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

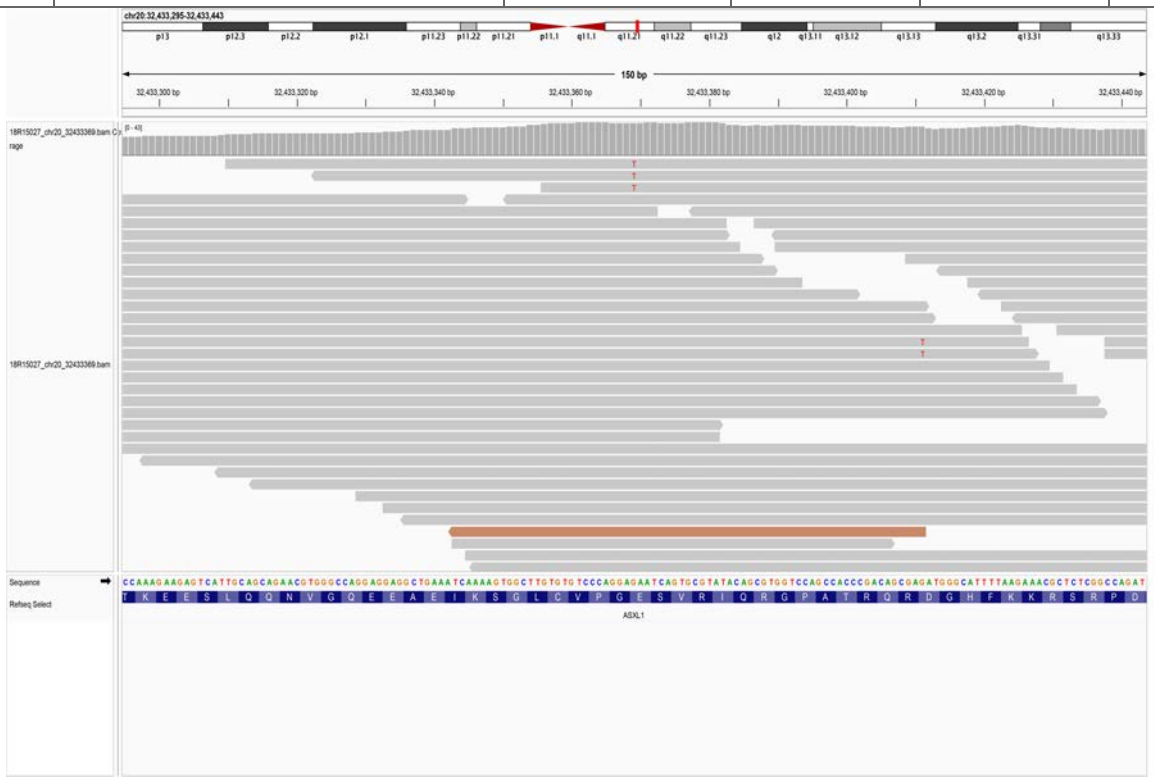
55.70. chr4_105269665_C/T ... 626
55.71. chr4_105269667_TTCTCAGGGGT/- ... 627
55.72. chr4_105269675_GGTC/- ... 628
55.73. chr4_105269691_G/C ... 629
55.74. chr4_105272591_C/T ... 630
55.75. chr4_105272623_G/T ... 632
55.76. chr4_105272700_G/A ... 633
55.77. chr4_105272717_G/A ... 634
55.78. chr4_105272774_C/T ... 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*

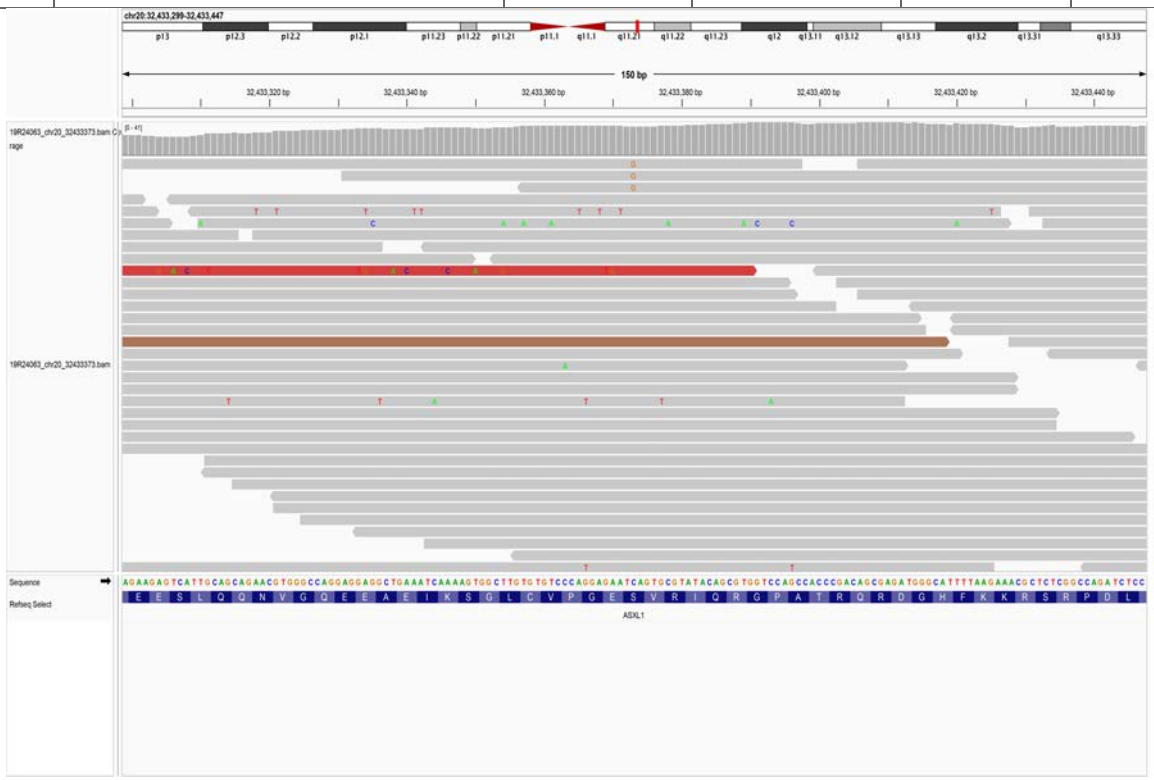
1.1. chr20_32433369_G/T

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



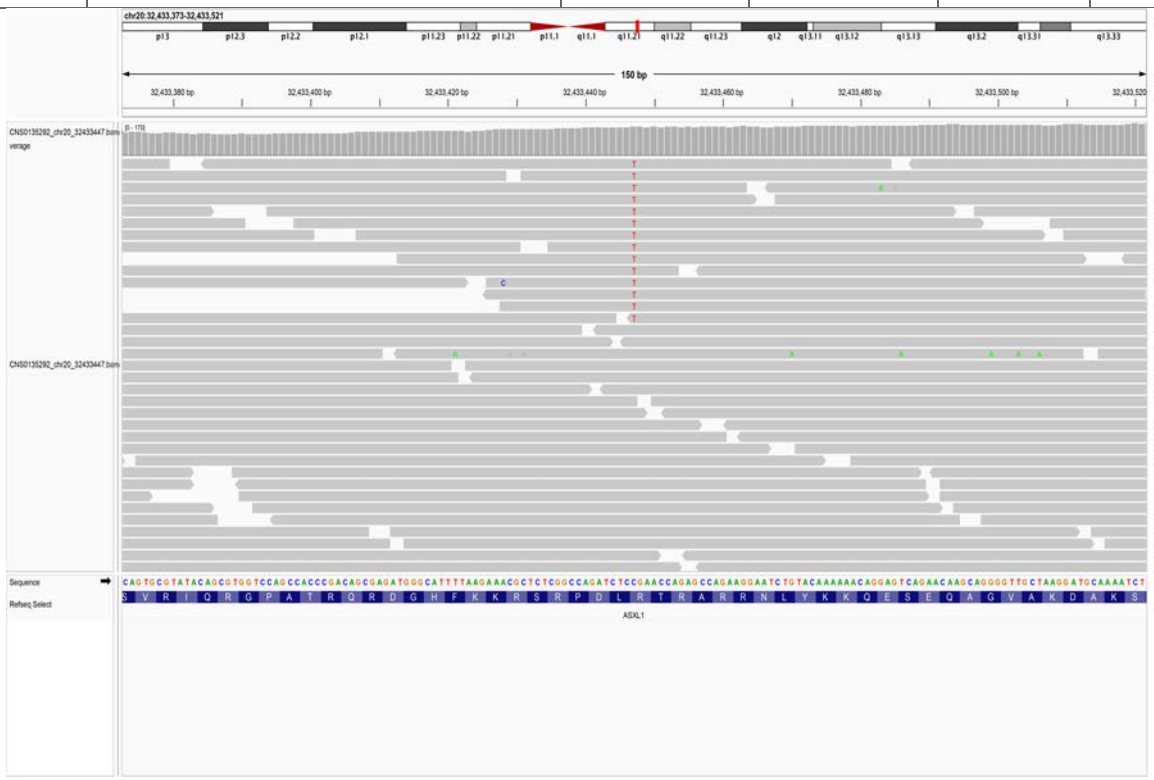
1.2. chr20_32433373_C/G

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



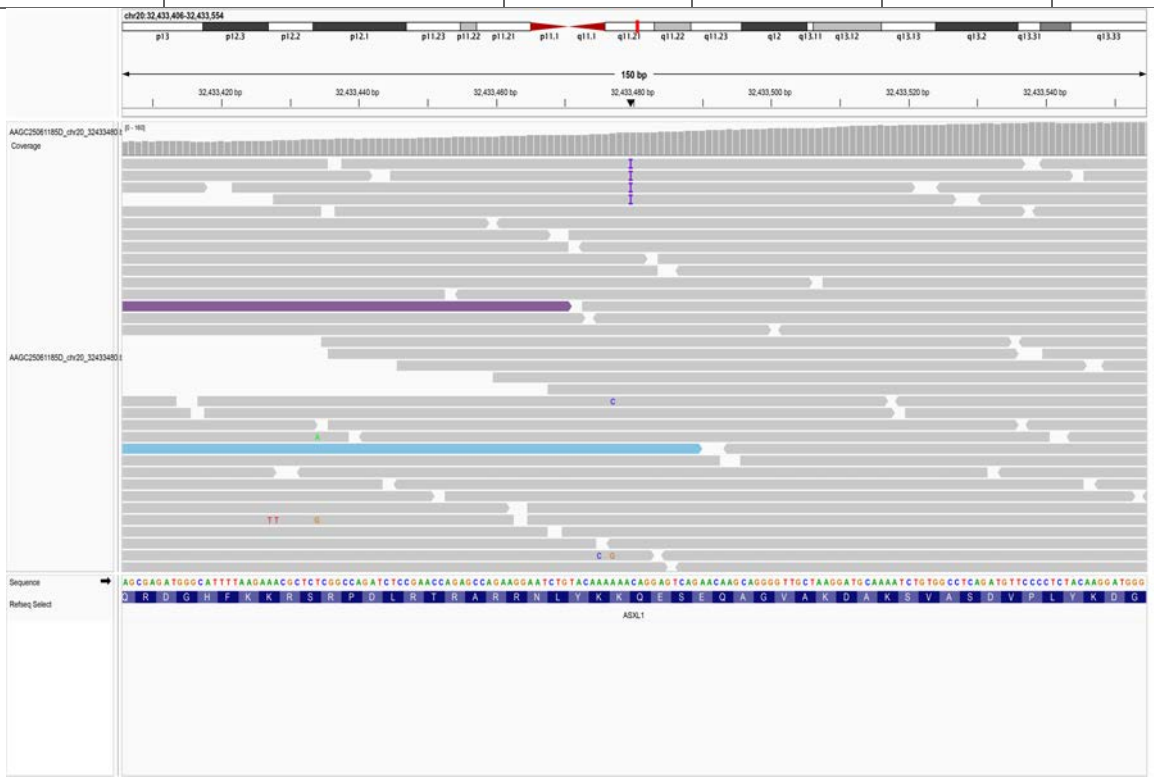
1.3. chr20_32433447_C/T

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



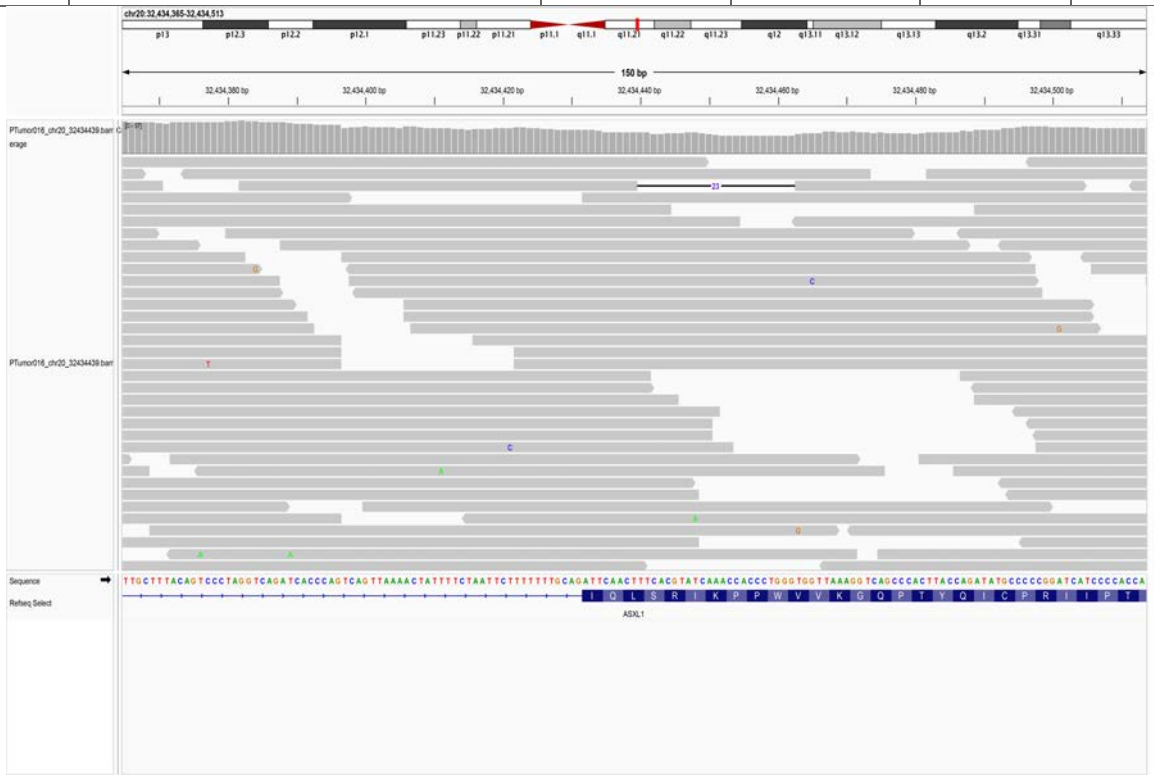
1.4. chr20_32433480_-/G

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



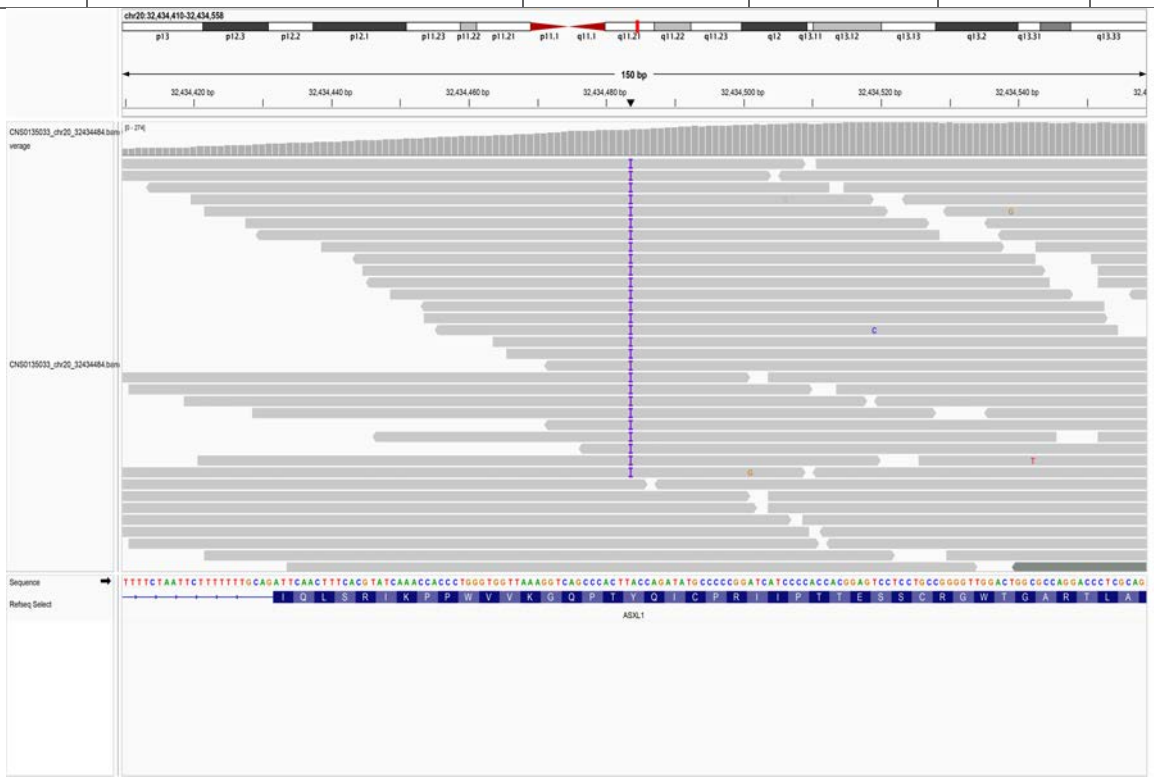
1.5. chr20_32434440_TTCACGTATCAAACCACCCTGGG/-

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



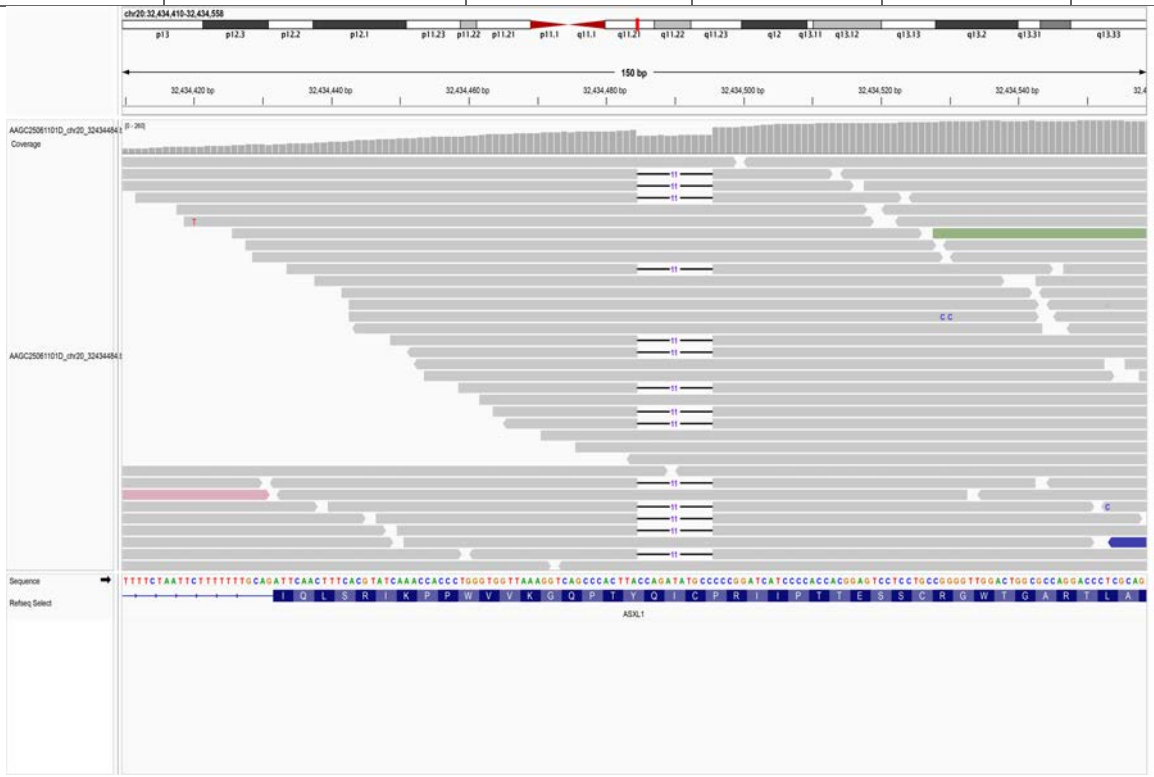
1.6. chr20_32434484_-/A

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



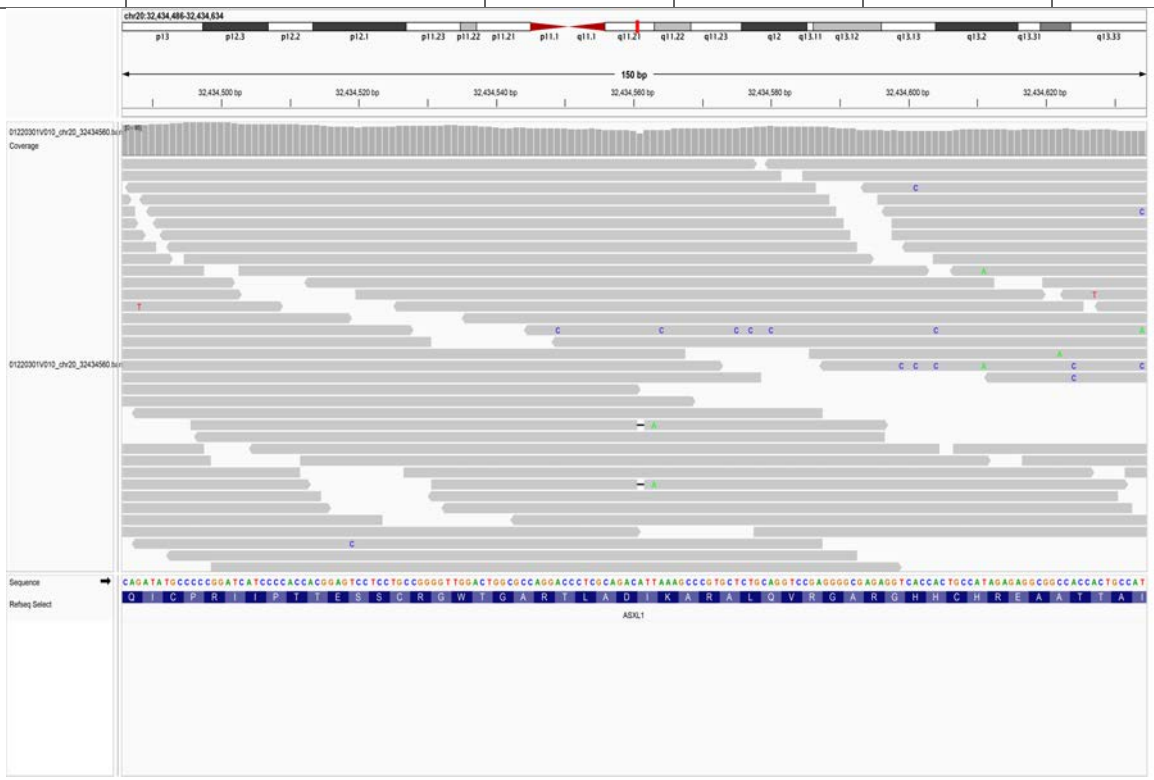
1.7. chr20_32434485_CCAGATATGCC/-

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



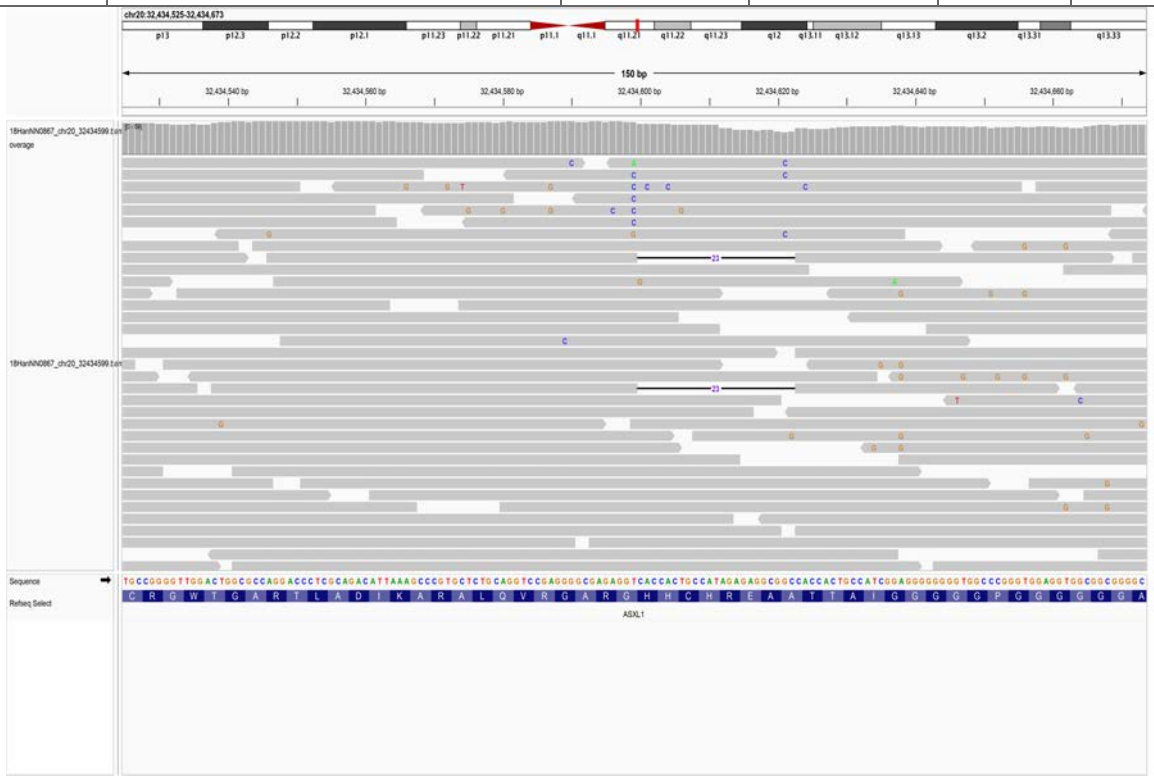
1.8. chr20_32434561_A/-

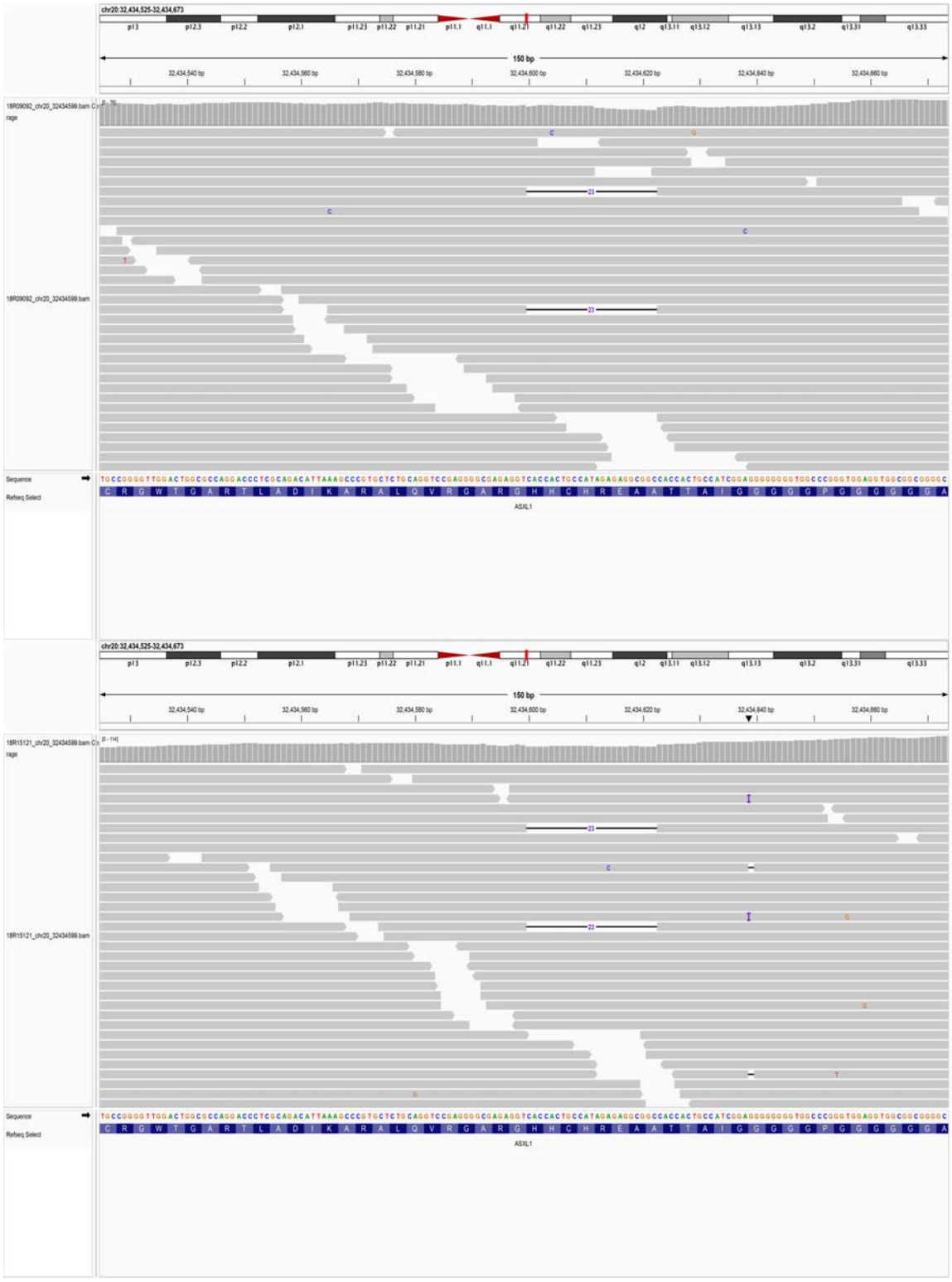
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
01220301V010	chr20_32434561_A/-	64	7	*ASXL1*	frameshift_variant



1.9. chr20_32434600_CACCACTGCCATAGAGAGGCGGC/-

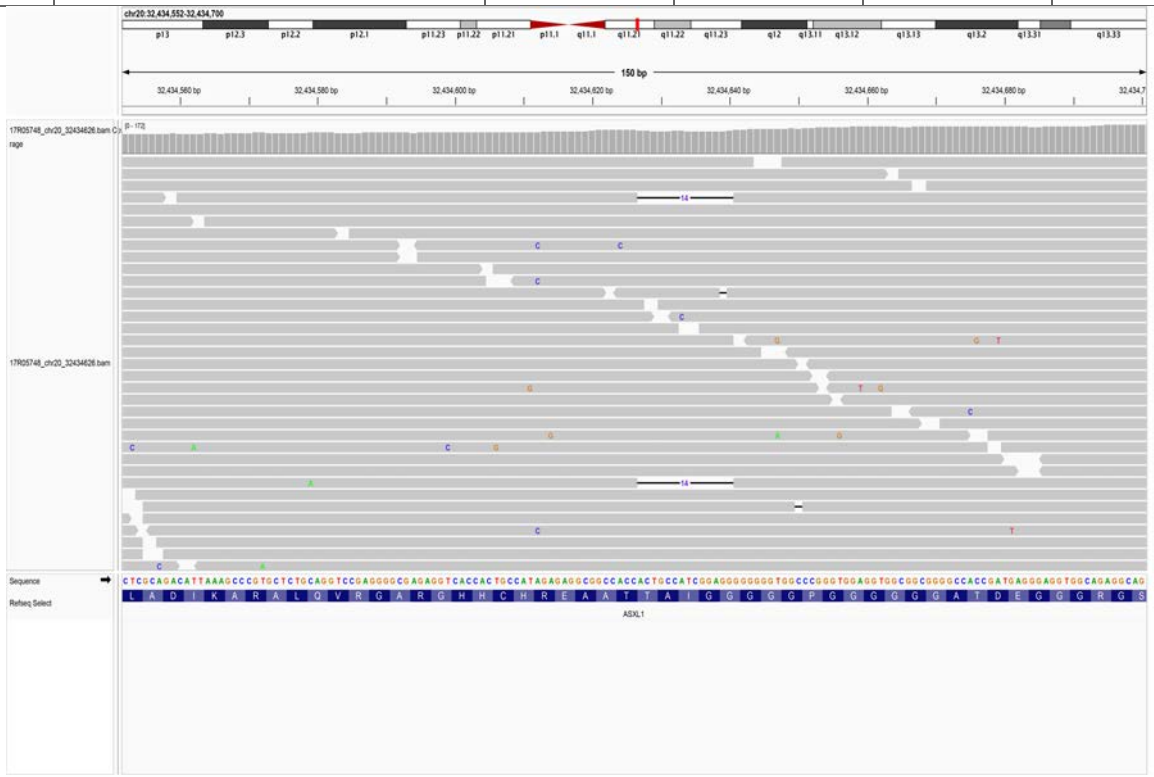
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0867	chr20_32434600_CACCACTGCCATAGAGAGGCGGC/-	45	11	*ASXL1*	frameshift_variant
18R09092	chr20_32434600_CACCACTGCCATAGAGAGGCGGC/-	50	13	*ASXL1*	frameshift_variant
18R15121	chr20_32434600_CACCACTGCCATAGAGAGGCGGC/-	68	9	*ASXL1*	frameshift_variant




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

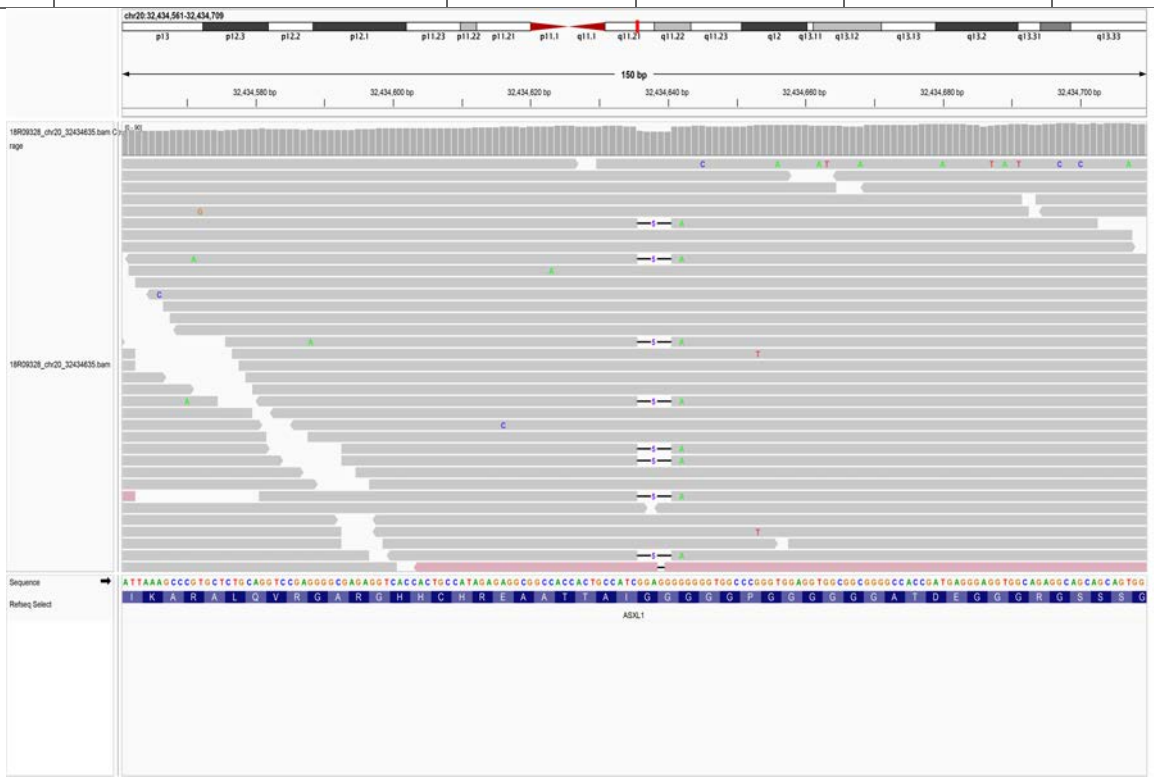
1.10. chr20_32434627_ACTGCCATCGGAGG/-

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



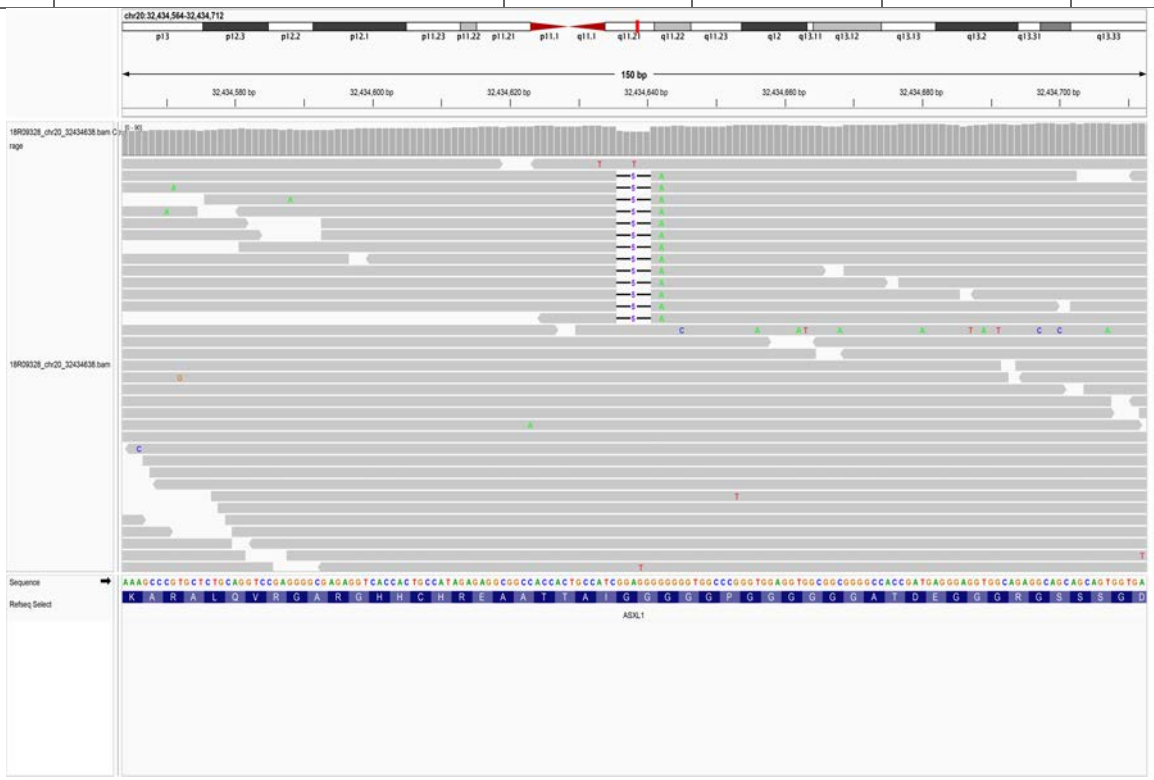
1.11. chr20_32434636_G/-

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



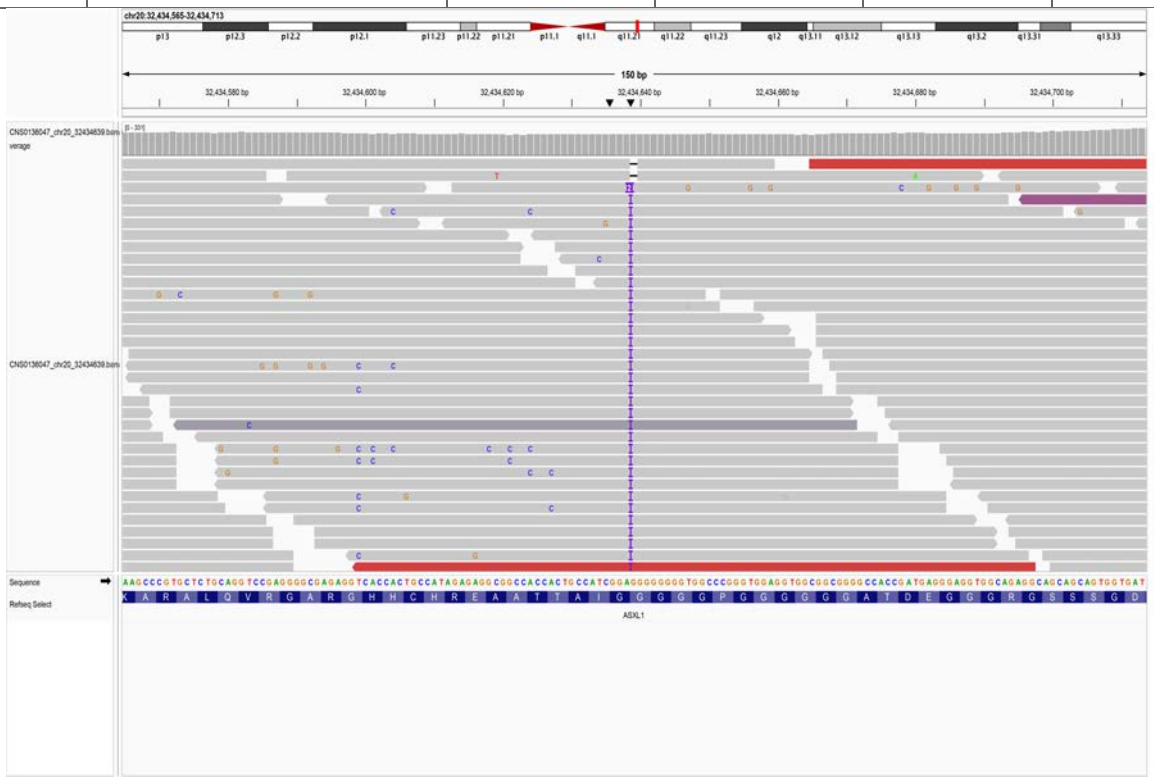
1.12. chr20_32434639_GGGG/-

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



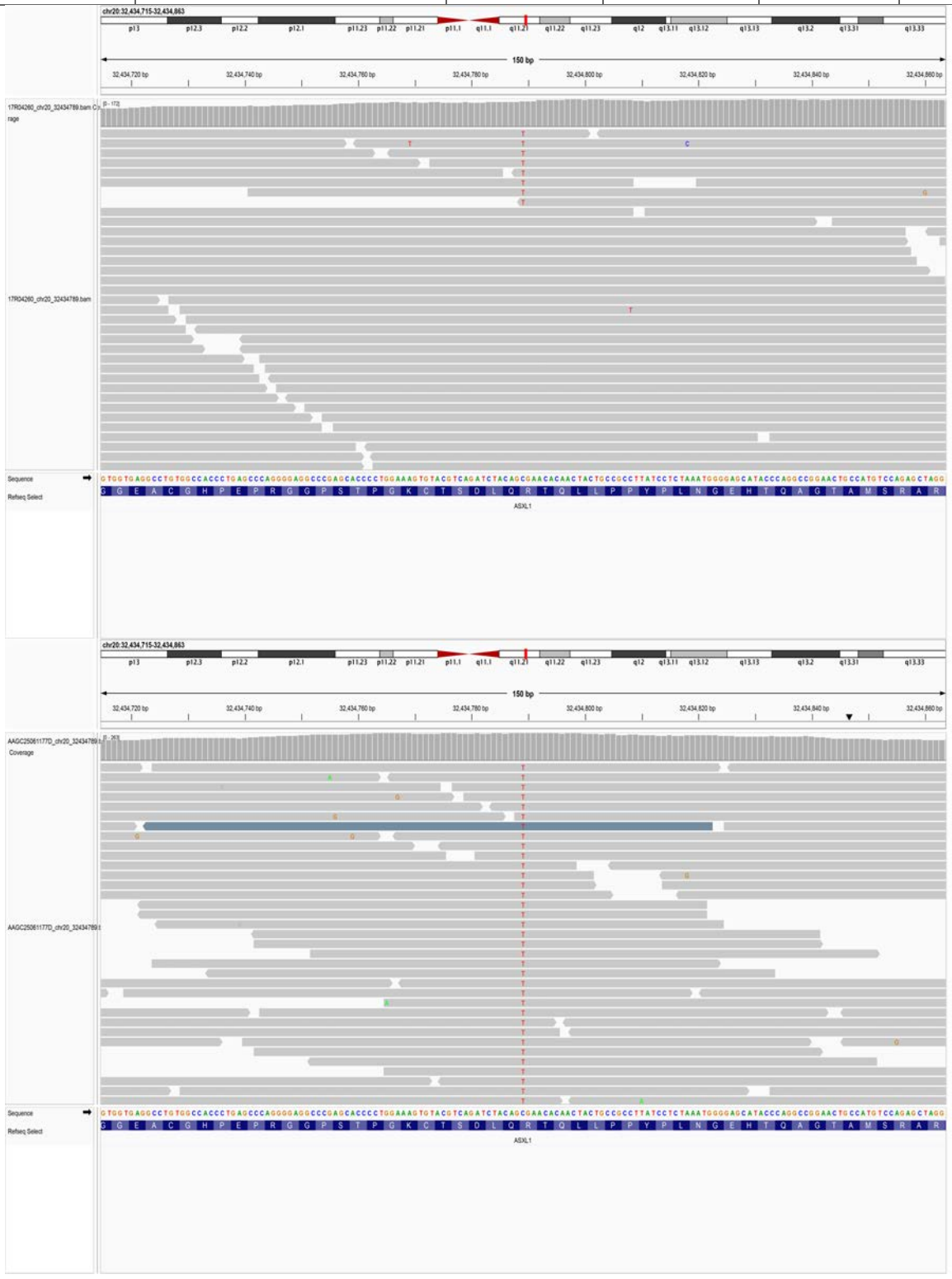
1.13. chr20_32434639_-/G

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



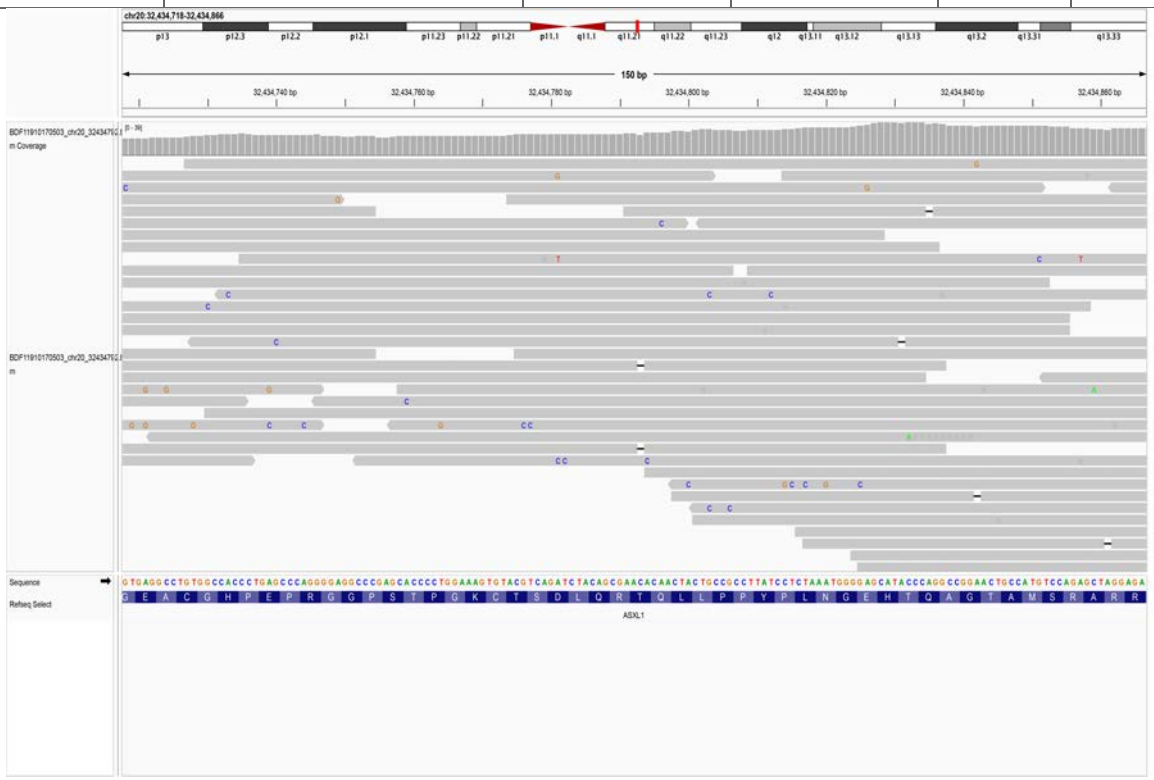
1.14. chr20_32434789_C/T

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



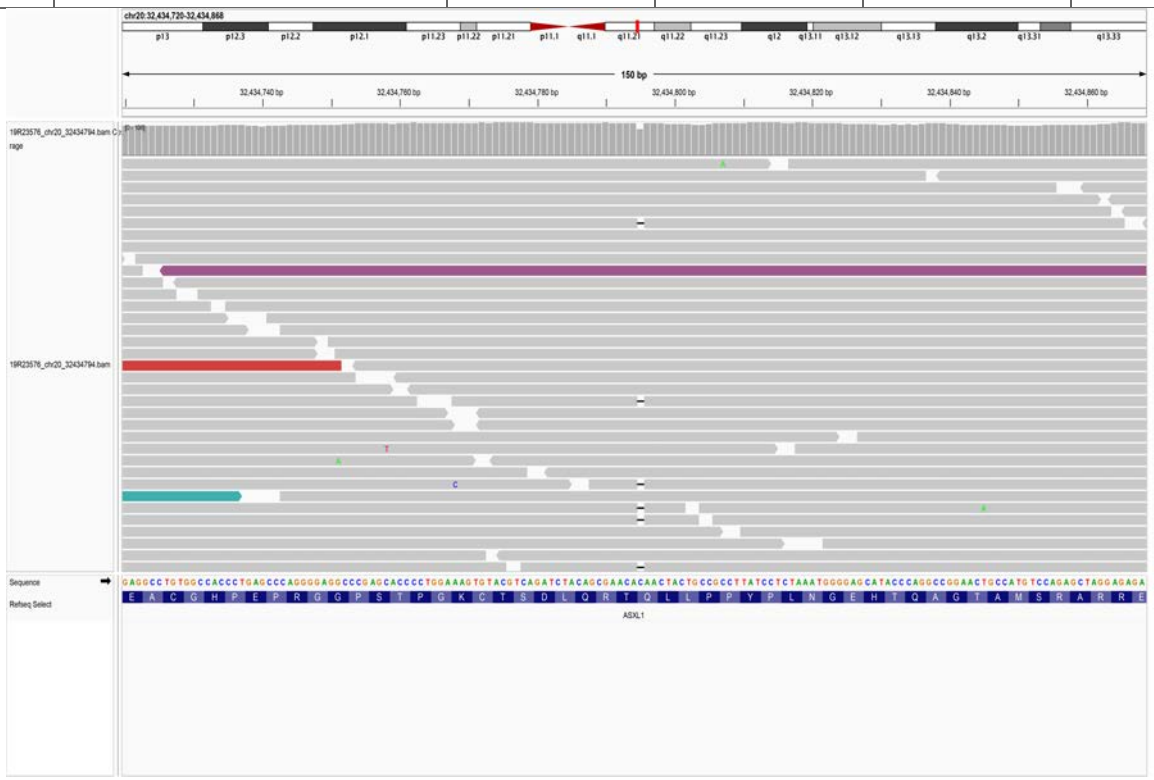
1.15. chr20_32434793_C/-

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



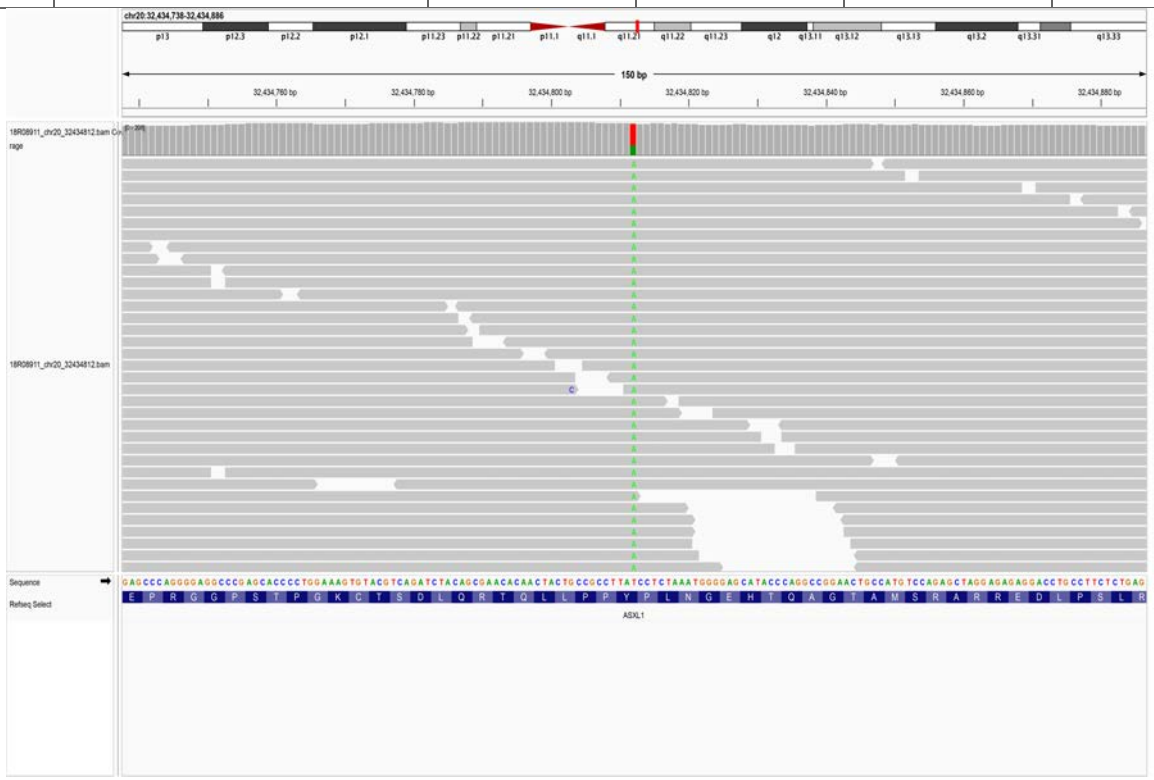
1.16. chr20_32434795_C/-

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



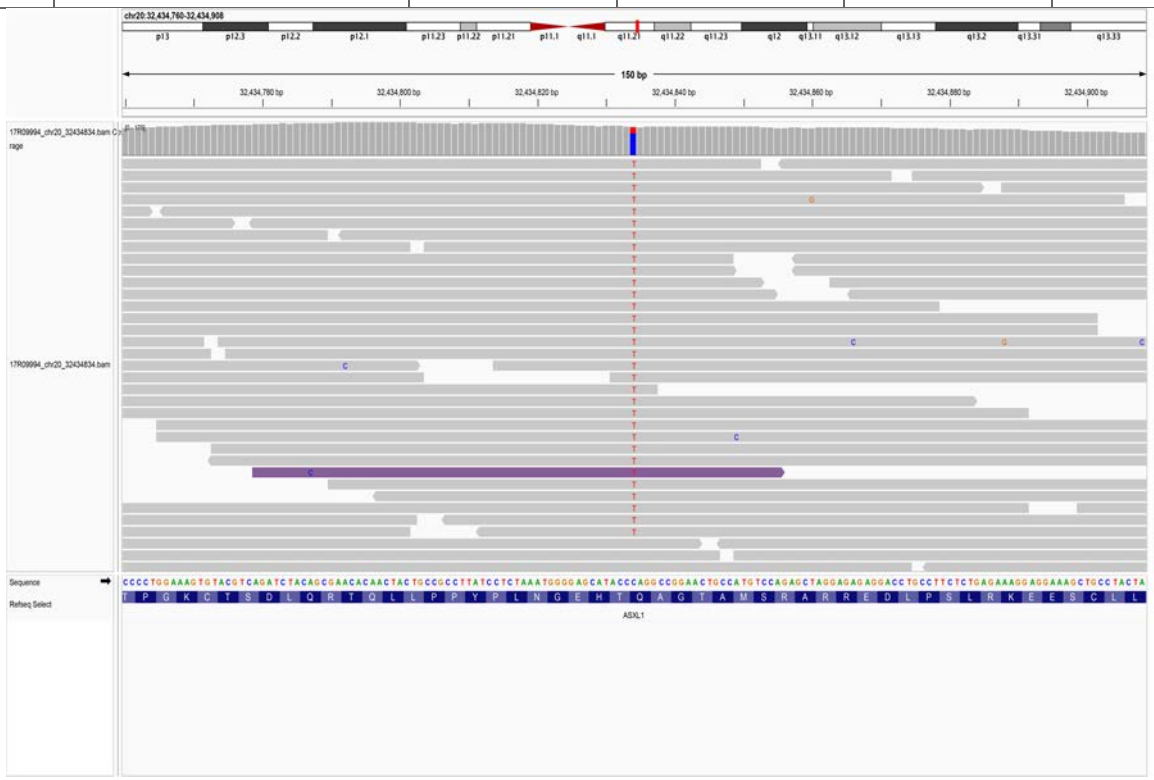
1.17. chr20_32434812_T/A

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



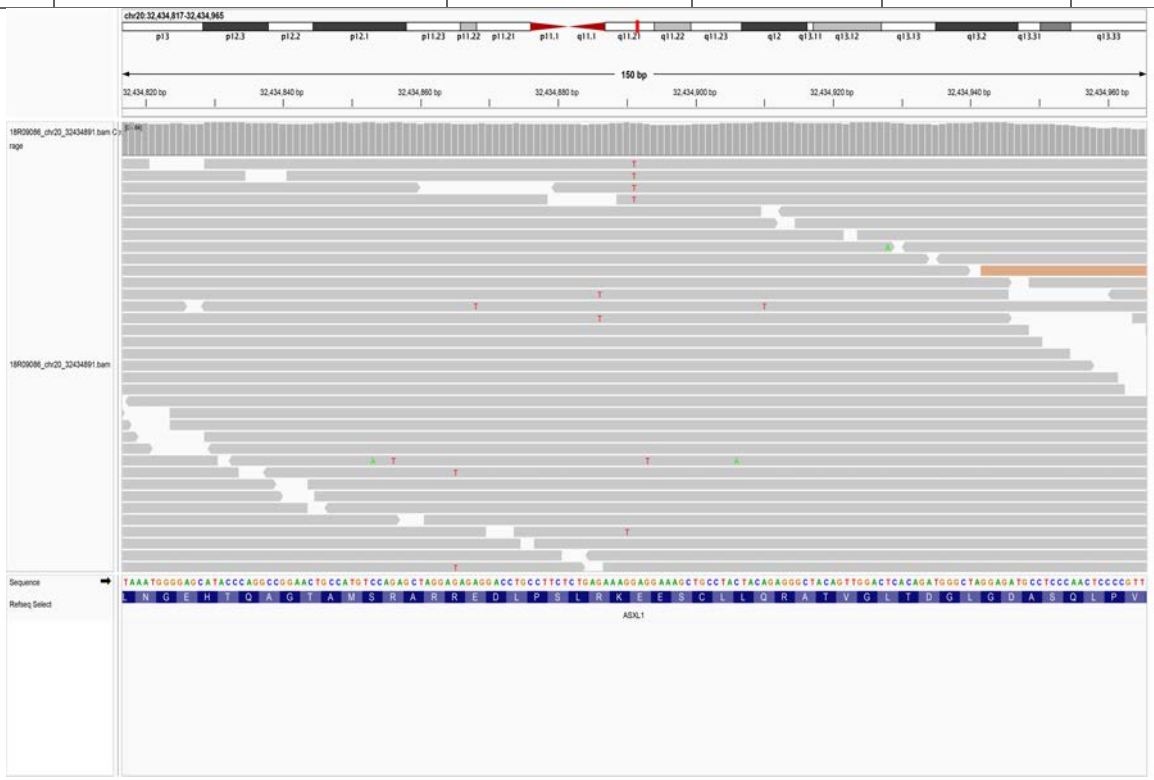
1.18. chr20_32434834_C/T

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



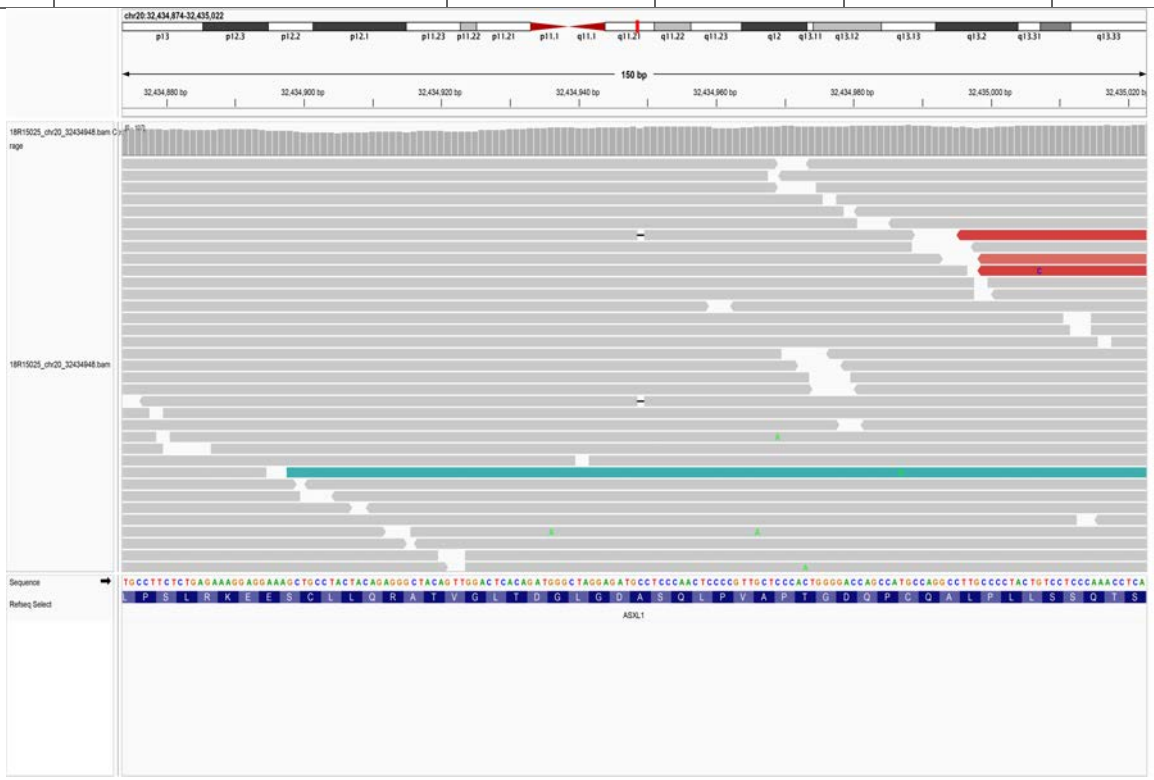
1.19. chr20_32434891_G/T

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



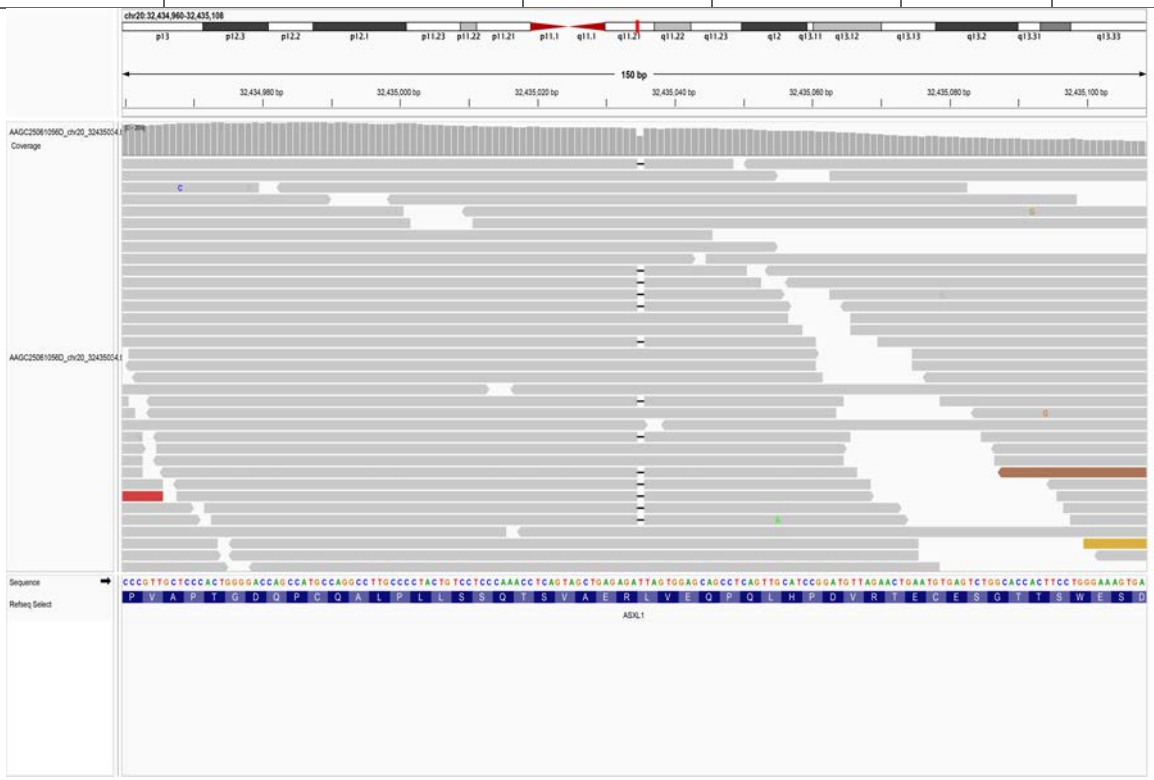
1.20. chr20_32434949_C/-

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



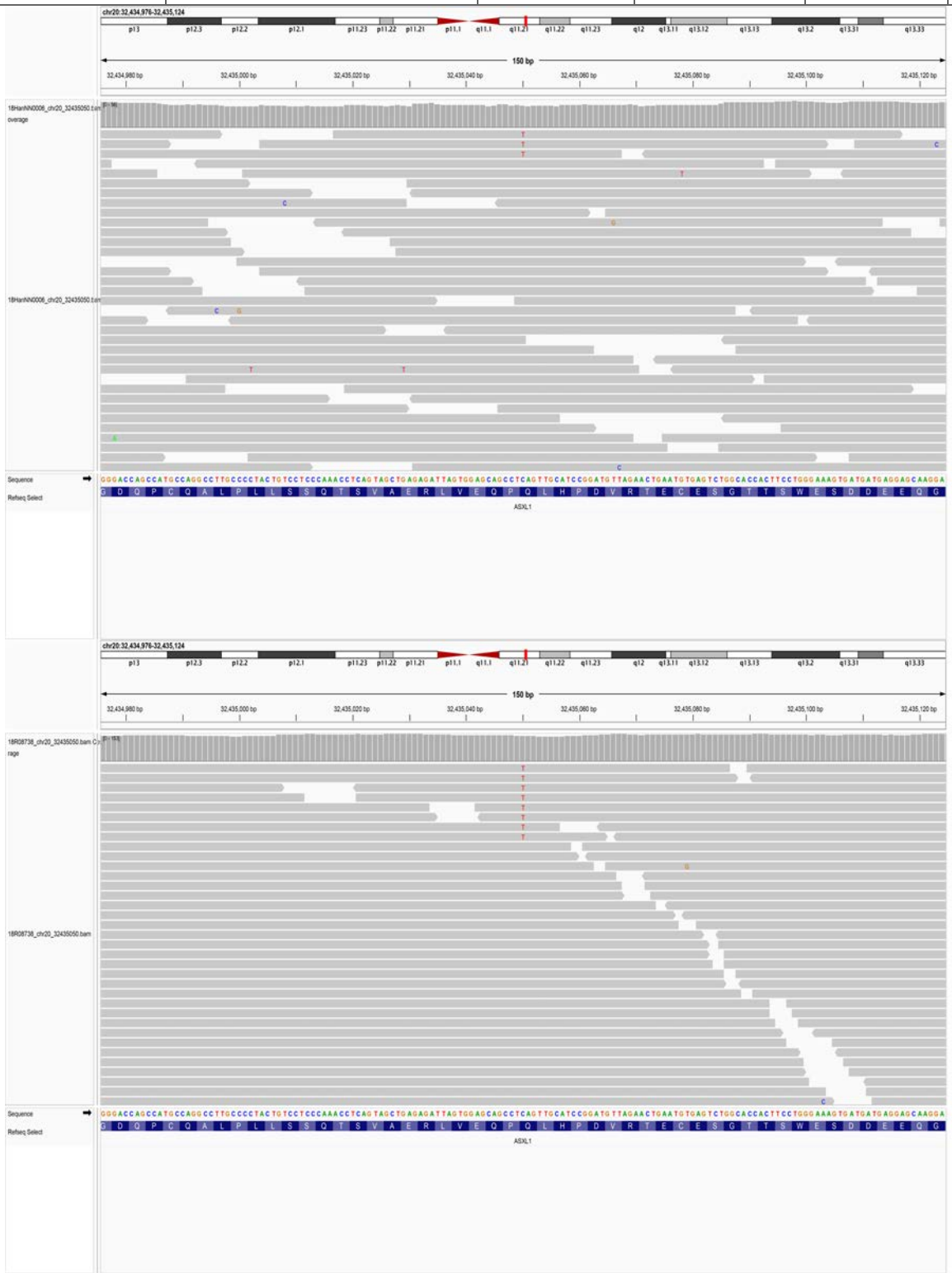
1.21. chr20_32435035_T/-

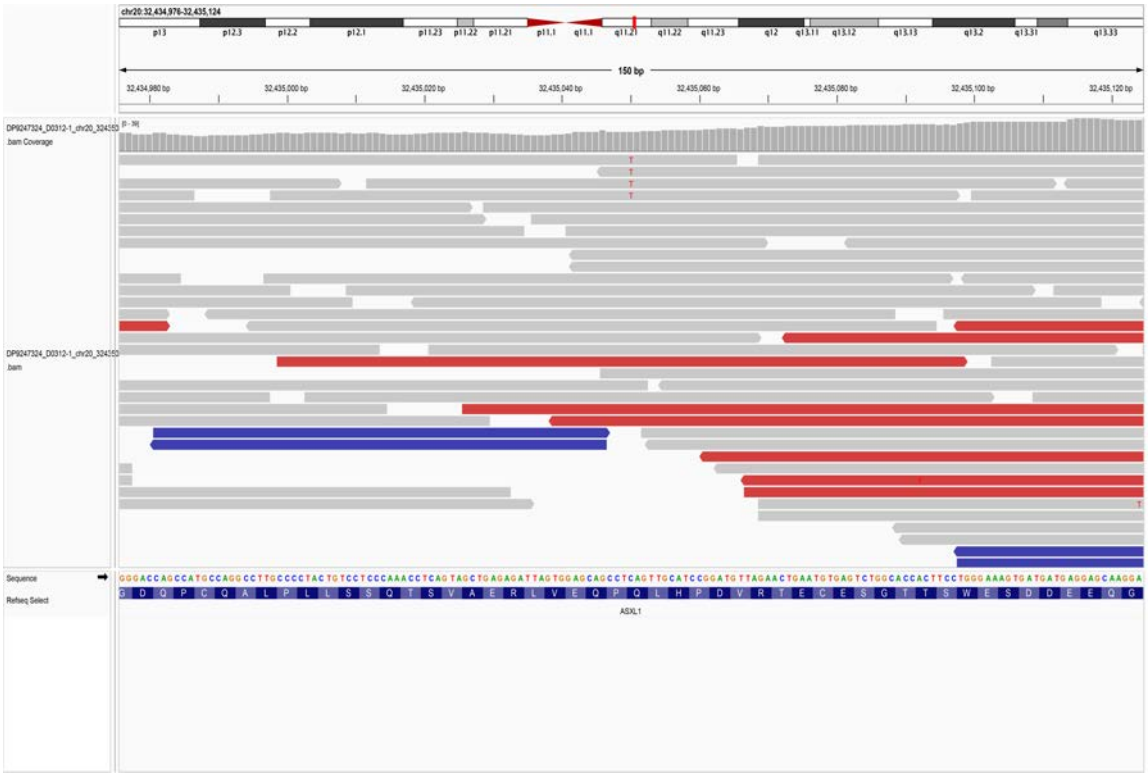
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061056D	chr20_32435035_T/-	117	49	*ASXL1*	frameshift_variant



1.22. chr20_32435050_C/T

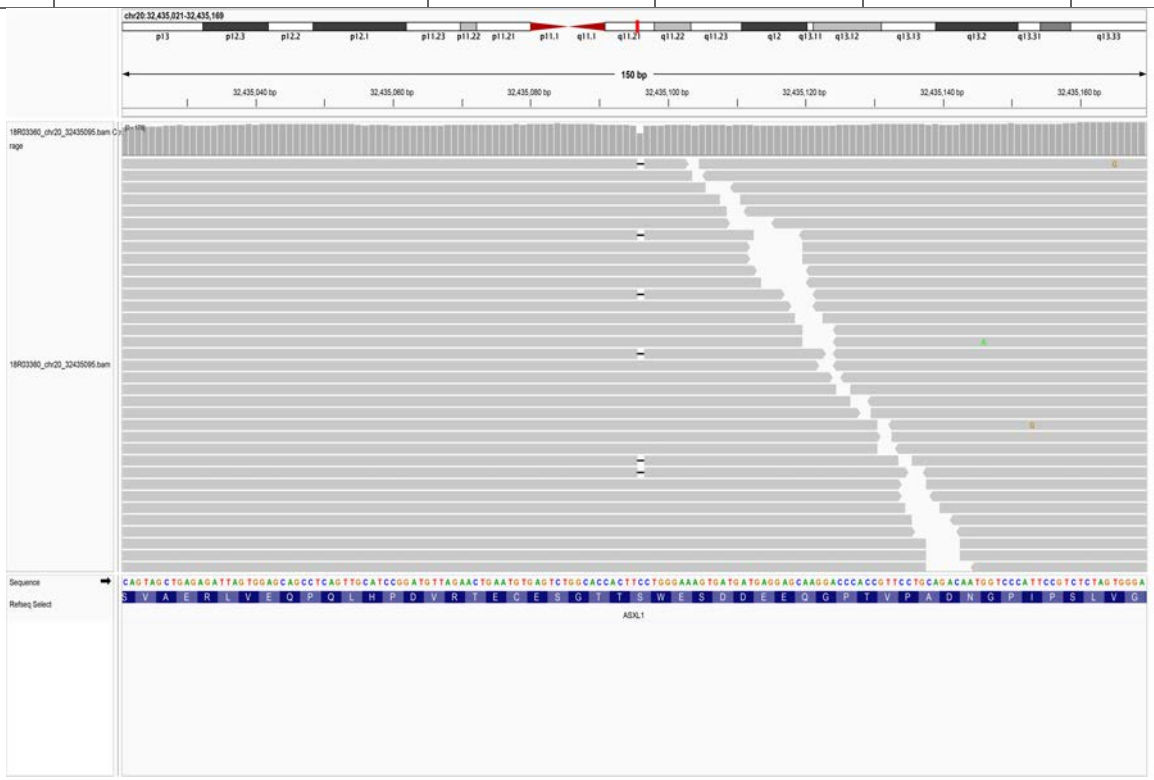
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0006	chr20_32435050_C/T	41	3	*ASXL1*	stop_gained
18R08738	chr20_32435050_C/T	130	8	*ASXL1*	stop_gained
DP9247324_D0312-1	chr20_32435050_C/T	19	4	*ASXL1*	stop_gained




chr20:32,434,976-32,435,124
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
.bam Coverage
.bam
Sequence
Refseq Select
ASXL1

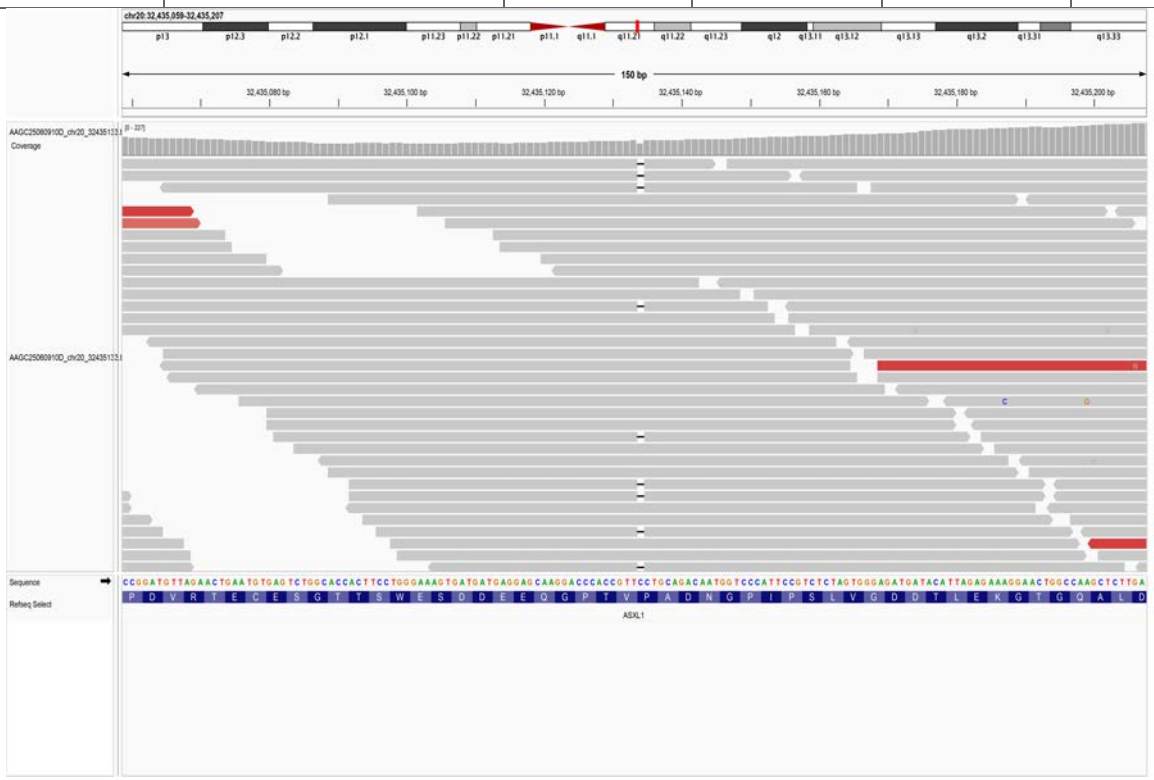
1.23. chr20_32435096_C/-

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



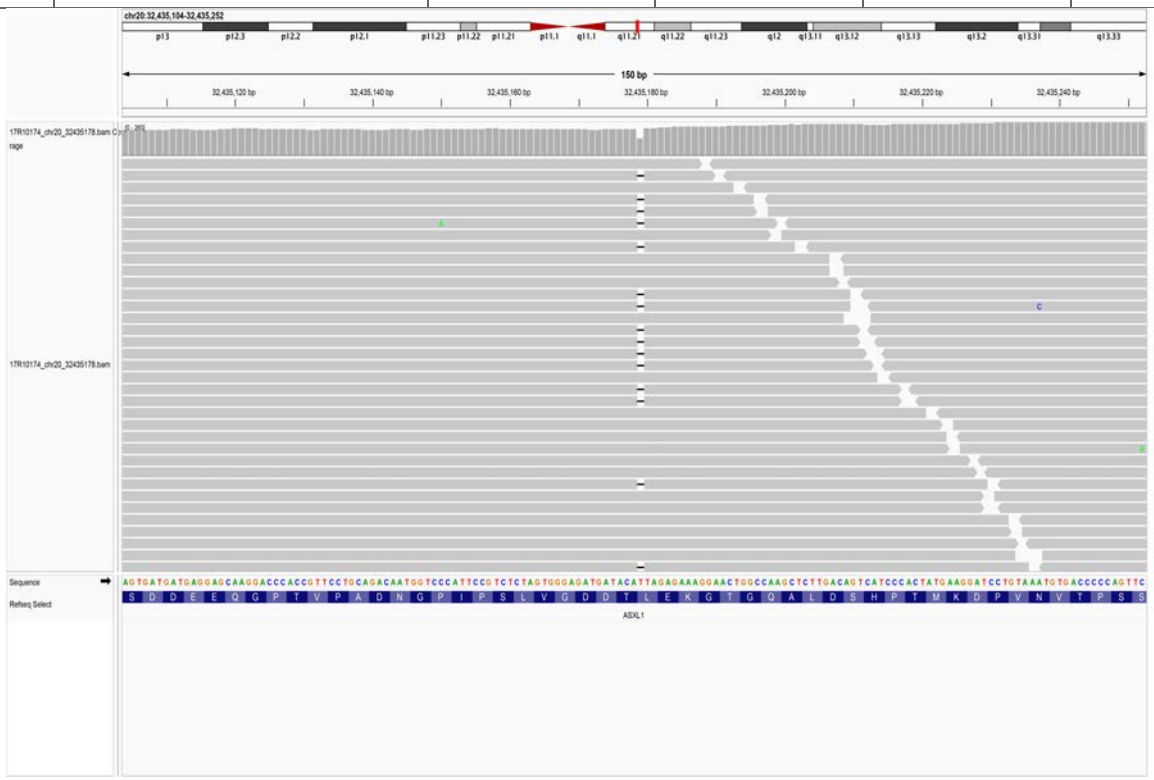
1.24. chr20_32435134_C/-

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



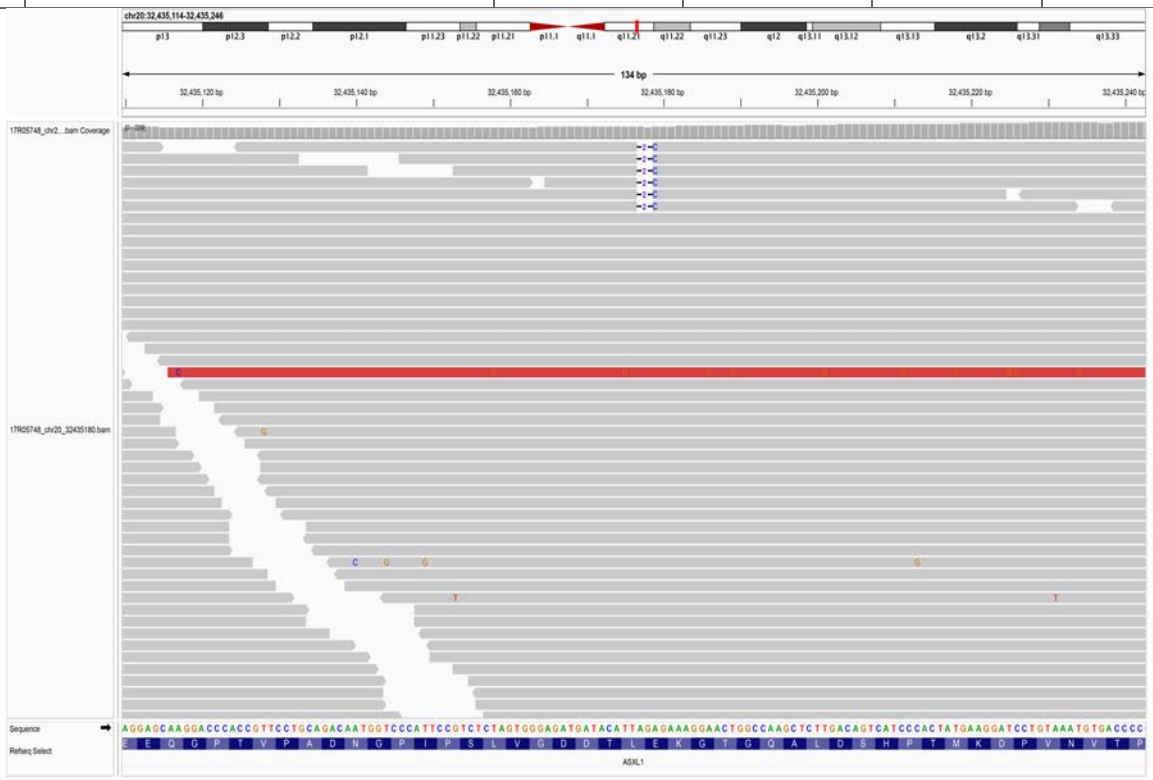
1.25. chr20_32435179_T/-

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



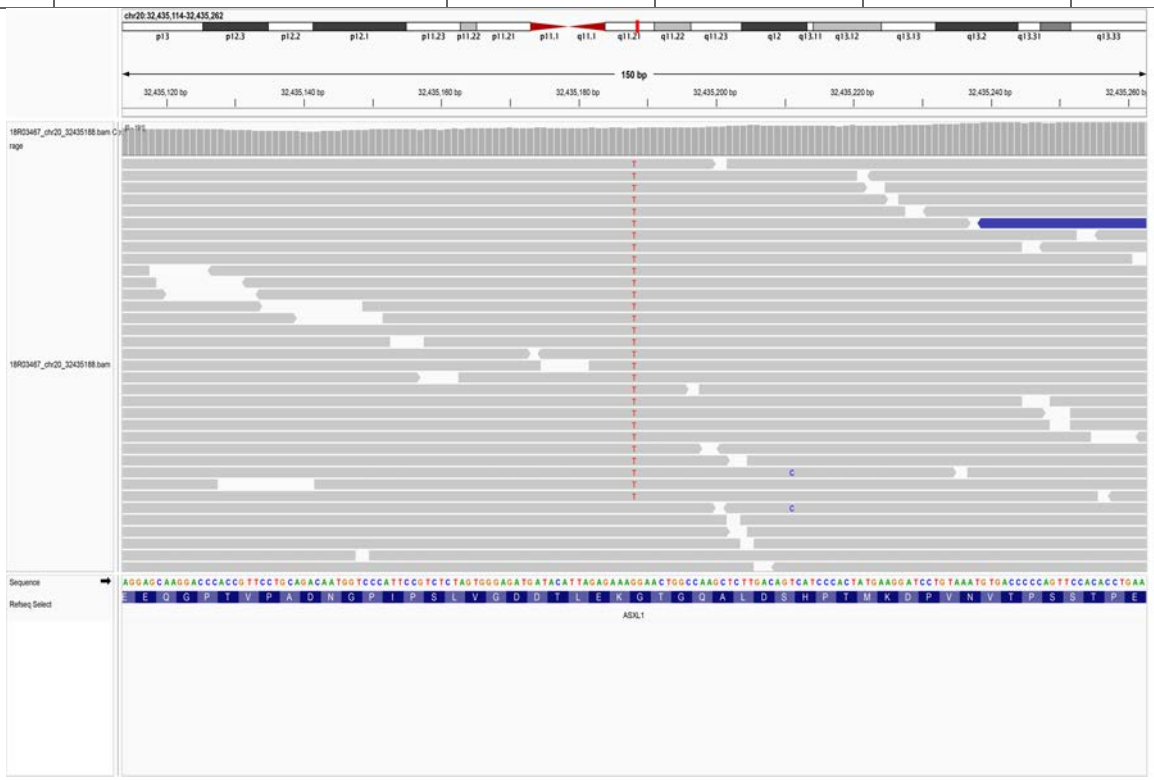
1.26. chr20_32435181_AG/-/AGAG

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



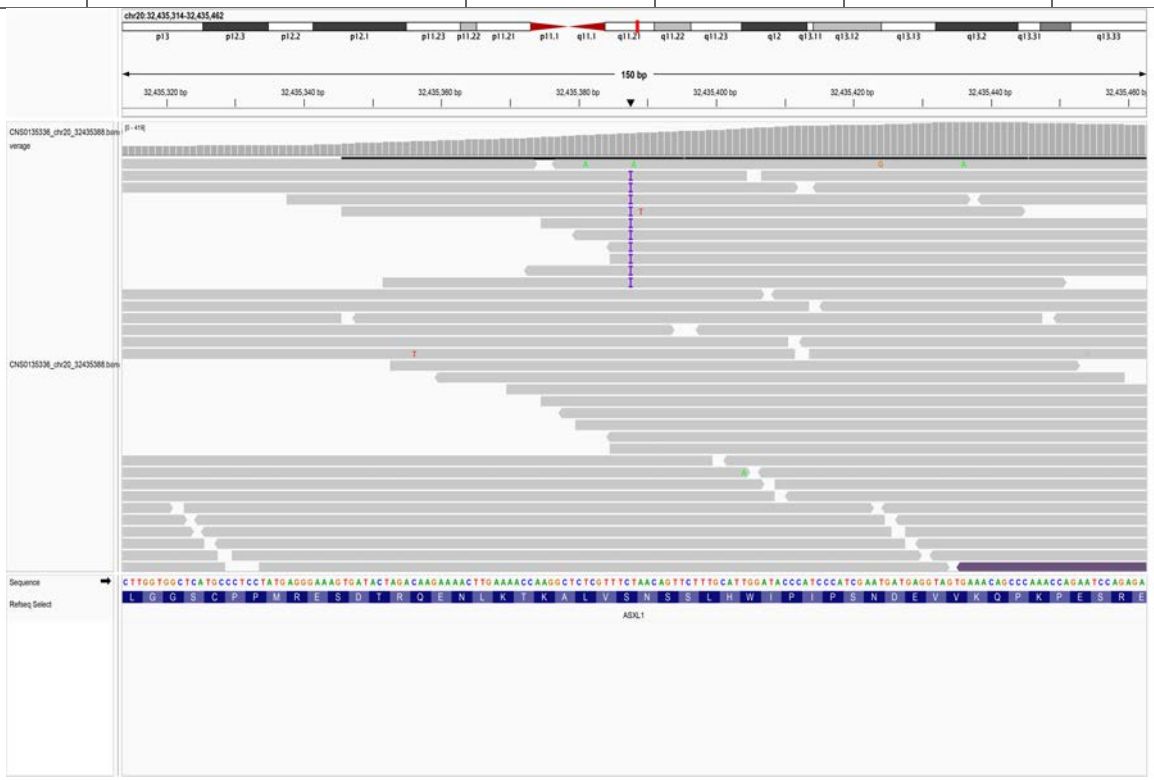
1.27. chr20_32435188_G/T

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



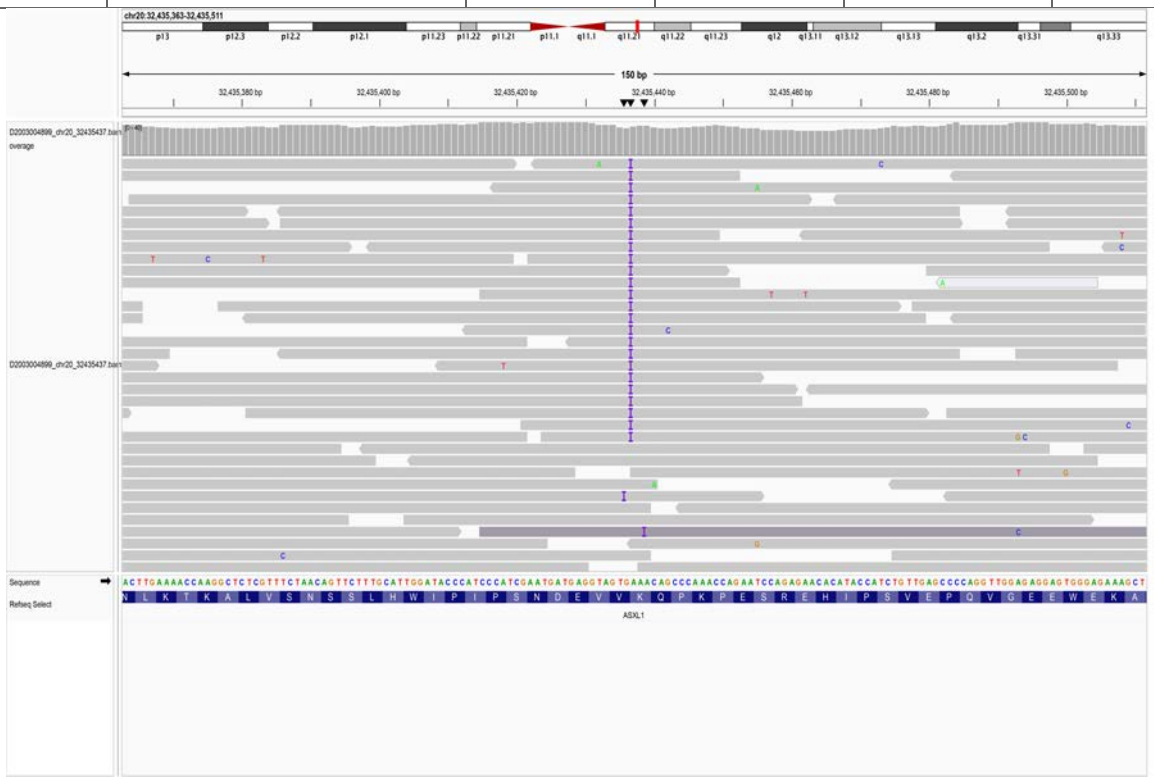
1.28. chr20_32435388_-/T

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



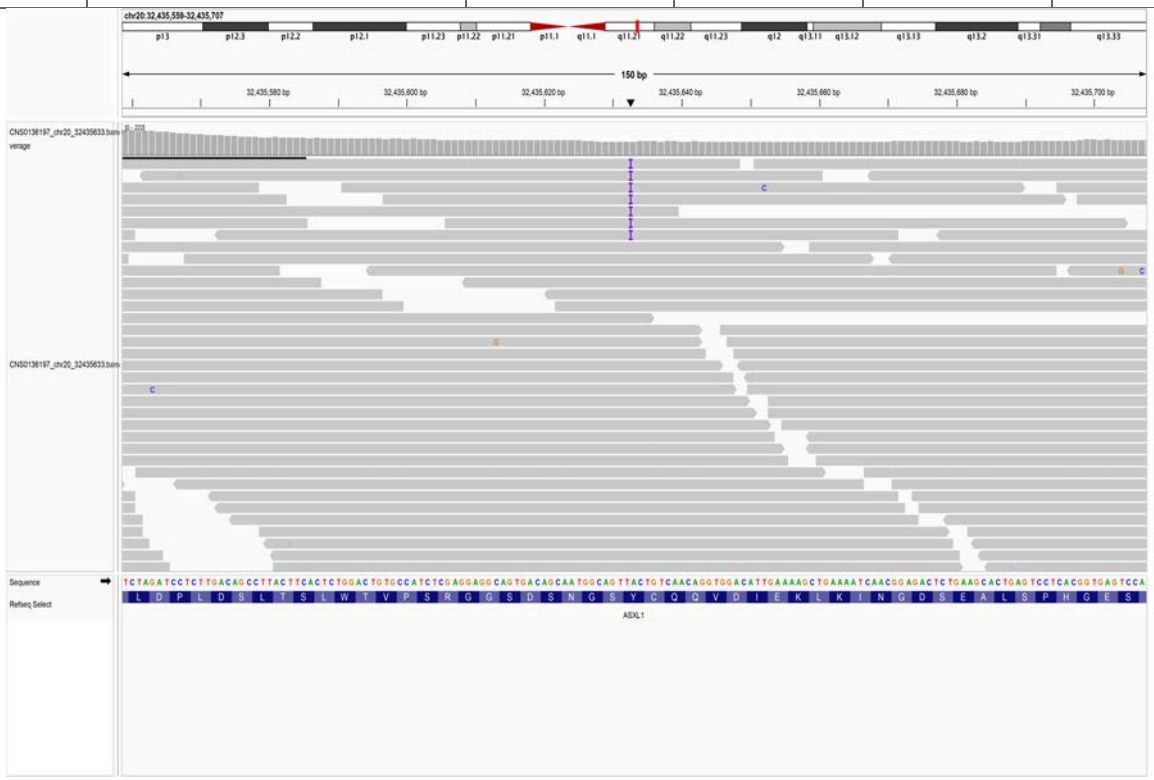
1.29. chr20_32435437_-/A

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



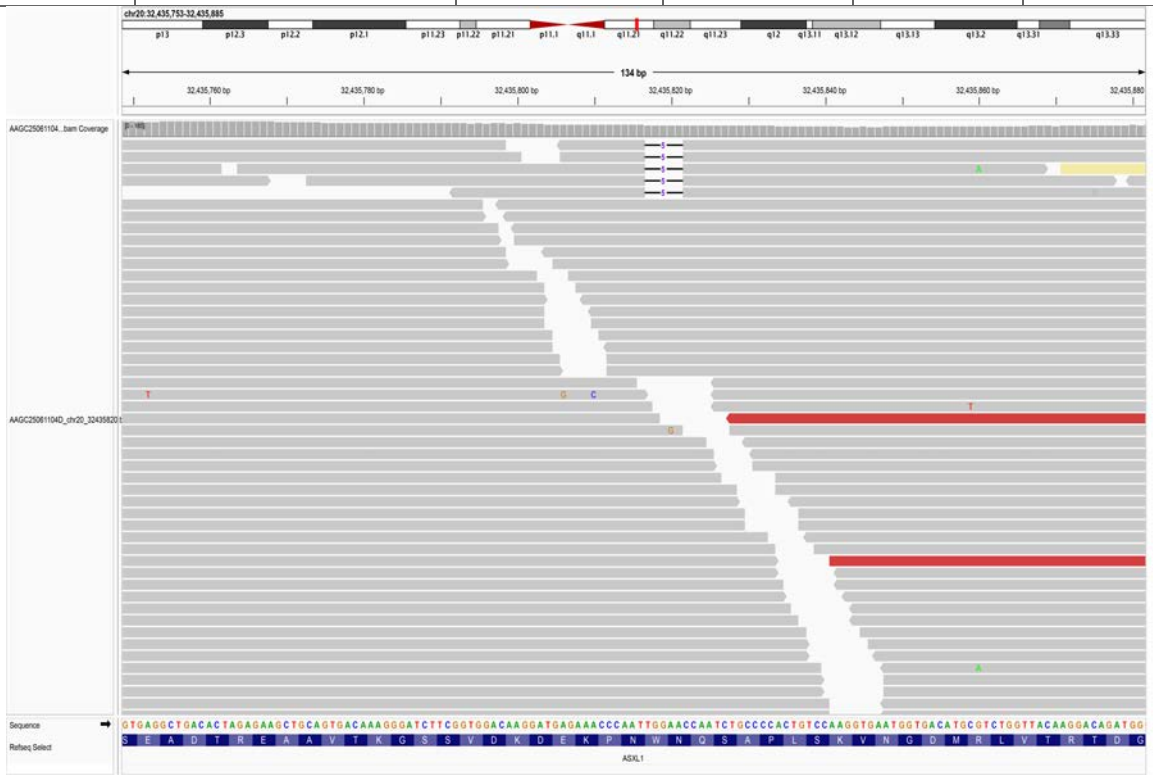
1.30. chr20_32435633_-/A

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



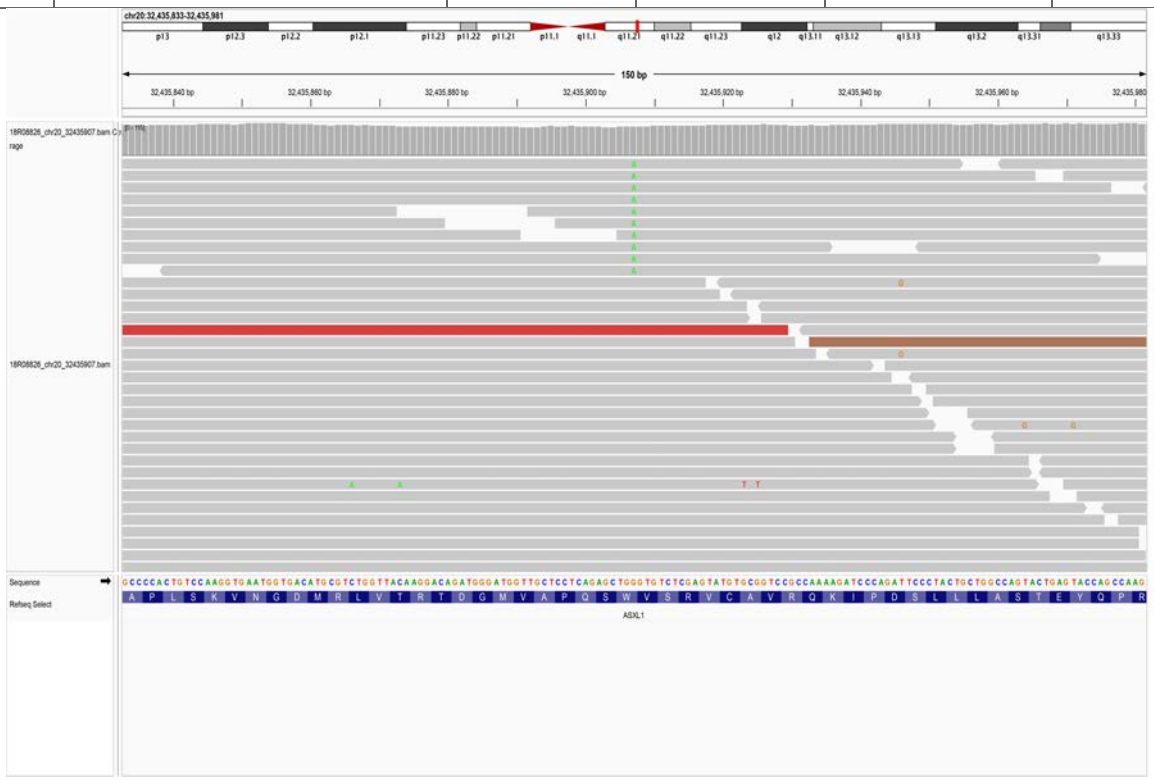
1.31. chr20_32435821_TGGAA/-

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



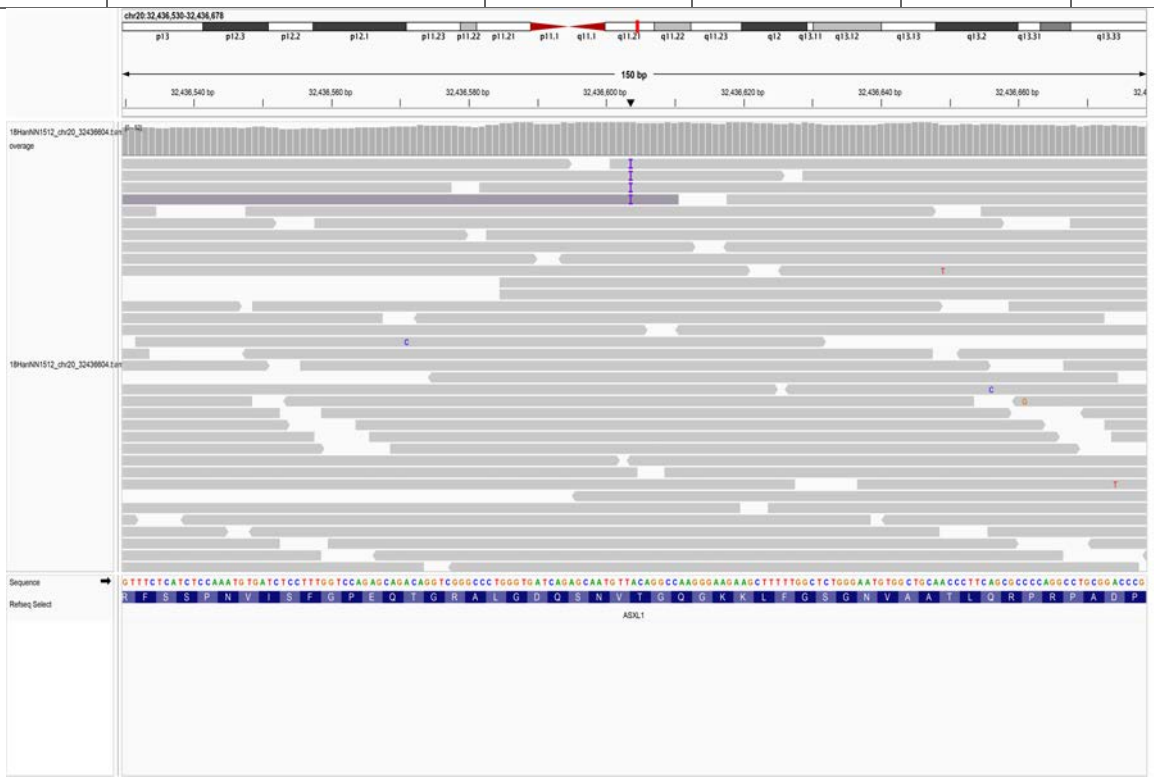
1.32. chr20_32435907_G/A

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



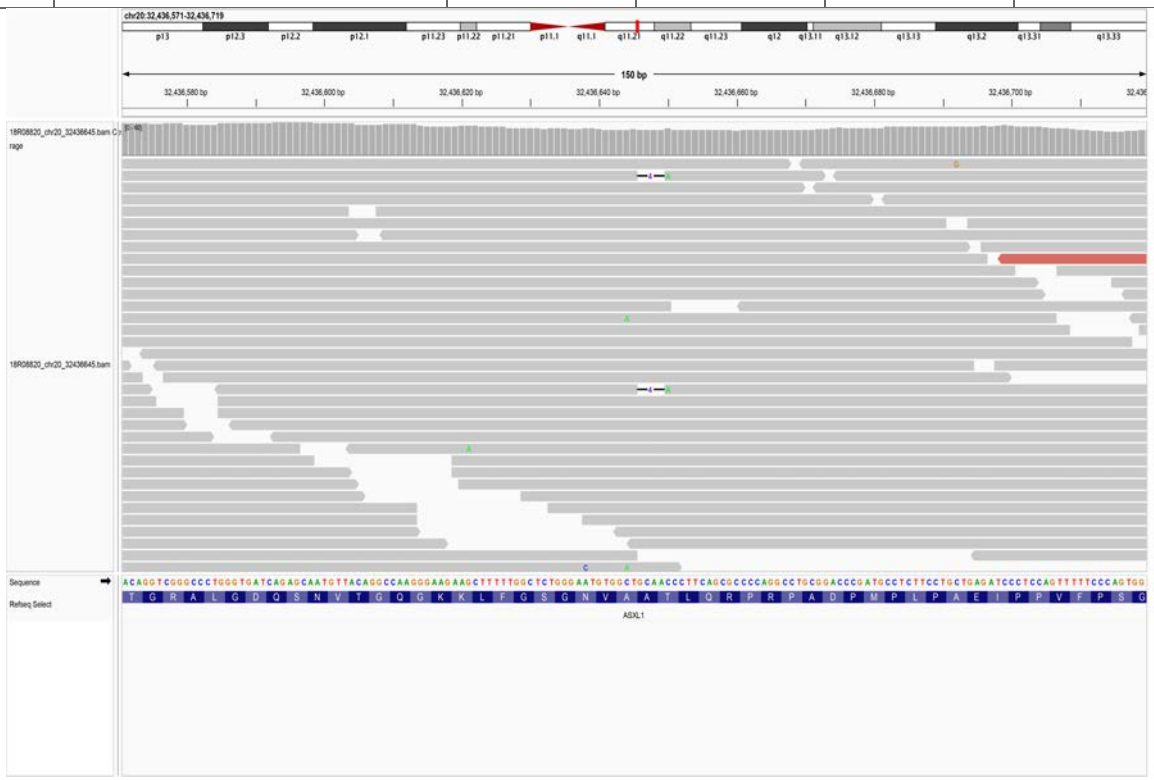
1.33. chr20_32436604_-/A

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



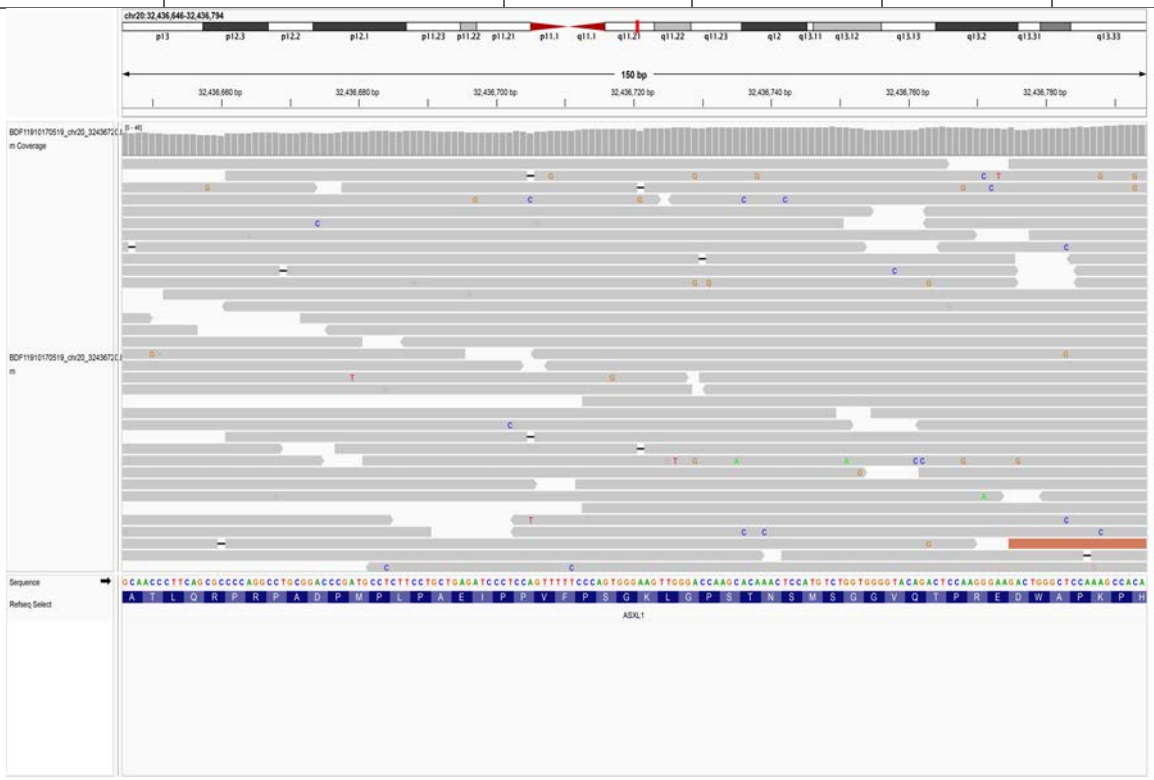
1.34. chr20_32436646_GC/-

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



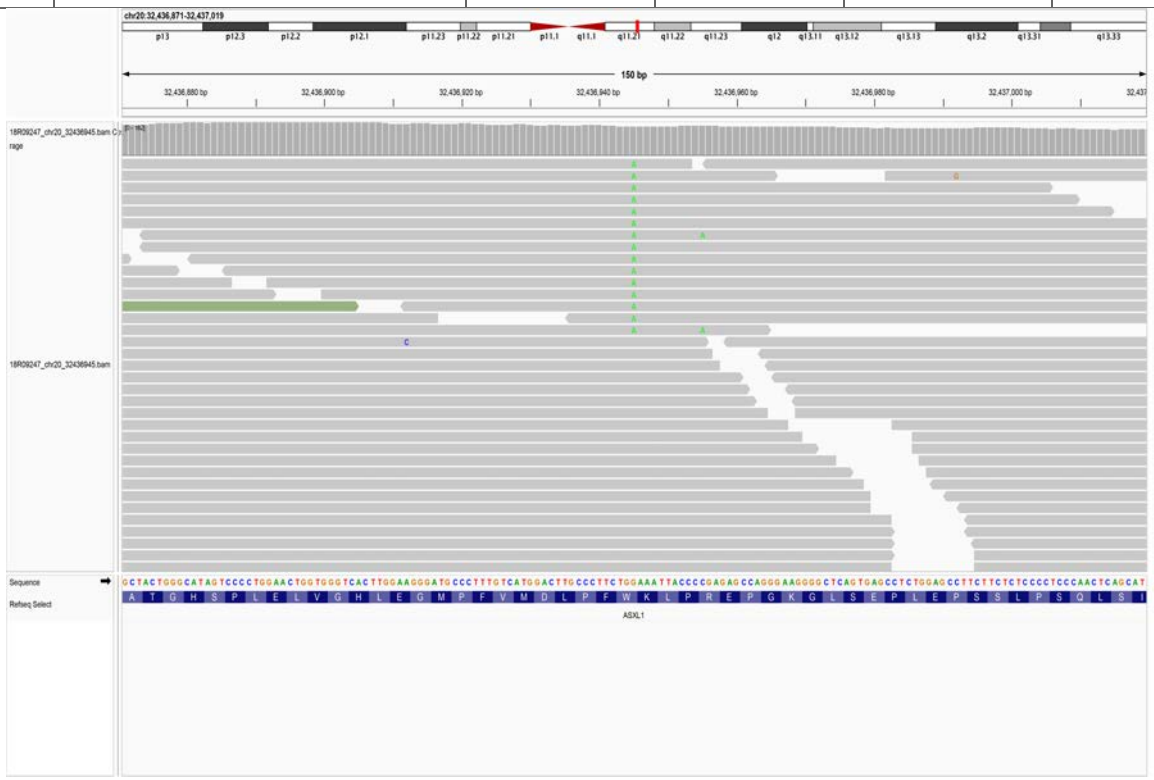
1.35. chr20_32436721_A/-

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



1.36. chr20_32436945_G/A

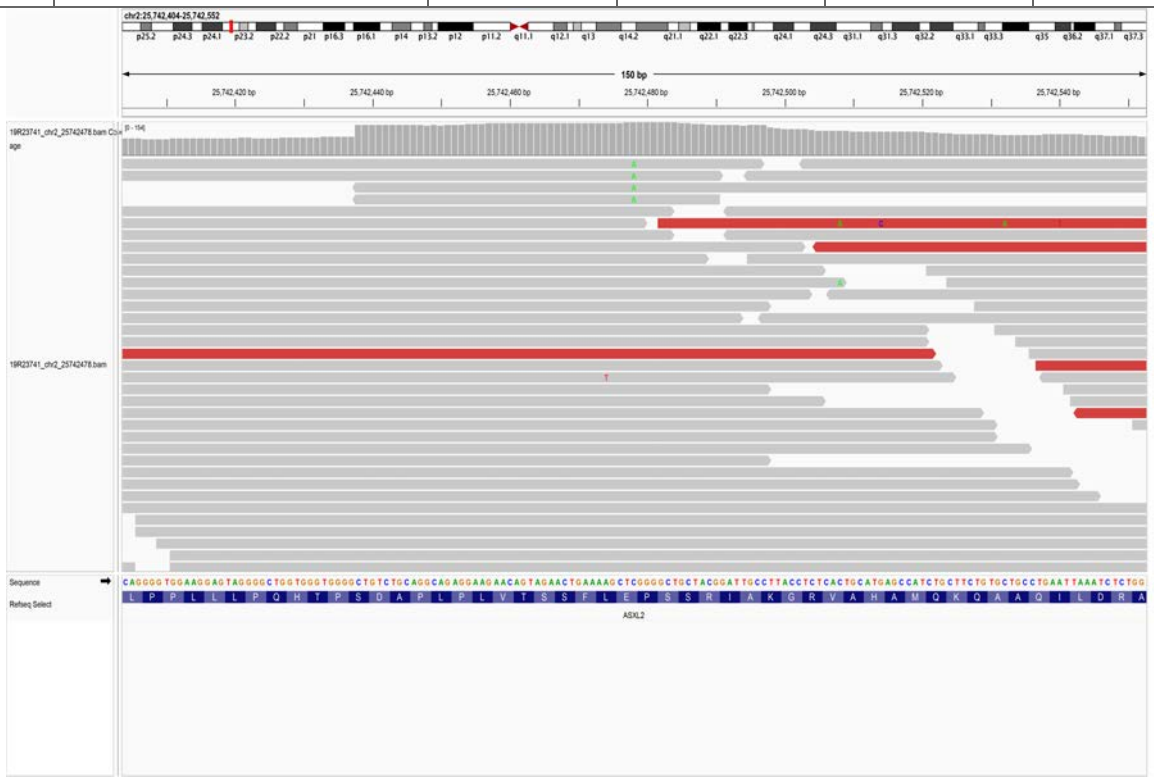
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09247	chr20_32436945_G/A	123	15	*ASXL1*	stop_gained



2. *ASXL2*

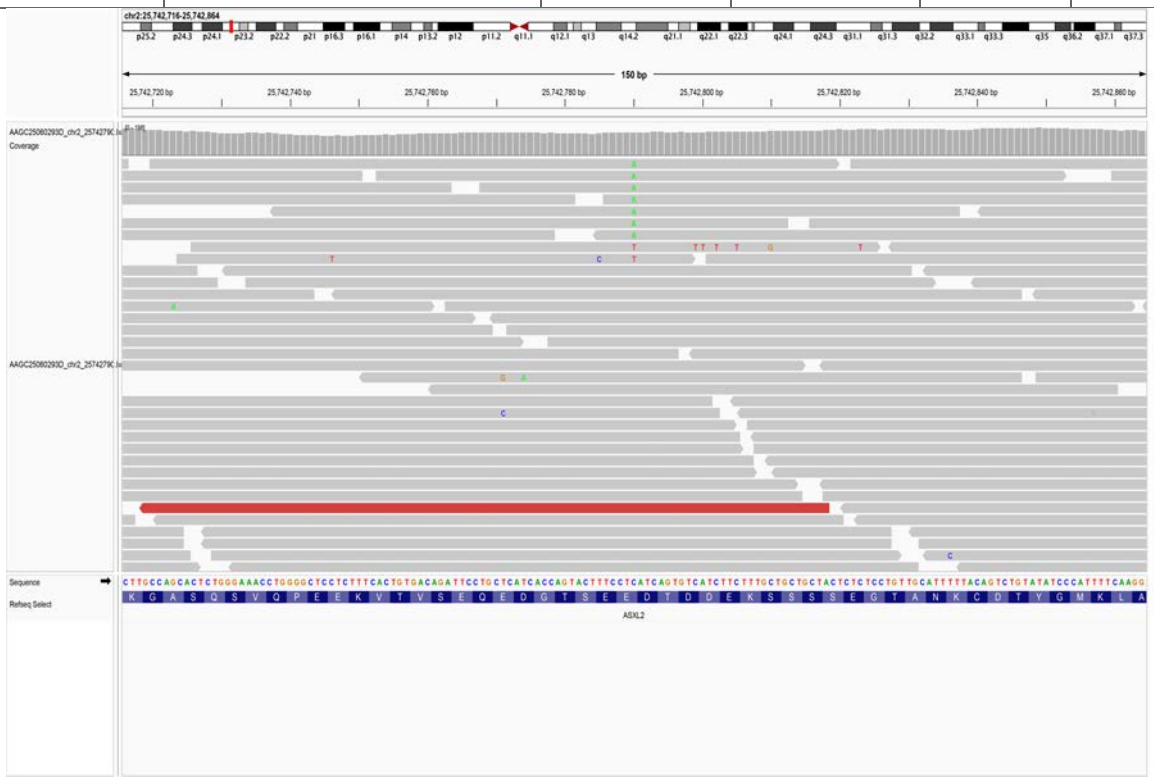
2.1. chr2_25742478_C/A

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



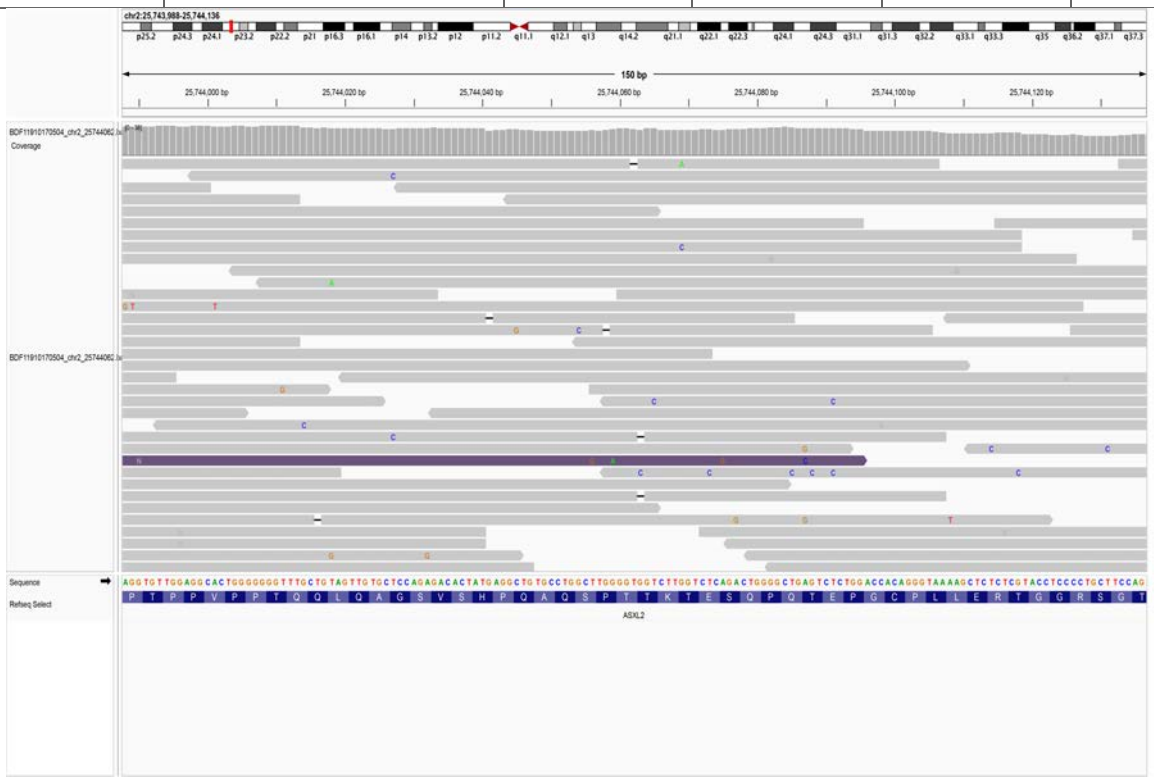
2.2. chr2_25742790_C/A

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



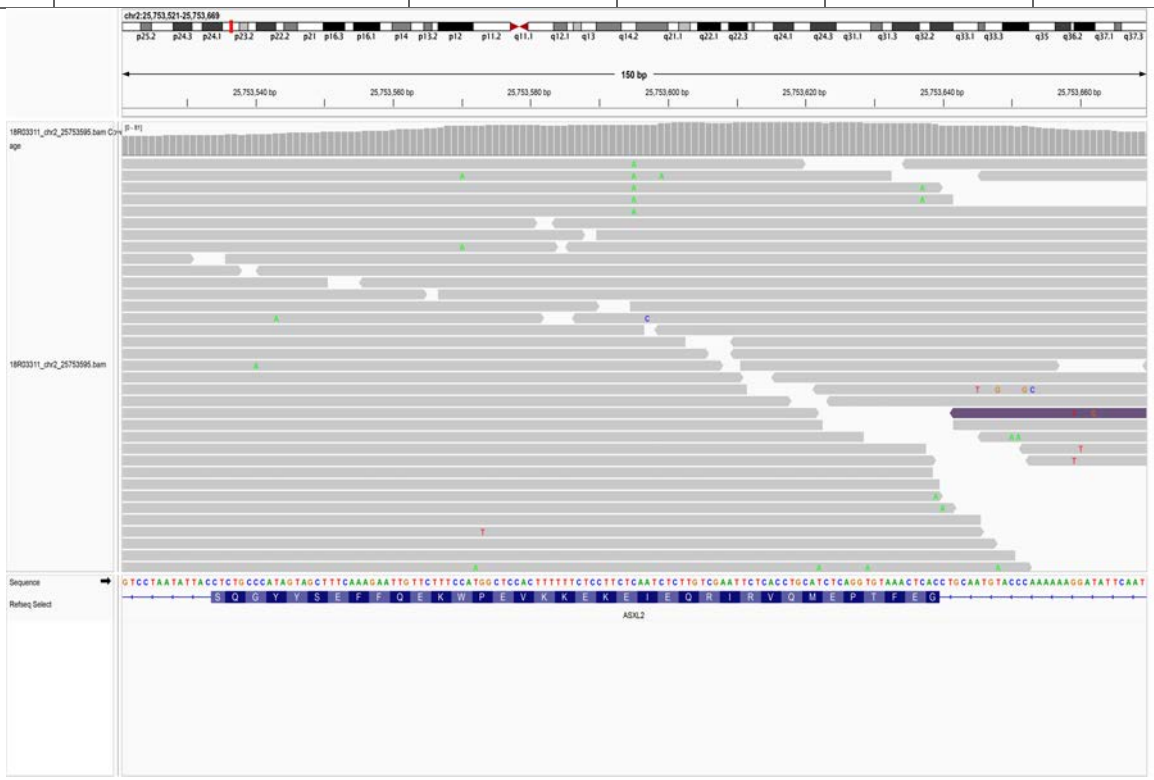
2.3. chr2_25744063_G/-

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



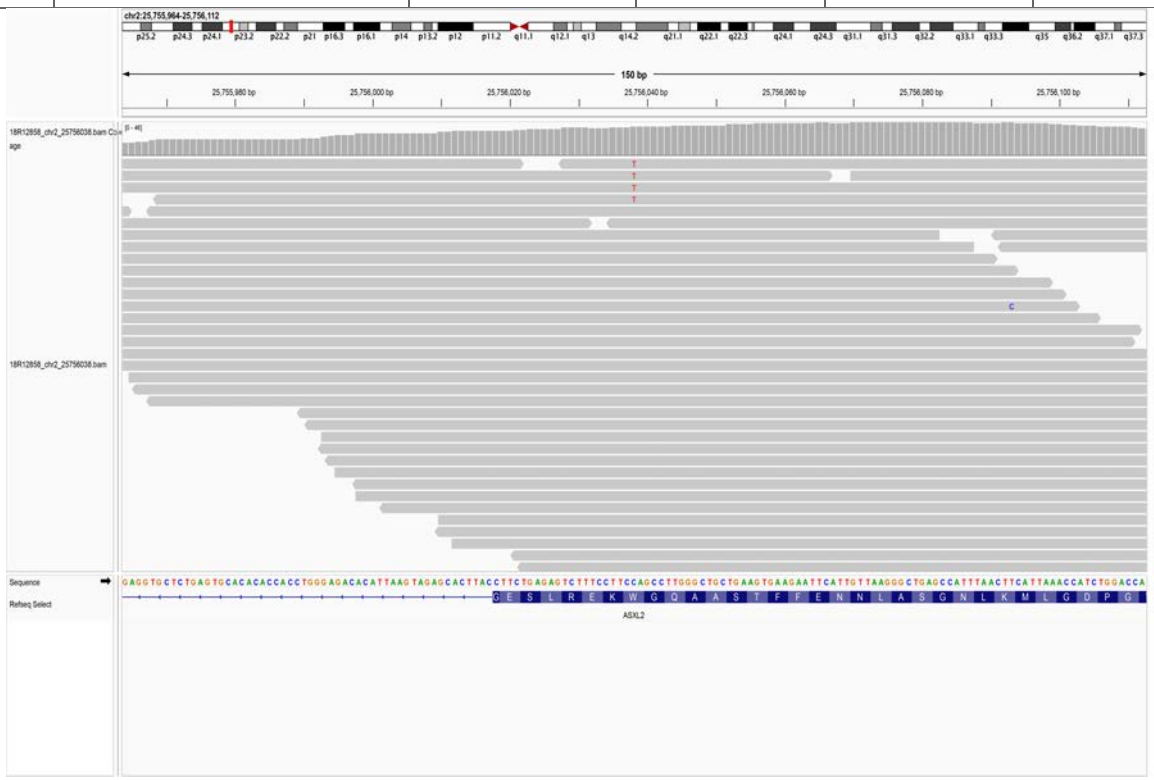
2.4. chr2_25753595_C/A

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



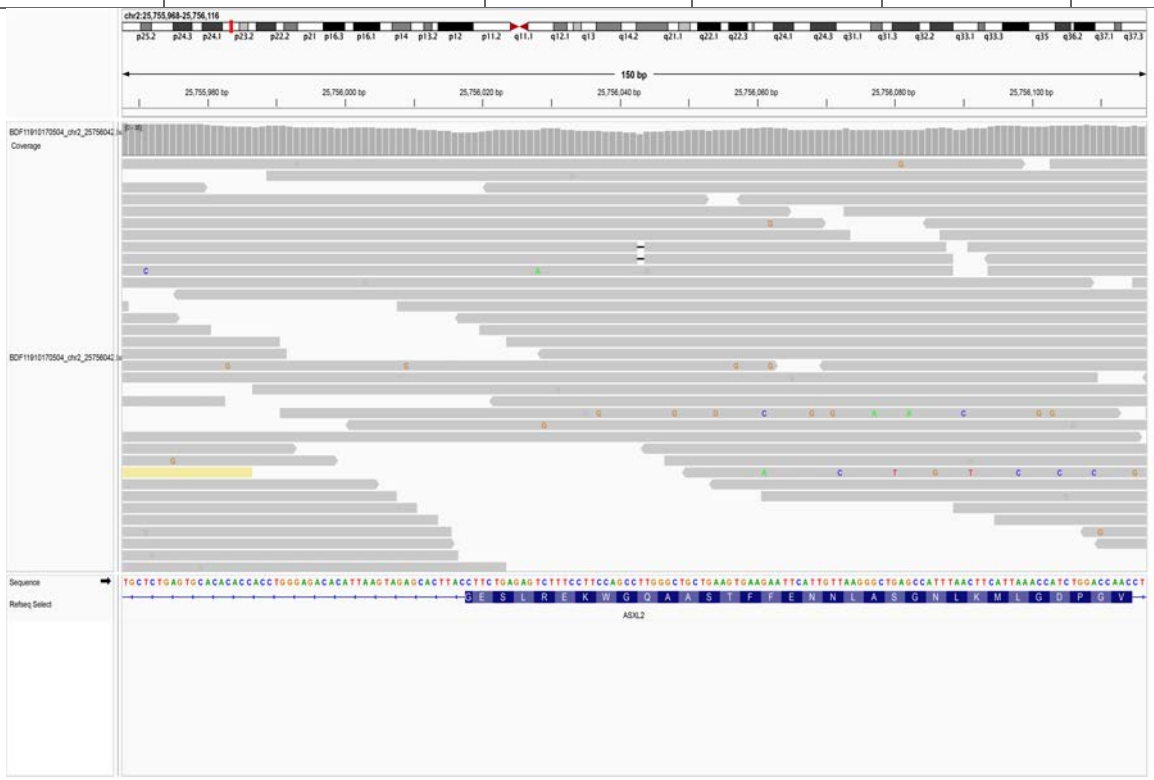
2.5. chr2_25756038_C/T

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



2.6. chr2_25756043_T/-

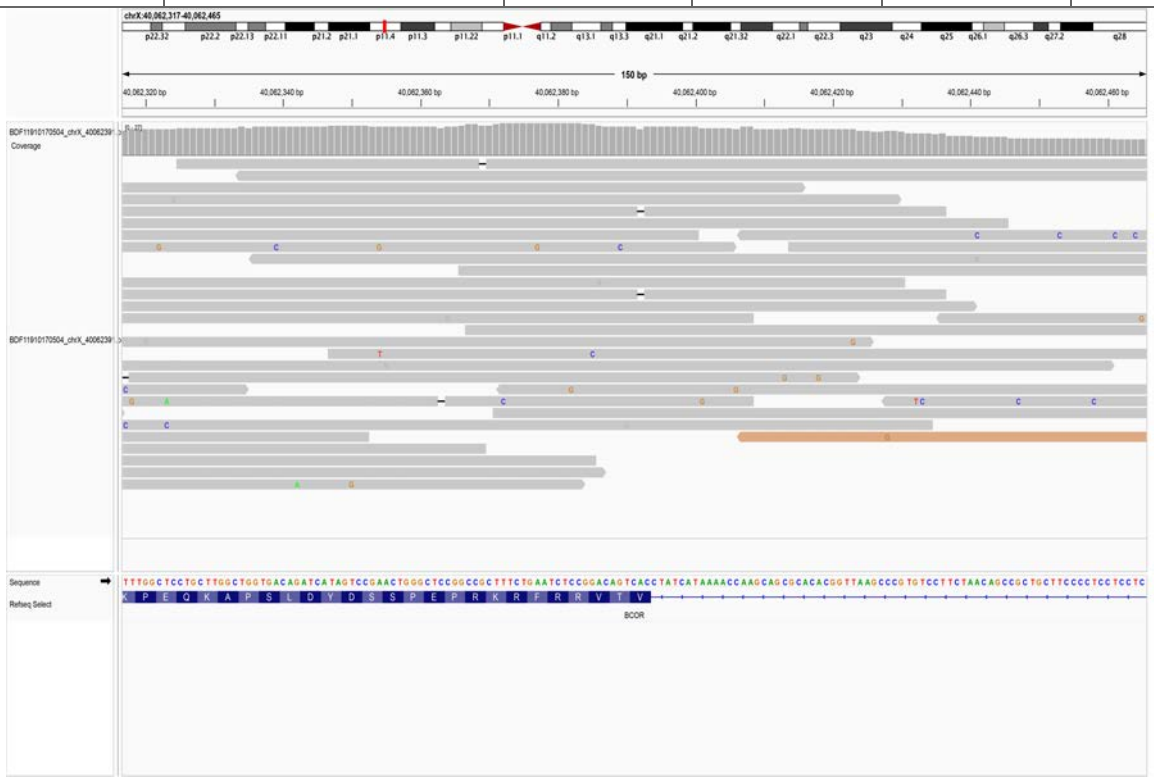
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chr2_25756043_T/-	21	2	*ASXL2*	frameshift_variant



3. *BCOR*

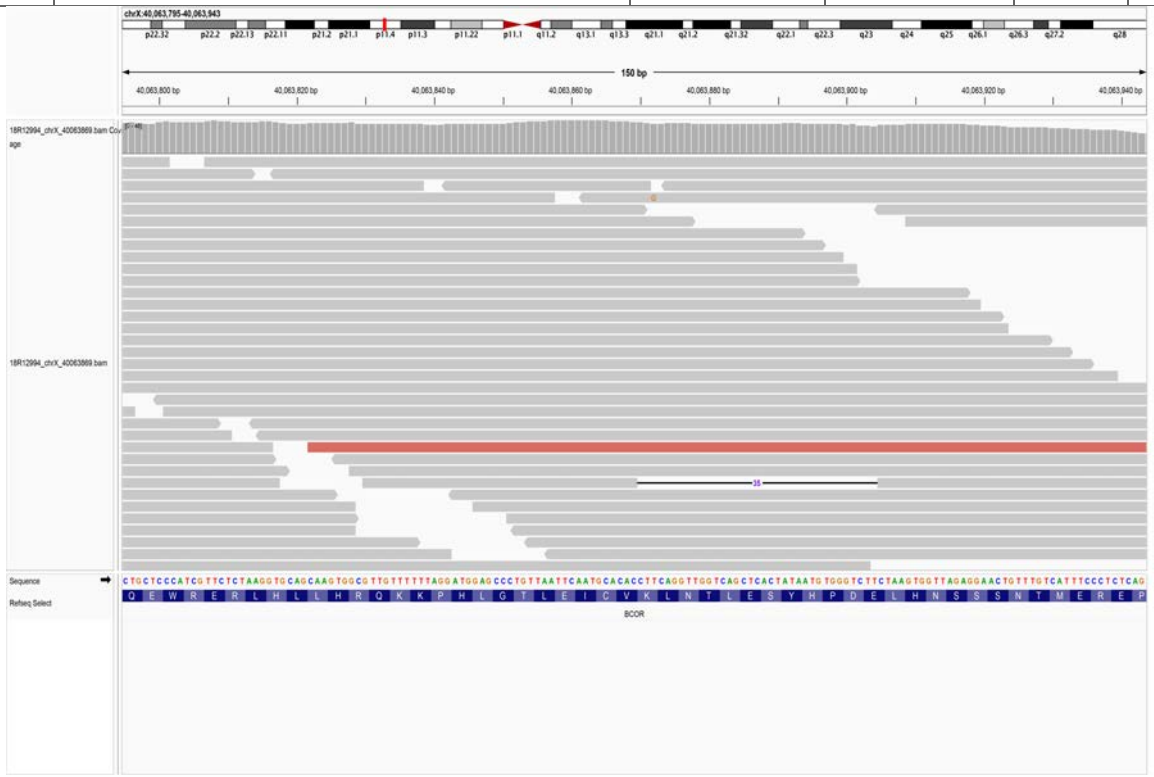
3.1. chrX_40062392_A/-

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



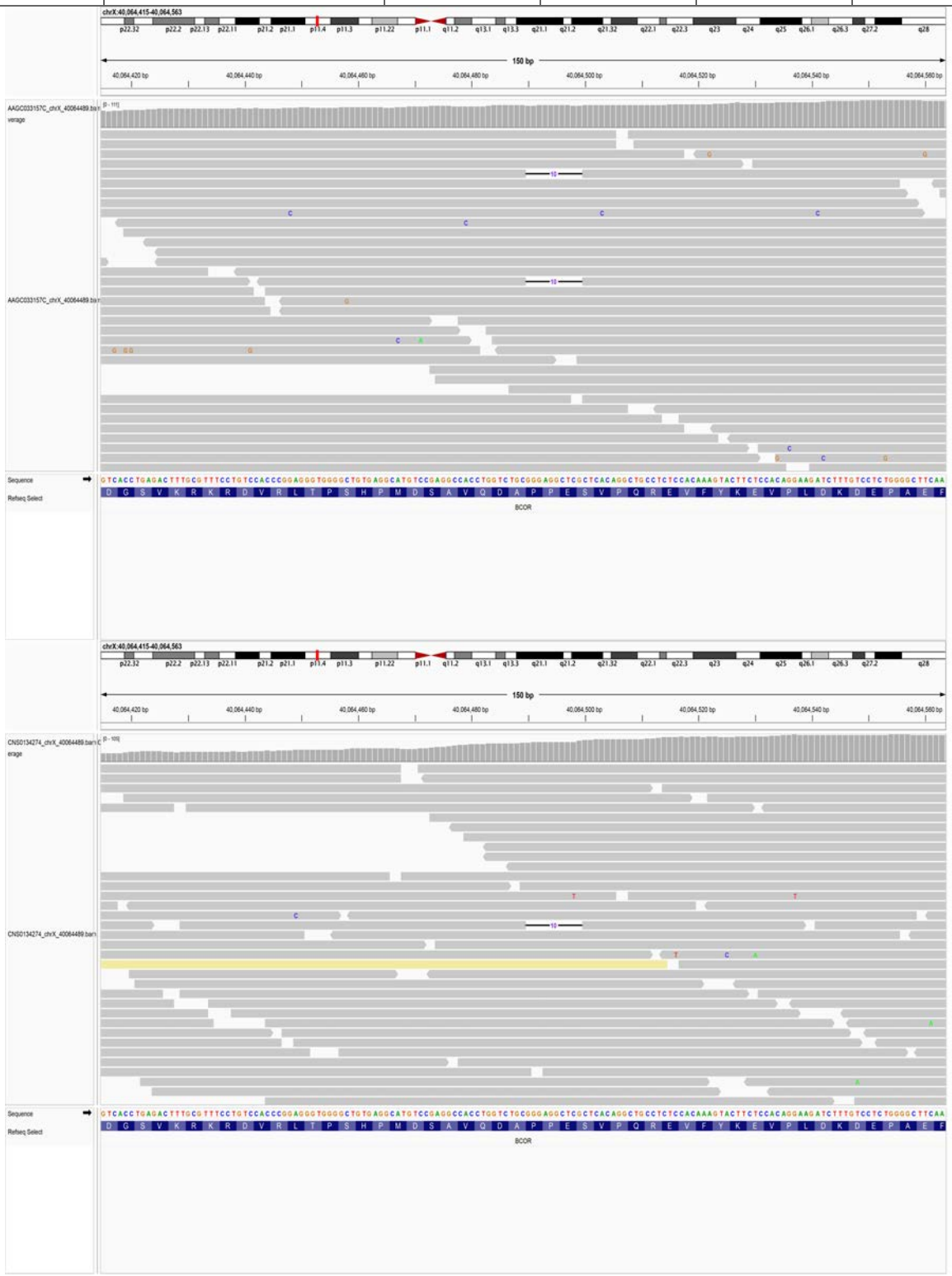
3.2. chrX_40063870_CTTCAGGTTGGTCAGCTCACTATAATGTGGGTCTT/-

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



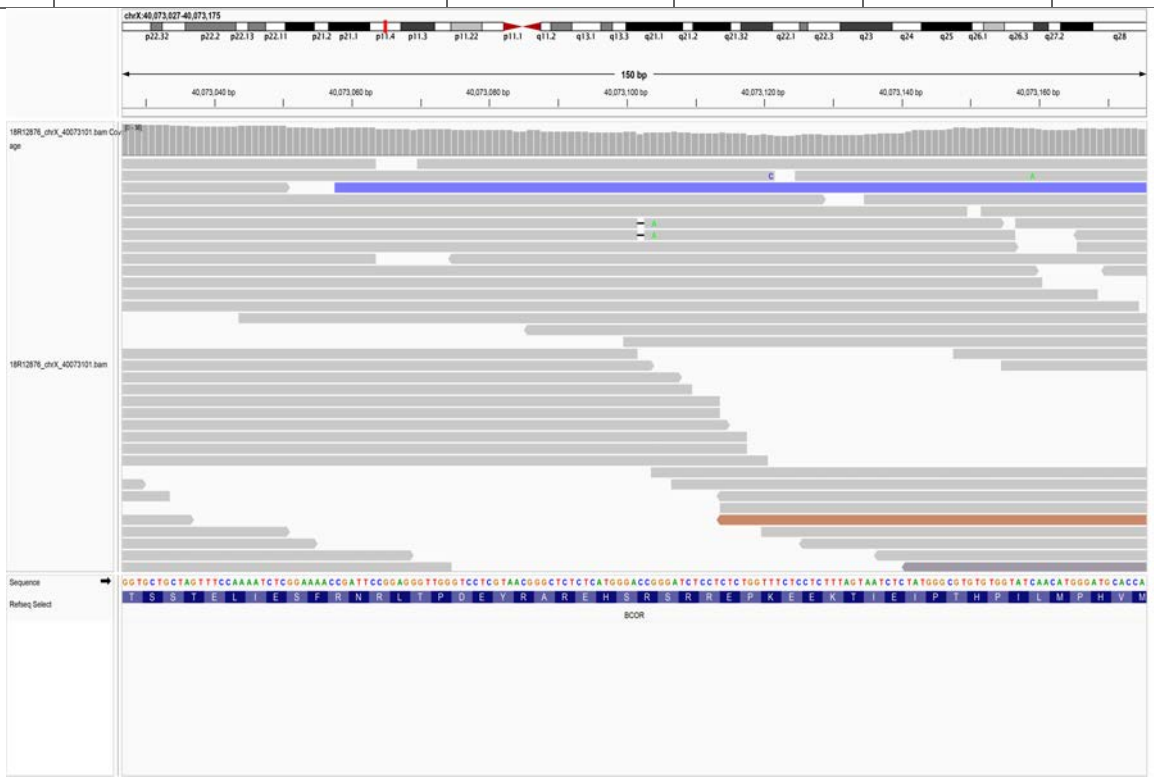
3.3. chrX_40064490_GGGAGGCTCG/-

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



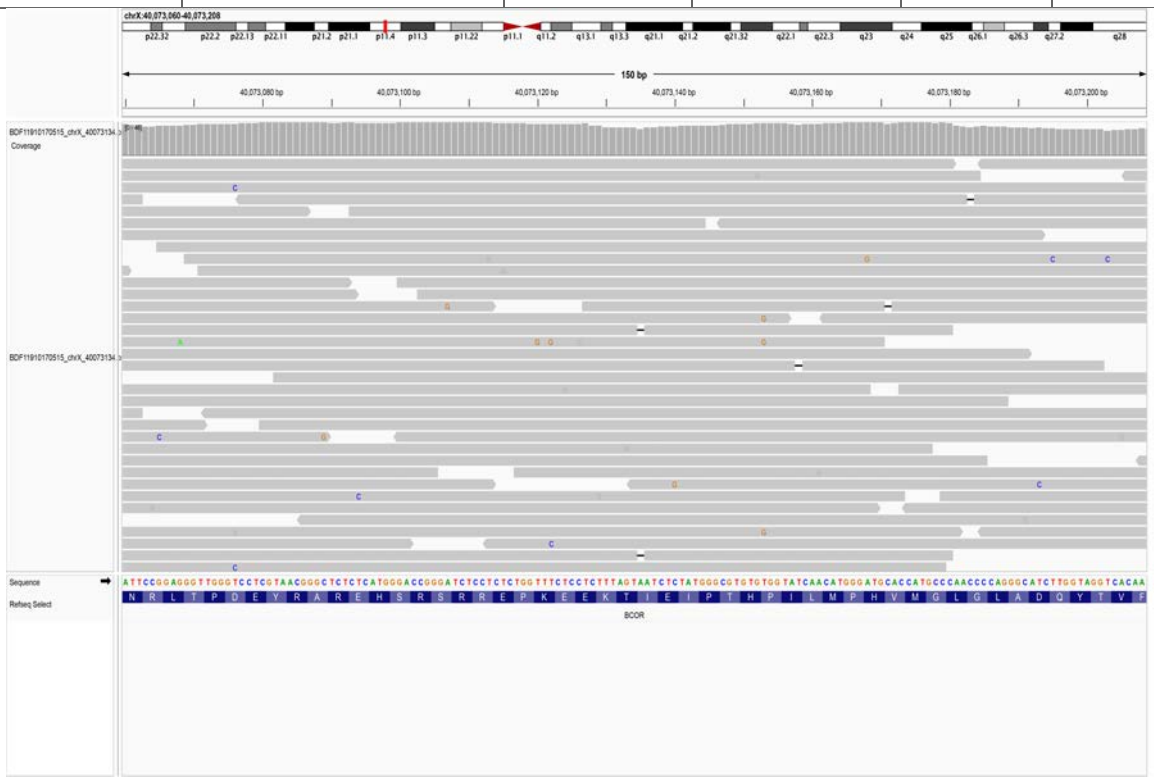
3.4. chrX_40073102_C/-

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



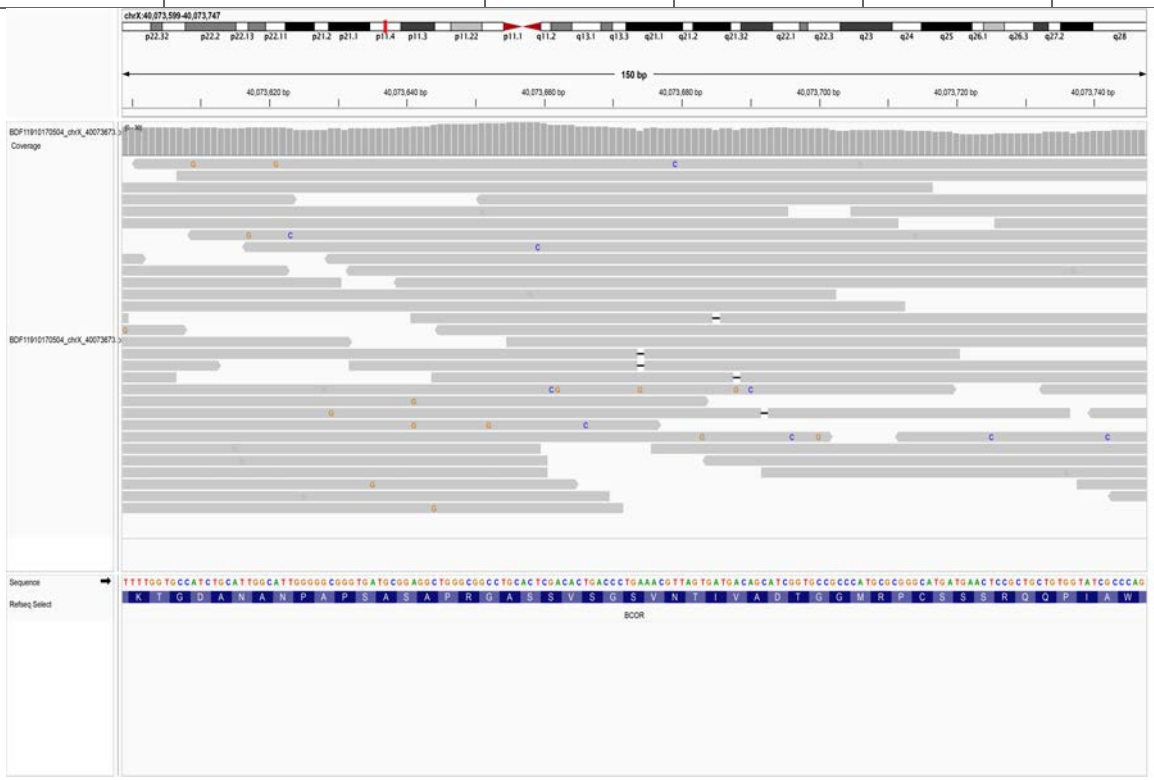
3.5. chrX_40073135_A/-

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



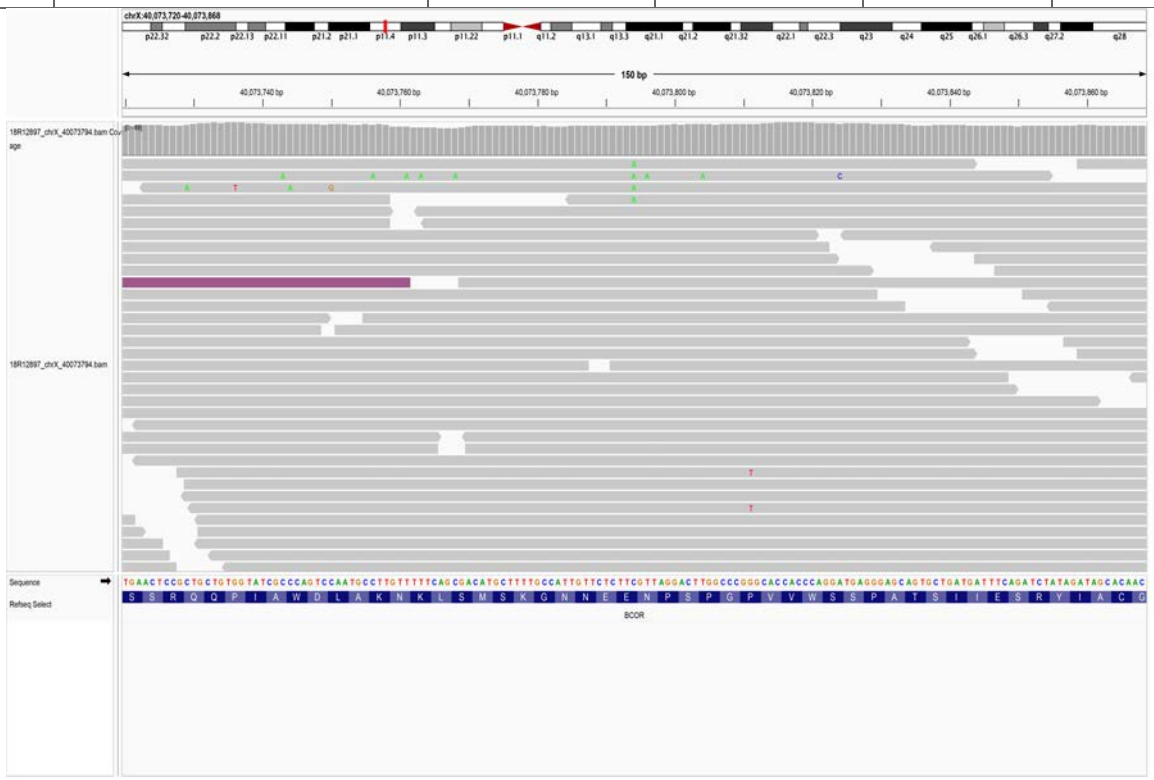
3.6. chrX_40073674_A/-

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



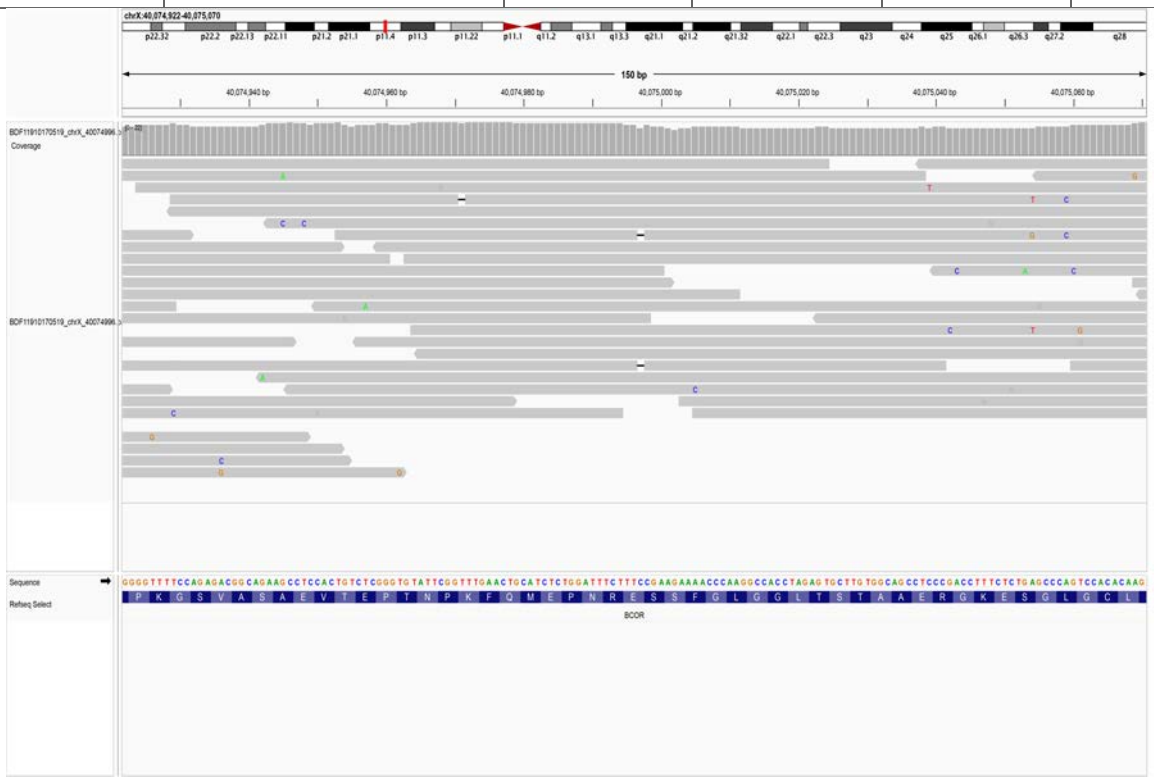
3.7. chrX_40073794_C/A

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



3.8. chrX_40074997_C/-

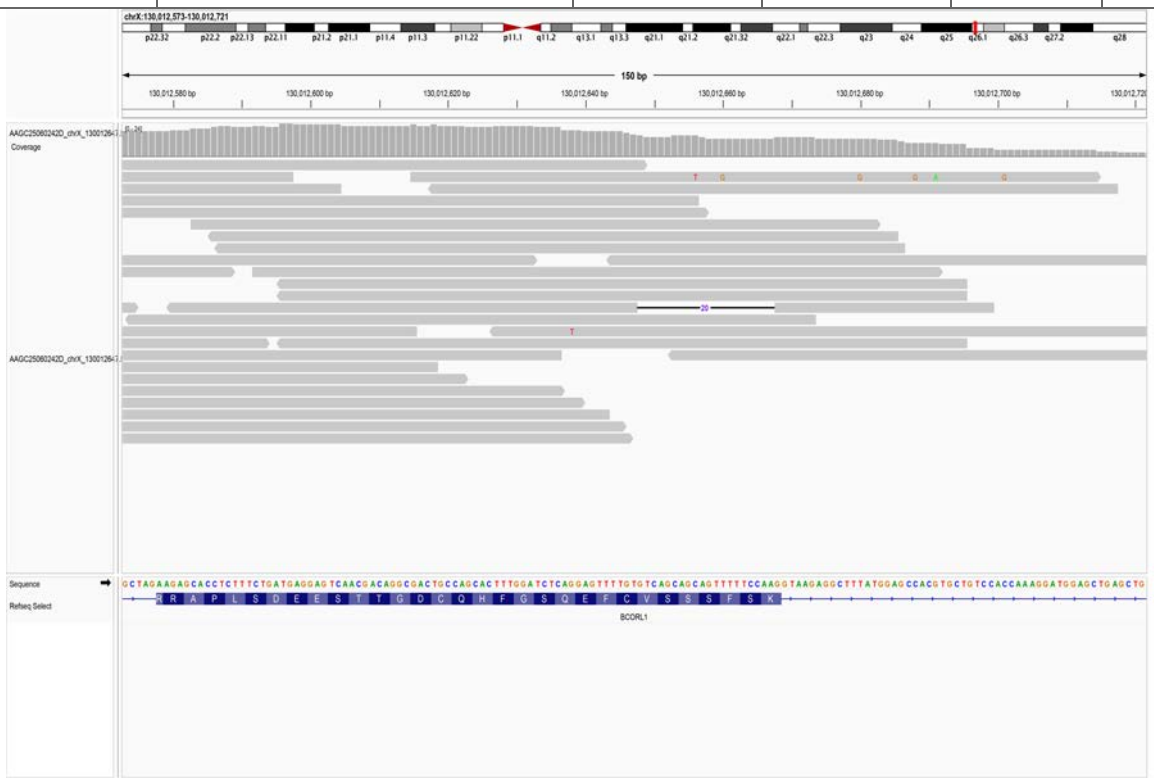
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chrX_40074997_C/-	17	2	*BCOR*	frameshift_variant



4. *BCORL1*

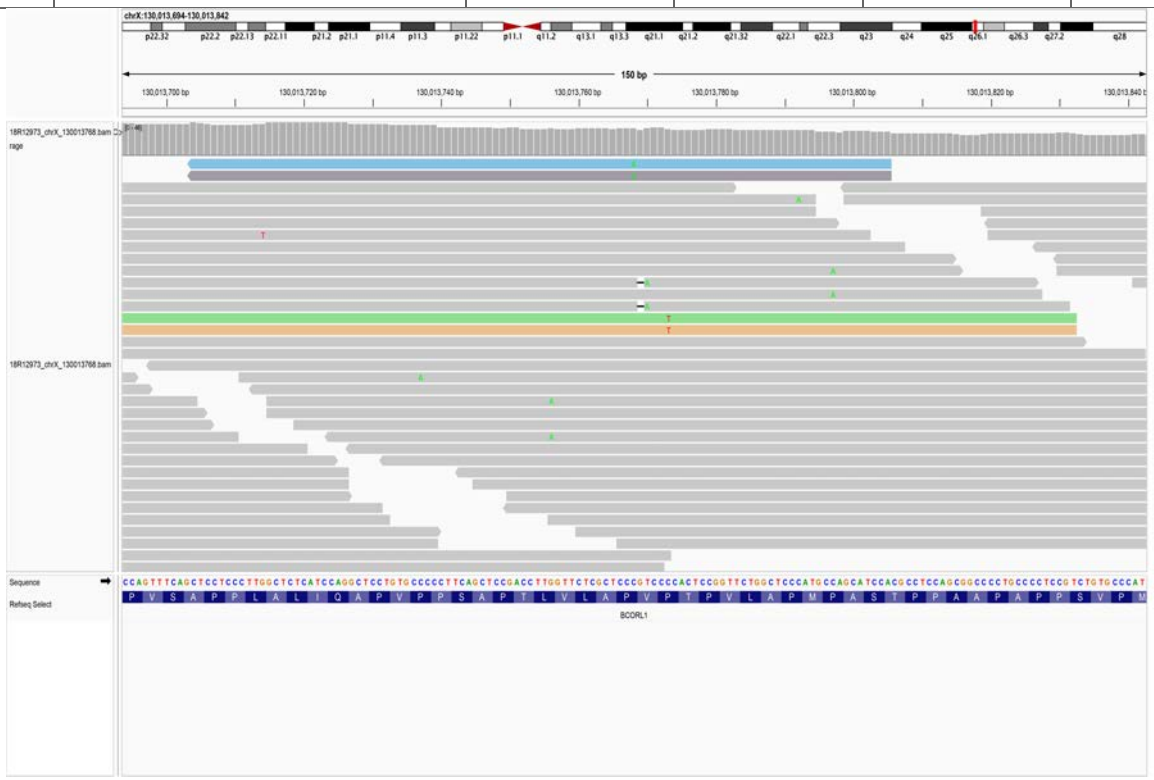
4.1. chrX_130012648_GTCAGCAGCAGTTTTTCCAA/-

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



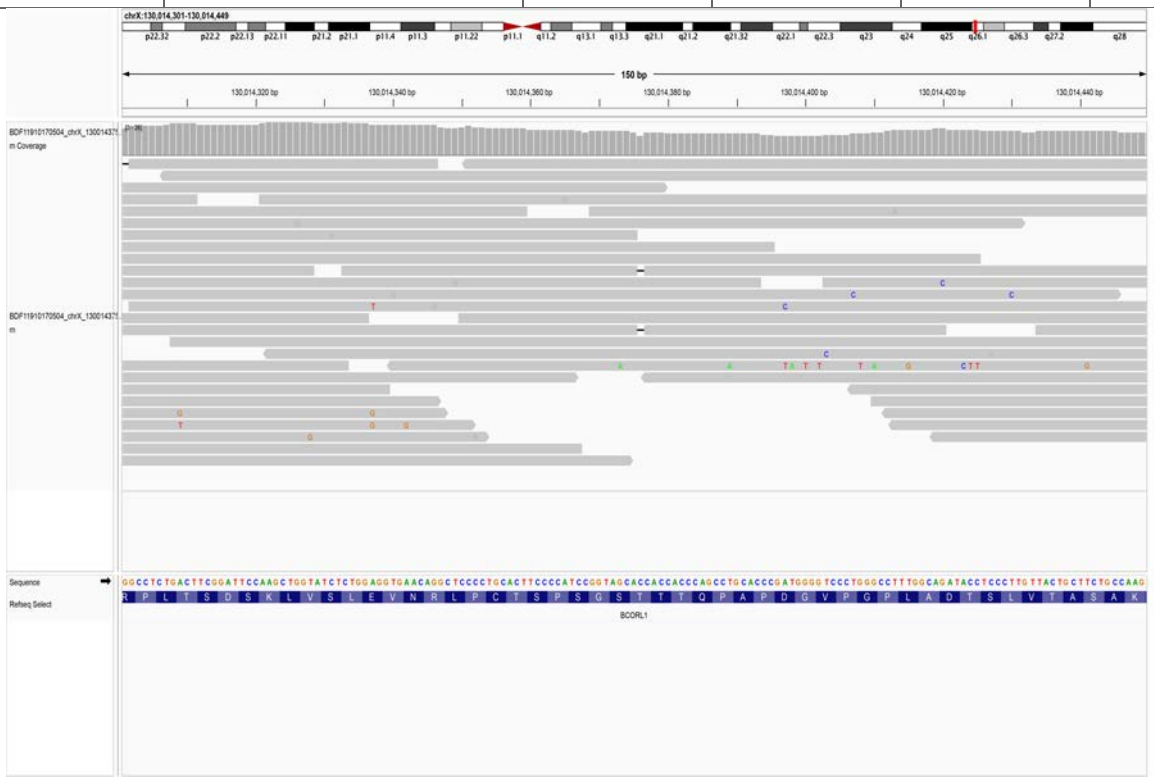
4.2. chrX_130013769_G/-

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



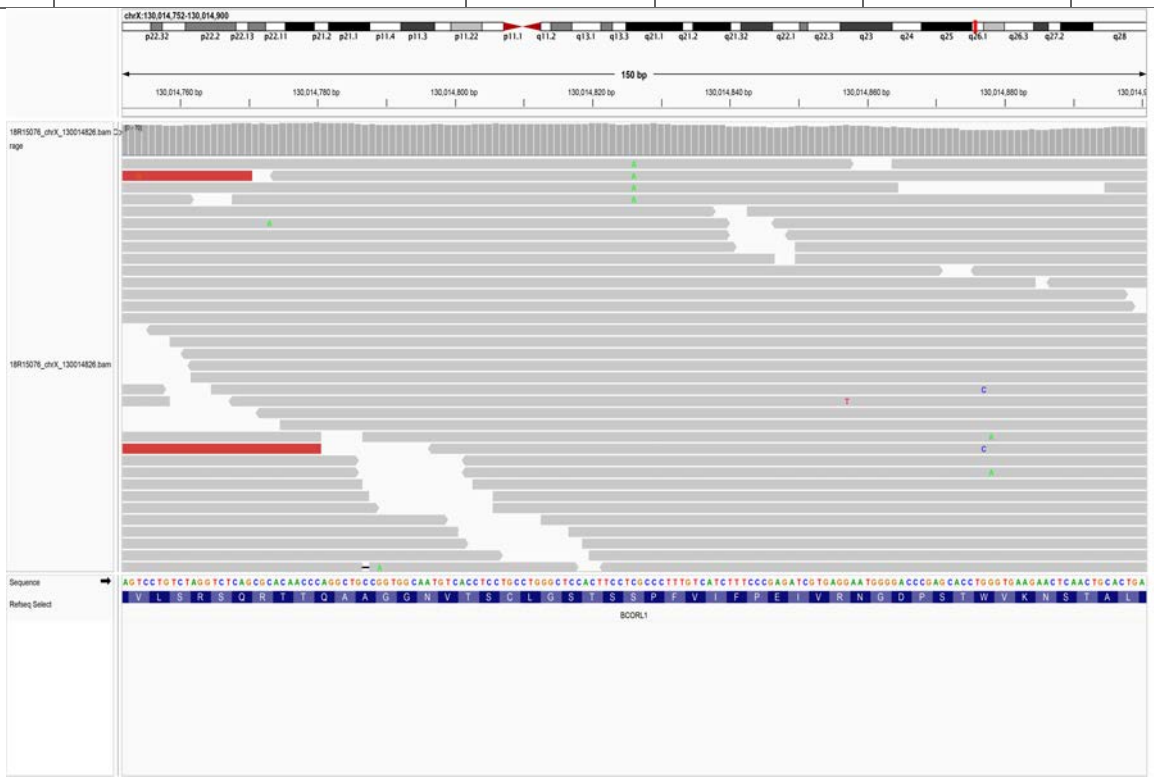
4.3. chrX_130014376_C/-

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



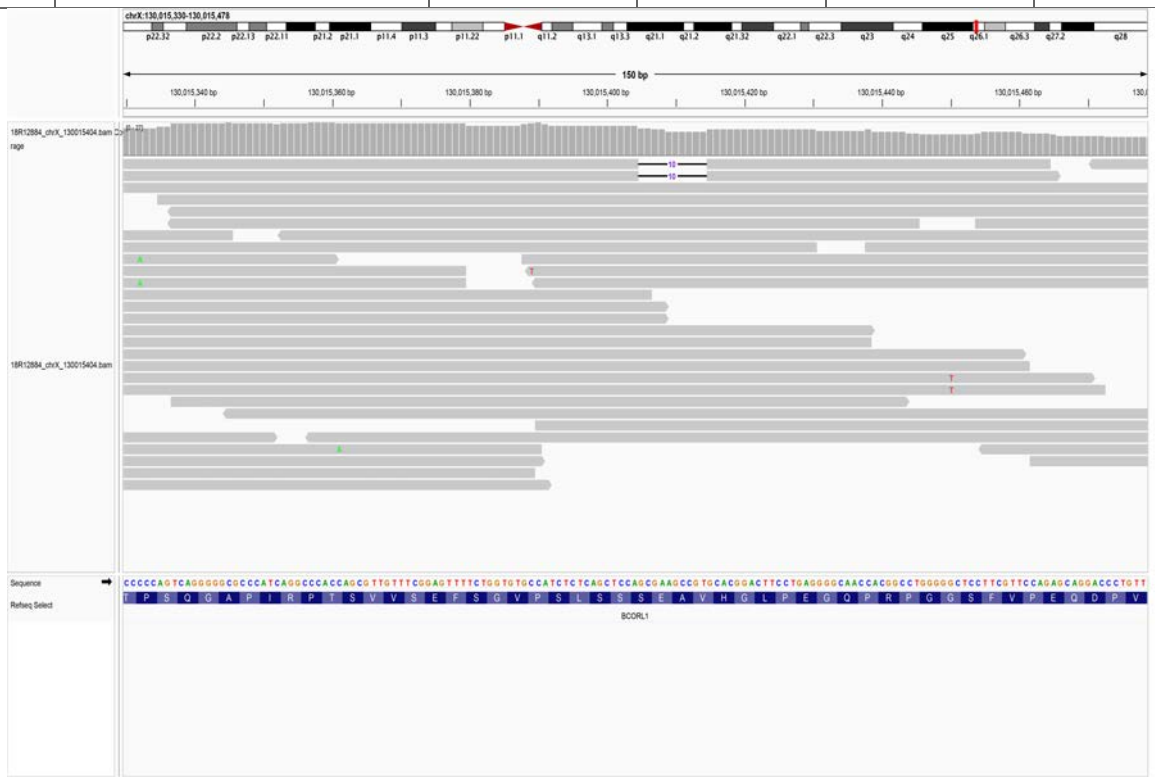
4.4. chrX_130014826_C/A

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



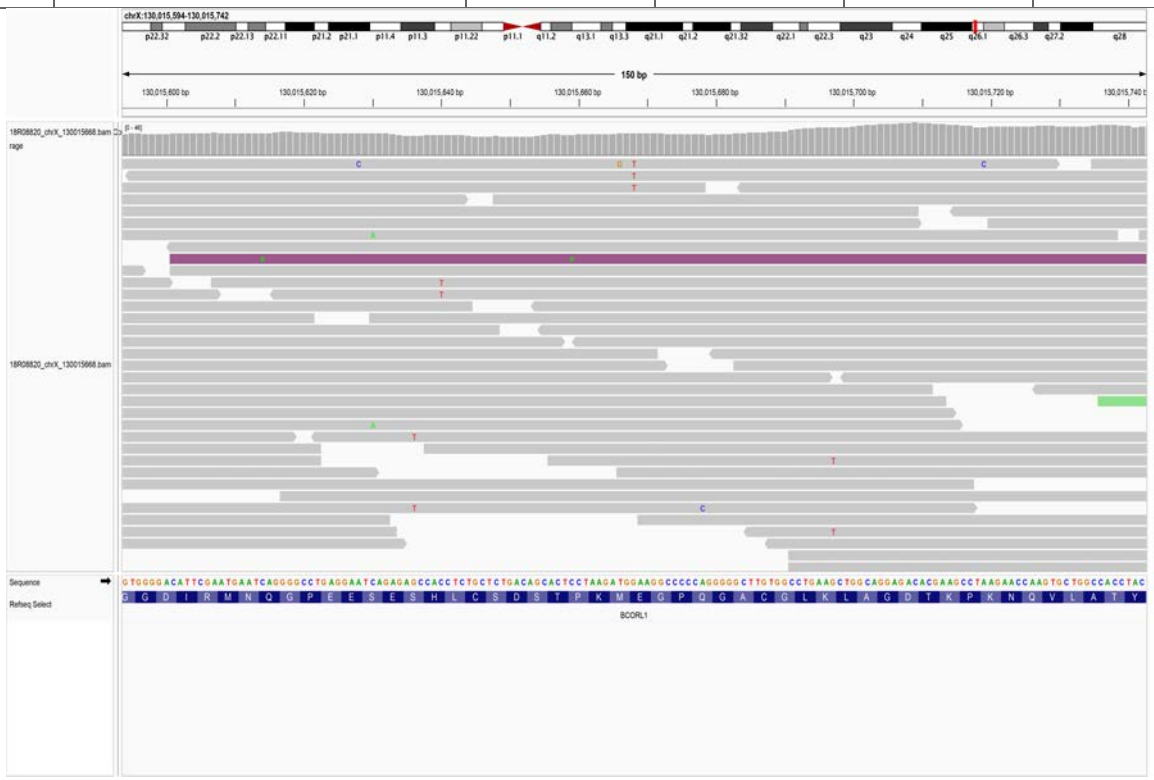
4.5. chrX_130015405_GCGAAGCCGT/-

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



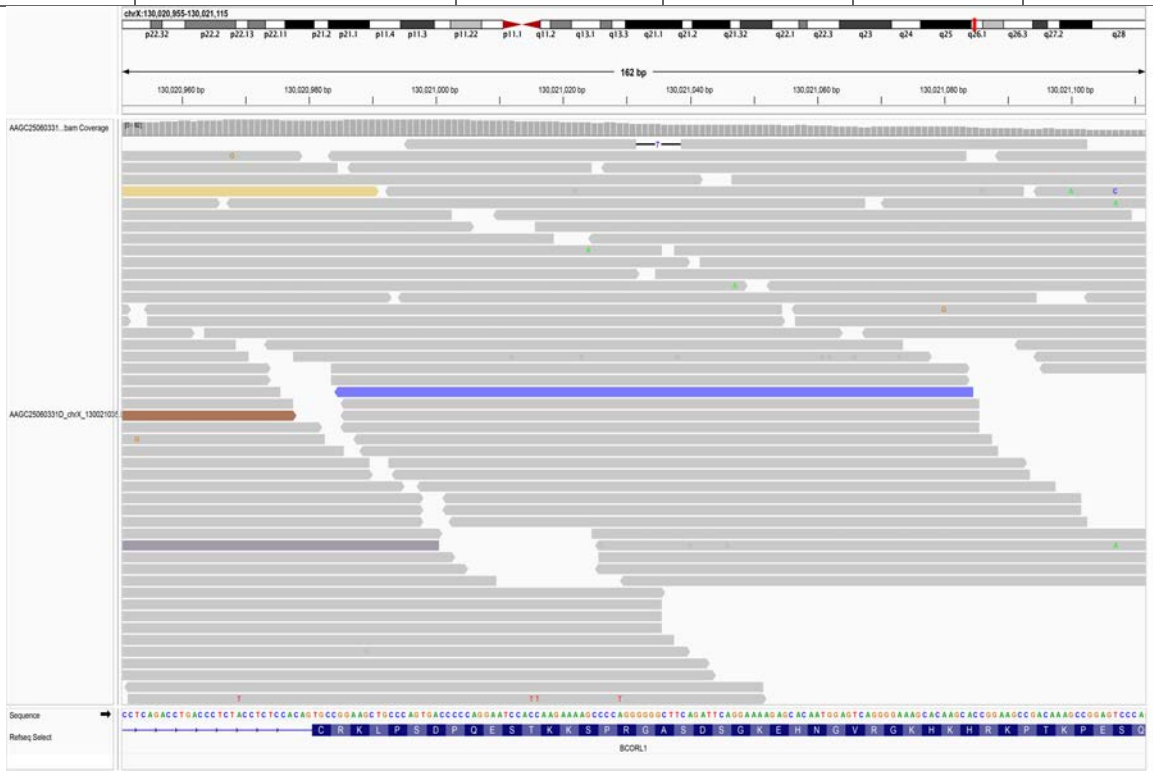
4.6. chrX_130015668_G/T

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



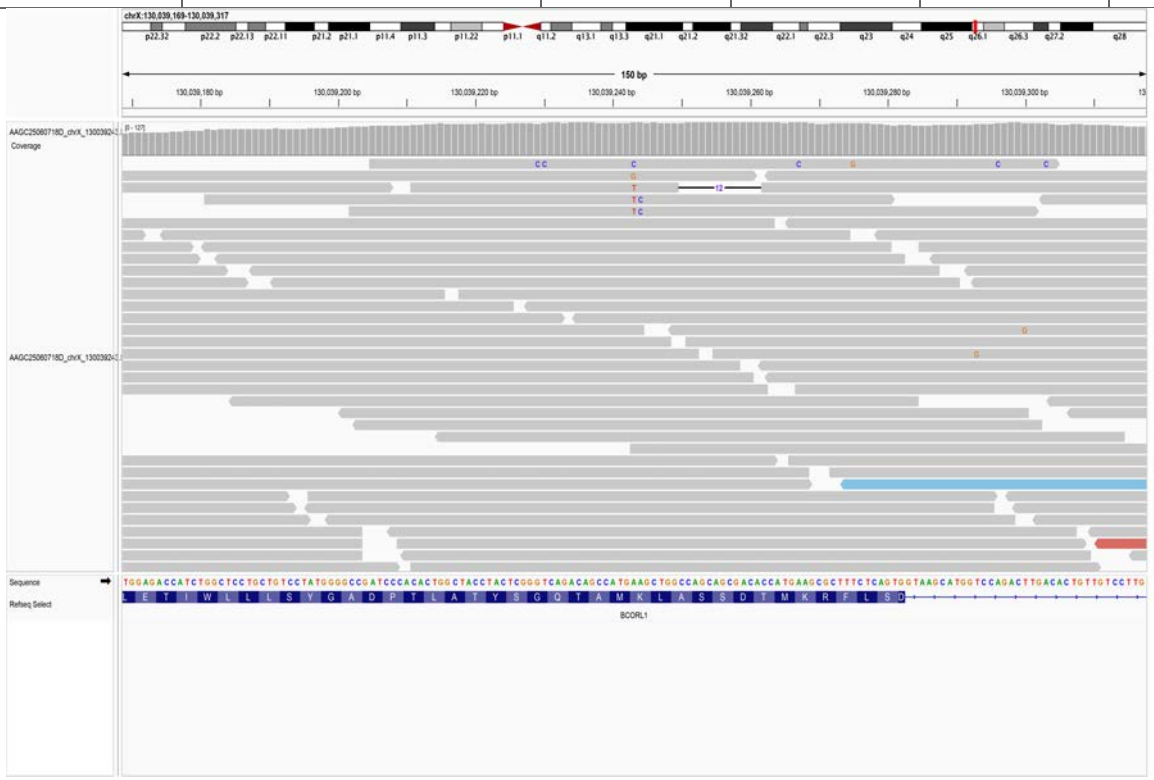
4.7. chrX_130021036_GGGGCTT/-

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

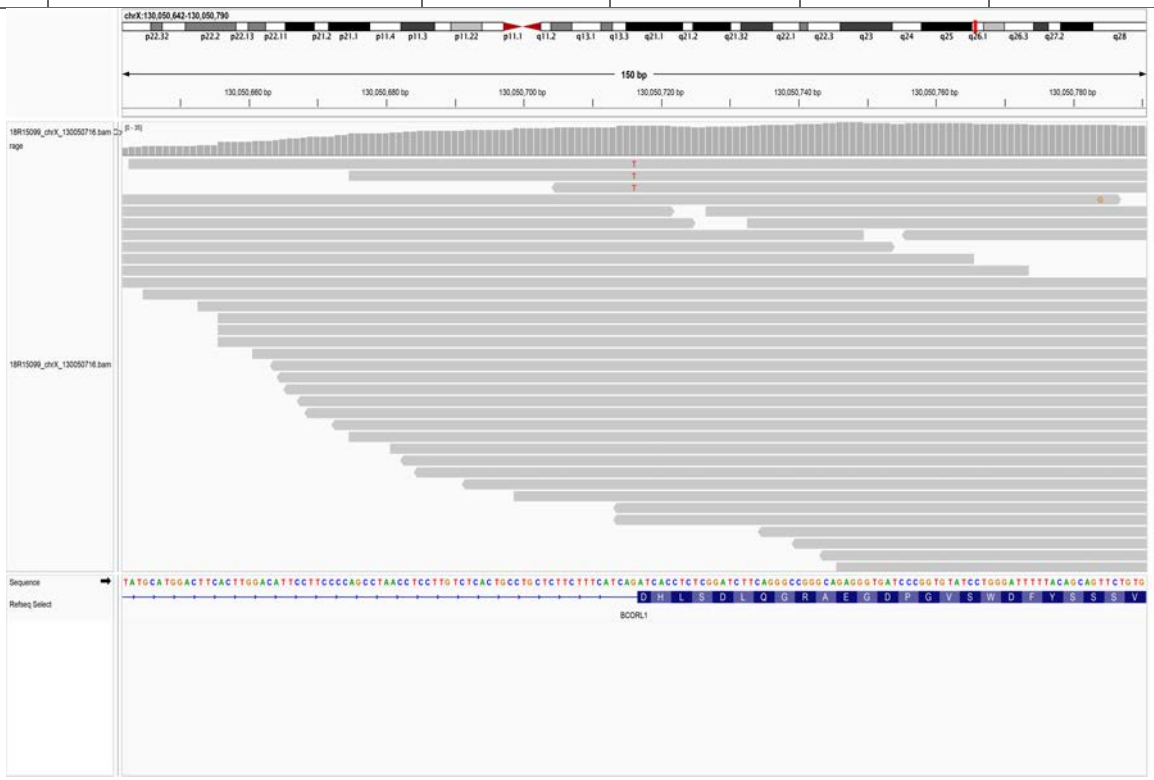


4.9. chrX_130039252_AGCAGCGACA/-

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

4.10. chrX_130050716_G/T

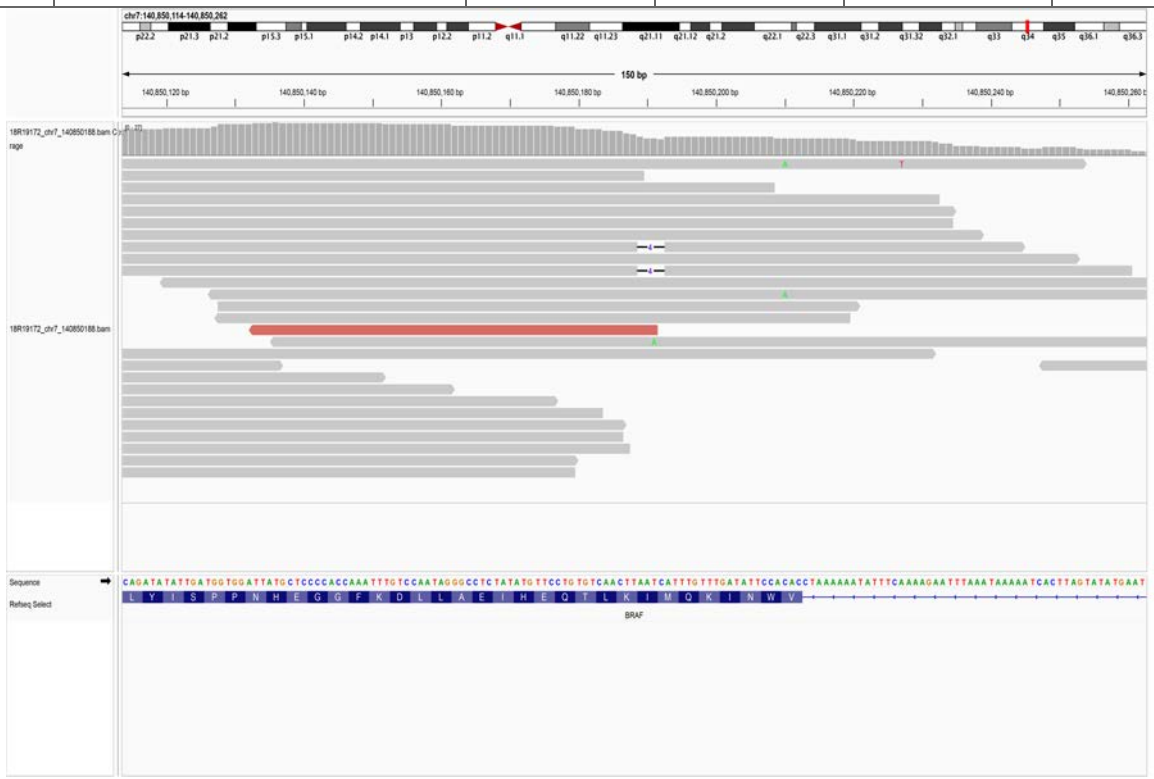
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15099	chrX_130050716_G/T	28	3	*BCORL1*	splice_acceptor_variant



5. *BRAF*

5.1. chr7_140850189_AATC/-

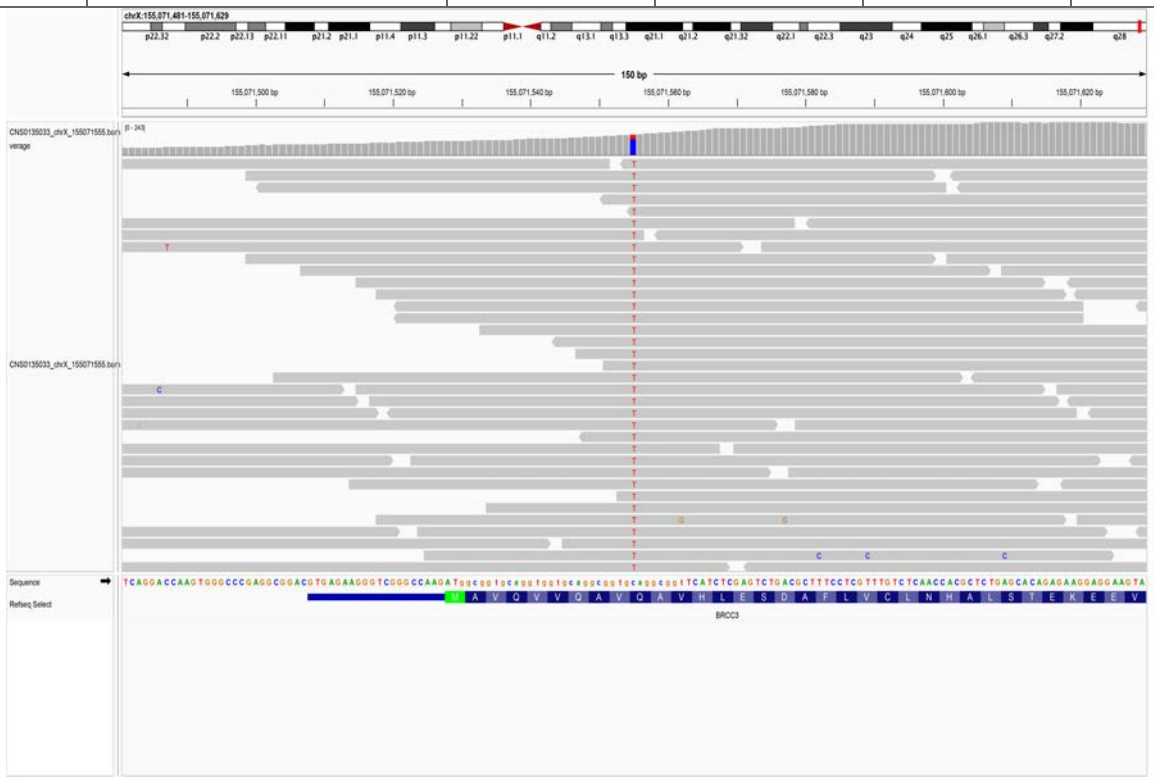
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19172	chr7_140850189_AATC/-	14	2	*BRAF*	frameshift_variant



6. *BRCC3*

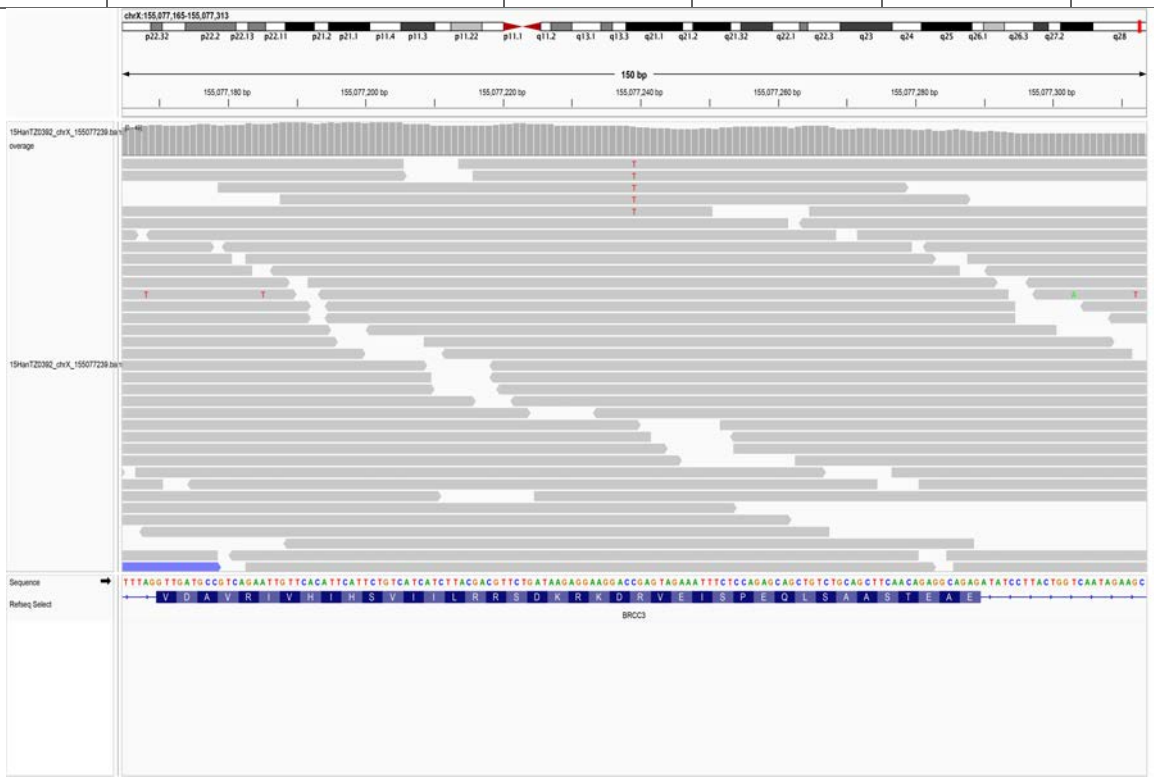
6.1. chrX_155071555_C/T

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

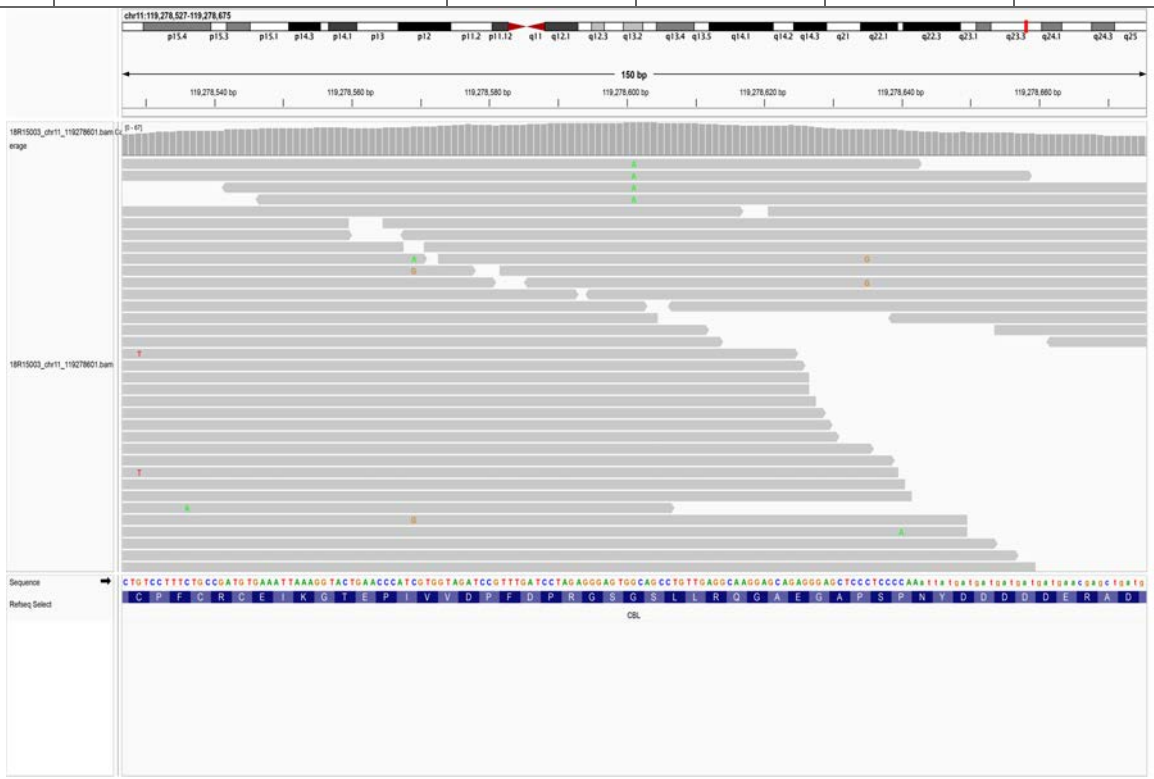
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0392	chrX_155077239_C/T	37	5	*BRCC3*	stop_gained



7. *CBL*

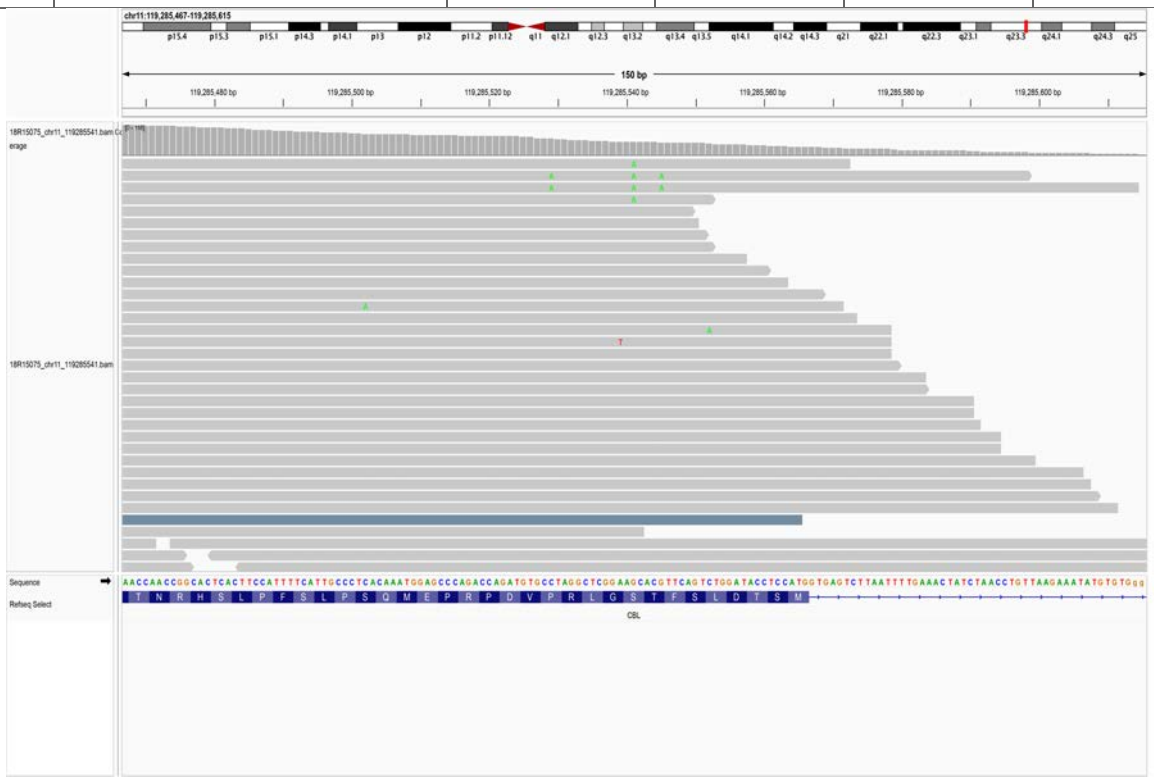
7.1. chr11_119278601_G/A

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



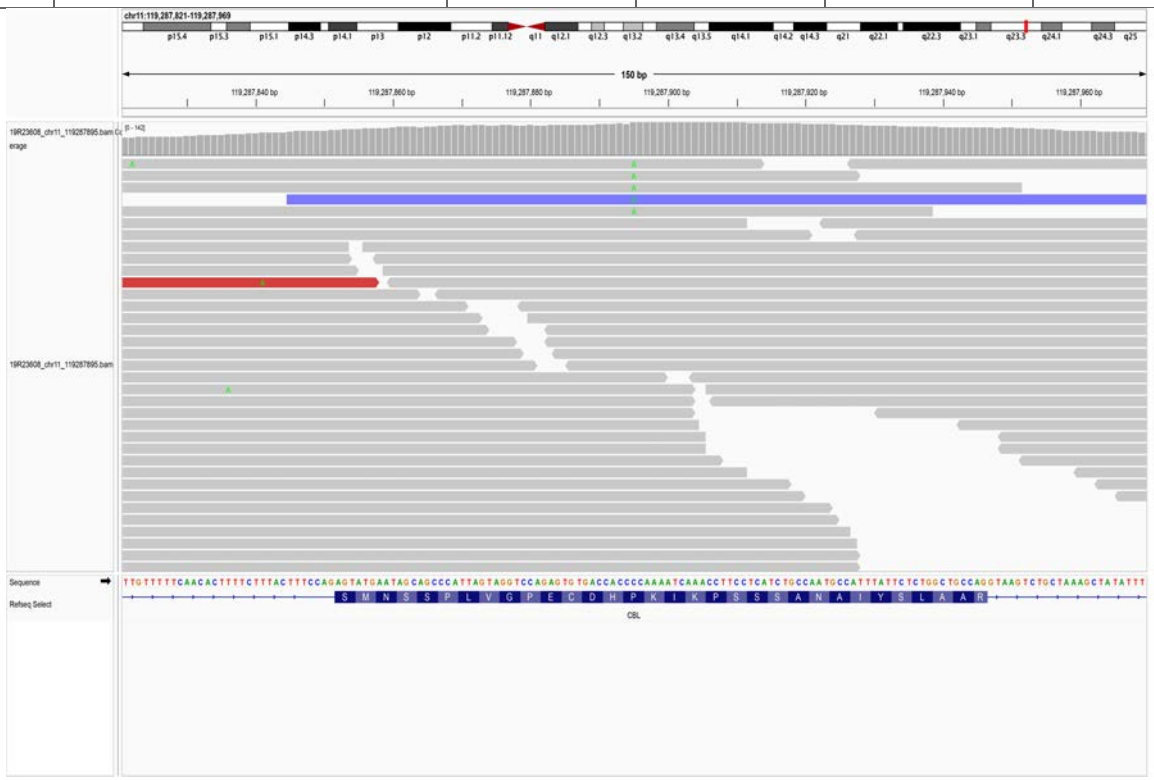
7.2. chr11_119285541_G/A

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



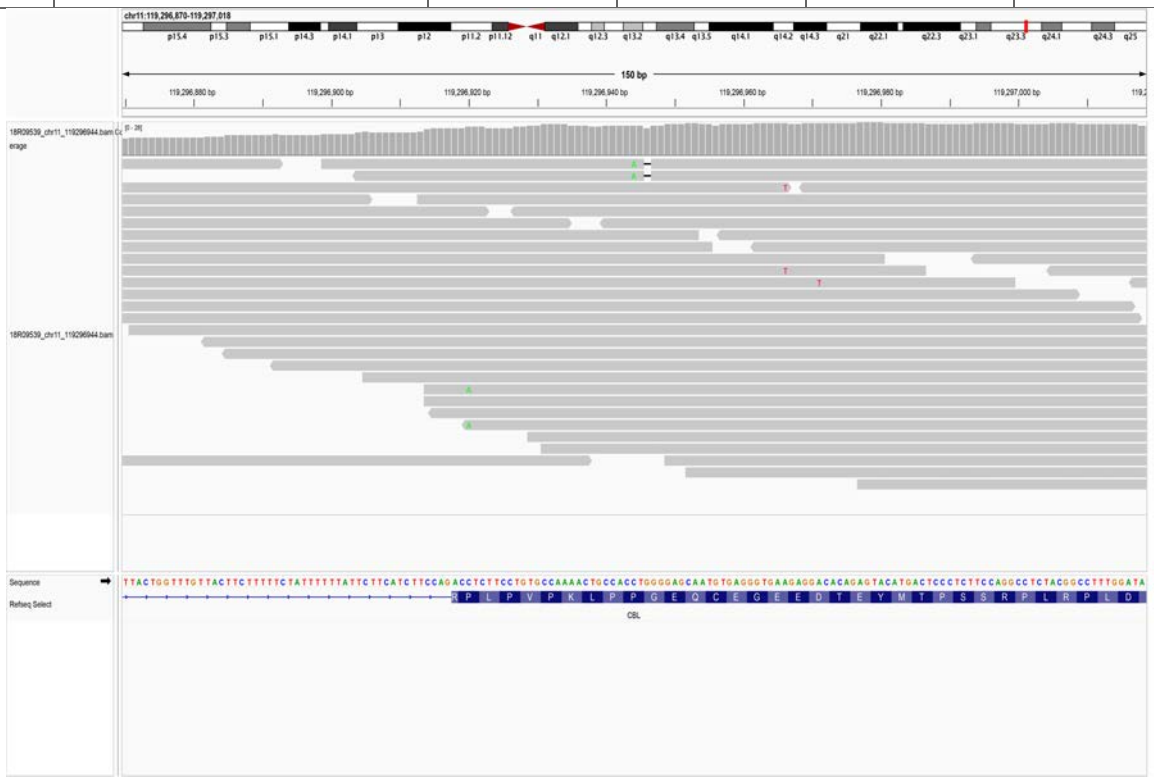
7.3. chr11_119287895_C/A

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



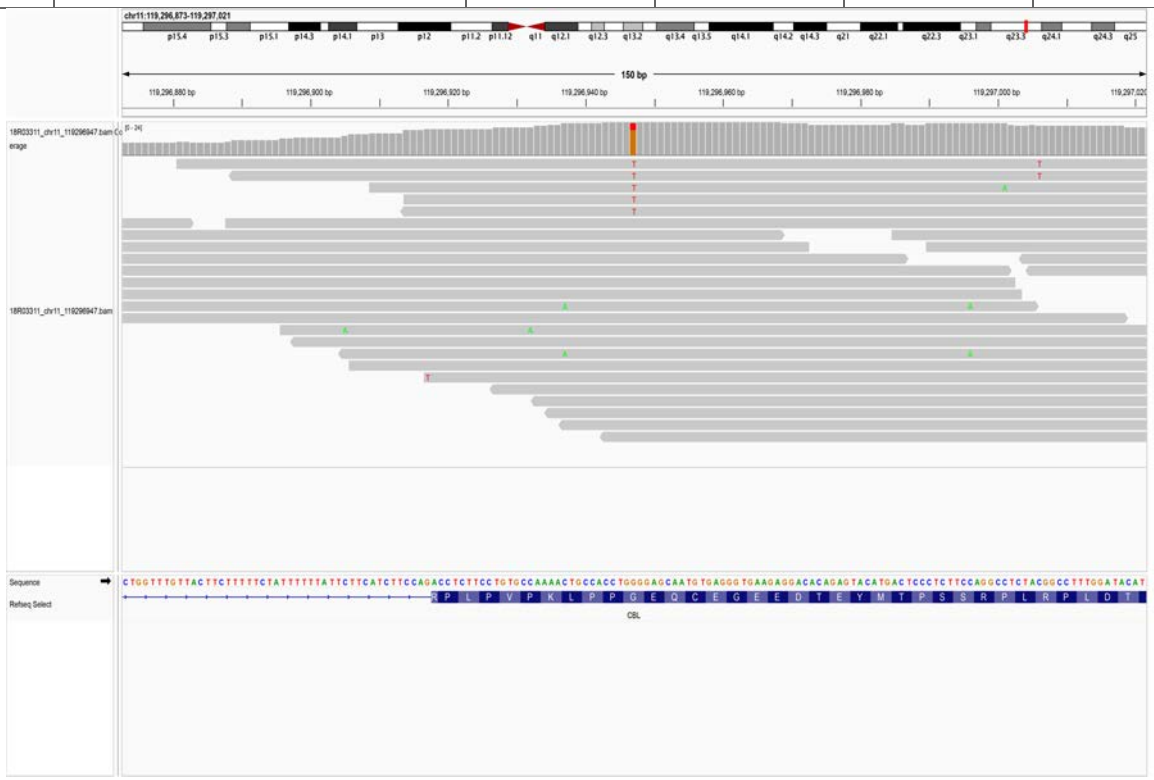
7.4. chr11_119296944_C/A

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



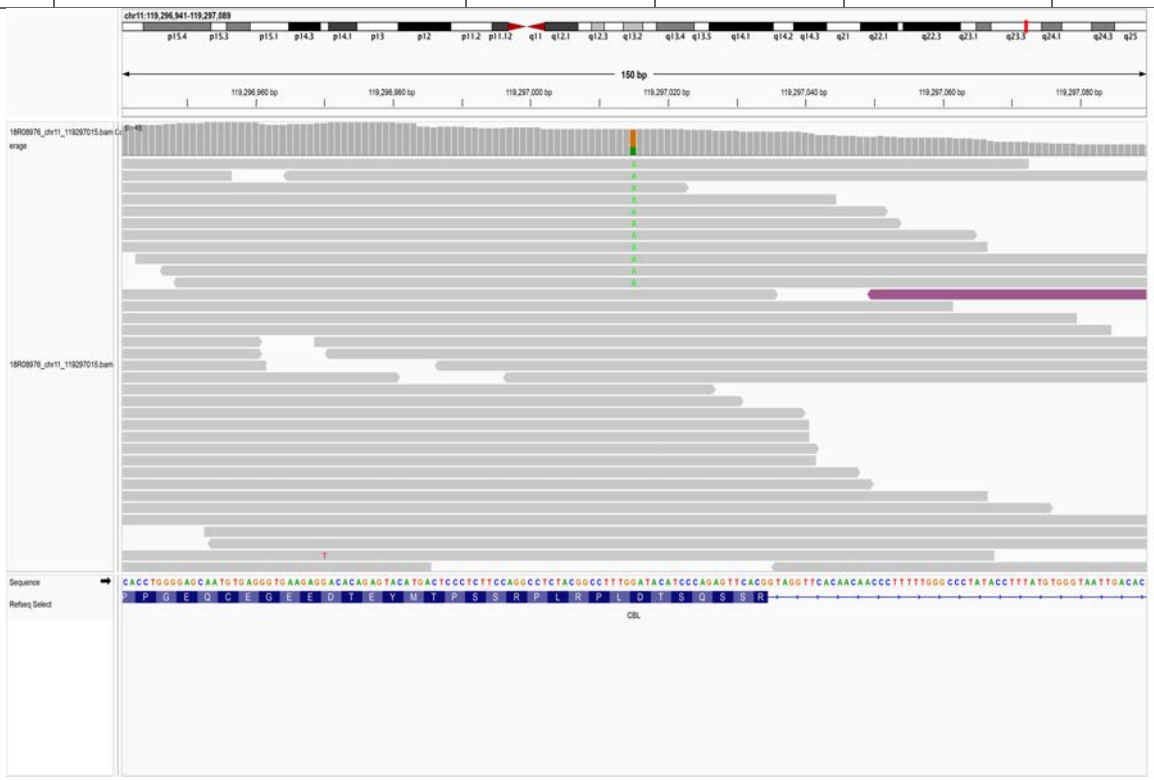
7.5. chr11_119296947_G/T

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



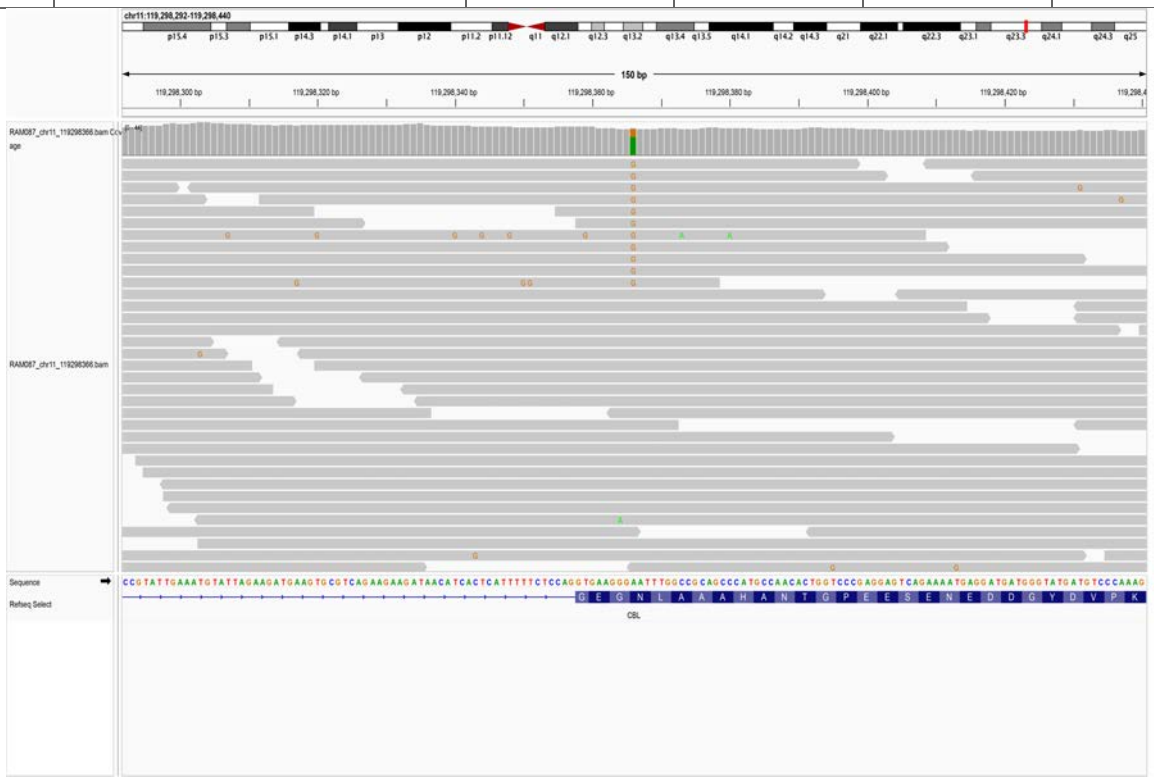
7.6. chr11_119297015_G/A

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



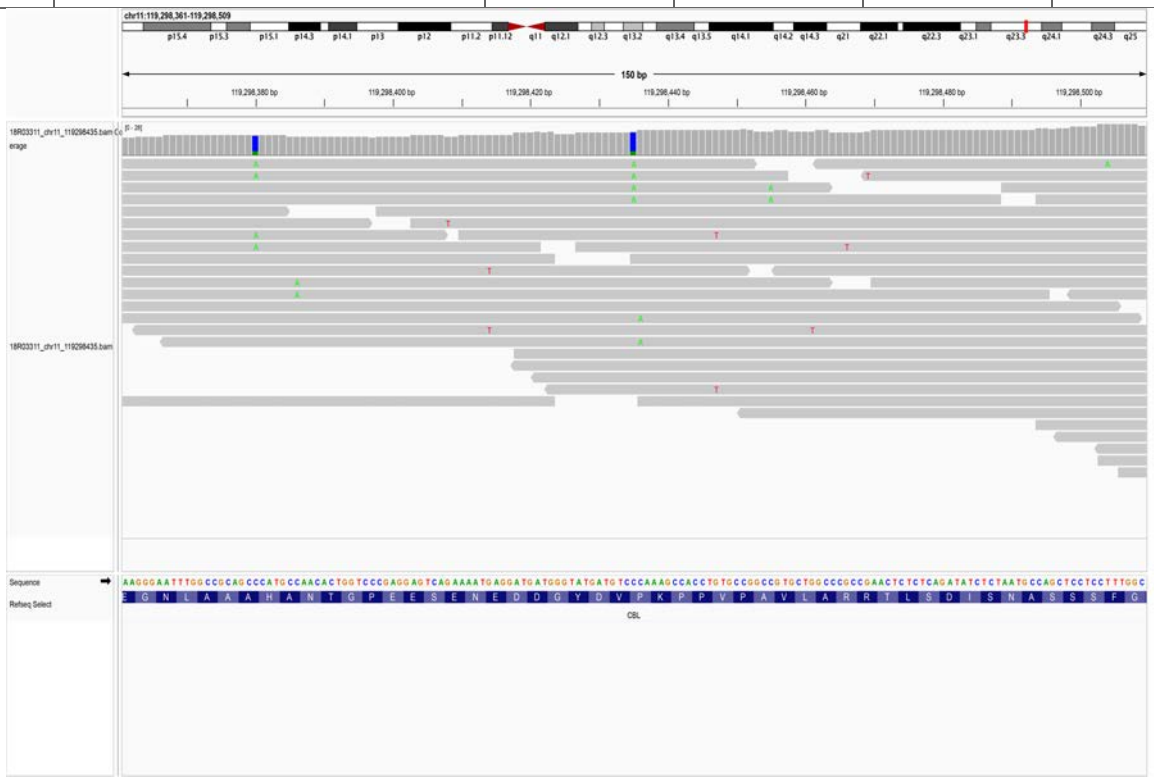
7.7. chr11_119298366_A/G

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



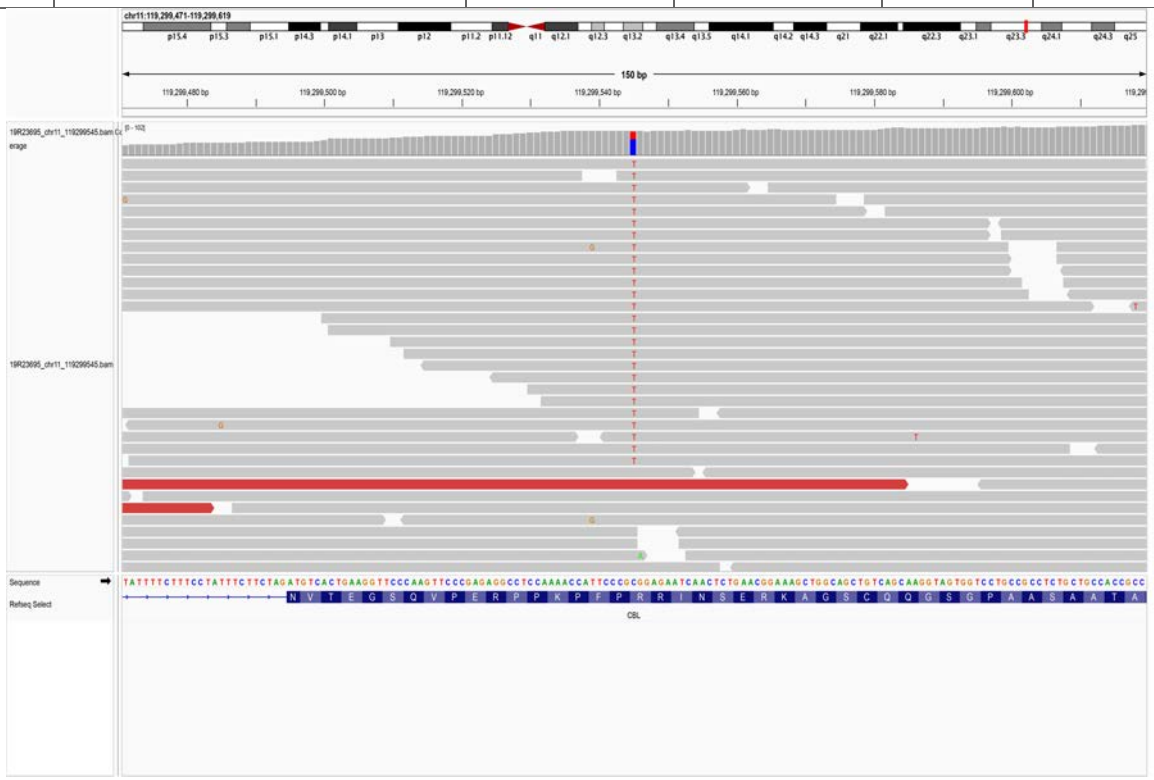
7.8. chr11_119298435_C/A

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



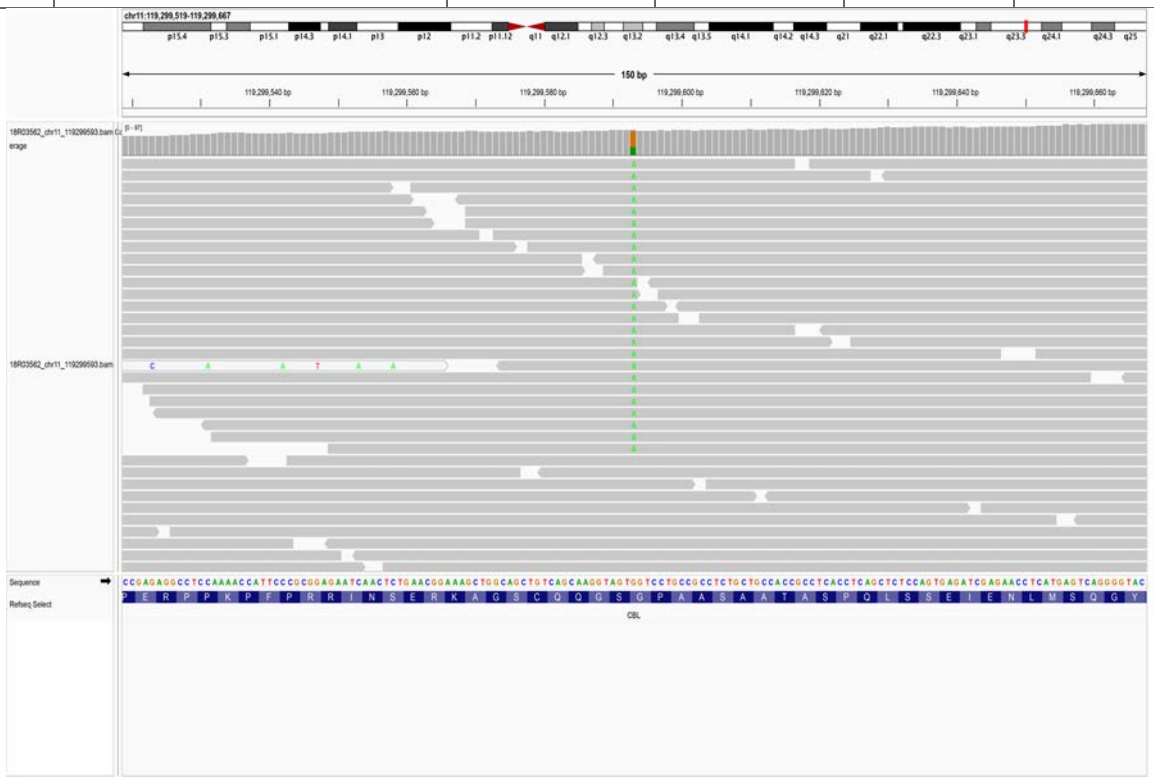
7.9. chr11_119299545_C/T

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



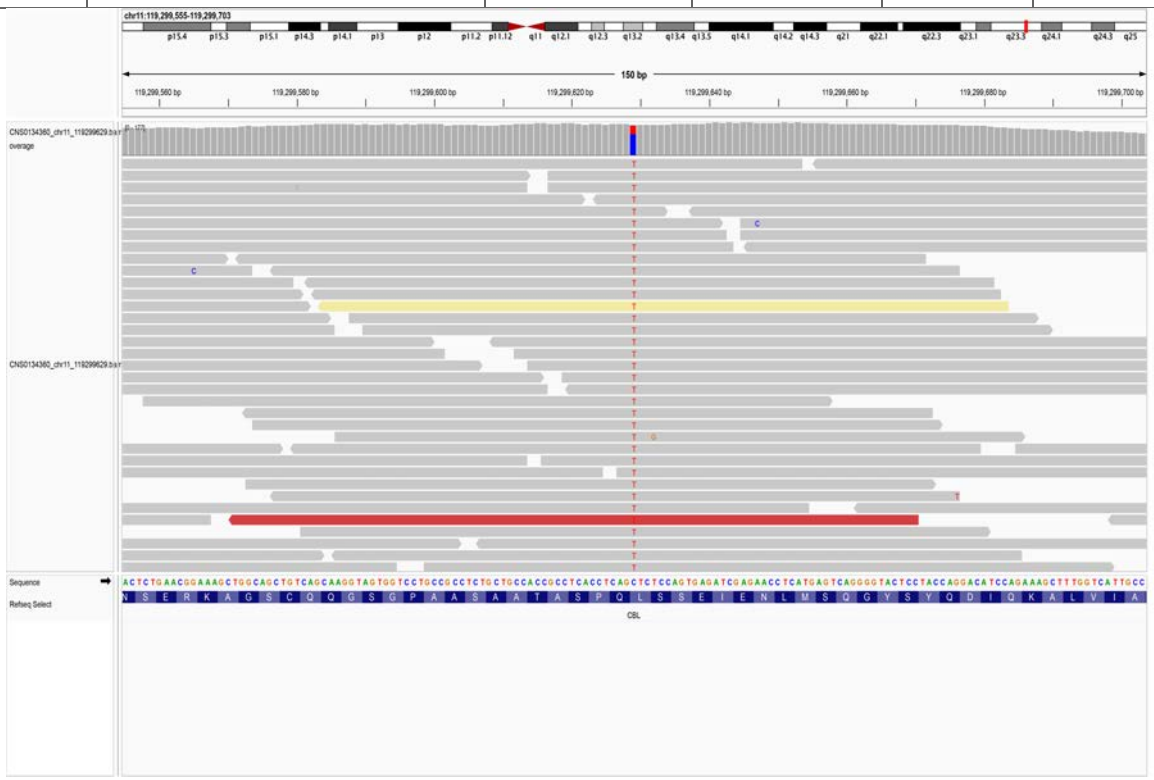
7.10. chr11_119299593_G/A

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



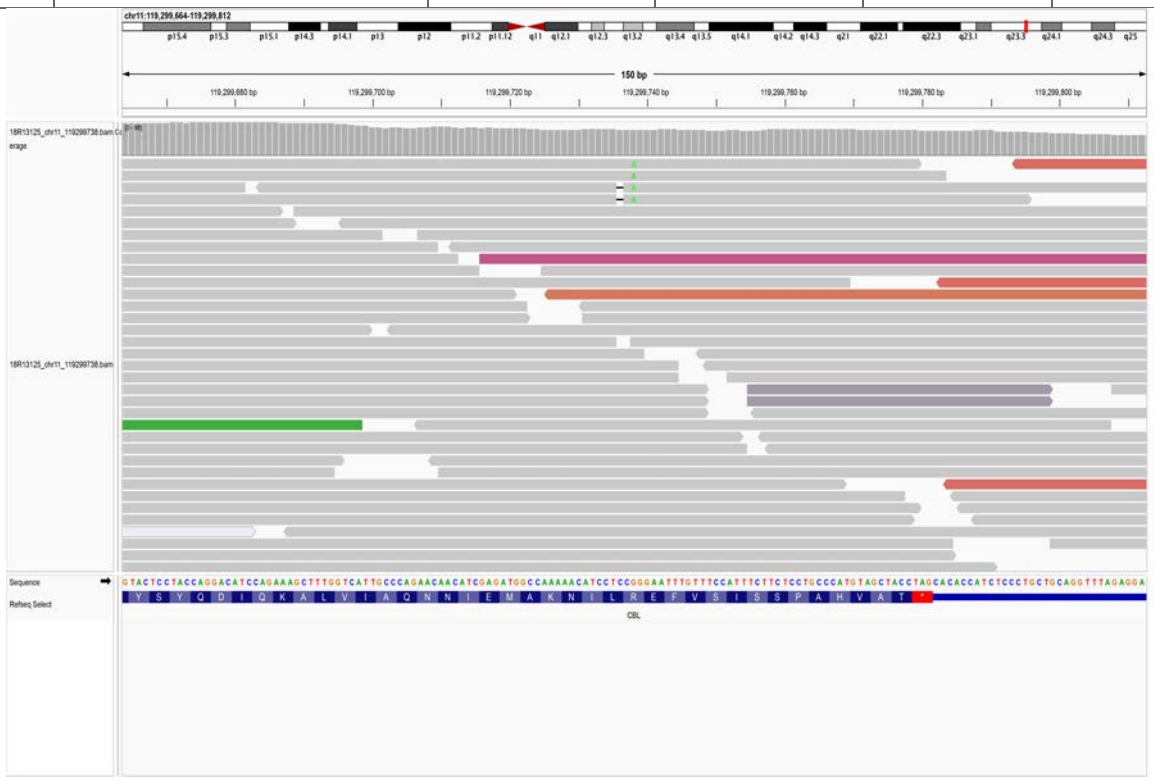
7.11. chr11_119299629_C/T

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

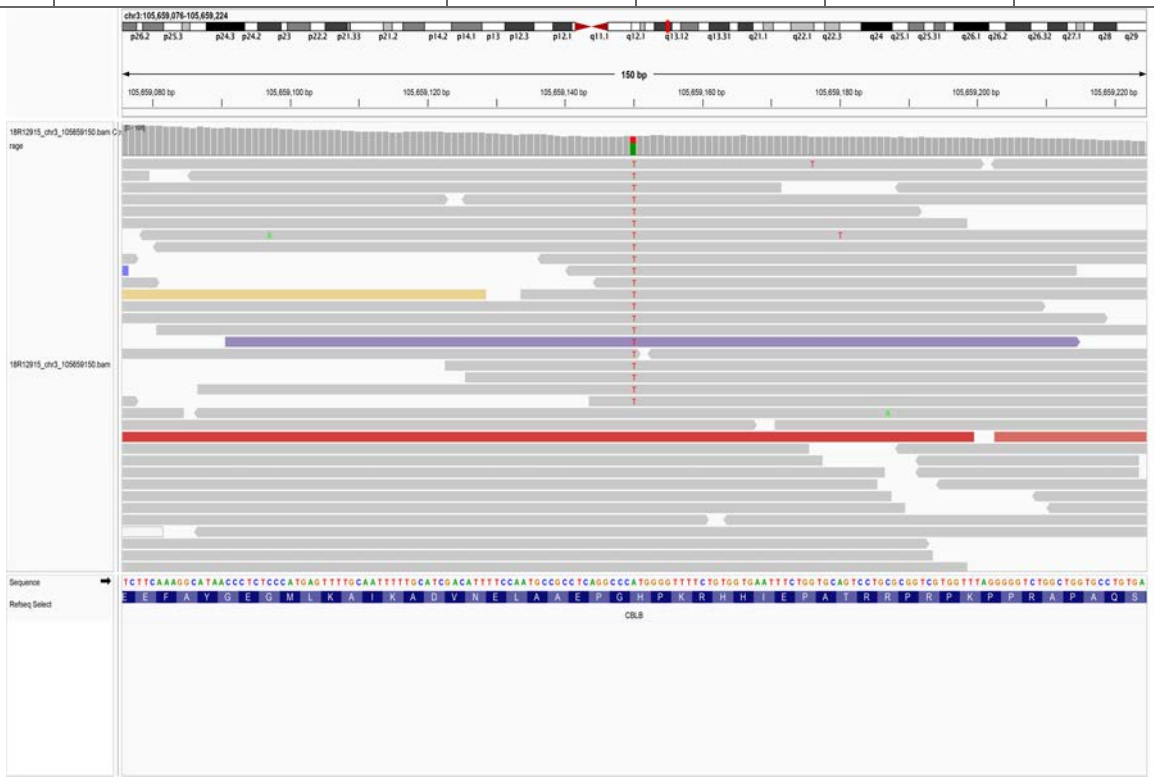
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13125	chr11_119299738_G/A	61	4	*CBL*	missense_variant



