Additional File 2

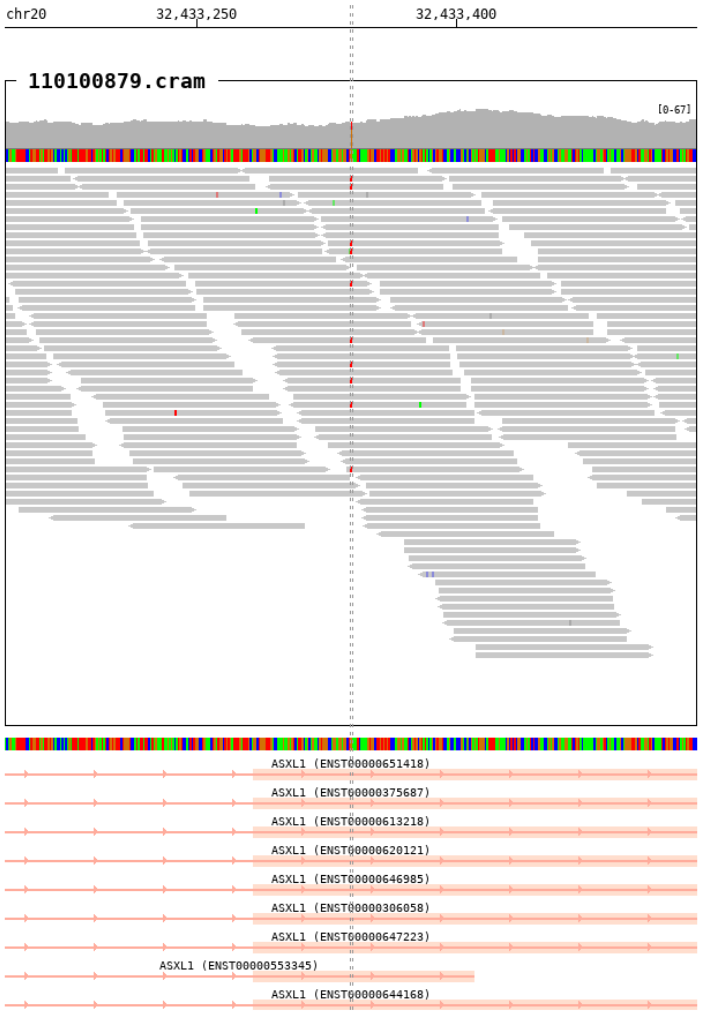
CHIP whitelist mutations identified and confirmed in the replication cohort. Listed are 476 CHIP whitelist mutations identified in 451 persons of the CYN16K cohort (N = 16,151). CHIP mutations identified as per the criteria used in Jaiswal et al.[1] Each CHIP variant has been manually reviewed independently by two researchers, by Integrative Genomics Viewer with reads support (related to **Table S5**).

Table of Contents

1. *ASXL1*

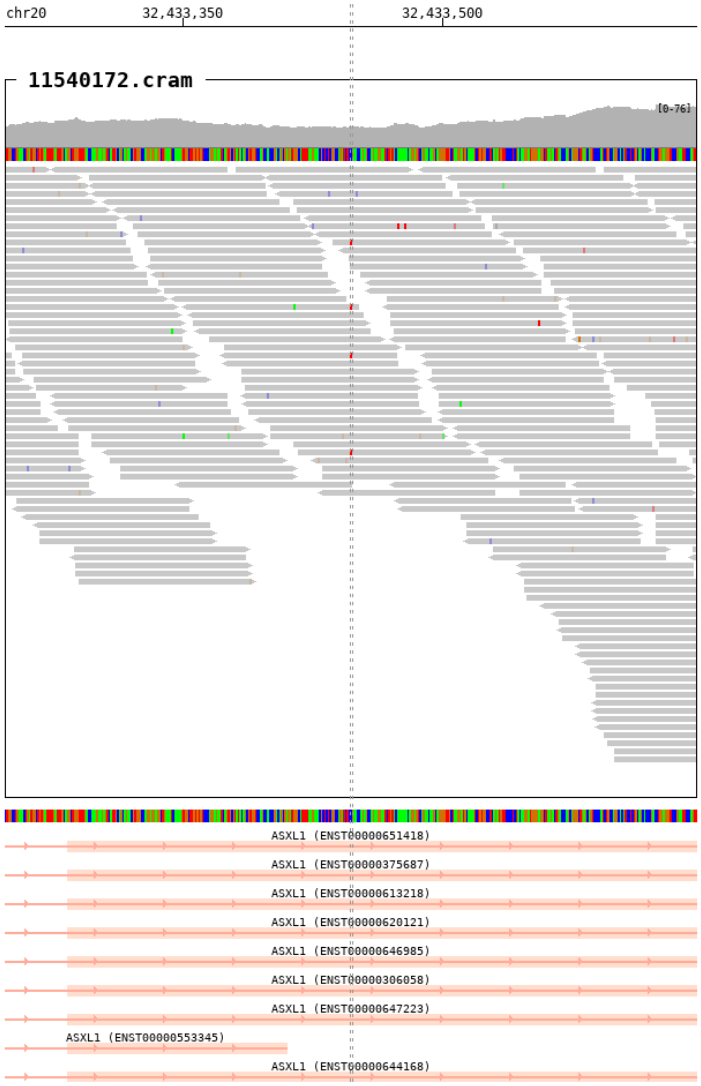
1.1. chr20_32433339_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110100879	chr20_32433339_G/T	28	10	*ASXL1*	stop_gained



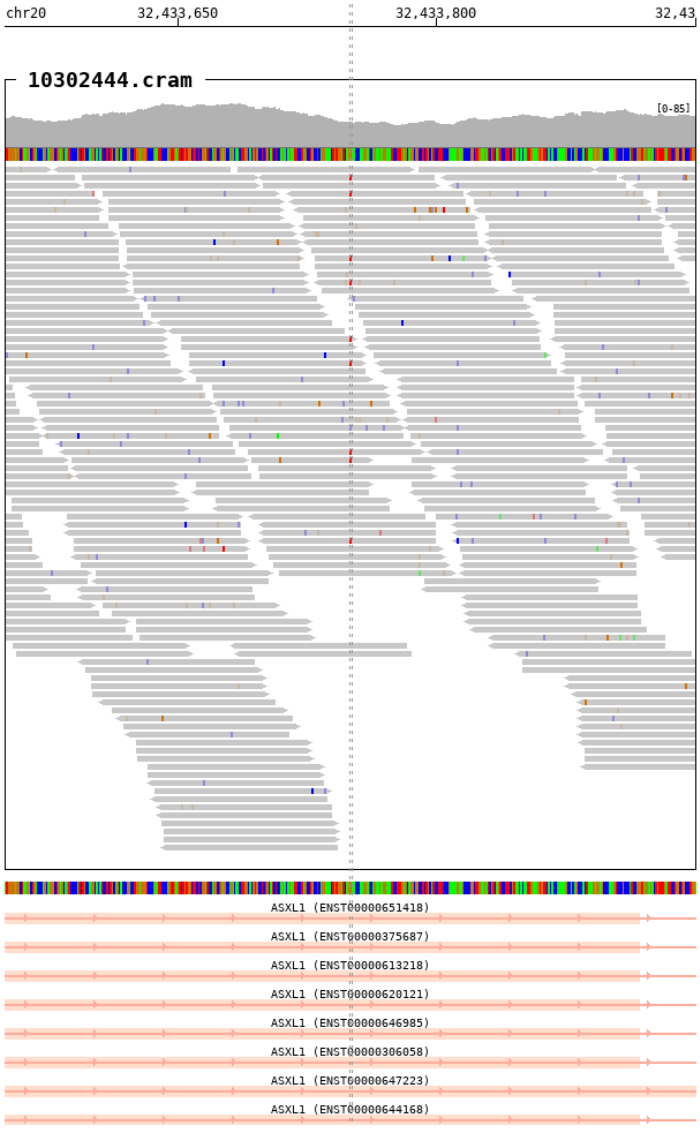
1.2. chr20_32433447_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11540172	chr20_32433447_C/T	30	4	*ASXL1*	stop_gained



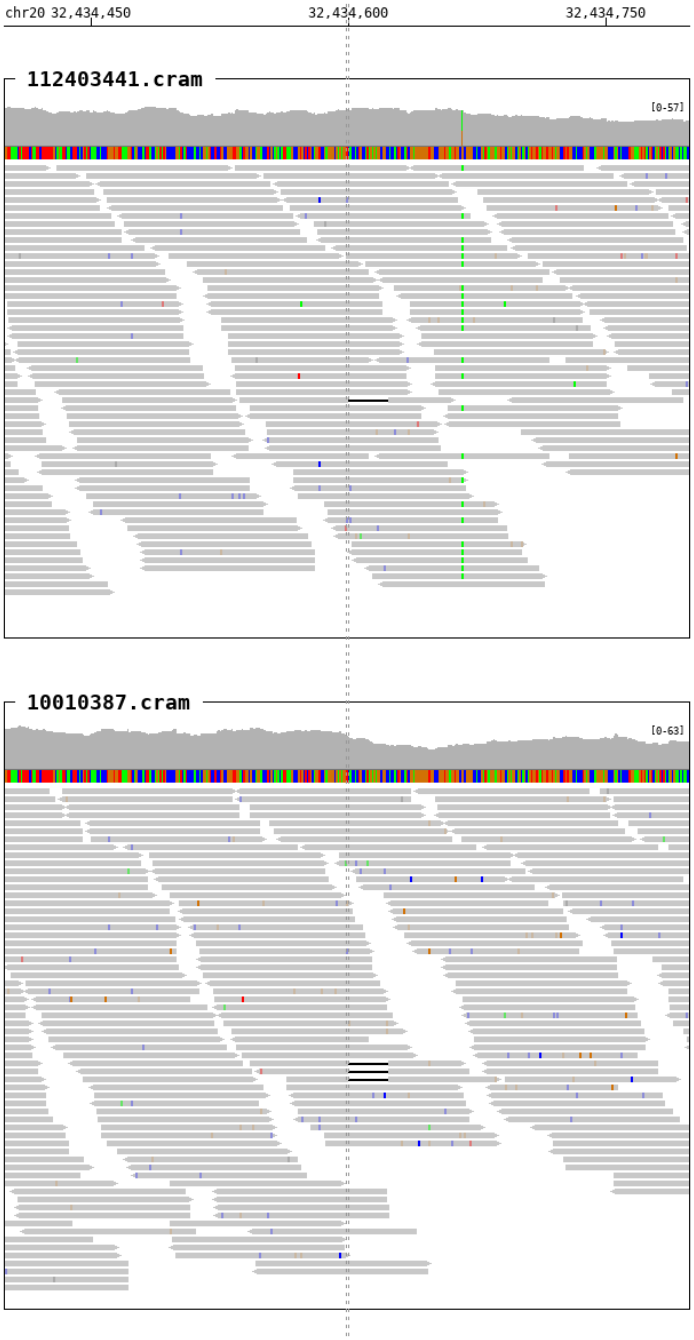
1.3. chr20_32433750_G/T

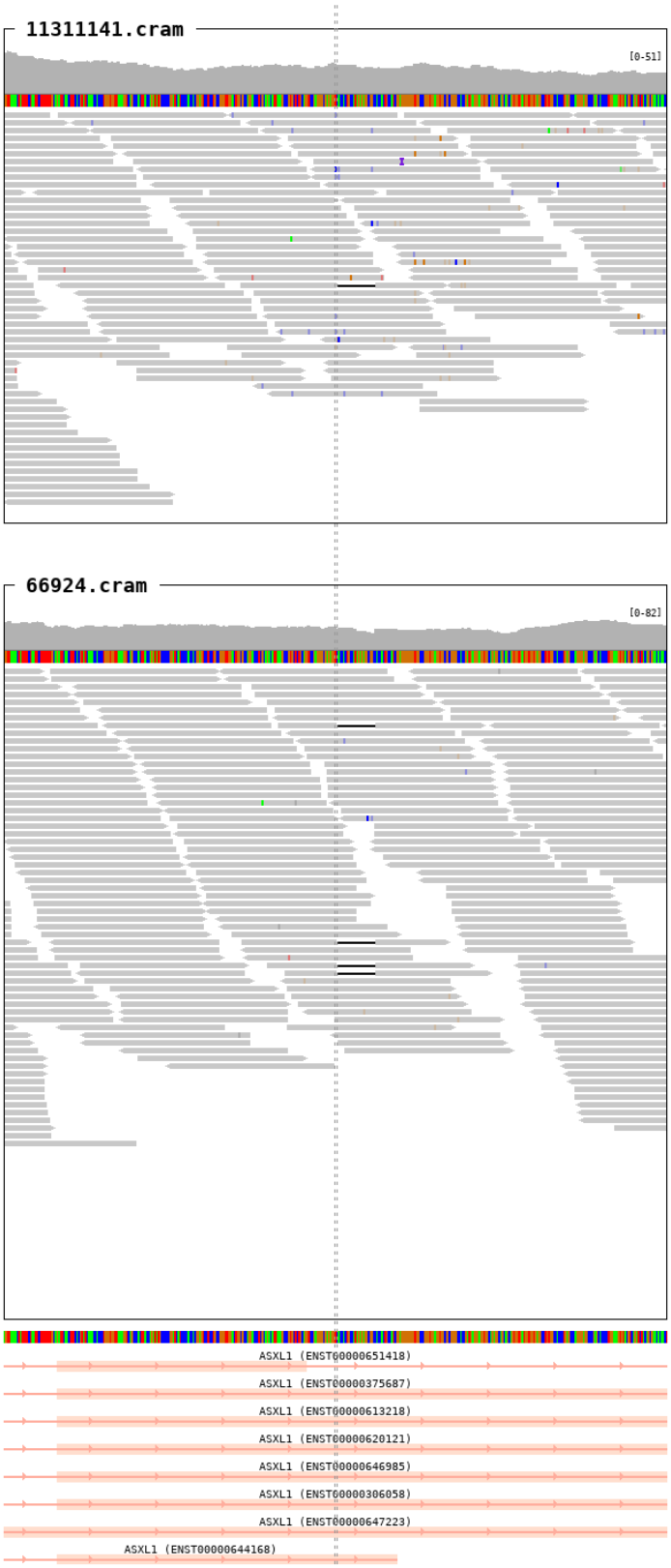
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10302444	chr20_32433750_G/T	33	7	*ASXL1*	stop_gained



1.4. chr20_32434599_CACCACTGCCATAGAGAGGCGGC/-

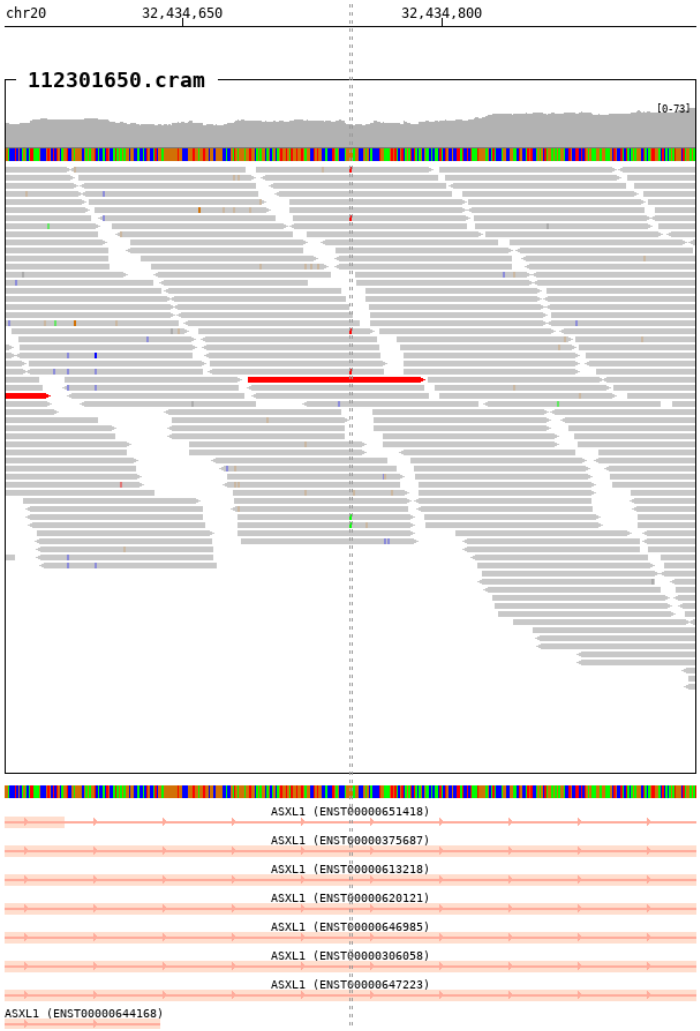
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10010387	chr20_32434599_CACCACTG CCATAGAGAGGCGGC/-	39	4	*ASXL1*	frameshift_variant
112403441	chr20_32434599_CACCACTG CCATAGAGAGGCGGC/-	48	5	*ASXL1*	frameshift_variant
11311141	chr20_32434599_CACCACTG CCATAGAGAGGCGGC/-	31	4	*ASXL1*	frameshift_variant
66924	chr20_32434599_CACCACTG CCATAGAGAGGCGGC/-	37	9	*ASXL1*	frameshift_variant




11311141.cram
[0-51]
66924.cram
[0-82]
ASXL1 (ENST00000651418)
ASXL1 (ENST00000375687)
ASXL1 (ENST00000613218)
ASXL1 (ENST00000620121)
ASXL1 (ENST00000646985)
ASXL1 (ENST00000306058)
ASXL1 (ENST00000647223)
ASXL1 (ENST00000644168)

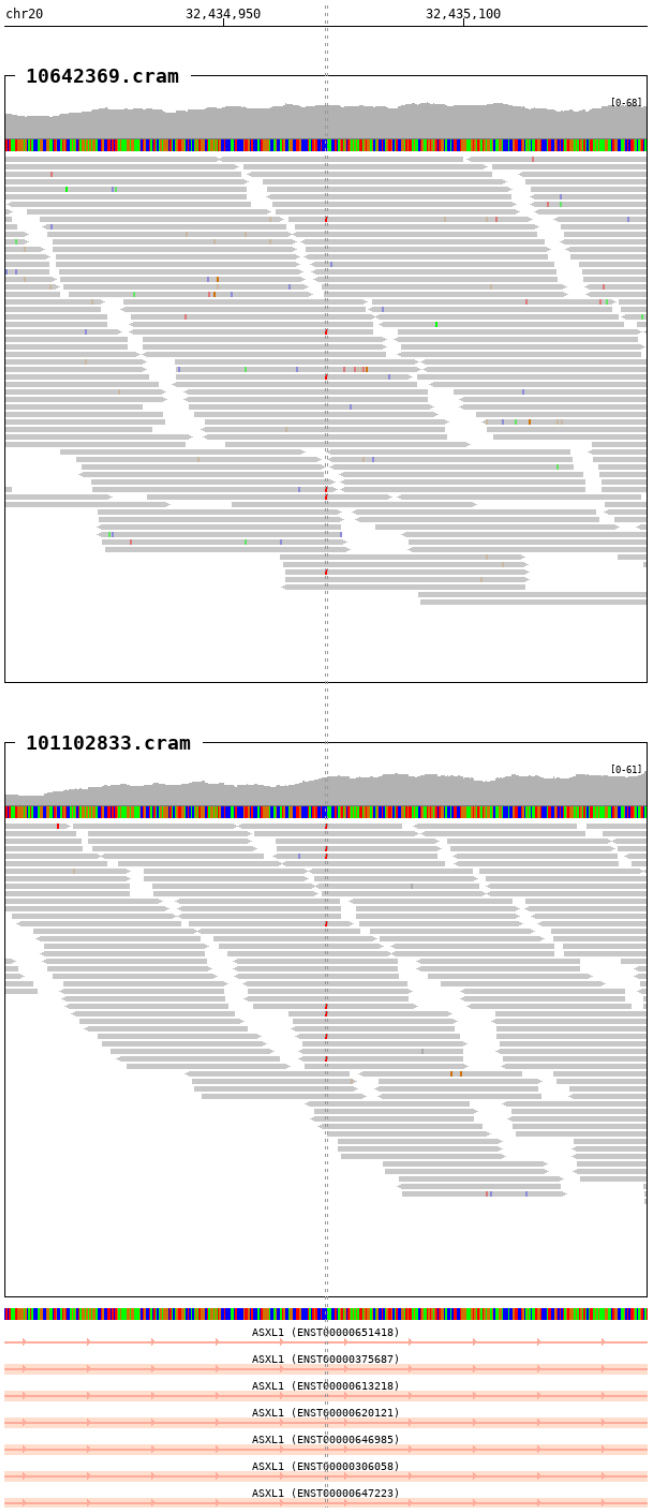
1.5. chr20_32434747_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301650	chr20_32434747_G/T	31	5	*ASXL1*	stop_gained



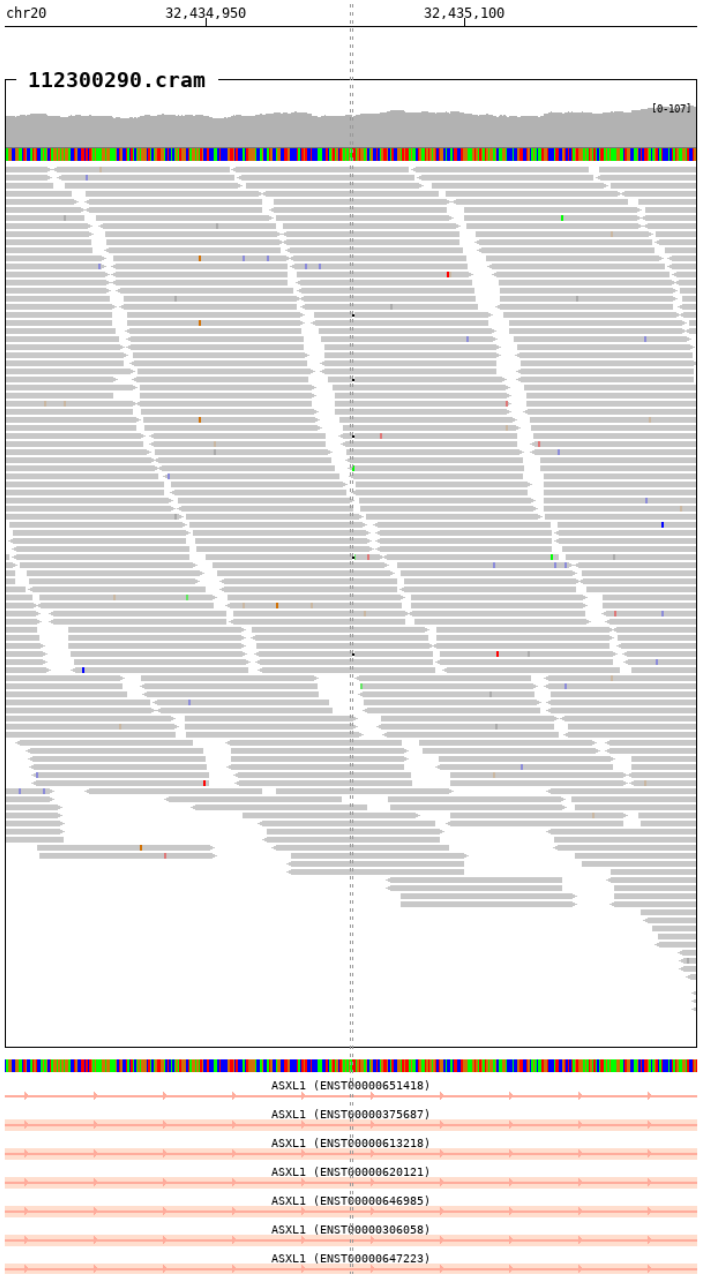
1.6. chr20_32435014_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101102833	chr20_32435014_C/T	30	8	*ASXL1*	stop_gained
10642369	chr20_32435014_C/T	47	6	*ASXL1*	stop_gained



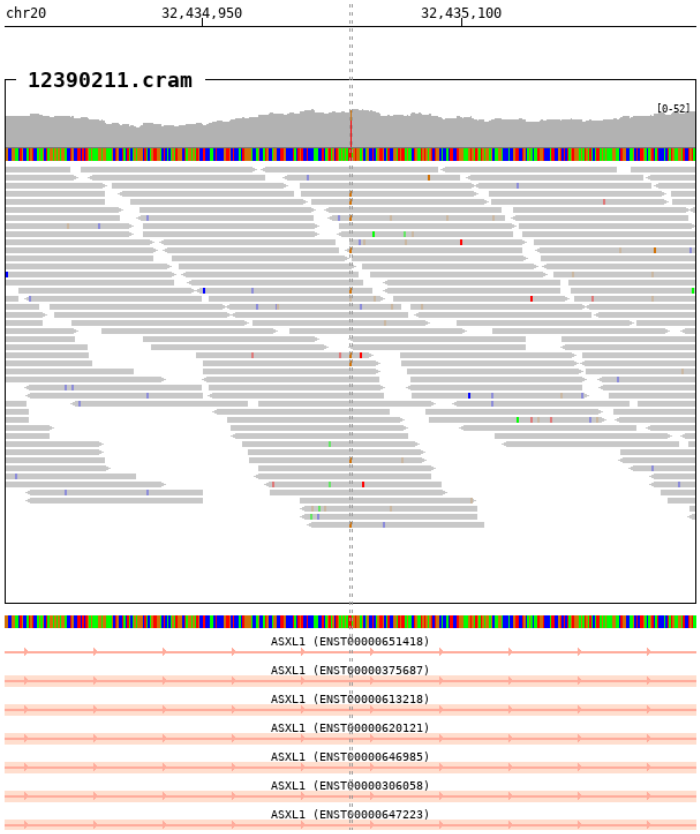
1.7. chr20_32435034_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112300290	chr20_32435034_T/-	66	9	*ASXL1*	frameshift_variant



1.8. chr20_32435036_T/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12390211	chr20_32435036_T/G	29	9	*ASXL1*	stop_gained



1.9. chr20_32435050_C/T

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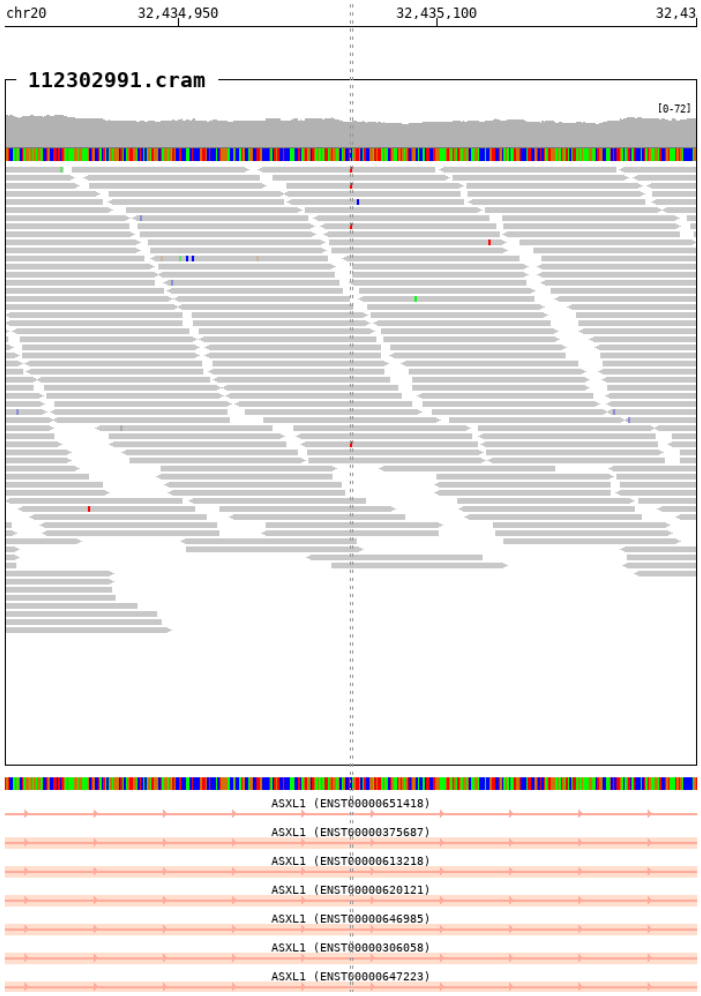
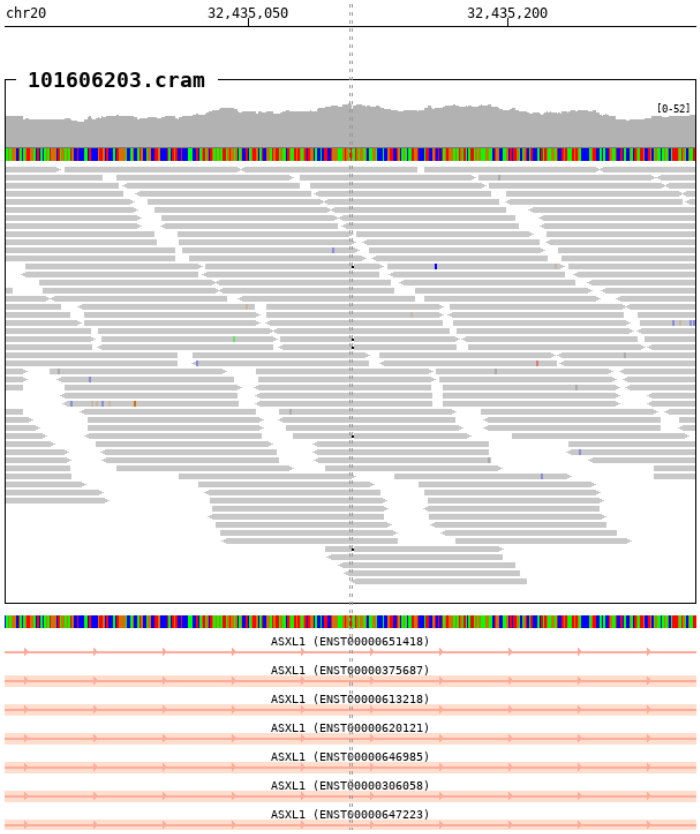
112302991	chr20_32435050_C/T	36	4	*ASXL1*	stop_gained



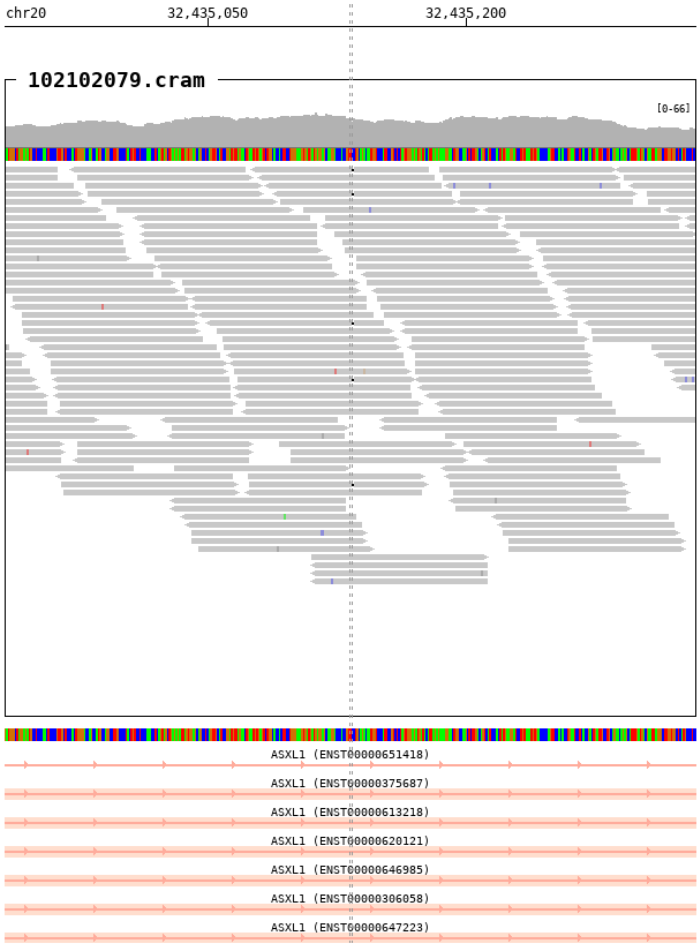
1.10. chr20_32435109_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101606203	chr20_32435109_G/-	42	5	*ASXL1*	frameshift_variant



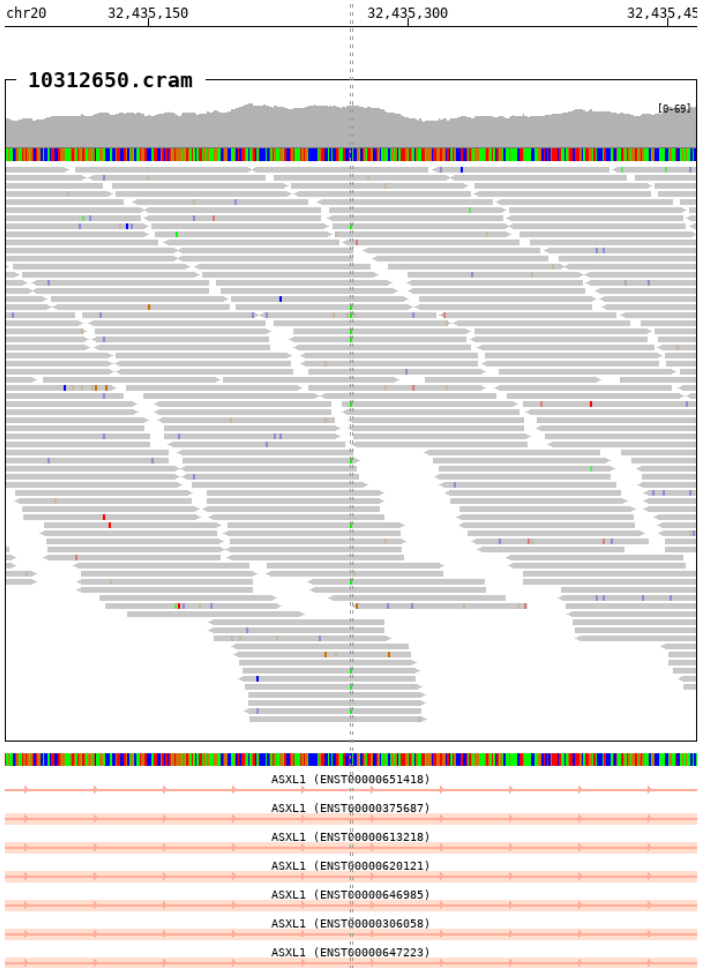
1.11. chr20_32435133_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102102079	chr20_32435133_C/-	37	5	*ASXL1*	frameshift_variant



1.12. chr20_32435267_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10312650	chr20_32435267_C/A	50	12	*ASXL1*	stop_gained



1.13. chr20_32435491_G/T

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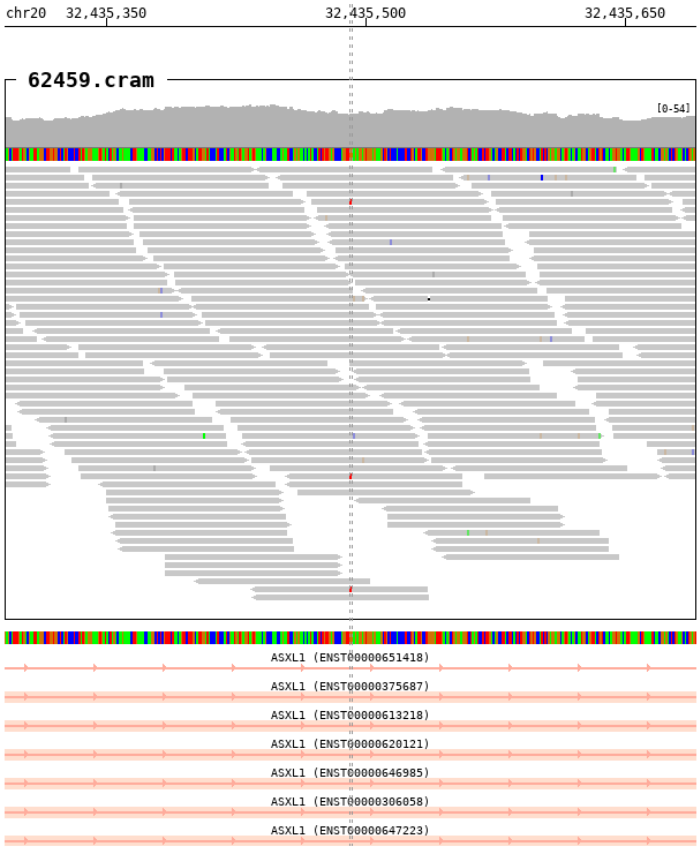
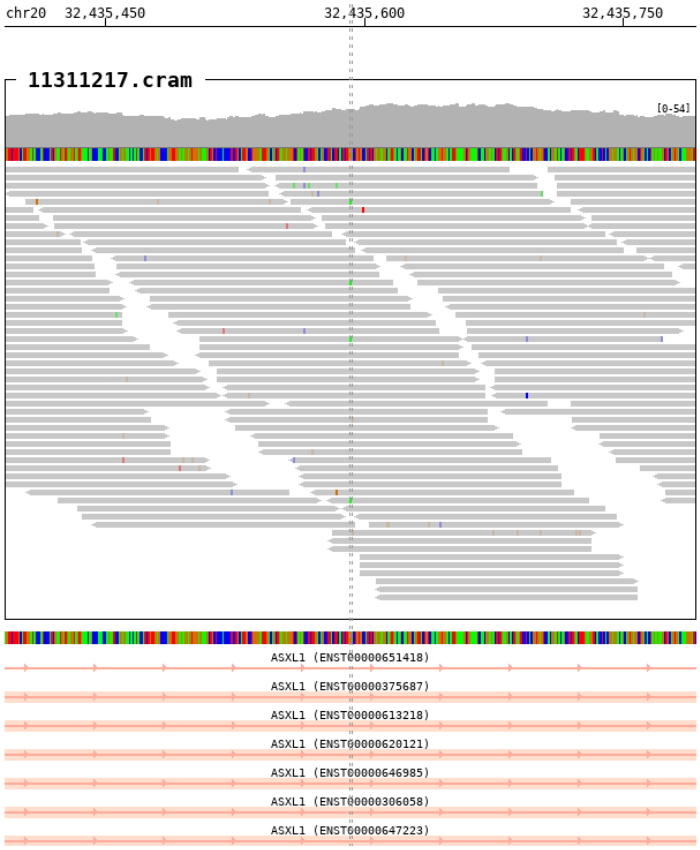
62459	chr20_32435491_G/T	37	3	*ASXL1*	stop_gained



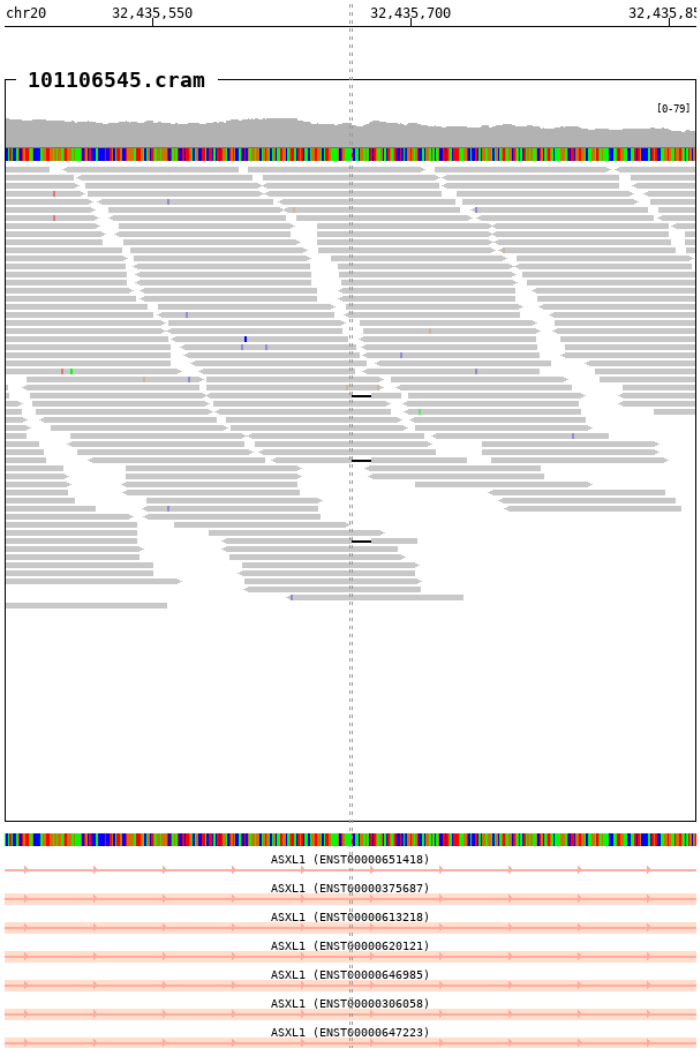
1.14. chr20_32435592_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11311217	chr20_32435592_G/A	38	4	*ASXL1*	stop_gained



1.15. chr20_32435665_TCAACGGAGAC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101106545	chr20_32435665_TCAACGGAGAC/-	45	4	*ASXL1*	frameshift_variant



1.16. chr20_32435696_-/A

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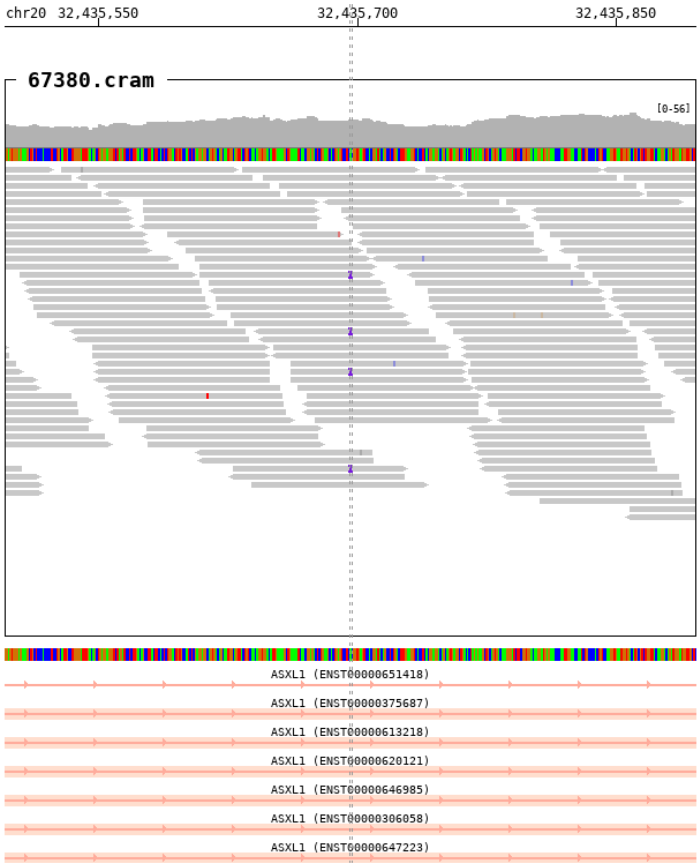
67380	chr20_32435696_-/A	30	4	*ASXL1*	frameshift_variant



1.17. chr20_32436442_A/T

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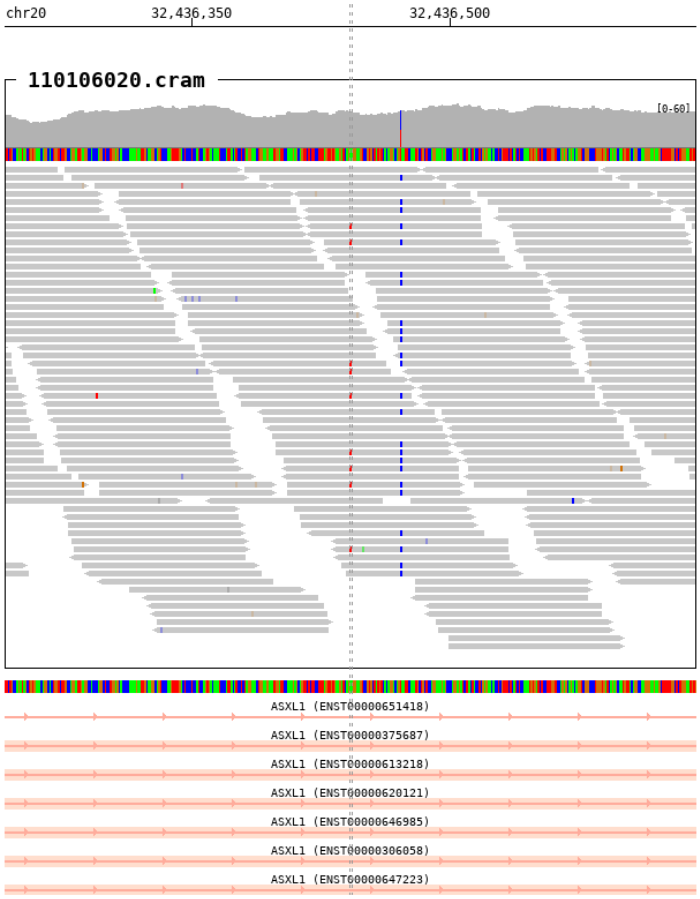
110106020	chr20_32436442_A/T	39	9	*ASXL1*	stop_gained



1.18. chr20_32436449_C/-

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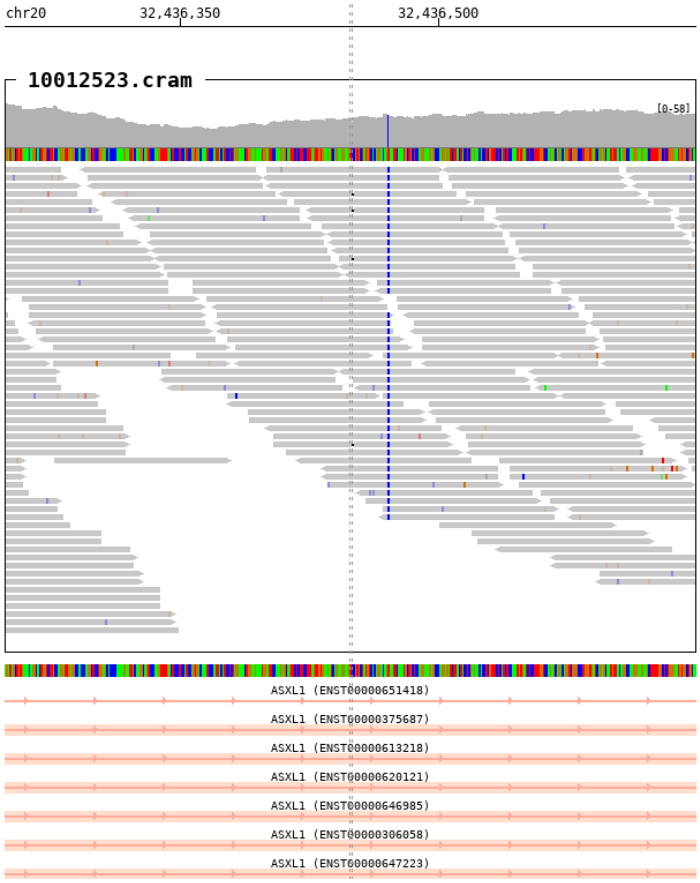
10012523	chr20_32436449_C/-	32	4	*ASXL1*	frameshift_variant



2. *BCOR*

2.1. chrX_40064489_GGGAGGCTCG/-

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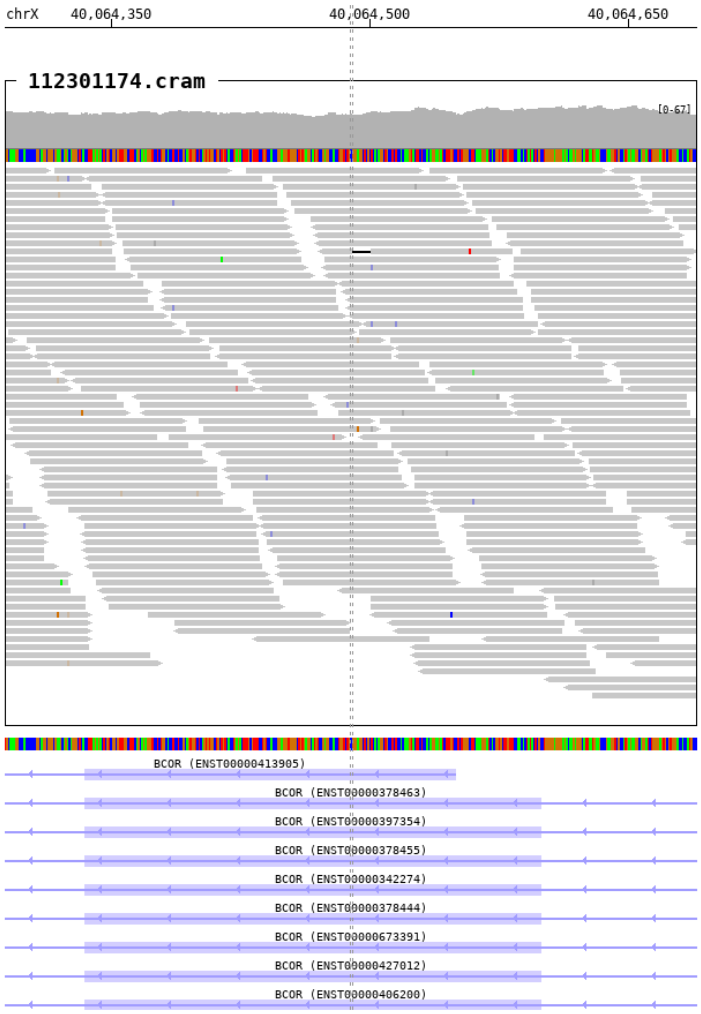
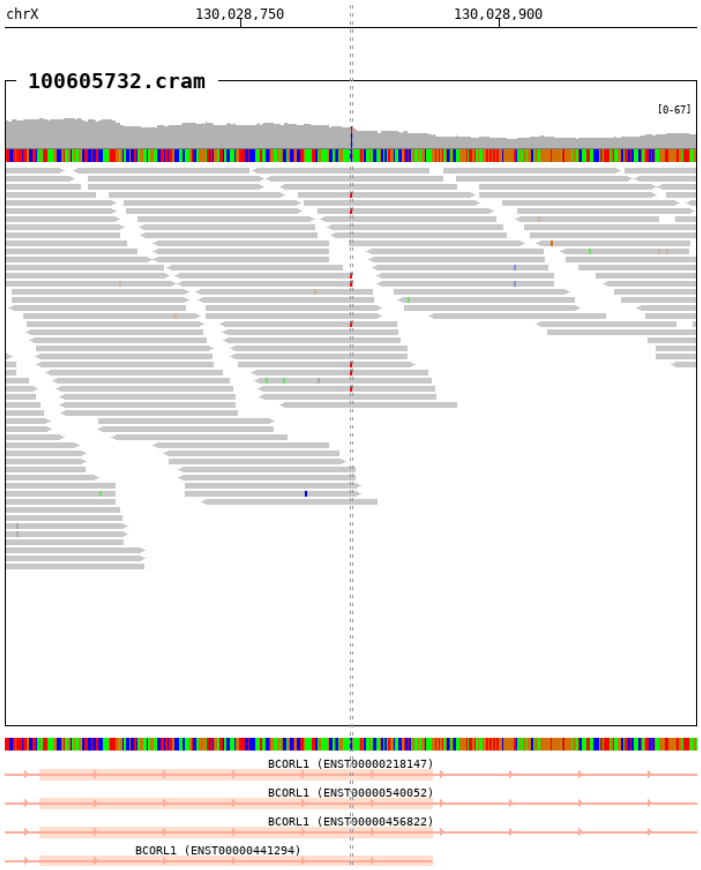
112301174	chrX_40064489_GGGAGGCTCG/-	53	2	*BCOR*	frameshift_variant



3. *BCORL1*

3.1. chrX_130028814_C/T

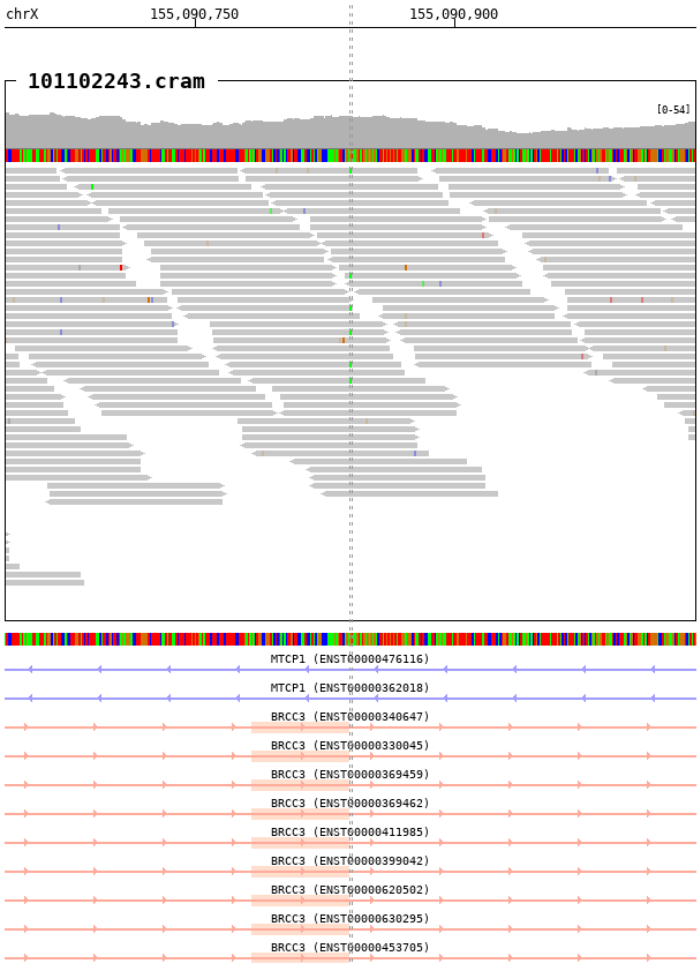
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100605732	chrX_130028814_C/T	21	8	*BCORL1*	stop_gained



4. *BRCC3*

4.1. chrX_155090840_G/A

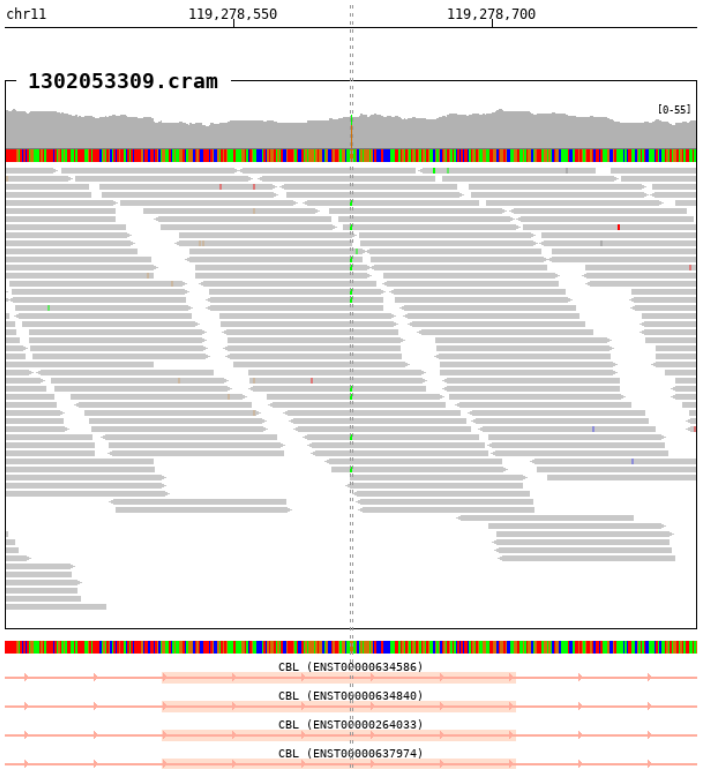
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101102243	chrX_155090840_G/A	32	6	*BRCC3*	splice_donor_variant



5. *CBL*

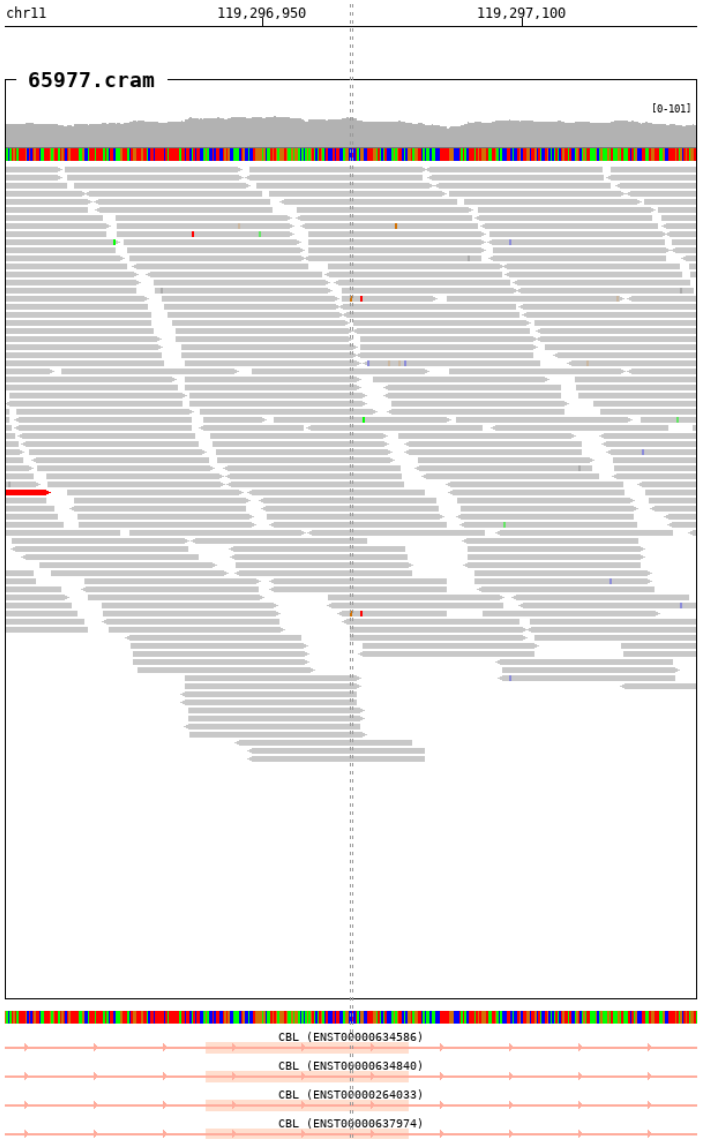
5.1. chr11_119278618_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
1302053309	chr11_119278618_G/A	30	9	*CBL*	missense_variant



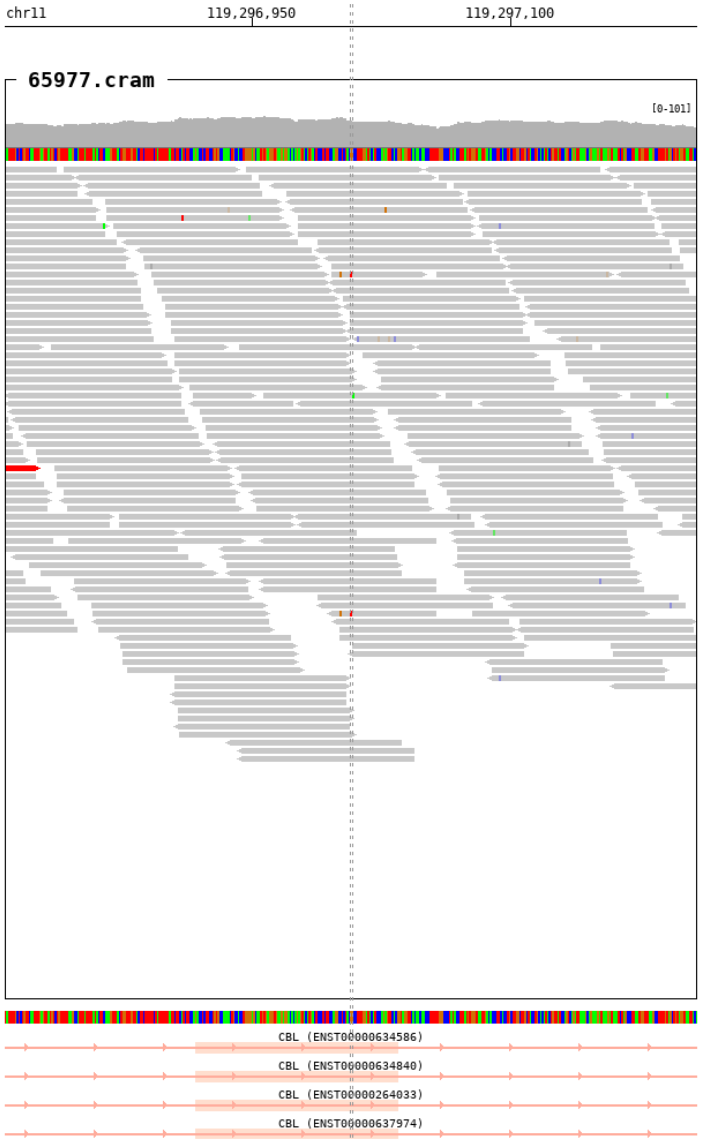
5.2. chr11_119297001_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
65977	chr11_119297001_C/G	59	2	*CBL*	missense_variant



5.3. chr11_119297007_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
65977	chr11_119297007_G/T	55	2	*CBL*	missense_variant



5.4. chr11_119298457_T/G

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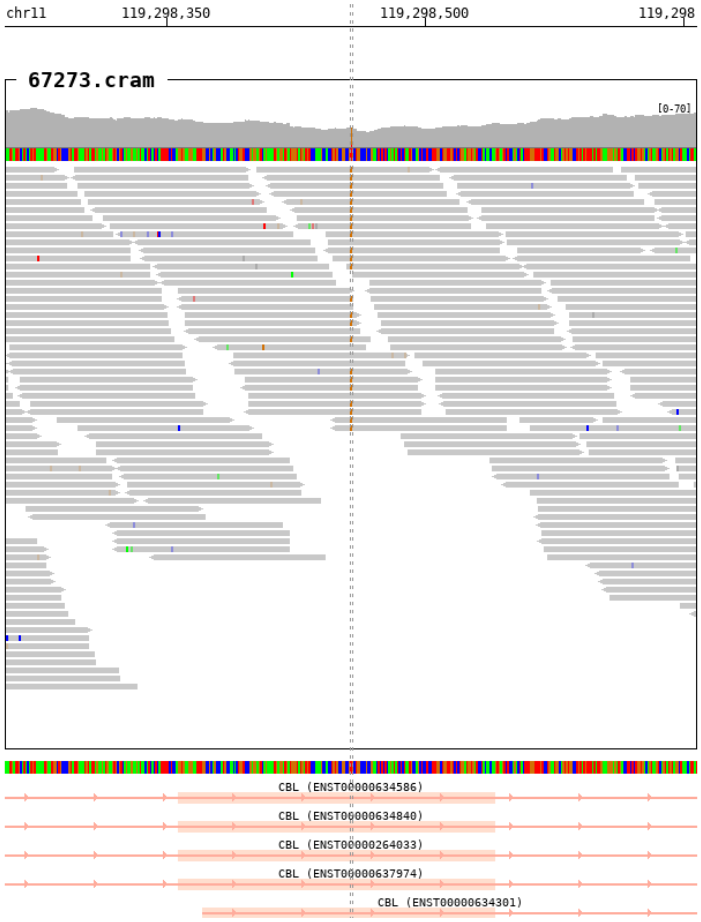
67273	chr11_119298457_T/G	7	23	*CBL*	missense_variant



5.5. chr11_119299593_G/A

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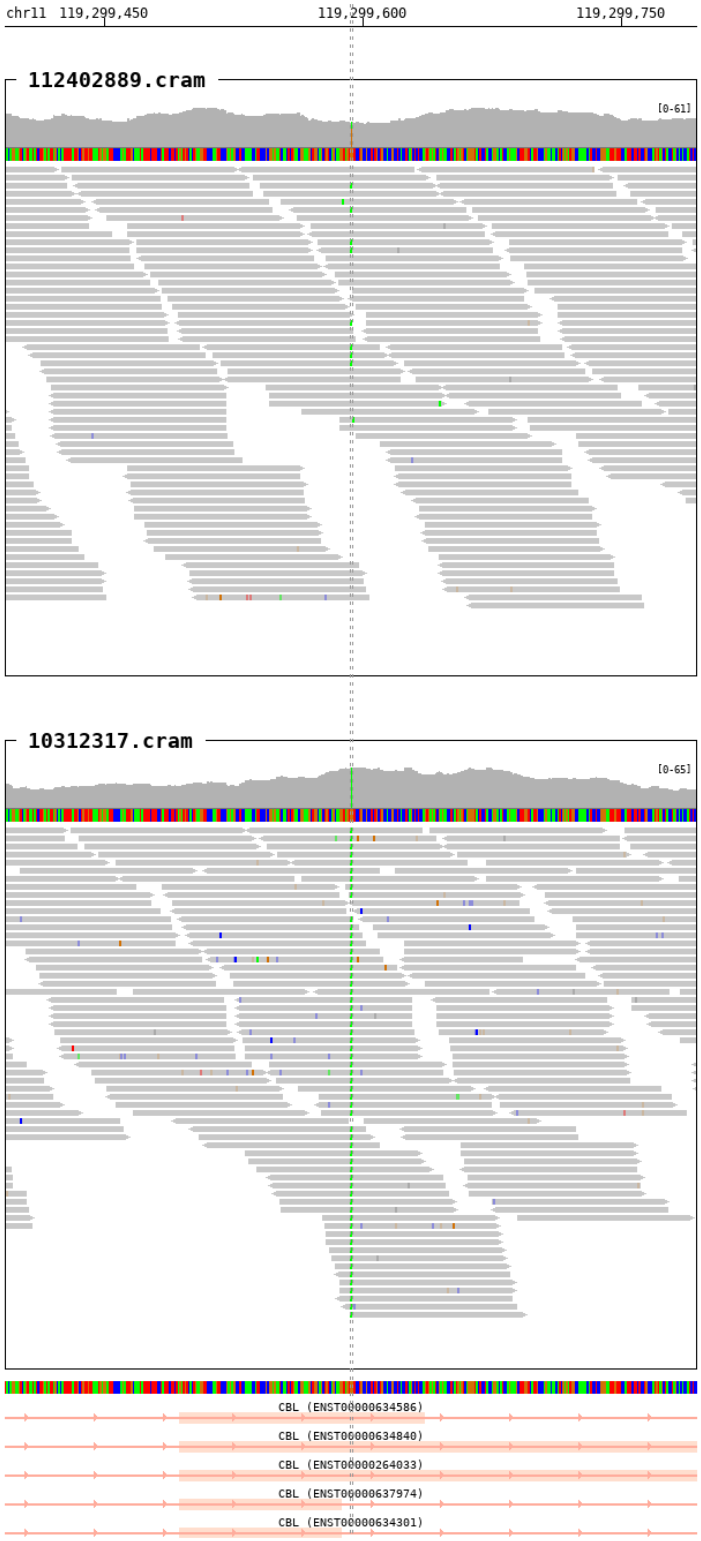
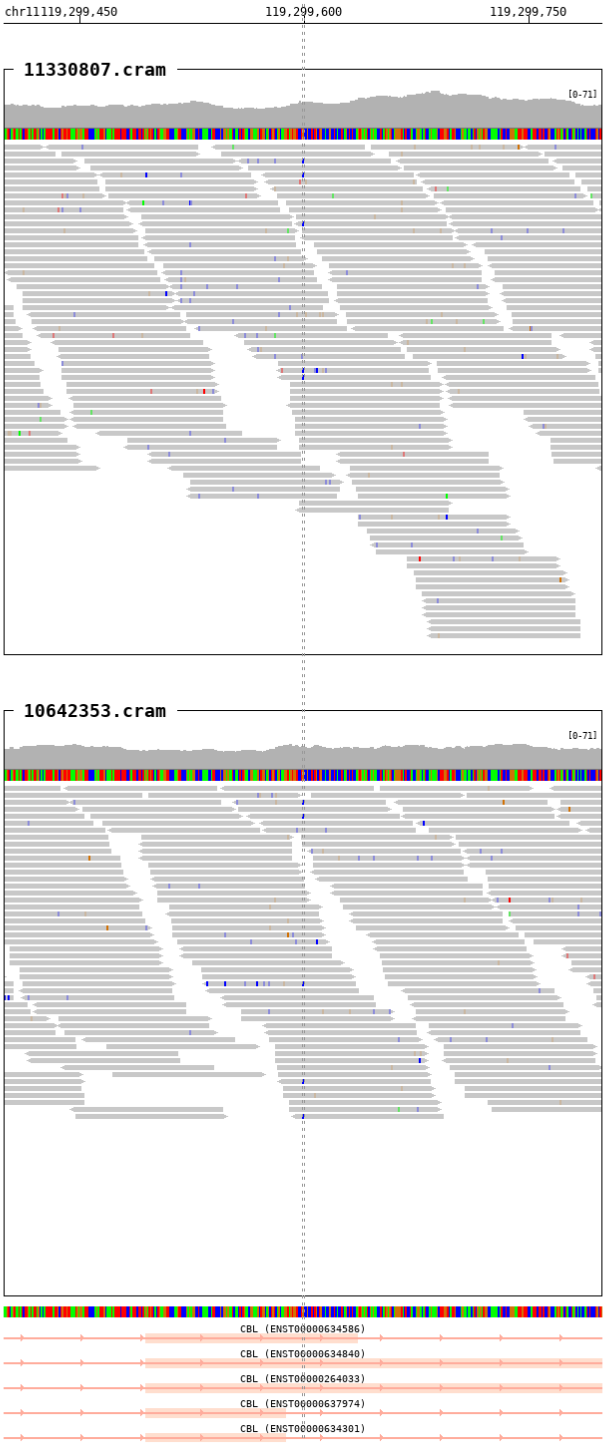
112402889	chr11_119299593_G/A	25	8	*CBL*	missense_variant



5.6. chr11_119299599_G/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10642353	chr11_119299599_G/C	33	5	*CBL*	missense_variant
11330807	chr11_119299599_G/C	38	4	*CBL*	missense_variant



6. *CBLB*

6.1. chr3_105659118_G/A

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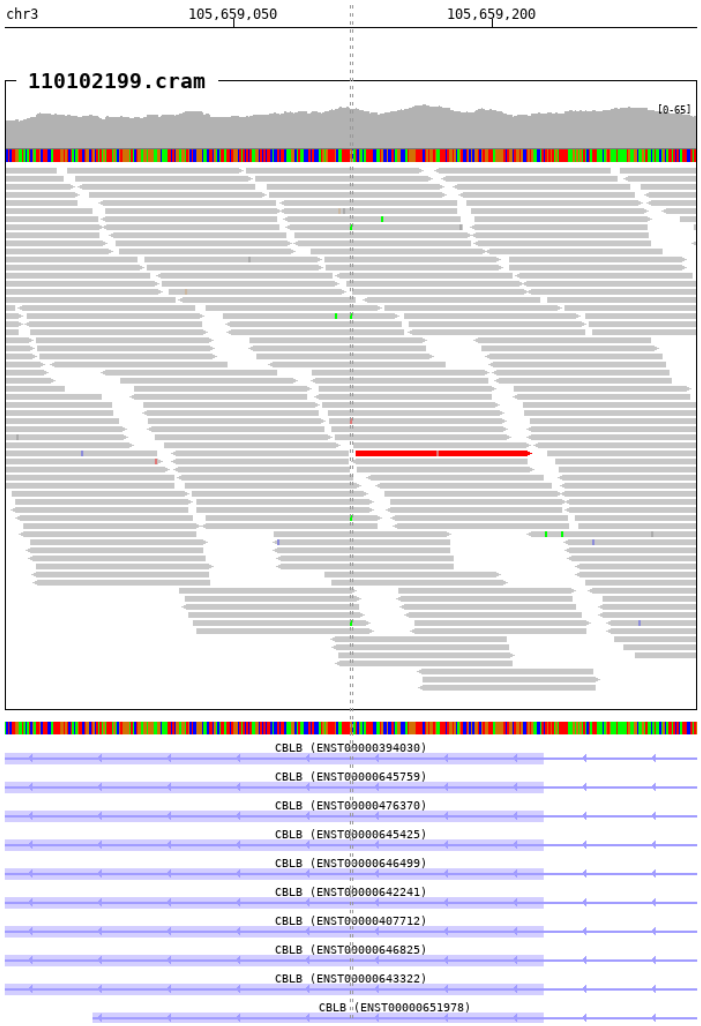
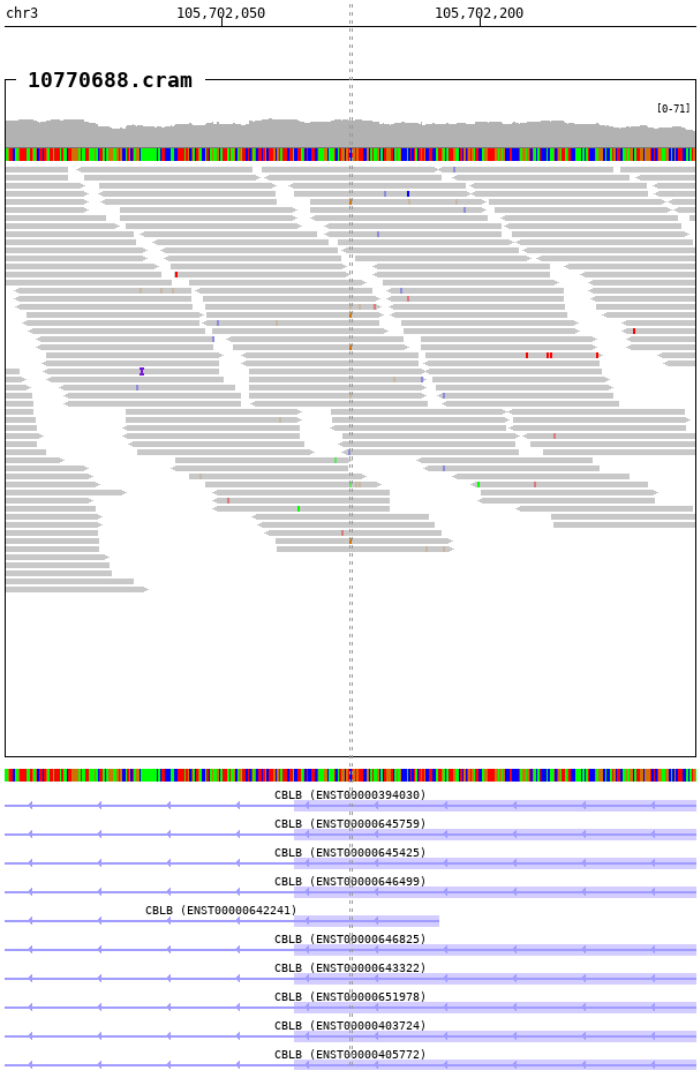
110102199	chr3_105659118_G/A	50	4	*CBLB*	missense_variant



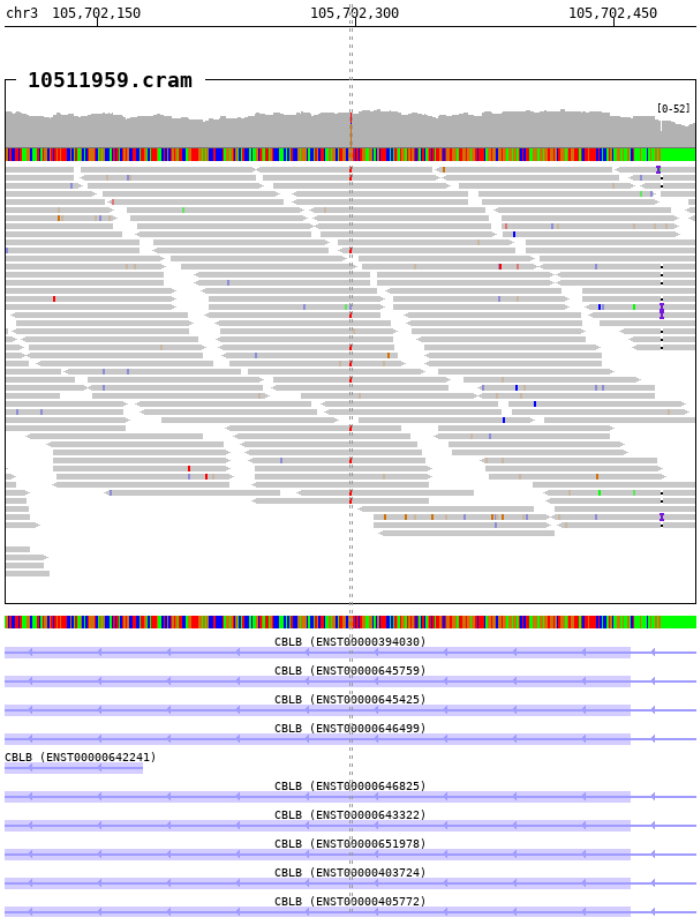
6.2. chr3_105702125_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10770688	chr3_105702125_C/G	36	5	*CBLB*	missense_variant



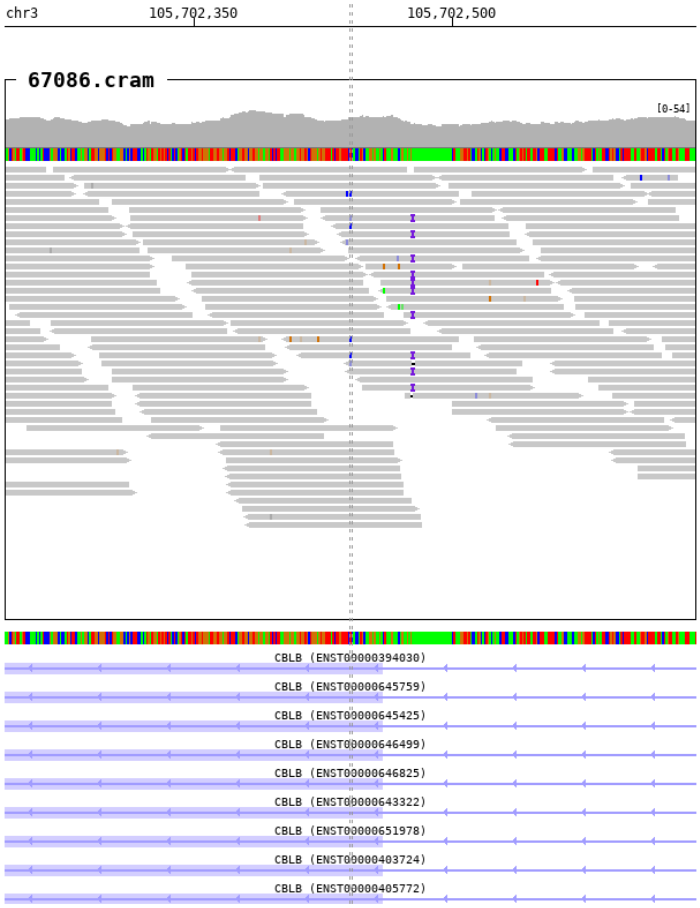
6.3. chr3_105702297_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10511959	chr3_105702297_G/T	28	10	*CBLB*	missense_variant



6.4. chr3_105702441_T/C

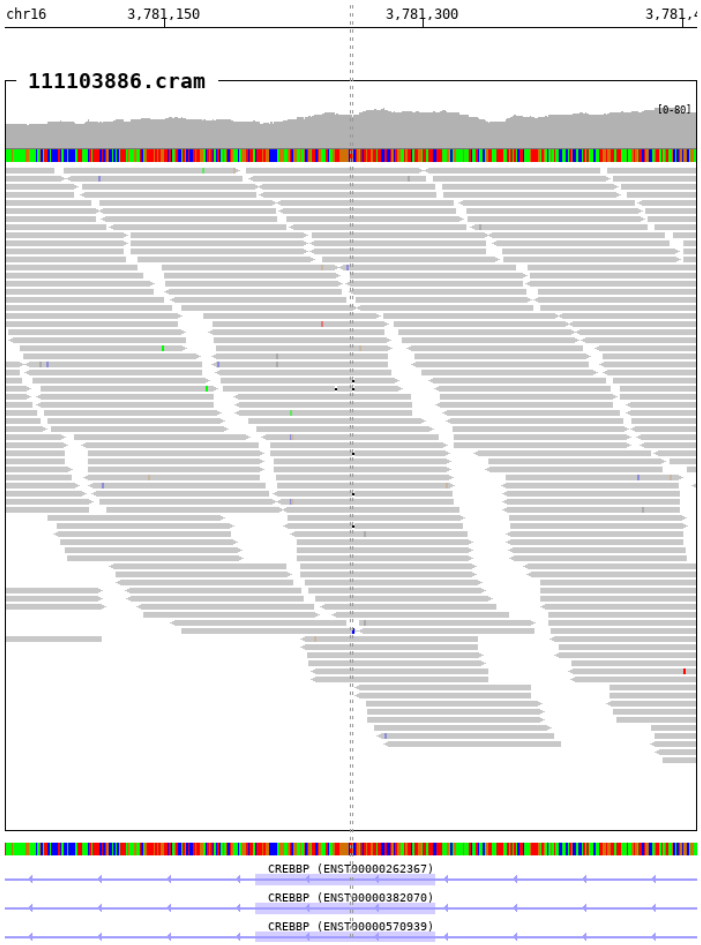
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
67086	chr3_105702441_T/C	31	6	*CBLB*	missense_variant



7. *CREBBP*

7.1. chr16_3781258_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
111103886	chr16_3781258_G/-	54	6	*CREBBP*	frameshift_variant



8. *CTCF*

8.1. chr16_67636801_GCGGAGAG/-

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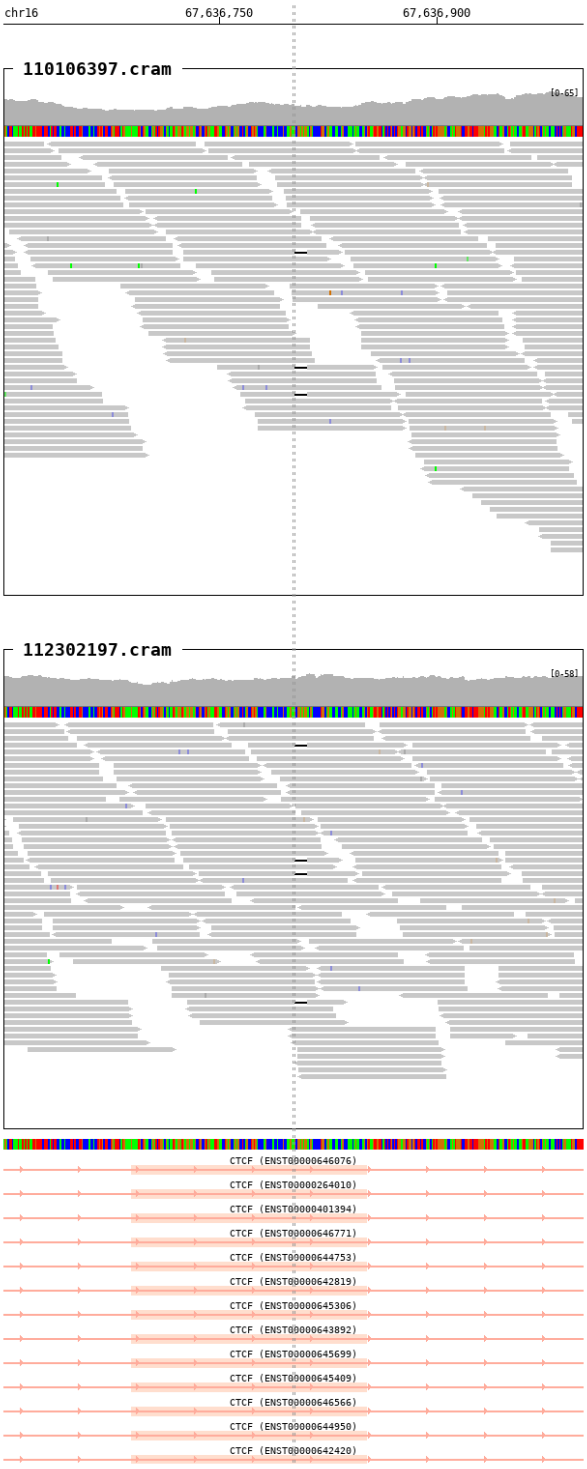
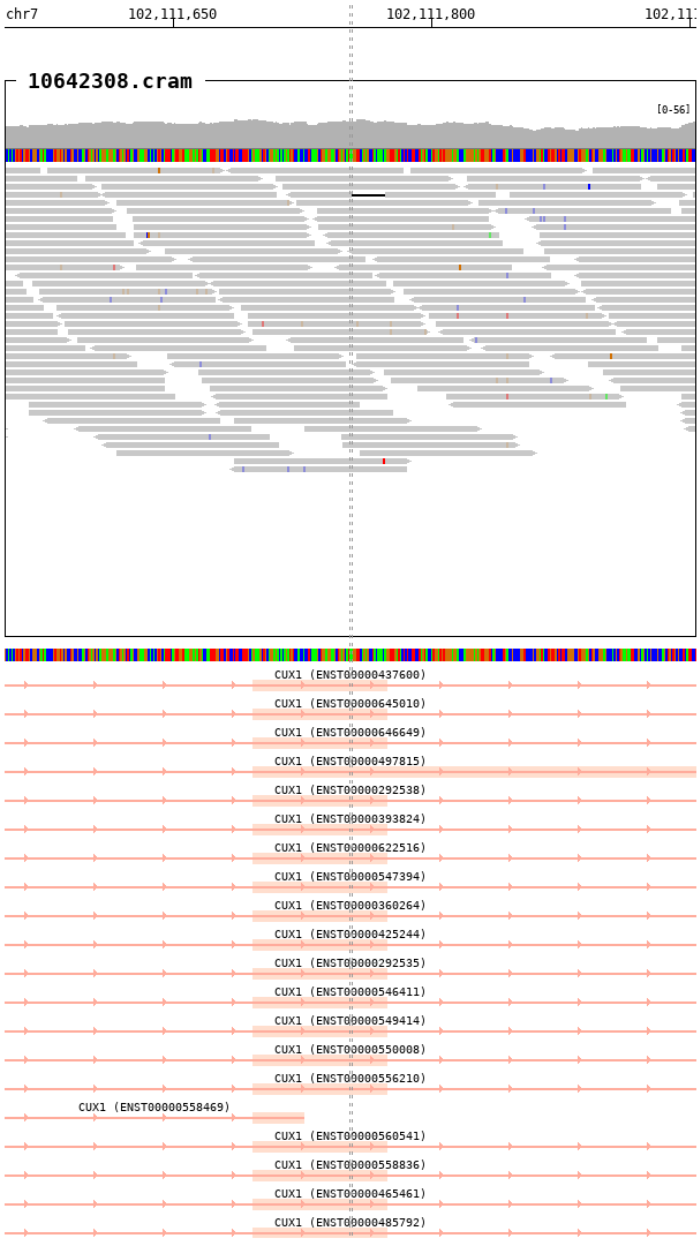
110106397	chr16_67636801_GCGGAGAG/-	35	3	*CTCF*	frameshift_variant
112302197	chr16_67636801_GCGGAGAG/-	47	4	*CTCF*	frameshift_variant



9. *CUX1*

9.1. chr7_102111753_AGGTTCAGAGCCTACAAAC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10642308	chr7_102111753_AGGTTCAGAGCCTACAAAC/-	37	3	*CUX1*	frameshift_variant



9.2. chr7_102196778_AAGTC/-

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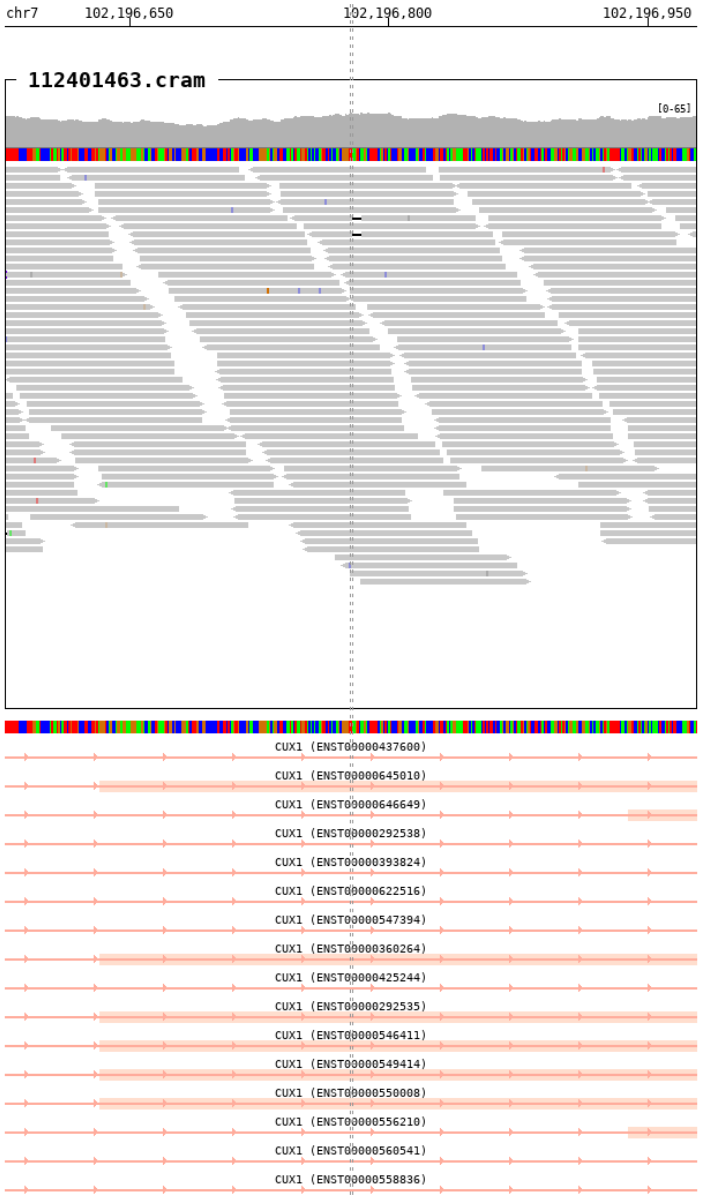
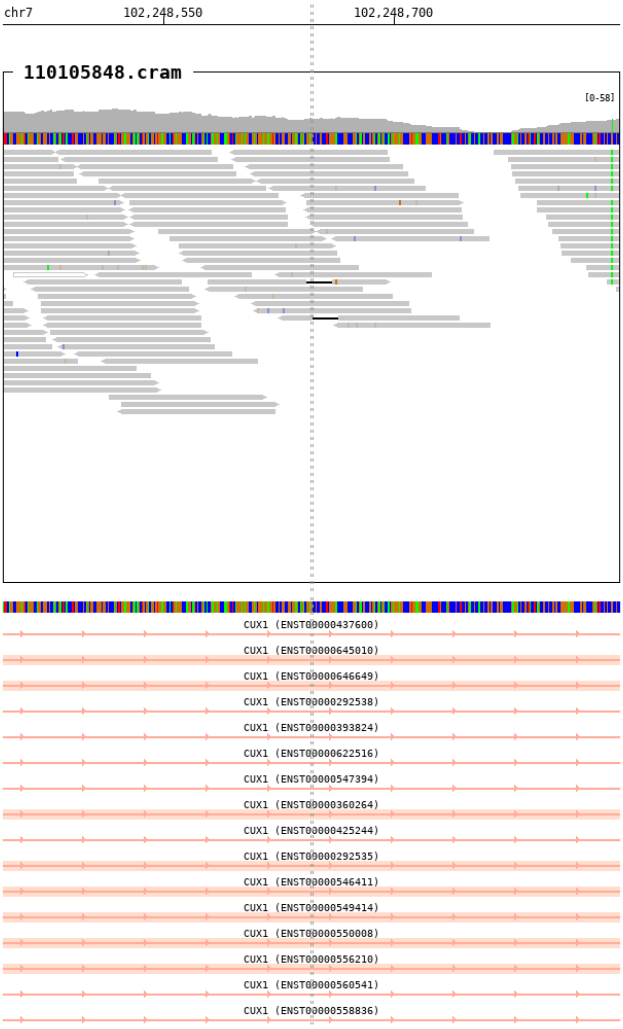
112401463	chr7_102196778_AAGTC/-	48	3	*CUX1*	frameshift_variant



9.3. chr7_102248646_CCGCCGCCCTCGGGGA/-

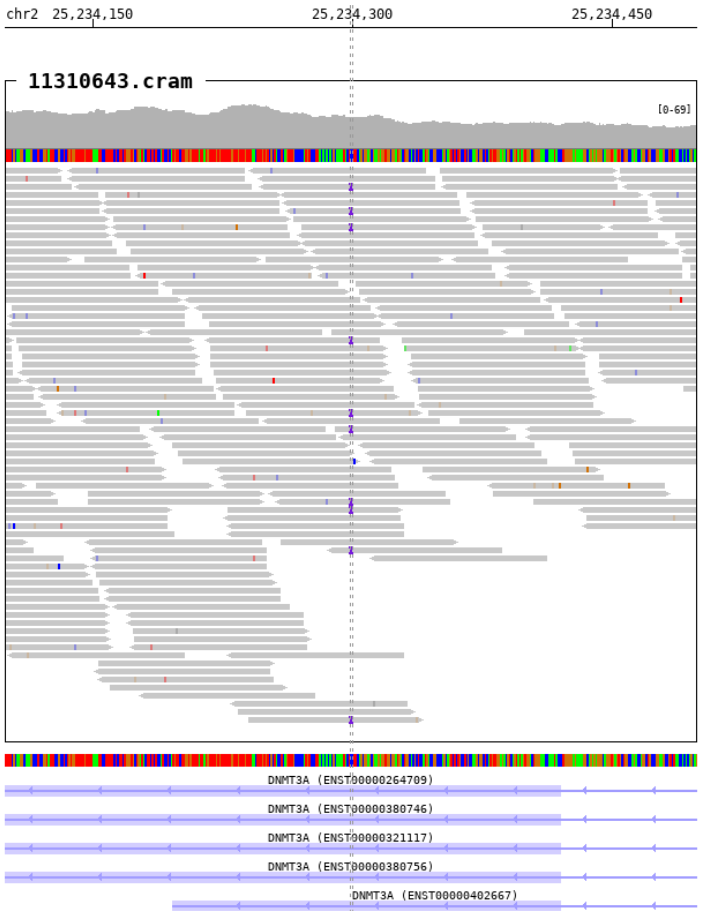
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110105848	chr7_102248646_CCGCCGCCCTCGGGGA/-	22	2	*CUX1*	frameshift_variant



10. *DNMT3A*

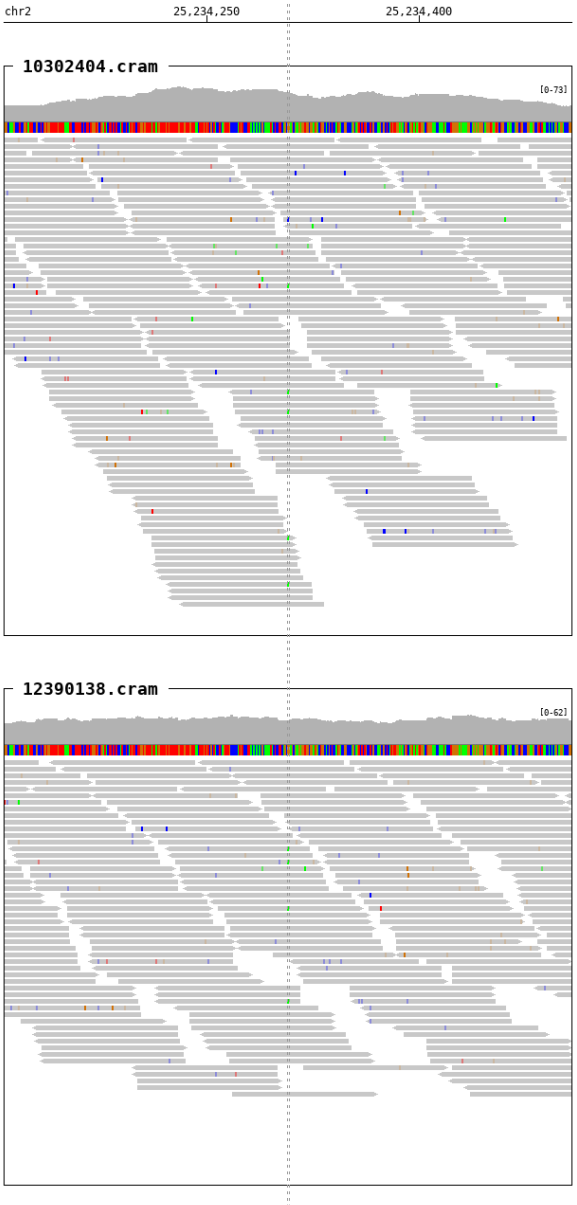
10.1. chr2_25234299_-/C

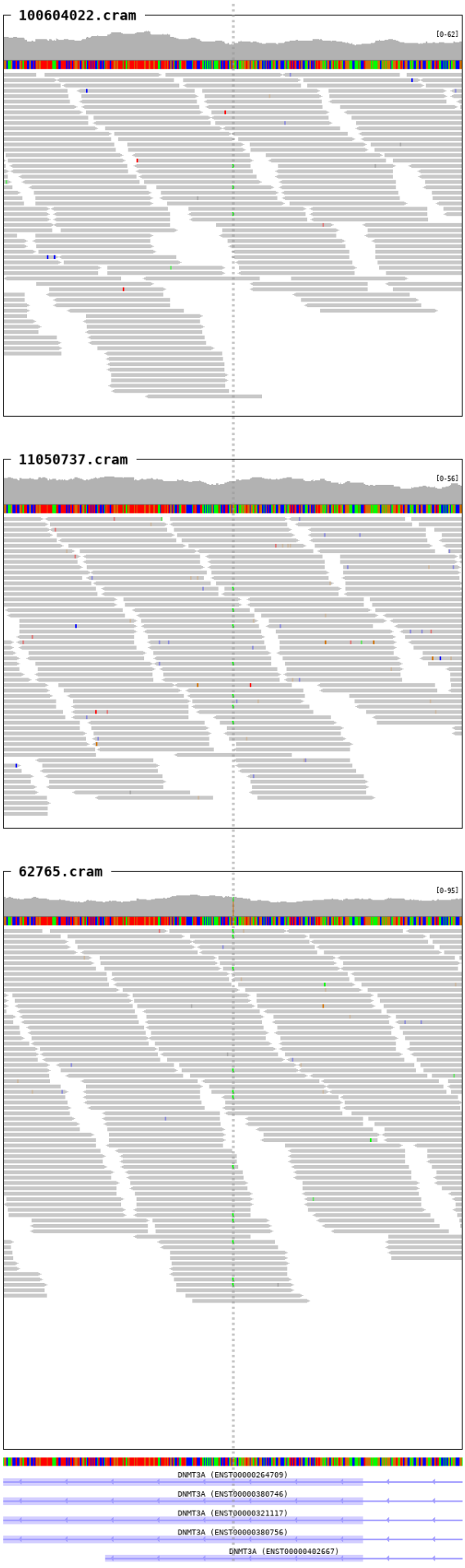
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11310643	chr2_25234299_-/C	37	11	*DNMT3A*	frameshift_variant



10.2. chr2_25234307_G/A

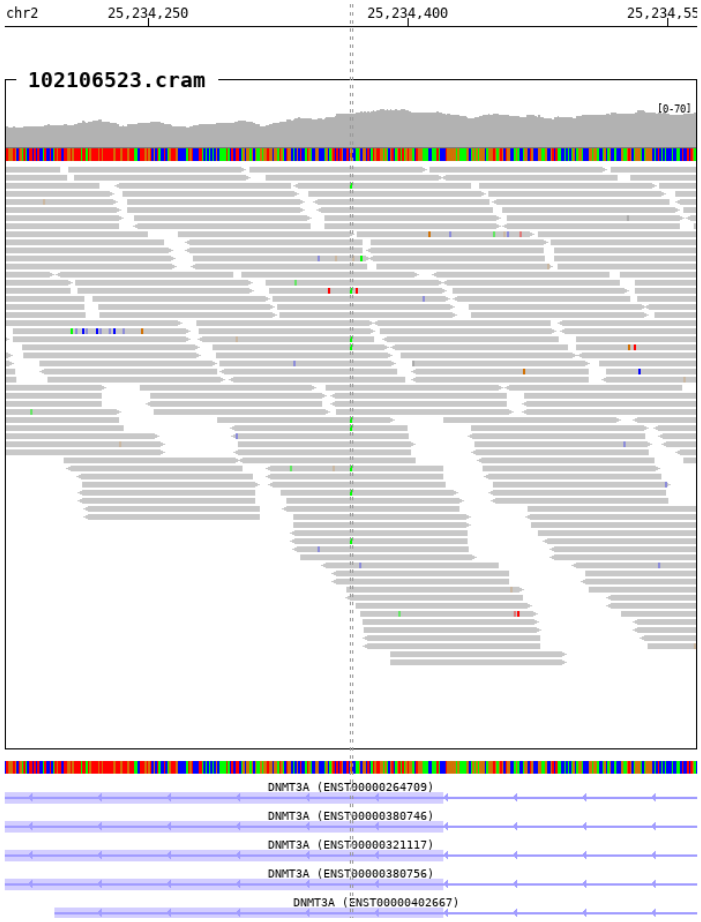
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100604022	chr2_25234307_G/A	29	3	*DNMT3A*	missense_variant
10302404	chr2_25234307_G/A	47	4	*DNMT3A*	missense_variant
11050737	chr2_25234307_G/A	35	7	*DNMT3A*	missense_variant
12390138	chr2_25234307_G/A	36	3	*DNMT3A*	missense_variant
62765	chr2_25234307_G/A	46	12	*DNMT3A*	missense_variant




100604022.cram
[0-62]
11050737.cram
[0-56]
62765.cram
[0-95]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)

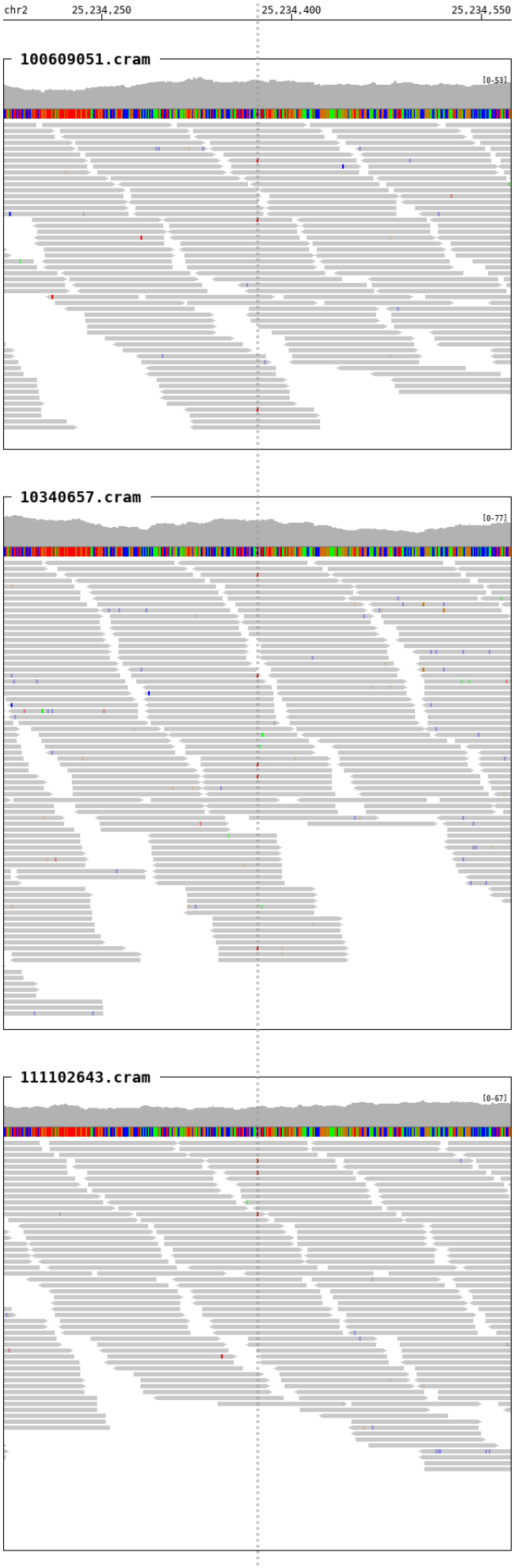
10.3. chr2_25234367_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102106523	chr2_25234367_G/A	42	8	*DNMT3A*	missense_variant



