Additional File 3

CHIP whitelist mutations identified and confirmed in the validation cohort. Listed are 93 CHIP whitelist mutations identified in 88 persons of the KGP Phase III cohort (N = 2,504 unrelated individuals). 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 S6**).

Table of Contents

1. *ASXL2*

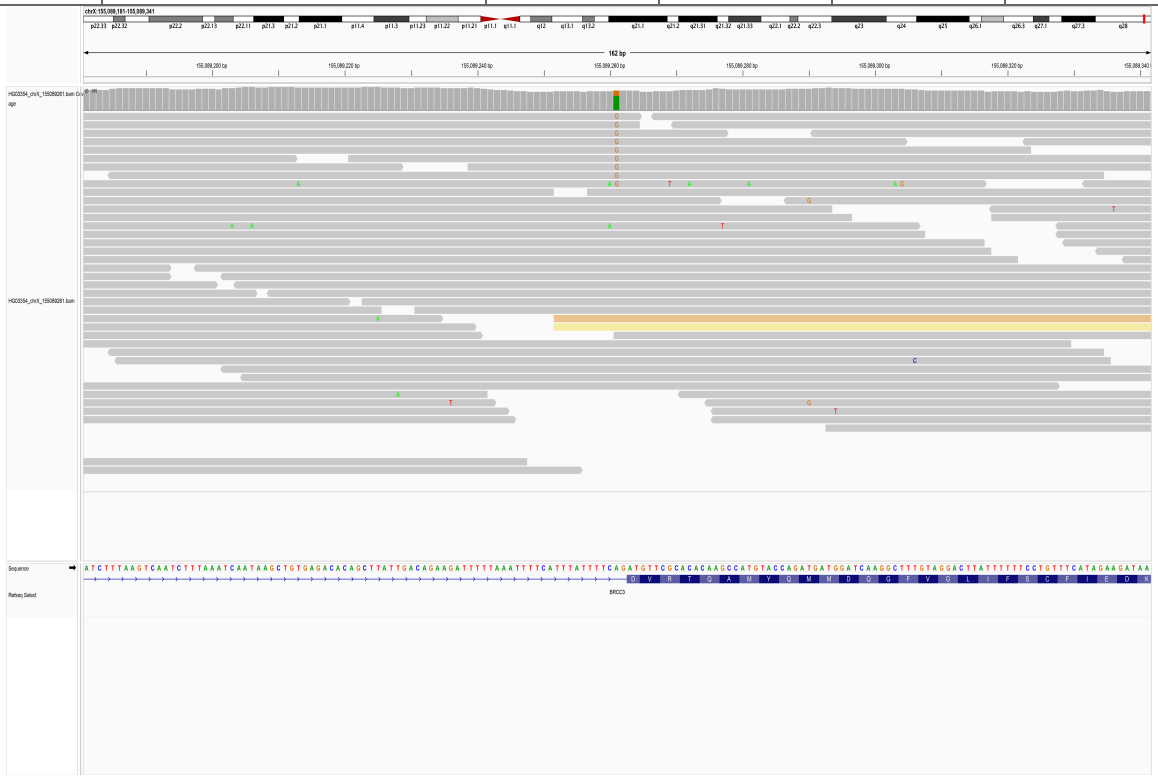
1.1. chr2_25878221_A/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA19004	chr2_25878221_A/C	48	6	*ASXL2*	start_lost

2. *BRCC3*

2.1. chrX_155089261_A/G

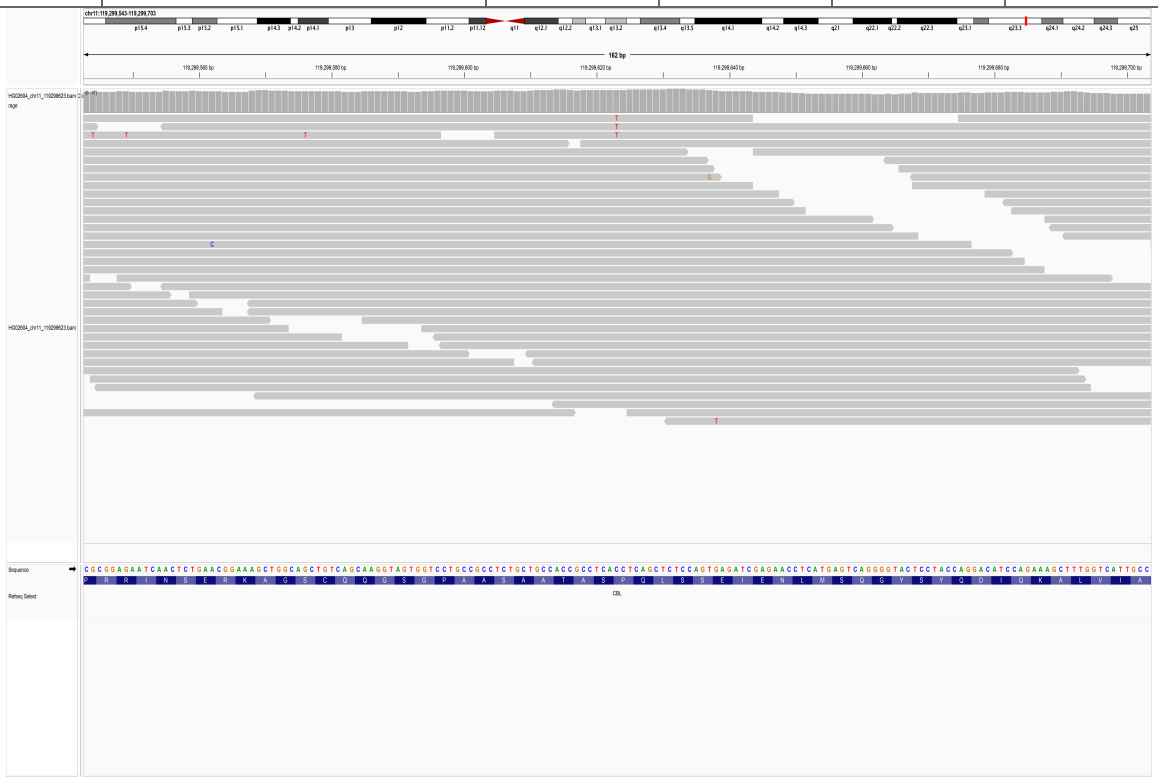
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03354	chrX_155089261_A/G	21	8	*BRCC3*	splice_acceptor_variant



3. *CBL*

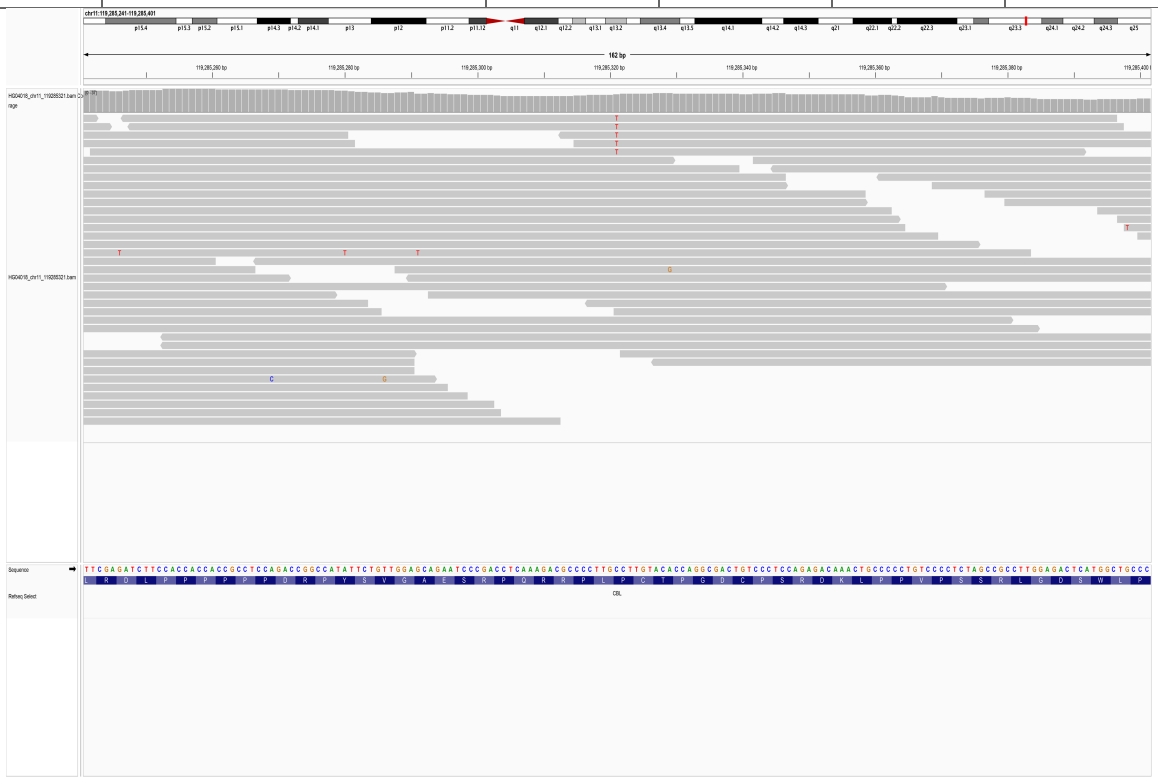
3.1. chr11_119299623_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02604	chr11_119299623_C/T	32	3	*CBL*	missense_variant



3.2. chr11_119285321_C/T

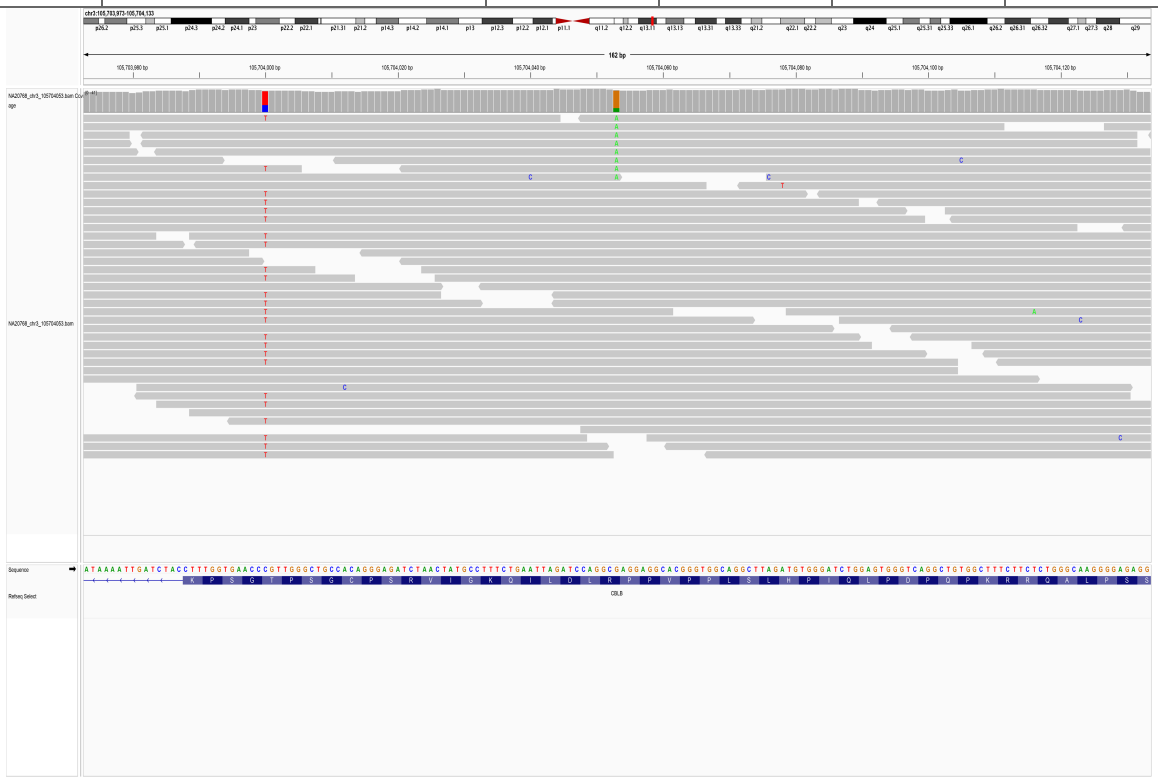
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG04018	chr11_119285321_C/T	22	5	*CBL*	missense_variant



4. *CBLB*

4.1. chr3_105704053_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA20768	chr3_105704053_G/A	30	8	*CBLB*	missense_variant



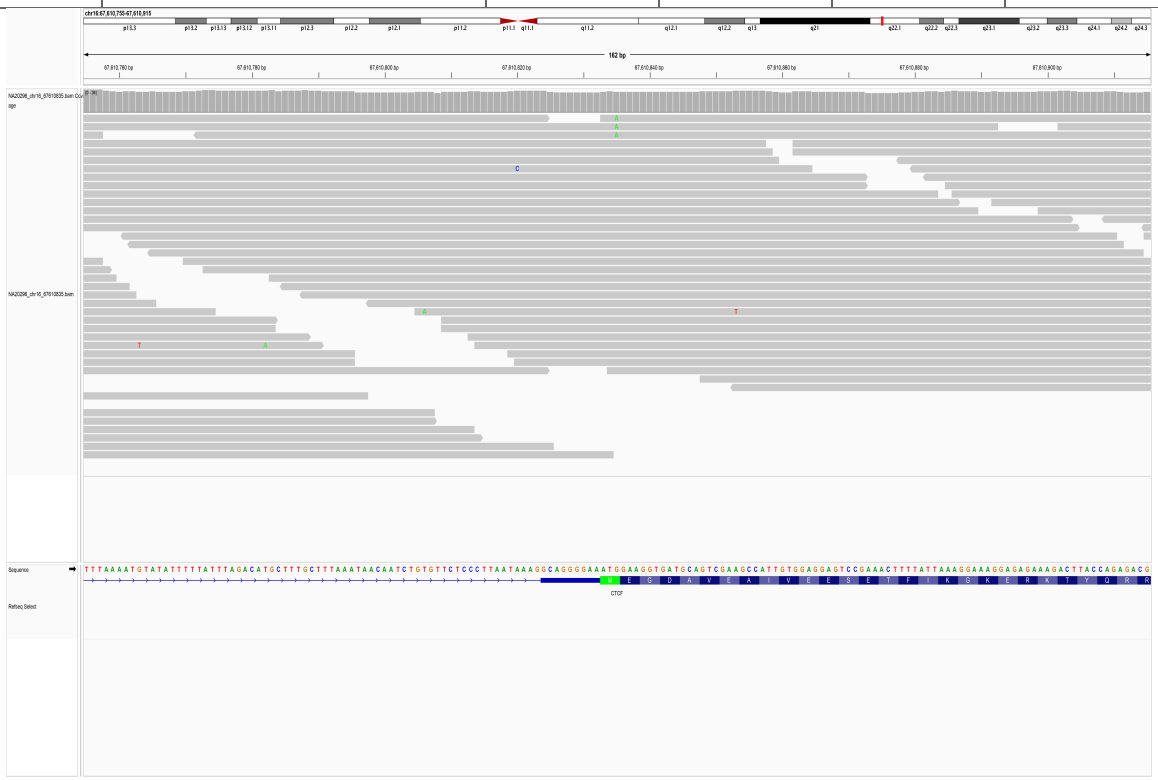
5. *CTCF*

5.1. chr16_67636812_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA18647	chr16_67636812_C/T	32	8	*CTCF*	stop_gained

5.2. chr16_67610835_G/A

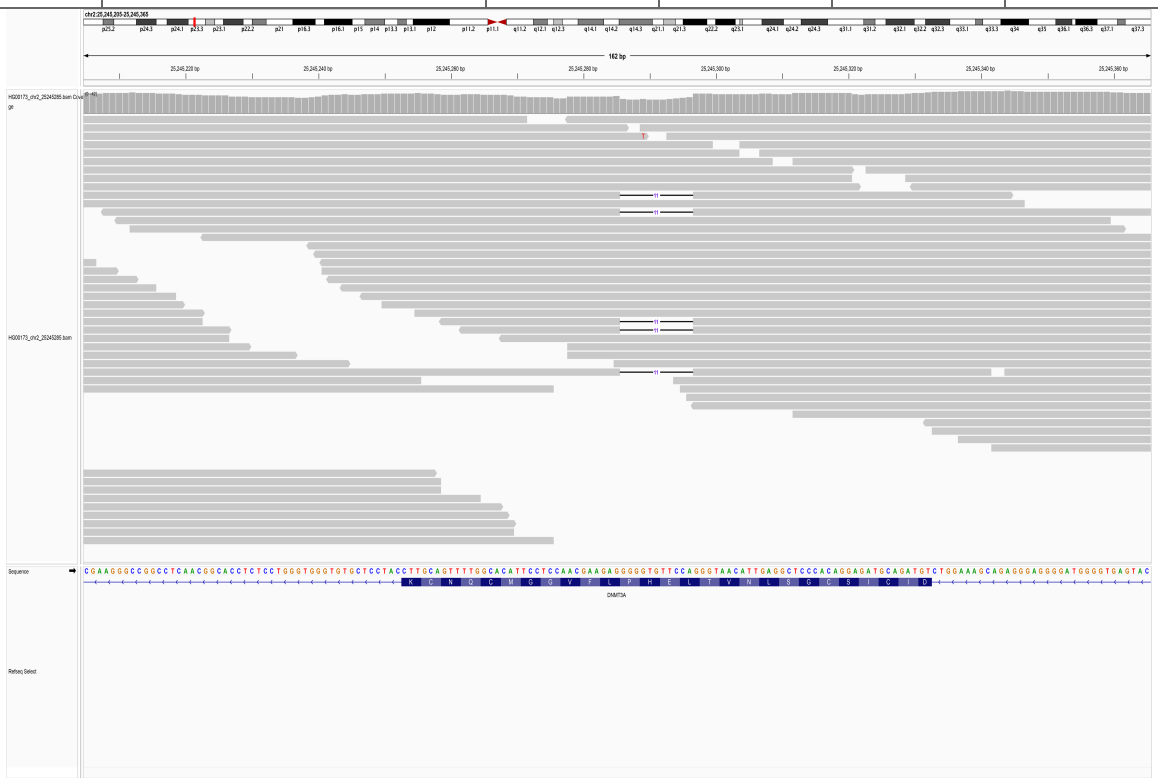
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA20296	chr16_67610835_G/A	28	3	*CTCF*	start_lost



6. *DNMT3A*

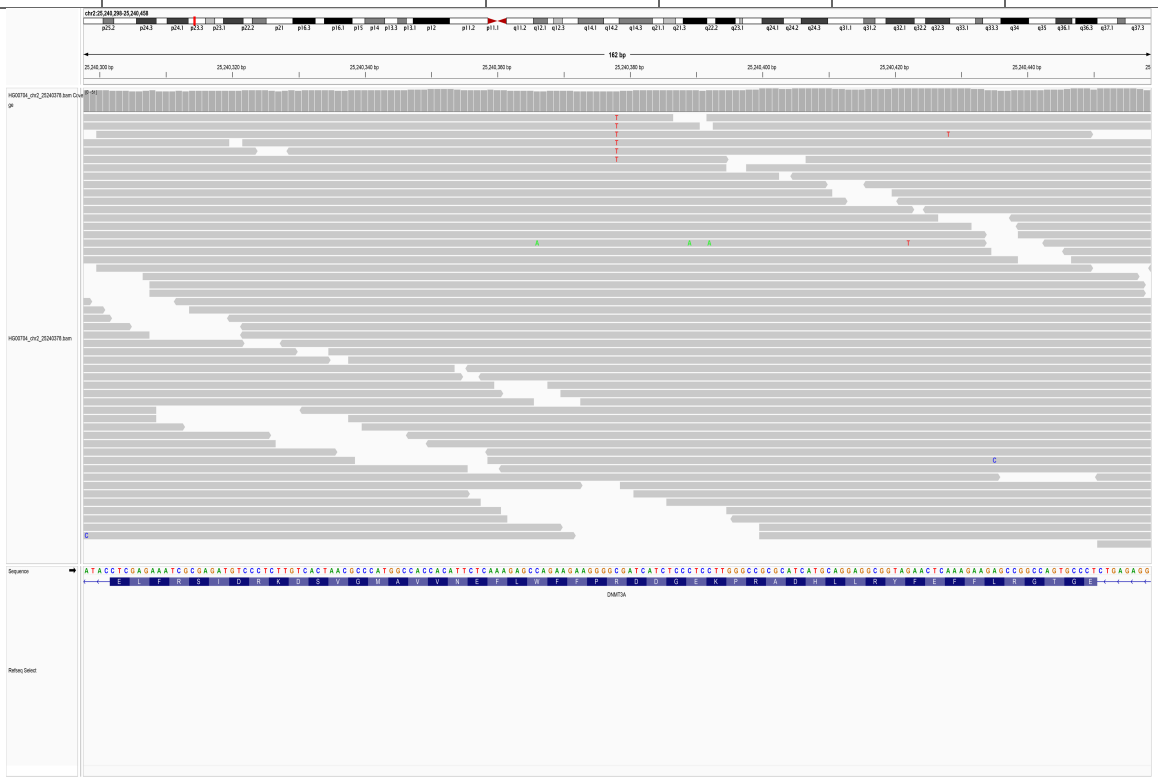
6.1. chr2_25245286_GGGGTGTTCCA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00173	chr2_25245286_GGGGTGTTCCA/-	29	7	*DNMT3A*	frameshift_variant



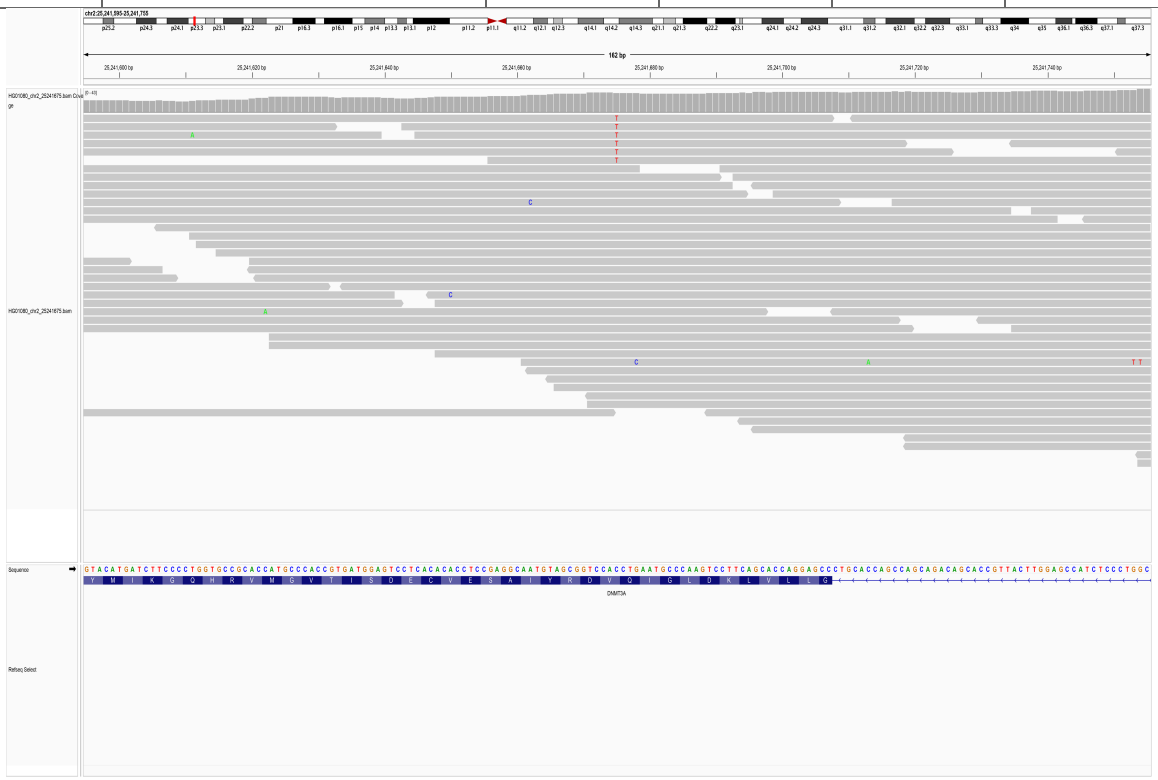
6.2. chr2_25240378_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00704	chr2_25240378_C/T	37	6	*DNMT3A*	missense_variant