8. *CBLB*

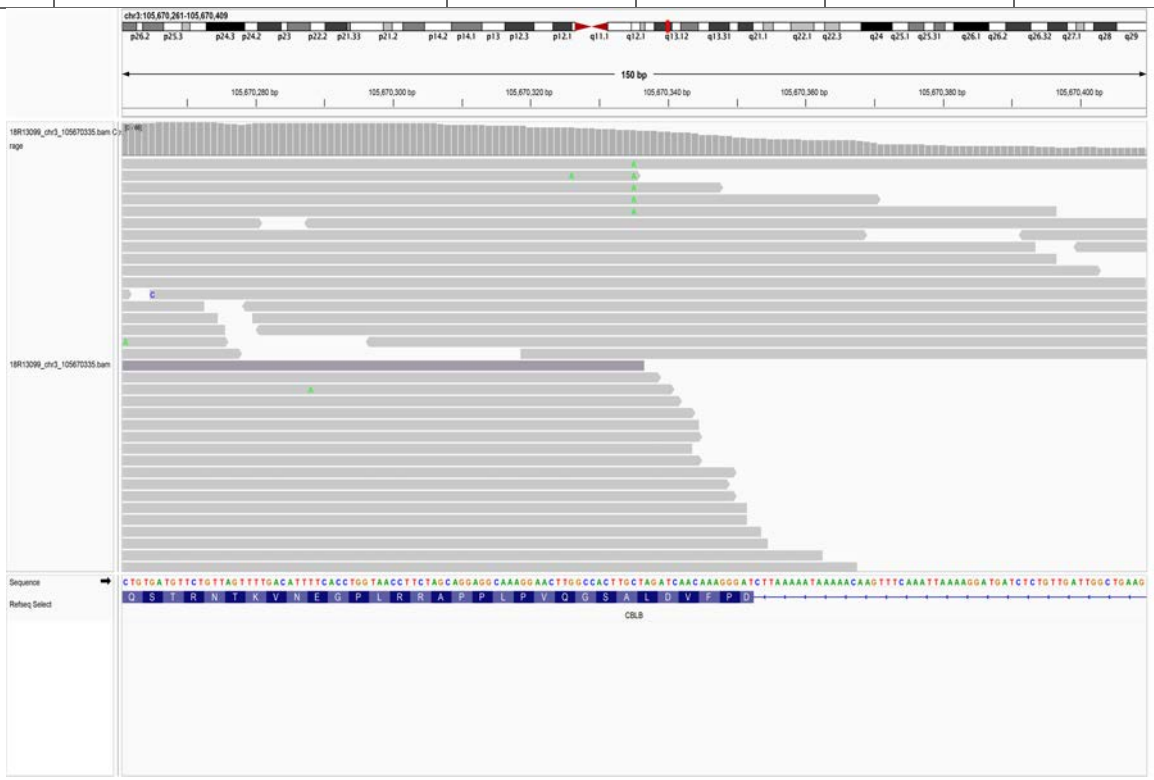
8.1. chr3_105659150_A/T

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



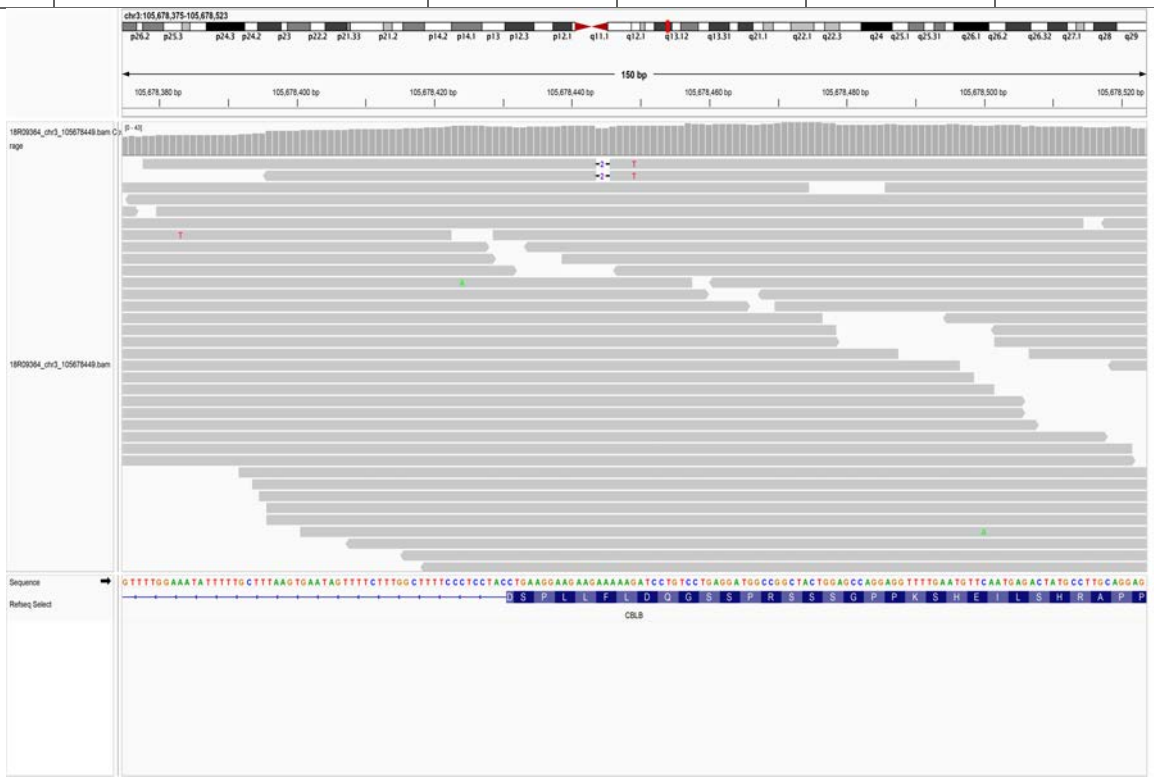
8.2. chr3_105670335_C/A

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



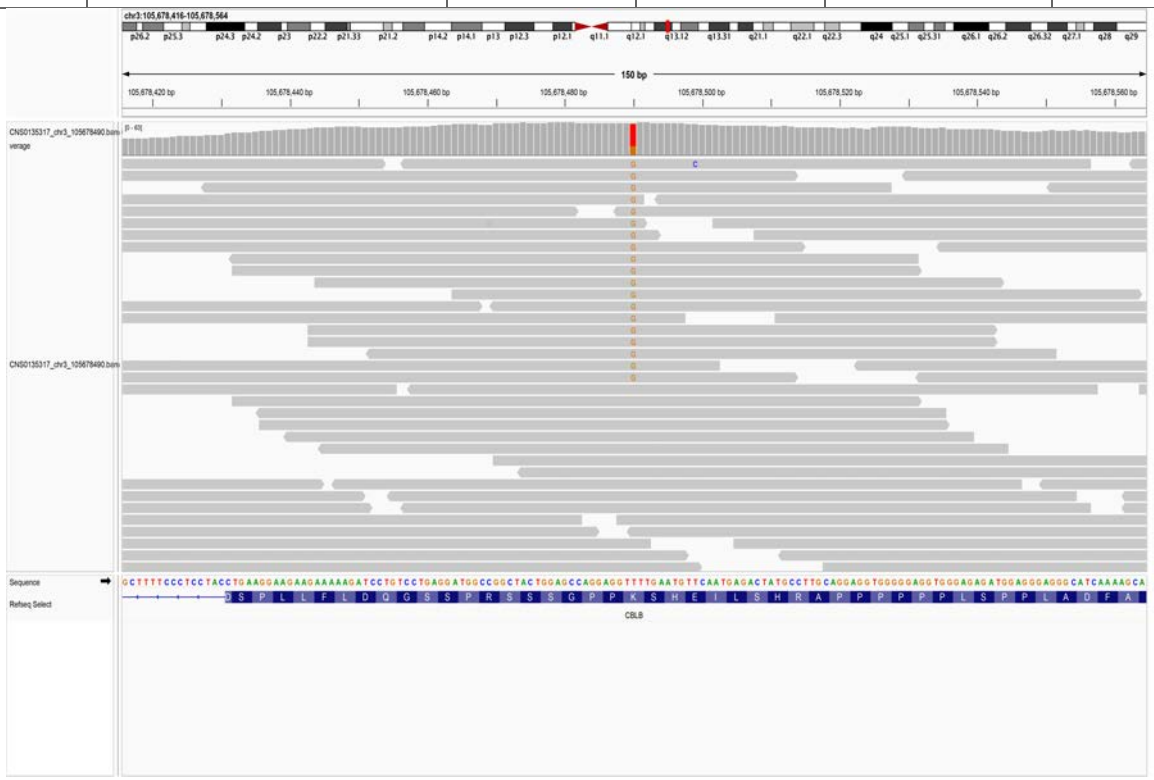
8.3. chr3_105678449_G/T

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



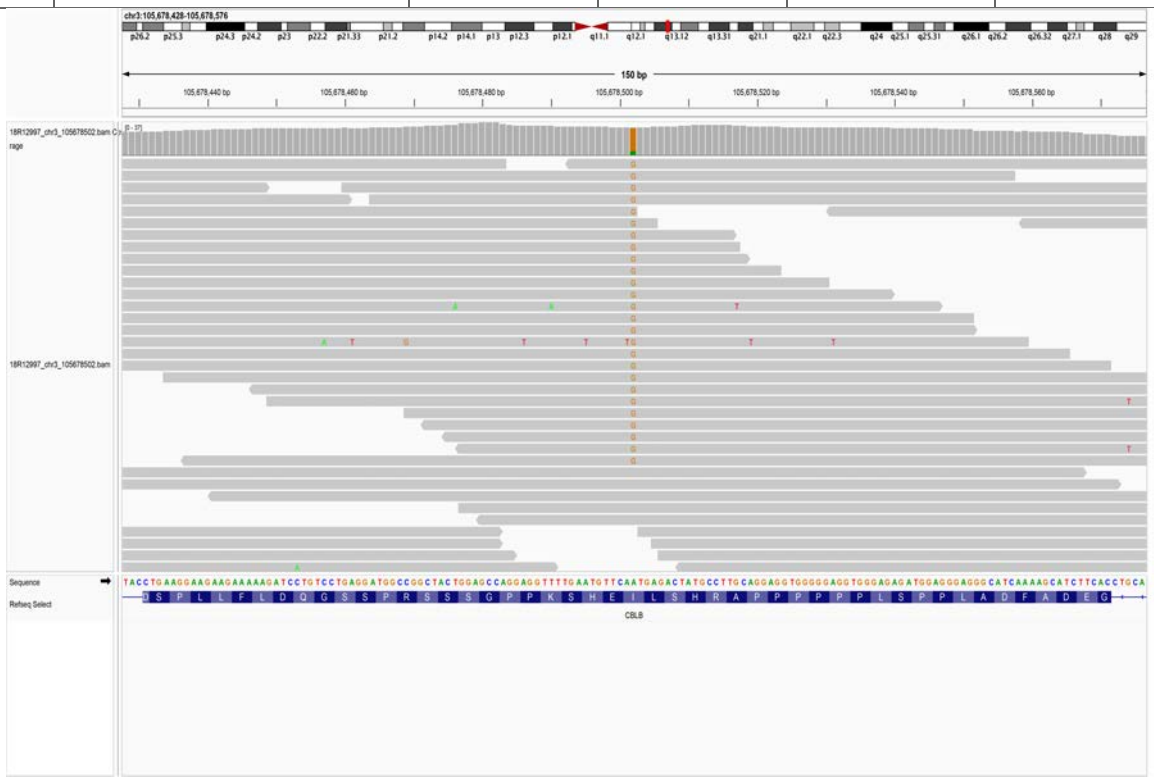
8.4. chr3_105678490_T/G

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



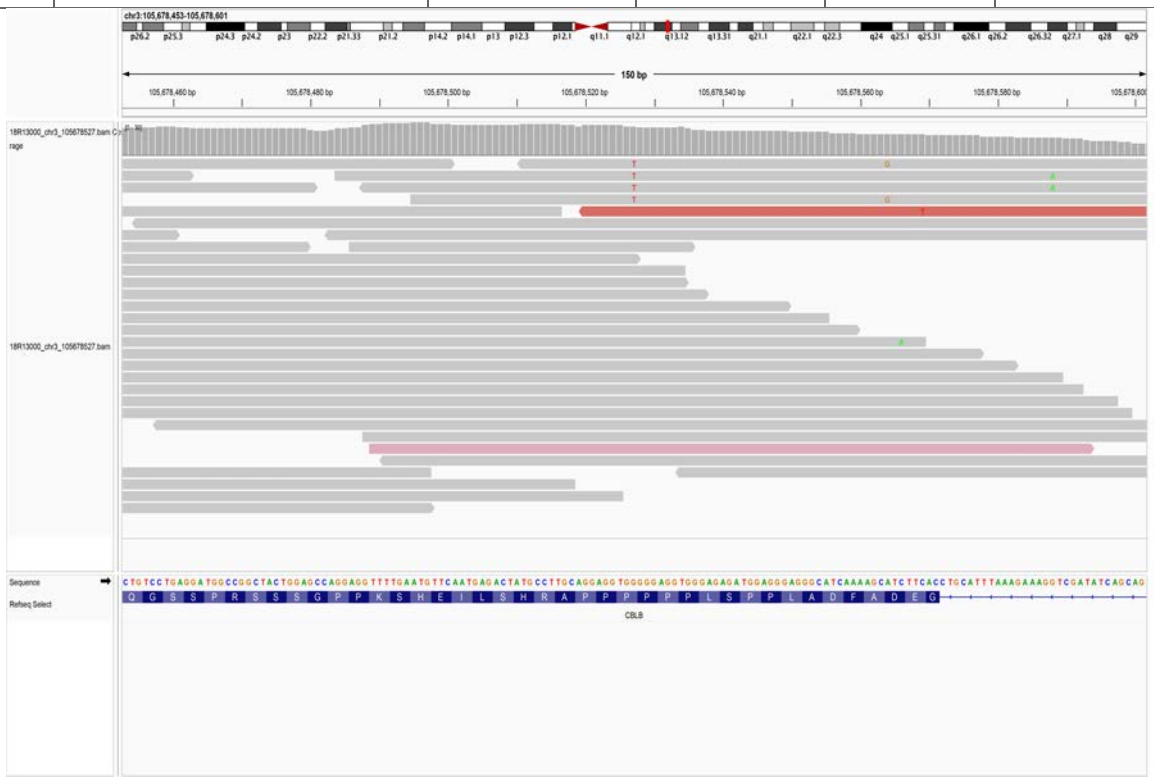
8.5. chr3_105678502_A/G

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



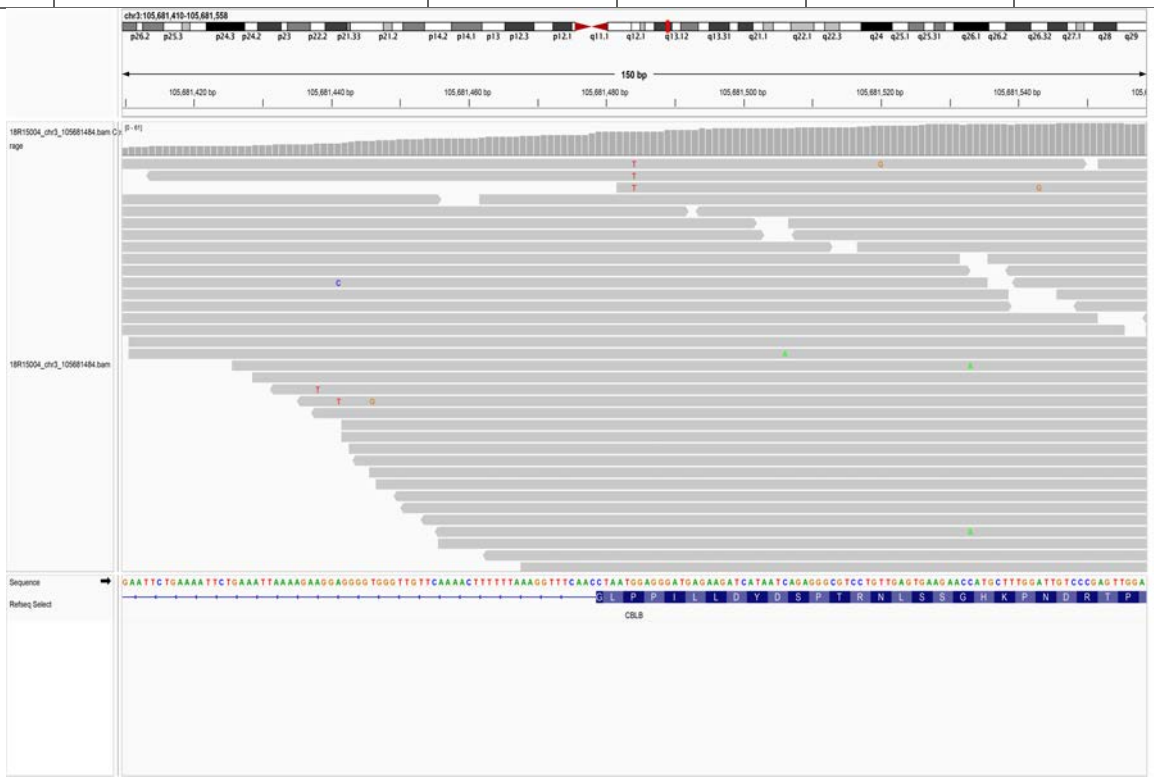
8.6. chr3_105678527_G/T

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



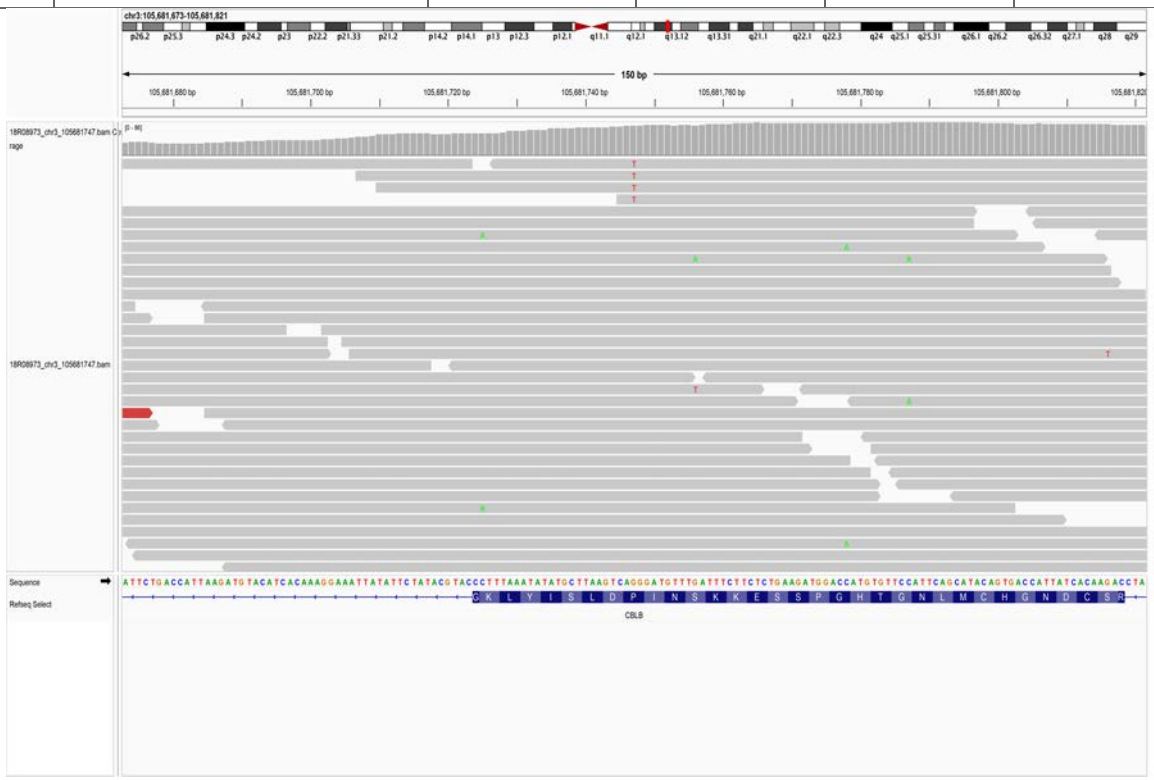
8.7. chr3_105681484_G/T

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



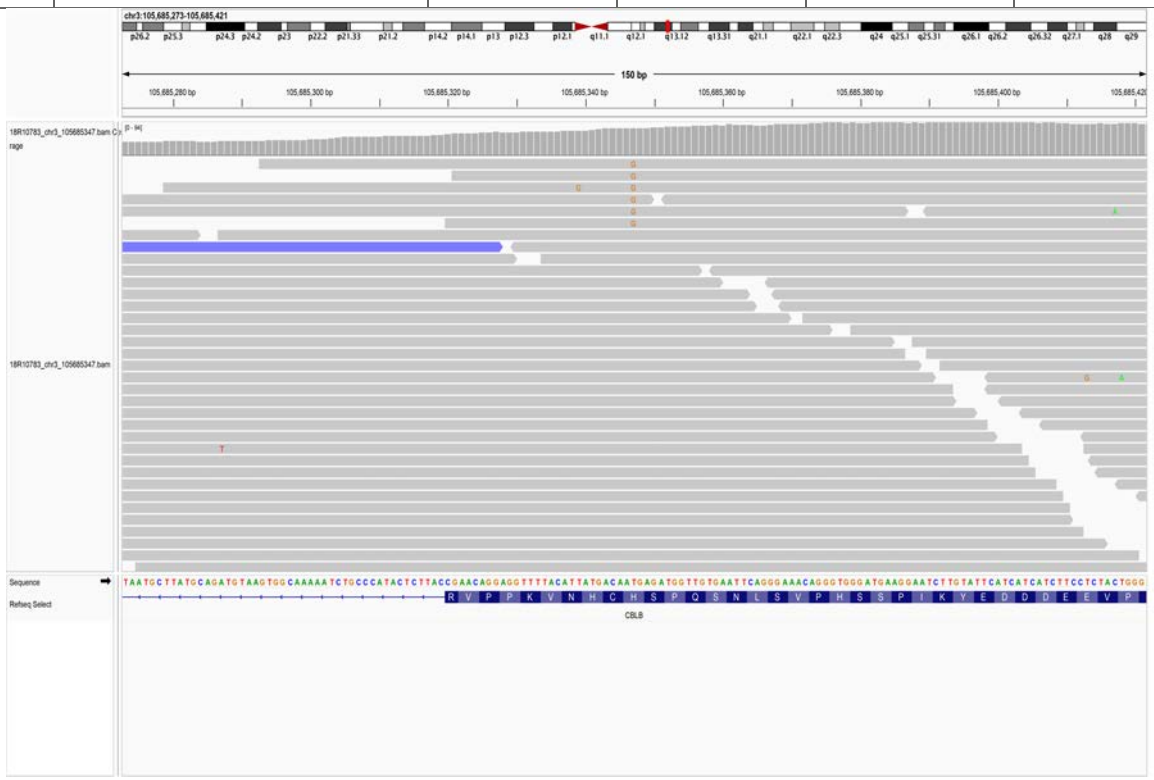
8.8. chr3_105681747_G/T

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



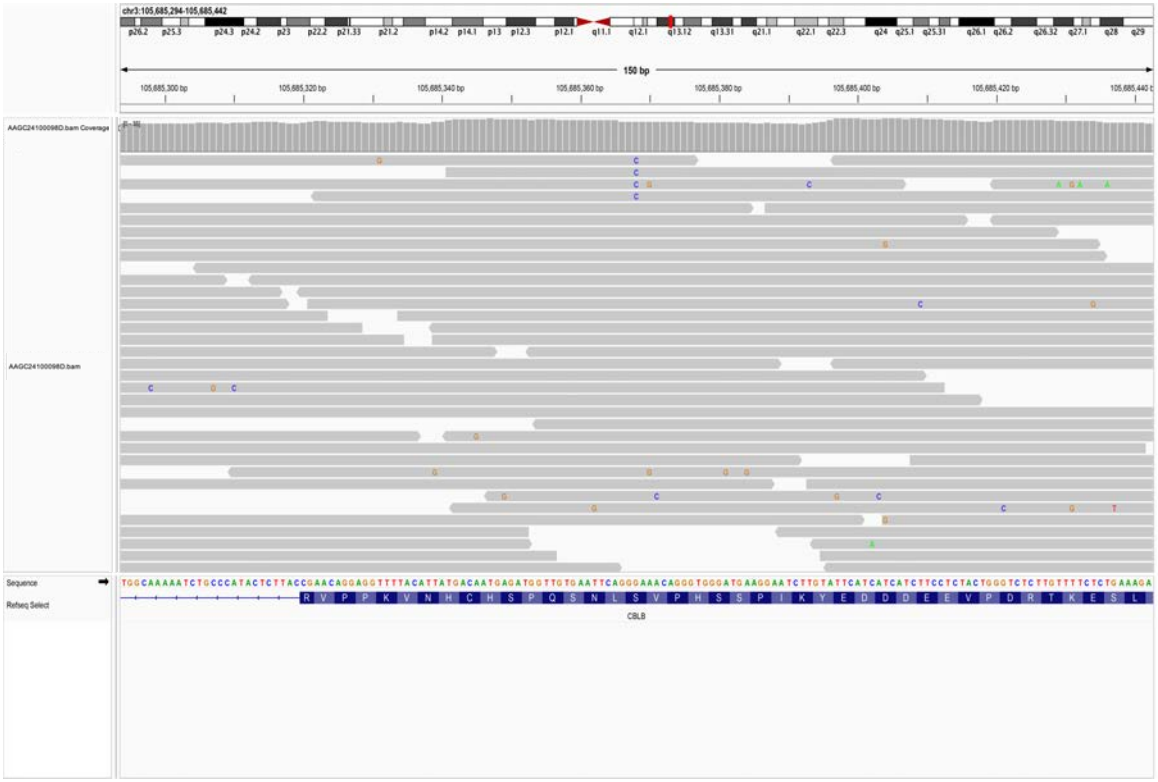
8.9. chr3_105685347_T/G

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



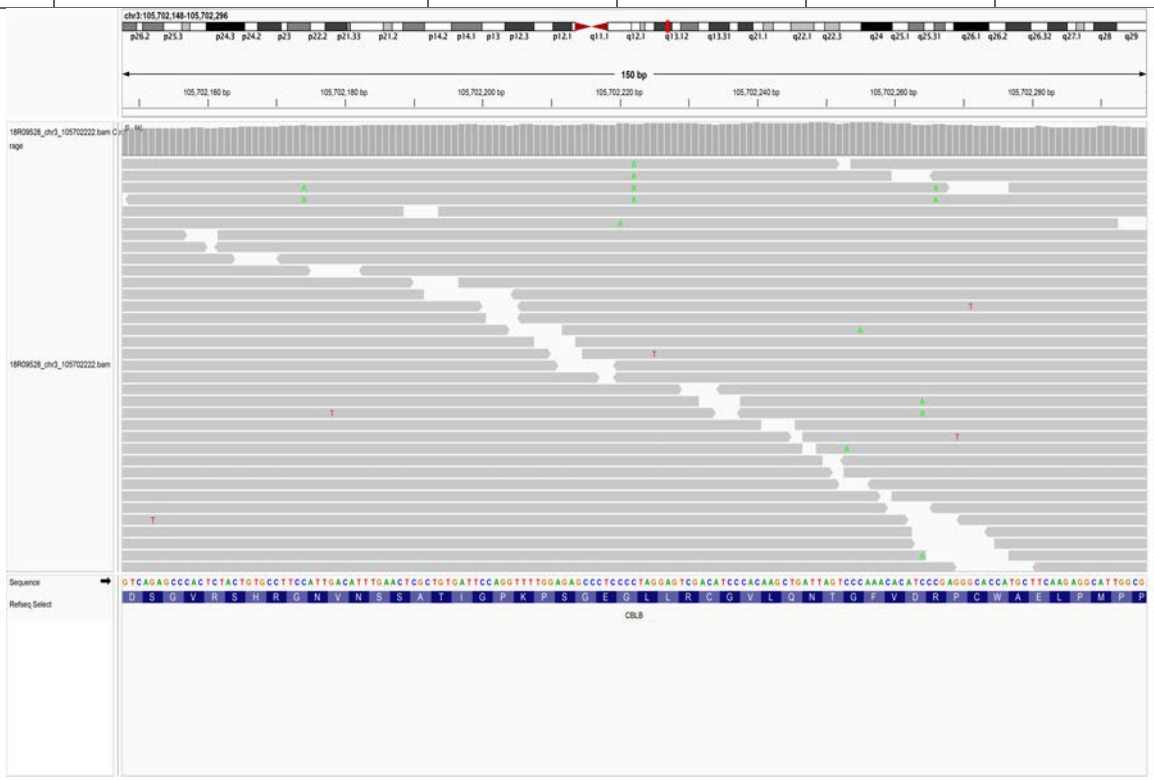
8.10. chr3_105685368_G/C

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



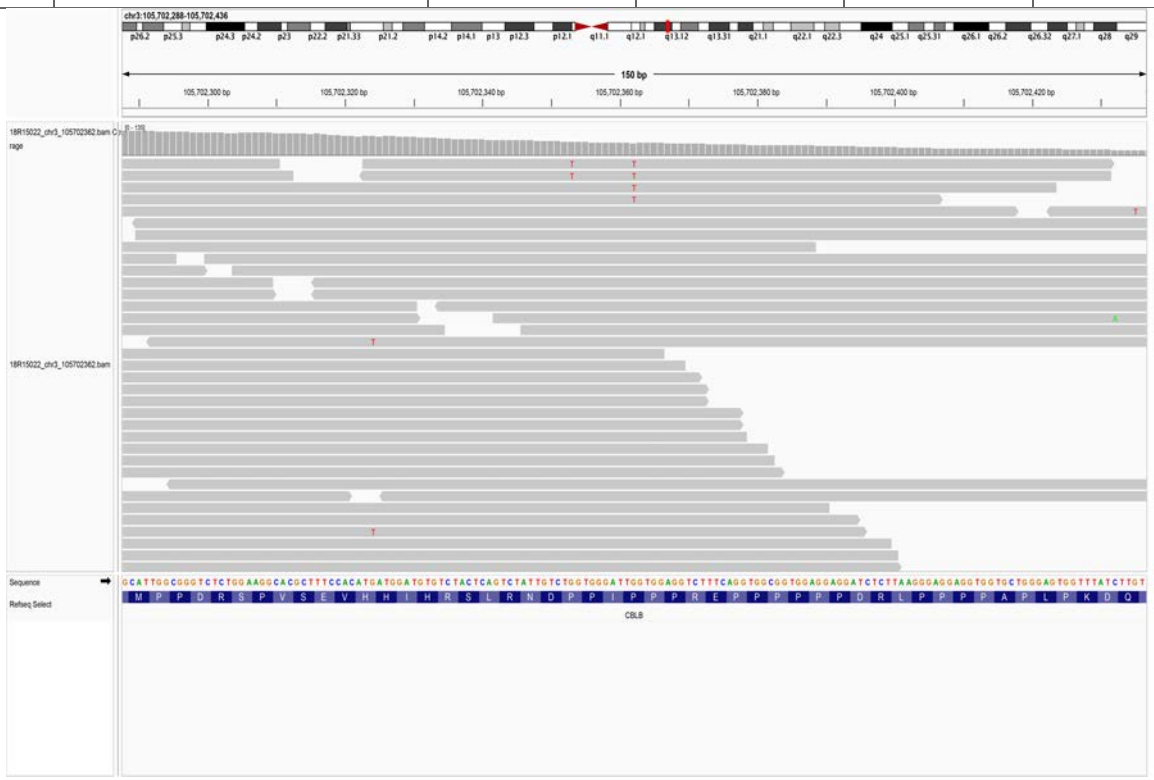
8.11. chr3_105702222_C/A

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



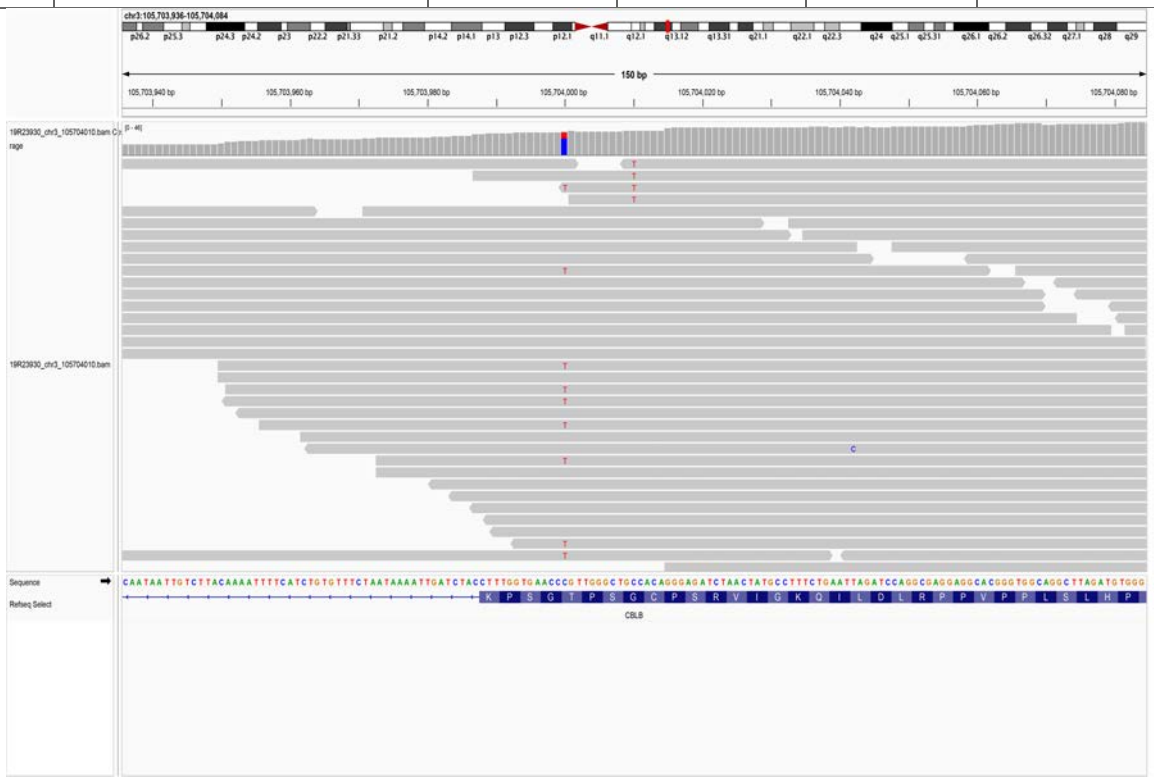
8.12. chr3_105702362_G/T

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



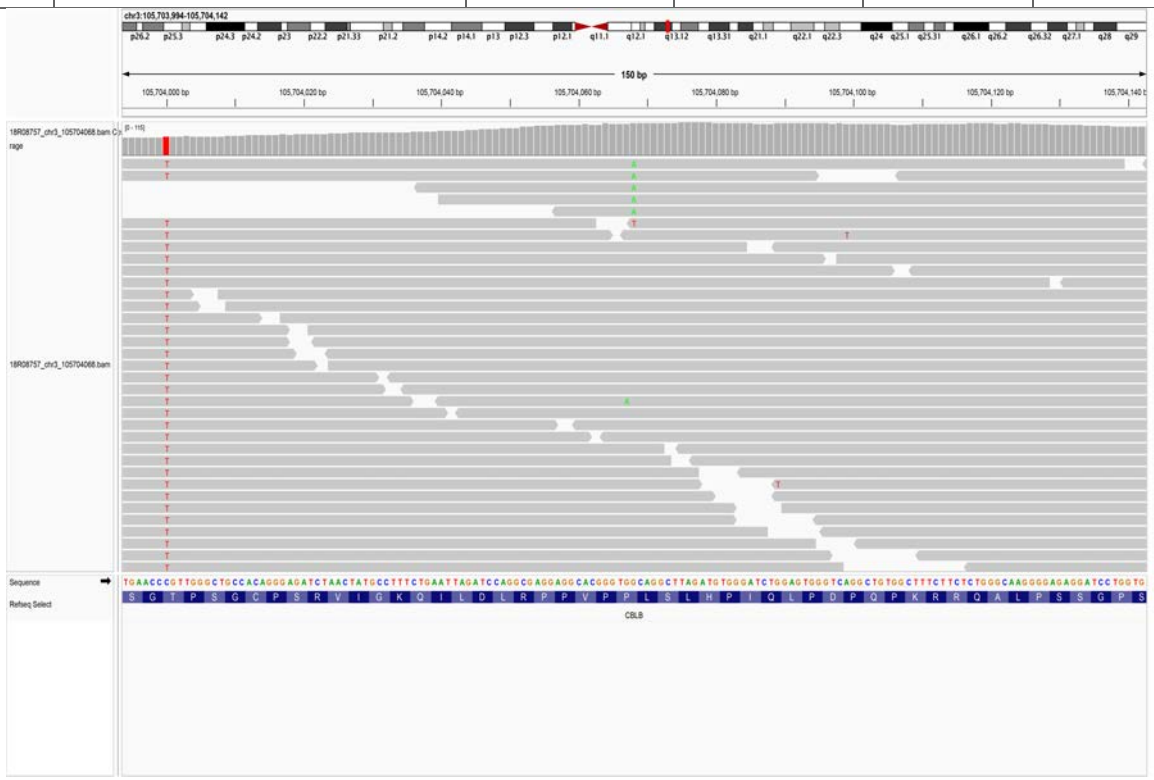
8.13. chr3_105704010_C/T

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



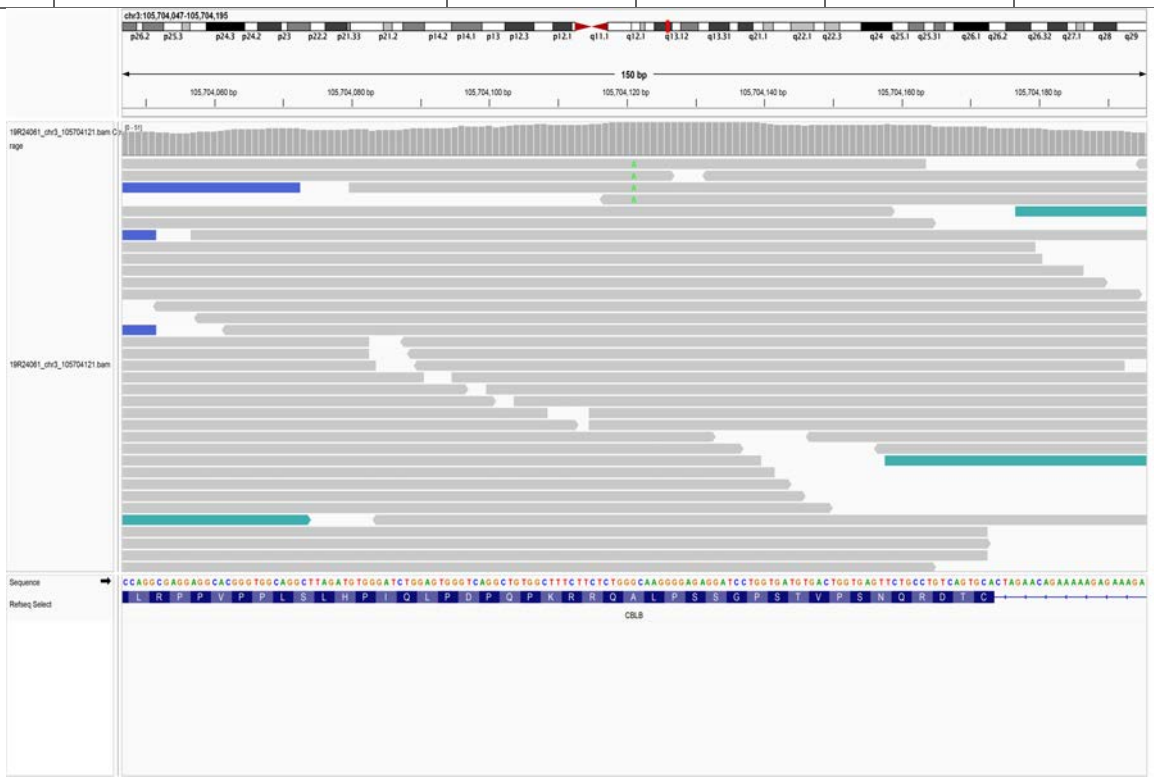
8.14. chr3_105704068_G/A

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



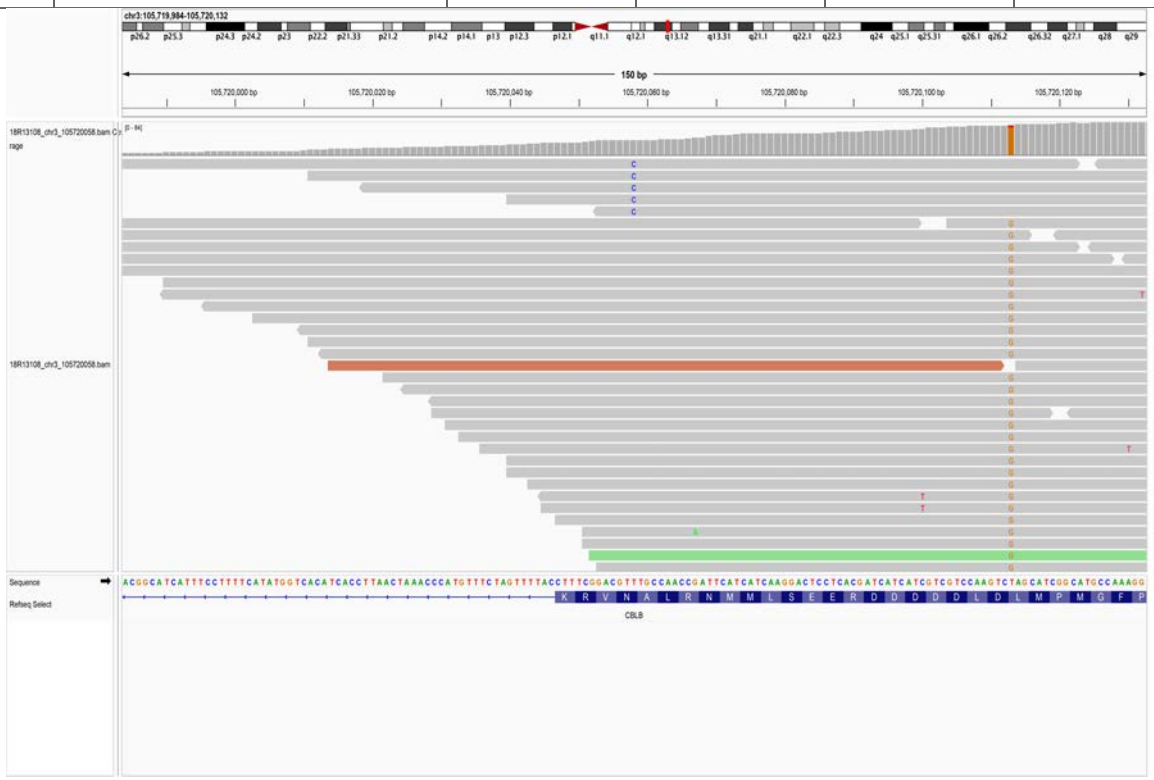
8.15. chr3_105704121_G/A

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



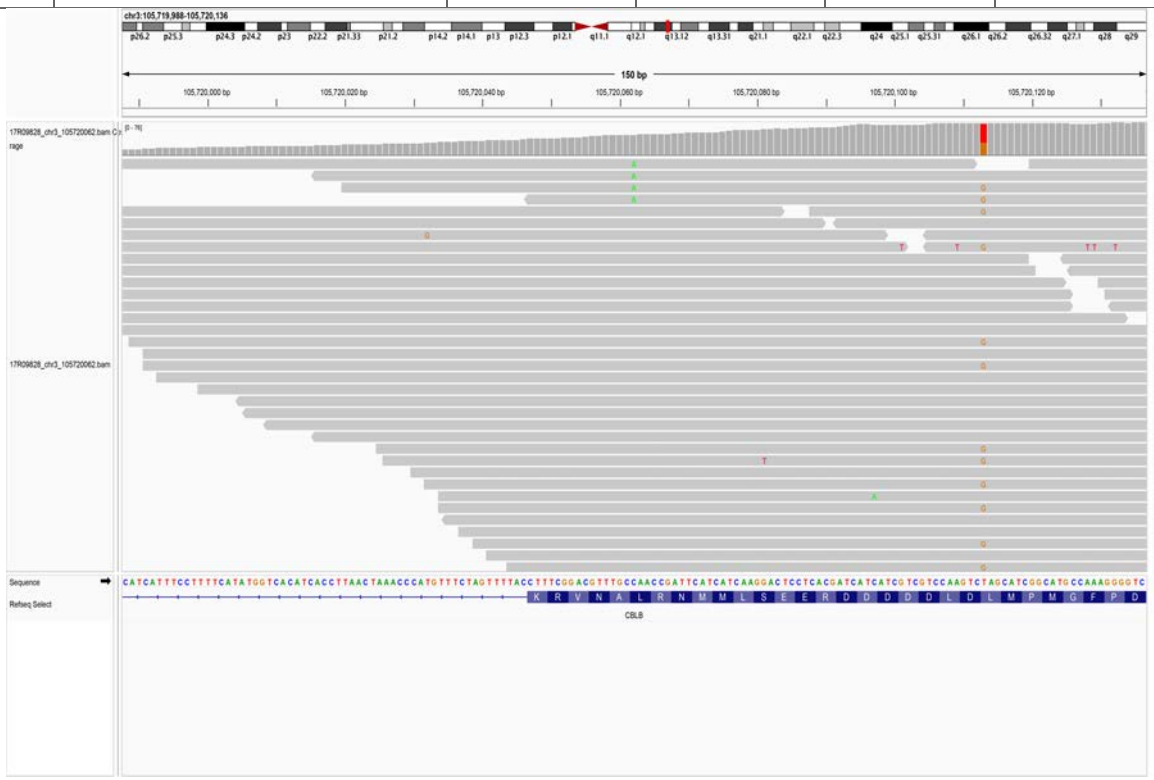
8.16. chr3_105720058_T/C

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



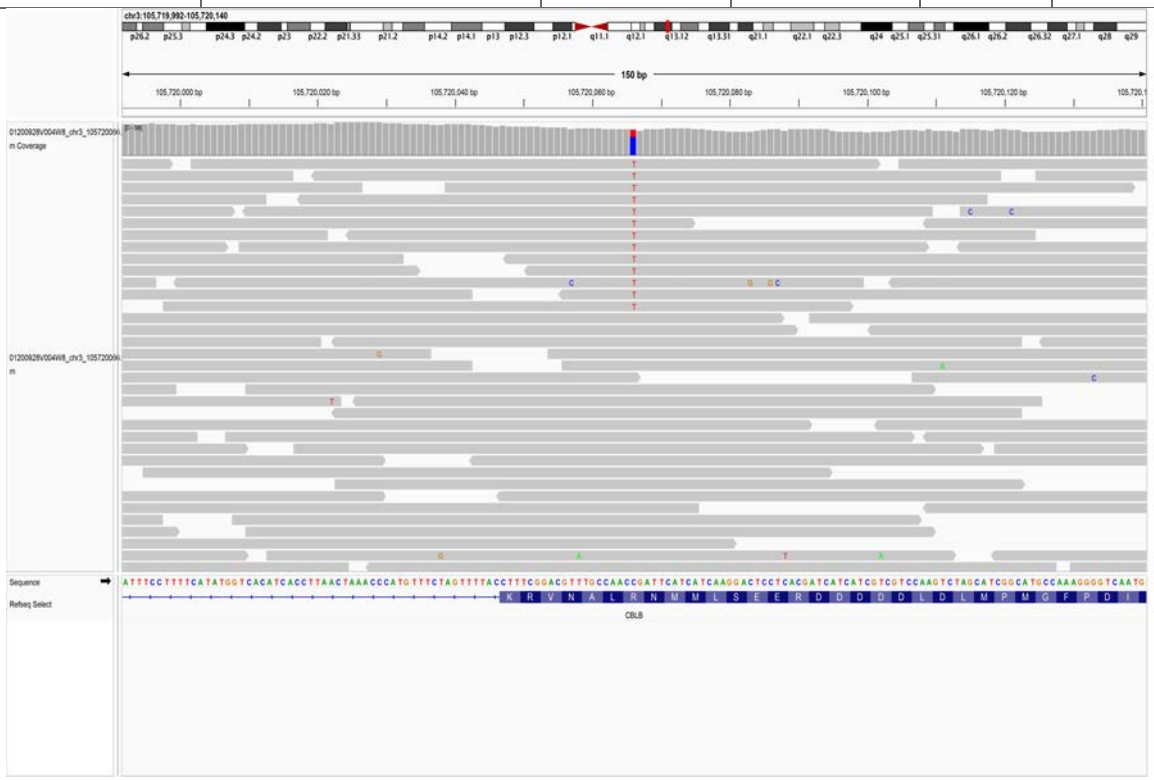
8.17. chr3_105720062_C/A

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



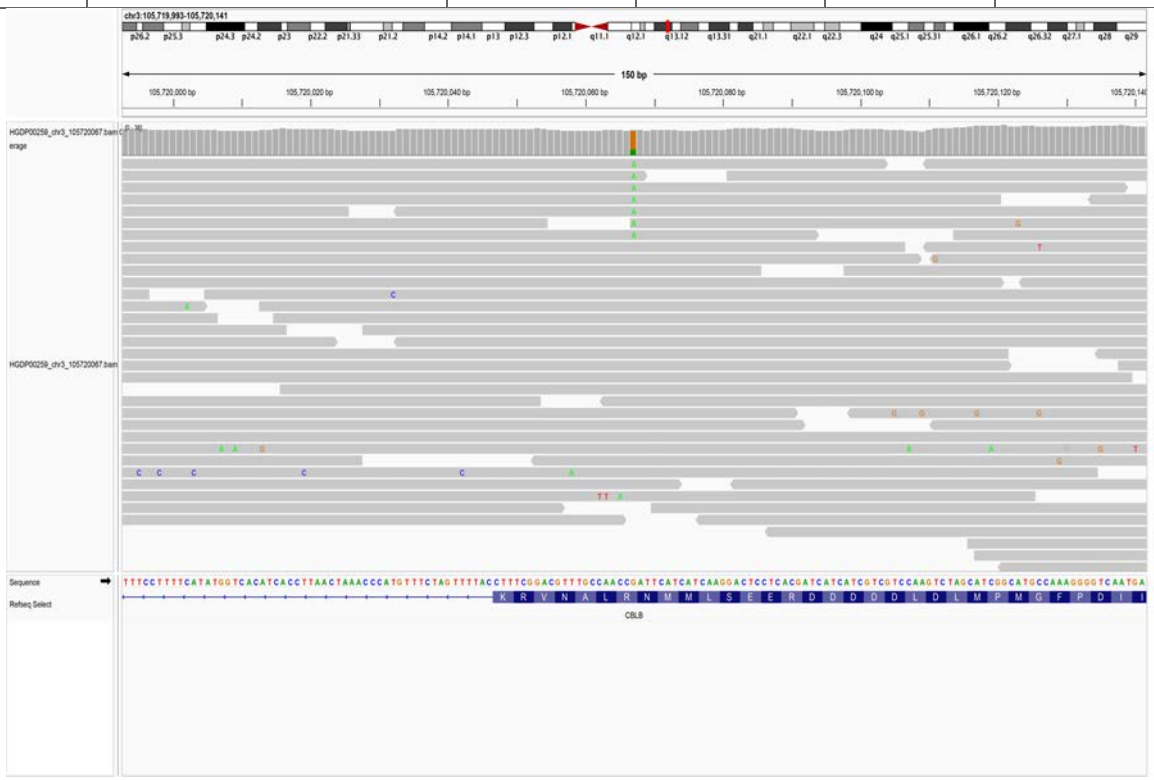
8.18. chr3_105720066_C/T

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



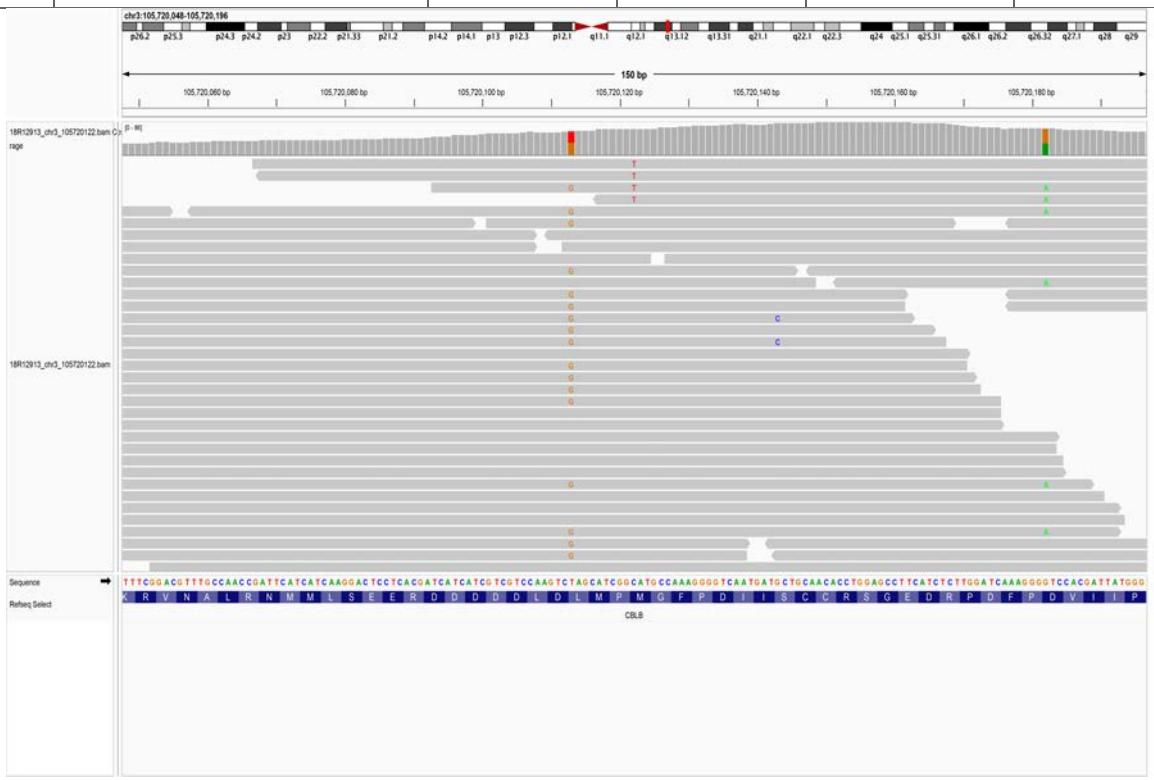
8.19. chr3_105720067_G/A

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



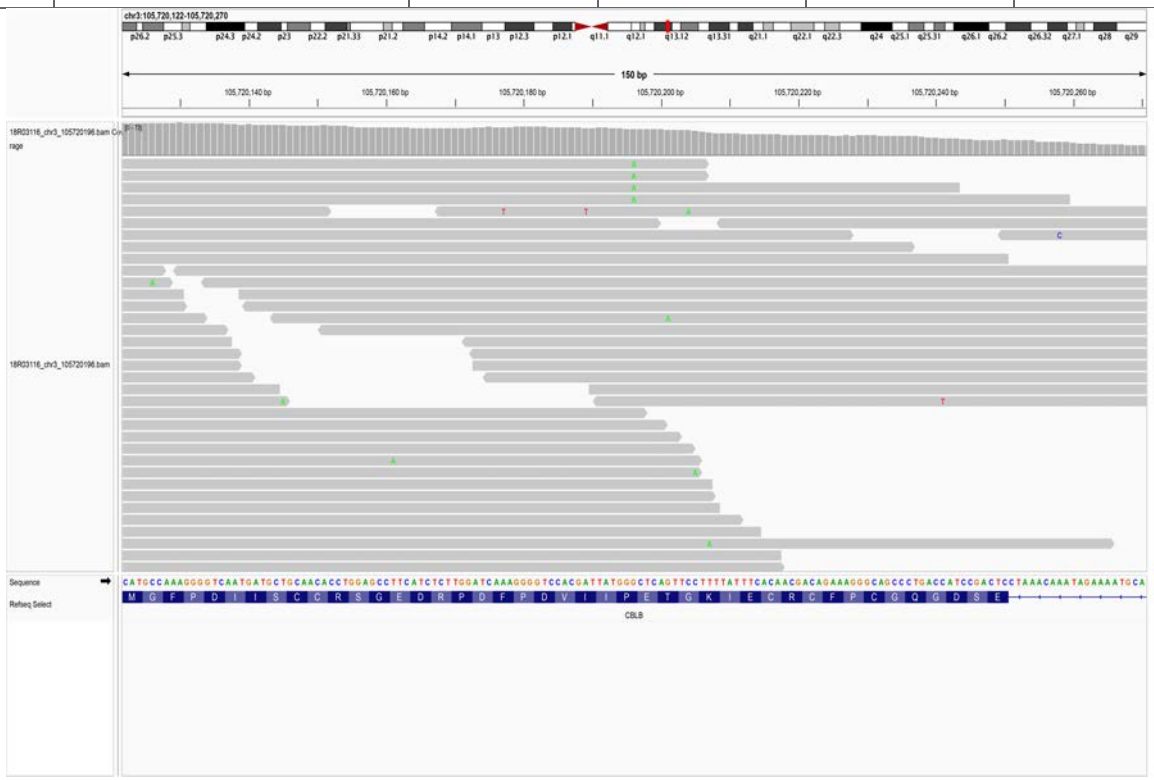
8.20. chr3_105720122_C/T

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

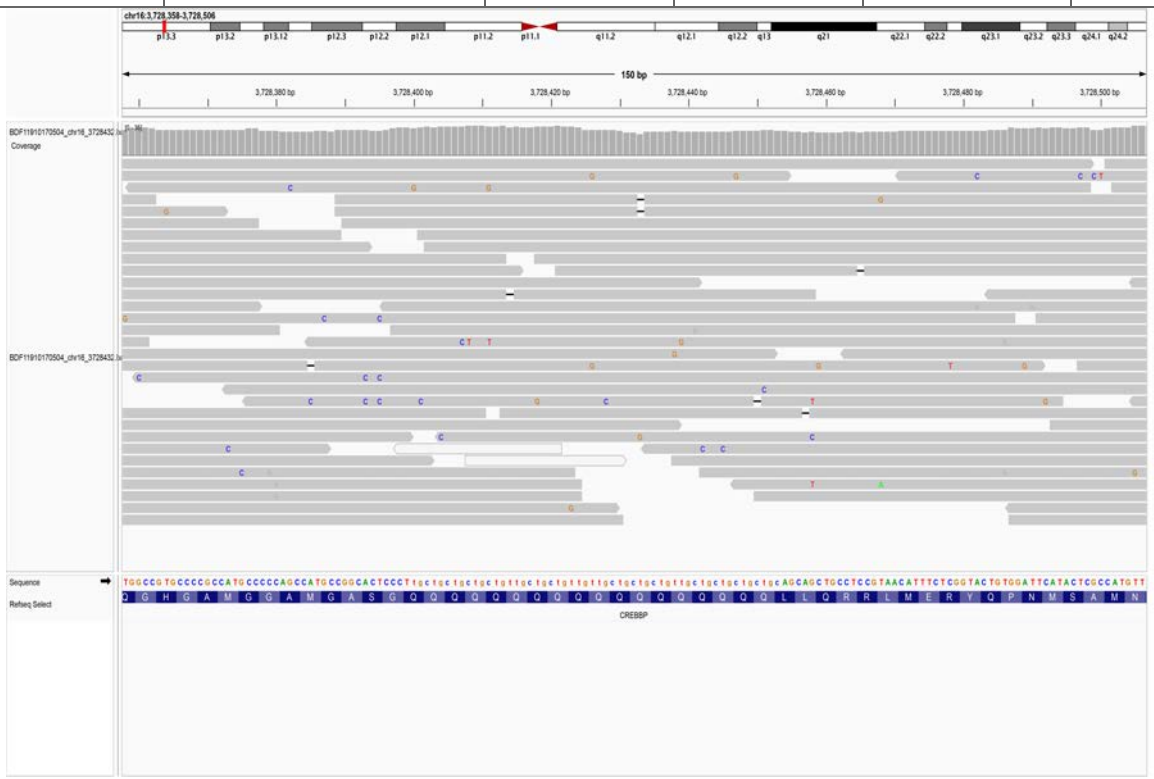
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03116	chr3_105720196_G/A	51	4	*CBLB*	missense_variant



9. *CREBBP*

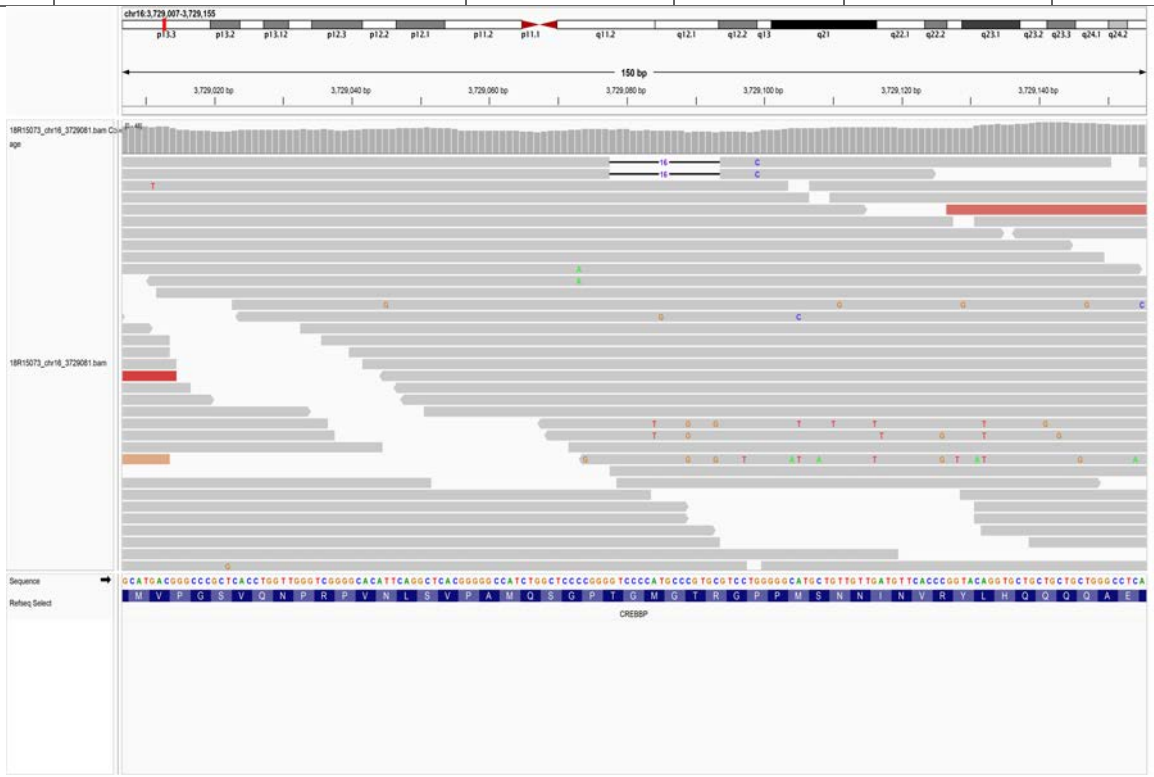
9.1. chr16_3728433_T/-

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



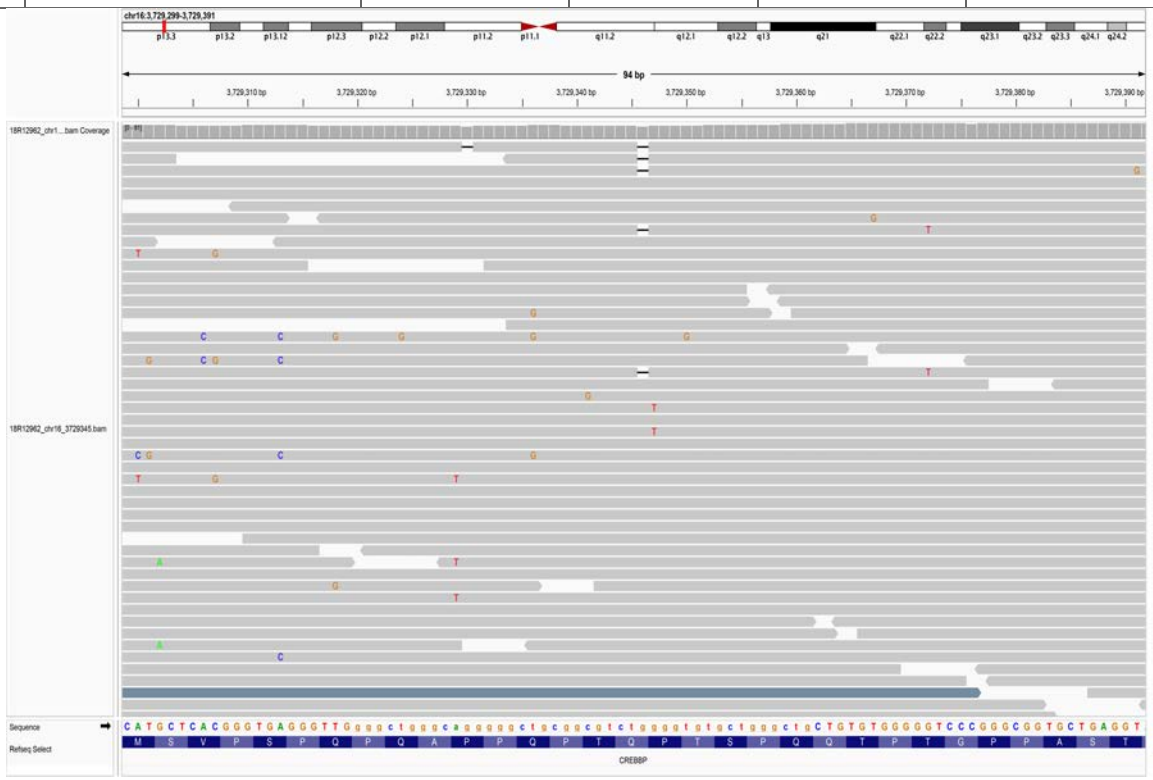
9.2. chr16_3729082_CCATGCCCGTGCG/-

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



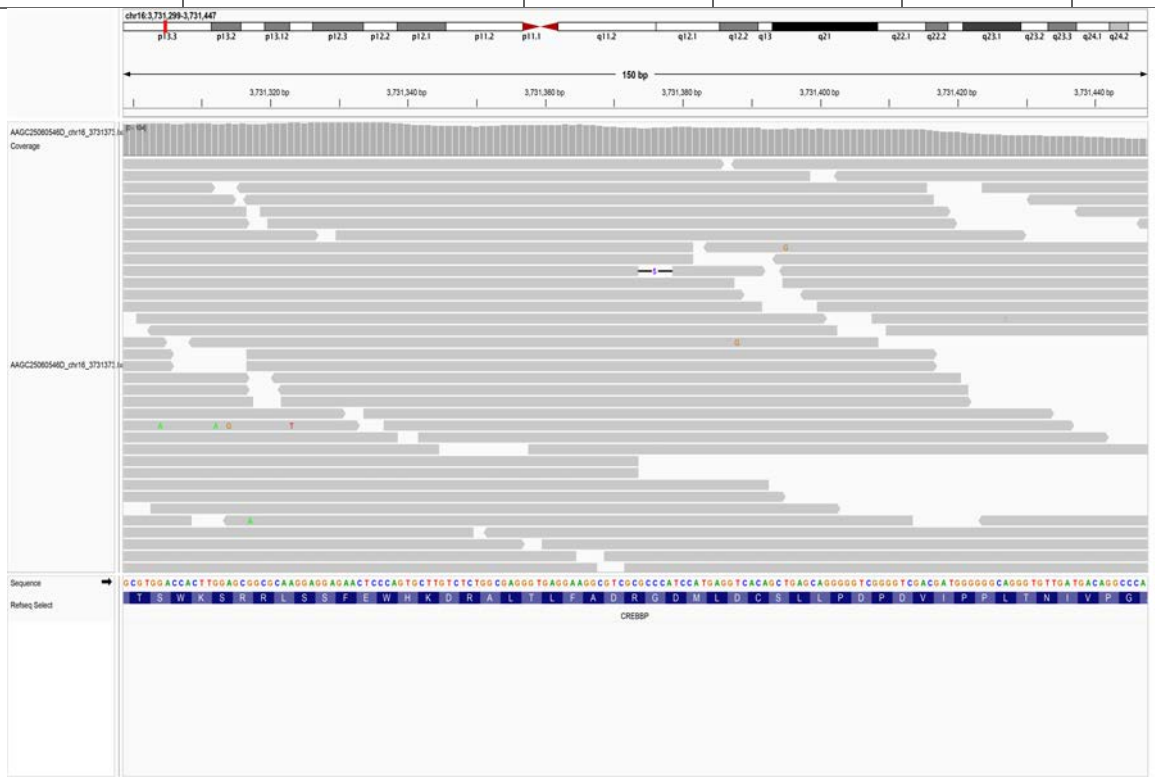
9.3. chr16_3729346_G/-

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



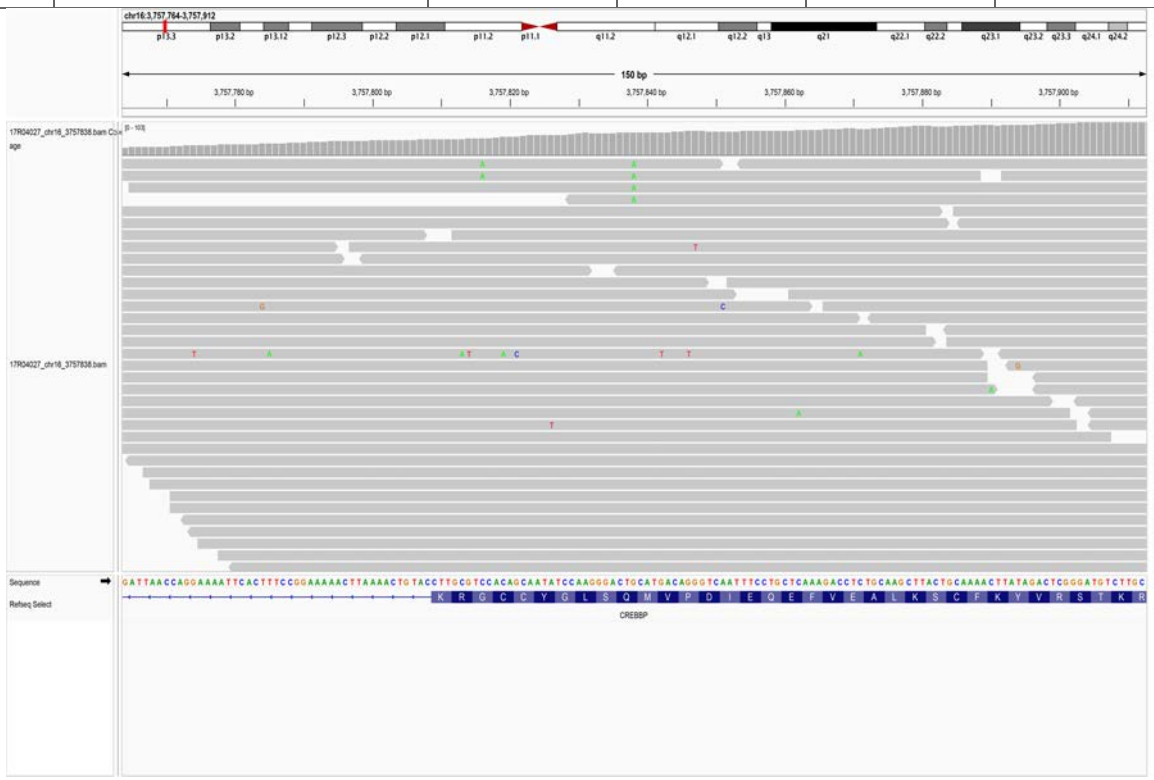
9.4. chr16_3731374_GCCCA/-

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



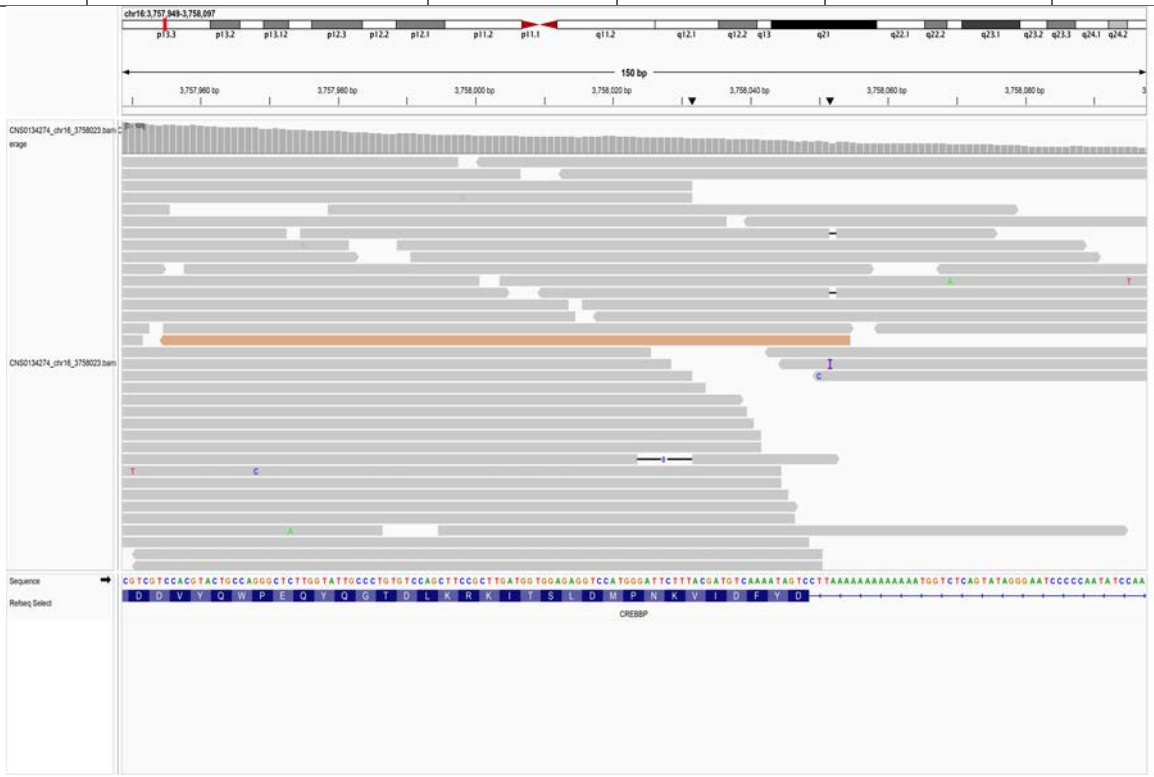
9.5. chr16_3757838_G/A

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



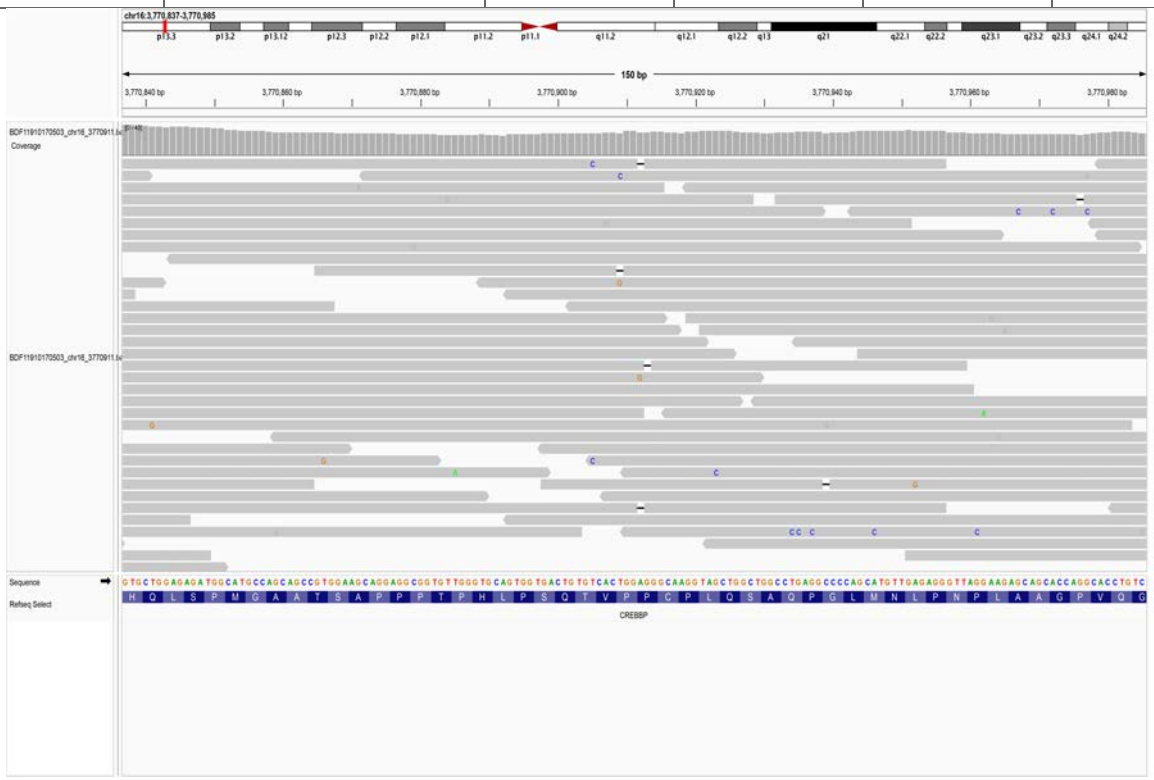
9.6. chr16_3758024_GATTCTTT/-

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



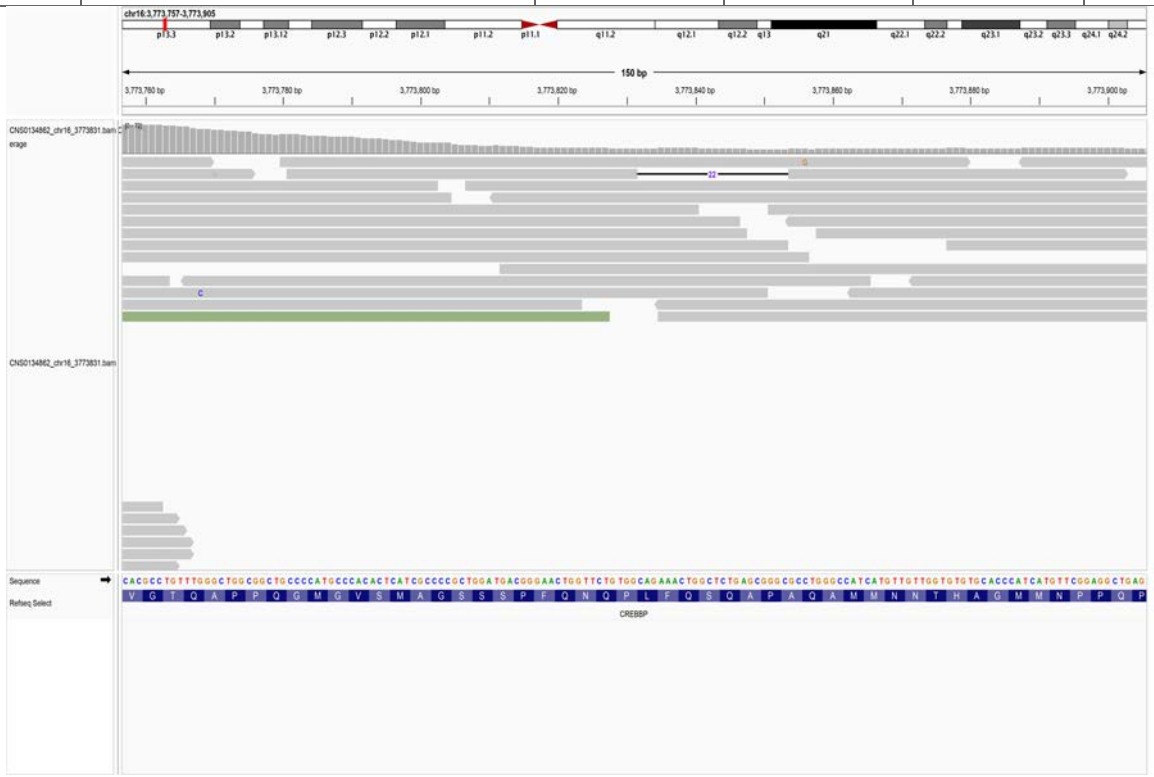
9.7. chr16_3770912_A/-

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



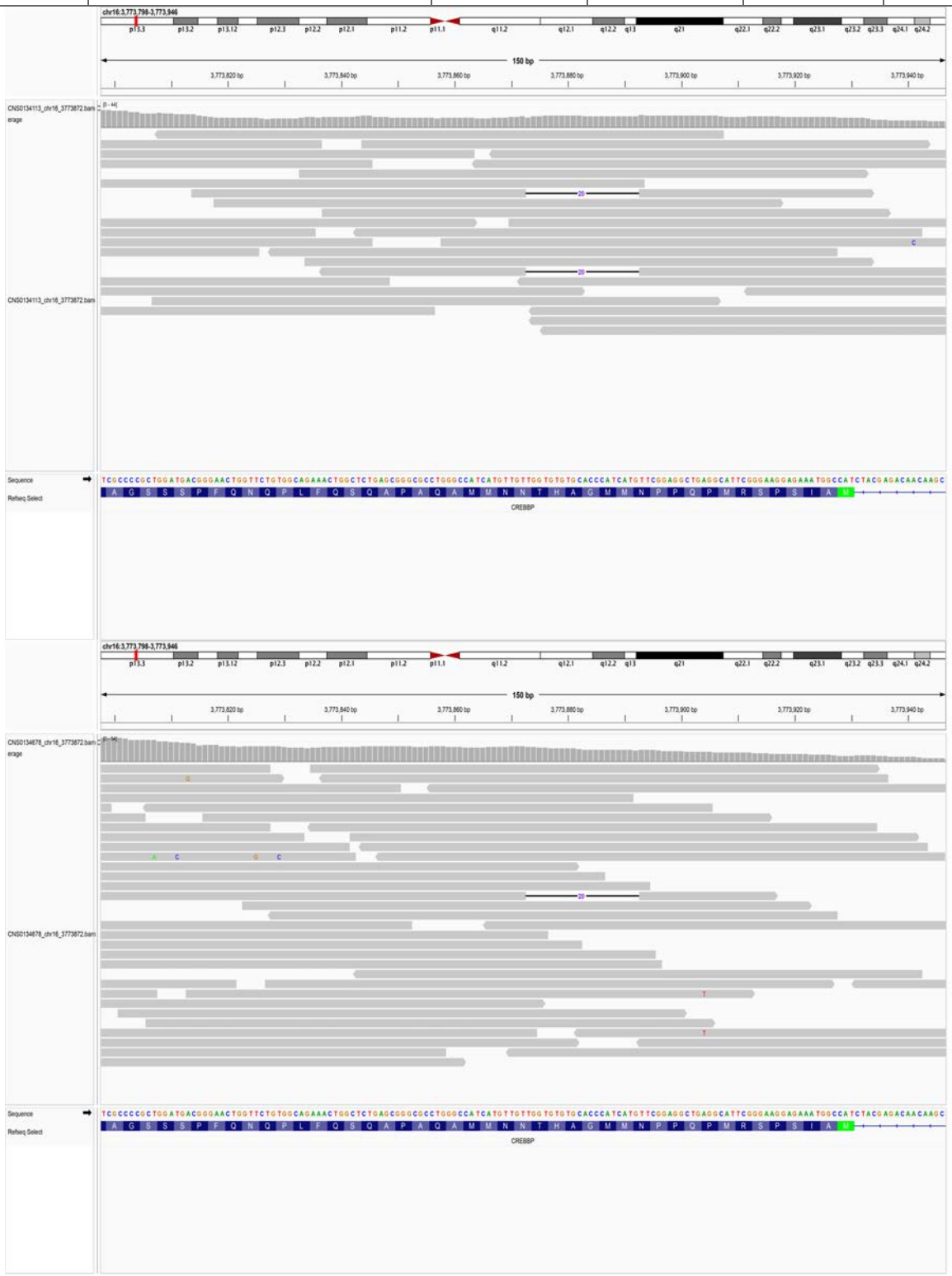
9.8. chr16_3773832_CAGAAACTGGCTCTGAGCGGGC/-

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



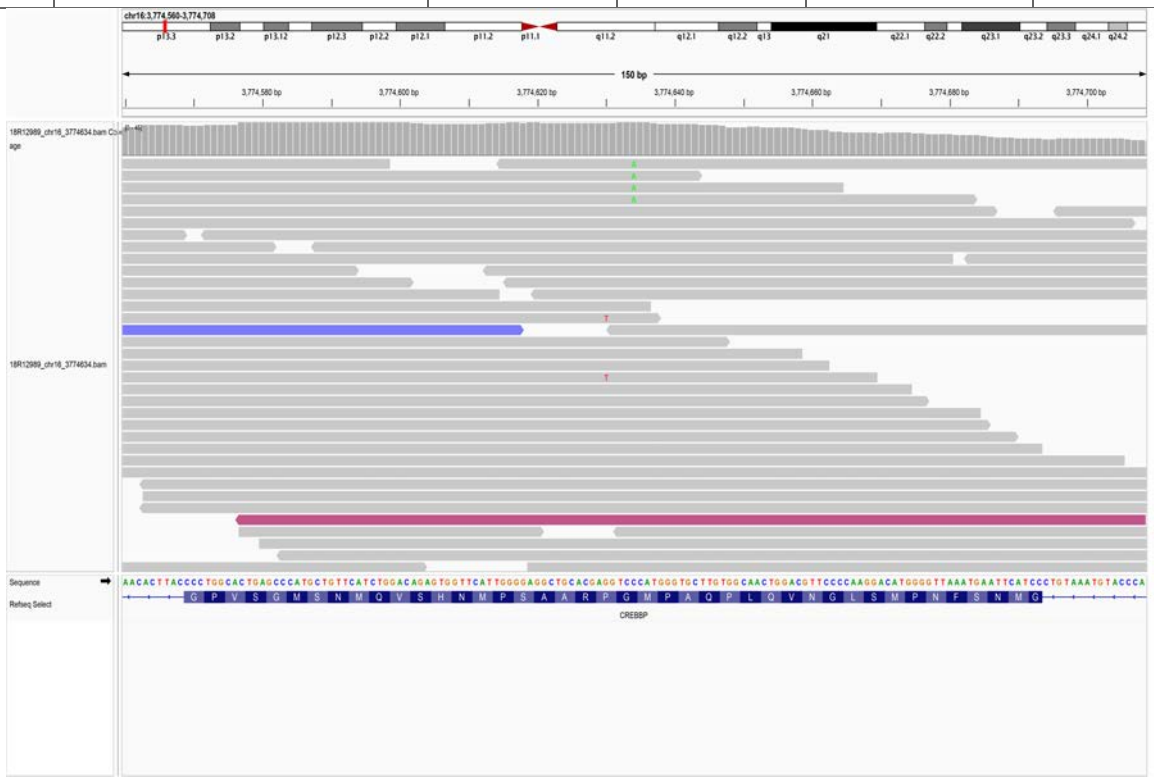
9.9. chr16_3773873_TGGTGTGTGCACCCATCATG/-

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



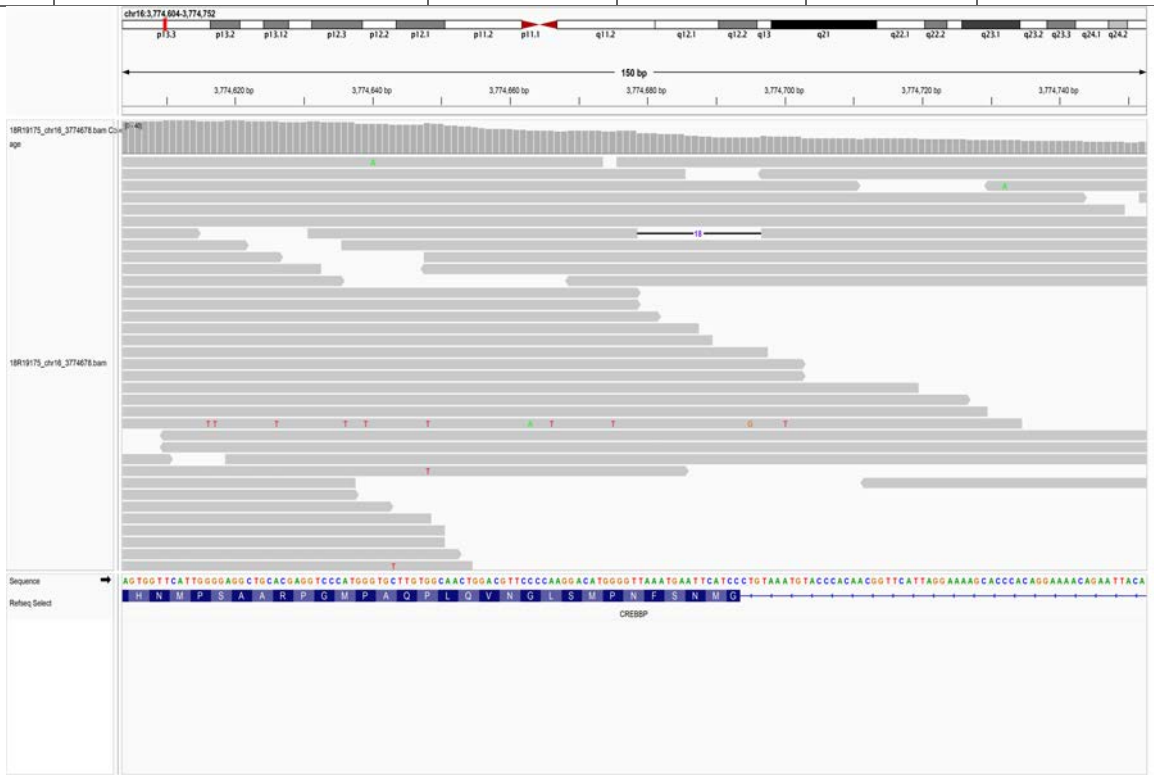
9.10. chr16_3774634_C/A

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



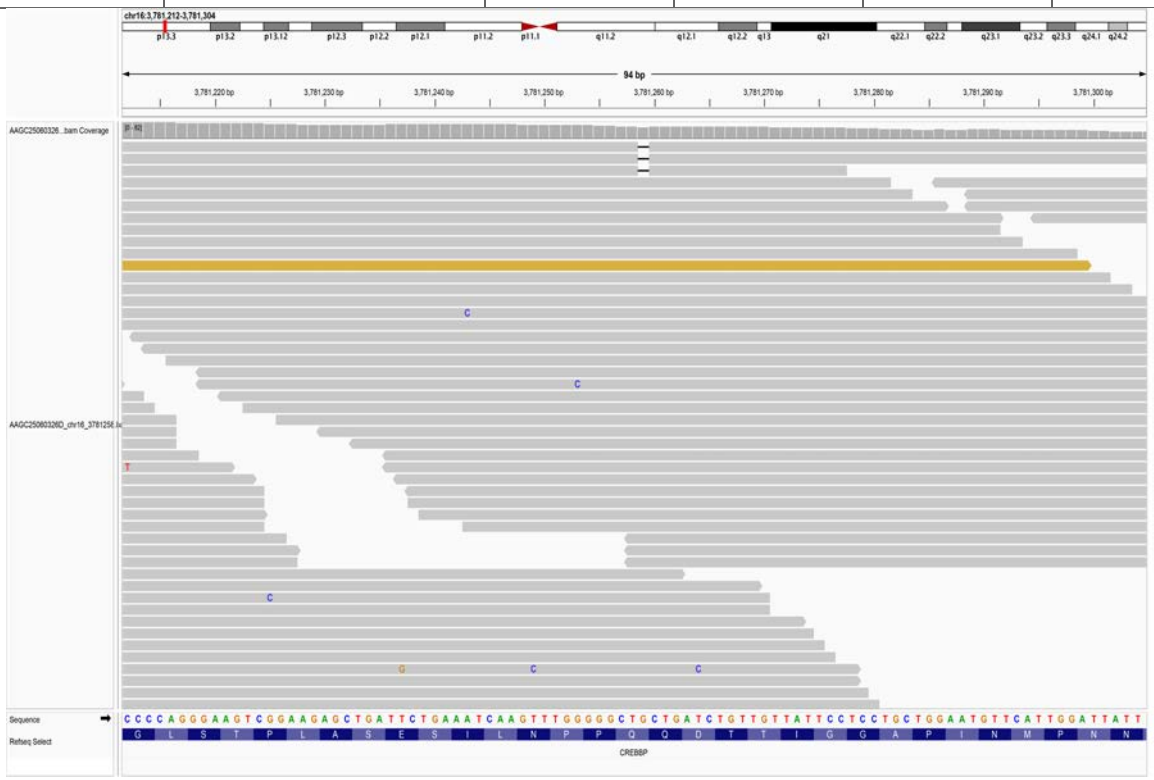
9.11. chr16_3774679_TAAATGAATTCATCCCTG/-

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



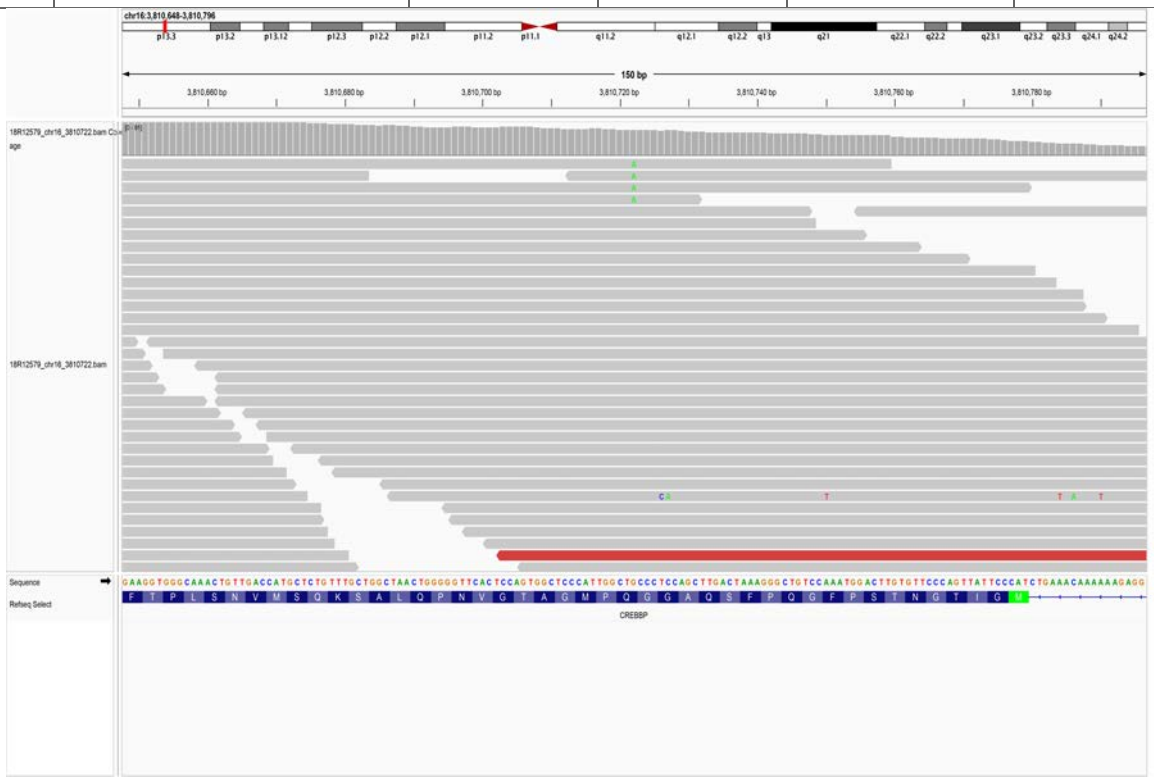
9.12. chr16_3781259_G/-

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



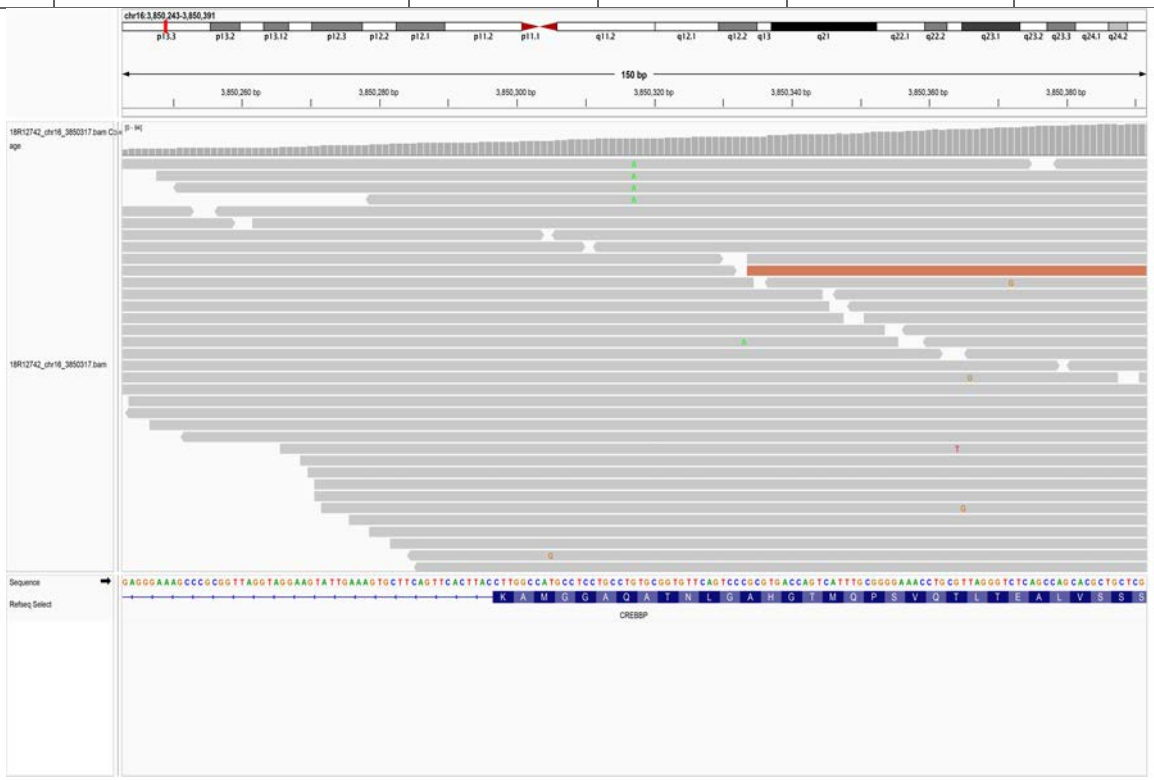
9.13. chr16_3810722_G/A

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



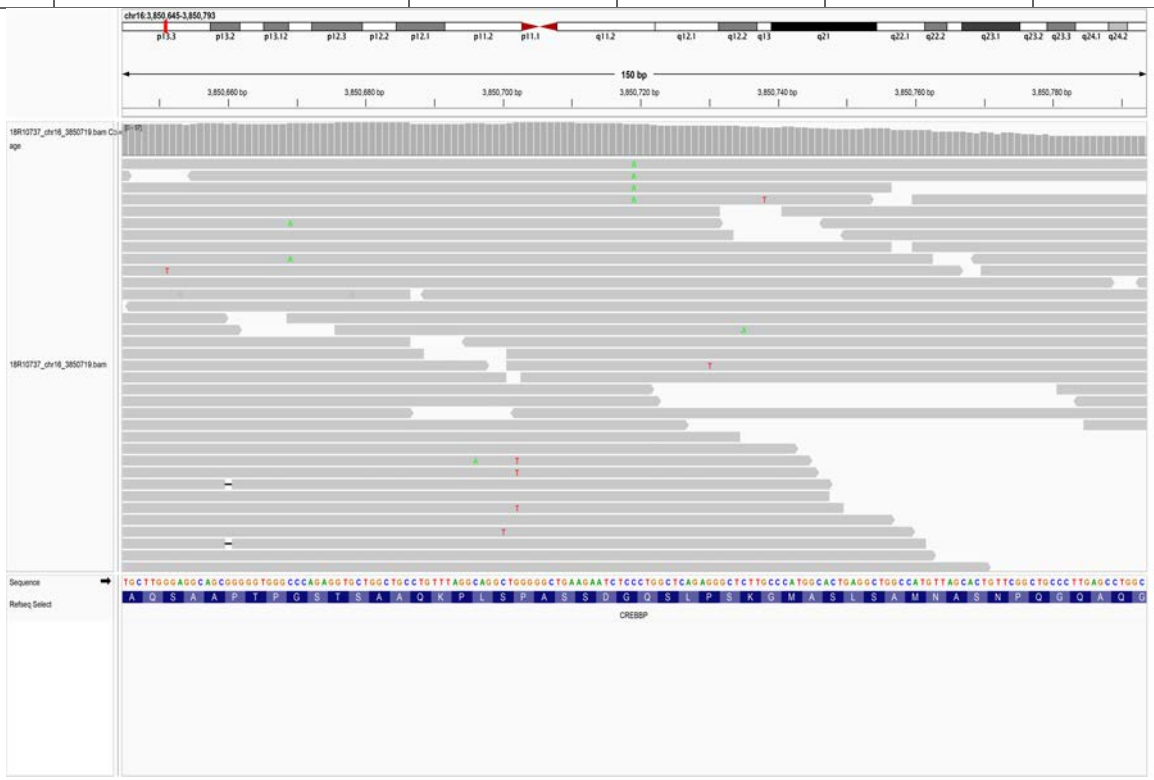
9.14. chr16_3850317_G/A

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

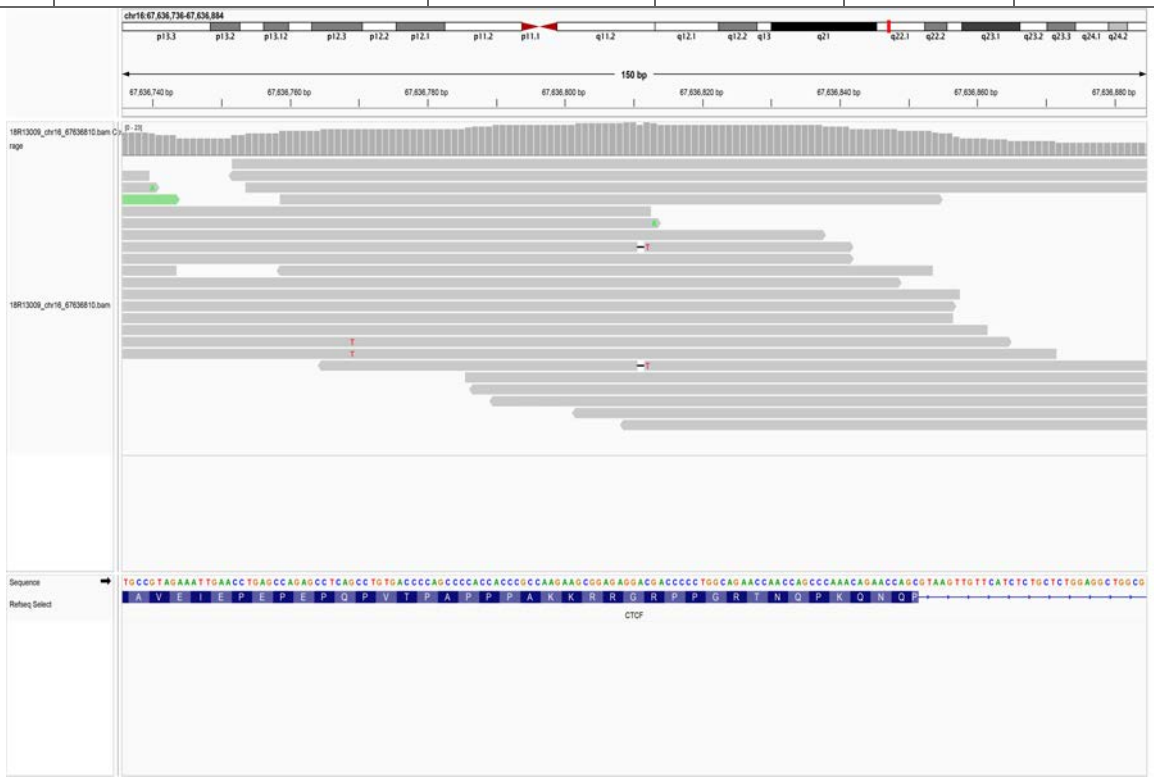
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10737	chr16_3850719_C/A	47	4	*CREBBP*	stop_gained



10. *CTCF*

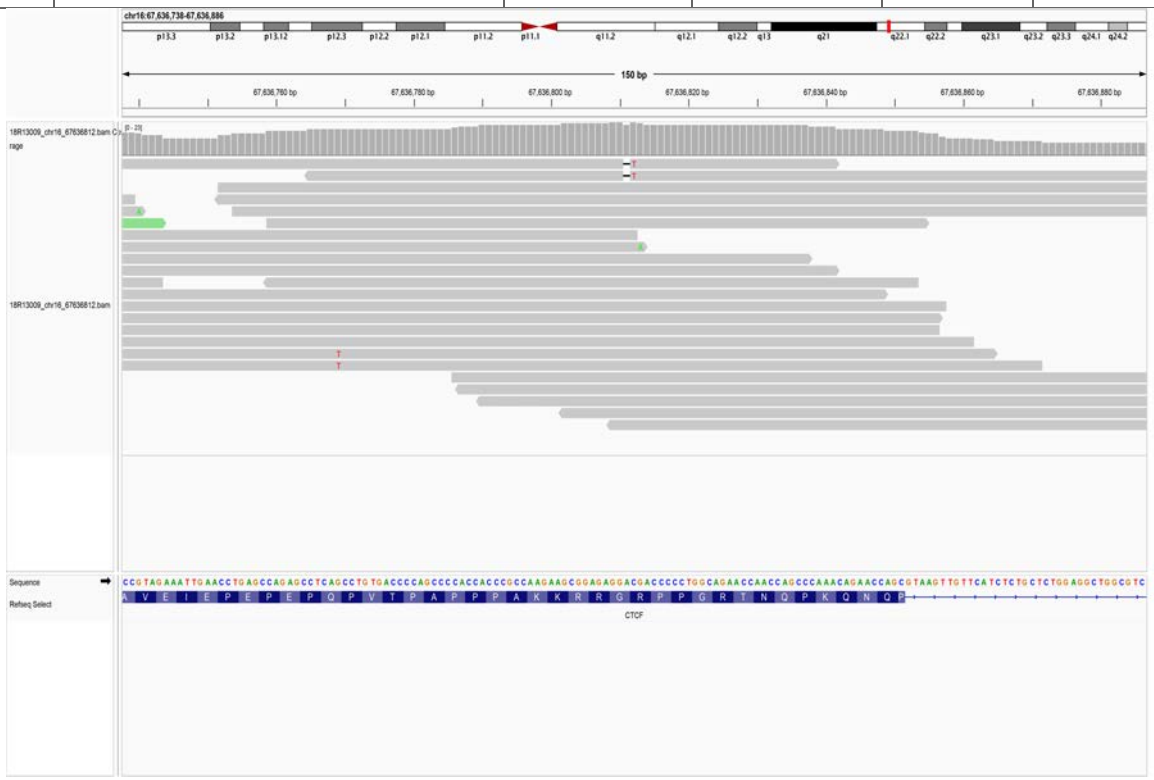
10.1. chr16_67636811_A/-

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



10.2. chr16_67636812_C/T

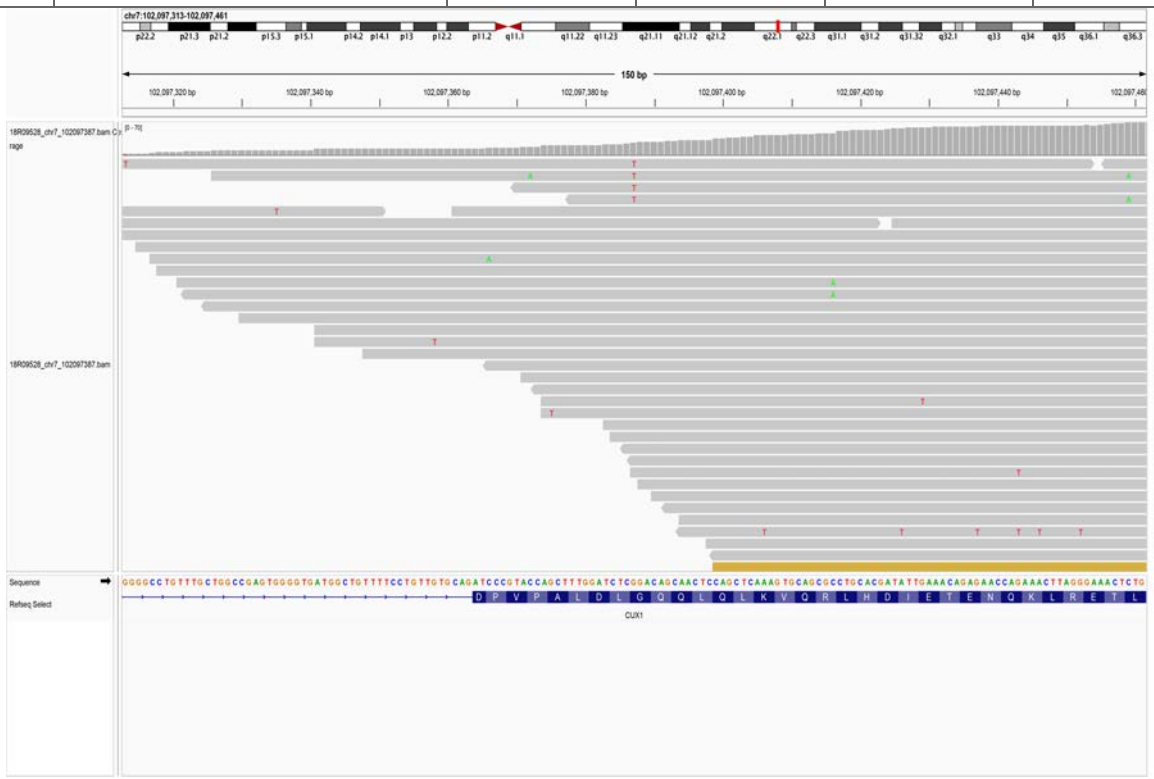
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13009	chr16_67636812_C/T	21	2	*CTCF*	stop_gained



11. *CUX1*

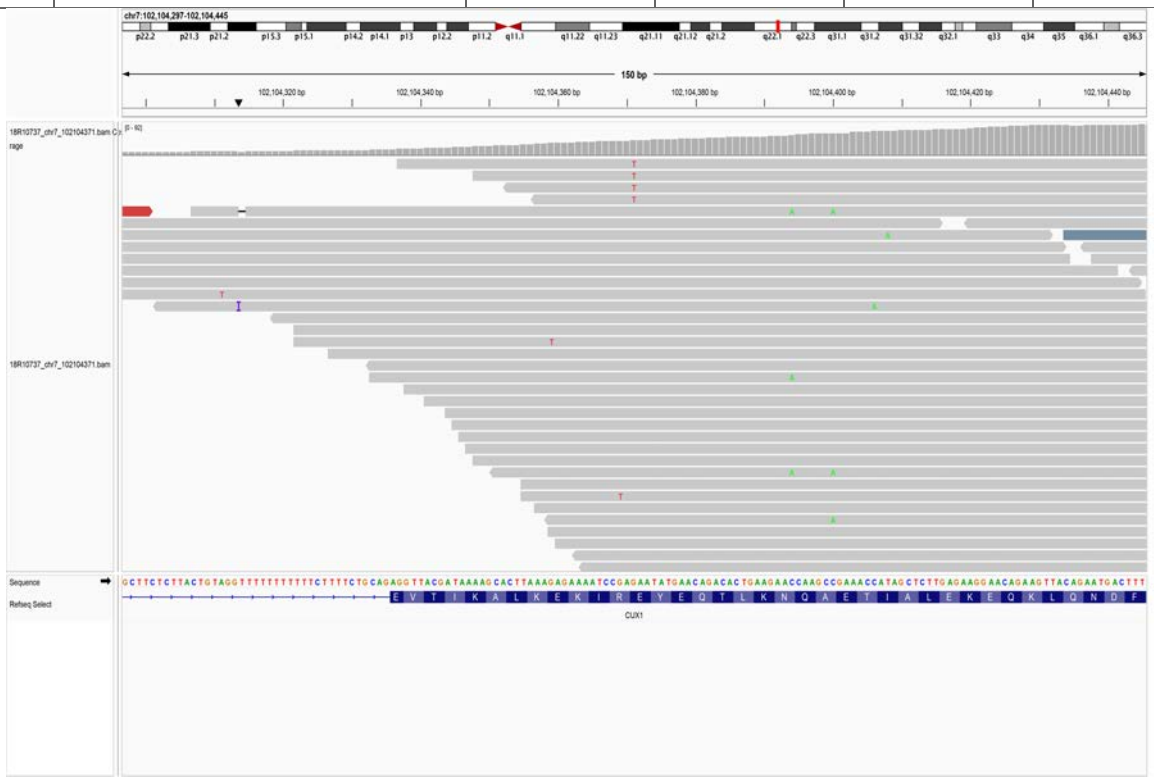
11.1. chr7_102097387_G/T

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



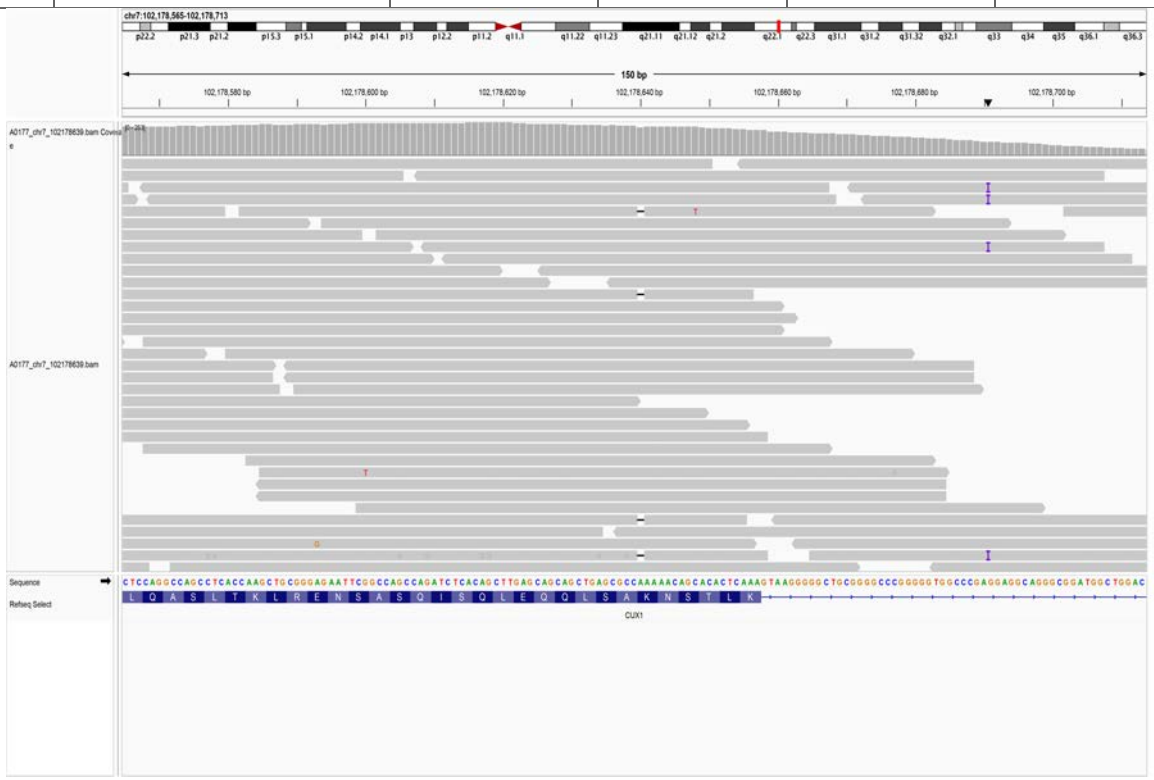
11.2. chr7_102104371_G/T

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



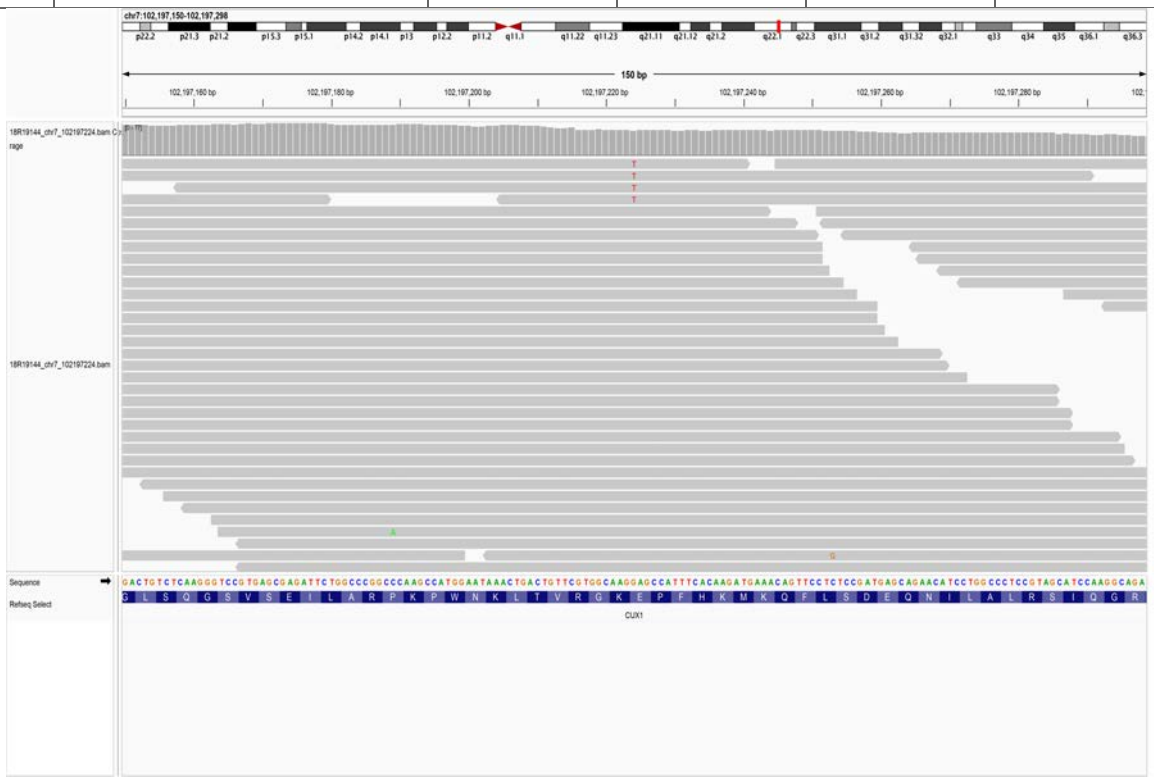
11.3. chr7_102178640_A/-

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



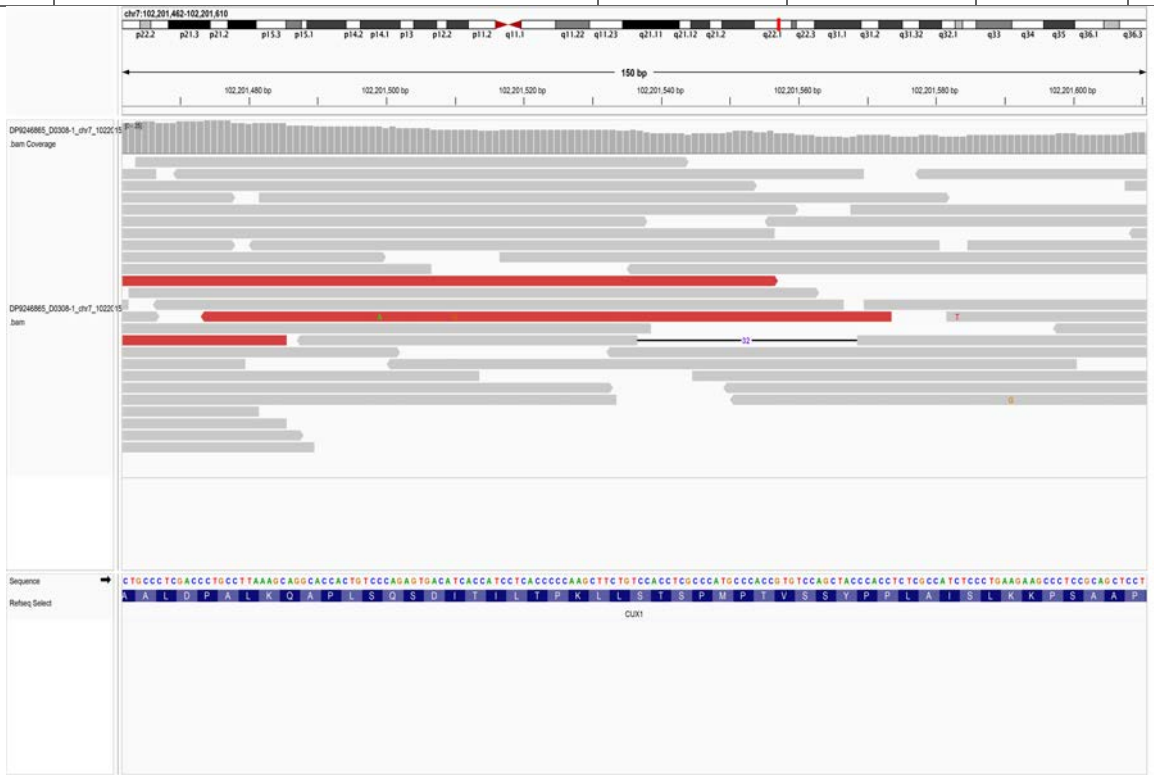
11.4. chr7_102197224_G/T

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



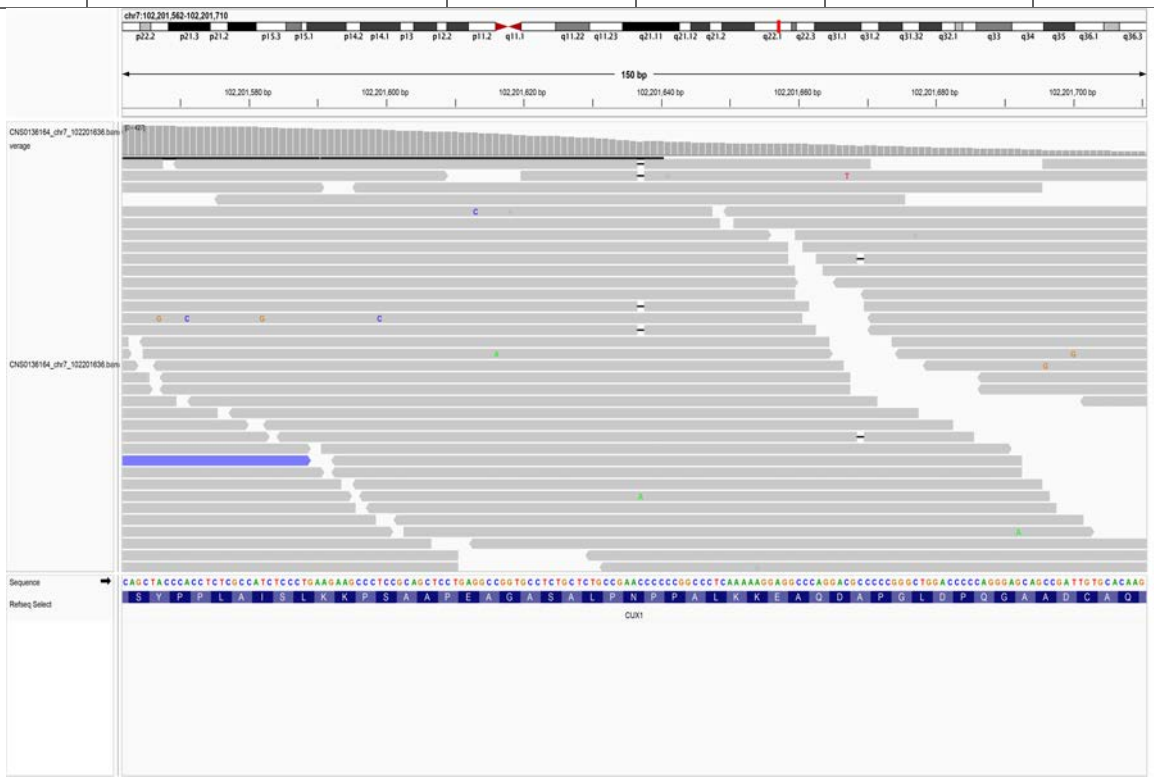
11.5. chr7_102201537_CCACCTCGCCCATGCCCACCGTGTCCAGCTAC/-

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



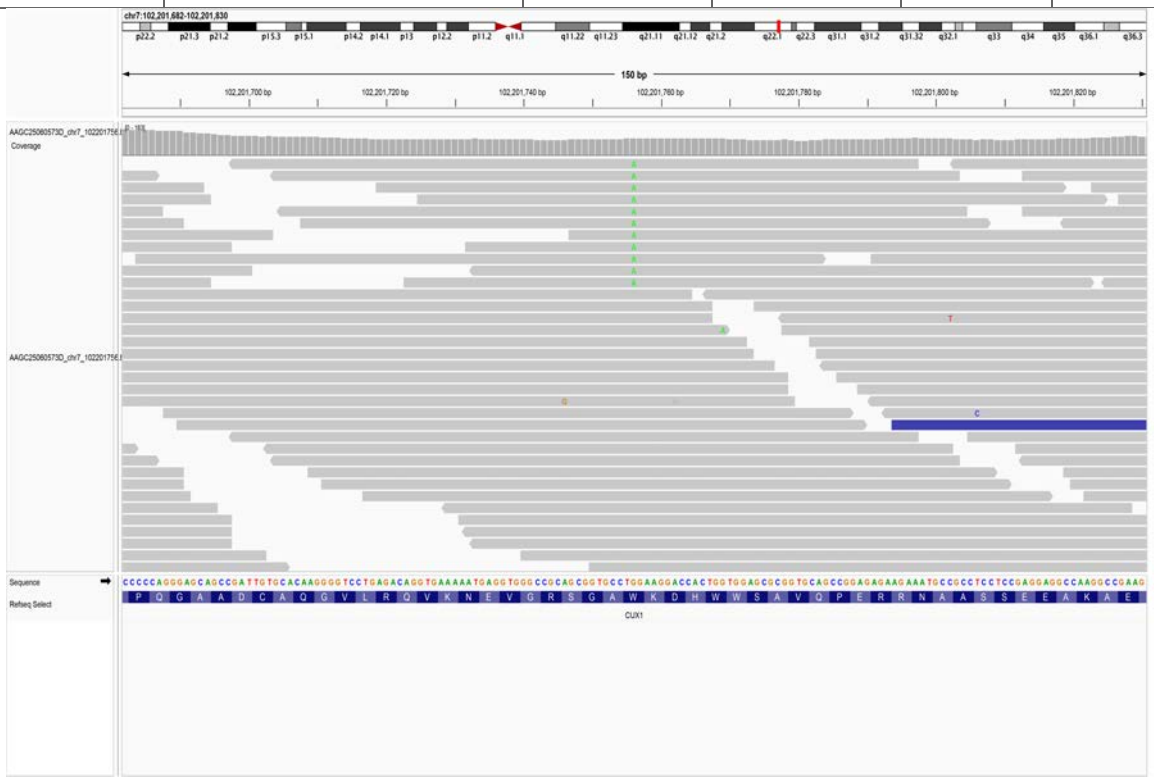
11.6. chr7_102201637_C/-

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



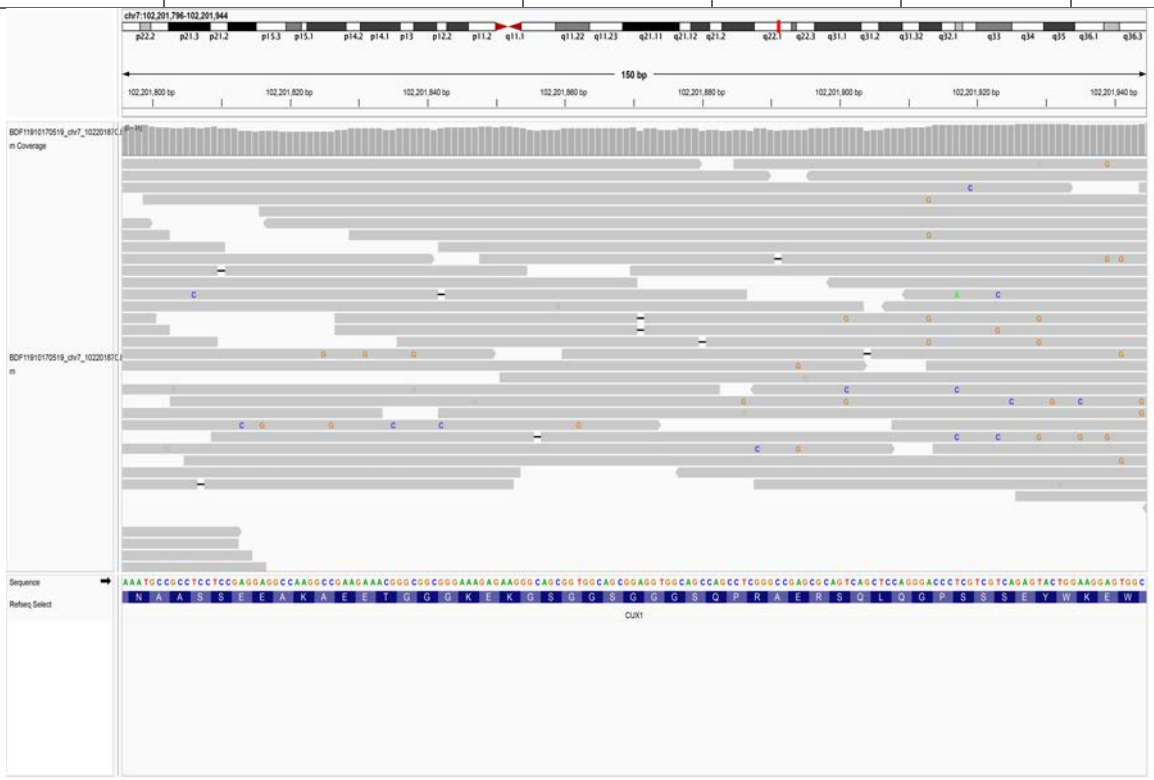
11.7. chr7_102201756_G/A

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



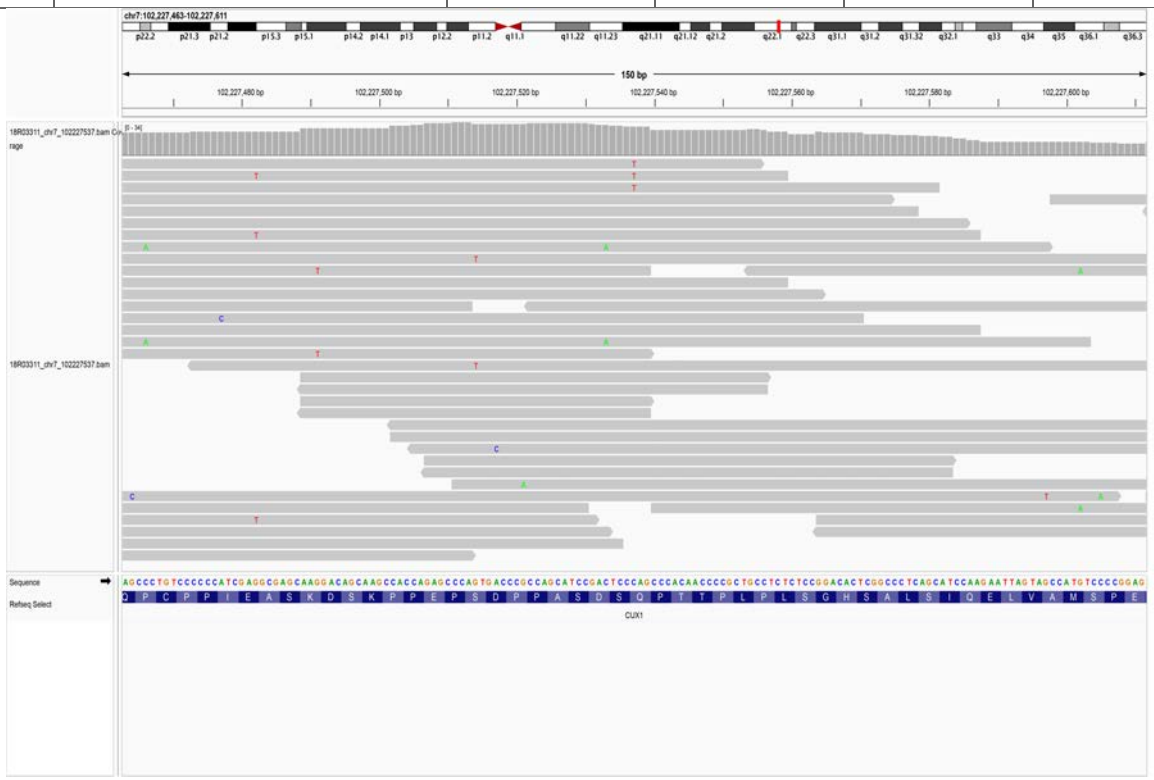
11.8. chr7_102201871_A/-

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



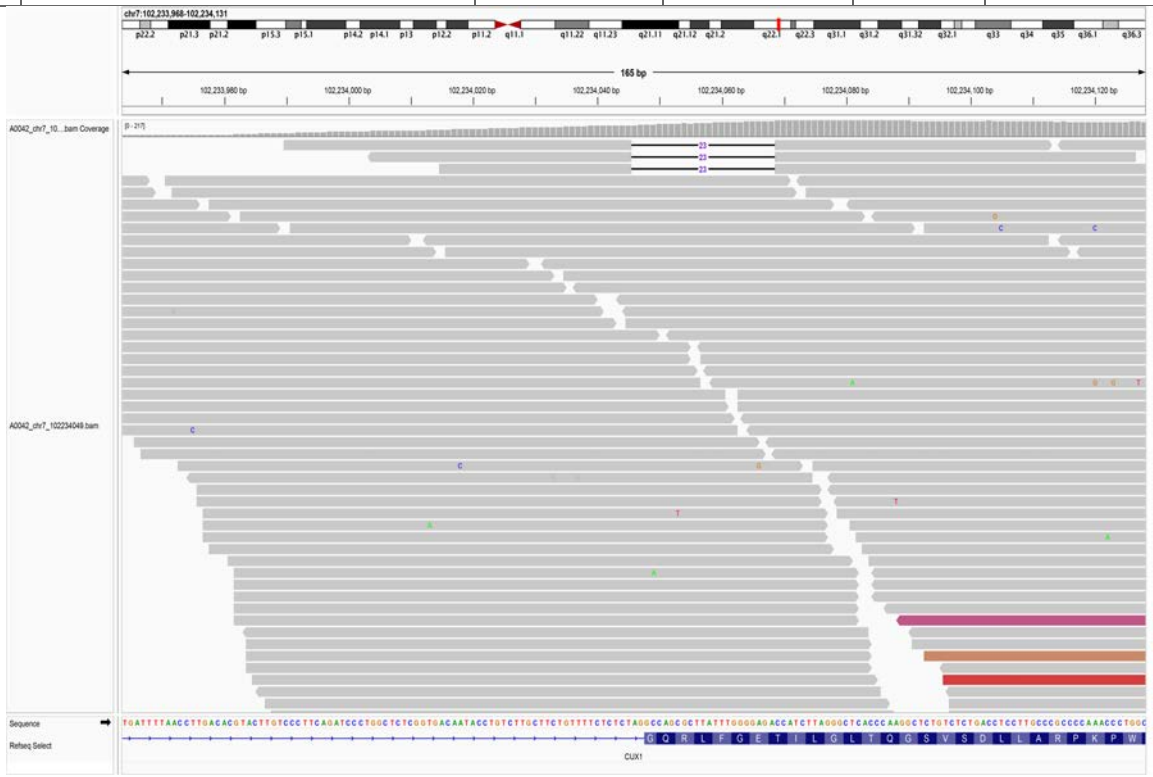
11.9. chr7_102227537_C/T

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



11.10. chr7_102234050_AGGCCAGCGCTTATTTGGGGAGA/-

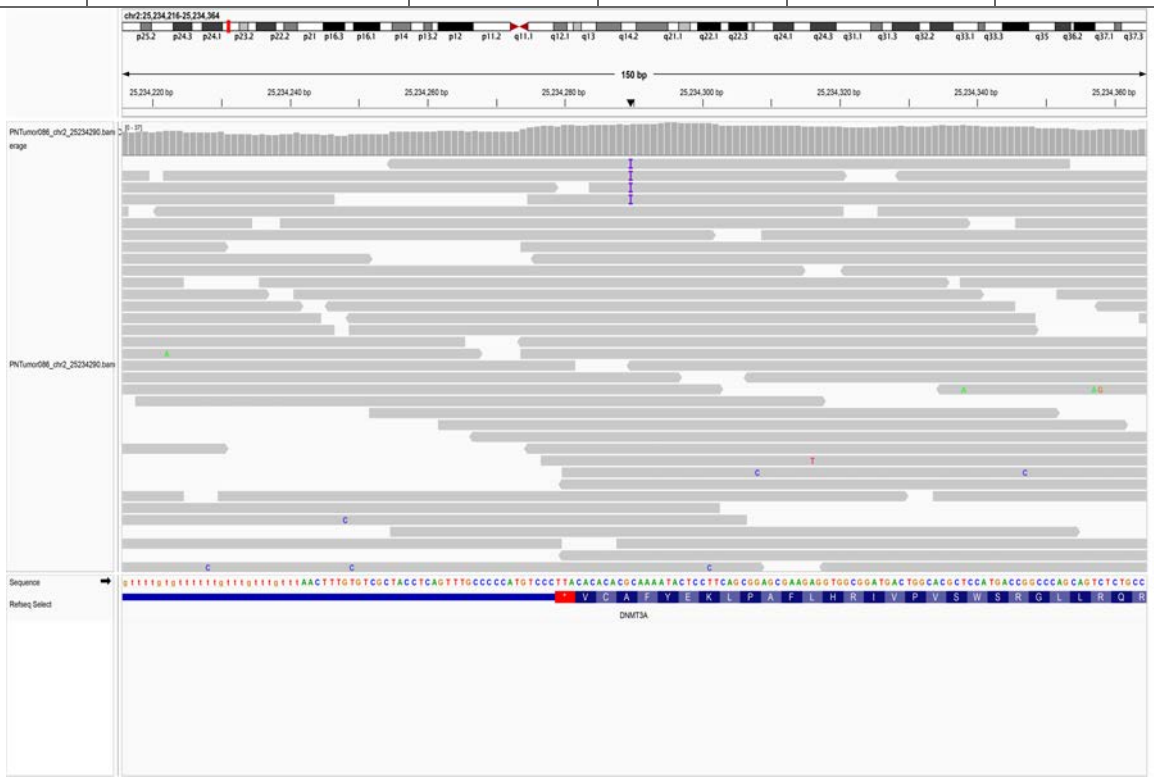
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0042	chr7_102234050_AGGCCAGCG CTTATTTGGGGAGA/-	213	3	*CUX1*	splice_acceptor_variant



12. *DNMT3A*

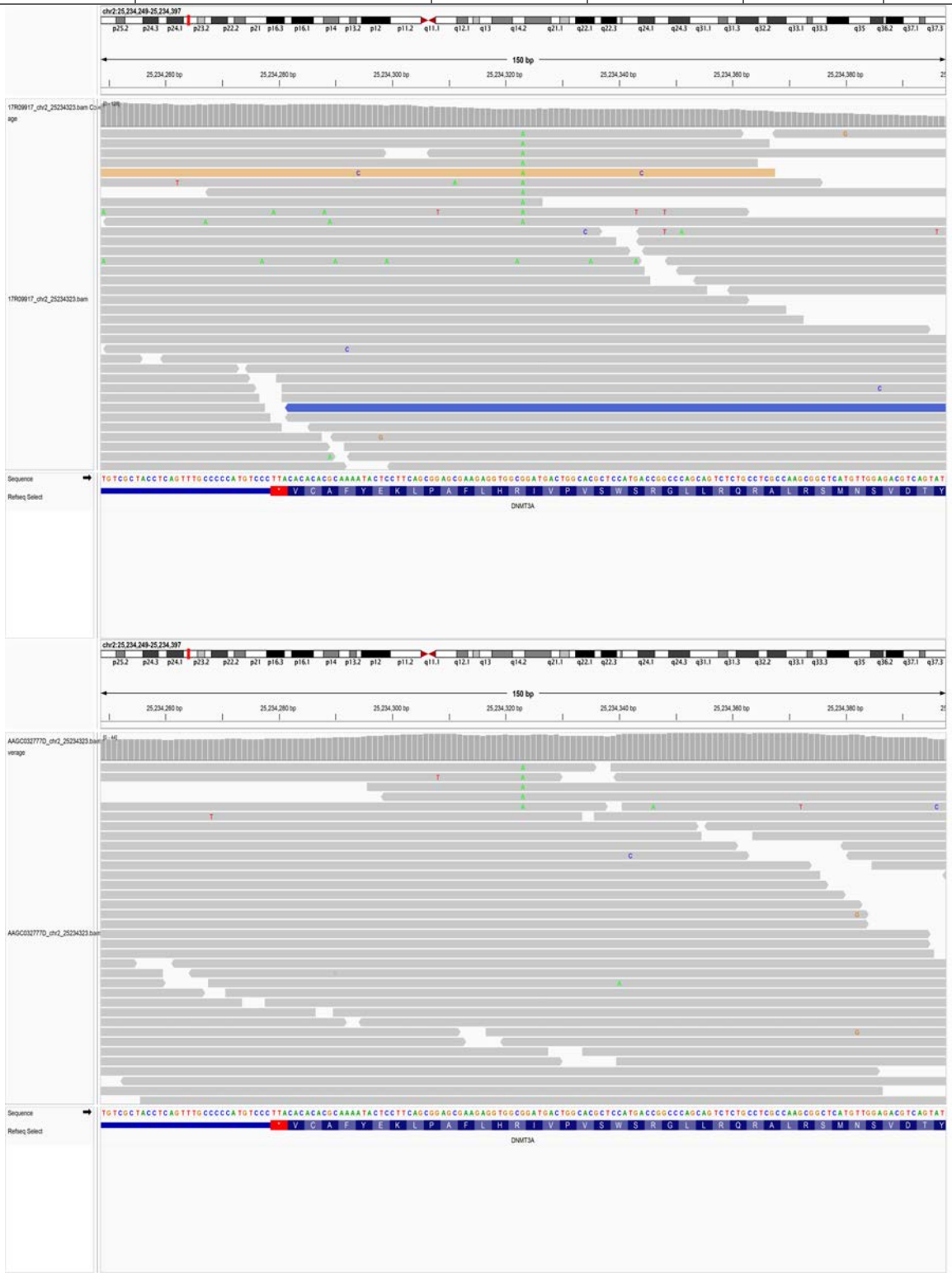
12.1. chr2_25234290_-/C

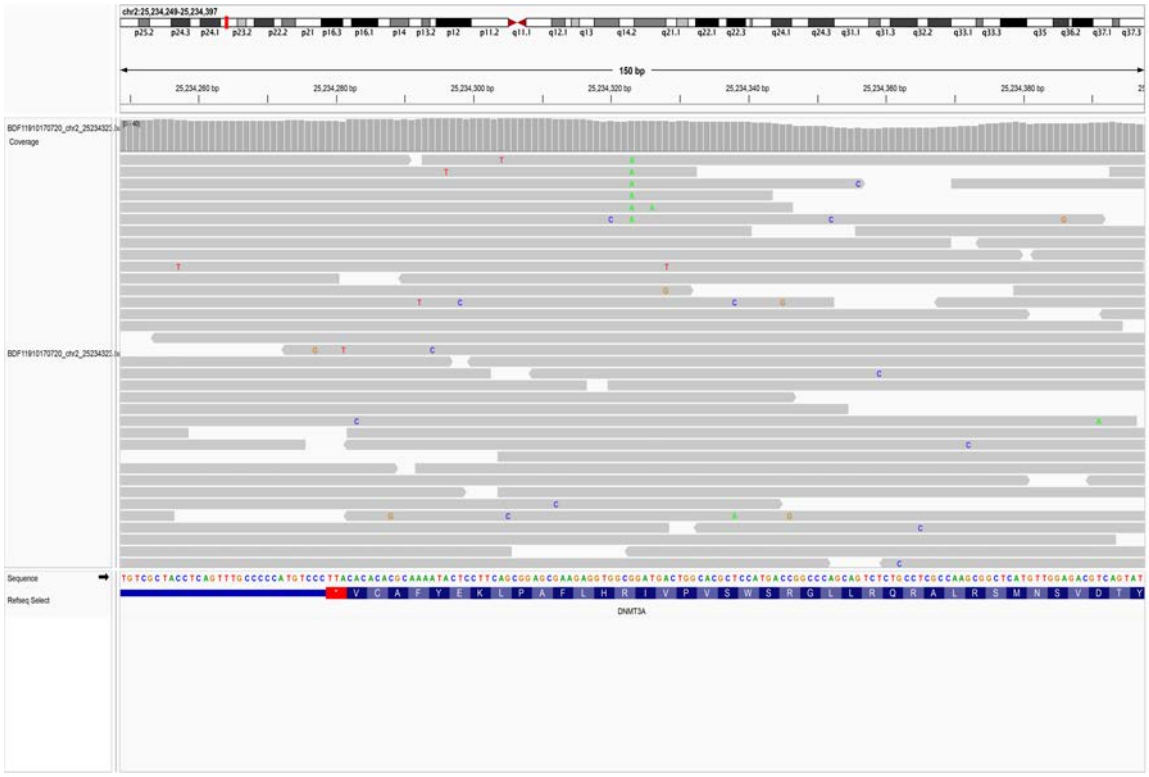
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
PNTumor086	chr2_25234290_-/C	30	4	*DNMT3A*	frameshift_variant



12.2. chr2_25234323_G/A

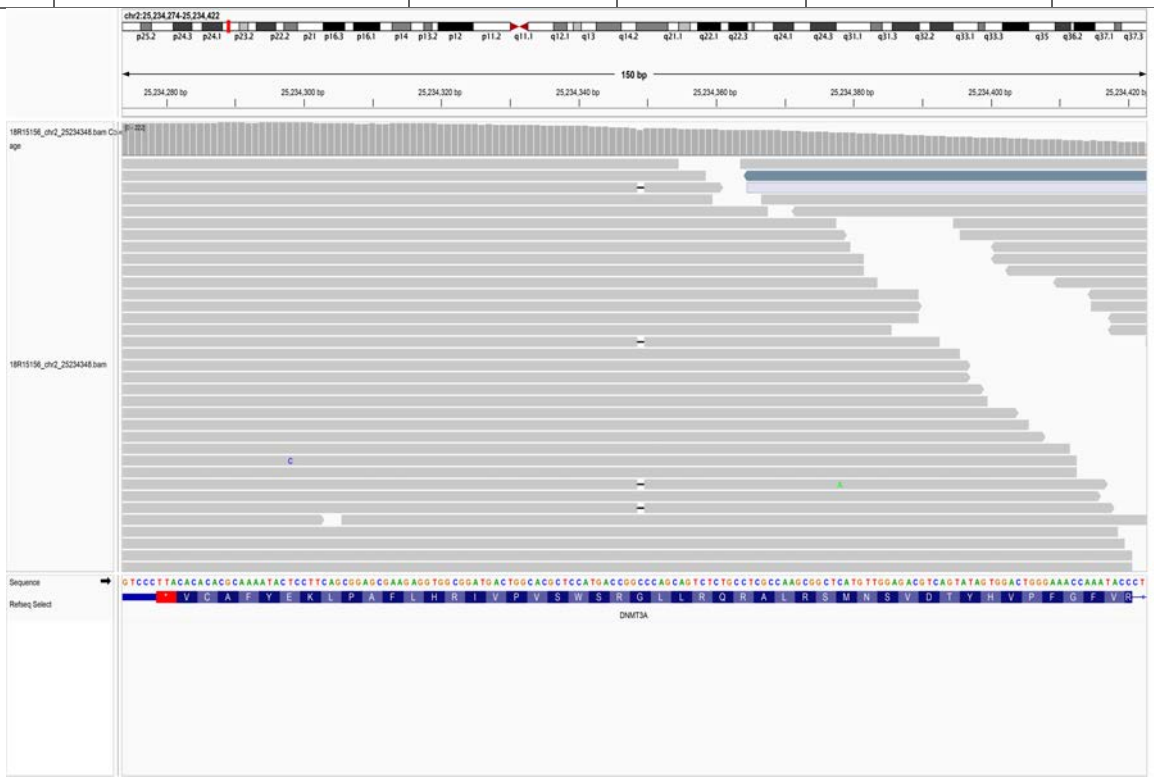
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09917	chr2_25234323_G/A	69	10	*DNMT3A*	missense_variant
AAGC032777D	chr2_25234323_G/A	34	5	*DNMT3A*	missense_variant
BDF11910170720	chr2_25234323_G/A	29	6	*DNMT3A*	missense_variant




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

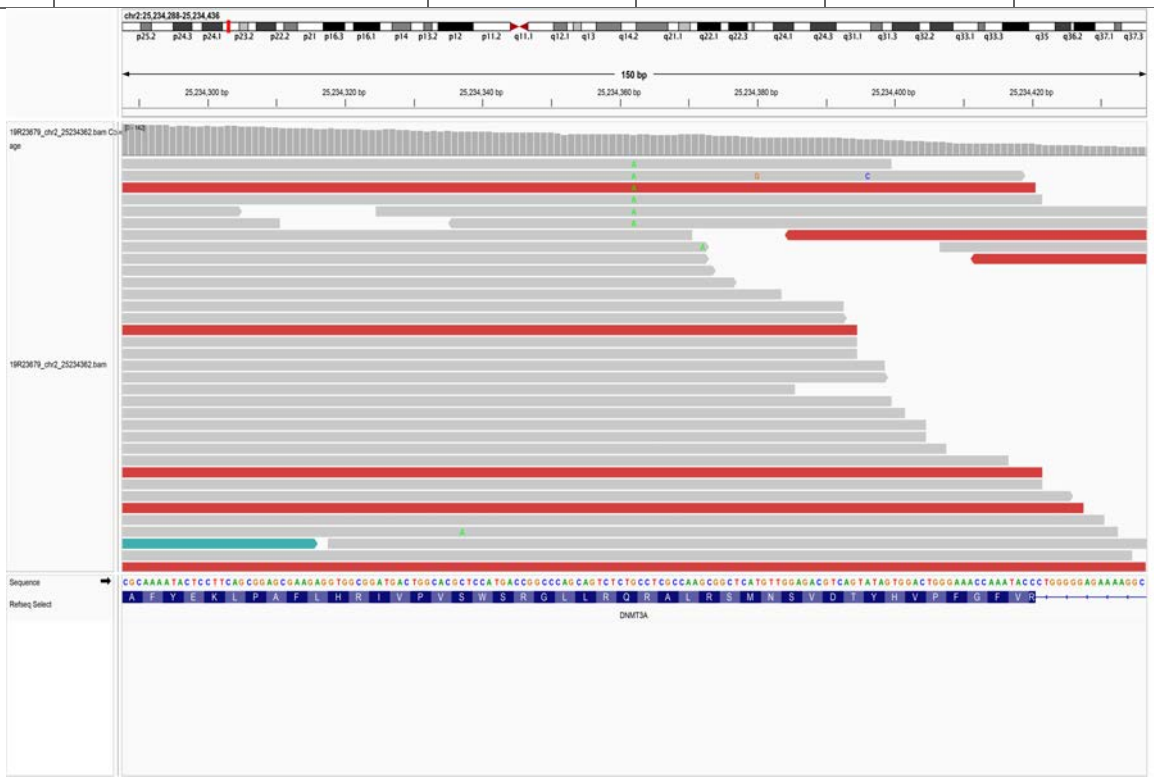
12.3. chr2_25234349_C/-

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



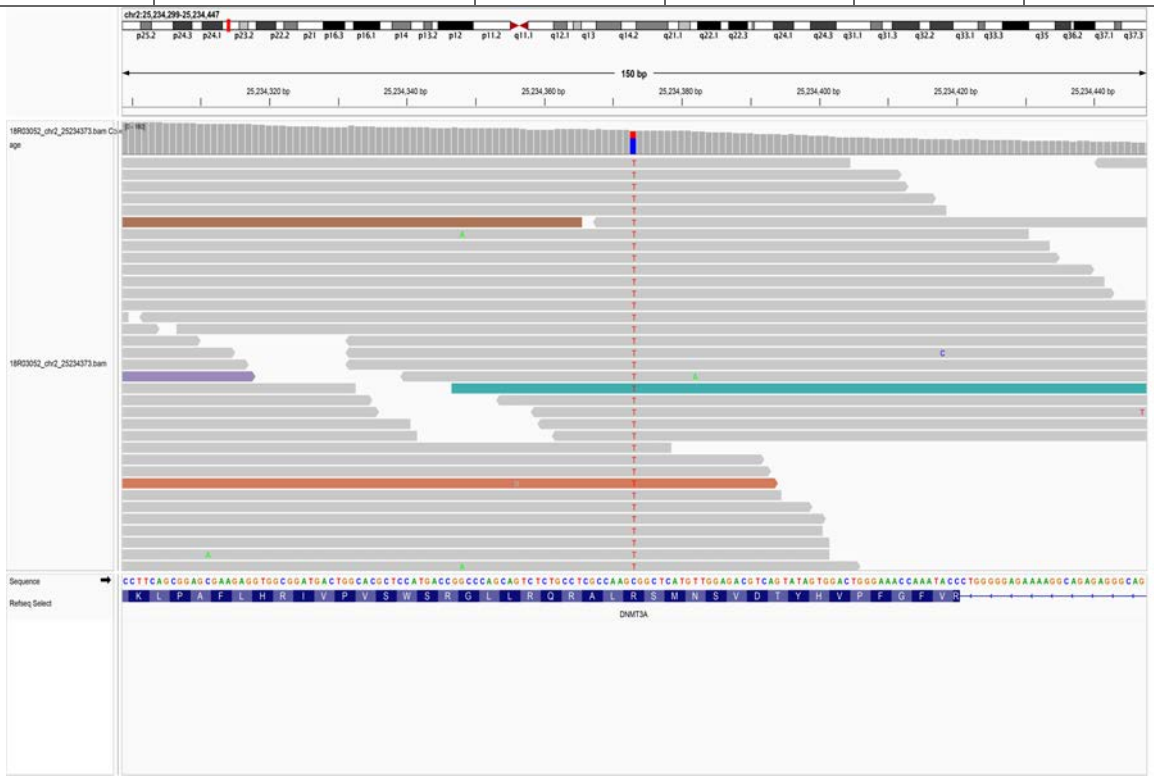
12.4. chr2_25234362_G/A

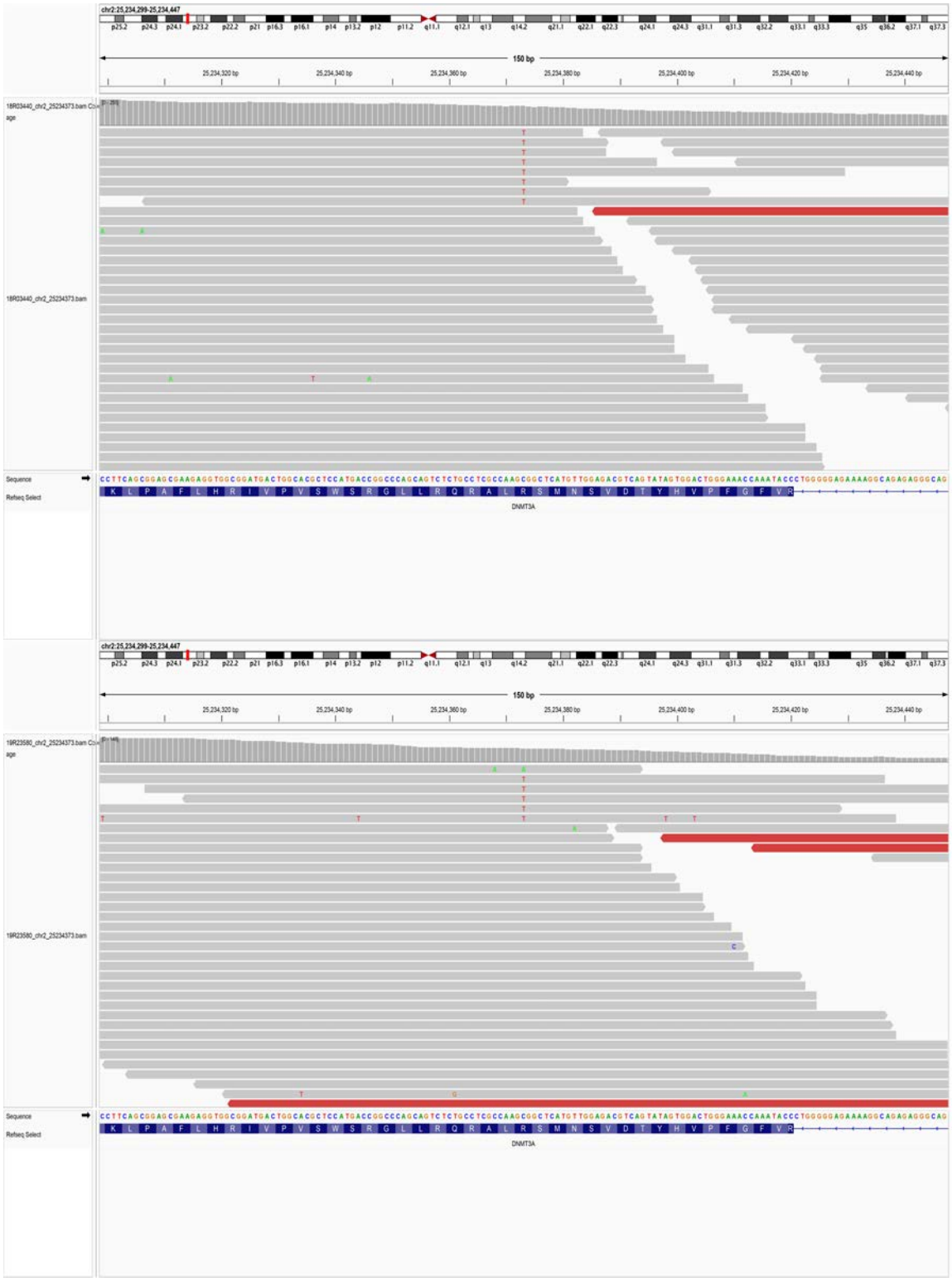
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23679	chr2_25234362_G/A	81	6	*DNMT3A*	stop_gained

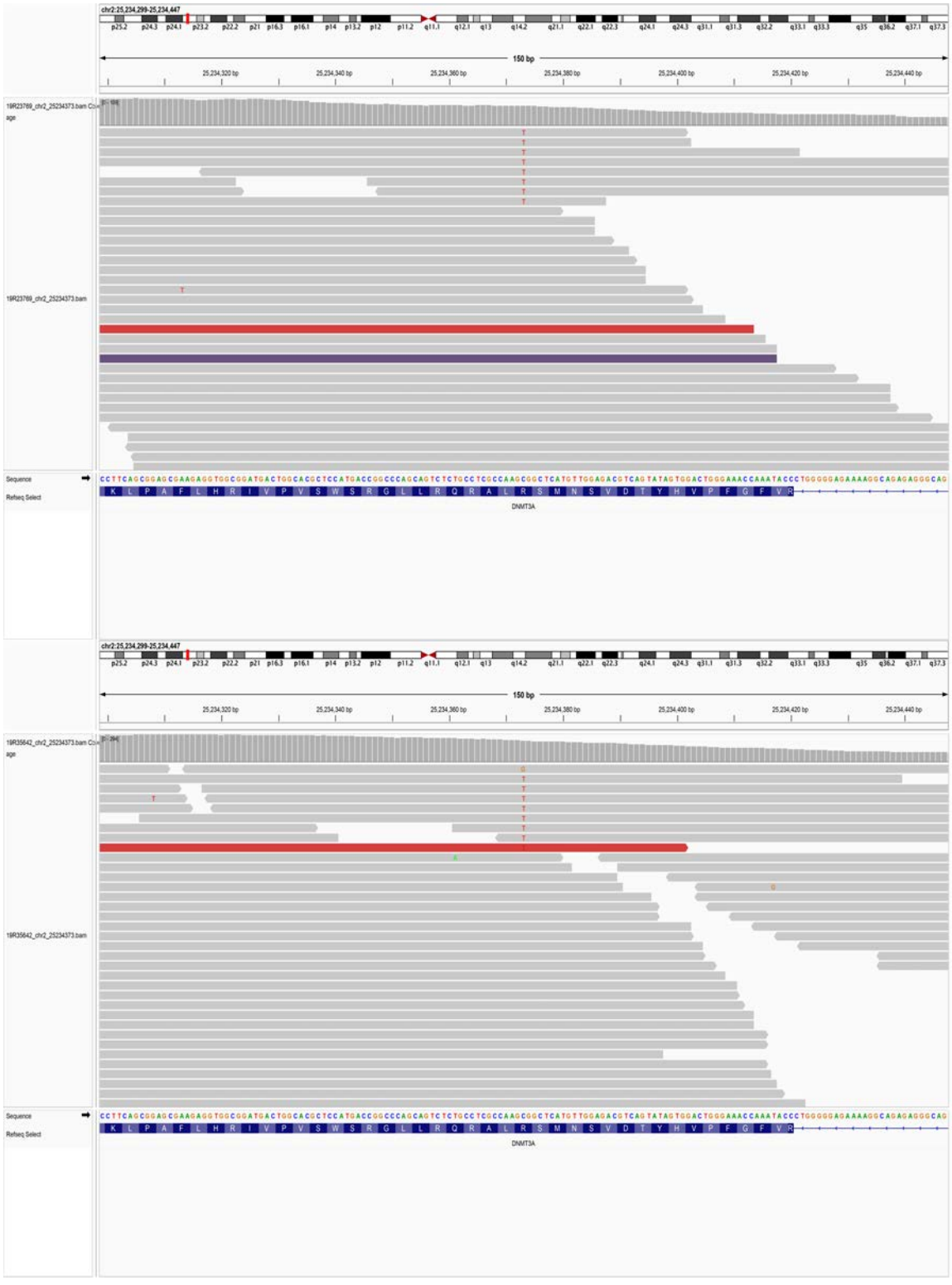


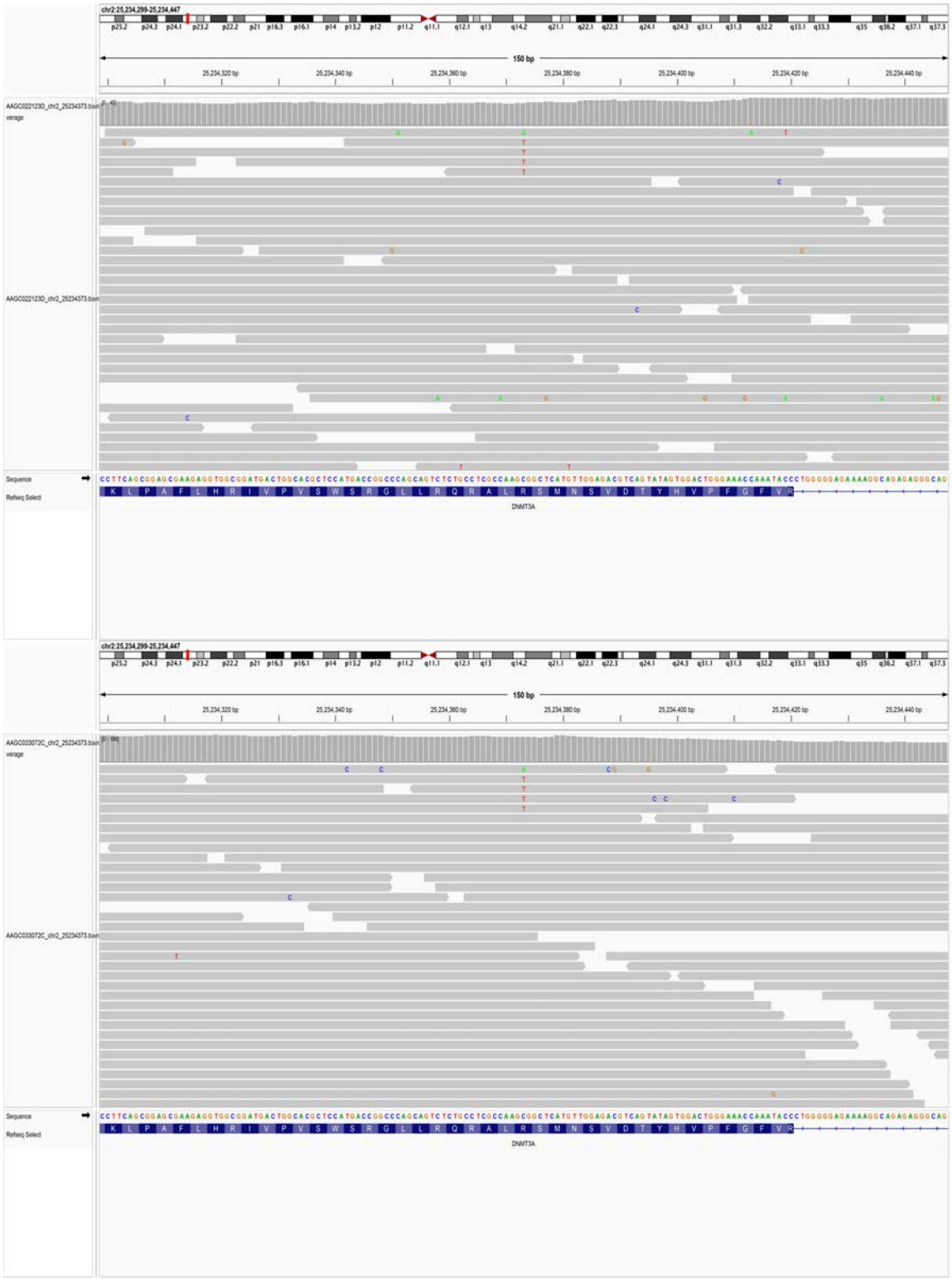
12.5. chr2_25234373_C/T

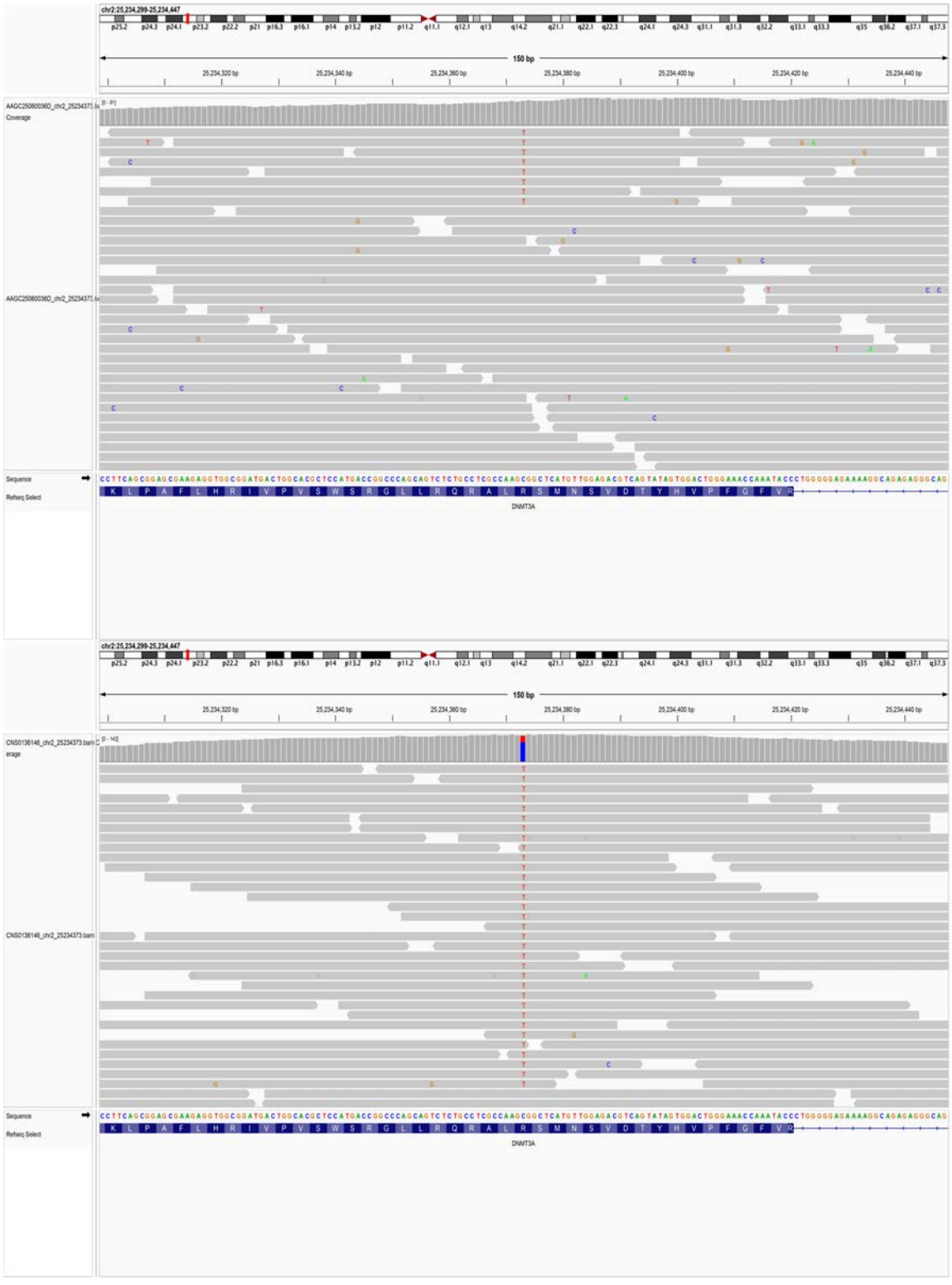
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03052	chr2_25234373_C/T	91	39	*DNMT3A*	missense_variant
18R03440	chr2_25234373_C/T	168	8	*DNMT3A*	missense_variant
19R23580	chr2_25234373_C/T	64	5	*DNMT3A*	missense_variant
19R23769	chr2_25234373_C/T	70	8	*DNMT3A*	missense_variant
19R35642	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

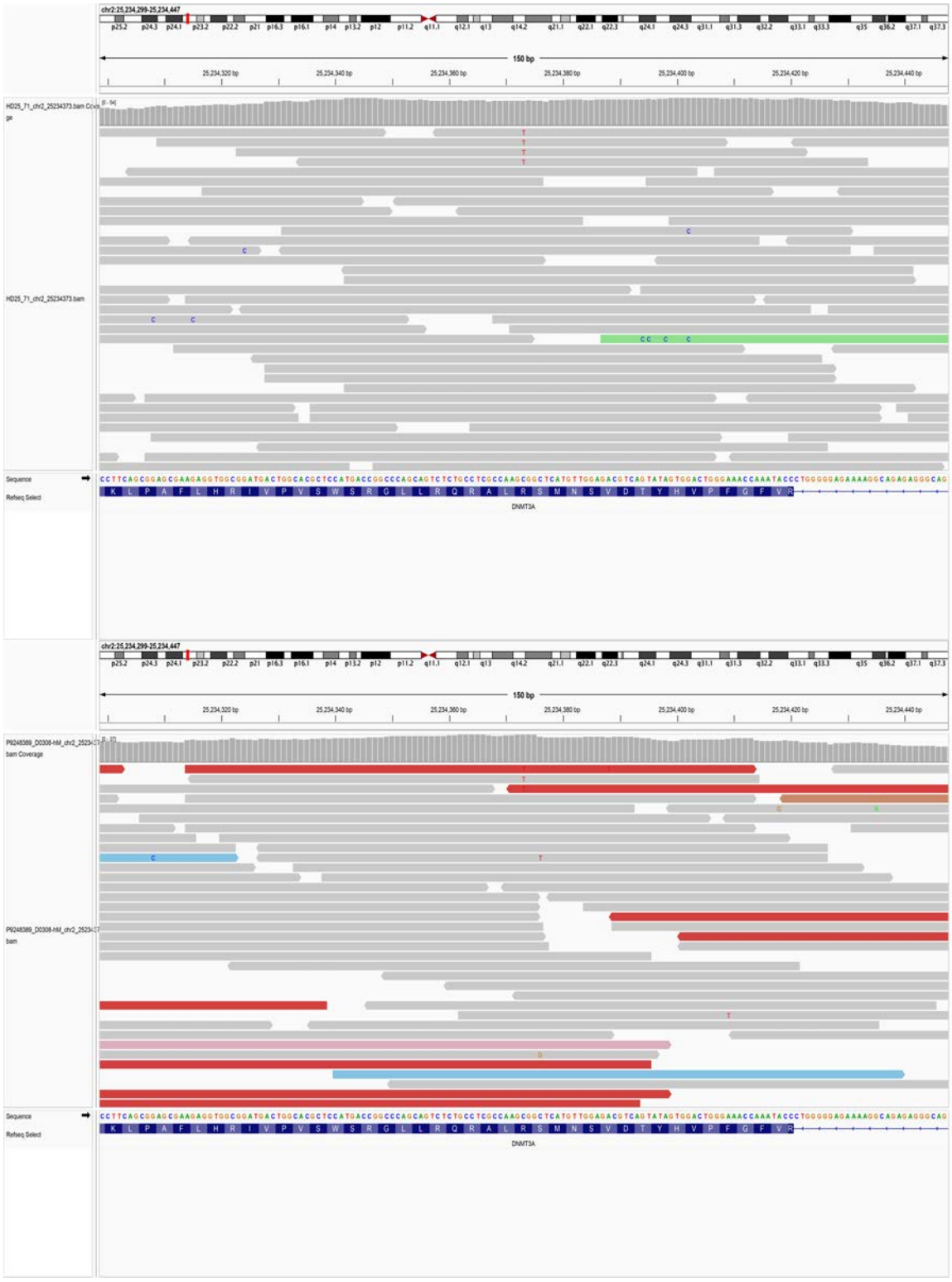


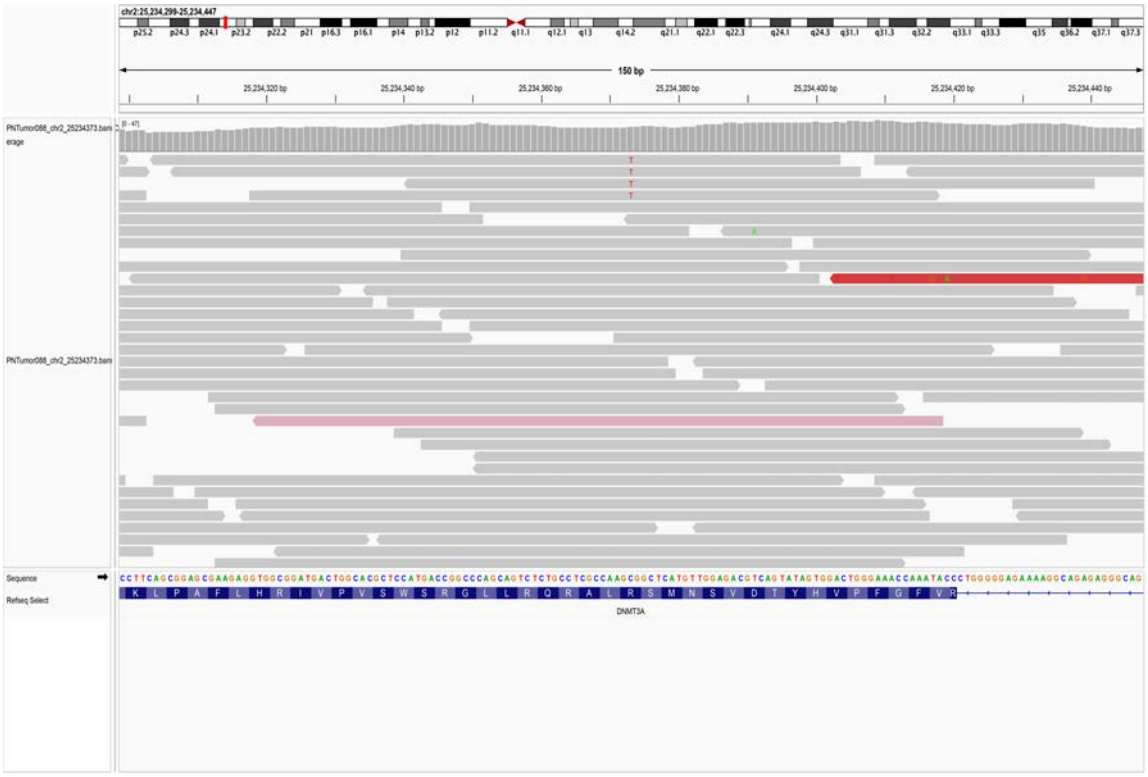

chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
18R03440_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A
19R23580_chr2_25234373.bam


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
19R35642_chr2_25234373.bam Coverage
19R35642_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
AAGC022123D_chr2_25234373.bam
verage
AAGC022123D_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
AAGC033072C_chr2_25234373.bam
verage
AAGC033072C_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A

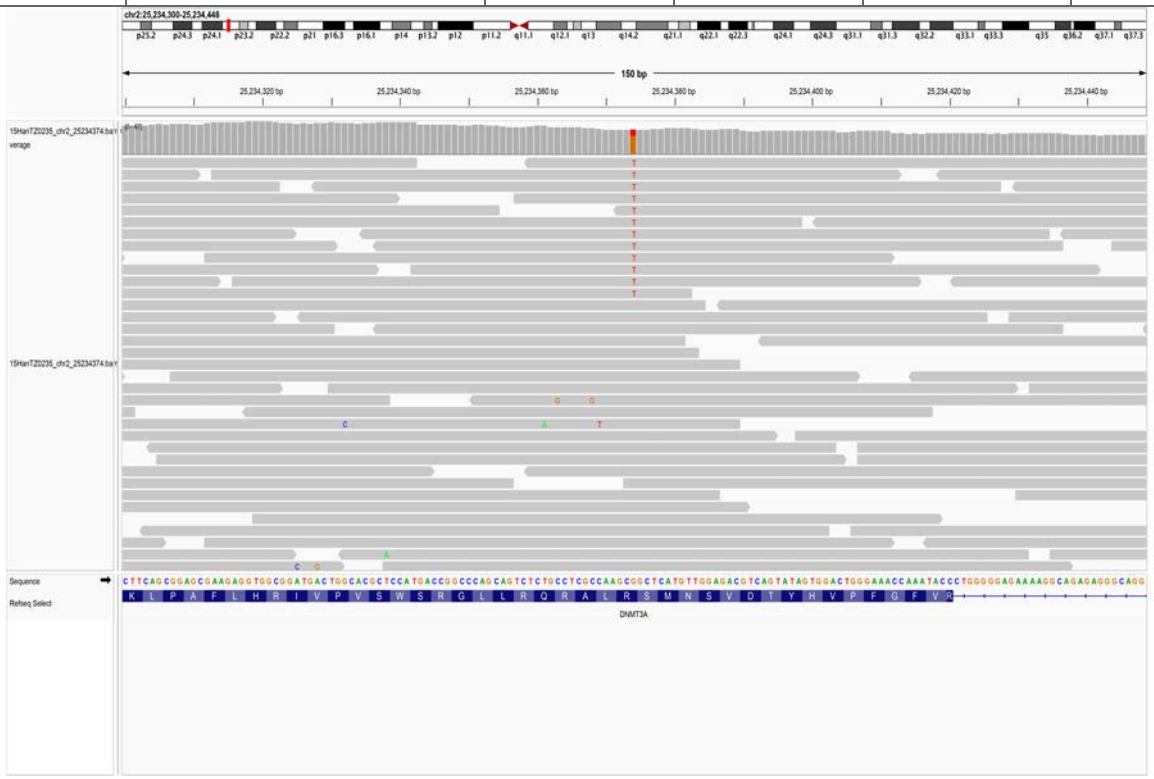

chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
Coverage
Sequence
Refseq Select
DNMT3A
chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp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

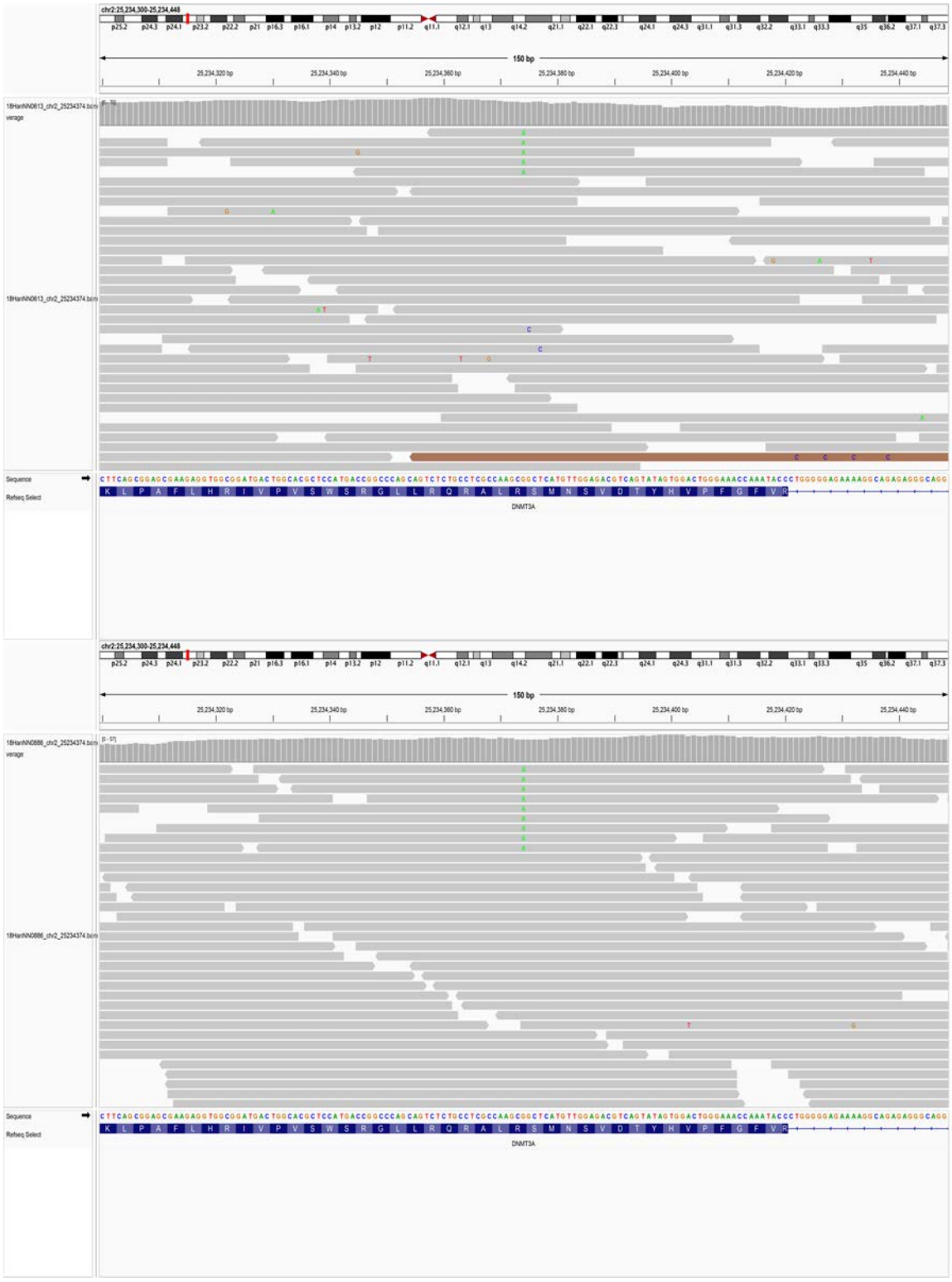

chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
HD25_71_chr2_25234373.bam Cover
ge
HD25_71_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A
chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380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

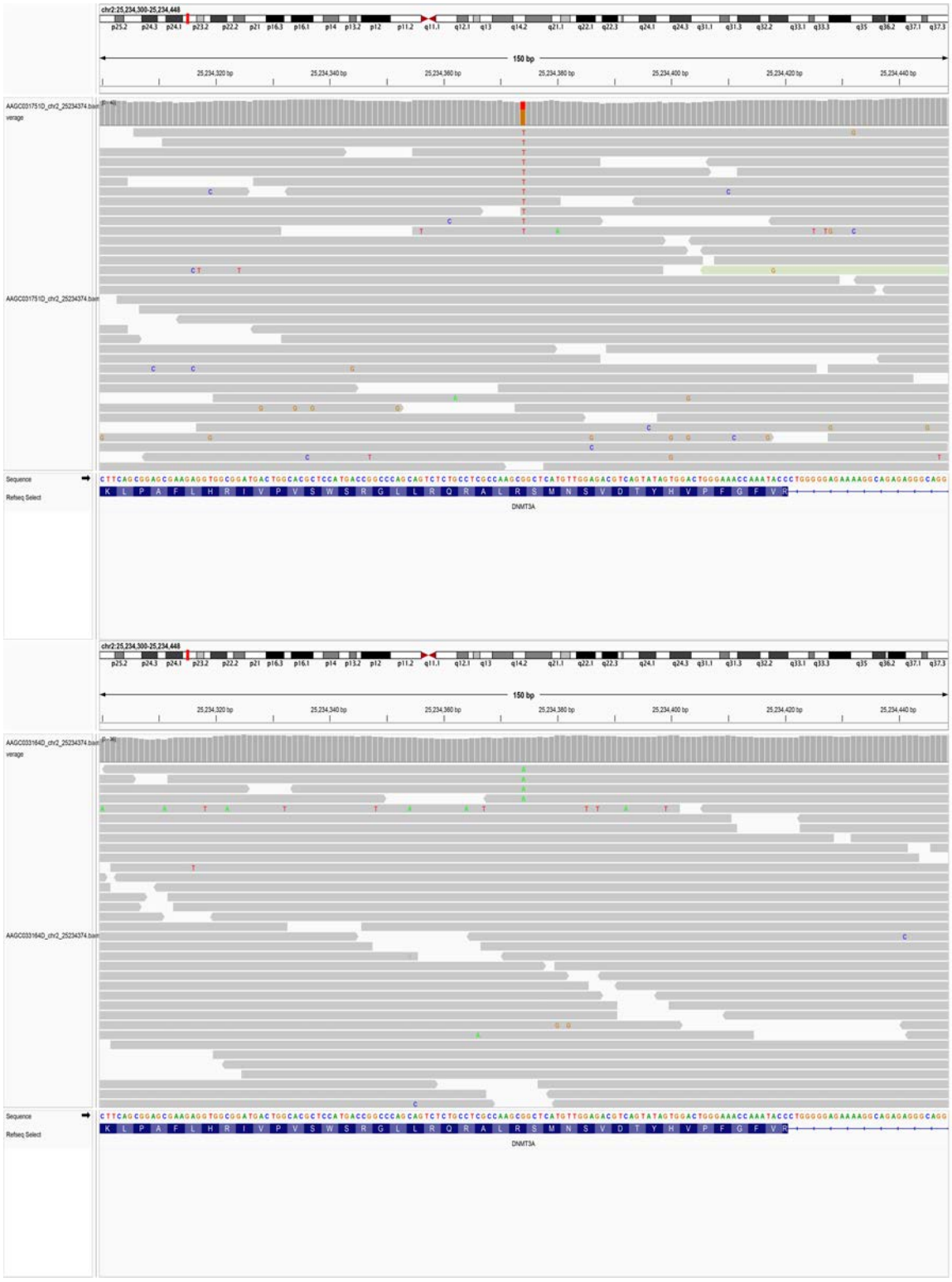

chr2:25,234,299-25,234,447
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
PNTumor088_chr2_25234373.bam
erage
PNTumor088_chr2_25234373.bam
Sequence
Refseq Select
DNMT3A

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

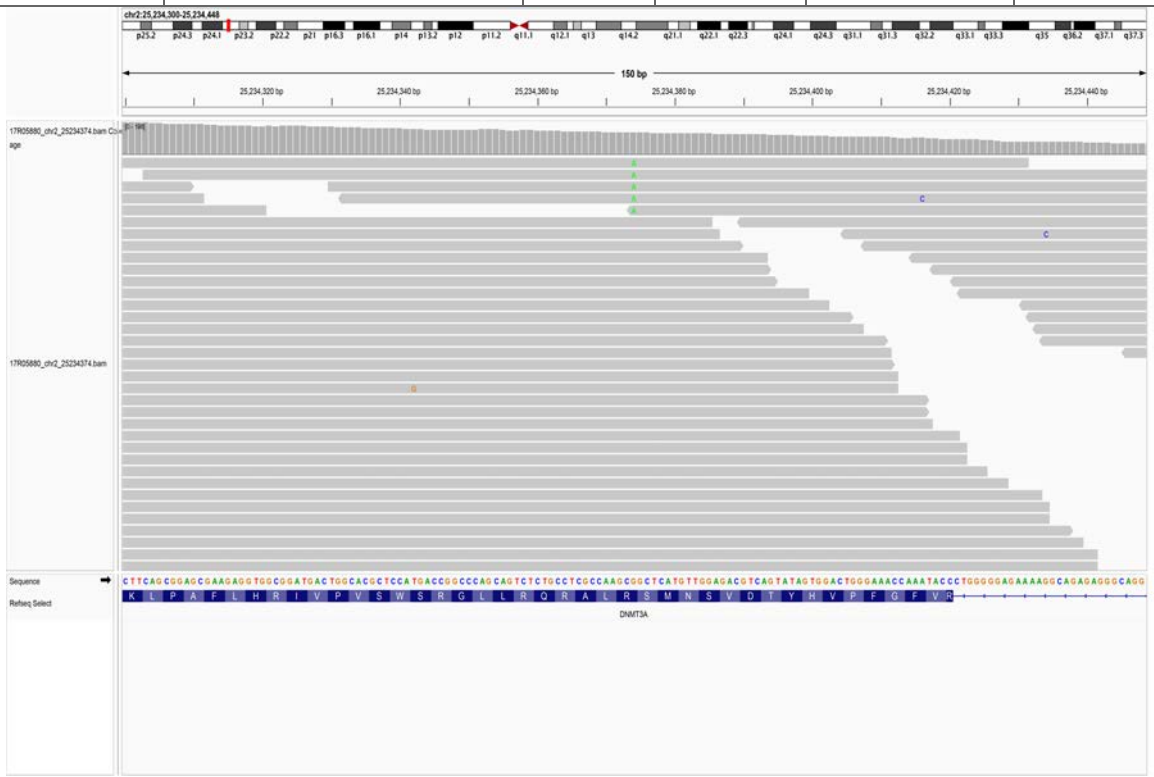


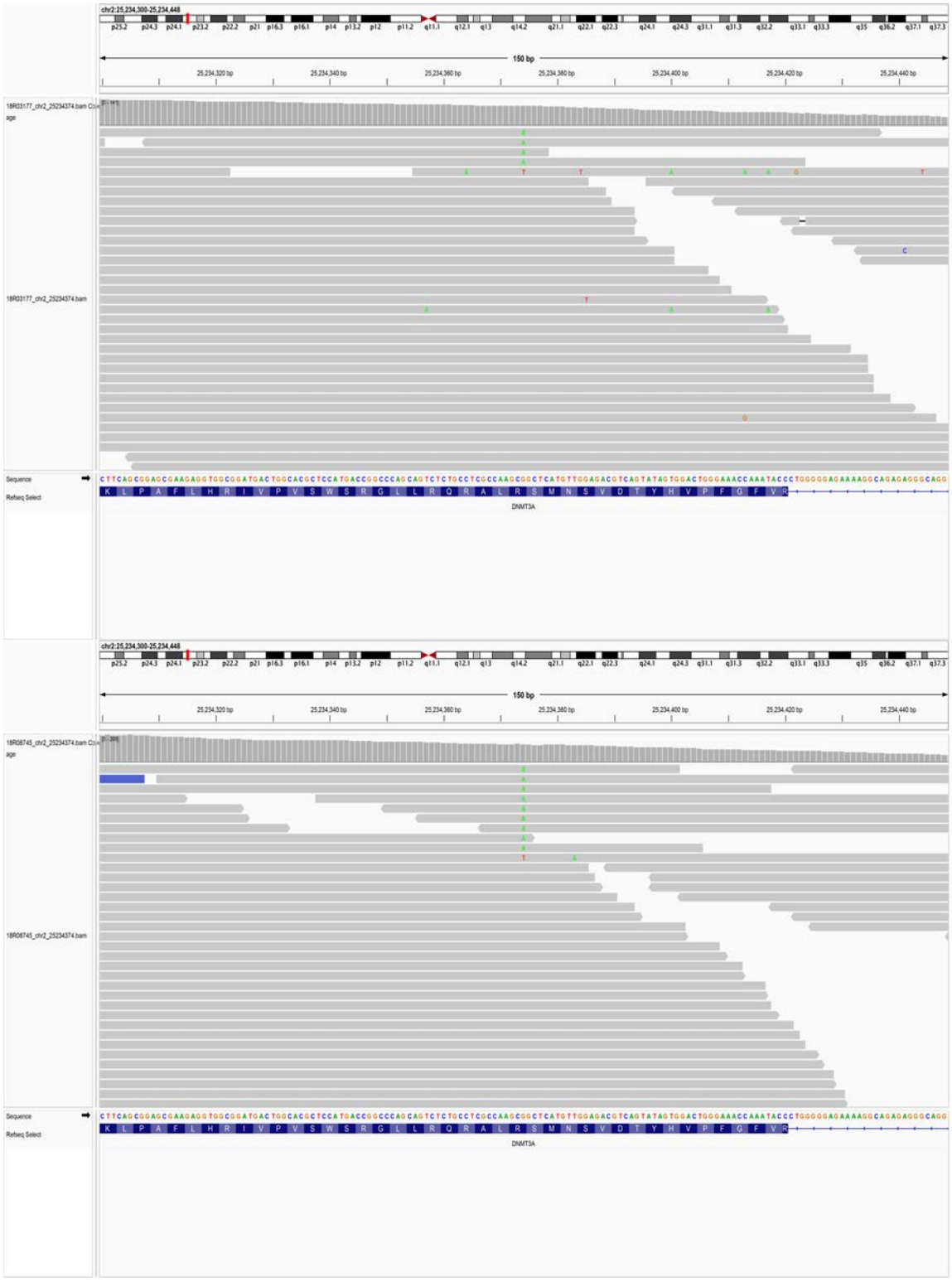

chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
1BHanNN0613_chr2_25234374.bam
verage
1BHanNN0613_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A
chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
1BHanNN0886_chr2_25234374.bam
verage
1BHanNN0886_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A

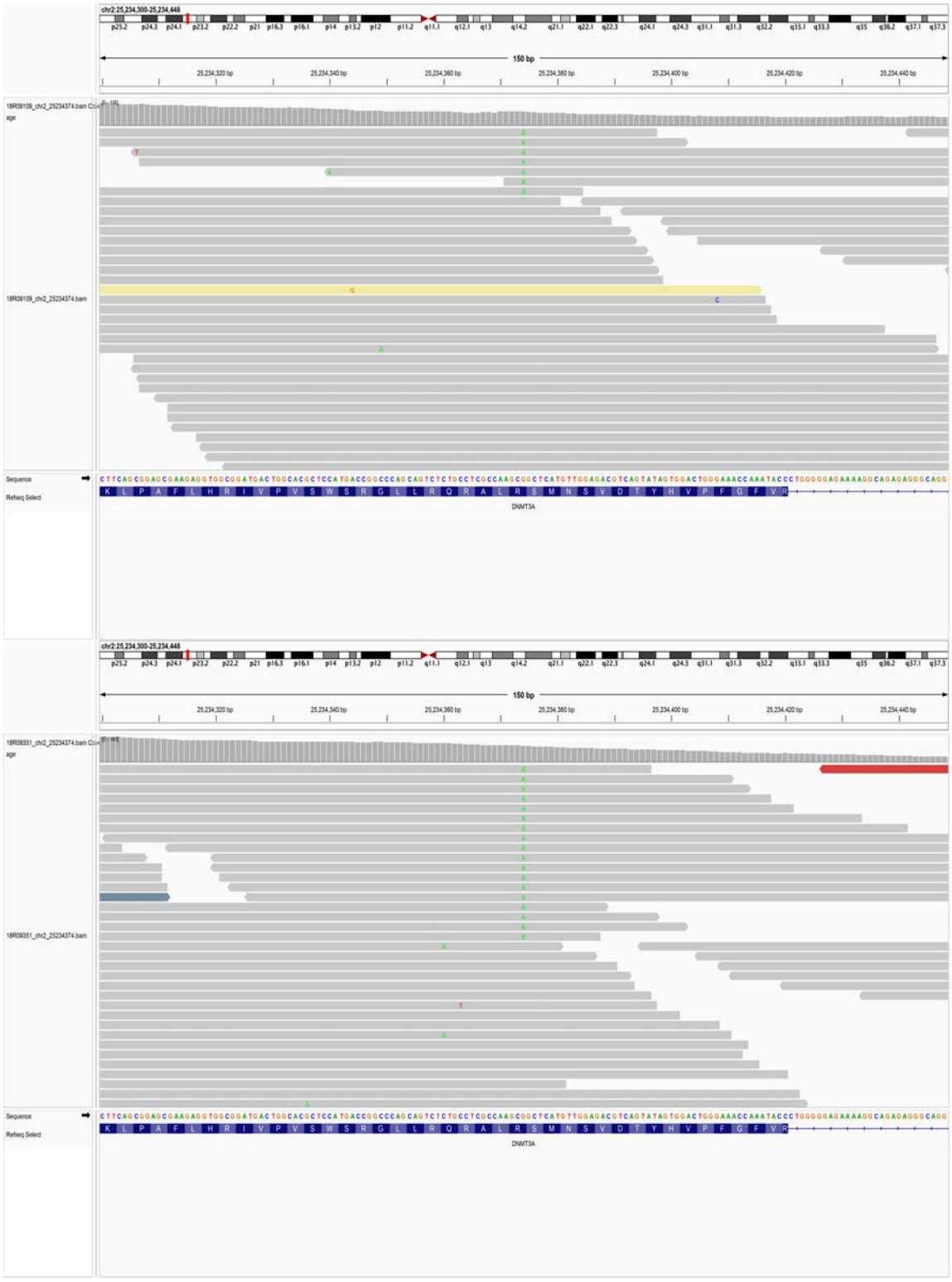

chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
AAGC031751D_chr2_25234374.bam
coverage
AAGC031751D_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A
chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360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

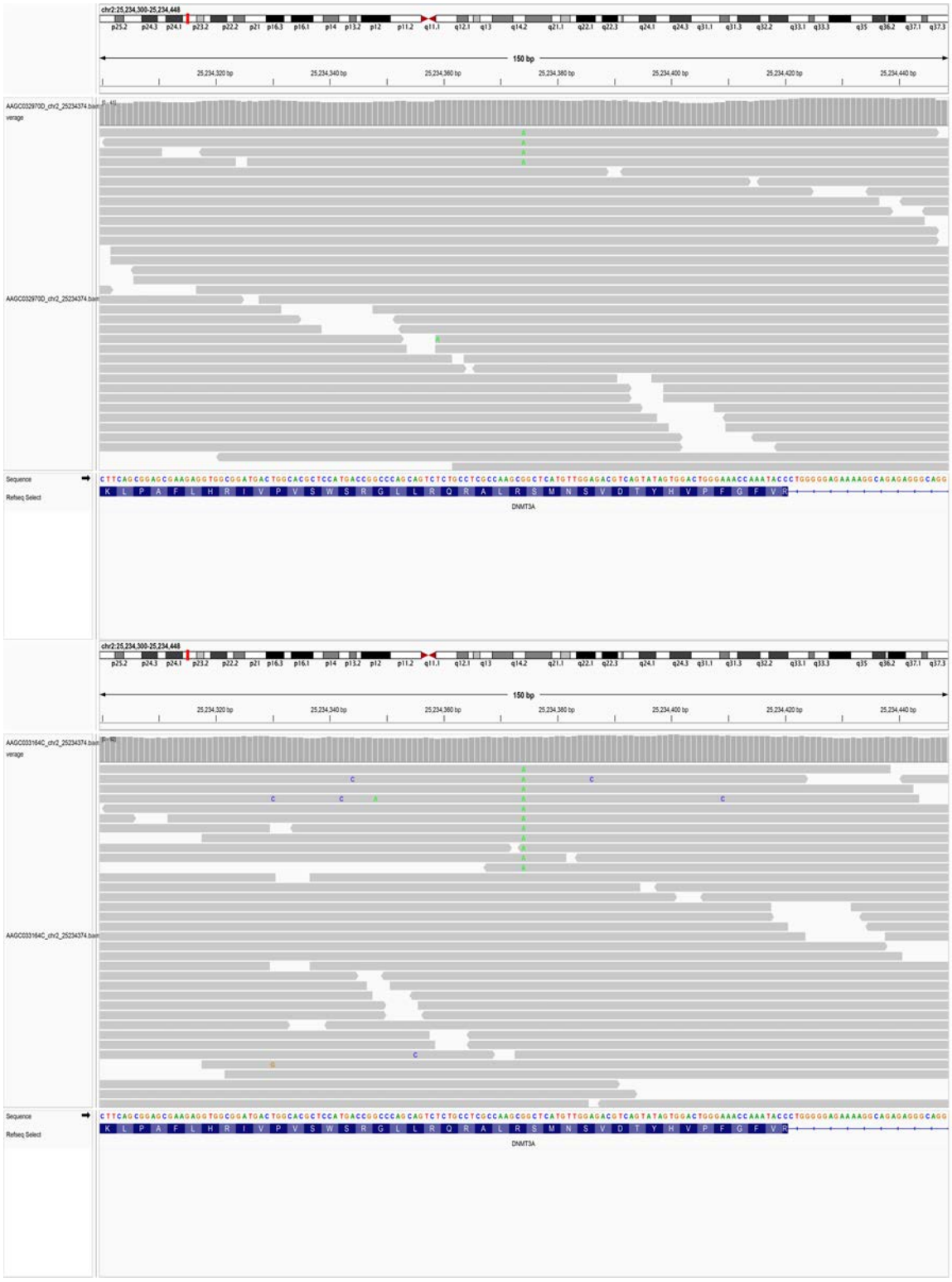
12.7. chr2_25234374_G/A

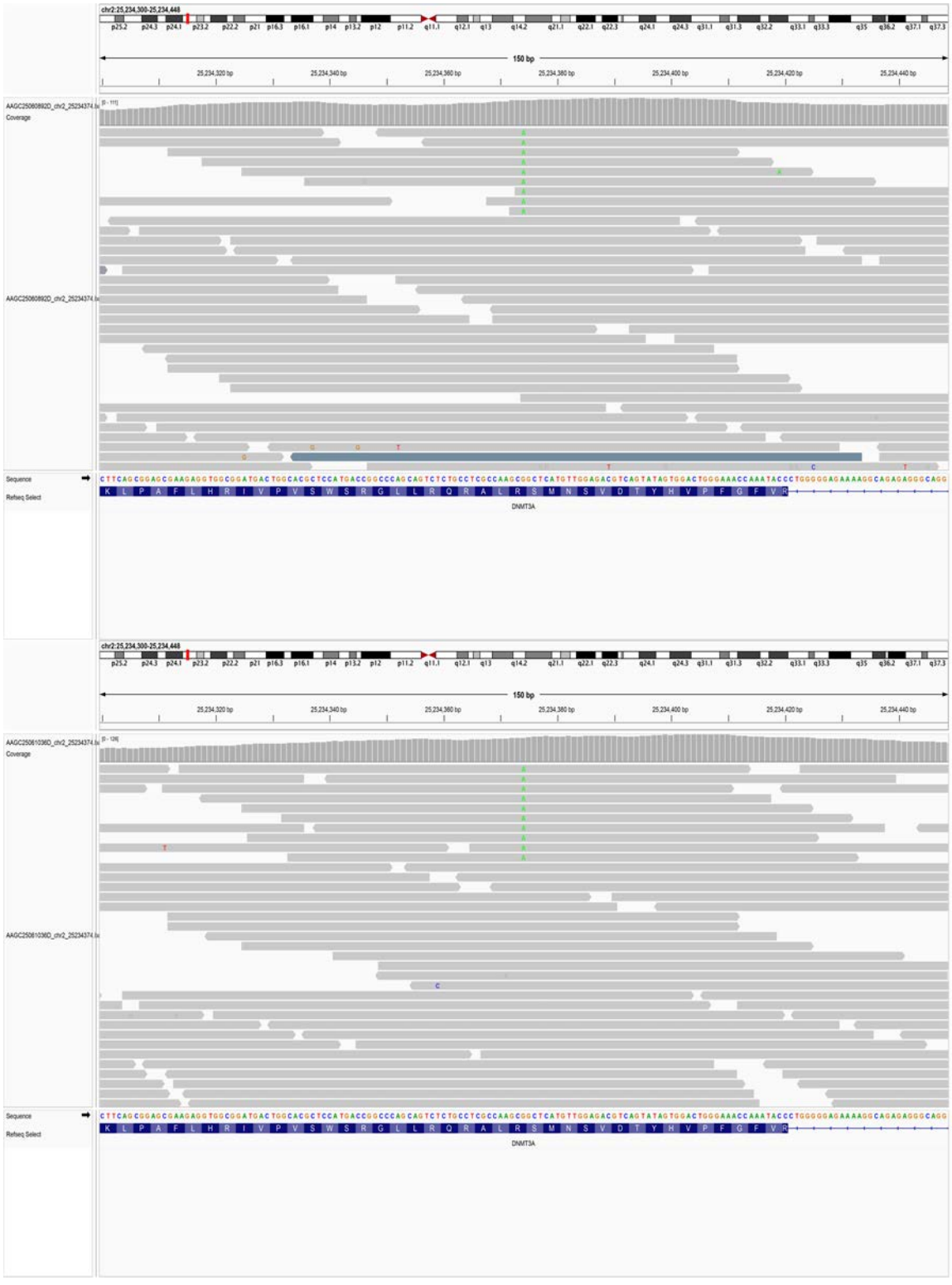
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05880	chr2_25234374_G/A	124	5	*DNMT3A*	missense_variant
18R03177	chr2_25234374_G/A	95	4	*DNMT3A*	missense_variant
18R08745	chr2_25234374_G/A	124	9	*DNMT3A*	missense_variant
18R09109	chr2_25234374_G/A	51	7	*DNMT3A*	missense_variant
18R09351	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

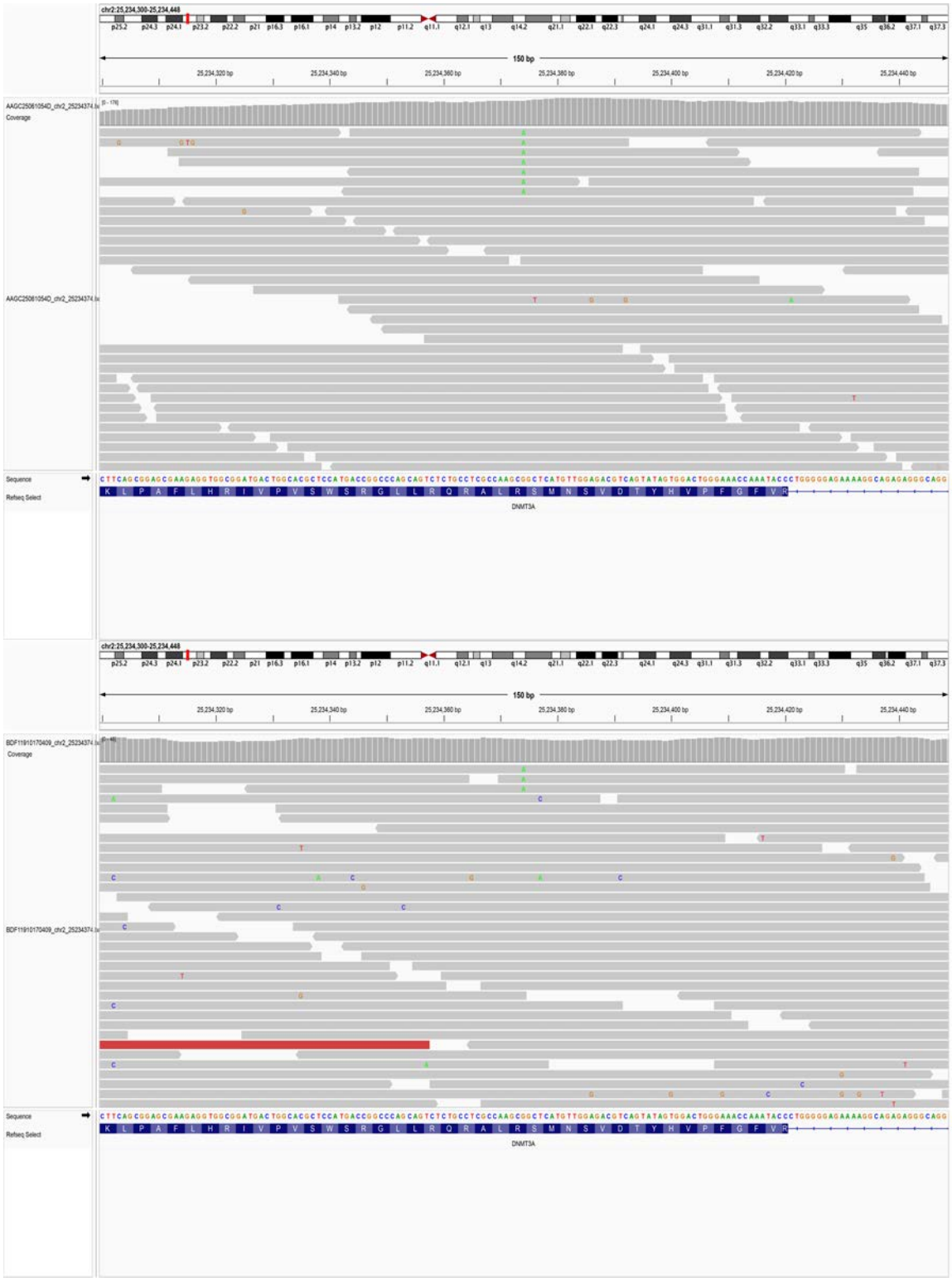


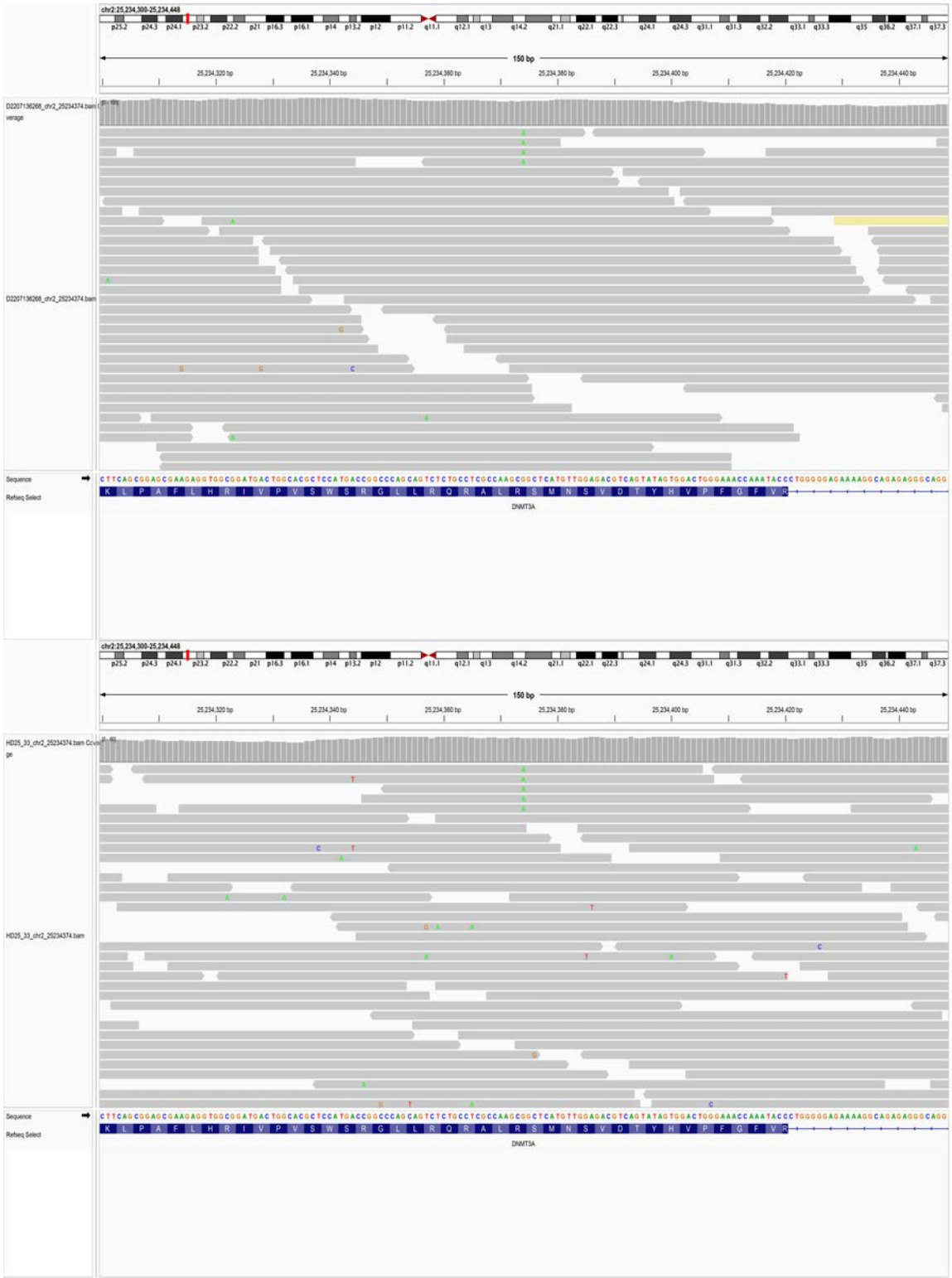

chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
18R03177_chr2_25234374.bam Coverage
18R03177_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A
chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
18R08745_chr2_25234374.bam Coverage
18R08745_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
18R09109_chr2_25234374.bam Coverage
18R09109_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
18R09351_chr2_25234374.bam Coverage
18R09351_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
AAGC032970D_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
AAGC033164C_chr2_25234374.bam
AAGC033164C_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A

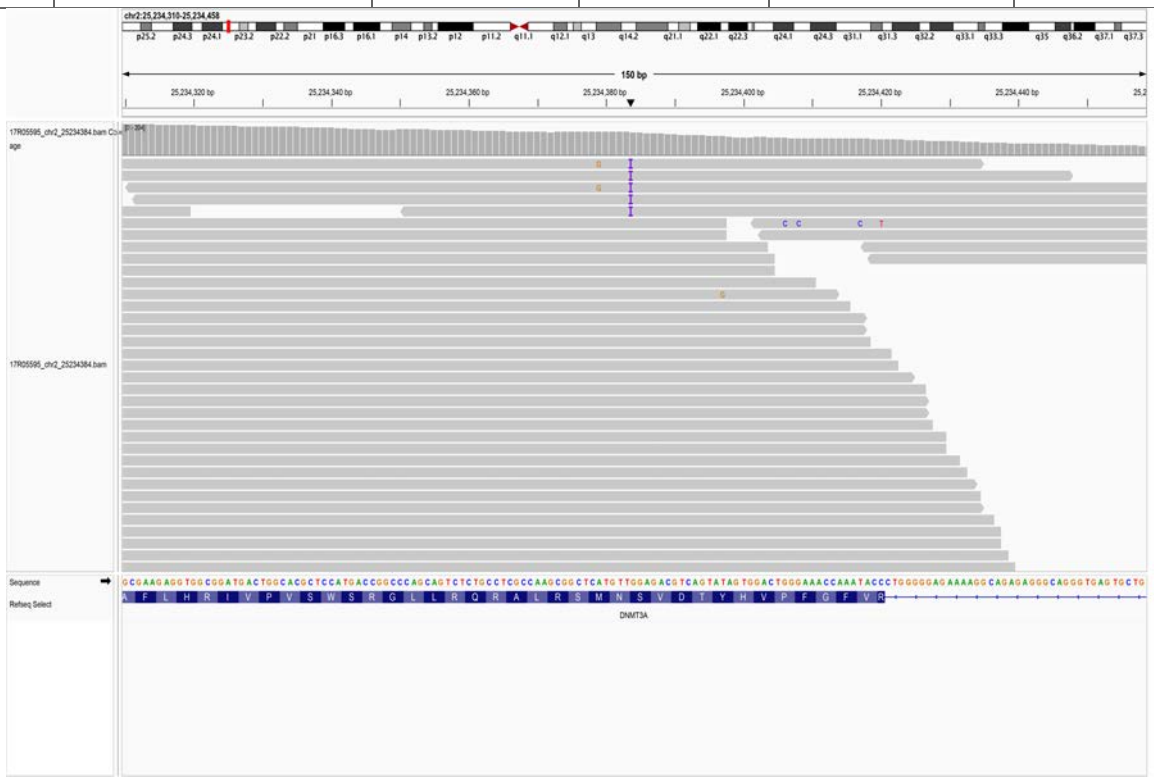

chr2:25,234,300-25,234,448
150 bp
25,234,320 bp
25,234,340 bp
25,234,360 bp
25,234,380 bp
25,234,400 bp
25,234,420 bp
25,234,440 bp
Coverage
Sequence
Refseq Select
DNMT3A
chr2:25,234,300-25,234,448
150 bp
Coverage
Sequence
Refseq Select
DNMT3A


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
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
D2207136268_chr2_25234374.bam
Sequence
Refseq Select
DNMT3A
HD25_33_chr2_25234374.bam

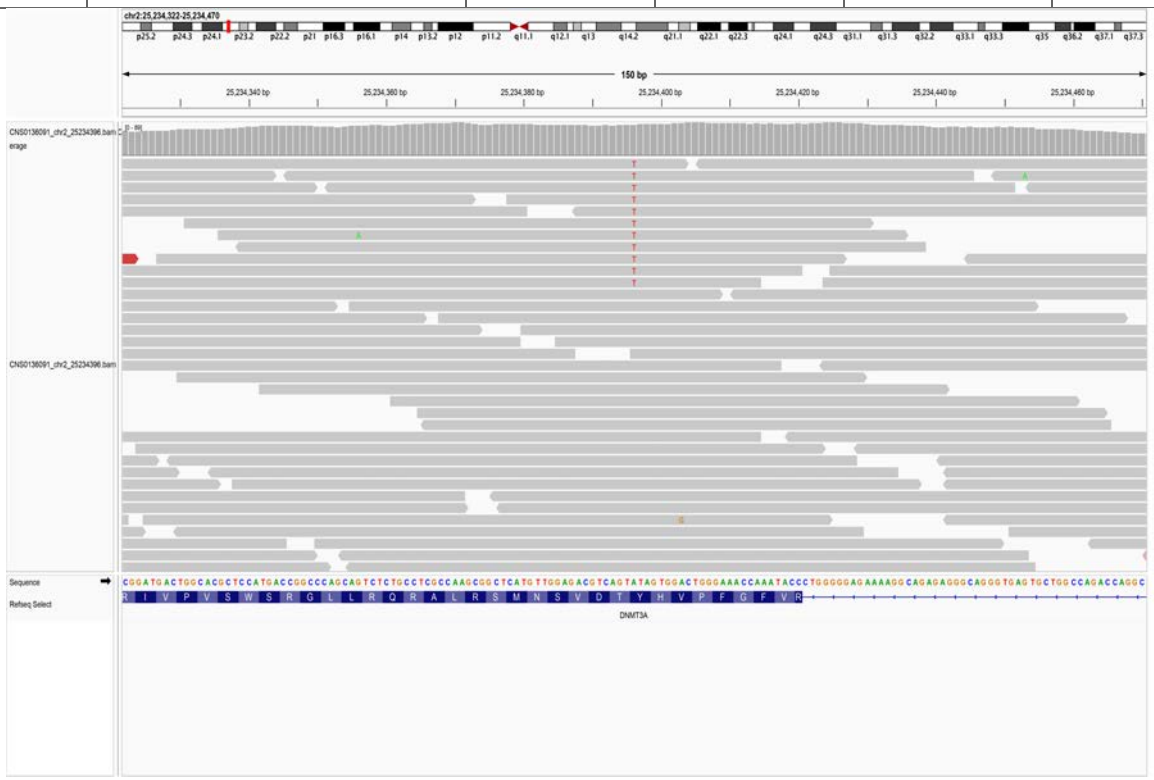
12.8. chr2_25234384_-/G

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



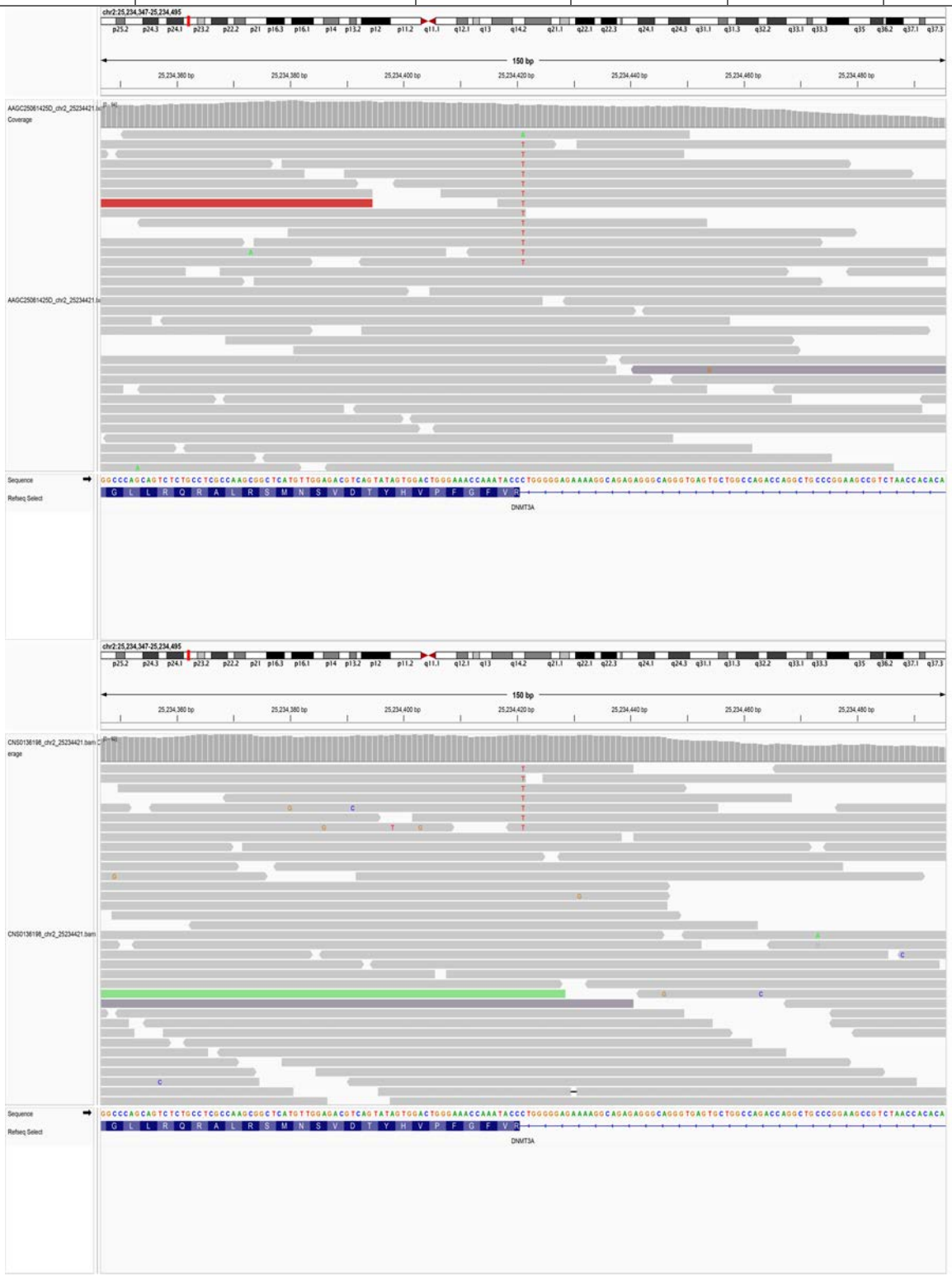
12.9. chr2_25234396_A/T

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



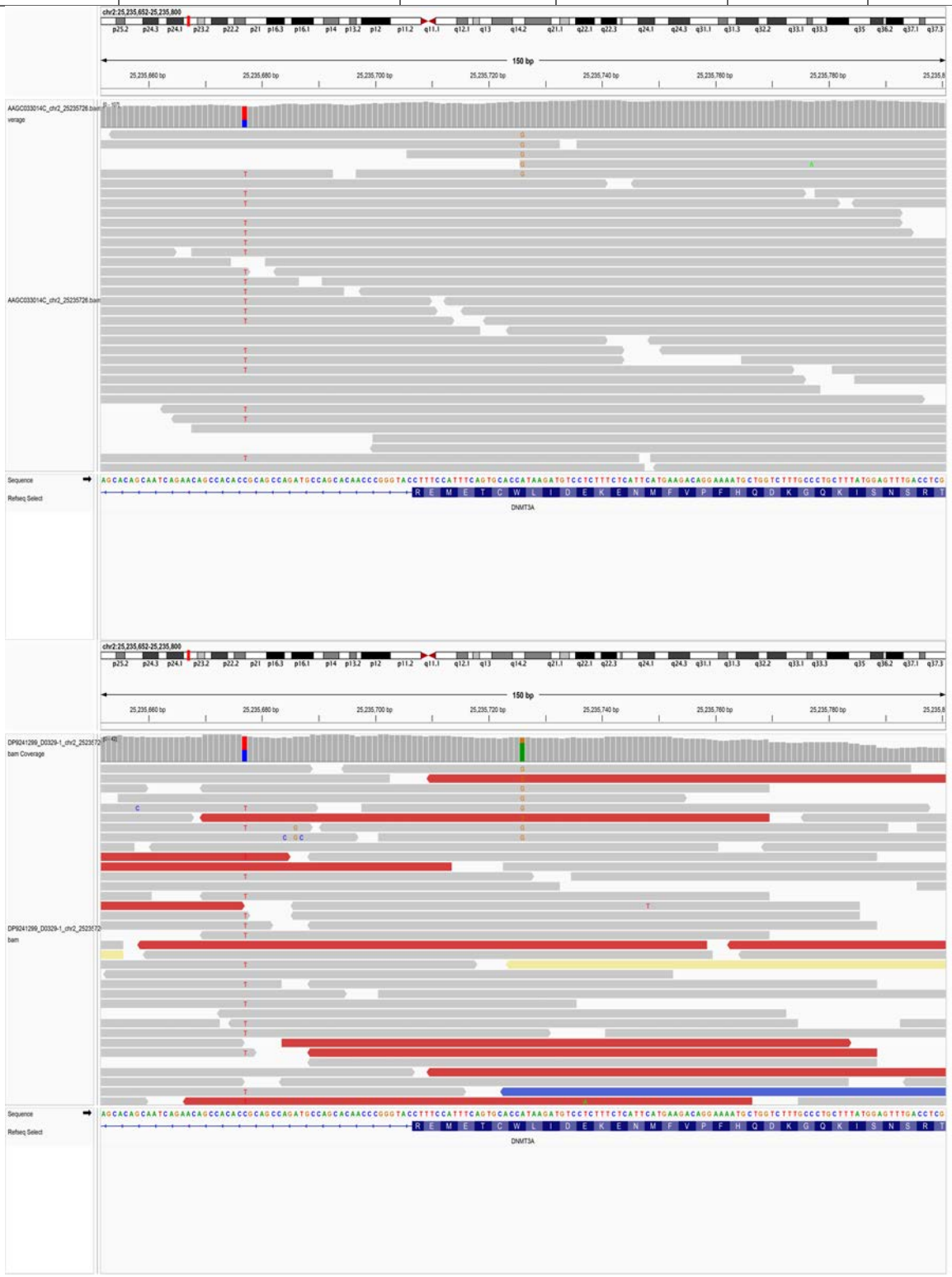
12.10. chr2_25234421_C/T

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



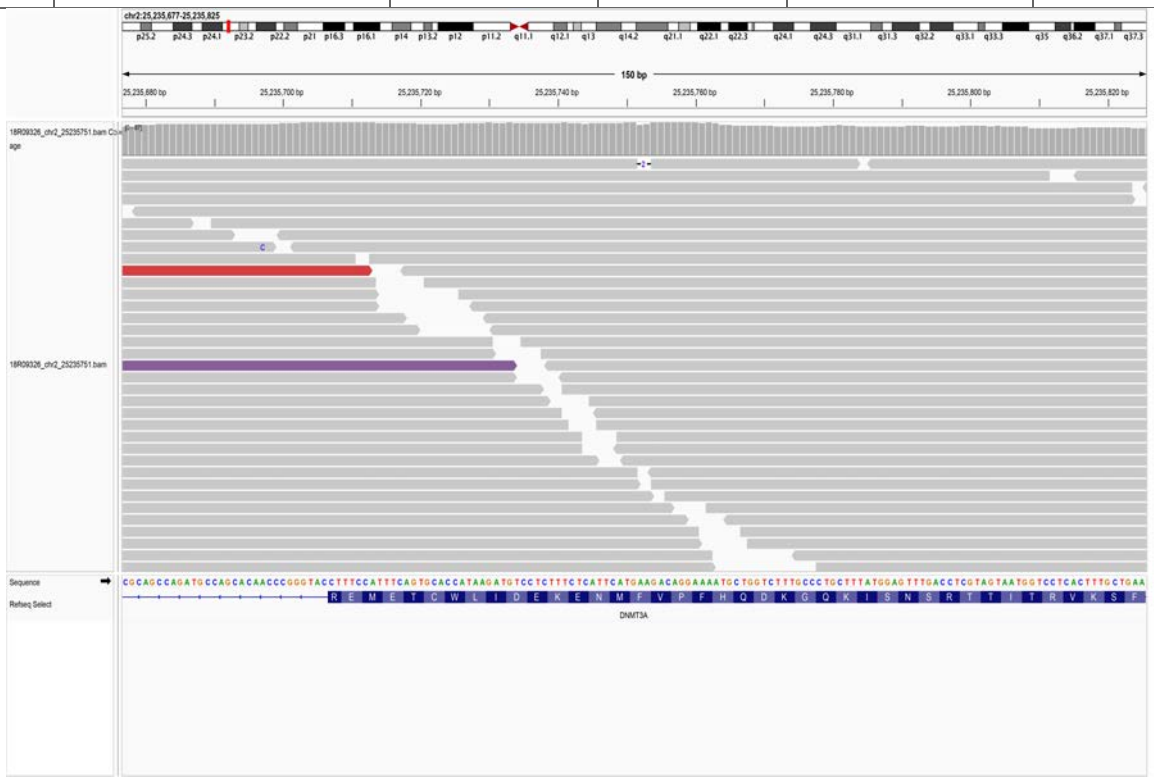
12.11. chr2_25235726_A/G

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



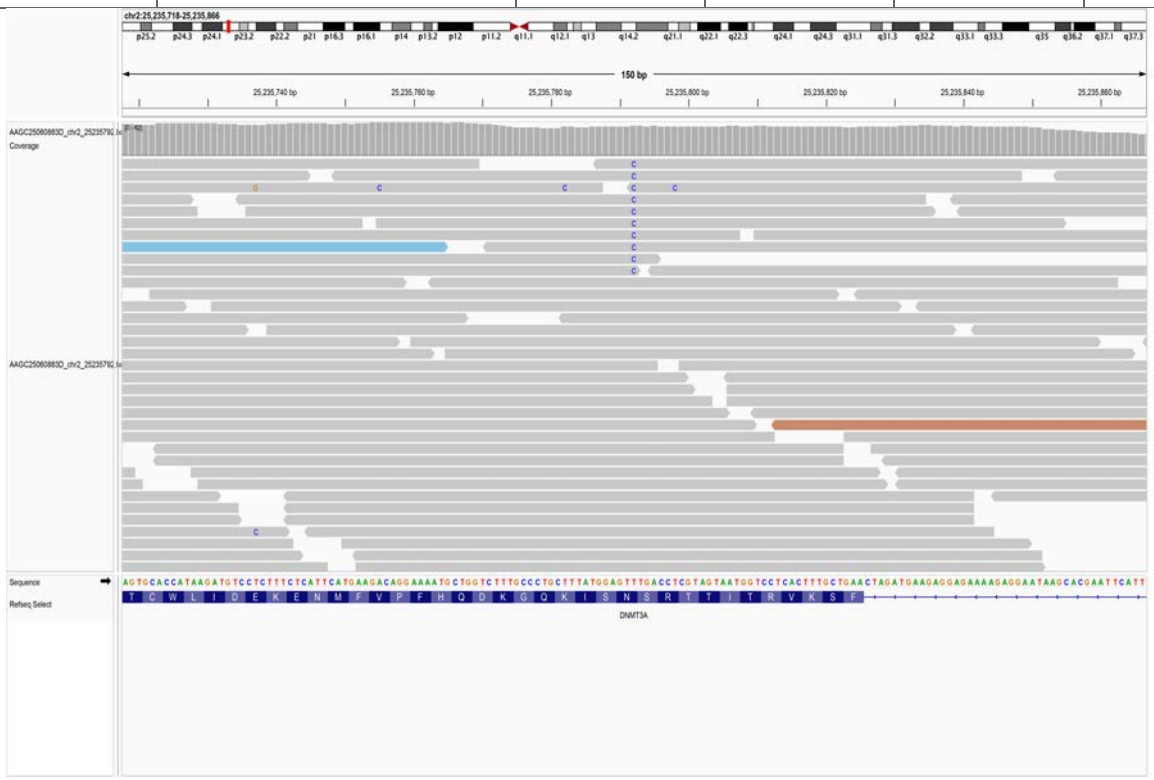
12.12. chr2_25235752_AA/-

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



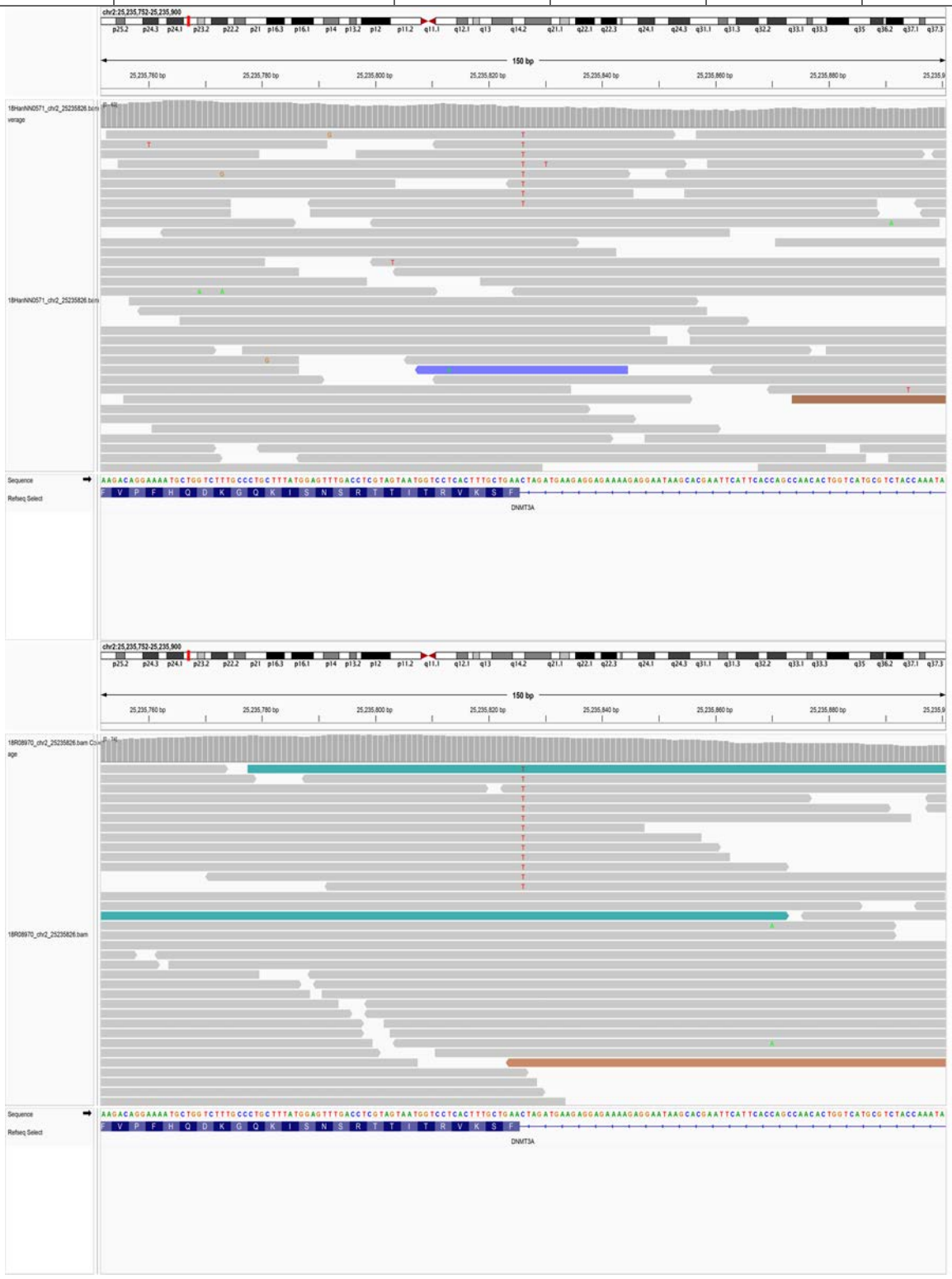
12.13. chr2_25235792_T/C

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



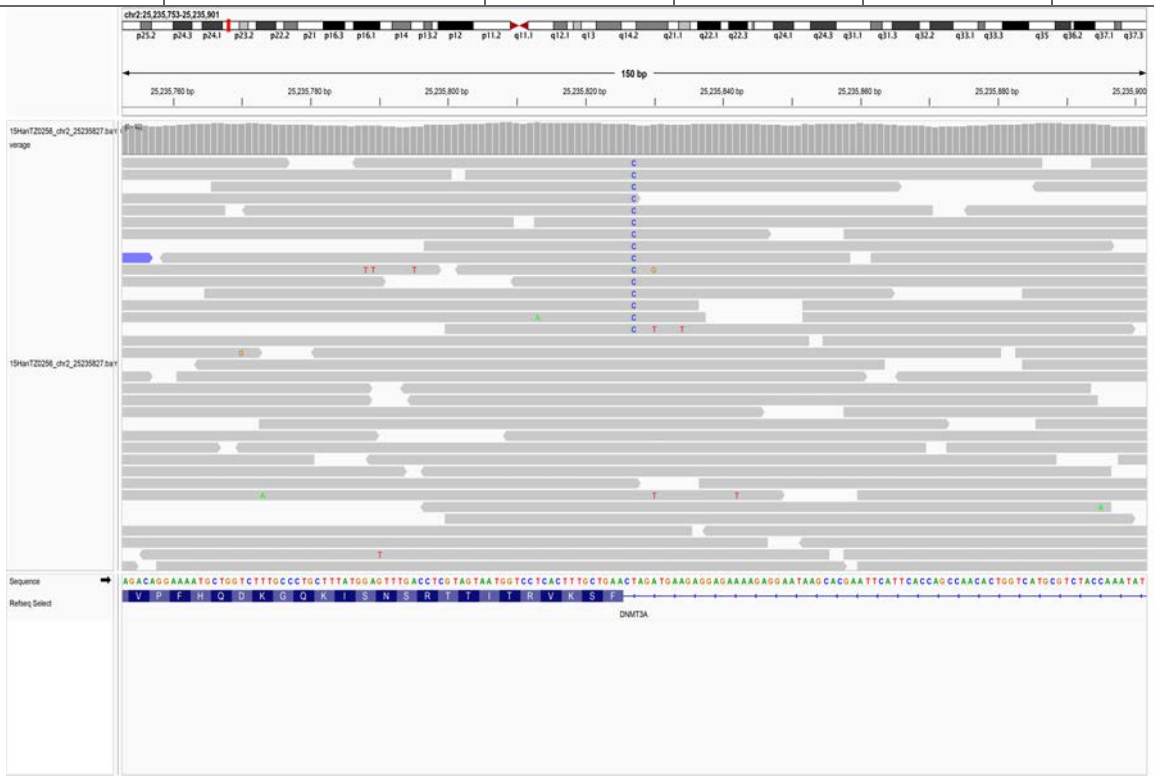
12.14. chr2_25235826_C/T

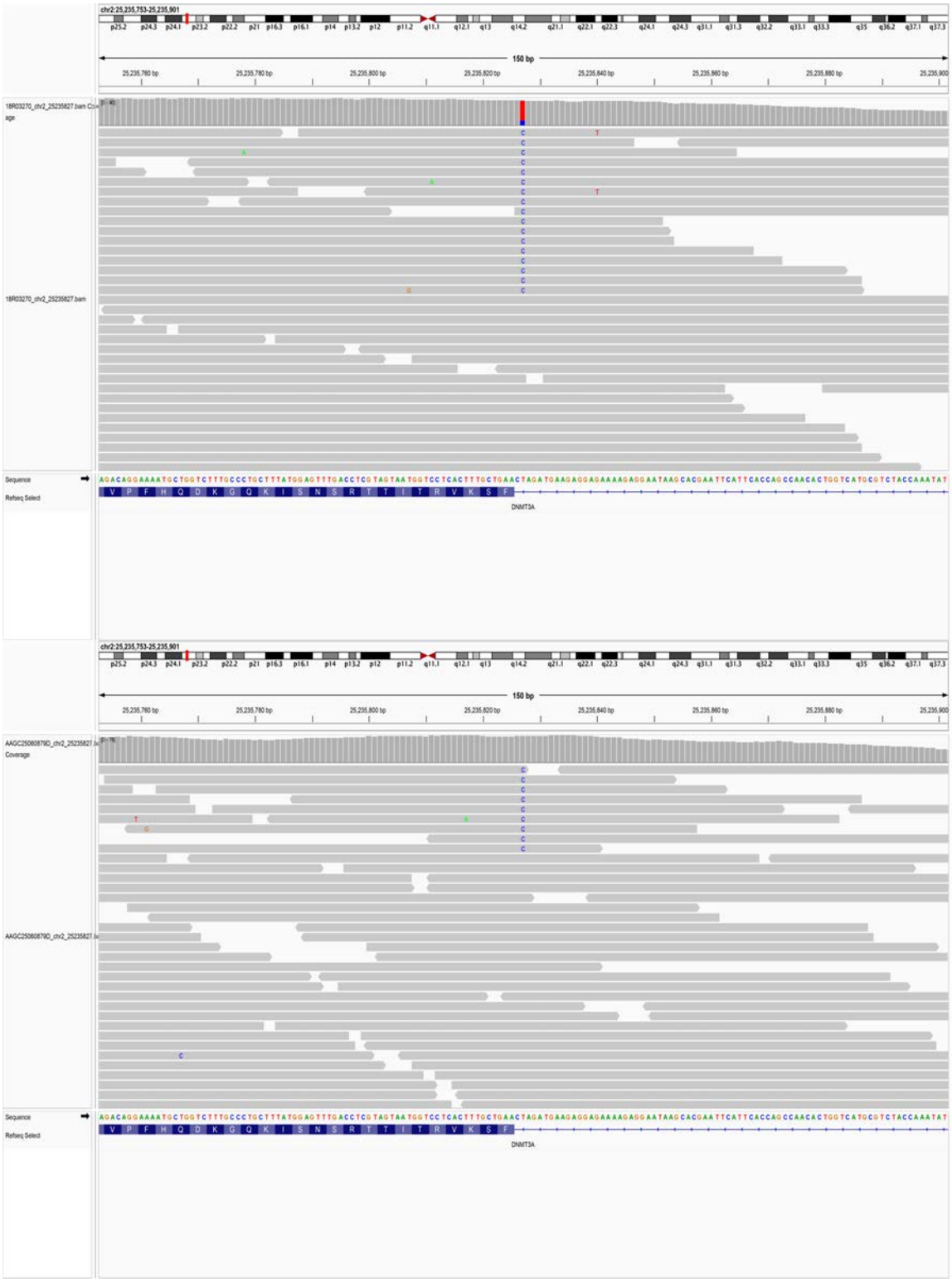
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18HanNN0571	chr2_25235826_C/T	38	7	*DNMT3A*	splice_acceptor_variant
18R08970	chr2_25235826_C/T	55	13	*DNMT3A*	splice_acceptor_variant



12.15. chr2_25235827_T/C

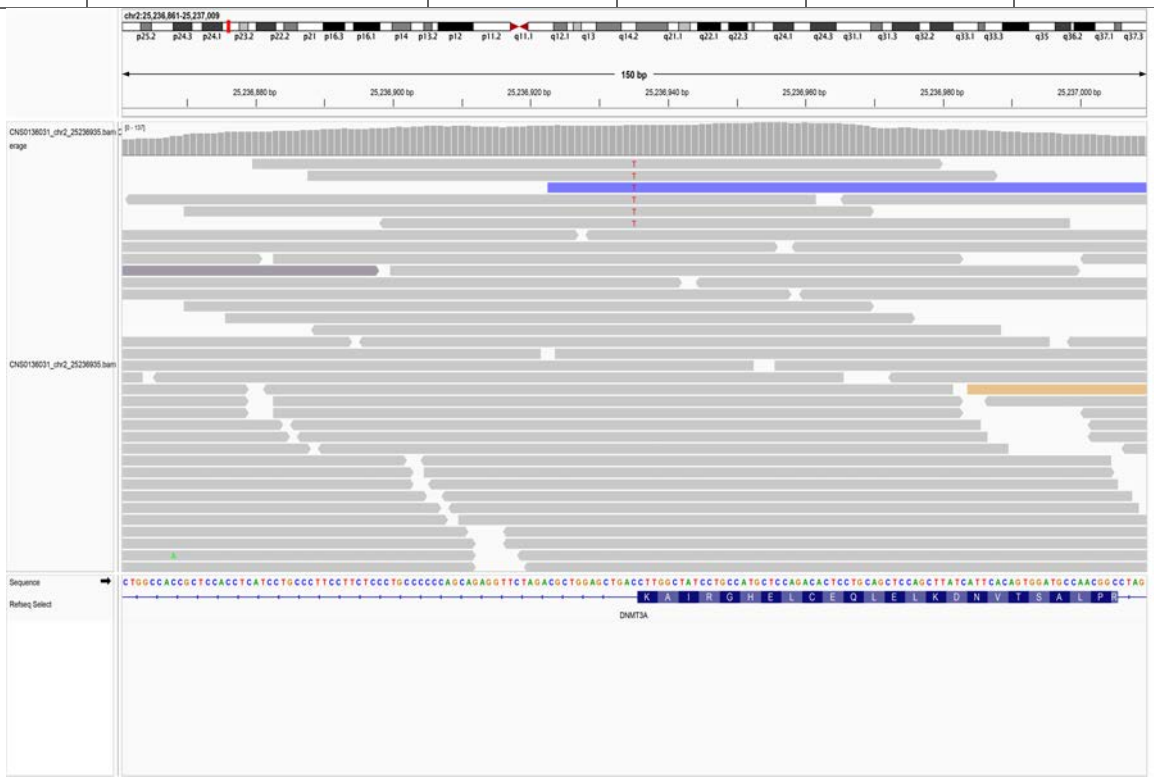
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
15HanTZ0256	chr2_25235827_T/C	63	14	*DNMT3A*	splice_acceptor_variant
18R03270	chr2_25235827_T/C	64	17	*DNMT3A*	splice_acceptor_variant
AAGC25060879D	chr2_25235827_T/C	66	9	*DNMT3A*	splice_acceptor_variant




chr2:25,235,753-25,235,901
150 bp
25,235,780 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
Sequence
Refseq Select
DNMT3A
AAGC2506087ID_chr2_25235827.bam

