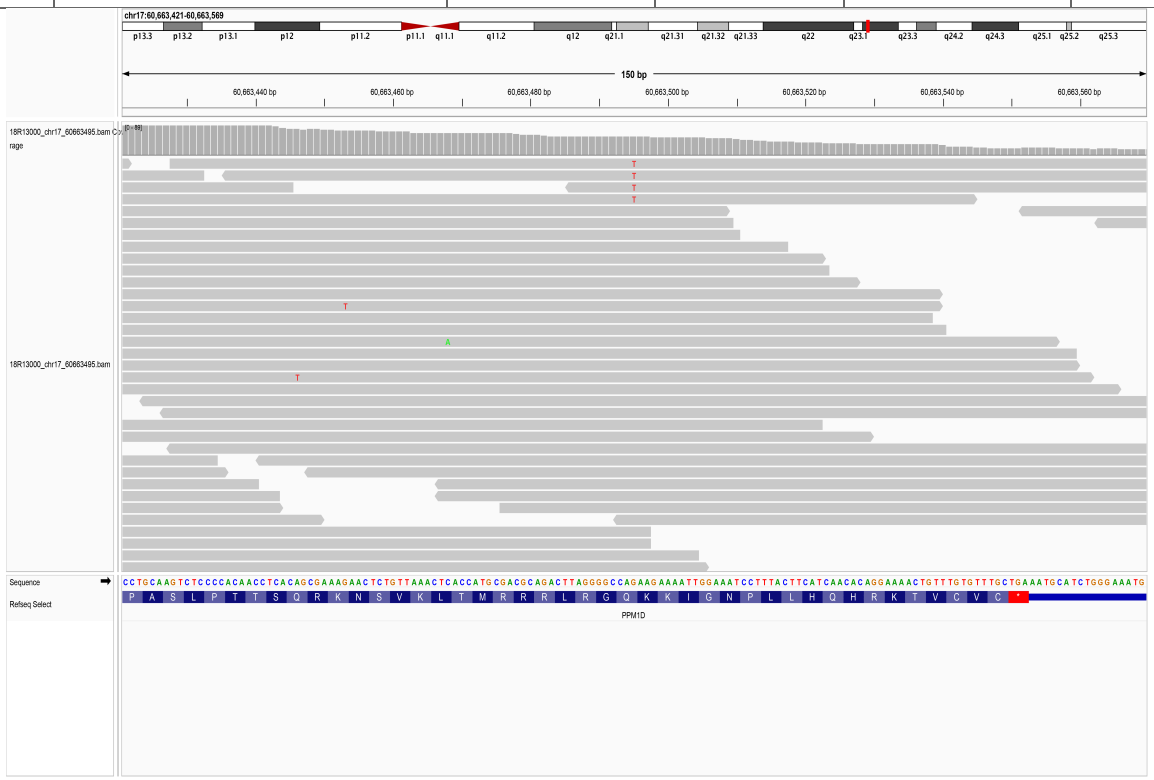
40.24. chr17_60663488_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HD30_52	chr17_60663488_G/A	40	17	*PPM1D*	missense_variant



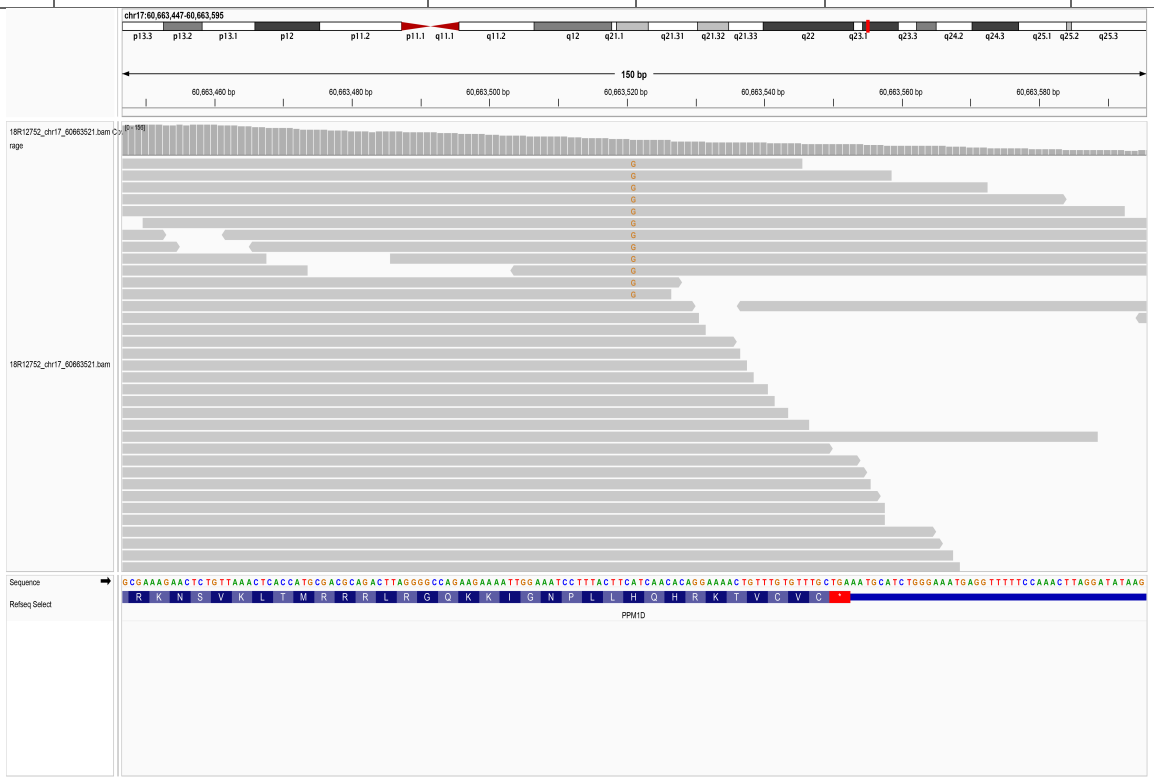
40.25. chr17_60663495_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13000	chr17_60663495_G/T	45	4	*PPM1D*	missense_variant



40.26. chr17_60663521_A/G

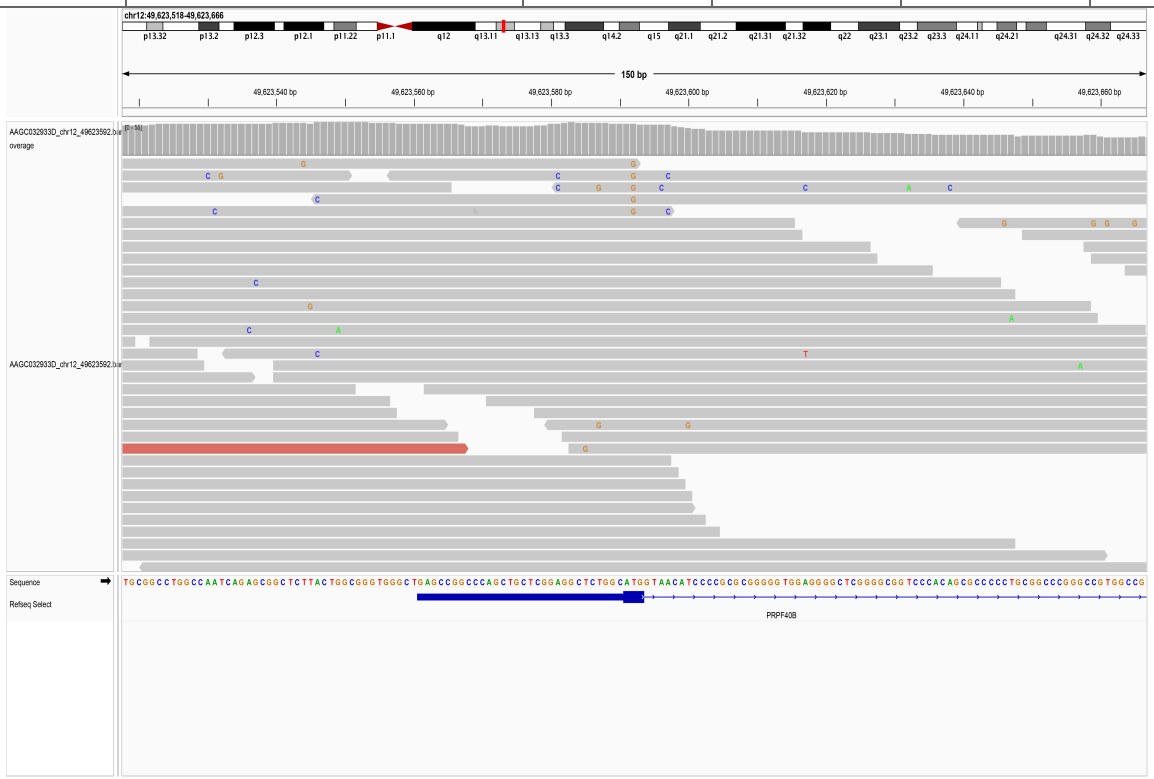
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12752	chr17_60663521_A/G	62	12	*PPM1D*	missense_variant



41. *PRPF40B*

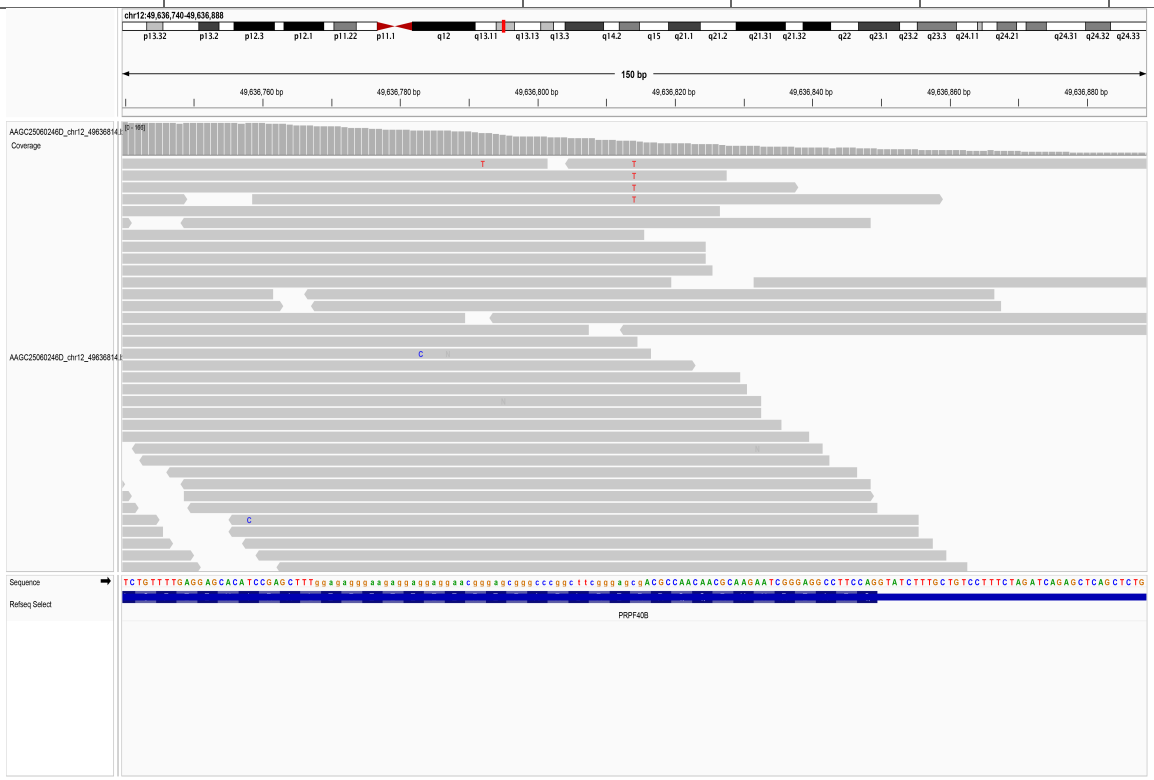
41.1. chr12_49623592_T/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC032933D	chr12_49623592_T/G	46	5	*PRPF40B*	start_lost



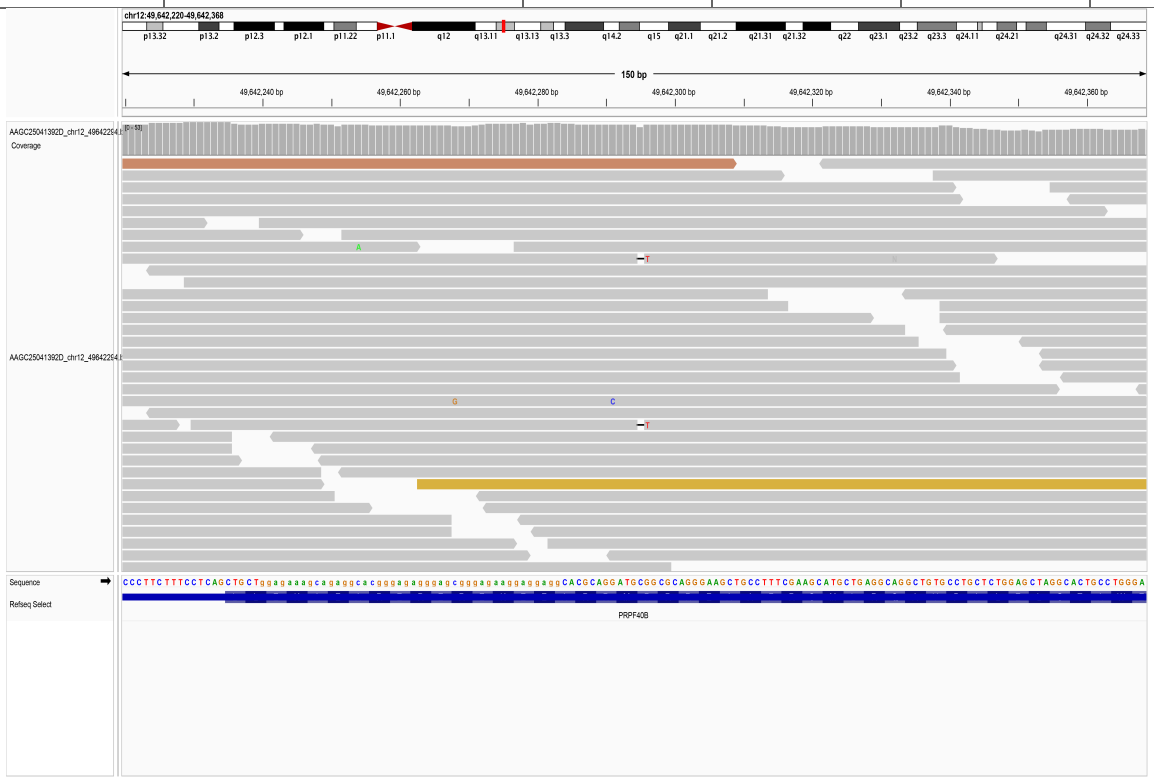
41.2. chr12_49636814_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060246D	chr12_49636814_C/T	67	4	*PRPF40B*	stop_gained



41.3. chr12_49642295_C/-

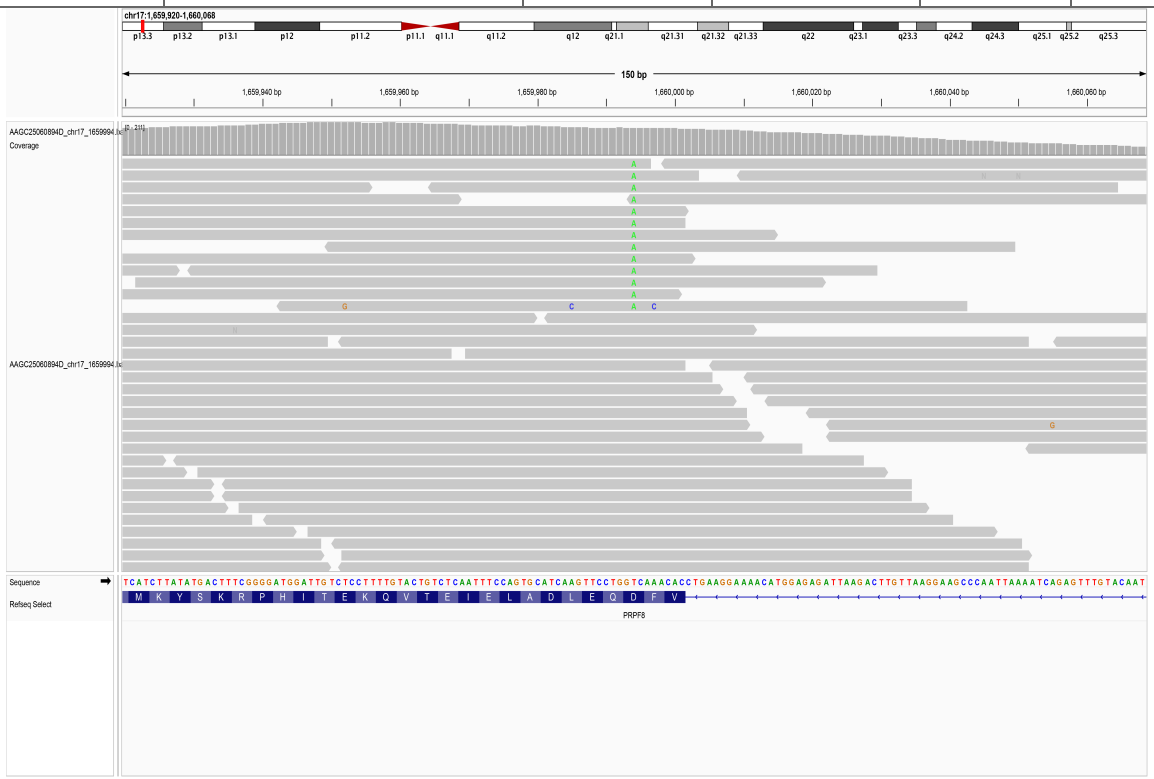
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25041392D	chr12_49642295_C/-	45	3	*PRPF40B*	frameshift_variant



42. *PRPF8*

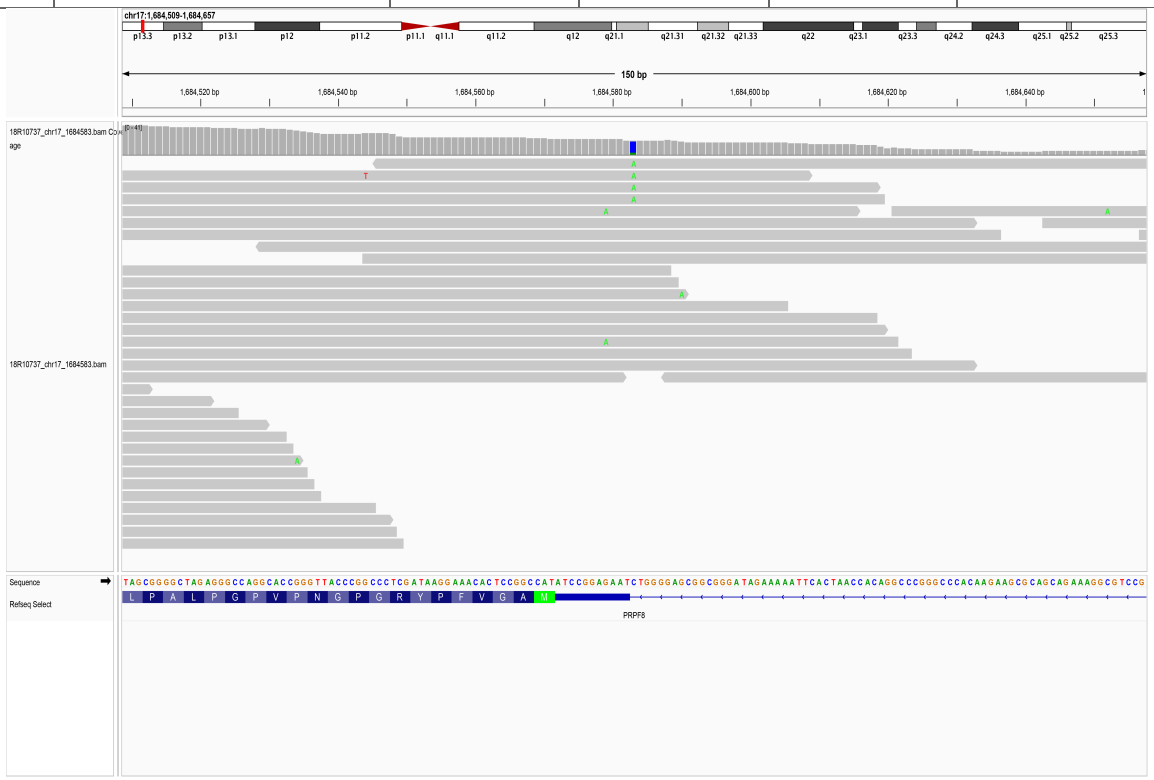
42.1. chr17_1659994_T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060894D	chr17_1659994_T/A	158	12	*PRPF8*	missense_variant



42.2. chr17_1684583_C/A

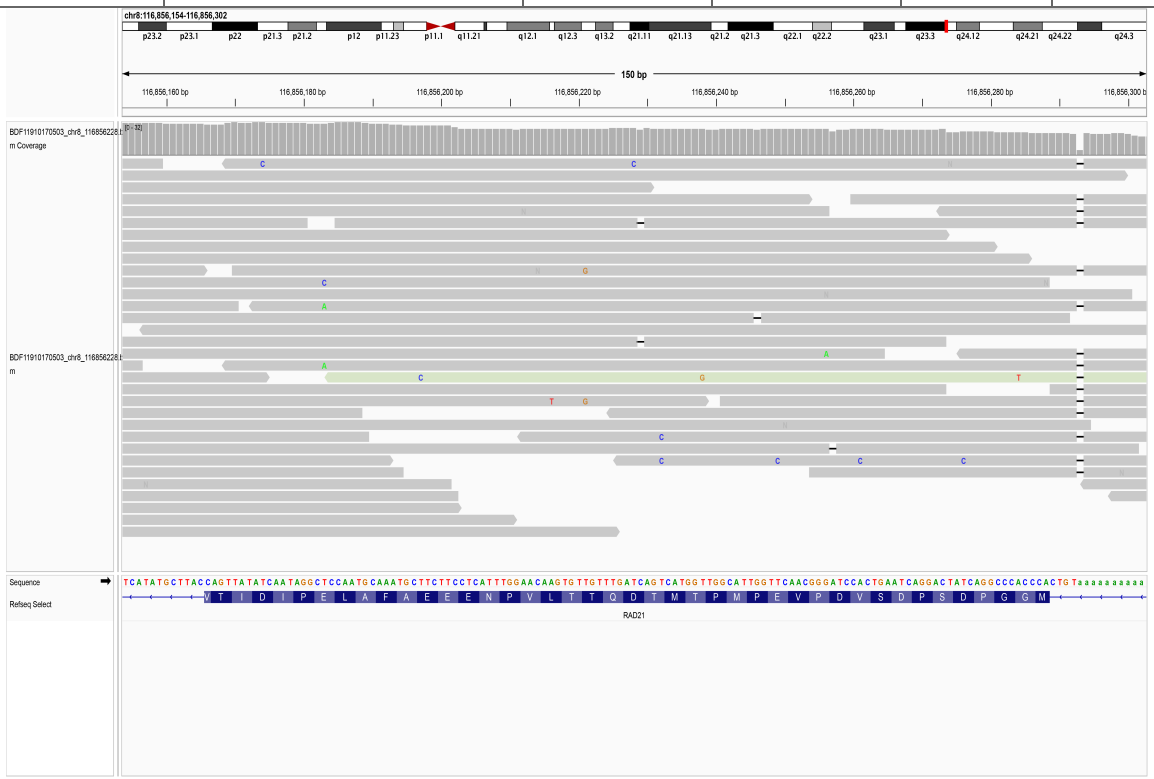
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10737	chr17_1684583_C/A	14	4	*PRPF8*	splice_acceptor_variant



43. *RAD21*

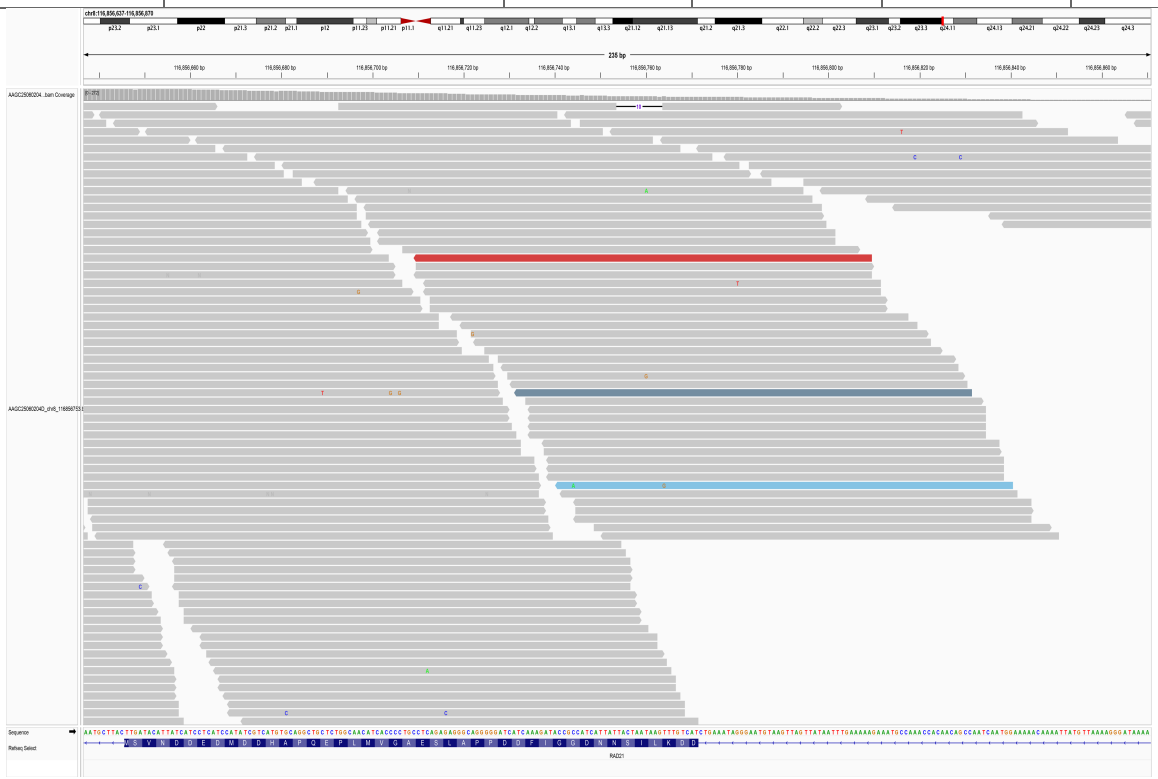
43.1. chr8_116856229_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr8_116856229_C/-	21	2	*RAD21*	frameshift_variant



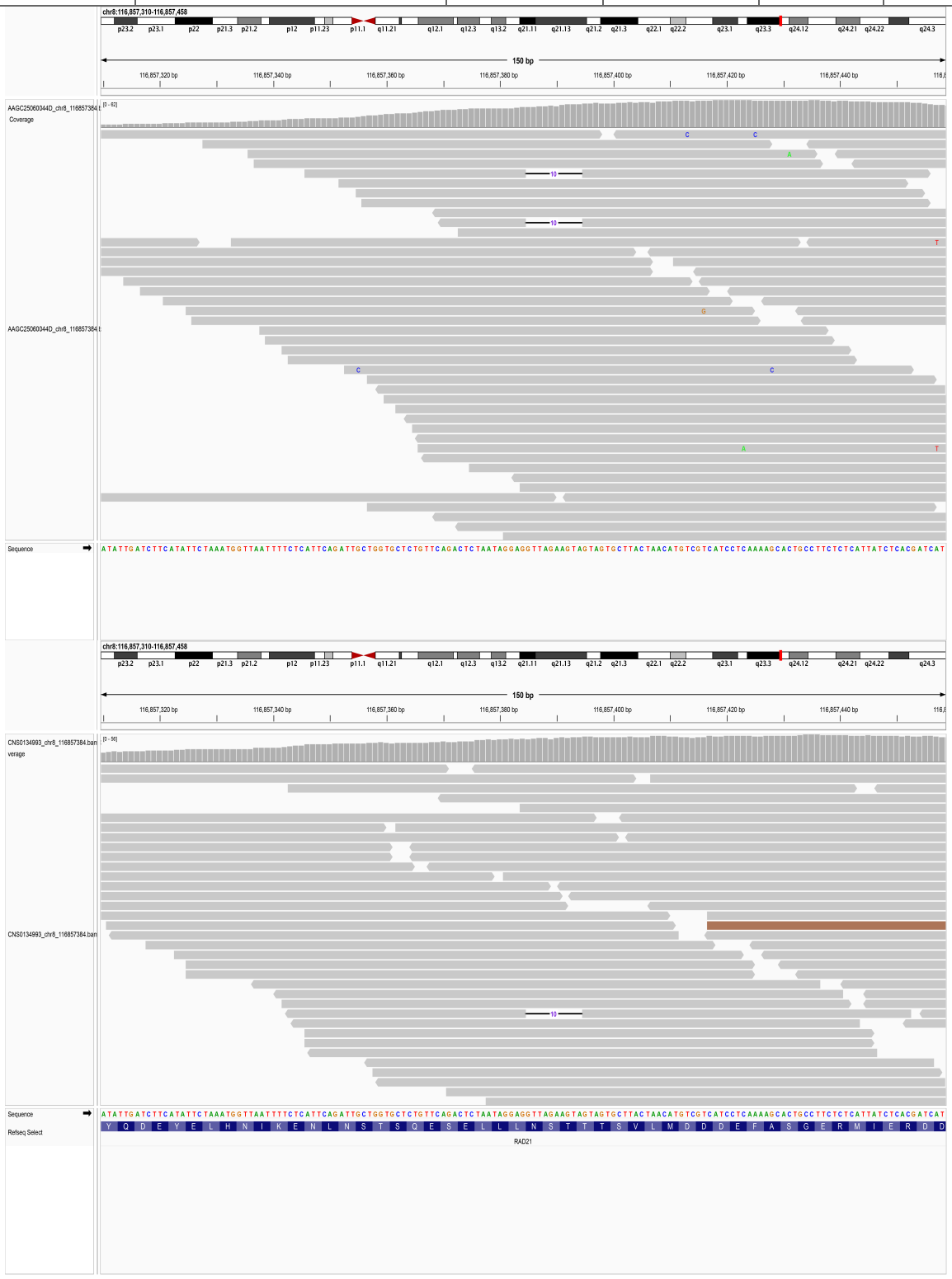
43.2. chr8_116856754_TACTAATAAG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060204D	chr8_116856754_TACTAATAAG/-	104	2	*RAD21*	frameshift_variant



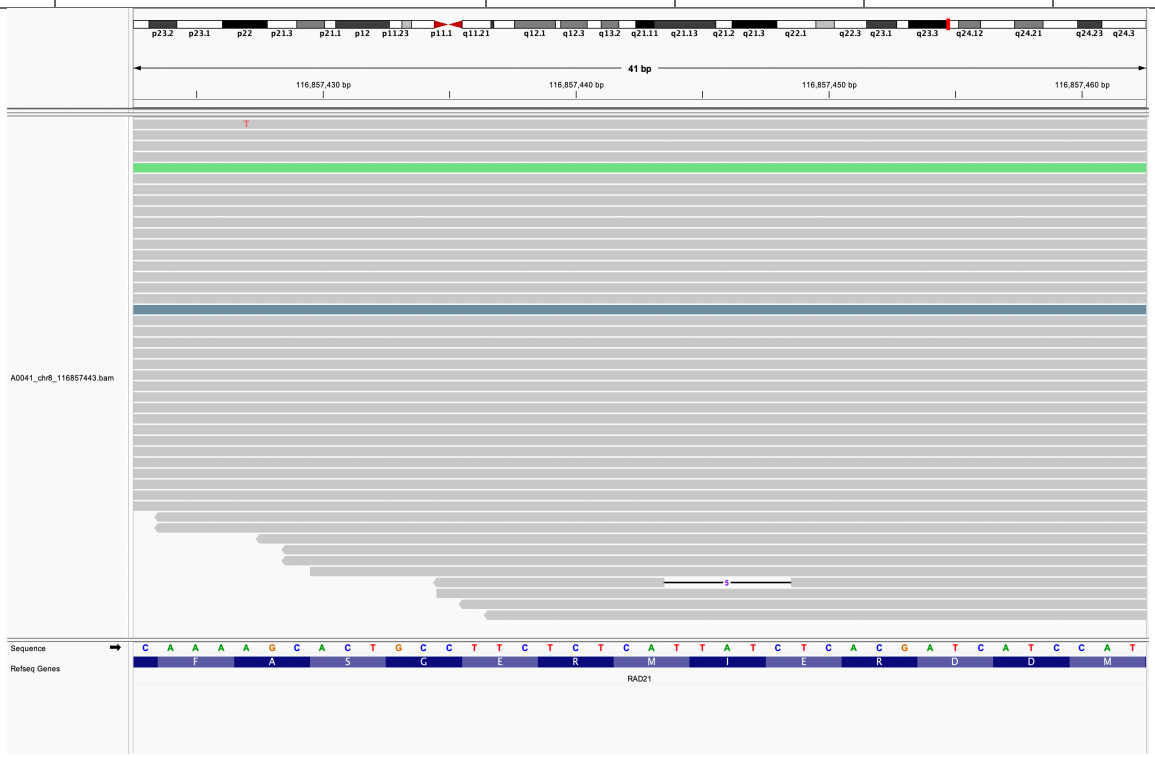
43.3. chr8_116857385_GTTAGAAGTA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060044D	chr8_116857385_GTTAGAAGTA/-	54	2	*RAD21*	frameshift_variant
CNS0134993	chr8_116857385_GTTAGAAGTA/-	53	2	*RAD21*	frameshift_variant



43.4. chr8_116857444_TTATC/-

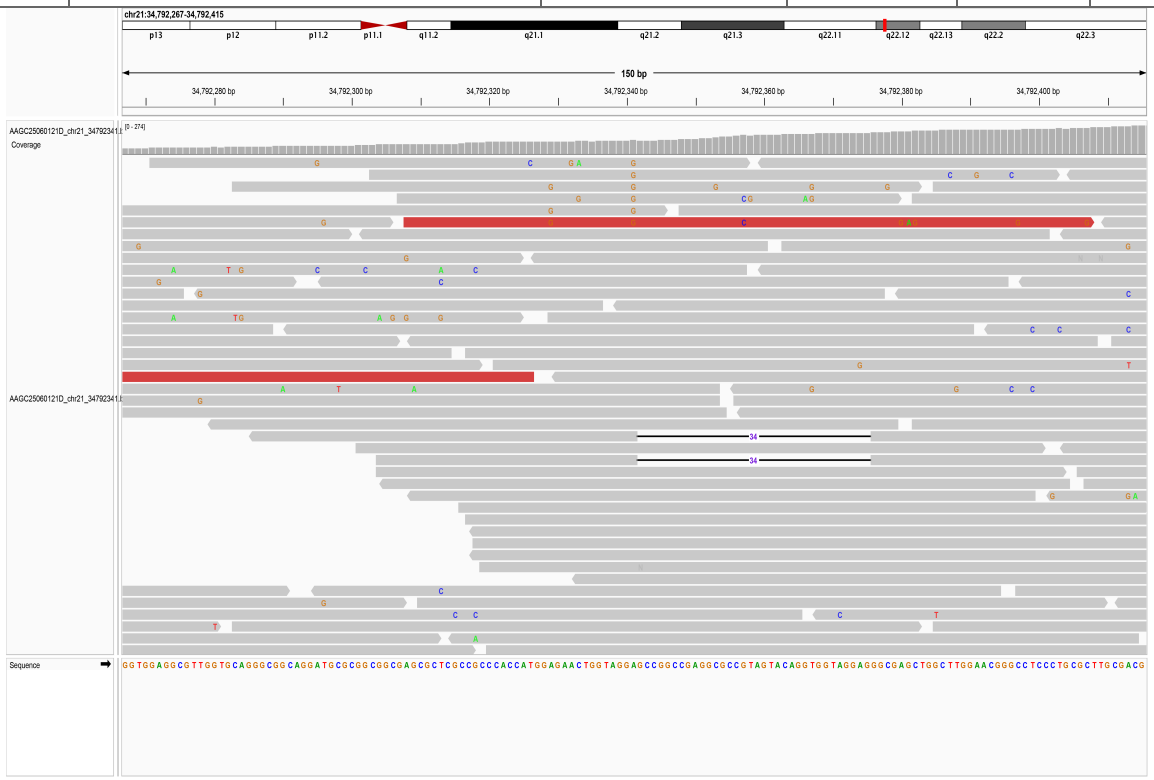
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0041	chr8_116857444_TTATC/-	115	2	*RAD21*	frameshift_variant



44. *RUNX1*

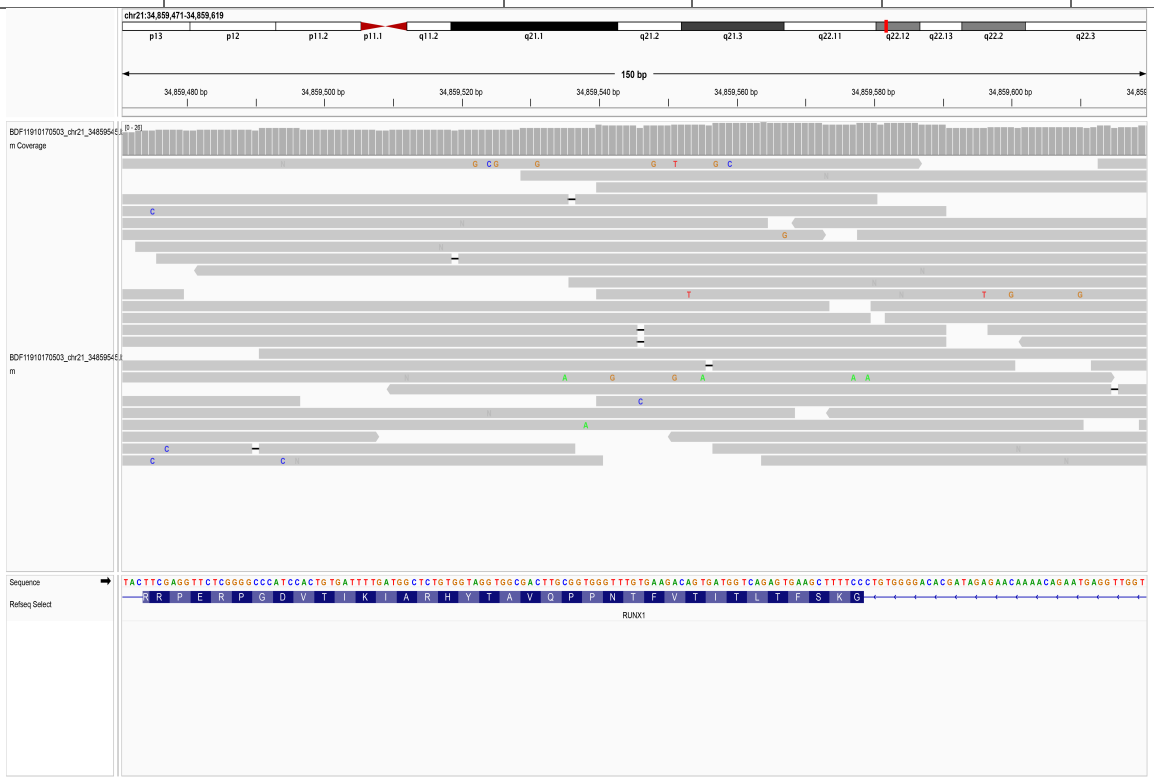
44.1. chr21_34792342_GCCGGCCGAGGCGCCGTAGTACAGGTGGTAGGAG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060121D	chr21_34792342_GCCGGCCGAGGCGCCGTAGTACAGGTGGTAGGAG/-	157	3	*RUNX1*	frameshift_variant



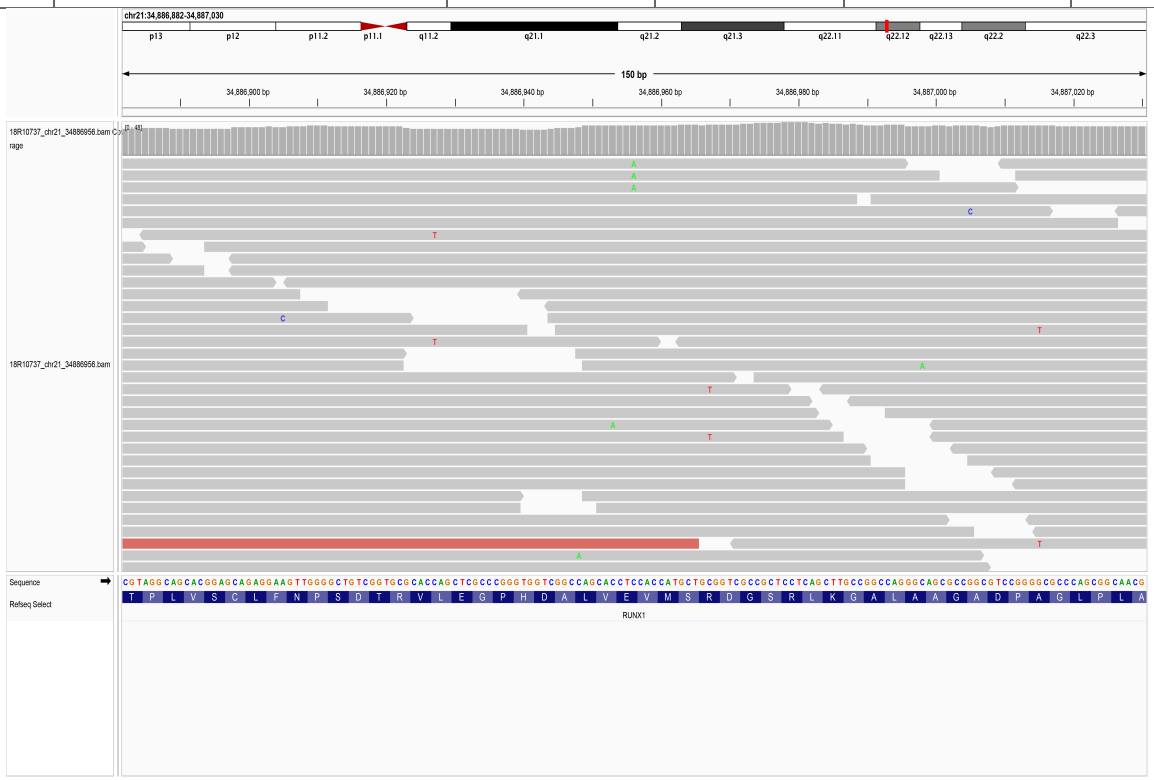
44.2. chr21_34859546_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr21_34859546_T/-	18	2	*RUNX1*	frameshift_variant



44.3. chr21_34886956_C/A

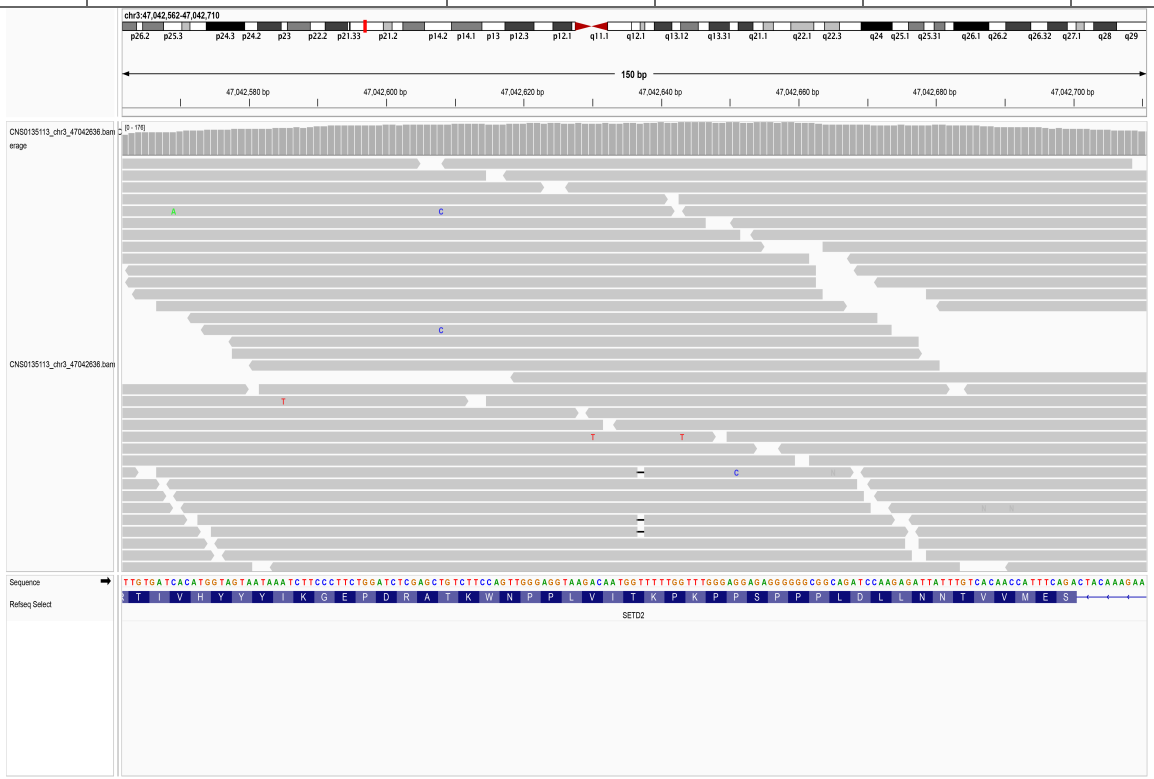
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10737	chr21_34886956_C/A	39	3	*RUNX1*	stop_gained



45. *SETD2*

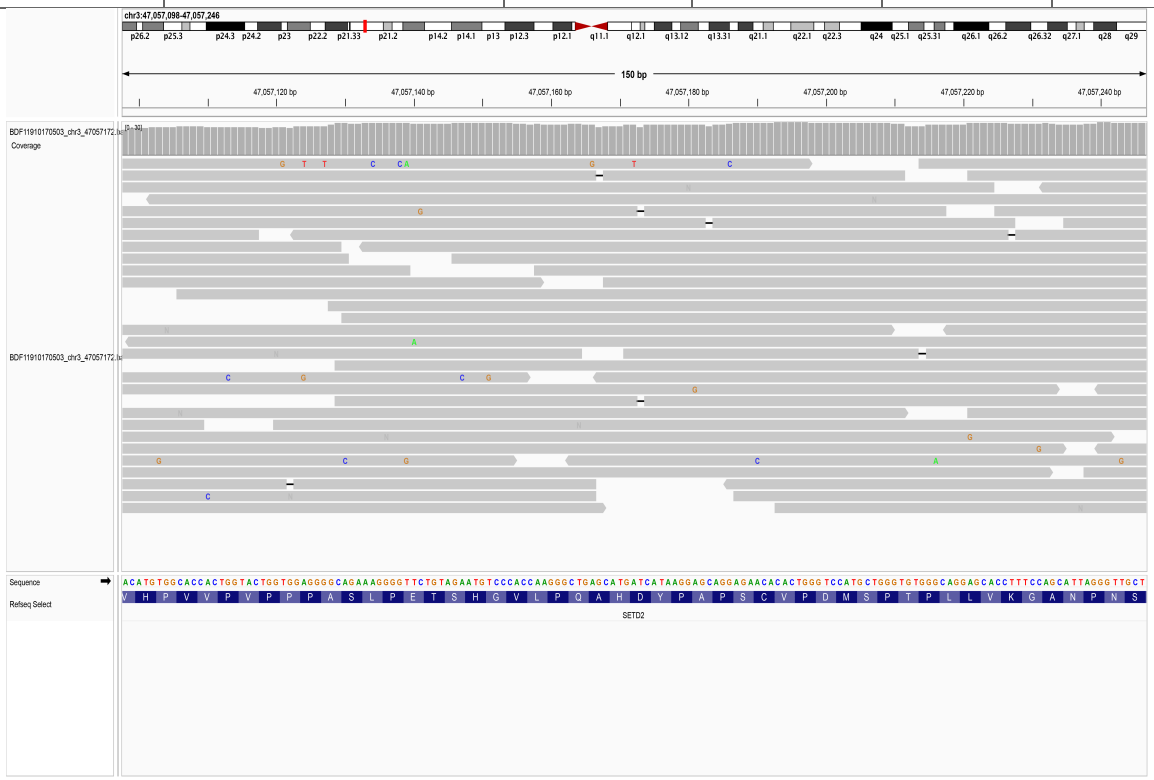
45.1. chr3_47042637_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135113	chr3_47042637_T/-	155	5	*SETD2*	frameshift_variant



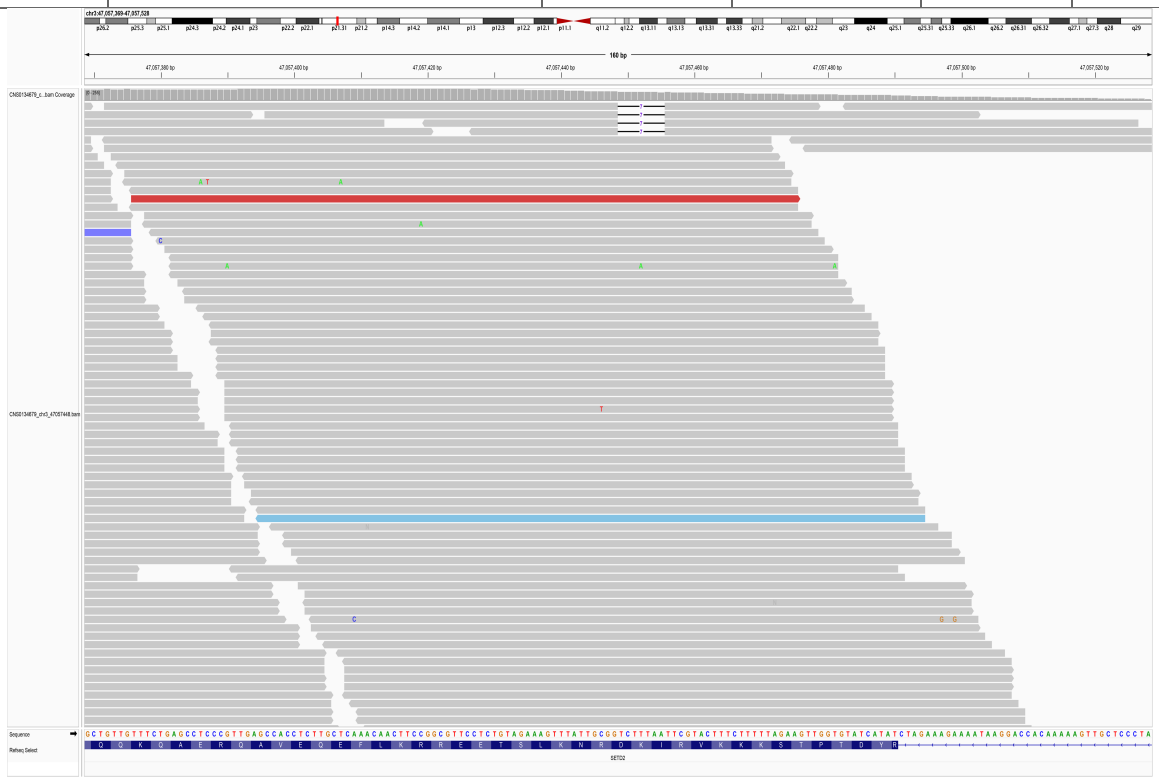
45.2. chr3_47057173_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr3_47057173_T/-	24	2	*SETD2*	frameshift_variant



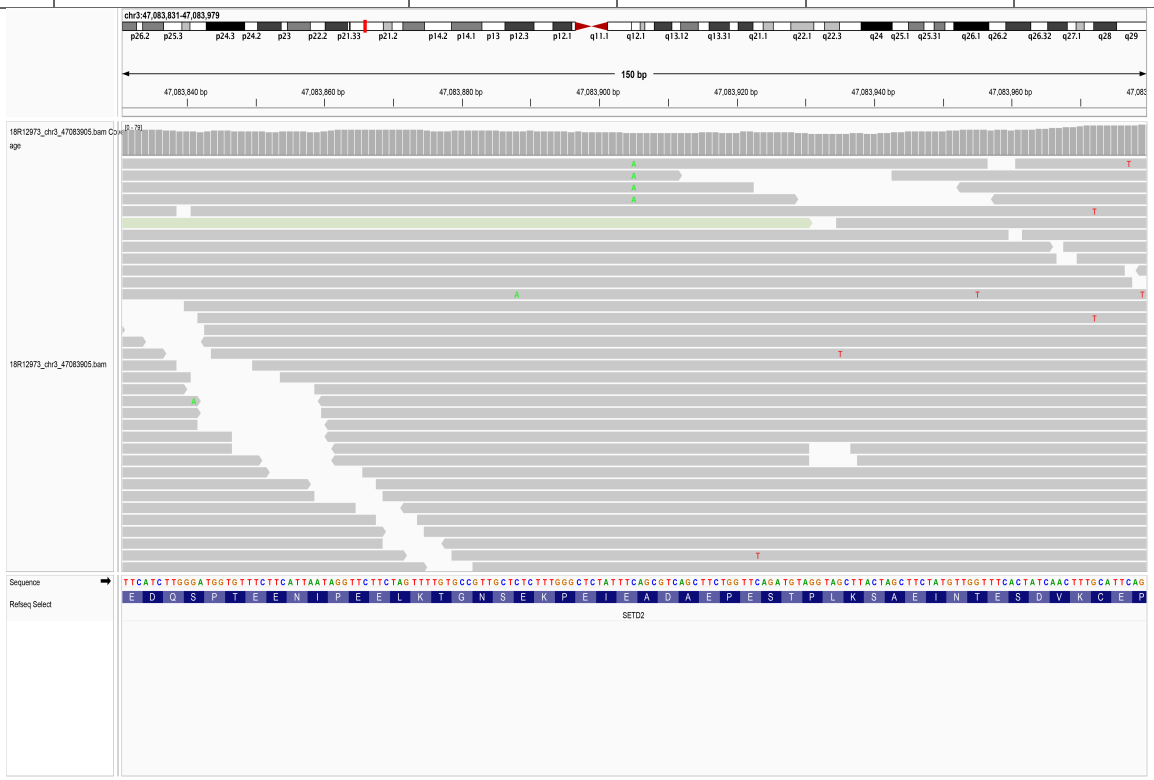
45.3. chr3_47057449_TCTTTAA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134679	chr3_47057449_TCTTTAA/-	183	4	*SETD2*	frameshift_variant



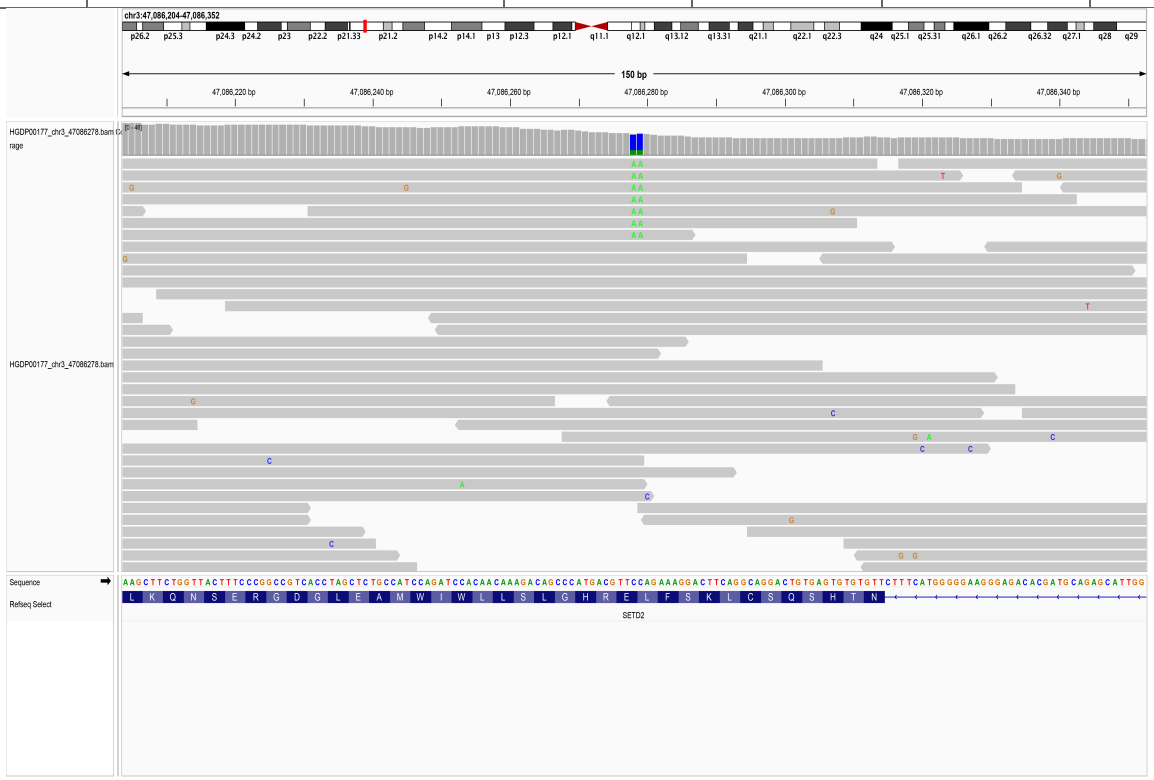
45.4. chr3_47083905_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12973	chr3_47083905_C/A	46	4	*SETD2*	stop_gained



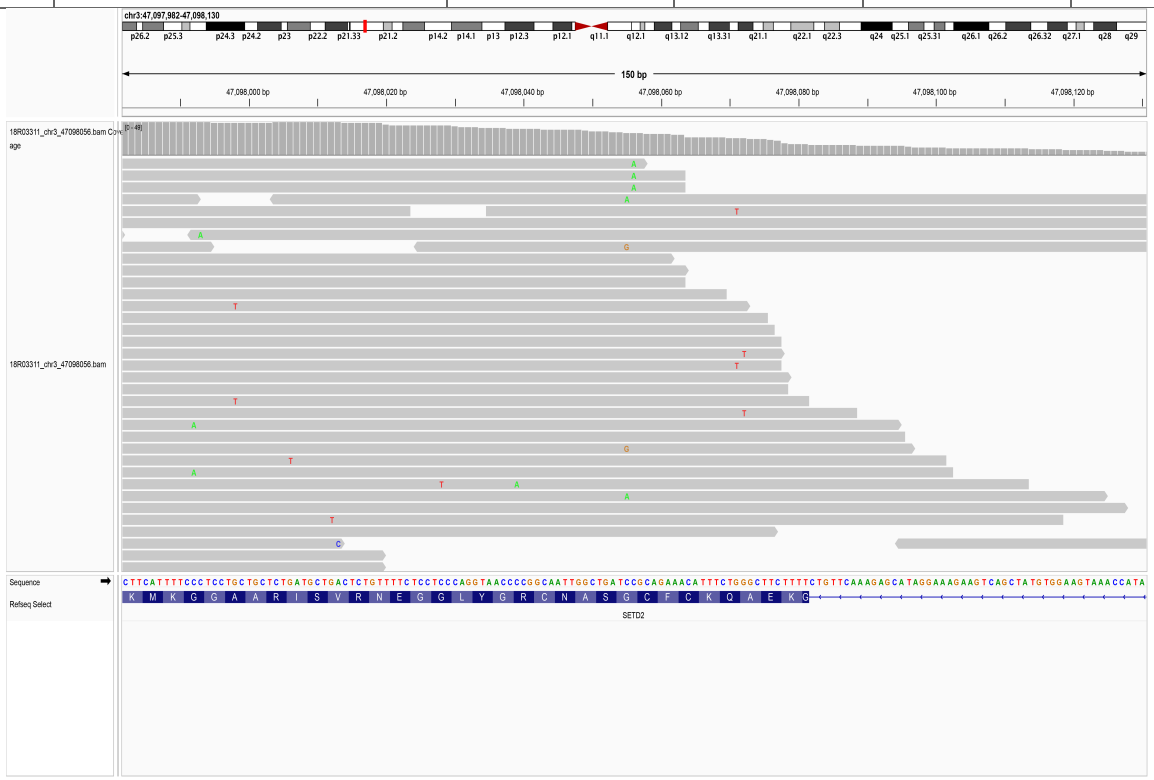
45.5. chr3_47086278_CC/AA

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HGDP00177	chr3_47086278_CC/AA	22	7	*SETD2*	stop_gained



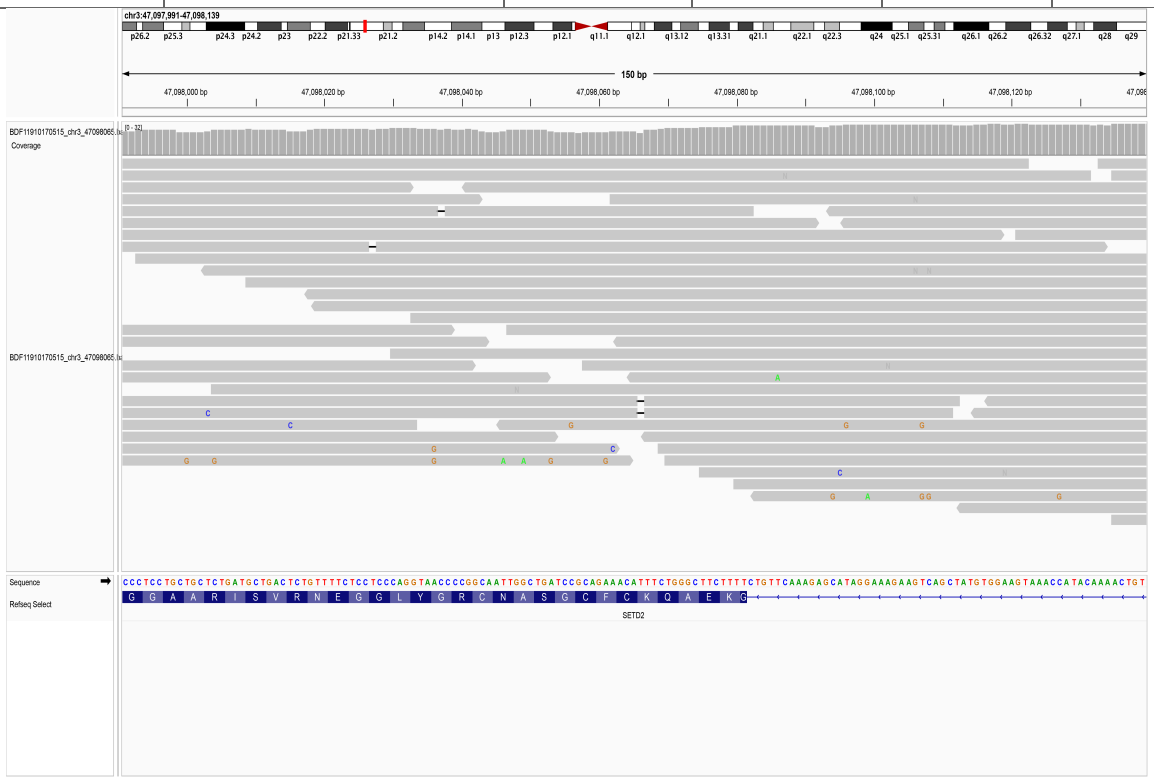
45.6. chr3_47098056_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr3_47098056_C/A	29	3	*SETD2*	stop_gained



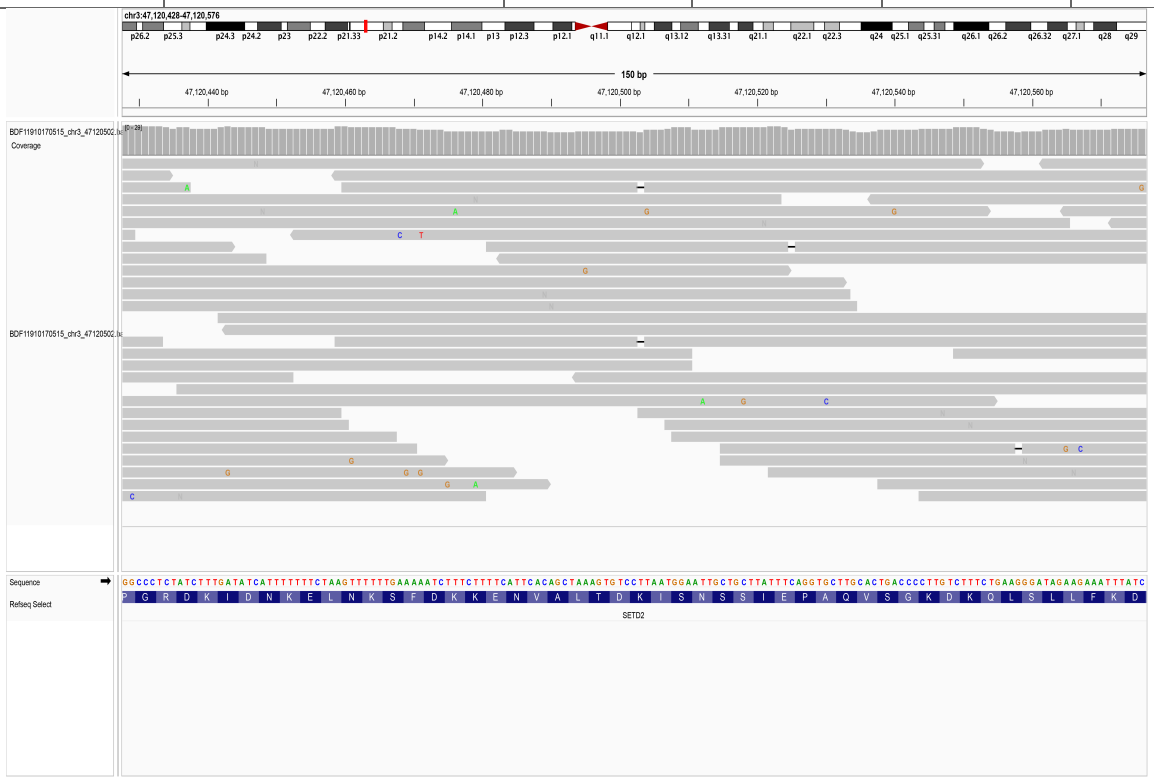
45.7. chr3_47098066_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170515	chr3_47098066_T/-	21	2	*SETD2*	frameshift_variant



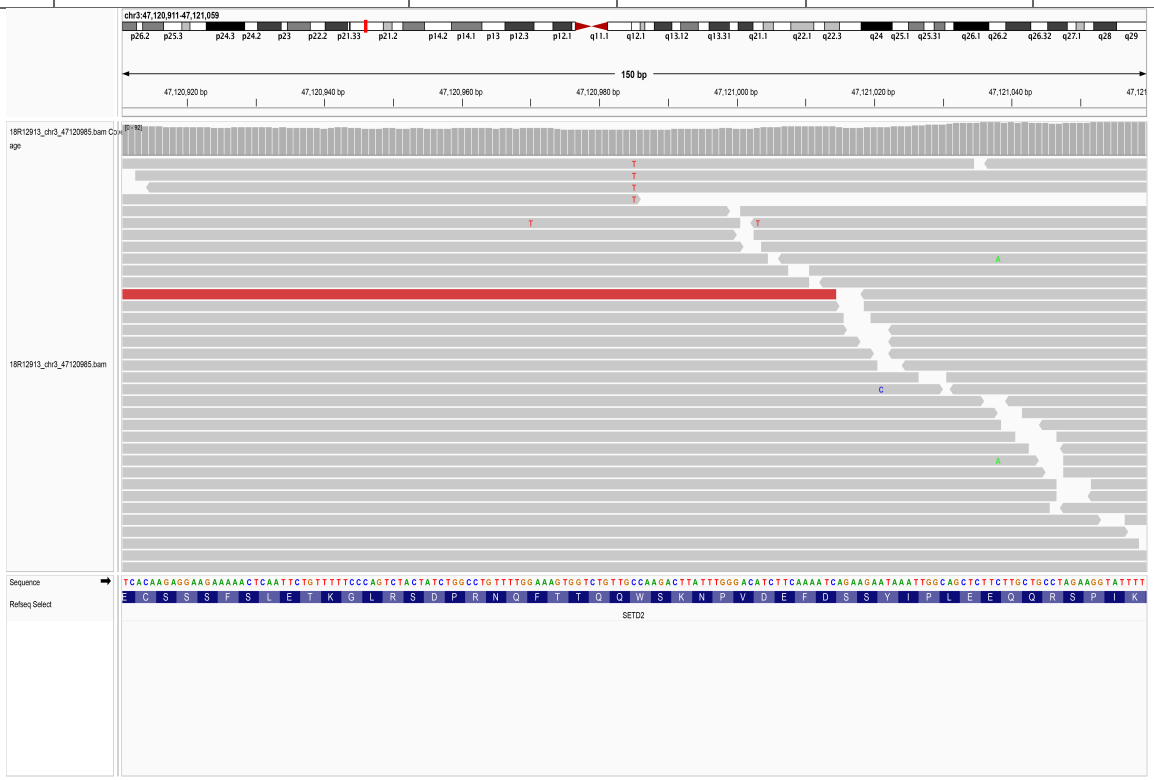
45.8. chr3_47120503_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170515	chr3_47120503_T/-	19	2	*SETD2*	frameshift_variant