10.4. chr2_25234373_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10012318	chr2_25234373_C/T	53	6	*DNMT3A*	missense_variant
10012653	chr2_25234373_C/T	36	6	*DNMT3A*	missense_variant
100605023	chr2_25234373_C/T	33	7	*DNMT3A*	missense_variant
100606074	chr2_25234373_C/T	30	4	*DNMT3A*	missense_variant
100609051	chr2_25234373_C/T	43	3	*DNMT3A*	missense_variant
100609394	chr2_25234373_C/T	43	4	*DNMT3A*	missense_variant
101606945	chr2_25234373_C/T	28	5	*DNMT3A*	missense_variant
10340657	chr2_25234373_C/T	47	4	*DNMT3A*	missense_variant
10511907	chr2_25234373_C/T	35	5	*DNMT3A*	missense_variant
10642231	chr2_25234373_C/T	55	9	*DNMT3A*	missense_variant
10672157	chr2_25234373_C/T	39	5	*DNMT3A*	missense_variant
110100971	chr2_25234373_C/T	45	4	*DNMT3A*	missense_variant
110108852	chr2_25234373_C/T	59	11	*DNMT3A*	missense_variant
111102643	chr2_25234373_C/T	37	3	*DNMT3A*	missense_variant
112302462	chr2_25234373_C/T	35	4	*DNMT3A*	missense_variant
11330885	chr2_25234373_C/T	36	4	*DNMT3A*	missense_variant
11560385	chr2_25234373_C/T	34	4	*DNMT3A*	missense_variant
1501033231	chr2_25234373_C/T	36	3	*DNMT3A*	missense_variant
61583	chr2_25234373_C/T	54	11	*DNMT3A*	missense_variant
63733	chr2_25234373_C/T	38	4	*DNMT3A*	missense_variant
66028	chr2_25234373_C/T	42	9	*DNMT3A*	missense_variant
66742	chr2_25234373_C/T	58	7	*DNMT3A*	missense_variant
67660	chr2_25234373_C/T	36	7	*DNMT3A*	missense_variant
68119	chr2_25234373_C/T	34	4	*DNMT3A*	missense_variant


chr2
25,234,250
25,234,400
25,234,550
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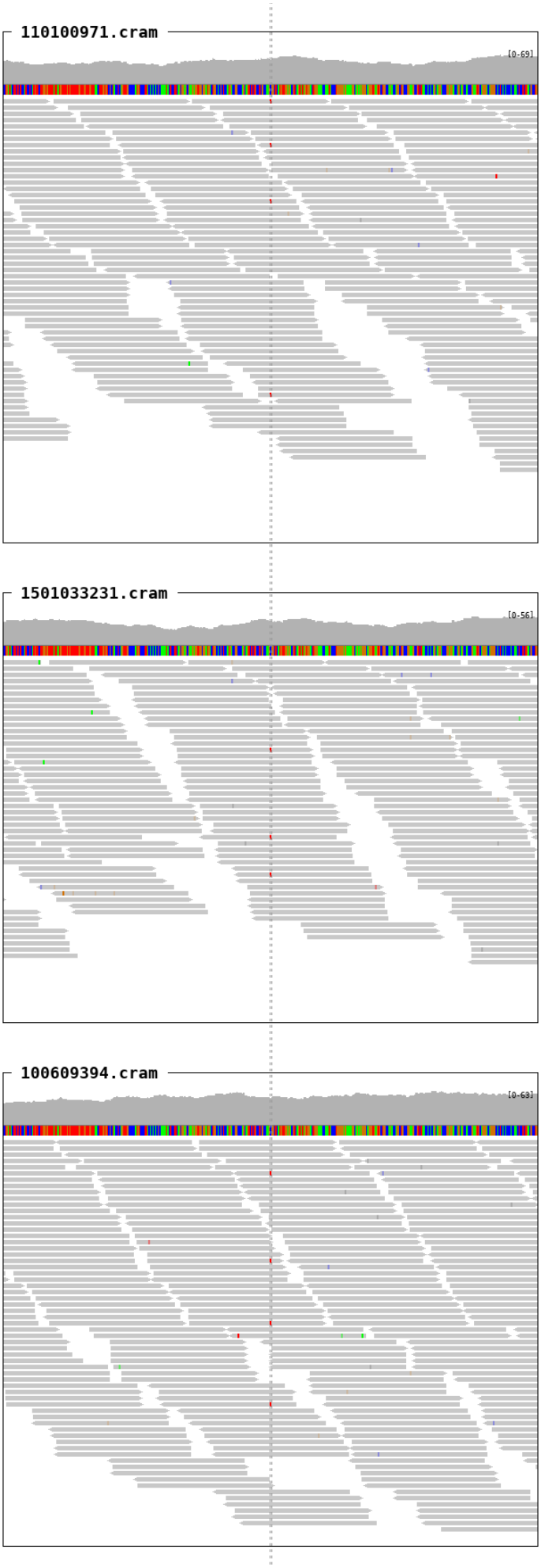
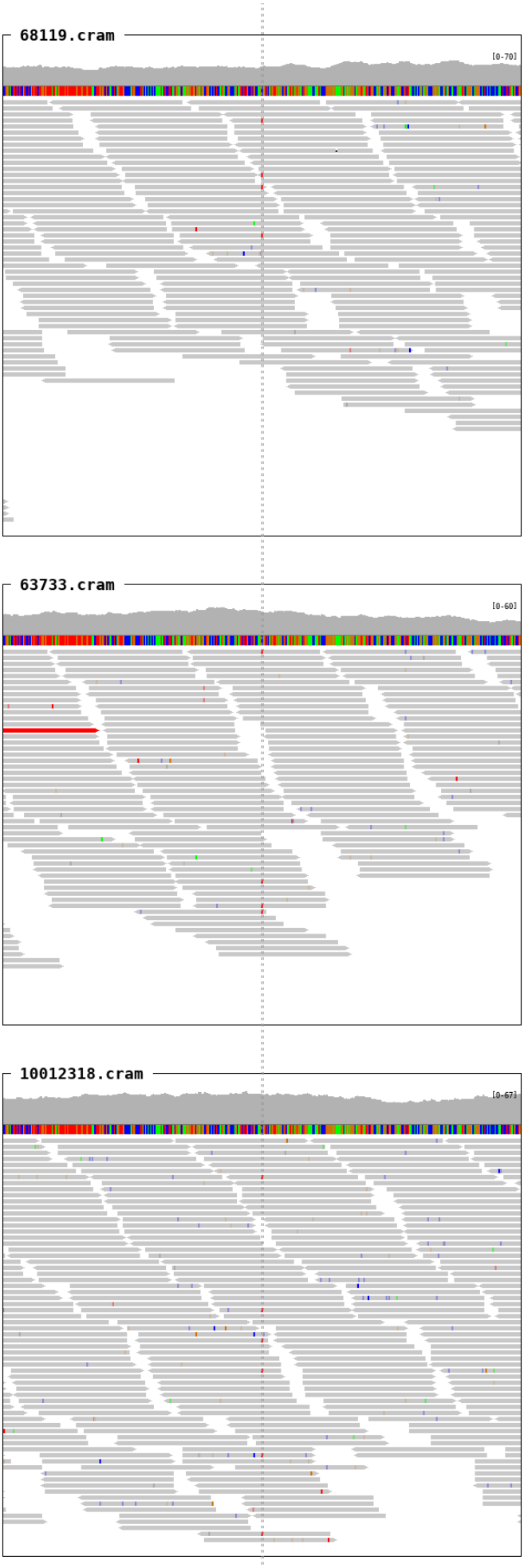
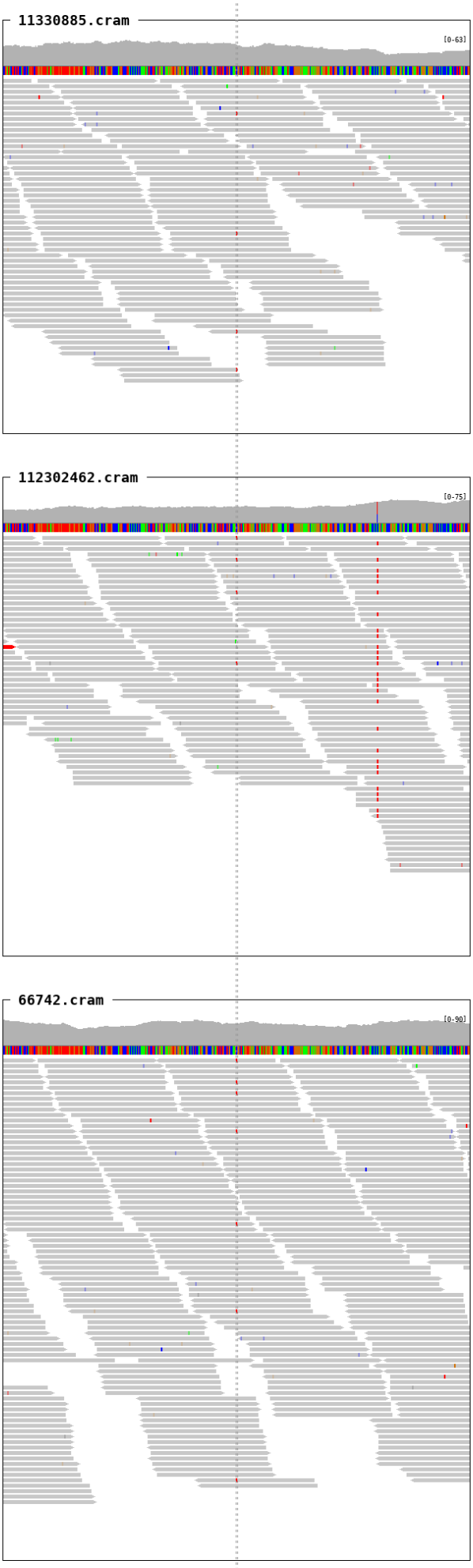
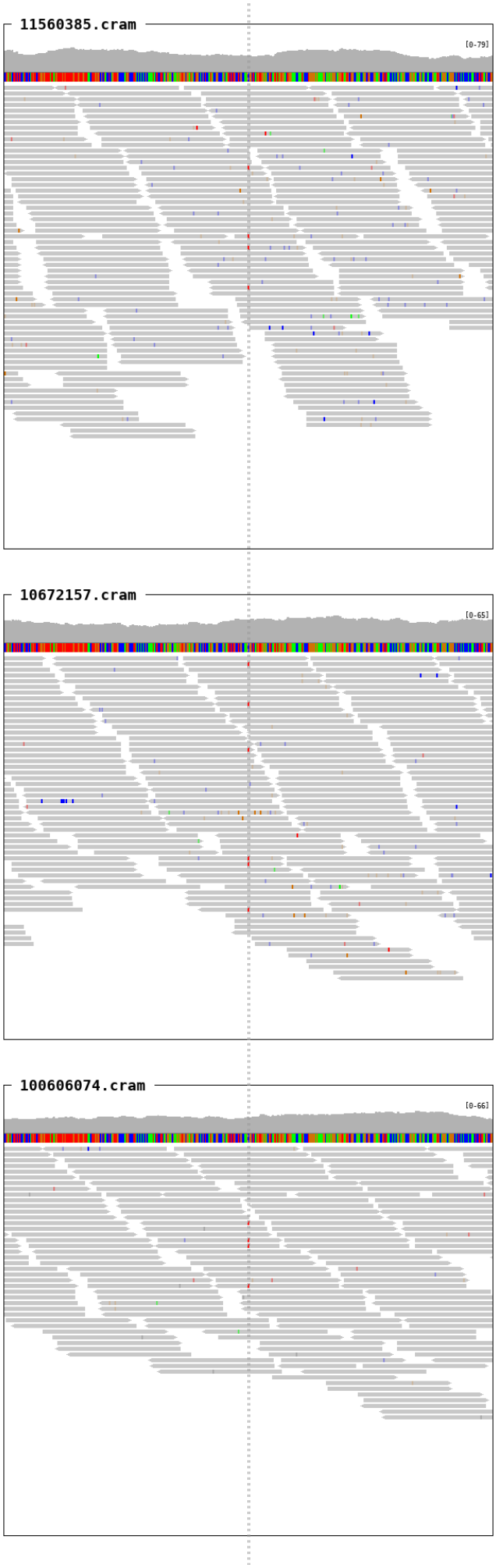
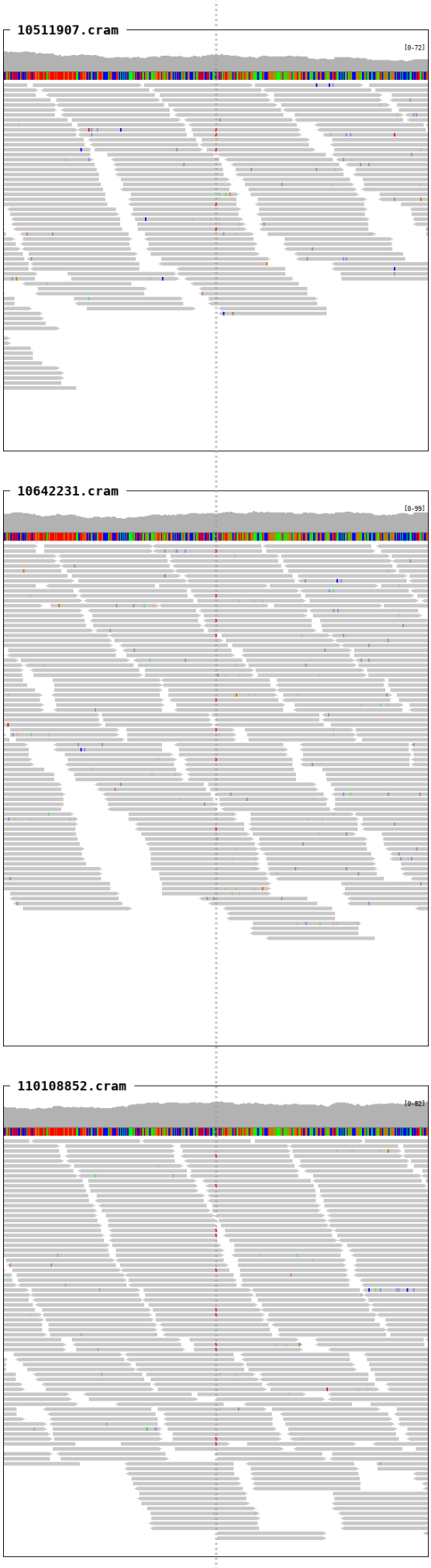
[0-53]
10340657.cram
[0-77]
111102643.cram
[0-67]

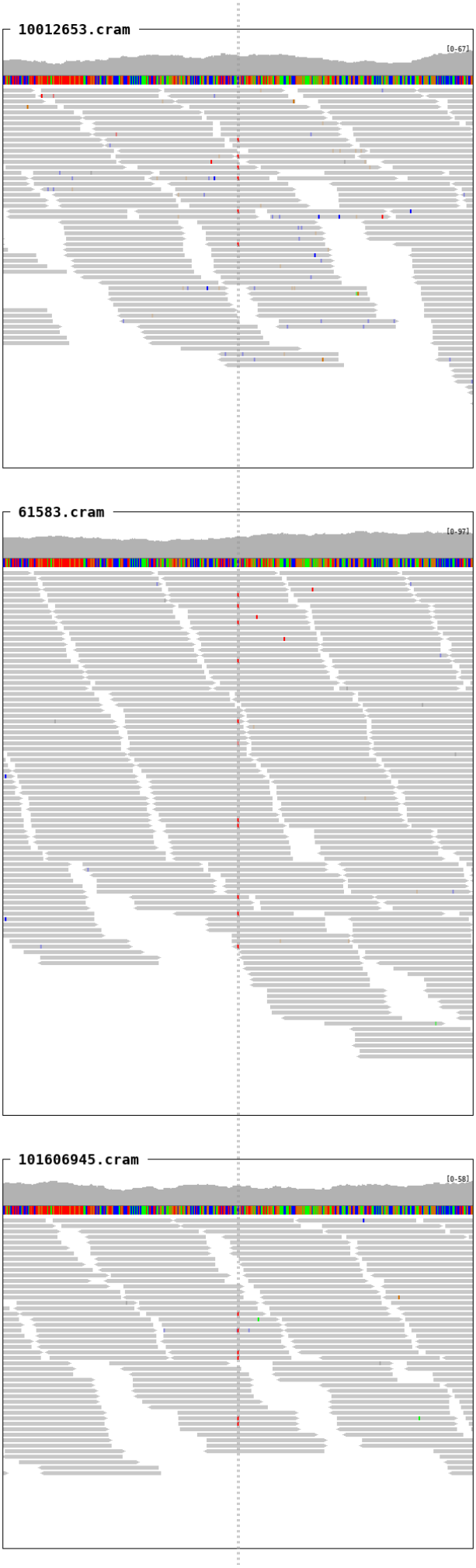

110100971.cram
[0-69]
1501033231.cram
[0-56]
100609394.cram
[0-63]

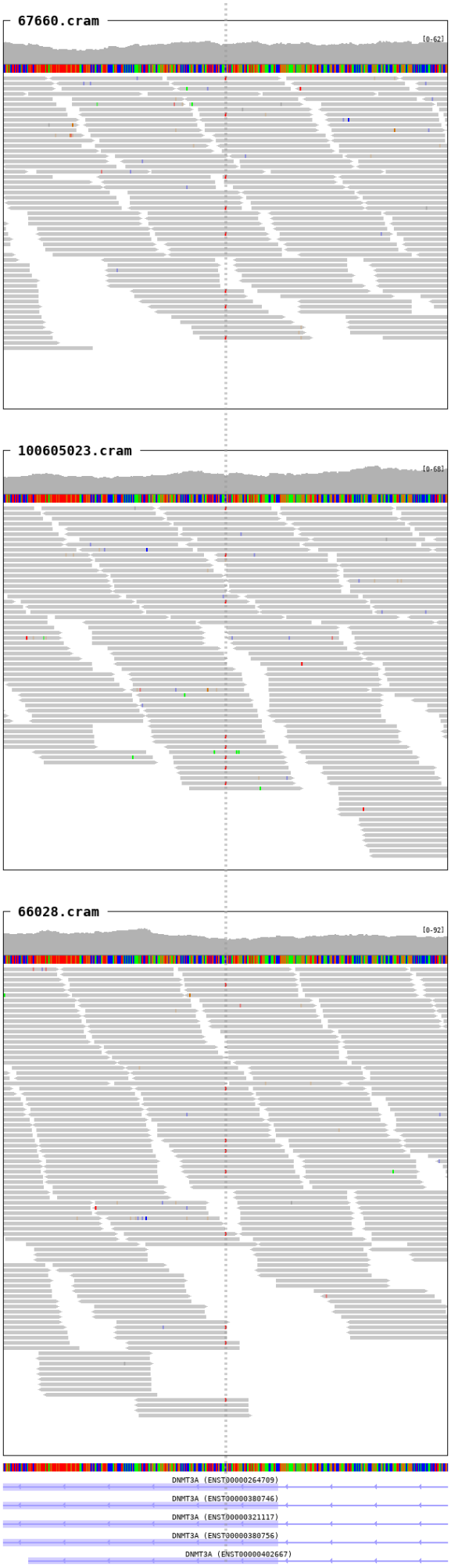

68119.cram
[0-70]
63733.cram
[0-60]
10012318.cram
[0-67]


11330885.cram
[0-63]
112302462.cram
[0-75]
66742.cram
[0-90]


11560385.cram
[0-79]
10672157.cram
[0-65]
100606074.cram
[0-66]

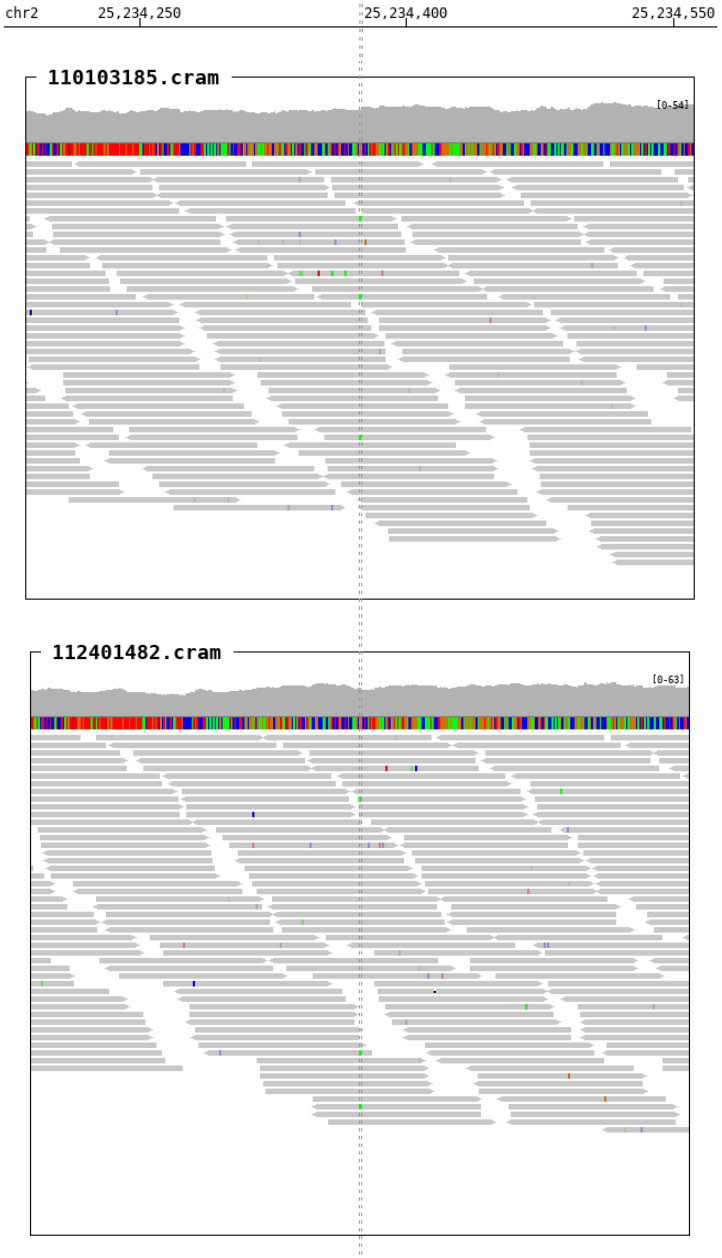

10511907.cram
[0-72]
10642231.cram
[0-99]
110108852.cram
[0-82]

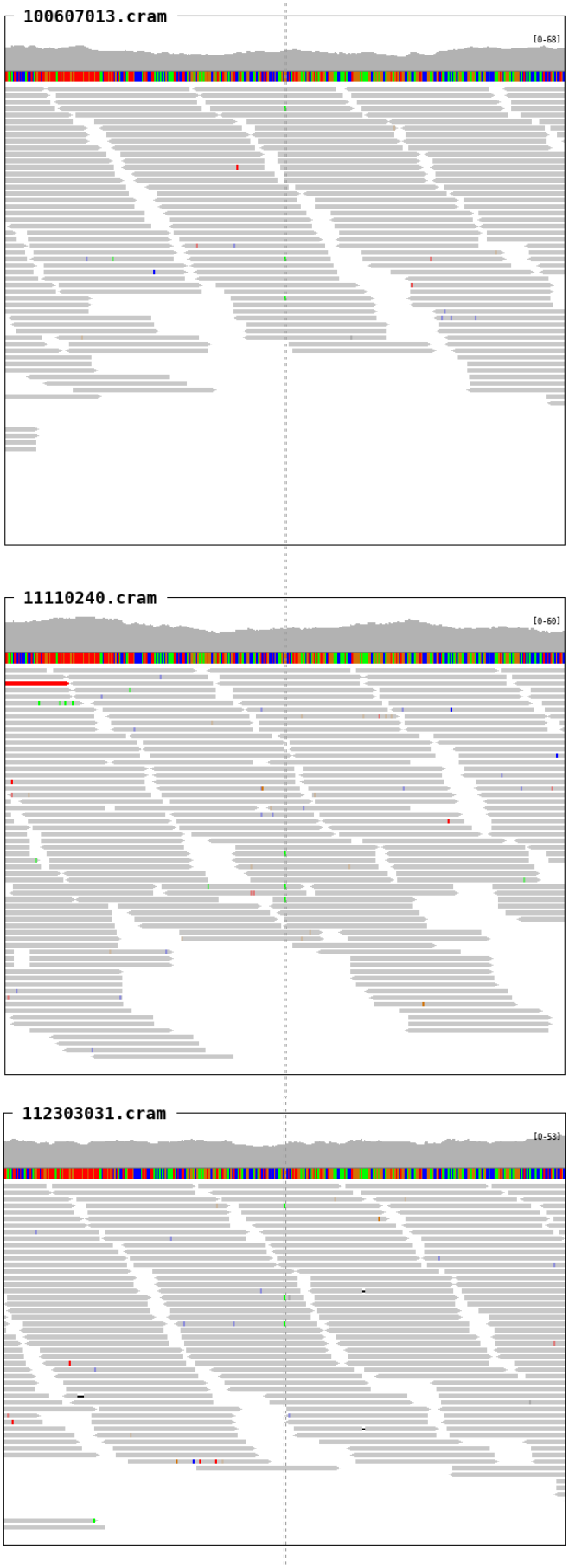

10012653.cram
[0-67]
61583.cram
[0-97]
101606945.cram
[0-58]

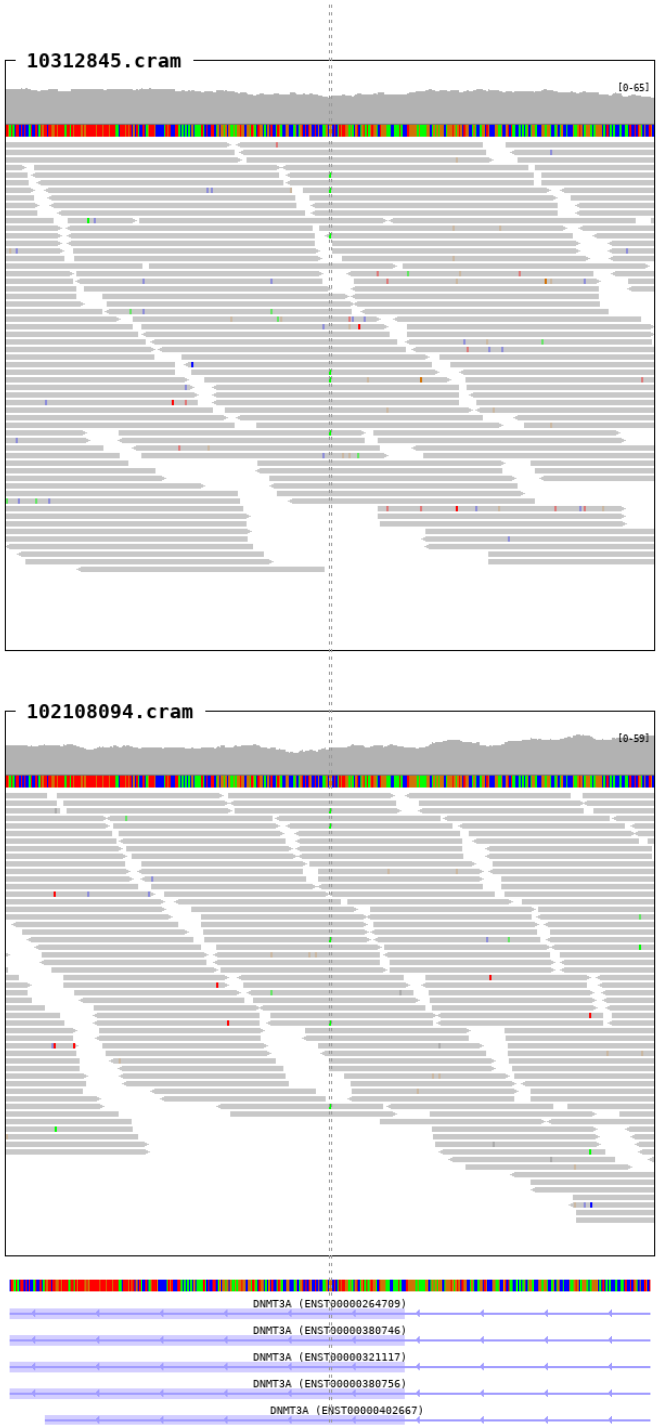

67660.cram
[0-62]
100605023.cram
[0-68]
66028.cram
[0-92]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)

10.5. chr2_25234374_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100607013	chr2_25234374_G/A	36	3	*DNMT3A*	missense_variant
102108094	chr2_25234374_G/A	32	5	*DNMT3A*	missense_variant
10312845	chr2_25234374_G/A	33	6	*DNMT3A*	missense_variant
110103185	chr2_25234374_G/A	36	3	*DNMT3A*	missense_variant
11110240	chr2_25234374_G/A	34	3	*DNMT3A*	missense_variant
112303031	chr2_25234374_G/A	32	3	*DNMT3A*	missense_variant
112401482	chr2_25234374_G/A	35	3	*DNMT3A*	missense_variant

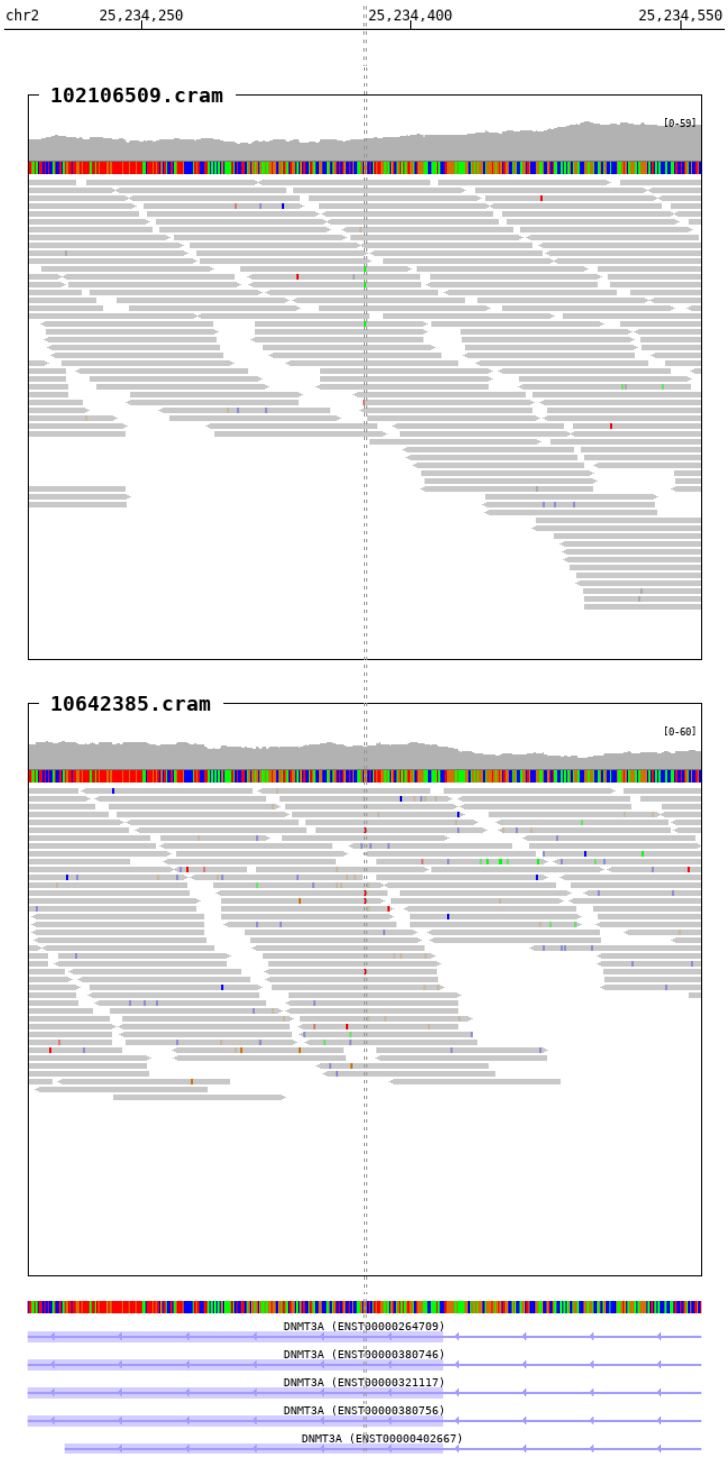



100607013.cram
[0-68]
11110240.cram
[0-60]
112303031.cram
[0-53]


10312845.cram
[0-65]
102108094.cram
[0-59]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)

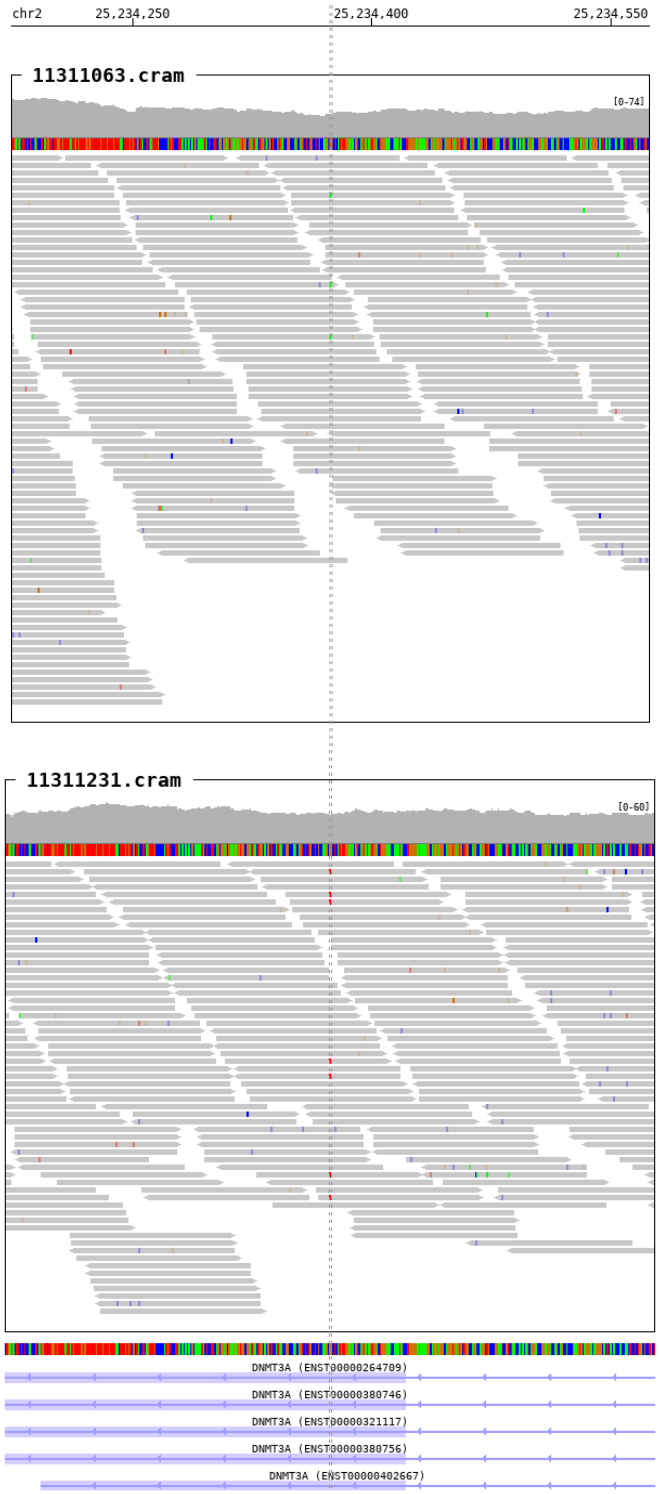
10.6. chr2_25234374_G/A/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102106509	chr2_25234374_G/A/T	28	3	*DNMT3A*	missense_variant
10642385	chr2_25234374_G/A/T	26	4	*DNMT3A*	missense_variant



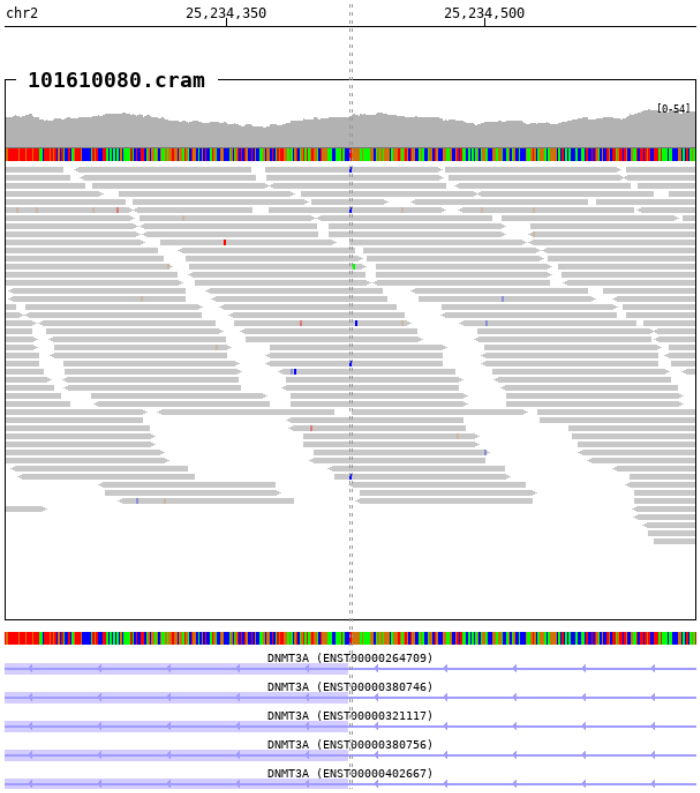
10.7. chr2_25234374_G/T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11311063	chr2_25234374_G/T/A	38	3	*DNMT3A*	missense_variant
11311231	chr2_25234374_G/T/A	32	7	*DNMT3A*	missense_variant



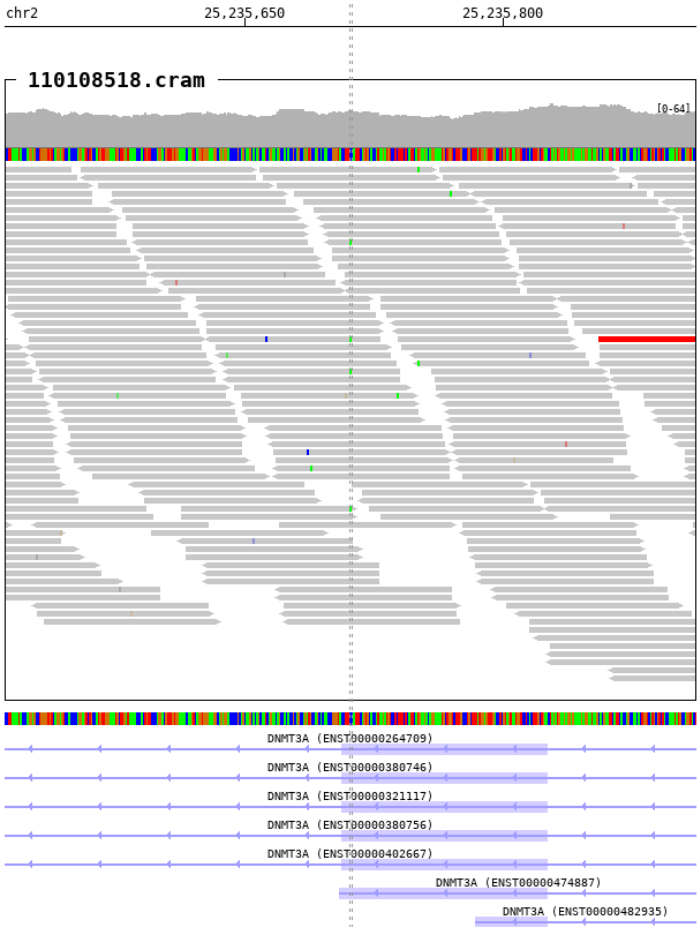
10.8. chr2_25234422_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101610080	chr2_25234422_T/C	32	4	*DNMT3A*	splice_acceptor_variant



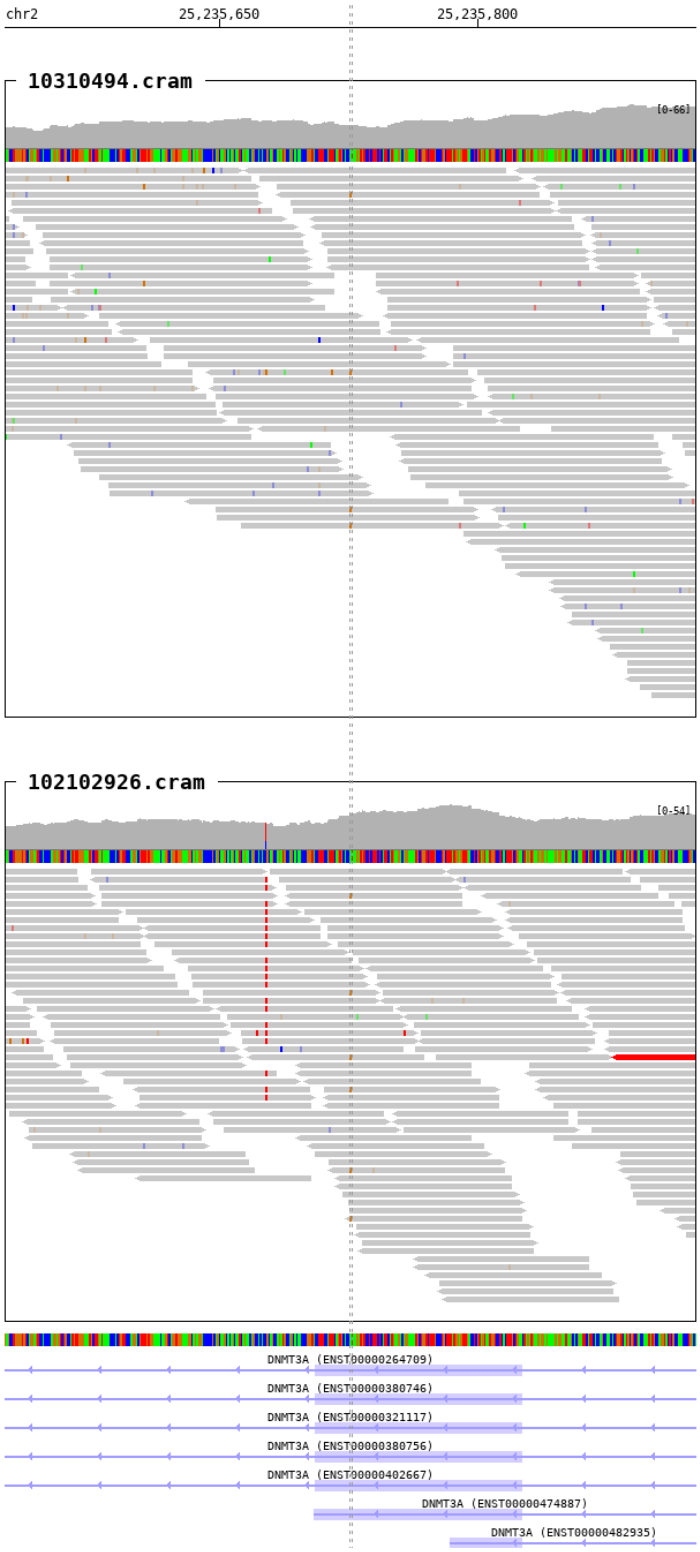
10.9. chr2_25235711_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110108518	chr2_25235711_C/A	47	4	*DNMT3A*	stop_gained



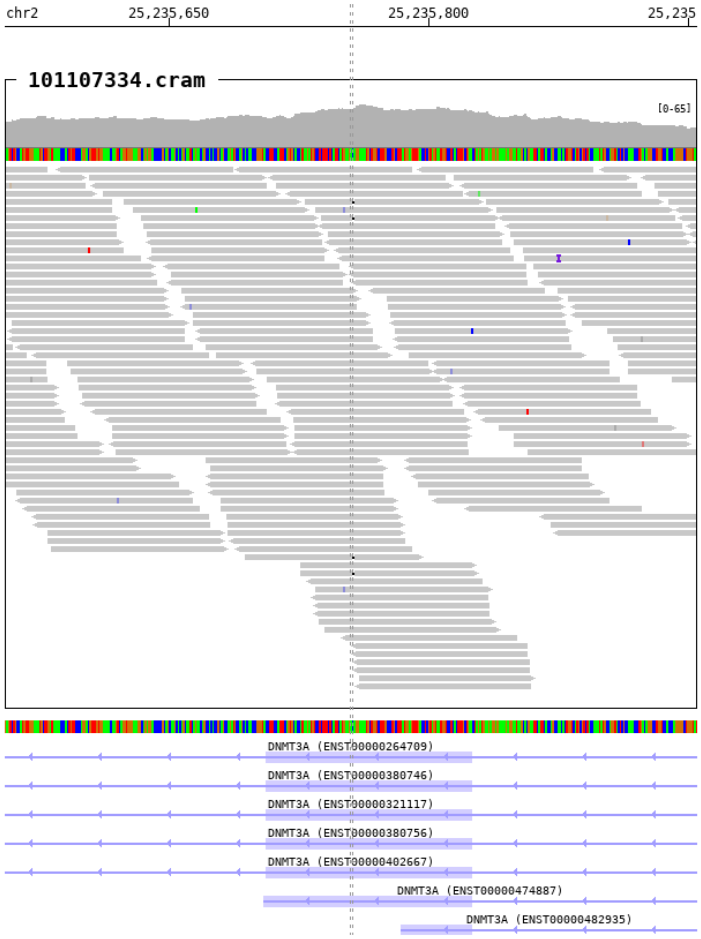
10.10. chr2_25235726_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102102926	chr2_25235726_A/G	37	6	*DNMT3A*	missense_variant
10310494	chr2_25235726_A/G	29	4	*DNMT3A*	missense_variant



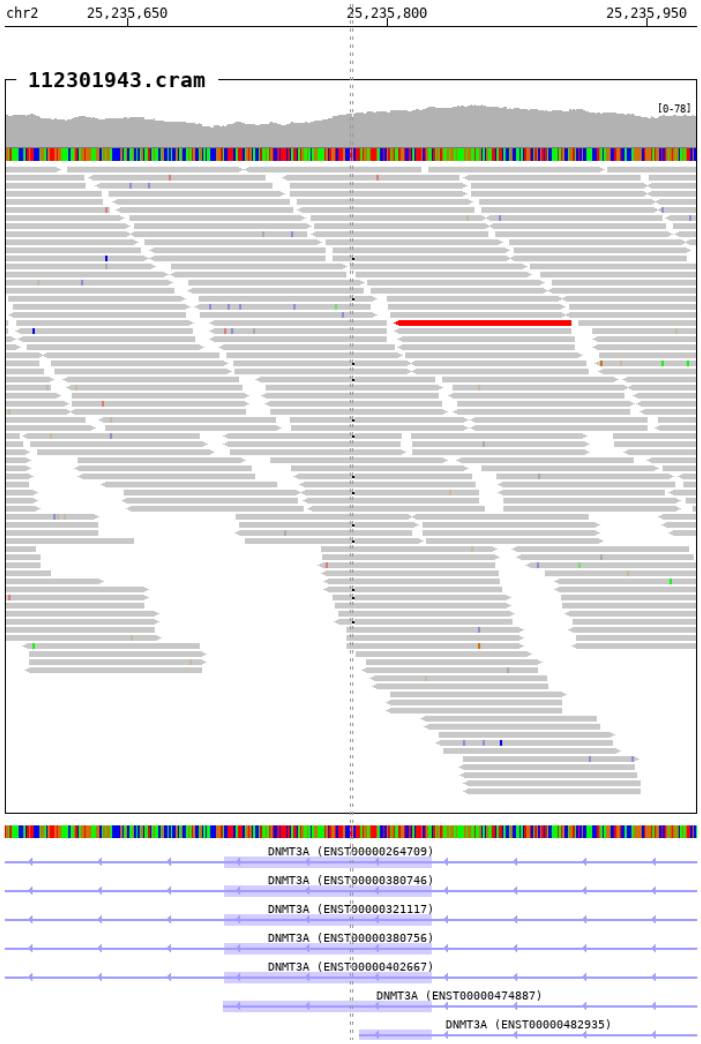
10.11. chr2_25235755_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101107334	chr2_25235755_C/-	43	4	*DNMT3A*	frameshift_variant



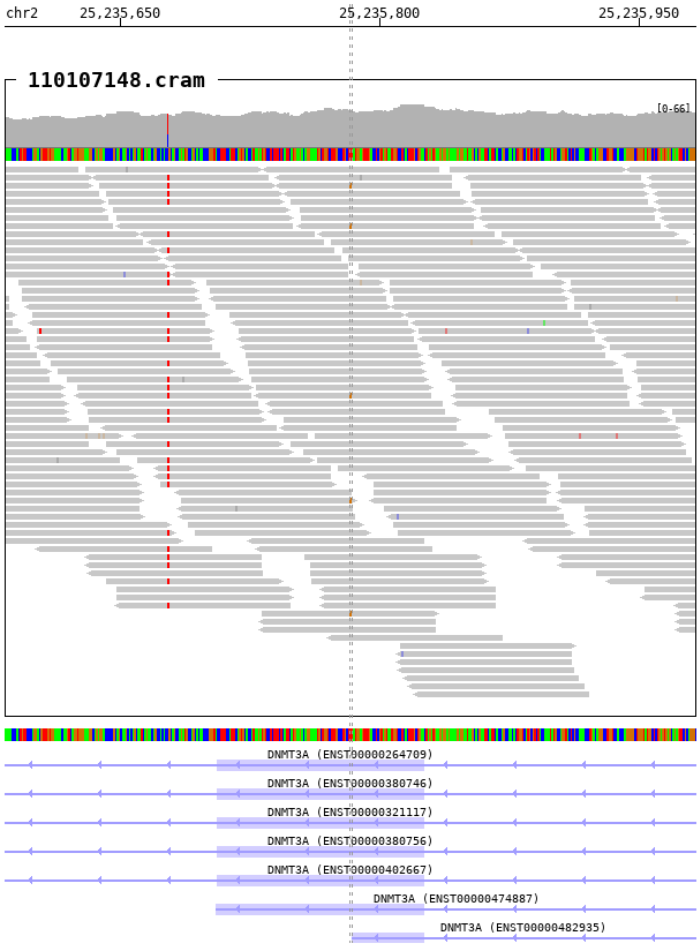
10.12. chr2_25235779_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301943	chr2_25235779_G/-	44	12	*DNMT3A*	frameshift_variant



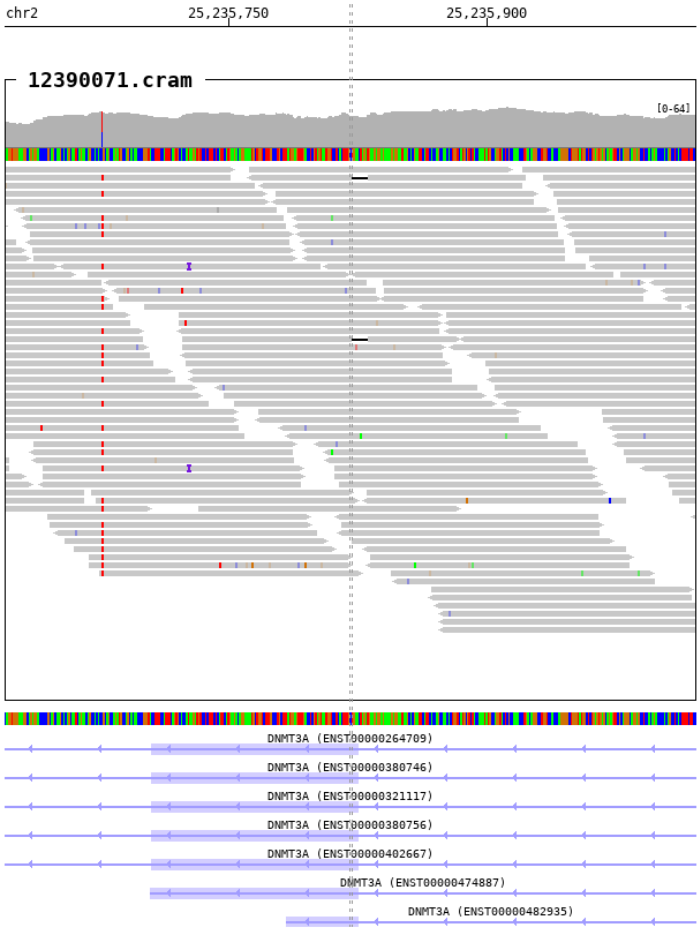
10.13. chr2_25235783_T/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110107148	chr2_25235783_T/G	48	5	*DNMT3A*	missense_variant



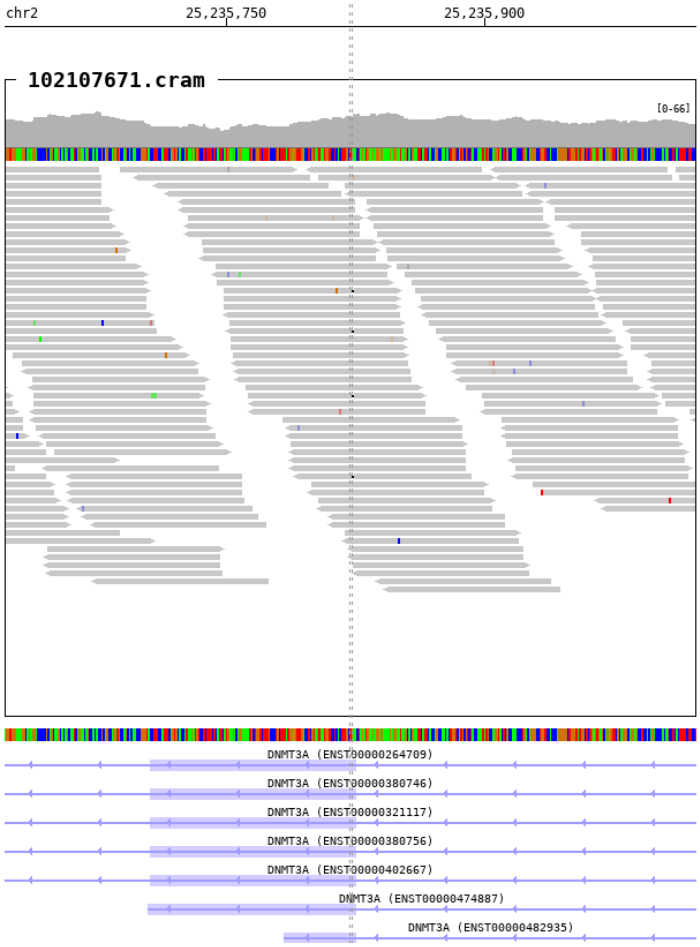
10.14. chr2_25235821_TGAACTAGA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12390071	chr2_25235821_TGAACTAGA/-	42	3	*DNMT3A*	splice_acceptor_variant



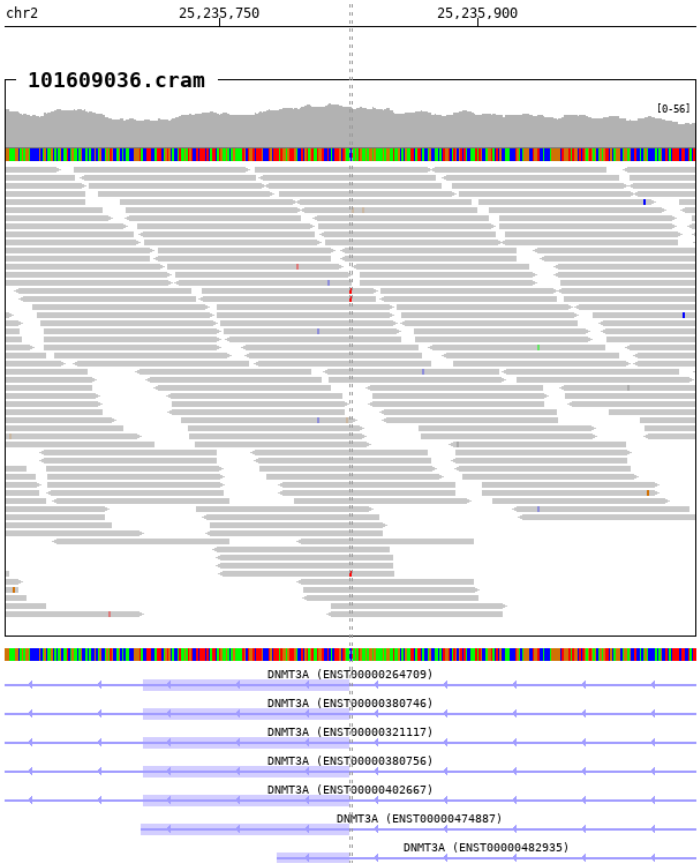
10.15. chr2_25235822_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102107671	chr2_25235822_G/-	40	4	*DNMT3A*	frameshift_variant



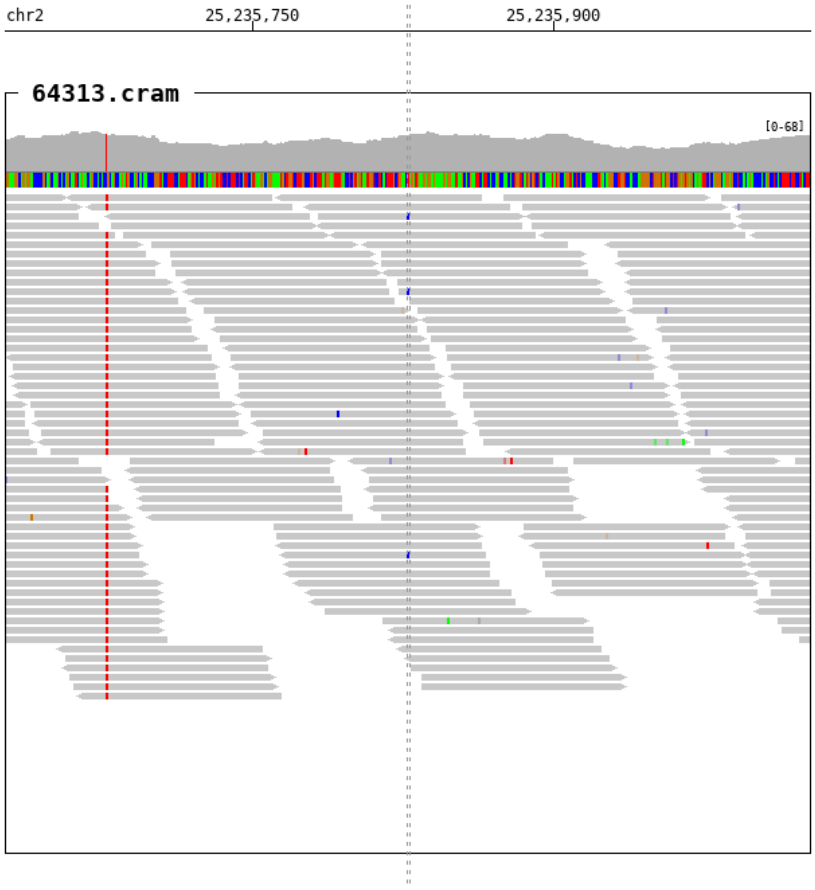
10.16. chr2_25235826_C/T

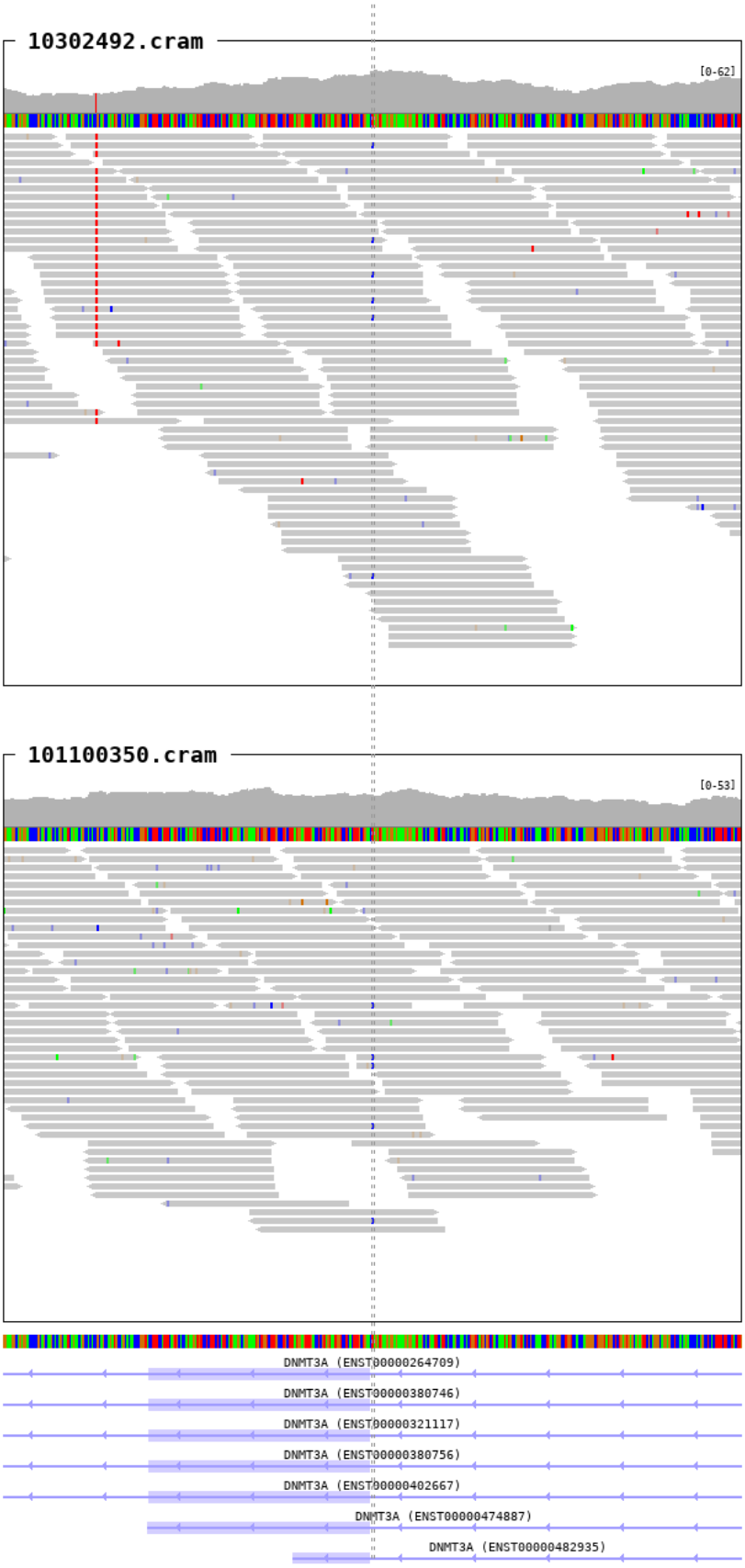
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101609036	chr2_25235826_C/T	46	3	*DNMT3A*	splice_acceptor_variant



10.17. chr2_25235827_T/C

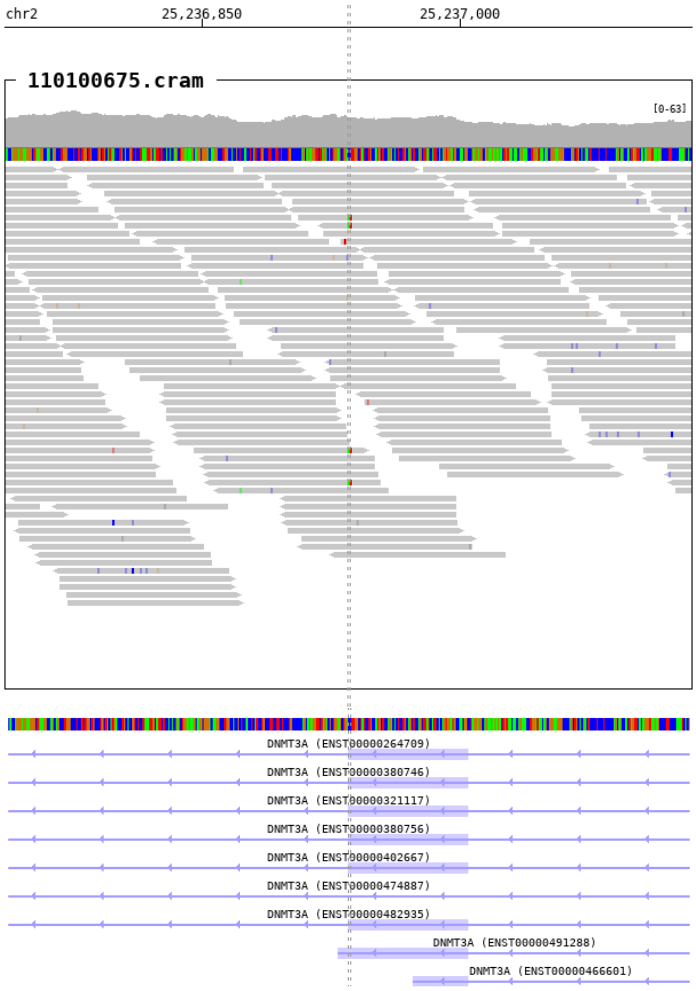
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101100350	chr2_25235827_T/C	30	4	*DNMT3A*	splice_acceptor_variant
10302492	chr2_25235827_T/C	47	6	*DNMT3A*	splice_acceptor_variant
64313	chr2_25235827_T/C	41	3	*DNMT3A*	splice_acceptor_variant




10302492.cram
[0-62]
101100350.cram
[0-53]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474887)
DNMT3A (ENST00000482935)

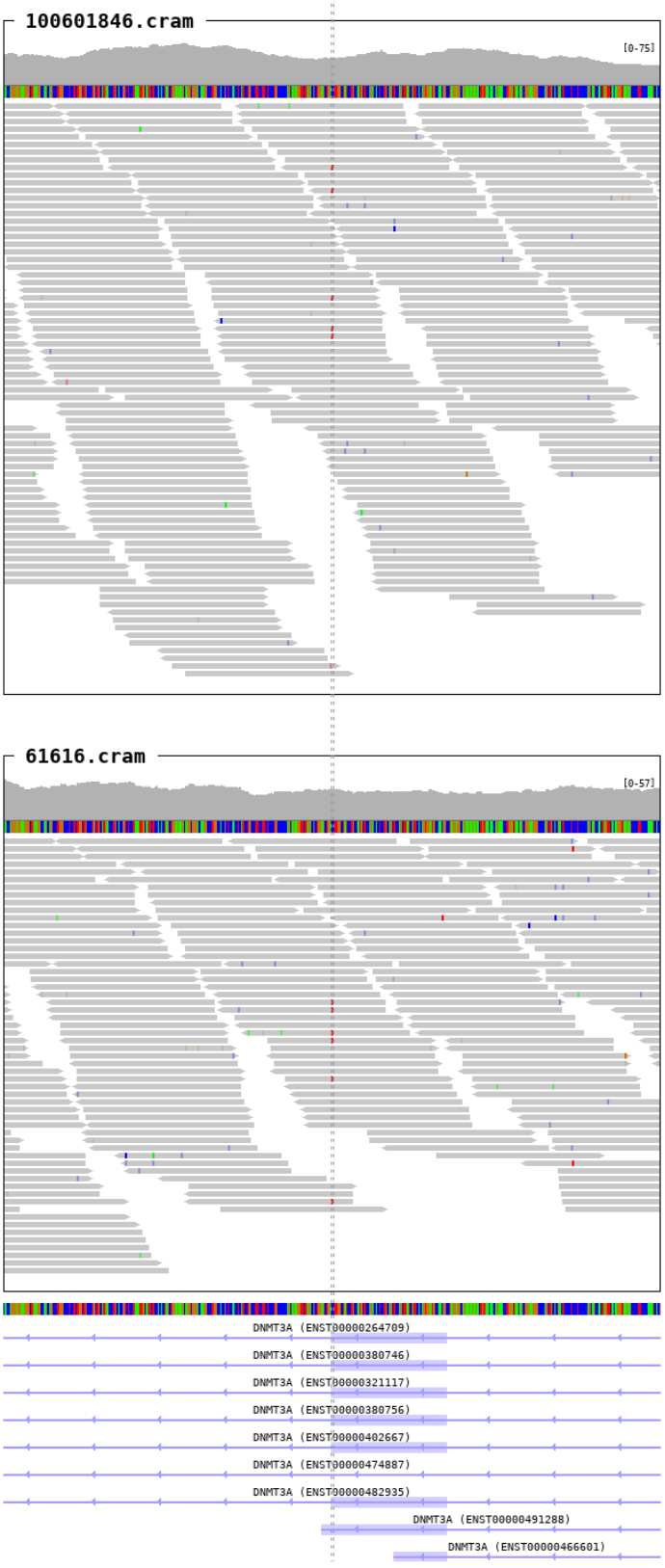
10.18. chr2_25236935_CC/AT

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110100675	chr2_25236935_CC/AT	37	4	*DNMT3A*	splice_donor_variant



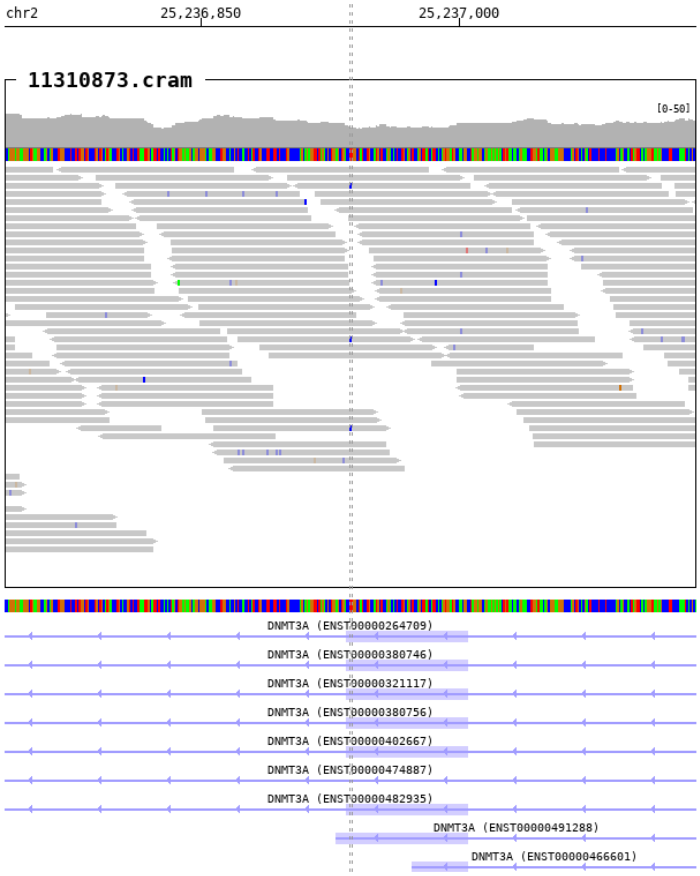
10.19. chr2_25236935_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100601846	chr2_25236935_C/T	43	5	*DNMT3A*	splice_donor_variant
61616	chr2_25236935_C/T	34	6	*DNMT3A*	splice_donor_variant



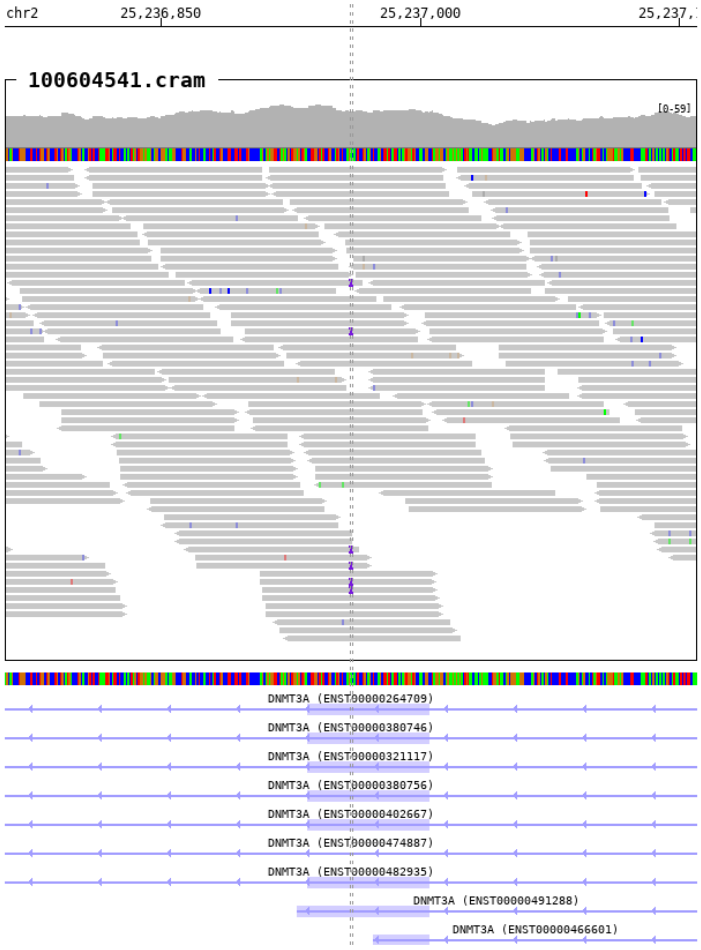
10.20. chr2_25236937_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11310873	chr2_25236937_T/C	20	3	*DNMT3A*	missense_variant



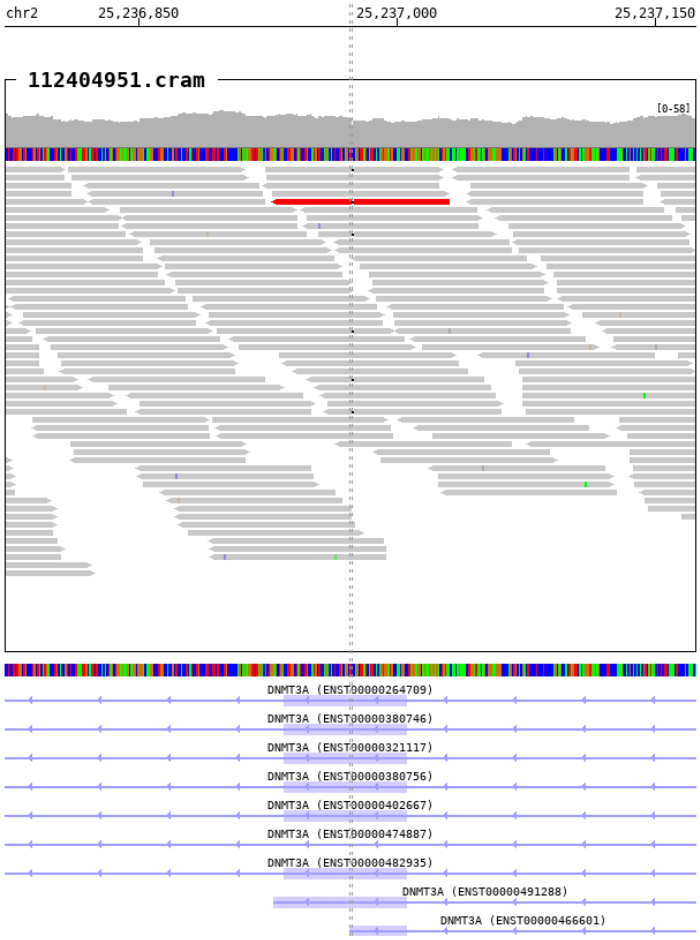
10.21. chr2_25236960_-/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100604541	chr2_25236960_-/A	39	6	*DNMT3A*	frameshift_variant



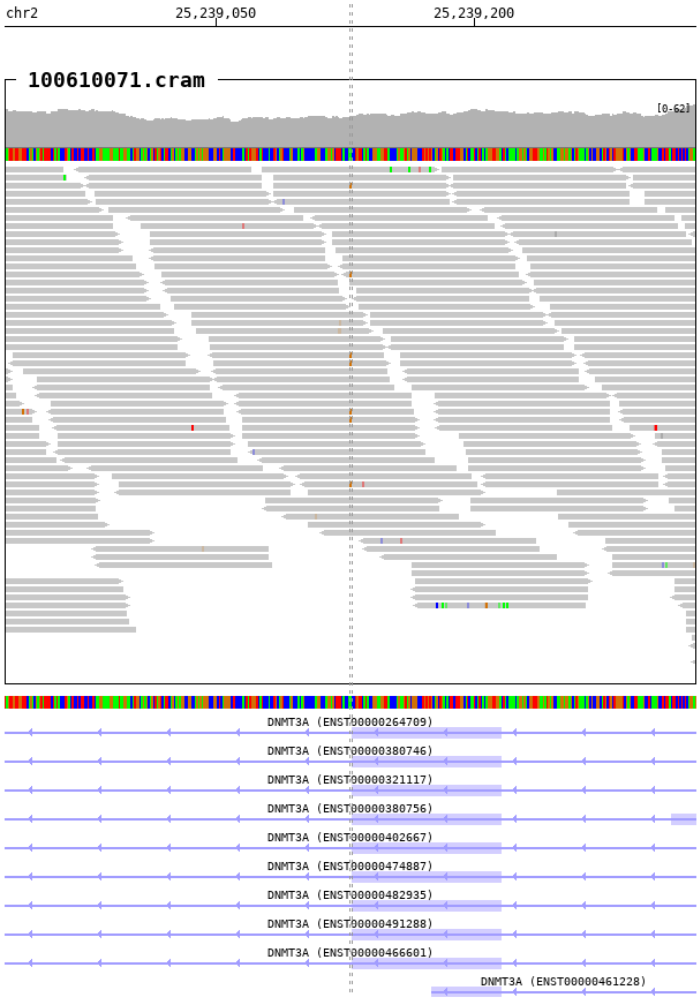
10.22. chr2_25236973_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112404951	chr2_25236973_C/-	29	6	*DNMT3A*	frameshift_variant



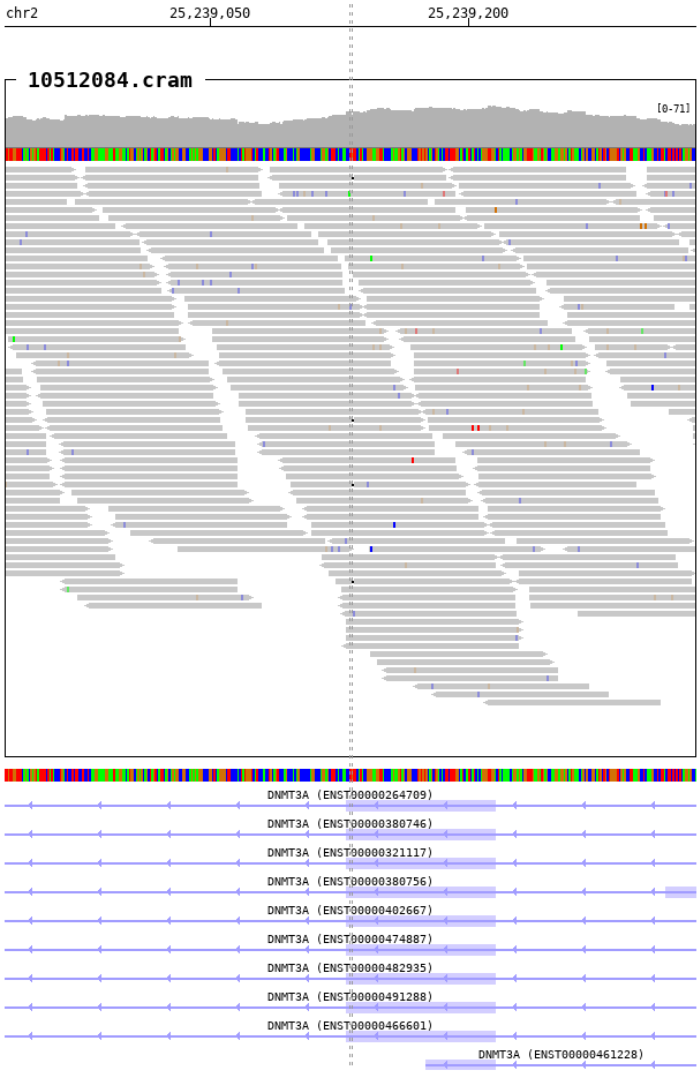
10.23. chr2_25239128_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100610071	chr2_25239128_A/G	32	7	*DNMT3A*	splice_donor_variant



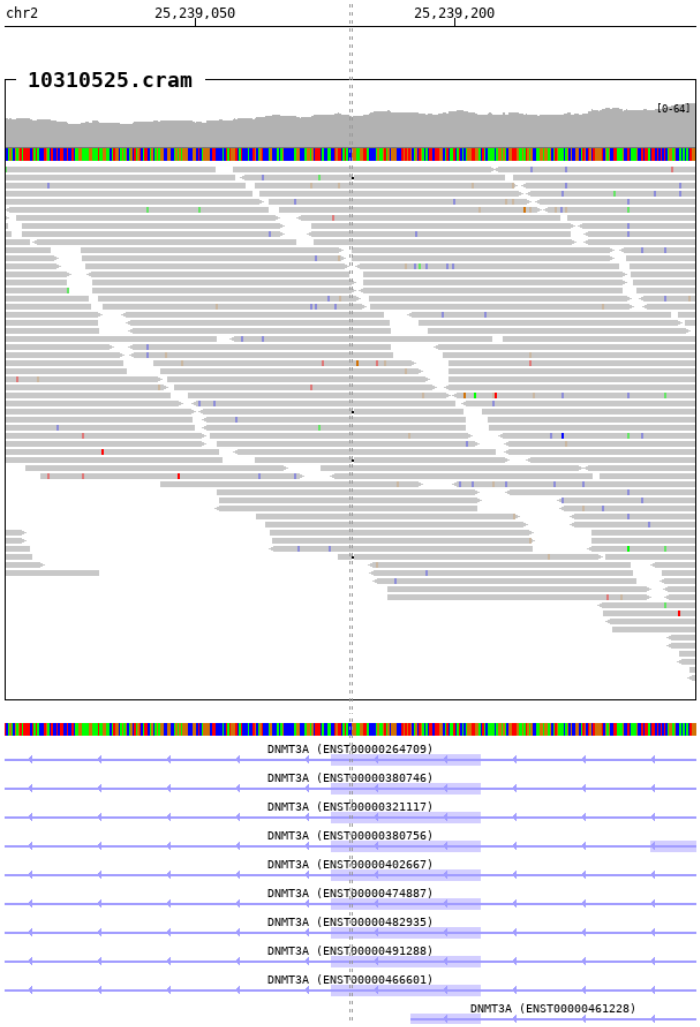
10.24. chr2_25239131_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10512084	chr2_25239131_G/-	51	4	*DNMT3A*	frameshift_variant



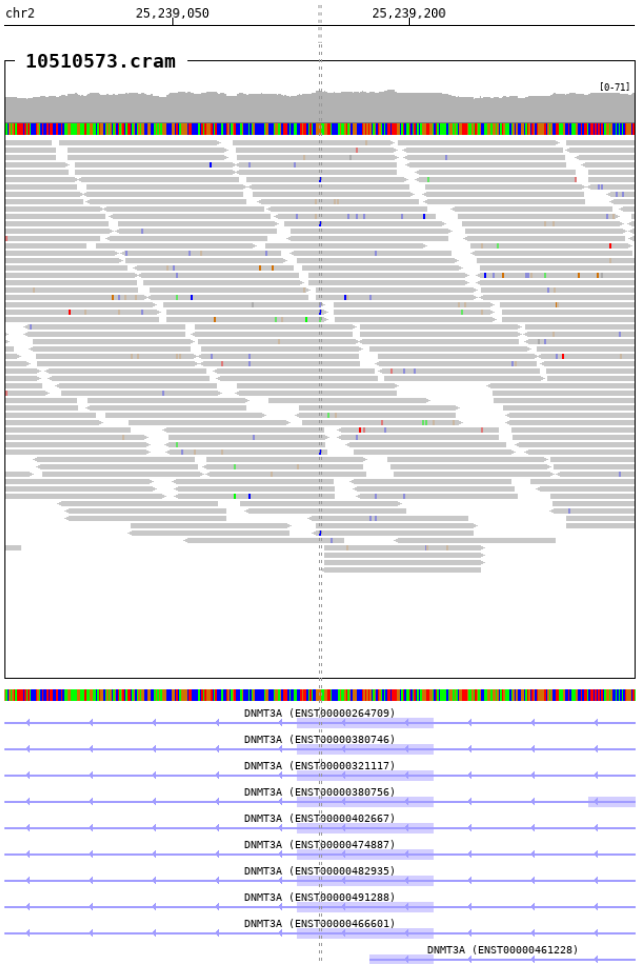
10.25. chr2_25239140_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10310525	chr2_25239140_G/-	40	4	*DNMT3A*	frameshift_variant



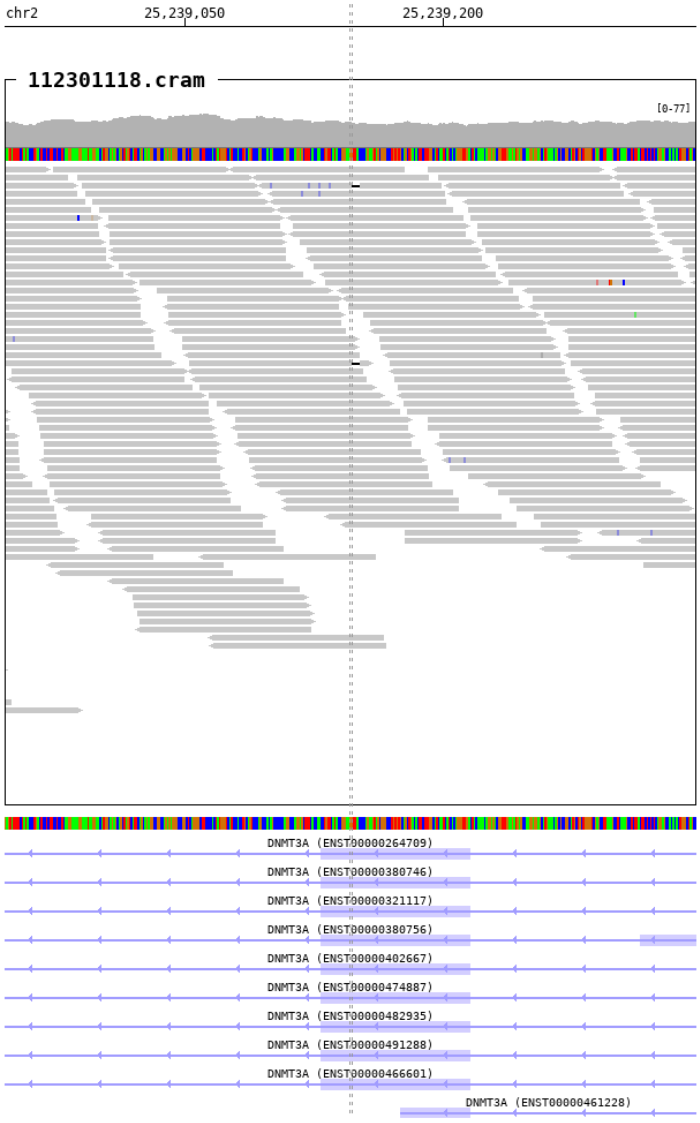
10.26. chr2_25239143_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
61668	chr2_25239143_G/A	38	4	*DNMT3A*	missense_variant



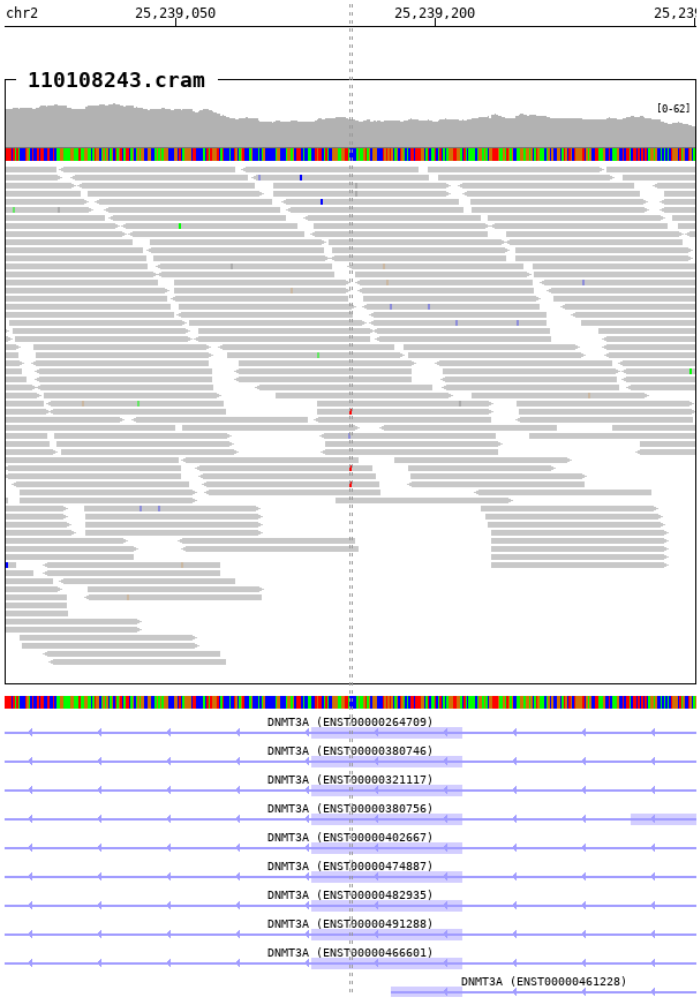
10.27. chr2_25239146_GTTA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301118	chr2_25239146_GTTA/-	43	2	*DNMT3A*	frameshift_variant



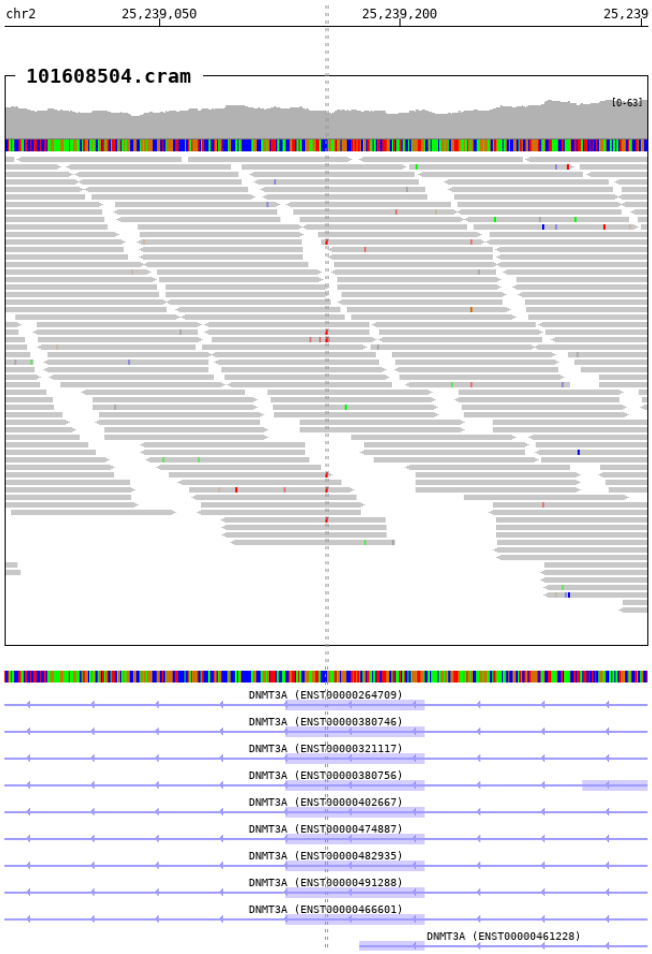
10.28. chr2_25239151_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110108243	chr2_25239151_C/T	33	3	*DNMT3A*	missense_variant



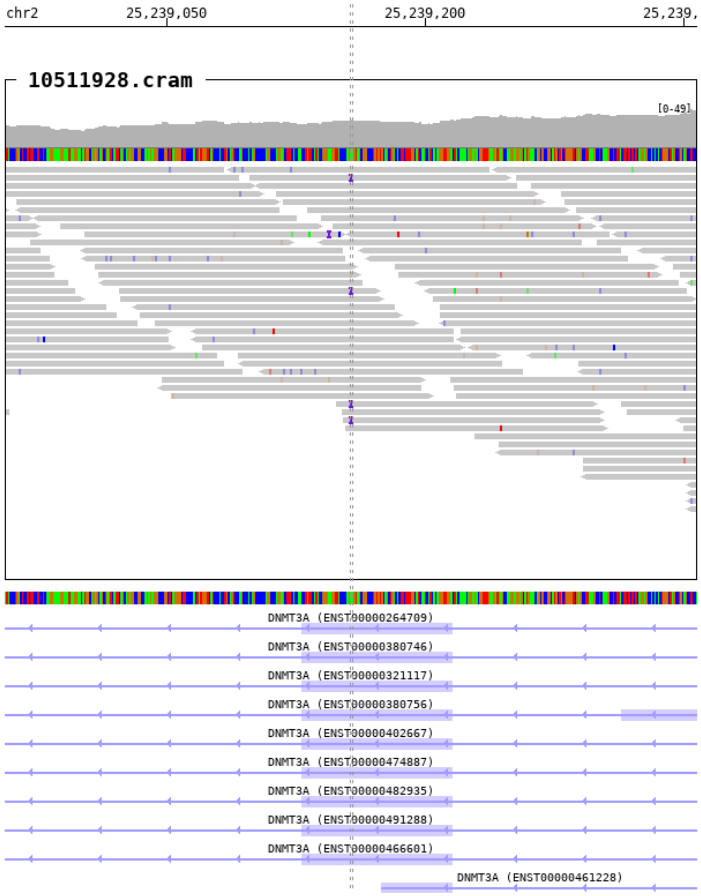
10.29. chr2_25239154_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101608504	chr2_25239154_C/T	31	5	*DNMT3A*	stop_gained



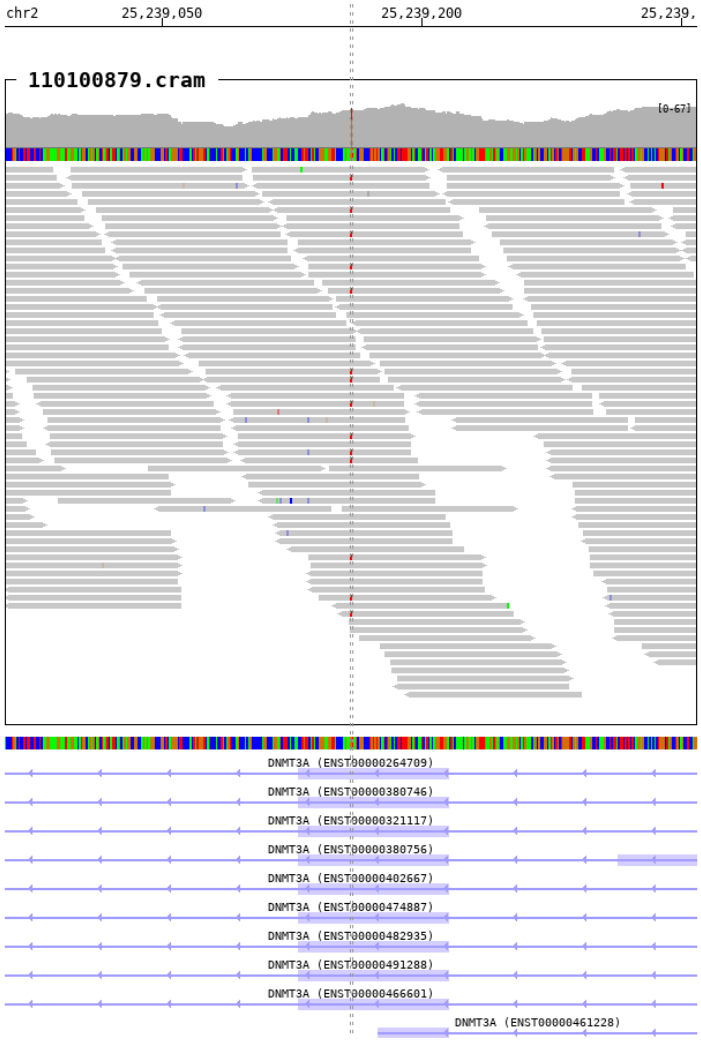
10.30. chr2_25239157_-/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10511928	chr2_25239157_-/T	25	4	*DNMT3A*	frameshift_variant



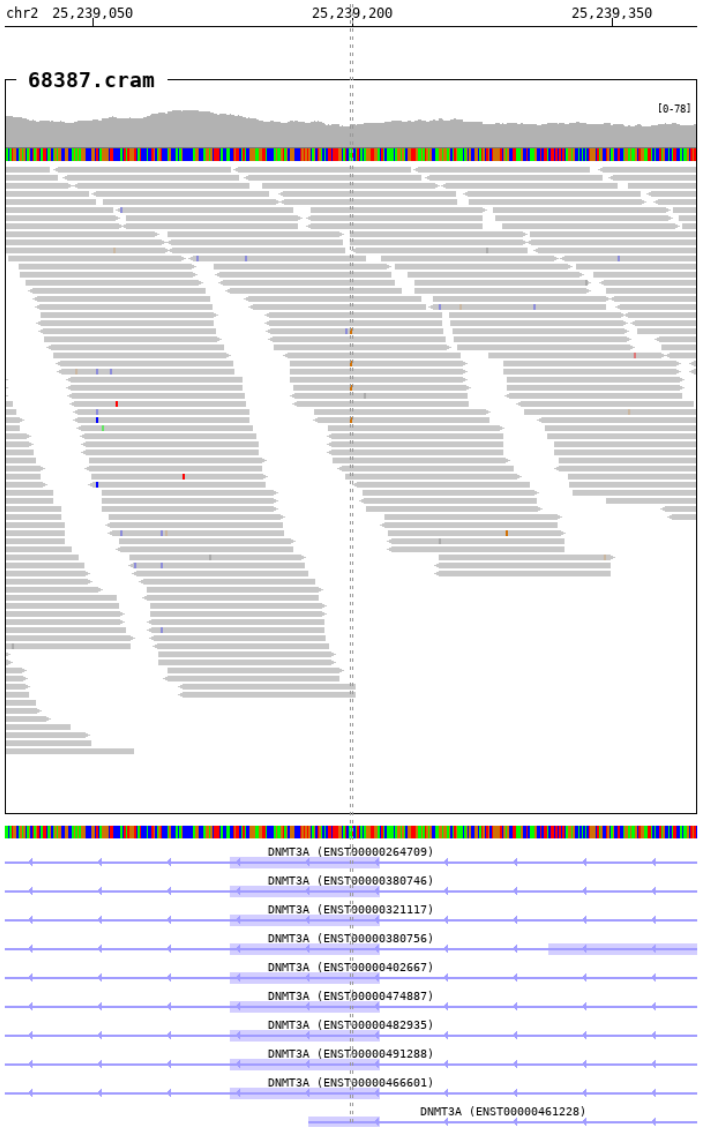
10.31. chr2_25239159_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110100879	chr2_25239159_G/T	41	14	*DNMT3A*	stop_gained



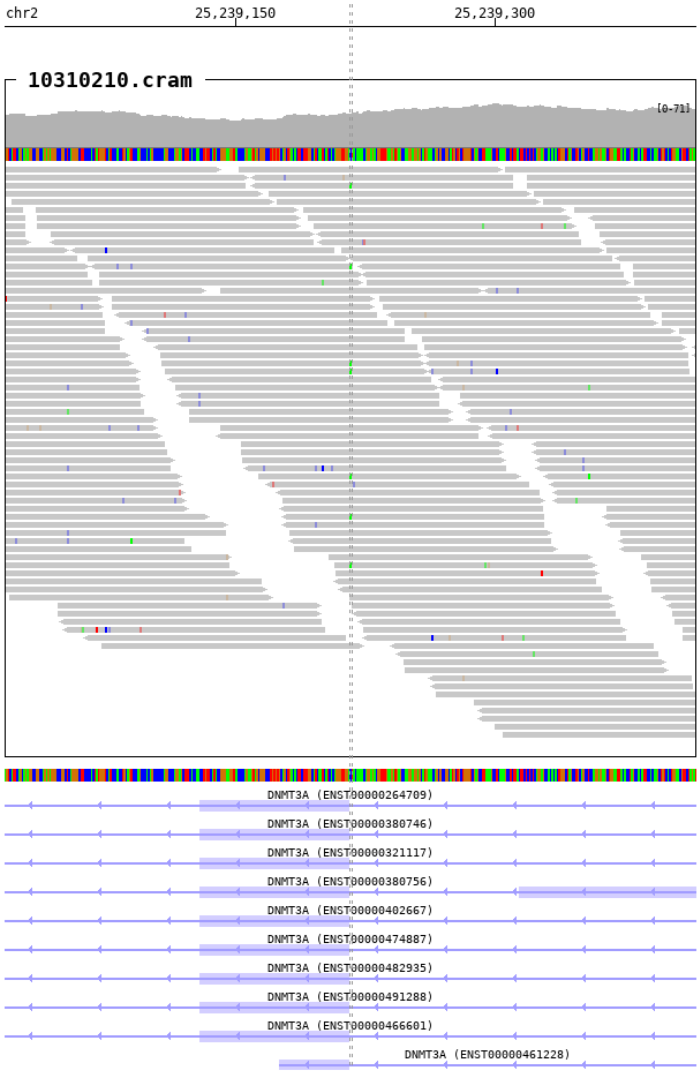
10.32. chr2_25239199_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
68387	chr2_25239199_A/G	36	4	*DNMT3A*	missense_variant



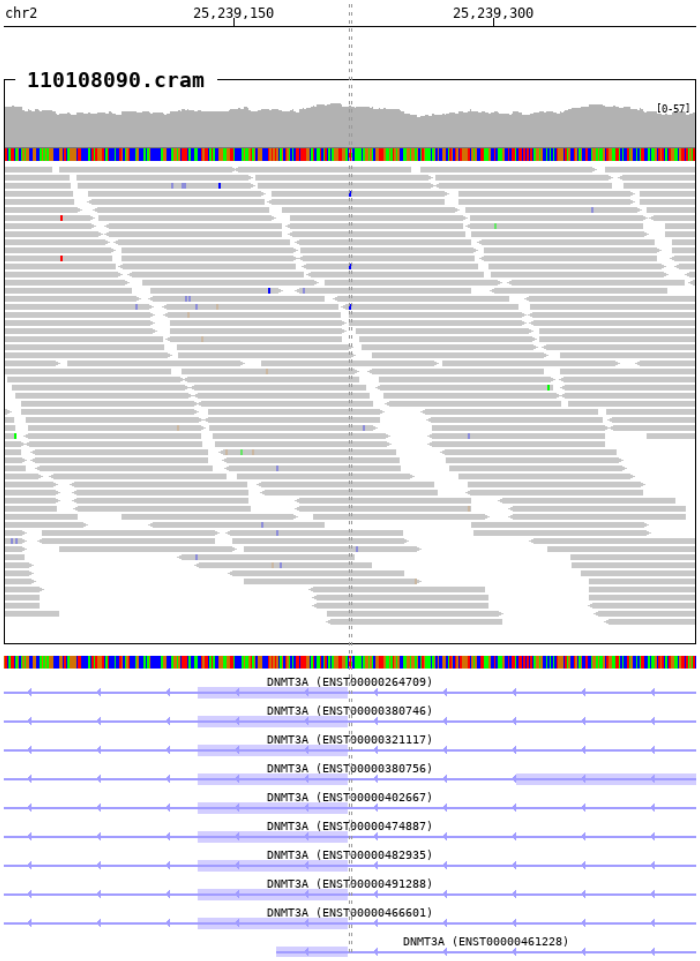
10.33. chr2_25239216_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10310210	chr2_25239216_C/A	44	7	*DNMT3A*	splice_acceptor_variant



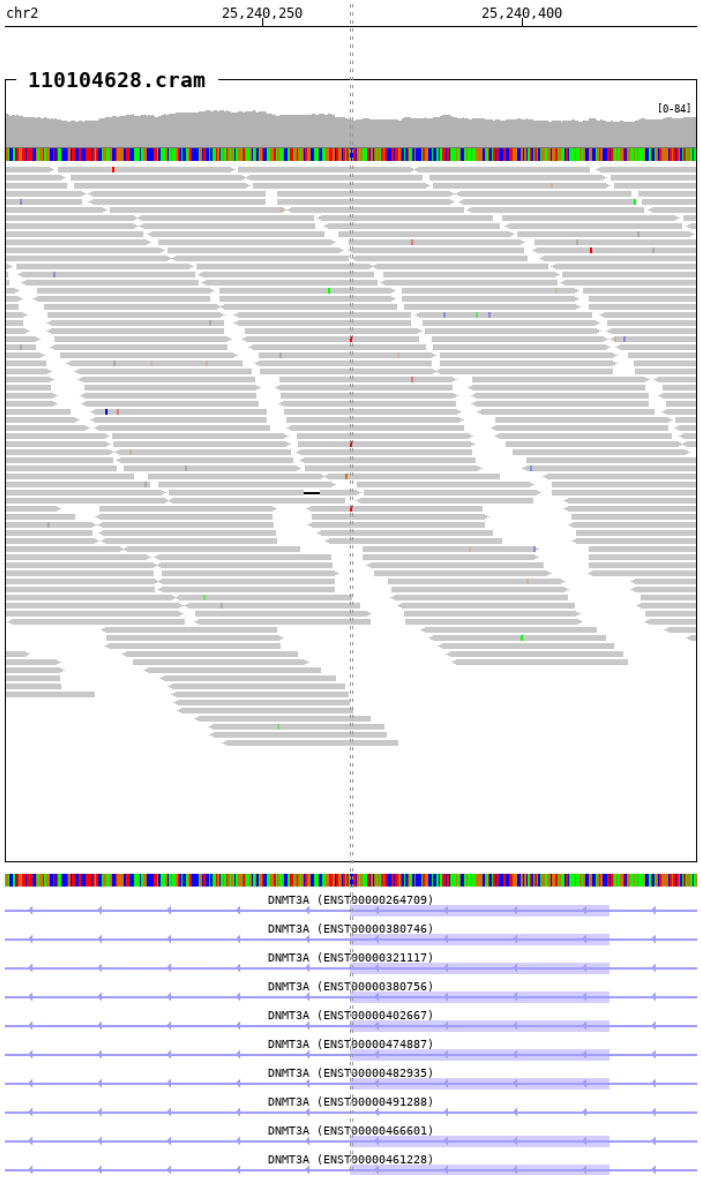
10.34. chr2_25239217_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110108090	chr2_25239217_T/C	46	3	*DNMT3A*	splice_acceptor_variant



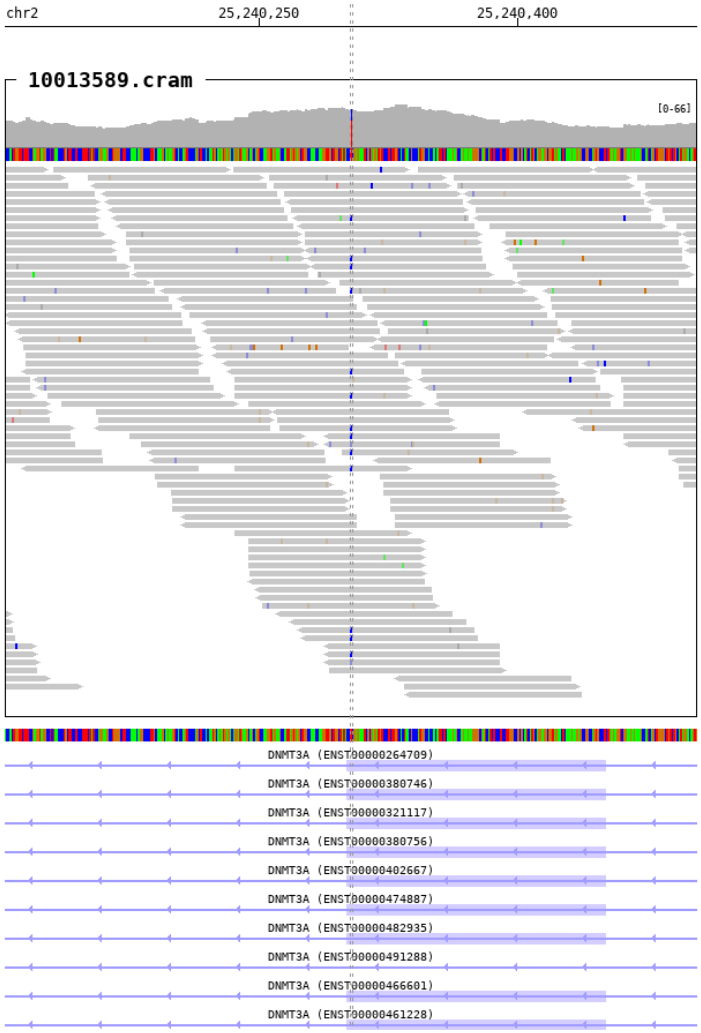
10.35. chr2_25240301_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110104628	chr2_25240301_C/T	45	3	*DNMT3A*	splice_donor_variant



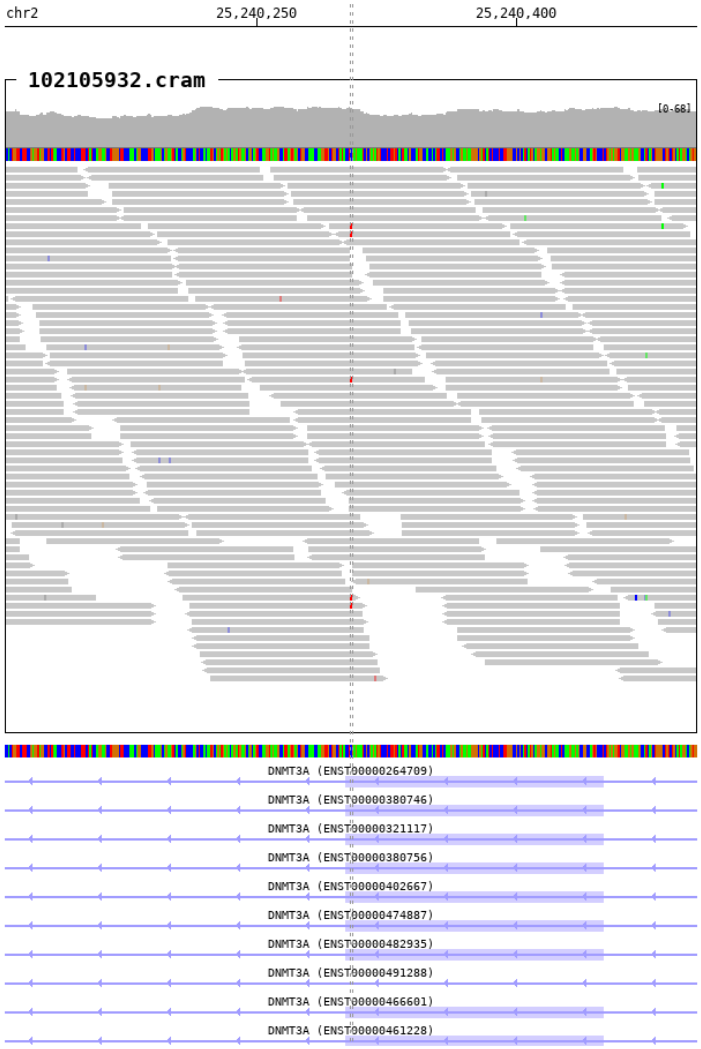
10.36. chr2_25240303_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10013589	chr2_25240303_T/C	39	14	*DNMT3A*	missense_variant