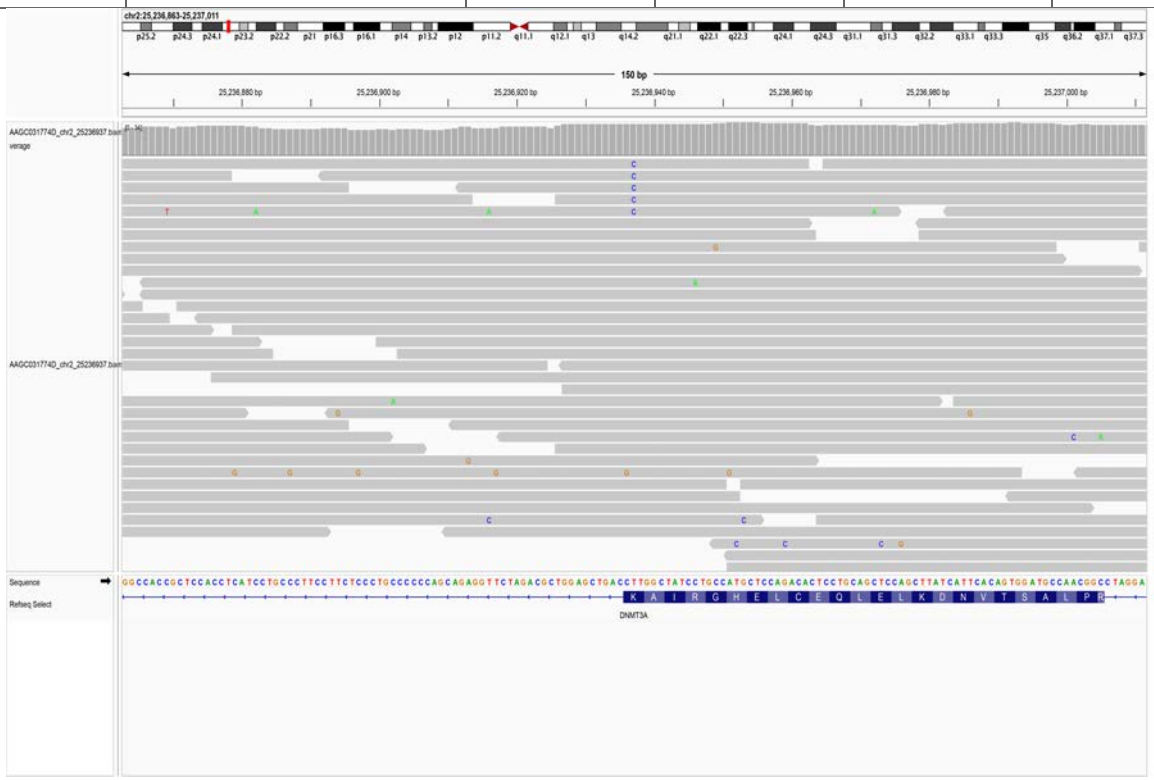
12.16. chr2_25236935_C/T

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



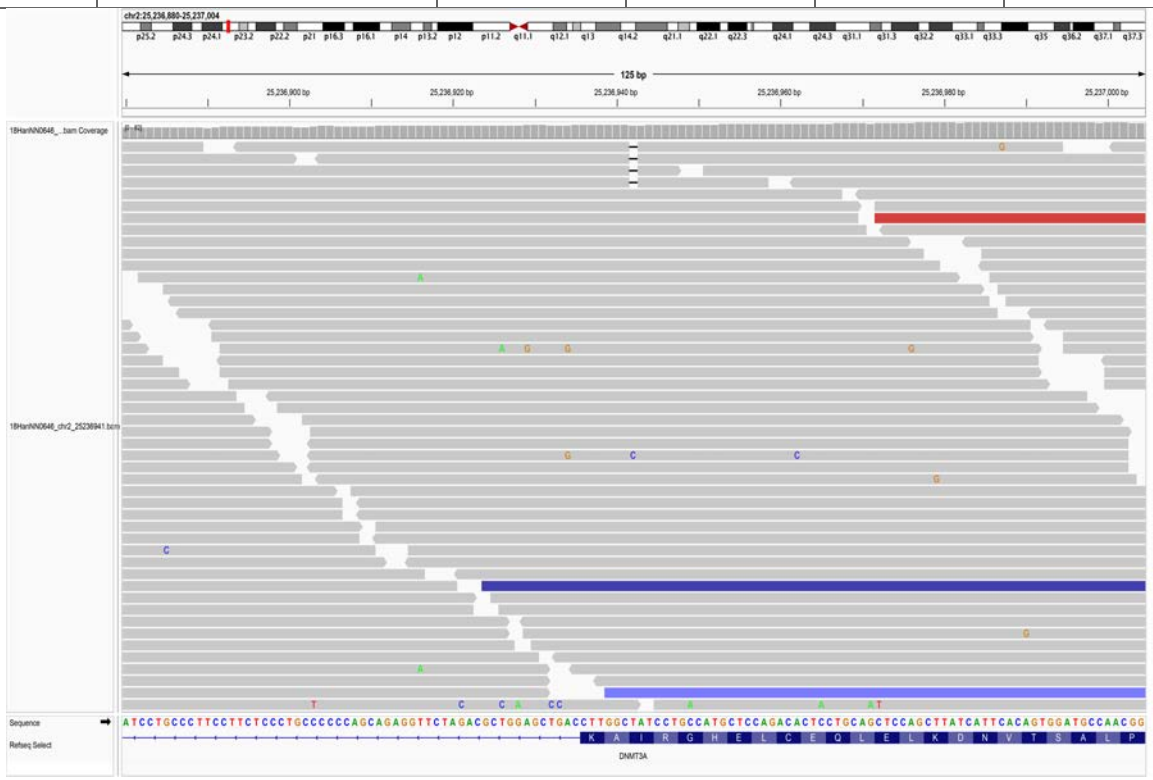
12.17. chr2_25236937_T/C

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



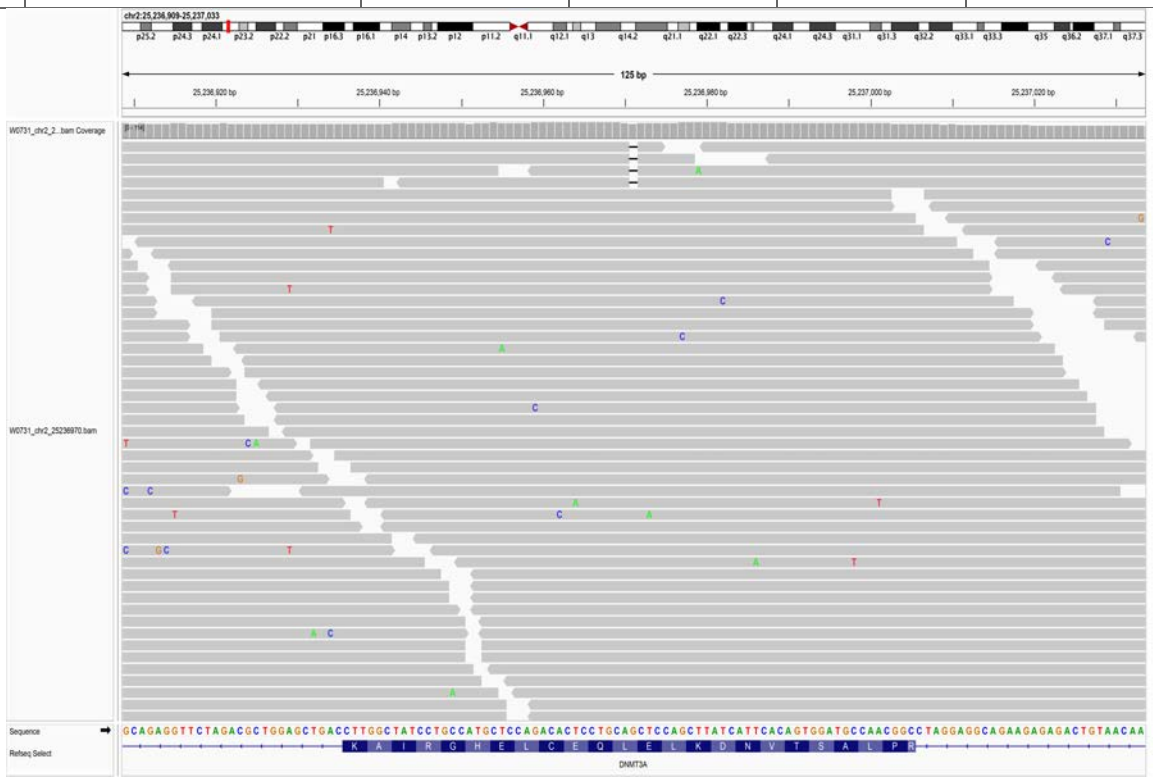
12.18. chr2_25236942_T/-

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



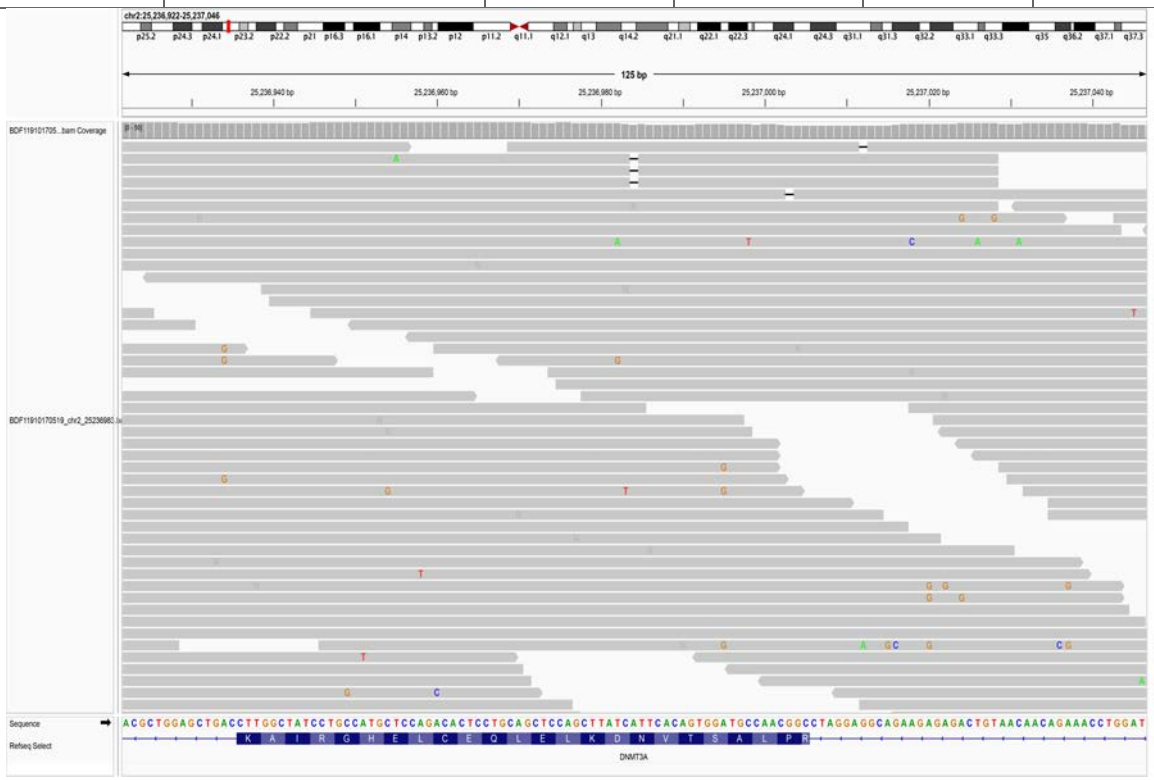
12.19. chr2_25236971_G/-

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



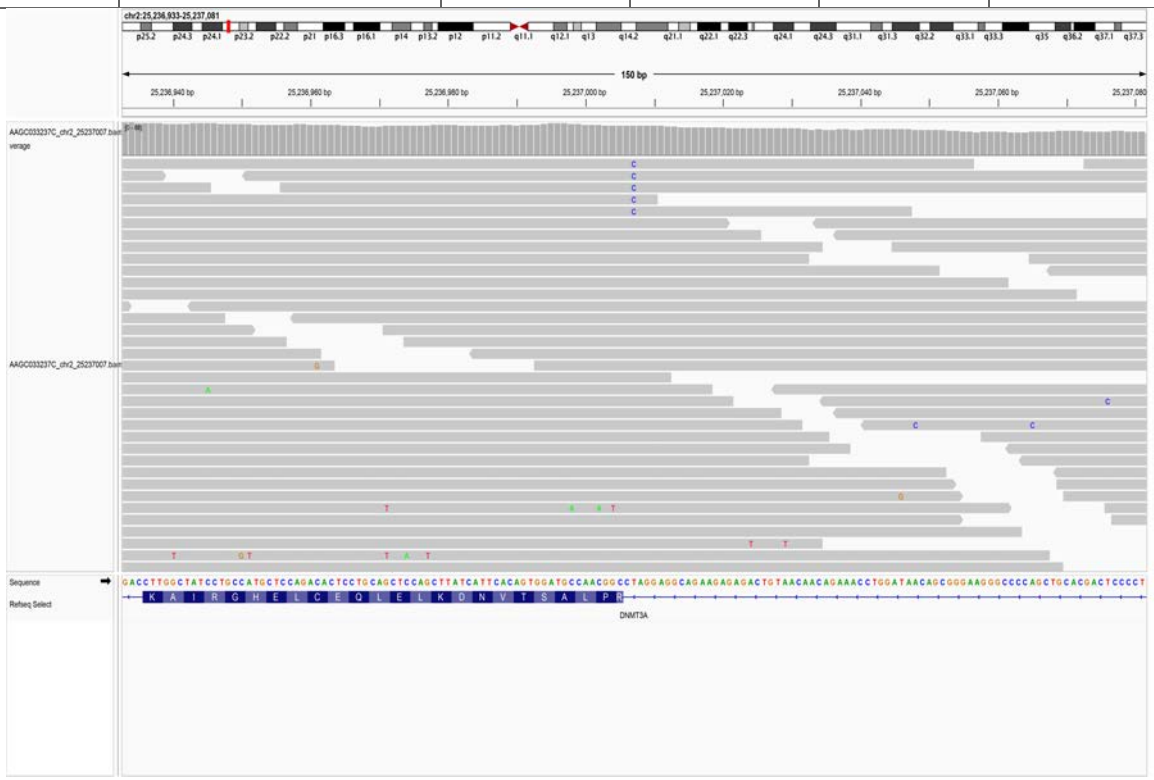
12.20. chr2_25236984_A/-

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



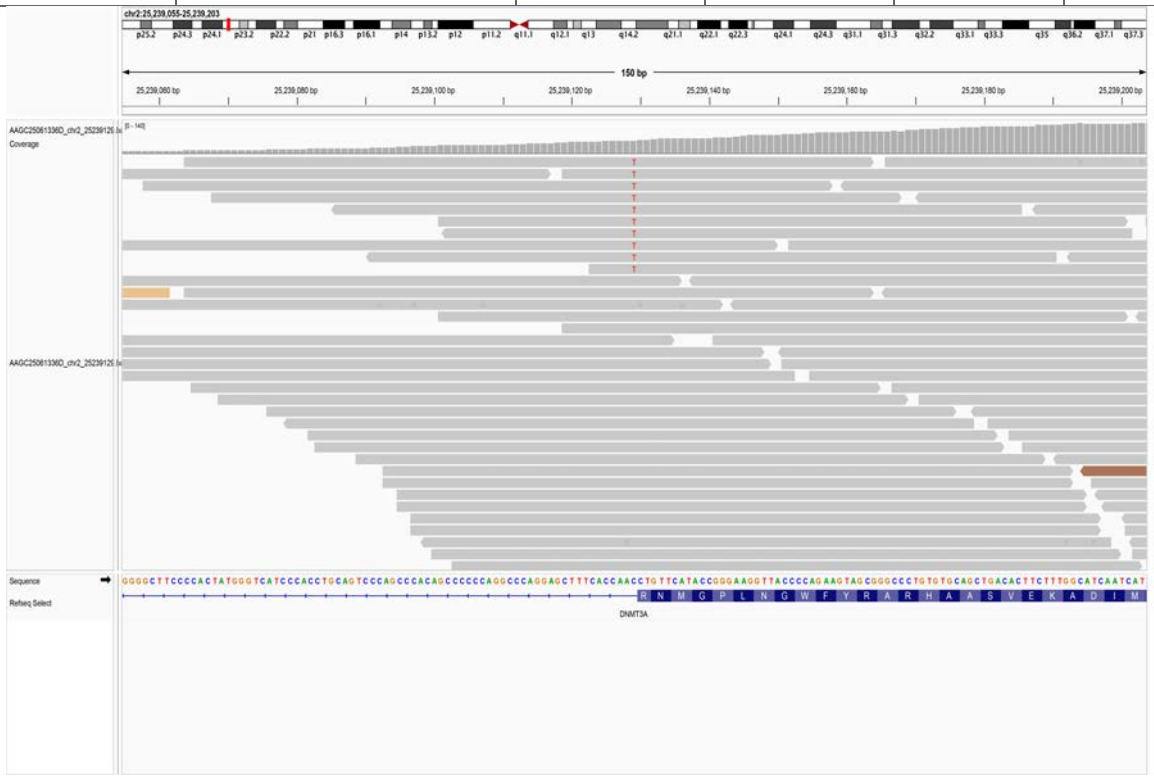
12.21. chr2_25237007_T/C

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



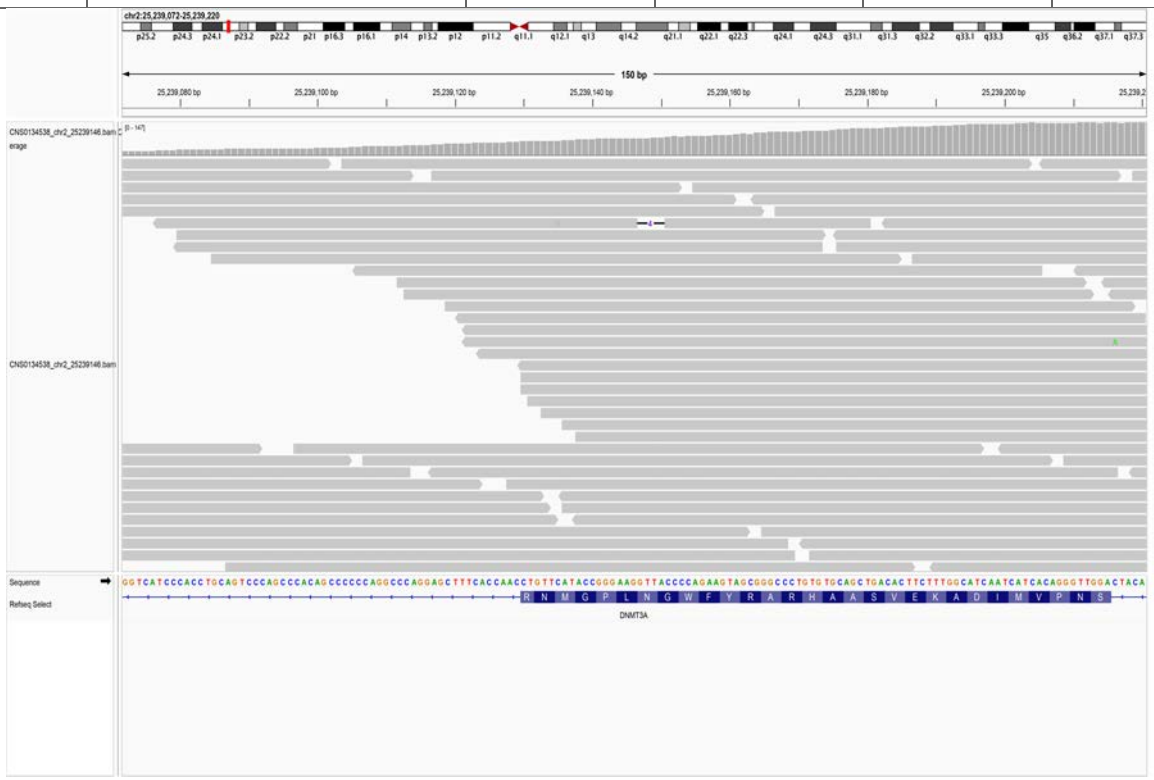
12.22. chr2_25239129_C/T

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



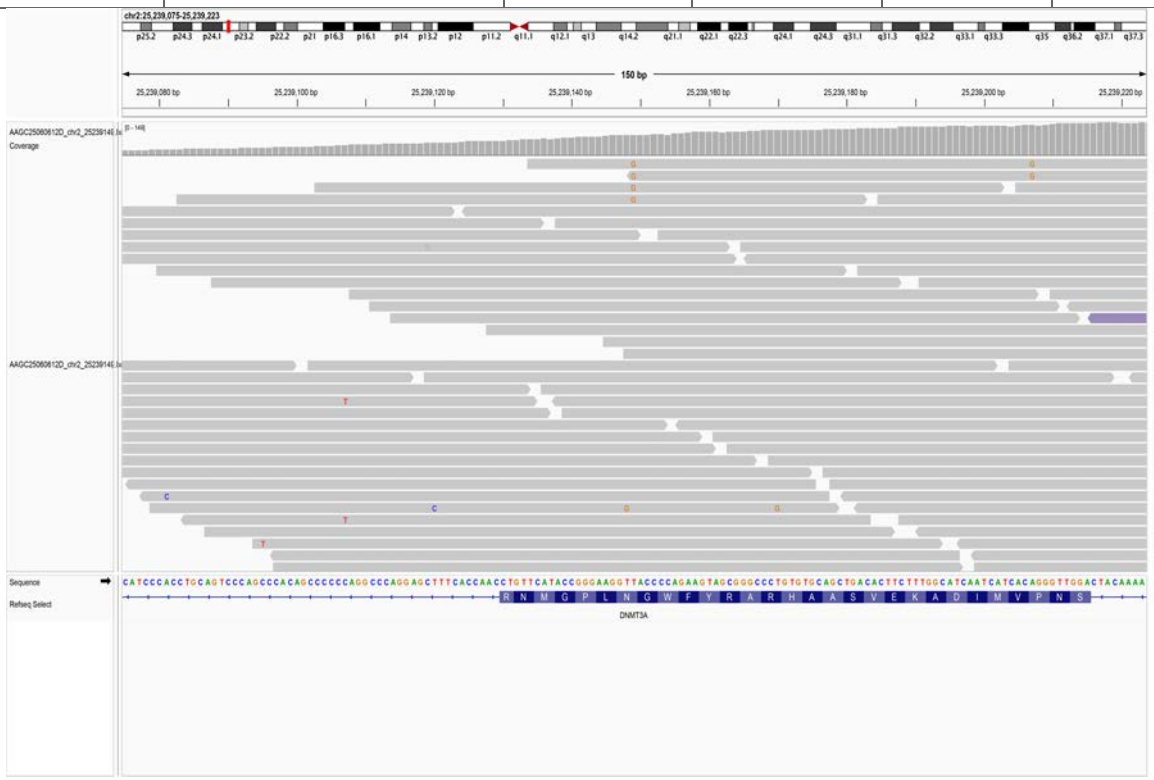
12.23. chr2_25239147_GTTA/-

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



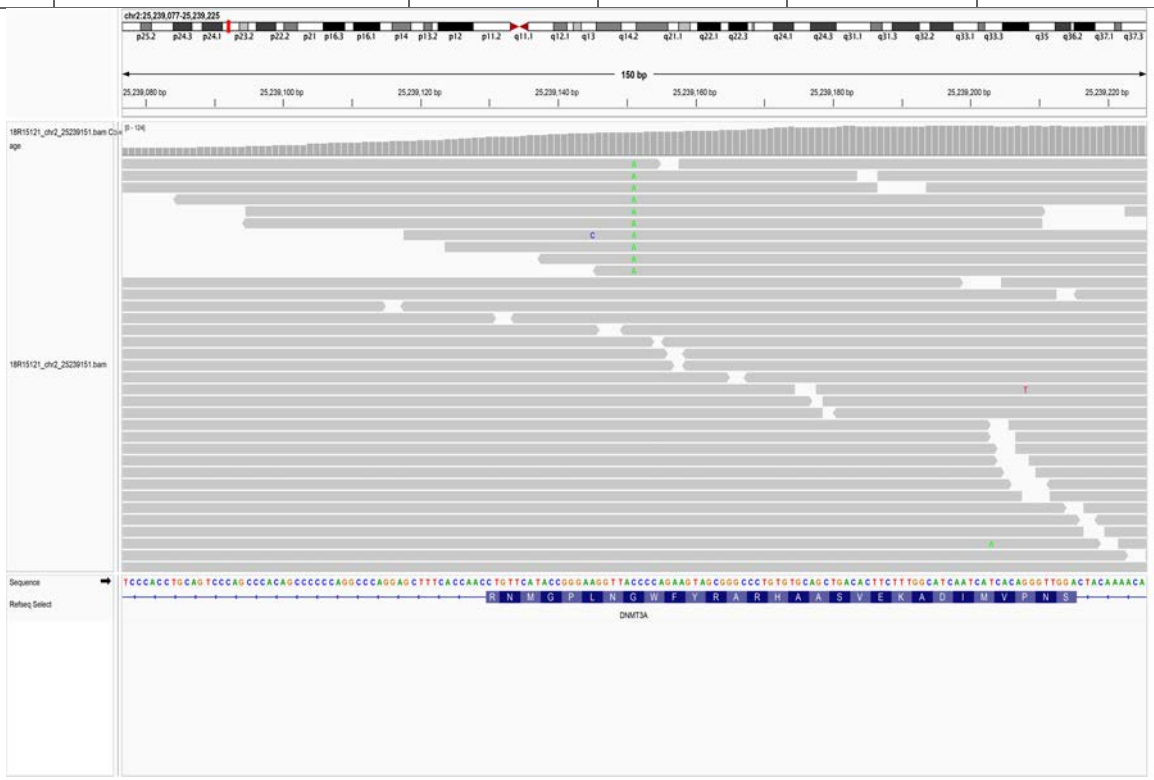
12.24. chr2_25239149_T/G

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



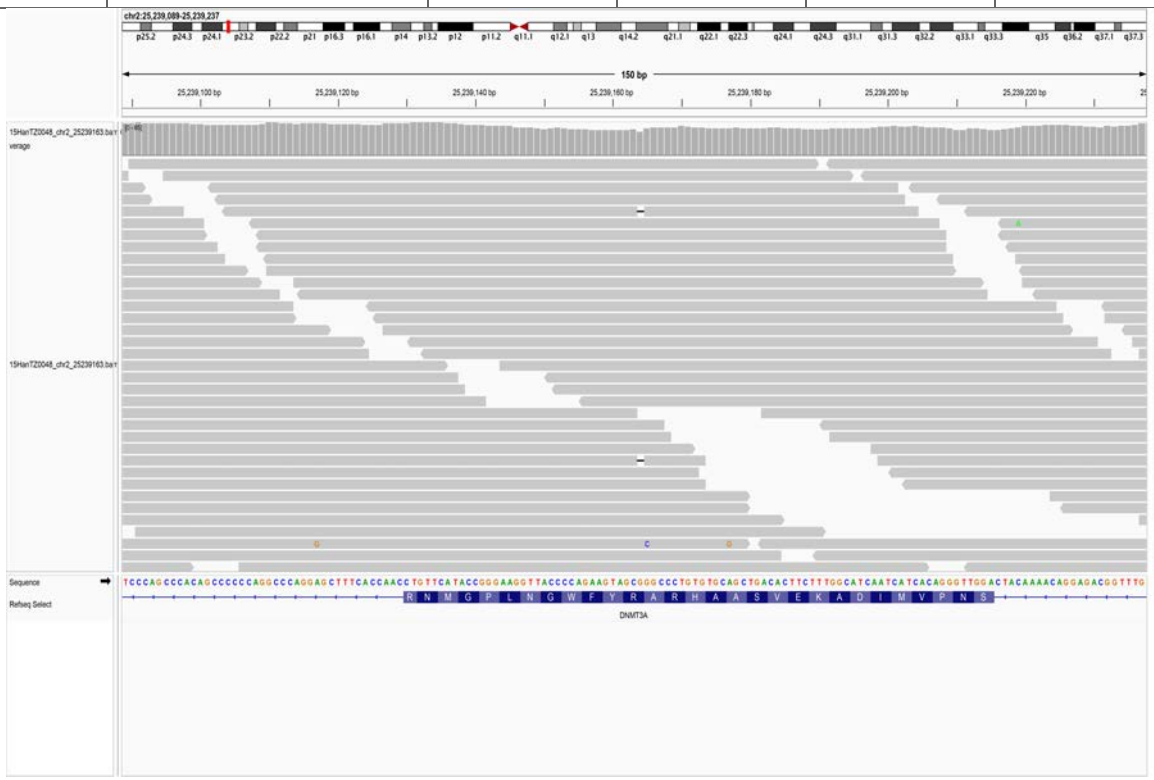
12.25. chr2_25239151_C/A

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



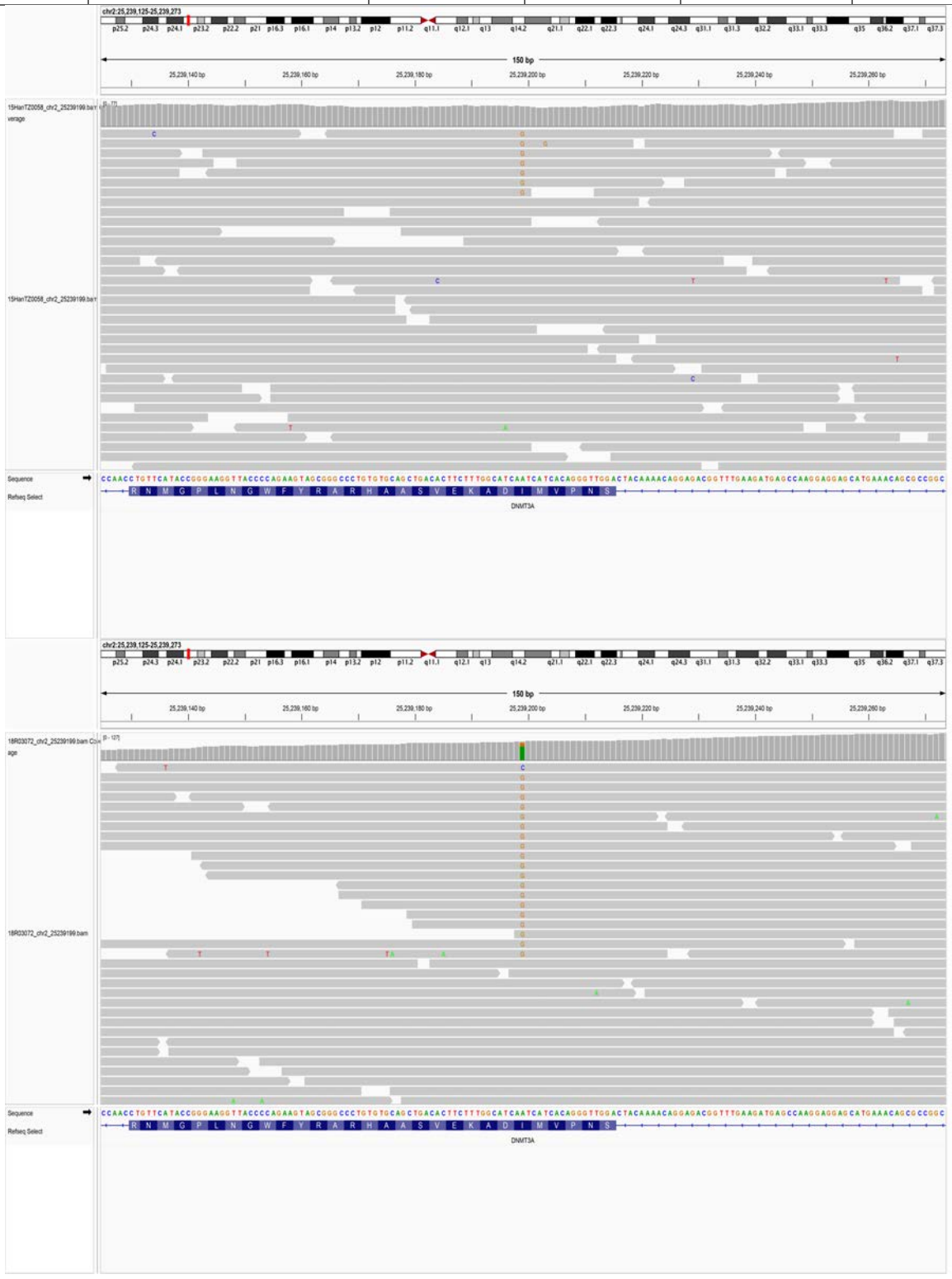
12.26. chr2_25239164_G/-

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



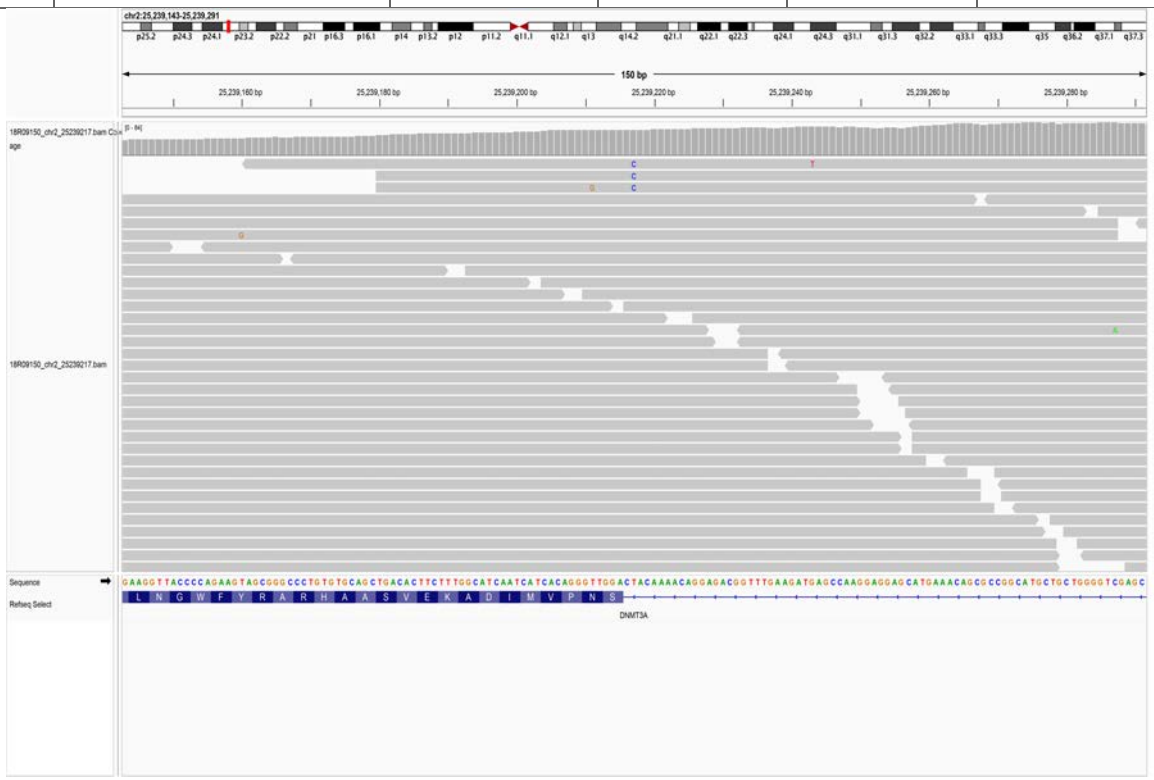
12.27. chr2_25239199_A/G

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



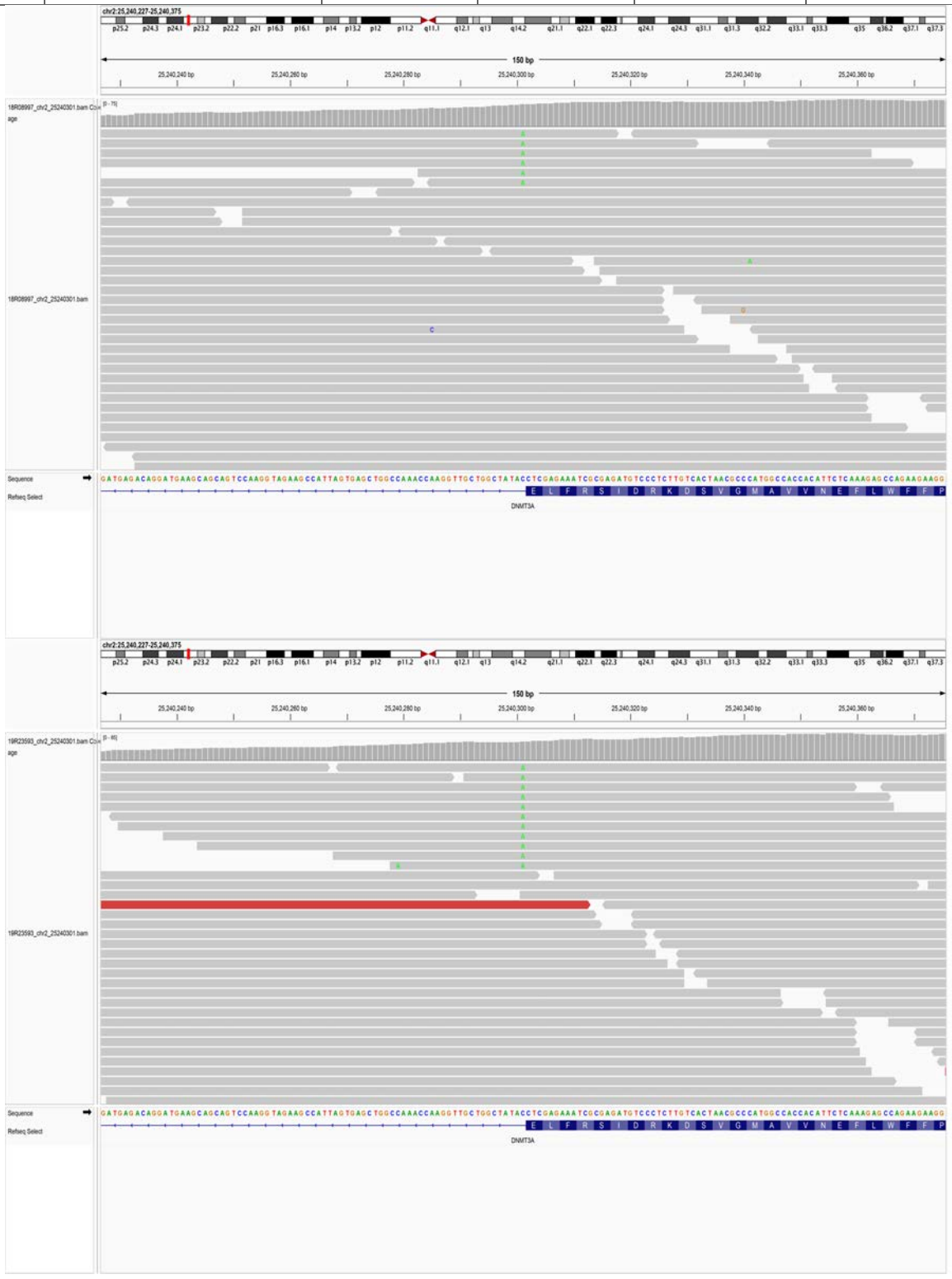
12.28. chr2_25239217_T/C

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



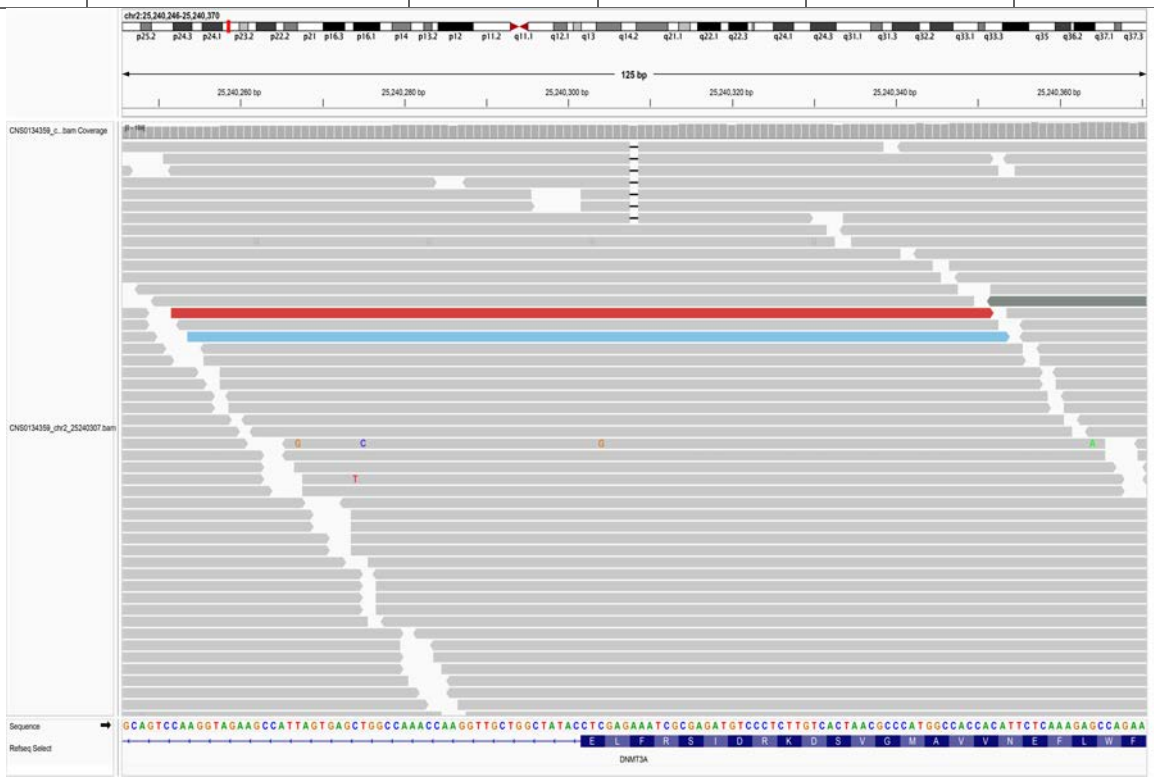
12.29. chr2_25240301_C/A

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



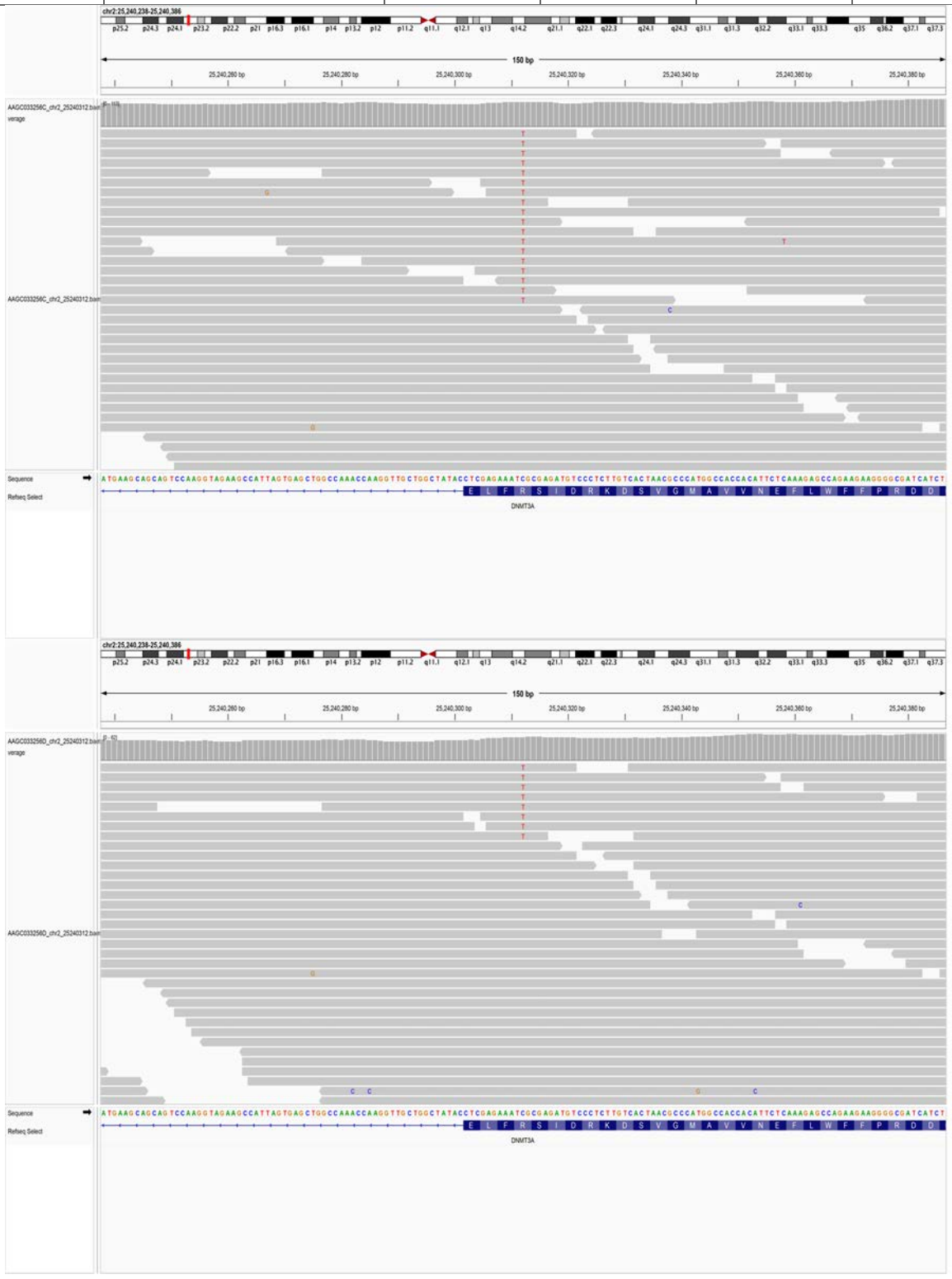
12.30. chr2_25240308_A/-

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



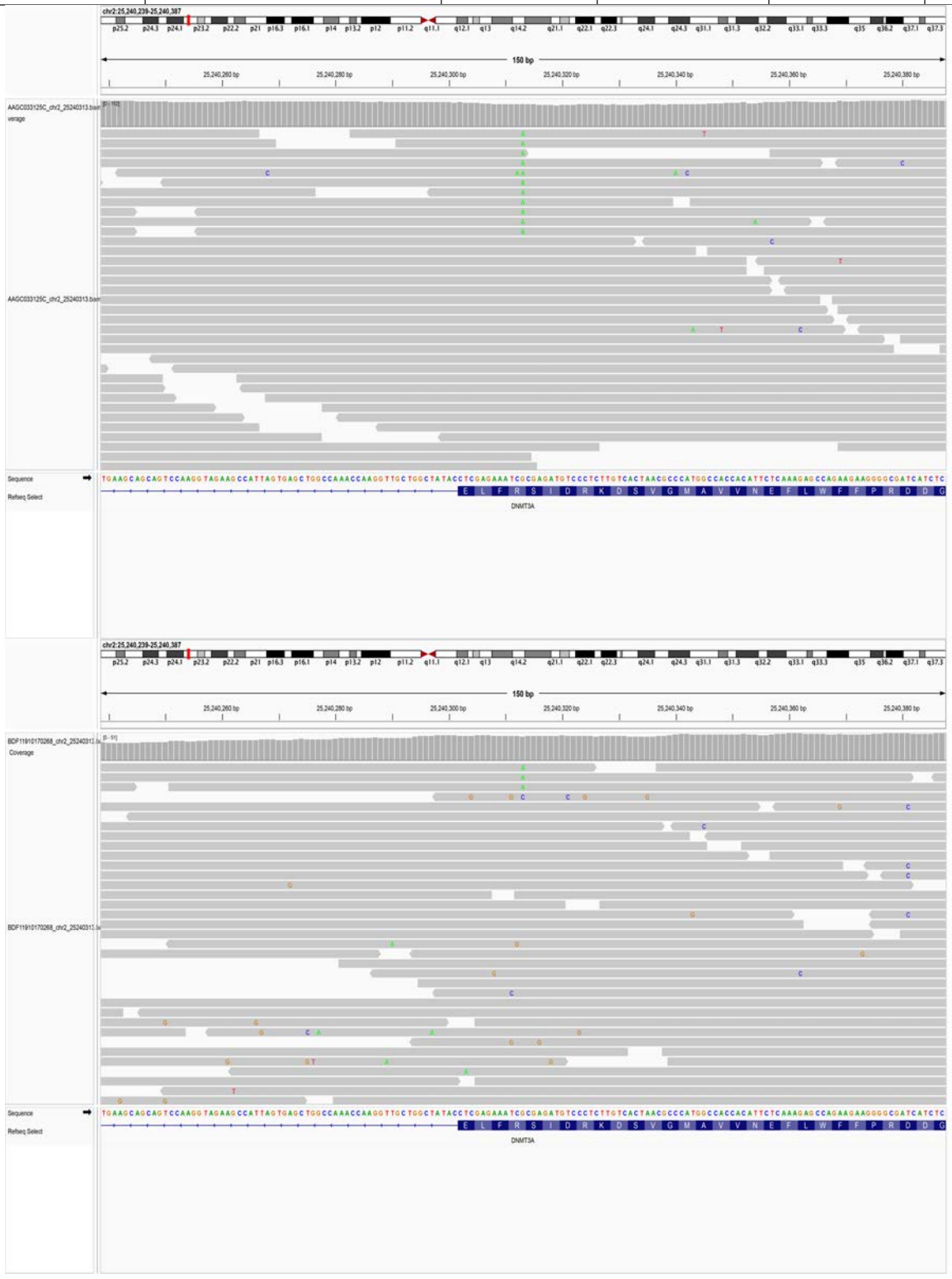
12.31. chr2_25240312_C/T

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



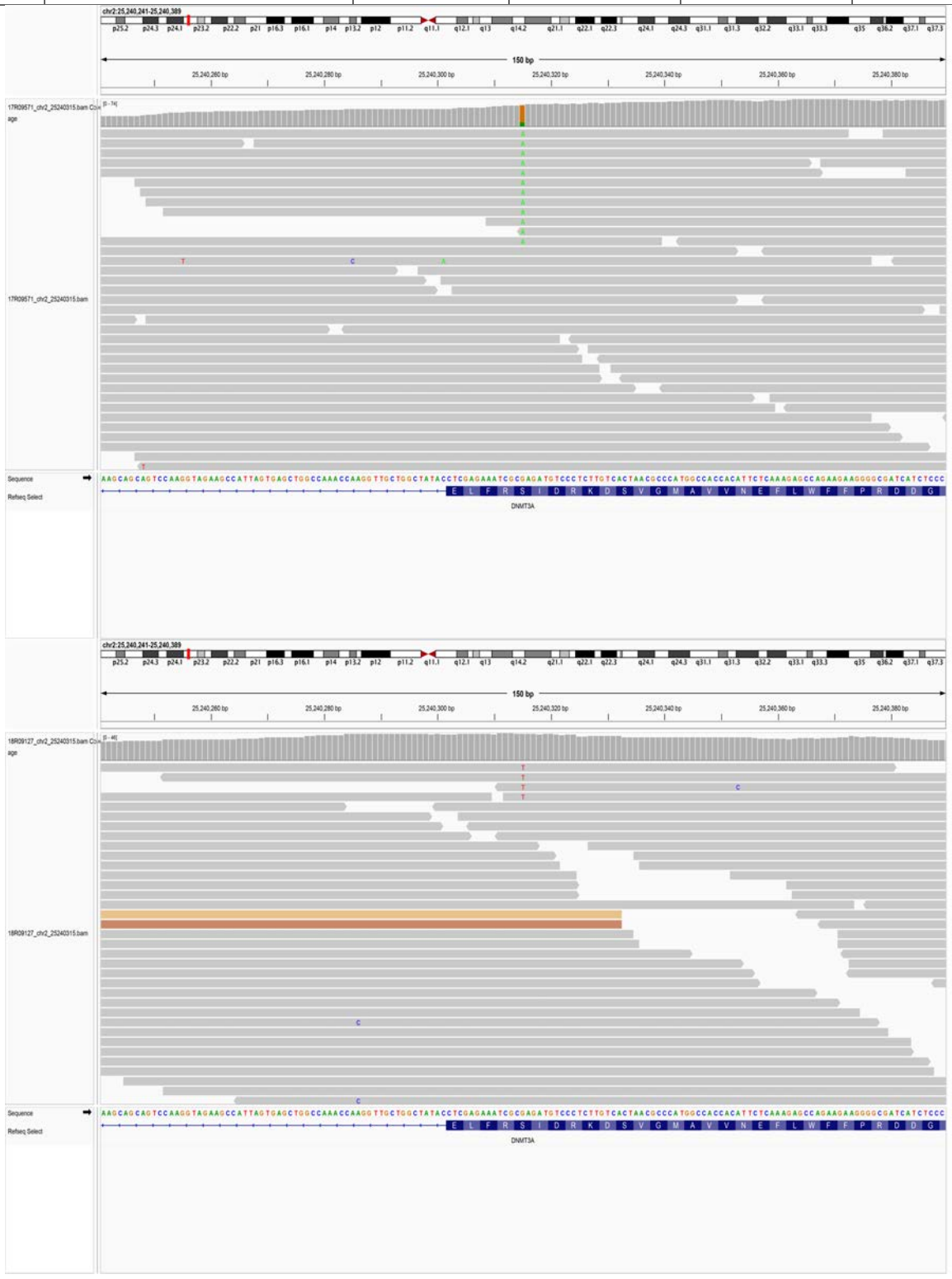
12.32. chr2_25240313_G/A

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



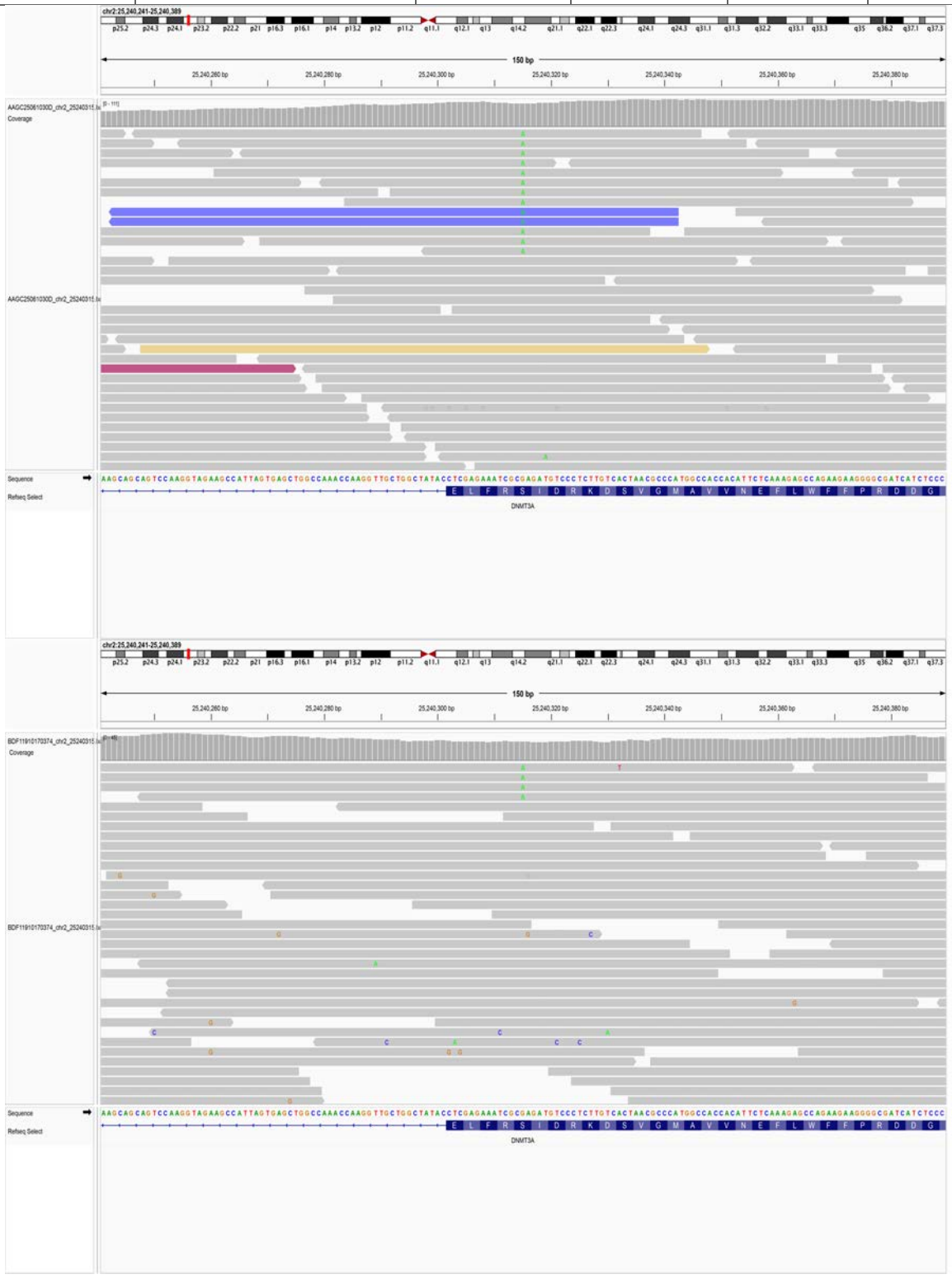
12.33. chr2_25240315_G/A/T

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



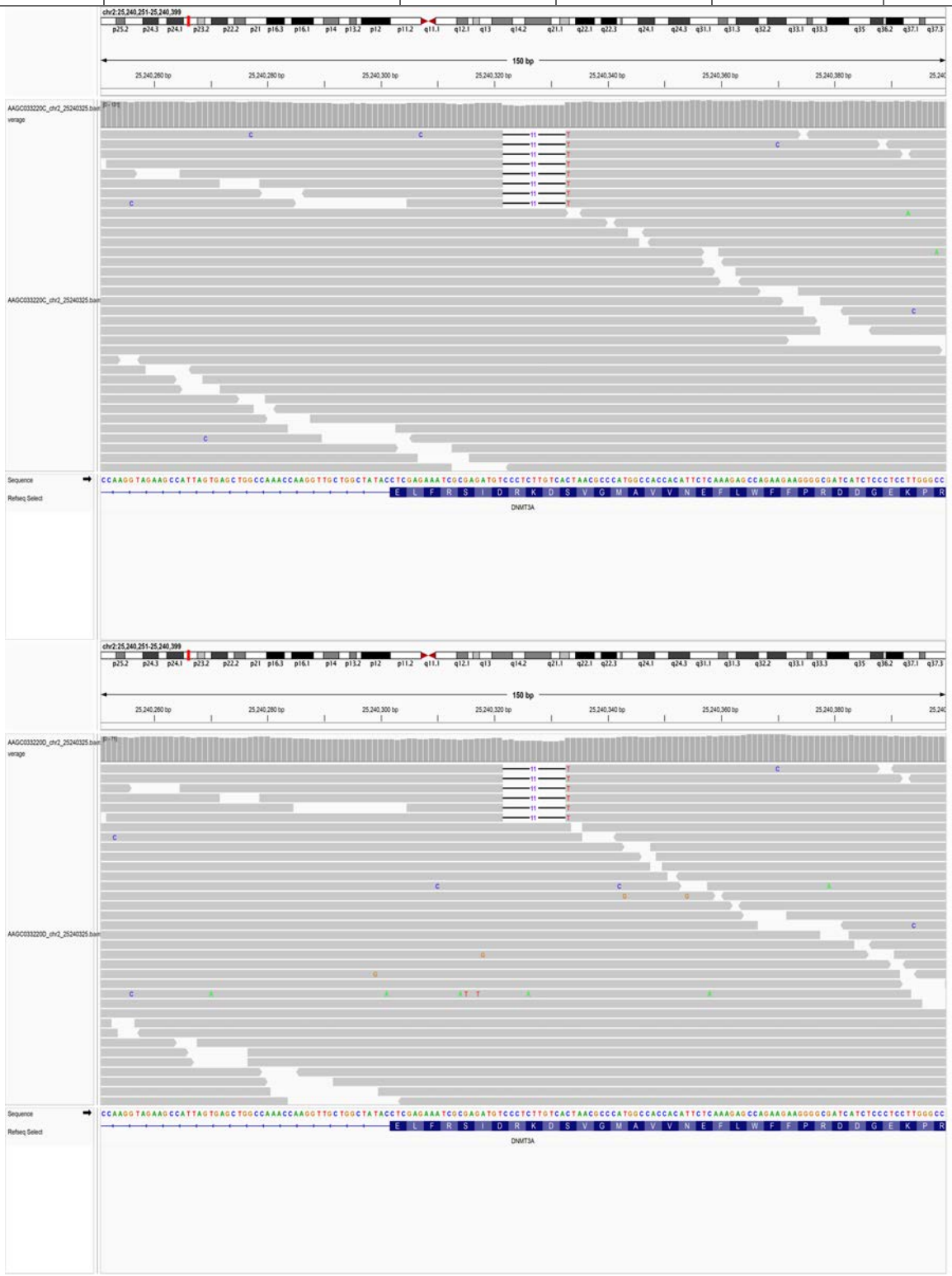
12.34. chr2_25240315_G/A

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



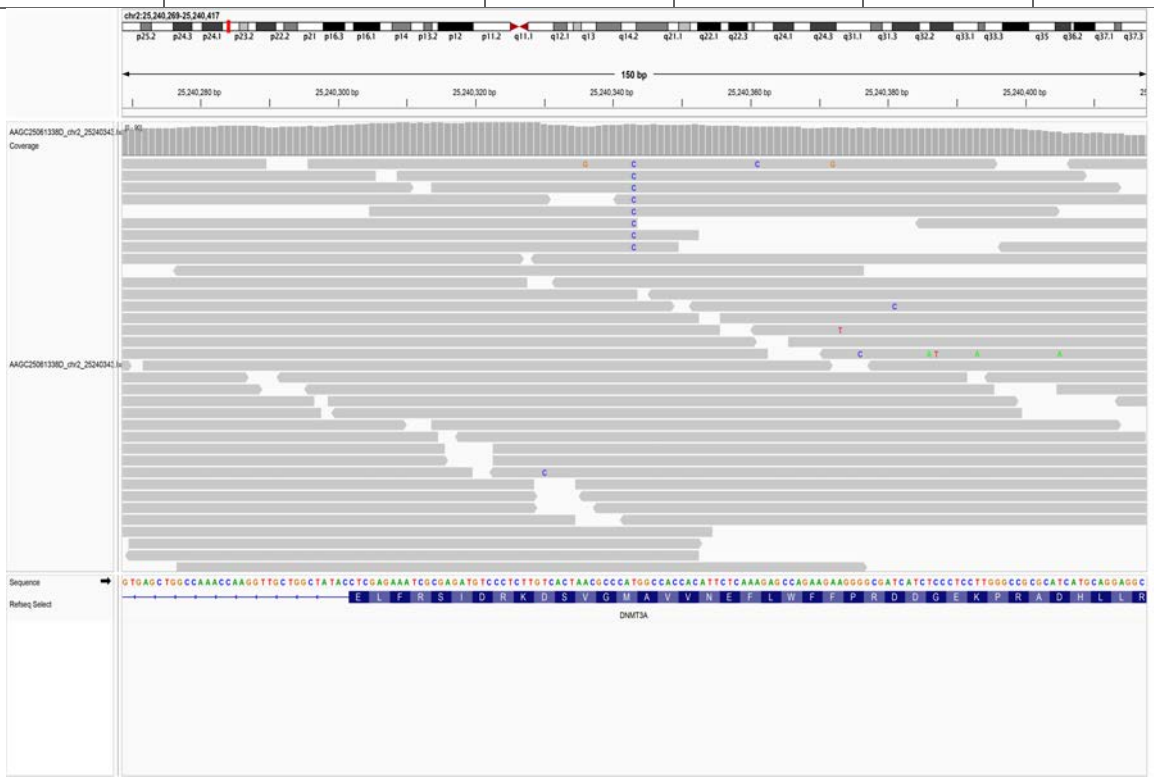
12.35. chr2_25240326_CTTGTCAC/-

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



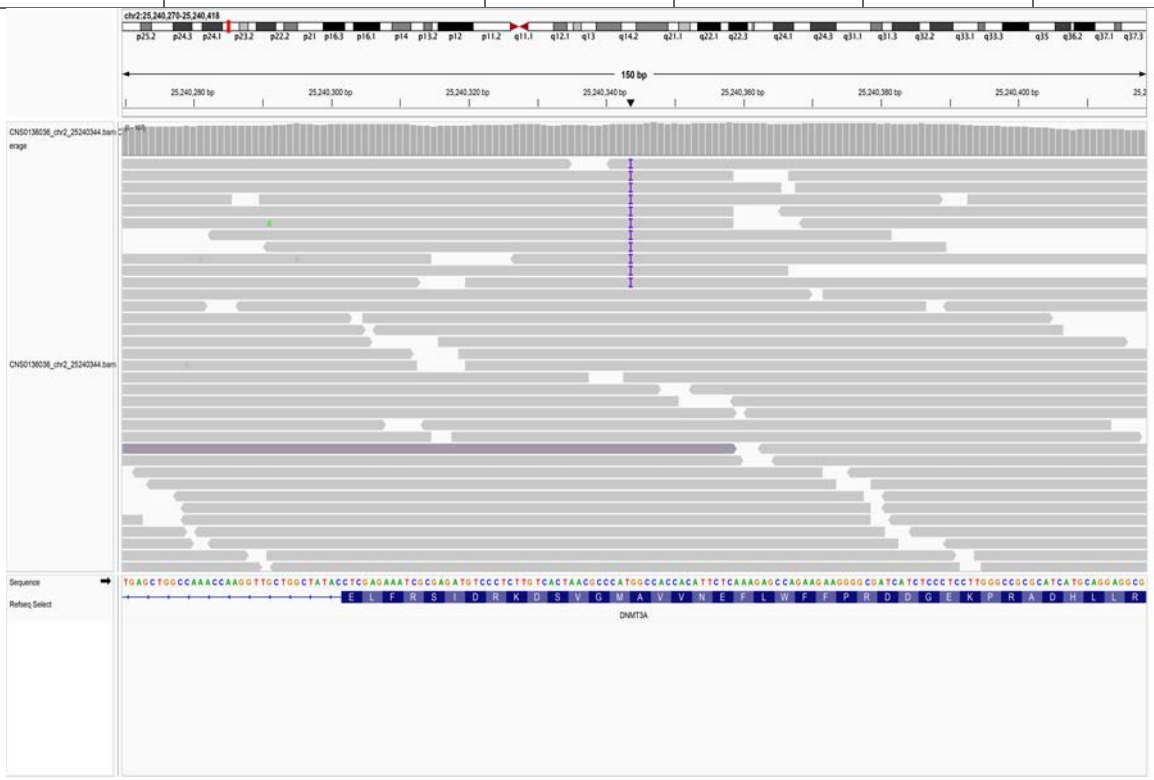
12.36. chr2_25240343_T/C

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



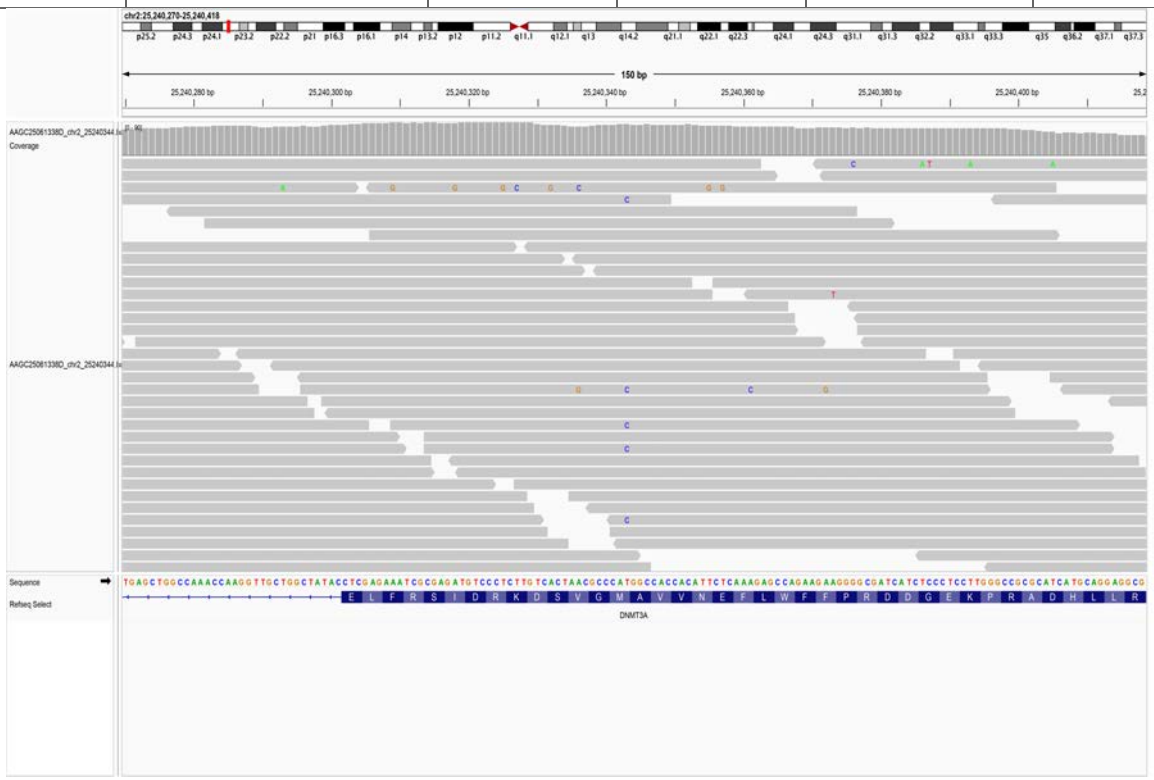
12.37. chr2_25240344_-/G

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



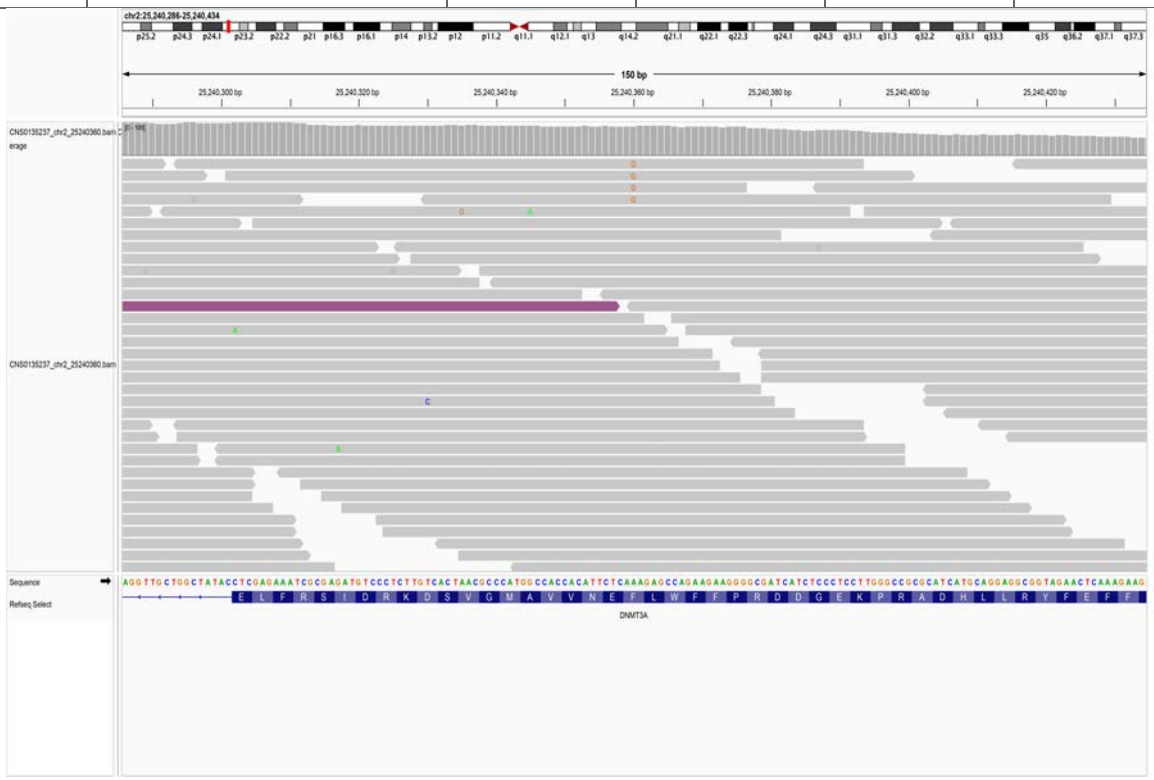
12.38. chr2_25240344_T/C

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



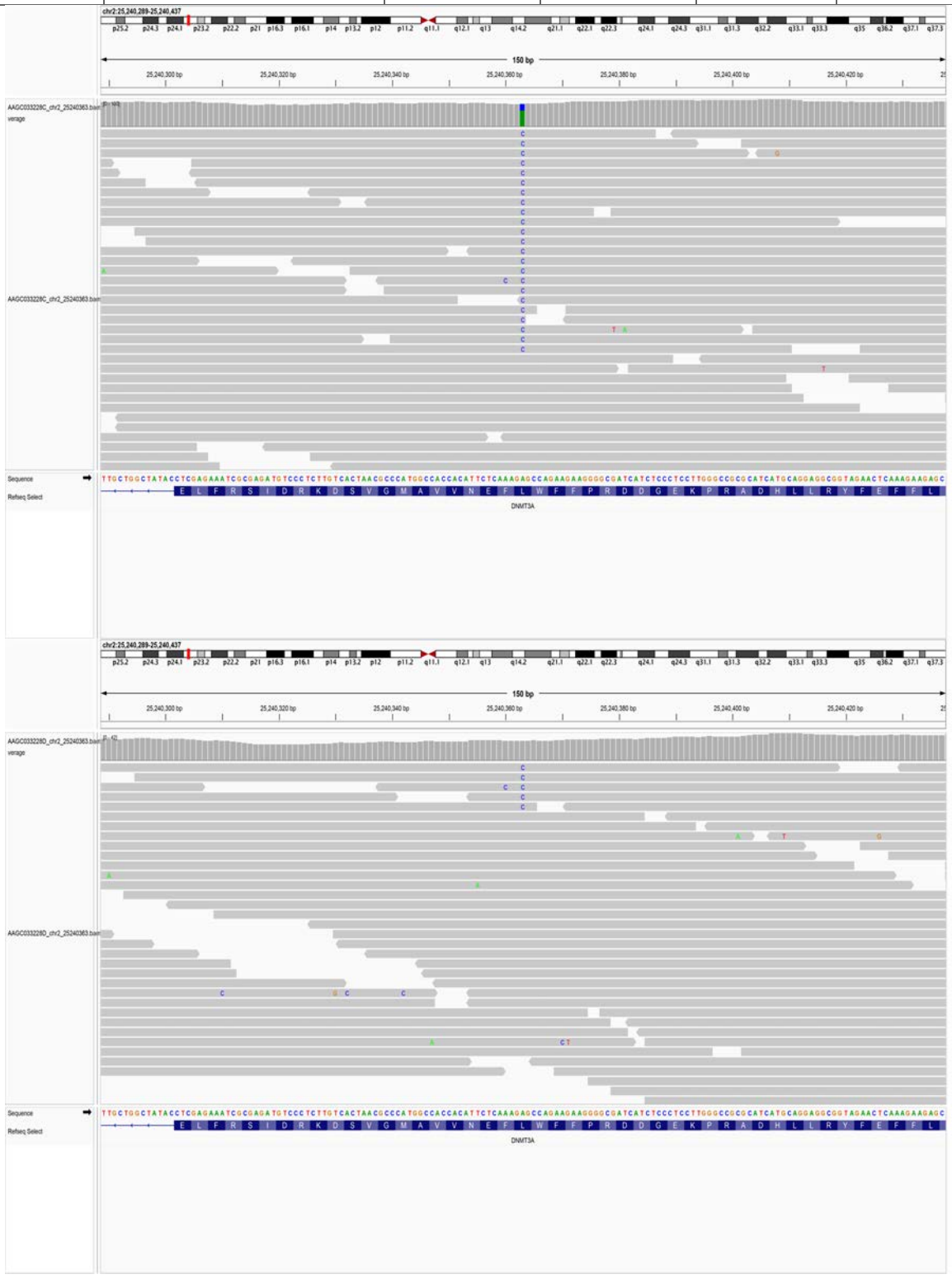
12.39. chr2_25240360_A/G

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



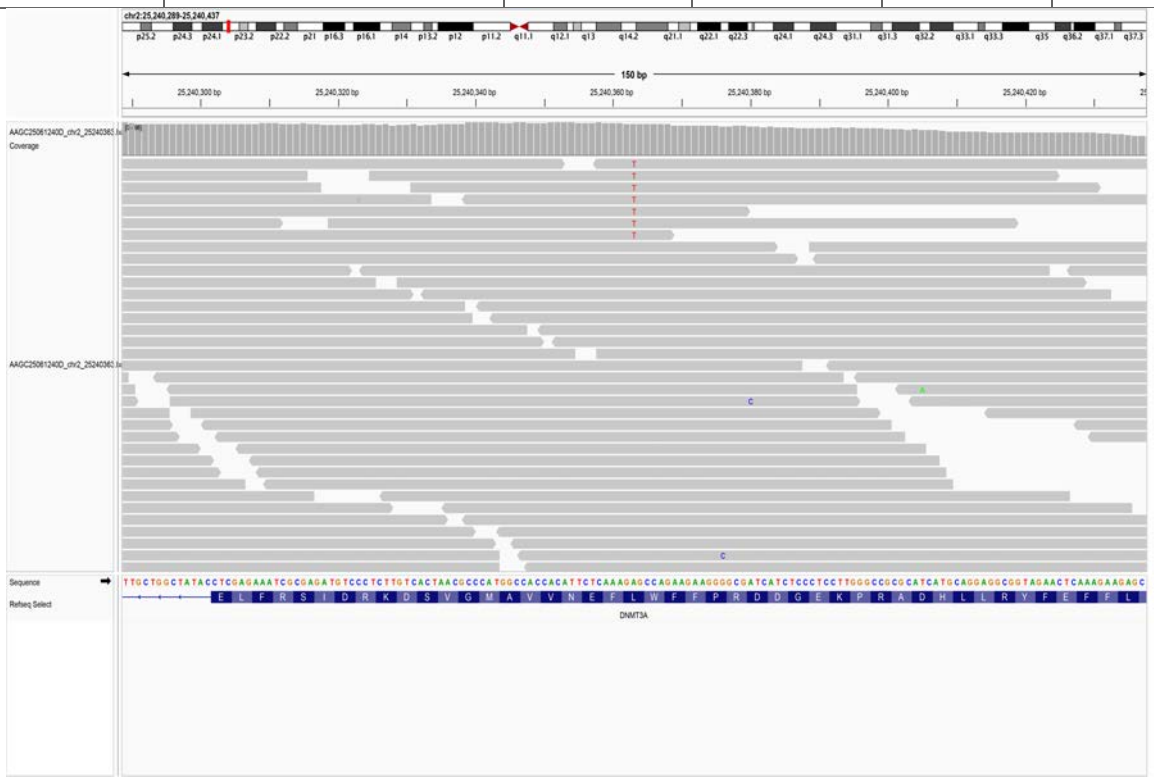
12.40. chr2_25240363_A/C

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



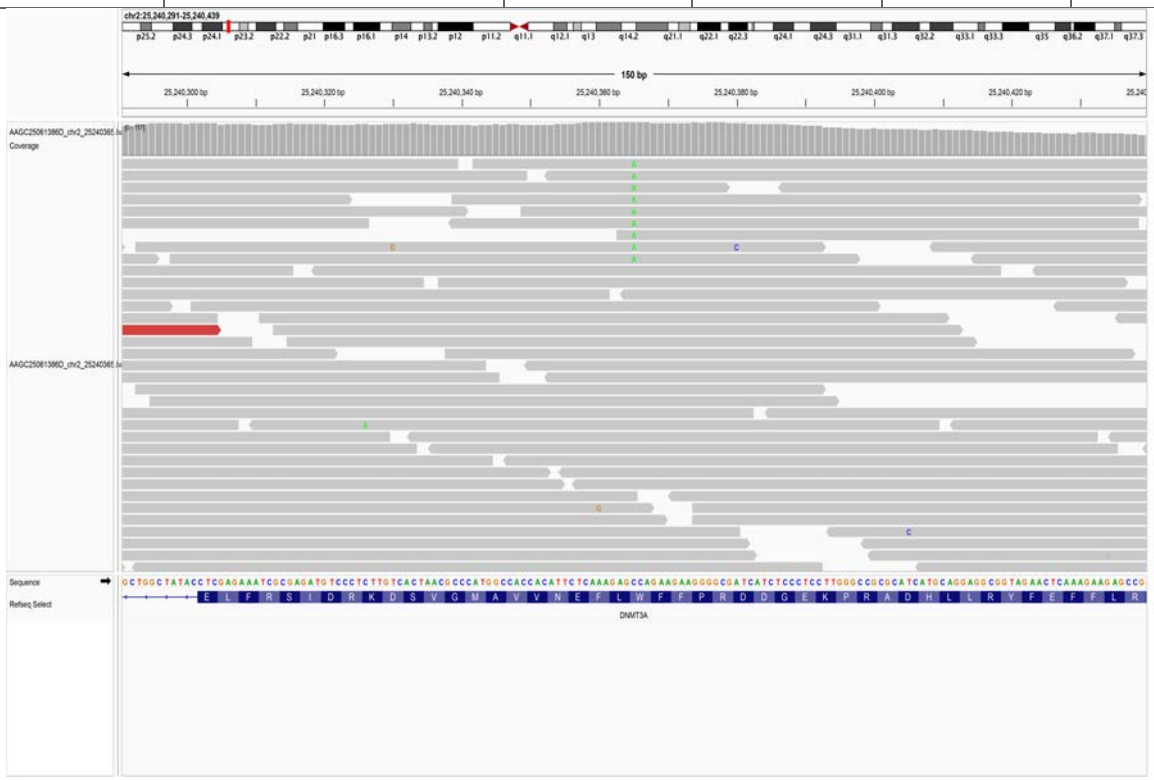
12.41. chr2_25240363_A/T

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



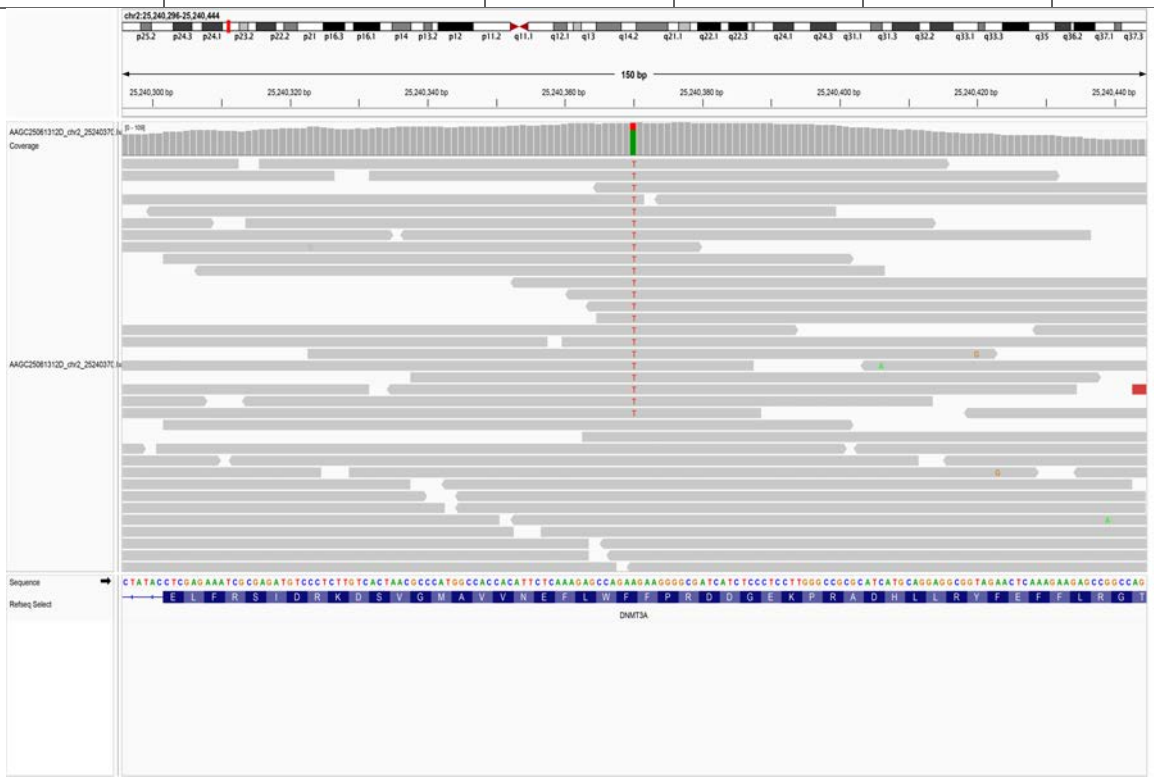
12.42. chr2_25240365_C/A

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



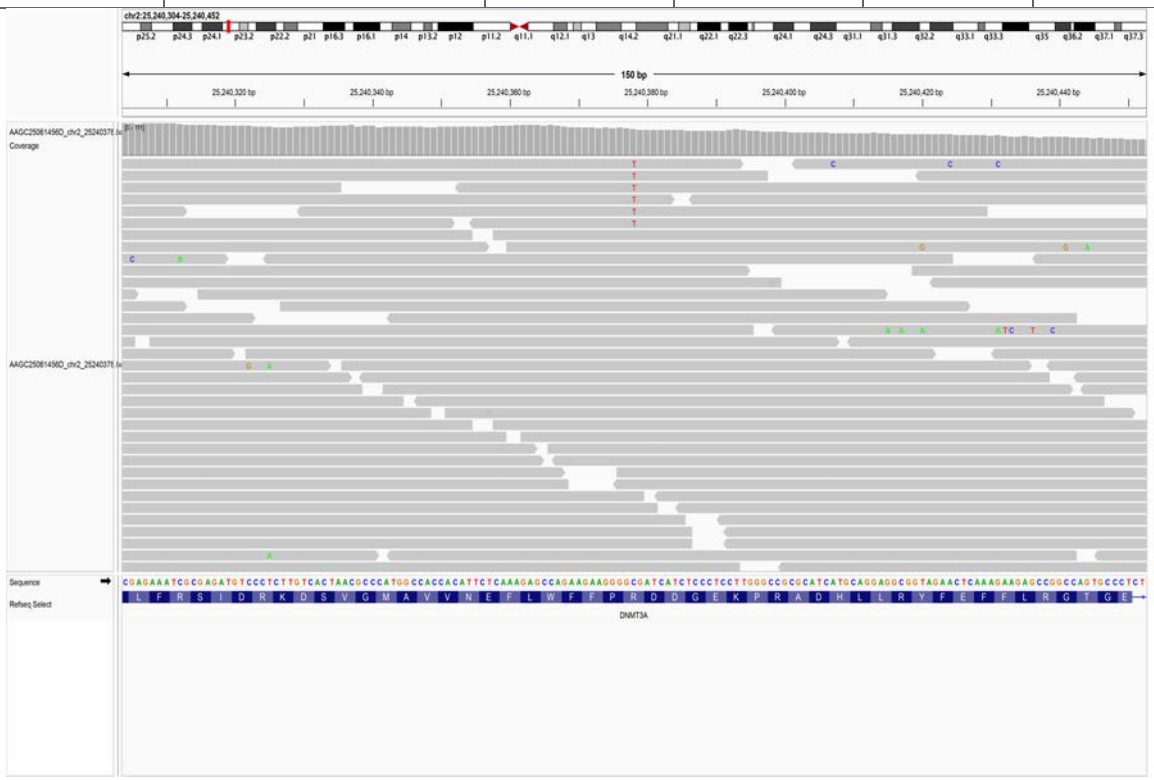
12.43. chr2_25240370_A/T

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



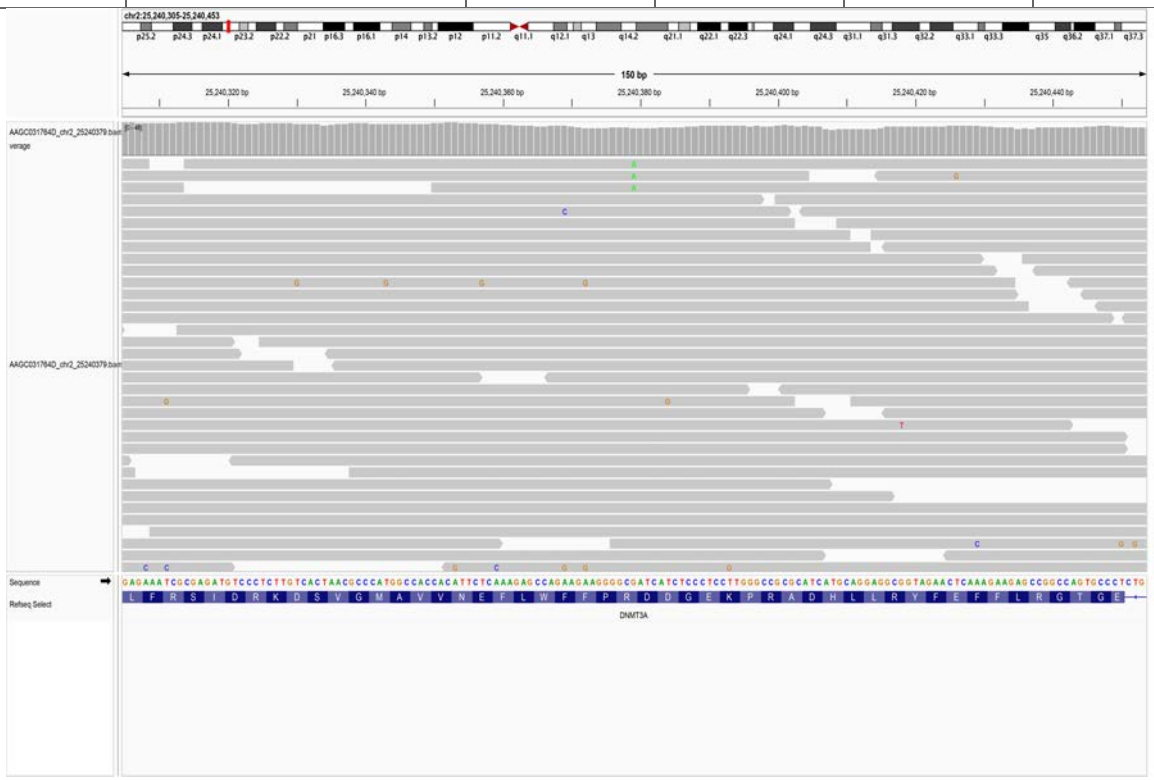
12.44. chr2_25240378_C/T

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



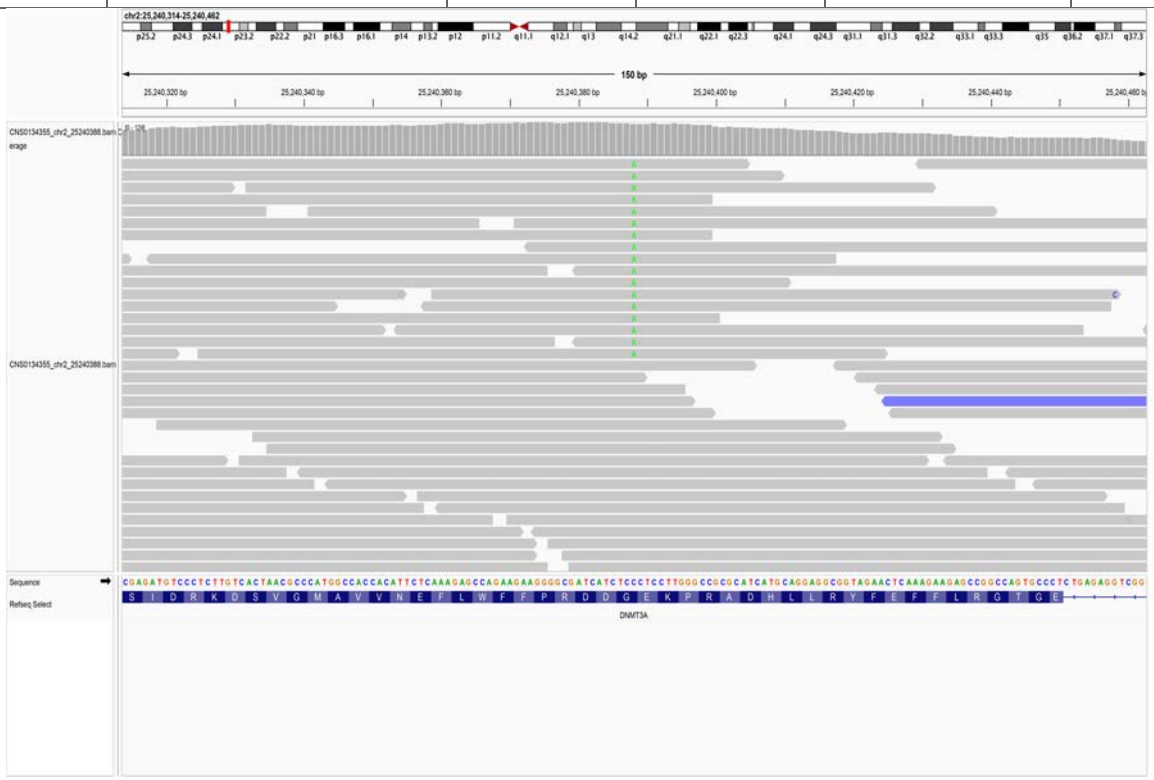
12.45. chr2_25240379_G/A

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



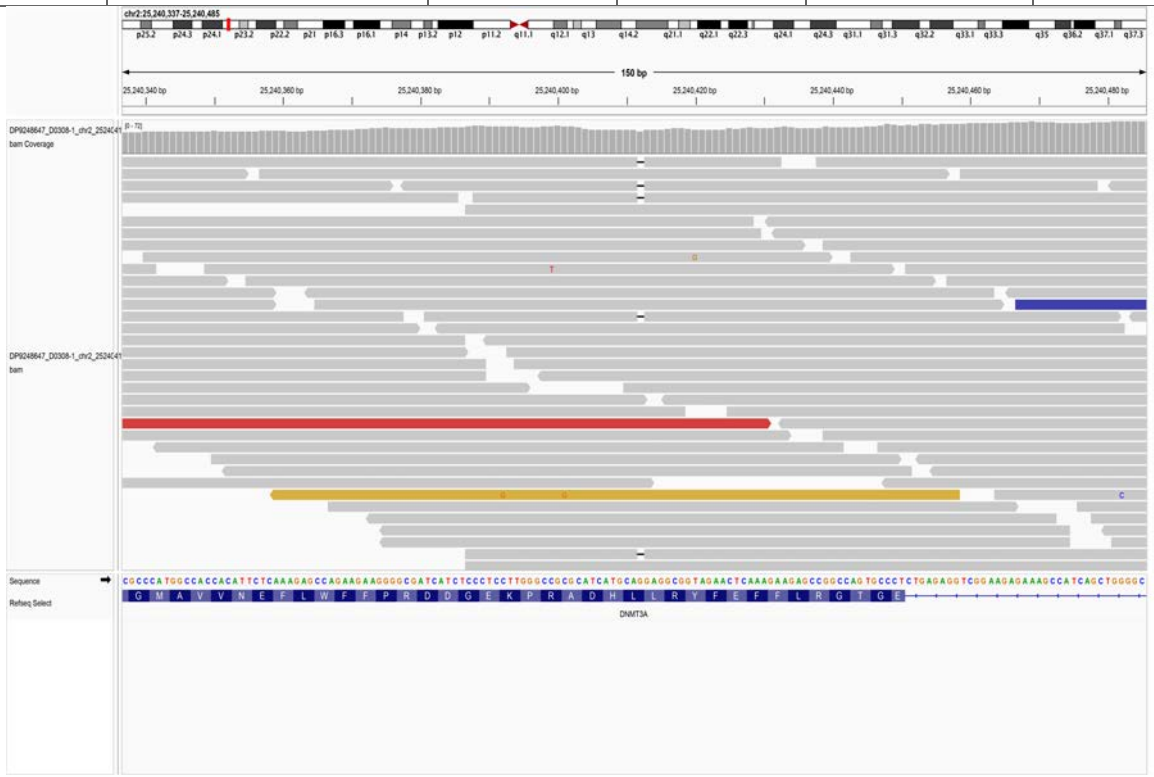
12.46. chr2_25240388_C/A

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



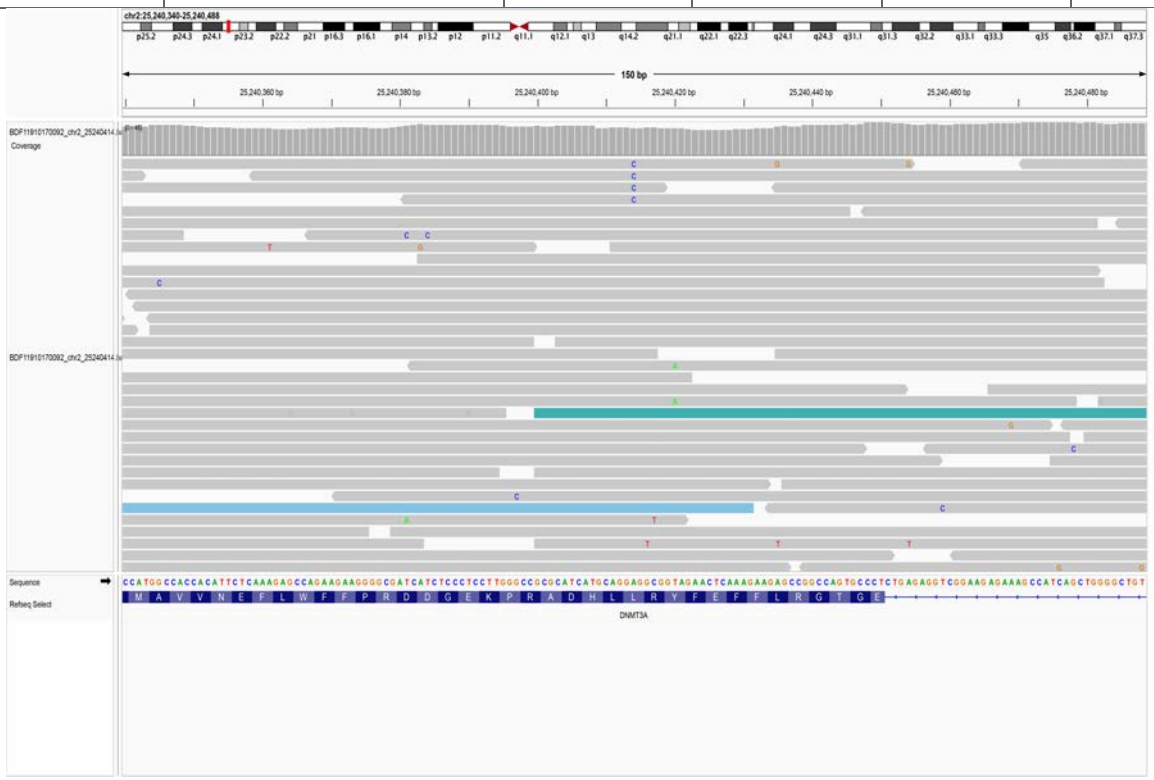
12.47. chr2_25240412_G/-

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



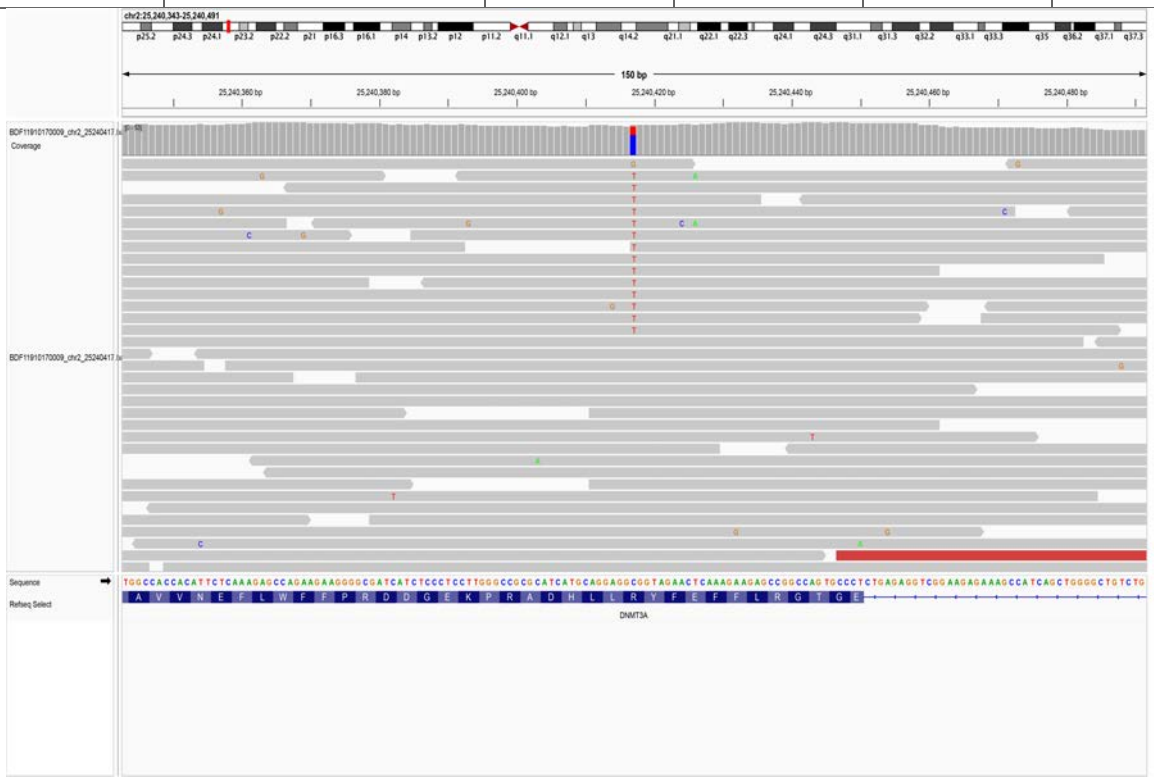
12.48. chr2_25240414_A/C

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



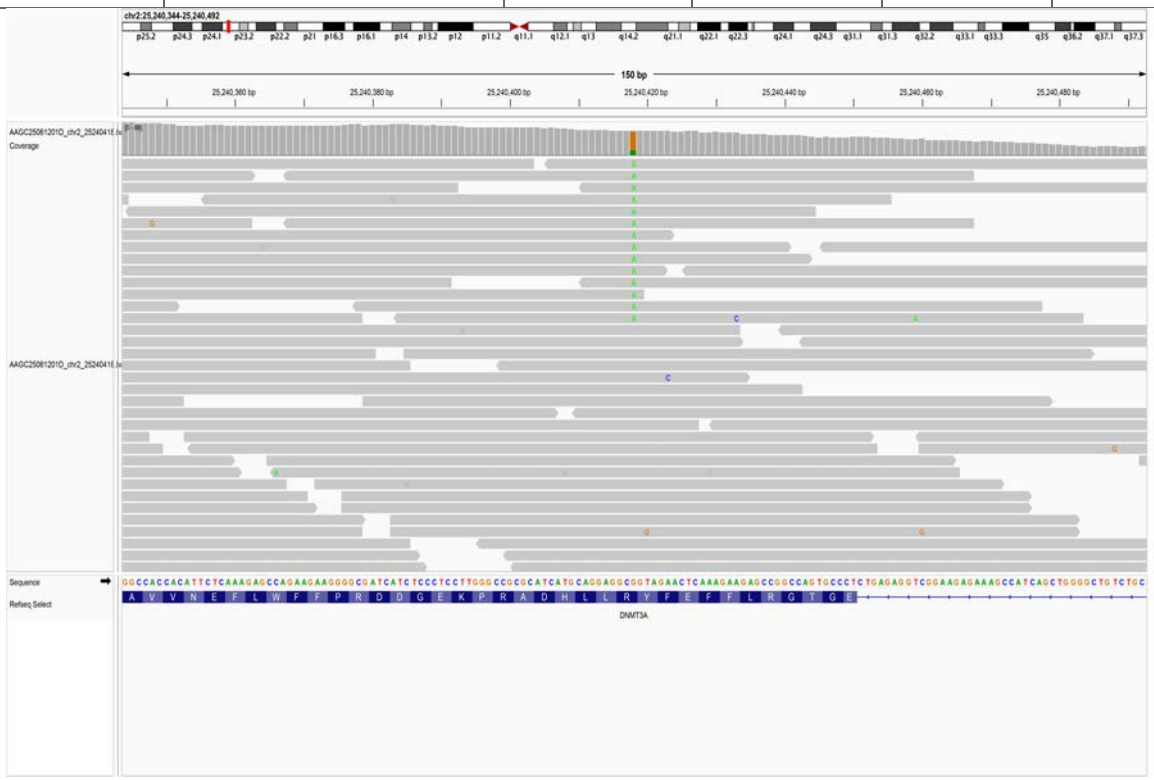
12.49. chr2_25240417_C/T

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



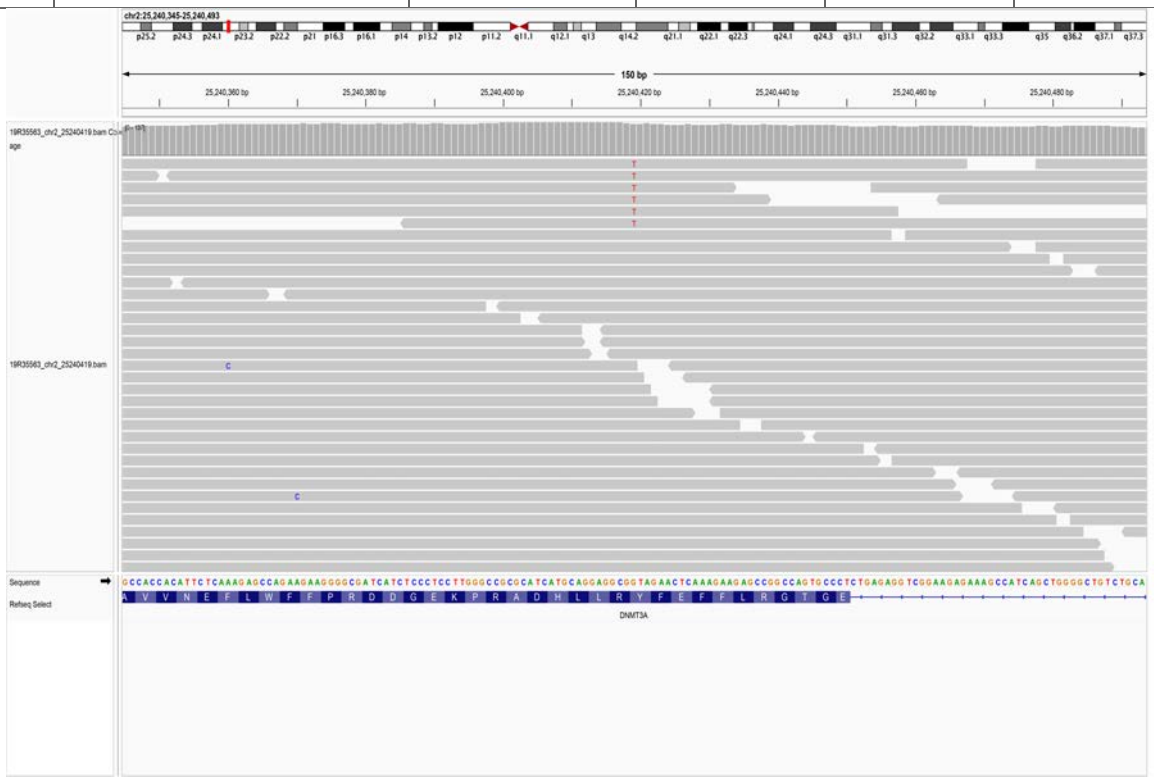
12.50. chr2_25240418_G/A

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



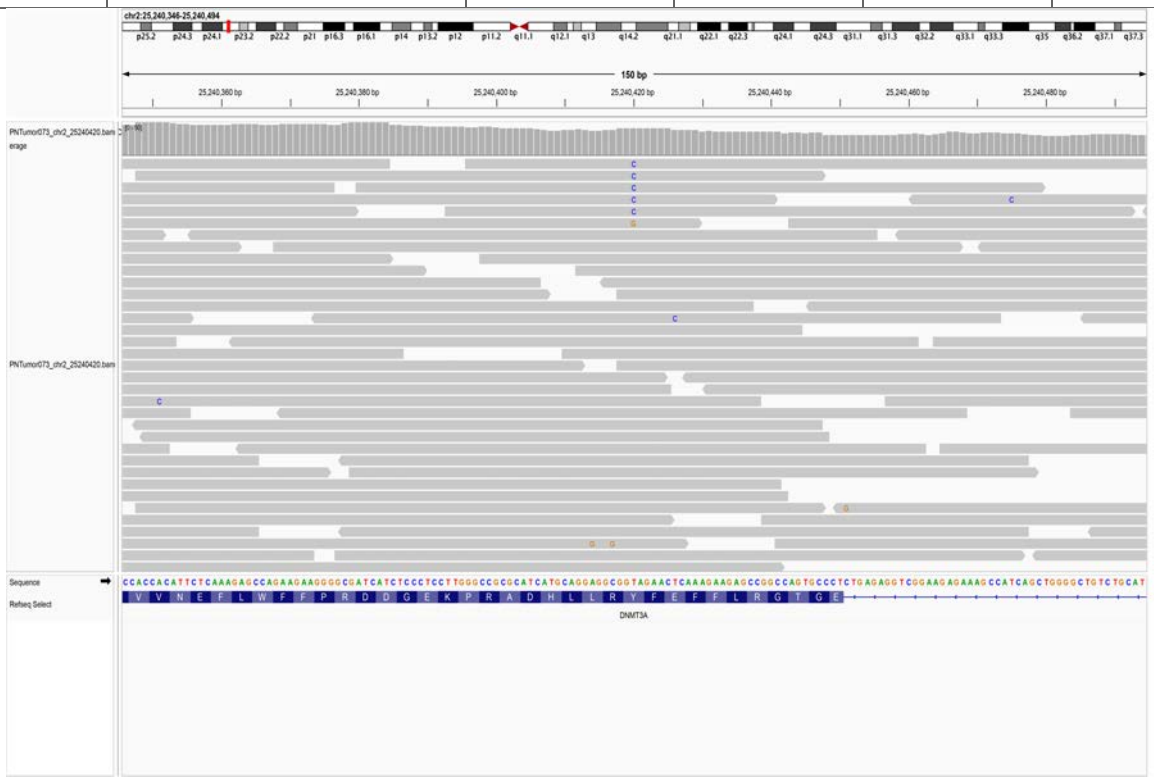
12.51. chr2_25240419_G/T

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



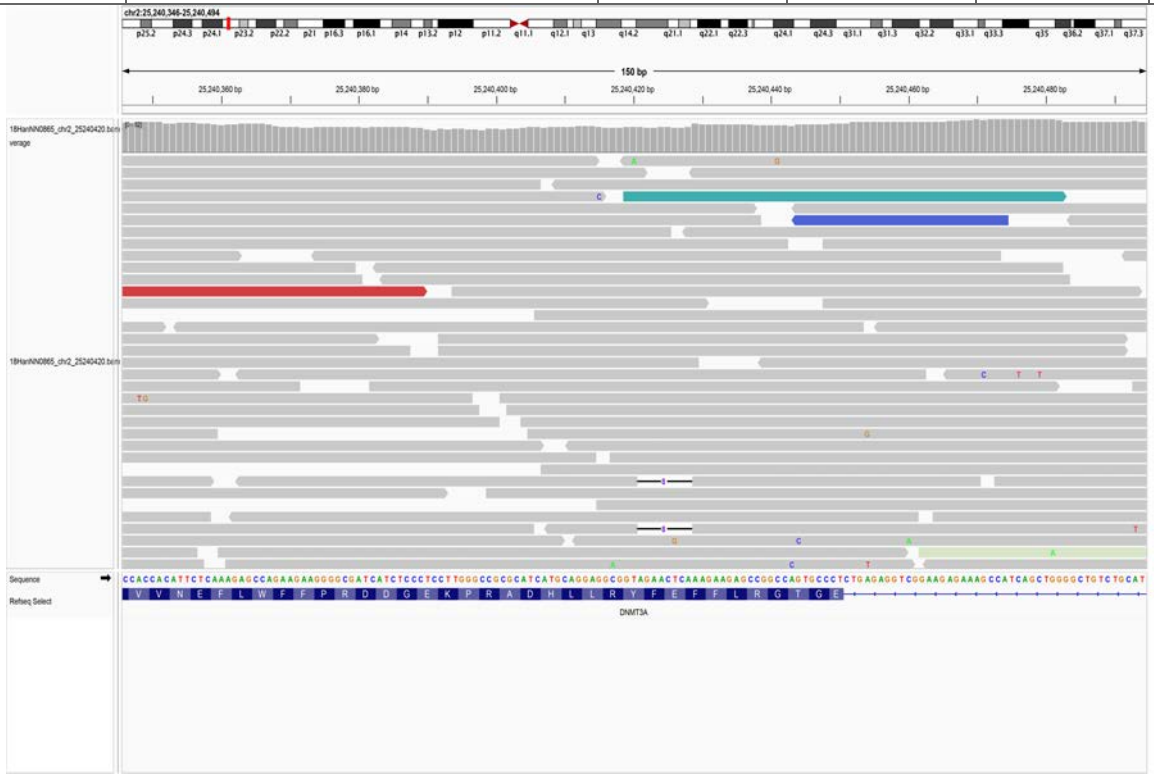
12.52. chr2_25240420_T/C

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



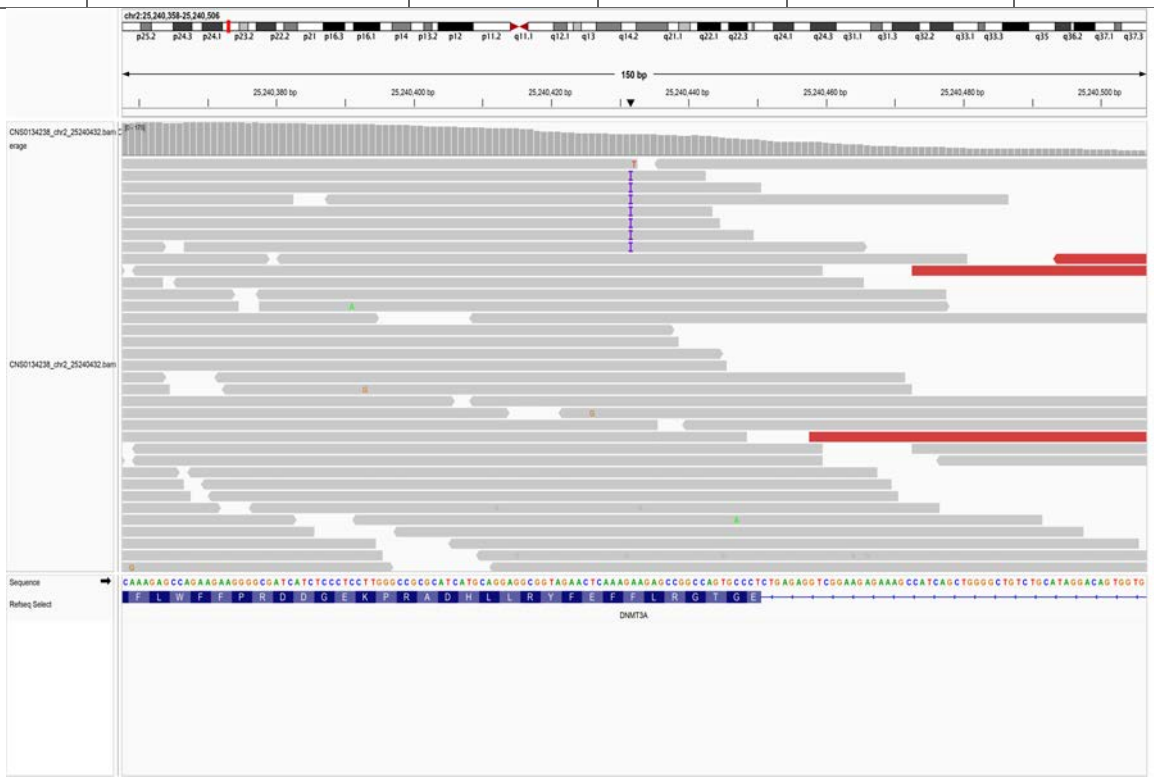
12.53. chr2_25240421_AGAACTCA/-

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



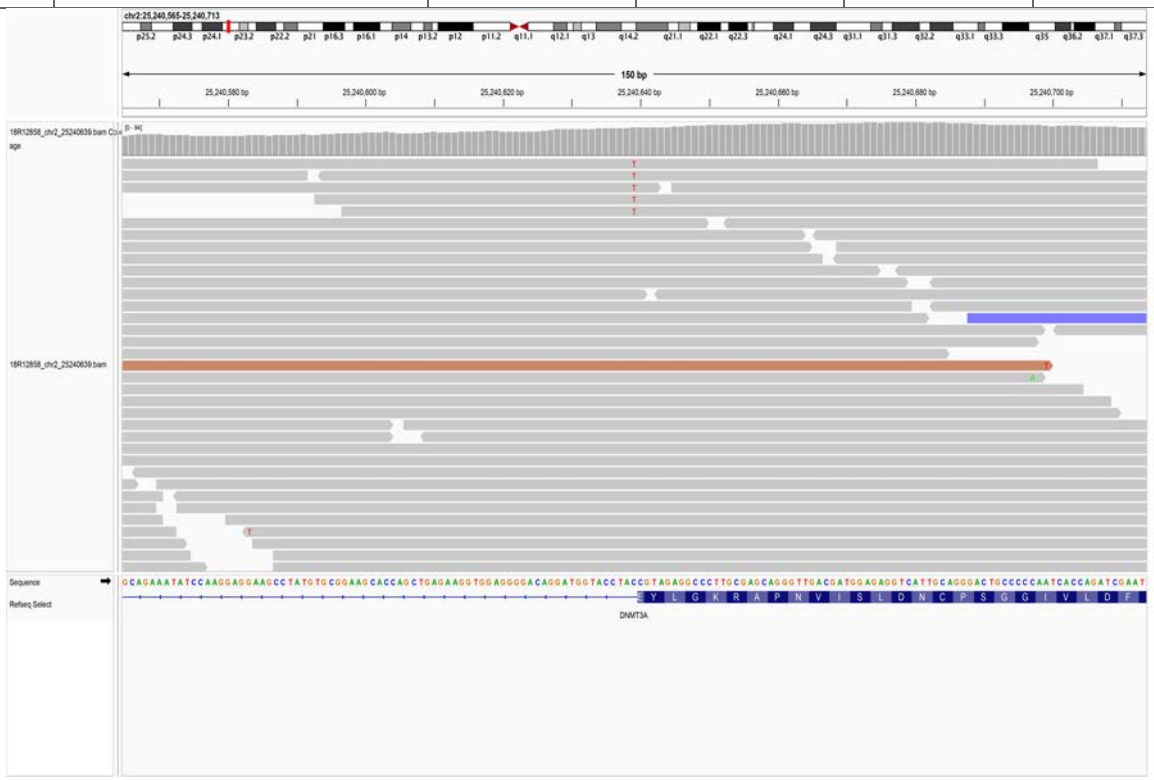
12.54. chr2_25240432_-/T

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



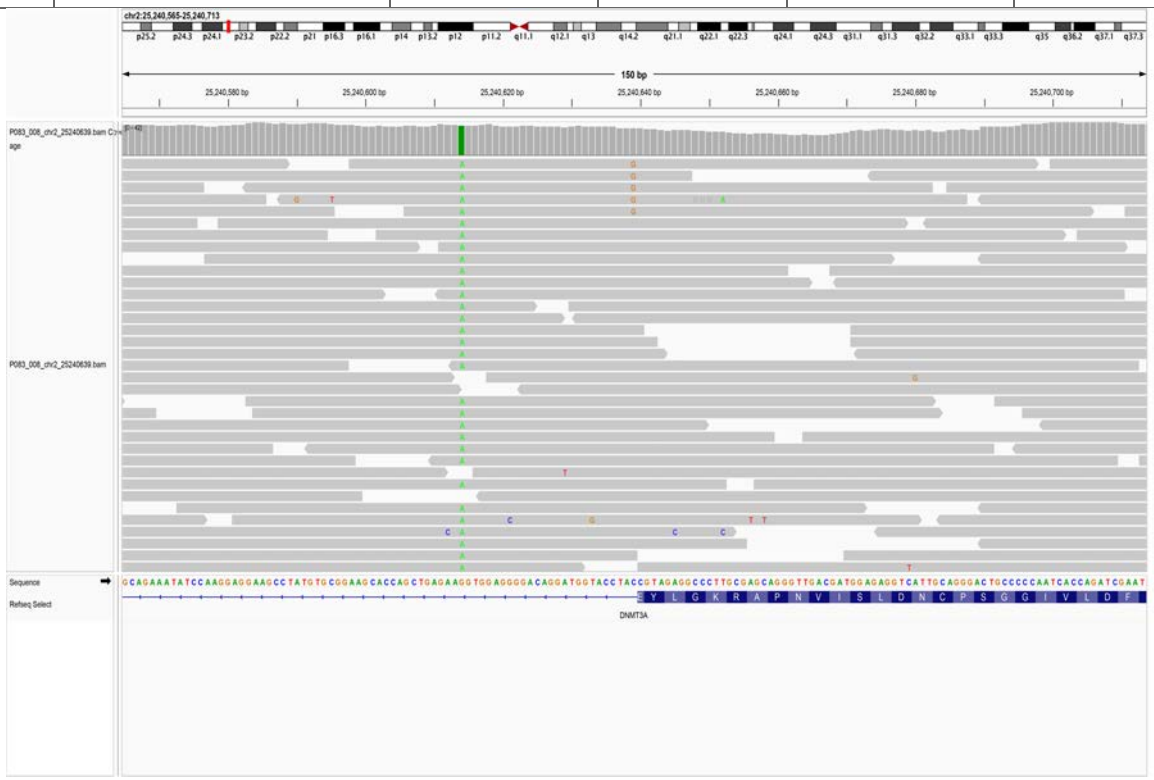
12.55. chr2_25240639_C/T

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



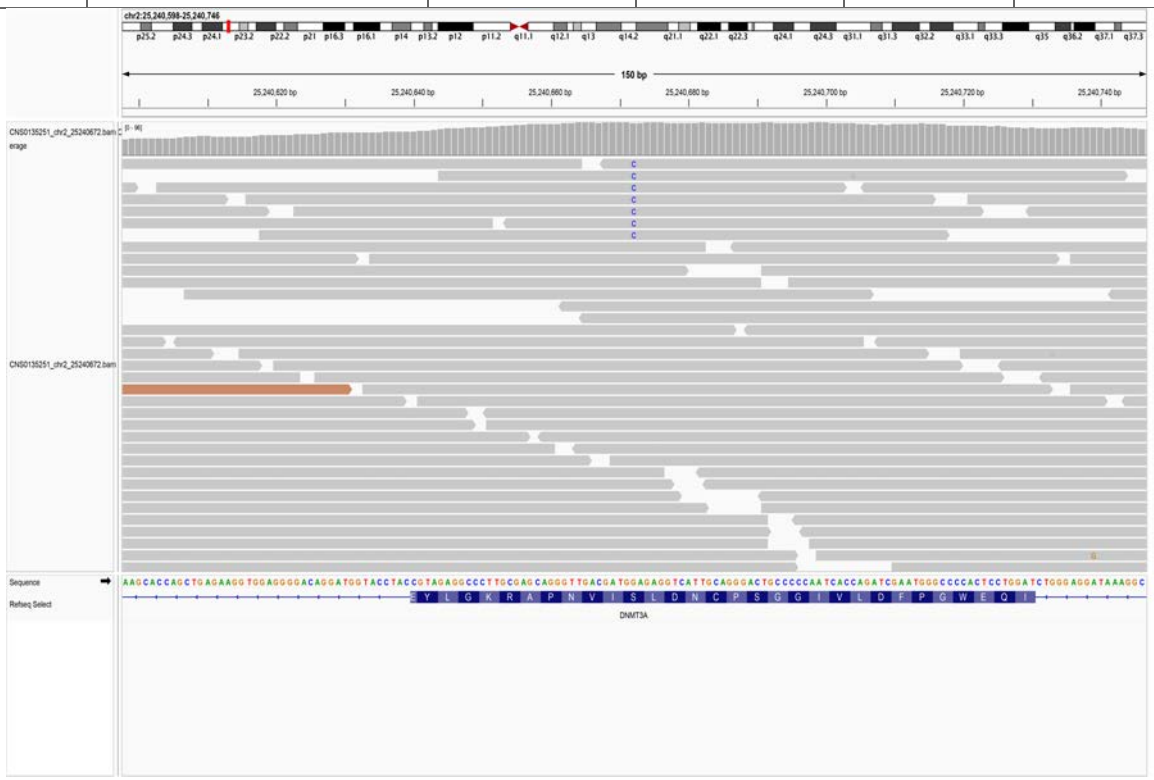
12.56. chr2_25240639_C/G

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



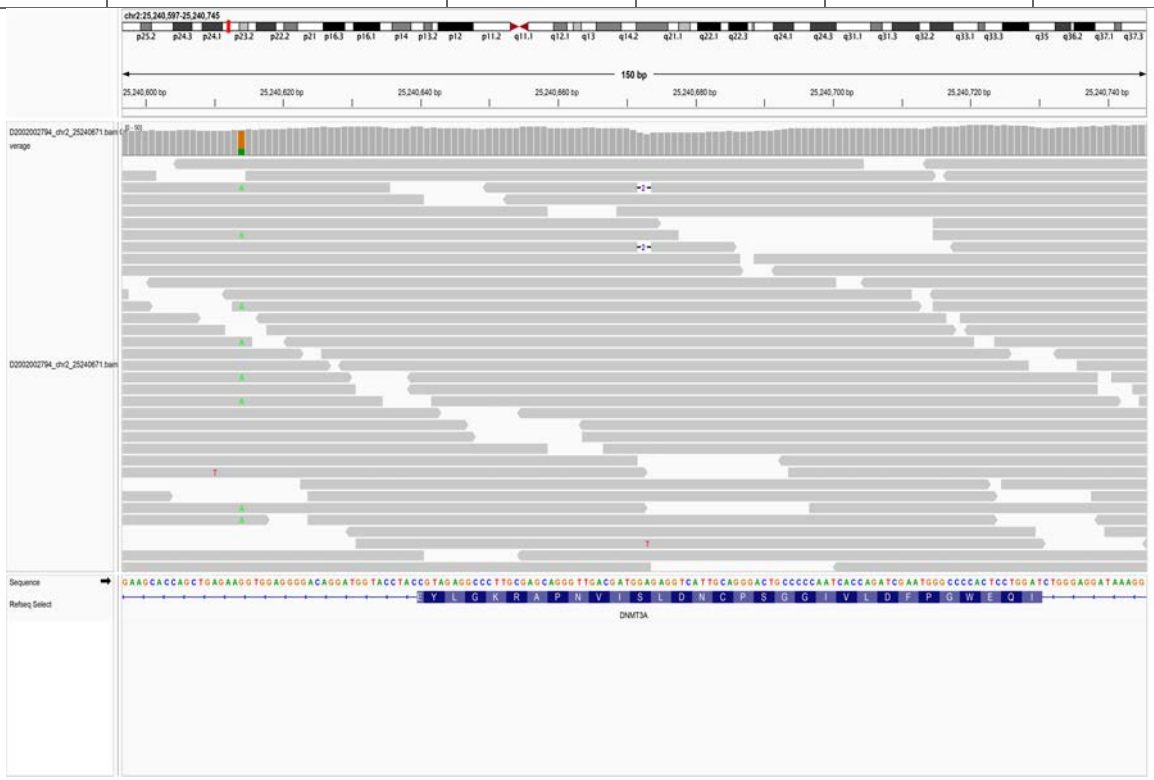
12.57. chr2_25240672_G/C

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



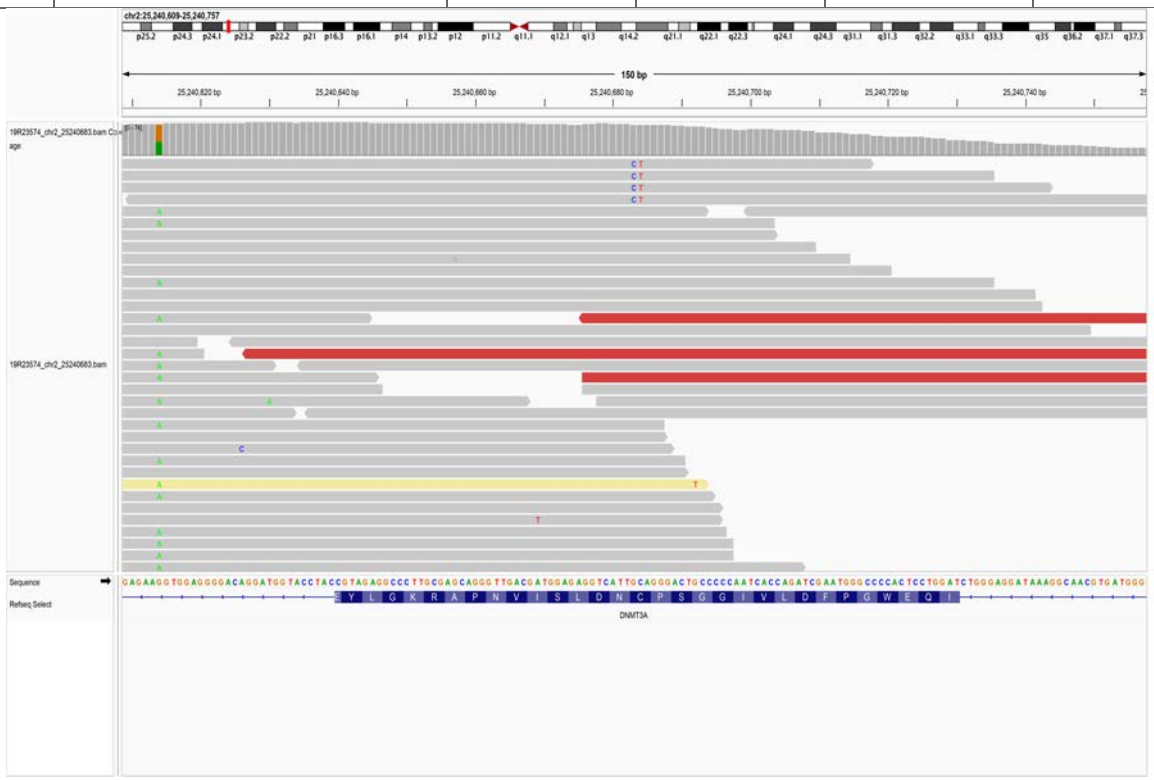
12.58. chr2_25240672_GA/-

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



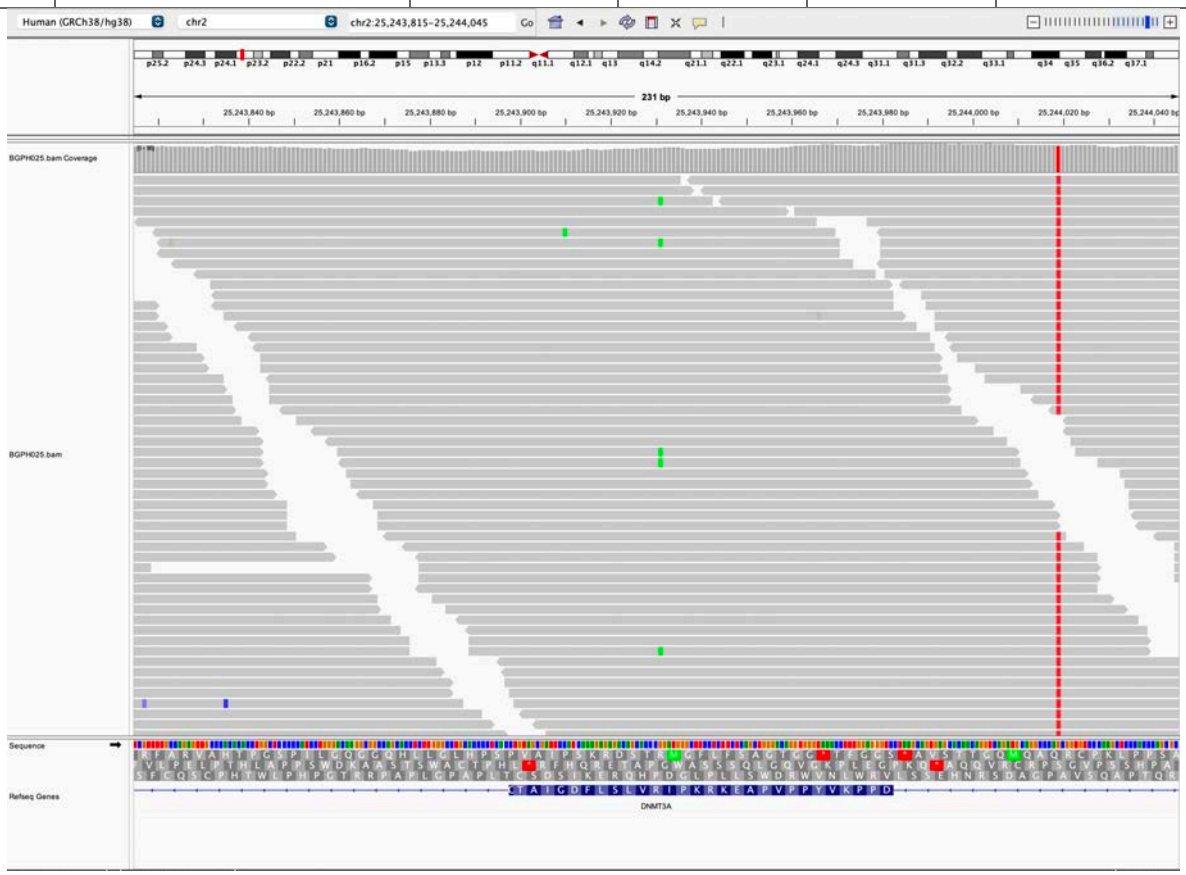
12.59. chr2_25240683_GC/CT

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



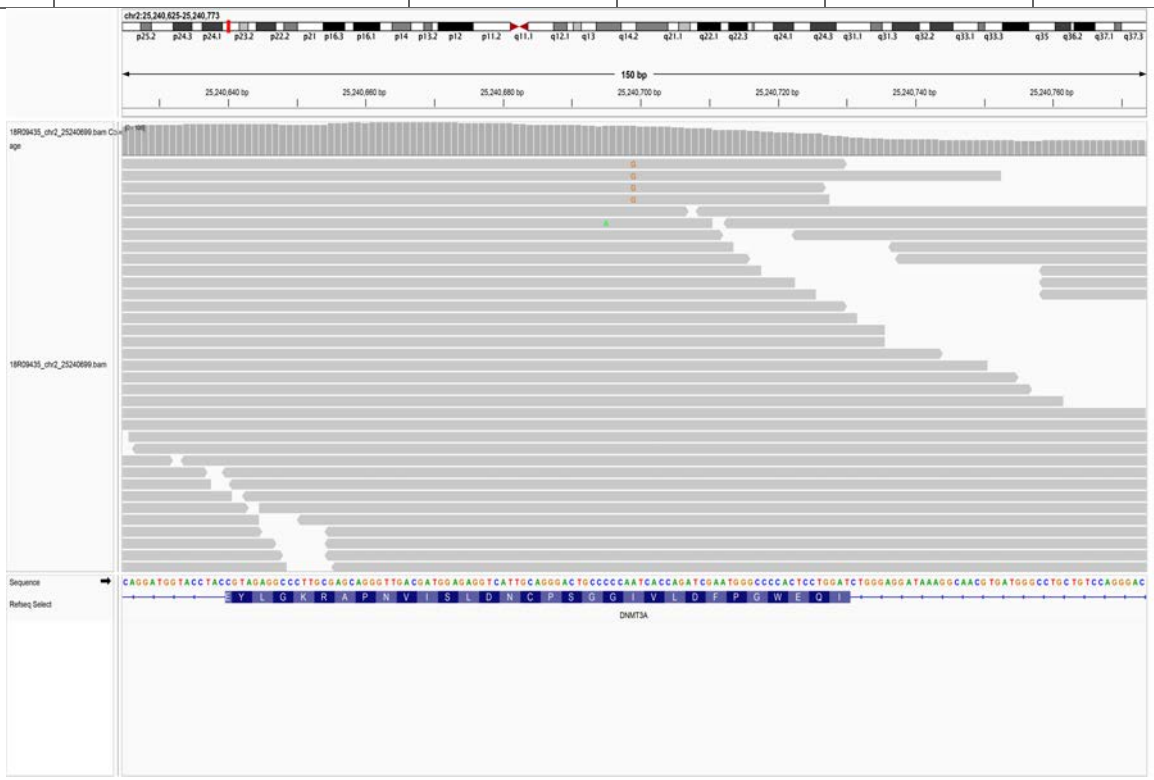
12.60. chr2_25240684_C/G

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



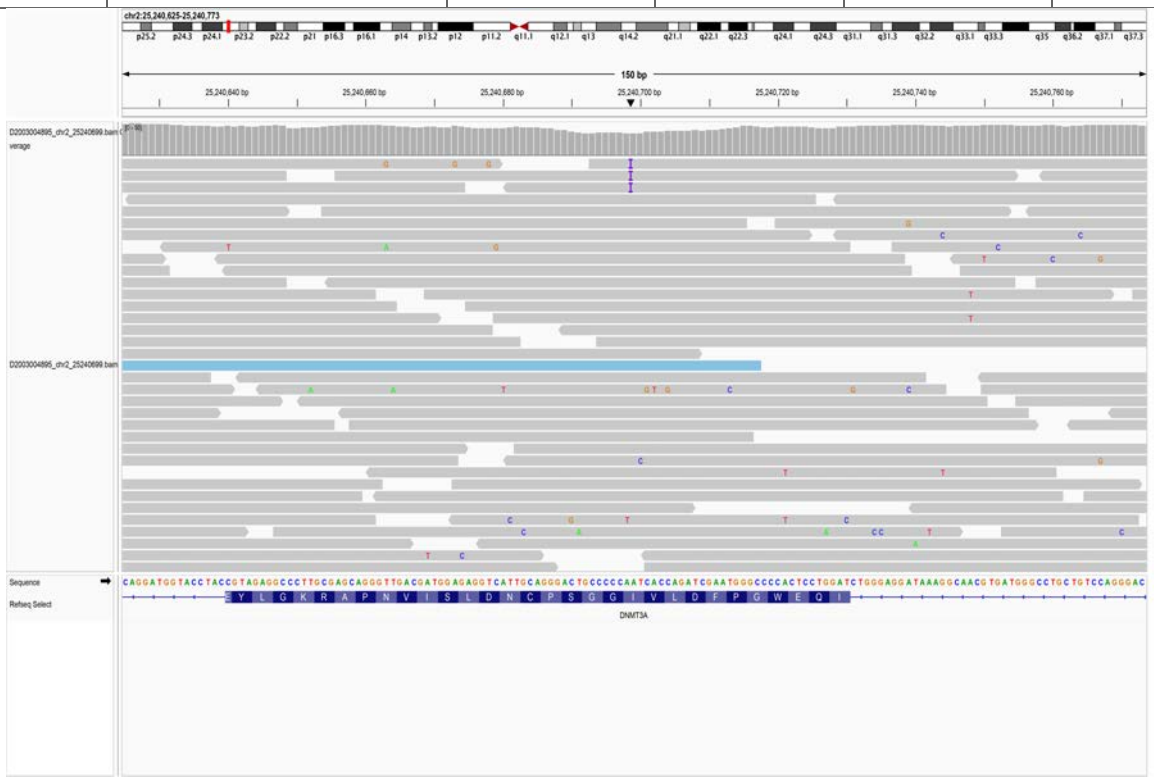
12.61. chr2_25240699_A/G

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



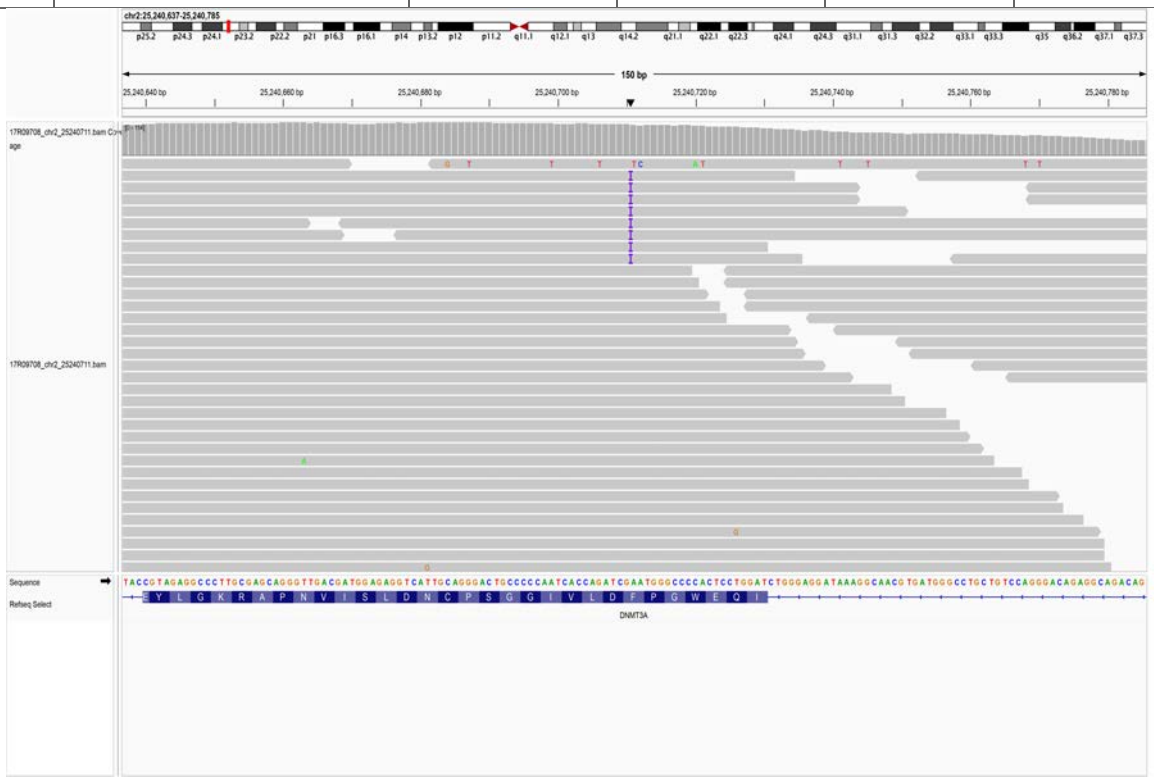
12.62. chr2_25240699_-/C

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



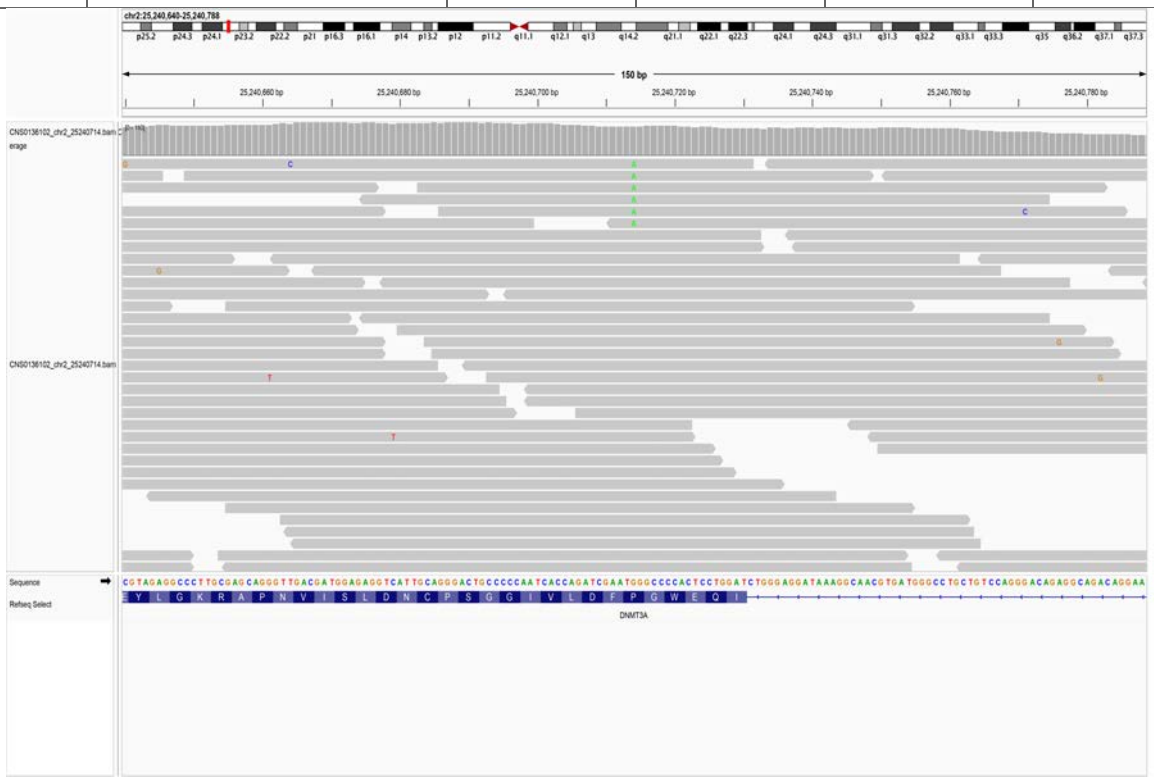
12.63. chr2_25240711_-/A

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



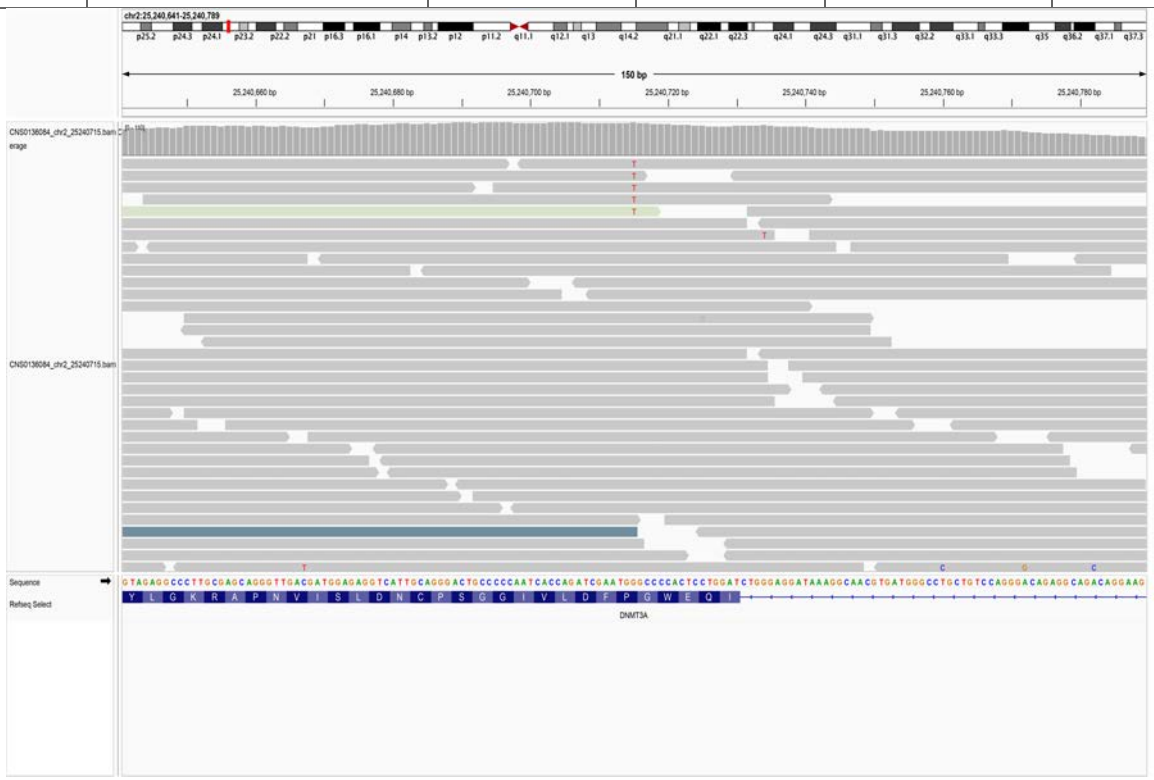
12.64. chr2_25240714_G/A

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



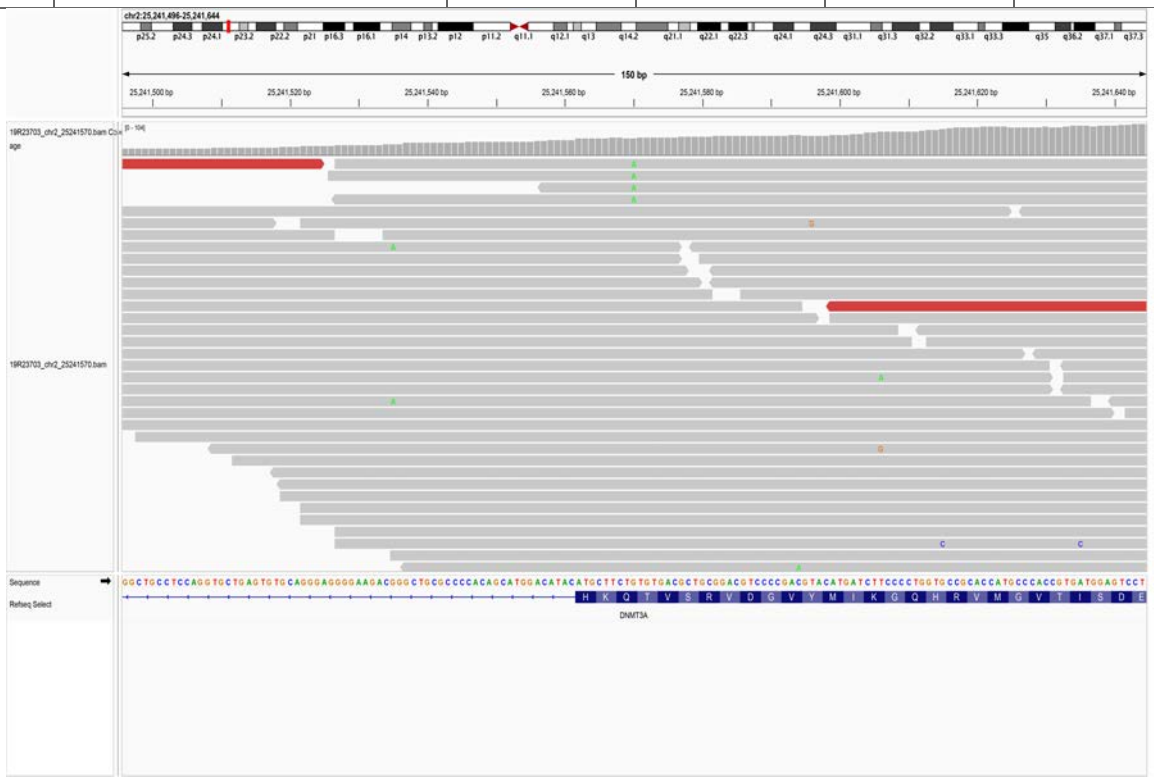
12.65. chr2_25240715_G/T

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



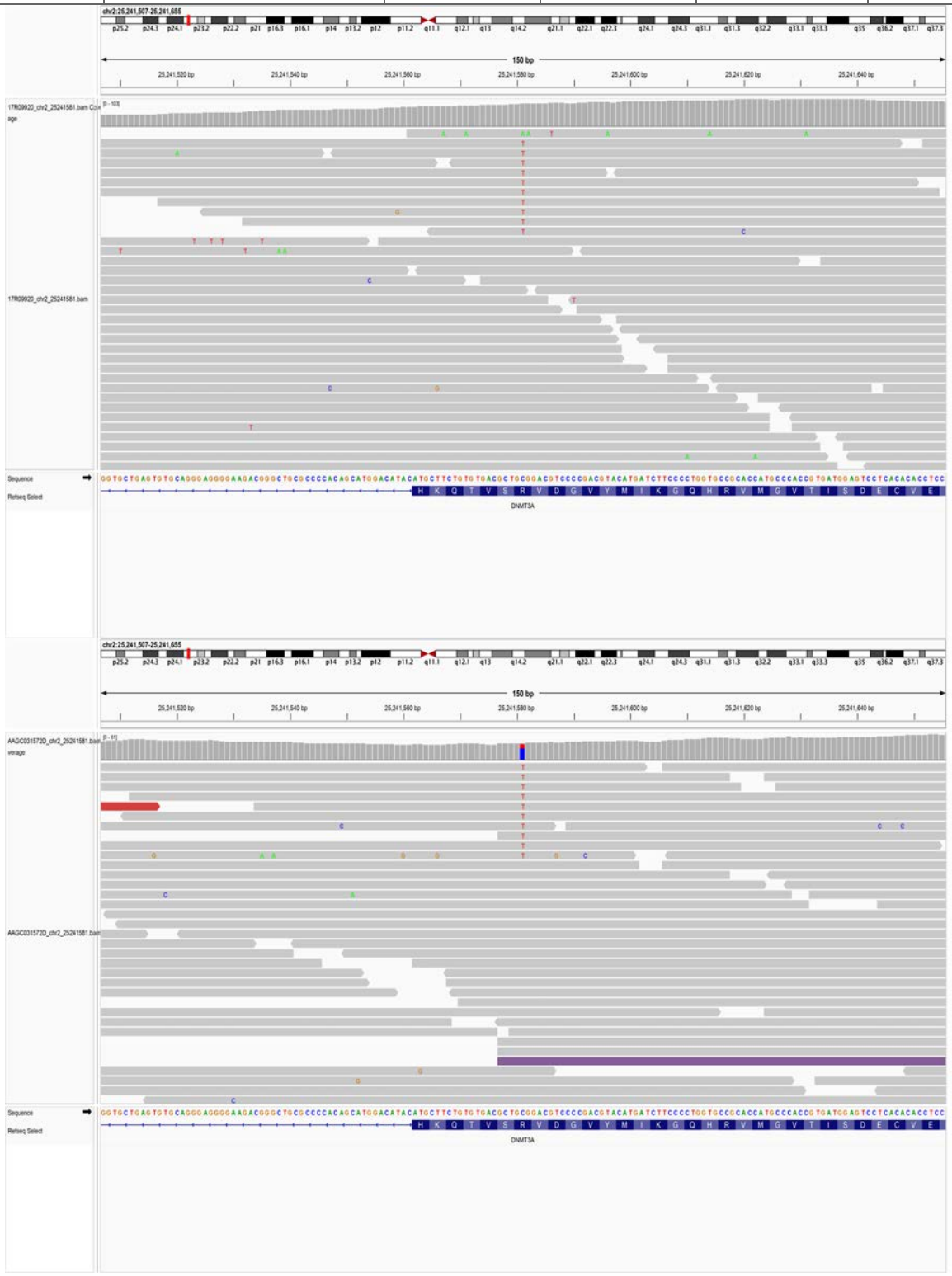
12.66. chr2_25241570_G/A

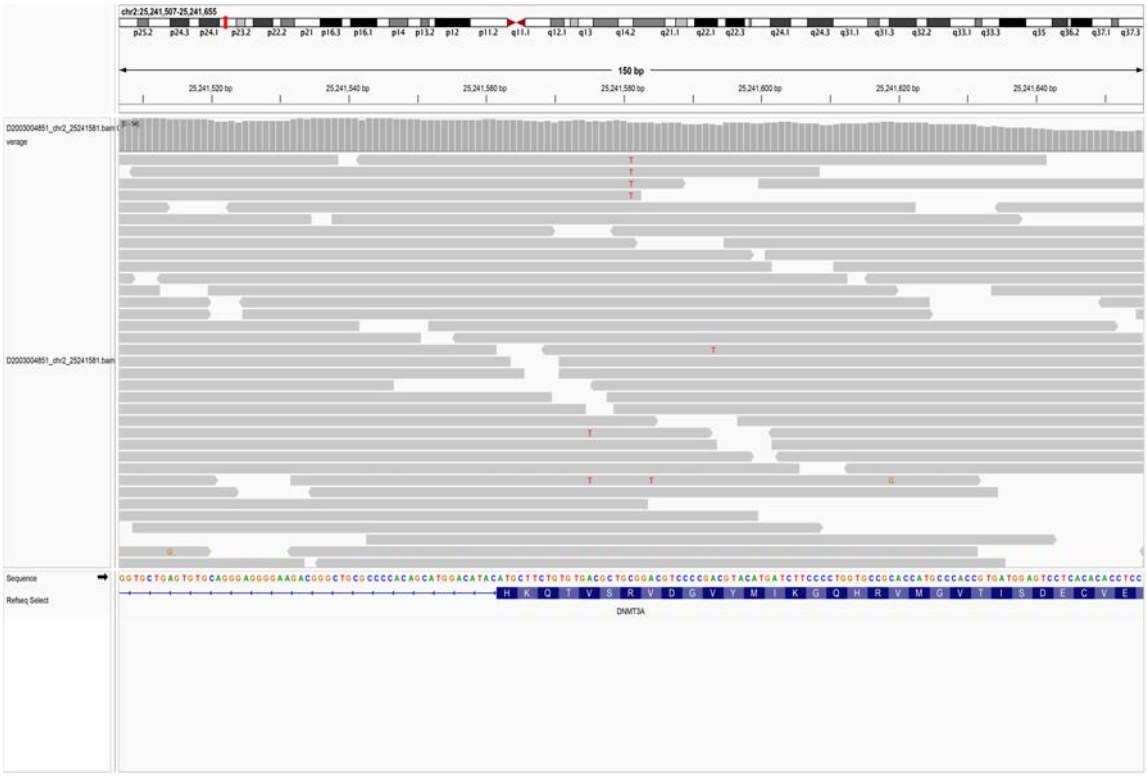
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23703	chr2_25241570_G/A	50	4	*DNMT3A*	stop_gained



12.67. chr2_25241581_C/T

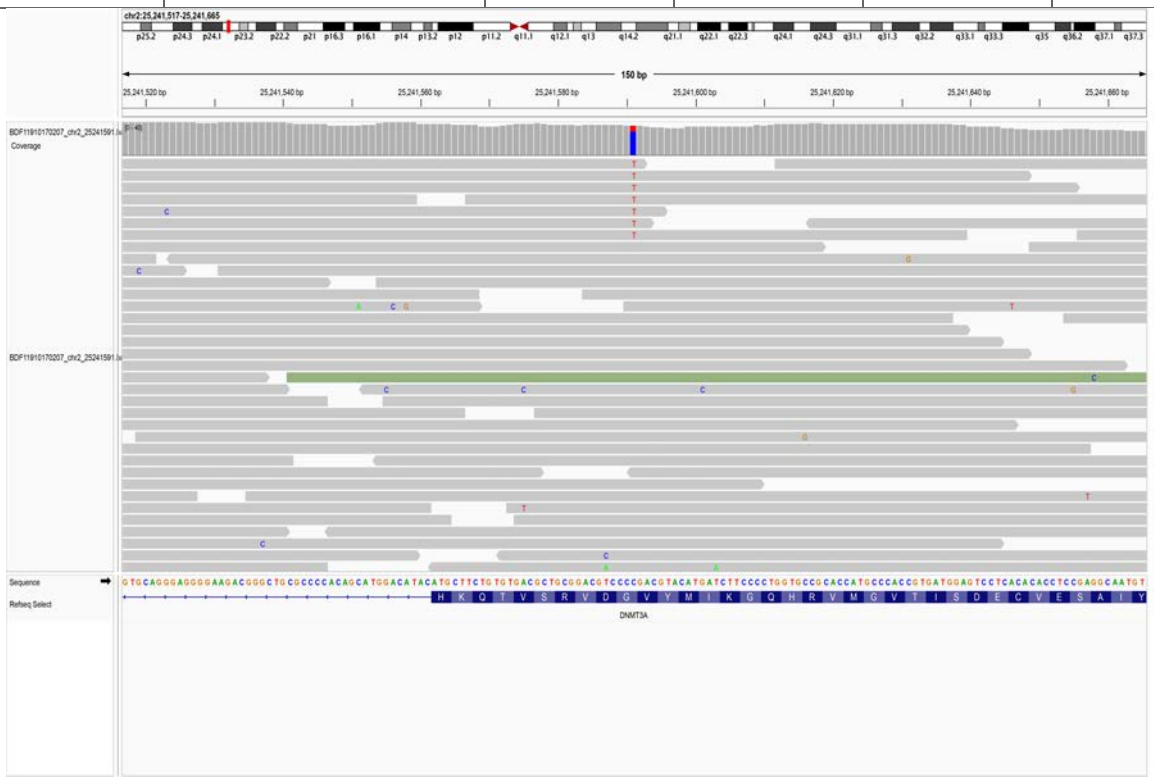
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09920	chr2_25241581_C/T	70	10	*DNMT3A*	missense_variant
AAGC031572D	chr2_25241581_C/T	27	9	*DNMT3A*	missense_variant
D2003004851	chr2_25241581_C/T	42	4	*DNMT3A*	missense_variant




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_2524158 1.bam
verage
D2003004851_chr2_2524158 1.bam
Sequence
Refseq Select
DNMT3A

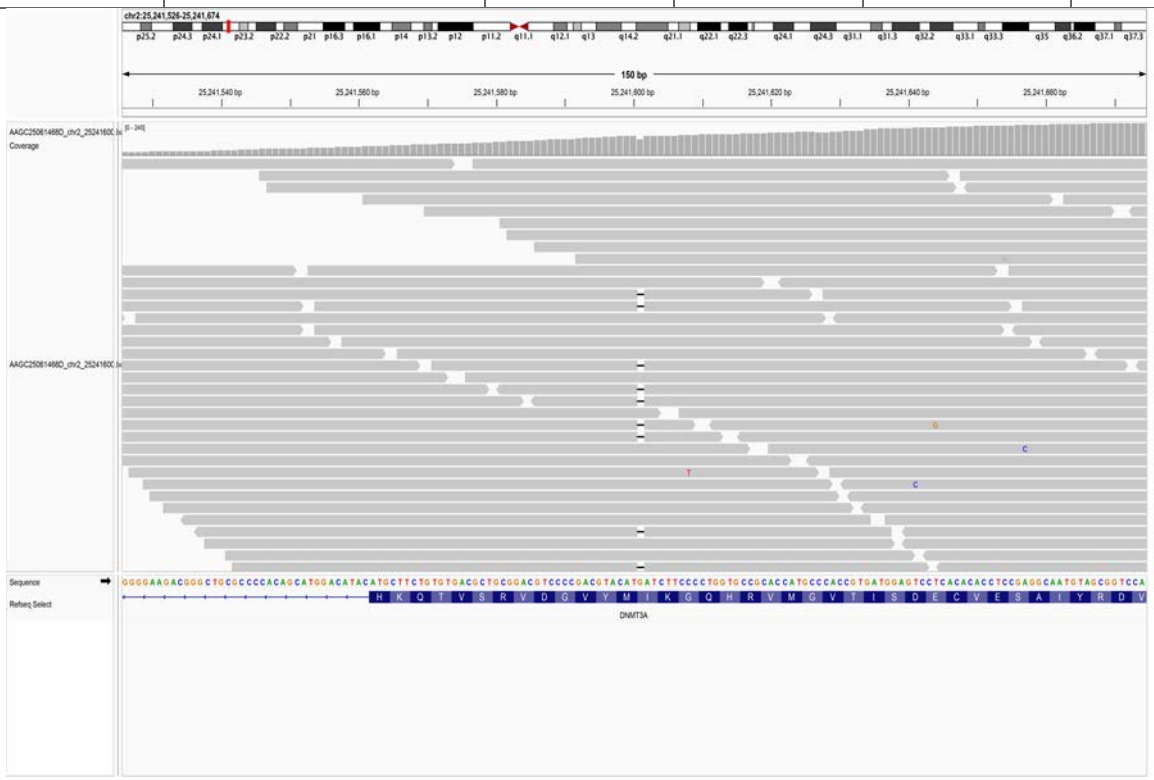
12.68. chr2_25241591_C/T

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



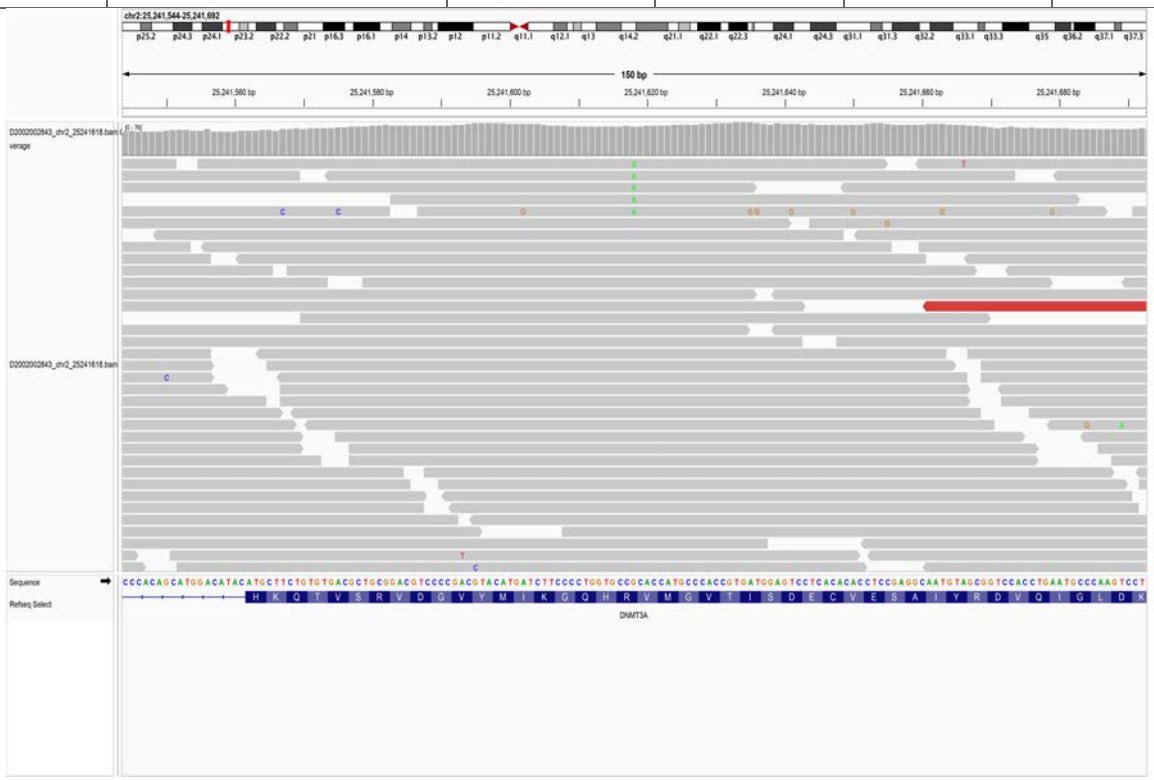
12.69. chr2_25241601_G/-

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



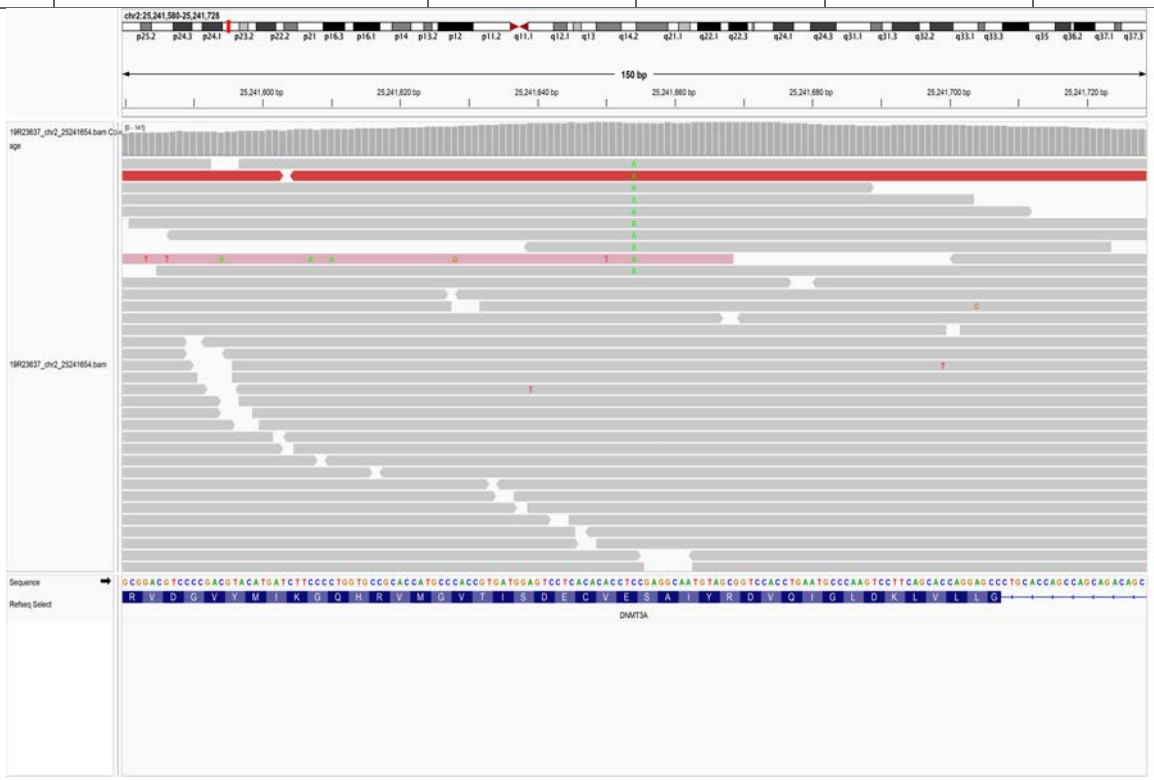
12.70. chr2_25241618_G/A

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



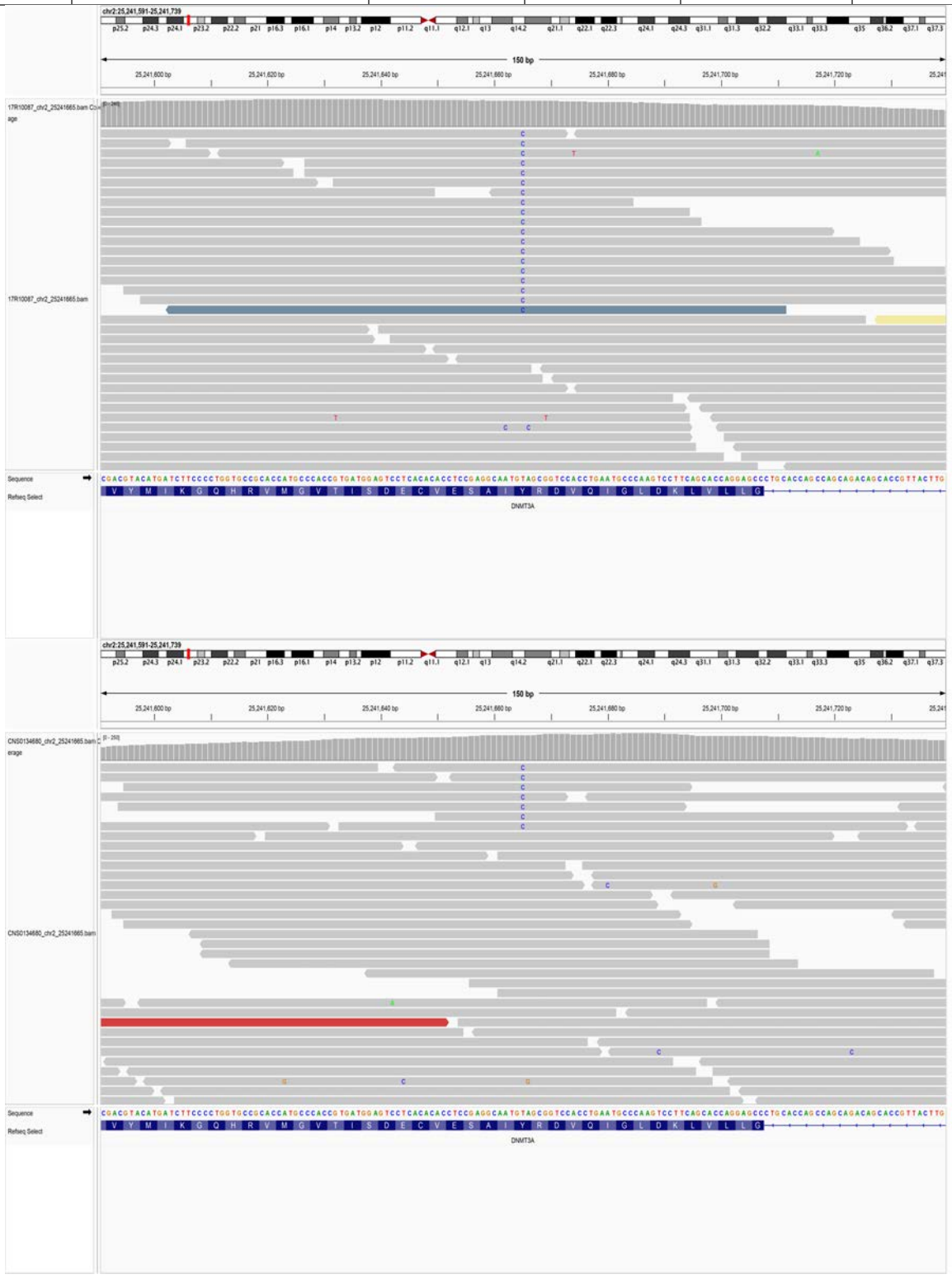
12.71. chr2_25241654_C/A

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



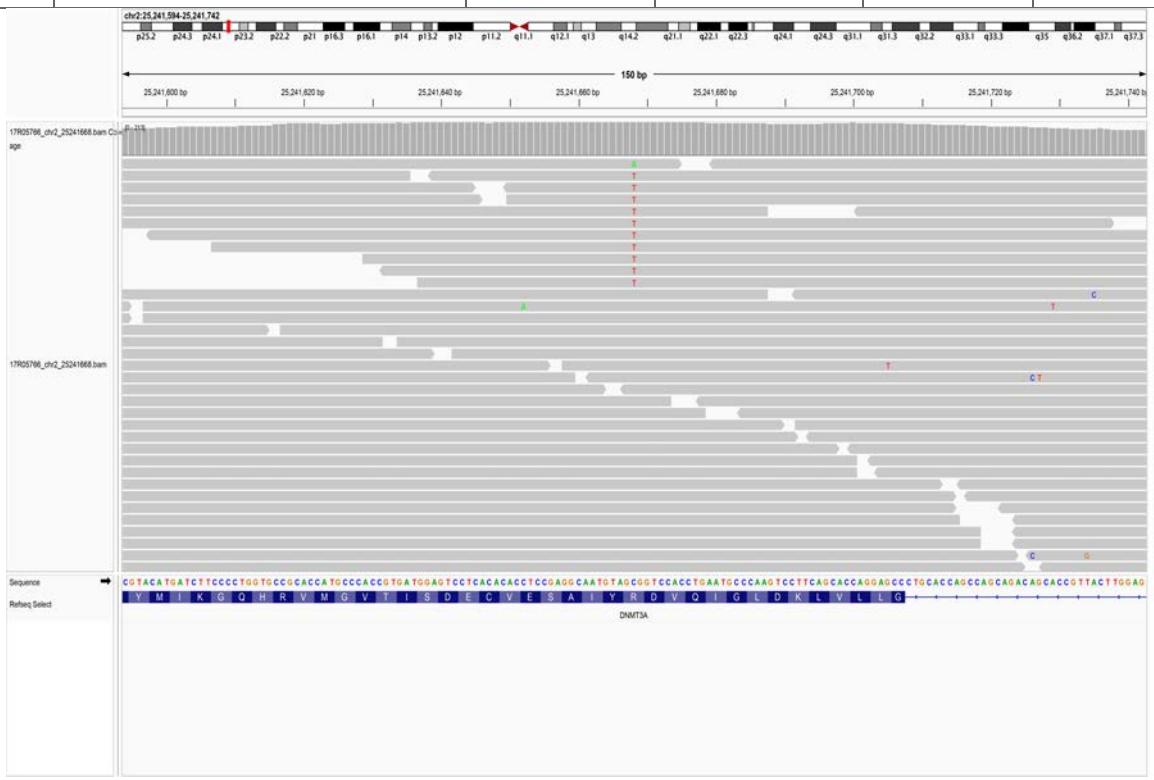
12.72. chr2_25241665_T/C

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



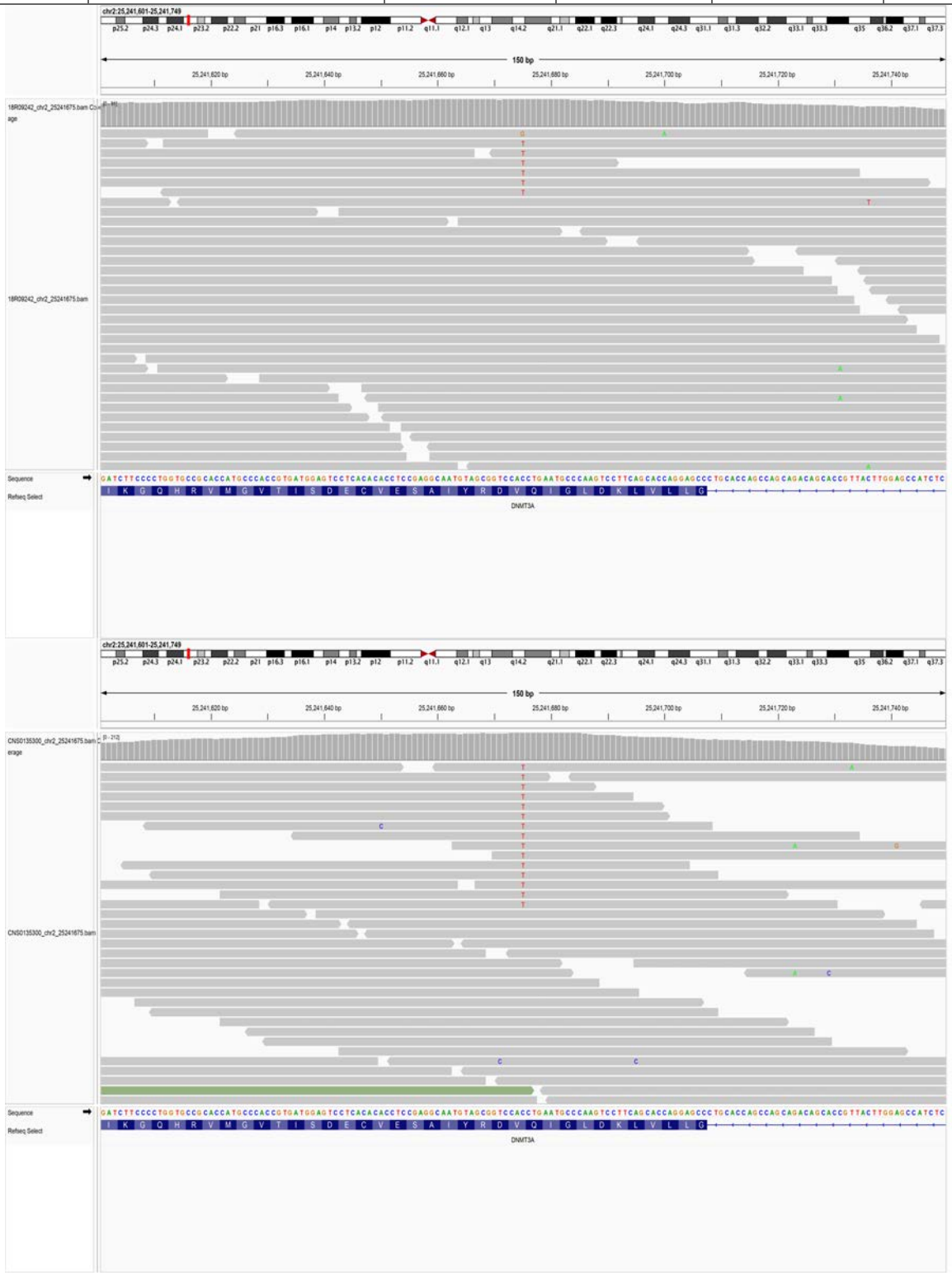
12.73. chr2_25241668_C/T

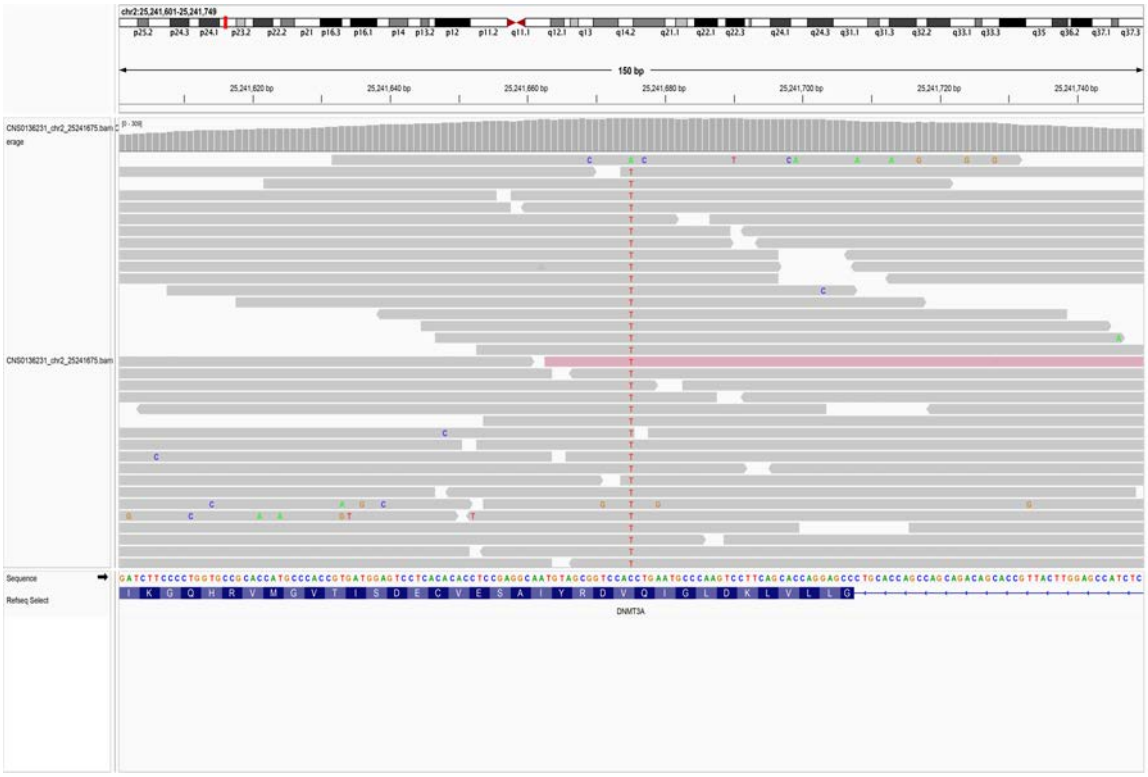
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05766	chr2_25241668_C/T	199	10	*DNMT3A*	missense_variant



12.74. chr2_25241675_C/T

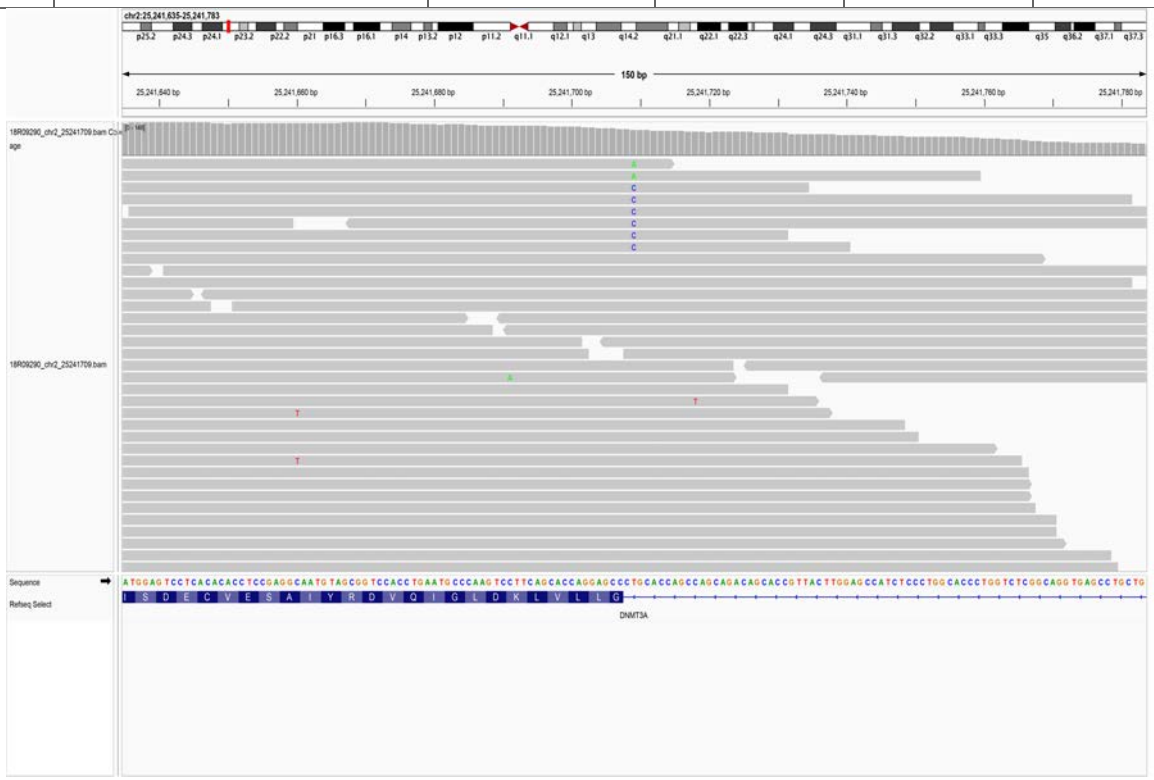
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09242	chr2_25241675_C/T	80	6	*DNMT3A*	missense_variant
CNS0135300	chr2_25241675_C/T	188	15	*DNMT3A*	missense_variant
CNS0136231	chr2_25241675_C/T	251	42	*DNMT3A*	missense_variant




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
erage
CNS0136231_chr2_25241675.bam
Sequence
Refseq Select
DNMT3A

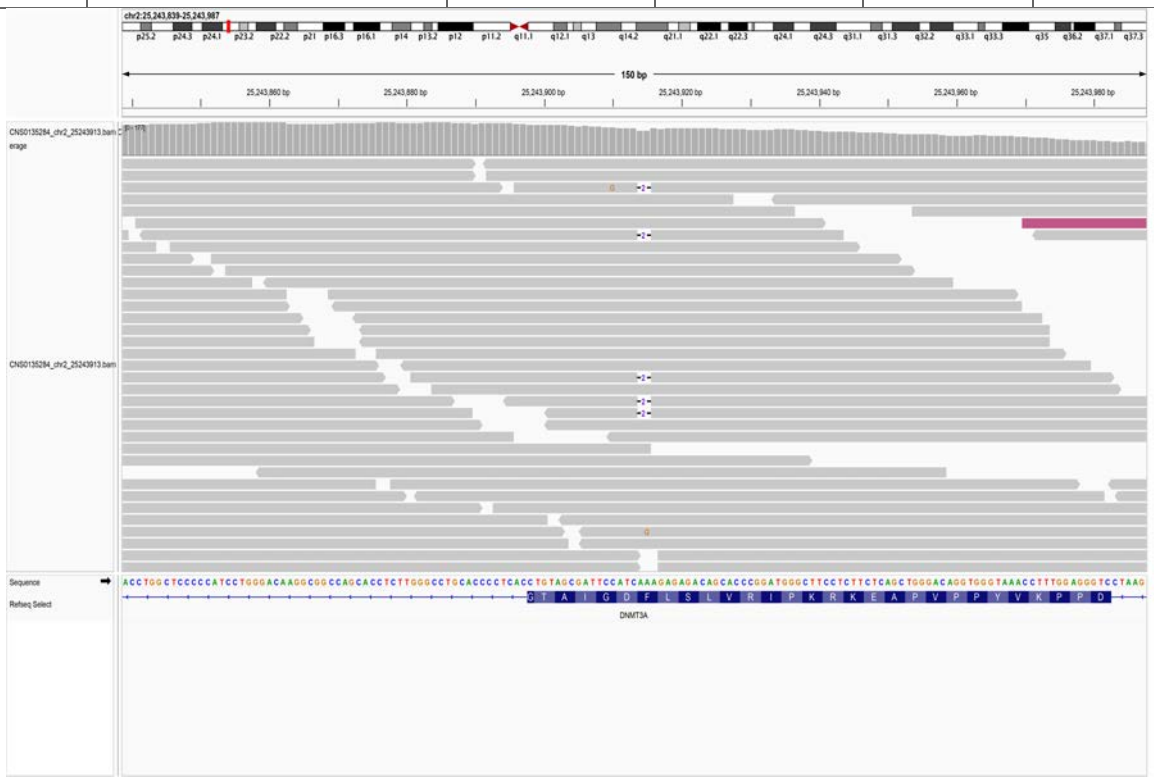
12.75. chr2_25241709_T/C

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



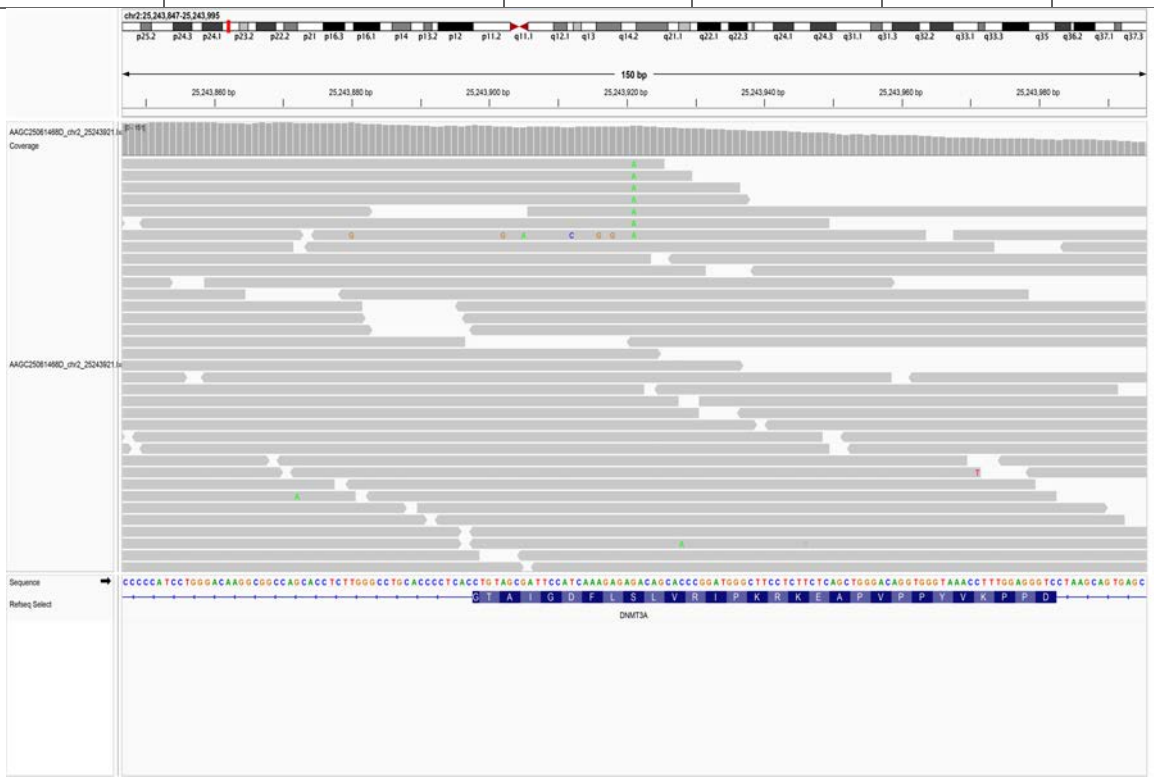
12.76. chr2_25243914_AA/-

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



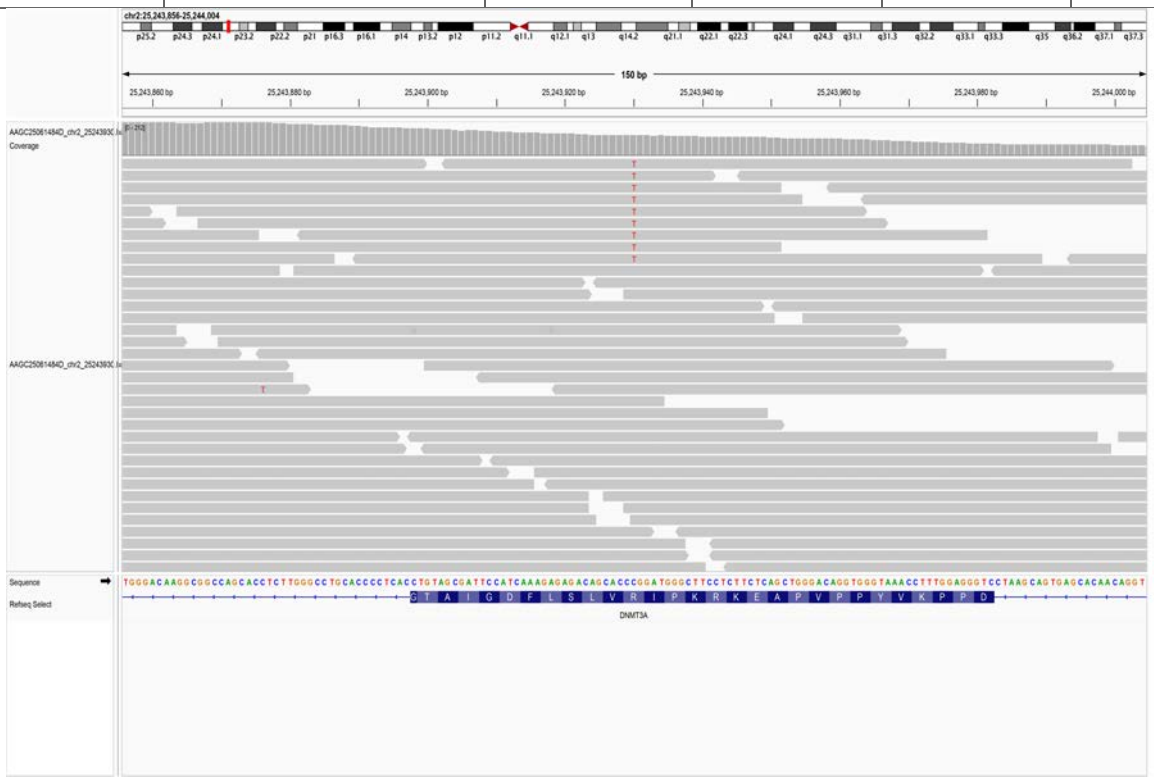
12.77. chr2_25243921_G/A

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



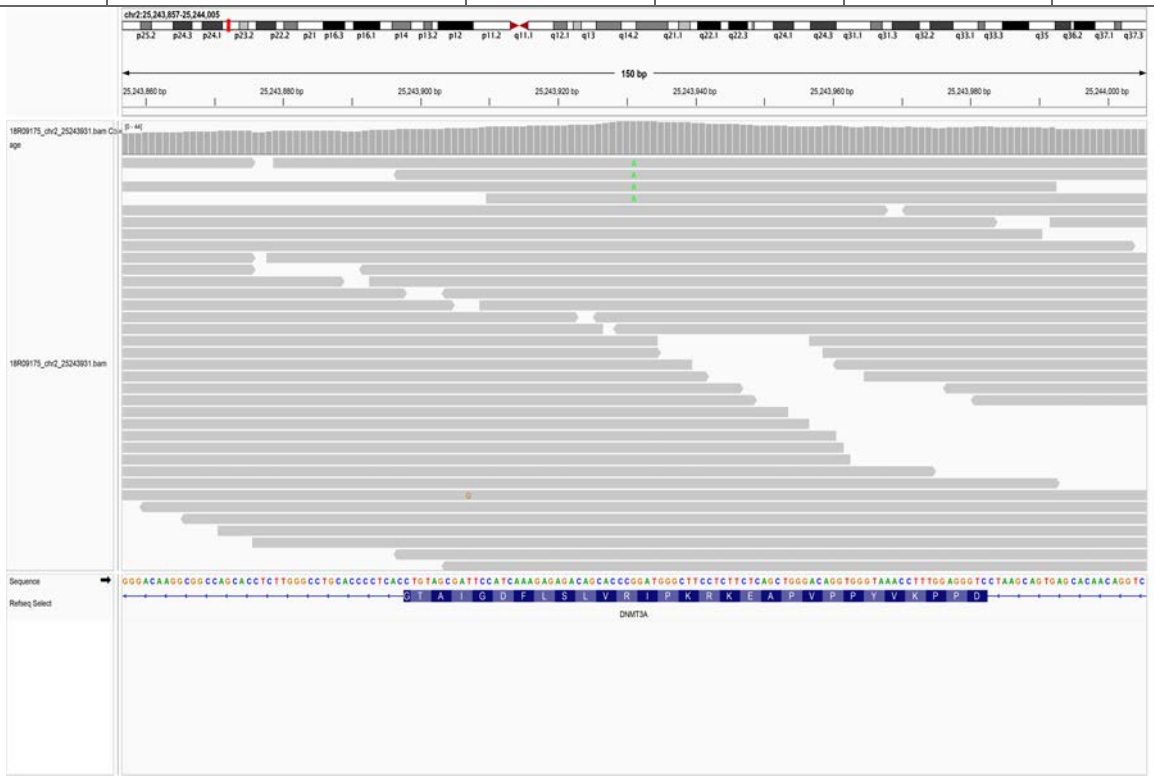
12.78. chr2_25243930_C/T

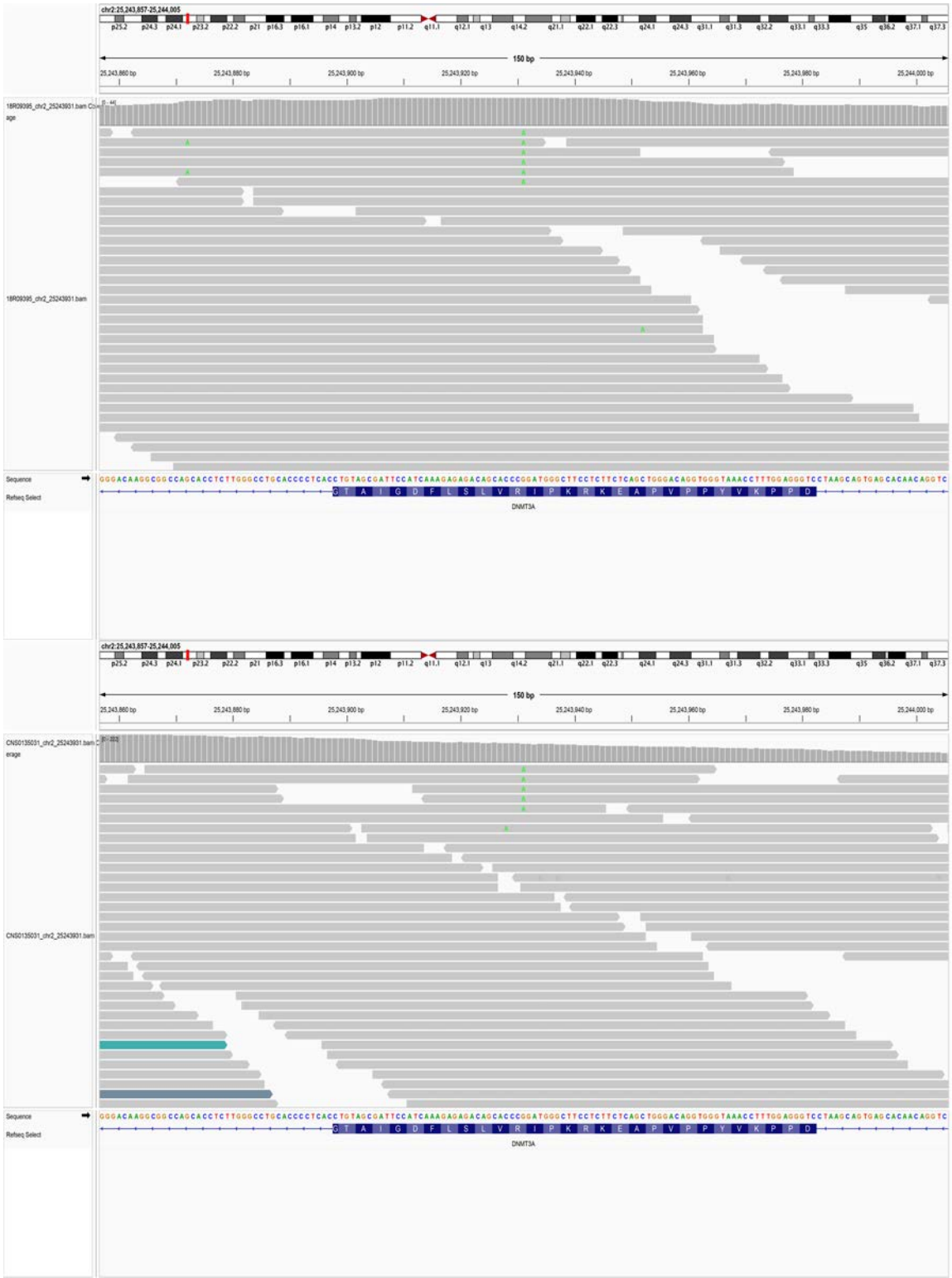
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061484D	chr2_25243930_C/T	118	9	*DNMT3A*	missense_variant

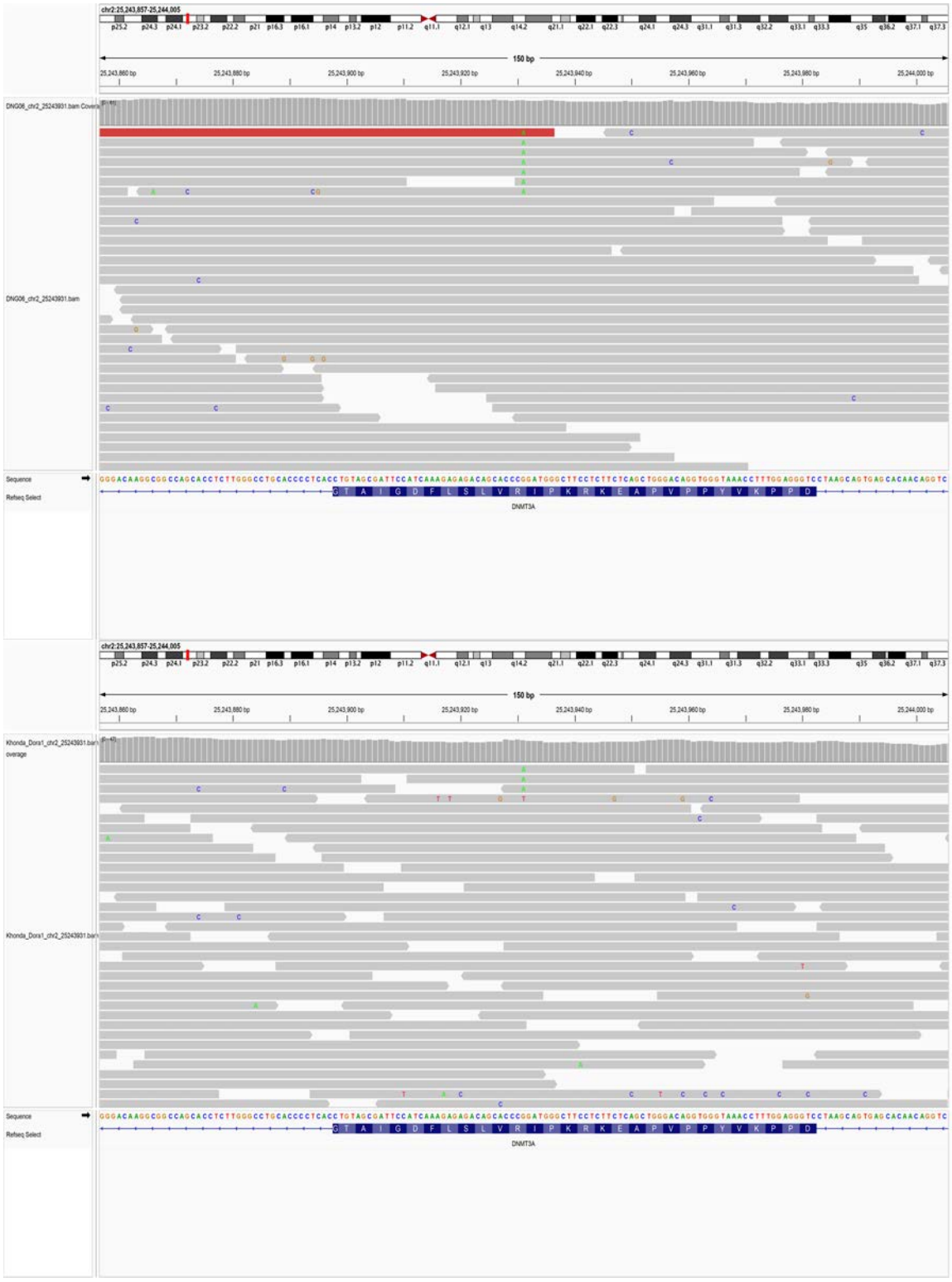


12.79. chr2_25243931_G/A

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

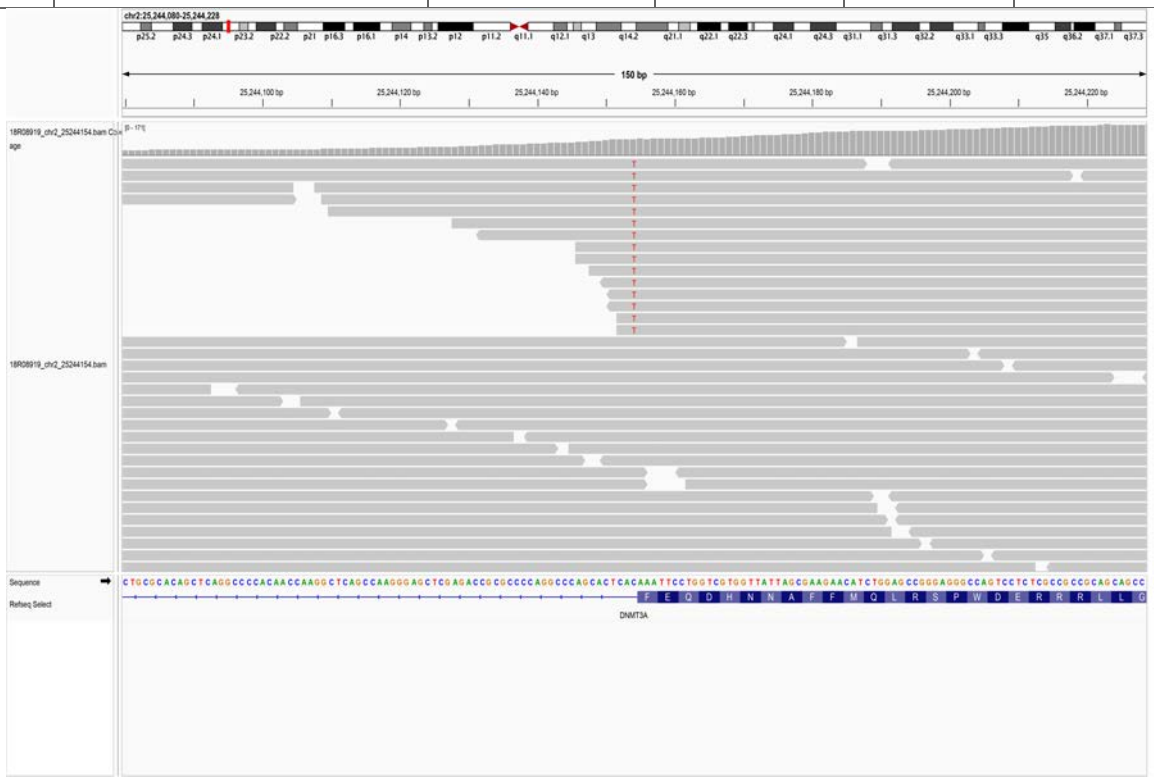



chr2:25,243,857-25,244,005
150 bp
25,243,860 bp
25,243,880 bp
25,243,900 bp
25,243,920 bp
25,243,940 bp
25,243,960 bp
25,243,980 bp
25,244,000 bp
18R09395_chr2_2524393l.bam Coverage
18R09395_chr2_2524393l.bam
Sequence
Refseq Select
DNMT3A
chr2:25,243,857-25,244,005
150 bp
CNS0135031_chr2_2524393l.bam Coverage
CNS0135031_chr2_2524393l.bam
Sequence
Refseq Select
DNMT3A


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

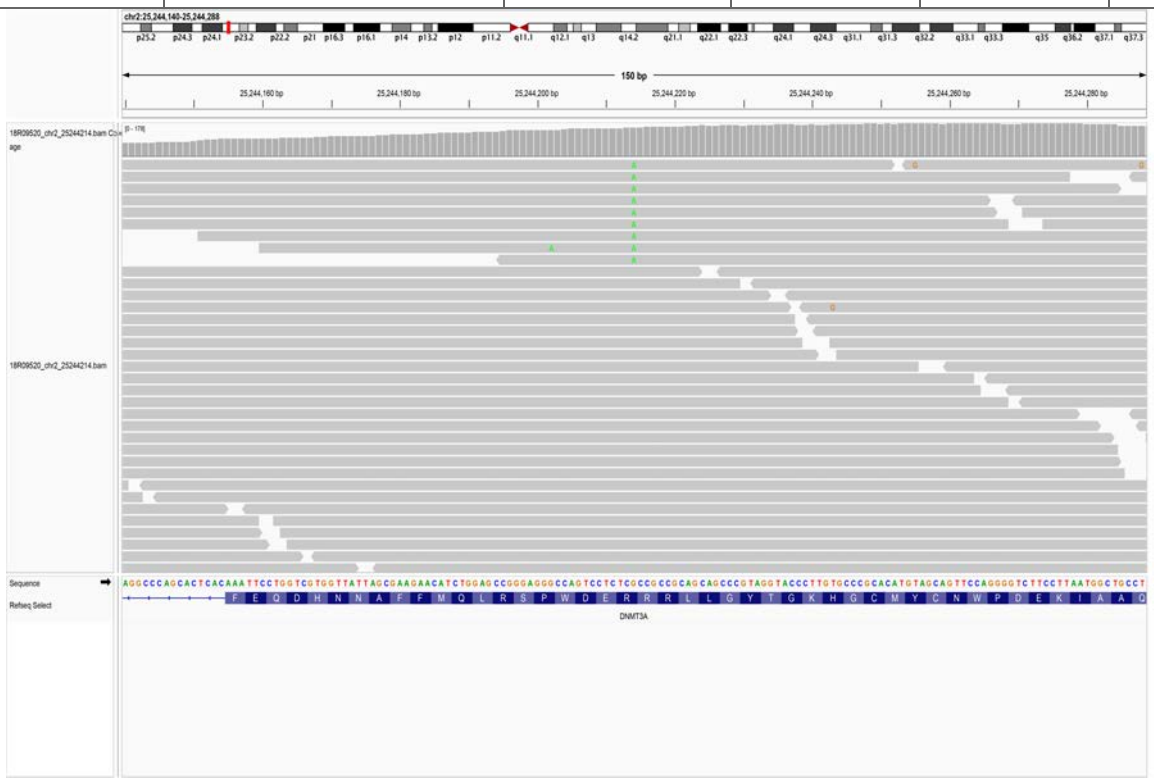
12.80. chr2_25244154_C/T

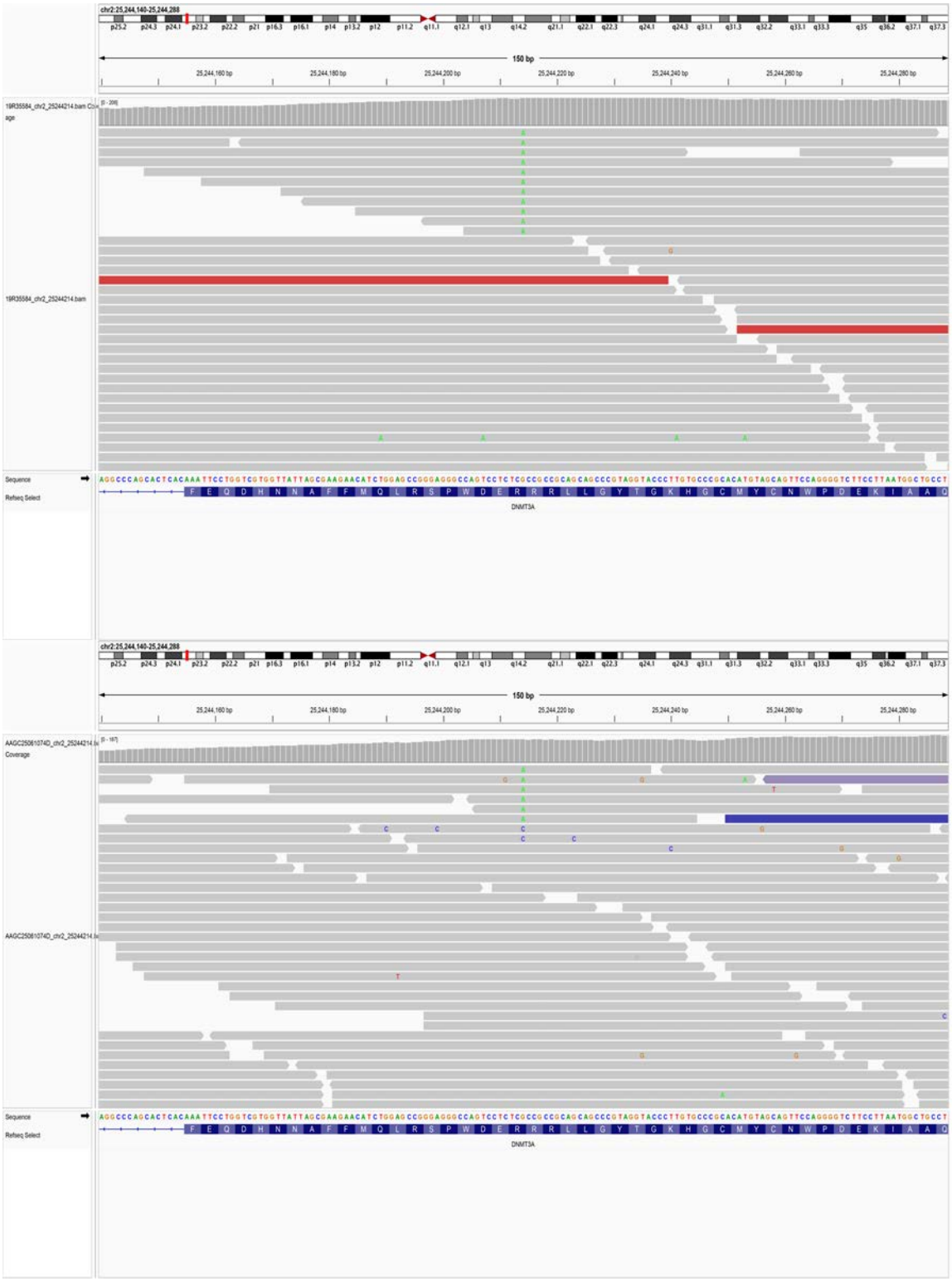
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08919	chr2_25244154_C/T	70	15	*DNMT3A*	splice_donor_variant

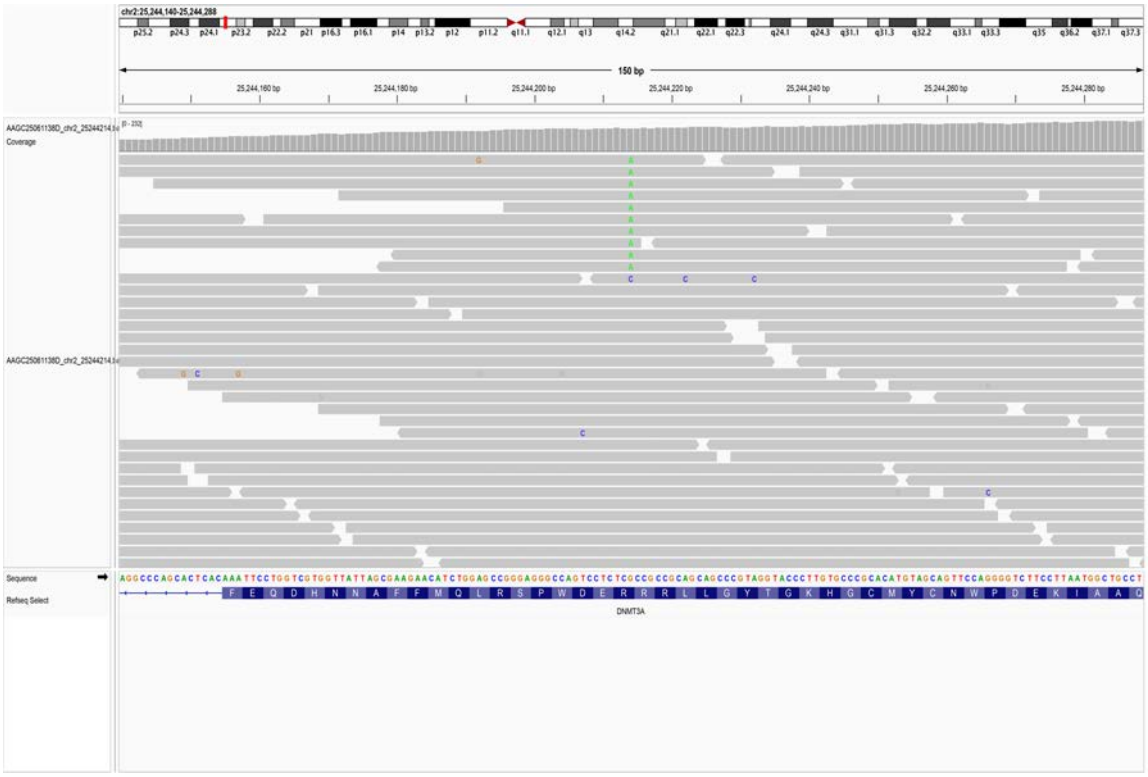


12.81. chr2_25244214_G/A

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

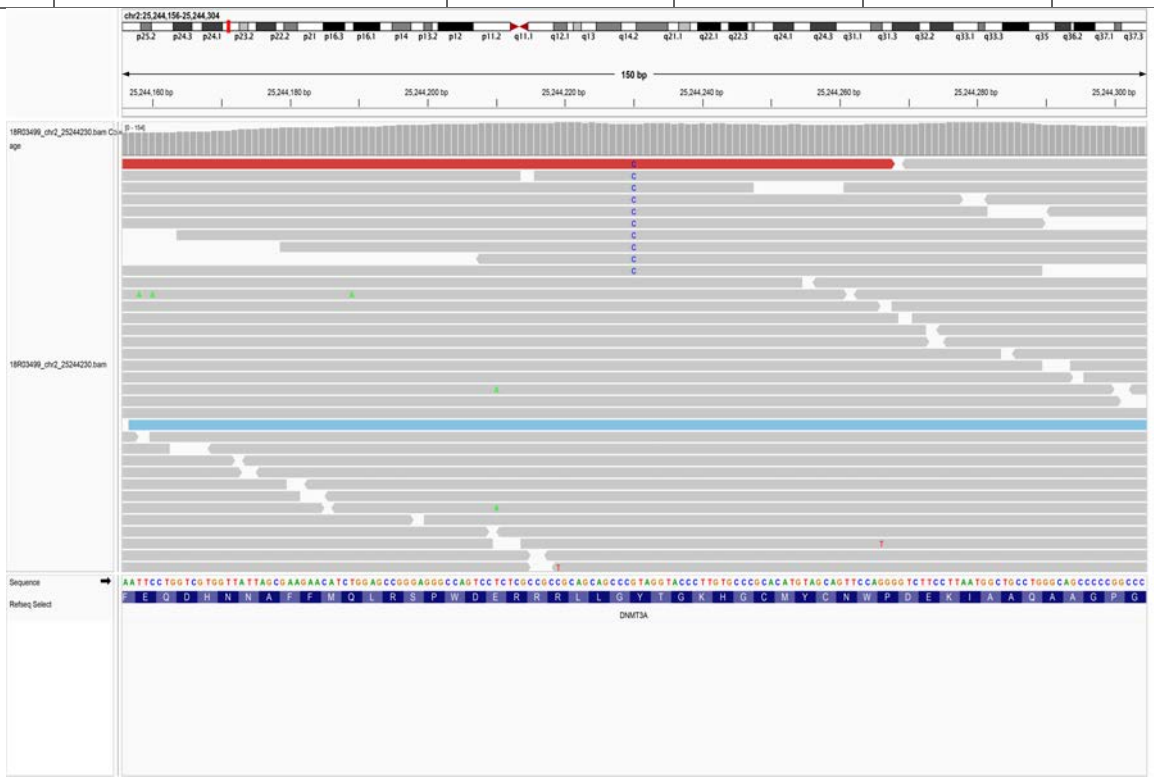



chr2:25,244,140-25,244,288
150 bp
25,244,160 bp
25,244,180 bp
25,244,200 bp
25,244,220 bp
25,244,240 bp
25,244,260 bp
25,244,280 bp
19R35584_chr2_25244214.bam Coverage
19R35584_chr2_25244214.bam
Sequence
Refseq Select
DNMT3A
AAGC25081074D_chr2_25244214.bam Coverage
AAGC25081074D_chr2_25244214.bam


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

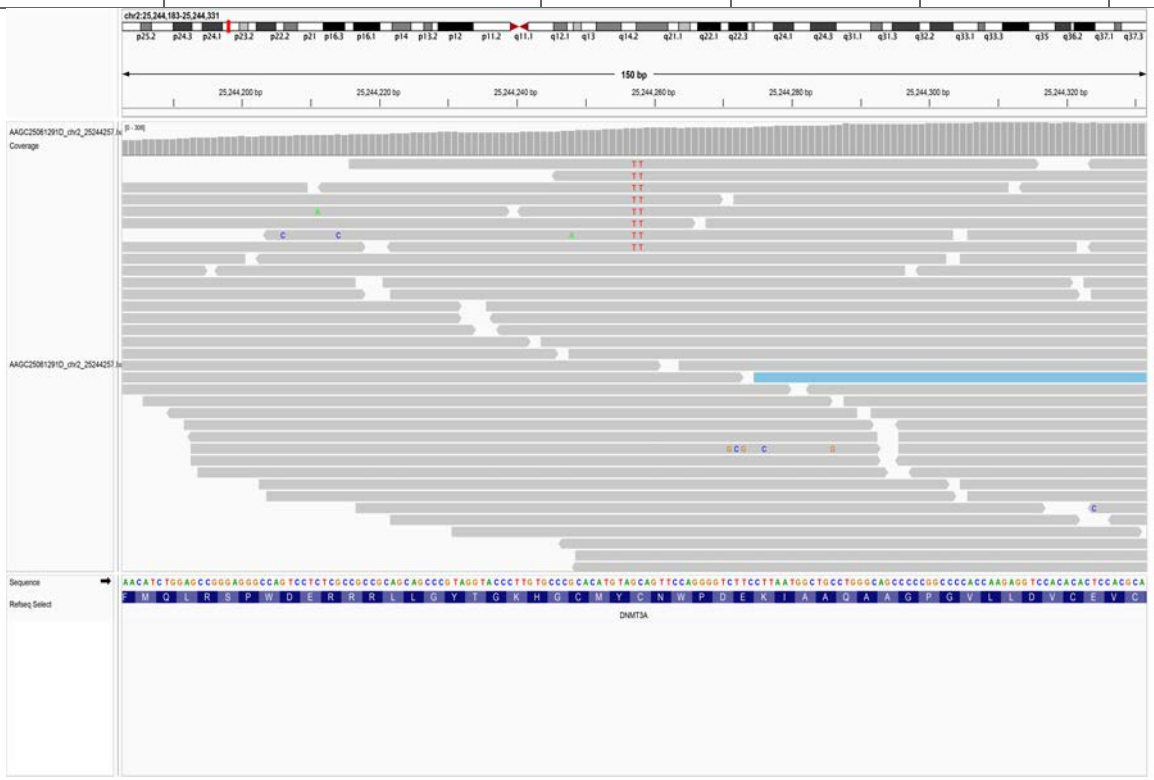
12.82. chr2_25244230_G/C

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



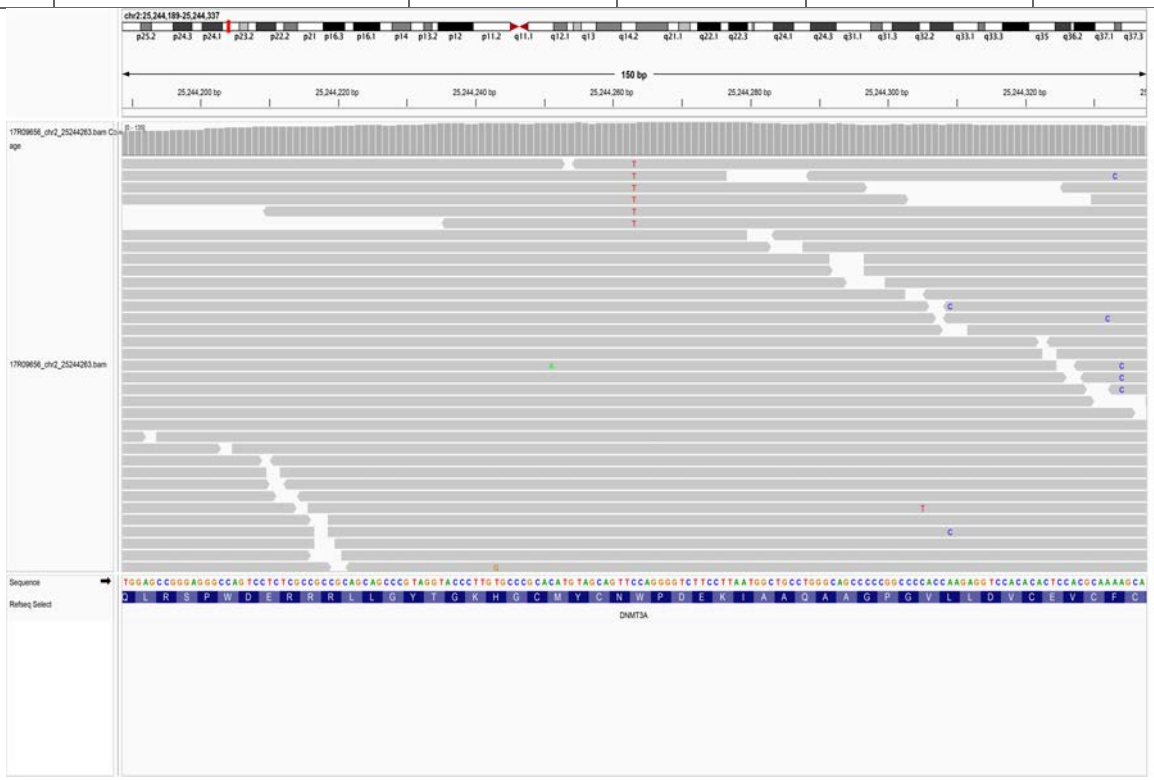
12.83. chr2_25244257_GC/TT

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



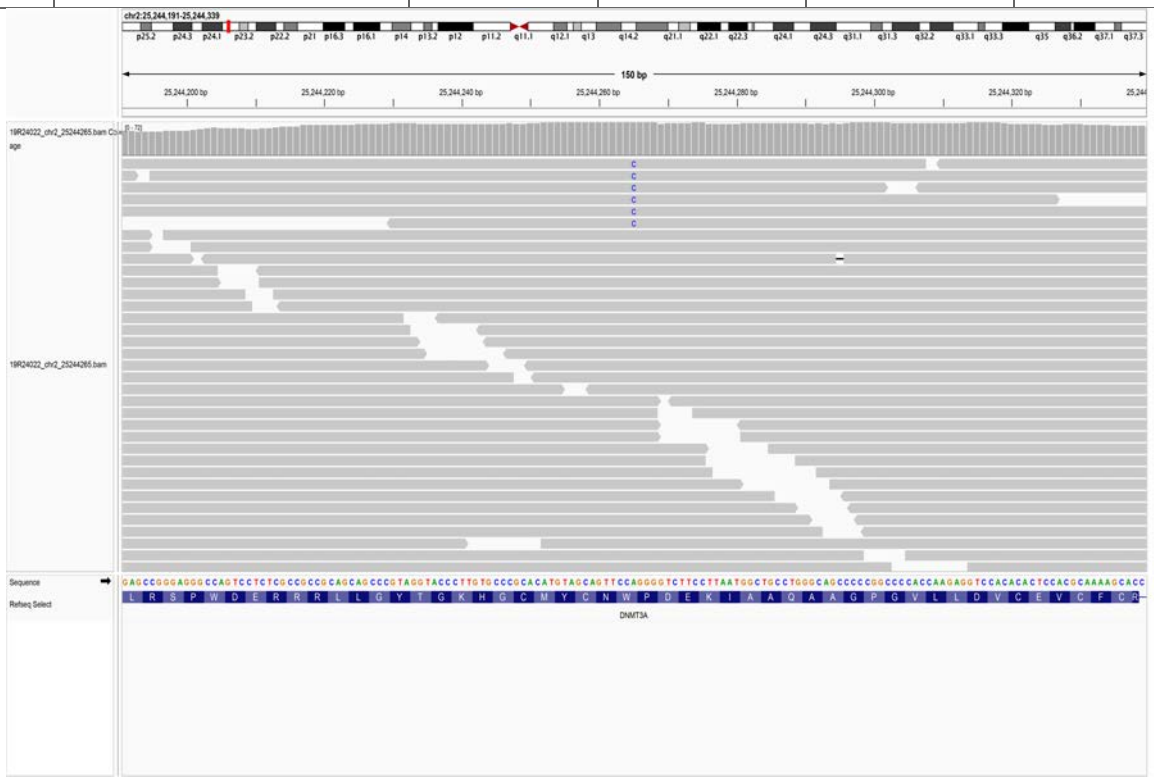
12.84. chr2_25244263_C/T

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



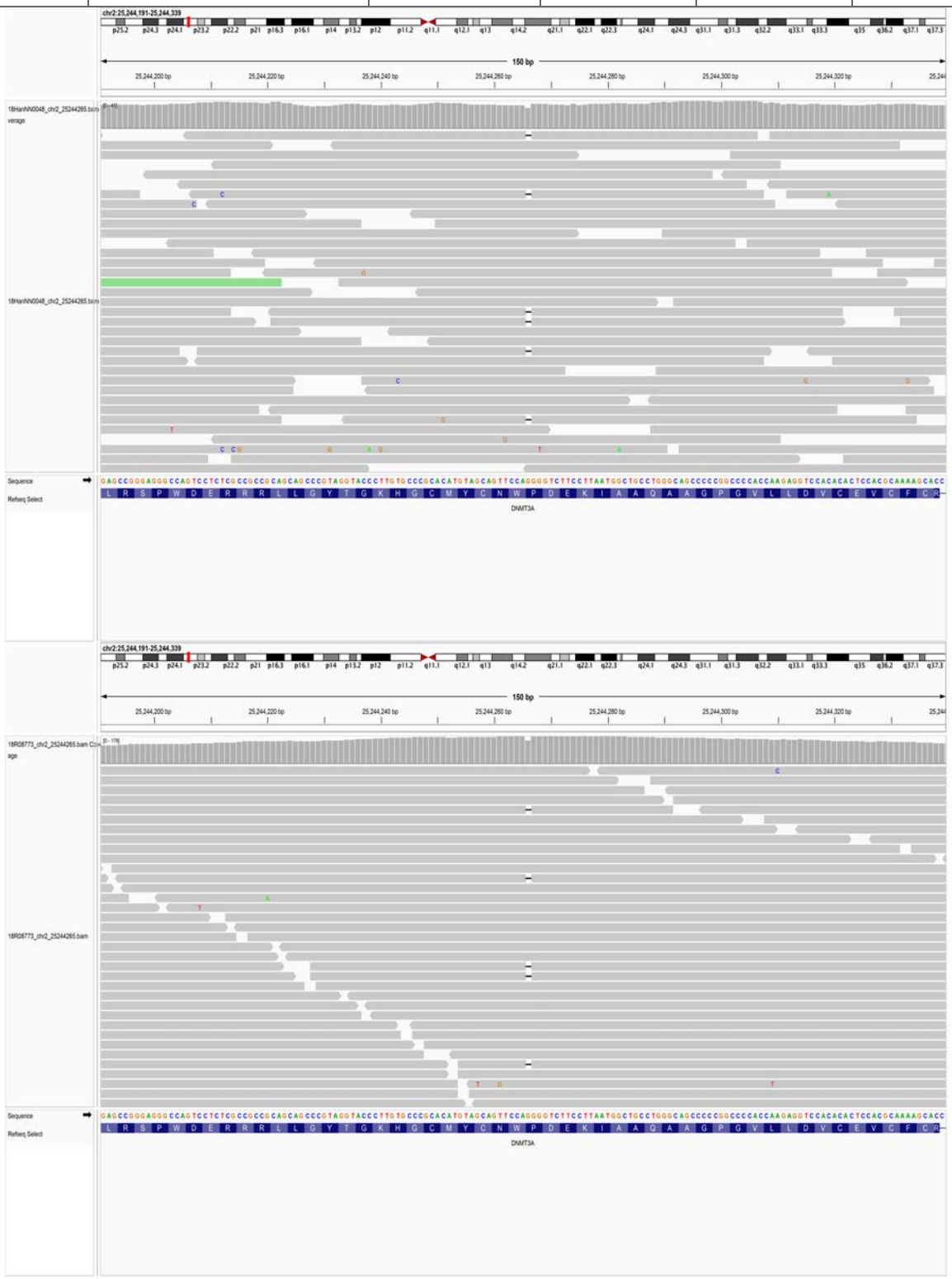
12.85. chr2_25244265_A/C

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



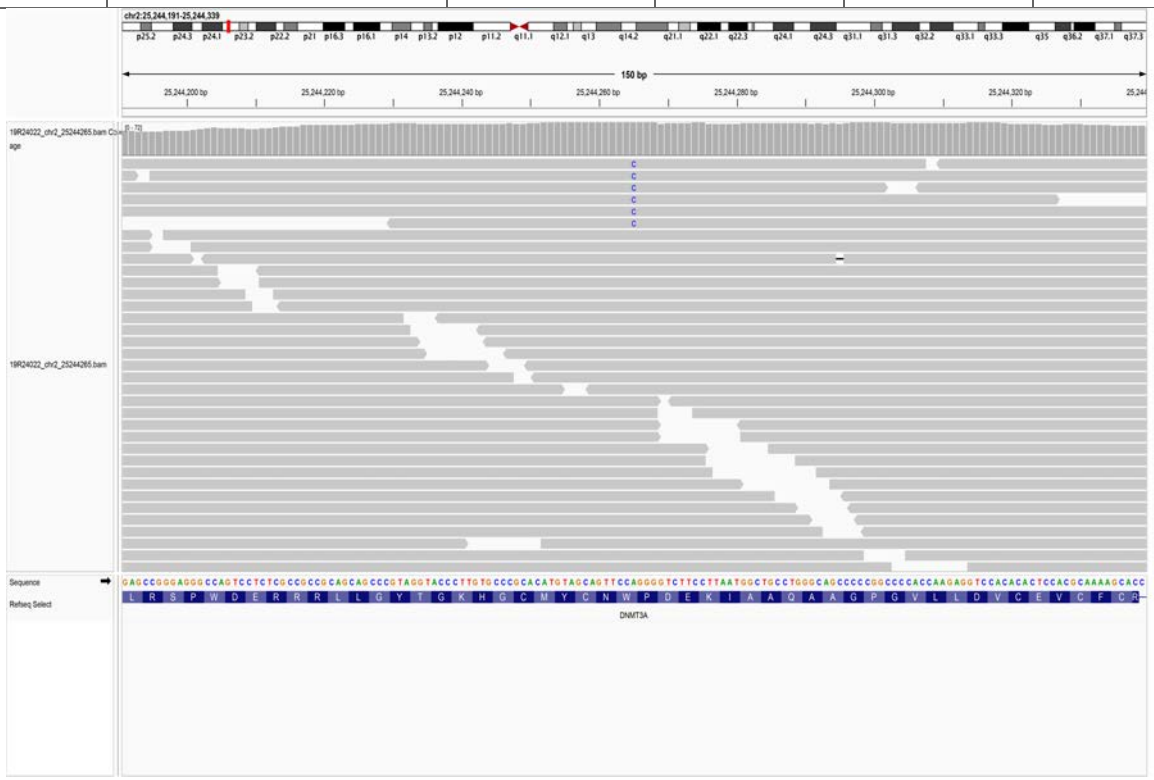
12.86. chr2_25244266_G/-

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



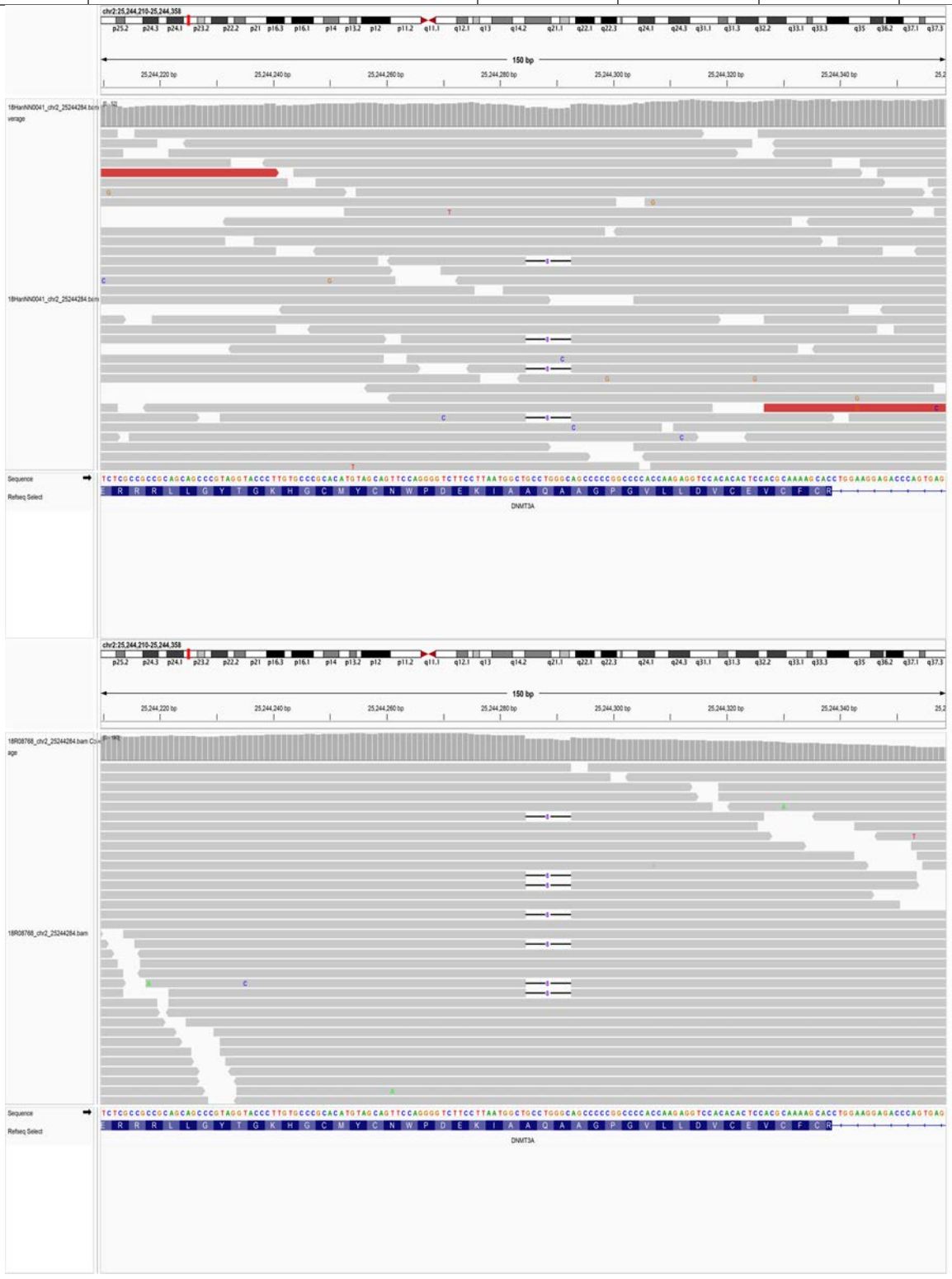
12.87. chr2_25244266_A/C

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



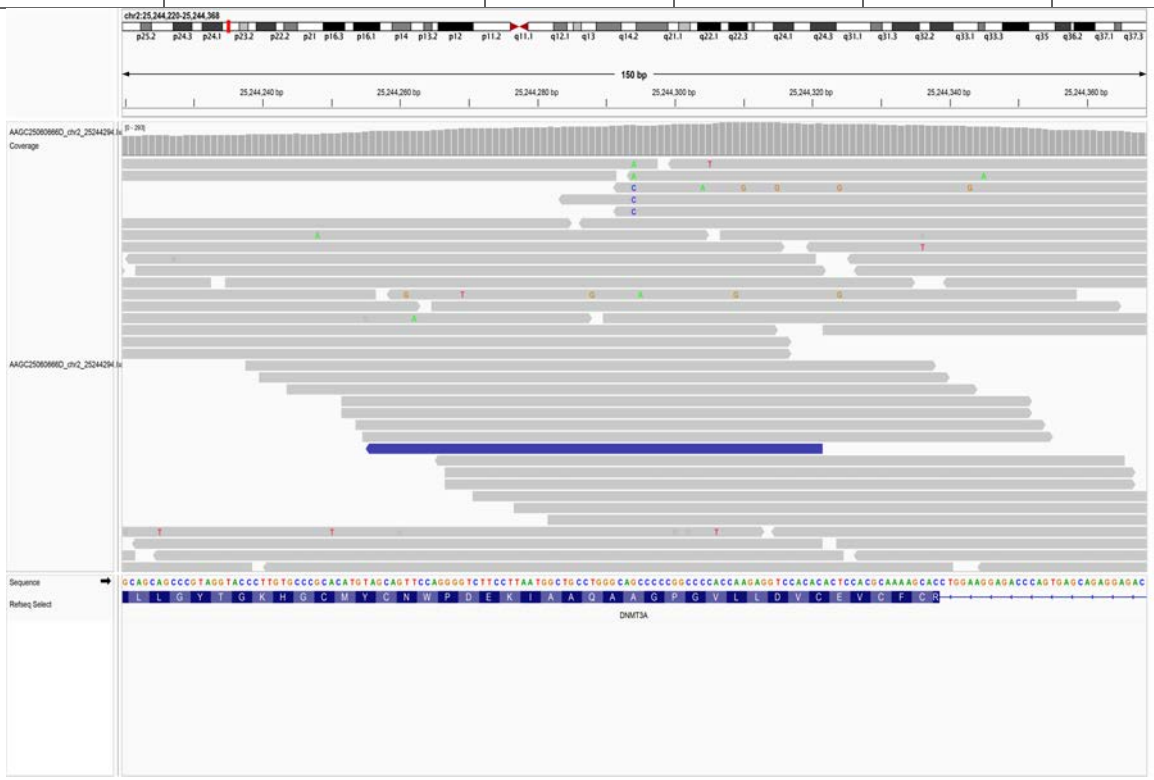
12.88. chr2_25244285_GCCTGGGC/-

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



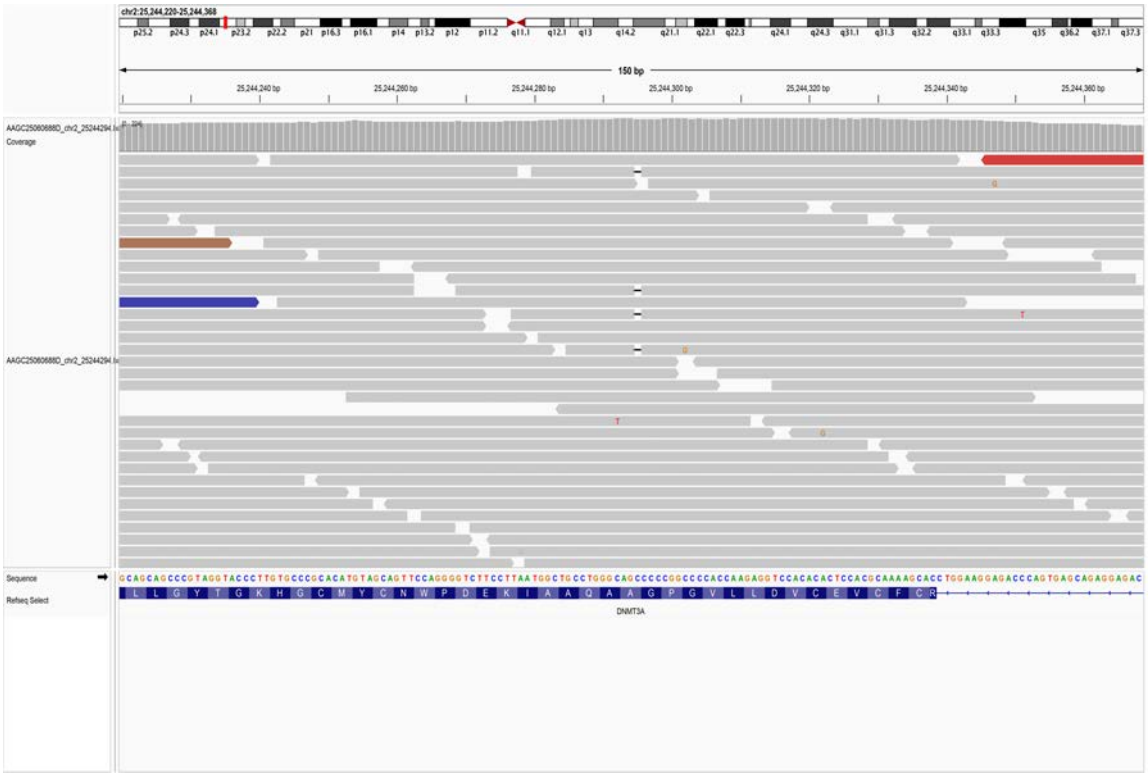
12.89. chr2_25244295_G/C

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



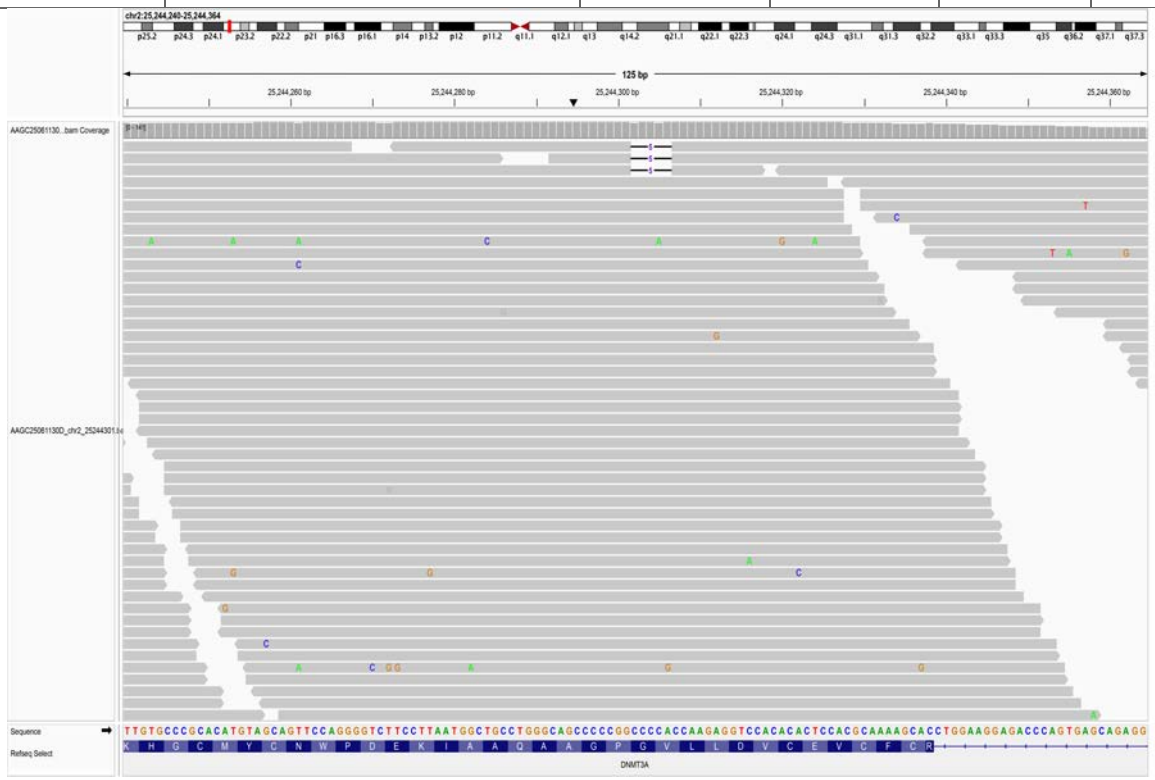
12.90. chr2_25244295_C/-

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



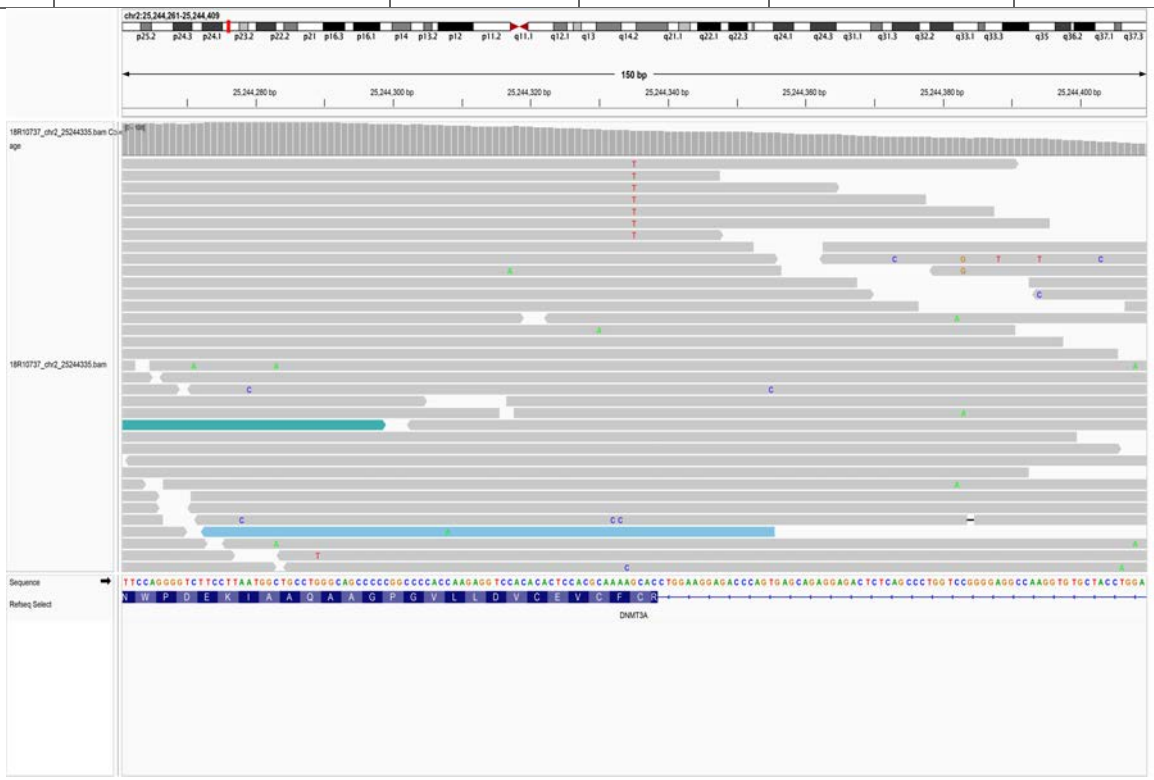
12.91. chr2_25244302_CCCCA/-

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



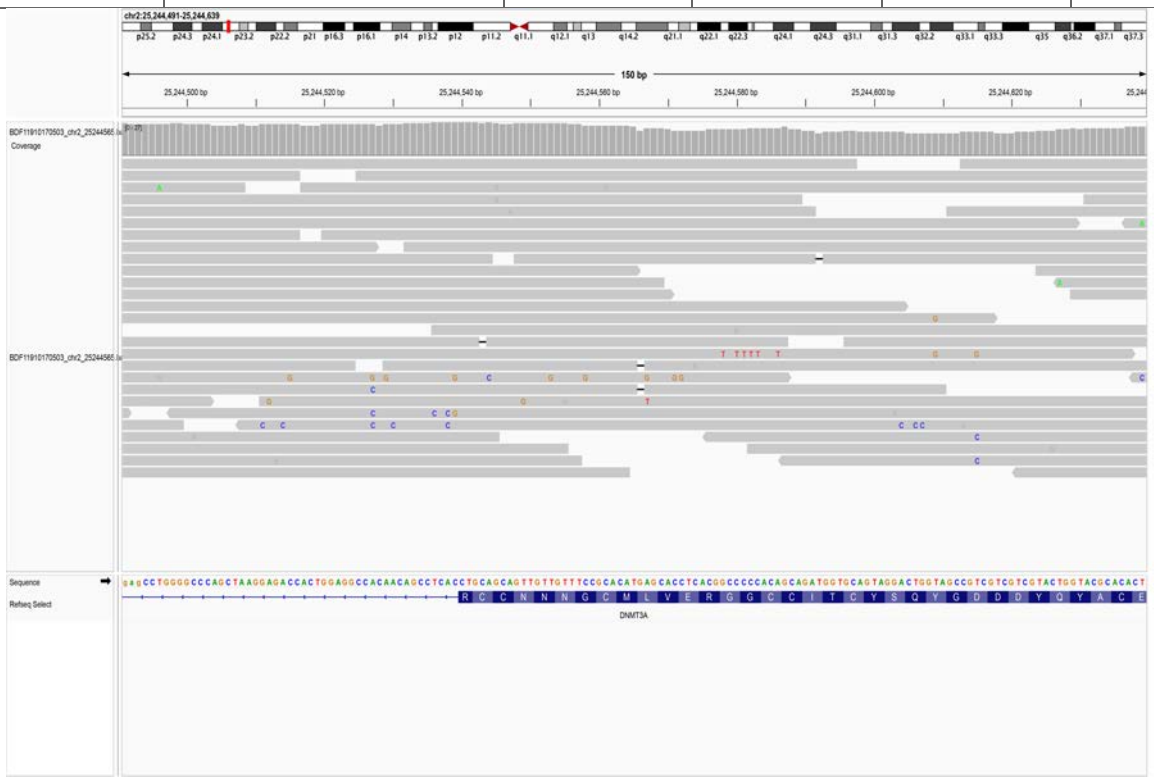
12.92. chr2_25244335_G/T

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



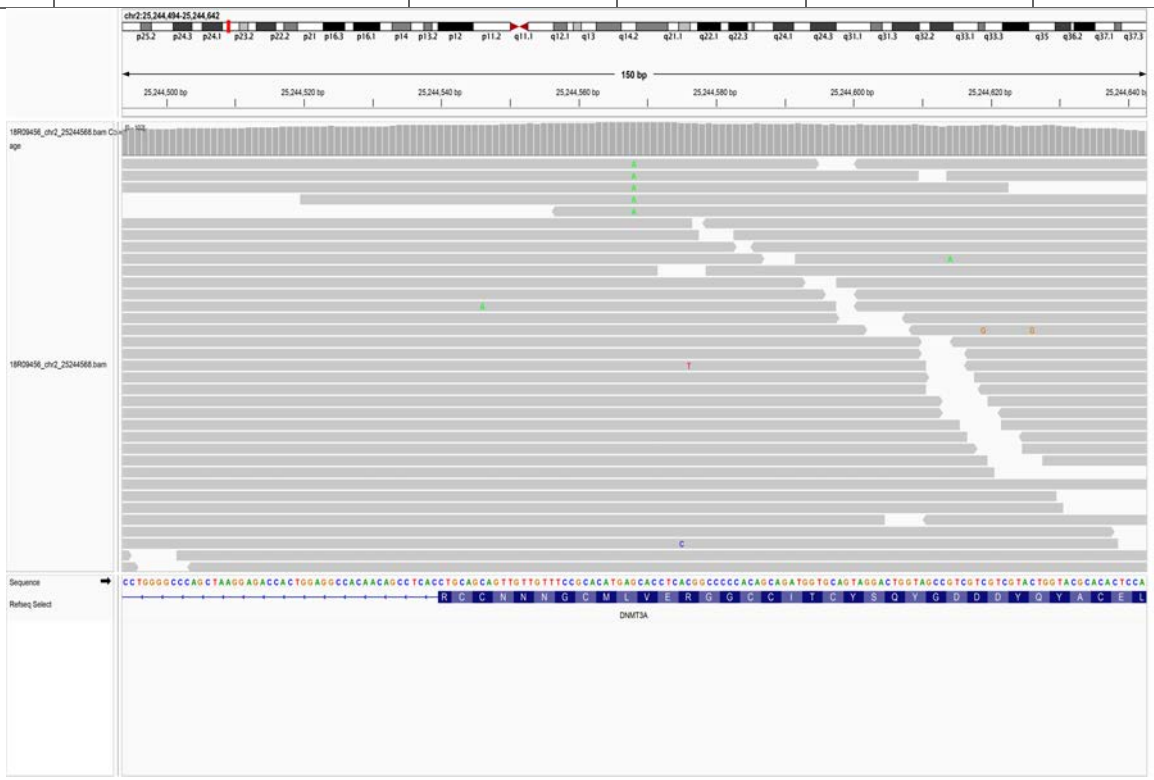
12.93. chr2_25244566_G/-

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



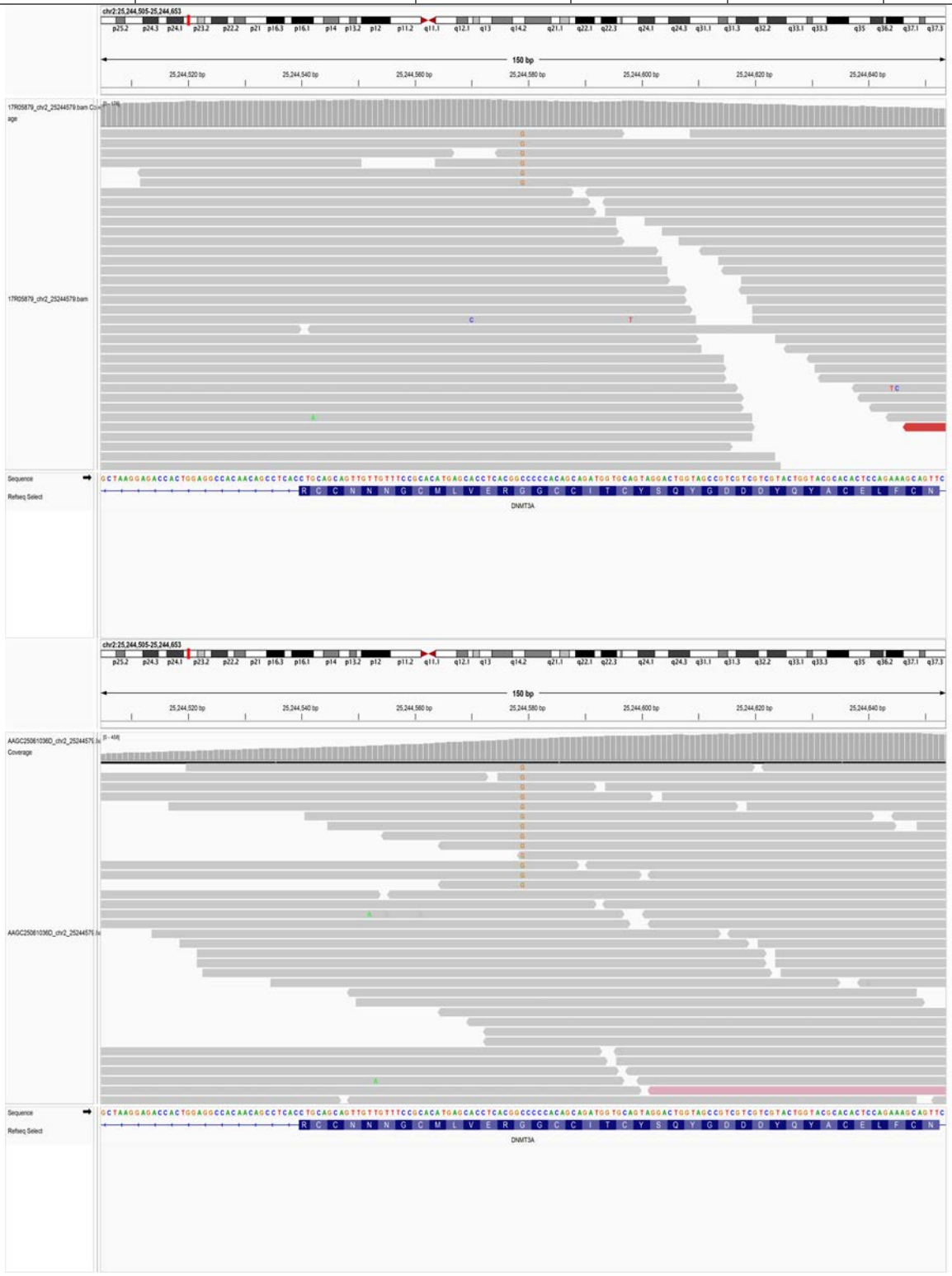
12.94. chr2_25244568_G/A

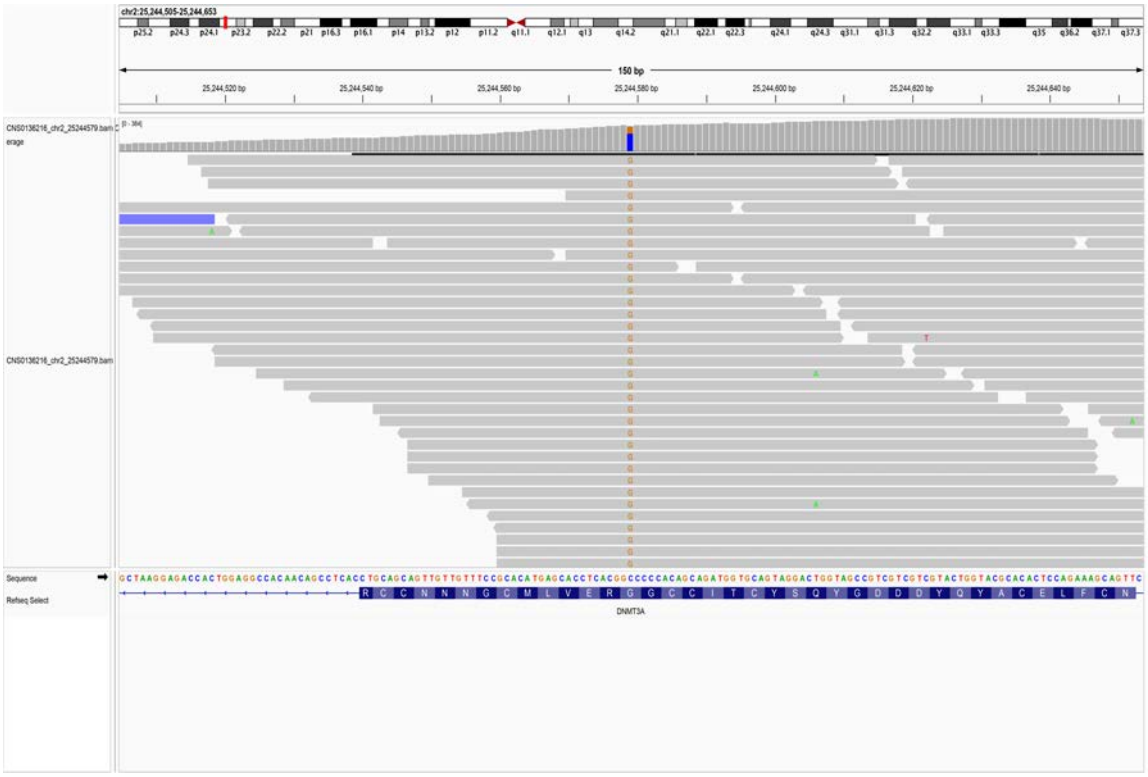
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09456	chr2_25244568_G/A	92	5	*DNMT3A*	missense_variant