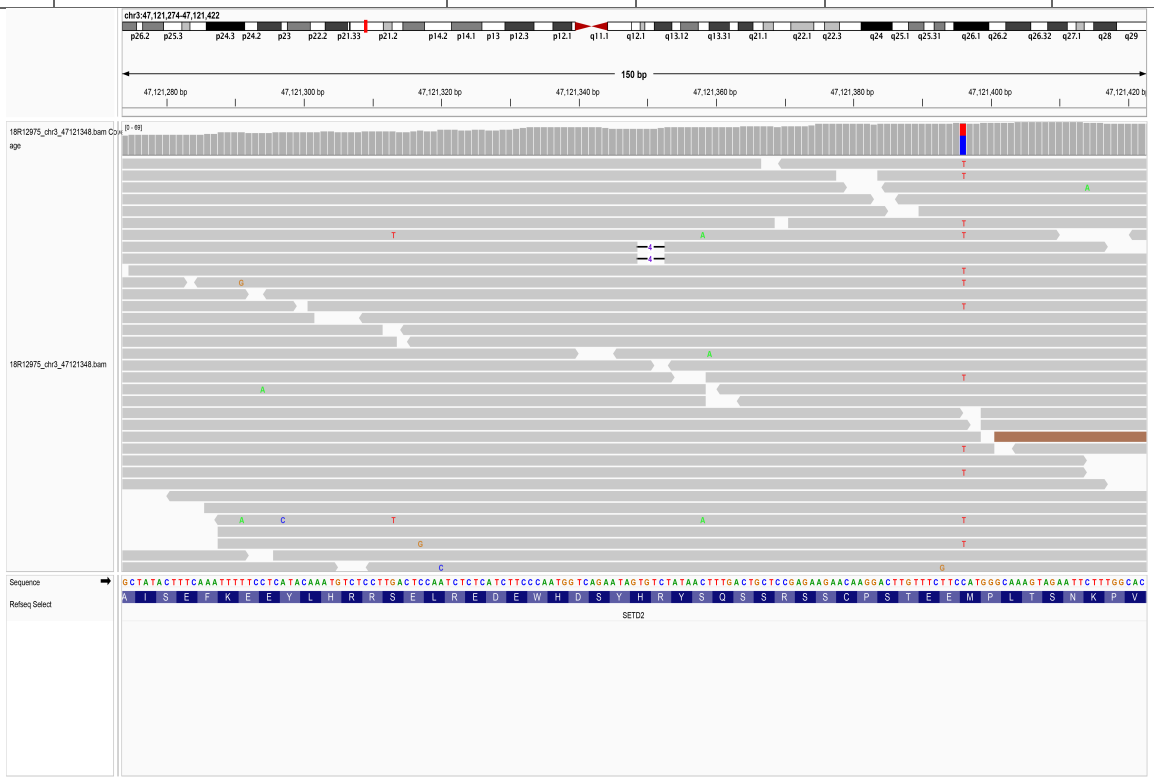
45.9. chr3_47120985_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12913	chr3_47120985_C/T	64	4	*SETD2*	stop_gained



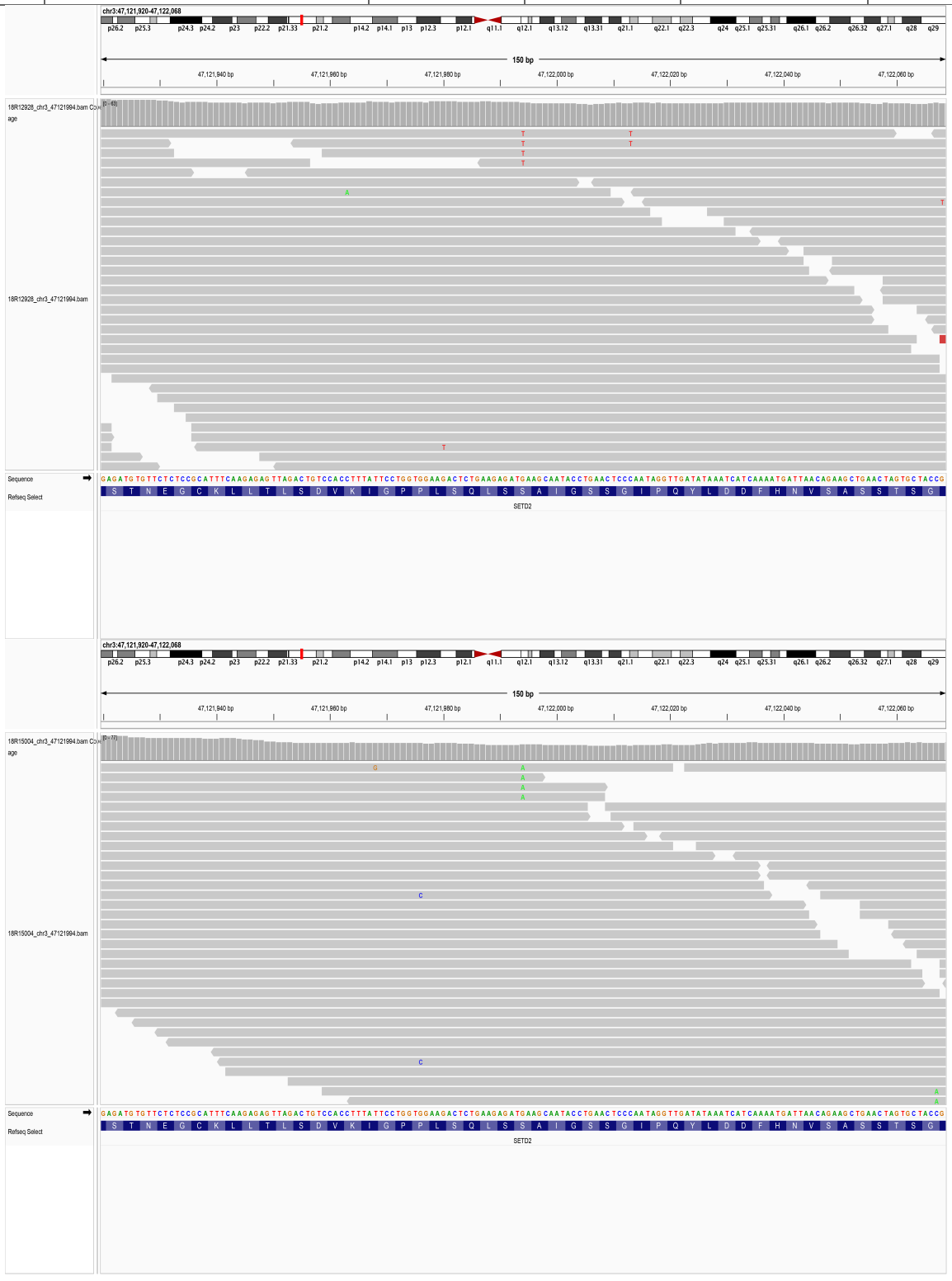
45.10. chr3_47121349_TGTC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12975	chr3_47121349_TGTC/-	56	2	*SETD2*	frameshift_variant



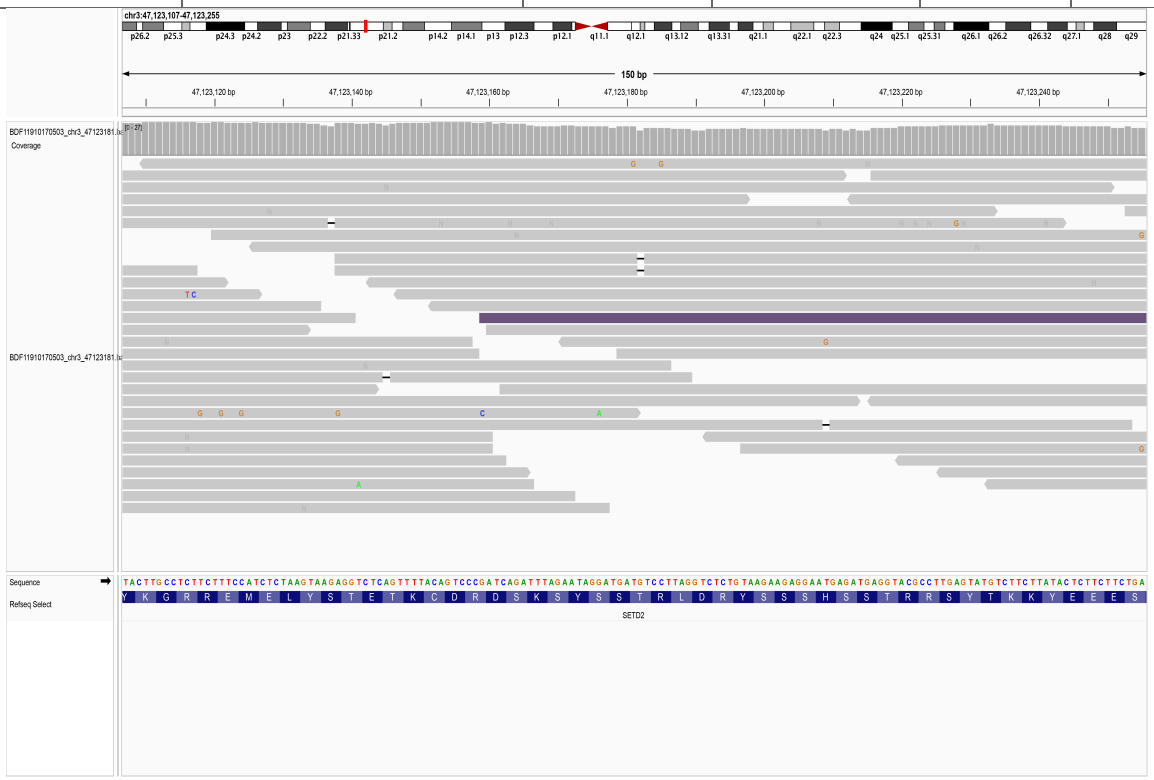
45.11. chr3_47121994_G/T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12928	chr3_47121994_G/T/A	50	4	*SETD2*	stop_gained
18R15004	chr3_47121994_G/T/A	41	4	*SETD2*	stop_gained



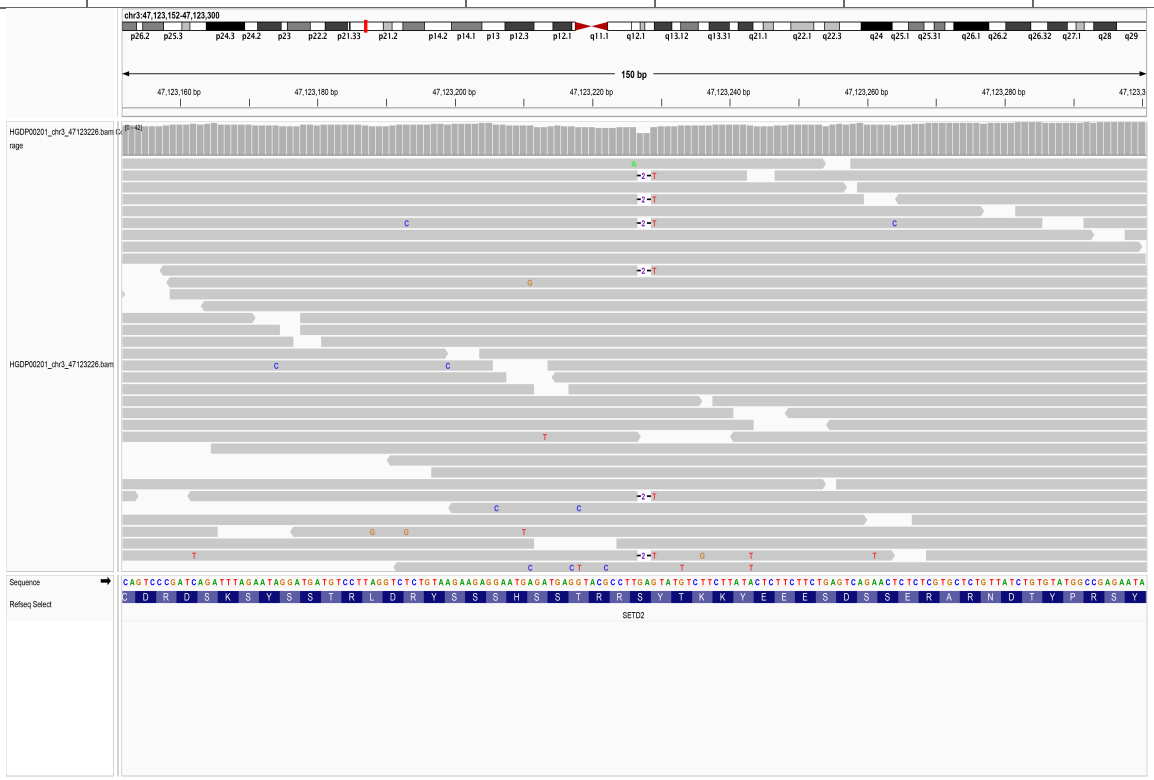
45.12. chr3_47123182_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr3_47123182_G/-	19	2	*SETD2*	frameshift_variant



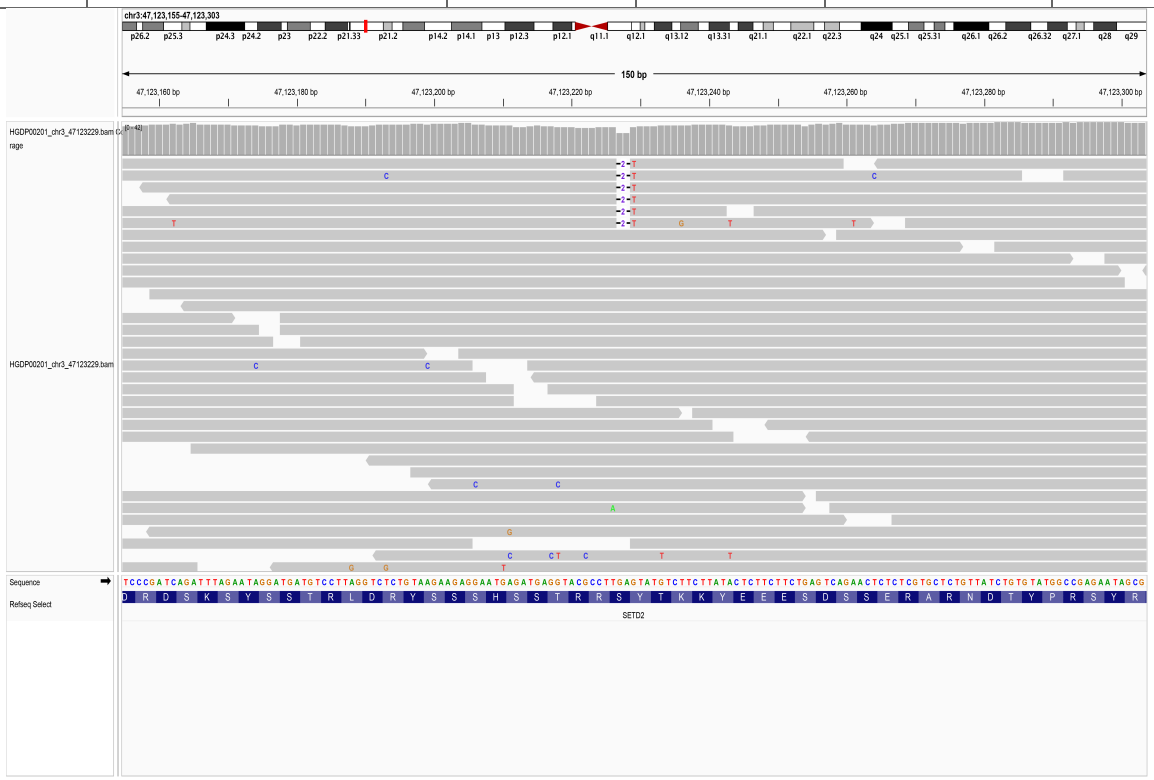
45.13. chr3_47123227_GA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HGDP00201	chr3_47123227_GA/-	28	6	*SETD2*	frameshift_variant



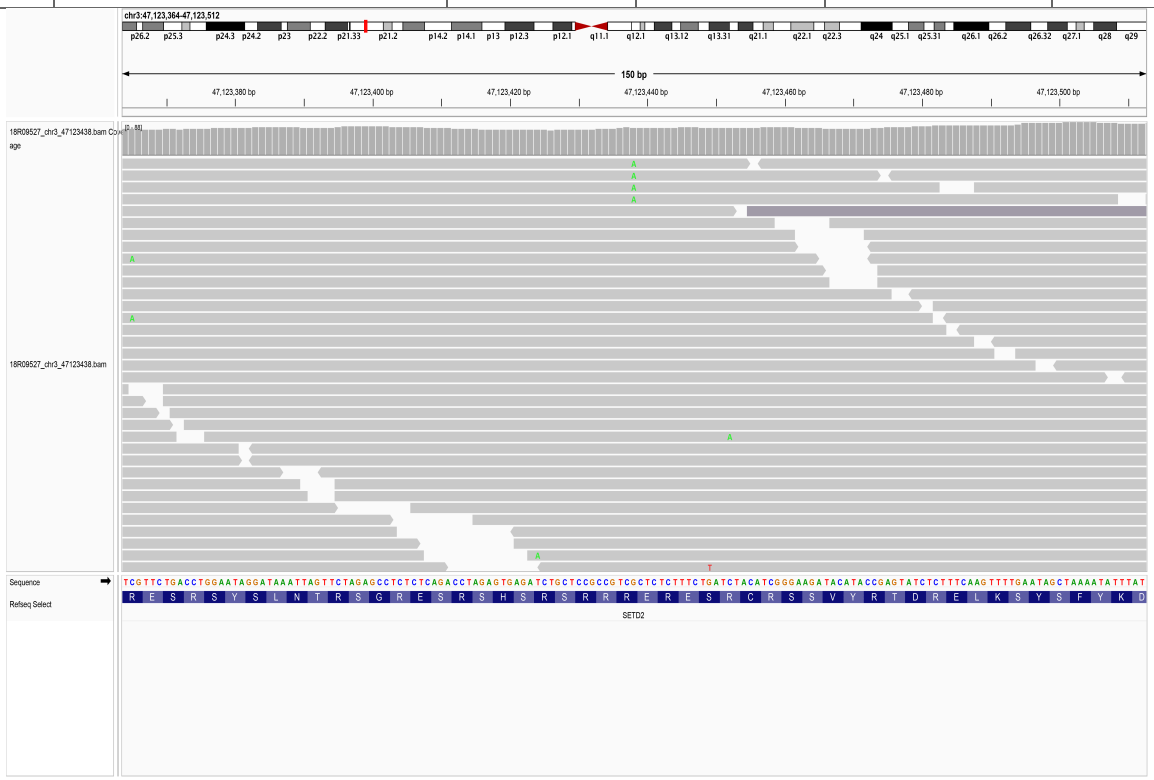
45.14. chr3_47123229_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HGDP00201	chr3_47123229_G/T	28	6	*SETD2*	stop_gained



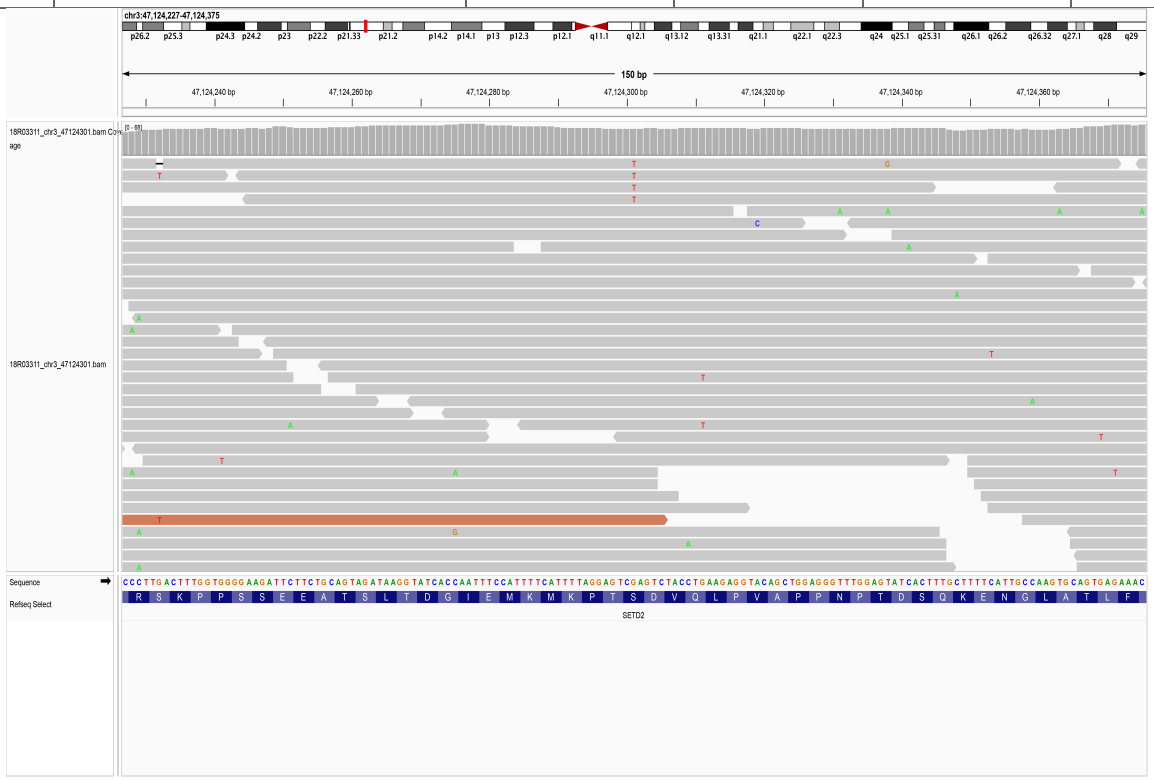
45.15. chr3_47123438_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09527	chr3_47123438_G/A	59	4	*SETD2*	stop_gained



45.16. chr3_47124301_G/T

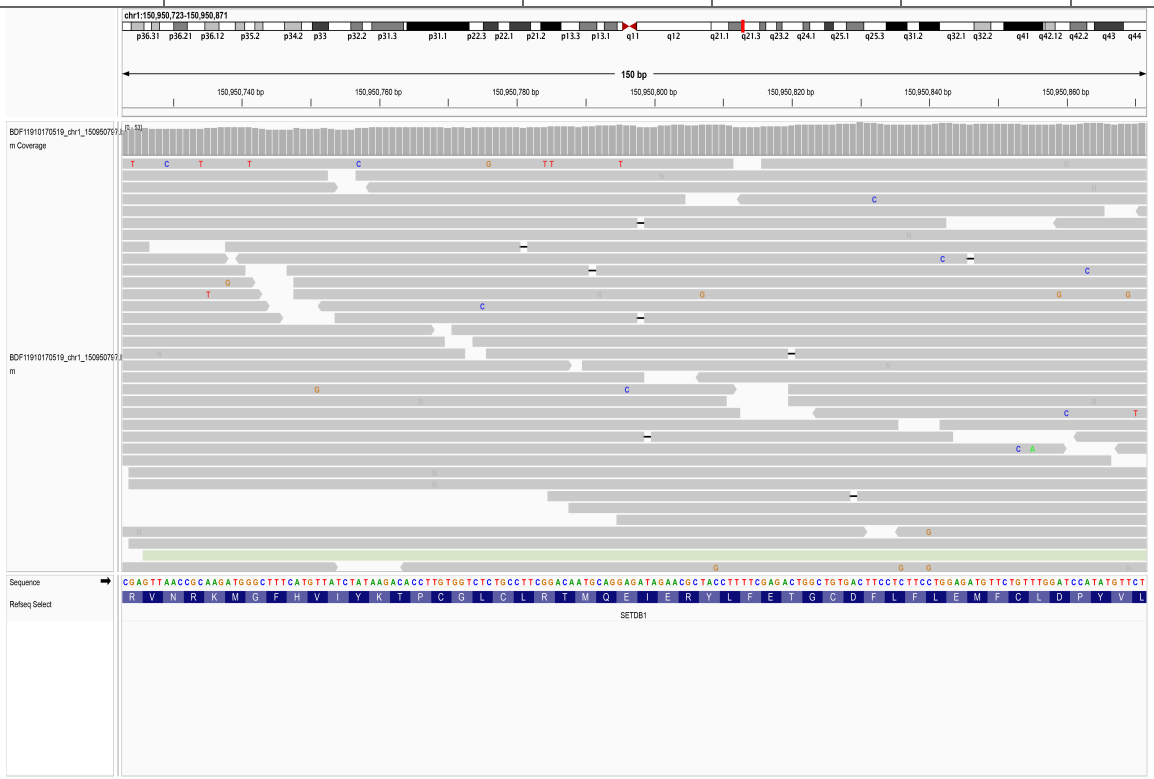
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr3_47124301_G/T	47	4	*SETD2*	stop_gained



46. *SETDB1*

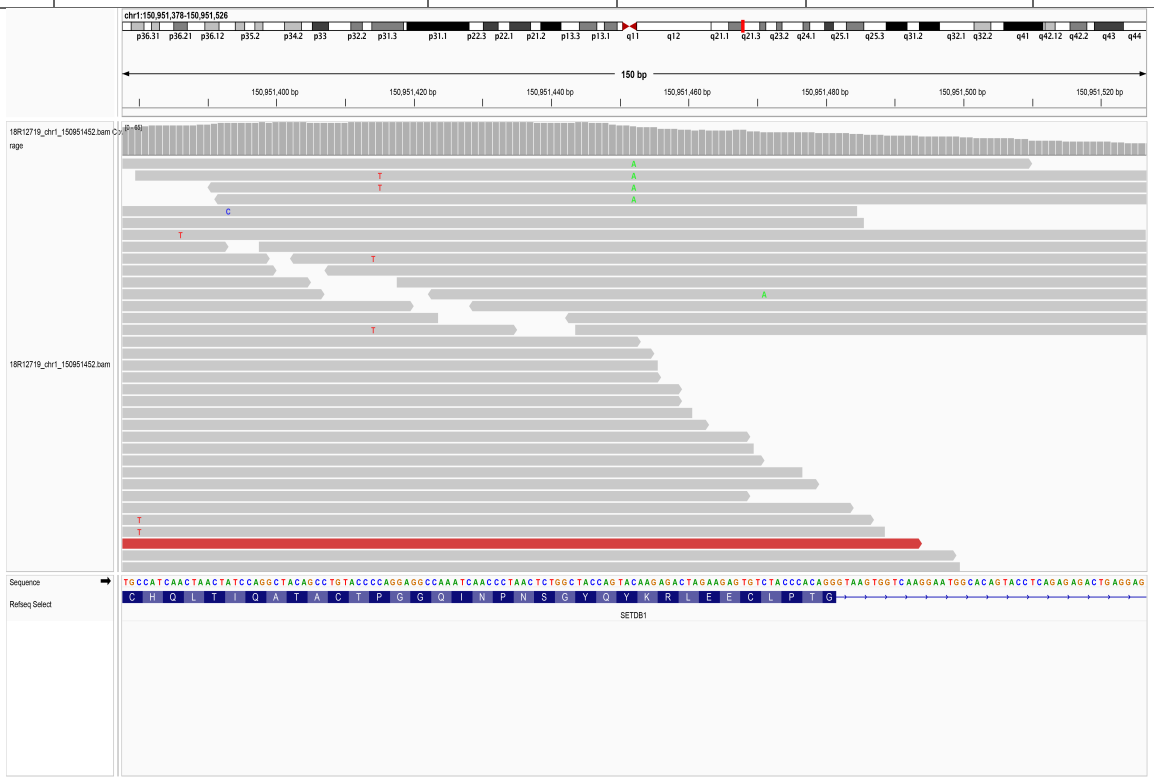
46.1. chr1_150950798_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chr1_150950798_A/-	38	3	*SETDB1*	frameshift_variant



46.2. chr1_150951452_C/A

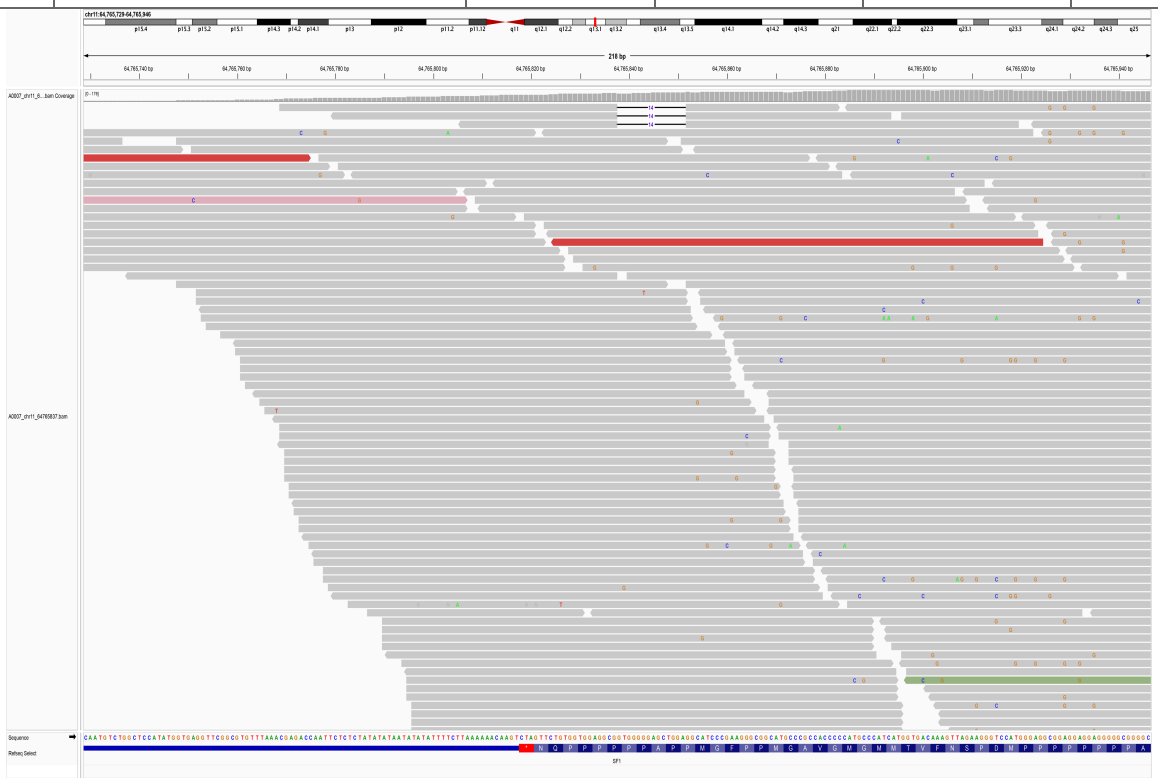
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12719	chr1_150951452_C/A	52	4	*SETDB1*	stop_gained



47. *SF1*

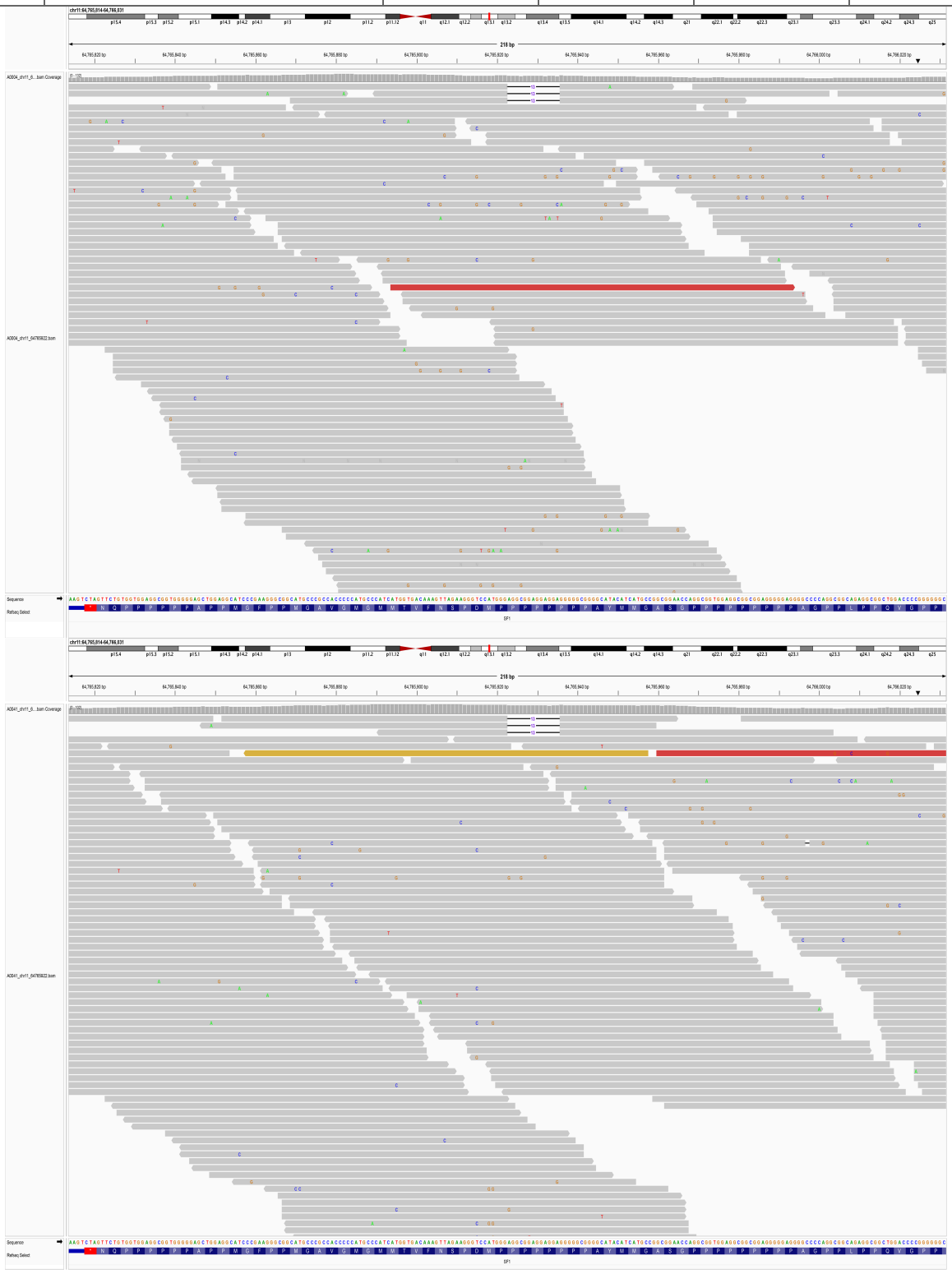
47.1. chr11_64765838_GTGGGGGAGCTGGA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0007	chr11_64765838_GTGGGGGAGCTGGA/-	137	3	*SF1*	frameshift_variant



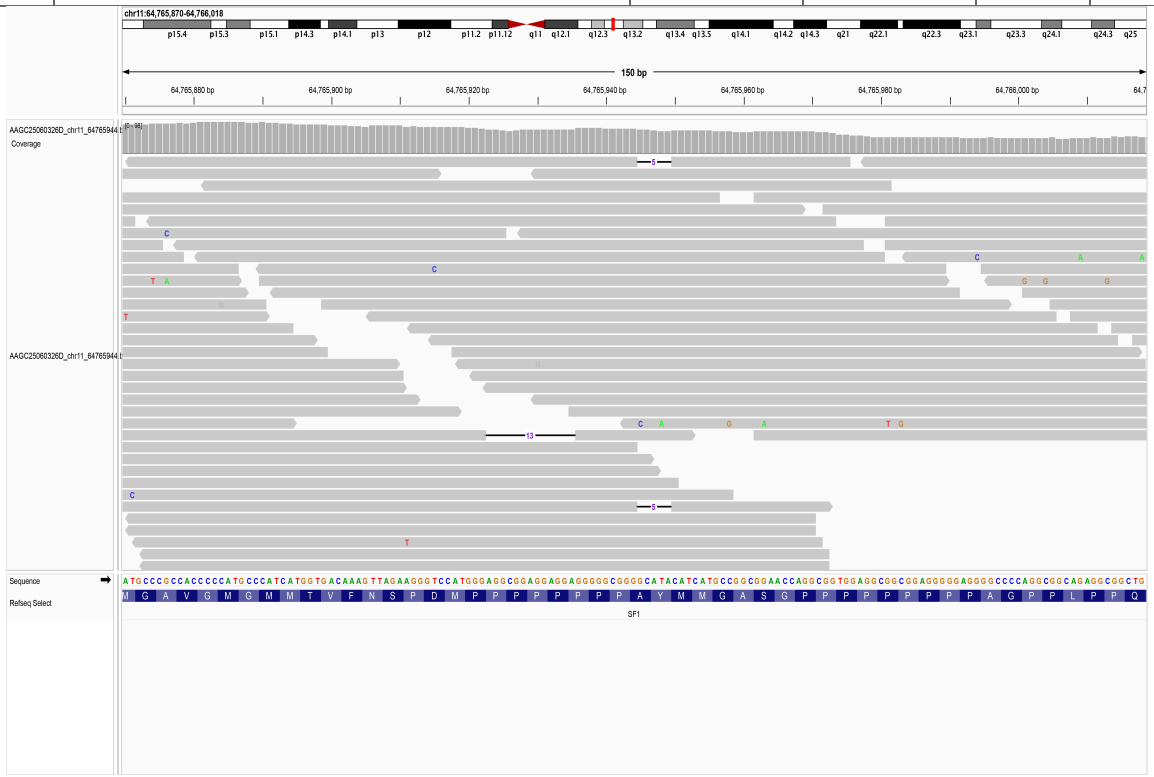
47.2. chr11_64765923_AGGCGGAGGAGGA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0004	chr11_64765923_AGGCGGAGGAGGA/-	67	3	*SF1*	frameshift_variant
A0041	chr11_64765923_AGGCGGAGGAGGA/-	95	3	*SF1*	frameshift_variant



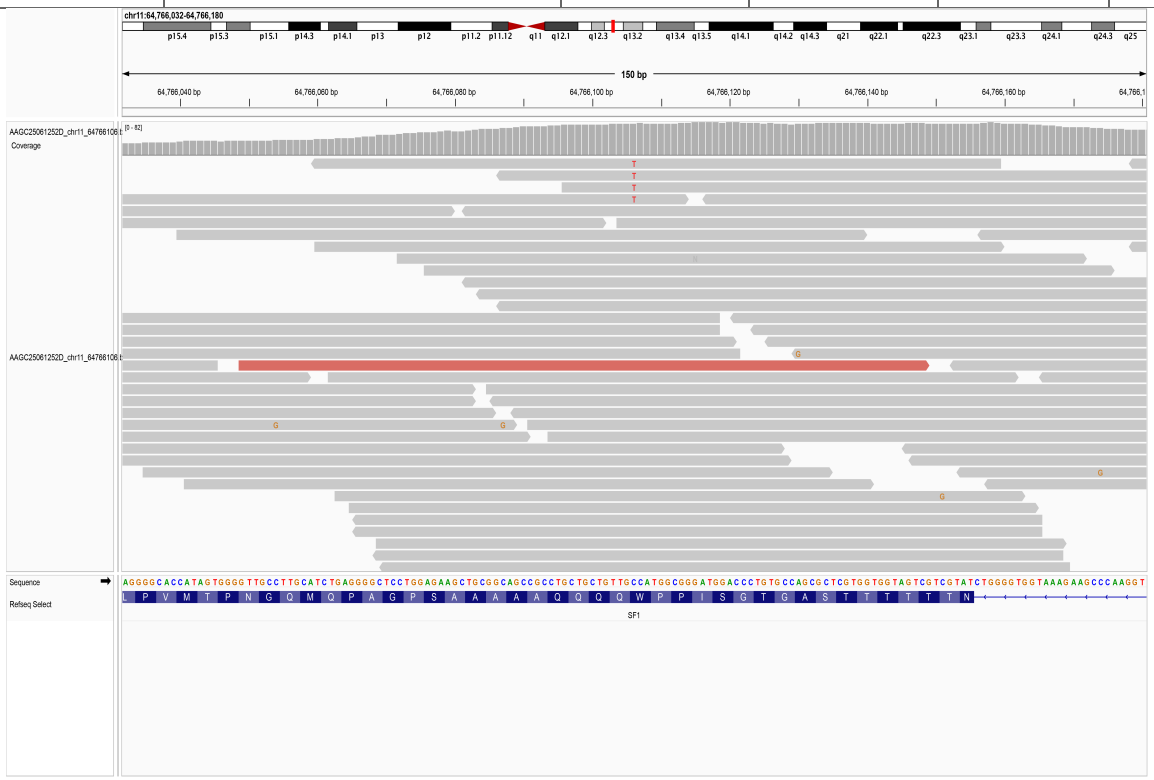
47.3. chr11_64765945_GCATA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060326D	chr11_64765945_GCATA/-	61	2	*SF1*	frameshift_variant



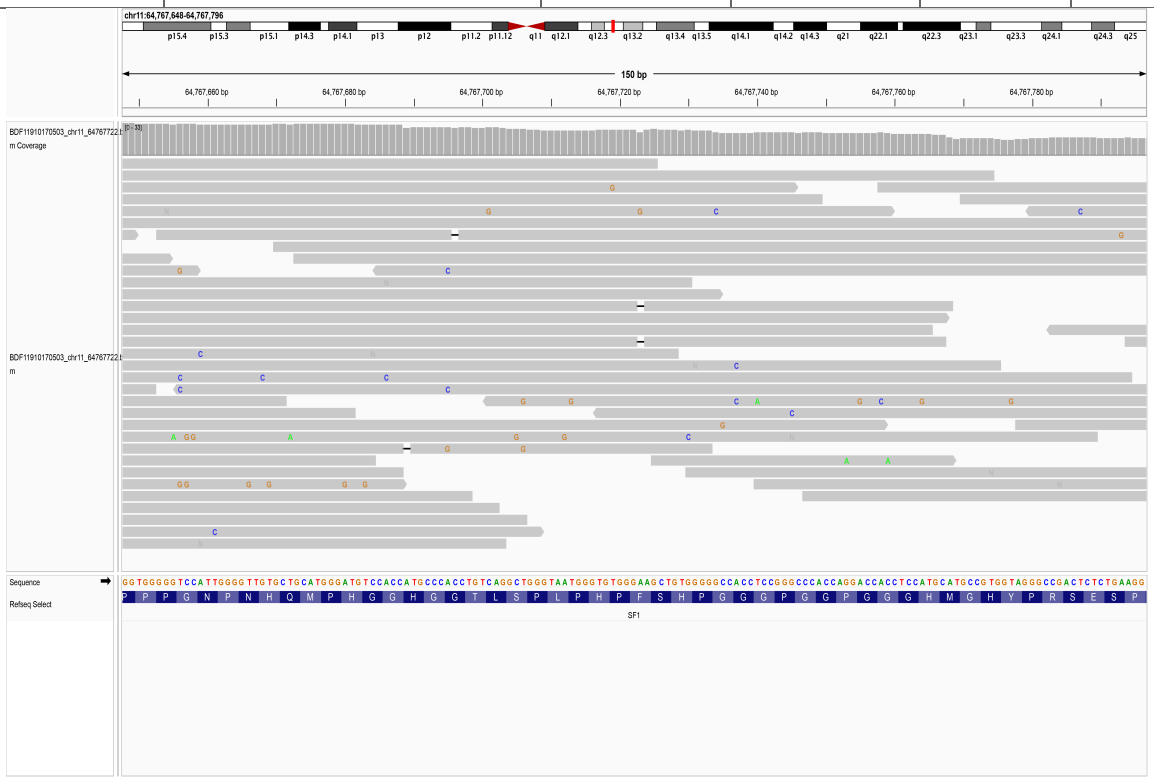
47.4. chr11_64766106_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061252D	chr11_64766106_C/T	72	4	*SF1*	stop_gained



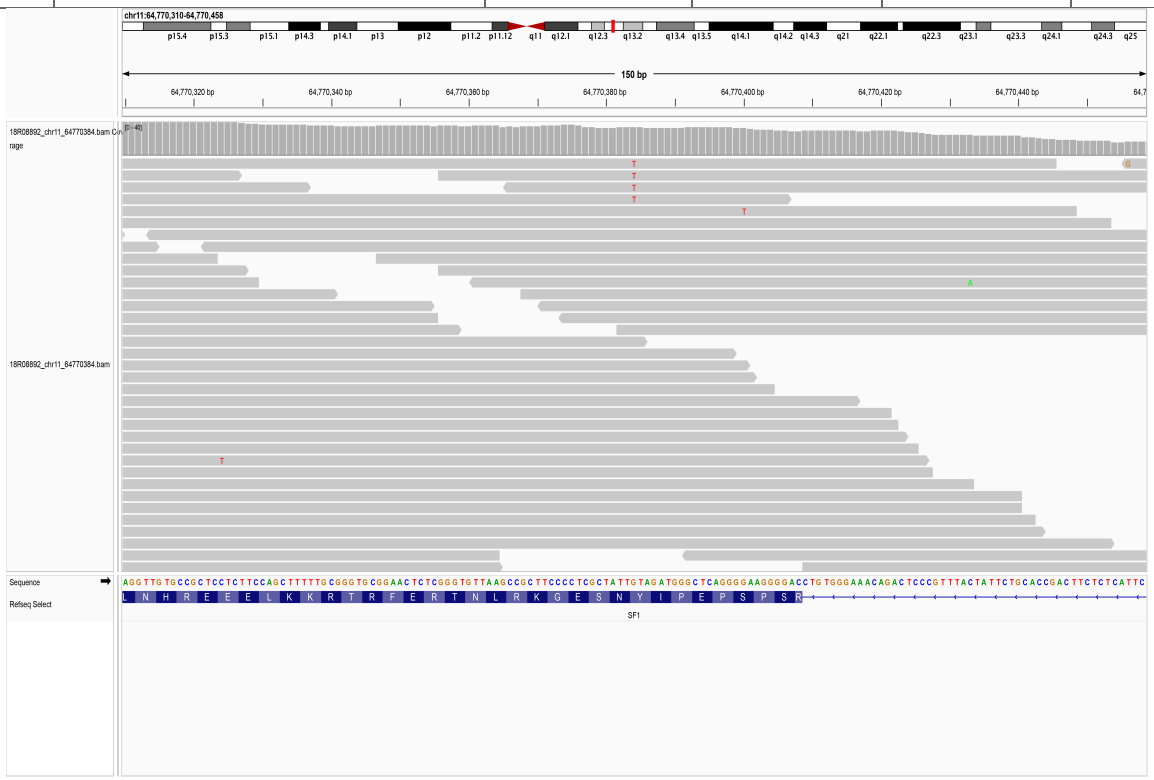
47.5. chr11_64767723_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr11_64767723_A/-	19	2	*SF1*	frameshift_variant



47.6. chr11_64770384_G/T

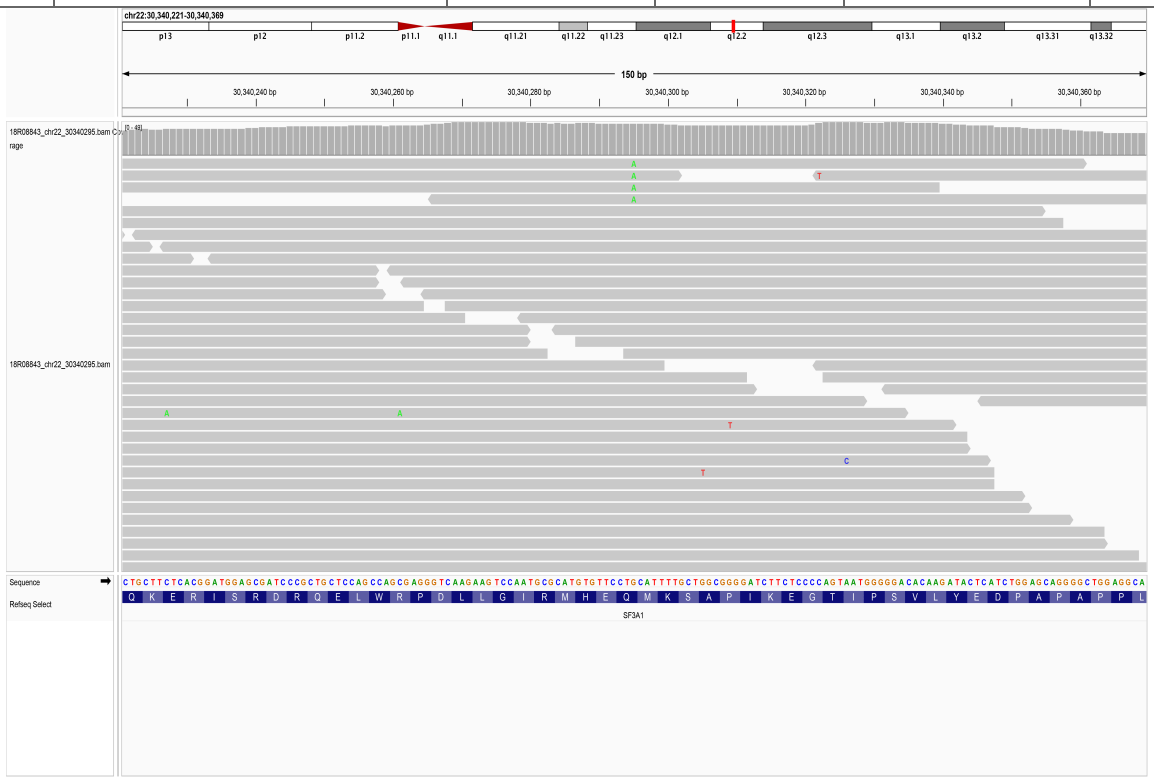
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08892	chr11_64770384_G/T	28	4	*SF1*	stop_gained



48. *SF3A1*

48.1. chr22_30340295_G/A

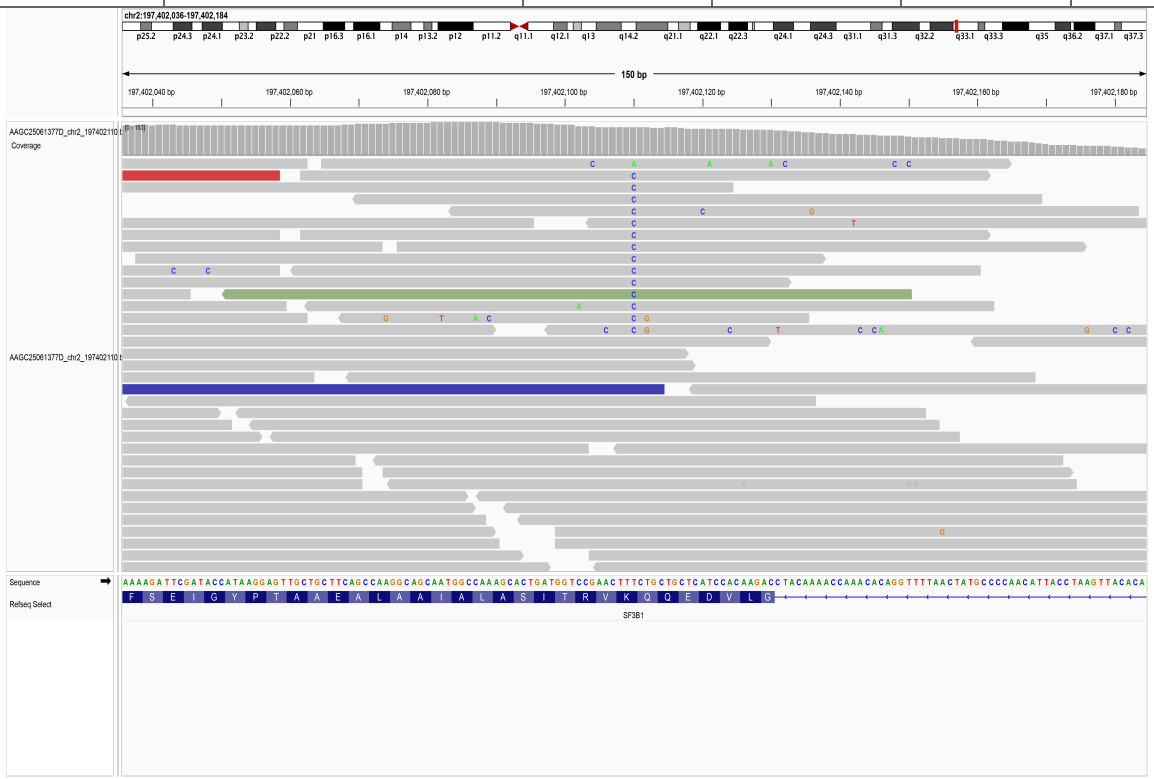
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08843	chr22_30340295_G/A	40	4	*SF3A1*	stop_gained



49. *SF3B1*

49.1. chr2_197402110_T/C

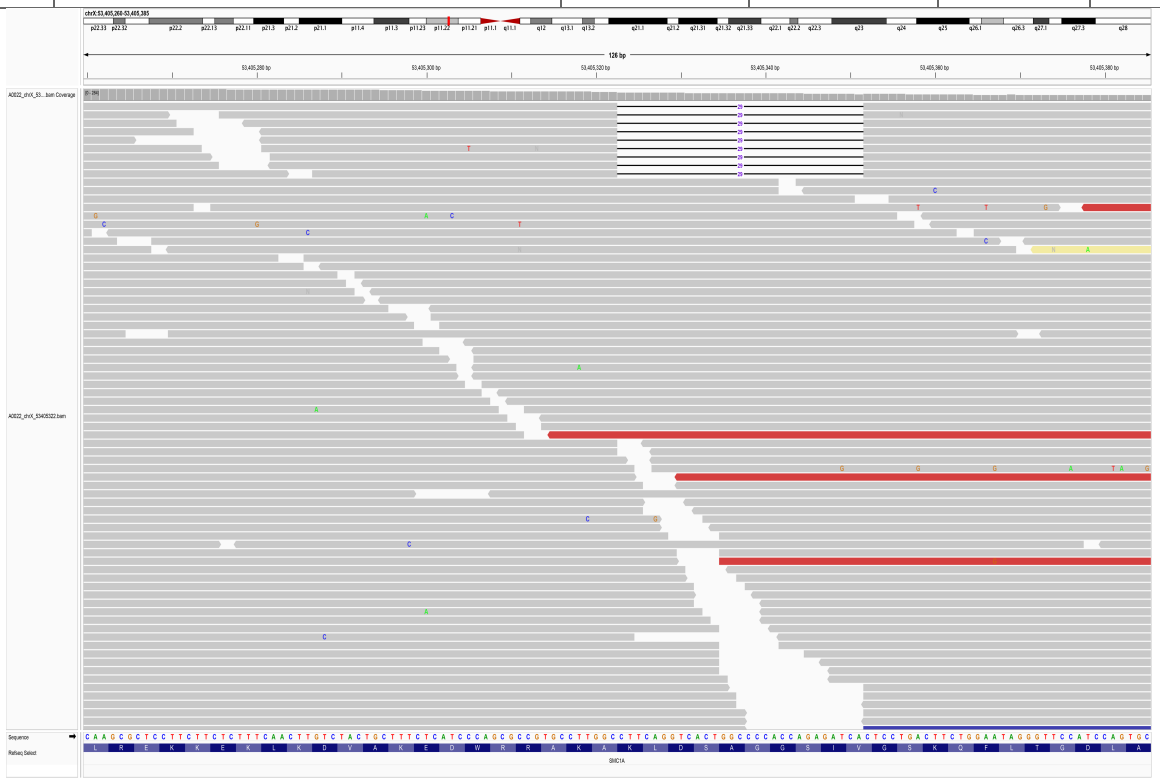
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061377D	chr2_197402110_T/C	111	13	*SF3B1*	missense_variant

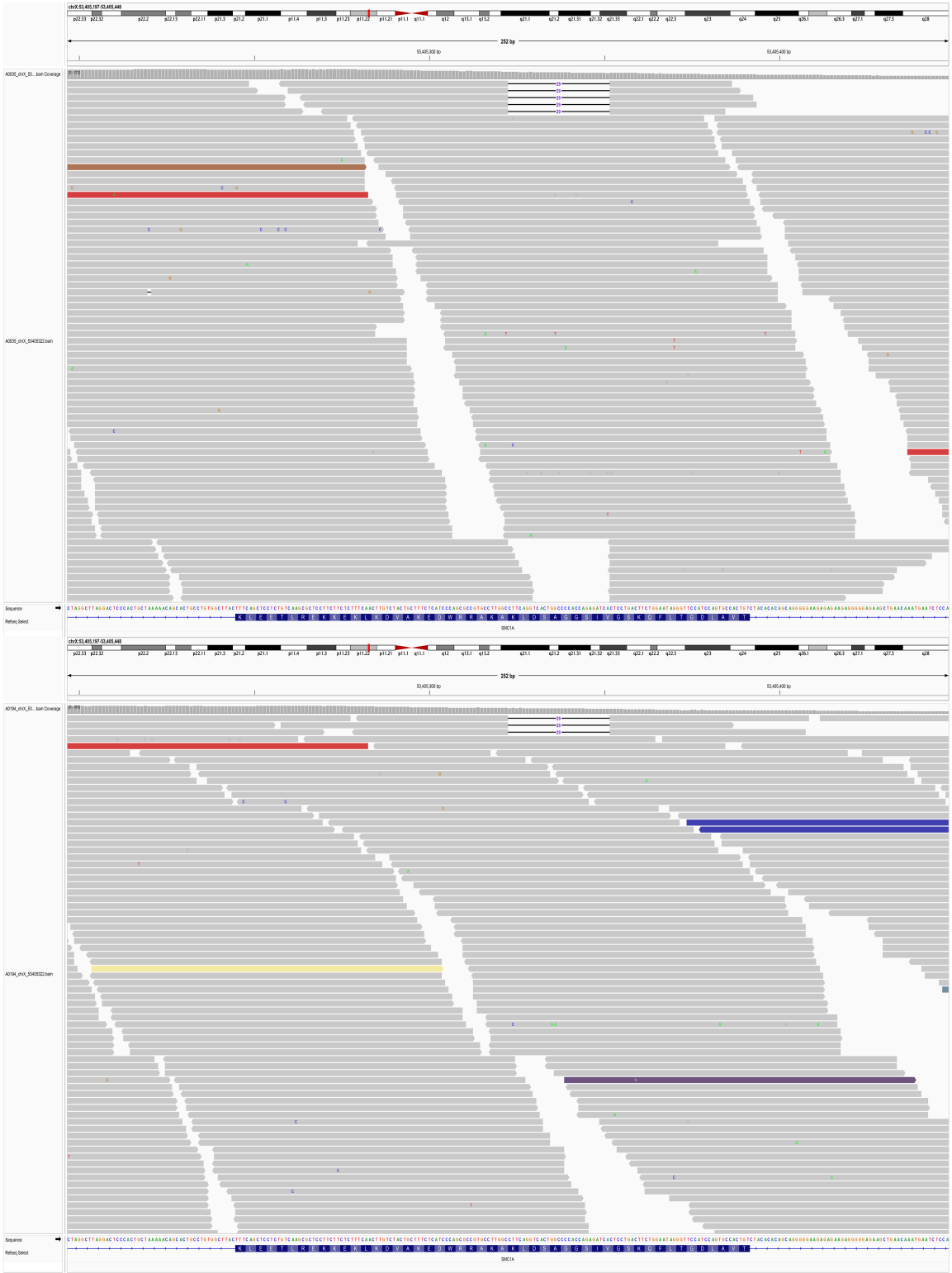


50. *SMC1A*

50.1. chrX_53405323_CTTCAGGTCACTGGCCCCACCAGAGATCA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0022	chrX_53405323_CTTCAGGTCACTGGCCCCACCAGAGATCA/-	217	9	*SMC1A*	frameshift_variant
A0035	chrX_53405323_CTTCAGGTCACTGGCCCCACCAGAGATCA/-	215	6	*SMC1A*	frameshift_variant
A0194	chrX_53405323_CTTCAGGTCACTGGCCCCACCAGAGATCA/-	166	3	*SMC1A*	frameshift_variant

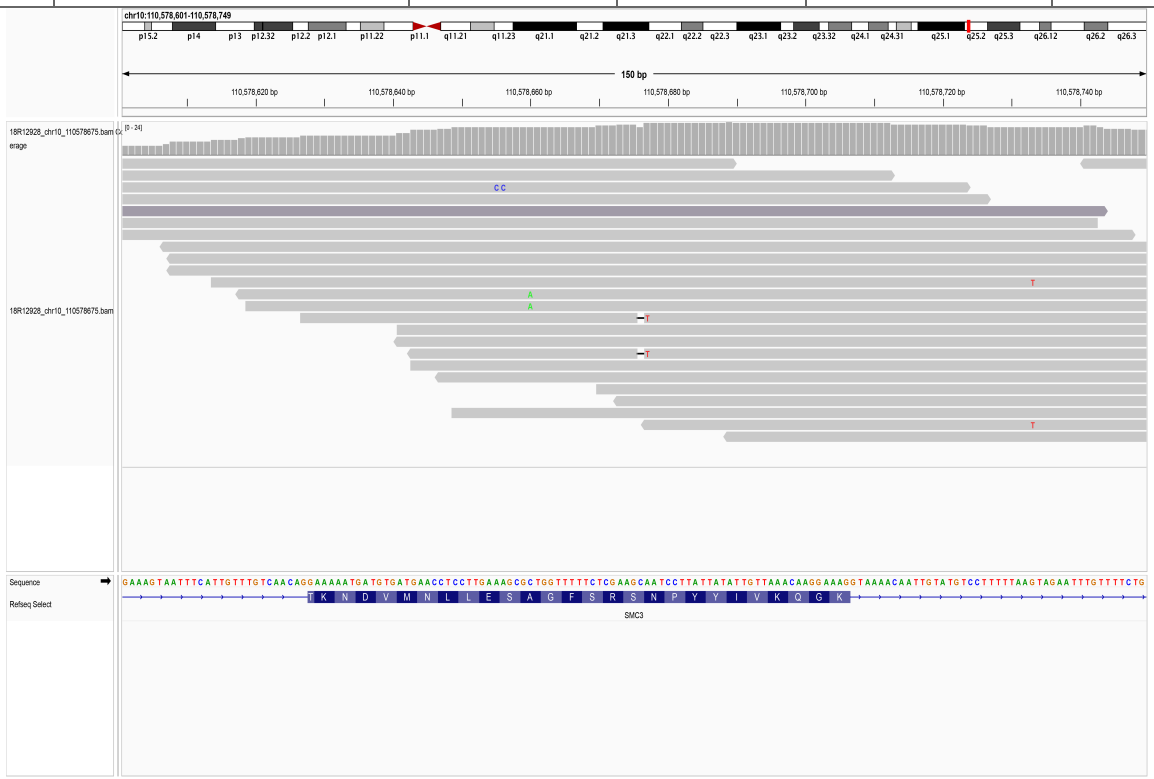



chrX:53,405,157-53,405,448
252 bp
53,405,300 bp
53,405,400 bp
A0035_chrX_53... bam Coverage
A0035_chrX_53405322.bam
Sequence
Refseq Select
SMC1A
chrX:53,405,157-53,405,448
252 bp
53,405,300 bp
53,405,400 bp
A0194_chrX_53... bam Coverage
A0194_chrX_53405322.bam
Sequence
Refseq Select
SMC1A

51. *SMC3*

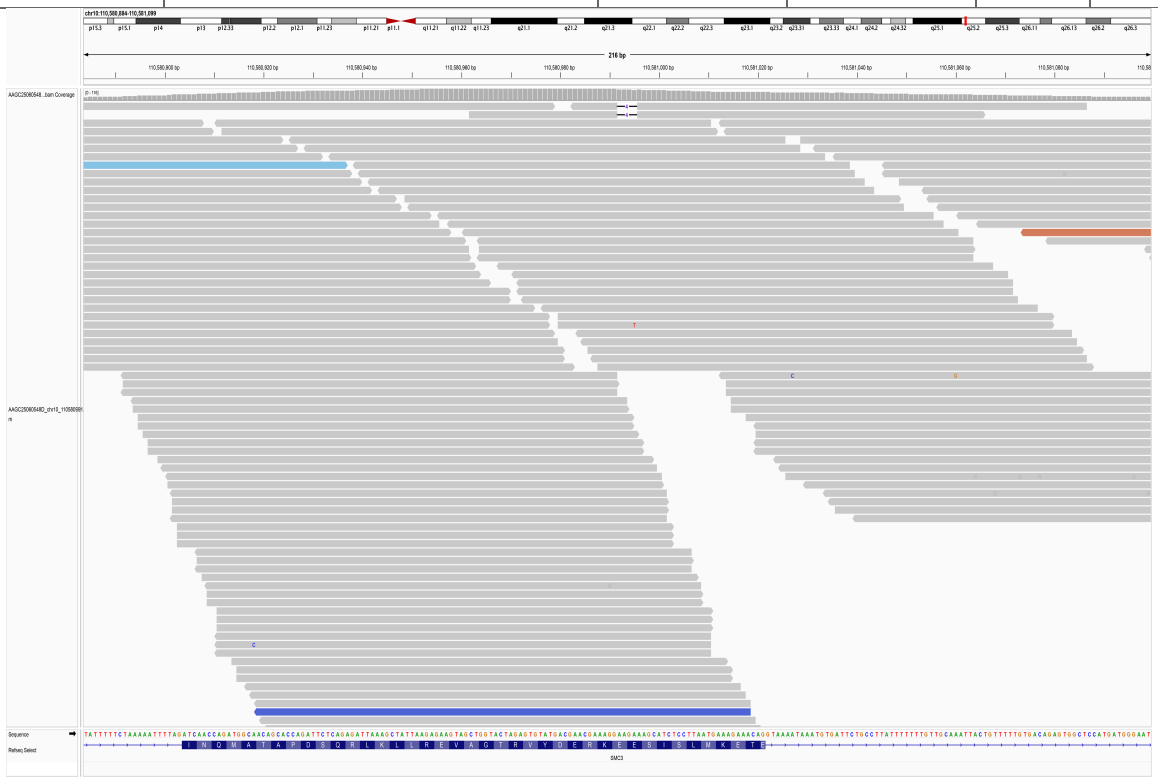
51.1. chr10_110578676_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12928	chr10_110578676_C/-	21	2	*SMC3*	frameshift_variant



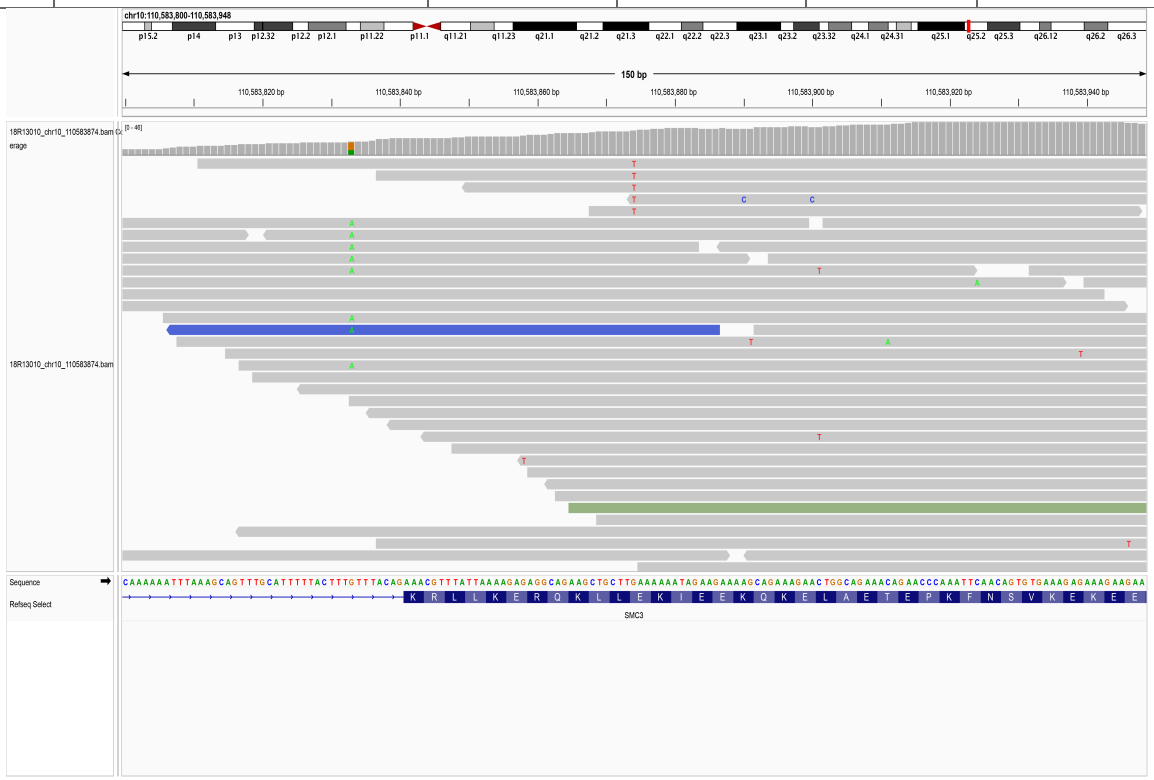
51.2. chr10_110580992_AAGA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060548D	chr10_110580992_AAGA/-	102	2	*SMC3*	frameshift_variant