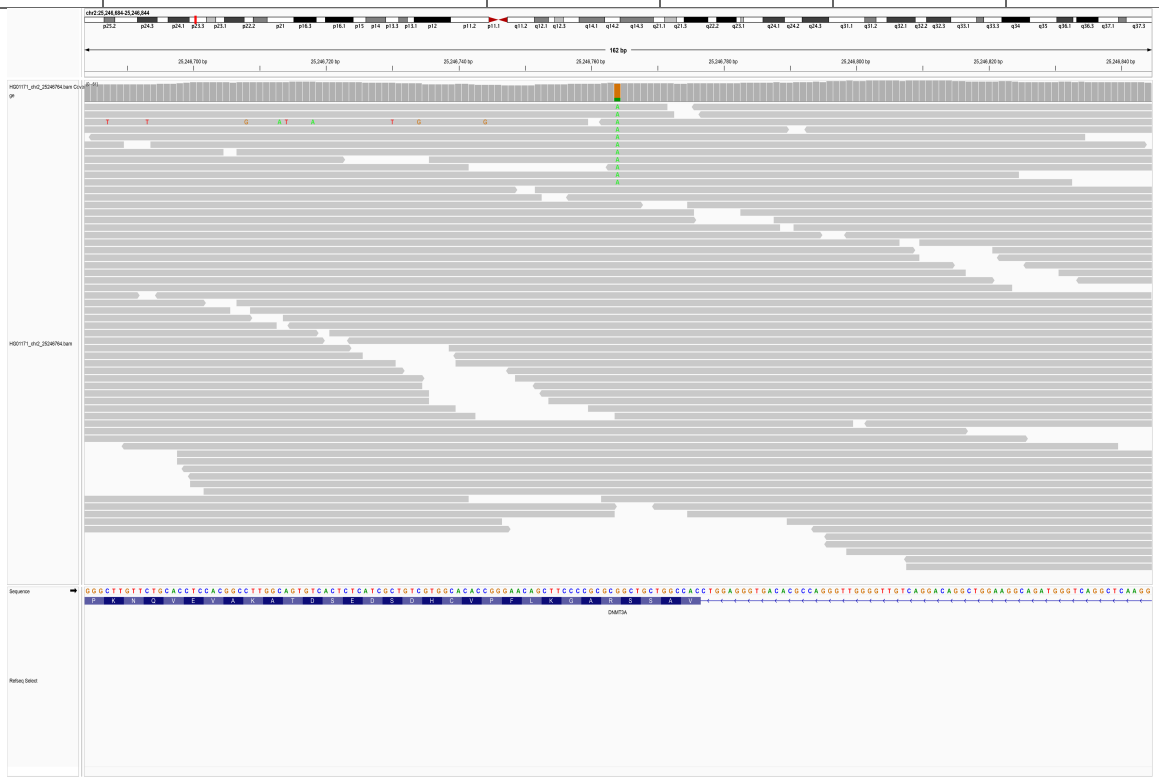
6.3. chr2_25241675_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01080	chr2_25241675_C/T	29	6	*DNMT3A*	missense_variant



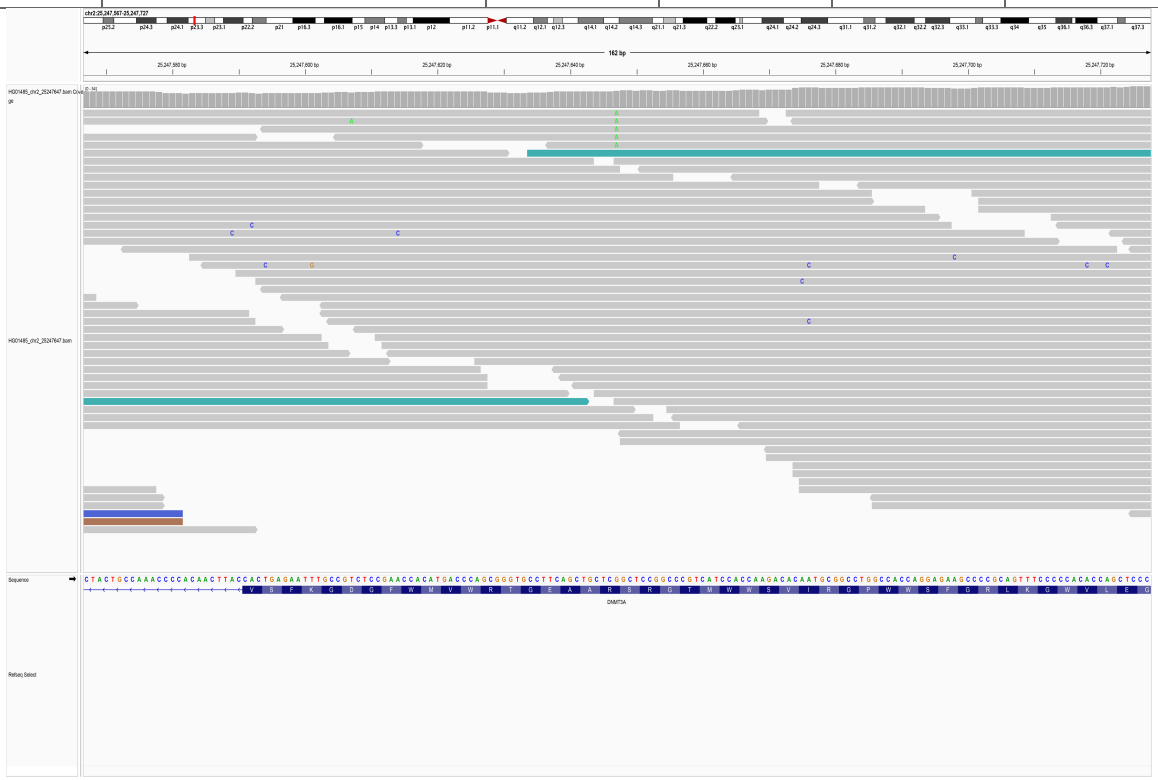
6.4. chr2_25246764_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01171	chr2_25246764_G/A	42	11	*DNMT3A*	missense_variant



6.5. chr2_25247647_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01485	chr2_25247647_G/A	35	5	*DNMT3A*	stop_gained



6.6. chr2_25247629_G/A

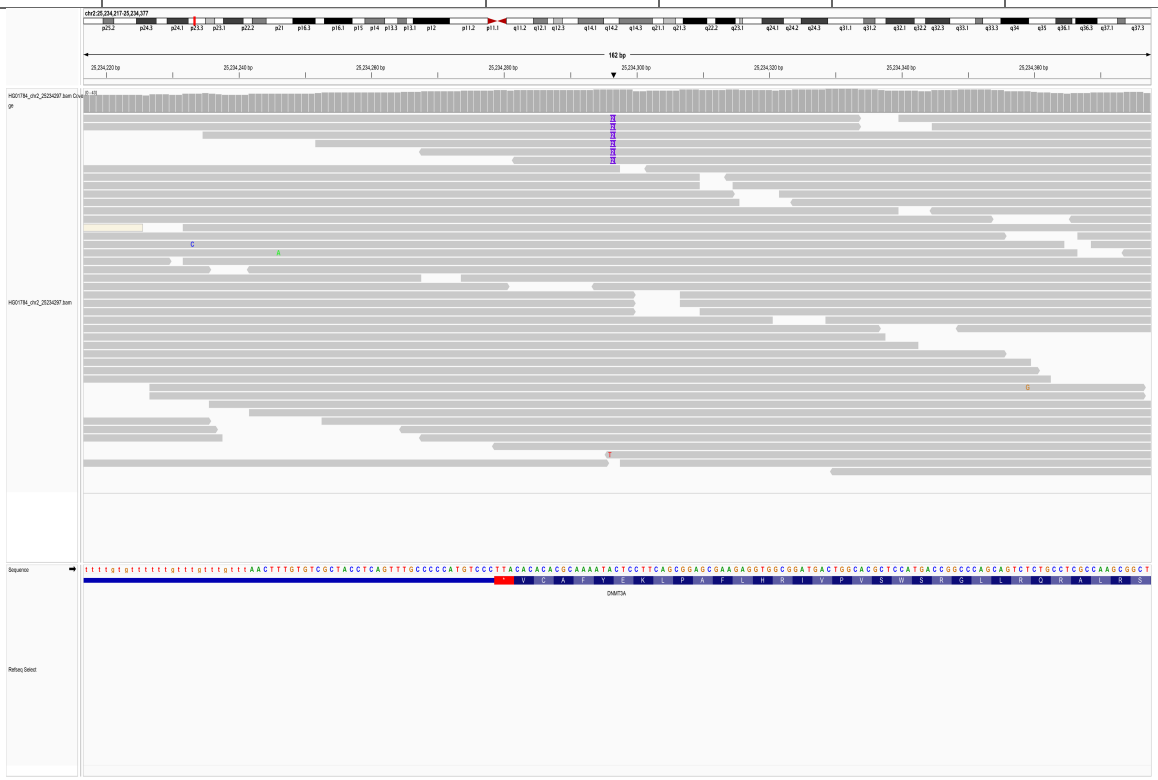
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01537	chr2_25247629_G/A	37	3	*DNMT3A*	missense_variant

6.7. chr2_25240718_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01765	chr2_25240718_C/T	32	7	*DNMT3A*	missense_variant

6.8. chr2_25234297_-/CT

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01784	chr2_25234297_-/CT	30	8	*DNMT3A*	frameshift_variant

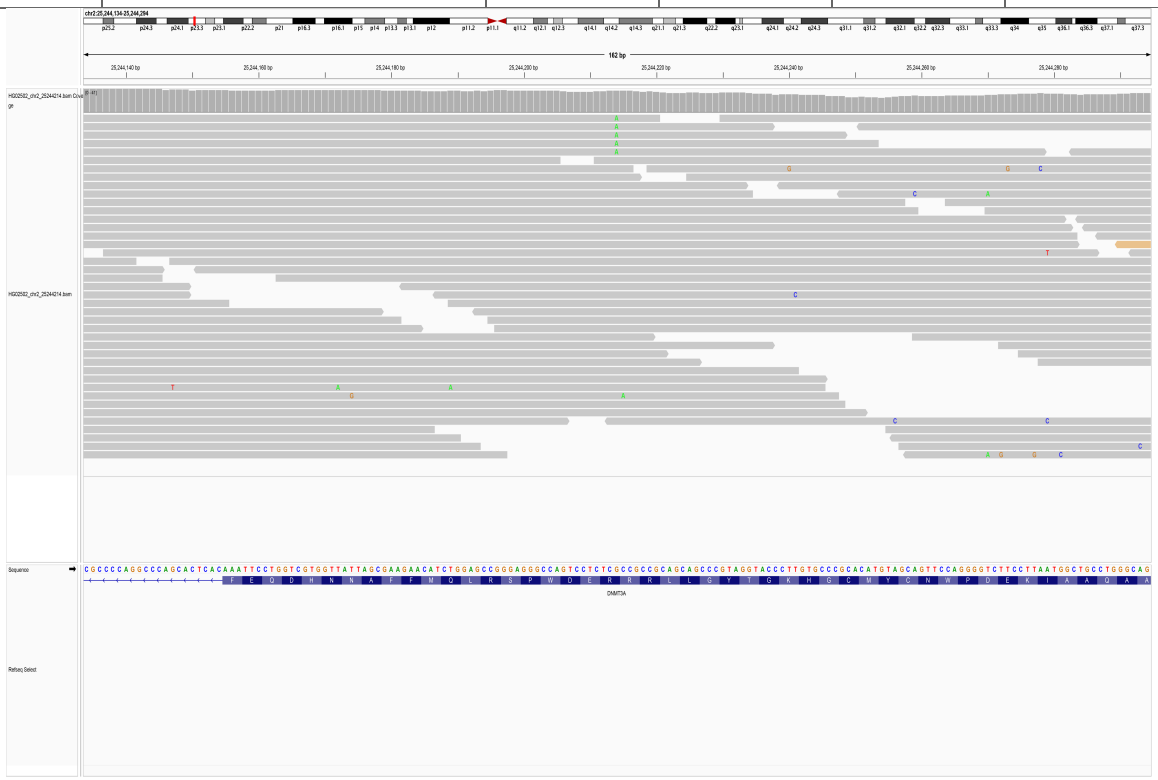


6.9. chr2_25240315_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02025	chr2_25240315_G/A	39	10	*DNMT3A*	missense_variant

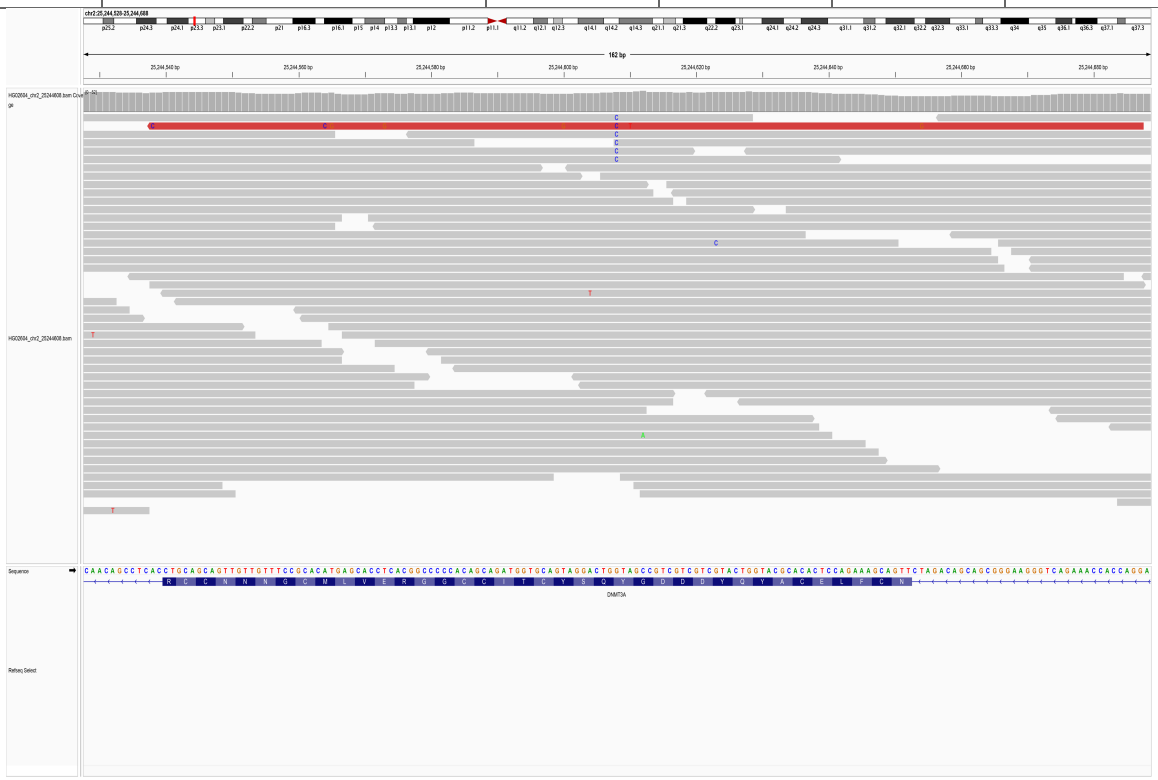
6.10. chr2_25244214_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02502	chr2_25244214_G/A	32	5	*DNMT3A*	stop_gained



6.11. chr2_25244608_G/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02604	chr2_25244608_G/C	35	5	*DNMT3A*	stop_gained

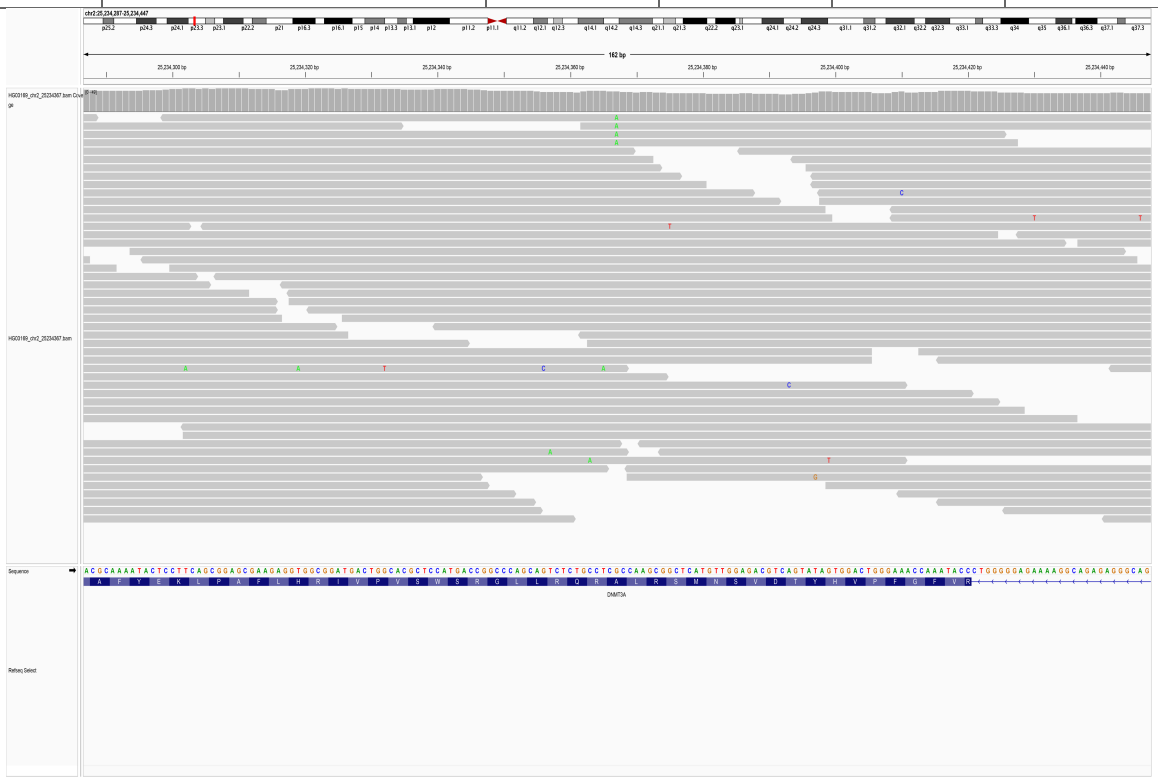


6.12. chr2_25236968_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02722	chr2_25236968_G/A	23	4	*DNMT3A*	stop_gained

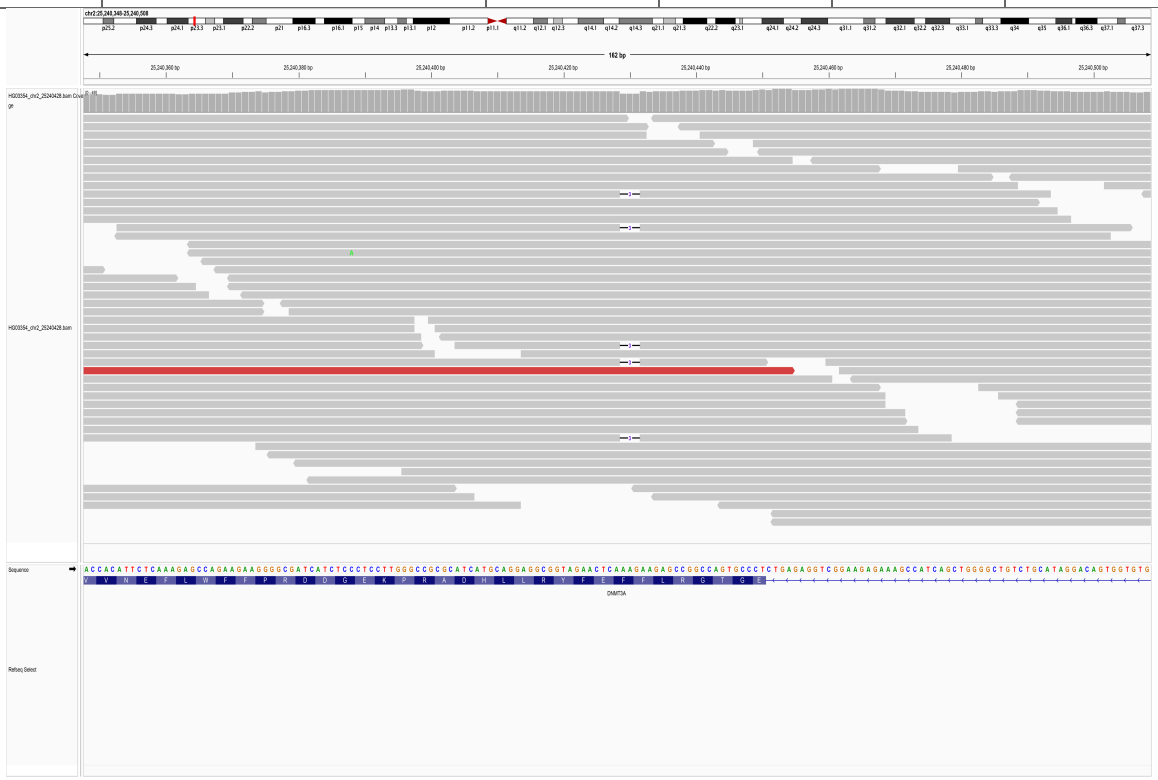
6.13. chr2_25234367_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03169	chr2_25234367_G/A	37	4	*DNMT3A*	missense_variant



6.14. chr2_25240429_AAG/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03354	chr2_25240429_AAG/-	37	6	*DNMT3A*	inframe_deletion



6.15. chr2_25240700_T/A

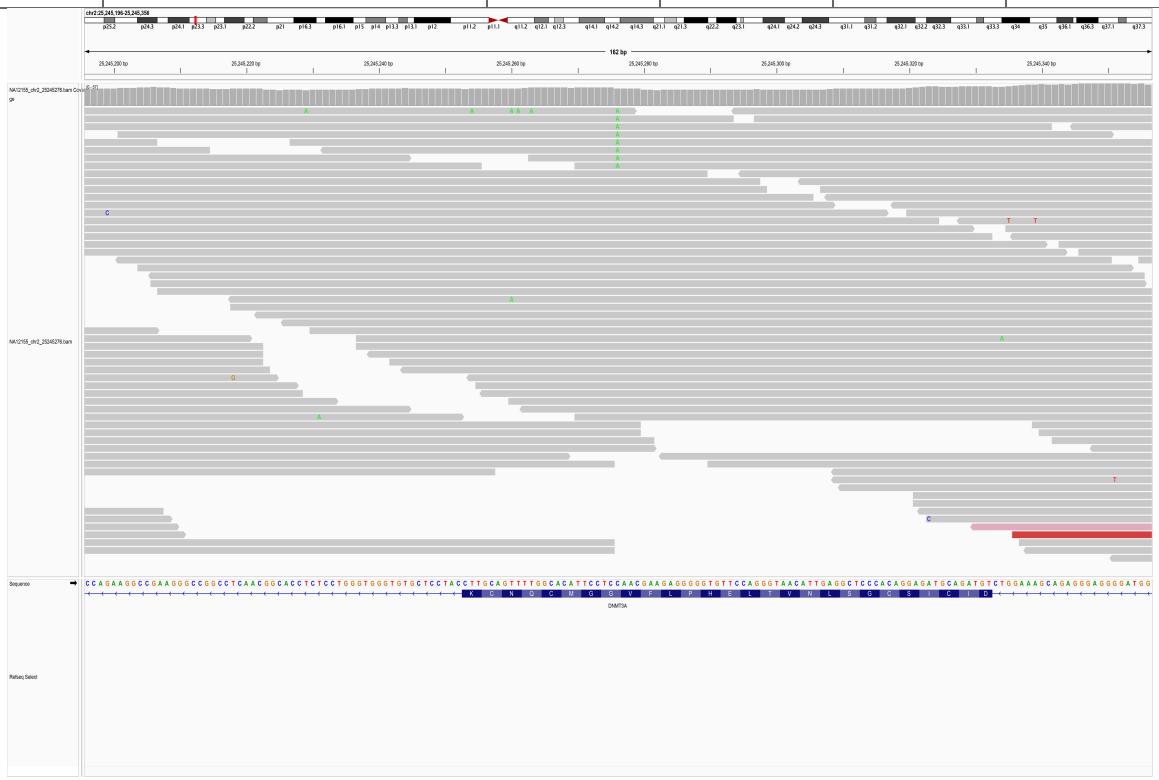
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03899	chr2_25240700_T/A	41	8	*DNMT3A*	missense_variant

6.16. chr2_25244654_T/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA11994	chr2_25244654_T/G	33	11	*DNMT3A*	splice_acceptor_variant

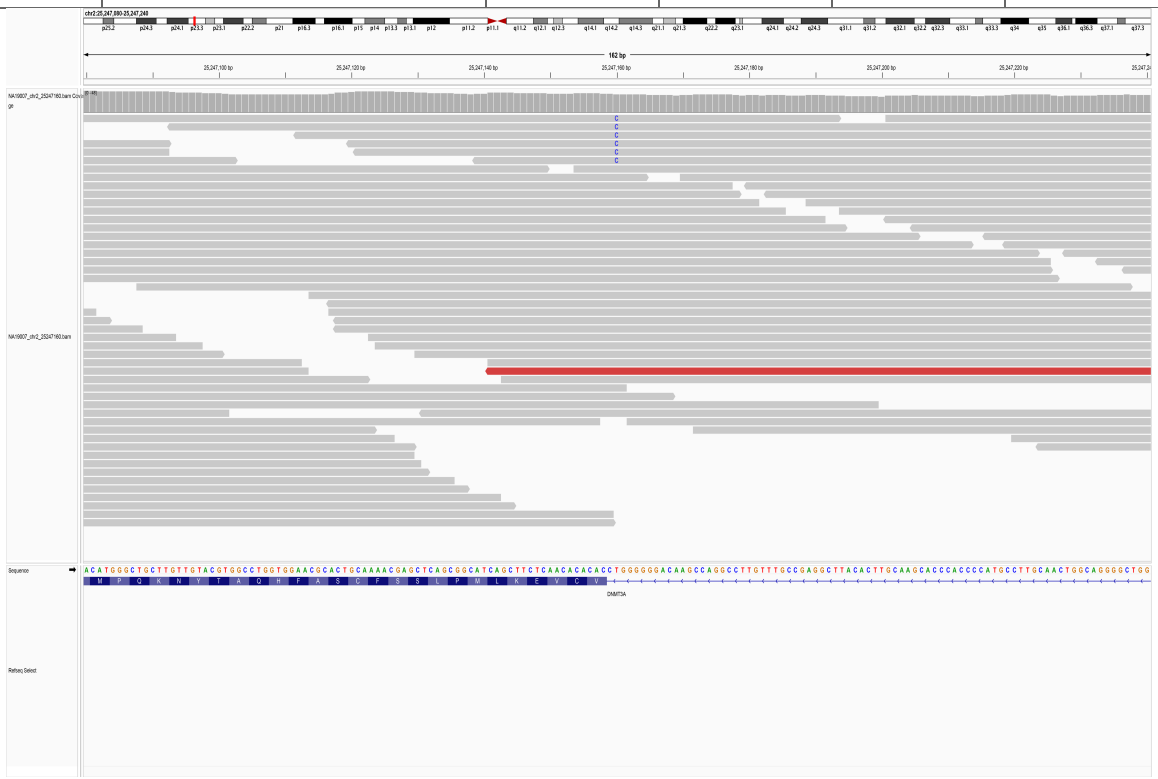
6.17. chr2_25245276_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA12155	chr2_25245276_C/A	36	7	*DNMT3A*	stop_gained