12.95. chr2_25244579_C/G

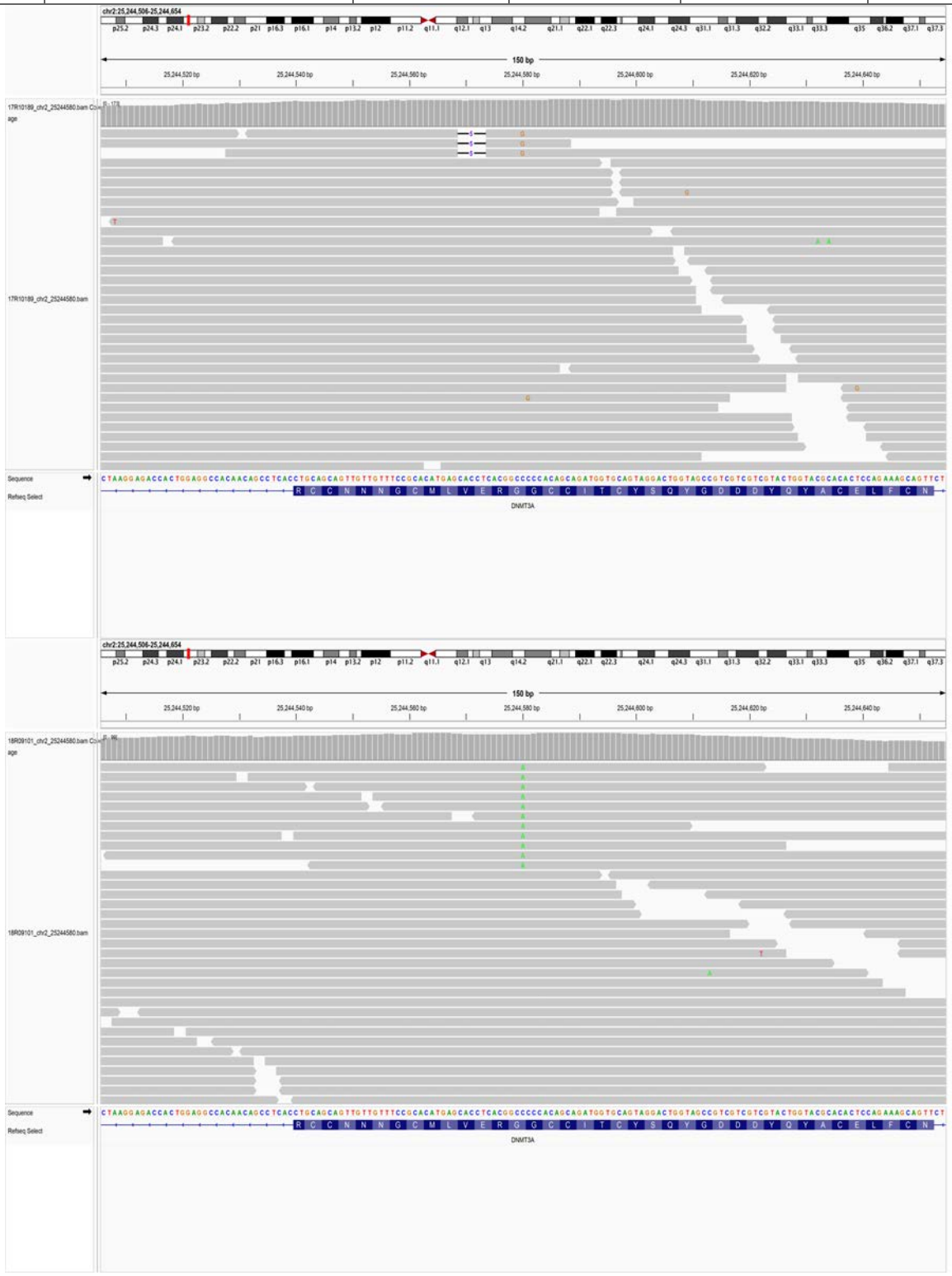
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05879	chr2_25244579_C/G	156	6	*DNMT3A*	missense_variant
AAGC25061036D	chr2_25244579_C/G	336	15	*DNMT3A*	missense_variant
CNS0136216	chr2_25244579_C/G	209	80	*DNMT3A*	missense_variant

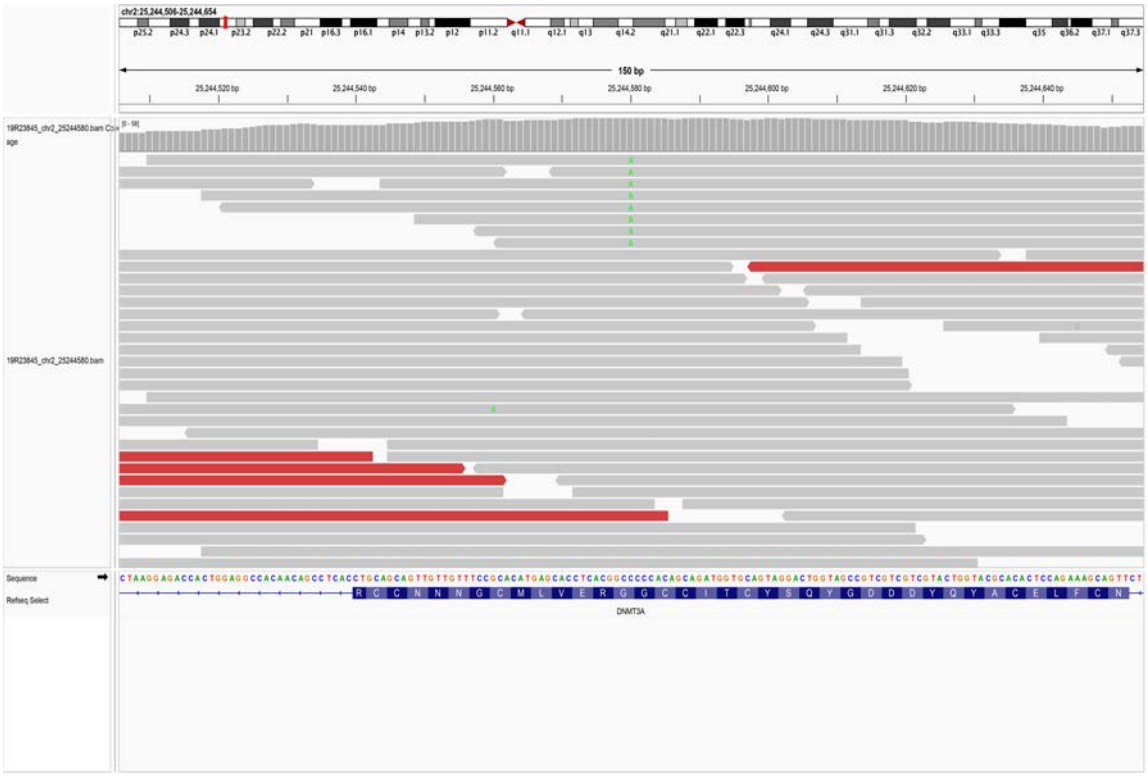



chr2:25,244,505-25,244,653
150 bp
25,244,520 bp
25,244,540 bp
25,244,560 bp
25,244,580 bp
25,244,600 bp
25,244,620 bp
25,244,640 bp
CNS0136216_chr2_25244579.bam
erage
CNS0136216_chr2_25244579.bam
Sequence
Refseq Select
DNMT3A

12.96. chr2_25244580_C/G/A

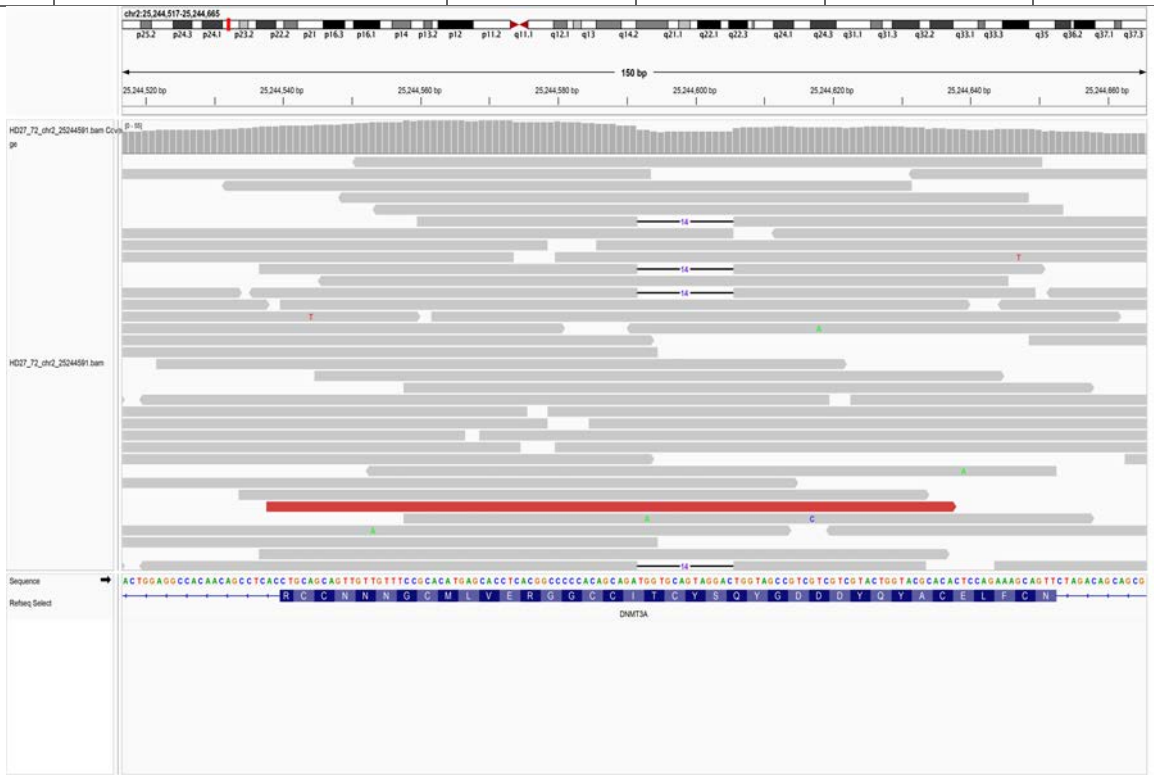
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R10189	chr2_25244580_C/G/A	165	3	*DNMT3A*	missense_variant
18R09101	chr2_25244580_C/G/A	82	11	*DNMT3A*	missense_variant
19R23845	chr2_25244580_C/G/A	49	8	*DNMT3A*	missense_variant




chr2:25,244,506-25,244,654
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
19R23845_chr2_25244580.bam
Sequence
Refseq Select
DNMT3A

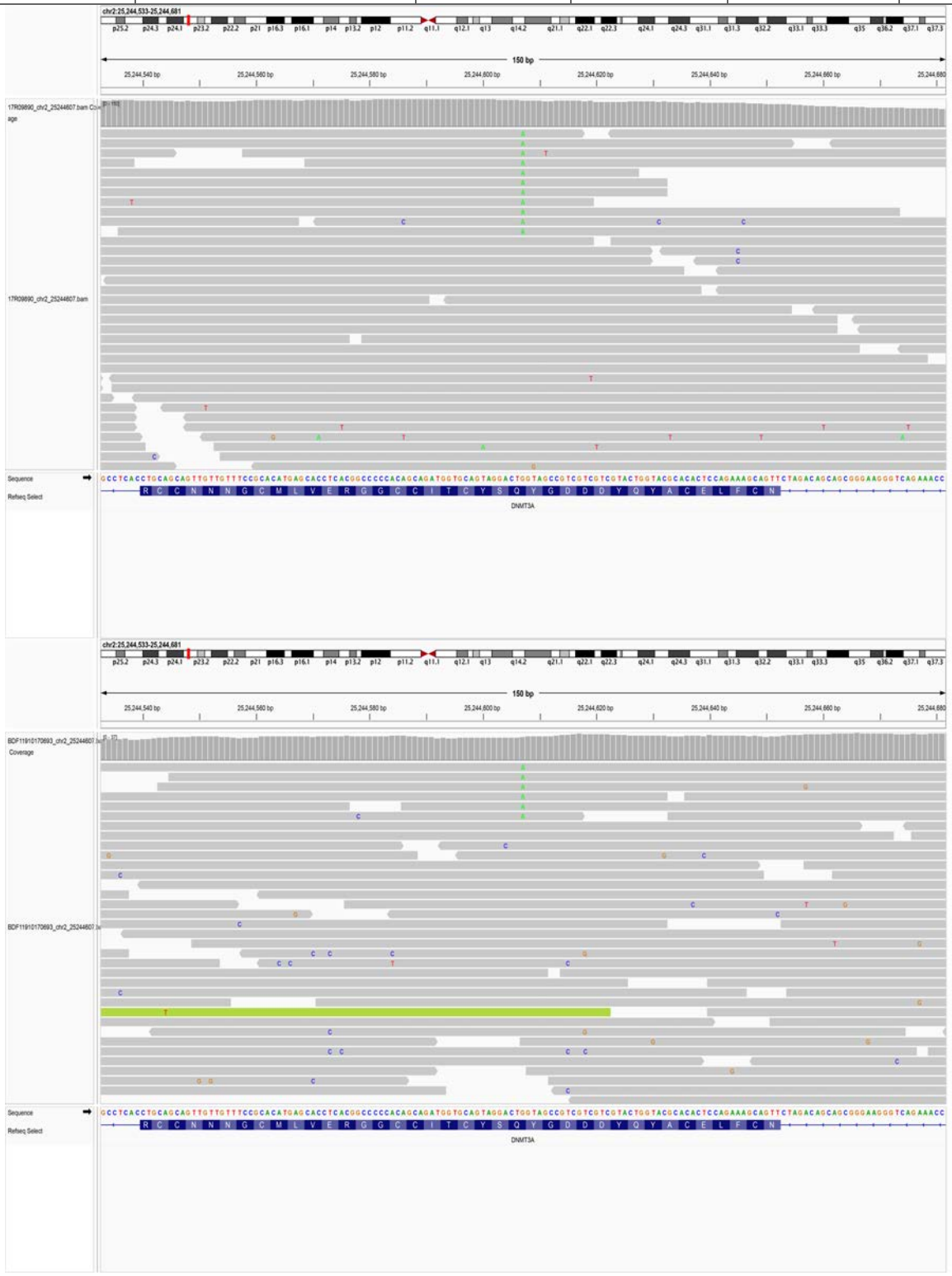
12.97. chr2_25244592_TGGTGCAGTAGGAC/-

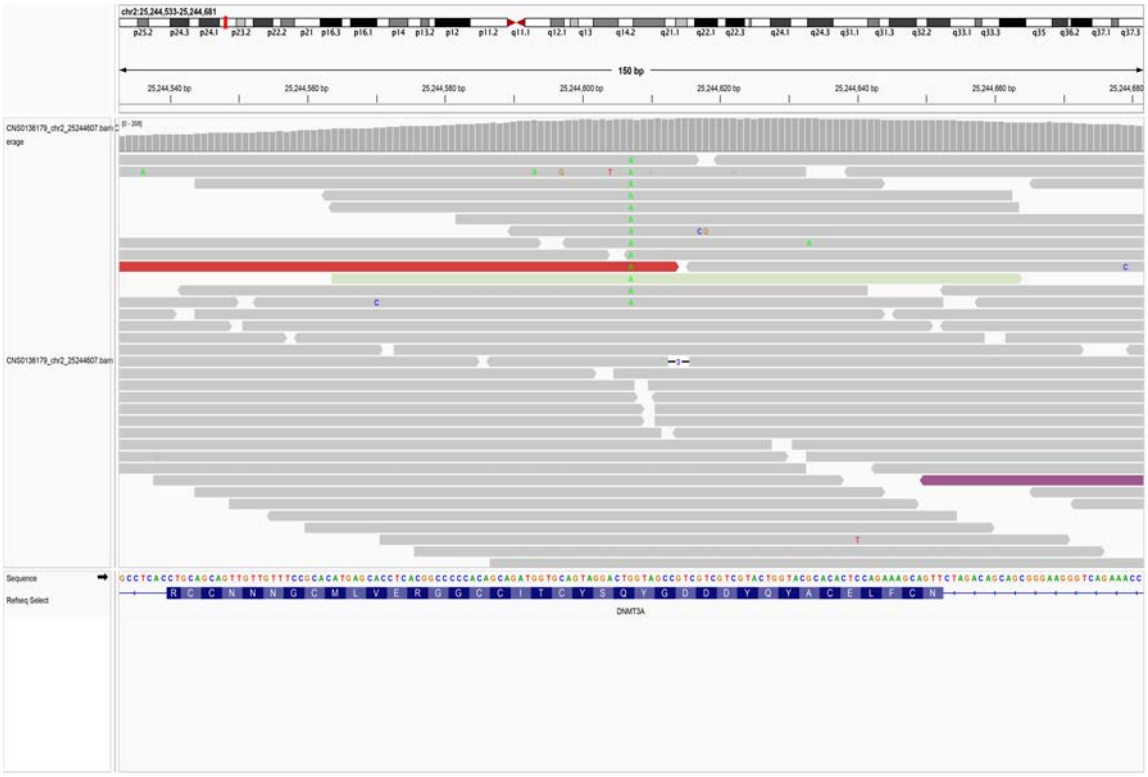
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HD27_72	chr2_25244592_TGGTGCAGTAGGAC/-	36	5	*DNMT3A*	frameshift_variant



12.98. chr2_25244607_G/A

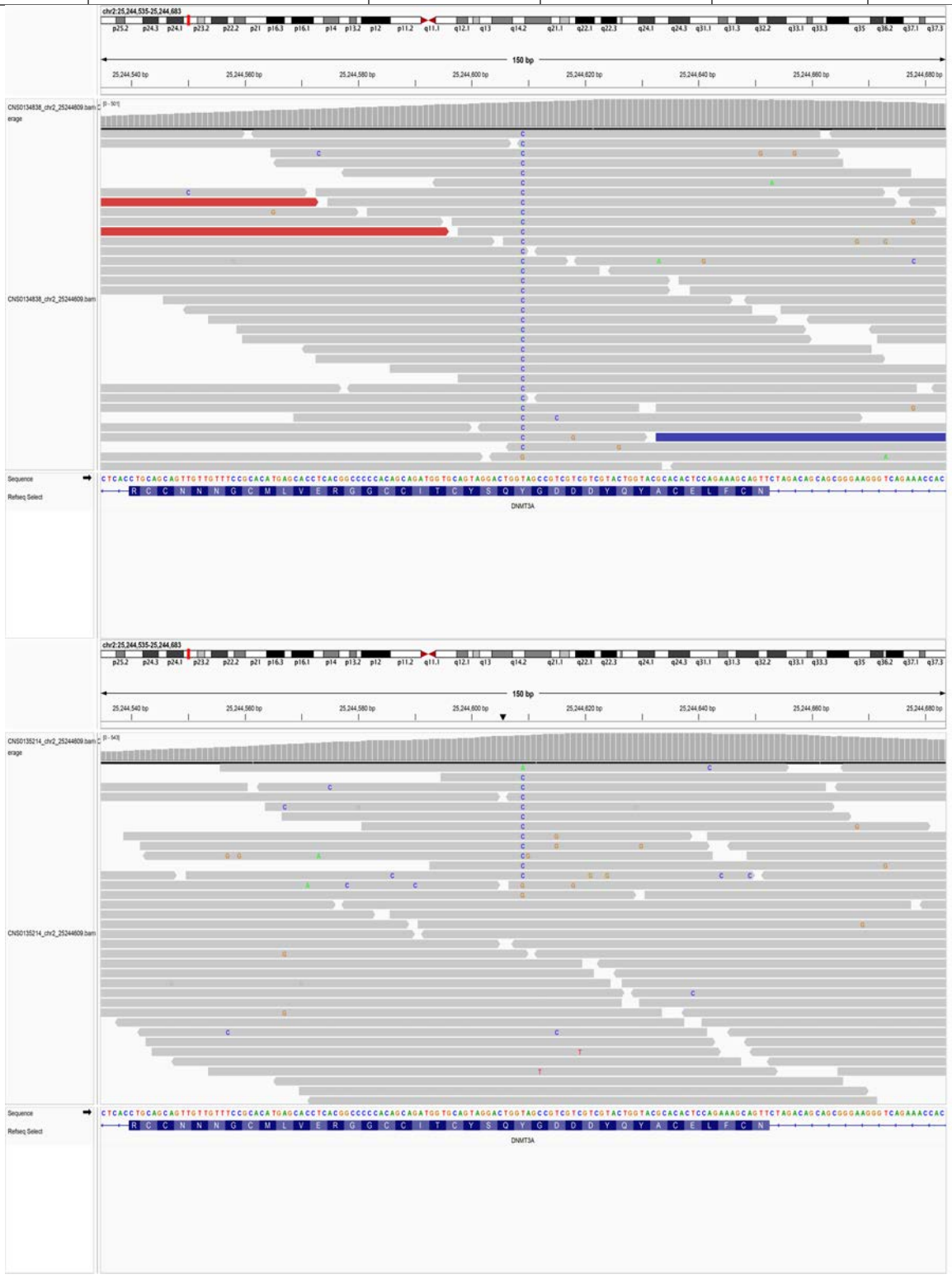
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09890	chr2_25244607_G/A	88	11	*DNMT3A*	stop_gained
BDF11910170693	chr2_25244607_G/A	24	6	*DNMT3A*	stop_gained
CNS0136179	chr2_25244607_G/A	182	11	*DNMT3A*	stop_gained




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
erage
CNS0136179_chr2_25244607.bam
Sequence
Refseq Select
DNMT3A

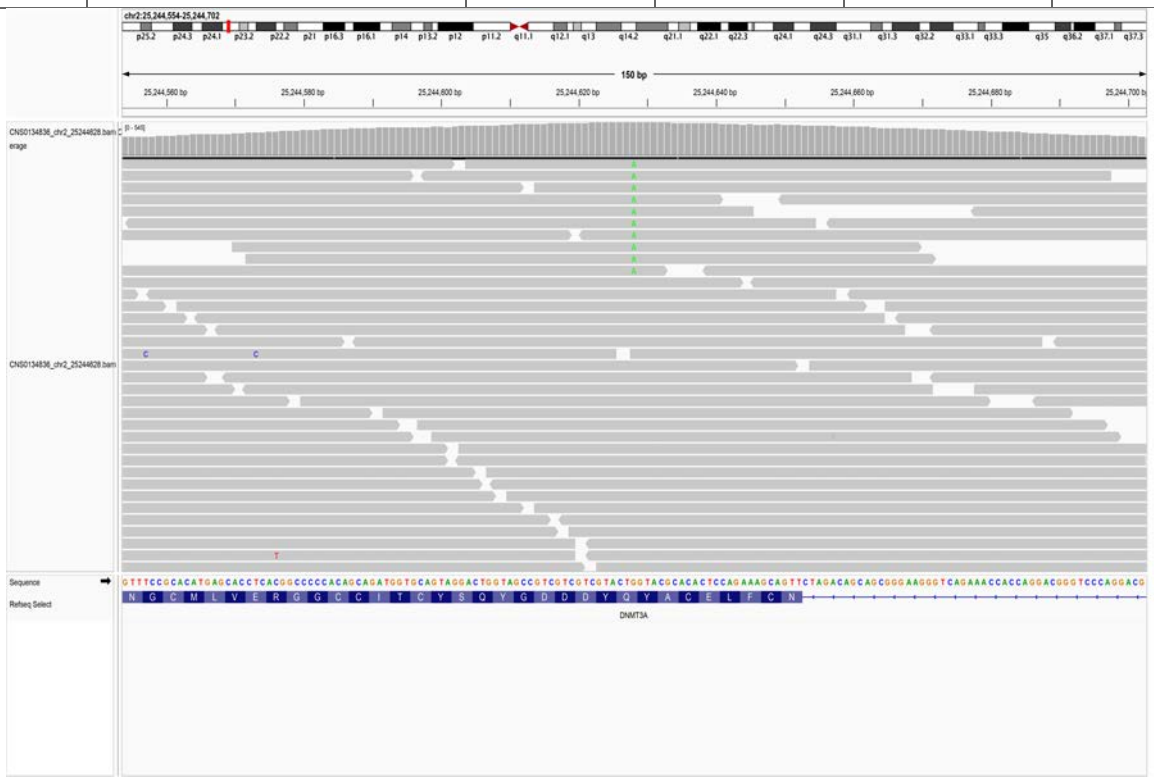
12.99. chr2_25244609_T/C

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



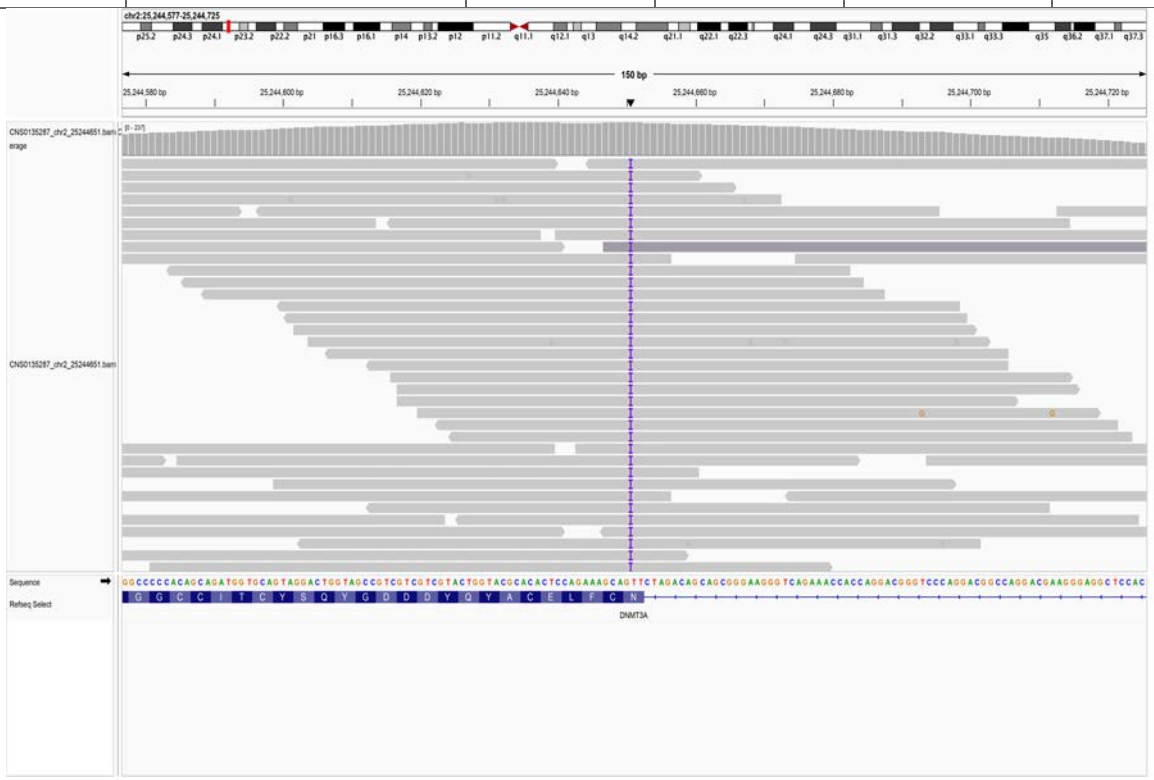
12.100. chr2_25244628_G/A

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



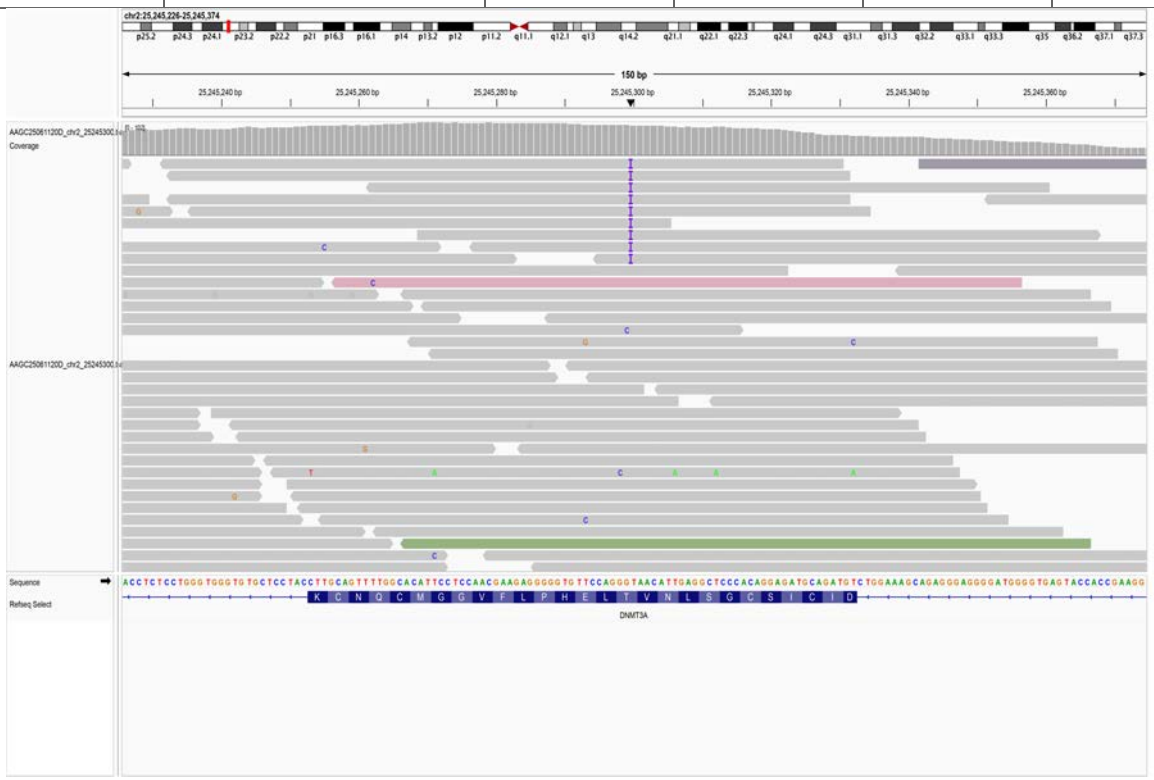
12.101. chr2_25244651_-/T

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



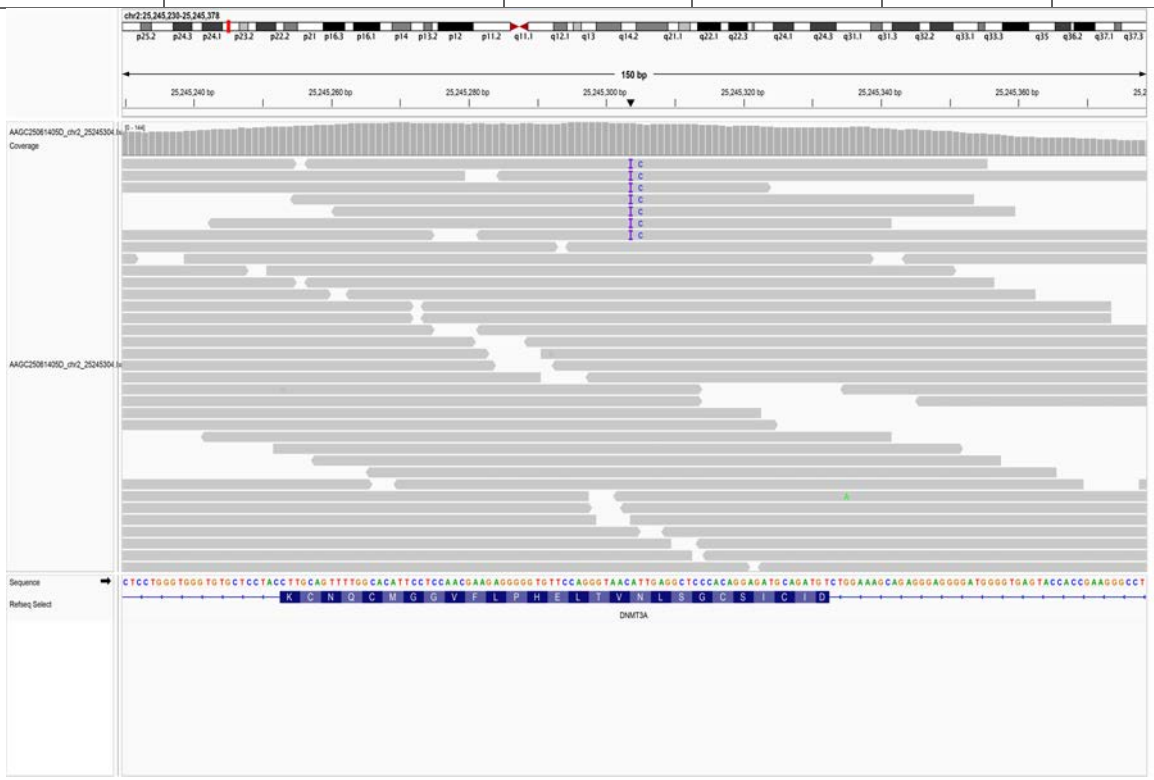
12.102. chr2_25245300_-/T

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



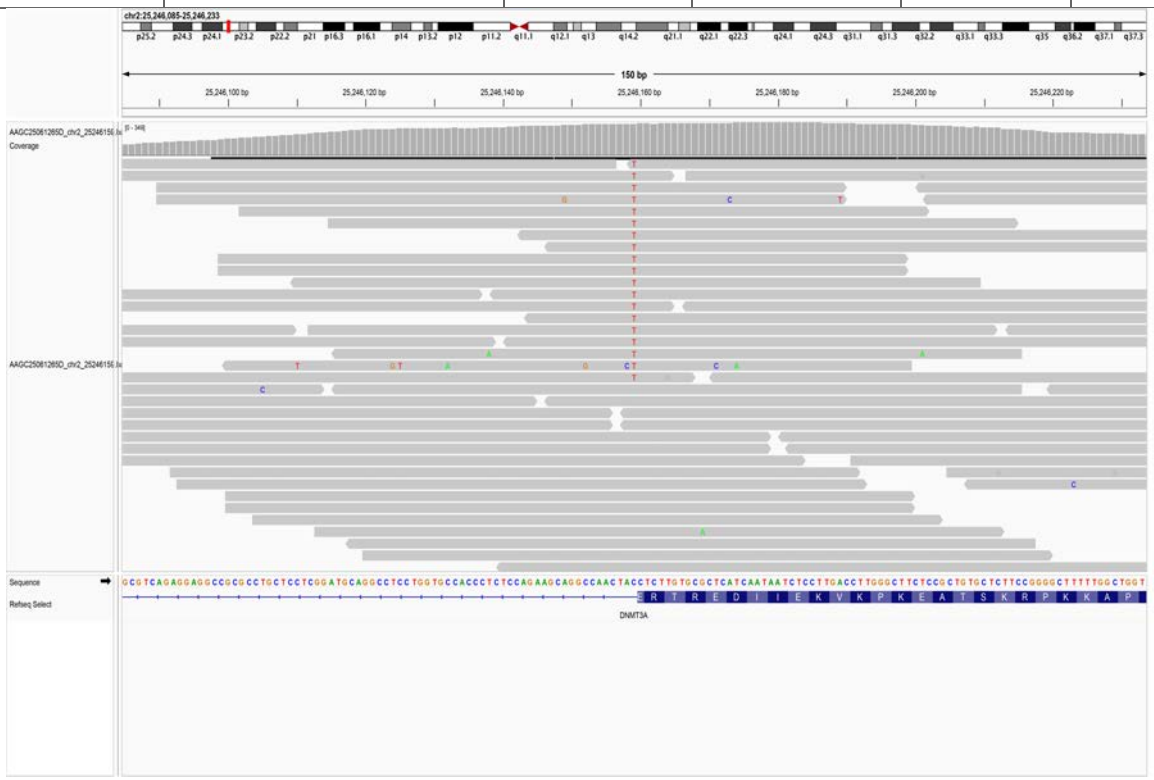
12.103. chr2_25245304_-/A

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



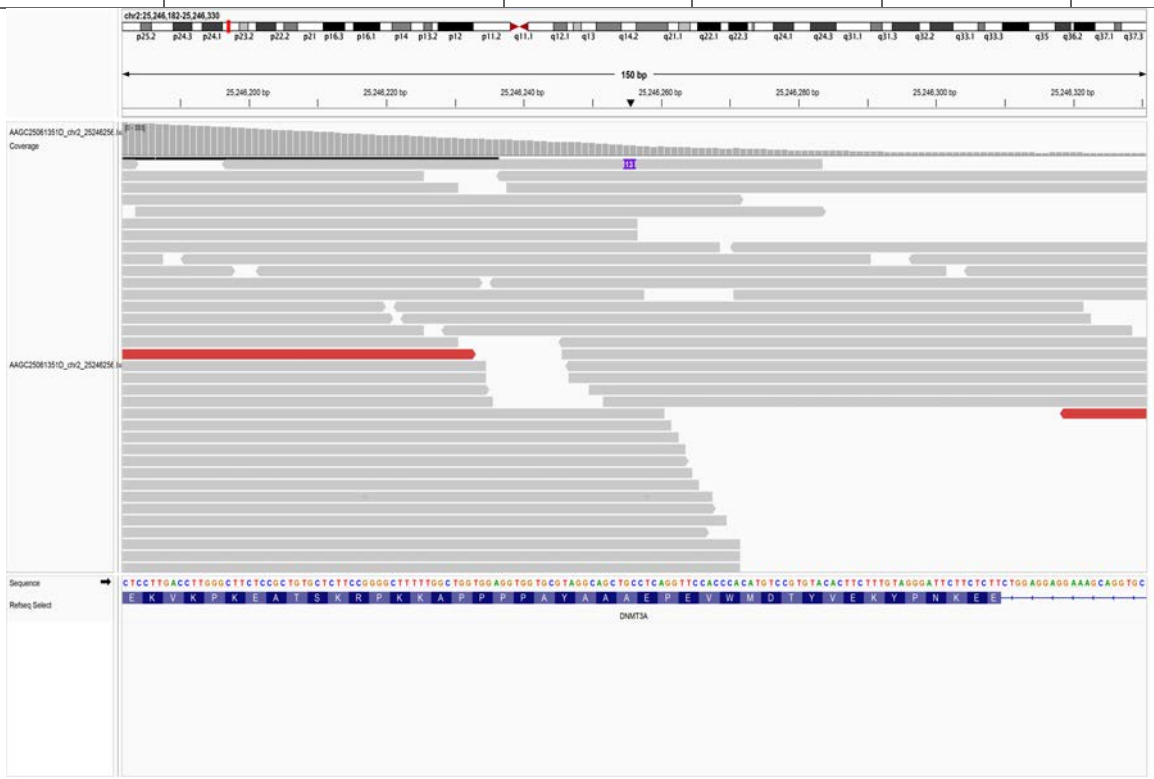
12.104. chr2_25246159_C/T

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



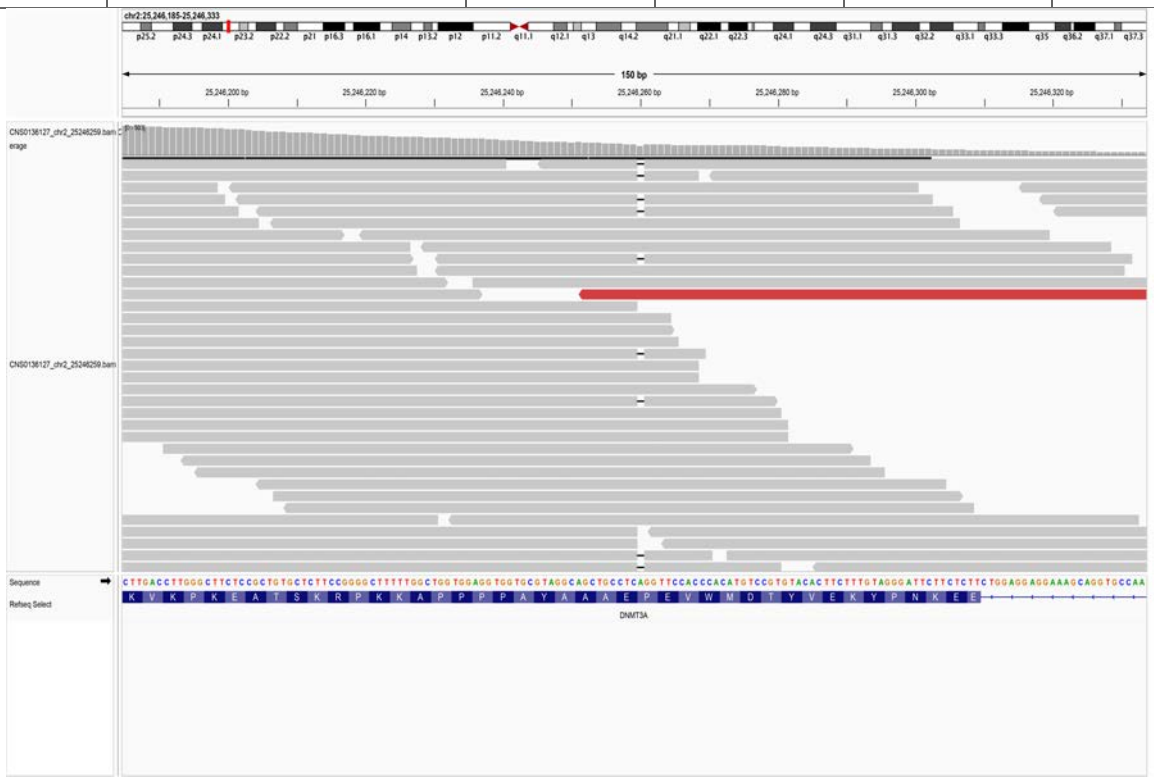
12.105. chr2_25246256_-/CCTCAGGTTCCCT

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



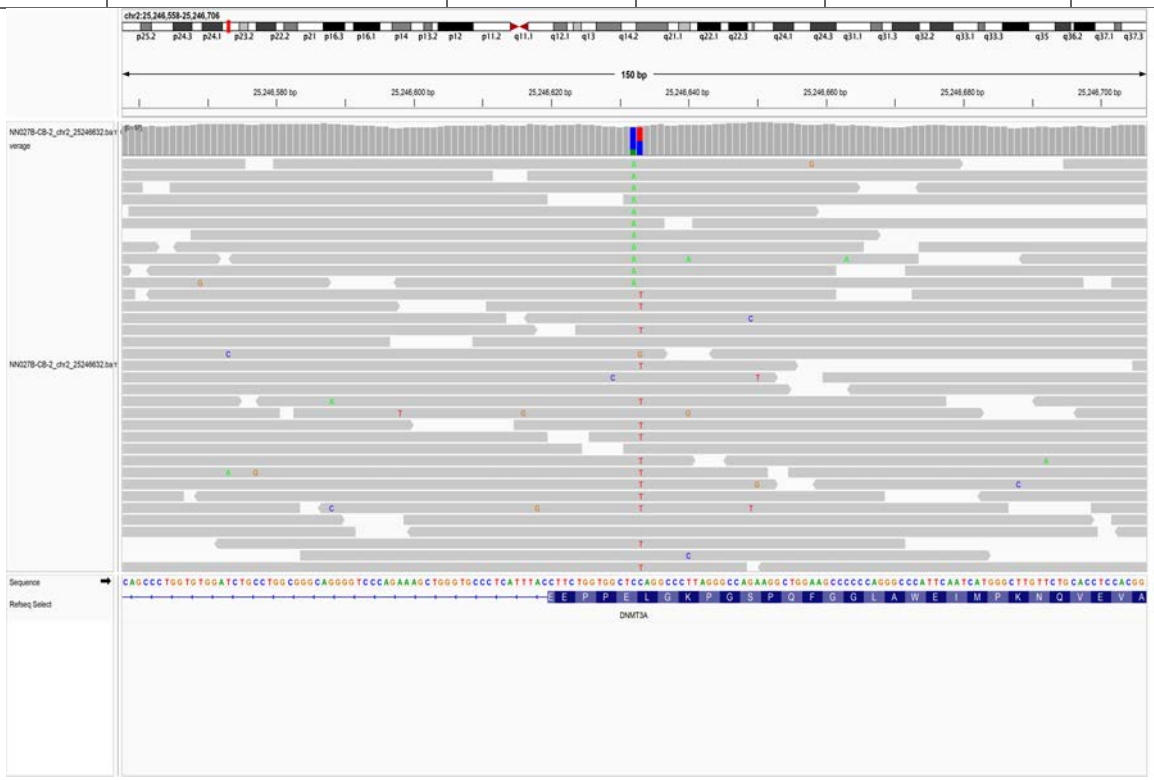
12.106. chr2_25246260_A/-

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



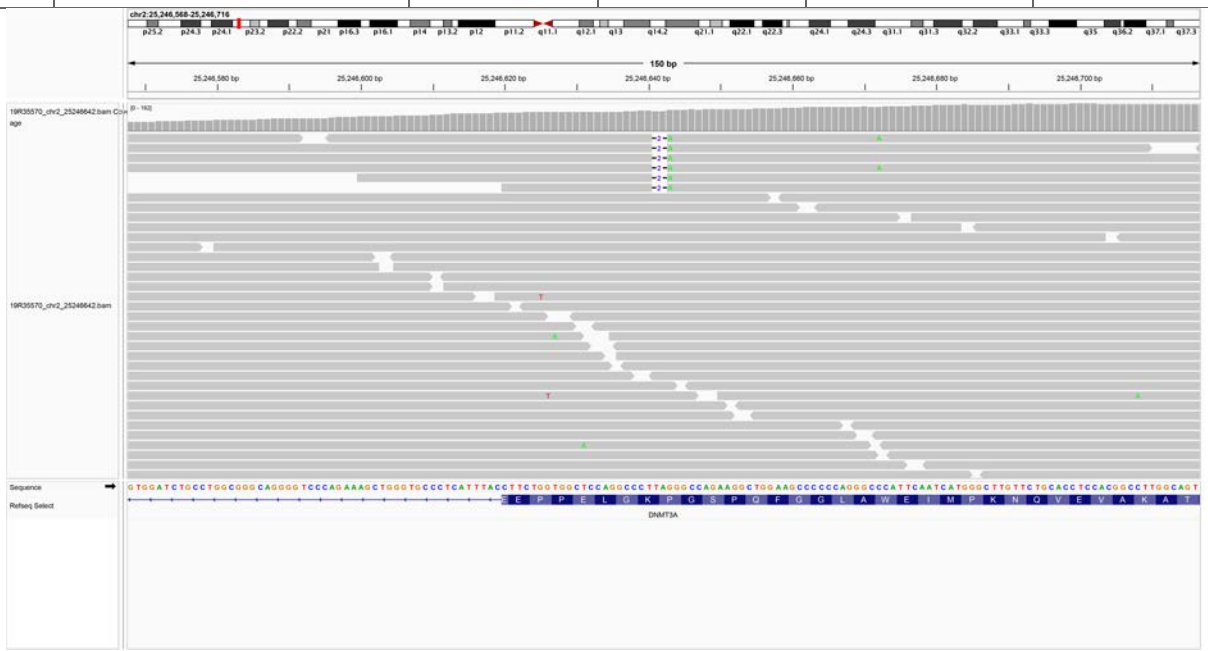
12.107. chr2_25246632_C/A

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



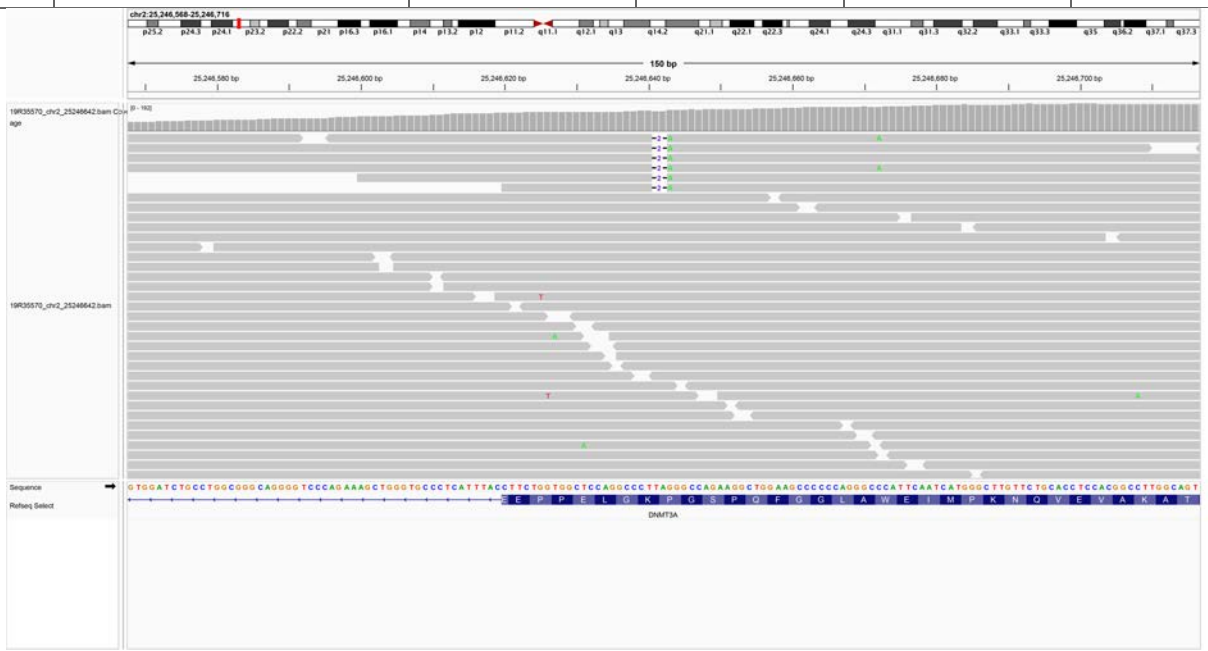
12.108. chr2_25246640_T/-

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



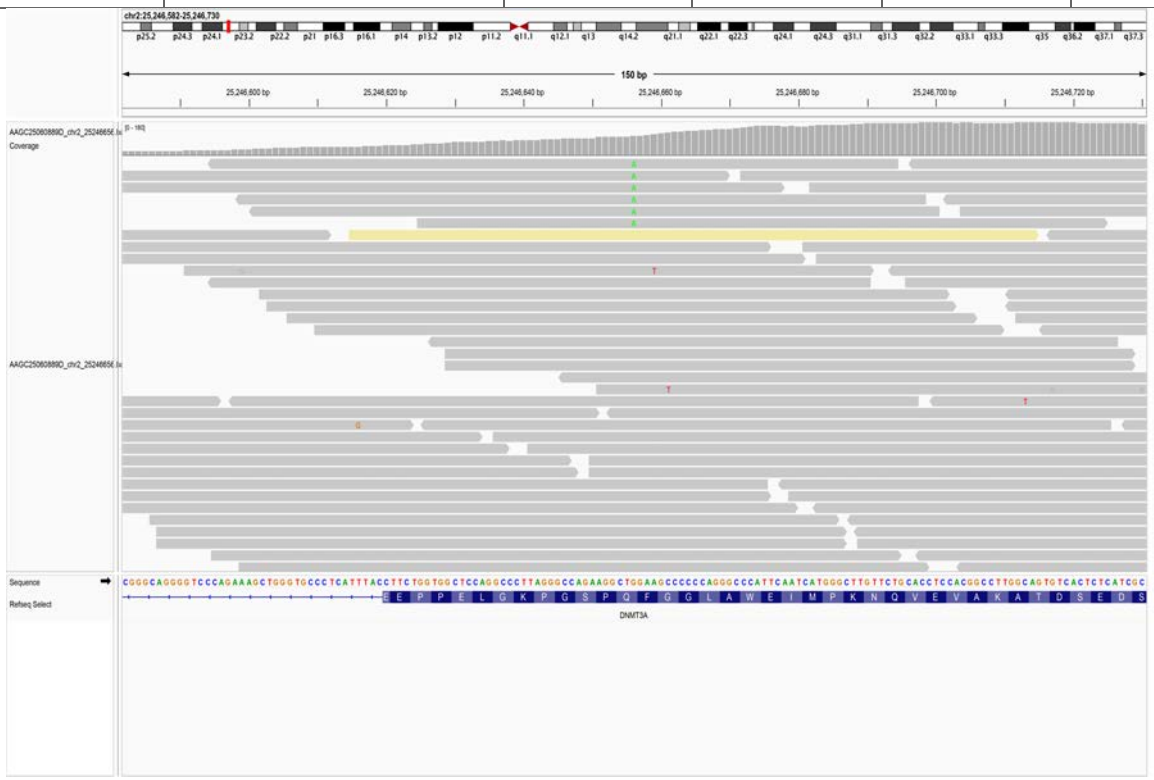
12.109. chr2_25246641_G/-

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



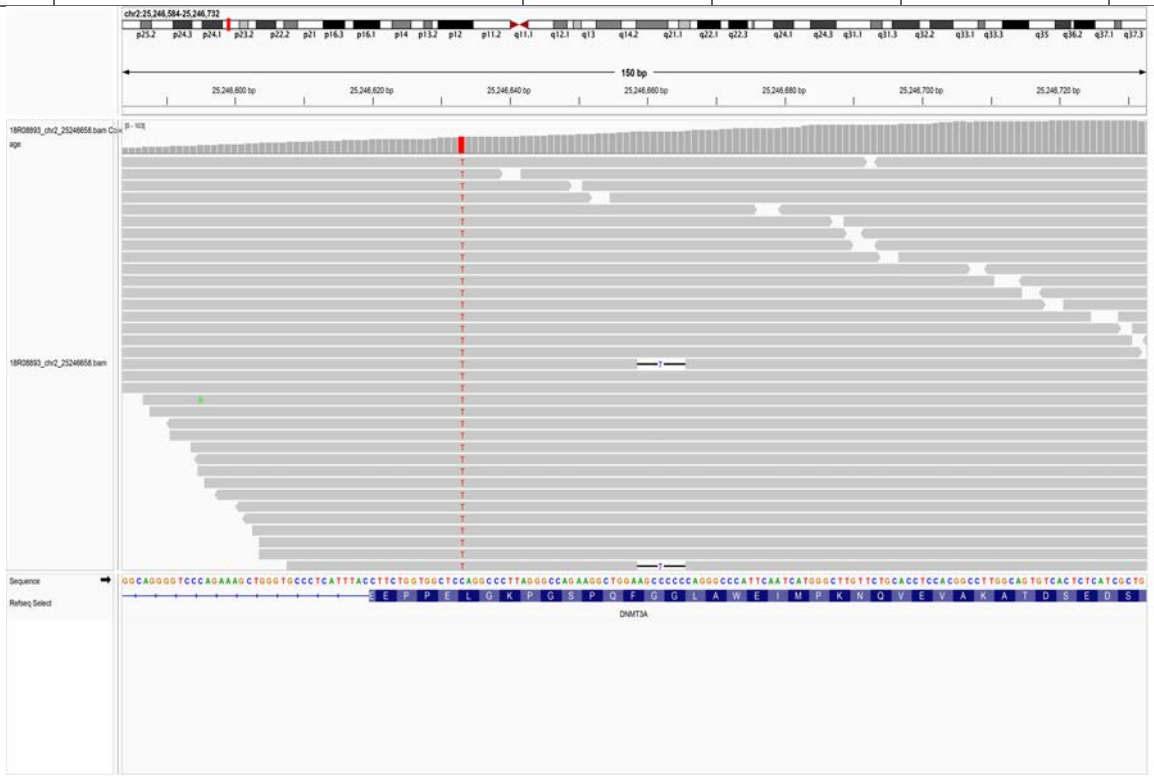
12.110. chr2_25246656_G/A

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



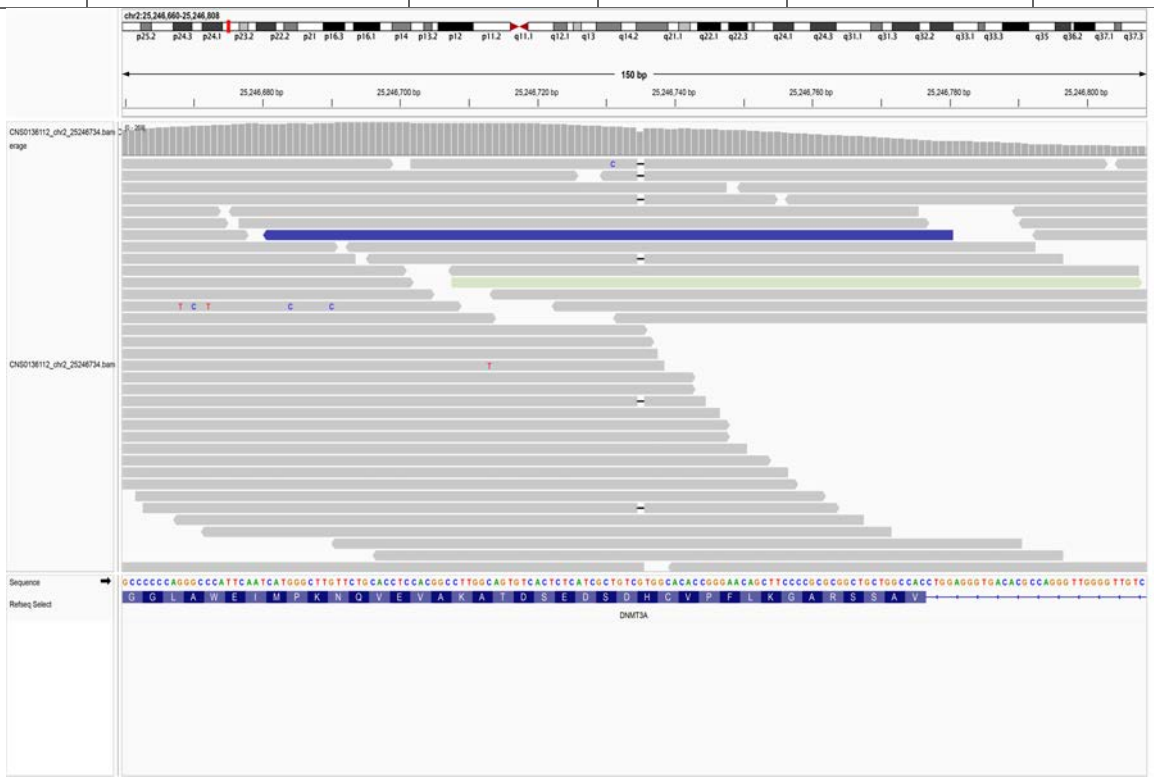
12.111. chr2_25246659_AGCCCCC/-

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



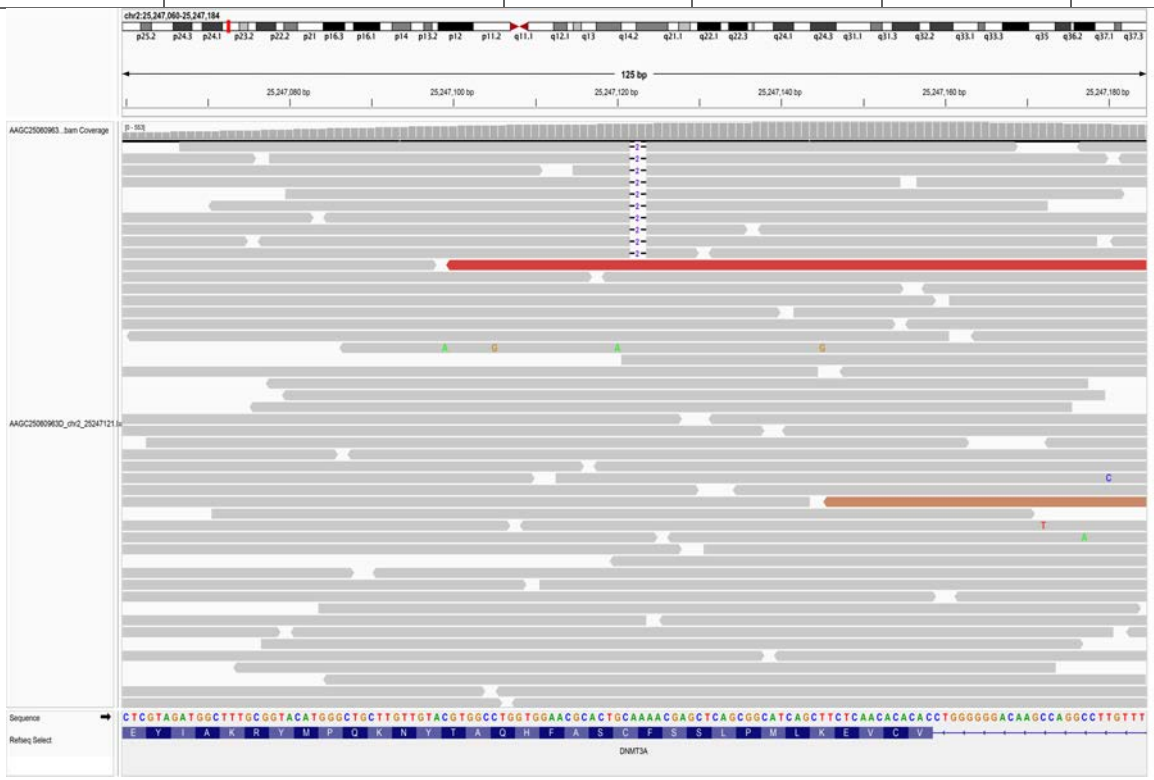
12.112. chr2_25246735_G/-

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



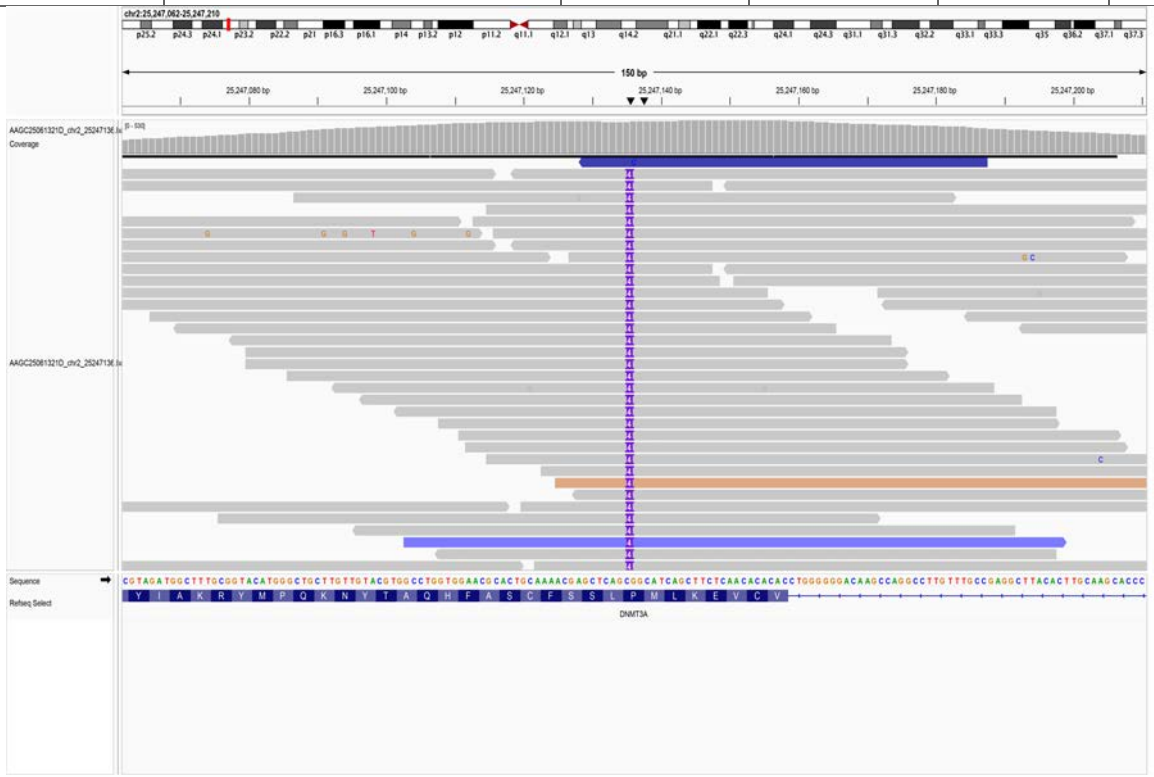
12.113. chr2_25247122_AA/-

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



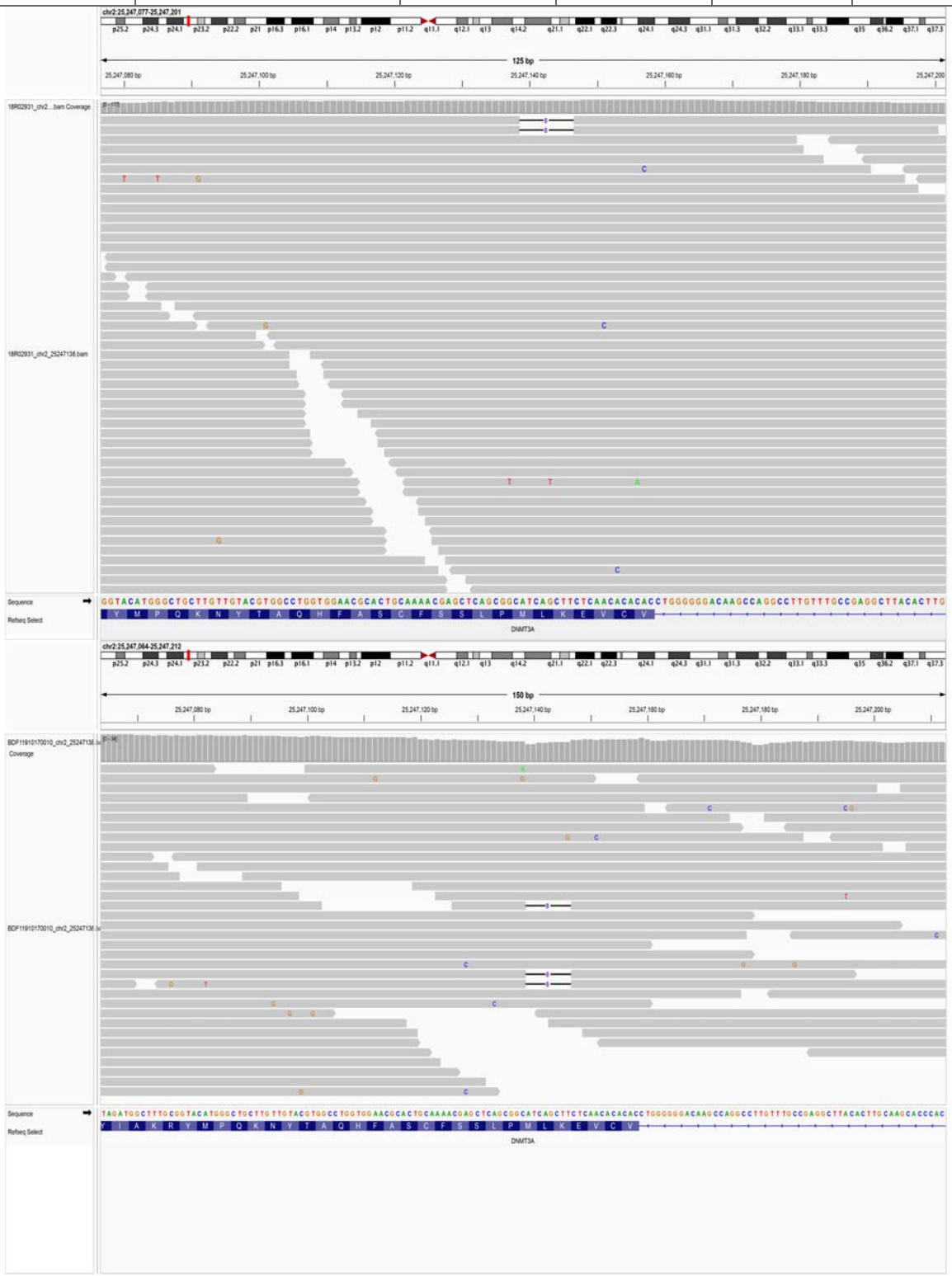
12.114. chr2_25247136_-/GGCA

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



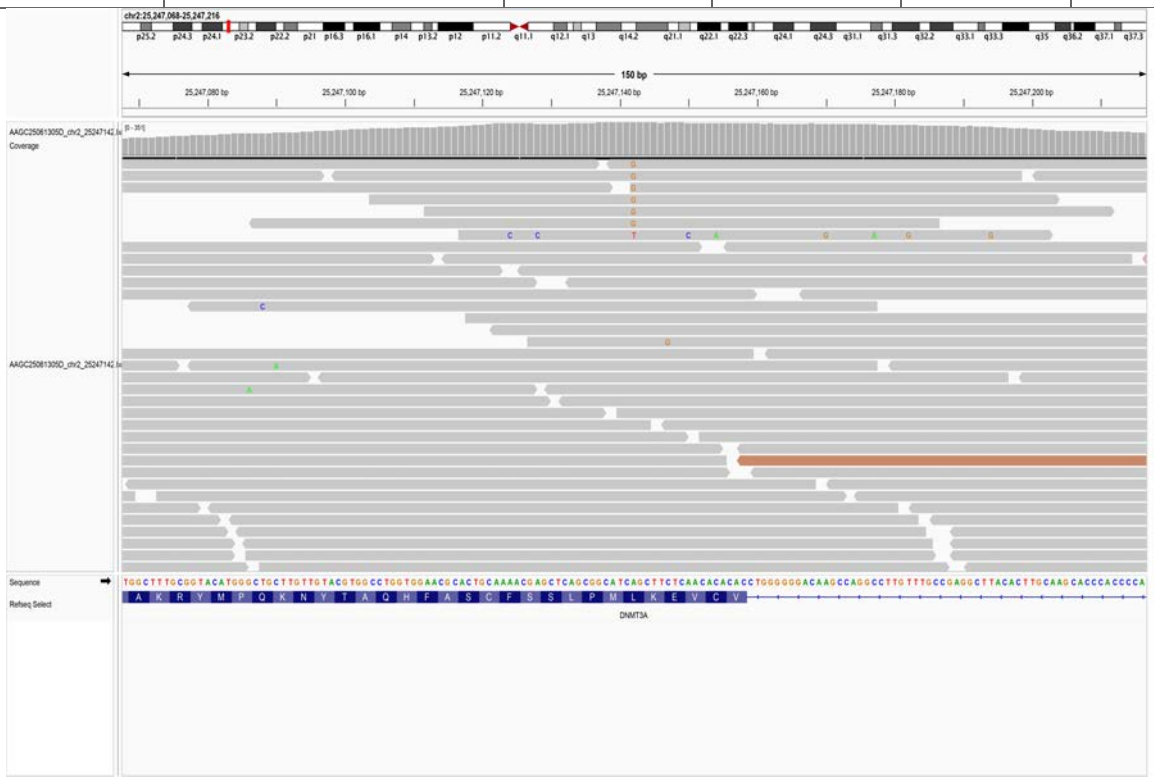
12.115. chr2_25247139_ATCAGCTT/-

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



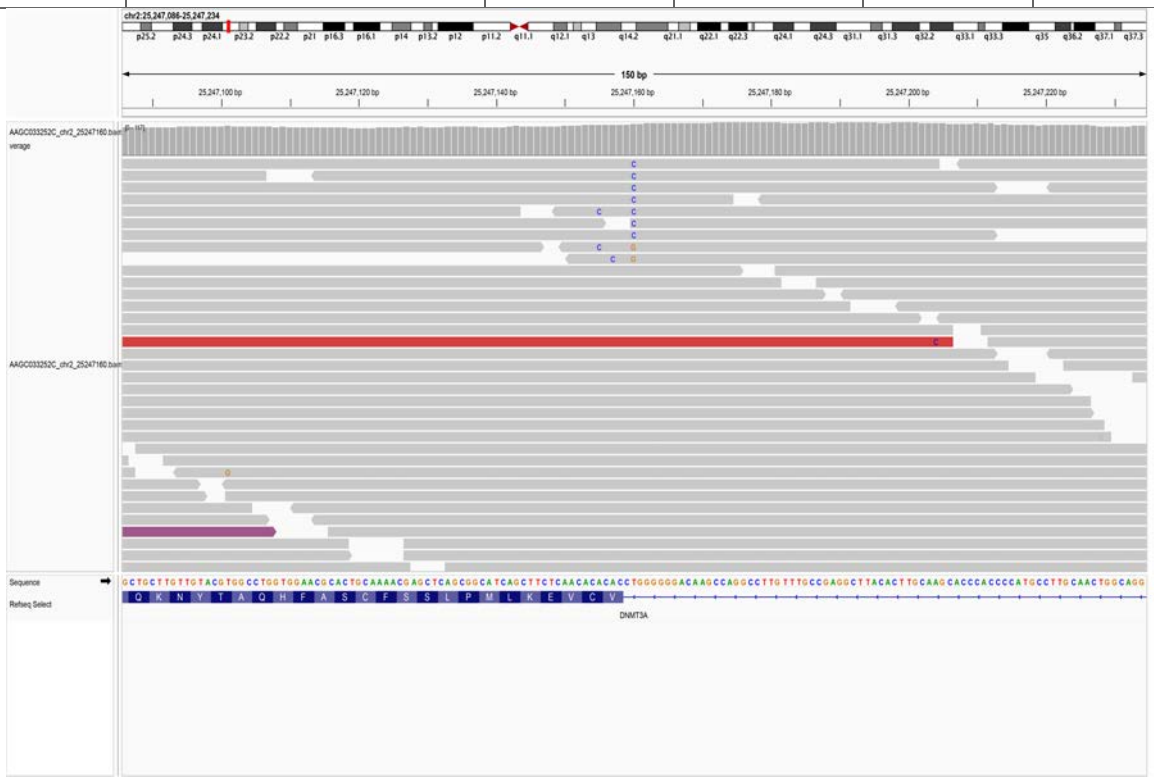
12.116. chr2_25247142_A/G

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



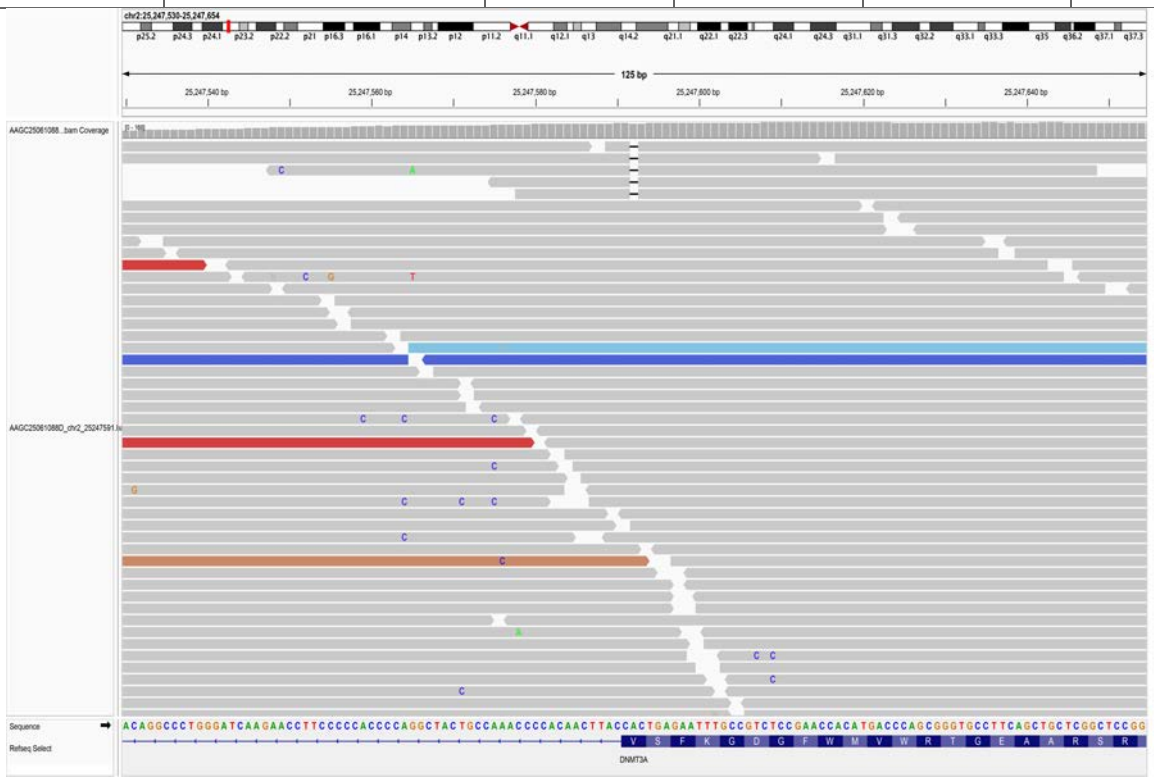
12.117. chr2_25247160_T/C

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



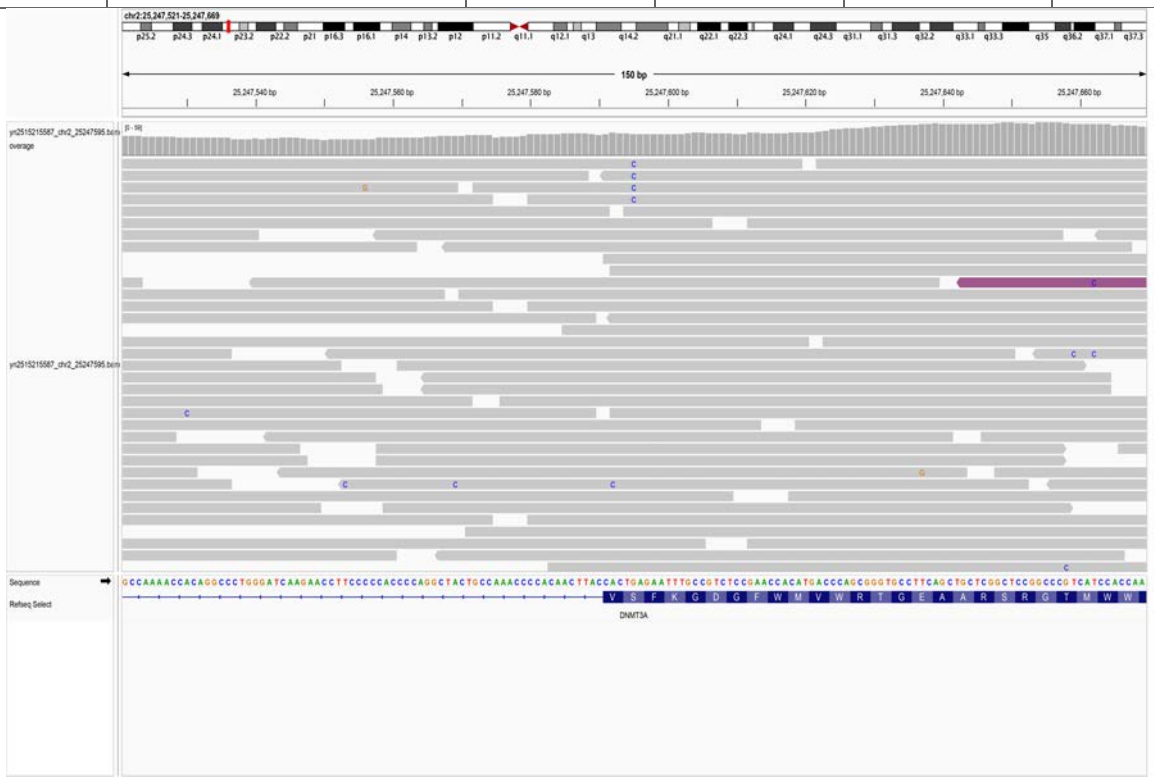
12.118. chr2_25247592_A/-

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



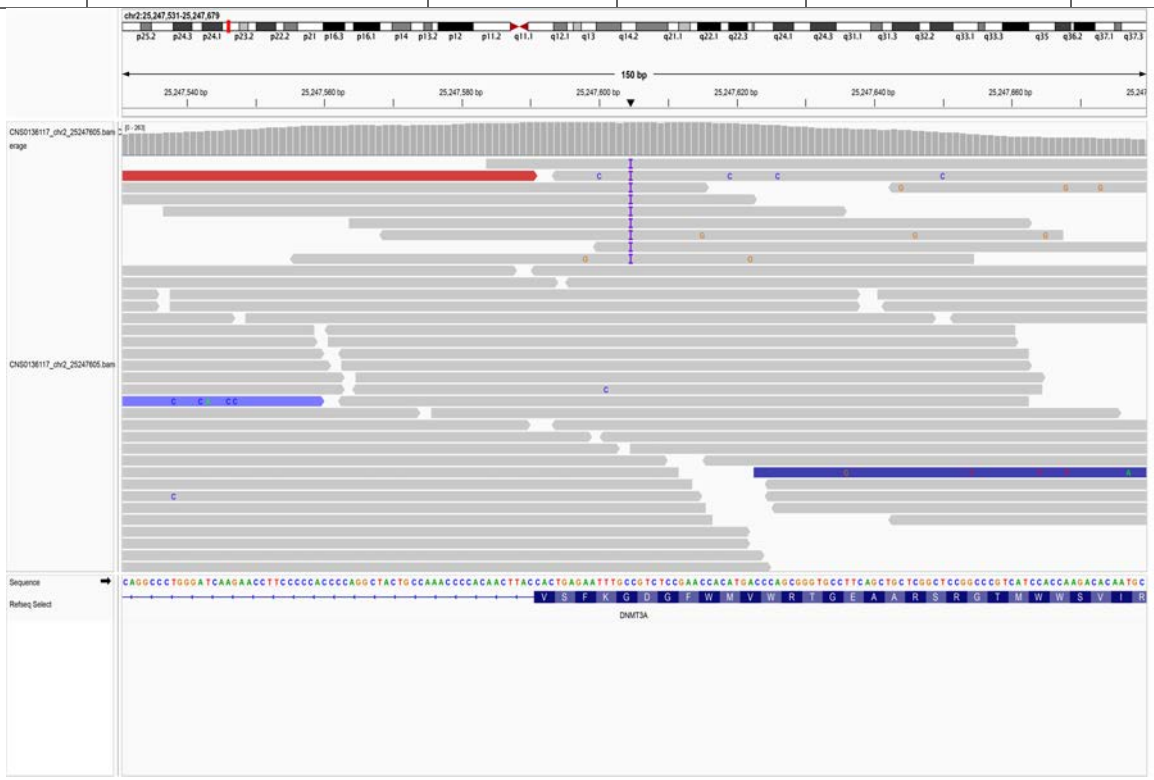
12.119. chr2_25247595_G/C

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



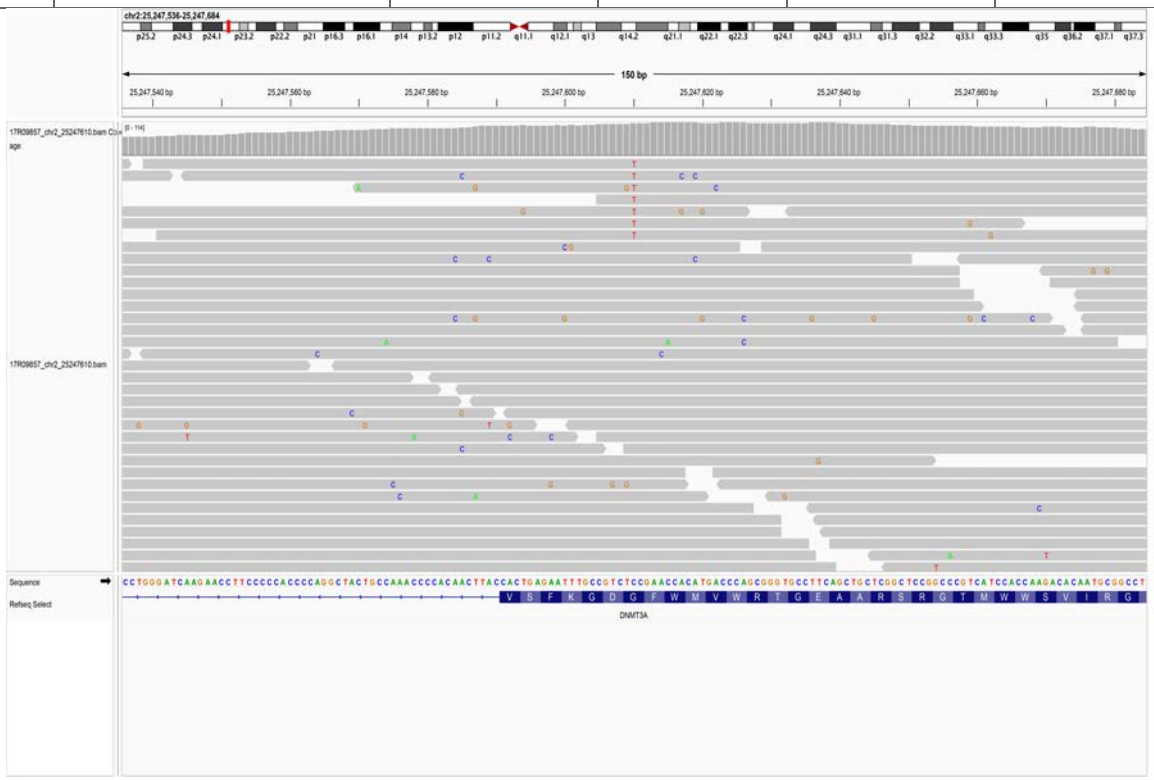
12.120. chr2_25247605_-/G

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



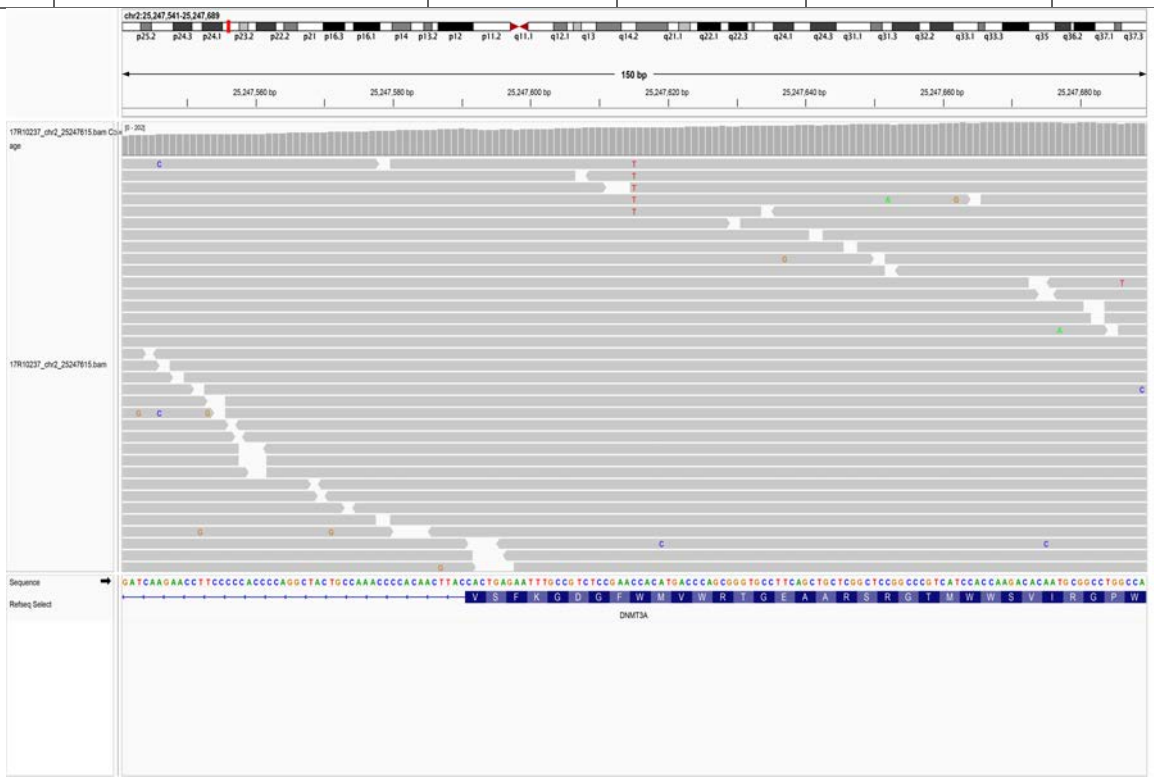
12.121. chr2_25247610_C/T

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



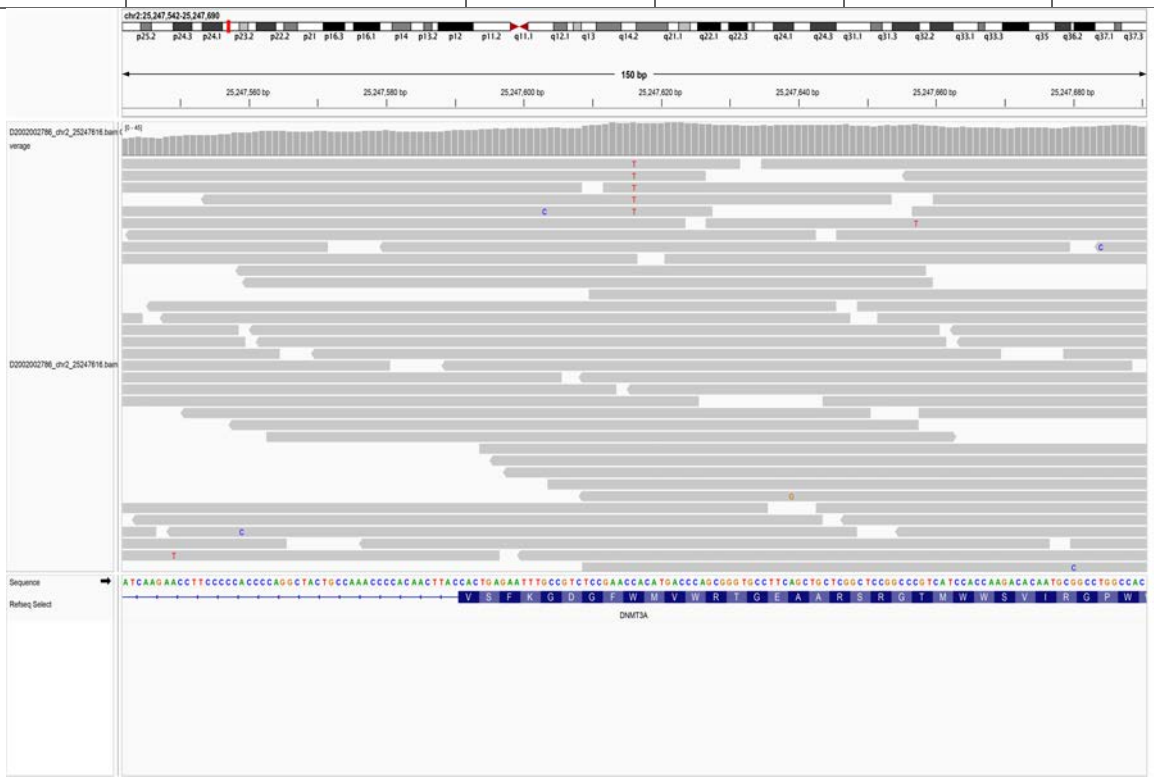
12.122. chr2_25247615_C/T

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



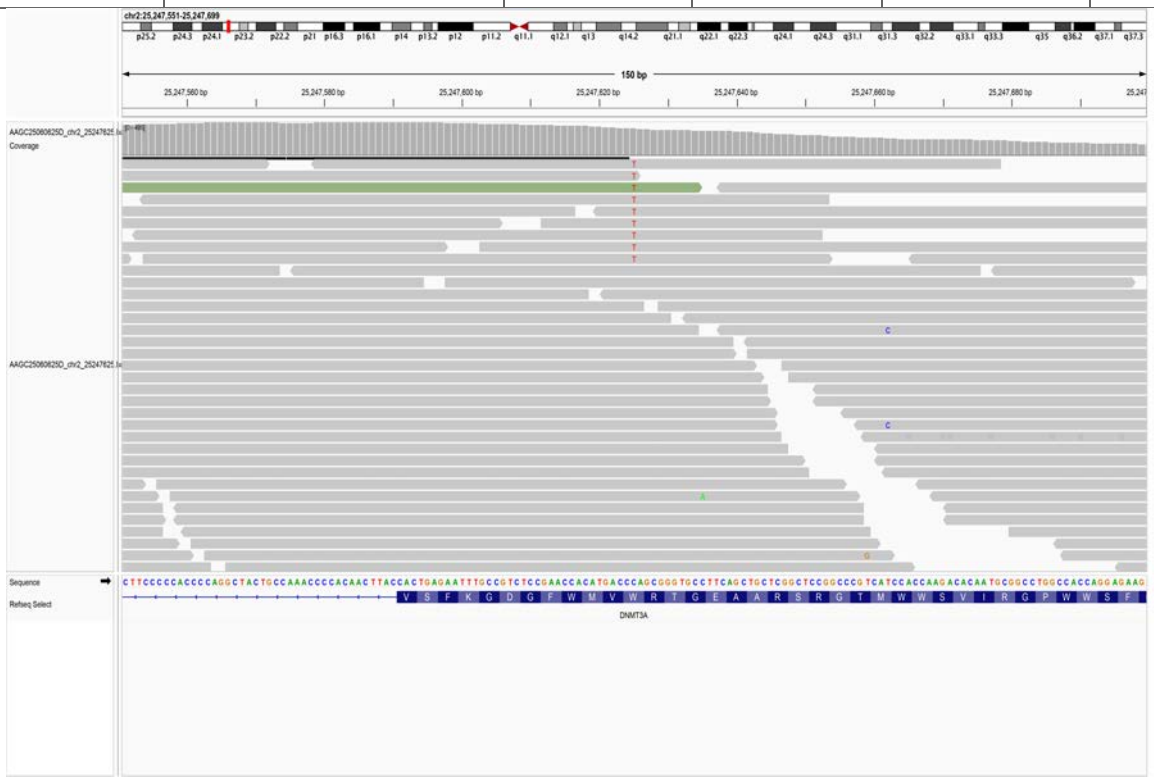
12.123. chr2_25247616_C/T

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



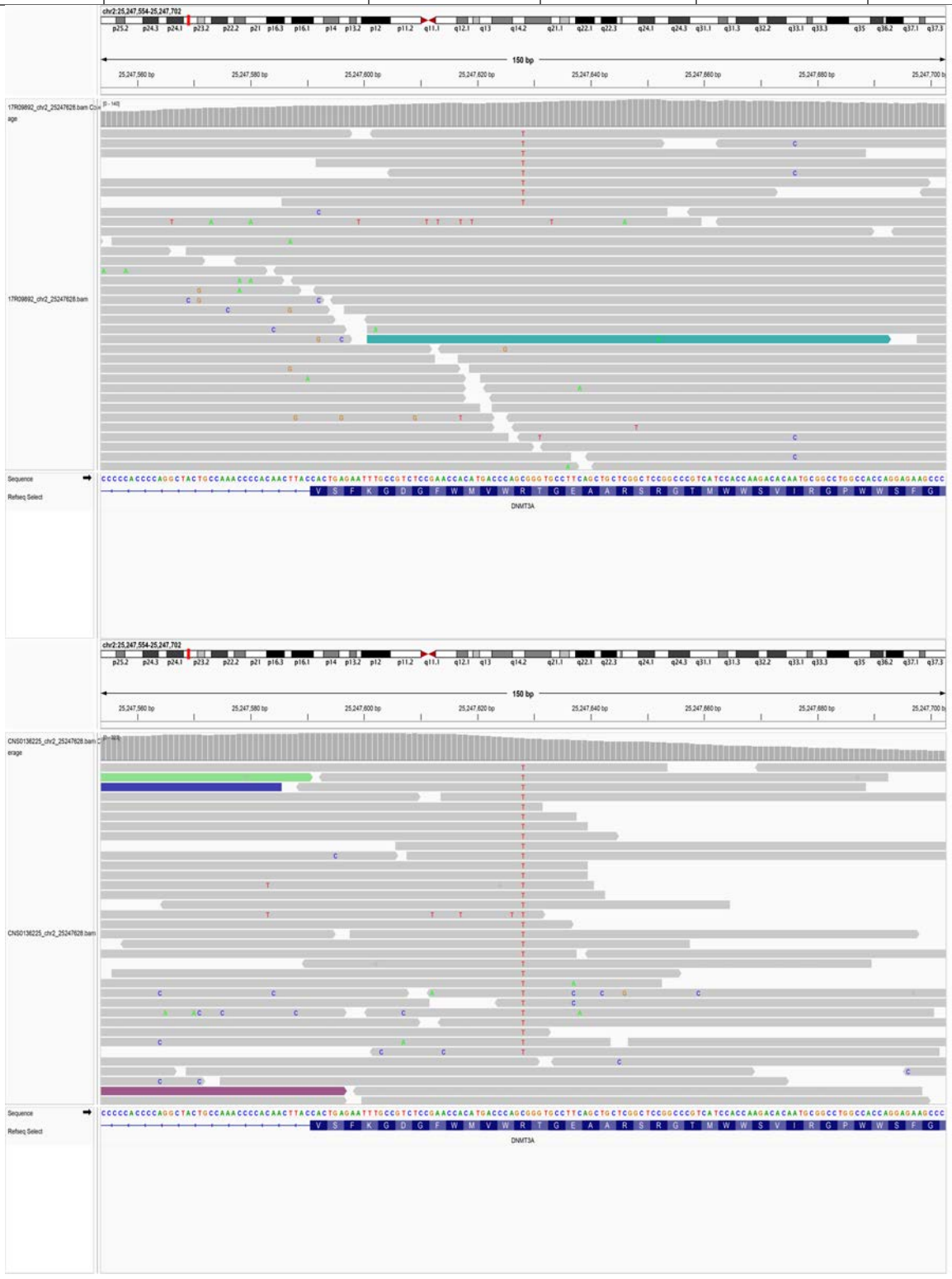
12.124. chr2_25247625_C/T

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



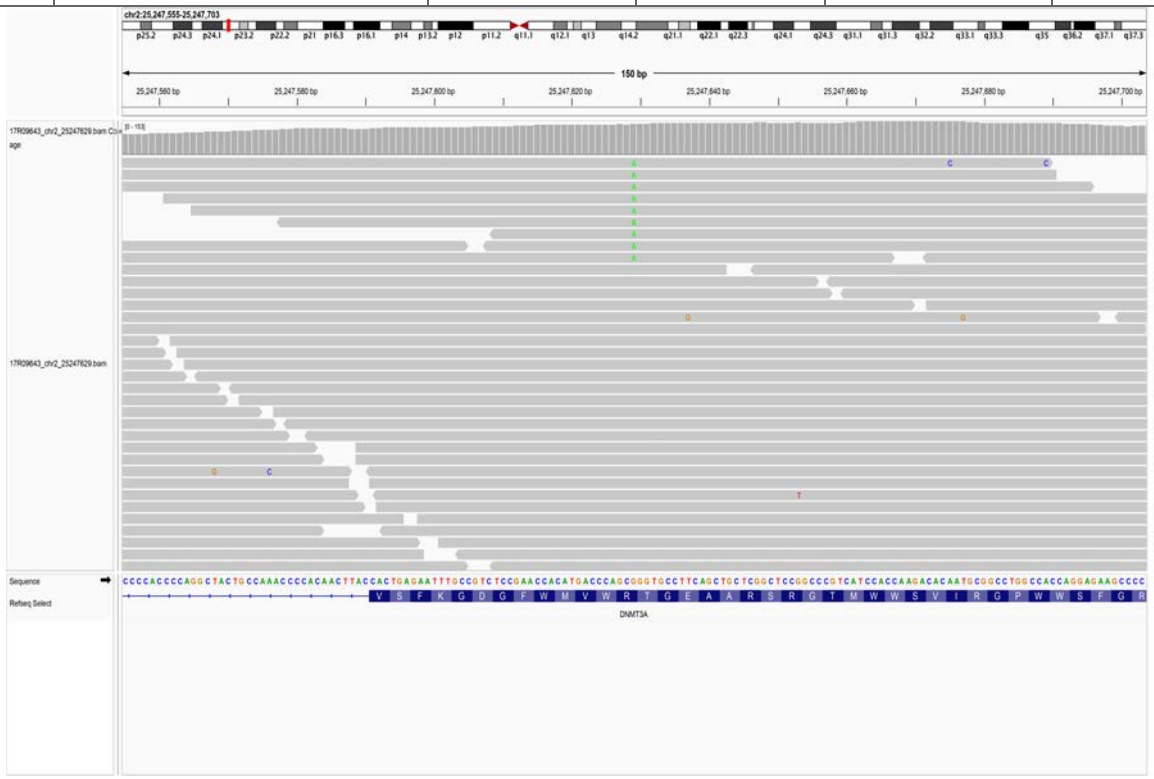
12.125. chr2_25247628_C/T

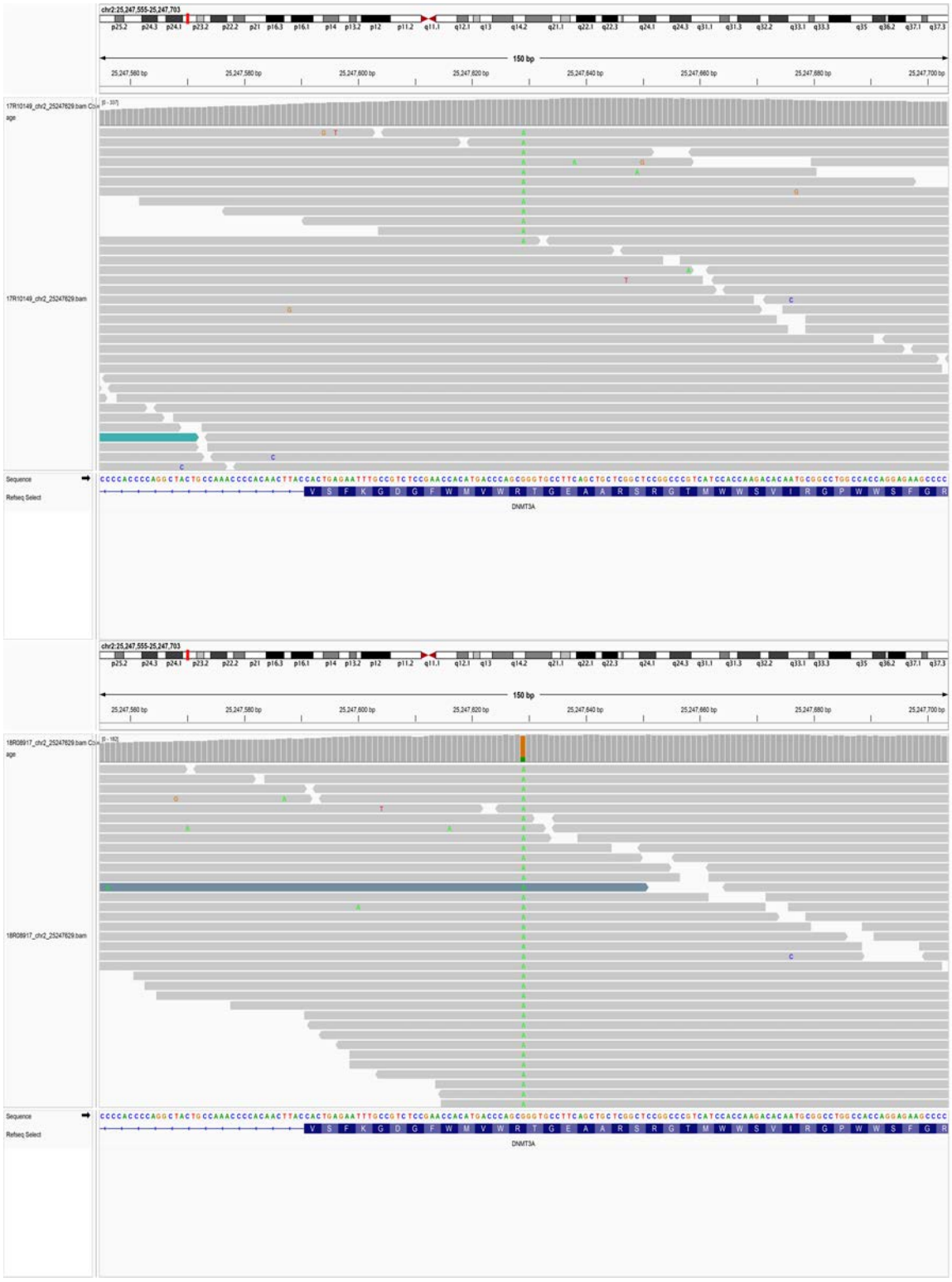
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09892	chr2_25247628_C/T	100	8	*DNMT3A*	missense_variant
CNS0136225	chr2_25247628_C/T	226	27	*DNMT3A*	missense_variant

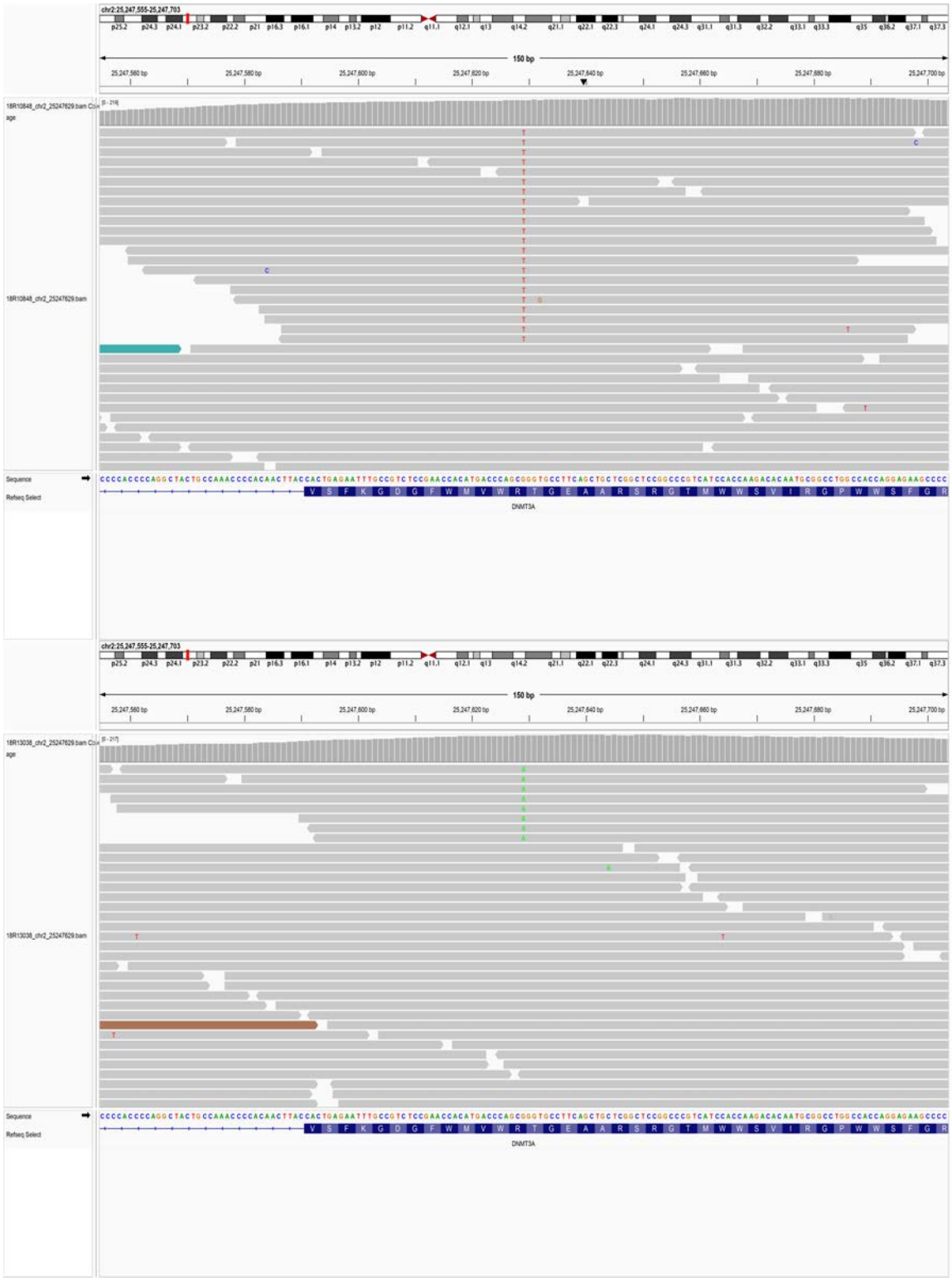


12.126. chr2_25247629_G/A/T

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

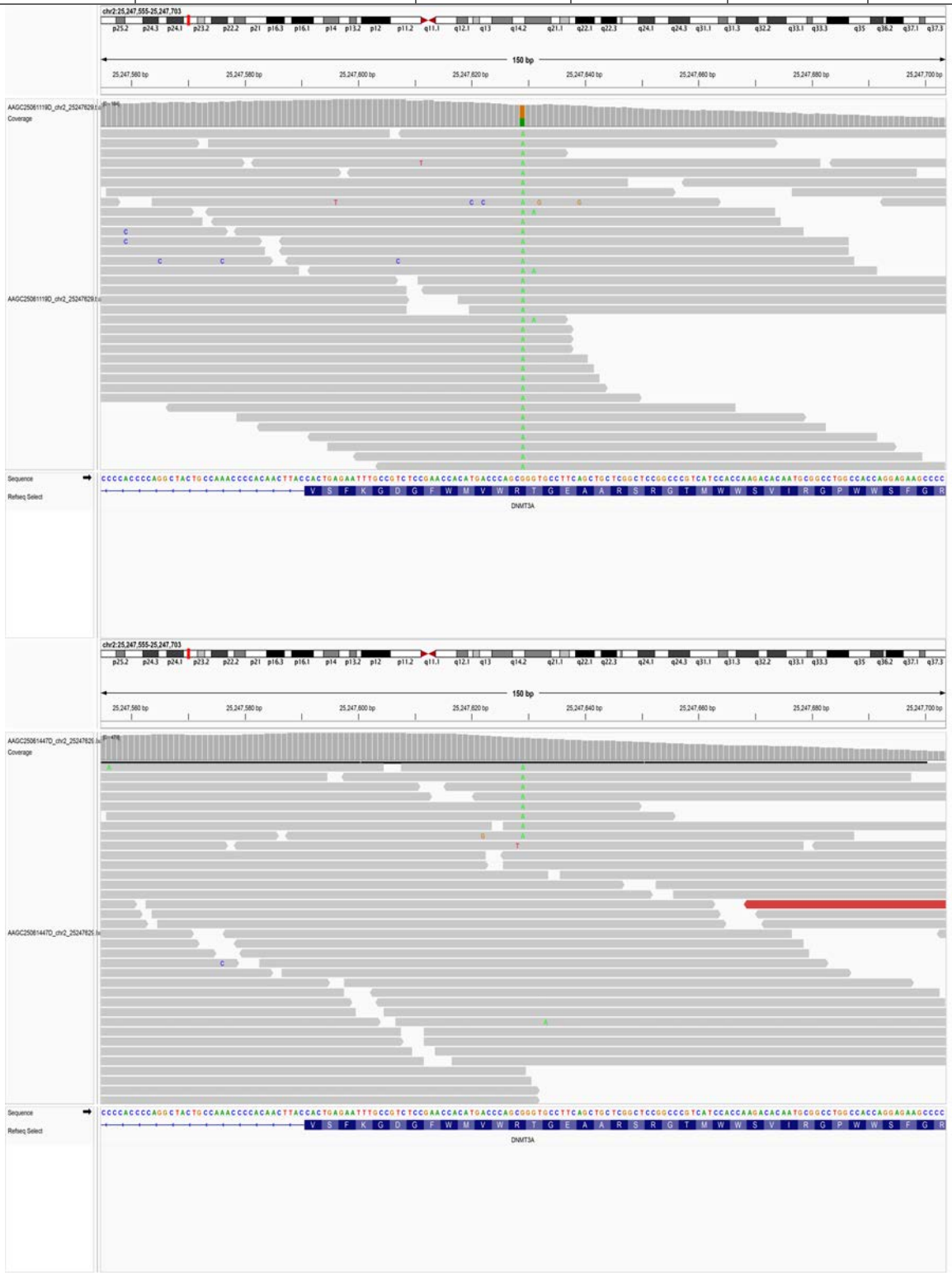


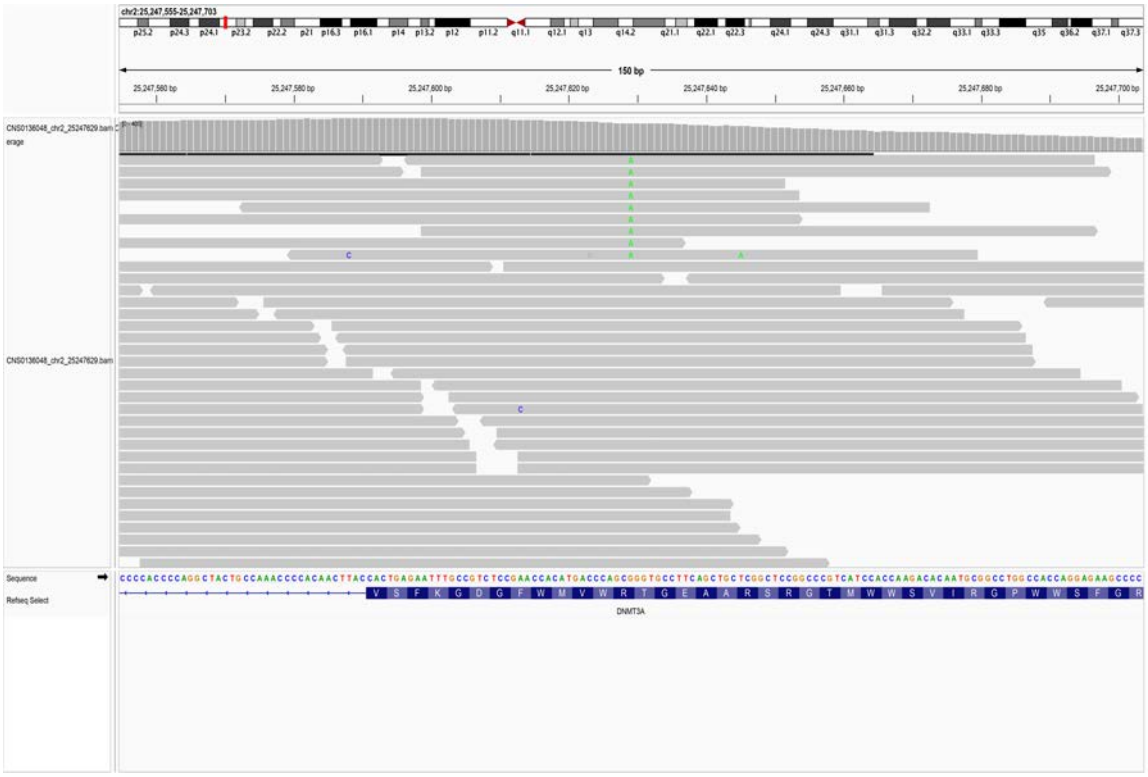

chr2:25,247,555-25,247,703
150 bp
25,247,560 bp
25,247,580 bp
25,247,600 bp
25,247,620 bp
25,247,640 bp
25,247,660 bp
25,247,680 bp
25,247,700 bp
17R10149_chr2_25247629.bam Coverage
17R10149_chr2_25247629.bam
Sequence
Refseq Select
DNMT3A
18R08917_chr2_25247629.bam Coverage
18R08917_chr2_25247629.bam


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

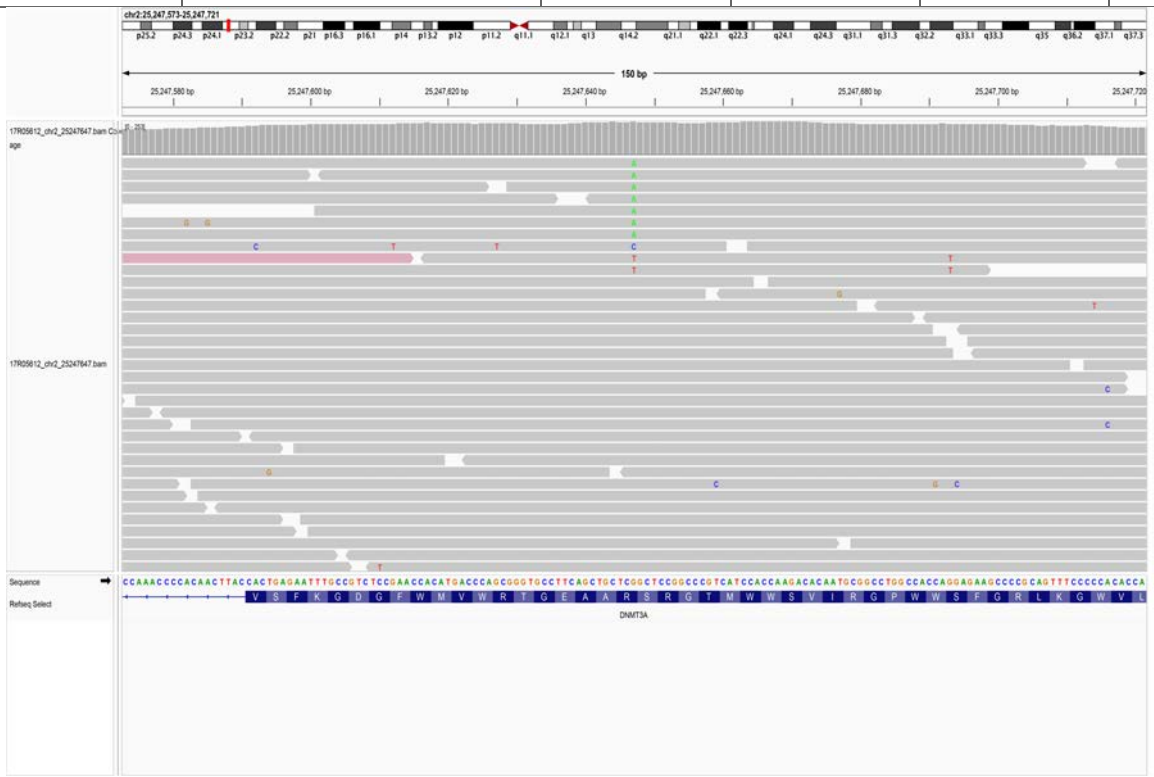
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061119D	chr2_25247629_G/A	83	53	*DNMT3A*	missense_variant
AAGC25061447D	chr2_25247629_G/A	379	10	*DNMT3A*	missense_variant
CNS0136048	chr2_25247629_G/A	327	9	*DNMT3A*	missense_variant

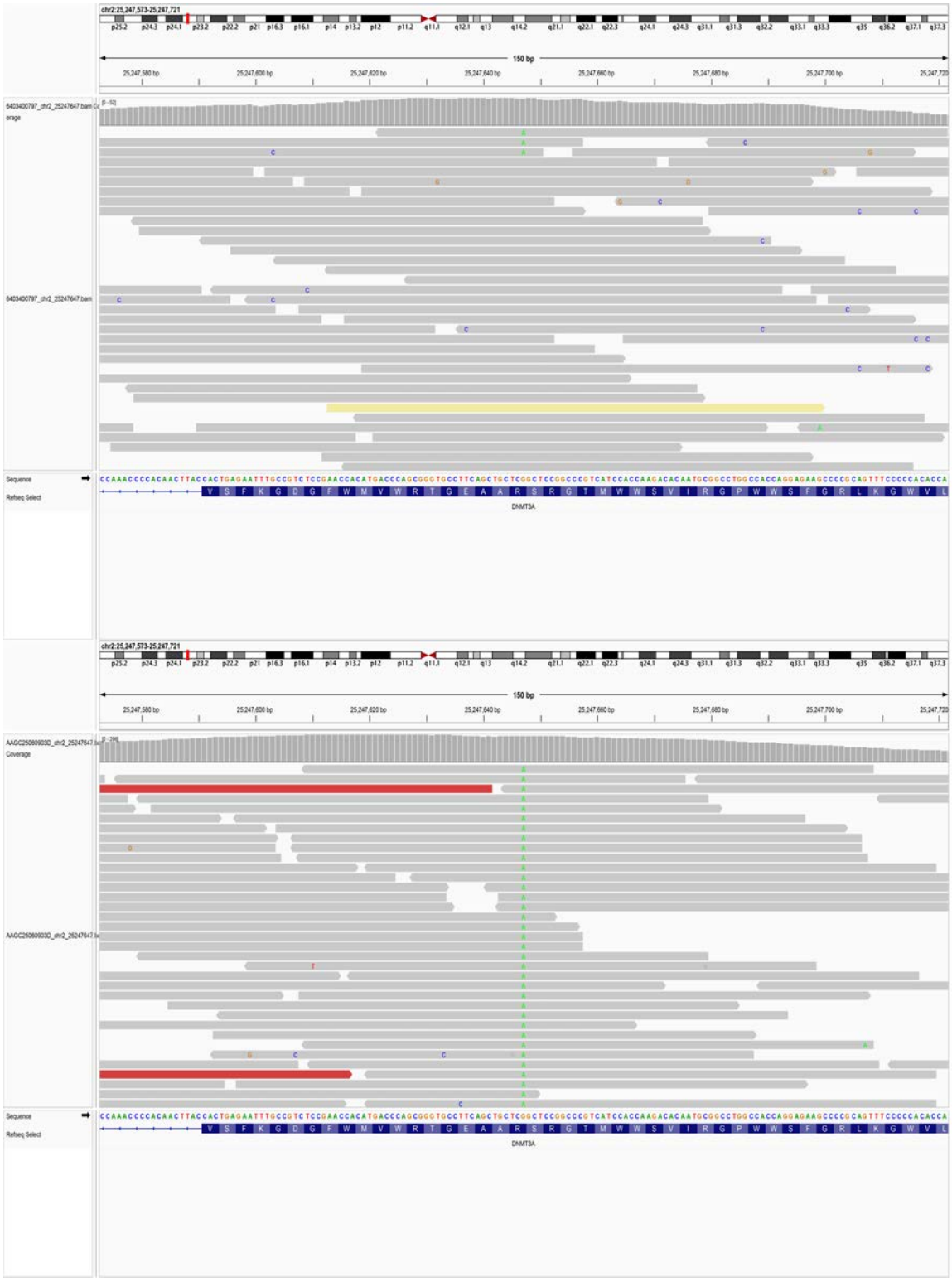


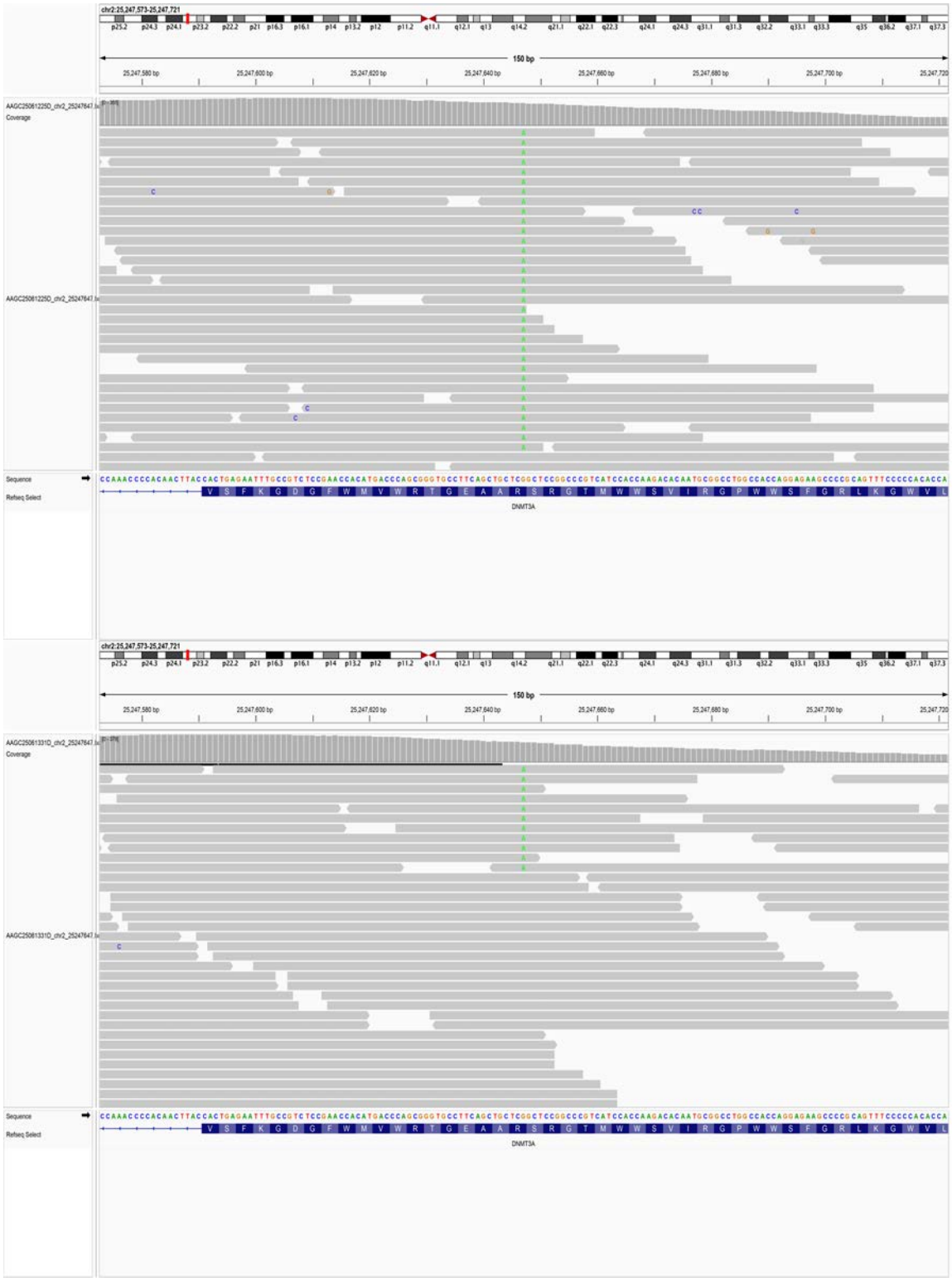

chr2:25,247,555-25,247,703
150 bp
25,247,560 bp
25,247,580 bp
25,247,600 bp
25,247,620 bp
25,247,640 bp
25,247,660 bp
25,247,680 bp
25,247,700 bp
CNS0136048_chr2_25247629.bam
erage
CNS0136048_chr2_25247629.bam
Sequence
Refseq Select
DNMT3A

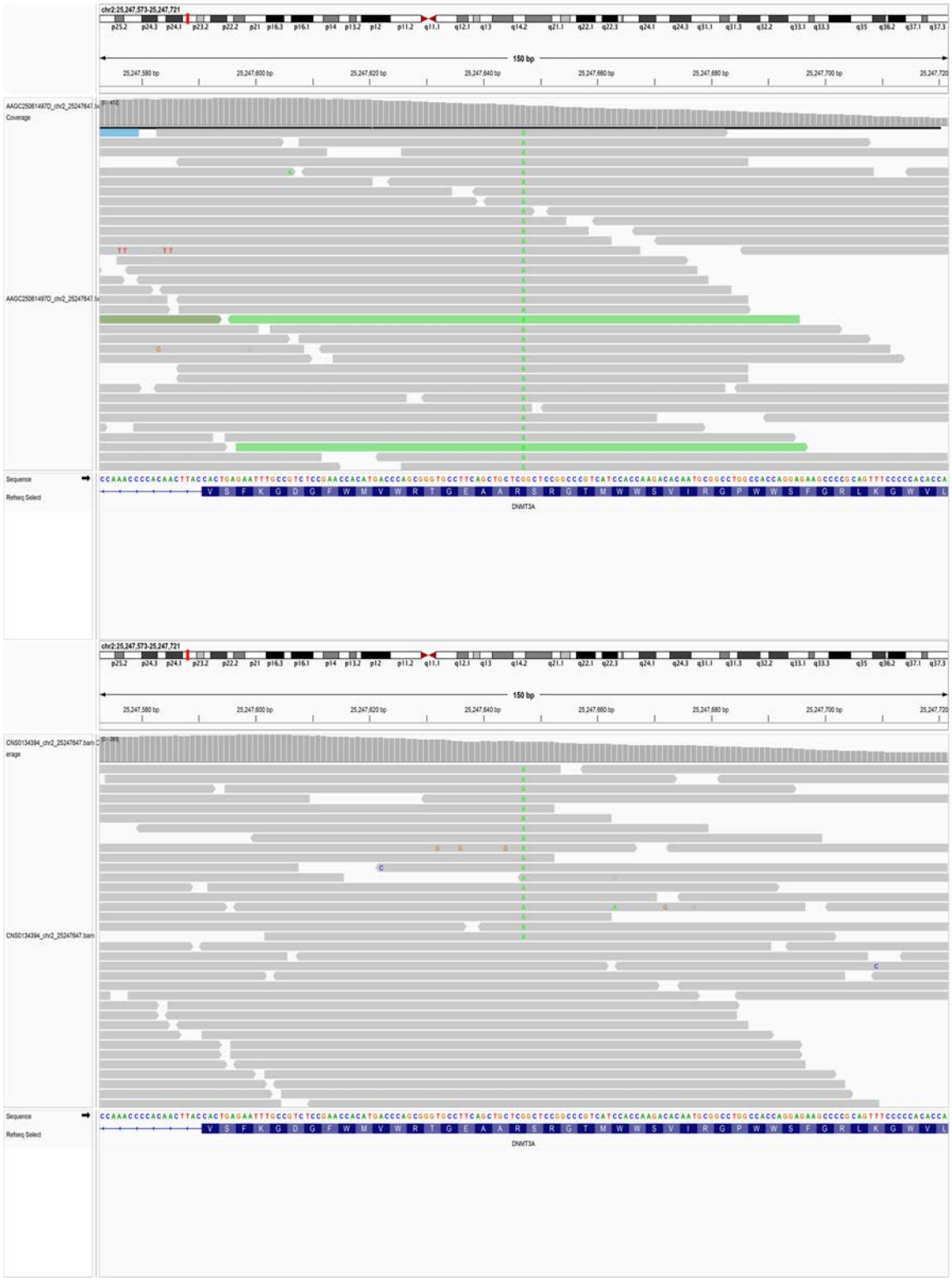
12.128. chr2_25247647_G/A

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



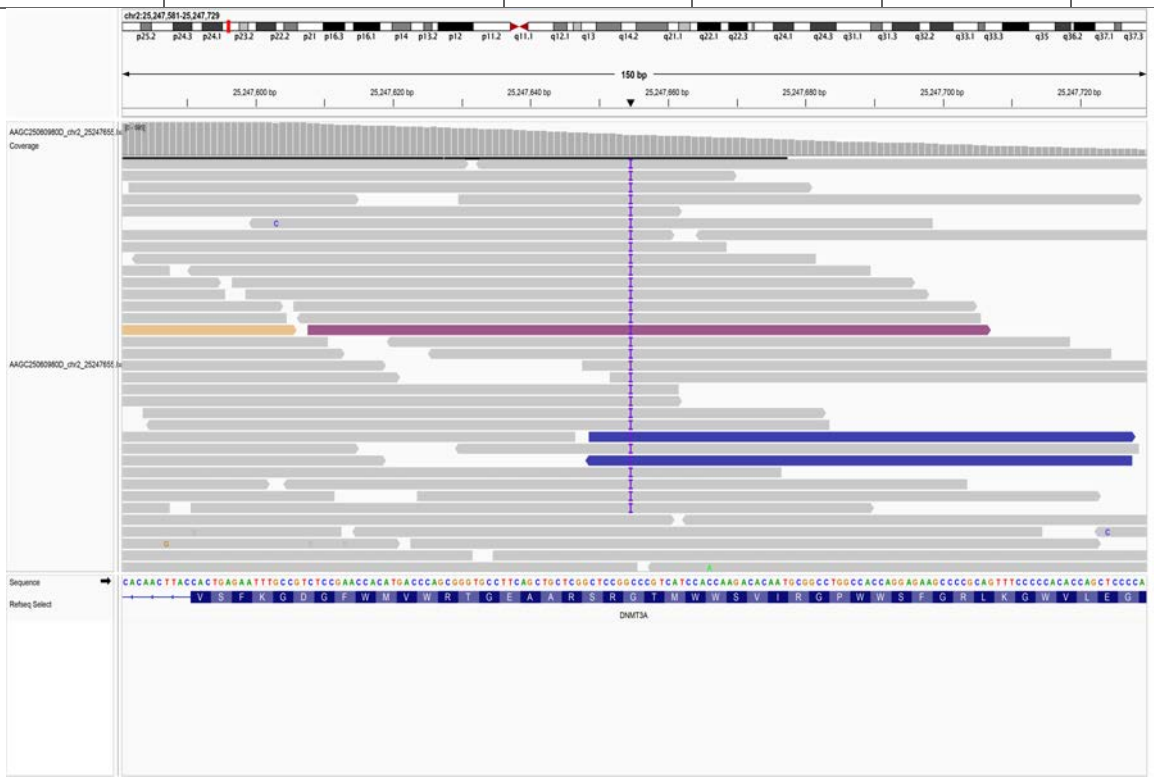

chr2:25,247,573-25,247,721
150 bp
25,247,580 bp
25,247,600 bp
25,247,620 bp
25,247,640 bp
25,247,660 bp
25,247,680 bp
25,247,700 bp
25,247,720
Coverage
Sequence
Refseq Select
DNMT3A
chr2:25,247,573-25,247,721
150 bp
Coverage
Sequence
Refseq Select
DNMT3A


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
Coverage
Sequence
Refseq Select
DNMT3A
chr2:25,247,573-25,247,721
150 bp
Coverage
Sequence
Refseq Select
DNMT3A


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
Coverage
Sequence
Refseq Select
DNMT3A
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
Sequence
Refseq Select
DNMT3A

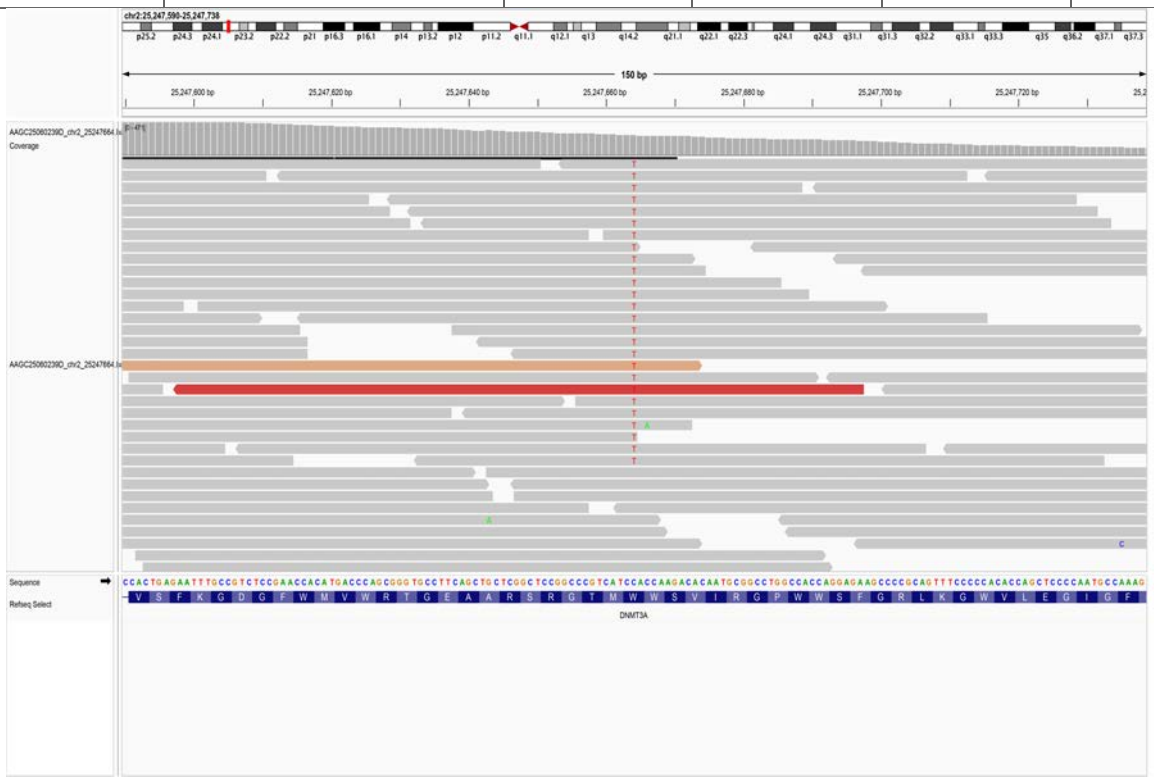
12.129. chr2_25247655_-/C

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



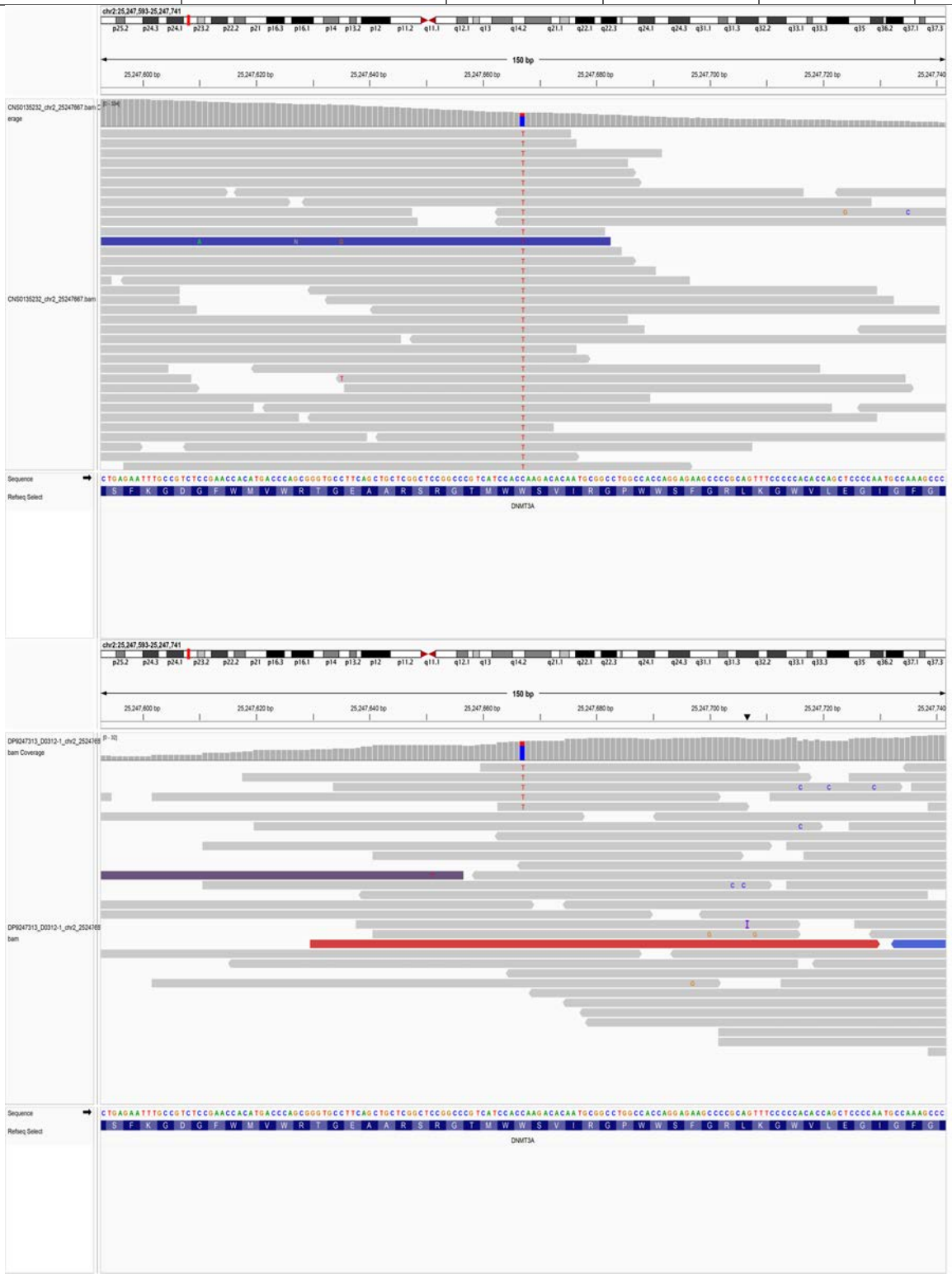
12.130. chr2_25247664_C/T

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



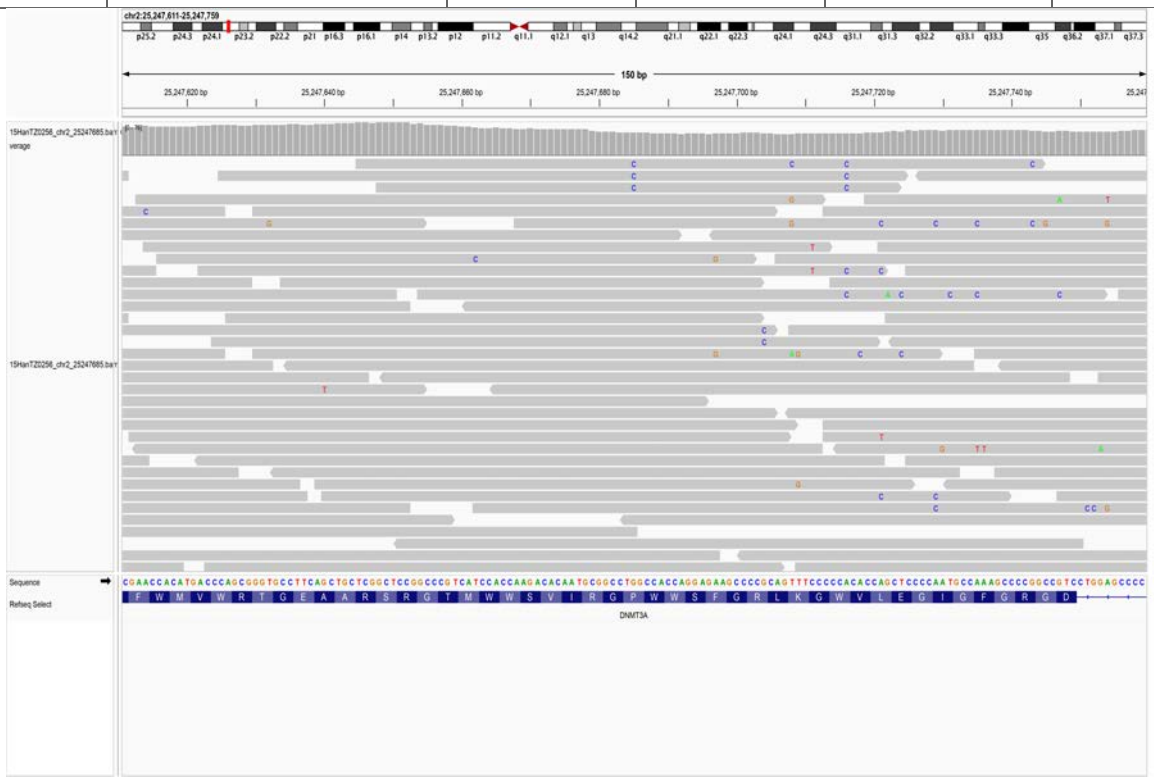
12.131. chr2_25247667_C/T

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



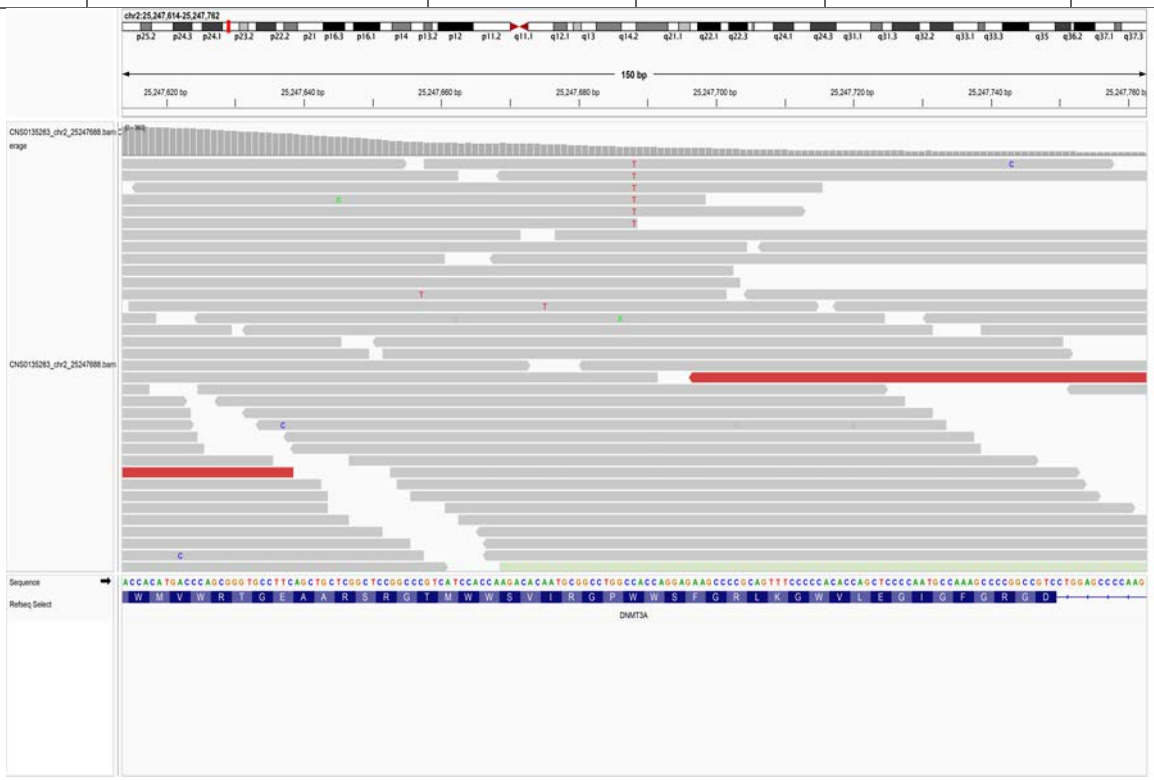
12.132. chr2_25247685_G/C

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



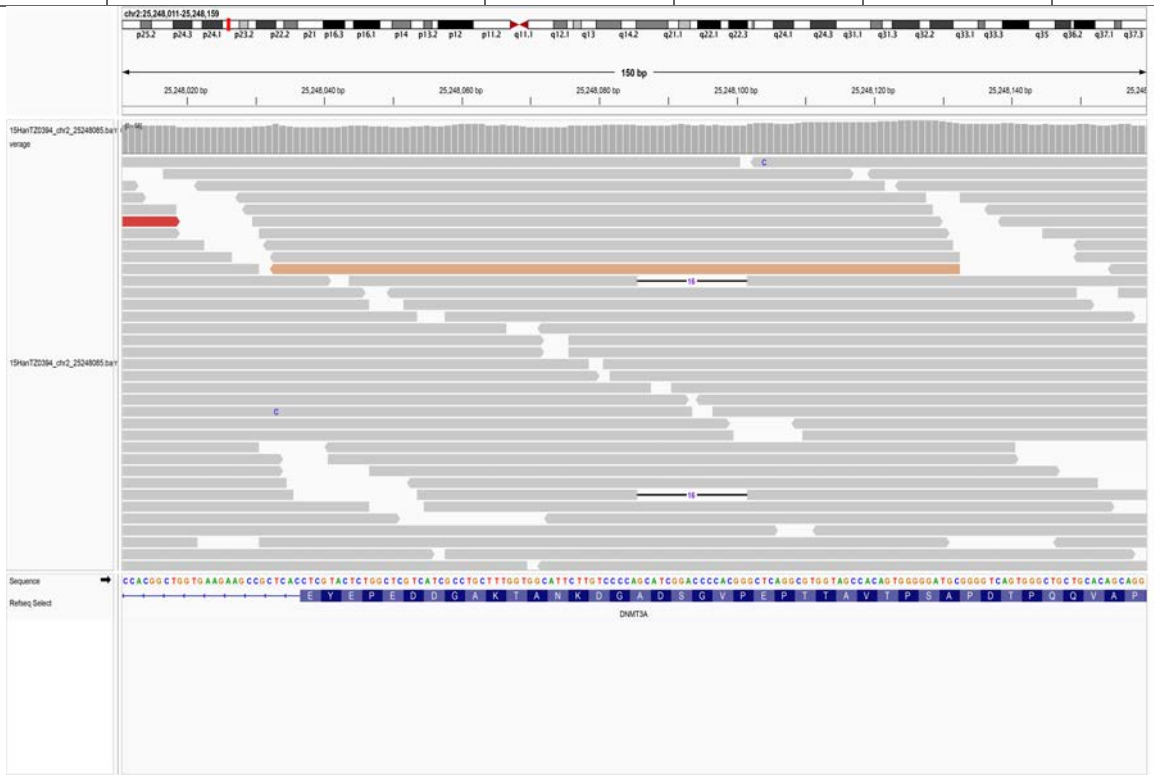
12.133. chr2_25247688_C/T

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



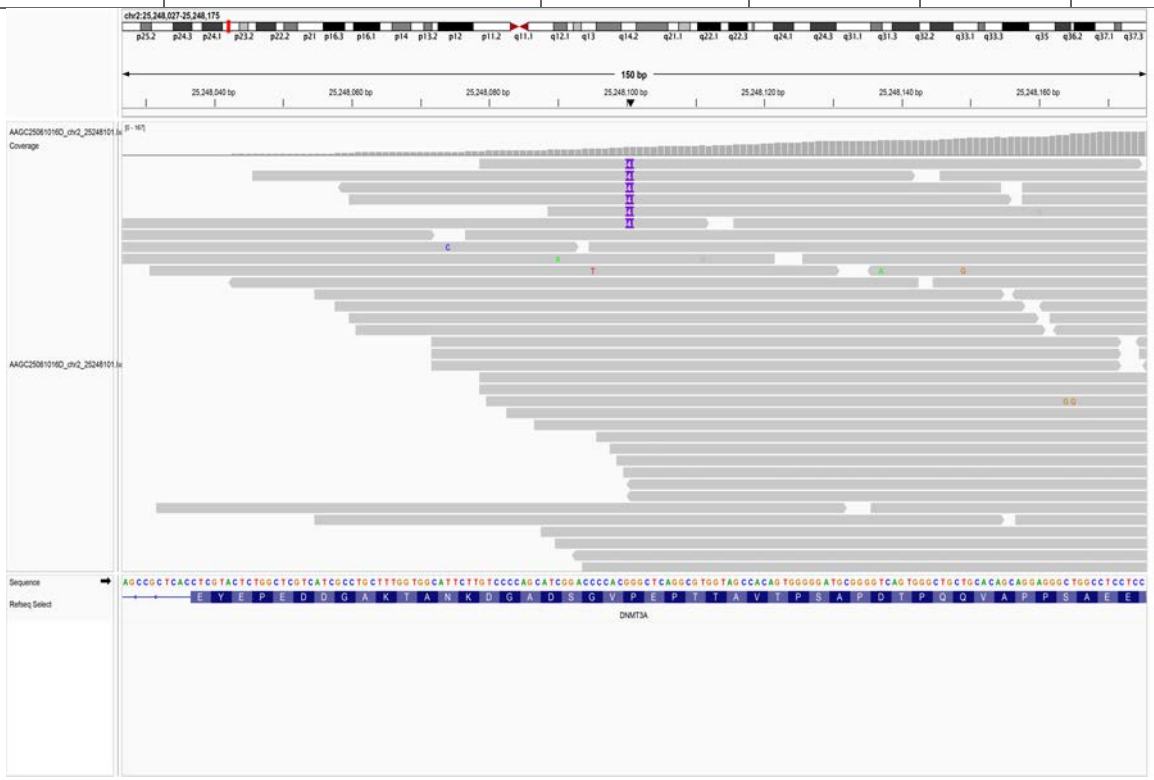
12.134. chr2_25248086_GCATCGGACCCCACGG/-

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



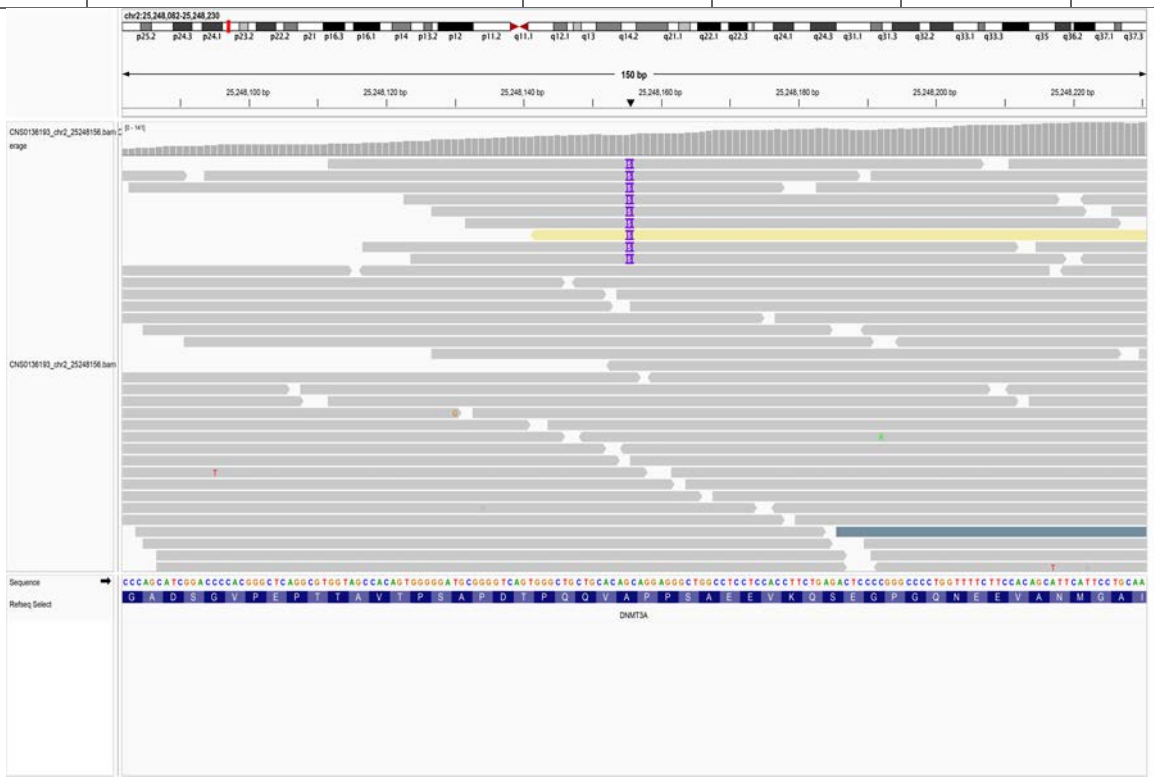
12.135. chr2_25248101_-/GGCC

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



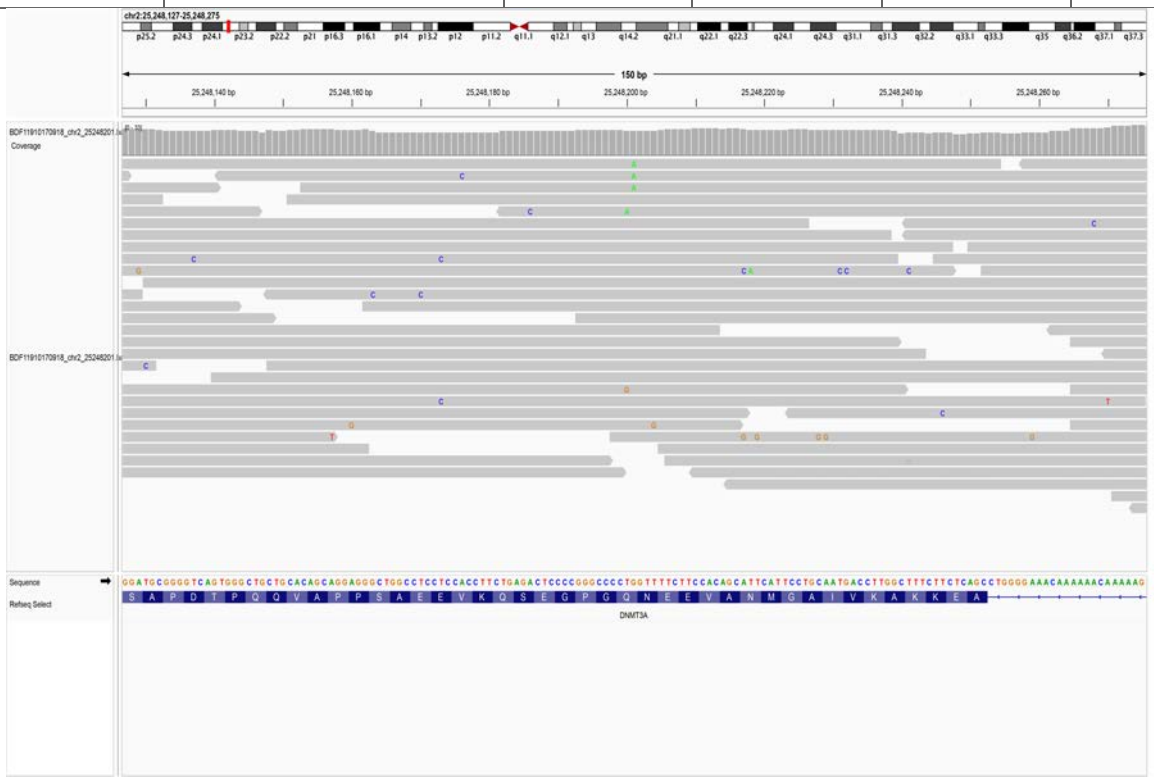
12.136. chr2_25248156_-/GAGGA

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



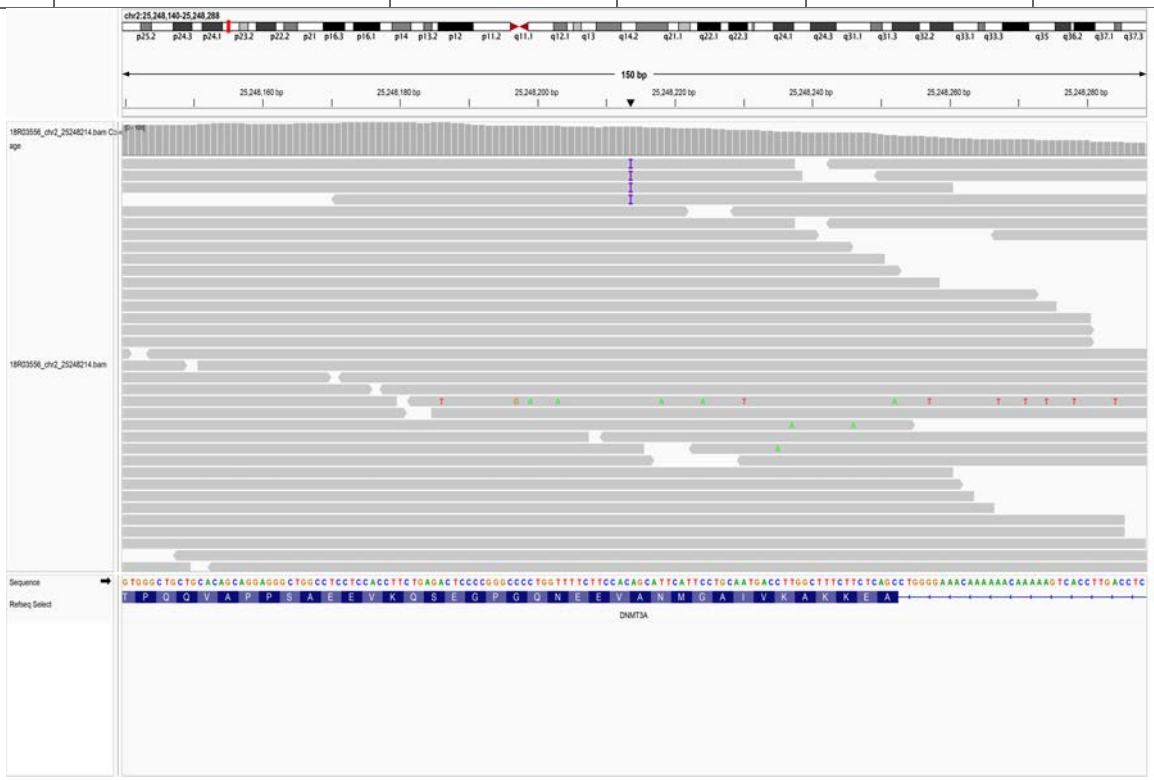
12.137. chr2_25248201_G/A

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



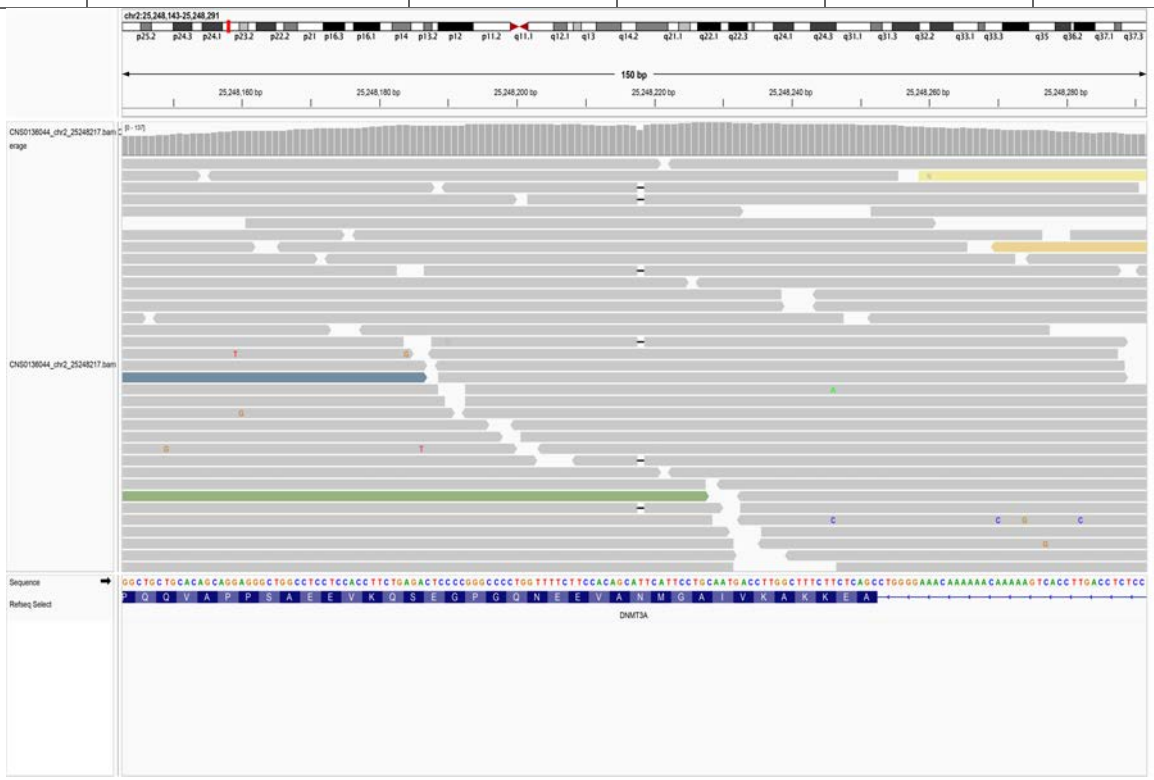
12.138. chr2_25248214_-/A

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



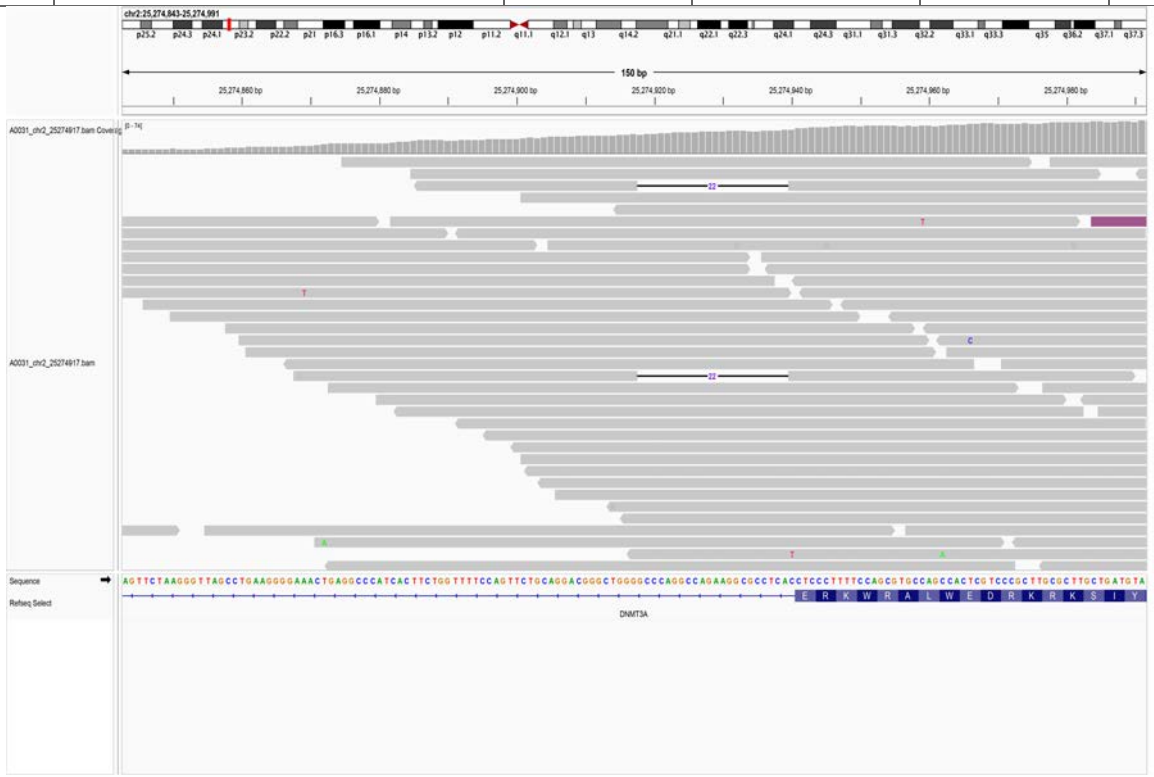
12.139. chr2_25248218_T/-

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



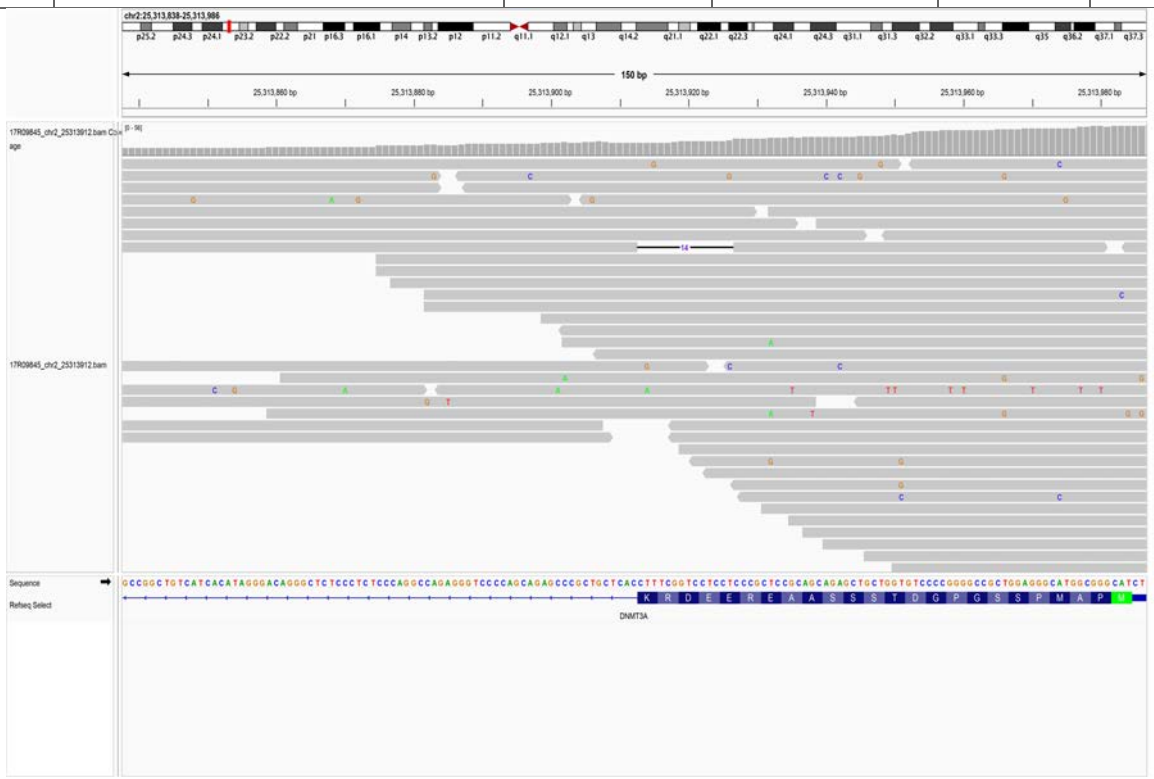
12.140. chr2_25274918_GCCCAGGCCAGAAGGCGCCTCA/-

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



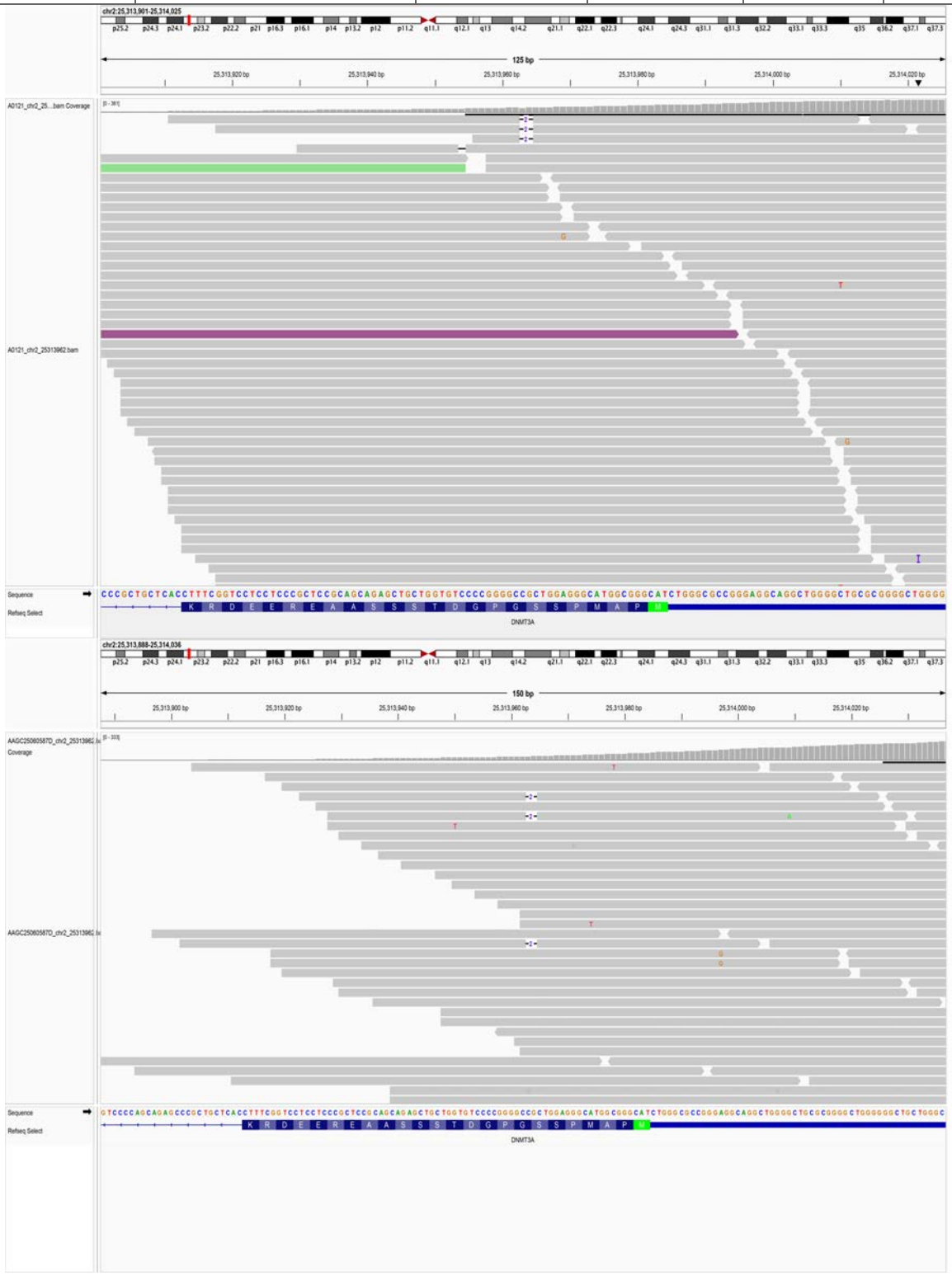
12.141. chr2_25313913_CTTTCGGTCCTCCT/-

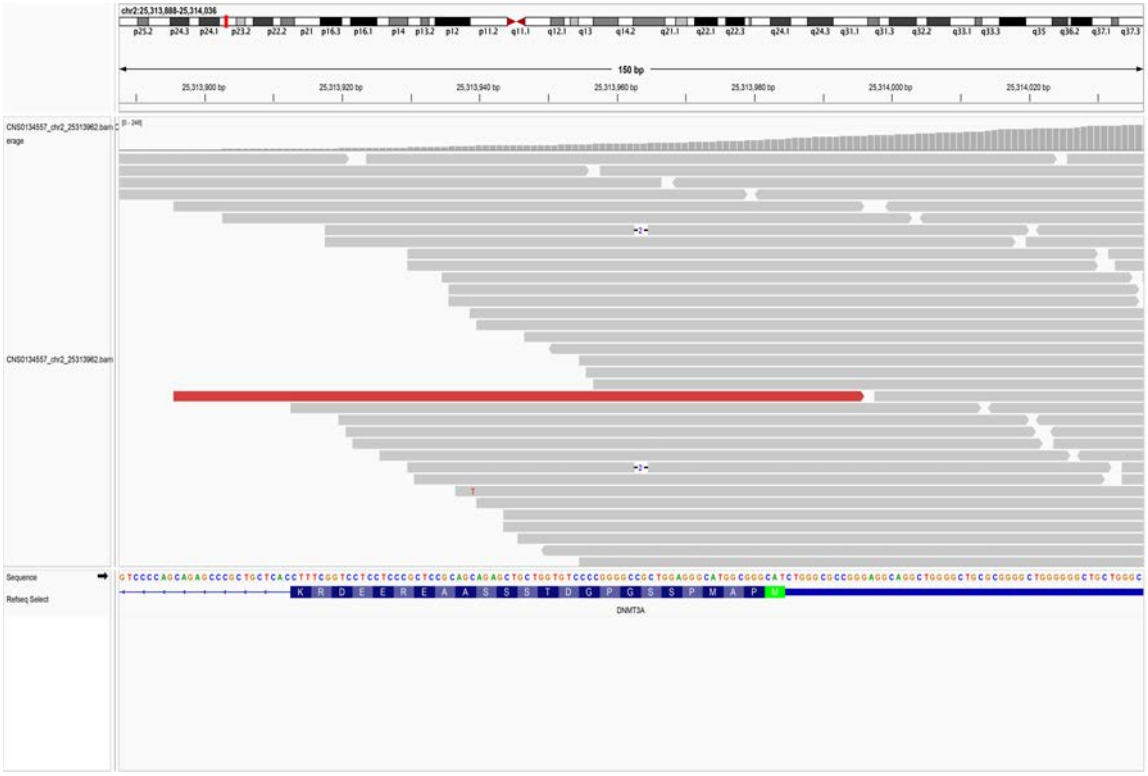
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R09845	chr2_25313913_CTTTCGGTCCTCCT/-	20	3	*DNMT3A*	frameshift_variant



12.142. chr2_25313963_CG/-

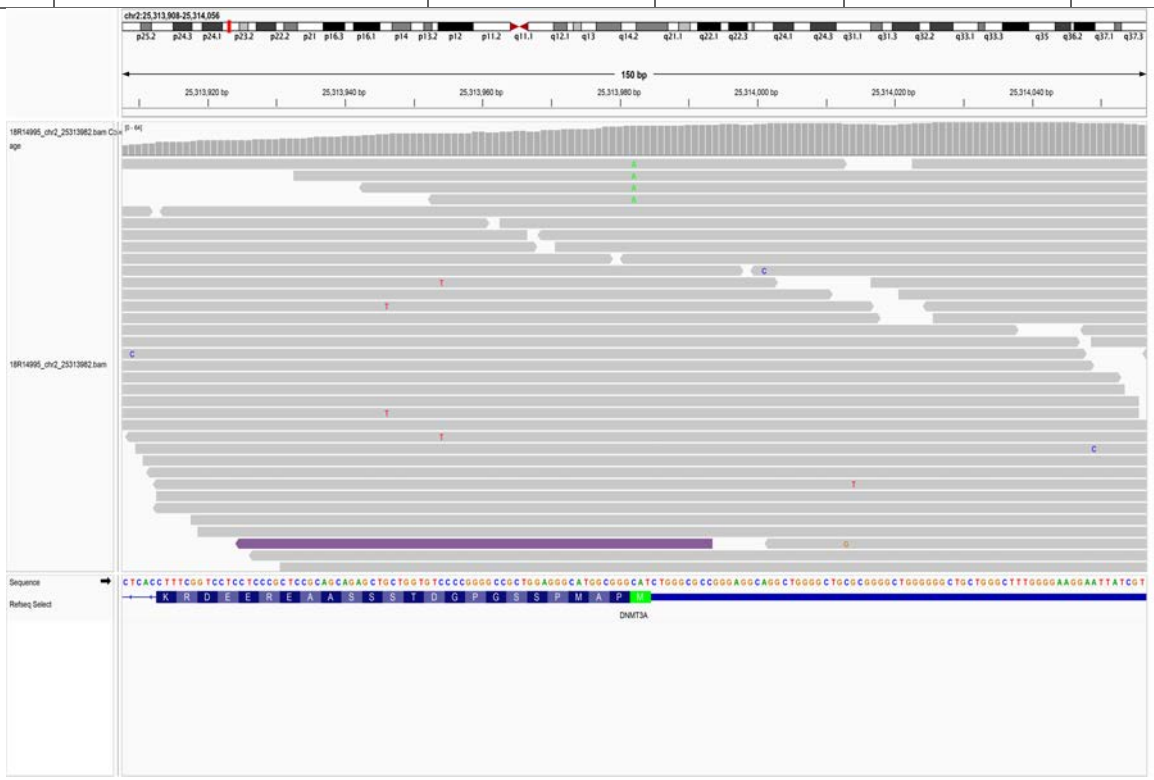
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0121	chr2_25313963_CG/-	132	3	*DNMT3A*	frameshift_variant
AAGC25060587D	chr2_25313963_CG/-	50	3	*DNMT3A*	frameshift_variant
CNS0134557	chr2_25313963_CG/-	51	3	*DNMT3A*	frameshift_variant




chr2:25,313,888-25,314,036
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
erage
CNS0134557_chr2_25313962.bam
Sequence
Refseq Select
DNMT3A

12.143. chr2_25313982_C/A

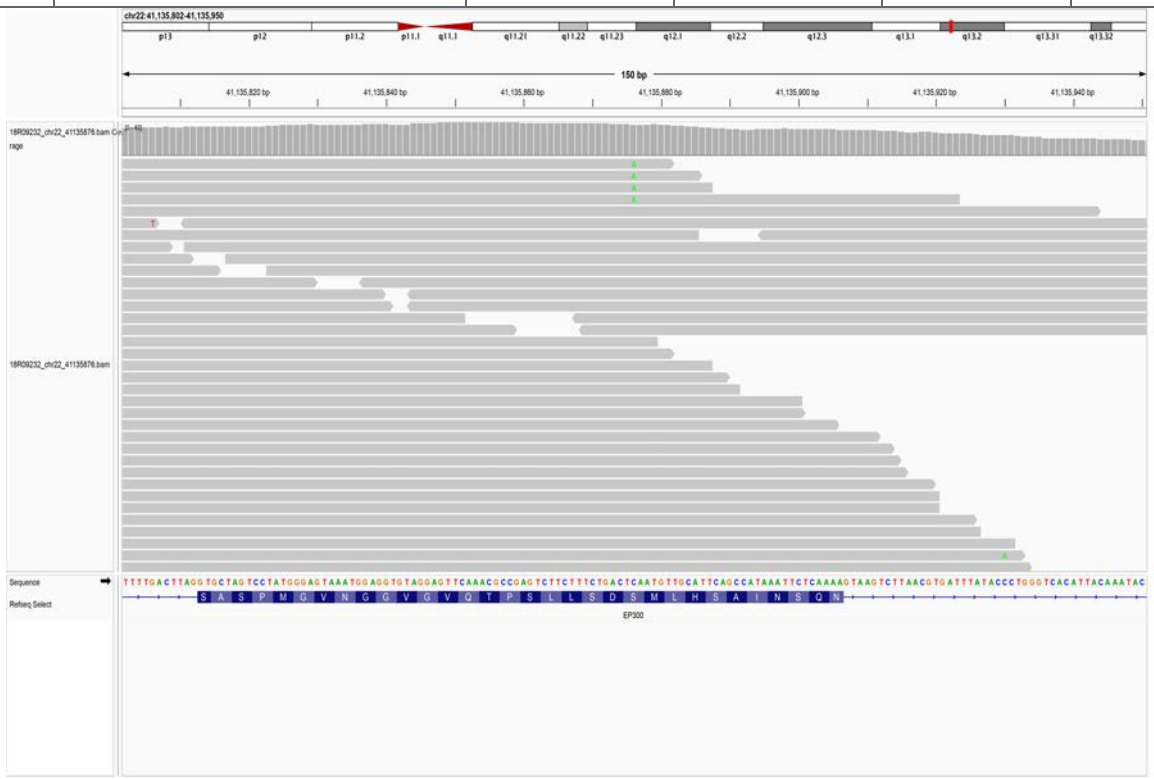
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R14995	chr2_25313982_C/A	52	4	*DNMT3A*	start_lost



13. *EP300*

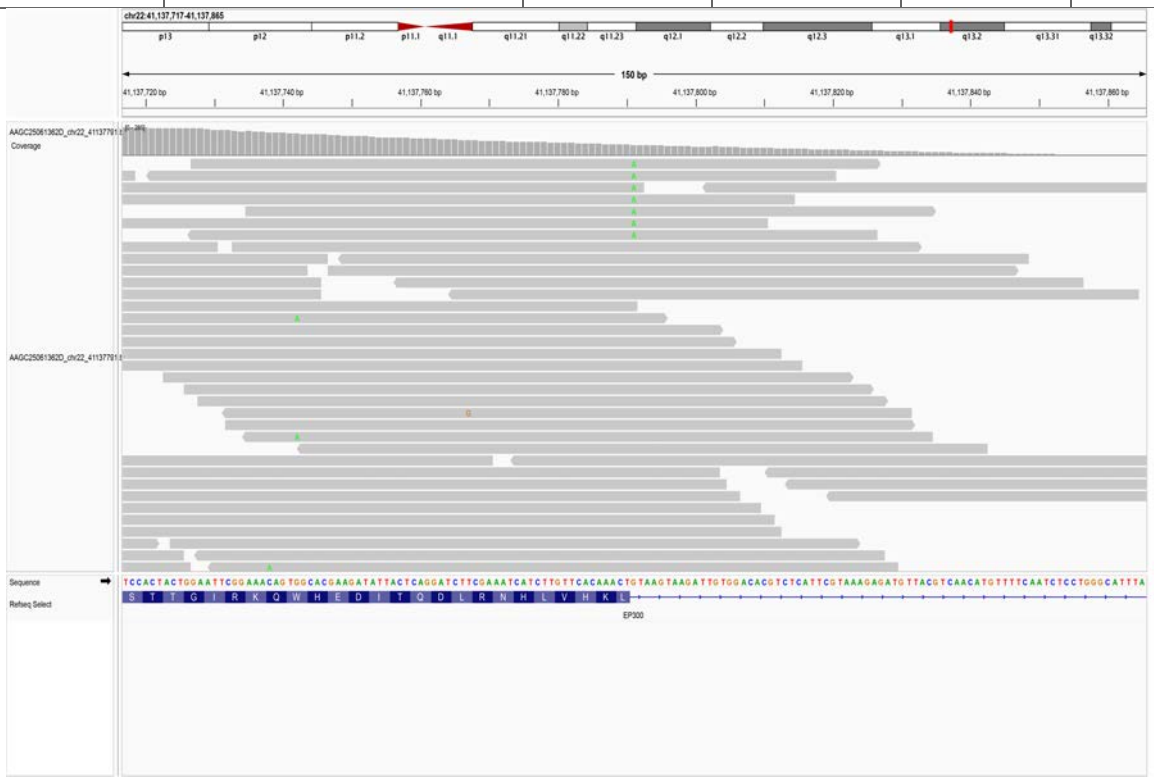
13.1. chr22_41135876_C/A

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



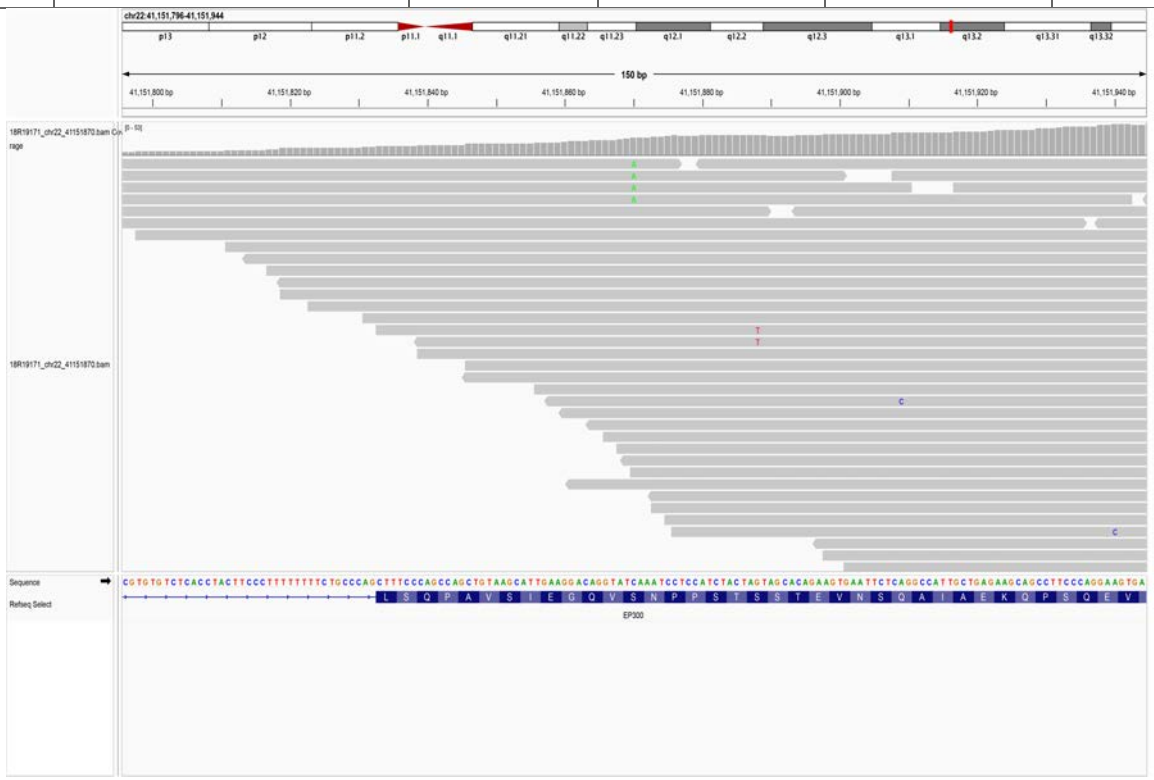
13.2. chr22_41137791_G/A

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



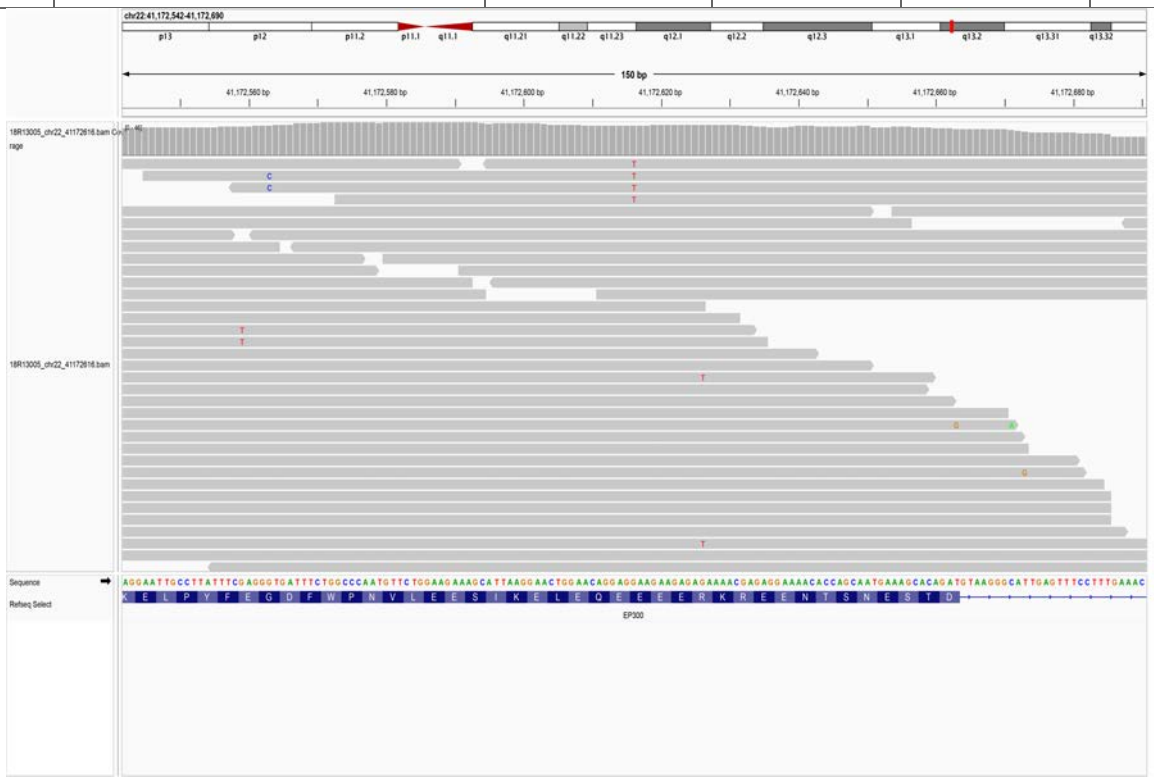
13.3. chr22_41151870_C/A

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



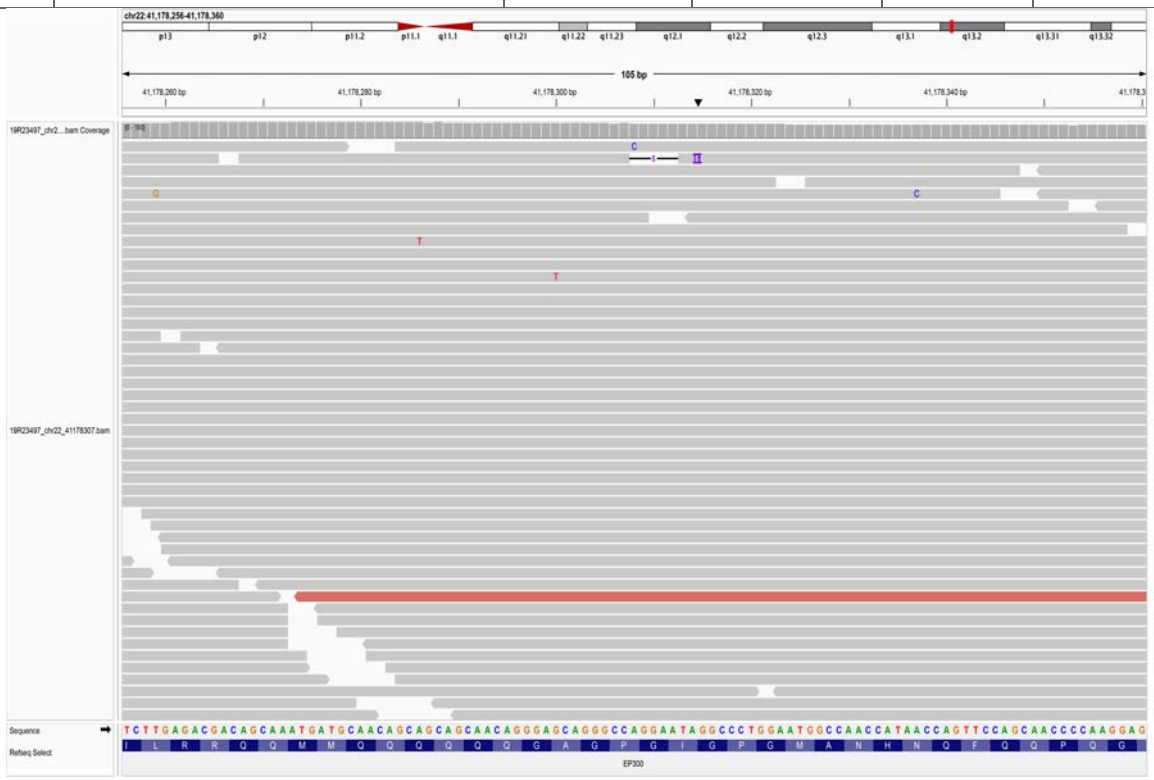
13.4. chr22_41172616_G/T

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



13.5. chr22_41178308_AGGAA/-

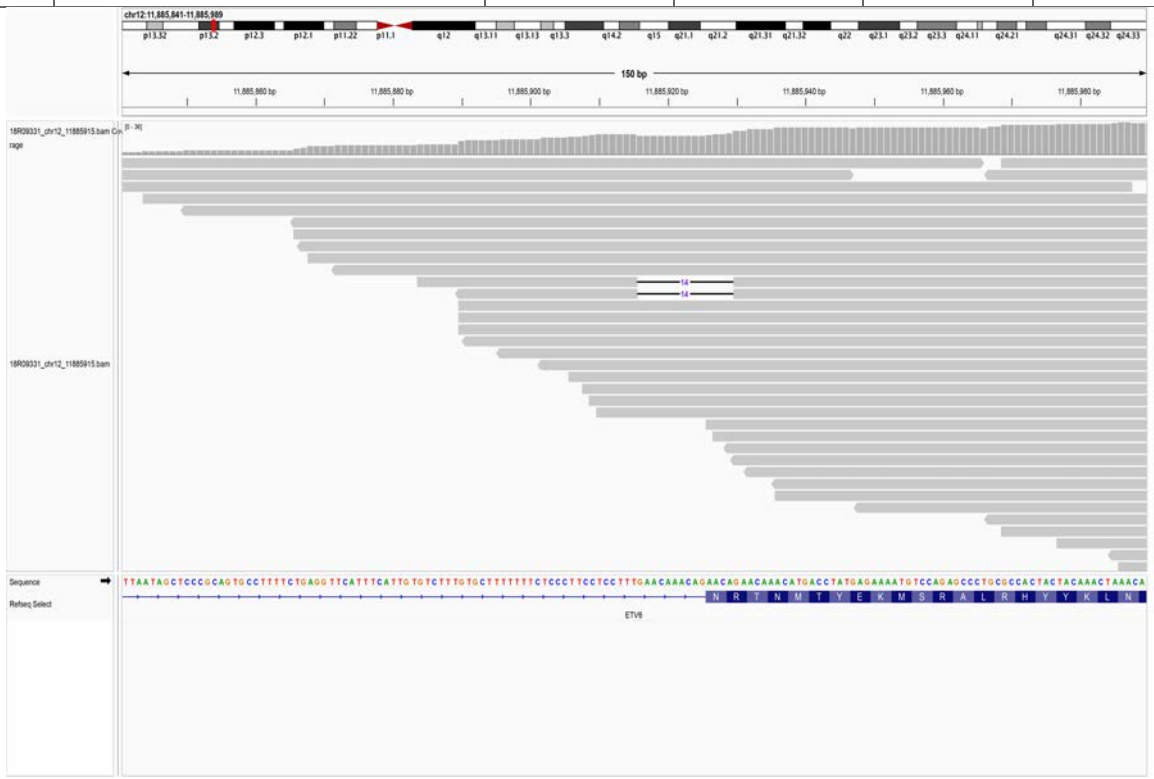
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23497	chr22_41178308_AGGAA/-	127	5	*EP300*	frameshift_variant

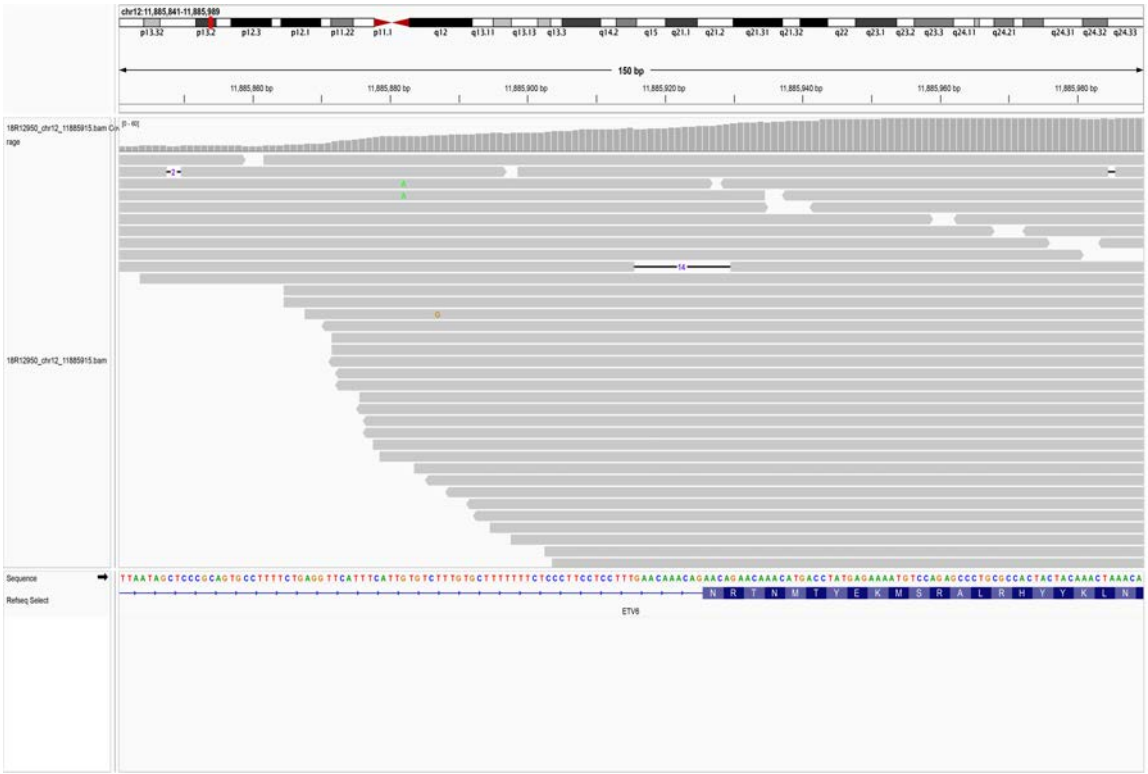


14. *ETV6*

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

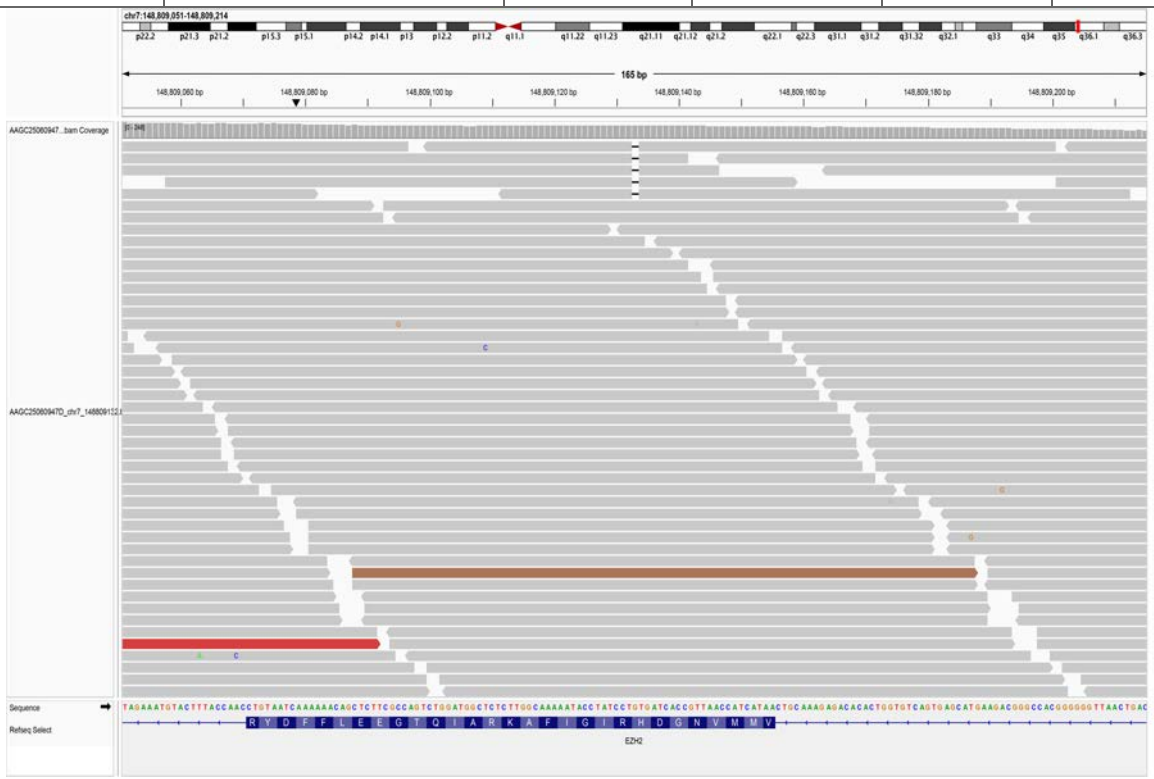



chr12:11,885,841-11,885,989
150 bp
11,885,860 bp
11,885,880 bp
11,885,900 bp
11,885,920 bp
11,885,940 bp
11,885,960 bp
11,885,980 bp
18R12950_chr12_11885915.bam Cov
rage
18R12950_chr12_11885915.bam
Sequence
Refseq Select
ETV6

15. *EZH2*

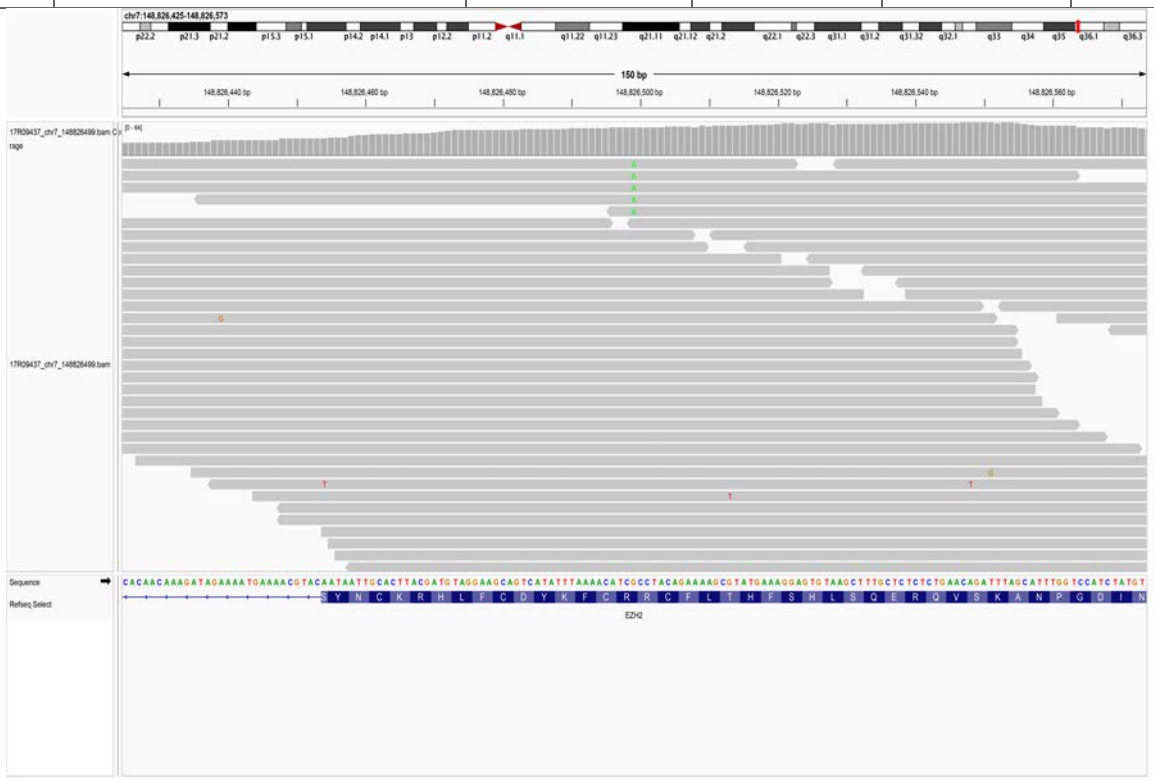
15.1. chr7_148809133_G/-

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



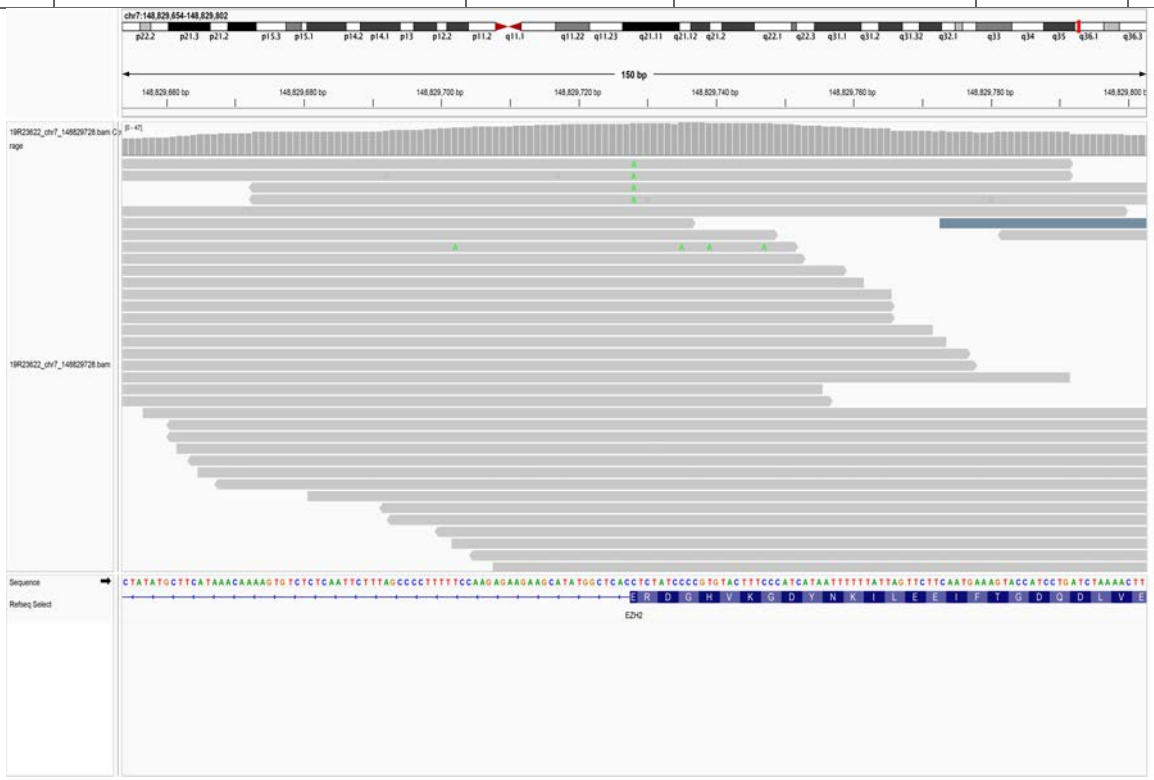
15.2. chr7_148826499_G/A

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



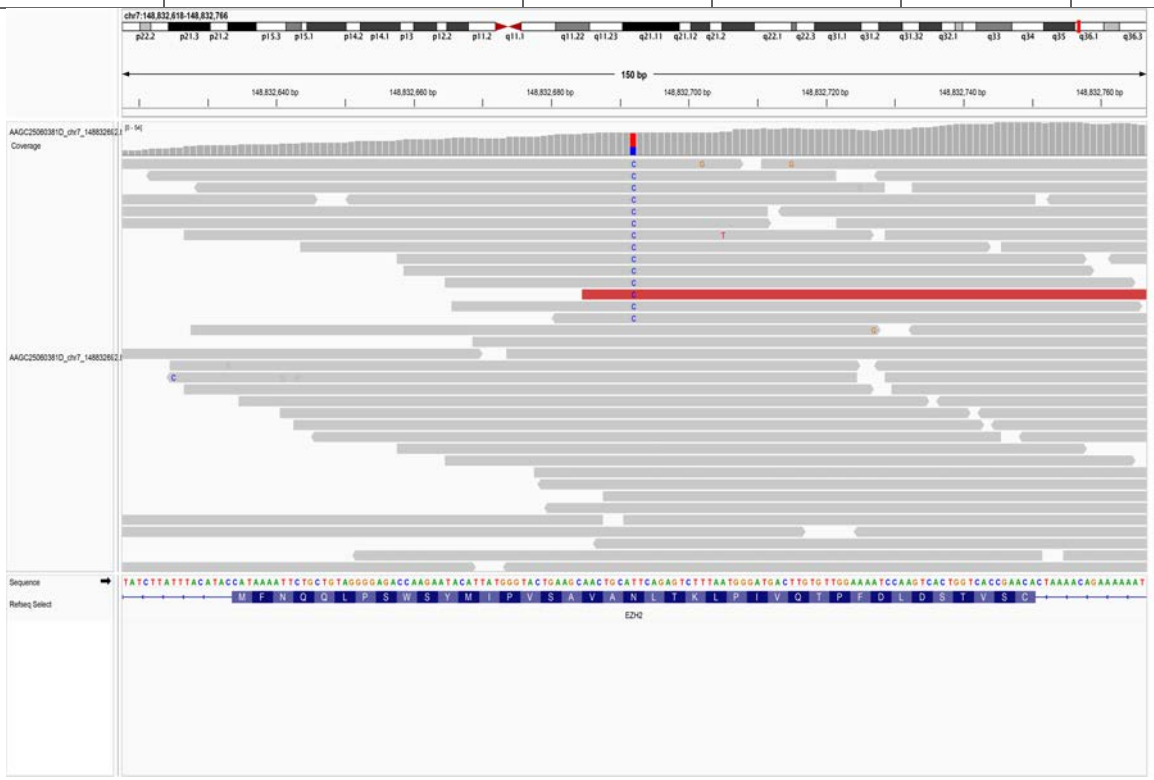
15.3. chr7_148829728_C/A

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

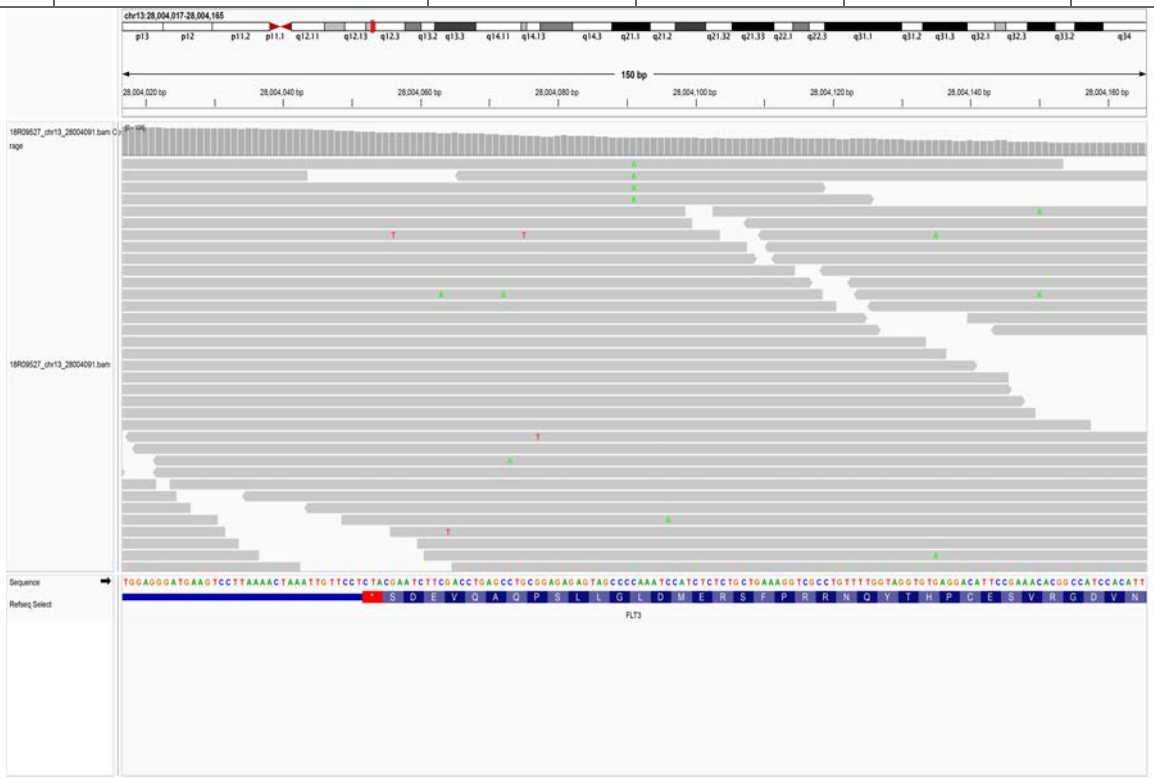
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060381D	chr7_148832692_T/C	23	14	*EZH2*	missense_variant



16. *FLT3*

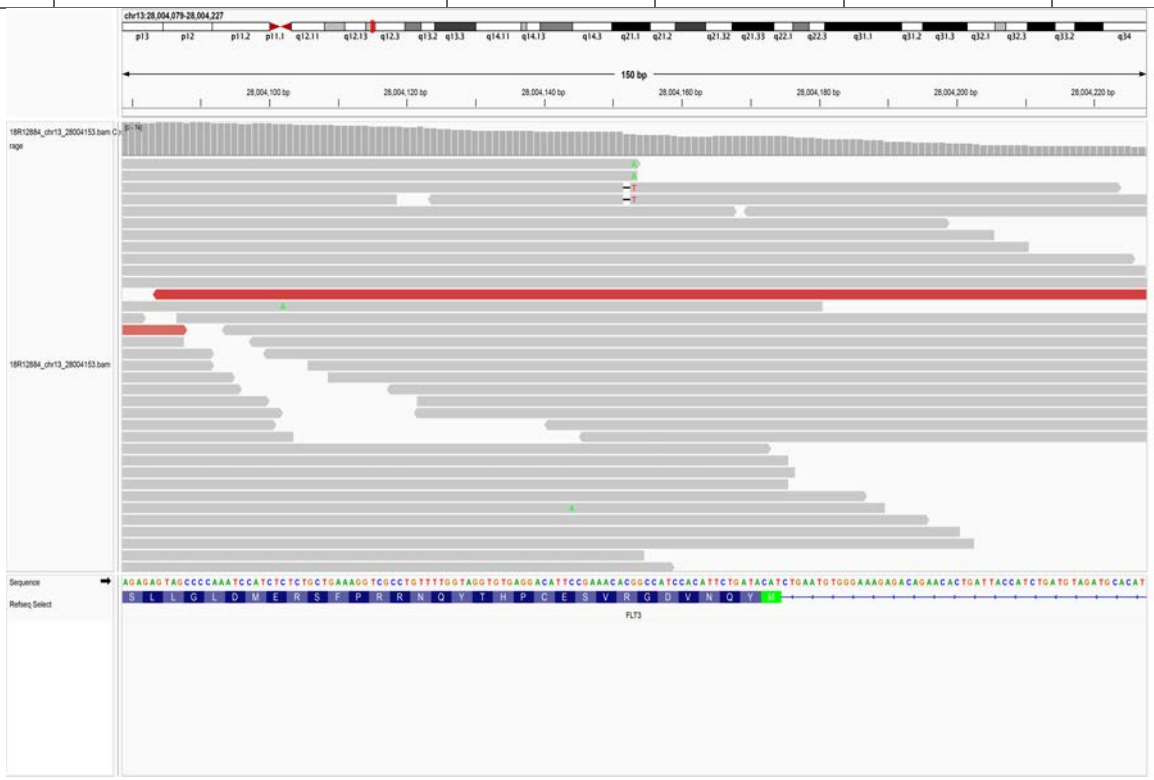
16.1. chr13_28004091_C/A

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

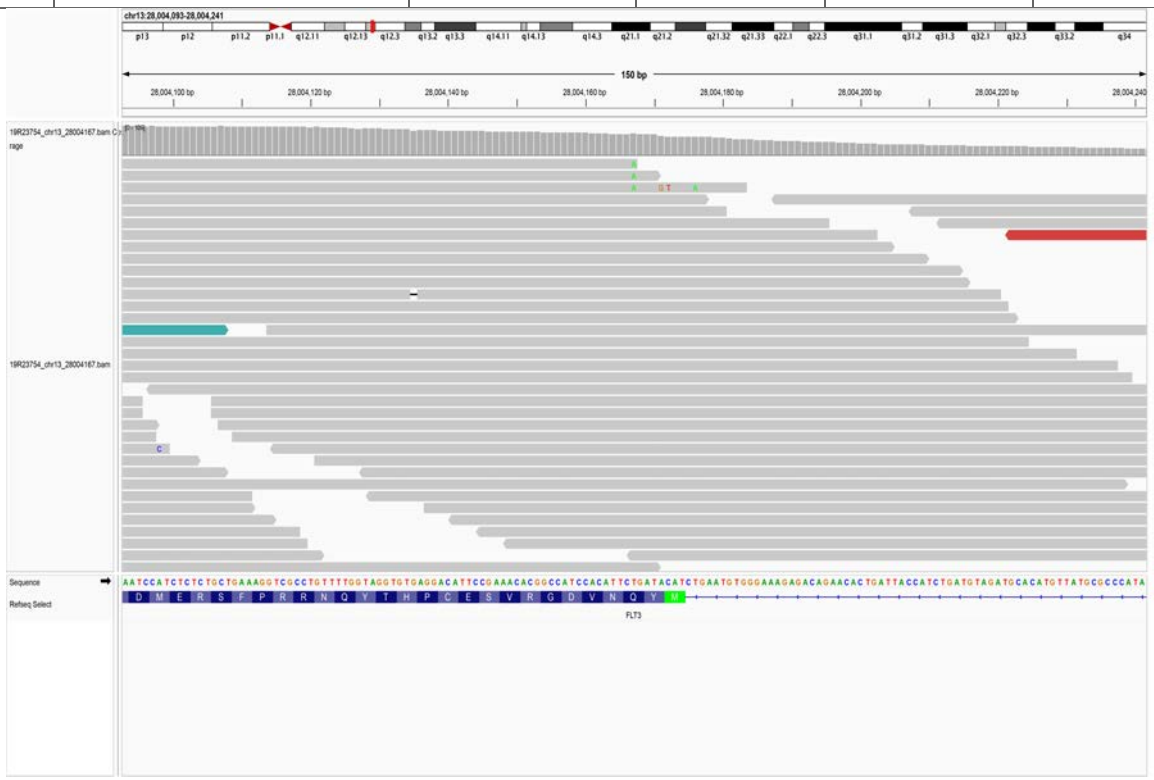


16.3. chr13_28004153_G/A

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

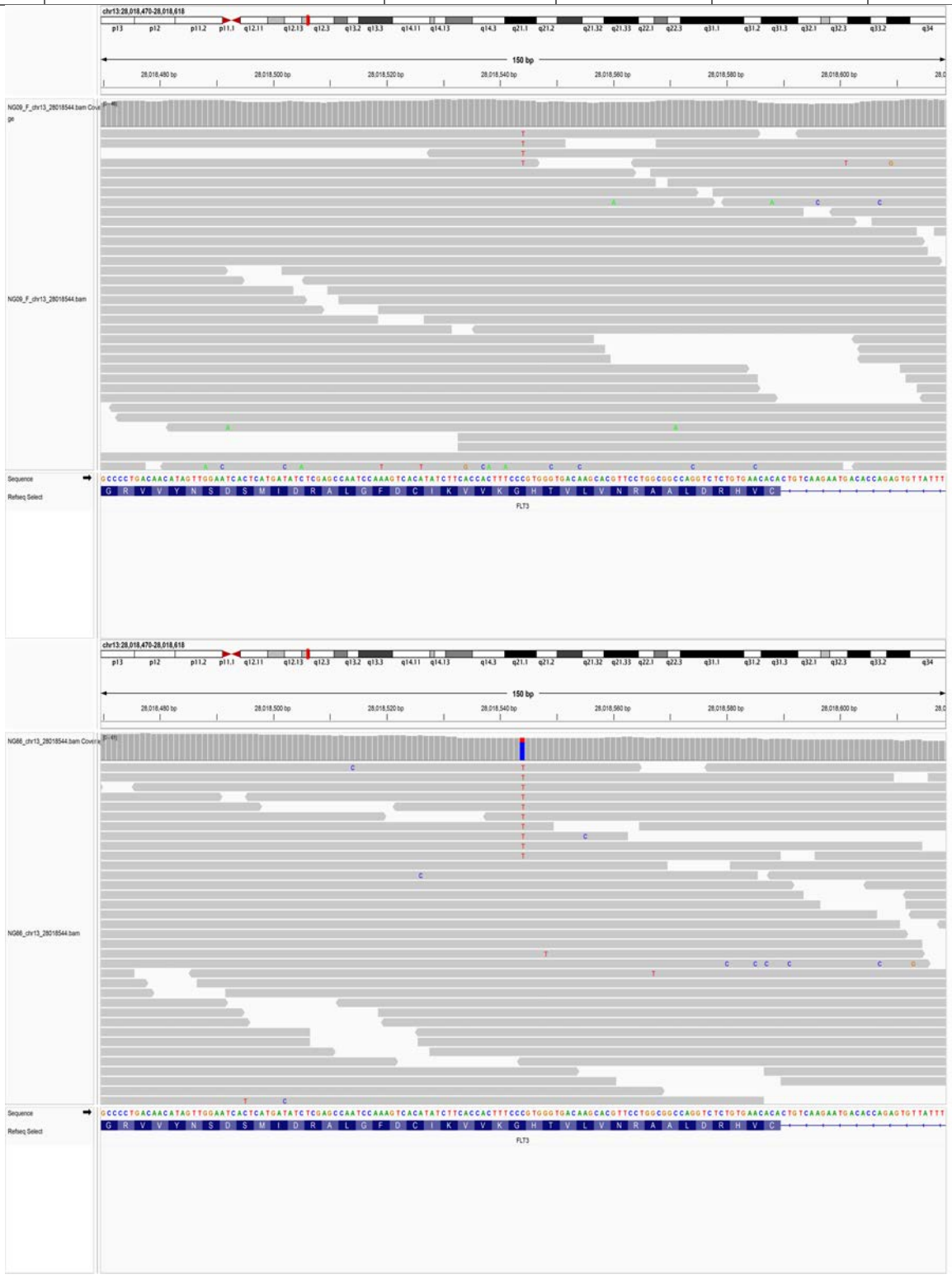
16.4. chr13_28004167_T/A

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



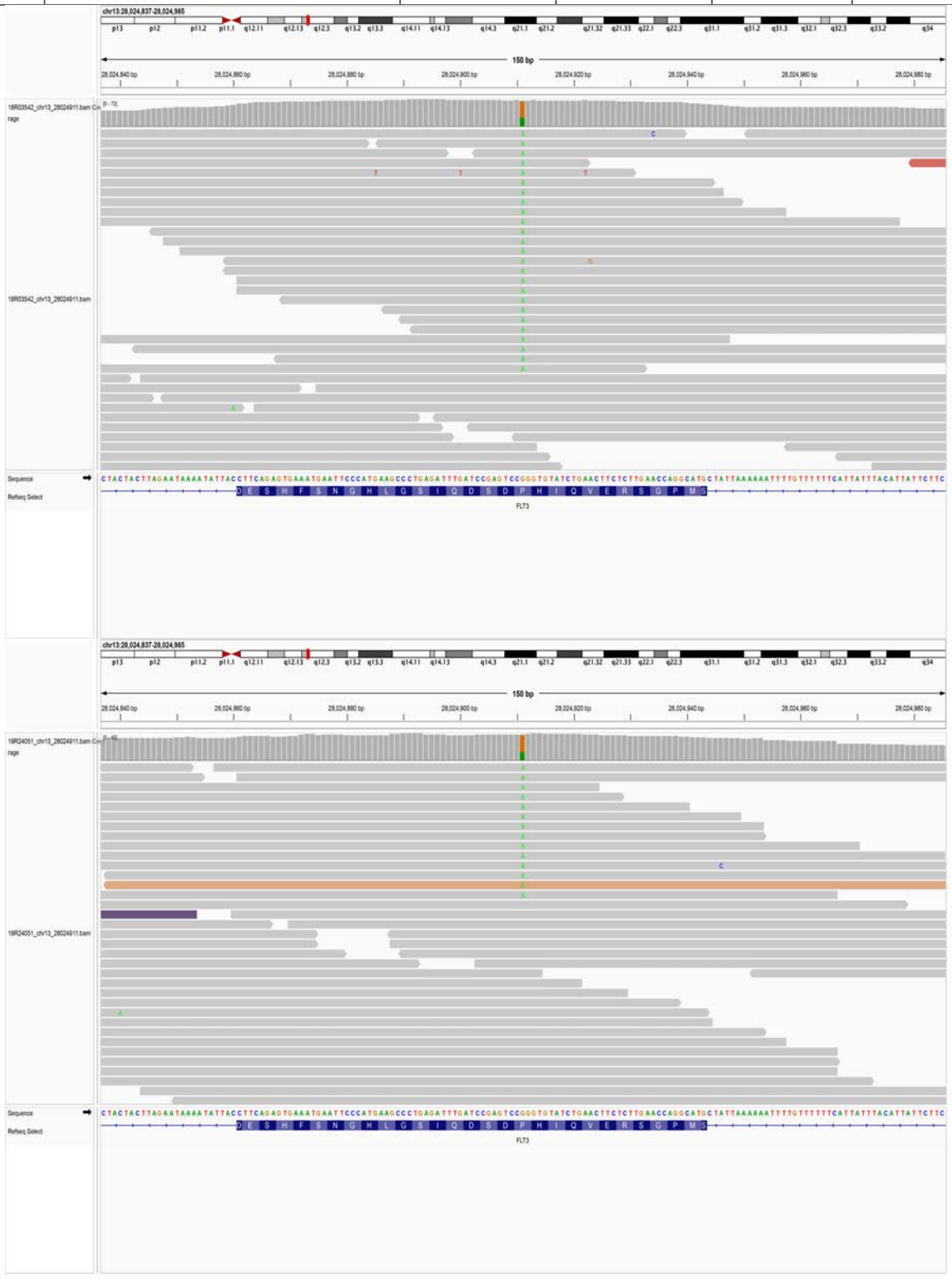
16.5. chr13_28018544_C/T

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



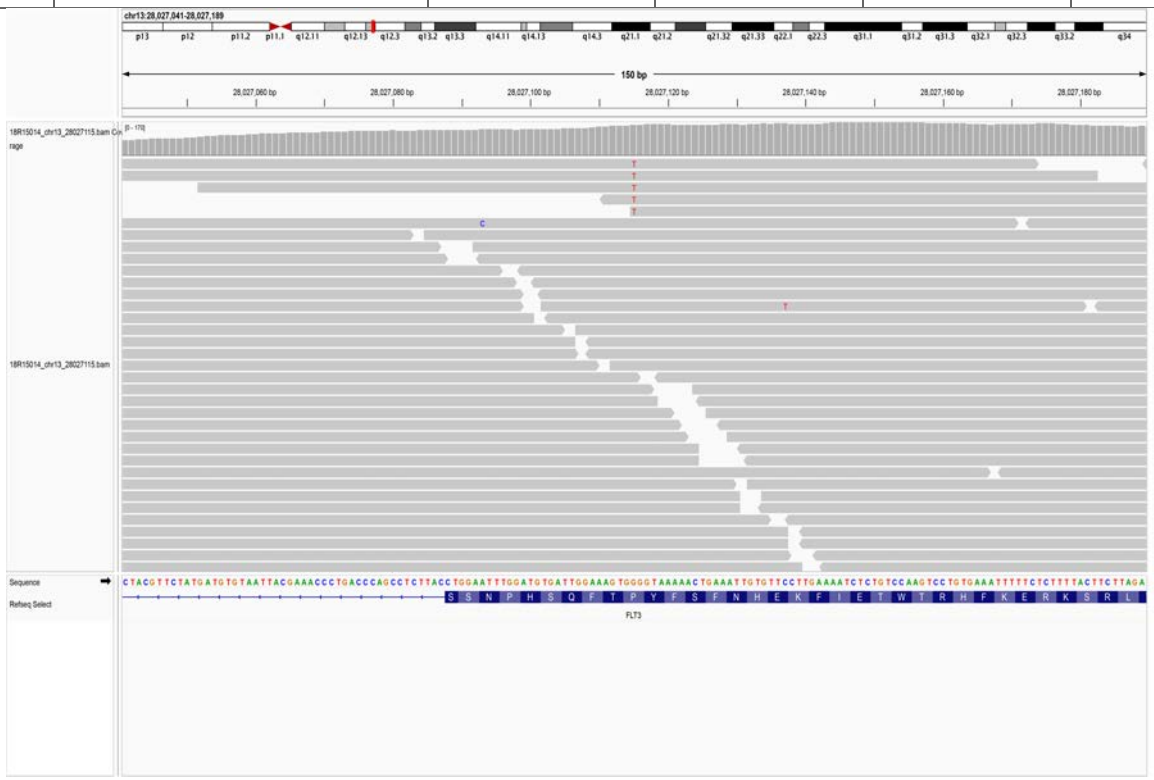
16.6. chr13_28024911_G/A

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



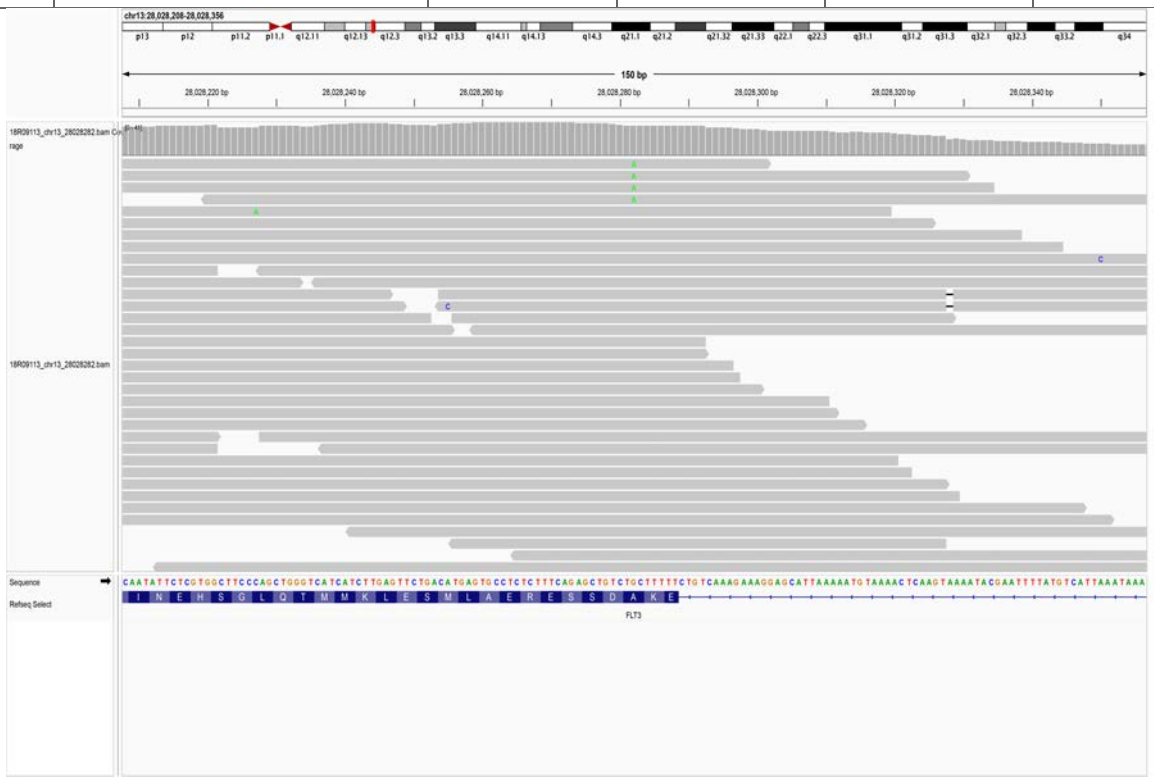
16.7. chr13_28027115_G/T

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

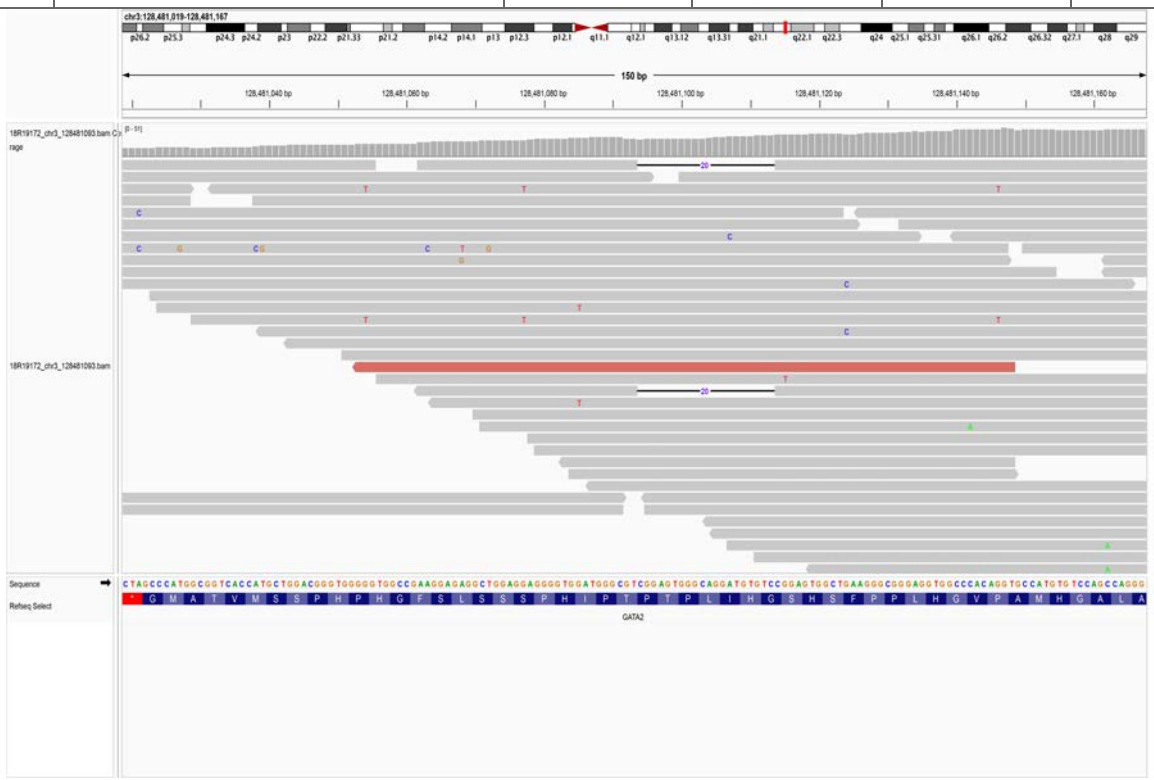
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R09113	chr13_28028282_G/A	32	4	*FLT3*	missense_variant



17. *GATA2*

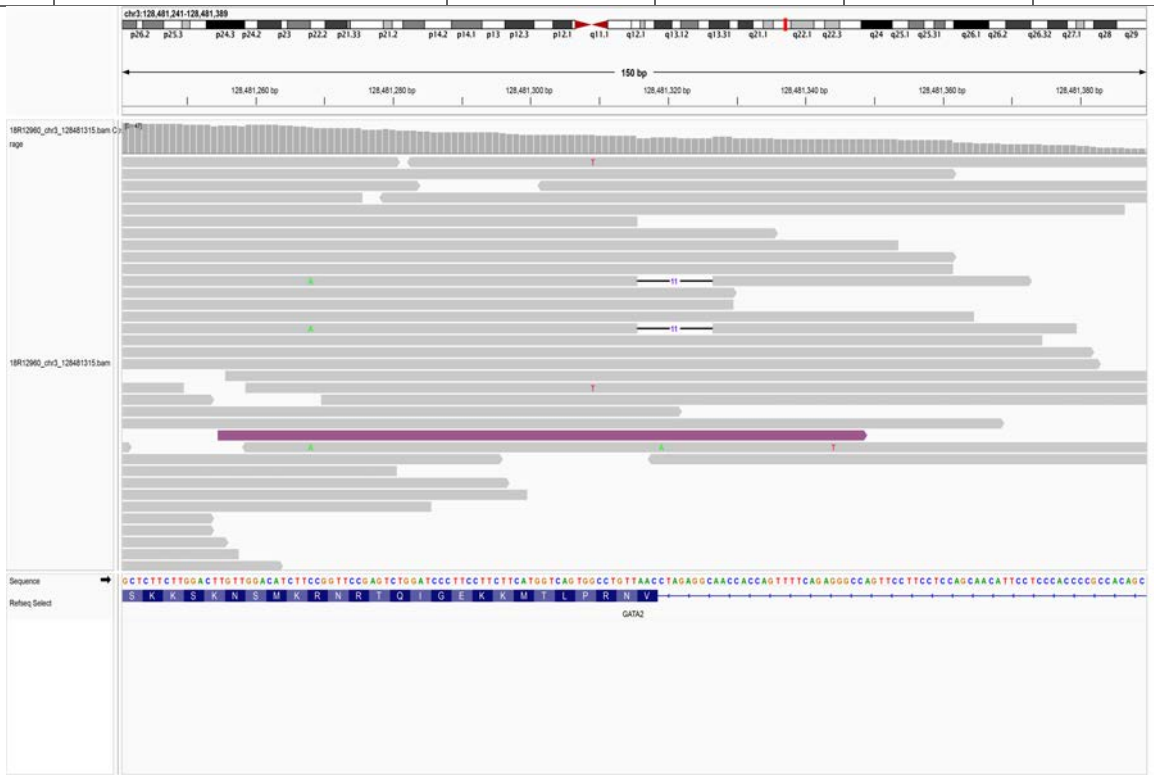
17.1. chr3_128481094_CGGAGTGGGCAGGATGTGTC/-

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



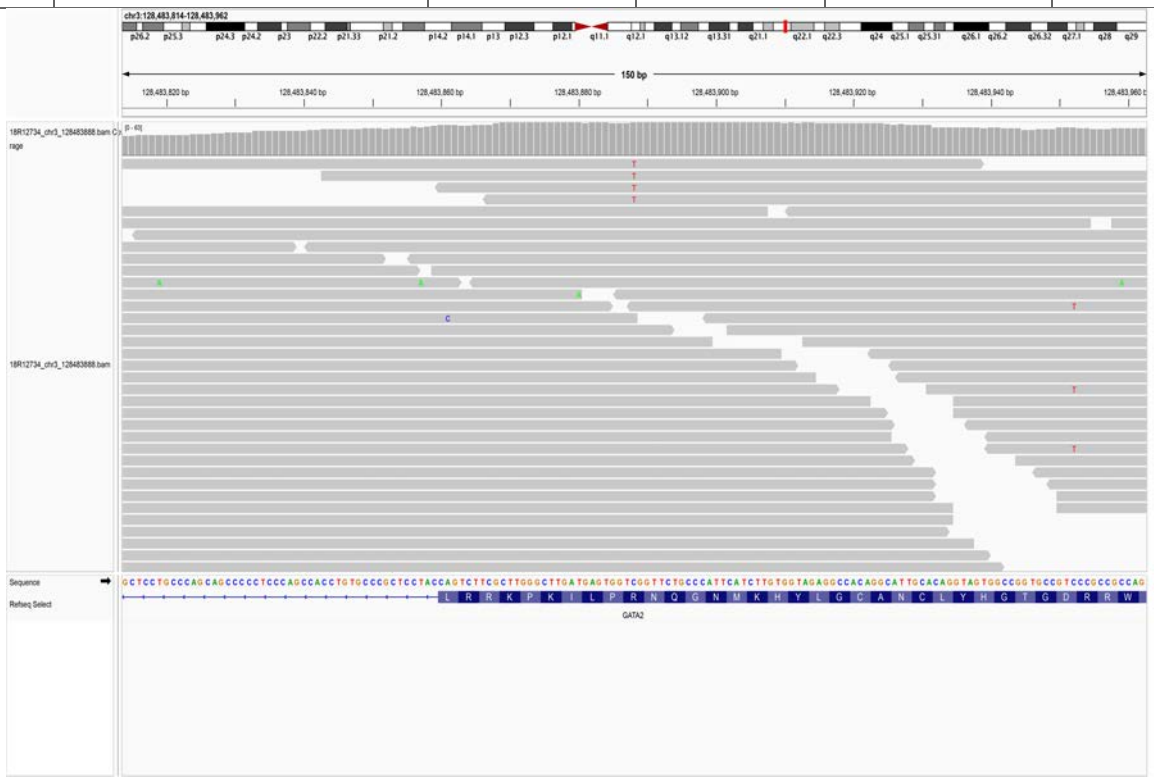
17.2. chr3_128481316_AACCTAGAGGC/-

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



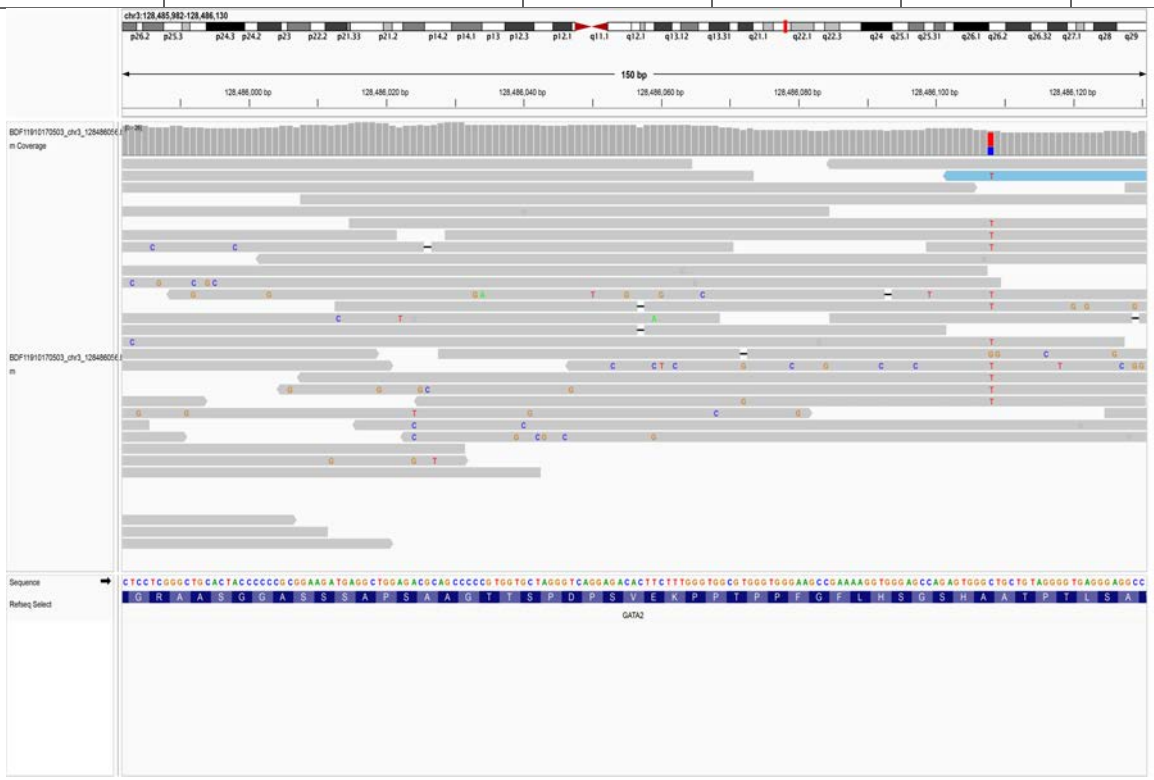
17.3. chr3_128483888_C/T

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



17.4. chr3_128486057_C/-

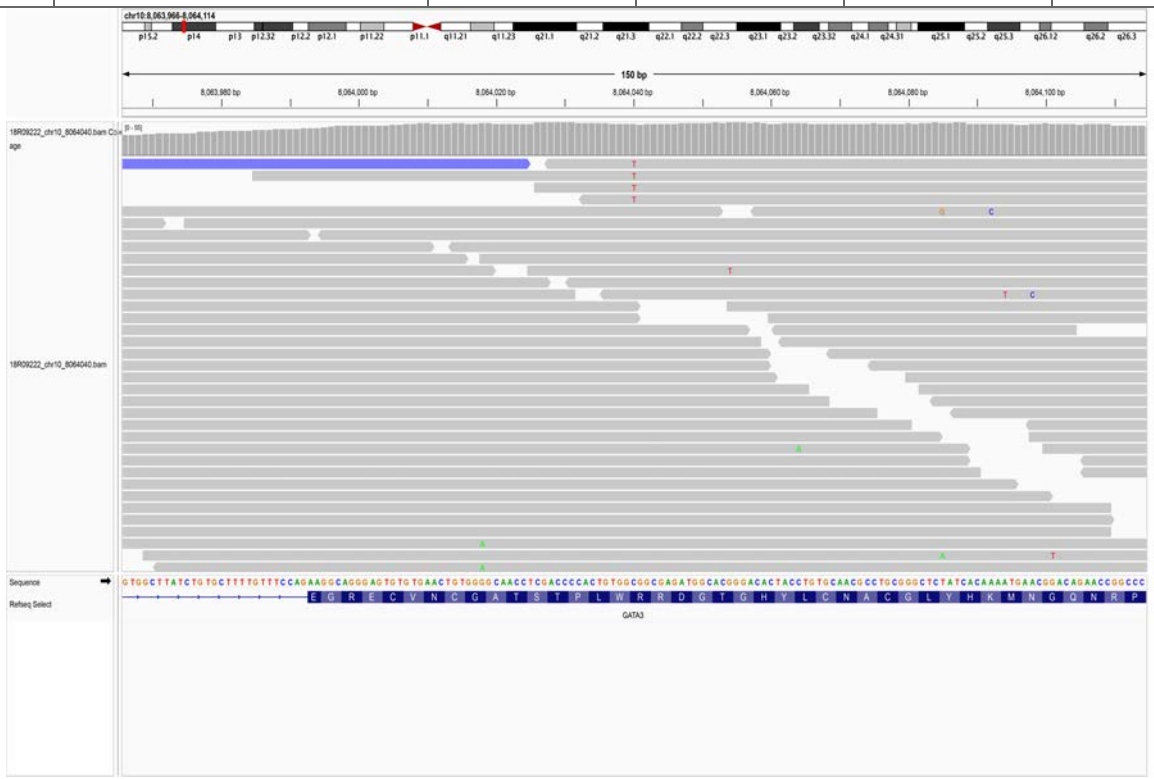
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170503	chr3_128486057_C/-	12	2	*GATA2*	frameshift_variant