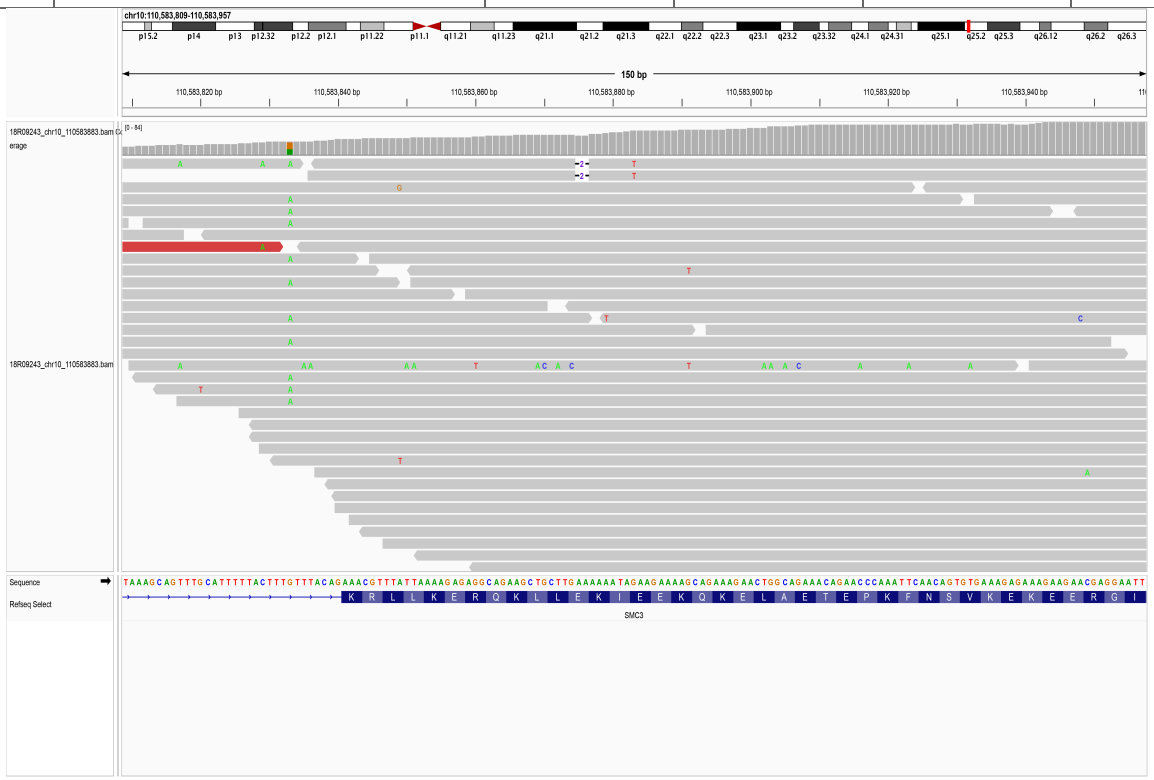
51.3. chr10_110583874_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13010	chr10_110583874_G/T	29	3	*SMC3*	stop_gained



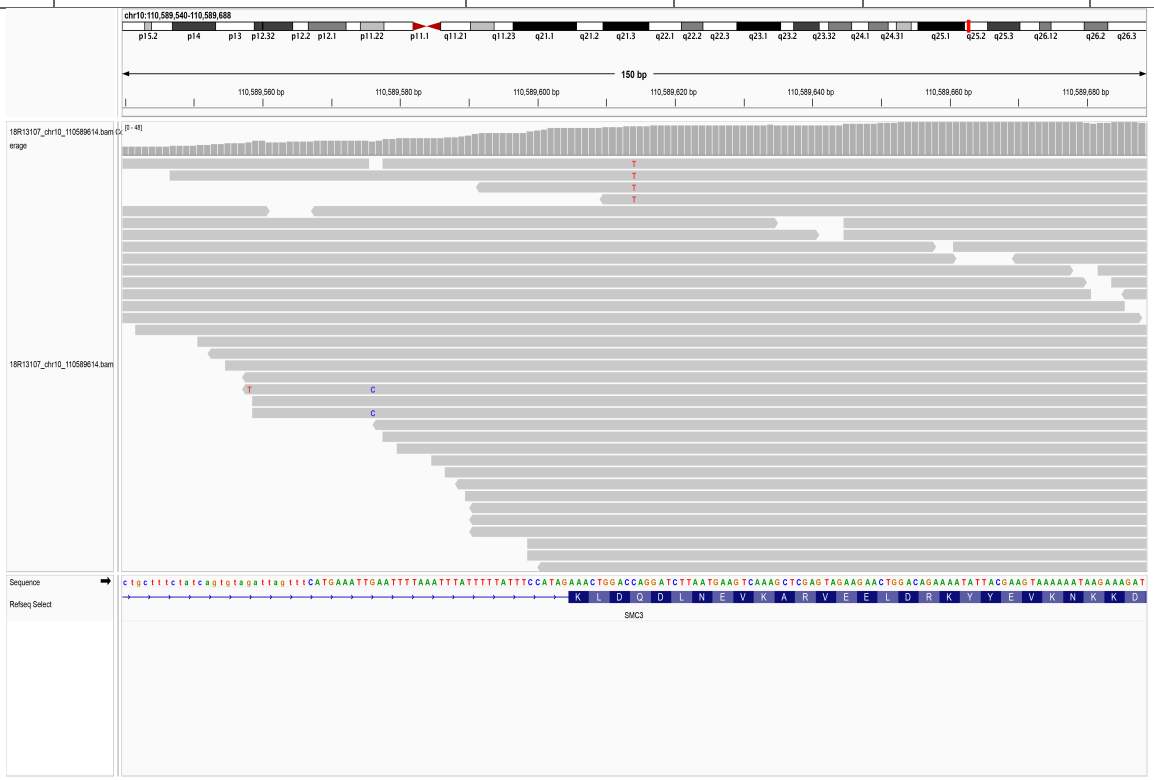
51.4. chr10_110583883_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09243	chr10_110583883_G/T	48	2	*SMC3*	stop_gained



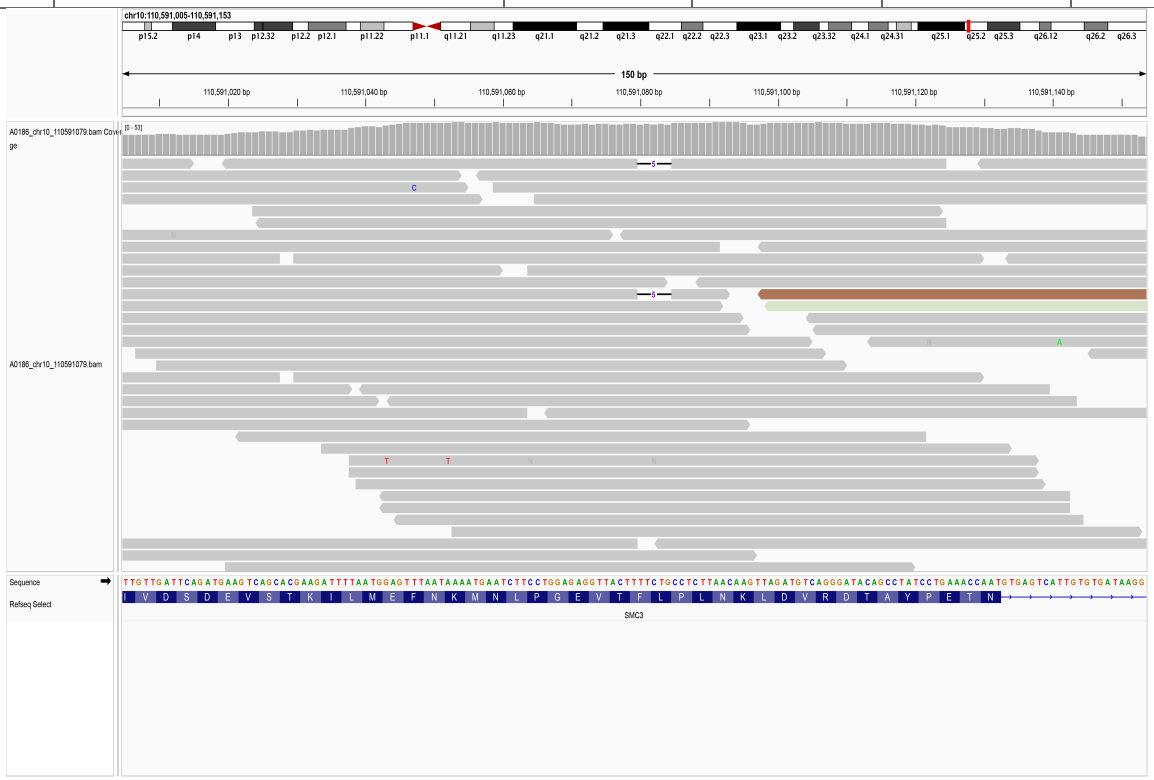
51.5. chr10_110589614_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13107	chr10_110589614_C/T	36	4	*SMC3*	stop_gained



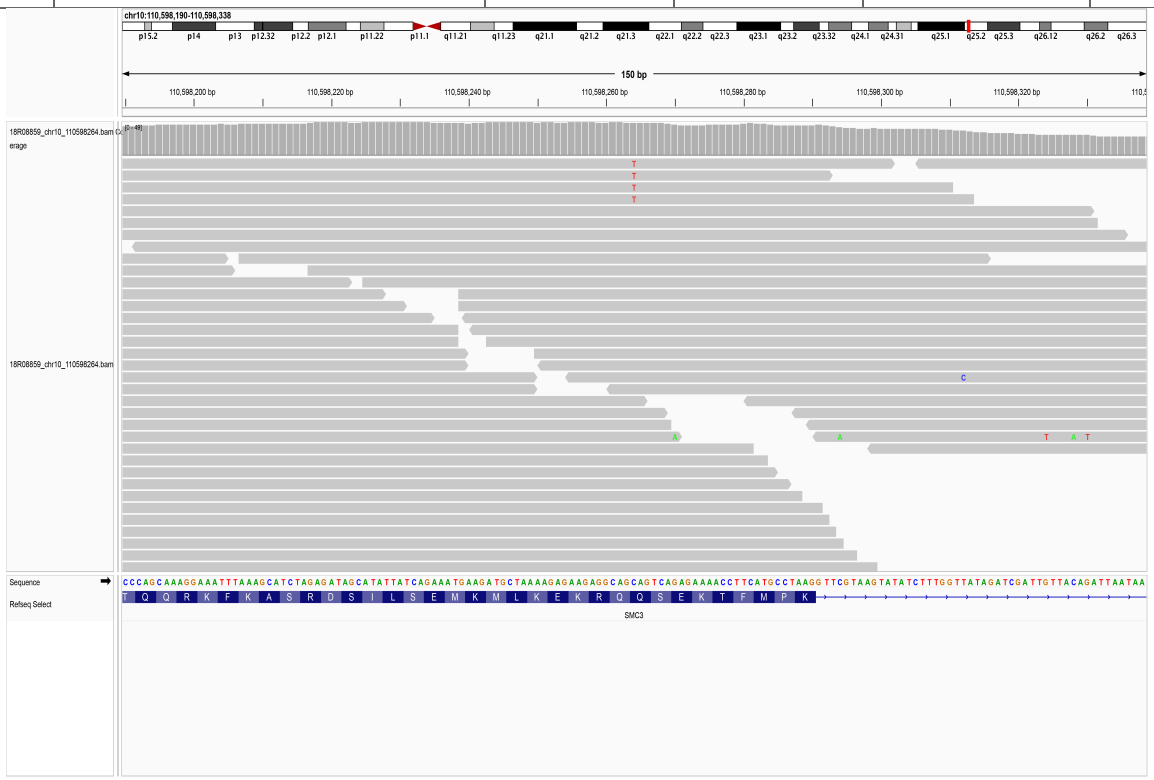
51.6. chr10_110591080_TTCTG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0186	chr10_110591080_TTCTG/-	51	2	*SMC3*	frameshift_variant



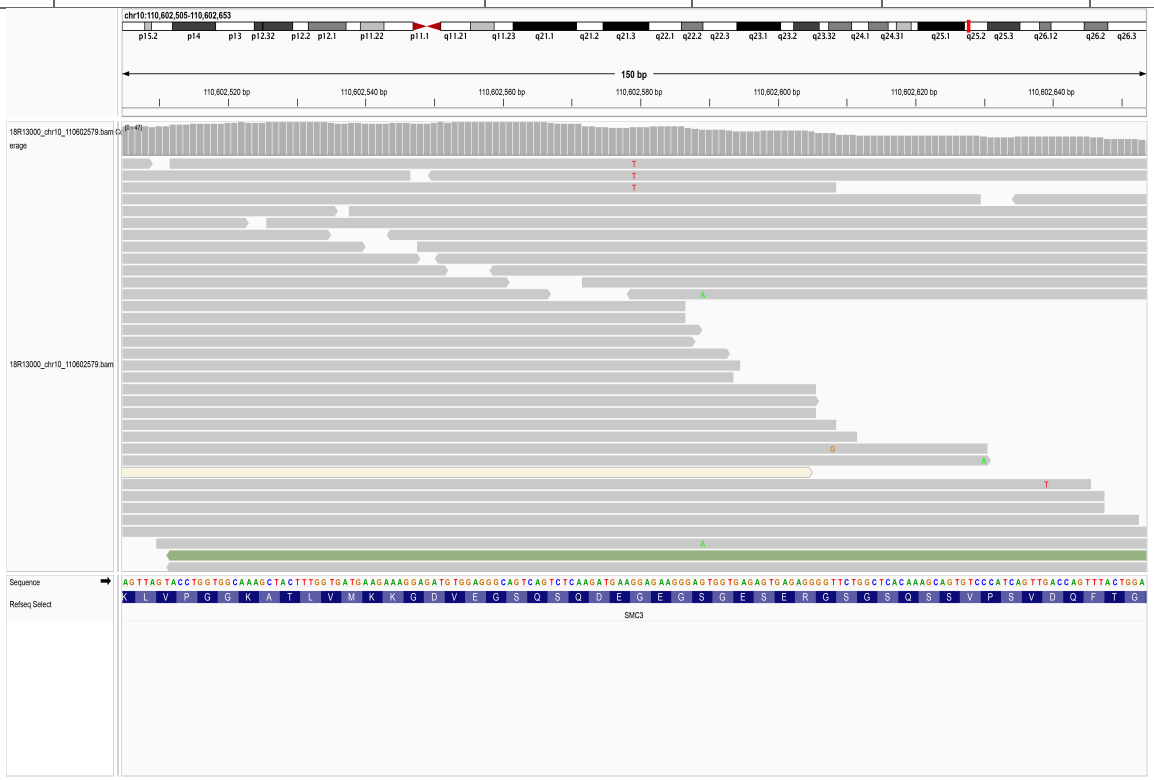
51.7. chr10_110598264_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08859	chr10_110598264_C/T	43	4	*SMC3*	stop_gained



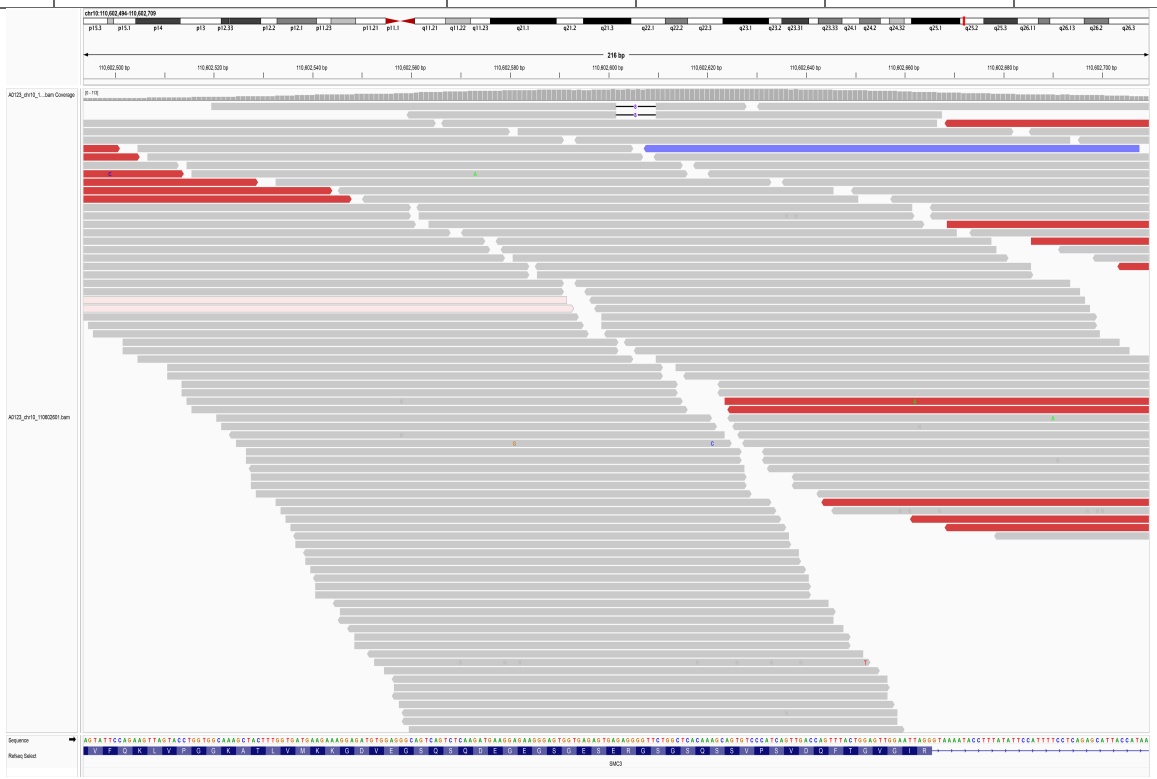
51.8. chr10_110602579_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13000	chr10_110602579_G/T	35	3	*SMC3*	stop_gained



51.9. chr10_110602602_GAGGGGTT/-

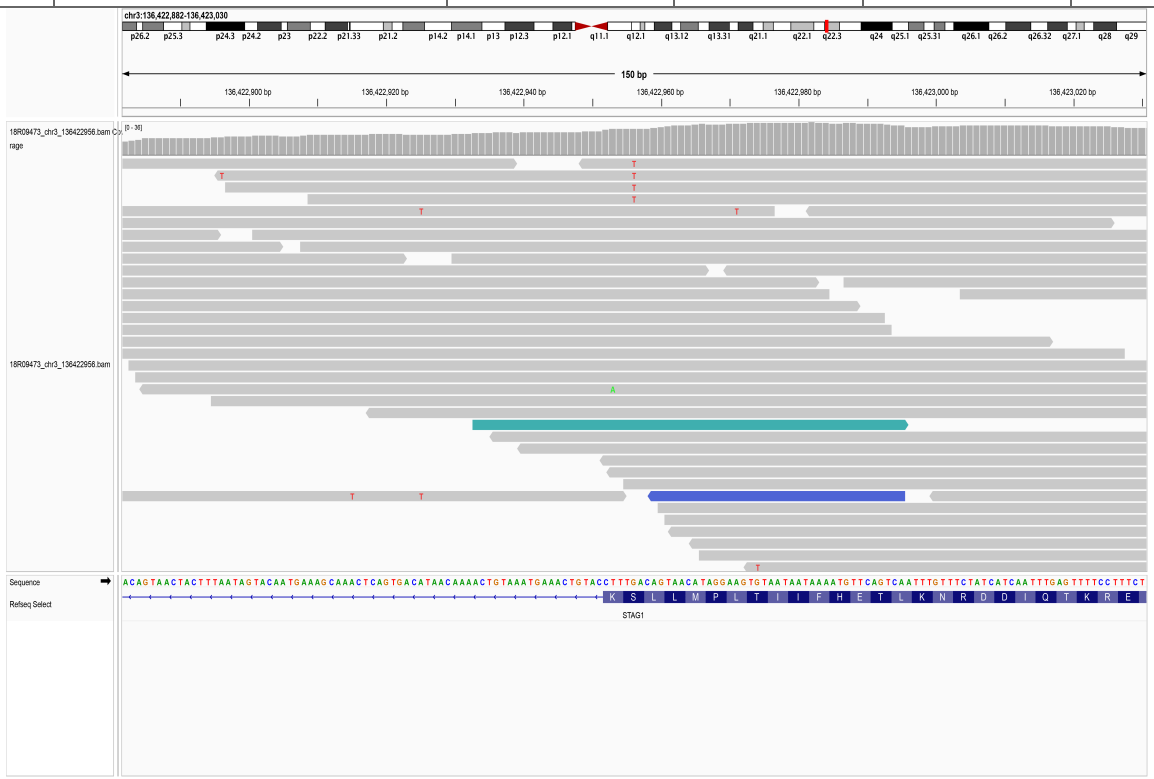
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0123	chr10_110602602_GAGGGGTT/-	111	2	*SMC3*	frameshift_variant



52. *STAG1*

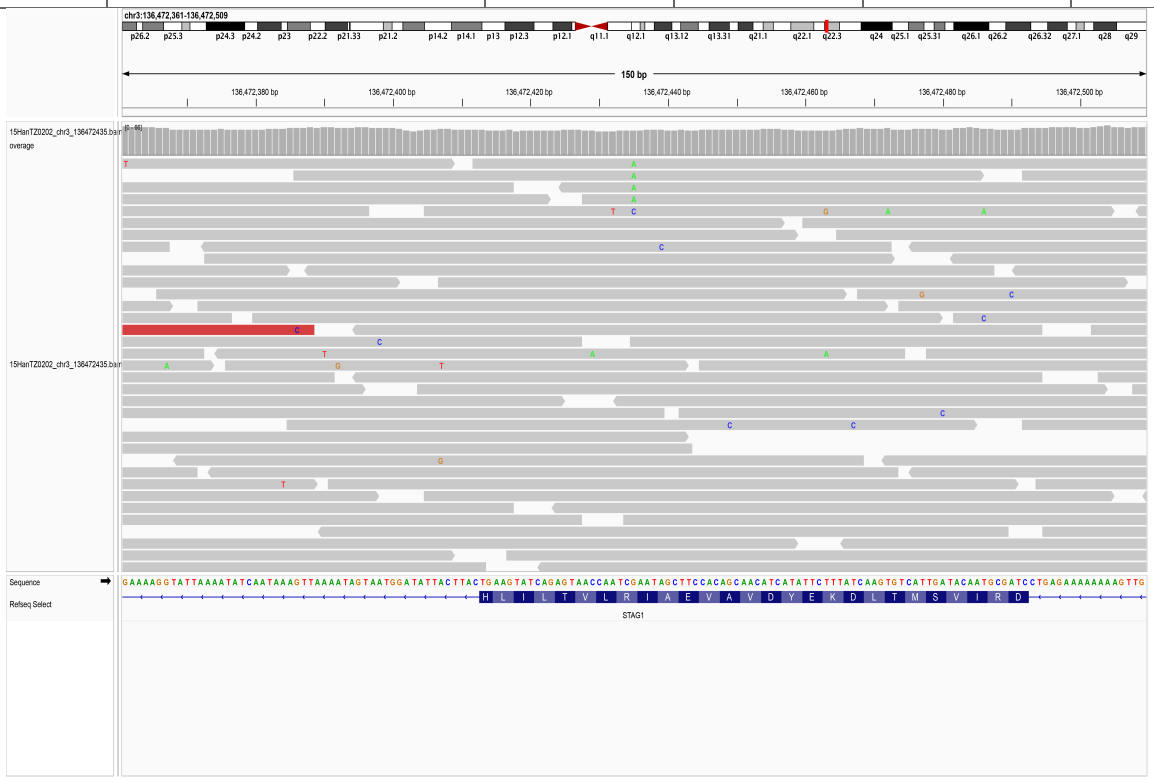
52.1. chr3_136422956_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09473	chr3_136422956_G/T	23	4	*STAG1*	stop_gained



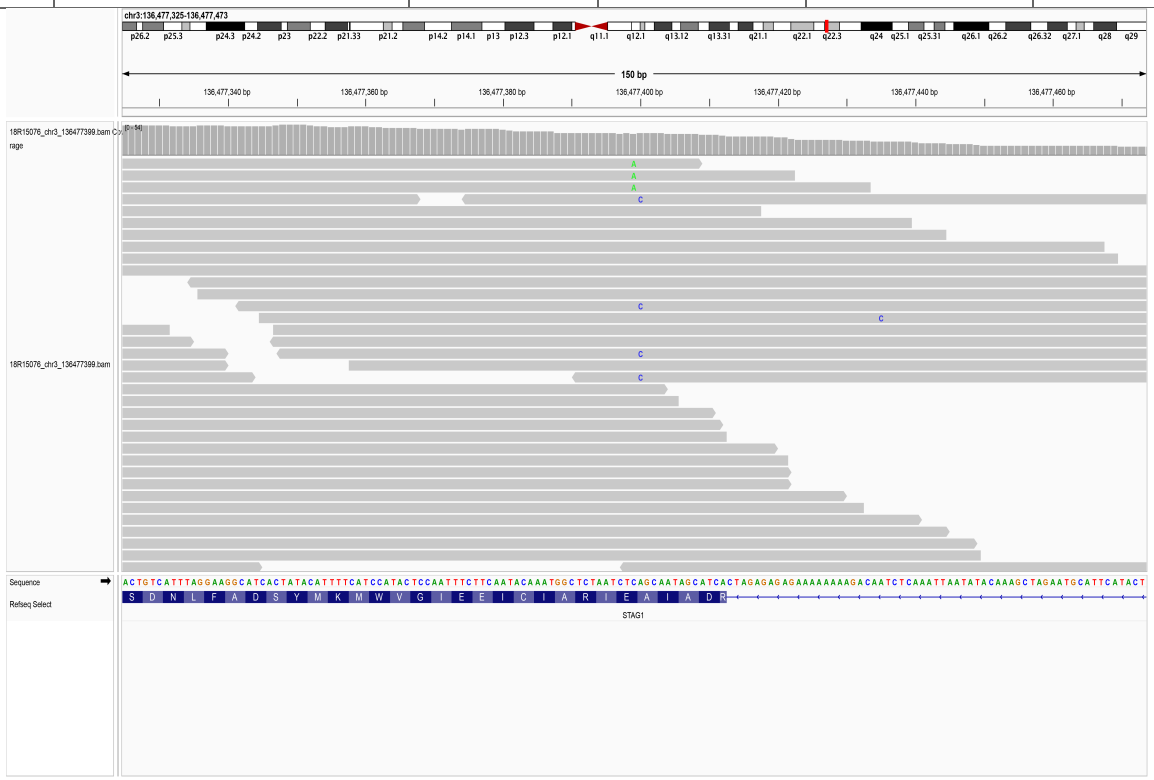
52.2. chr3_136472435_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0202	chr3_136472435_G/A	39	4	*STAG1*	stop_gained



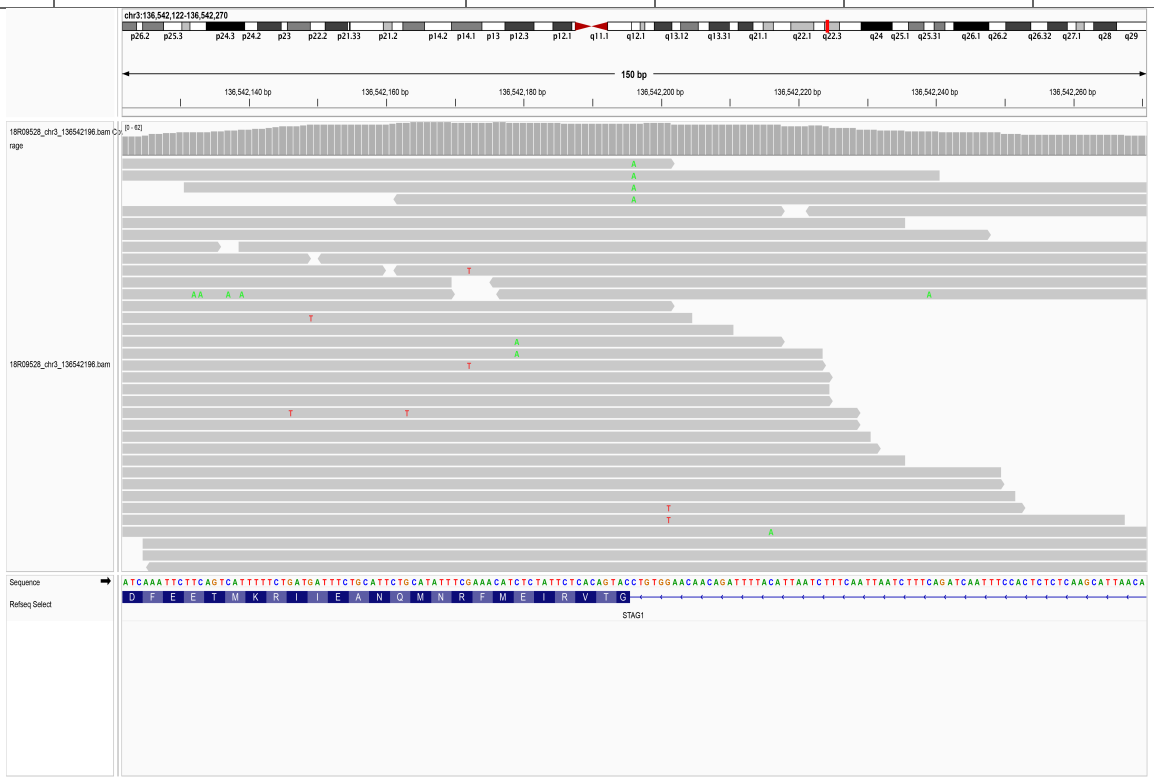
52.3. chr3_136477399_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15076	chr3_136477399_C/A	32	3	*STAG1*	stop_gained



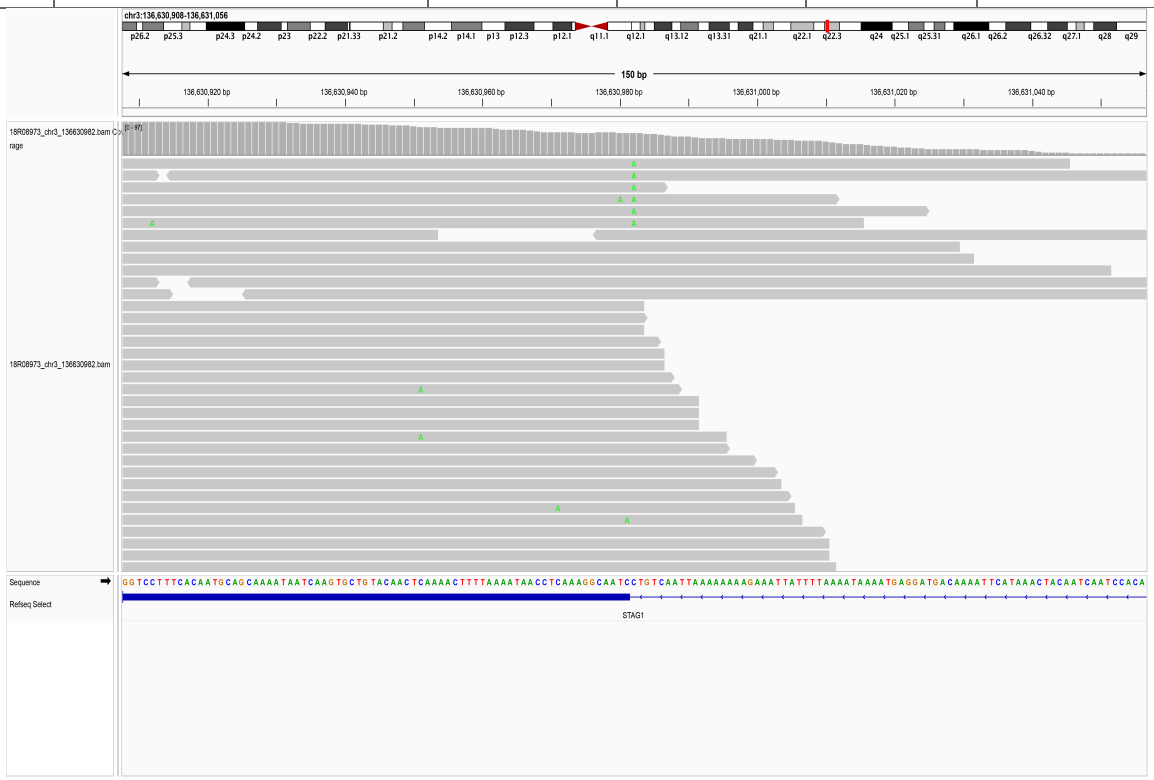
52.4. chr3_136542196_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09528	chr3_136542196_C/A	54	4	*STAG1*	splice_acceptor_variant



52.5. chr3_136630982_C/A

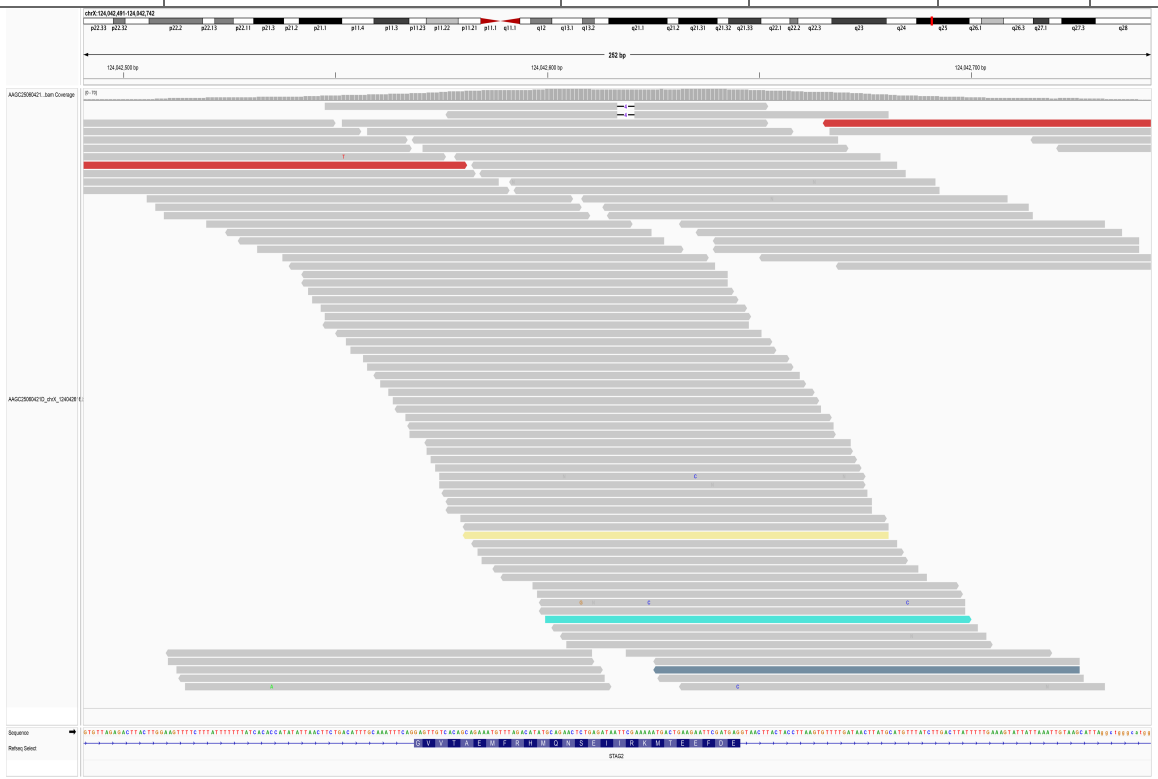
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08973	chr3_136630982_C/A	54	6	*STAG1*	splice_acceptor_variant



53. *STAG2*

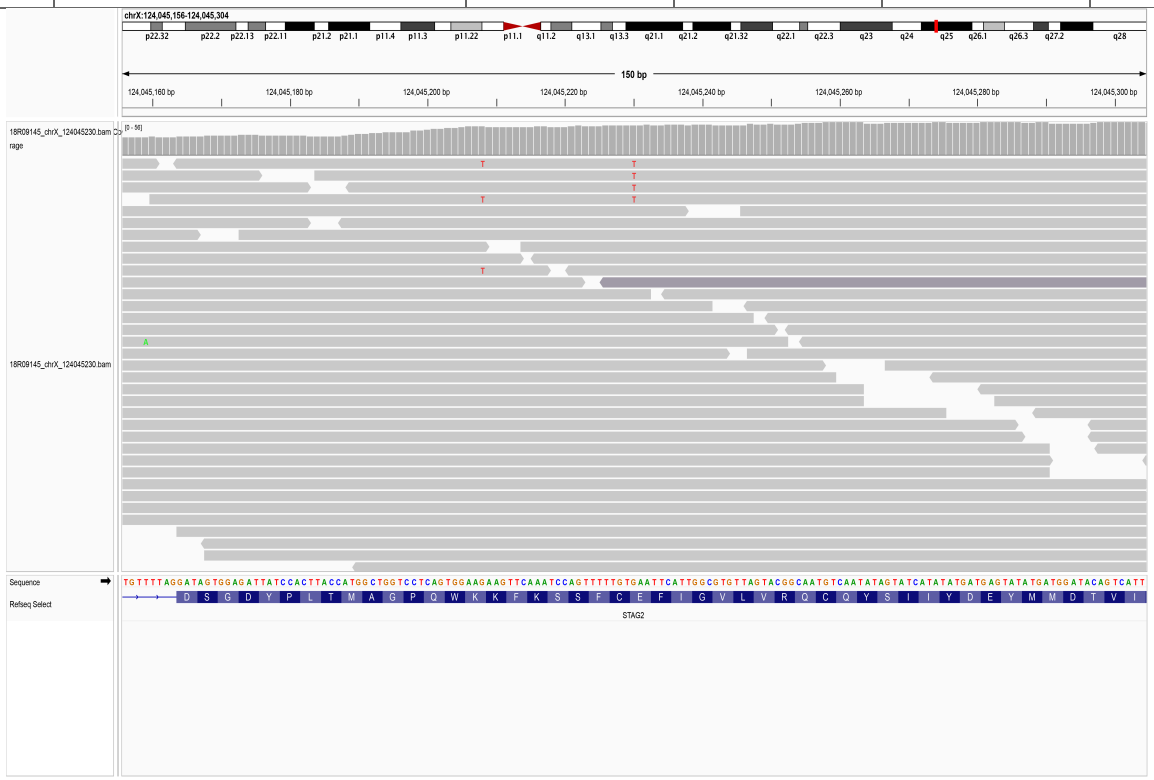
53.1. chrX_124042617_TTCG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060421D	chrX_124042617_TTCG/-	64	2	*STAG2*	frameshift_variant



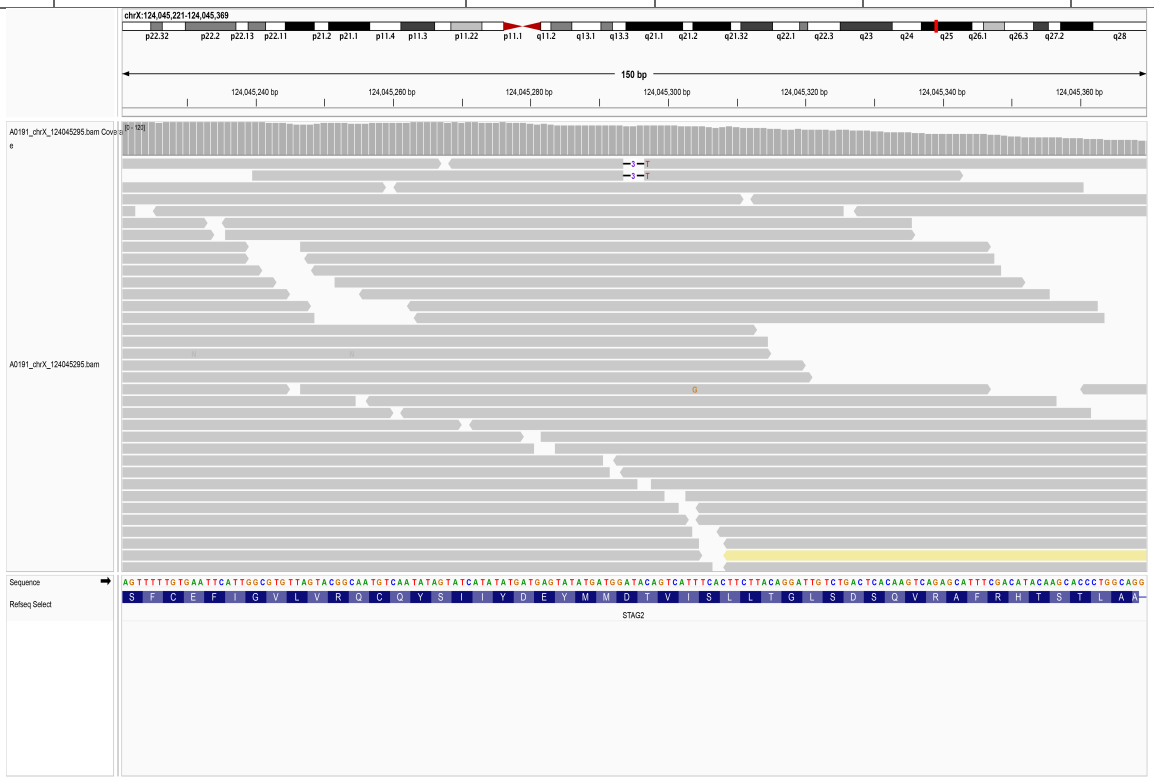
53.2. chrX_124045230_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09145	chrX_124045230_G/T	46	4	*STAG2*	stop_gained



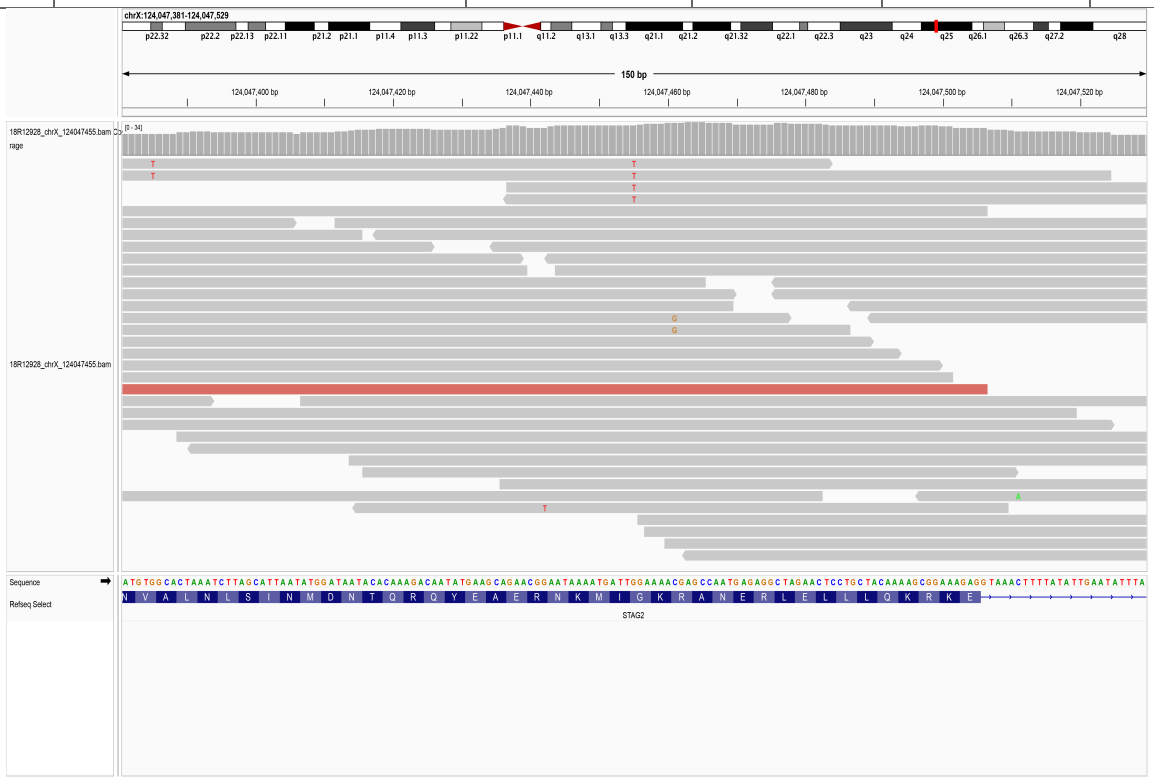
53.3. chrX_124045296_AC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0191	chrX_124045296_AC/-	106	2	*STAG2*	frameshift_variant



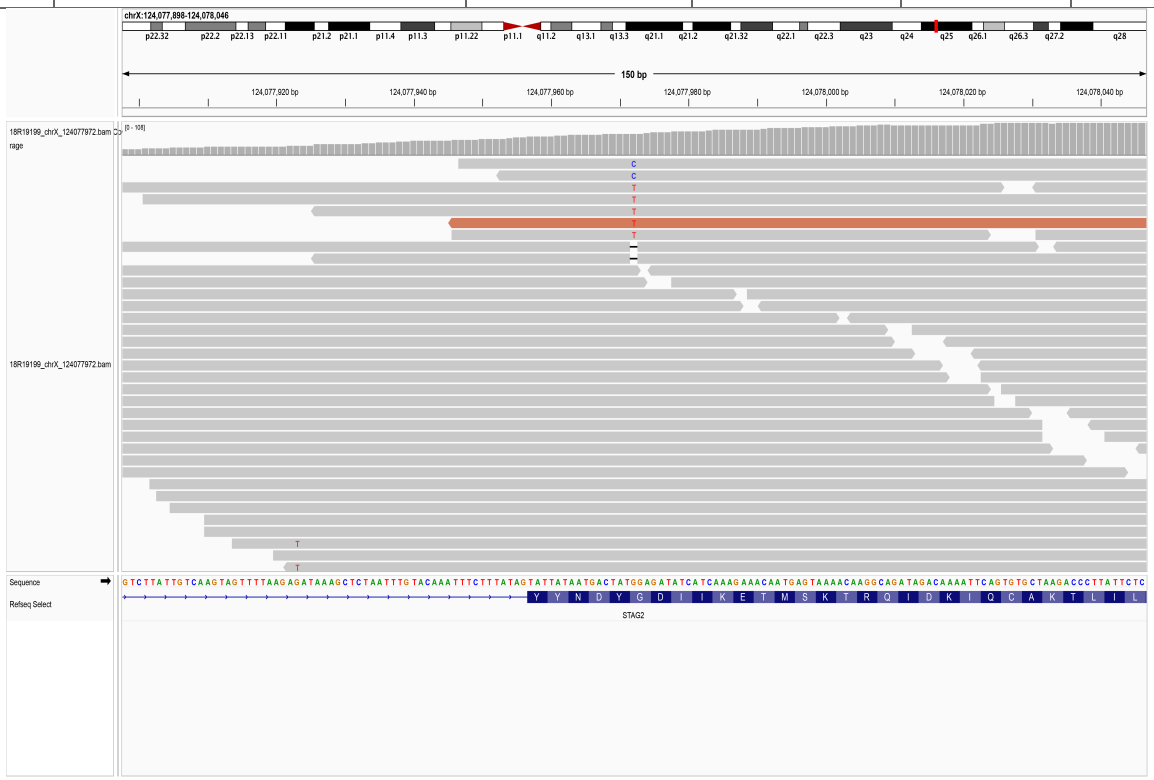
53.4. chrX_124047455_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12928	chrX_124047455_G/T	25	4	*STAG2*	stop_gained



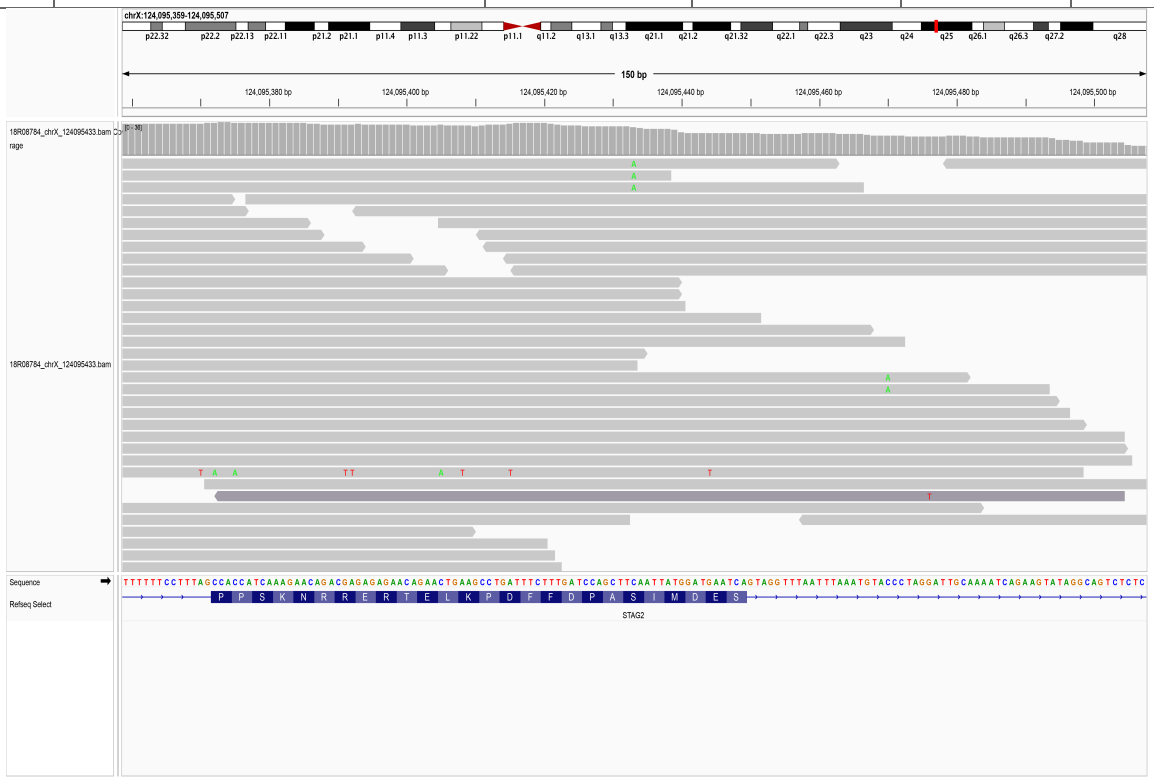
53.5. chrX_124077972_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19199	chrX_124077972_G/T	62	4	*STAG2*	stop_gained



53.6. chrX_124095433_C/A

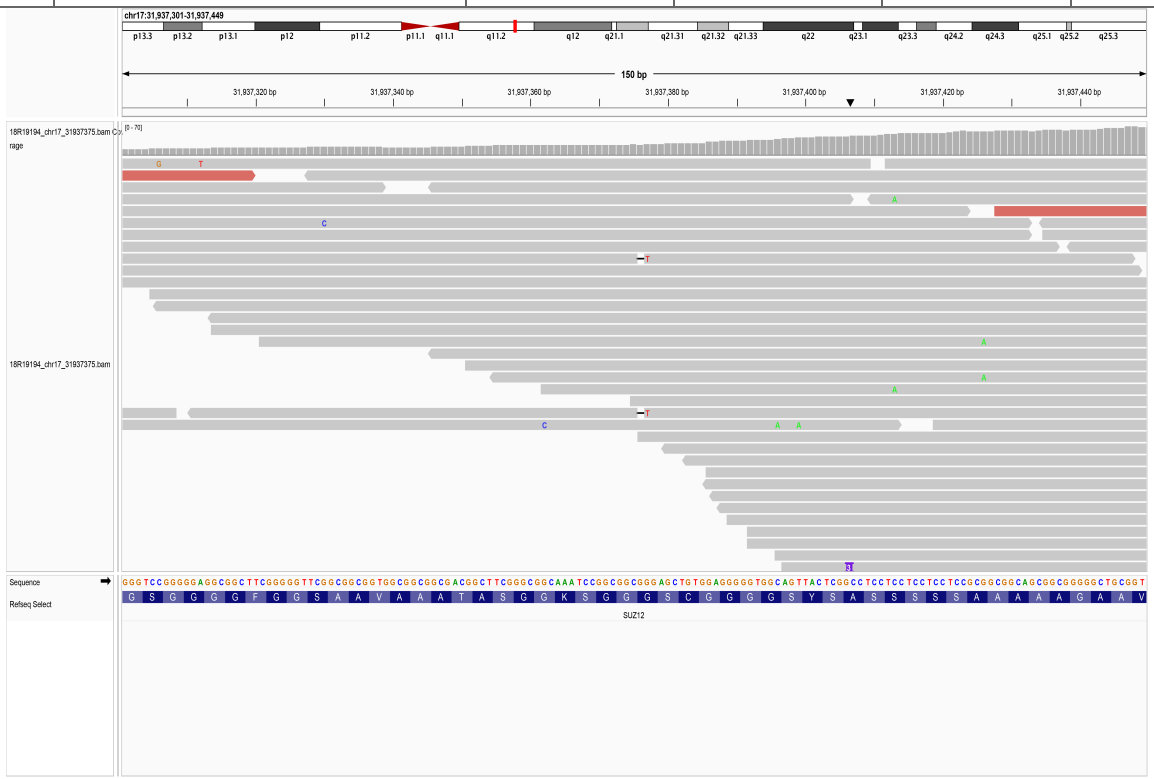
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08784	chrX_124095433_C/A	27	3	*STAG2*	stop_gained



54. *SUZ12*

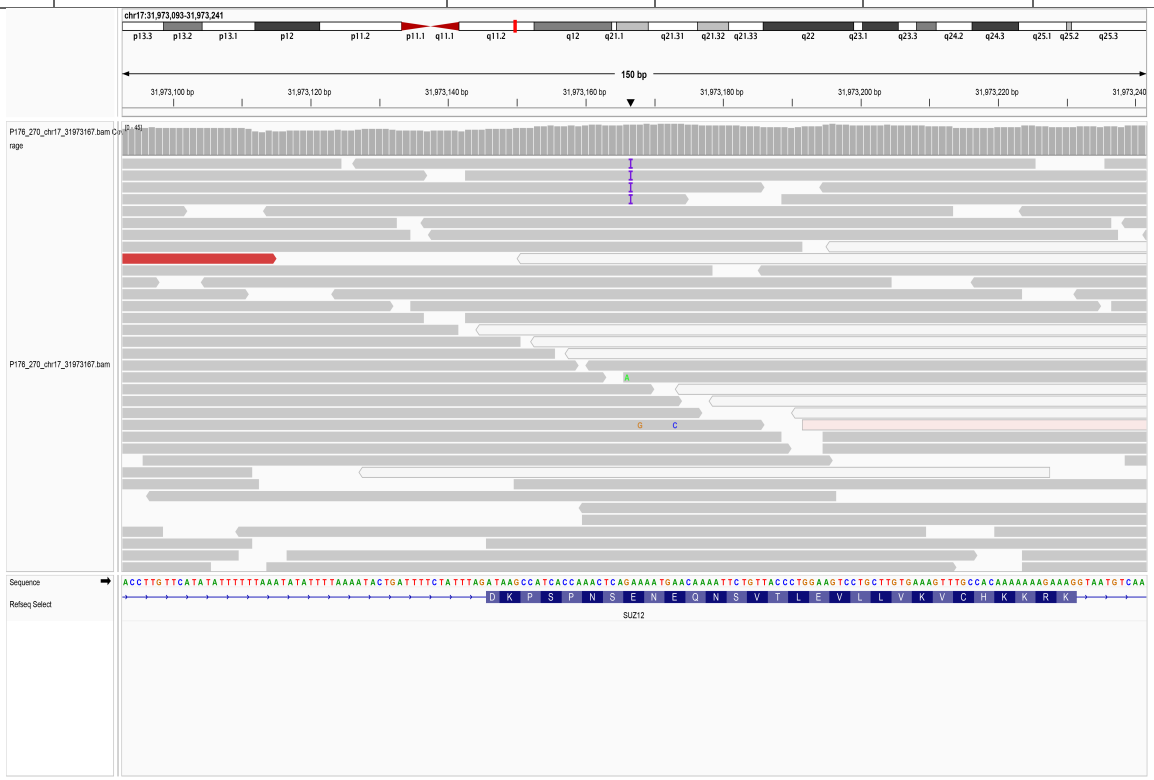
54.1. chr17_31937376_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19194	chr17_31937376_G/-	21	2	*SUZ12*	frameshift_variant



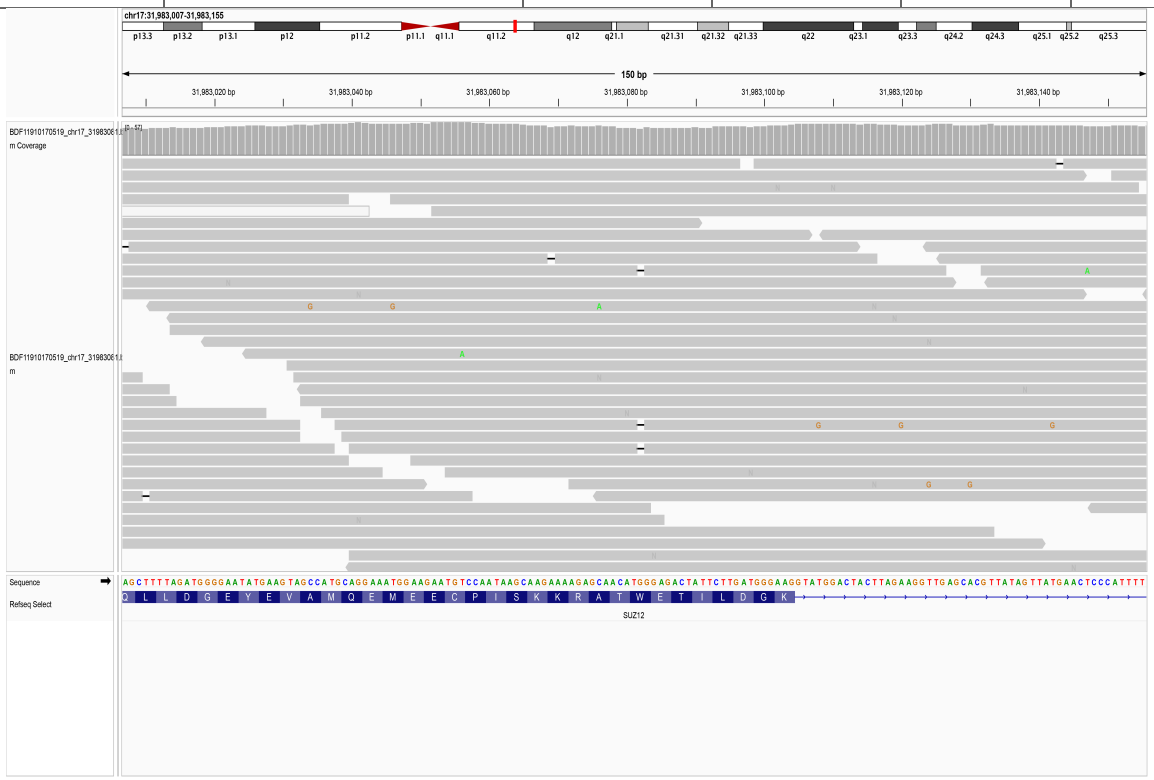
54.2. chr17_31973167_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
P176_270	chr17_31973167_-/A	27	5	*SUZ12*	frameshift_variant



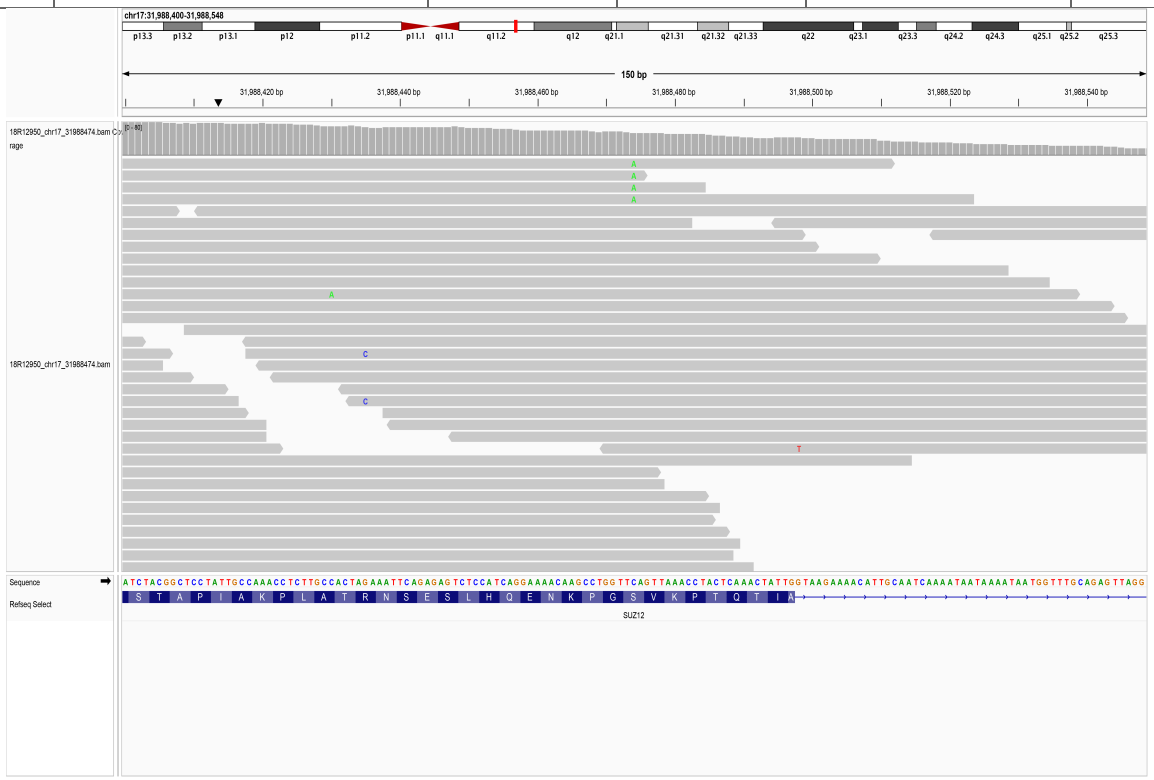
54.3. chr17_31983082_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chr17_31983082_G/-	44	3	*SUZ12*	frameshift_variant



54.4. chr17_31988474_C/A

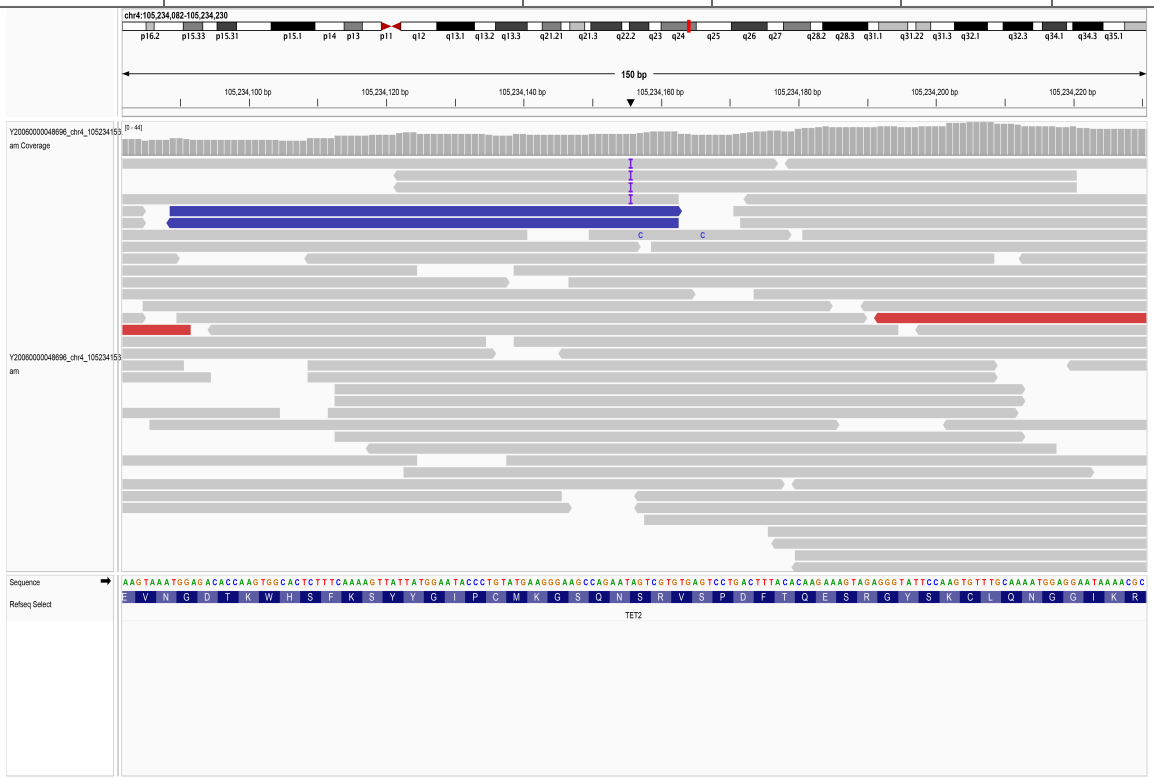
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12950	chr17_31988474_C/A	48	4	*SUZ12*	stop_gained



55. *TET2*

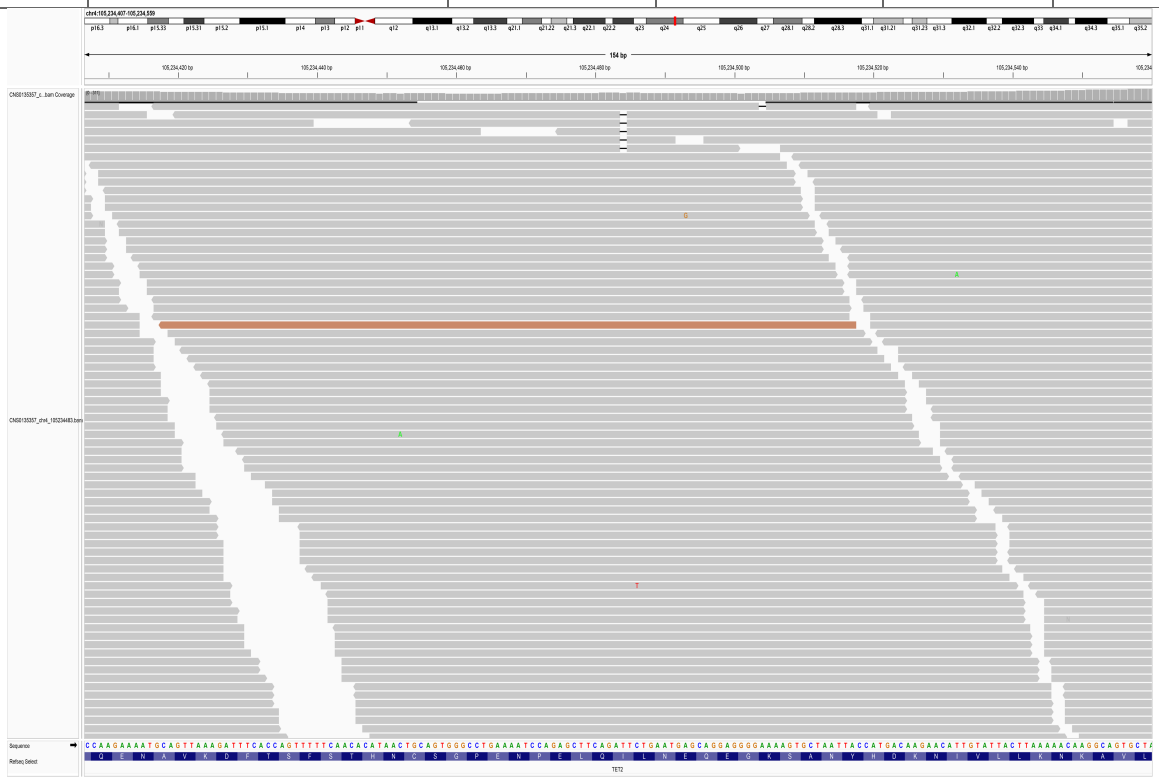
55.1. chr4_105234156_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
Y20060000048696	chr4_105234156_-/A	20	4	*TET2*	frameshift_variant