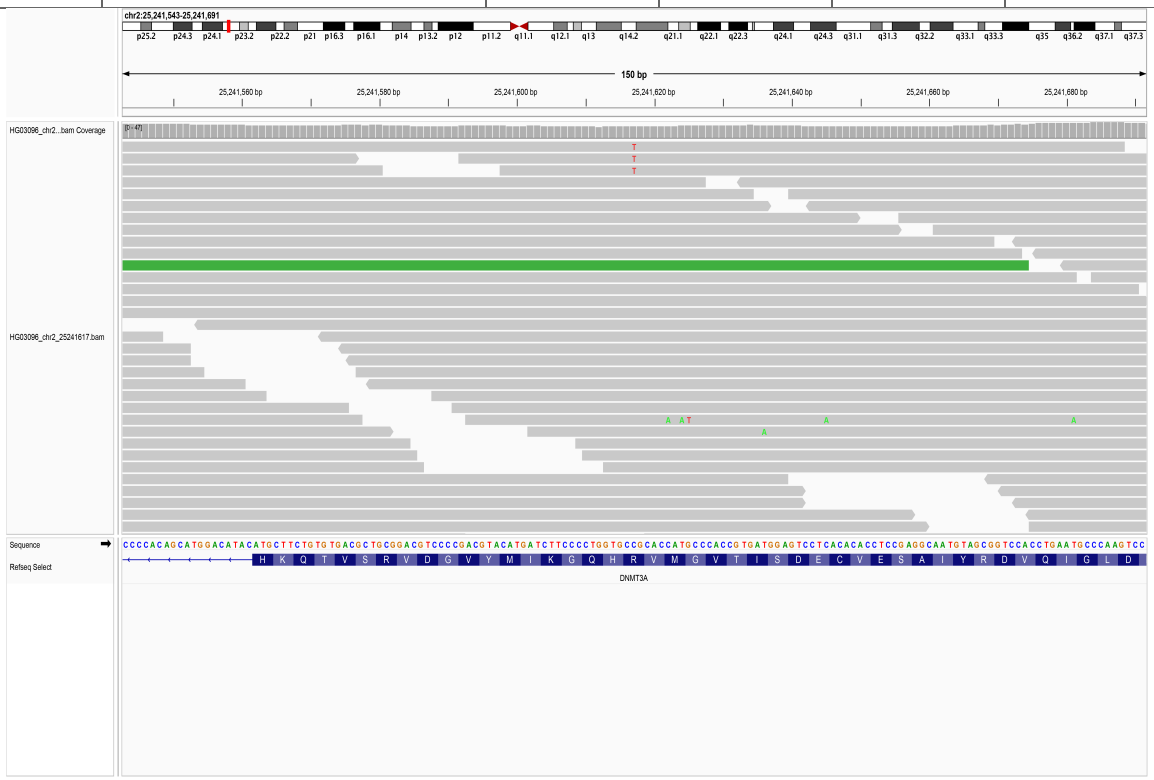
6.18. chr2_25247160_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA19007	chr2_25247160_T/C	30	6	*DNMT3A*	splice_acceptor_variant



6.19. chr2_25241617_C/T

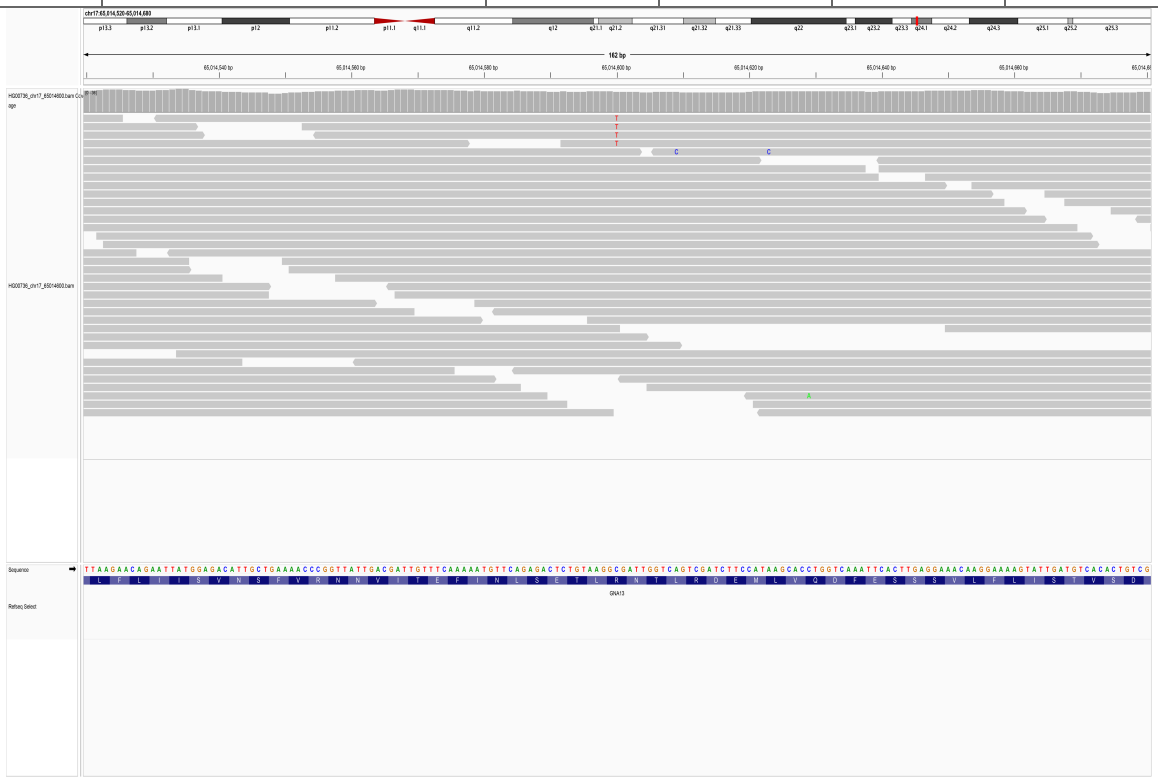
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03096	chr2_25241617_C/T	29	3	*DNMT3A*	missense_variant



7. *GNA13*

7.1. chr17_65014600_C/T

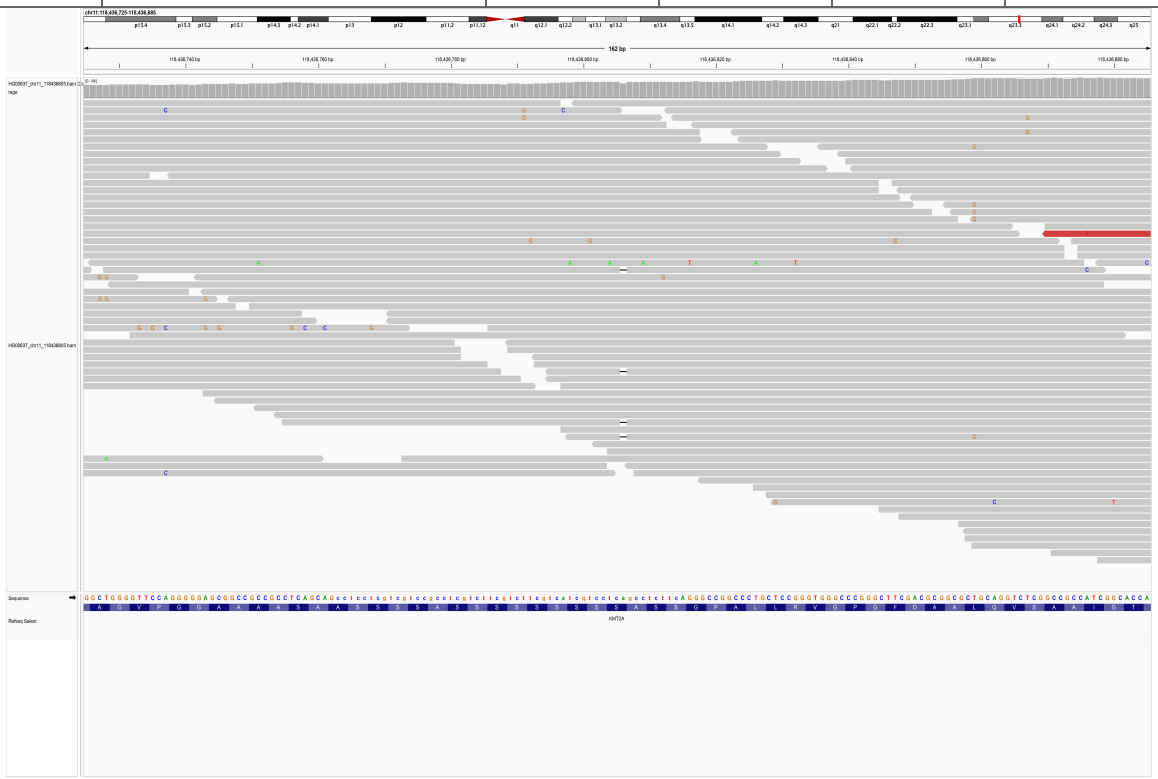
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00736	chr17_65014600_C/T	27	4	*GNA13*	missense_variant



8. *KMT2A*

8.1. chr11_118436806_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00637	chr11_118436806_A/-	43	4	*KMT2A*	frameshift_variant



9. *KMT2D*

9.1. chr12_49037395_G/A

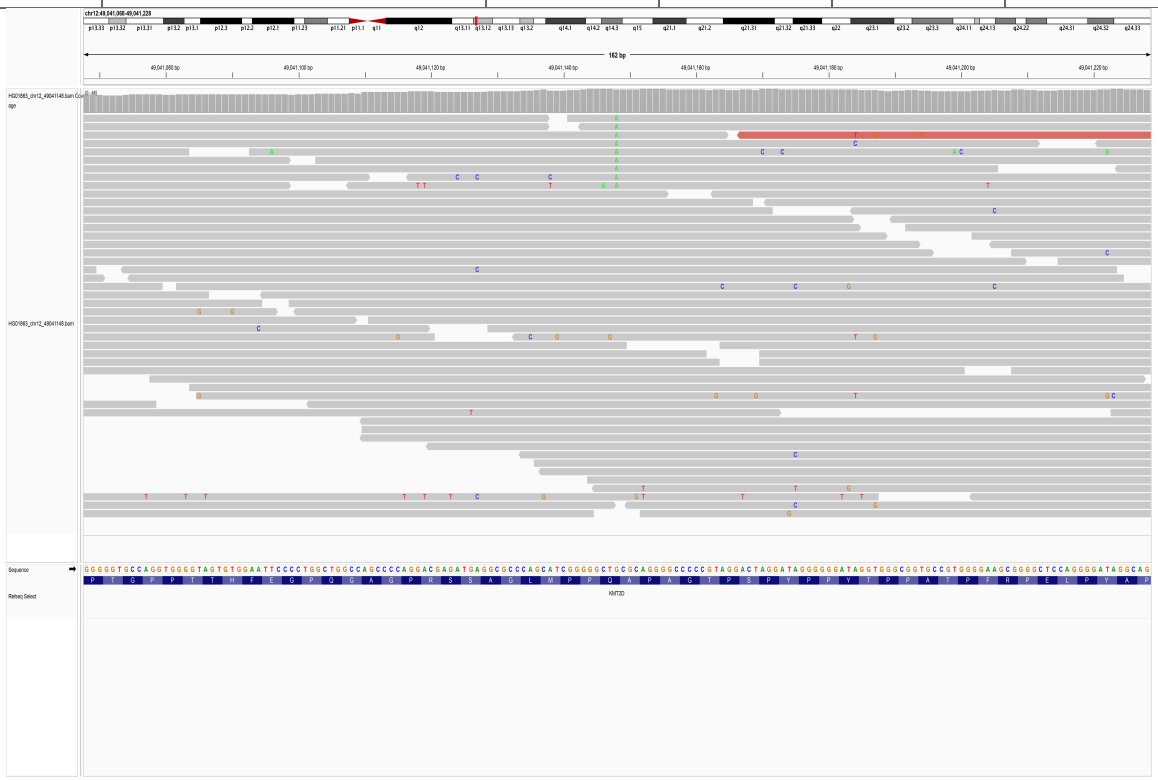
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00613	chr12_49037395_G/A	31	4	*KMT2D*	stop_gained

9.2. chr12_49037173_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01771	chr12_49037173_G/A	40	4	*KMT2D*	stop_gained

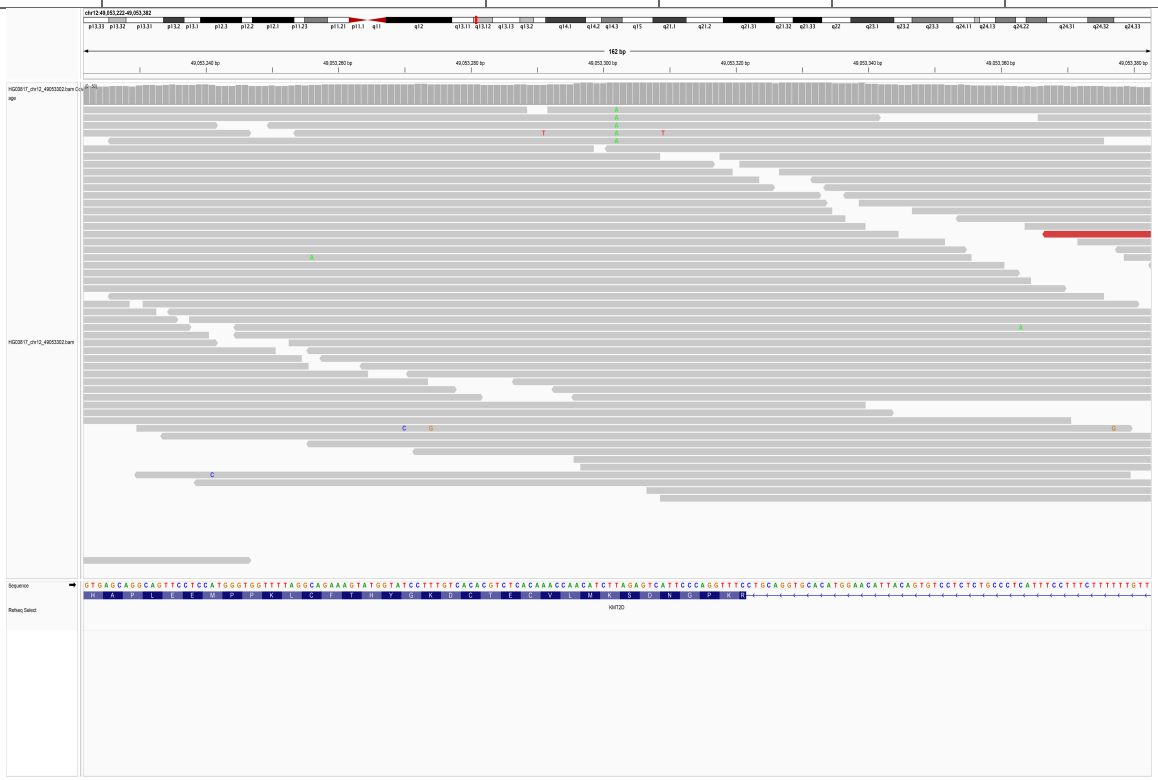
9.3. chr12_49041148_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01863	chr12_49041148_G/A	35	8	*KMT2D*	stop_gained



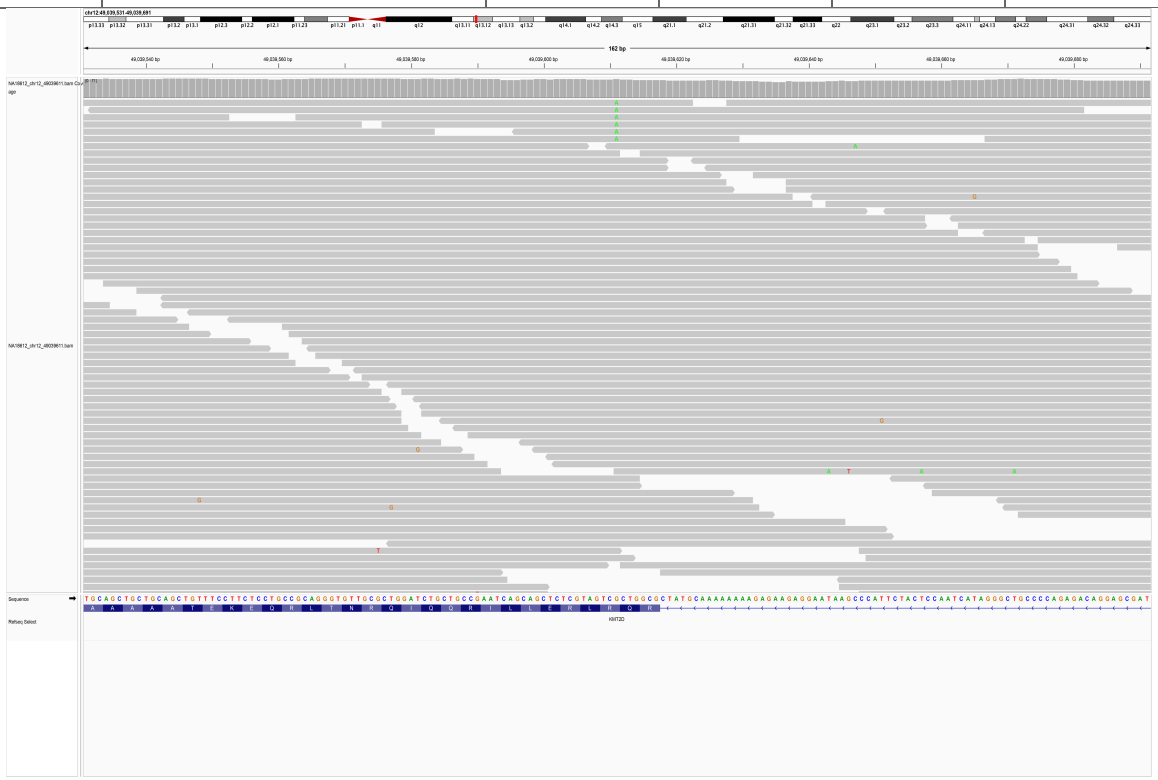
9.4. chr12_49053302_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03817	chr12_49053302_T/A	44	4	*KMT2D*	stop_gained



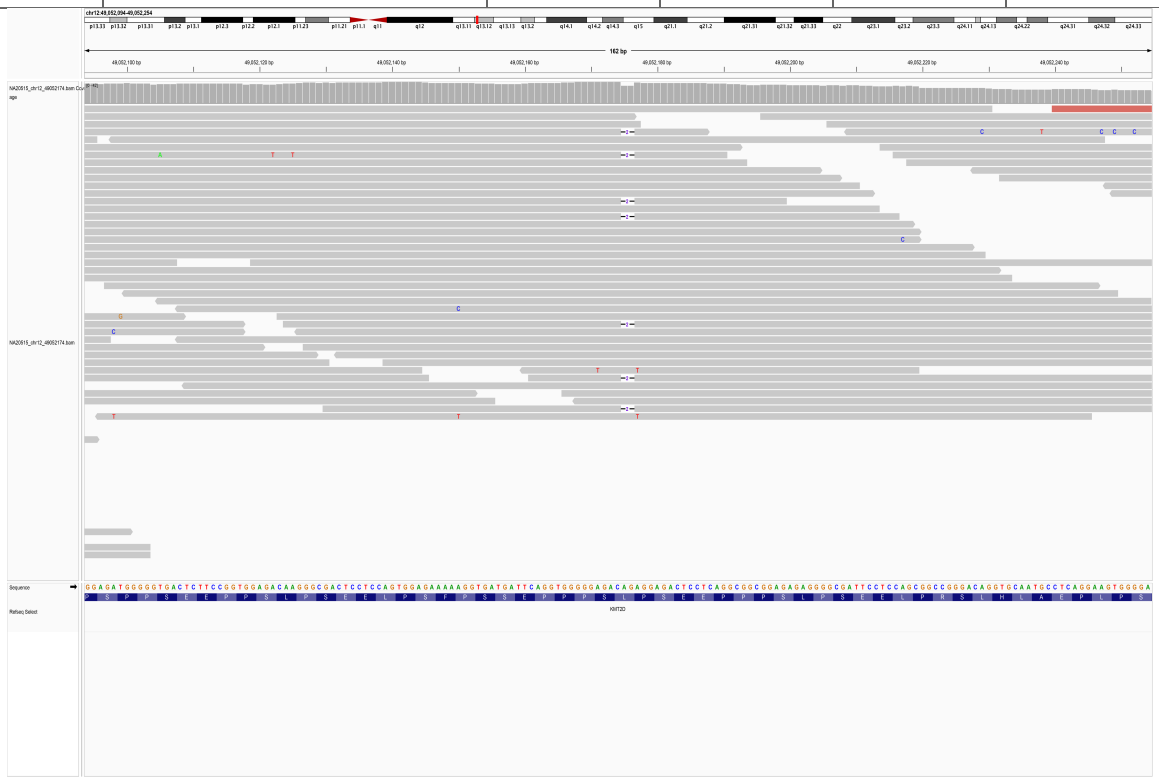
9.5. chr12_49039611_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA18612	chr12_49039611_G/A	58	6	*KMT2D*	stop_gained



9.6. chr12_49052175_AG/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA20515	chr12_49052175_AG/-	32	7	*KMT2D*	frameshift_variant



10. *MPL*

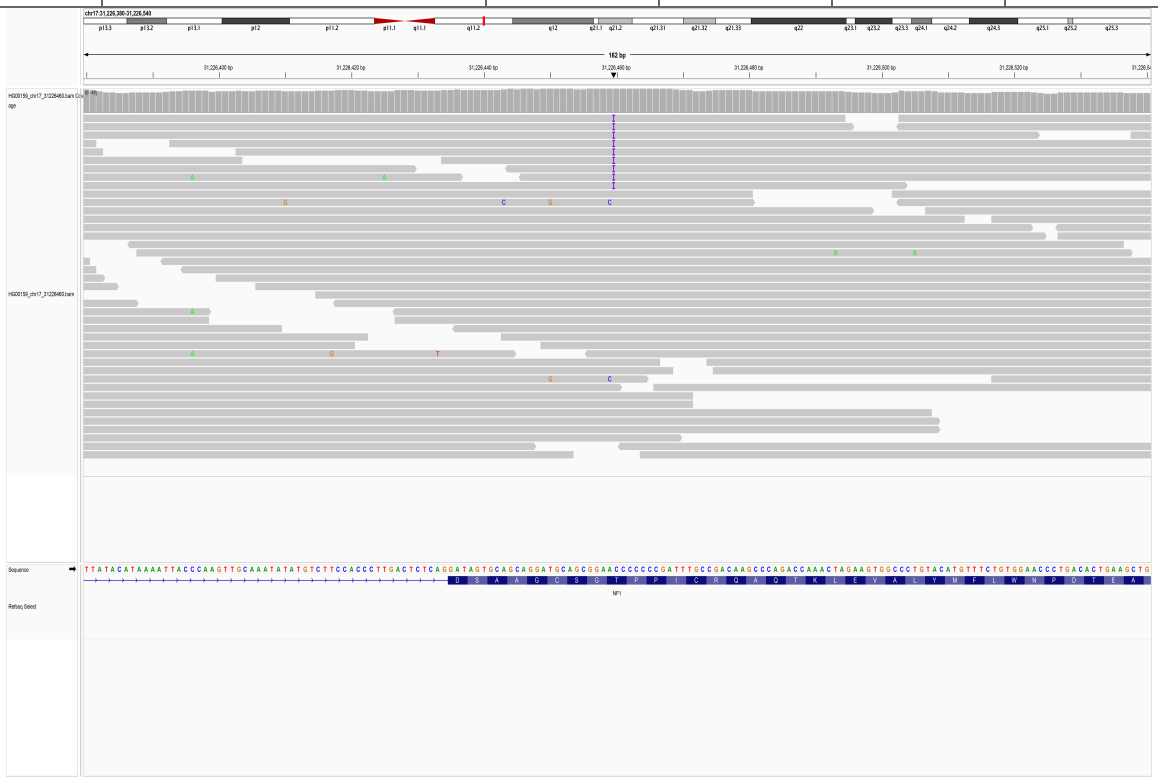
10.1. chr1_43352251_A/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA18976	chr1_43352251_A/T	26	10	*MPL*	missense_variant