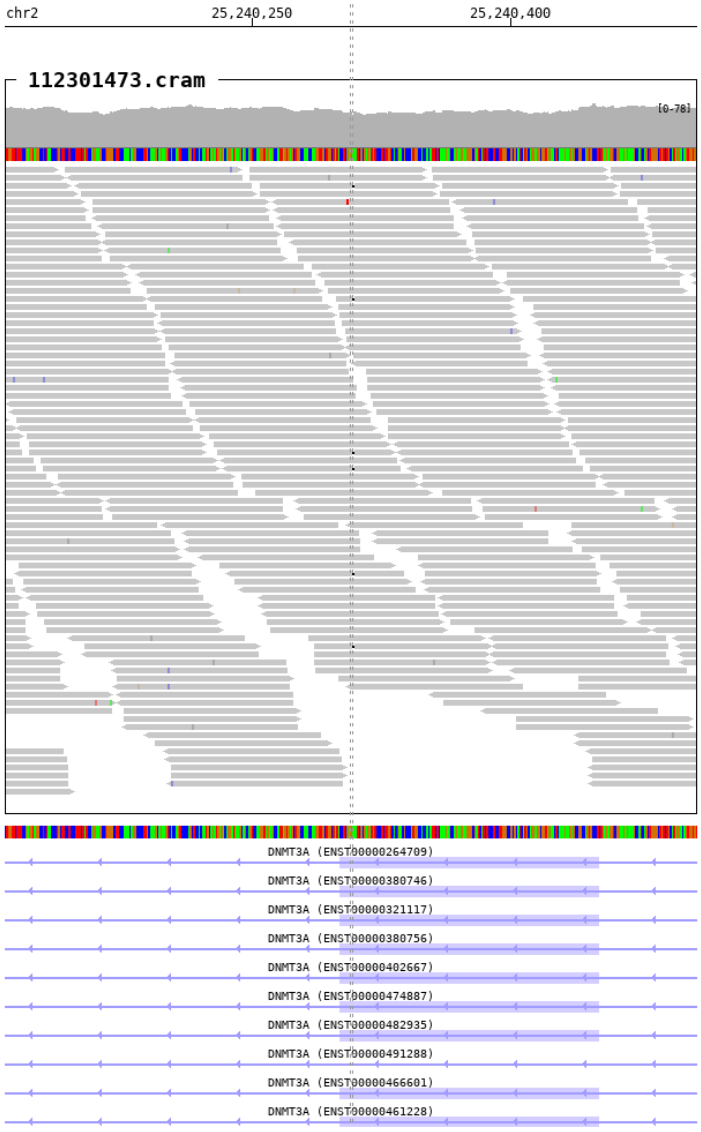
10.37. chr2_25240304_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102105932	chr2_25240304_C/T	53	5	*DNMT3A*	missense_variant



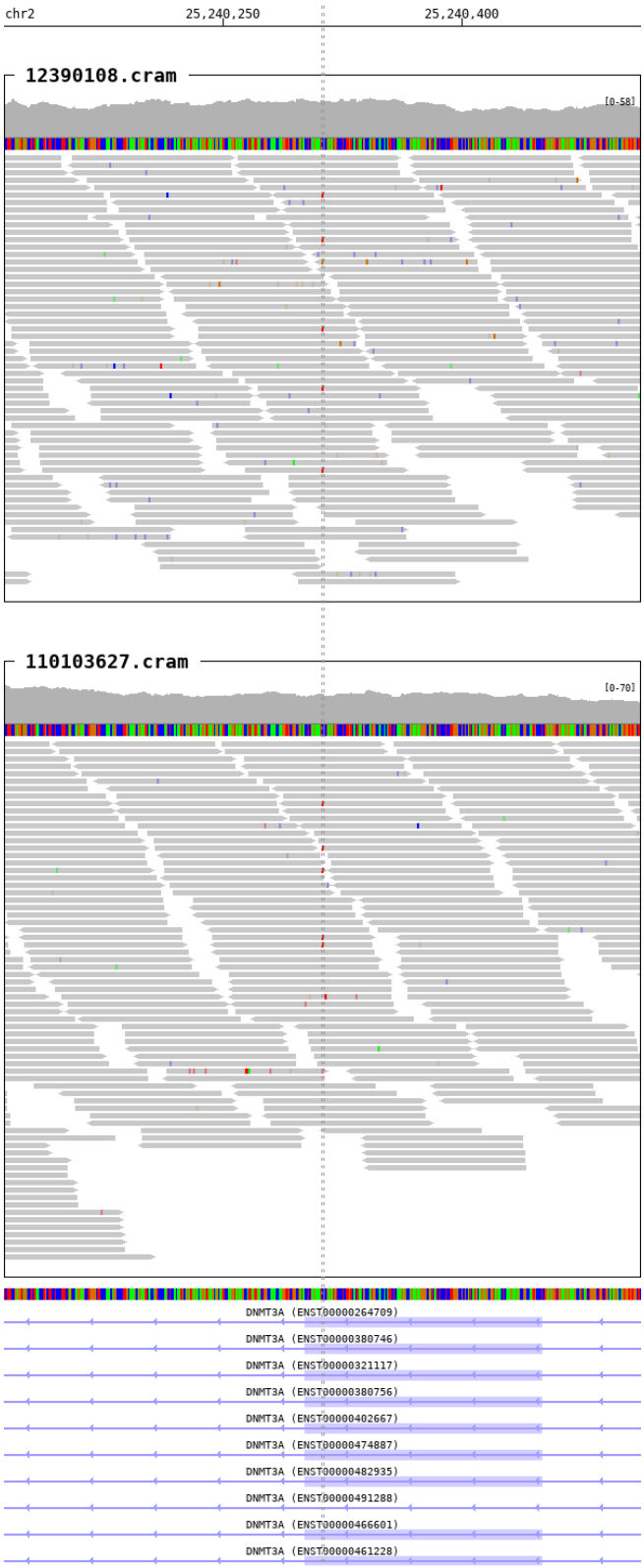
10.38. chr2_25240307_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301473	chr2_25240307_A/-	53	7	*DNMT3A*	frameshift_variant



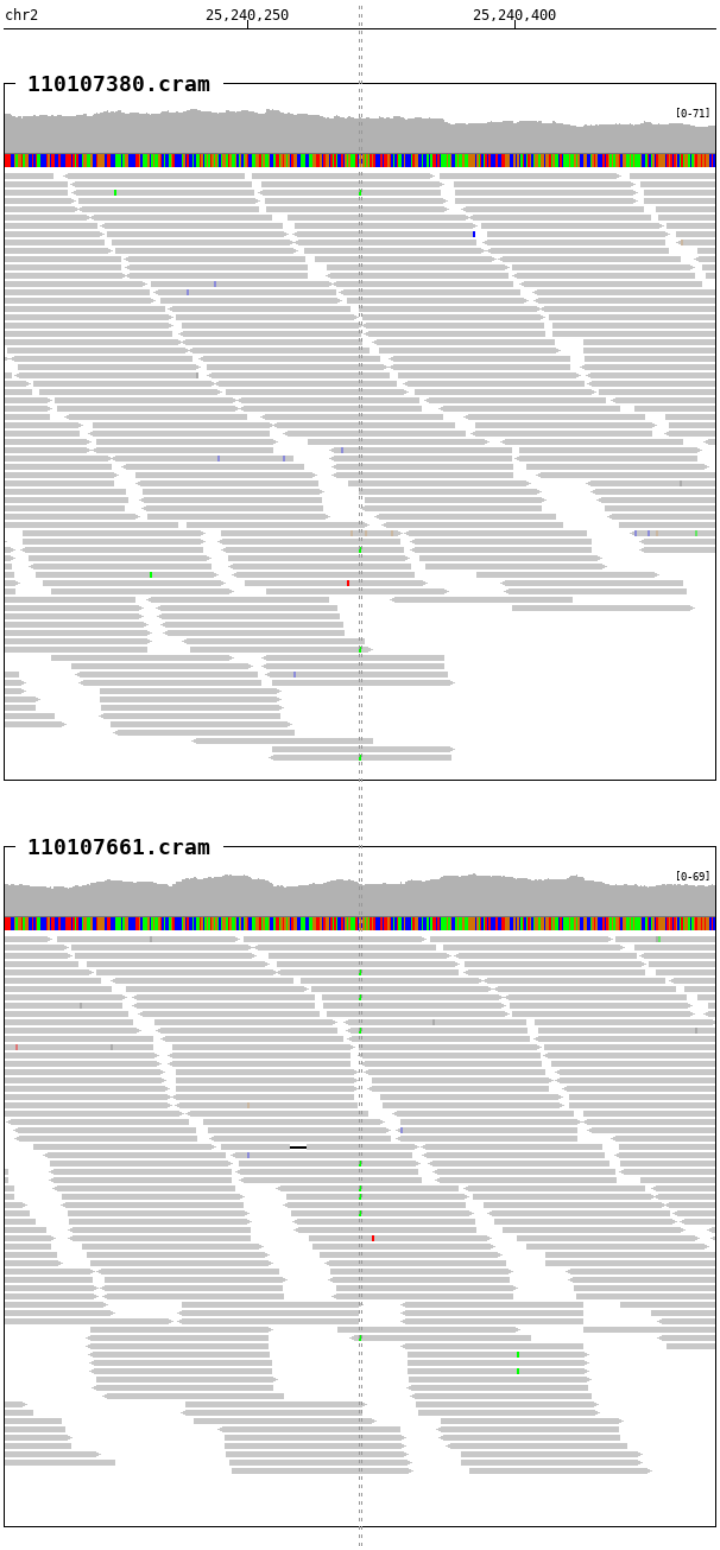
10.39. chr2_25240312_C/T

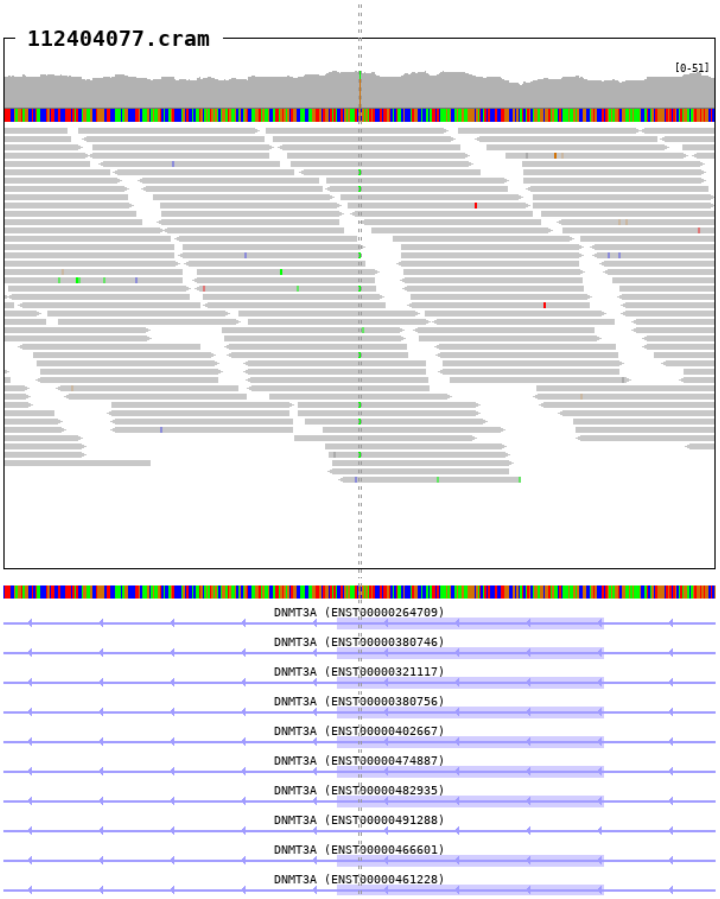
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110103627	chr2_25240312_C/T	42	6	*DNMT3A*	missense_variant
12390108	chr2_25240312_C/T	40	5	*DNMT3A*	missense_variant



10.40. chr2_25240313_G/A

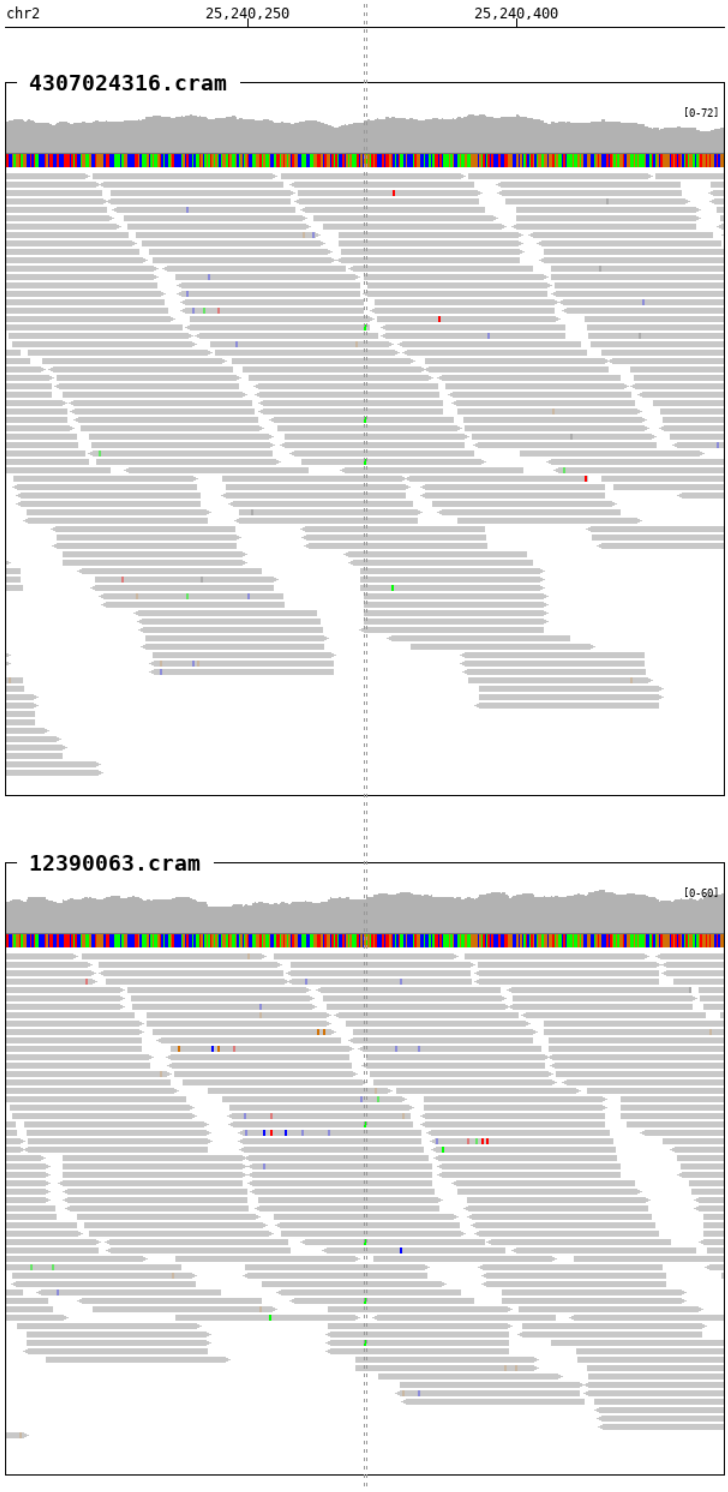
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110107380	chr2_25240313_G/A	49	4	*DNMT3A*	stop_gained
110107661	chr2_25240313_G/A	39	7	*DNMT3A*	stop_gained
112404077	chr2_25240313_G/A	32	8	*DNMT3A*	stop_gained

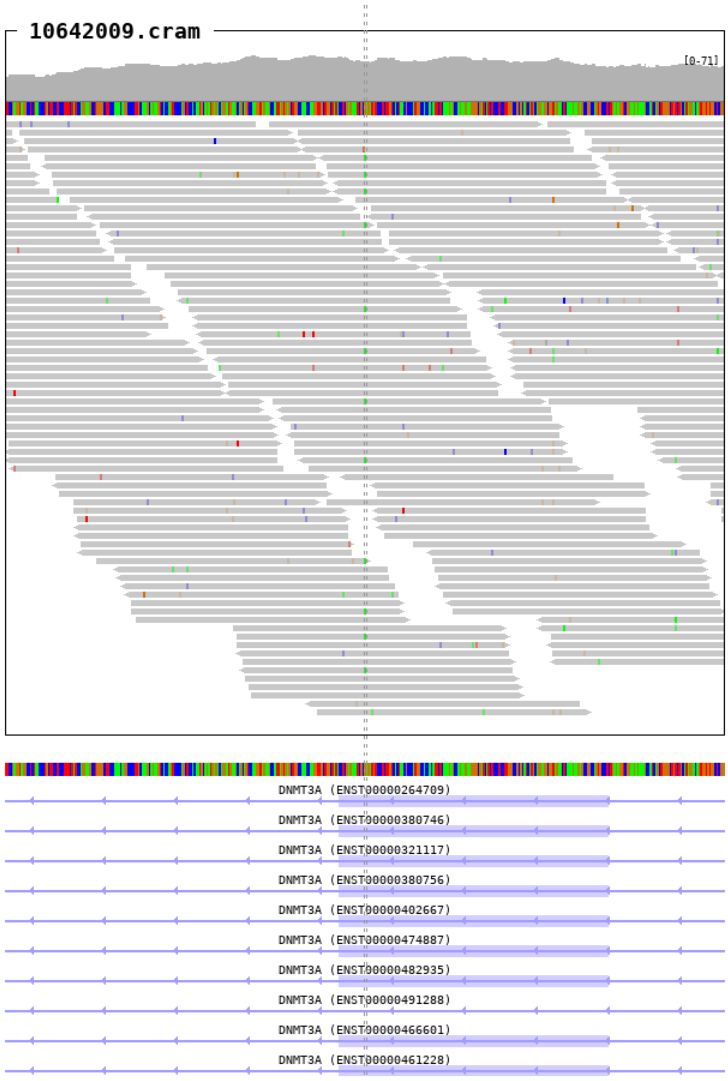



112404077.cram
[0-51]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474887)
DNMT3A (ENST00000482935)
DNMT3A (ENST00000491288)
DNMT3A (ENST00000466601)
DNMT3A (ENST00000461228)

10.41. chr2_25240315_G/A

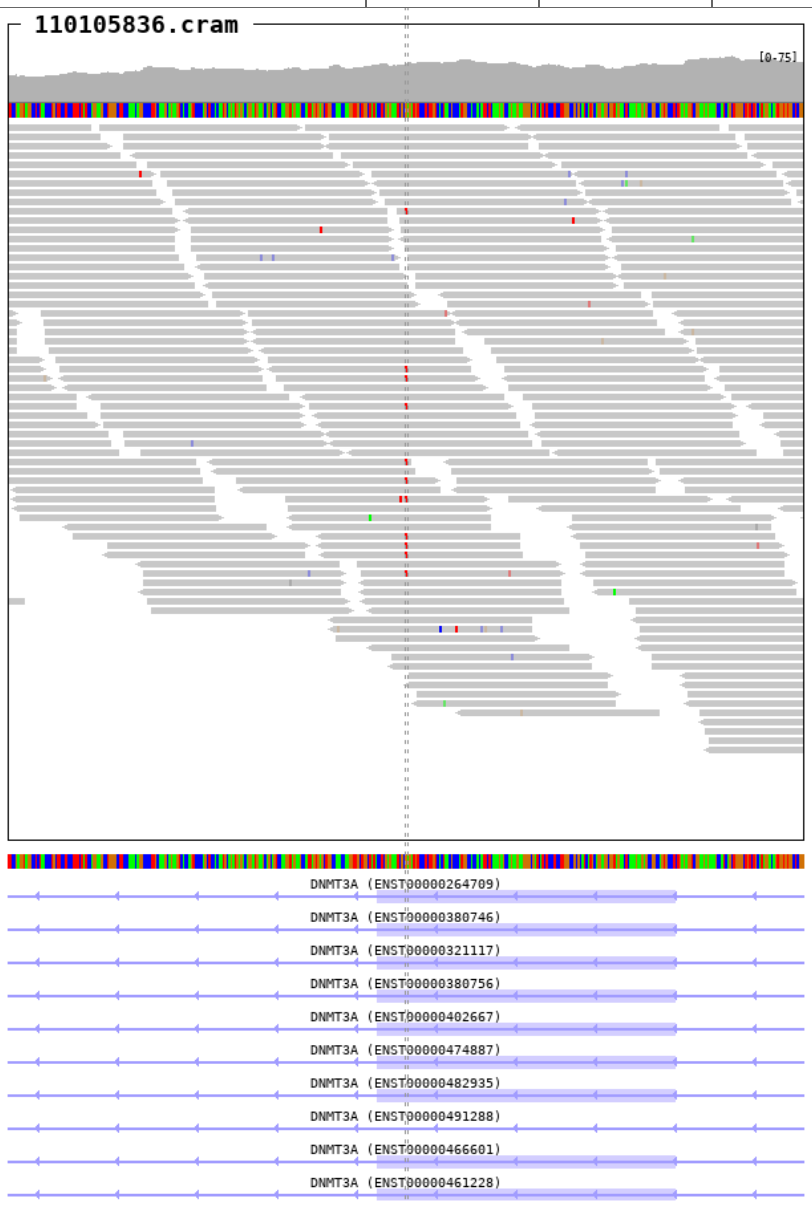
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10642009	chr2_25240315_G/A	48	12	*DNMT3A*	missense_variant
12390063	chr2_25240315_G/A	36	4	*DNMT3A*	missense_variant
4307024316	chr2_25240315_G/A	45	3	*DNMT3A*	missense_variant




10642009.cram
[0-71]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474887)
DNMT3A (ENST00000482935)
DNMT3A (ENST00000491288)
DNMT3A (ENST00000466601)
DNMT3A (ENST00000461228)

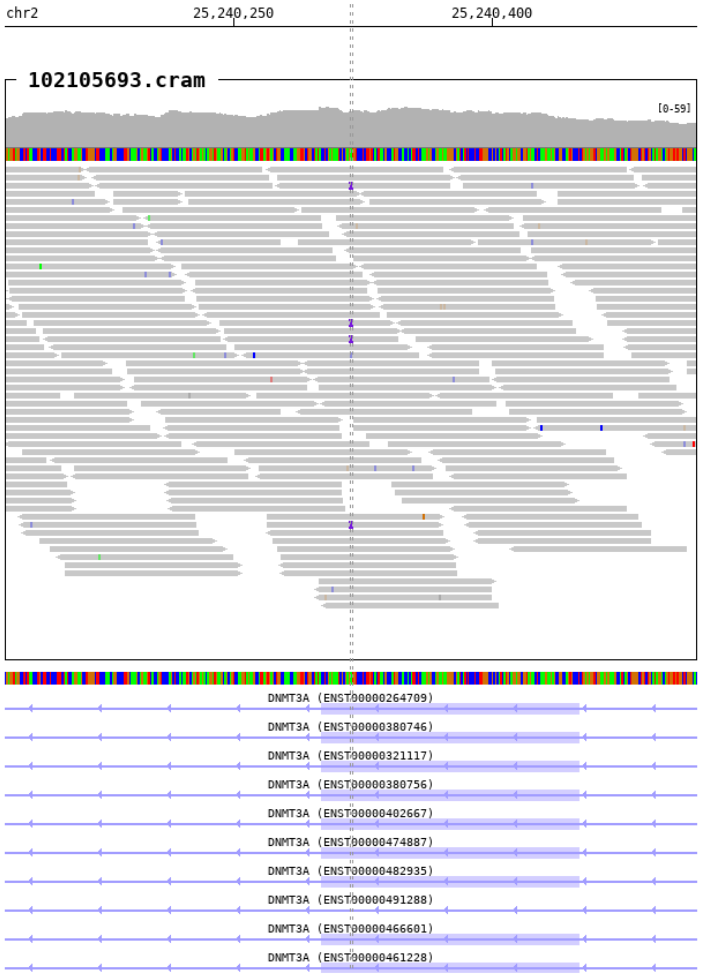
10.42. chr2_25240315_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110105836	chr2_25240315_G/T	41	10	*DNMT3A*	stop_gained



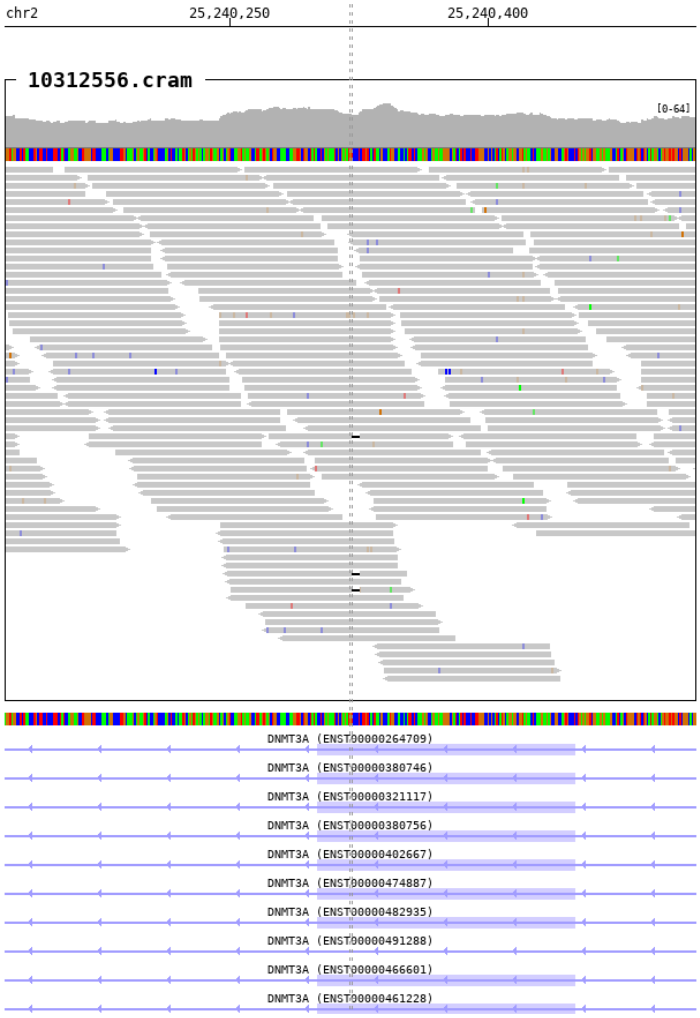
10.43. chr2_25240318_-/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102105693	chr2_25240318_-/T	42	4	*DNMT3A*	frameshift_variant



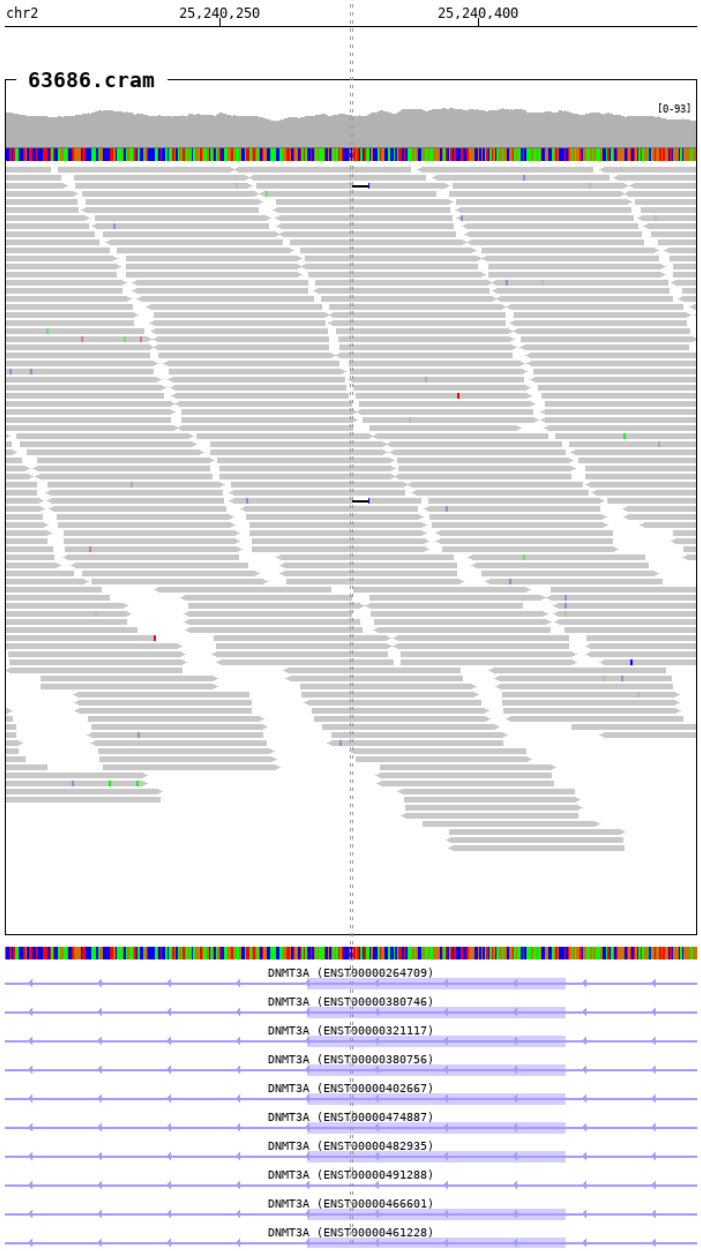
10.44. chr2_25240320_TCCC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10312556	chr2_25240320_TCCC/-	45	4	*DNMT3A*	frameshift_variant



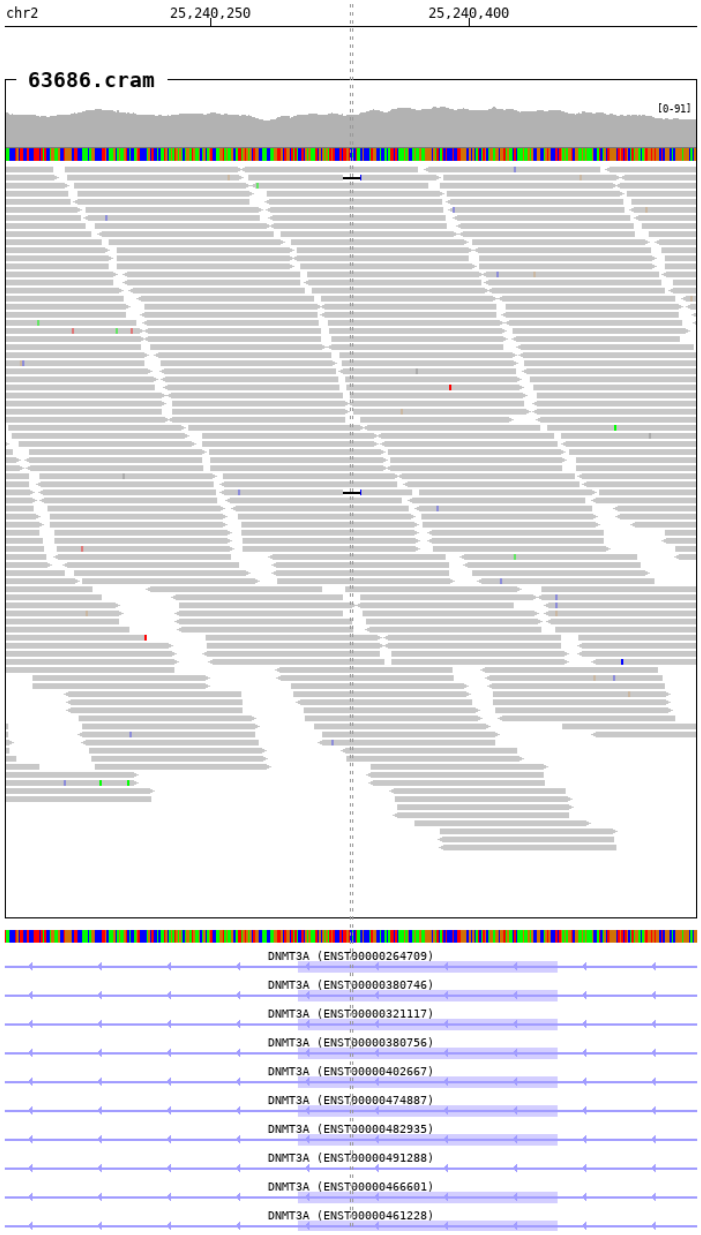
10.45. chr2_25240326_TTGT/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
63686	chr2_25240326_TTGT/-	70	6	*DNMT3A*	frameshift_variant



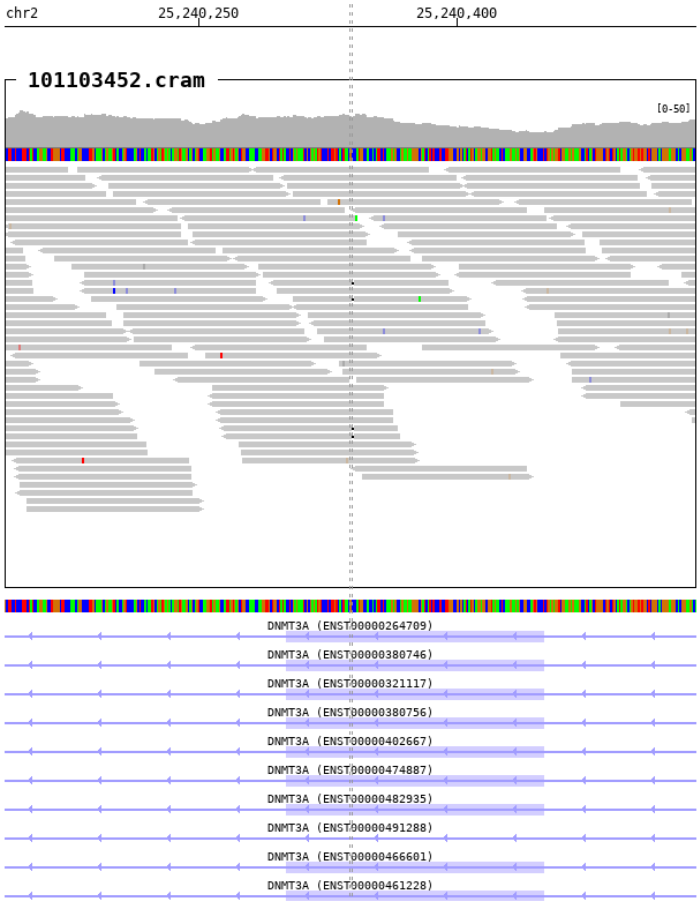
10.46. chr2_25240331_ACTAA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
63686	chr2_25240331_ACTAA/-	68	6	*DNMT3A*	frameshift_variant



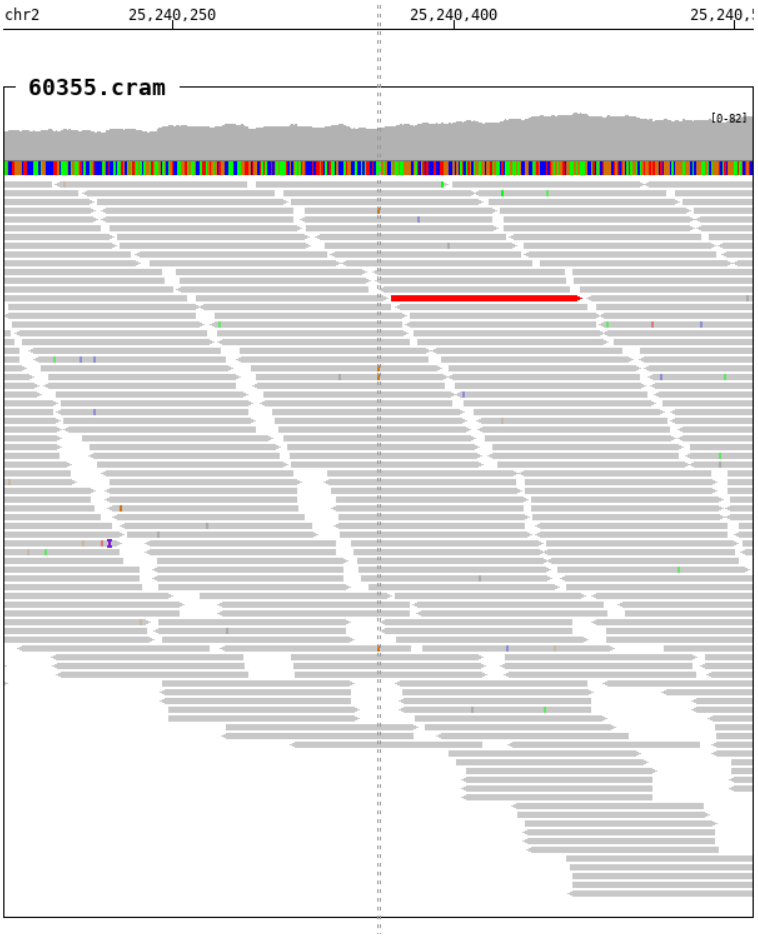
10.47. chr2_25240338_C/-

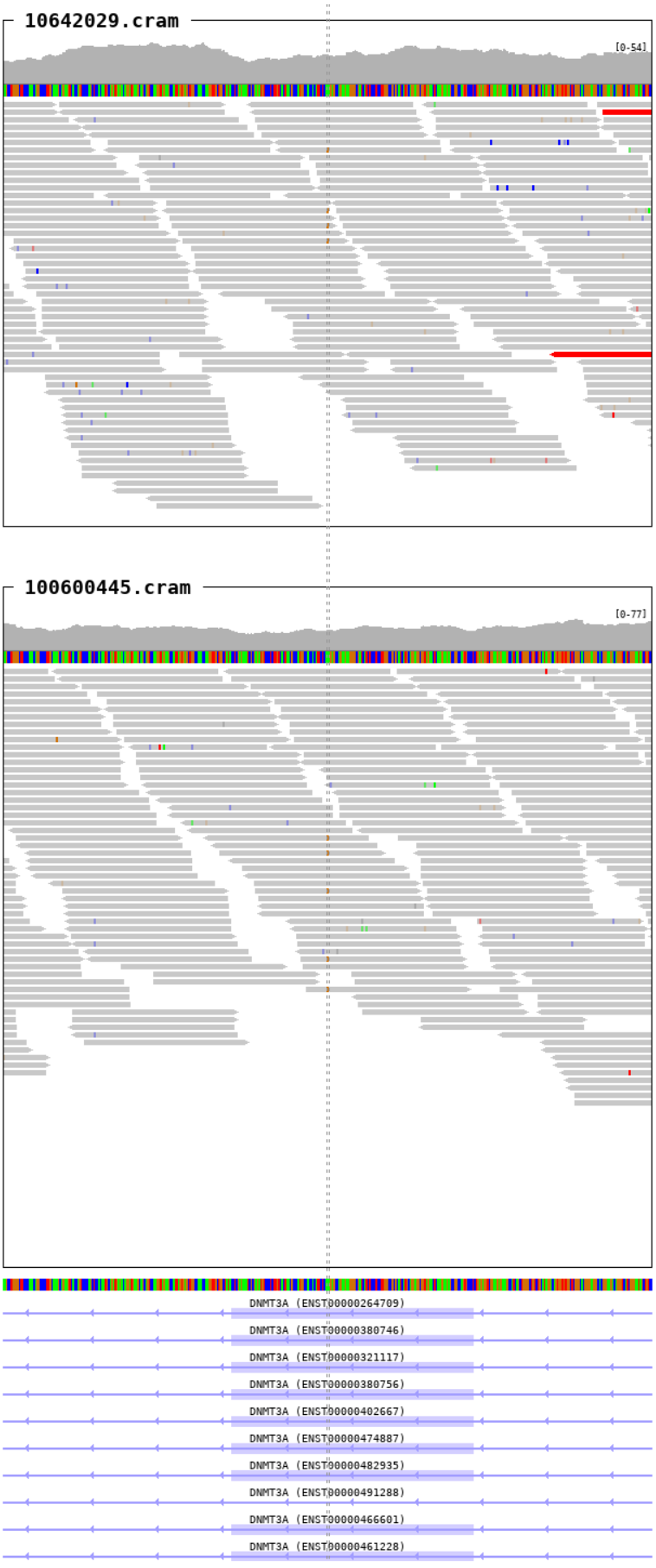
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101103452	chr2_25240338_C/-	30	5	*DNMT3A*	frameshift_variant



10.48. chr2_25240360_A/G

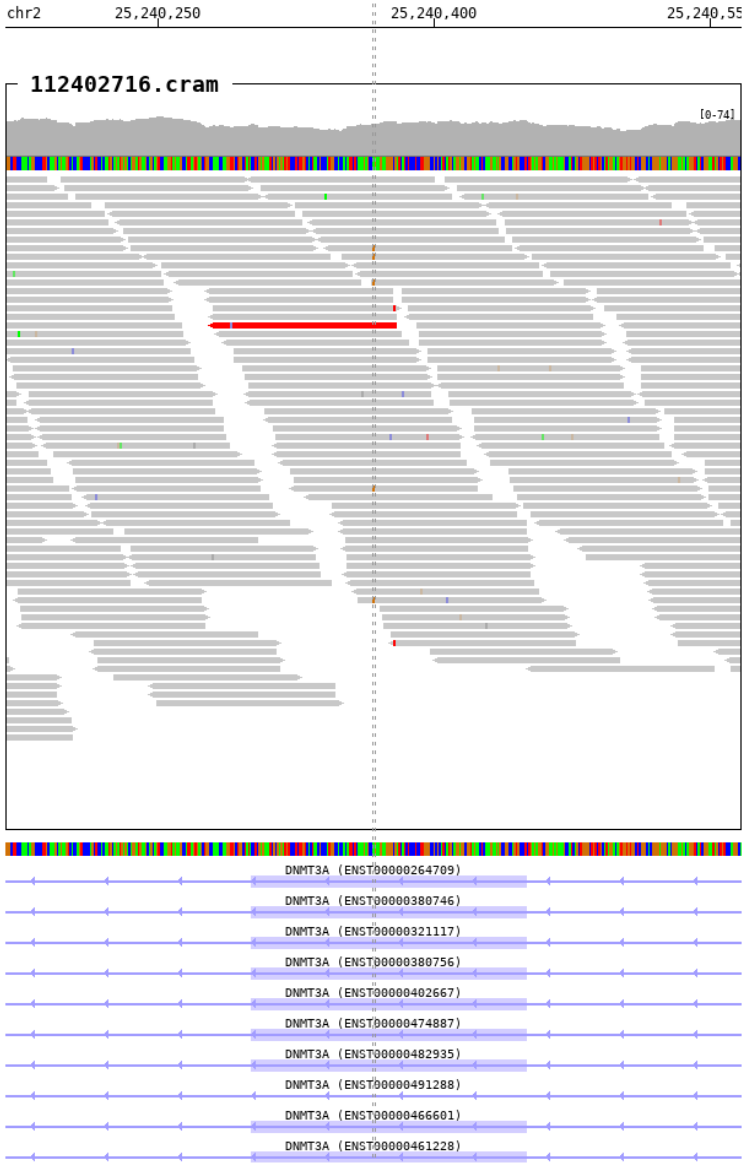
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100600445	chr2_25240360_A/G	33	5	*DNMT3A*	missense_variant
10642029	chr2_25240360_A/G	33	4	*DNMT3A*	missense_variant
60355	chr2_25240360_A/G	50	4	*DNMT3A*	missense_variant




10642029.cram
[0-54]
100600445.cram
[0-77]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474887)
DNMT3A (ENST00000482935)
DNMT3A (ENST00000491288)
DNMT3A (ENST00000466601)
DNMT3A (ENST00000461228)

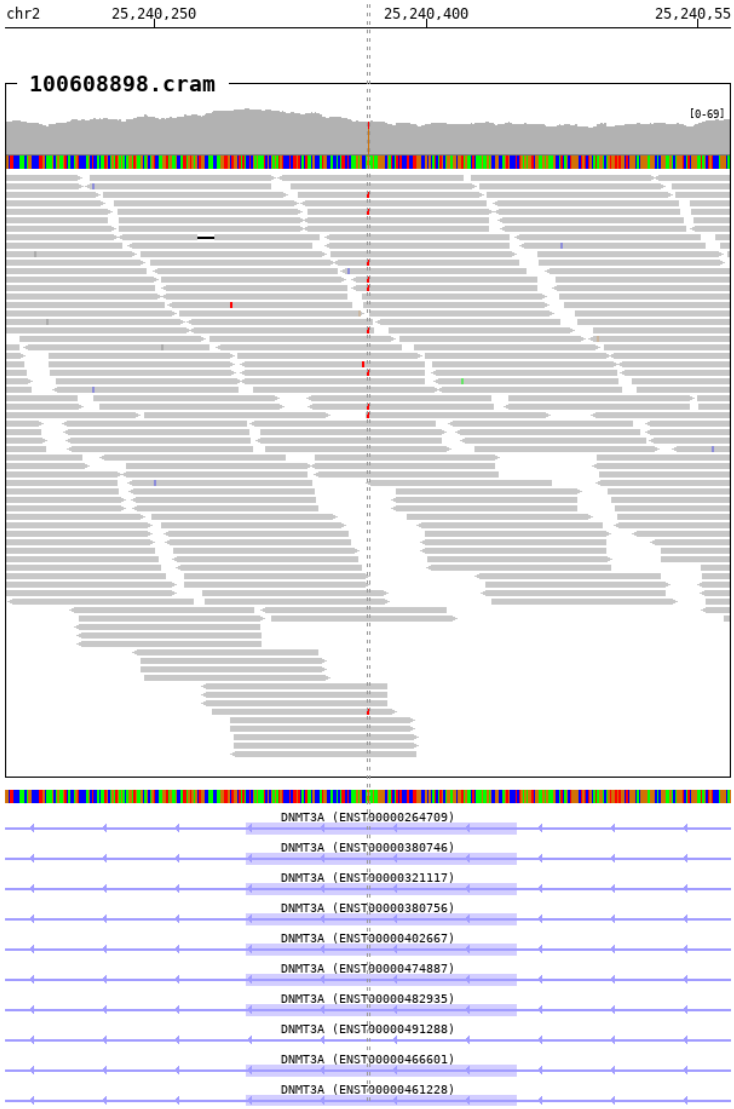
10.49. chr2_25240367_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112402716	chr2_25240367_A/G	44	5	*DNMT3A*	missense_variant



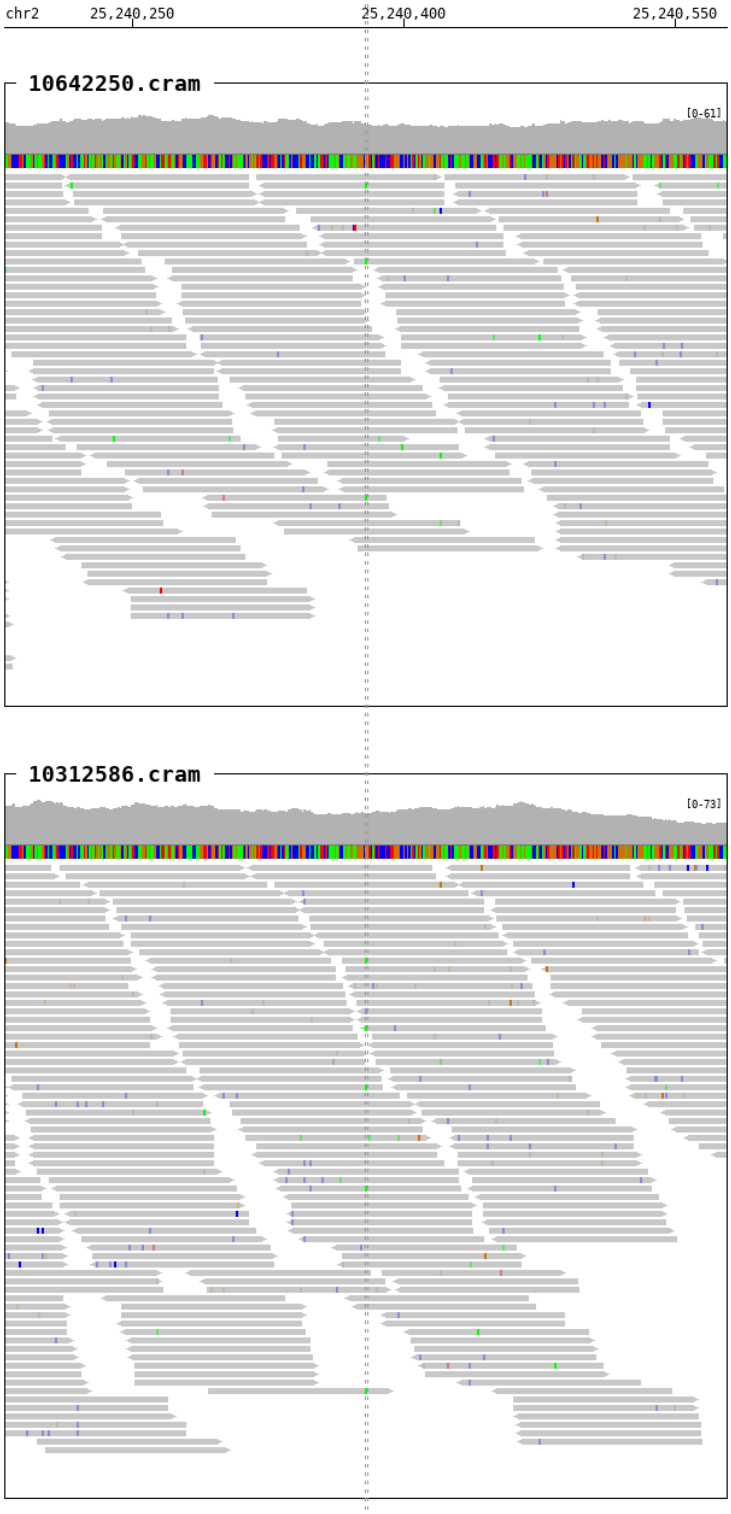
10.50. chr2_25240368_G/T

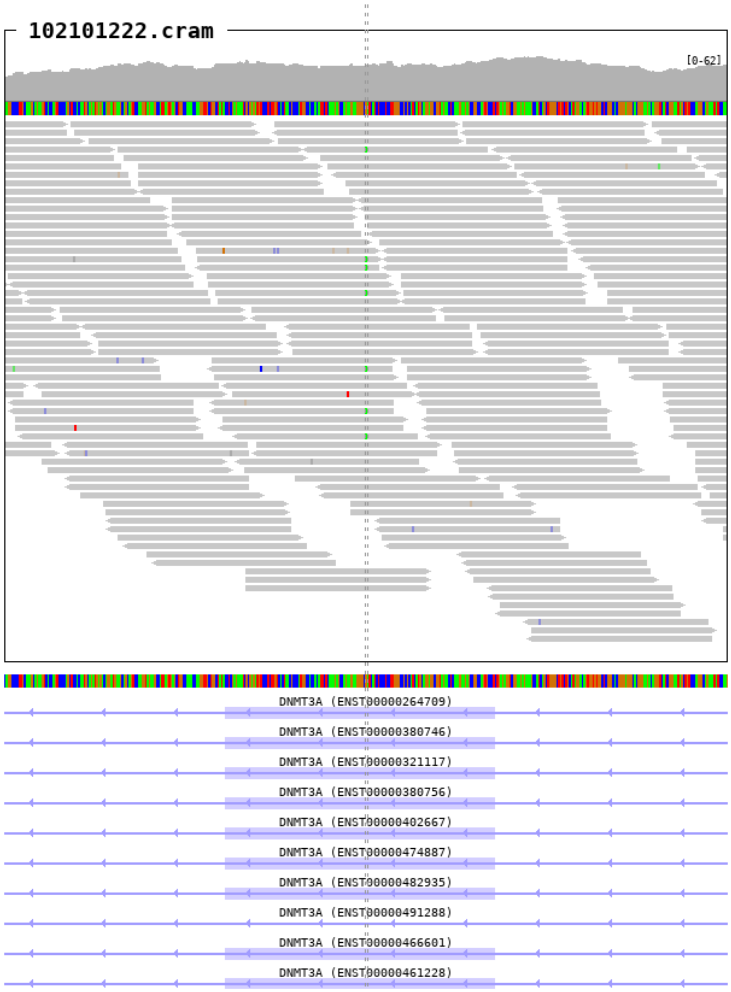
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100608898	chr2_25240368_G/T	35	9	*DNMT3A*	missense_variant



10.51. chr2_25240379_G/A

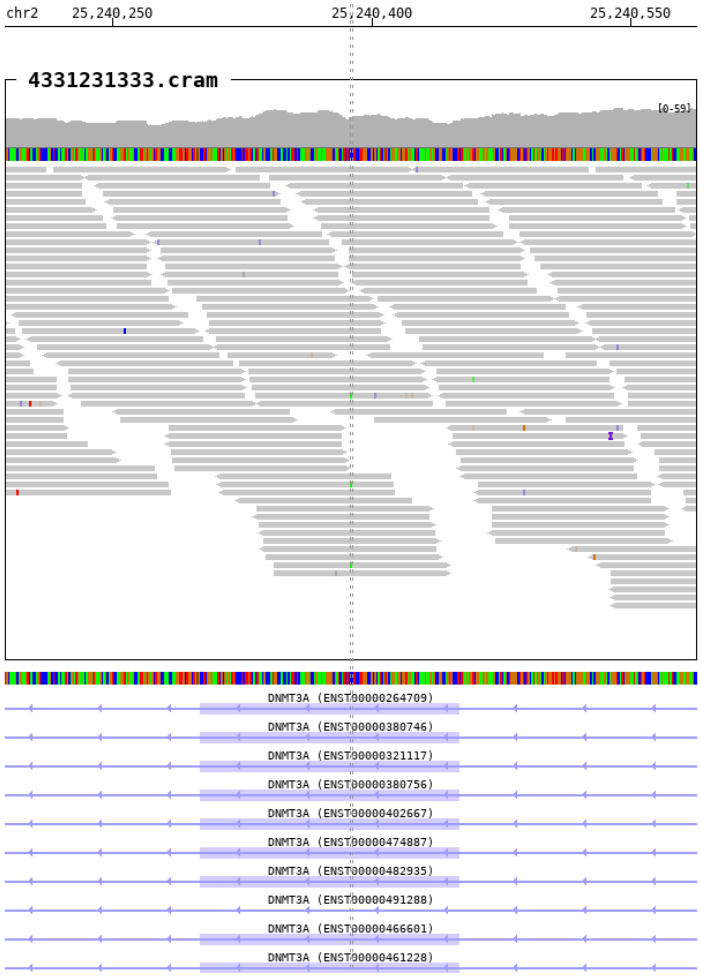
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102101222	chr2_25240379_G/A	39	7	*DNMT3A*	missense_variant
10312586	chr2_25240379_G/A	41	5	*DNMT3A*	missense_variant
10642250	chr2_25240379_G/A	33	3	*DNMT3A*	missense_variant




102101222.cram
[0-62]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474887)
DNMT3A (ENST00000482935)
DNMT3A (ENST00000491288)
DNMT3A (ENST00000466601)
DNMT3A (ENST00000461228)

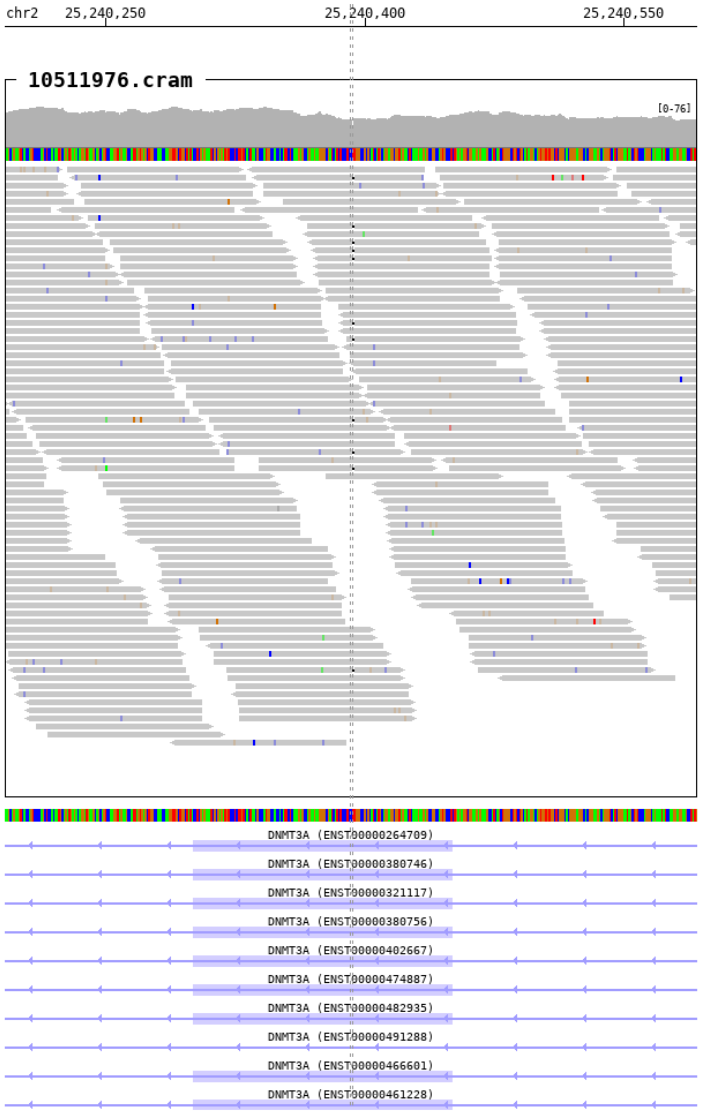
10.52. chr2_25240388_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
4331231333	chr2_25240388_C/A	36	3	*DNMT3A*	stop_gained



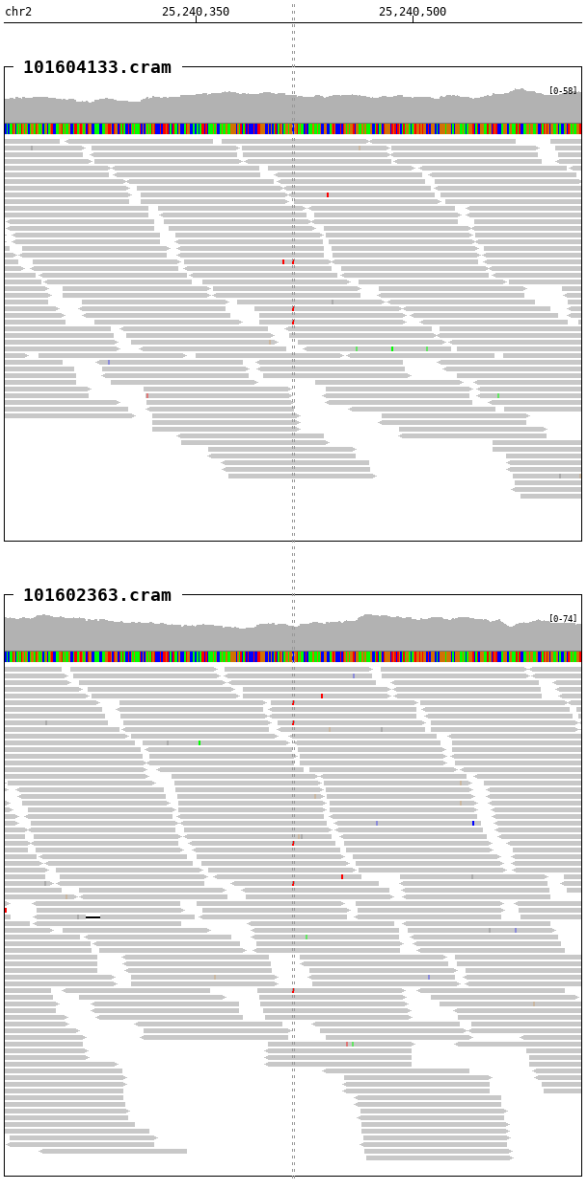
10.53. chr2_25240392_T/-

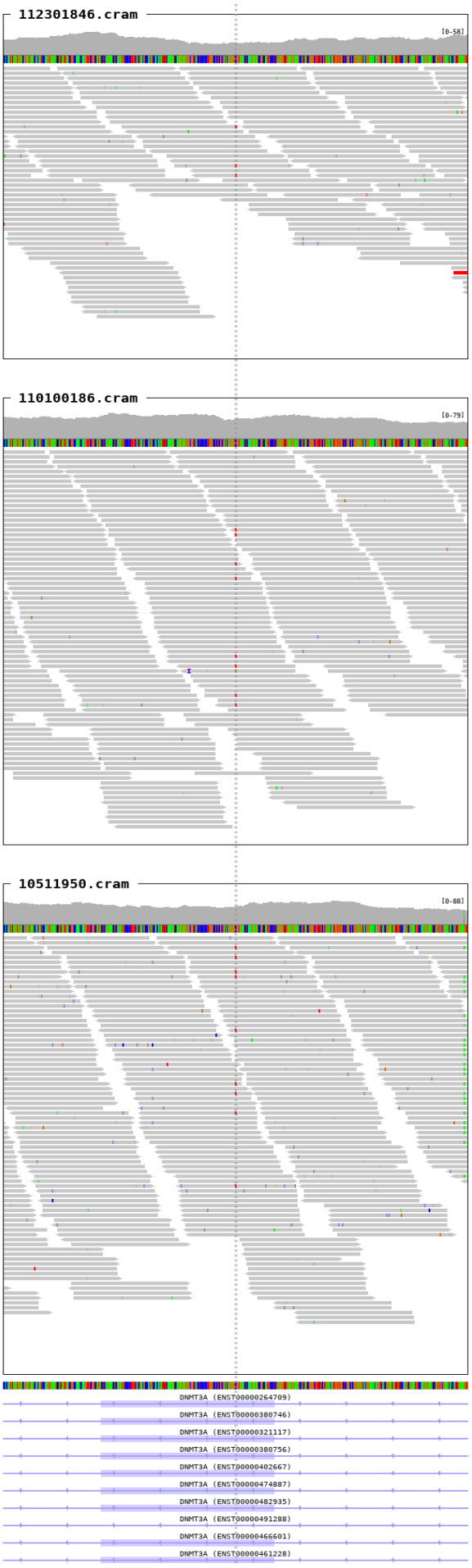
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10511976	chr2_25240392_T/-	32	11	*DNMT3A*	frameshift_variant



10.54. chr2_25240417_C/T

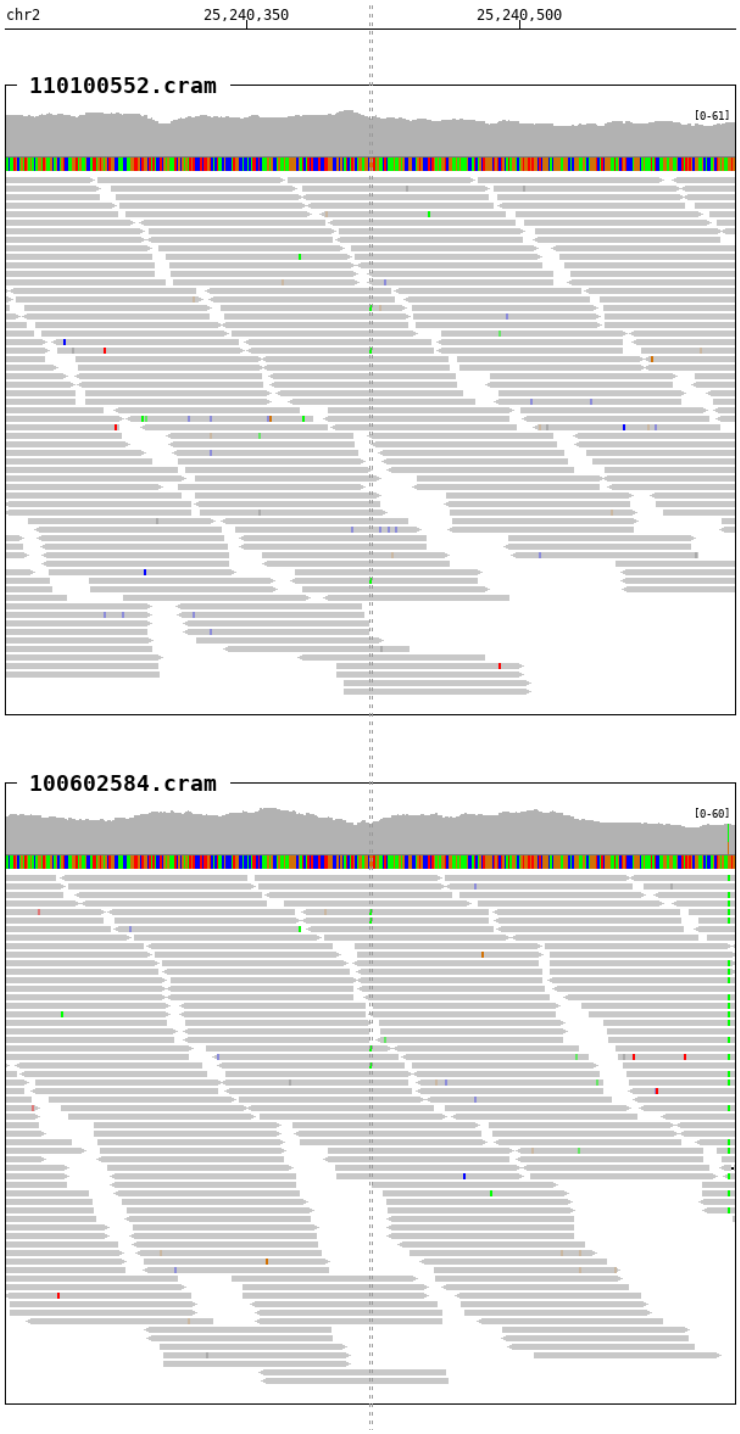
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101602363	chr2_25240417_C/T	41	5	*DNMT3A*	missense_variant
101604133	chr2_25240417_C/T	41	3	*DNMT3A*	missense_variant
10511950	chr2_25240417_C/T	47	9	*DNMT3A*	missense_variant
110100186	chr2_25240417_C/T	49	8	*DNMT3A*	missense_variant
112301846	chr2_25240417_C/T	24	3	*DNMT3A*	missense_variant

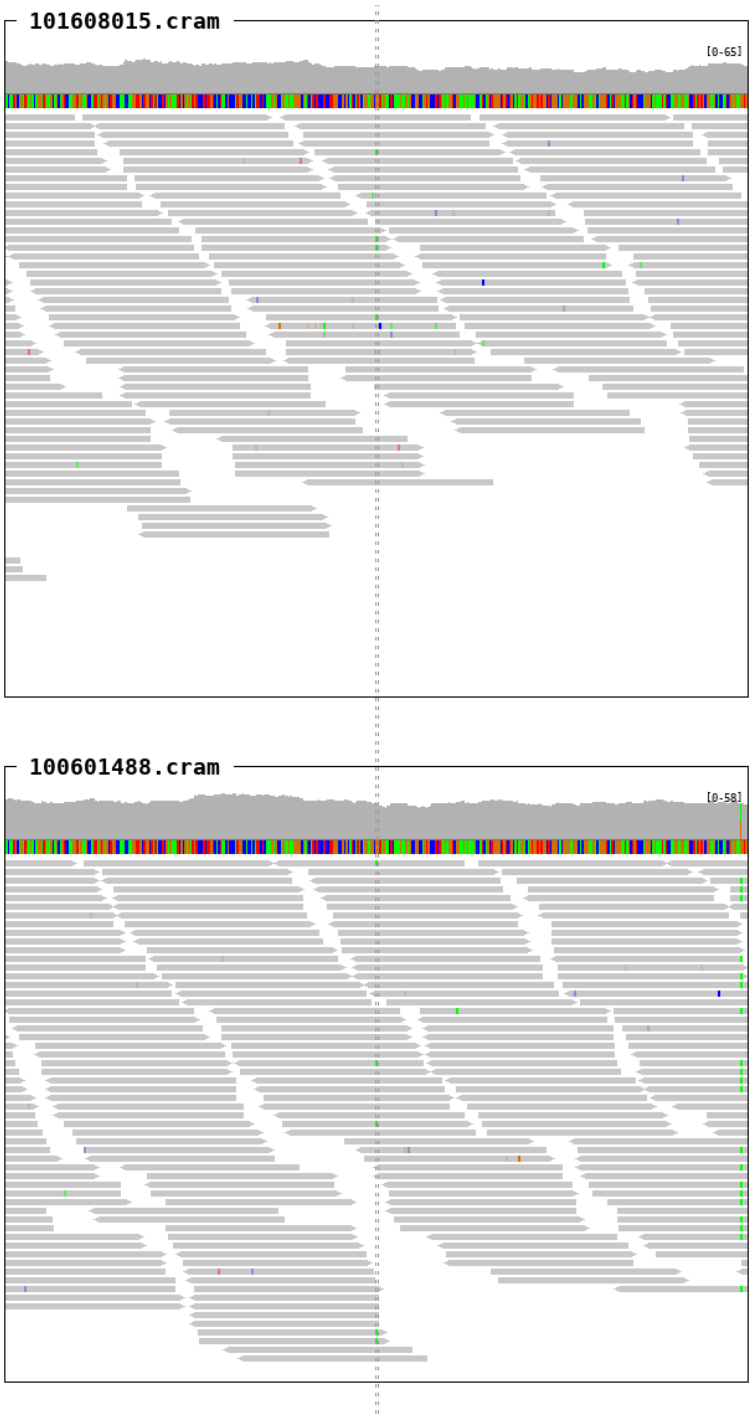


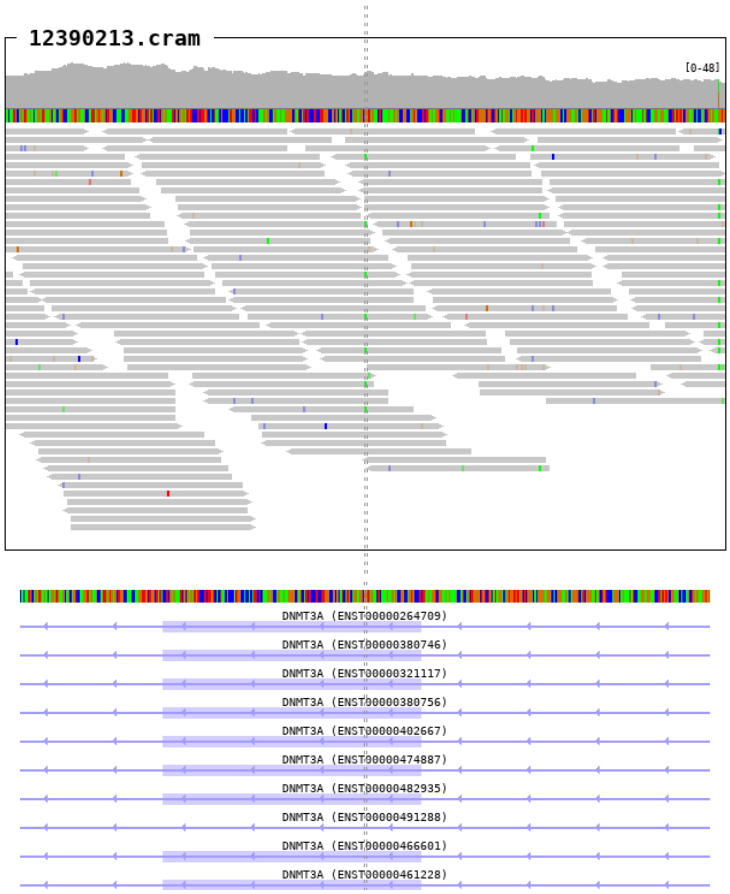

112301846.cram
[0-58]
110100186.cram
[0-79]
10511950.cram
[0-88]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474887)
DNMT3A (ENST00000482935)
DNMT3A (ENST00000491288)
DNMT3A (ENST00000466601)
DNMT3A (ENST00000461228)

10.55. chr2_25240418_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100601488	chr2_25240418_G/A	35	5	*DNMT3A*	missense_variant
100602584	chr2_25240418_G/A	34	3	*DNMT3A*	missense_variant
101608015	chr2_25240418_G/A	33	3	*DNMT3A*	missense_variant
110100552	chr2_25240418_G/A	44	3	*DNMT3A*	missense_variant
12390213	chr2_25240418_G/A	30	7	*DNMT3A*	missense_variant




101608015.cram
[0-65]
100601488.cram
[0-58]


12390213.cram
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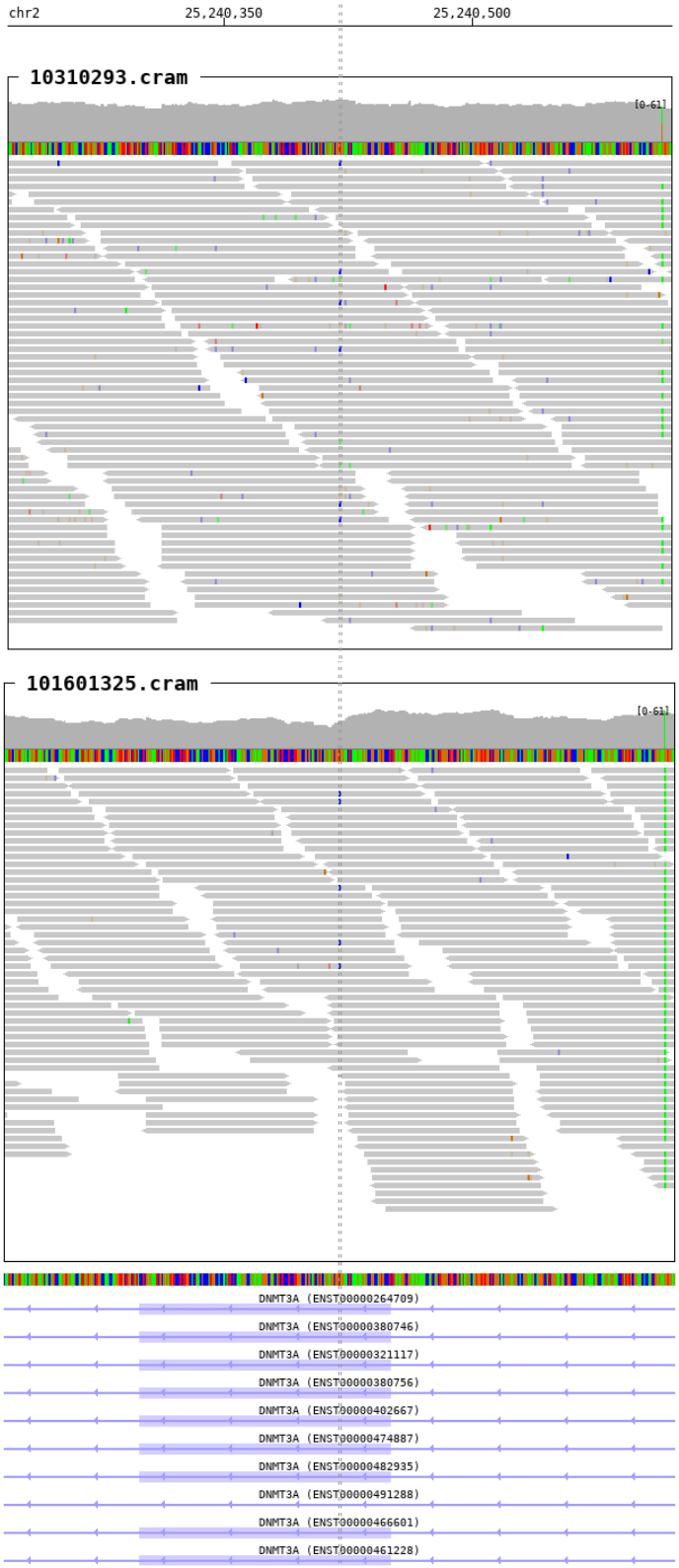
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474887)
DNMT3A (ENST00000482935)
DNMT3A (ENST00000491288)
DNMT3A (ENST00000466601)
DNMT3A (ENST00000461228)

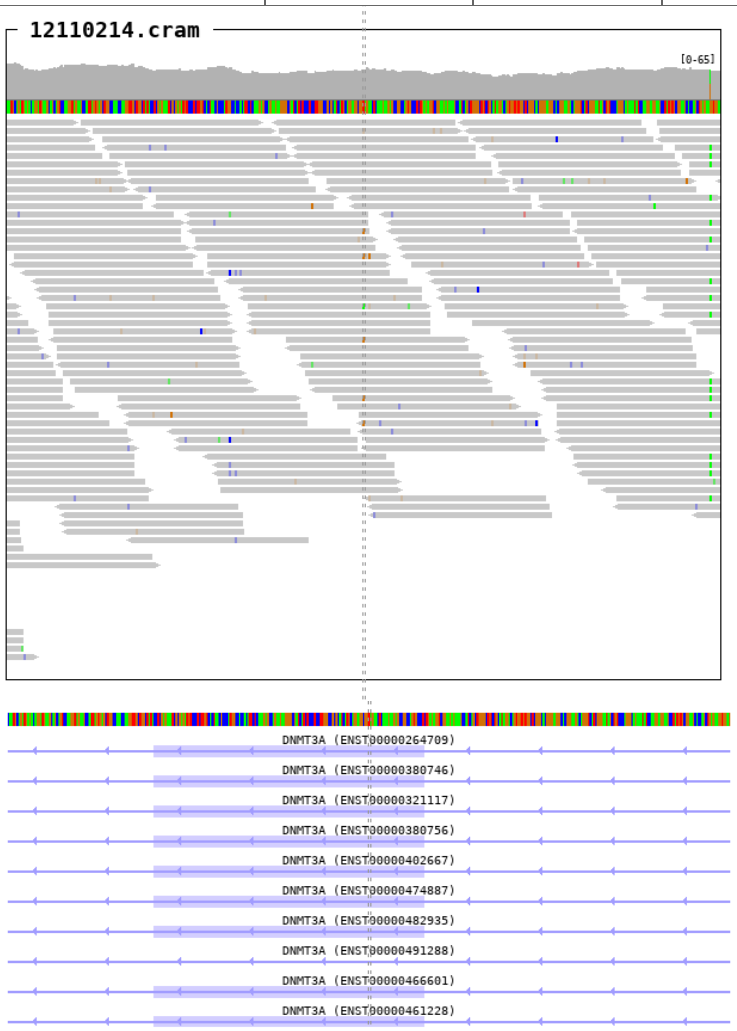
10.56. chr2_25240420_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101601325	chr2_25240420_T/C	32	5	*DNMT3A*	missense_variant
10310293	chr2_25240420_T/C	44	5	*DNMT3A*	missense_variant



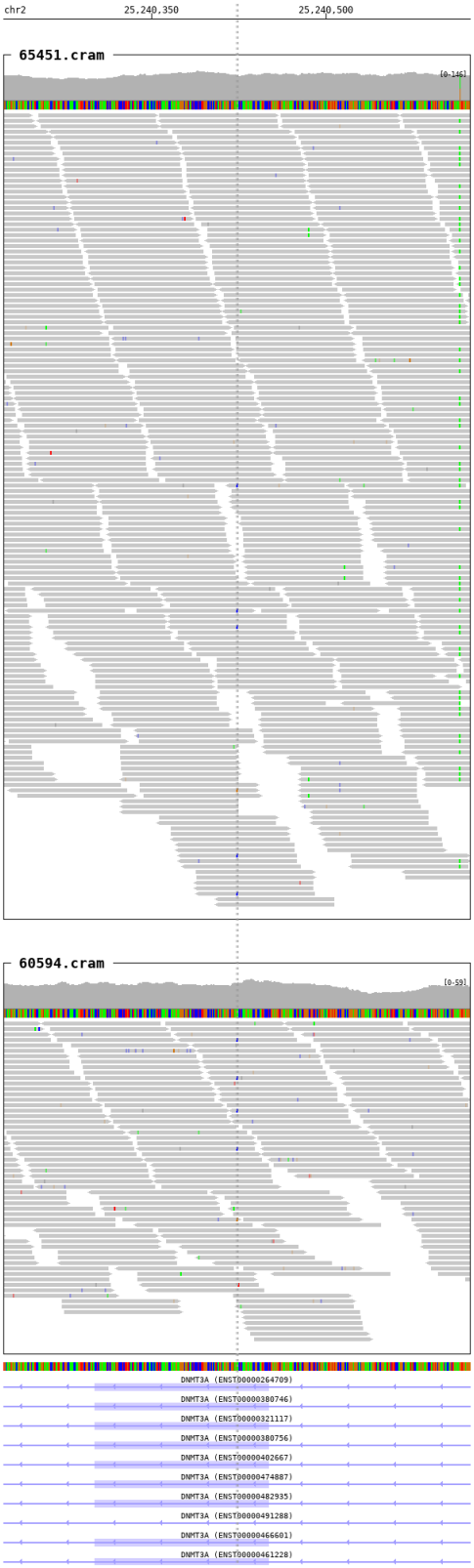
10.57. chr2_25240420_T/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12110214	chr2_25240420_T/G	33	5	*DNMT3A*	missense_variant



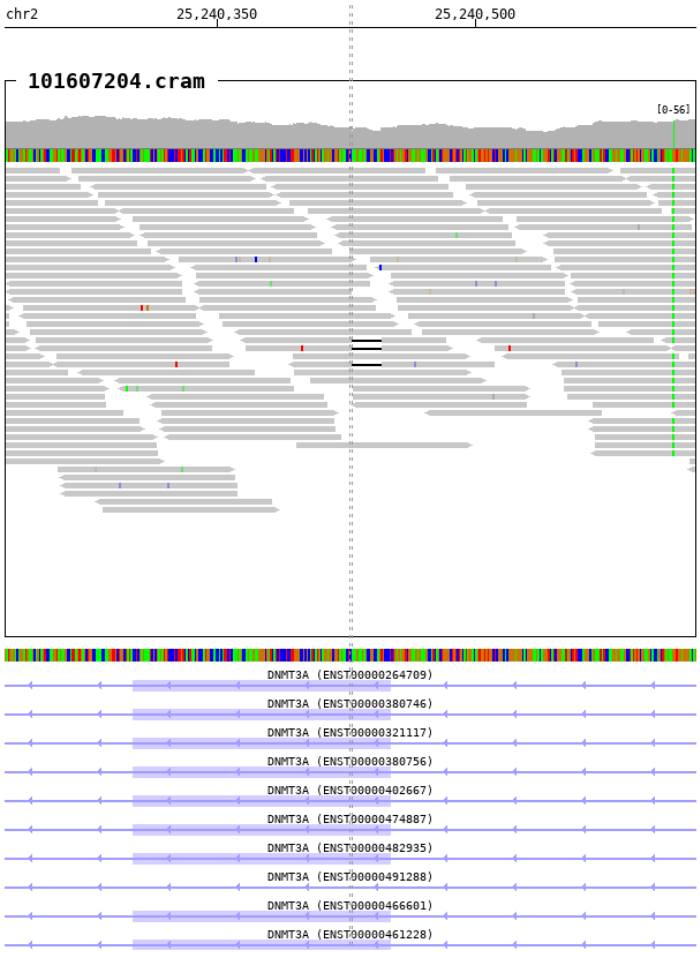
10.58. chr2_25240423_A/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
60594	chr2_25240423_A/C	42	4	*DNMT3A*	missense_variant
65451	chr2_25240423_A/C	111	5	*DNMT3A*	missense_variant



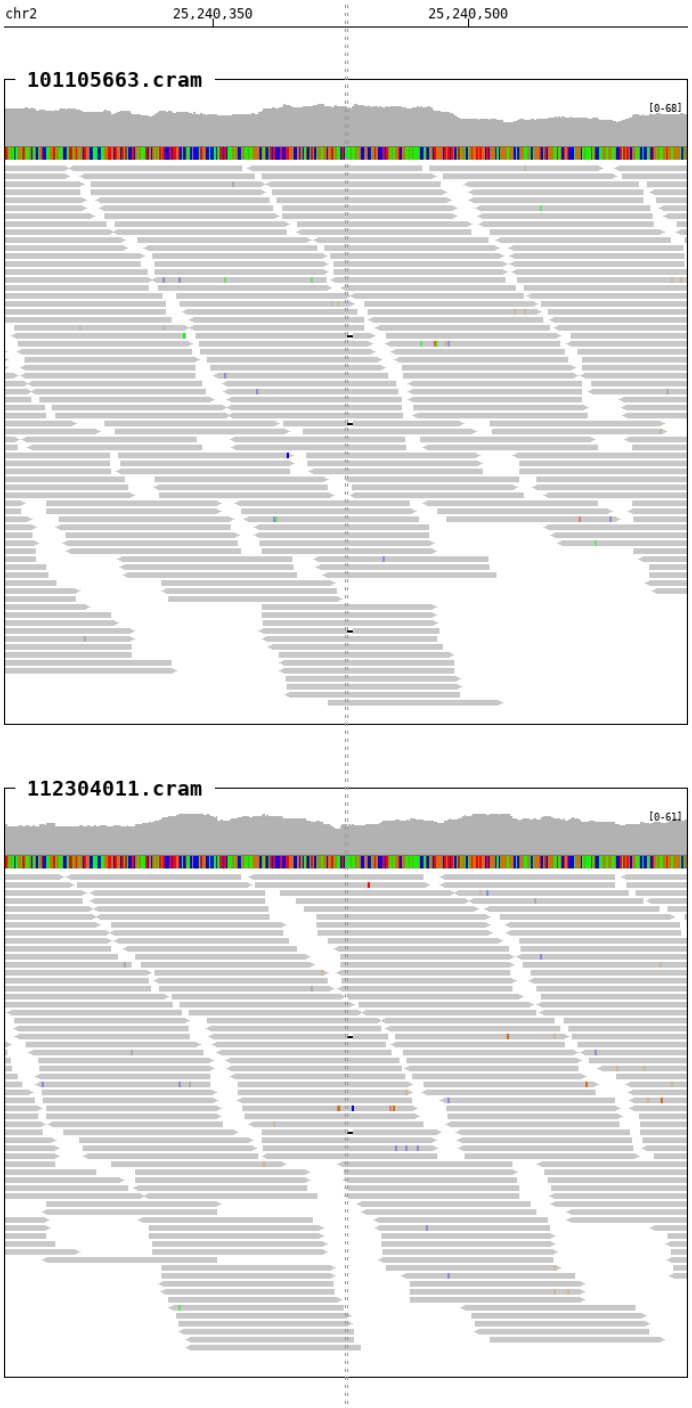
10.59. chr2_25240427_AAAGAAGAGCCGGCCAG/-

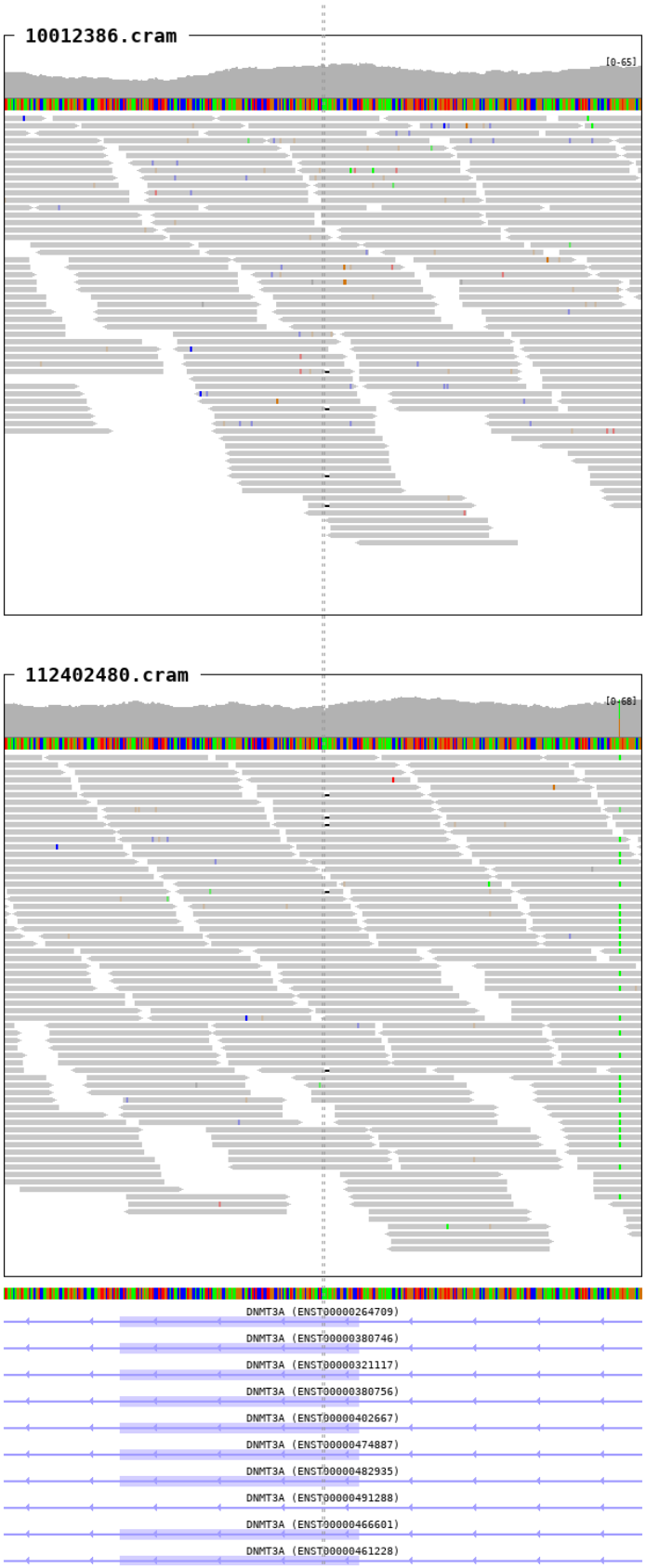
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101607204	chr2_25240427_AAAGAAGAGCCGGCCAG/-	27	5	*DNMT3A*	frameshift_variant



10.60. chr2_25240428_AAG/-

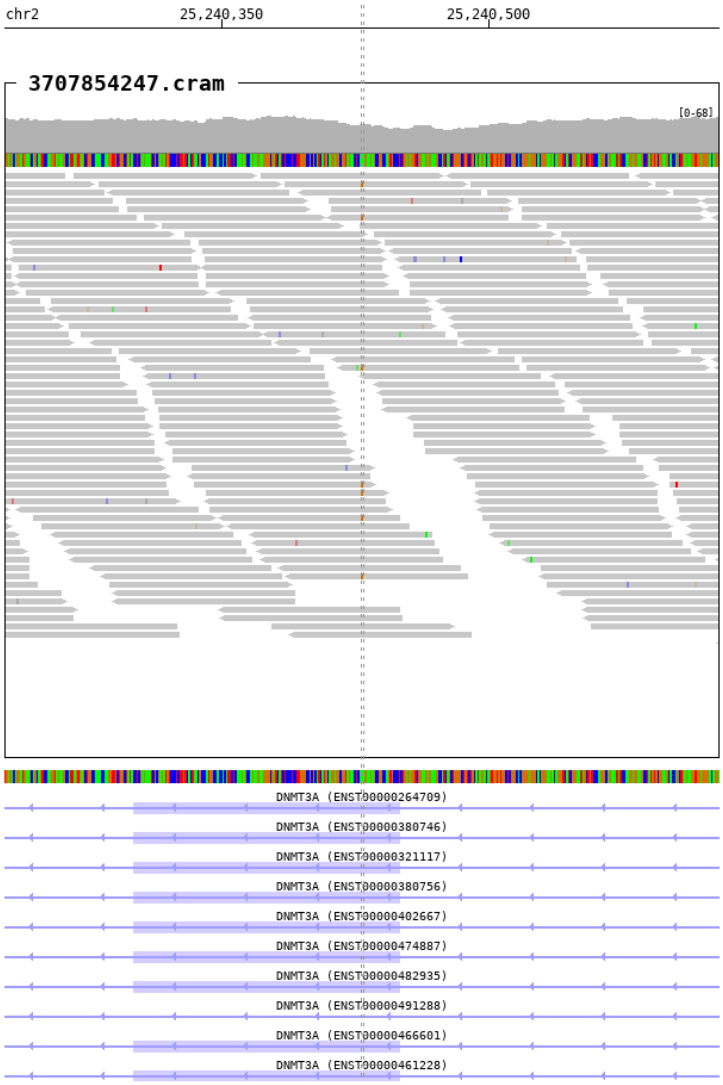
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10012386	chr2_25240428_AAG/-	41	4	*DNMT3A*	inframe_deletion
101105663	chr2_25240428_AAG/-	55	4	*DNMT3A*	inframe_deletion
112304011	chr2_25240428_AAG/-	37	3	*DNMT3A*	inframe_deletion
112402480	chr2_25240428_AAG/-	45	5	*DNMT3A*	inframe_deletion




10012386.cram
[0-65]
112402480.cram
[0-68]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474887)
DNMT3A (ENST00000482935)
DNMT3A (ENST00000491288)
DNMT3A (ENST00000466601)
DNMT3A (ENST00000461228)

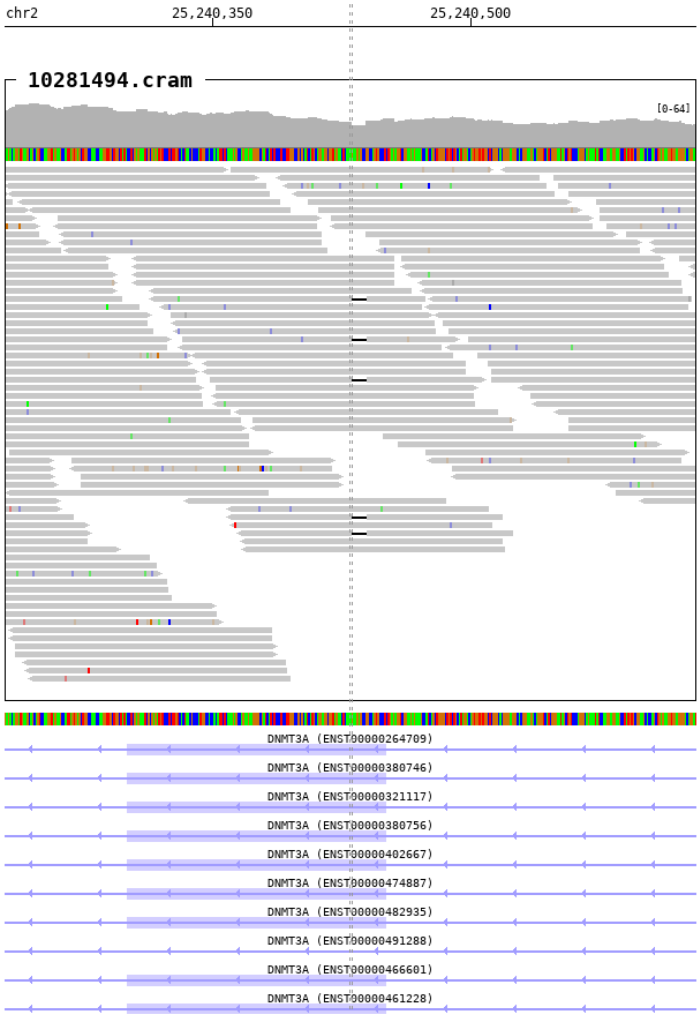
10.61. chr2_25240429_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
3707854247	chr2_25240429_A/G	34	7	*DNMT3A*	missense_variant



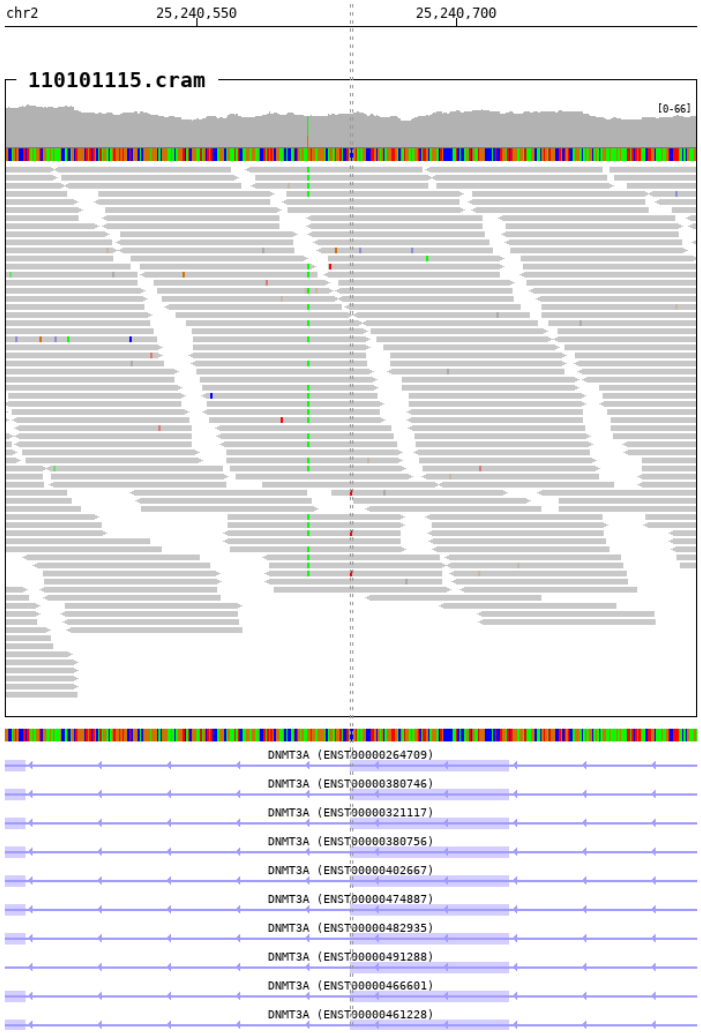
10.62. chr2_25240430_GAAGAGCC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10281494	chr2_25240430_GAAGAGCC/-	30	6	*DNMT3A*	frameshift_variant



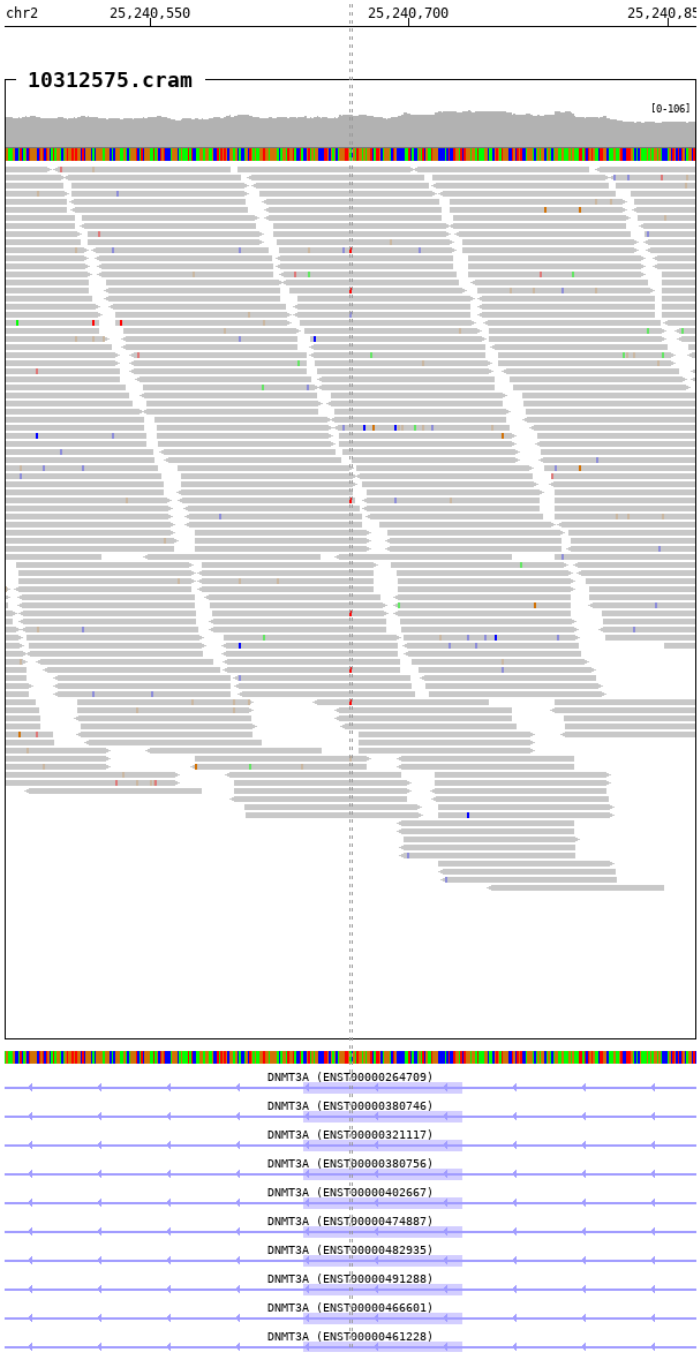
10.63. chr2_25240639_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110101115	chr2_25240639_C/T	43	3	*DNMT3A*	splice_donor_variant



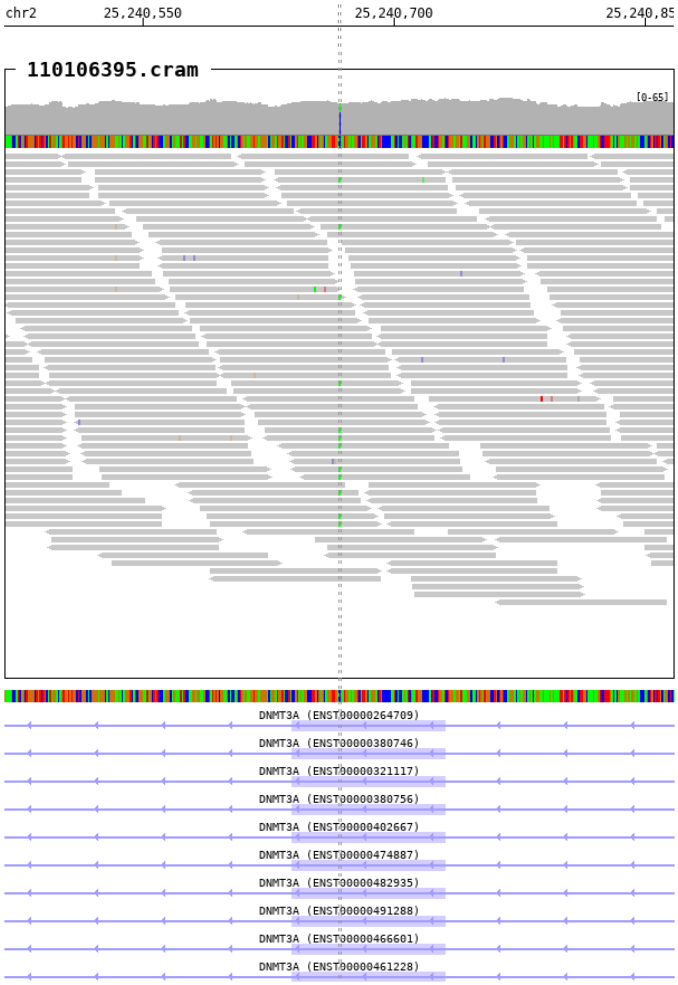
10.64. chr2_25240666_A/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10312575	chr2_25240666_A/T	67	6	*DNMT3A*	missense_variant



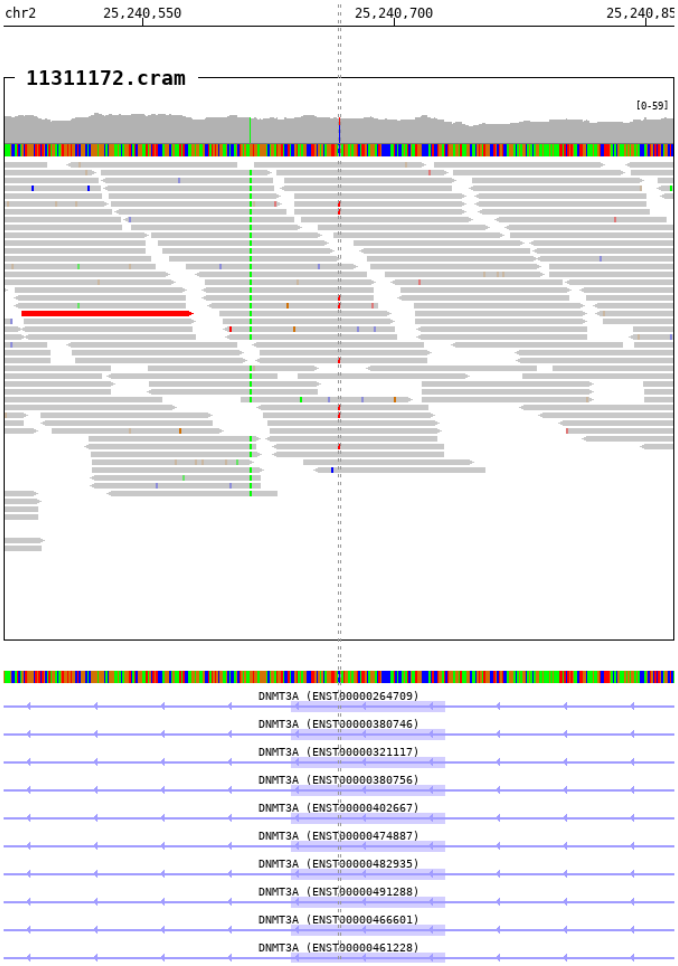
10.65. chr2_25240667_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110106395	chr2_25240667_C/A	34	12	*DNMT3A*	missense_variant



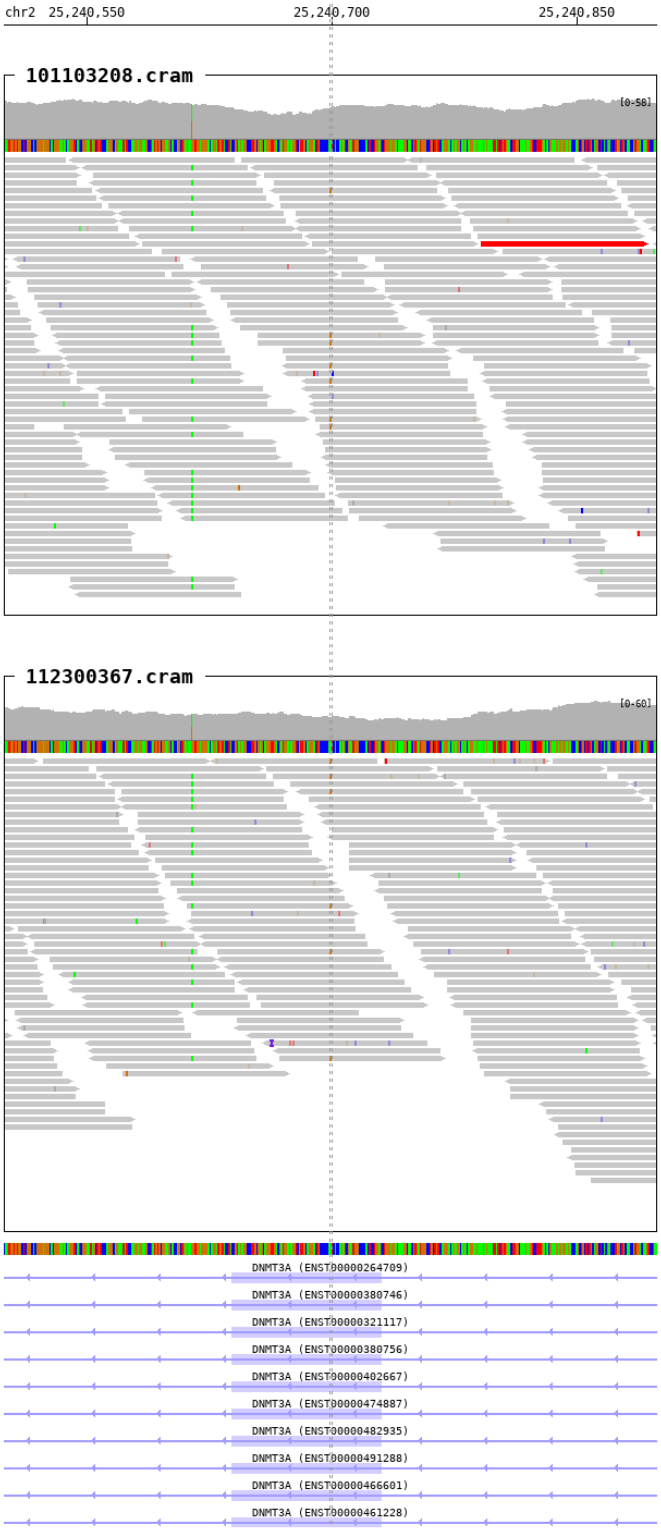
10.66. chr2_25240667_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11311172	chr2_25240667_C/T	24	7	*DNMT3A*	missense_variant