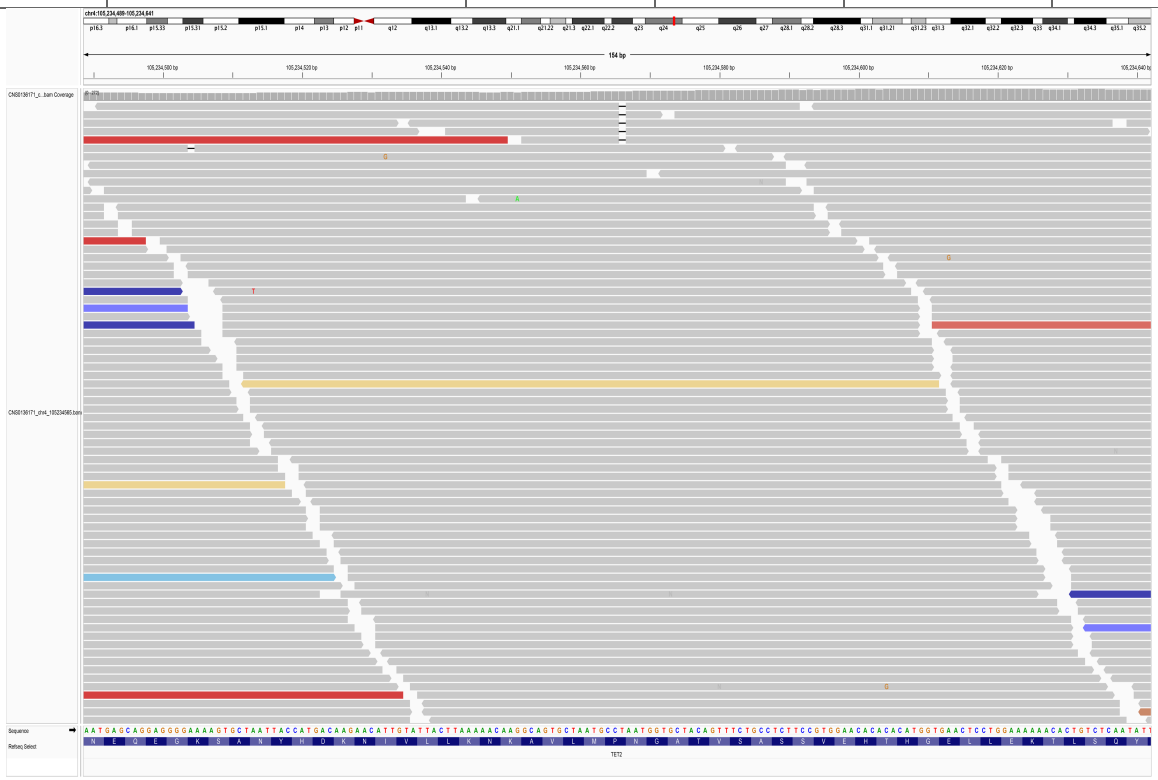
55.2. chr4_105234484_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135357	chr4_105234484_T/-	195	7	*TET2*	frameshift_variant



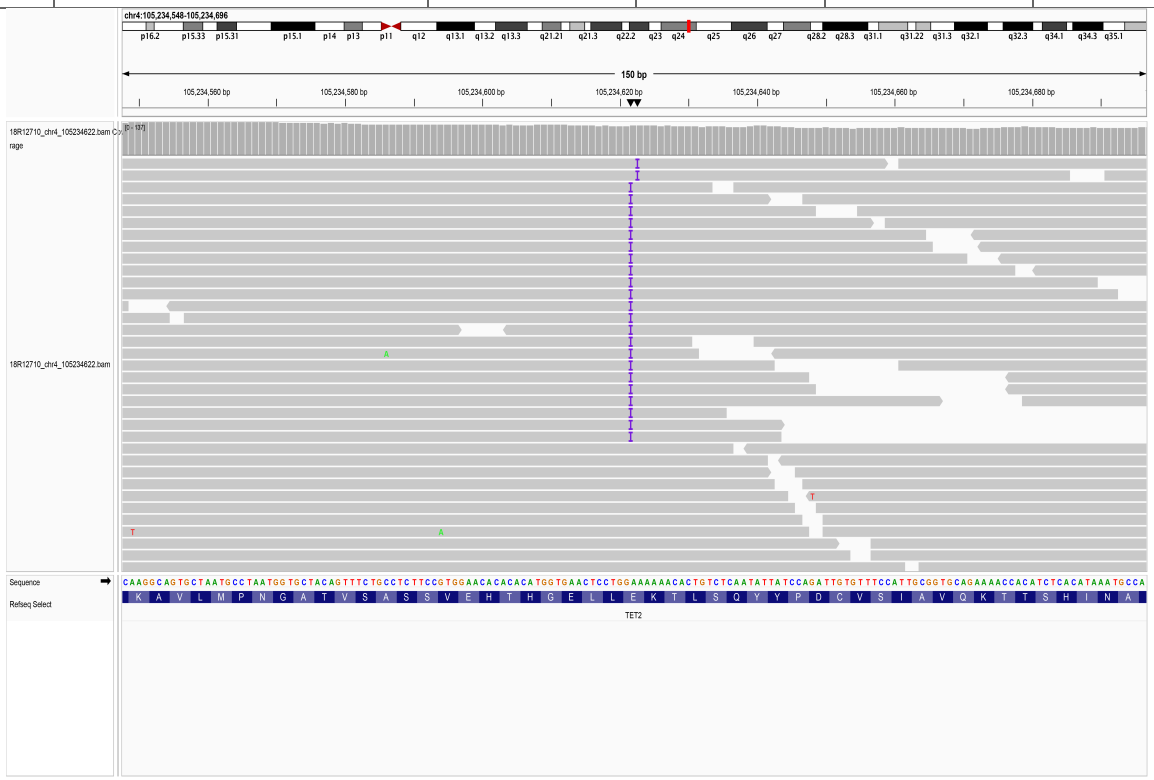
55.3. chr4_105234566_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136171	chr4_105234566_T/-	203	5	*TET2*	frameshift_variant



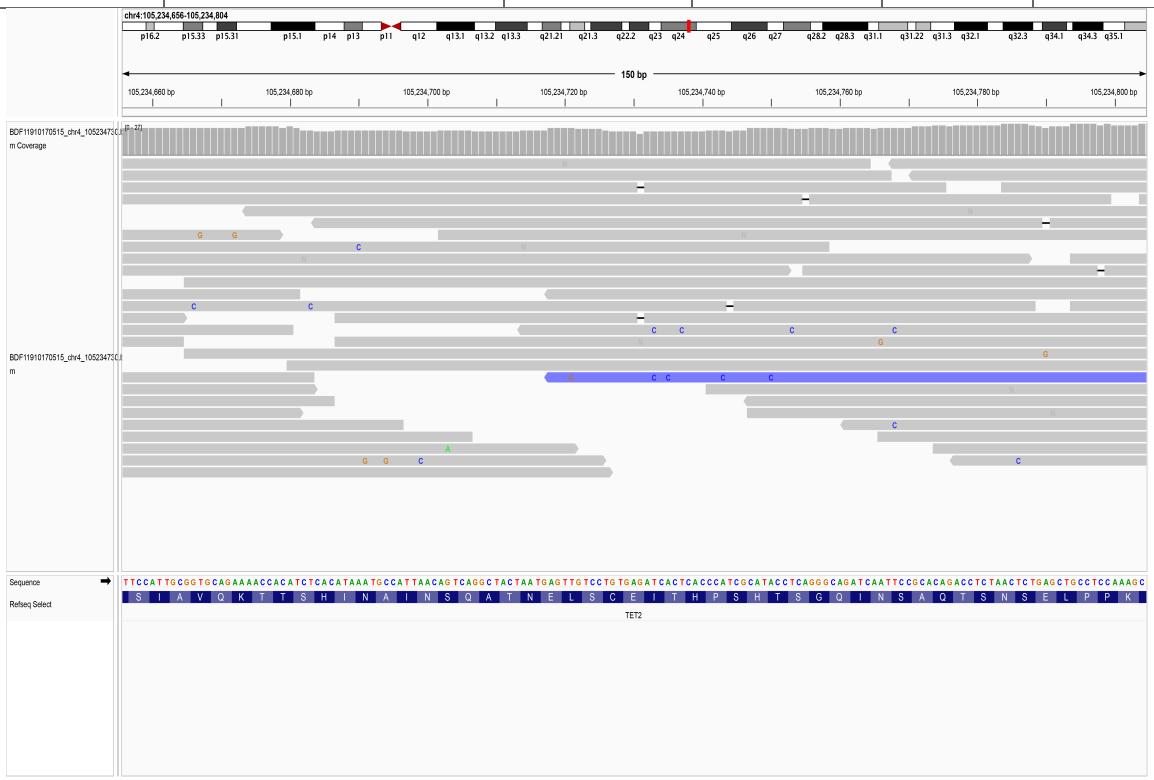
55.4. chr4_105234622_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12710	chr4_105234622_-/A	87	25	*TET2*	frameshift_variant



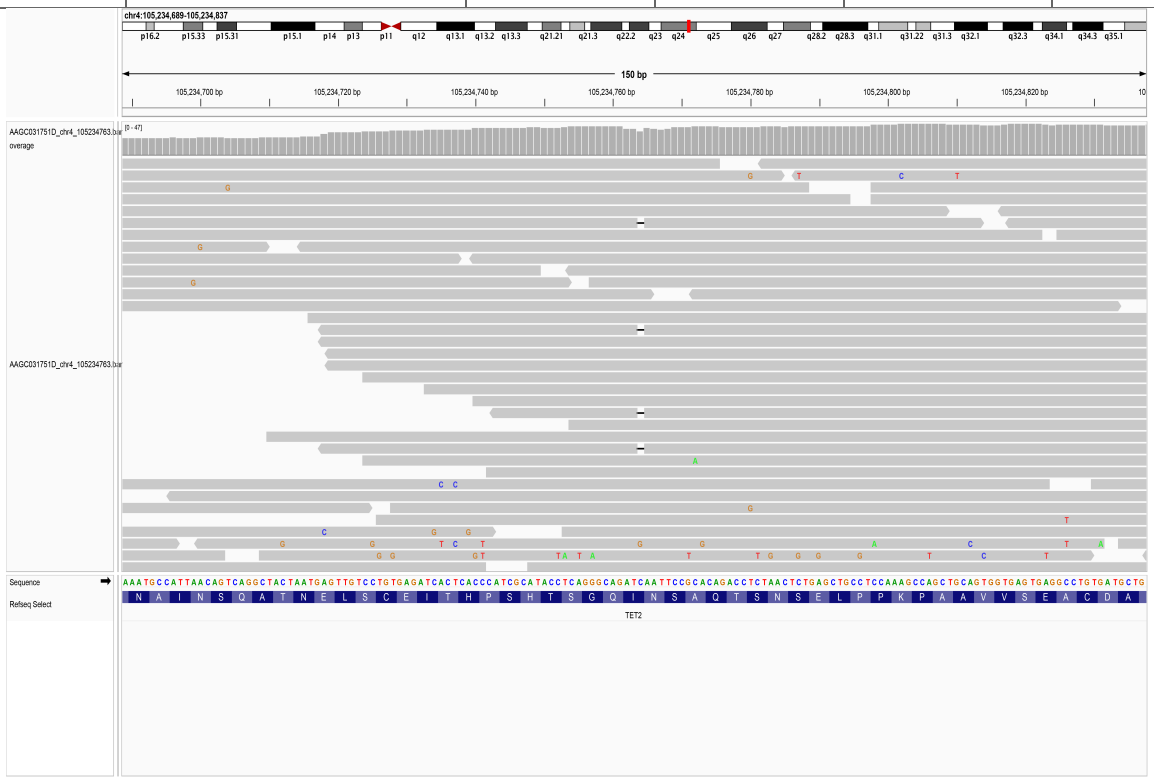
55.5. chr4_105234731_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170515	chr4_105234731_G/-	14	2	*TET2*	frameshift_variant



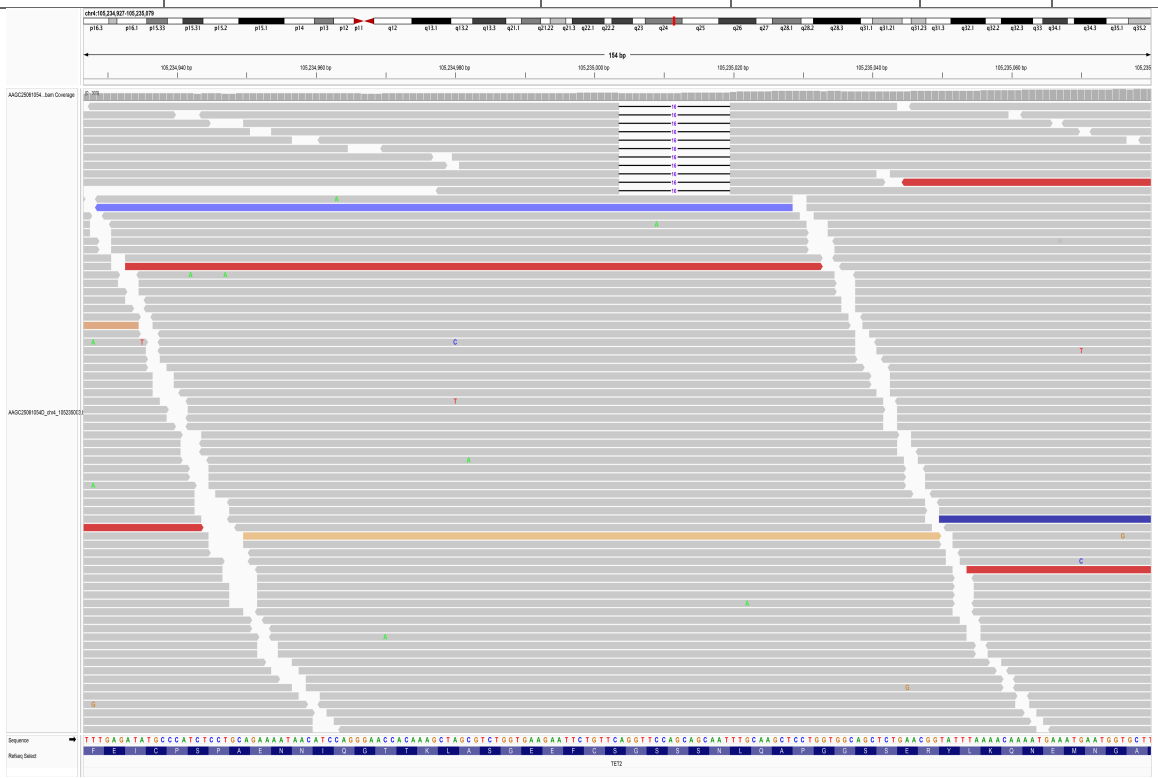
55.6. chr4_105234764_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC031751D	chr4_105234764_C/-	31	5	*TET2*	frameshift_variant



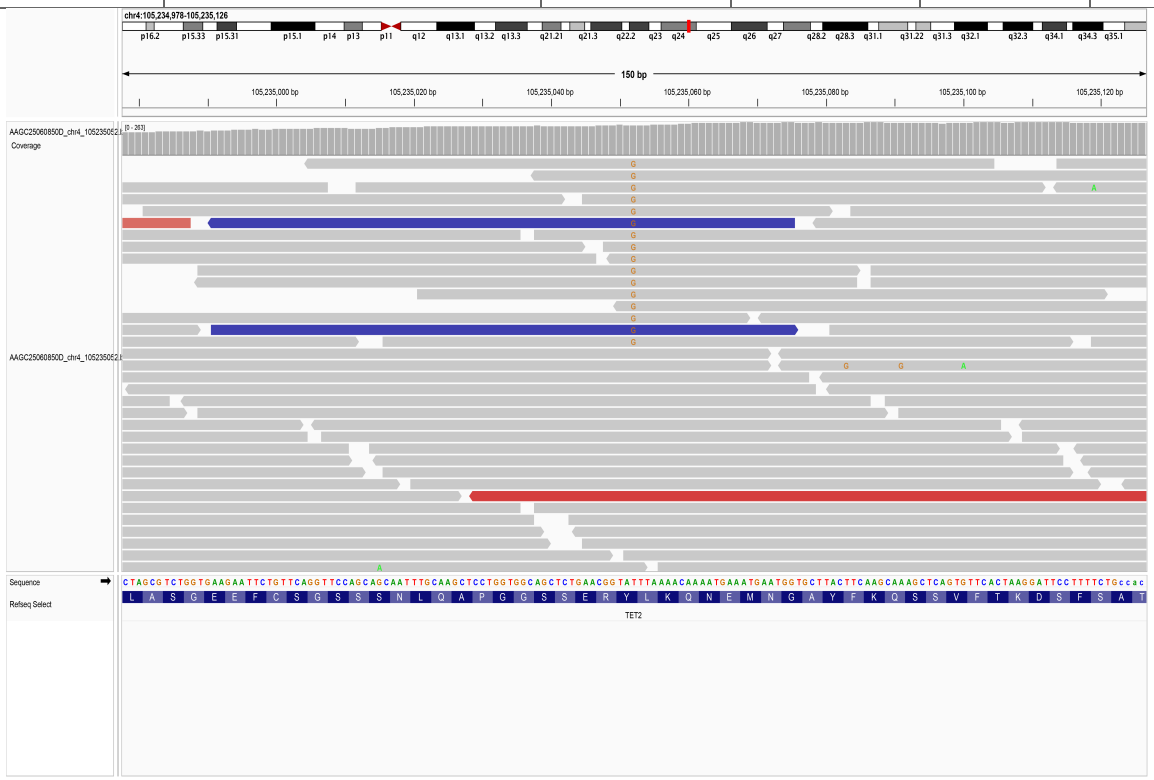
55.7. chr4_105235004_AGGTTCCAGCAGCAAT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061054D	chr4_105235004_AGGTTCCAGCAGCAAT/-	224	20	*TET2*	frameshift_variant



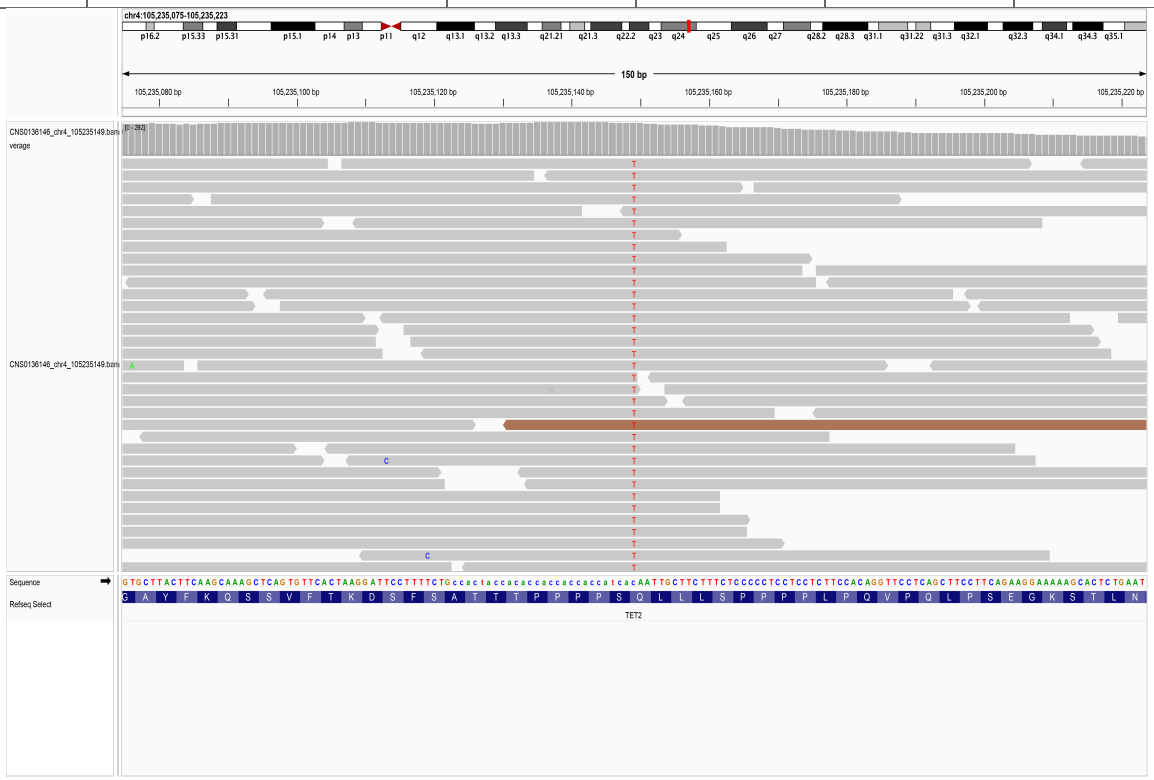
55.8. chr4_105235052_T/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060850D	chr4_105235052_T/G	216	16	*TET2*	stop_gained



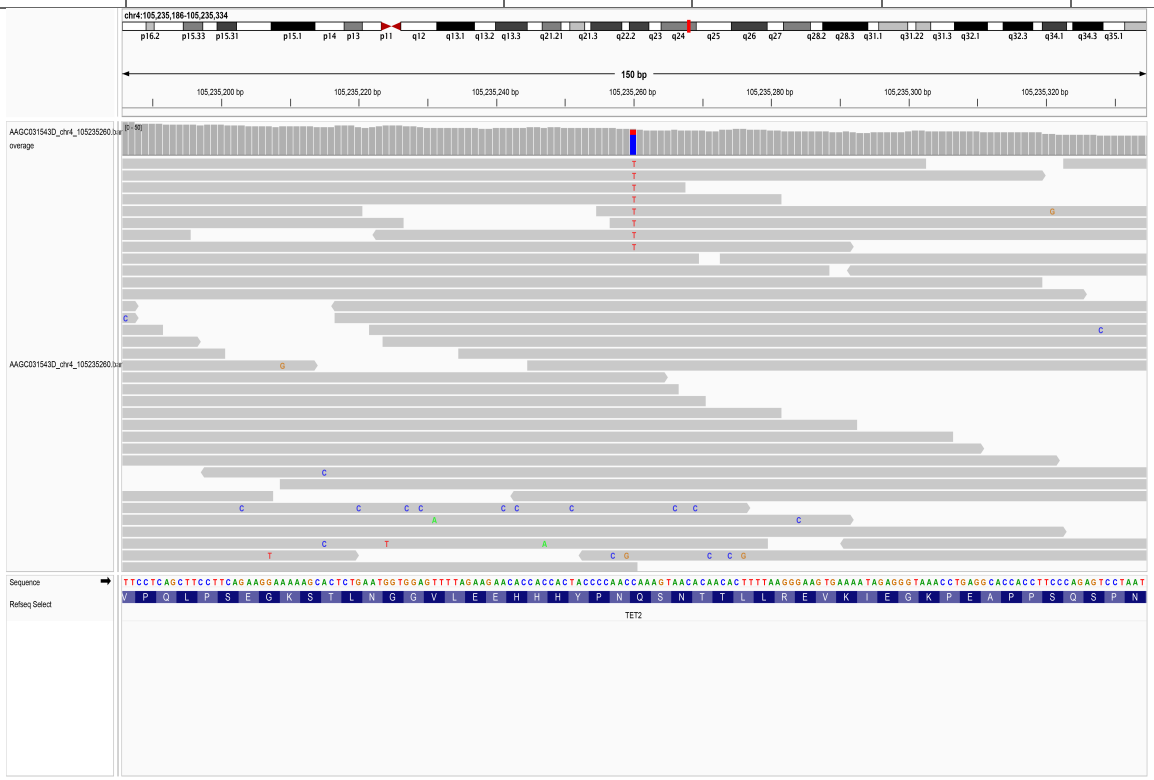
55.9. chr4_105235149_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136146	chr4_105235149_C/T	228	52	*TET2*	stop_gained



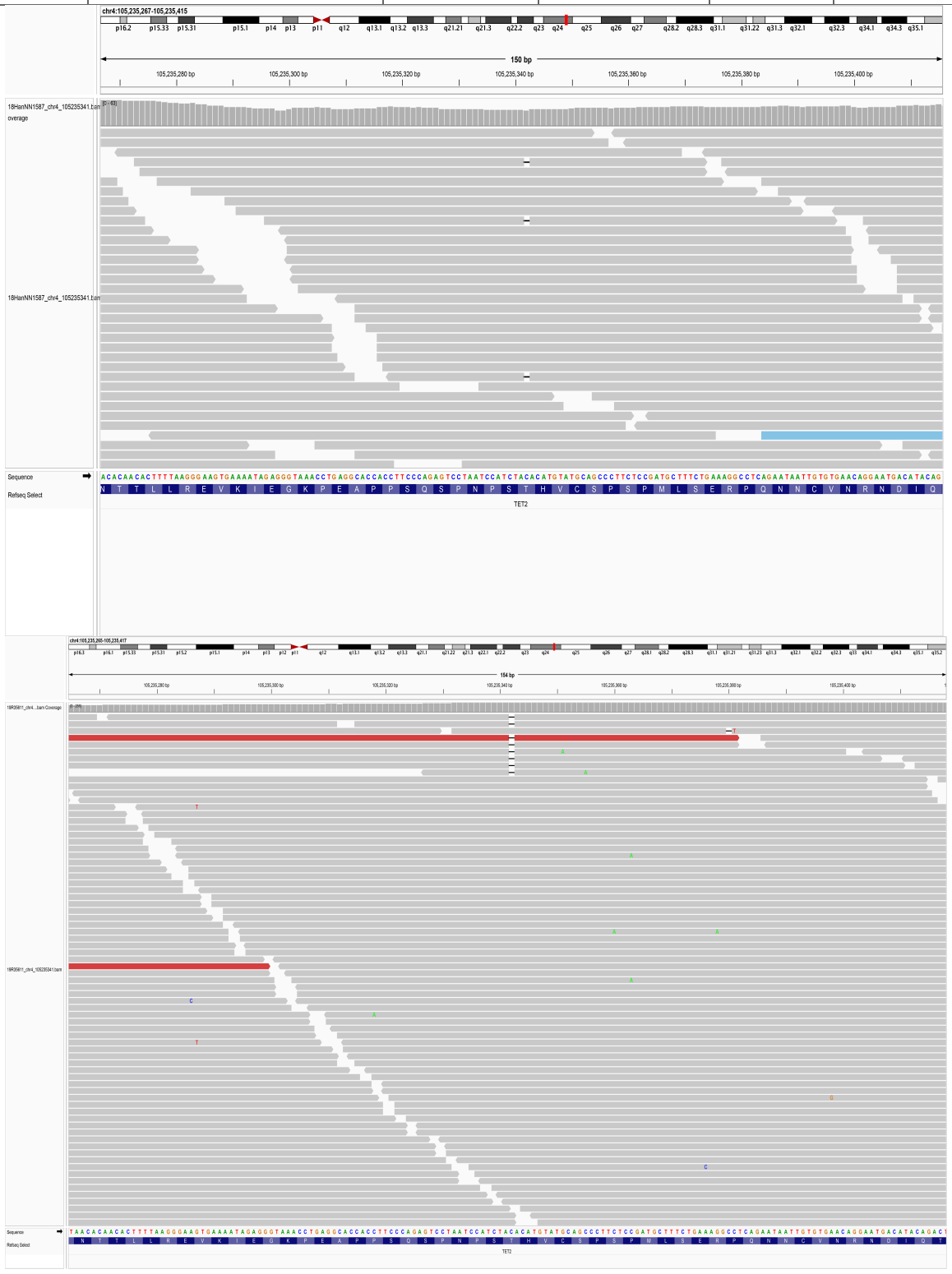
55.10. chr4_105235260_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC031543D	chr4_105235260_C/T	28	8	*TET2*	stop_gained



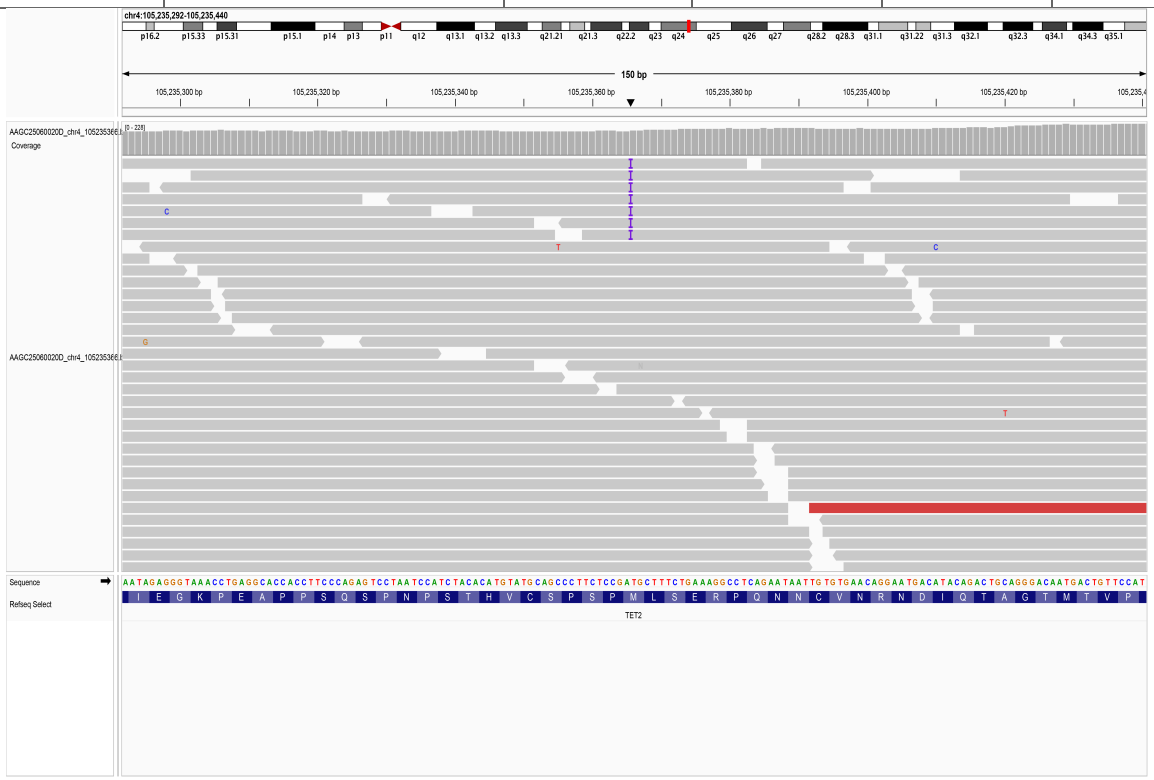
55.11. chr4_105235342_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN1587	chr4_105235342_C/-	35	3	*TET2*	frameshift_variant
19R35611	chr4_105235342_C/-	241	8	*TET2*	frameshift_variant



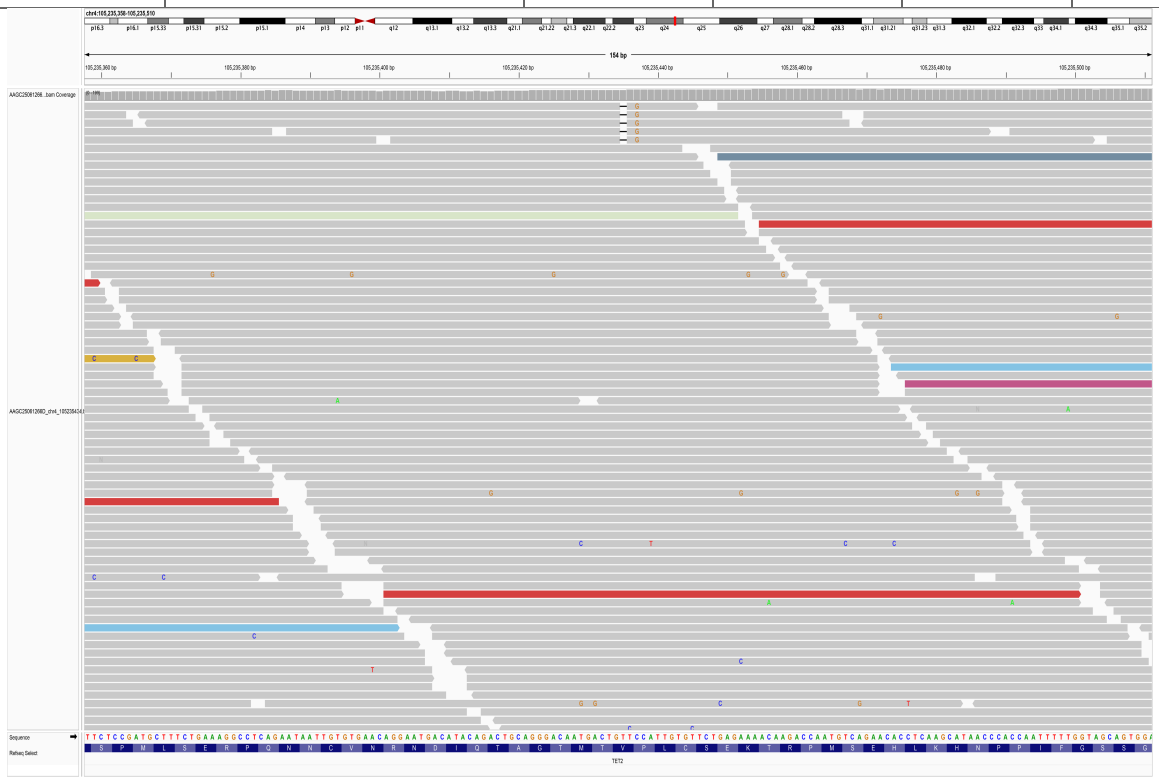
55.12. chr4_105235366_-/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060020D	chr4_105235366_-/T	152	7	*TET2*	frameshift_variant



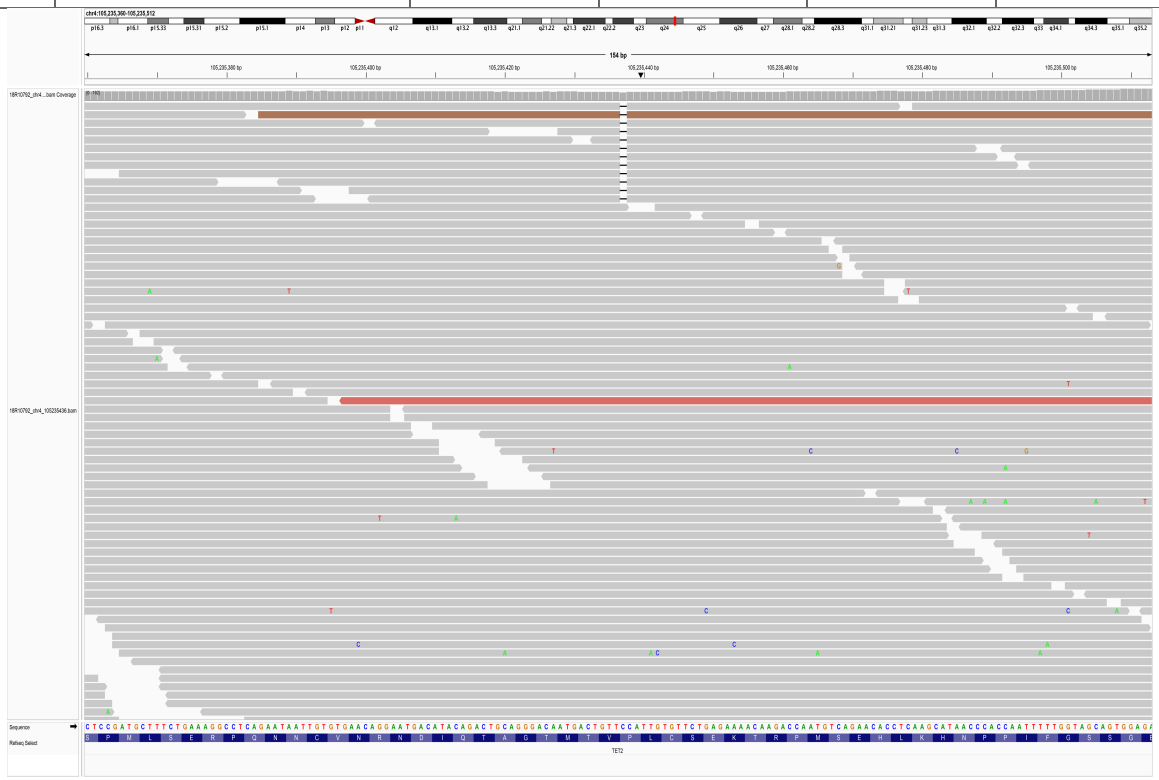
55.13. chr4_105235435_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061266D	chr4_105235435_T/-	173	7	*TET2*	frameshift_variant



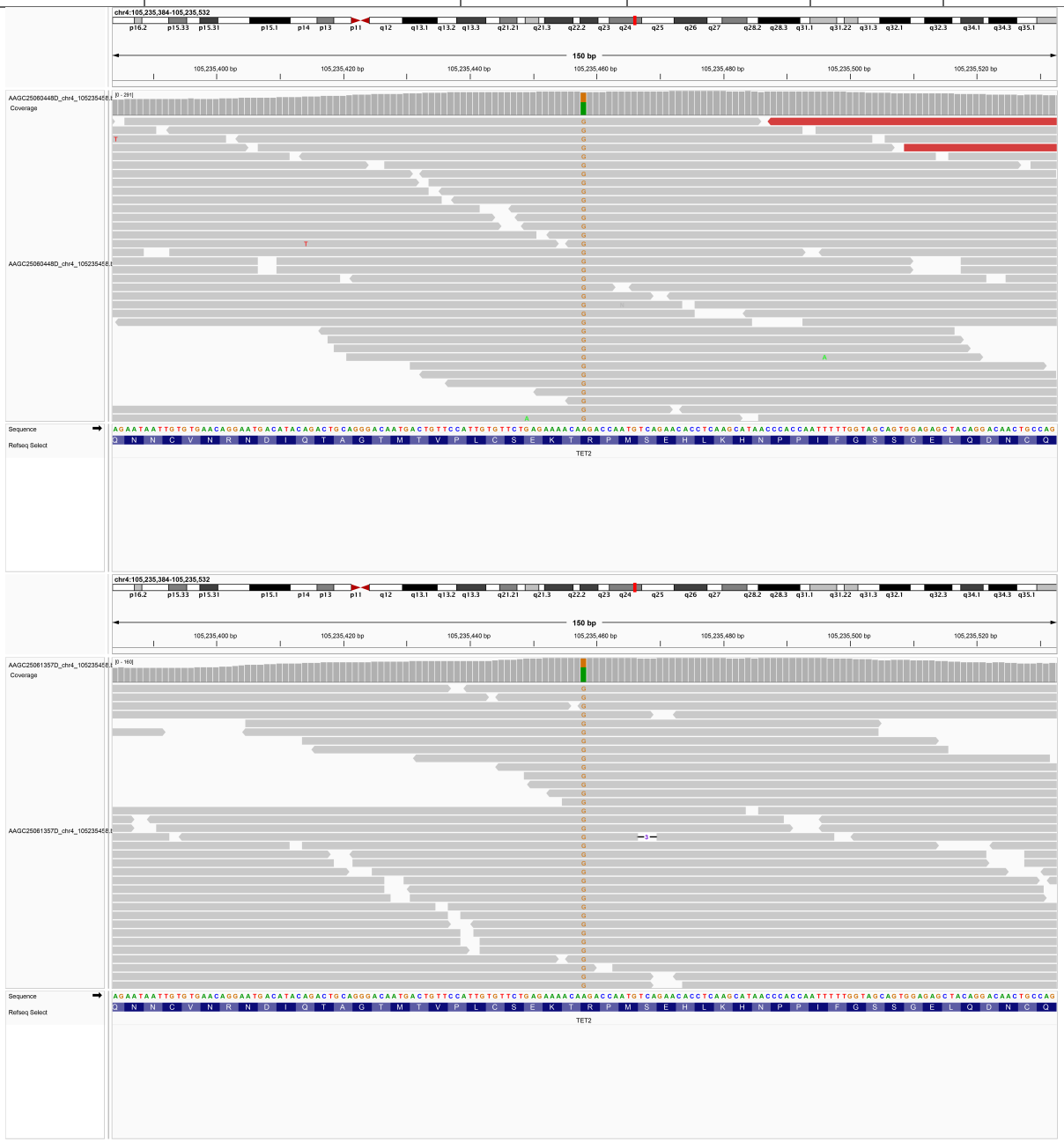
55.14. chr4_105235437_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10792	chr4_105235437_C/-	119	13	*TET2*	frameshift_variant



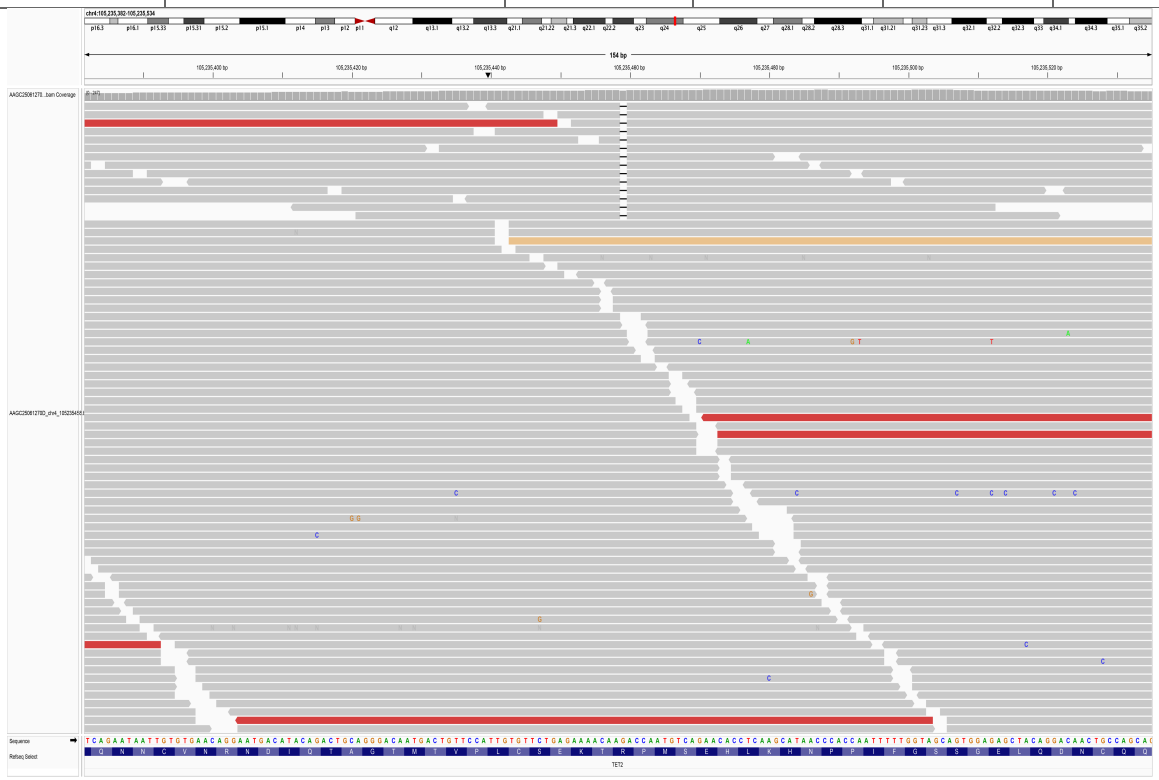
55.15. chr4_105235459_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060448D	chr4_105235459_A/G	161	113	*TET2*	frameshift_variant
AAGC25061357D	chr4_105235459_A/G	99	60	*TET2*	frameshift_variant



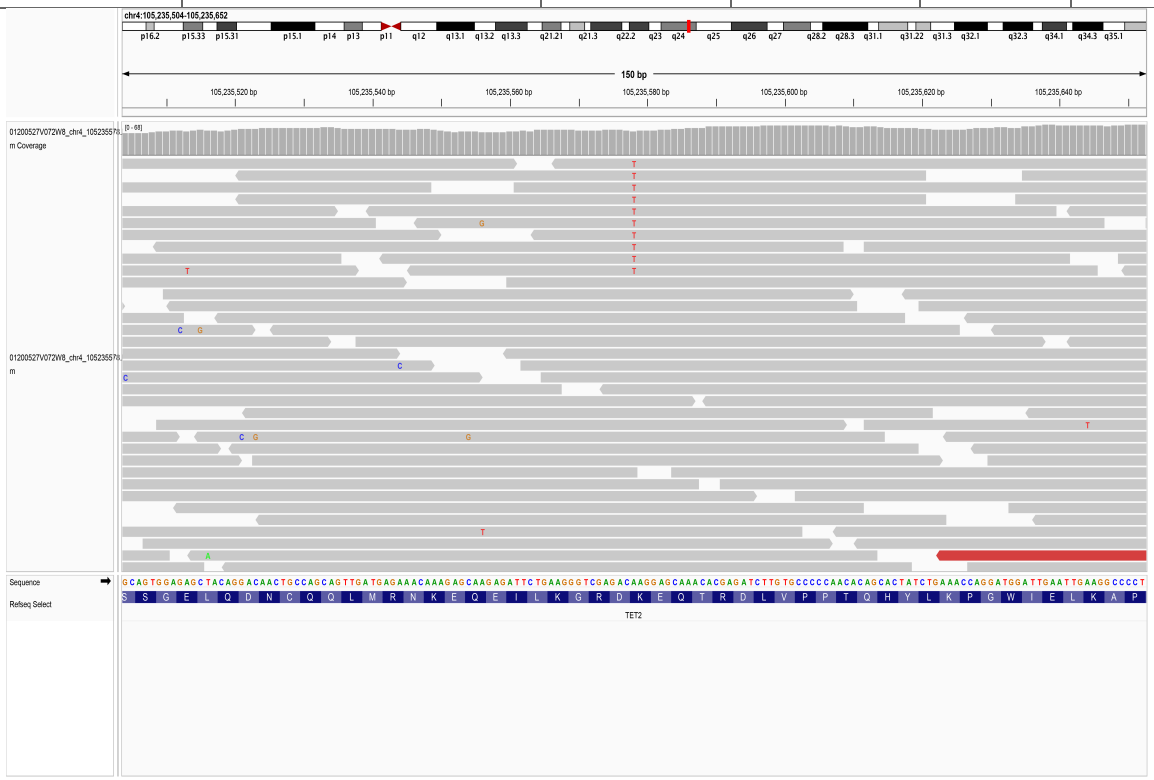
55.16. chr4_105235459_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061270D	chr4_105235459_G/-	199	14	*TET2*	frameshift_variant



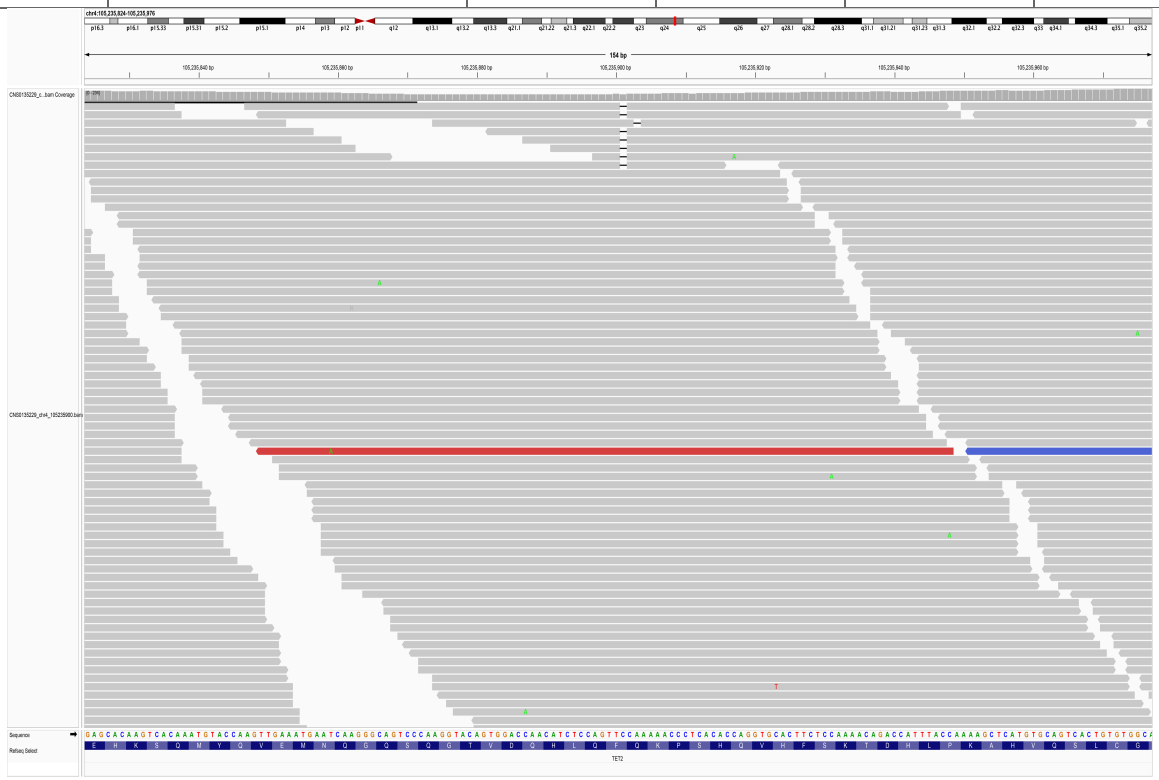
55.17. chr4_105235578_A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
01200527V072W8	chr4_105235578_A/T	39	10	*TET2*	stop_gained



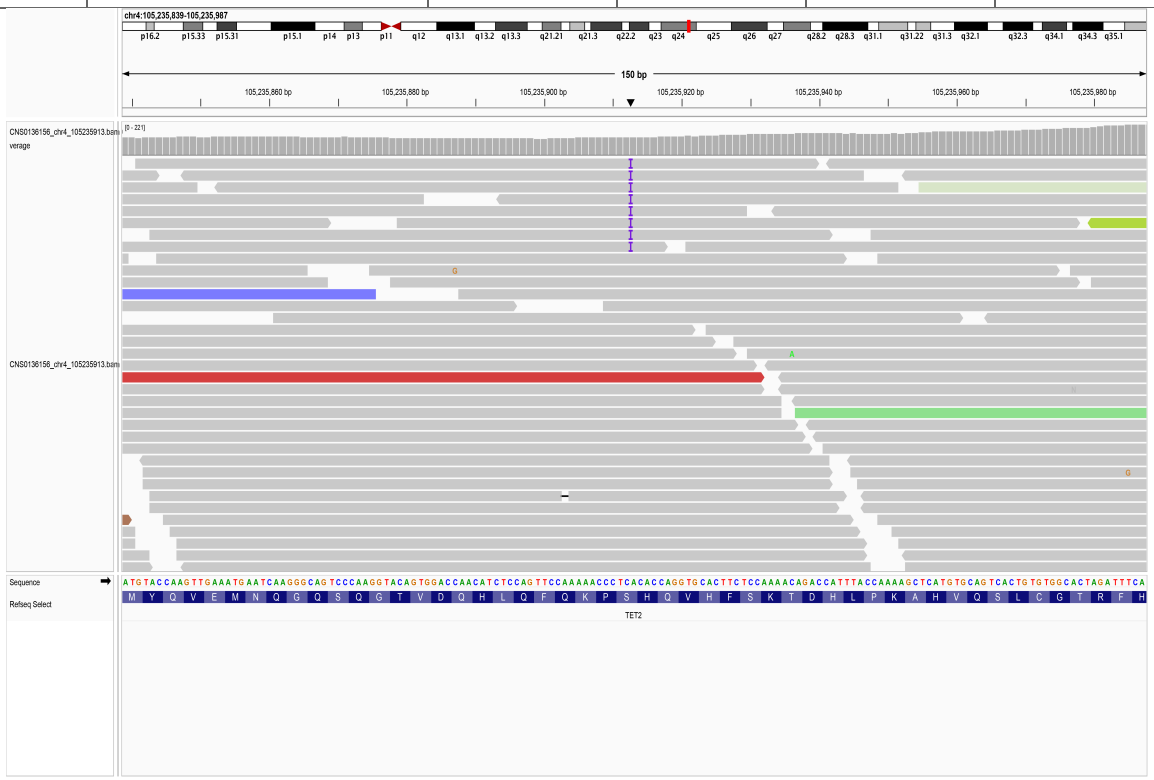
55.18. chr4_105235901_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135229	chr4_105235901_C/-	120	7	*TET2*	frameshift_variant



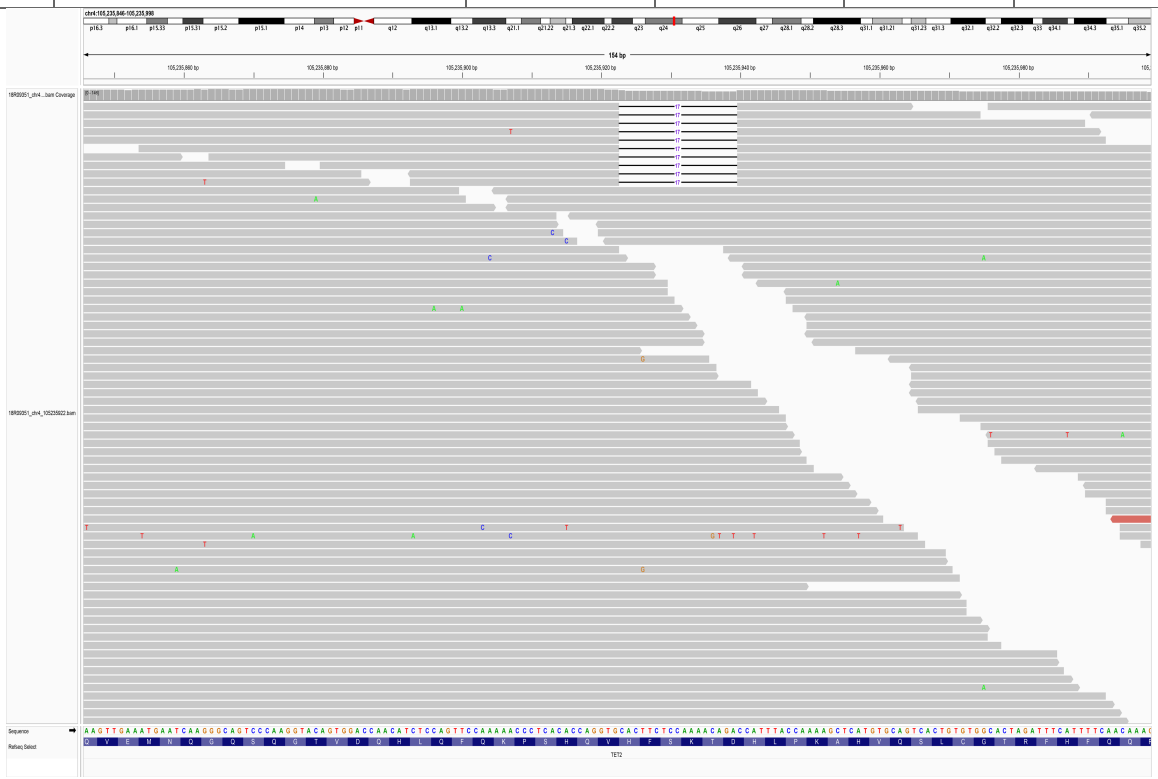
55.19. chr4_105235913_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136156	chr4_105235913_-/A	109	8	*TET2*	frameshift_variant



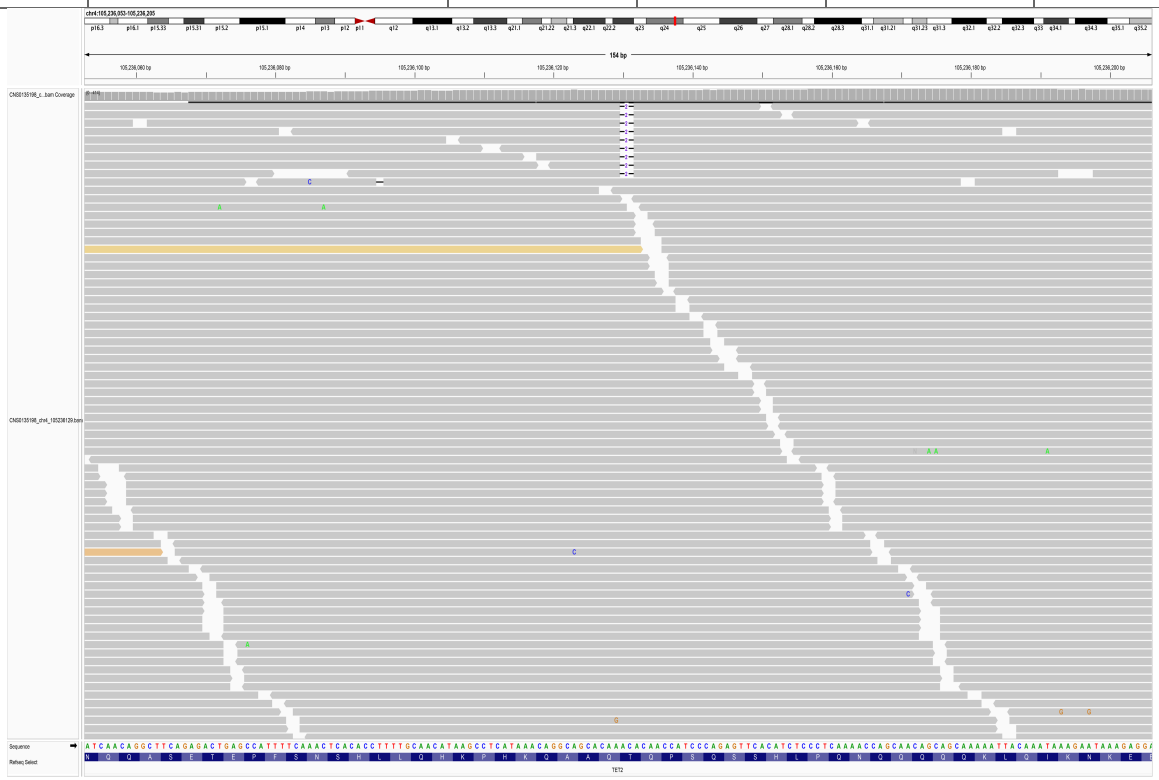
55.20. chr4_105235923_CACTTCTCCAAAACAGA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09351	chr4_105235923_CACTTCTCCAAAACAGA/-	127	13	*TET2*	frameshift_variant



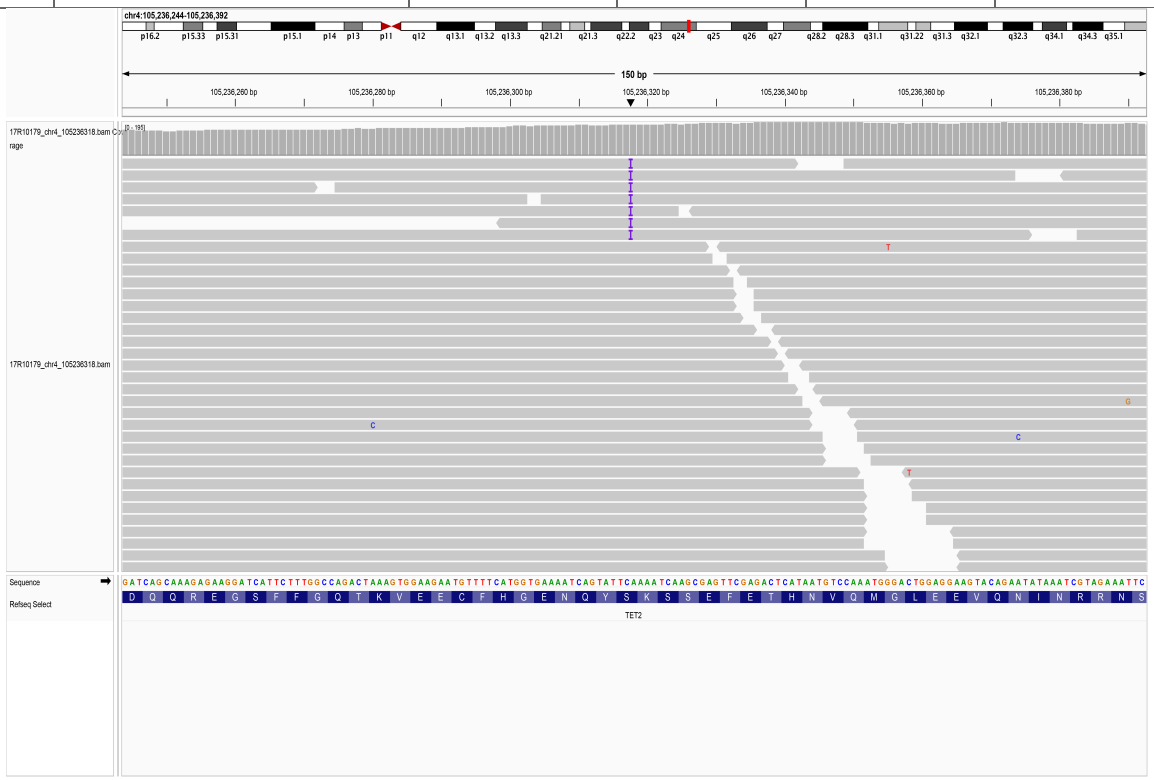
55.21. chr4_105236130_AC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135198	chr4_105236130_AC/-	347	11	*TET2*	frameshift_variant



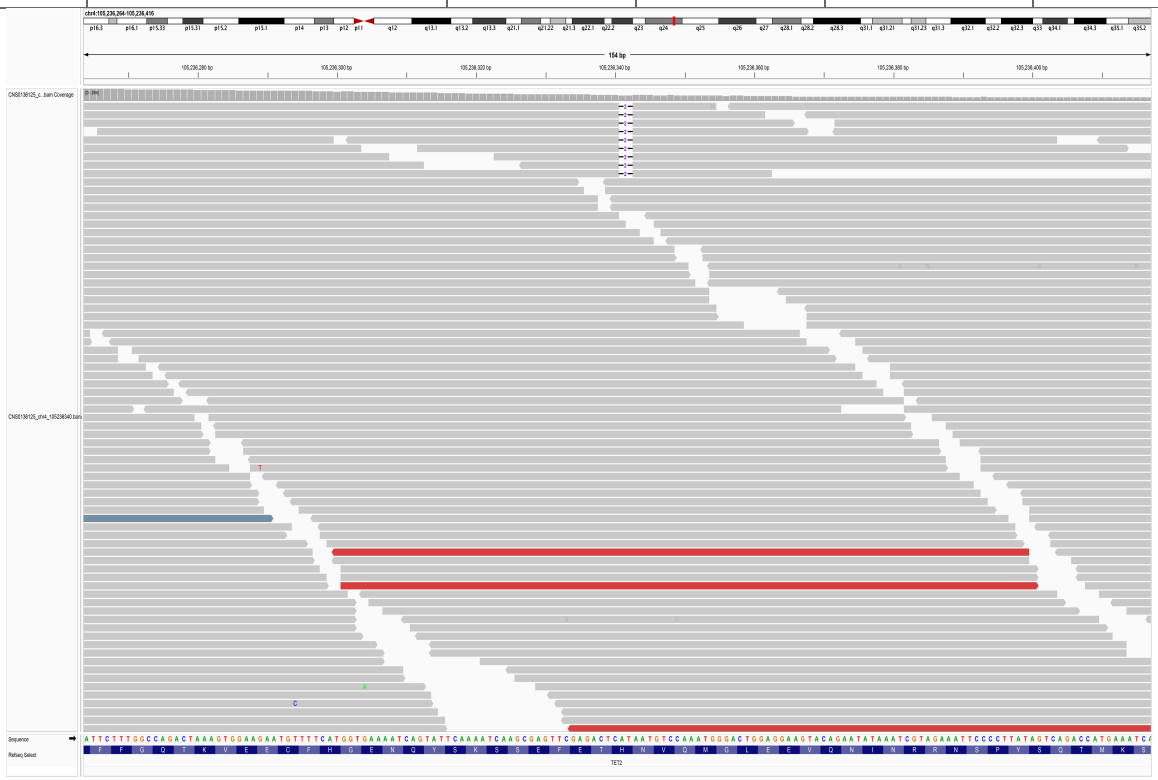
55.22. chr4_105236318_-/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R10179	chr4_105236318_-/A	163	7	*TET2*	frameshift_variant



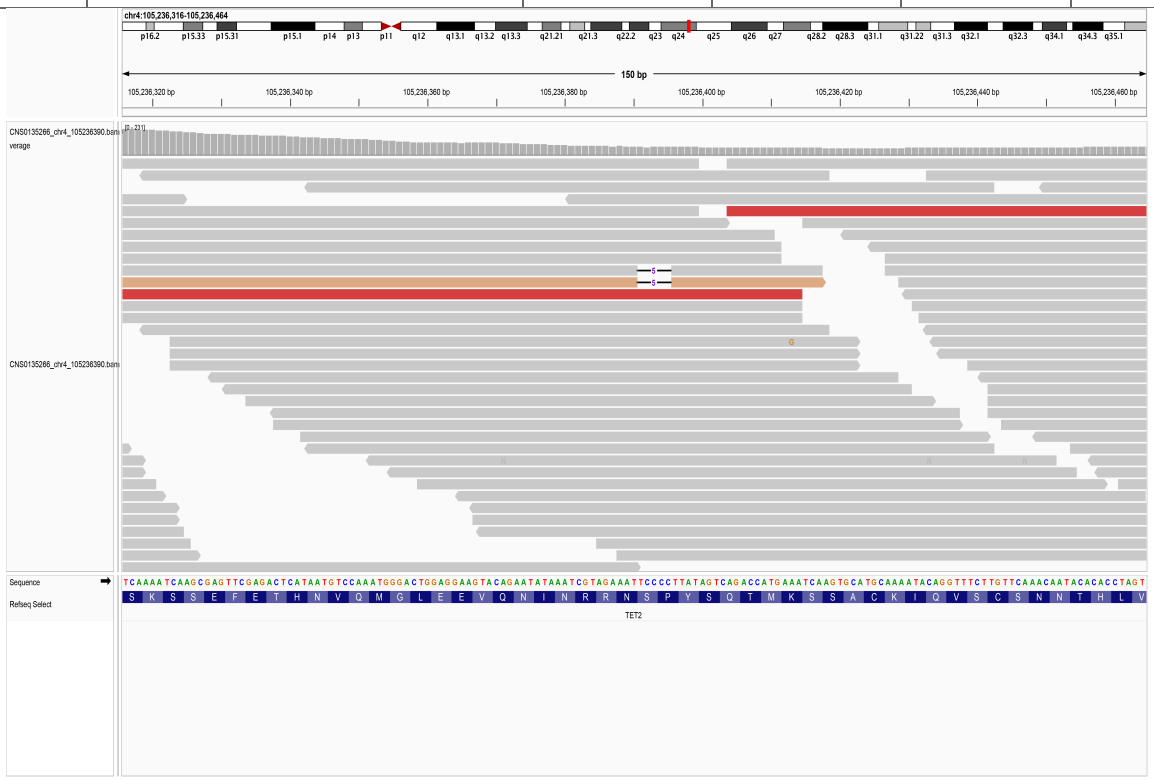
55.23. chr4_105236341_AT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136125	chr4_105236341_AT/-	112	9	*TET2*	frameshift_variant



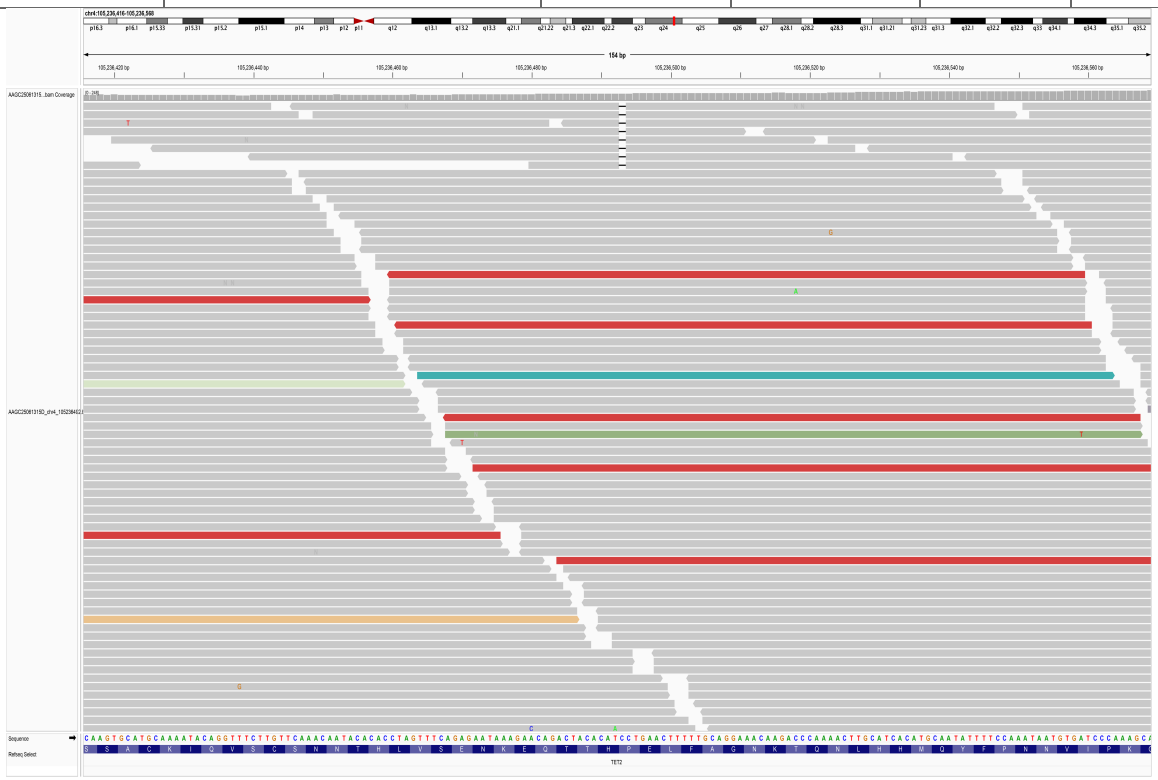
55.24. chr4_105236391_TCCCC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135266	chr4_105236391_TCCCC/-	59	3	*TET2*	frameshift_variant