11. *NF1*

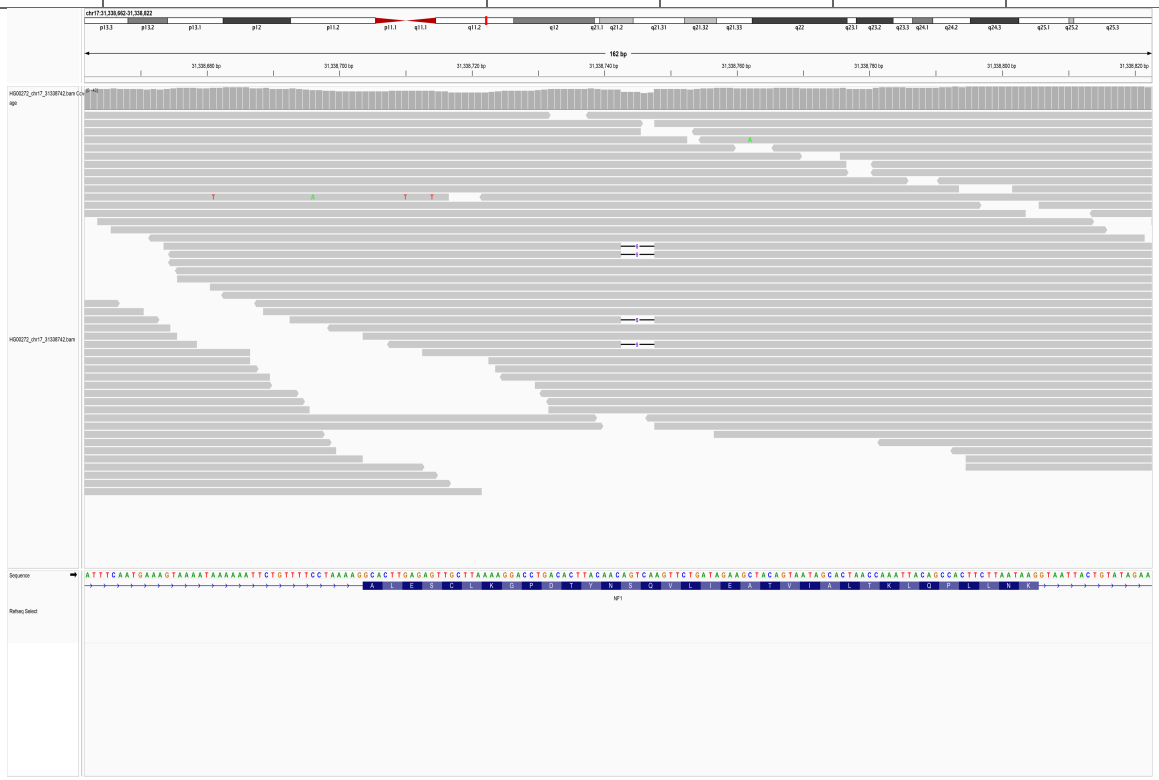
11.1. chr17_31226460_-/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00159	chr17_31226460_-/C	26	9	*NF1*	frameshift_variant



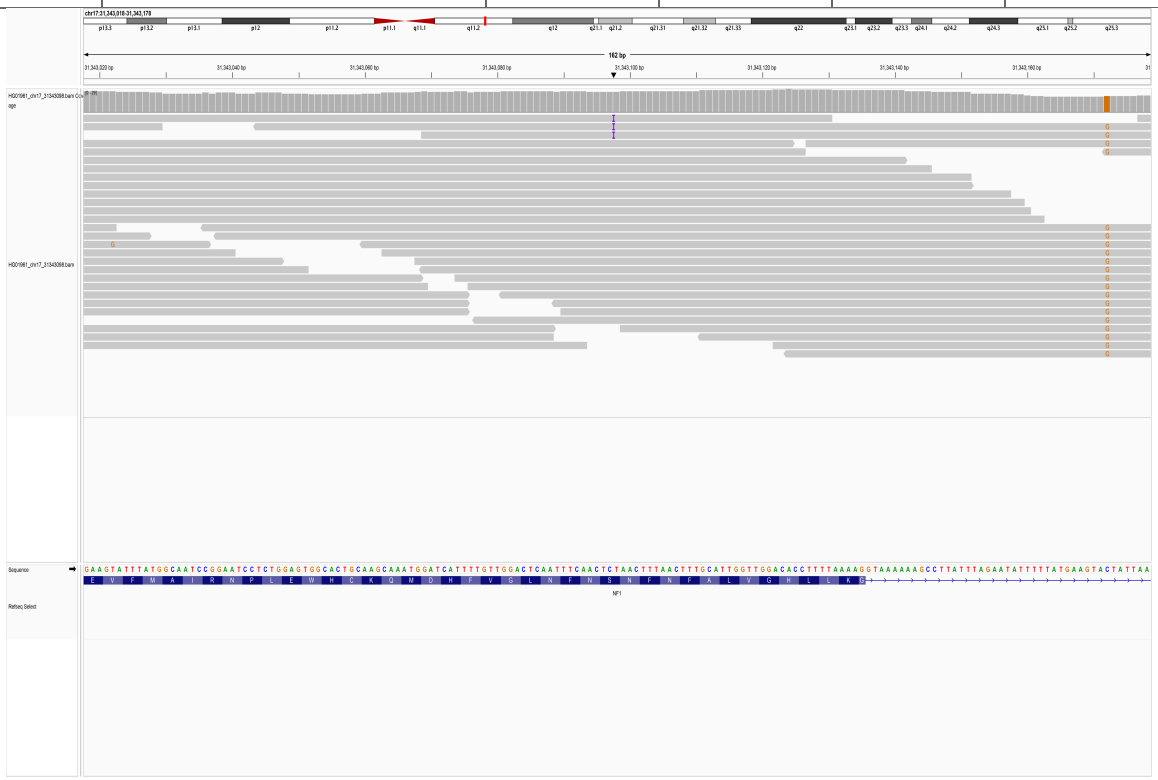
11.2. chr17_31338743_AGTCA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00272	chr17_31338743_AGTCA/-	32	6	*NF1*	frameshift_variant



11.3. chr17_31343098_-/T

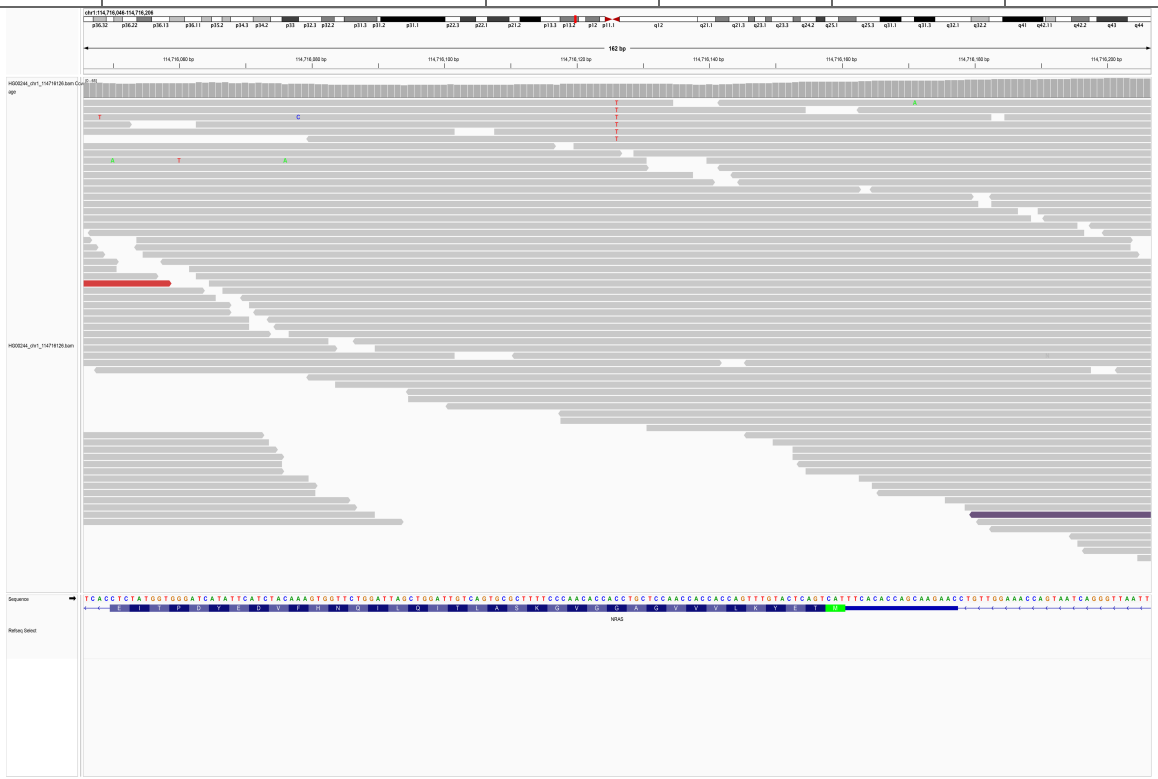
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01961	chr17_31343098_-/T	22	3	*NF1*	frameshift_variant



12. *NRAS*

12.1. chr1_114716126_C/T

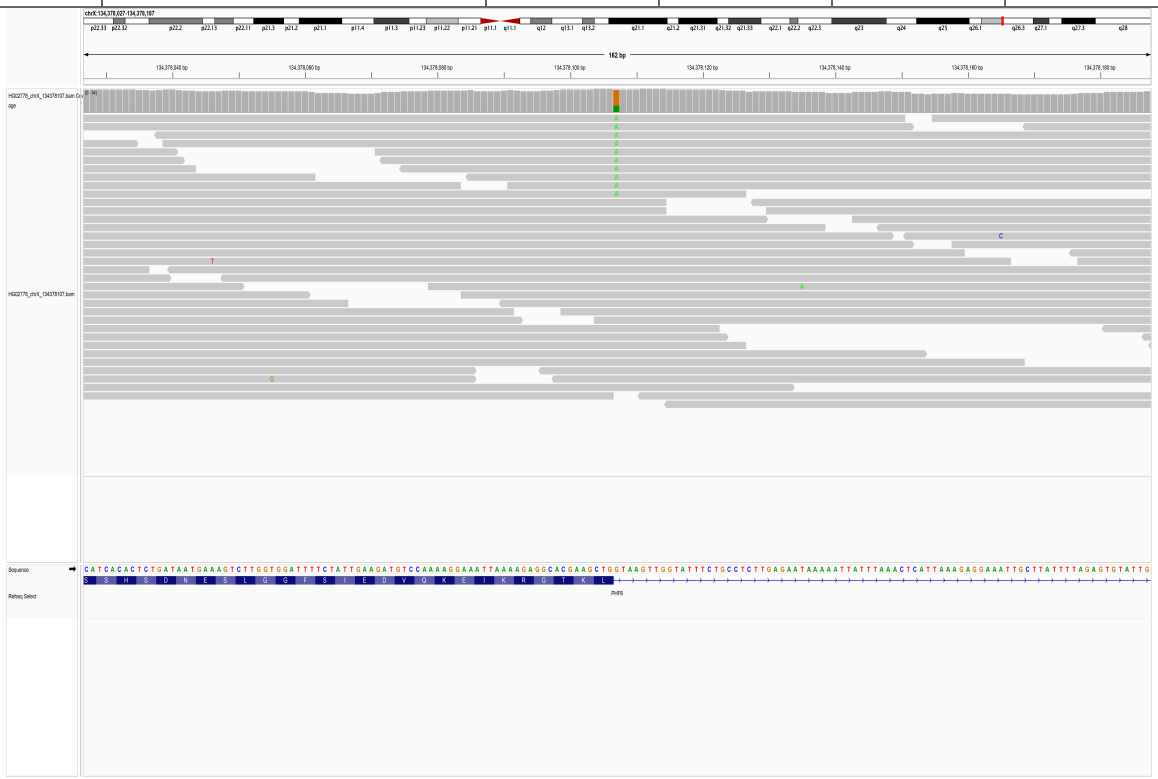
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00244	chr1_114716126_C/T	39	6	*NRAS*	missense_variant



13. *PHF6*

13.1. chrX_134378107_G/A

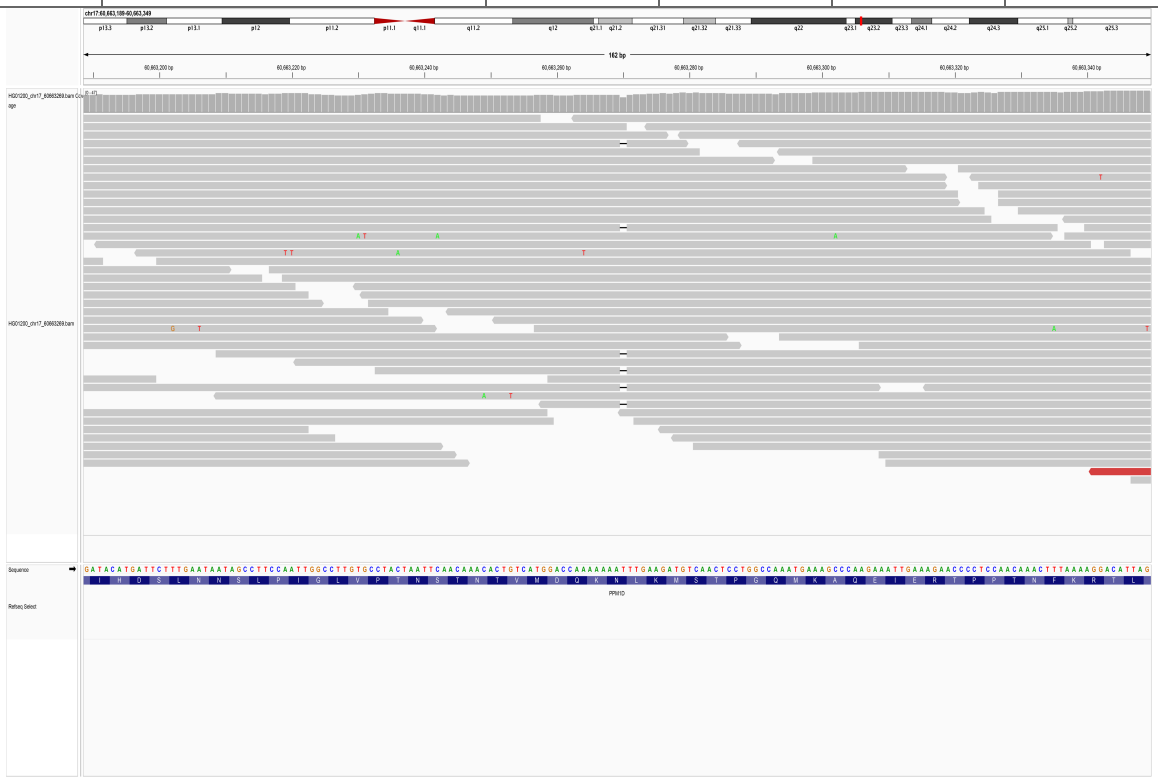
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02778	chrX_134378107_G/A	23	10	*PHF6*	splice_donor_variant



14. *PPM1D*

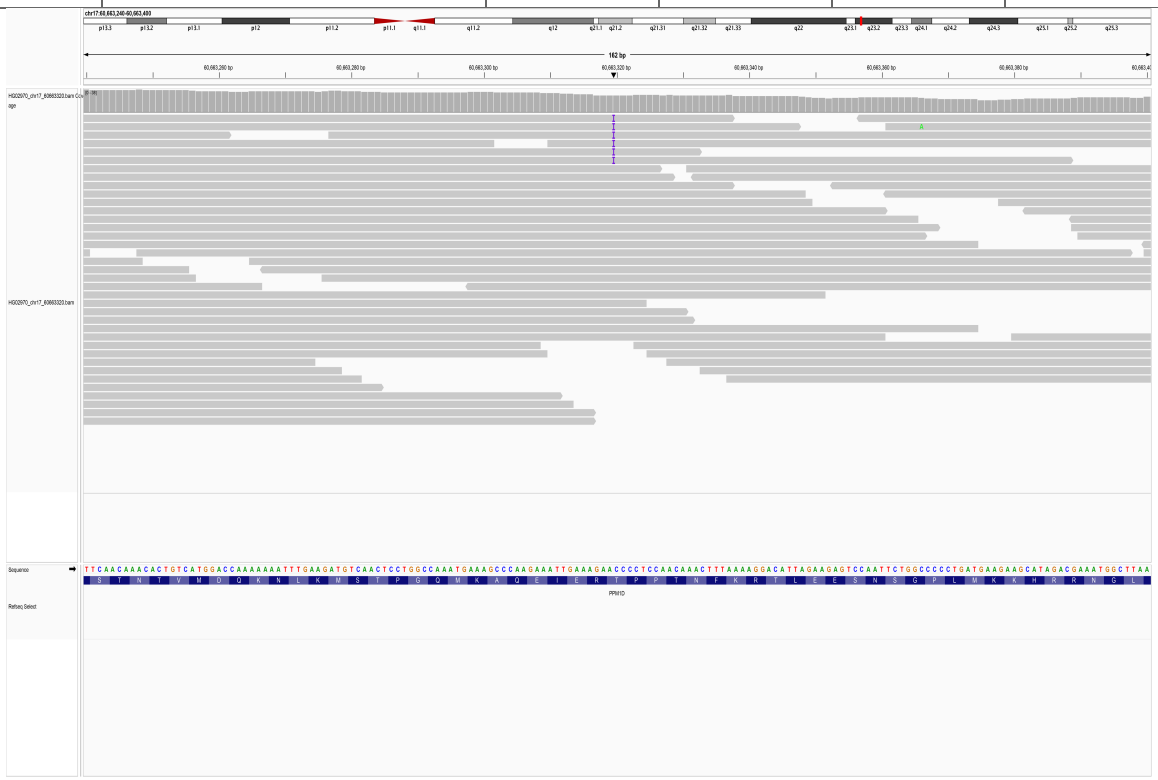
14.1. chr17_60663270_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01200	chr17_60663270_T/-	27	6	*PPM1D*	frameshift_variant



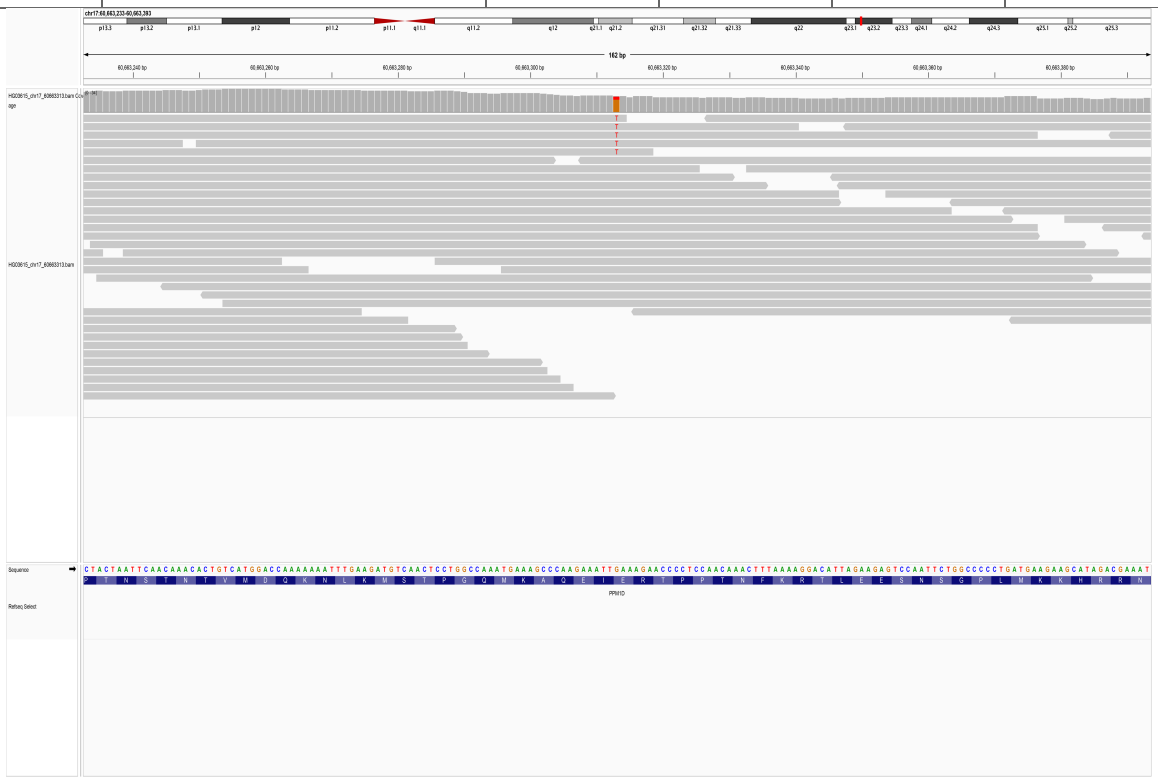
14.2. chr17_60663320_-/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02970	chr17_60663320_-/C	21	6	*PPM1D*	frameshift_variant



14.3. chr17_60663313_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03615	chr17_60663313_G/T	18	5	*PPM1D*	stop_gained

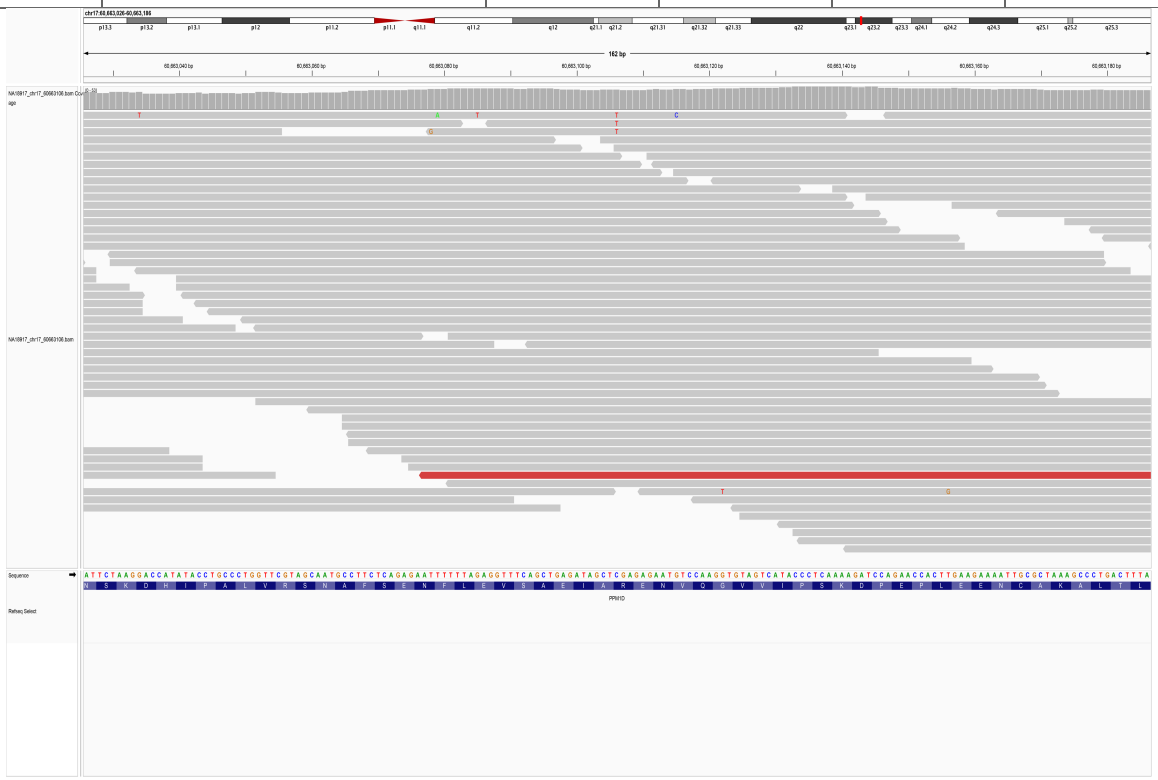


14.4. chr17_60662995_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG04022	chr17_60662995_T/A	31	7	*PPM1D*	missense_variant

14.5. chr17_60663106_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA18917	chr17_60663106_C/T	43	3	*PPM1D*	stop_gained



15. *PRPF40B*

15.1. chr12_49643754_T/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00640	chr12_49643754_T/G	27	6	*PRPF40B*	splice_donor_variant

16. *PTEN*

16.1. chr10_87933035_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA20899	chr10_87933035_C/A	32	4	*PTEN*	missense_variant

17. *RAD21*

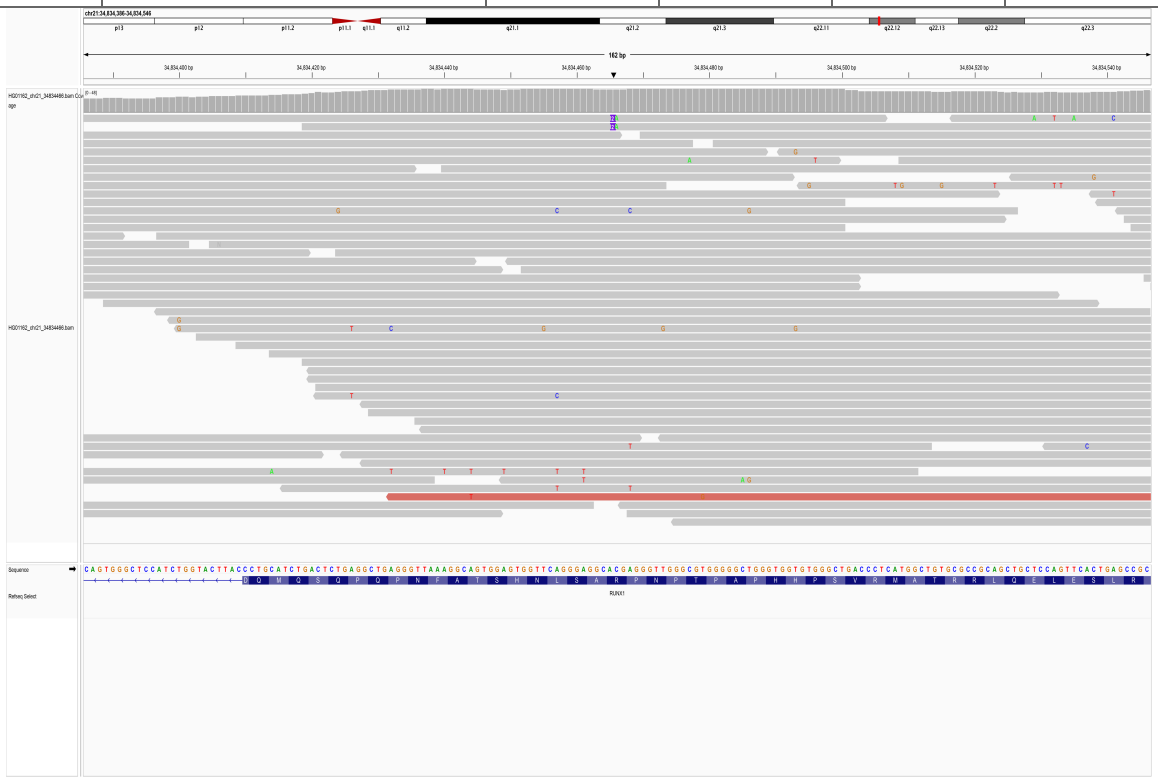
17.1. chr8_116850698_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00159	chr8_116850698_G/A	19	7	*RAD21*	stop_gained