18. *GATA3*

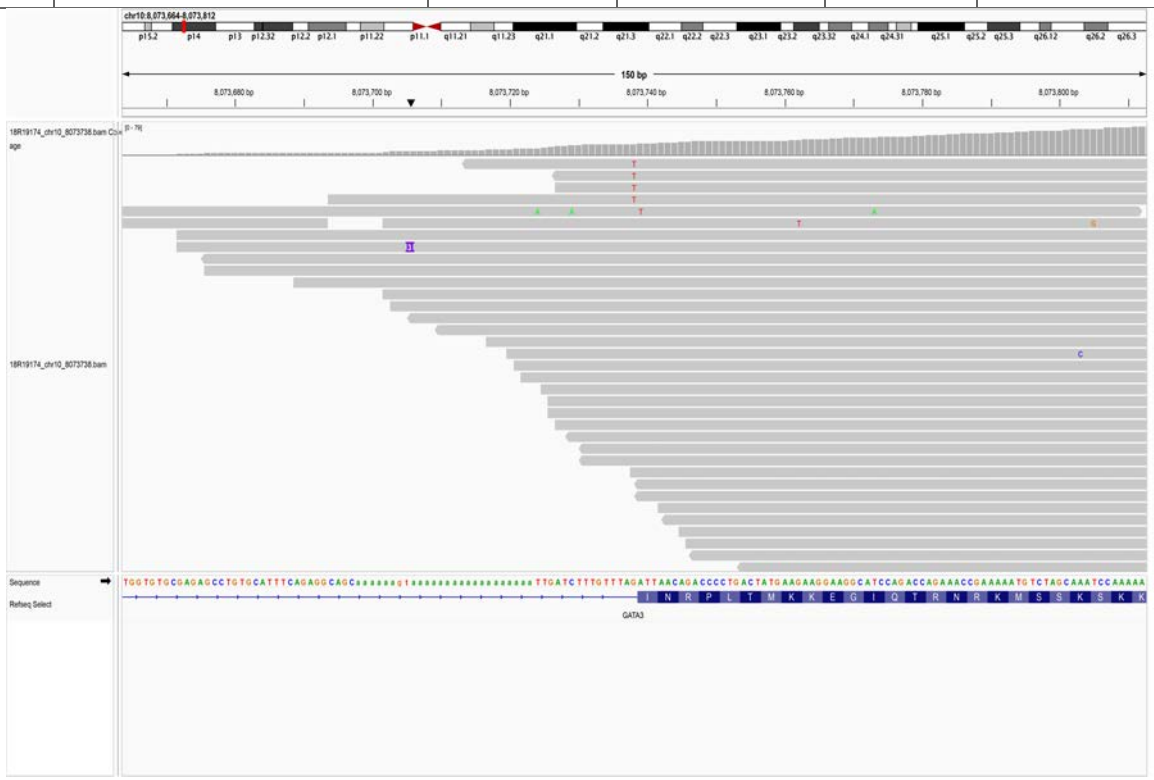
18.1. chr10_8064040_C/T

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

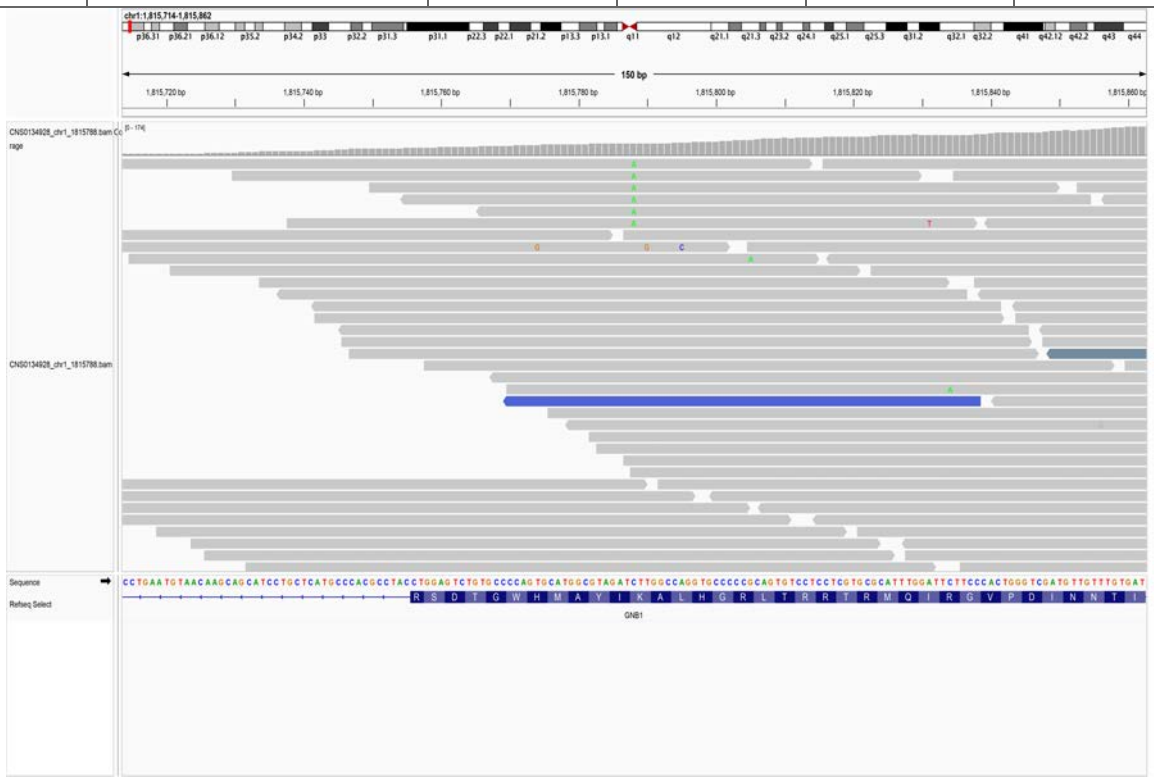
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19174	chr10_8073738_G/T	22	4	*GATA3*	splice_acceptor_variant



19. *GNB1*

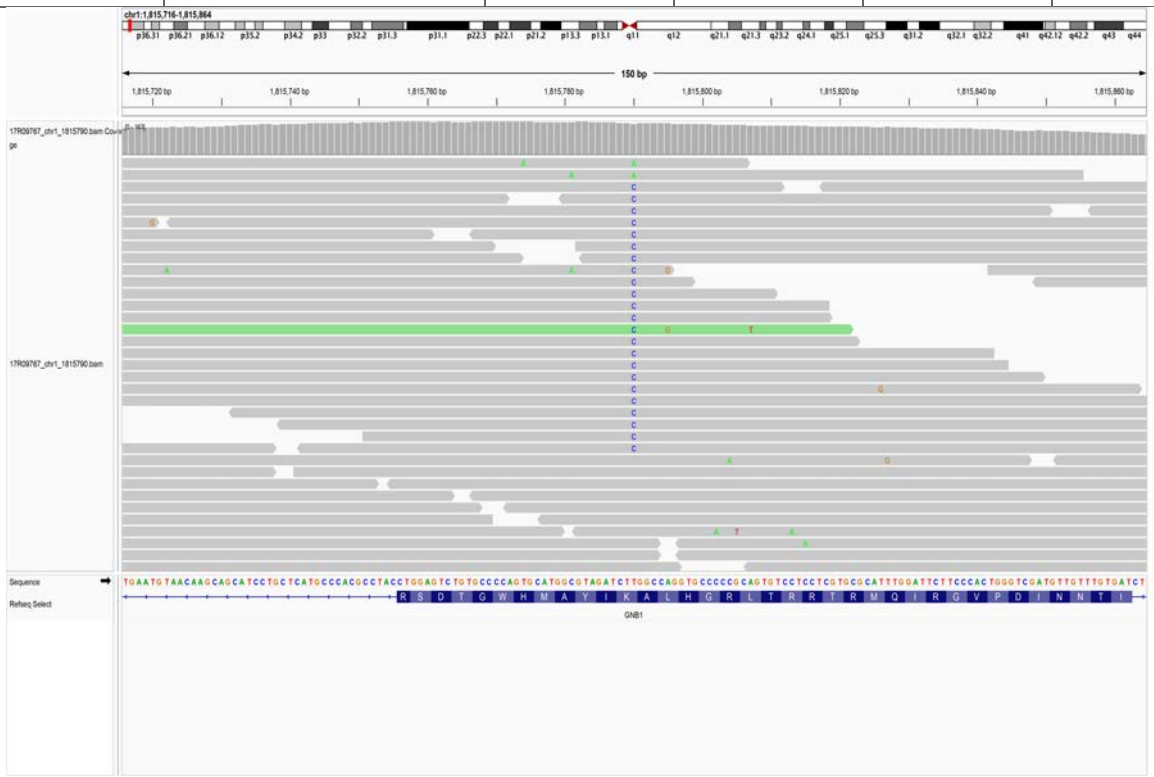
19.1. chr1_1815788_C/A

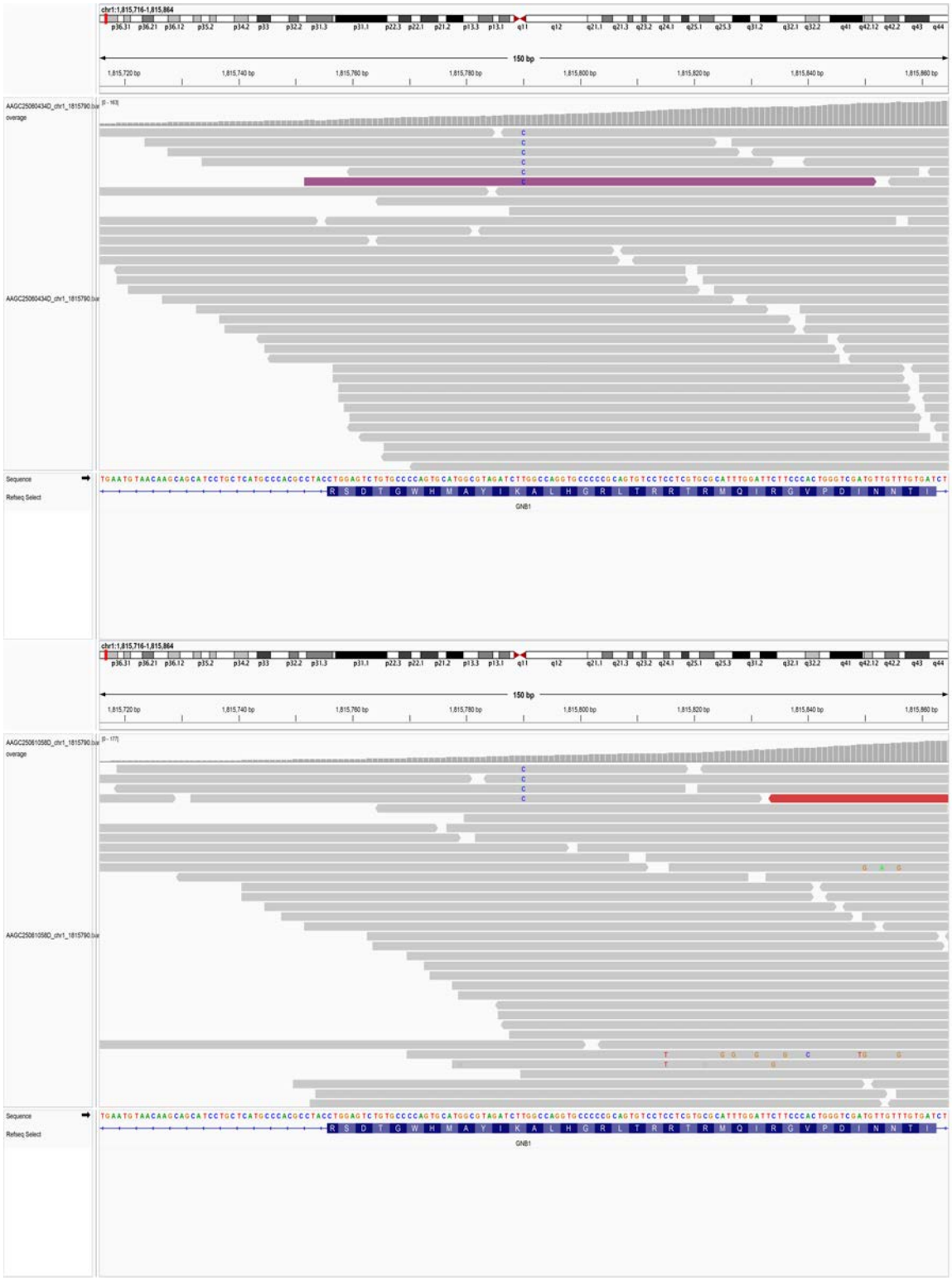
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134928	chr1_1815788_C/A	55	6	*GNB1*	missense_variant

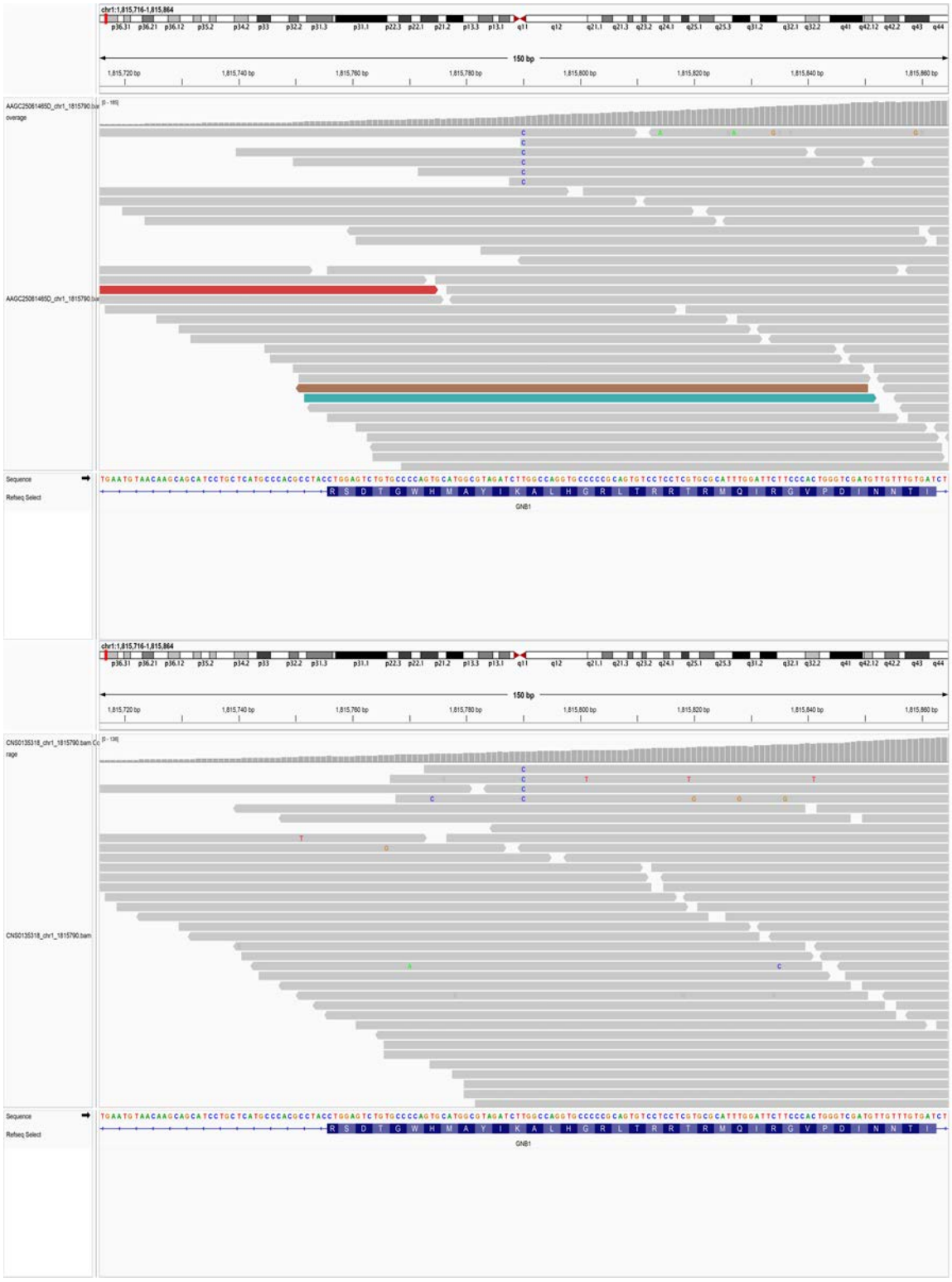


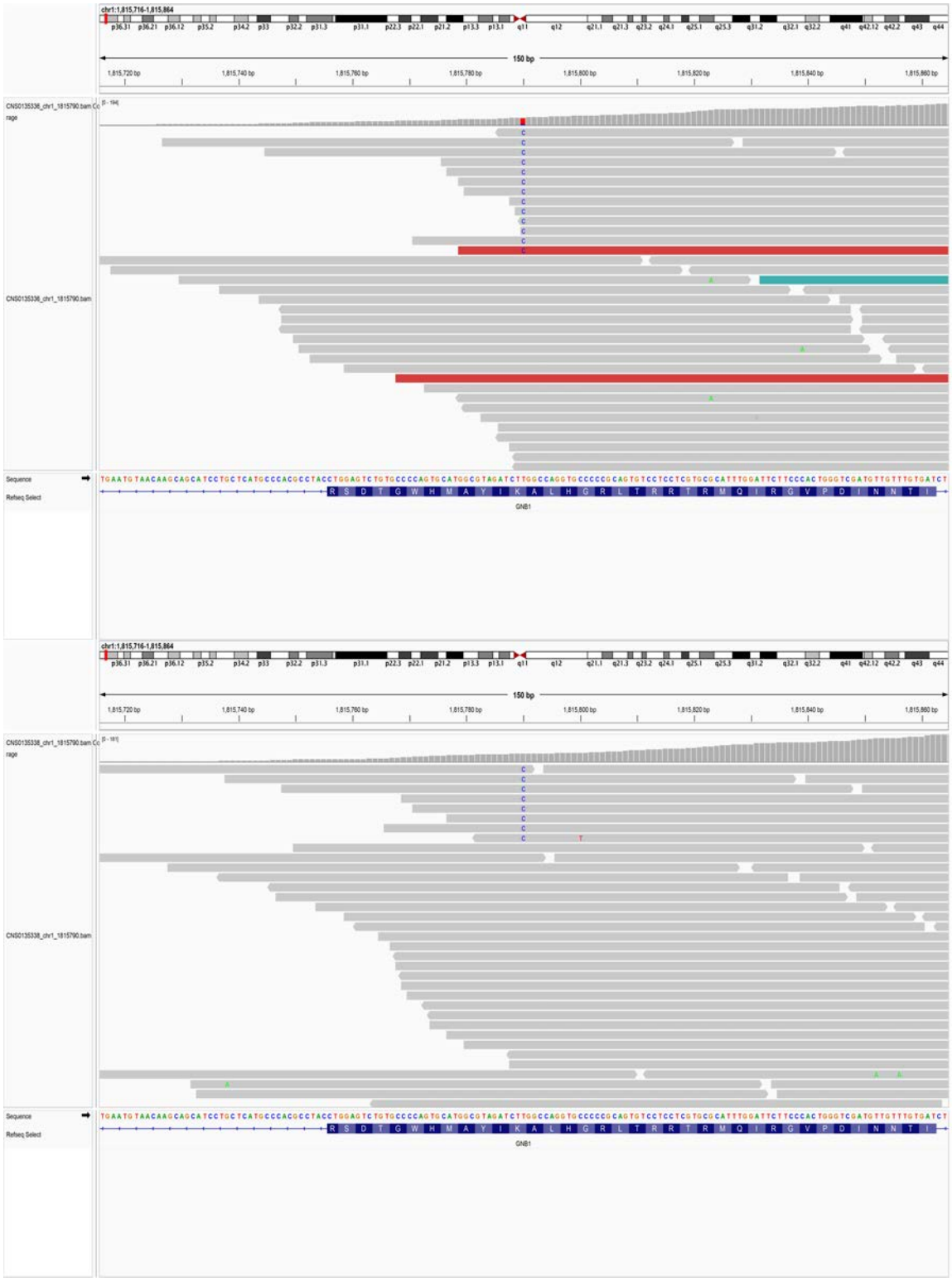
19.2. chr1_1815790_T/C

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
TGAATGTAACAAGCAGCATCCTGCTCATGCCCACGCCTACCTGGAGTCTGTGCCCCAGTGCATGGCGTAGATCTTGGCCAGGTGCCCCCGCAGTGTCCTCCTCGTGCGCATTTGGATTCTTCCCACTGGGTCGATGTTGTTTGTGATCT
R S D T G W H M A Y I K A L H G R L T R R T R M Q I R G V P D I N N T I
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
AAGC25061058D_chr1_1815790.bai
overage
AAGC25061058D_chr1_1815790.bai
Sequence
Refseq Select
TGAATGTAACAAGCAGCATCCTGCTCATGCCCACGCCTACCTGGAGTCTGTGCCCCAGTGCATGGCGTAGATCTTGGCCAGGTGCCCCCGCAGTGTCCTCCTCGTGCGCATTTGGATTCTTCCCACTGGGTCGATGTTGTTTGTGATCT
R S D T G W H M A Y I K A L H G R L T R R T R M Q I R G V P D I N N T I
GNB1

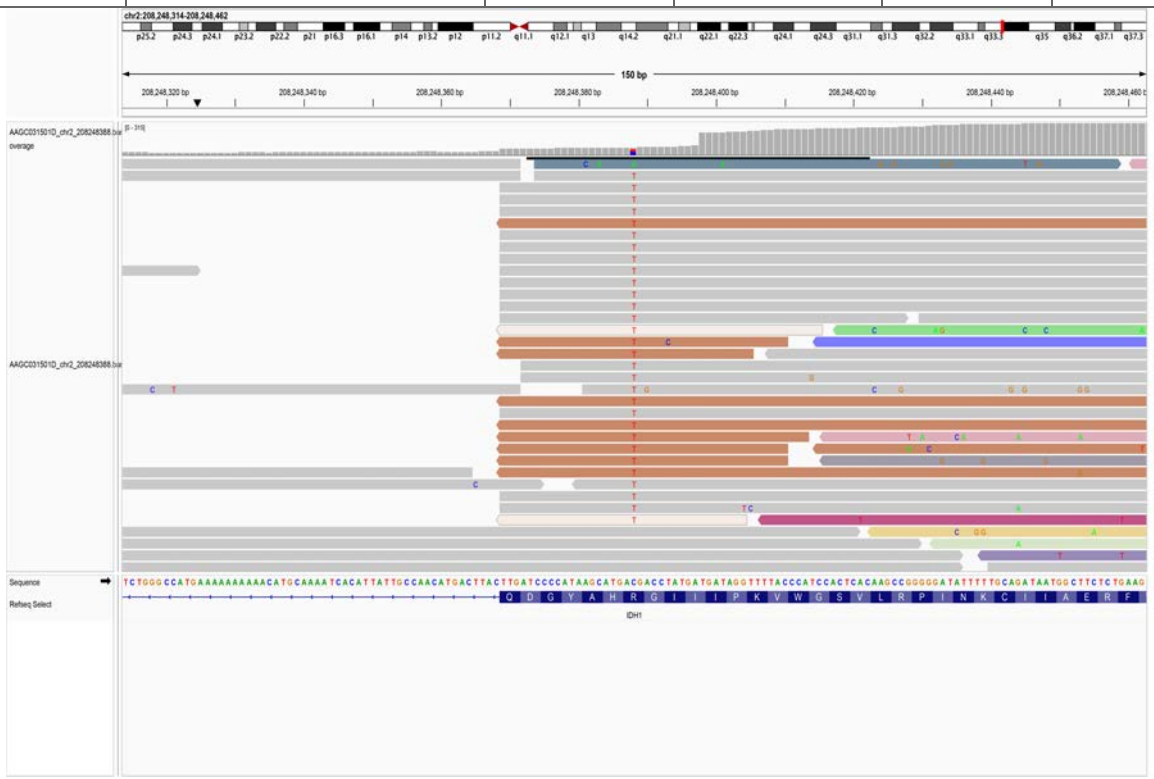

chr1:1,815,716-1,815,864
150 bp
1,815,720 bp
1,815,740 bp
1,815,760 bp
1,815,780 bp
1,815,800 bp
1,815,820 bp
1,815,840 bp
1,815,860 bp
Sequence
Refseq Select
GNB1
chr1:1,815,716-1,815,864
150 bp
CNS0135318_chr1_1815790.bam
Sequence
Refseq Select
GNB1


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
CNS0135336_chr1_1815790.bam
Sequence
Refseq Select
GNB1
chr1:1,815,716-1,815,864
150 bp
CNS0135338_chr1_1815790.bam
Sequence
Refseq Select
GNB1

20. *IDH1*

20.1. chr2_208248388_C/T

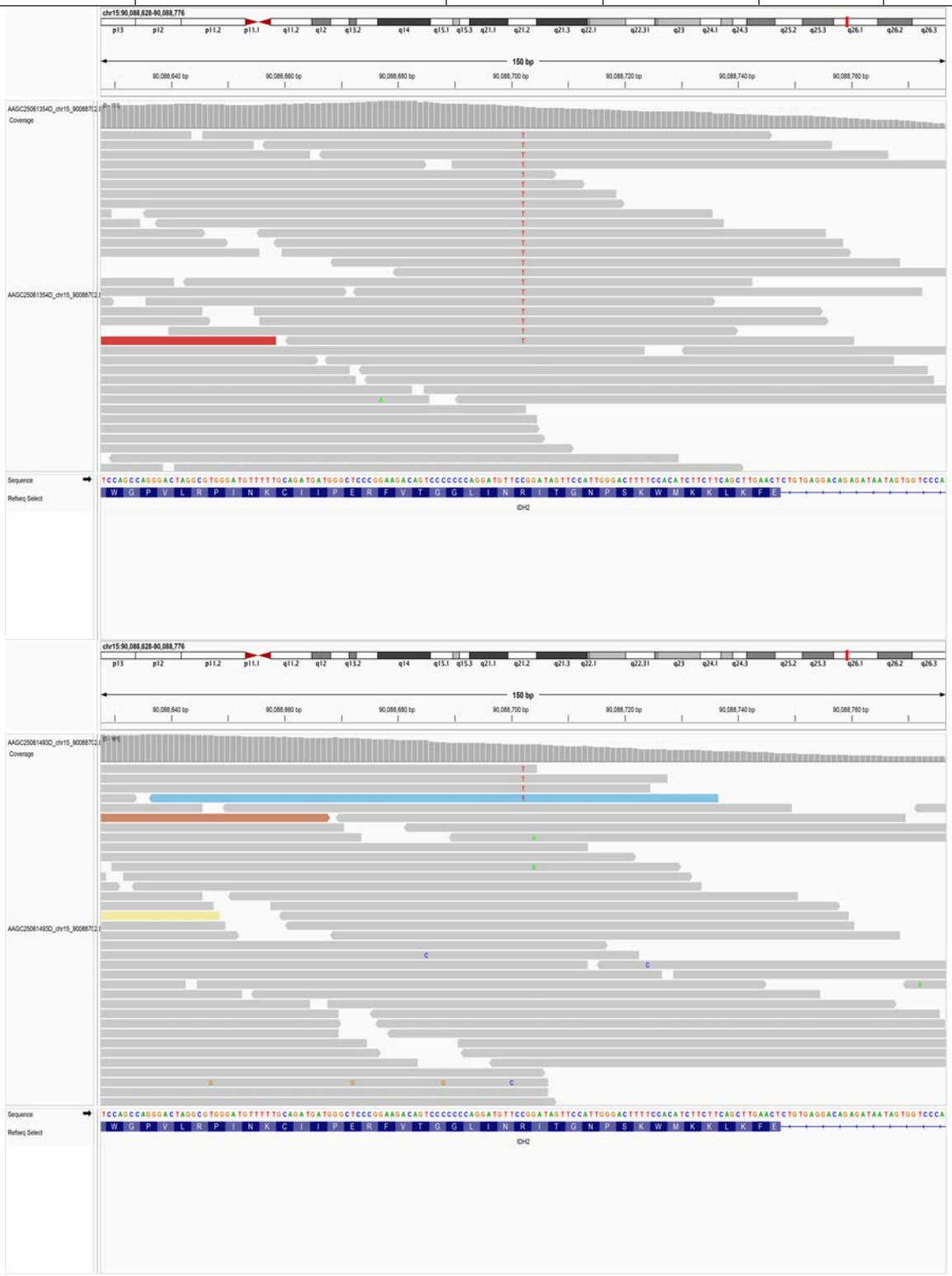
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC031501D	chr2_208248388_C/T	38	6	*IDH1*	missense_variant



21. *IDH2*

21.1. chr15_90088702_C/T

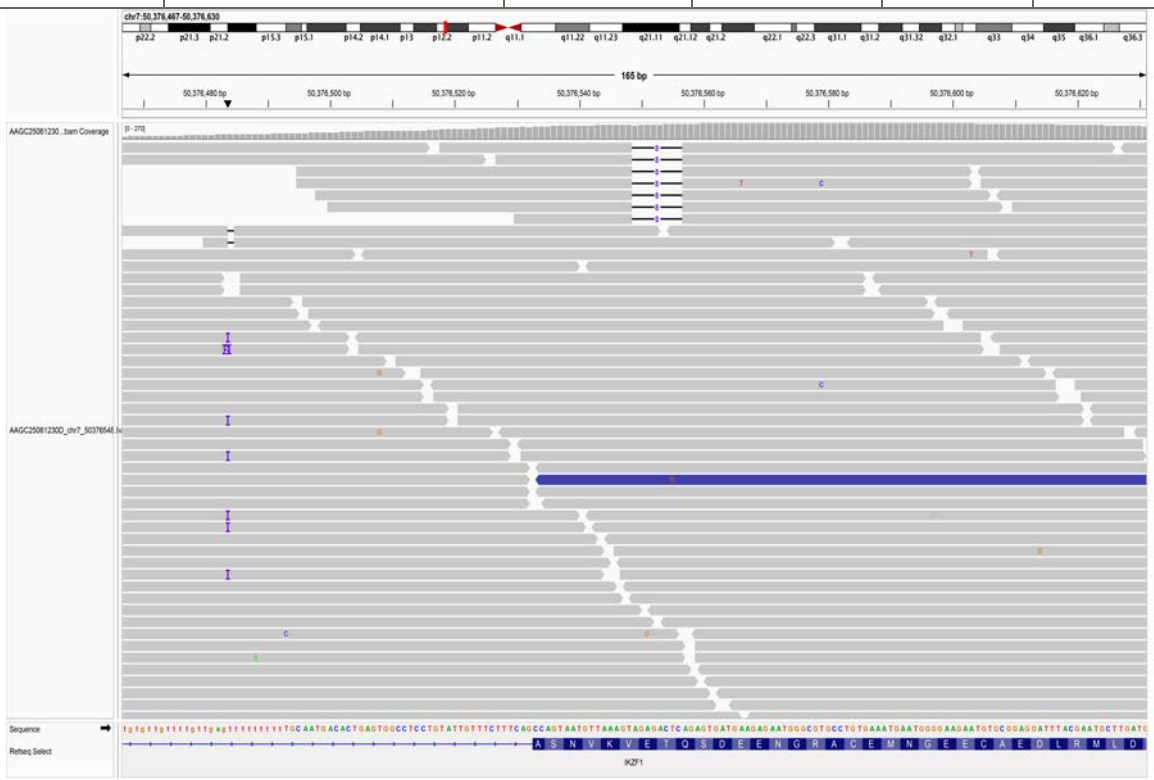
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061354D	chr15_90088702_C/T	96	22	*IDH2*	missense_variant
AAGC25061493D	chr15_90088702_C/T	97	4	*IDH2*	missense_variant



22. *IKZF1*

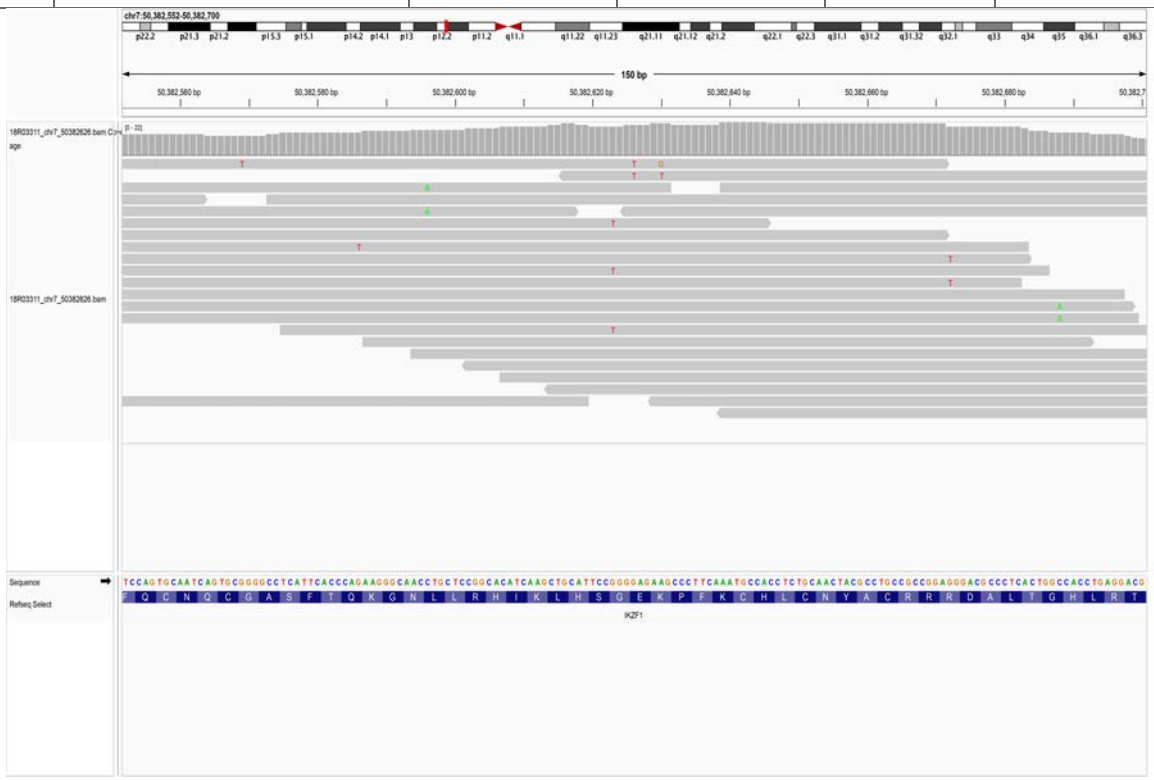
22.1. chr7_50376549_AGAGACTC/-

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



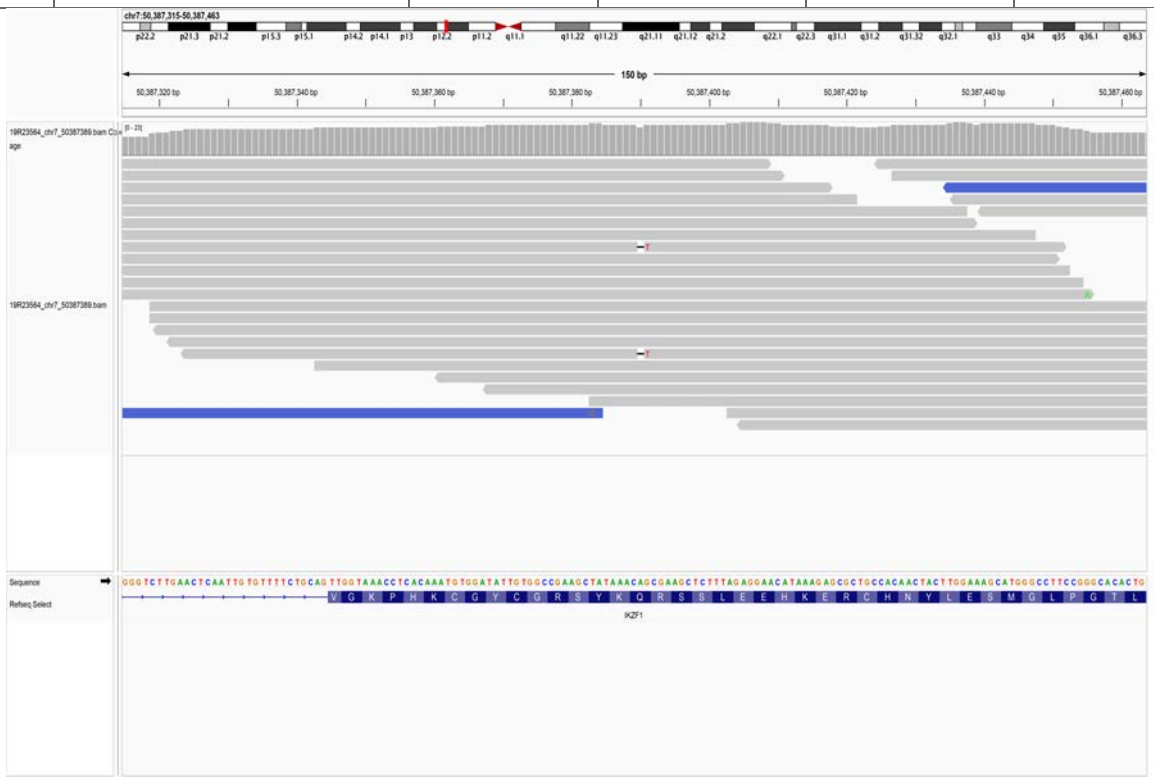
22.2. chr7_50382626_G/T

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



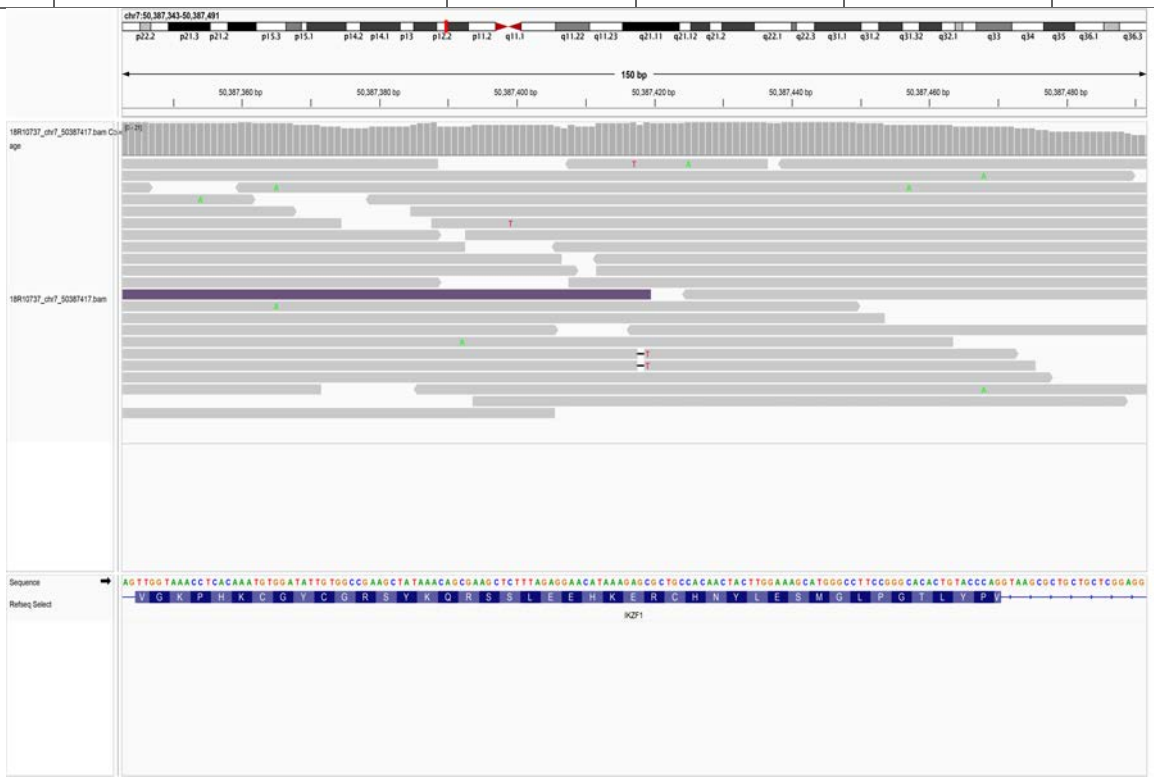
22.3. chr7_50387390_A/-

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



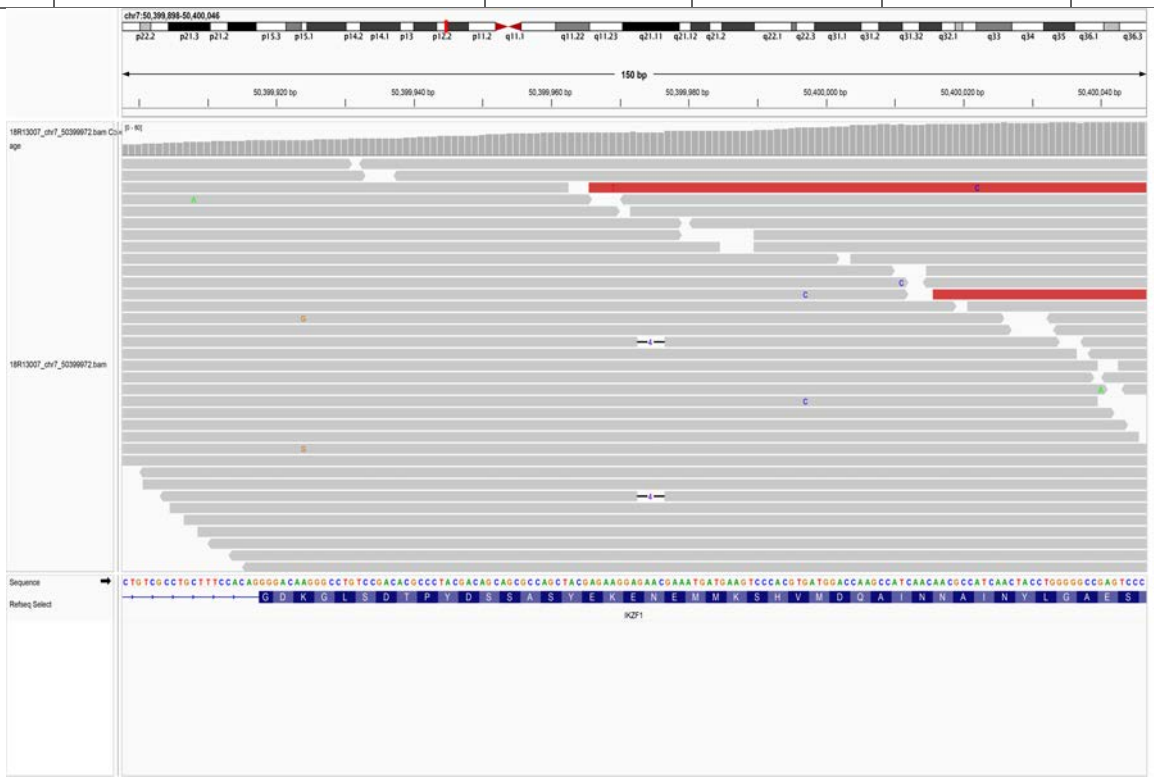
22.4. chr7_50387418_G/-

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



22.5. chr7_50399973_GAAC/-

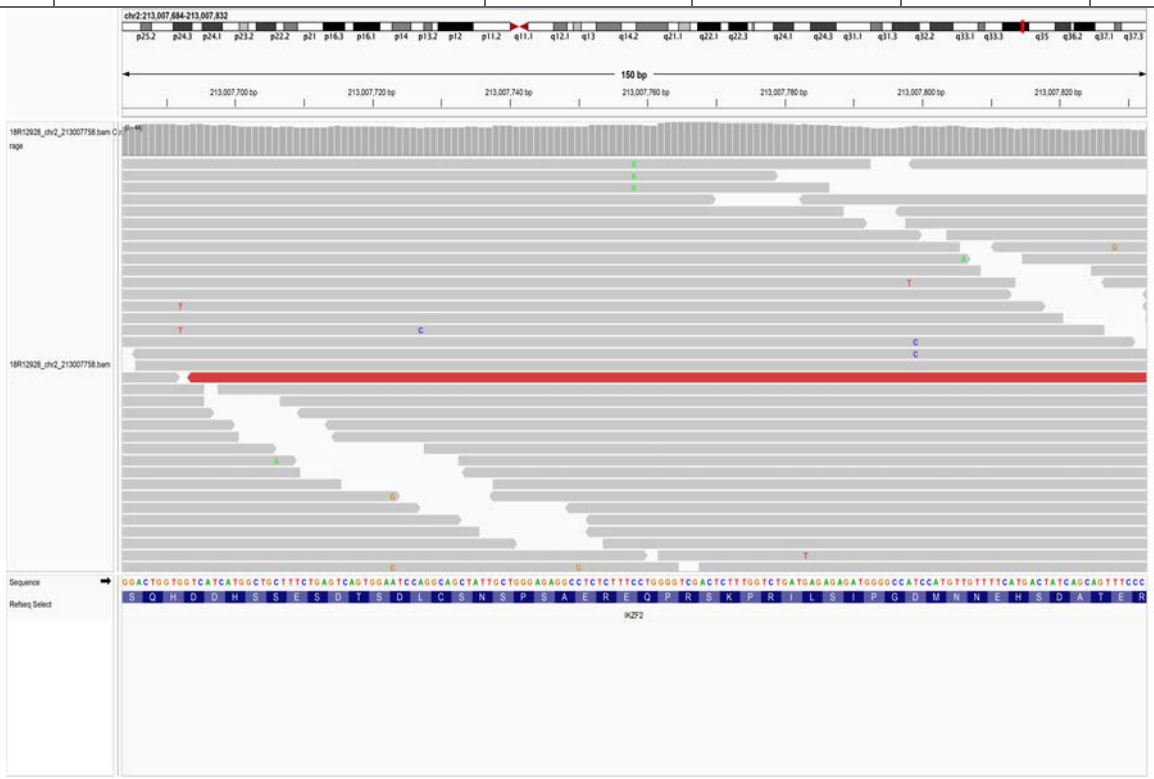
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13007	chr7_50399973_GAAC/-	55	2	*IKZF1*	frameshift_variant



23. *IKZF2*

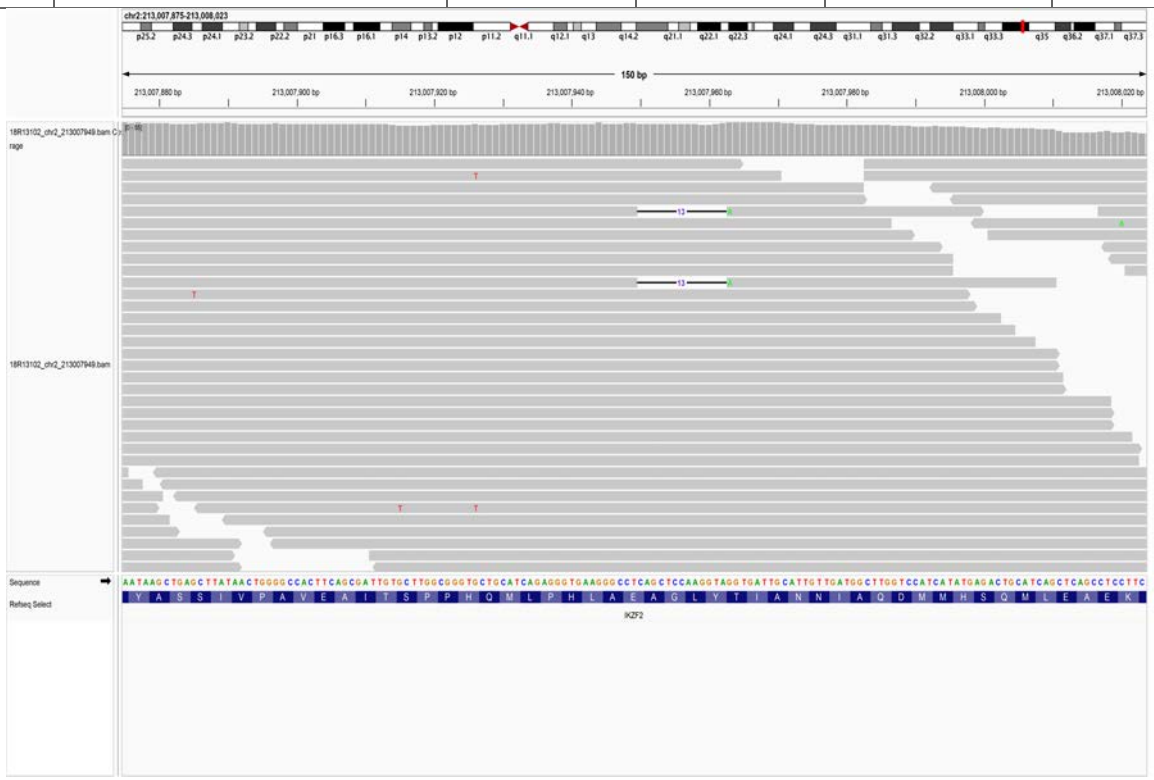
23.1. chr2_213007758_C/A

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



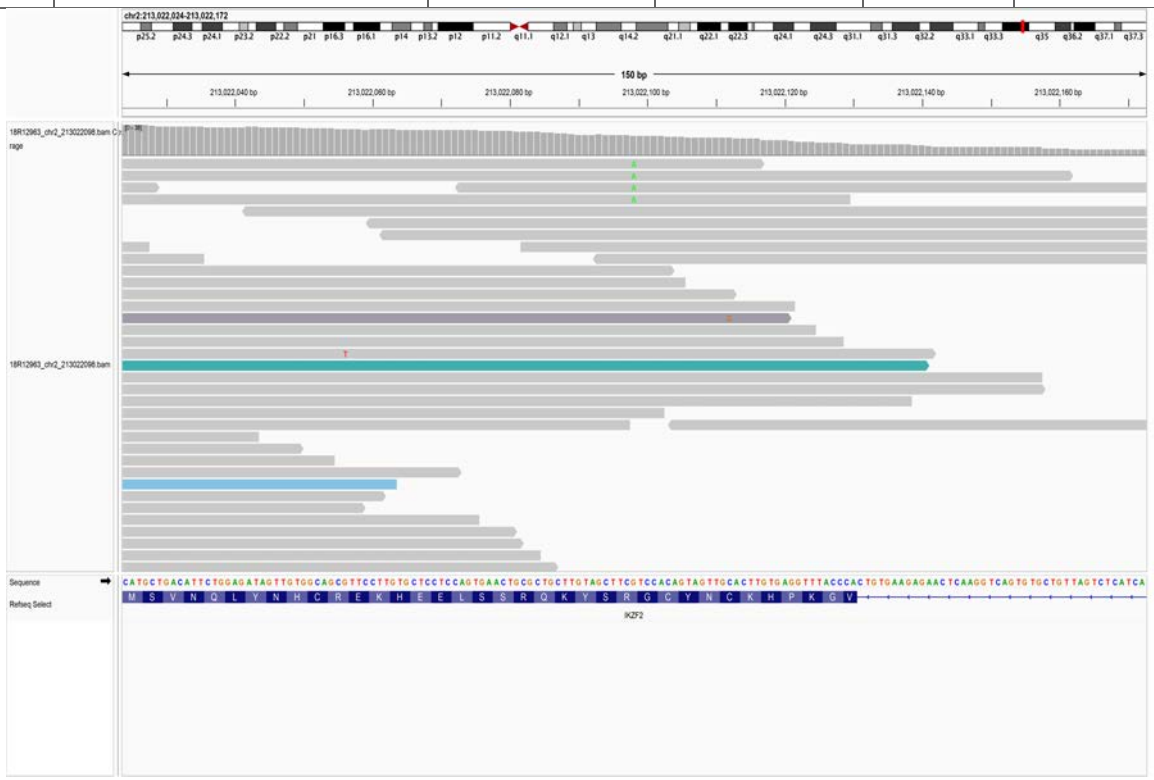
23.2. chr2_213007950_C/-

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



23.3. chr2_213022098_G/A

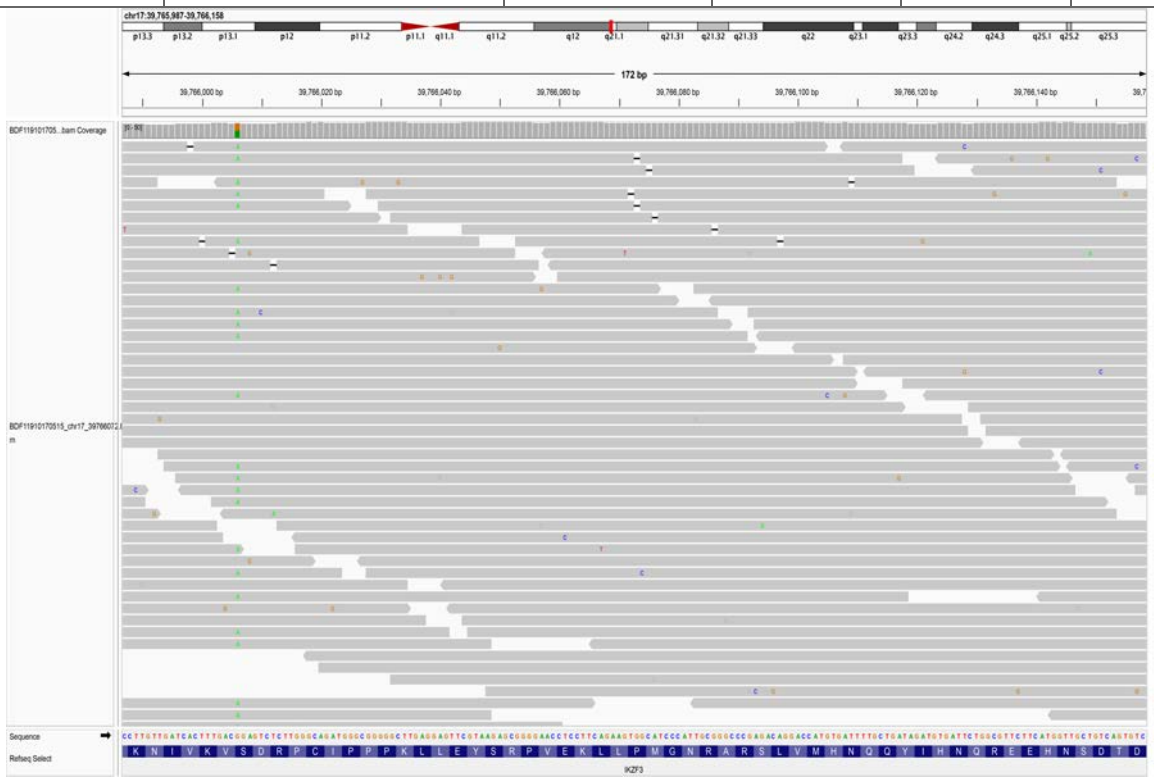
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12963	chr2_213022098_G/A	17	4	*IKZF2*	stop_gained



24. *IKZF3*

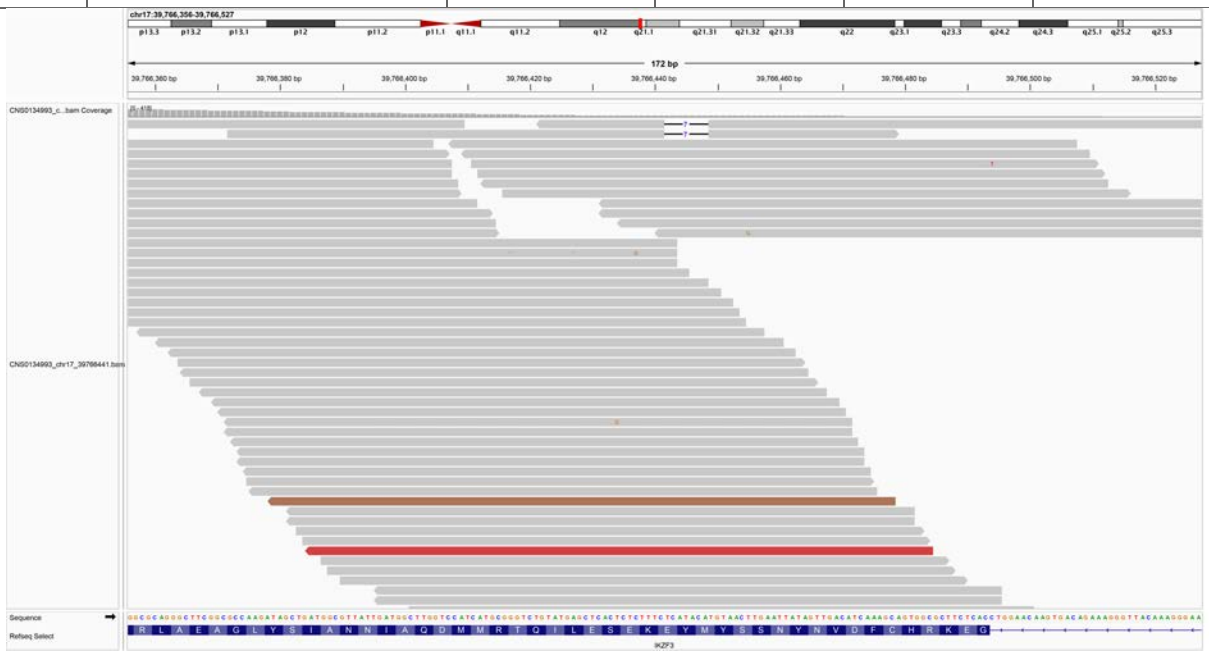
24.1. chr17_39766073_G/-

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



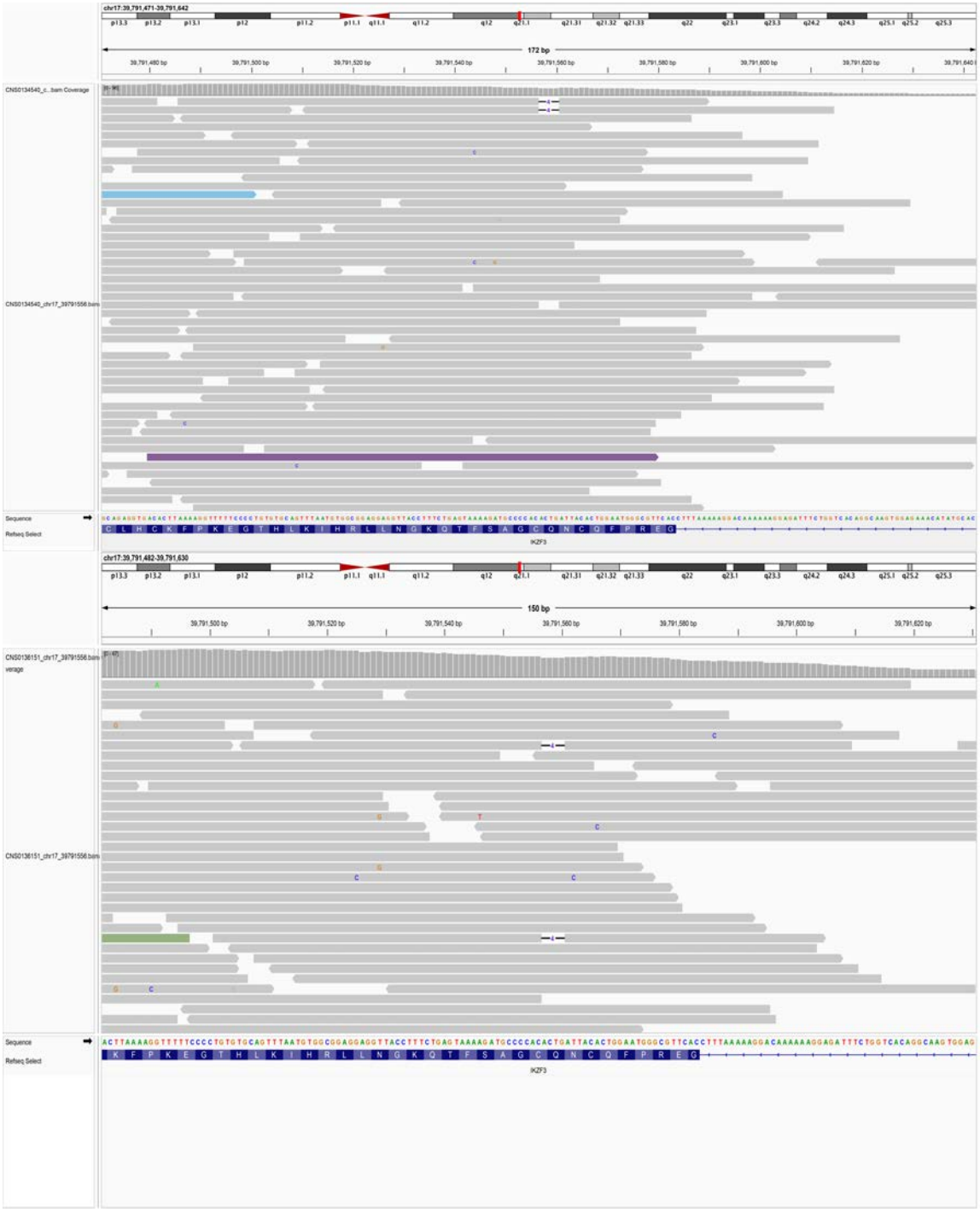
24.2. chr17_39766442_TCATACA/-

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



24.3. chr17_39791557_ACTG/-

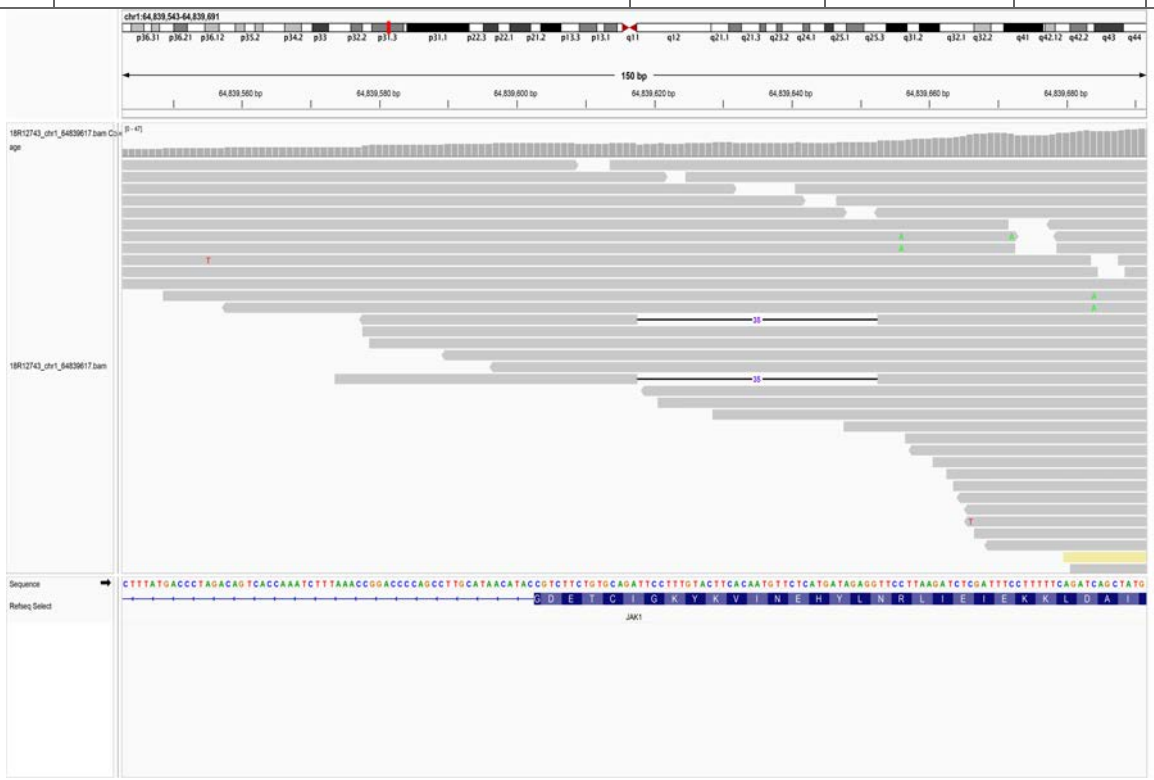
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0134540	chr17_39791557_ACTG/-	59	2	*IKZF3*	frameshift_variant
CNS0136151	chr17_39791557_ACTG/-	46	2	*IKZF3*	frameshift_variant



25. *JAK1*

25.1. chr1_64839618_TTCCTTTGTACTTCACAATGTTCTCATGATAGAGG/-

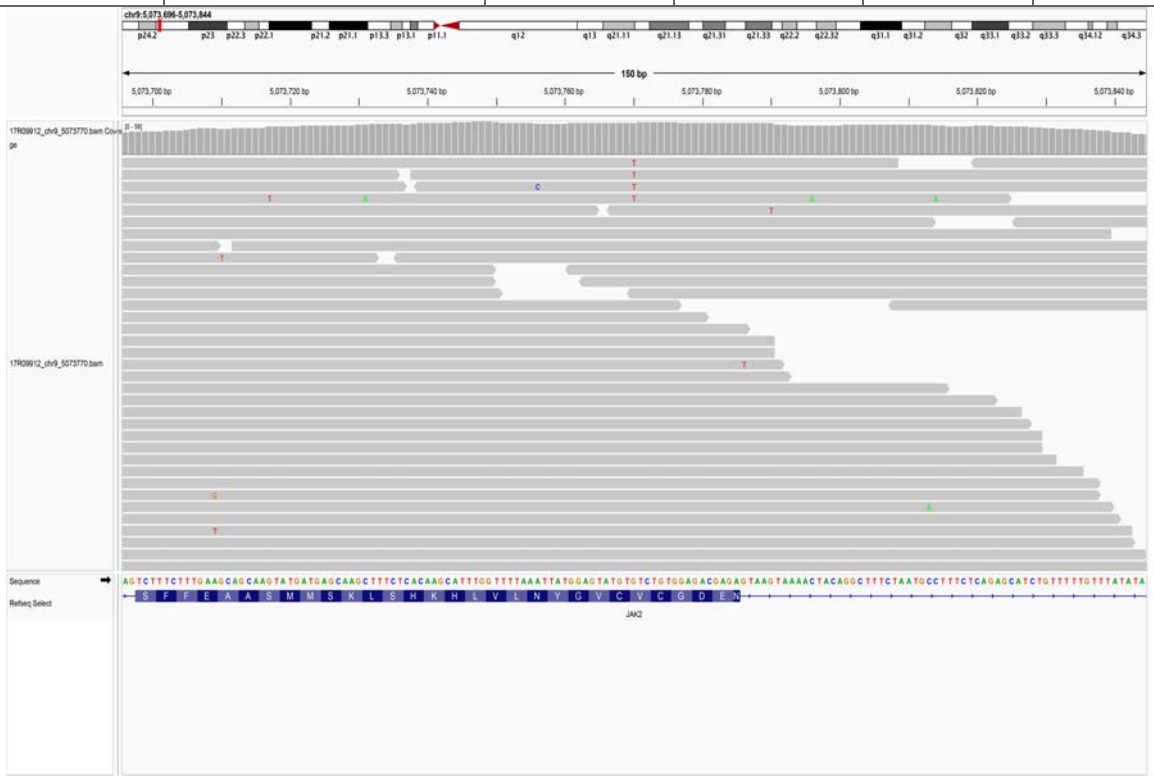
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12743	chr1_64839618_TTCCTTTGTACTTCACAATGTTCTCATGATAGAGG/-	23	2	*JAK1*	frameshift_variant

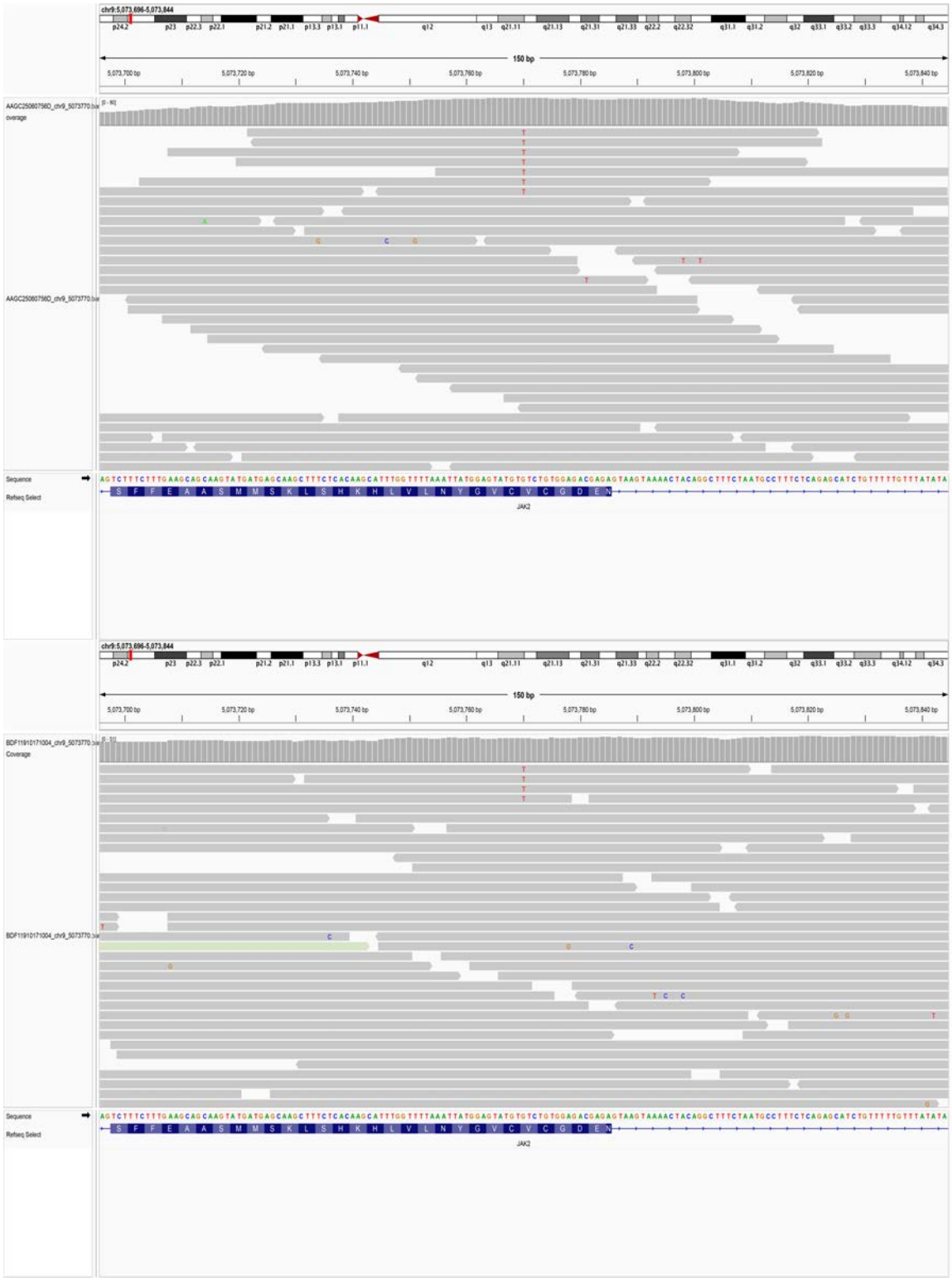


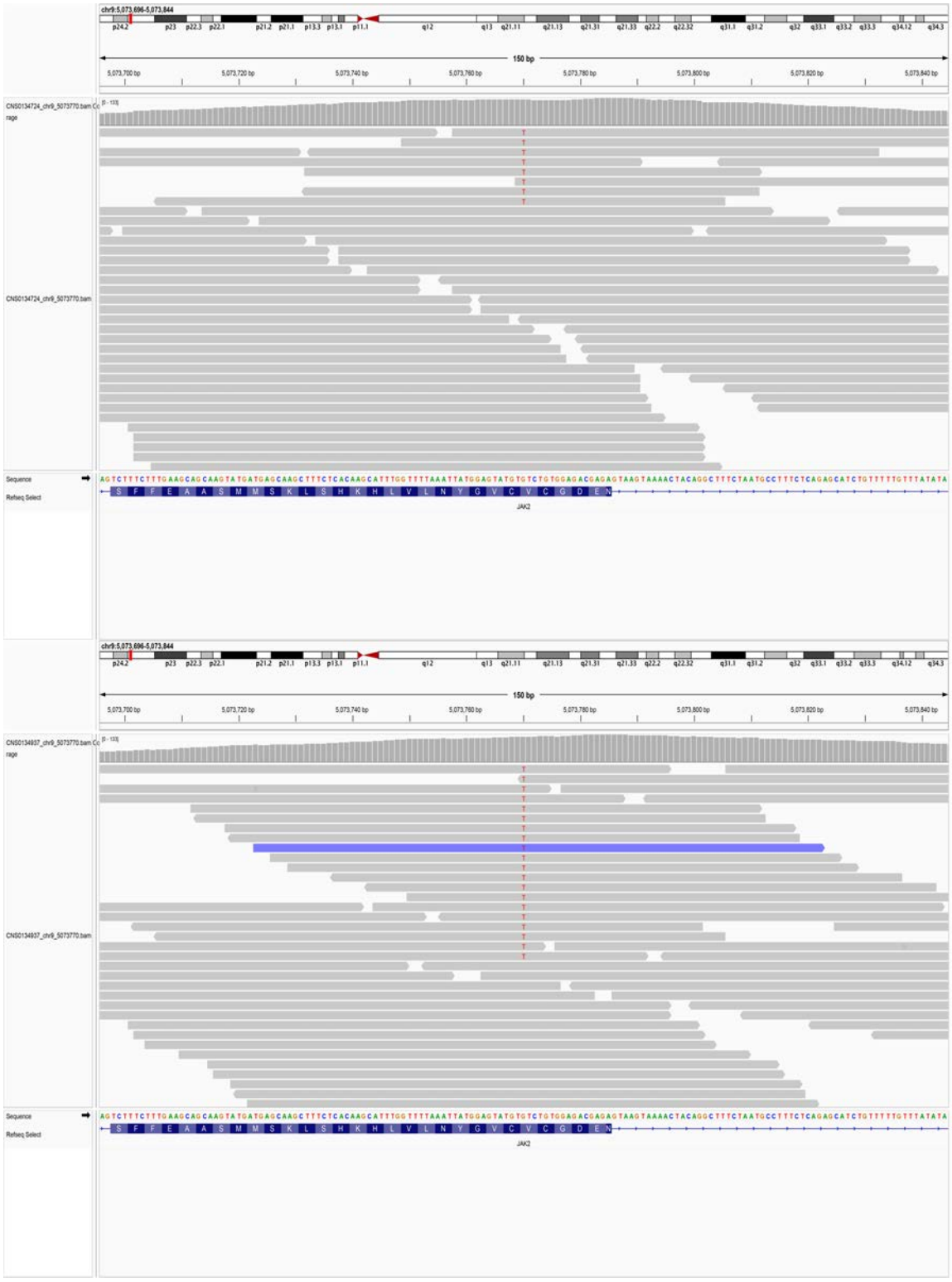
26. *JAK2*

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



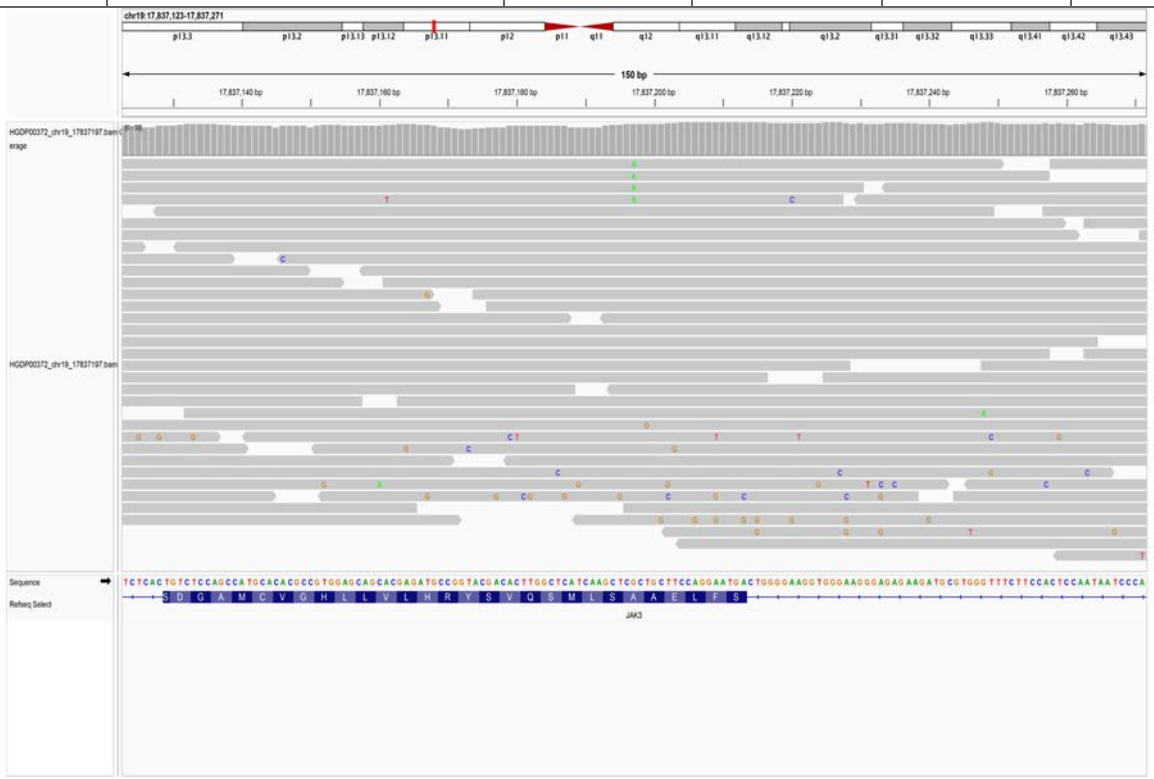

chr9:5,073,696-5,073,844
150 bp
5,073,700 bp
5,073,720 bp
5,073,740 bp
5,073,760 bp
5,073,780 bp
5,073,800 bp
5,073,820 bp
5,073,840 bp
AAGC25060756D_chr9_5073770.bai
overage
Sequence
Refseq Select
JAK2
chr9:5,073,696-5,073,844
150 bp
BDF11910171004_chr9_5073770.bai
Coverage
Sequence
Refseq Select
JAK2


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
Sequence
Refseq Select
JAK2
chr9:5,073,696-5,073,844
150 bp
CNS0134937_chr9_5073770.bam
Sequence
Refseq Select
JAK2

27. *JAK3*

27.1. chr19_17837197_G/A

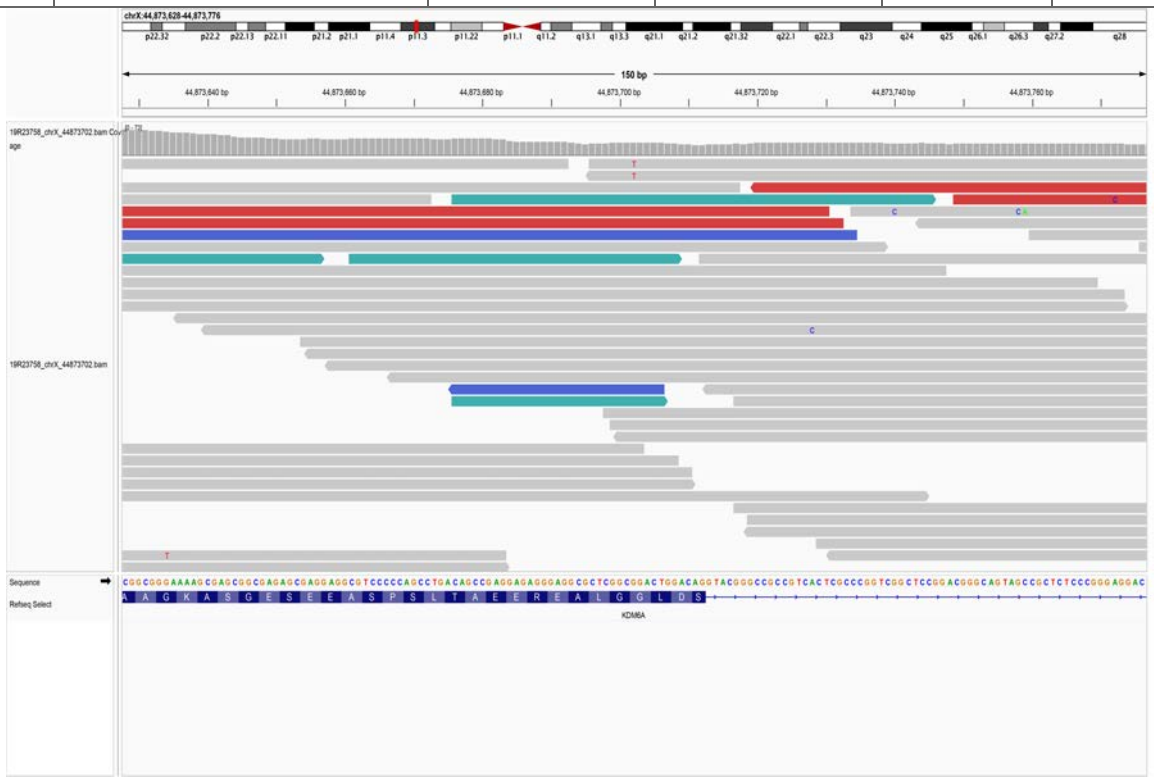
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HGDP00372	chr19_17837197_G/A	23	4	*JAK3*	missense_variant



28. *KDM6A*

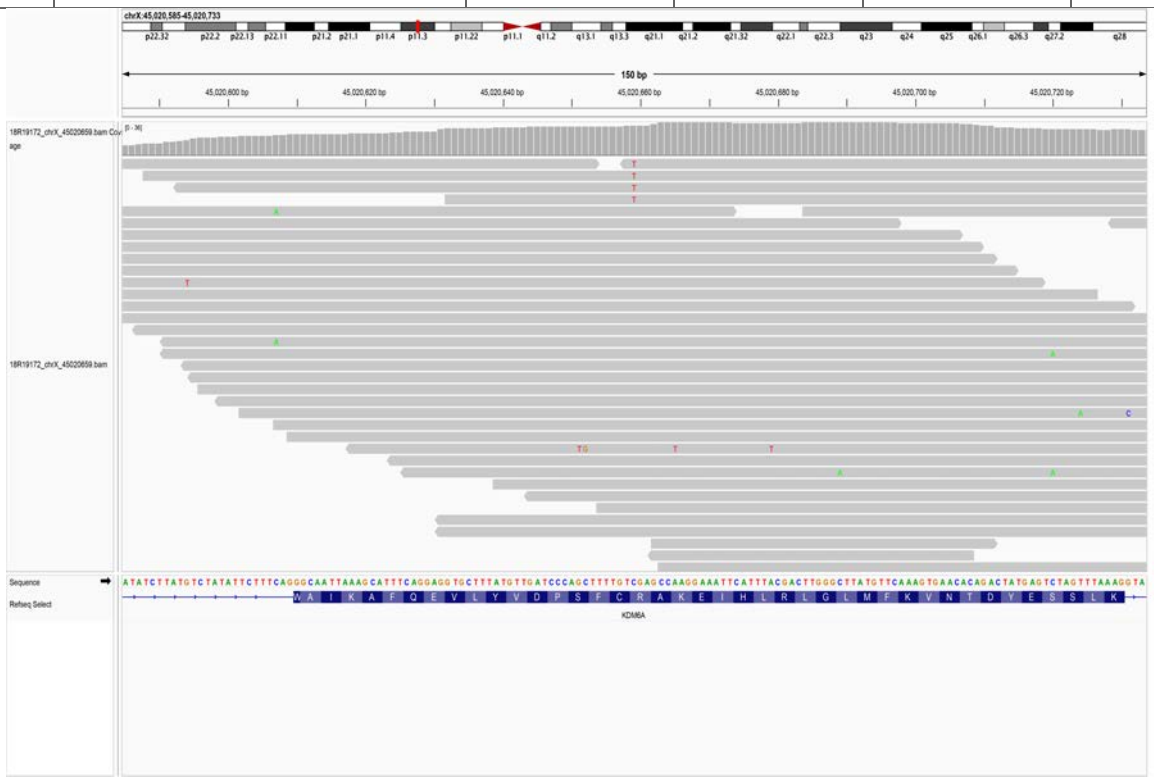
28.1. chrX_44873702_G/T

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



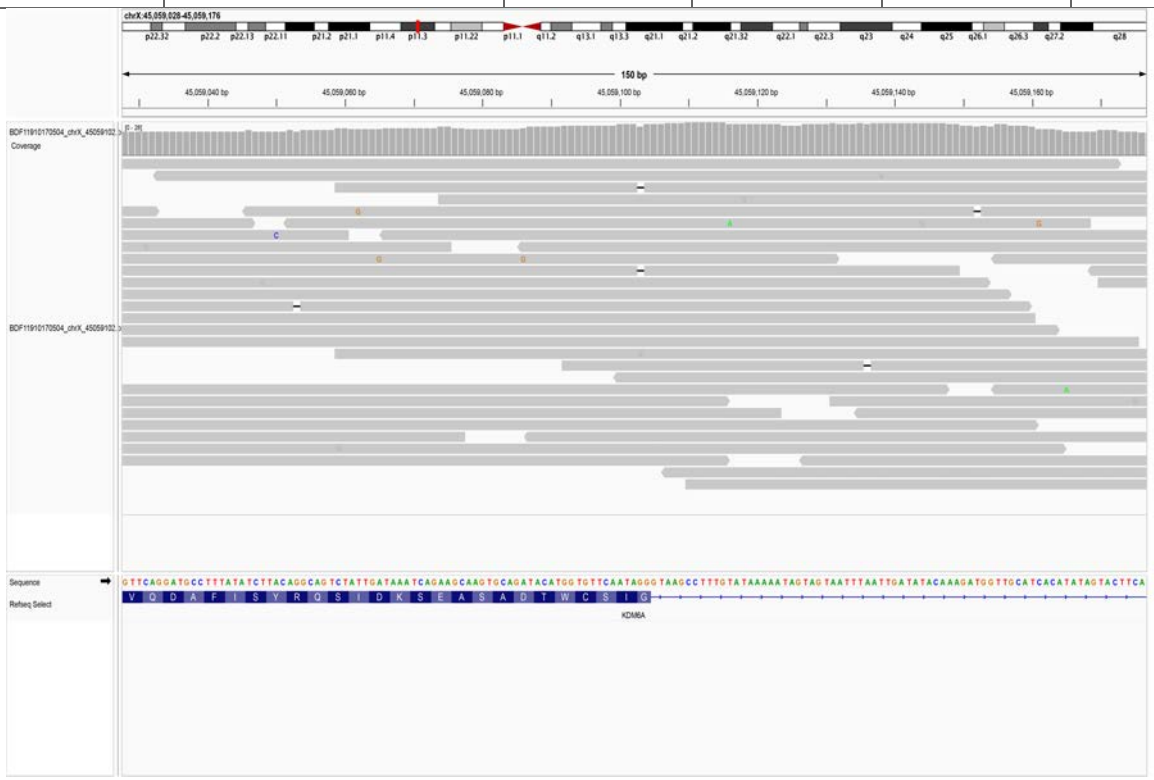
28.2. chrX_45020659_C/T

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



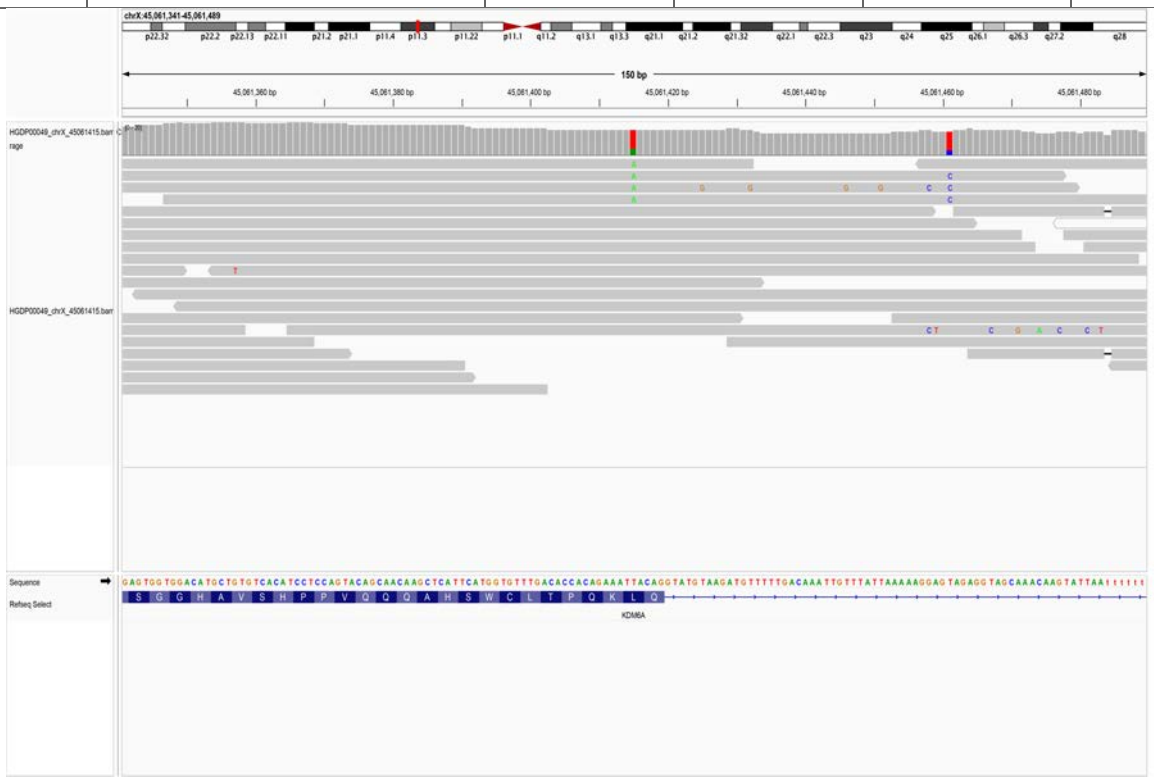
28.3. chrX_45059103_G/-

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



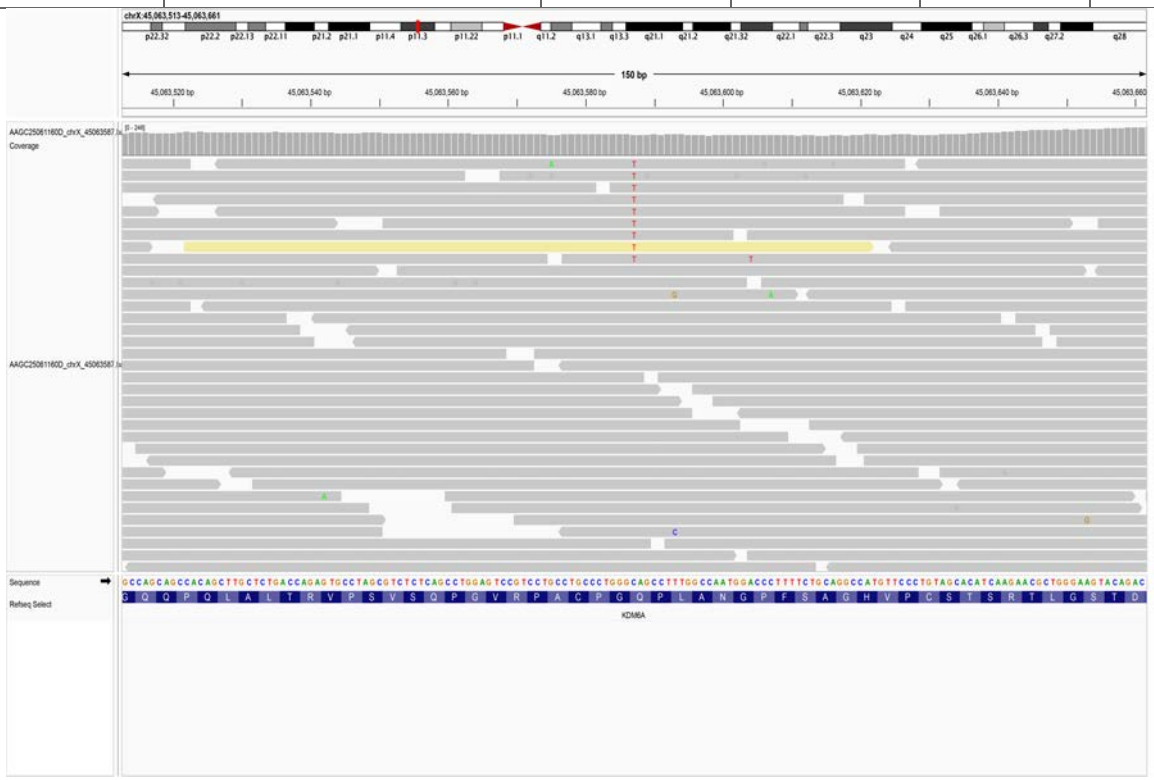
28.4. chrX_45061415_T/A

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



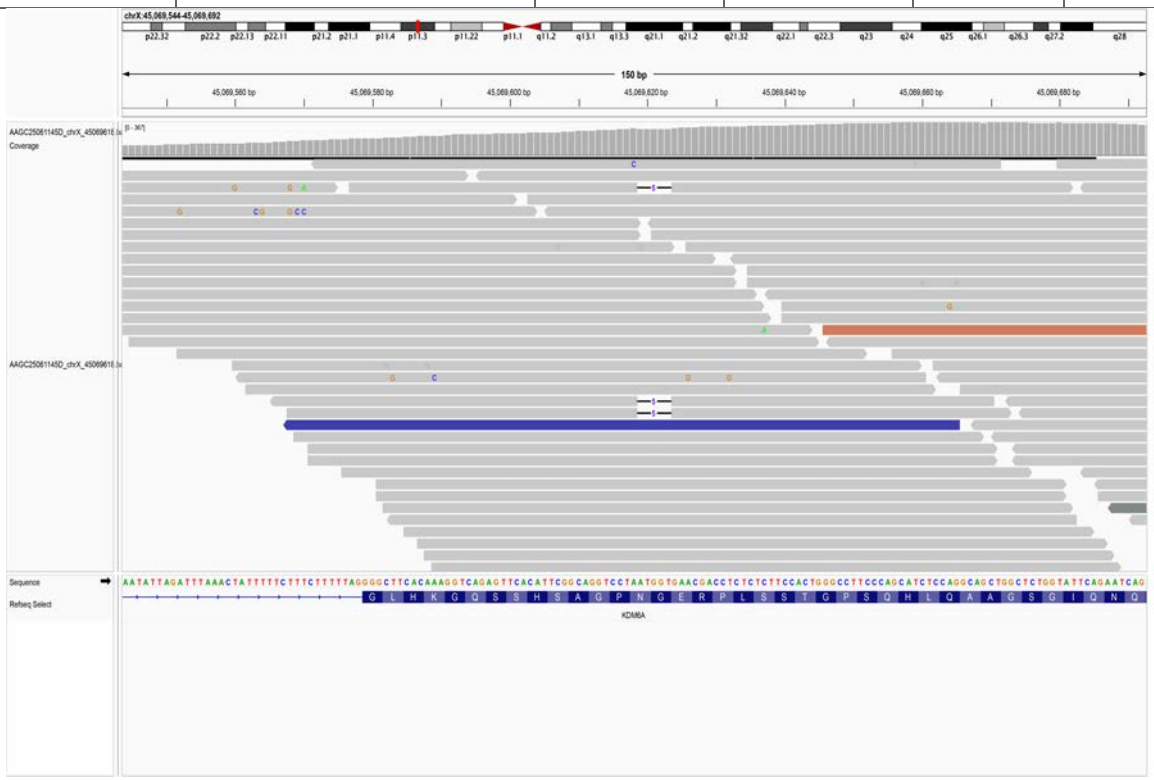
28.5. chrX_45063587_C/T

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



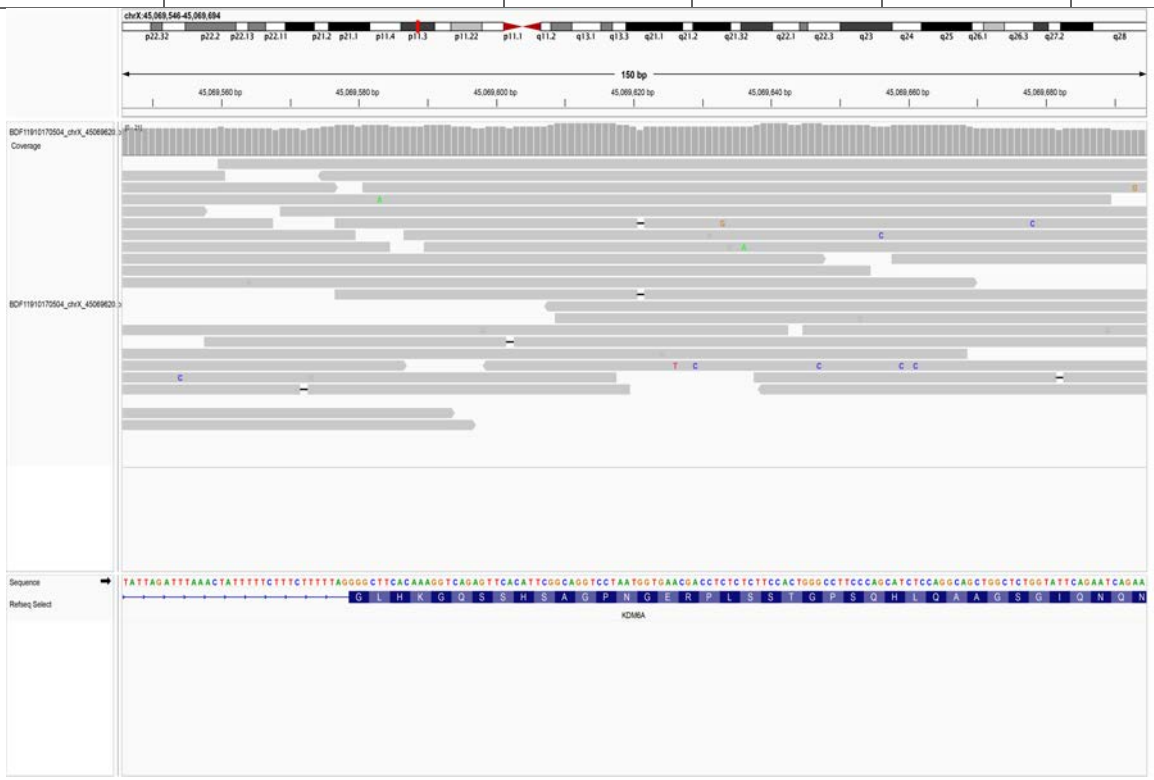
28.6. chrX_45069619_ATGGT/-

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



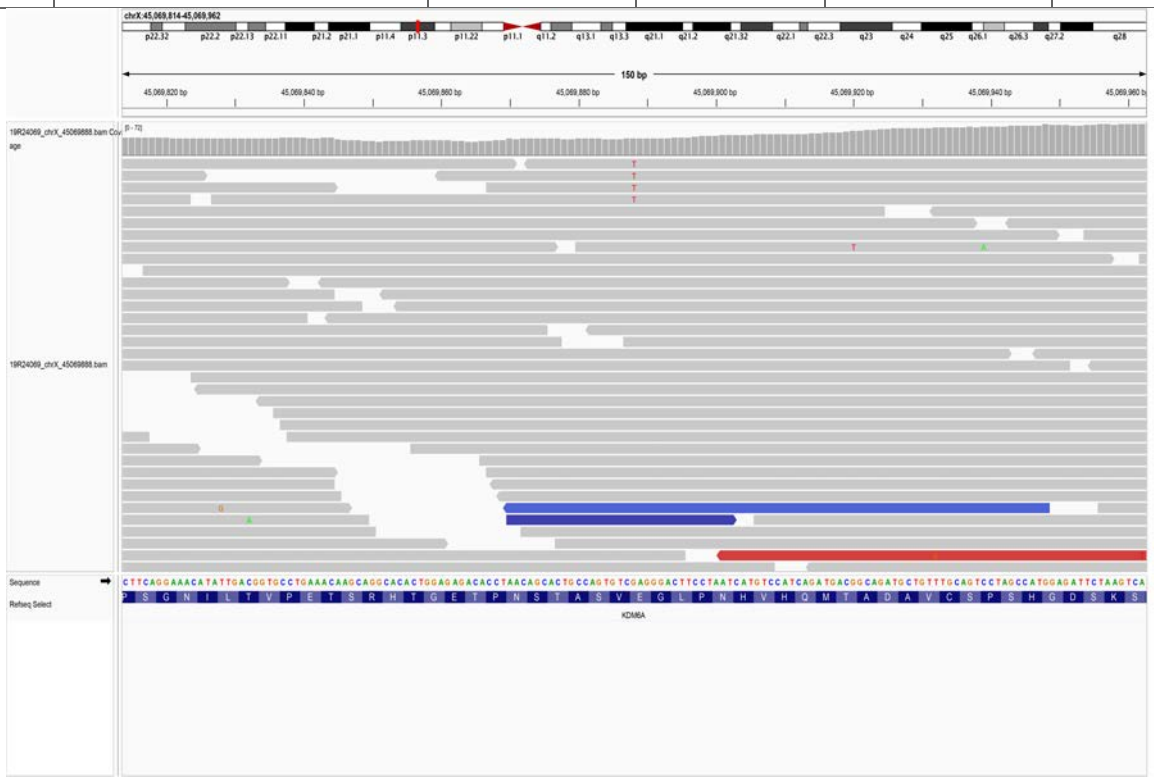
28.7. chrX_45069621_G/-

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



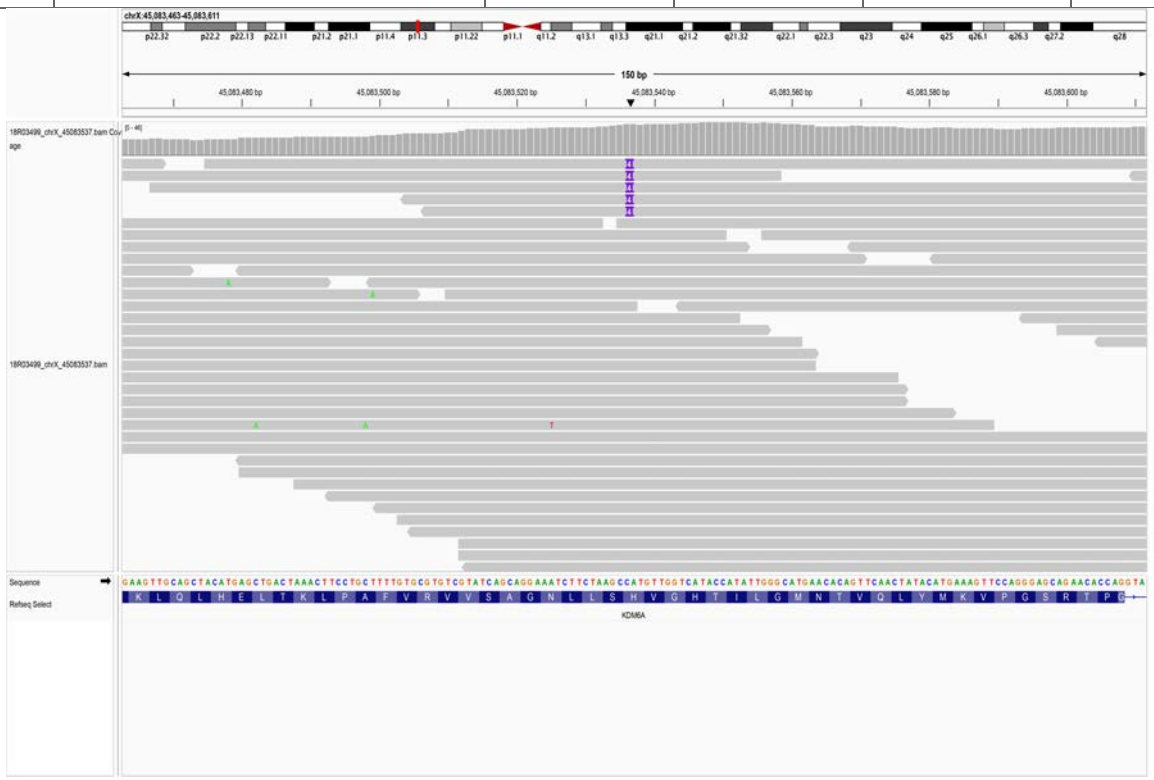
28.8. chrX_45069888_G/T

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



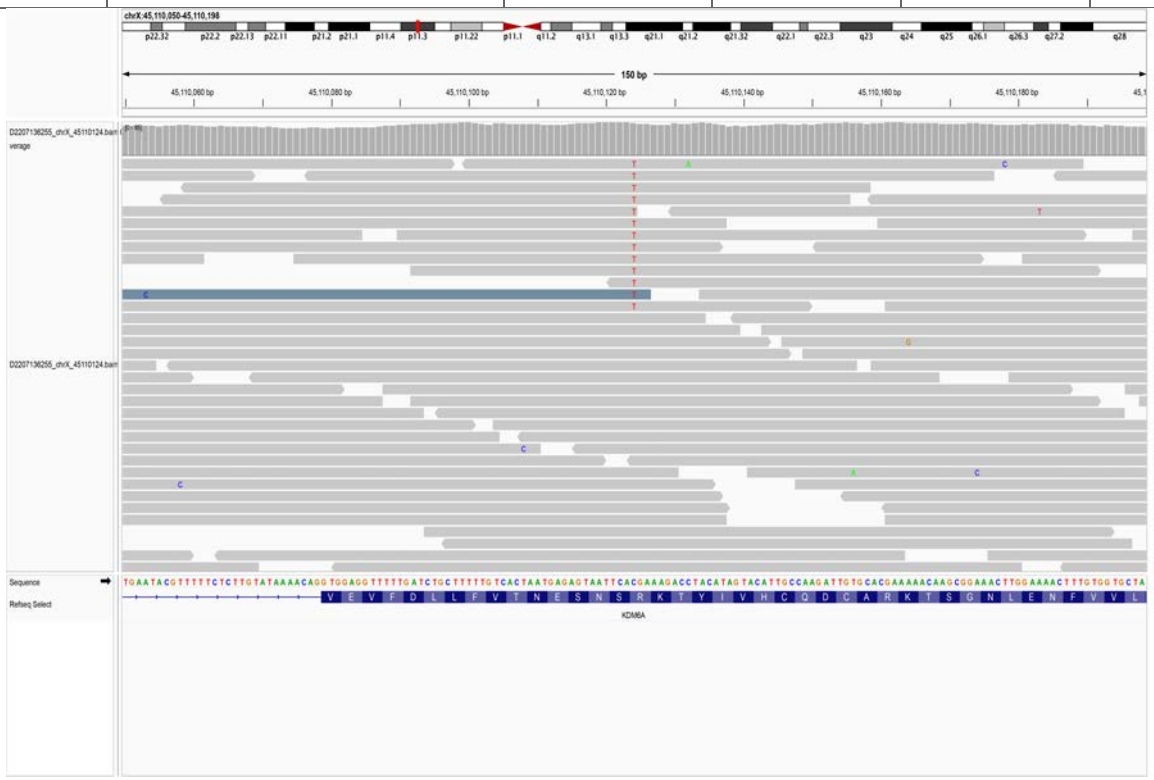
28.9. chrX_45083537_-/ACAT

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



28.10. chrX_45110124_C/T

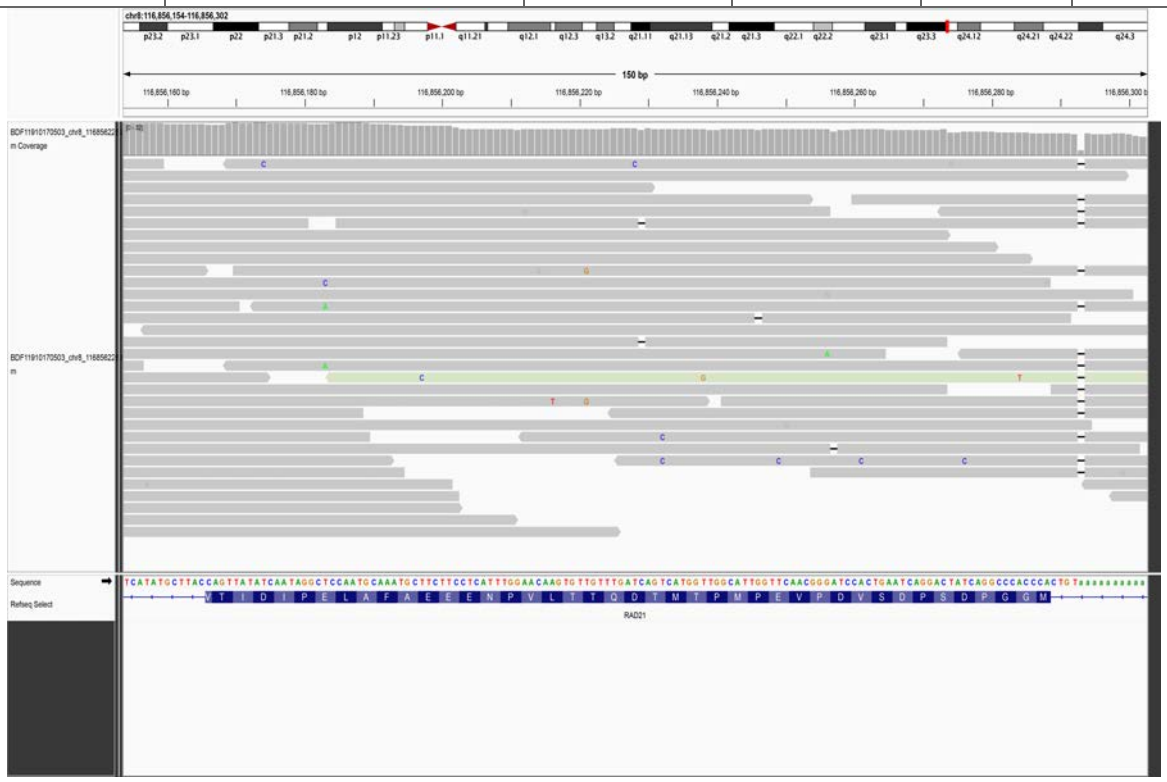
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
D2207136255	chrX_45110124_C/T	67	13	*KDM6A*	stop_gained



29. *KMT2A*

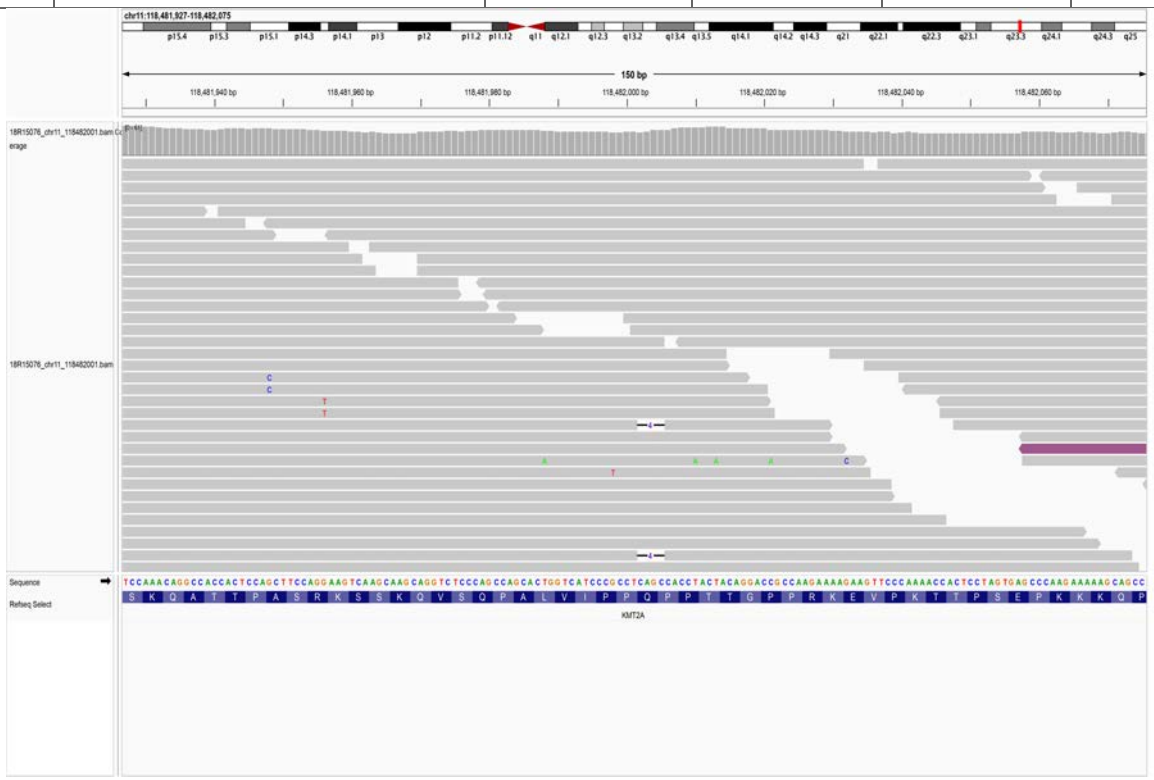
29.1. chr11_118473674_T/-

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



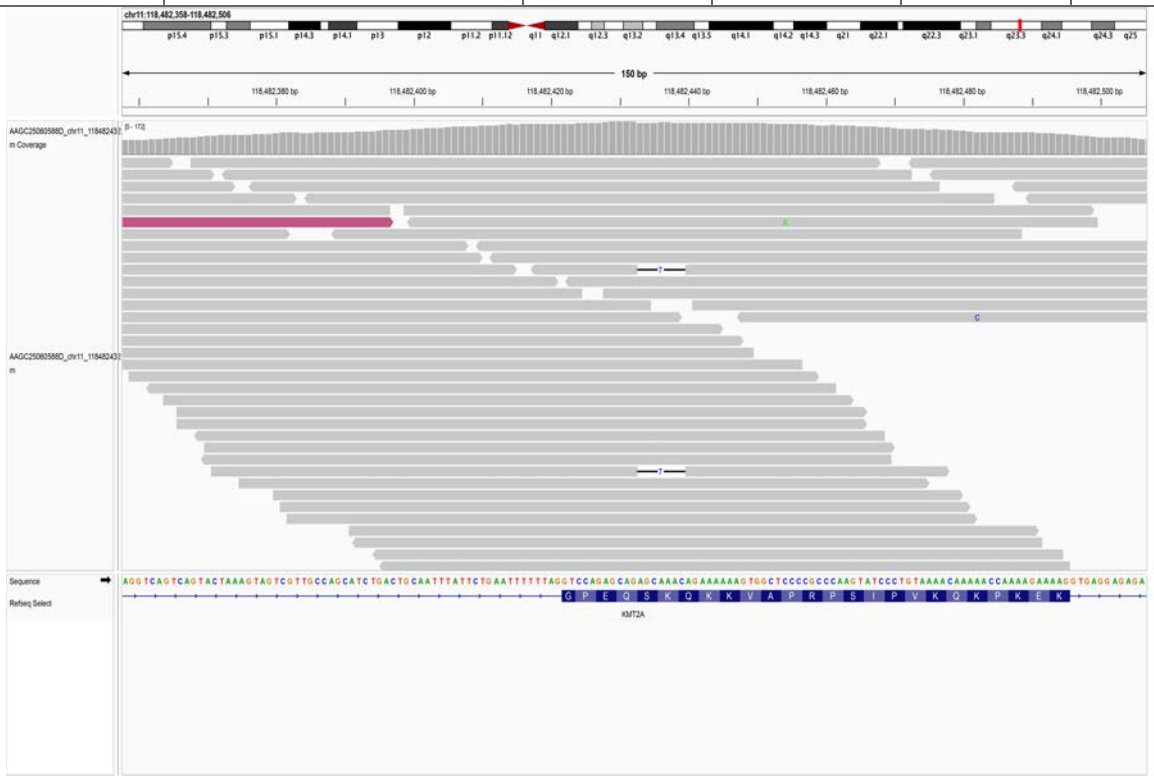
29.2. chr11_118482002_CAGC/-

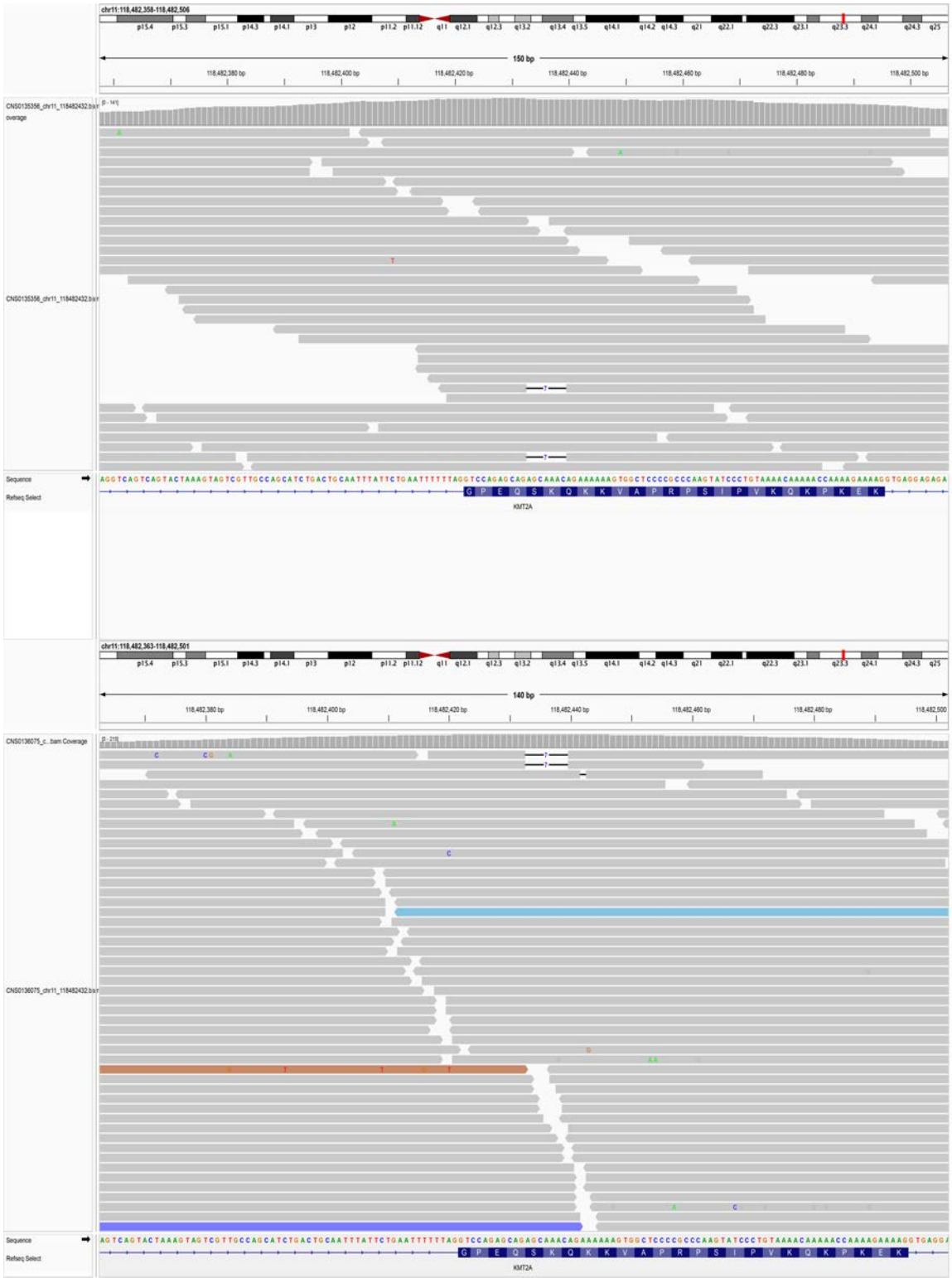
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R15076	chr11_118482002_CAGC/-	44	2	*KMT2A*	frameshift_variant



29.3. chr11_118482433_AGCAAAC/-

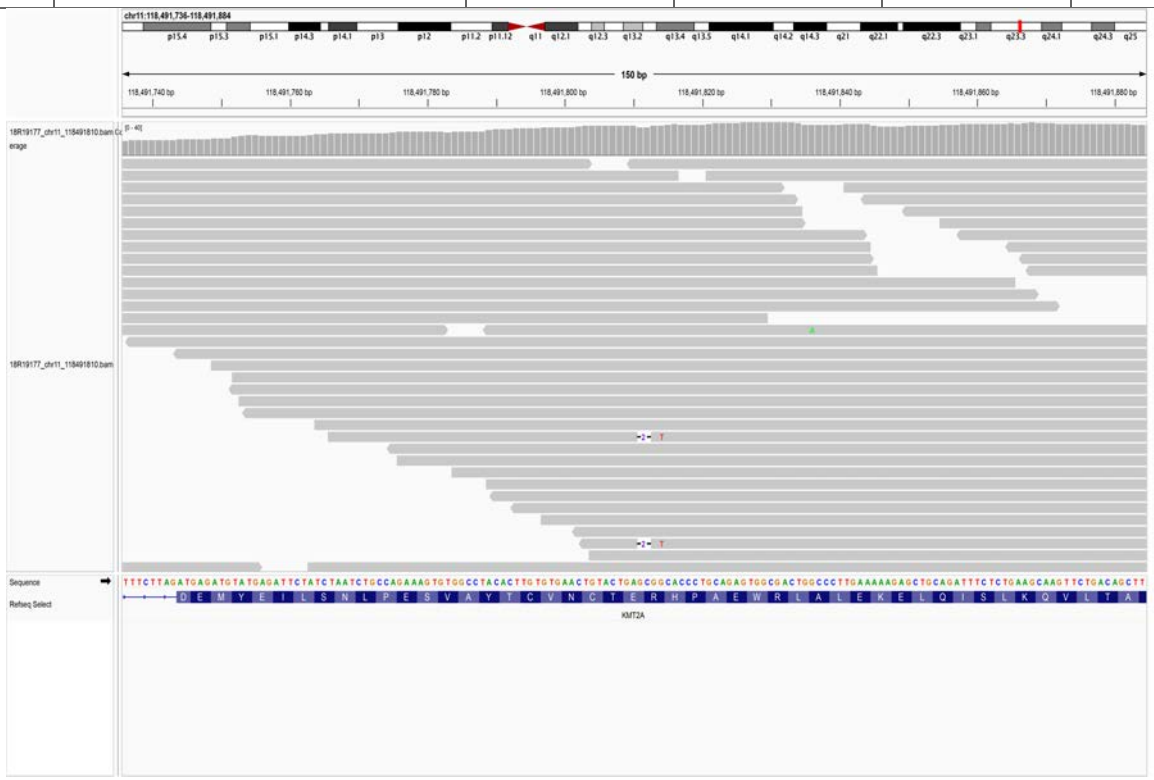
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060588D	chr11_118482433_AGCAAAC/-	166	4	*KMT2A*	frameshift_variant
CNS0135356	chr11_118482433_AGCAAAC/-	136	4	*KMT2A*	frameshift_variant
CNS0136075	chr11_118482433_AGCAAAC/-	206	4	*KMT2A*	frameshift_variant




chr11:118,482,358-118,482,506
150 bp
CNS0135356_chr11_118482432.bam
overage
CNS0135356_chr11_118482432.bam
Sequence
Refseq Select
KMT2A
chr11:118,482,363-118,482,501
140 bp
CNS0136075_c...bam Coverage
CNS0136075_chr11_118482432.bam
Sequence
Refseq Select
KMT2A

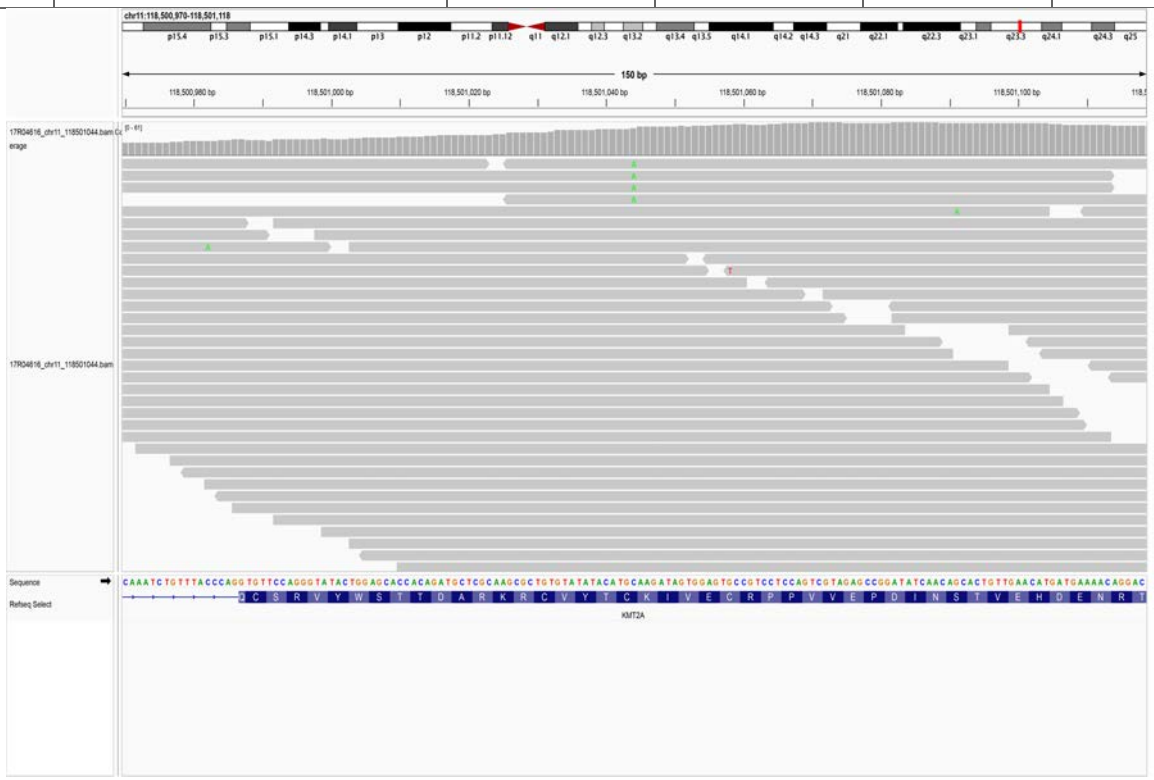
29.4. chr11_118491811_GC/-

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



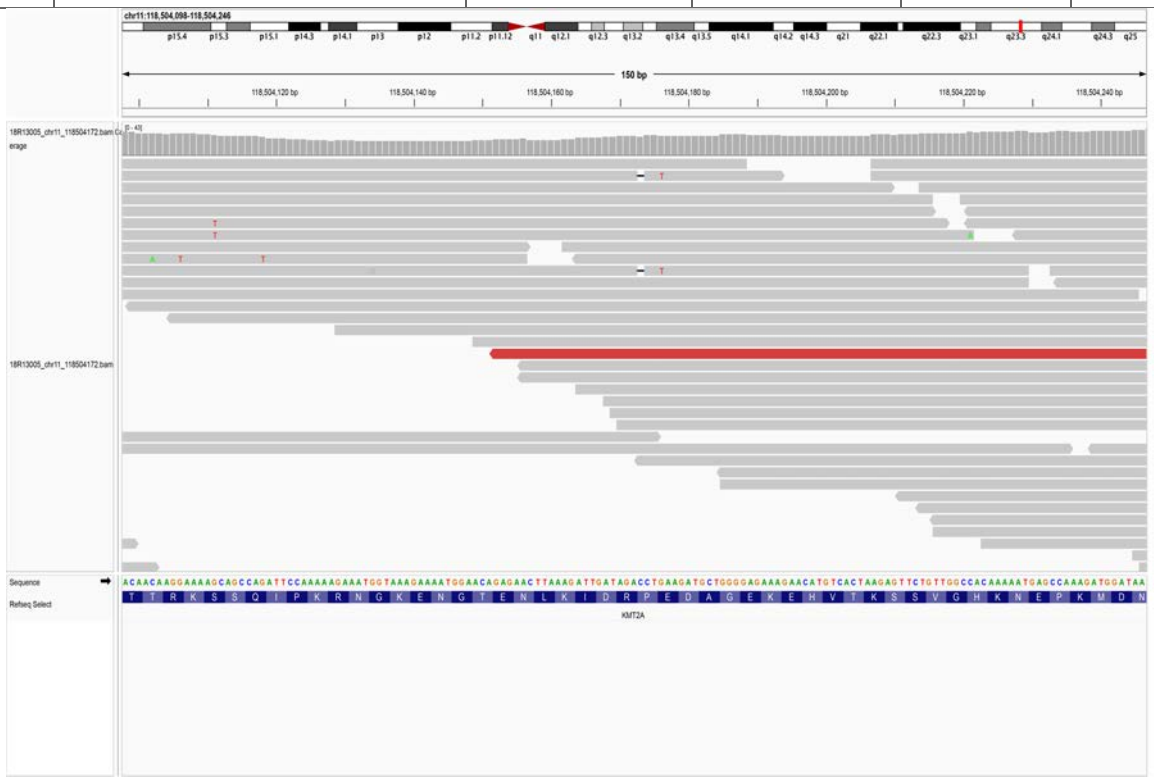
29.5. chr11_118501044_C/A

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



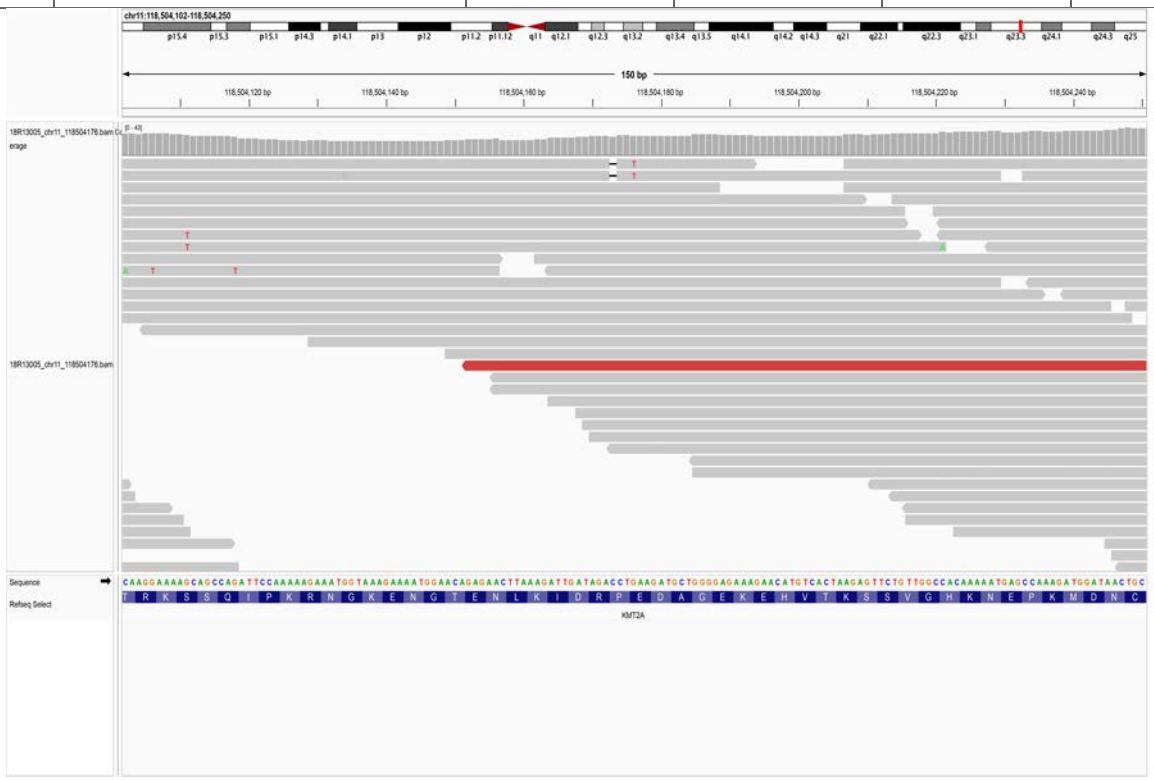
29.6. chr11_118504173_C/-

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



29.7. chr11_118504176_G/T

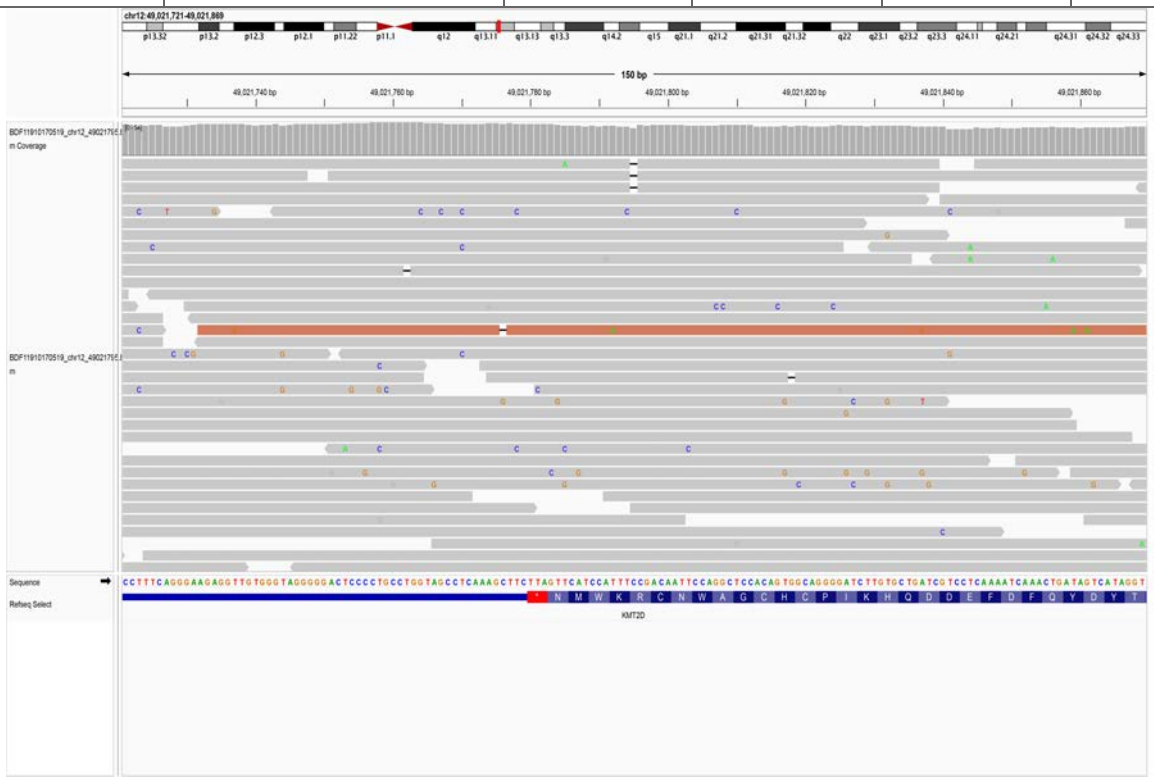
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13005	chr11_118504176_G/T	24	2	*KMT2A*	stop_gained



30. *KMT2D*

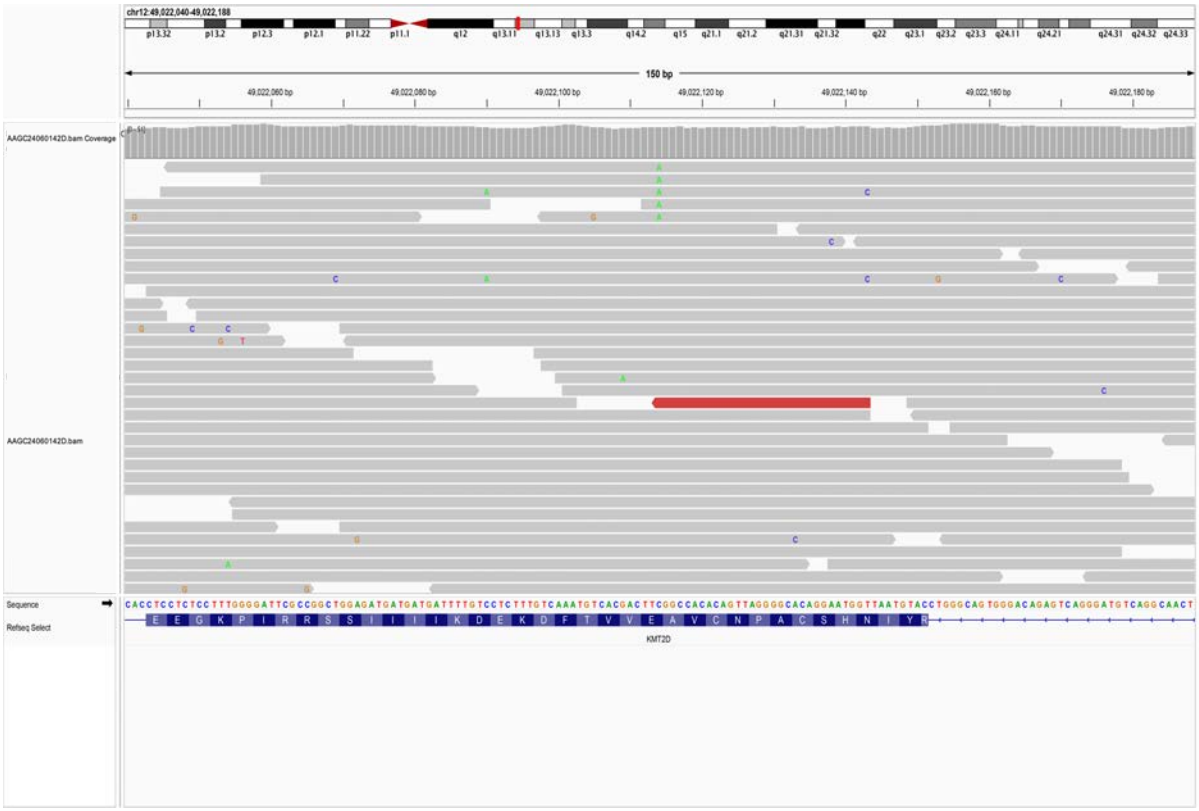
30.1. chr12_49021795_C/-

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



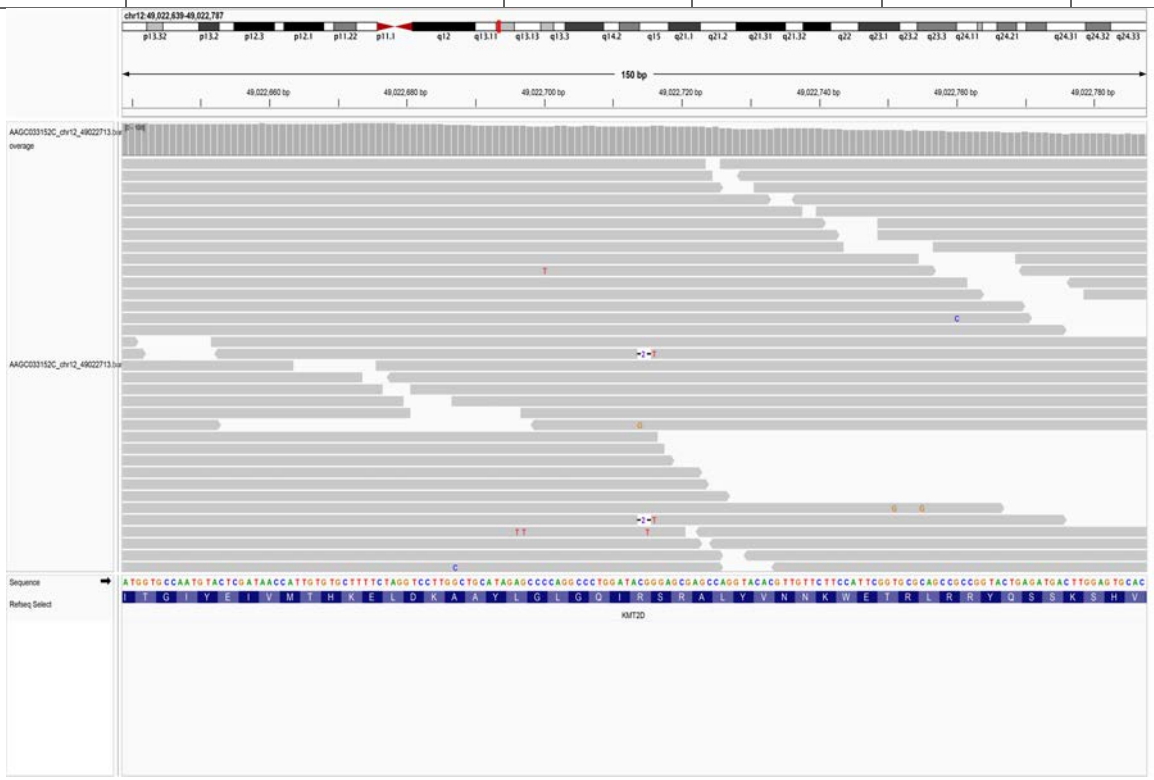
30.2. chr12_49022114_C/A

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



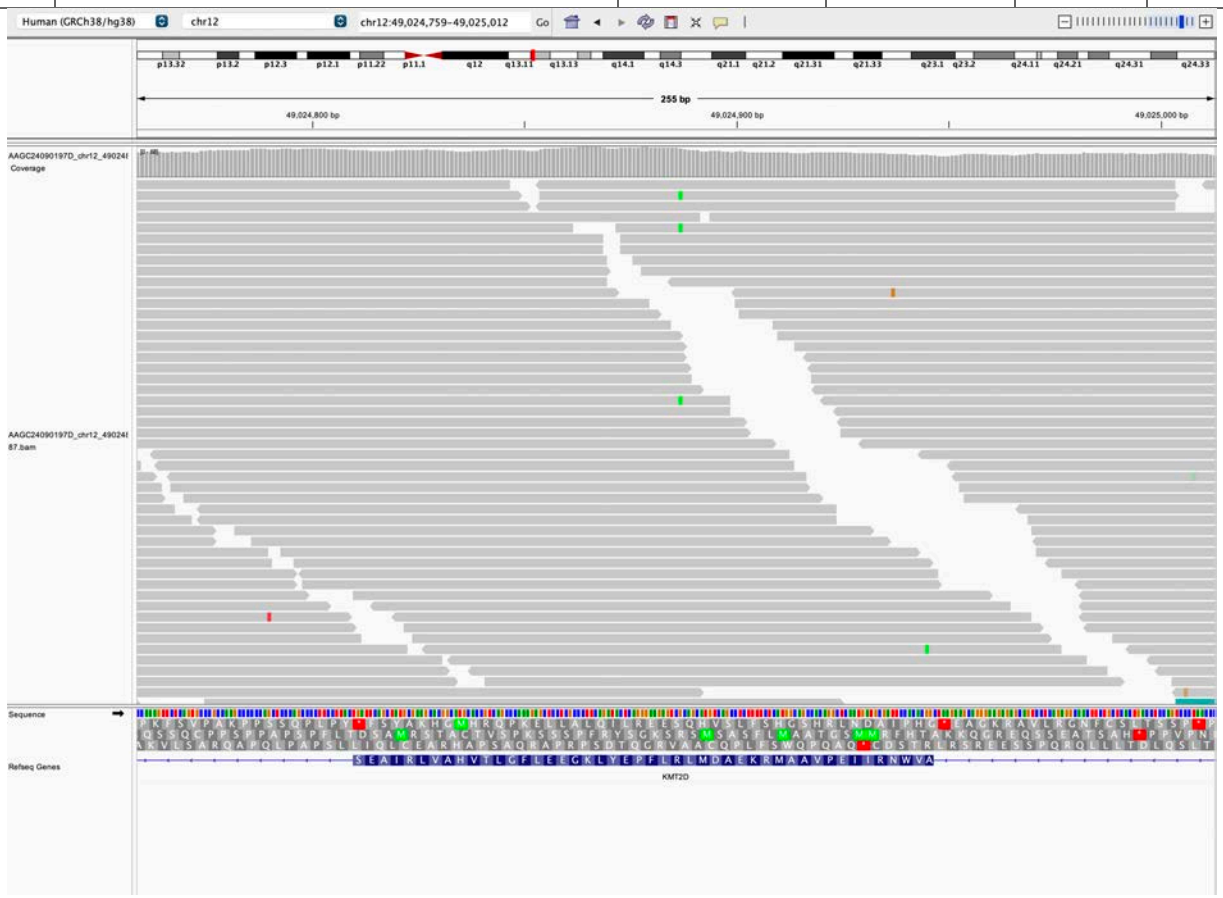
30.3. chr12_49022714_CG/-

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



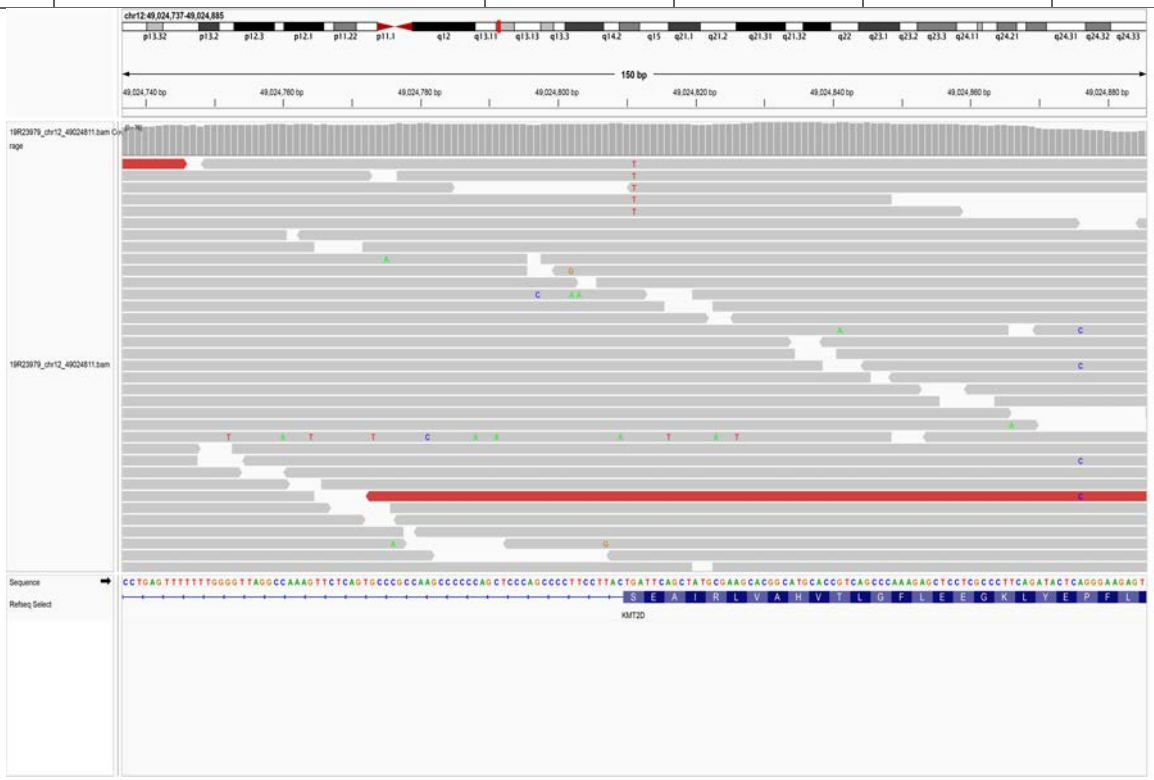
30.4. chr12_49027229_C/A

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



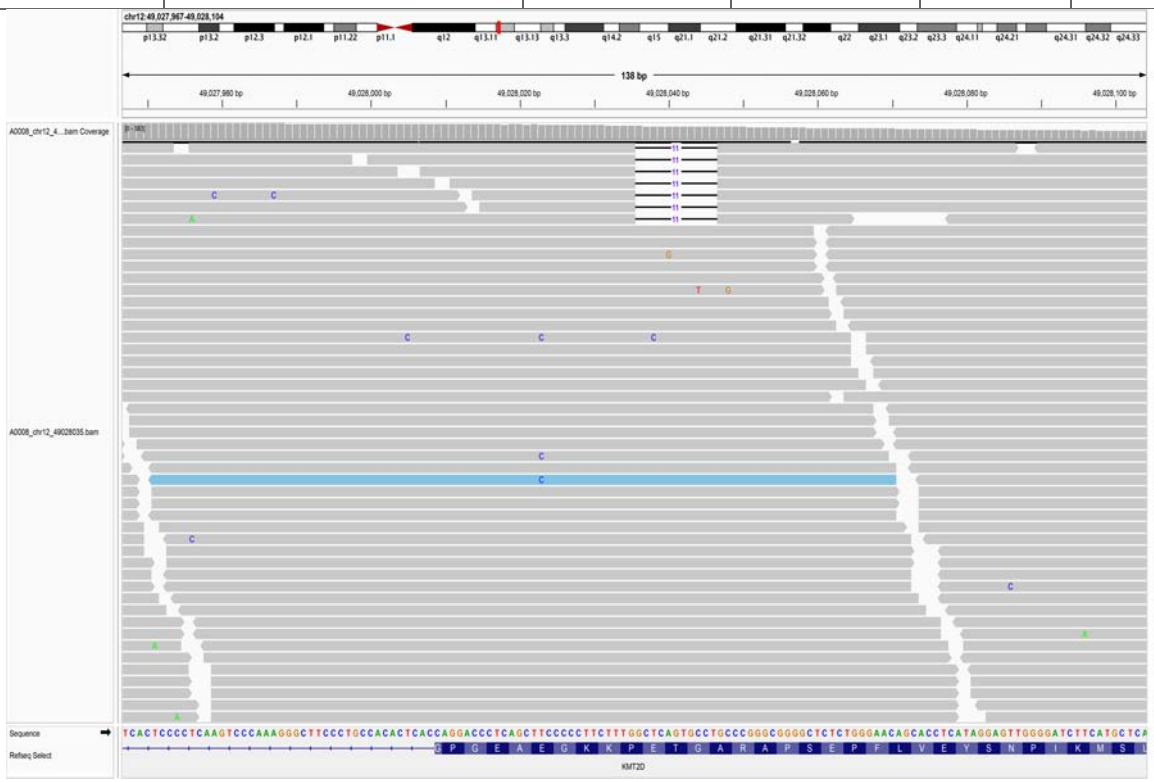
30.5. chr12_49024811_G/T

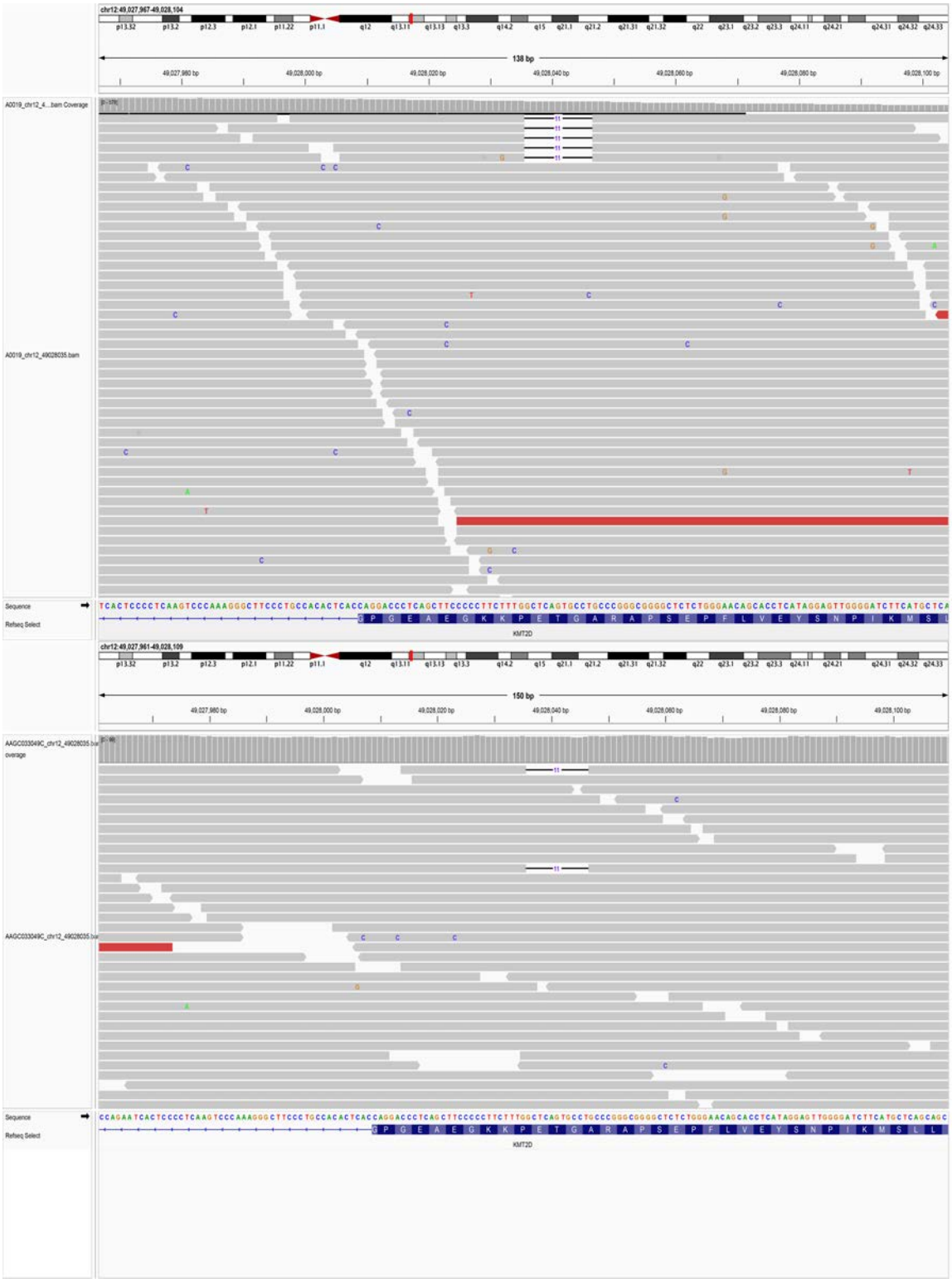
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23979	chr12_49024811_G/T	60	5	*KMT2D*	stop_gained

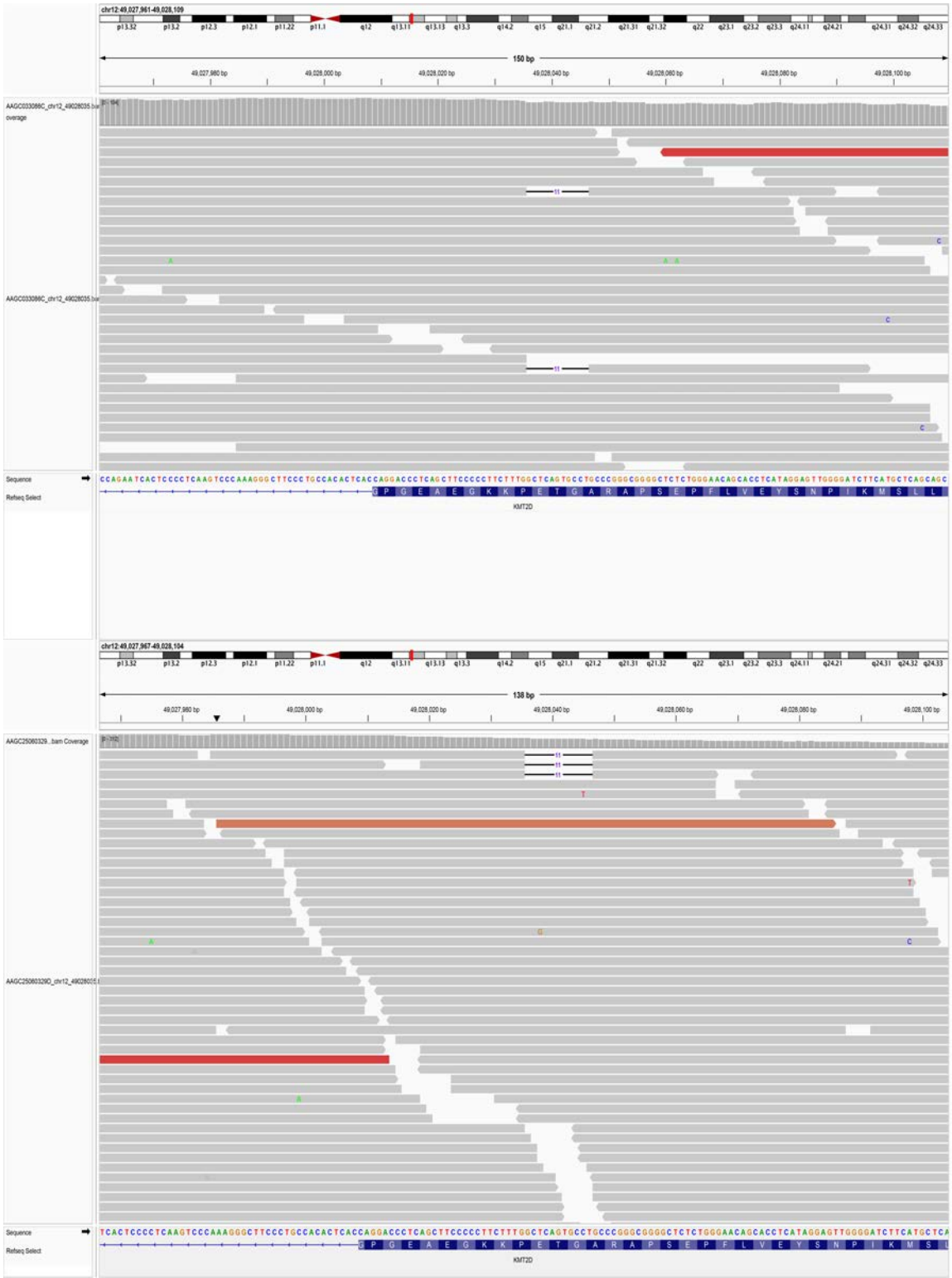


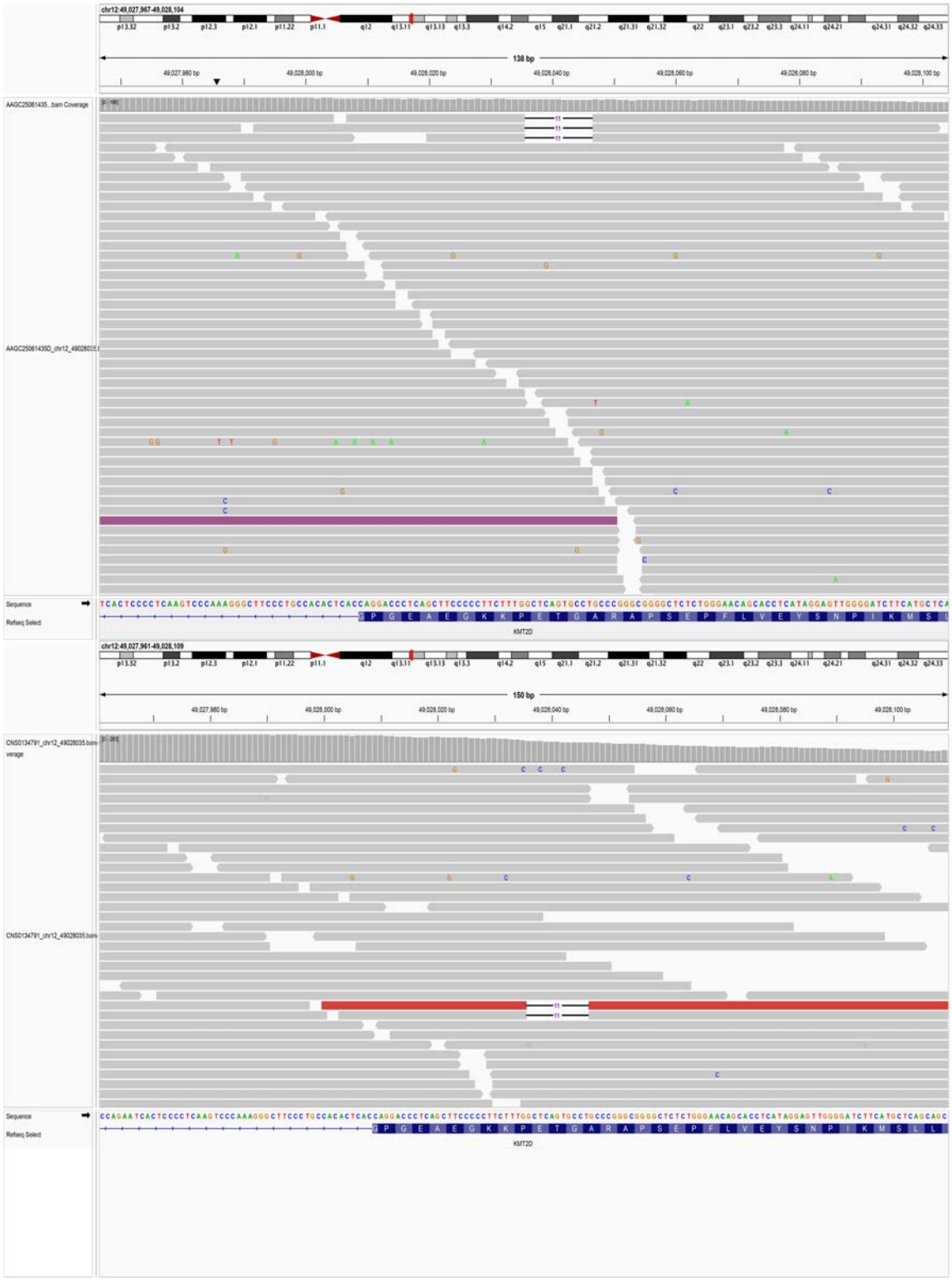
30.6. chr12_49028036_GCTCAGTGCCT/-

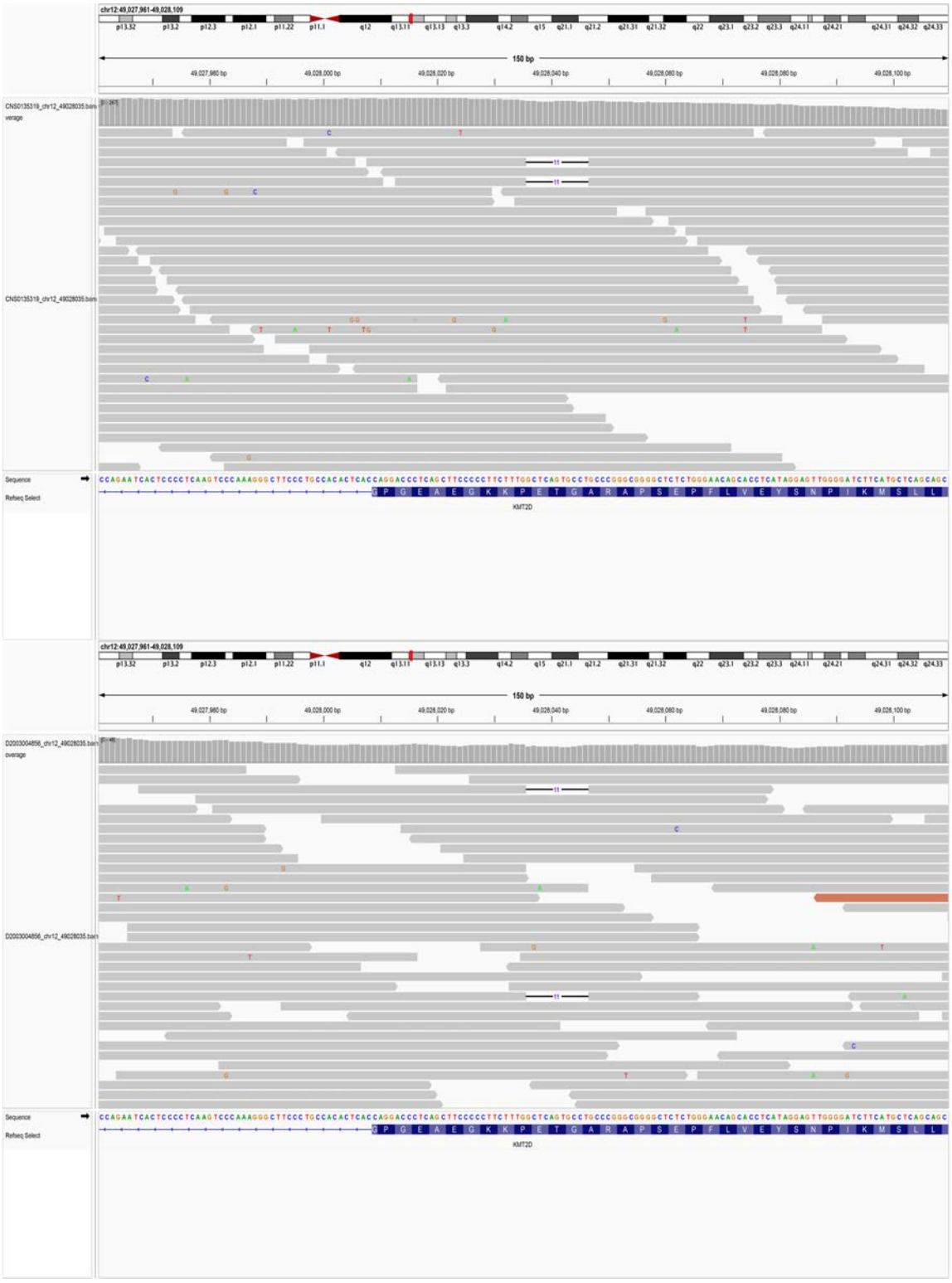
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0008	chr12_49028036_GCTCAGTGCCT/-	471	8	*KMT2D*	frameshift_variant
A0019	chr12_49028036_GCTCAGTGCCT/-	418	6	*KMT2D*	frameshift_variant
AAGC033049C	chr12_49028036_GCTCAGTGCCT/-	91	3	*KMT2D*	frameshift_variant
AAGC033086C	chr12_49028036_GCTCAGTGCCT/-	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

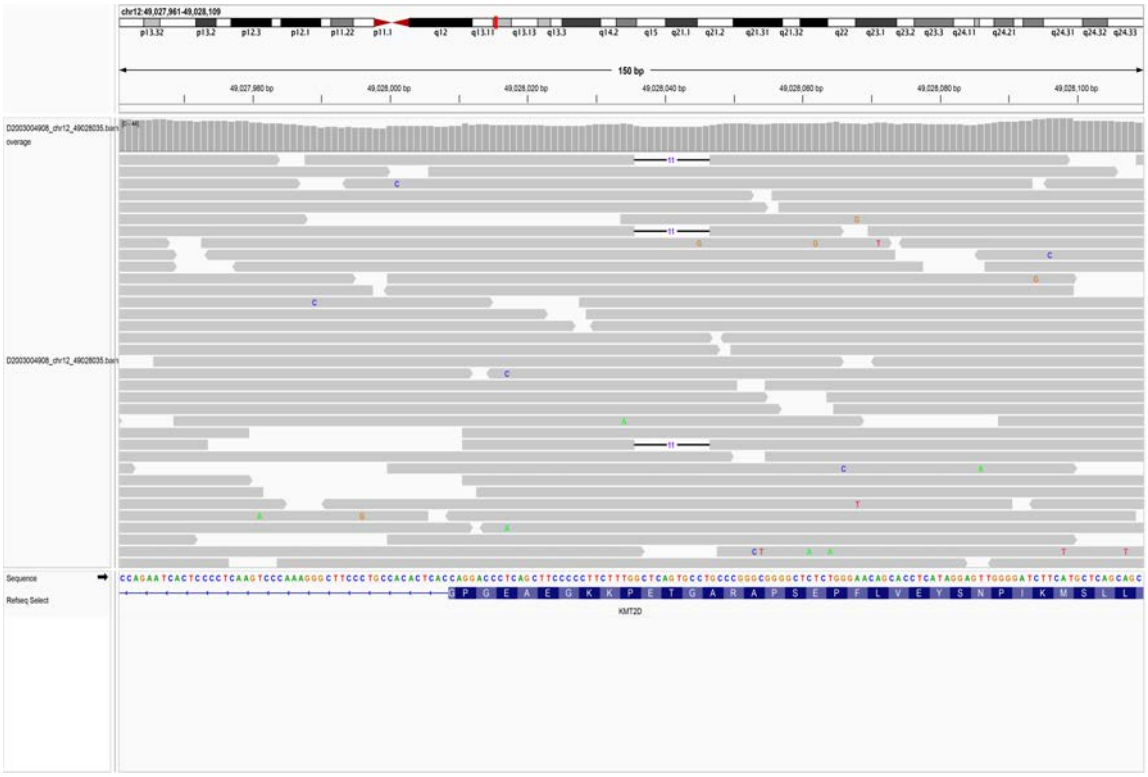



chr12:49,027,967-49,028,104
138 bp
A0019_chr12_4....bam Coverage
A0019_chr12_49028035.bam
Sequence
Refseq Select
KMT2D
chr12:49,027,961-49,028,109
150 bp
AAGC033049C_chr12_49028035.bam coverage
AAGC033049C_chr12_49028035.bam
Sequence
Refseq Select
KMT2D


chr12:49,027,961-49,028,109
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
Coverage
Sequence
Refseq Select
KMT2D
chr12:49,027,967-49,028,104
138 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
Coverage
Sequence
Refseq Select
KMT2D

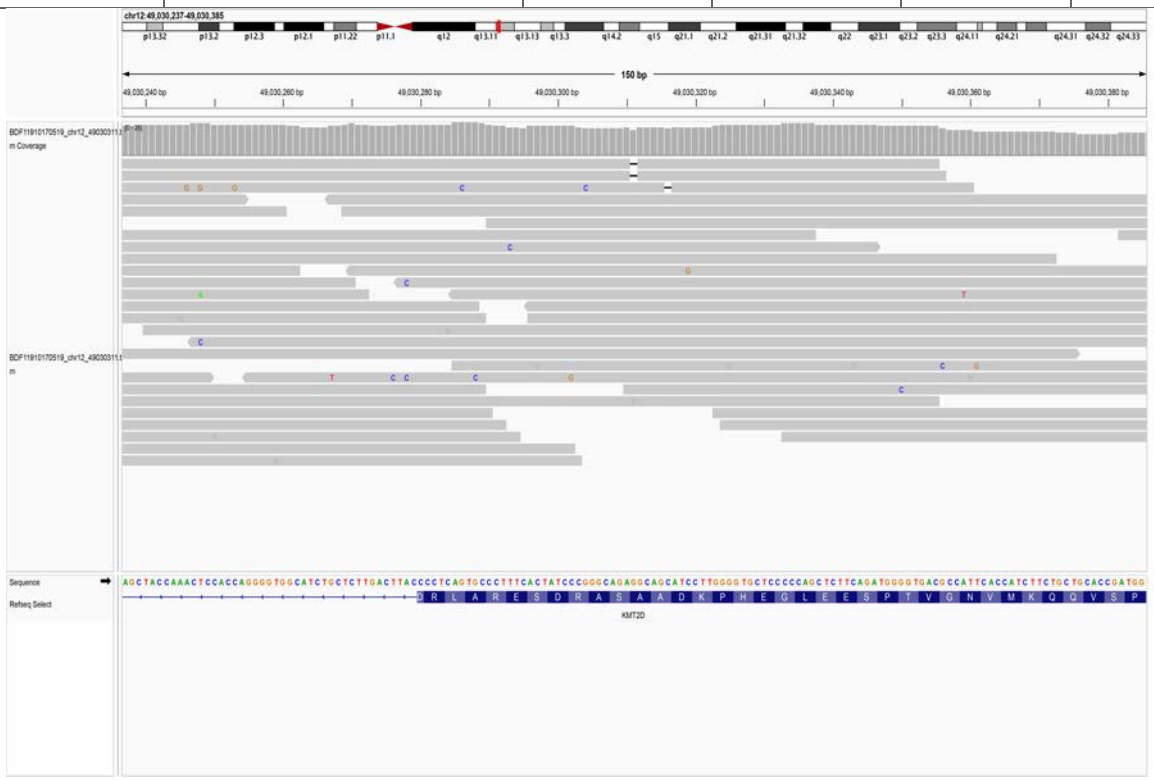

chr12:49,027,967-49,028,104
138 bp
AAGC25061435...bam Coverage
Sequence
Refseq Select
KMT2D
chr12:49,027,961-49,028,109
150 bp
CNS0134791_chr12_49028035.bam
CNS0134791_chr12_49028035.bam
Sequence
Refseq Select
KMT2D


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


chr12:49,027,961-49,028,109
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

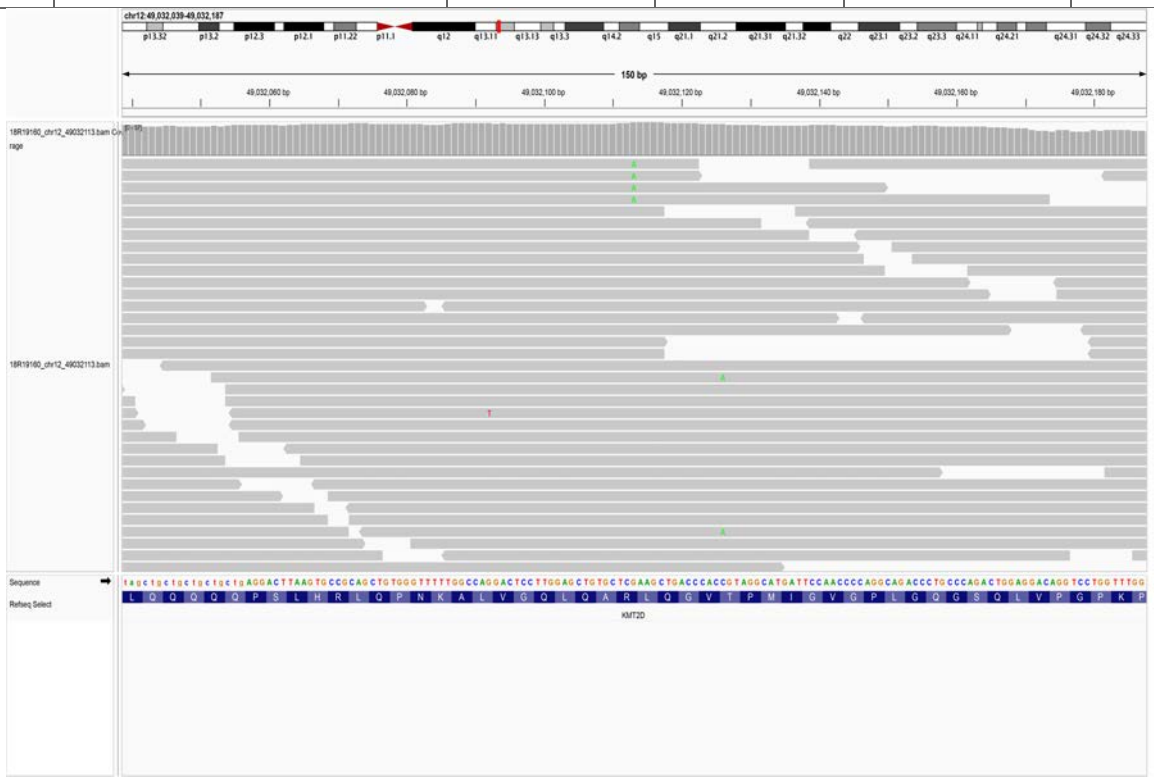
30.7. chr12_49030311_G/-

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



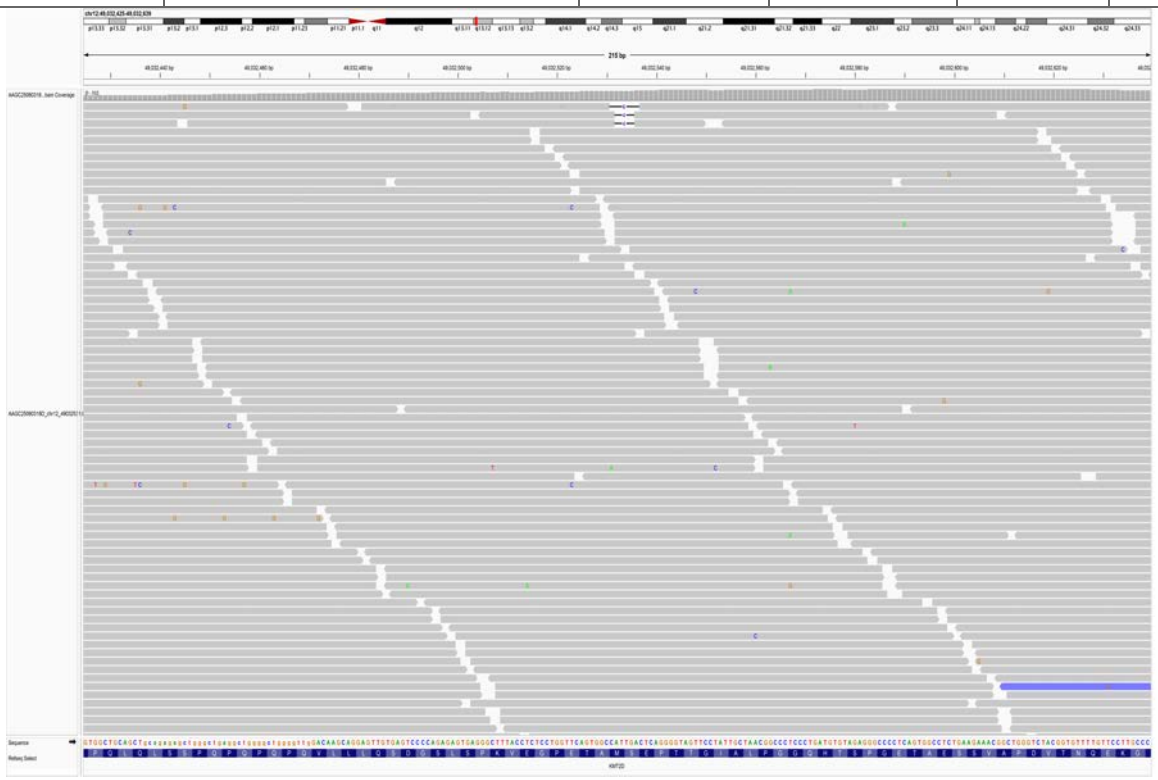
30.8. chr12_49032113_G/A

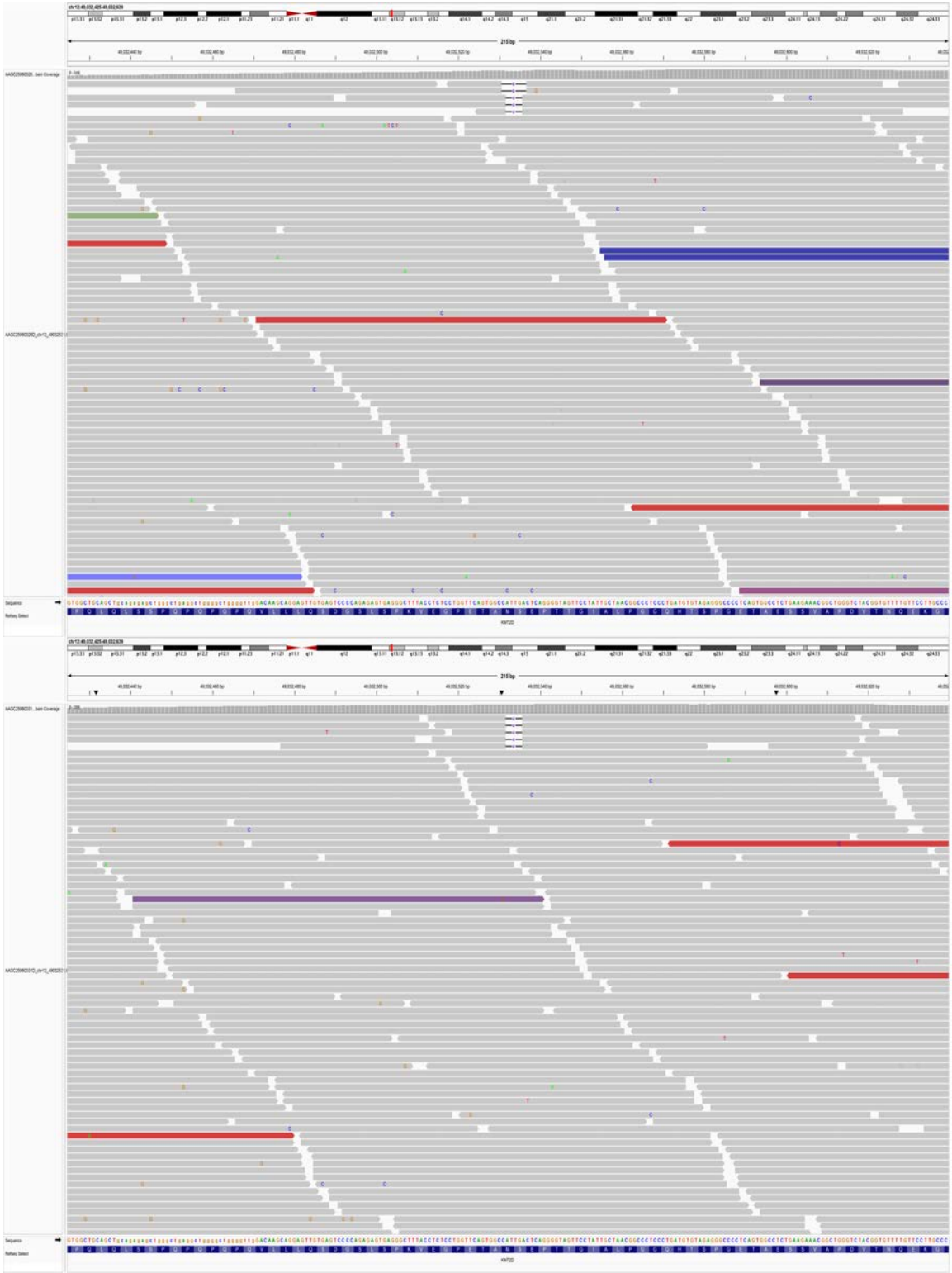
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R19160	chr12_49032113_G/A	52	4	*KMT2D*	stop_gained

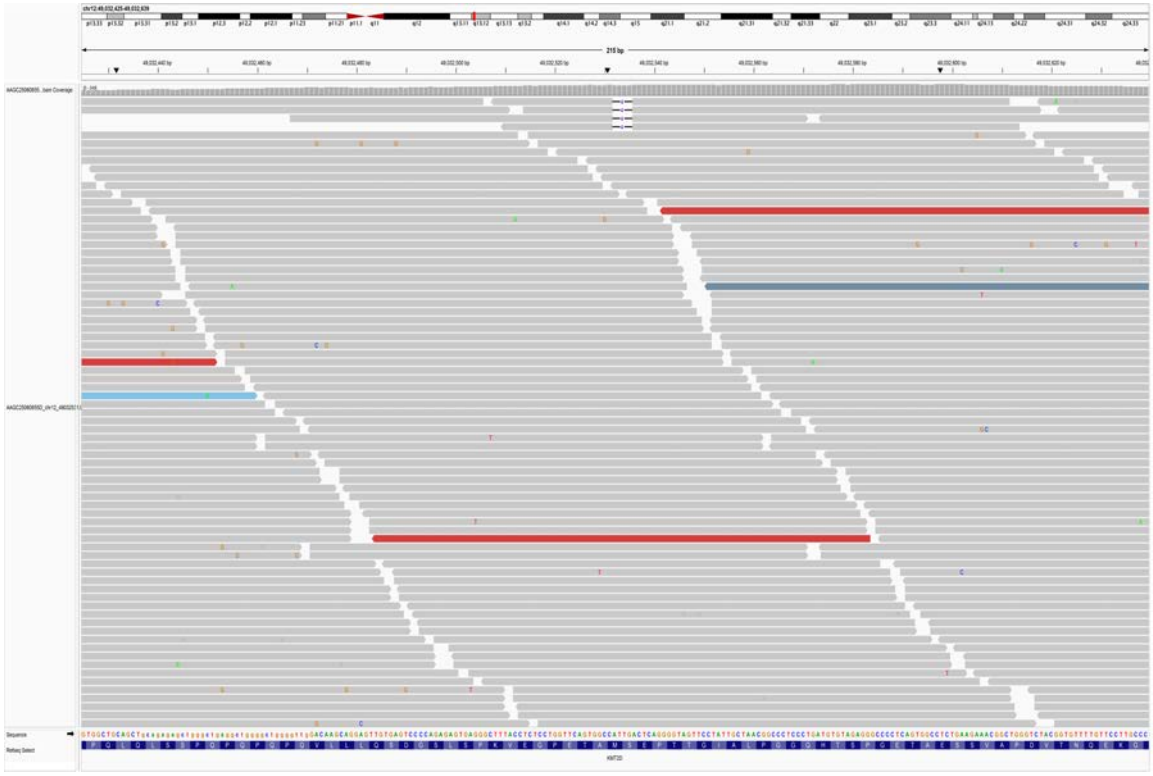


30.9. chr12_49032532_ATTG/-

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

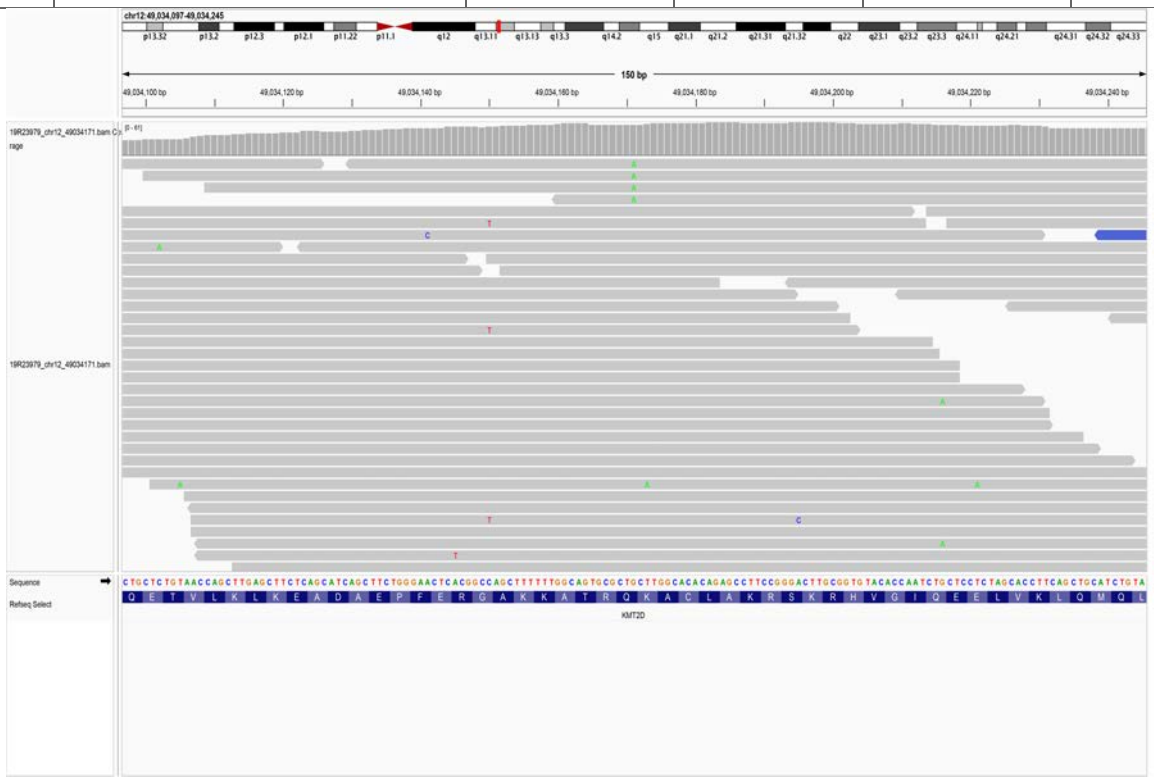






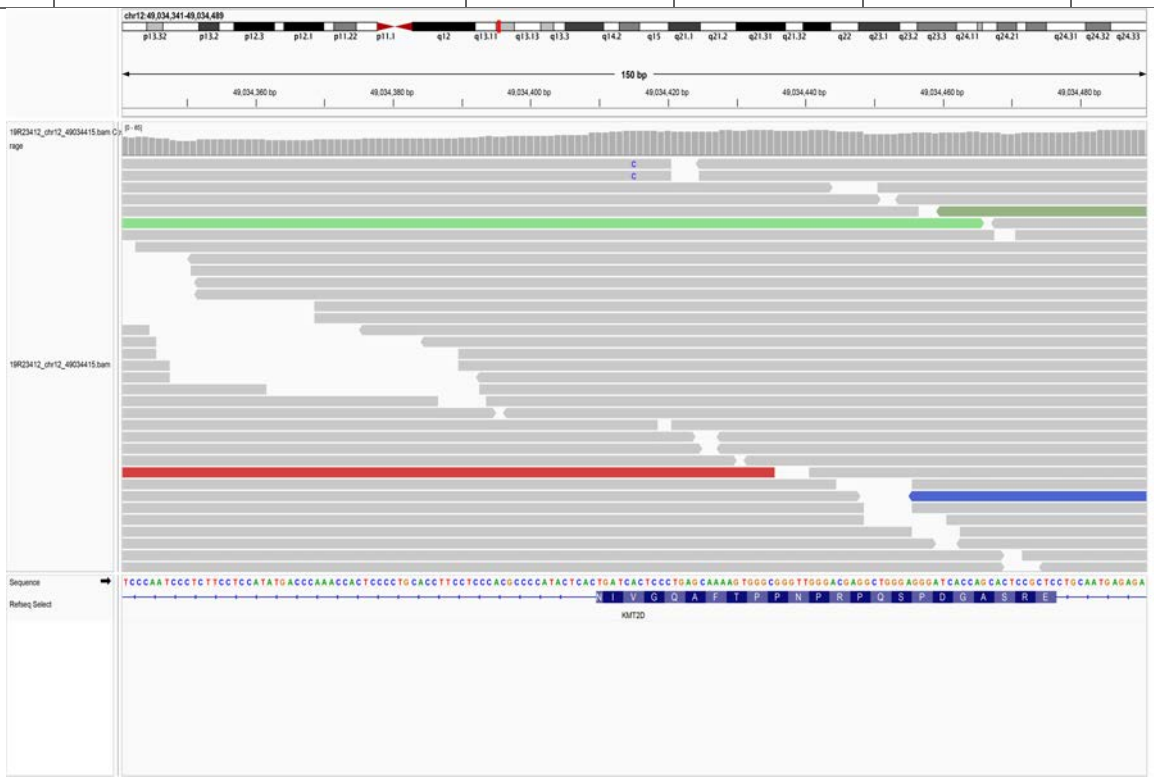
30.10. chr12_49034171_G/A

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



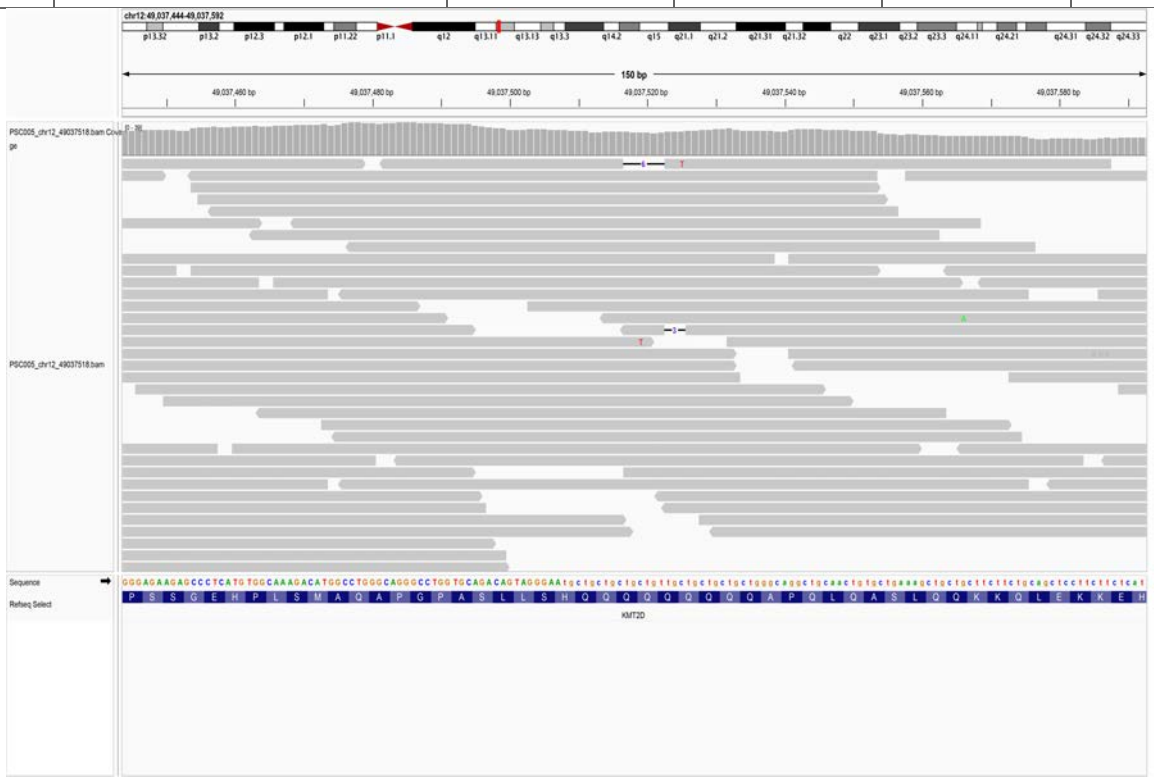
30.11. chr12_49034415_A/C

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



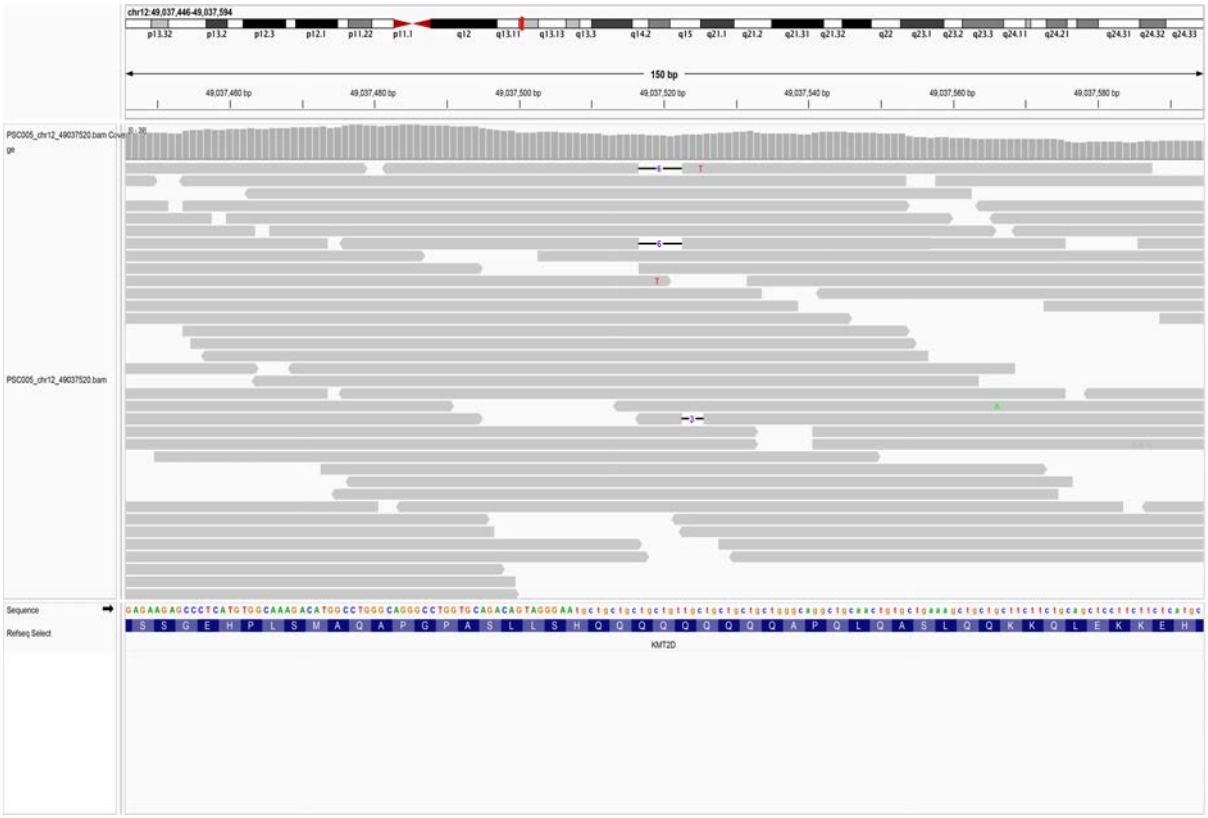
30.12. chr12_49037519_C/-

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



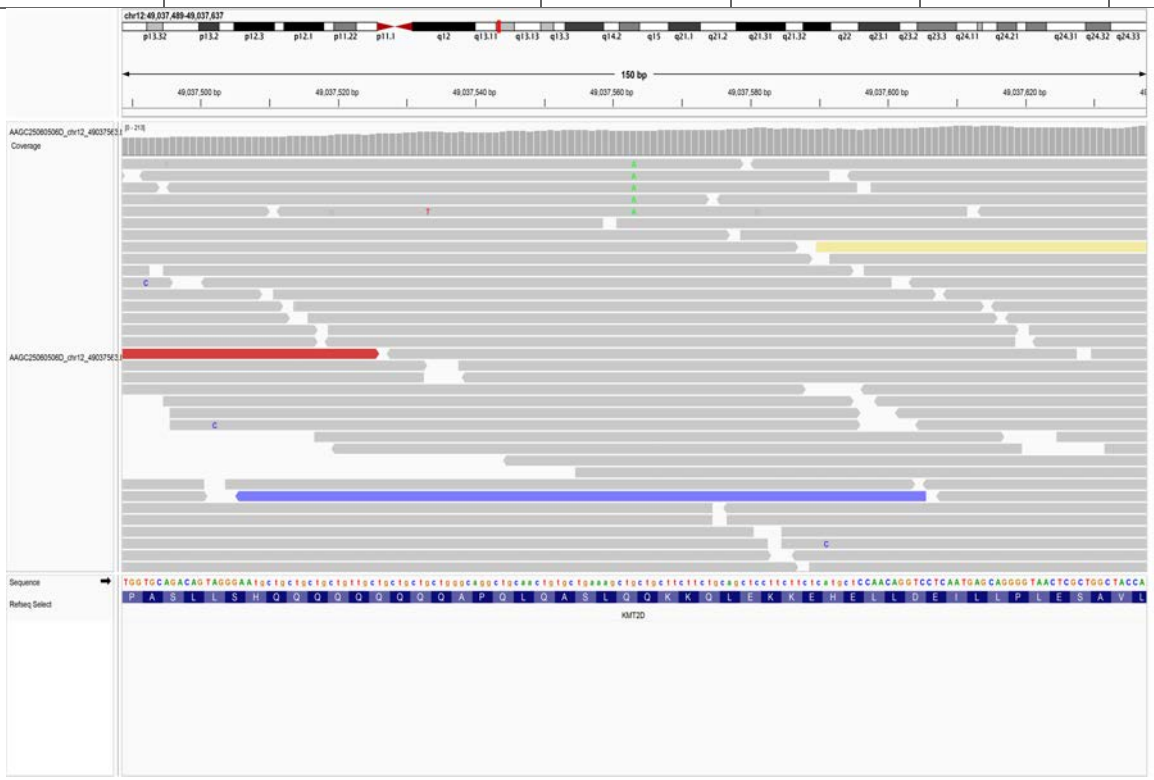
30.13. chr12_49037521_GTTGC/-

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



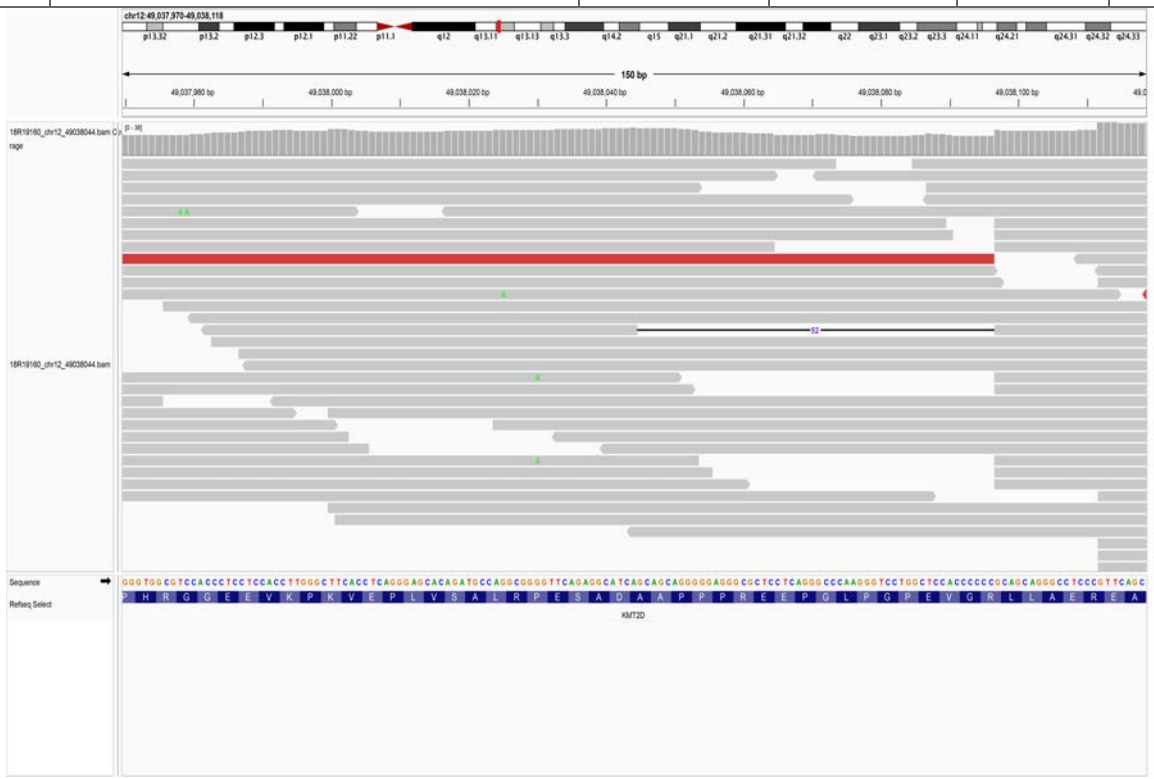
30.14. chr12_49037563_G/A

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



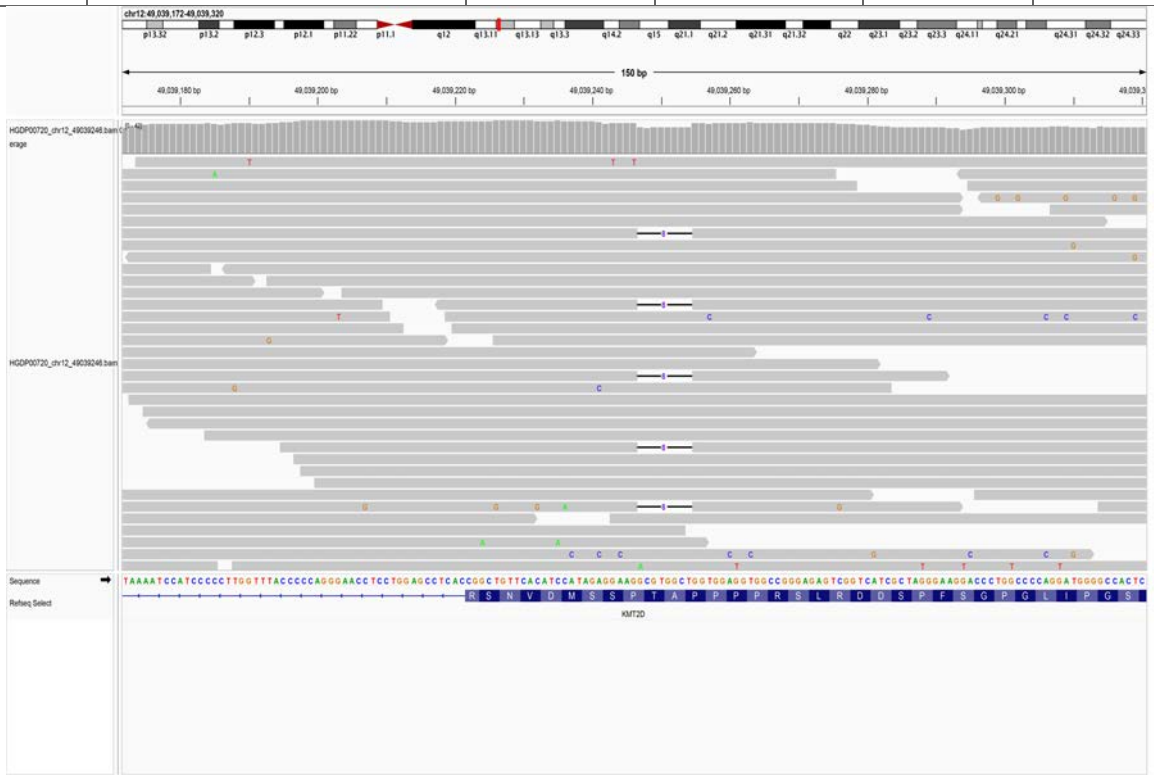
30.15. chr12_49038045_GCAGCAGGGGGAGGGCGCTCCTCAGGGCCCAAGGGTCCTGGCTCCACCCCCC/-

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



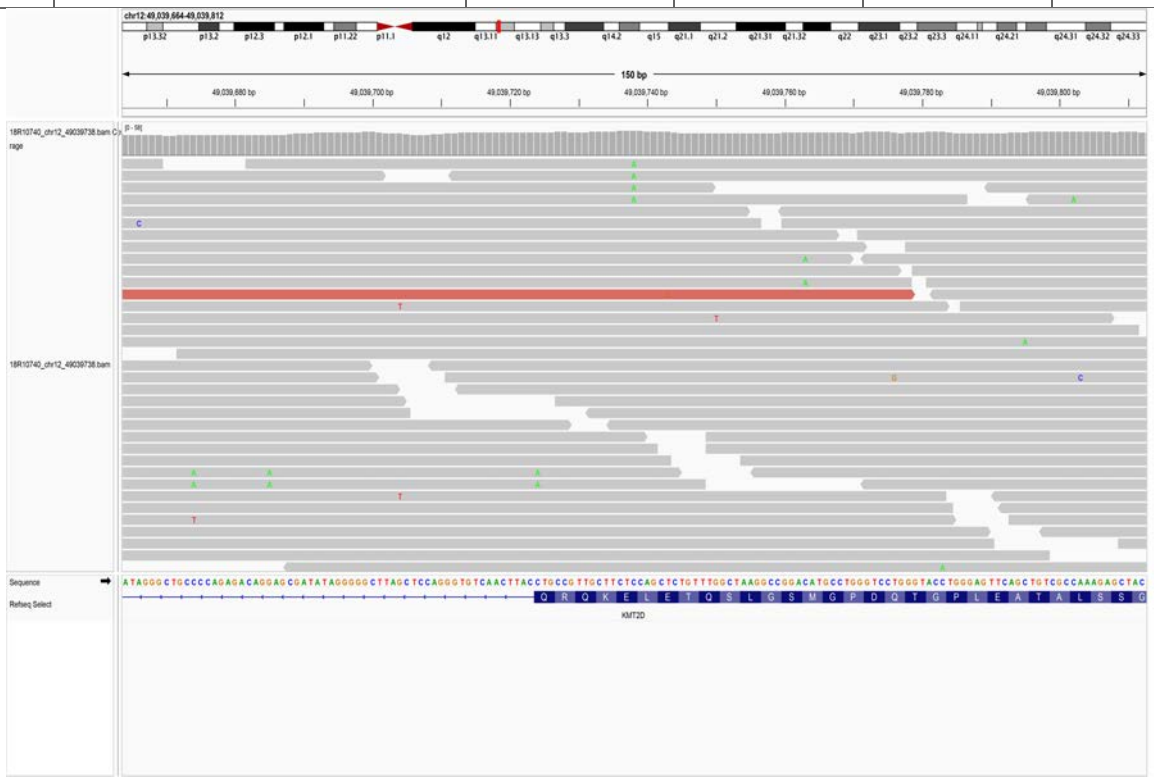
30.16. chr12_49039247_GCGTGGCT/-

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



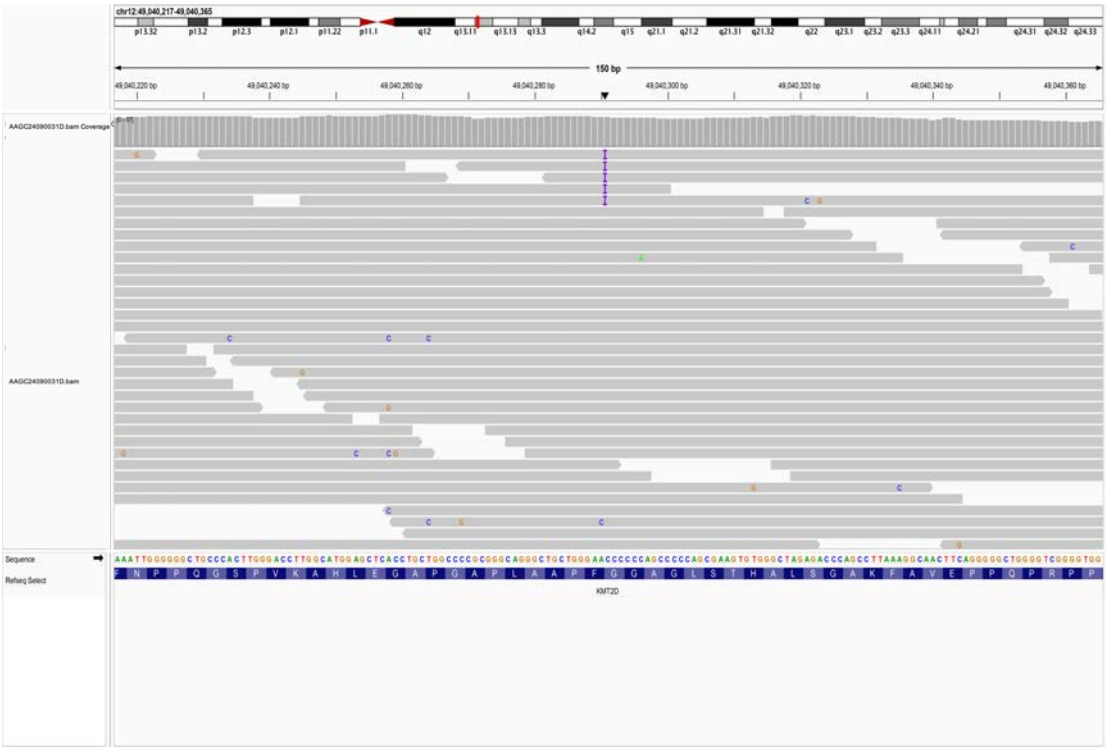
30.17. chr12_49039738_C/A

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



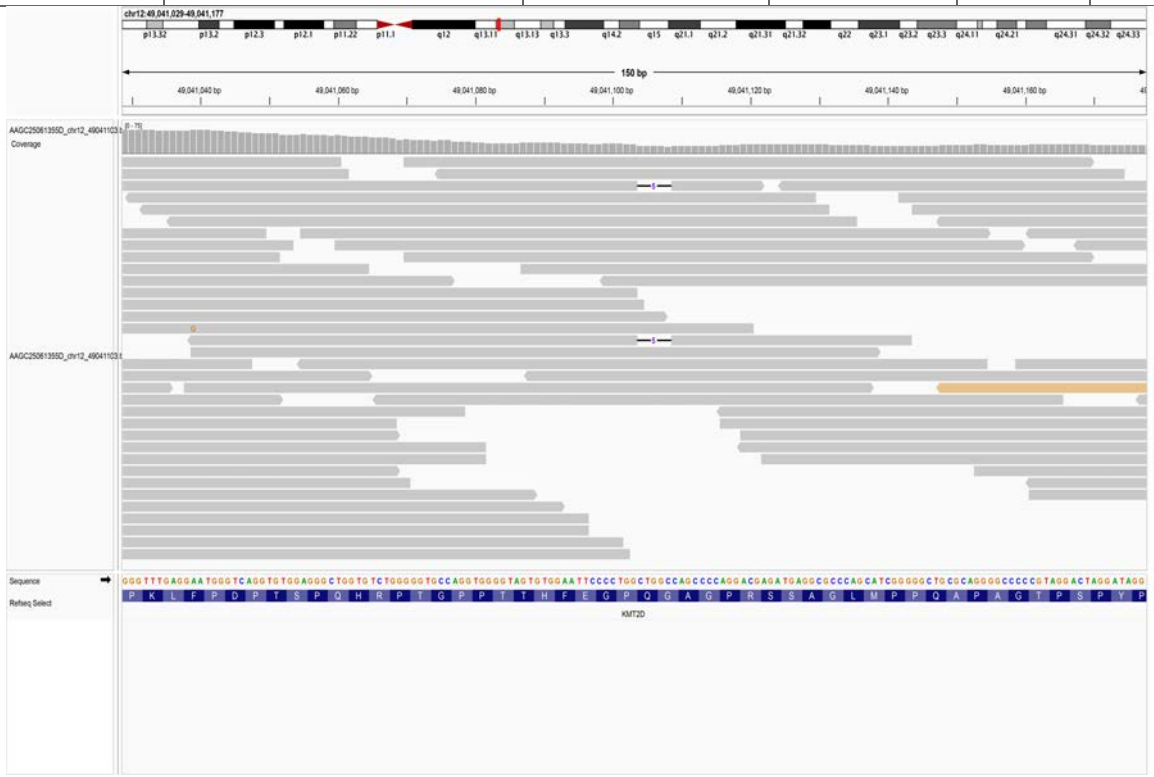
30.18. chr12_49040291_-/C

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



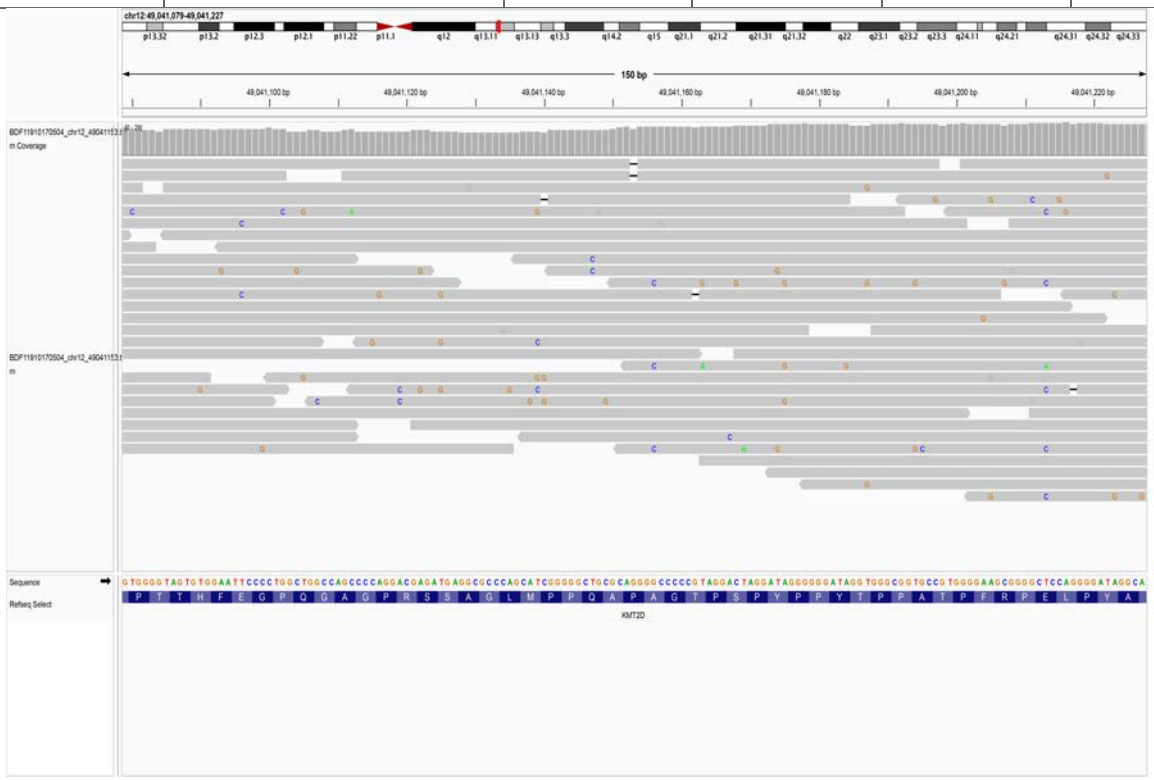
30.19. chr12_49041104_CTGGC/-

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



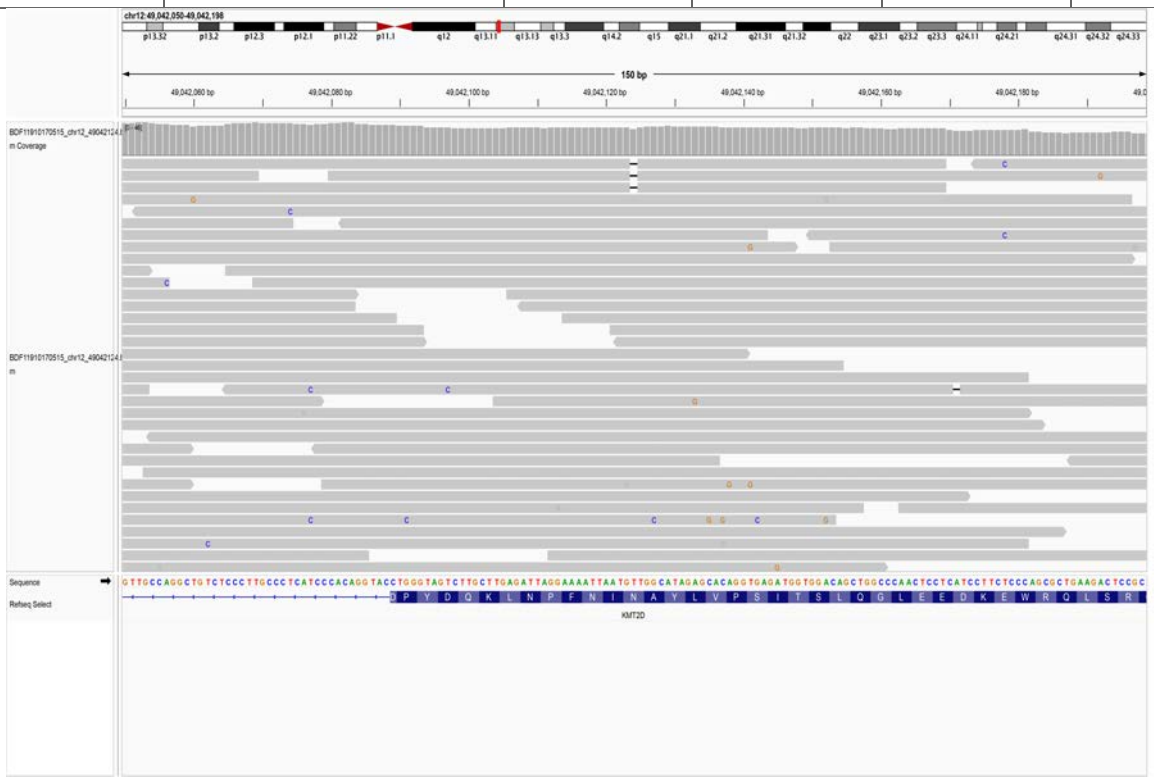
30.20. chr12_49041153_G/-

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



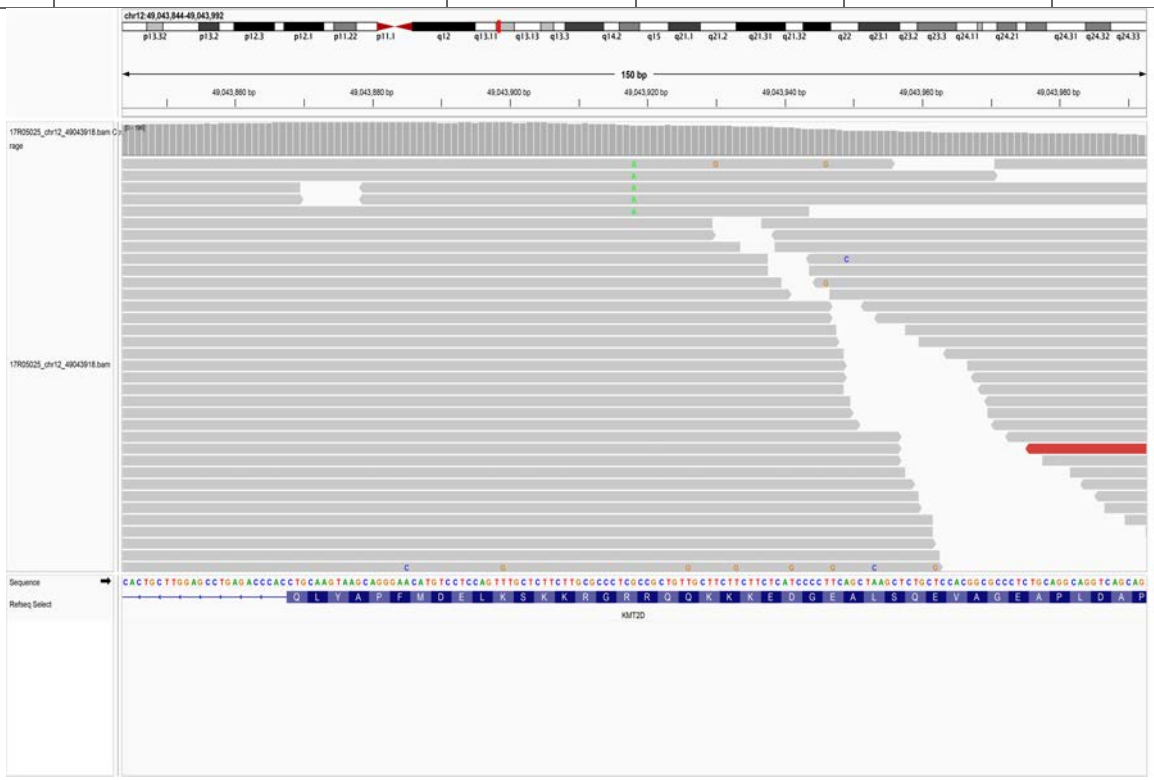
30.21. chr12_49042124_T/-

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



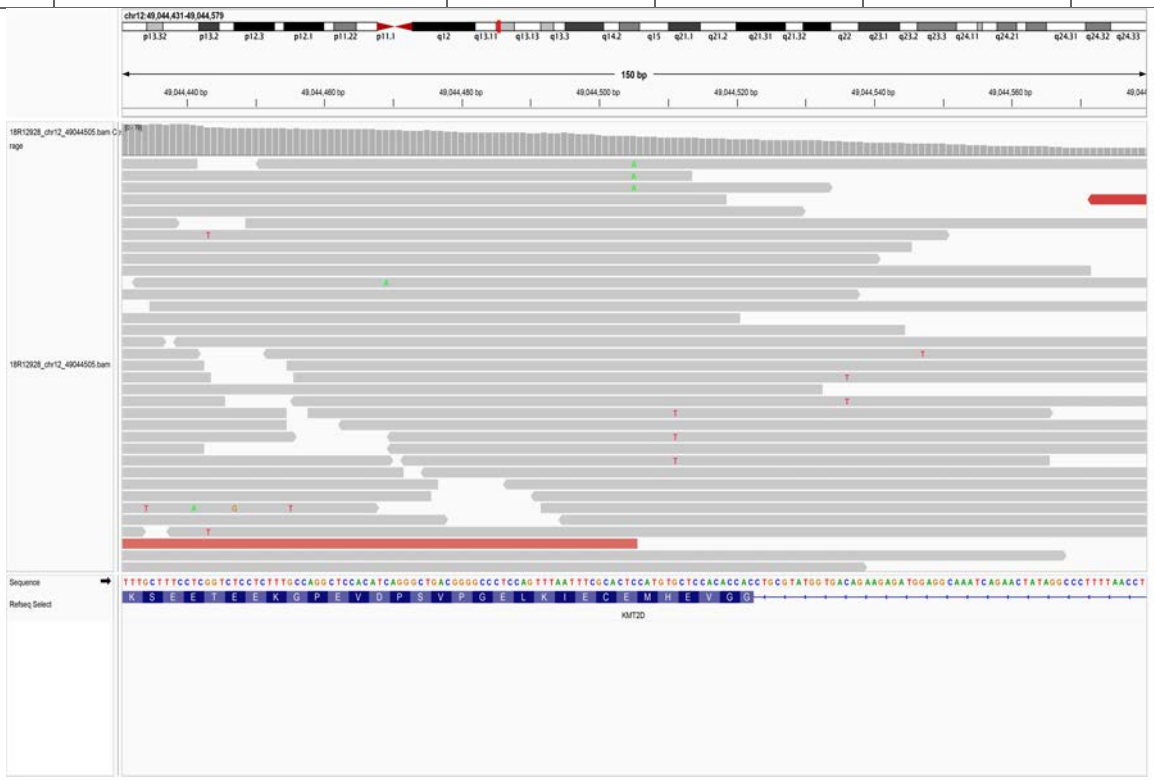
30.22. chr12_49043918_G/A

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



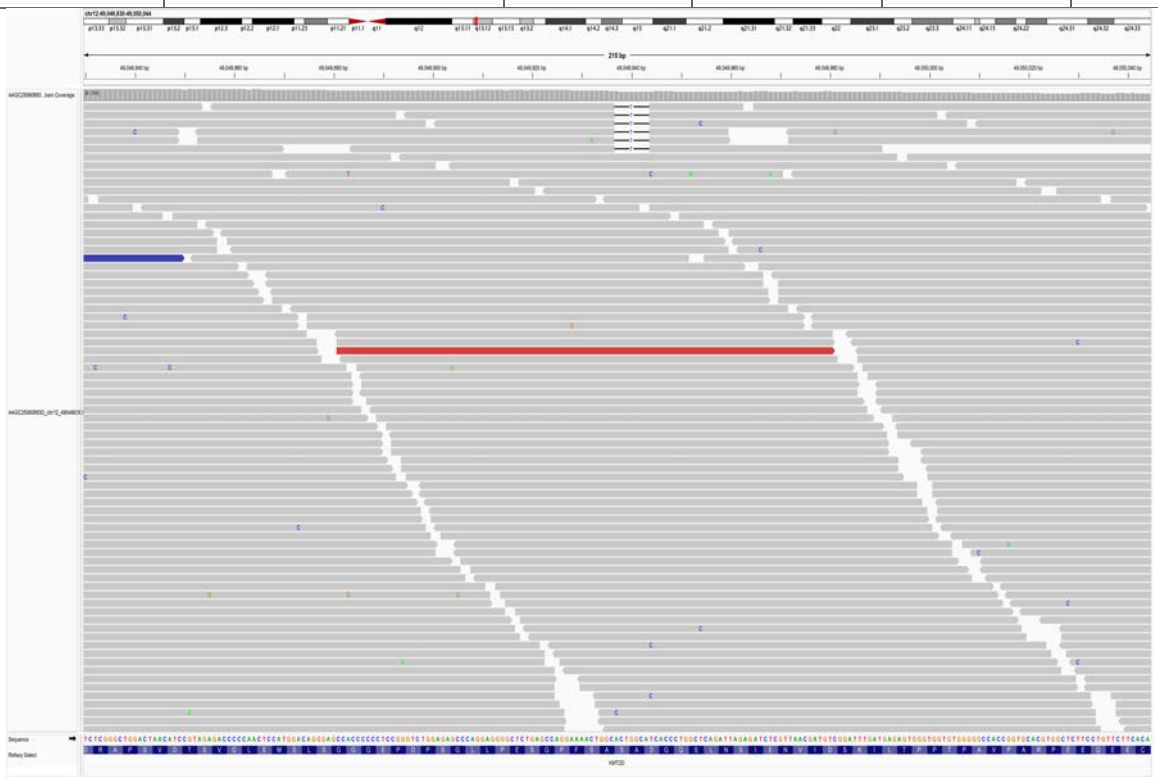
30.23. chr12_49044505_C/A

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



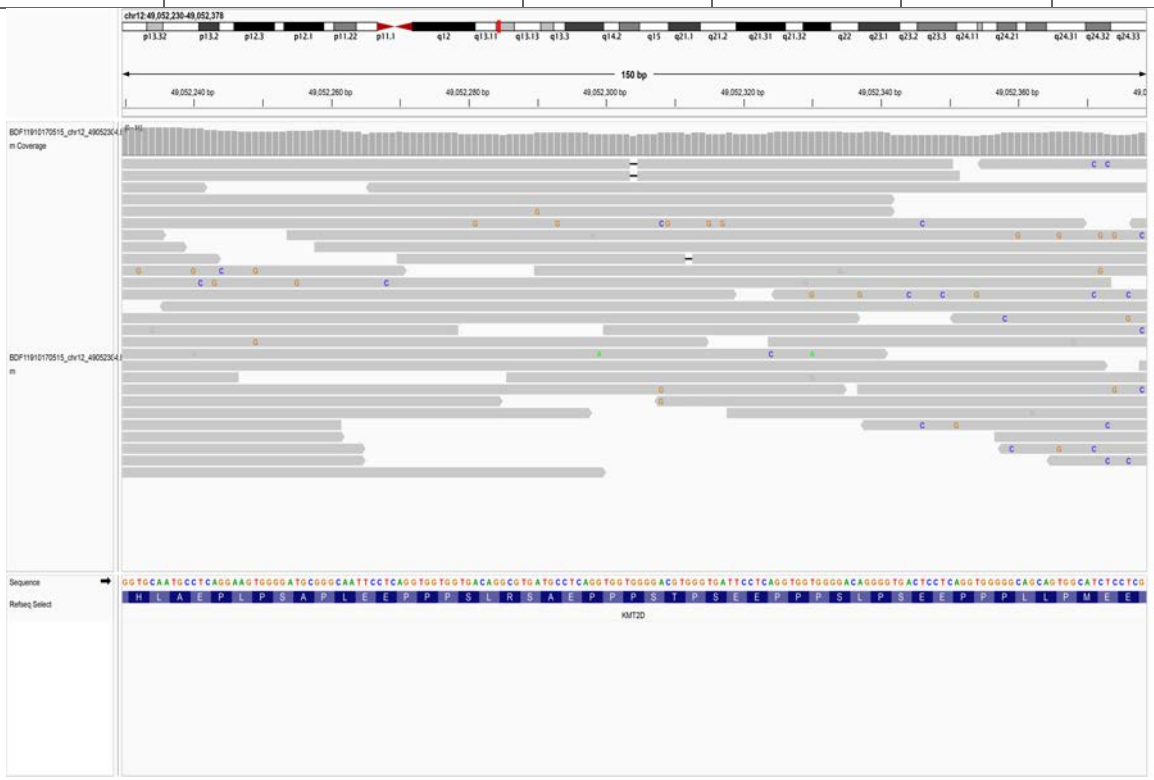
30.24. chr12_49049937_ACTGGCA/-

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



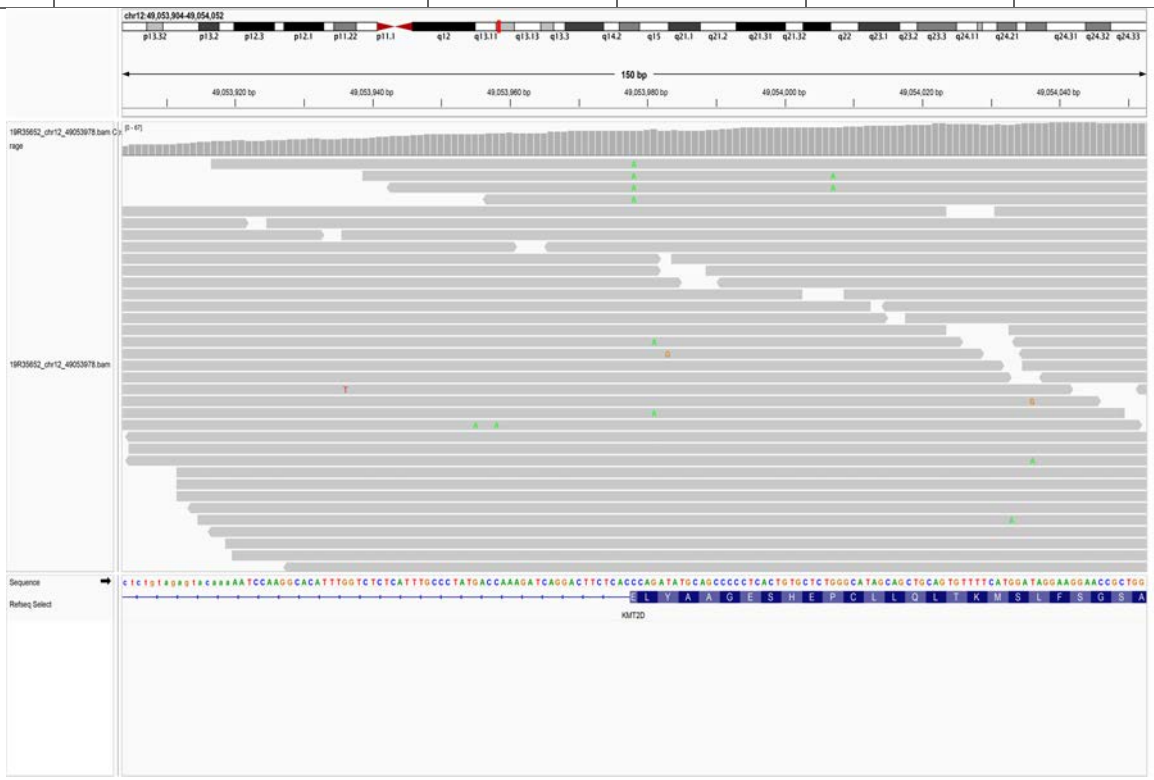
30.25. chr12_49052304_G/-

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



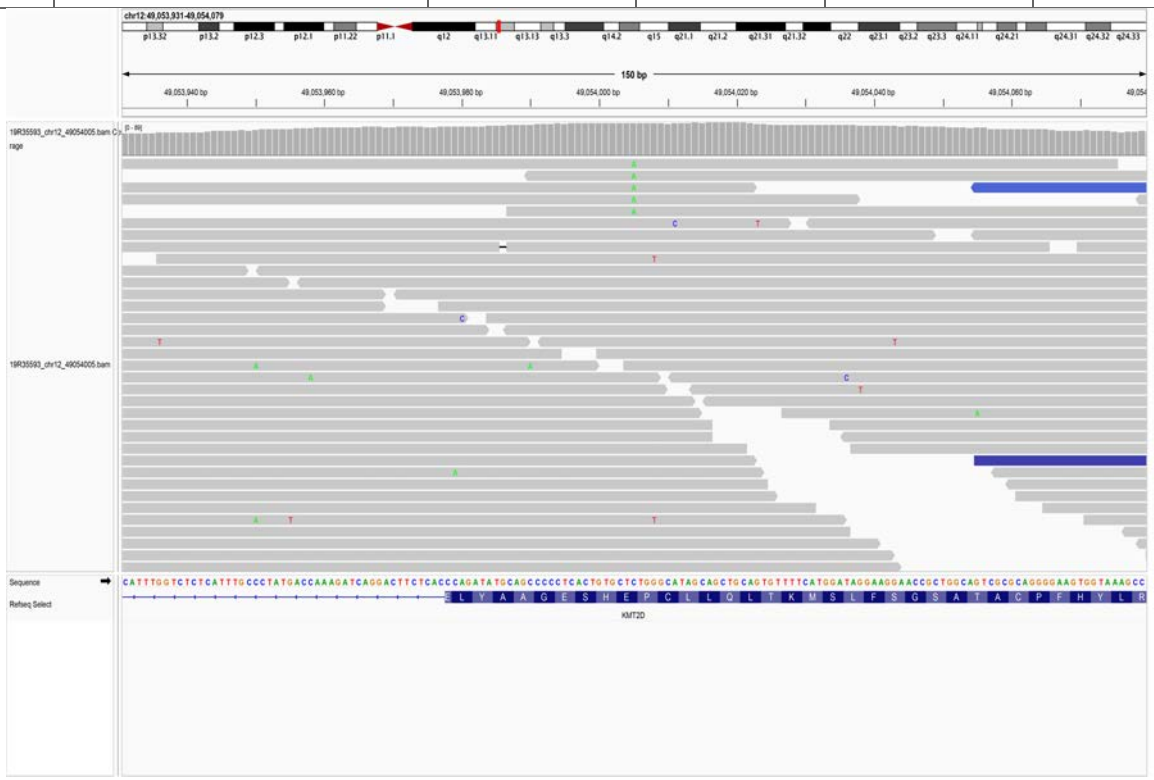
30.26. chr12_49053978_C/A

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



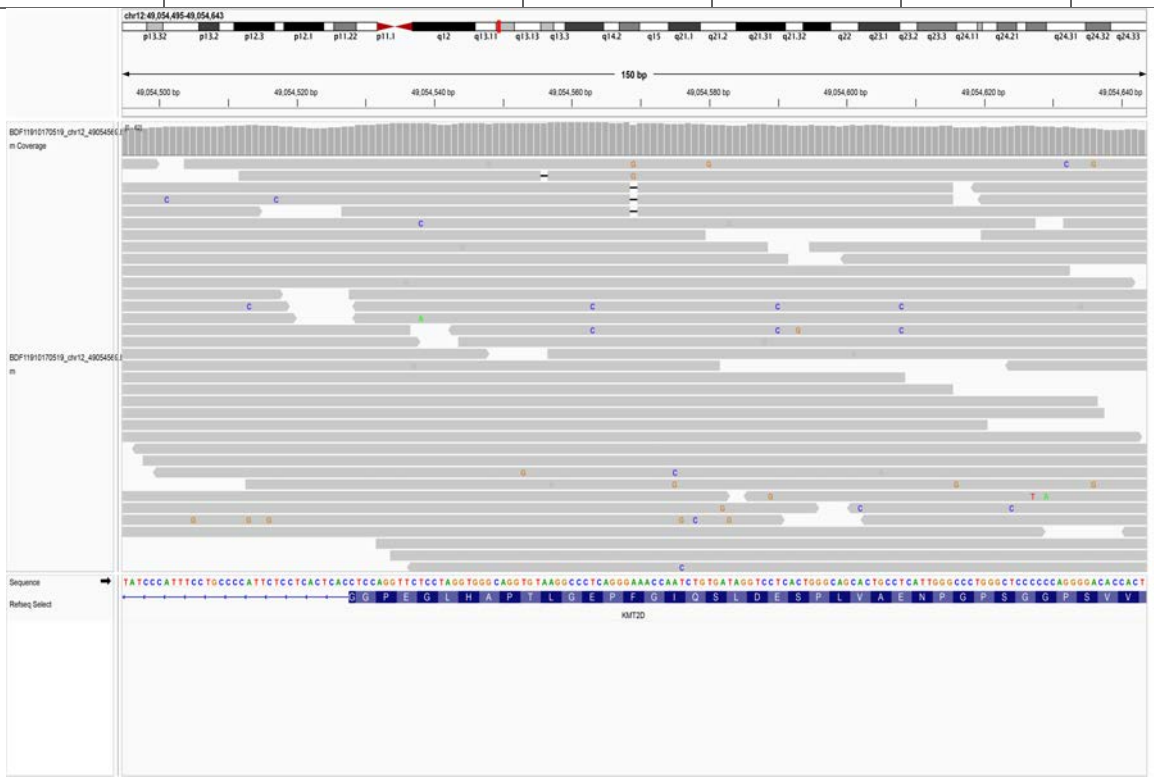
30.27. chr12_49054005_C/A

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



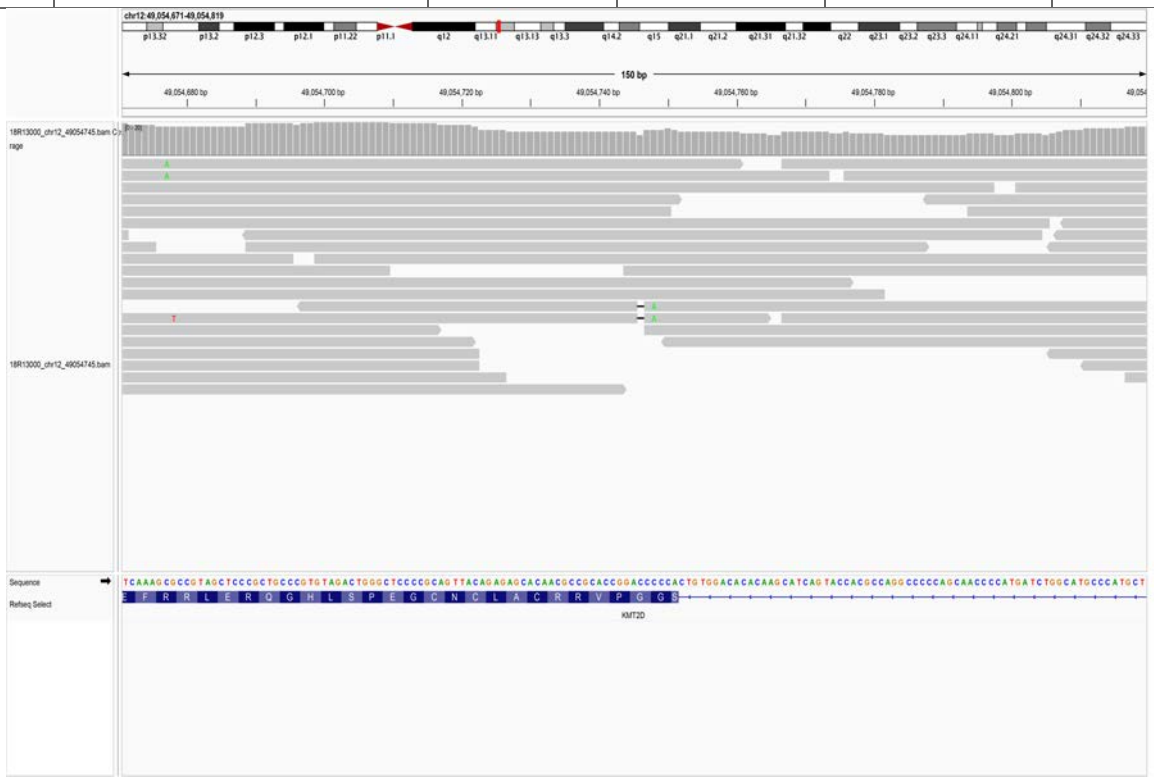
30.28. chr12_49054569_A/-

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



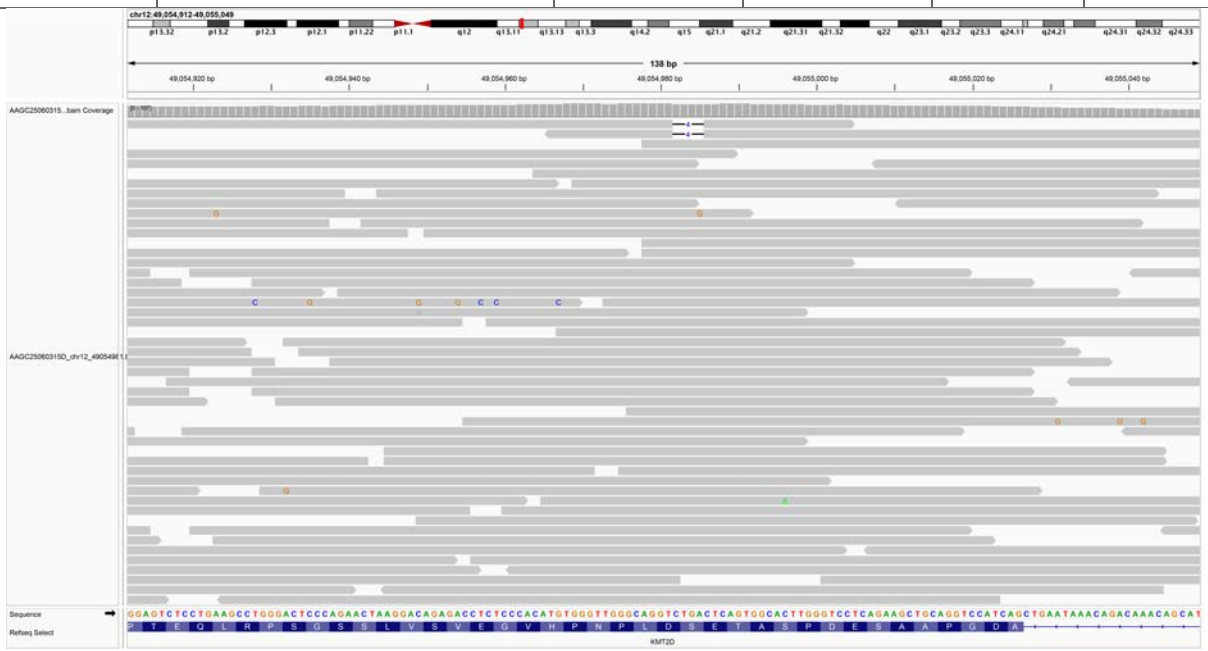
30.29. chr12_49054746_C/-

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



30.30. chr12_49054982_CTGA/-

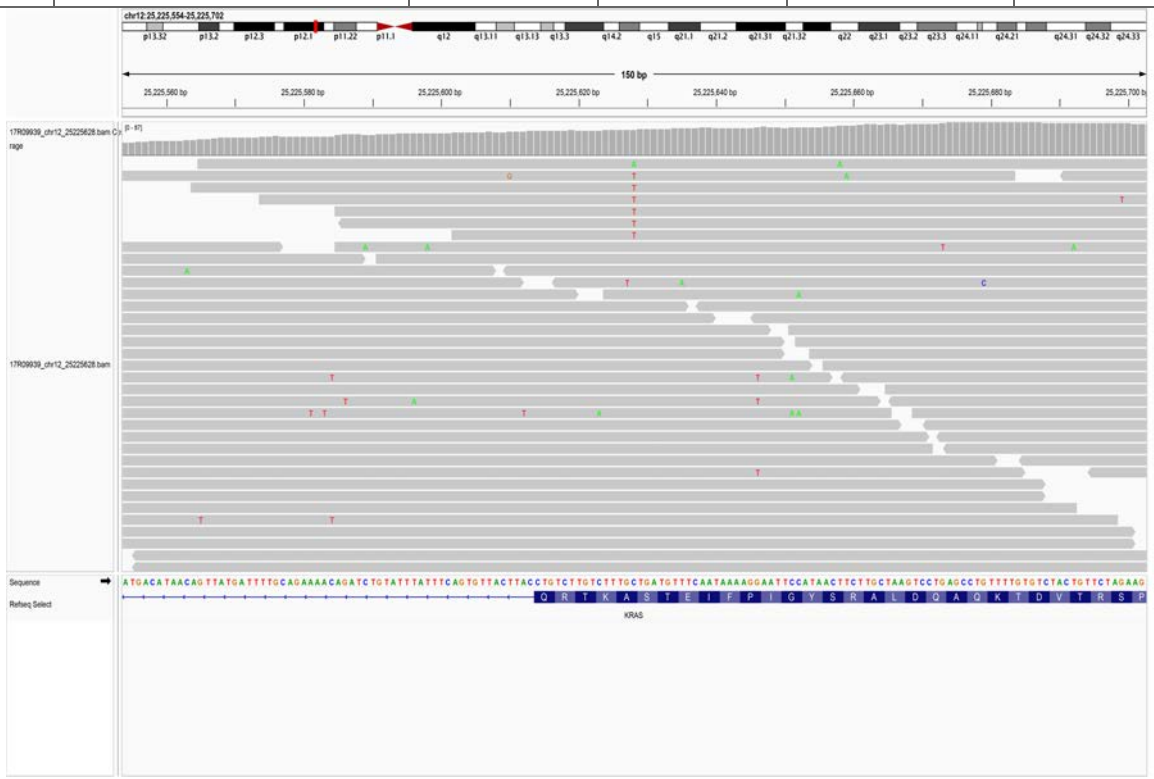
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060315D	chr12_49054982_CTGA/-	99	2	*KMT2D*	frameshift_variant