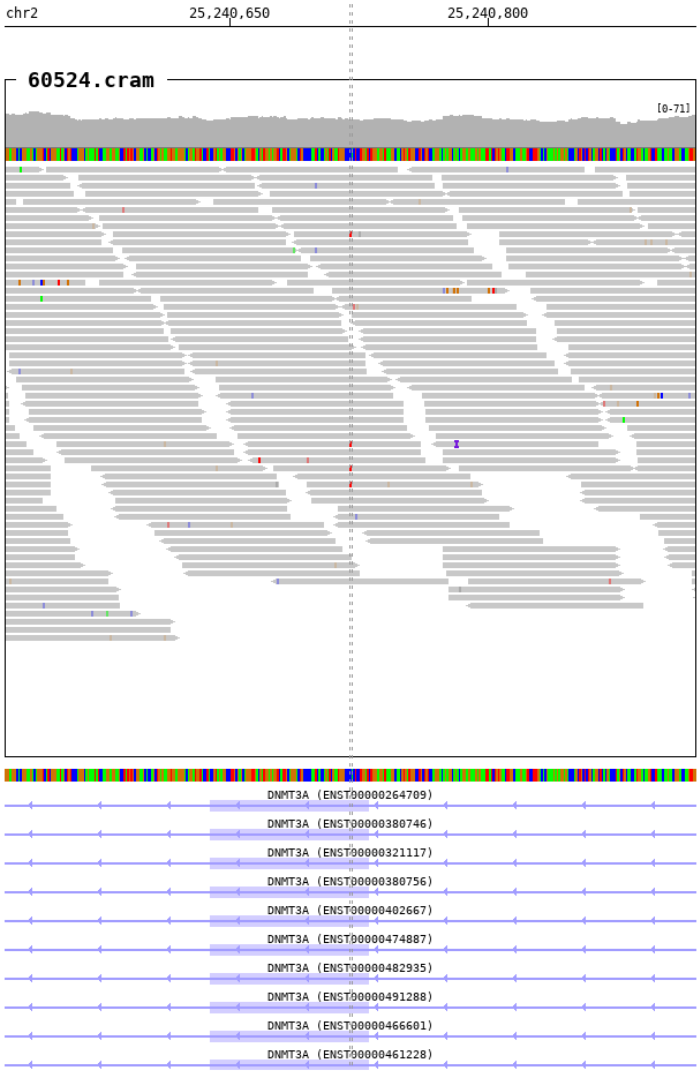
10.67. chr2_25240699_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101103208	chr2_25240699_A/G	35	7	*DNMT3A*	missense_variant
112300367	chr2_25240699_A/G	25	6	*DNMT3A*	missense_variant



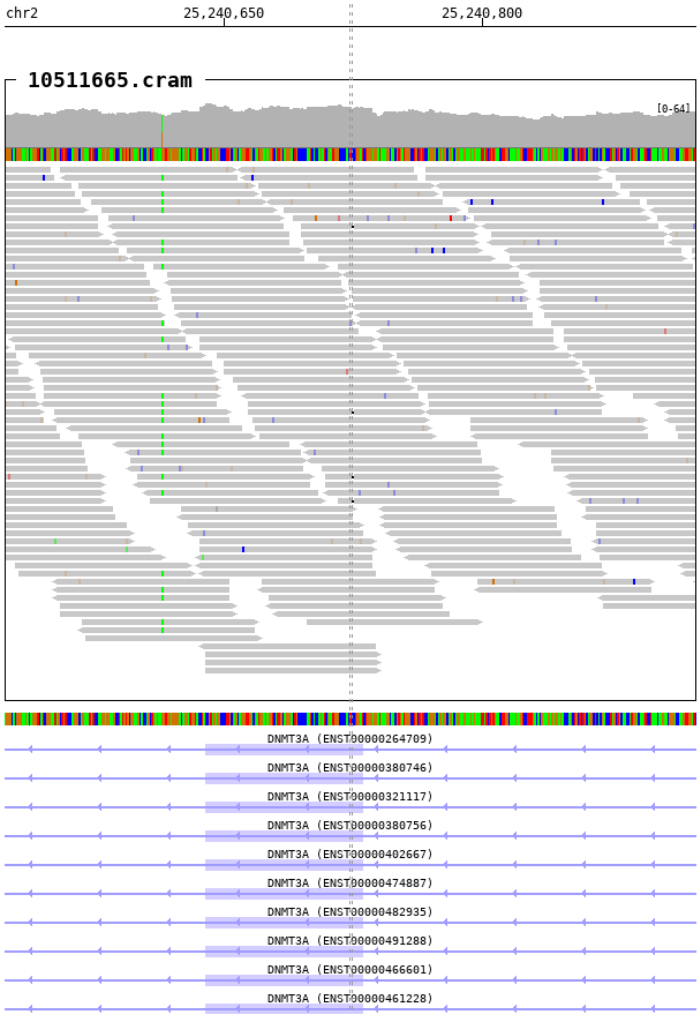
10.68. chr2_25240720_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
60524	chr2_25240720_C/T	38	4	*DNMT3A*	stop_gained



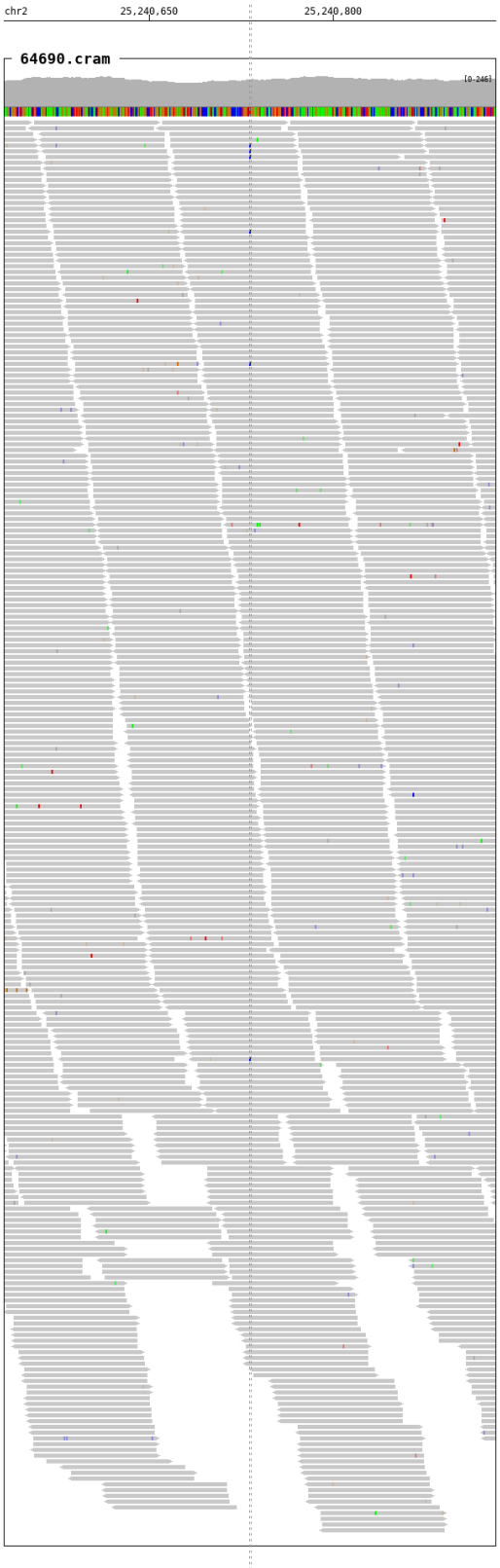
10.69. chr2_25240723_C/-

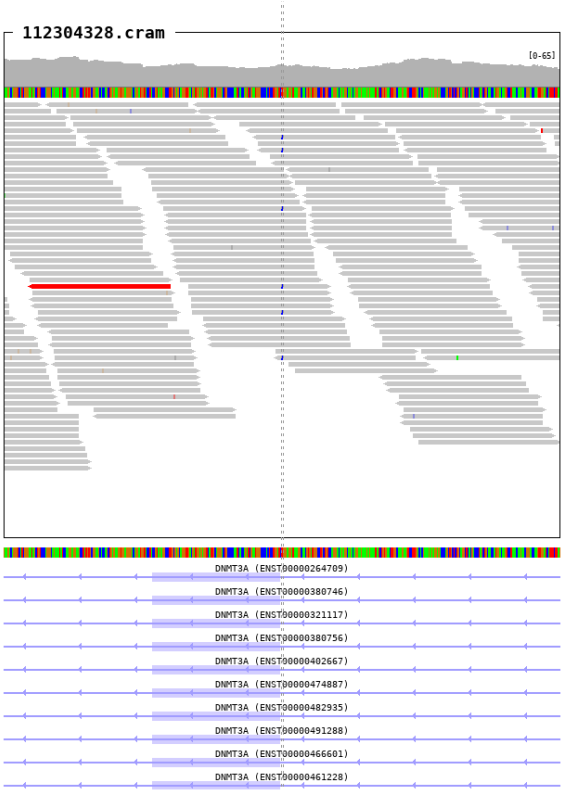
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10511665	chr2_25240723_C/-	48	4	*DNMT3A*	frameshift_variant



10.70. chr2_25240732_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112304328	chr2_25240732_T/C	34	6	*DNMT3A*	splice_acceptor_variant
64690	chr2_25240732_T/C	188	6	*DNMT3A*	splice_acceptor_variant




112304328.cram
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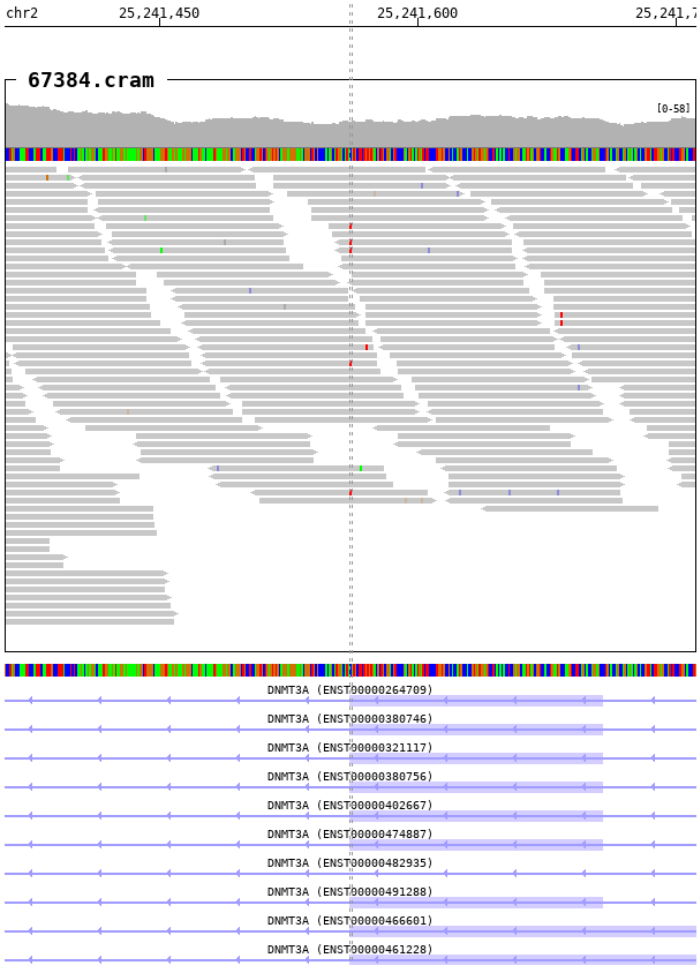
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474887)
DNMT3A (ENST00000482935)
DNMT3A (ENST00000491288)
DNMT3A (ENST00000466601)
DNMT3A (ENST00000461228)

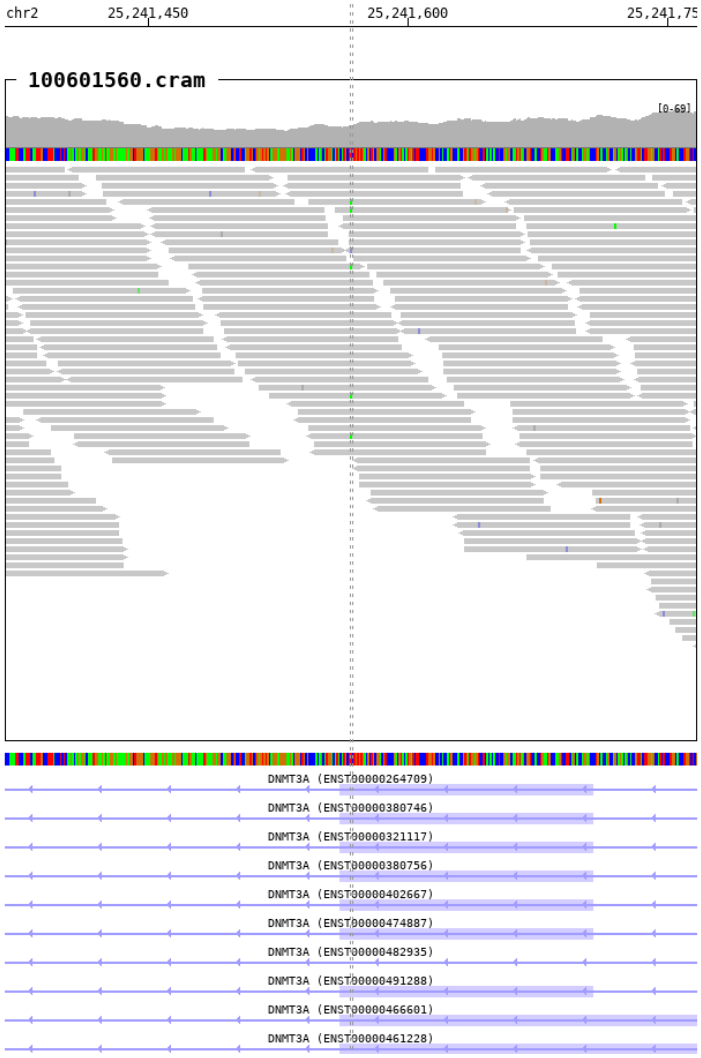
10.71. chr2_25241561_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
67384	chr2_25241561_C/T	26	5	*DNMT3A*	splice_donor_variant



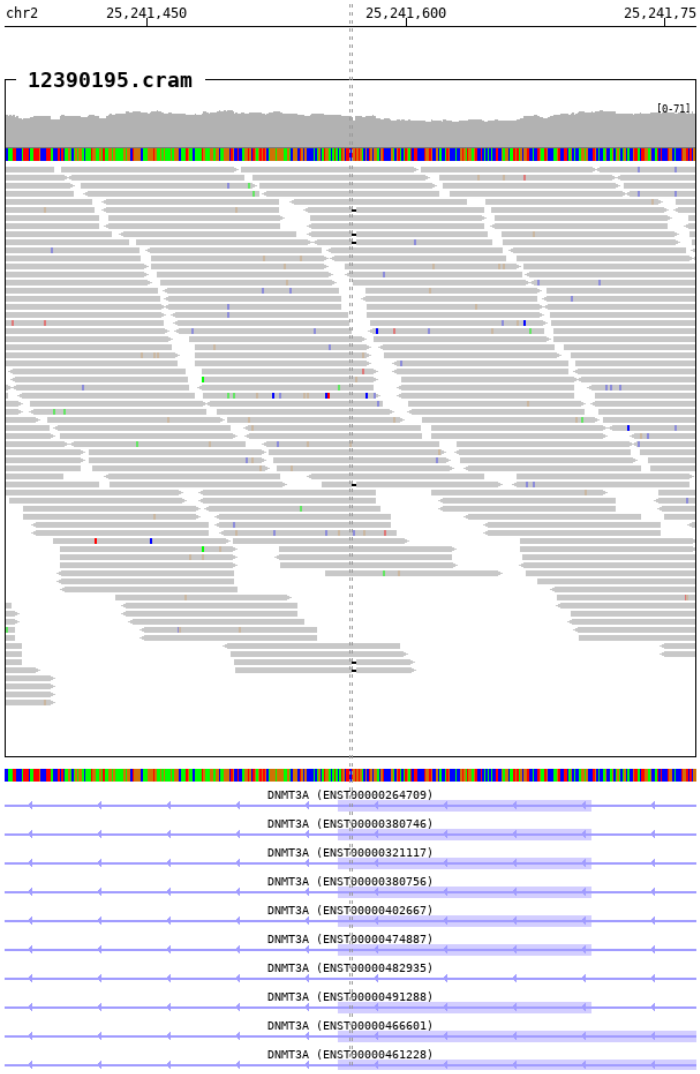
10.72. chr2_25241567_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100601560	chr2_25241567_T/A	29	5	*DNMT3A*	stop_gained



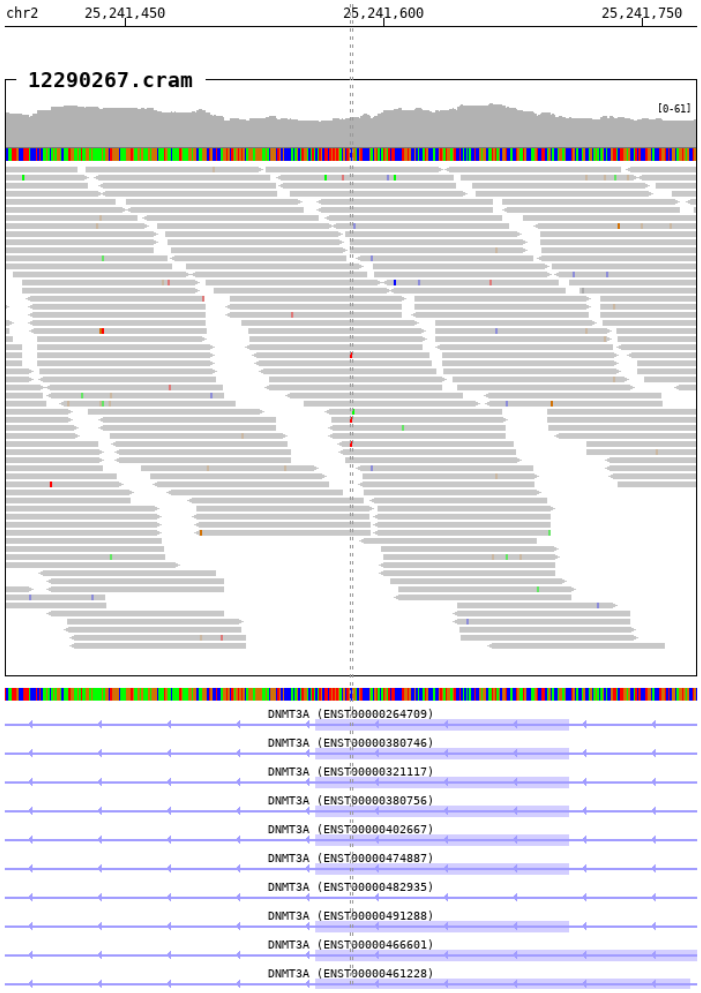
10.73. chr2_25241568_TG/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12390195	chr2_25241568_TG/-	40	6	*DNMT3A*	frameshift_variant



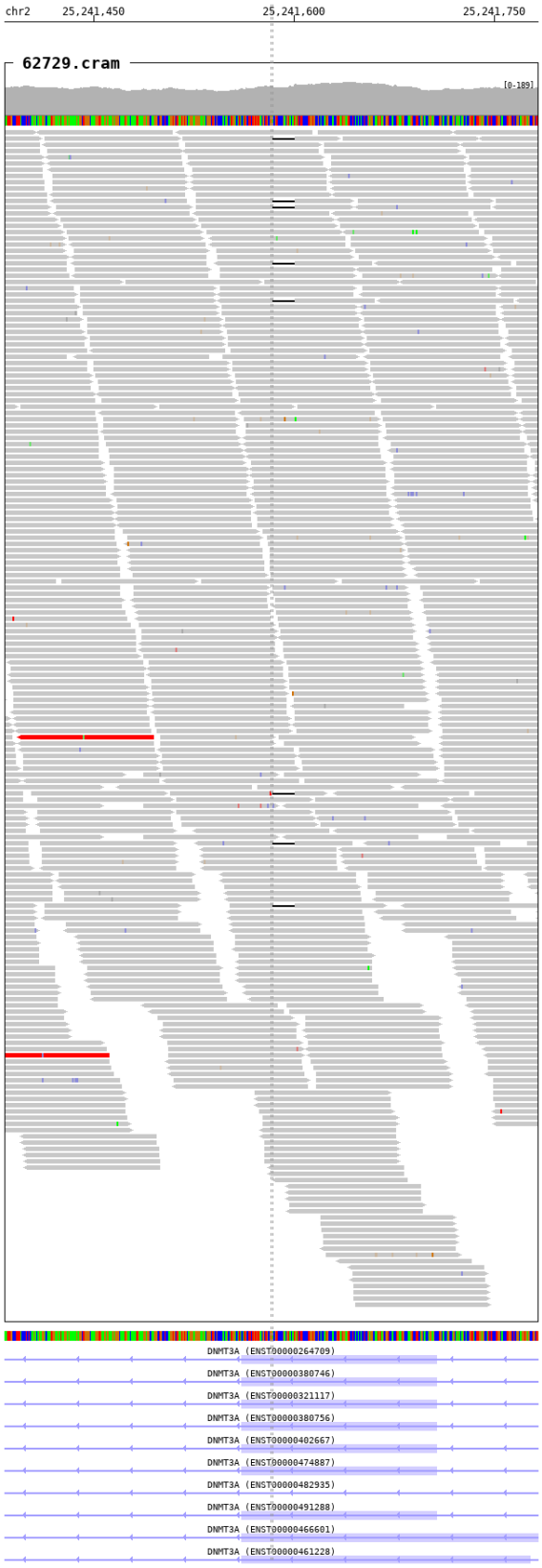
10.74. chr2_25241581_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12290267	chr2_25241581_C/T	34	3	*DNMT3A*	missense_variant



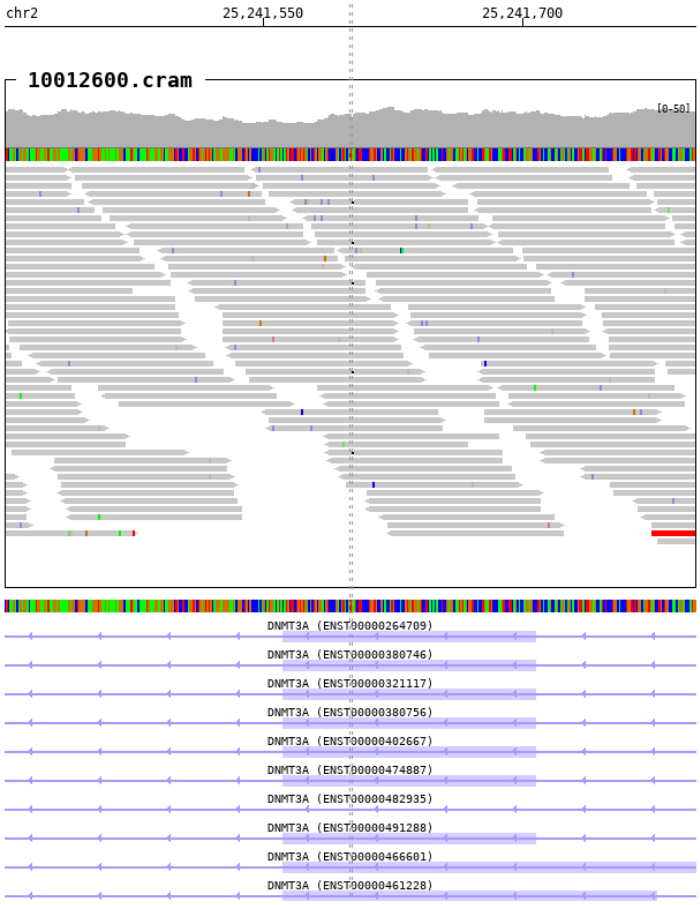
10.75. chr2_25241583_ACGTCCCCGACGTACA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
62729	chr2_25241583_ACGTCCCCGACGTACA/-	173	10	*DNMT3A*	frameshift_variant



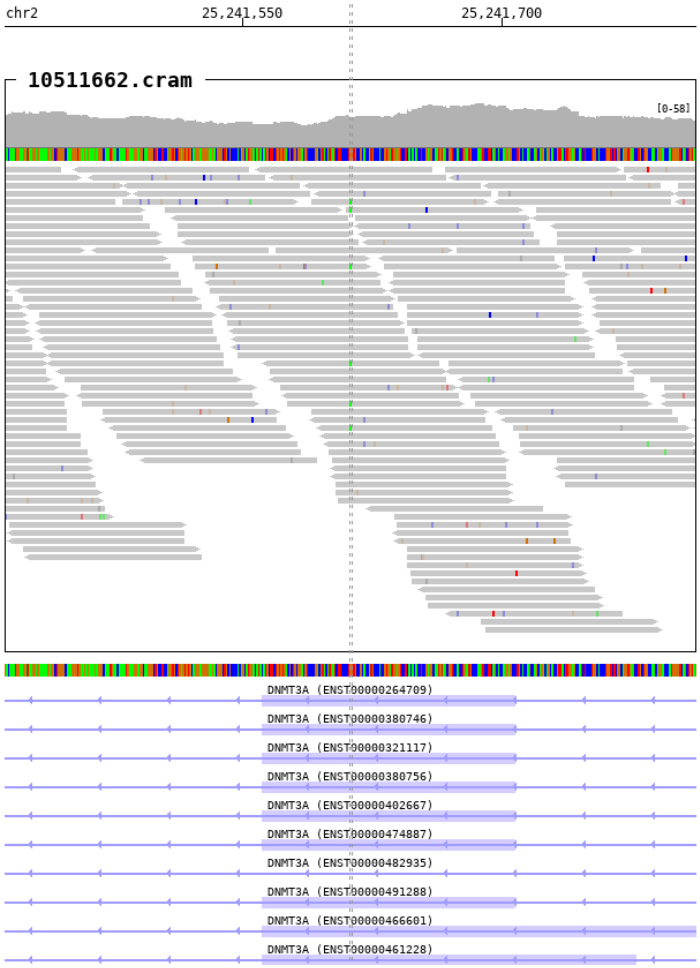
10.76. chr2_25241600_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10012600	chr2_25241600_G/-	31	4	*DNMT3A*	frameshift_variant



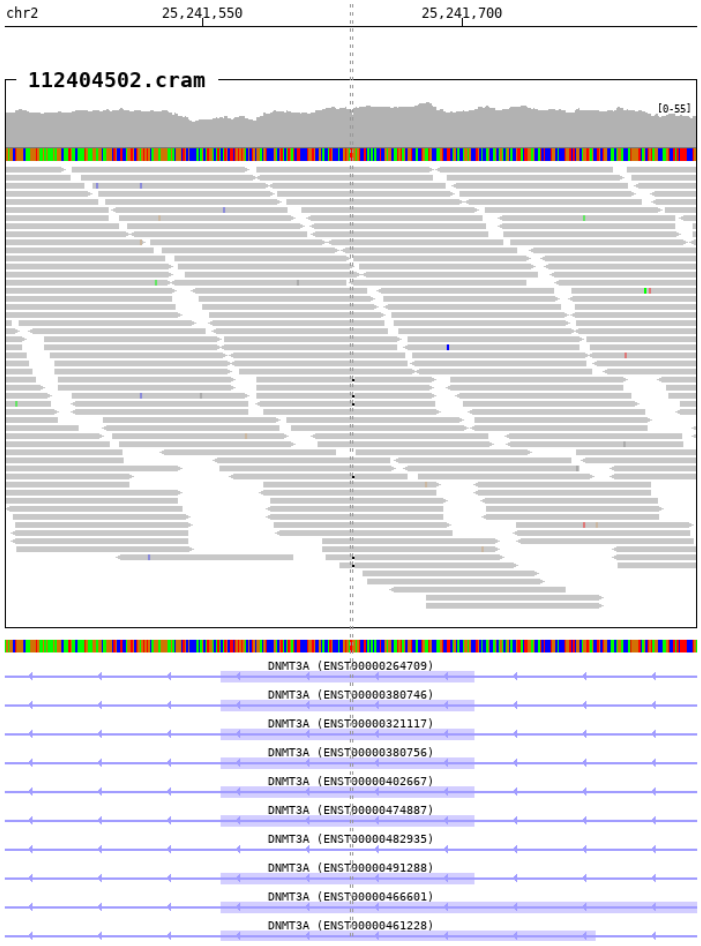
10.77. chr2_25241612_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10511662	chr2_25241612_G/A	32	6	*DNMT3A*	stop_gained



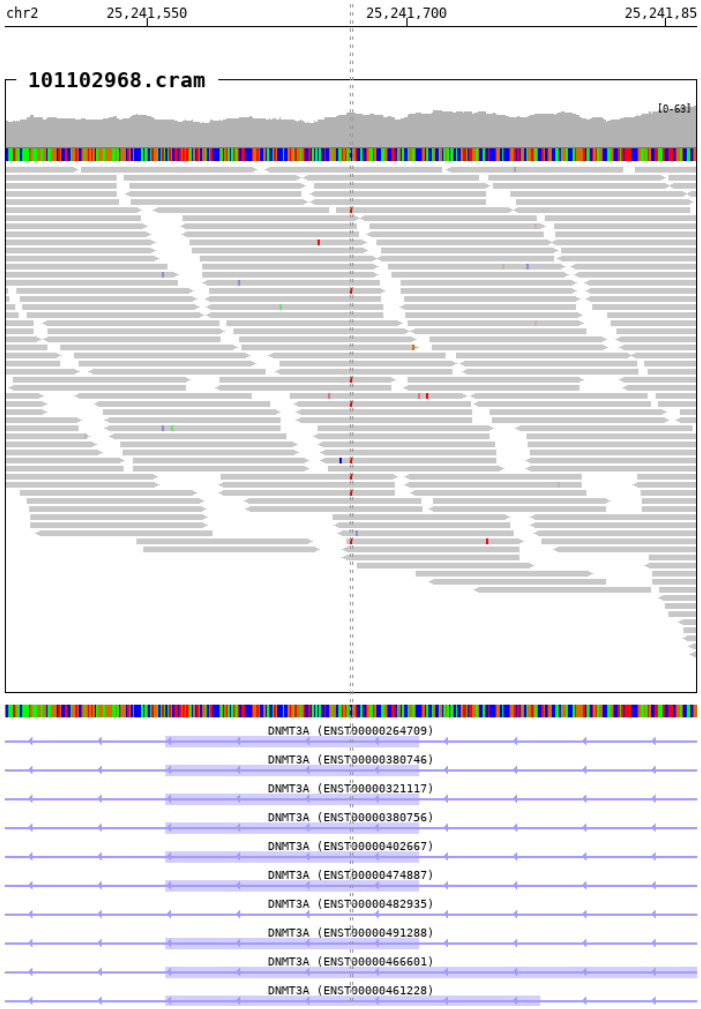
10.78. chr2_25241636_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112404502	chr2_25241636_G/-	39	6	*DNMT3A*	frameshift_variant



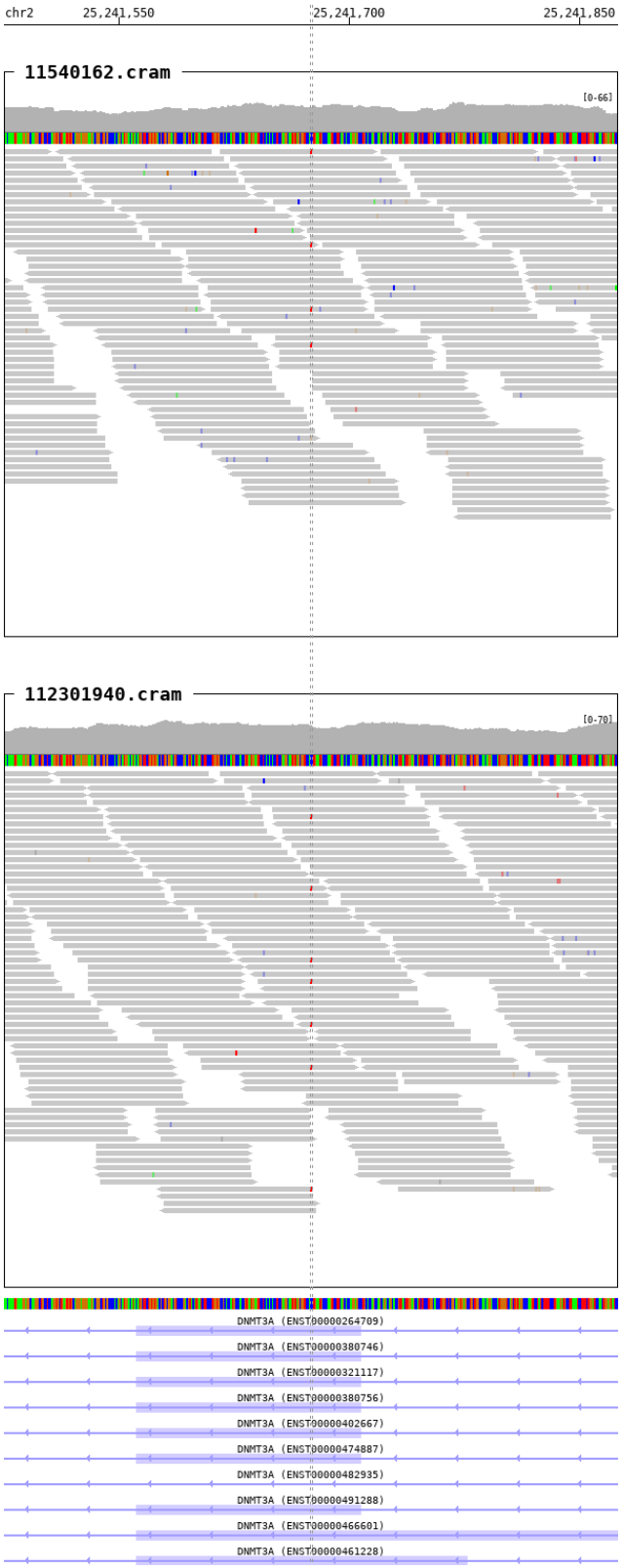
10.79. chr2_25241668_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101102968	chr2_25241668_C/T	37	8	*DNMT3A*	missense_variant



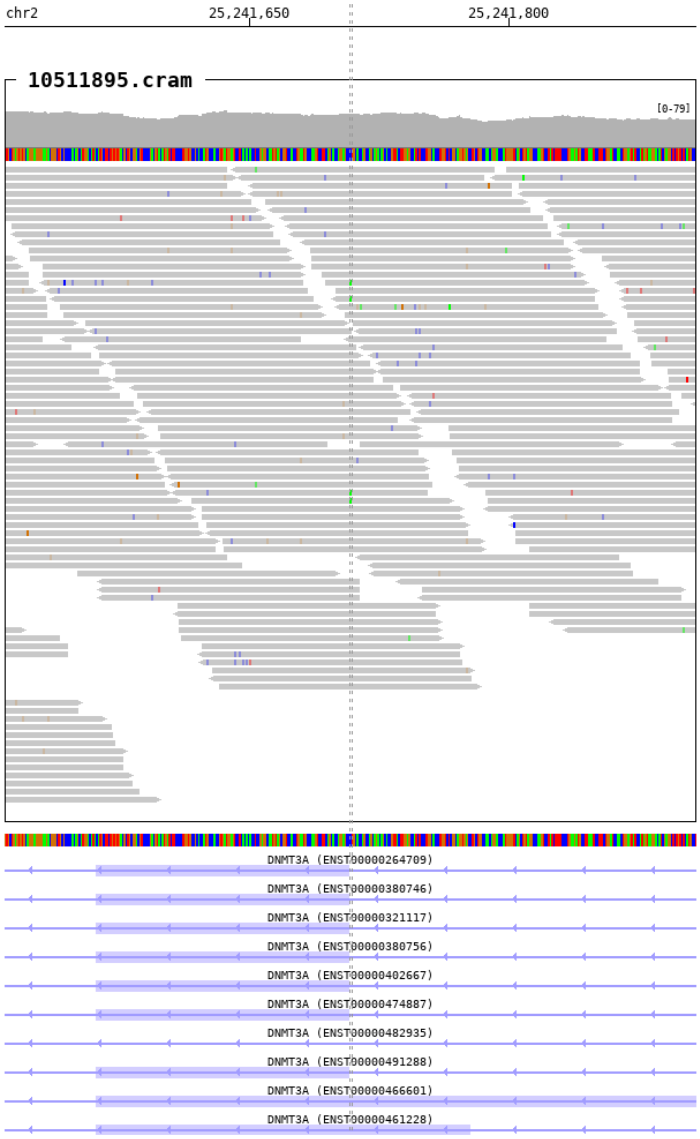
10.80. chr2_25241675_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301940	chr2_25241675_C/T	43	7	*DNMT3A*	missense_variant
11540162	chr2_25241675_C/T	36	4	*DNMT3A*	missense_variant



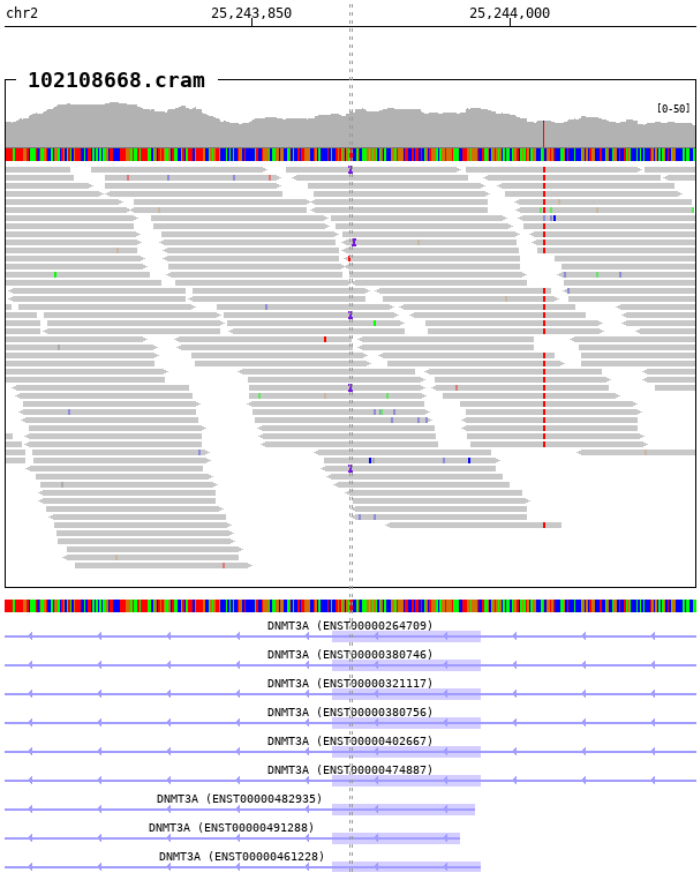
10.81. chr2_25241708_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10511895	chr2_25241708_C/A	55	4	*DNMT3A*	splice_acceptor_variant



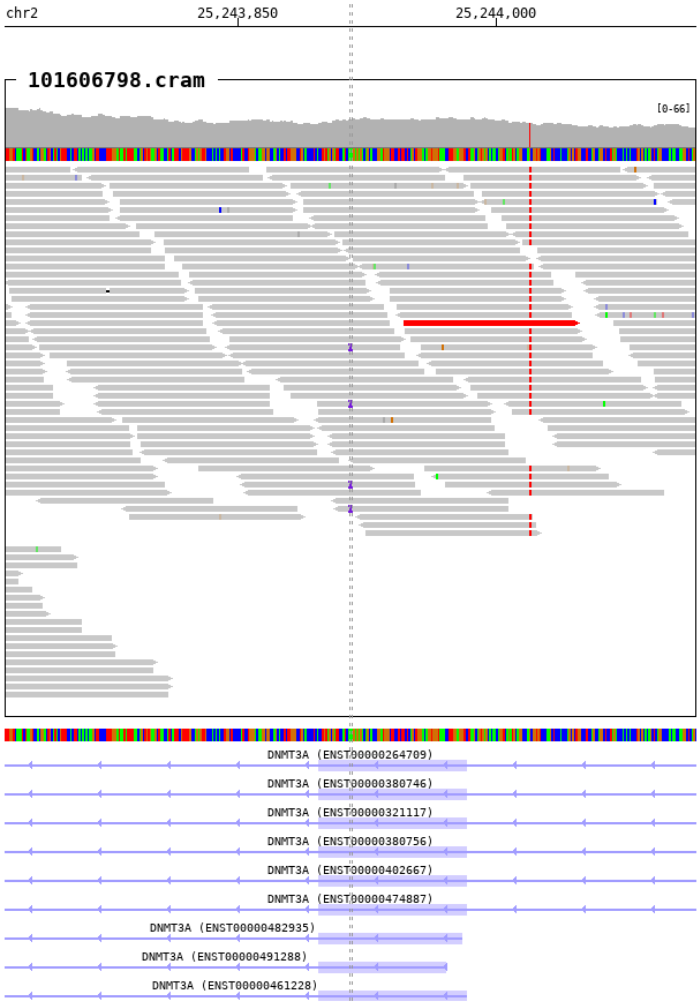
10.82. chr2_25243907_-/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102108668	chr2_25243907_-/T	29	6	*DNMT3A*	frameshift_variant



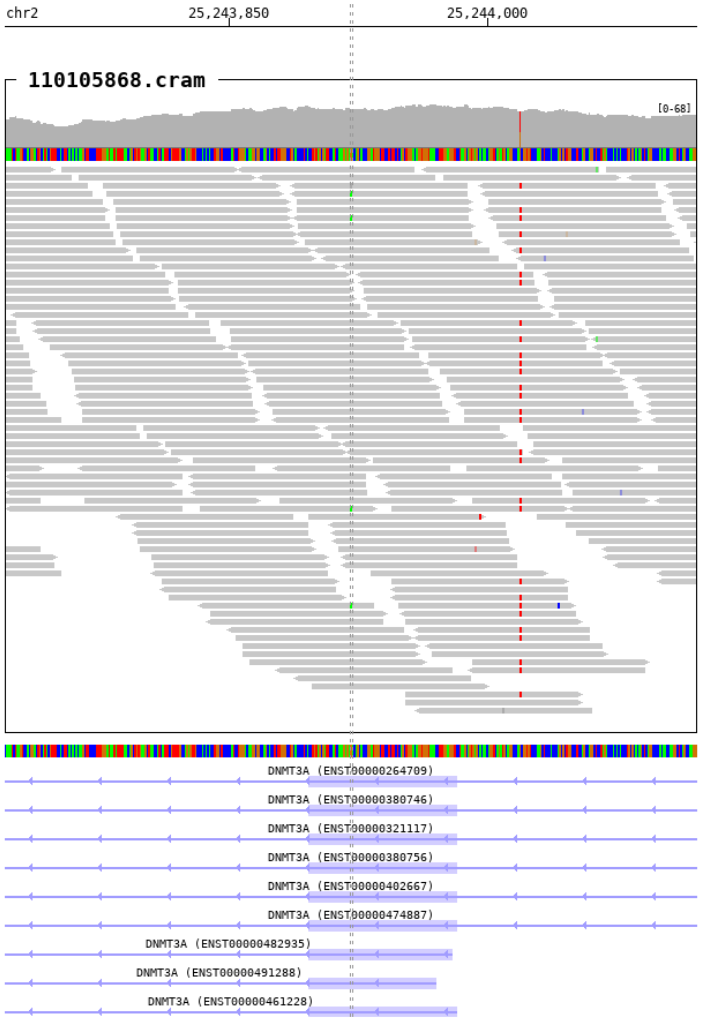
10.83. chr2_25243915_-/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101606798	chr2_25243915_-/T	35	4	*DNMT3A*	frameshift_variant



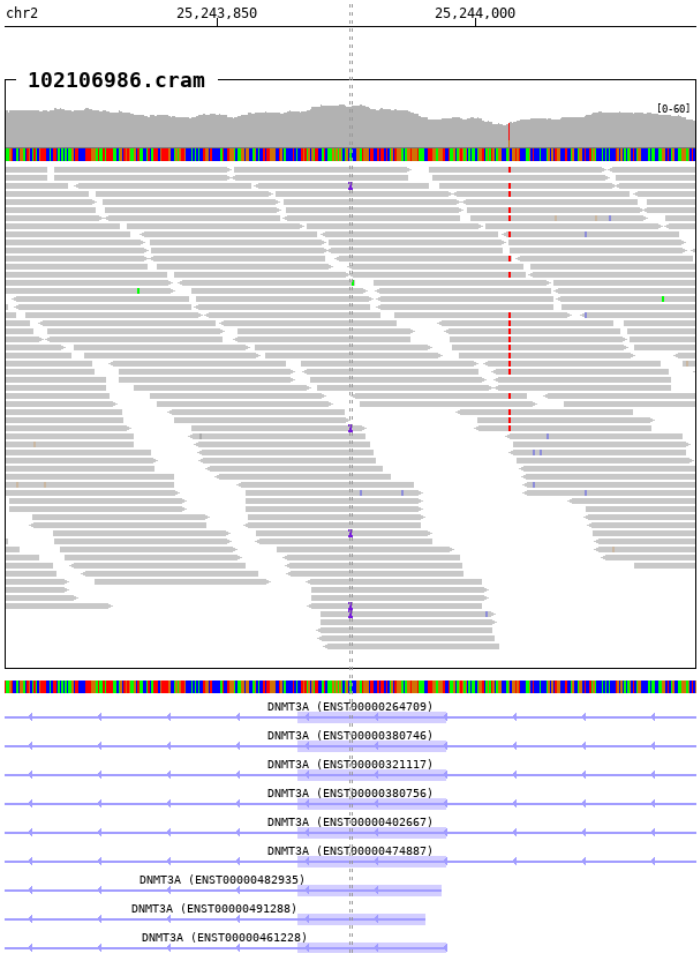
10.84. chr2_25243921_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110105868	chr2_25243921_G/A	52	4	*DNMT3A*	missense_variant



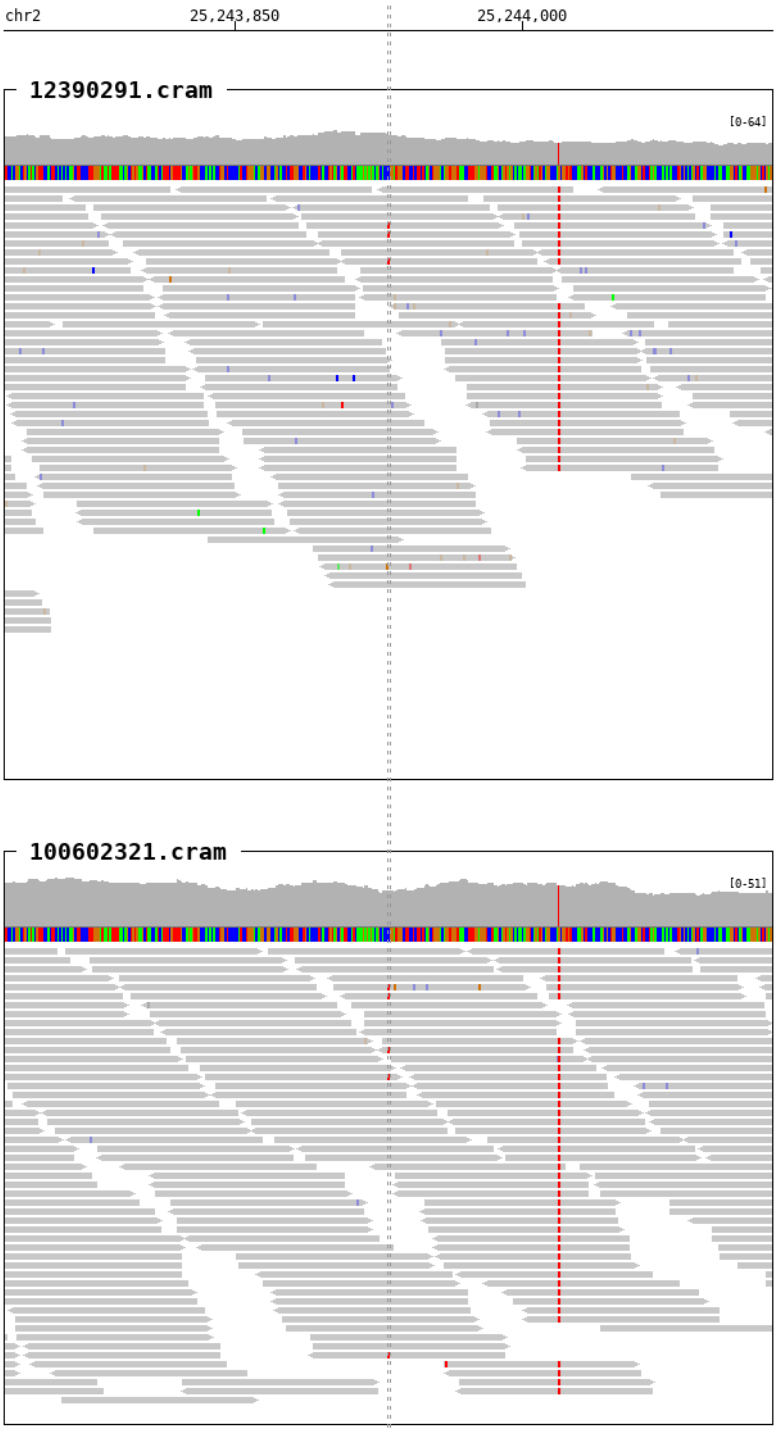
10.85. chr2_25243927_-/A

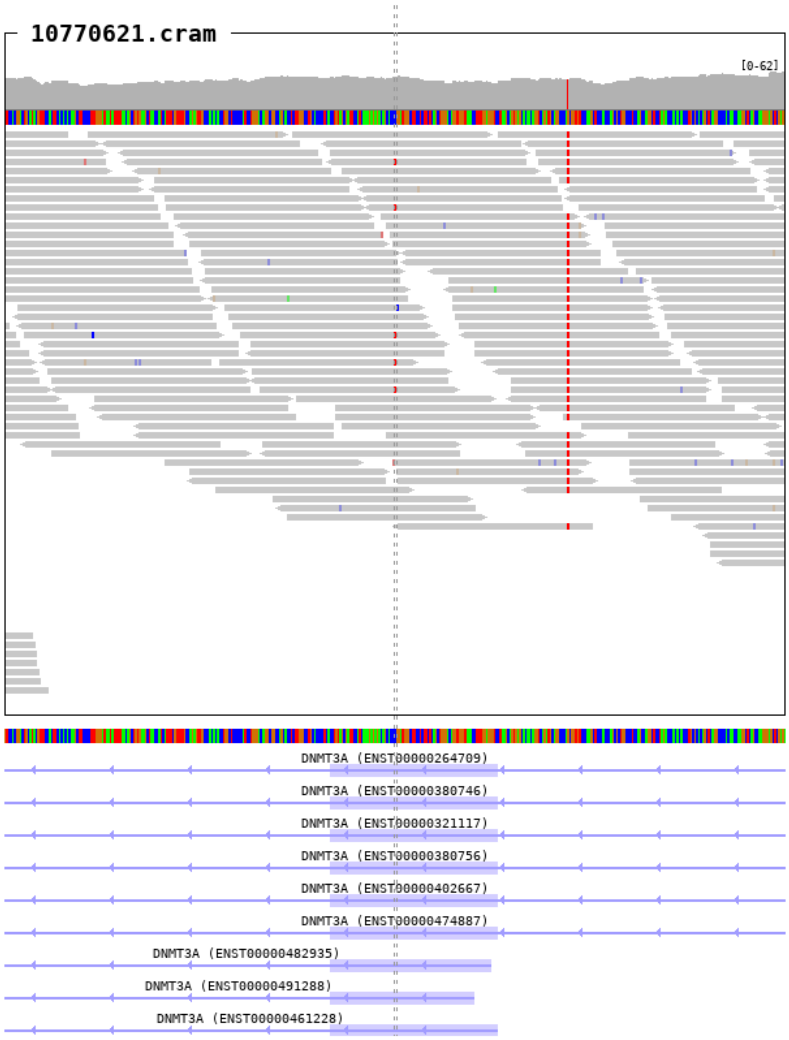
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102106986	chr2_25243927_-/A	47	6	*DNMT3A*	frameshift_variant



10.86. chr2_25243930_C/T

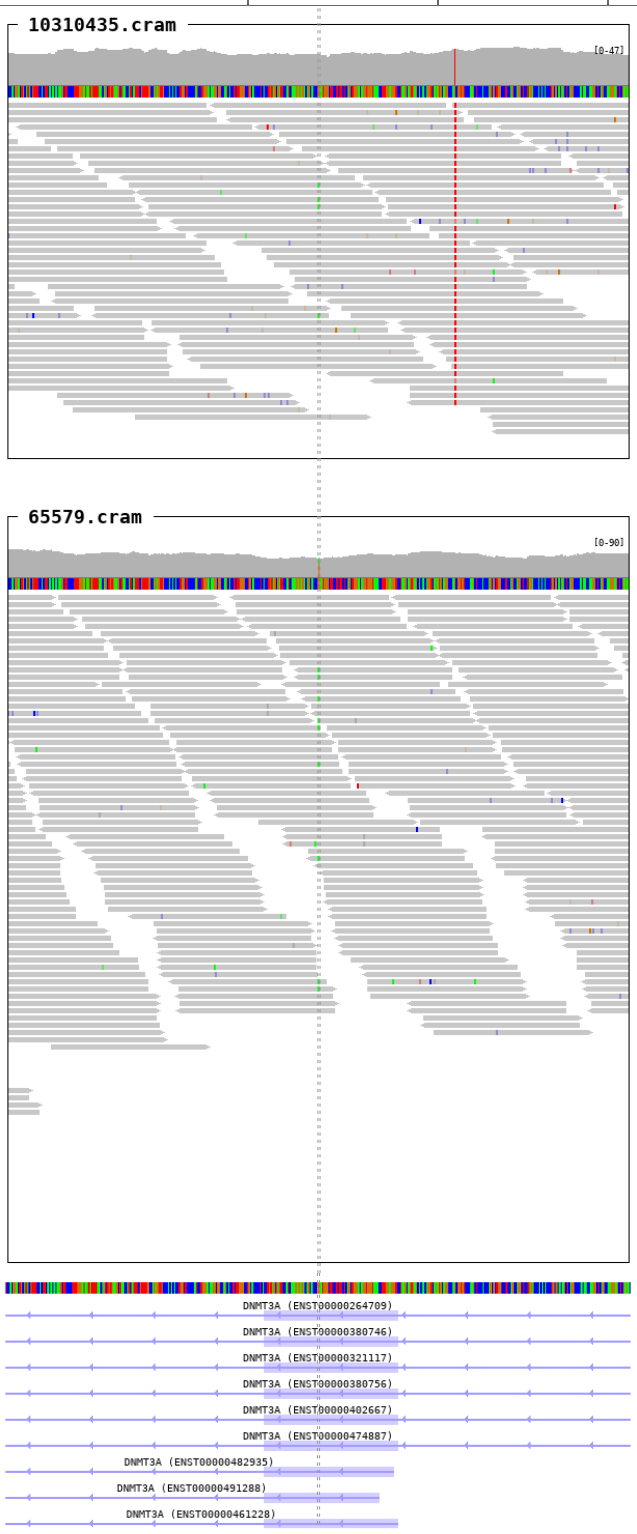
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100602321	chr2_25243930_C/T	32	4	*DNMT3A*	missense_variant
10770621	chr2_25243930_C/T	35	5	*DNMT3A*	missense_variant
12390291	chr2_25243930_C/T	35	3	*DNMT3A*	missense_variant




10770621.cram
[0-62]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474887)
DNMT3A (ENST00000482935)
DNMT3A (ENST00000491288)
DNMT3A (ENST00000461228)

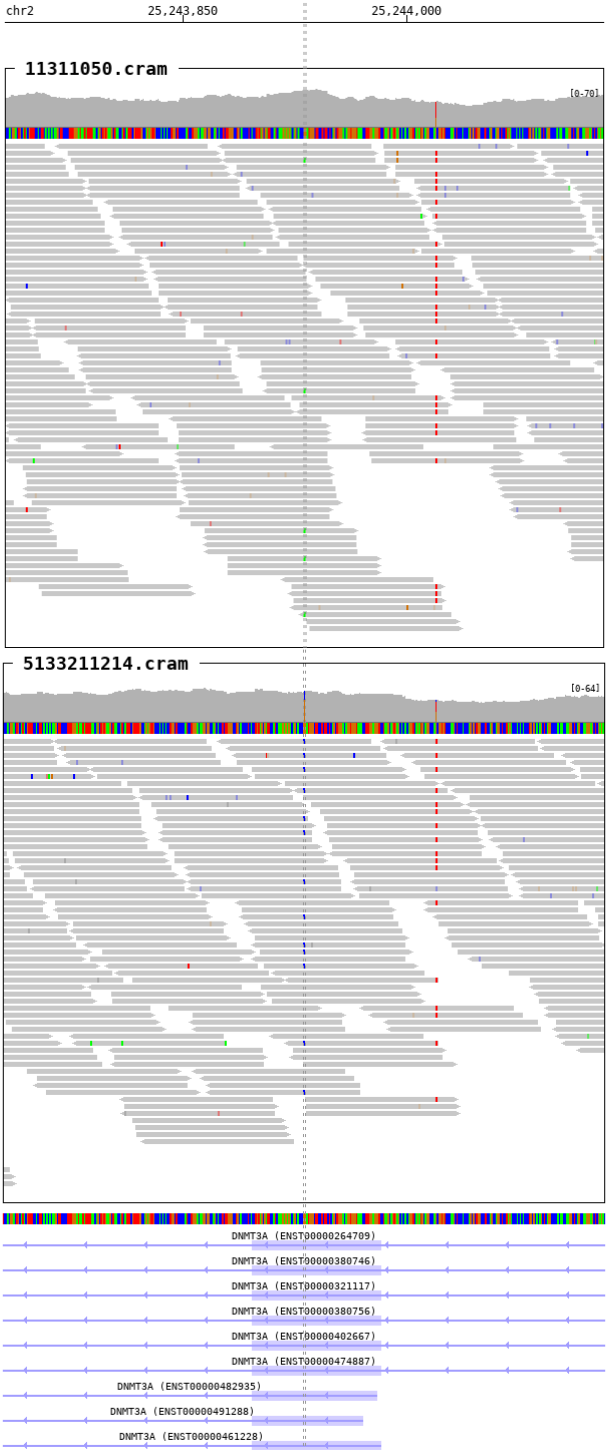
10.87. chr2_25243931_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10310435	chr2_25243931_G/A	30	4	*DNMT3A*	missense_variant
65579	chr2_25243931_G/A	33	9	*DNMT3A*	missense_variant



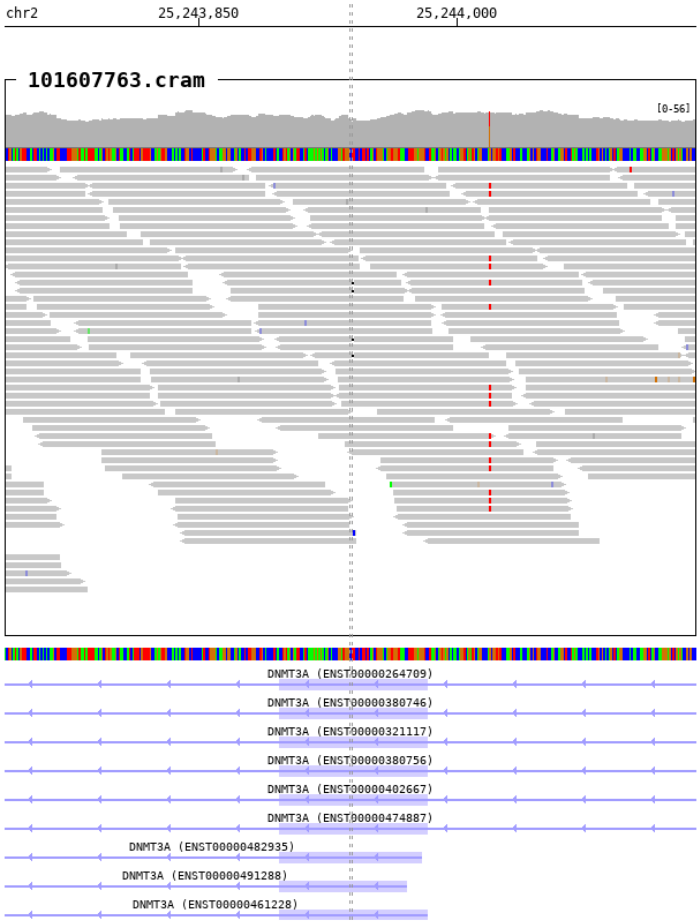
10.88. chr2_25243931_G/C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11311050	chr2_25243931_G/C/A	57	5	*DNMT3A*	missense_variant
5133211214	chr2_25243931_G/C/A	37	13	*DNMT3A*	missense_variant



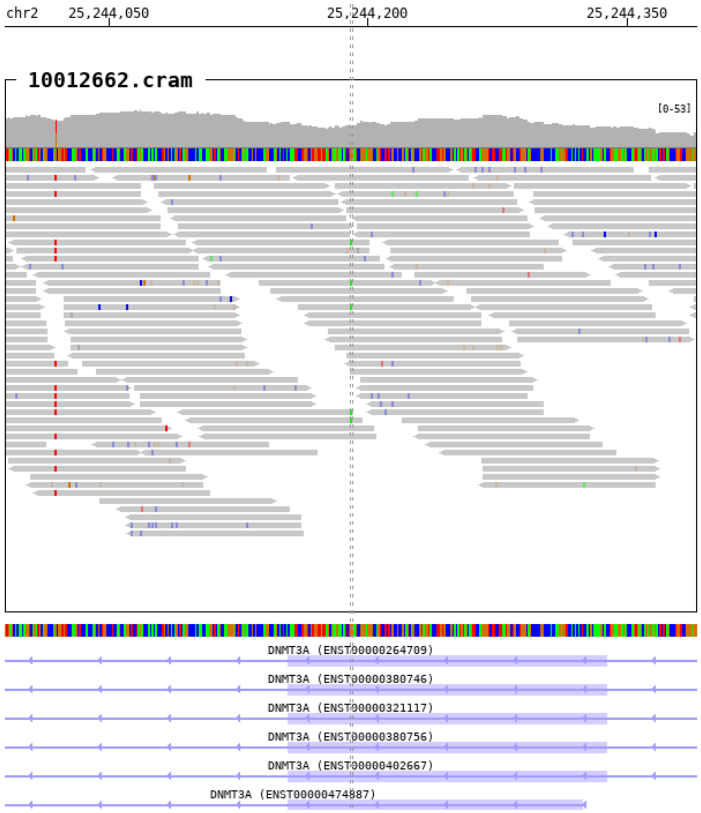
10.89. chr2_25243938_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101607763	chr2_25243938_T/-	30	5	*DNMT3A*	frameshift_variant



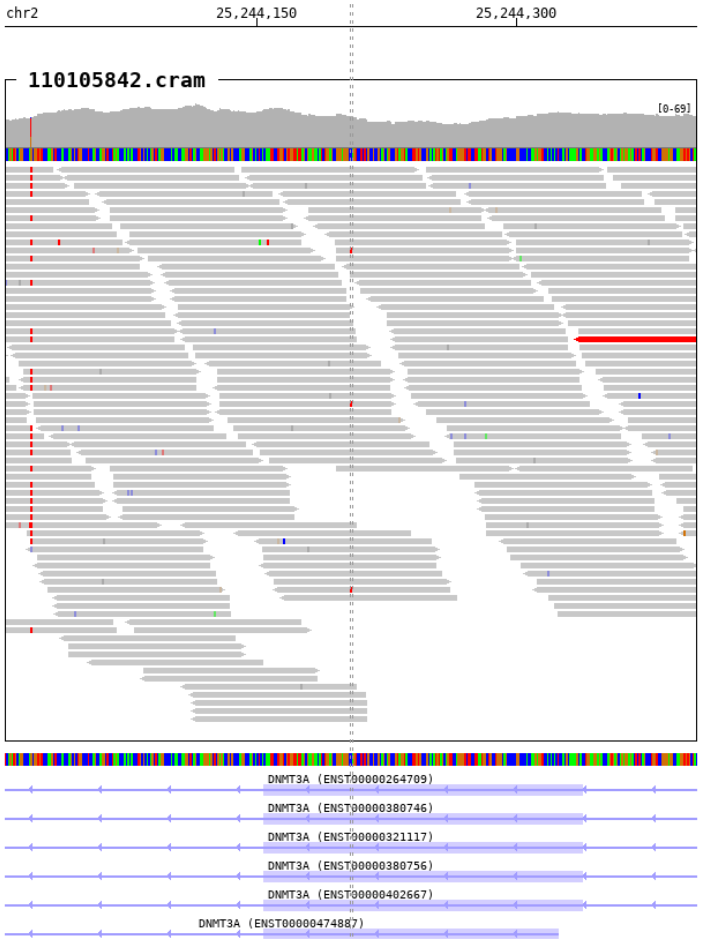
10.90. chr2_25244190_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10012662	chr2_25244190_G/A	22	5	*DNMT3A*	stop_gained



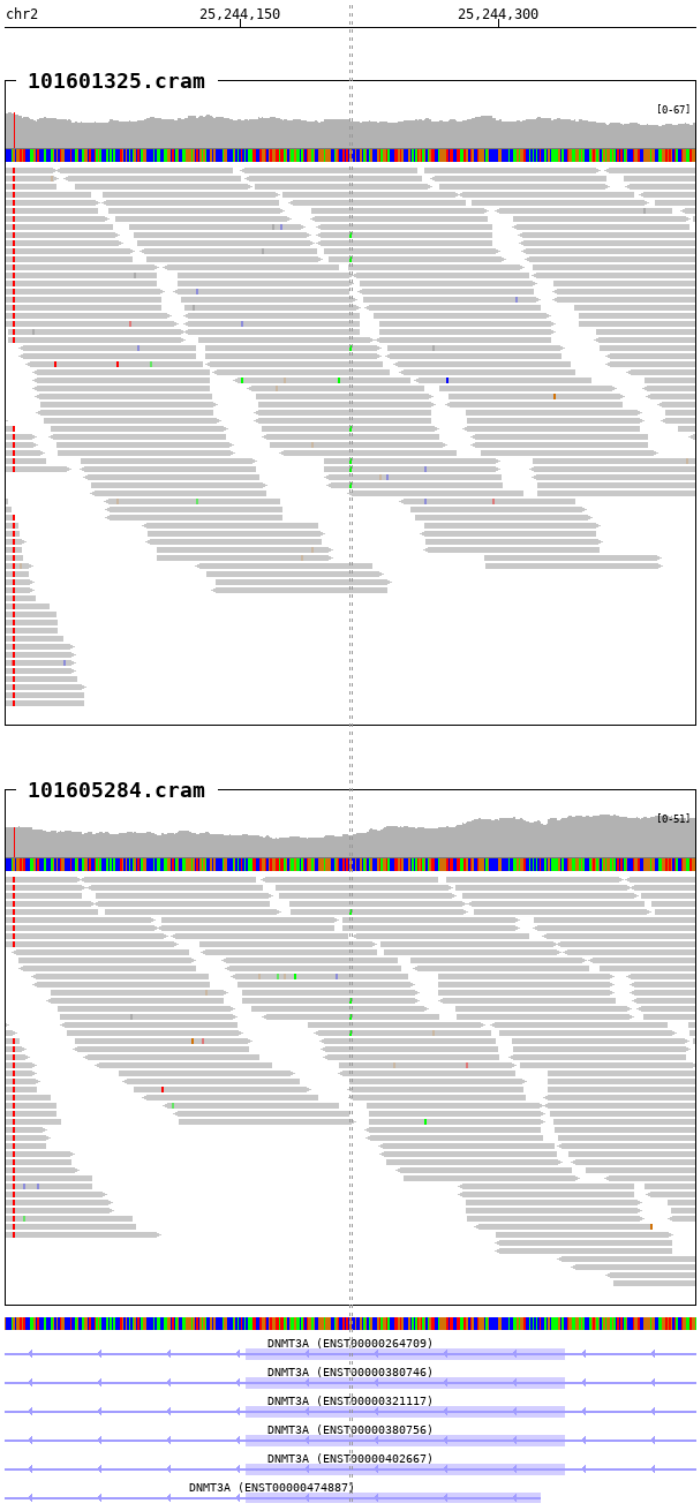
10.91. chr2_25244204_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110105842	chr2_25244204_C/T	45	3	*DNMT3A*	stop_gained



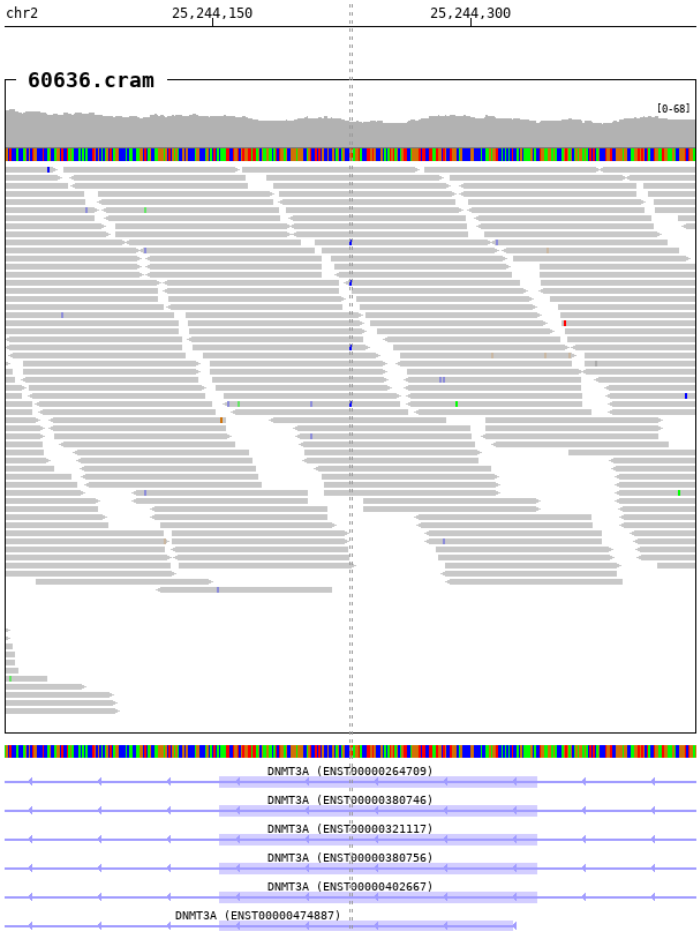
10.92. chr2_25244214_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101601325	chr2_25244214_G/A	33	6	*DNMT3A*	stop_gained
101605284	chr2_25244214_G/A	21	4	*DNMT3A*	stop_gained



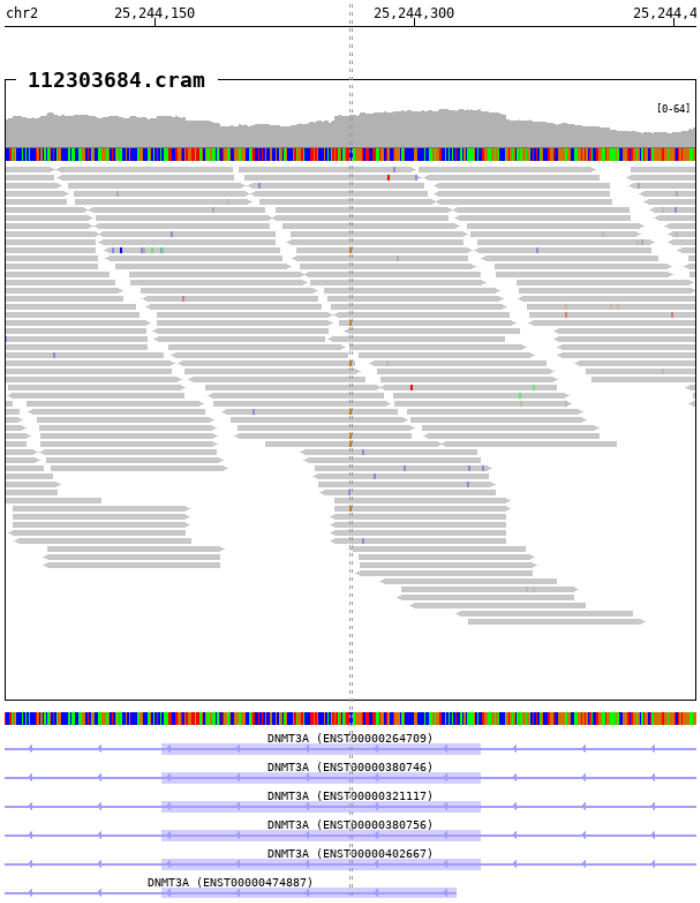
10.93. chr2_25244230_G/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
60636	chr2_25244230_G/C	35	4	*DNMT3A*	stop_gained



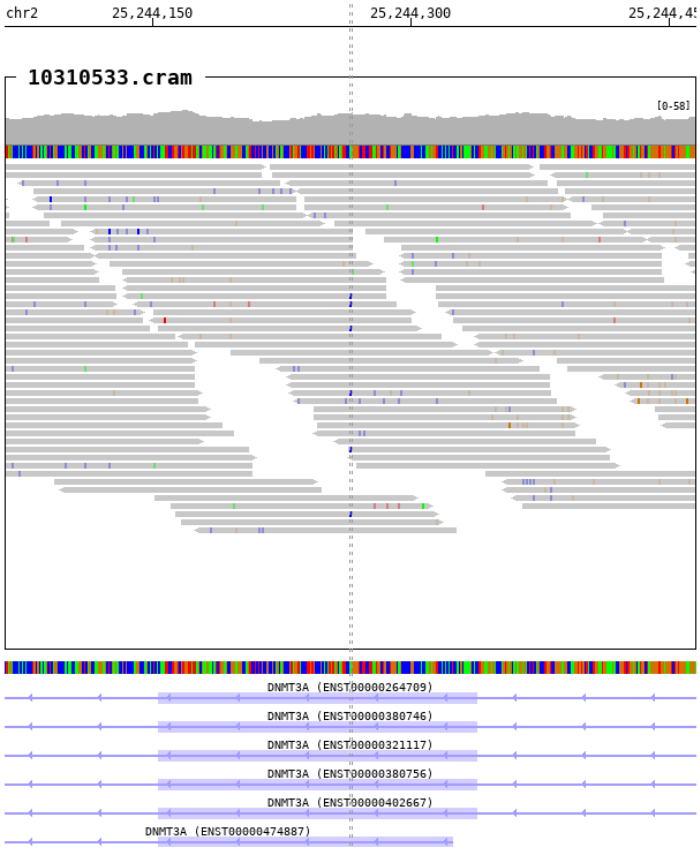
10.94. chr2_25244263_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112303684	chr2_25244263_C/G	38	7	*DNMT3A*	missense_variant



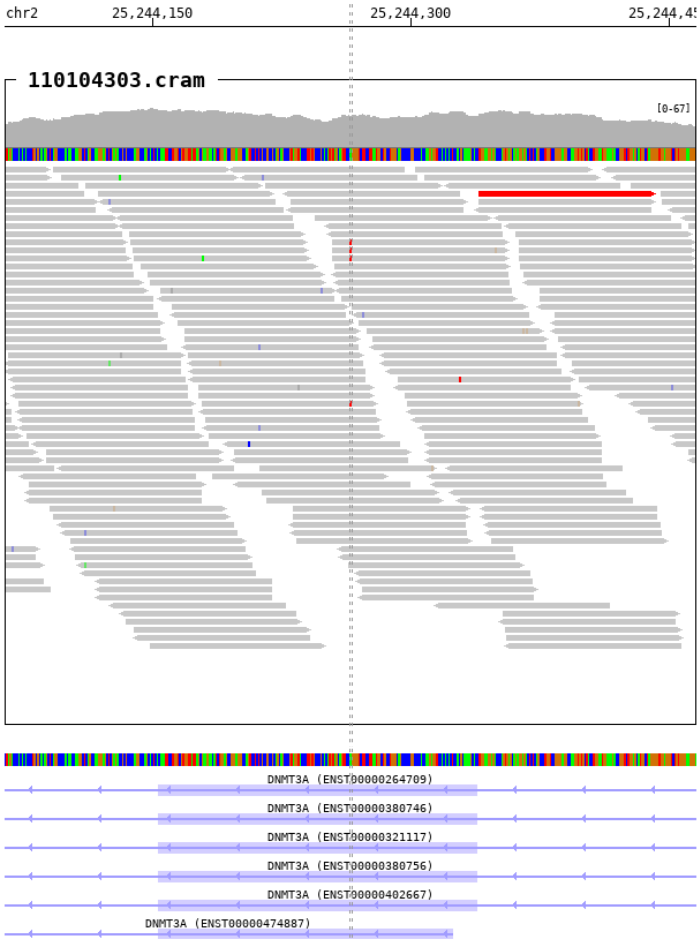
10.95. chr2_25244265_A/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10310533	chr2_25244265_A/C	33	6	*DNMT3A*	missense_variant



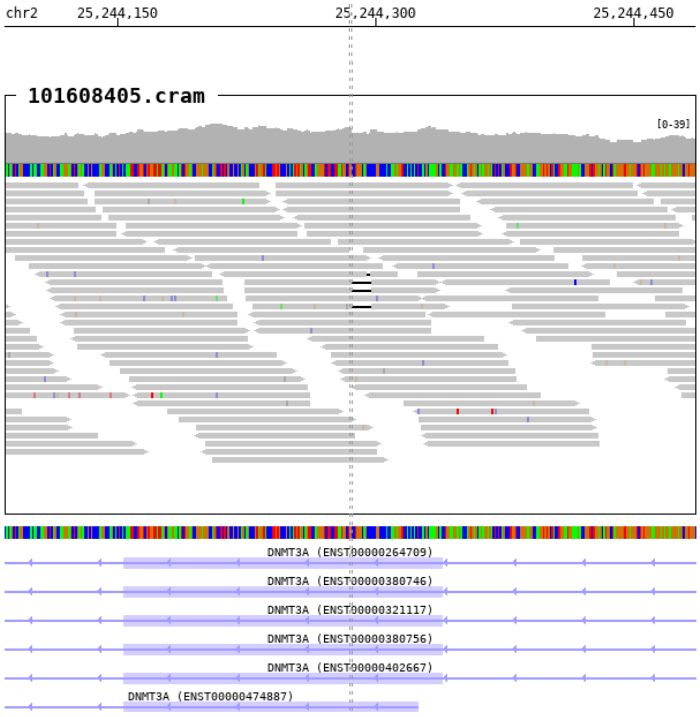
10.96. chr2_25244265_A/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110104303	chr2_25244265_A/T	42	3	*DNMT3A*	missense_variant



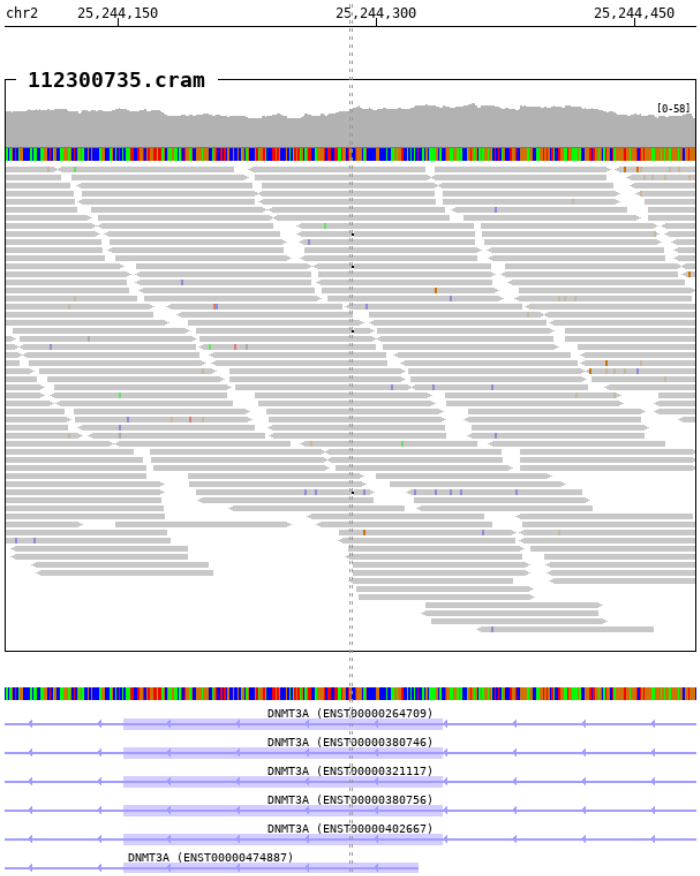
10.97. chr2_25244285_CCTGGGCAGCC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101608405	chr2_25244285_CCTGGGCAGCC/-	27	3	*DNMT3A*	frameshift_variant



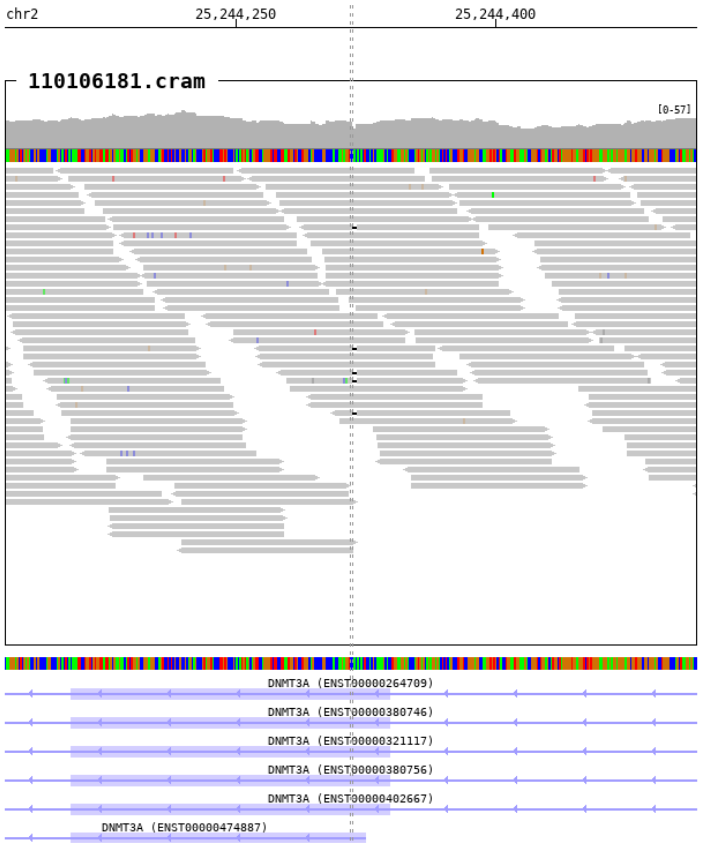
10.98. chr2_25244285_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112300735	chr2_25244285_C/-	44	5	*DNMT3A*	frameshift_variant



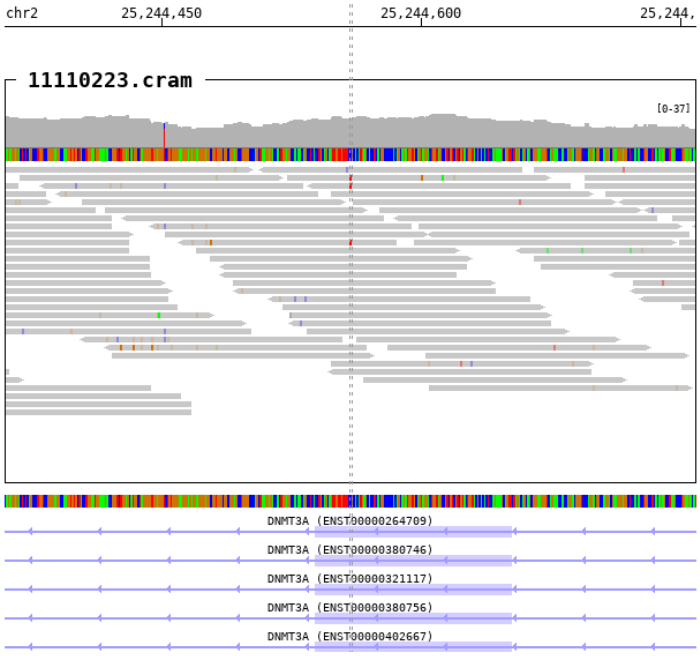
10.99. chr2_25244316_CA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110106181	chr2_25244316_CA/-	25	6	*DNMT3A*	frameshift_variant



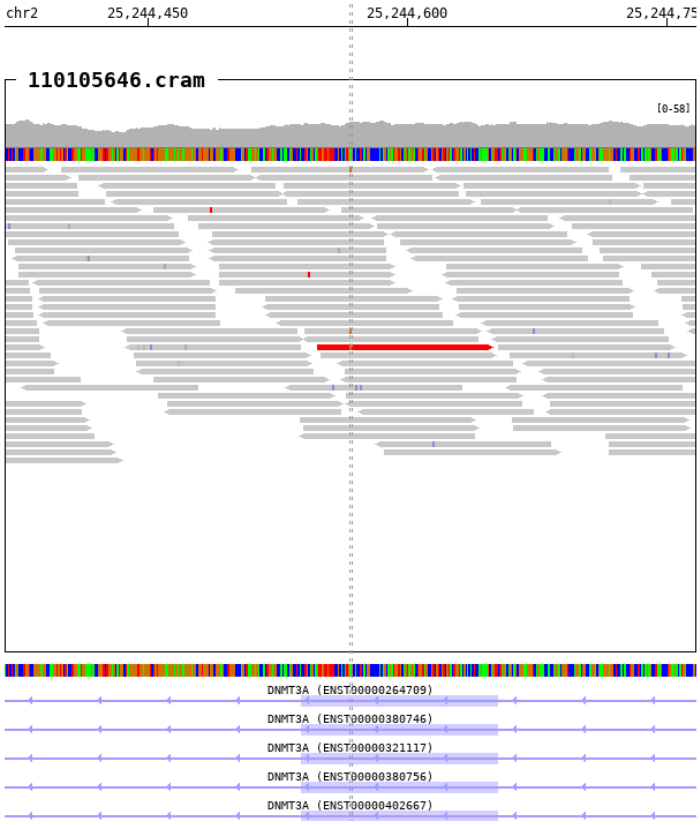
10.100. chr2_25244559_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11110223	chr2_25244559_C/T	21	3	*DNMT3A*	missense_variant



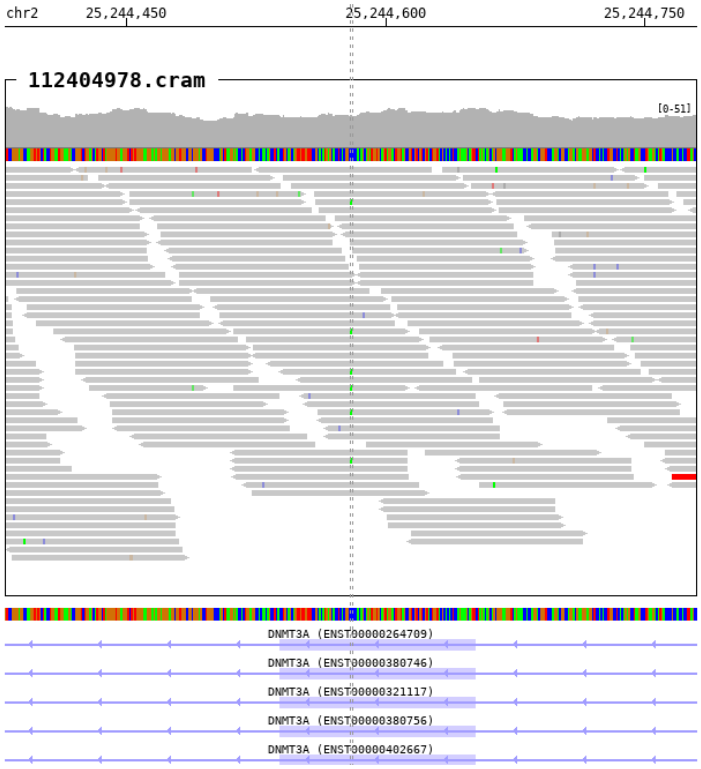
10.101. chr2_25244567_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110105646	chr2_25244567_A/G	28	3	*DNMT3A*	missense_variant



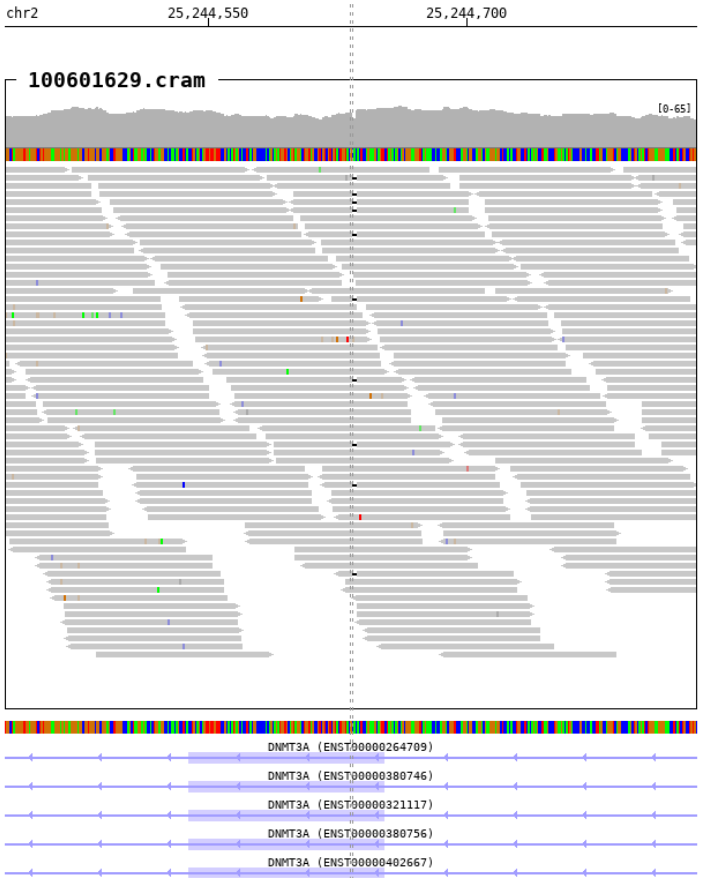
10.102. chr2_25244580_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112404978	chr2_25244580_C/A	30	5	*DNMT3A*	missense_variant



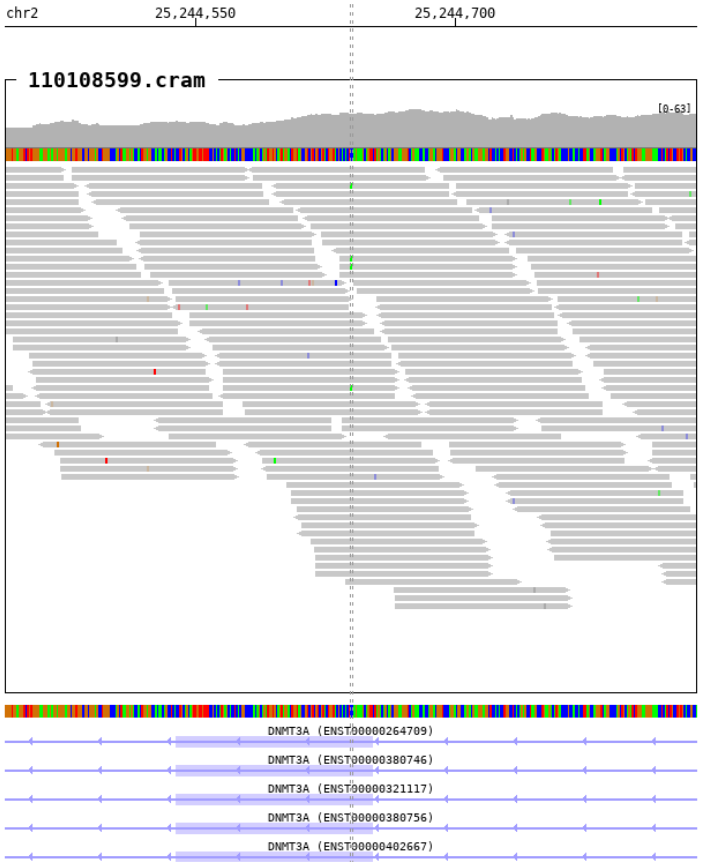
10.103. chr2_25244633_CA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100601629	chr2_25244633_CA/-	39	10	*DNMT3A*	frameshift_variant



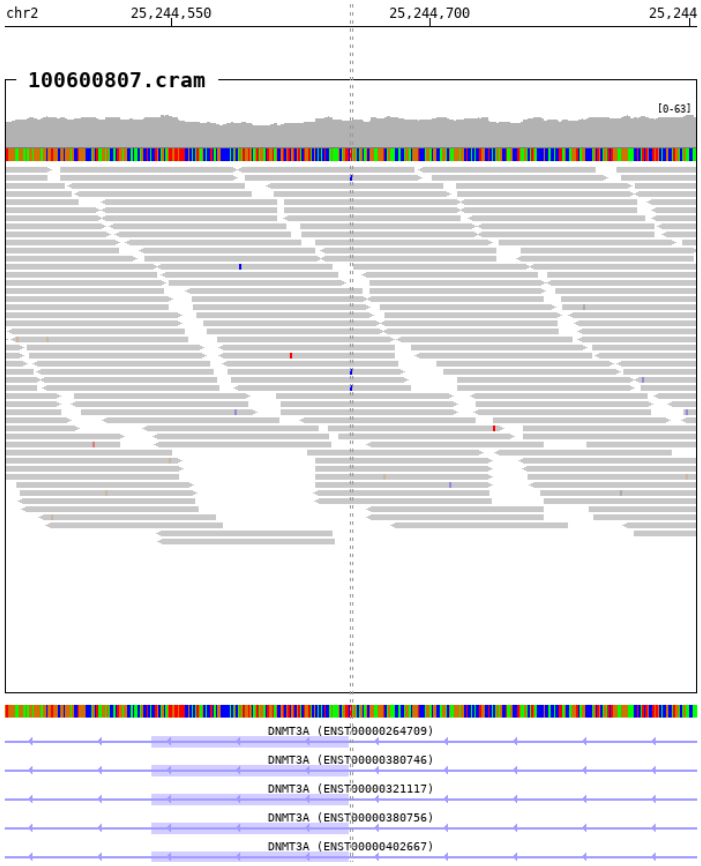
10.104. chr2_25244640_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110108599	chr2_25244640_C/A	42	4	*DNMT3A*	stop_gained



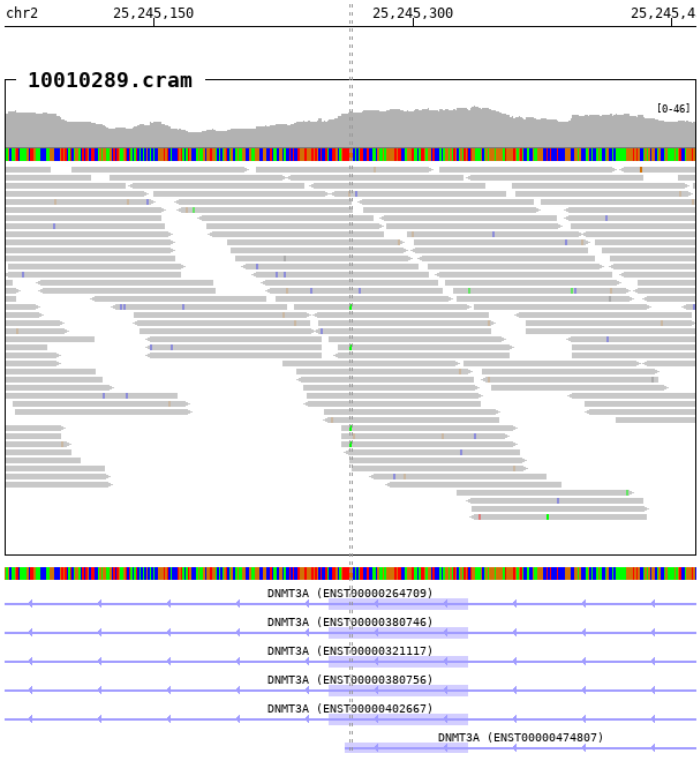
10.105. chr2_25244654_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100600807	chr2_25244654_T/C	33	3	*DNMT3A*	splice_acceptor_variant



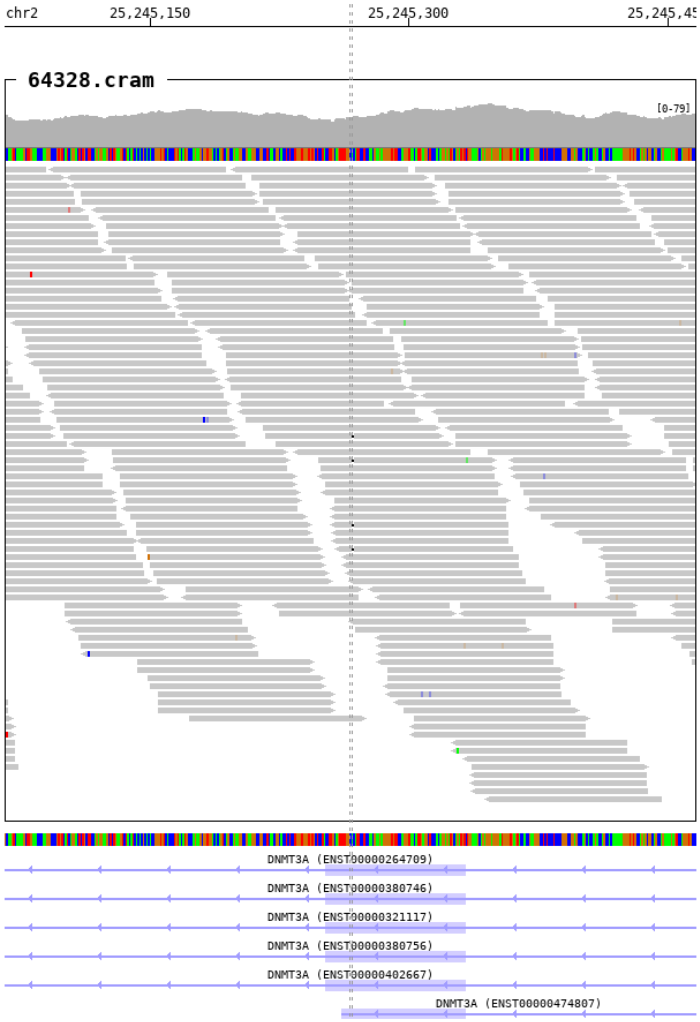
10.106. chr2_25245264_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10010289	chr2_25245264_G/A	32	4	*DNMT3A*	stop_gained



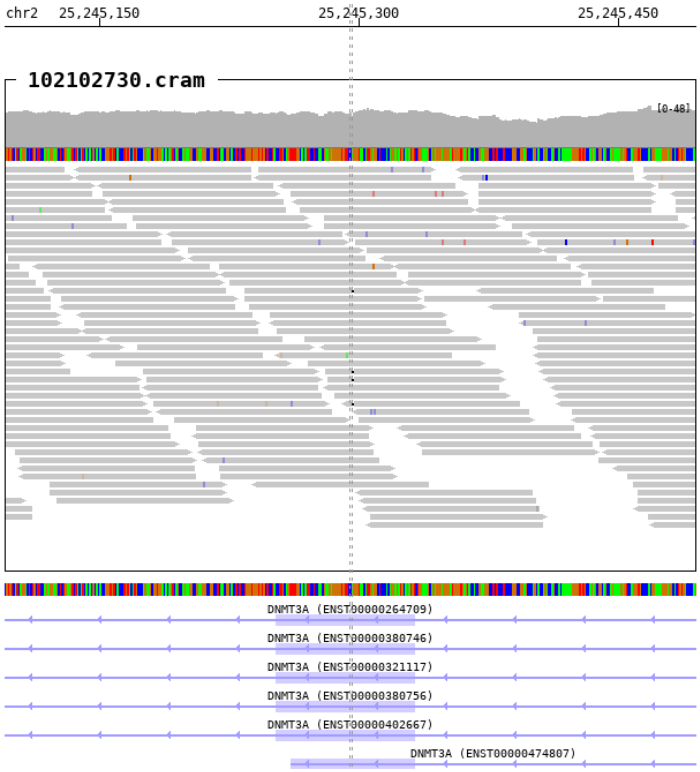
10.107. chr2_25245266_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
64328	chr2_25245266_A/-	48	4	*DNMT3A*	frameshift_variant



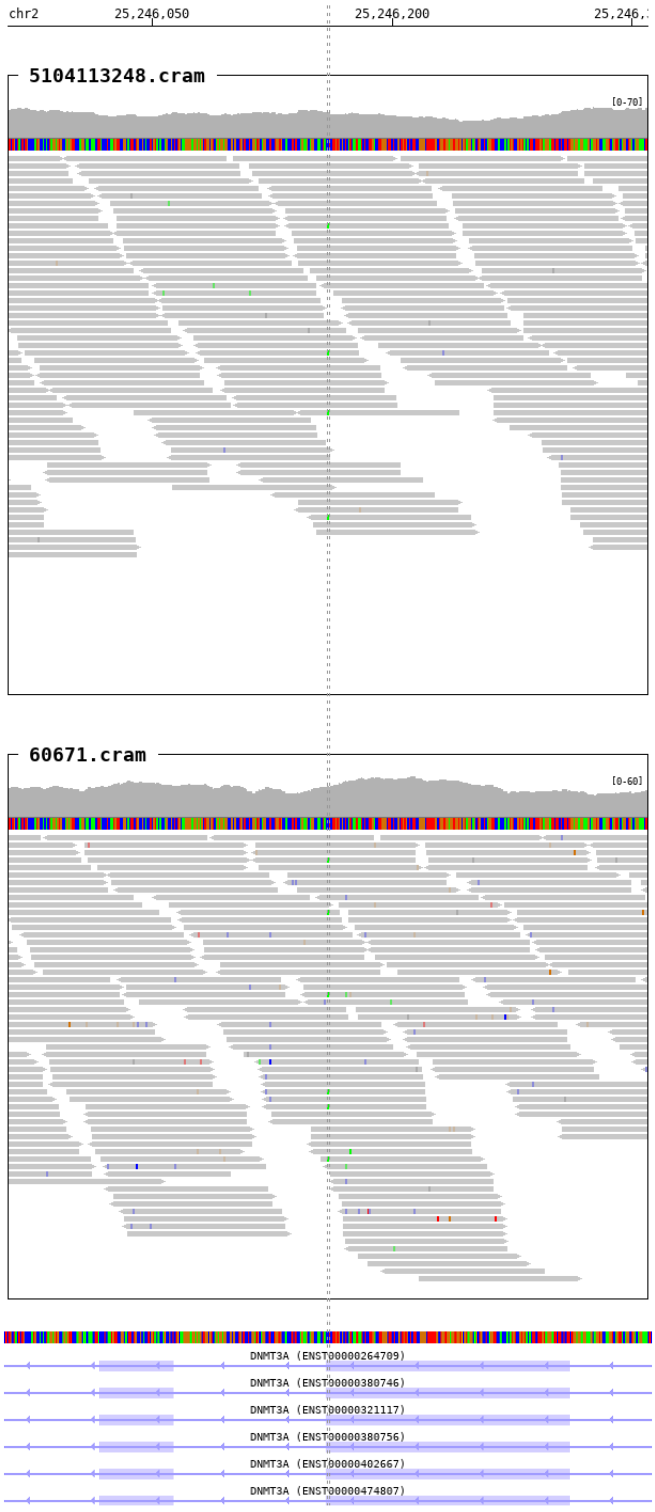
10.108. chr2_25245295_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102102730	chr2_25245295_A/-	33	4	*DNMT3A*	frameshift_variant



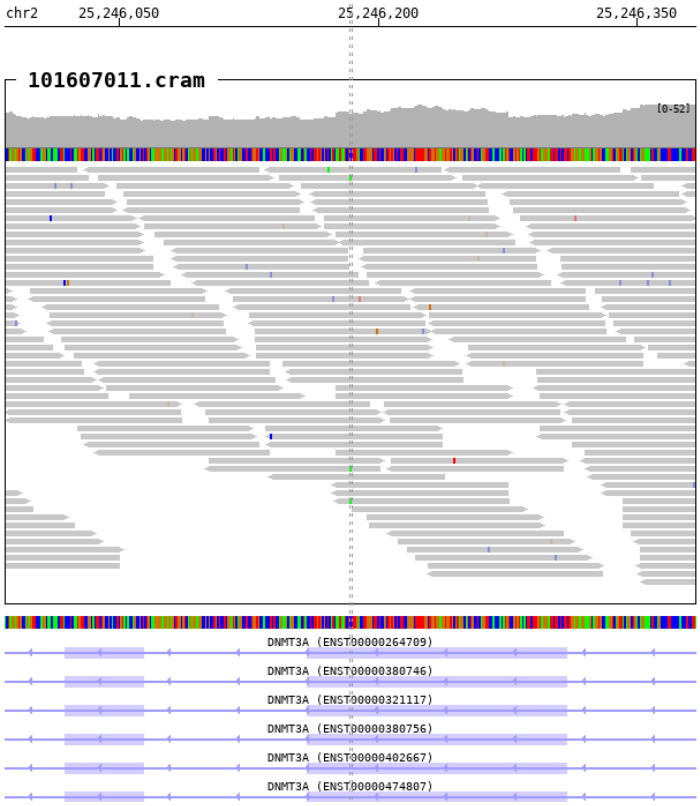
10.109. chr2_25246160_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
5104113248	chr2_25246160_C/A	38	4	*DNMT3A*	stop_gained
60671	chr2_25246160_C/A	38	6	*DNMT3A*	stop_gained



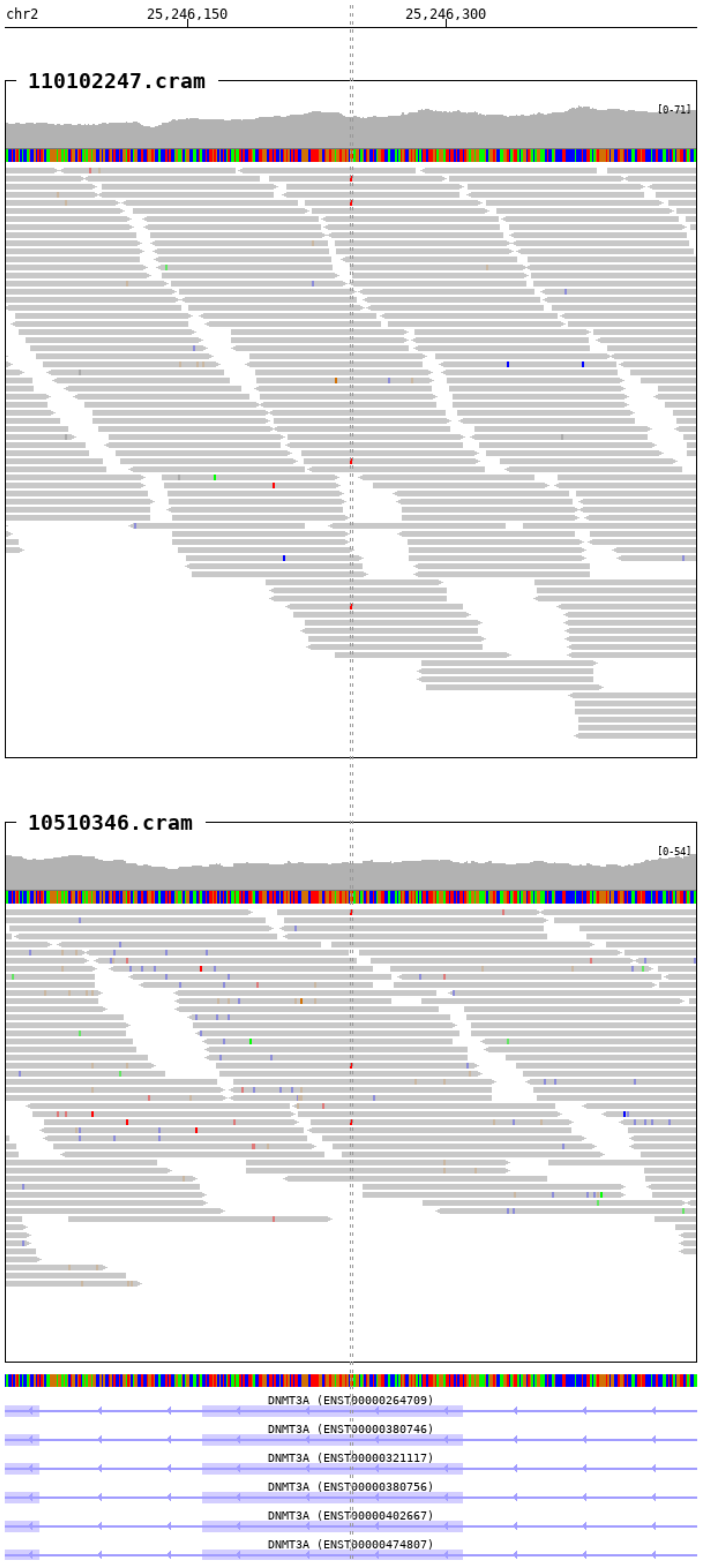
10.110. chr2_25246184_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101607011	chr2_25246184_C/A	33	3	*DNMT3A*	stop_gained