18. *RUNX1*

18.1. chr21_34834466_-/GG

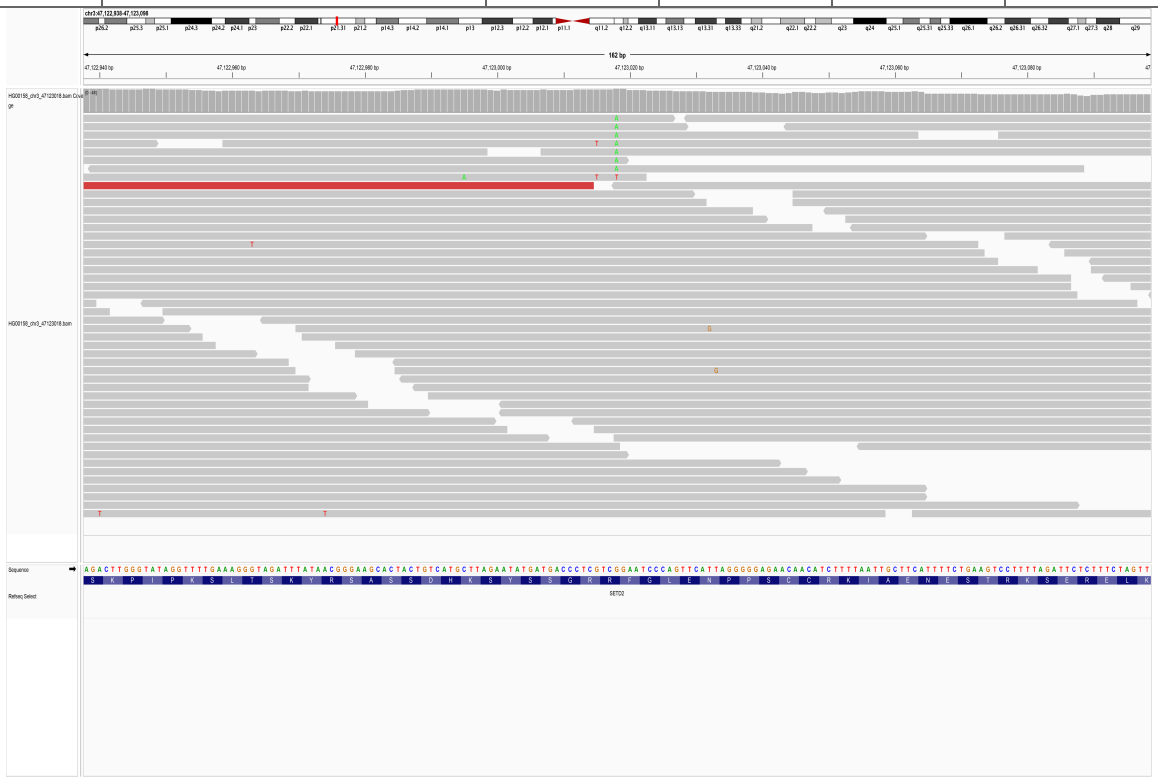
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01162	chr21_34834466_-/GG	40	3	*RUNX1*	frameshift_variant



19. *SETD2*

19.1. chr3_47123018_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00158	chr3_47123018_G/A	40	8	*SETD2*	stop_gained

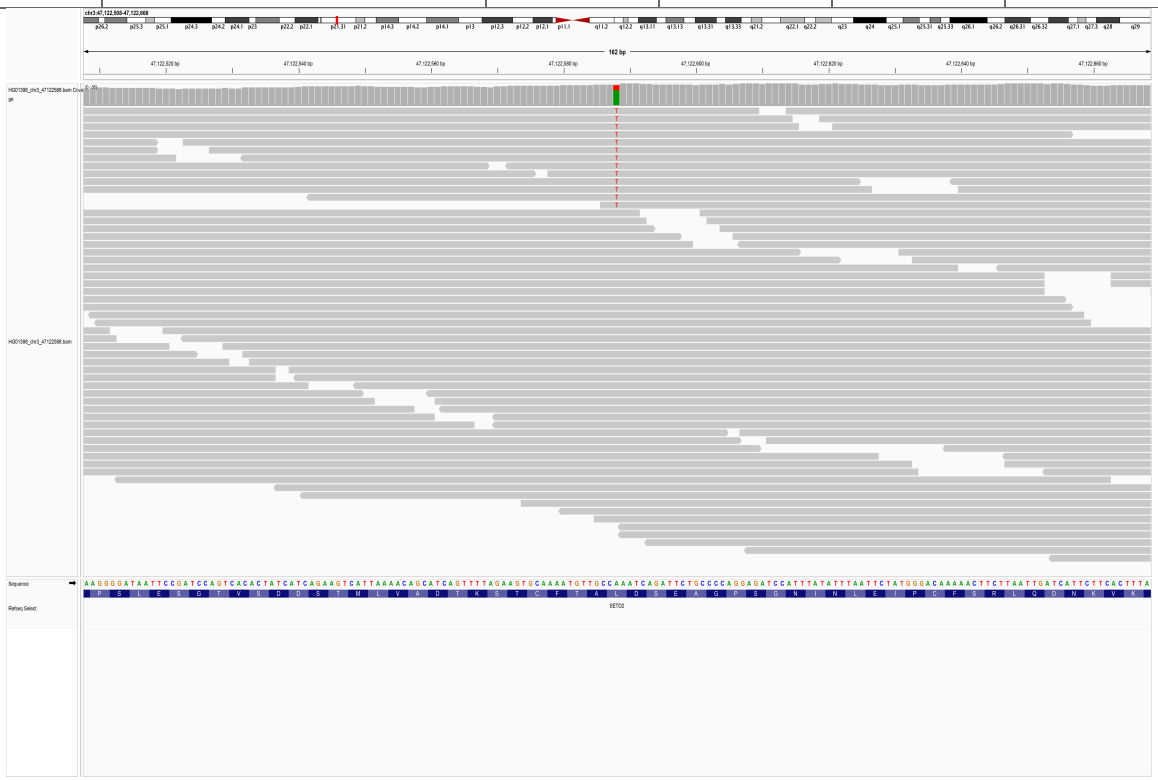


19.2. chr3_47124063_-/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00729	chr3_47124063_-/A	27	8	*SETD2*	frameshift_variant

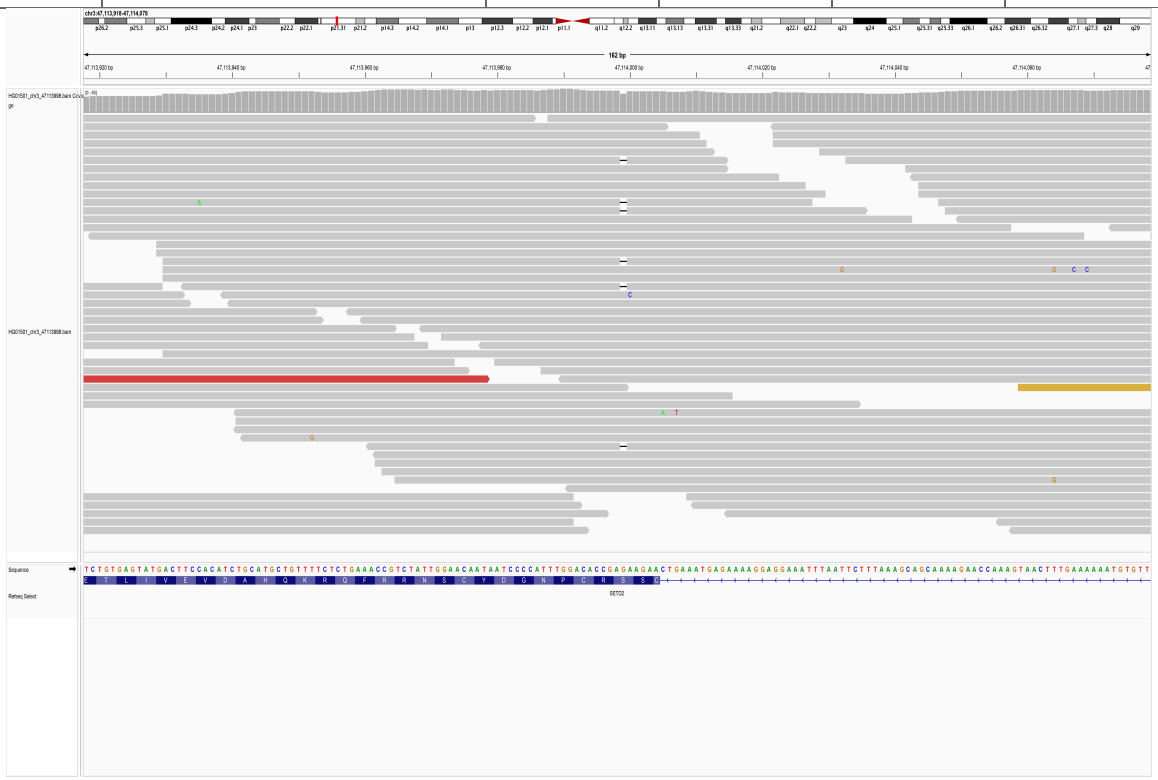
19.3. chr3_47122588_A/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01398	chr3_47122588_A/T	40	13	*SETD2*	stop_gained



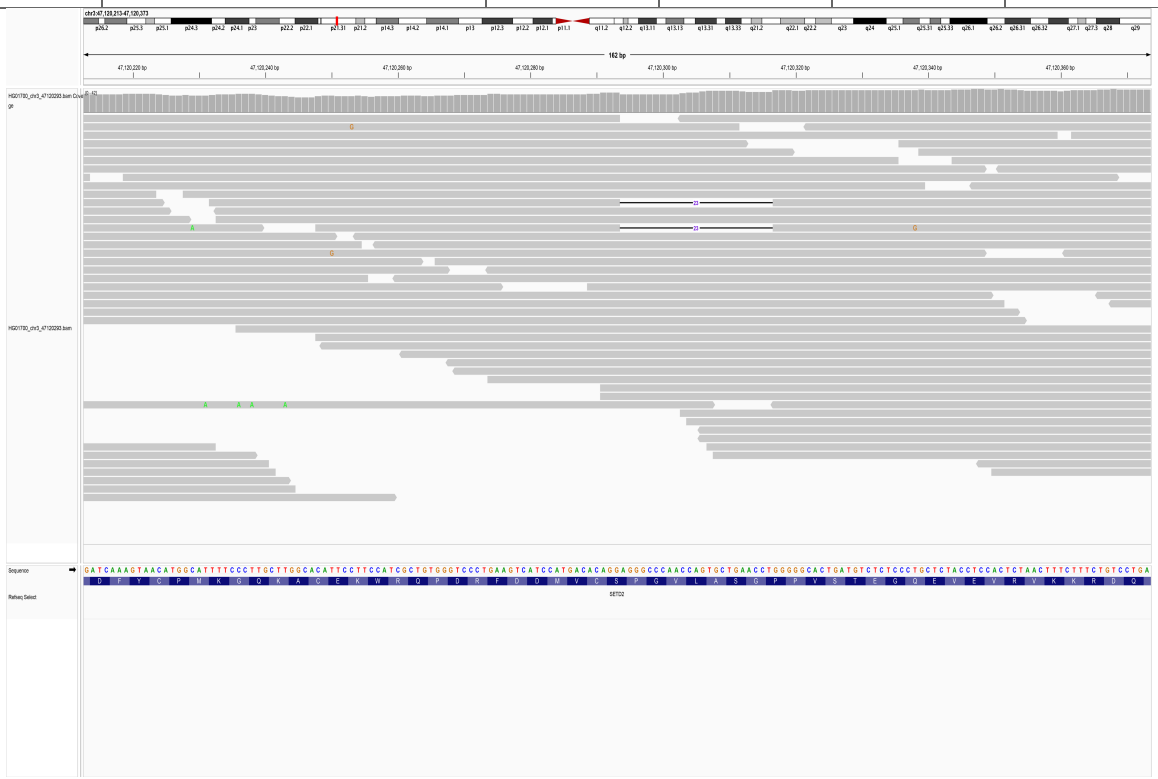
19.4. chr3_47113999_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01501	chr3_47113999_G/-	38	6	*SETD2*	frameshift_variant



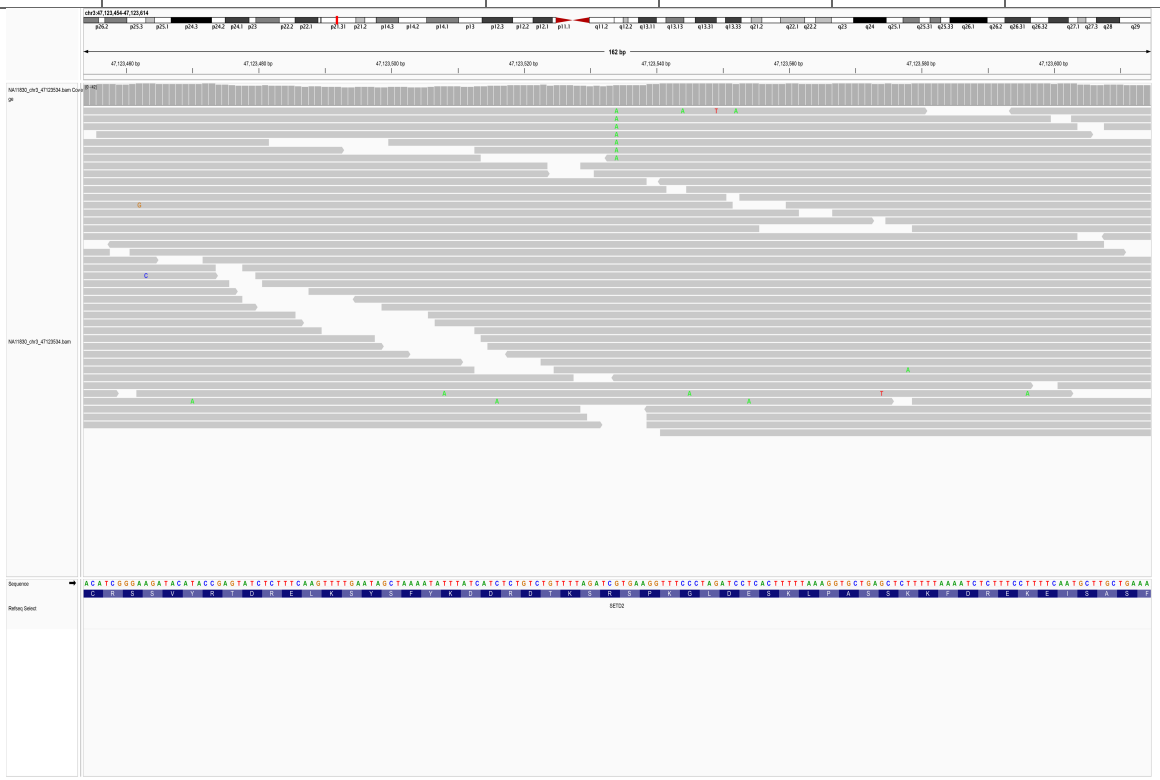
19.5. chr3_47120294_AGGGCCCAACCAGTGCTGAACCT/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01700	chr3_47120294_AGGGCCCAACCAGTGCTGAACCT/-	39	3	*SETD2*	frameshift_variant



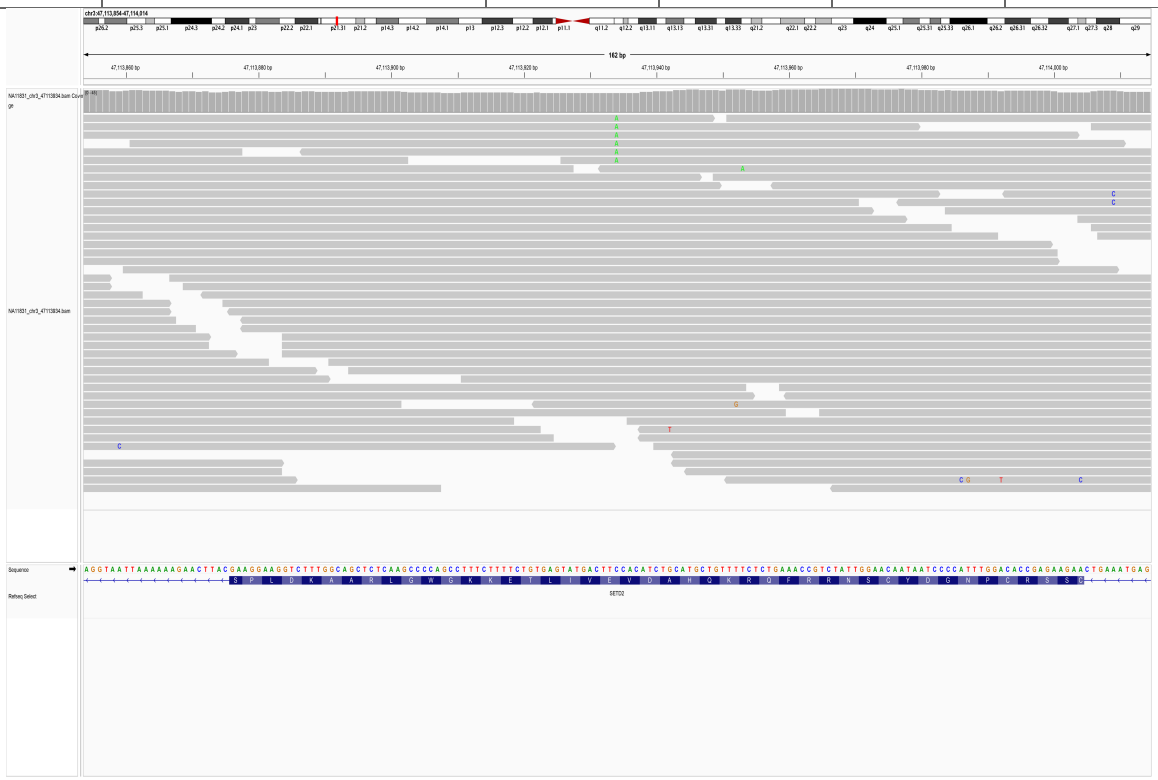
19.6. chr3_47123534_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA11830	chr3_47123534_G/A	29	6	*SETD2*	stop_gained



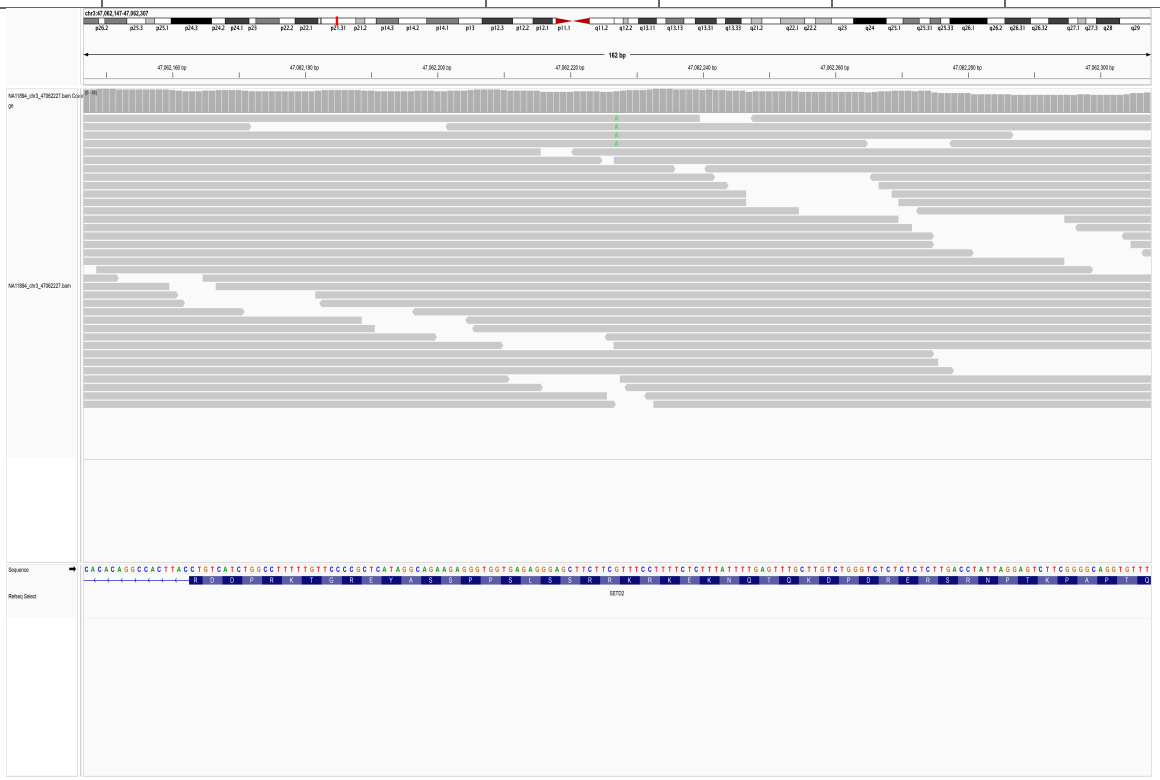
19.7. chr3_47113934_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA11831	chr3_47113934_C/A	30	6	*SETD2*	stop_gained



19.8. chr3_47062227_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA11894	chr3_47062227_G/A	27	4	*SETD2*	stop_gained

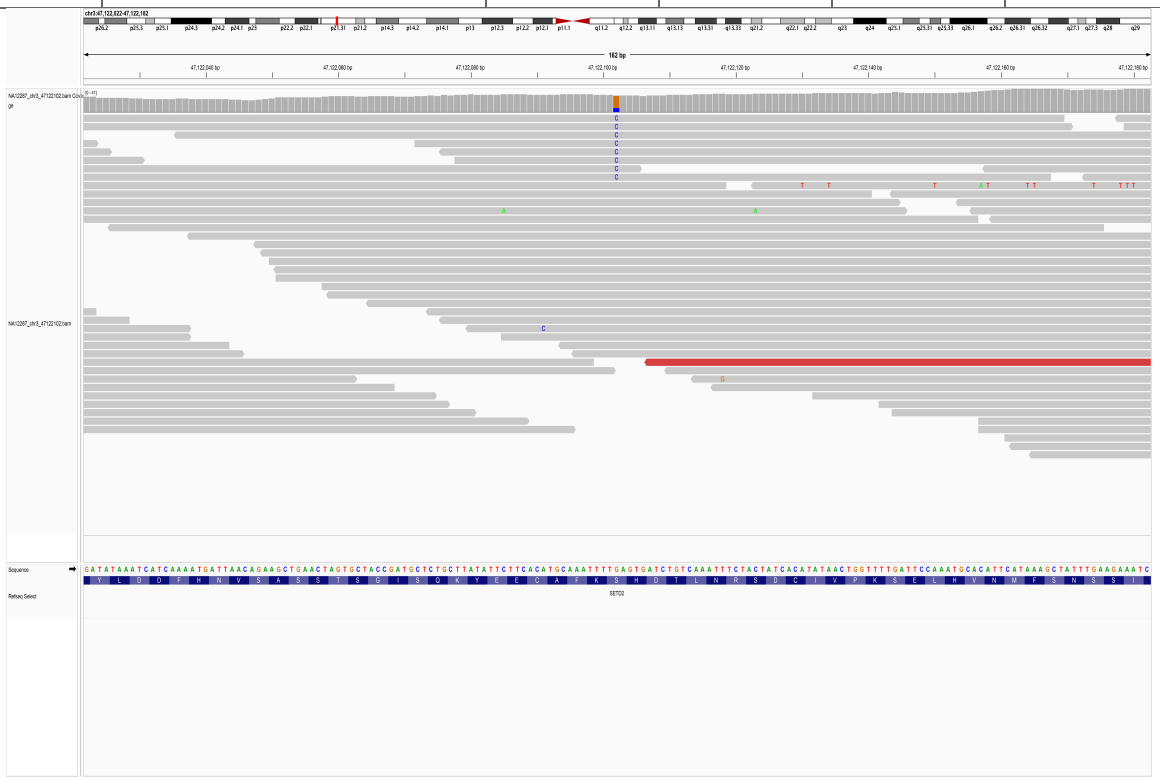


19.9. chr3_47101520_-/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA12282	chr3_47101520_-/A	32	5	*SETD2*	frameshift_variant