31. *KRAS*

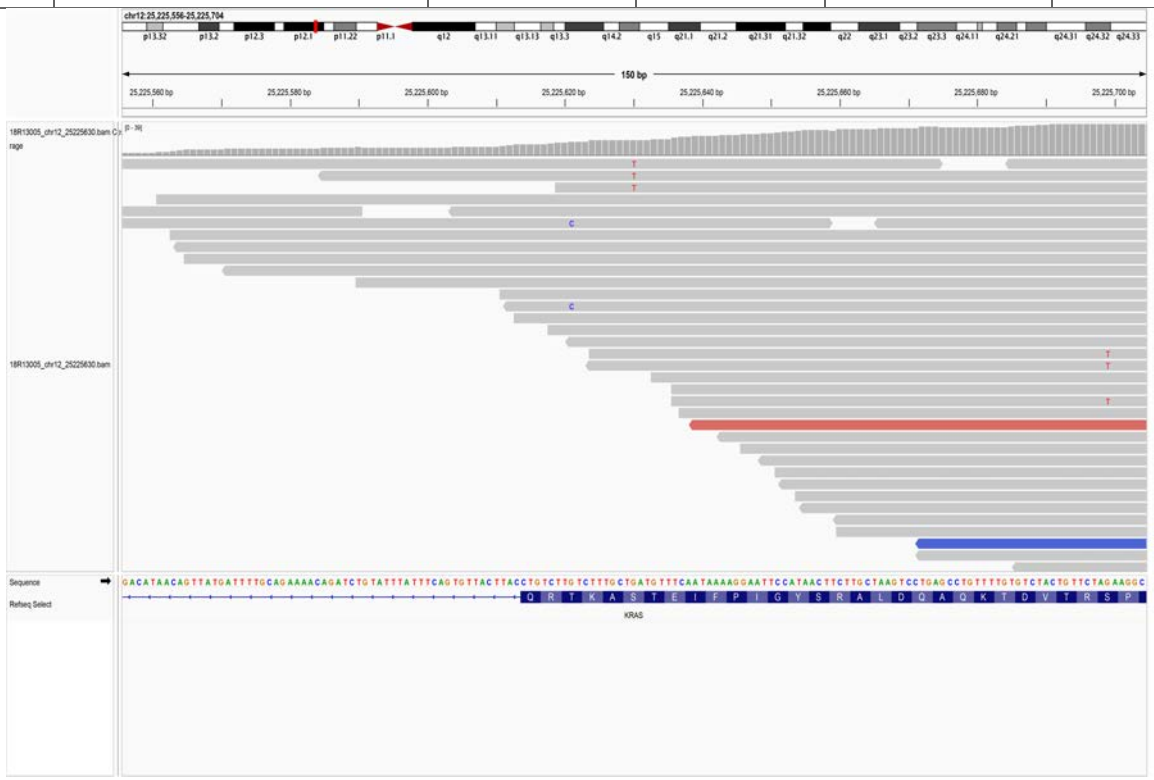
31.1. chr12_25225628_C/T

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

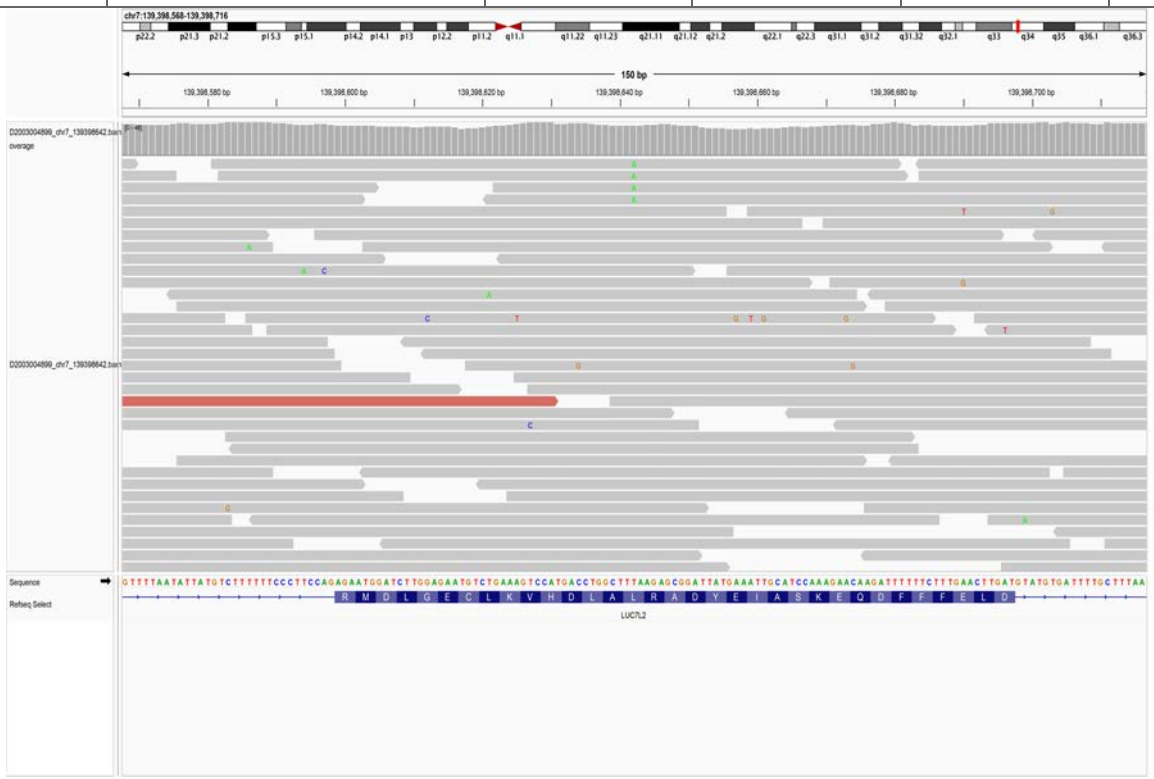
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13005	chr12_25225630_G/T	15	3	*KRAS*	stop_gained



32. *LUC7L2*

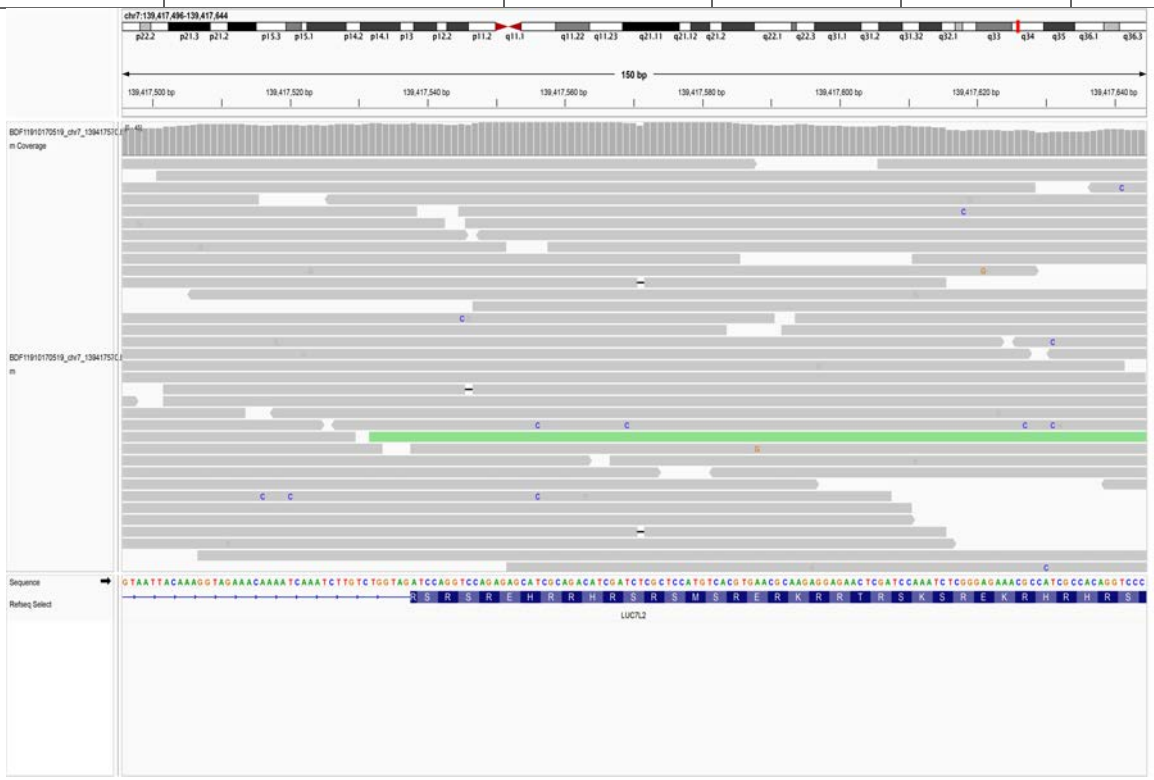
32.1. chr7_139398642_T/A

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



32.2. chr7_139417571_T/-

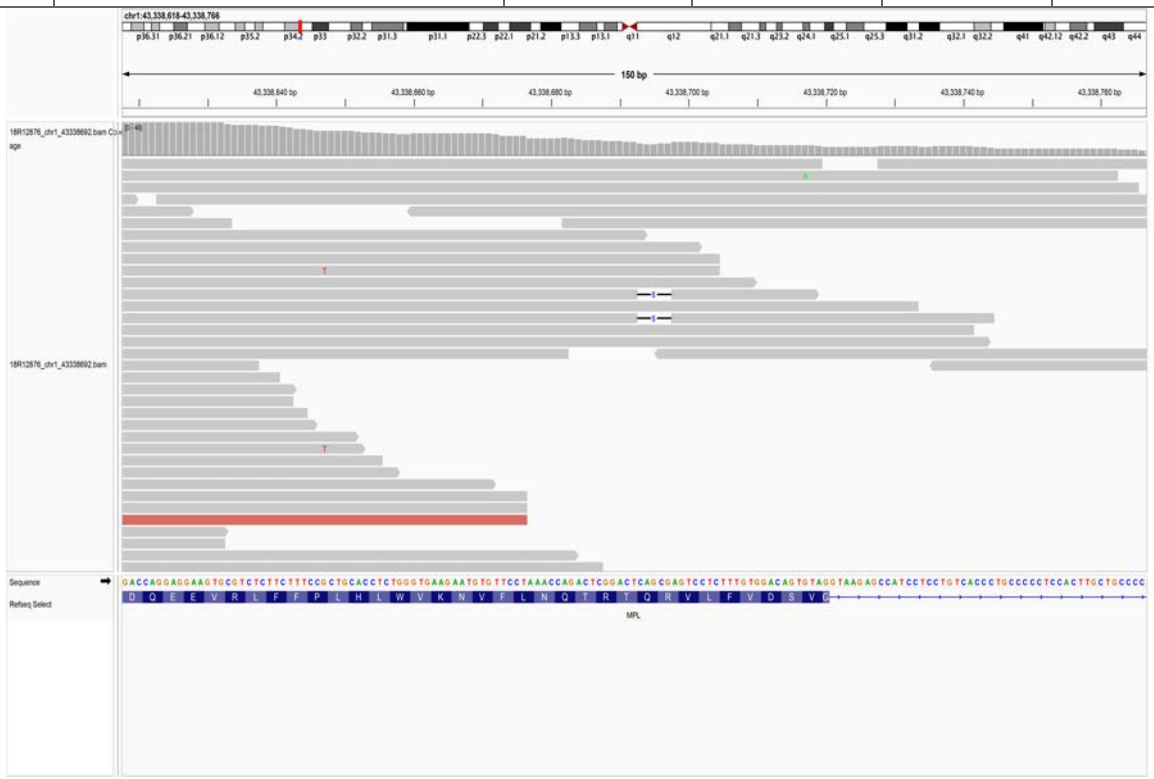
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170519	chr7_139417571_T/-	38	3	*LUC7L2*	frameshift_variant



33. *MPL*

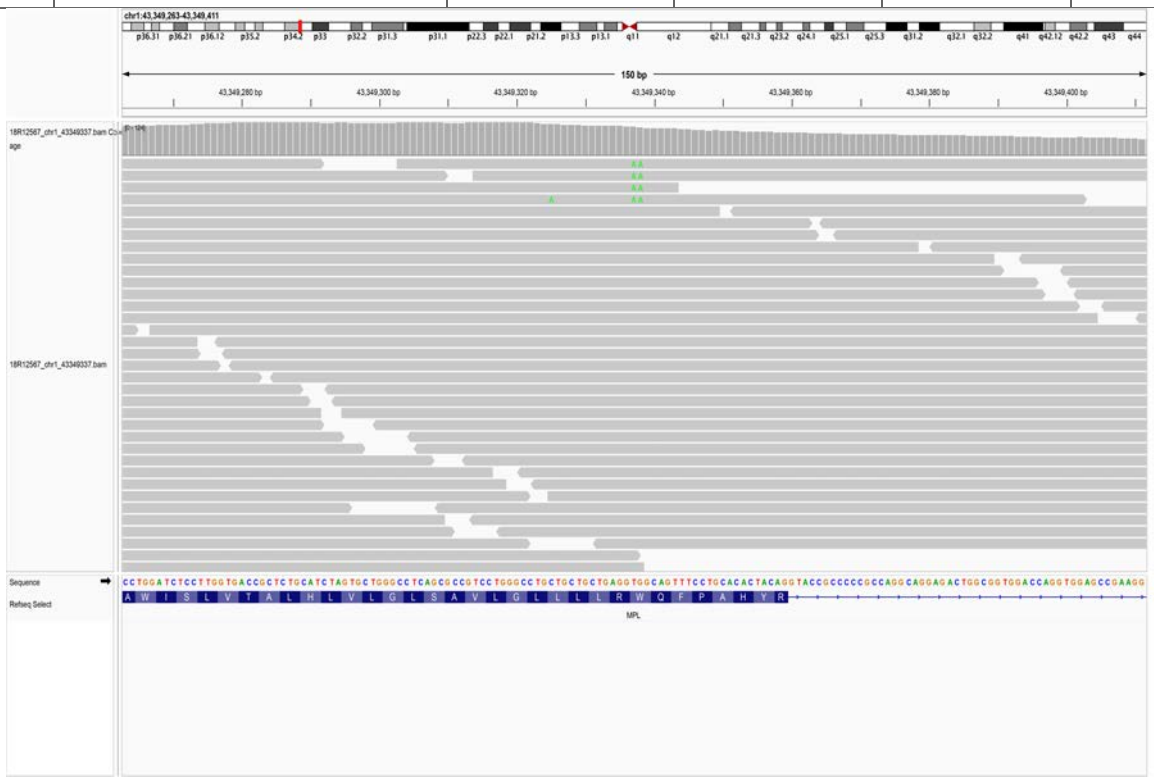
33.1. chr1_43338693_CAGCG/-

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



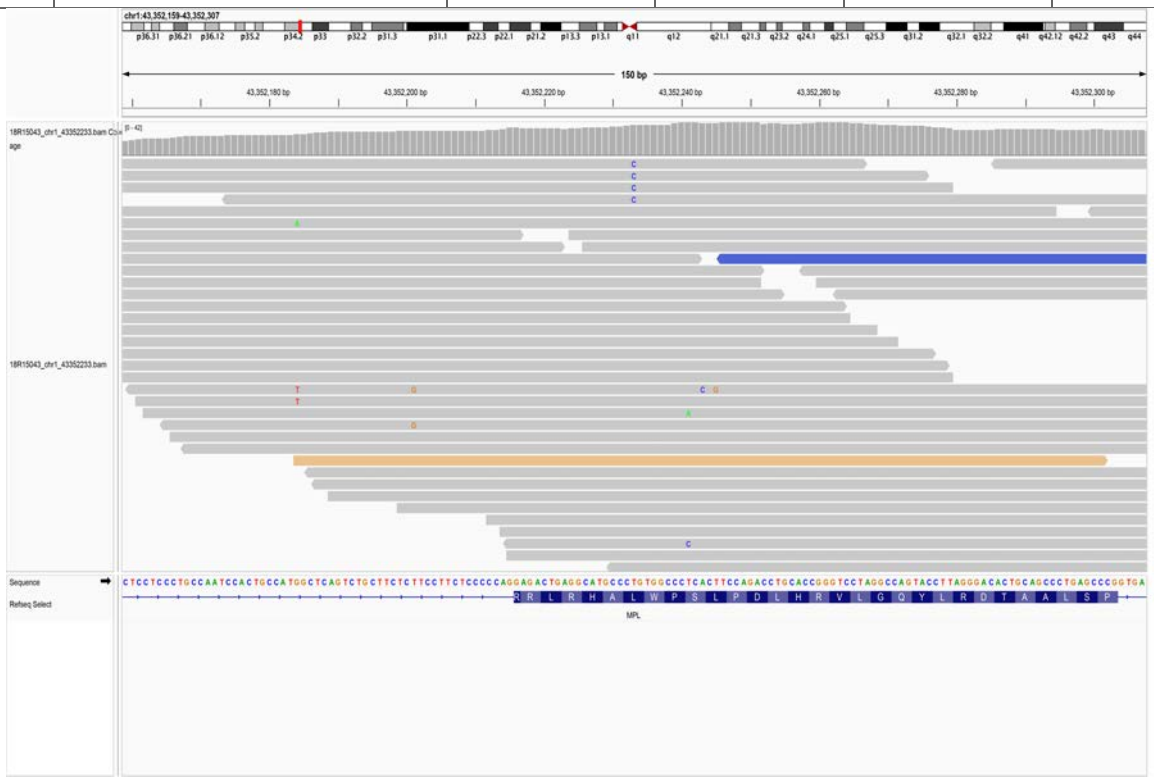
33.2. chr1_43349337_TG/AA

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



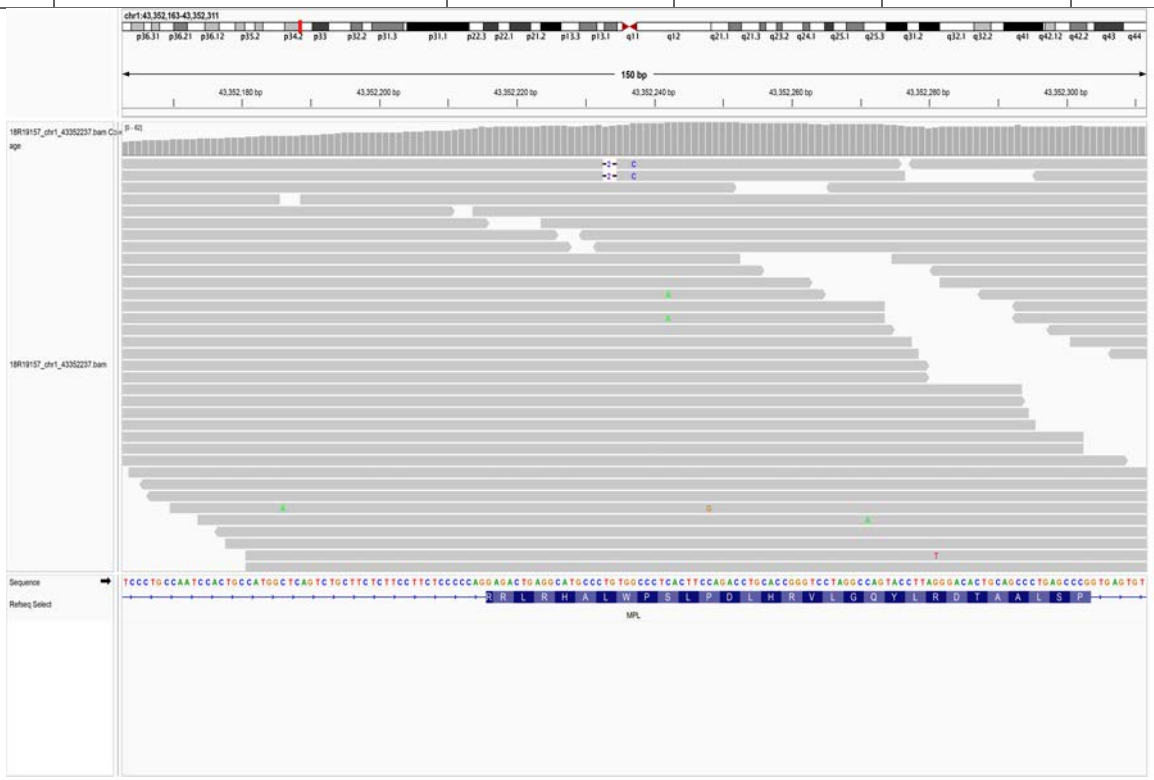
33.3. chr1_43352233_T/C

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



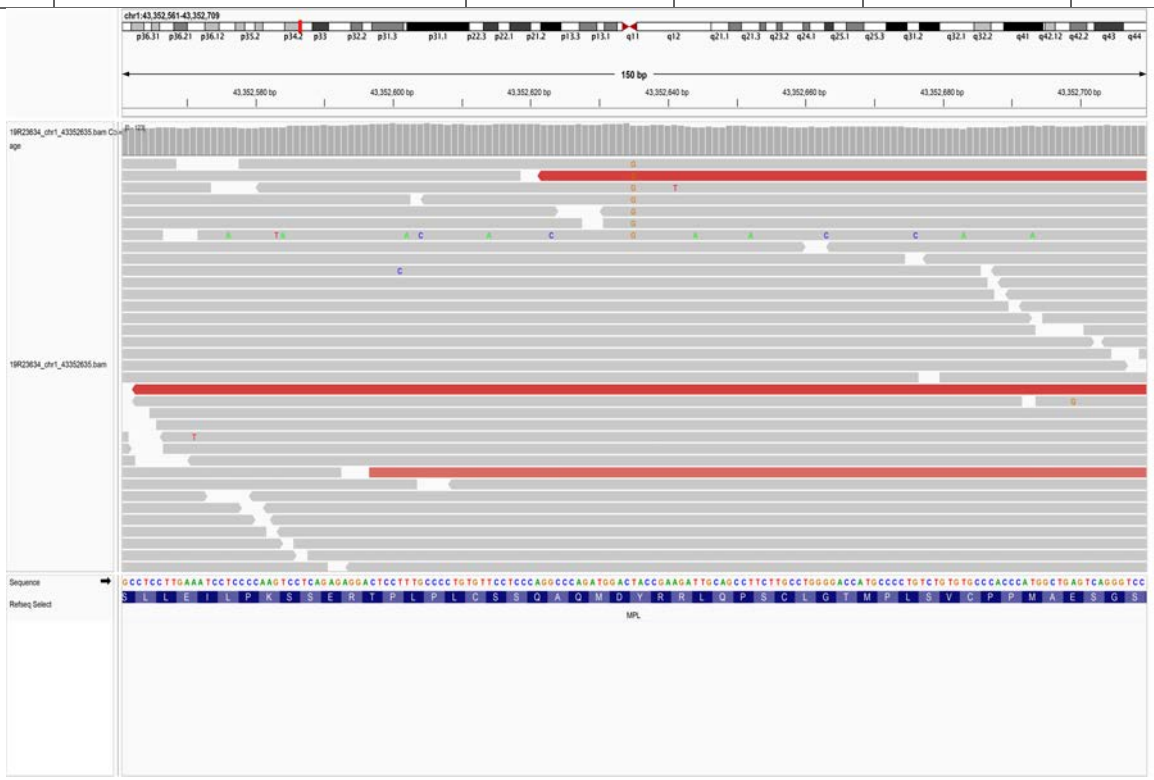
33.4. chr1_43352237_G/C

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



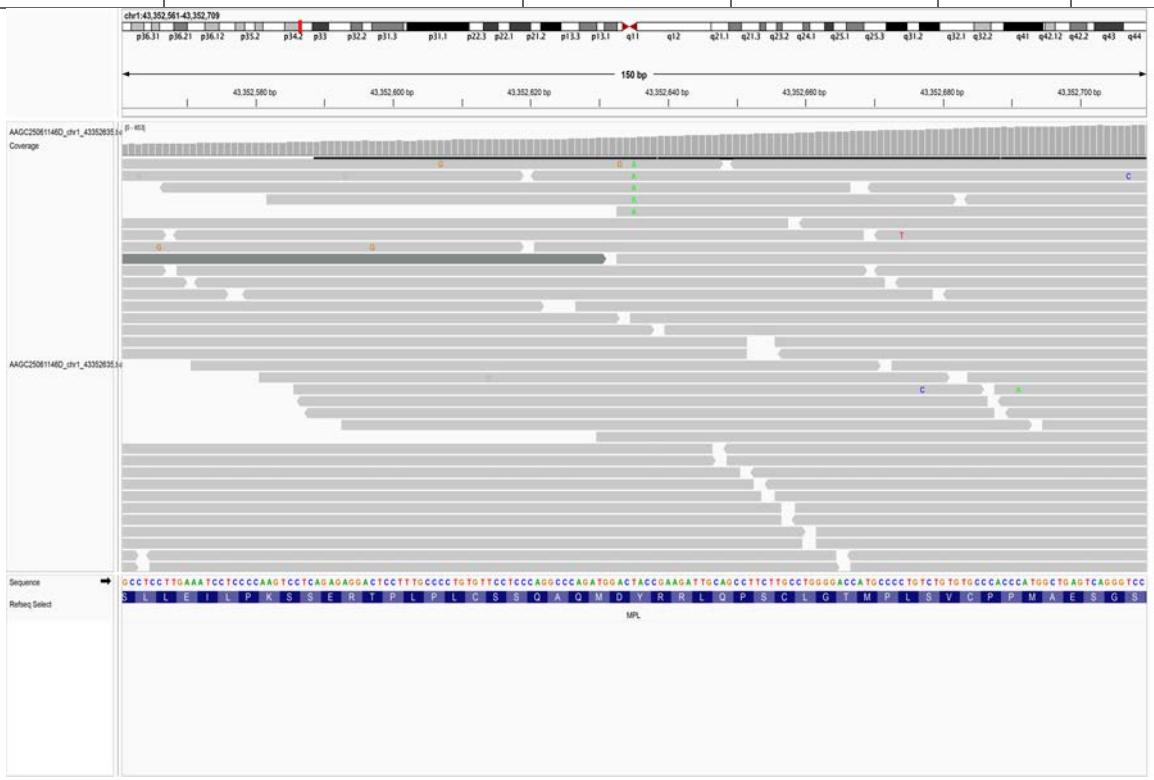
33.5. chr1_43352635_T/G

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



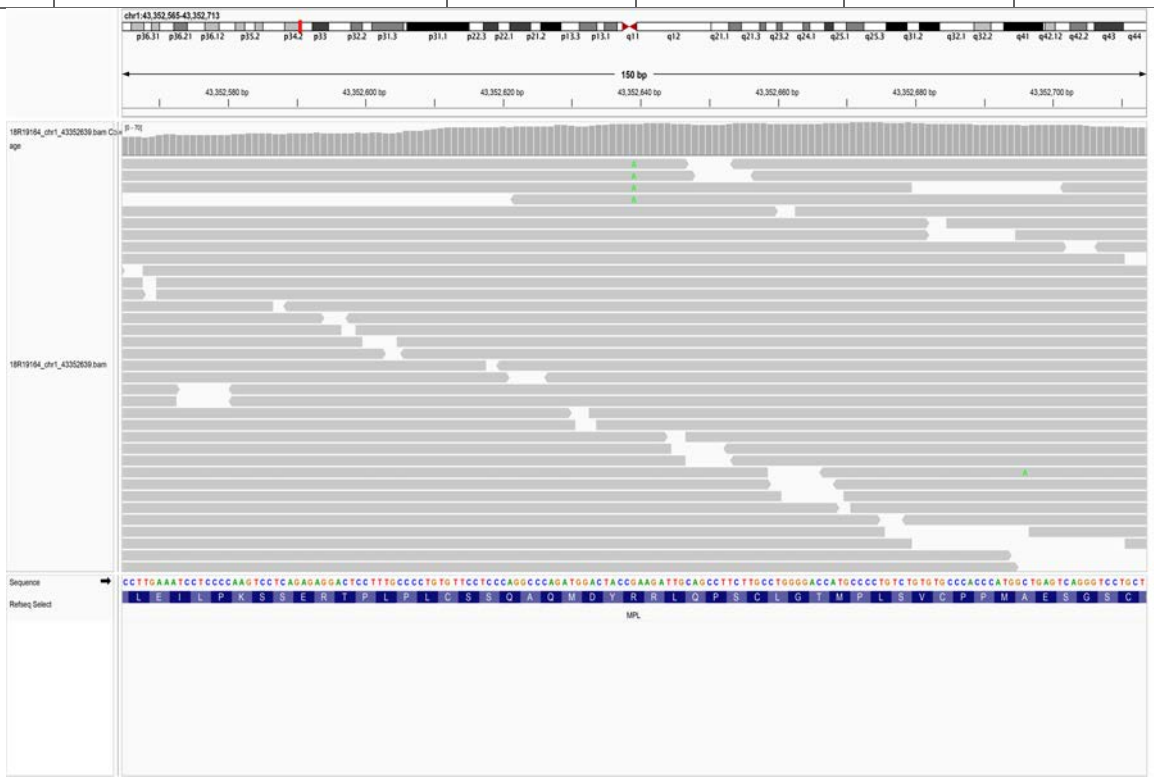
33.6. chr1_43352635_T/A

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



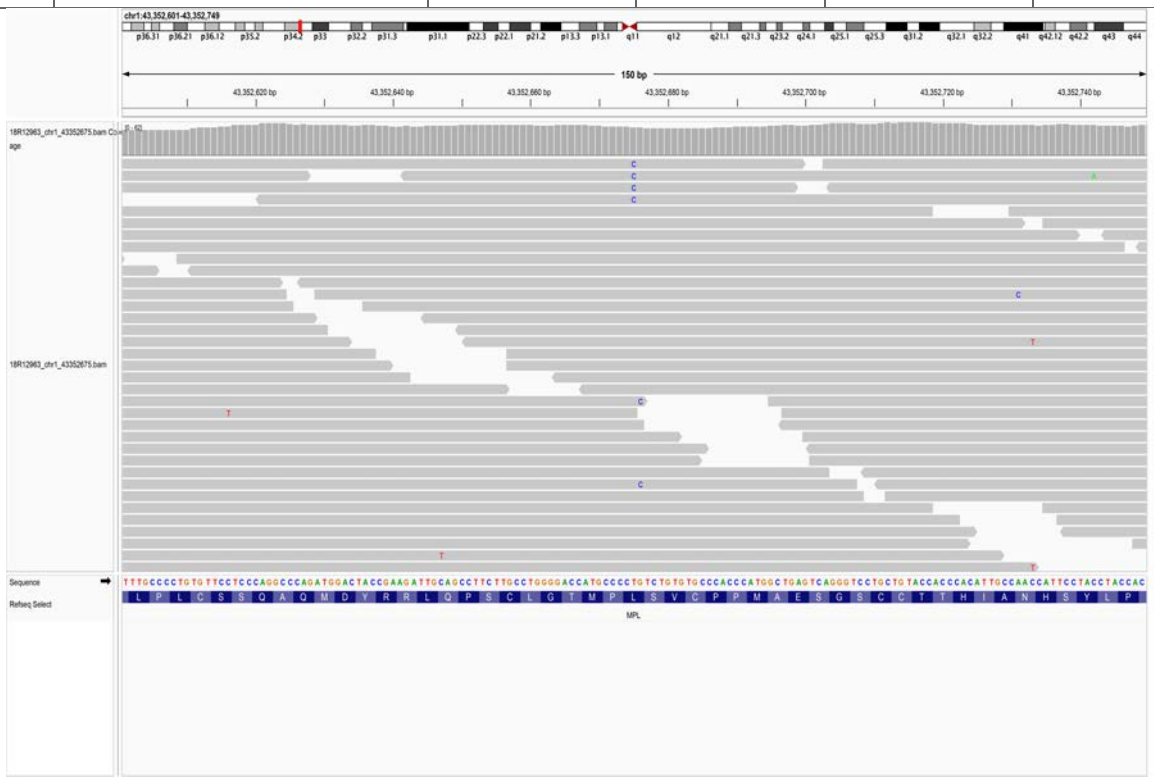
33.7. chr1_43352639_G/A

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

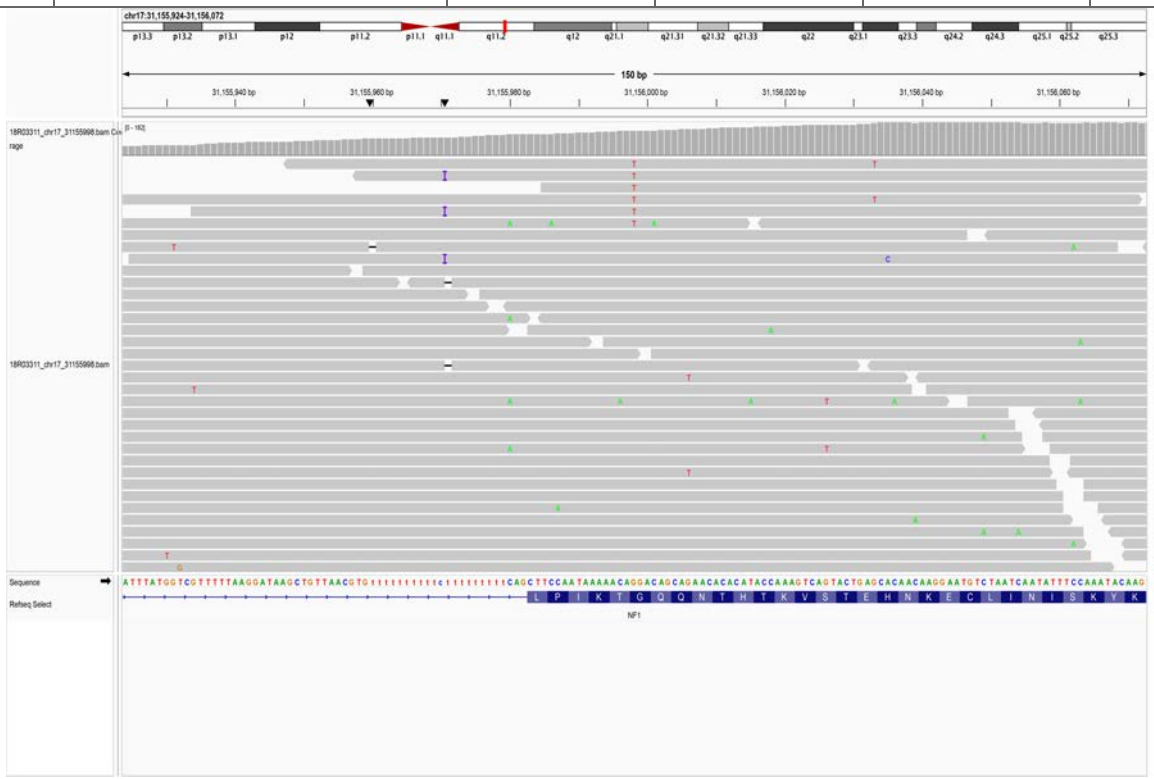
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12963	chr1_43352675_T/C	48	4	*MPL*	missense_variant



34. *NF1*

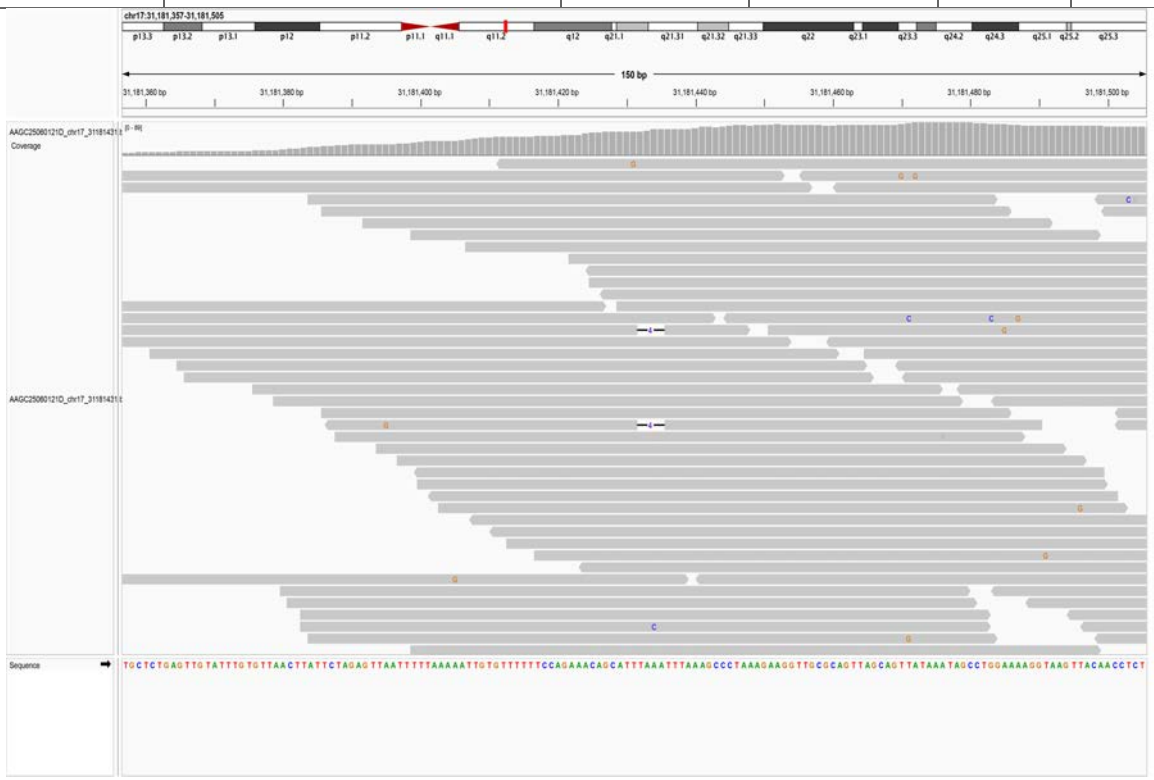
34.1. chr17_31155998_G/T

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



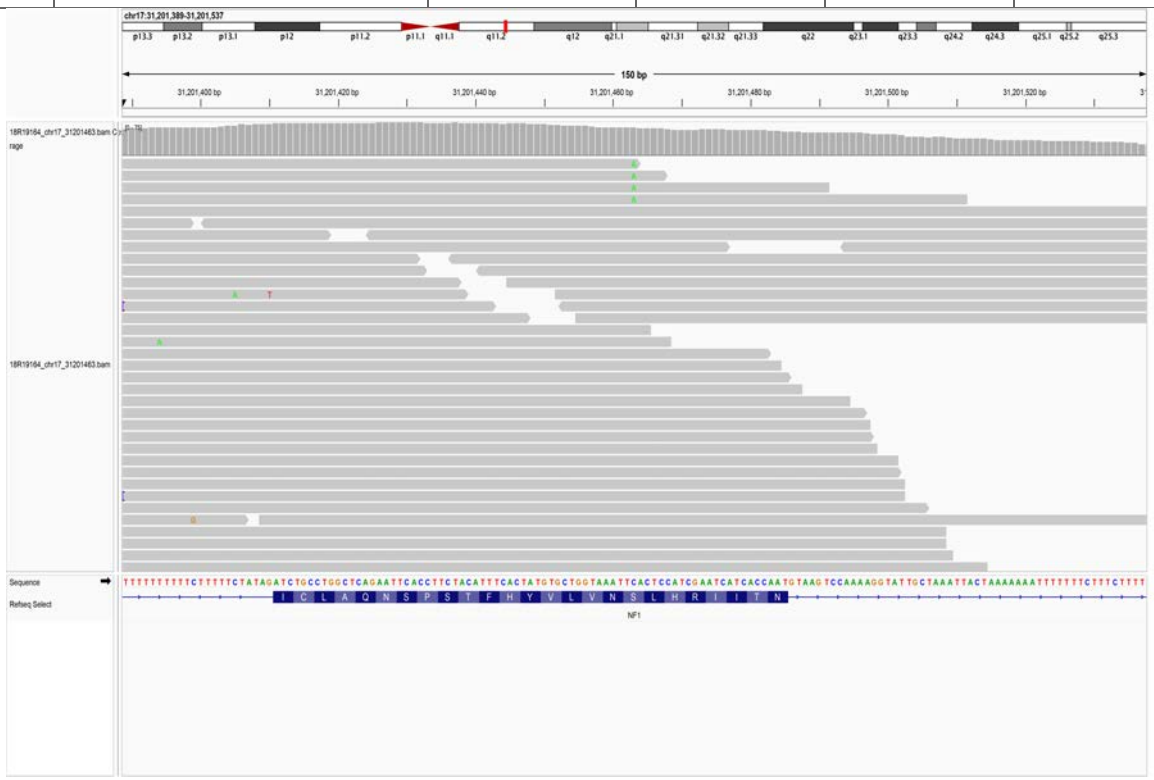
34.2. chr17_31181432_TAAA/-

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



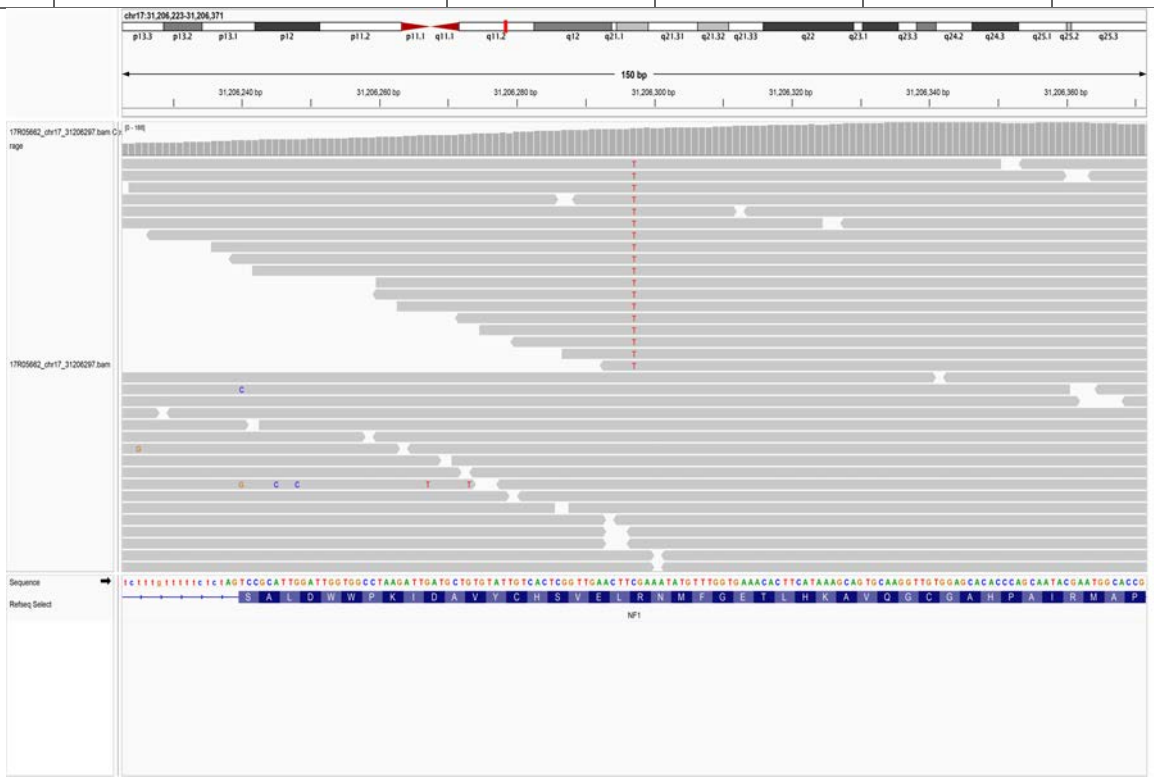
34.3. chr17_31201463_C/A

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



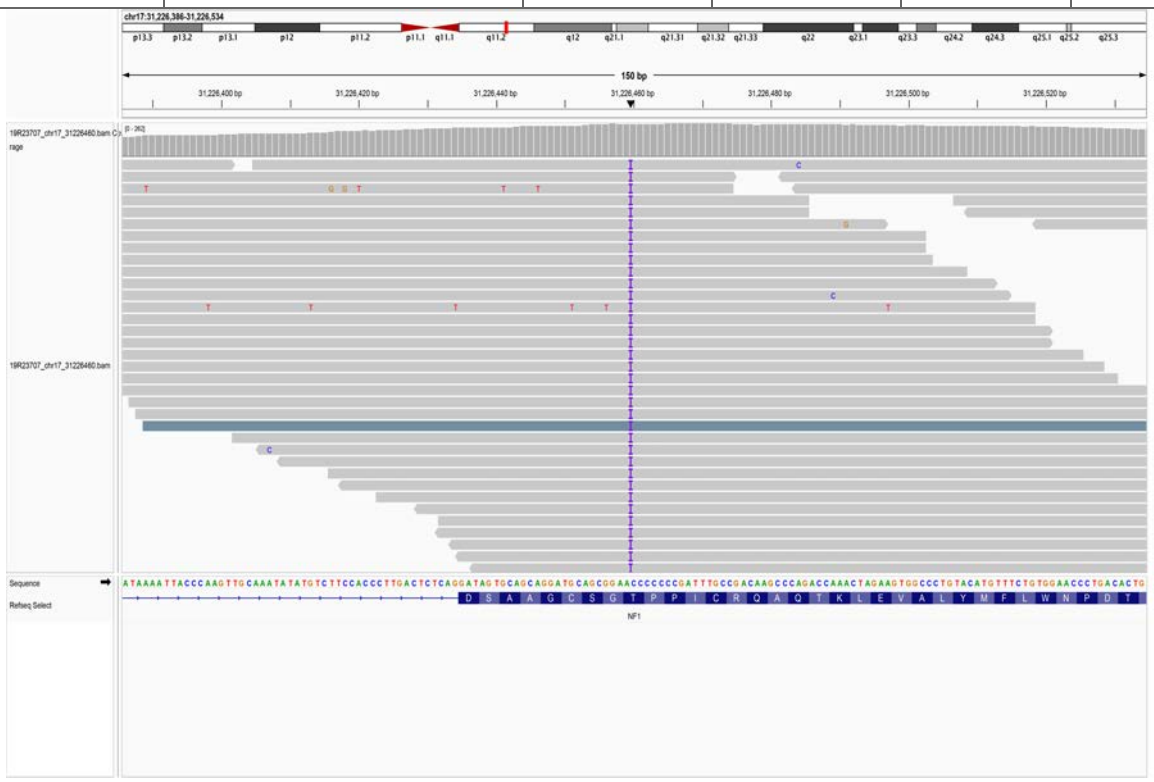
34.4. chr17_31206297_C/T

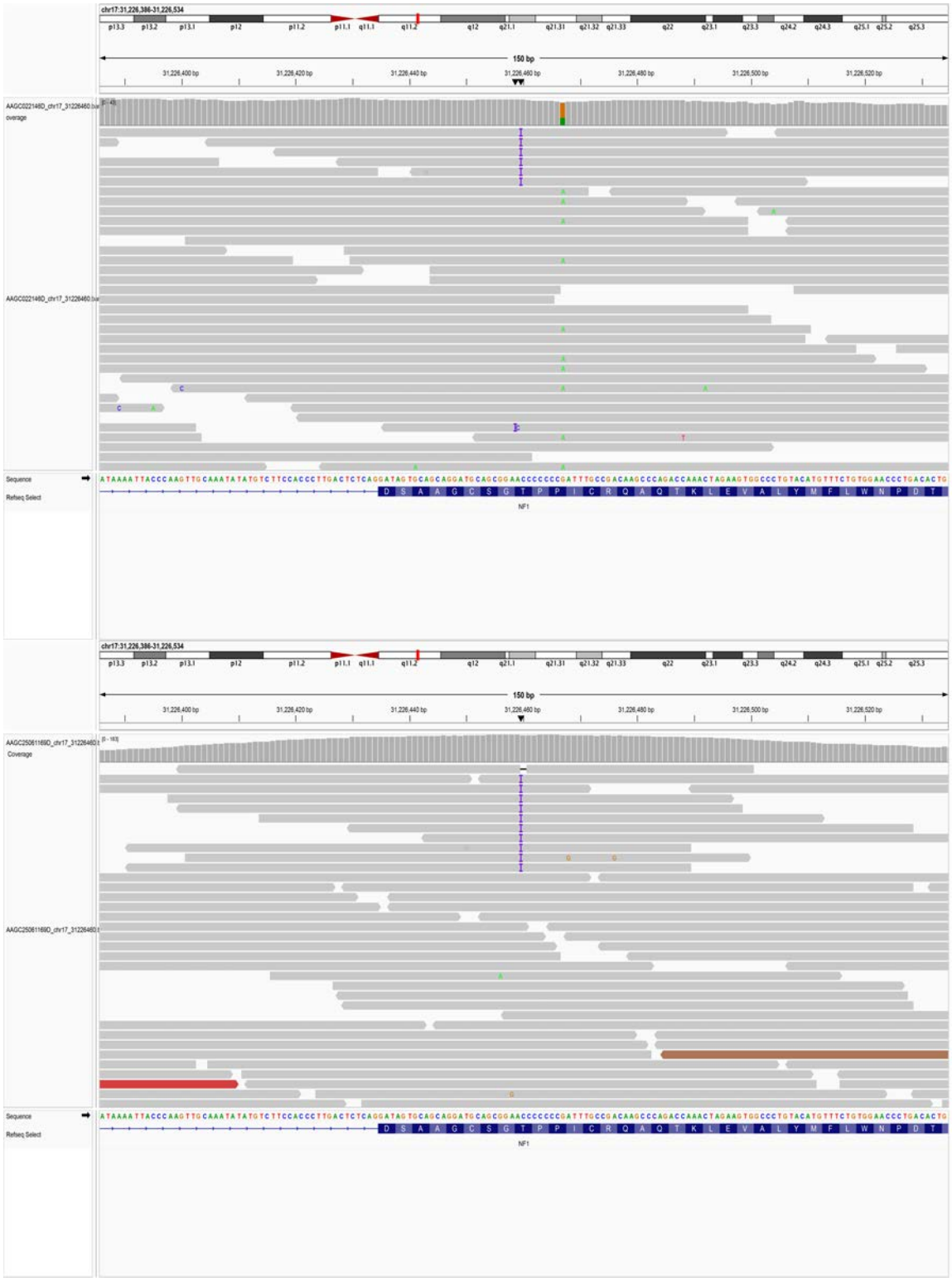
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
17R05662	chr17_31206297_C/T	130	18	*NF1*	stop_gained

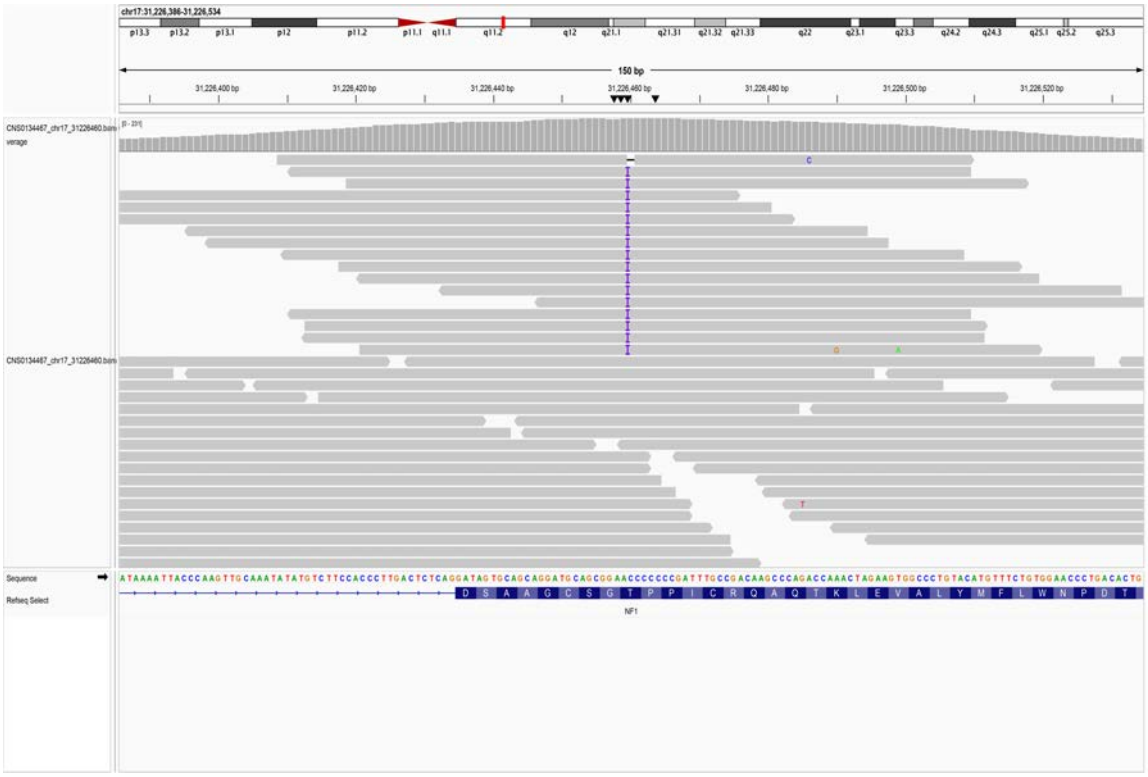


34.5. chr17_31226460_-/C

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

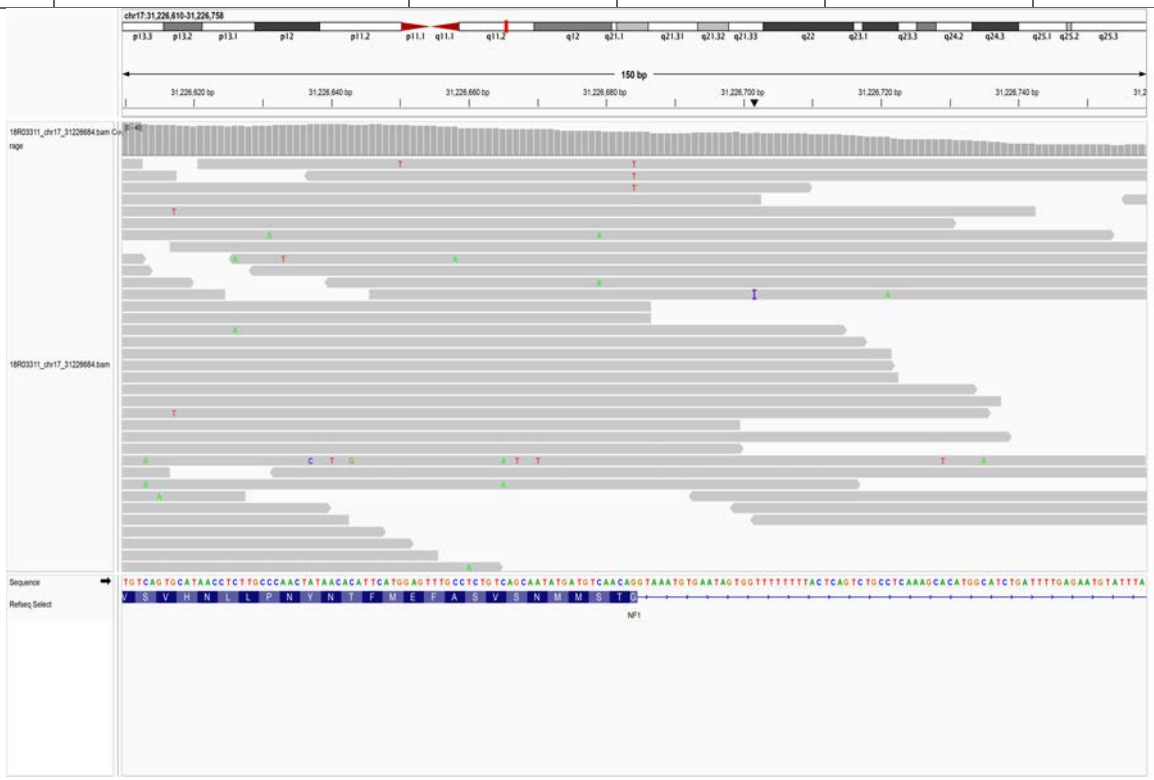



chr17:31,226,386-31,226,534
150 bp
31,226,400 bp
31,226,420 bp
31,226,440 bp
31,226,460 bp
31,226,480 bp
31,226,500 bp
31,226,520 bp
Coverage
Sequence
Refseq Select
NF1


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
CNS0134467_chr17_31226460.bam
verage
CNS0134467_chr17_31226460.bam
Sequence
Refseq Select
NF1

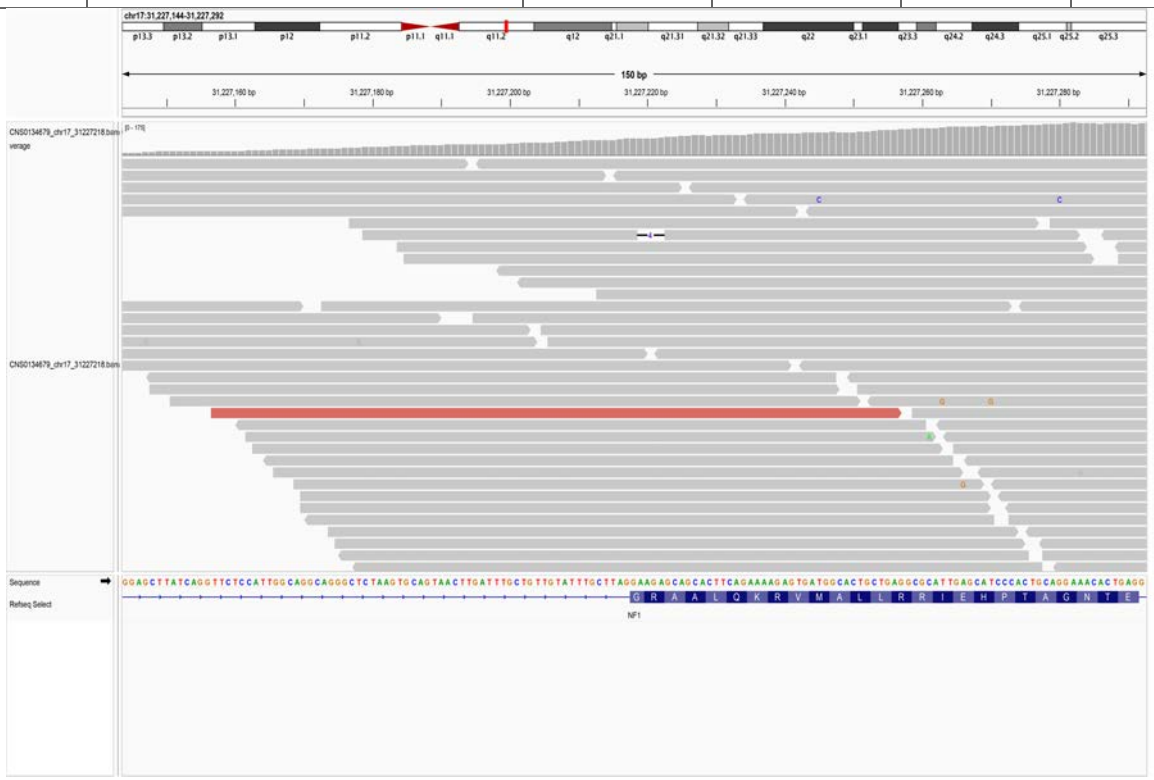
34.6. chr17_31226684_G/T

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



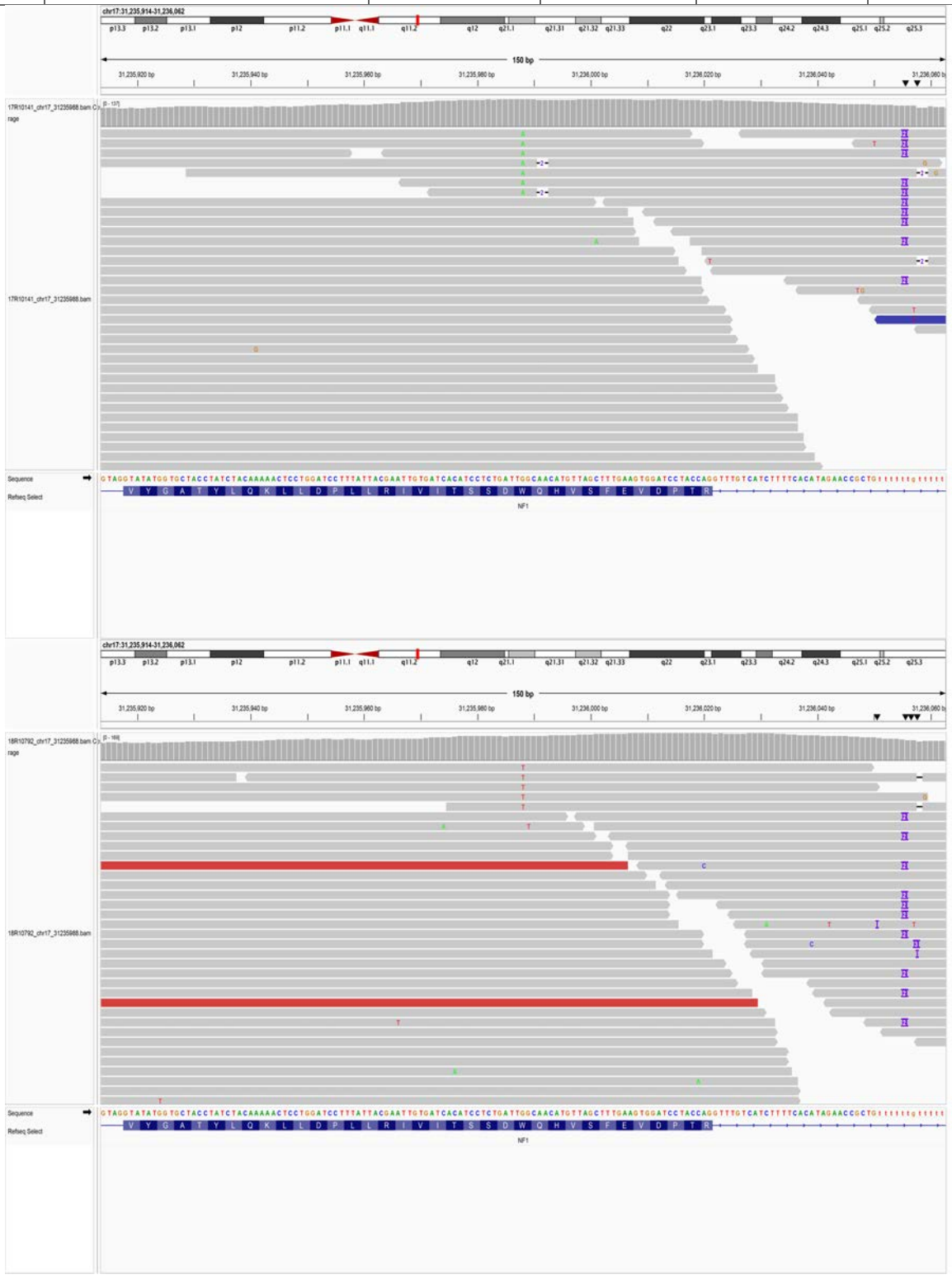
34.7. chr17_31227219_AAGA/-

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



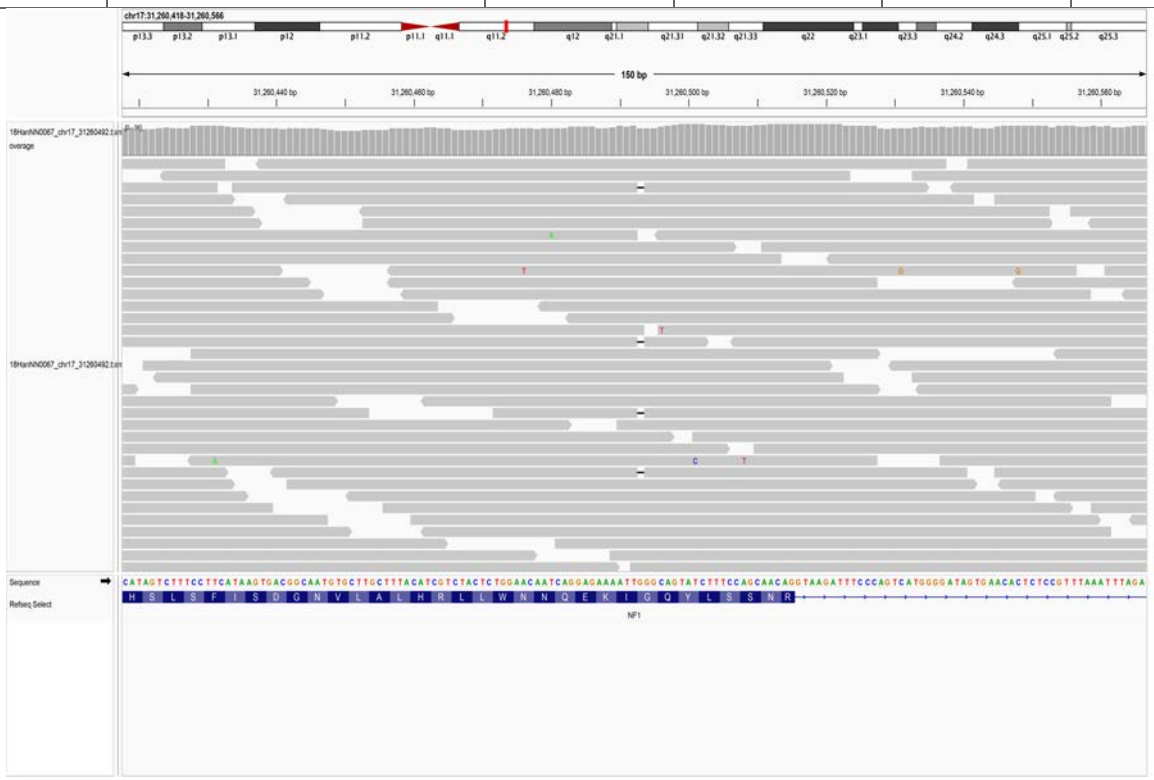
34.8. chr17_31235988_G/A/T

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



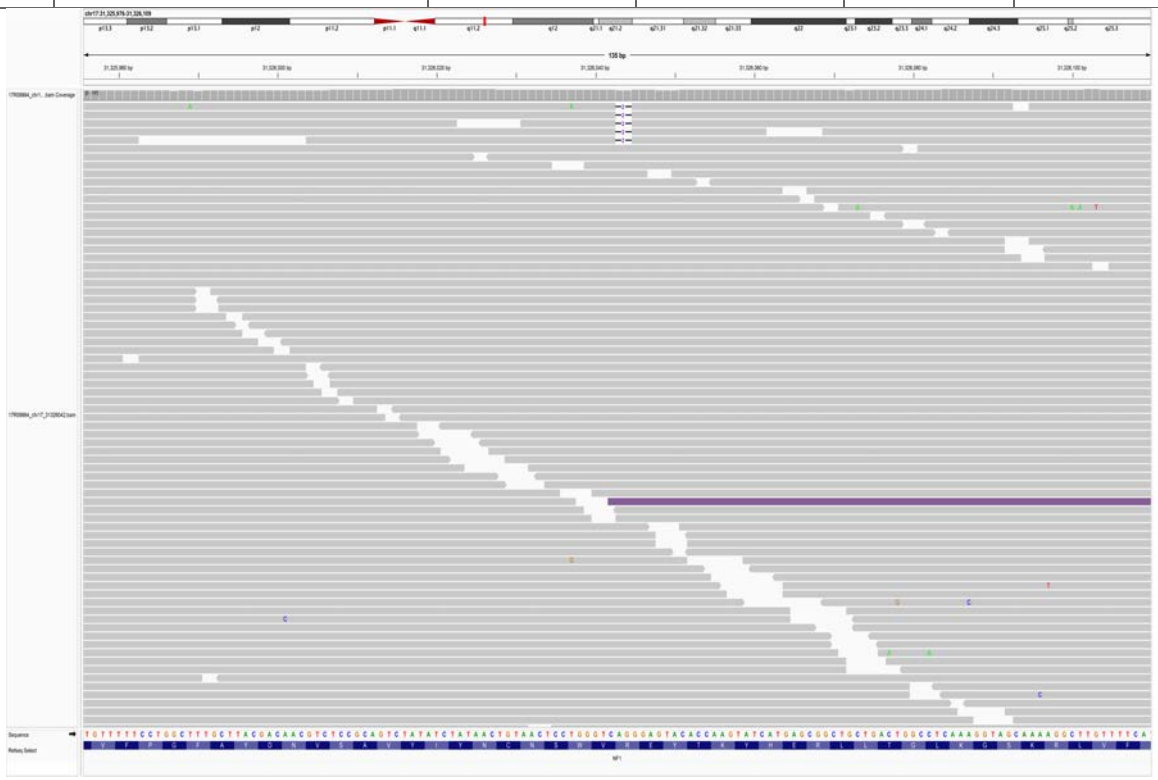
34.9. chr17_31260493_G/-

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



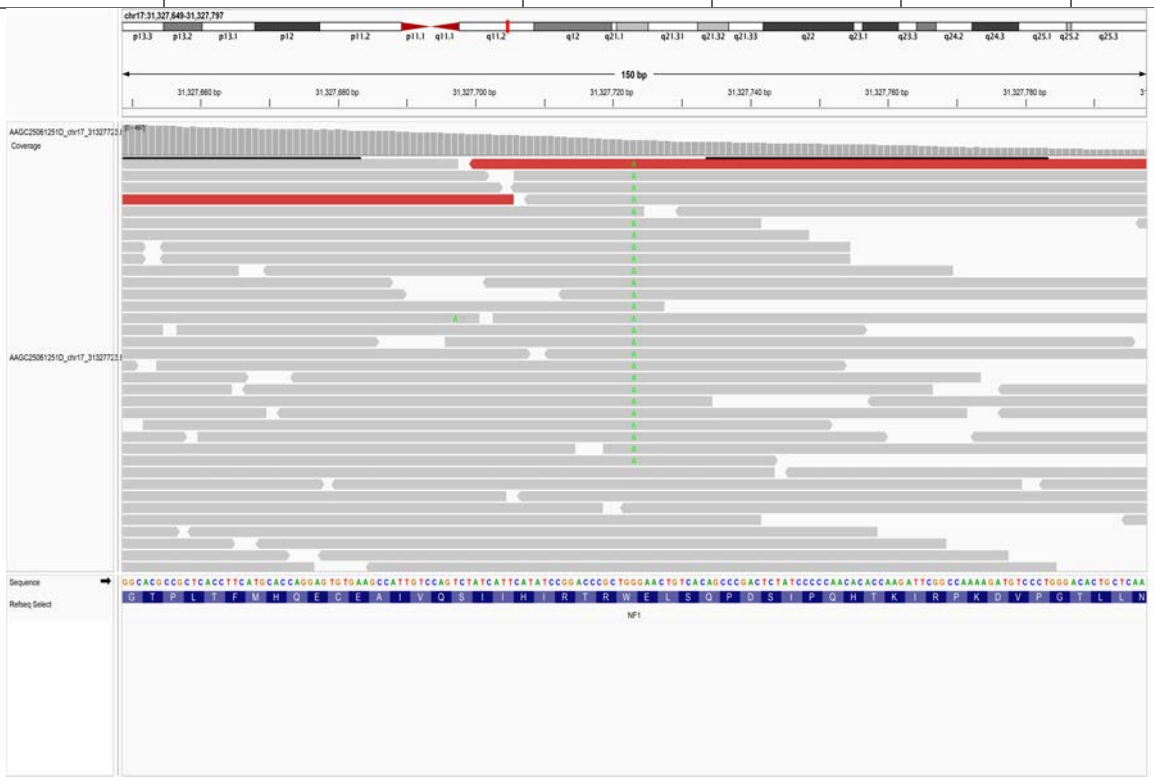
34.10. chr17_31326043_AG/-

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



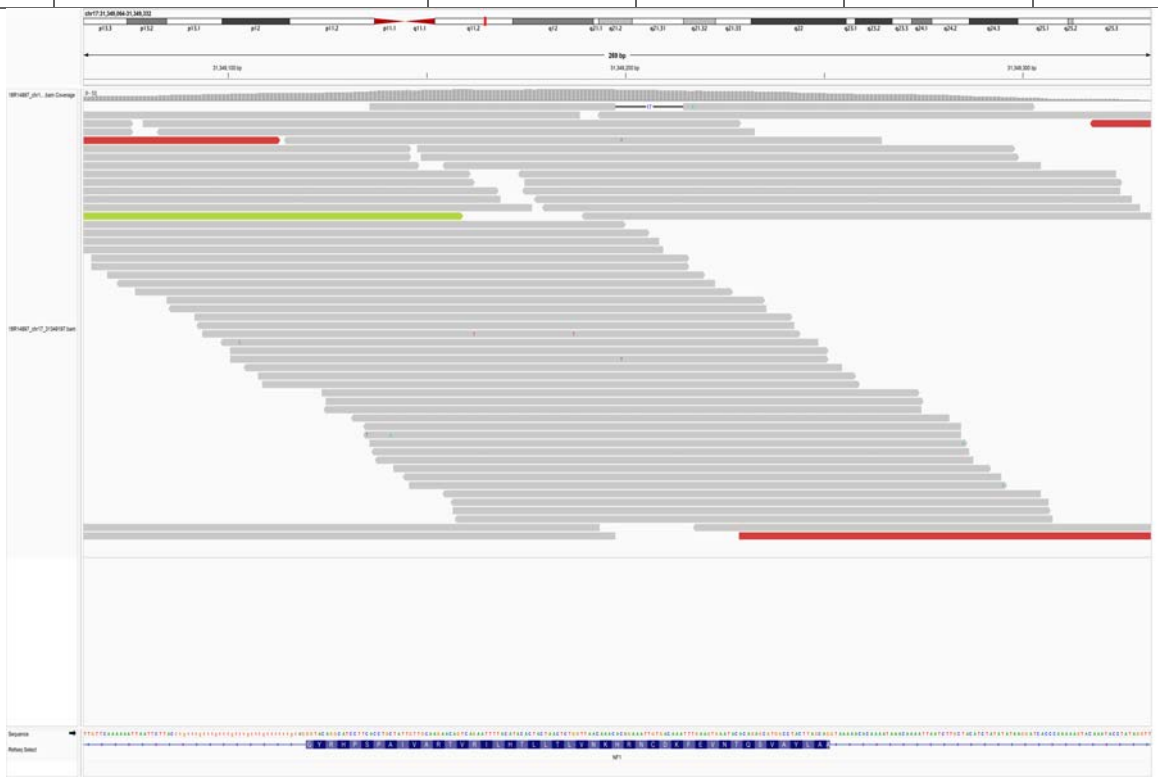
34.11. chr17_31327723_G/A

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



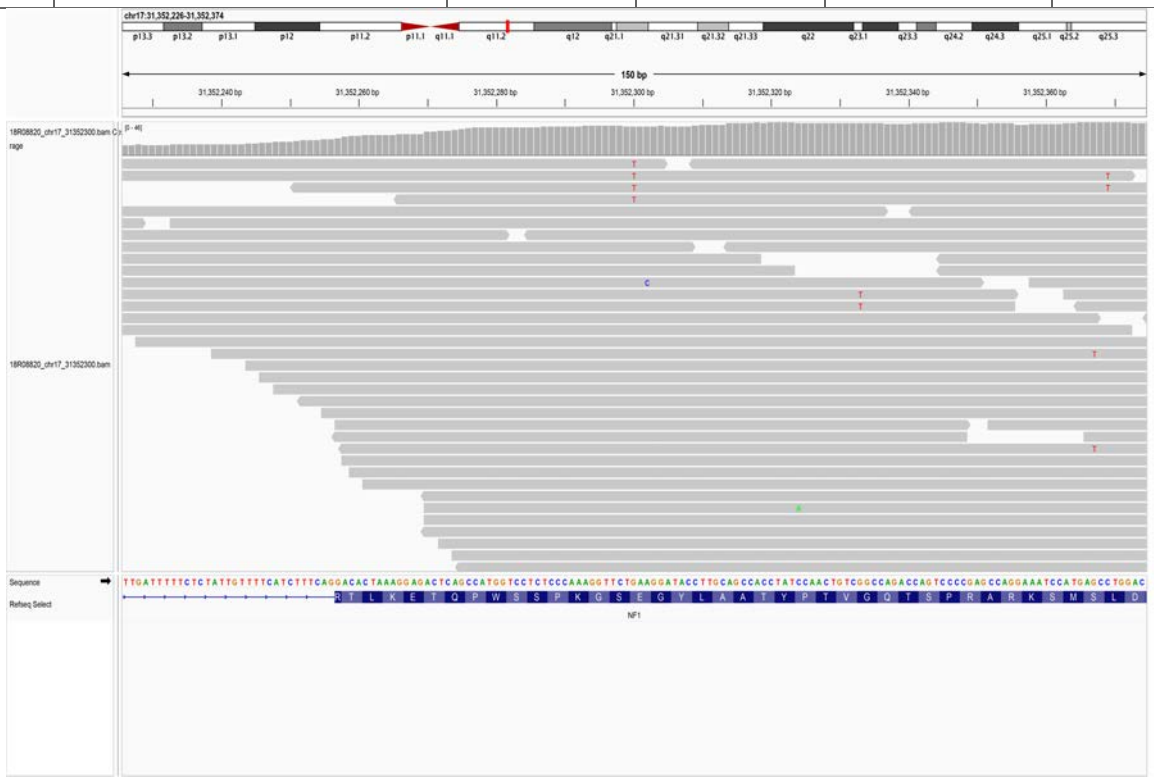
34.12. chr17_31349198_ACAGAAATTGTGACAAA/-

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



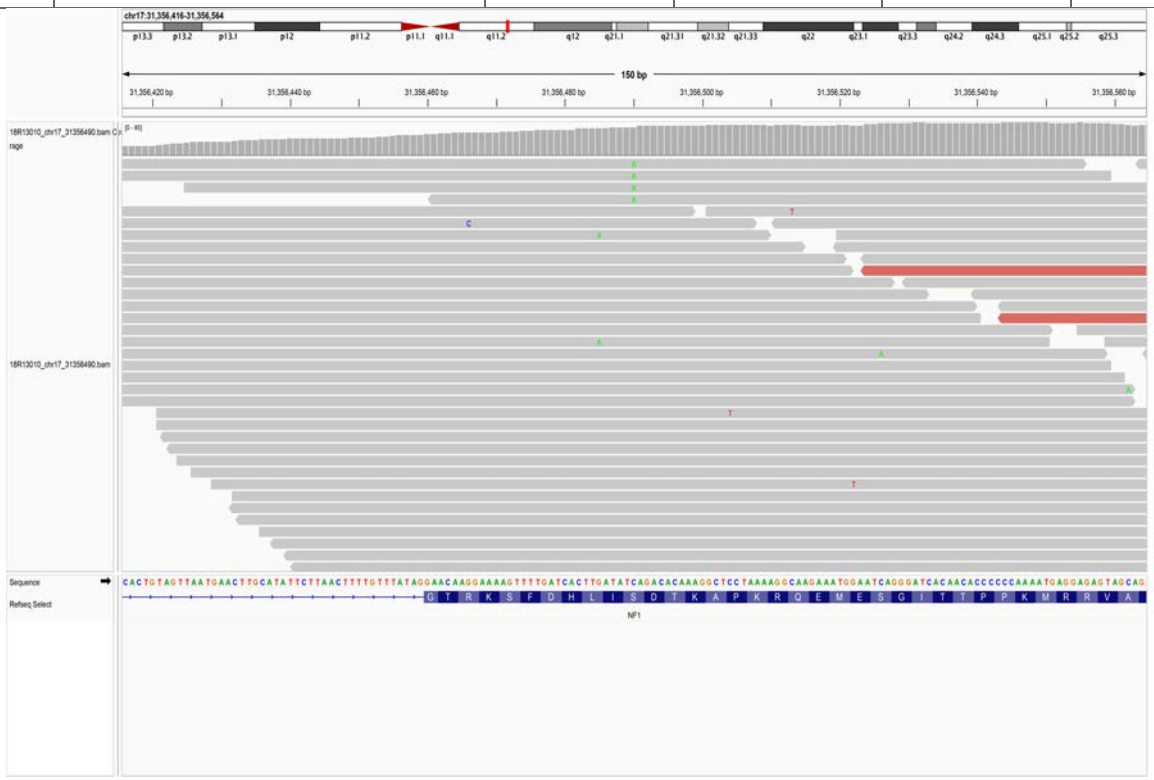
34.13. chr17_31352300_G/T

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

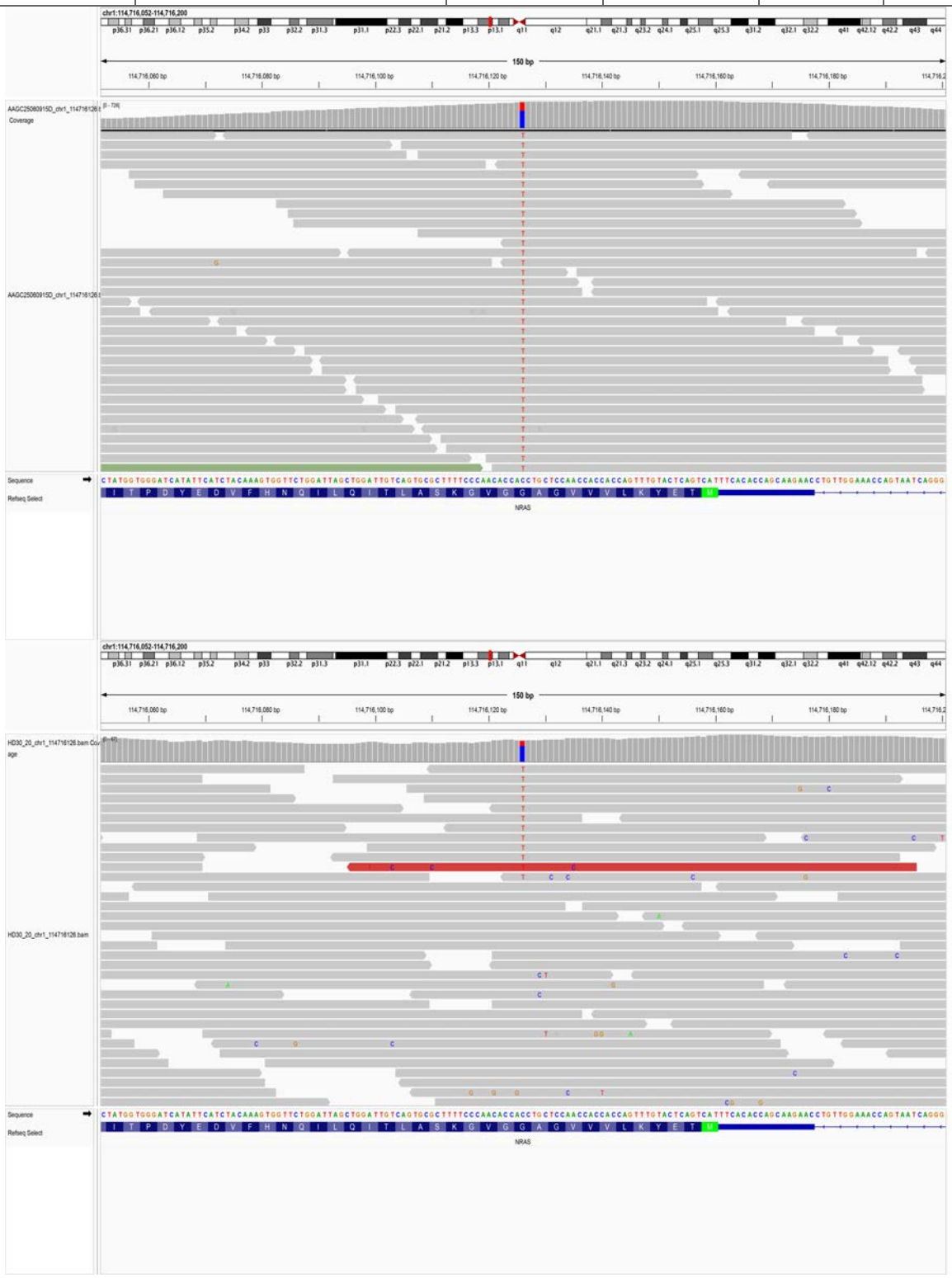
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R13010	chr17_31356490_C/A	51	4	*NF1*	stop_gained



35. *NRAS*

35.1. chr1_114716126_C/T

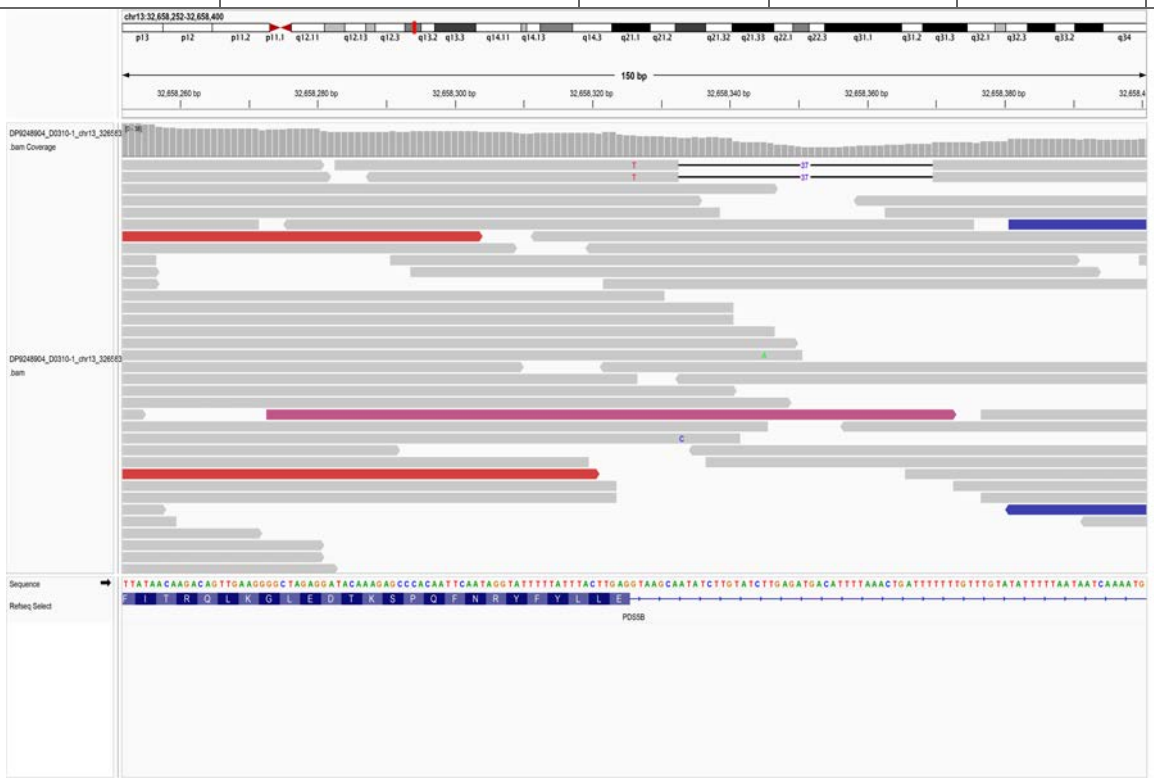
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25060915D	chr1_114716126_C/T	457236	457236	*NRAS*	missense_variant
HD30_20	chr1_114716126_C/T	36	11	*NRAS*	missense_variant



36. *PDS5B*

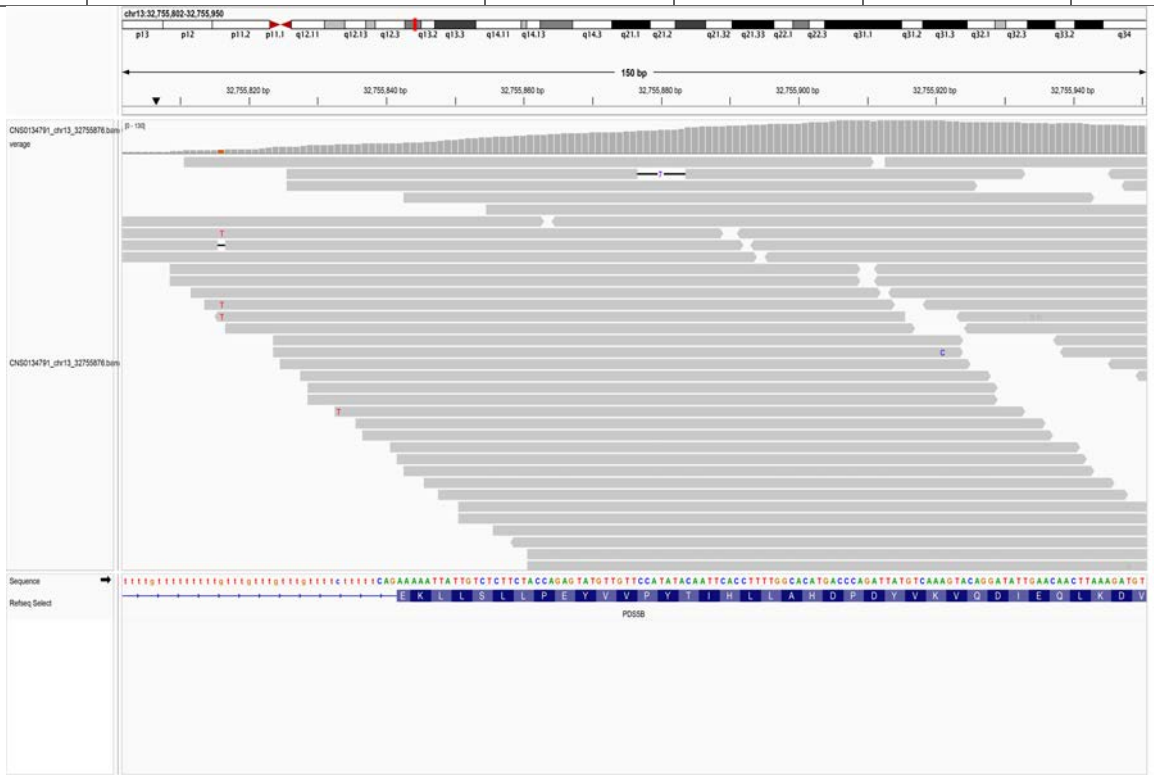
36.1. chr13_32658326_G/T

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



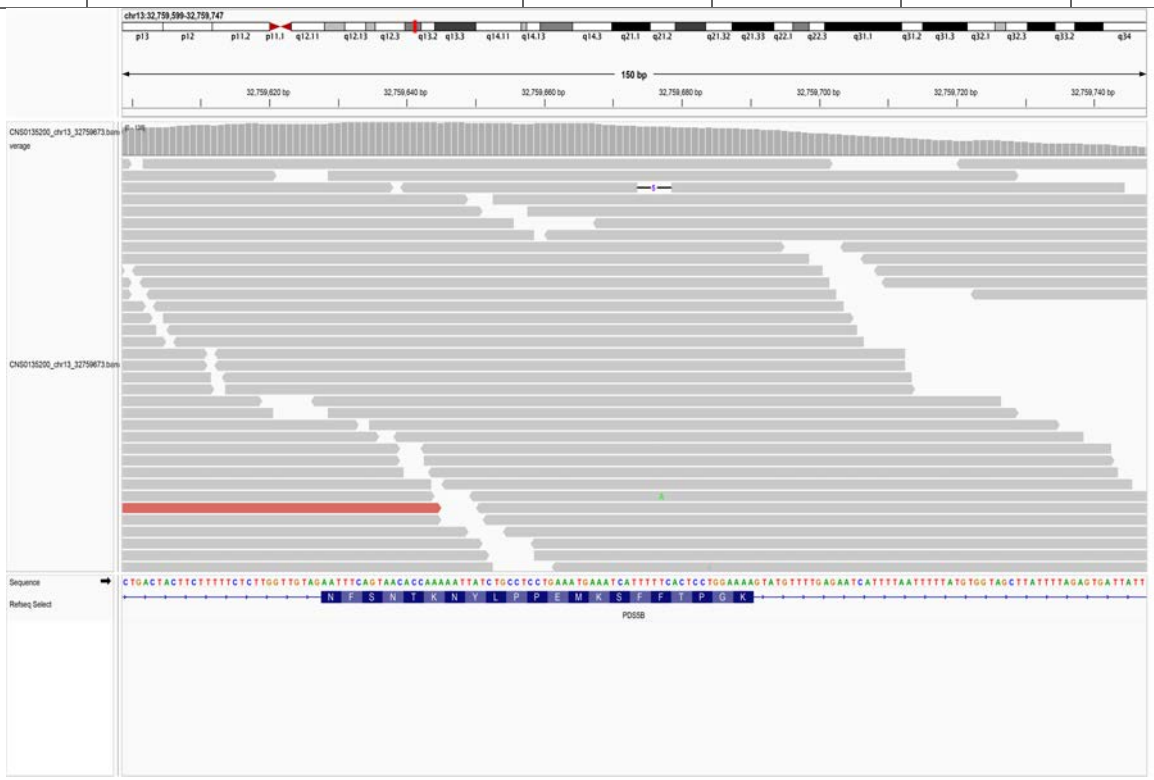
36.2. chr13_32755877_CCATATA/-

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



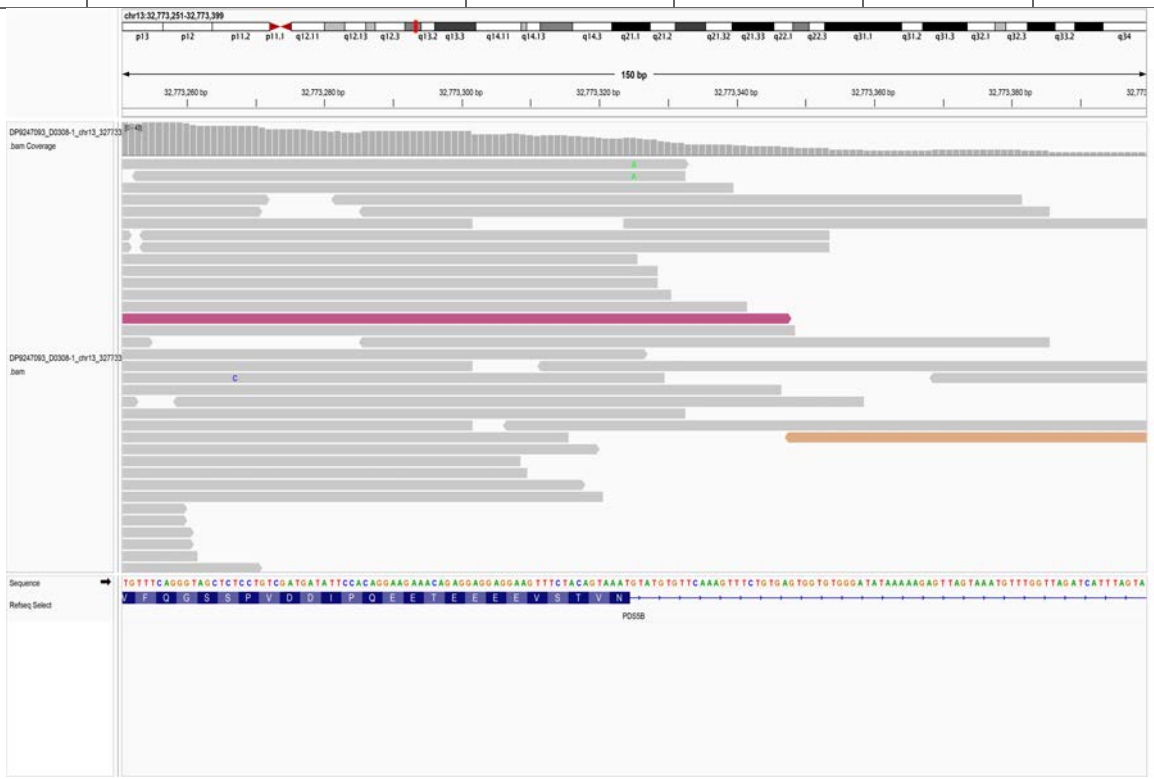
36.3. chr13_32759674_TTTTC/-

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



36.4. chr13_32773325_G/A

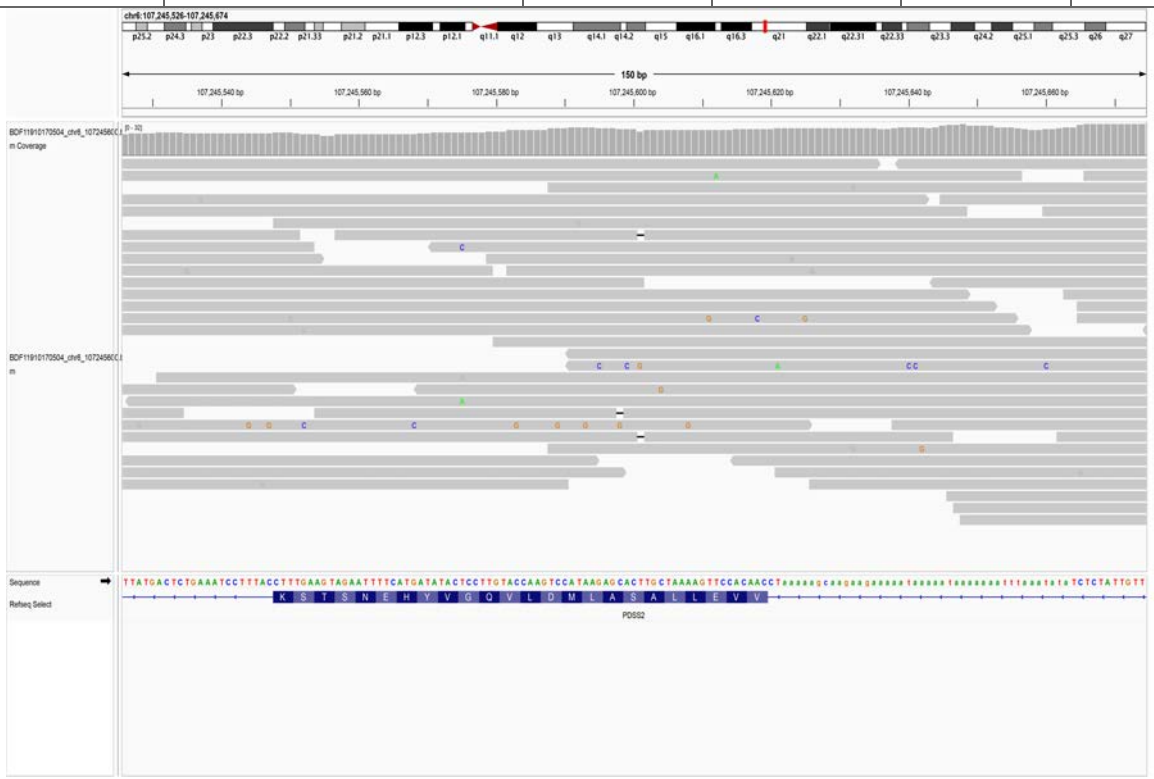
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
DP9247093_D0308-1	chr13_32773325_G/A	21	2	*PDS5B*	splice_donor_variant



37. *PDSS2*

37.1. chr6_107245601_T/-

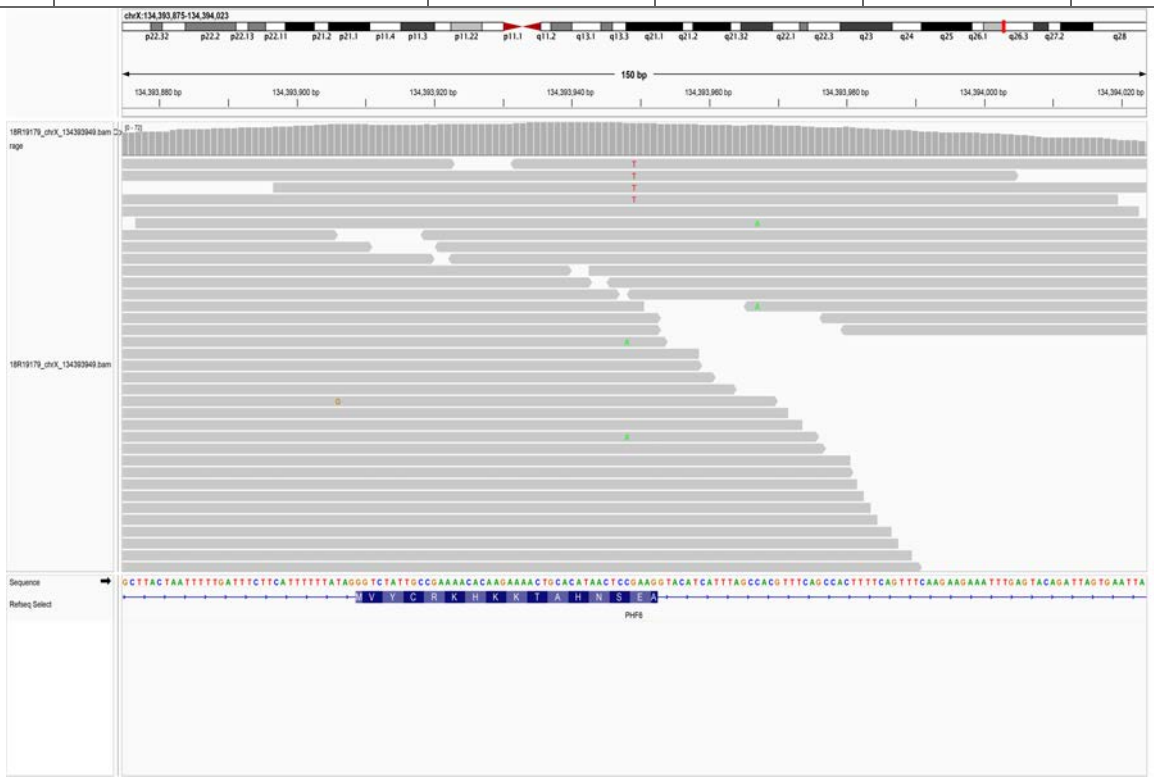
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
BDF11910170504	chr6_107245601_T/-	20	2	*PDSS2*	frameshift_variant



38. *PHF6*

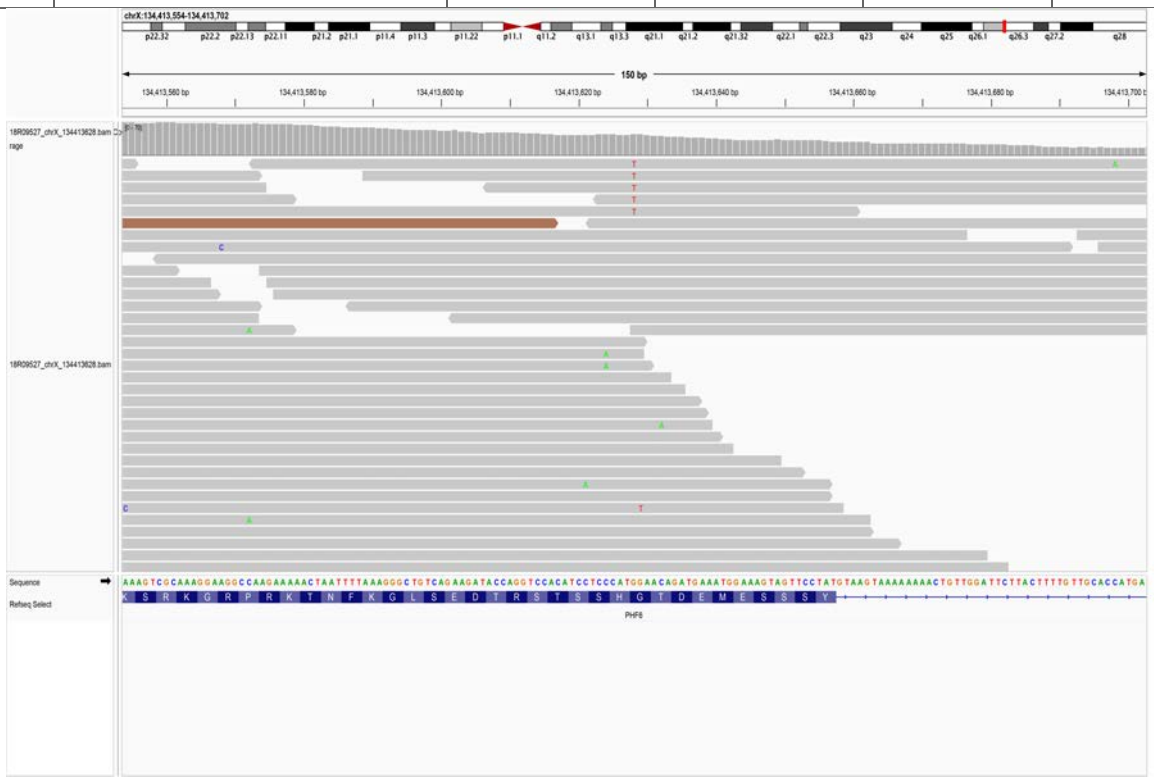
38.1. chrX_134393949_G/T

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



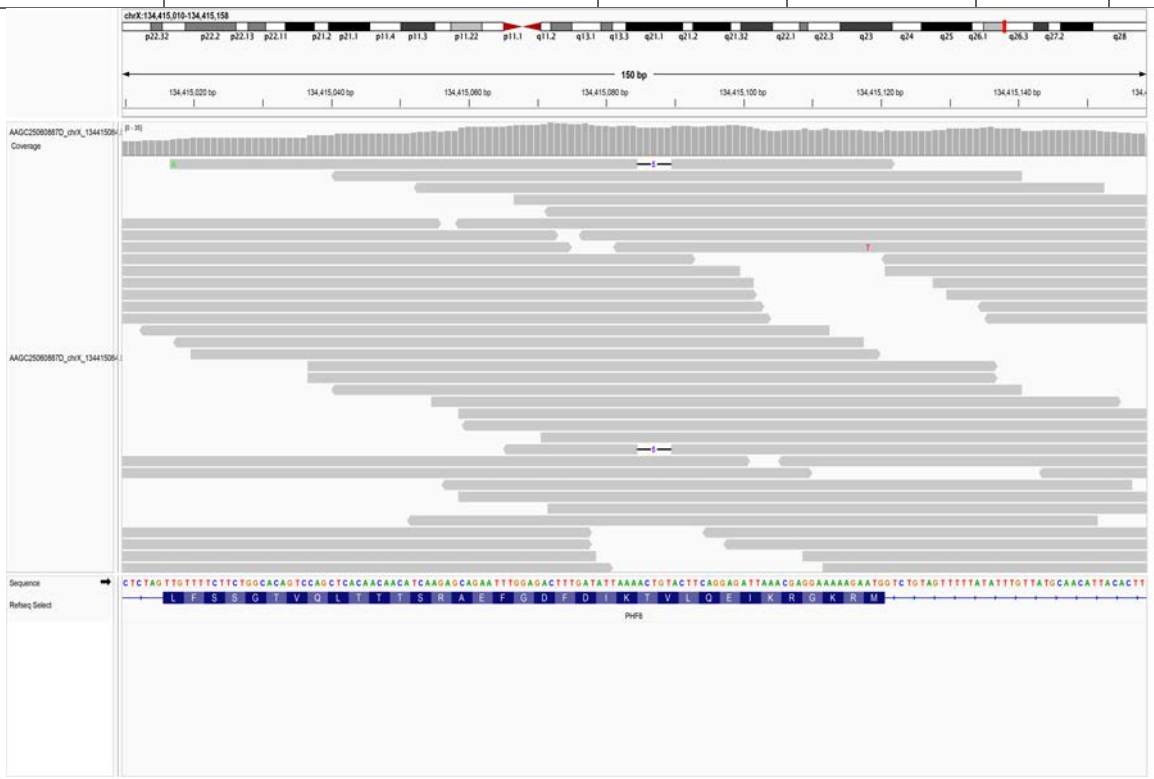
38.2. chrX_134413628_G/T

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



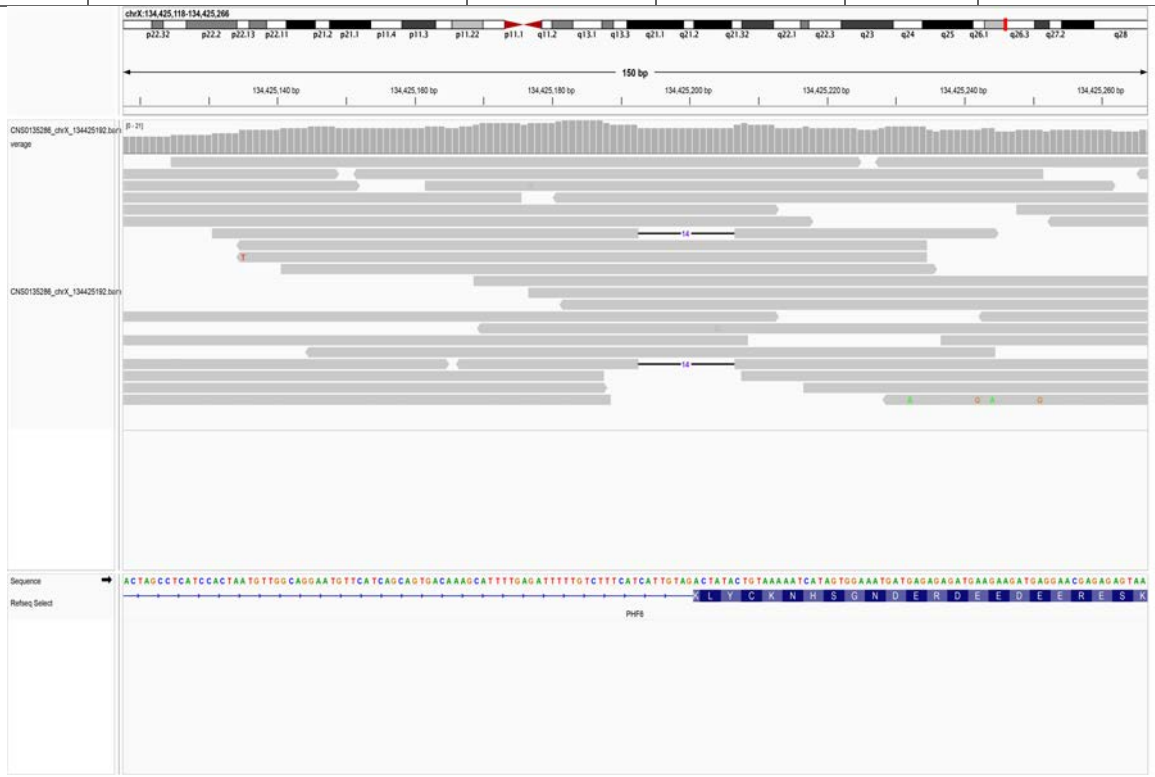
38.3. chrX_134415085_ACTGT/-

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



38.4. chrX_134425193_CATTGTAGACTATA/-

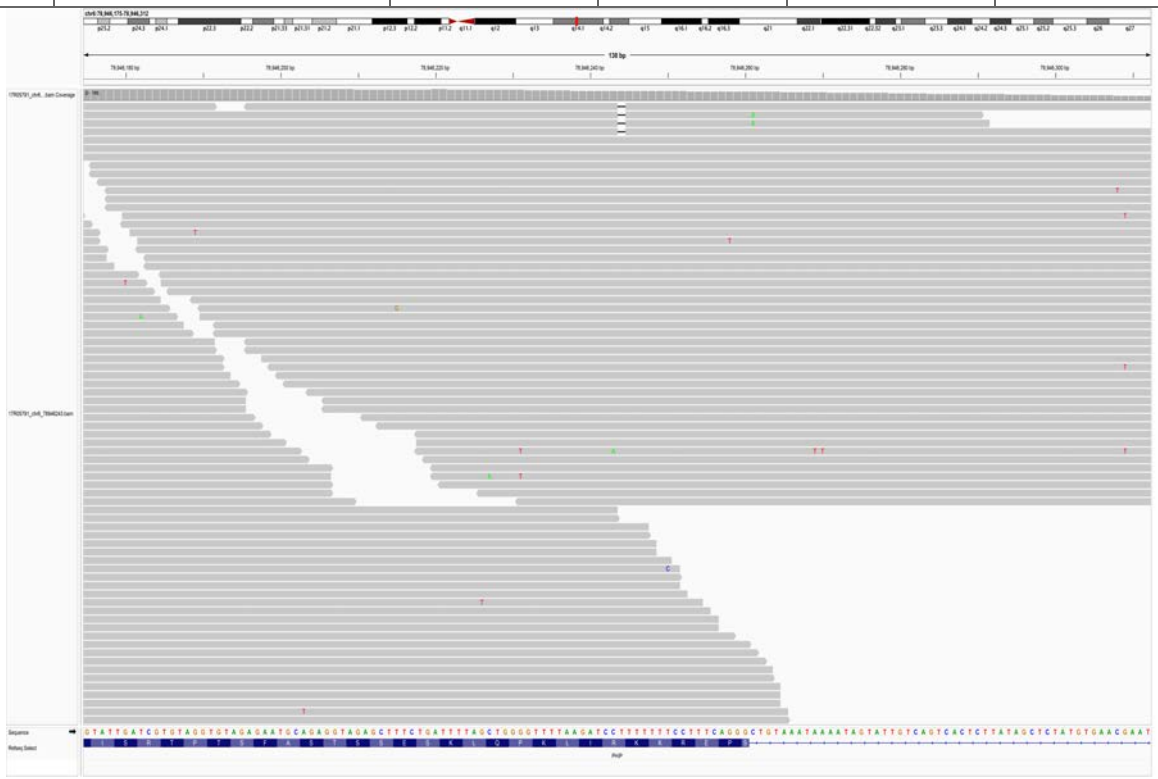
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
CNS0135286	chrX_134425193_CATTGTAGACTATA/-	15	2	*PHF6*	splice_acceptor_variant



39. *PHIP*

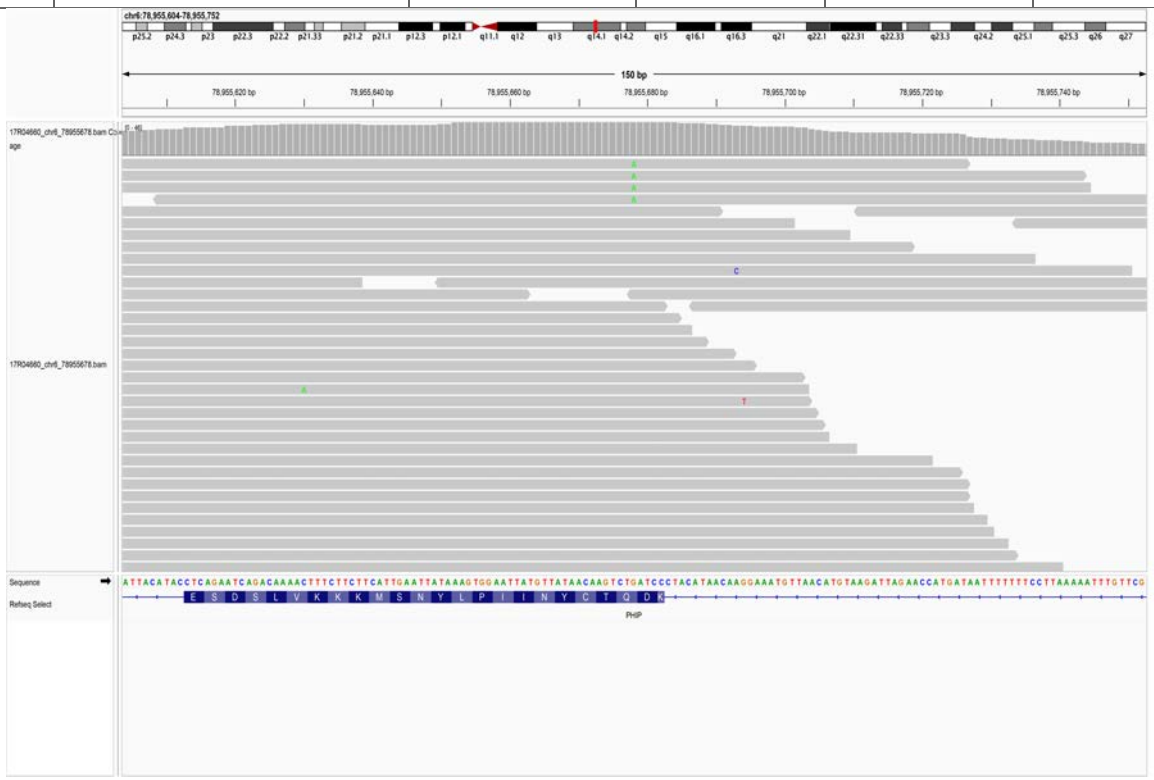
39.1. chr6_78946244_T/-

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



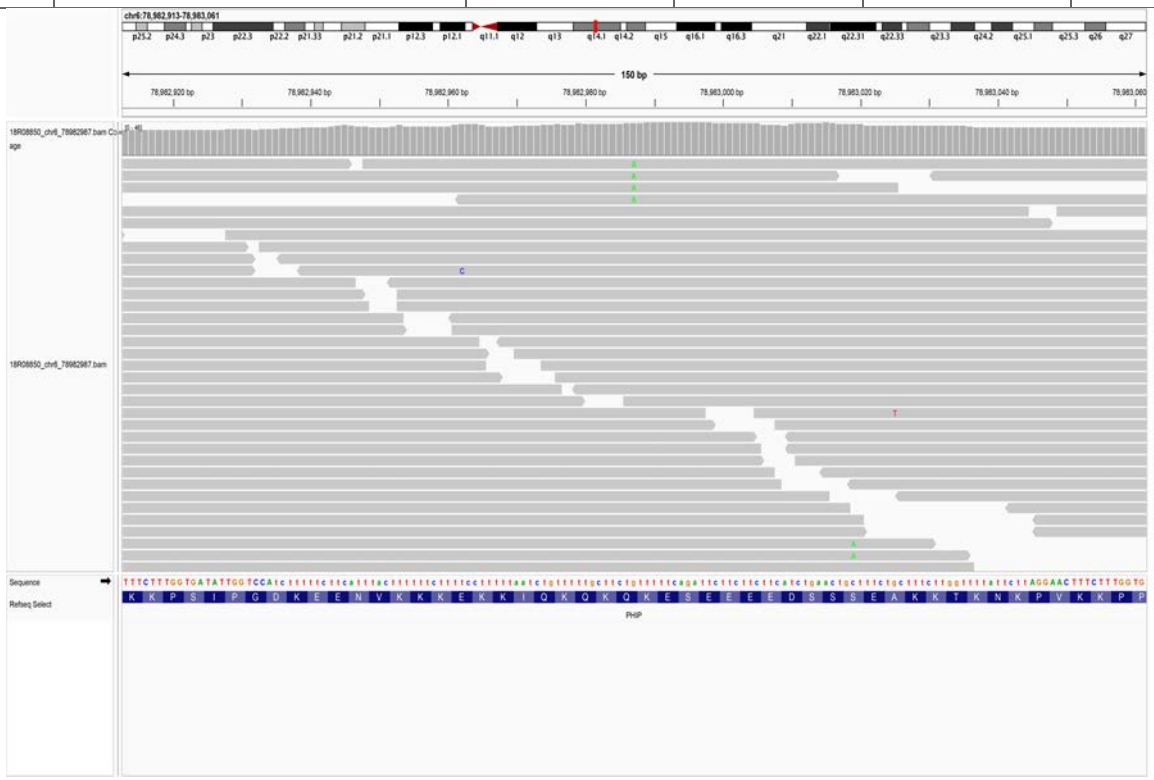
39.2. chr6_78955678_G/A

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



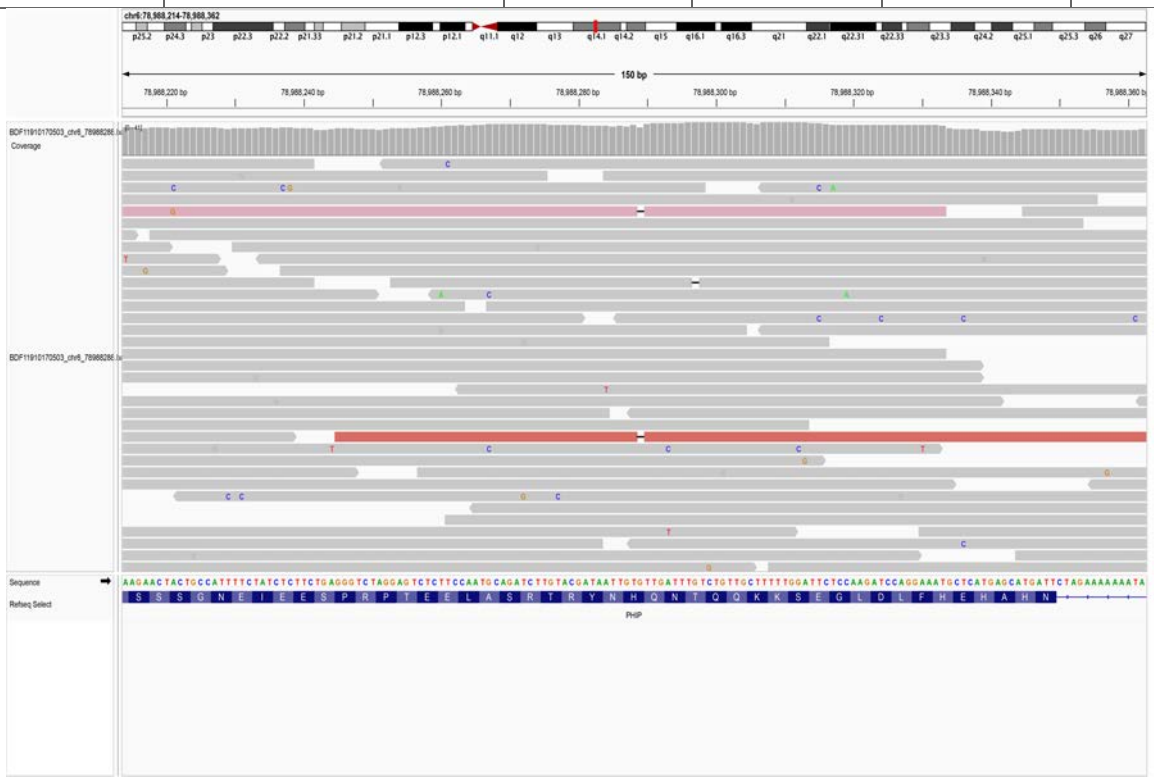
39.3. chr6_78982987_G/A

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



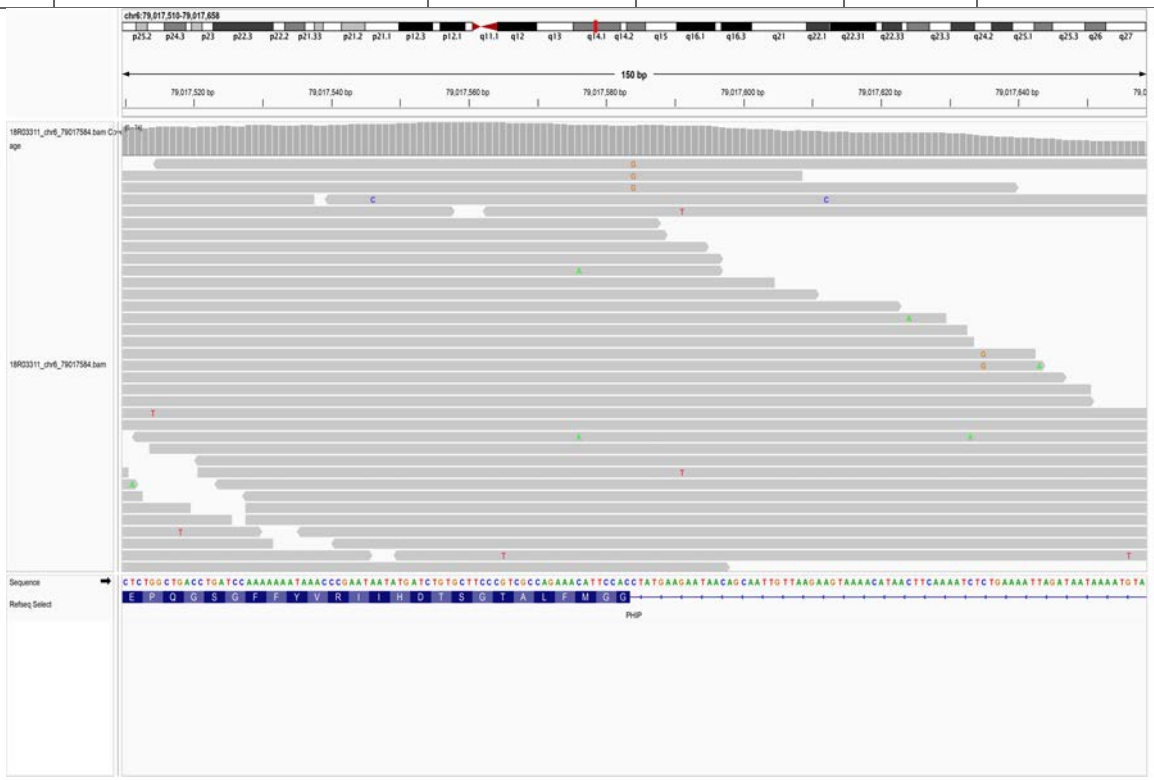
39.4. chr6_78988289_G/-

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



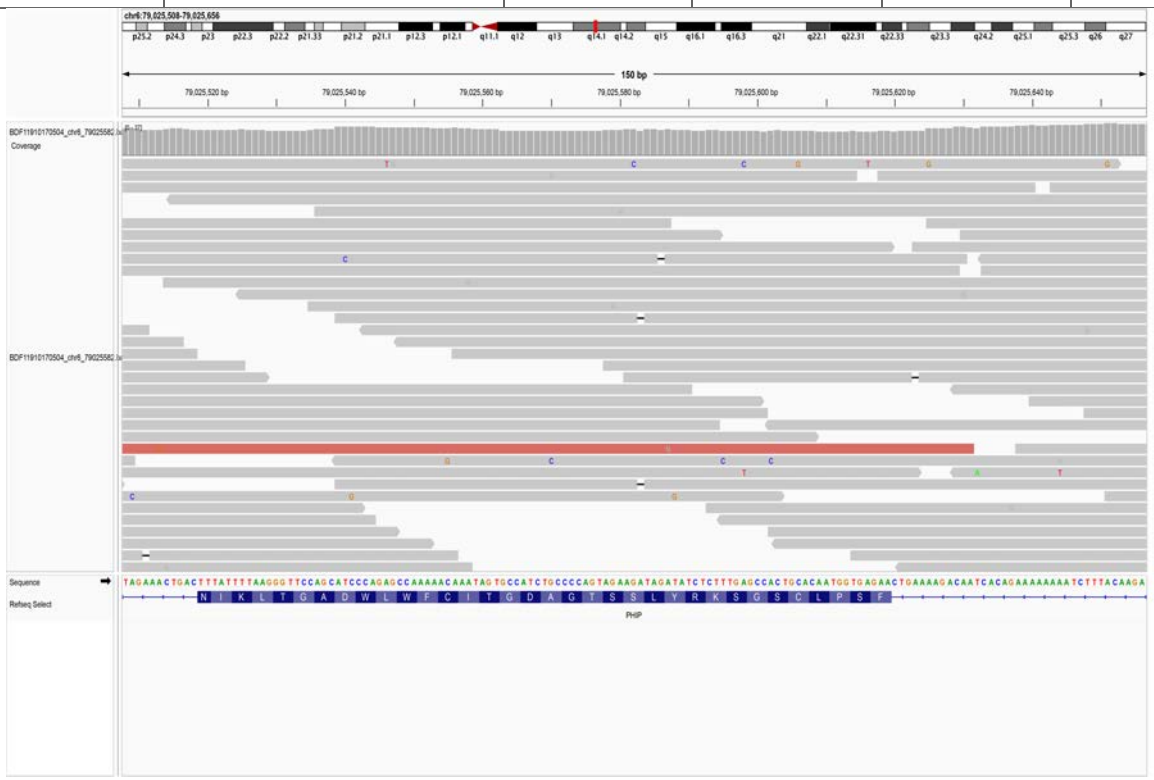
39.5. chr6_79017584_C/G

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



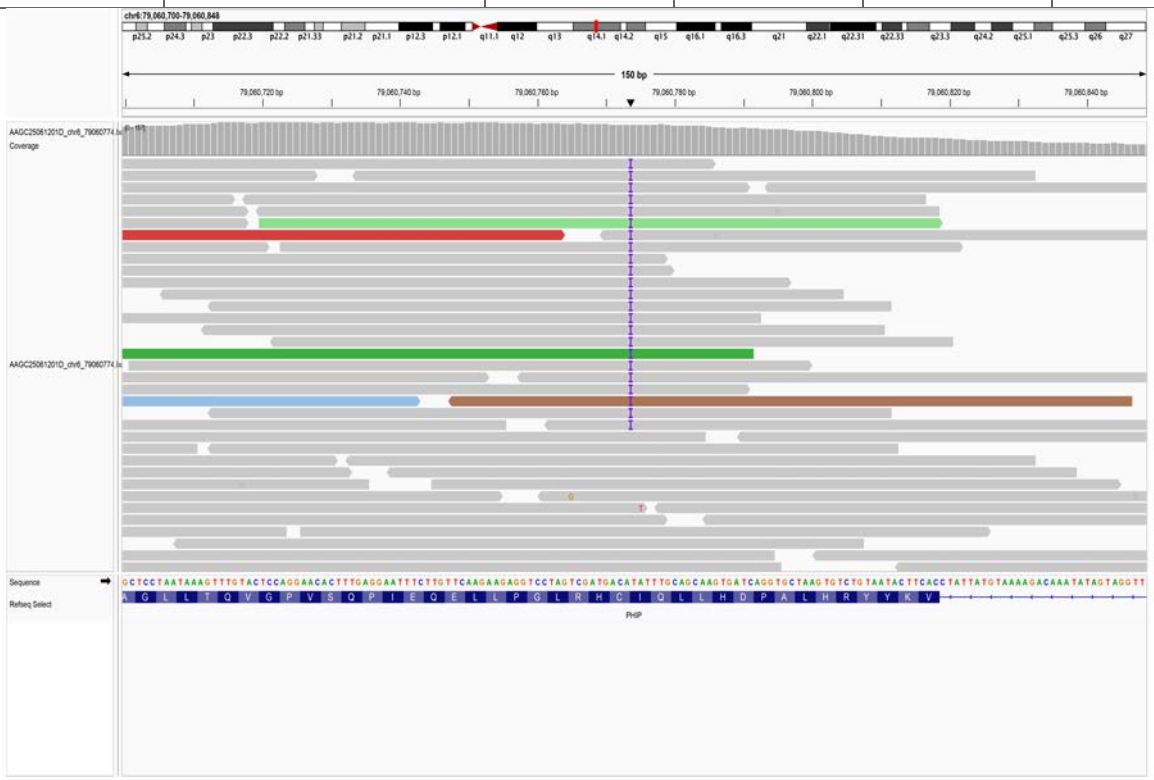
39.6. chr6_79025583_A/-

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



39.7. chr6_79060774_-/T

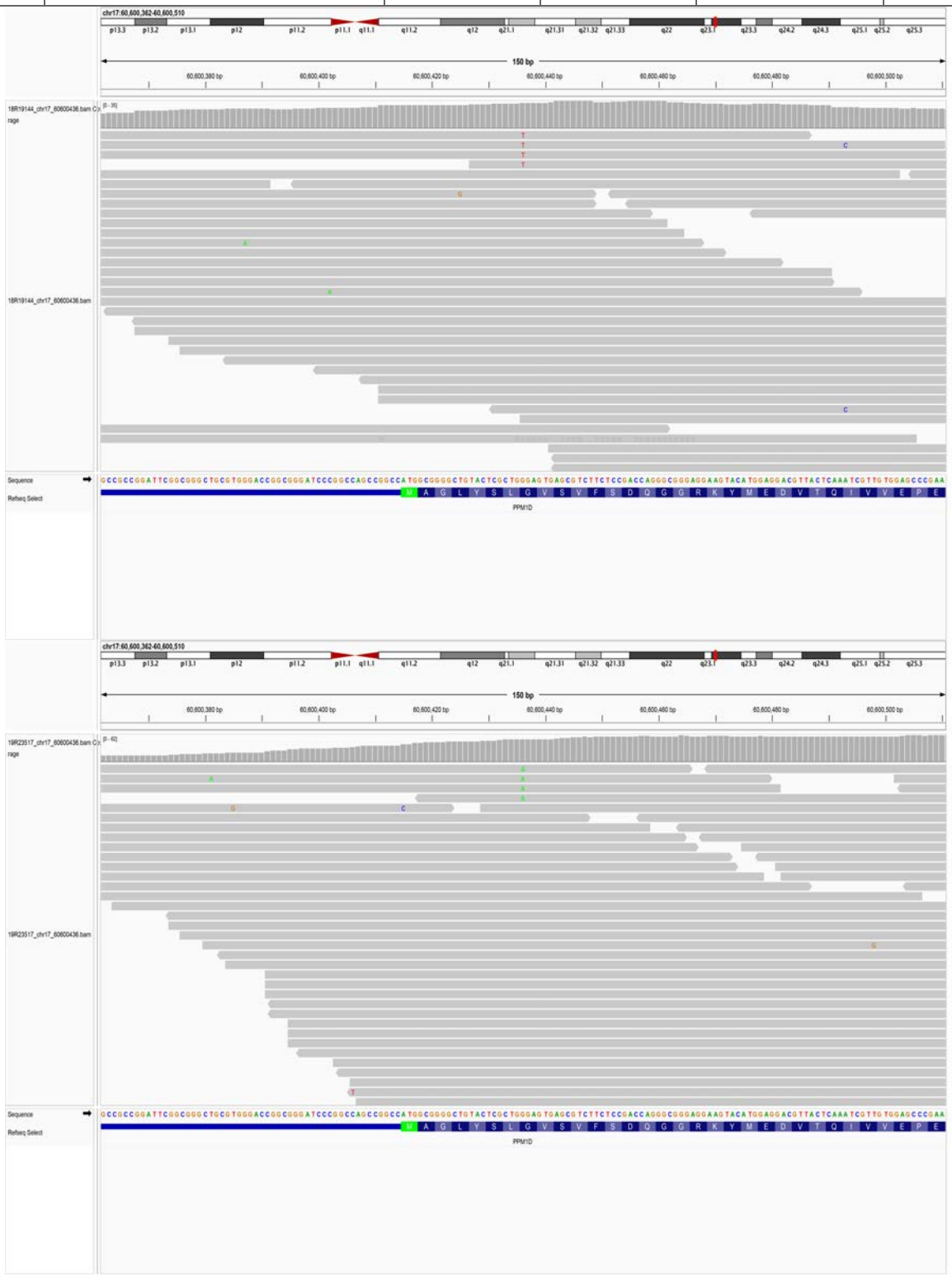
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061201D	chr6_79060774_-/T	116	23	*PHIP*	frameshift_variant



40. *PPM1D*

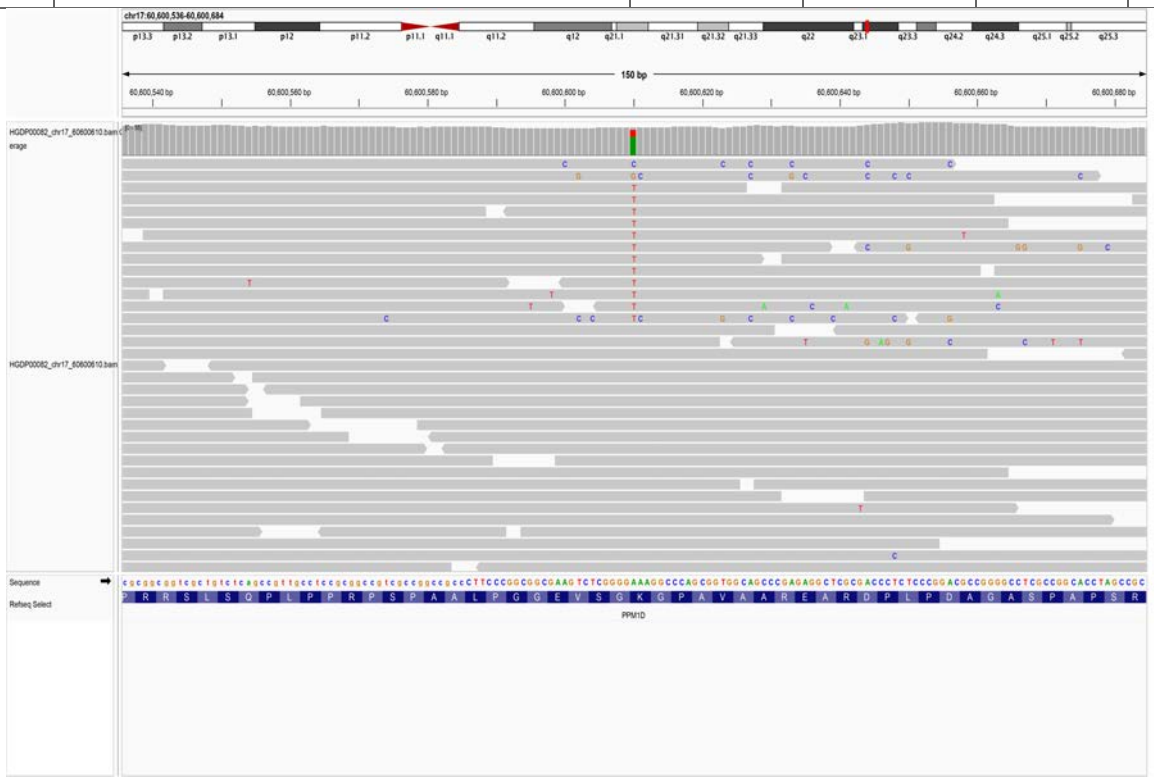
40.1. chr17_60600436_G/T/A

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



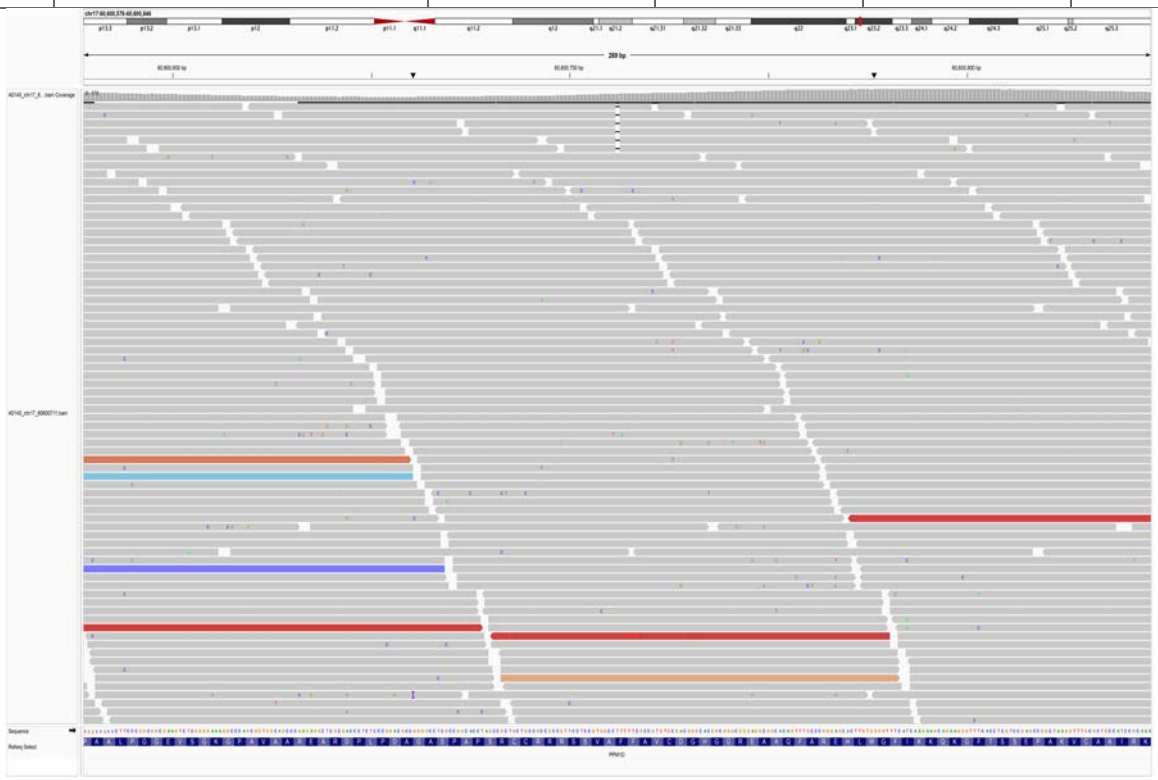
40.2. chr17_60600610_A/T

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



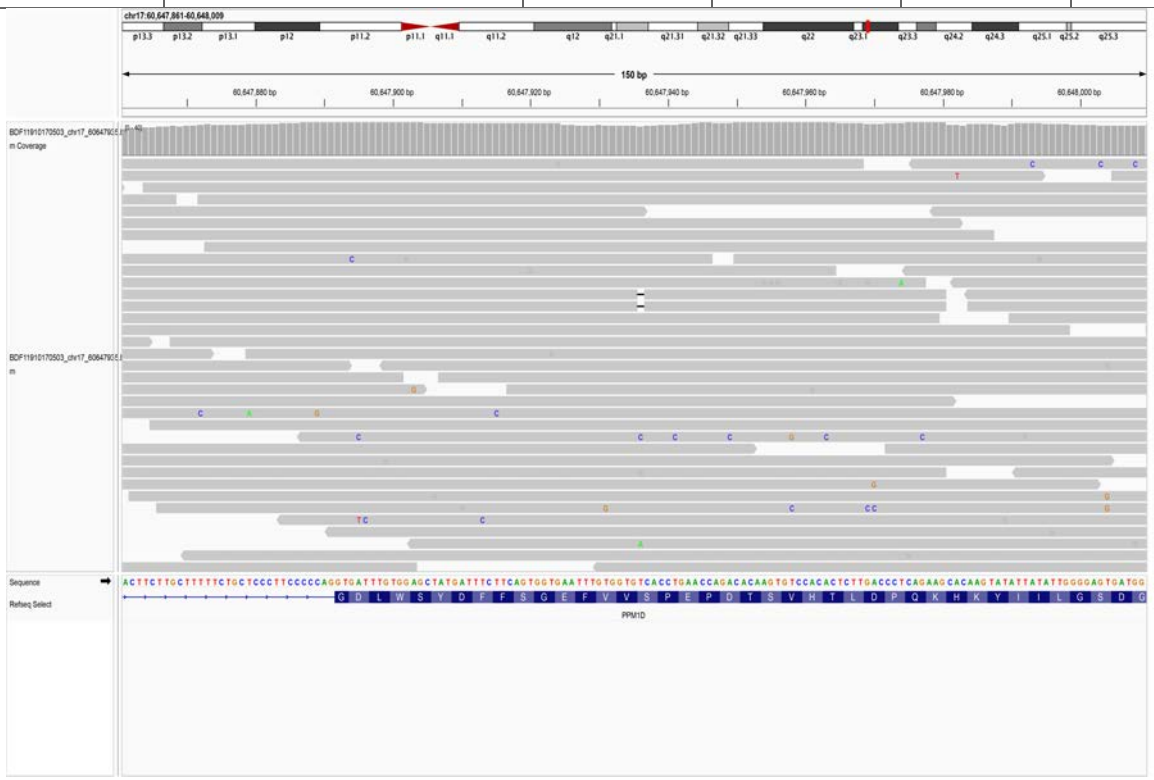
40.3. chr17_60600712_T/-

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



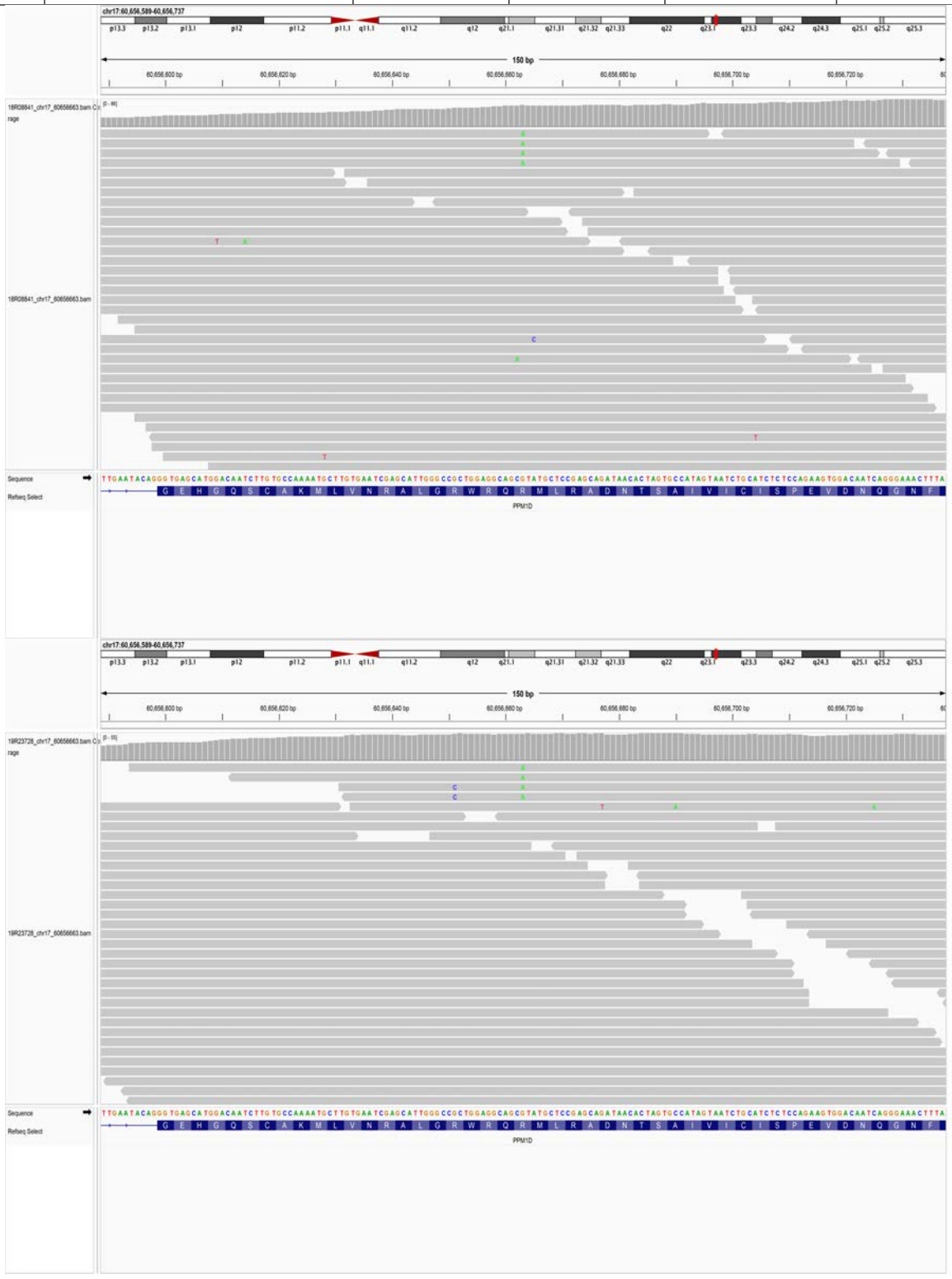
40.4. chr17_60647936_T/-

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



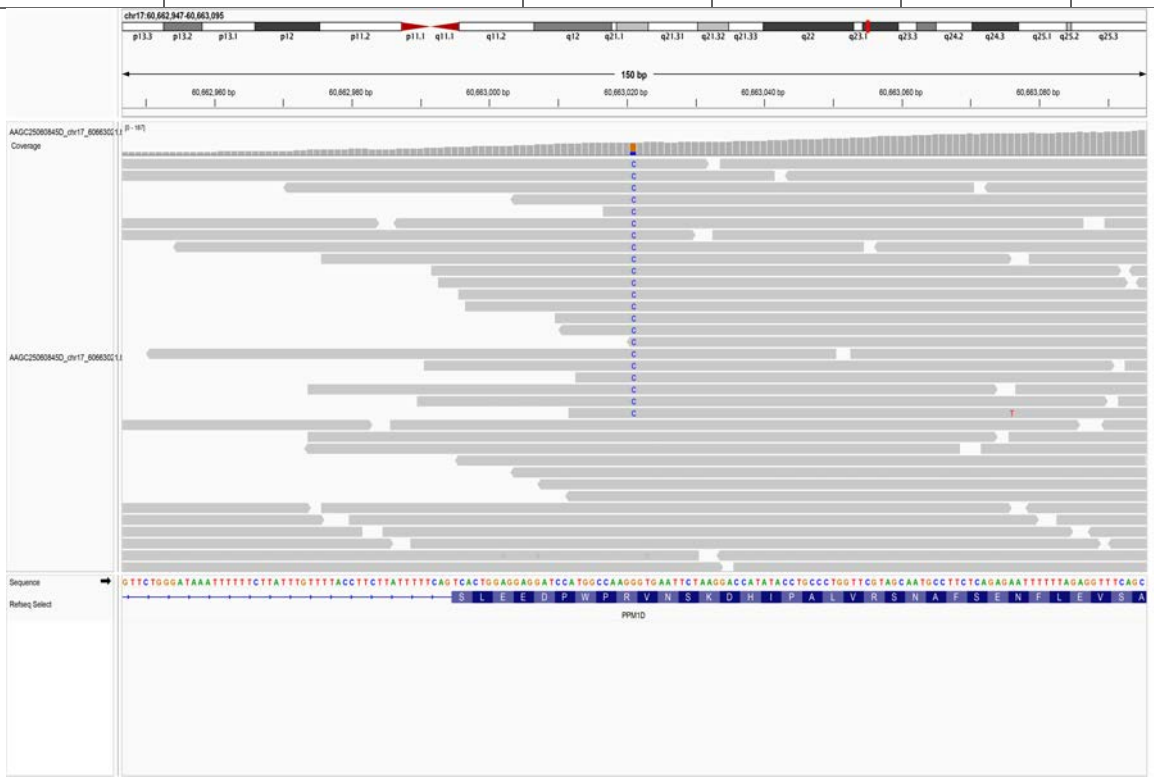
40.5. chr17_60656663_G/A

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



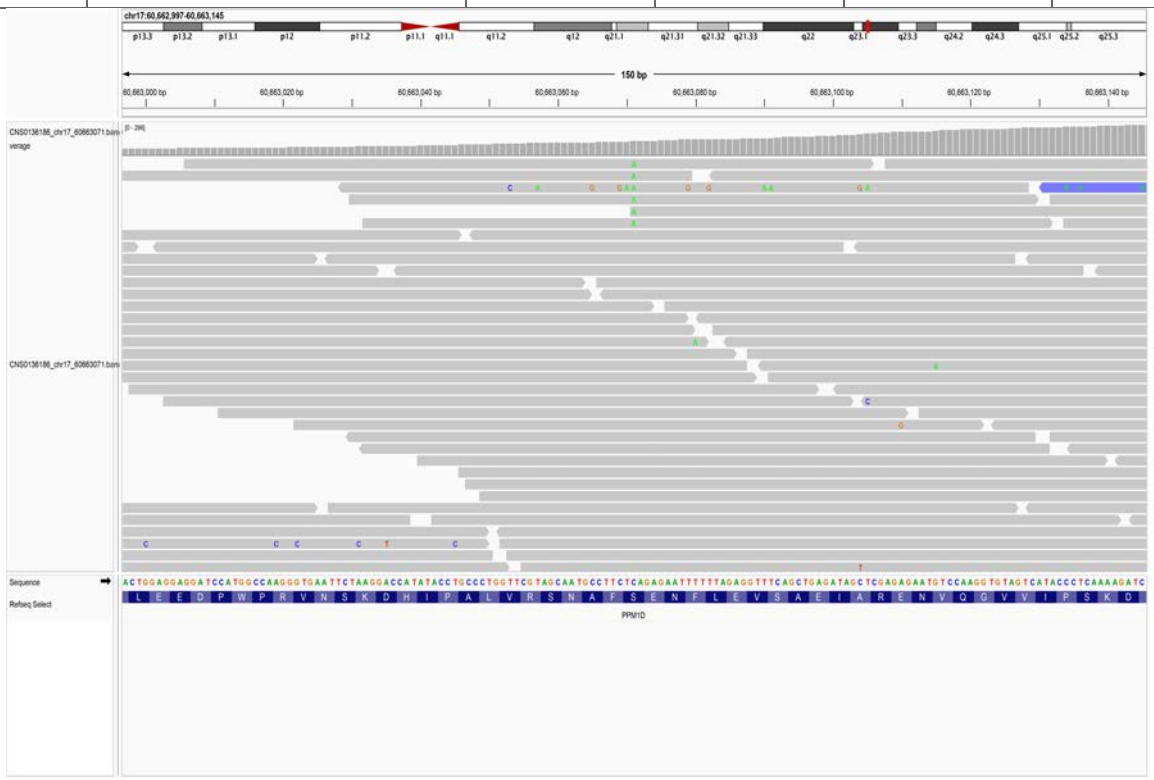
40.6. chr17_60663021_G/C

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



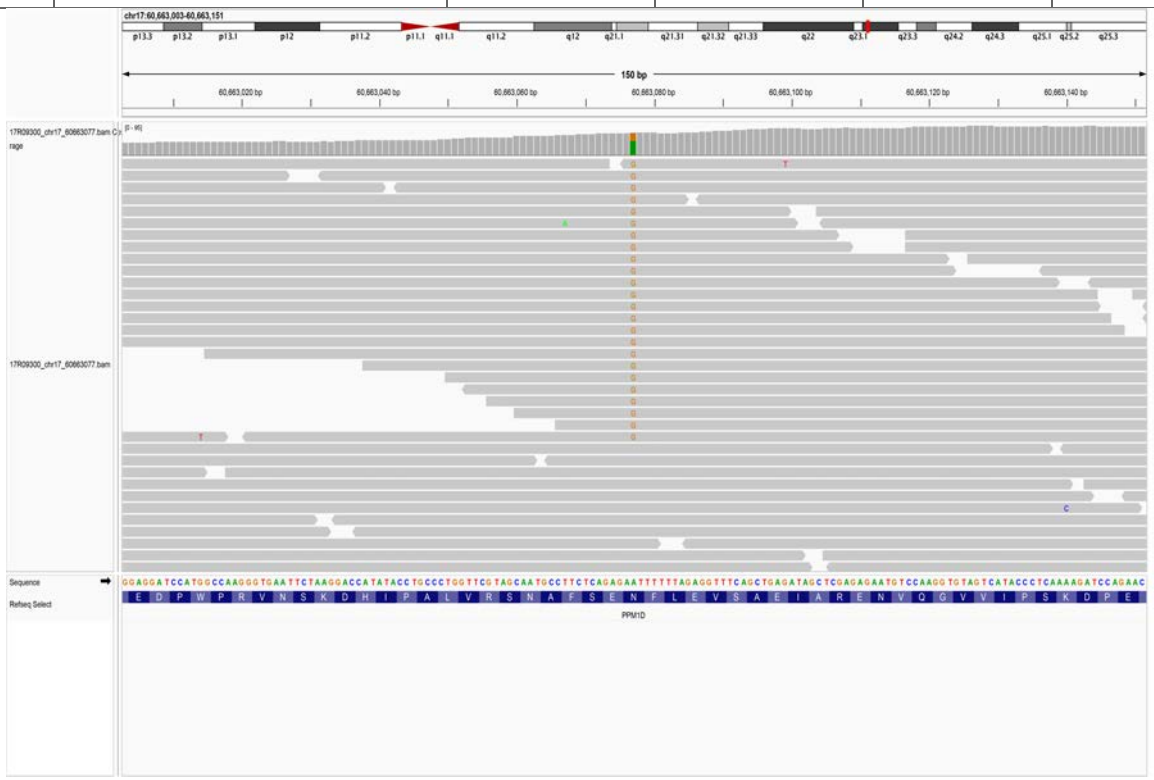
40.7. chr17_60663071_C/A

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



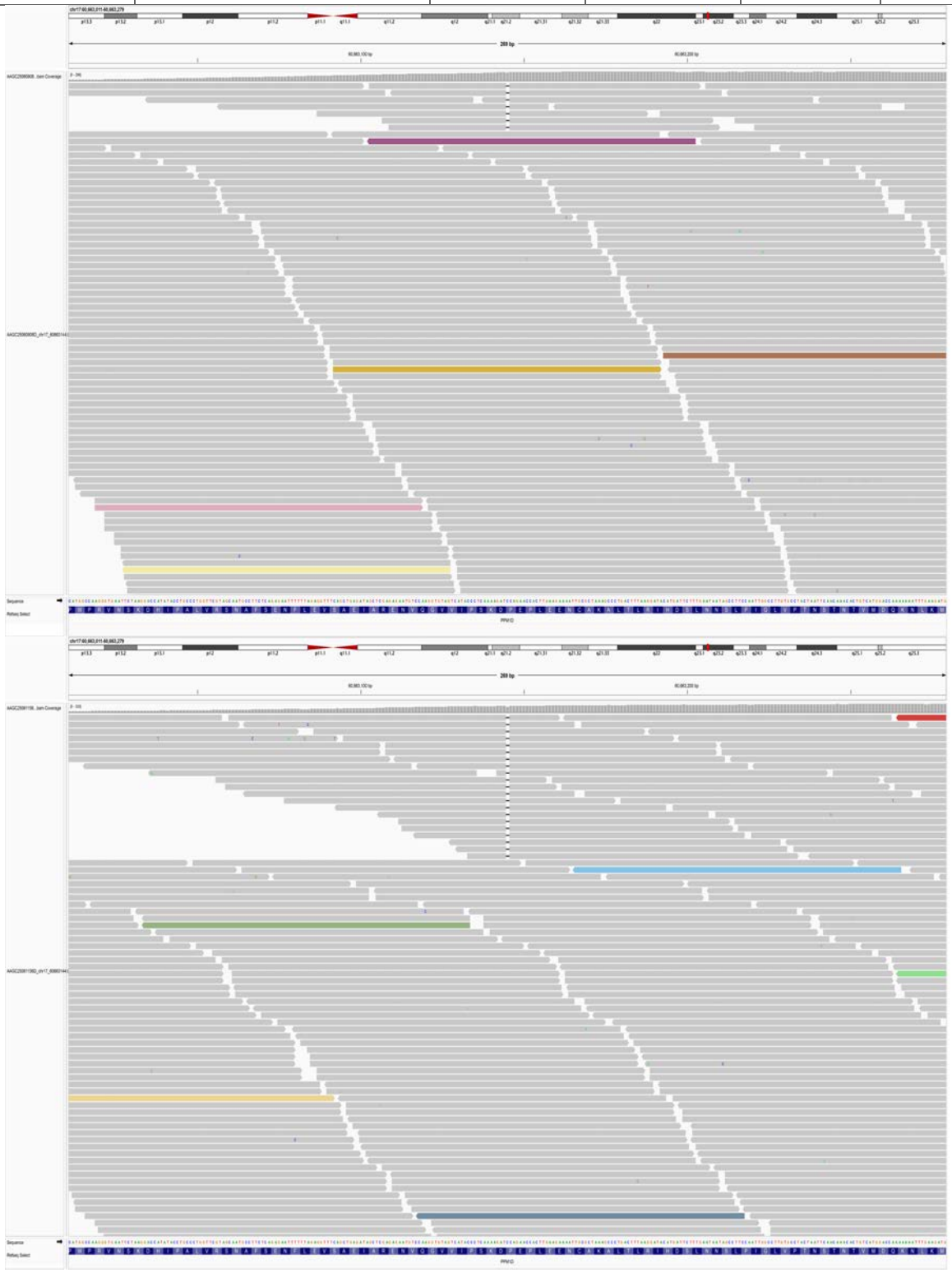
40.8. chr17_60663077_A/G

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



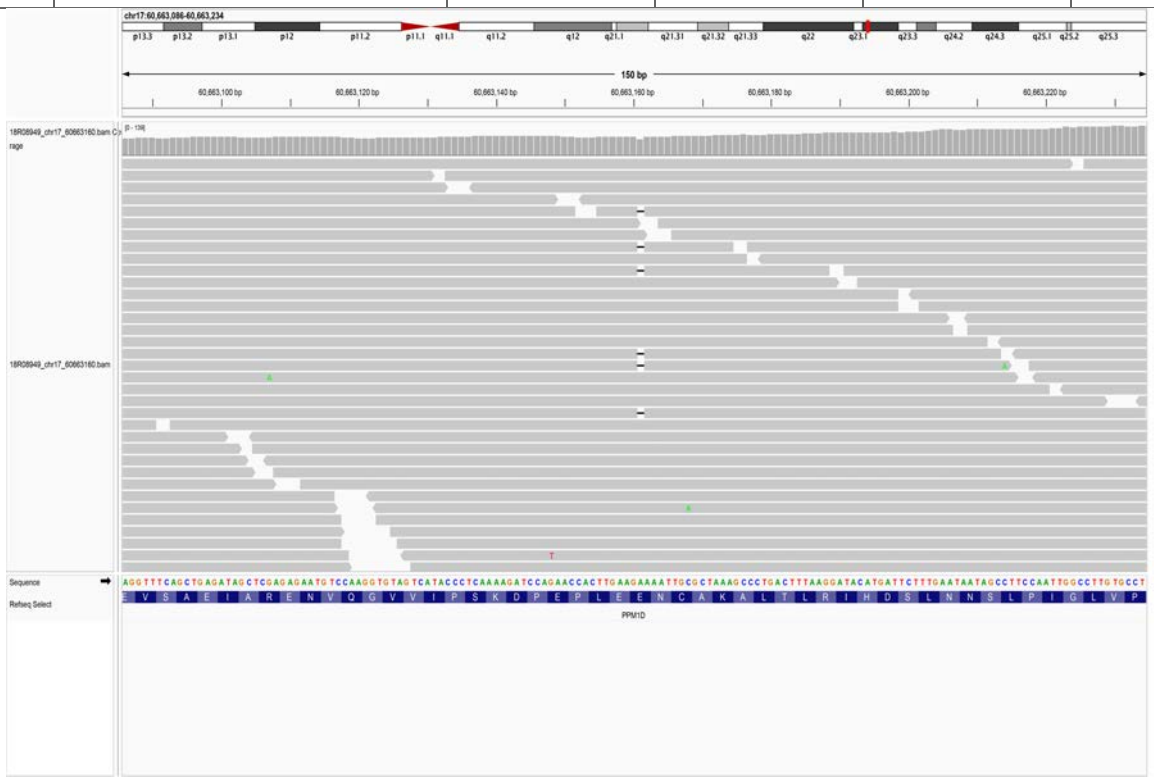
40.9. chr17_60663145_C/-

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



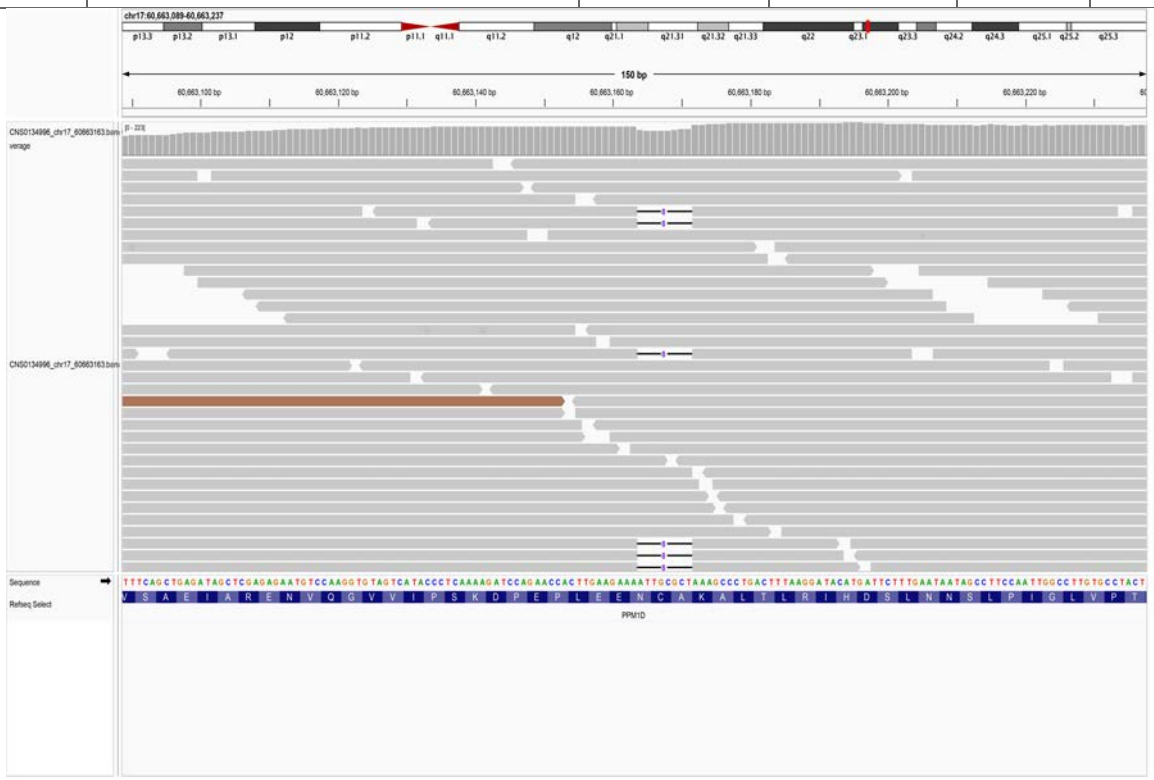
40.10. chr17_60663161_A/-

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



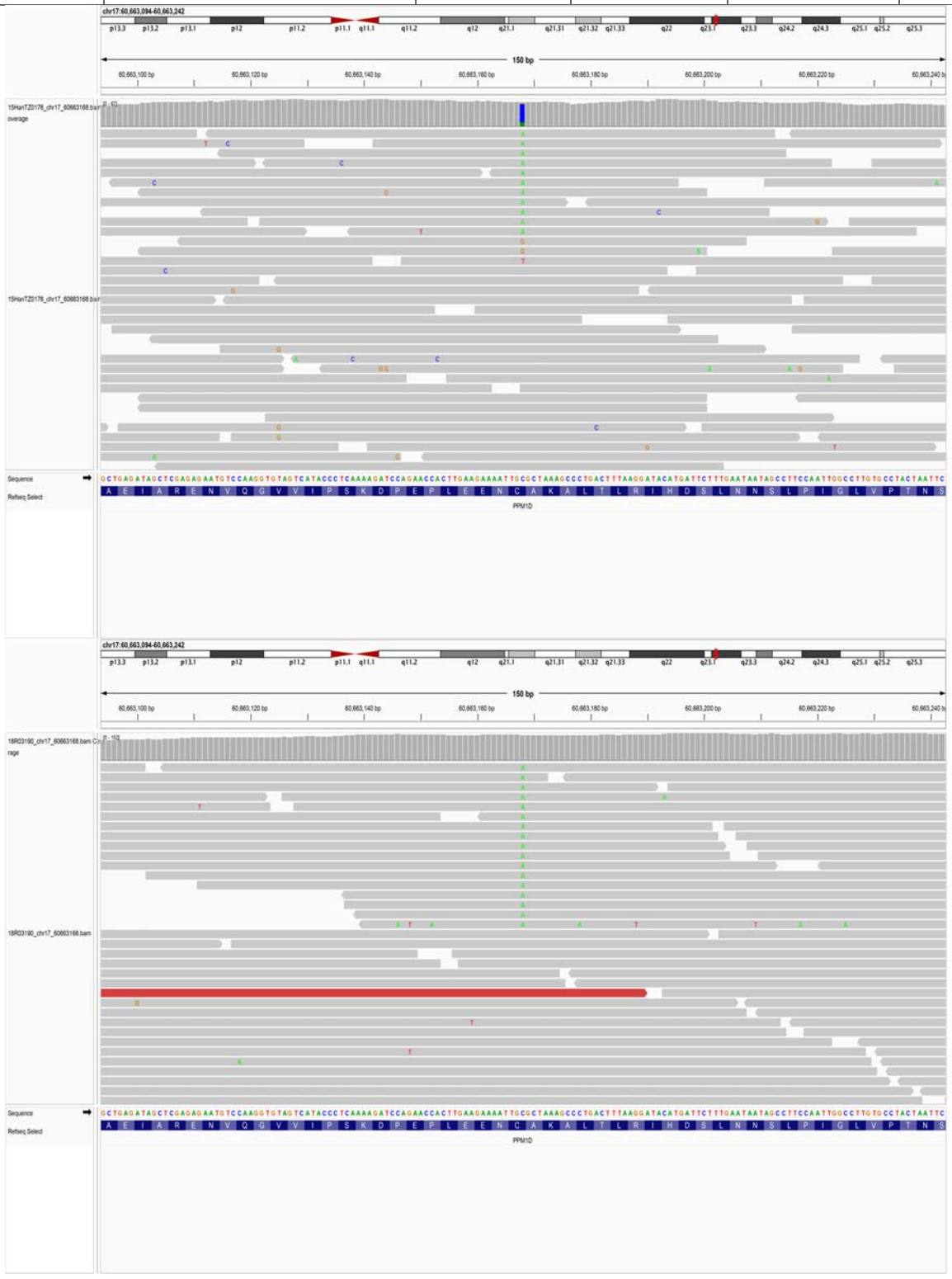
40.11. chr17_60663164_ATTGCGCT/-

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



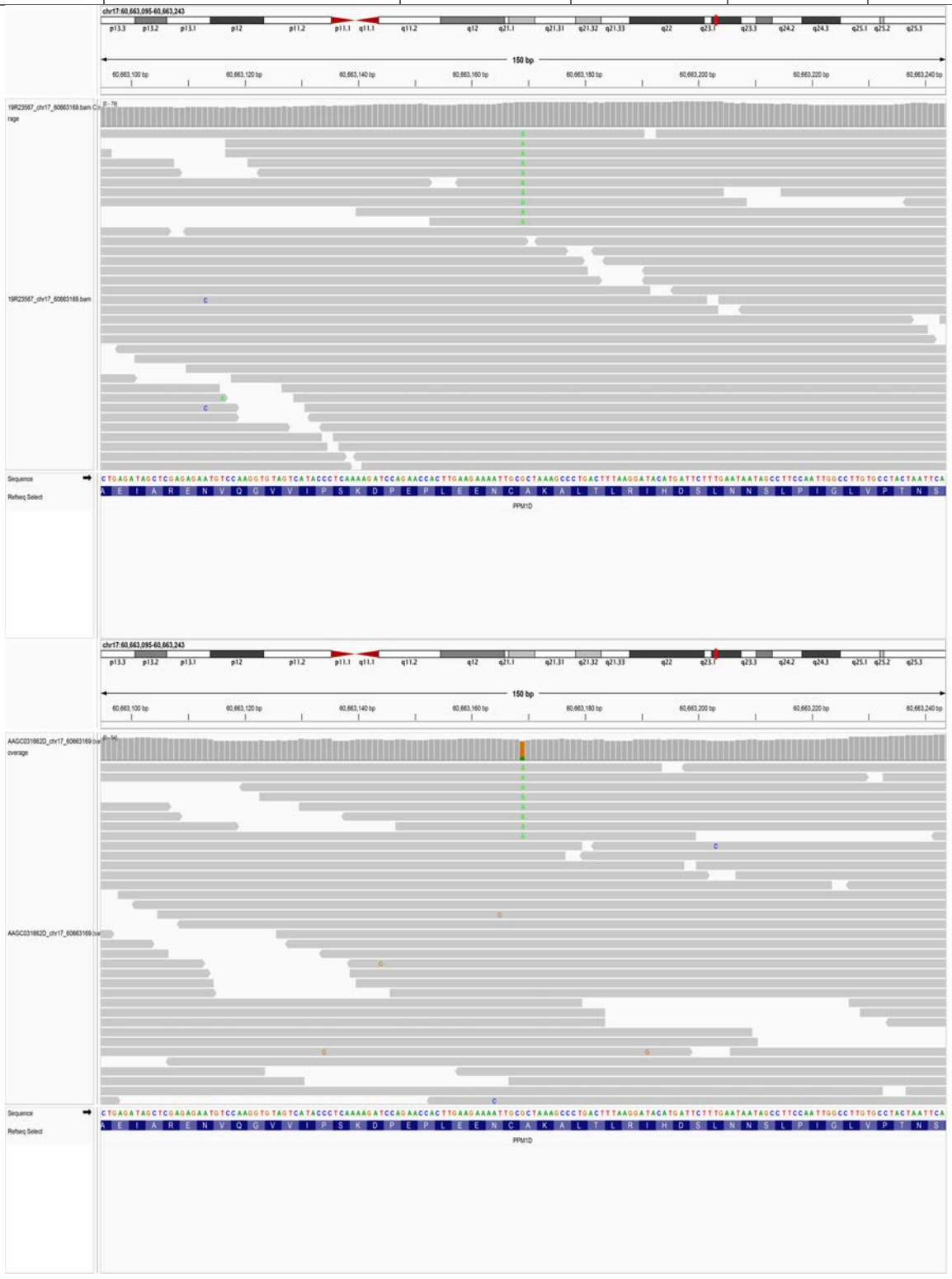
40.12. chr17_60663168_C/A

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



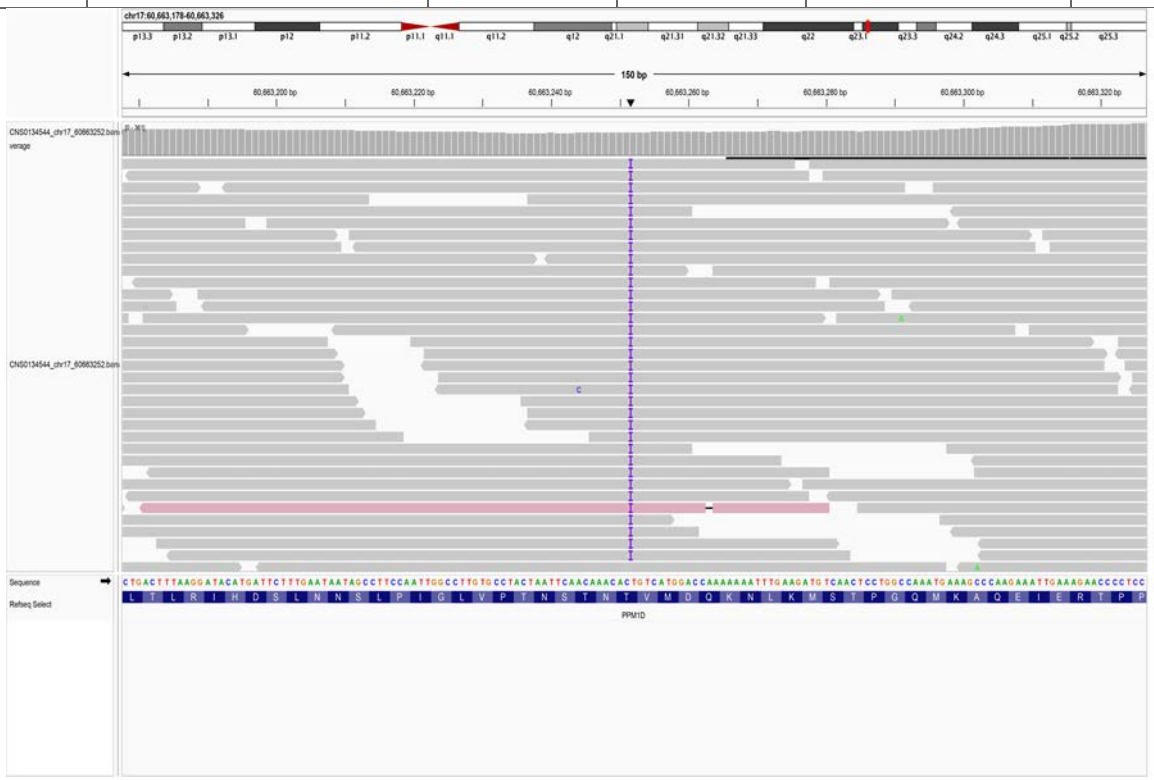
40.13. chr17_60663169_G/A

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



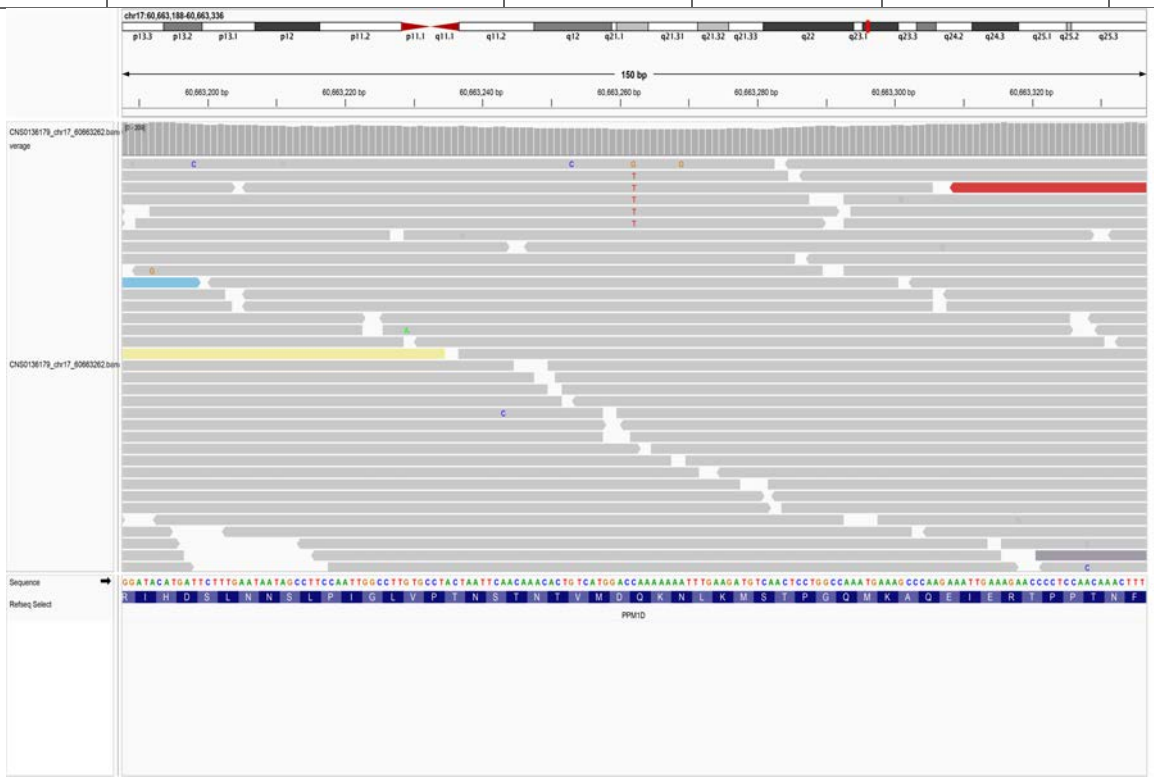
40.14. chr17_60663252_-/T

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



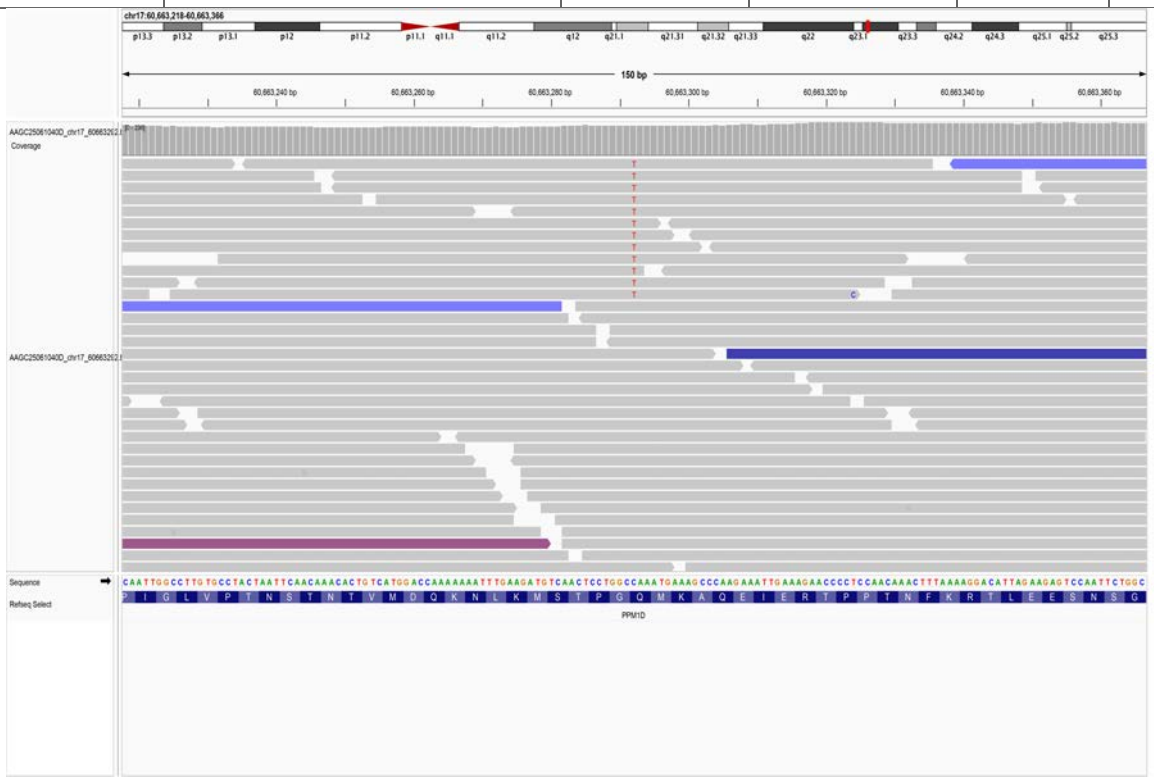
40.15. chr17_60663262_C/T

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



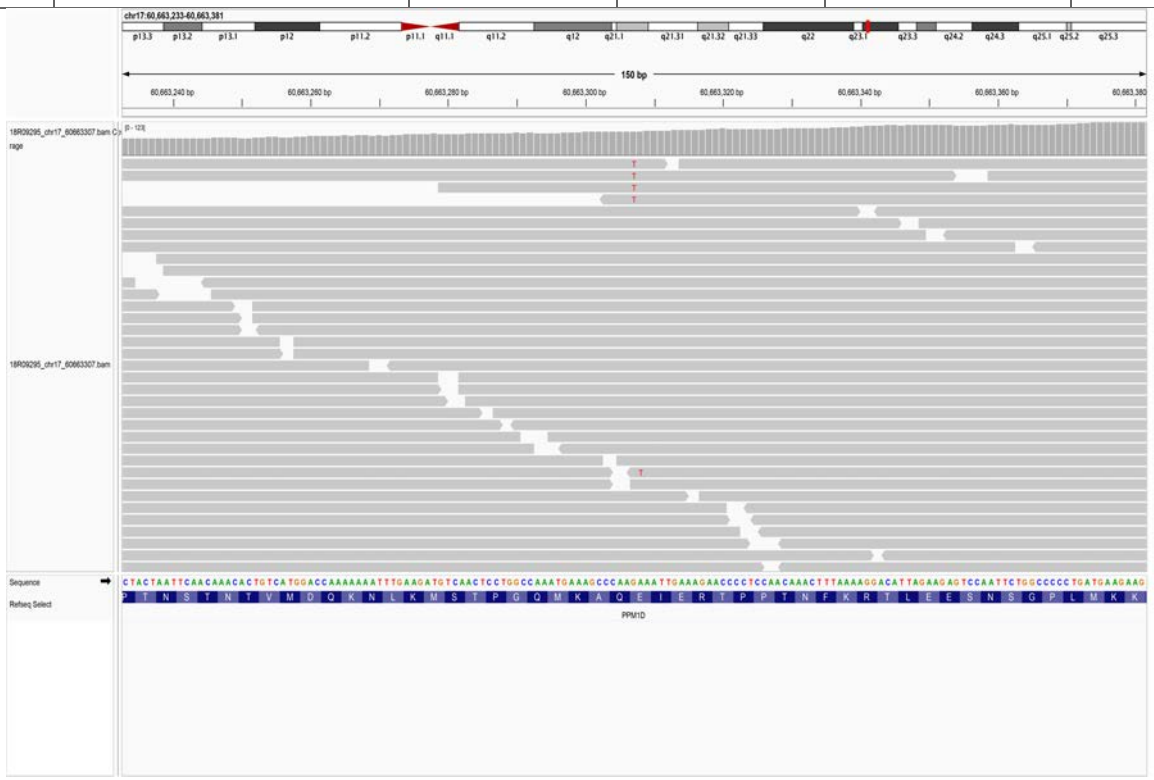
40.16. chr17_60663292_C/T

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



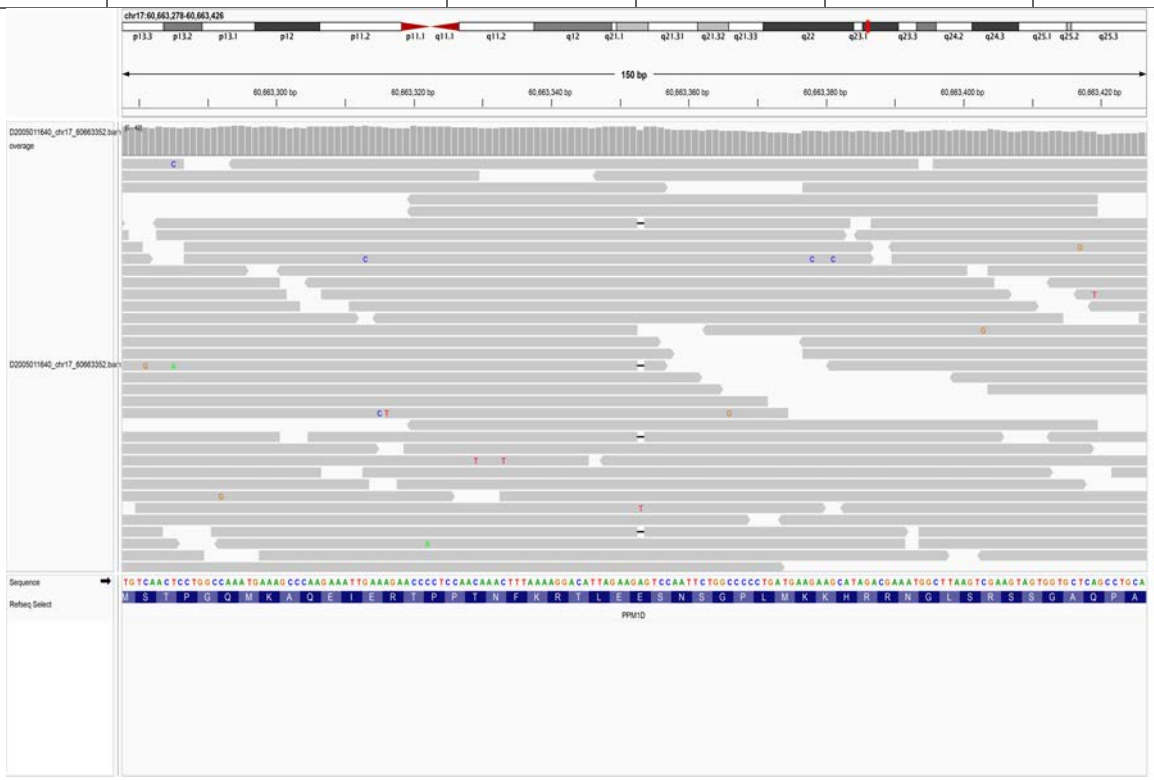
40.17. chr17_60663307_G/T

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



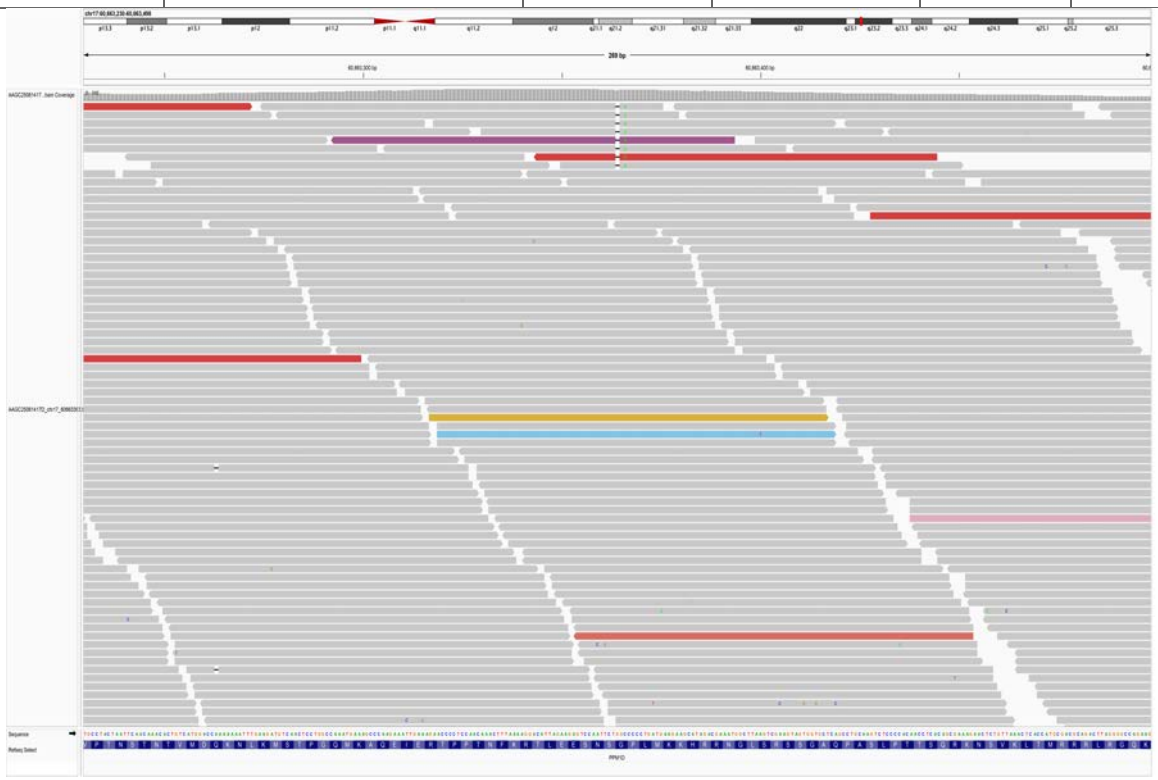
40.18. chr17_60663353_A/-

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



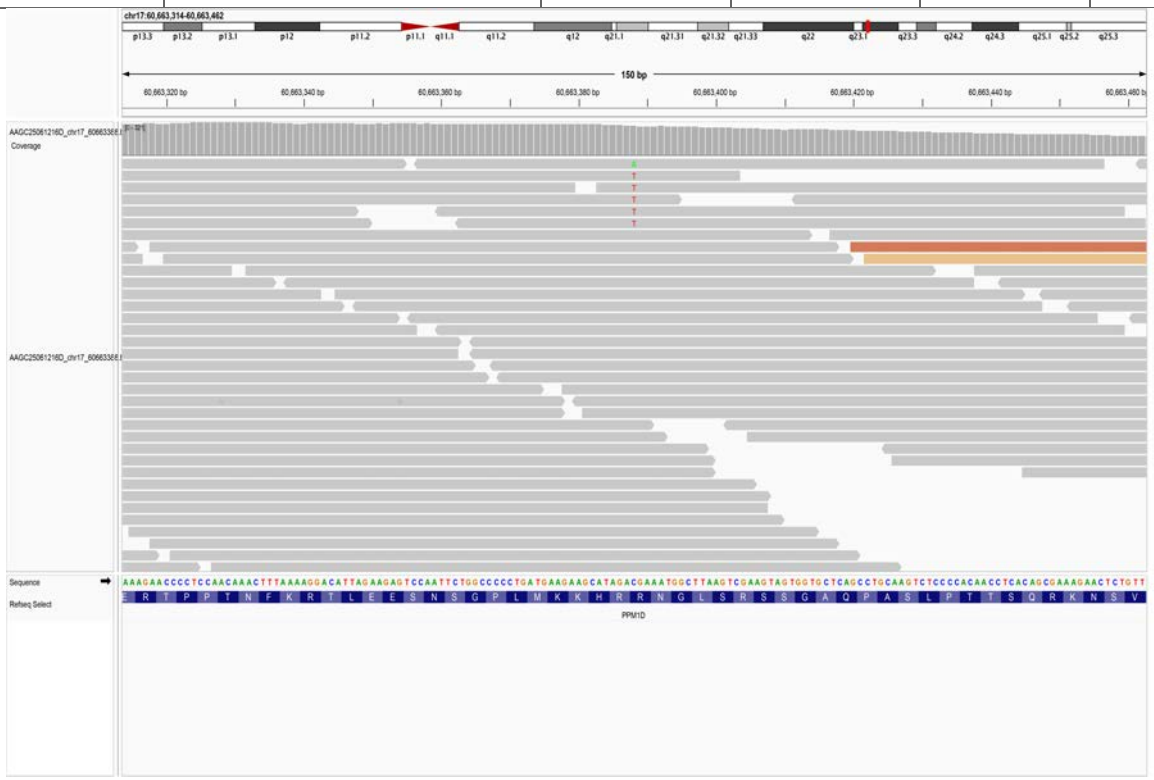
40.19. chr17_60663364_G/-

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



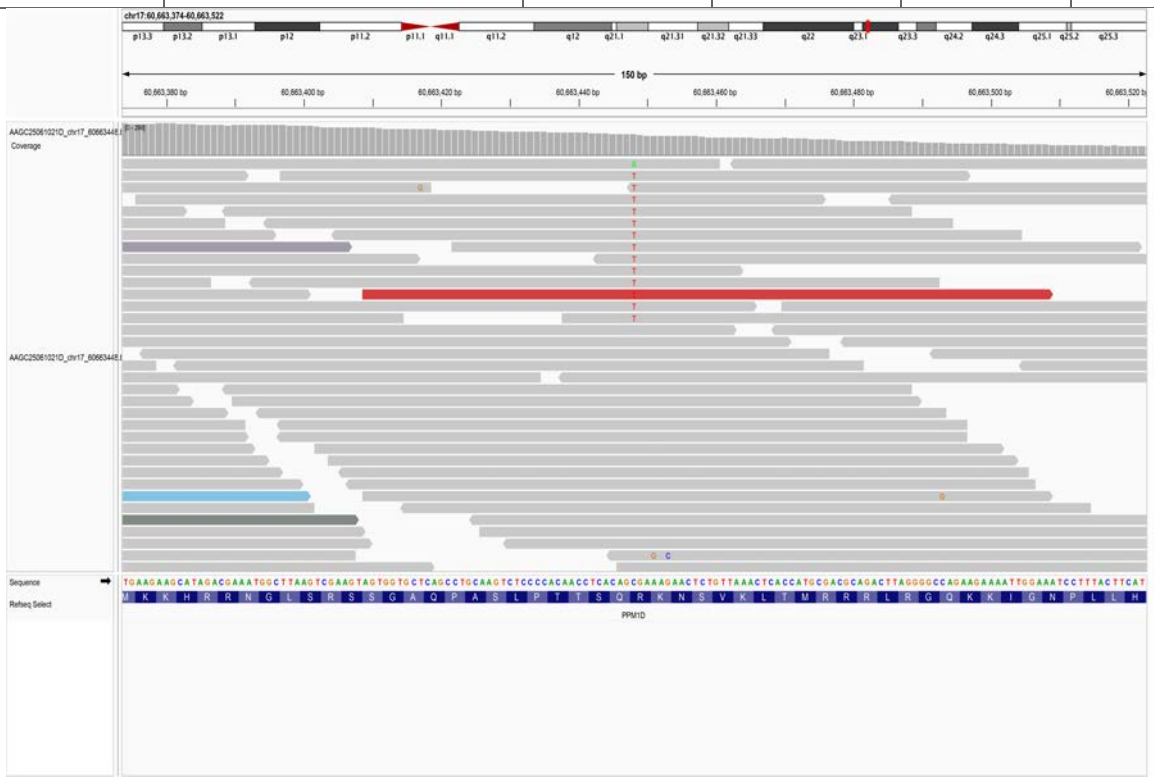
40.20. chr17_60663388_C/T

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



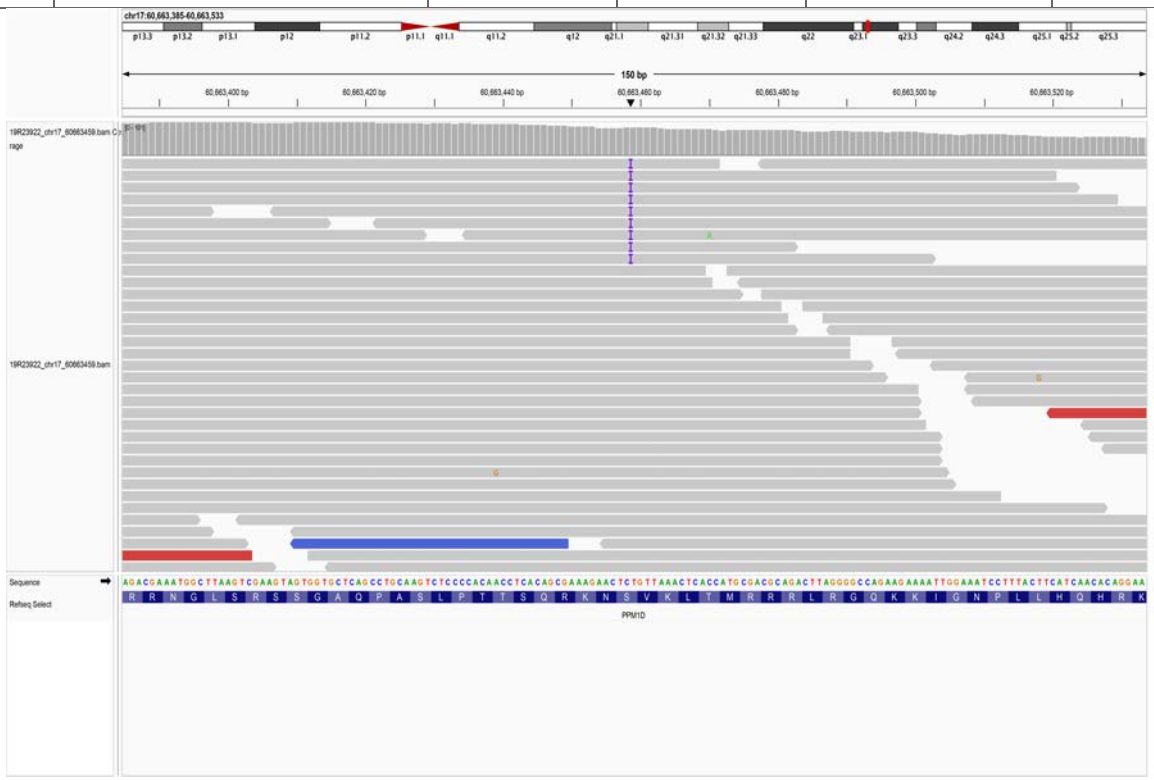
40.21. chr17_60663448_C/T

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



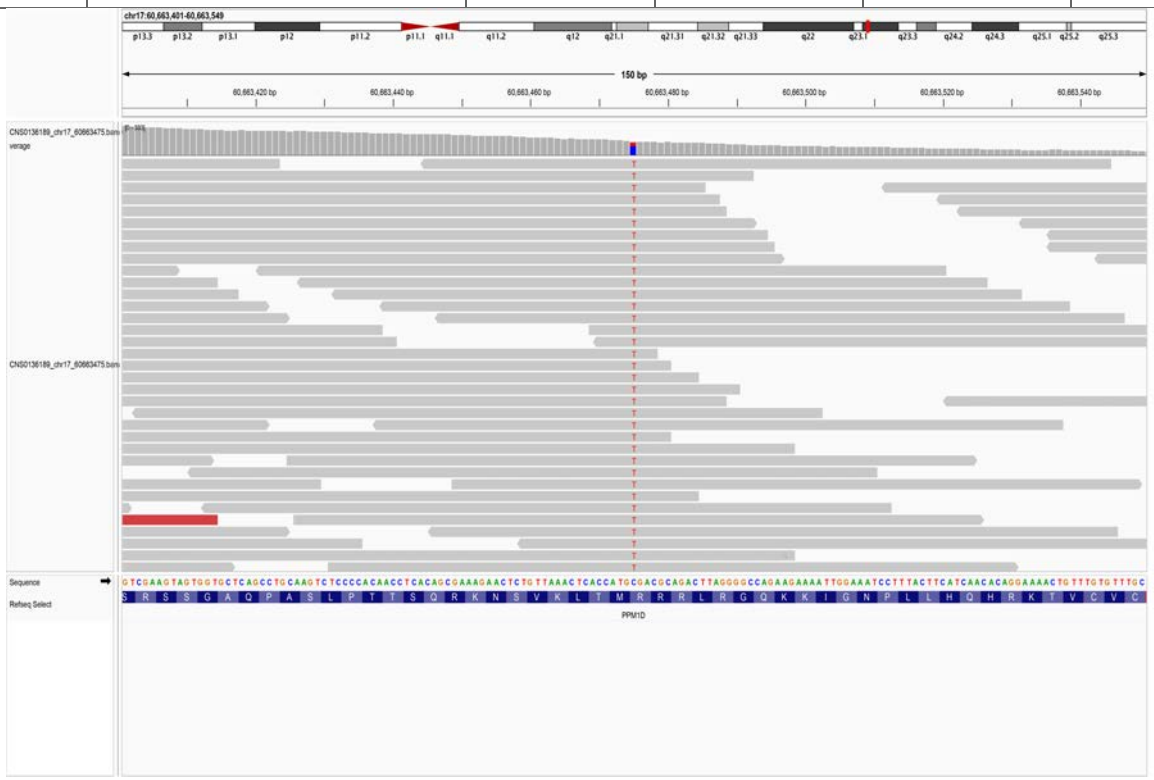
40.22. chr17_60663459_-/T

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



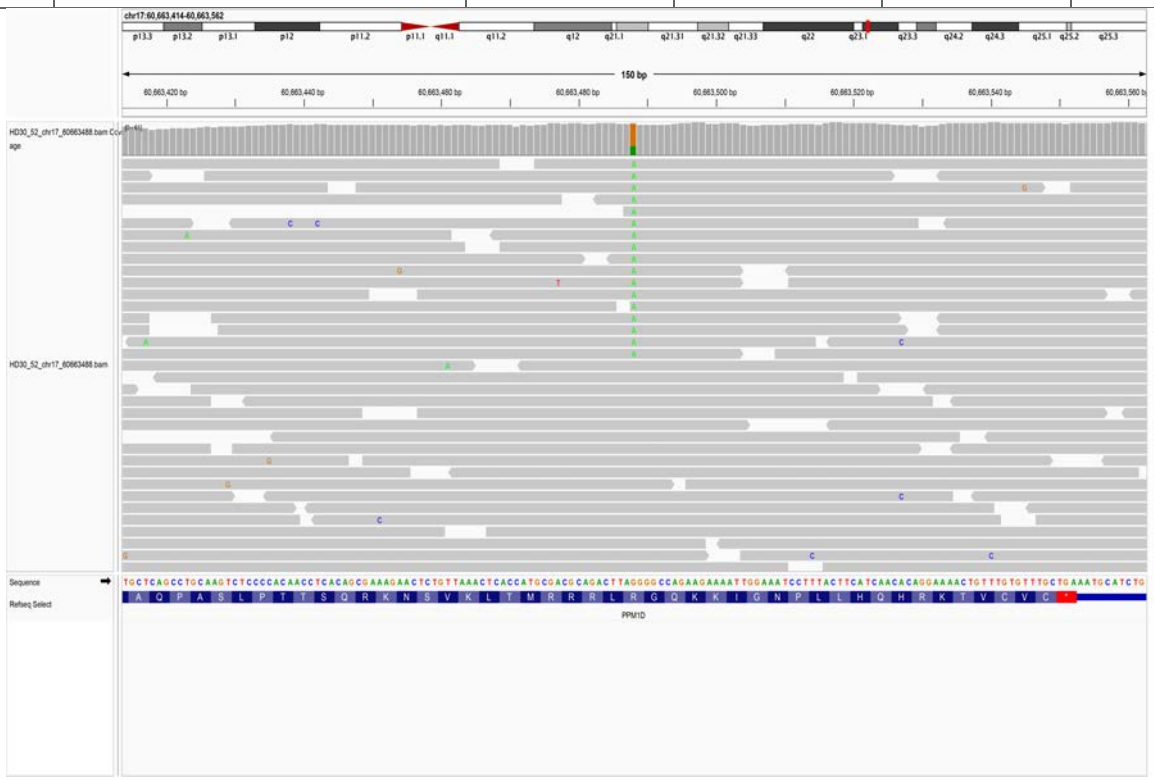
40.23. chr17_60663475_C/T

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



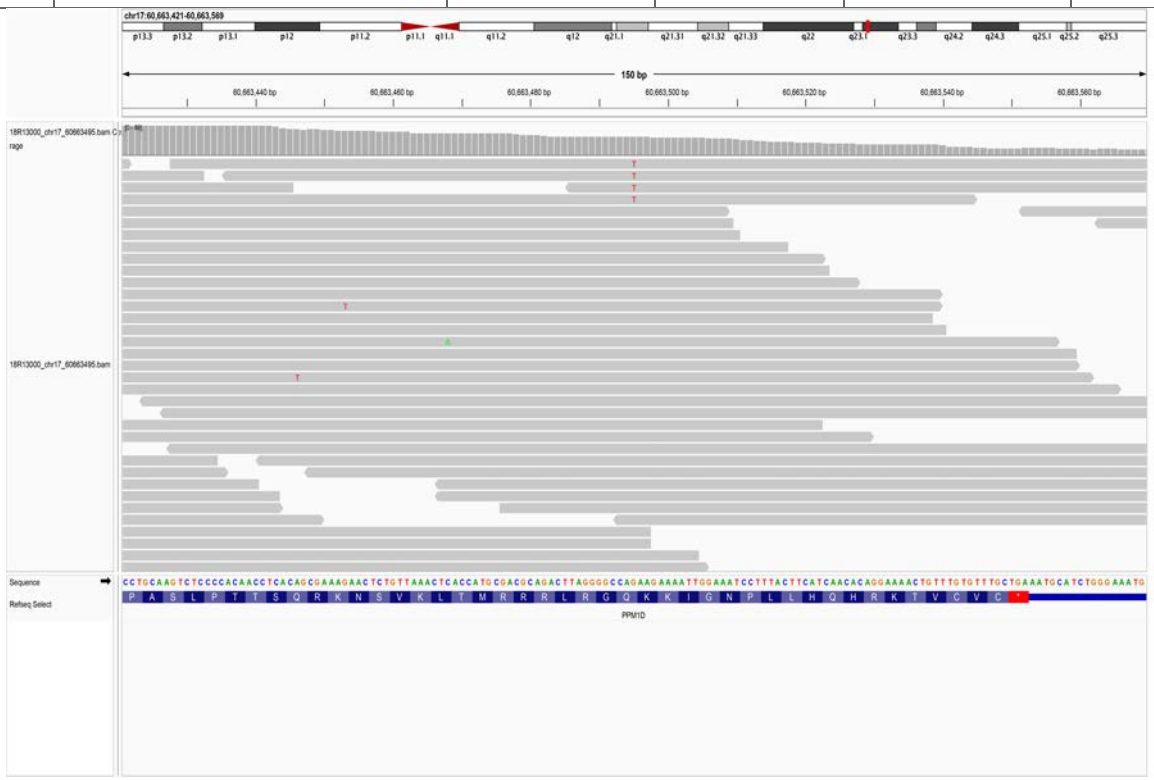
40.24. chr17_60663488_G/A

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



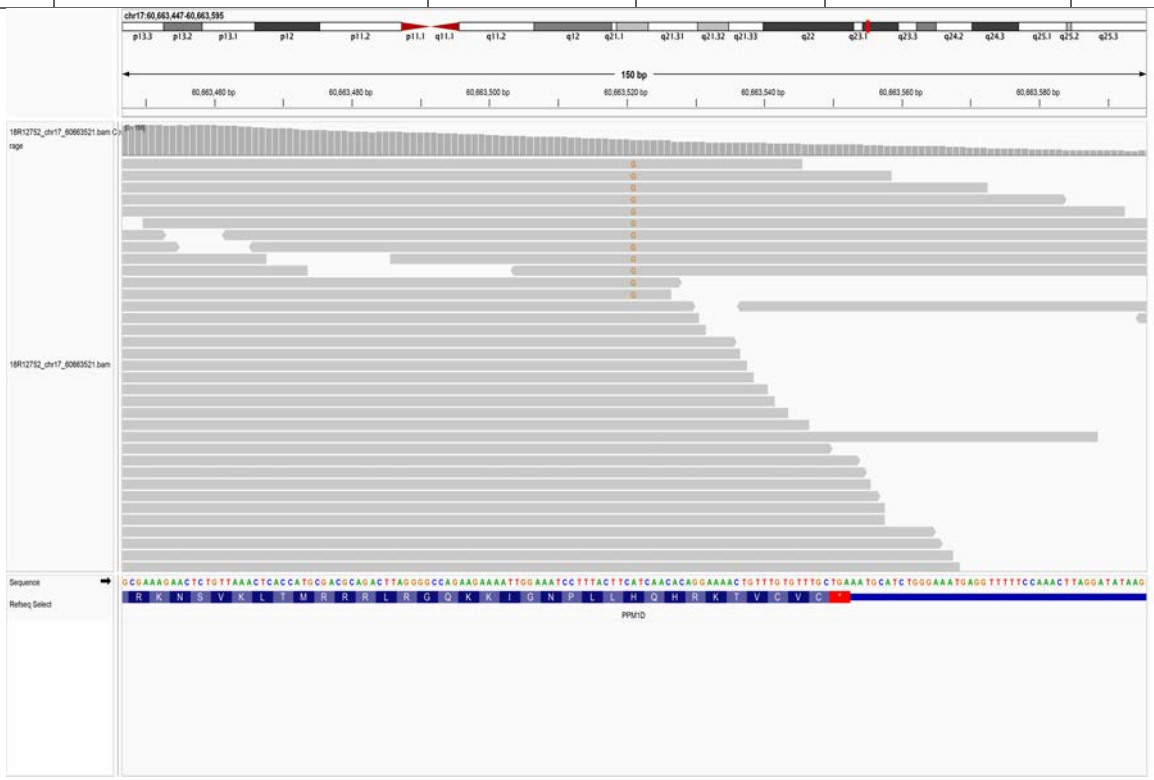
40.25. chr17_60663495_G/T

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

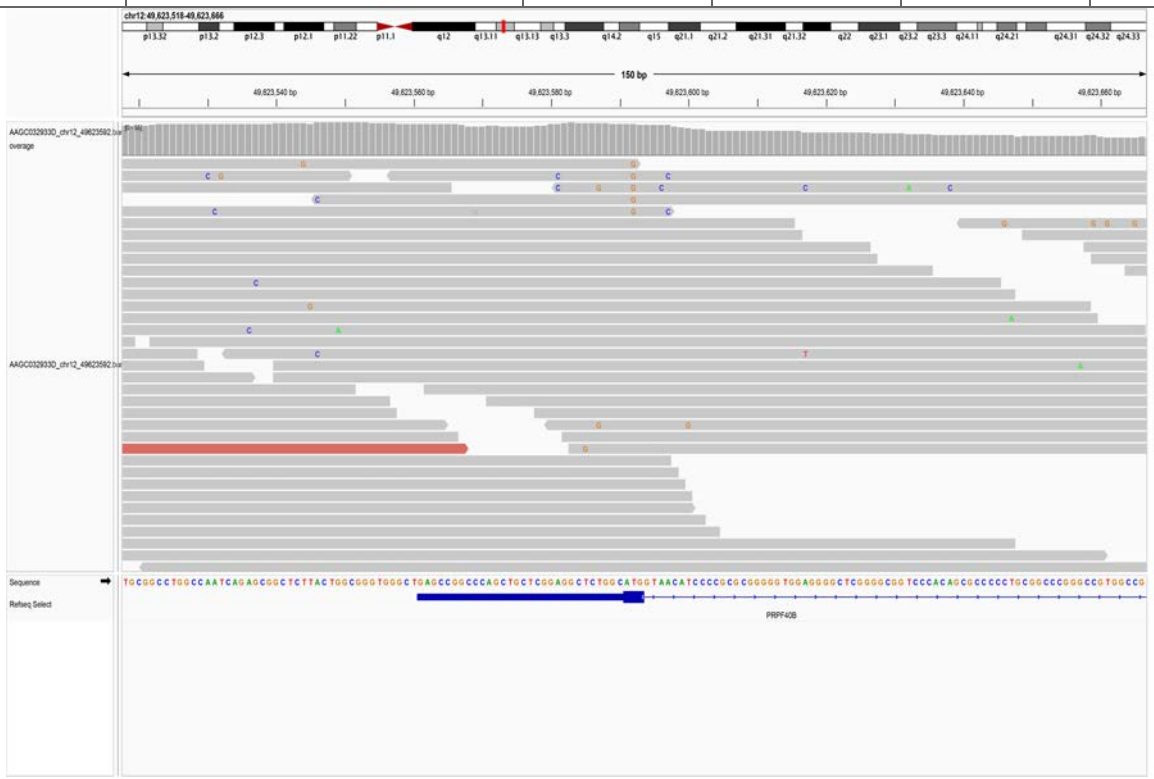
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12752	chr17_60663521_A/G	62	12	*PPM1D*	missense_variant



41. *PRPF40B*

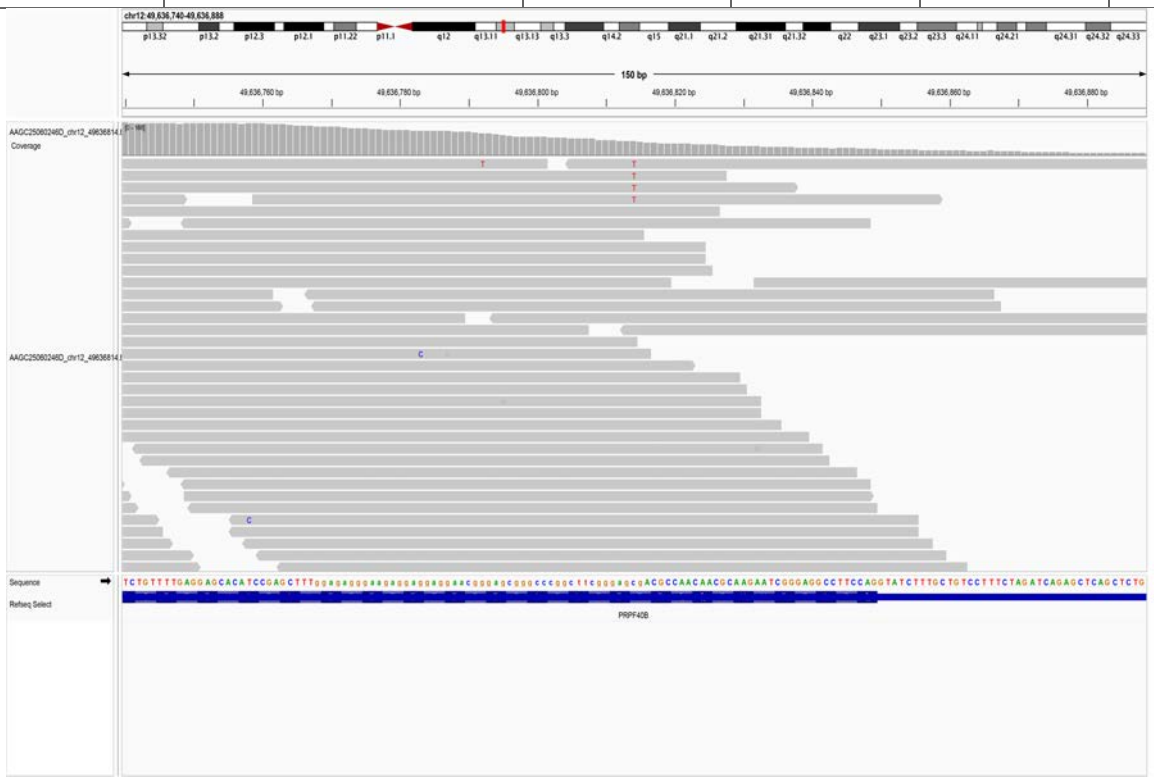
41.1. chr12_49623592_T/G

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



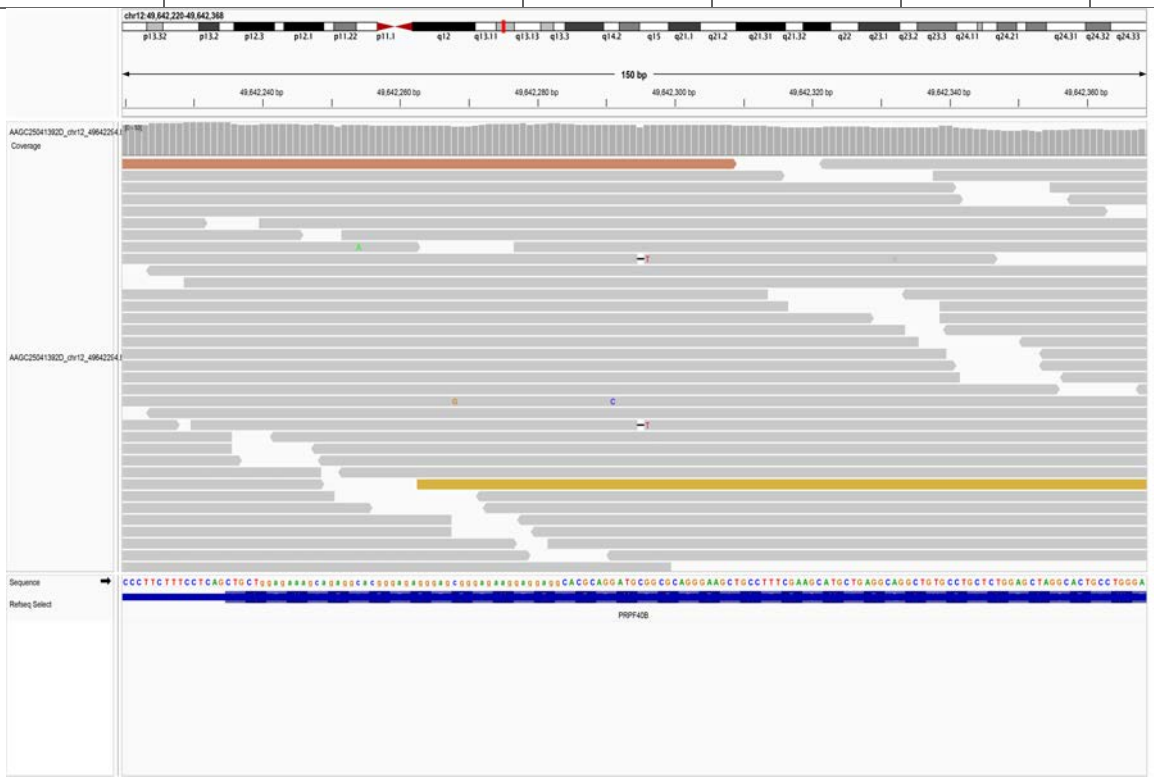
41.2. chr12_49636814_C/T

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



41.3. chr12_49642295_C/-

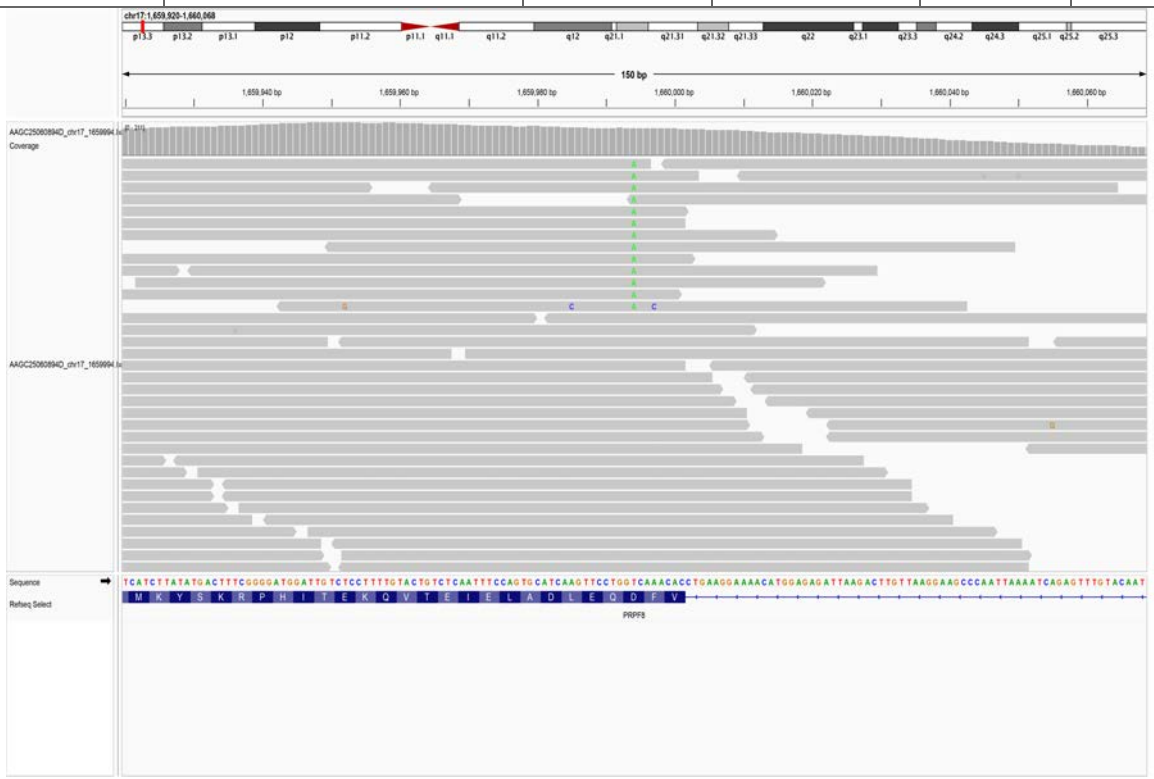
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25041392D	chr12_49642295_C/-	45	3	*PRPF40B*	frameshift_variant



42. *PRPF8*

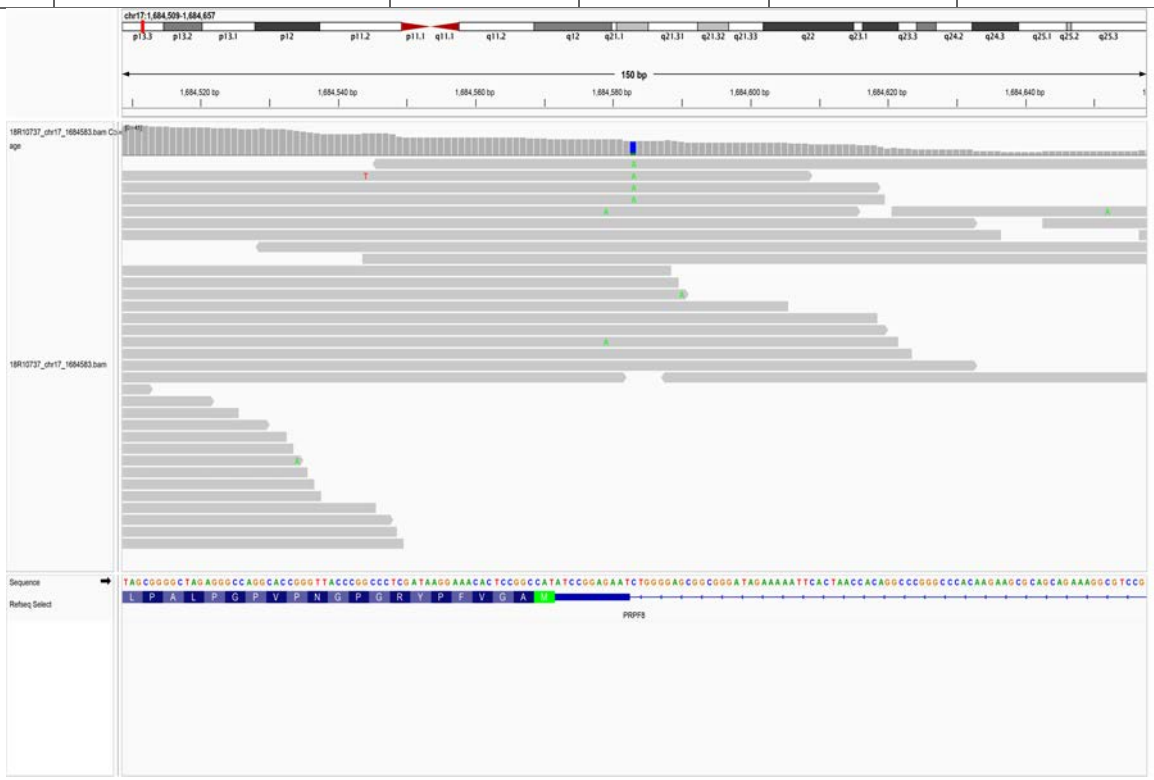
42.1. chr17_1659994_T/A

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

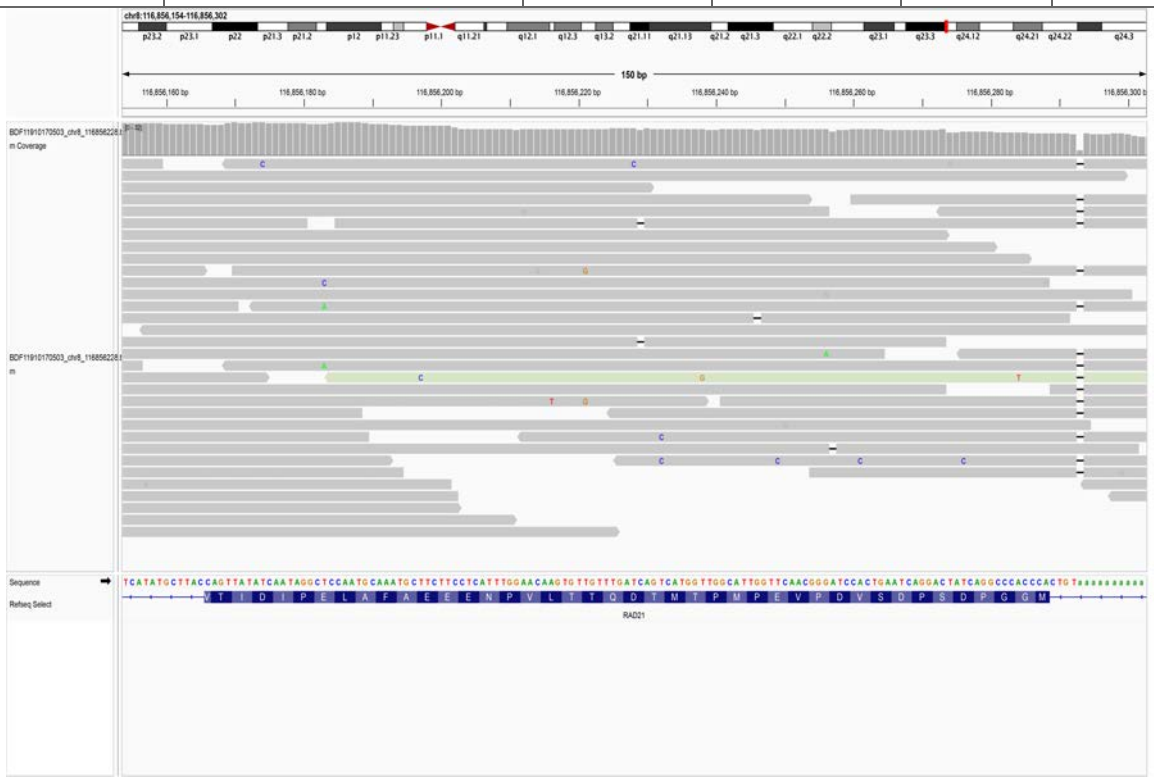
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10737	chr17_1684583_C/A	14	4	*PRPF8*	splice_acceptor_variant



43. *RAD21*

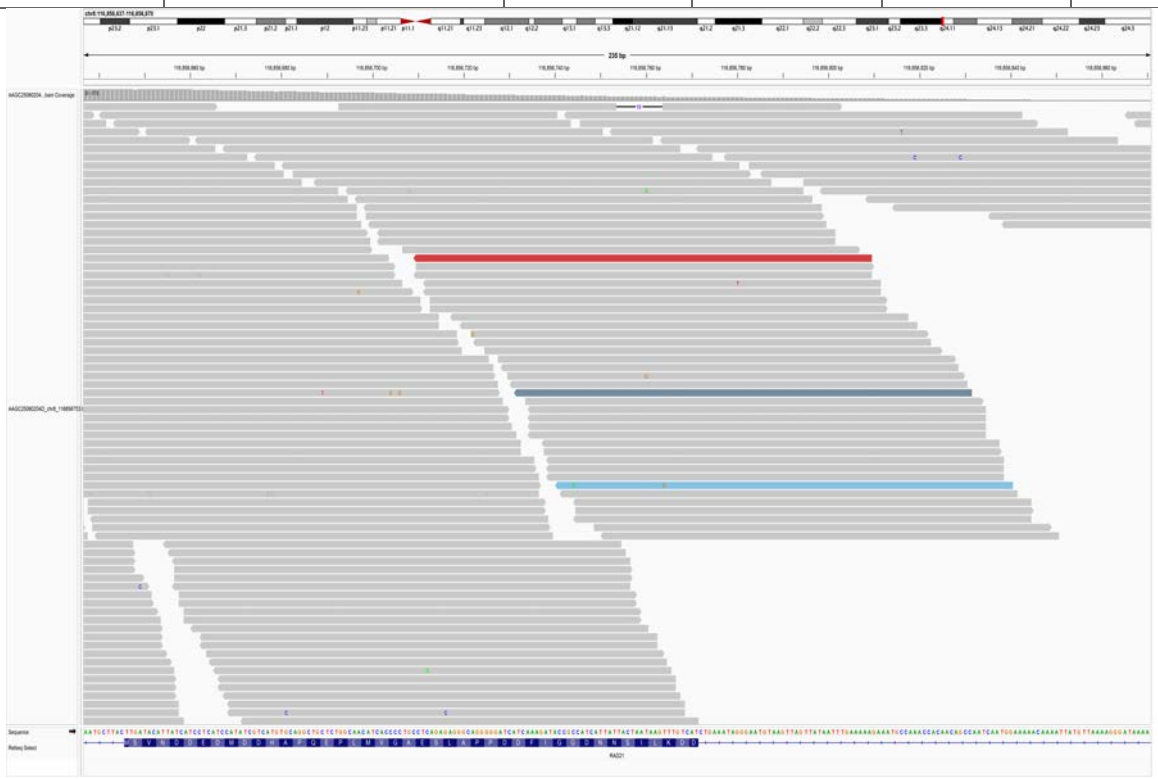
43.1. chr8_116856229_C/-

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



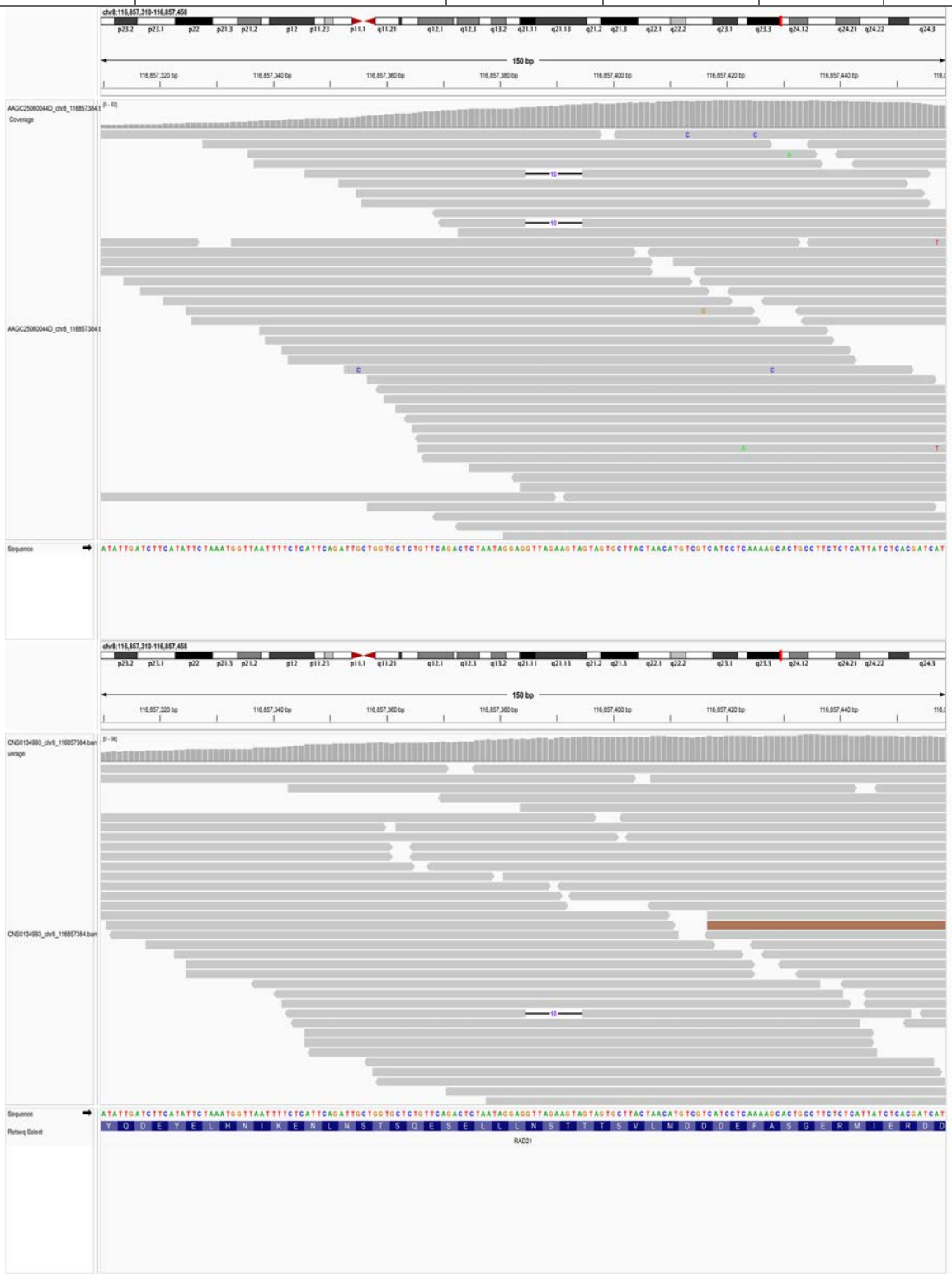
43.2. chr8_116856754_TACTAATAAG/-

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



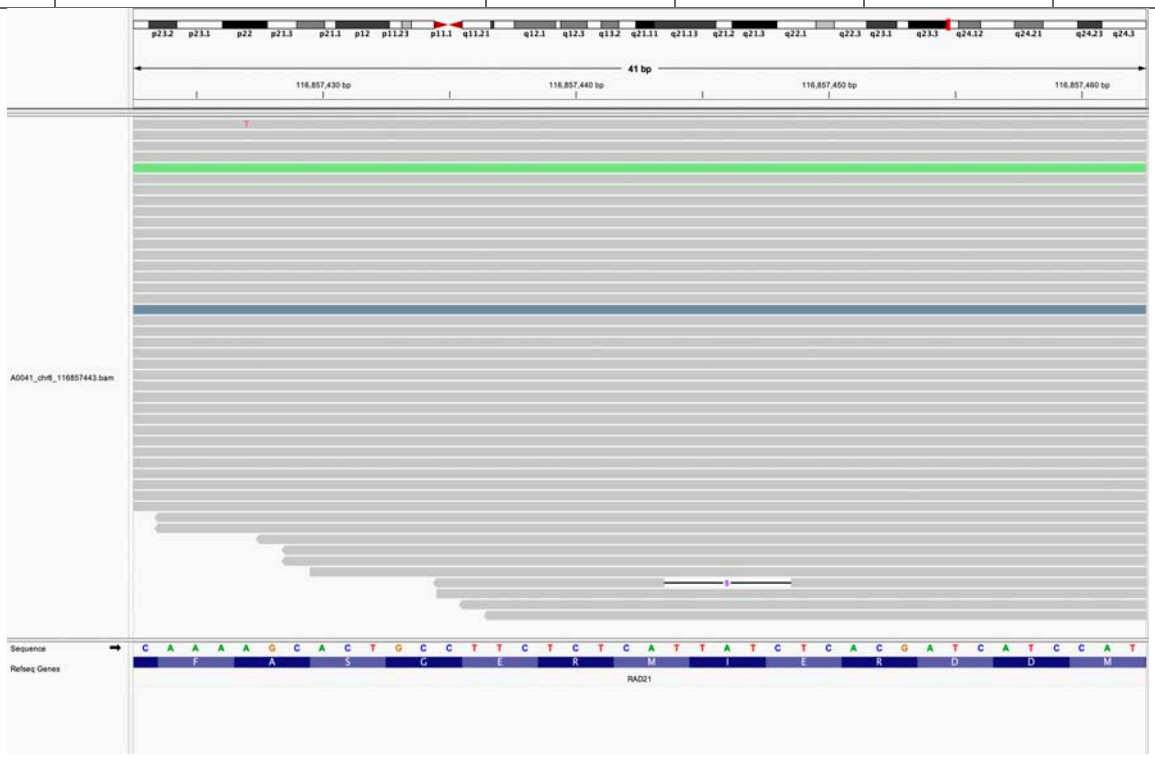
43.3. chr8_116857385_GTTAGAAGTA/-

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/-

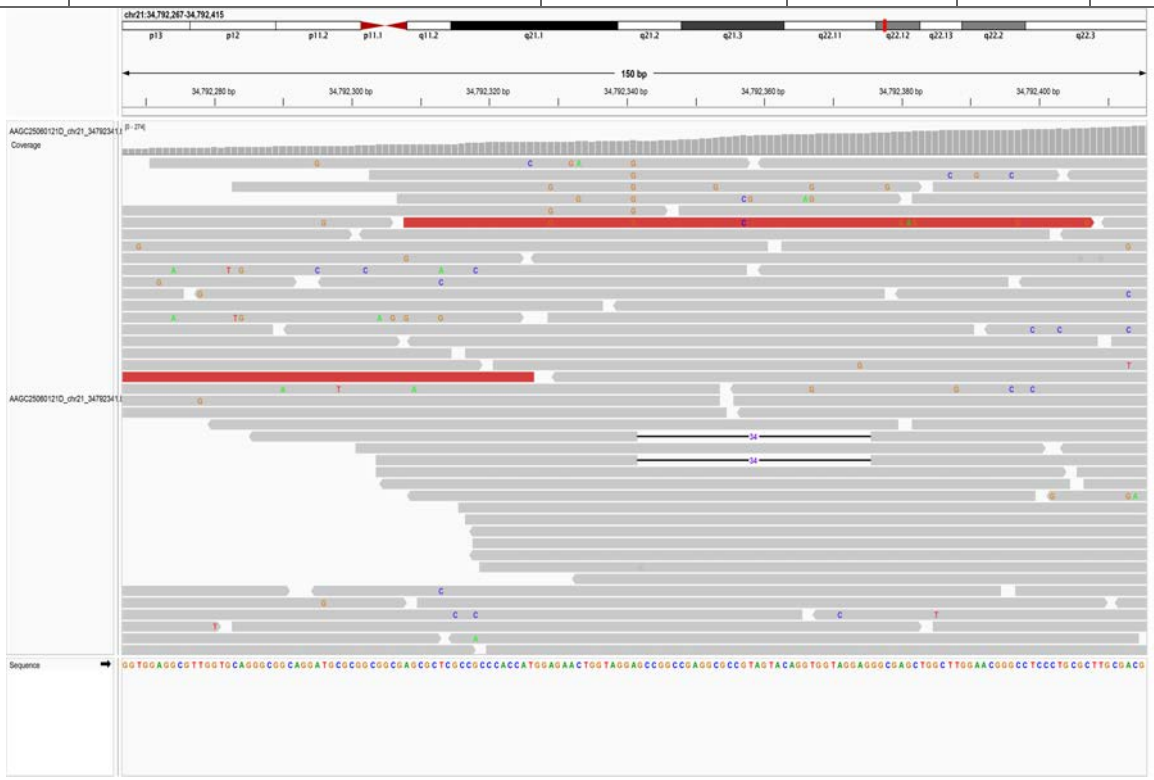
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0041	chr8_116857444_TTATC/-	115	2	*RAD21*	frameshift_variant



44. *RUNX1*

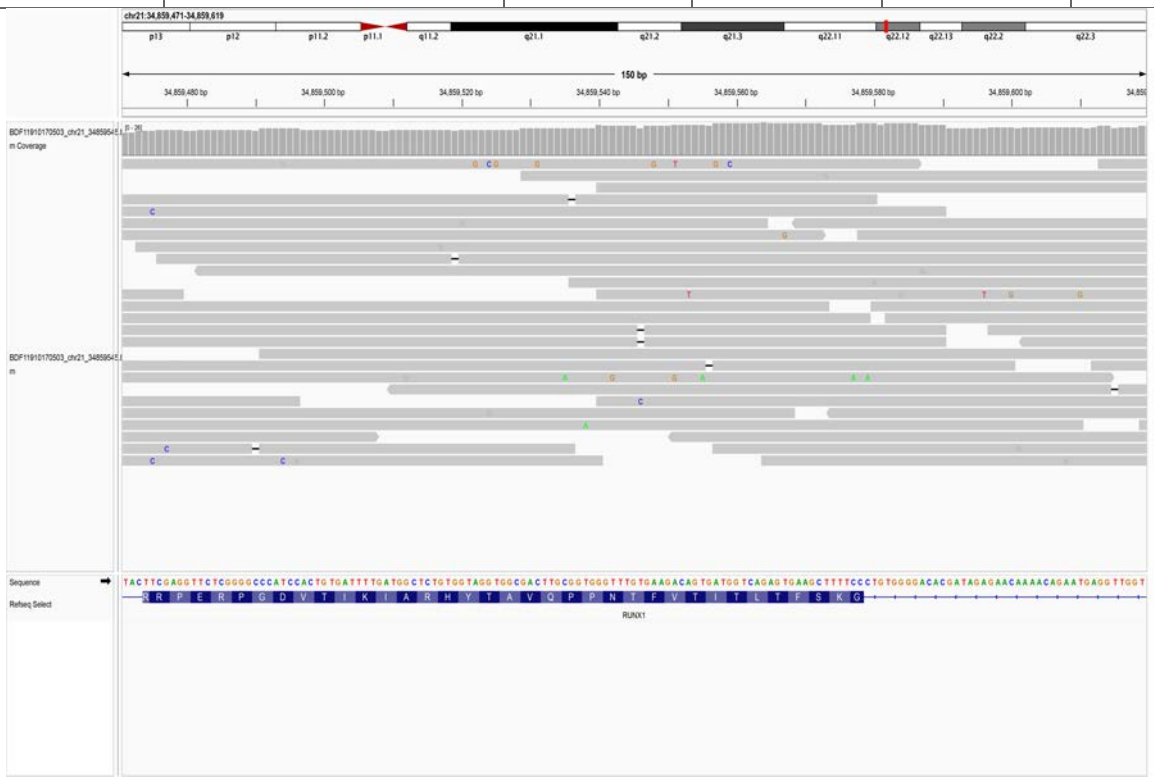
44.1. chr21_34792342_GCCGGCCGAGGCGCCGTAGTACAGGTGGTAGGAG/-

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



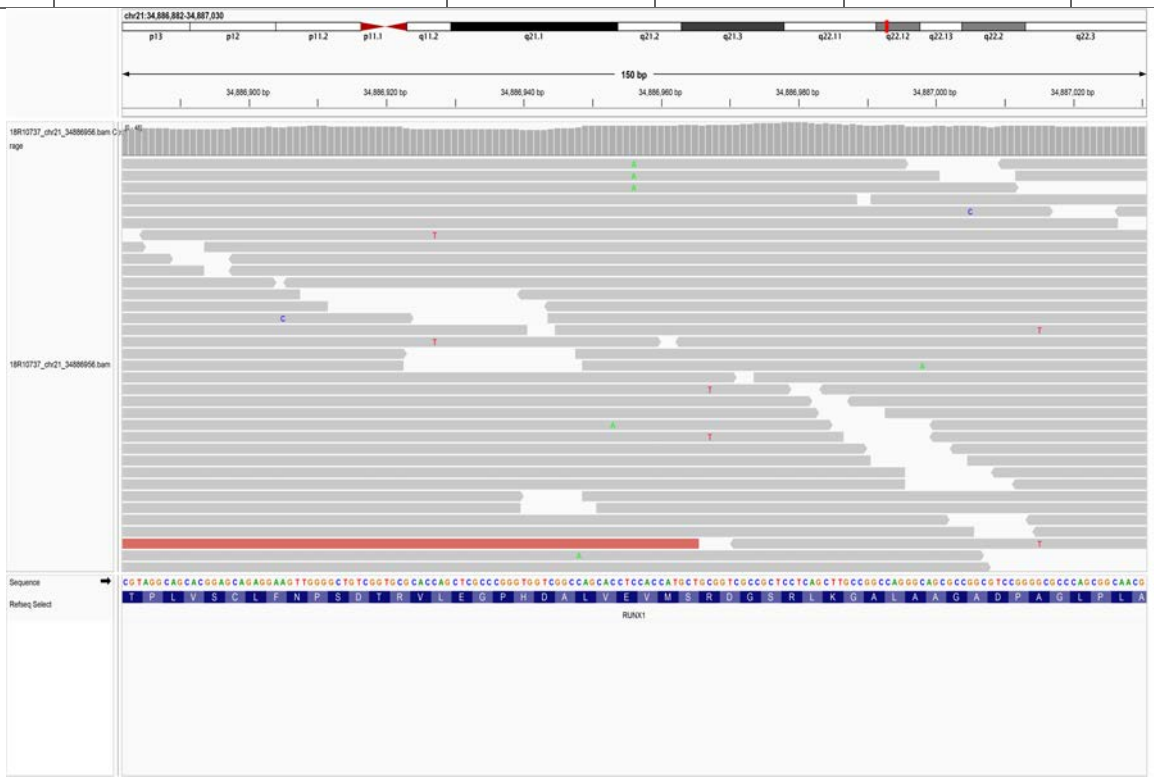
44.2. chr21_34859546_T/-

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



44.3. chr21_34886956_C/A

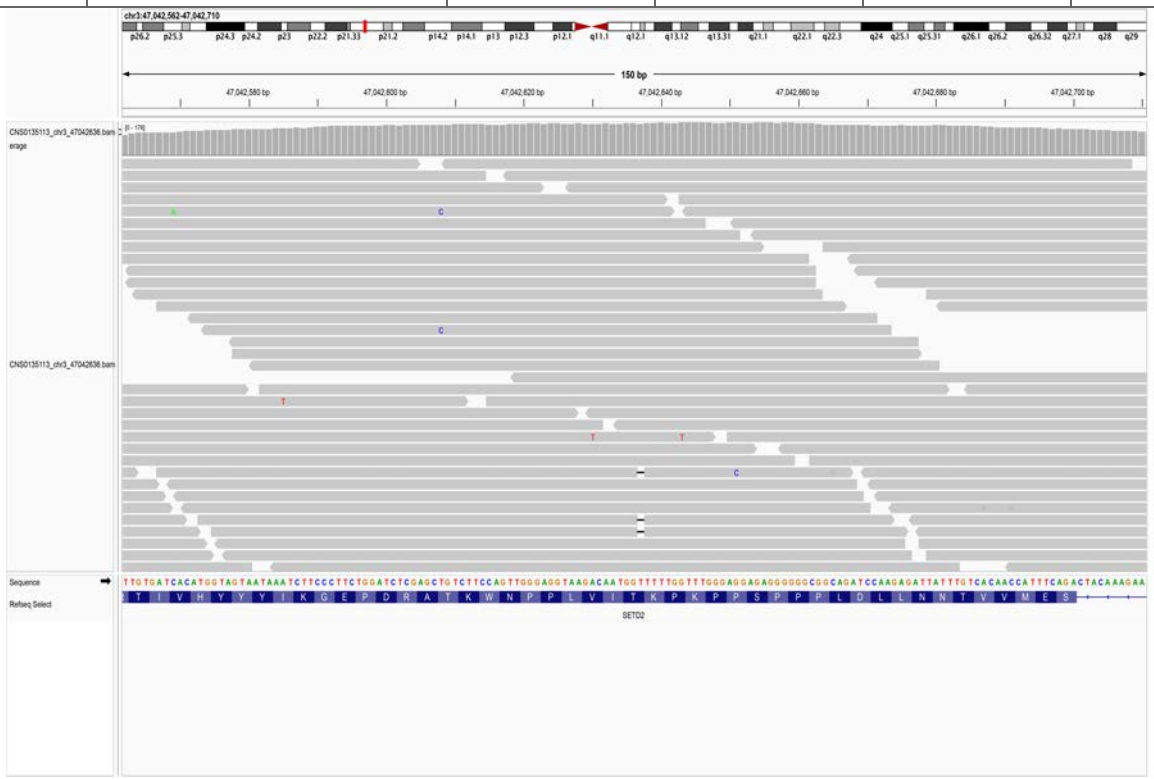
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R10737	chr21_34886956_C/A	39	3	*RUNX1*	stop_gained