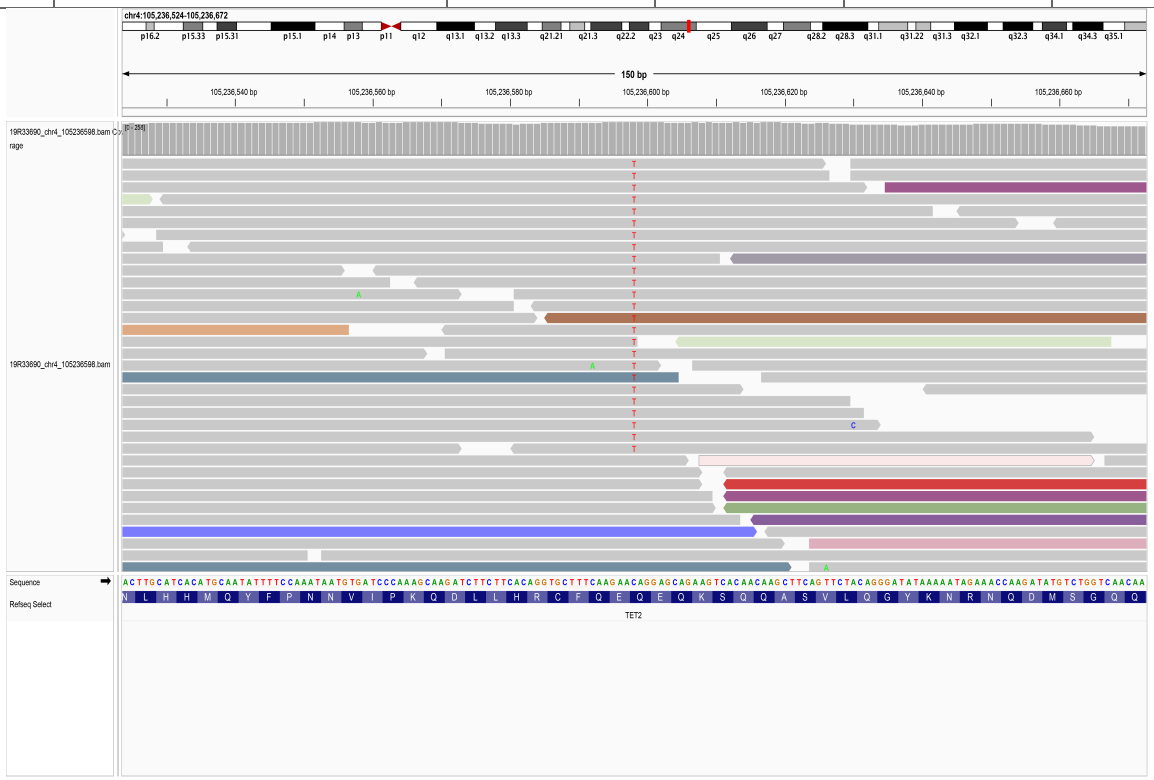
55.25. chr4_105236493_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061315D	chr4_105236493_C/-	137	8	*TET2*	frameshift_variant



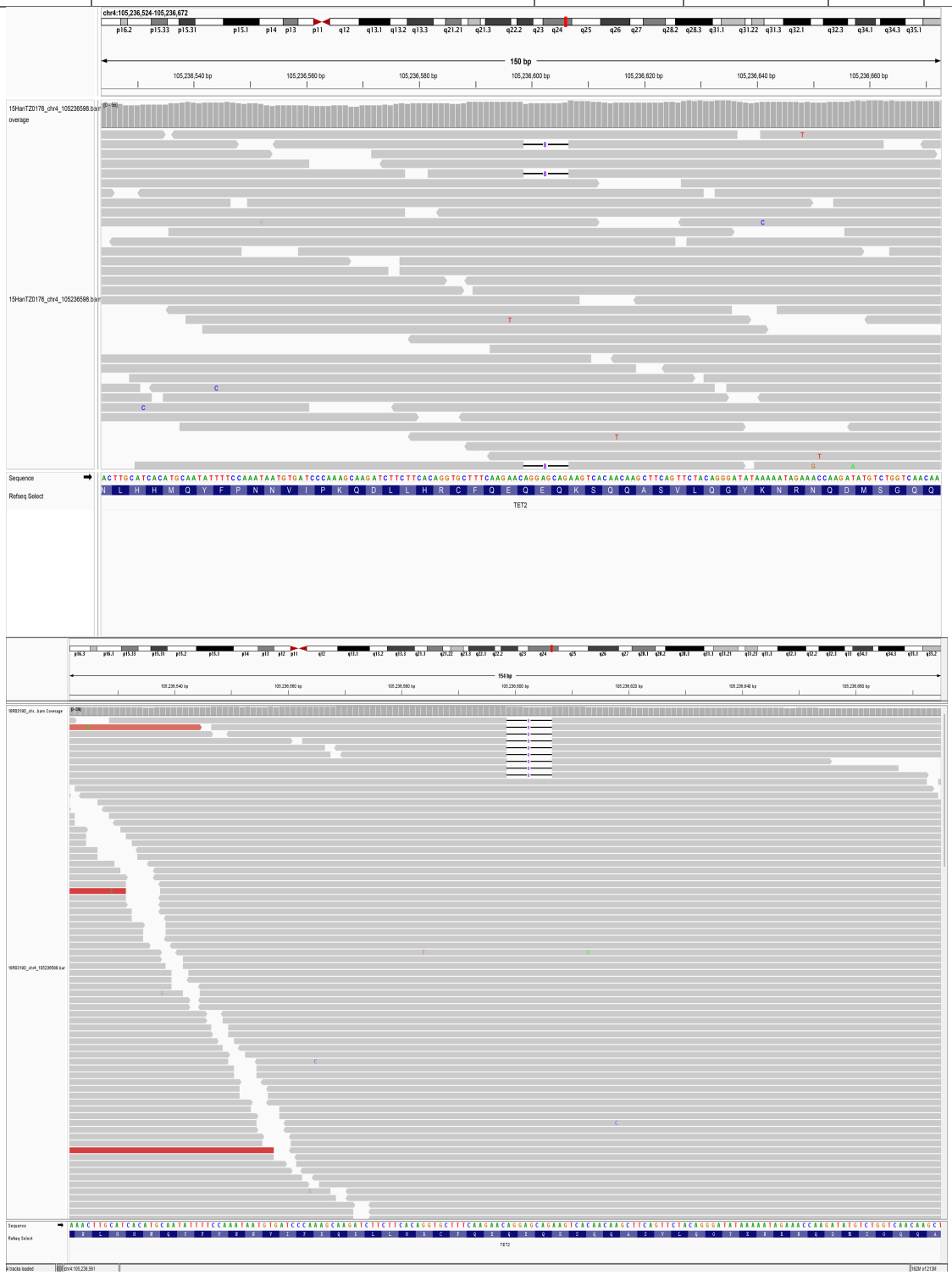
55.26. chr4_105236598_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R33690	chr4_105236598_C/T	216	24	*TET2*	stop_gained



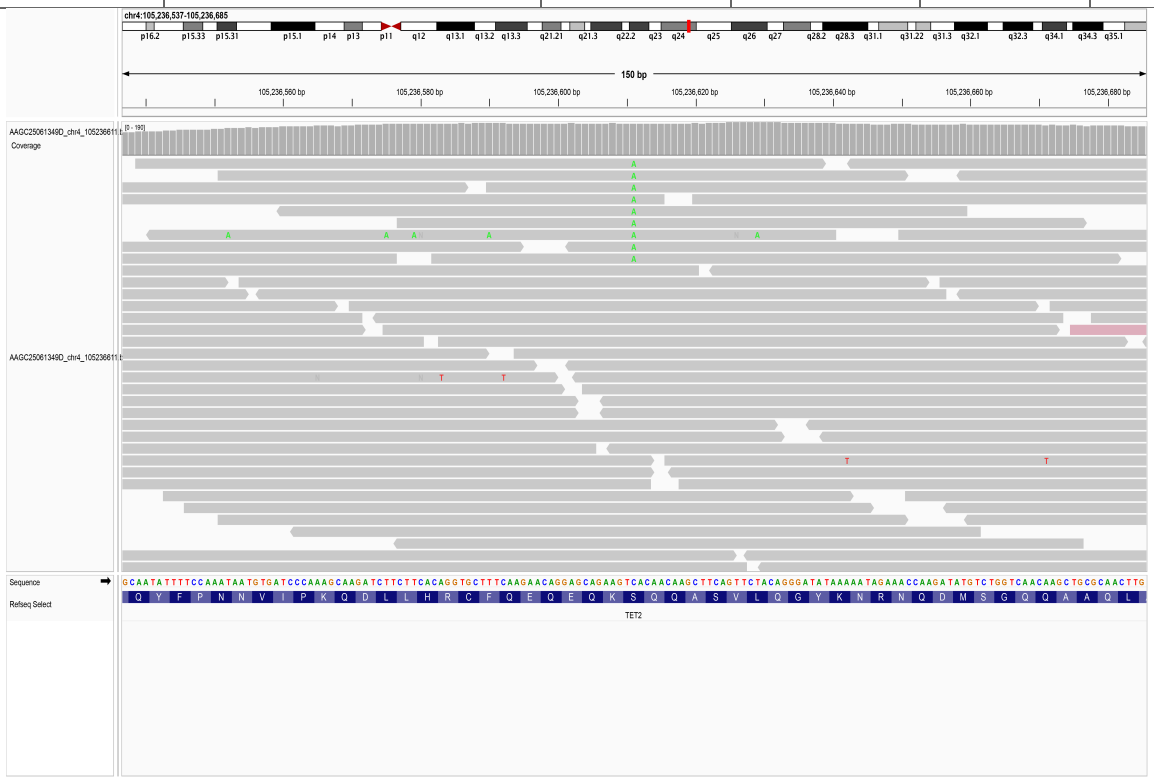
55.27. chr4_105236599_AGGAGCAG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0176	chr4_105236599_AGGAGCAG/-	53	4	*TET2*	frameshift_variant
18R03190	chr4_105236599_AGGAGCAG/-	217	10	*TET2*	frameshift_variant



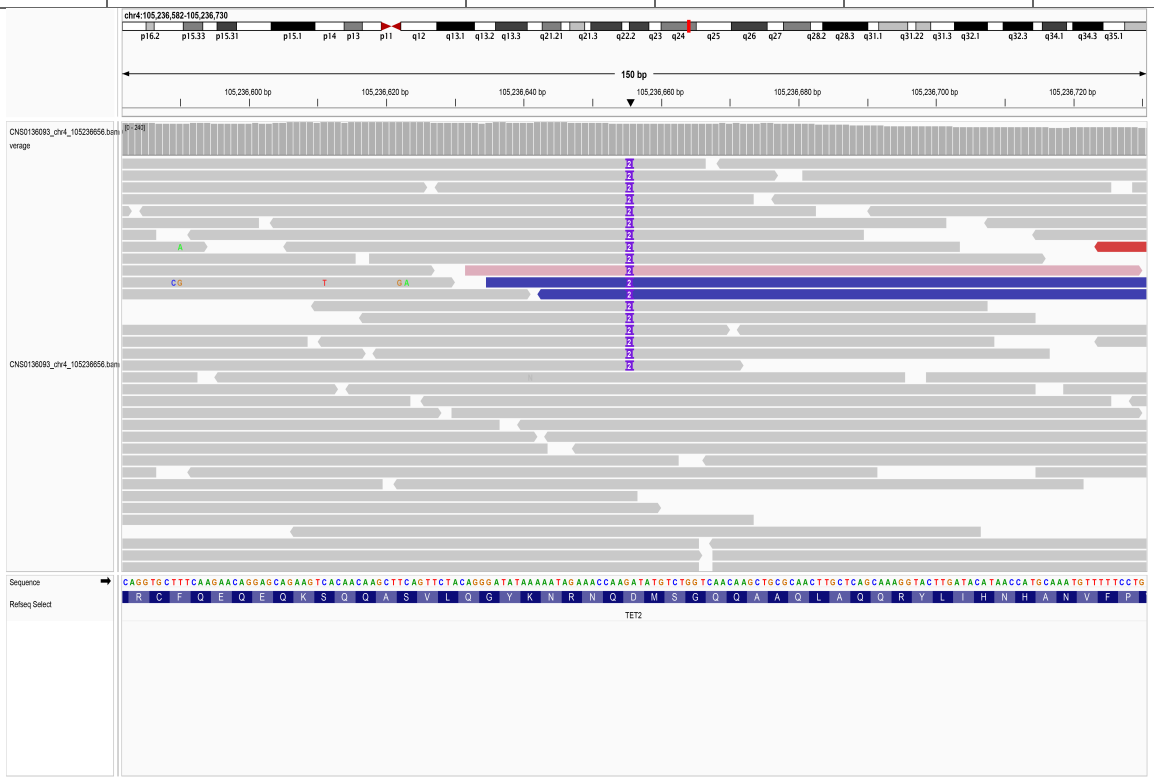
55.28. chr4_105236611_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061349D	chr4_105236611_C/A	168	8	*TET2*	stop_gained



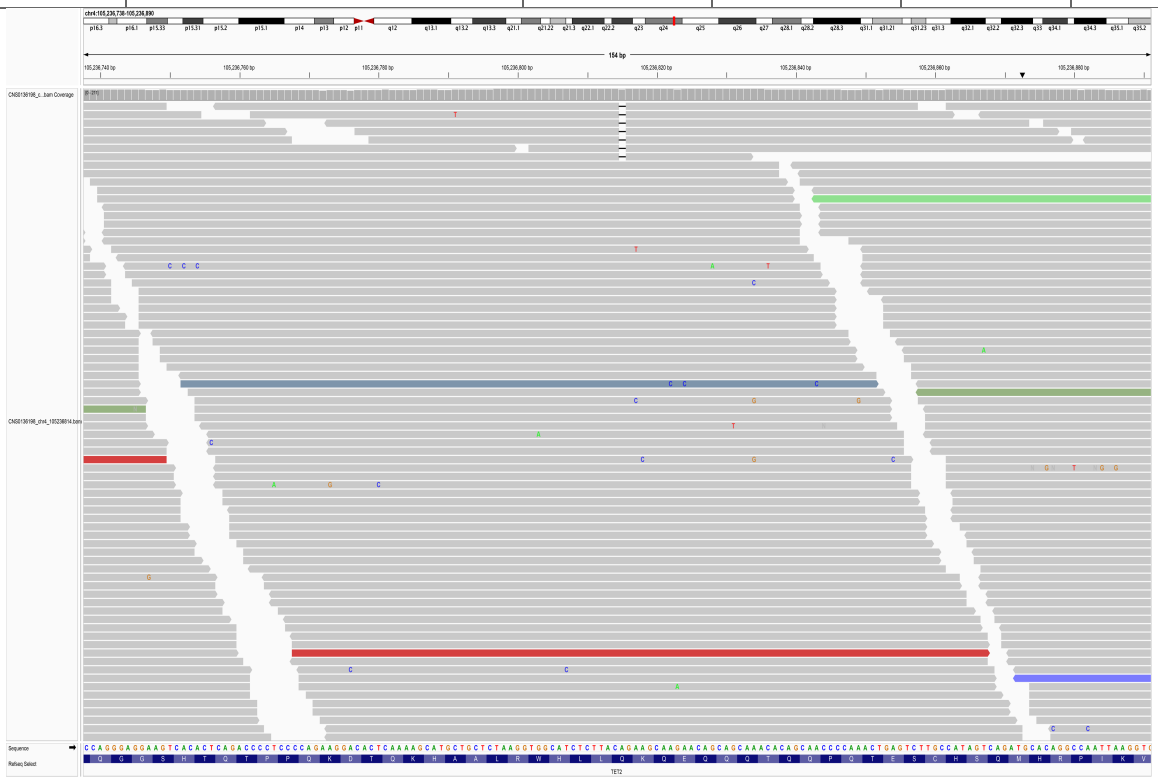
55.29. chr4_105236656_-/AT

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136093	chr4_105236656_-/AT	194	19	*TET2*	frameshift_variant



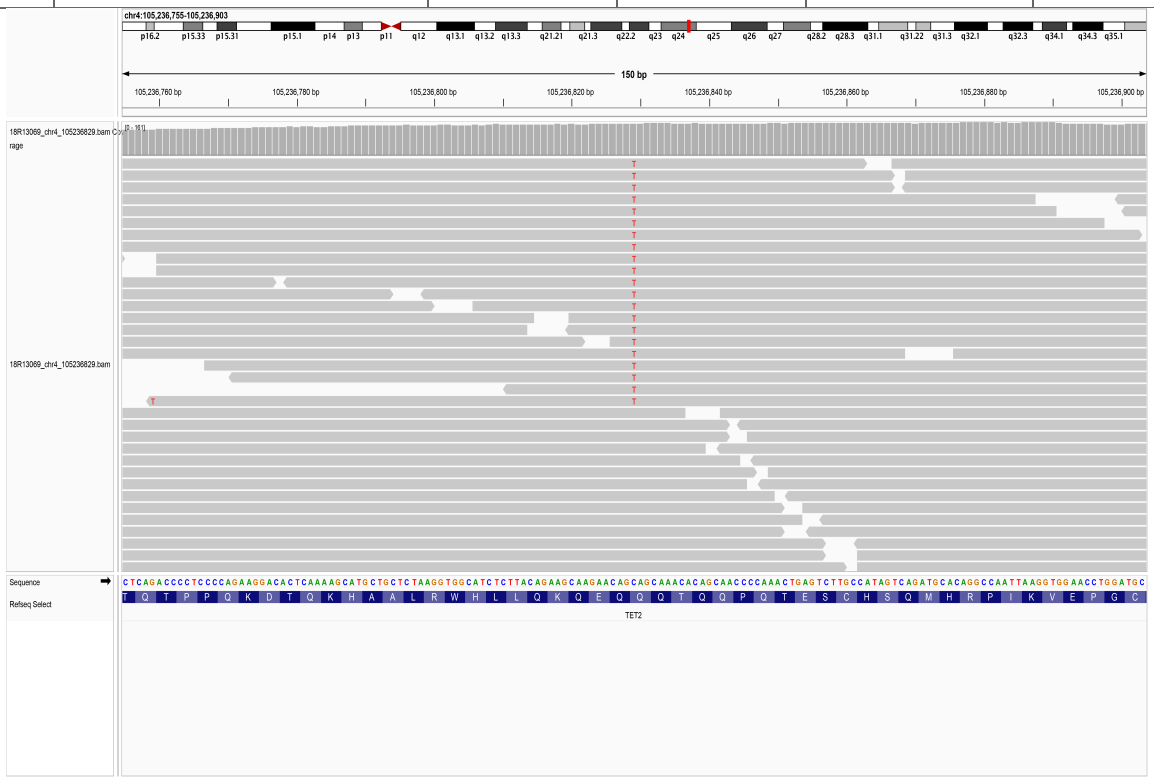
55.30. chr4_105236815_A/AA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136198	chr4_105236815_A/AA/-	87	6	*TET2*	frameshift_variant



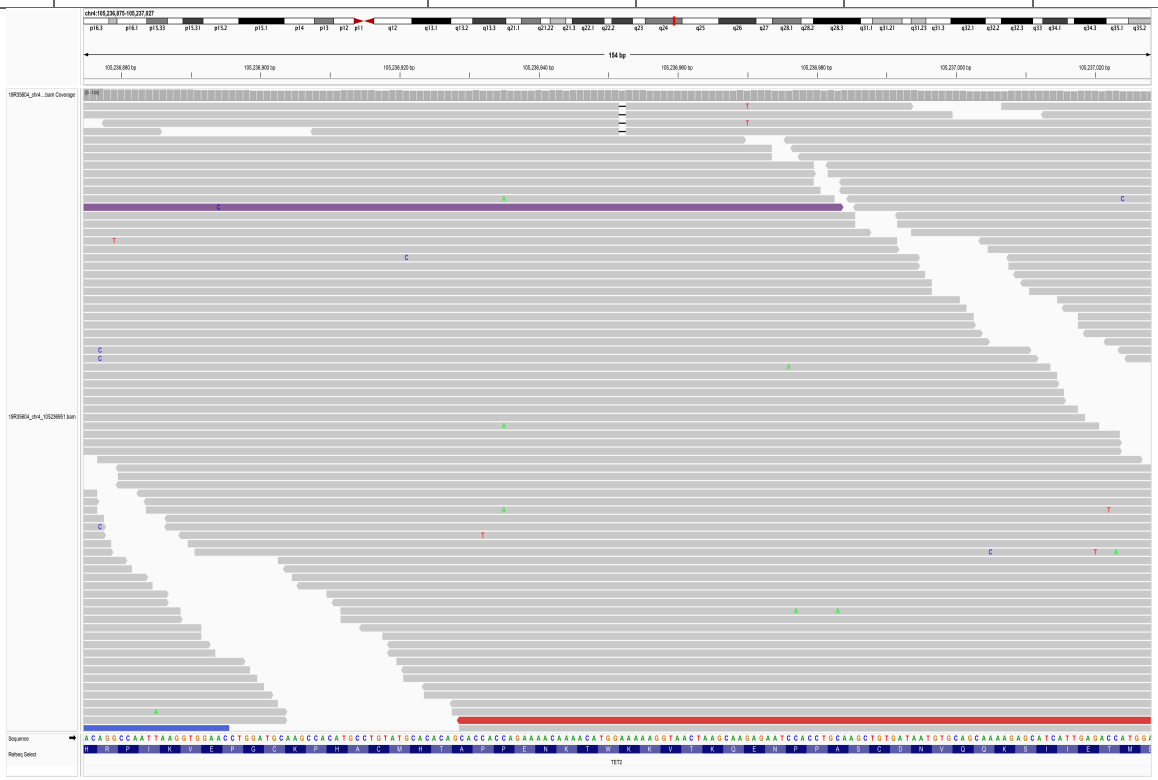
55.31. chr4_105236829_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13069	chr4_105236829_C/T	125	21	*TET2*	stop_gained



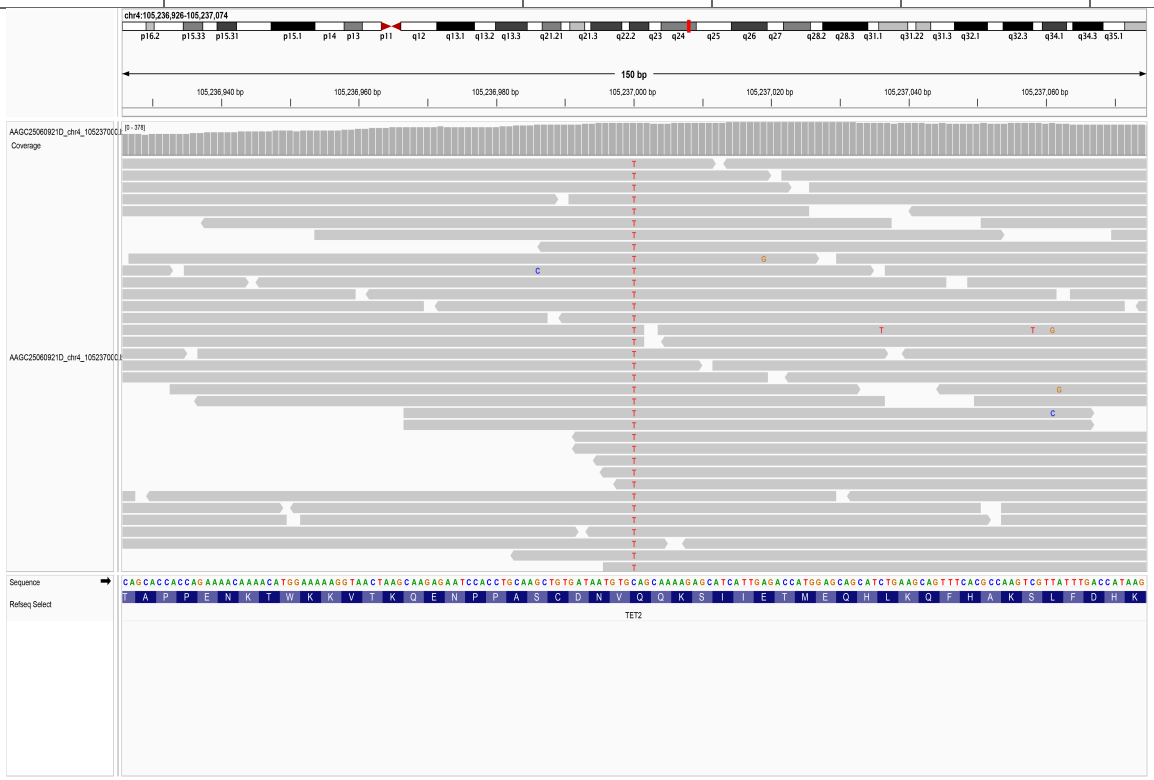
55.32. chr4_105236952_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R35604	chr4_105236952_A/-	107	4	*TET2*	frameshift_variant



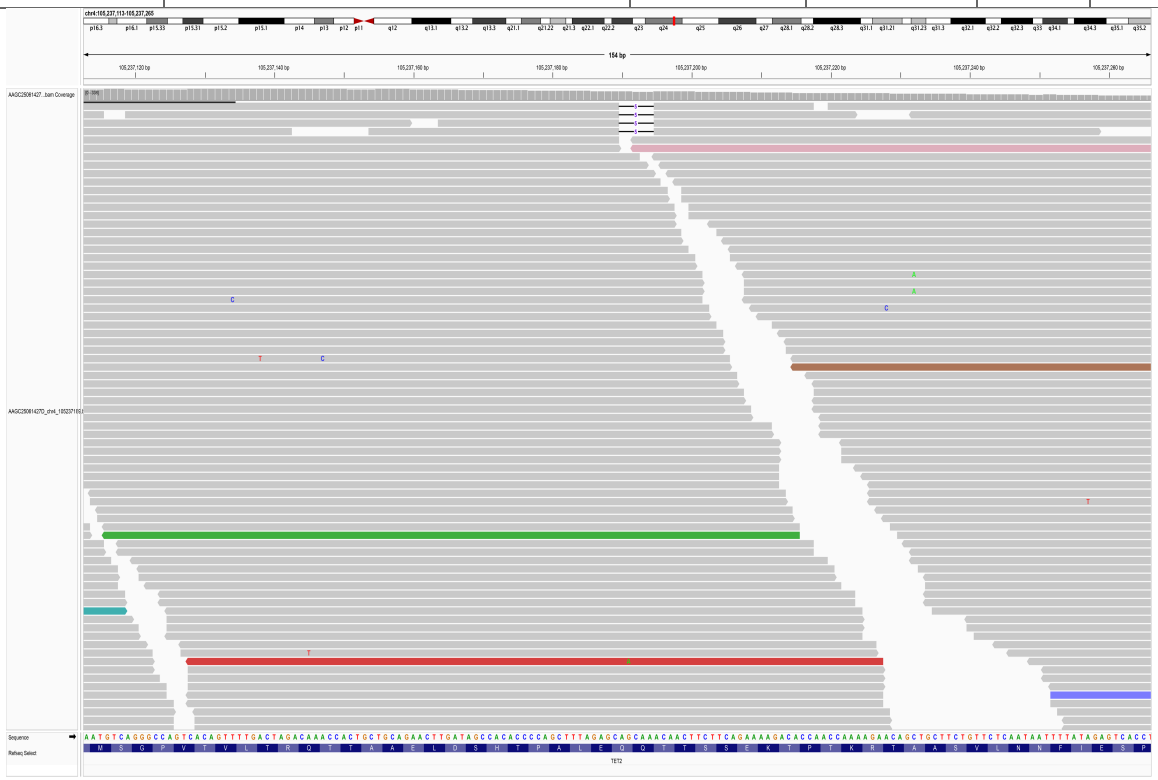
55.33. chr4_105237000_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060921D	chr4_105237000_C/T	312	42	*TET2*	stop_gained



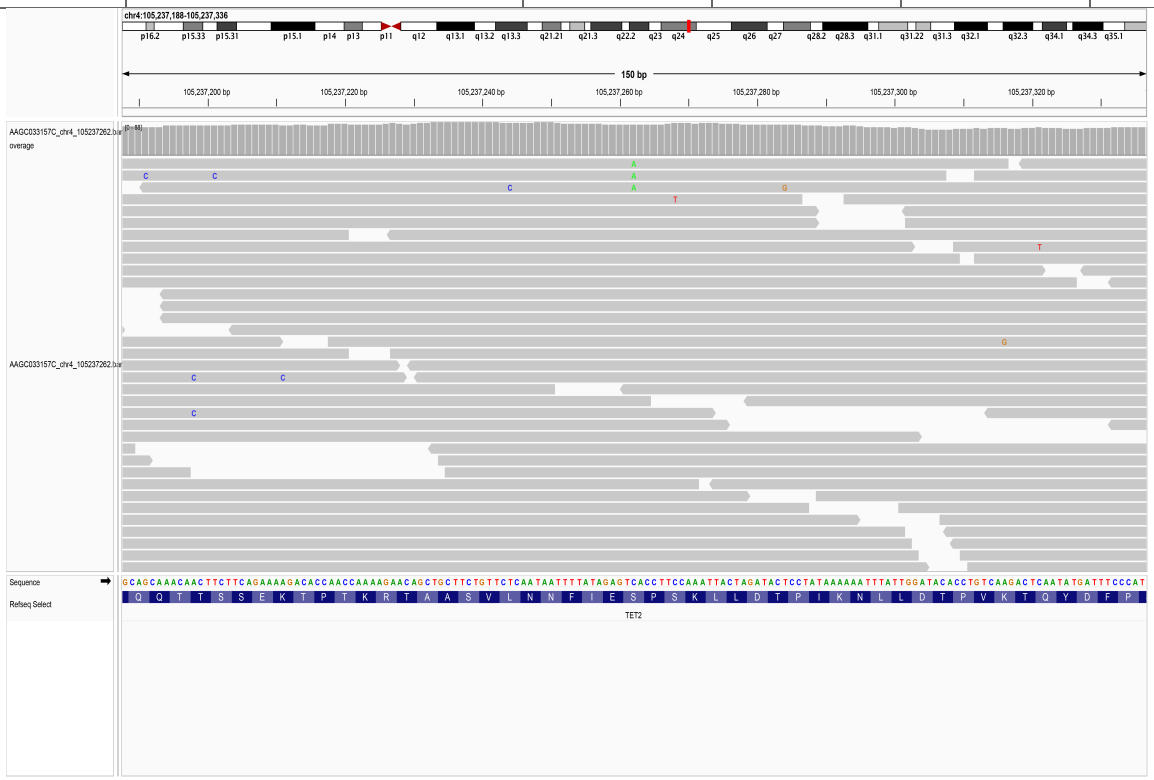
55.34. chr4_105237190_AGCAA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061427D	chr4_105237190_AGCAA/-	258	5	*TET2*	frameshift_variant



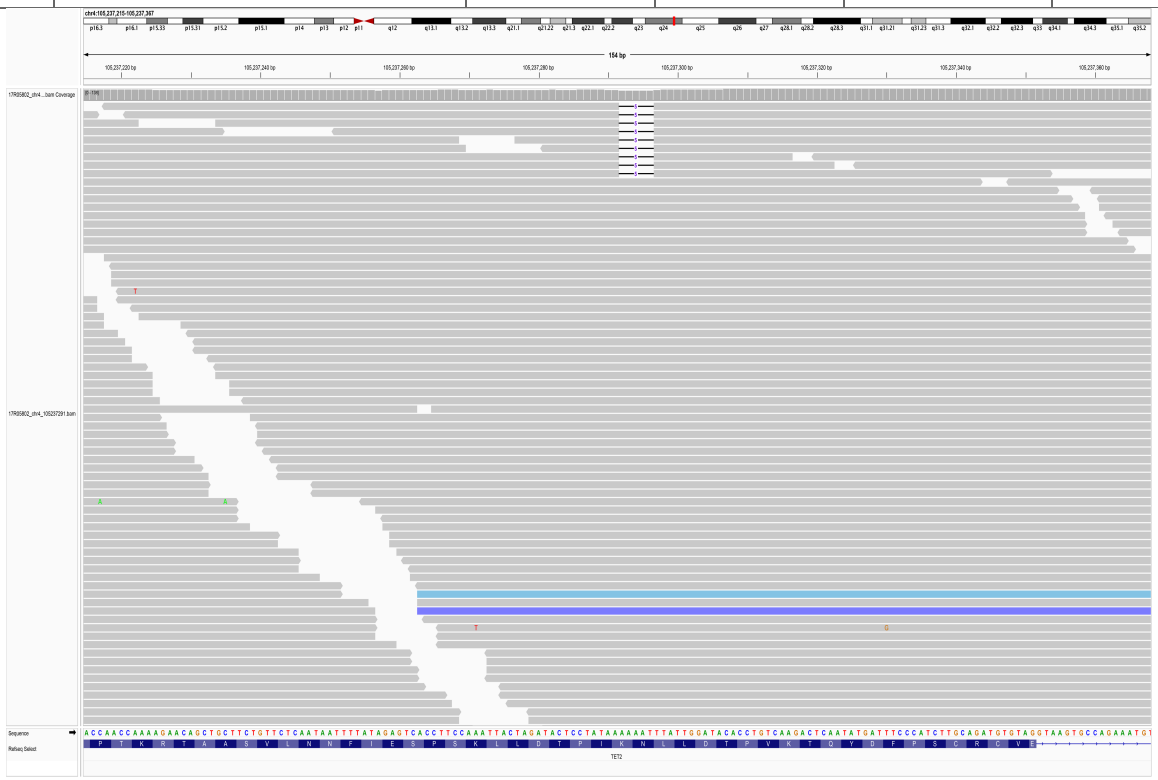
55.35. chr4_105237262_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033157C	chr4_105237262_C/A	78	3	*TET2*	stop_gained



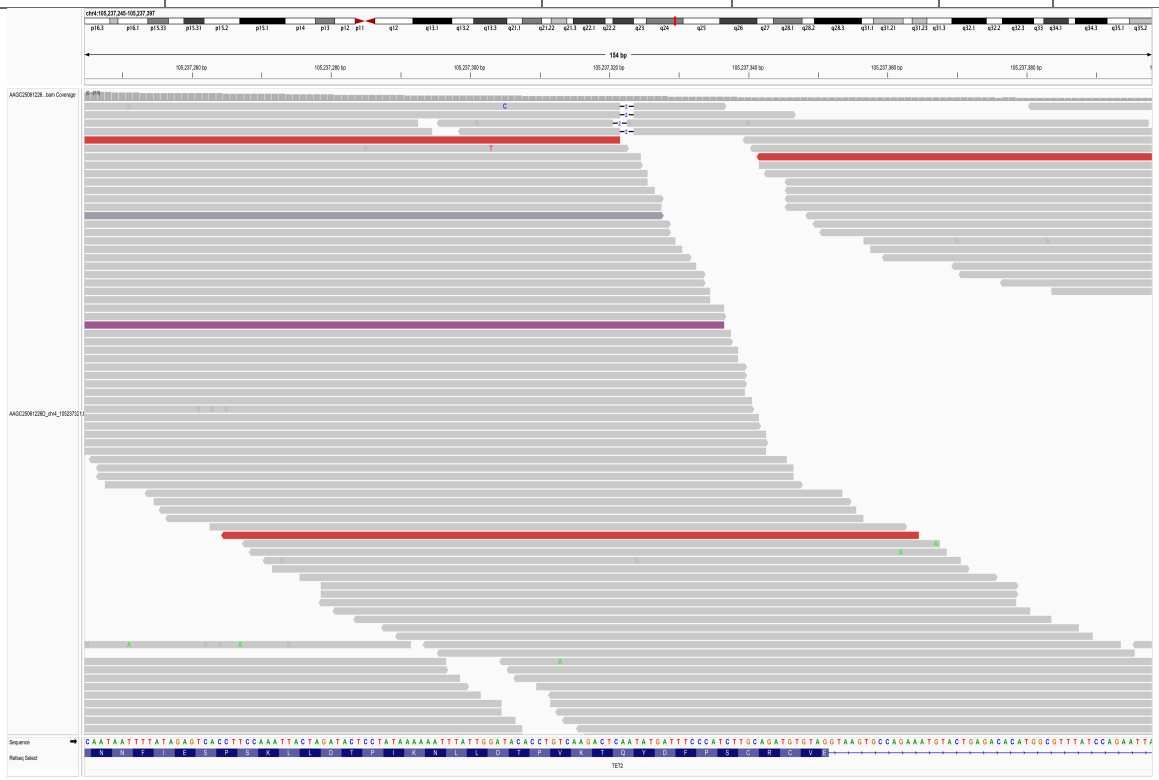
55.36. chr4_105237292_AAAAT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05802	chr4_105237292_AAAAT/-	110	10	*TET2*	frameshift_variant



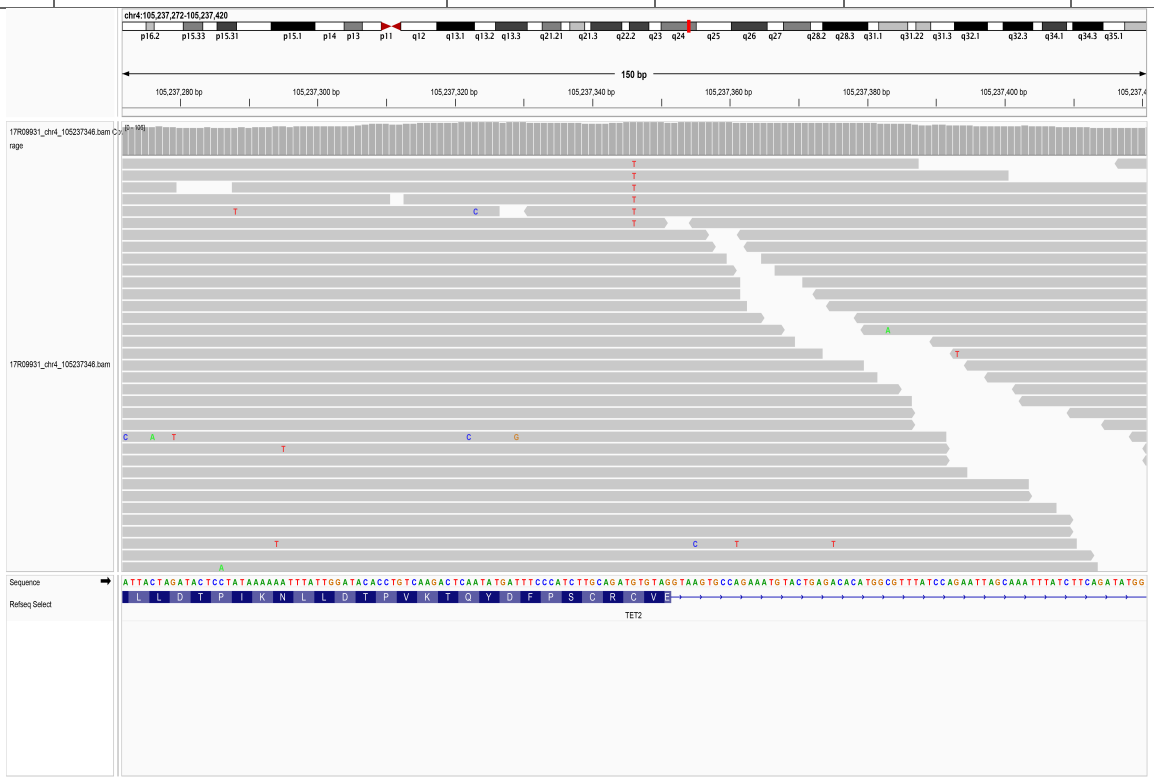
55.37. chr4_105237322_AA/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061226D	chr4_105237322_AA/-	77	4	*TET2*	frameshift_variant



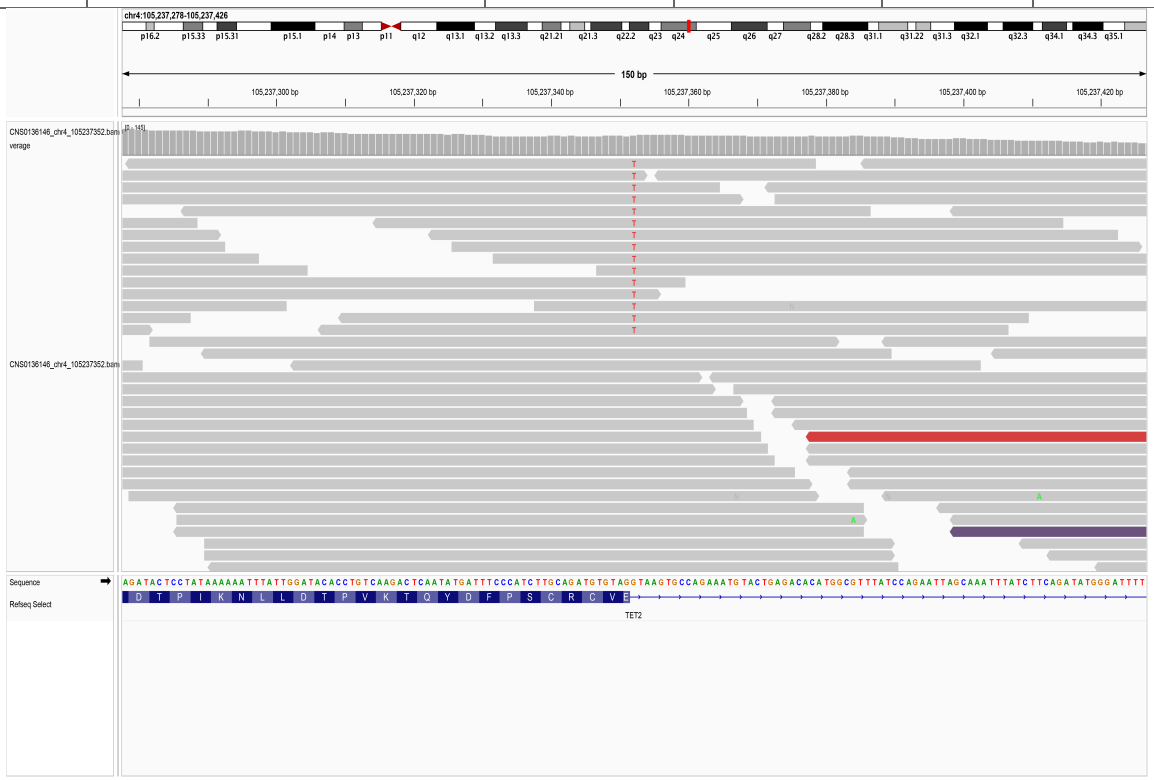
55.38. chr4_105237346_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09931	chr4_105237346_G/T	89	6	*TET2*	missense_variant



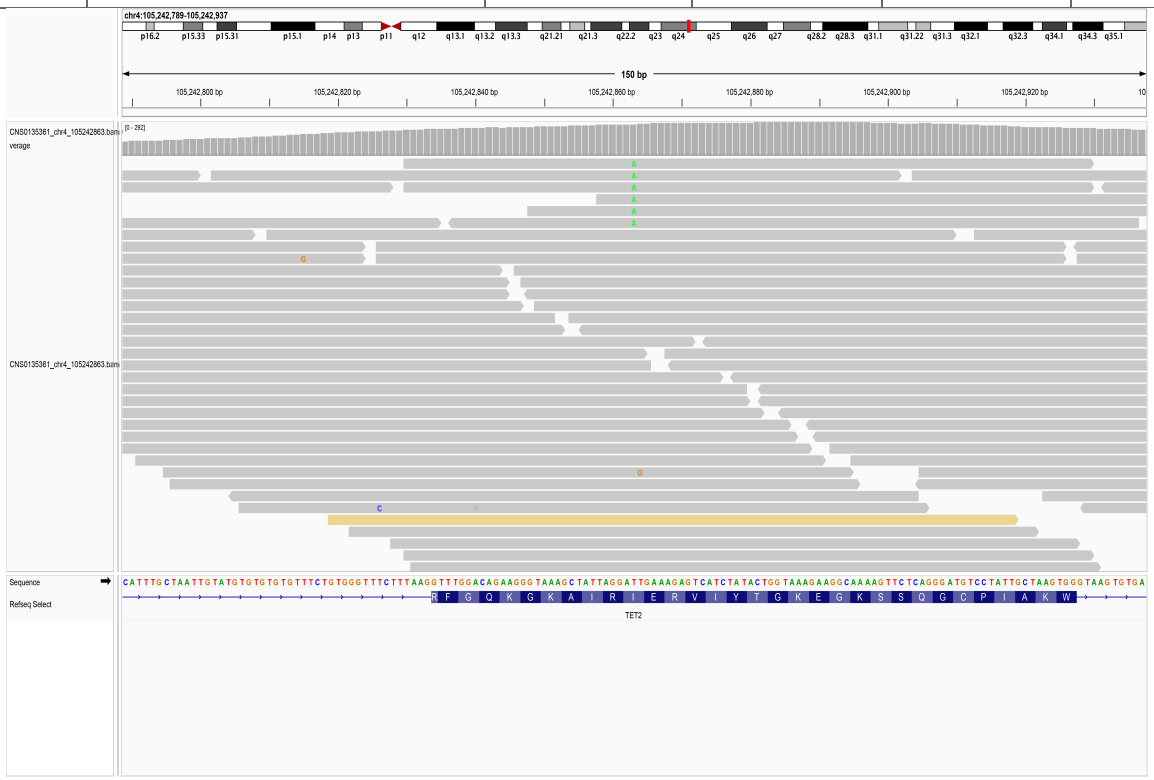
55.39. chr4_105237352_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136146	chr4_105237352_G/T	71	15	*TET2*	splice_donor_variant



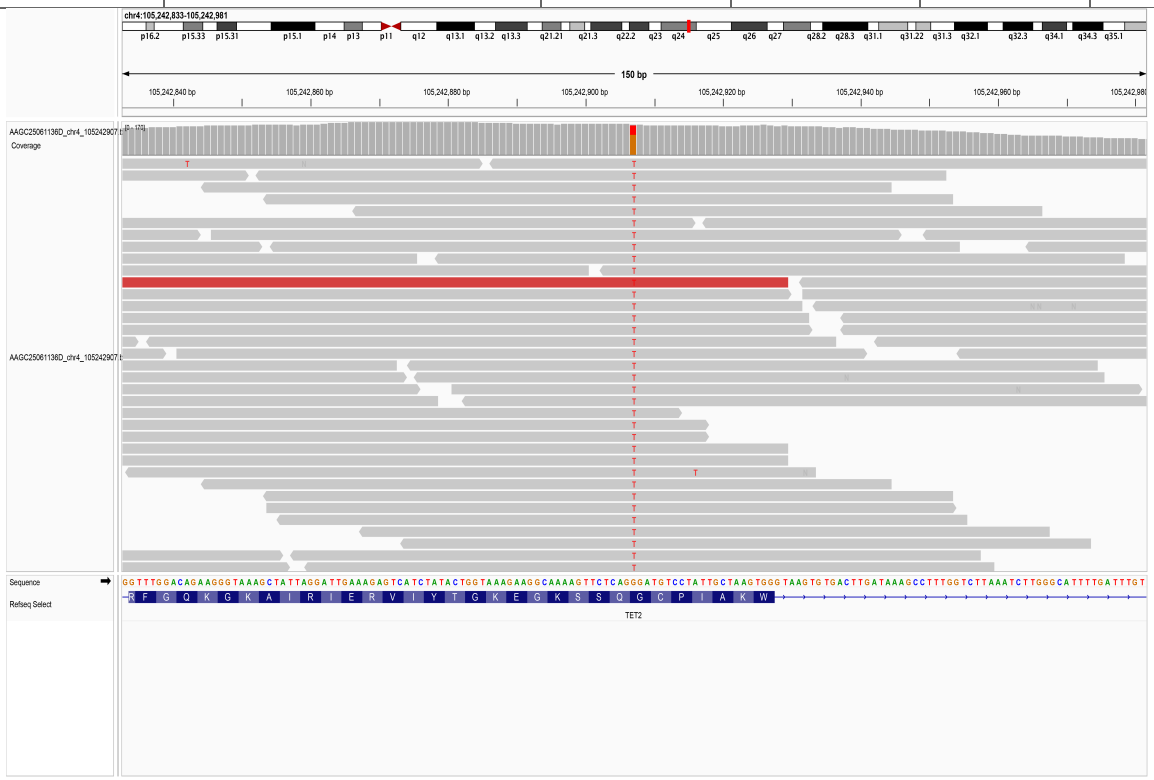
55.40. chr4_105242863_T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135361	chr4_105242863_T/A	262	6	*TET2*	missense_variant



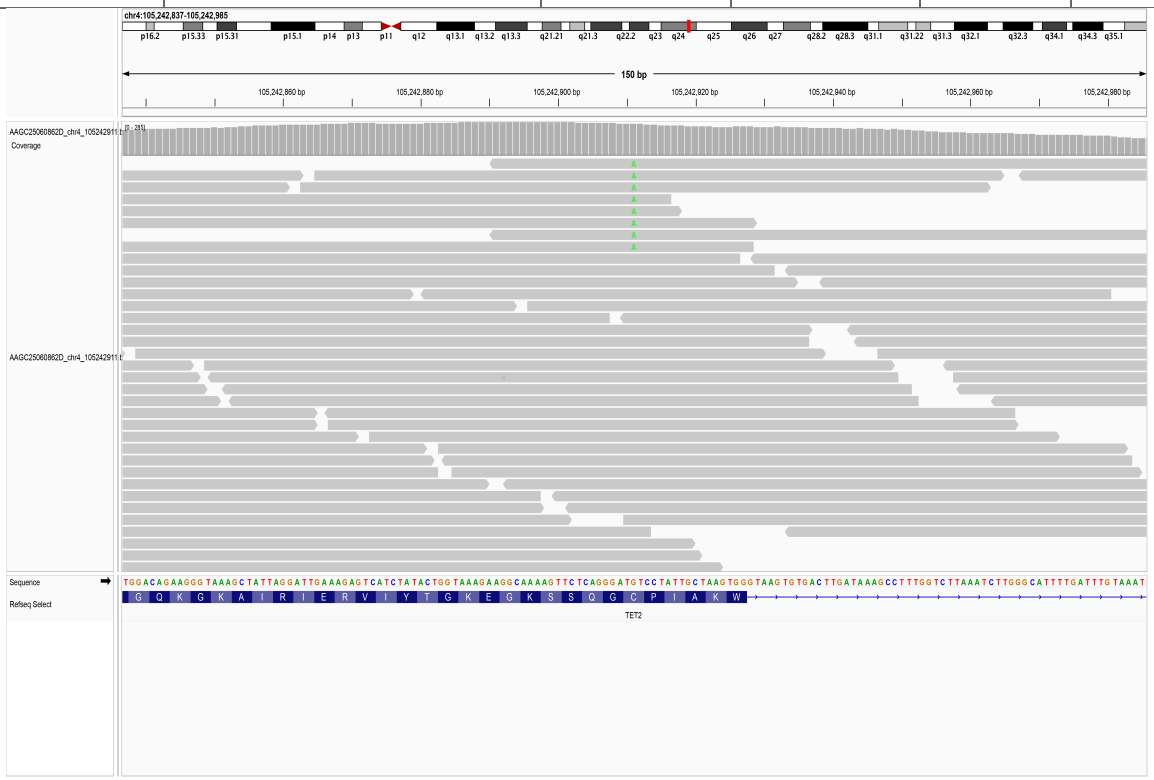
55.41. chr4_105242907_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061136D	chr4_105242907_G/T	105	49	*TET2*	stop_gained



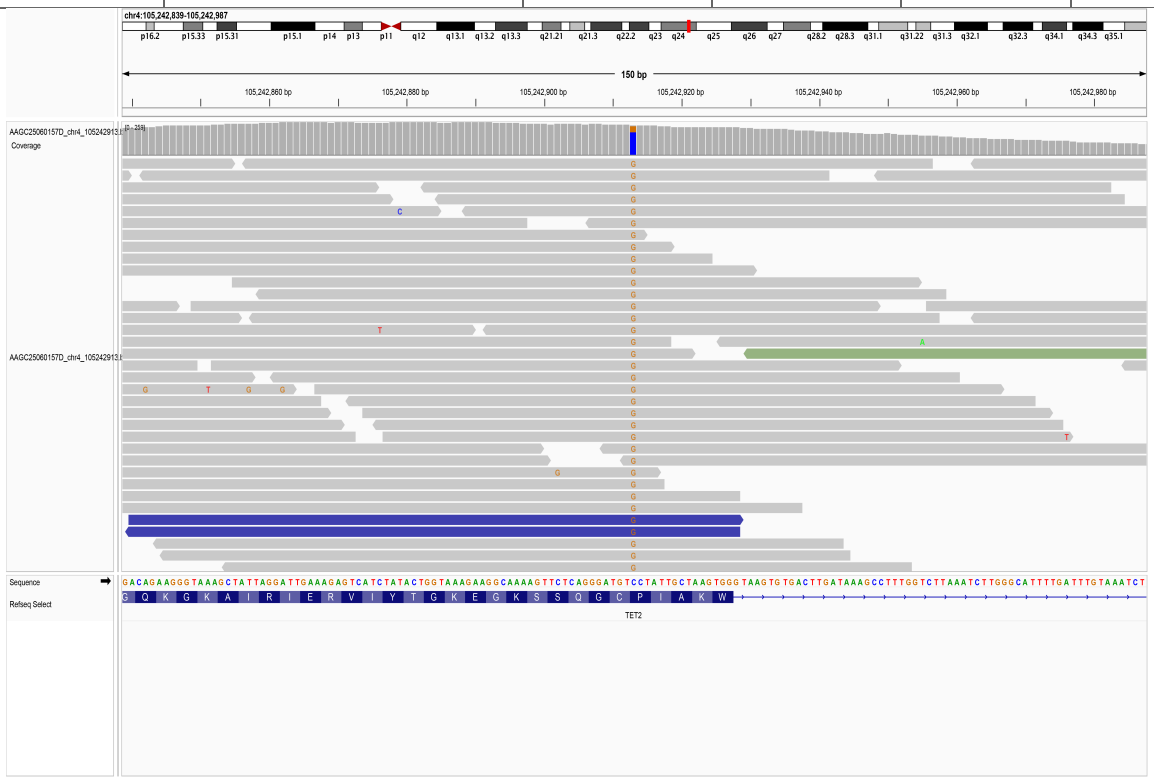
55.42. chr4_105242911_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060862D	chr4_105242911_G/A	255	8	*TET2*	missense_variant



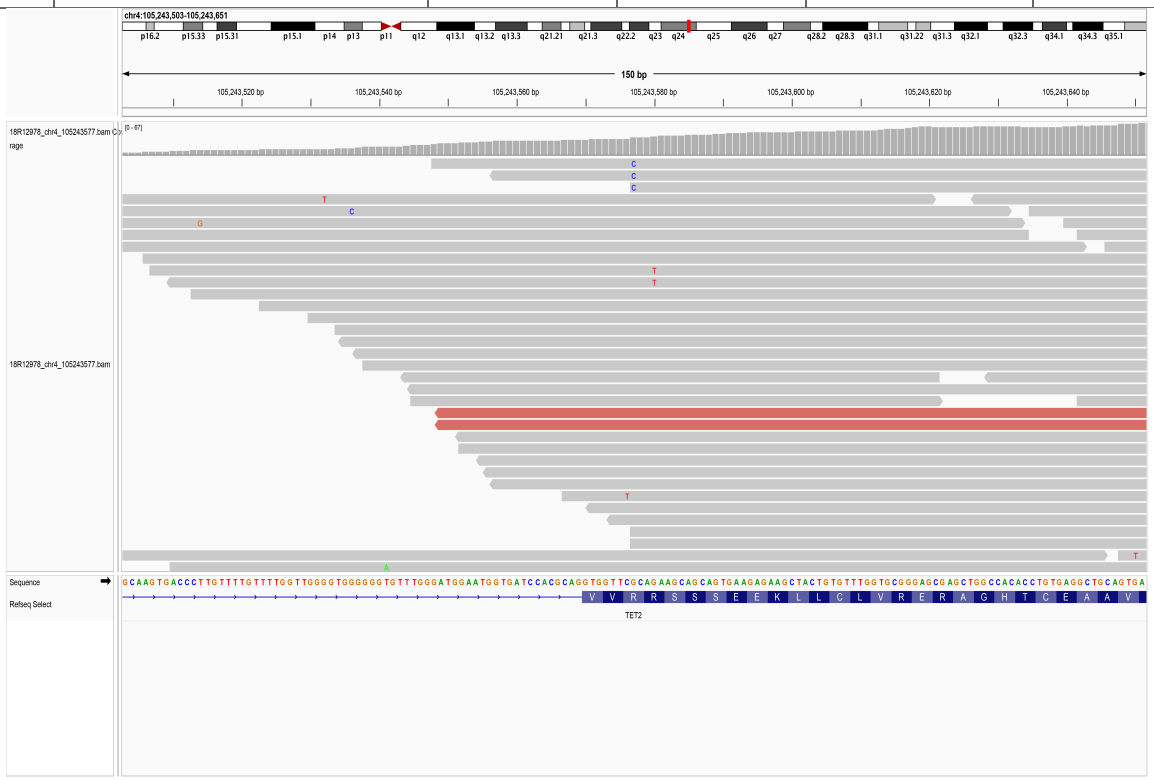
55.43. chr4_105242913_C/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060157D	chr4_105242913_C/G	178	52	*TET2*	missense_variant



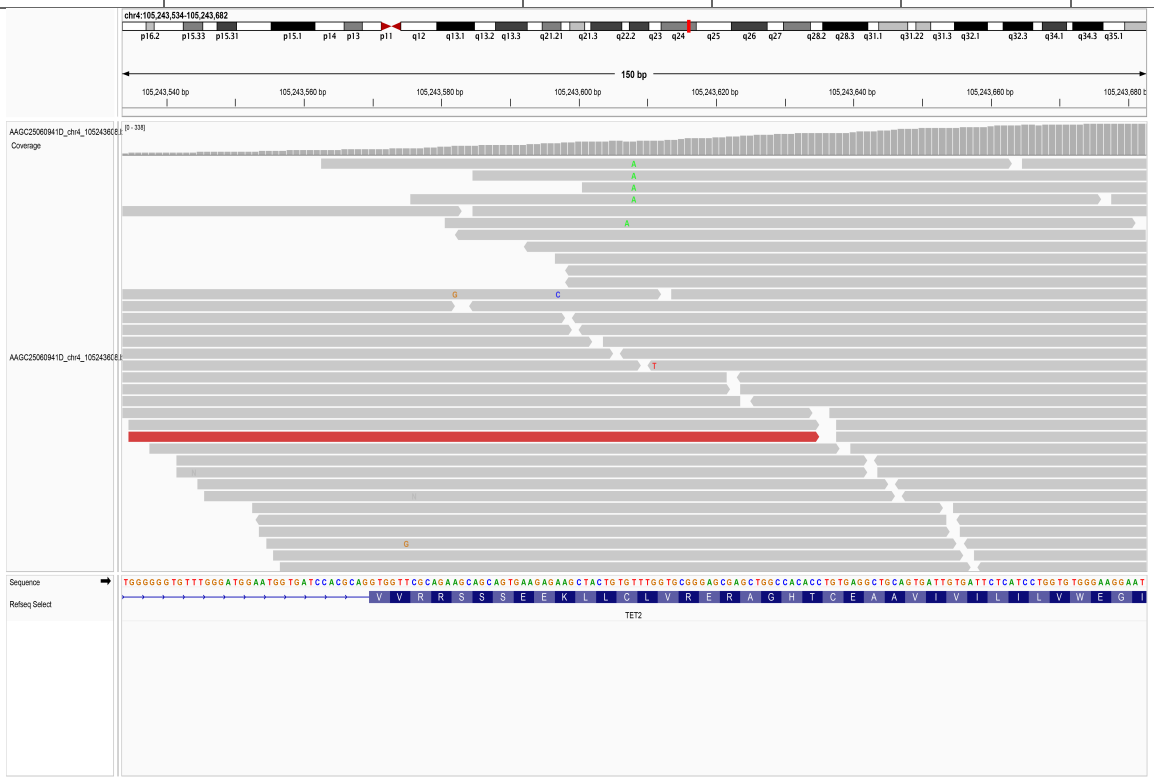
55.44. chr4_105243577_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12978	chr4_105243577_G/C	32	3	*TET2*	missense_variant



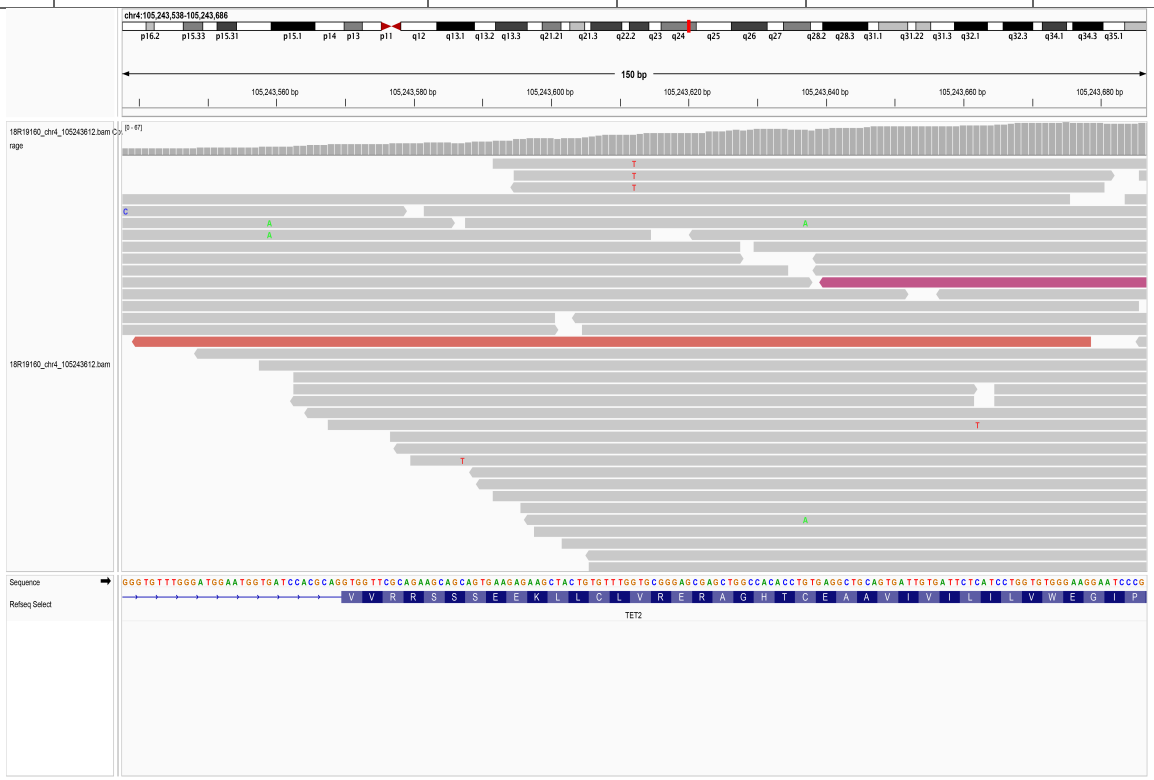
55.45. chr4_105243608_T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060941D	chr4_105243608_T/A	134	4	*TET2*	stop_gained



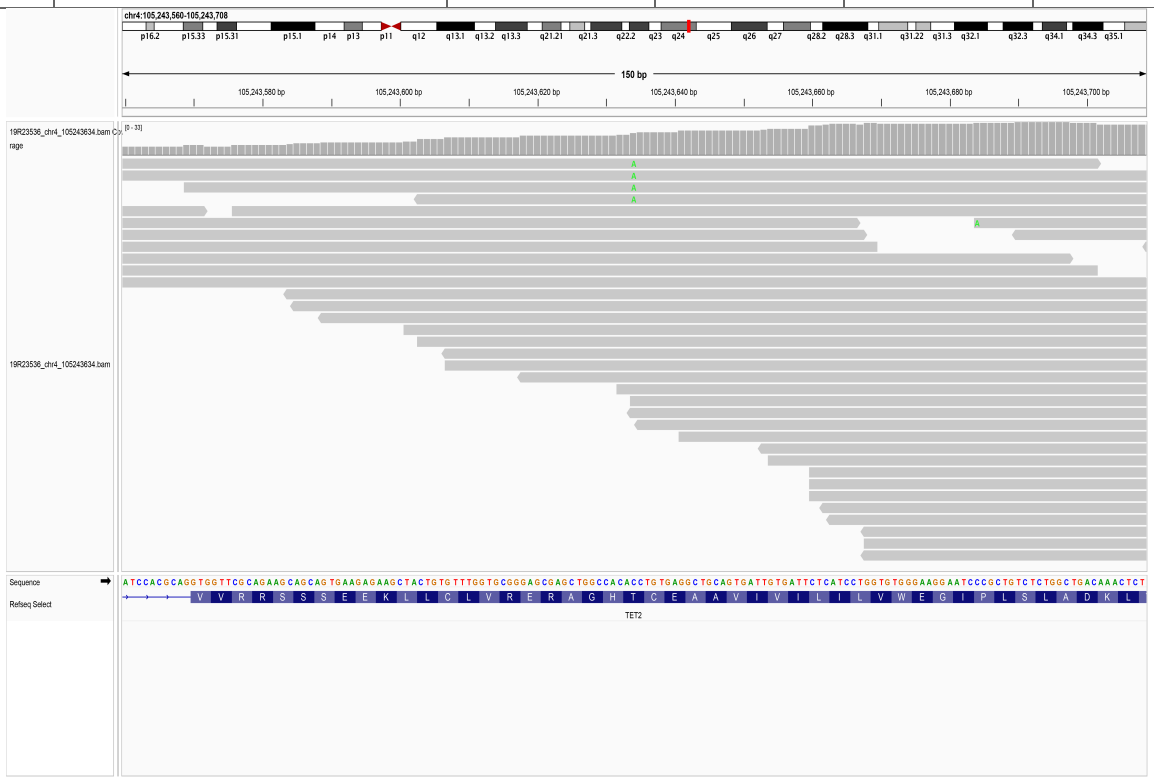
55.46. chr4_105243612_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19160	chr4_105243612_G/T	38	3	*TET2*	missense_variant



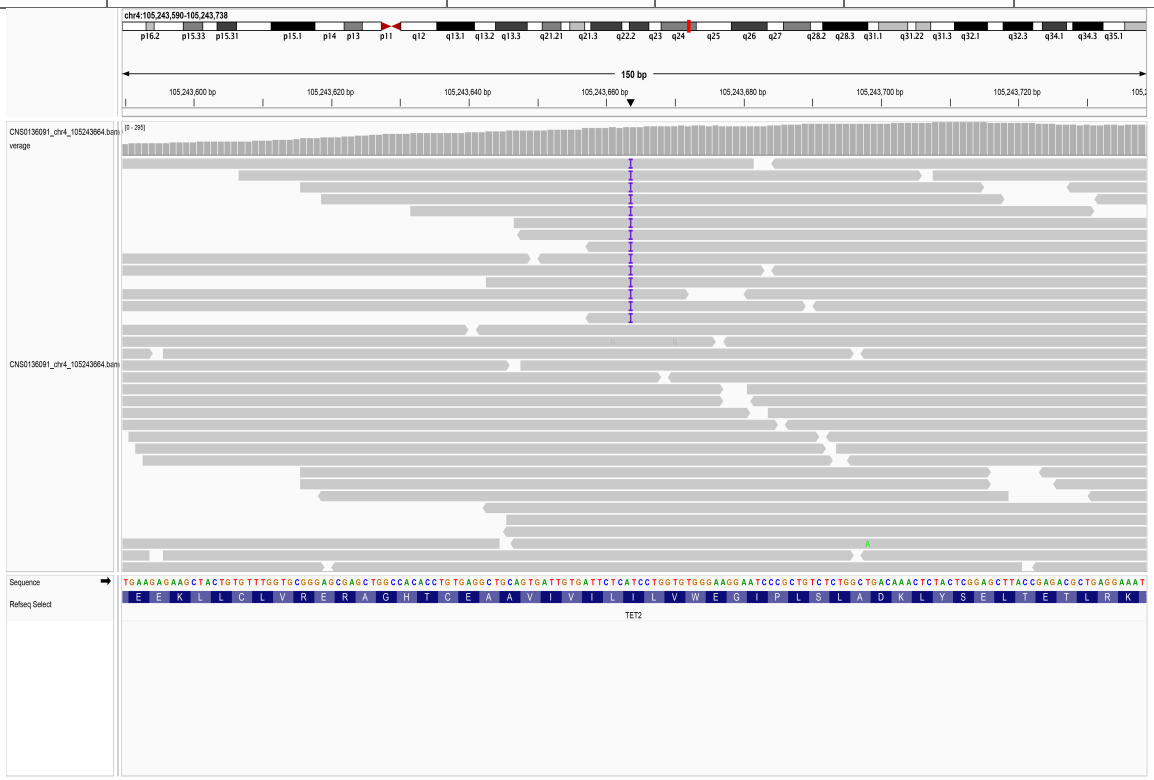
55.47. chr4_105243634_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23536	chr4_105243634_C/A	18	4	*TET2*	missense_variant