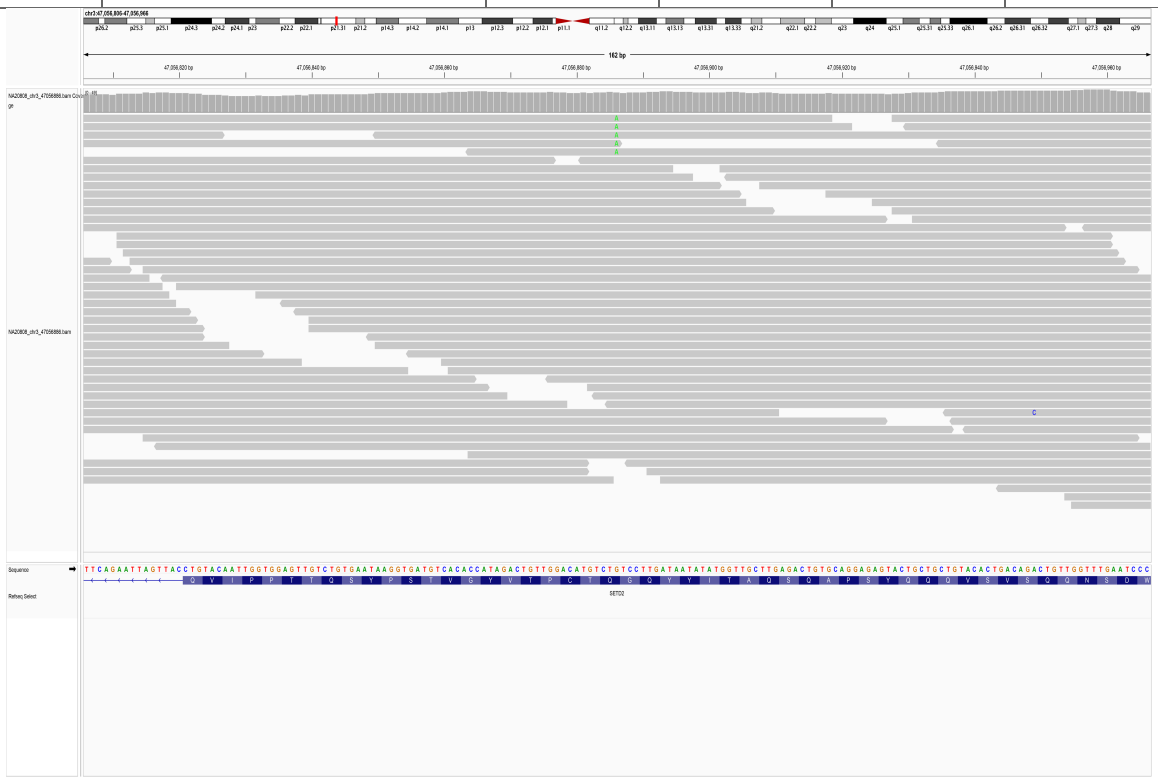
19.10. chr3_47122102_G/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA12287	chr3_47122102_G/C	21	8	*SETD2*	stop_gained



19.11. chr3_47056886_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA20808	chr3_47056886_G/A	36	5	*SETD2*	stop_gained

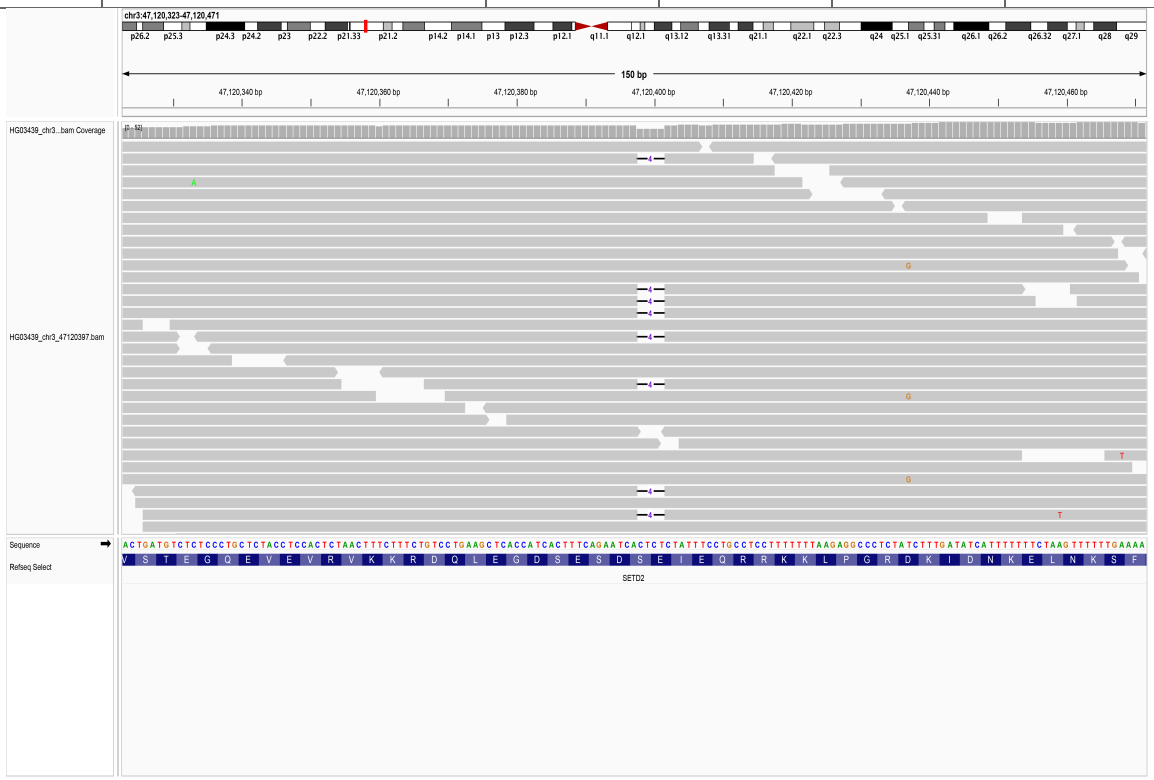


19.12. chr3_47121944_AG/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA20896	chr3_47121944_AG/-	36	5	*SETD2*	frameshift_variant

19.13. chr3_47120398_CTCT/-

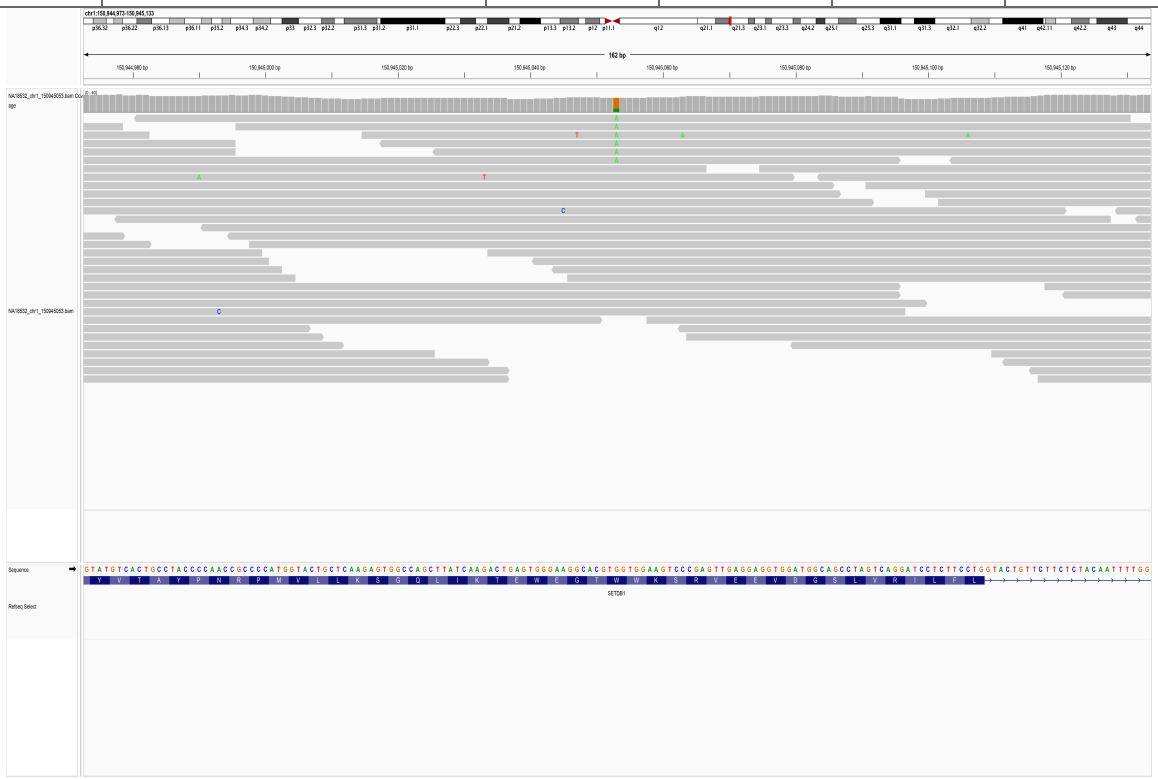
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03439	chr3_47120398_CTCT/-	31	9	*SETD2*	frameshift_variant



20. *SETDB1*

20.1. chr1_150945053_G/A

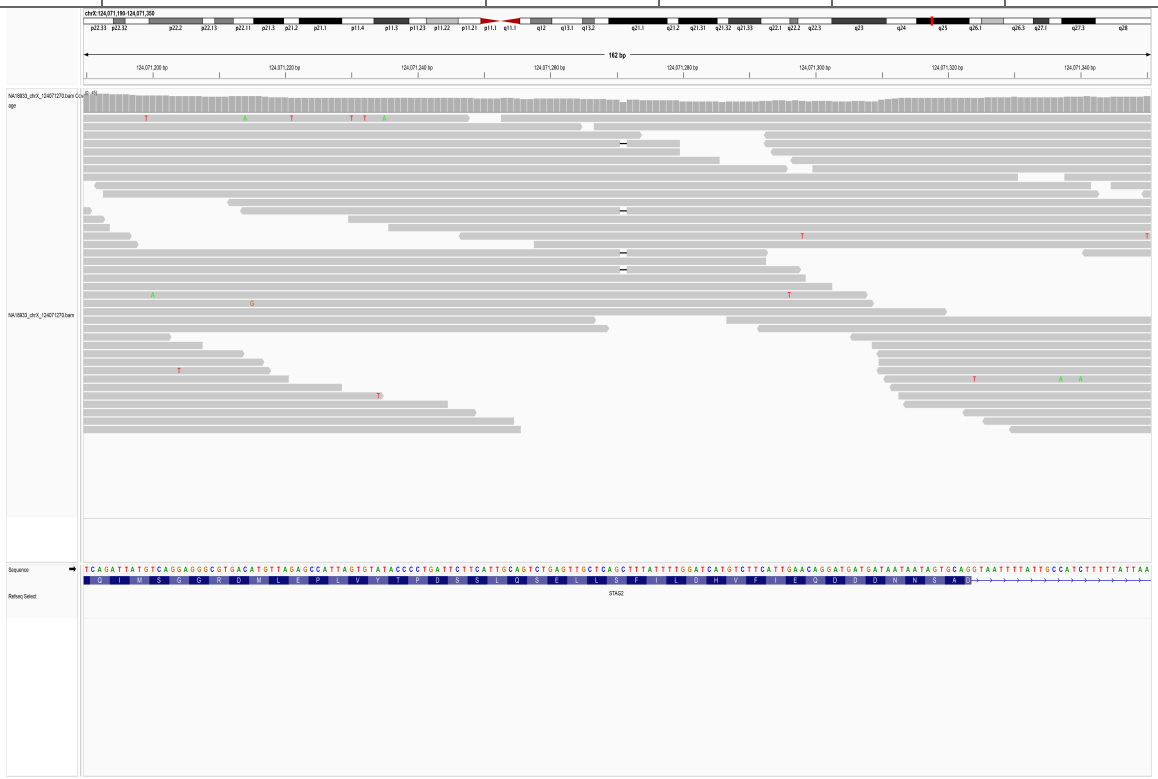
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA18532	chr1_150945053_G/A	18	6	*SETDB1*	stop_gained



21. *STAG2*

21.1. chrX_124071271_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA18933	chrX_124071271_C/-	20	4	*STAG2*	frameshift_variant



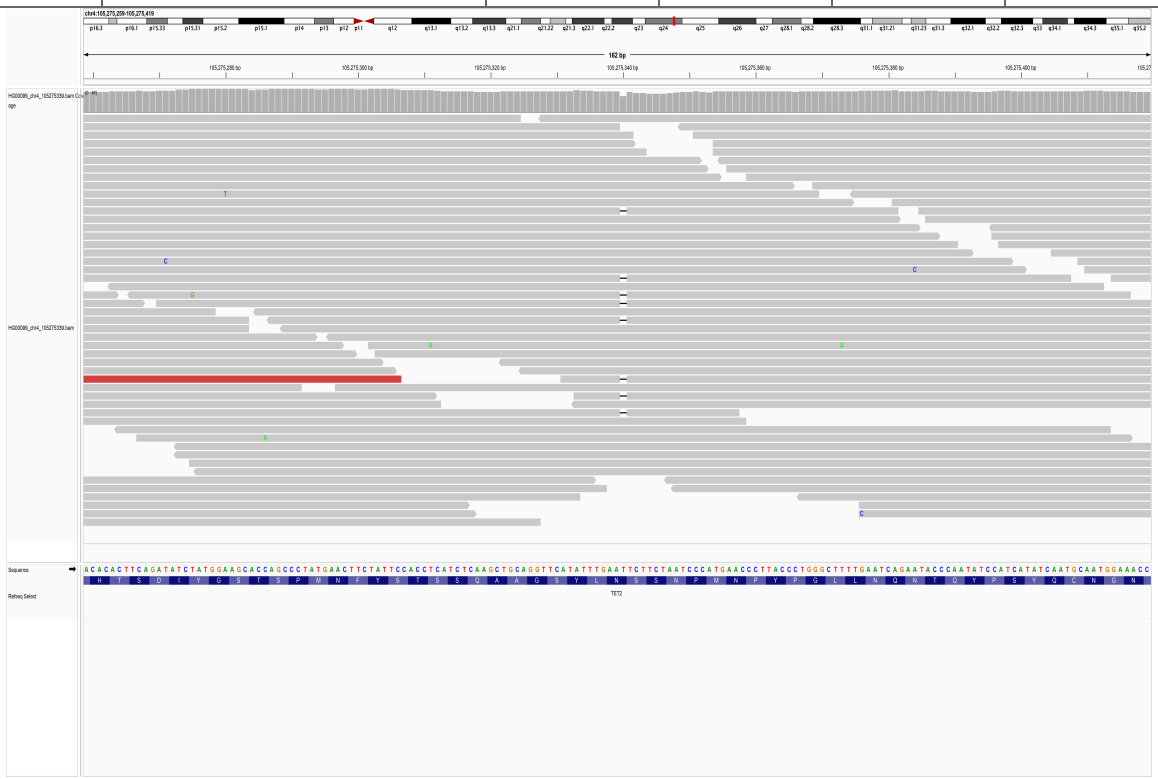
21.2. chrX_124066217_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA20281	chrX_124066217_C/A	8	2	*STAG2*	stop_gained

22. *TET2*

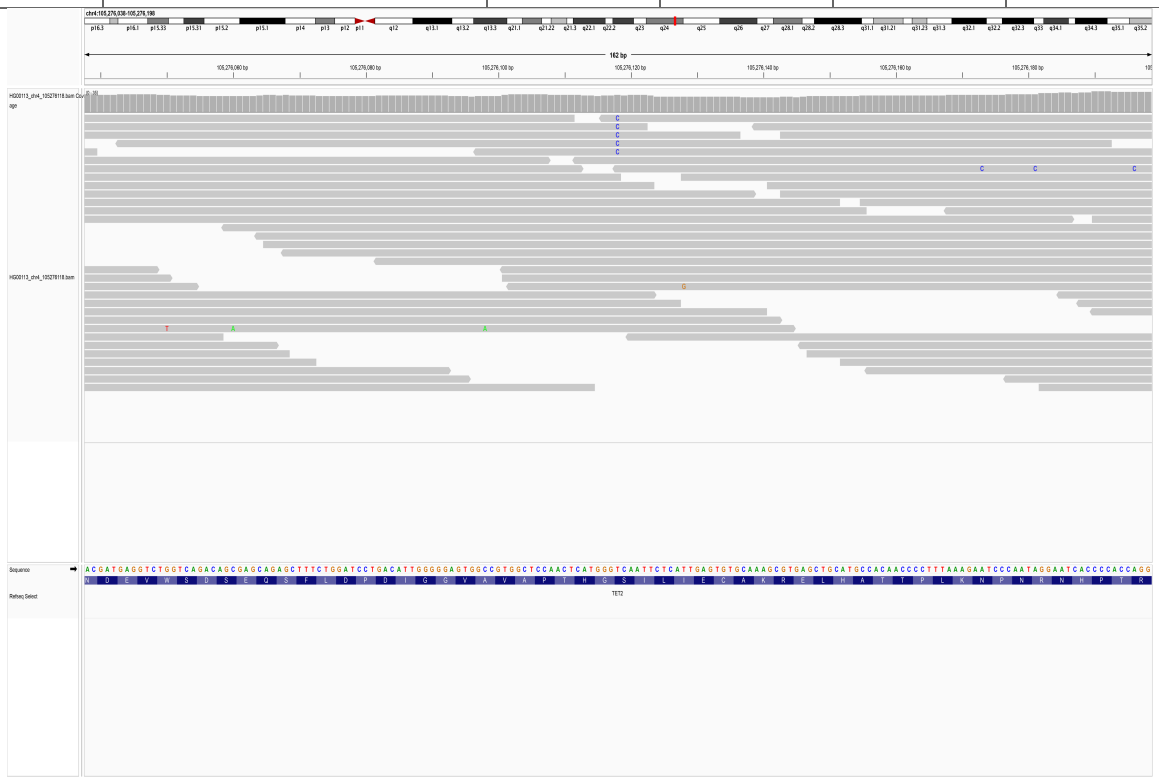
22.1. chr4_105275340_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00099	chr4_105275340_T/-	34	8	*TET2*	frameshift_variant



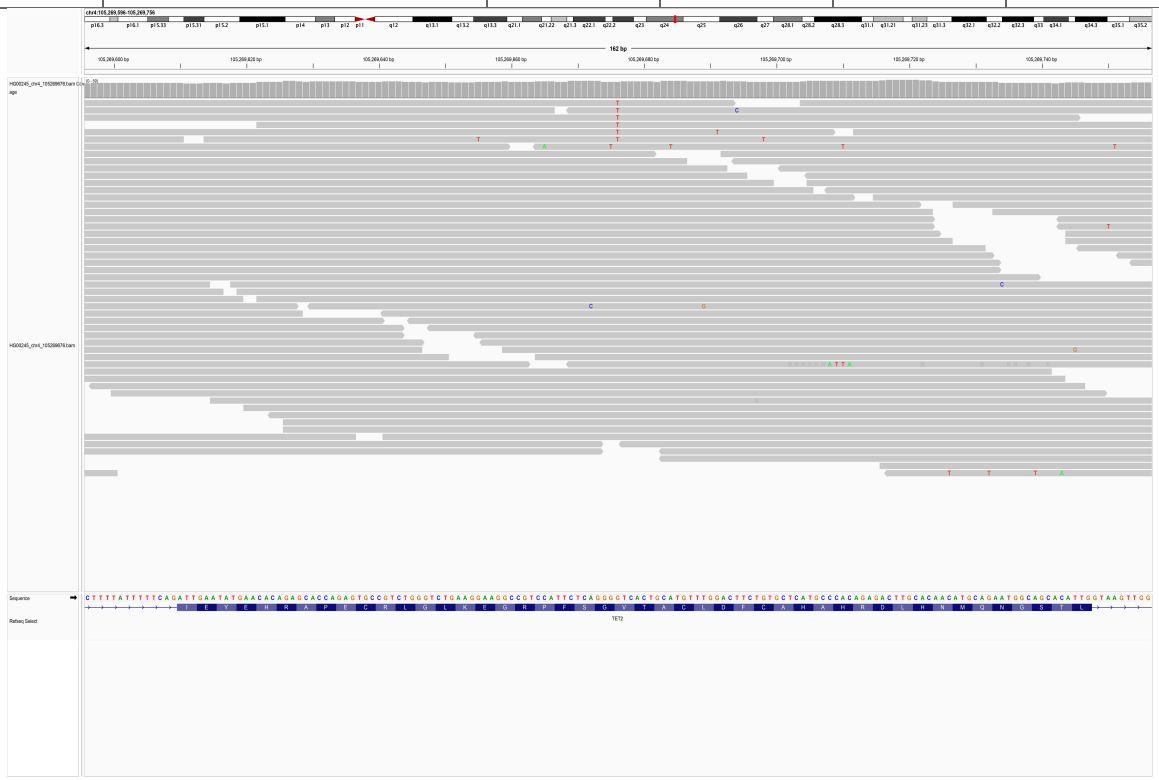
22.2. chr4_105276118_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00113	chr4_105276118_T/C	21	5	*TET2*	missense_variant



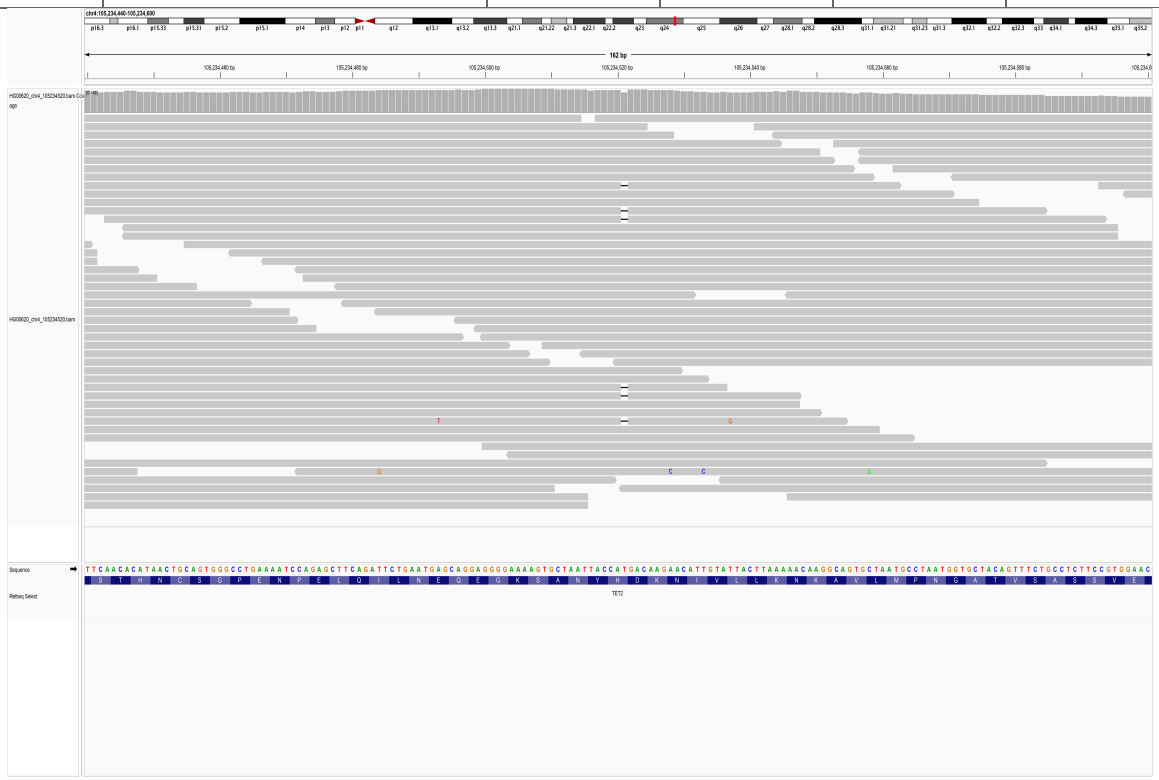
22.3. chr4_105269676_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00245	chr4_105269676_G/T	40	6	*TET2*	missense_variant



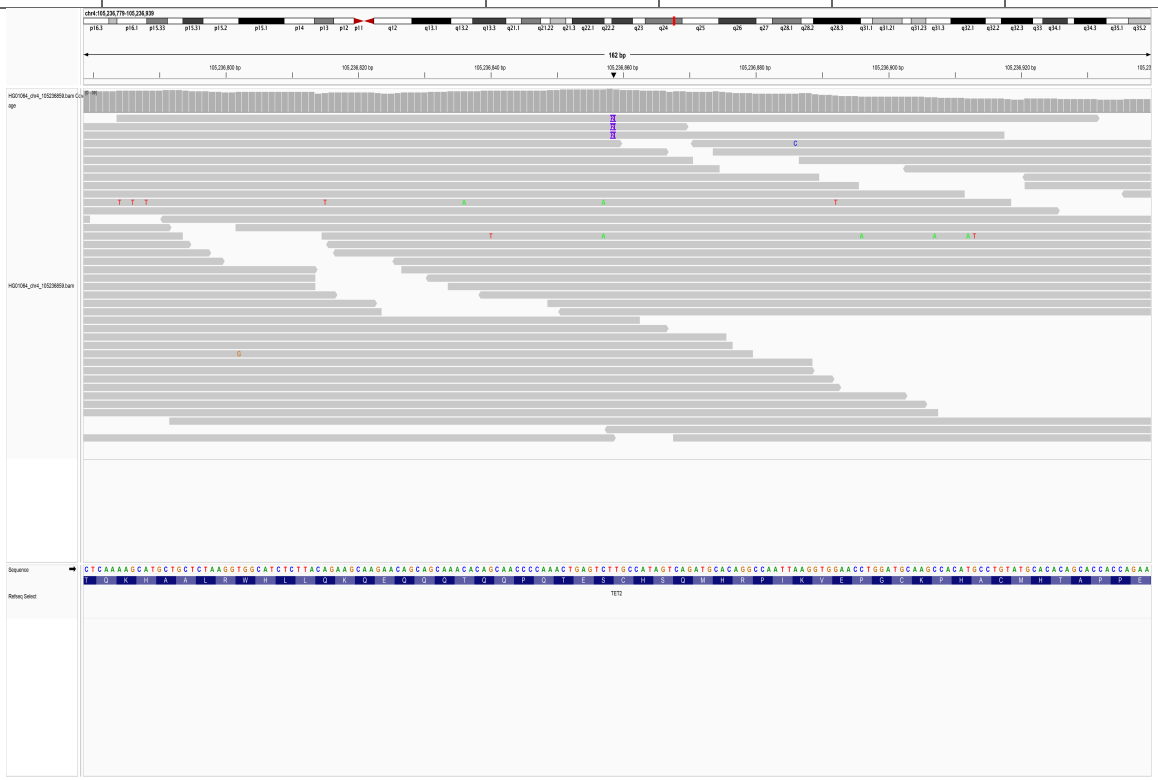
22.4. chr4_105234521_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG00620	chr4_105234521_T/-	37	6	*TET2*	frameshift_variant