45. *SETD2*

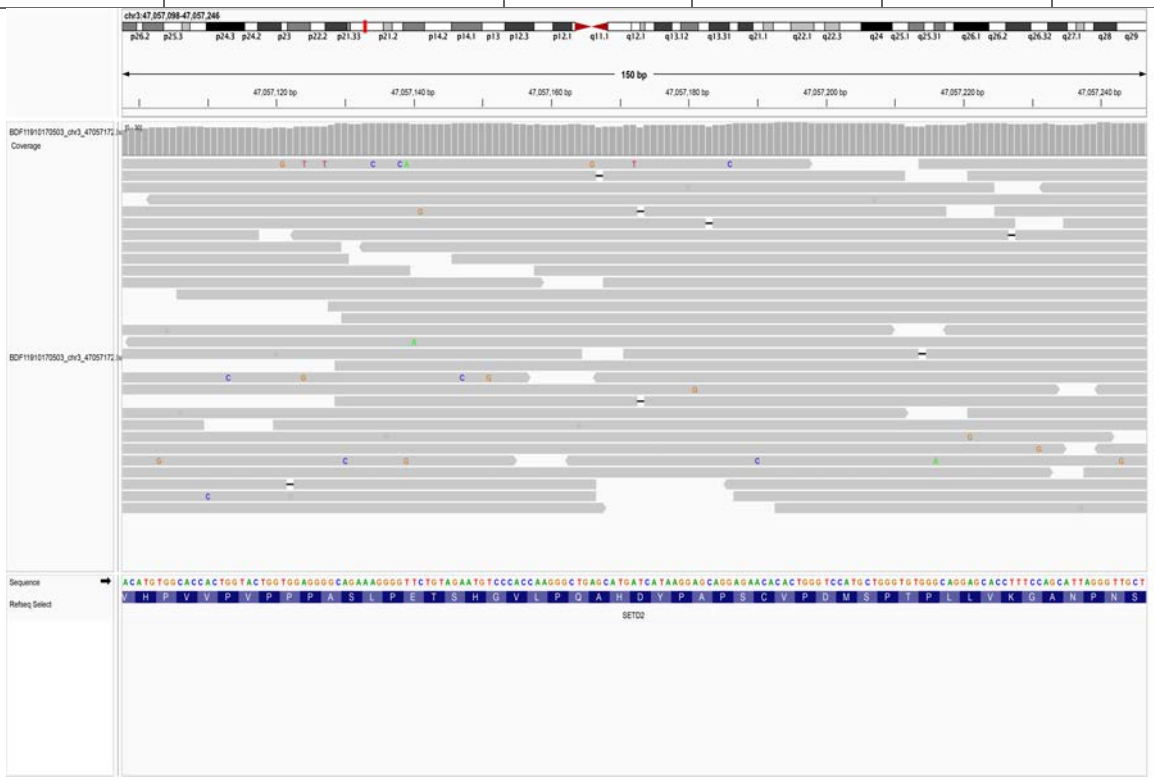
45.1. chr3_47042637_T/-

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



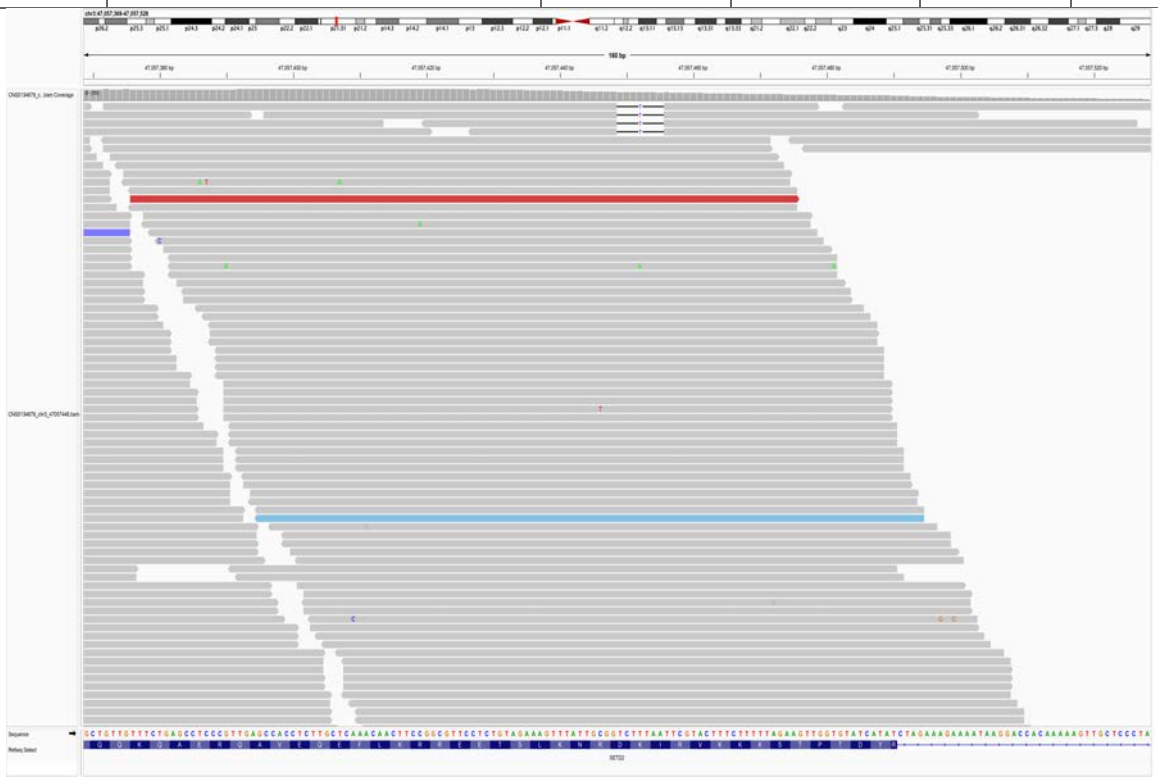
45.2. chr3_47057173_T/-

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



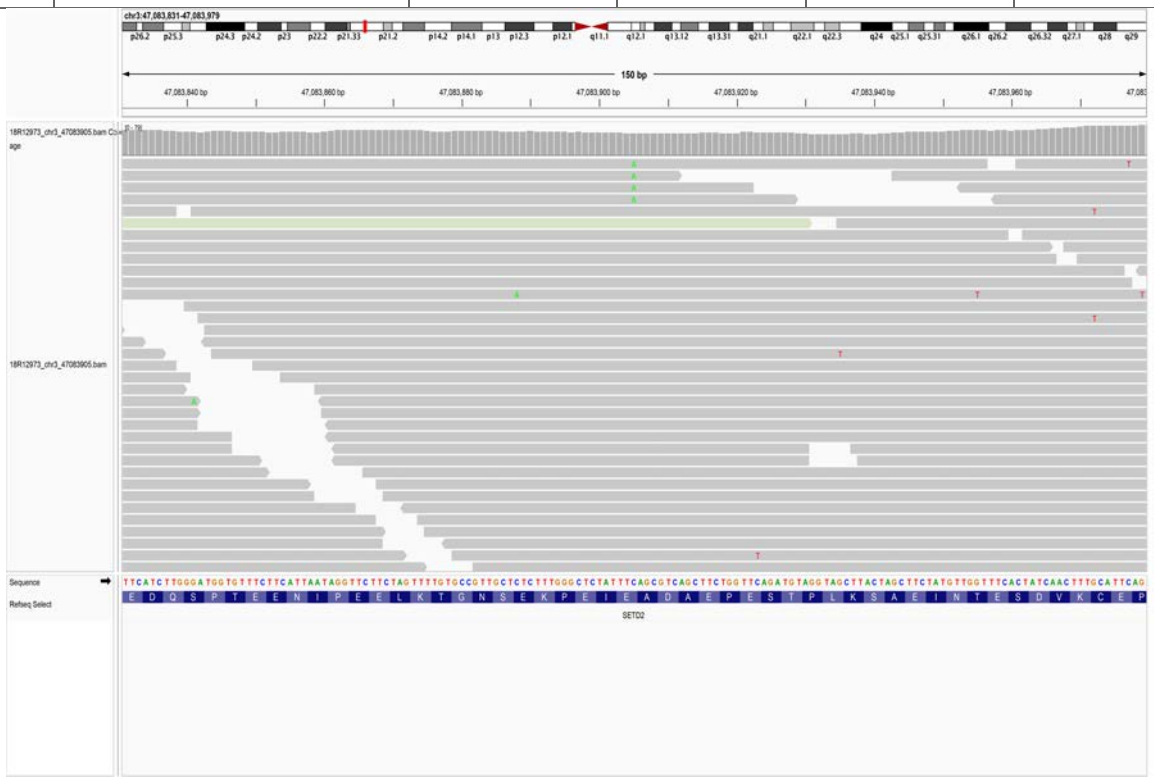
45.3. chr3_47057449_TCTTTAA/-

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



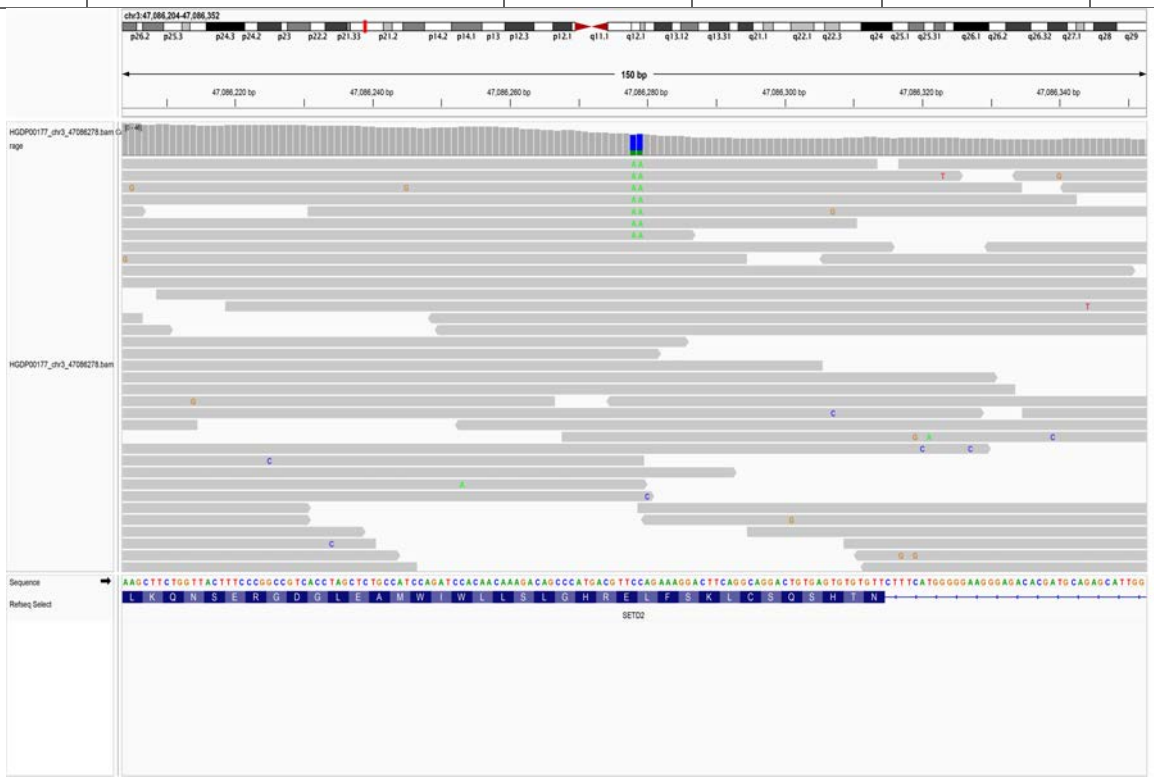
45.4. chr3_47083905_C/A

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



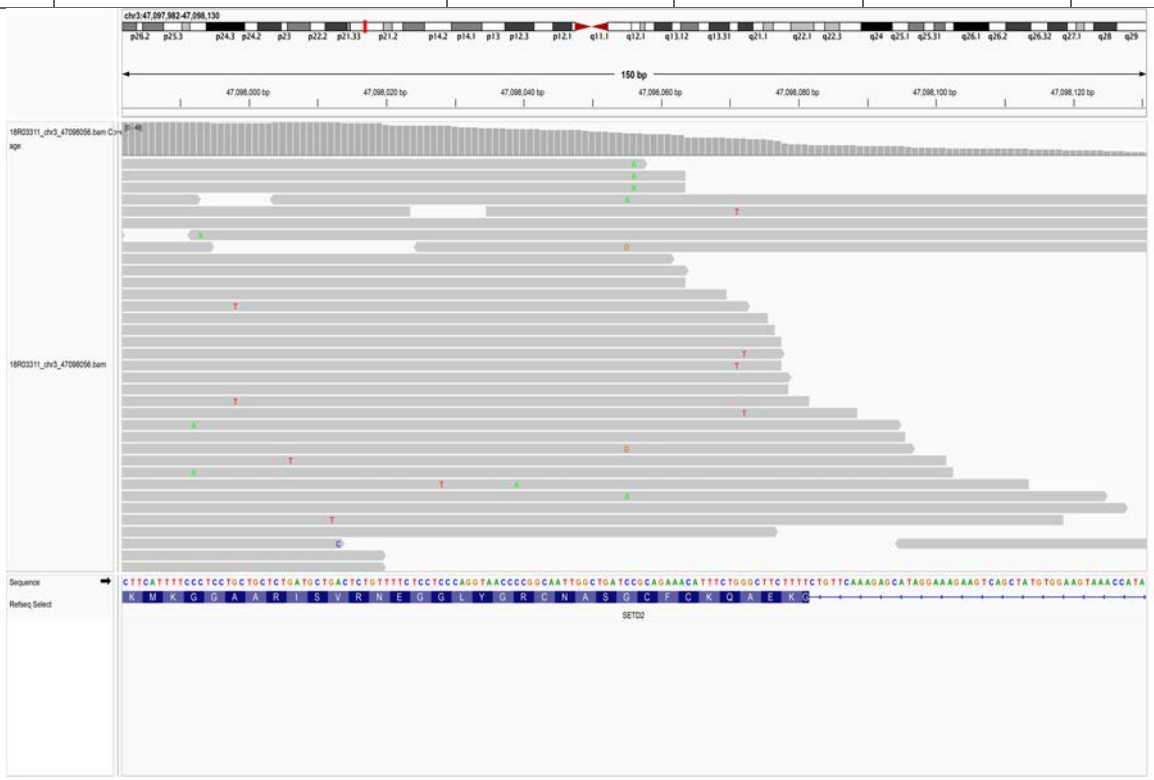
45.5. chr3_47086278_CC/AA

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



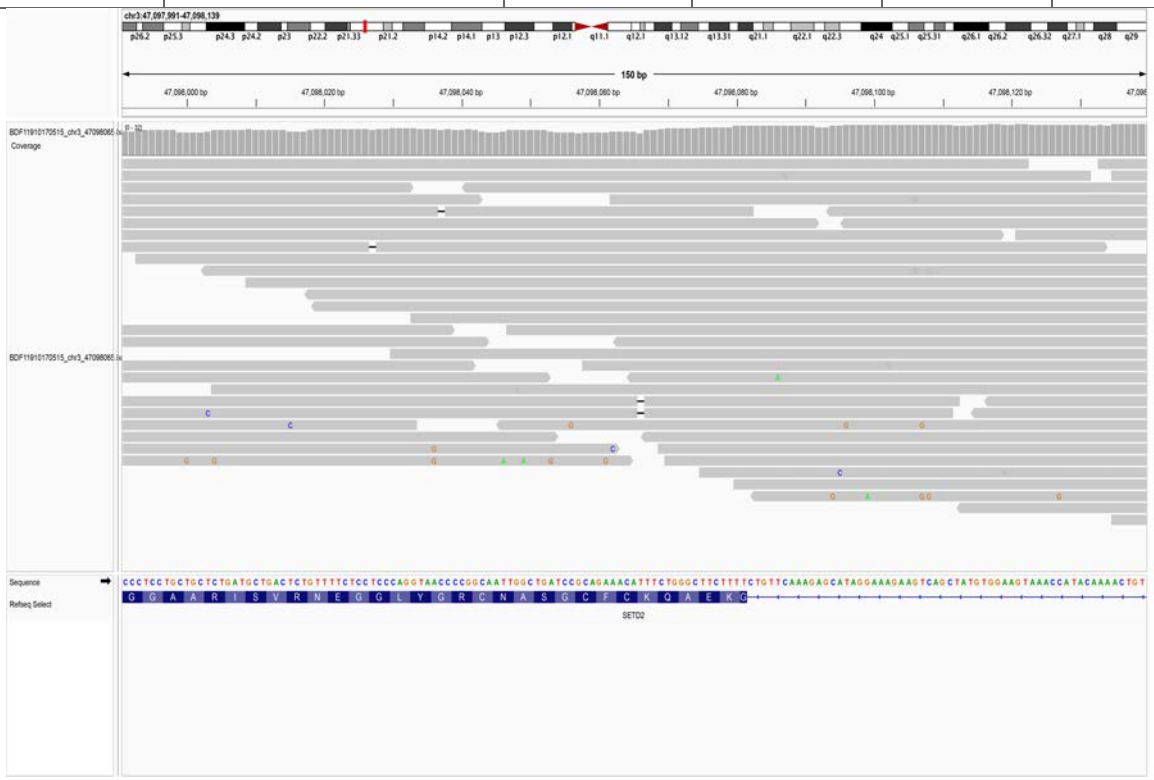
45.6. chr3_47098056_C/A

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



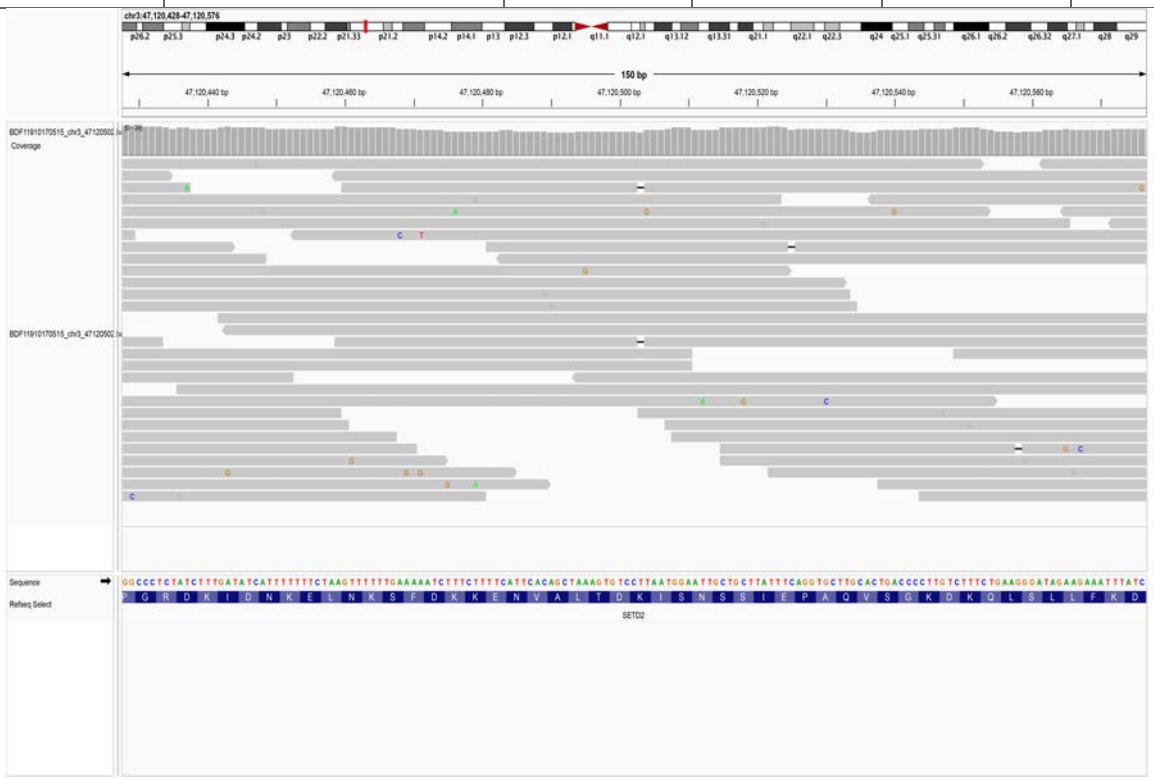
45.7. chr3_47098066_T/-

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



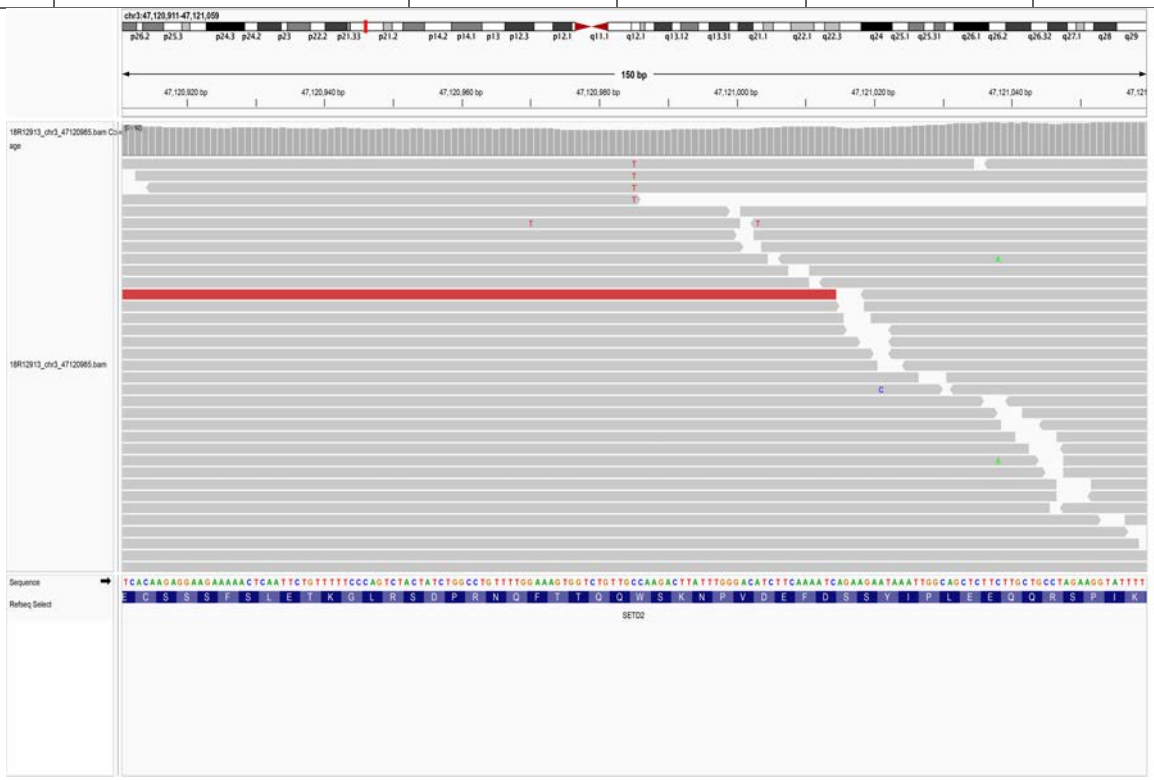
45.8. chr3_47120503_T/-

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



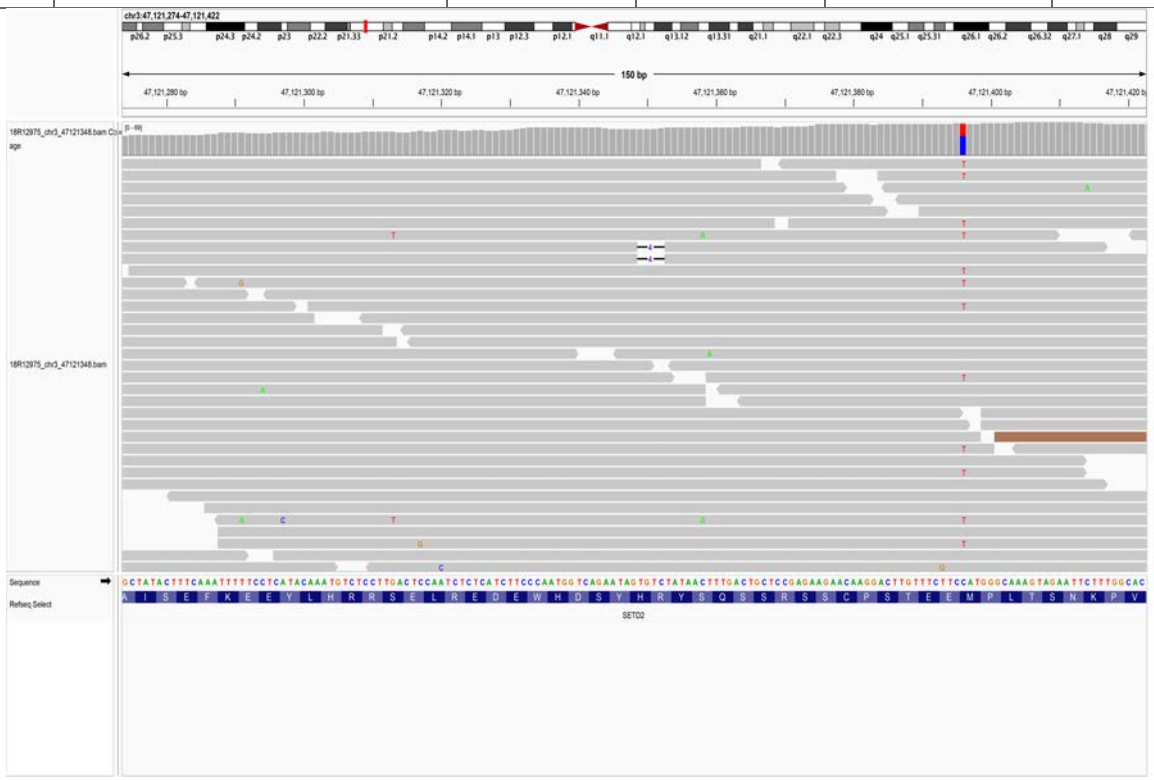
45.9. chr3_47120985_C/T

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



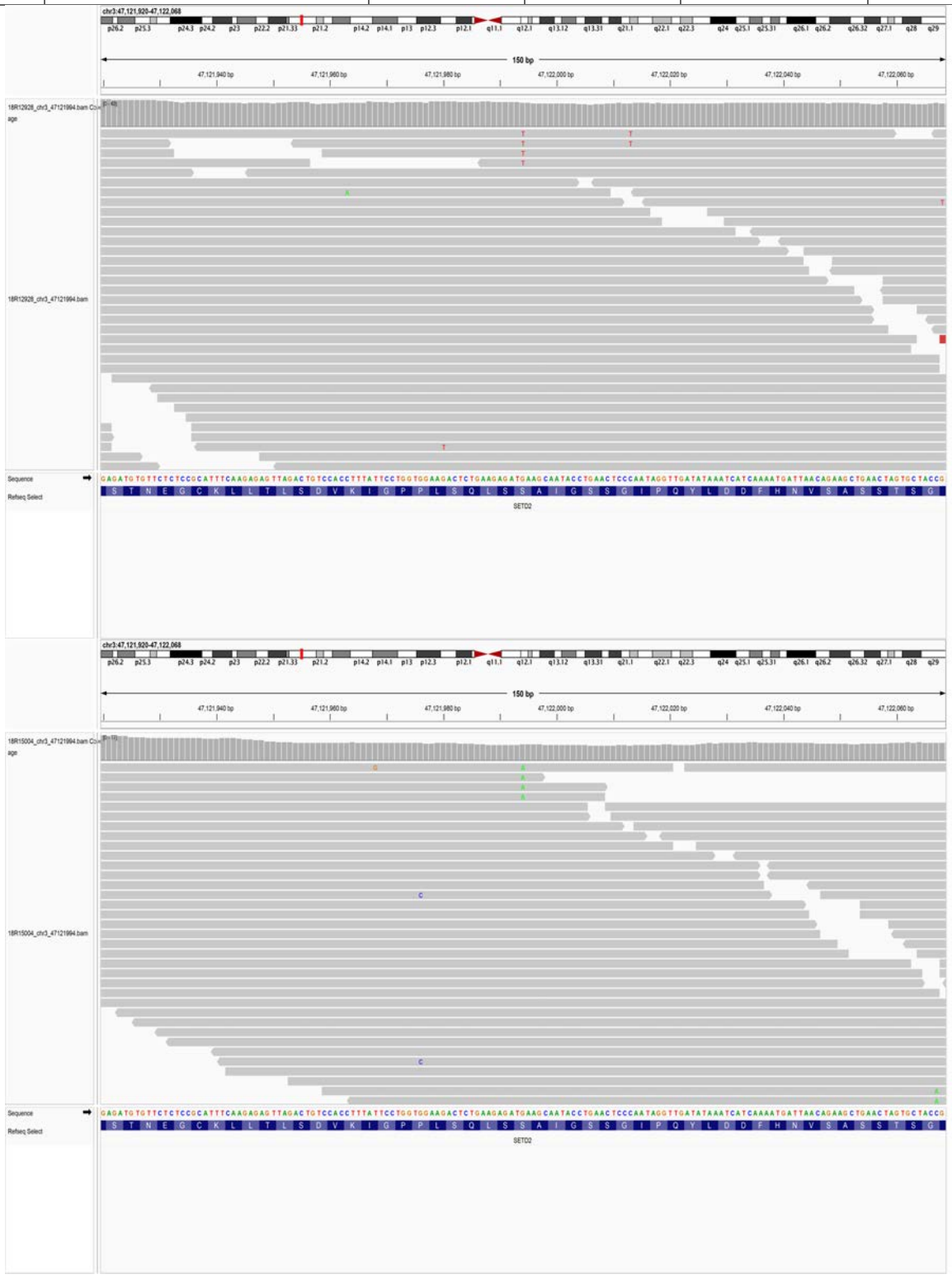
45.10. chr3_47121349_TGTC/-

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



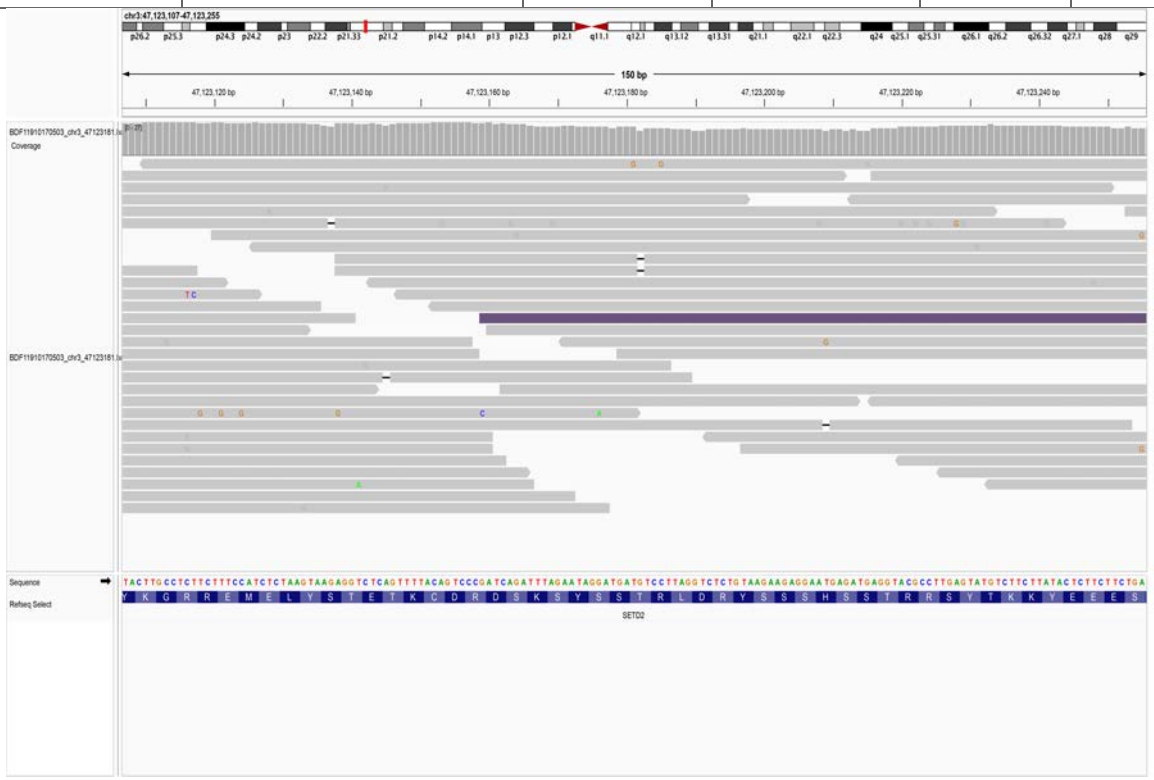
45.11. chr3_47121994_G/T/A

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



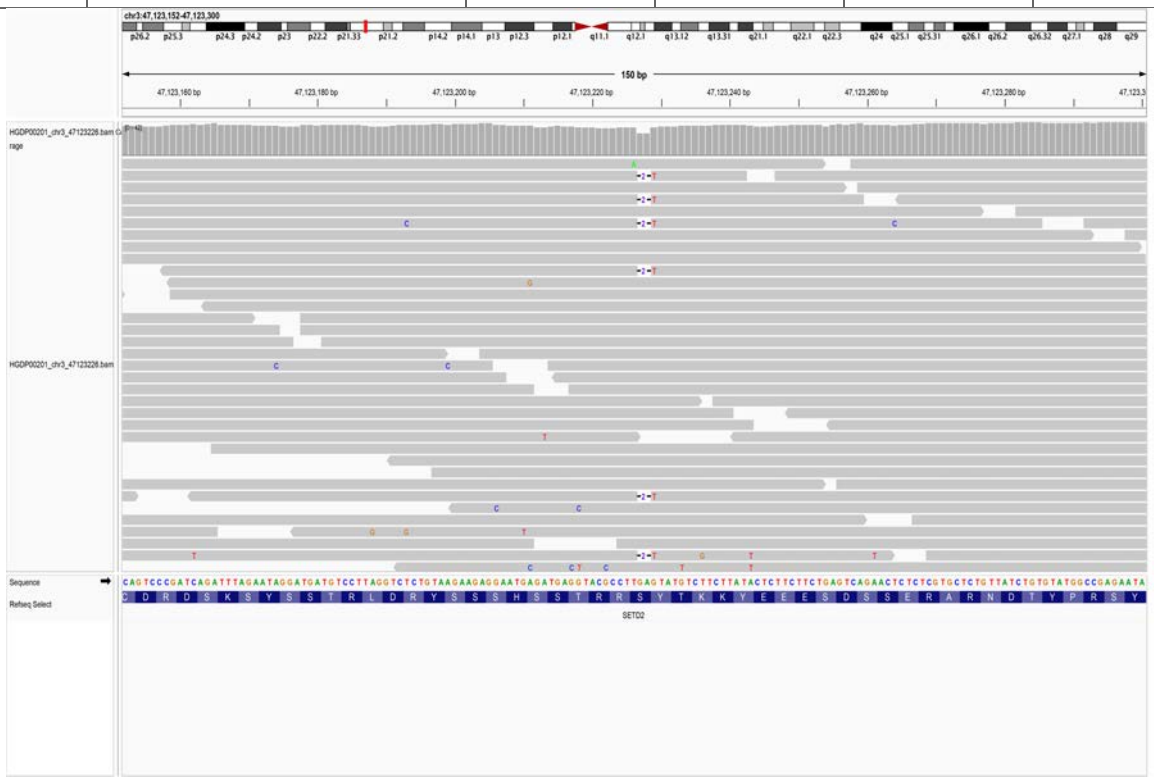
45.12. chr3_47123182_G/-

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



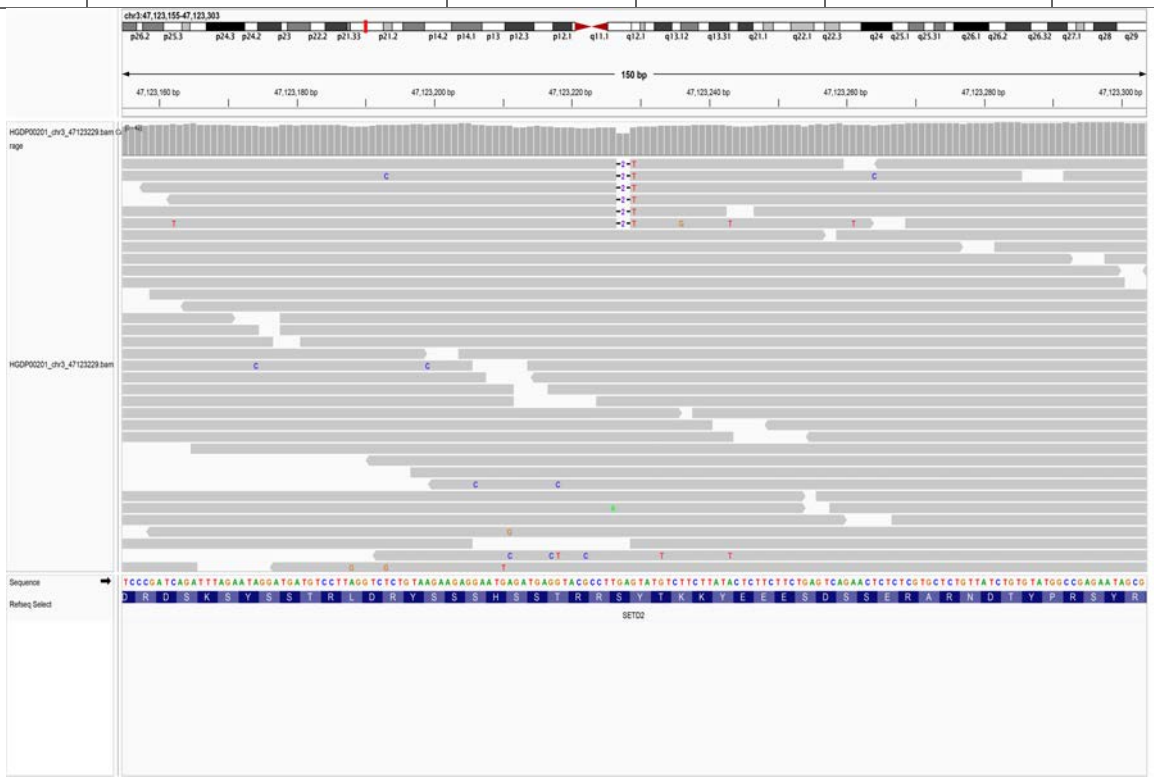
45.13. chr3_47123227_GA/-

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



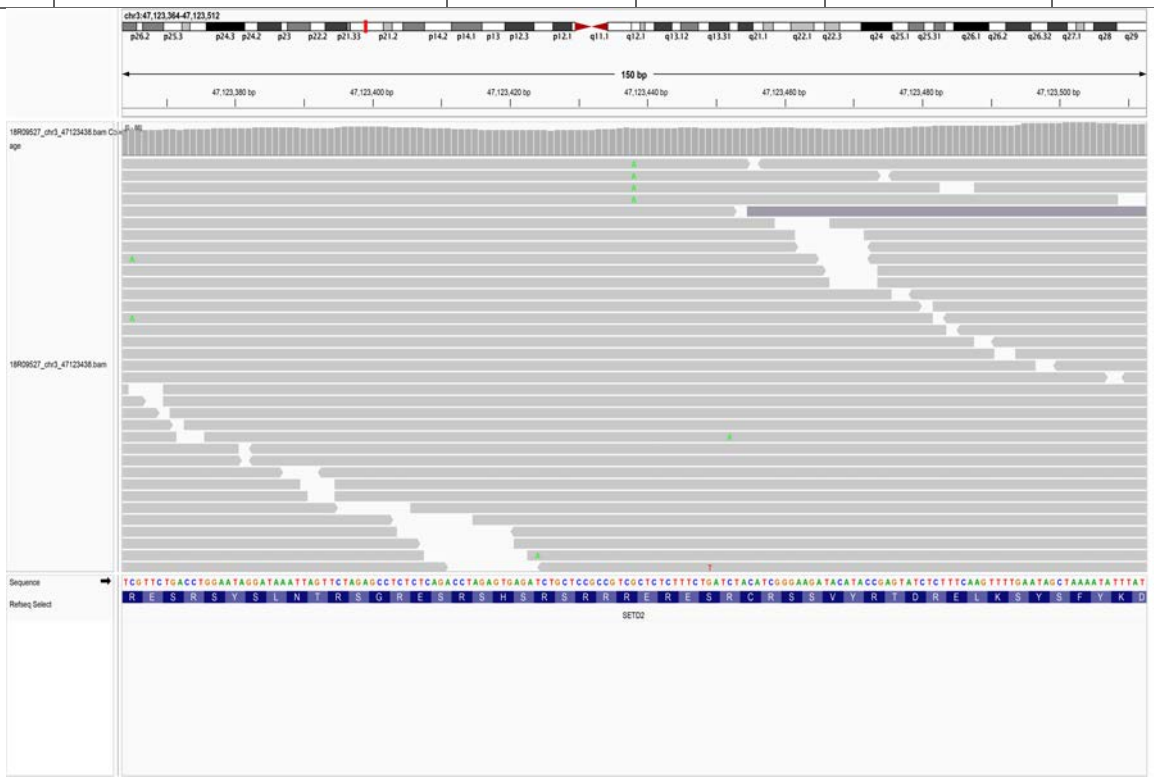
45.14. chr3_47123229_G/T

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



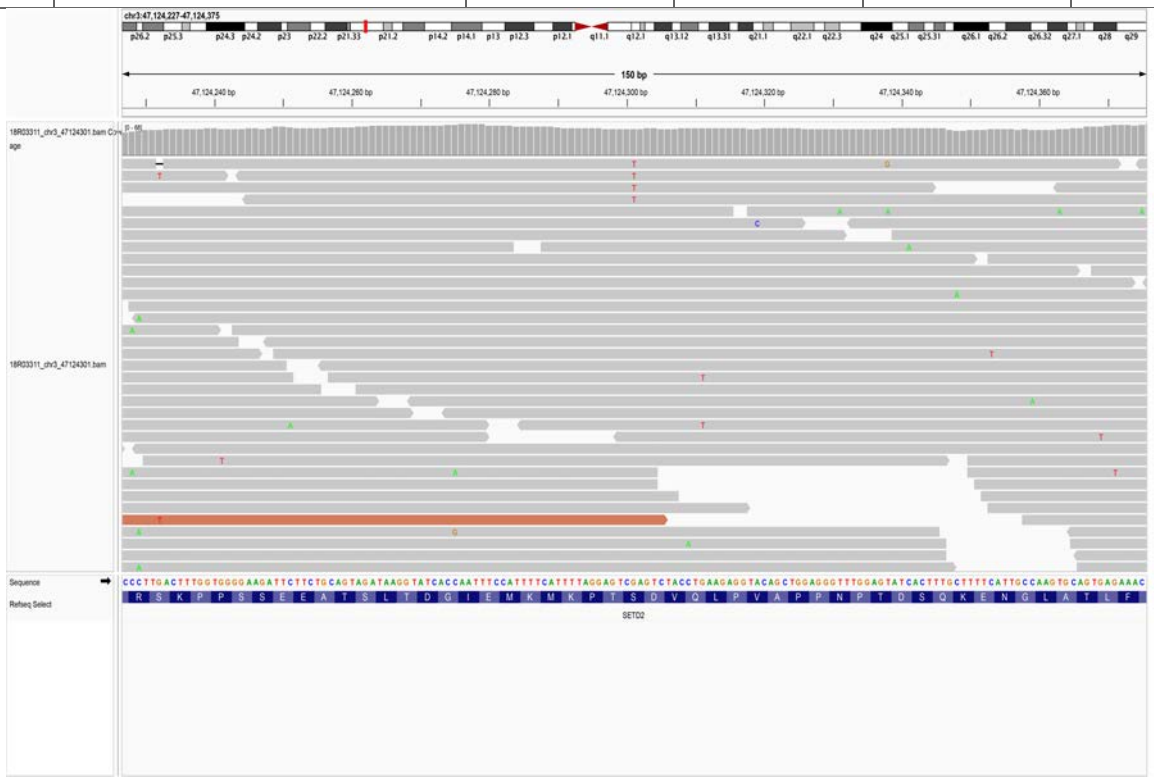
45.15. chr3_47123438_G/A

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

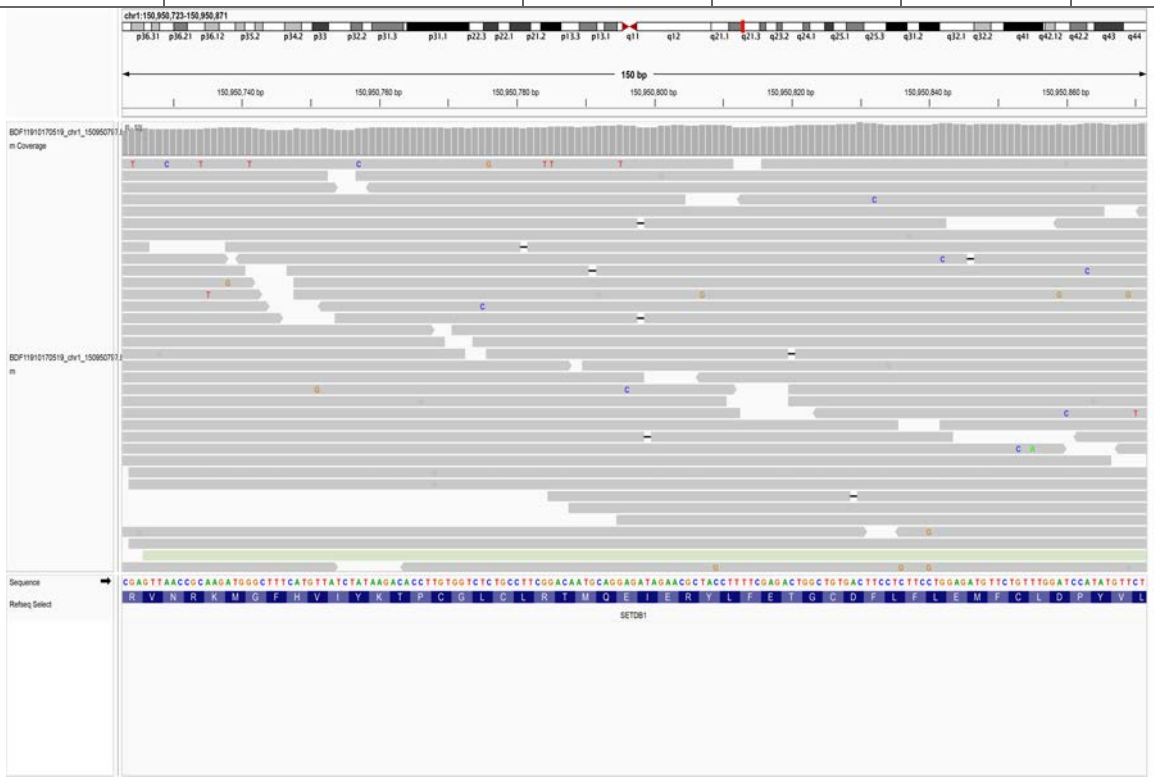
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R03311	chr3_47124301_G/T	47	4	*SETD2*	stop_gained



46. *SETDB1*

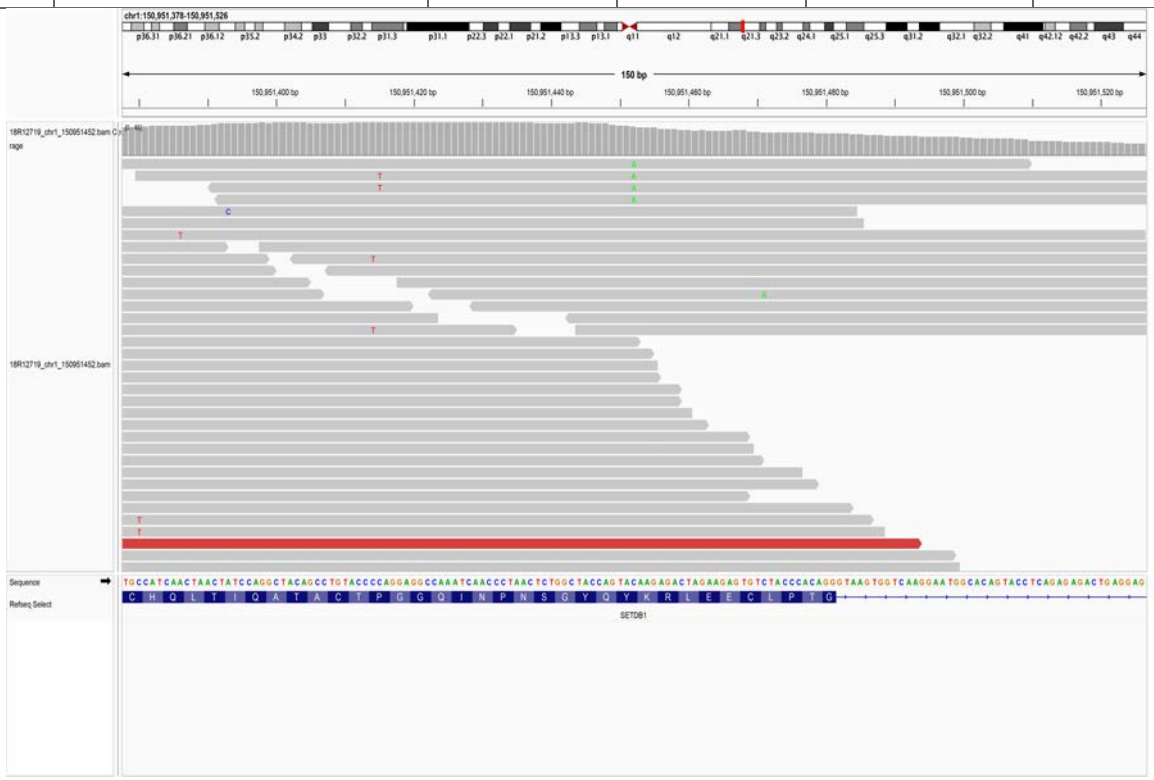
46.1. chr1_150950798_A/-

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



46.2. chr1_150951452_C/A

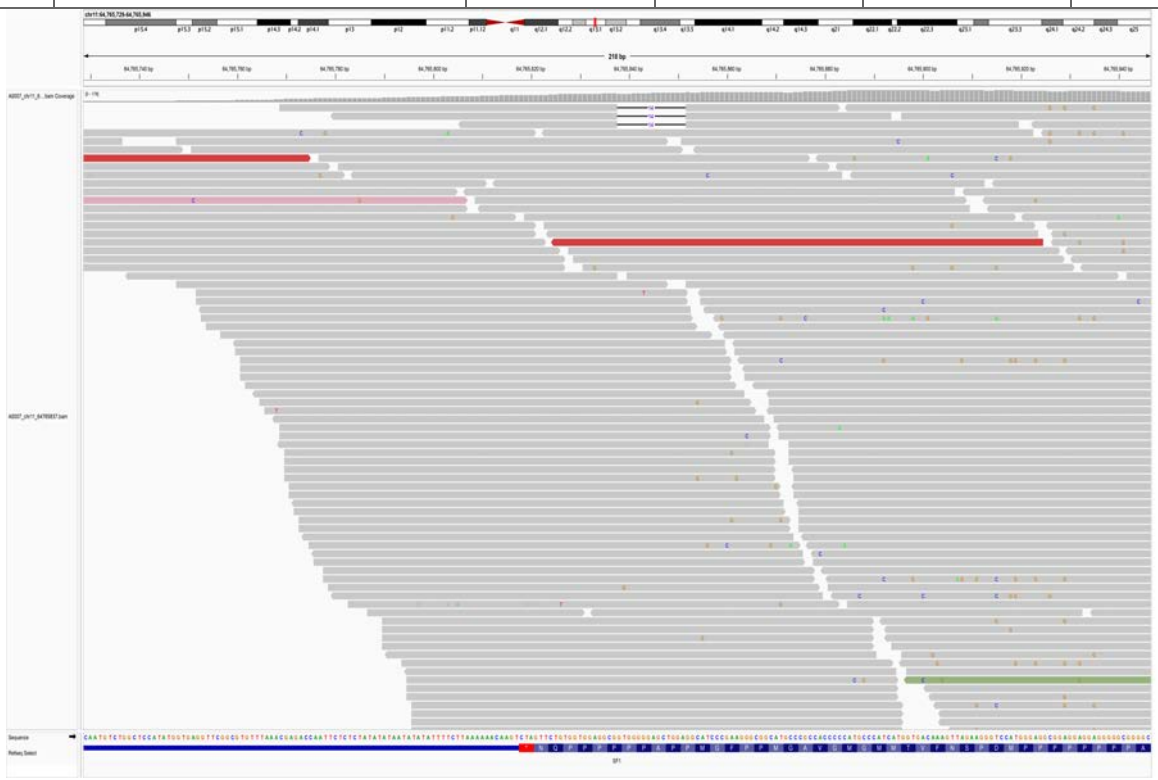
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12719	chr1_150951452_C/A	52	4	*SETDB1*	stop_gained



47. *SF1*

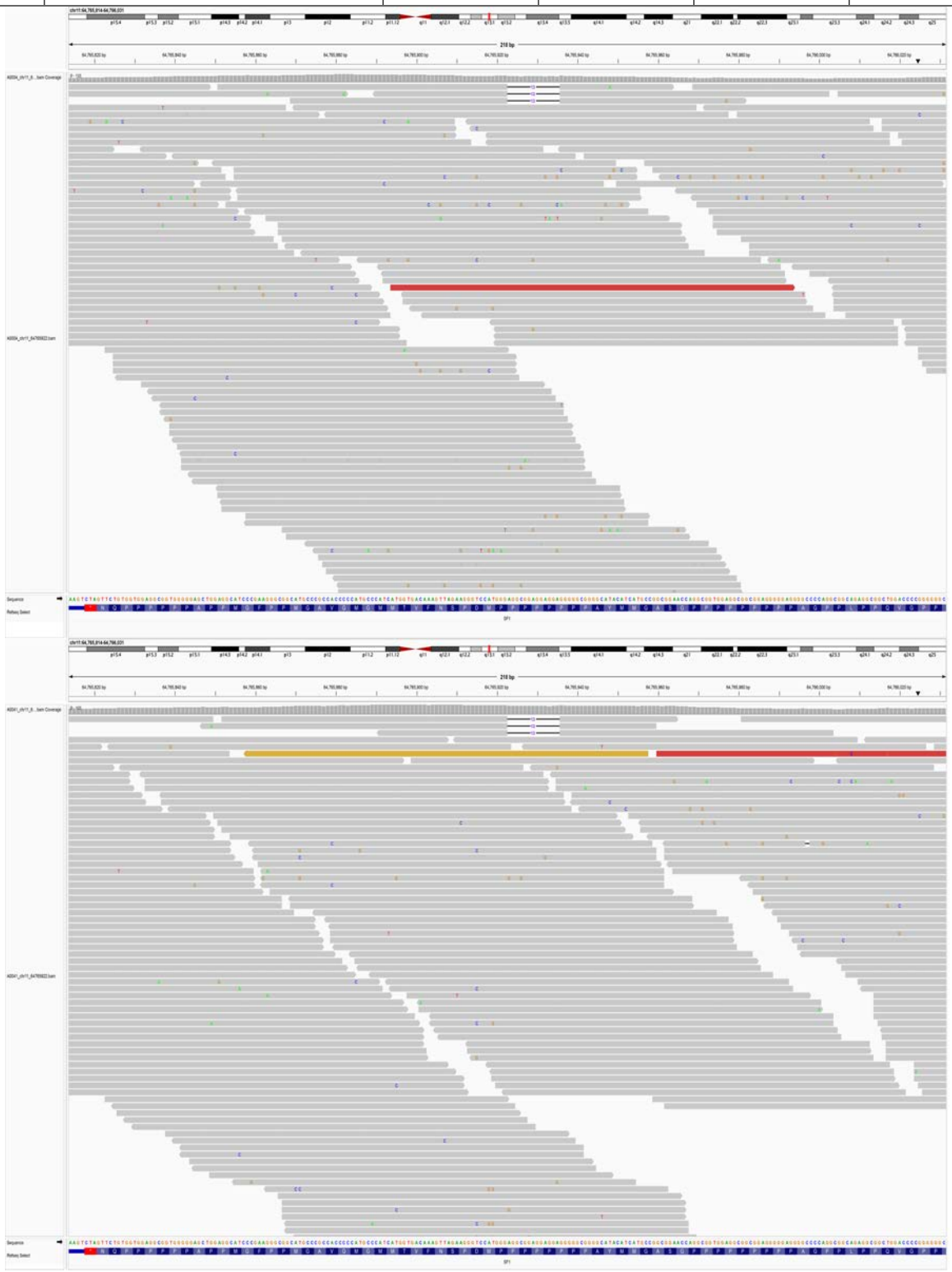
47.1. chr11_64765838_GTGGGGGAGCTGGA/-

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



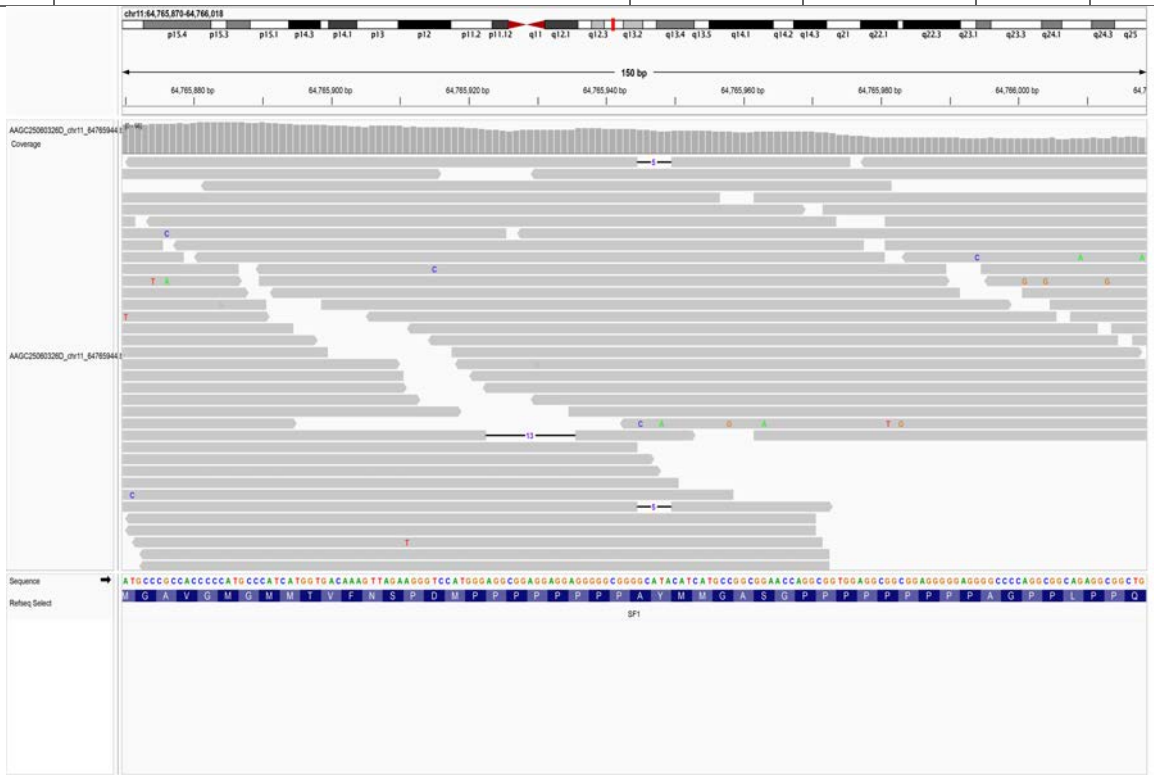
47.2. chr11_64765923_AGGCGGAGGAGGA/-

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



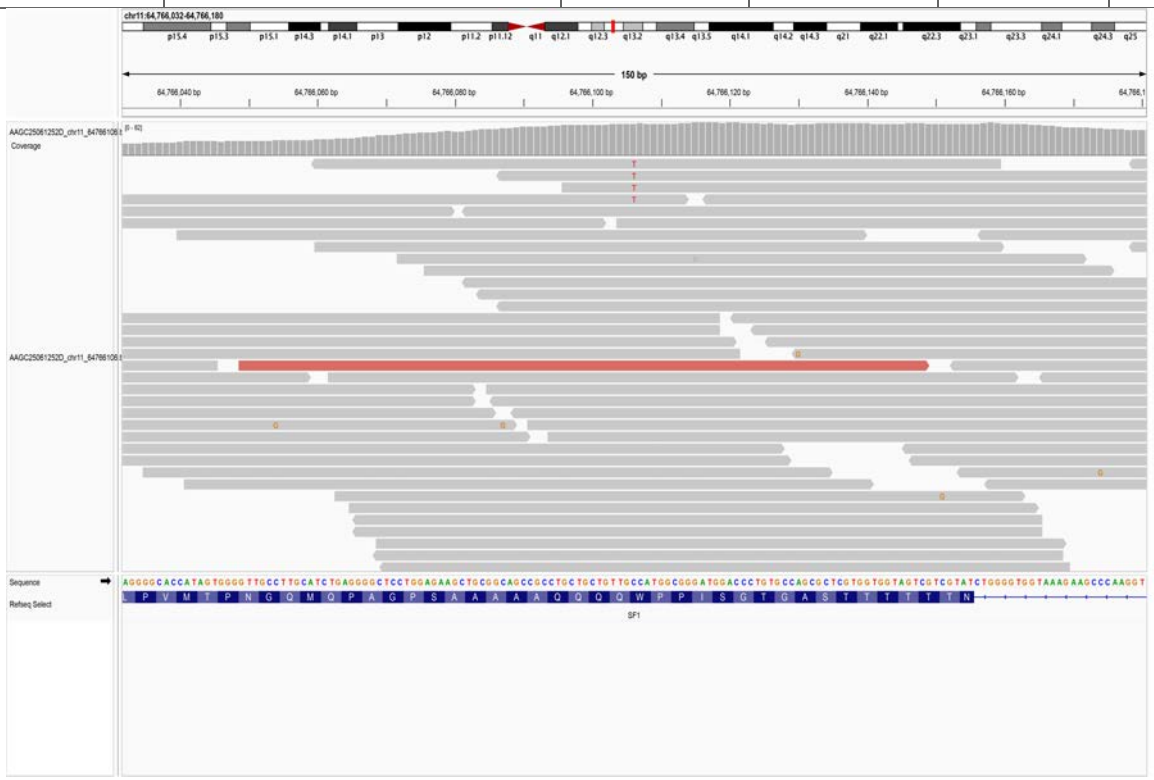
47.3. chr11_64765945_GCATA/-

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



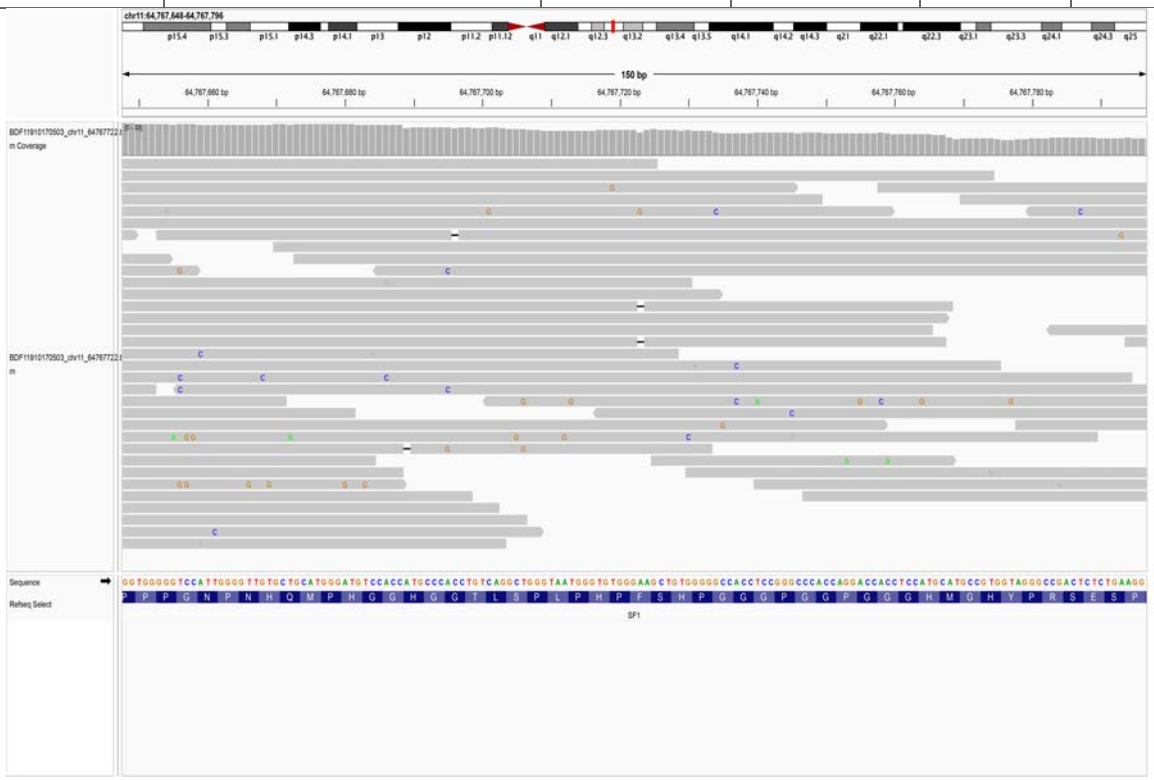
47.4. chr11_64766106_C/T

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



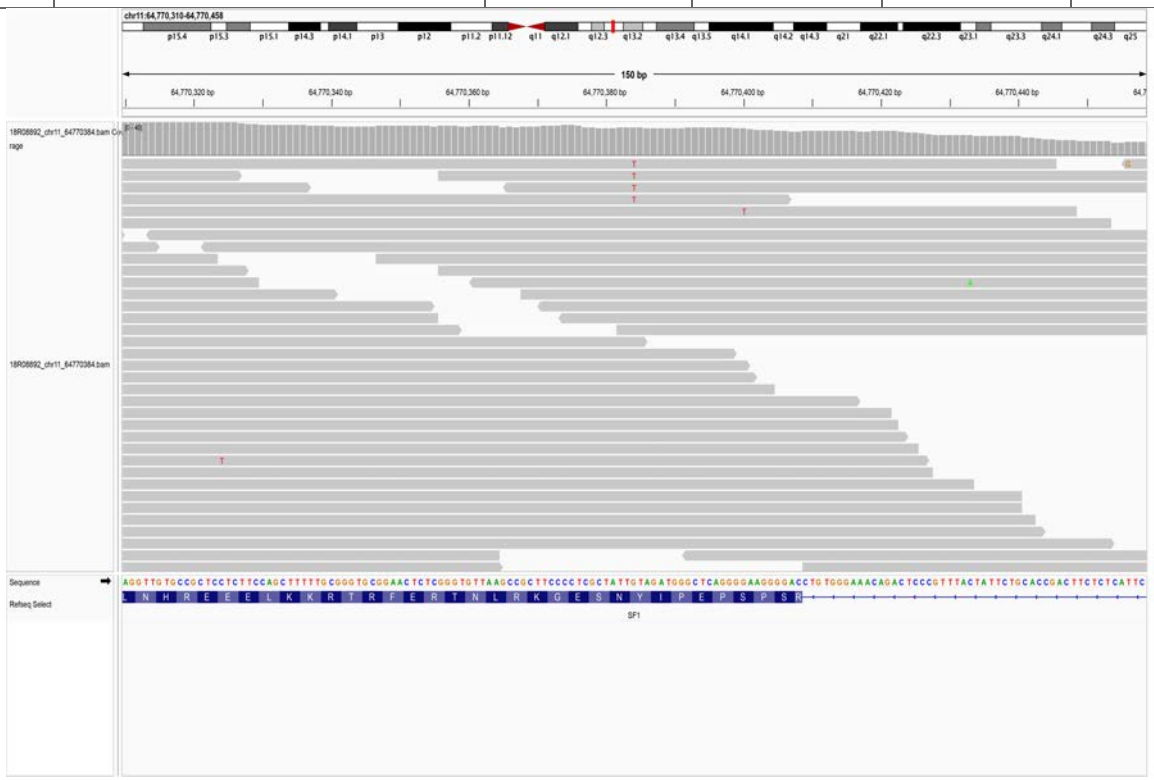
47.5. chr11_64767723_A/-

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



47.6. chr11_64770384_G/T

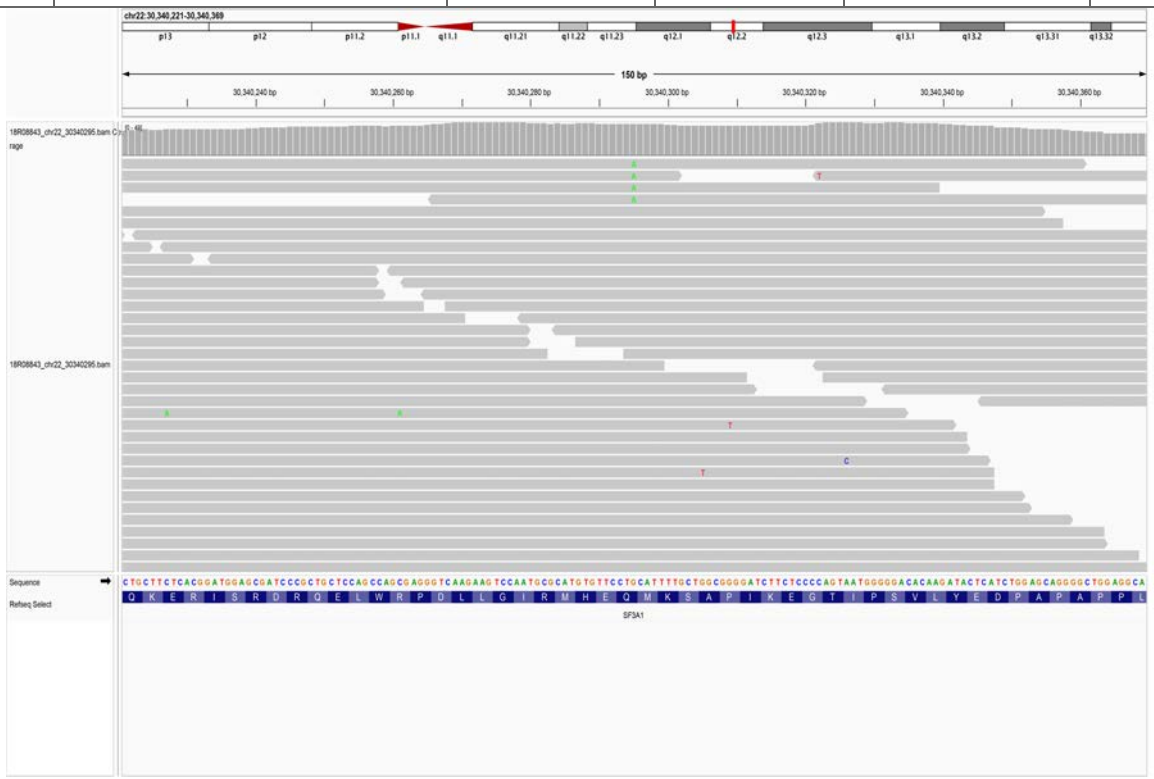
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08892	chr11_64770384_G/T	28	4	*SF1*	stop_gained



48. *SF3A1*

48.1. chr22_30340295_G/A

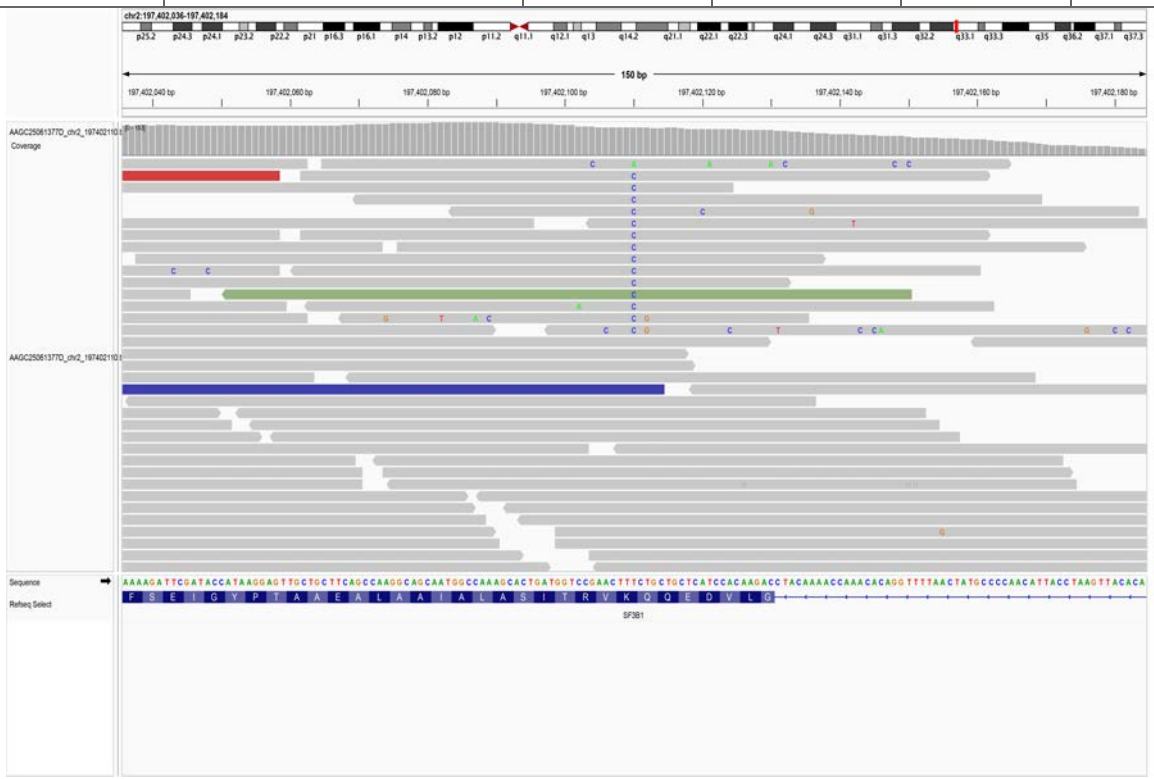
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08843	chr22_30340295_G/A	40	4	*SF3A1*	stop_gained



49. *SF3B1*

49.1. chr2_197402110_T/C

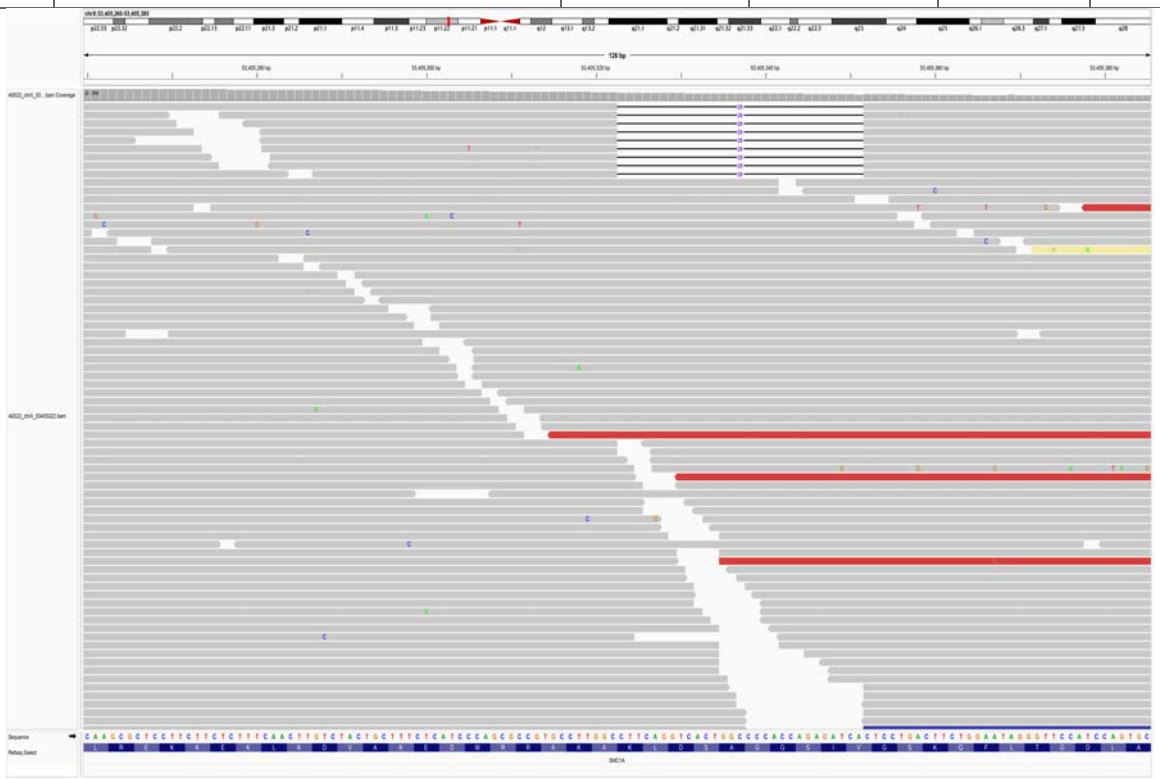
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061377D	chr2_197402110_T/C	111	13	*SF3B1*	missense_variant

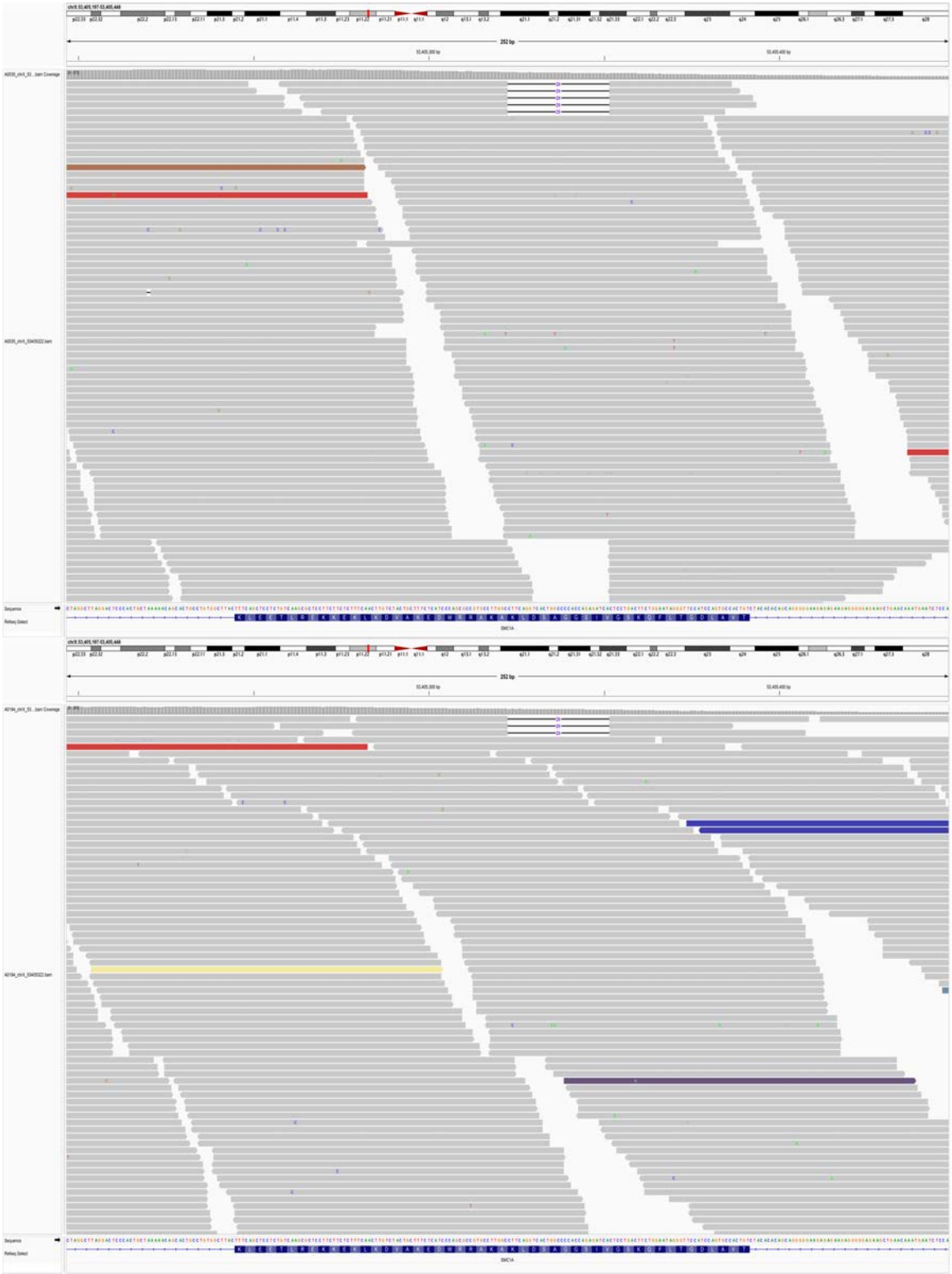


50. *SMC1A*

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

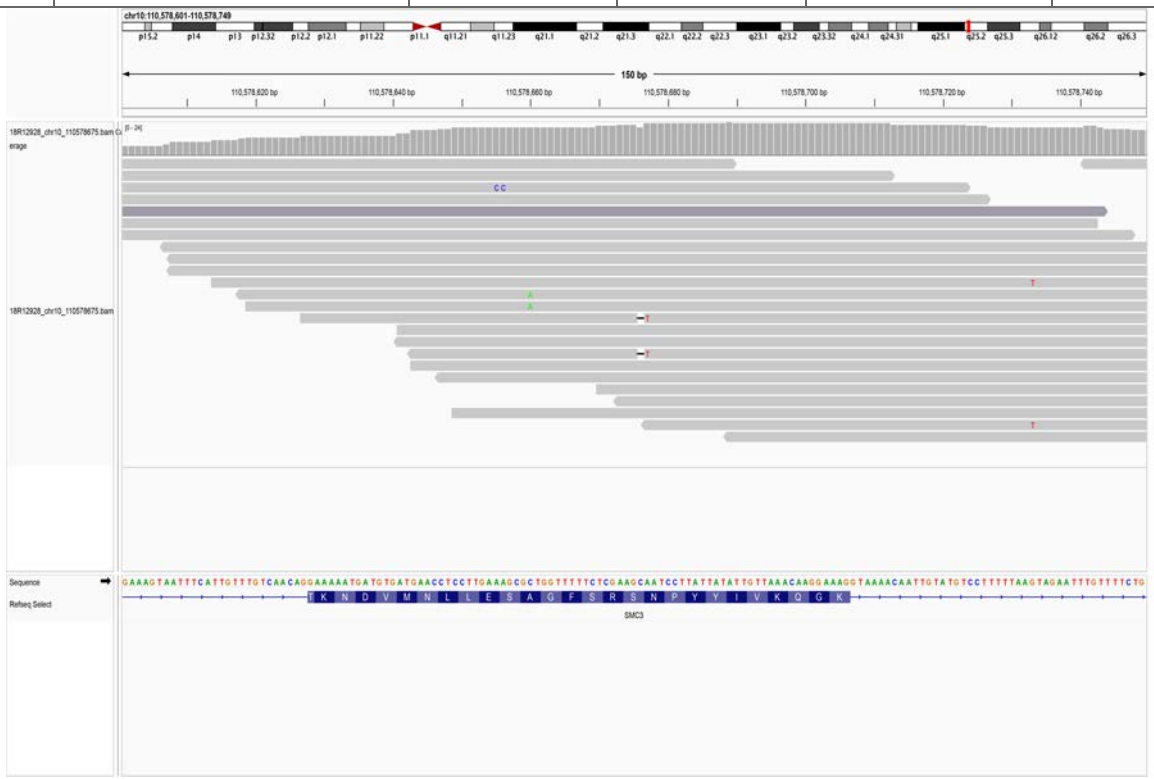




51. *SMC3*

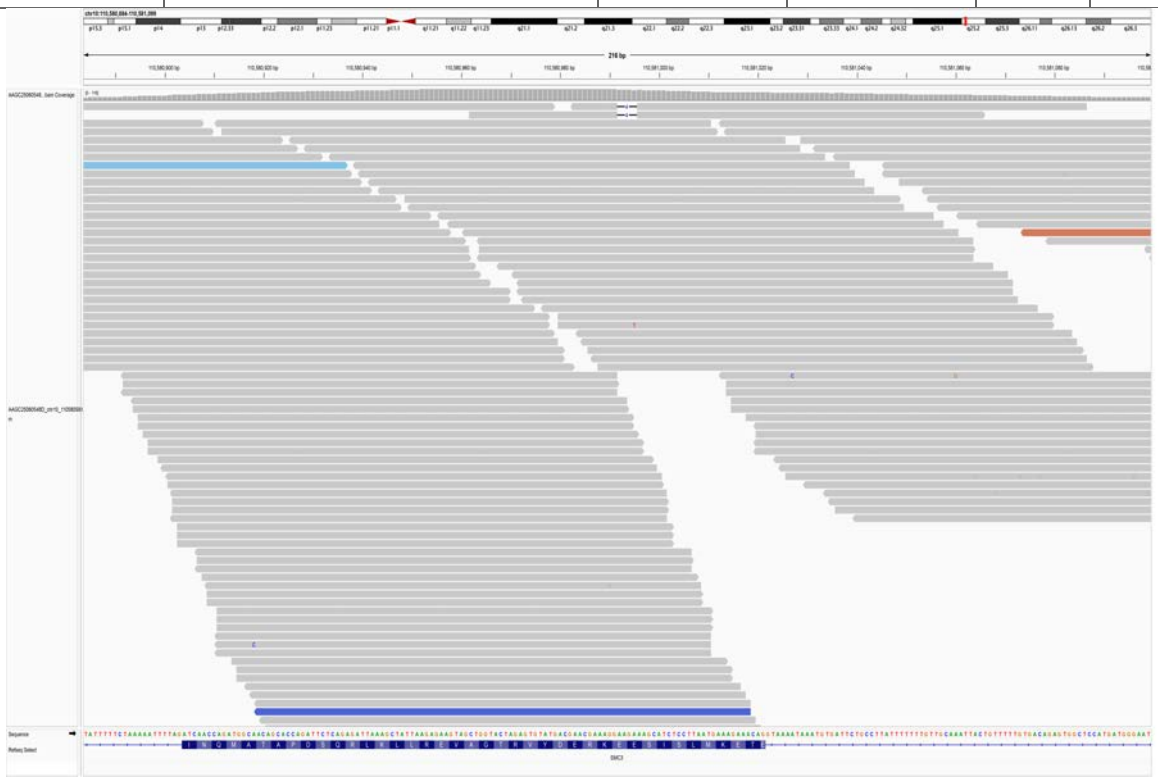
51.1. chr10_110578676_C/-

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



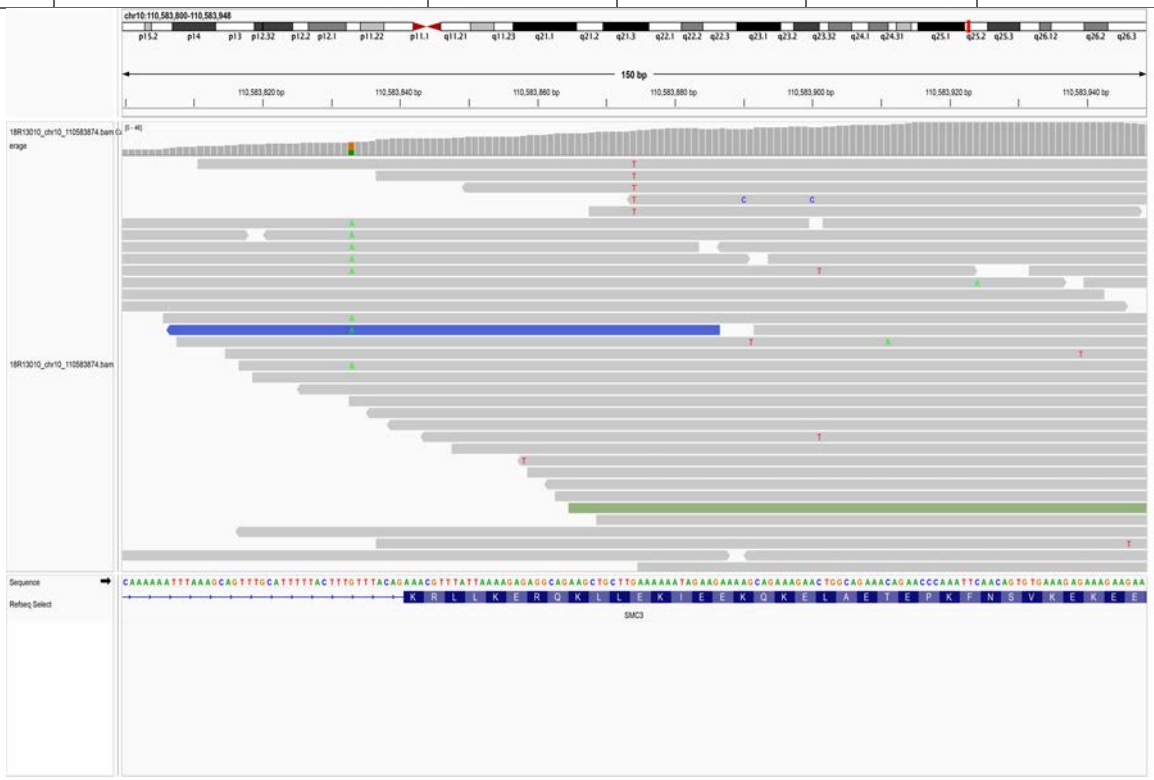
51.2. chr10_110580992_AAGA/-

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



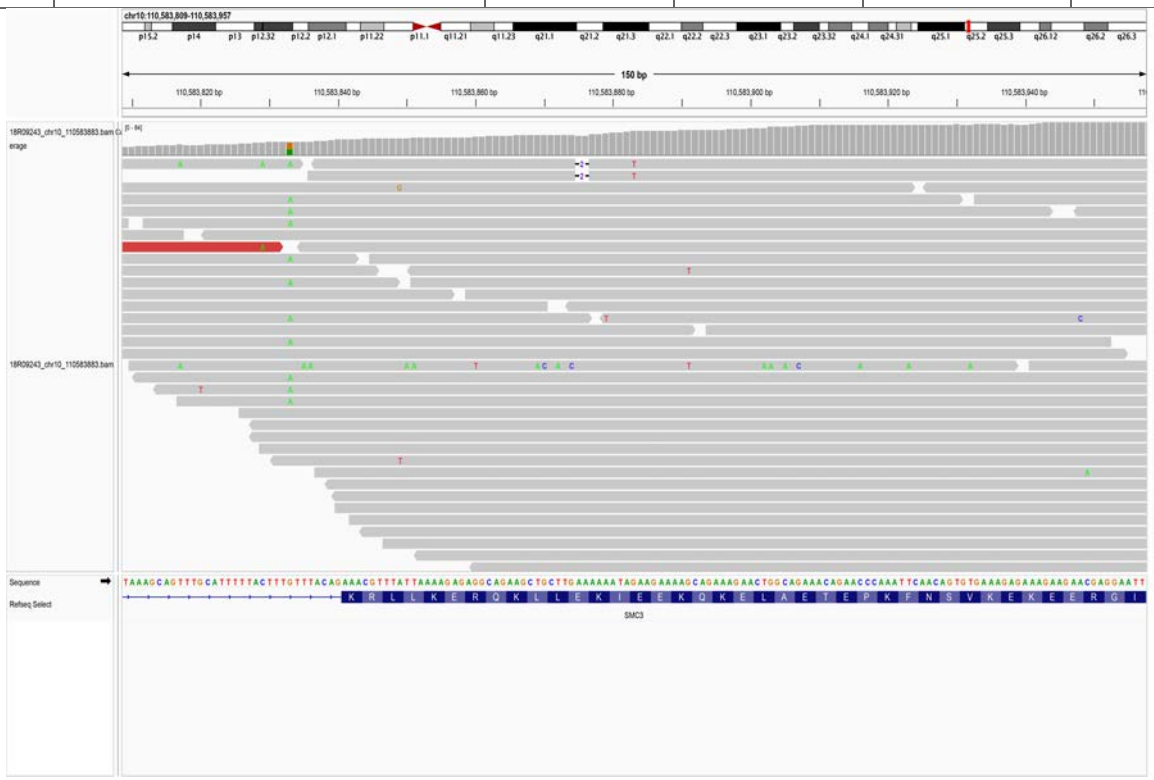
51.3. chr10_110583874_G/T

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



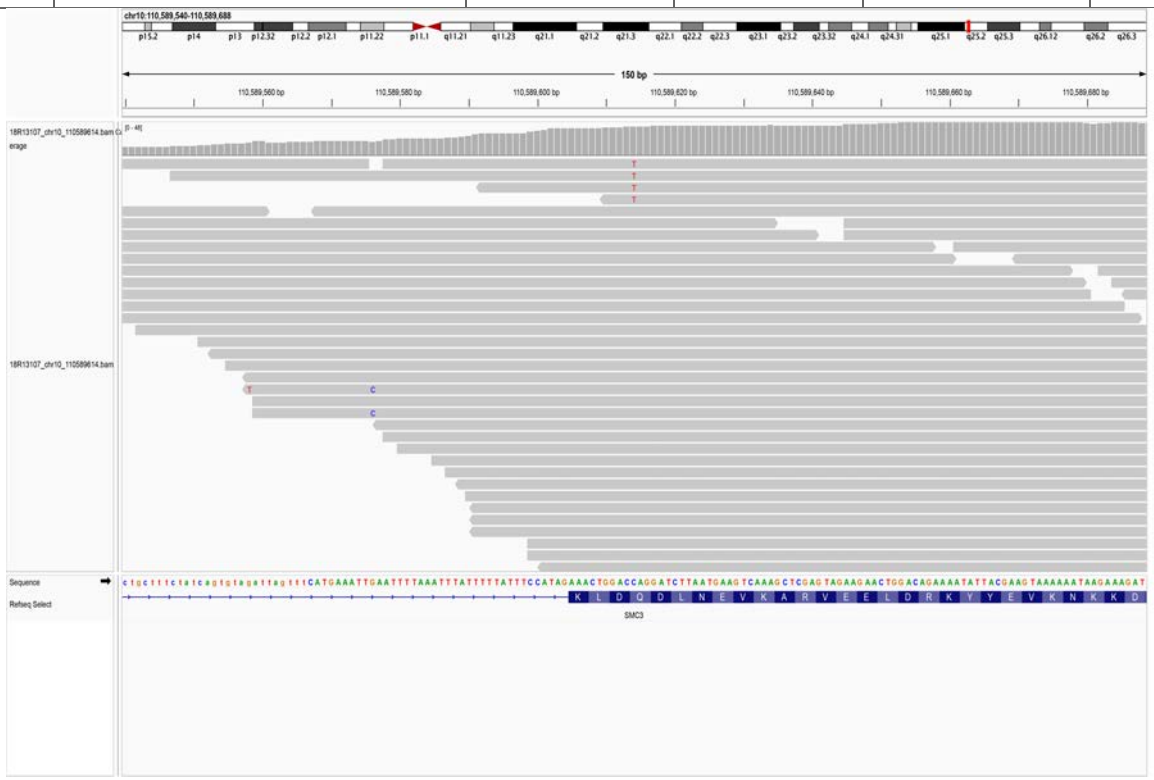
51.4. chr10_110583883_G/T

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



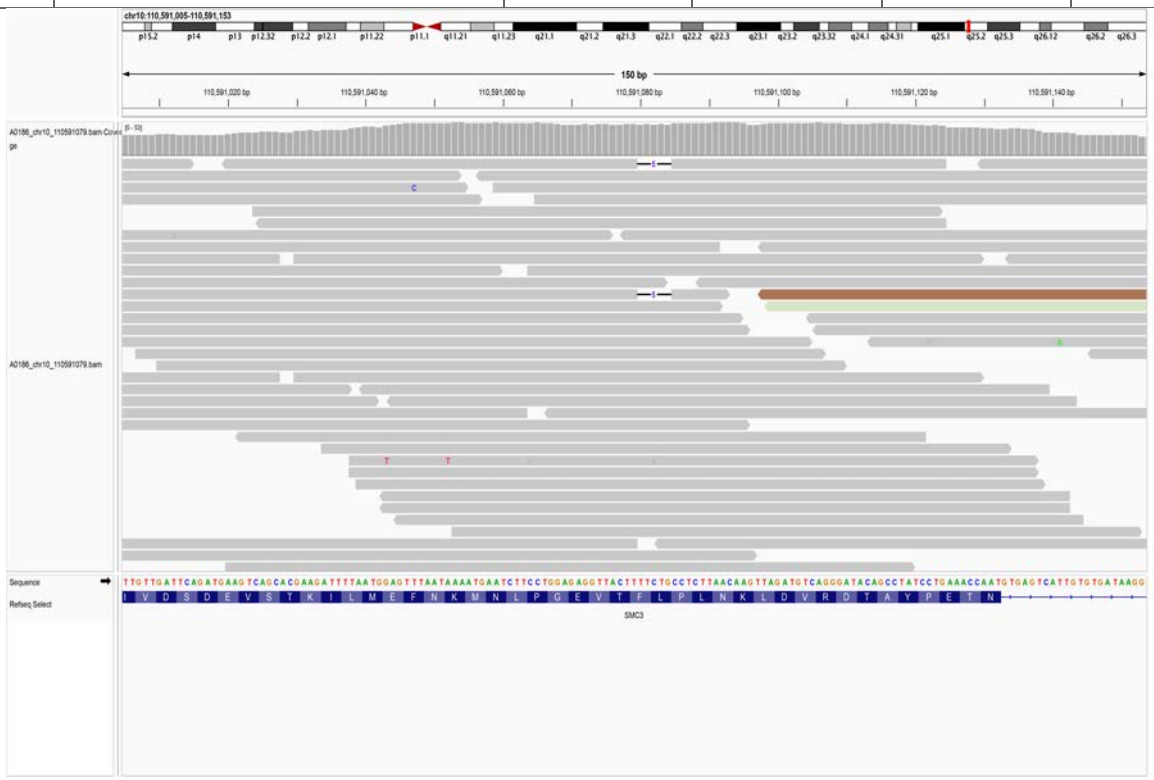
51.5. chr10_110589614_C/T

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



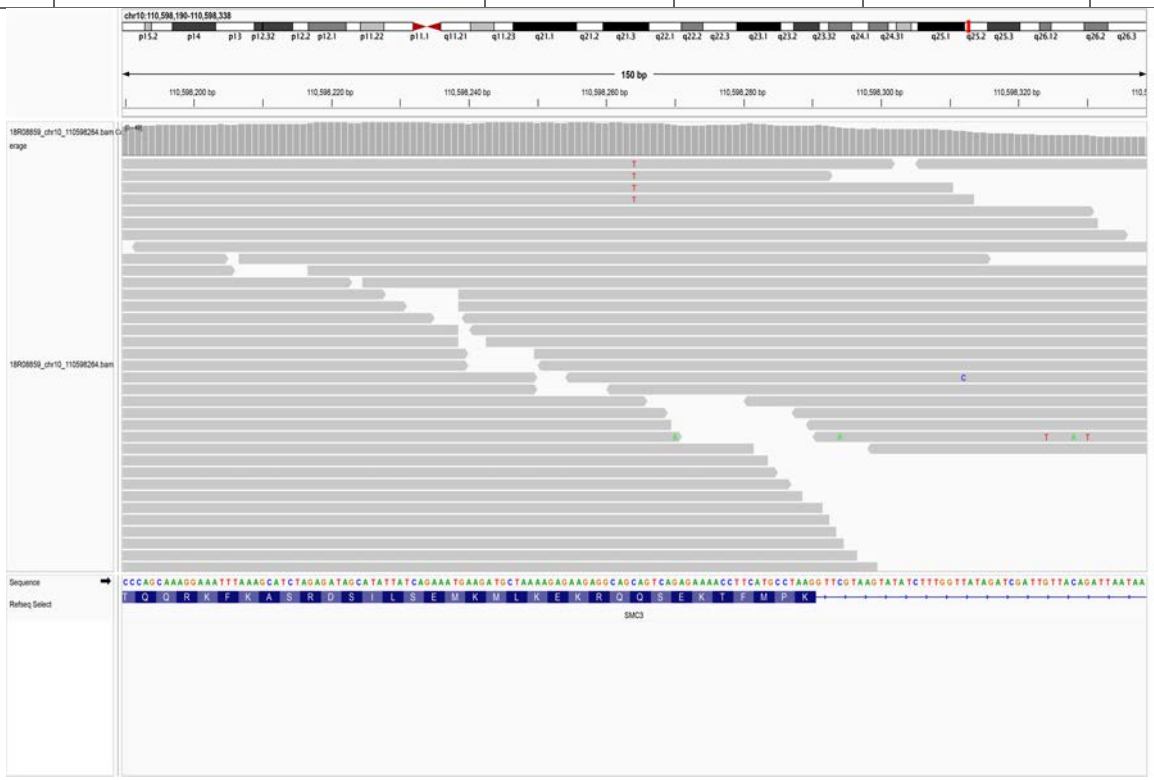
51.6. chr10_110591080_TTCTG/-

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



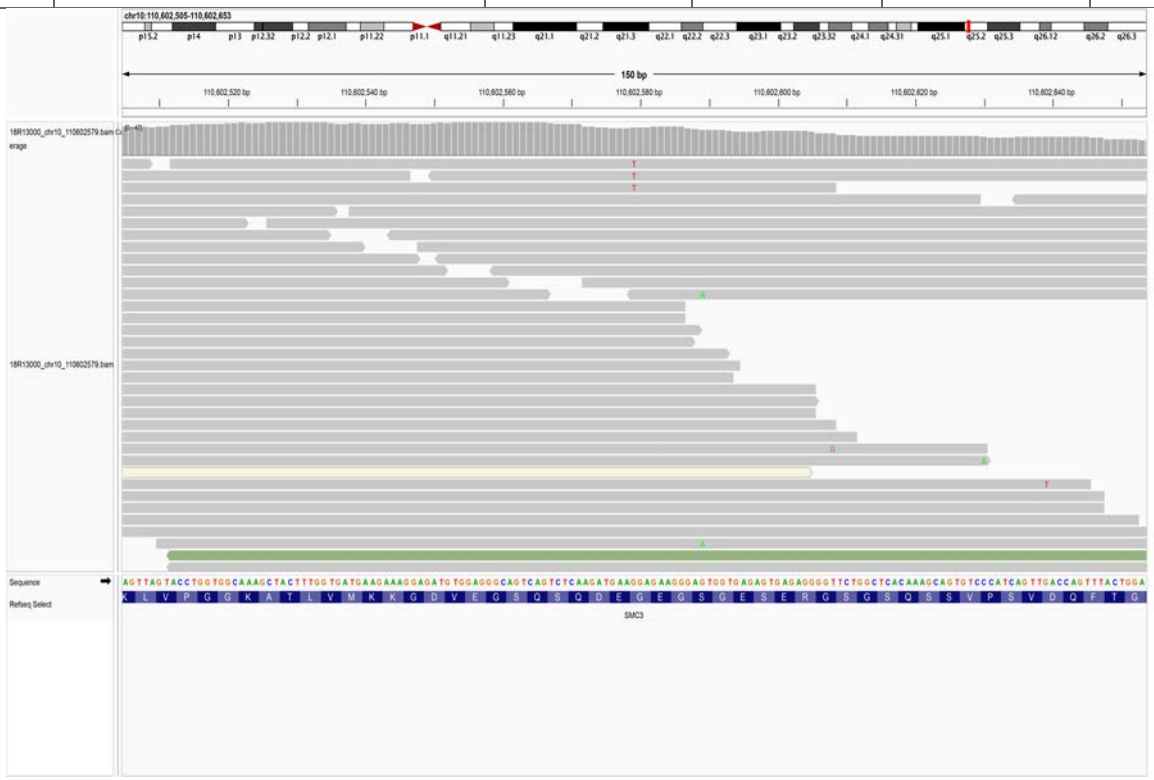
51.7. chr10_110598264_C/T

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



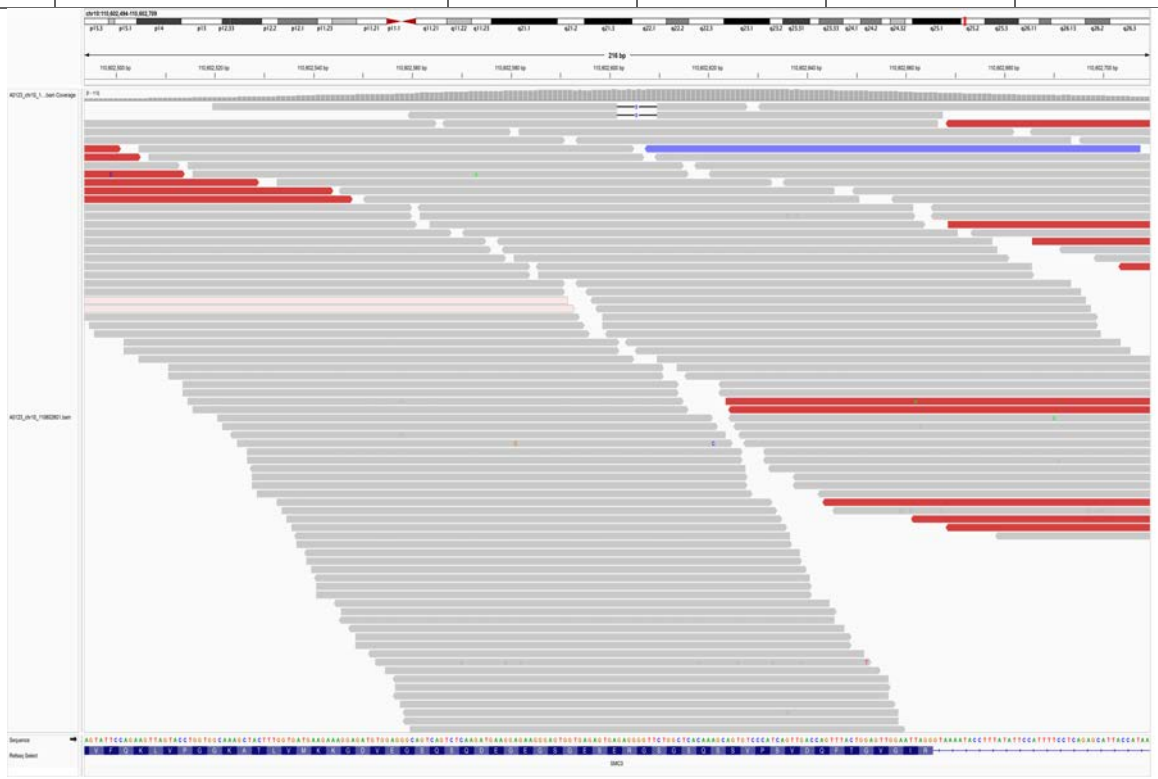
51.8. chr10_110602579_G/T

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



51.9. chr10_110602602_GAGGGGTT/-

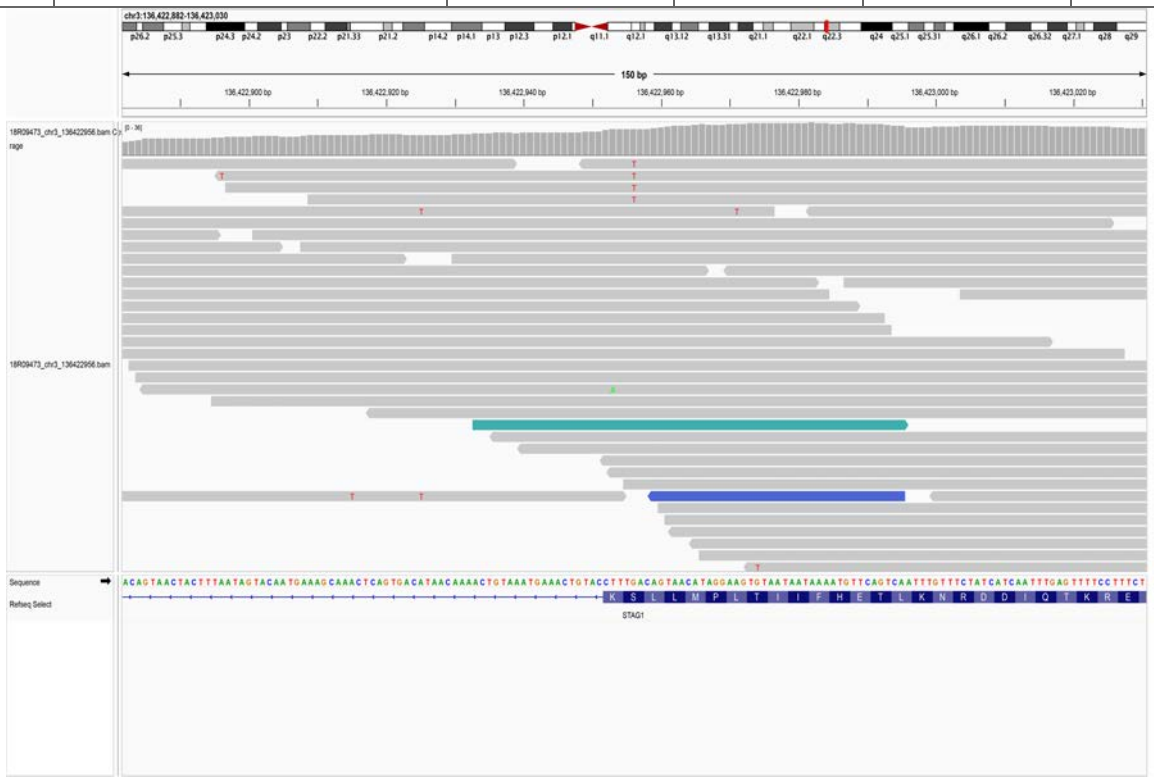
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0123	chr10_110602602_GAGGGGTT/-	111	2	*SMC3*	frameshift_variant



52. *STAG1*

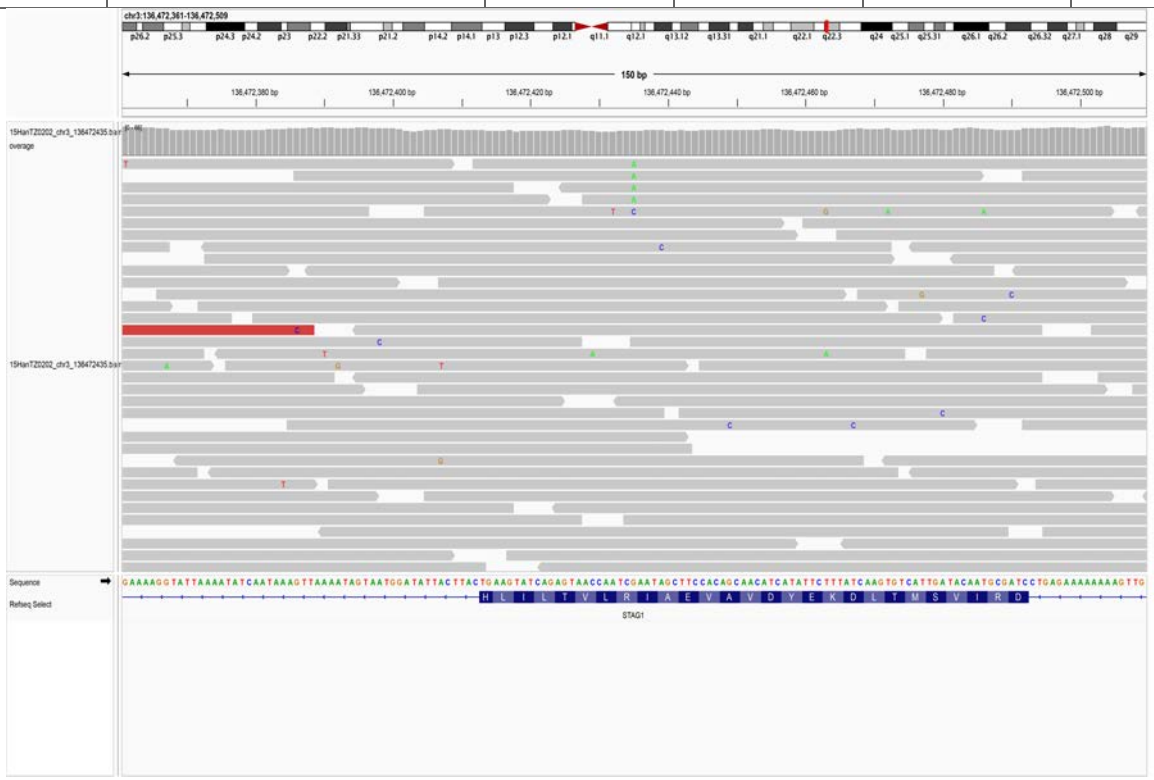
52.1. chr3_136422956_G/T

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



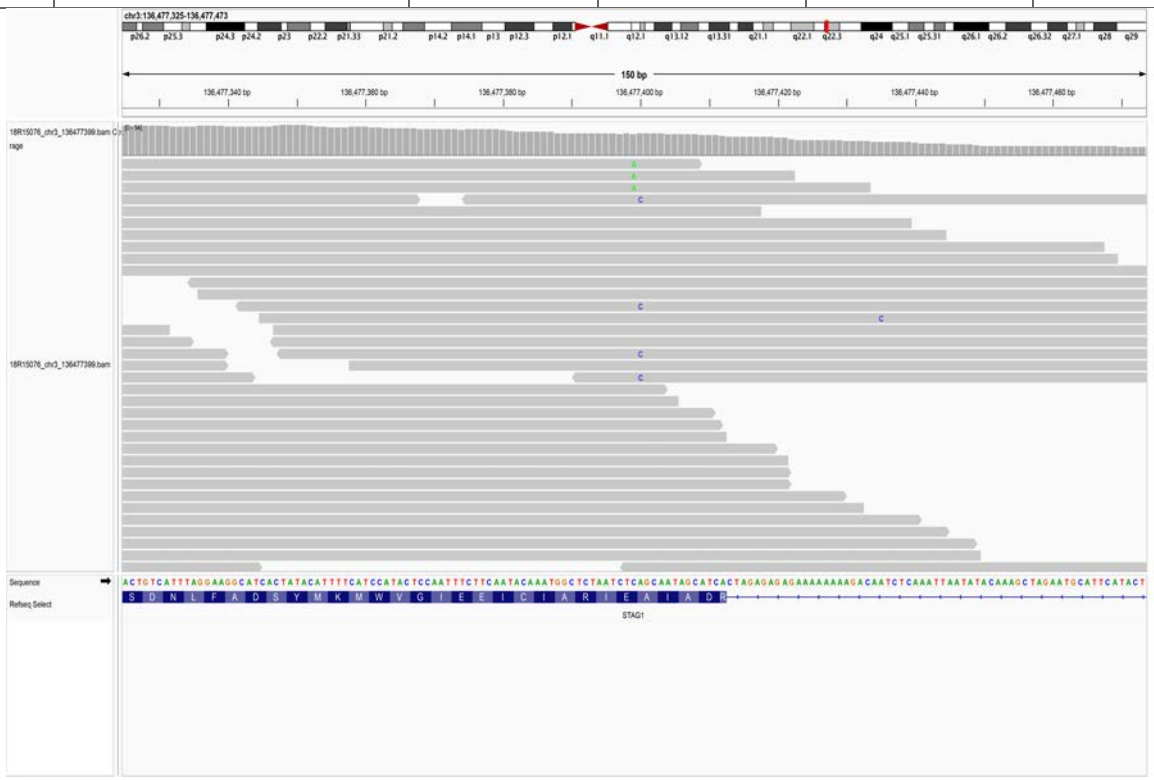
52.2. chr3_136472435_G/A

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



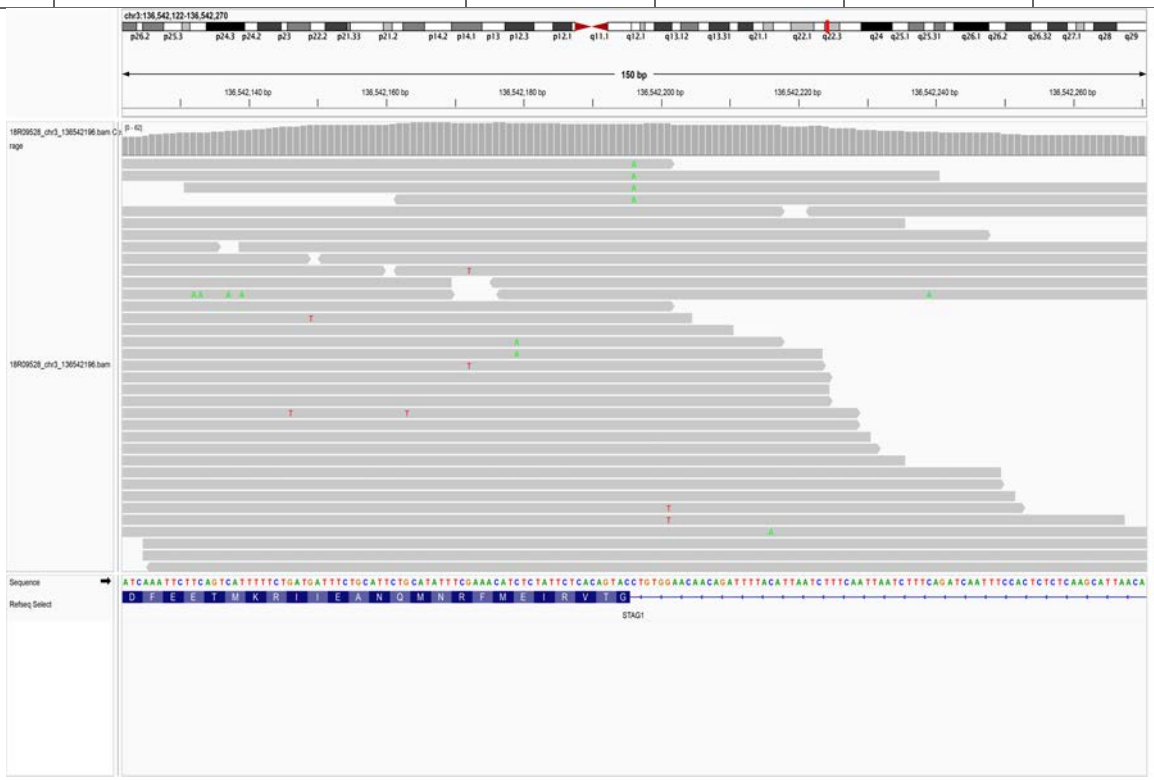
52.3. chr3_136477399_C/A

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



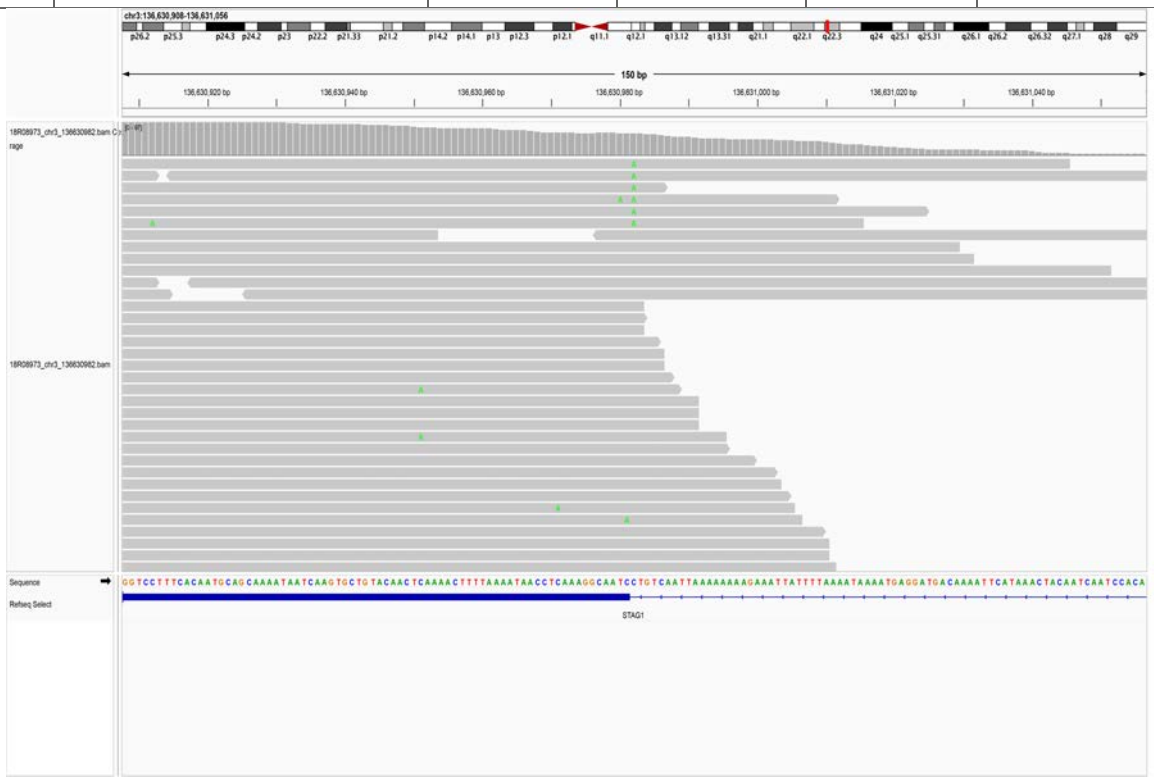
52.4. chr3_136542196_C/A

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

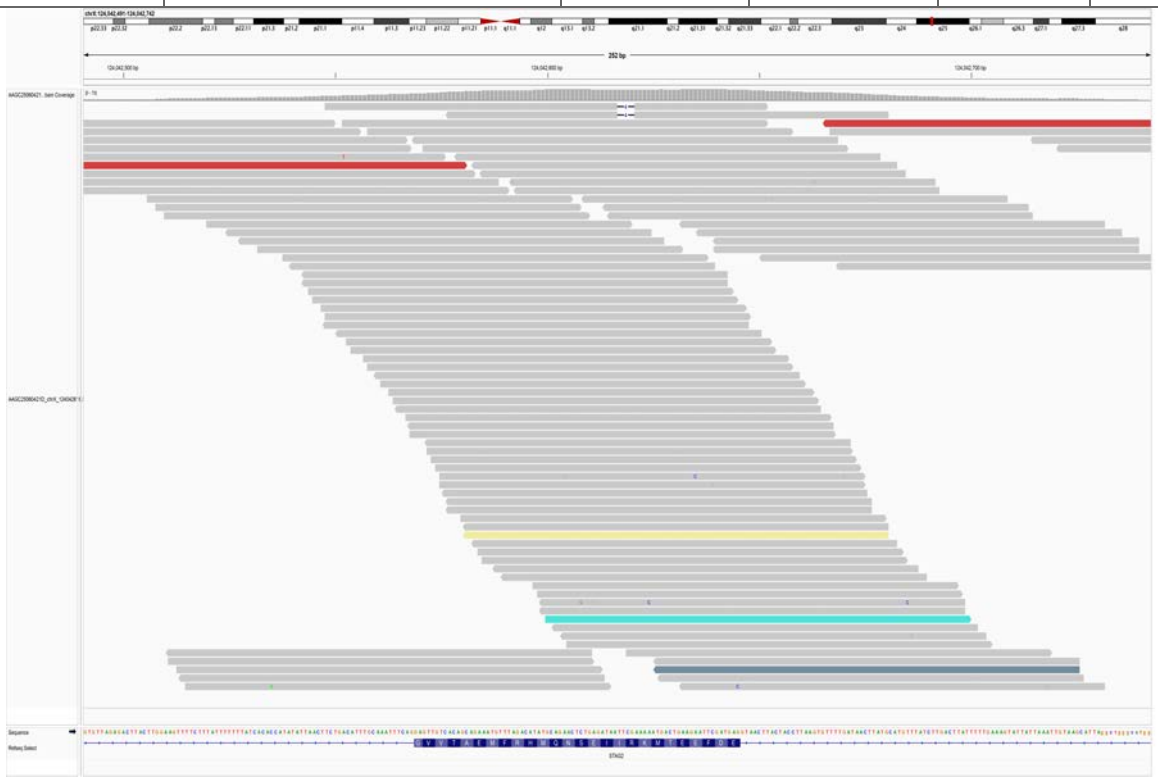
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08973	chr3_136630982_C/A	54	6	*STAG1*	splice_acceptor_variant



53. *STAG2*

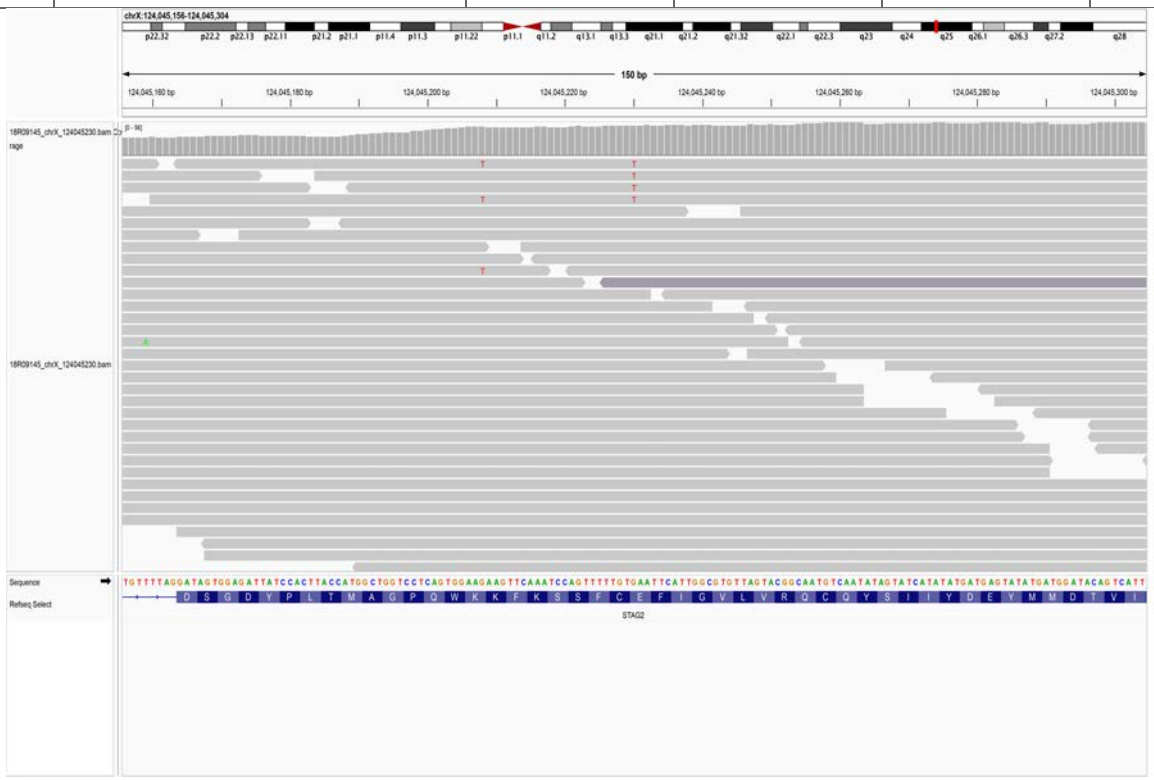
53.1. chrX_124042617_TTCG/-

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



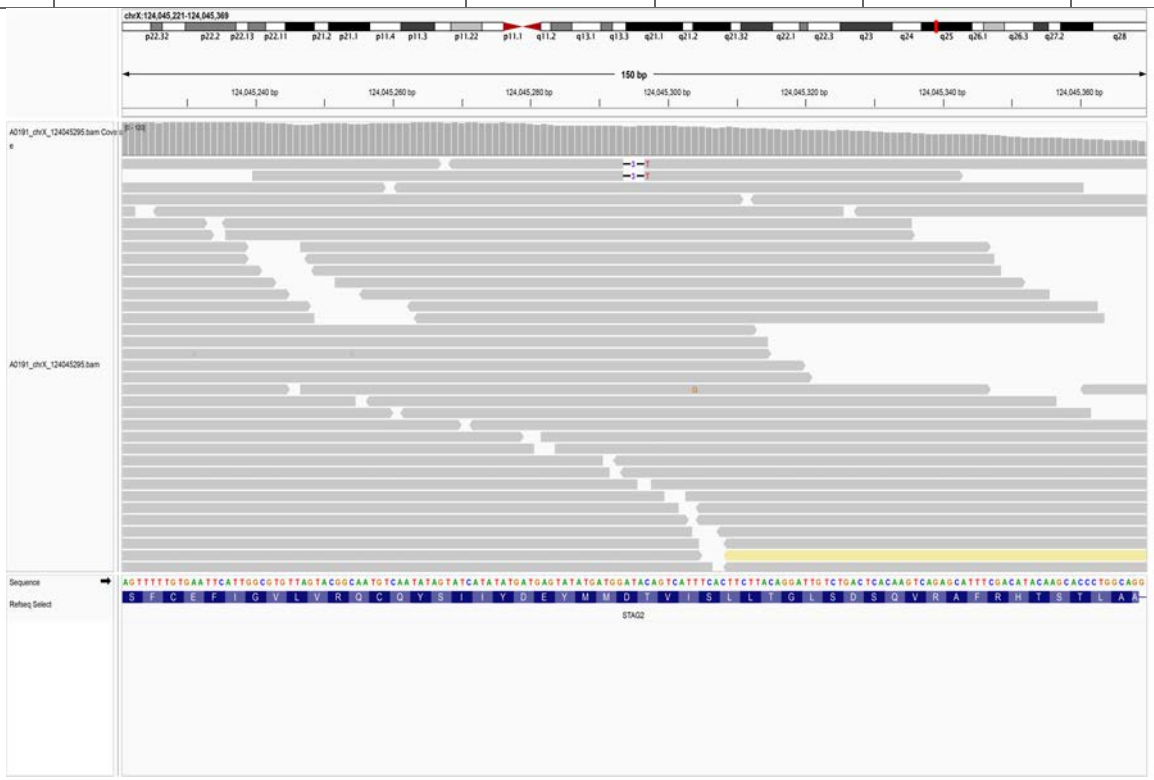
53.2. chrX_124045230_G/T

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



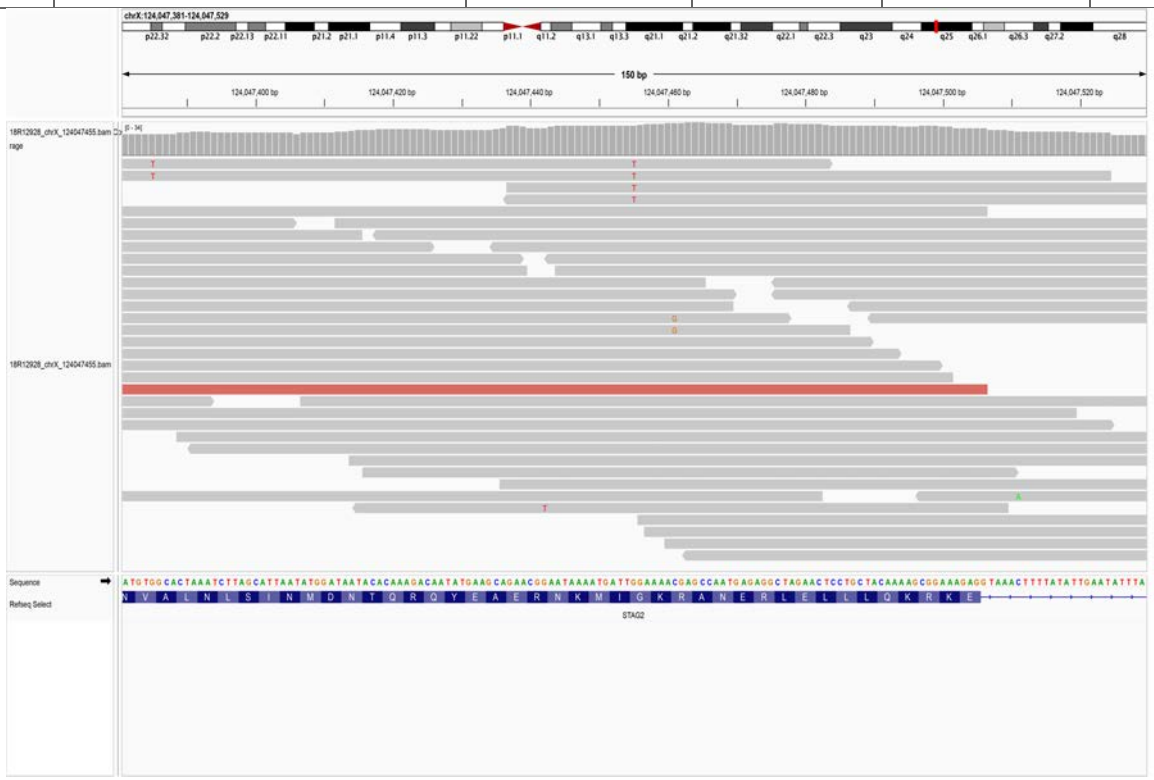
53.3. chrX_124045296_AC/-

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



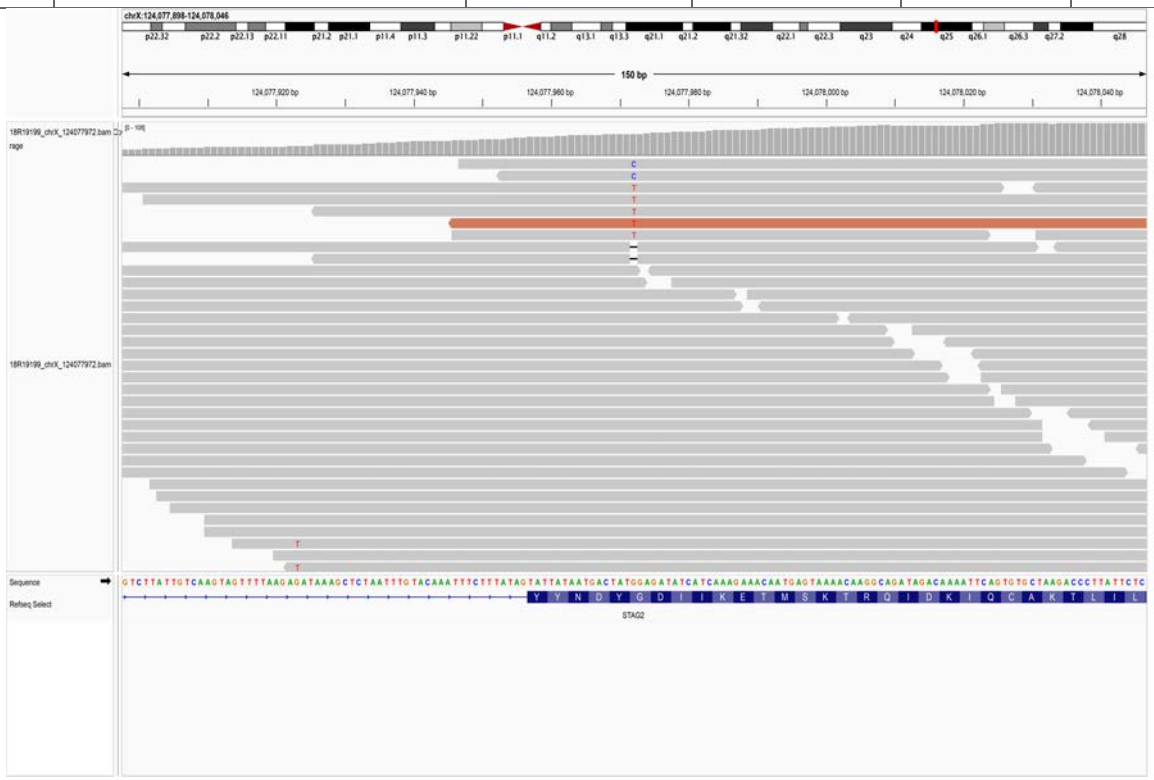
53.4. chrX_124047455_G/T

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



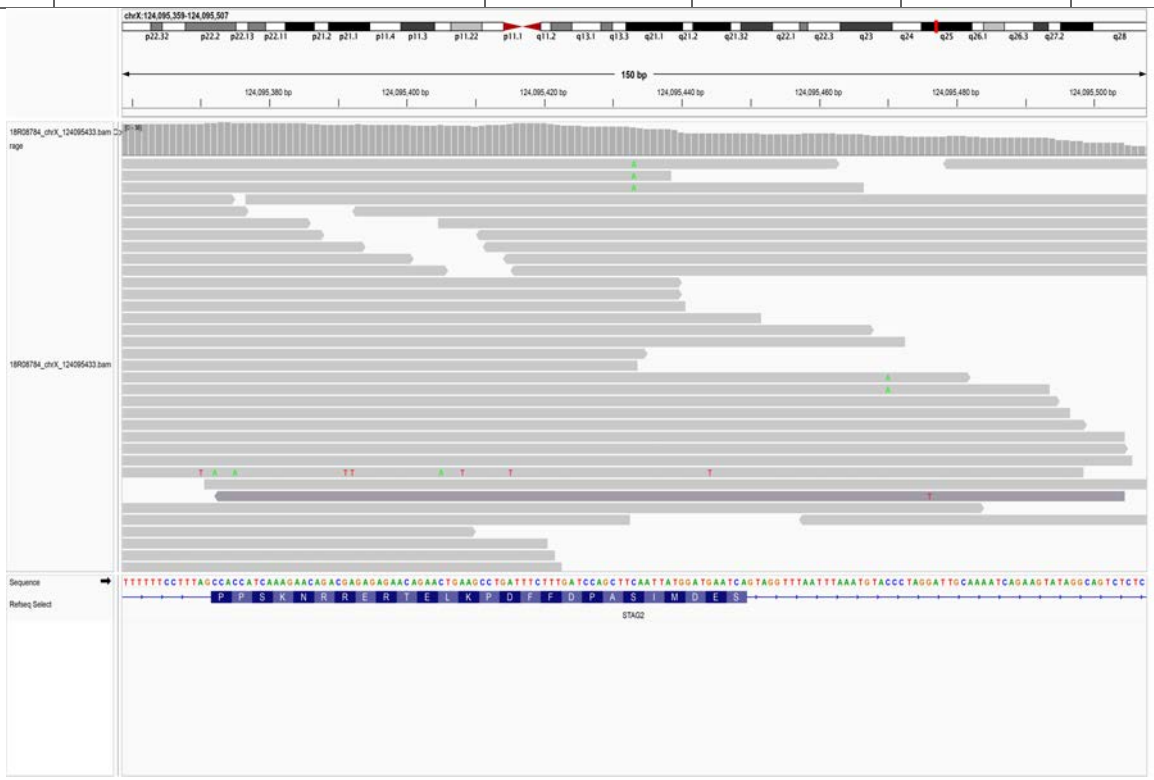
53.5. chrX_124077972_G/T

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

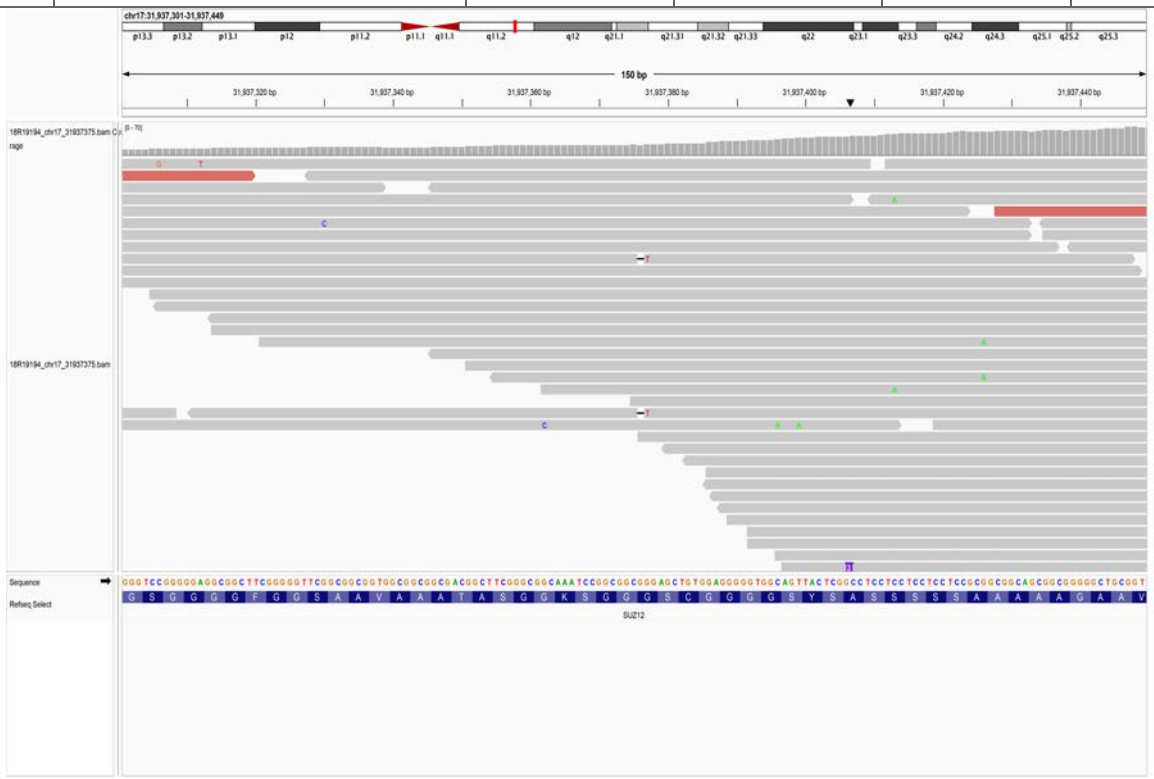
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08784	chrX_124095433_C/A	27	3	*STAG2*	stop_gained



54. *SUZ12*

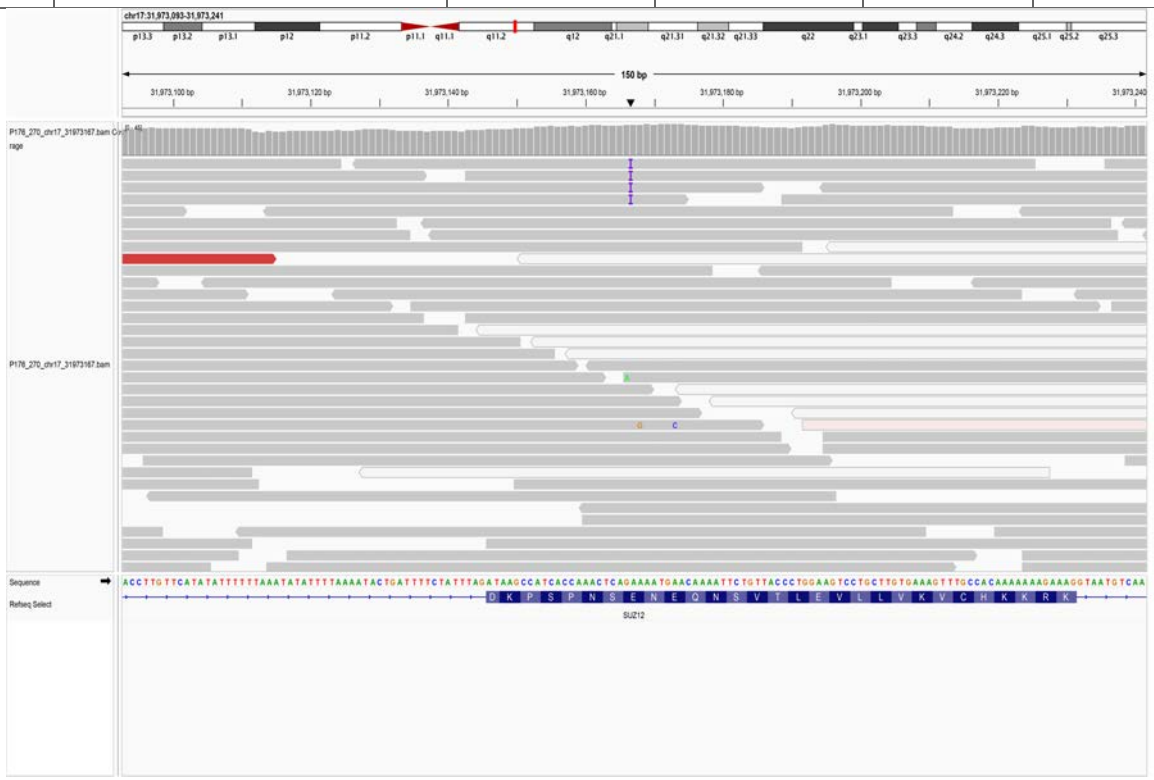
54.1. chr17_31937376_G/-

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



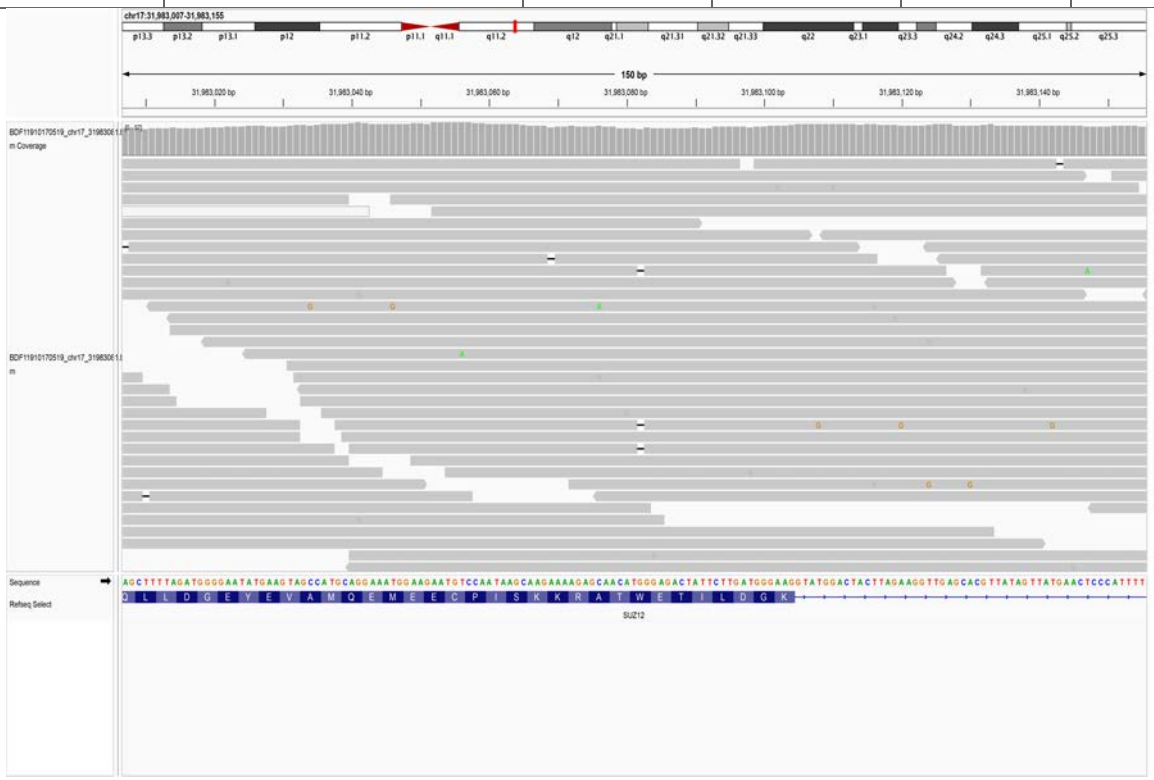
54.2. chr17_31973167_-/A

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



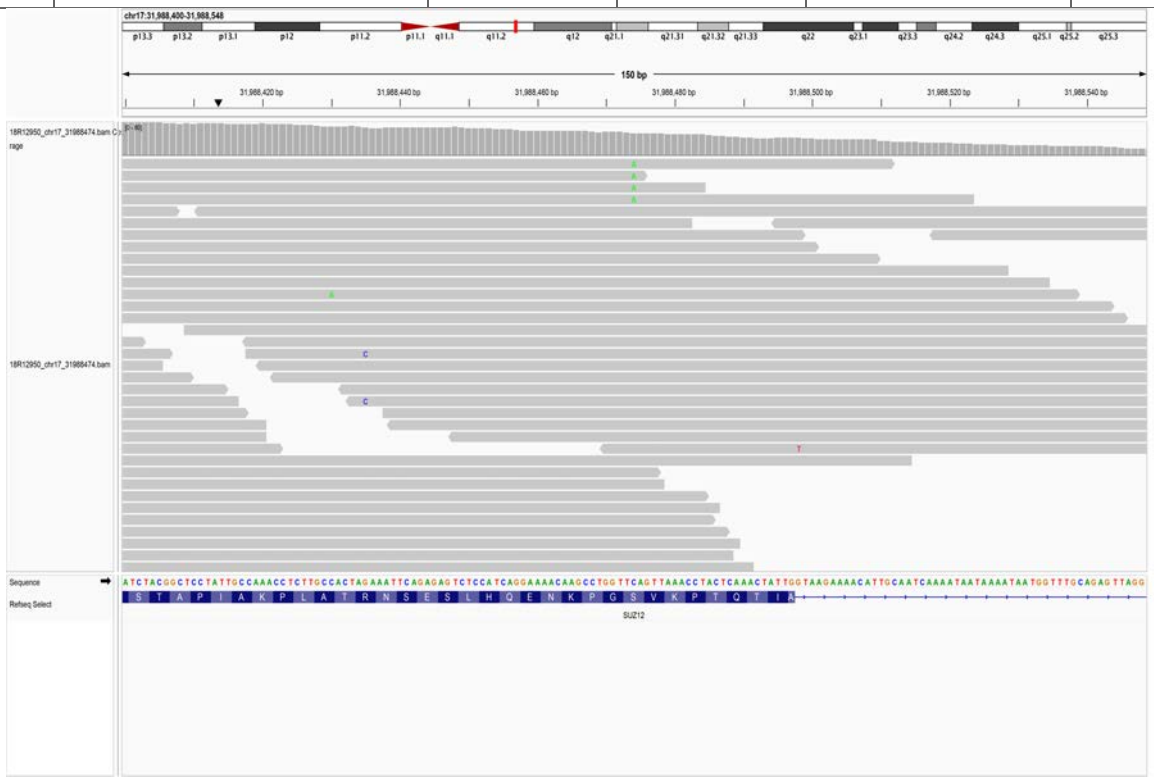
54.3. chr17_31983082_G/-

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



54.4. chr17_31988474_C/A

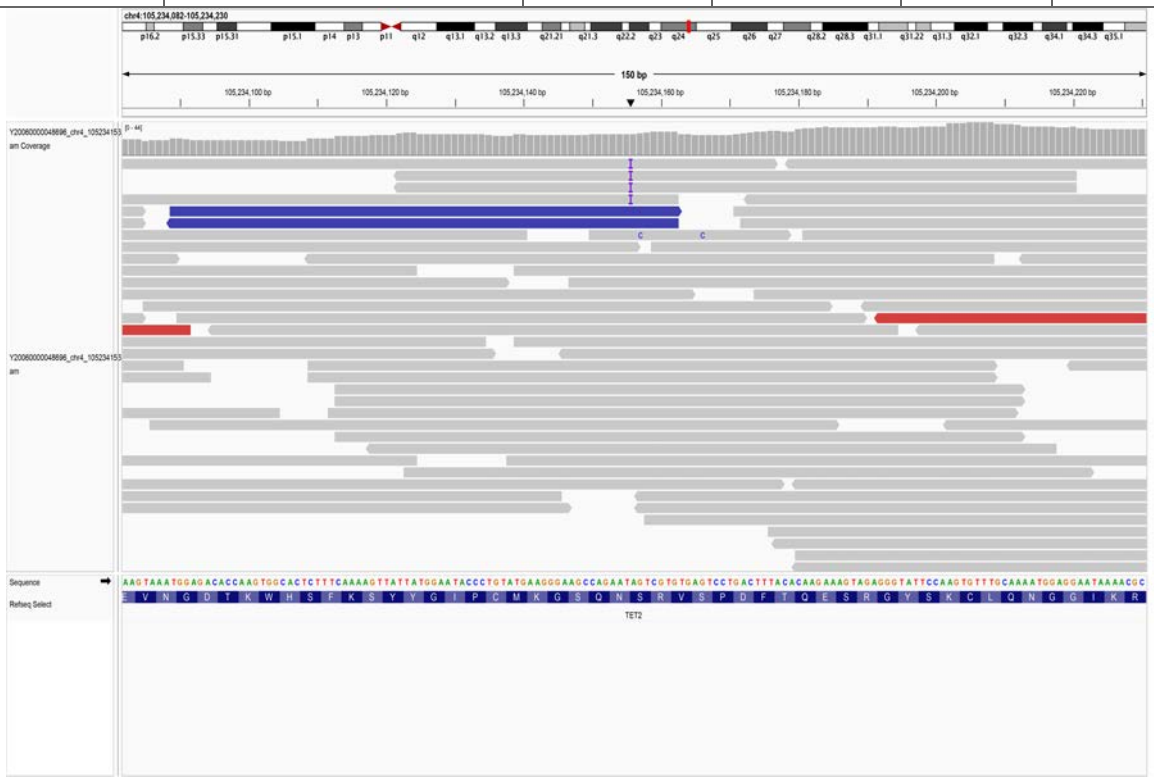
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R12950	chr17_31988474_C/A	48	4	*SUZ12*	stop_gained



55. *TET2*

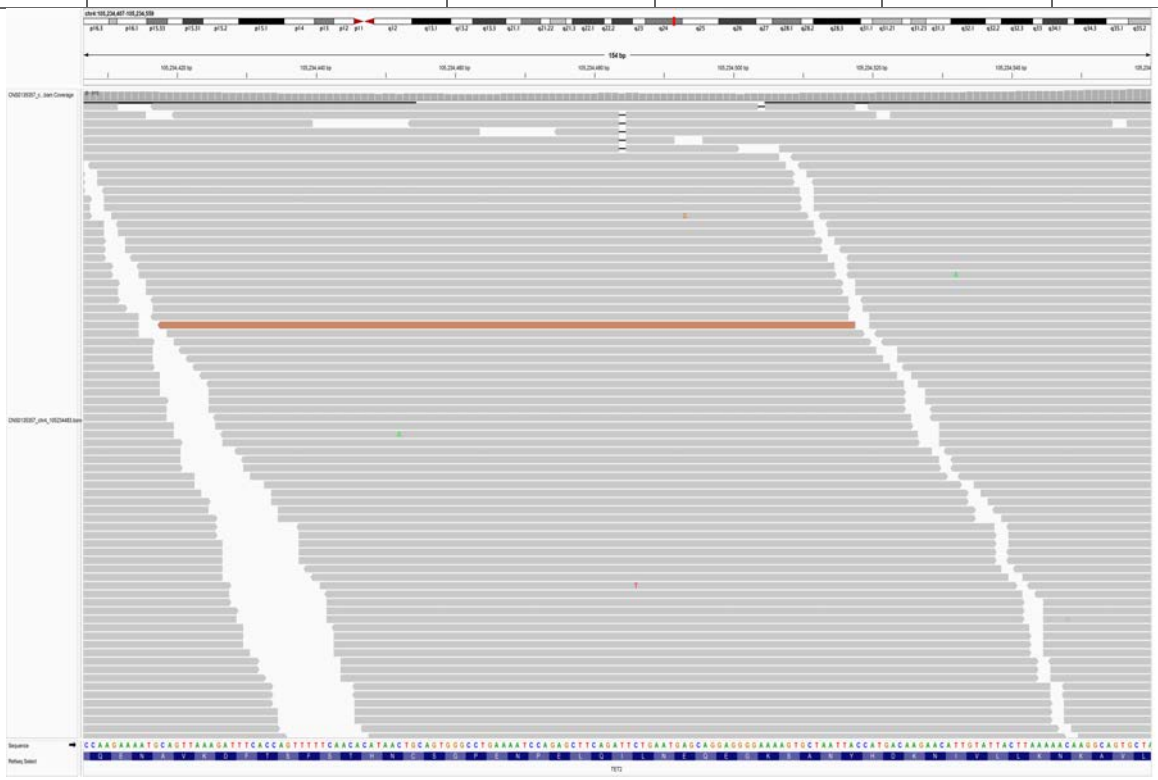
55.1. chr4_105234156_-/A

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



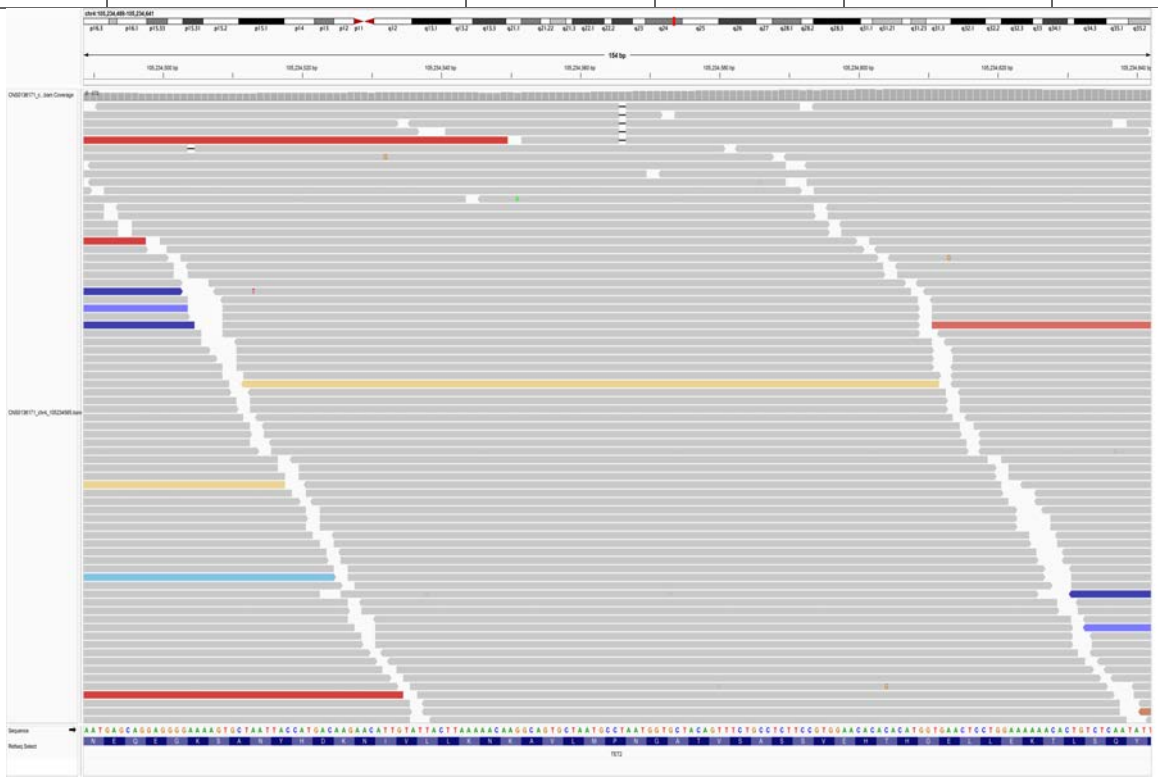
55.2. chr4_105234484_T/-

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



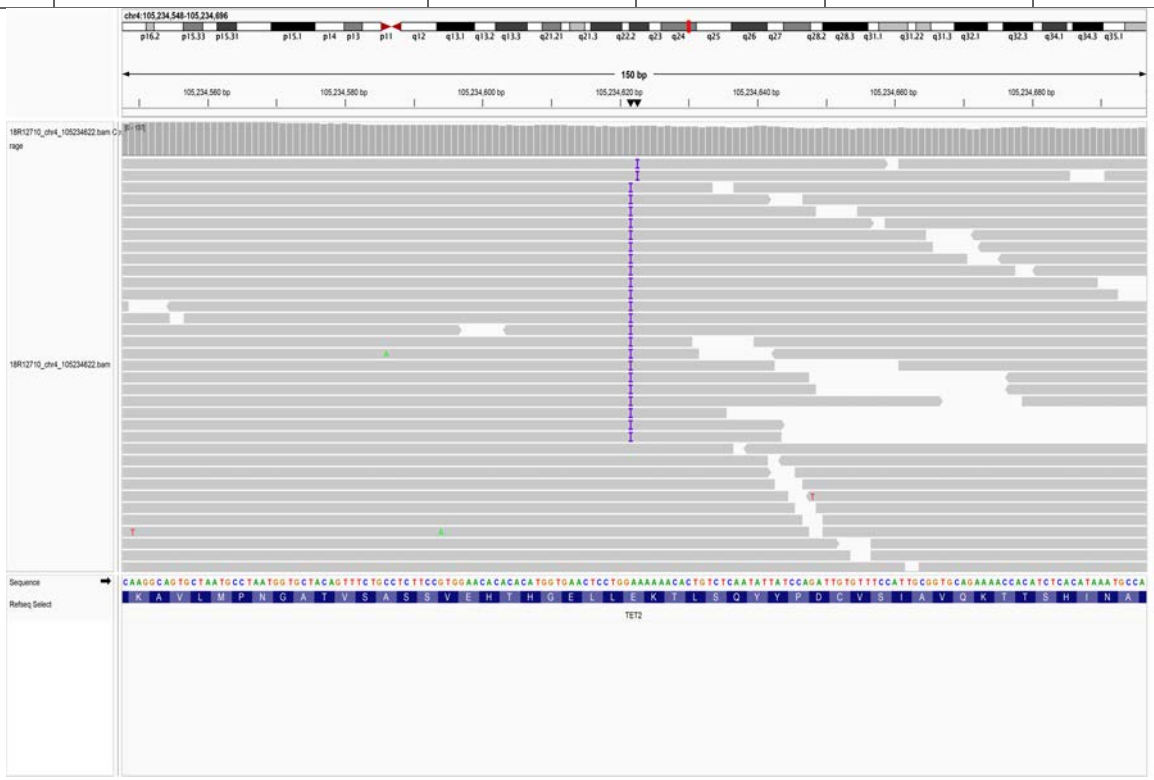
55.3. chr4_105234566_T/-

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



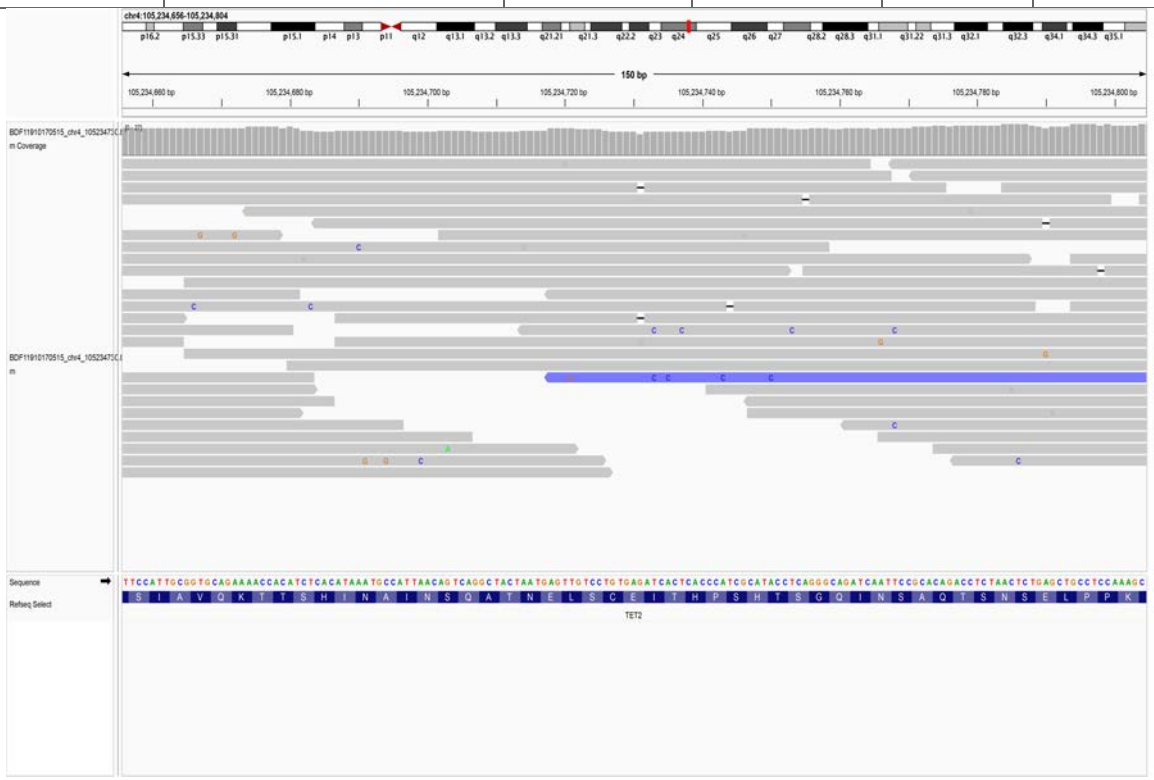
55.4. chr4_105234622_-/A

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



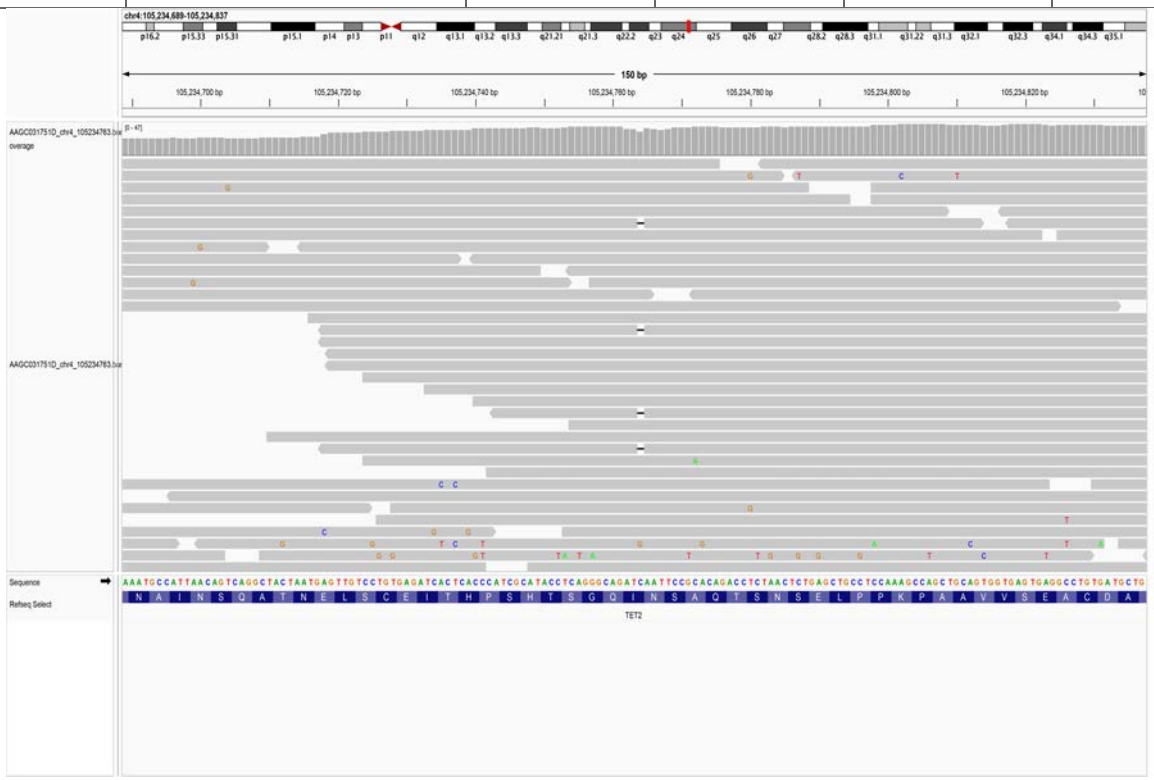
55.5. chr4_105234731_G/-

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



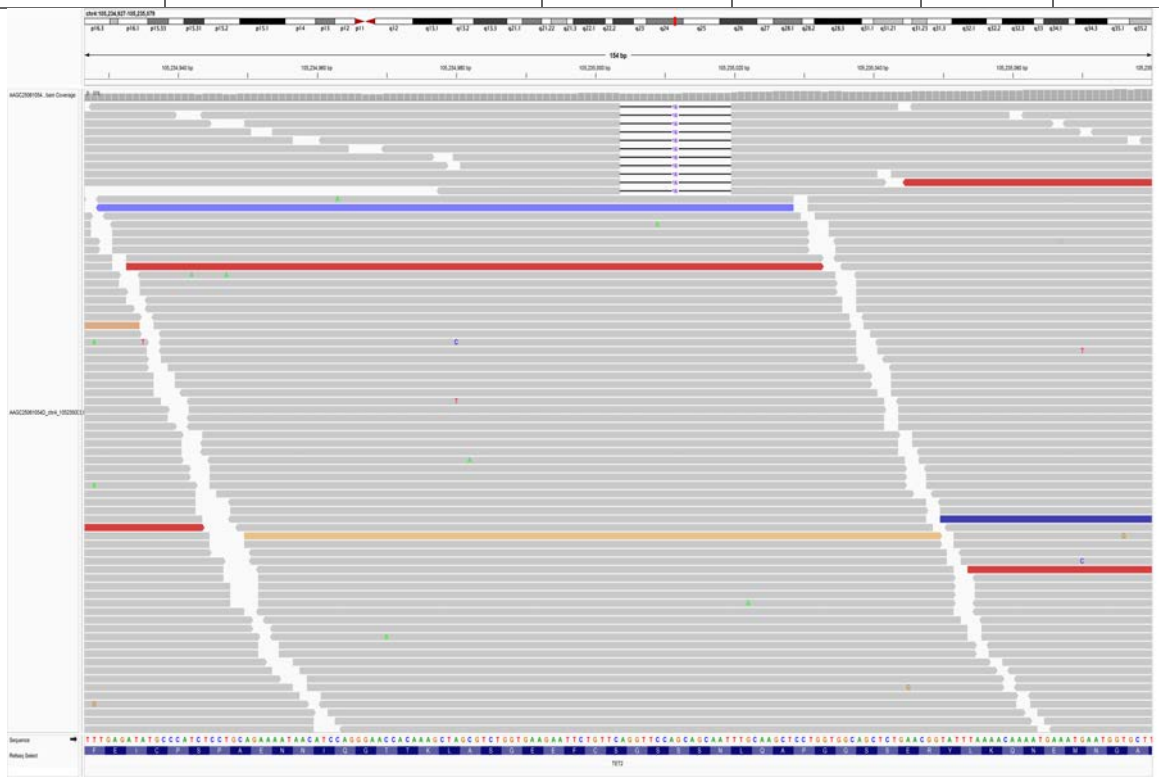
55.6. chr4_105234764_C/-

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



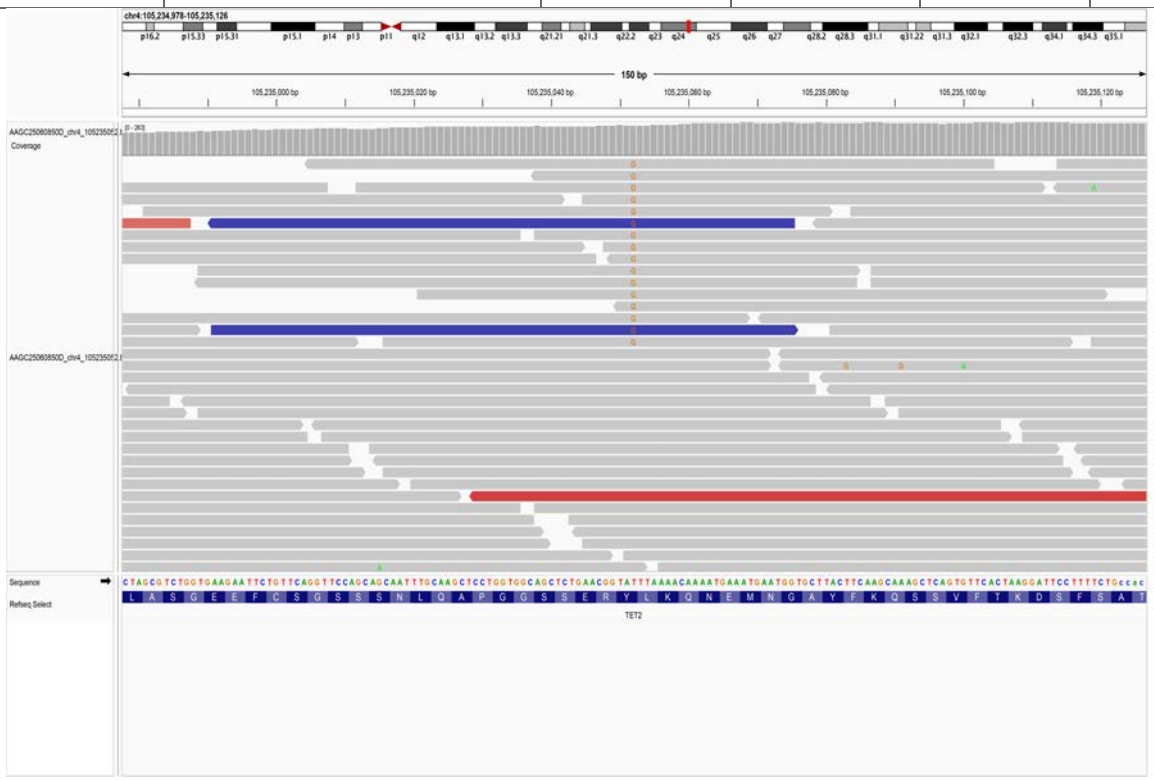
55.7. chr4_105235004_AGGTTCCAGCAGCAAT/-

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



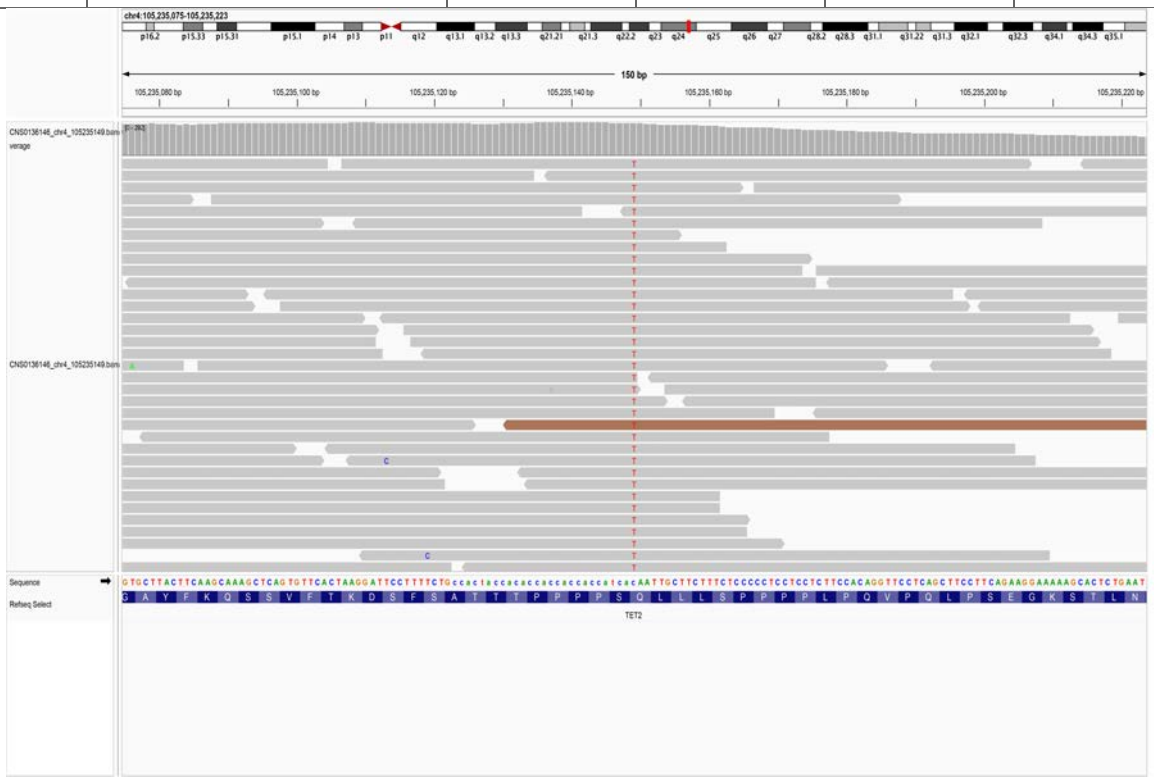
55.8. chr4_105235052_T/G

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



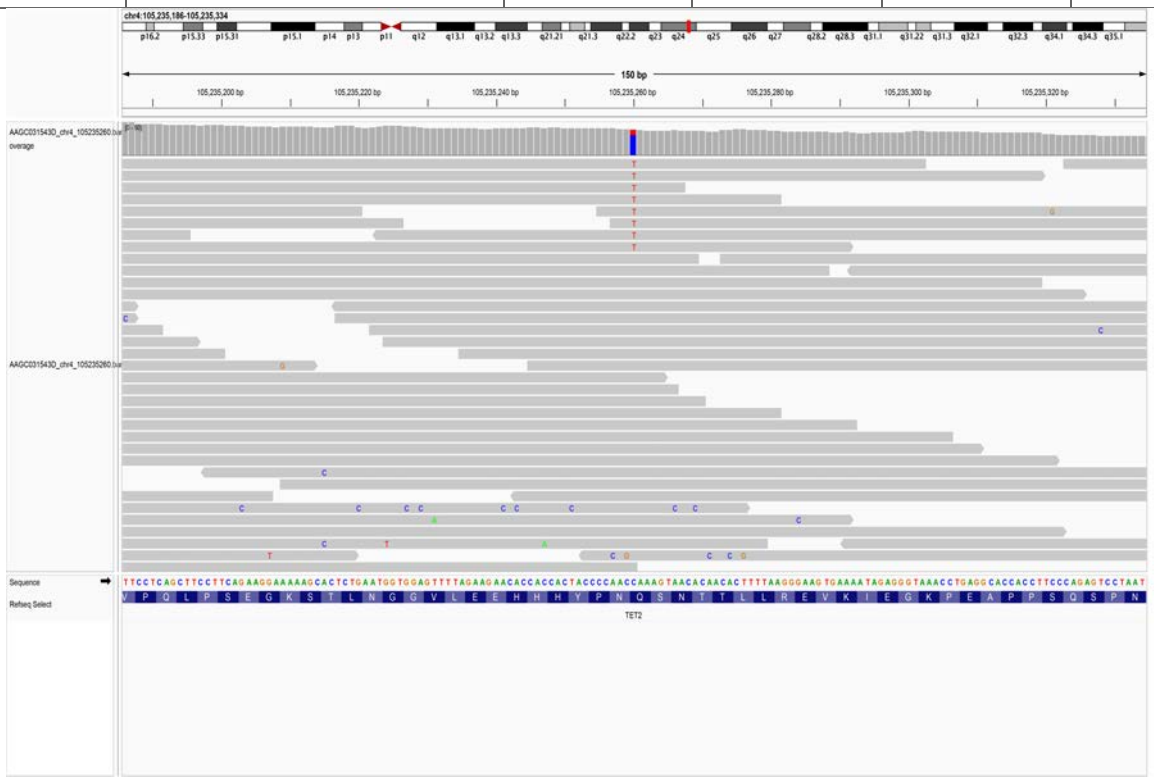
55.9. chr4_105235149_C/T

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



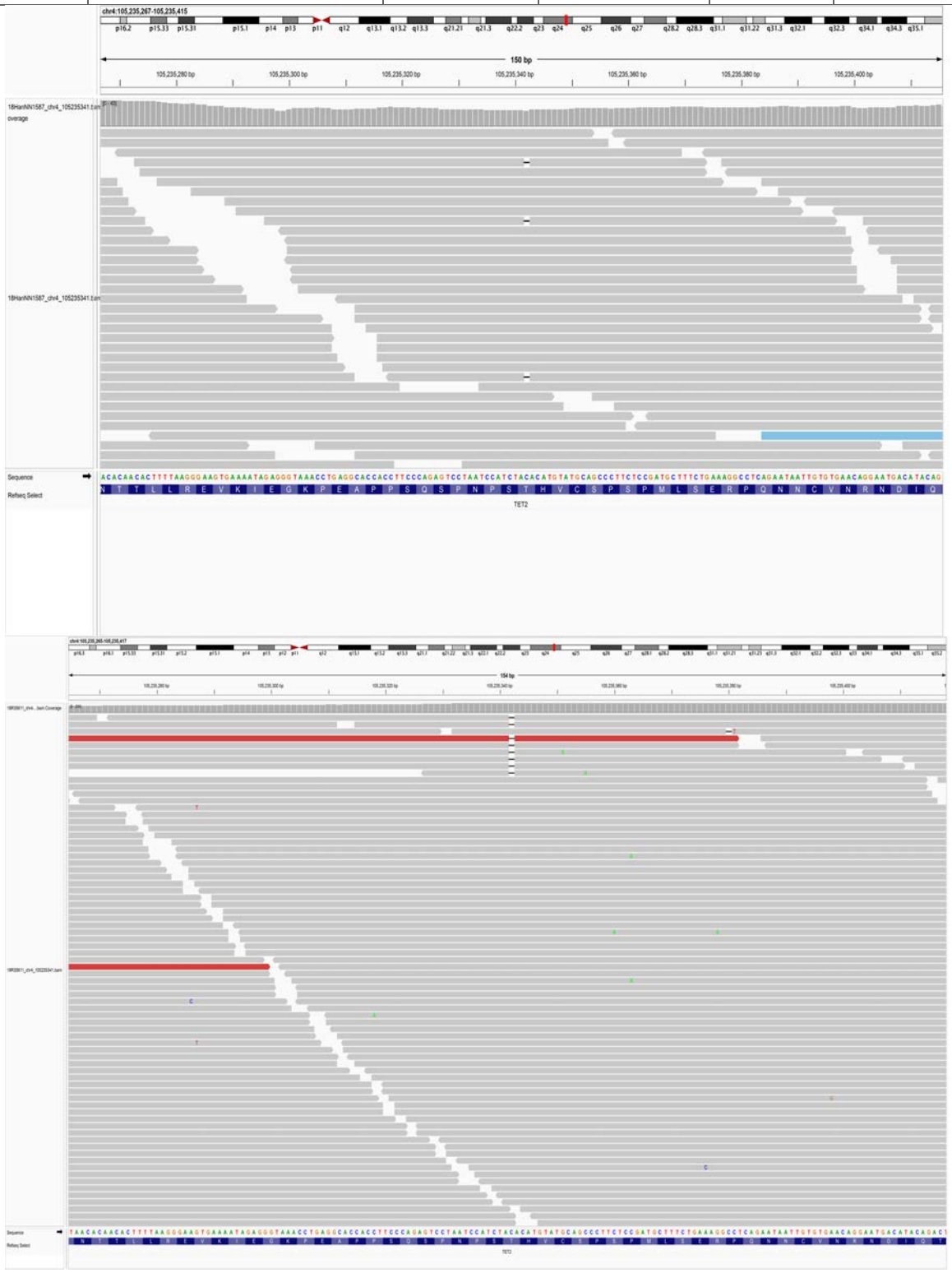
55.10. chr4_105235260_C/T

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



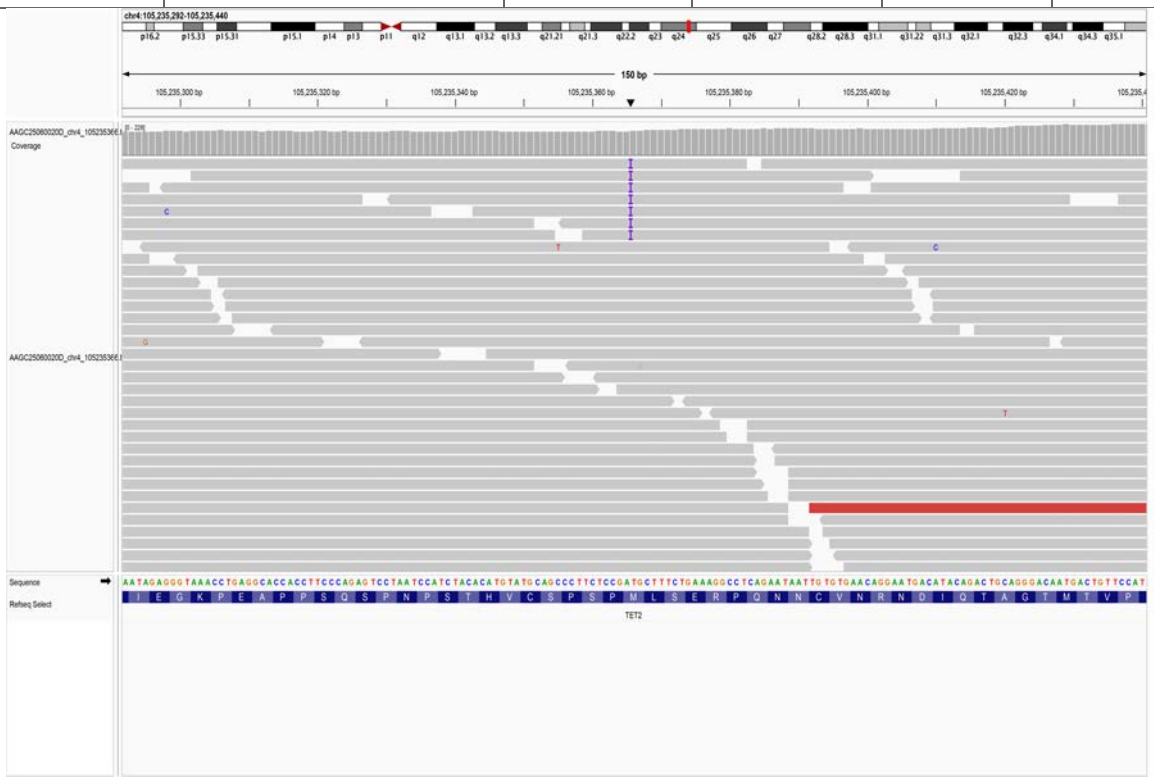
55.11. chr4_105235342_C/-

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



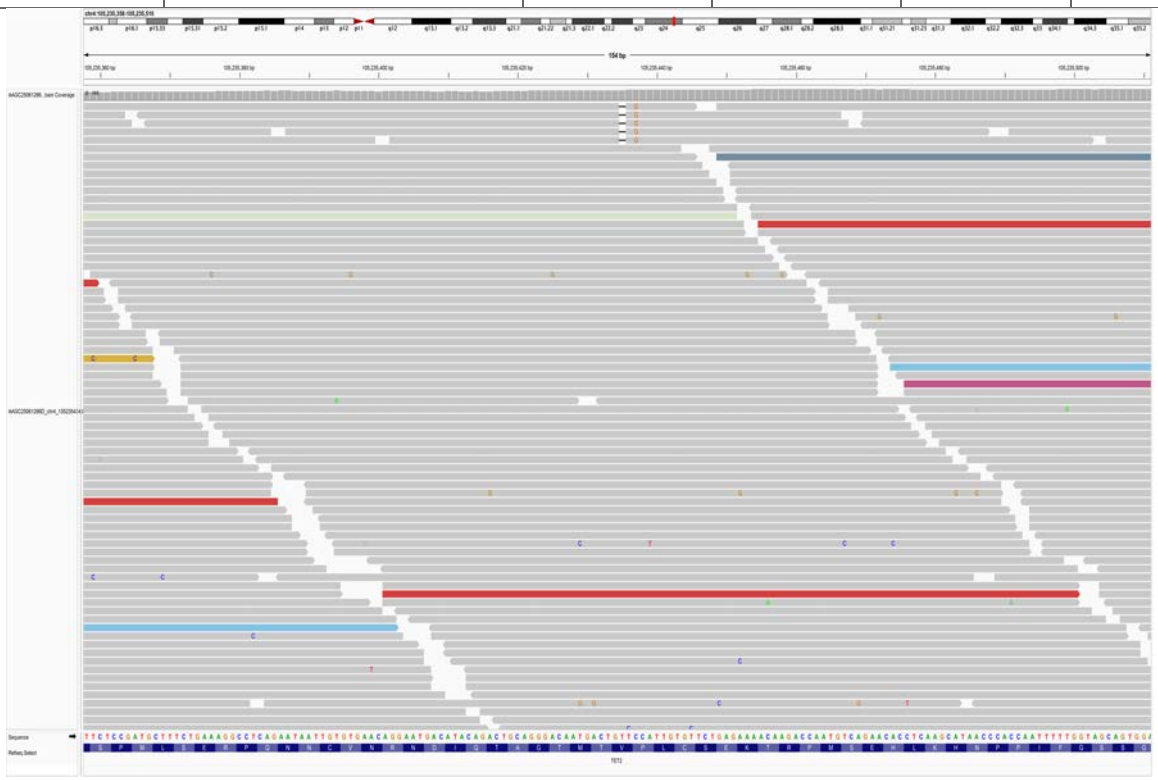
55.12. chr4_105235366_-/T

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



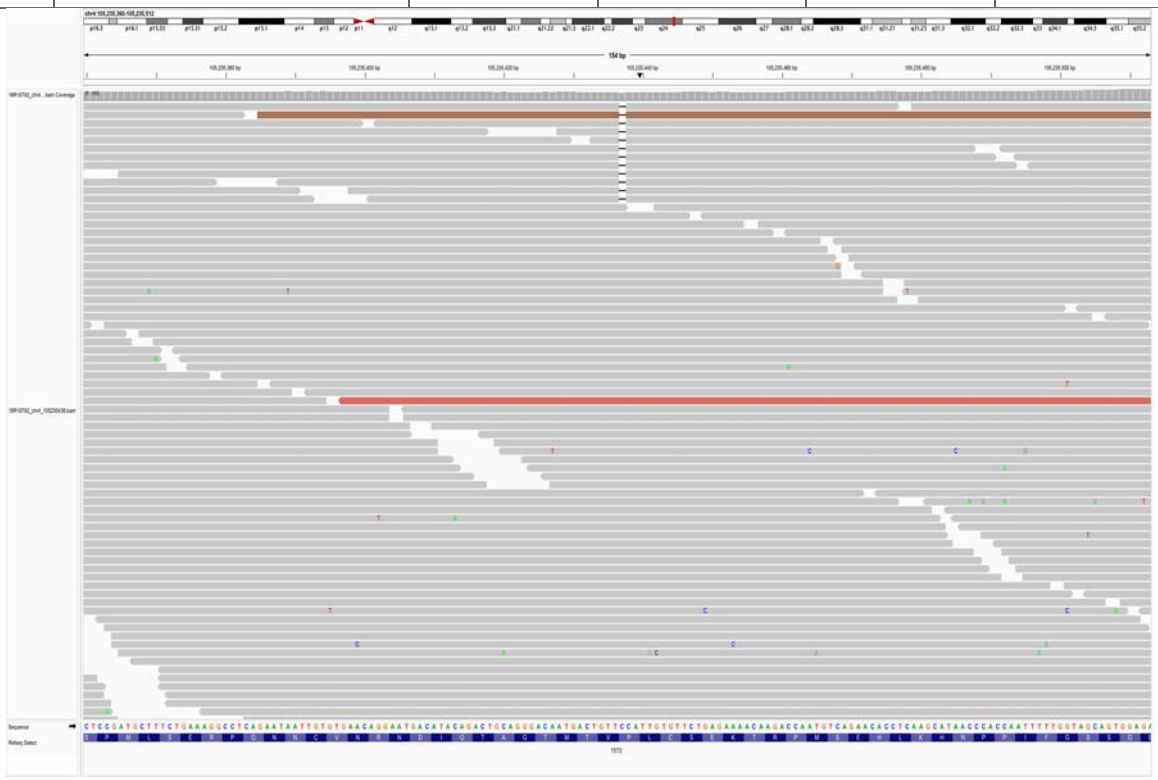
55.13. chr4_105235435_T/-

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



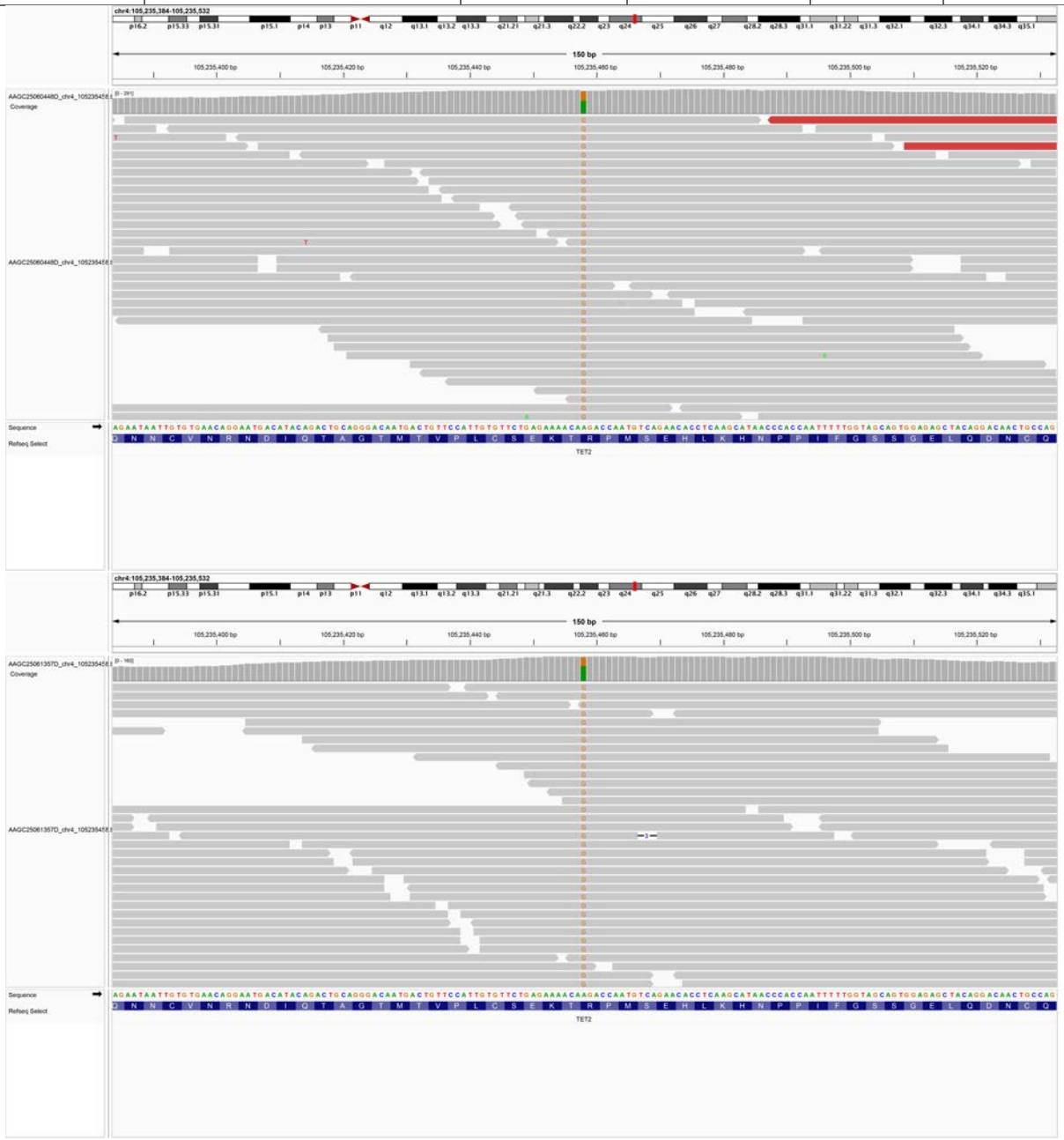
55.14. chr4_105235437_C/-

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



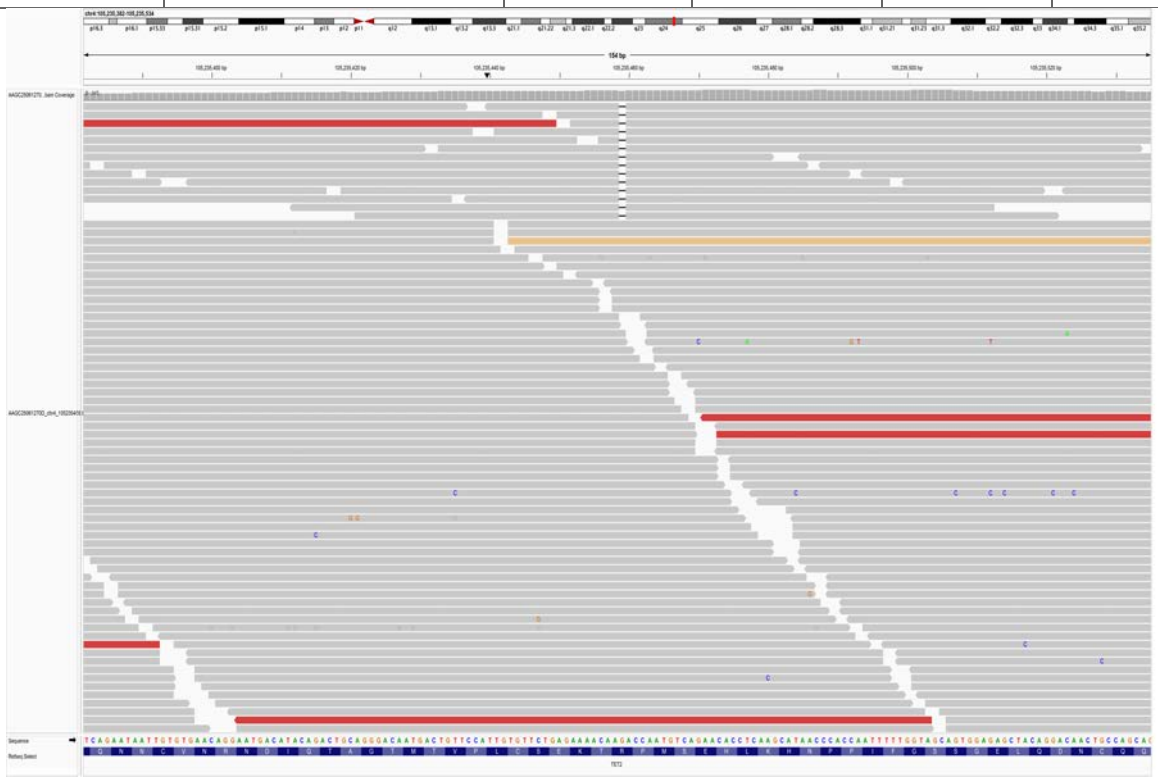
55.15. chr4_105235459_A/G

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



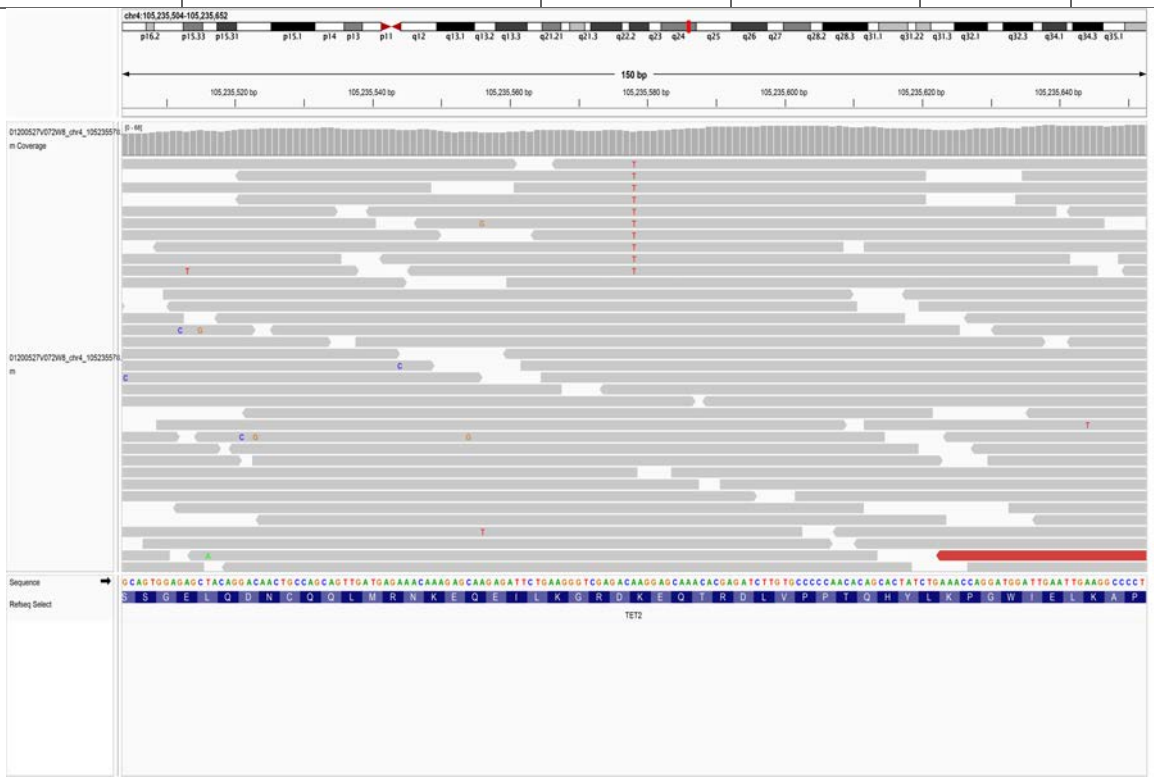
55.16. chr4_105235459_G/-

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



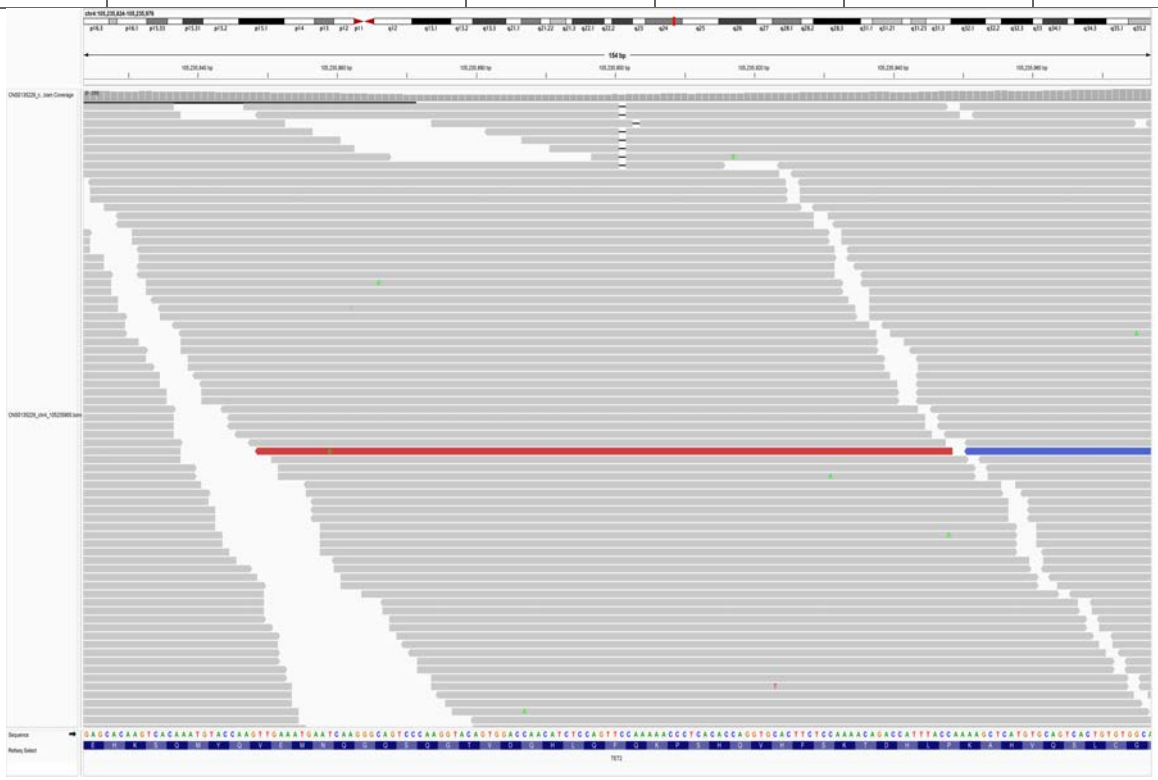
55.17. chr4_105235578_A/T

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



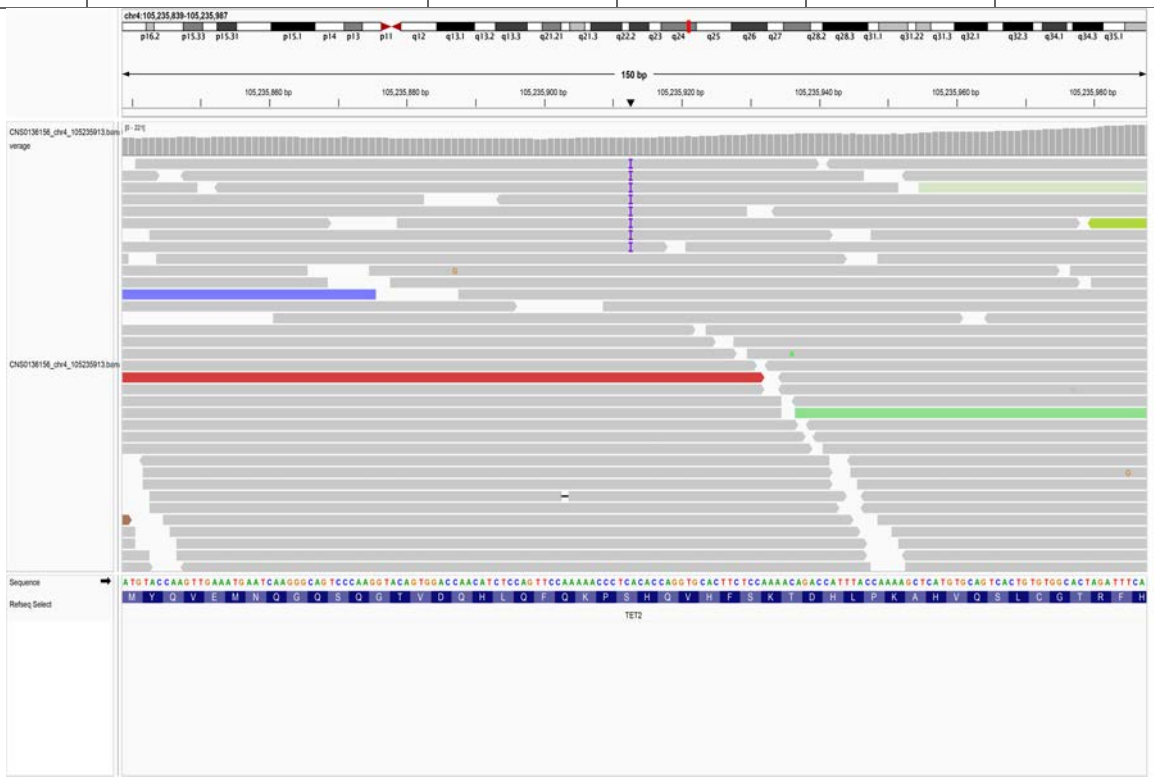
55.18. chr4_105235901_C/-

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



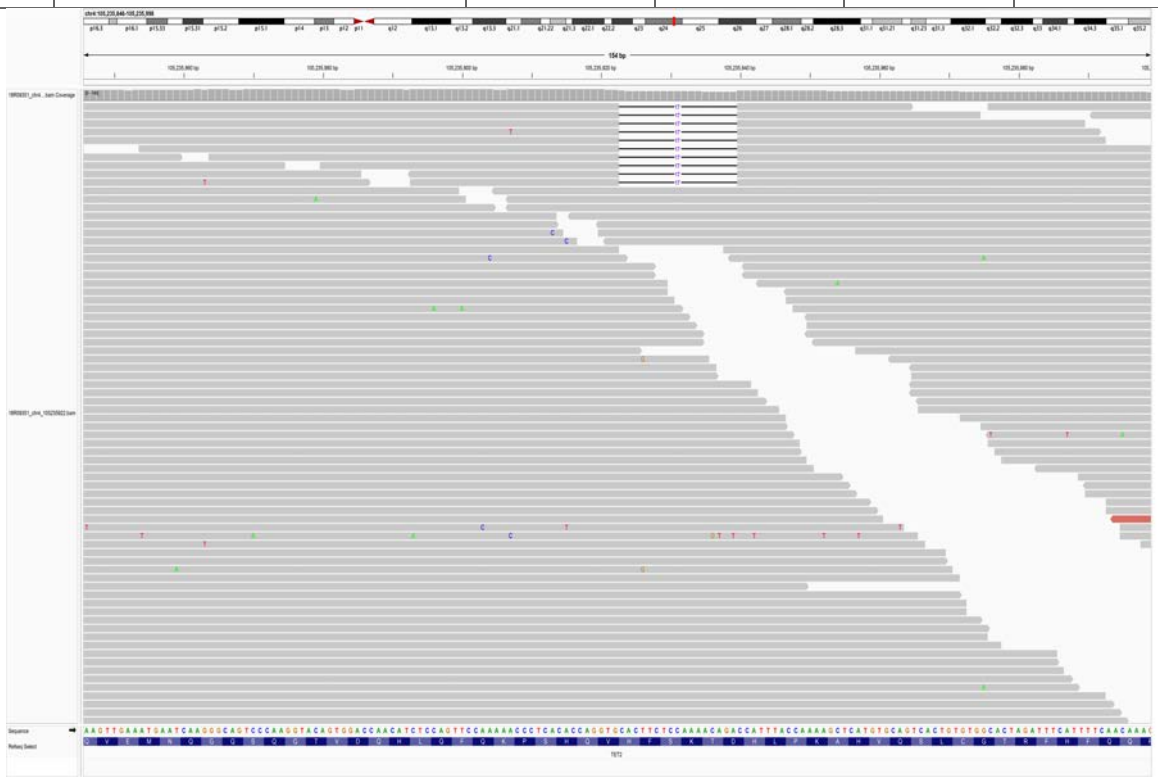
55.19. chr4_105235913_-/A

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



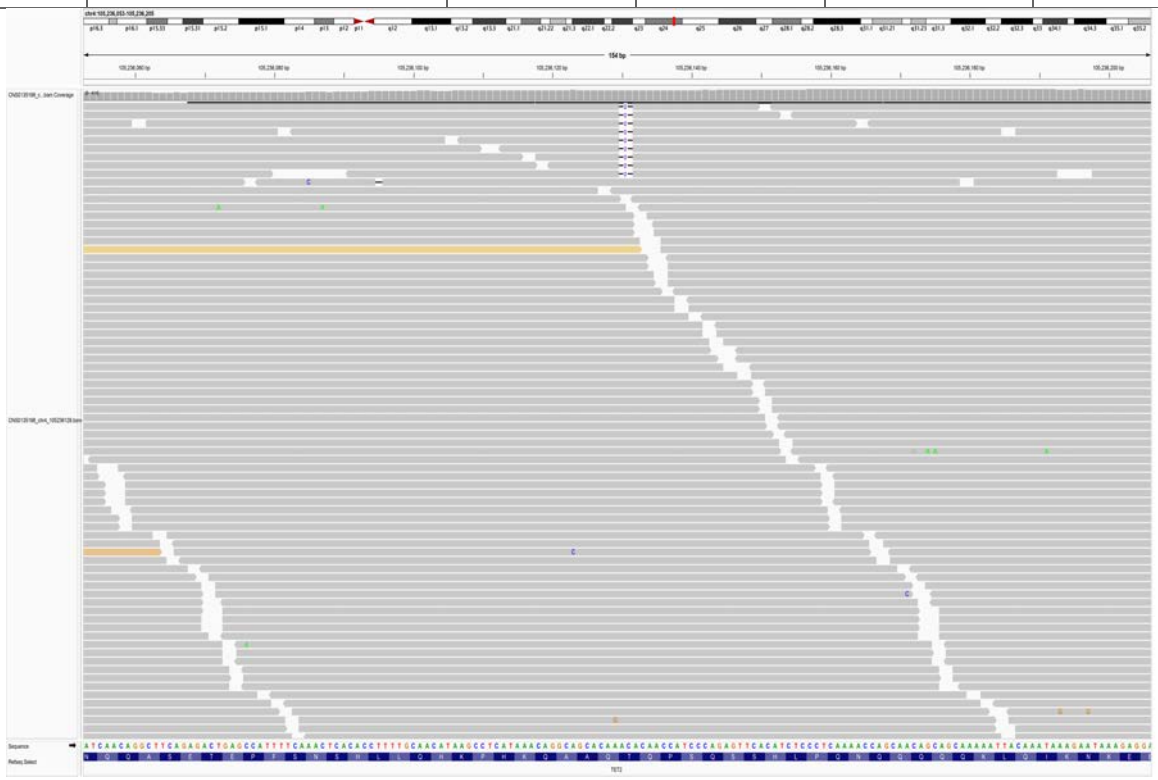
55.20. chr4_105235923_CACTTCTCCAAAACAGA/-