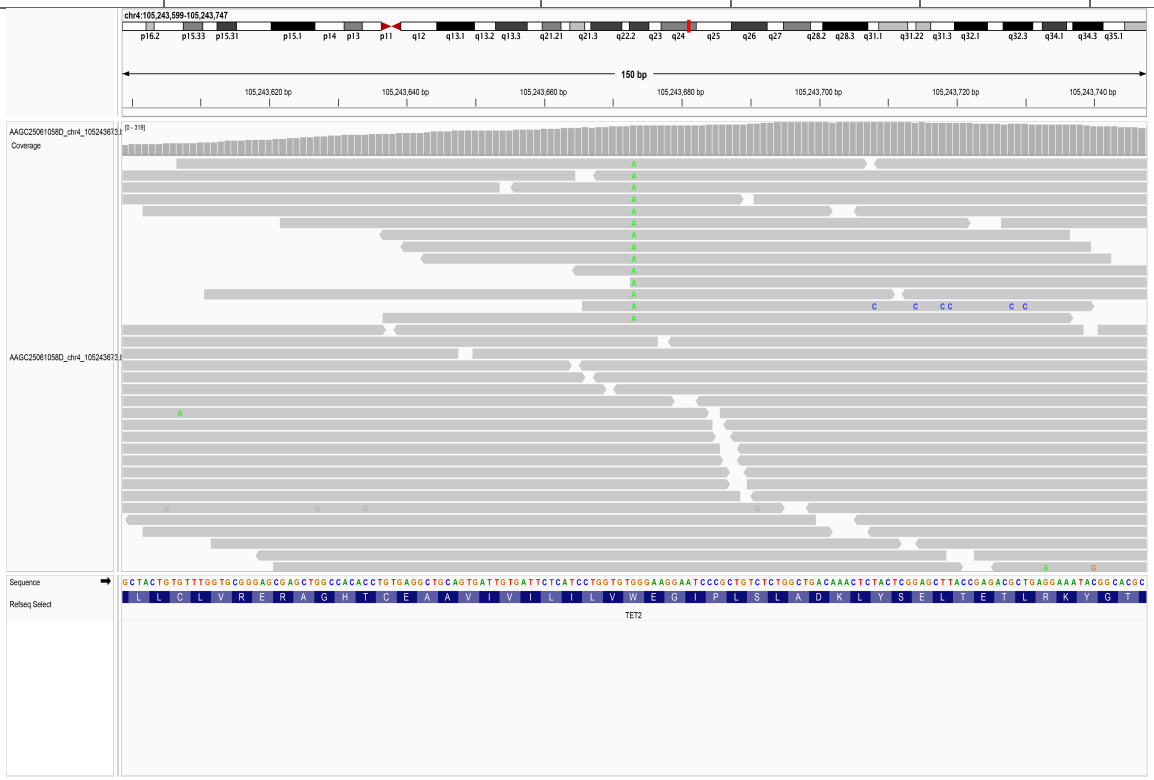
55.48. chr4_105243664_-/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136091	chr4_105243664_-/T	225	16	*TET2*	frameshift_variant



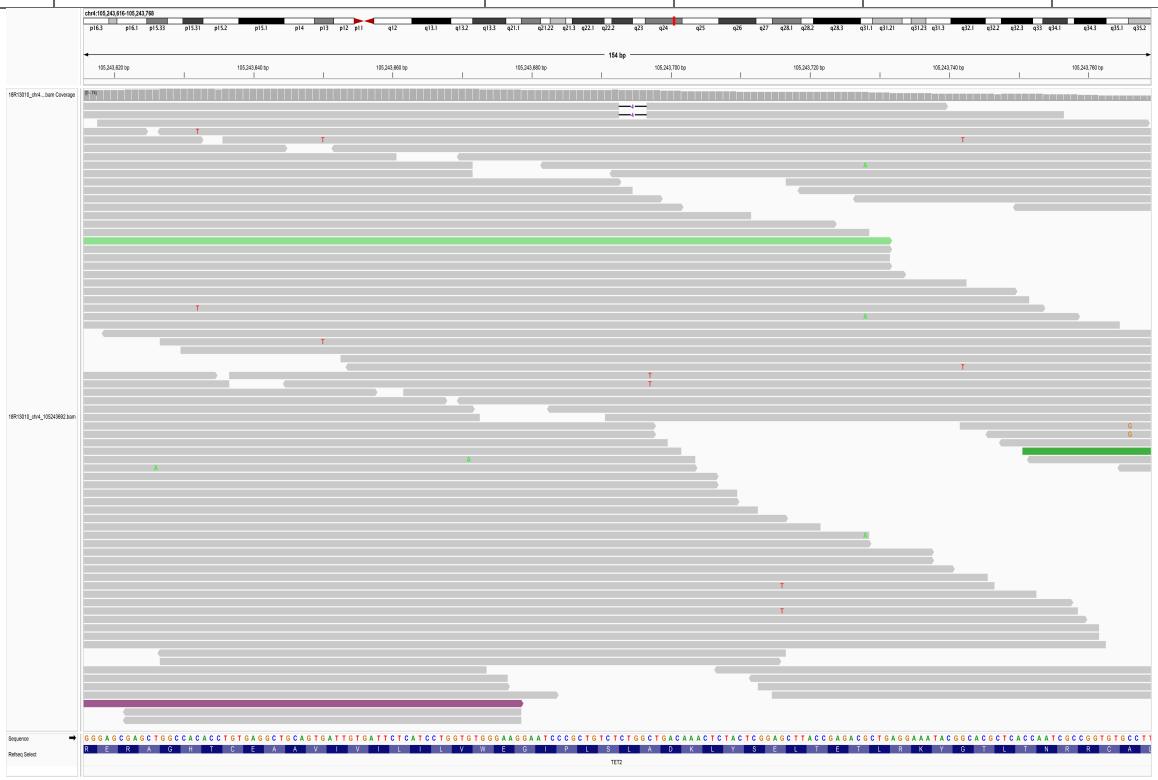
55.49. chr4_105243673_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061058D	chr4_105243673_G/A	262	14	*TET2*	stop_gained



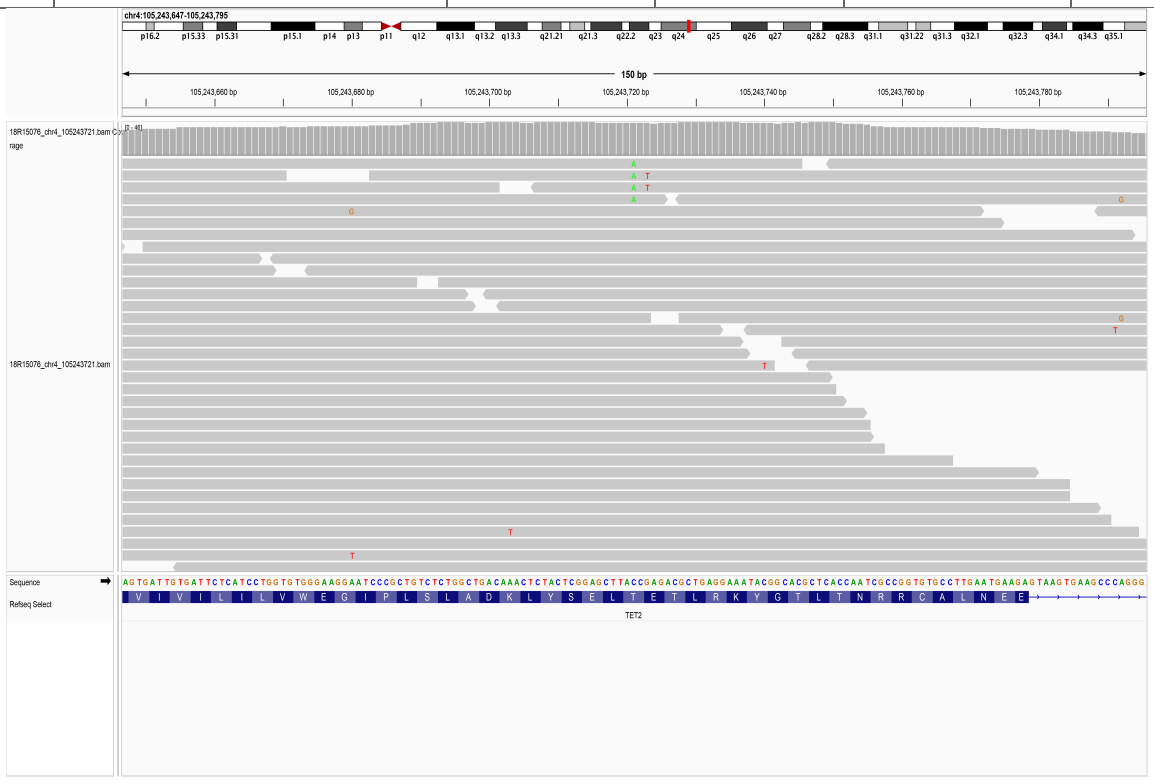
55.50. chr4_105243693_CTGG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13010	chr4_105243693_CTGG/-	62	2	*TET2*	frameshift_variant



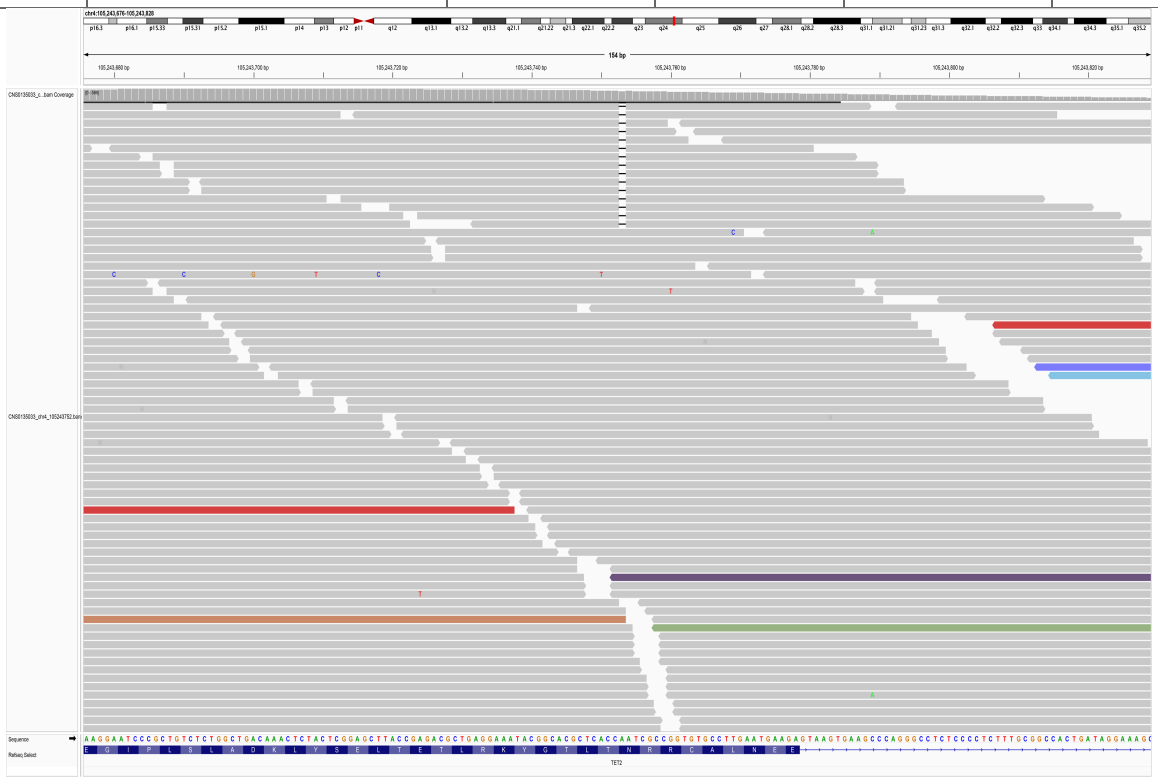
55.51. chr4_105243721_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15076	chr4_105243721_C/A	39	4	*TET2*	missense_variant



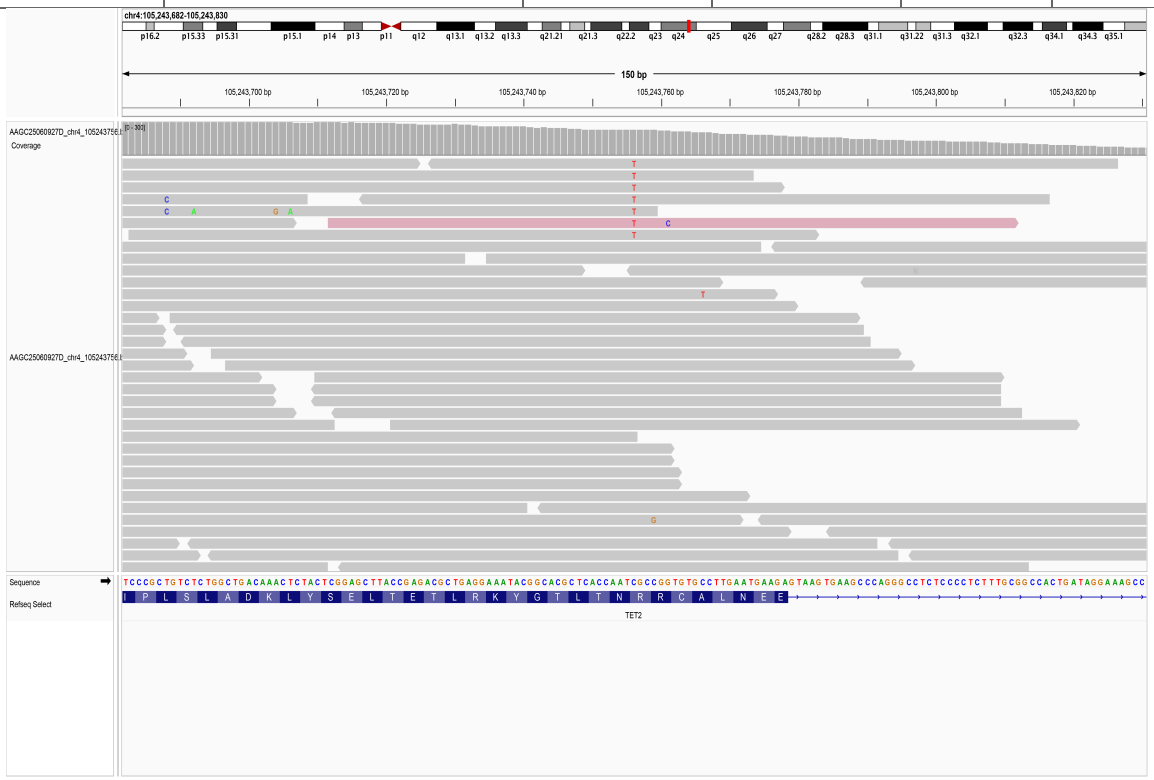
55.52. chr4_105243753_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135033	chr4_105243753_A/-	441	28	*TET2*	frameshift_variant



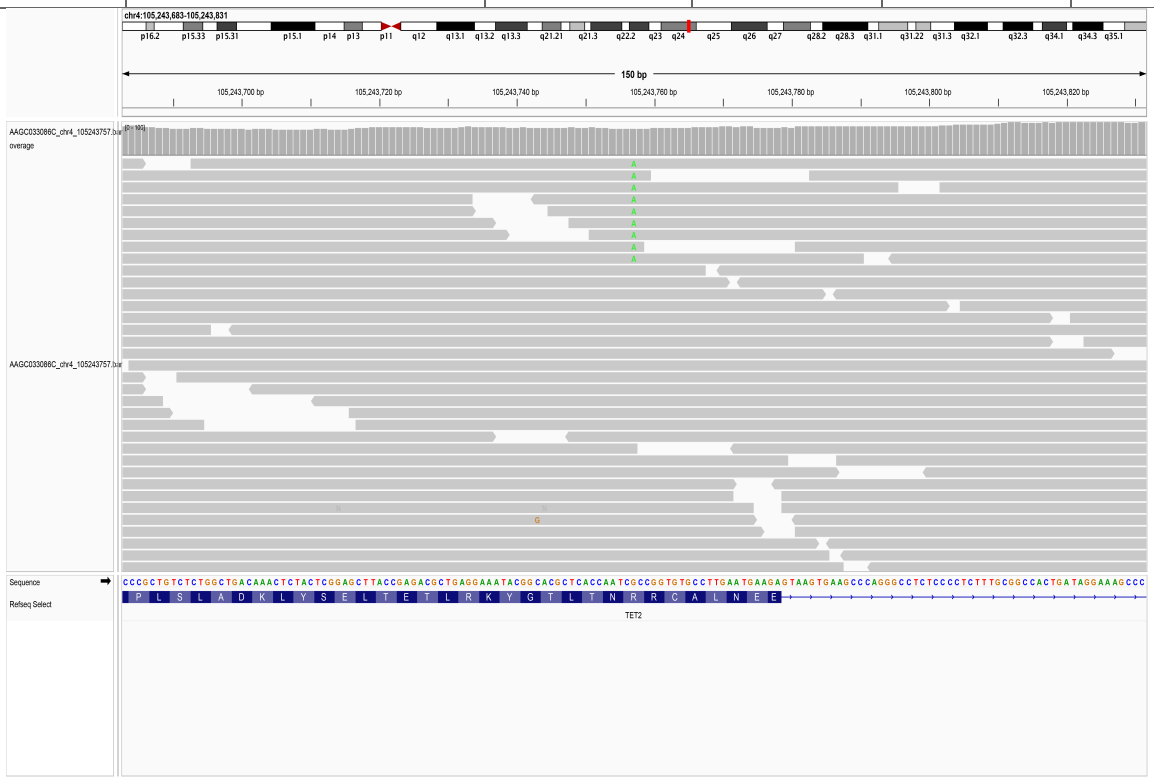
55.53. chr4_105243756_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060927D	chr4_105243756_C/T	222	7	*TET2*	missense_variant



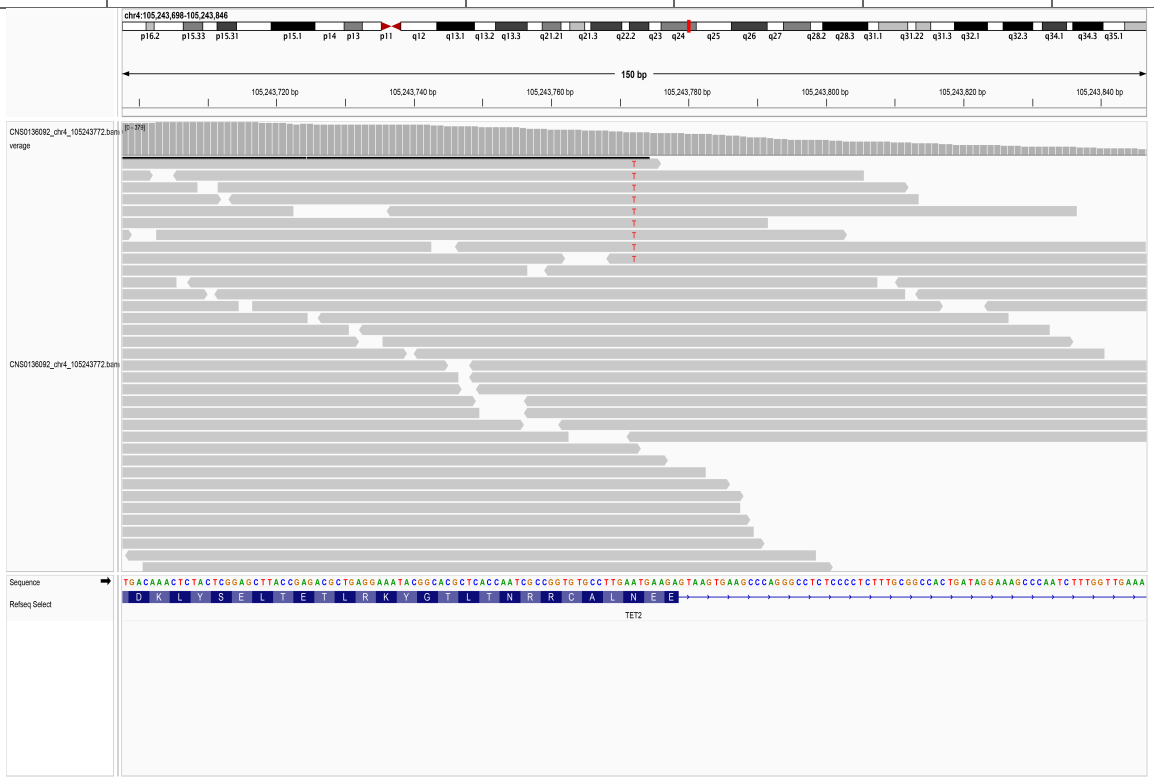
55.54. chr4_105243757_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033086C	chr4_105243757_G/A	68	9	*TET2*	missense_variant



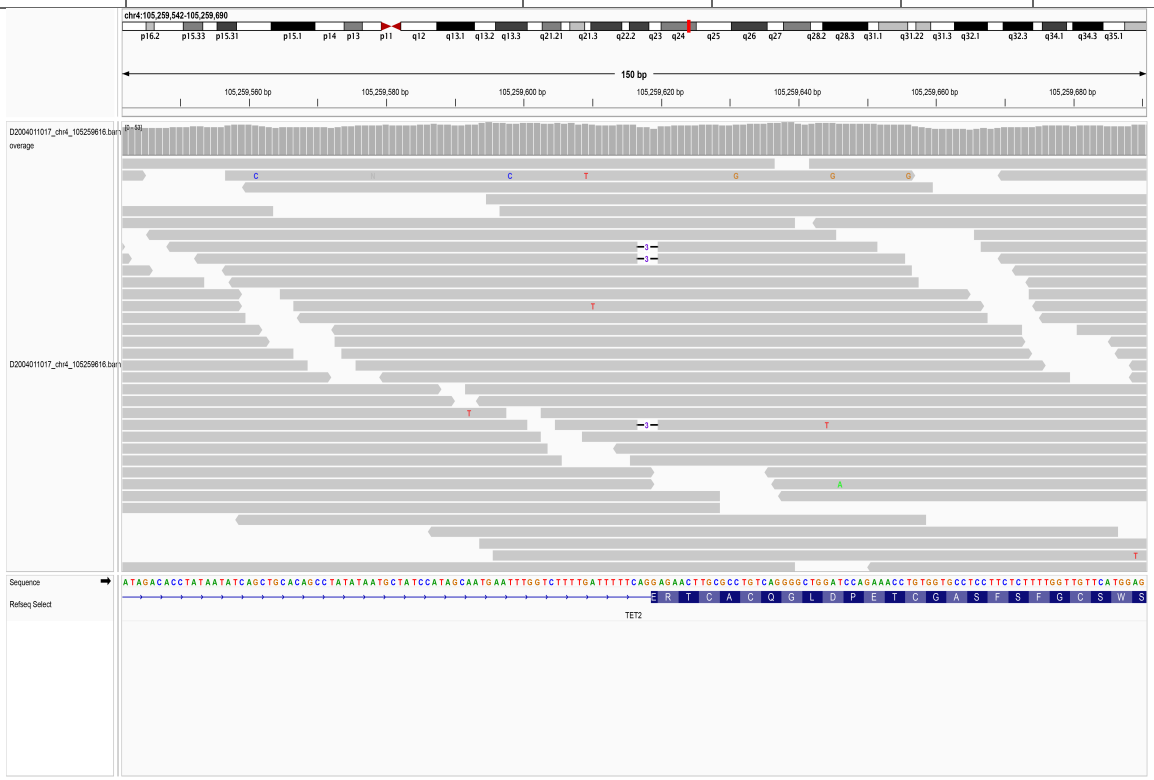
55.55. chr4_105243772_A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136092	chr4_105243772_A/T	251	9	*TET2*	missense_variant



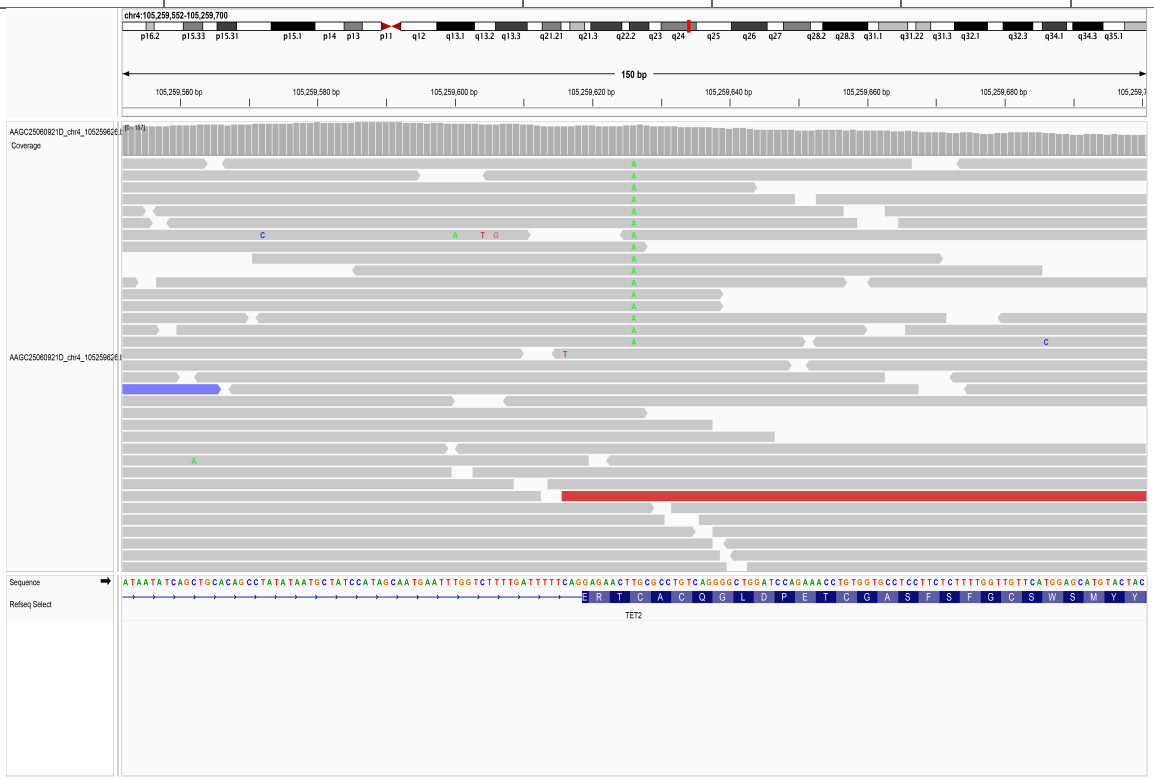
55.56. chr4_105259617_AGG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2004011017	chr4_105259617_AGG/-	41	4	*TET2*	splice_acceptor_variant



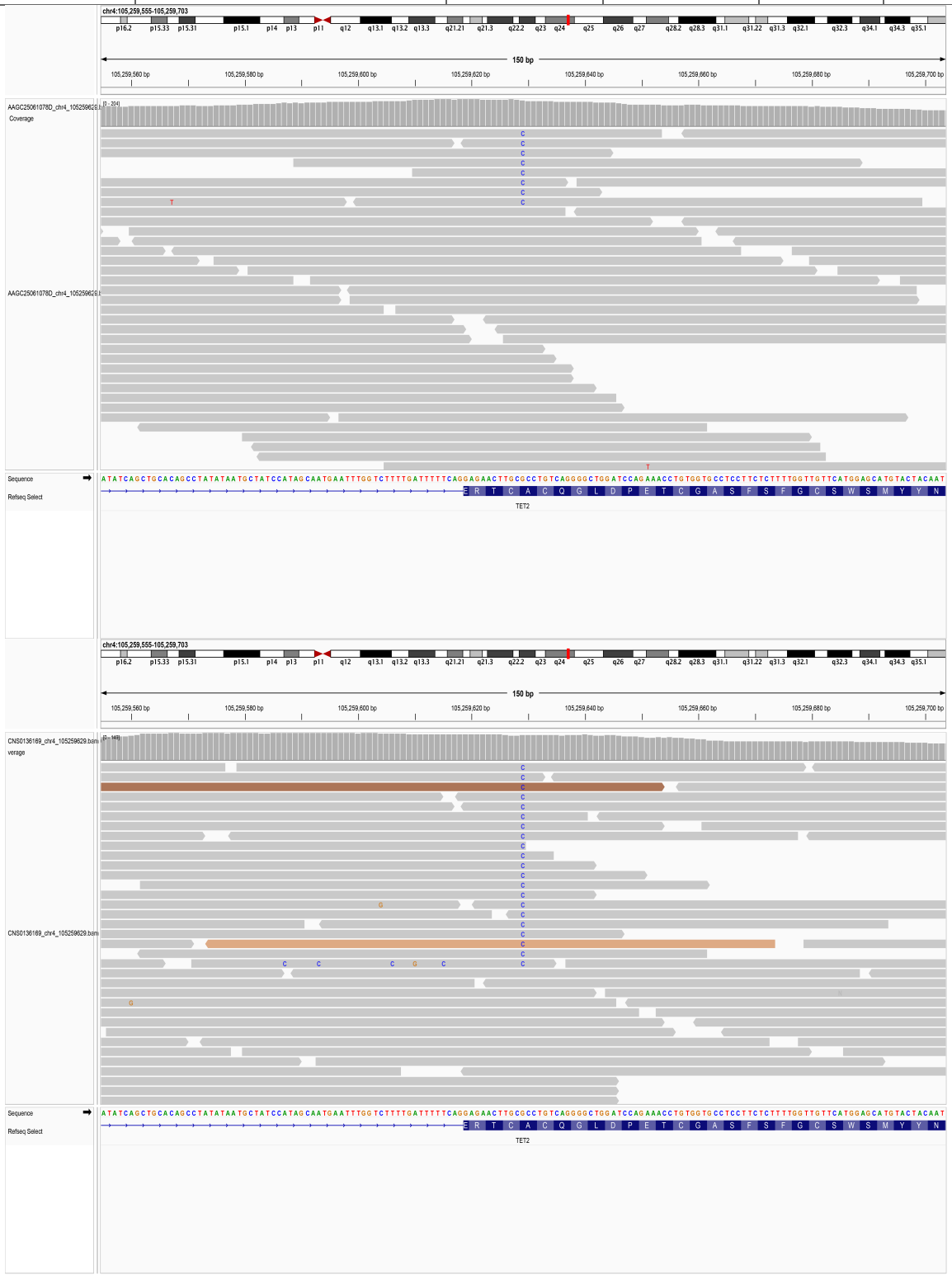
55.57. chr4_105259626_T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060921D	chr4_105259626_T/A	121	16	*TET2*	missense_variant



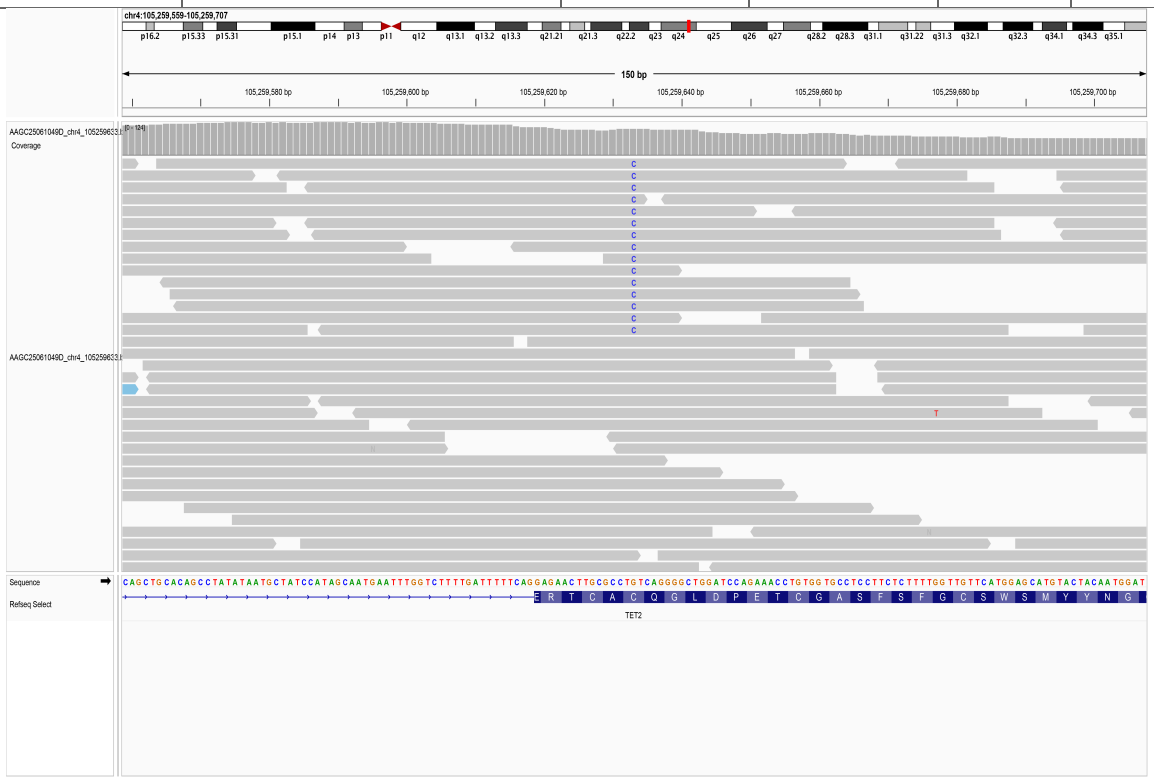
55.58. chr4_105259629_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061078D	chr4_105259629_G/C	181	8	*TET2*	missense_variant
CNS0136169	chr4_105259629_G/C	114	20	*TET2*	missense_variant



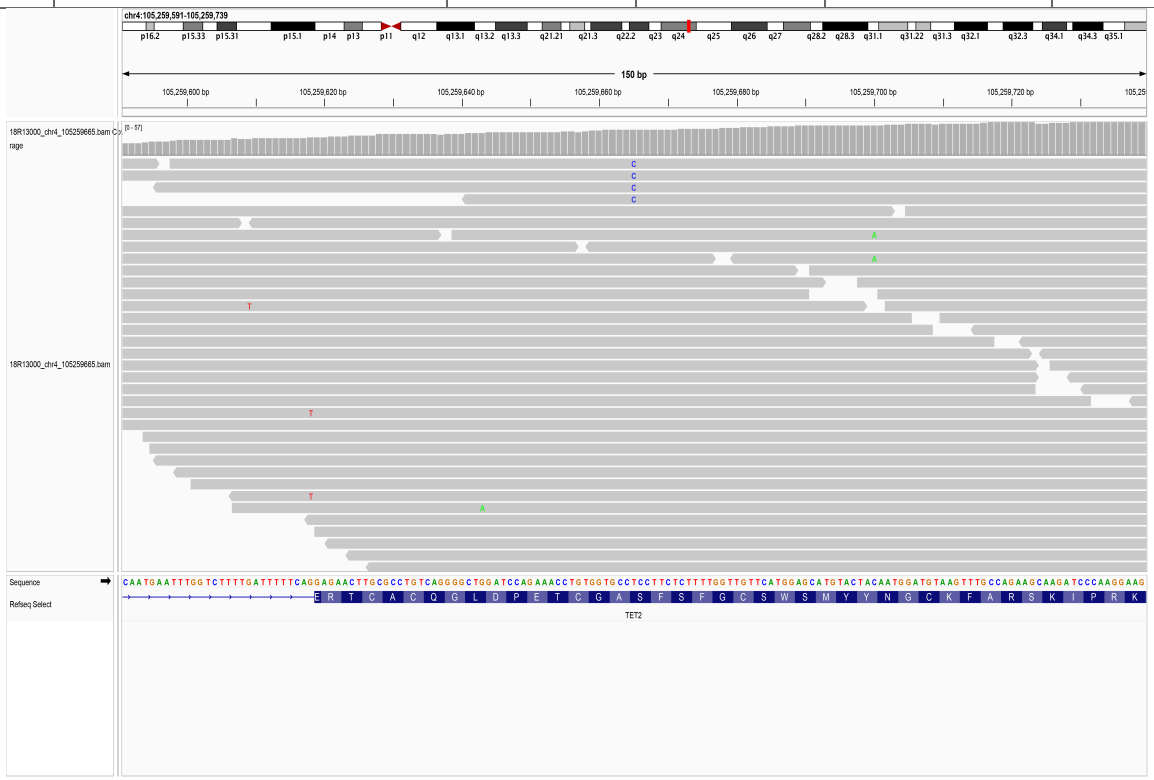
55.59. chr4_105259633_G/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061049D	chr4_105259633_G/C	82	15	*TET2*	missense_variant



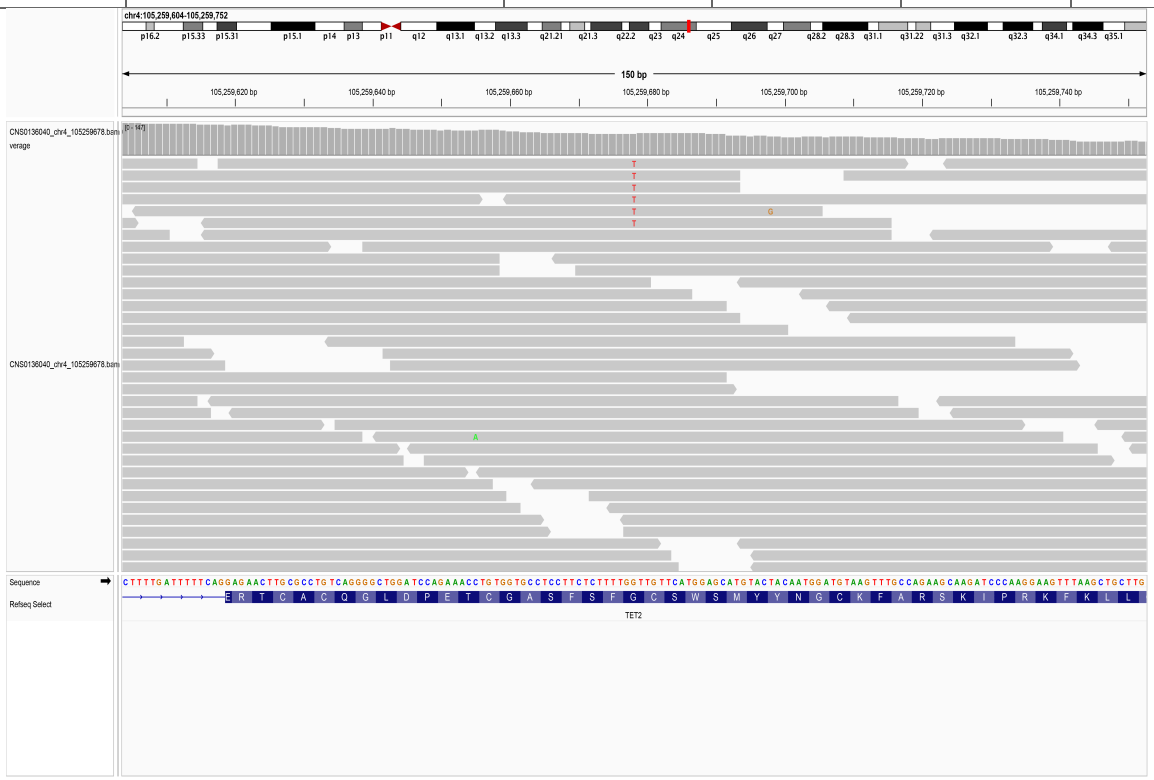
55.60. chr4_105259665_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13000	chr4_105259665_T/C	40	4	*TET2*	missense_variant



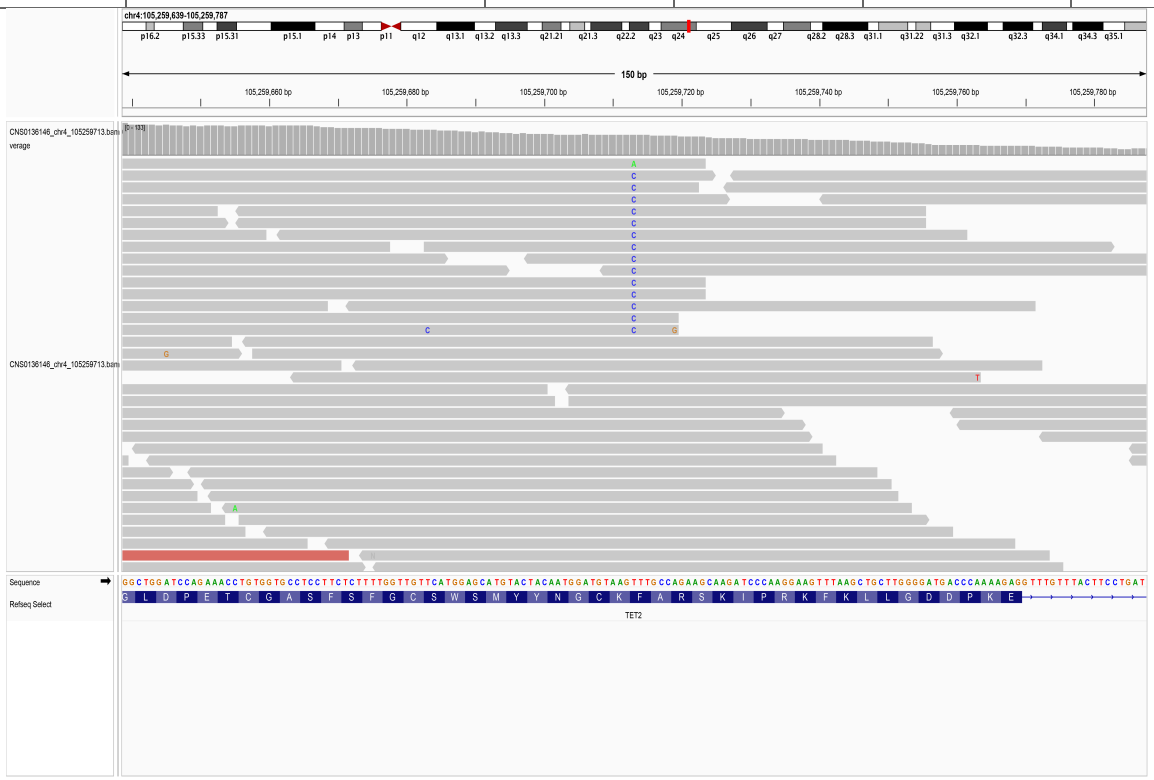
55.61. chr4_105259678_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136040	chr4_105259678_G/T	89	6	*TET2*	missense_variant



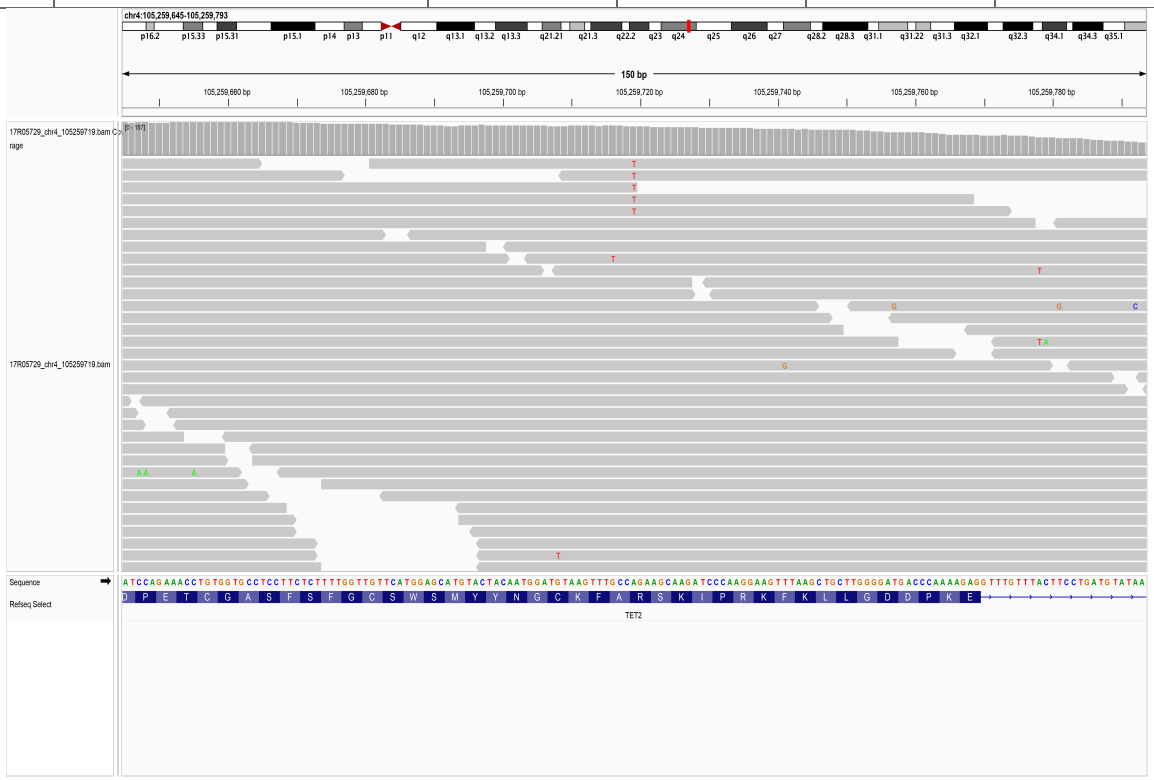
55.62. chr4_105259713_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136146	chr4_105259713_T/C	66	14	*TET2*	missense_variant



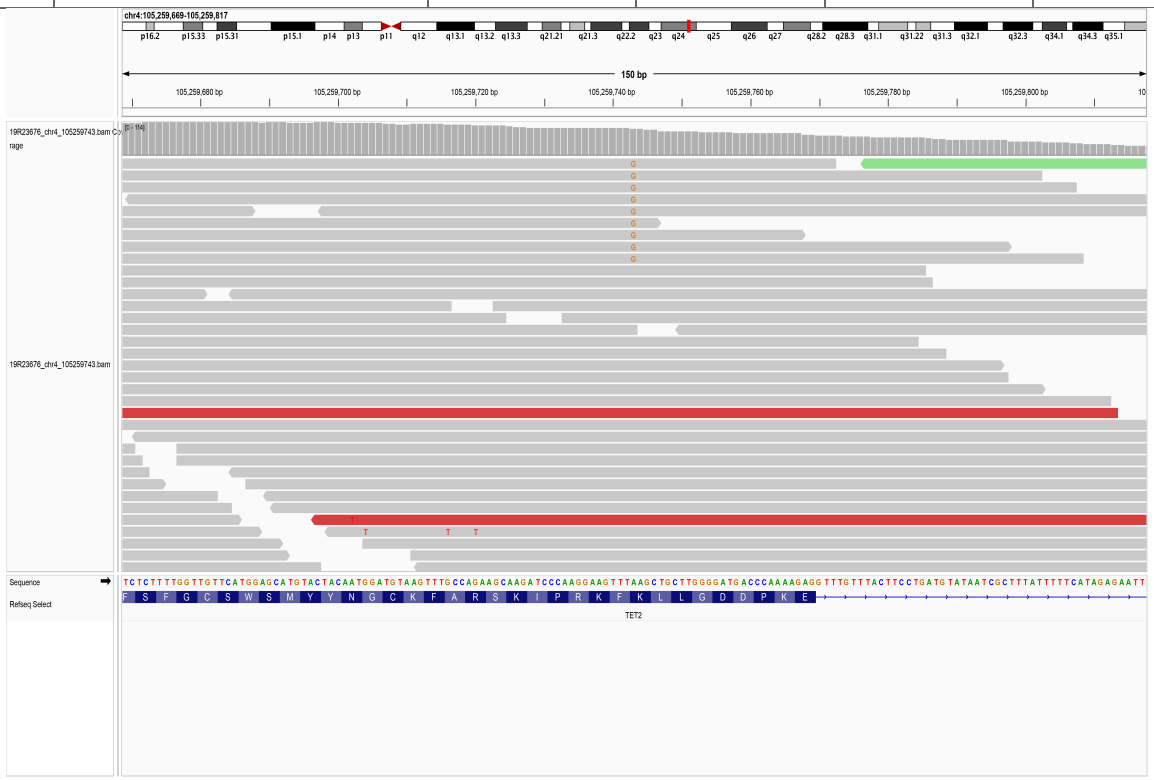
55.63. chr4_105259719_A/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05729	chr4_105259719_A/T	129	5	*TET2*	stop_gained



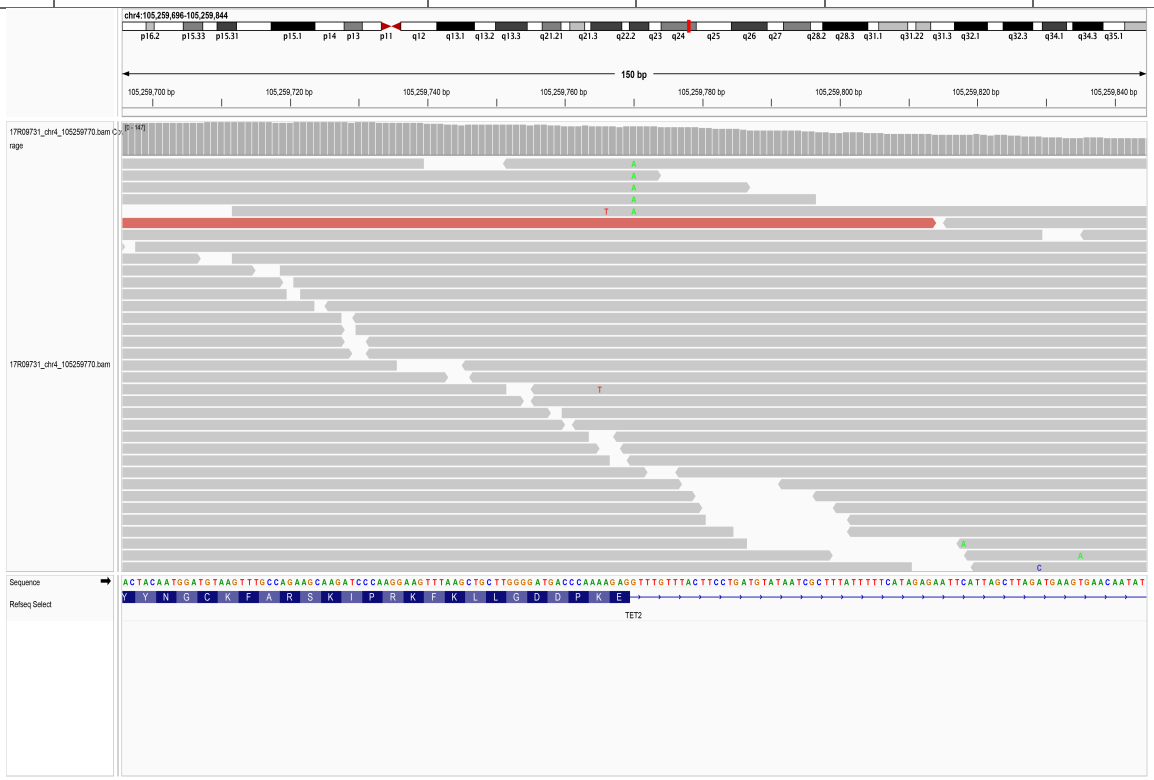
55.64. chr4_105259743_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23676	chr4_105259743_A/G	79	9	*TET2*	missense_variant



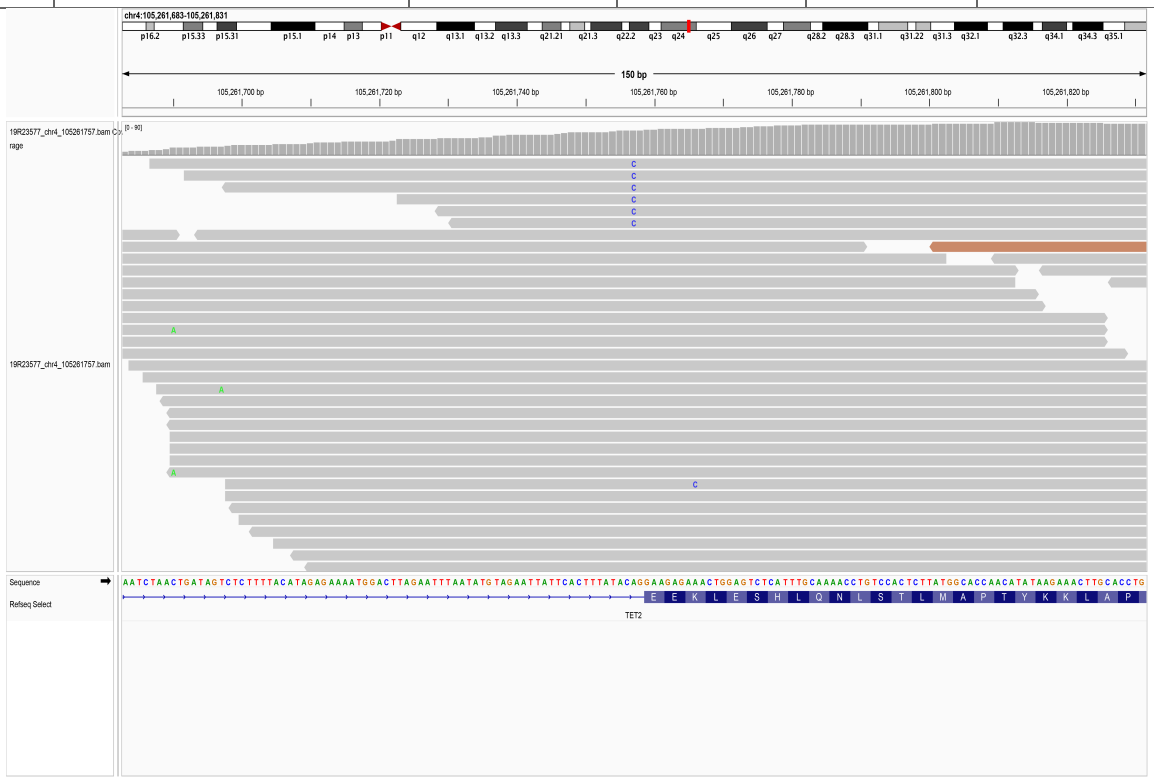
55.65. chr4_105259770_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09731	chr4_105259770_G/A	121	5	*TET2*	splice_donor_variant



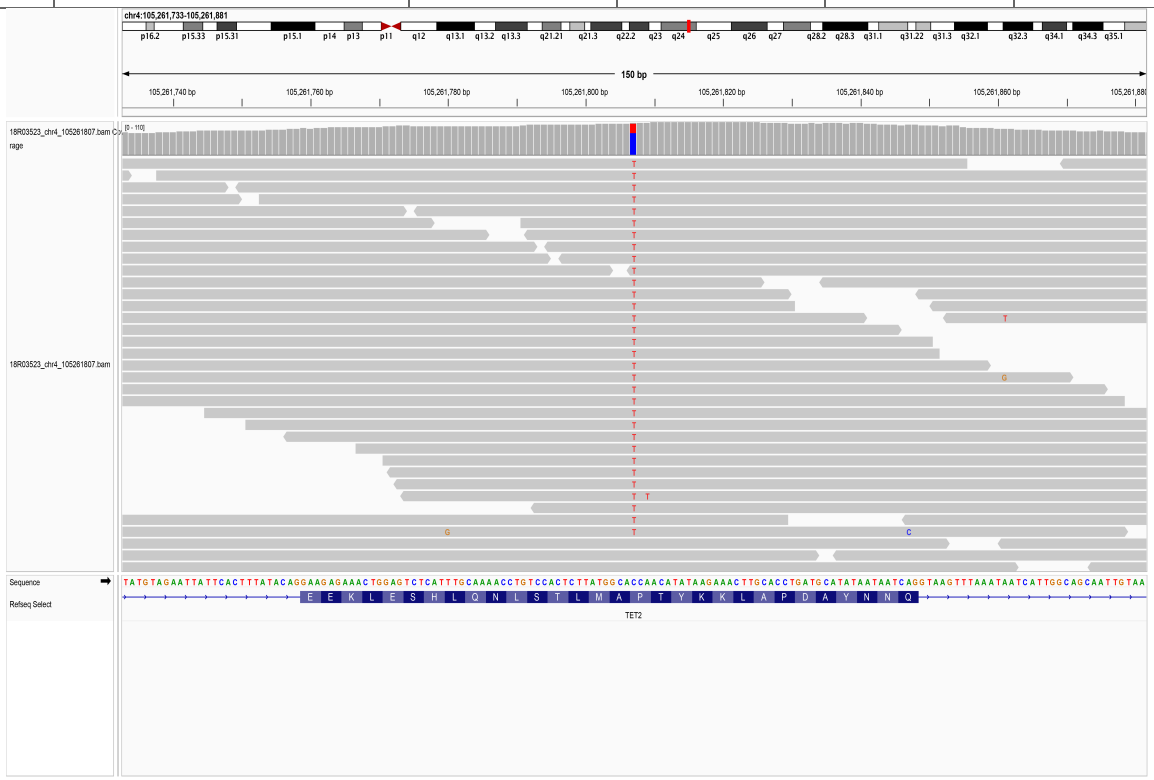
55.66. chr4_105261757_A/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23577	chr4_105261757_A/C	60	6	*TET2*	splice_acceptor_variant



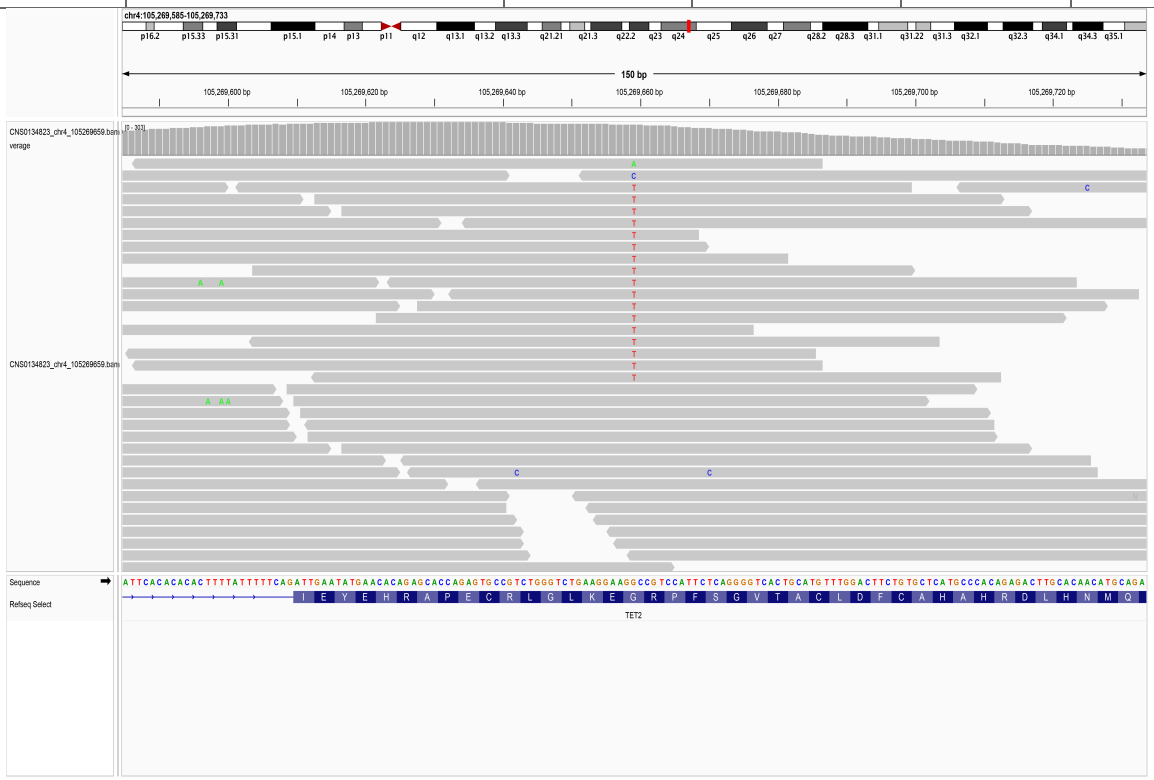
55.67. chr4_105261807_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03523	chr4_105261807_C/T	71	32	*TET2*	missense_variant



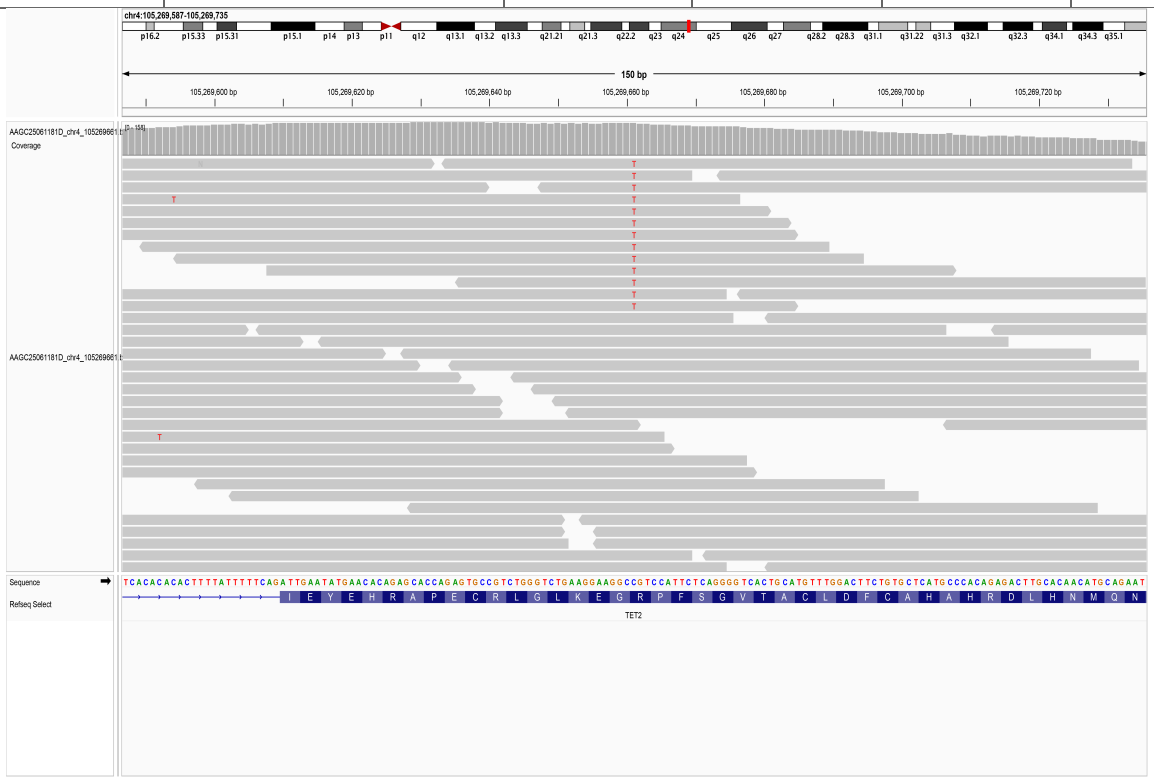
55.68. chr4_105269659_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134823	chr4_105269659_G/T	245	17	*TET2*	missense_variant



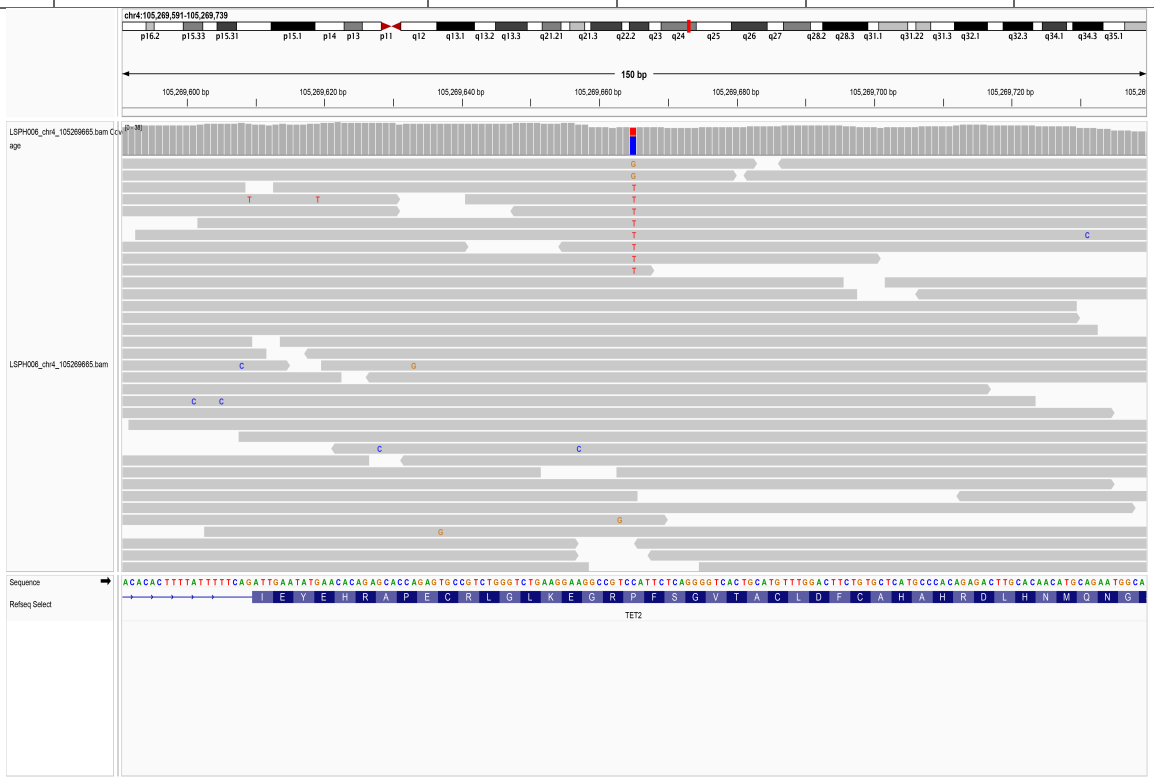
55.69. chr4_105269661_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061181D	chr4_105269661_C/T	131	13	*TET2*	missense_variant



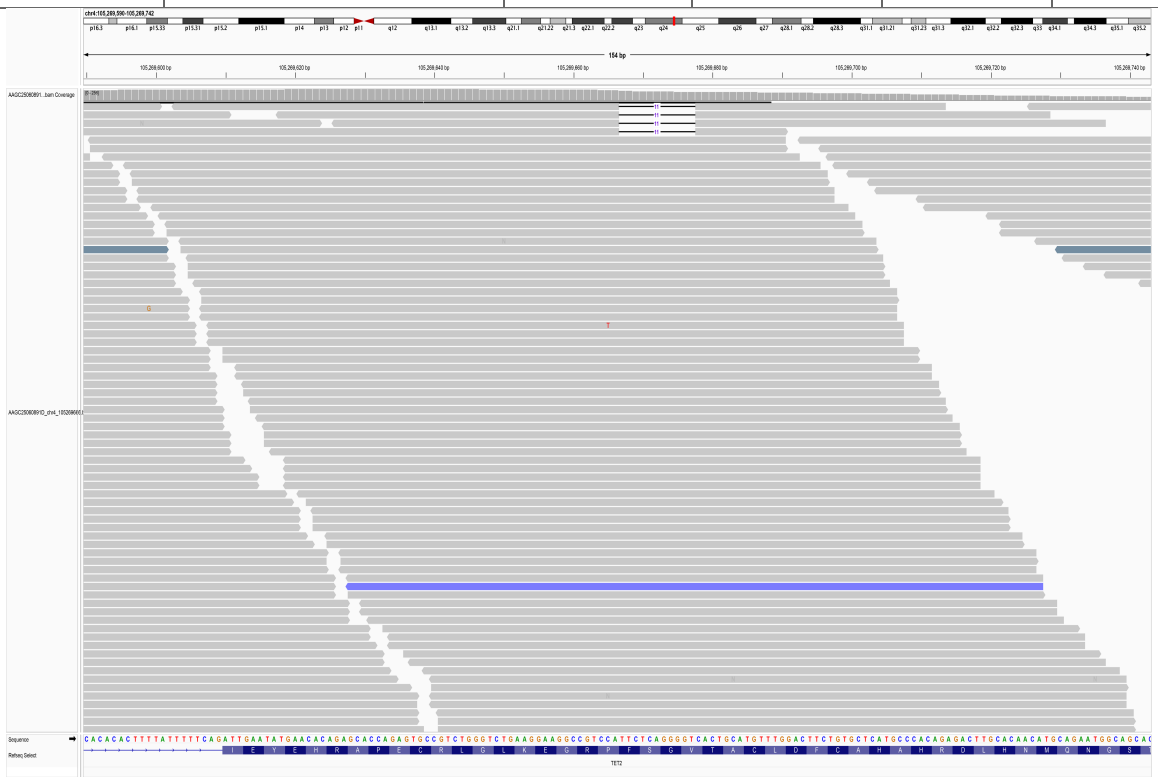
55.70. chr4_105269665_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
LSPH006	chr4_105269665_C/T	22	8	*TET2*	missense_variant