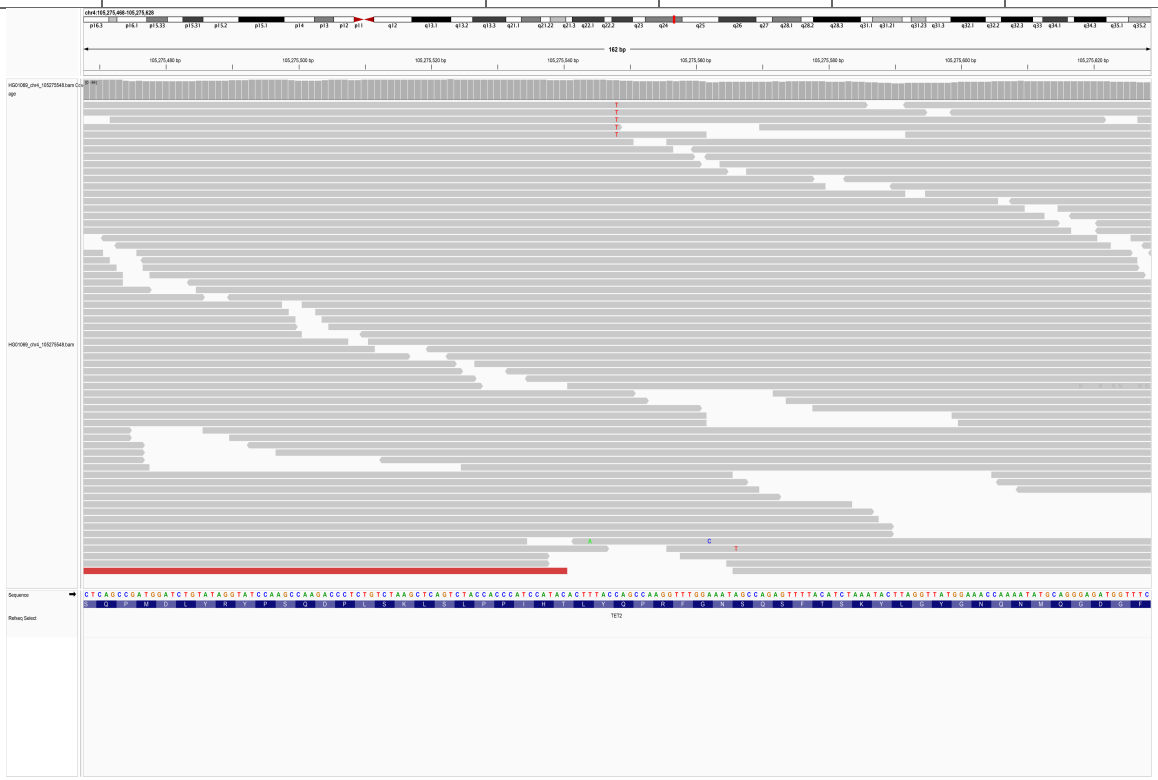
22.5. chr4_105236859_-/TG

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01064	chr4_105236859_-/TG	32	3	*TET2*	frameshift_variant



22.6. chr4_105275548_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01069	chr4_105275548_C/T	54	5	*TET2*	stop_gained

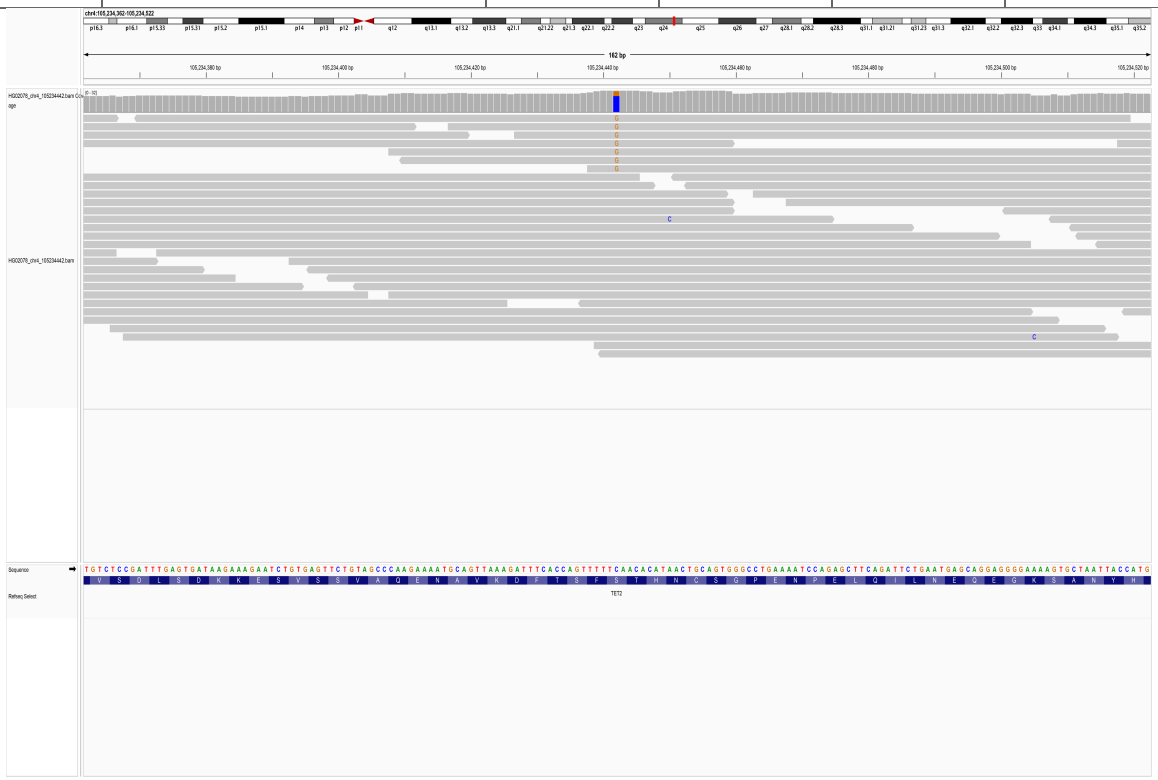


22.7. chr4_105241383_-/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG01606	chr4_105241383_-/G	28	9	*TET2*	frameshift_variant

22.8. chr4_105234442_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02078	chr4_105234442_C/G	22	7	*TET2*	stop_gained



22.9. chr4_105241421_G/A

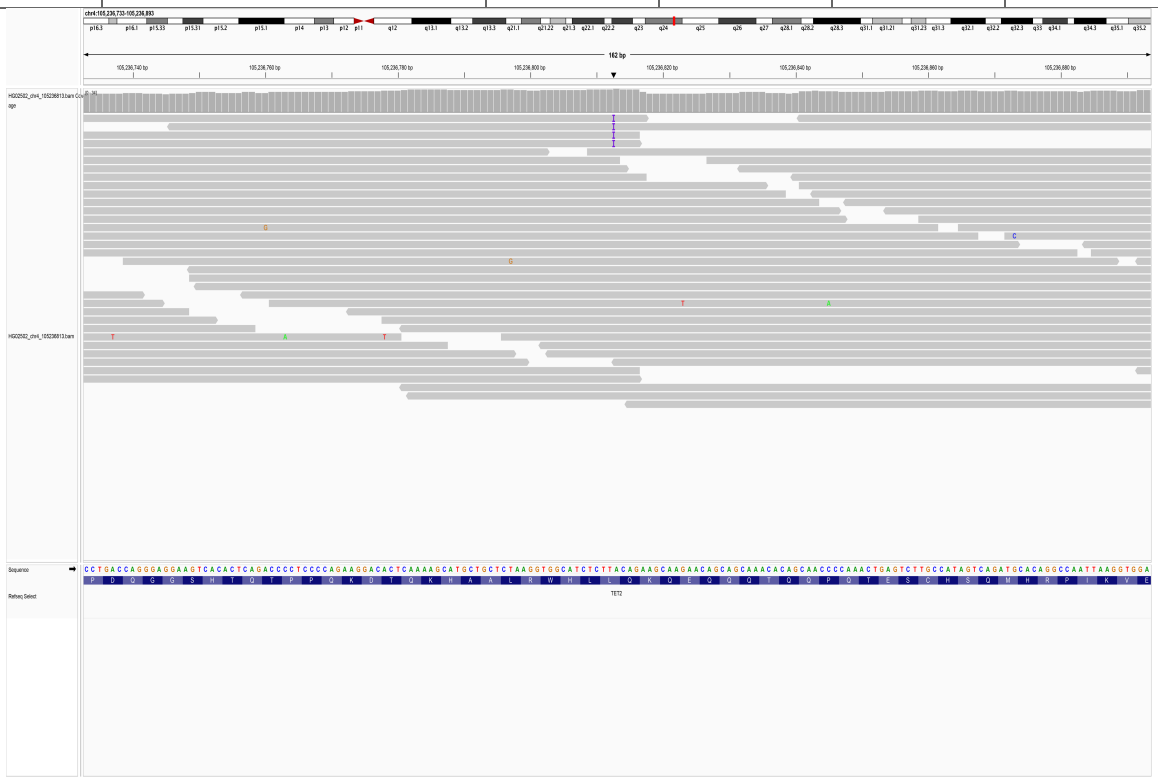
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02107	chr4_105241421_G/A	44	10	*TET2*	missense_variant

22.10. chr4_105259617_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02484	chr4_105259617_A/G	38	6	*TET2*	splice_acceptor_variant

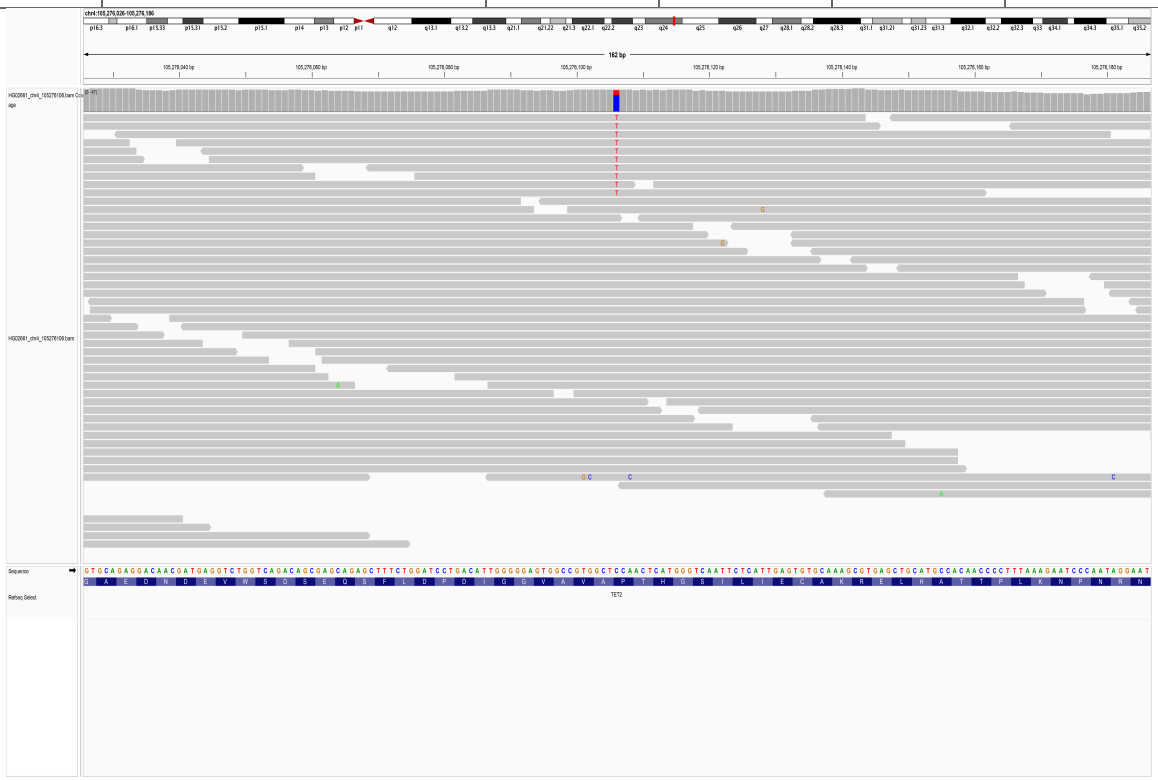
22.11. chr4_105236813_-/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02502	chr4_105236813_-/A	28	4	*TET2*	frameshift_variant



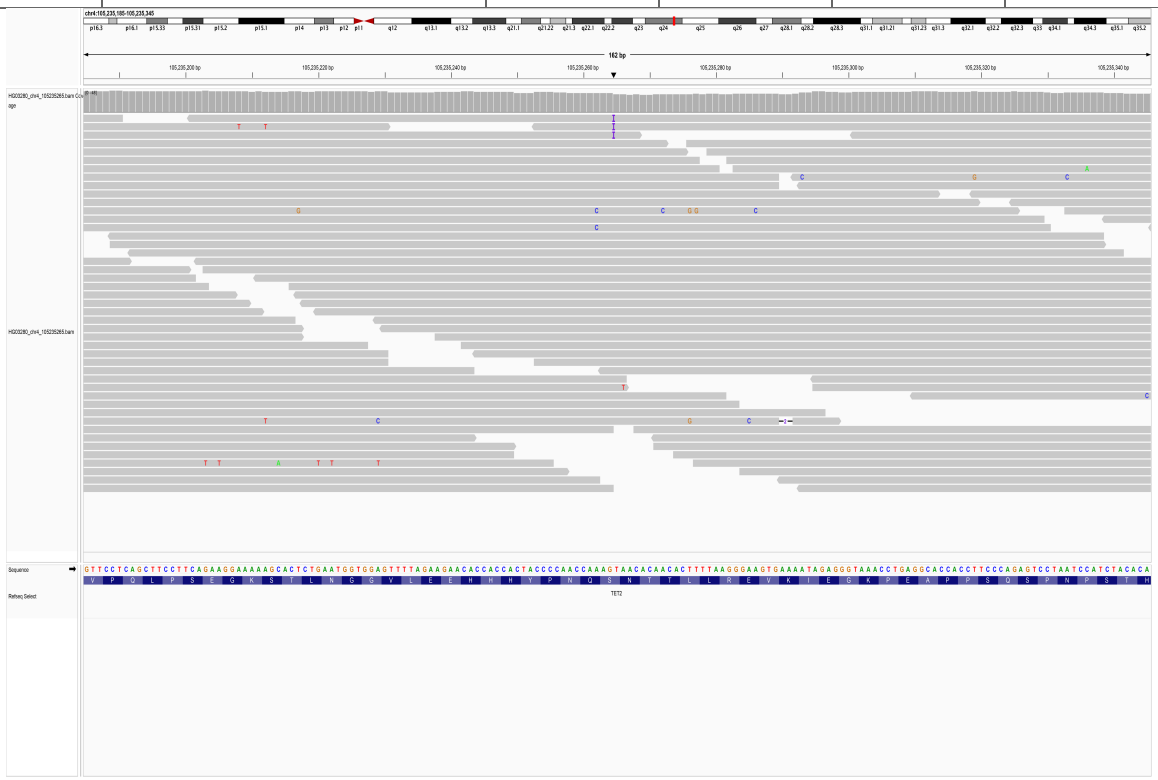
22.12. chr4_105276106_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02661	chr4_105276106_C/T	33	10	*TET2*	missense_variant



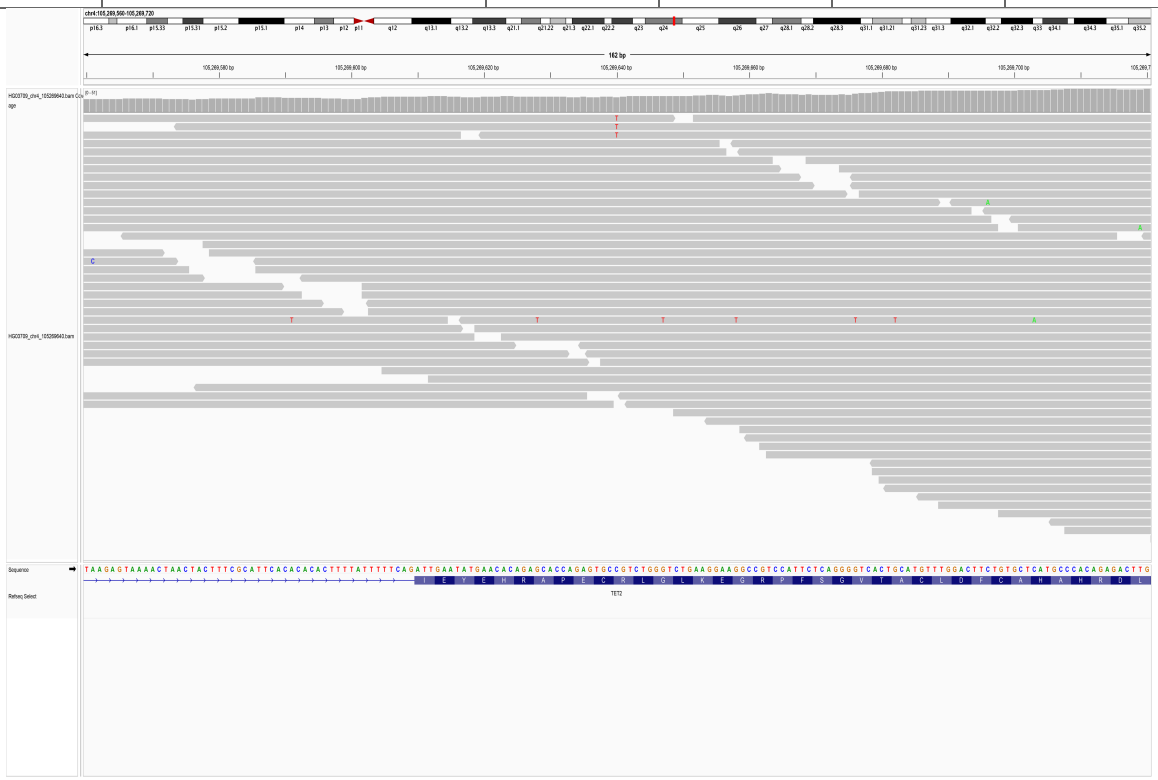
22.13. chr4_105235265_-/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03280	chr4_105235265_-/T	31	4	*TET2*	frameshift_variant



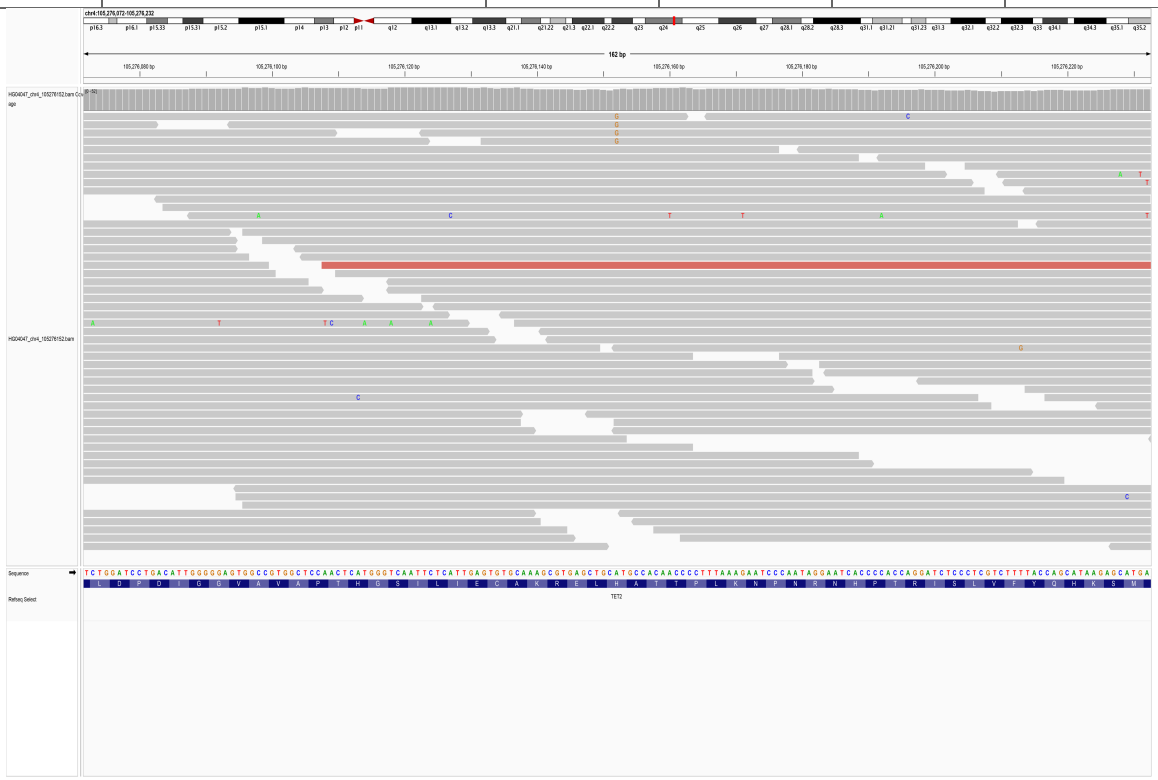
22.14. chr4_105269640_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03709	chr4_105269640_C/T	29	3	*TET2*	missense_variant



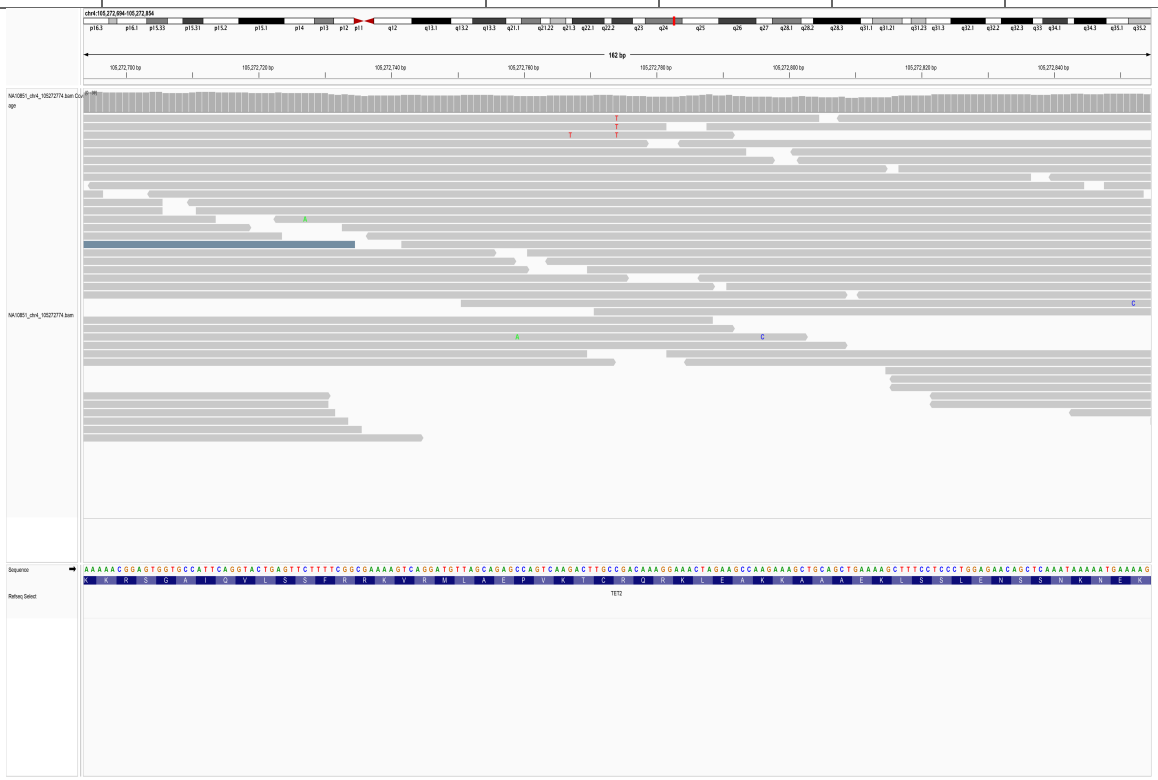
22.15. chr4_105276152_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG04047	chr4_105276152_A/G	43	4	*TET2*	missense_variant



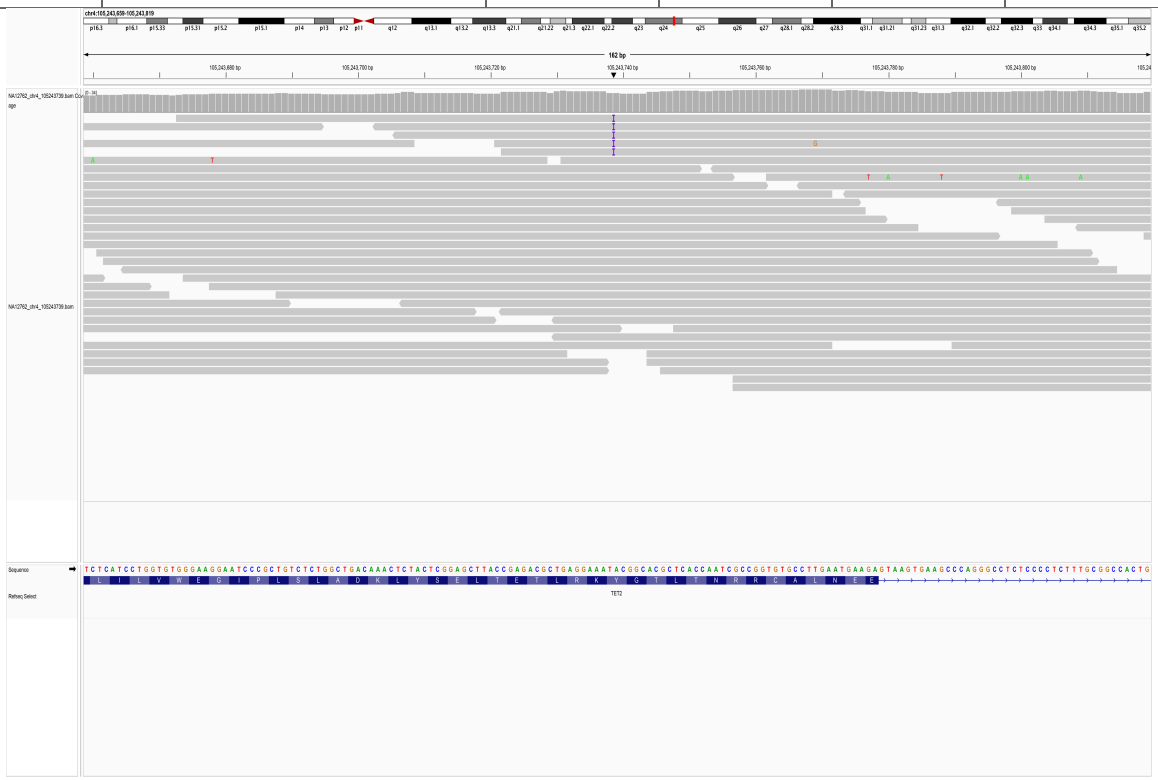
22.16. chr4_105272774_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA10851	chr4_105272774_C/T	25	3	*TET2*	stop_gained