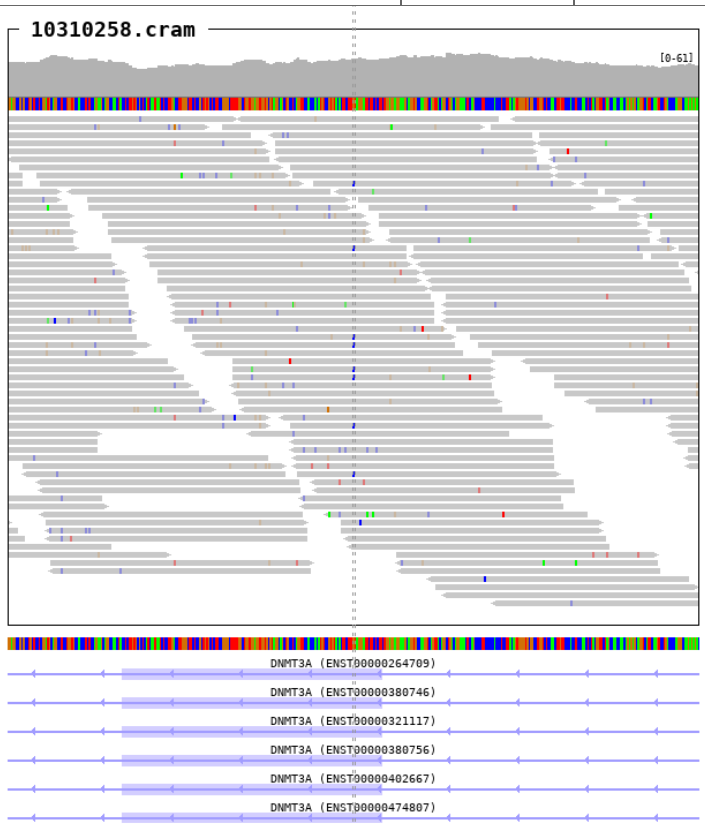
10.111. chr2_25246245_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10510346	chr2_25246245_G/T	30	3	*DNMT3A*	stop_gained
110102247	chr2_25246245_G/T	44	4	*DNMT3A*	stop_gained



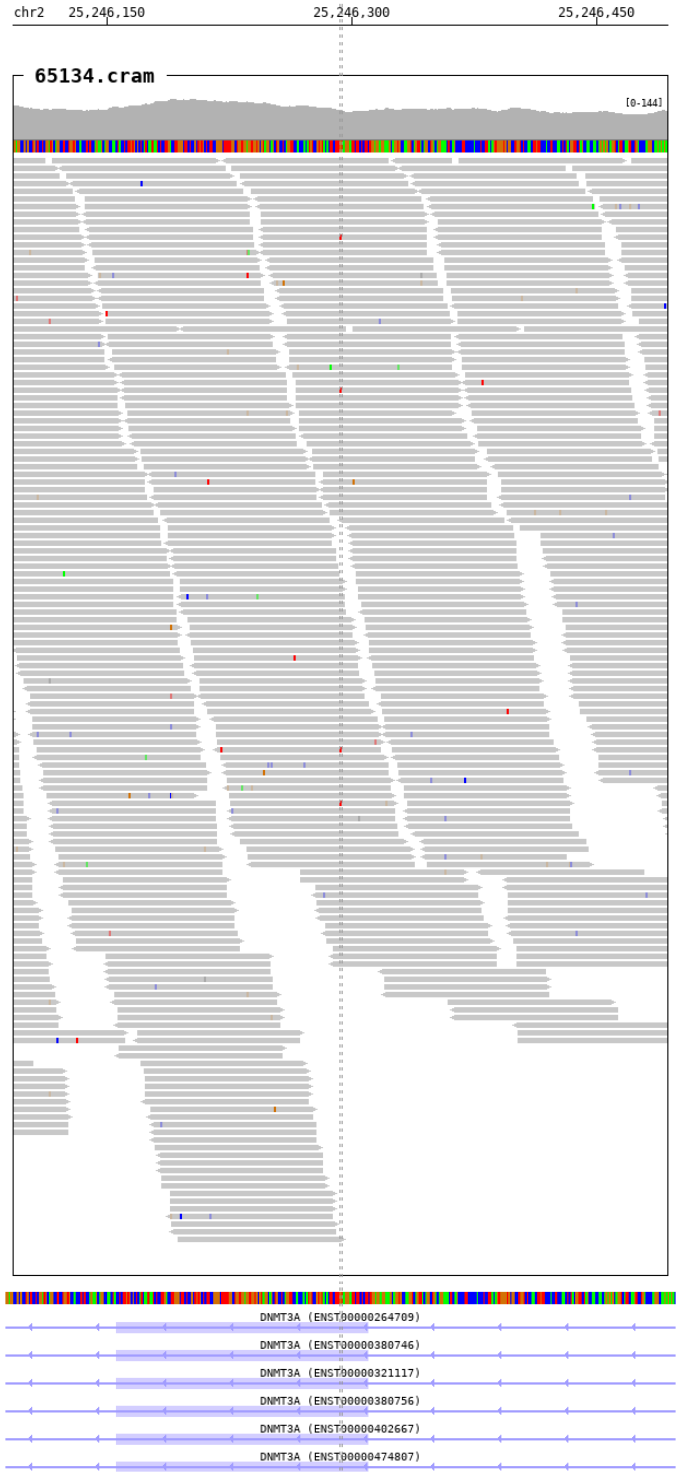
10.112. chr2_25246293_G/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10310258	chr2_25246293_G/C	38	7	*DNMT3A*	stop_gained



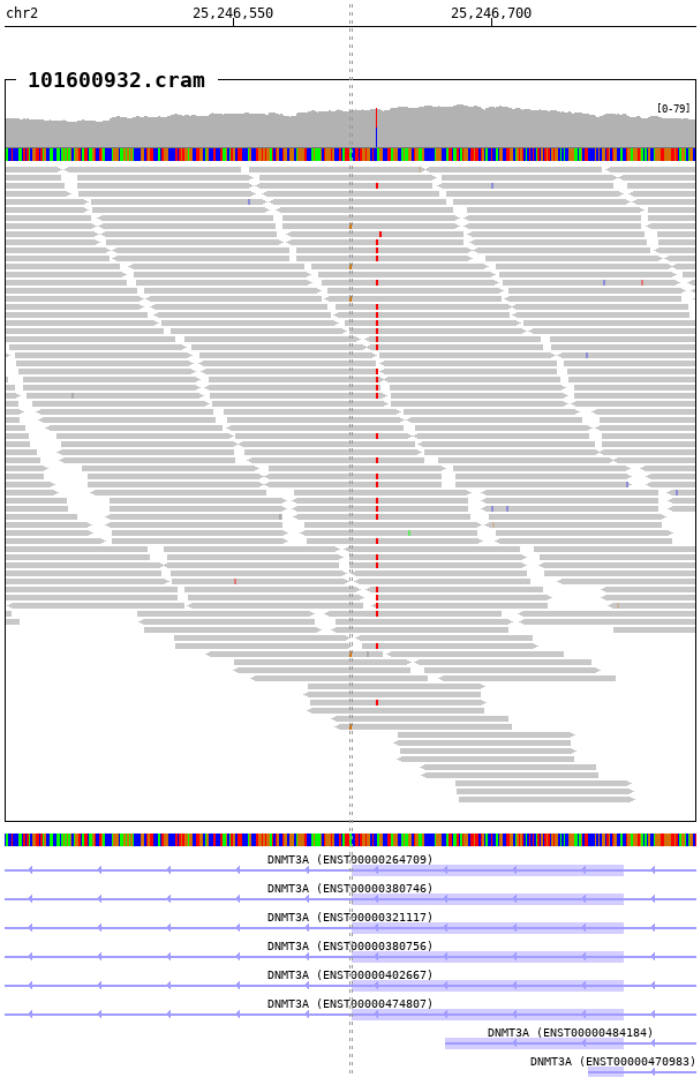
10.113. chr2_25246293_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
65134	chr2_25246293_G/T	92	4	*DNMT3A*	stop_gained



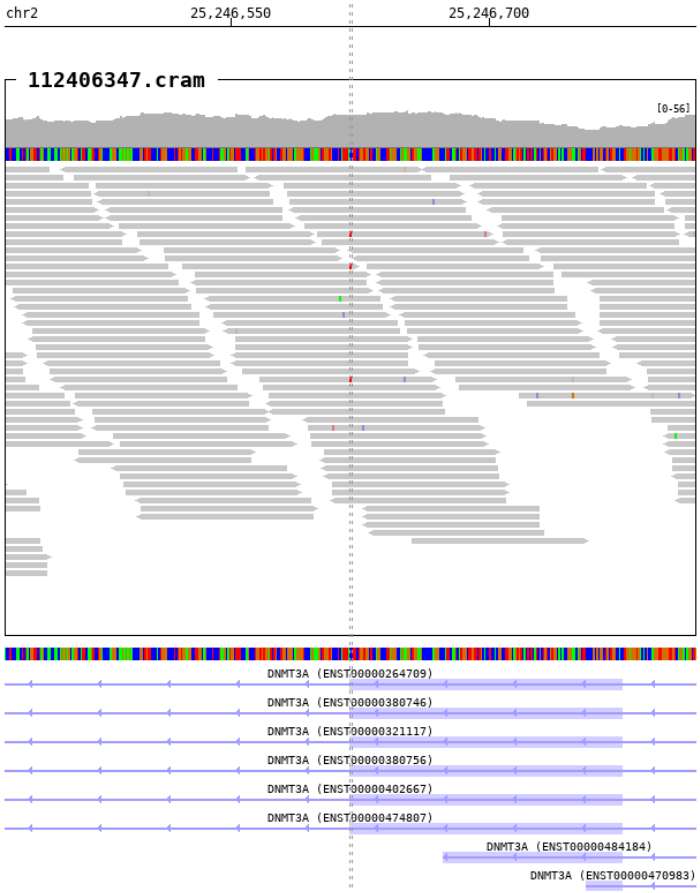
10.114. chr2_25246618_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101600932	chr2_25246618_A/G	59	5	*DNMT3A*	splice_donor_variant



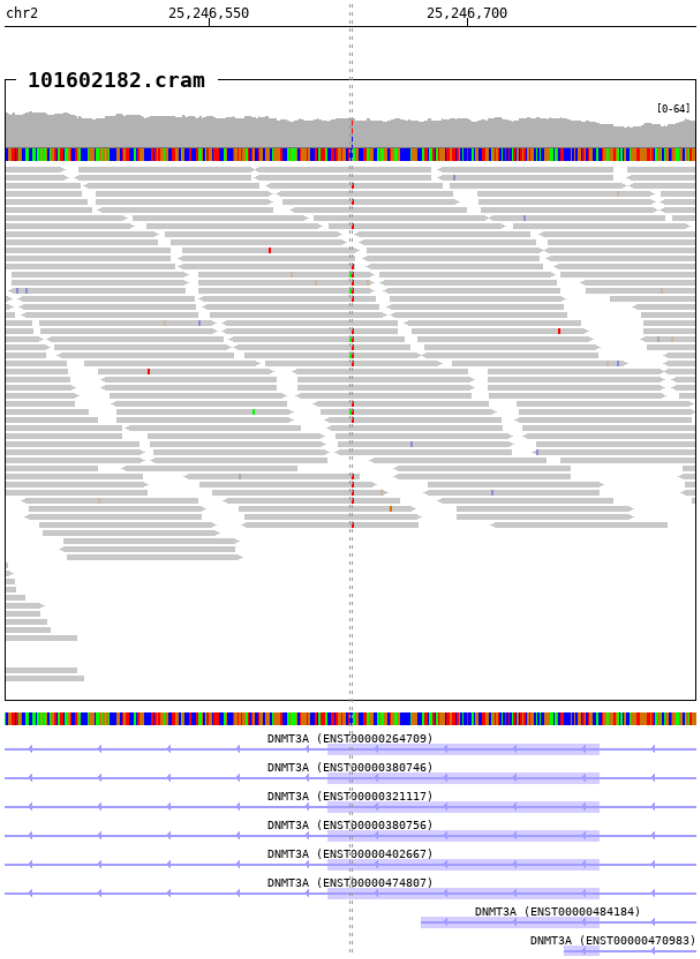
10.115. chr2_25246619_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112406347	chr2_25246619_C/T	36	3	*DNMT3A*	splice_donor_variant



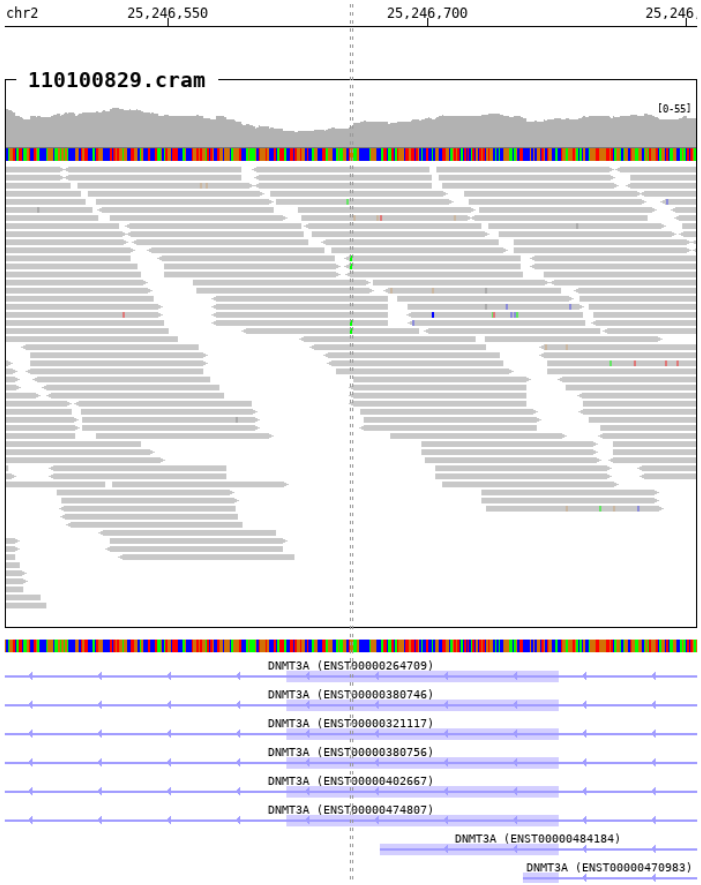
10.116. chr2_25246632_CC/AT

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101602182	chr2_25246632_CC/AT	35	4	*DNMT3A*	stop_gained



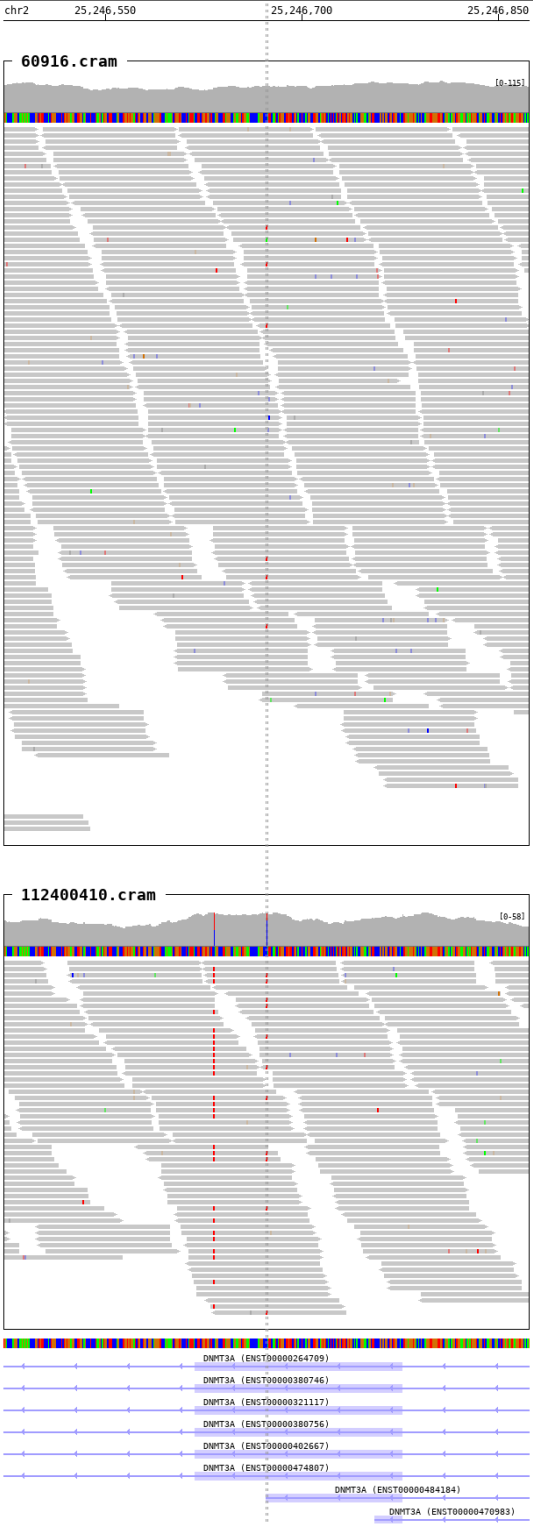
10.117. chr2_25246656_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110100829	chr2_25246656_G/A	20	3	*DNMT3A*	stop_gained



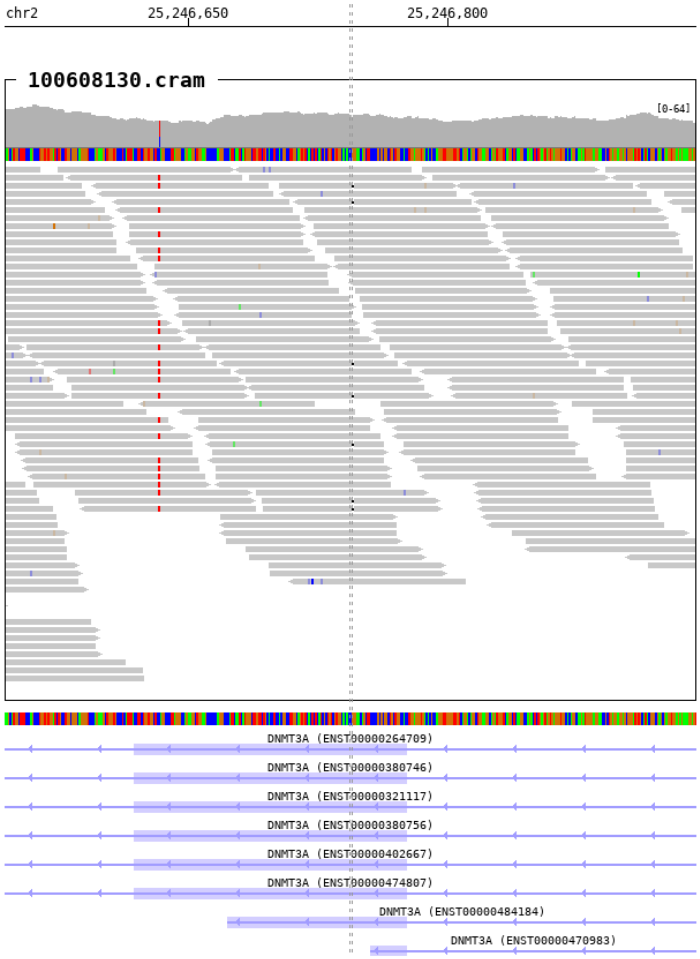
10.118. chr2_25246673_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112400410	chr2_25246673_C/T	39	11	*DNMT3A*	stop_gained
60916	chr2_25246673_C/T	75	6	*DNMT3A*	stop_gained



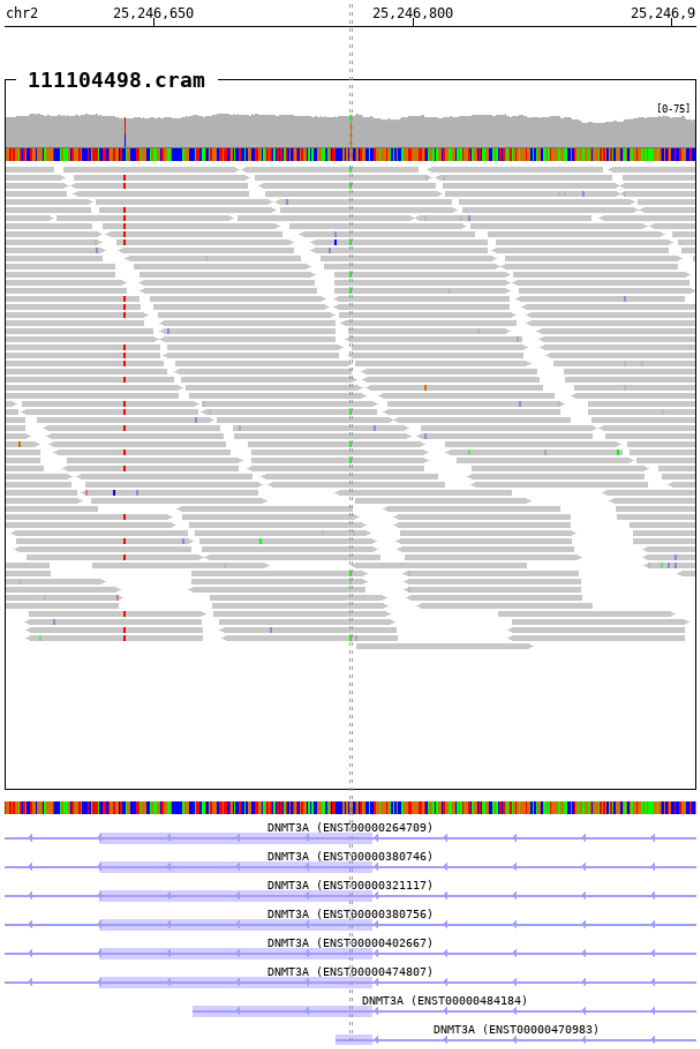
10.119. chr2_25246744_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100608130	chr2_25246744_G/-	35	7	*DNMT3A*	frameshift_variant



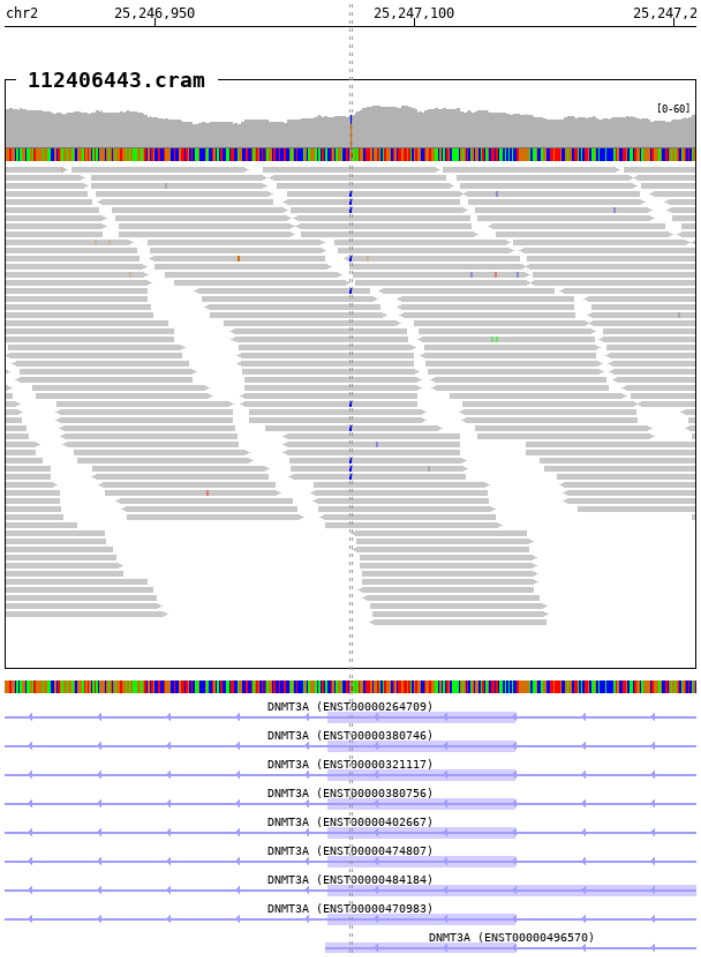
10.120. chr2_25246764_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
111104498	chr2_25246764_G/A	42	9	*DNMT3A*	missense_variant



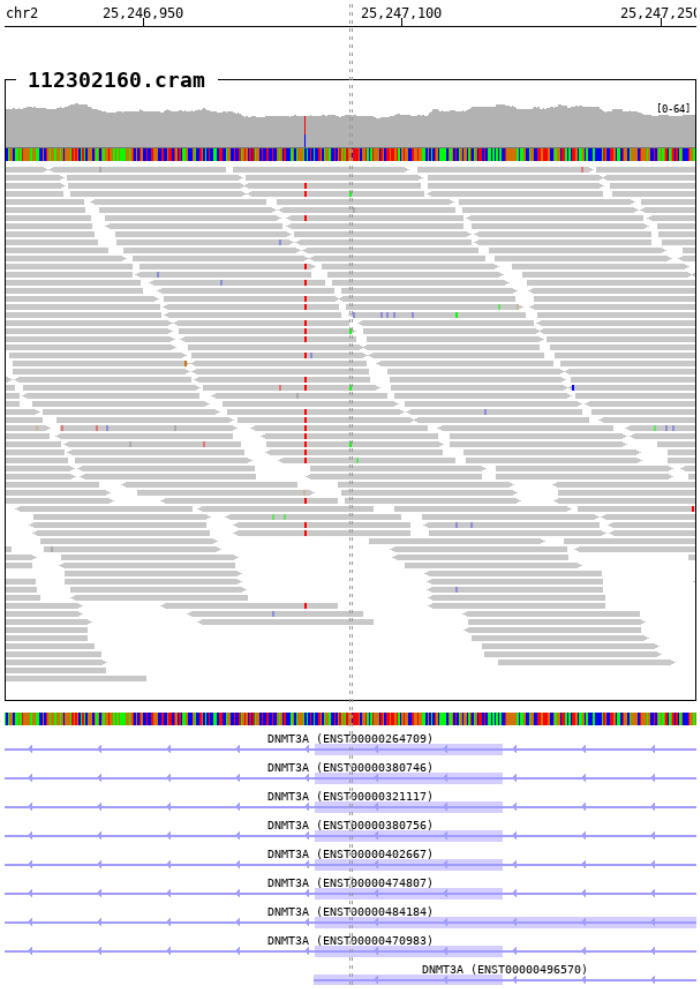
10.121. chr2_25247063_G/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112406443	chr2_25247063_G/C	31	10	*DNMT3A*	stop_gained



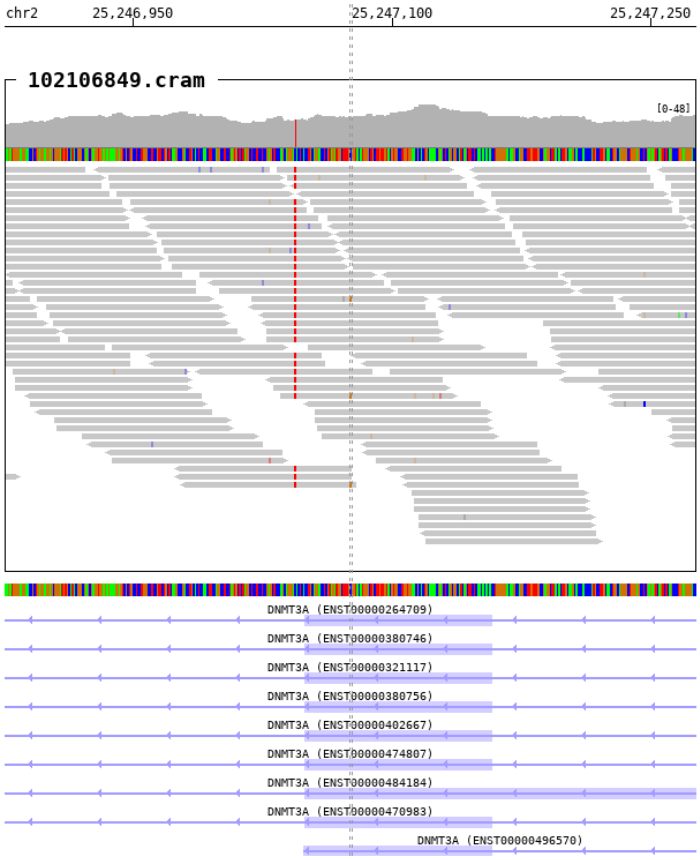
10.122. chr2_25247070_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112302160	chr2_25247070_G/A	41	4	*DNMT3A*	missense_variant



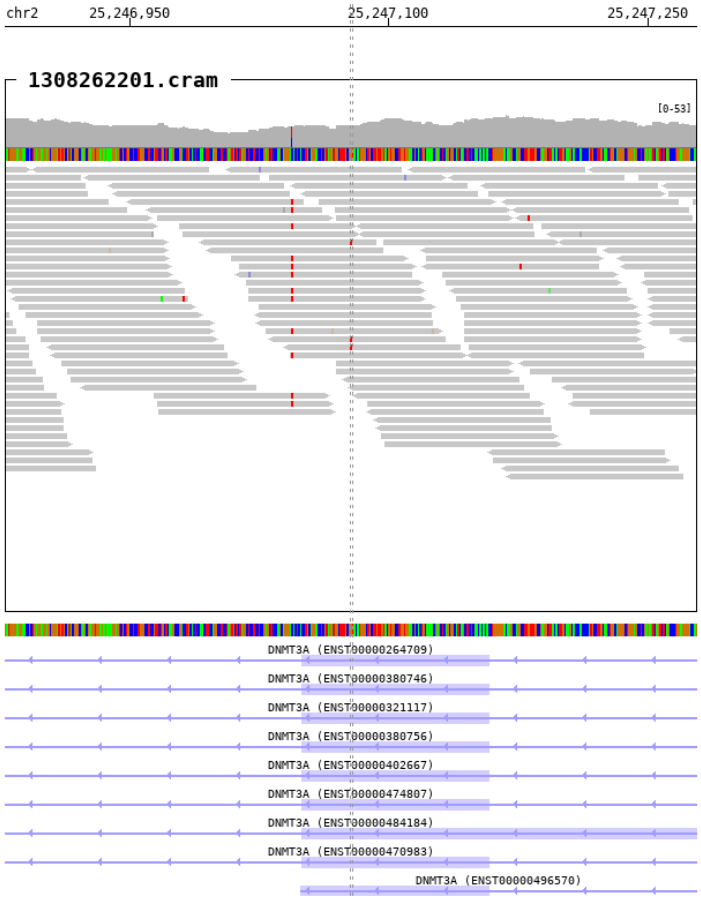
10.123. chr2_25247076_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102106849	chr2_25247076_C/G	30	3	*DNMT3A*	missense_variant



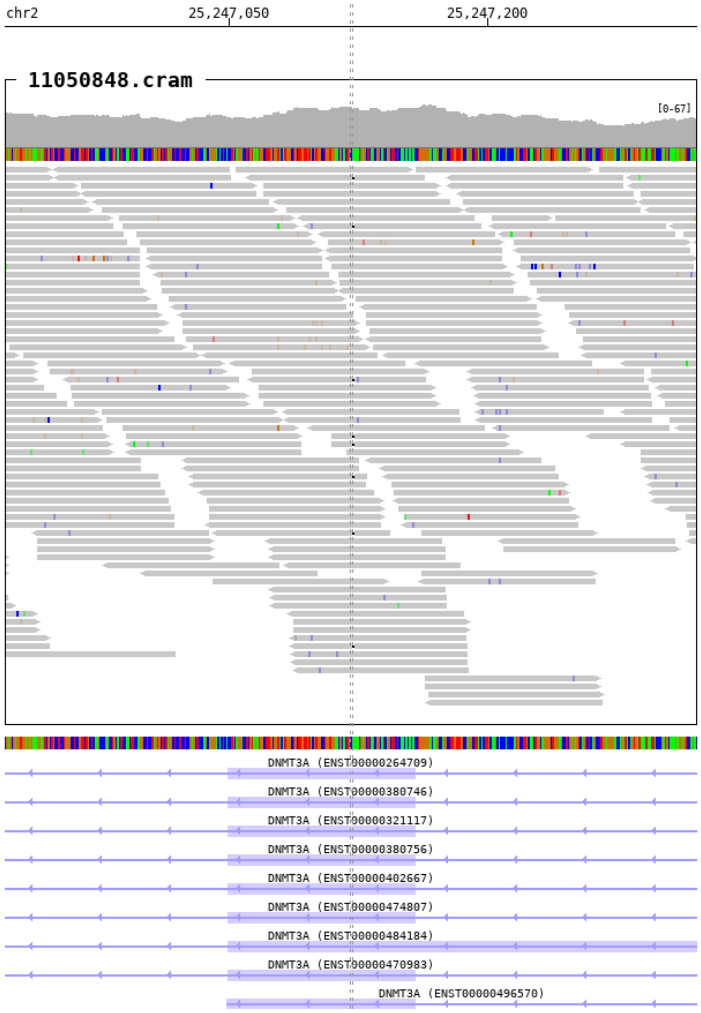
10.124. chr2_25247078_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
1308262201	chr2_25247078_G/T	23	3	*DNMT3A*	stop_gained



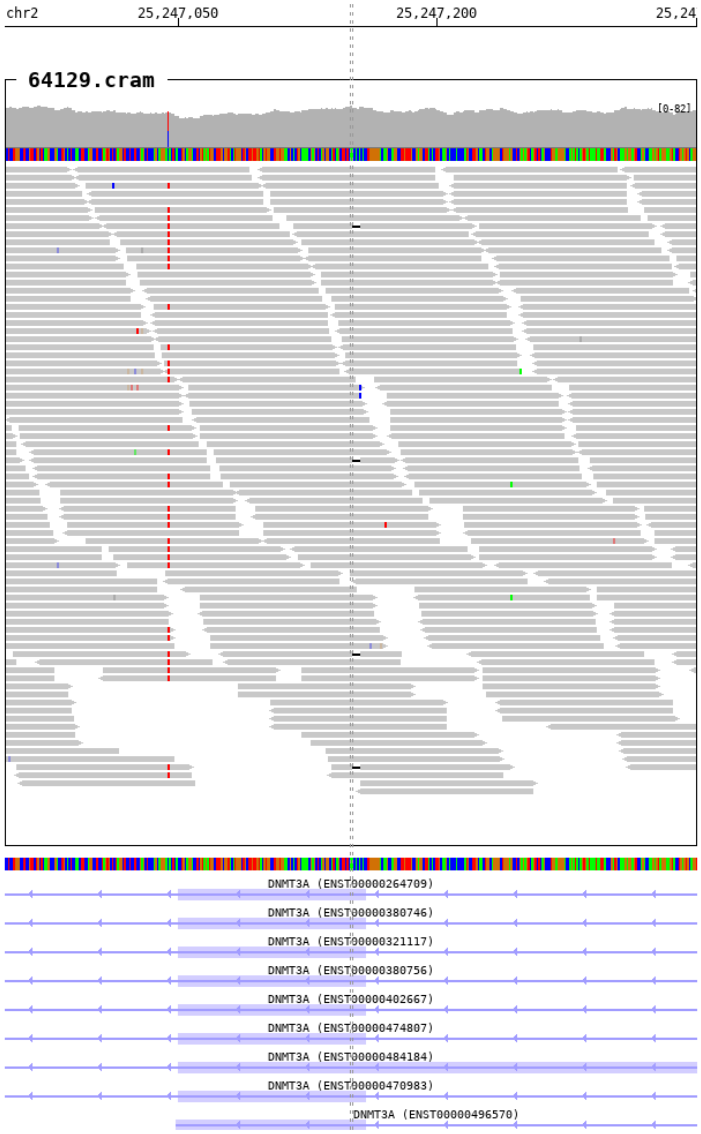
10.125. chr2_25247121_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11050848	chr2_25247121_A/-	44	8	*DNMT3A*	frameshift_variant



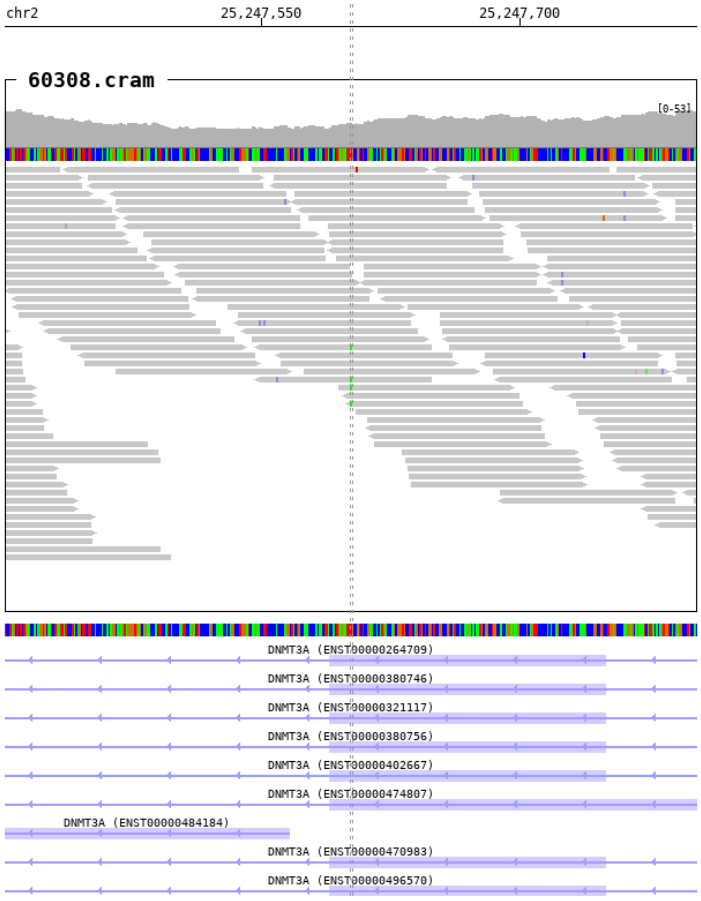
10.126. chr2_25247150_ACAC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
64129	chr2_25247150_ACAC/-	65	6	*DNMT3A*	frameshift_variant



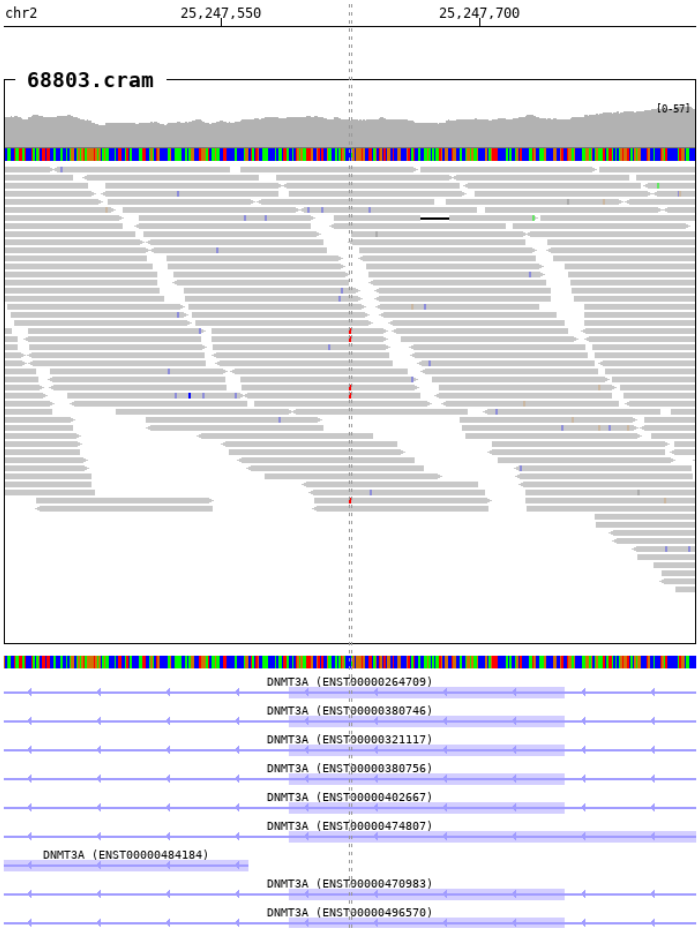
10.127. chr2_25247602_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
60308	chr2_25247602_T/A	24	4	*DNMT3A*	stop_gained



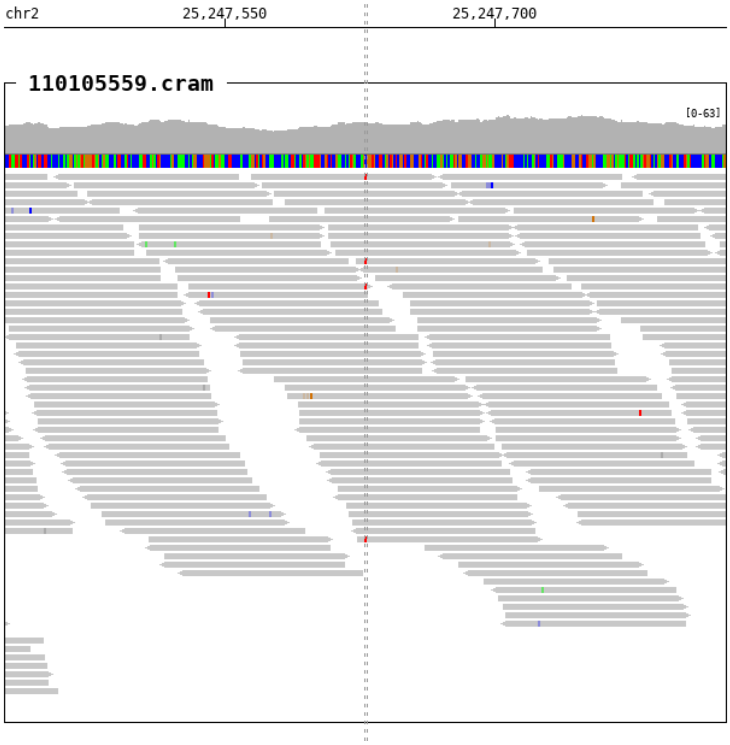
10.128. chr2_25247625_C/T

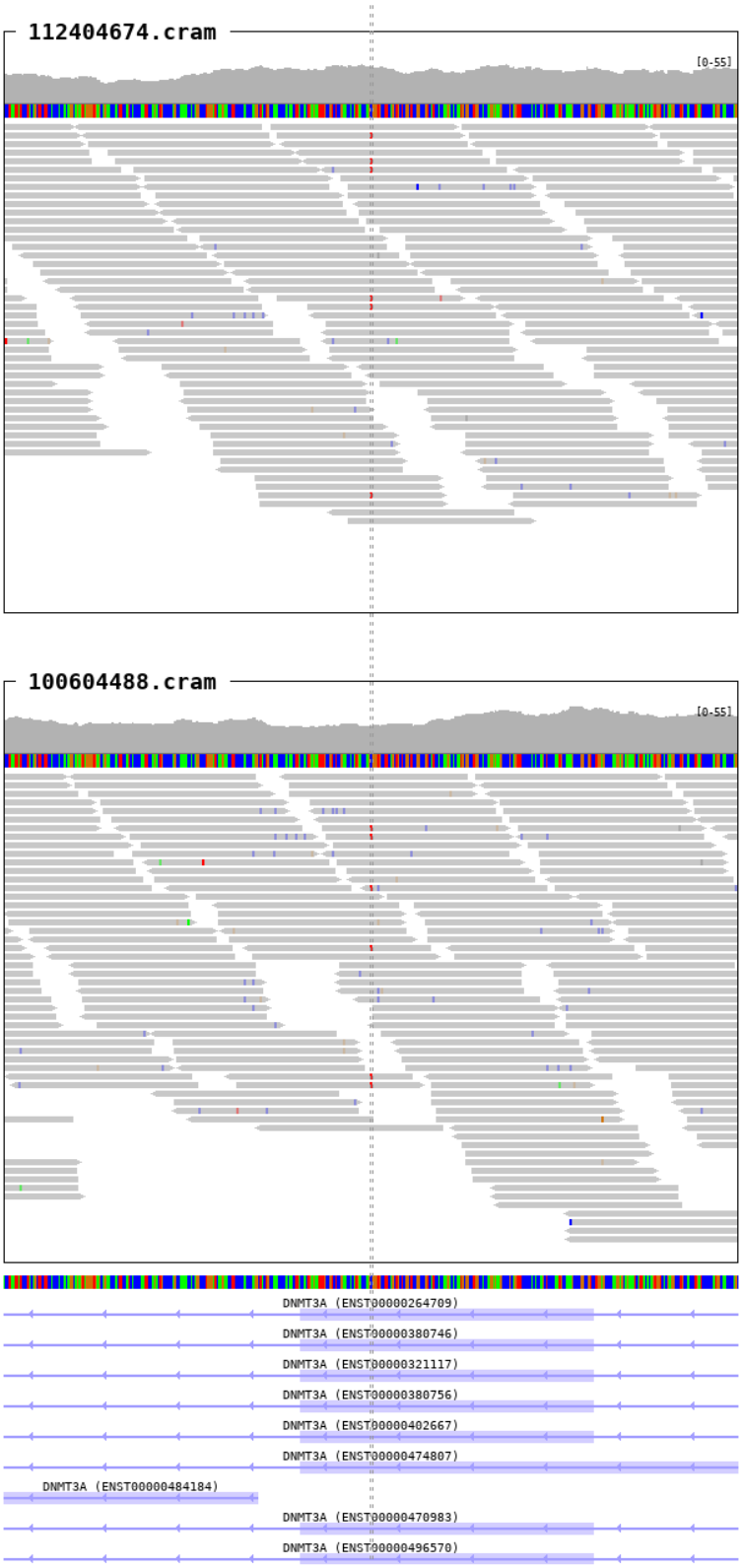
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
68803	chr2_25247625_C/T	29	5	*DNMT3A*	stop_gained



10.129. chr2_25247628_C/T

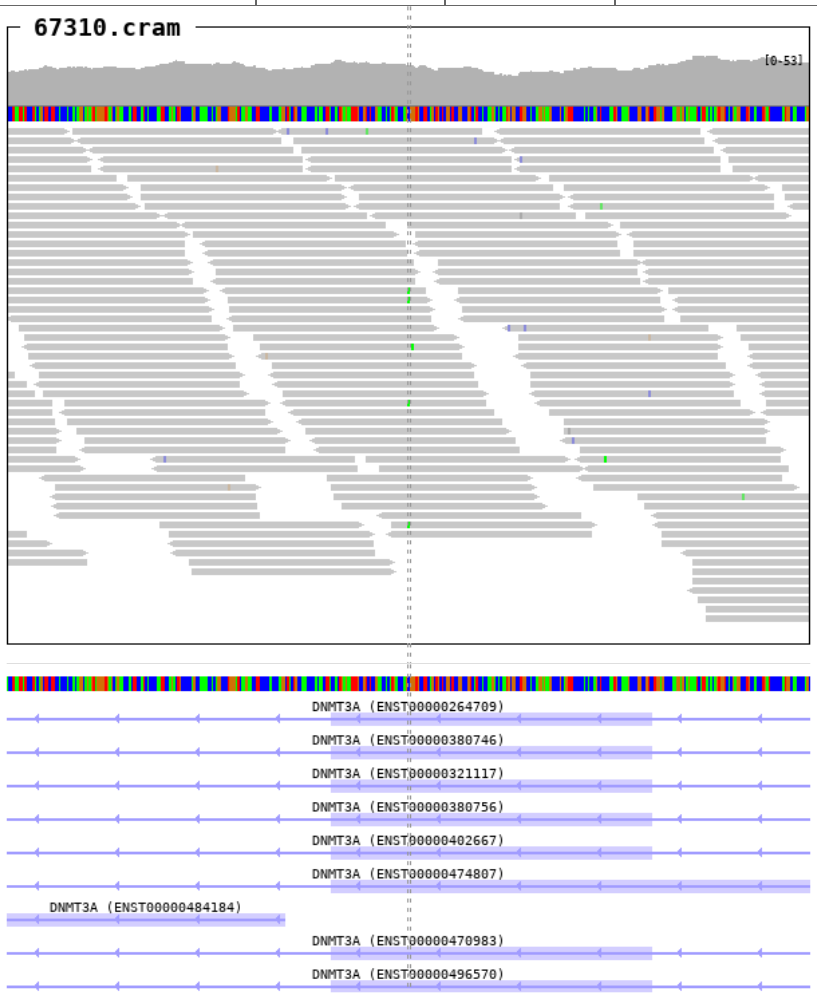
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100604488	chr2_25247628_C/T	23	6	*DNMT3A*	missense_variant
110105559	chr2_25247628_C/T	39	4	*DNMT3A*	missense_variant
112404674	chr2_25247628_C/T	34	6	*DNMT3A*	missense_variant




112404674.cram
[0-55]
100604488.cram
[0-55]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474807)
DNMT3A (ENST00000484184)
DNMT3A (ENST00000470983)
DNMT3A (ENST00000496570)

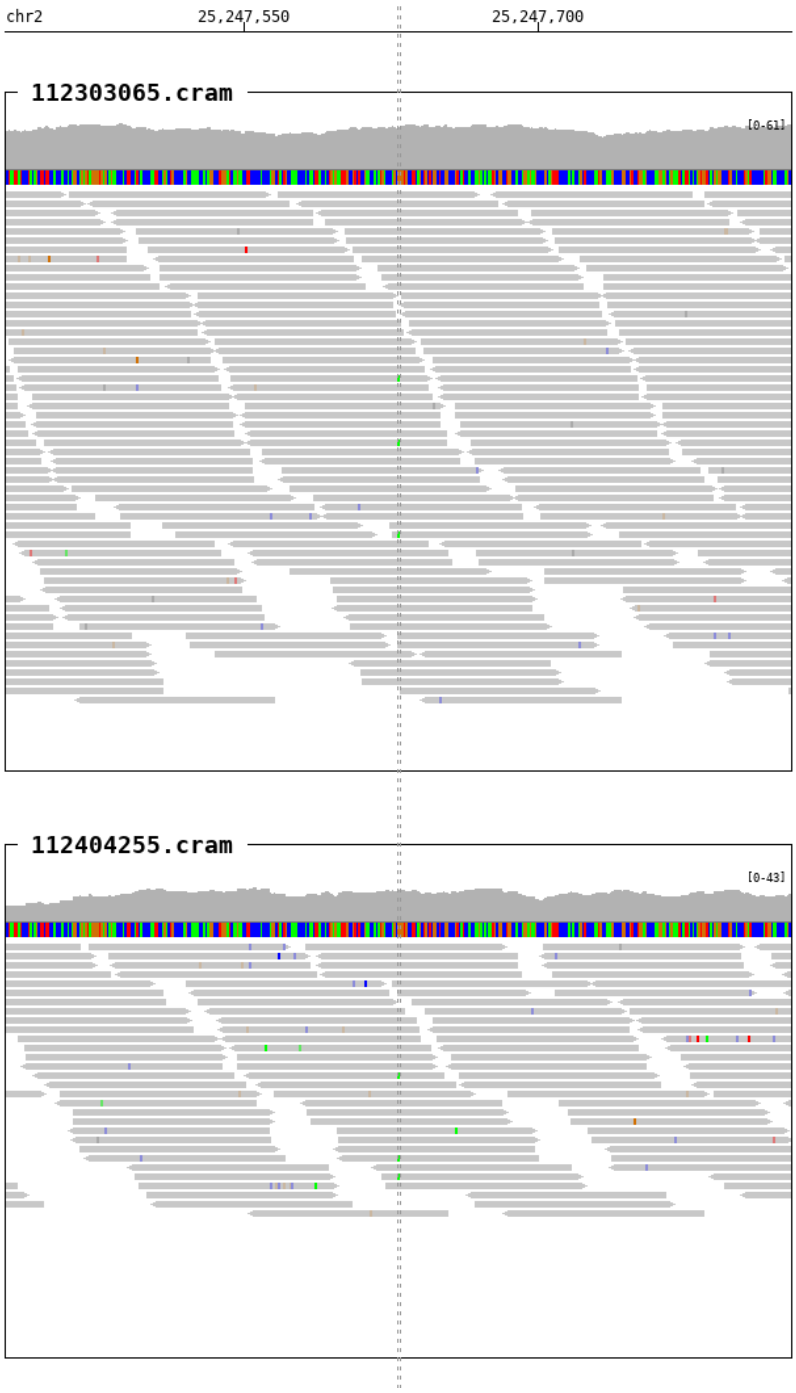
10.130. chr2_25247628_C/A

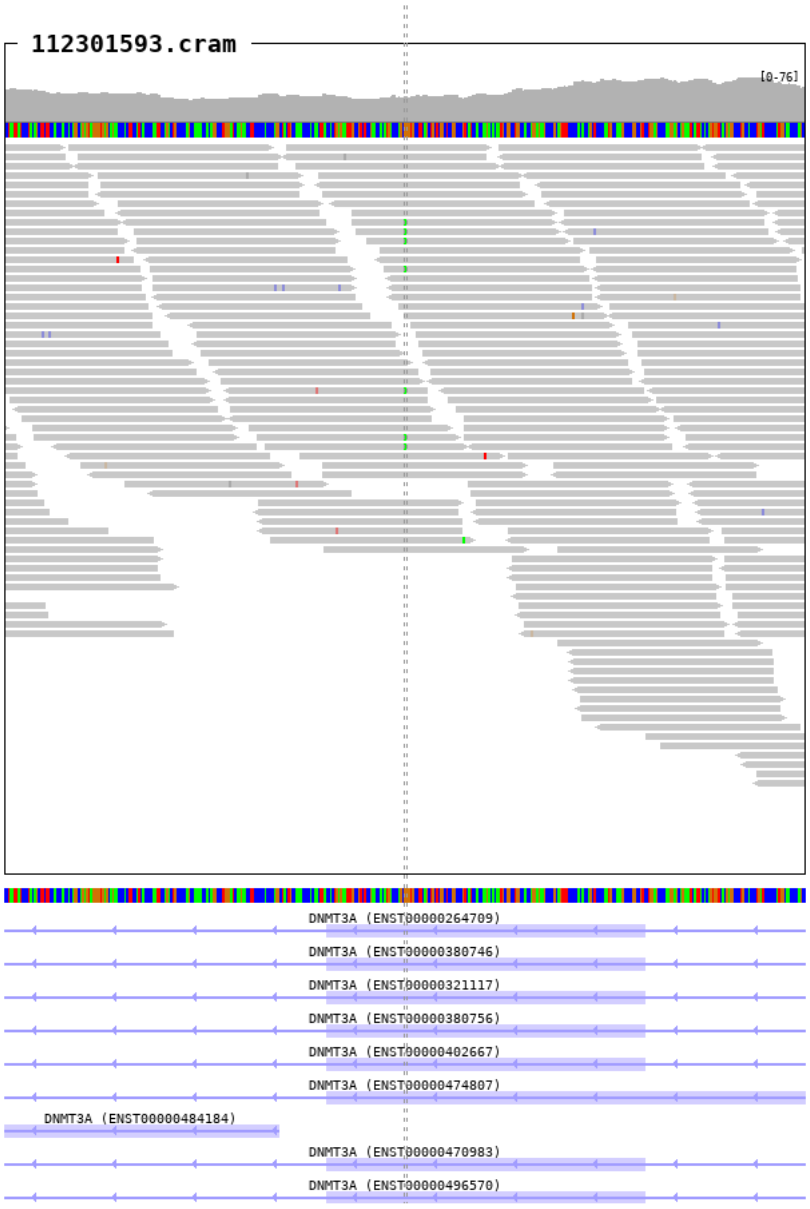
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
67310	chr2_25247628_C/A	36	4	*DNMT3A*	missense_variant



10.131. chr2_25247629_G/A

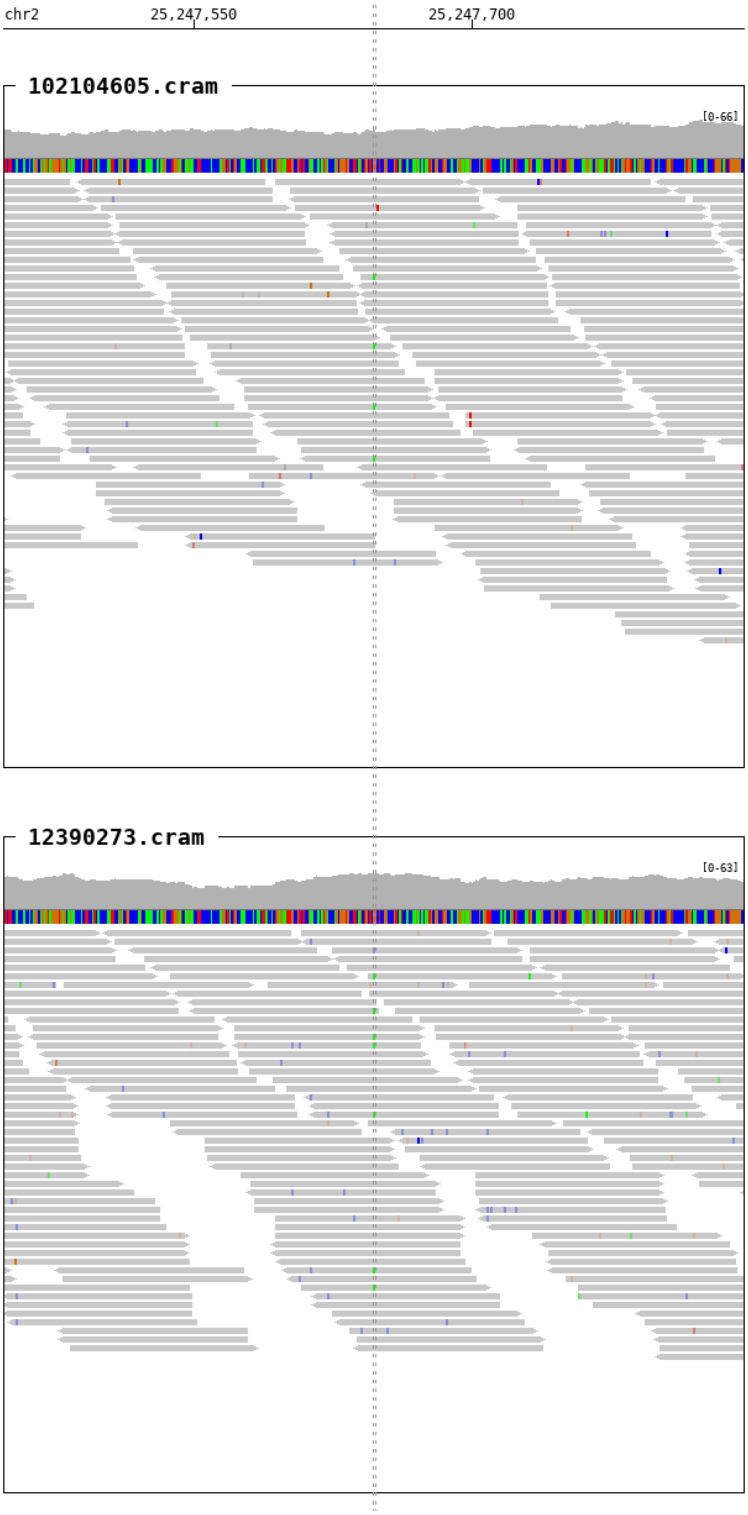
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301593	chr2_25247629_G/A	31	7	*DNMT3A*	missense_variant
112303065	chr2_25247629_G/A	46	3	*DNMT3A*	missense_variant
112404255	chr2_25247629_G/A	23	3	*DNMT3A*	missense_variant

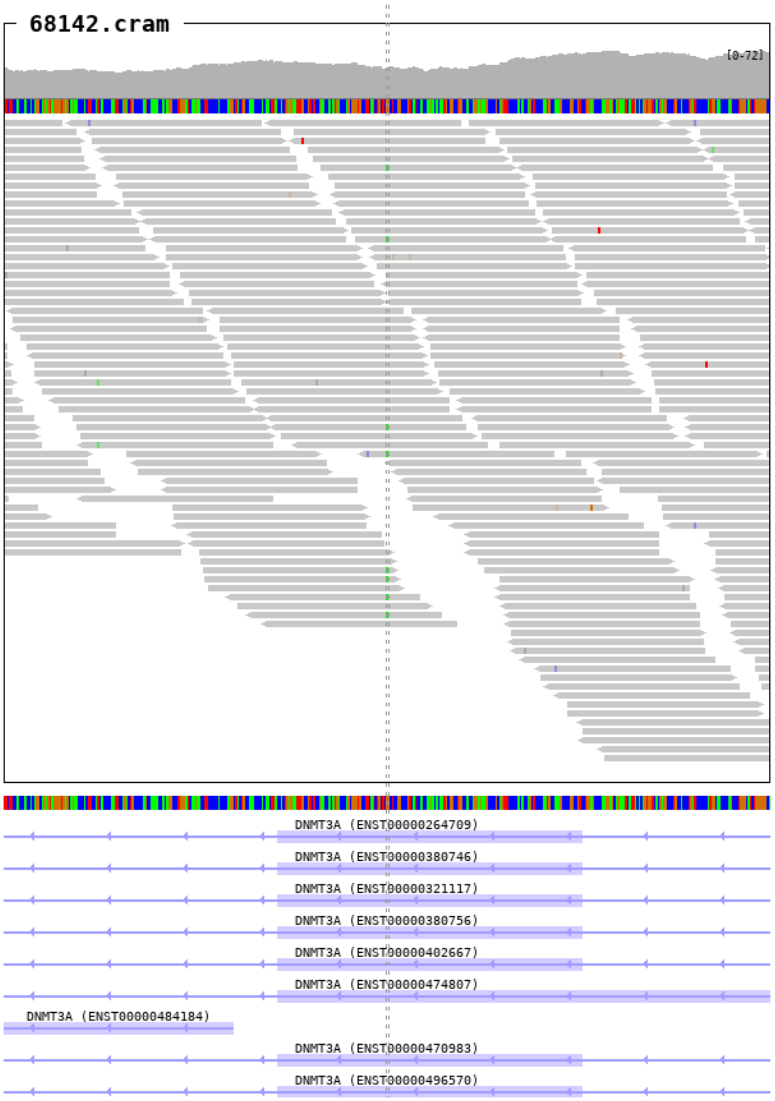



112301593.cram
[0-76]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474807)
DNMT3A (ENST00000484184)
DNMT3A (ENST00000470983)
DNMT3A (ENST00000496570)

10.132. chr2_25247647_G/A

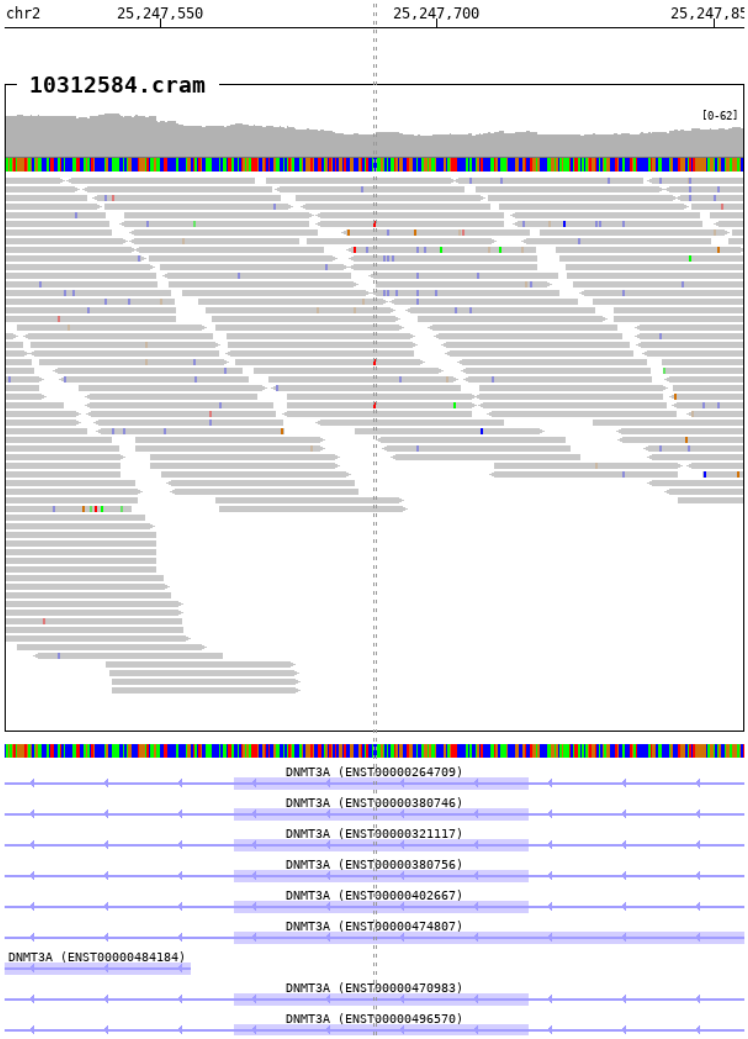
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102104605	chr2_25247647_G/A	33	4	*DNMT3A*	stop_gained
12390273	chr2_25247647_G/A	39	7	*DNMT3A*	stop_gained
68142	chr2_25247647_G/A	36	8	*DNMT3A*	stop_gained




68142.cram
[0-72]
DNMT3A (ENST00000264709)
DNMT3A (ENST00000380746)
DNMT3A (ENST00000321117)
DNMT3A (ENST00000380756)
DNMT3A (ENST00000402667)
DNMT3A (ENST00000474807)
DNMT3A (ENST00000484184)
DNMT3A (ENST00000470983)
DNMT3A (ENST00000496570)

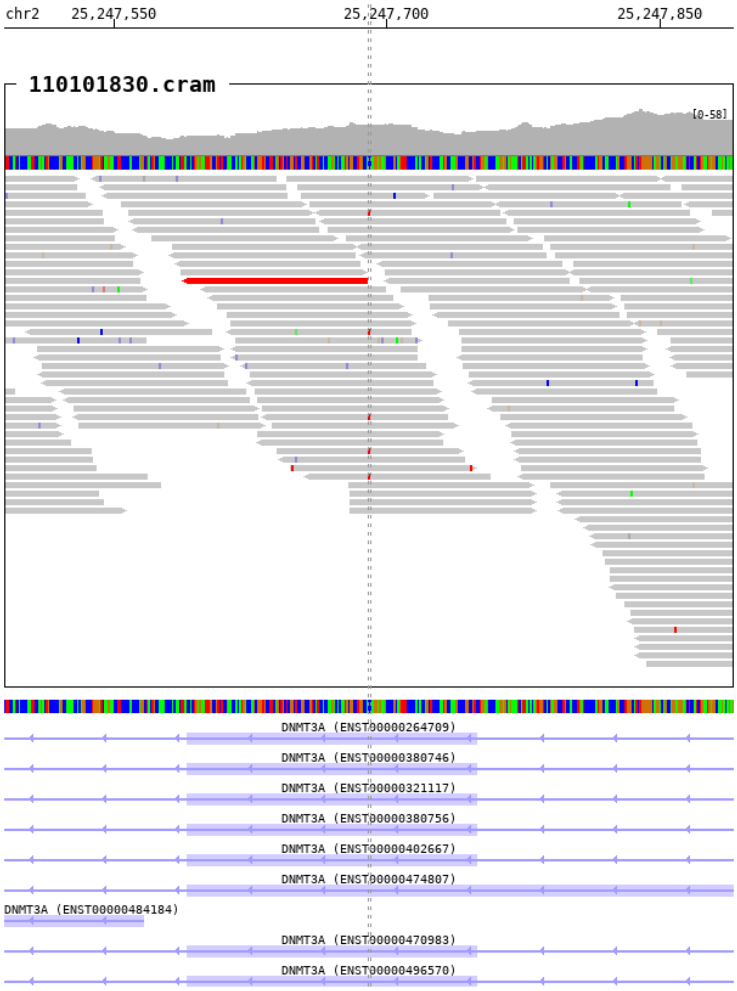
10.133. chr2_25247666_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10312584	chr2_25247666_C/T	24	3	*DNMT3A*	stop_gained



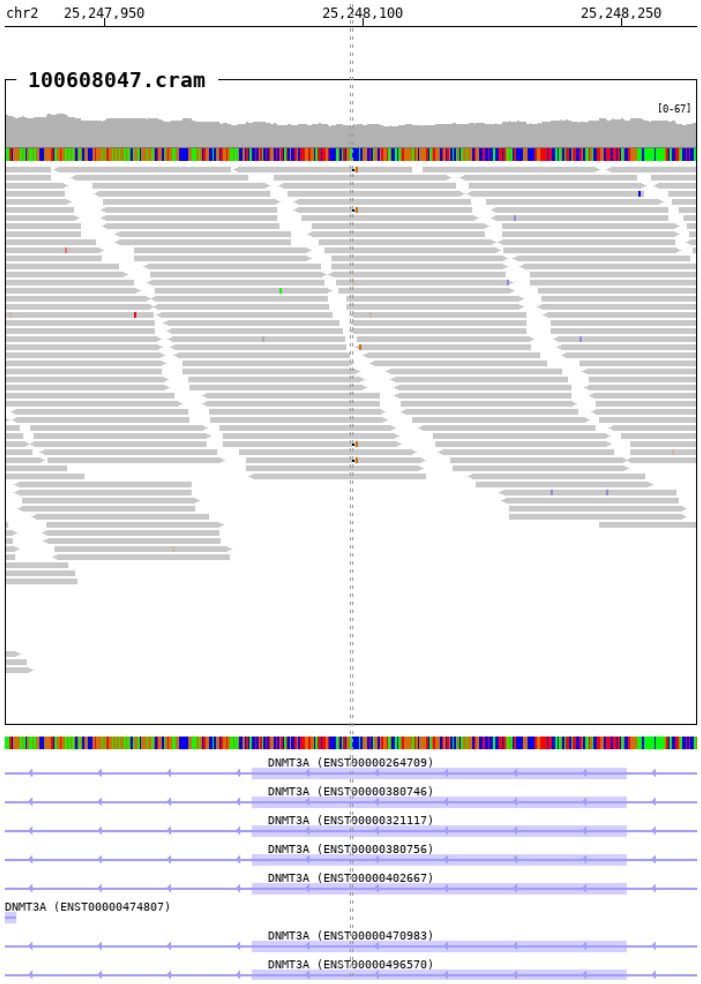
10.134. chr2_25247690_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110101830	chr2_25247690_C/T	31	5	*DNMT3A*	stop_gained



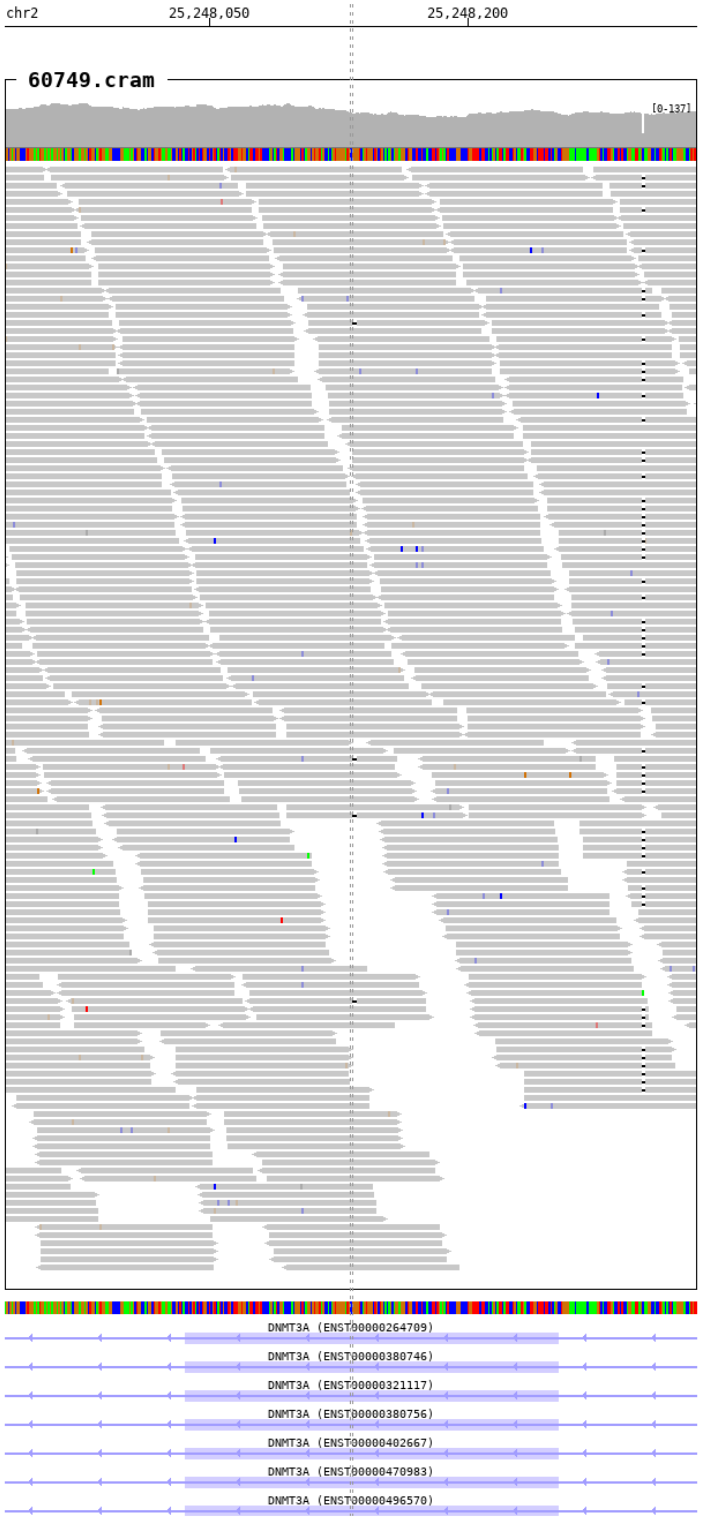
10.135. chr2_25248093_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100608047	chr2_25248093_C/-	30	5	*DNMT3A*	frameshift_variant



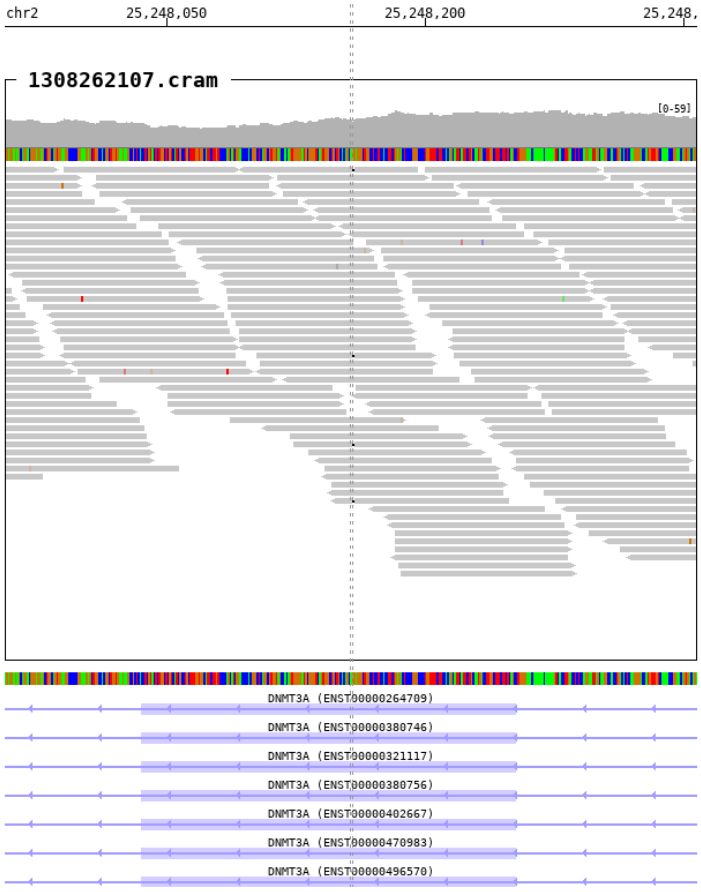
10.136. chr2_25248132_GG/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
60749	chr2_25248132_GG/-	98	4	*DNMT3A*	frameshift_variant



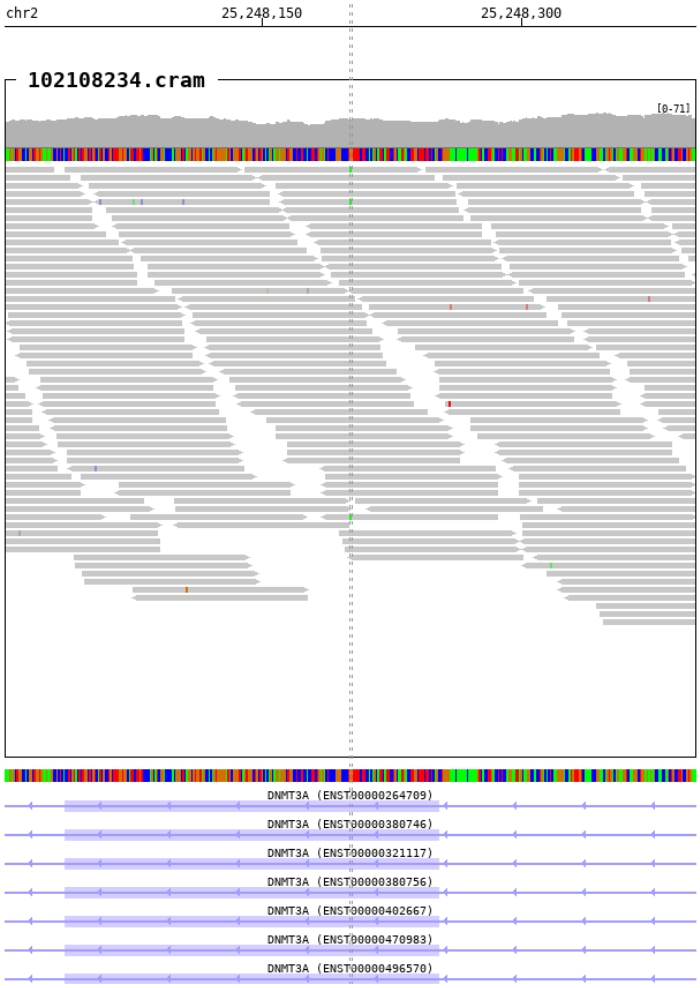
10.137. chr2_25248157_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
1308262107	chr2_25248157_G/-	31	4	*DNMT3A*	frameshift_variant



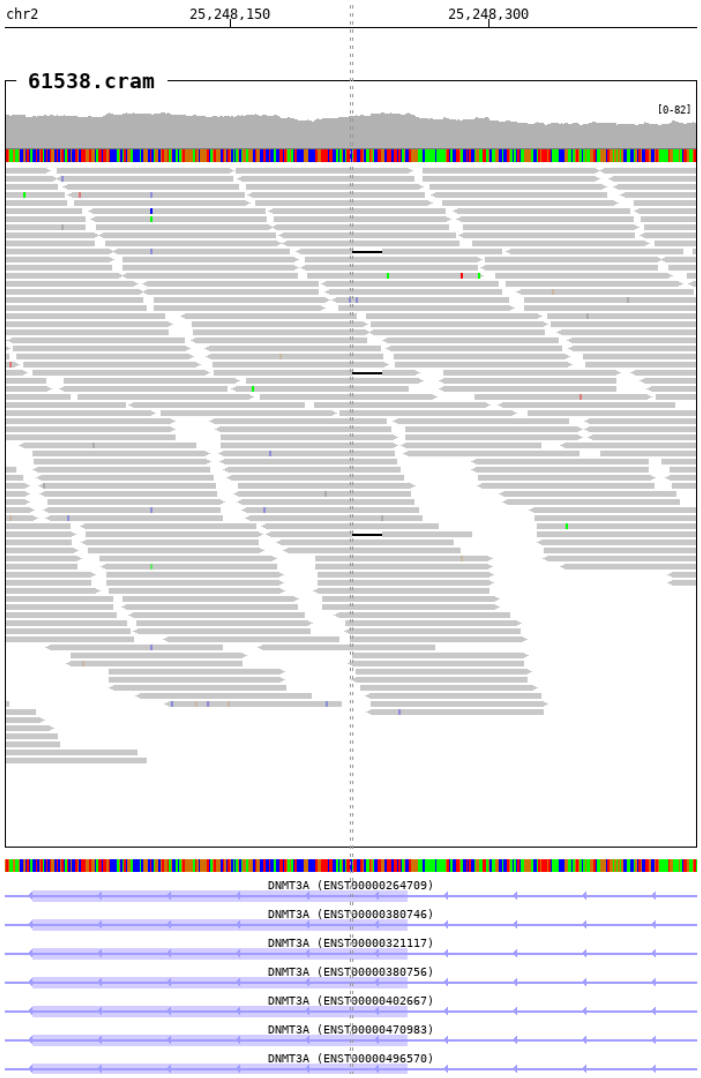
10.138. chr2_25248201_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102108234	chr2_25248201_G/A	37	3	*DNMT3A*	stop_gained



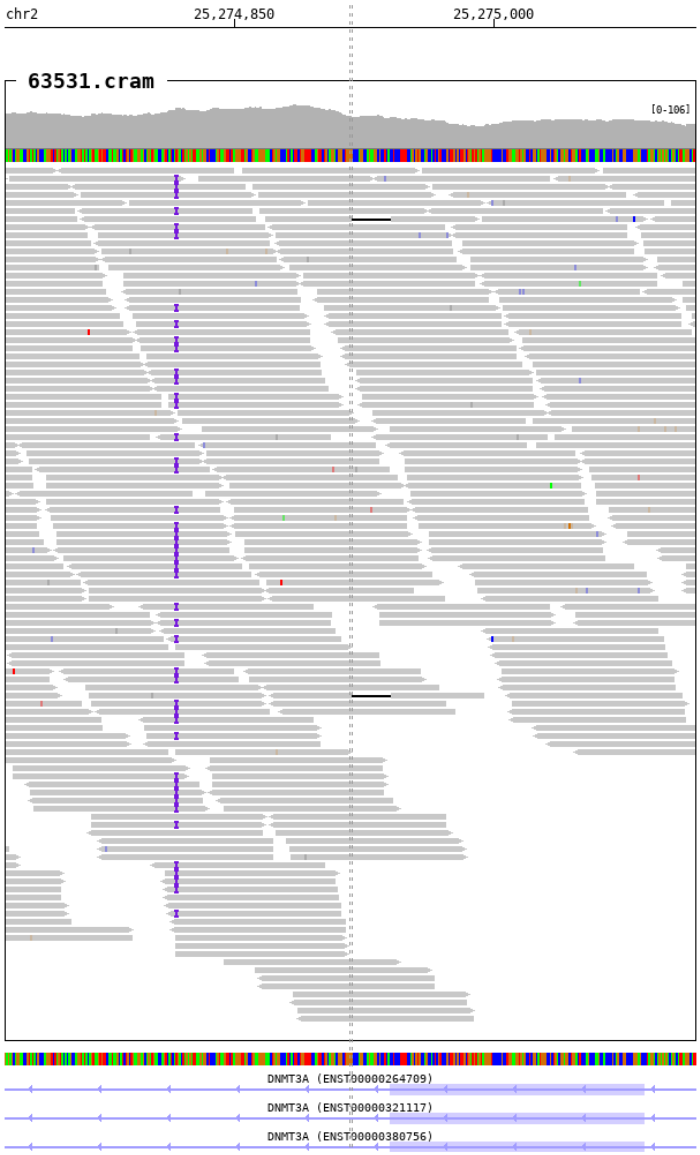
10.139. chr2_25248220_ATTCCTGCAATGACCTT/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
61538	chr2_25248220_ATTCCTGCAATGACCTT/-	65	3	*DNMT3A*	frameshift_variant



10.140. chr2_25274917_GCCCAGGCCAGAAGGCGCCTCA/-

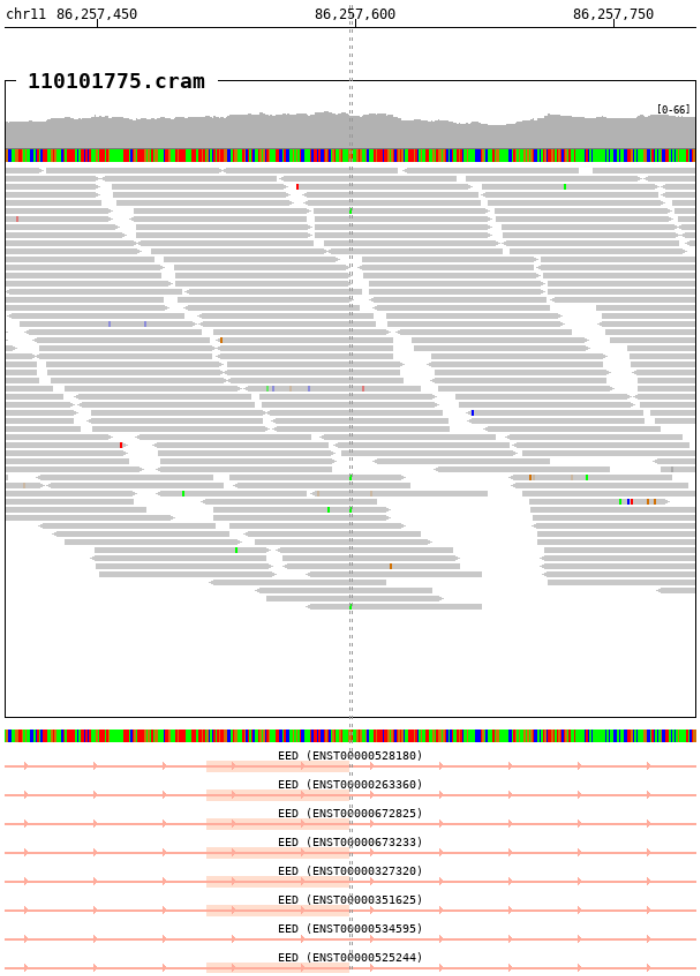
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
63531	chr2_25274917_GCCCAGGCCAGAAGGCGCCTCA/-	83	3	*DNMT3A*	splice_donor_variant



11. *EED*

11.1. chr11_86257597_G/A

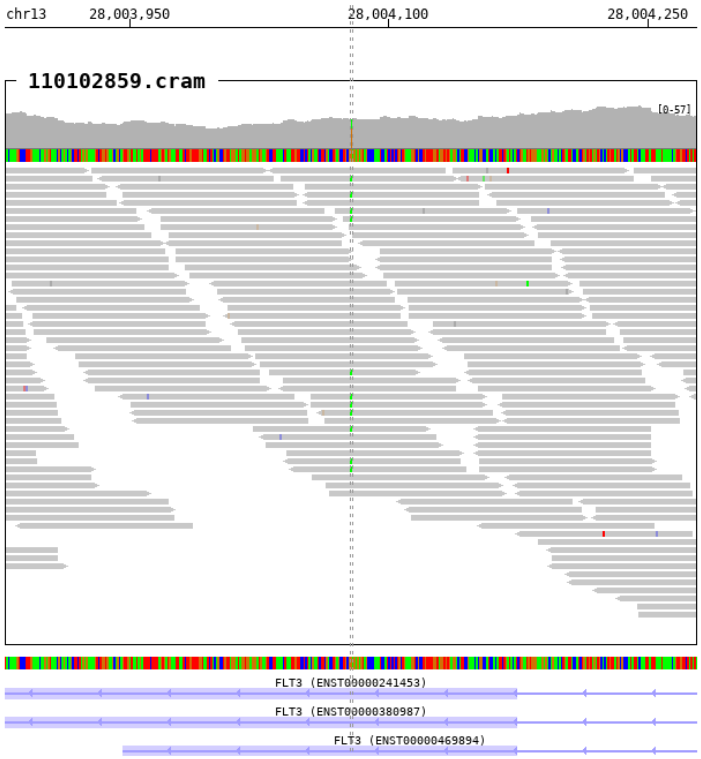
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110101775	chr11_86257597_G/A	40	4	*EED*	splice_donor_variant



12. *FLT3*

12.1. chr13_28004078_G/A

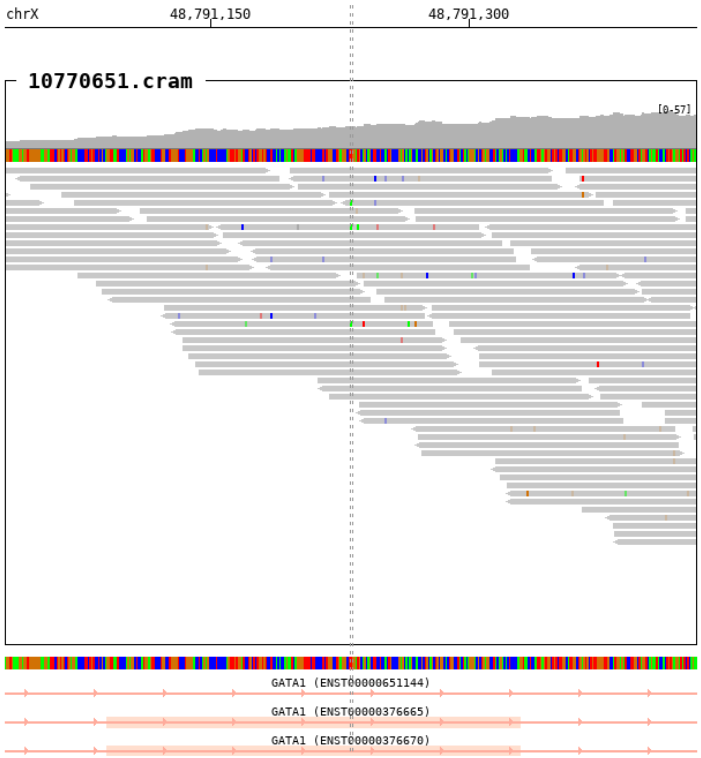
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110102859	chr13_28004078_G/A	26	10	*FLT3*	missense_variant



13. *GATA1*

13.1. chrX_48791231_T/A

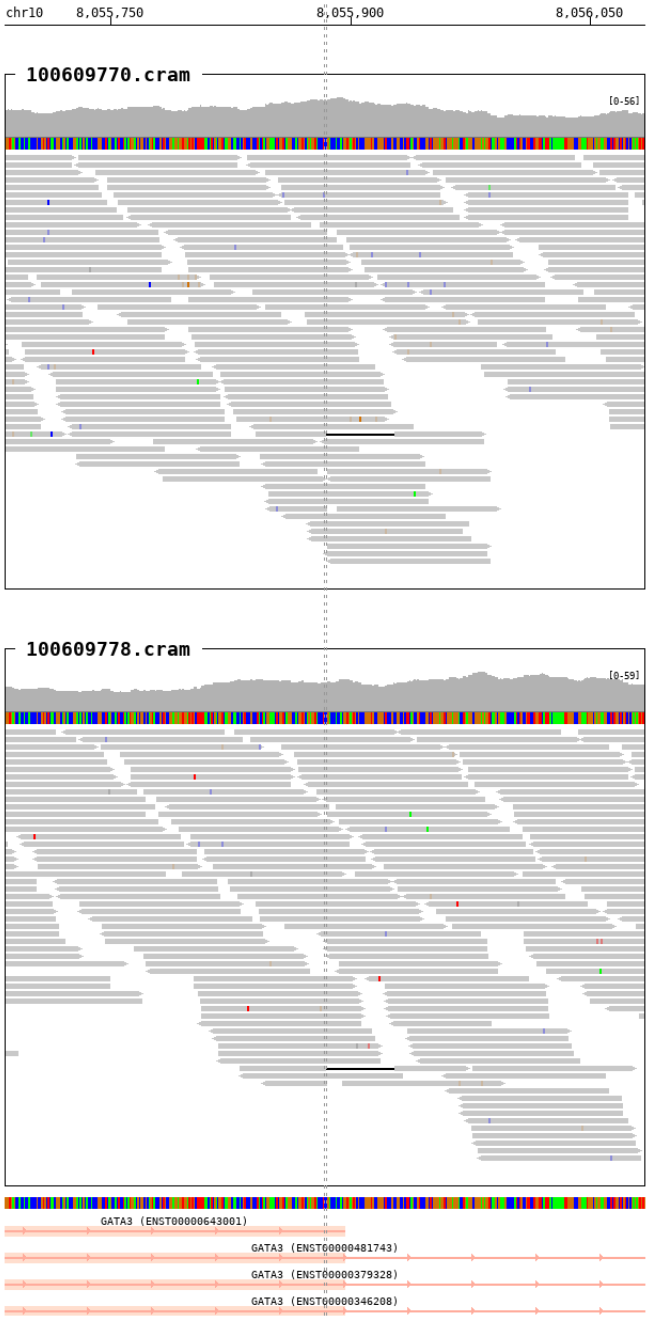
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10770651	chrX_48791231_T/A	24	3	*GATA1*	stop_gained



14. *GATA3*

14.1. chr10_8055884_CGACCCACCACGGTGAGTGCGCCCGGGGTGCCGGGGCTCCCG/-

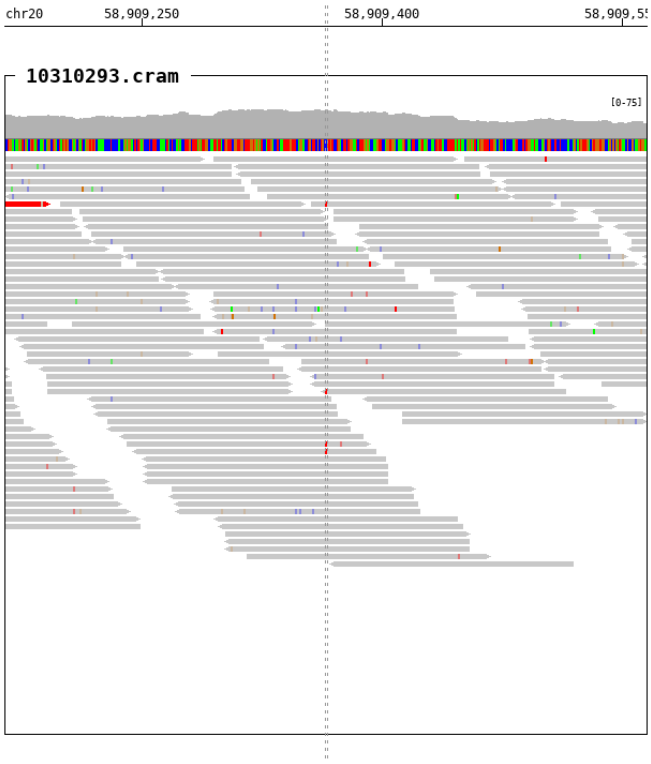
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100609770	chr10_8055884_CGACCCACCACGGTGAGTGCGCCCGGGGTGCCGGGGCTCCCG/-	59	3	*GATA3*	splice_donor_variant
100609778	chr10_8055884_CGACCCACCACGGTGAGTGCGCCCGGGGTGCCGGGGCTCCCG/-	62	3	*GATA3*	splice_donor_variant

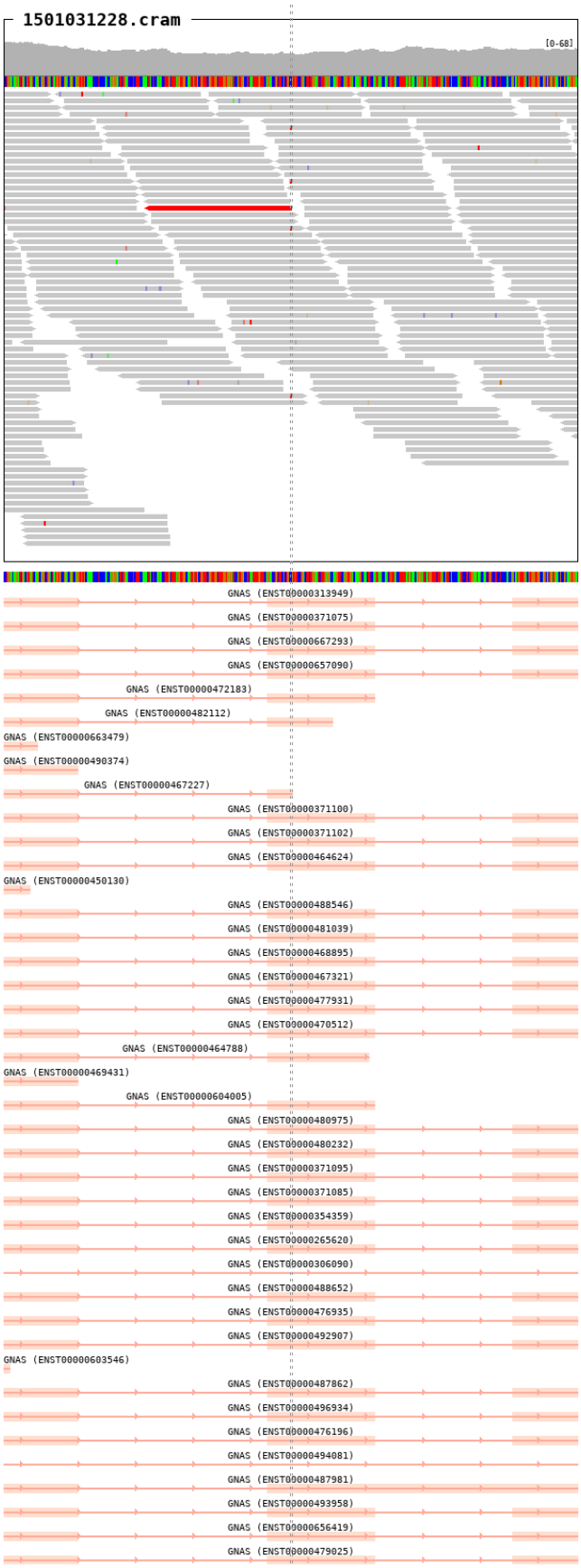


15. *GNAS*

15.1. chr20_58909365_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10310293	chr20_58909365_C/T	43	4	*GNAS*	missense_variant
1501031228	chr20_58909365_C/T	37	4	*GNAS*	missense_variant




1501031228.cram
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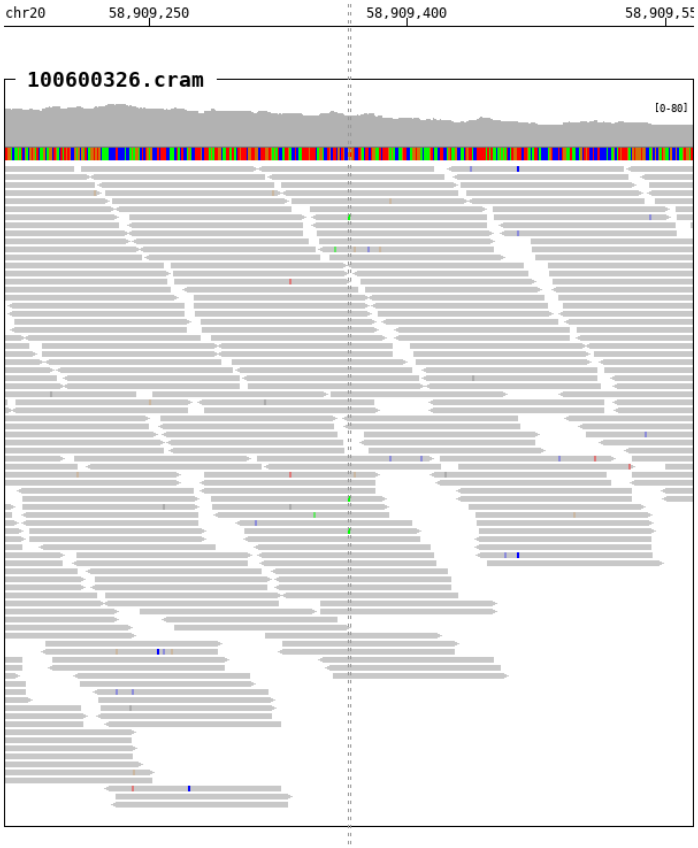
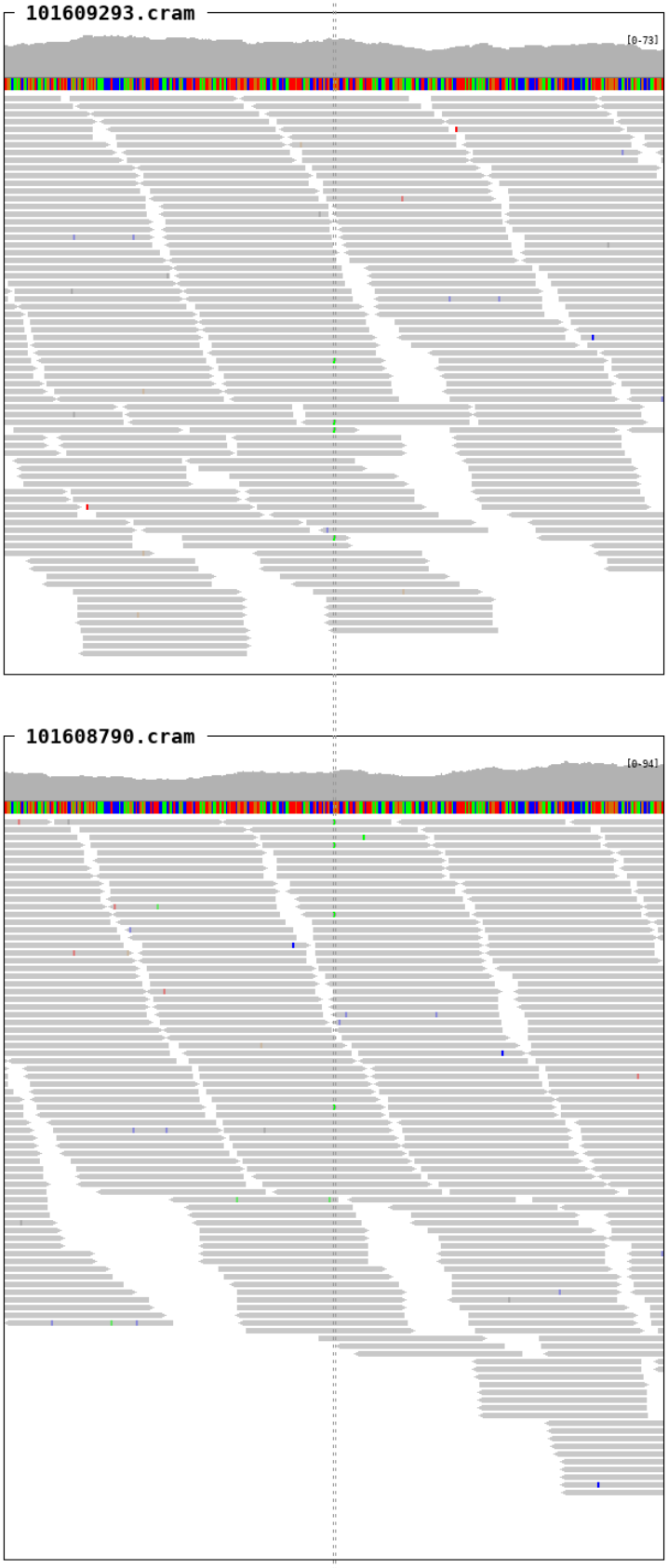
GNAS (ENST00000371075)
GNAS (ENST00000667293)
GNAS (ENST00000657090)
GNAS (ENST00000472183)
GNAS (ENST00000482112)
GNAS (ENST00000663479)
GNAS (ENST00000490374)
GNAS (ENST00000467227)
GNAS (ENST00000371100)
GNAS (ENST00000371102)
GNAS (ENST00000464624)
GNAS (ENST00000450130)
GNAS (ENST00000488546)
GNAS (ENST00000481039)
GNAS (ENST00000468895)
GNAS (ENST00000467321)
GNAS (ENST00000477931)
GNAS (ENST00000470512)
GNAS (ENST00000464788)
GNAS (ENST00000469431)
GNAS (ENST00000604005)
GNAS (ENST00000480975)
GNAS (ENST00000480232)
GNAS (ENST00000371095)
GNAS (ENST00000371085)
GNAS (ENST00000354359)
GNAS (ENST00000265620)
GNAS (ENST00000306090)
GNAS (ENST00000488652)
GNAS (ENST00000476935)
GNAS (ENST00000492907)
GNAS (ENST00000603546)
GNAS (ENST00000487862)
GNAS (ENST00000496934)
GNAS (ENST00000476196)
GNAS (ENST00000494081)
GNAS (ENST00000487981)
GNAS (ENST00000493958)
GNAS (ENST00000656419)
GNAS (ENST00000479025)

15.2. chr20_58909366_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100600326	chr20_58909366_G/A	50	3	*GNAS*	missense_variant
101102640	chr20_58909366_G/A	39	4	*GNAS*	missense_variant
101104757	chr20_58909366_G/A	39	4	*GNAS*	missense_variant
101608790	chr20_58909366_G/A	60	4	*GNAS*	missense_variant
101609293	chr20_58909366_G/A	60	4	*GNAS*	missense_variant
102102513	chr20_58909366_G/A	37	8	*GNAS*	missense_variant
110106805	chr20_58909366_G/A	43	4	*GNAS*	missense_variant




101609293.cram
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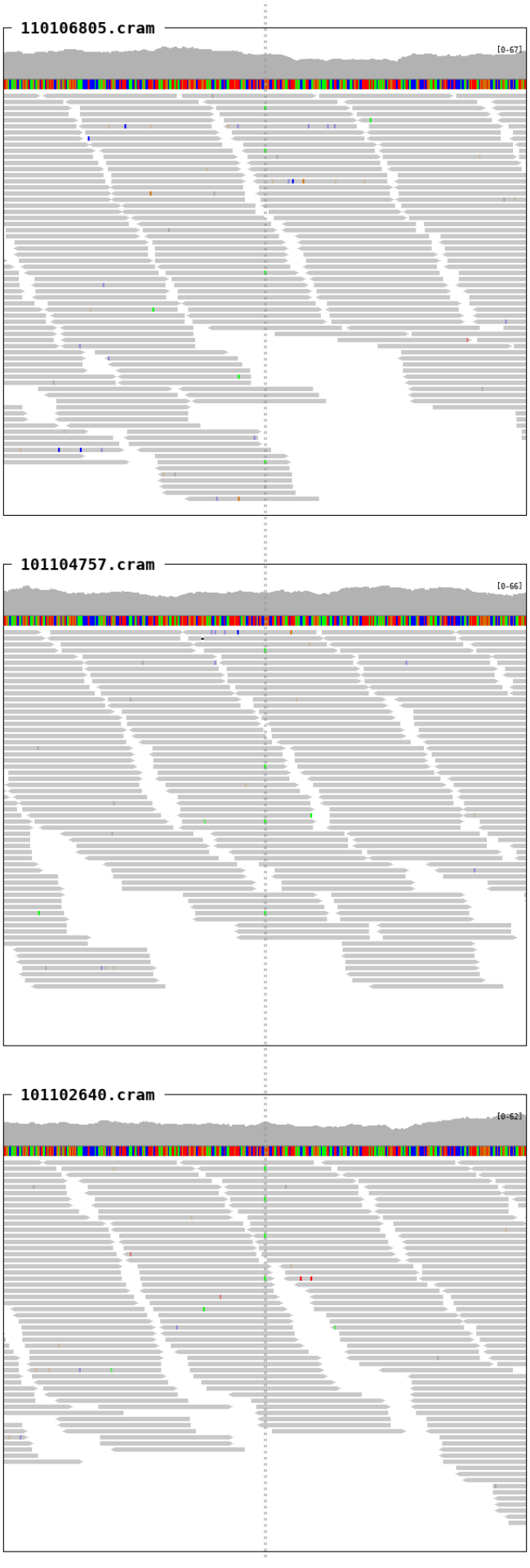
101608790.cram
[0-94]