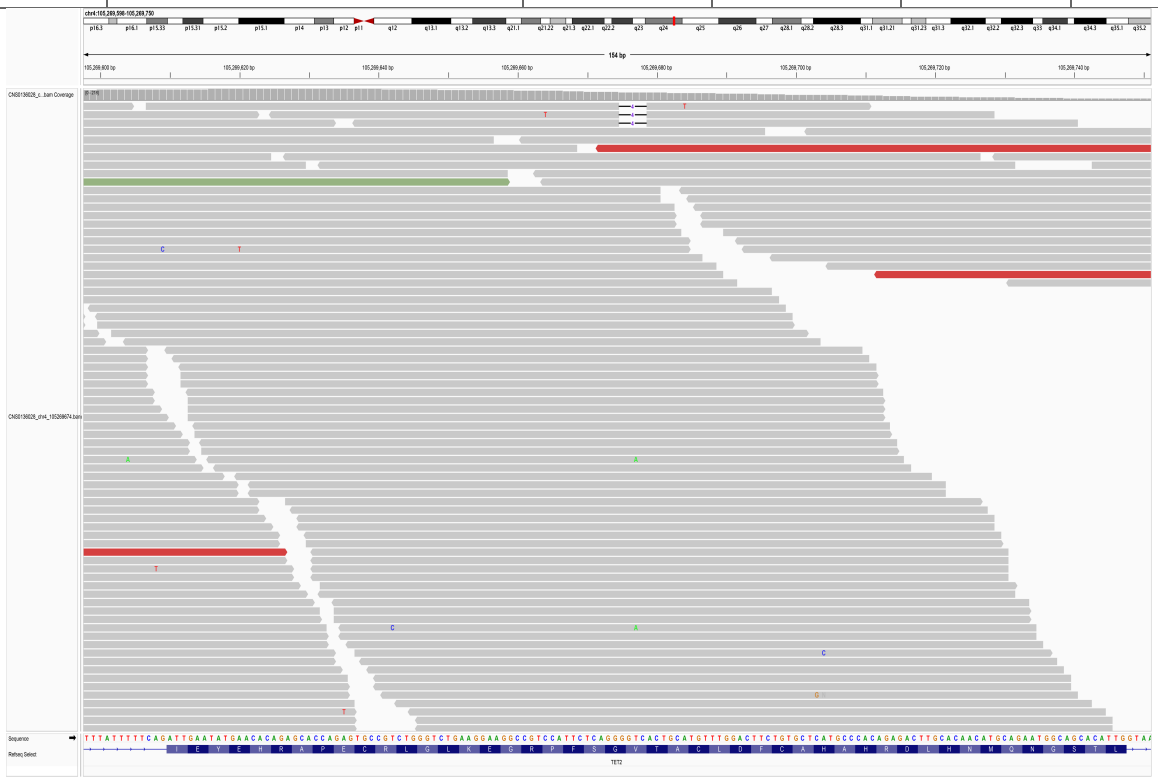
55.71. chr4_105269667_TTCTCAGGGGT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060891D	chr4_105269667_TTCTCAGGGGT/-	224	6	*TET2*	frameshift_variant



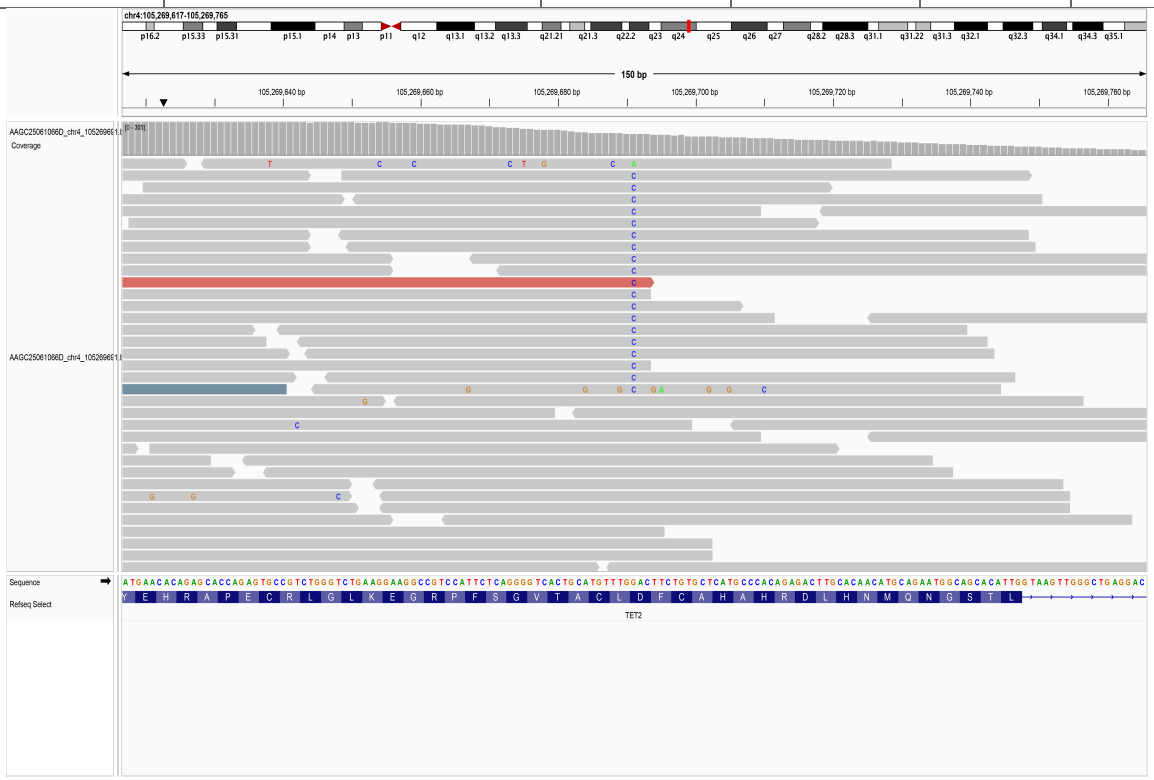
55.72. chr4_105269675_GGTC/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136028	chr4_105269675_GGTC/-	148	3	*TET2*	frameshift_variant



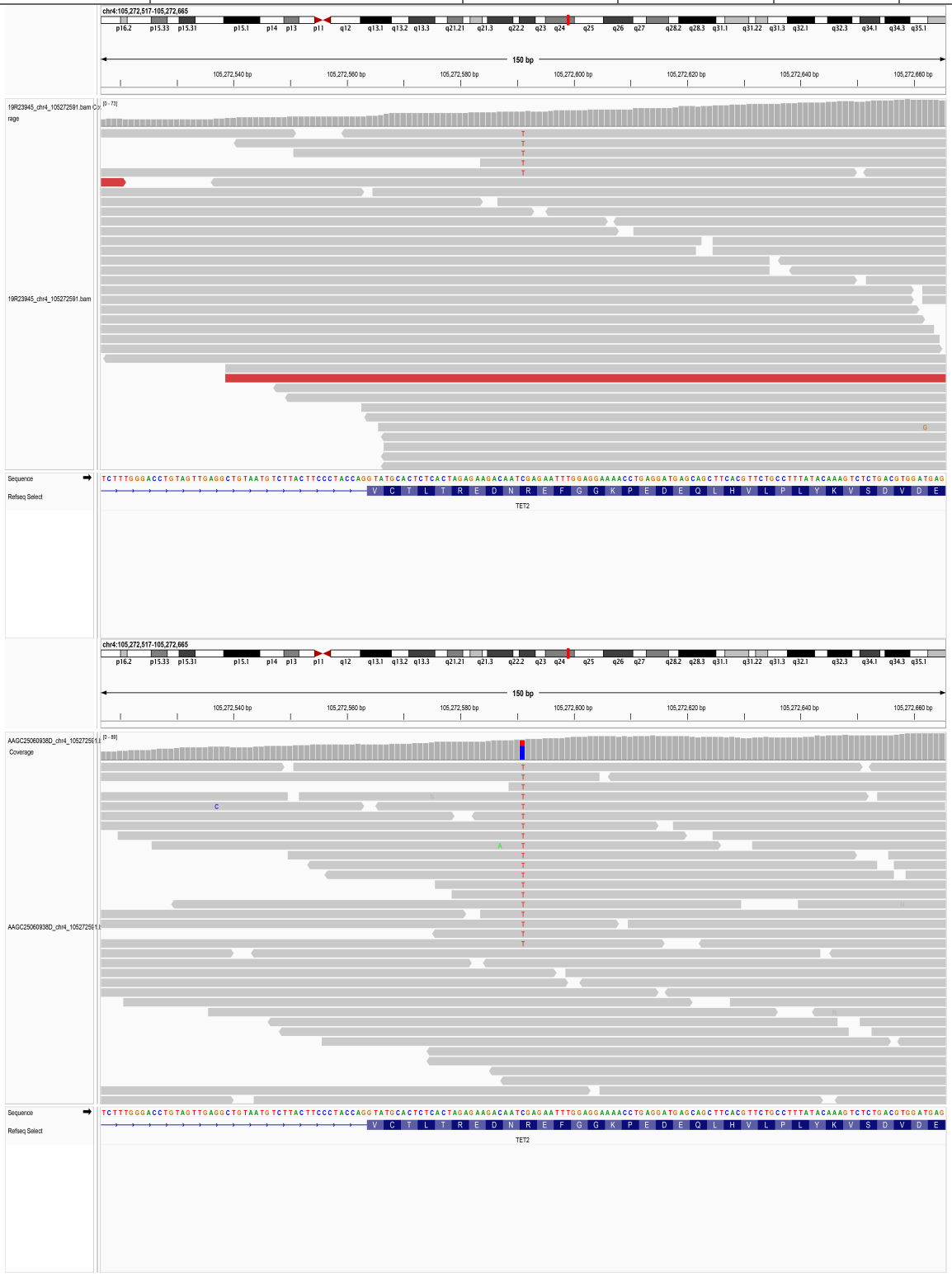
55.73. chr4_105269691_G/C

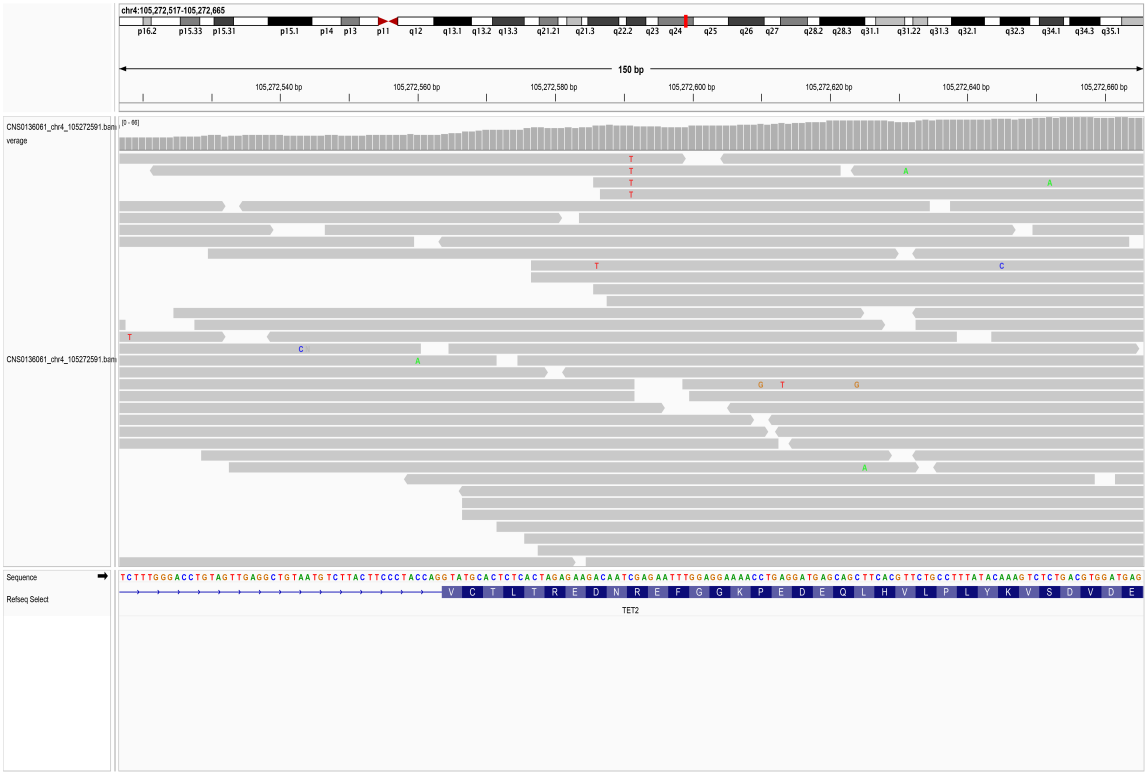
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061066D	chr4_105269691_G/C	169	18	*TET2*	missense_variant



55.74. chr4_105272591_C/T

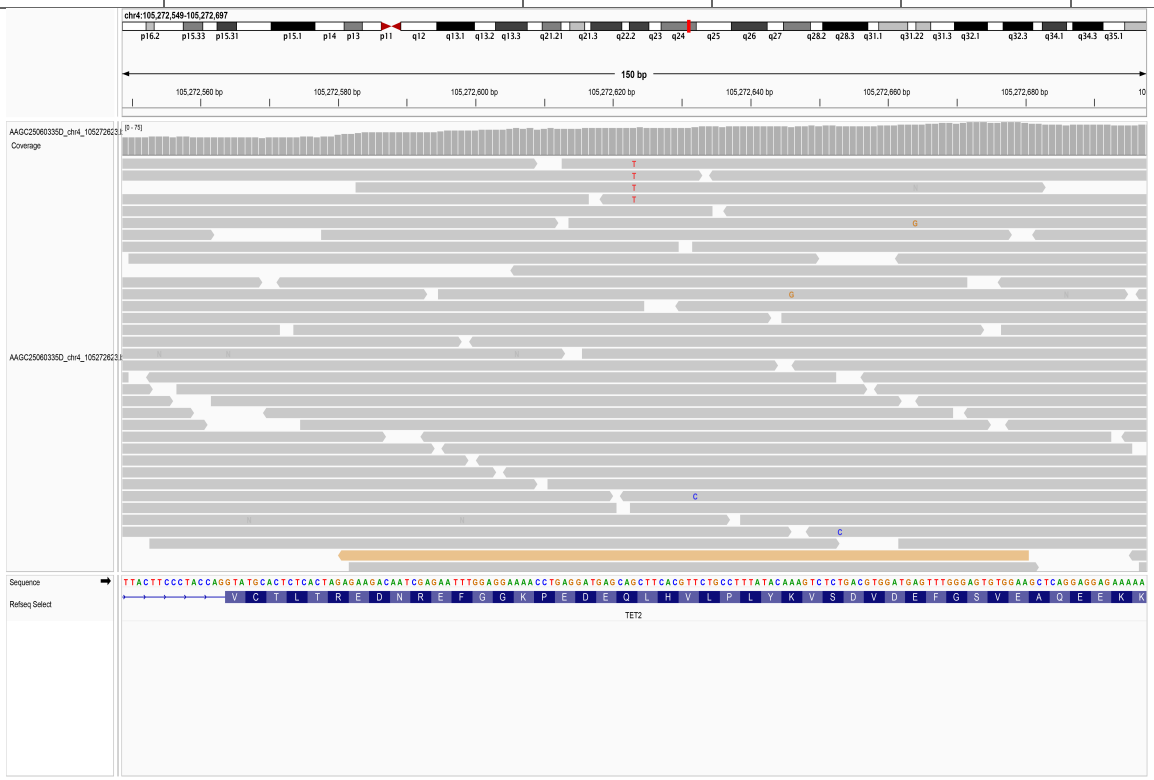
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23945	chr4_105272591_C/T	35	5	*TET2*	stop_gained
AAGC25060938D	chr4_105272591_C/T	47	19	*TET2*	stop_gained
CNS0136061	chr4_105272591_C/T	45	4	*TET2*	stop_gained




chr4:105,272,517-105,272,665
150 bp
105,272,540 bp
105,272,560 bp
105,272,580 bp
105,272,600 bp
105,272,620 bp
105,272,640 bp
105,272,660 bp
CNS0136061_chr4_105272591.bam
verage
CNS0136061_chr4_105272591.bam
Sequence
Refseq Select
TET2

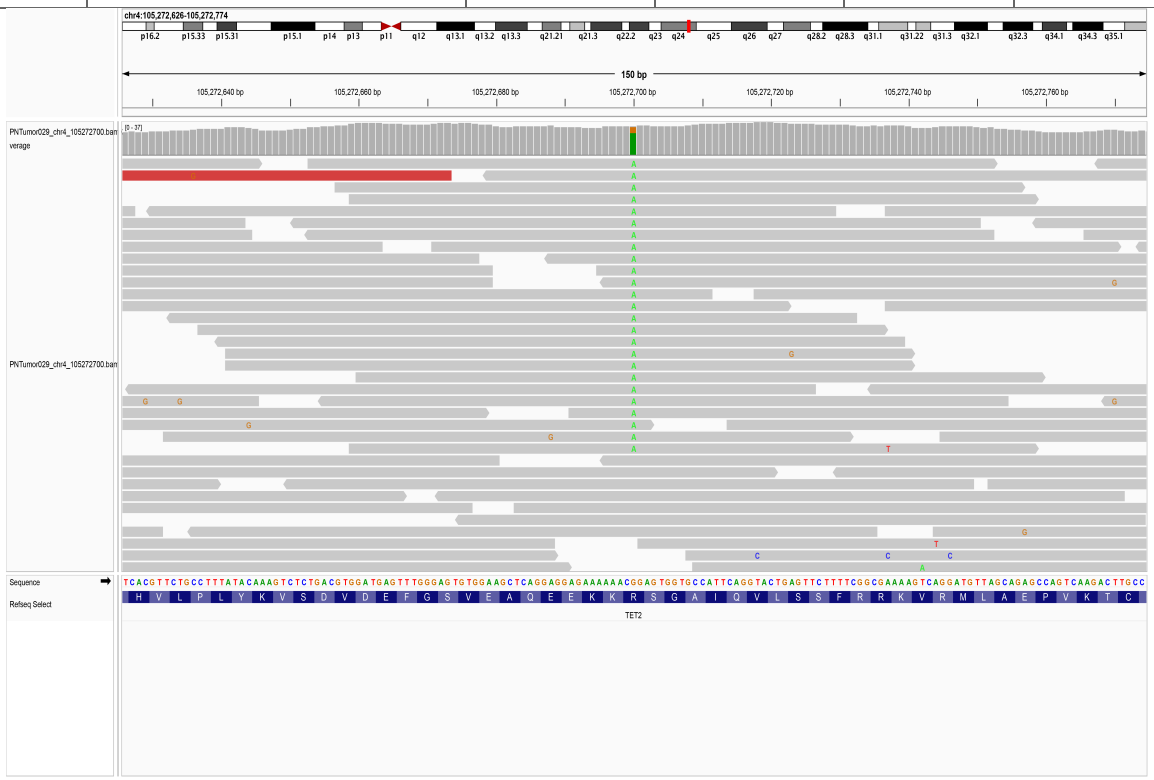
55.75. chr4_105272623_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060335D	chr4_105272623_G/T	56	4	*TET2*	missense_variant



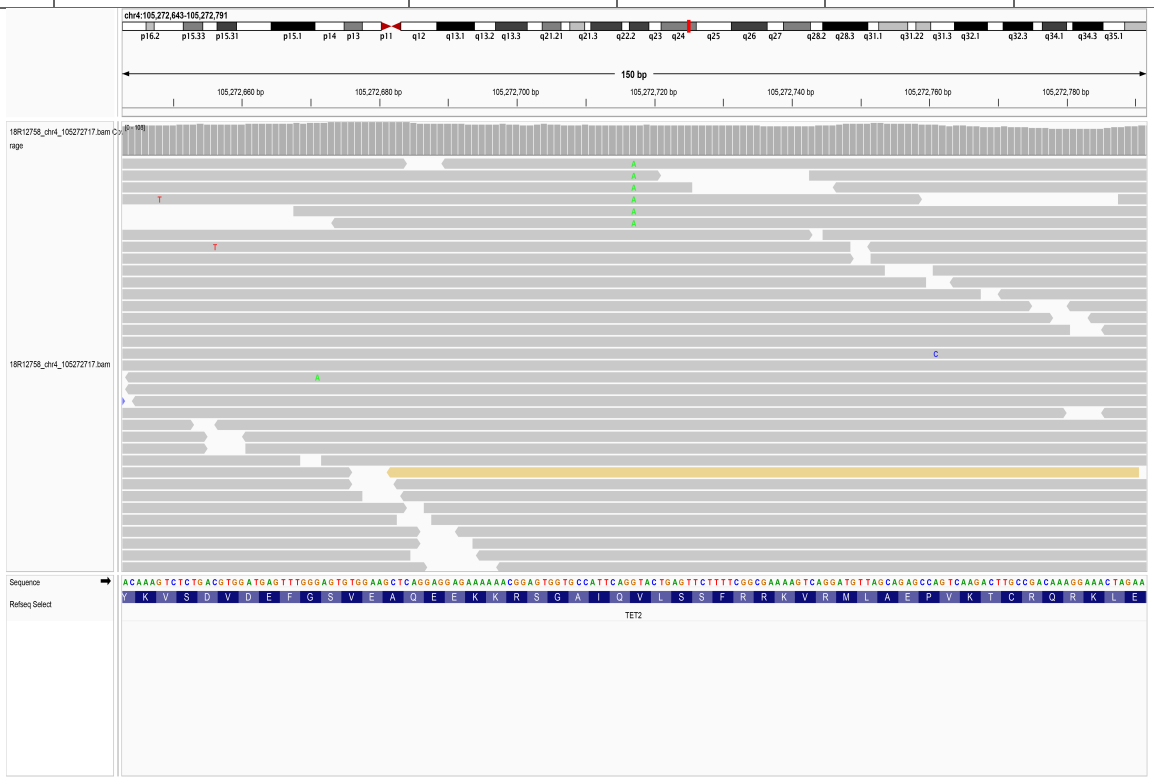
55.76. chr4_105272700_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
PNTumor029	chr4_105272700_G/A	7	25	*TET2*	missense_variant



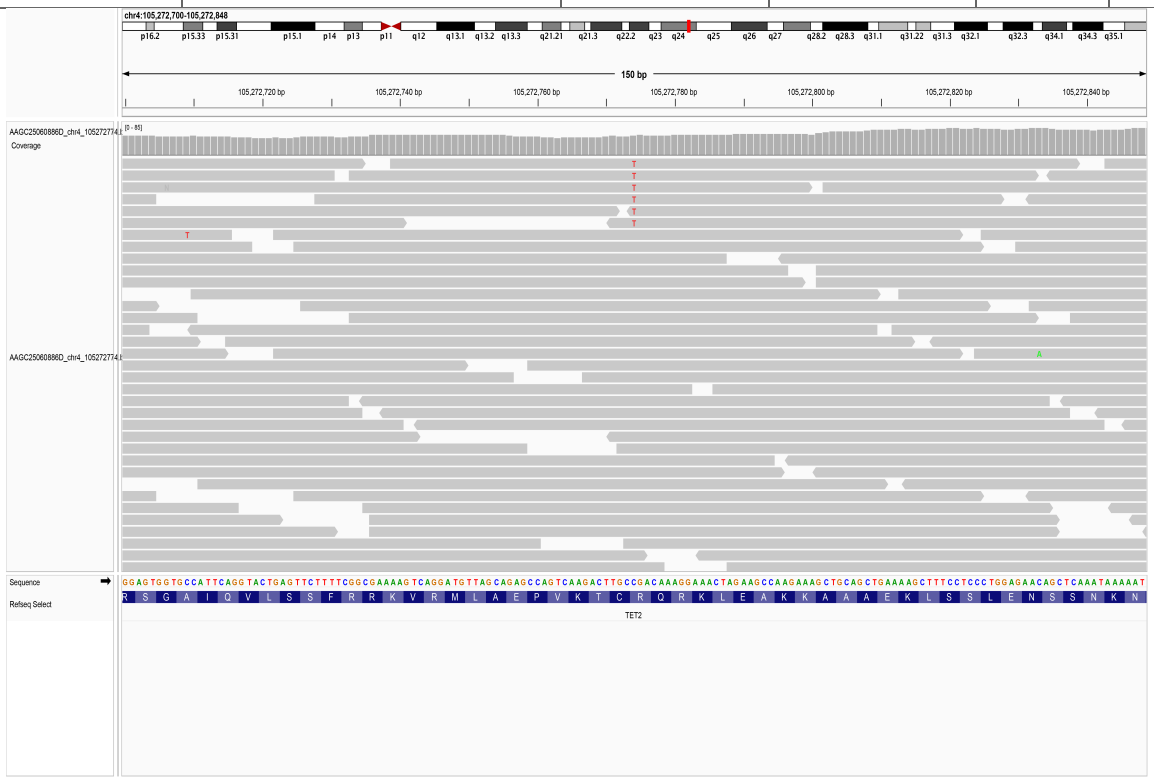
55.77. chr4_105272717_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12758	chr4_105272717_G/A	89	6	*TET2*	missense_variant



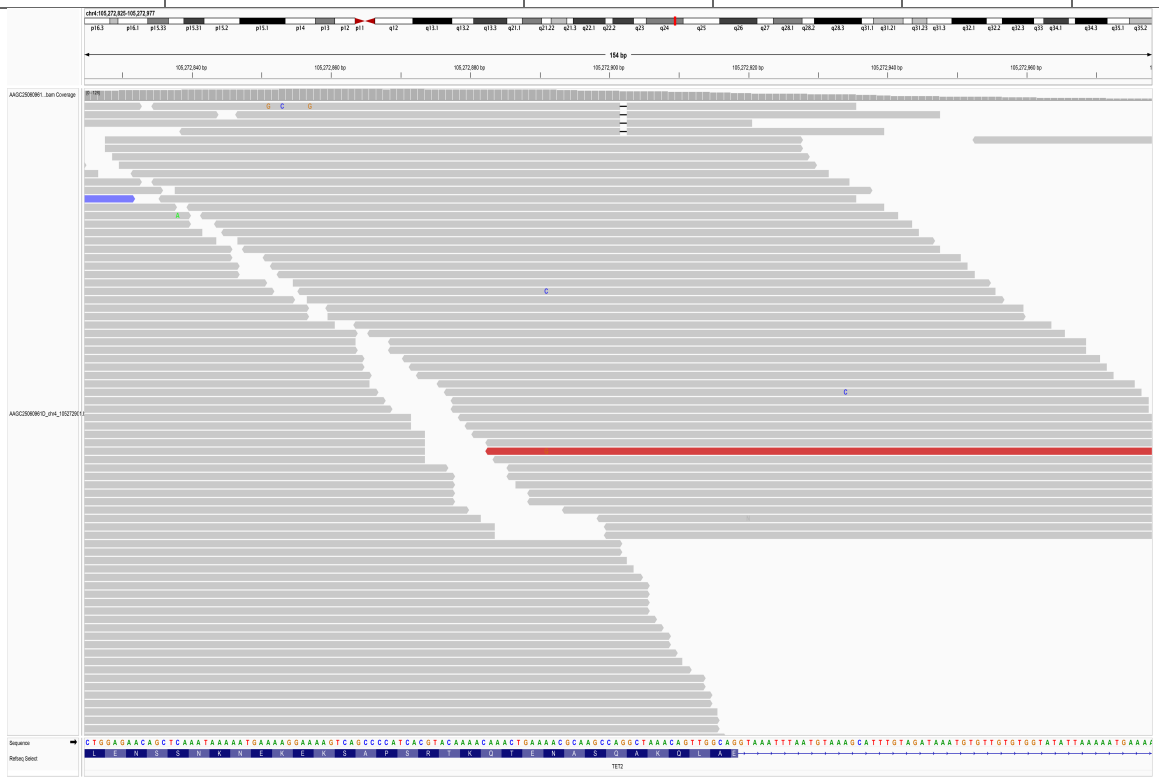
55.78. chr4_105272774_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060886D	chr4_105272774_C/T	44	6	*TET2*	stop_gained



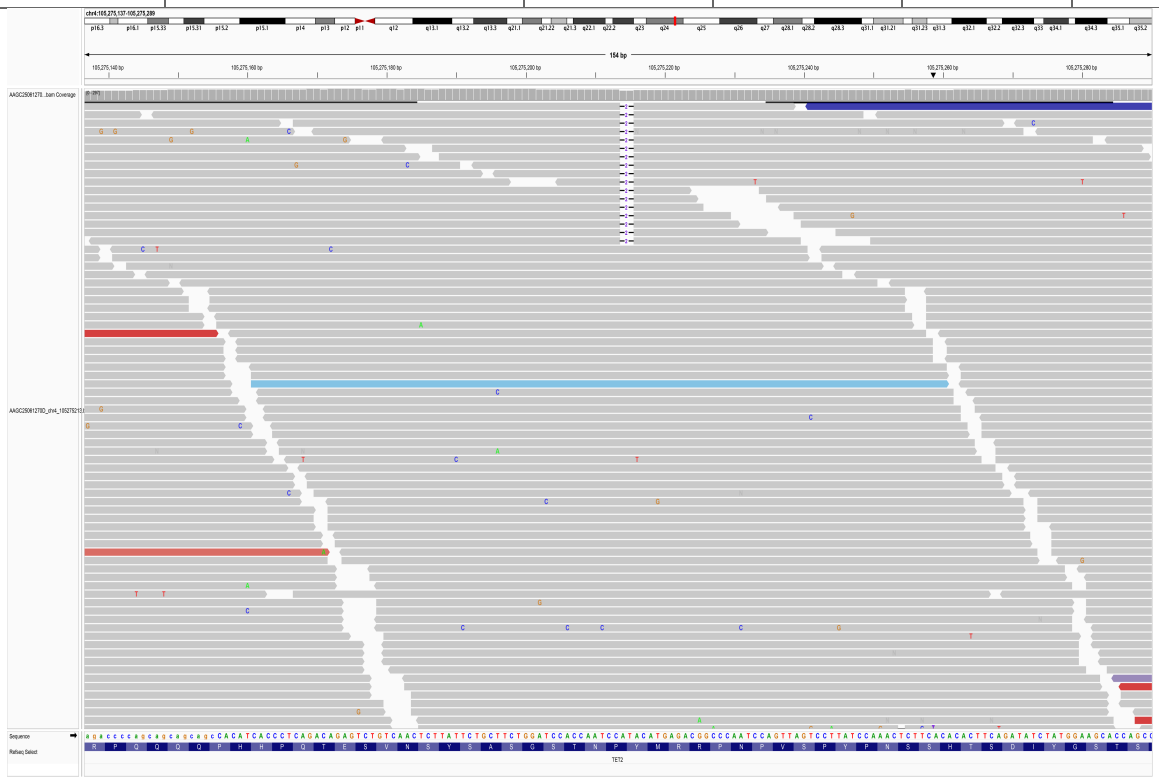
55.79. chr4_105272902_G/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060961D	chr4_105272902_G/-	97	4	*TET2*	frameshift_variant



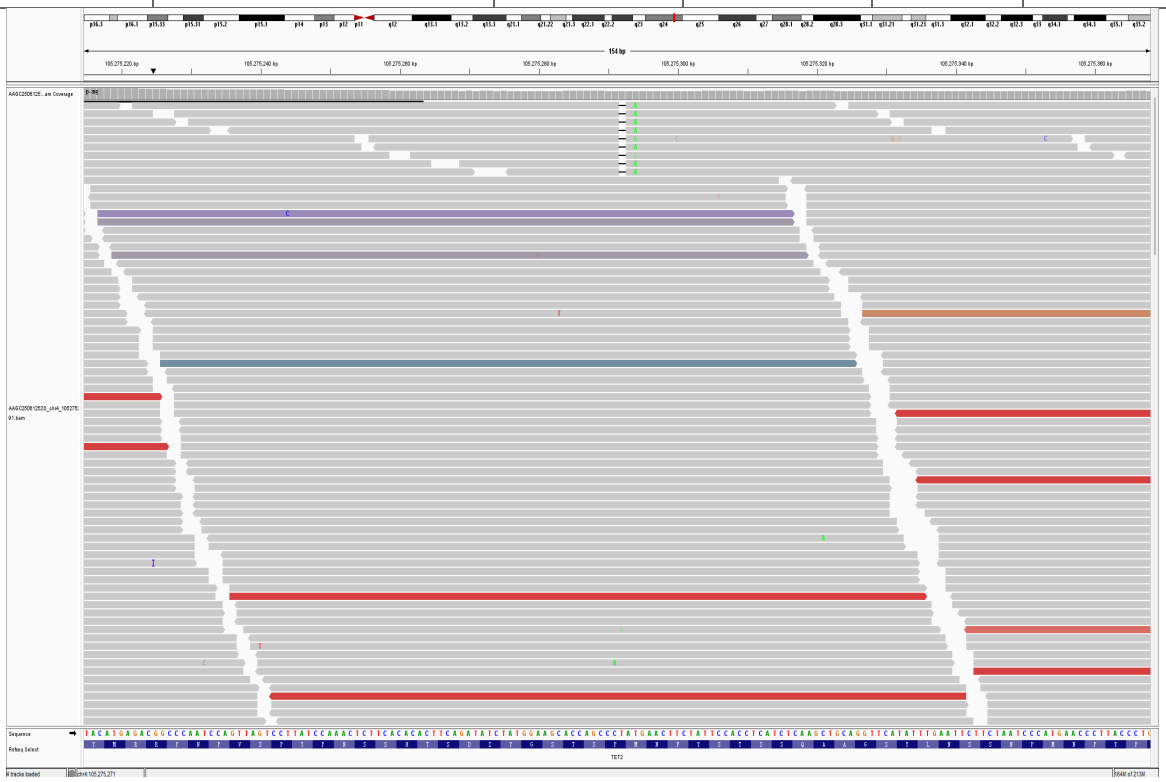
55.80. chr4_105275214_AT/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061270D	chr4_105275214_AT/-	231	19	*TET2*	frameshift_variant



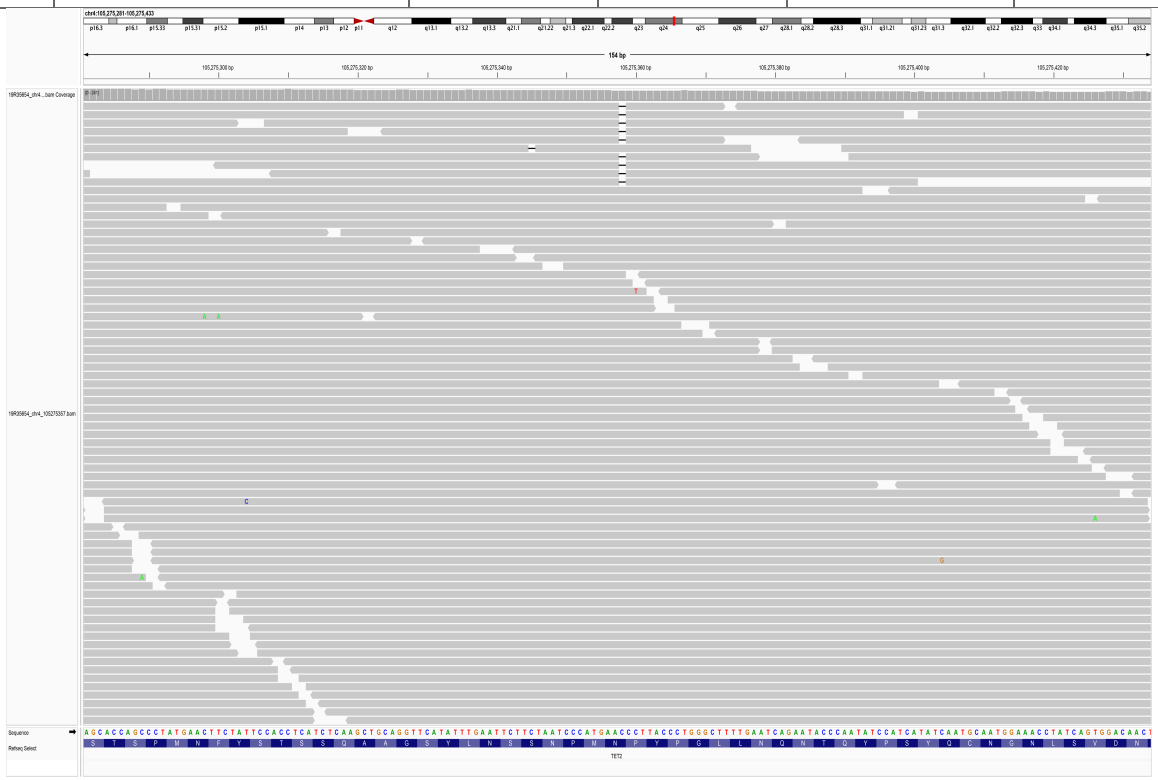
55.81. chr4_105275292_T/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061252D	chr4_105275292_T/-	275	12	*TET2*	frameshift_variant



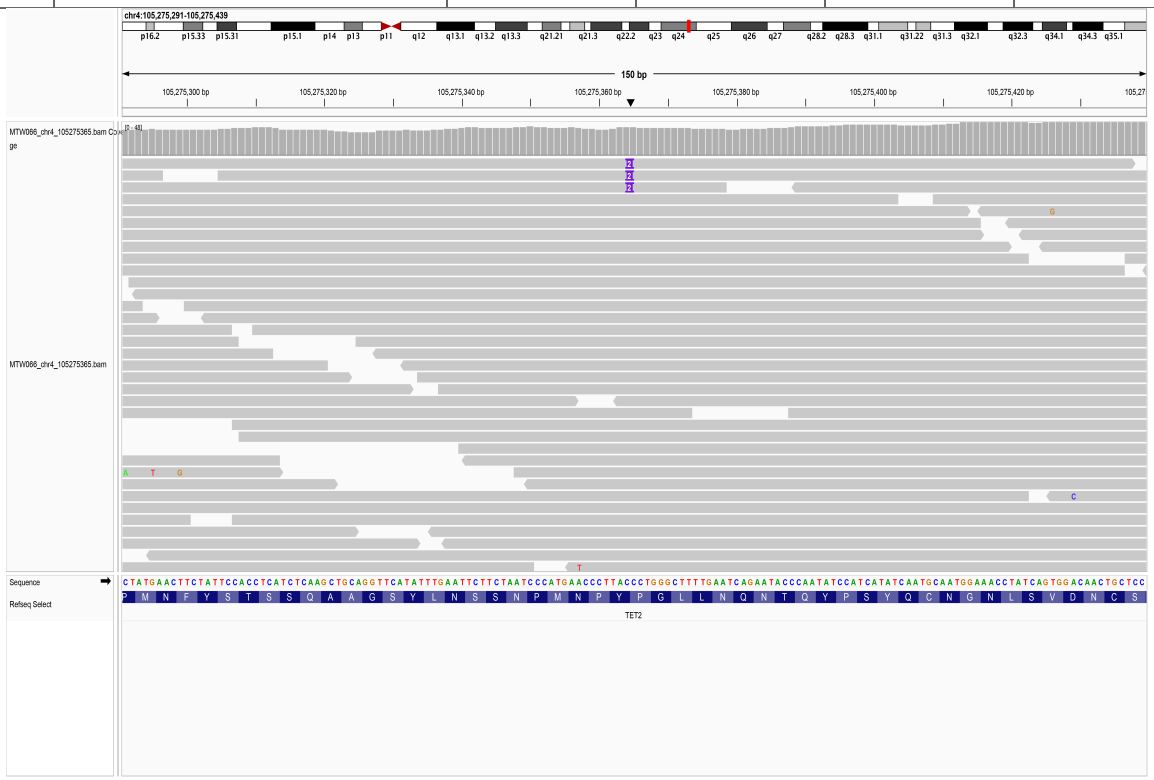
55.82. chr4_105275358_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R35654	chr4_105275358_C/-	188	10	*TET2*	frameshift_variant



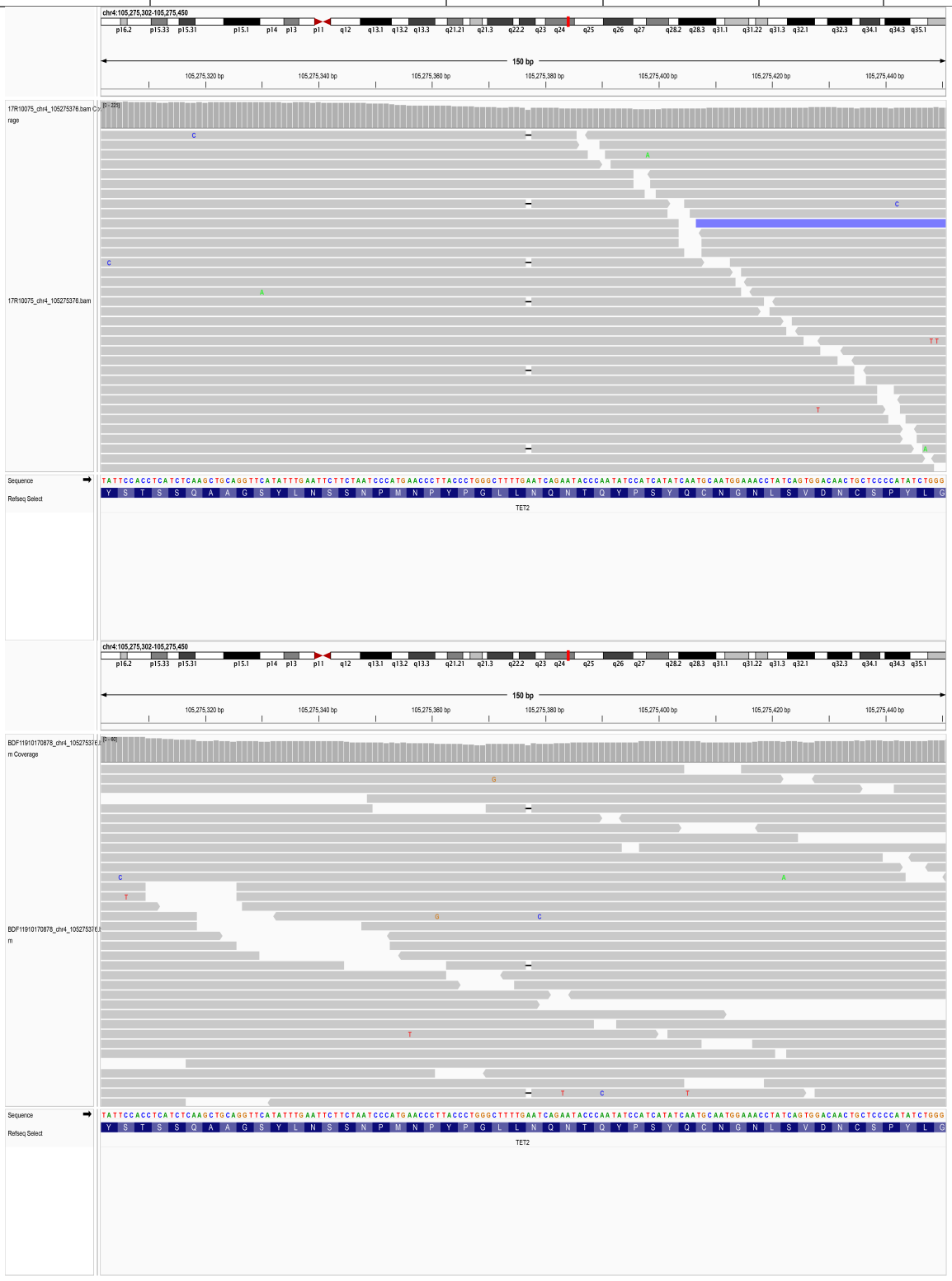
55.83. chr4_105275365_-/AA

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
MTW066	chr4_105275365_-/AA	37	3	*TET2*	frameshift_variant



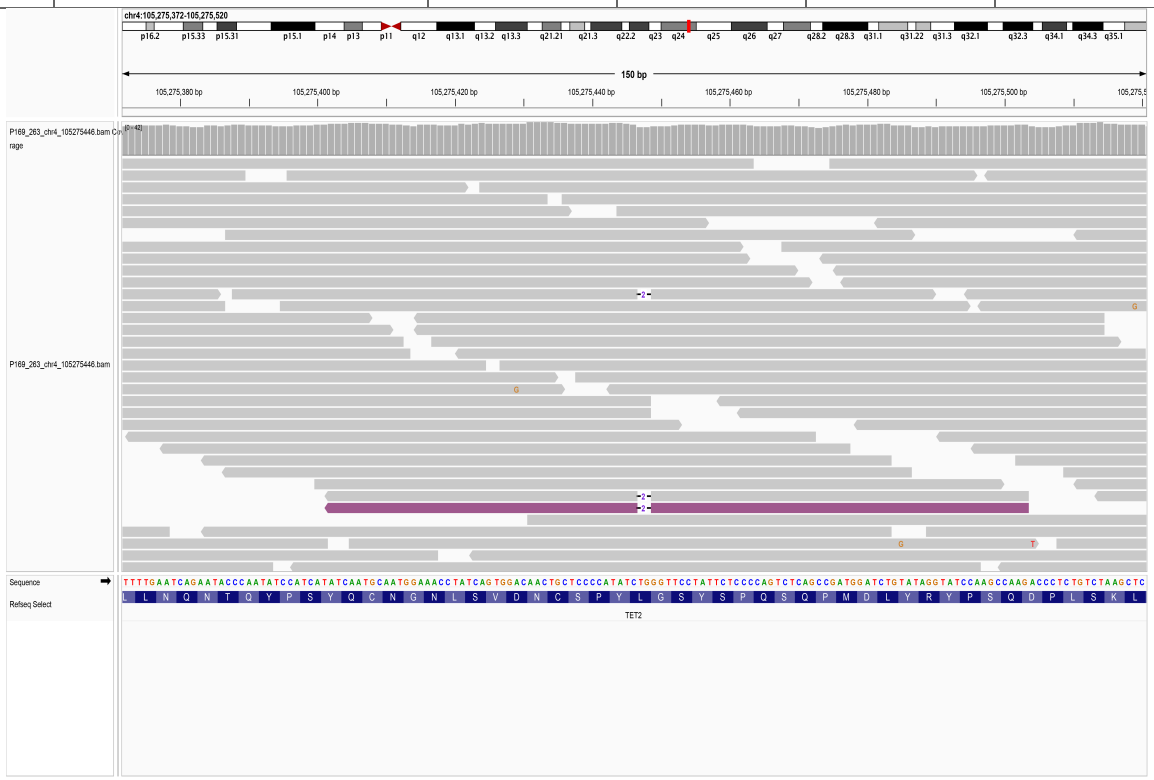
55.84. chr4_105275377_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R10075	chr4_105275377_A/-	147	14	*TET2*	frameshift_variant
BDF11910170878	chr4_105275377_A/-	36	4	*TET2*	frameshift_variant



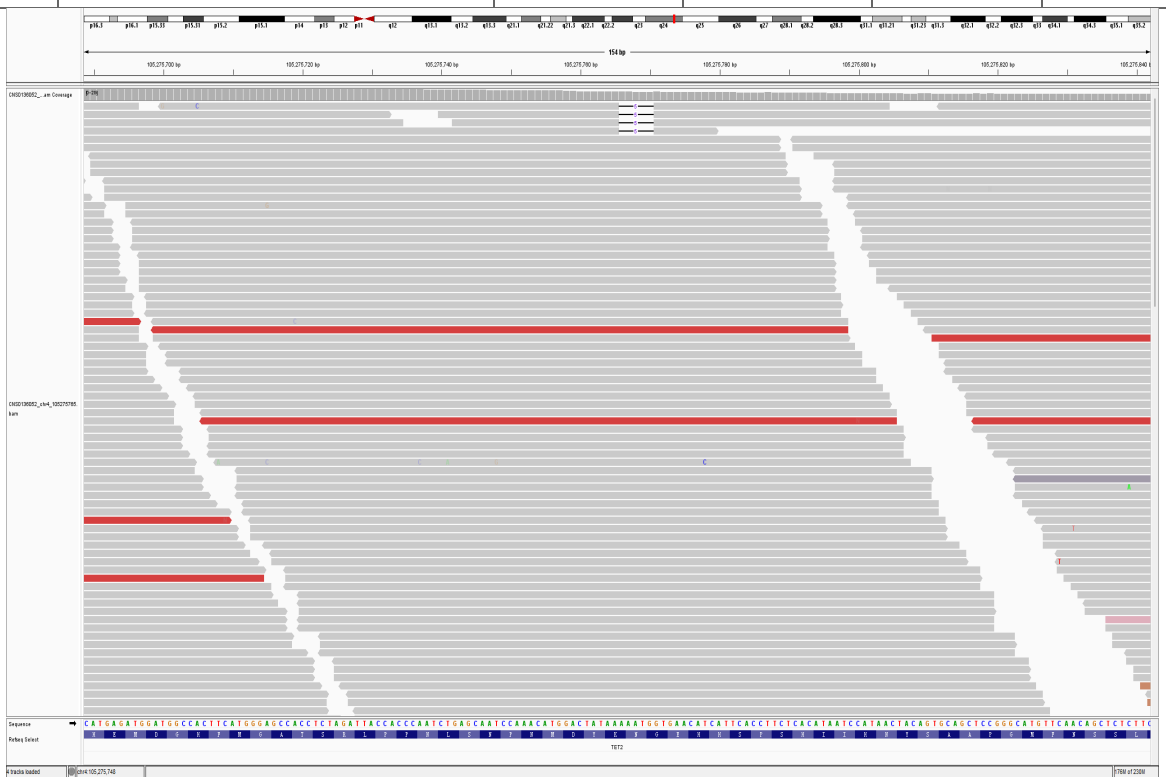
55.85. chr4_105275447_TG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
P169_263	chr4_105275447_TG/-	35	3	*TET2*	frameshift_variant



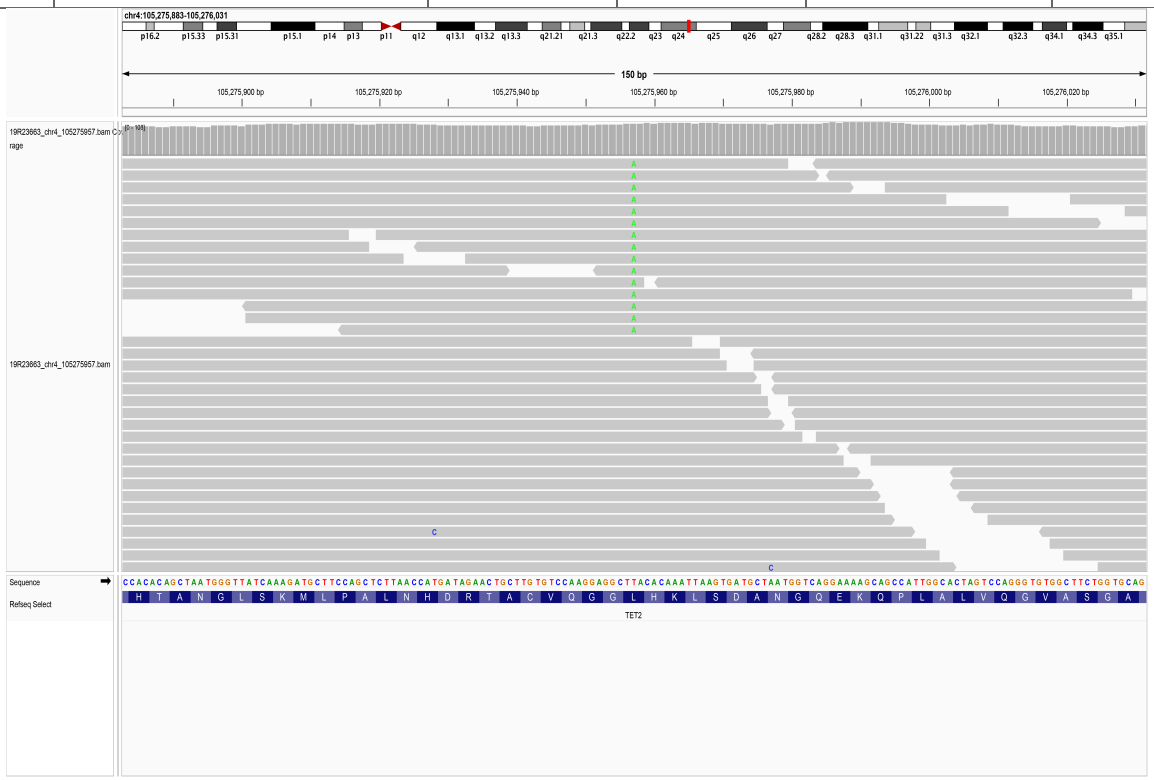
55.86. chr4_105275766_AAATG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136052	chr4_105275766_AAATG/-	167	5	*TET2*	frameshift_variant



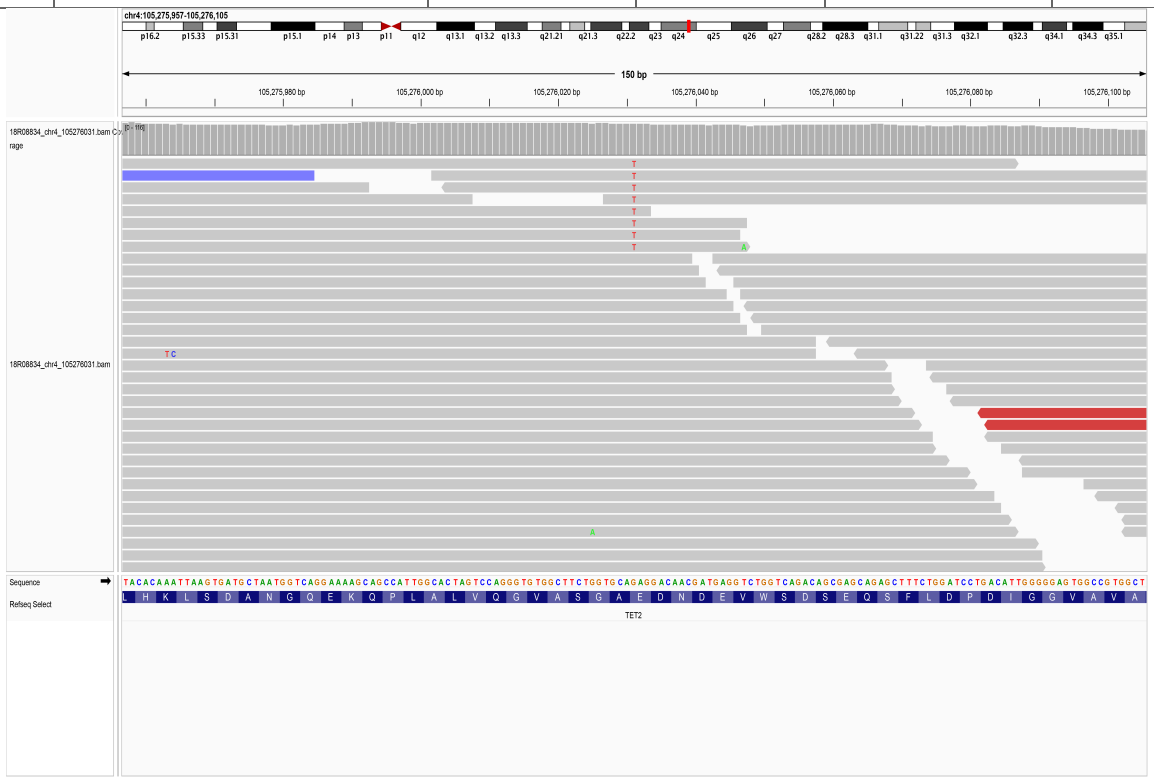
55.87. chr4_105275957_T/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23663	chr4_105275957_T/A	86	15	*TET2*	stop_gained



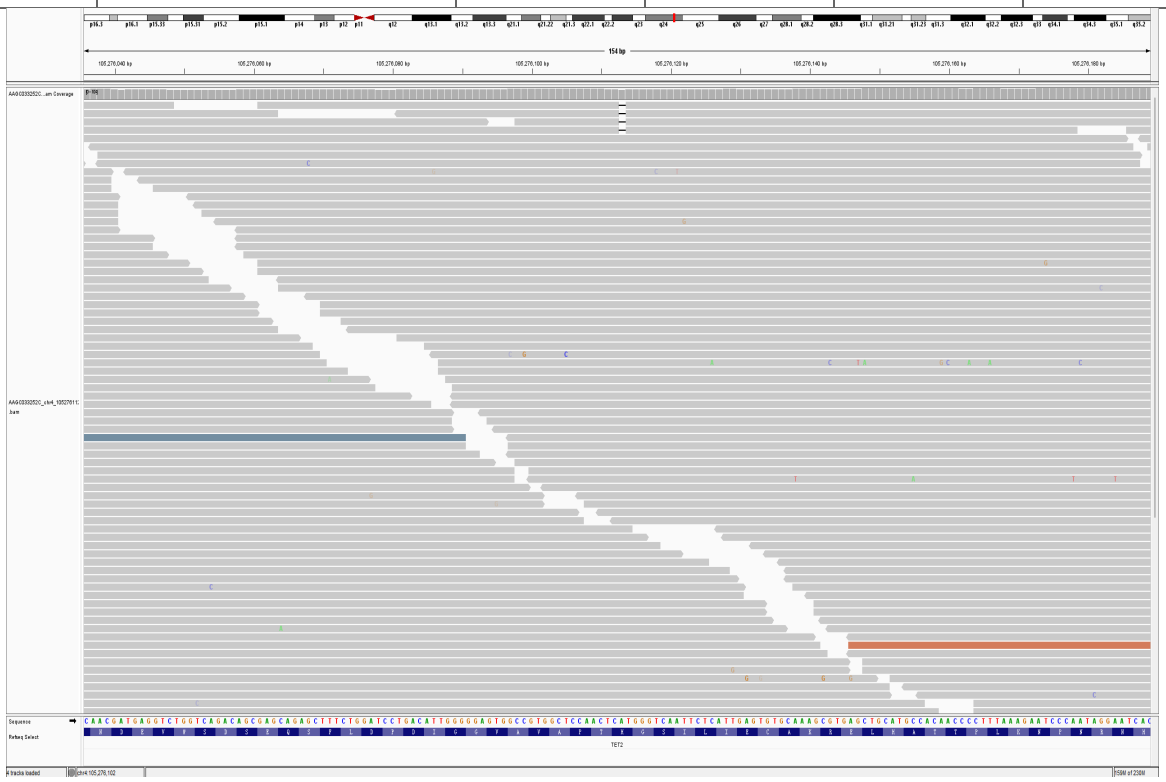
55.88. chr4_105276031_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08834	chr4_105276031_G/T	98	8	*TET2*	stop_gained



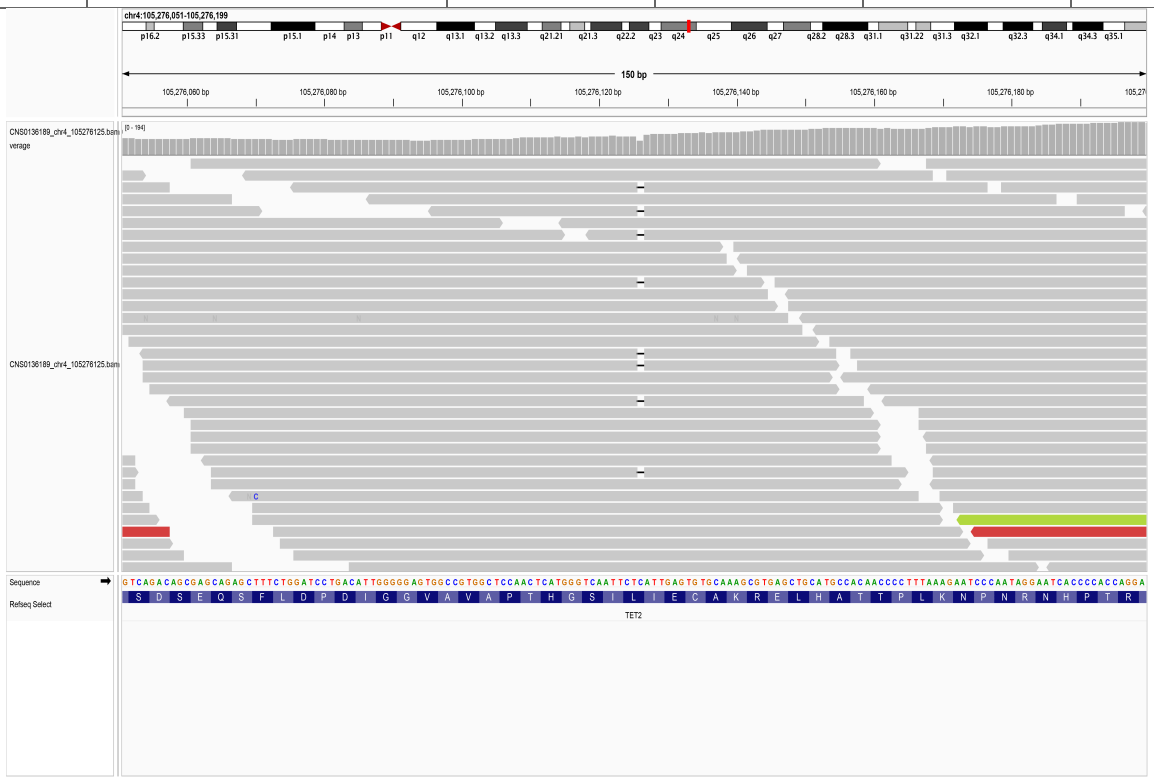
55.89. chr4_105276113_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033252C	chr4_105276113_A/-	83	5	*TET2*	frameshift_variant



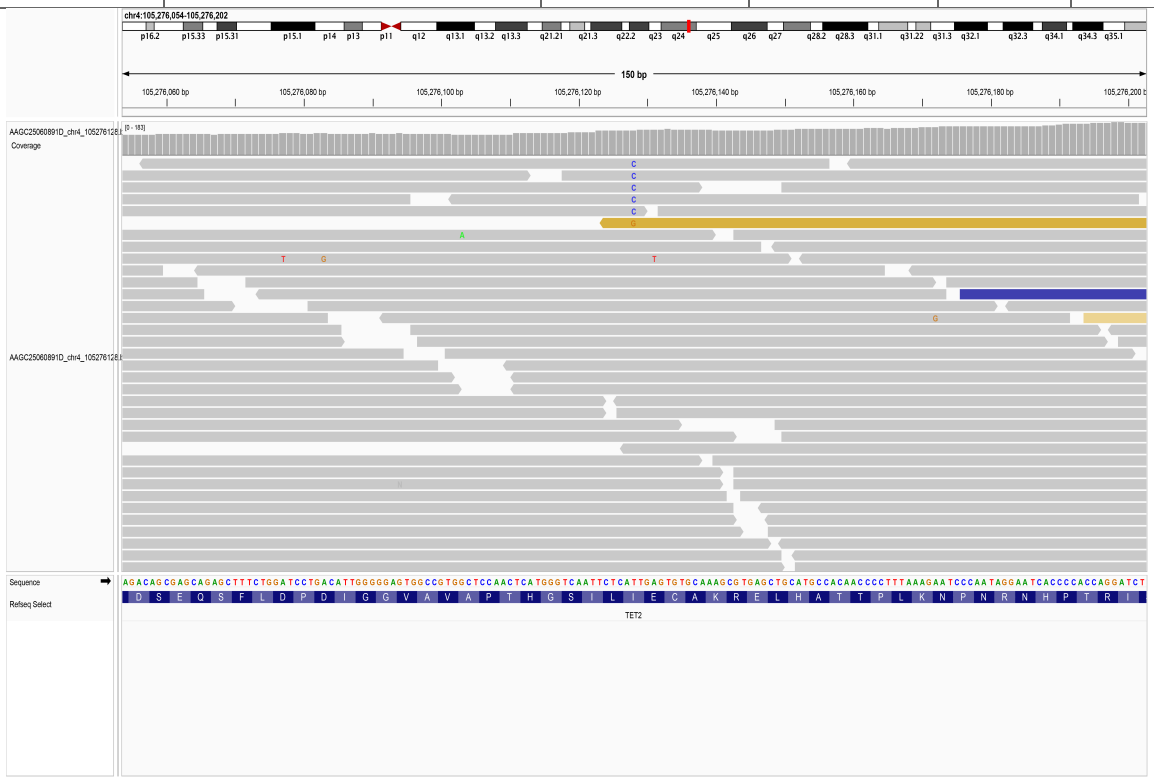
55.90. chr4_105276126_C/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0136189	chr4_105276126_C/-	81	30	*TET2*	frameshift_variant



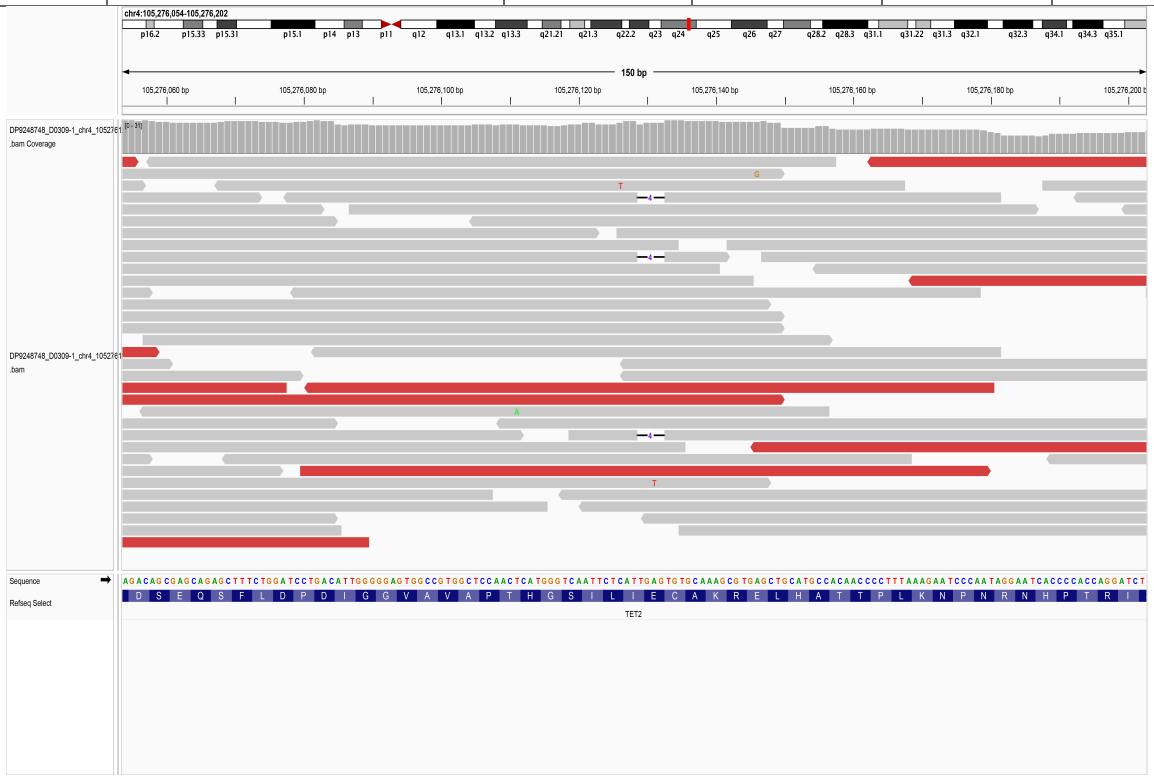
55.91. chr4_105276128_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060891D	chr4_105276128_T/C	131	5	*TET2*	missense_variant



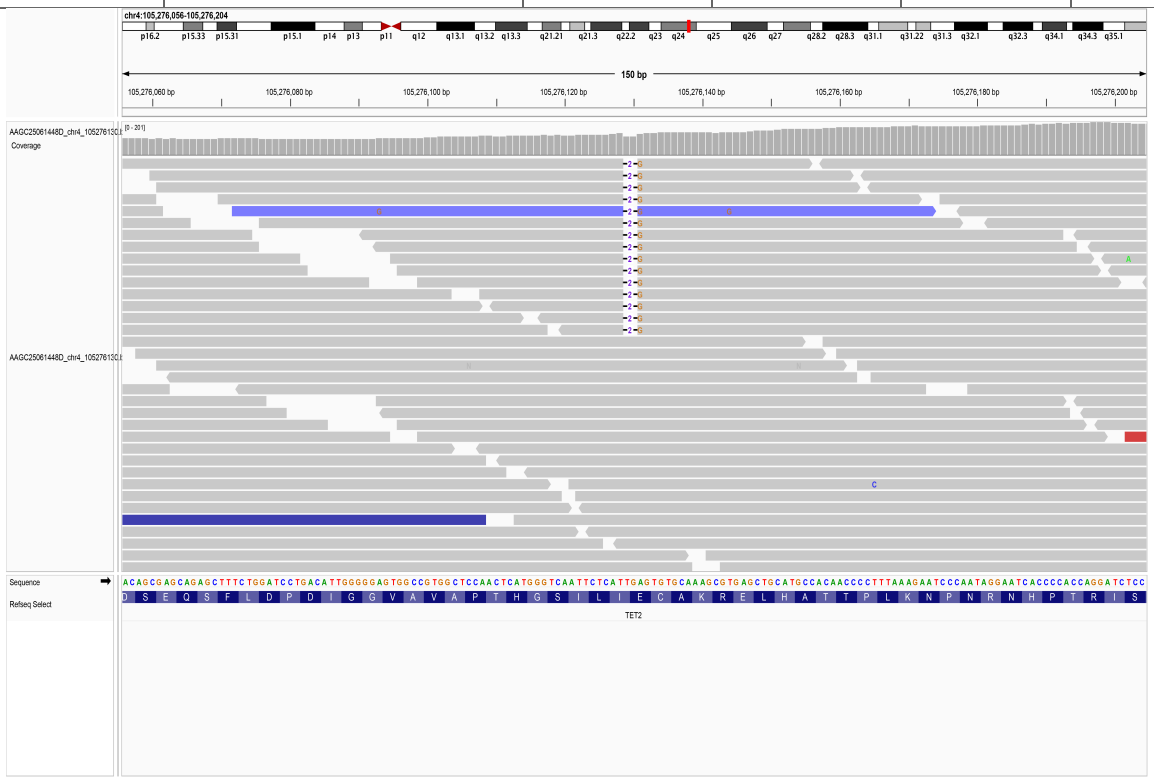
55.92. chr4_105276129_TGAG/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
DP9248748_D0309-1	chr4_105276129_TGAG/-	28	3	*TET2*	frameshift_variant