22.17. chr4_105243739_-/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA12762	chr4_105243739_-/A	22	5	*TET2*	stop_gained

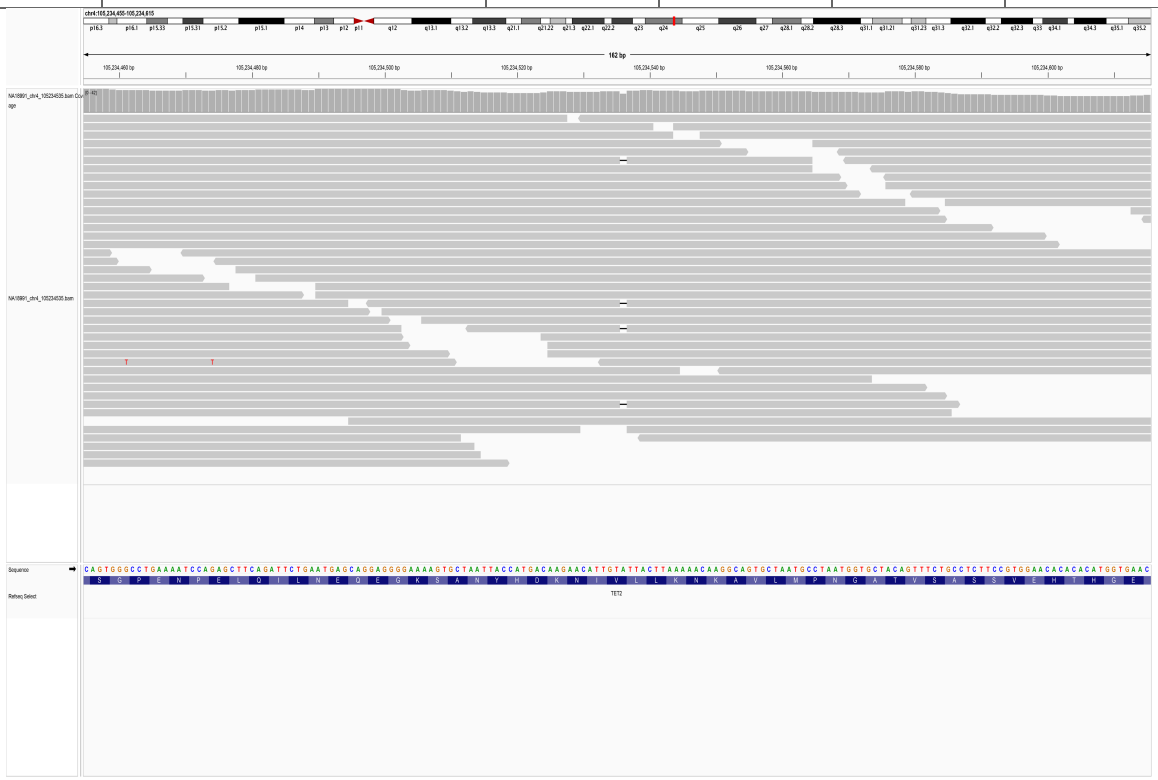


22.18. chr4_105235590_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA18634	chr4_105235590_C/T	29	8	*TET2*	stop_gained

22.19. chr4_105234536_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA18991	chr4_105234536_A/-	33	4	*TET2*	frameshift_variant

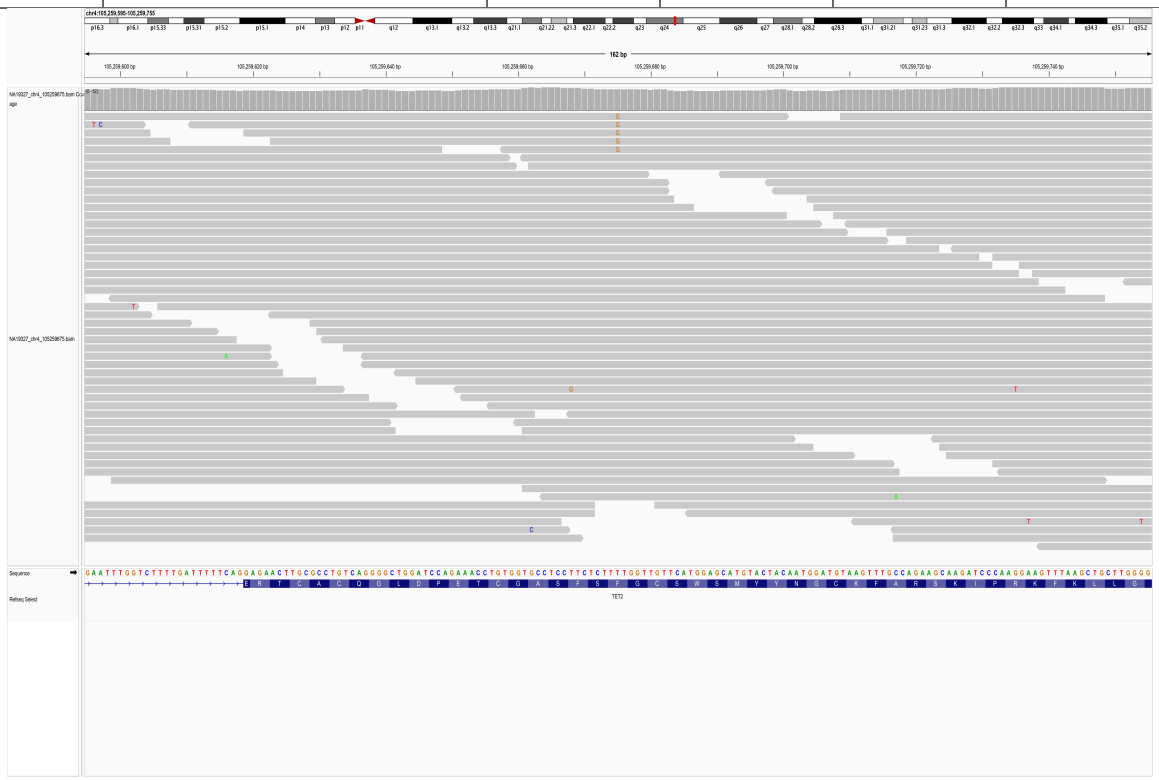


22.20. chr4_105237346_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA19222	chr4_105237346_G/A	26	3	*TET2*	missense_variant

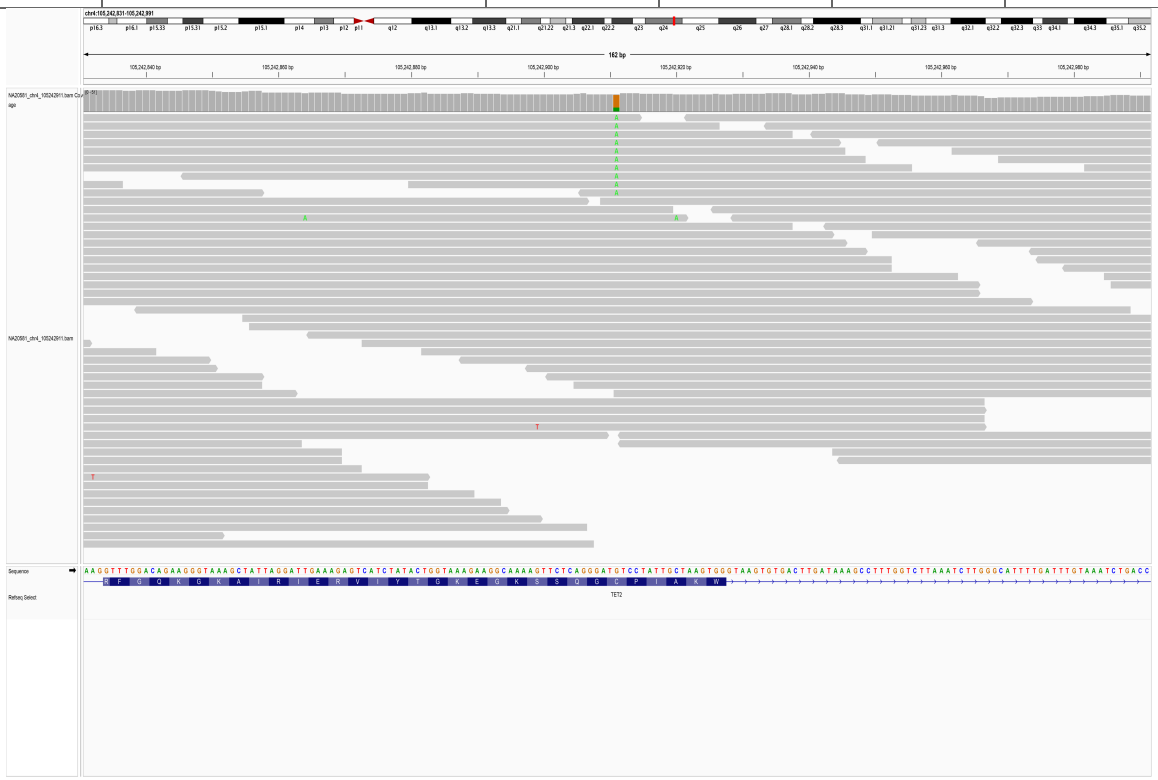
22.21. chr4_105259675_T/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA19327	chr4_105259675_T/G	42	5	*TET2*	missense_variant



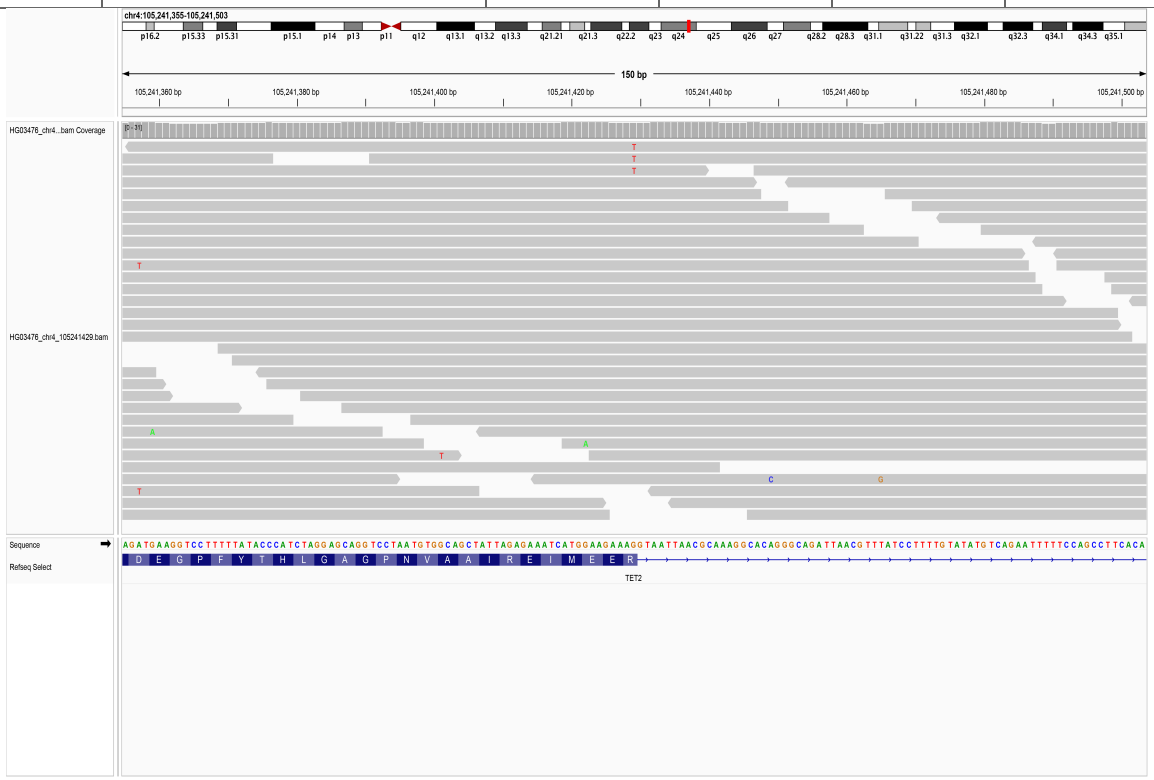
22.22. chr4_105242911_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA20581	chr4_105242911_G/A	27	10	*TET2*	missense_variant



22.23. chr4_105241429_G/T

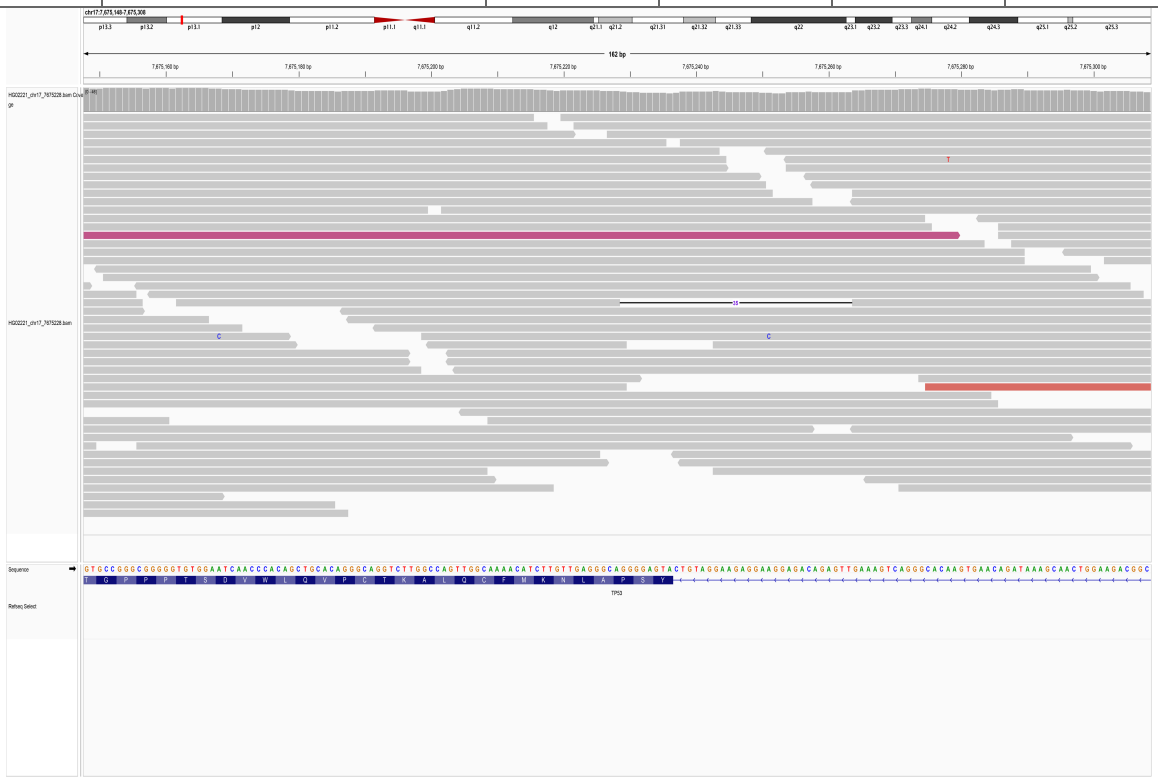
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03476	chr4_105241429_G/T	26	3	*TET2*	missense_variant



23. *TP53*

23.1. chr17_7675229_GGGGAGTACTGTAGGAAGAGGAAGGAGACAGAGTT/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG02221	chr17_7675229_GGGGAGTACTGTAGGAAGAGGAAGGAGACAGAGTT/-	47	4	*TP53*	splice_acceptor_variant



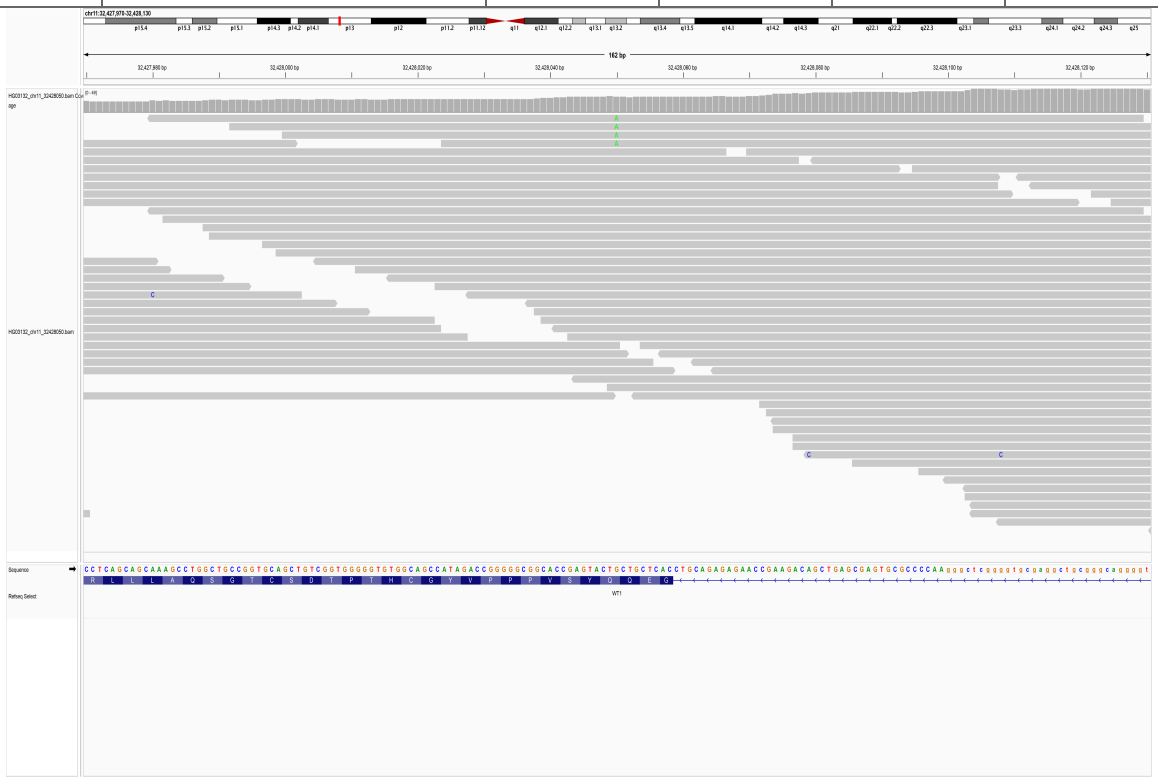
23.2. chr17_7674252_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03742	chr17_7674252_C/T	31	4	*TP53*	missense_variant

24. *WT1*

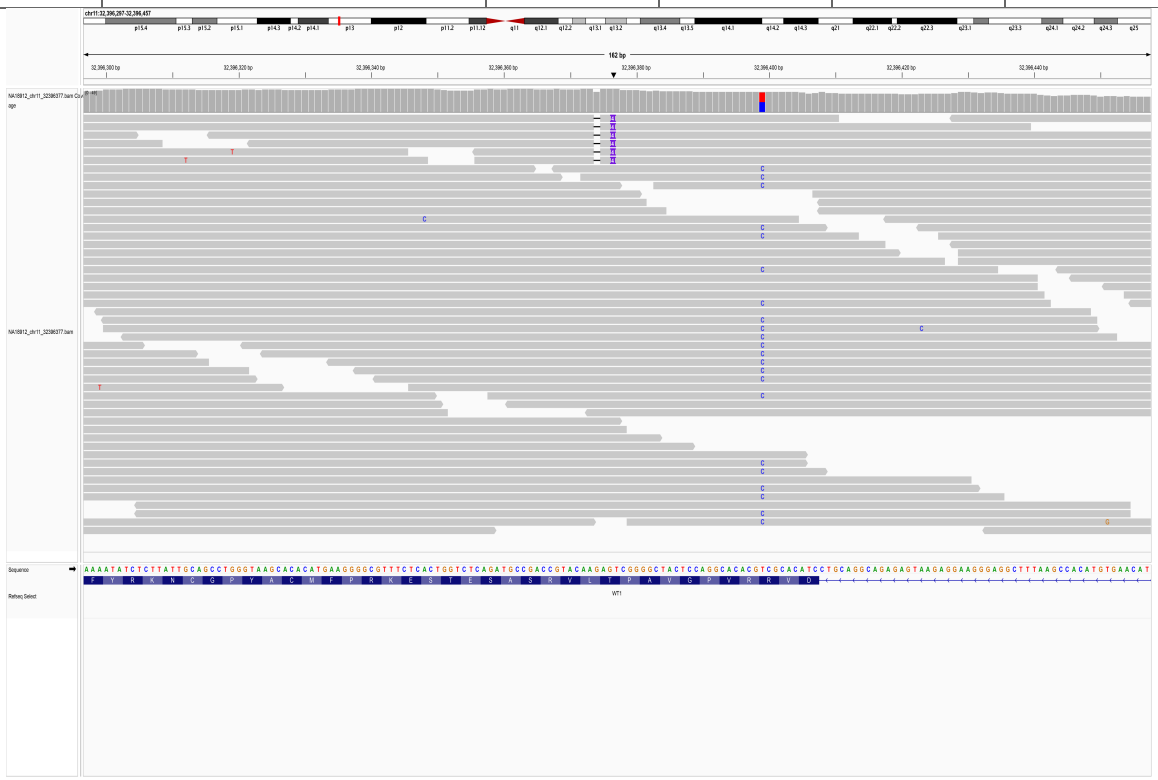
24.1. chr11_32428050_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
HG03132	chr11_32428050_G/A	29	4	*WT1*	stop_gained



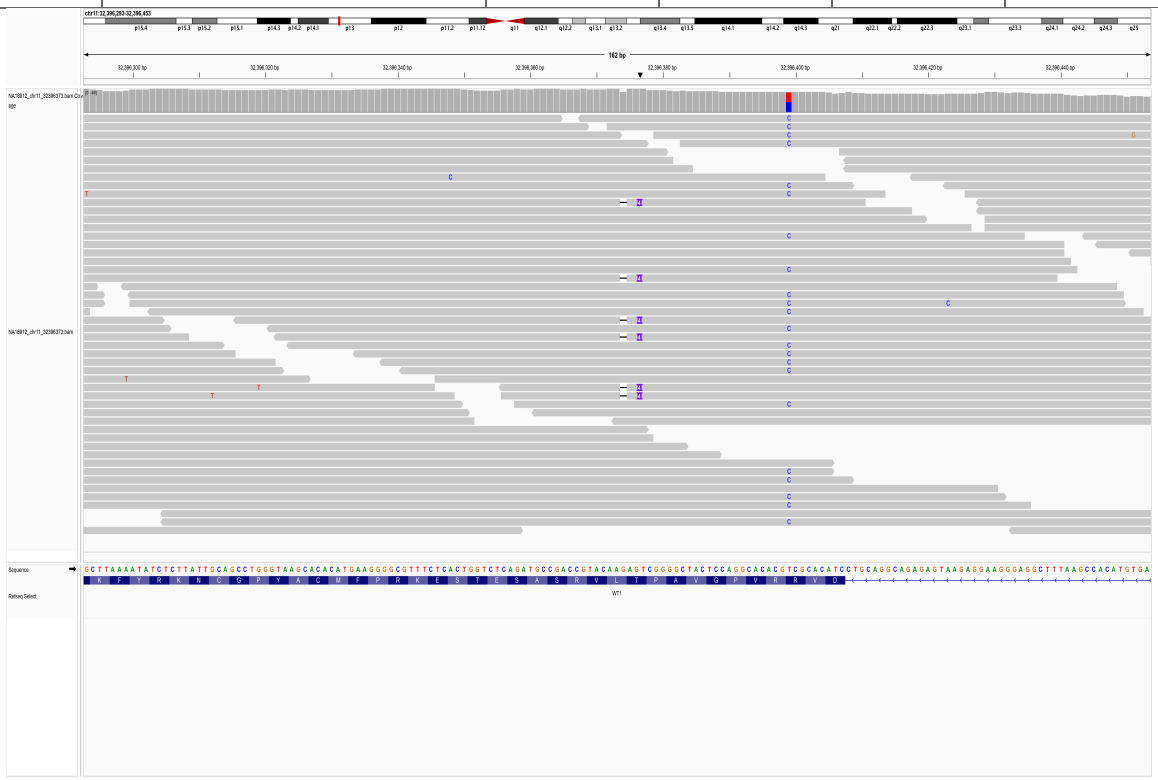
24.2. chr11_32396377_-/GACC

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA18912	chr11_32396377_-/GACC	42	6	*WT1*	frameshift_variant



24.3. chr11_32396374_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
NA18912	chr11_32396374_G/-	42	6	*WT1*	frameshift_variant



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.