110106805.cram
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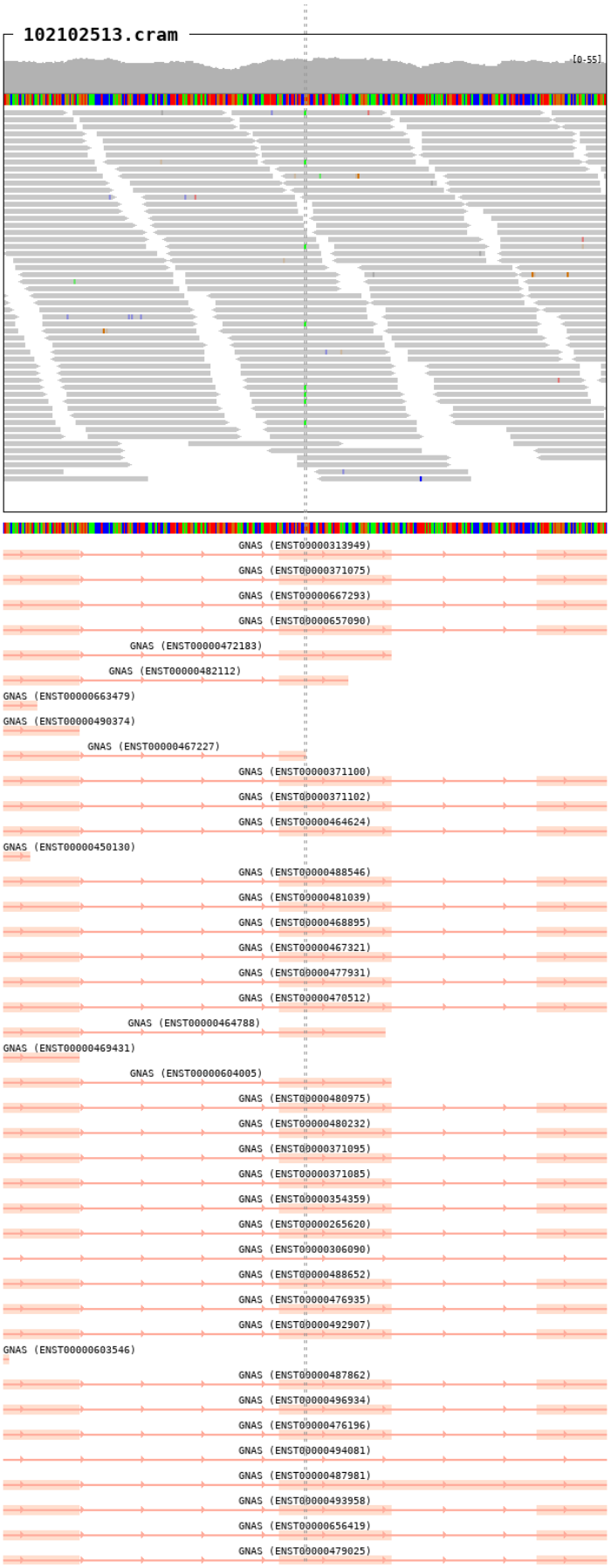
101104757.cram
[0-66]
101102640.cram
[0-62]


102102513.cram
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GNAS (ENST00000371075)
GNAS (ENST00000667293)
GNAS (ENST00000657090)
GNAS (ENST00000472183)
GNAS (ENST00000482112)
GNAS (ENST00000663479)
GNAS (ENST00000490374)
GNAS (ENST00000467227)
GNAS (ENST00000371100)
GNAS (ENST00000371102)
GNAS (ENST00000464624)
GNAS (ENST00000450130)
GNAS (ENST00000488546)
GNAS (ENST00000481039)
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GNAS (ENST00000467321)
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GNAS (ENST00000470512)
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GNAS (ENST00000265620)
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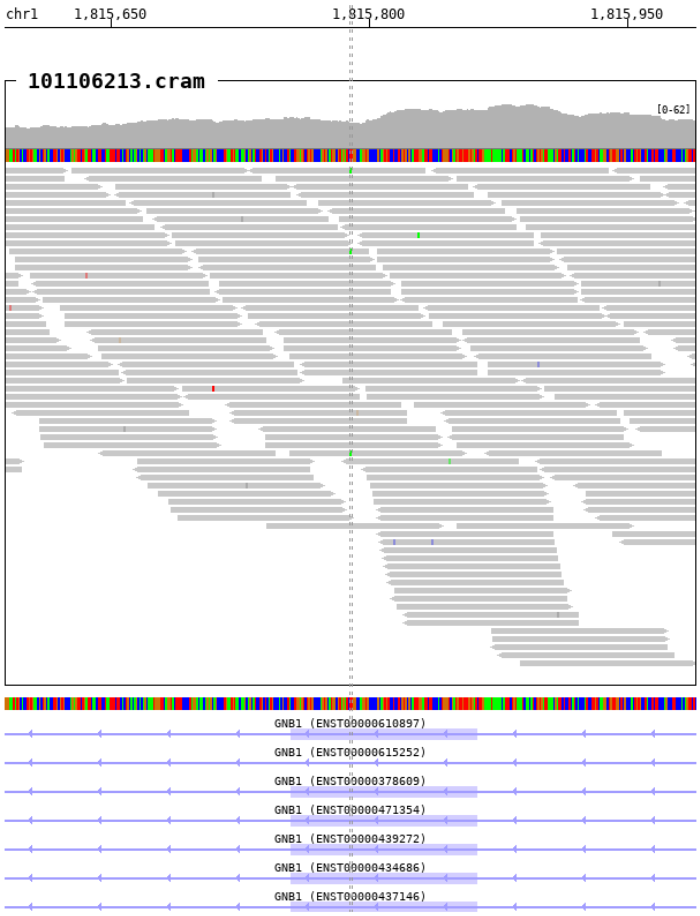
GNAS (ENST00000476935)
GNAS (ENST00000492907)
GNAS (ENST00000603546)
GNAS (ENST00000487862)
GNAS (ENST00000496934)
GNAS (ENST00000476196)
GNAS (ENST00000494081)
GNAS (ENST00000487981)
GNAS (ENST00000493958)
GNAS (ENST00000656419)
GNAS (ENST00000479025)

16. *GNB1*

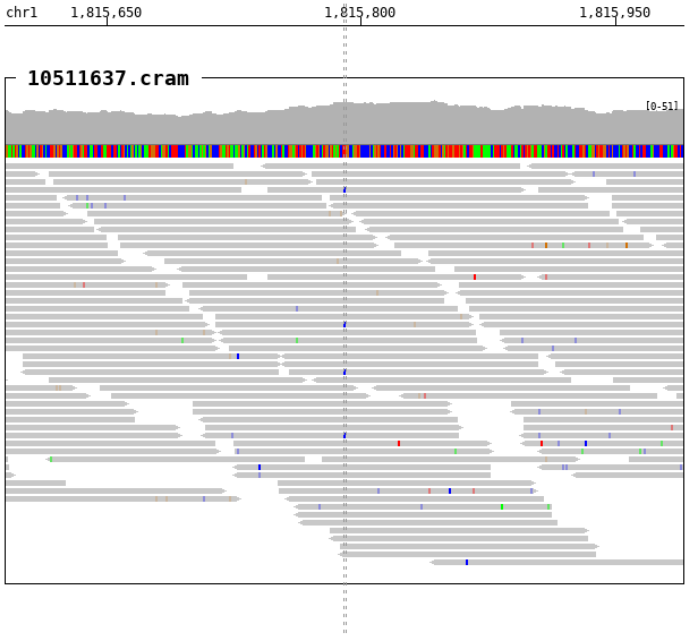
16.1. chr1_1815789_T/A

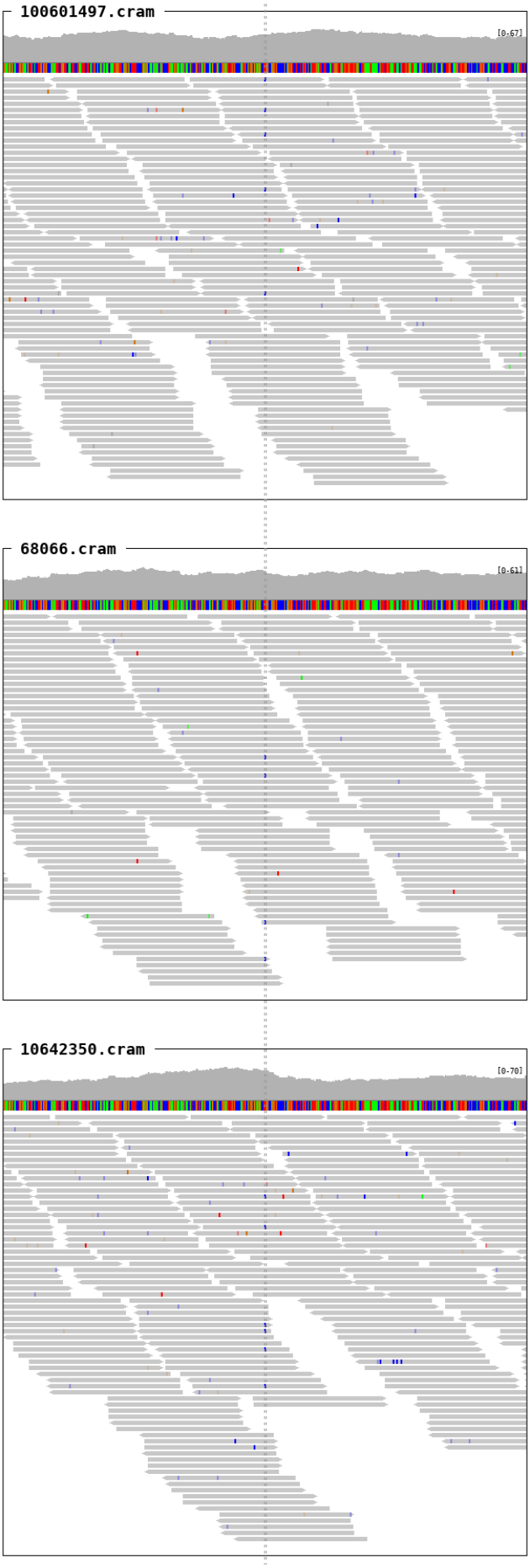
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101106213	chr1_1815789_T/A	32	3	*GNB1*	missense_variant



16.2. chr1_1815790_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100601497	chr1_1815790_T/C	50	5	*GNB1*	missense_variant
101104686	chr1_1815790_T/C	34	4	*GNB1*	missense_variant
102104451	chr1_1815790_T/C	36	5	*GNB1*	missense_variant
10310279	chr1_1815790_T/C	39	7	*GNB1*	missense_variant
10511637	chr1_1815790_T/C	45	4	*GNB1*	missense_variant
10642350	chr1_1815790_T/C	51	6	*GNB1*	missense_variant
11050788	chr1_1815790_T/C	46	7	*GNB1*	missense_variant
112401604	chr1_1815790_T/C	30	4	*GNB1*	missense_variant
68066	chr1_1815790_T/C	45	4	*GNB1*	missense_variant

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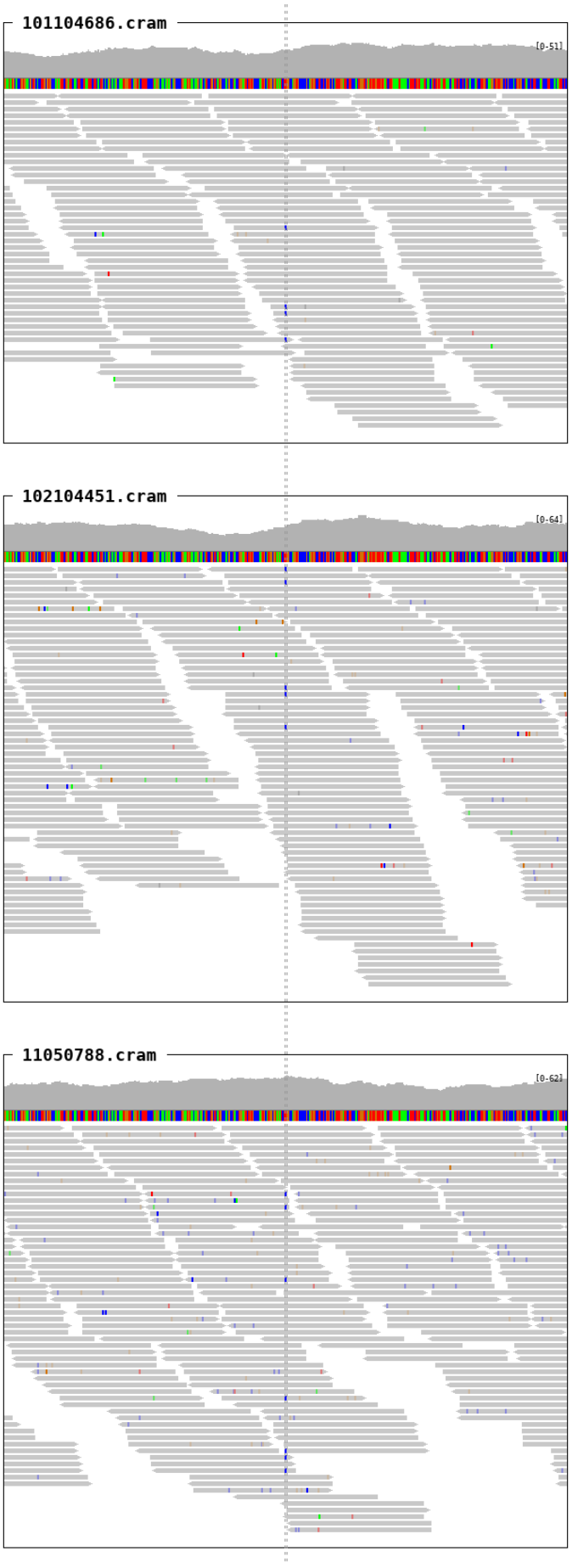
68066.cram
[0-61]
10642350.cram
[0-70]


101104686.cram
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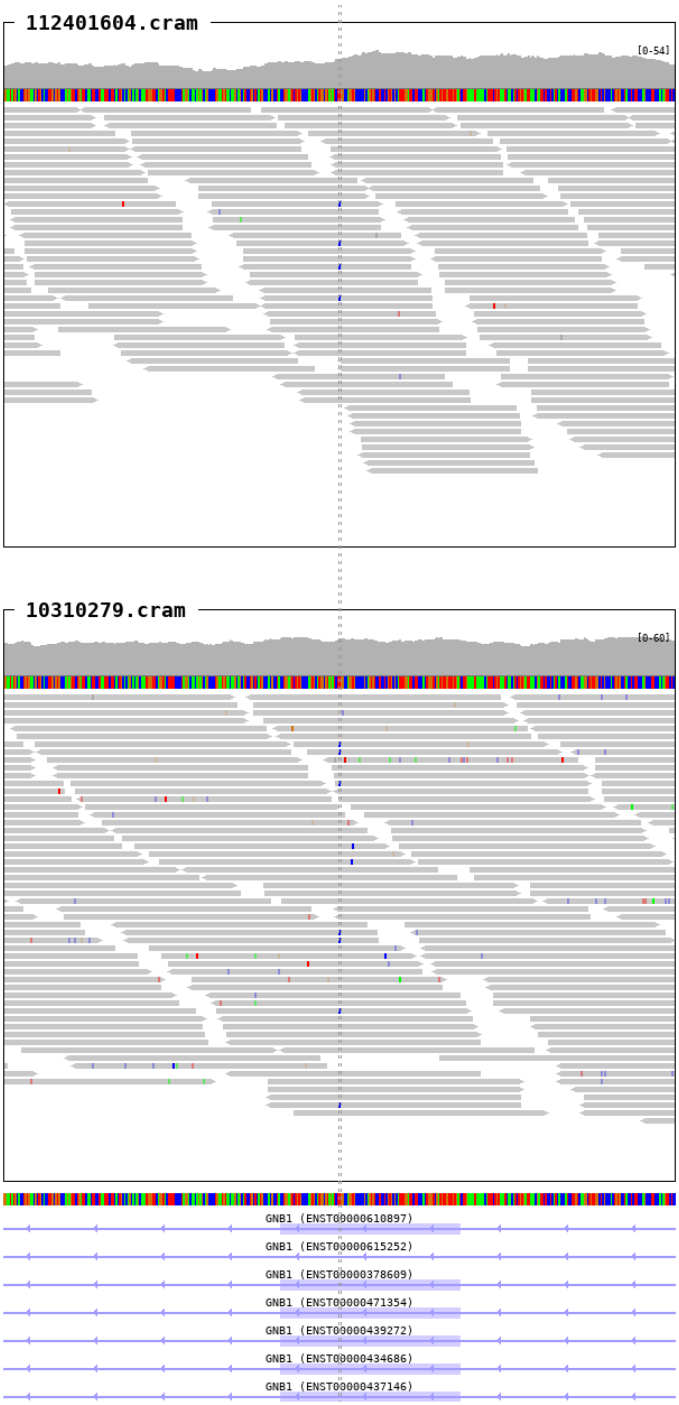
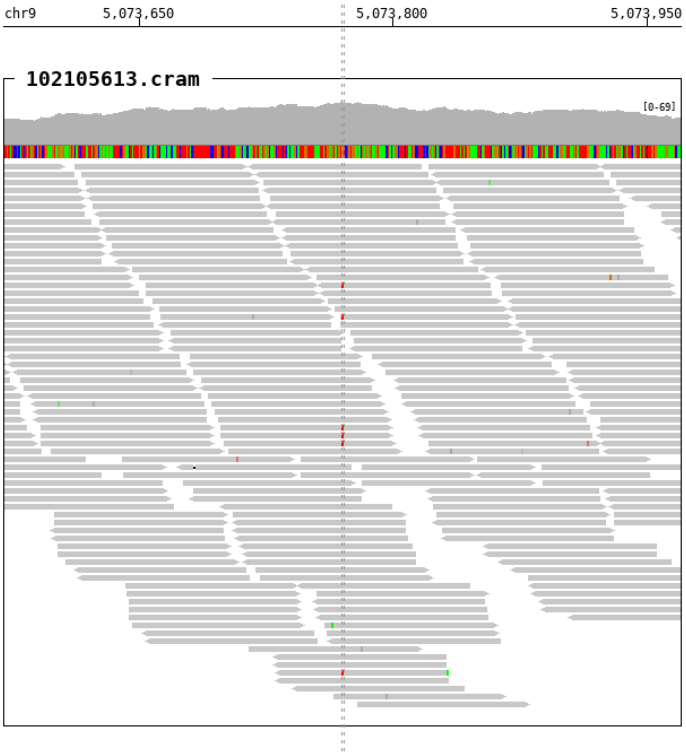
102104451.cram
[0-64]
11050788.cram
[0-62]

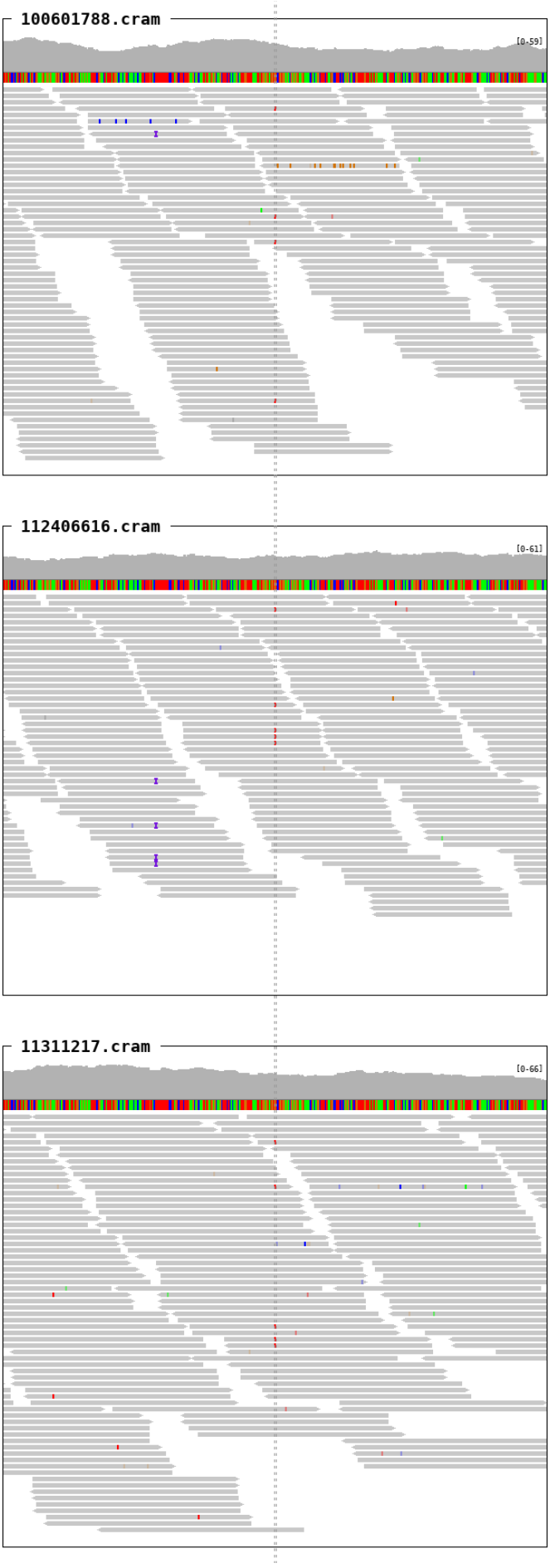

112401604.cram
[0-54]
10310279.cram
[0-60]
GNB1 (ENST00000610897)
GNB1 (ENST00000615252)
GNB1 (ENST00000378609)
GNB1 (ENST00000471354)
GNB1 (ENST00000439272)
GNB1 (ENST00000434686)
GNB1 (ENST00000437146)

17. *JAK2*

17.1. chr9_5073770_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10010583	chr9_5073770_G/T	26	5	*JAK2*	missense_variant
100601788	chr9_5073770_G/T	41	4	*JAK2*	missense_variant
101608575	chr9_5073770_G/T	33	6	*JAK2*	missense_variant
102104826	chr9_5073770_G/T	5	32	*JAK2*	missense_variant
102105613	chr9_5073770_G/T	57	6	*JAK2*	missense_variant
102105991	chr9_5073770_G/T	37	5	*JAK2*	missense_variant
10510596	chr9_5073770_G/T	41	6	*JAK2*	missense_variant
112300508	chr9_5073770_G/T	37	5	*JAK2*	missense_variant
112406616	chr9_5073770_G/T	34	4	*JAK2*	missense_variant
11311217	chr9_5073770_G/T	44	5	*JAK2*	missense_variant
1308262135	chr9_5073770_G/T	6	41	*JAK2*	missense_variant
1504233344	chr9_5073770_G/T	34	7	*JAK2*	missense_variant

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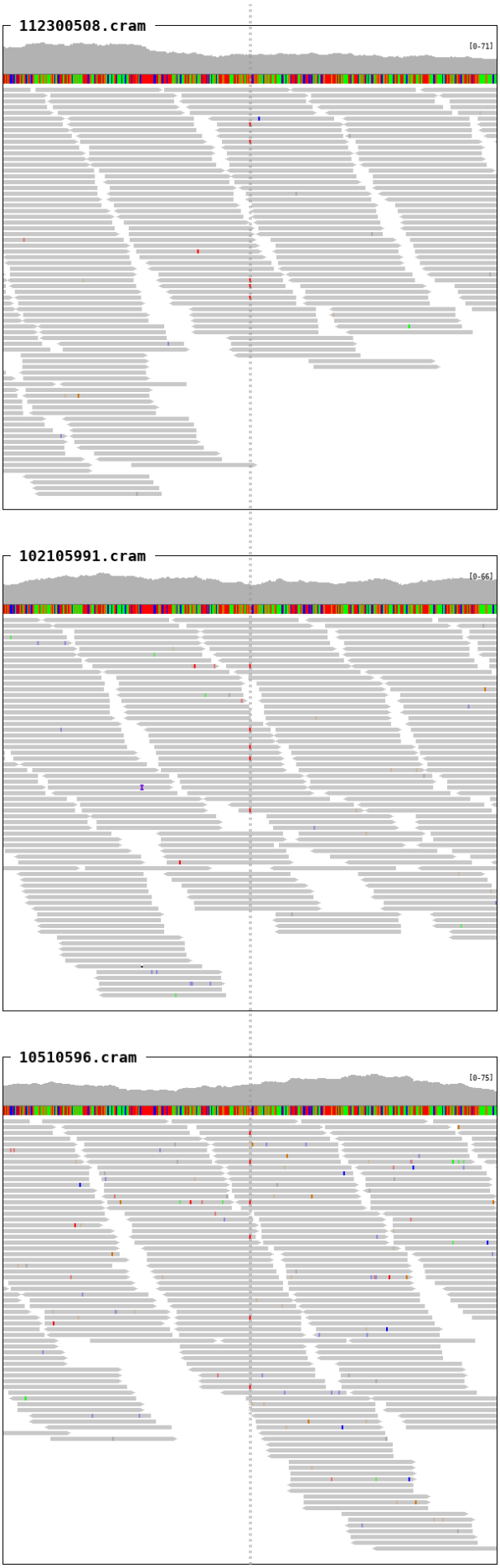
112406616.cram
[0-61]
11311217.cram
[0-66]


112300508.cram
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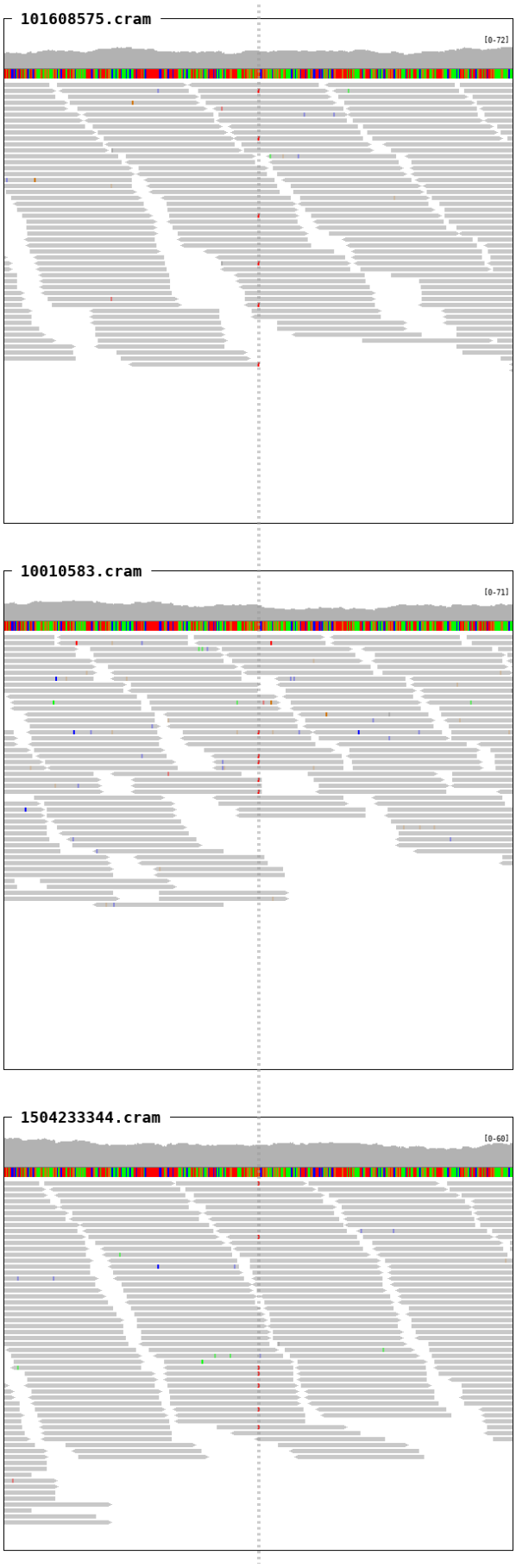
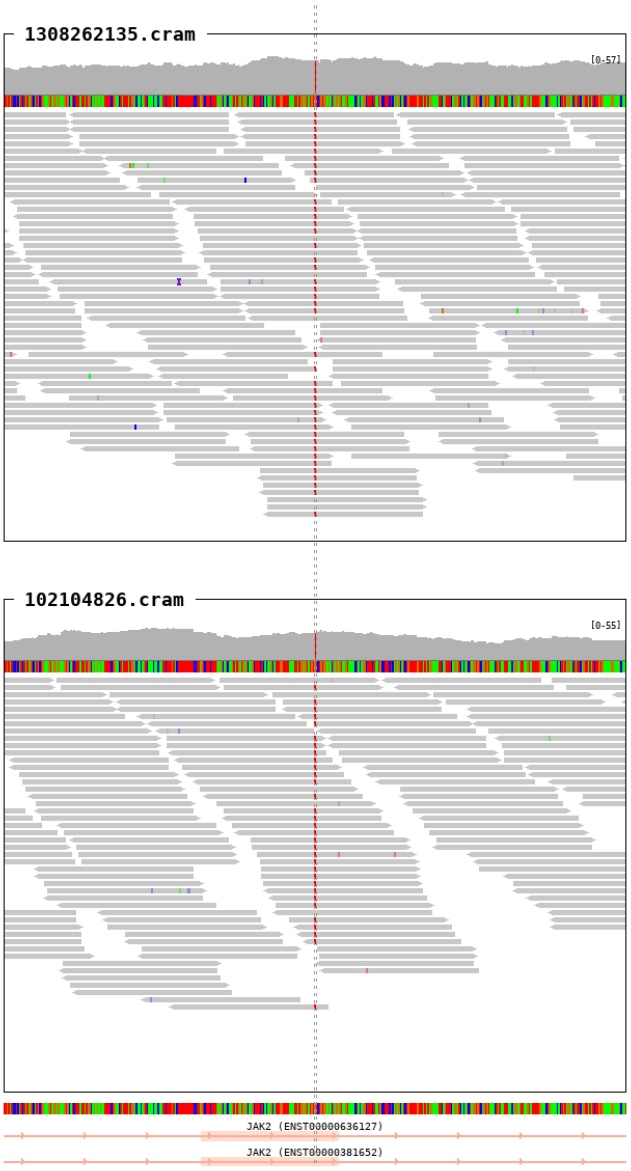
102105991.cram
[0-66]
10510596.cram
[0-75]

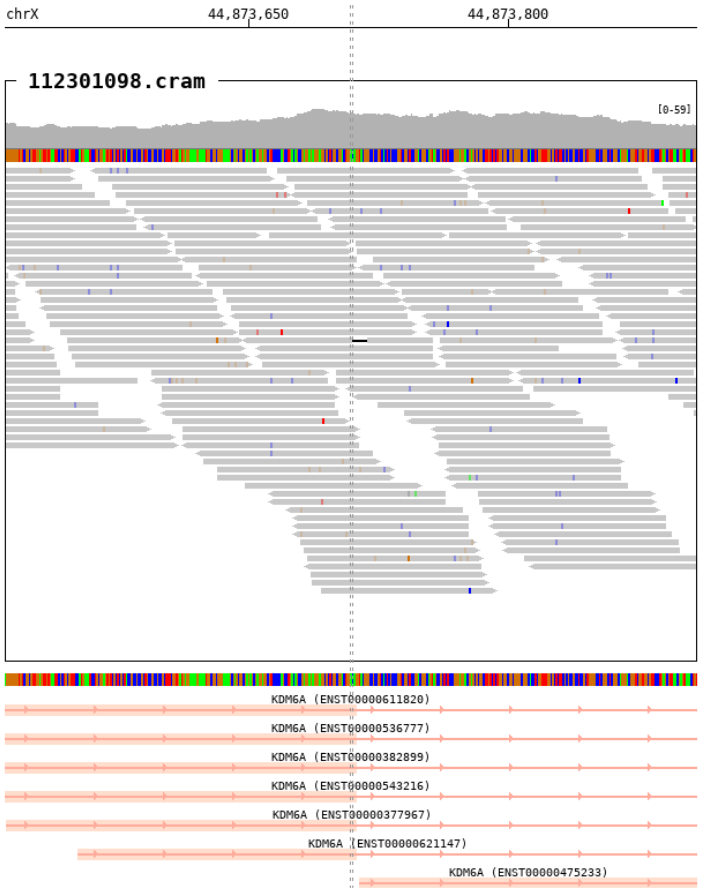

101608575.cram
[0-72]
10010583.cram
[0-71]
1504233344.cram
[0-60]


1308262135.cram
[0-57]
102104826.cram
[0-55]
JAK2 (ENST00000636127)
JAK2 (ENST00000381652)

18. *KDM6A*

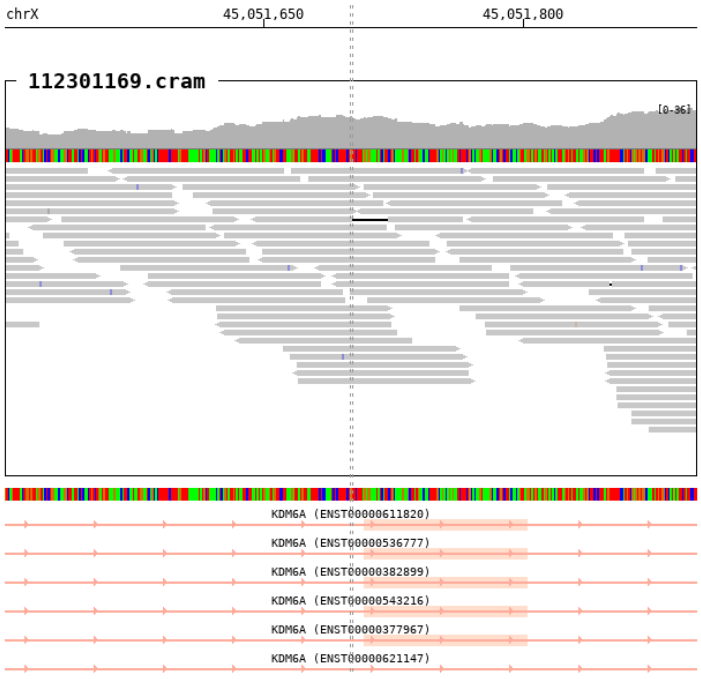
18.1. chrX_44873709_CAGGTACG/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301098	chrX_44873709_CAGGTACG/-	47	2	*KDM6A*	splice_donor_variant



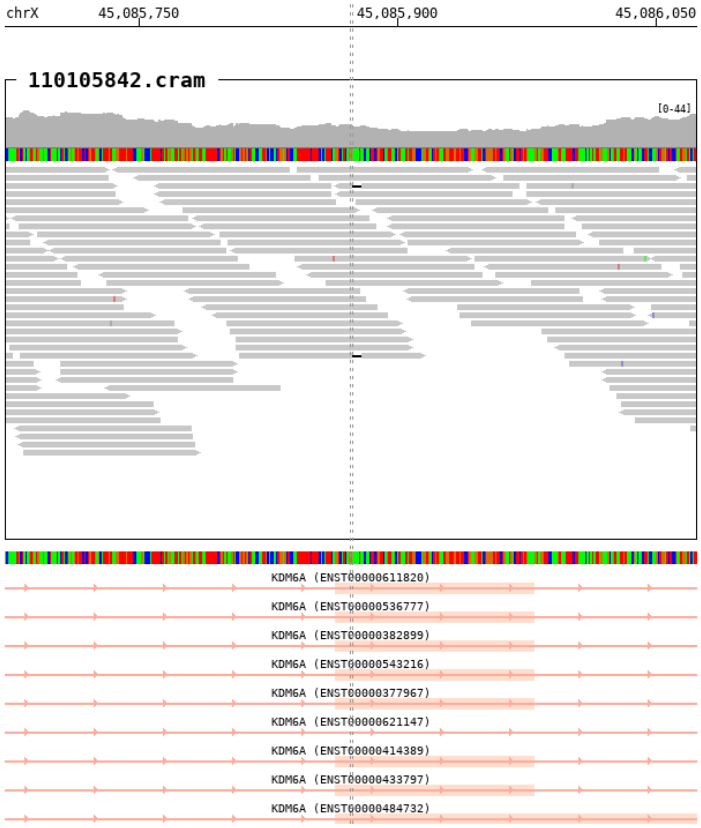
18.2. chrX_45051700_TTCTTTAGAGGAAATATCAT/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301169	chrX_45051700_TTCTTTAGAGGAAATATCAT/-	28	2	*KDM6A*	splice_acceptor_variant



18.3. chrX_45085873_AAAAT/-

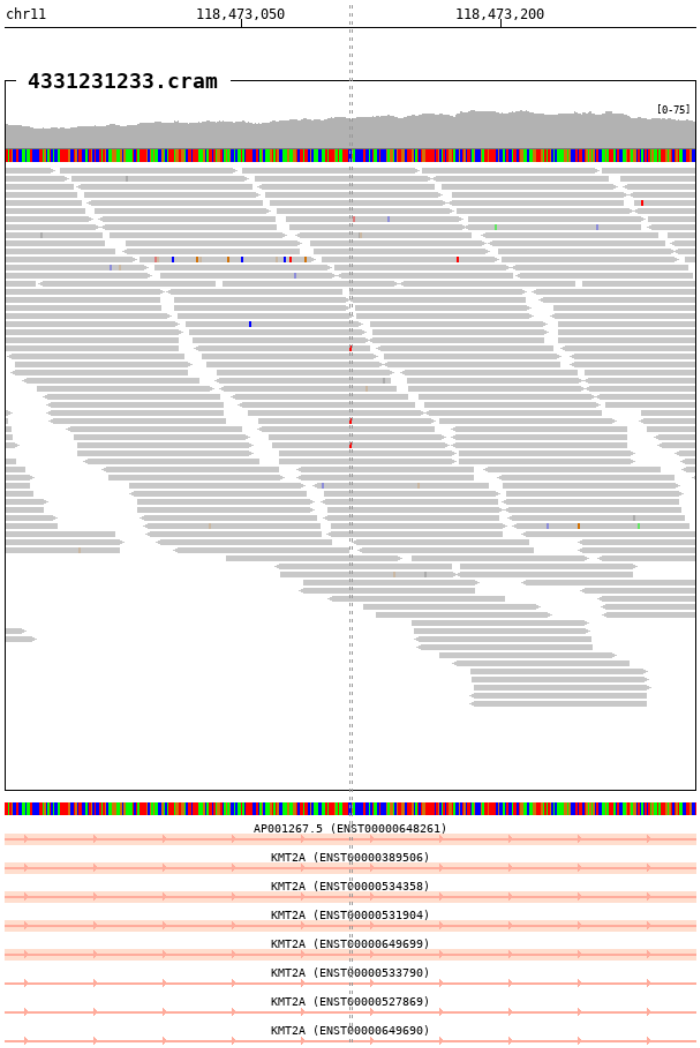
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110105842	chrX_45085873_AAAAT/-	21	2	*KDM6A*	frameshift_variant



19. *KMT2A*

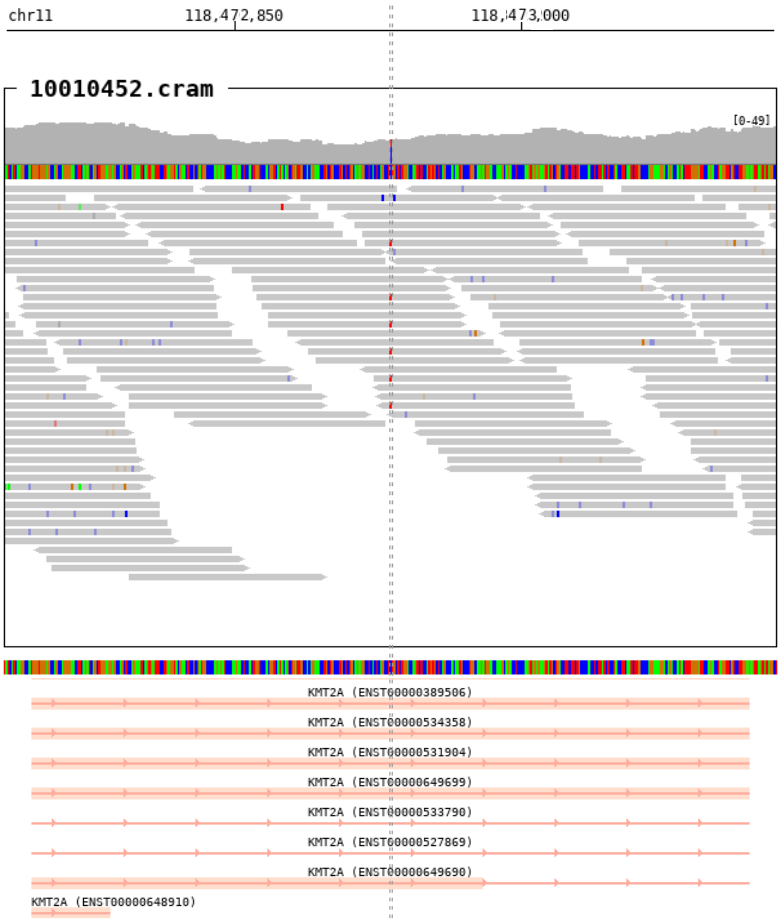
19.1. chr11_118473113_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
4331231233	chr11_118473113_C/T	46	3	*KMT2A*	stop_gained



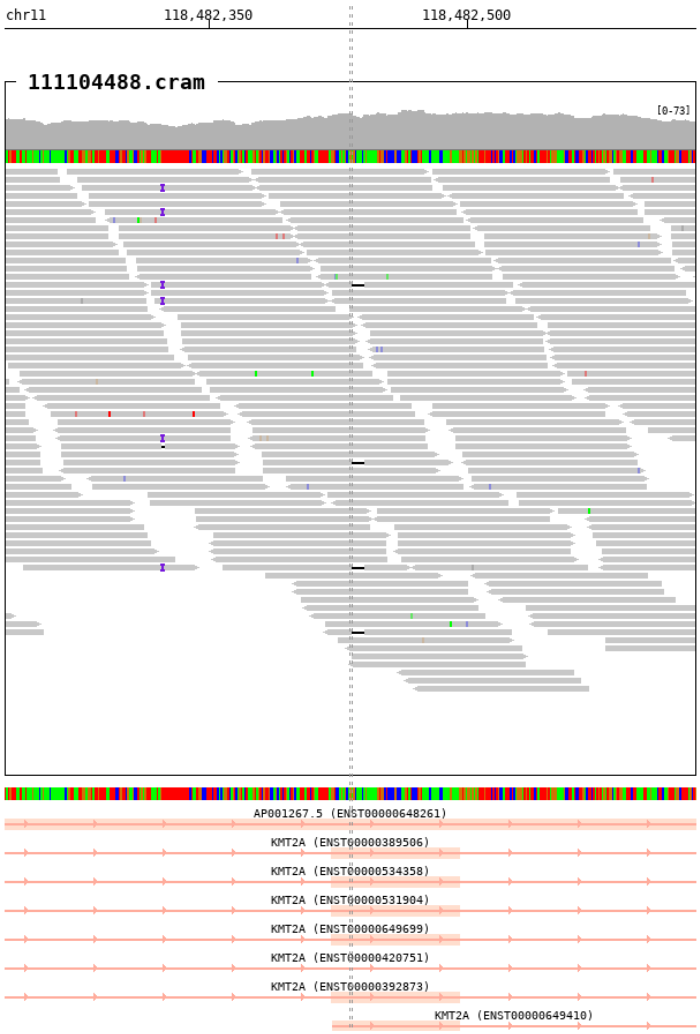
19.2. chr11_118472981_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10010452	chr11_118472981_C/T	28	6	*KMT2A*	stop_gained



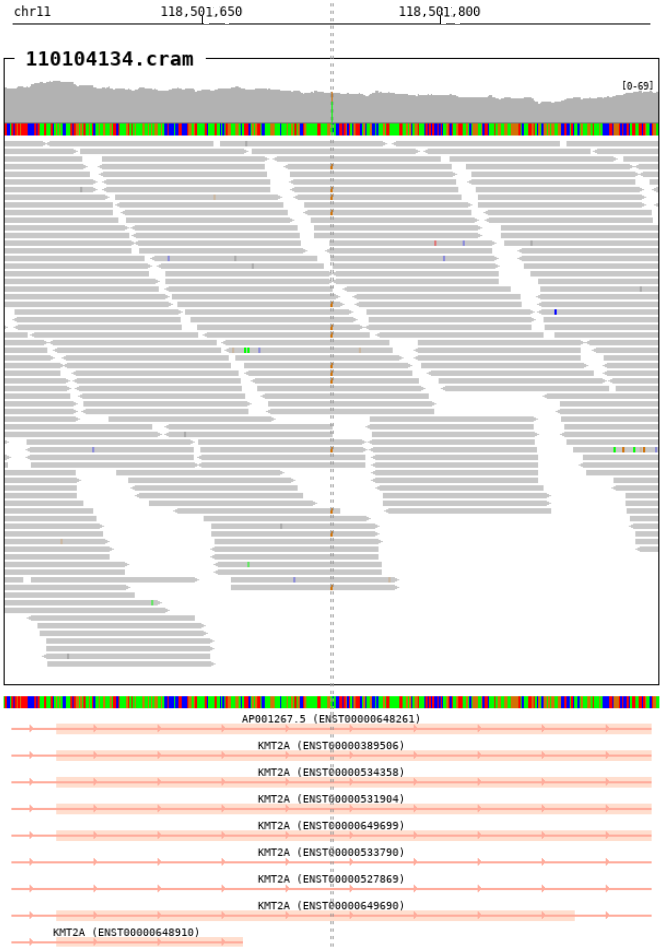
19.3. chr11_118482432_AGCAAAC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
111104488	chr11_118482432_AGCAAAC/-	54	4	*KMT2A*	frameshift_variant



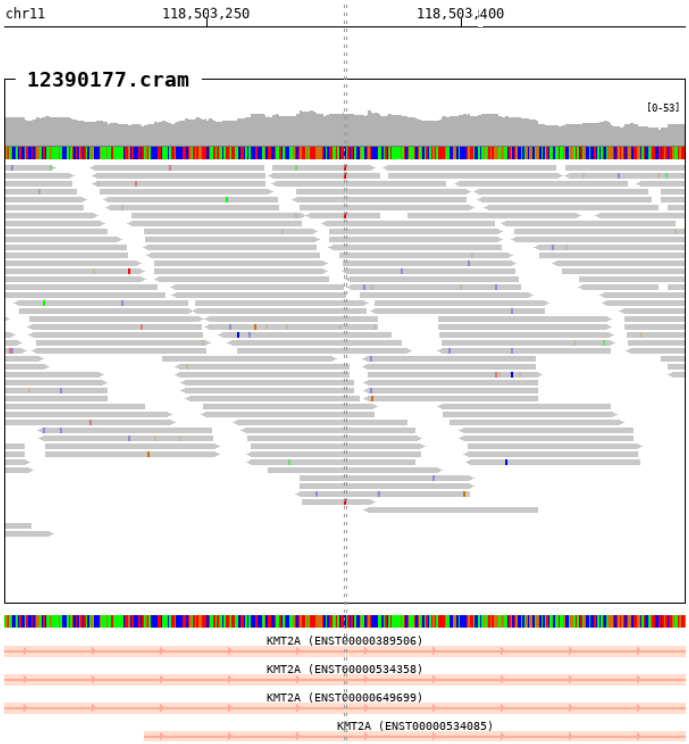
19.4. chr11_118501780_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110104134	chr11_118501780_C/G	53	14	*KMT2A*	stop_gained



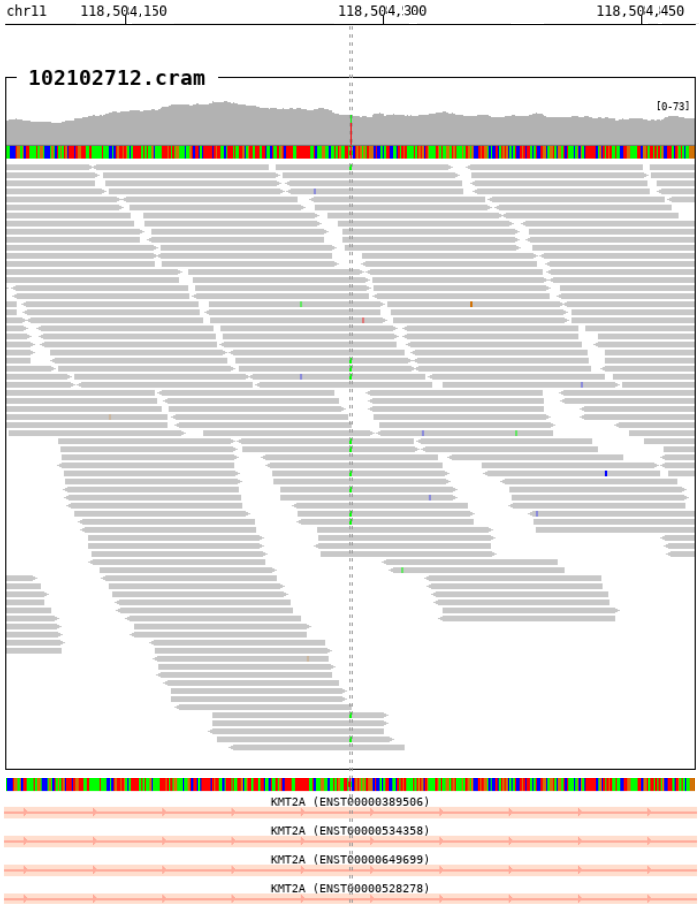
19.5. chr11_118503327_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12390177	chr11_118503327_C/T	32	4	*KMT2A*	stop_gained



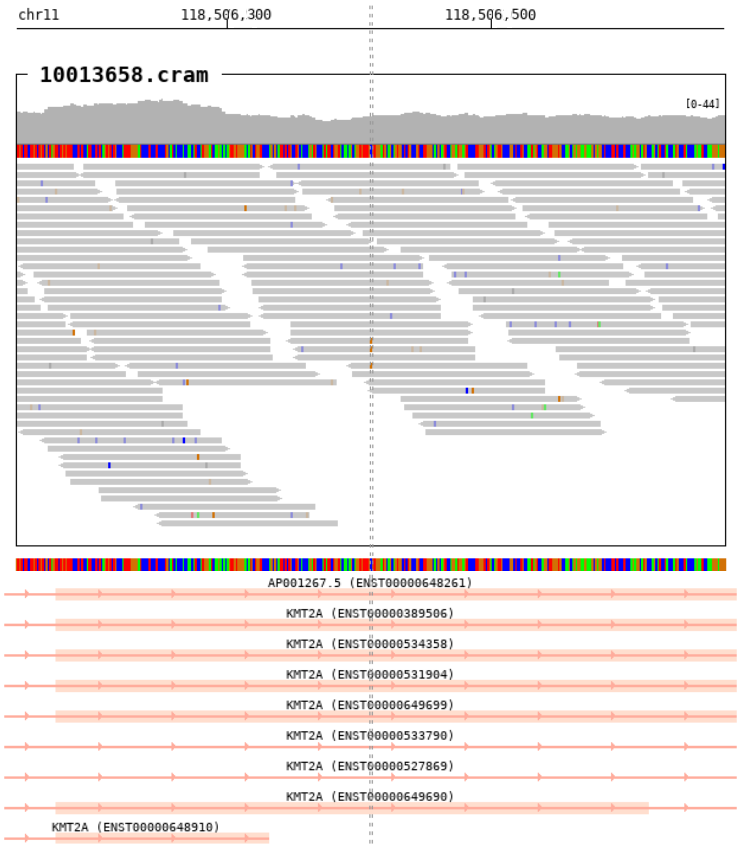
19.6. chr11_118504291_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102102712	chr11_118504291_T/A	36	12	*KMT2A*	stop_gained



19.7. chr11_118506409_C/G

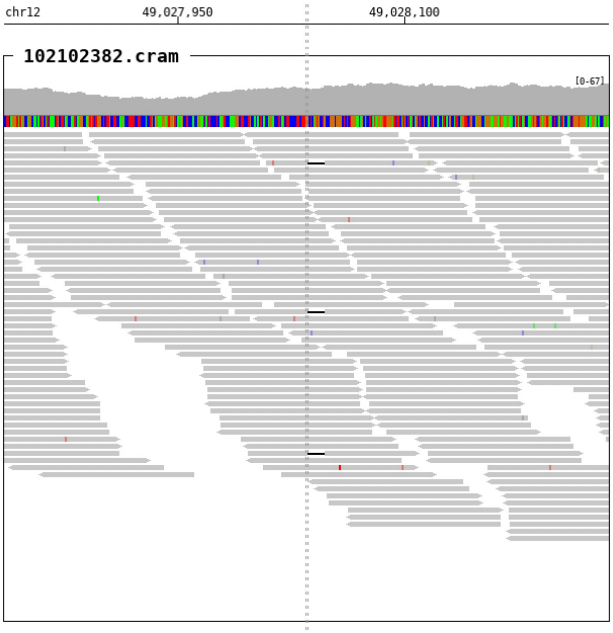
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10013658	chr11_118506409_C/G	22	4	*KMT2A*	stop_gained

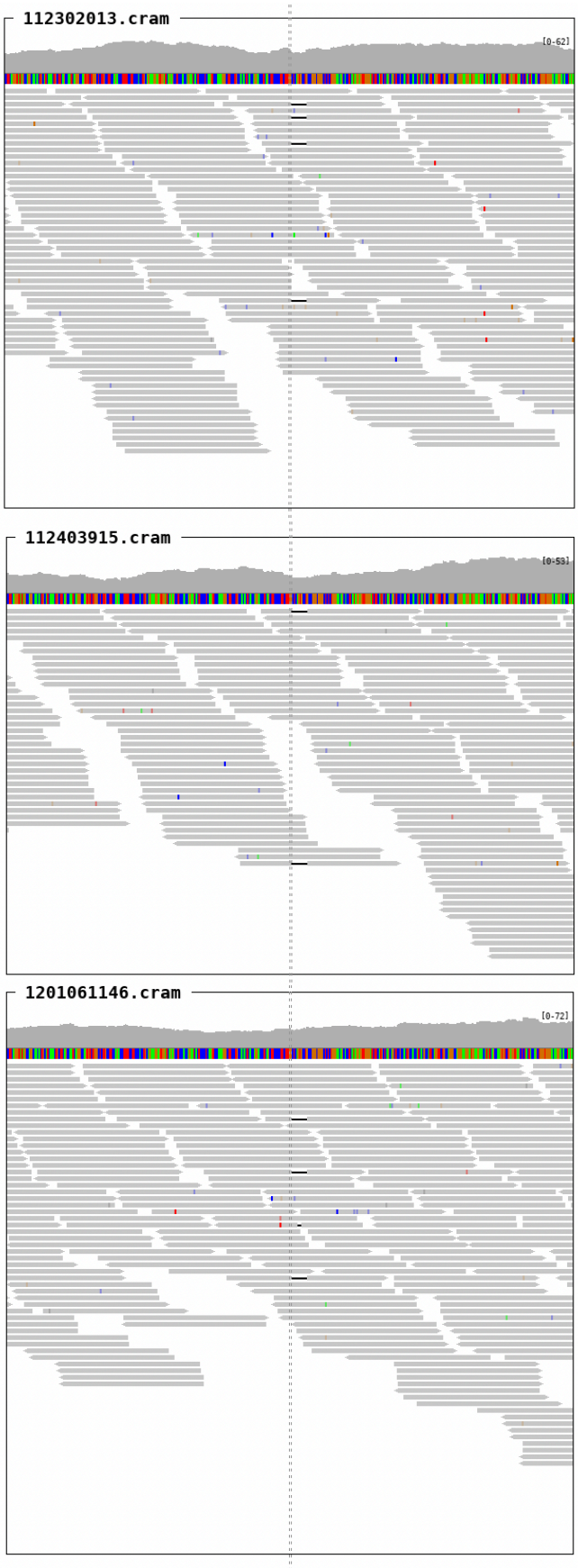


20. *KMT2D*

20.1. chr12_49028035_GCTCAGTGCCT/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102102382	chr12_49028035_GCTCAGTGCCT/-	46	3	*KMT2D*	frameshift_variant
112302013	chr12_49028035_GCTCAGTGCCT/-	40	4	*KMT2D*	frameshift_variant
112303742	chr12_49028035_GCTCAGTGCCT/-	35	5	*KMT2D*	frameshift_variant
112403915	chr12_49028035_GCTCAGTGCCT/-	25	3	*KMT2D*	frameshift_variant
1201061146	chr12_49028035_GCTCAGTGCCT/-	39	3	*KMT2D*	frameshift_variant
1202252316	chr12_49028035_GCTCAGTGCCT/-	30	3	*KMT2D*	frameshift_variant
1303022235	chr12_49028035_GCTCAGTGCCT/-	44	3	*KMT2D*	frameshift_variant
5401023125	chr12_49028035_GCTCAGTGCCT/-	39	3	*KMT2D*	frameshift_variant
5401023333	chr12_49028035_GCTCAGTGCCT/-	39	3	*KMT2D*	frameshift_variant
60076	chr12_49028035_GCTCAGTGCCT/-	26	3	*KMT2D*	frameshift_variant
102100137	chr12_49028035_GCTCAGTGCCT/-	46	5	*KMT2D*	frameshift_variant
102105394	chr12_49028035_GCTCAGTGCCT/-	36	4	*KMT2D*	frameshift_variant
112301159	chr12_49028035_GCTCAGTGCCT/-	83	11	*KMT2D*	frameshift_variant
102100162	chr12_49028035_GCTCAGTGCCT/-	40	4	*KMT2D*	frameshift_variant

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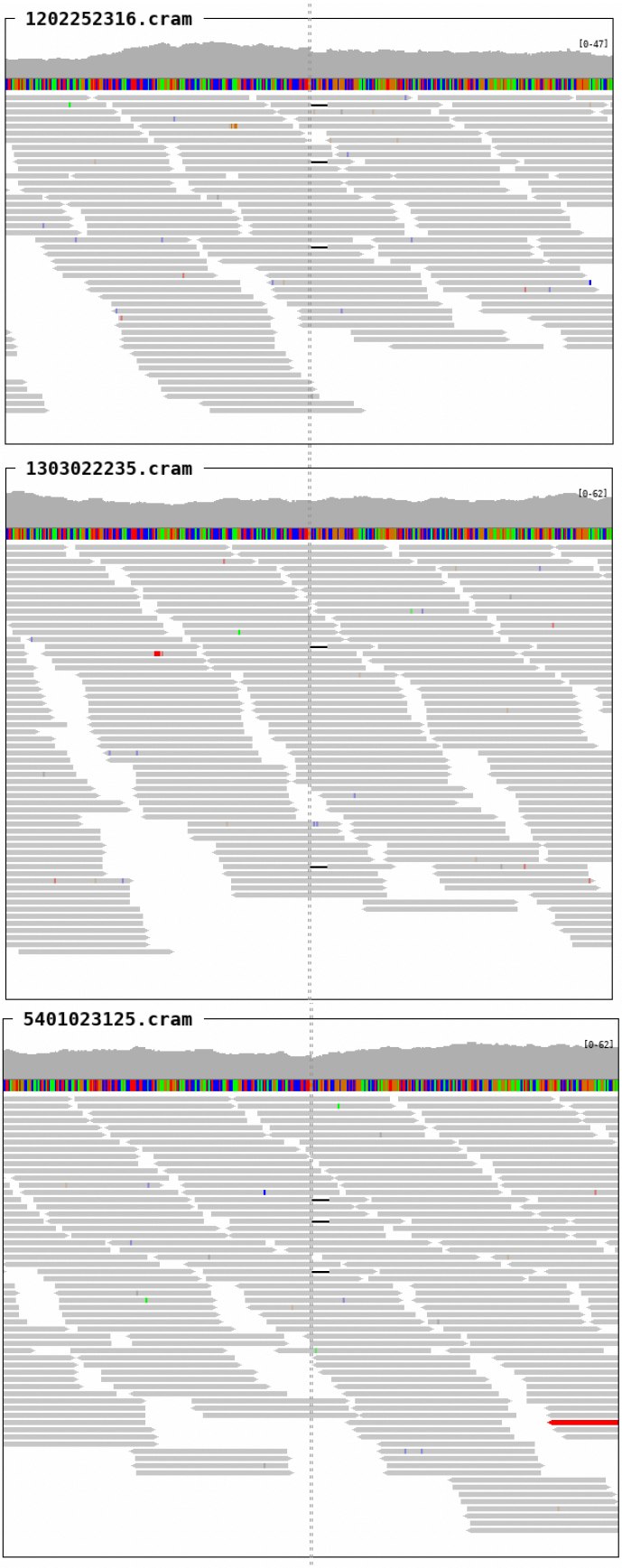
112403915.cram
[0-53]
1201061146.cram
[0-72]


1202252316.cram
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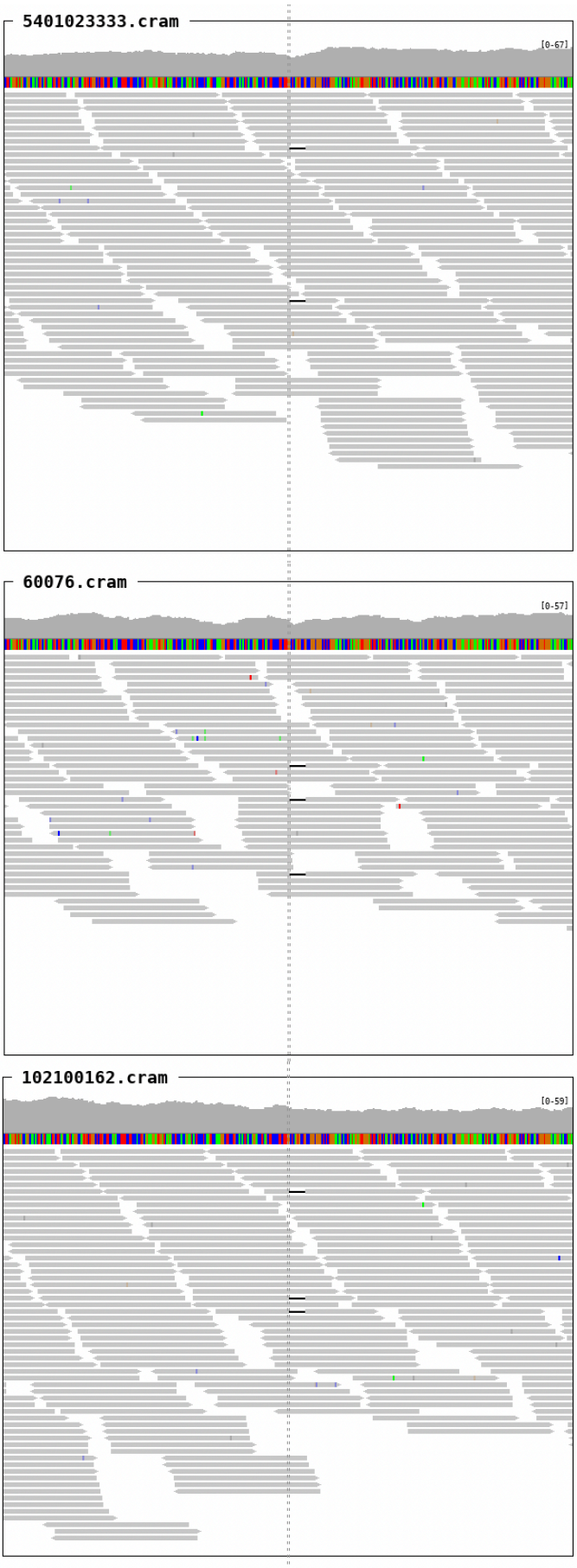
1303022235.cram
[0-62]
5401023125.cram
[0-62]


5401023333.cram
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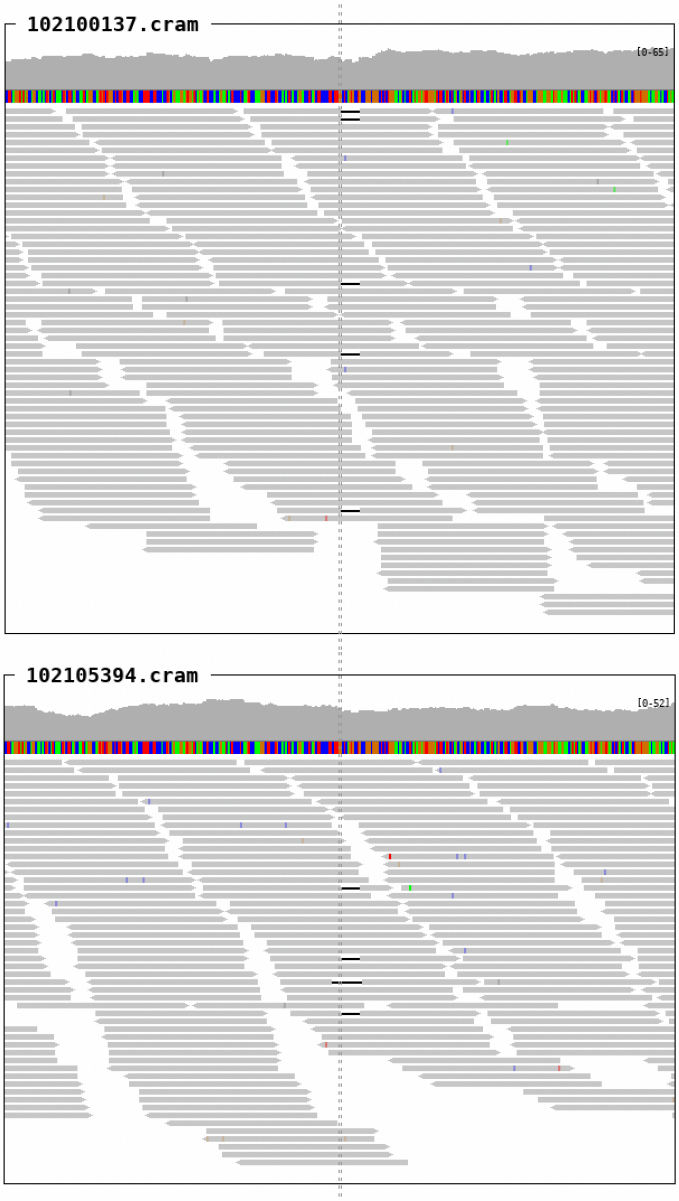
60076.cram
[0-57]
102100162.cram
[0-59]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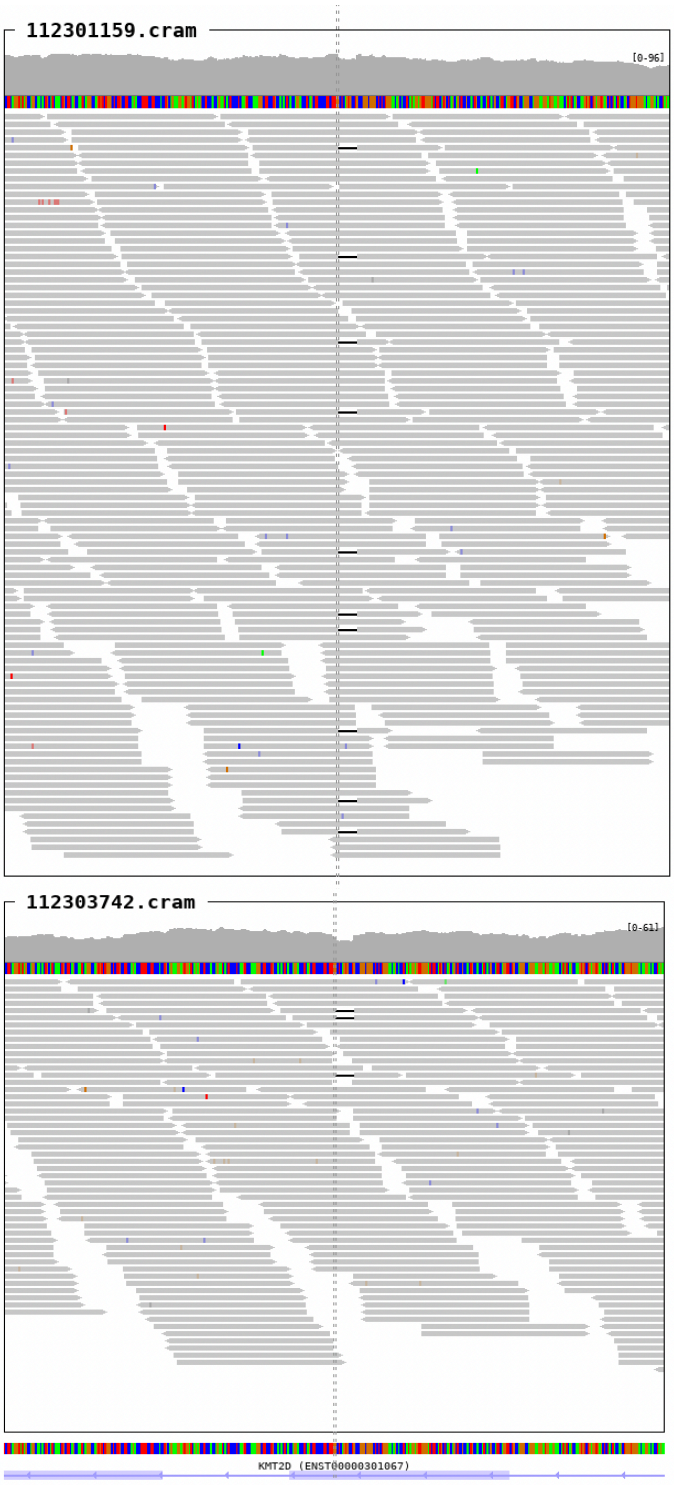
102105394.cram
[0-52]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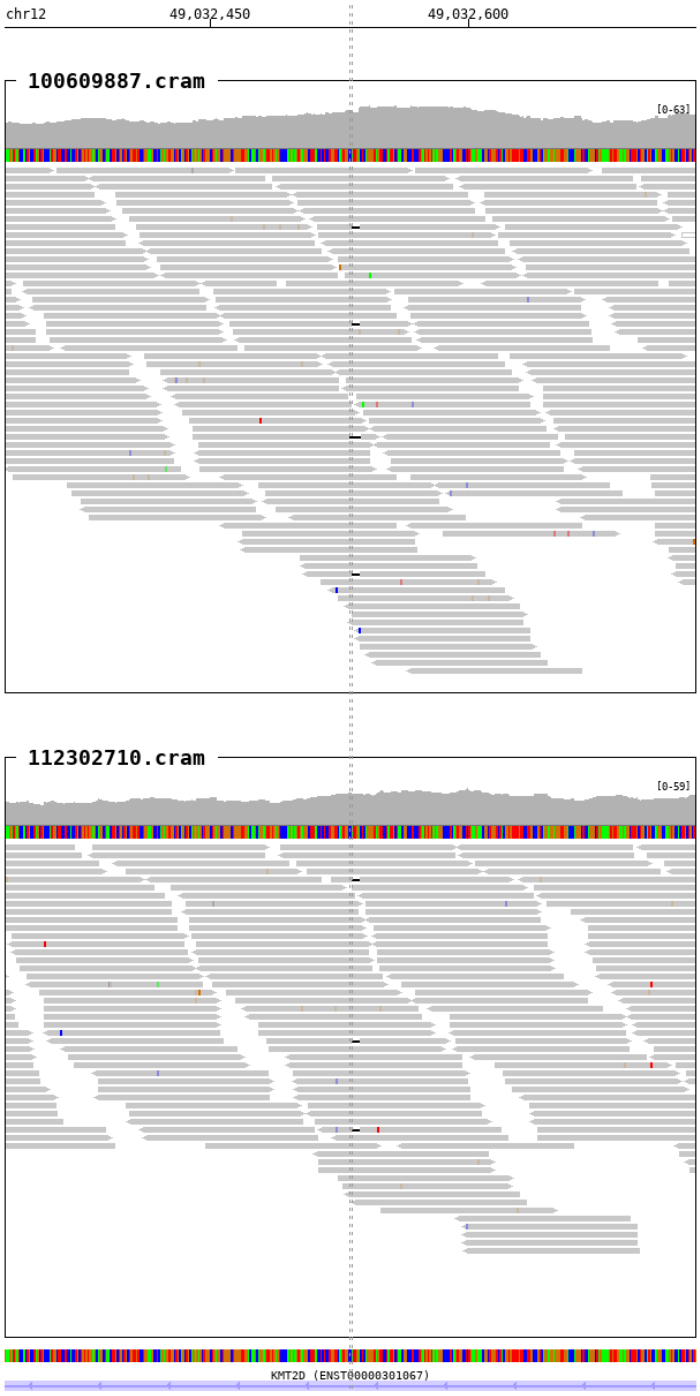
112303742.cram
[0-61]
KMT2D (ENST00000301067)

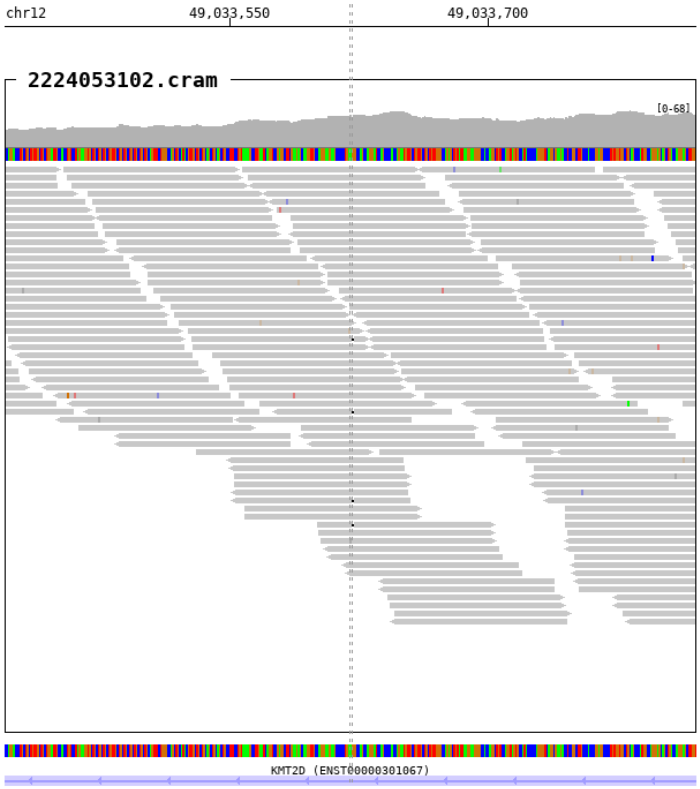
20.2. chr12_49032531_ATTG/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100609887	chr12_49032531_ATTG/-	49	5	*KMT2D*	frameshift_variant
112302710	chr12_49032531_ATTG/-	41	3	*KMT2D*	frameshift_variant



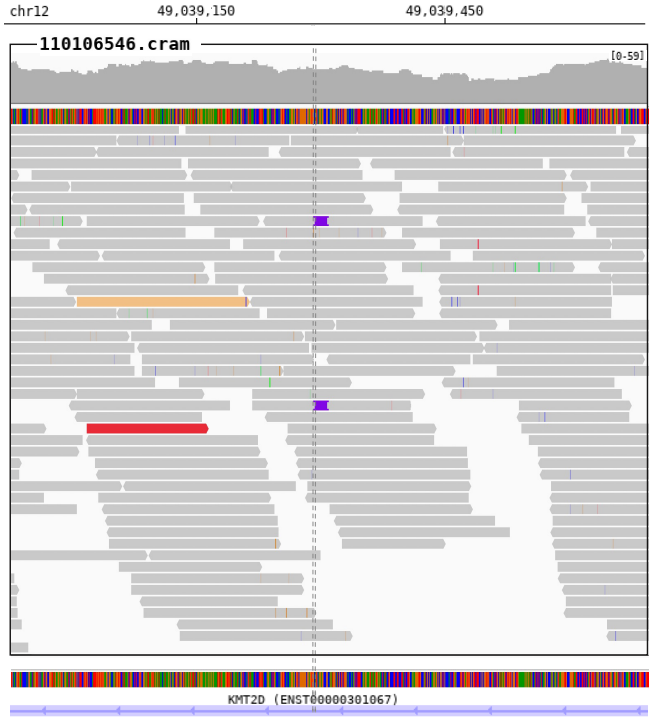
20.3. chr12_49033620_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
2224053102	chr12_49033620_G/-	44	4	*KMT2D*	frameshift_variant



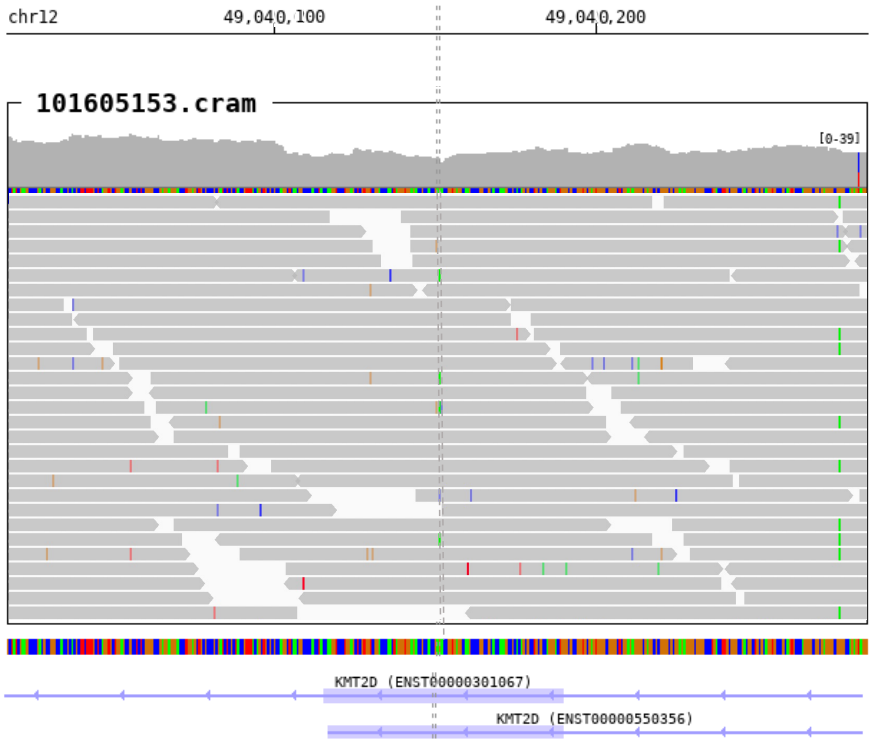
20.4. chr12_ 49039304_-/CCATCCTGGGG

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110106546	chr12_49039304_-/CCATCCTGGGG	31	2	*KMT2D*	frameshift_variant



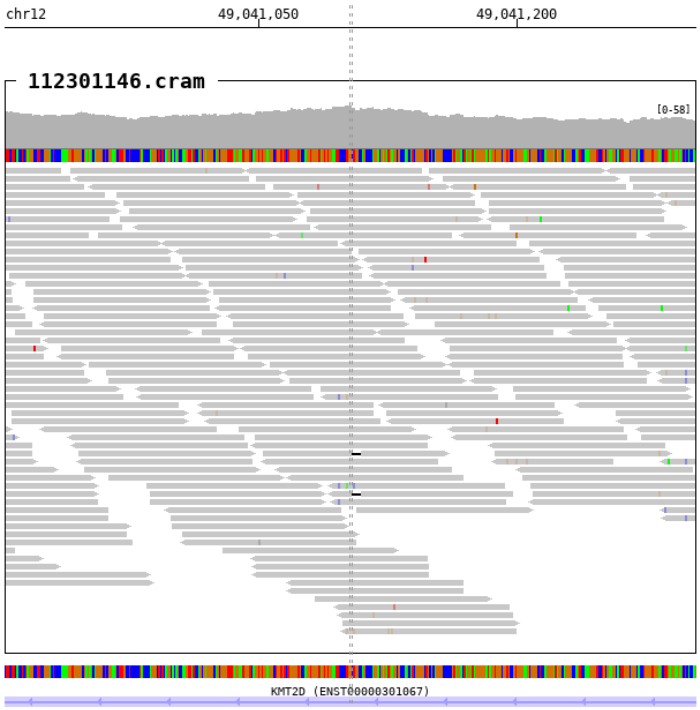
20.5. chr12_49040152_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101605153	chr12_49040152_G/A	31	5	*KMT2D*	stop_gained



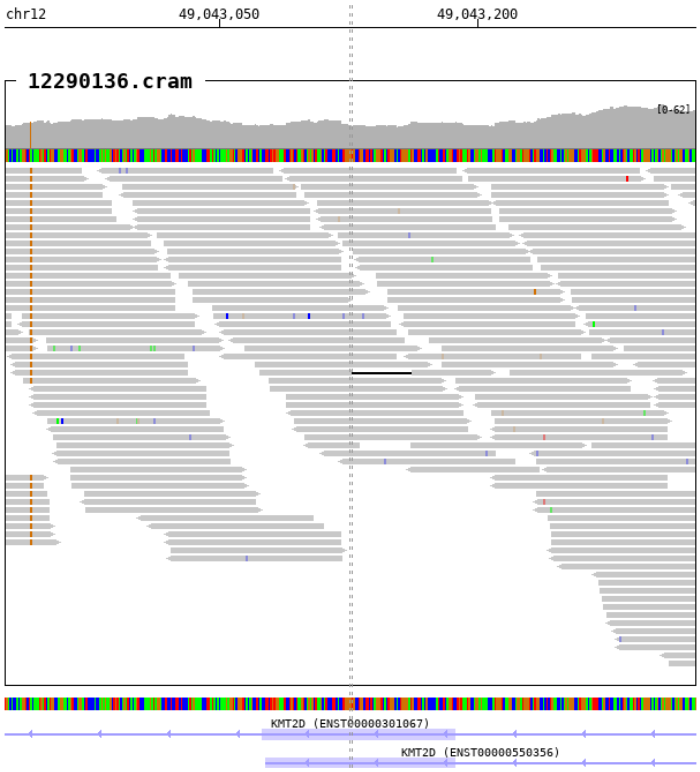
20.6. chr12_49041103_CTGGC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301146	chr12_49041103_CTGGC/-	54	2	*KMT2D*	frameshift_variant



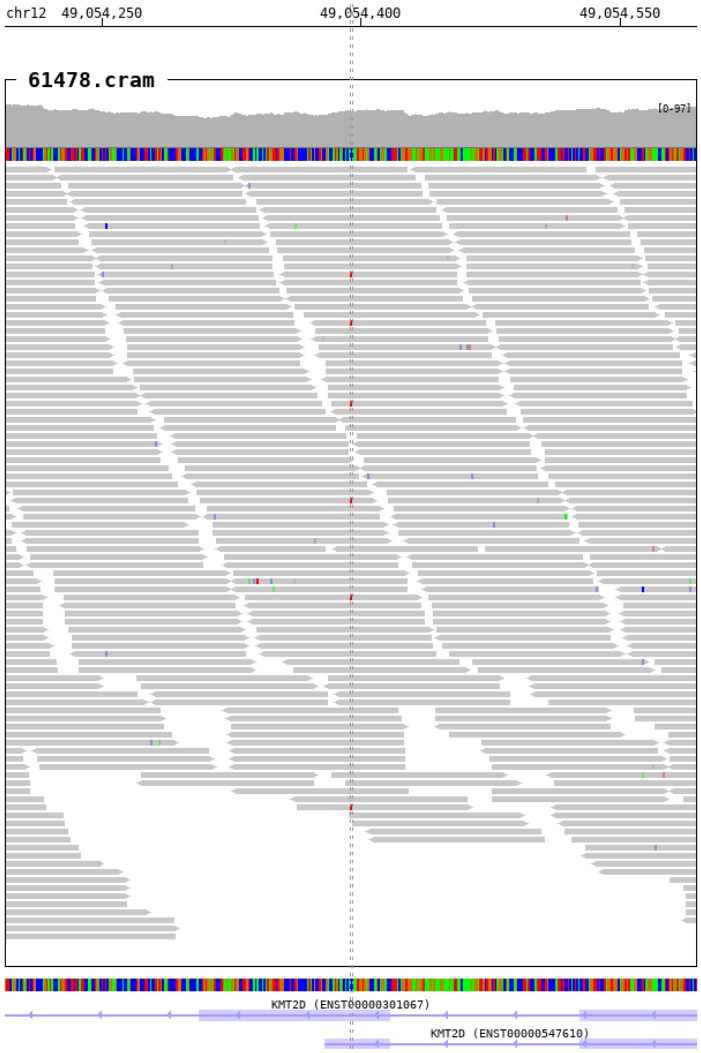
20.7. chr12_49043126_TGCCTGGCTTCTCAGGGTCACTGGGCACTGGGGA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12290136	chr12_49043126_TGCCTGGCTTCT CAGGGTCACTGGGCACTGGGGA/-	36	3	*KMT2D*	frameshift_variant



20.8. chr12_49054394_C/T

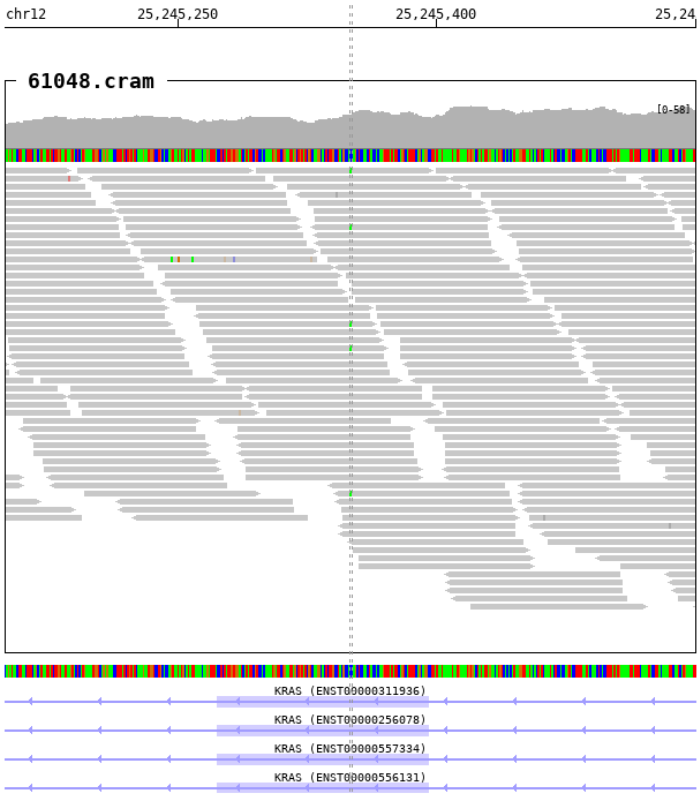
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
61478	chr12_49054394_C/T	68	6	*KMT2D*	stop_gained



21. *KRAS*

21.1. chr12_25245350_C/A

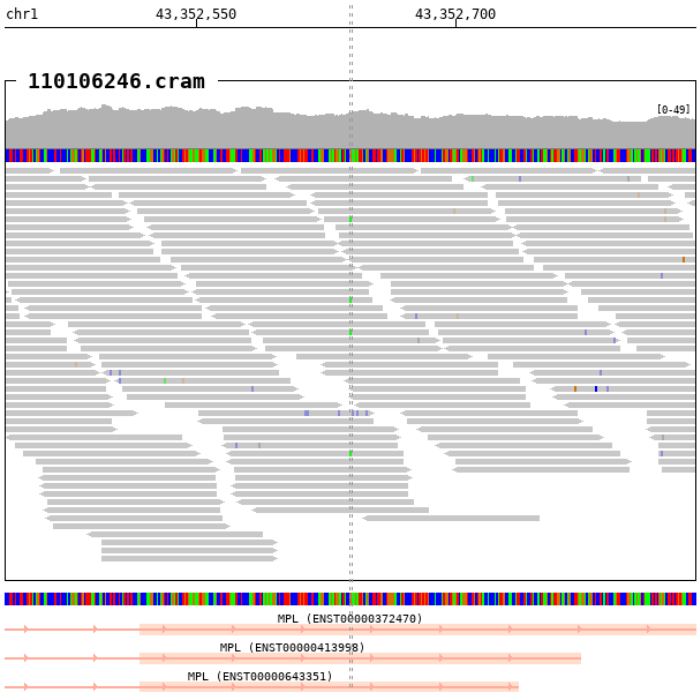
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
61048	chr12_25245350_C/A	38	5	*KRAS*	missense_variant



22. *MPL*

22.1. chr1_43352639_G/A

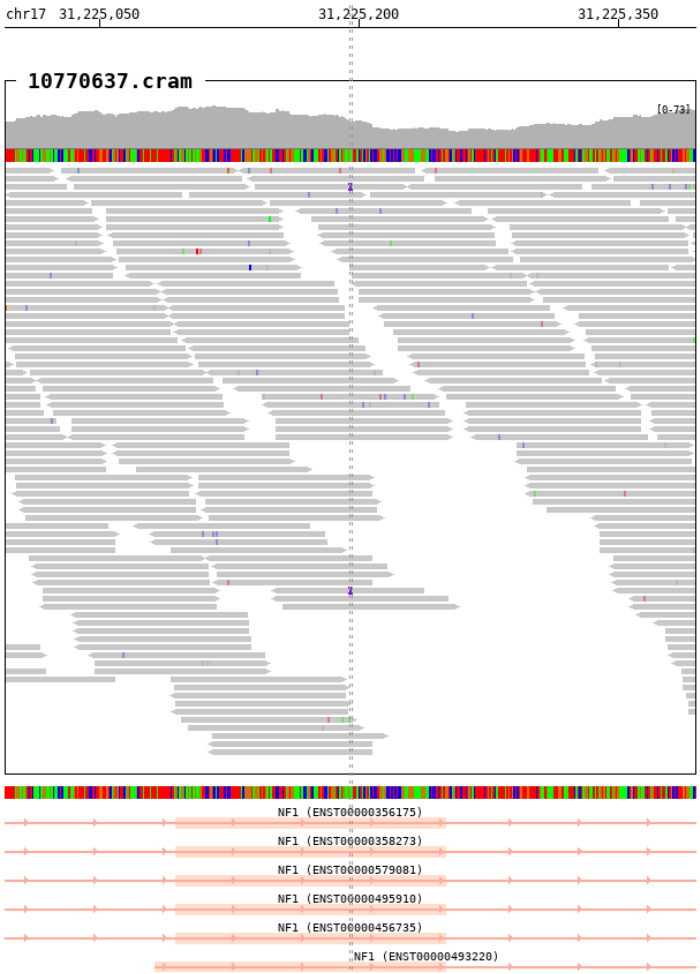
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110106246	chr1_43352639_G/A	34	4	*MPL*	missense_variant



23. *NF1*

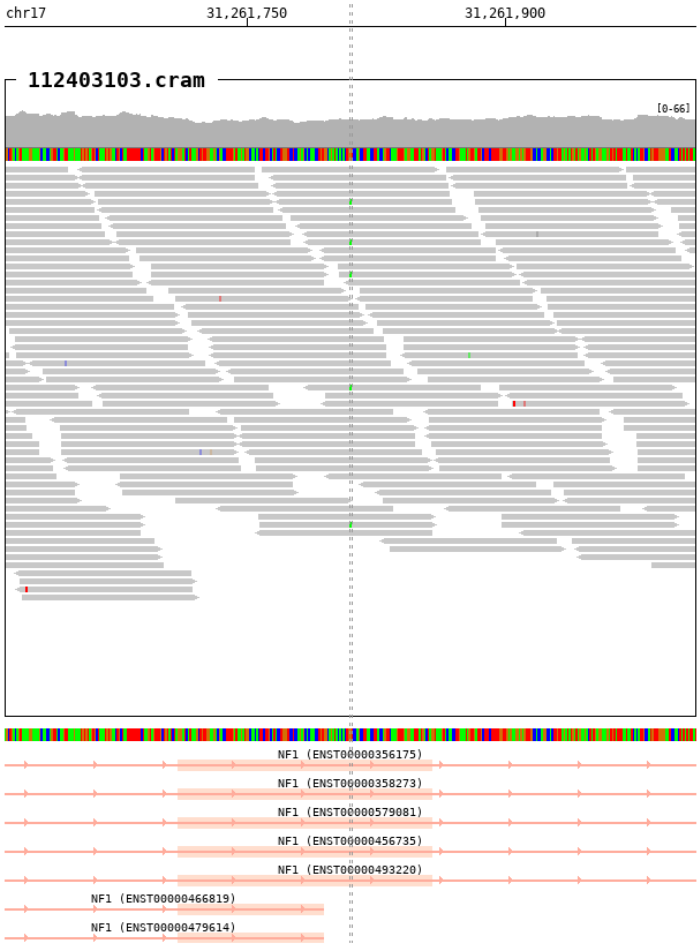
23.1. chr17_31225195_-/AATTACTACGTACA

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10770637	chr17_31225195_-/AATTACTACGTACA	26	7	*NF1*	frameshift_variant



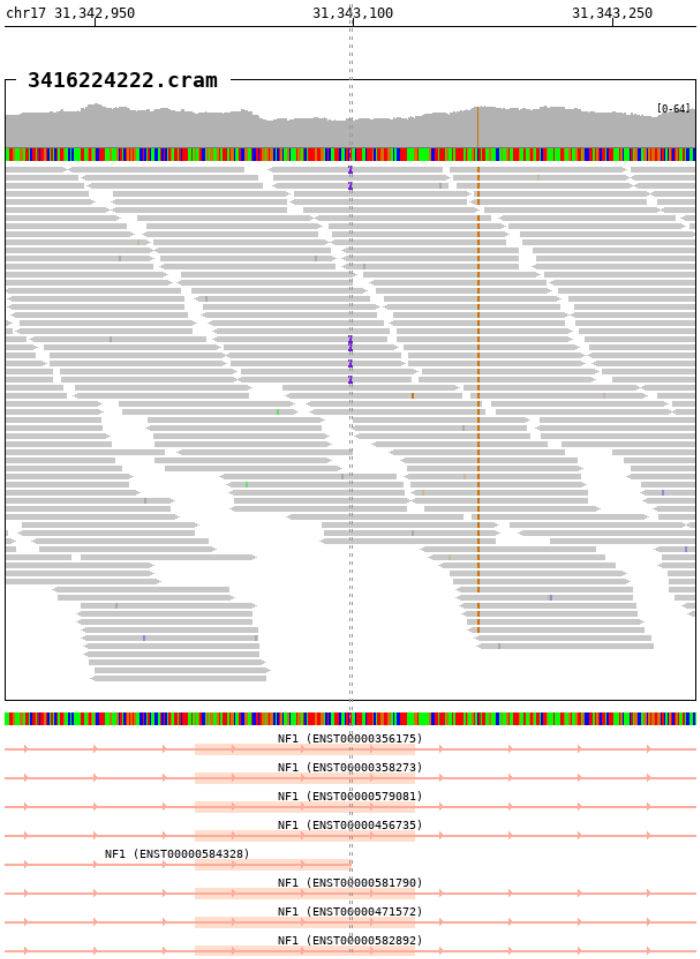
23.2. chr17_31261810_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112403103	chr17_31261810_G/A	35	4	*NF1*	stop_gained



23.3. chr17_31343098_-/T

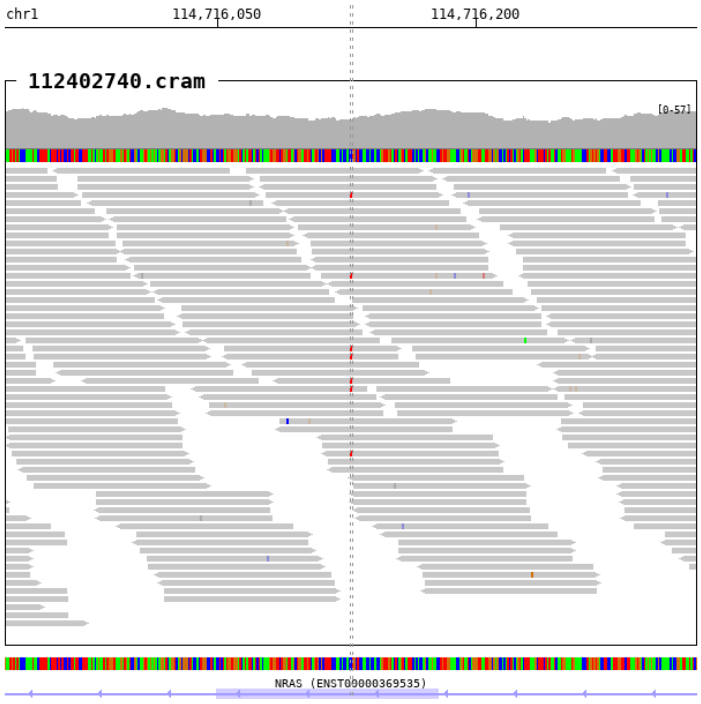
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
3416224222	chr17_31343098_-/T	32	6	*NF1*	frameshift_variant



24. *NRAS*

24.1. chr1_114716127_C/T

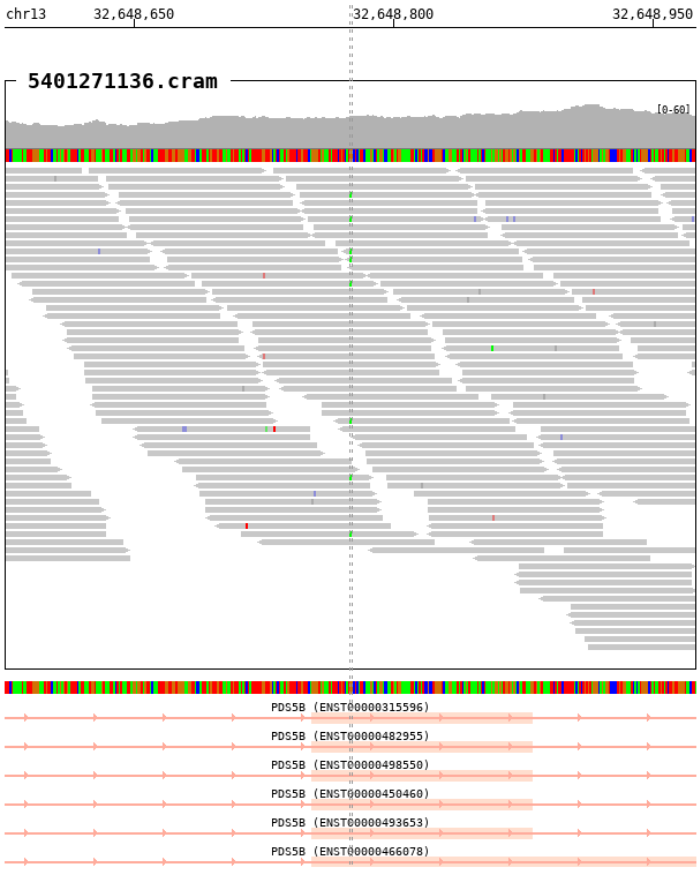
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112402740	chr1_114716127_C/T	30	7	*NRAS*	missense_variant



25. *PDS5B*

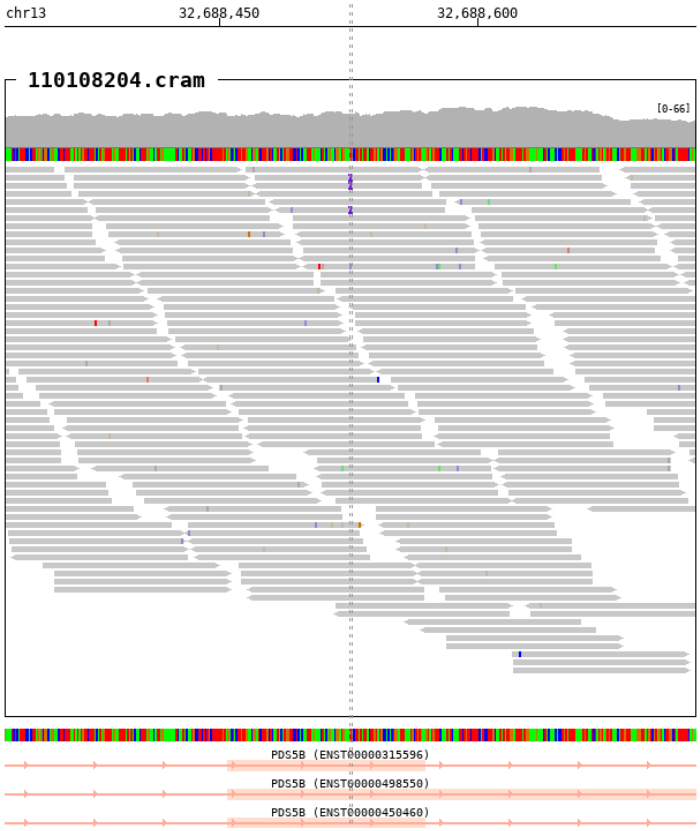
25.1. chr13_32648775_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
5401271136	chr13_32648775_G/A	35	8	*PDS5B*	start_lost



25.2. chr13_32688526_-/TGCT

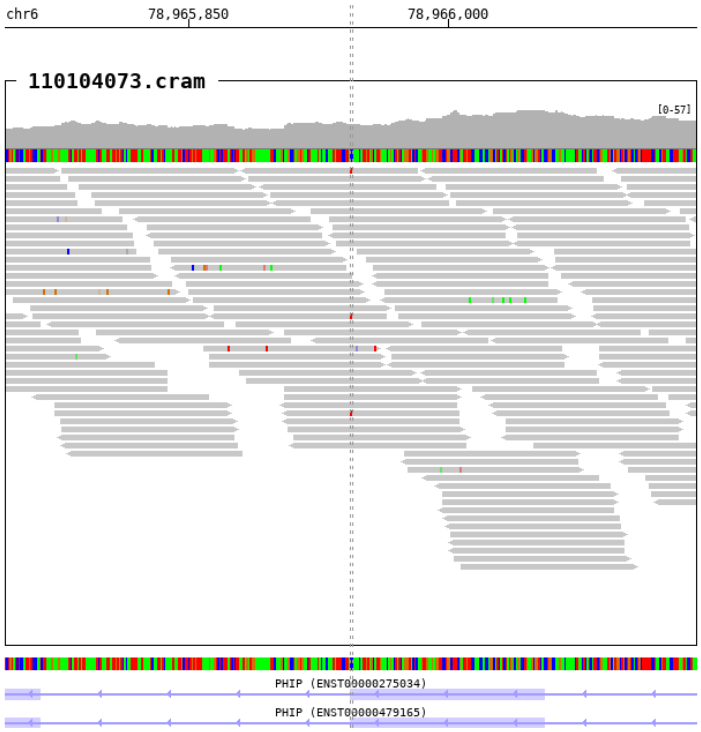
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110108204	chr13_32688526_-/TGCT	41	4	*PDS5B*	frameshift_variant



26. *PHIP*

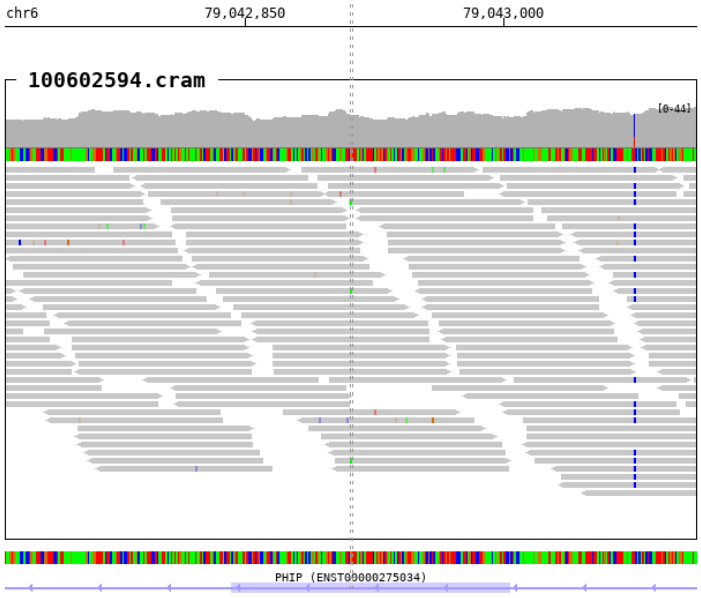
26.1. chr6_78965944_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110104073	chr6_78965944_C/T	27	3	*PHIP*	splice_donor_variant



26.2. chr6_79042911_G/A

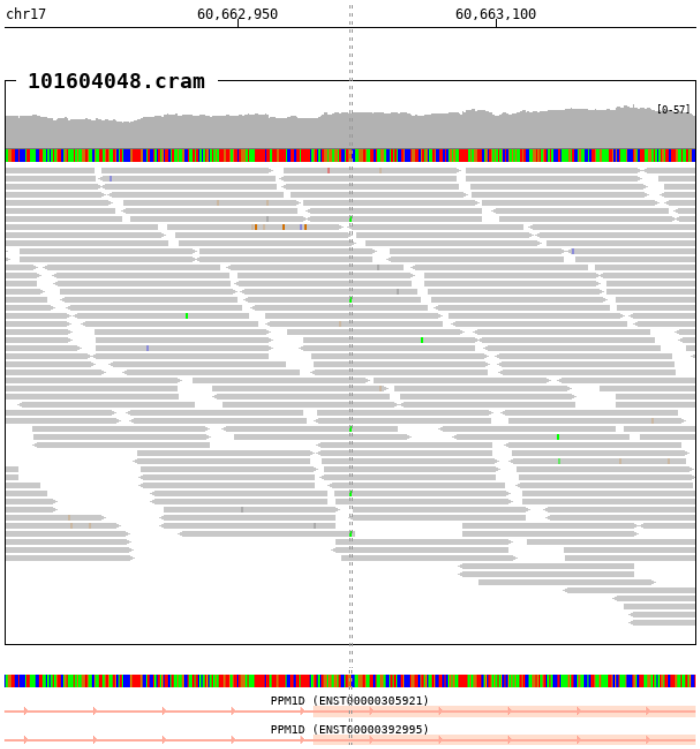
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100602594	chr6_79042911_G/A	25	3	*PHIP*	stop_gained



27. *PPM1D*

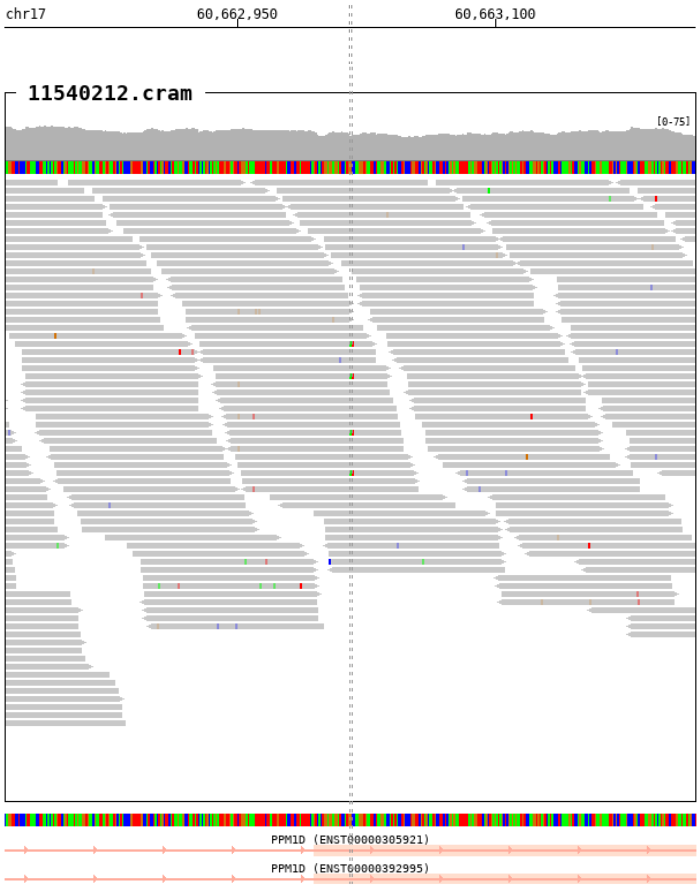
27.1. chr17_60663015_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101604048	chr17_60663015_G/A	39	5	*PPM1D*	stop_gained



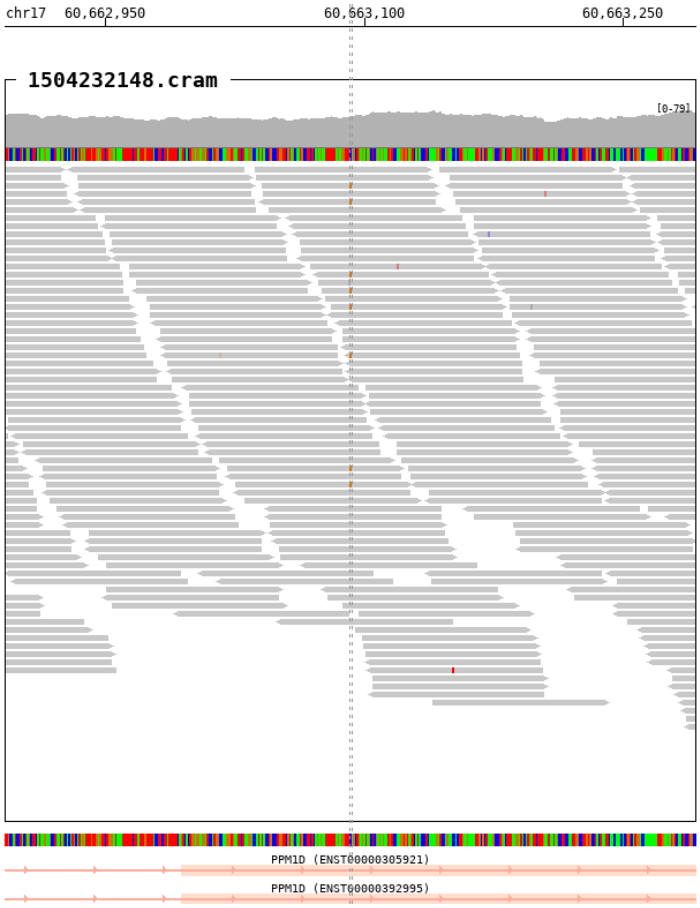
27.2. chr17_60663015_GC/AT

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11540212	chr17_60663015_GC/AT	37	6	*PPM1D*	stop_gained