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



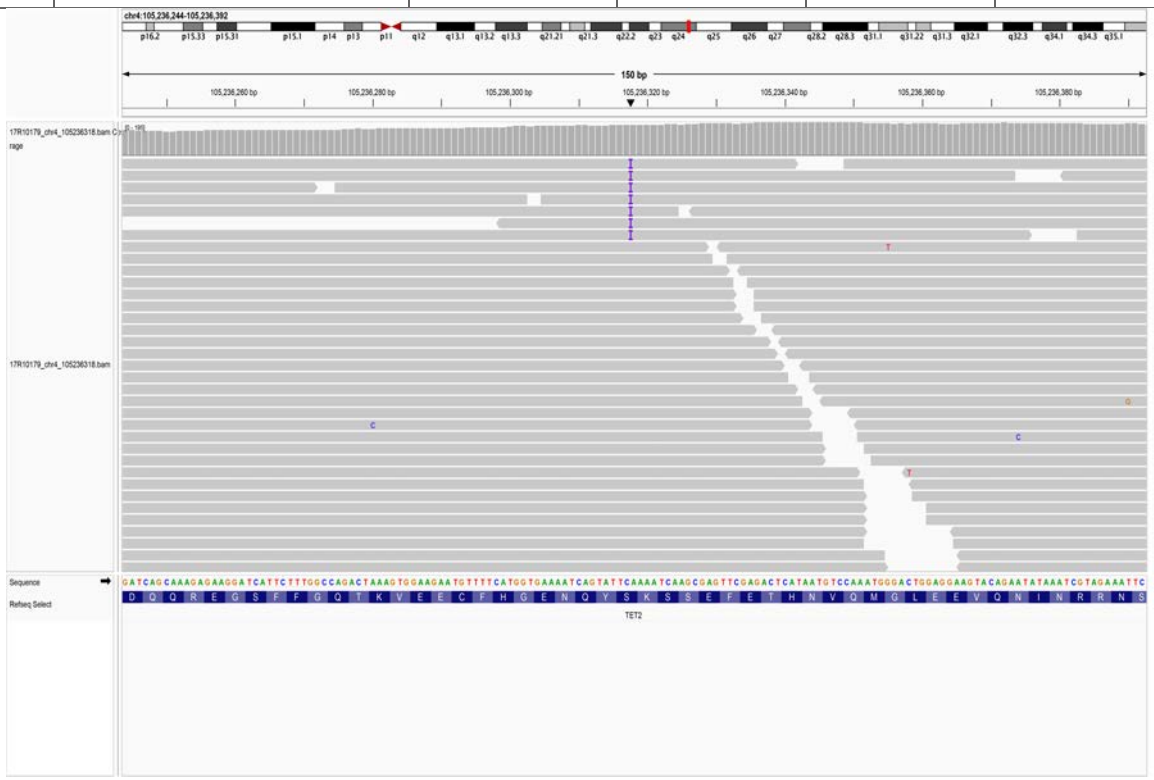
55.21. chr4_105236130_AC/-

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



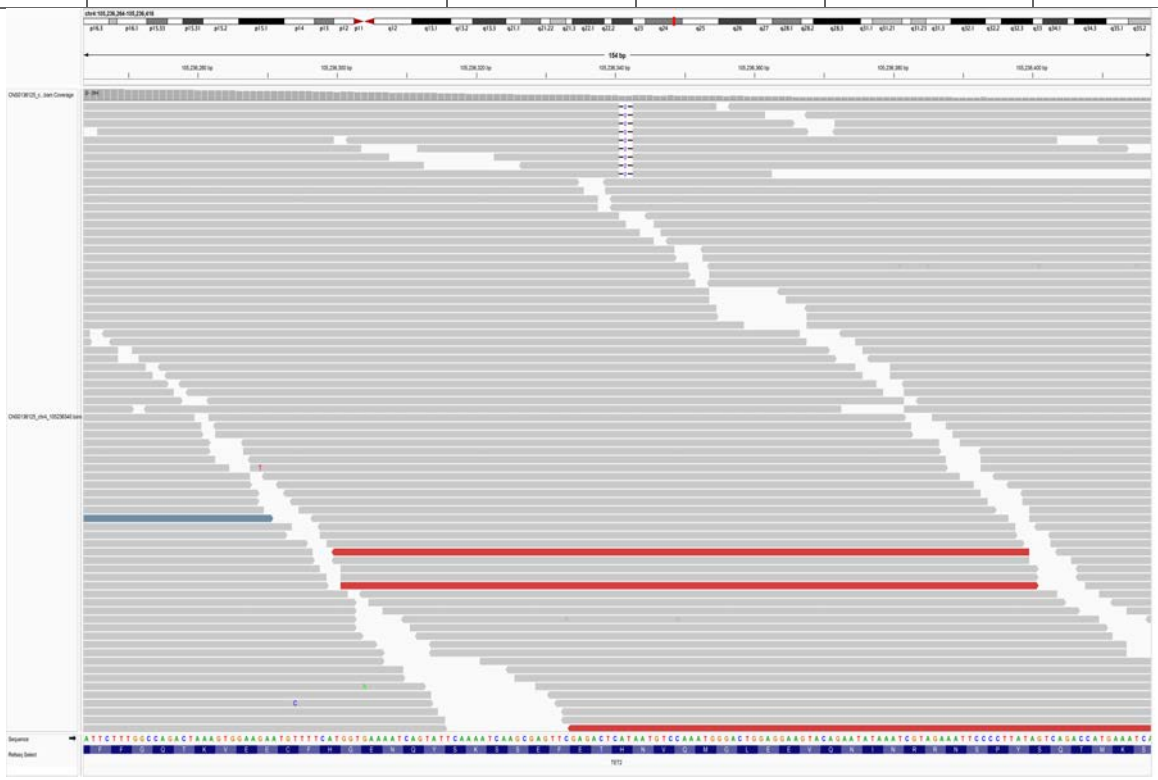
55.22. chr4_105236318_-/A

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



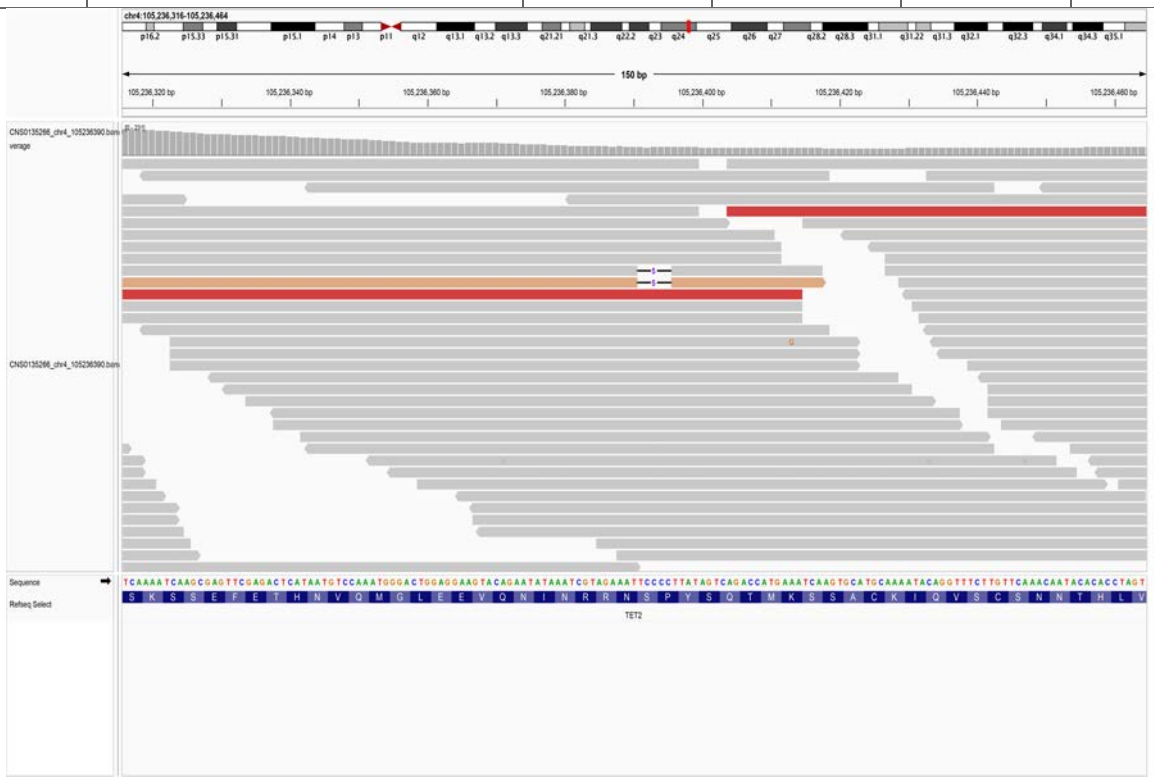
55.23. chr4_105236341_AT/-

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



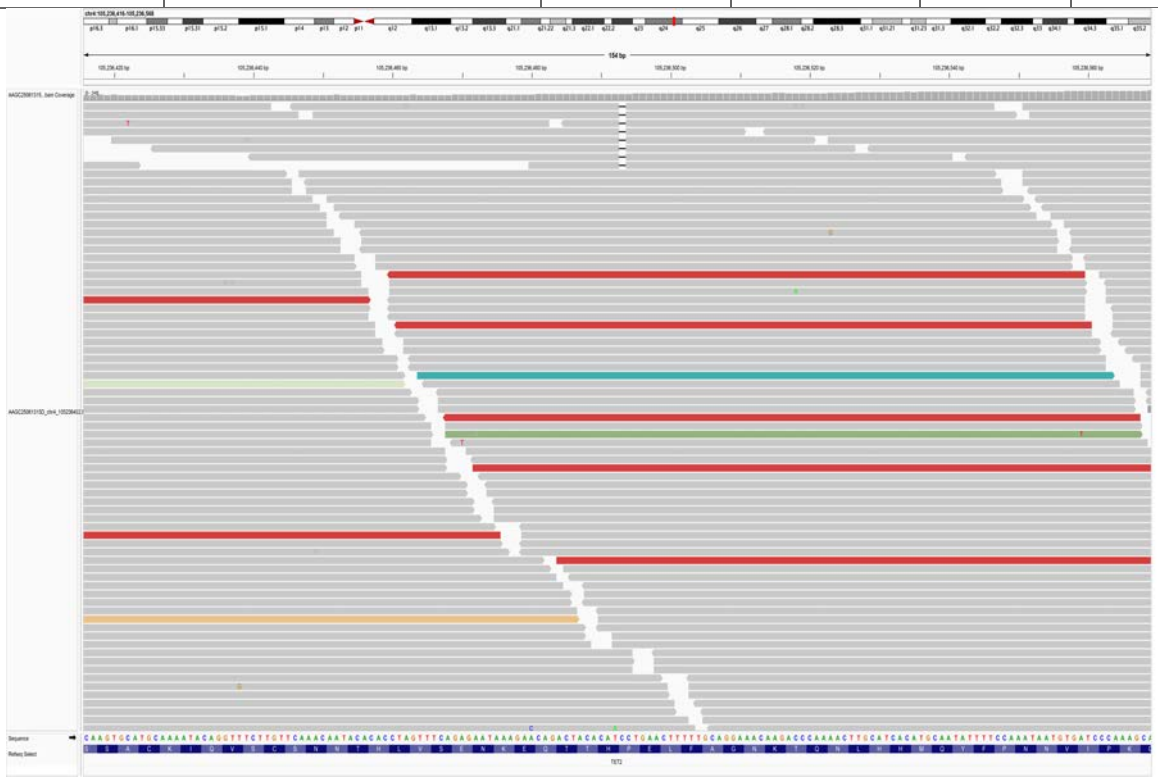
55.24. chr4_105236391_TCCCC/-

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



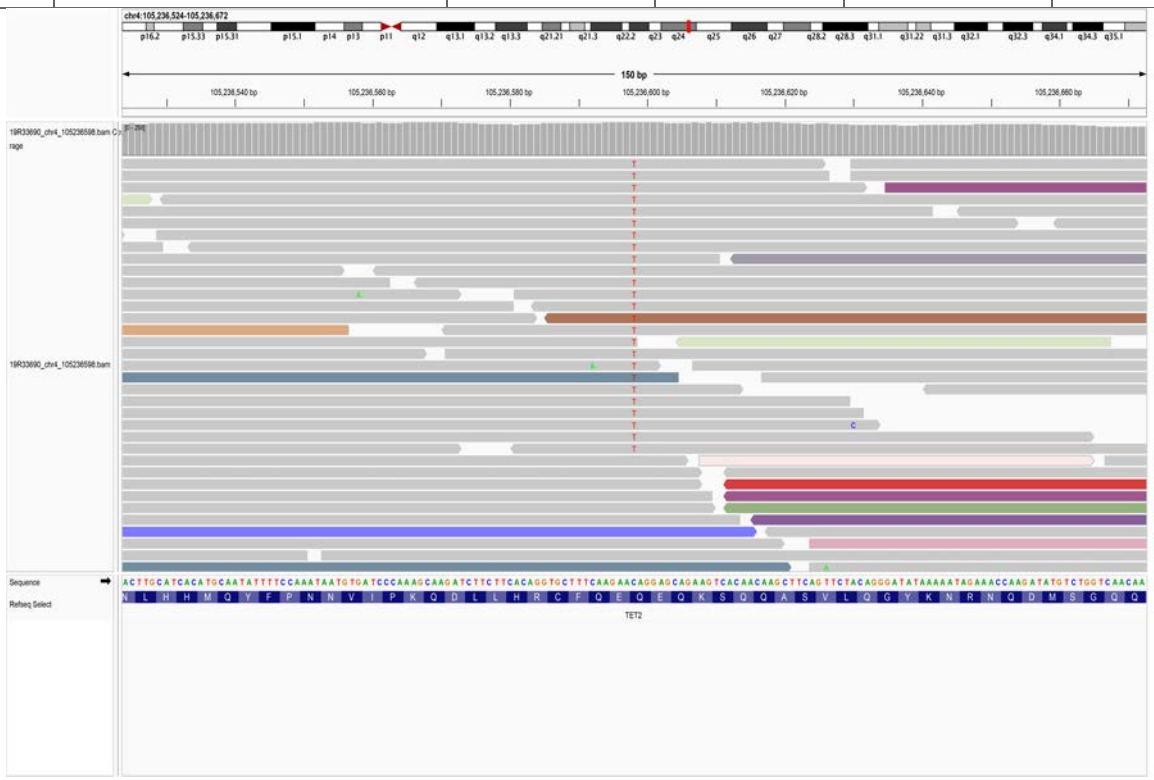
55.25. chr4_105236493_C/-

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



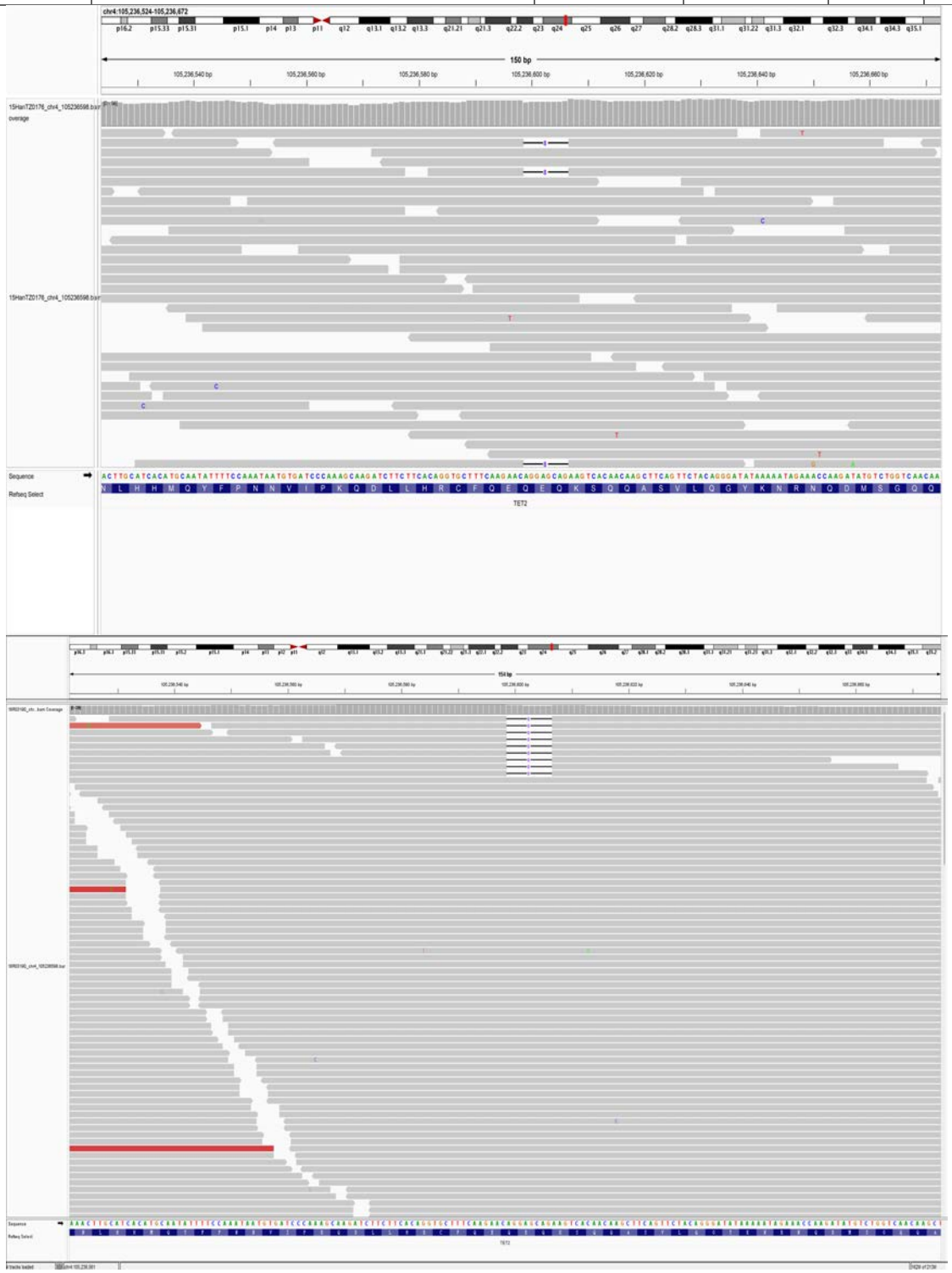
55.26. chr4_105236598_C/T

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



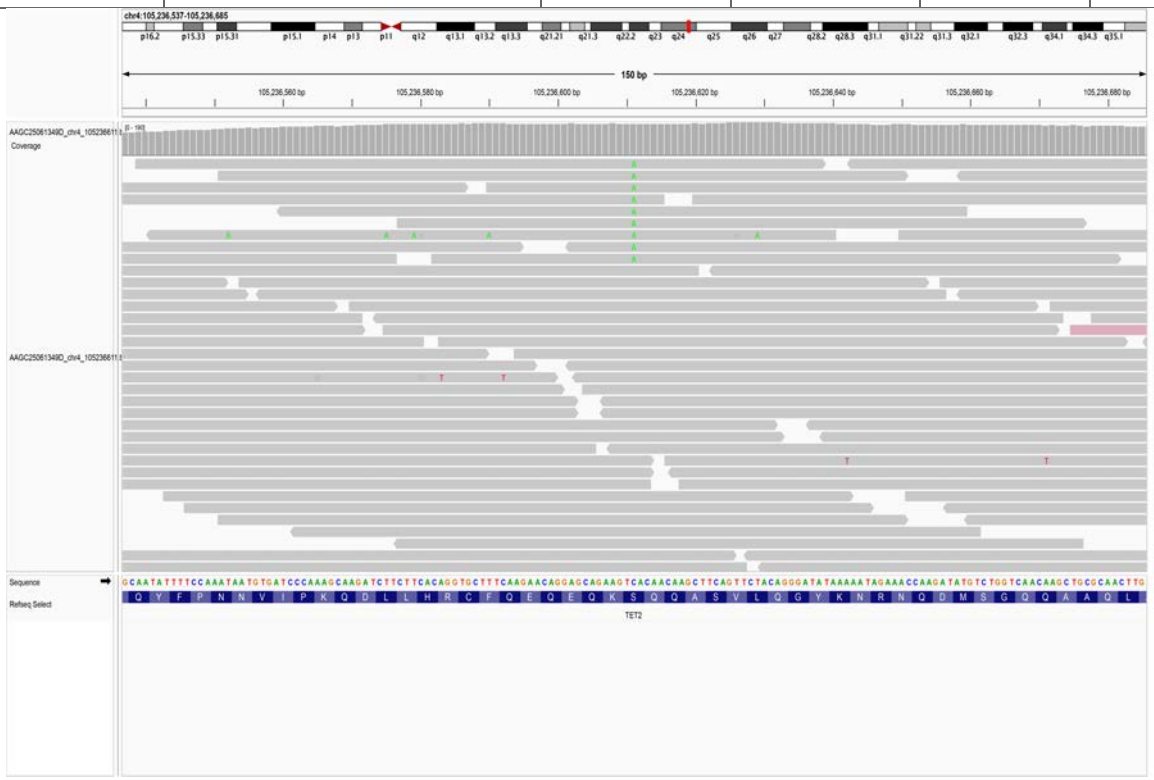
55.27. chr4_105236599_AGGAGCAG/-

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



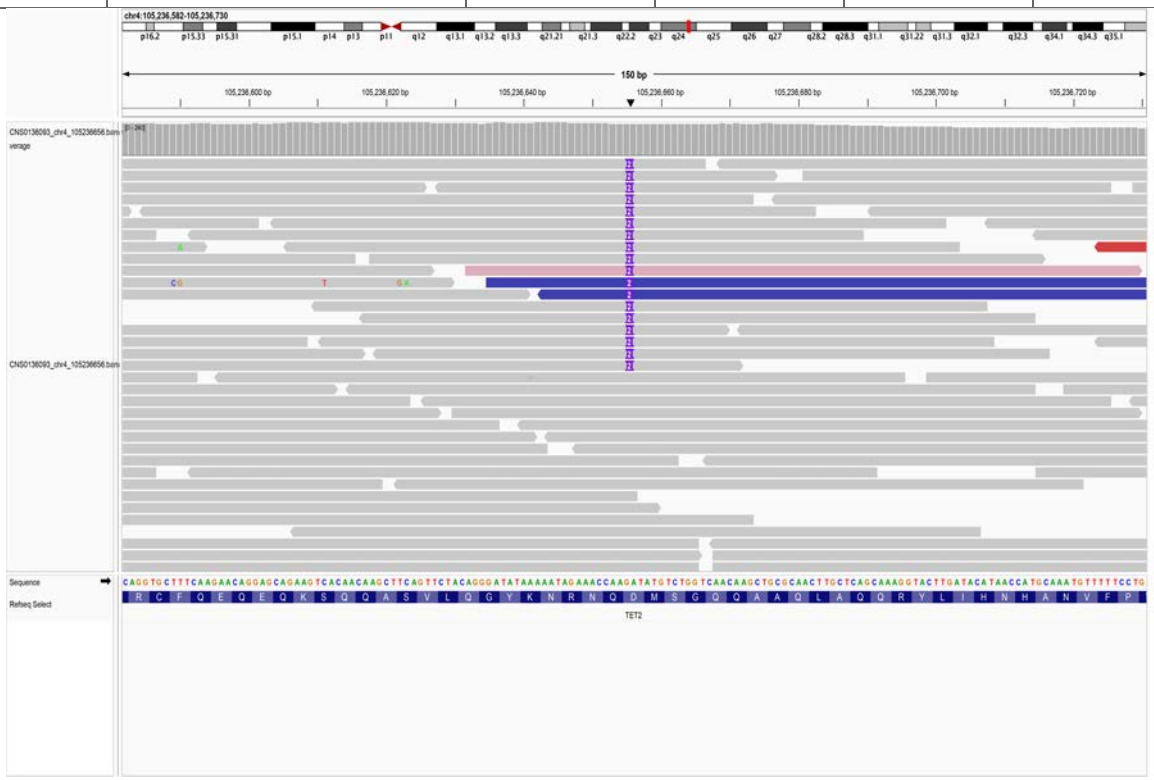
55.28. chr4_105236611_C/A

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



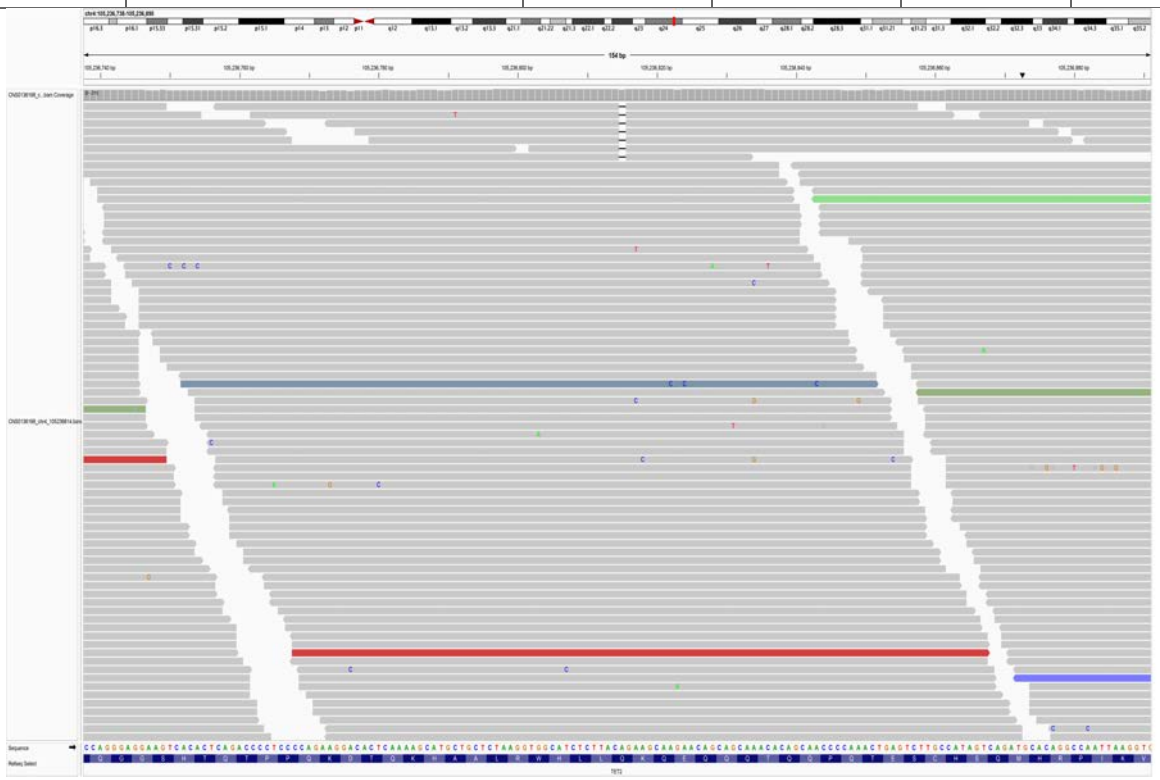
55.29. chr4_105236656_-/AT

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



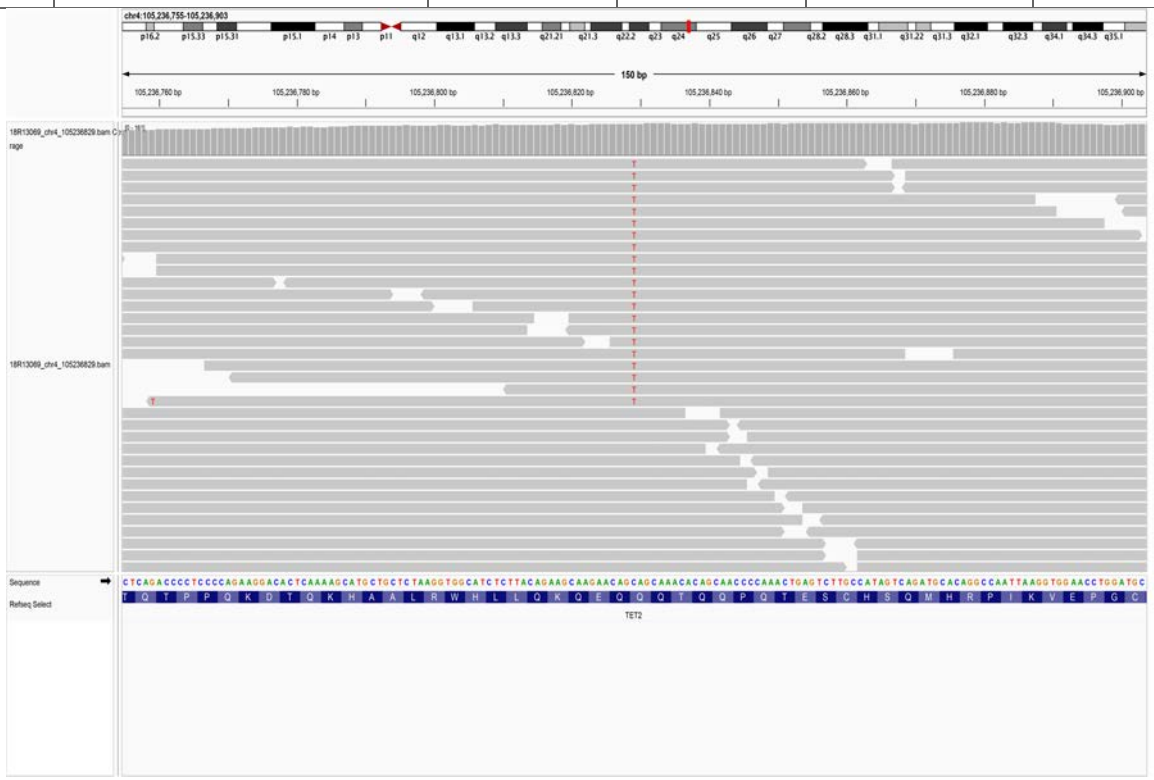
55.30. chr4_105236815_A/AA/-

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



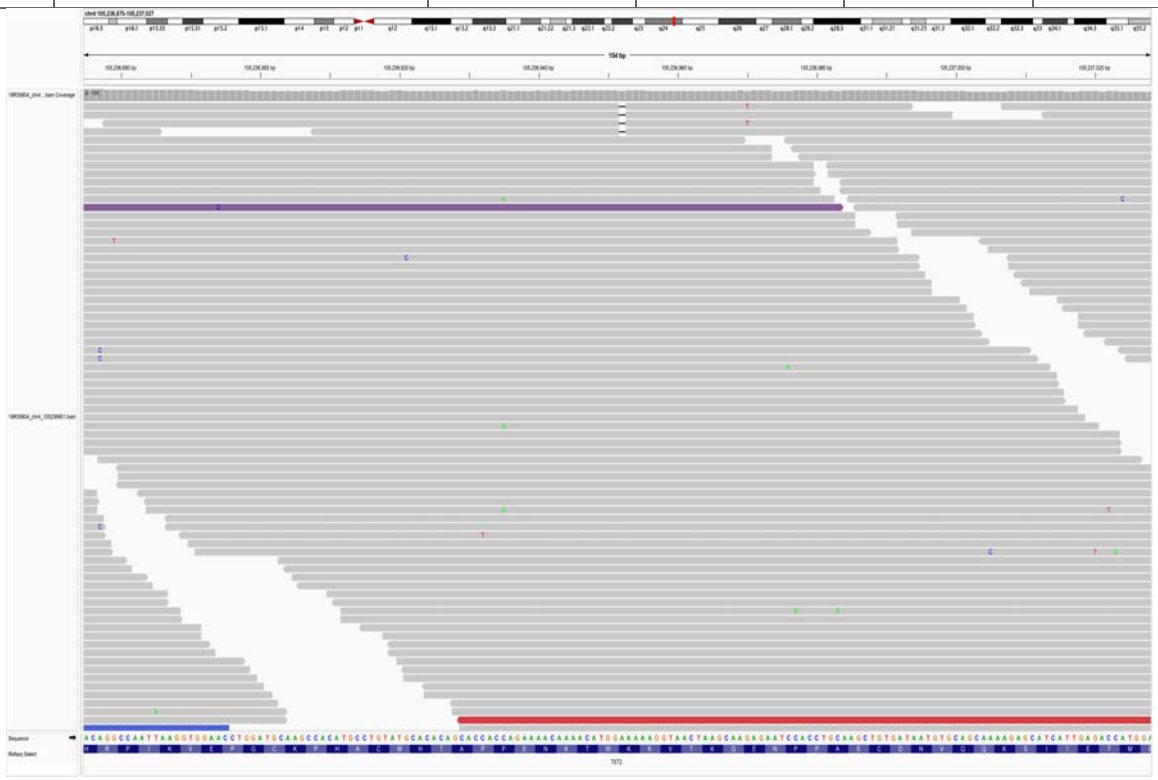
55.31. chr4_105236829_C/T

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



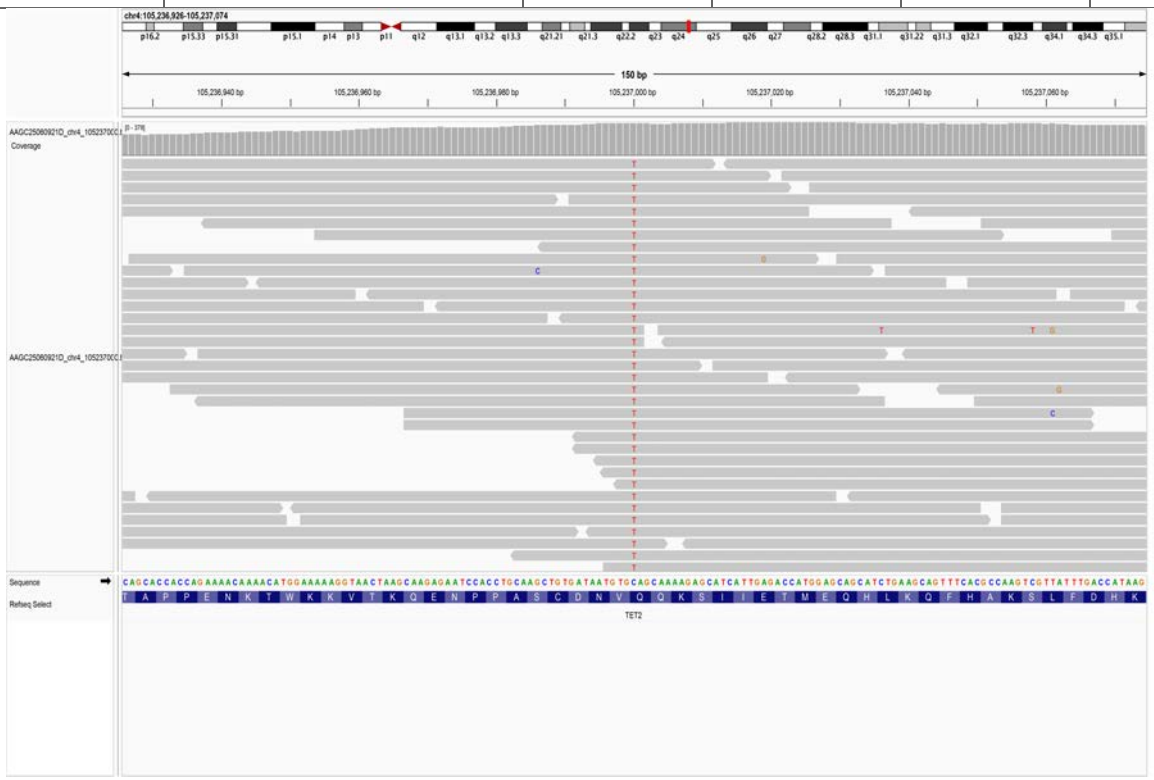
55.32. chr4_105236952_A/-

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



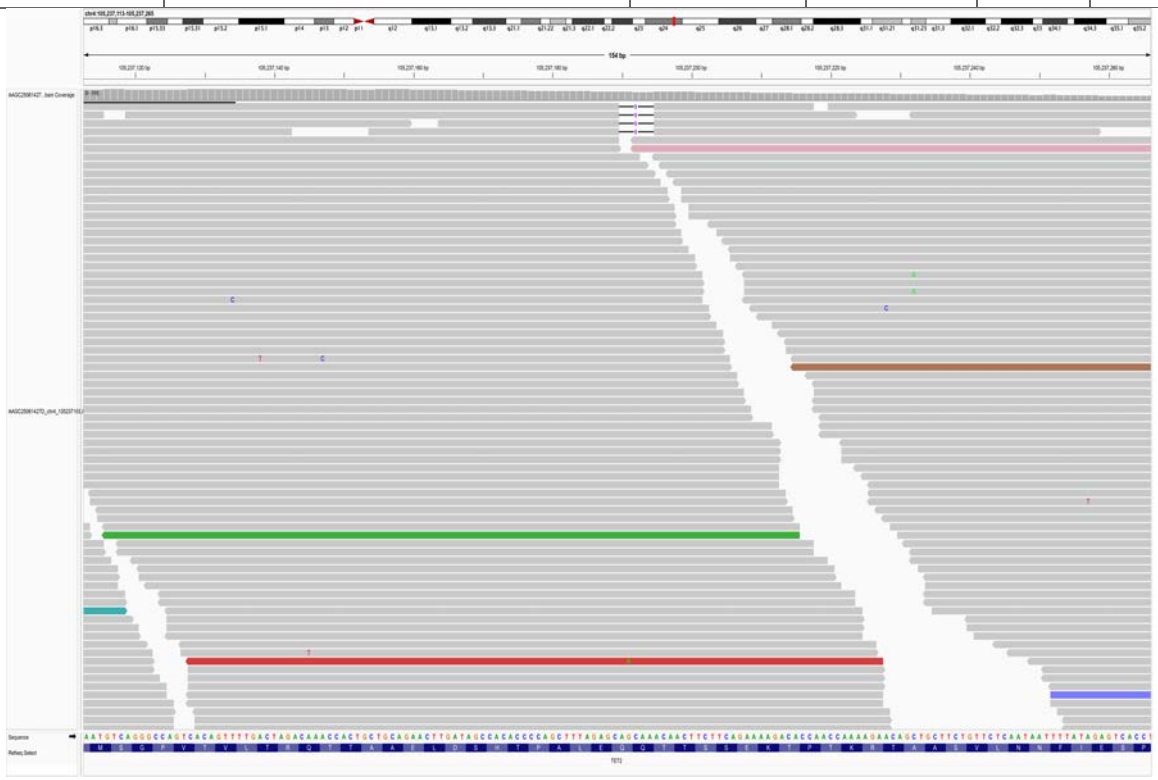
55.33. chr4_105237000_C/T

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



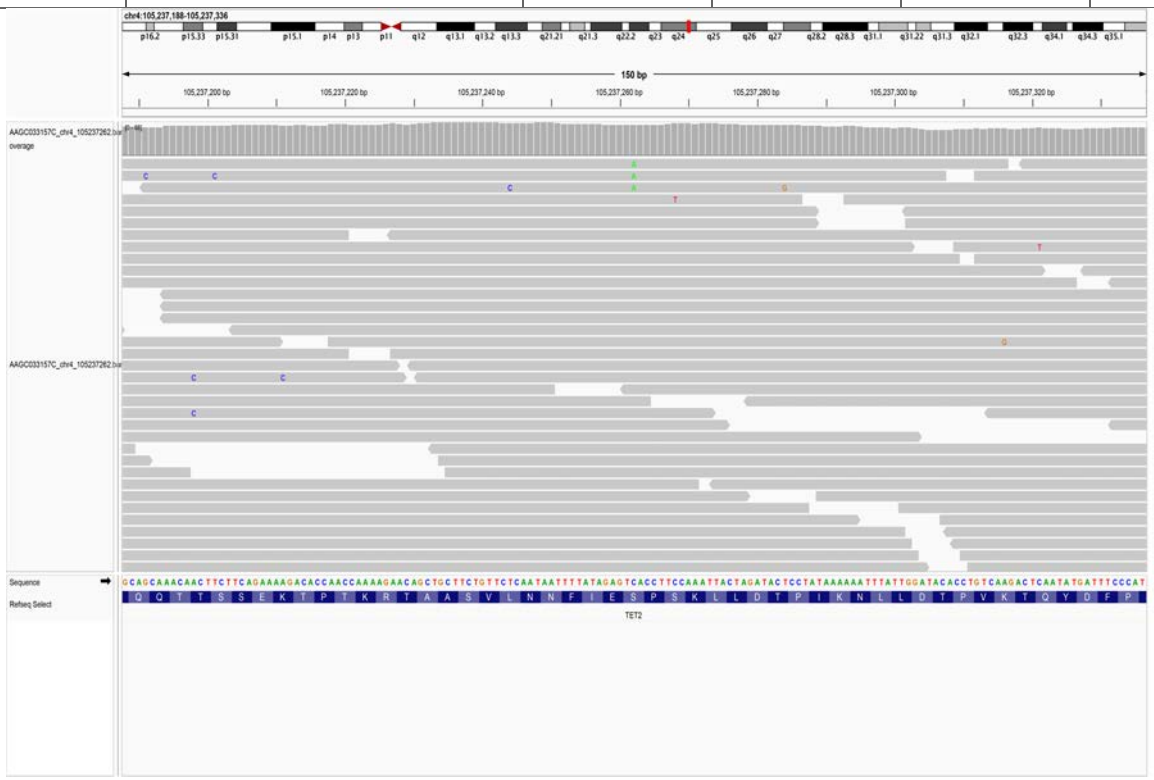
55.34. chr4_105237190_AGCAA/-

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



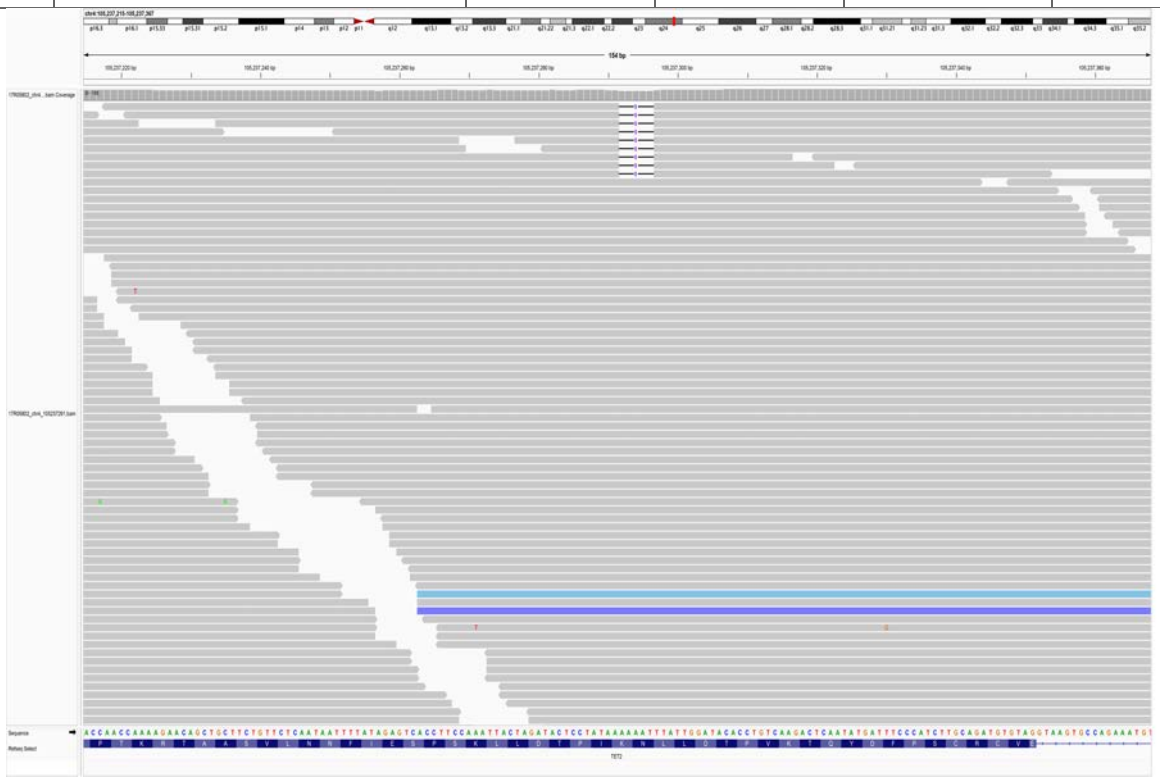
55.35. chr4_105237262_C/A

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



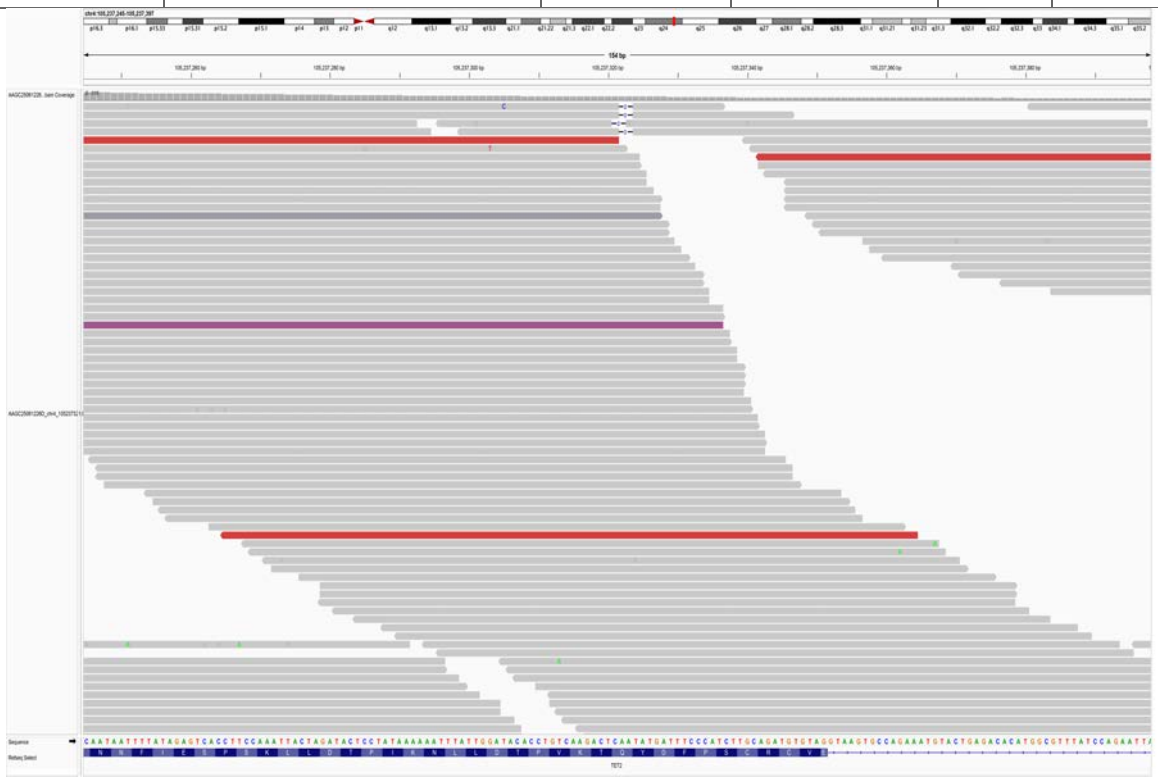
55.36. chr4_105237292_AAAAT/-

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



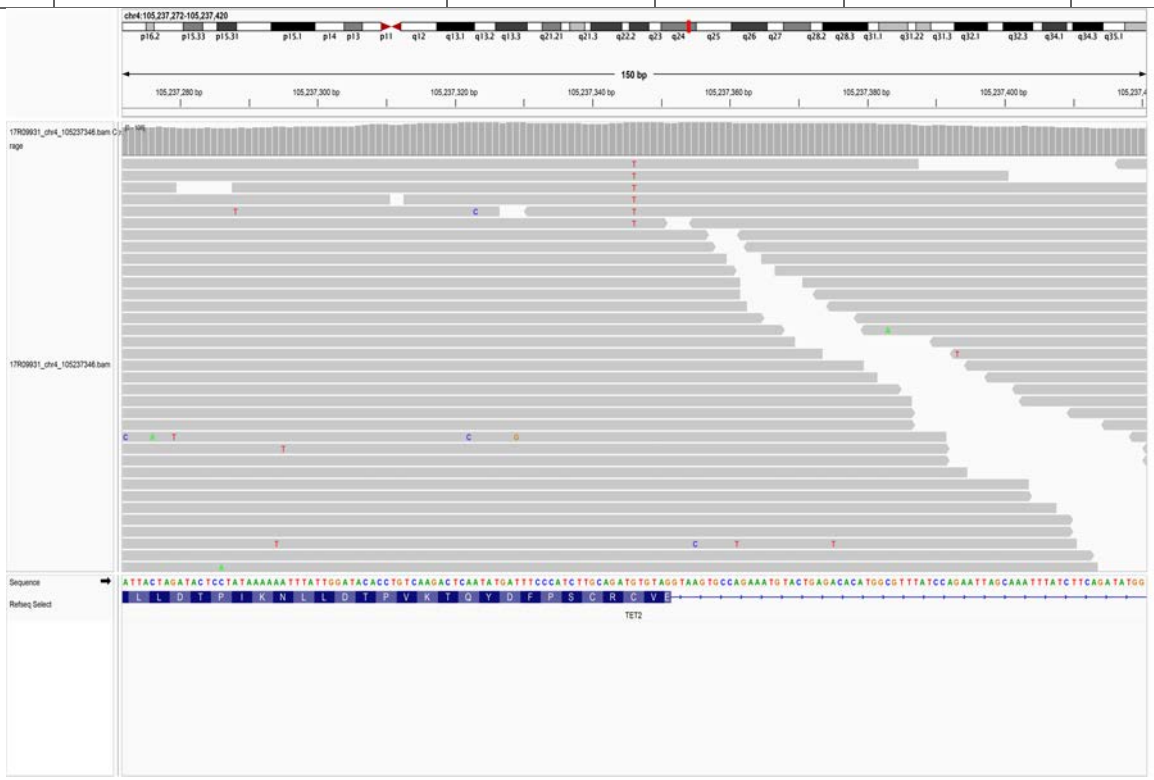
55.37. chr4_105237322_AA/-

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



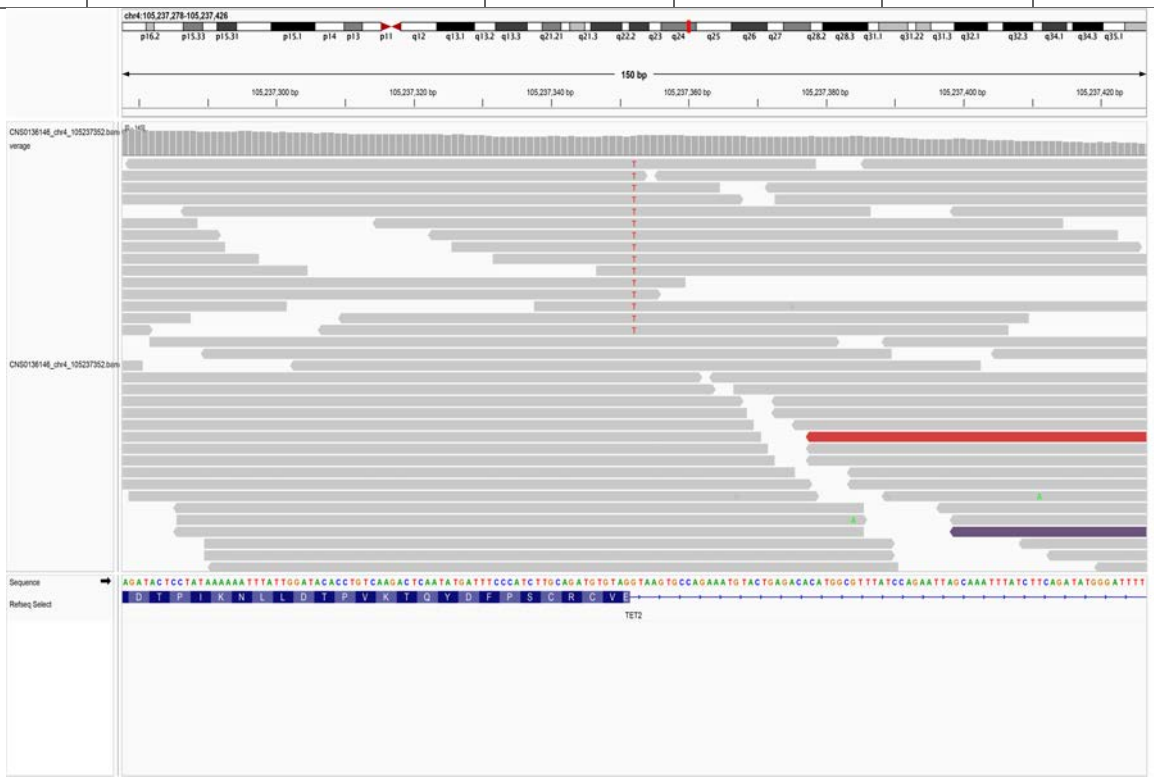
55.38. chr4_105237346_G/T

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



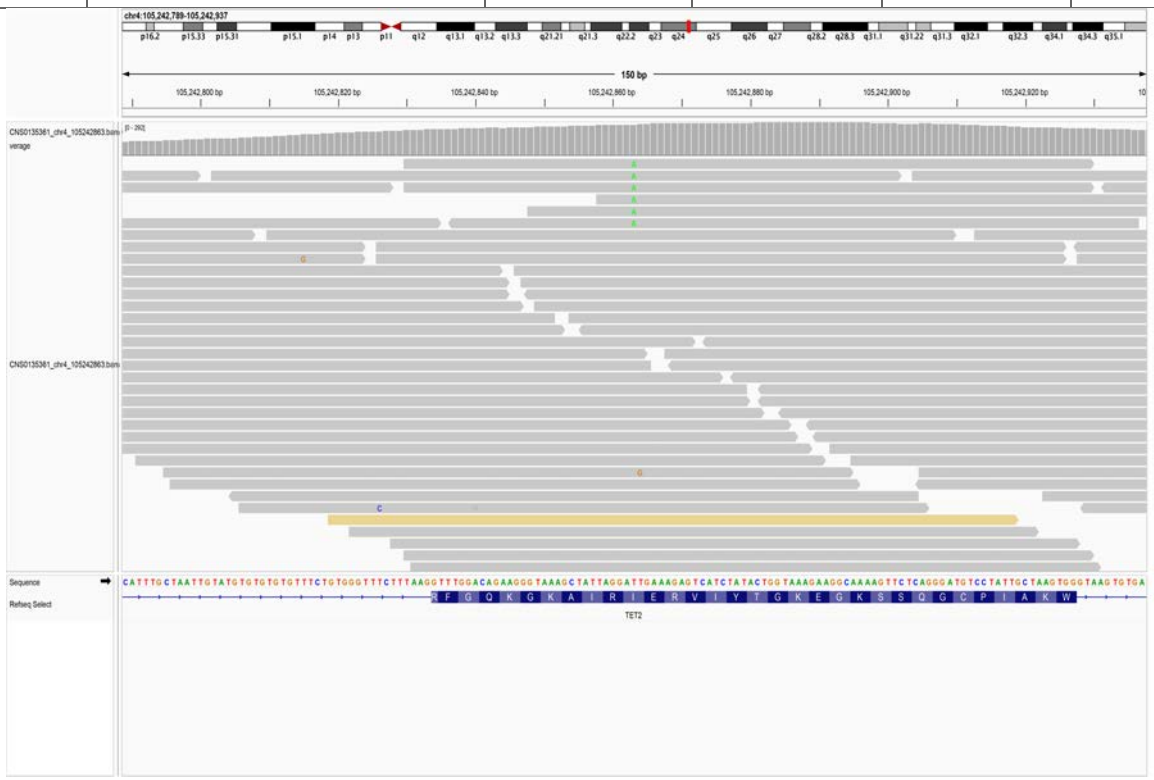
55.39. chr4_105237352_G/T

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



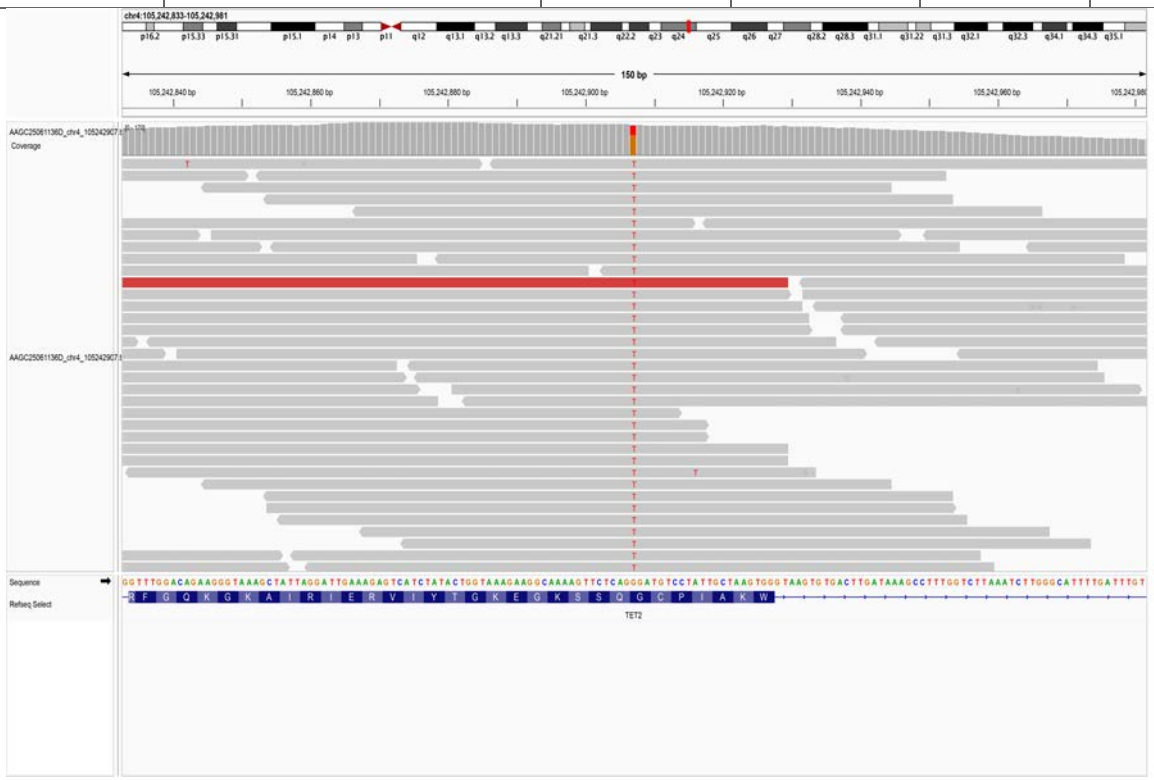
55.40. chr4_105242863_T/A

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



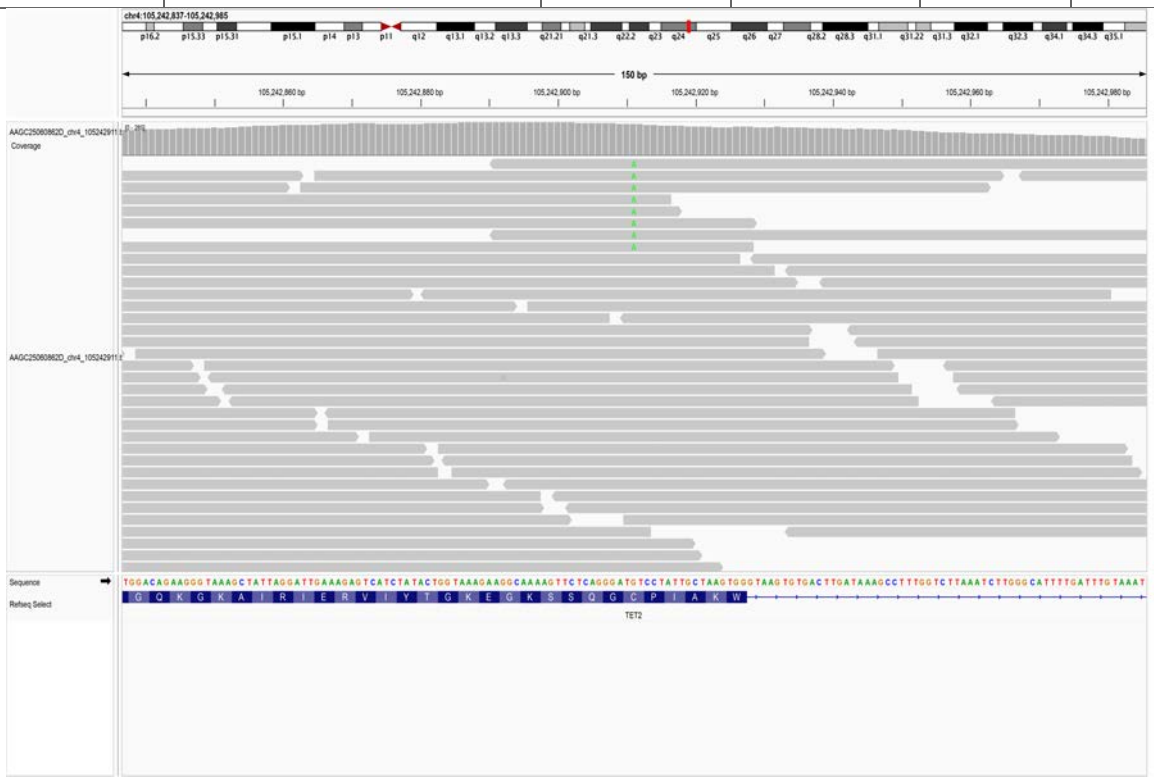
55.41. chr4_105242907_G/T

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



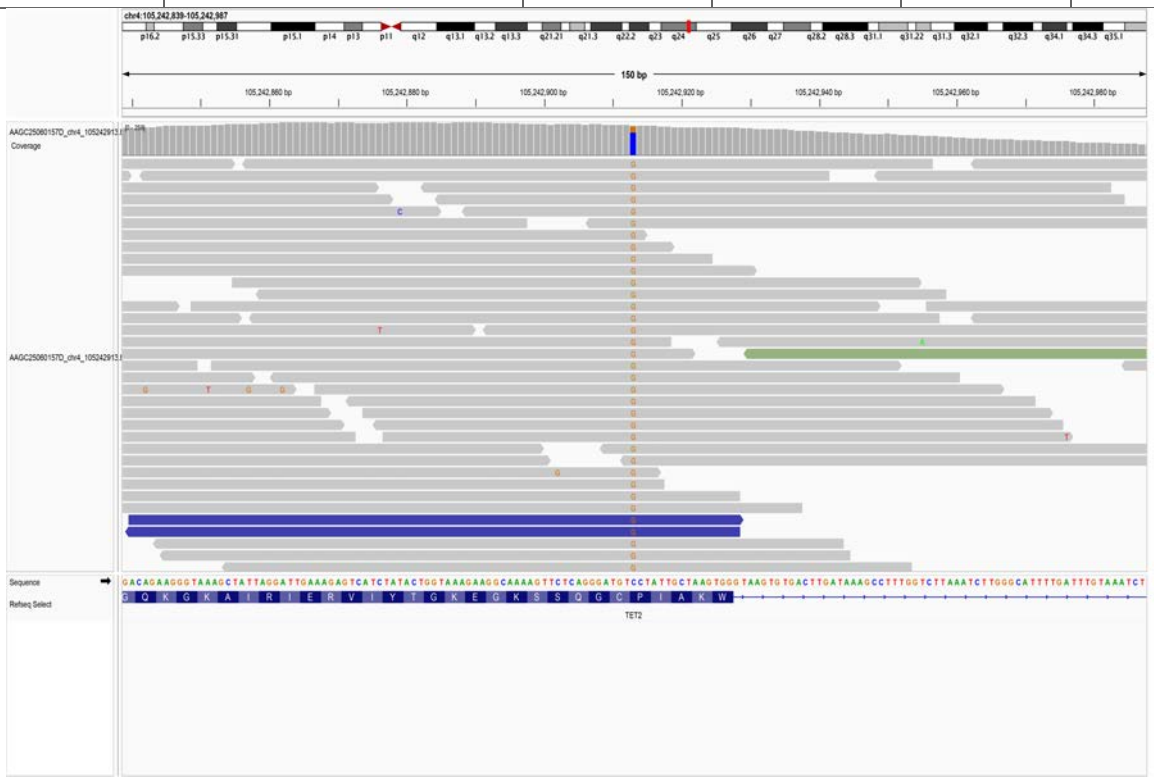
55.42. chr4_105242911_G/A

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



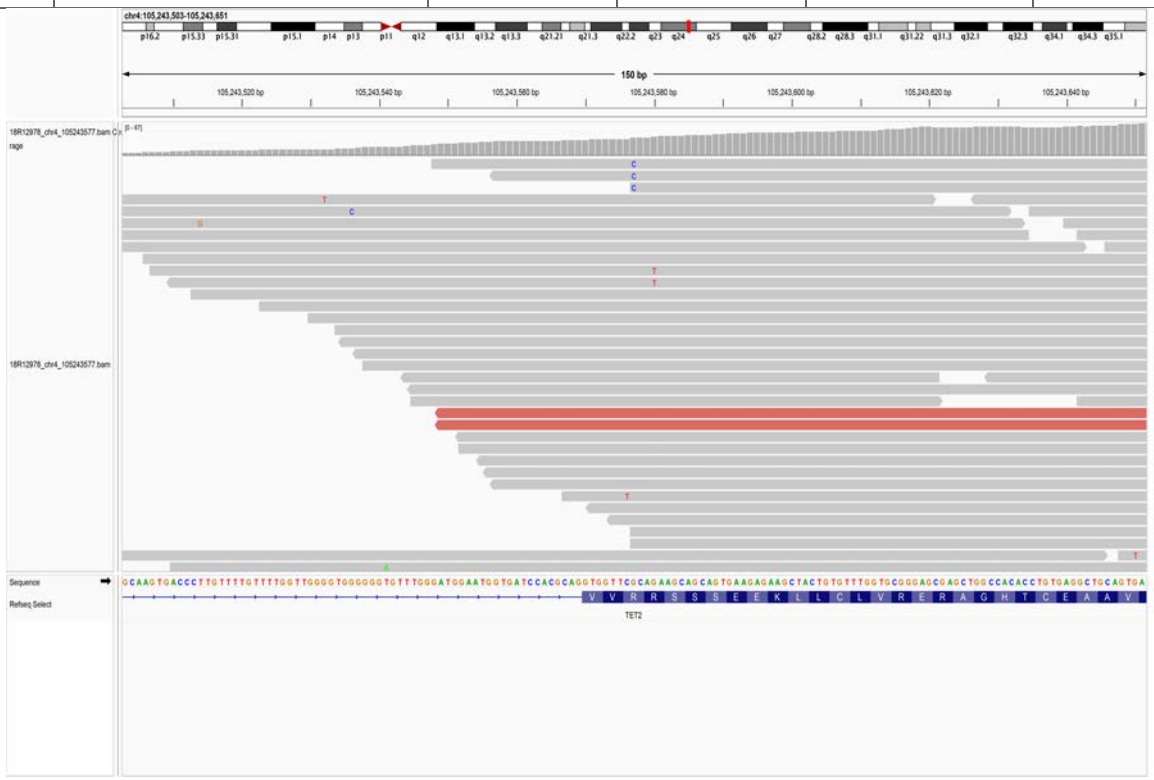
55.43. chr4_105242913_C/G

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



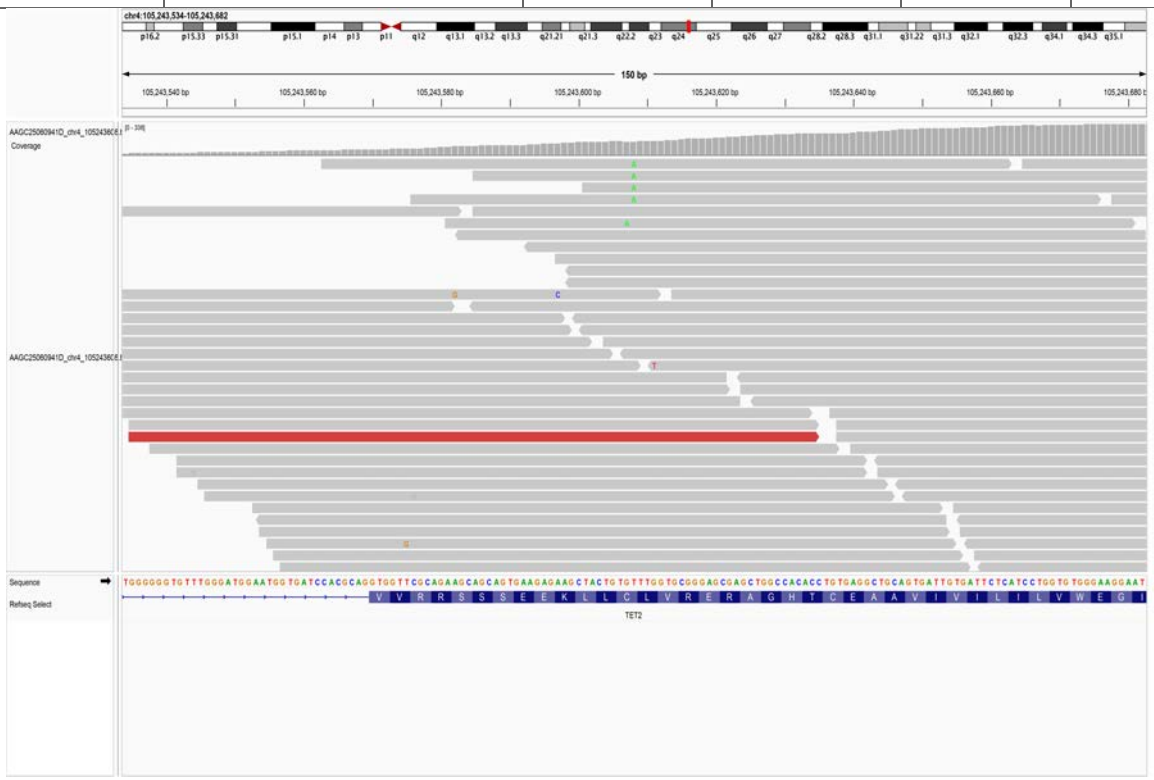
55.44. chr4_105243577_G/C

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



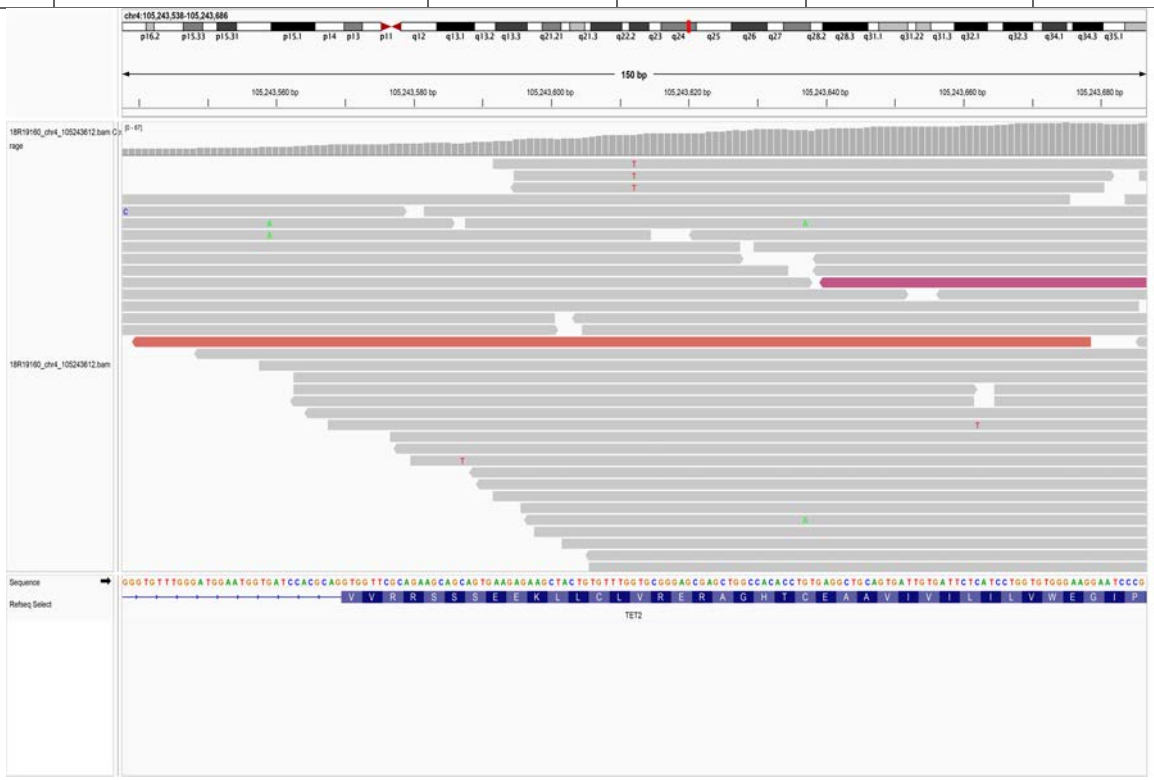
55.45. chr4_105243608_T/A

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



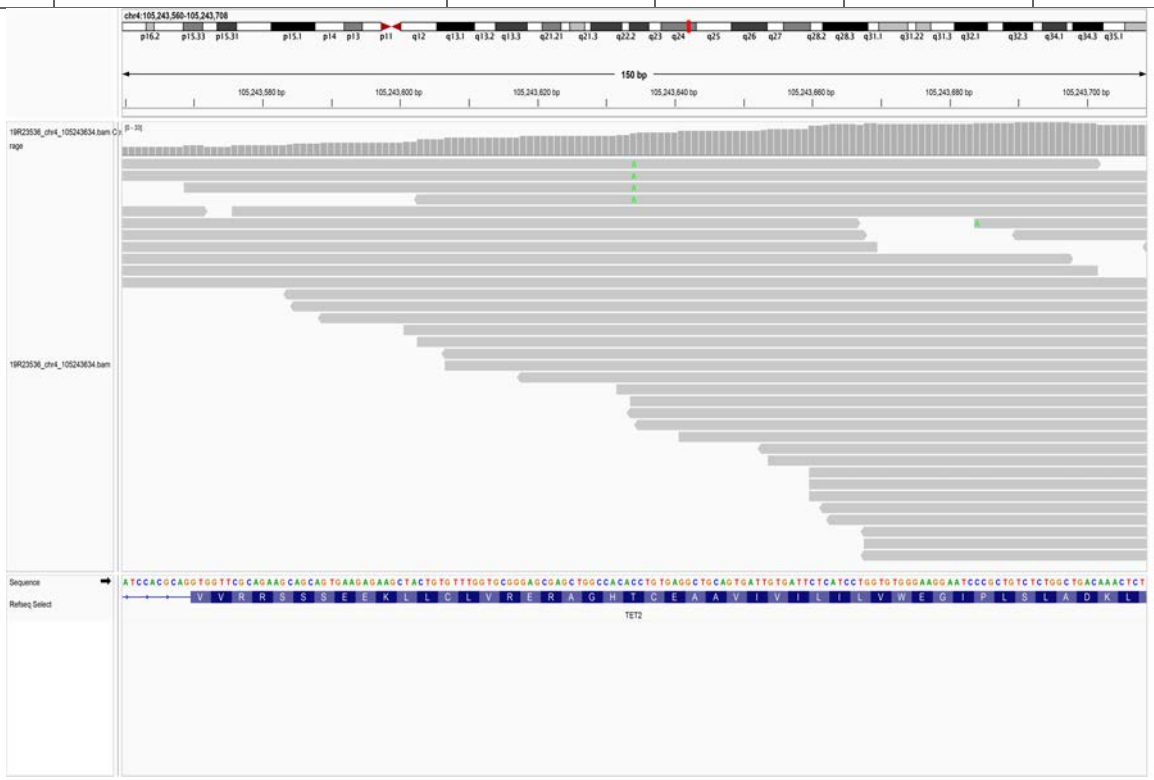
55.46. chr4_105243612_G/T

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



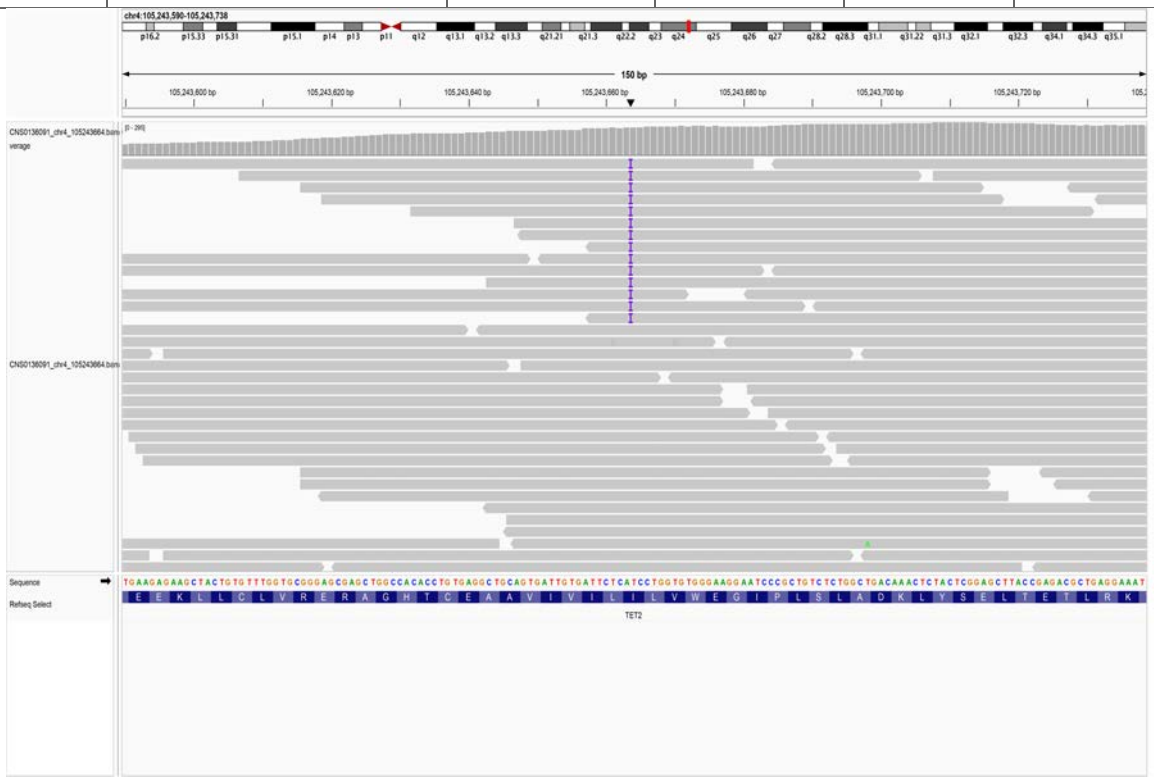
55.47. chr4_105243634_C/A

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



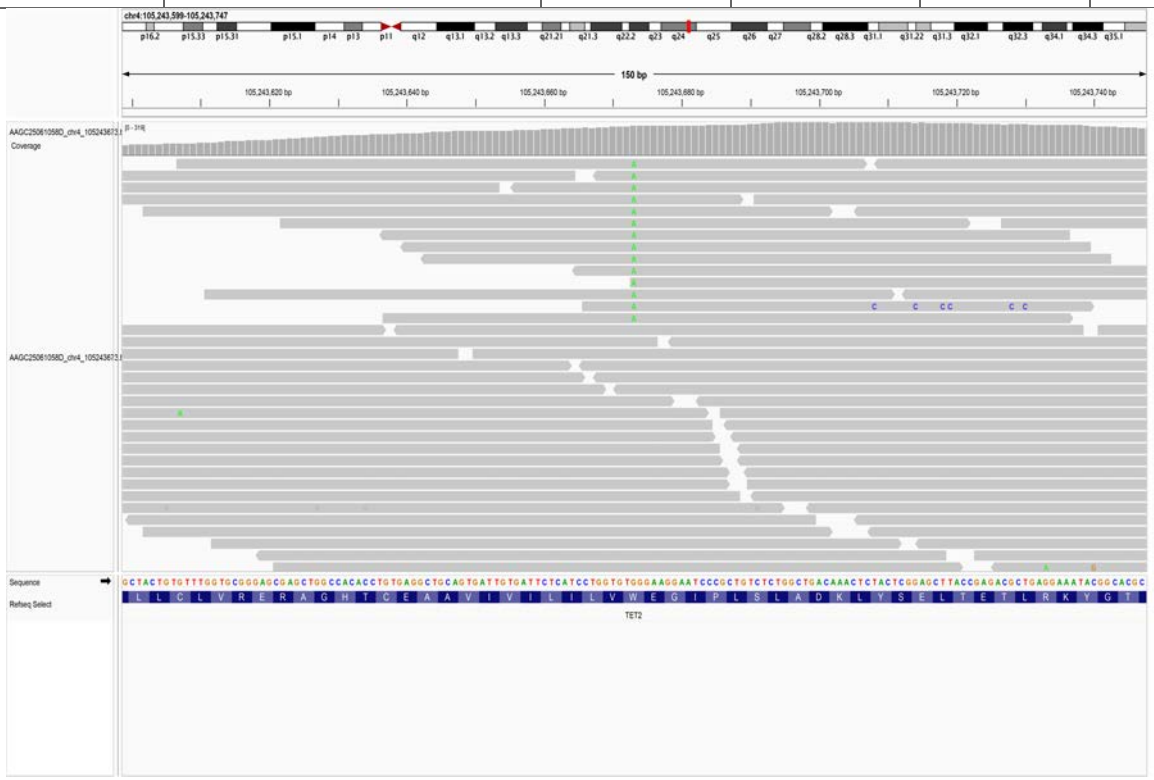
55.48. chr4_105243664_-/T

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



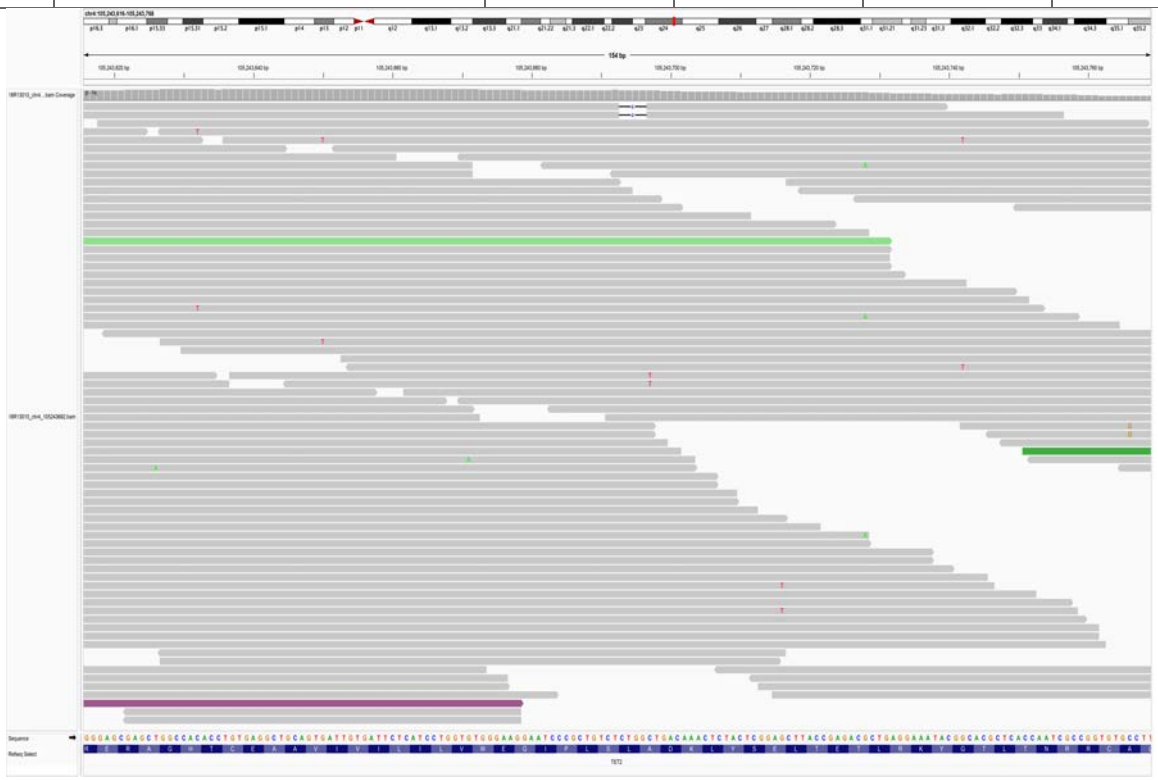
55.49. chr4_105243673_G/A

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



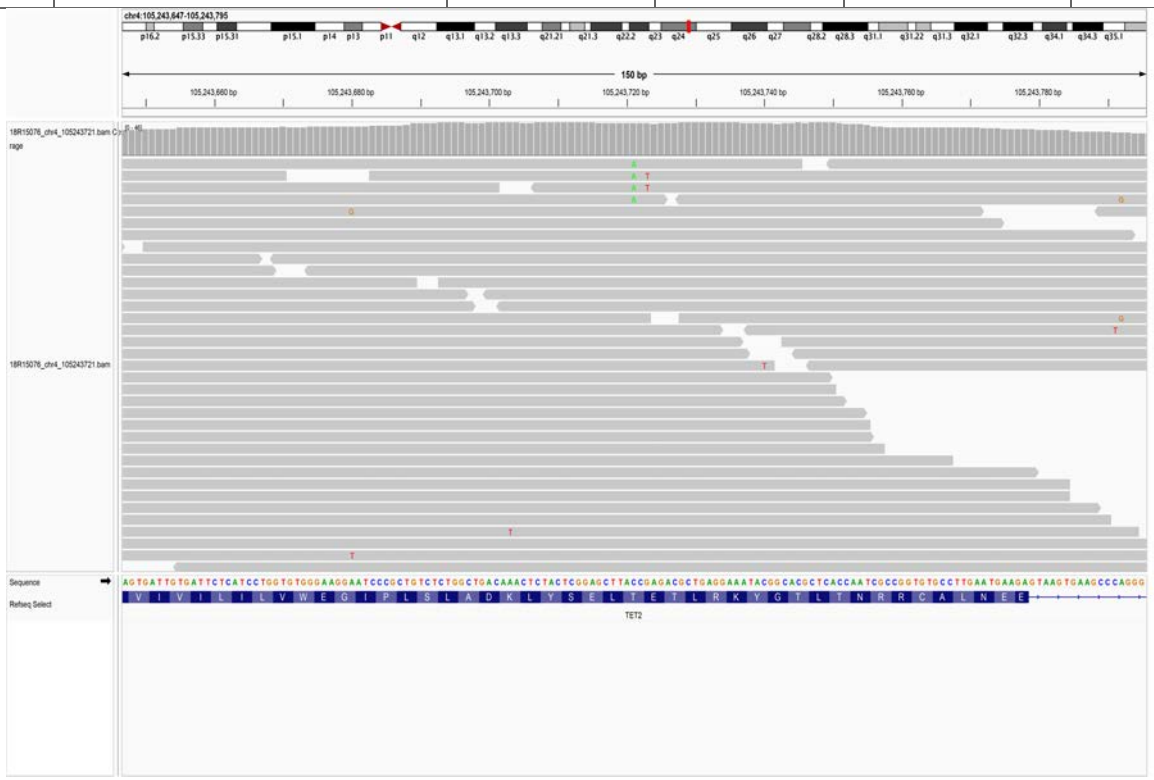
55.50. chr4_105243693_CTGG/-

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



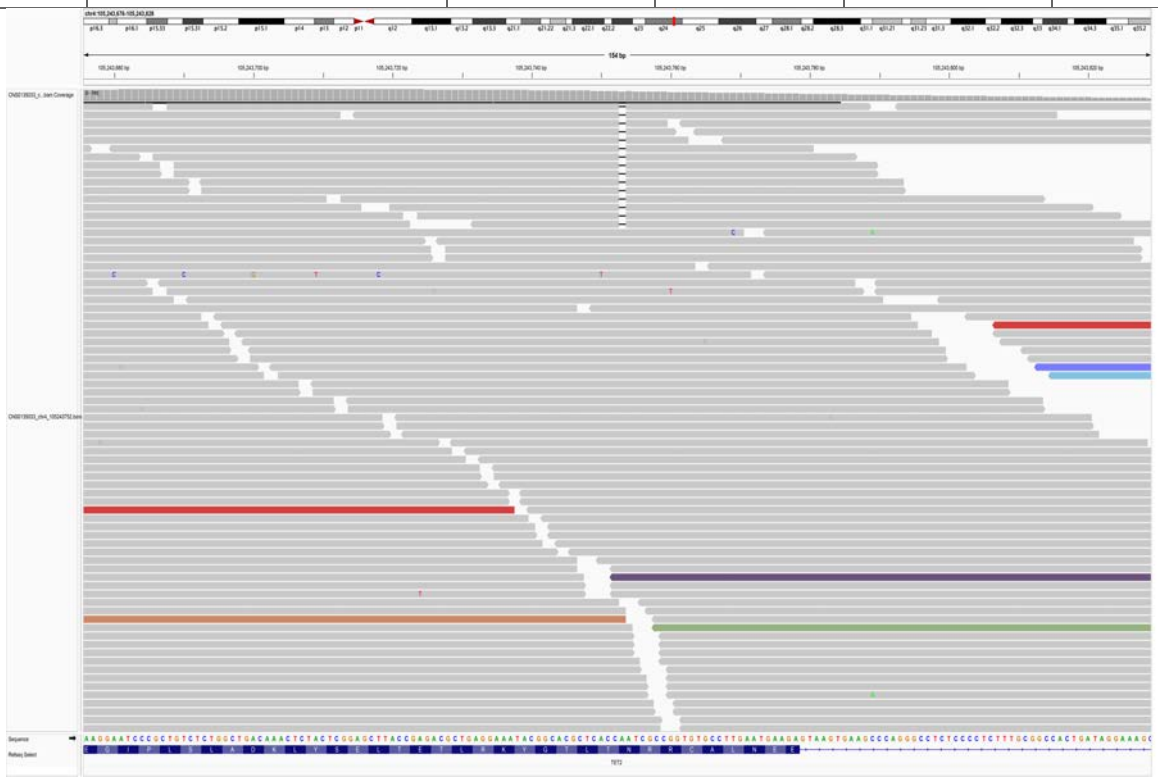
55.51. chr4_105243721_C/A

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



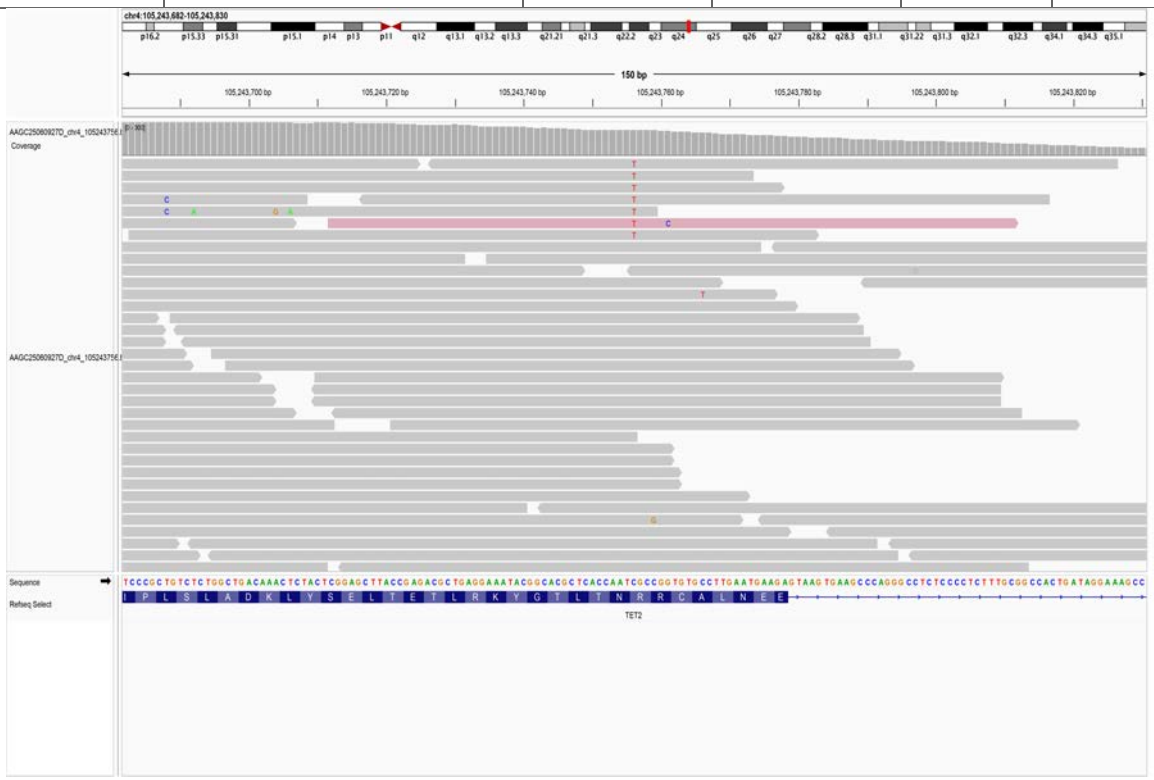
55.52. chr4_105243753_A/-

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



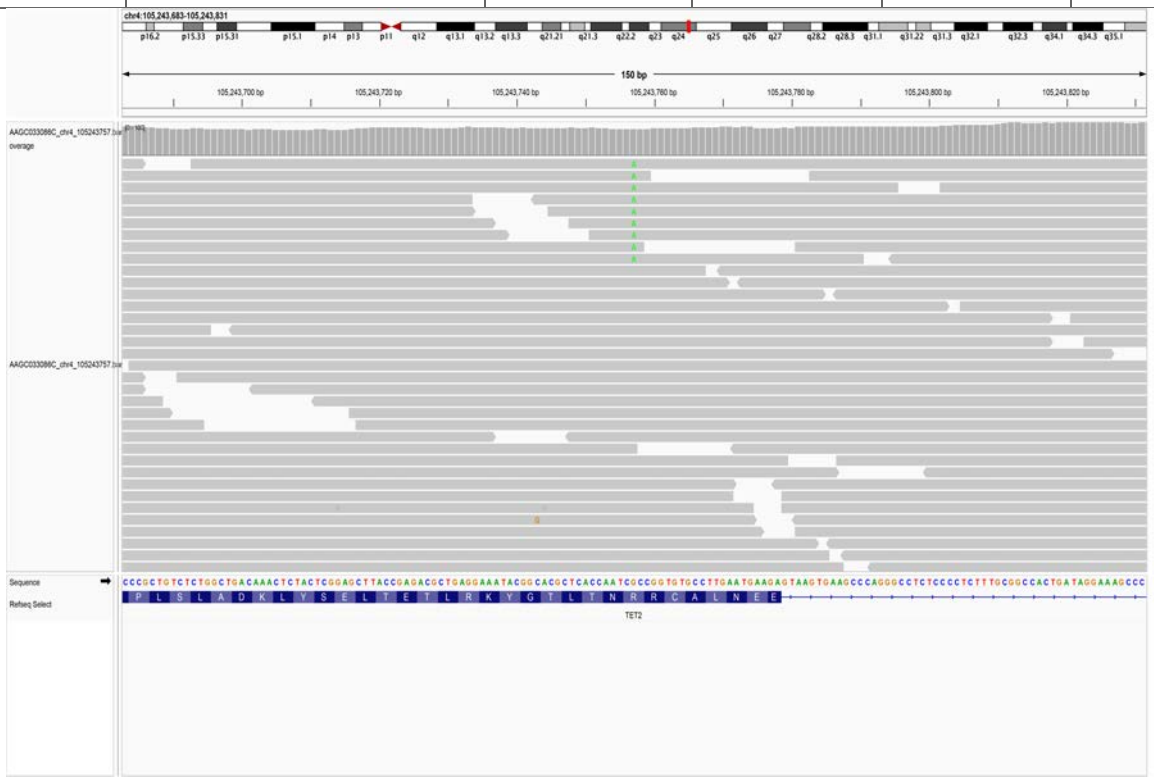
55.53. chr4_105243756_C/T

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



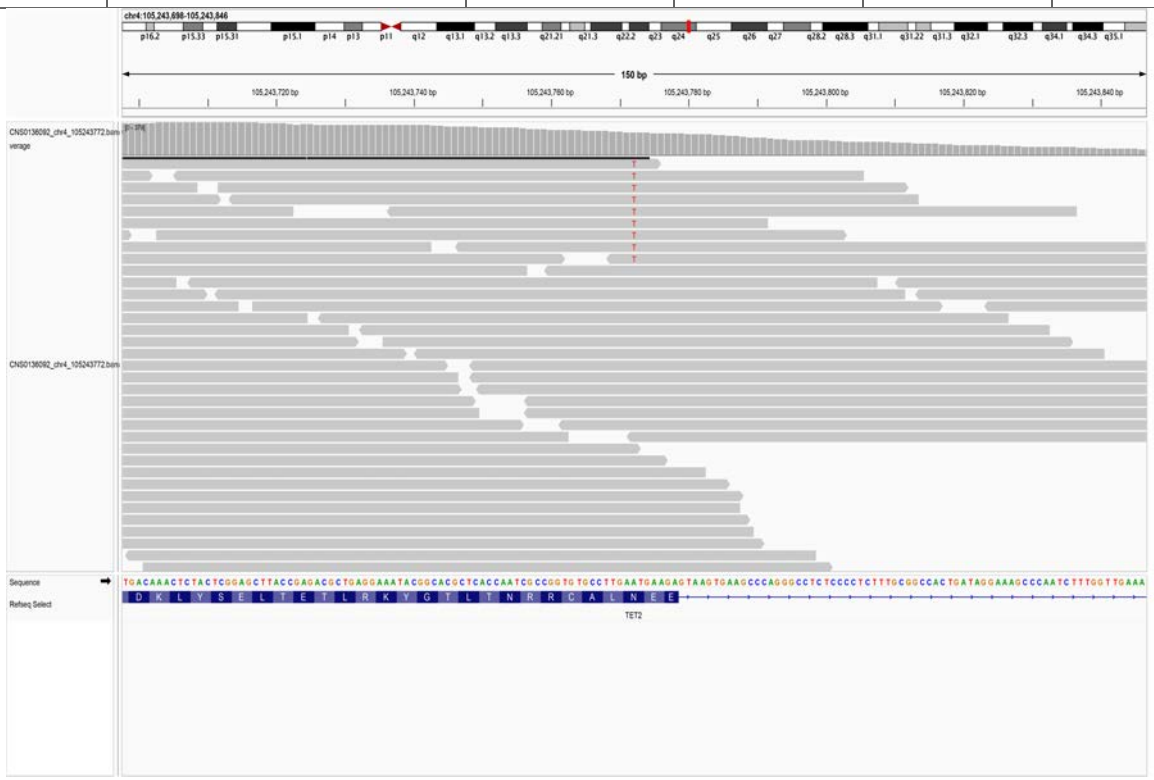
55.54. chr4_105243757_G/A

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



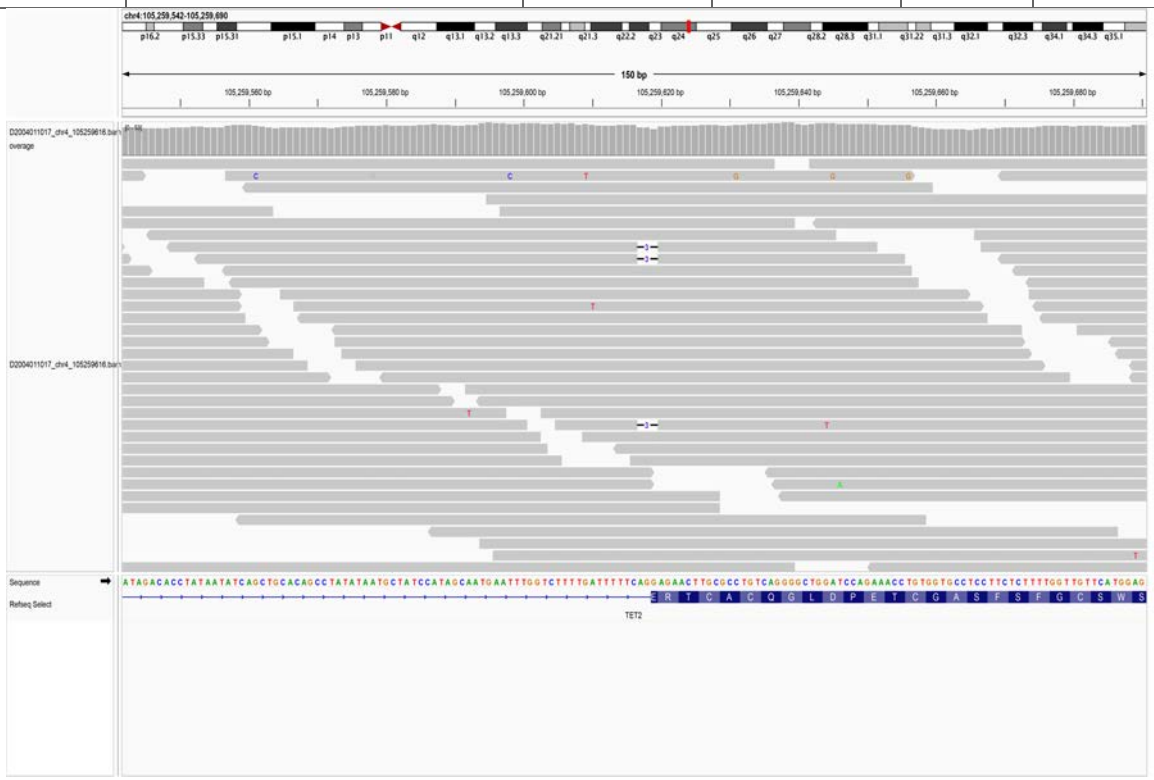
55.55. chr4_105243772_A/T

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



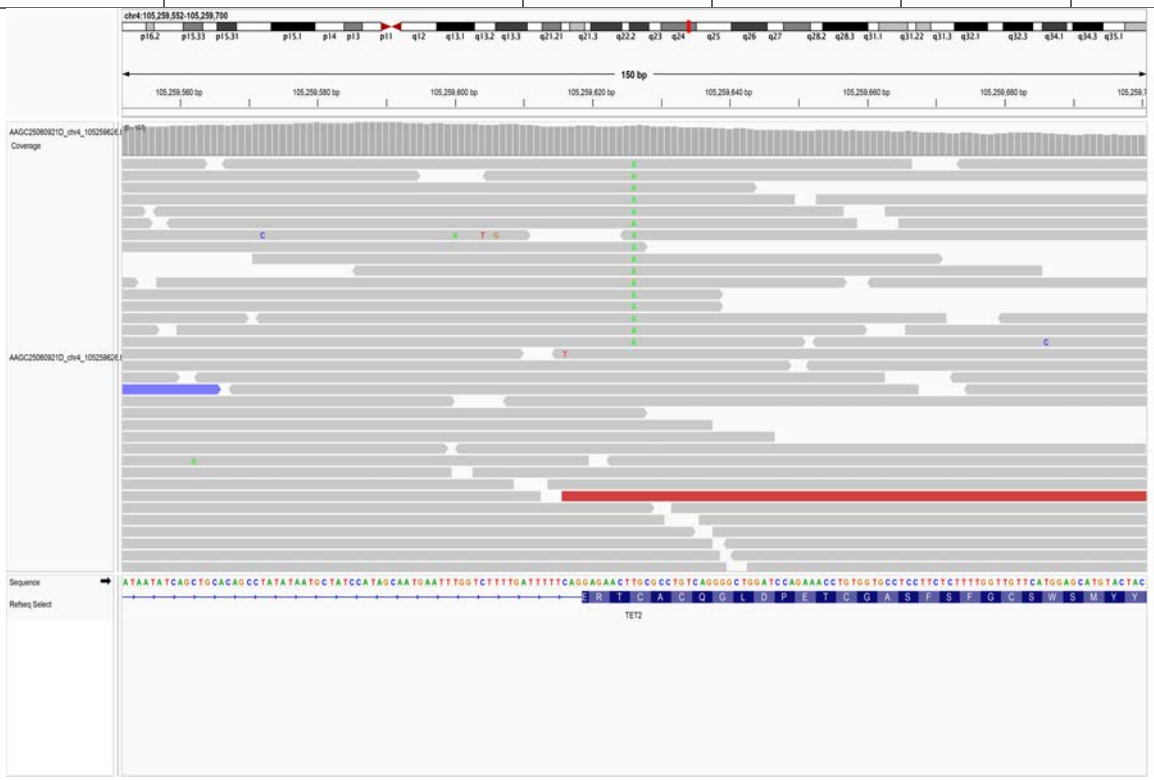
55.56. chr4_105259617_AGG/-

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



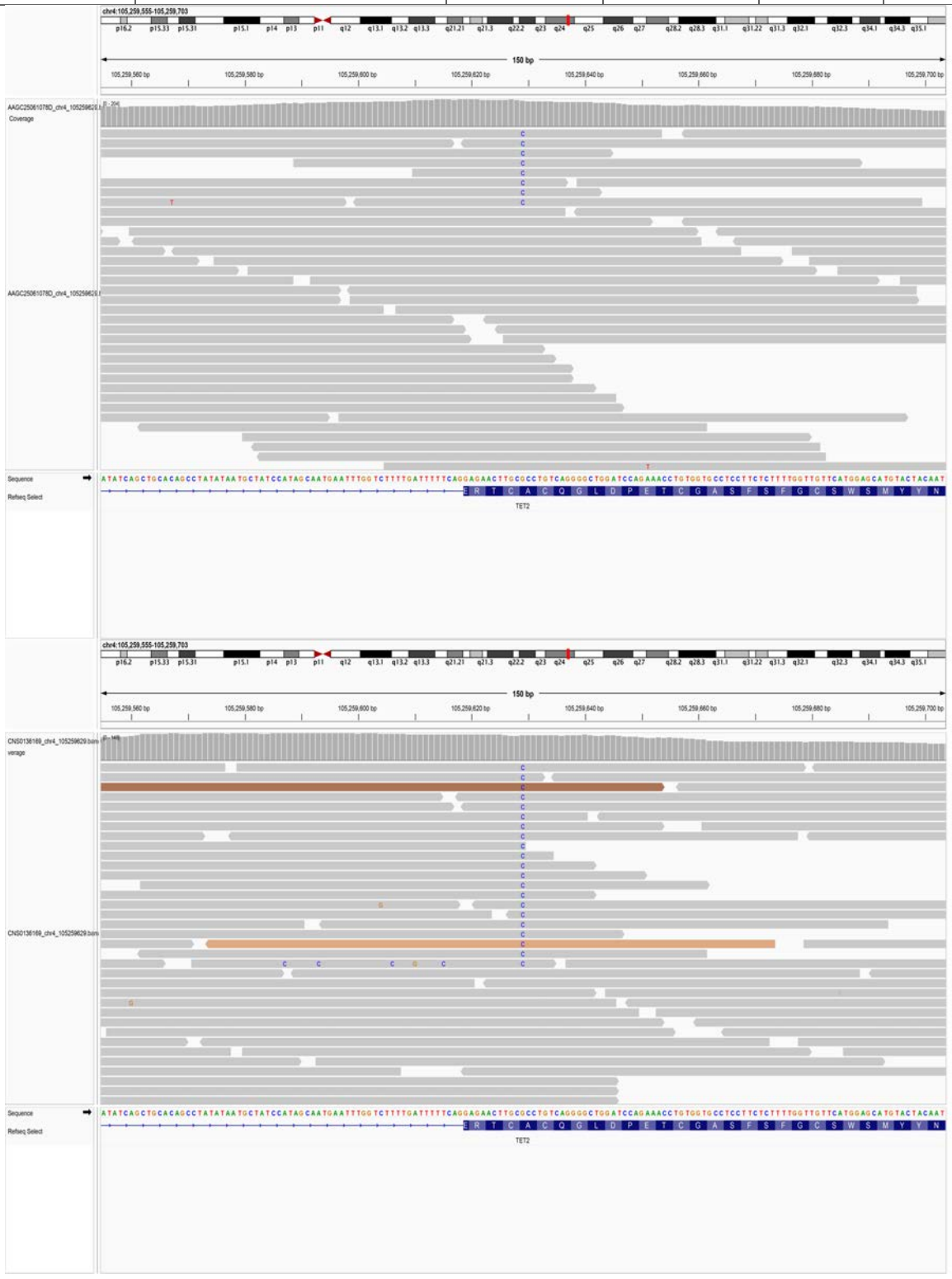
55.57. chr4_105259626_T/A

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



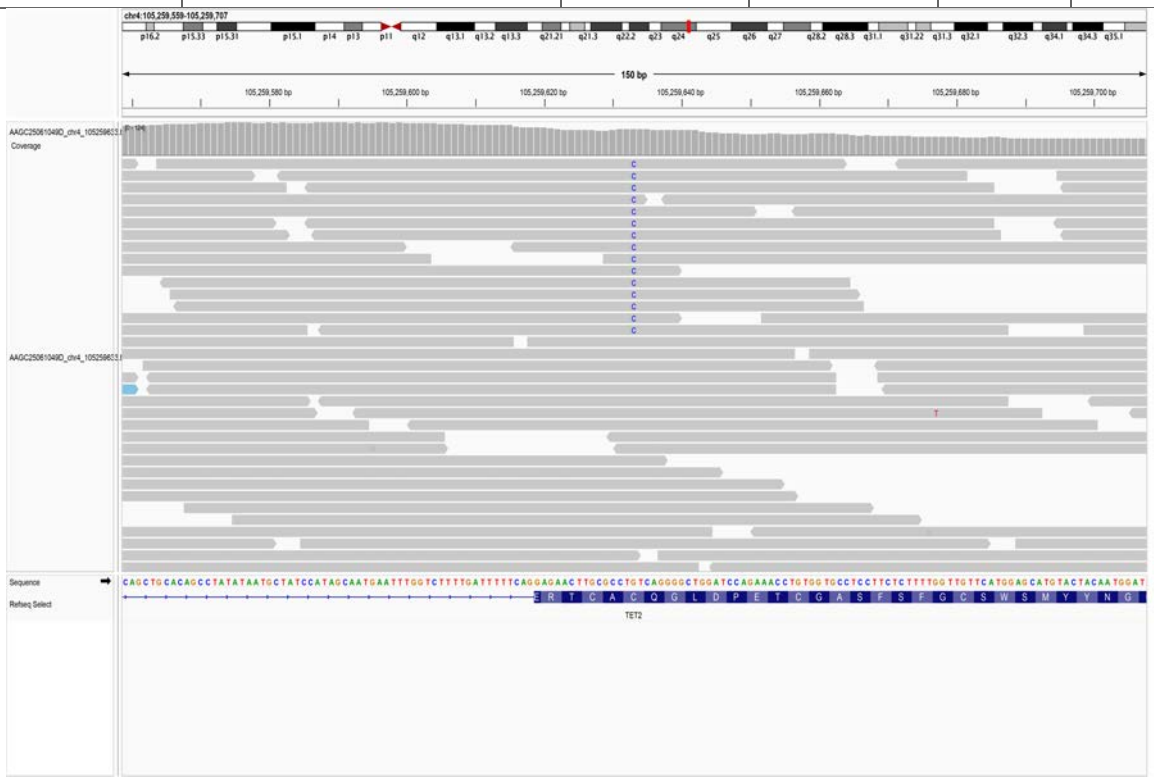
55.58. chr4_105259629_G/C

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



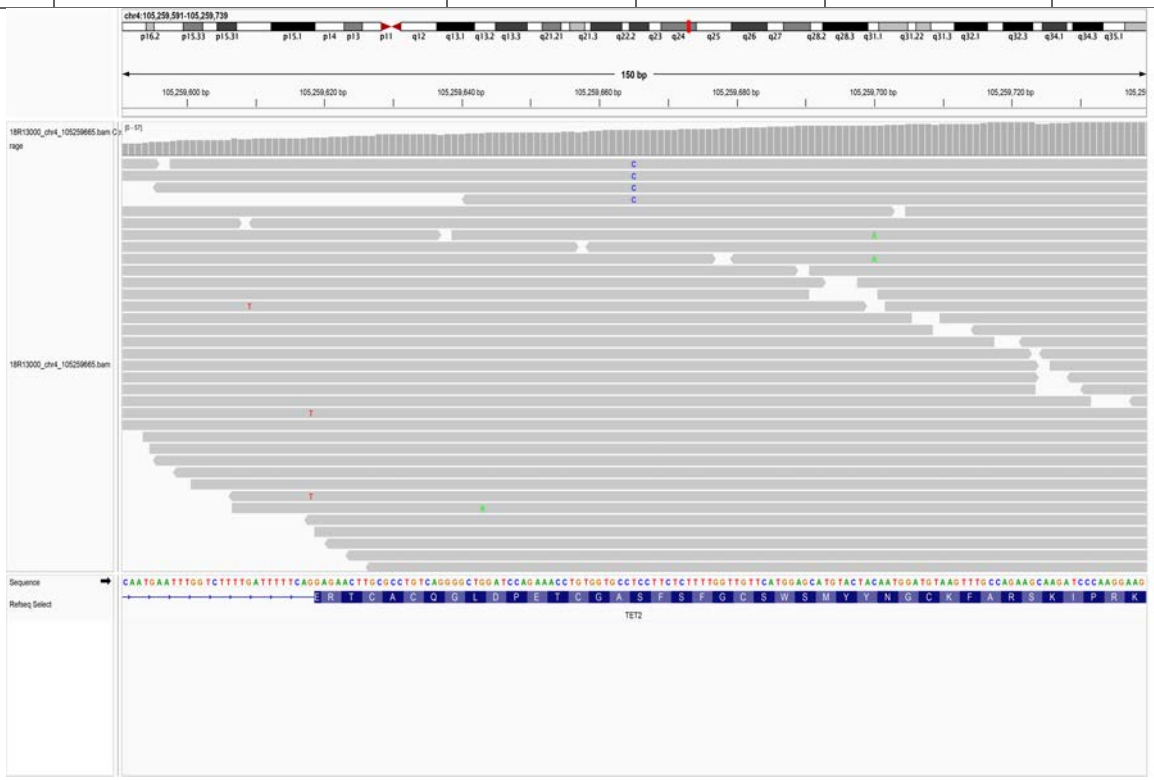
55.59. chr4_105259633_G/C

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



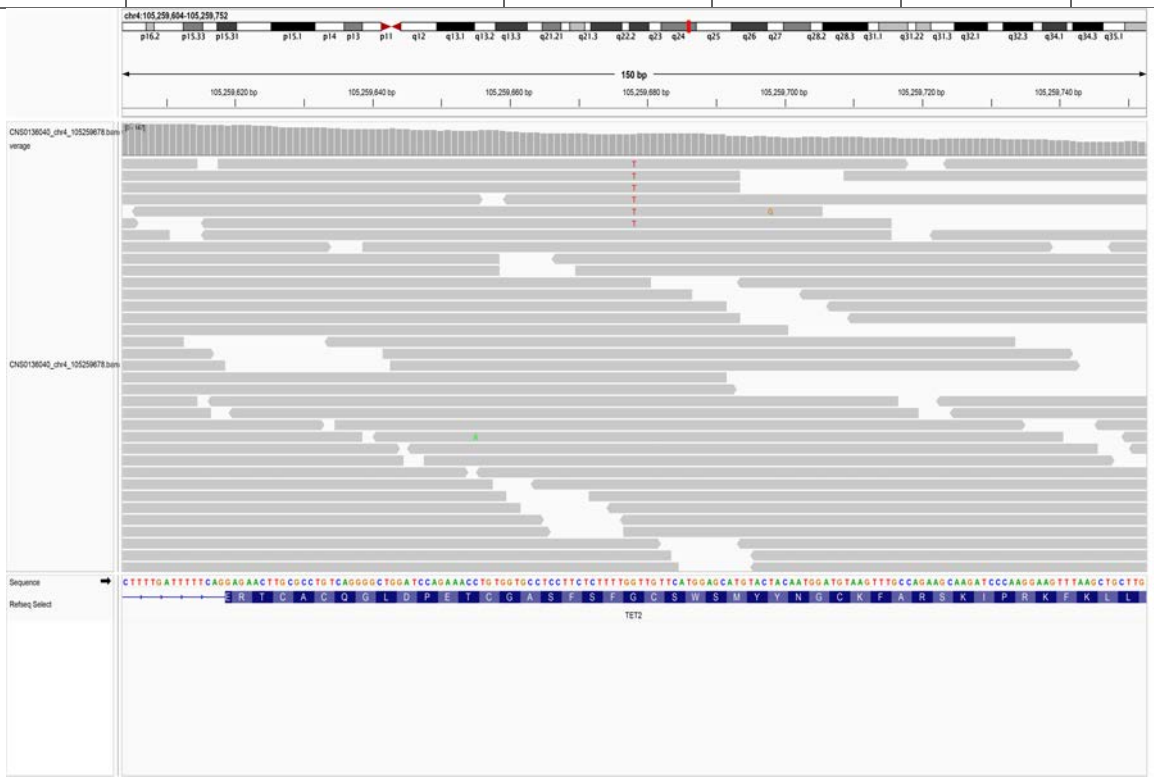
55.60. chr4_105259665_T/C

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



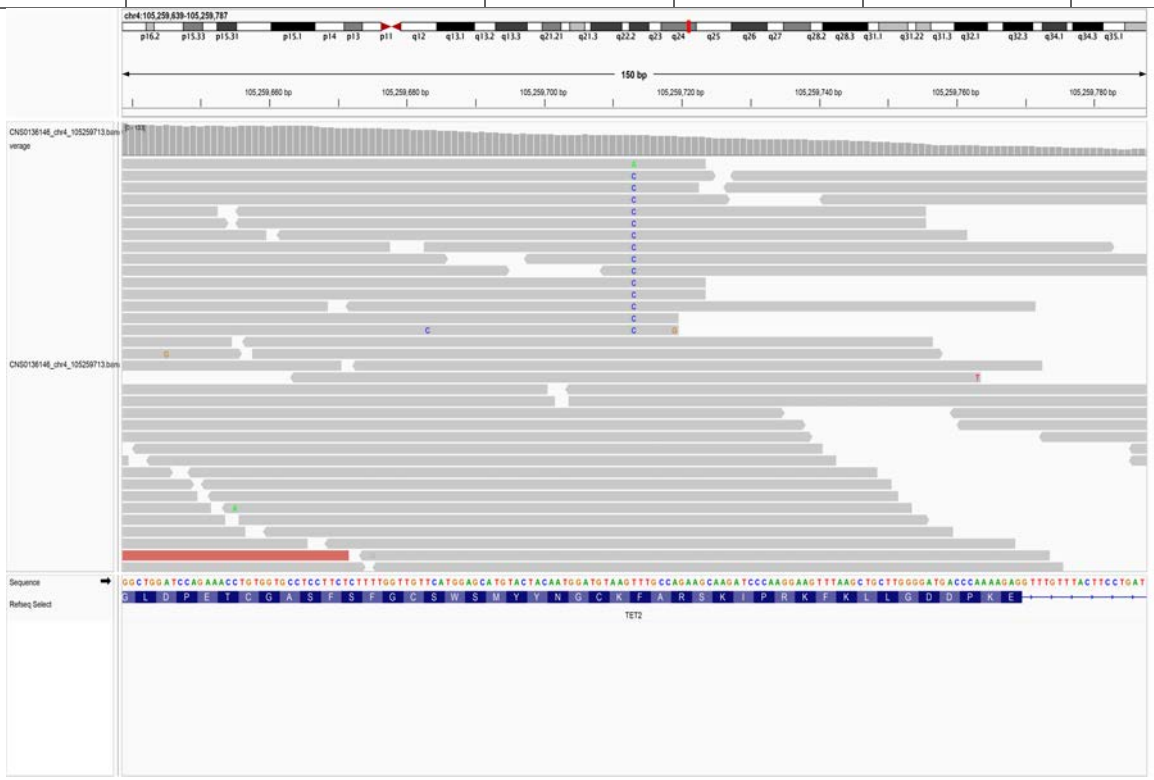
55.61. chr4_105259678_G/T

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



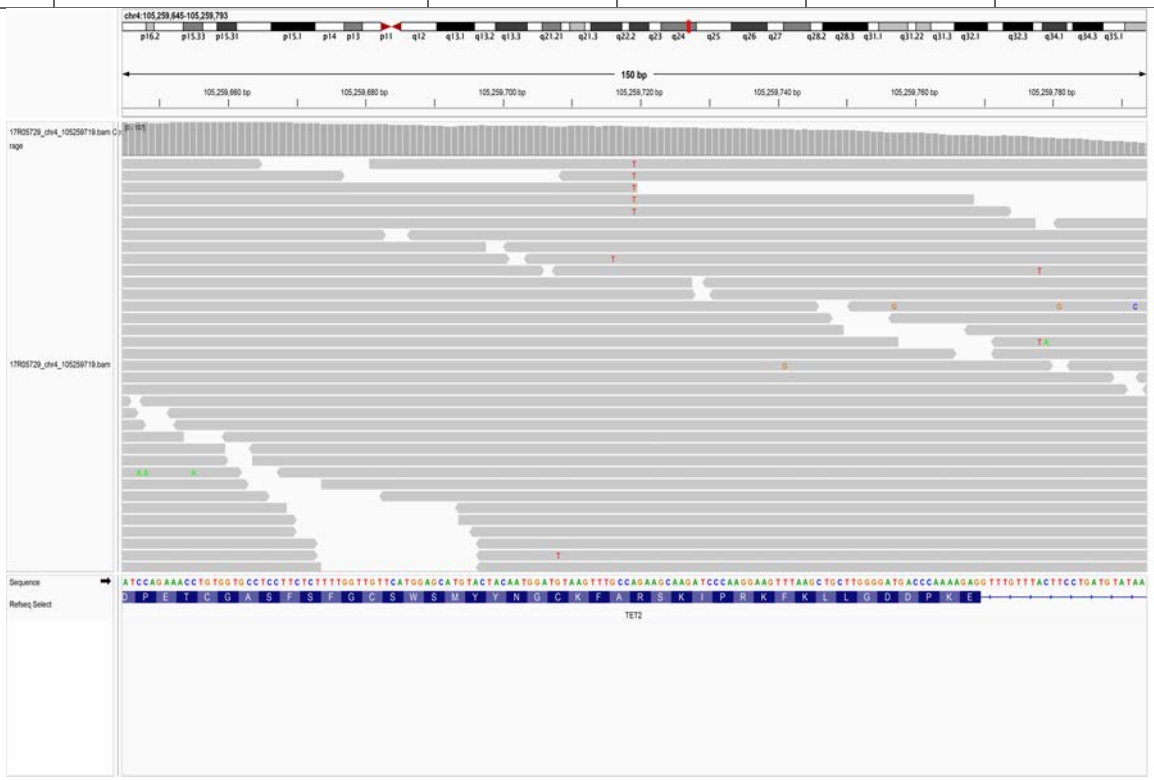
55.62. chr4_105259713_T/C

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



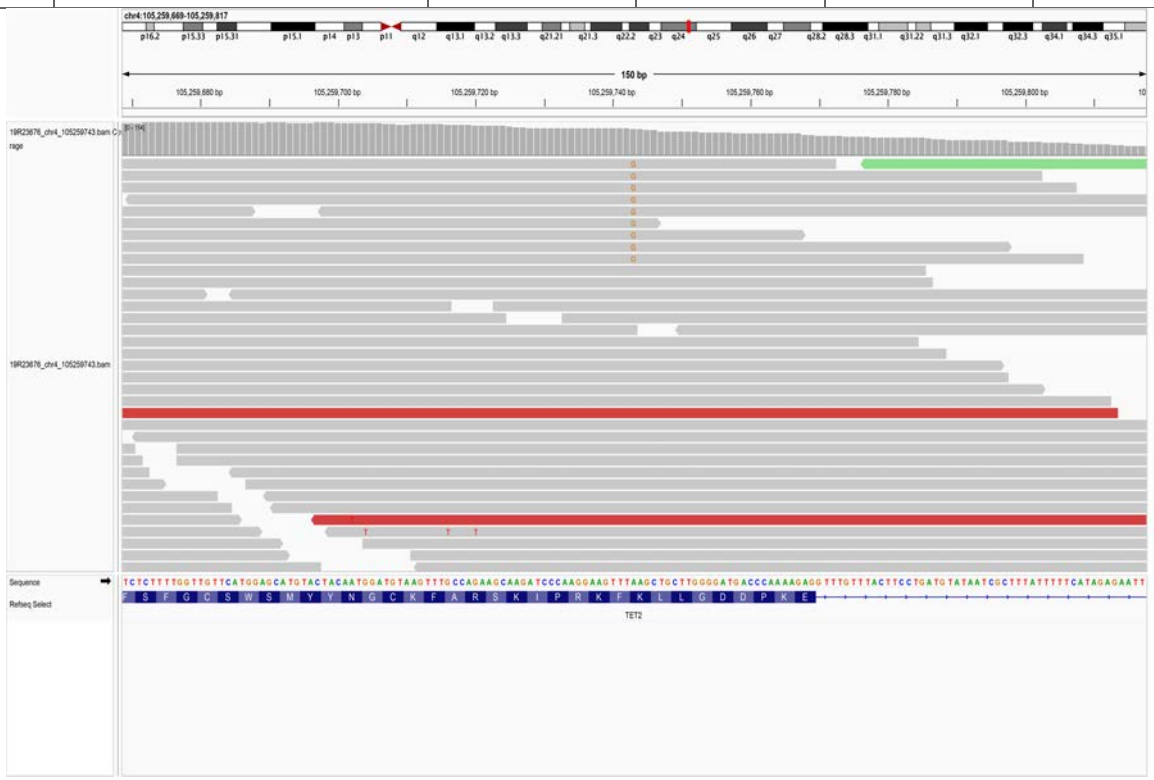
55.63. chr4_105259719_A/T

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



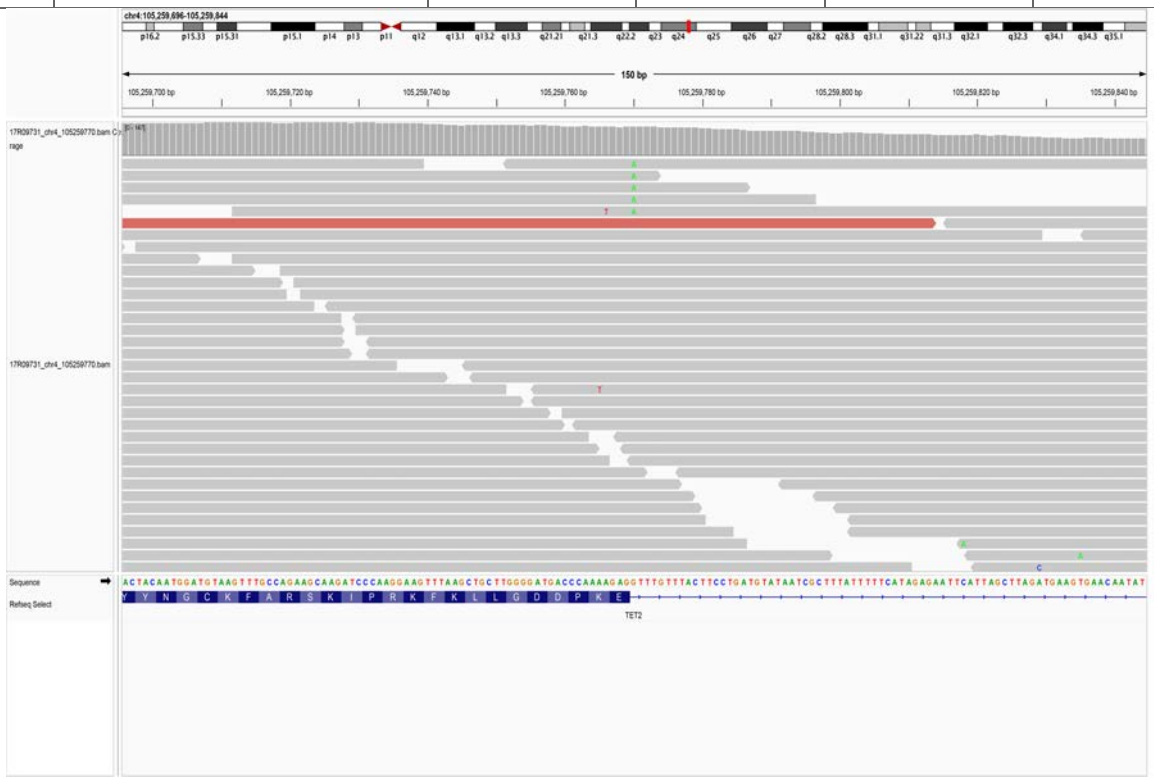
55.64. chr4_105259743_A/G

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



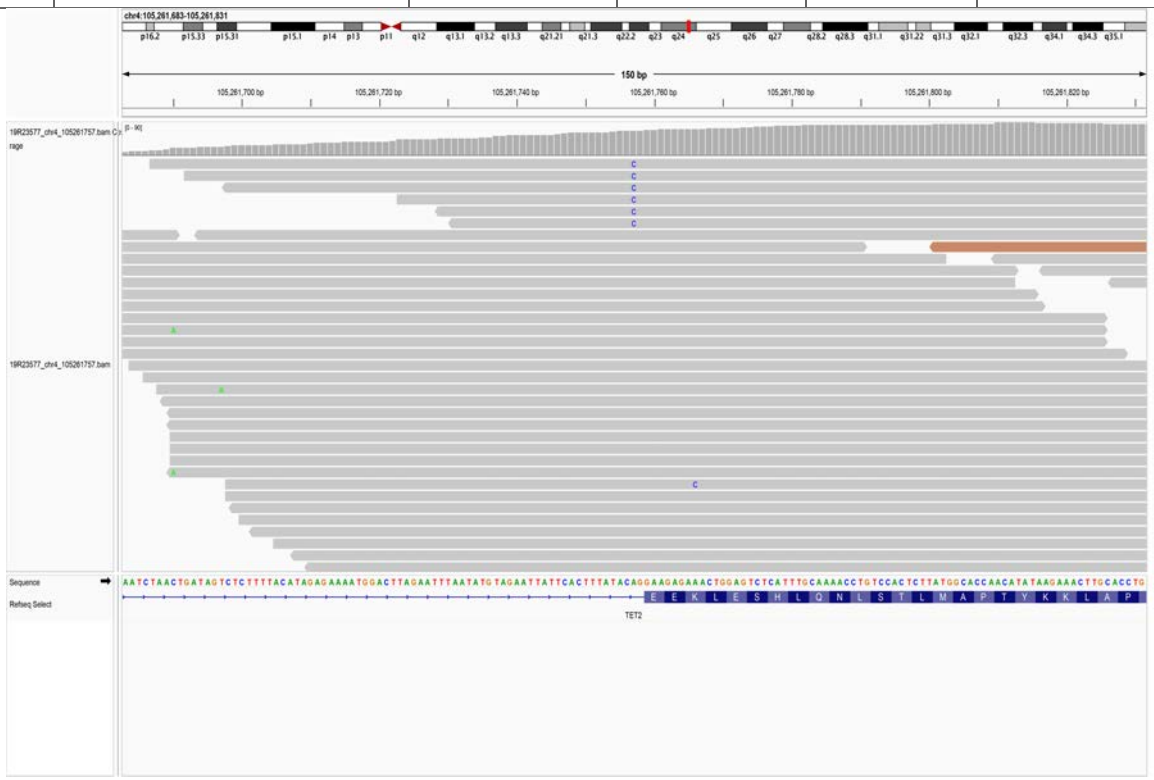
55.65. chr4_105259770_G/A

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



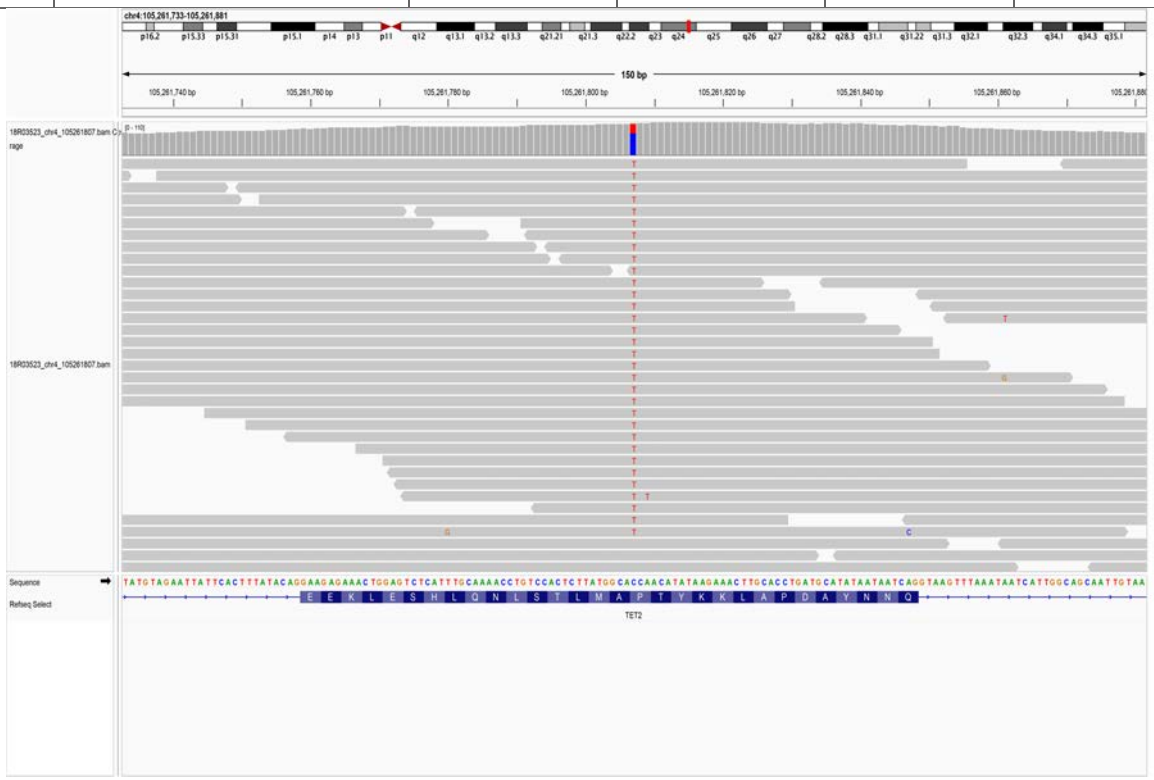
55.66. chr4_105261757_A/C

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



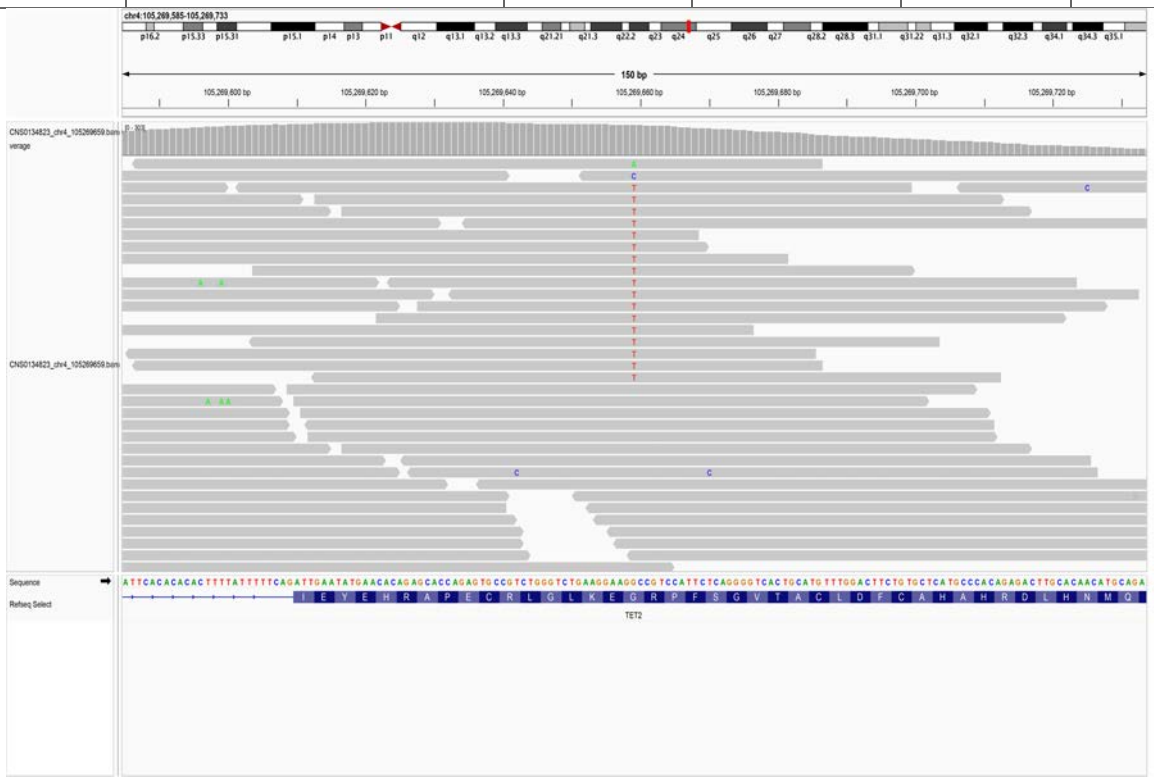
55.67. chr4_105261807_C/T

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



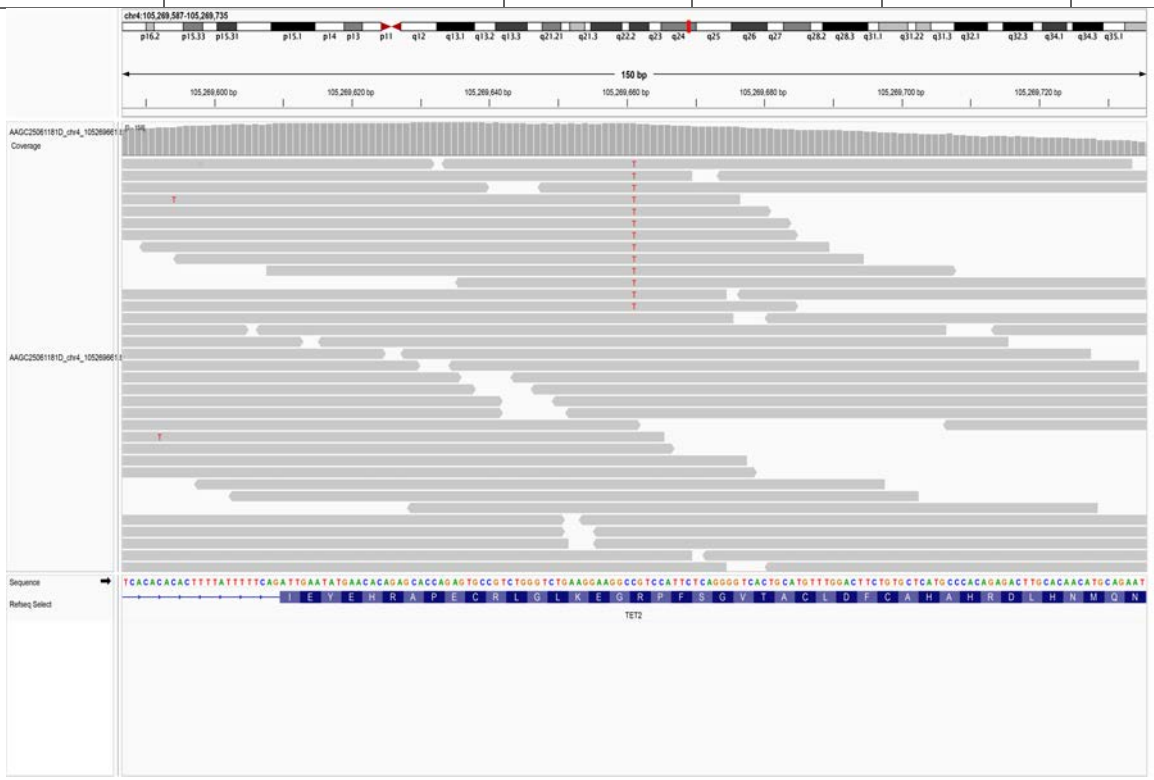
55.68. chr4_105269659_G/T

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



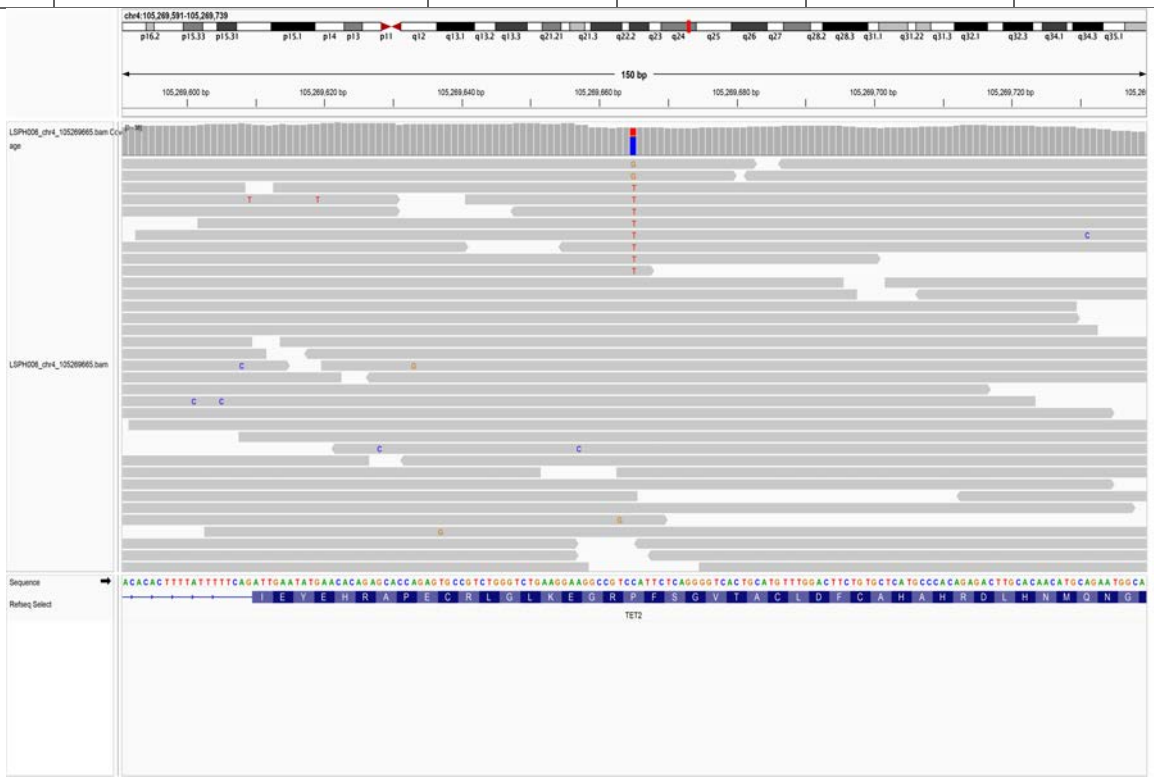
55.69. chr4_105269661_C/T

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



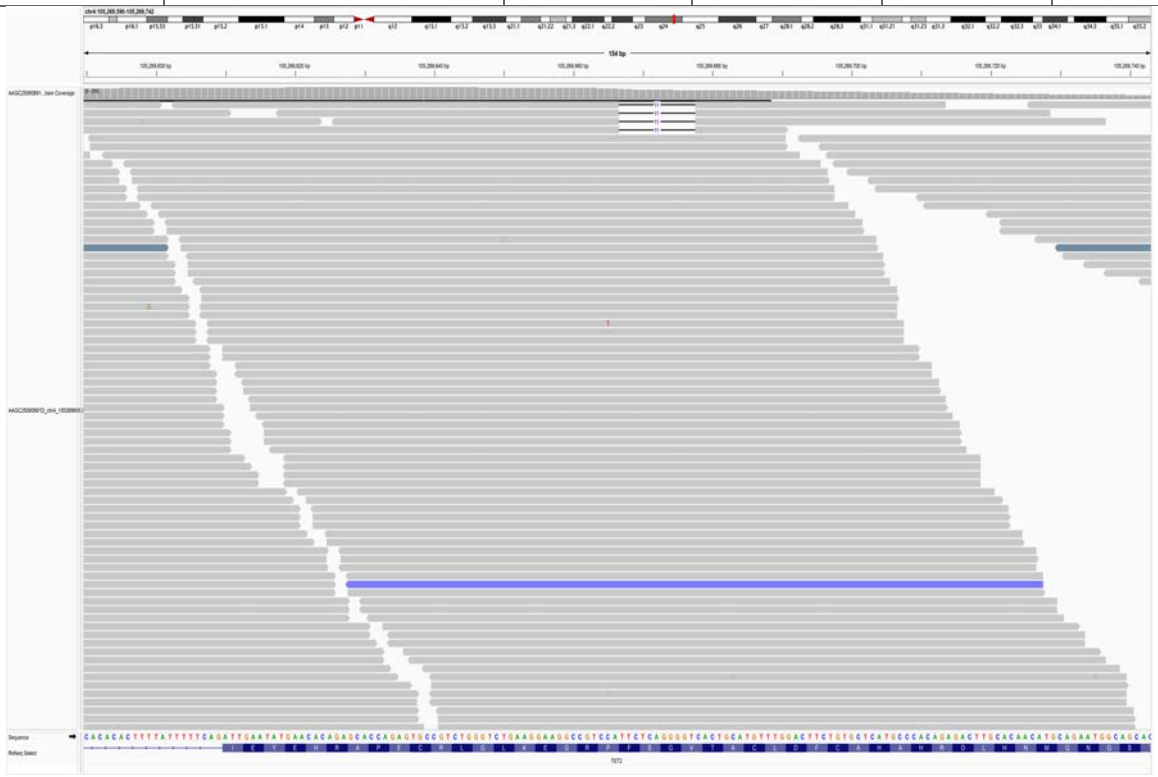
55.70. chr4_105269665_C/T

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



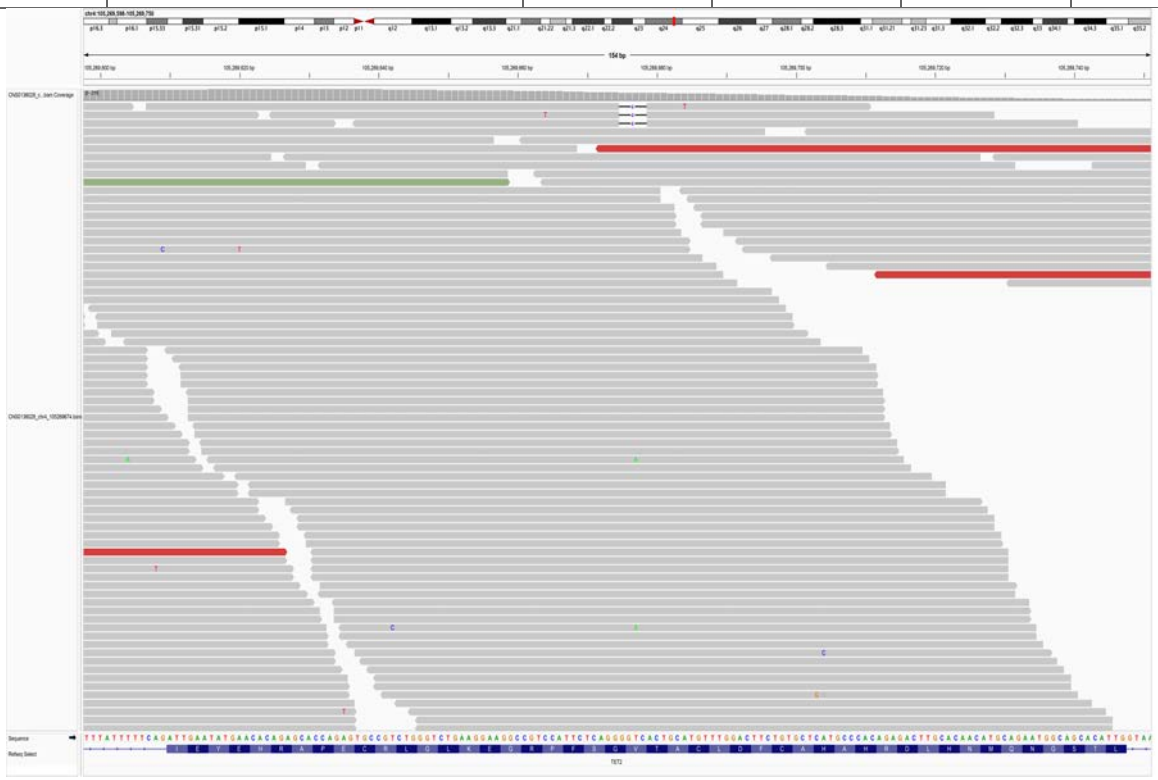
55.71. chr4_105269667_TTCTCAGGGGT/-

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



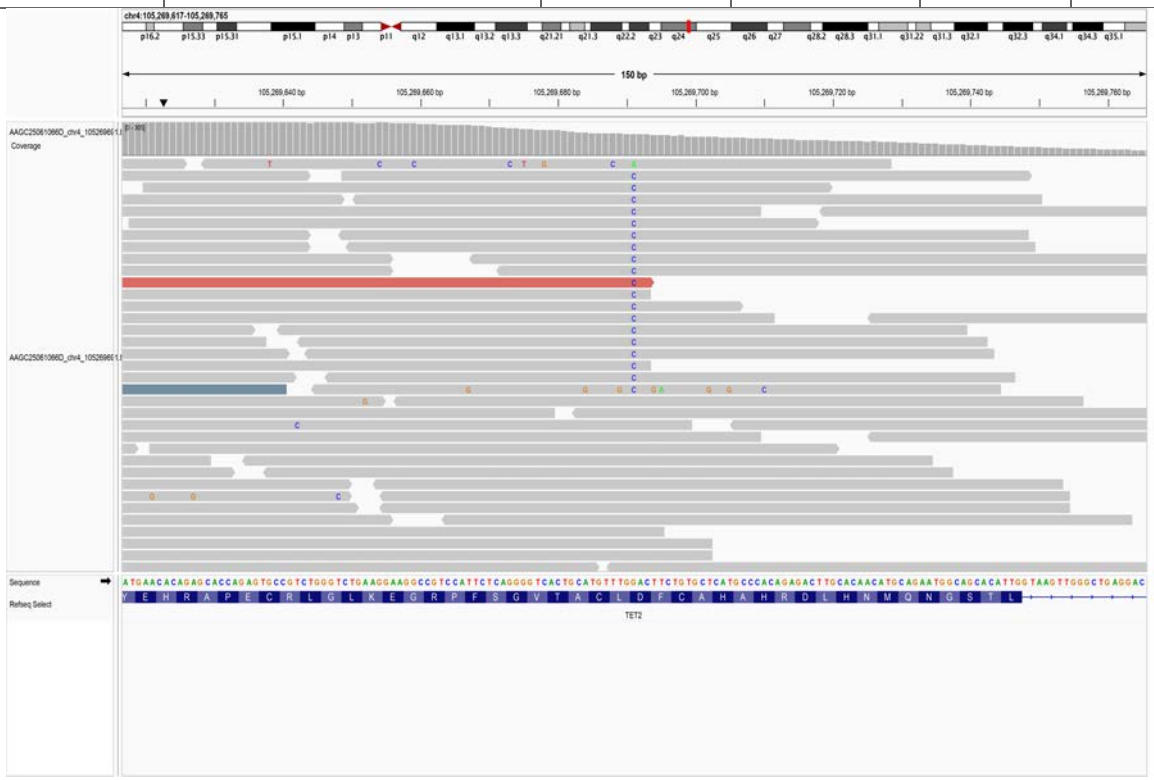
55.72. chr4_105269675_GGTC/-

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



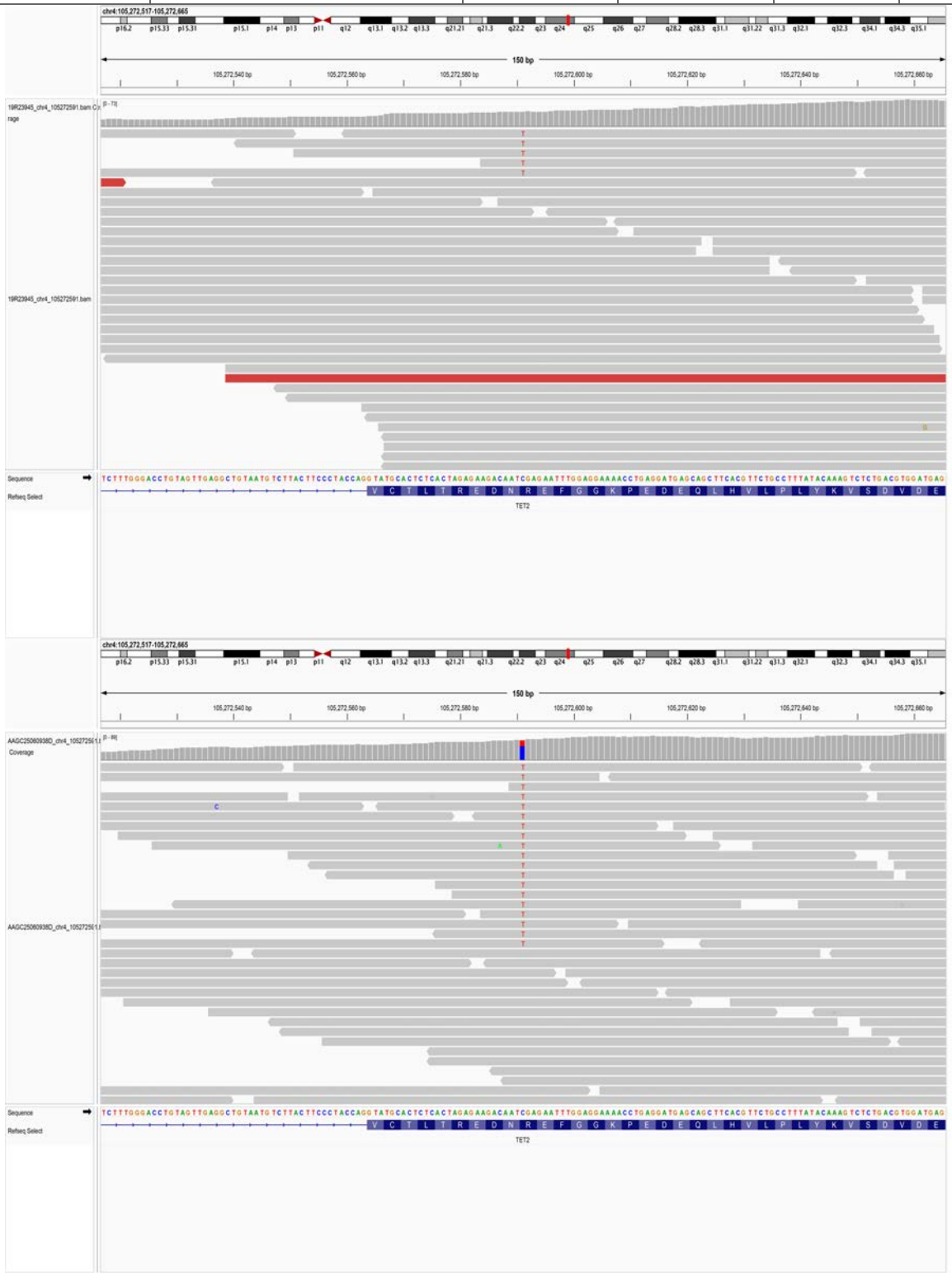
55.73. chr4_105269691_G/C

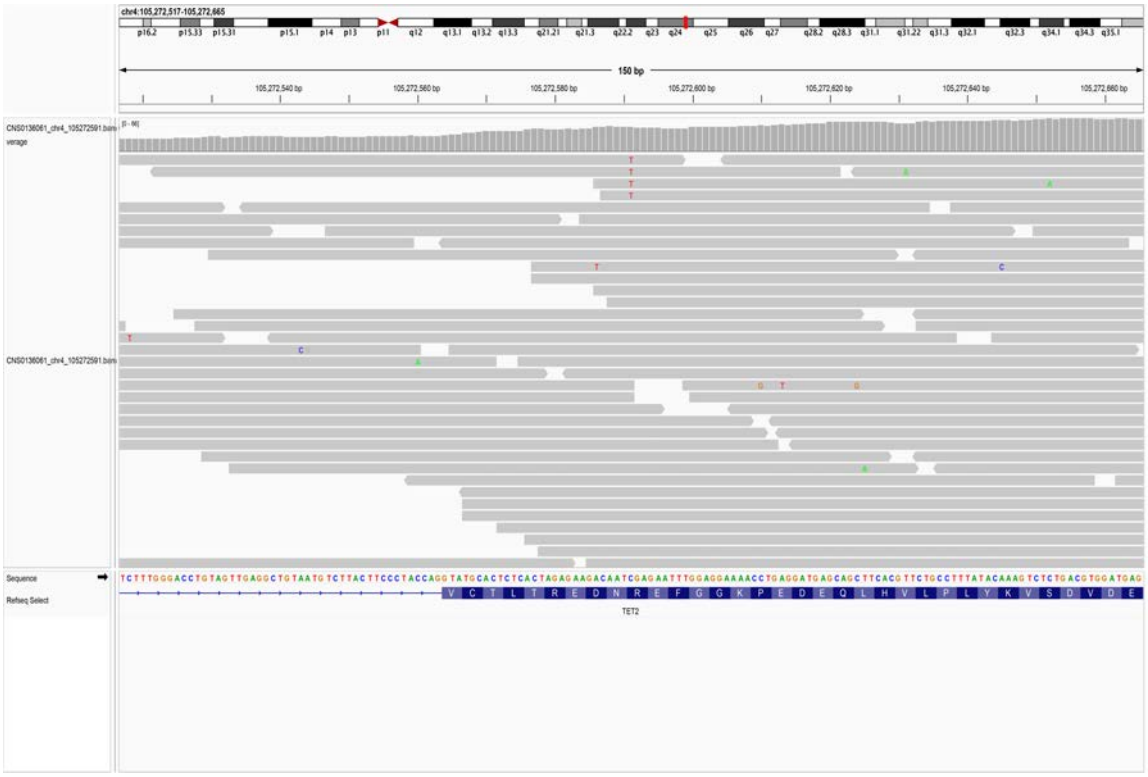
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC25061066D	chr4_105269691_G/C	169	18	*TET2*	missense_variant



55.74. chr4_105272591_C/T

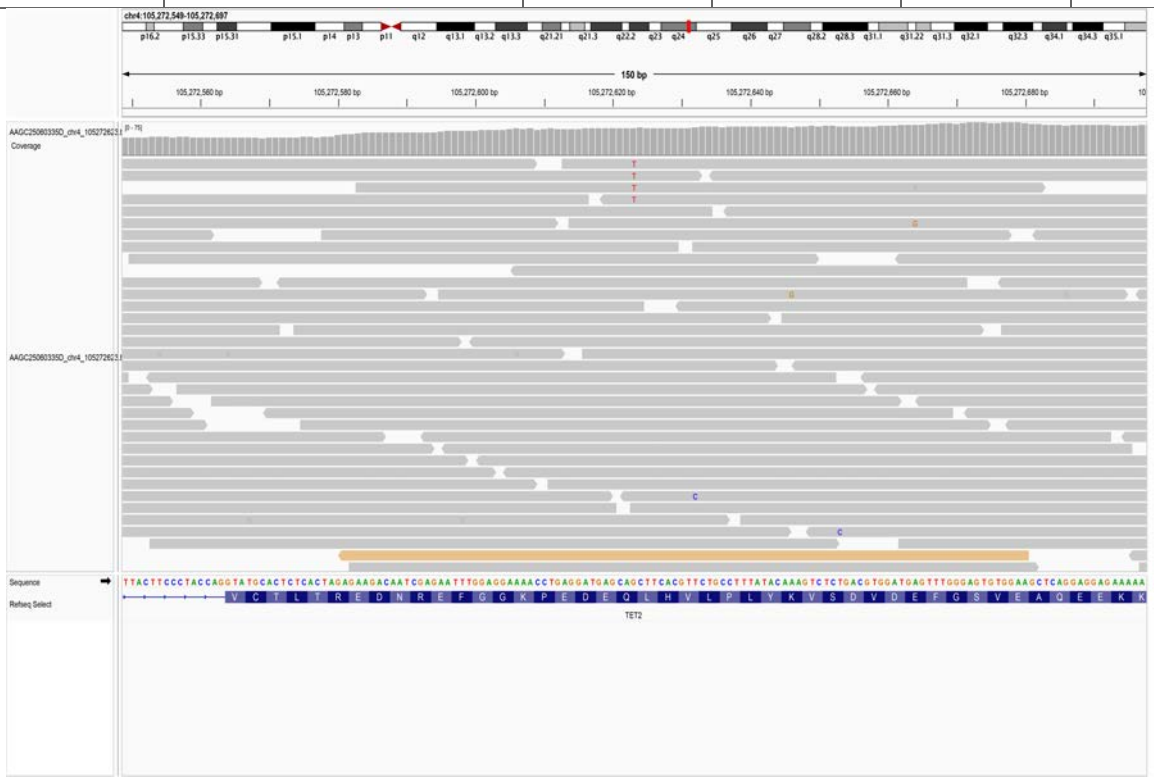
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
19R23945	chr4_105272591_C/T	35	5	*TET2*	stop_gained
AAGC25060938D	chr4_105272591_C/T	47	19	*TET2*	stop_gained
CNS0136061	chr4_105272591_C/T	45	4	*TET2*	stop_gained




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

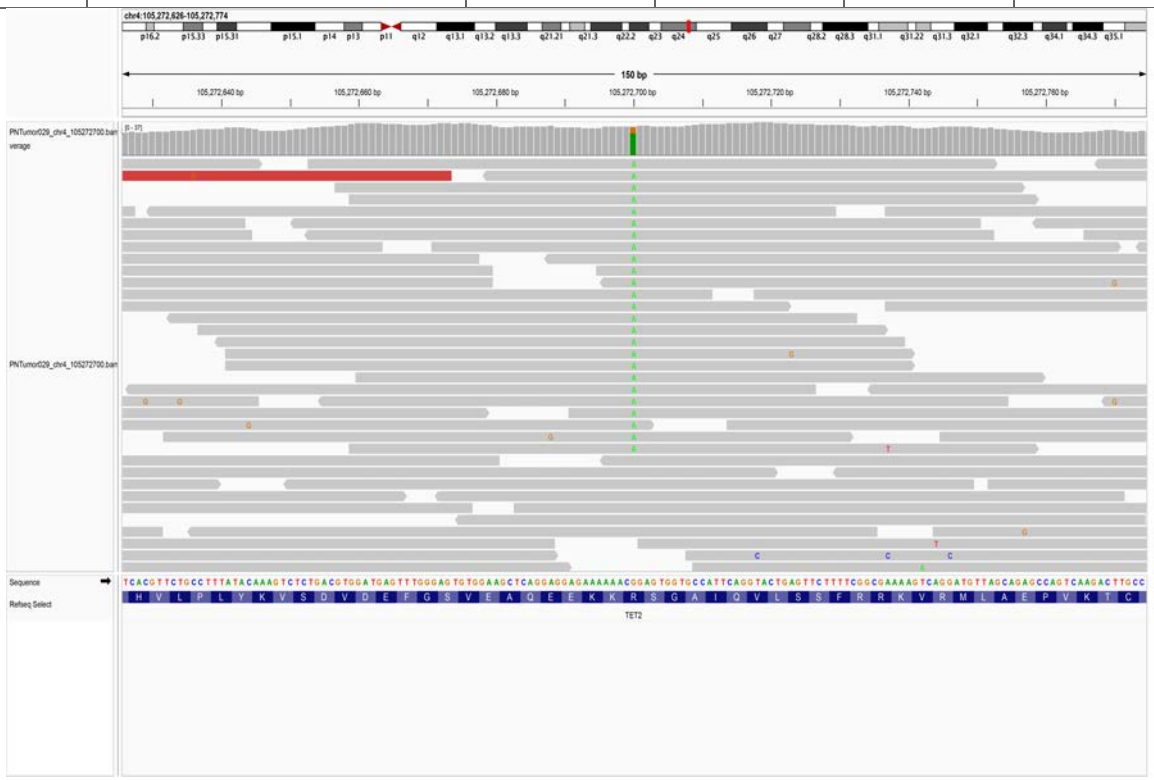
55.75. chr4_105272623_G/T

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



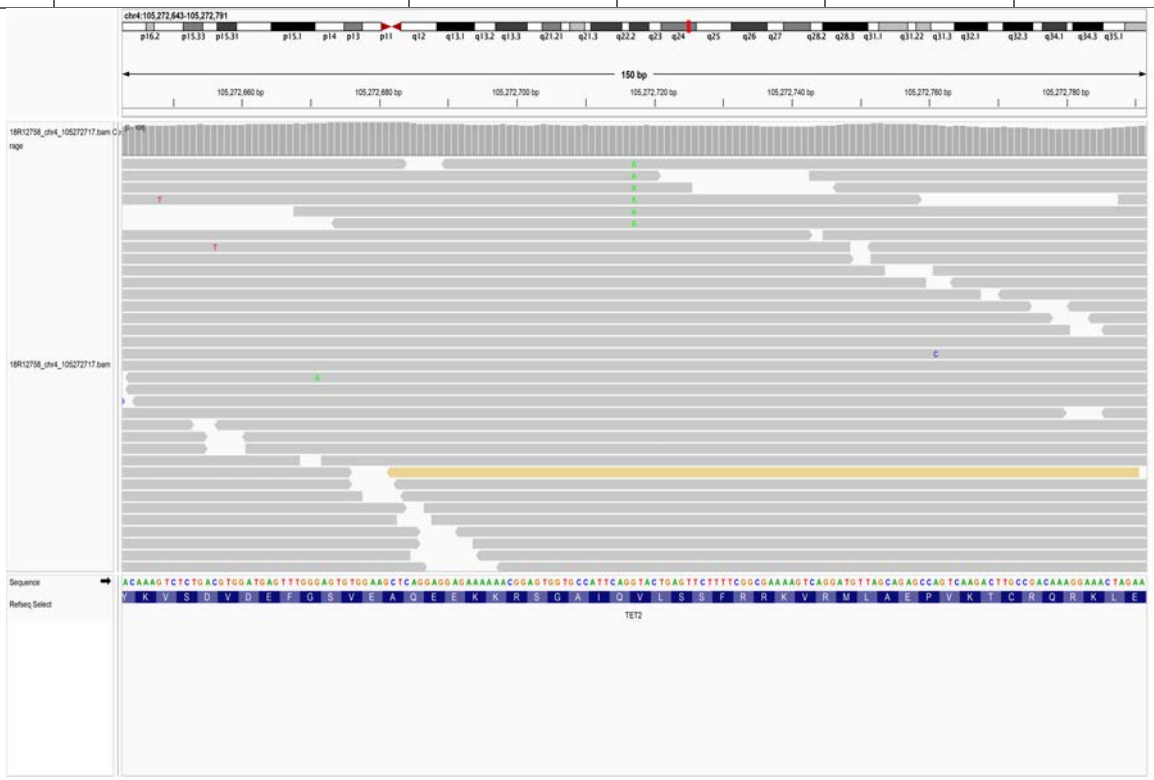
55.76. chr4_105272700_G/A

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



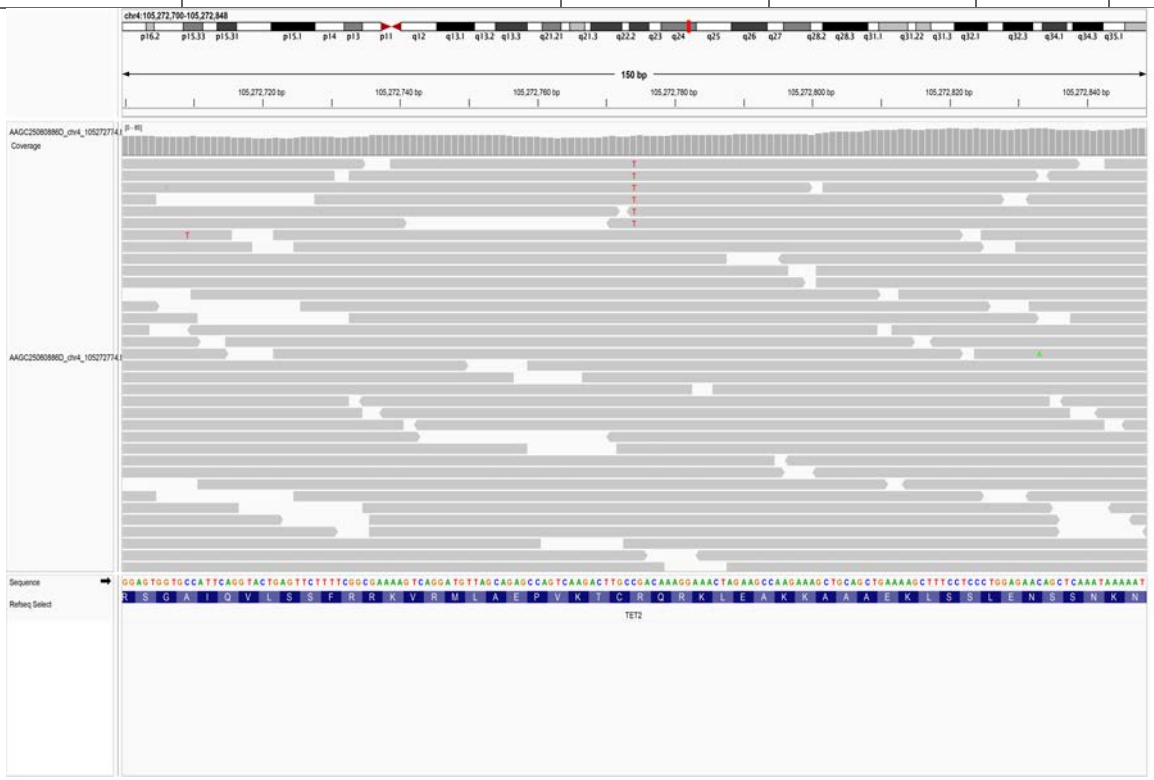
55.77. chr4_105272717_G/A

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



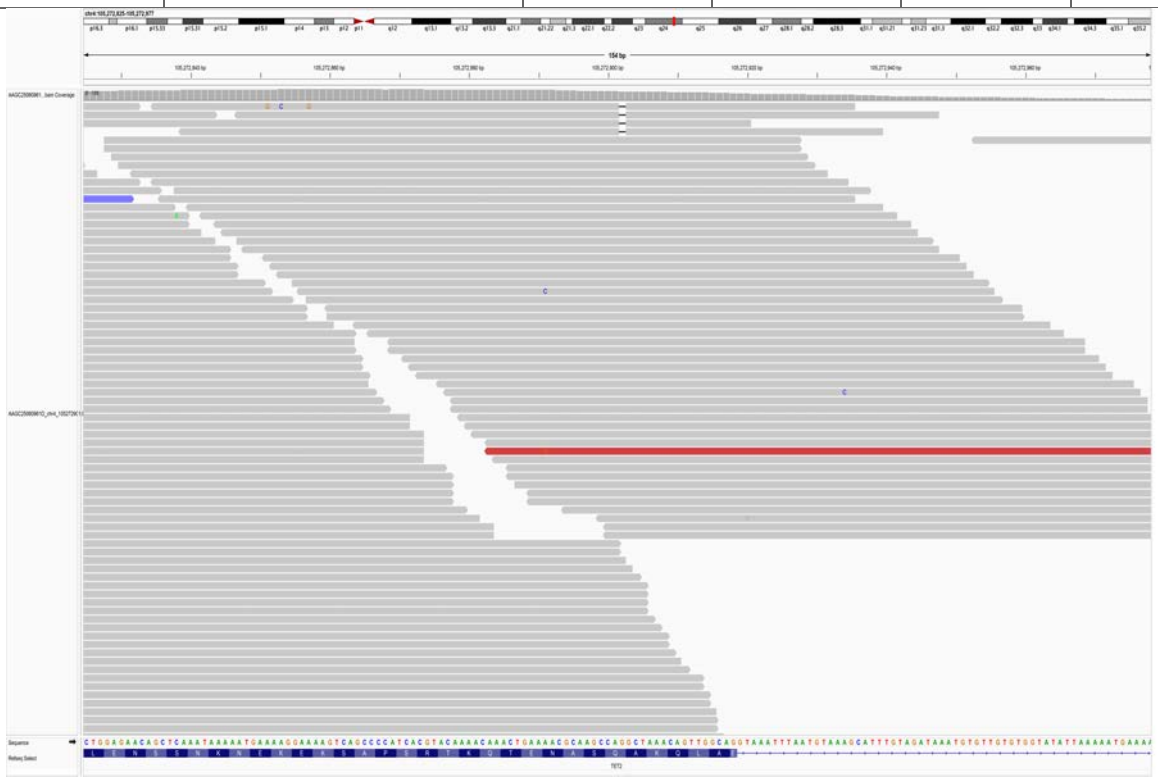
55.78. chr4_105272774_C/T

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



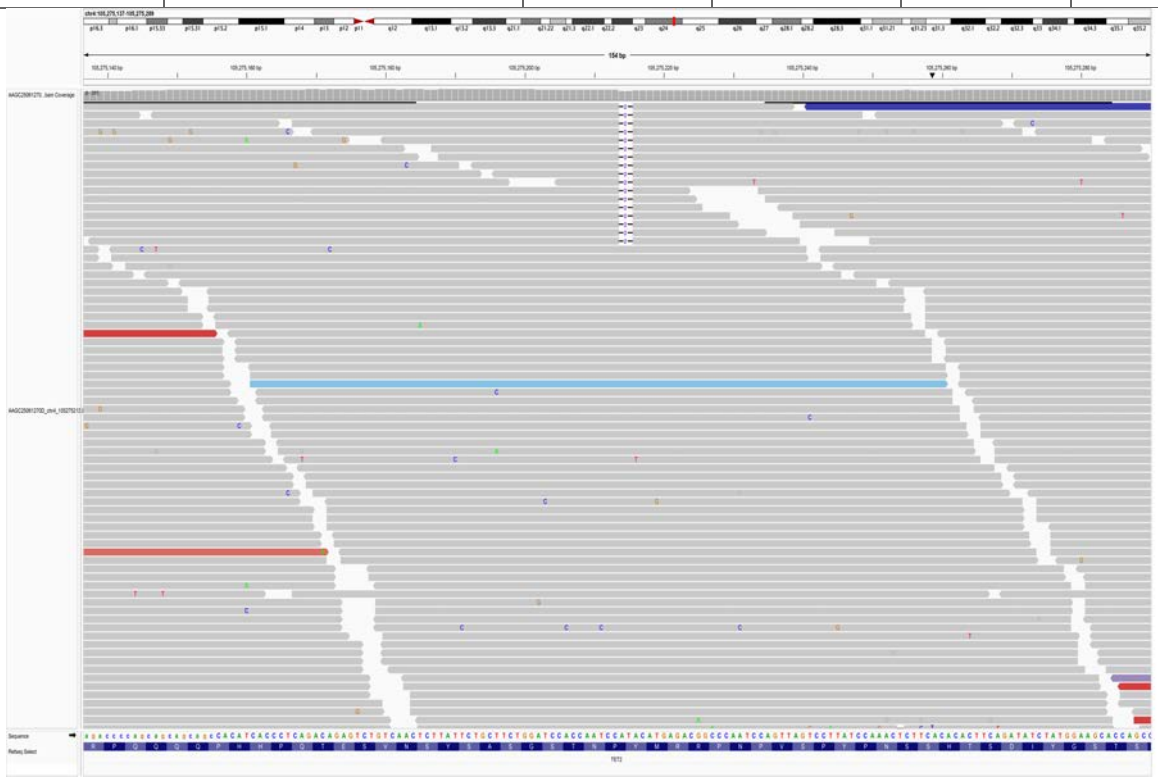
55.79. chr4_105272902_G/-

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



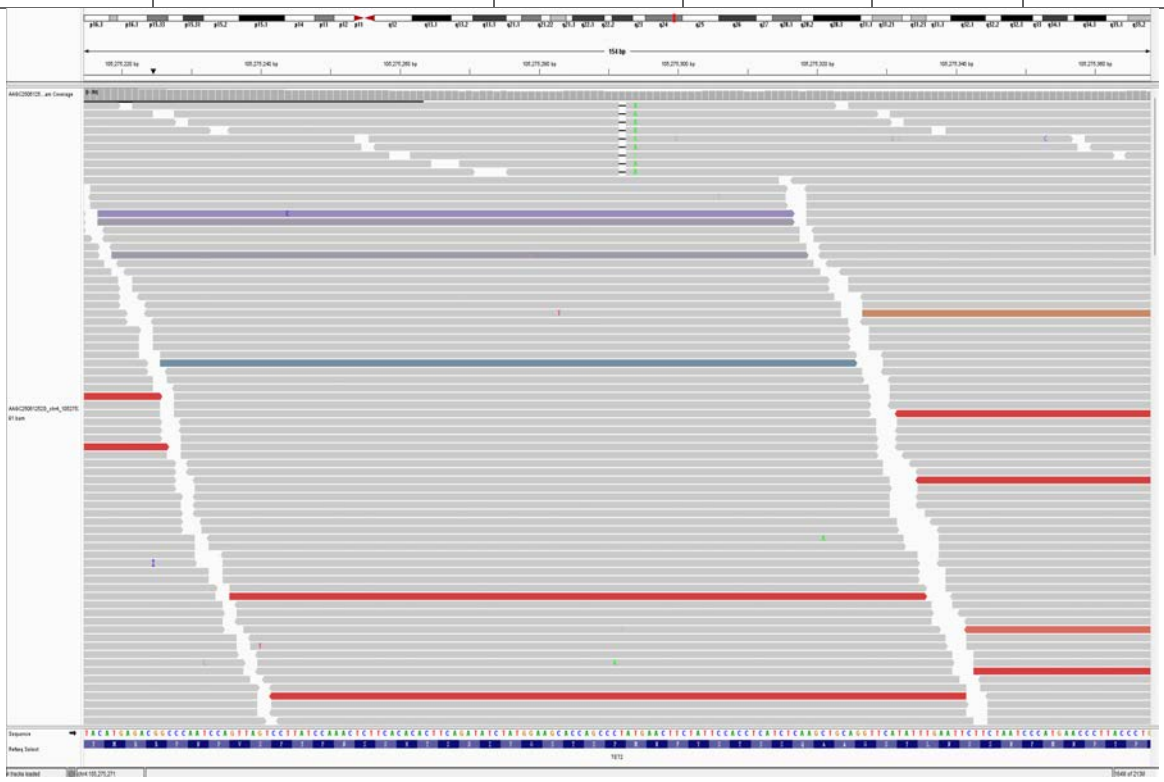
55.80. chr4_105275214_AT/-

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



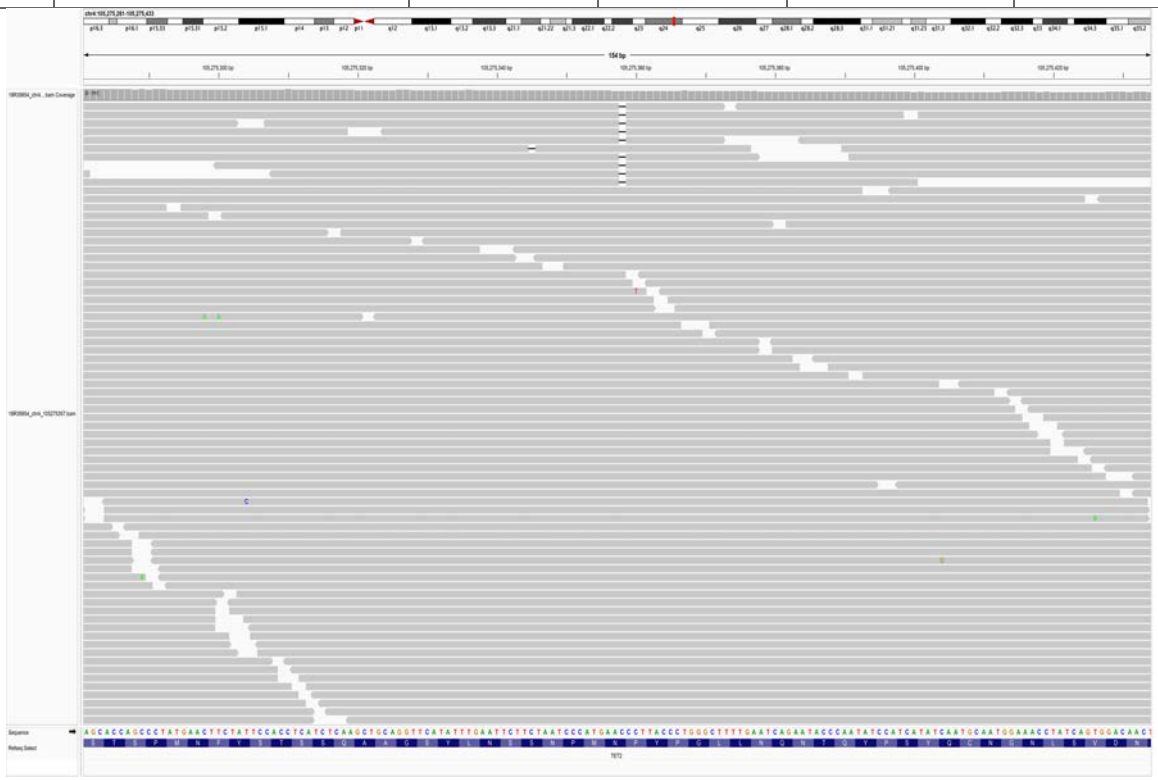
55.81. chr4_105275292_T/-

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



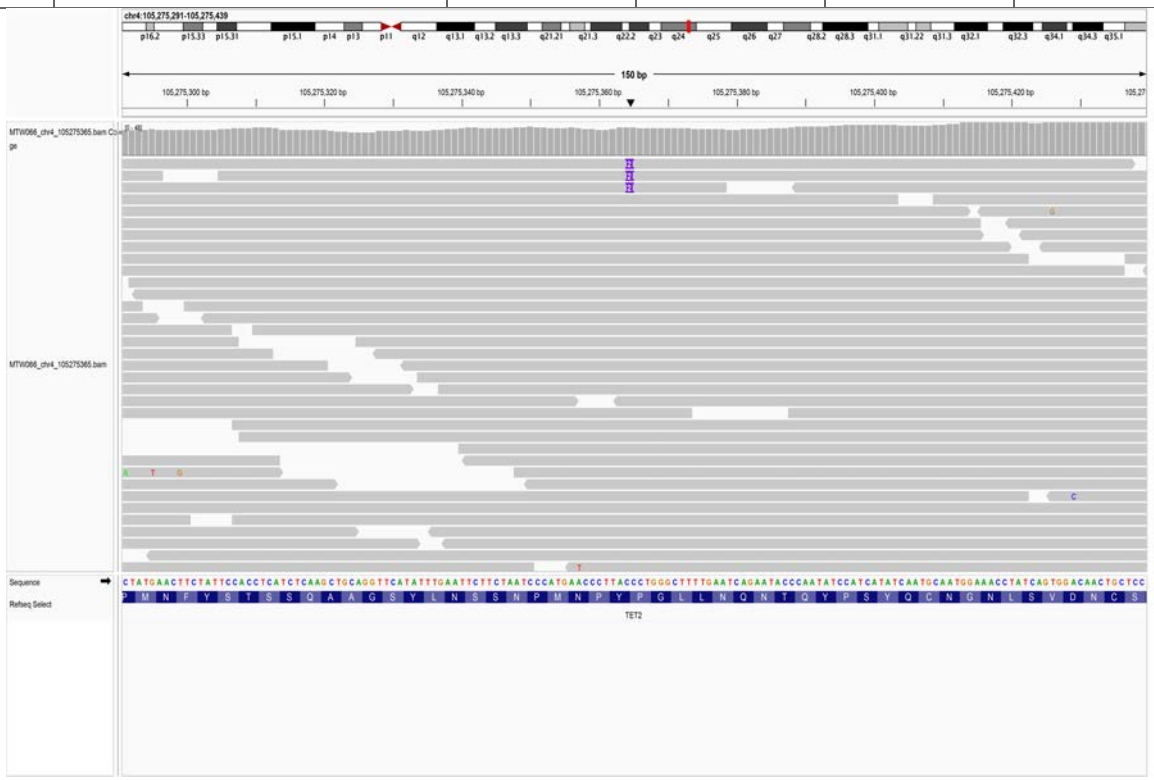
55.82. chr4_105275358_C/-

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



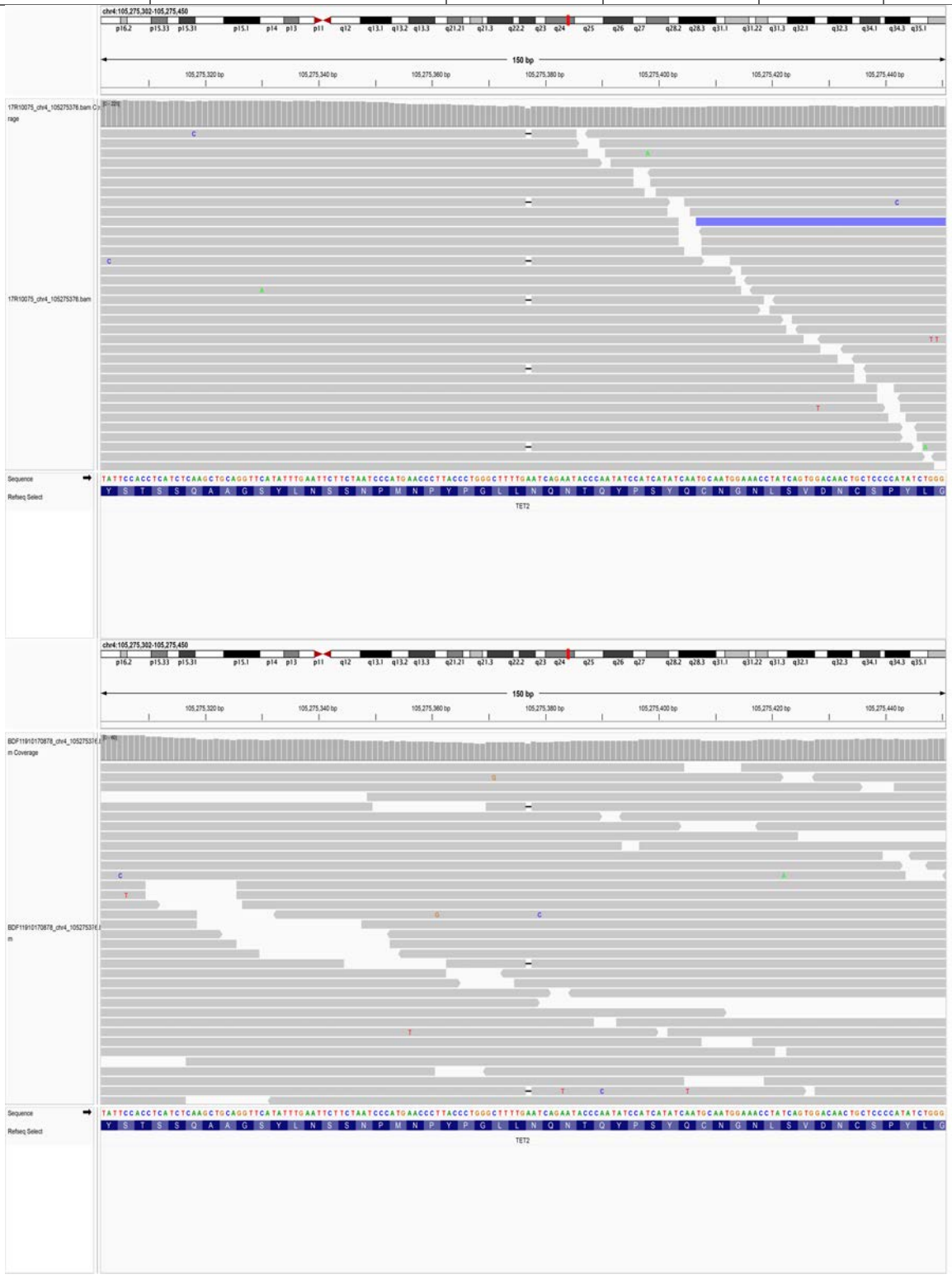
55.83. chr4_105275365_-/AA

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



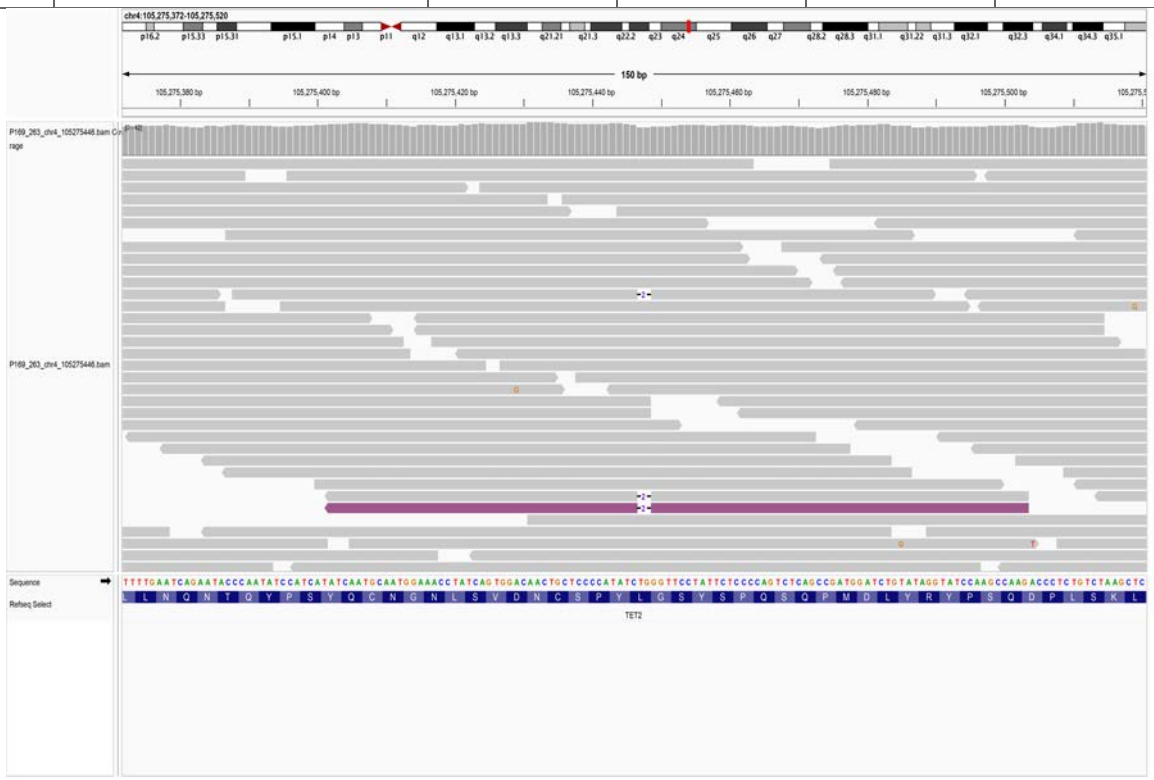
55.84. chr4_105275377_A/-

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



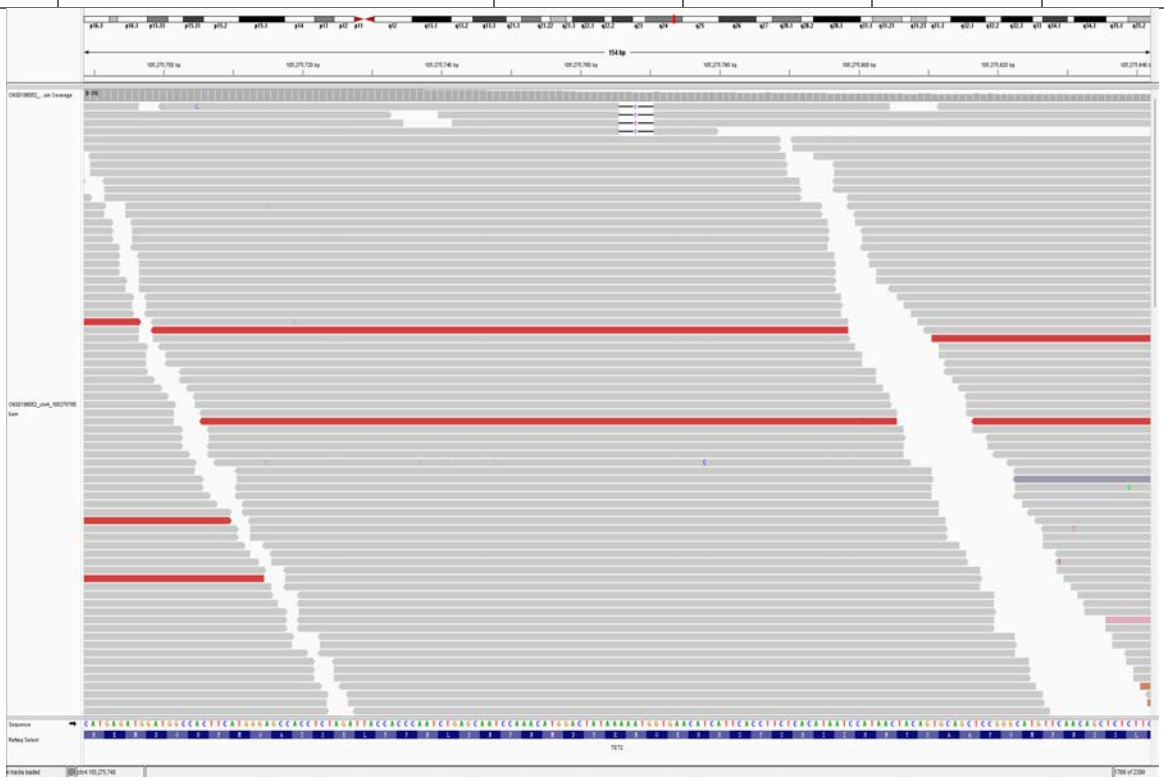
55.85. chr4_105275447_TG/-

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



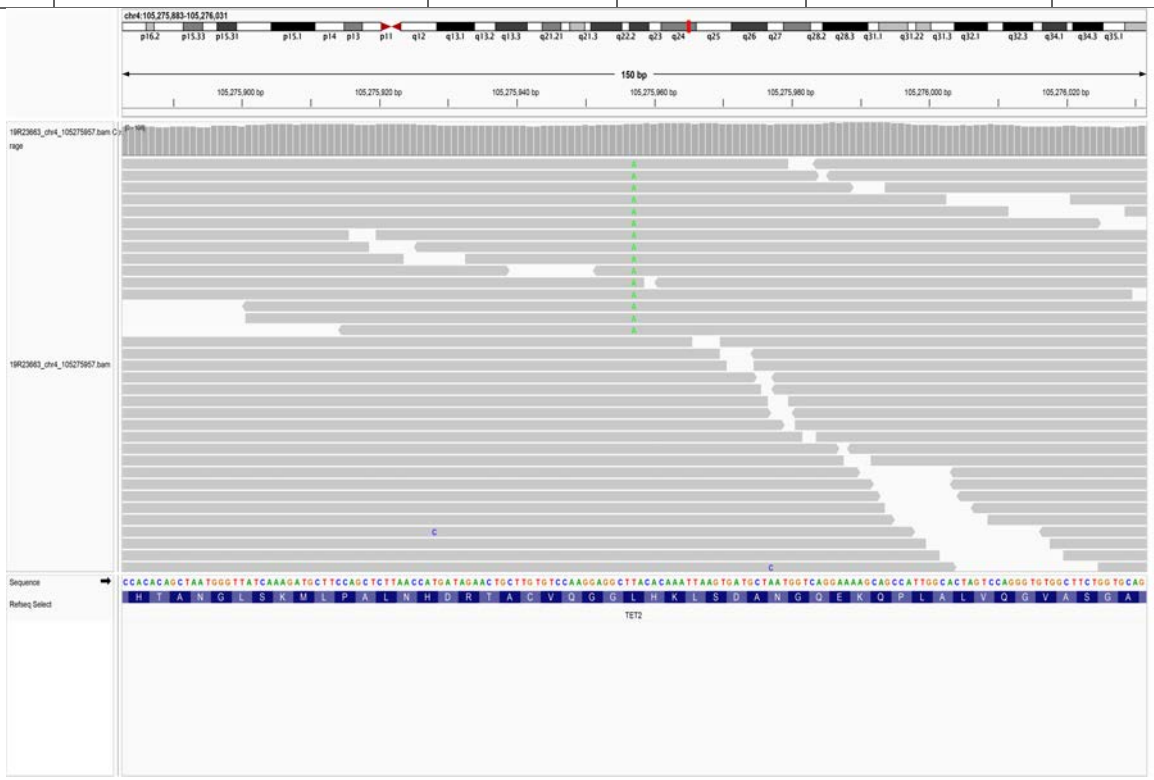
55.86. chr4_105275766_AAATG/-

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



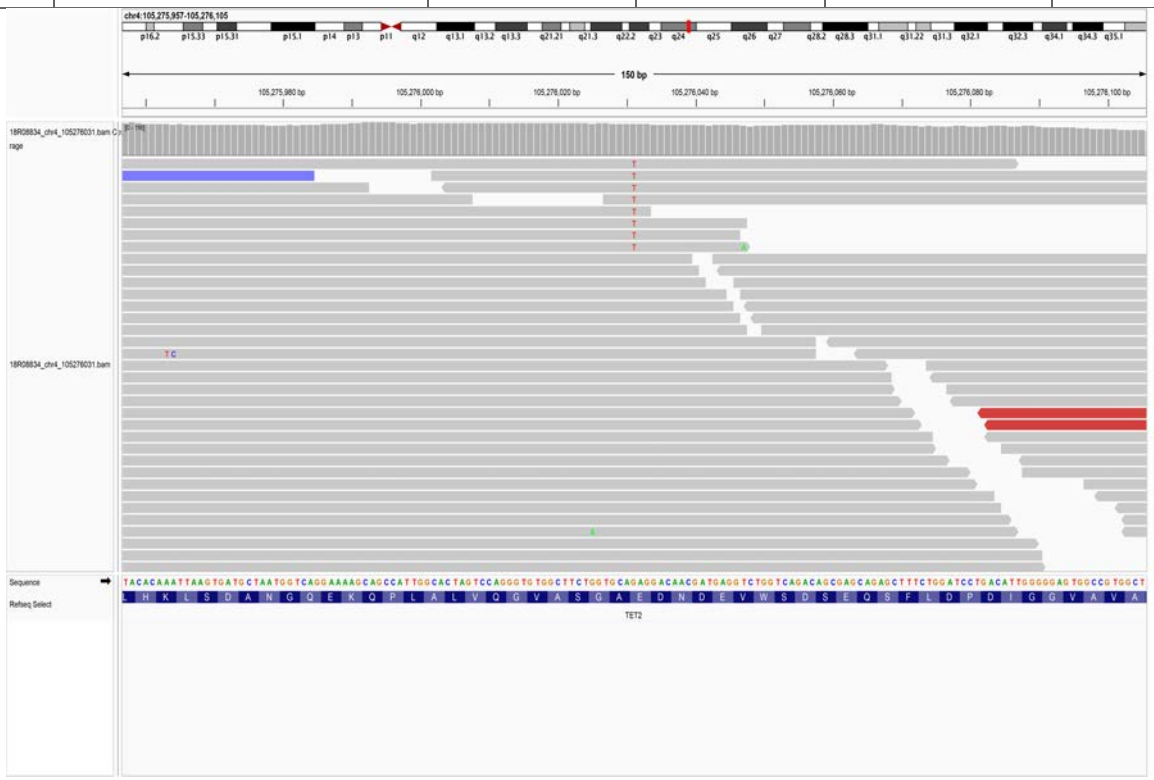
55.87. chr4_105275957_T/A

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



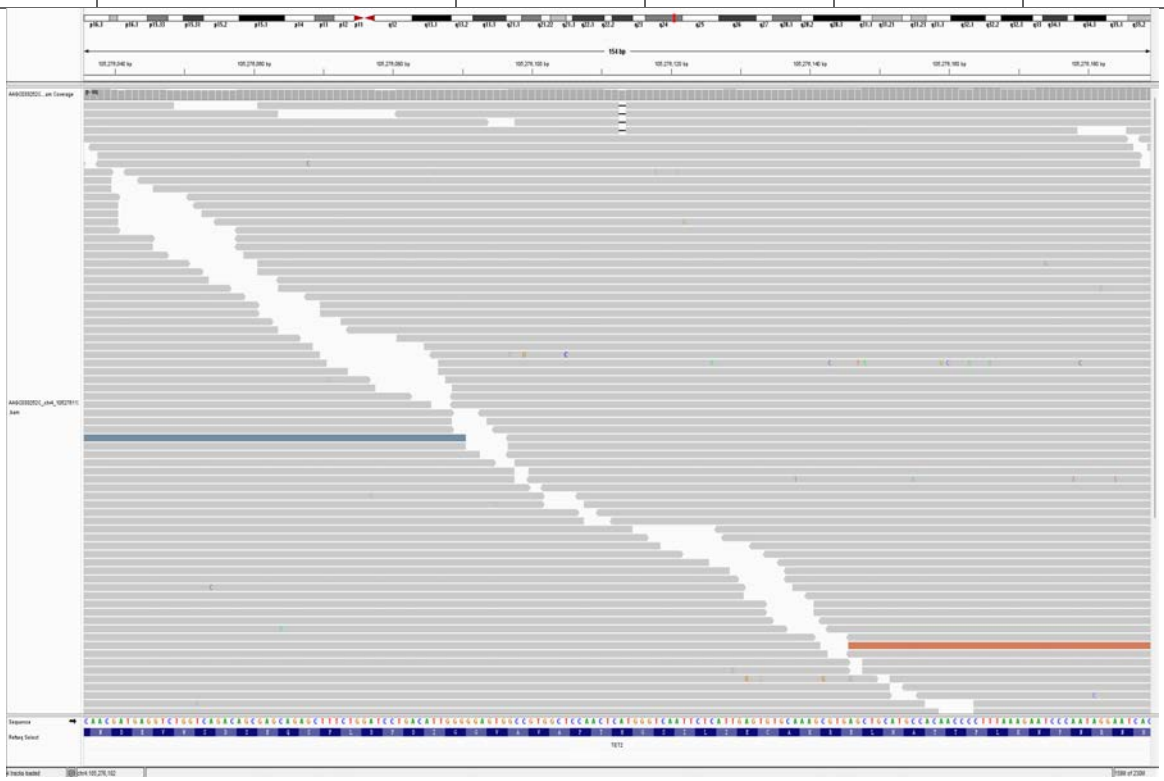
55.88. chr4_105276031_G/T

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



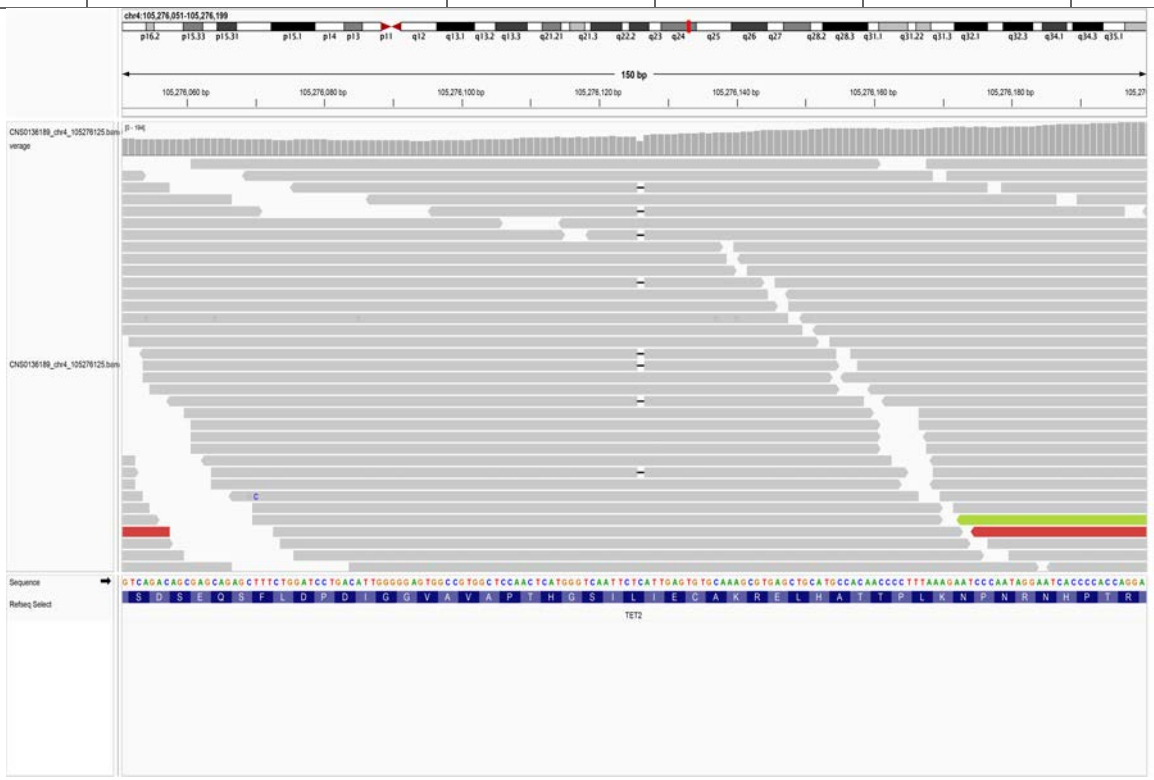
55.89. chr4_105276113_A/-

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



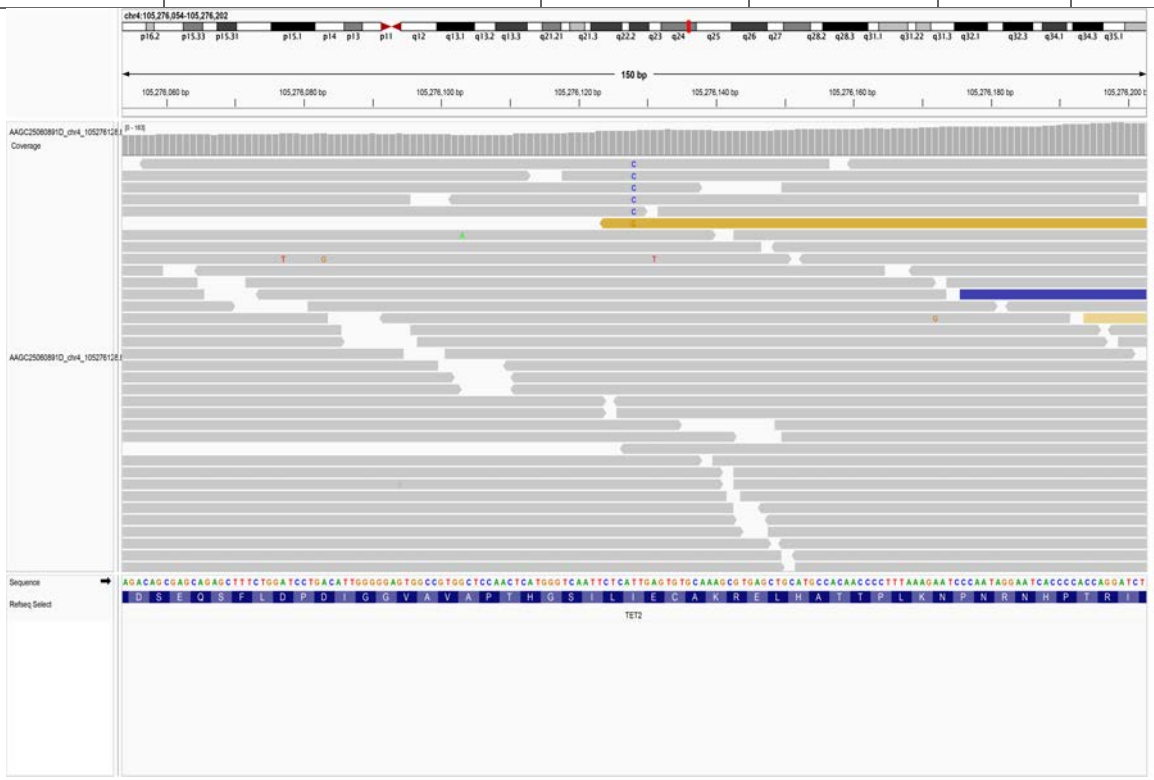
55.90. chr4_105276126_C/-

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



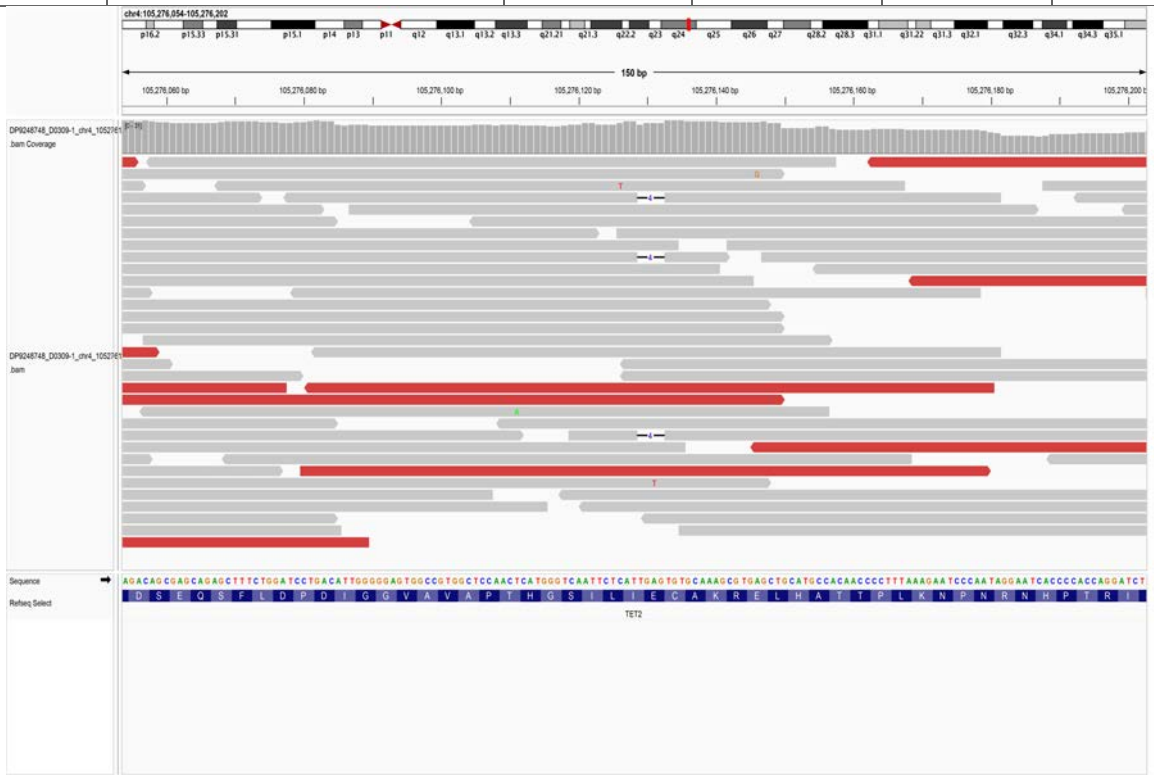
55.91. chr4_105276128_T/C

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



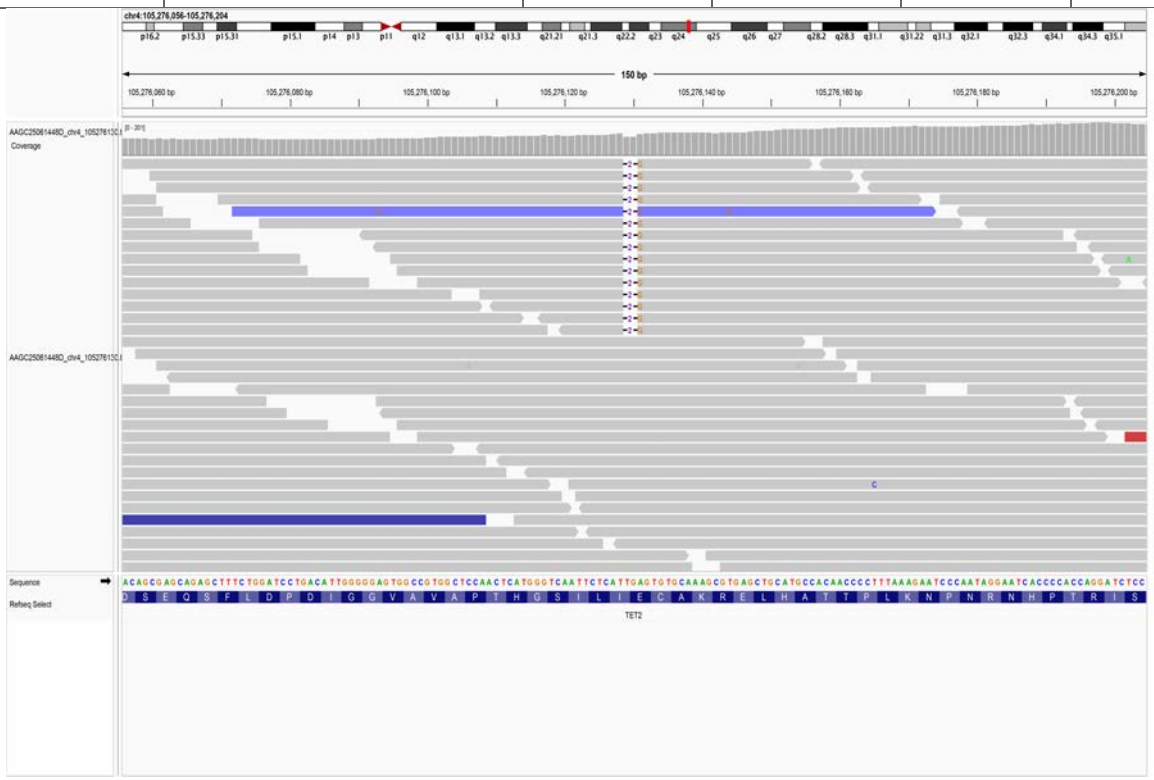
55.92. chr4_105276129_TGAG/-

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



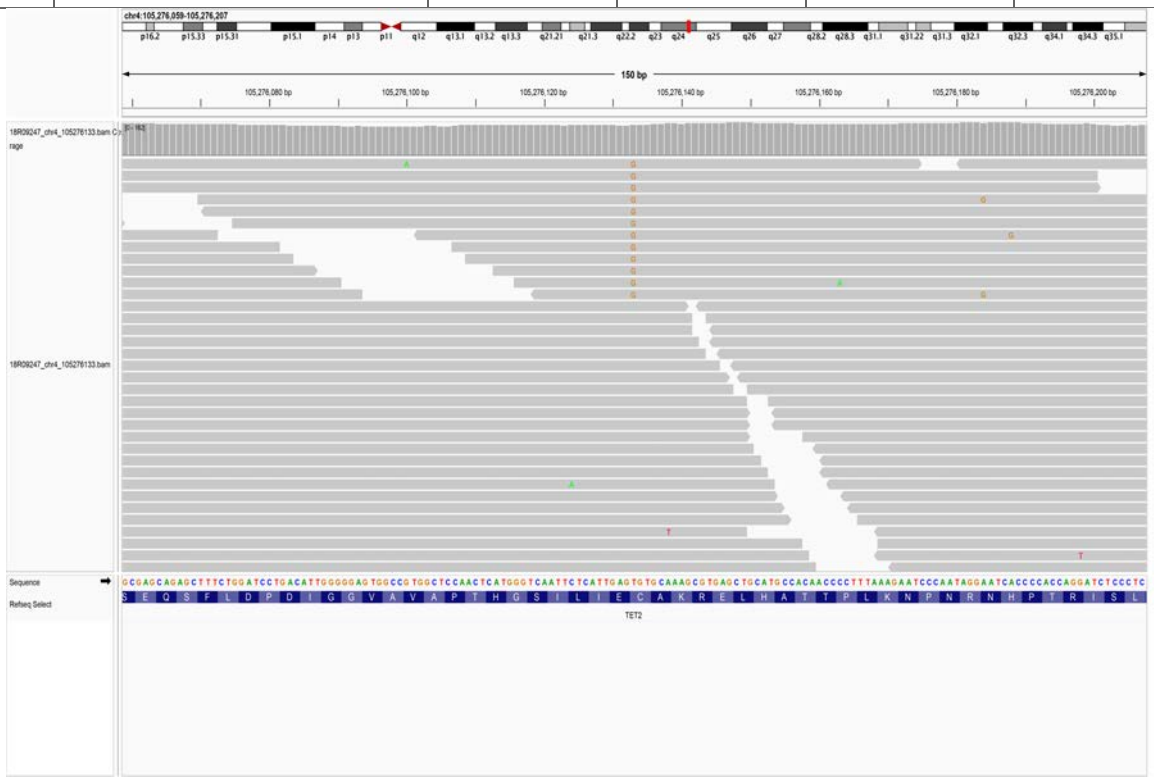
55.93. chr4_105276131_A/-

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



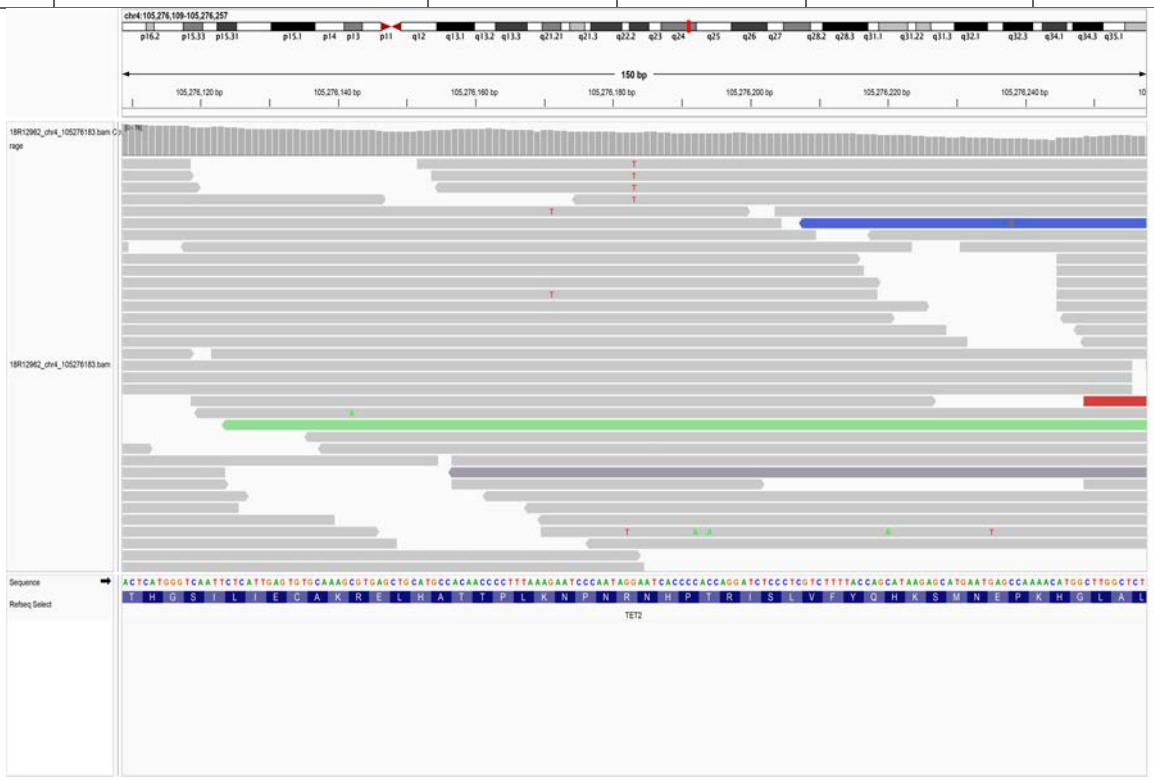
55.94. chr4_105276133_T/G

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



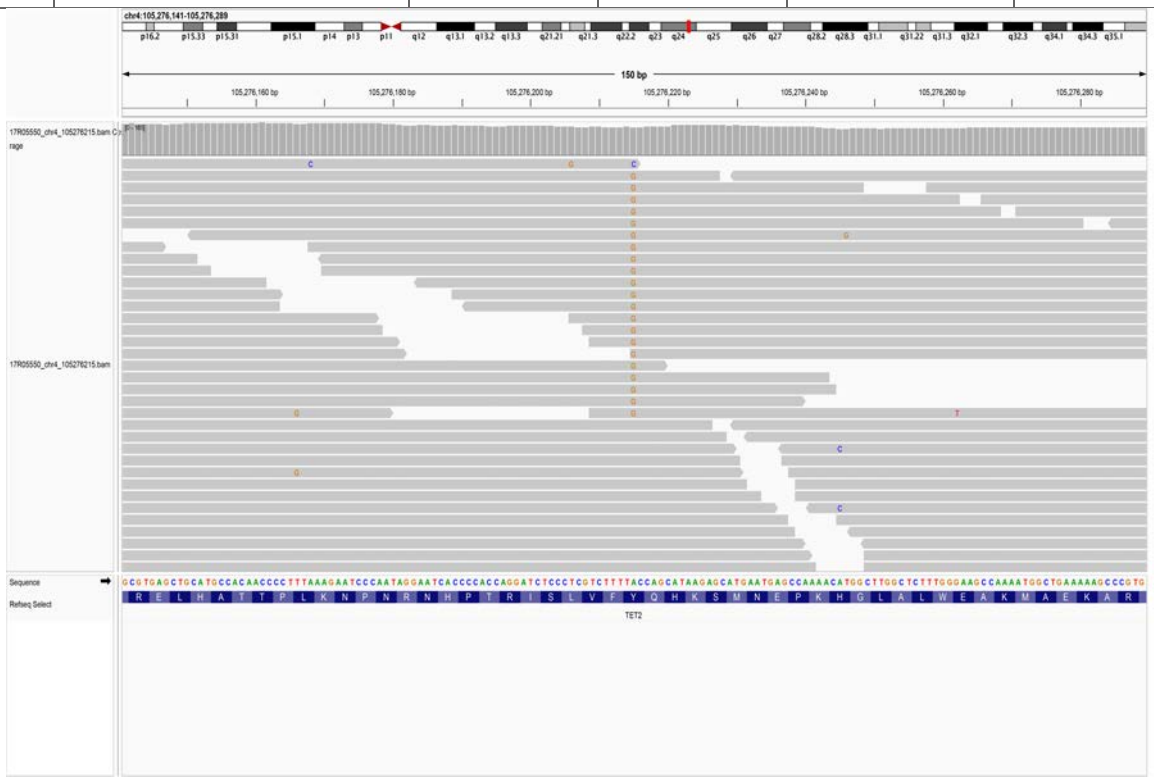
55.95. chr4_105276183_G/T

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



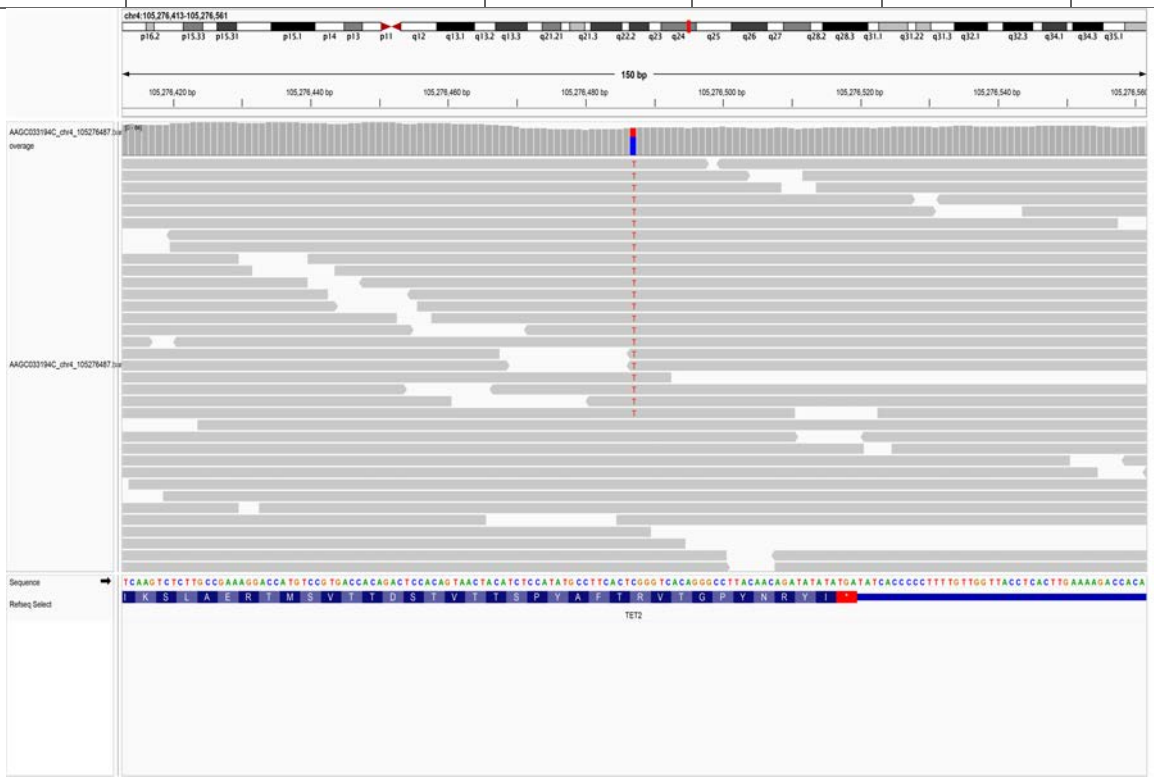
55.96. chr4_105276215_A/G

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

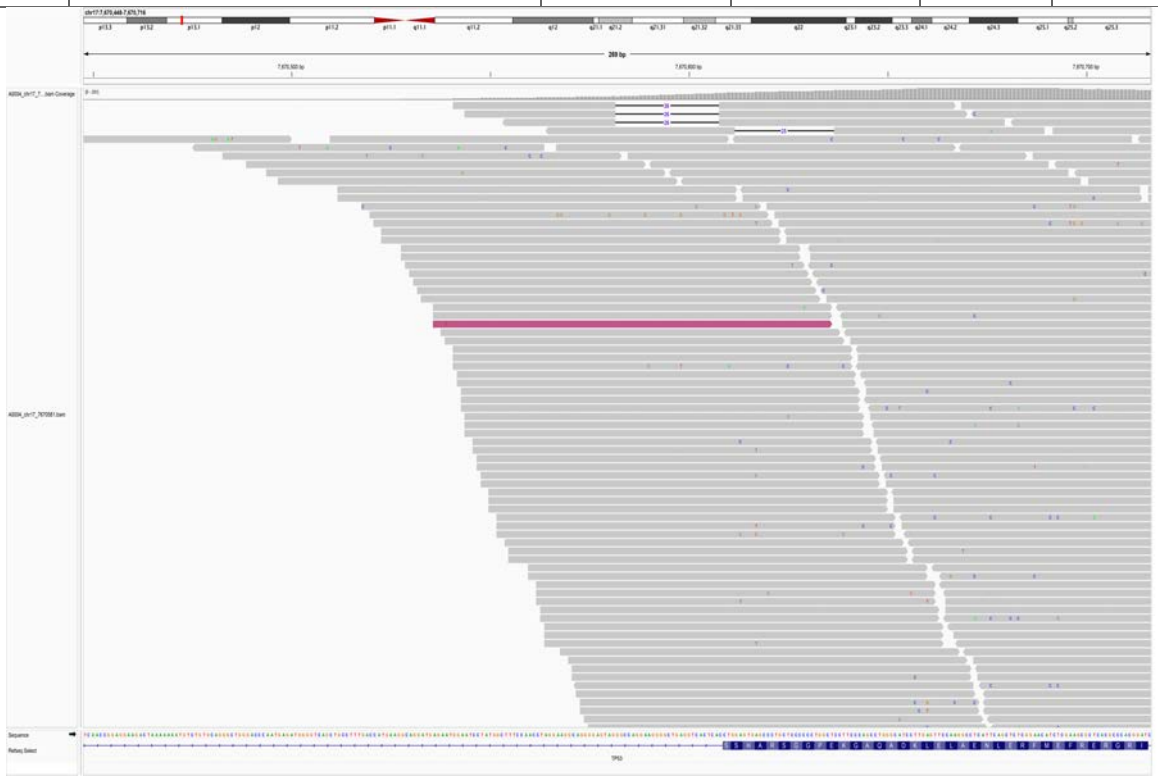
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
AAGC033194C	chr4_105276487_C/T	46	22	*TET2*	missense_variant

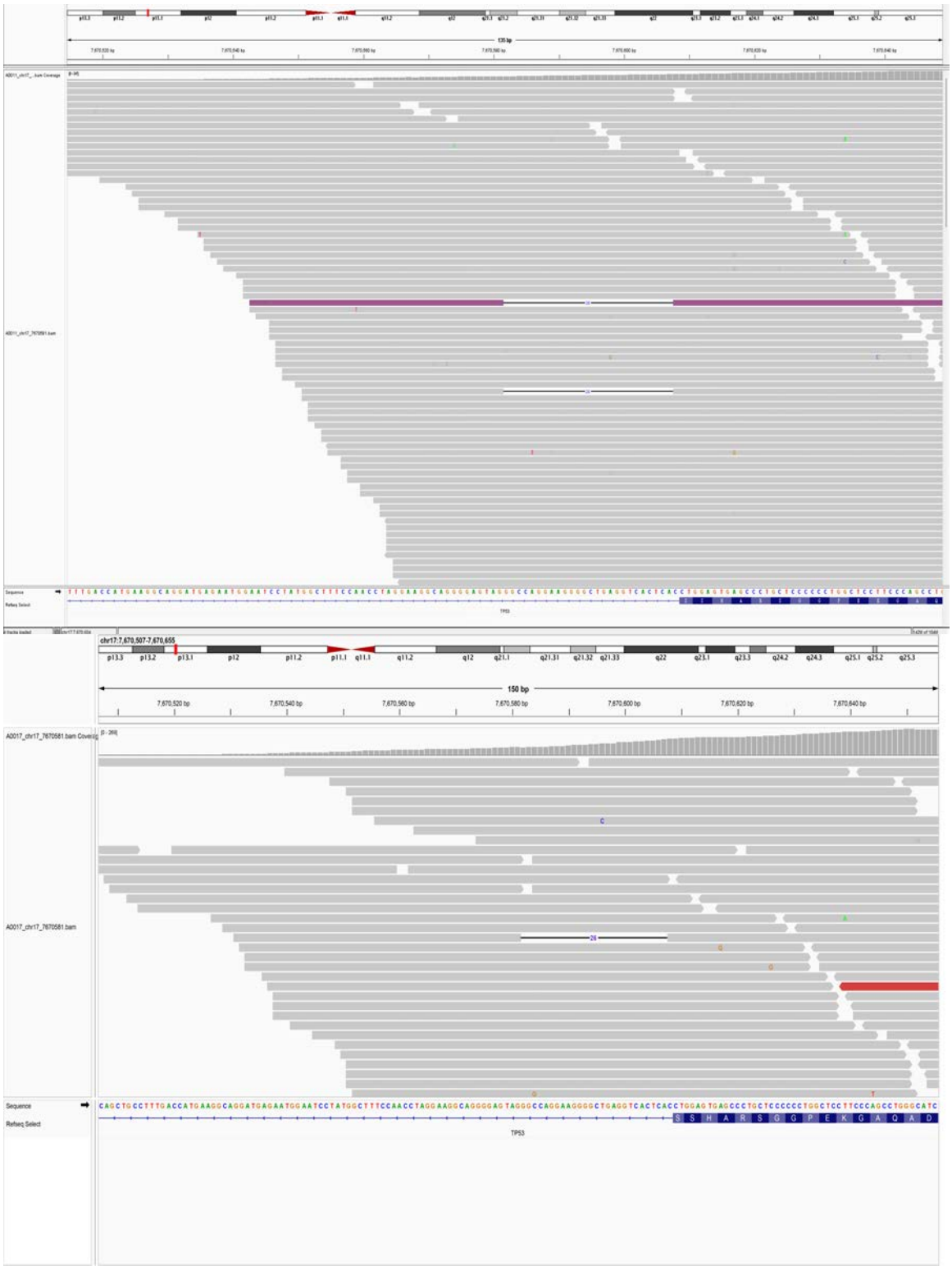


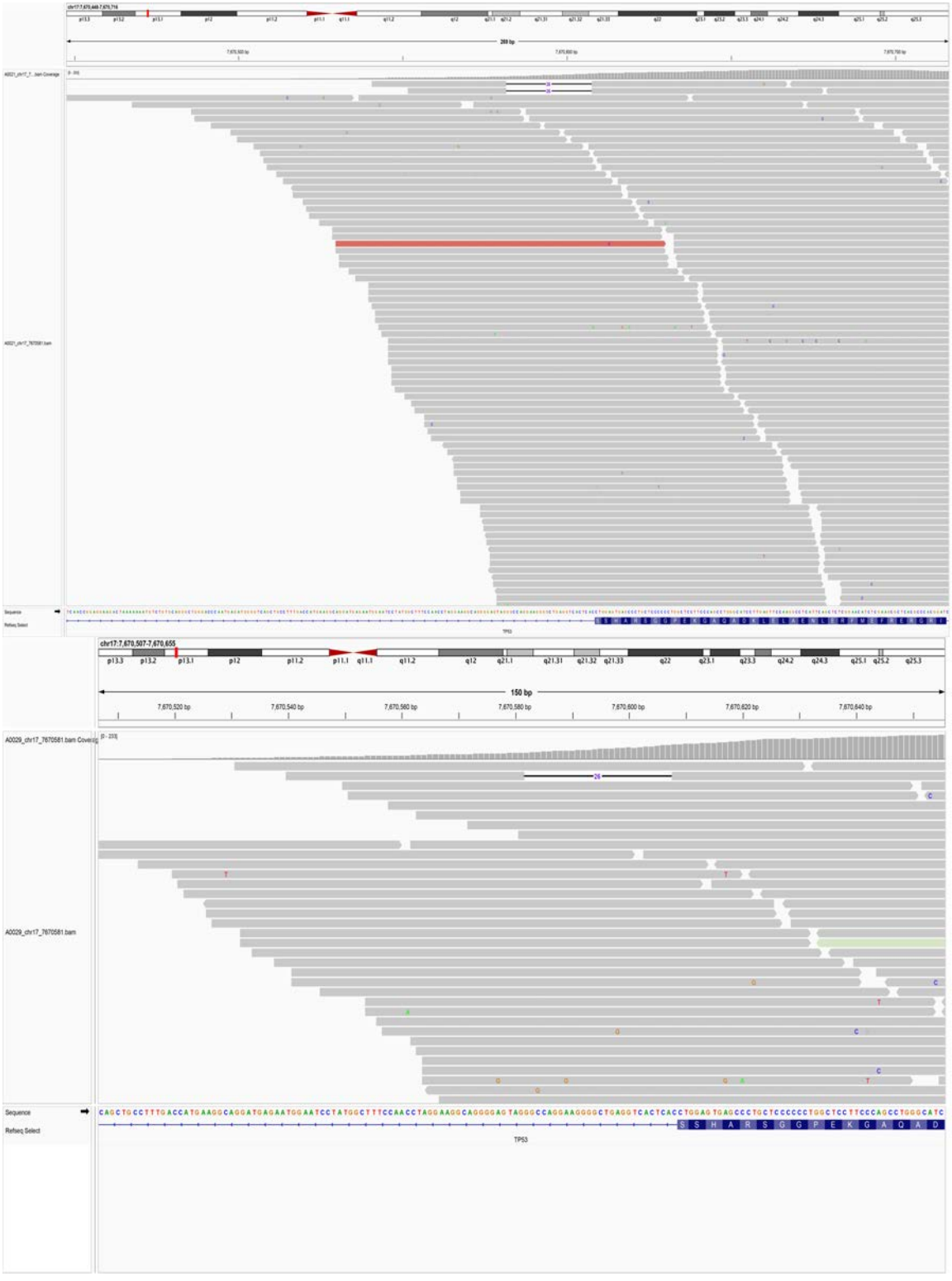
56. *TP53*

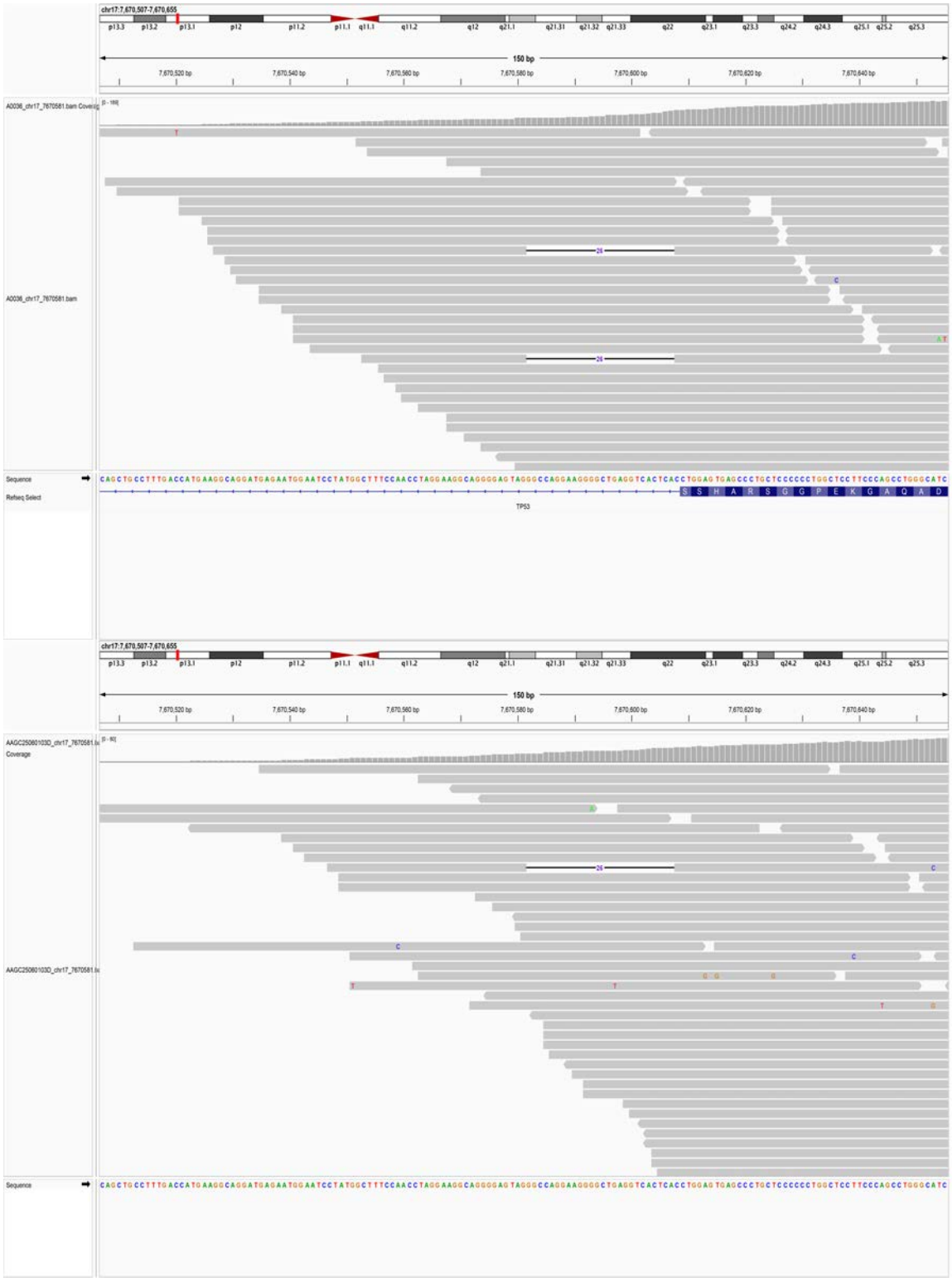
56.1. chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-

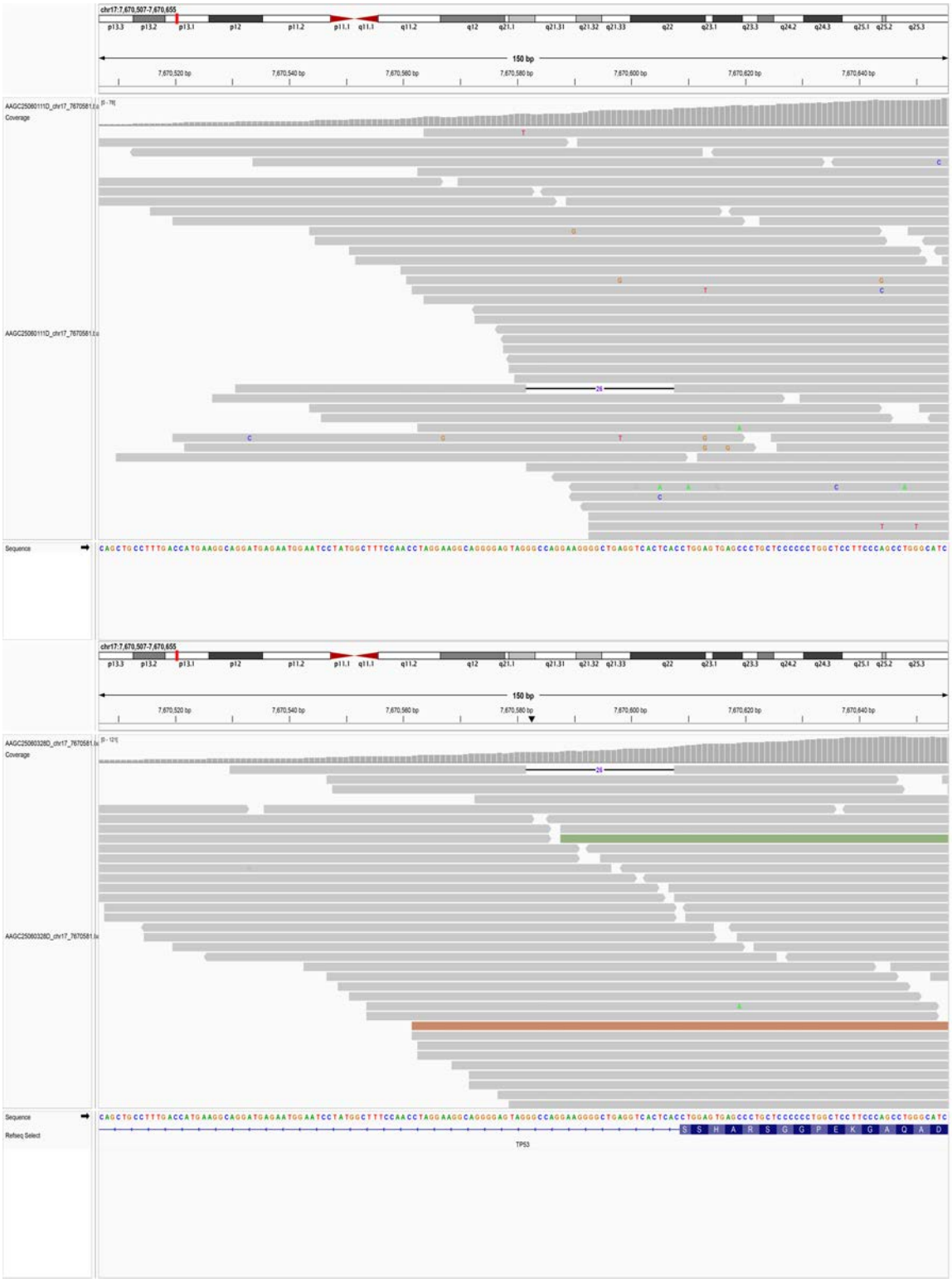
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
A0004	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	155	4	*TP53*	splice_donor_variant
A0011	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	146	3	*TP53*	splice_donor_variant
A0017	chr17_7670582_GGCCAGGAAGGGGCTGAGGTCACTCA/-	154	4	*TP53*	splice_donor_variant
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

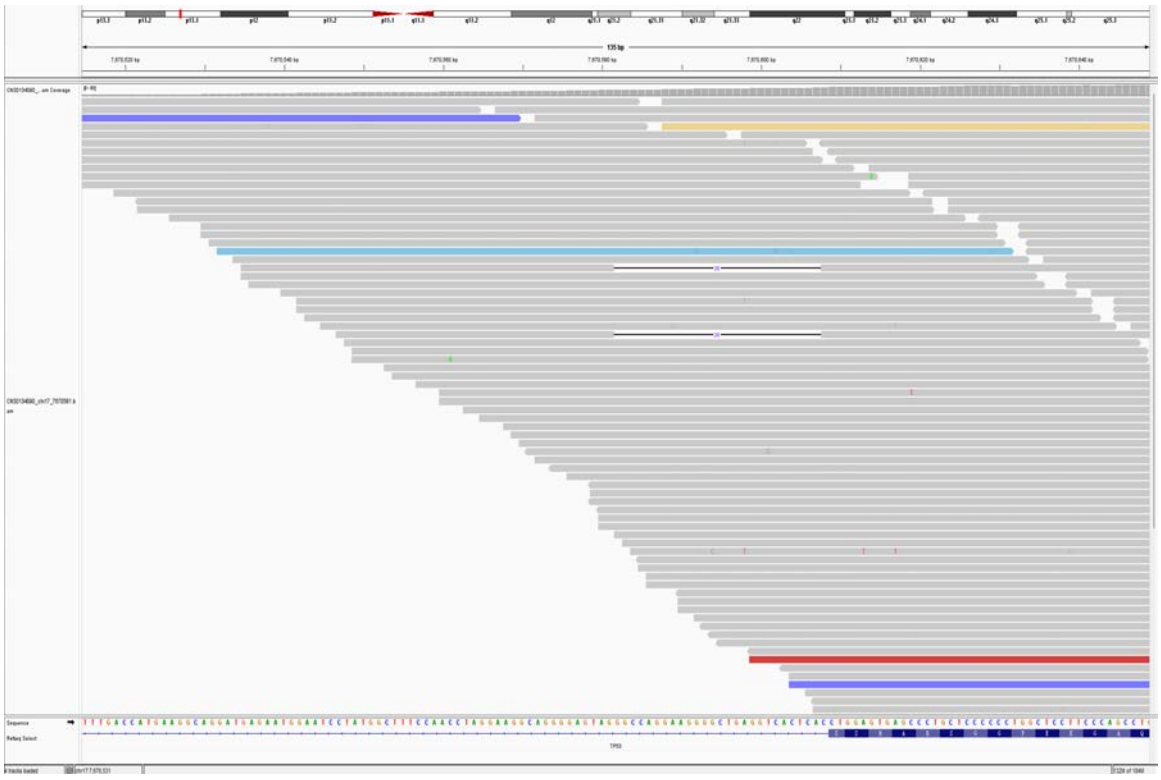



chr17:7,670,507-7,670,655
150 bp
7,670,520 bp
7,670,540 bp
7,670,560 bp
7,670,580 bp
7,670,600 bp
7,670,620 bp
7,670,640 bp
A0017_chr17_7670581.bam
Sequence
Refseq Select
TP53


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
Sequence
Refseq Select
TP53

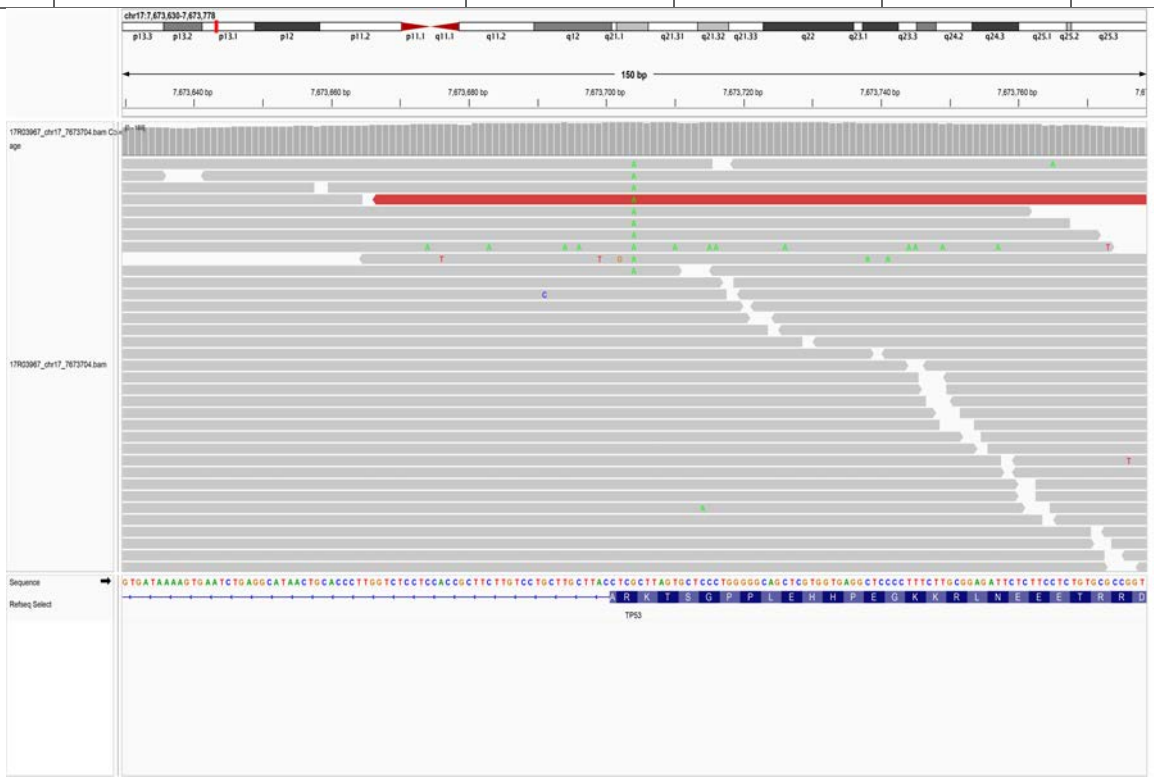

chr17:7,670,507-7,670,655
150 bp
7,670,520 bp
7,670,540 bp
7,670,560 bp
7,670,580 bp
7,670,600 bp
7,670,620 bp
7,670,640 bp
A0036_chr17_7670581.bam
Sequence
Refseq Select
TP53
CAGCTGCCTTTGACCATGAAGGCAGGATGAGAATGGAATCCTATGGCTTTCCAACCTAGGAAGGCAGGGGAGTAGGGCCAGGAAGGGGCTGAGGTCACTCACCTGGAGTGAGCCCTGCTCCCCCCTGGCTCCTTCCCAGCCTGGGCATC
S S H A R S G G P E K G A Q A D
AAGC25060103D_chr17_7670581.ba
Coverage


chr17:7,670,507-7,670,655
150 bp
Coverage
Sequence
Refseq Select
TP53



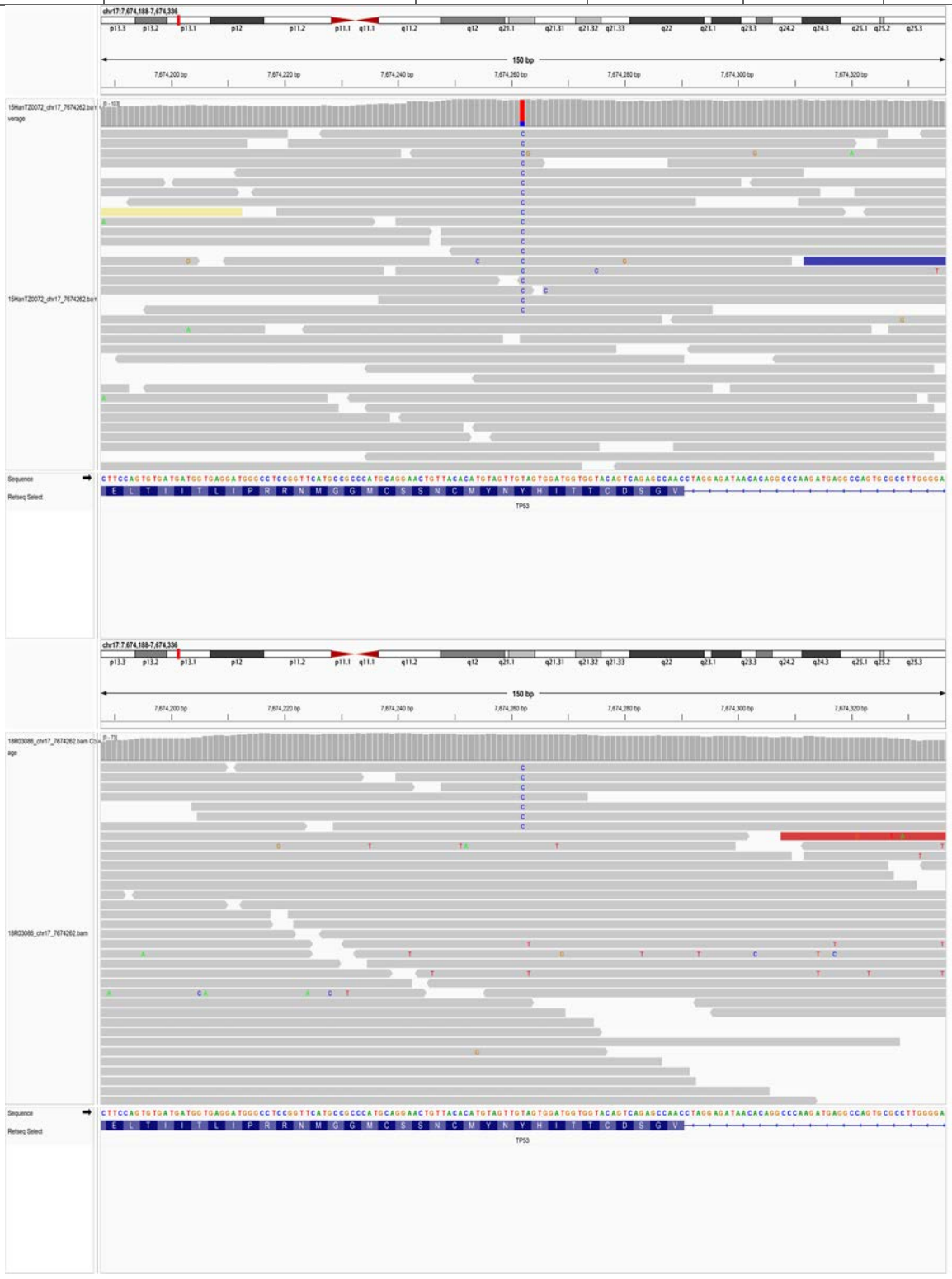
56.2. chr17_7673704_G/A

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



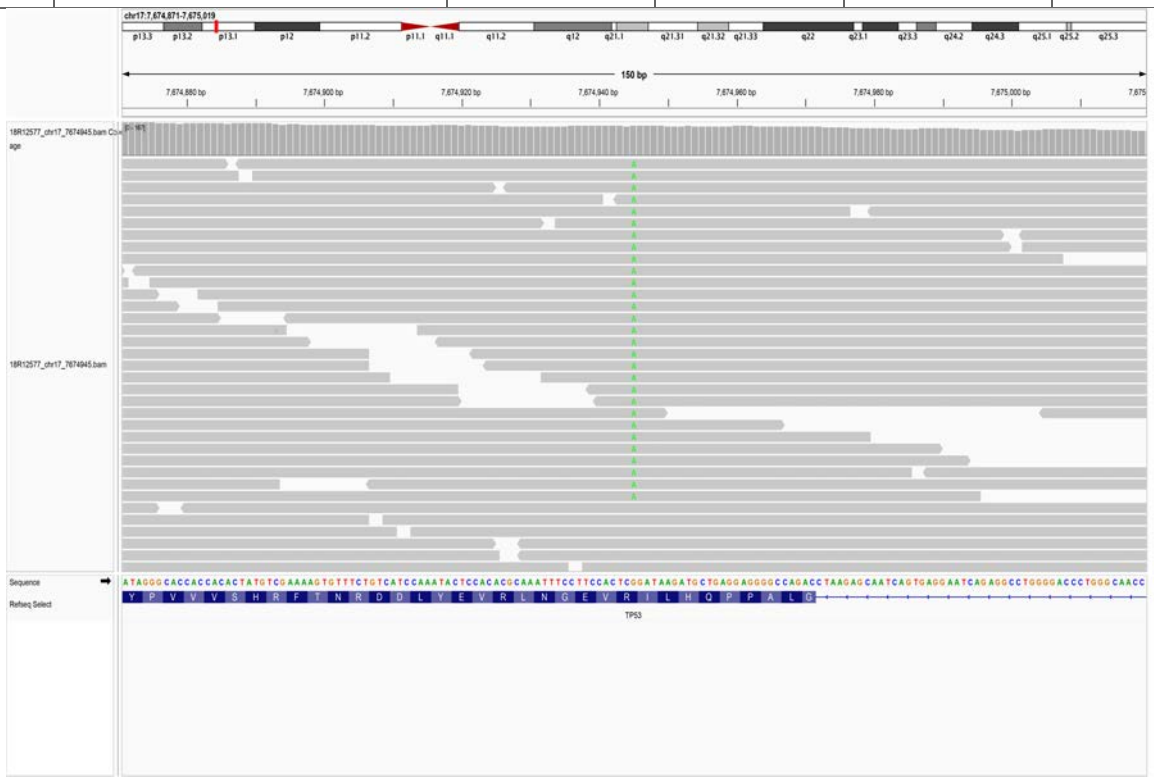
56.3. chr17_7674262_T/C

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



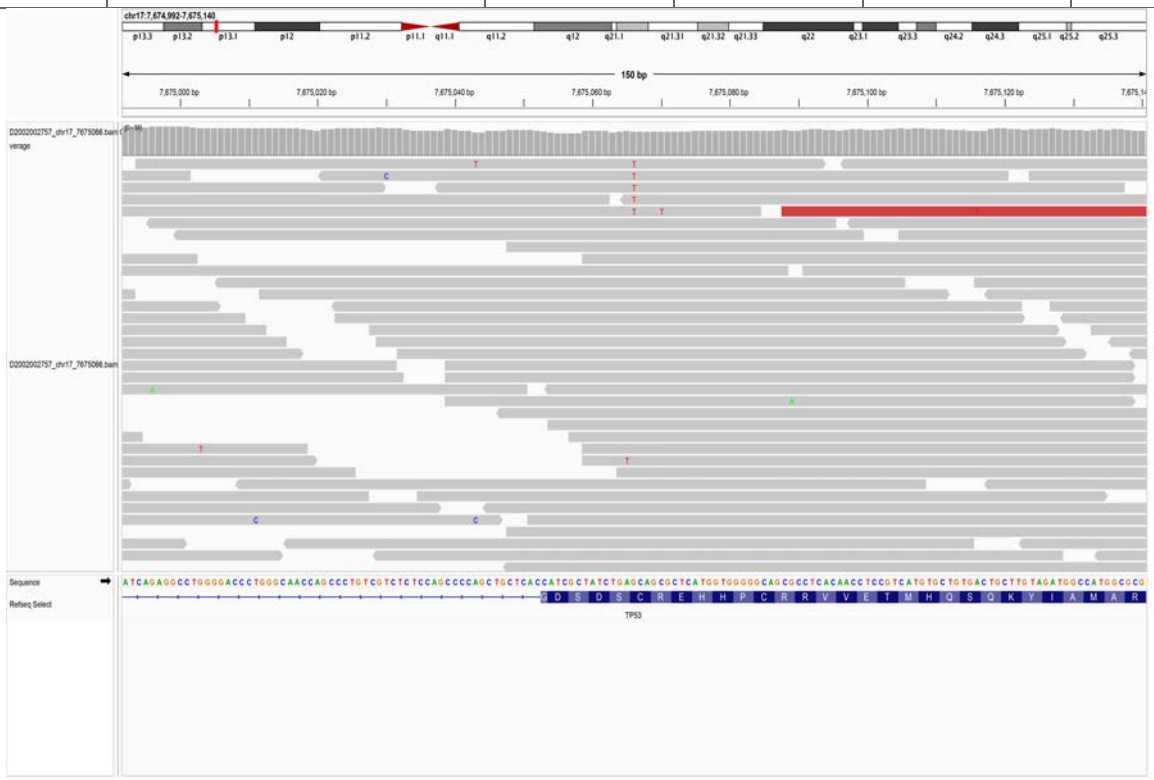
56.4. chr17_7674945_G/A

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



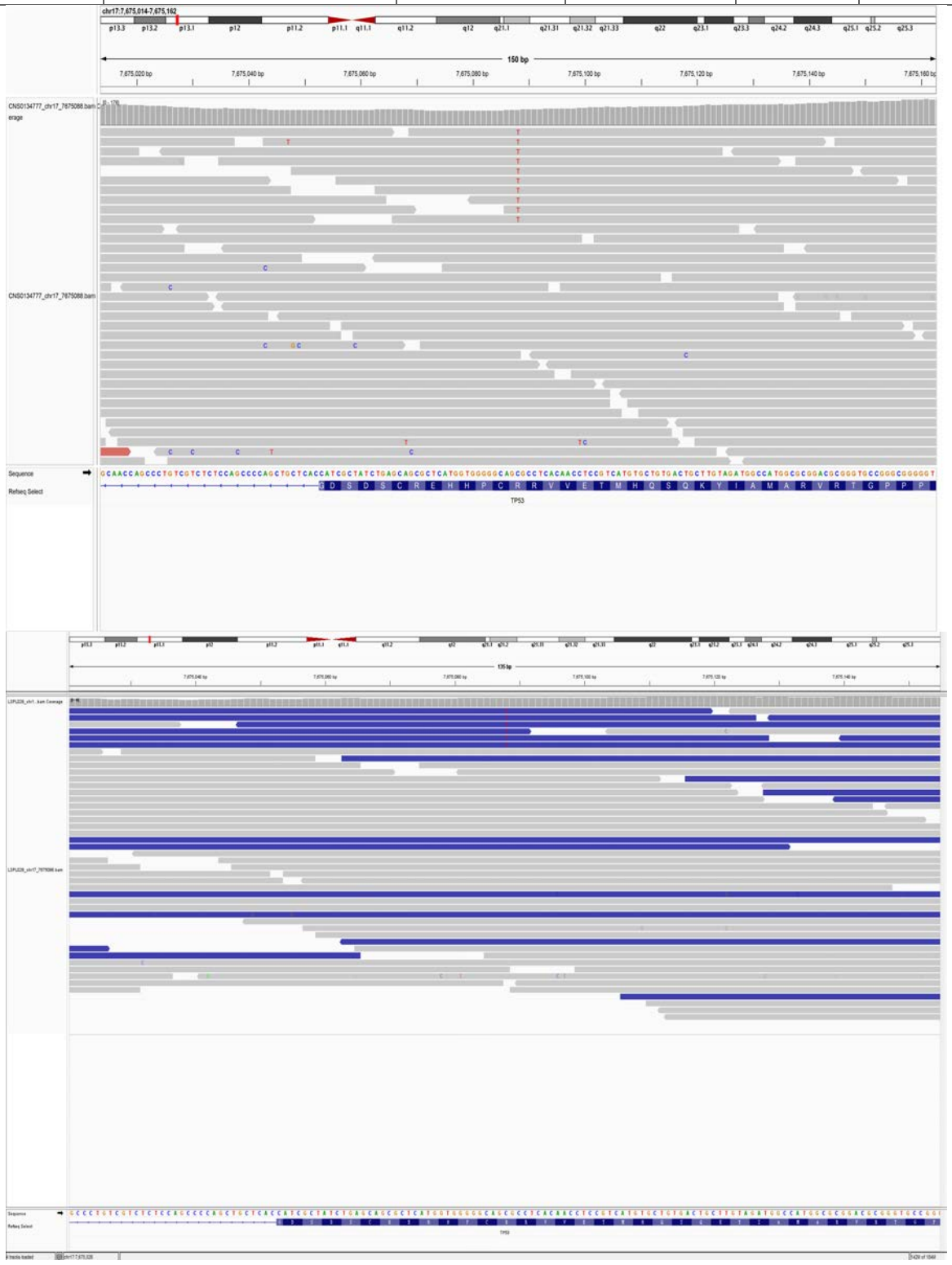
56.5. chr17_7675066_G/T

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



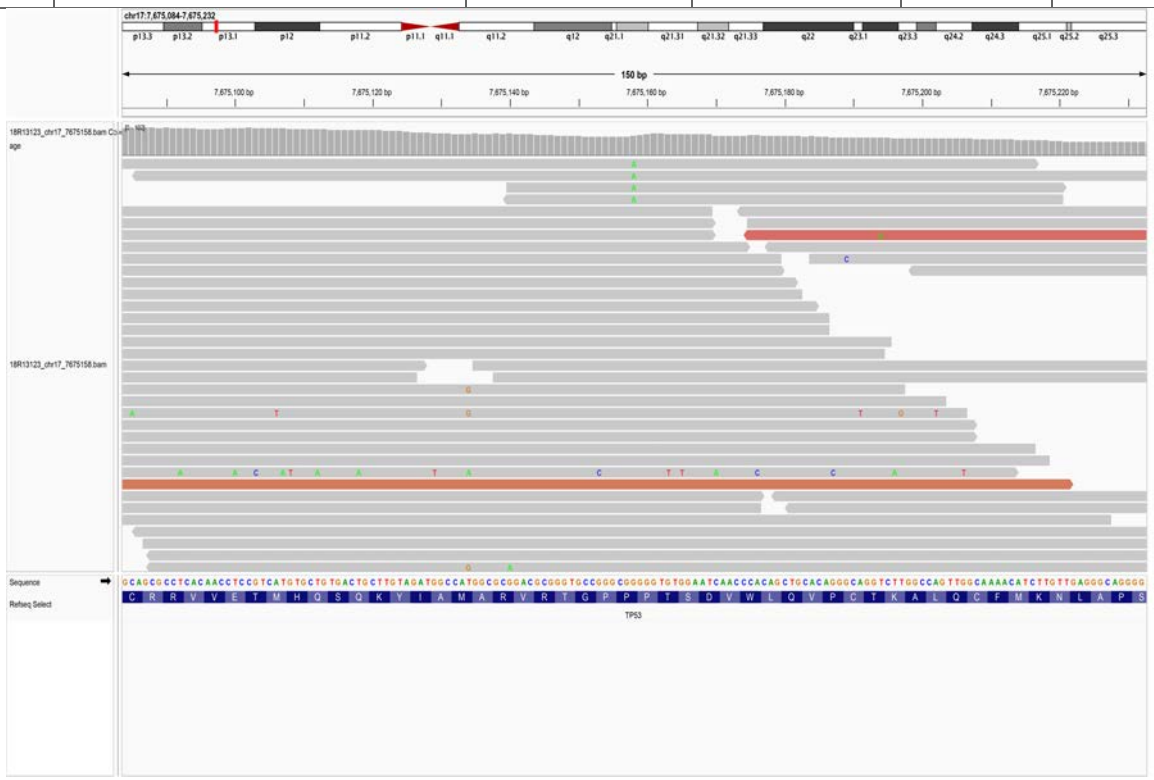
56.6. chr17_7675088_C/T

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



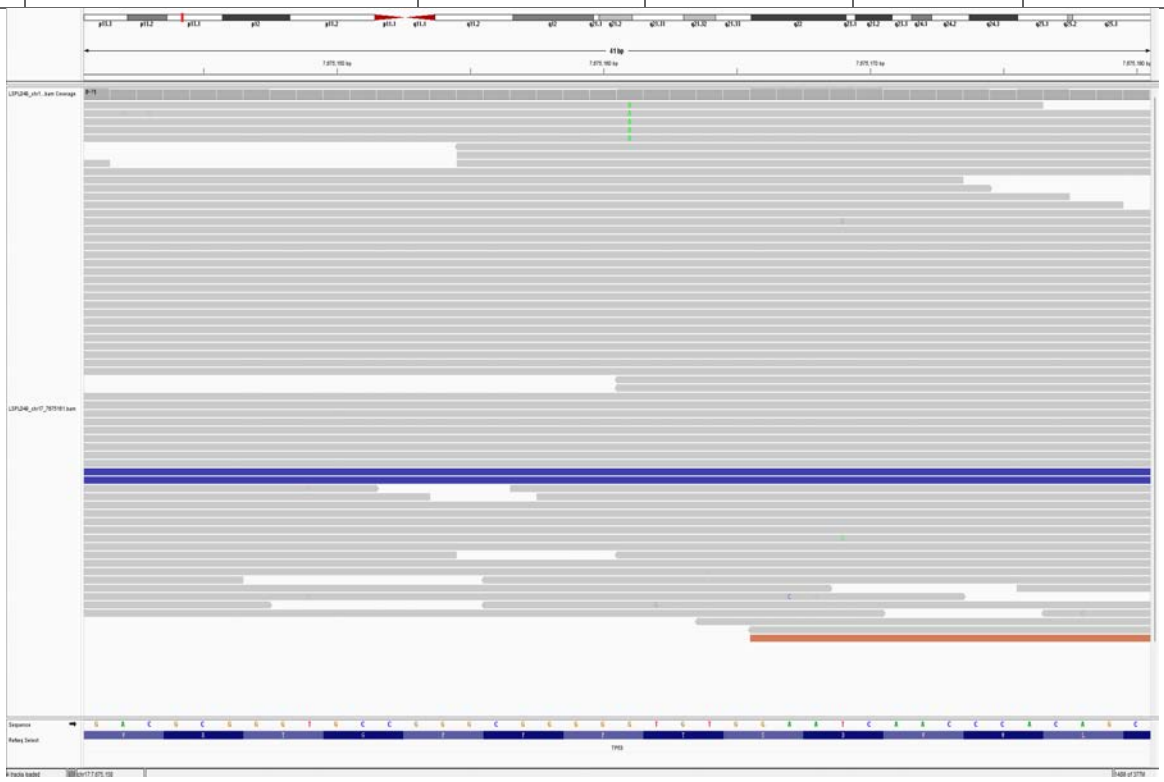
56.7. chr17_7675158_G/A

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



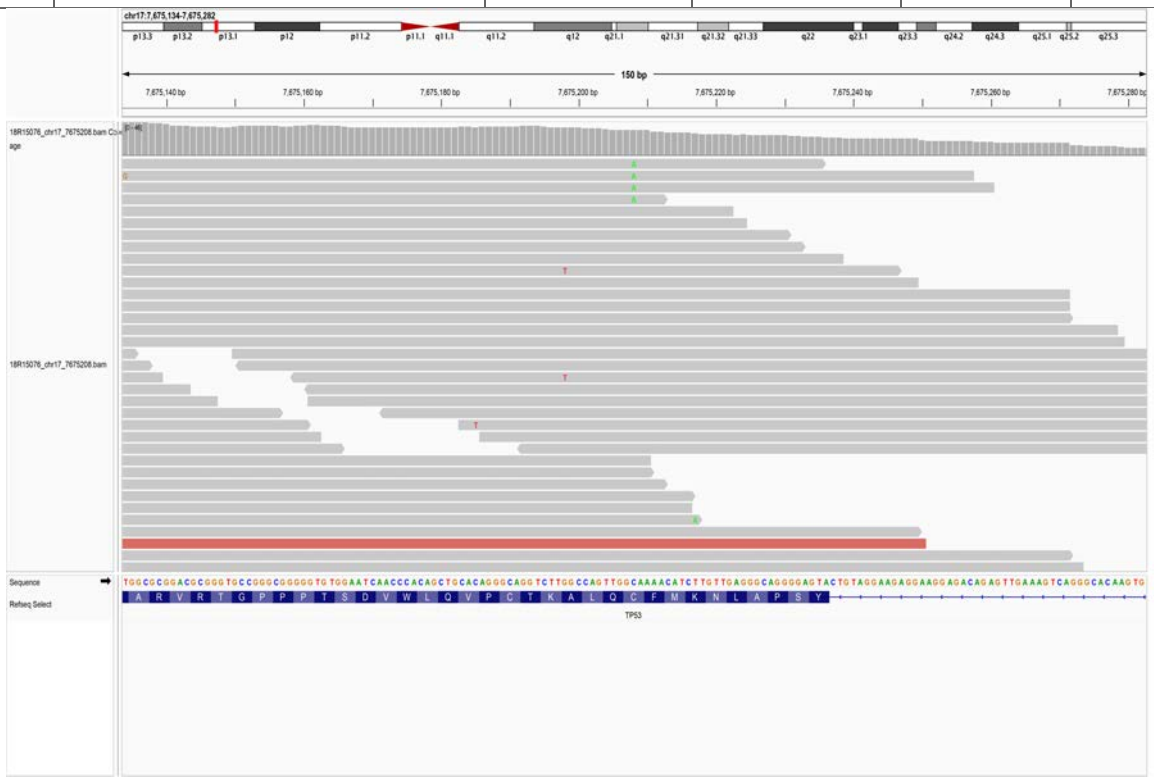
56.8. chr17_7675161_G/A

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



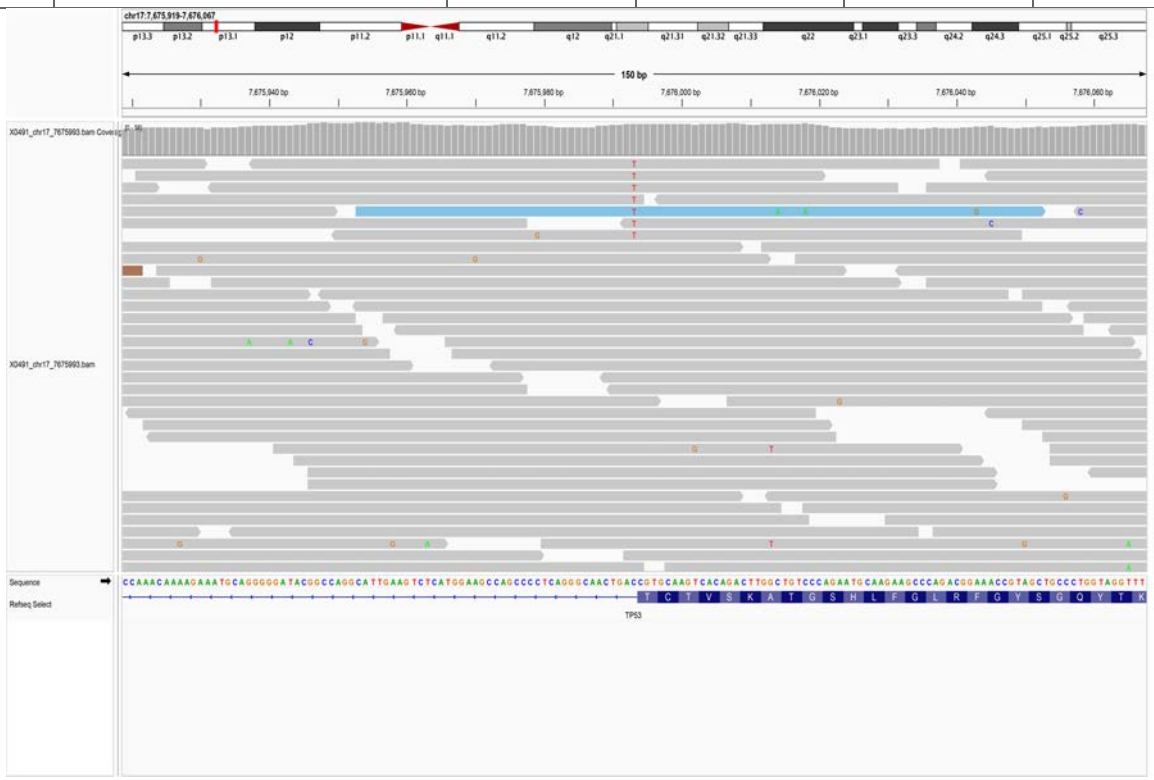
56.9. chr17_7675208_C/A

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

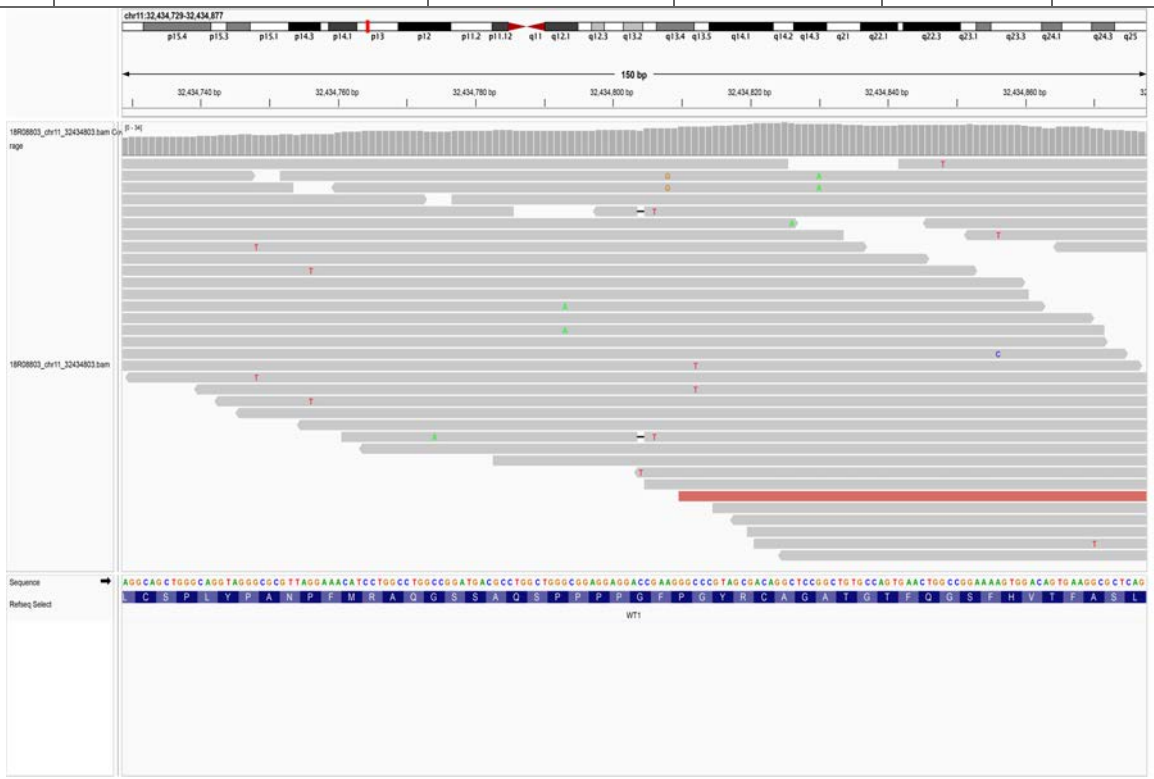
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
X0491	chr17_7675993_C/T	44	6	*TP53*	splice_donor_variant



57. *WT1*

57.1. chr11_32434804_C/-

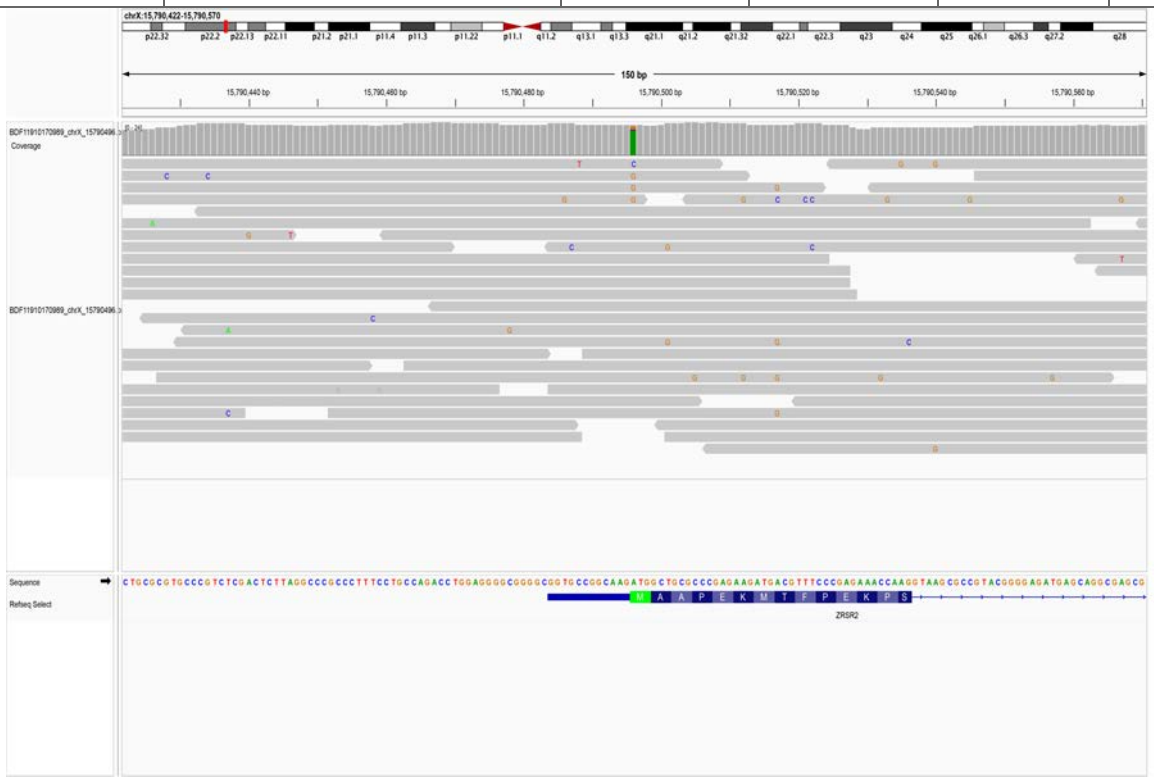
SampleID	Variant (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
18R08803	chr11_32434804_C/-	26	2	*WT1*	frameshift_variant



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.