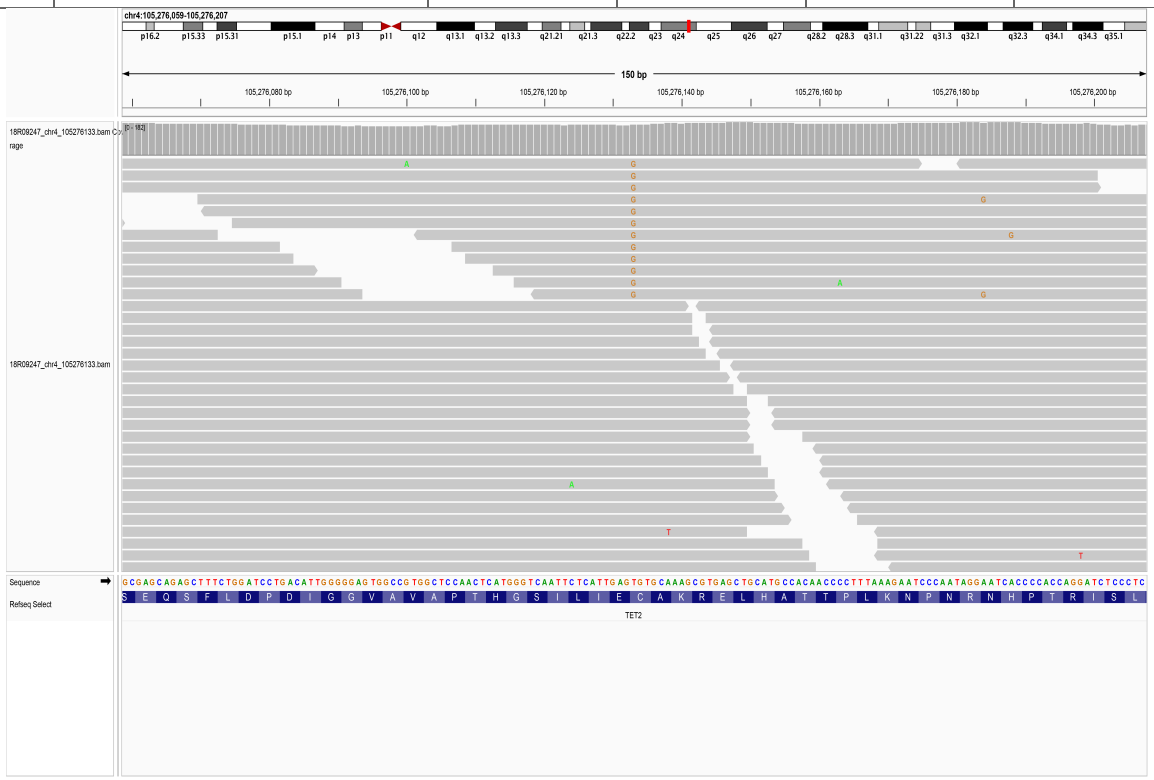
55.93. chr4_105276131_A/-

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061448D	chr4_105276131_A/-	114	18	*TET2*	frameshift_variant



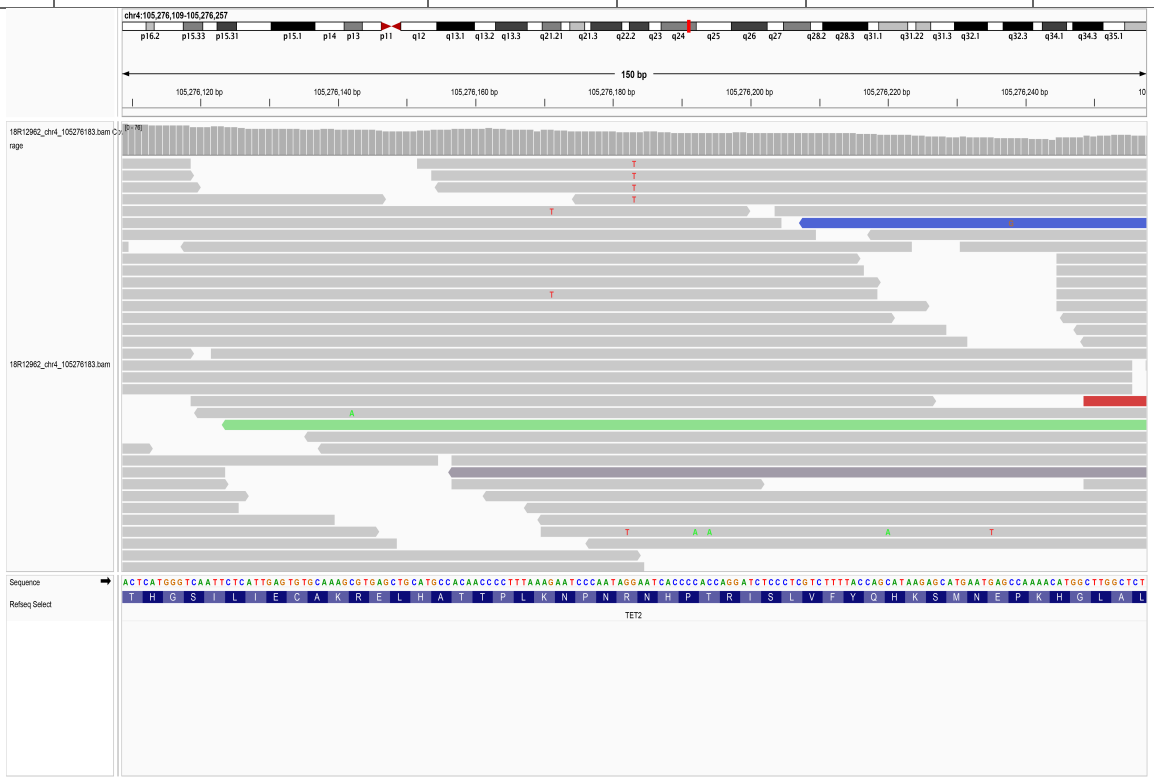
55.94. chr4_105276133_T/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09247	chr4_105276133_T/G	149	12	*TET2*	missense_variant



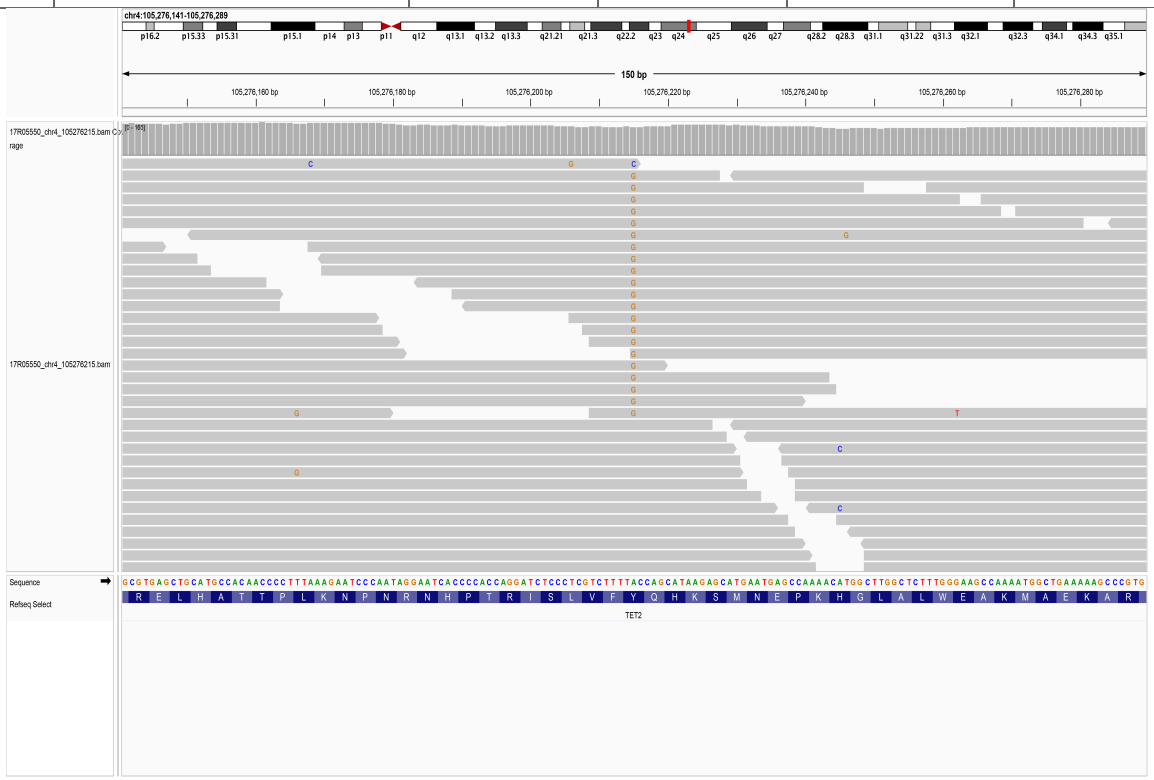
55.95. chr4_105276183_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12962	chr4_105276183_G/T	47	4	*TET2*	missense_variant



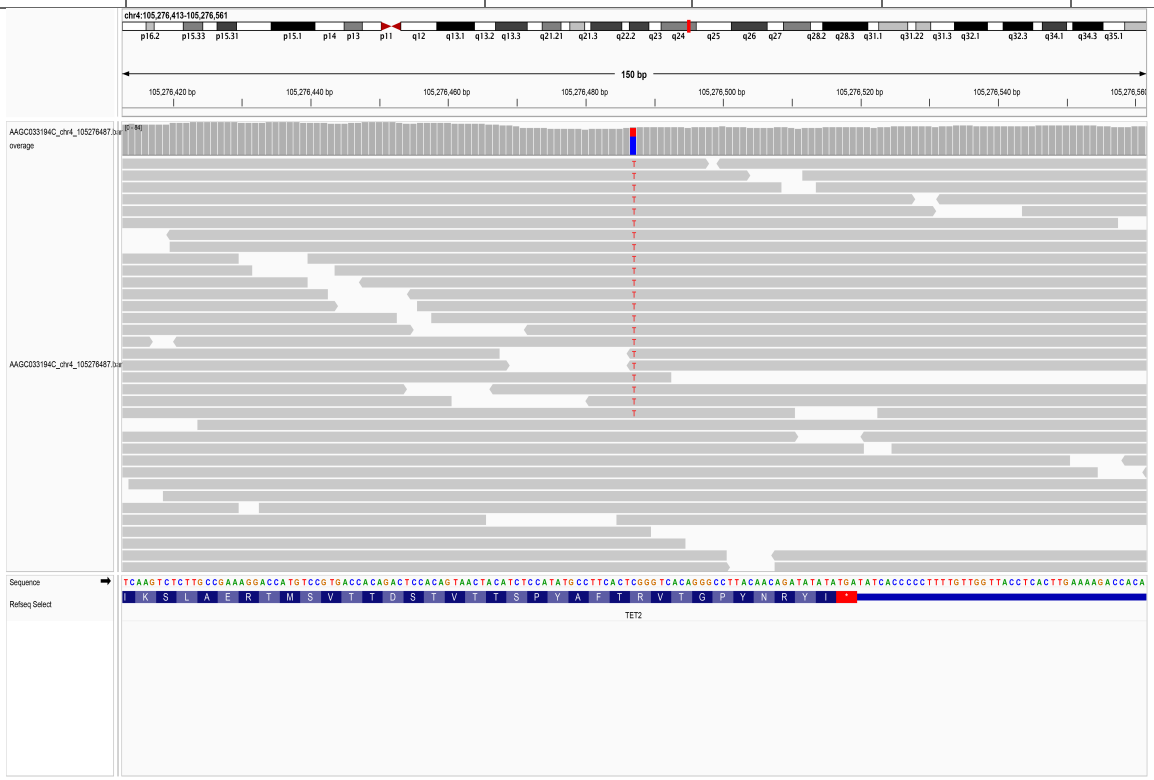
55.96. chr4_105276215_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05550	chr4_105276215_A/G	118	21	*TET2*	missense_variant



55.97. chr4_105276487_C/T

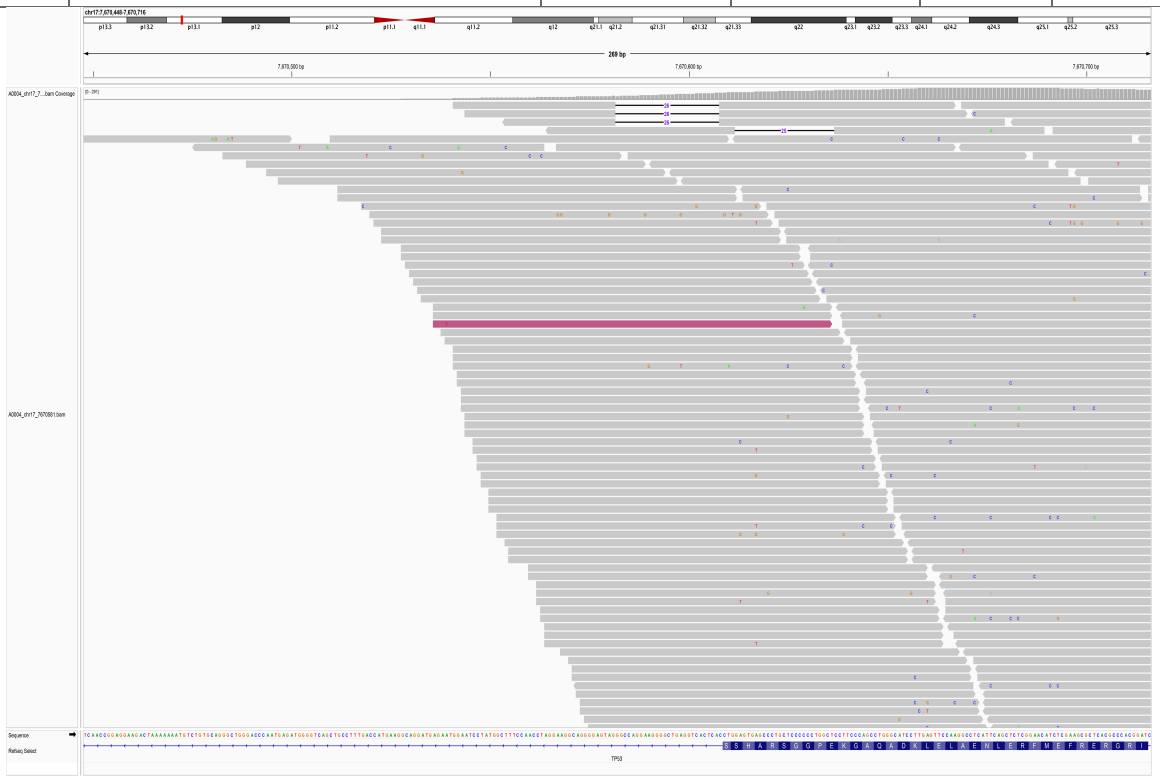
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033194C	chr4_105276487_C/T	46	22	*TET2*	missense_variant

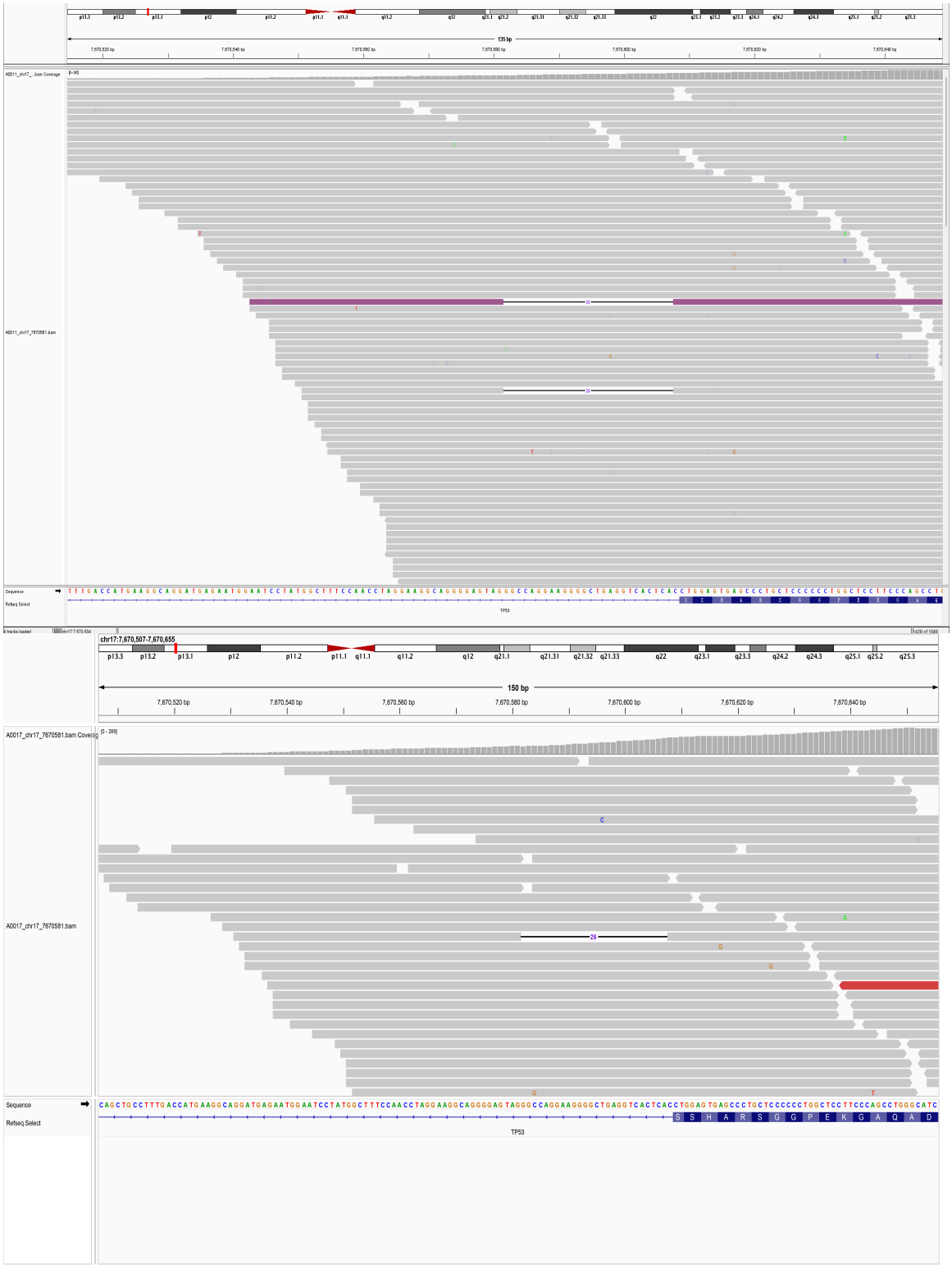


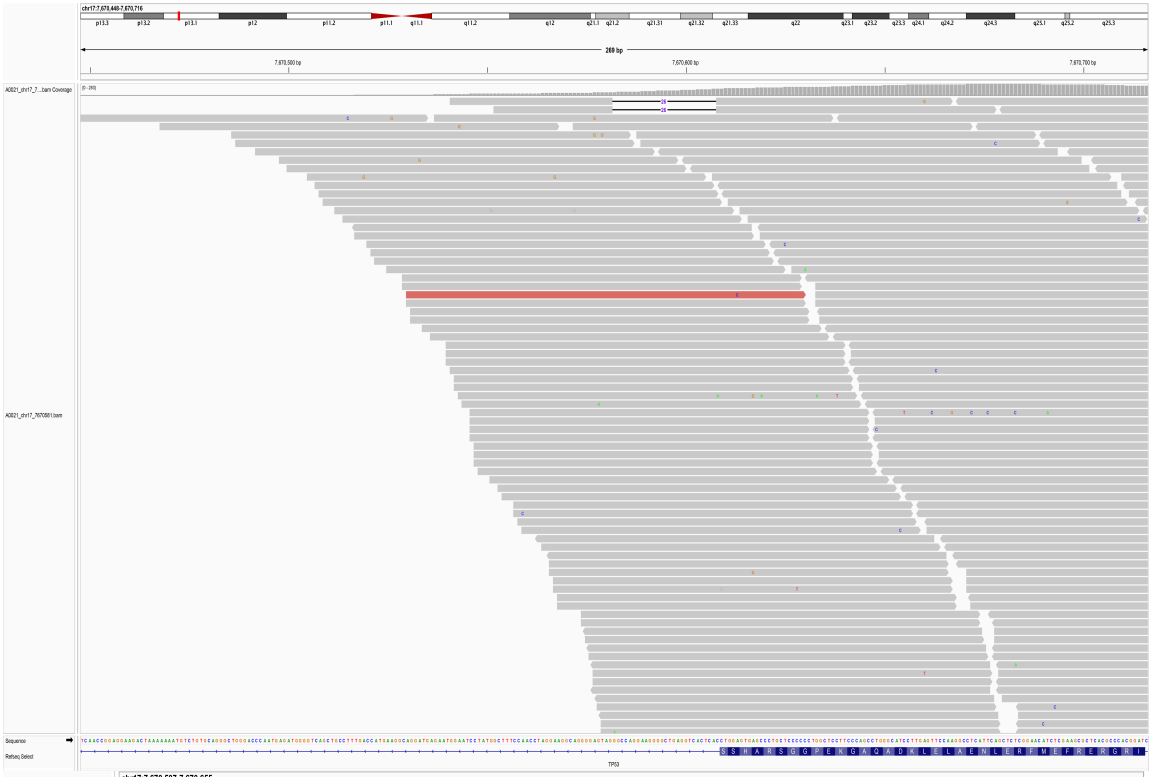
56. *TP53*

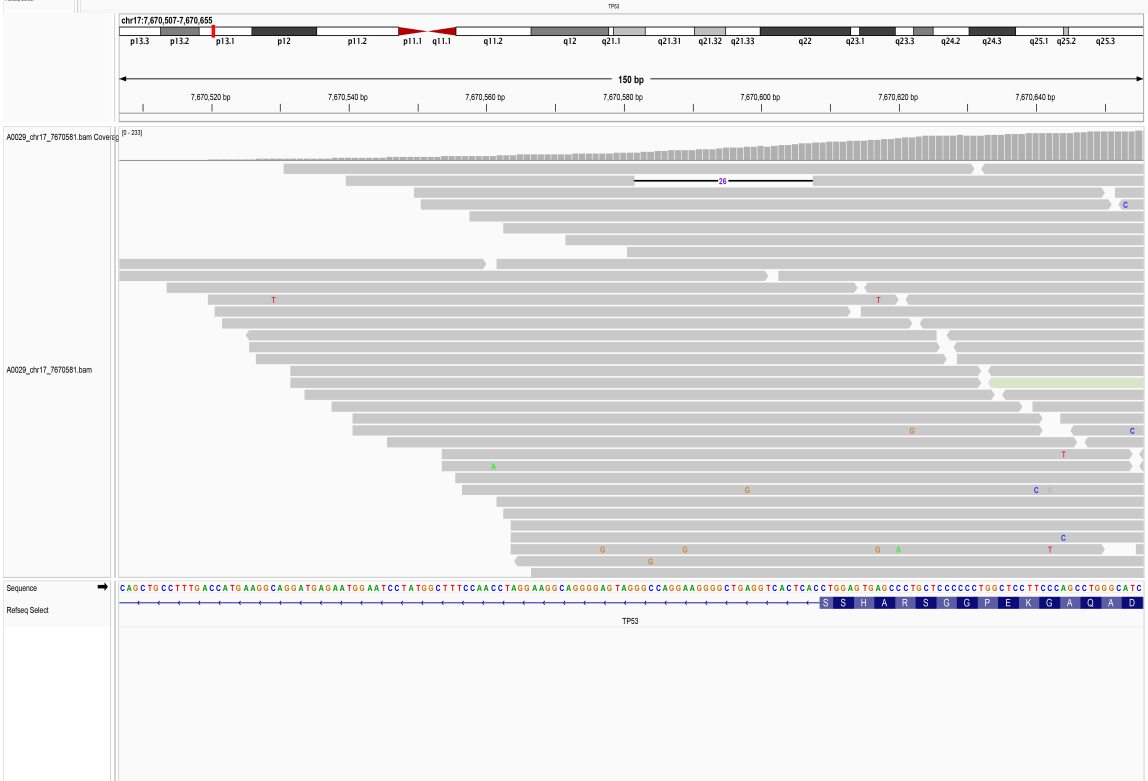
56.1. chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-

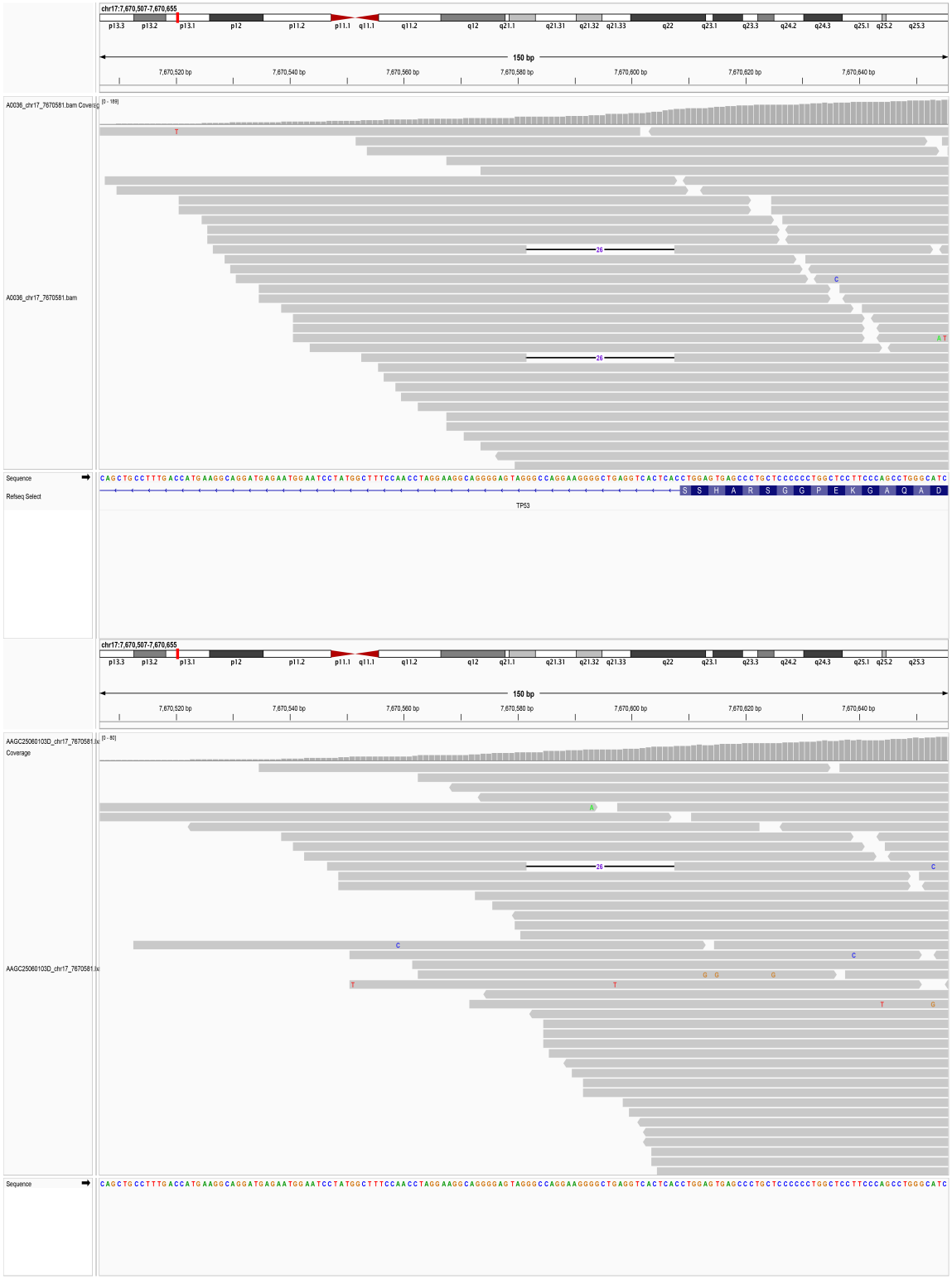
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0004	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	155	4	*TP53*	splice_donor_variant
A0011	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	146	3	*TP53*	splice_donor_variant
A0017	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	154	4	*TP53*	splice_donor_variant
A0021	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	159	4	*TP53*	splice_donor_variant
A0029	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	117	3	*TP53*	splice_donor_variant
A0036	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	103	3	*TP53*	splice_donor_variant
AAGC25060103D	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	40	2	*TP53*	splice_donor_variant
AAGC25060111D	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	45	2	*TP53*	splice_donor_variant
AAGC25060328D	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	73	4	*TP53*	splice_donor_variant
CNS0134090	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	74	3	*TP53*	splice_donor_variant

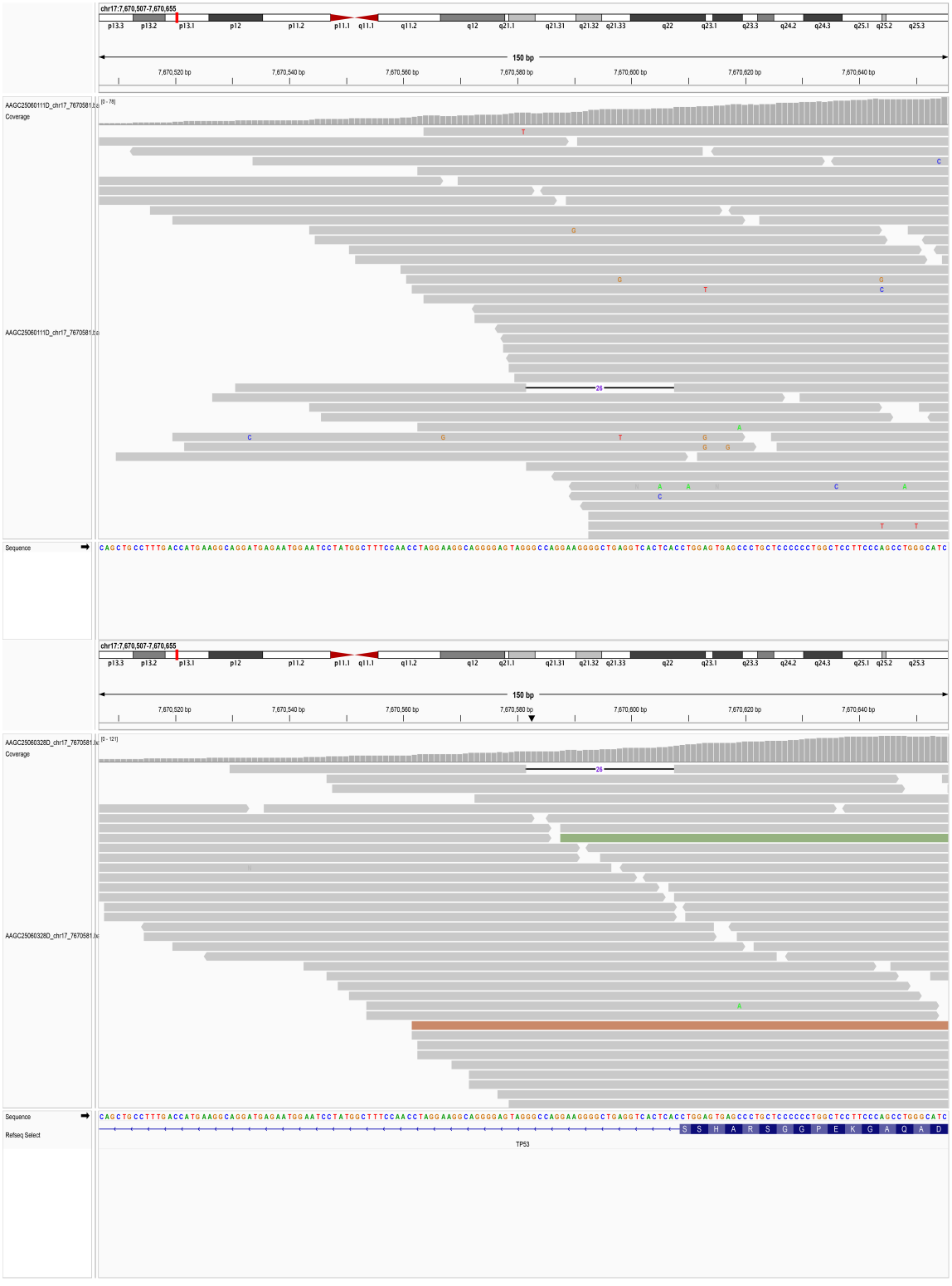


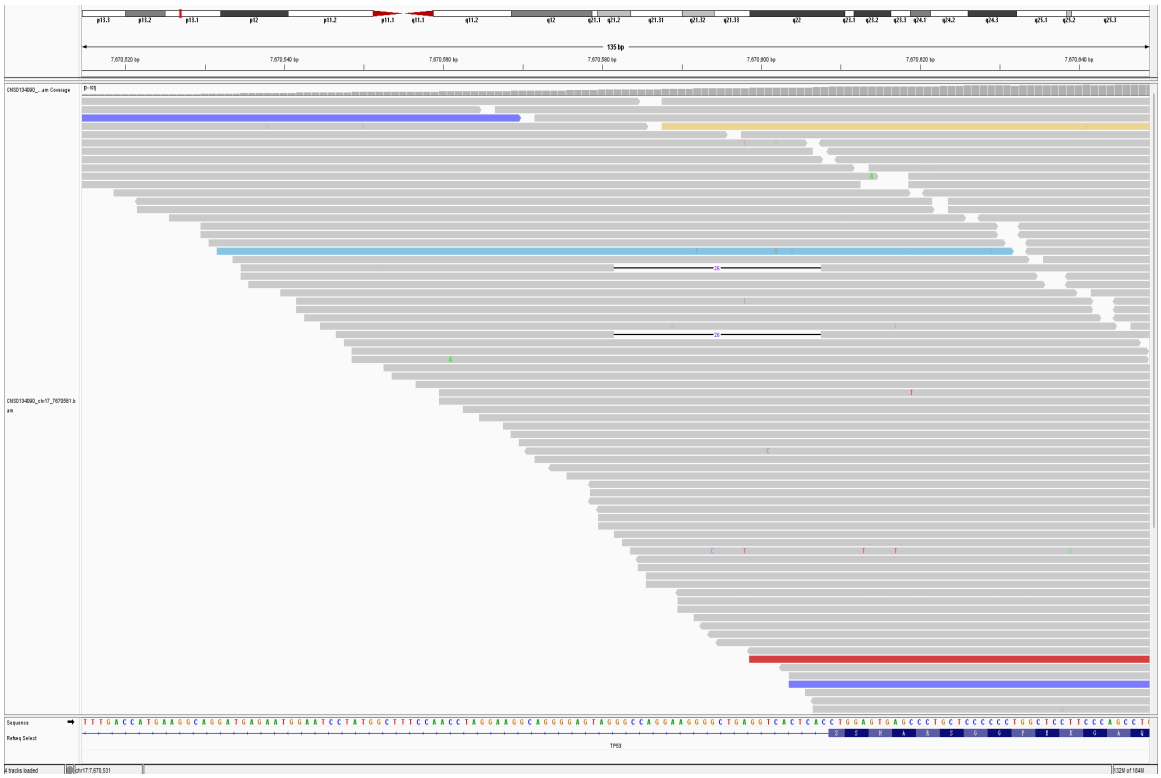

chr17:7,670,507-7,670,655
150 bp
7,670,520 bp
7,670,540 bp
7,670,560 bp
7,670,580 bp
7,670,600 bp
7,670,620 bp
7,670,640 bp
A0017_chr17_7670581.bam Coverage
A0017_chr17_7670581.bam
Sequence
Refseq Select
TP53


chr17:7,670,440-7,670,716
260 bp
A0021_chr17_7...bam Coverage
A0021_chr17_7670581.bam
Sequence
Refseq Select
TP53


chr17:7,670,507-7,670,655
150 bp
7,670,520 bp
7,670,540 bp
7,670,560 bp
7,670,580 bp
7,670,600 bp
7,670,620 bp
7,670,640 bp
A0029_chr17_7670581.bam Coverag
A0029_chr17_7670581.bam
Sequence
Refseq Select
TP53

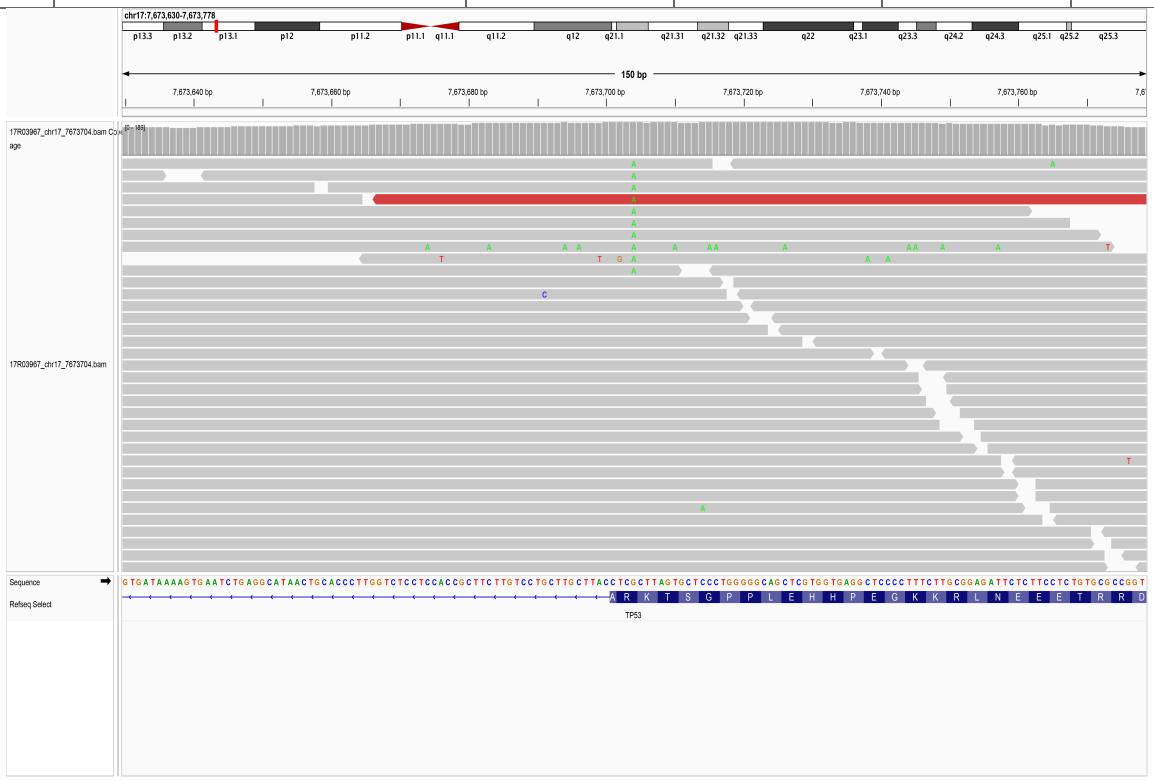

chr17:7,670,507-7,670,655
150 bp
7,670,520 bp
7,670,540 bp
7,670,560 bp
7,670,580 bp
7,670,600 bp
7,670,620 bp
7,670,640 bp
A0036_chr17_7670581.bam Coverag
A0036_chr17_7670581.bam
Sequence
Refseq Select
TP53
S S H A R S G G P E K G A Q A D
AAGC2506103D_chr17_7670581.ba
Coverage
AAGC2506103D_chr17_7670581.ba


chr17:7,670,507-7,670,655
150 bp
7,670,520 bp
7,670,540 bp
7,670,560 bp
7,670,580 bp
7,670,600 bp
7,670,620 bp
7,670,640 bp
Coverage
Sequence
CAGCTGCCTTTGACCATGAAGGCAGGATGAGAATGGAATCCTATGGCTTTCCAACCTAGGAAGGCAGGGGAGTAGGGCCAGGAAGGGGCTGAGGTCACTCACCTGGAGTGAGCCCTGCTCCCCCCTGGCTCCTTCCCAGCCTGGGCATC
Refseq Select
TP53


135 bp
TP53

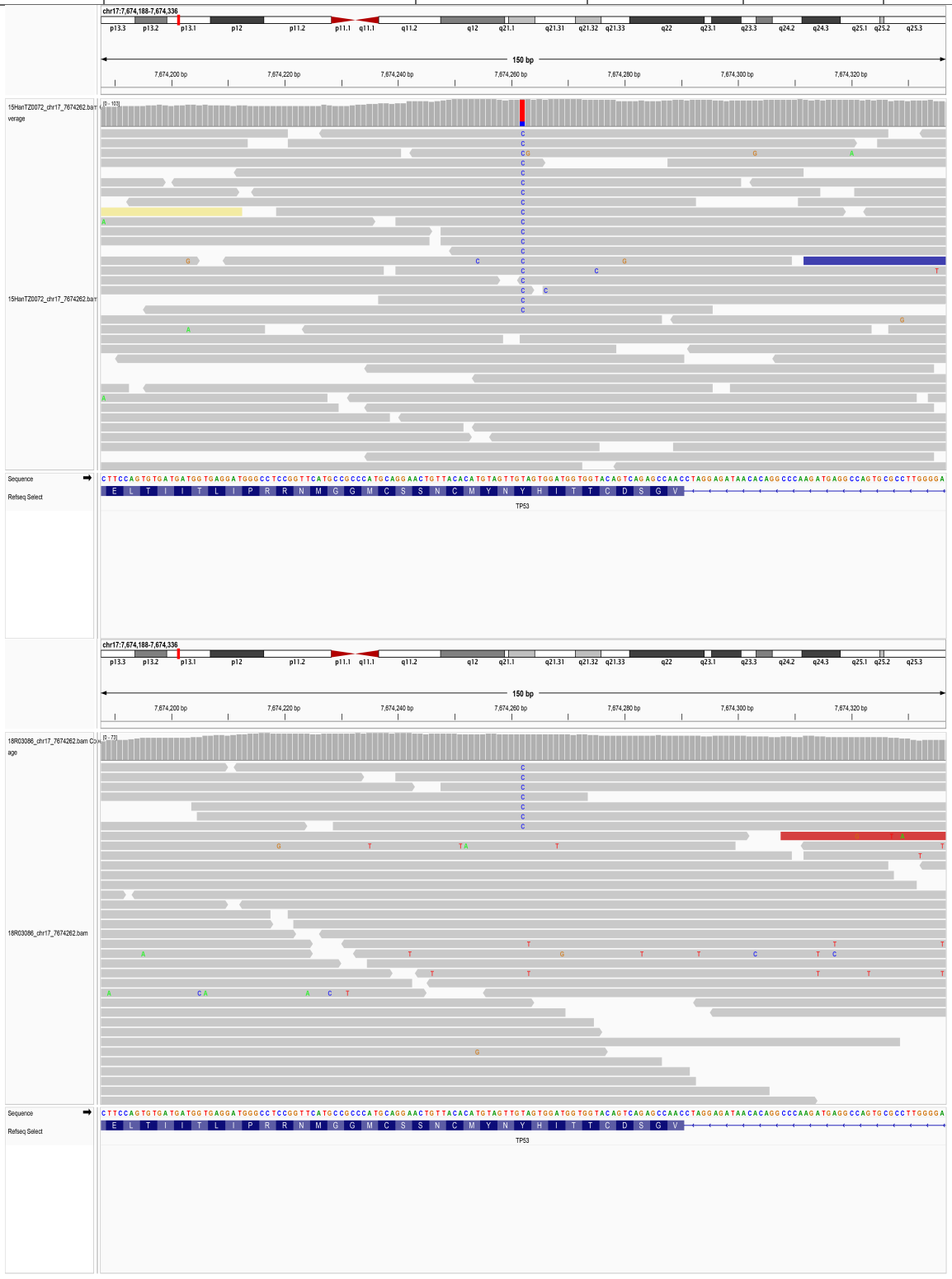
56.2. chr17_7673704_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R03967	chr17_7673704_G/A	167	8	*TP53*	stop_gained



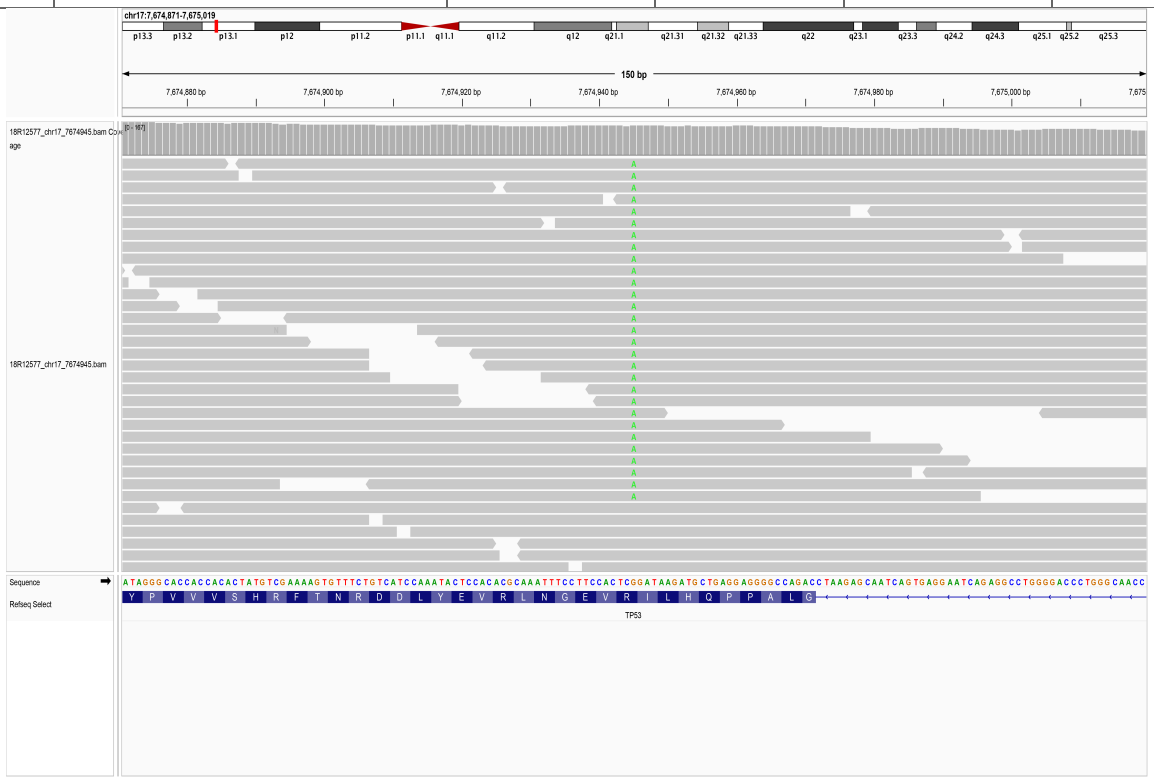
56.3. chr17_7674262_T/C

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0072	chr17_7674262_T/C	80	19	*TP53*	missense_variant
18R03086	chr17_7674262_T/C	54	7	*TP53*	missense_variant



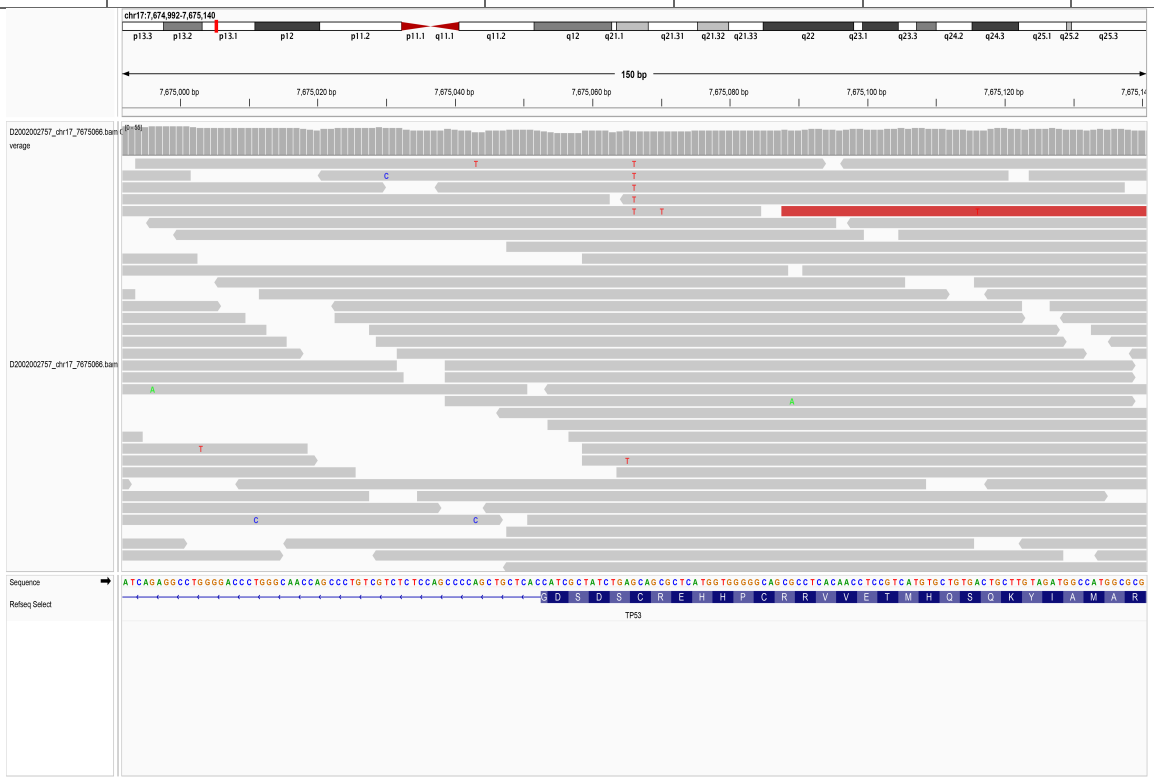
56.4. chr17_7674945_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12577	chr17_7674945_G/A	116	29	*TP53*	stop_gained



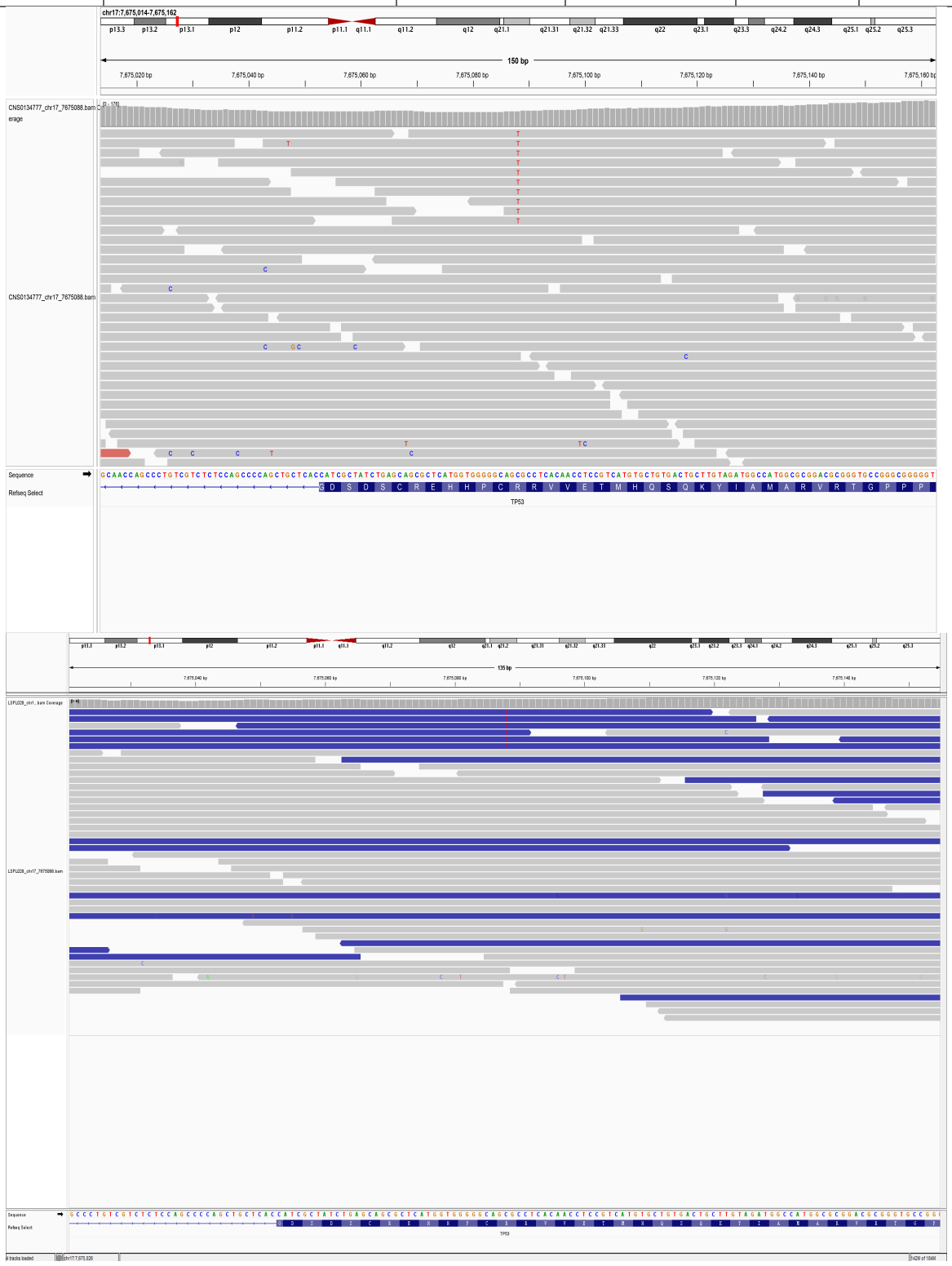
56.5. chr17_7675066_G/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2002002757	chr17_7675066_G/T	31	5	*TP53*	stop_gained



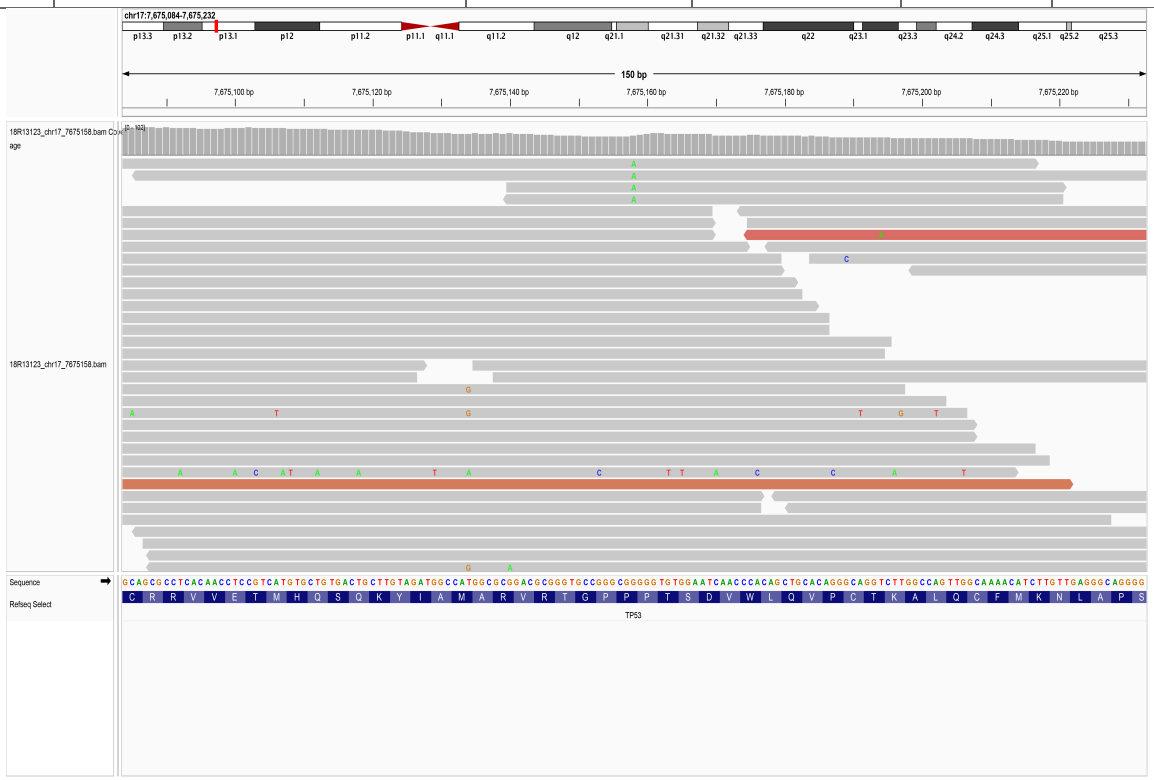
56.6. chr17_7675088_C/T

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134777	chr17_7675088_C/T	87	10	*TP53*	missense_variant
LSPL028	chr17_7675088_C/T	33	6	*TP53*	missense_variant



56.7. chr17_7675158_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13123	chr17_7675158_G/A	53	4	*TP53*	missense_variant



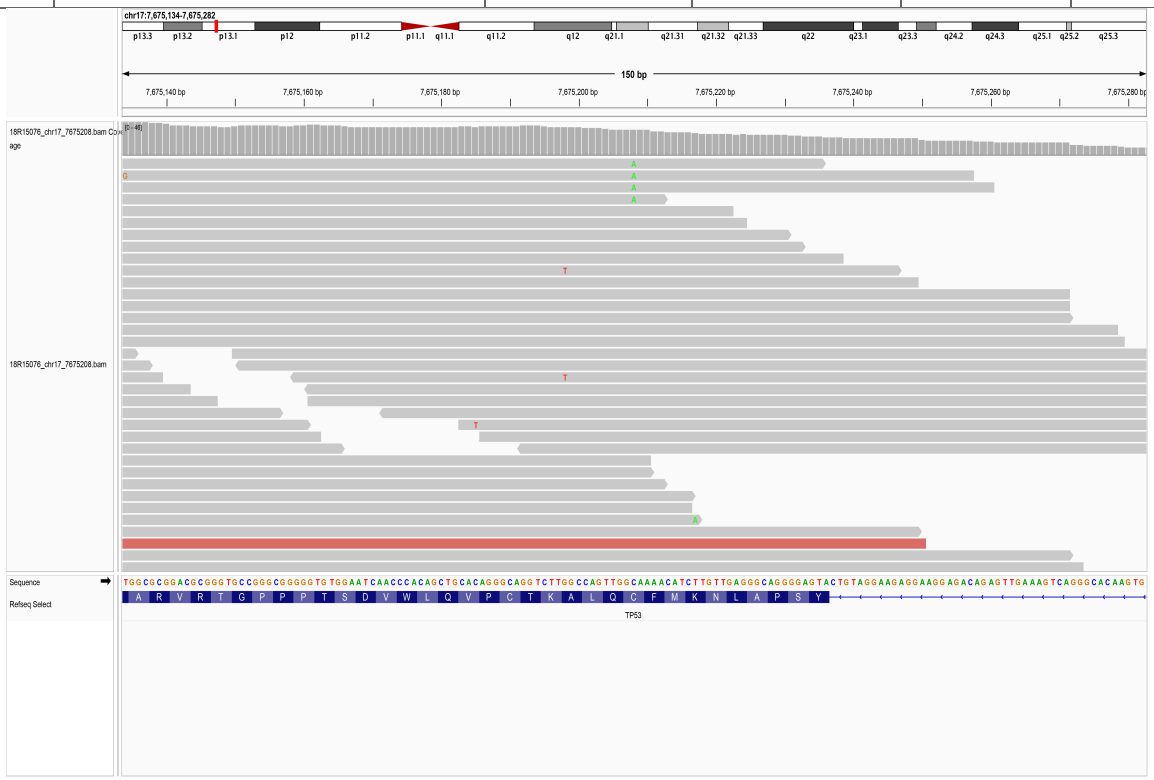
56.8. chr17_7675161_G/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
LSPL049	chr17_7675161_G/A	51	4	*TP53*	missense_variant



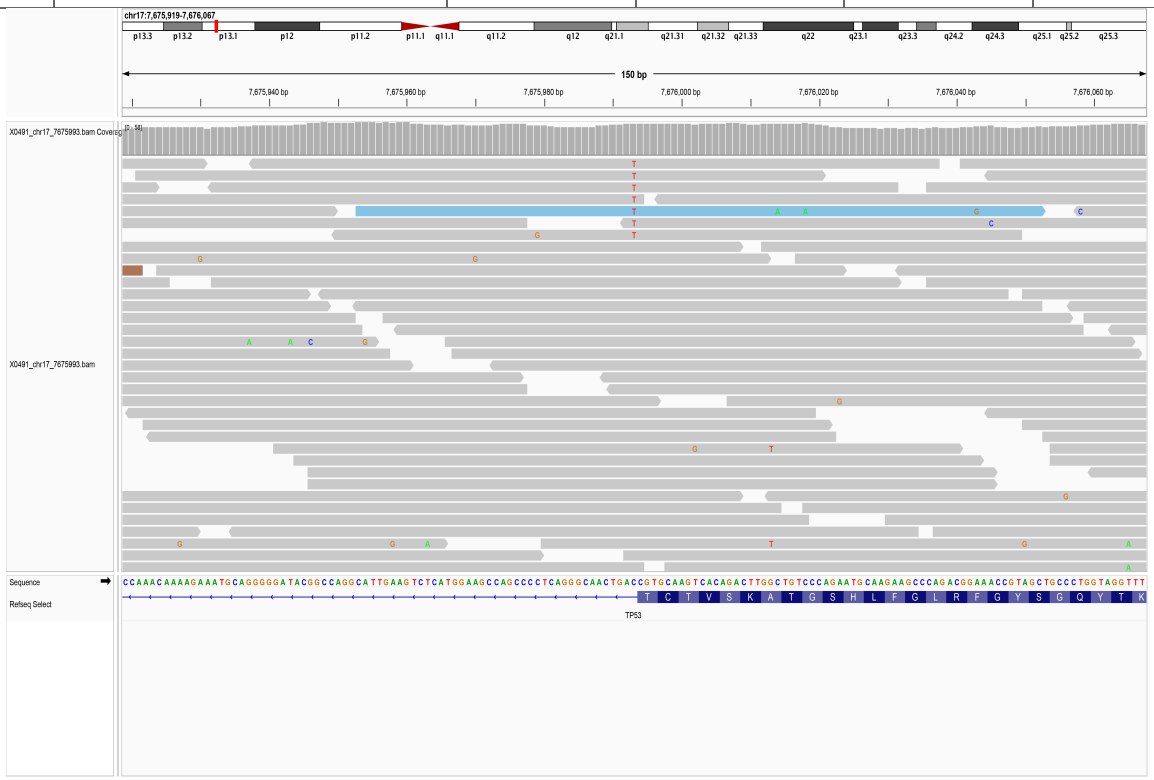
56.9. chr17_7675208_C/A

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15076	chr17_7675208_C/A	30	4	*TP53*	missense_variant



56.10. chr17_7675993_C/T

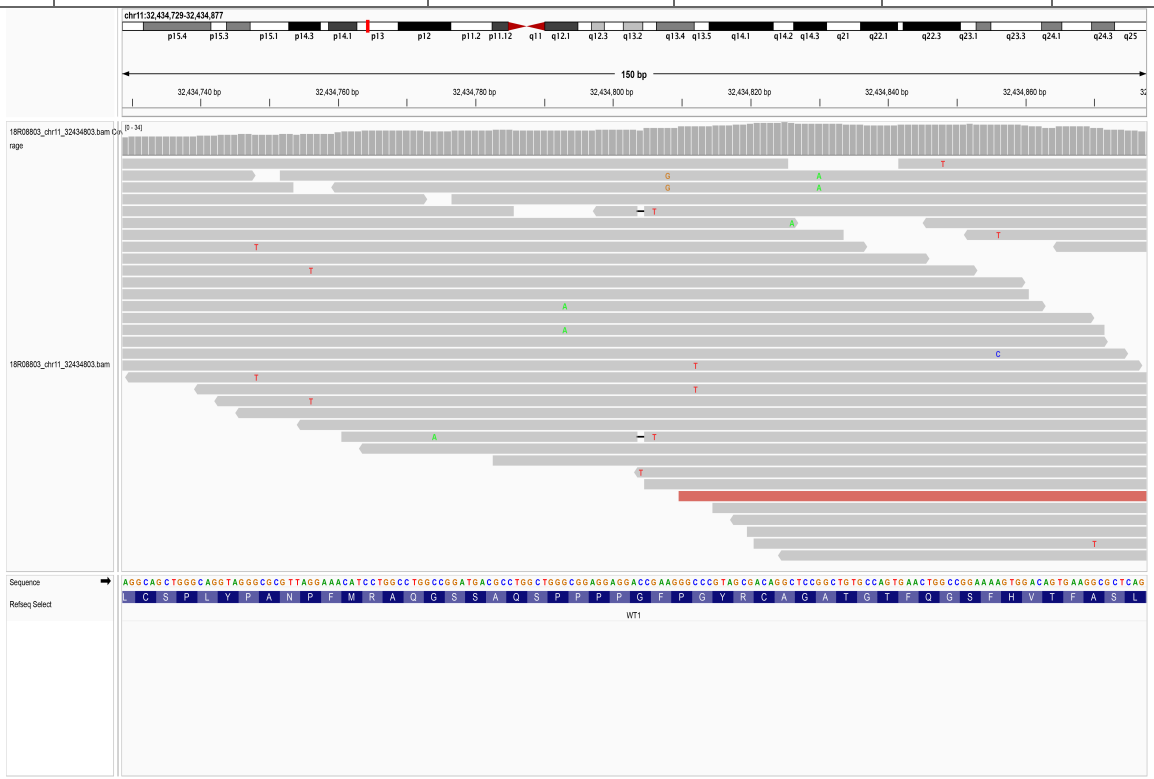
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
X0491	chr17_7675993_C/T	44	6	*TP53*	splice_donor_variant



57. *WT1*

57.1. chr11_32434804_C/-

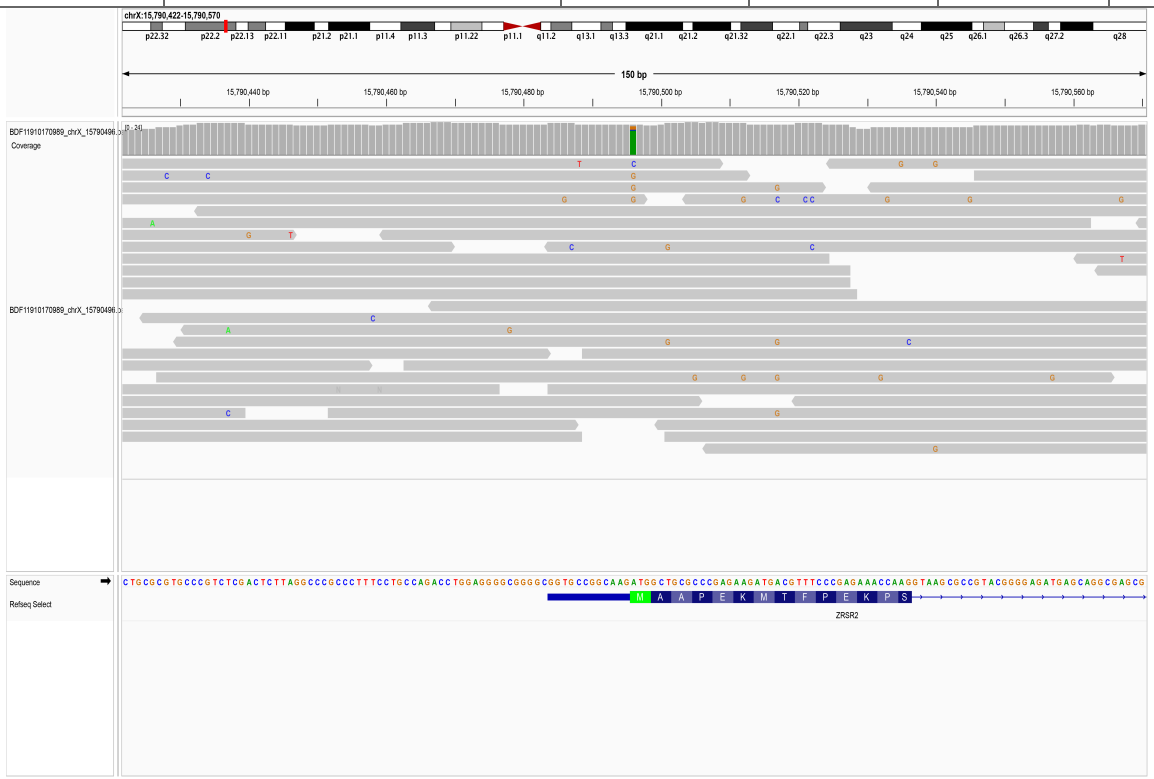
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08803	chr11_32434804_C/-	26	2	*WT1*	frameshift_variant



58. *ZRSR2*

58.1. chrX_15790496_A/G

SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170989	chrX_15790496_A/G	16	3	*ZRSR2*	start_lost



Reference:

1. Jaiswal, S., Natarajan, P., Silver, A.J., Gibson, C.J., Bick, A.G., Shvartz, E., McConkey, M., Gupta, N., Gabriel, S., Ardissino, D., et al. (2017). Clonal Hematopoiesis and Risk of Atherosclerotic Cardiovascular Disease. N. Engl. J. Med. *377*, 111–121.