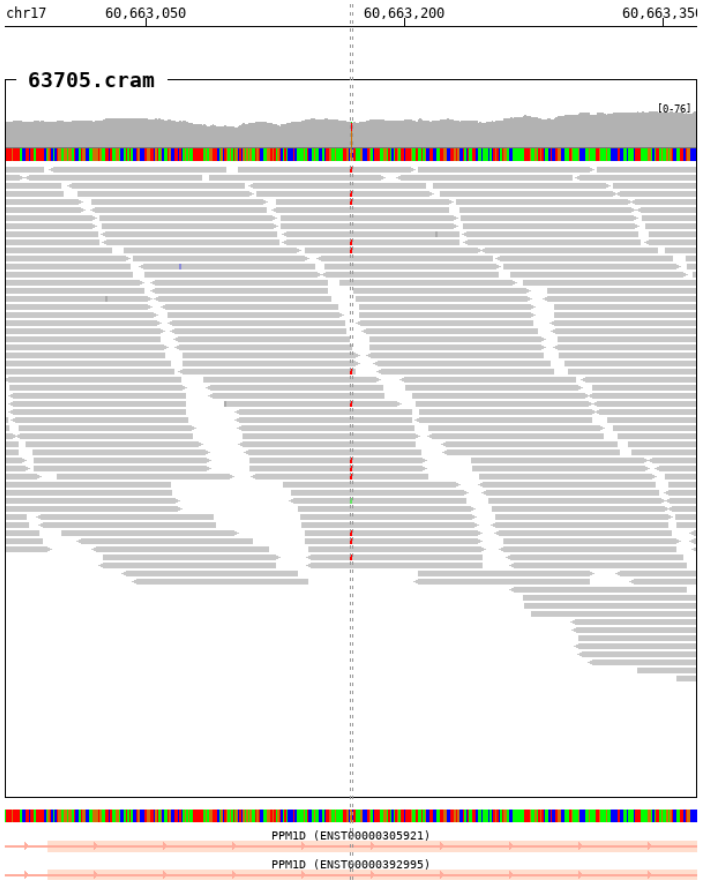
27.3. chr17_60663092_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
1504232148	chr17_60663092_C/G	47	8	*PPM1D*	stop_gained



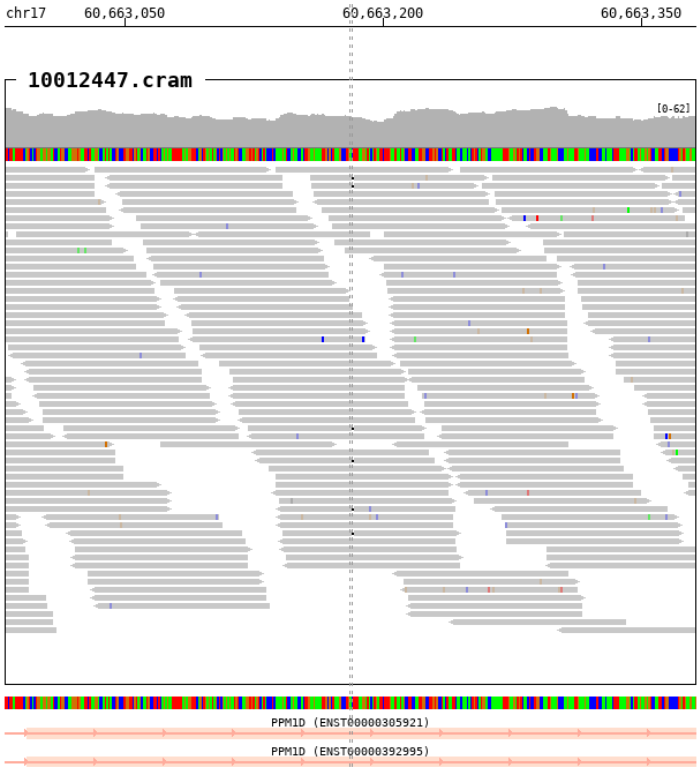
27.4. chr17_60663169_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
63705	chr17_60663169_G/T	29	12	*PPM1D*	missense_variant



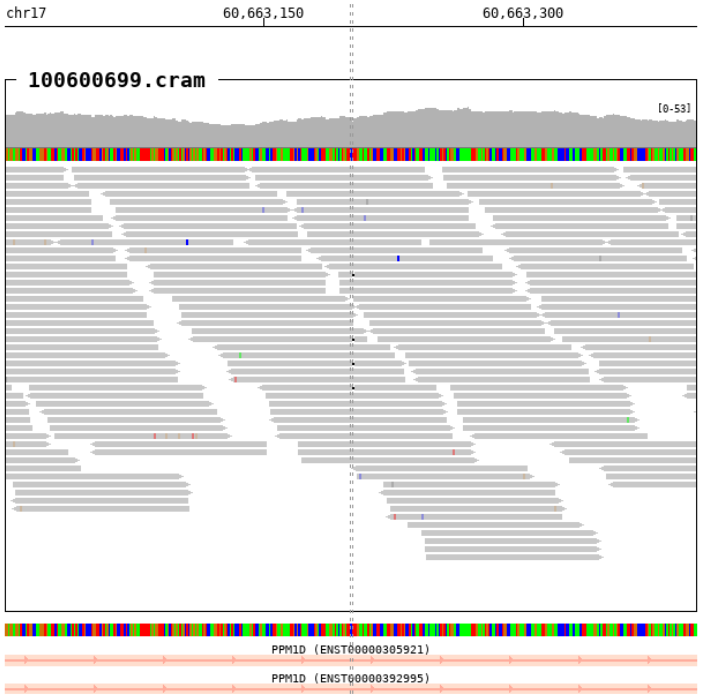
27.5. chr17_60663181_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10012447	chr17_60663181_C/-	37	5	*PPM1D*	frameshift_variant



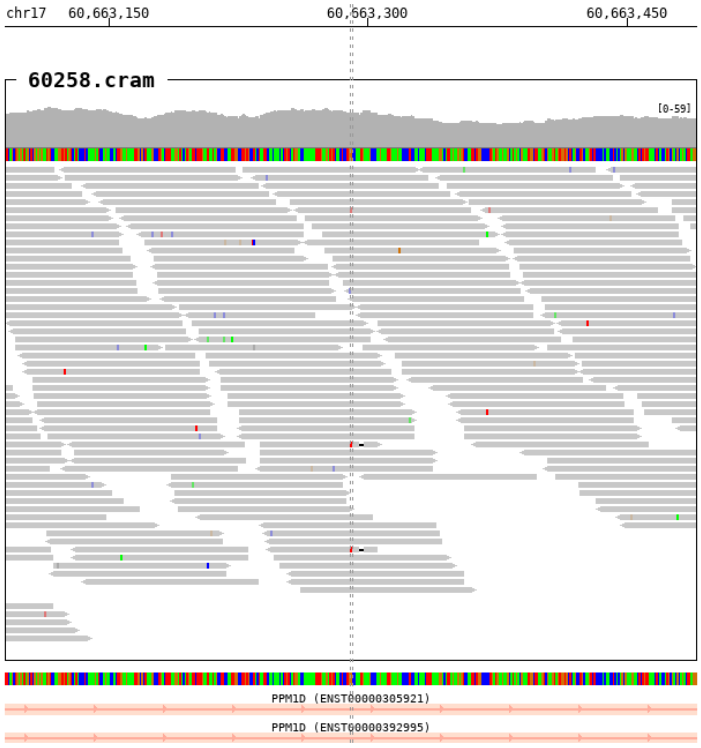
27.6. chr17_60663200_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100600699	chr17_60663200_T/-	29	4	*PPM1D*	frameshift_variant



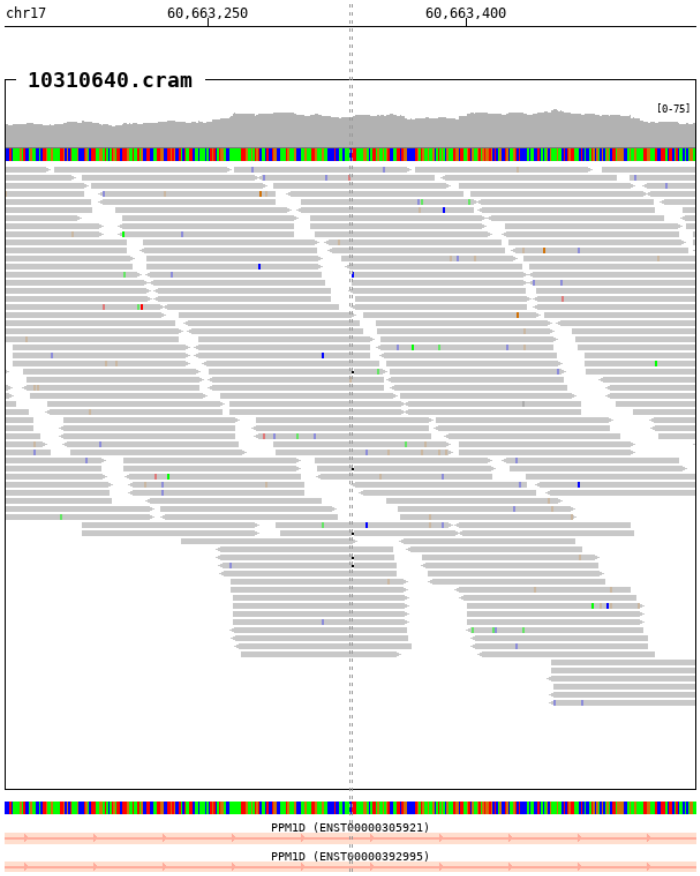
27.7. chr17_60663290_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
60258	chr17_60663290_G/T	43	2	*PPM1D*	missense_variant



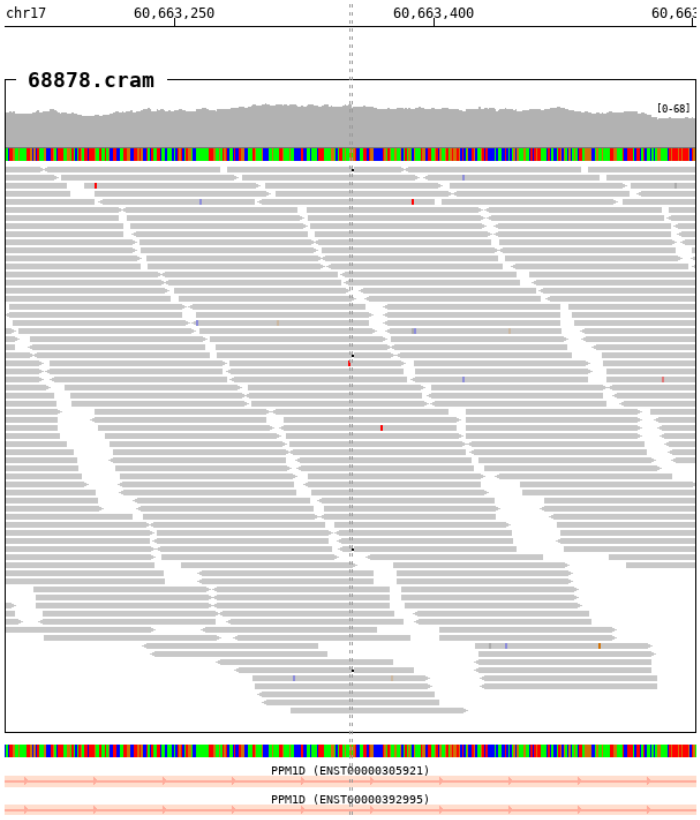
27.8. chr17_60663333_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10310640	chr17_60663333_T/-	43	6	*PPM1D*	frameshift_variant



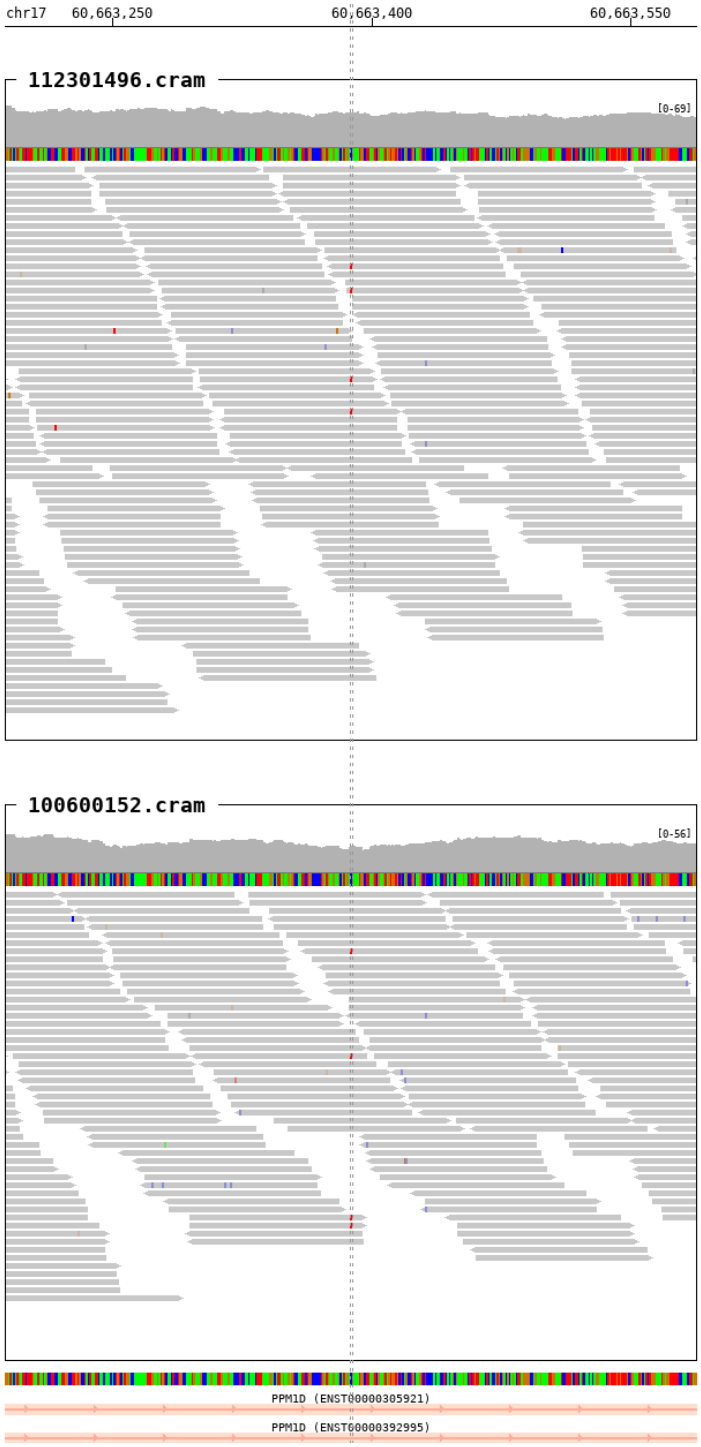
27.9. chr17_60663352_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
68878	chr17_60663352_A/-	59	4	*PPM1D*	frameshift_variant



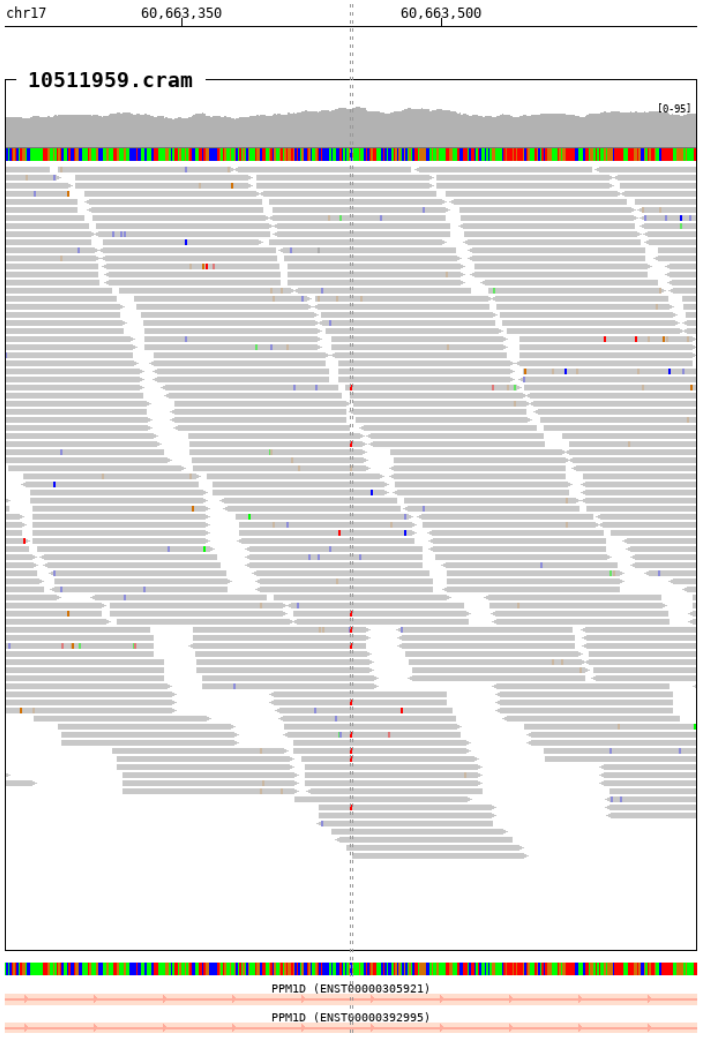
27.10. chr17_60663388_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100600152	chr17_60663388_C/T	29	4	*PPM1D*	stop_gained
112301496	chr17_60663388_C/T	48	4	*PPM1D*	stop_gained



27.11. chr17_60663448_C/T

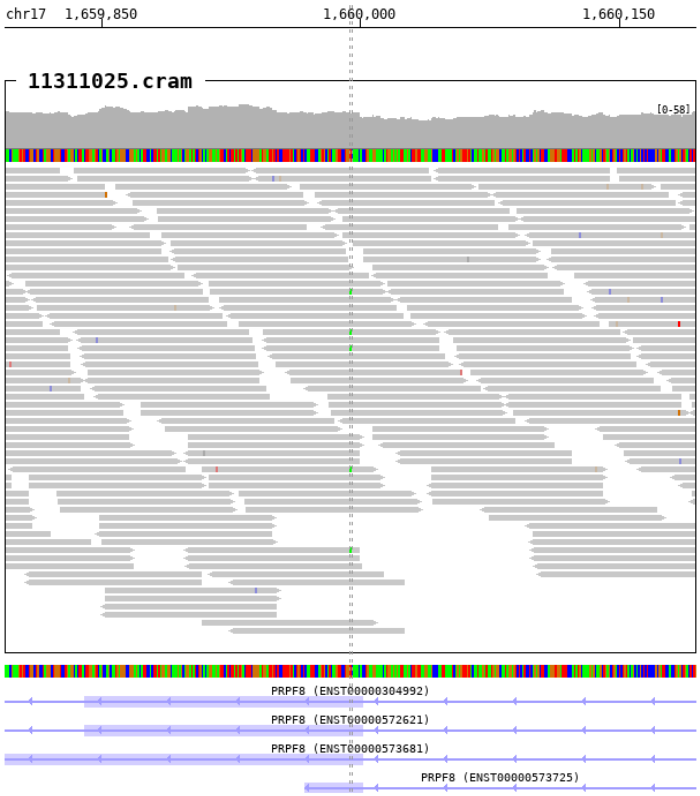
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10511959	chr17_60663448_C/T	64	7	*PPM1D*	stop_gained



28. *PRPF8*

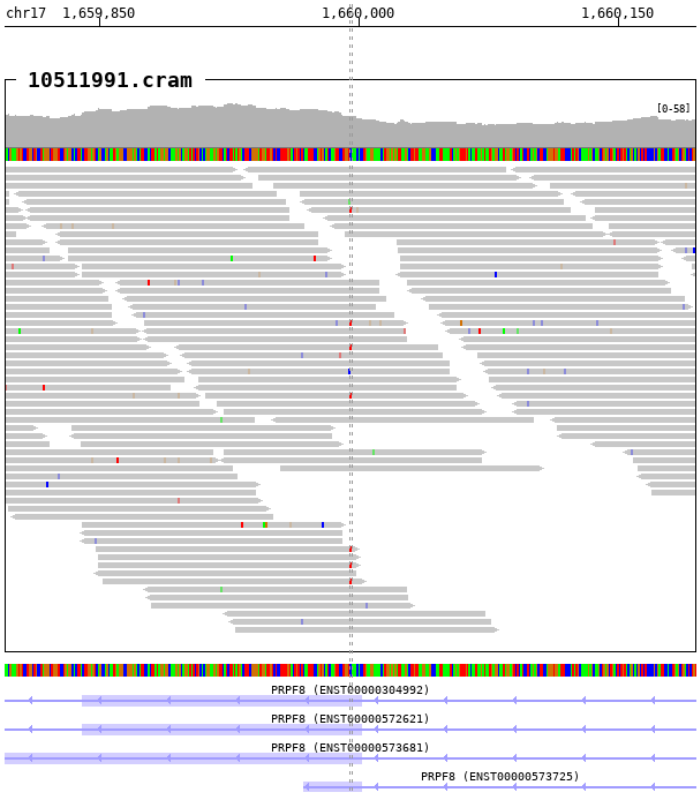
28.1. chr17_1659994_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11311025	chr17_1659994_T/A	37	5	*PRPF8*	missense_variant



28.2. chr17_1659995_C/T

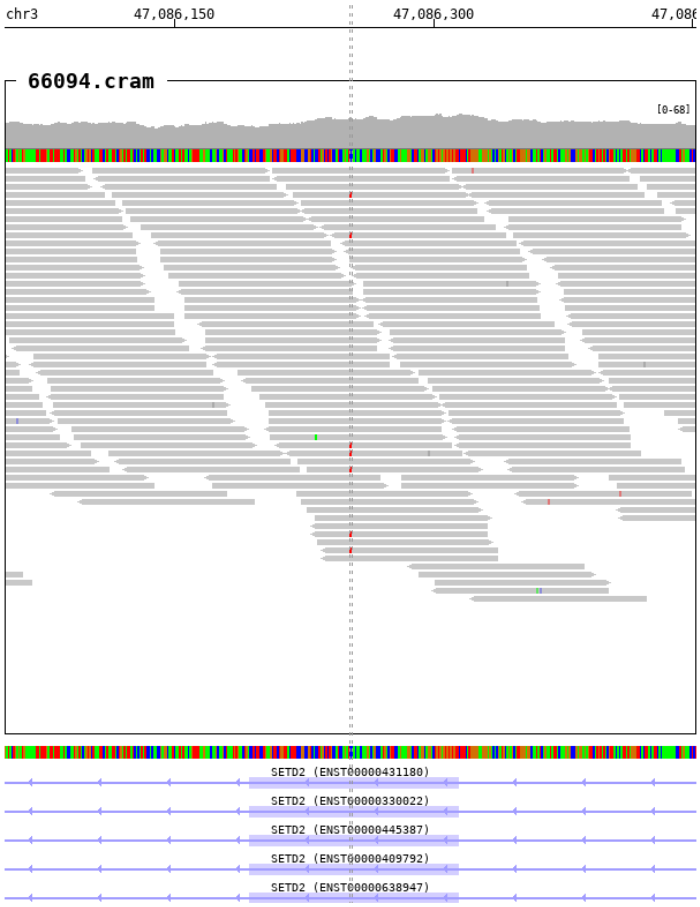
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10511991	chr17_1659995_C/T	33	6	*PRPF8*	missense_variant



29. *SETD2*

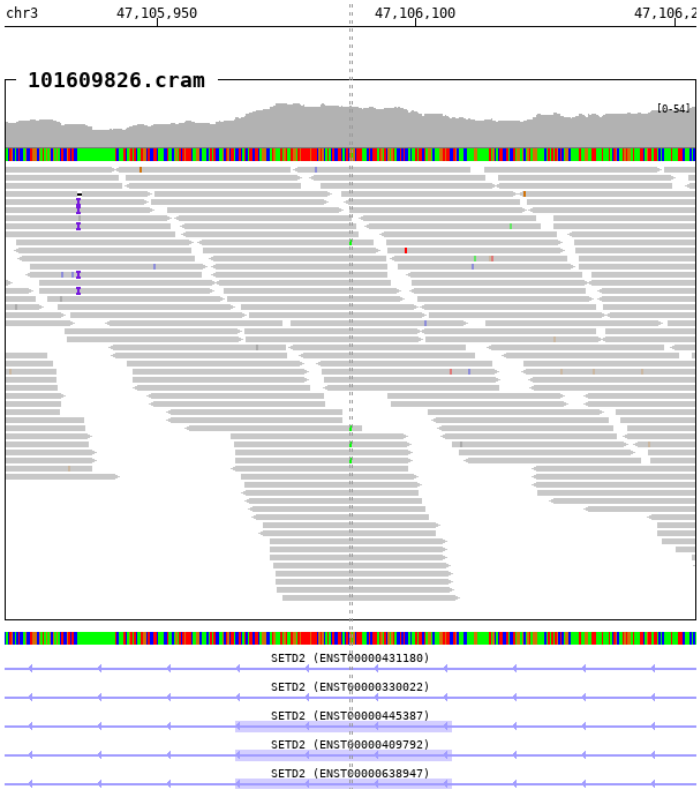
29.1. chr3_47086252_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
66094	chr3_47086252_C/T	40	7	*SETD2*	stop_gained



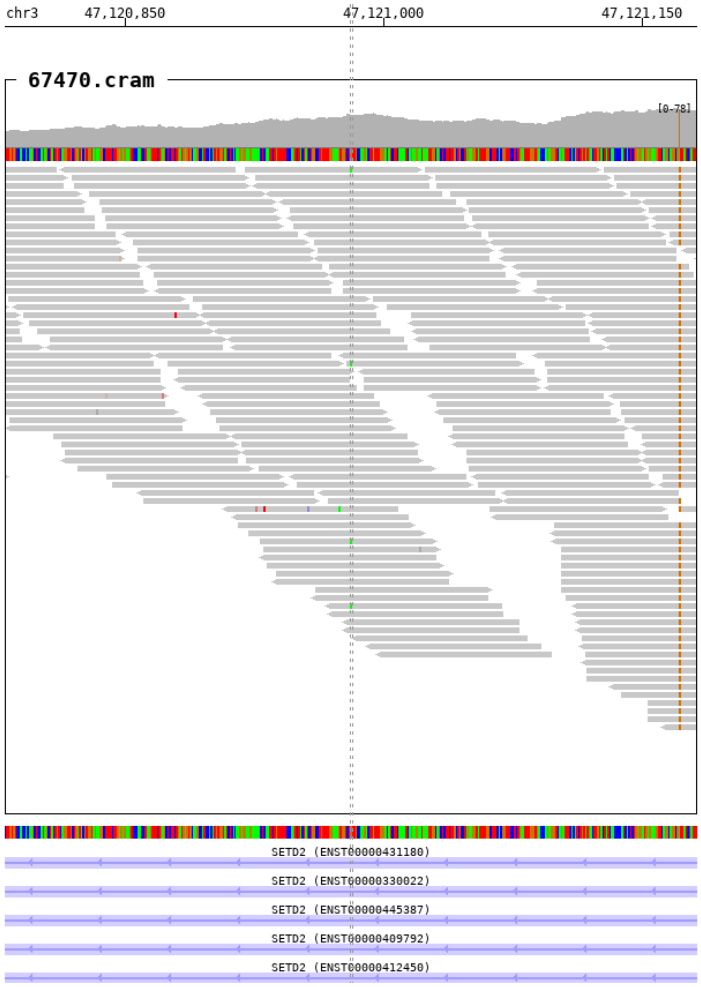
29.2. chr3_47106062_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101609826	chr3_47106062_G/A	45	4	*SETD2*	stop_gained



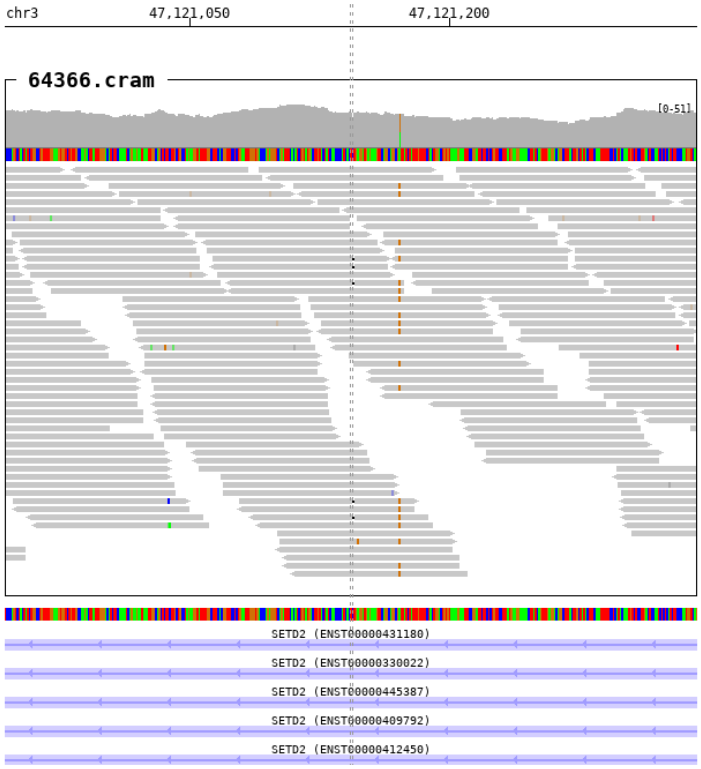
29.3. chr3_47120981_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
67470	chr3_47120981_G/A	51	4	*SETD2*	stop_gained



29.4. chr3_47121143_C/-

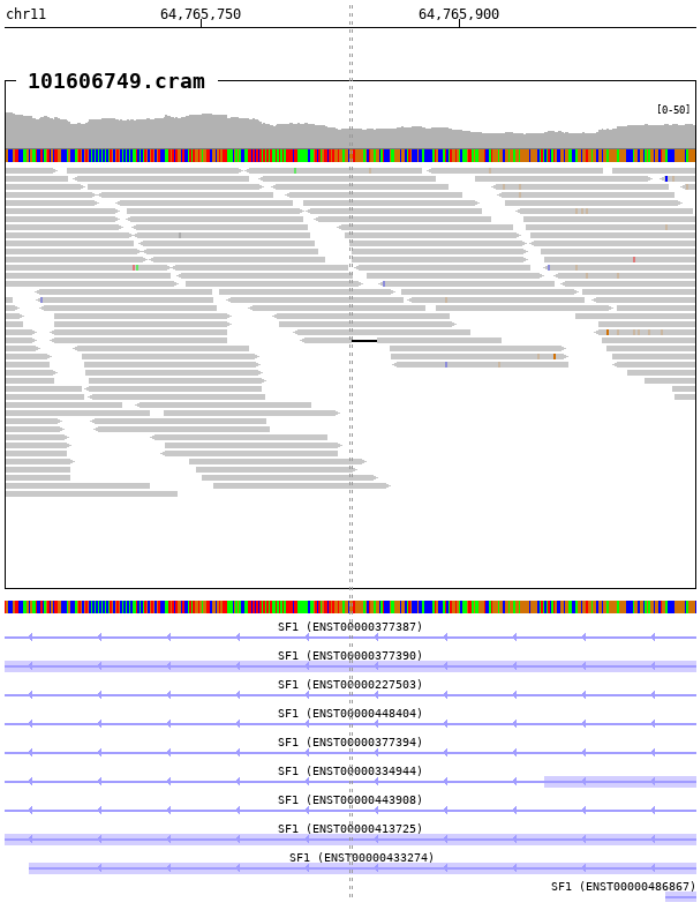
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
64366	chr3_47121143_C/-	33	5	*SETD2*	frameshift_variant



30. *SF1*

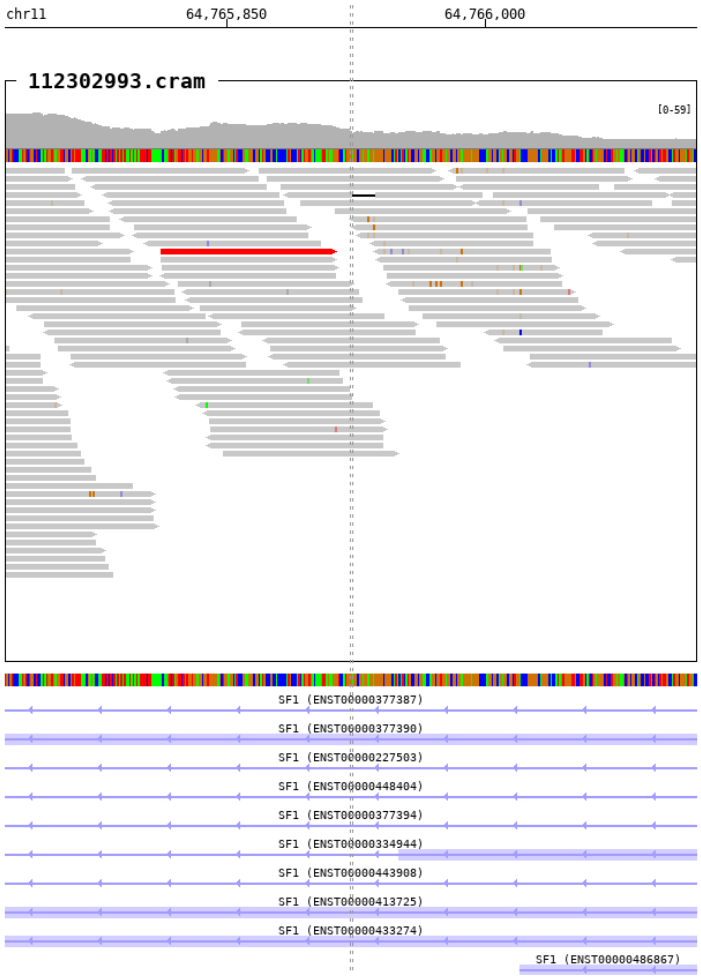
30.1. chr11_64765837_GTGGGGGAGCTGGA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101606749	chr11_64765837_GTGGGGGAGCTGGA/-	24	2	*SF1*	frameshift_variant



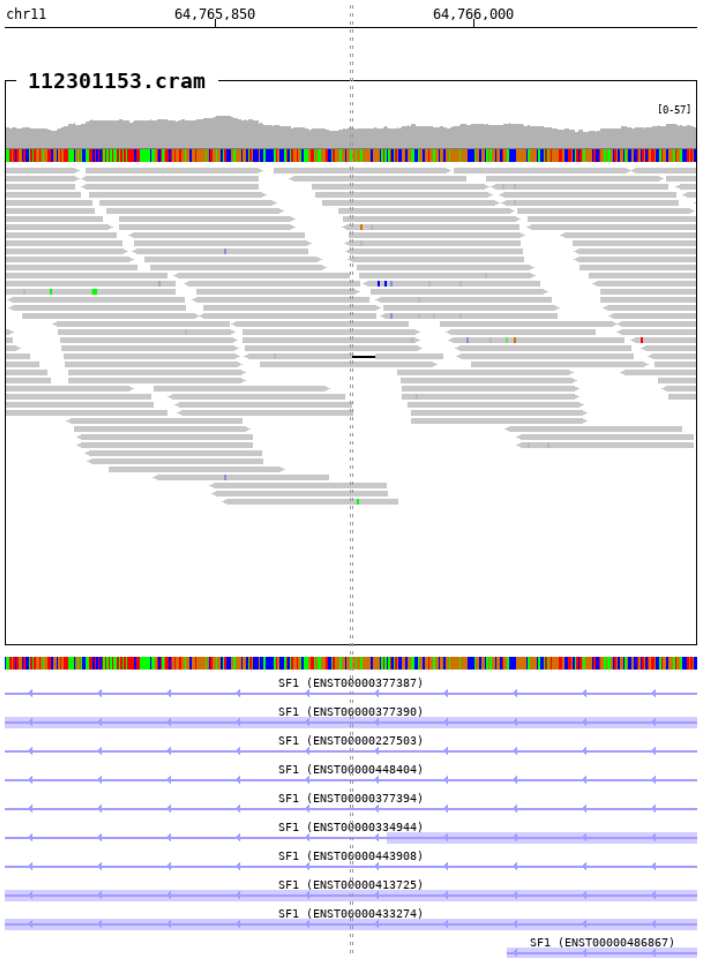
30.2. chr11_64765922_AGGCGGAGGAGGA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112302993	chr11_64765922_AGGCGGAGGAGGA/-	24	2	*SF1*	frameshift_variant



30.3. chr11_64765929_GGAGGAGGGGGCG/-

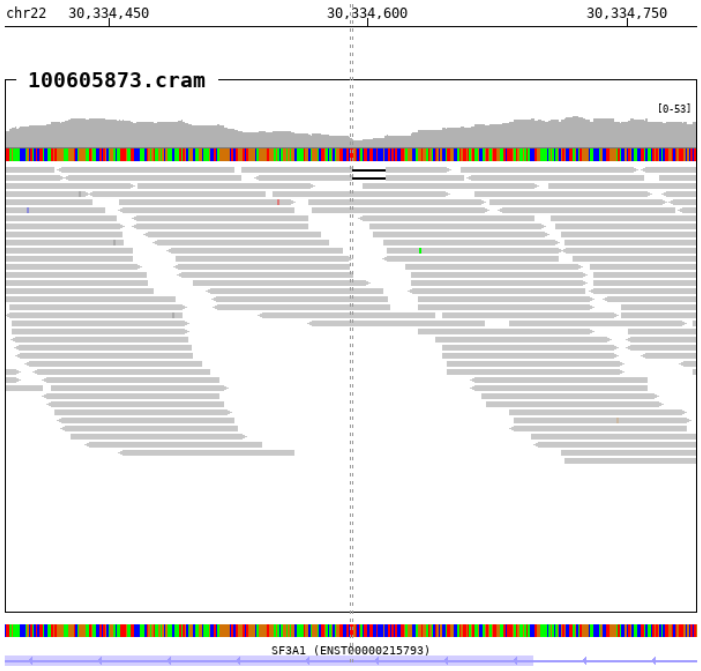
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301153	chr11_64765929_GGAGGAGGGGGCG/-	27	2	*SF1*	frameshift_variant



31. *SF3A1*

31.1. chr22_30334590_TGTCTACTTCTTCCTCCCG/-

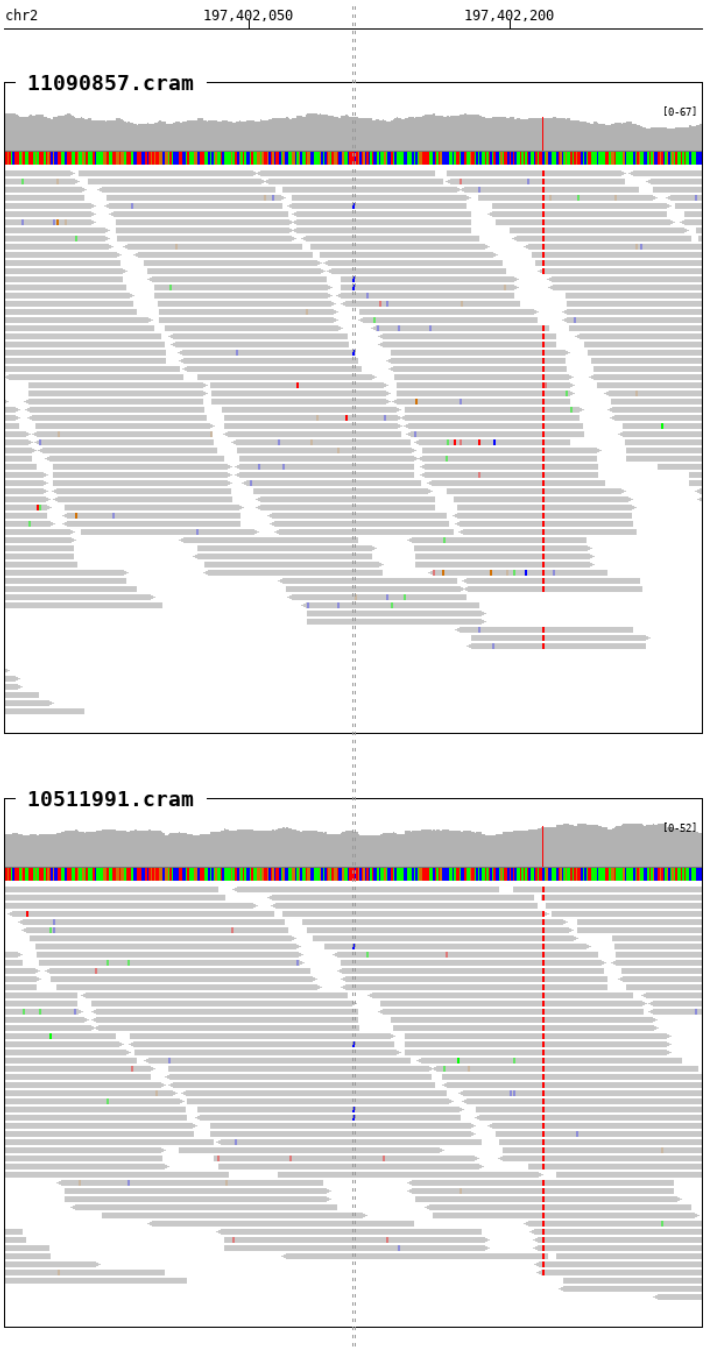
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100605873	chr22_30334590_TGTCTACTTCTTCCTCCCG/-	15	2	*SF3A1*	stop_lost

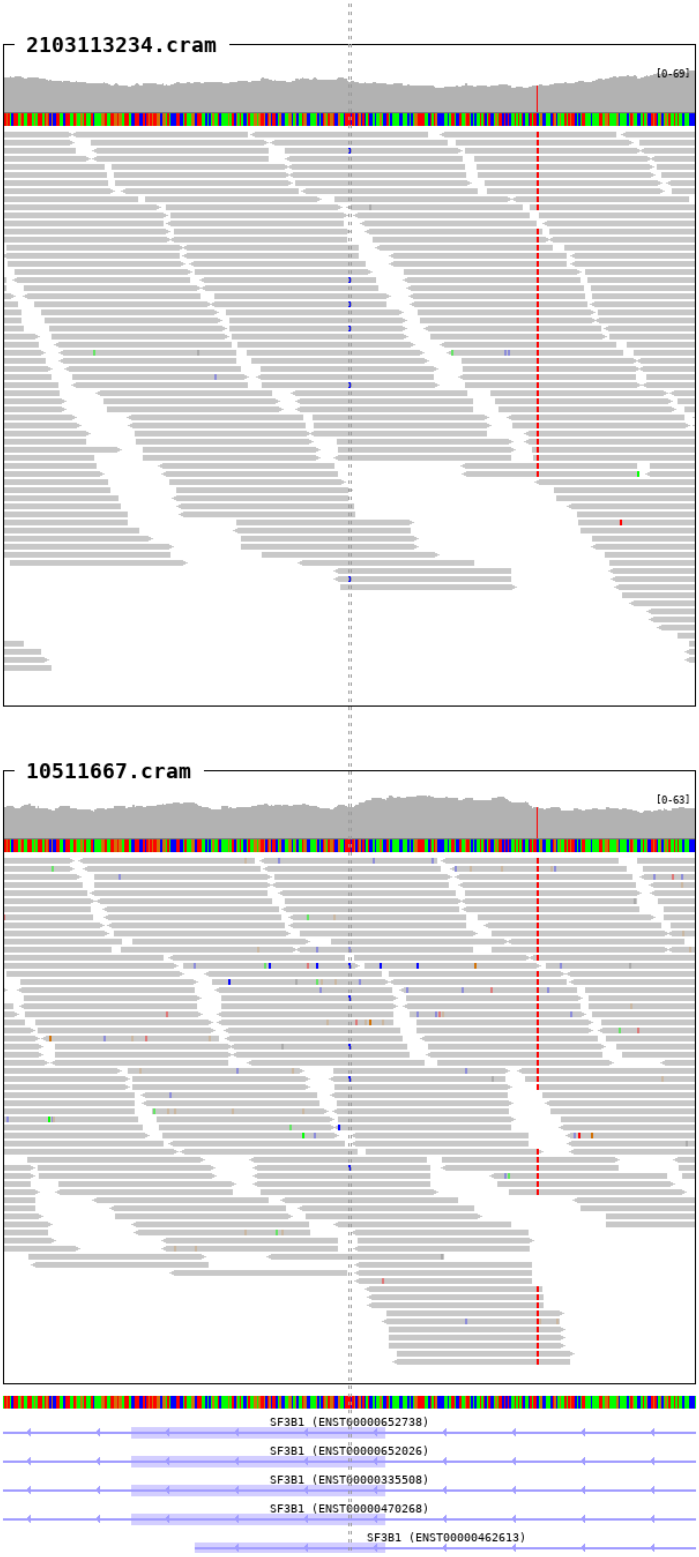


32. *SF3B1*

32.1. chr2_197402110_T/C

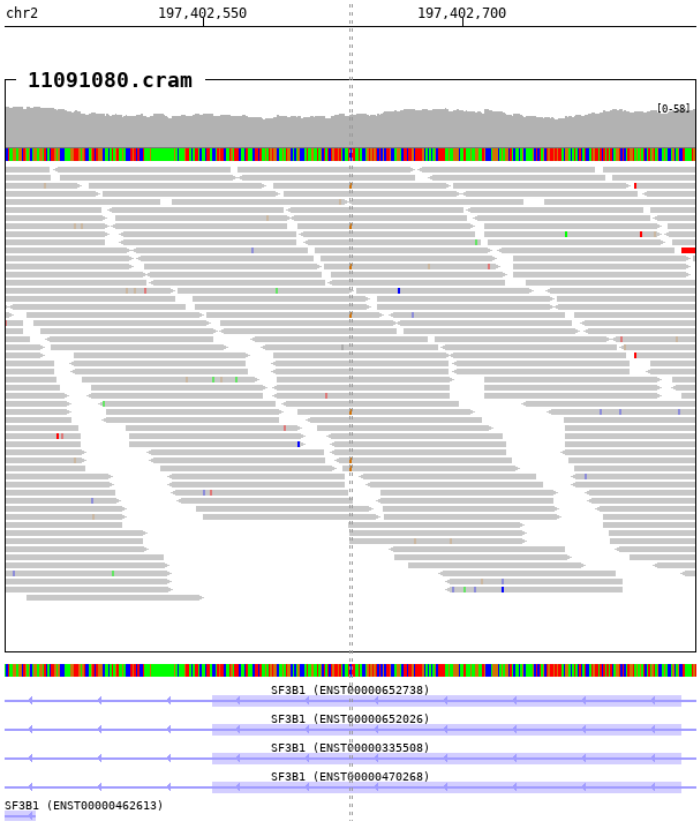
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10511667	chr2_197402110_T/C	35	5	*SF3B1*	missense_variant
10511991	chr2_197402110_T/C	36	4	*SF3B1*	missense_variant
11090857	chr2_197402110_T/C	43	4	*SF3B1*	missense_variant
2103113234	chr2_197402110_T/C	41	6	*SF3B1*	missense_variant




2103113234.cram
[0-69]
10511667.cram
[0-63]
SF3B1 (ENST00000652738)
SF3B1 (ENST00000652026)
SF3B1 (ENST00000335508)
SF3B1 (ENST00000470268)
SF3B1 (ENST00000462613)

32.2. chr2_197402635_C/G

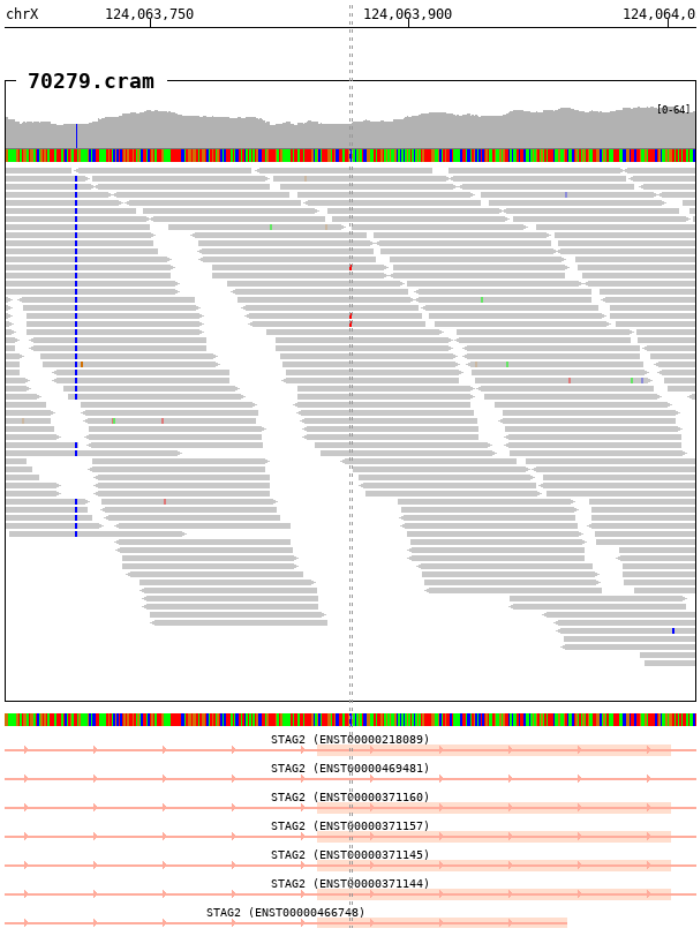
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11091080	chr2_197402635_C/G	34	6	*SF3B1*	missense_variant



33. *STAG2*

33.1. chrX_124063866_C/T

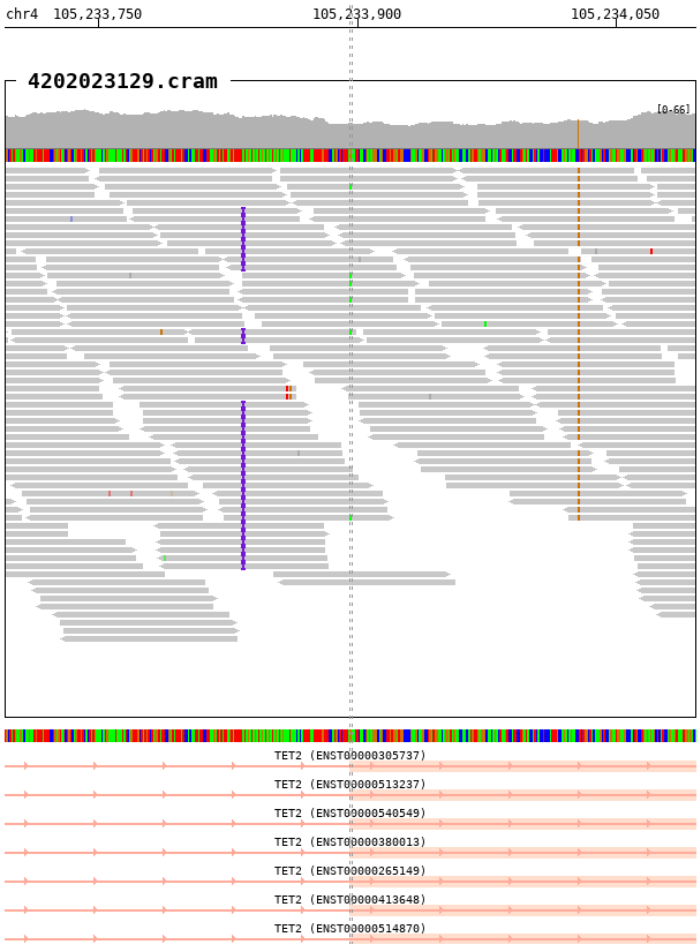
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
70279	chrX_124063866_C/T	33	3	*STAG2*	stop_gained



34. *TET2*

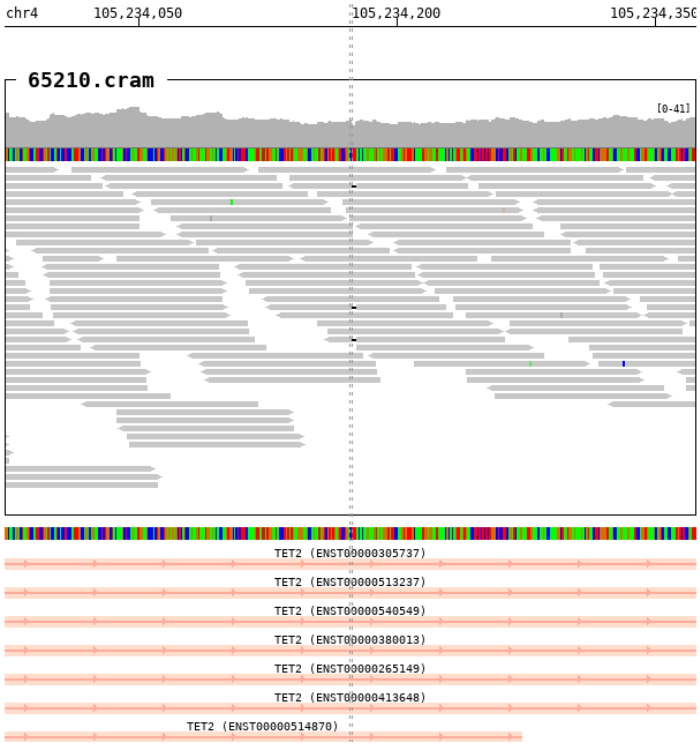
34.1. chr4_105233896_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
4202023129	chr4_105233896_G/A	32	6	*TET2*	splice_acceptor_variant



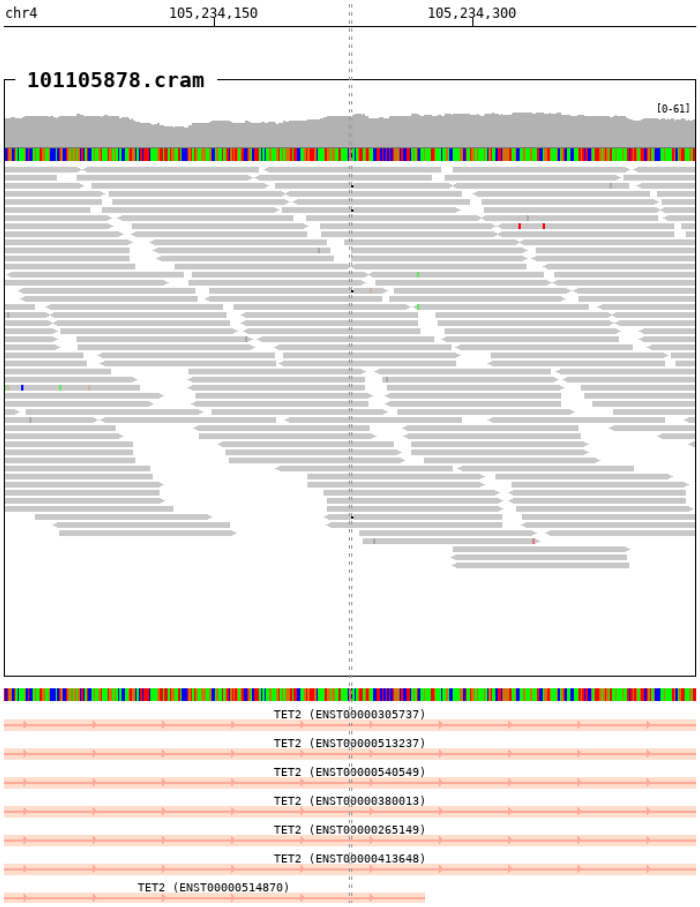
34.2. chr4_105234173_TT/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
65210	chr4_105234173_TT/-	20	3	*TET2*	frameshift_variant



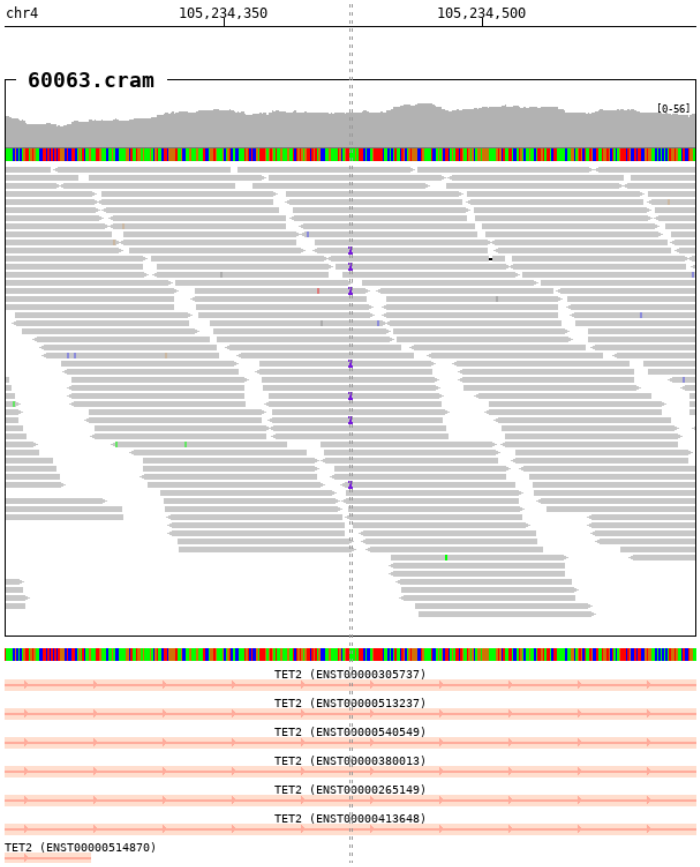
34.3. chr4_105234229_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101105878	chr4_105234229_C/-	39	4	*TET2*	frameshift_variant



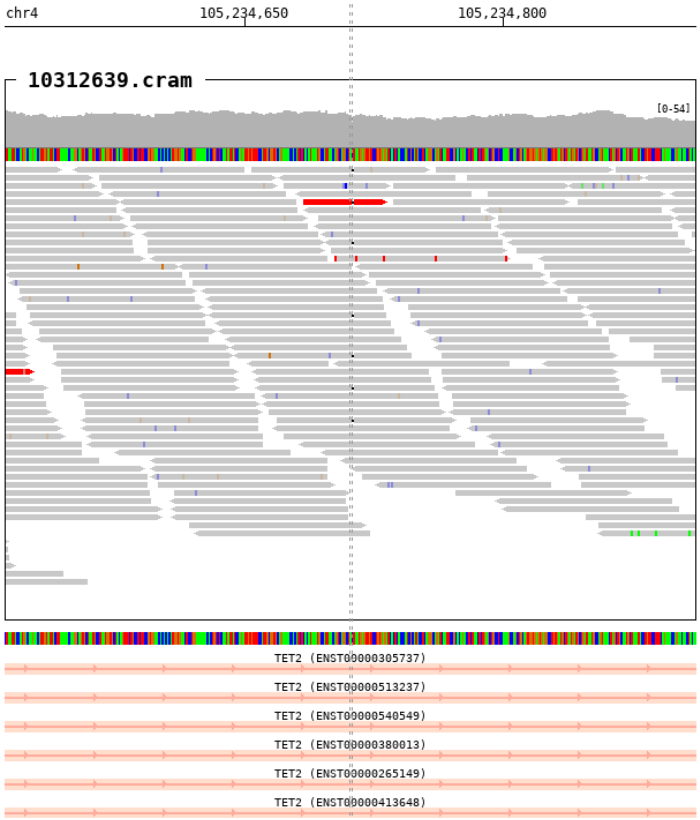
34.4. chr4_105234423_-/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
60063	chr4_105234423_-/A	35	7	*TET2*	frameshift_variant



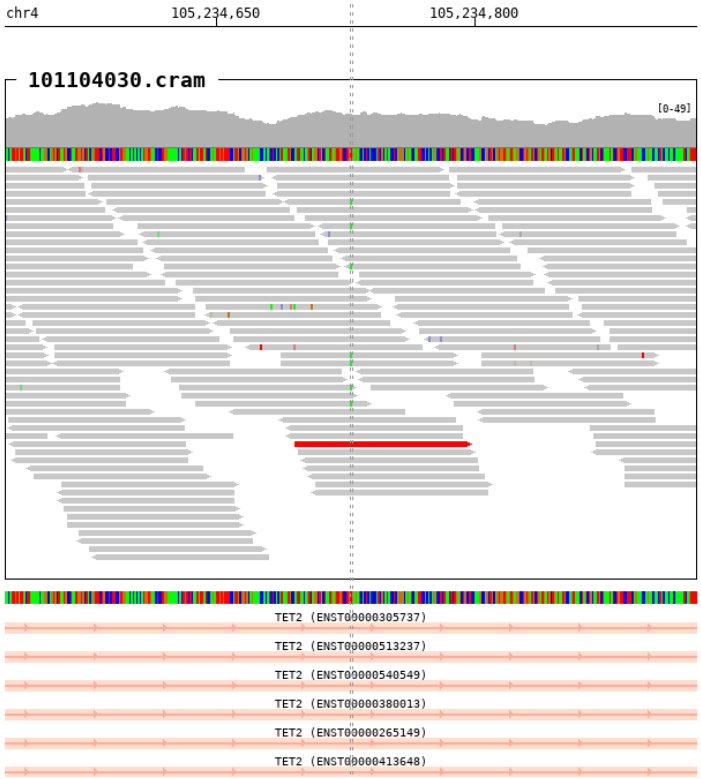
34.5. chr4_105234711_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10312639	chr4_105234711_C/-	29	8	*TET2*	frameshift_variant



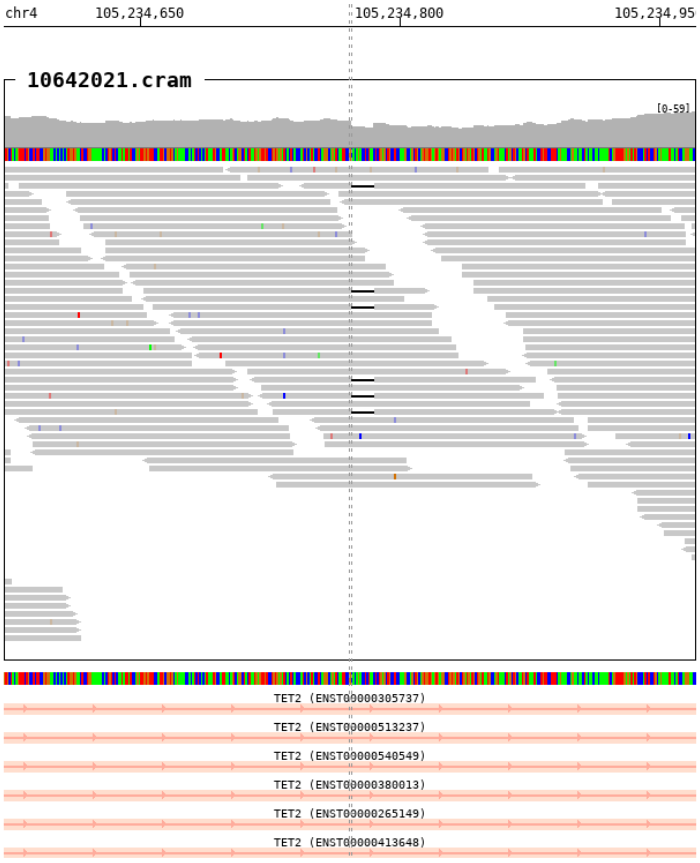
34.6. chr4_105234728_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101104030	chr4_105234728_T/A	29	6	*TET2*	stop_gained



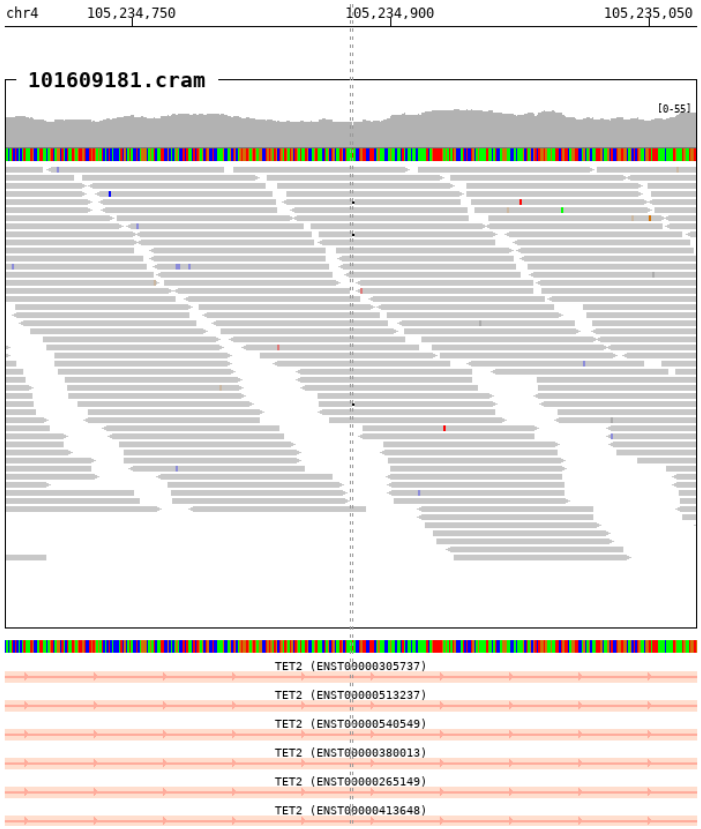
34.7. chr4_105234771_CACAGACCTCTAA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10642021	chr4_105234771_CACAGACCTCTAA/-	25	7	*TET2*	frameshift_variant



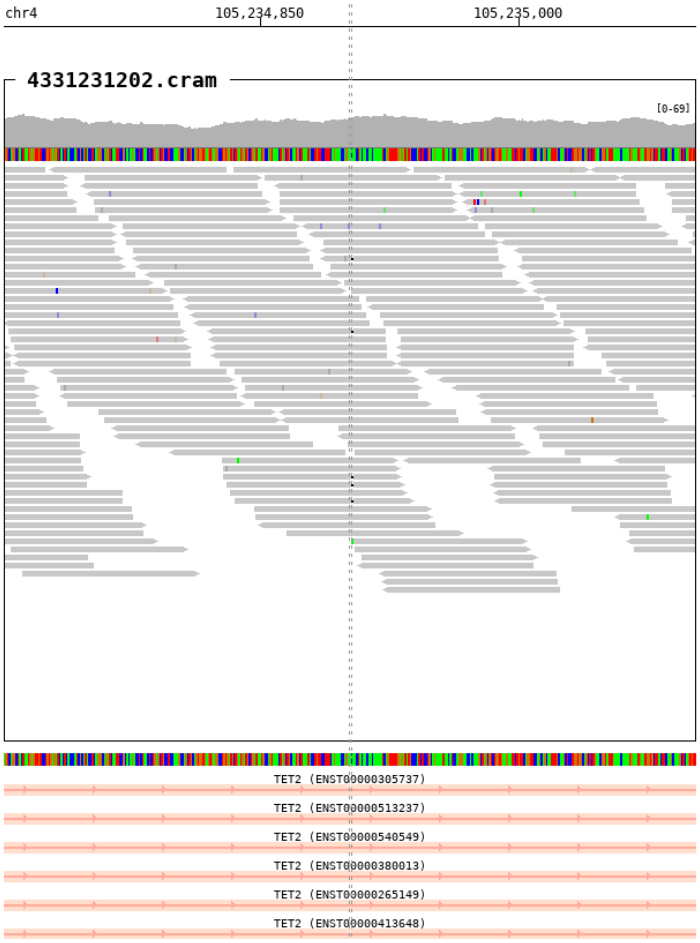
34.8. chr4_105234877_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101609181	chr4_105234877_T/-	28	3	*TET2*	frameshift_variant



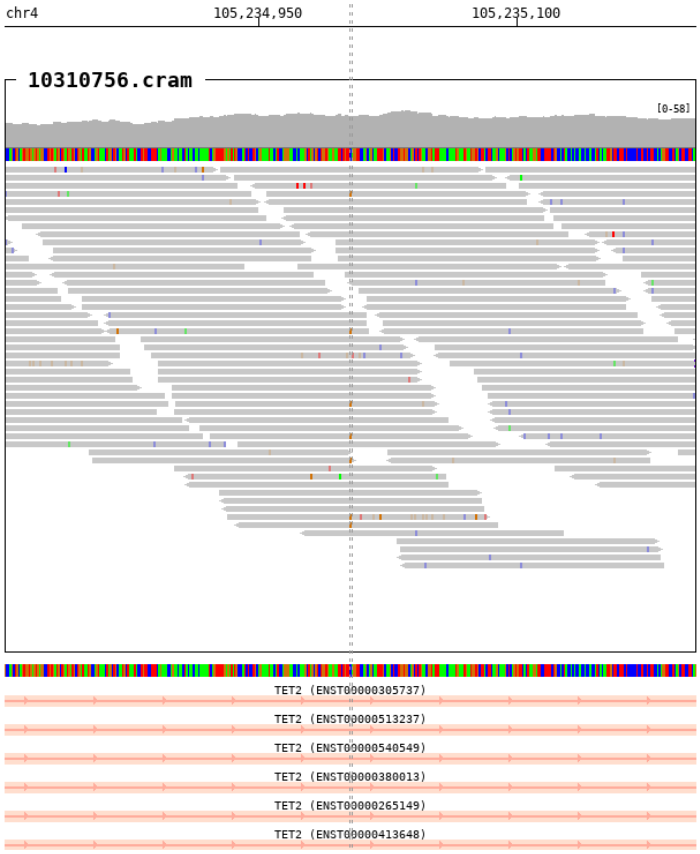
34.9. chr4_105234902_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
4331231202	chr4_105234902_C/-	40	6	*TET2*	frameshift_variant



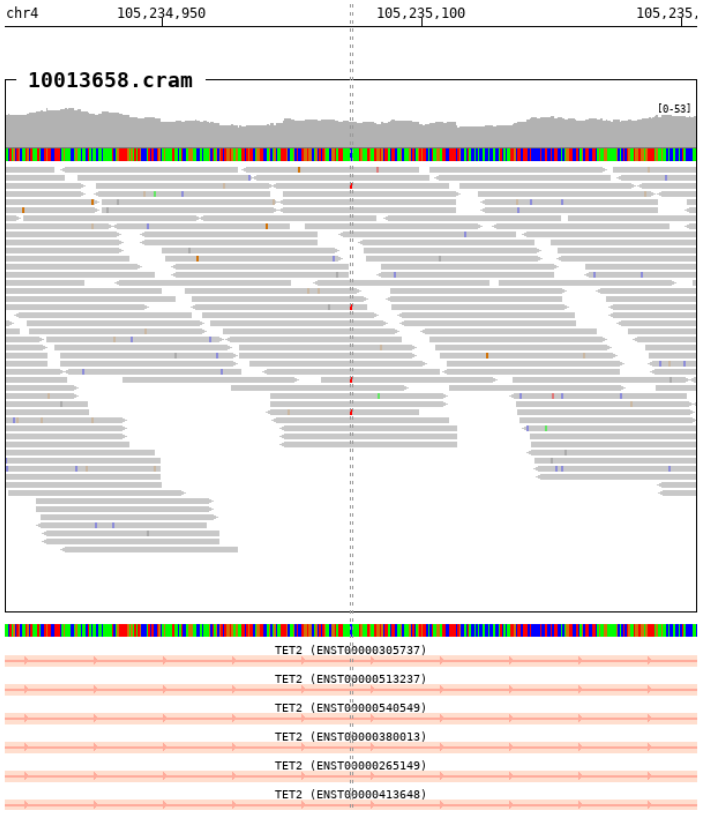
34.10. chr4_105235003_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10310756	chr4_105235003_C/G	33	7	*TET2*	stop_gained



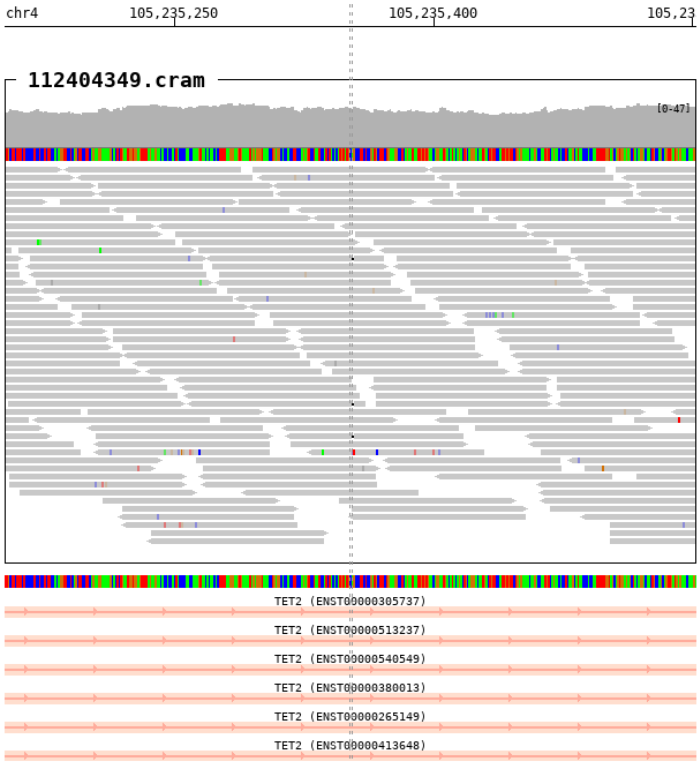
34.11. chr4_105235059_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10013658	chr4_105235059_C/T	26	4	*TET2*	stop_gained



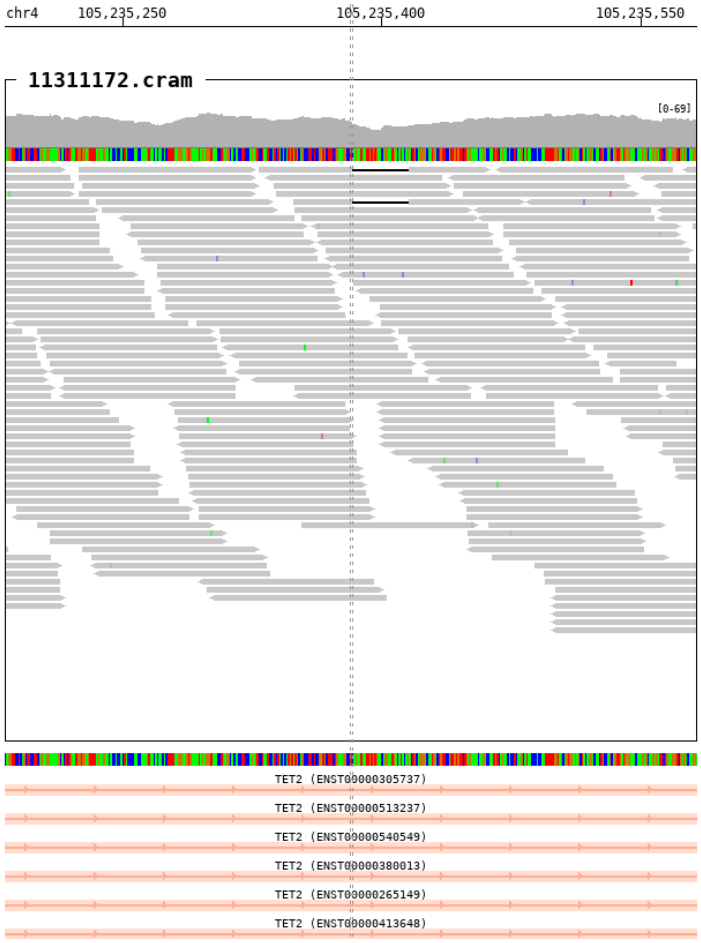
34.12. chr4_105235352_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112404349	chr4_105235352_A/-	36	3	*TET2*	frameshift_variant



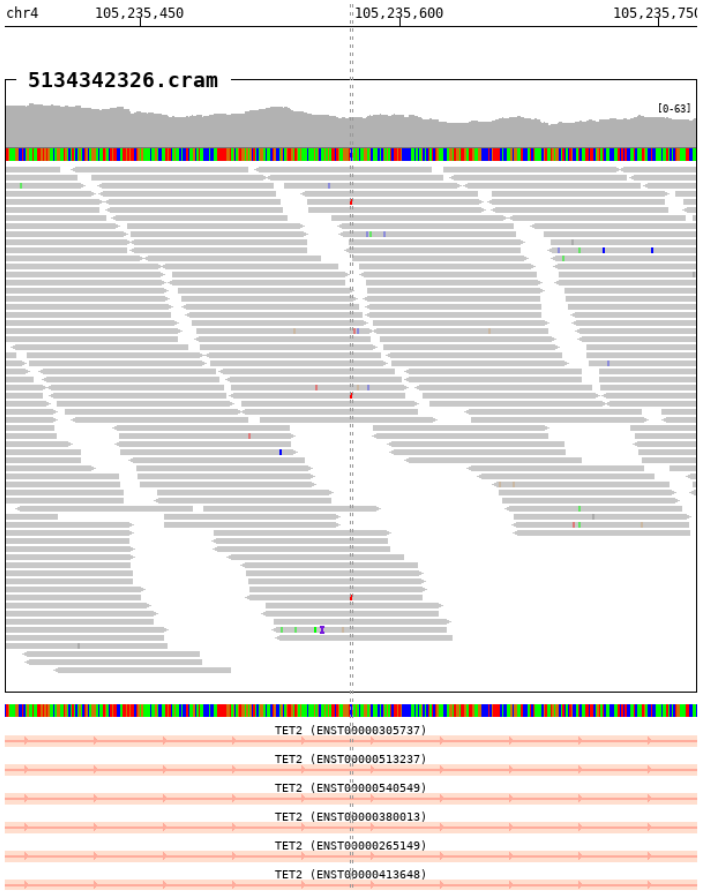
34.13. chr4_105235382_CAGAATAATTGTGTGAACAGGAATGACATACA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11311172	chr4_105235382_CAGAATAATTGTGTGAACAGGAATGACATACA/-	48	3	*TET2*	frameshift_variant



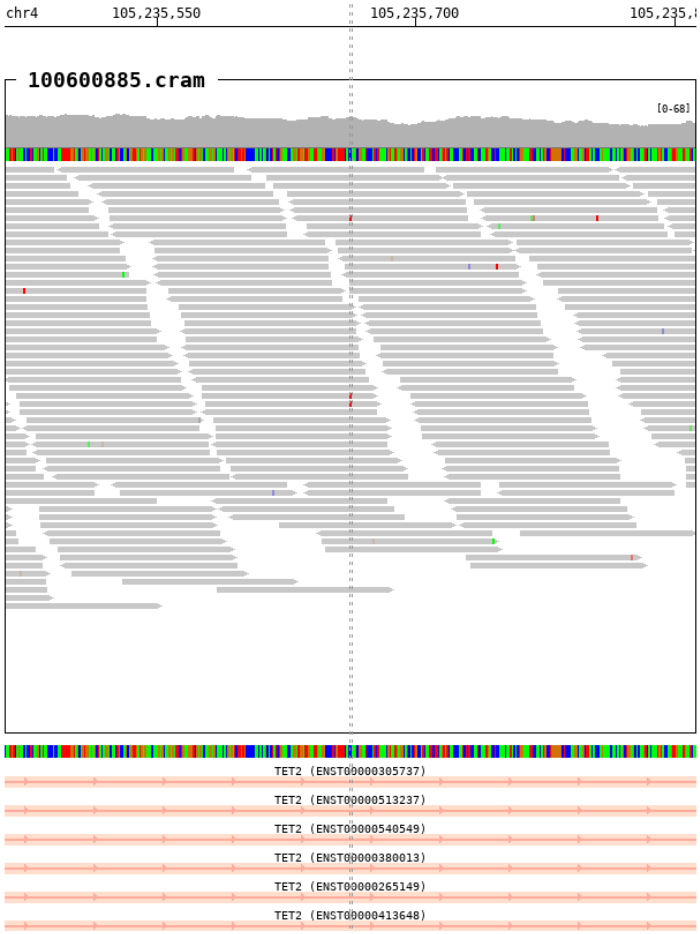
34.14. chr4_105235572_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
5134342326	chr4_105235572_C/T	35	3	*TET2*	stop_gained



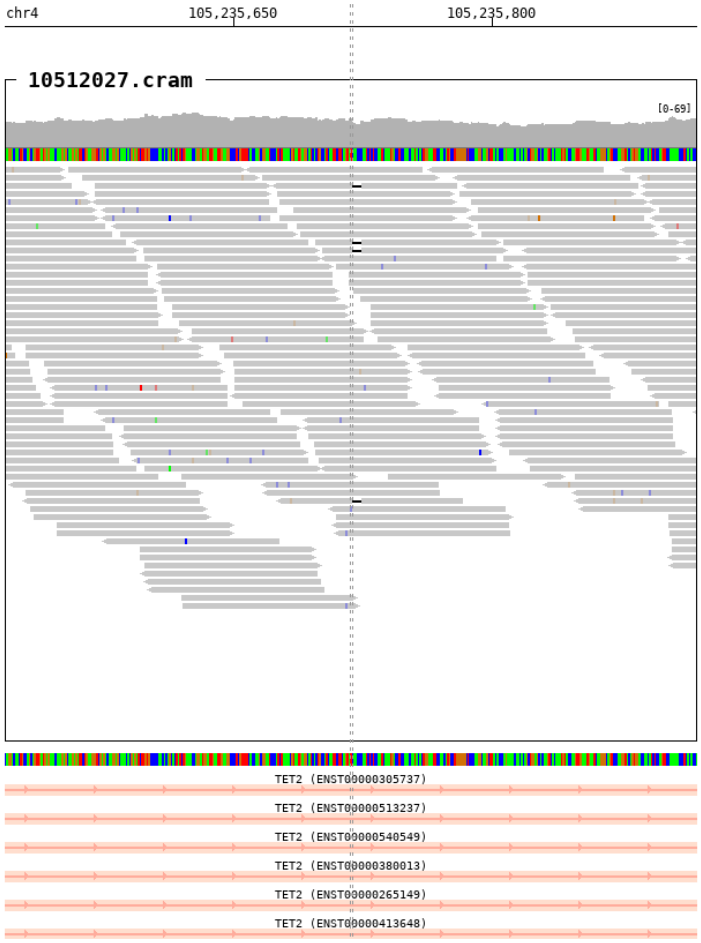
34.15. chr4_105235662_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100600885	chr4_105235662_C/T	43	3	*TET2*	stop_gained



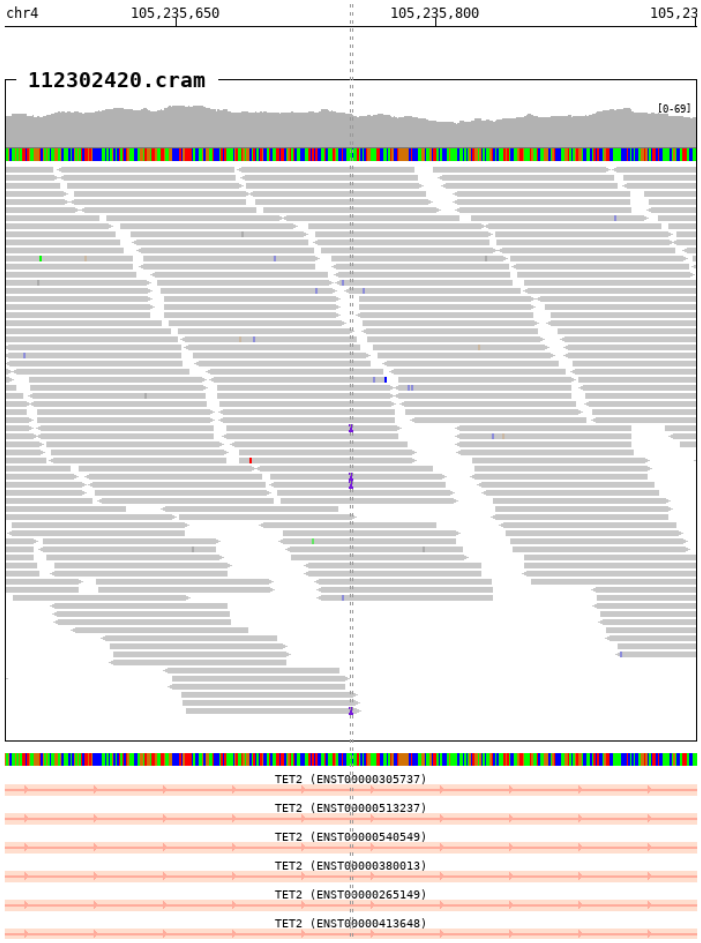
34.16. chr4_105235718_CAACC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10512027	chr4_105235718_CAACC/-	37	5	*TET2*	frameshift_variant



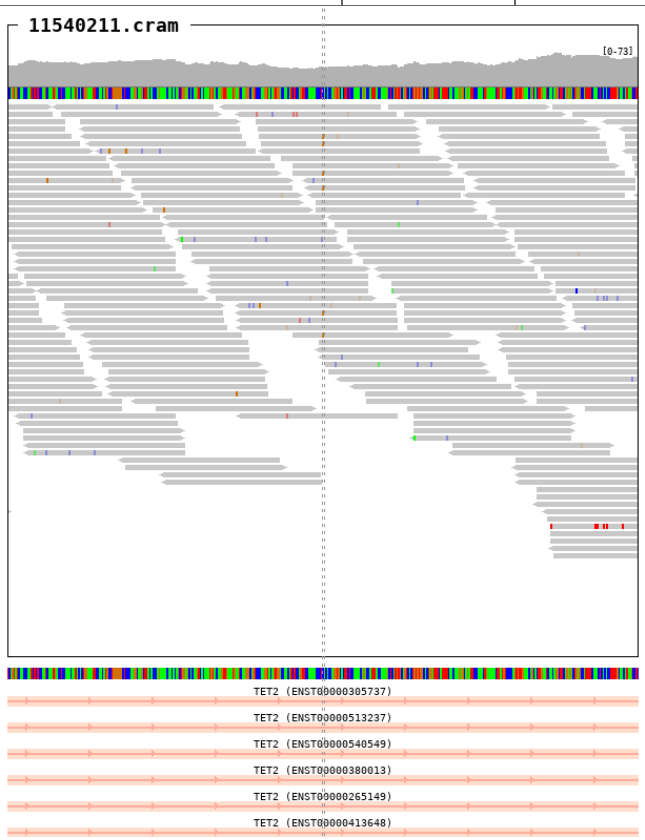
34.17. chr4_105235751_-/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112302420	chr4_105235751_-/C	46	4	*TET2*	frameshift_variant



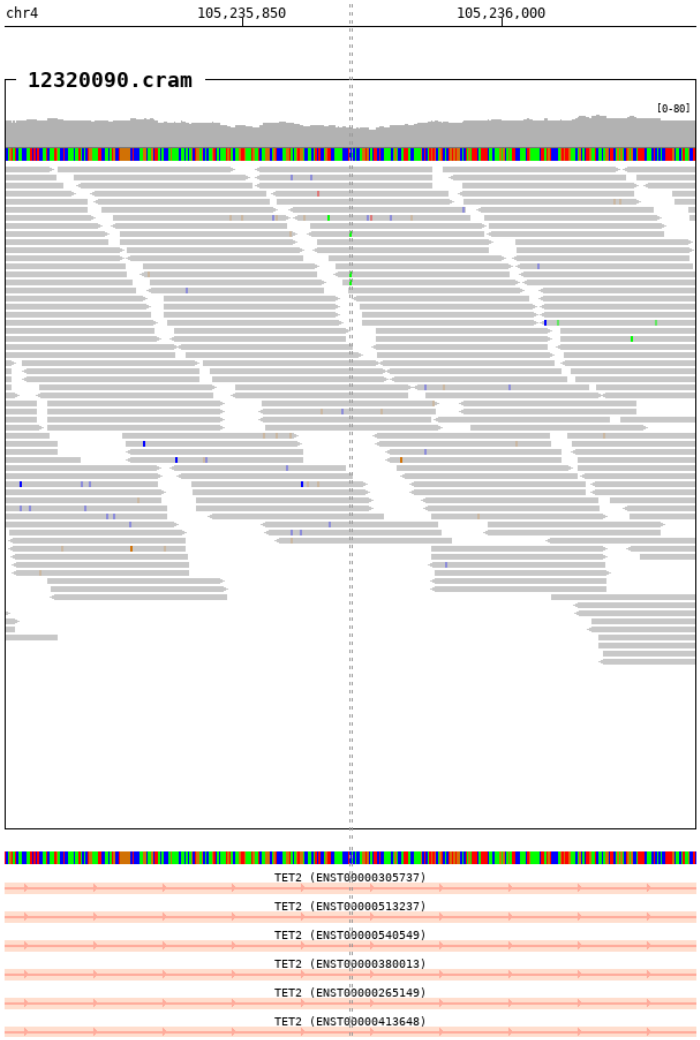
34.18. chr4_105235912_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11540211	chr4_105235912_C/G	26	5	*TET2*	stop_gained



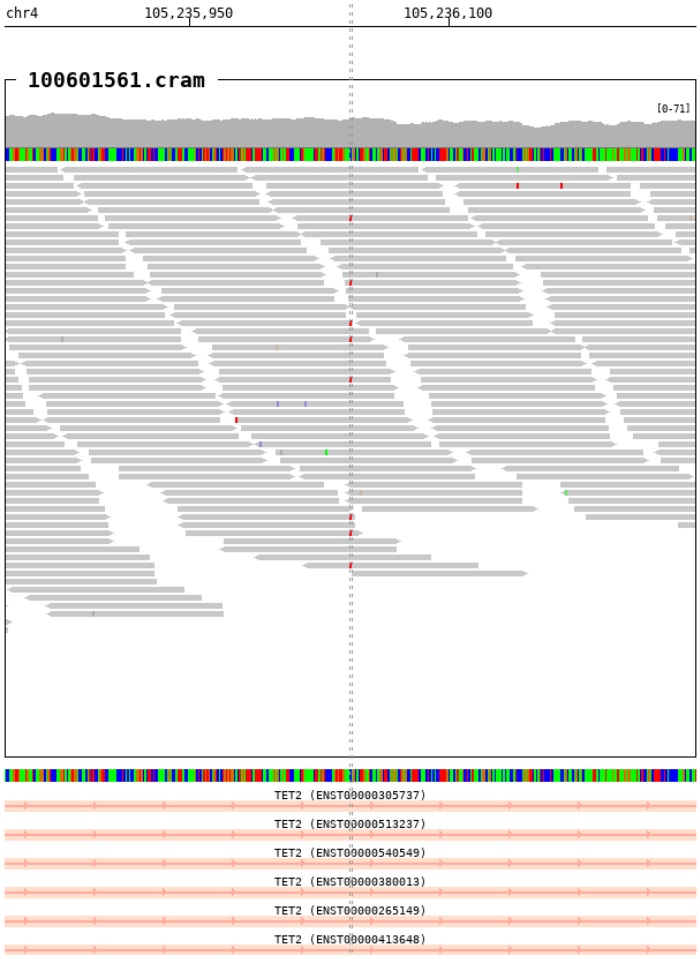
34.19. chr4_105235912_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12320090	chr4_105235912_C/A	31	3	*TET2*	stop_gained



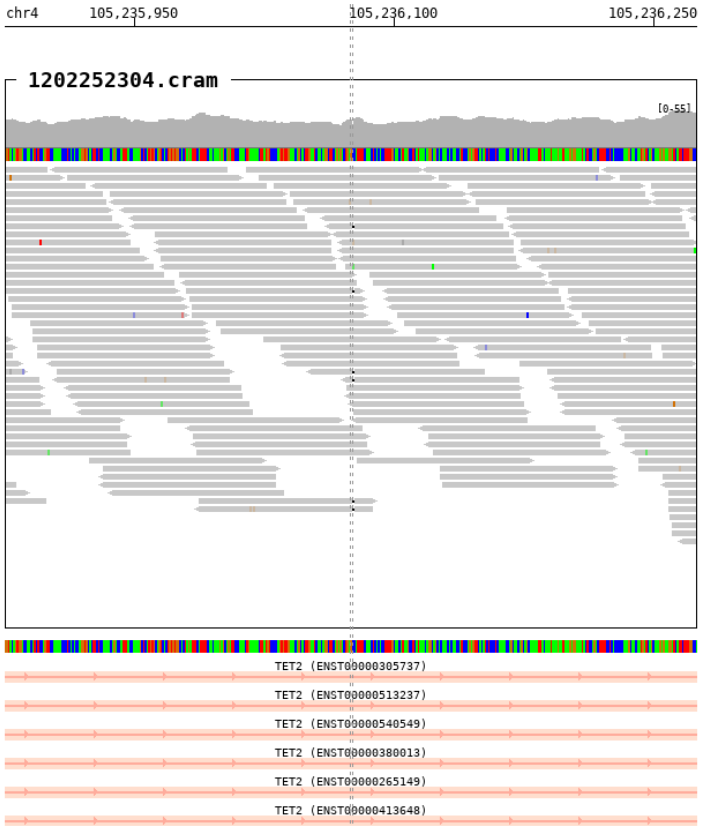
34.20. chr4_105236043_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100601561	chr4_105236043_C/T	37	8	*TET2*	stop_gained



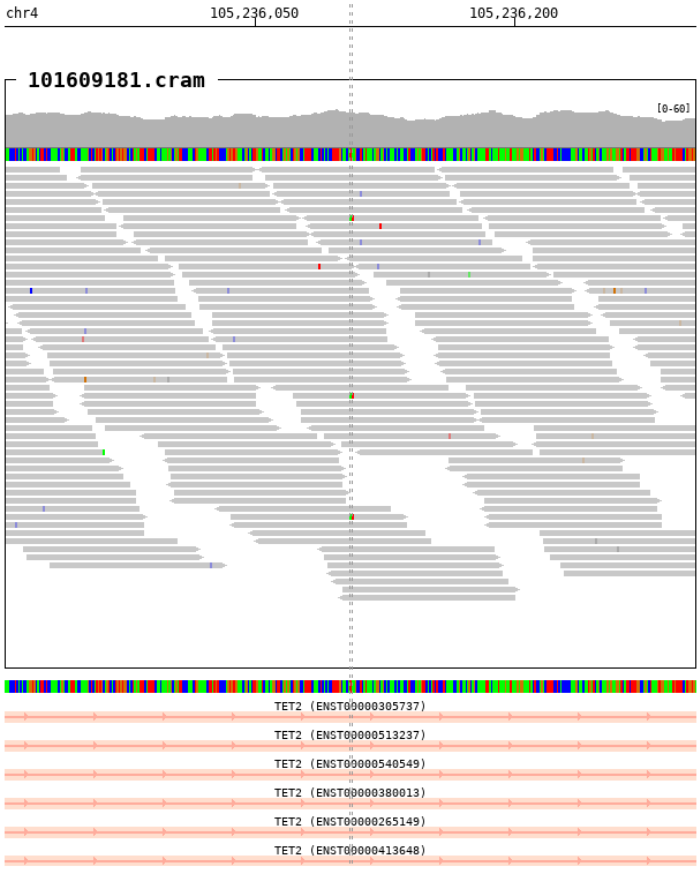
34.21. chr4_105236075_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
1202252304	chr4_105236075_C/-	29	6	*TET2*	frameshift_variant



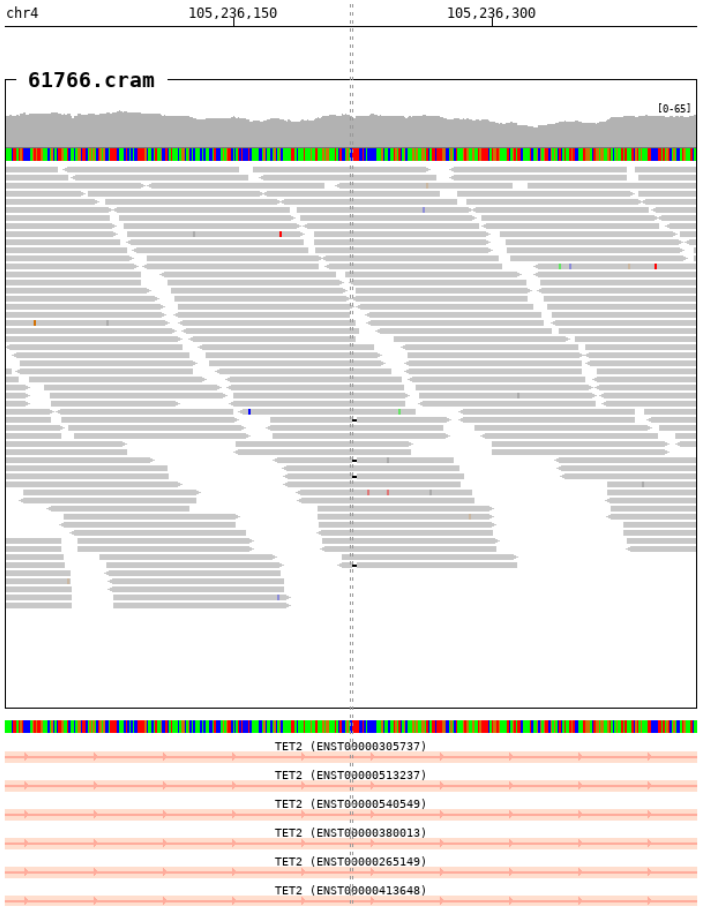
34.22. chr4_105236105_TA/AT

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101609181	chr4_105236105_TA/AT	44	3	*TET2*	stop_gained



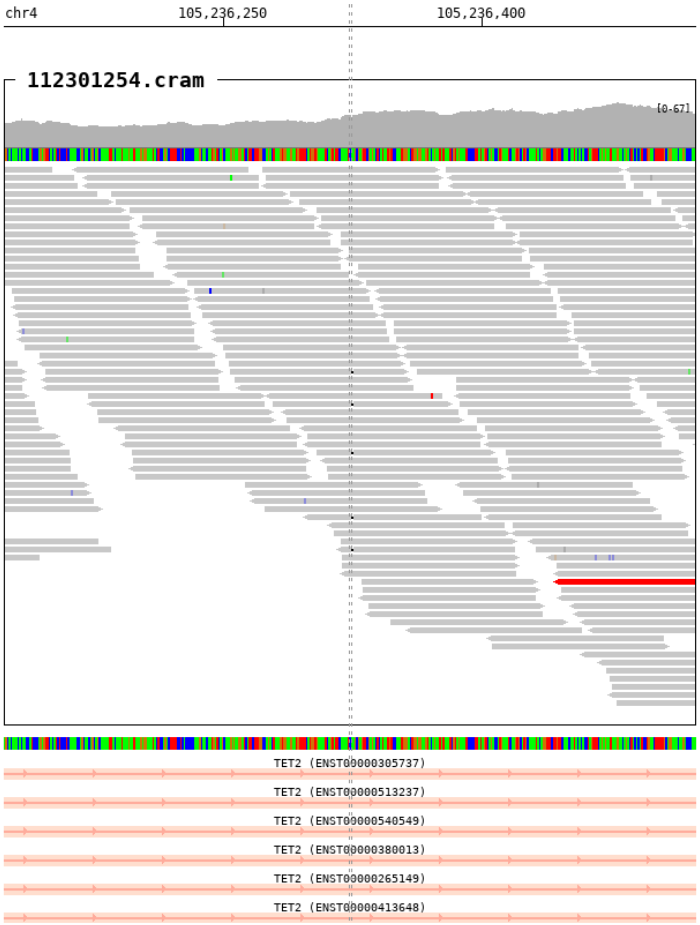
34.23. chr4_105236218_TT/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
61766	chr4_105236218_TT/-	40	5	*TET2*	frameshift_variant



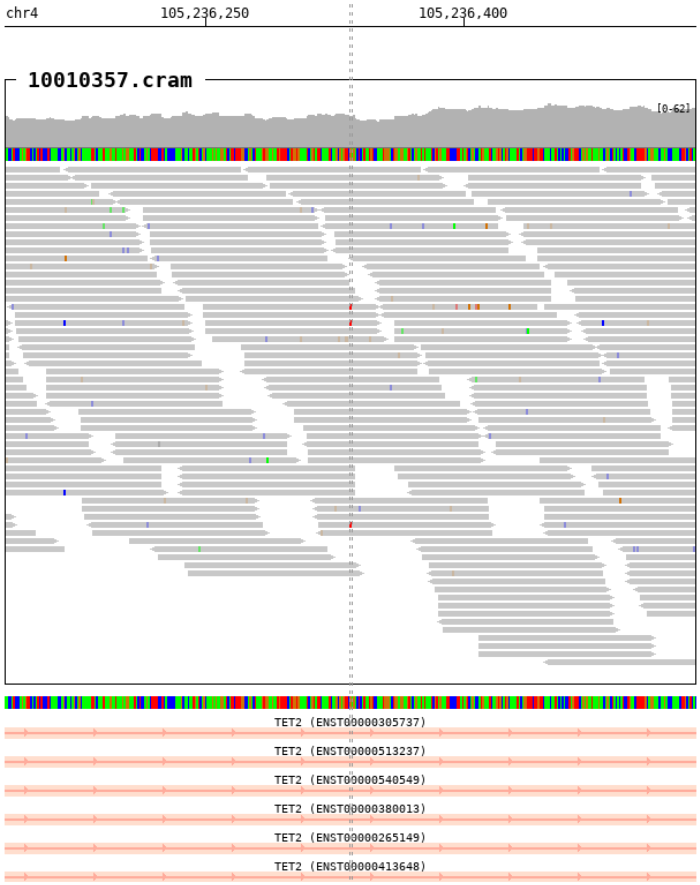
34.24. chr4_105236323_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301254	chr4_105236323_A/-	44	5	*TET2*	frameshift_variant



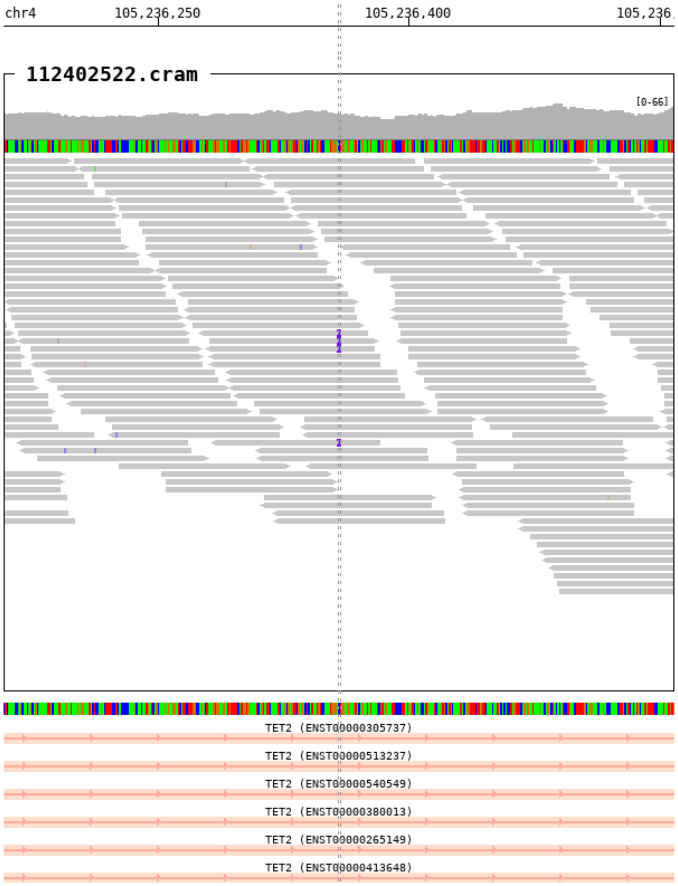
34.25. chr4_105236334_G/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10010357	chr4_105236334_G/T	39	3	*TET2*	stop_gained



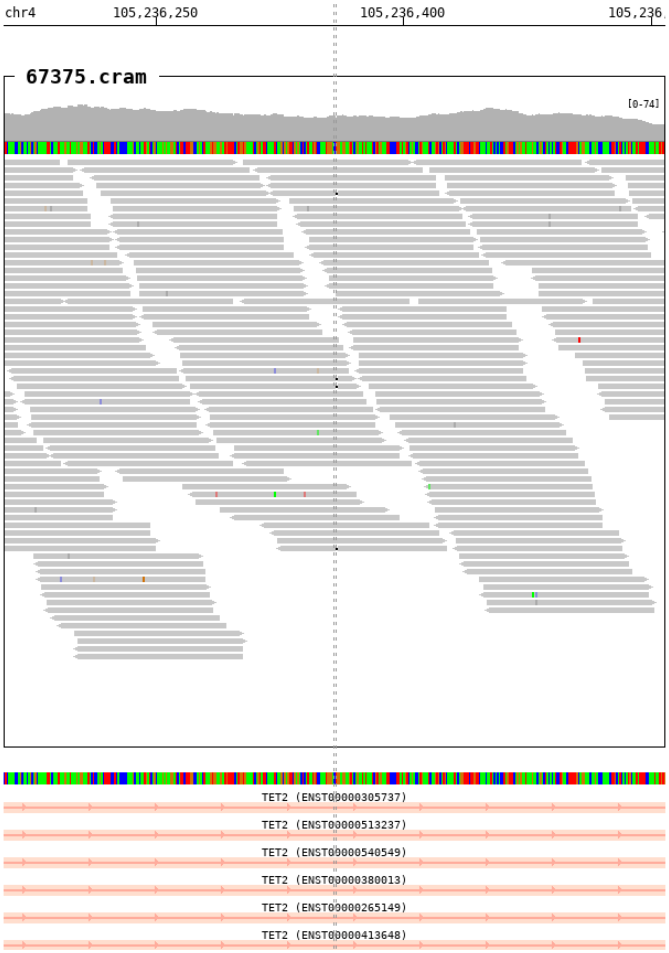
34.26. chr4_105236358_-/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112402522	chr4_105236358_-/C	34	4	*TET2*	frameshift_variant



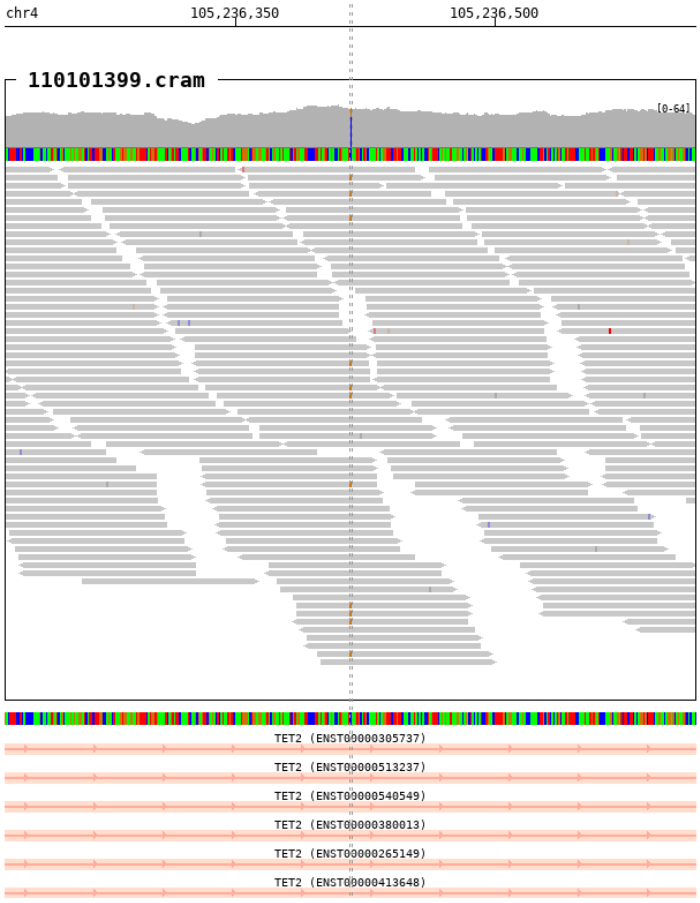
34.27. chr4_105236358_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
67375	chr4_105236358_T/-	40	4	*TET2*	frameshift_variant



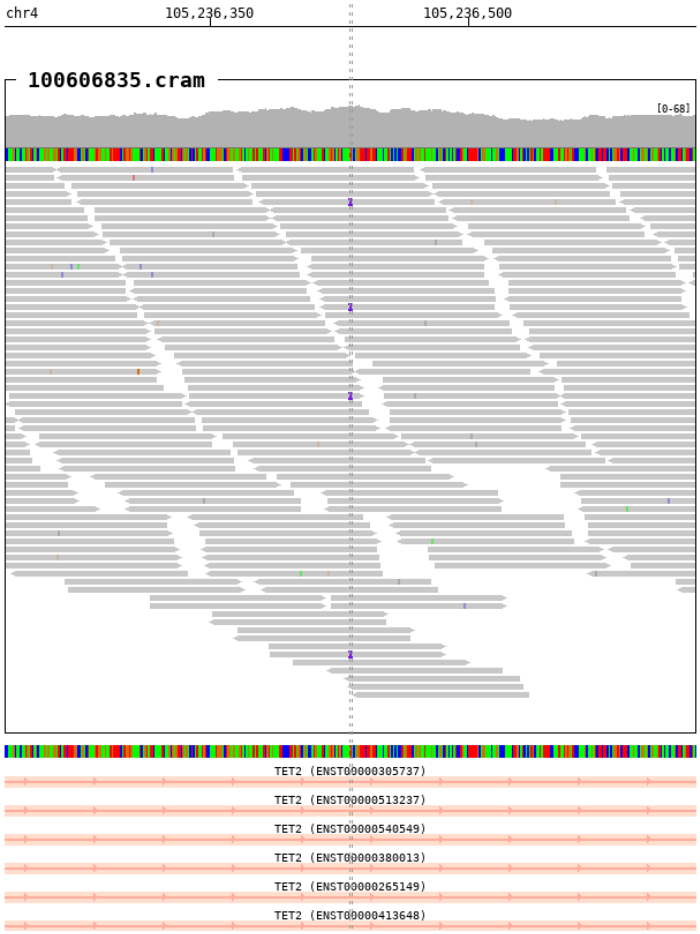
34.28. chr4_105236416_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110101399	chr4_105236416_C/G	43	10	*TET2*	stop_gained



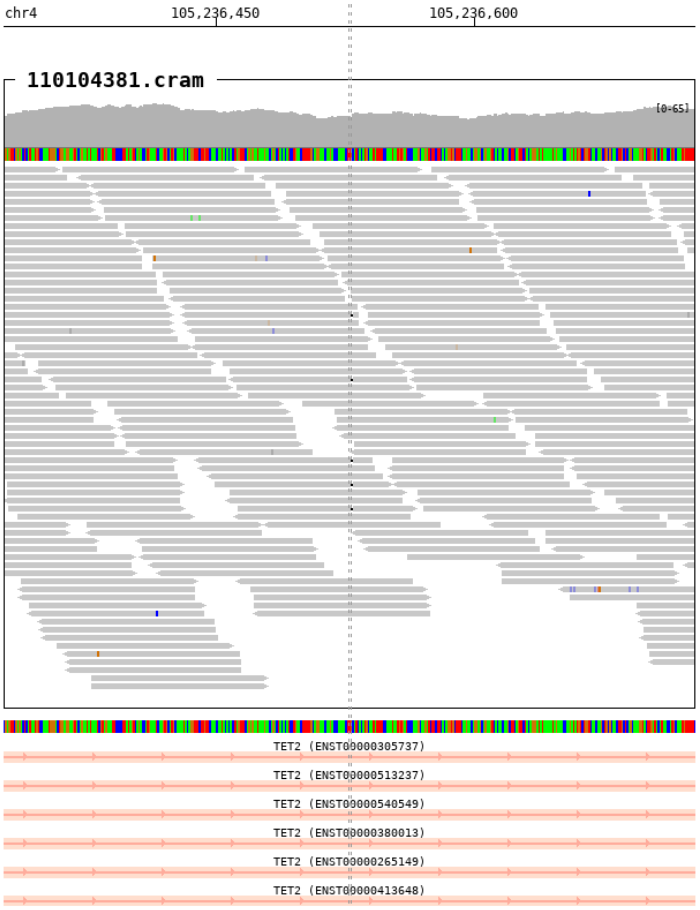
34.29. chr4_105236431_-/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100606835	chr4_105236431_-/T	58	5	*TET2*	frameshift_variant



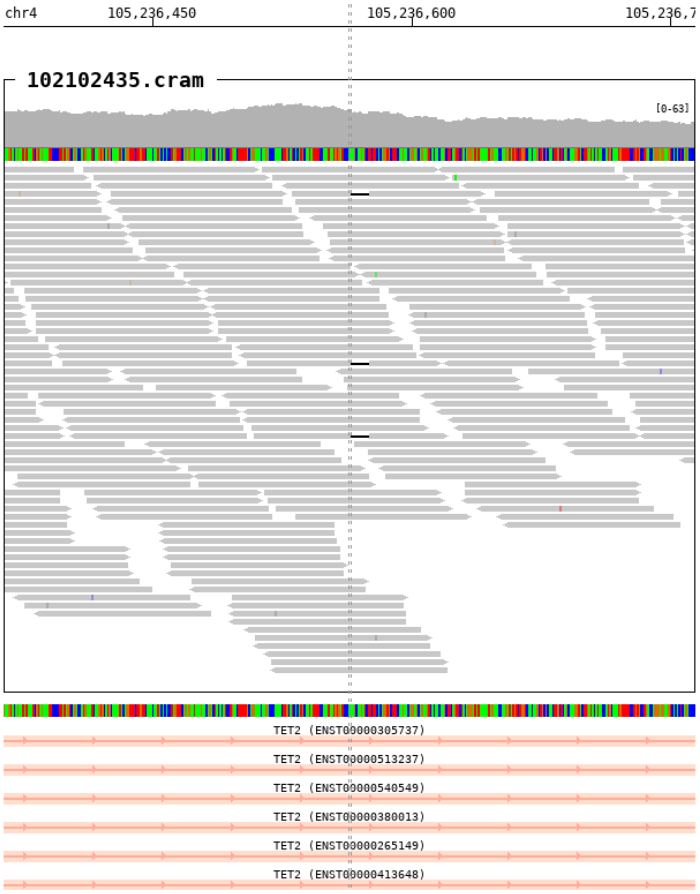
34.30. chr4_105236527_G/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110104381	chr4_105236527_G/-	41	5	*TET2*	frameshift_variant



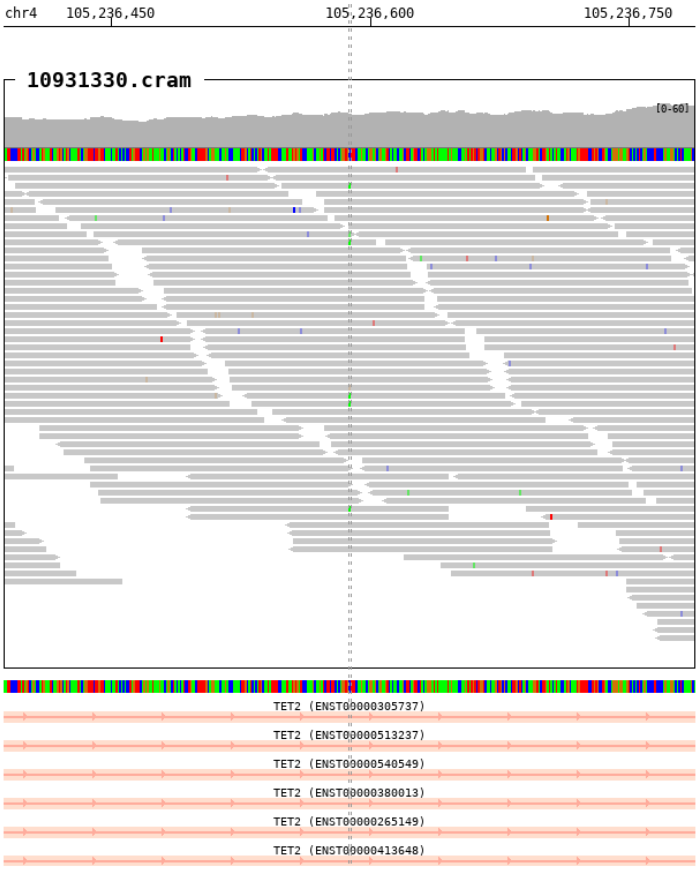
34.31. chr4_105236564_AAGCAAGATC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102102435	chr4_105236564_AAGCAAGATC/-	49	4	*TET2*	frameshift_variant



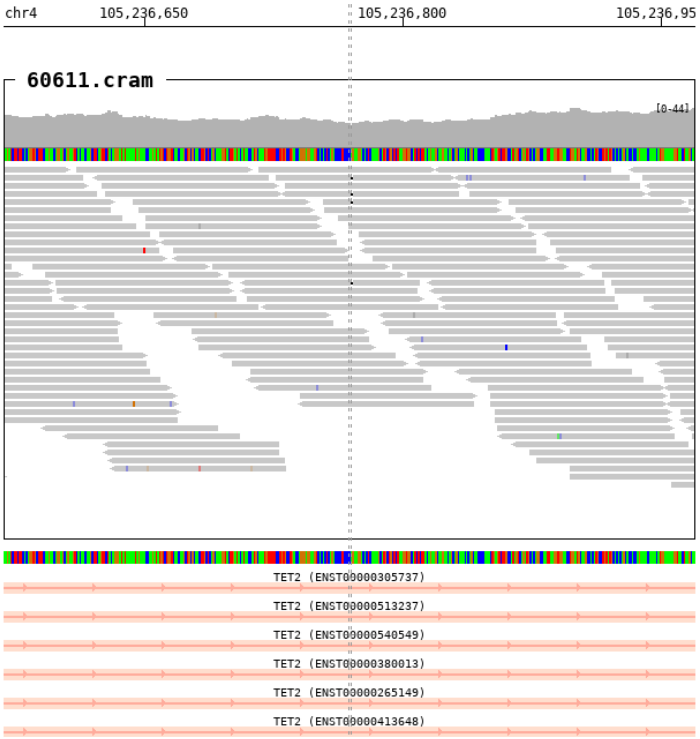
34.32. chr4_105236588_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10931330	chr4_105236588_C/A	38	6	*TET2*	stop_gained



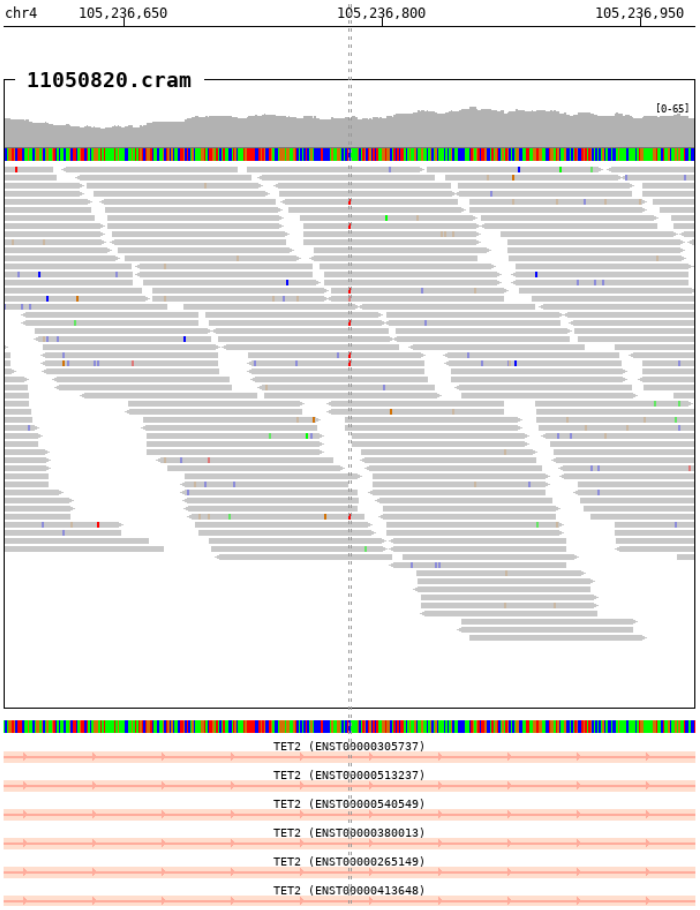
34.33. chr4_105236769_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
60611	chr4_105236769_A/-	20	4	*TET2*	frameshift_variant



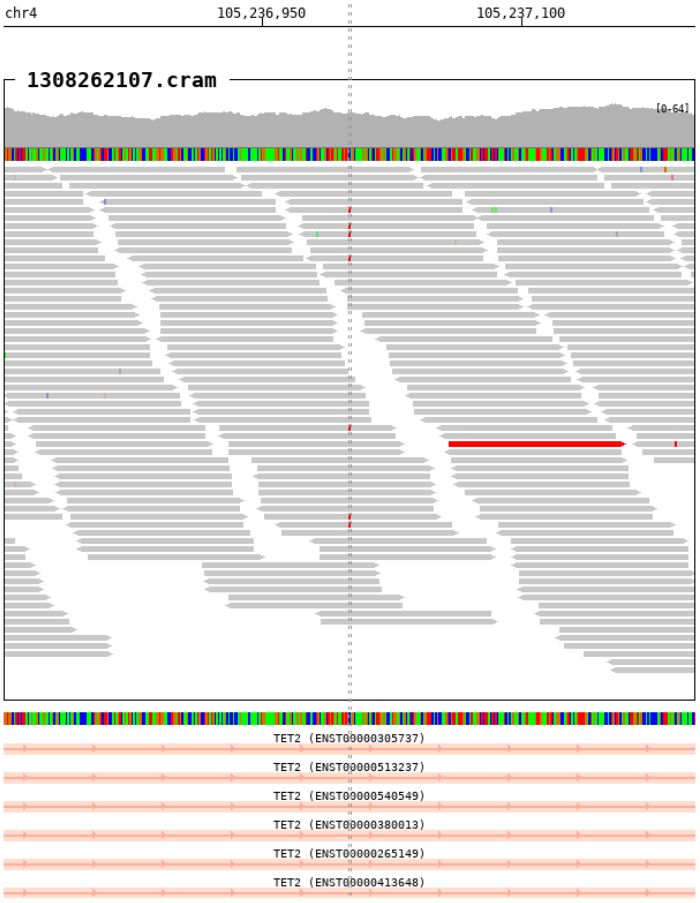
34.34. chr4_105236781_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11050820	chr4_105236781_C/T	34	7	*TET2*	stop_gained



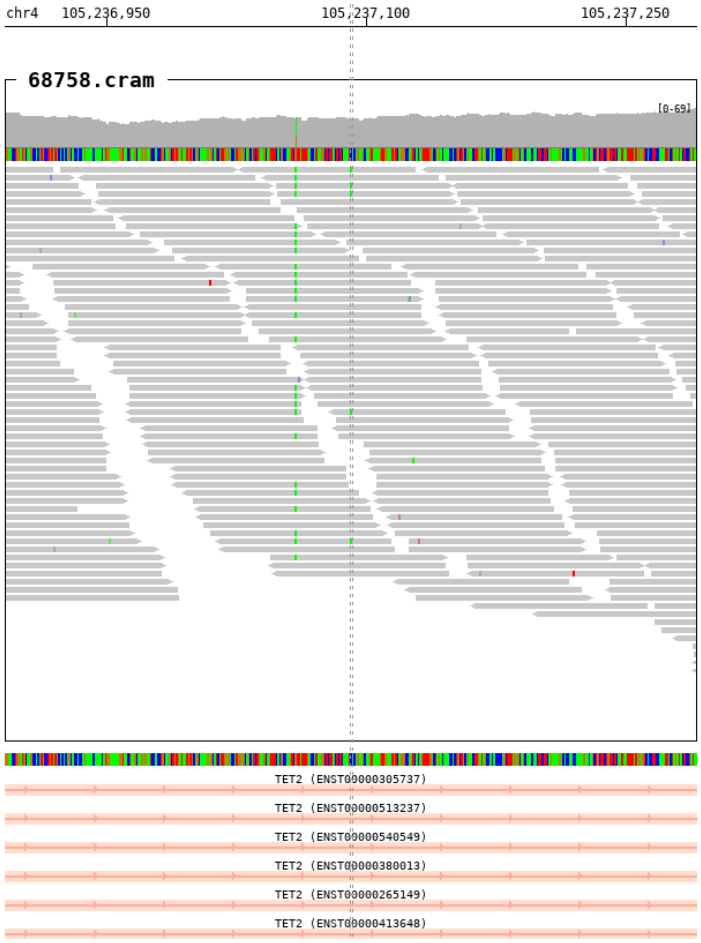
34.35. chr4_105237000_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
1308262107	chr4_105237000_C/T	40	7	*TET2*	stop_gained



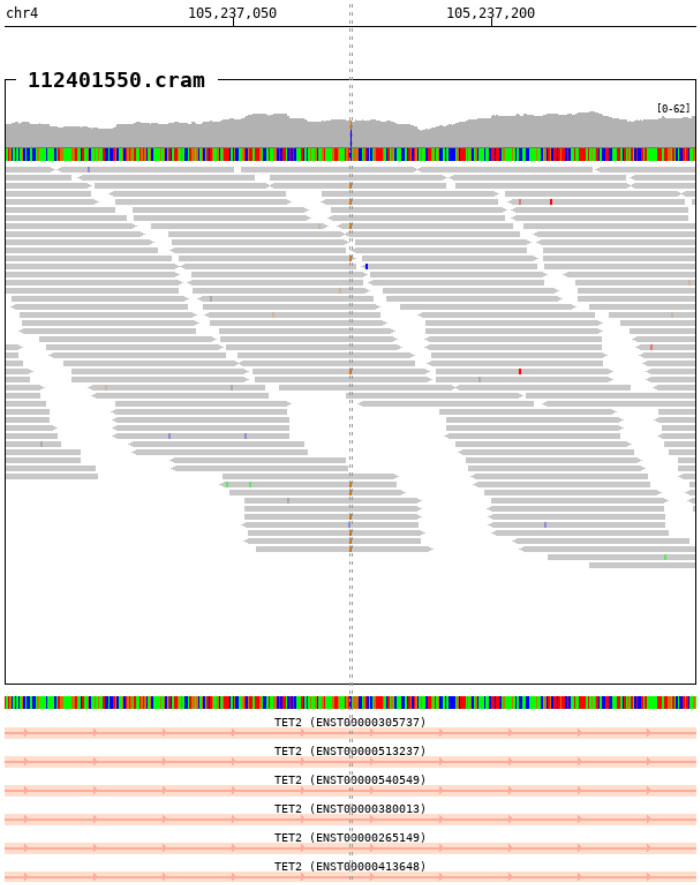
34.36. chr4_105237091_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
68758	chr4_105237091_C/A	39	5	*TET2*	stop_gained



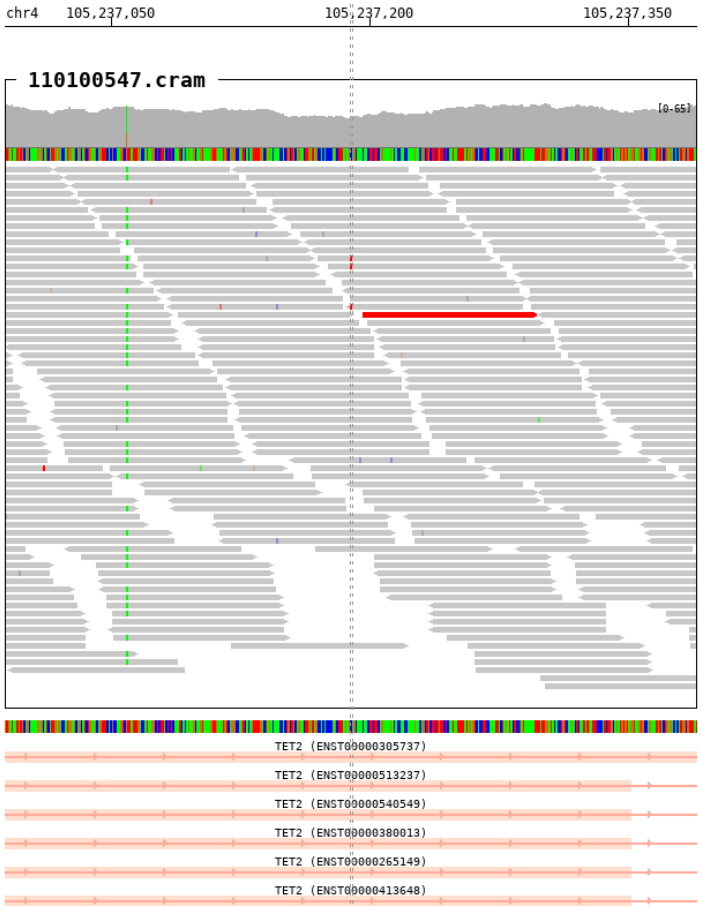
34.37. chr4_105237118_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112401550	chr4_105237118_C/G	26	11	*TET2*	stop_gained



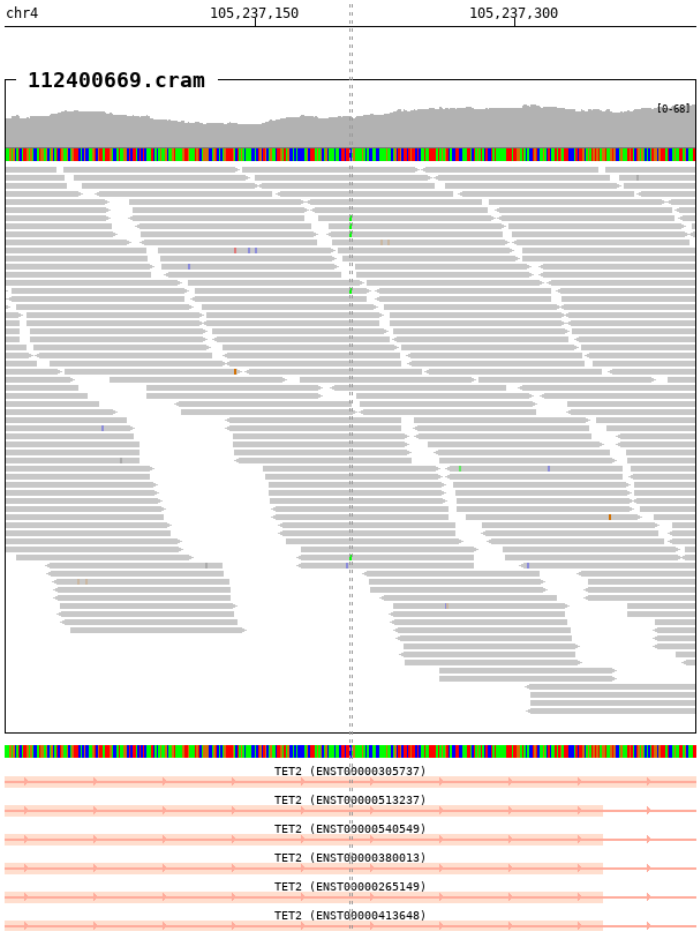
34.38. chr4_105237189_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110100547	chr4_105237189_C/T	41	3	*TET2*	stop_gained



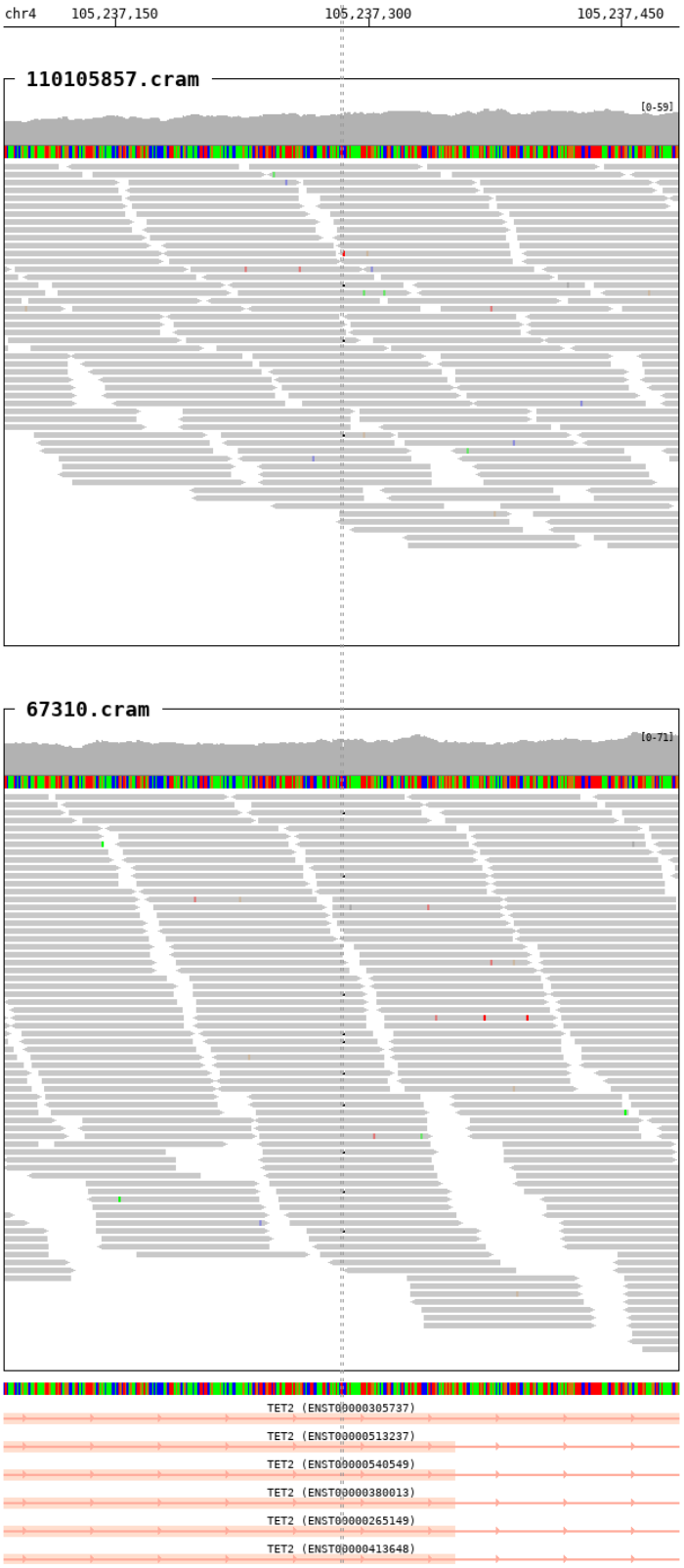
34.39. chr4_105237205_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112400669	chr4_105237205_C/A	41	5	*TET2*	stop_gained



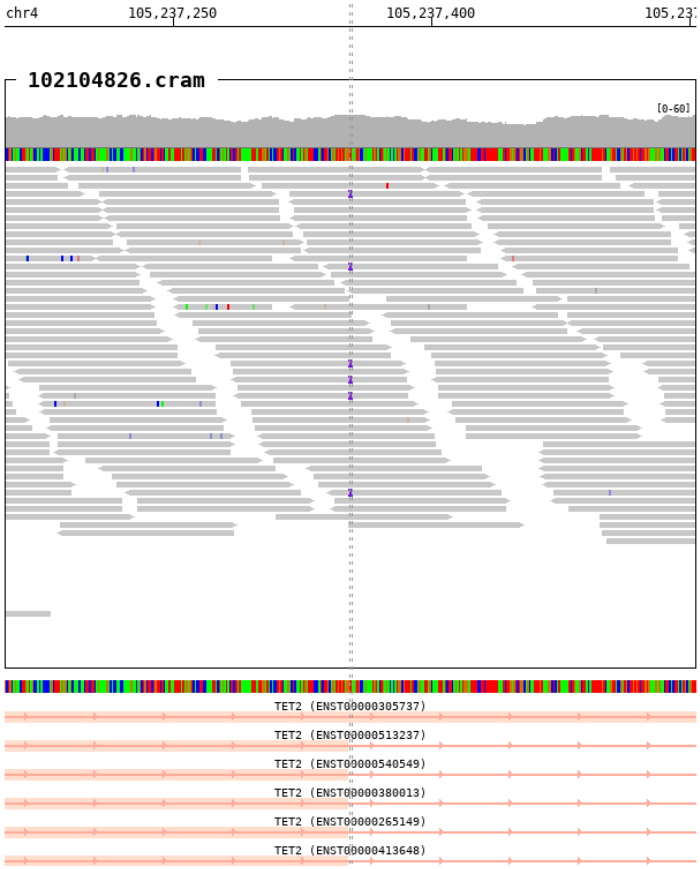
34.40. chr4_105237284_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110105857	chr4_105237284_C/-	39	4	*TET2*	frameshift_variant
67310	chr4_105237284_C/-	44	10	*TET2*	frameshift_variant



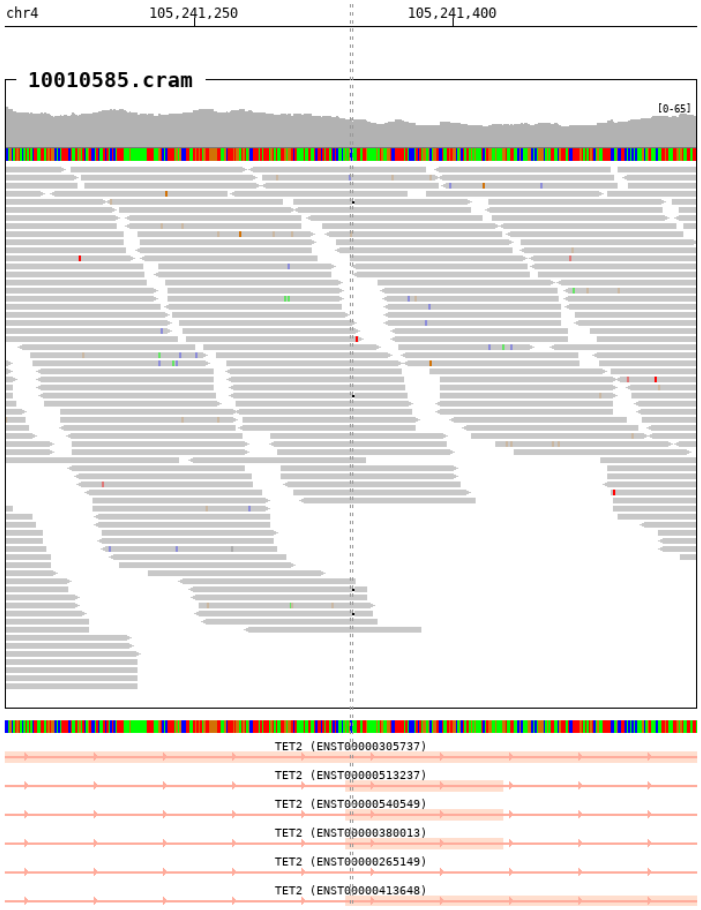
34.41. chr4_105237353_-/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102104826	chr4_105237353_-/T	36	6	*TET2*	splice_donor_variant



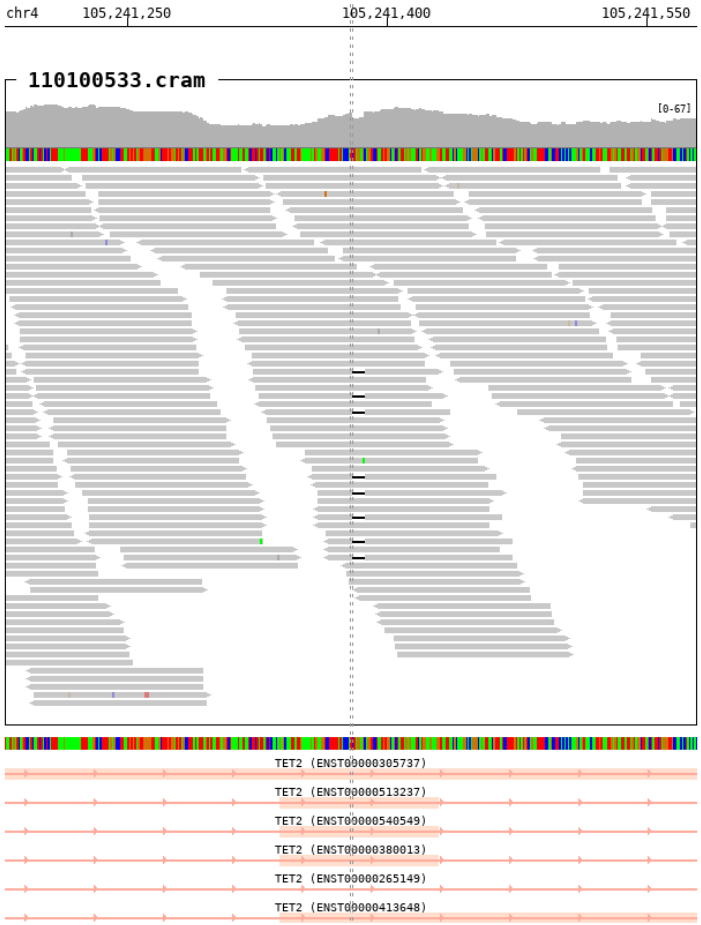
34.42. chr4_105241341_A/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10010585	chr4_105241341_A/-	34	5	*TET2*	frameshift_variant



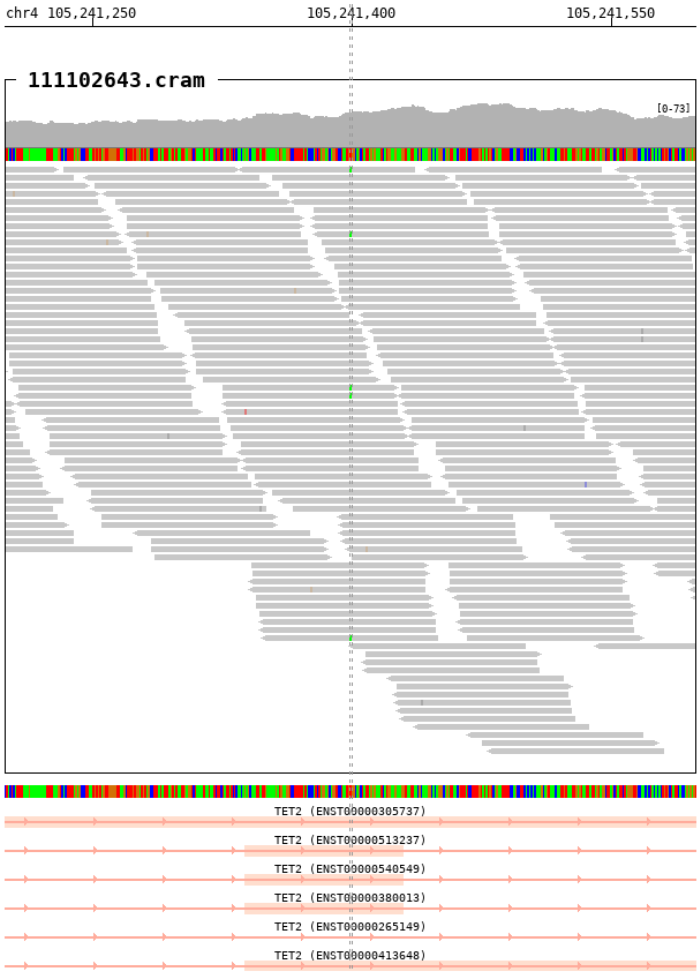
34.43. chr4_105241379_CTAGGAG/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110100533	chr4_105241379_CTAGGAG/-	46	7	*TET2*	frameshift_variant



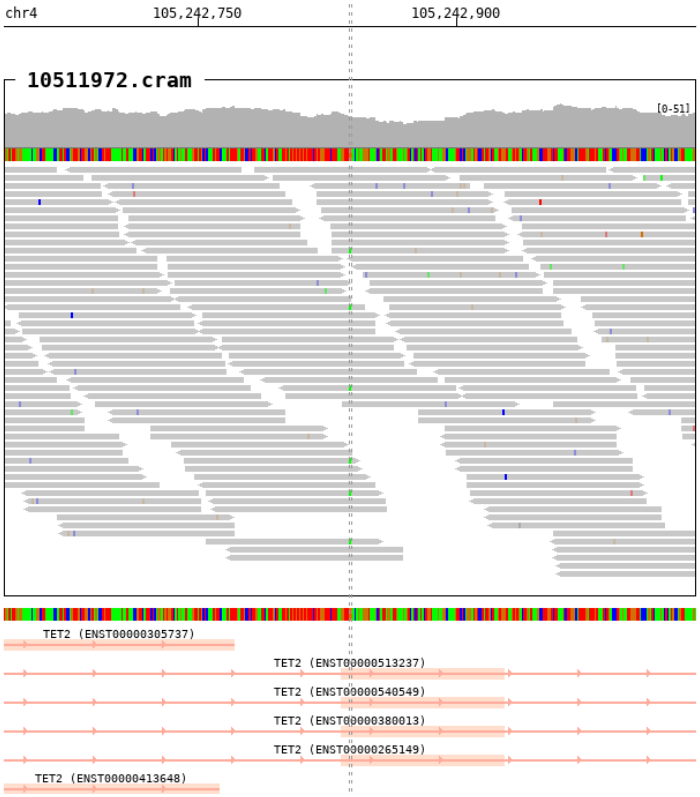
34.44. chr4_105241399_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
111102643	chr4_105241399_T/A	49	5	*TET2*	missense_variant



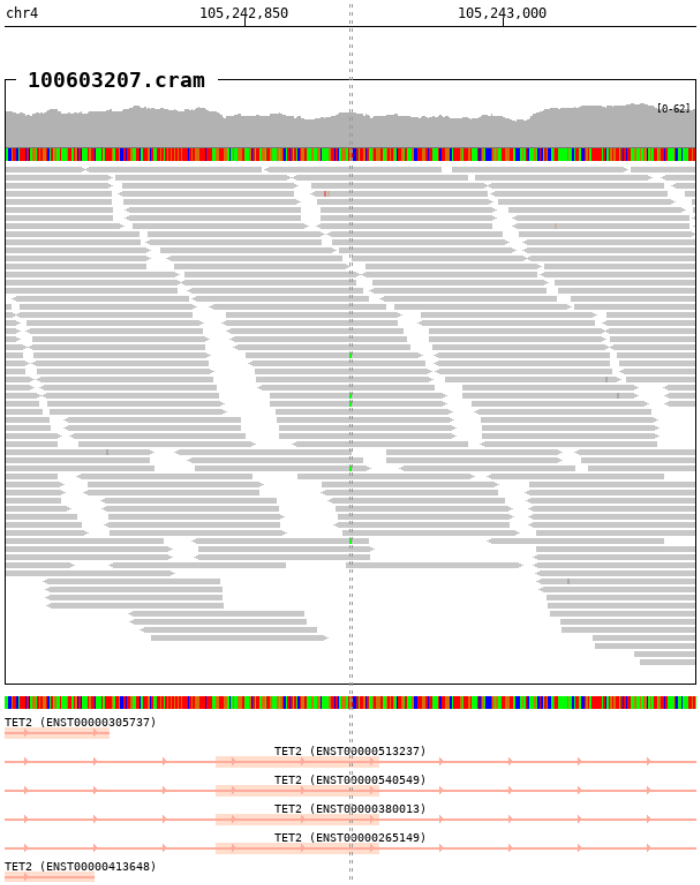
34.45. chr4_105242838_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10511972	chr4_105242838_G/A	30	6	*TET2*	missense_variant



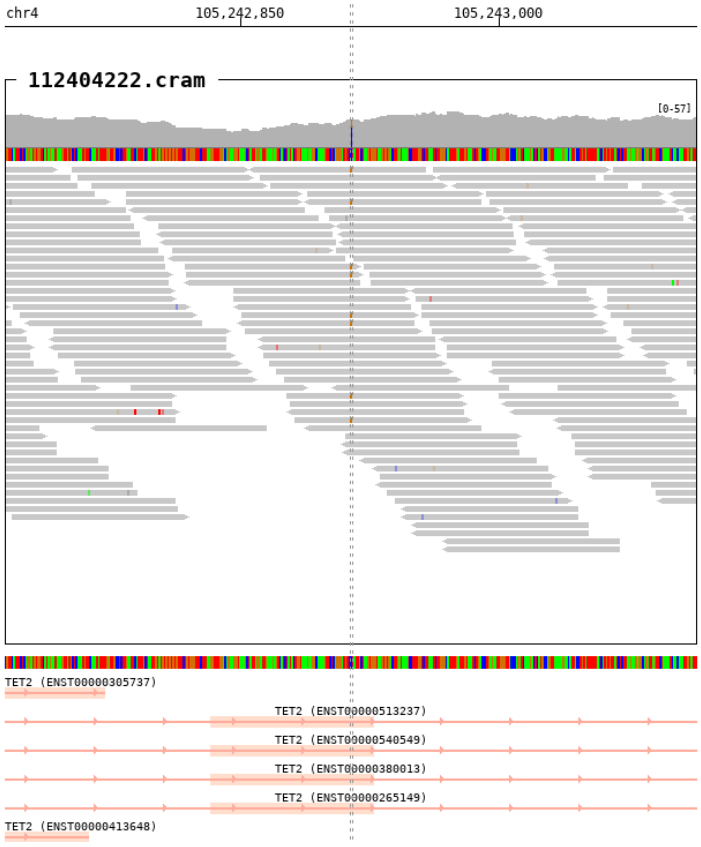
34.46. chr4_105242911_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100603207	chr4_105242911_G/A	41	4	*TET2*	missense_variant



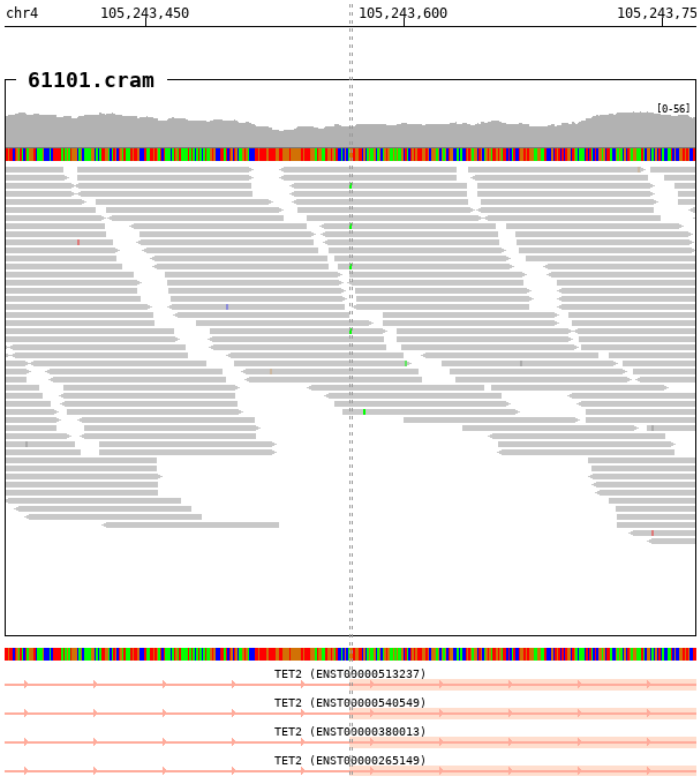
34.47. chr4_105242914_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112404222	chr4_105242914_C/G	26	8	*TET2*	missense_variant



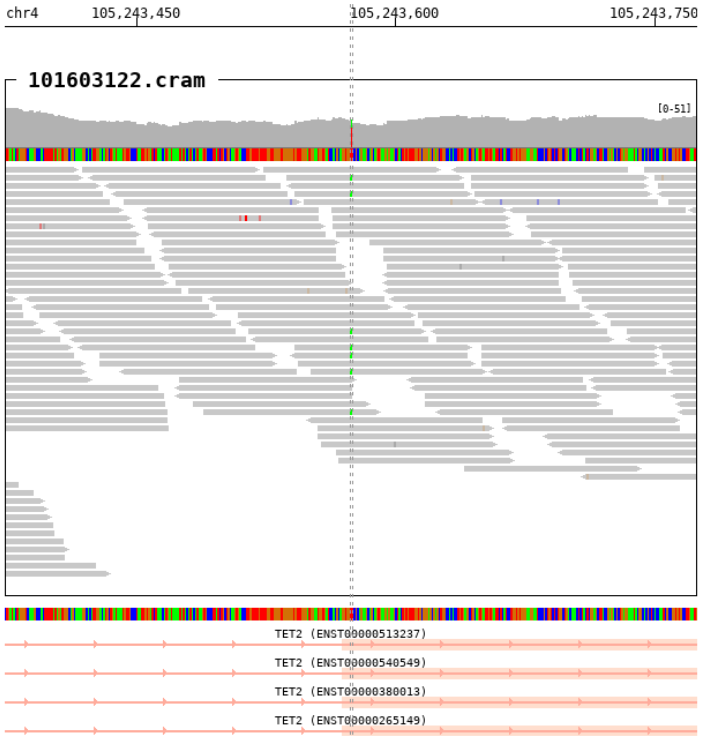
34.48. chr4_105243569_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
61101	chr4_105243569_G/A	20	4	*TET2*	splice_acceptor_variant



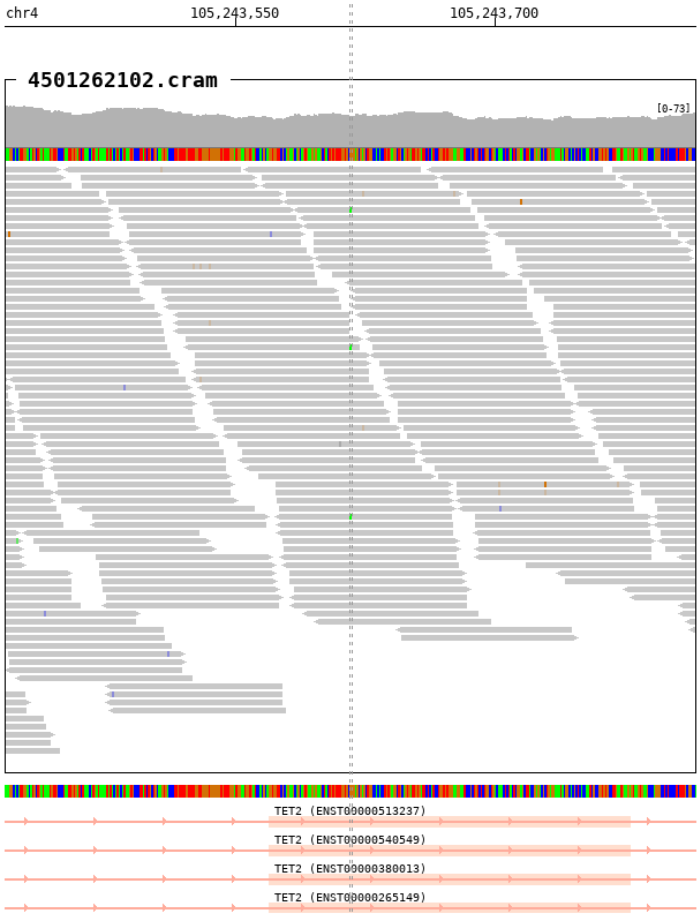
34.49. chr4_105243574_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101603122	chr4_105243574_T/A	22	6	*TET2*	missense_variant



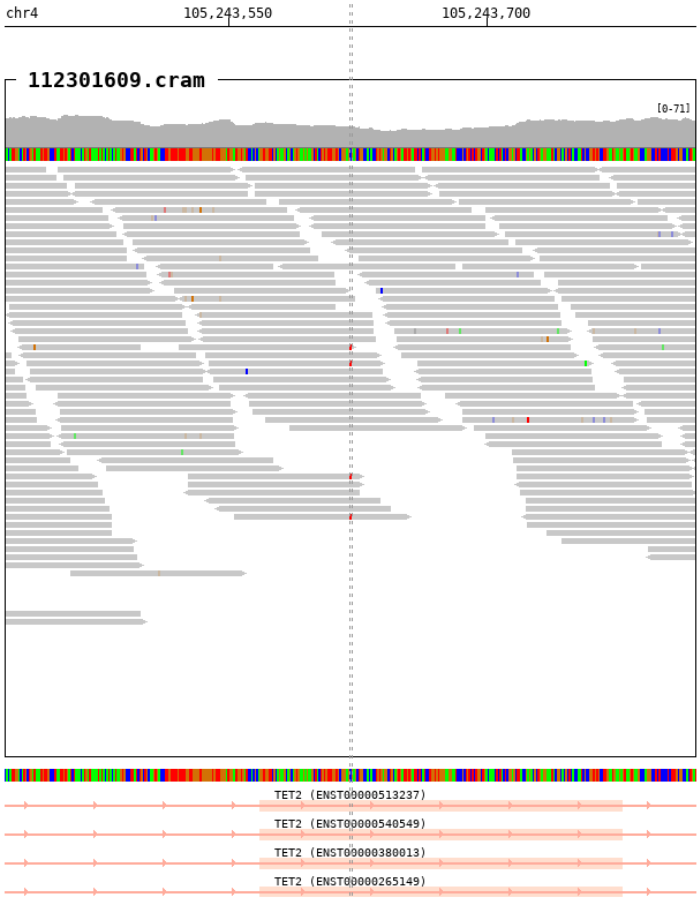
34.50. chr4_105243616_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
4501262102	chr4_105243616_G/A	45	3	*TET2*	missense_variant



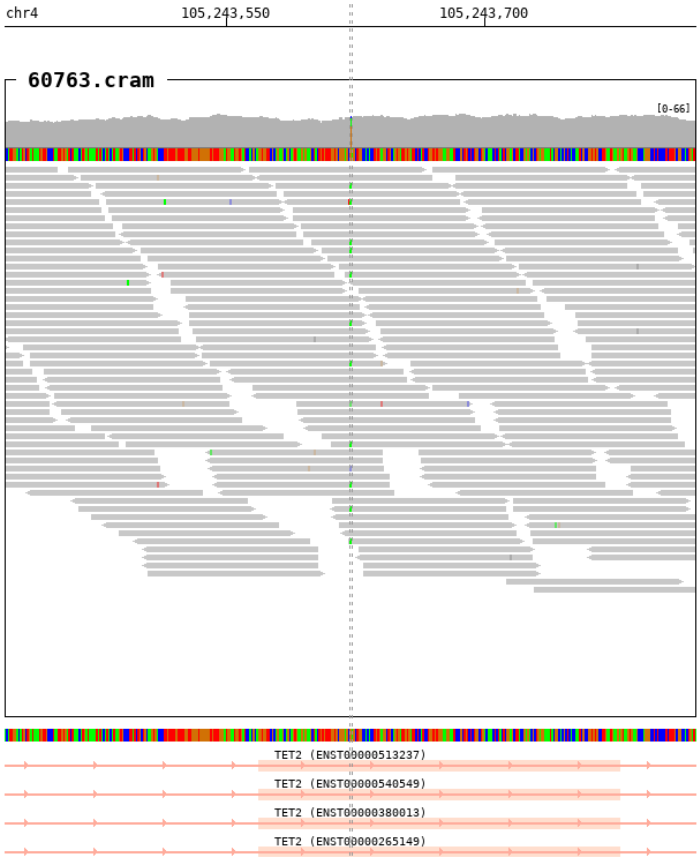
34.51. chr4_105243621_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112301609	chr4_105243621_C/T	30	4	*TET2*	stop_gained



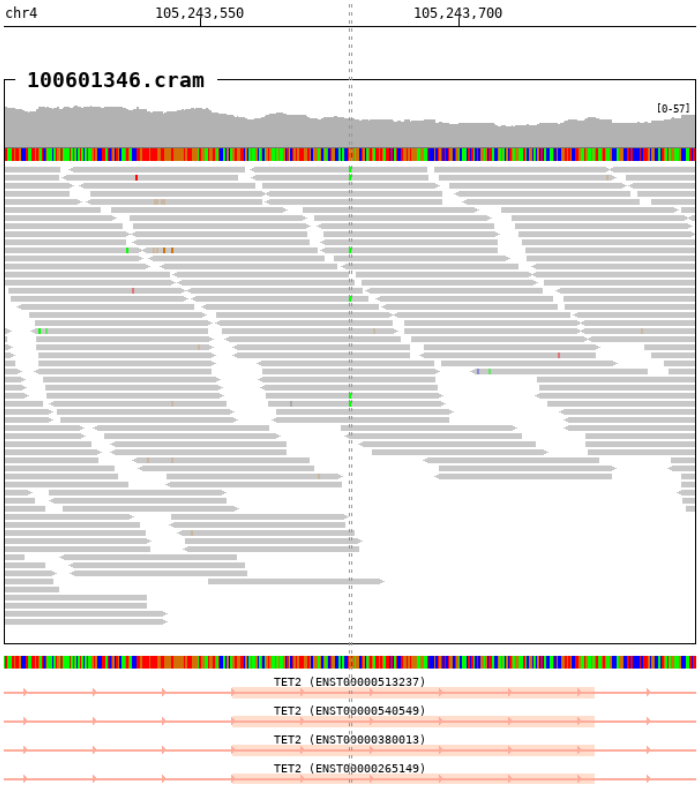
34.52. chr4_105243622_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
60763	chr4_105243622_G/A	31	12	*TET2*	missense_variant



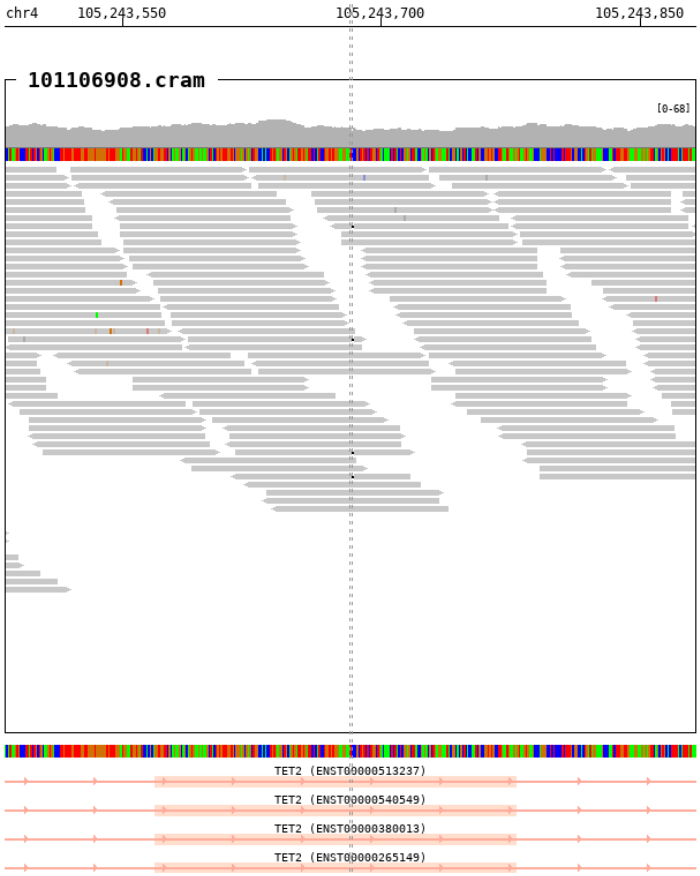
34.53. chr4_105243637_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100601346	chr4_105243637_G/A	30	6	*TET2*	missense_variant



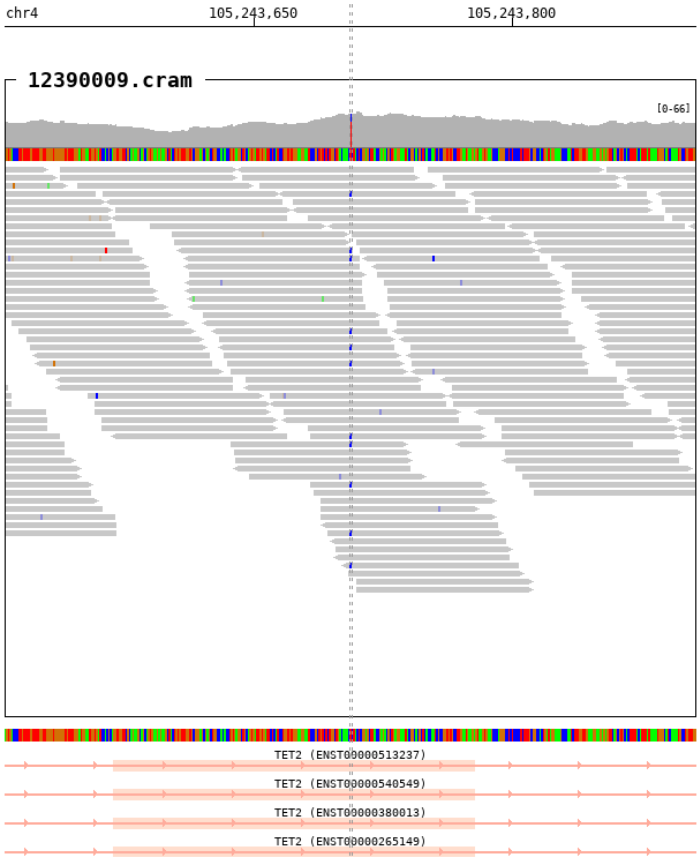
34.54. chr4_105243682_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101106908	chr4_105243682_C/-	24	4	*TET2*	frameshift_variant



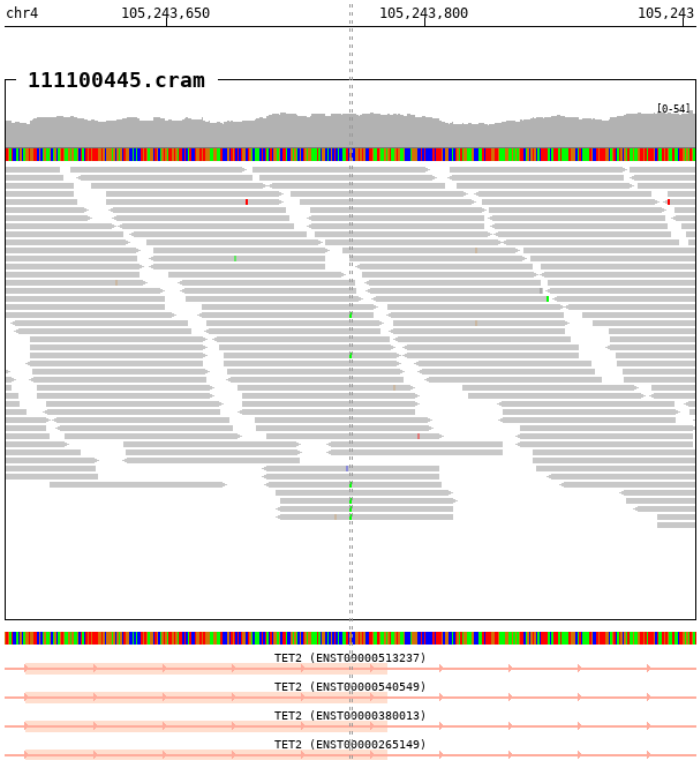
34.55. chr4_105243706_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12390009	chr4_105243706_T/C	38	11	*TET2*	missense_variant



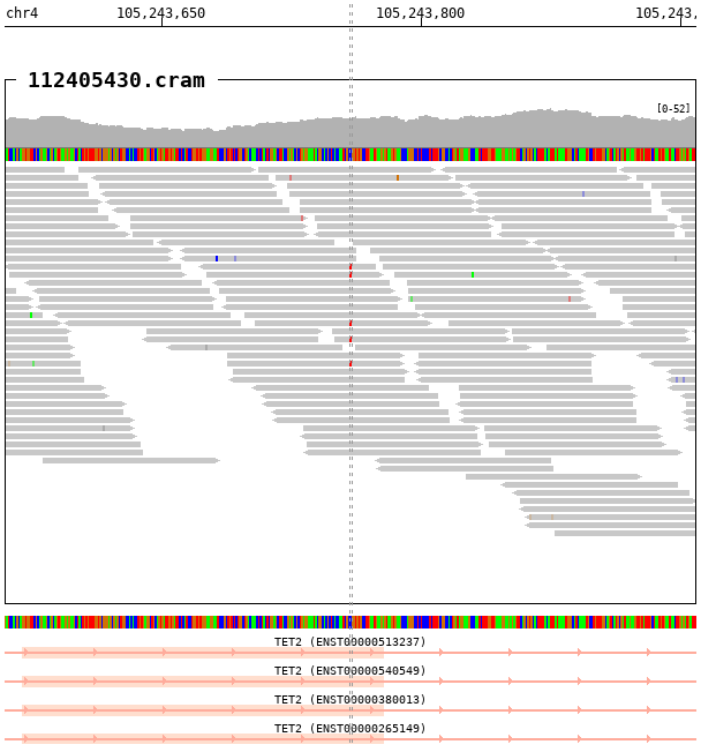
34.56. chr4_105243757_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
111100445	chr4_105243757_G/A	34	5	*TET2*	missense_variant



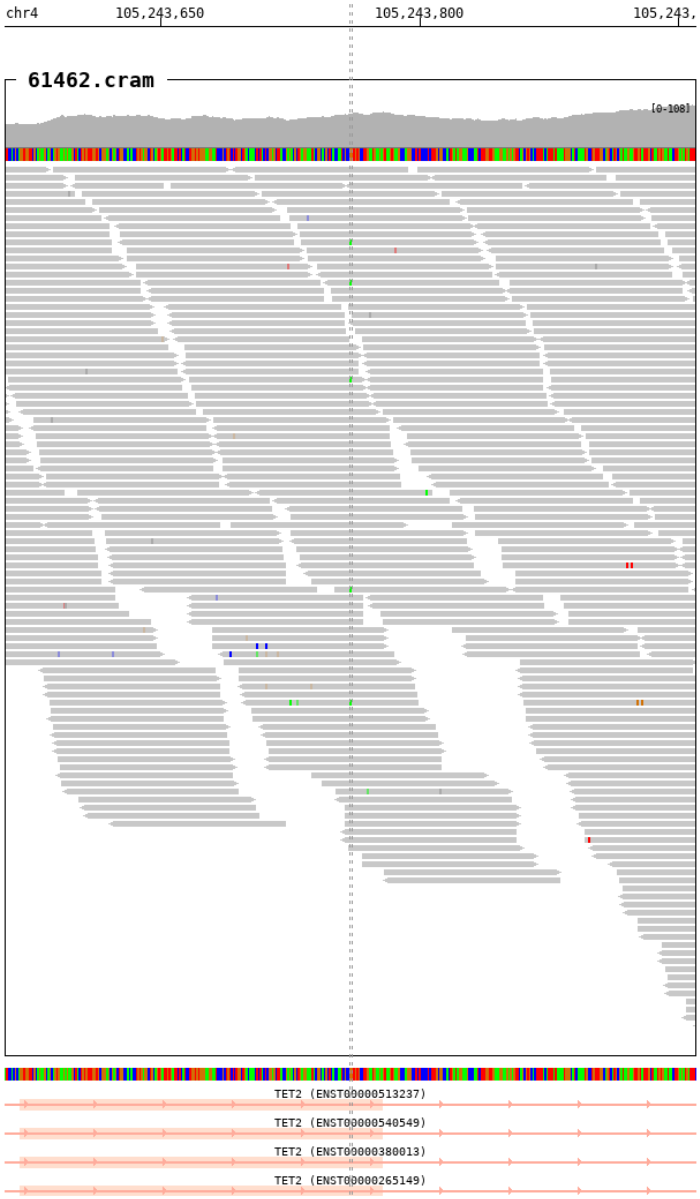
34.57. chr4_105243759_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112405430	chr4_105243759_C/T	28	5	*TET2*	missense_variant



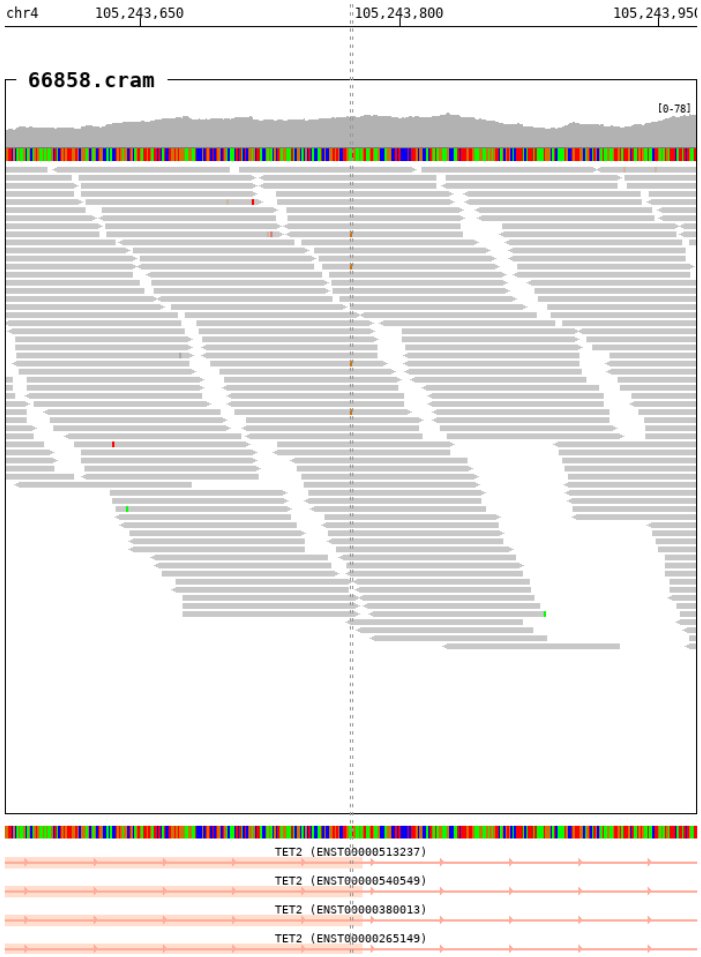
34.58. chr4_105243760_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
61462	chr4_105243760_G/A	72	5	*TET2*	missense_variant



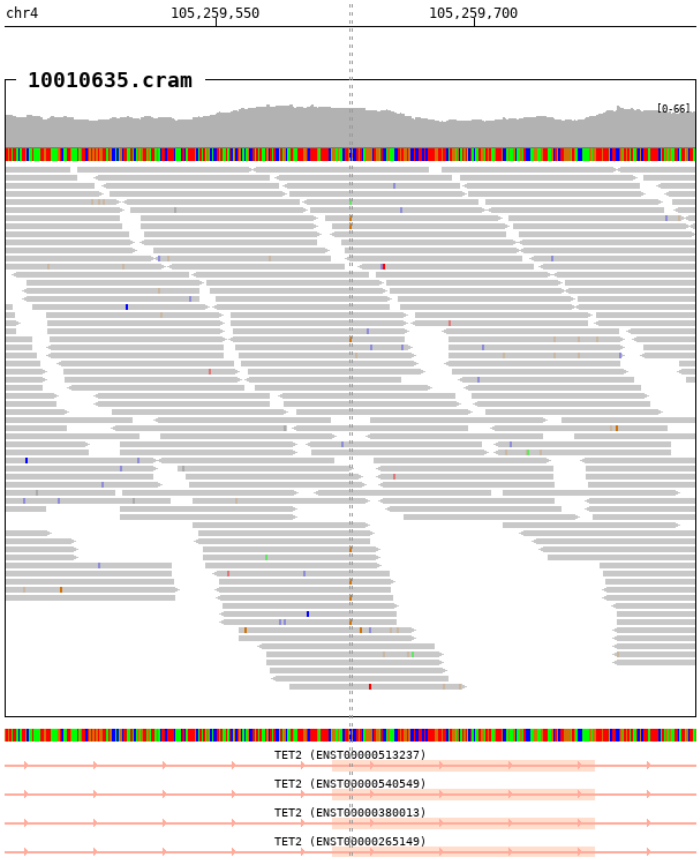
34.59. chr4_105243772_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
66858	chr4_105243772_A/G	50	4	*TET2*	missense_variant



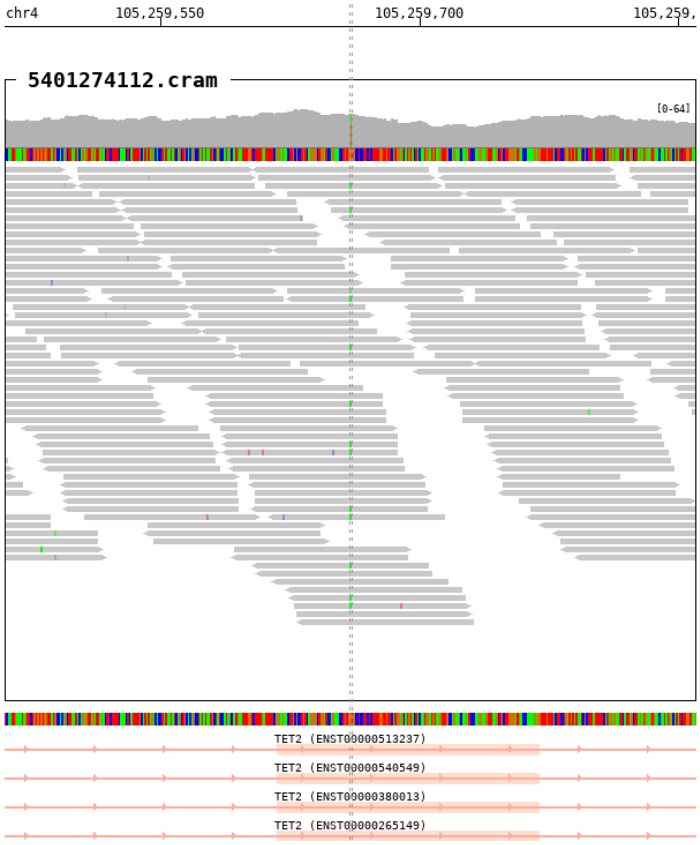
34.60. chr4_105259628_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10010635	chr4_105259628_C/G	48	7	*TET2*	missense_variant



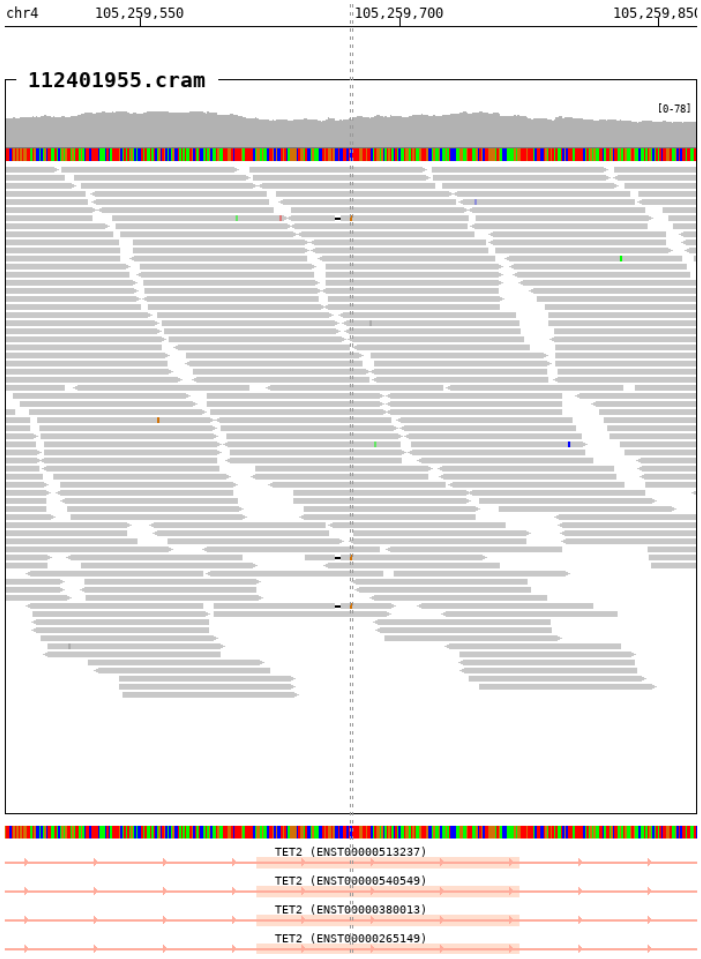
34.61. chr4_105259660_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
5401274112	chr4_105259660_G/A	35	13	*TET2*	missense_variant



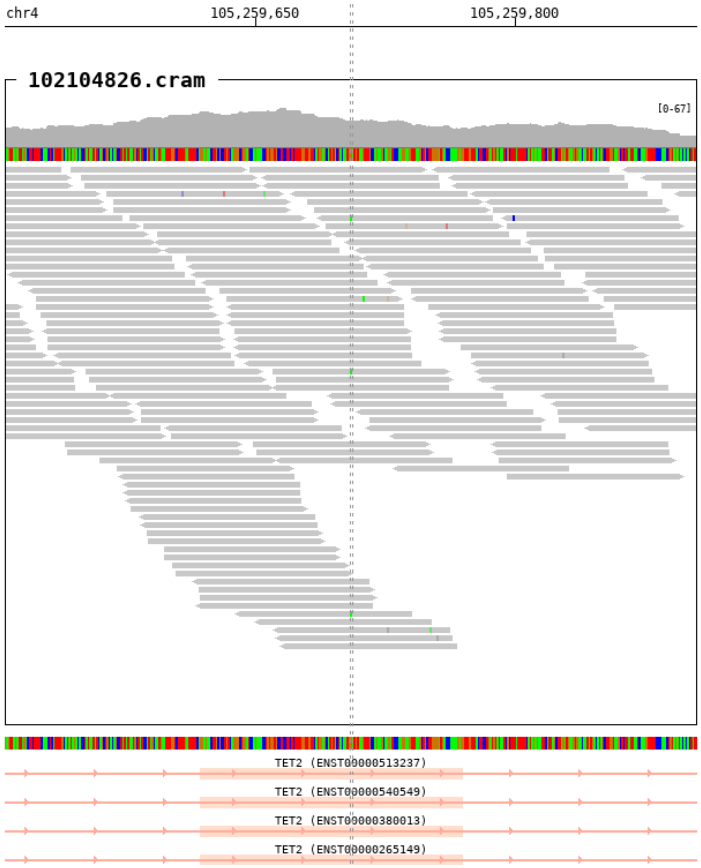
34.62. chr4_105259672_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112401955	chr4_105259672_C/G	46	3	*TET2*	missense_variant



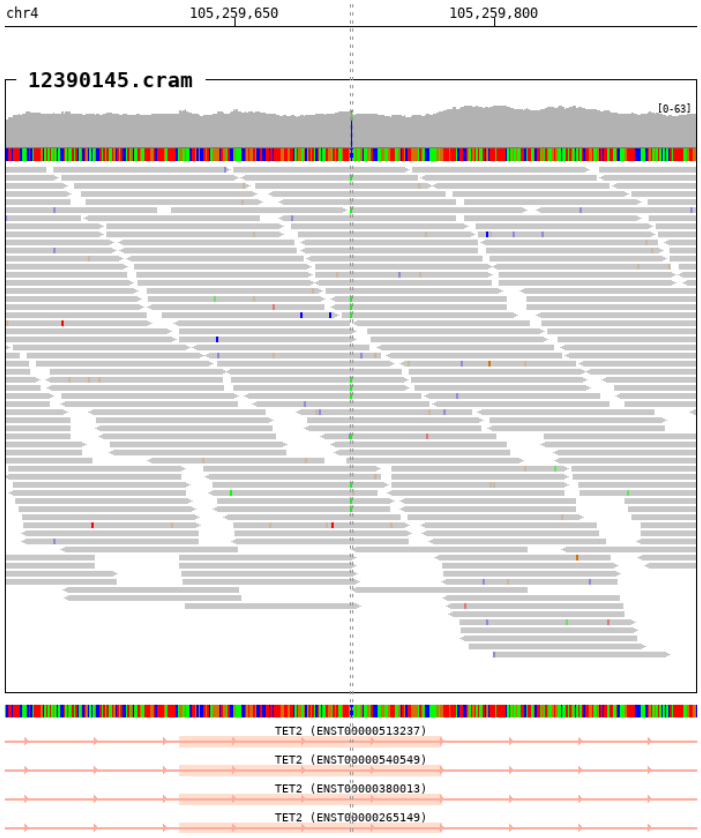
34.63. chr4_105259705_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102104826	chr4_105259705_G/A	38	3	*TET2*	missense_variant



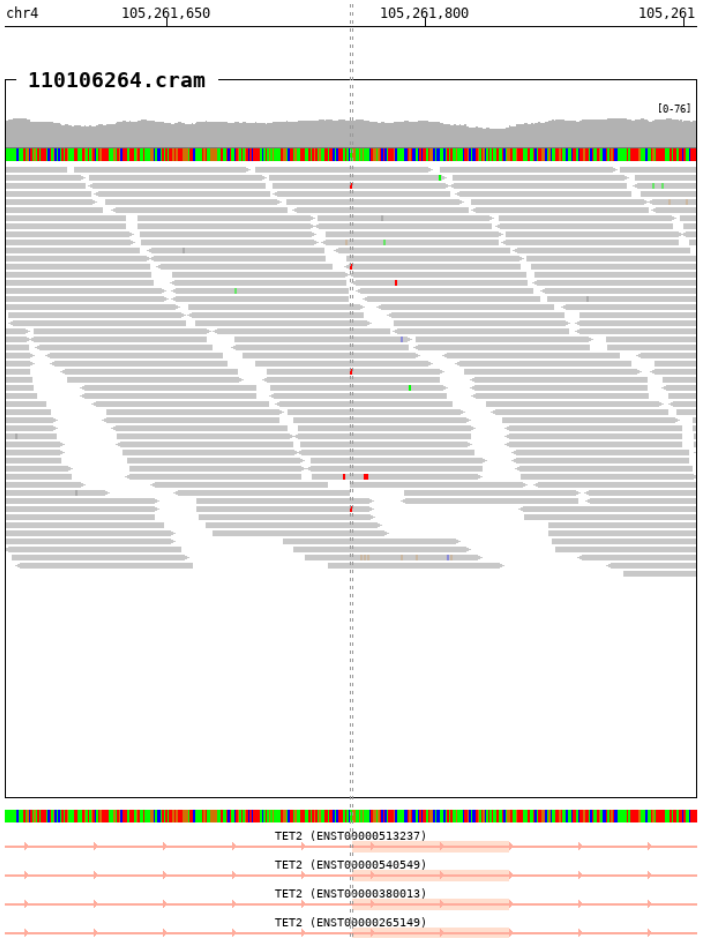
34.64. chr4_105259717_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12390145	chr4_105259717_C/A	36	12	*TET2*	missense_variant



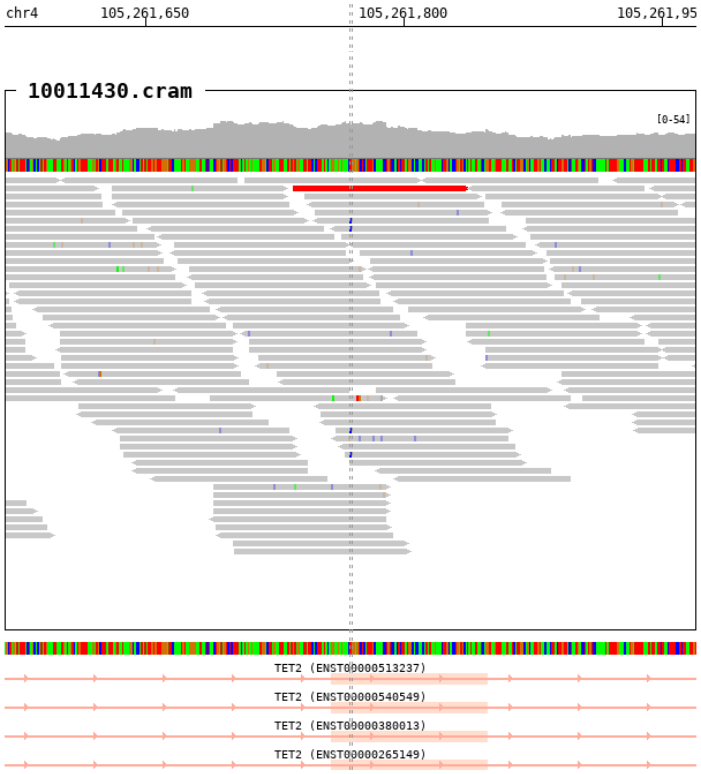
34.65. chr4_105261757_A/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110106264	chr4_105261757_A/T	37	4	*TET2*	splice_acceptor_variant



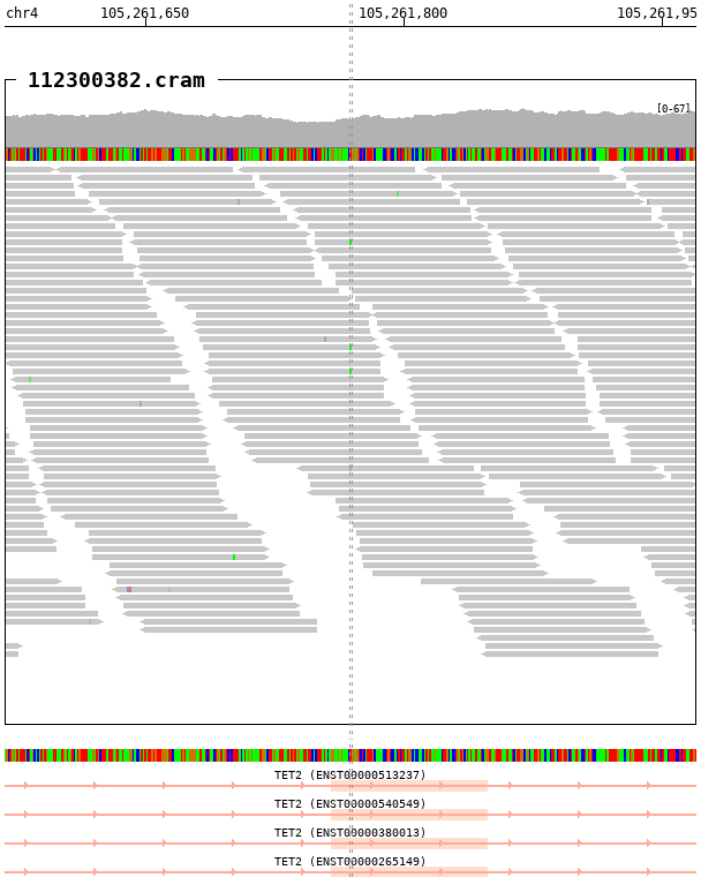
34.66. chr4_105261769_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10011430	chr4_105261769_T/C	34	4	*TET2*	missense_variant



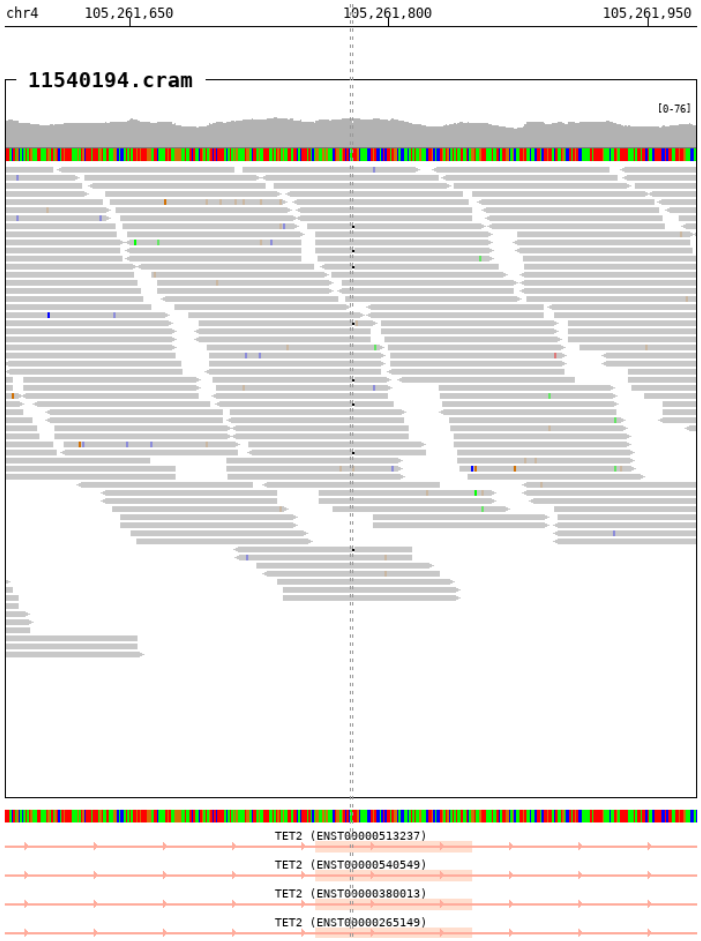
34.67. chr4_105261769_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112300382	chr4_105261769_T/A	37	3	*TET2*	missense_variant



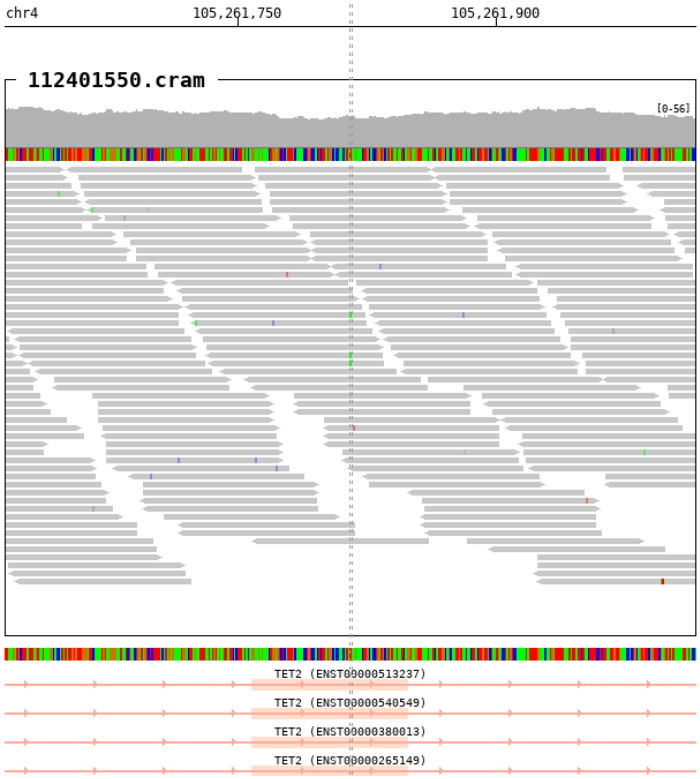
34.68. chr4_105261778_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11540194	chr4_105261778_T/-	41	8	*TET2*	frameshift_variant



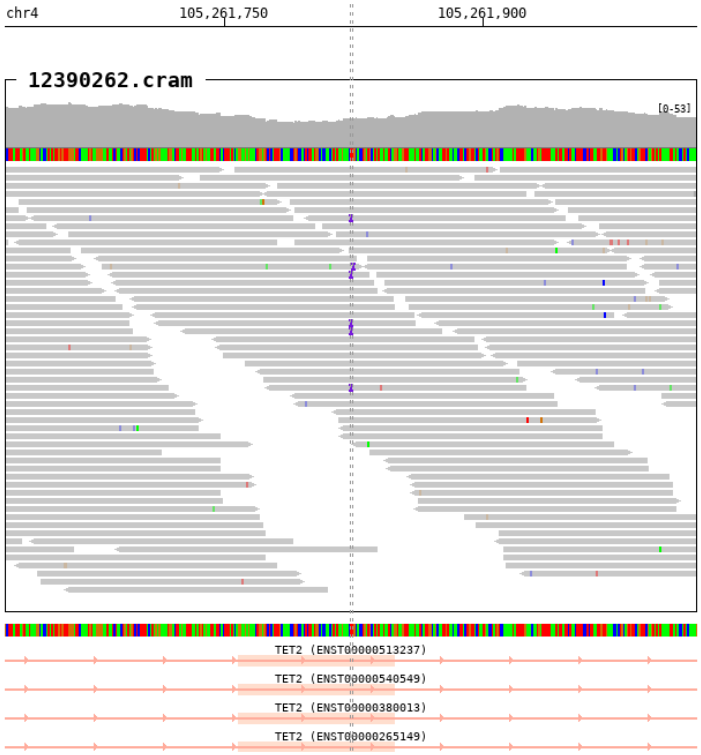
34.69. chr4_105261815_T/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112401550	chr4_105261815_T/A	33	3	*TET2*	stop_gained



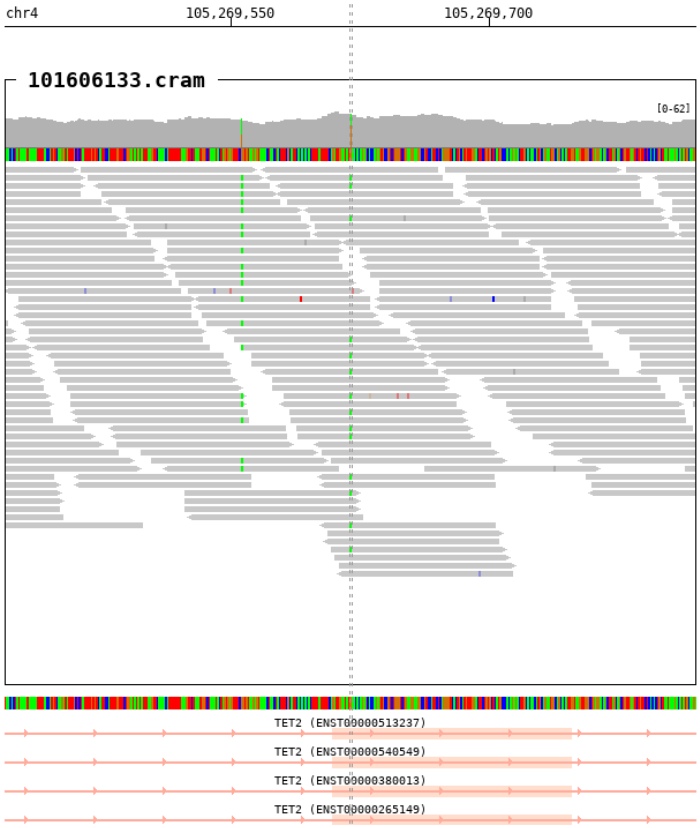
34.70. chr4_105261823_-/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12390262	chr4_105261823_-/T	29	6	*TET2*	frameshift_variant



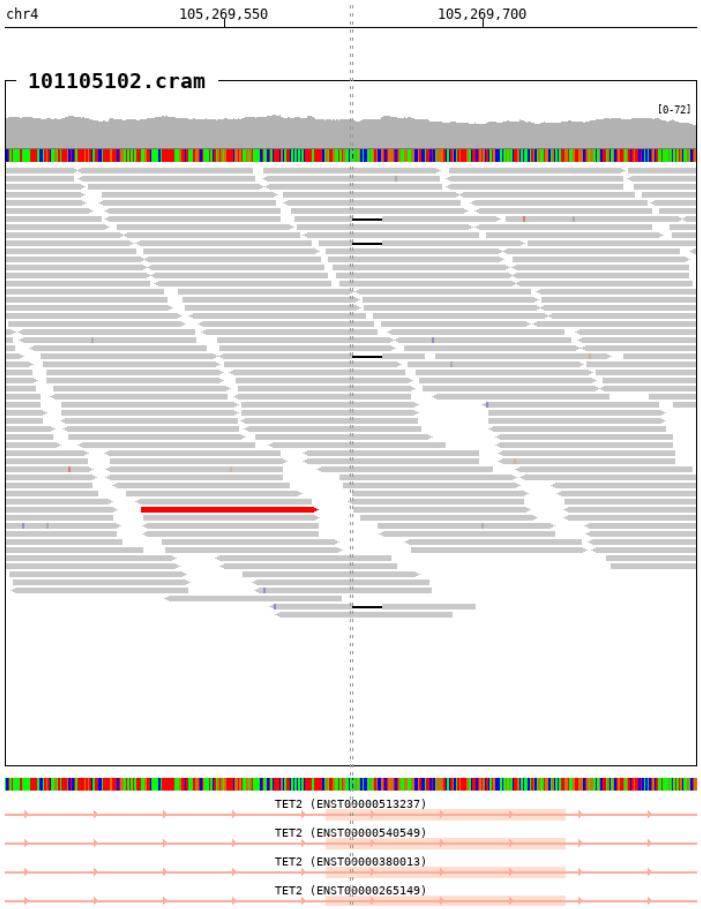
34.71. chr4_105269619_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101606133	chr4_105269619_G/A	31	14	*TET2*	missense_variant



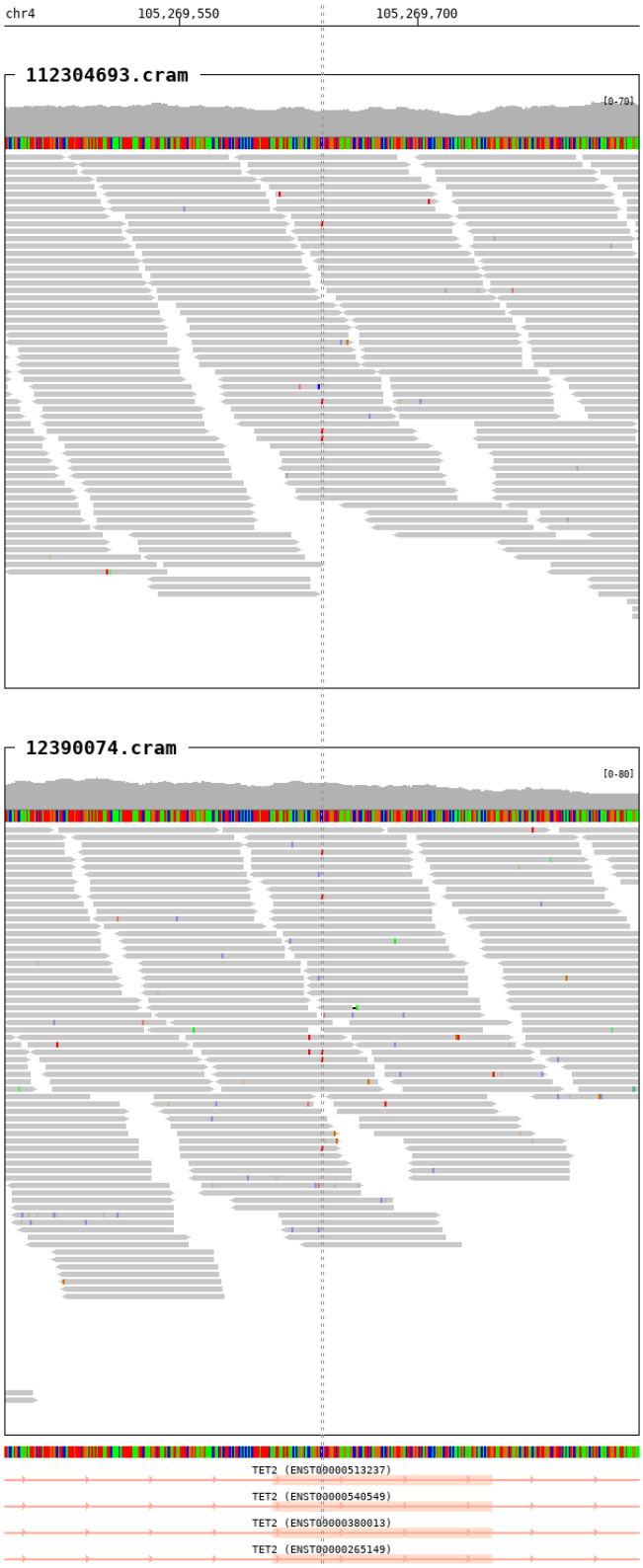
34.72. chr4_105269623_CAGAGCACCAGAGTGCC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101105102	chr4_105269623_CAGAGCACCAGAGTGCC/-	51	5	*TET2*	frameshift_variant



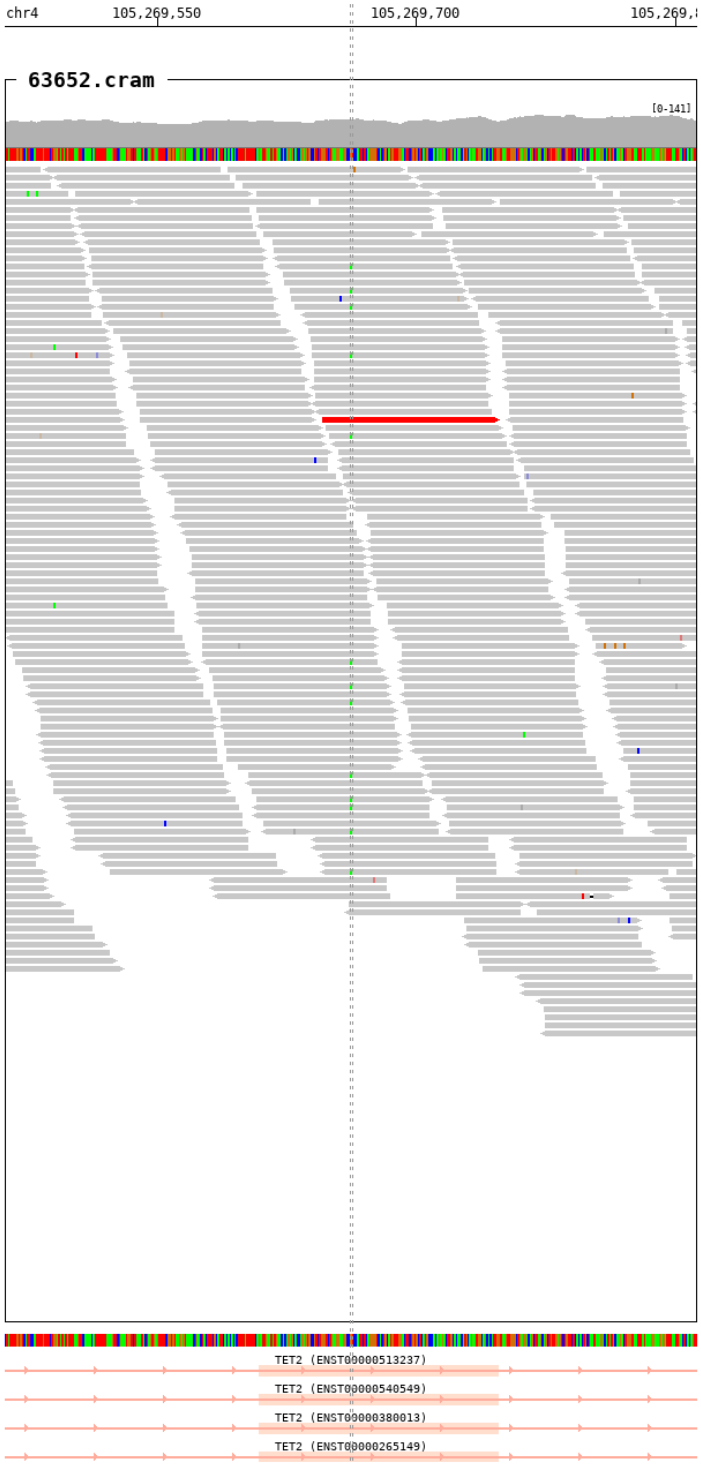
34.73. chr4_105269640_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112304693	chr4_105269640_C/T	38	4	*TET2*	missense_variant
12390074	chr4_105269640_C/T	42	5	*TET2*	missense_variant



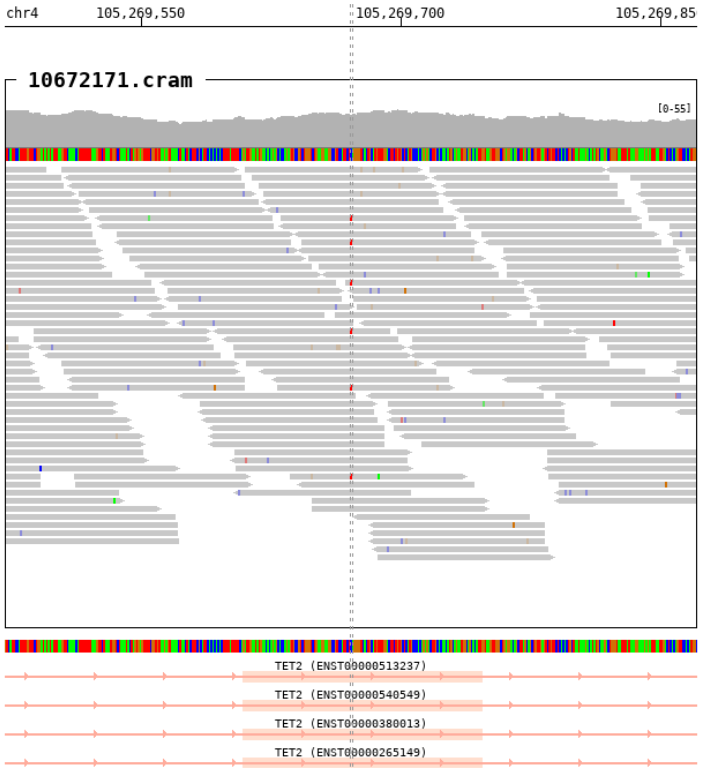
34.74. chr4_105269662_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
63652	chr4_105269662_G/A	71	13	*TET2*	missense_variant



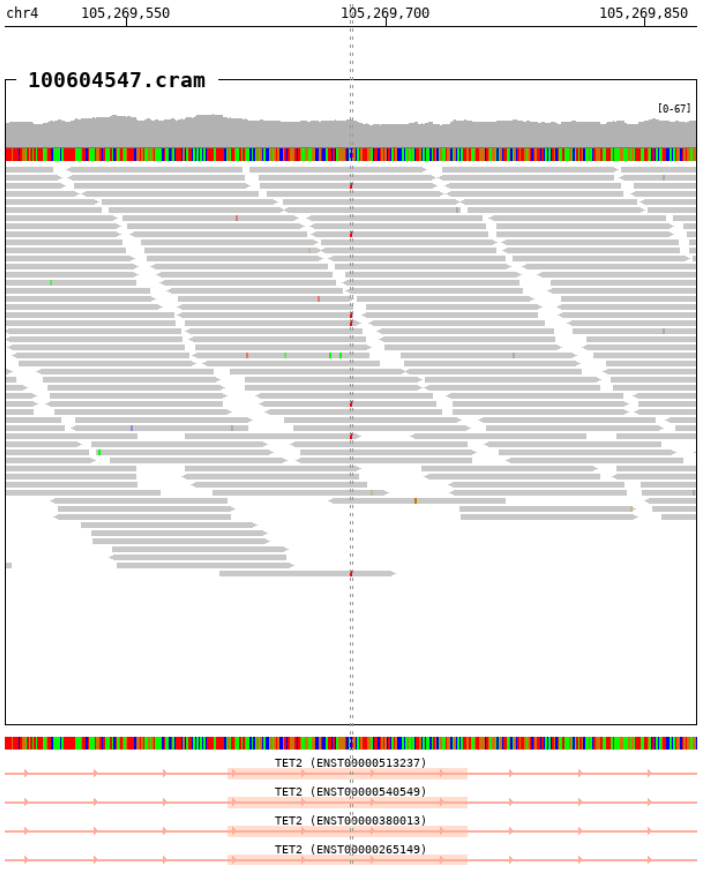
34.75. chr4_105269671_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10672171	chr4_105269671_C/T	33	6	*TET2*	missense_variant



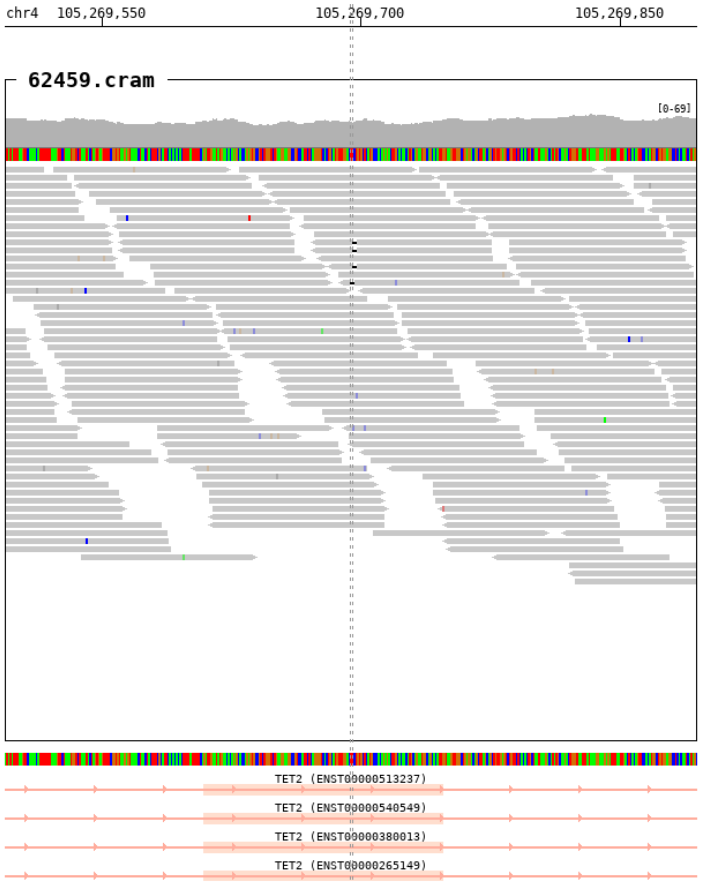
34.76. chr4_105269680_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100604547	chr4_105269680_C/T	34	7	*TET2*	missense_variant



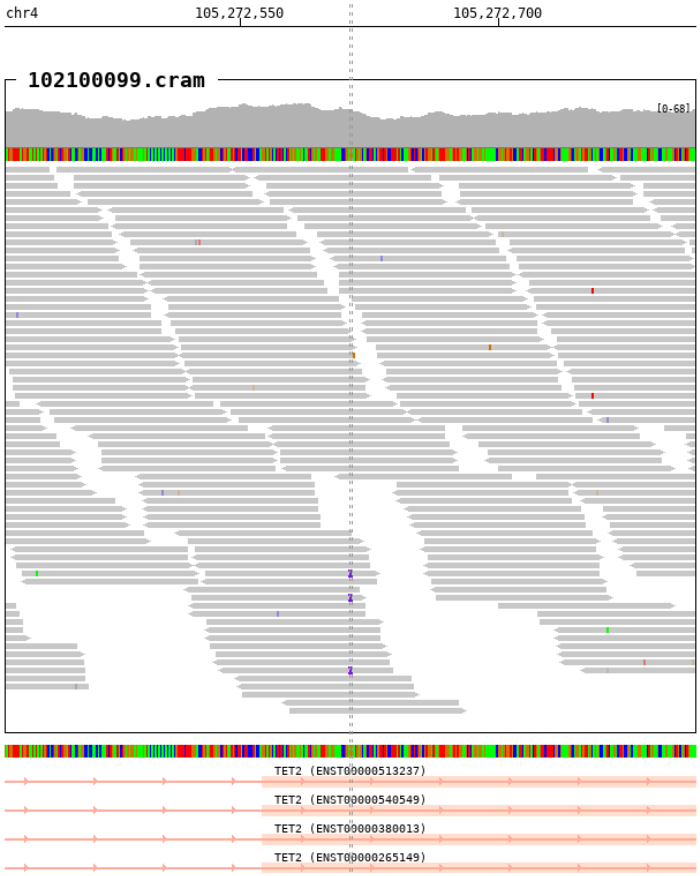
34.77. chr4_105269694_TC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
62459	chr4_105269694_TC/-	38	4	*TET2*	frameshift_variant



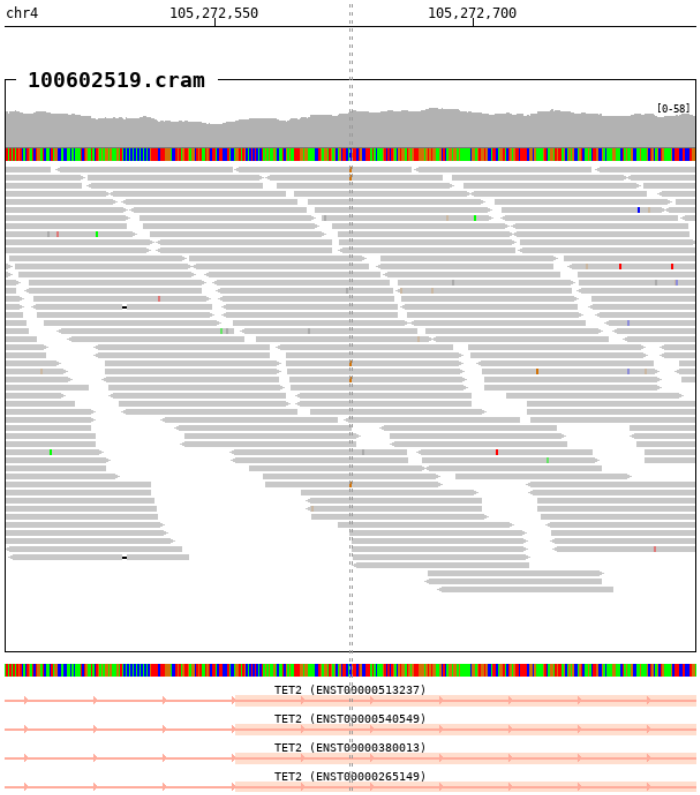
34.78. chr4_105272614_-/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102100099	chr4_105272614_-/G	46	4	*TET2*	frameshift_variant



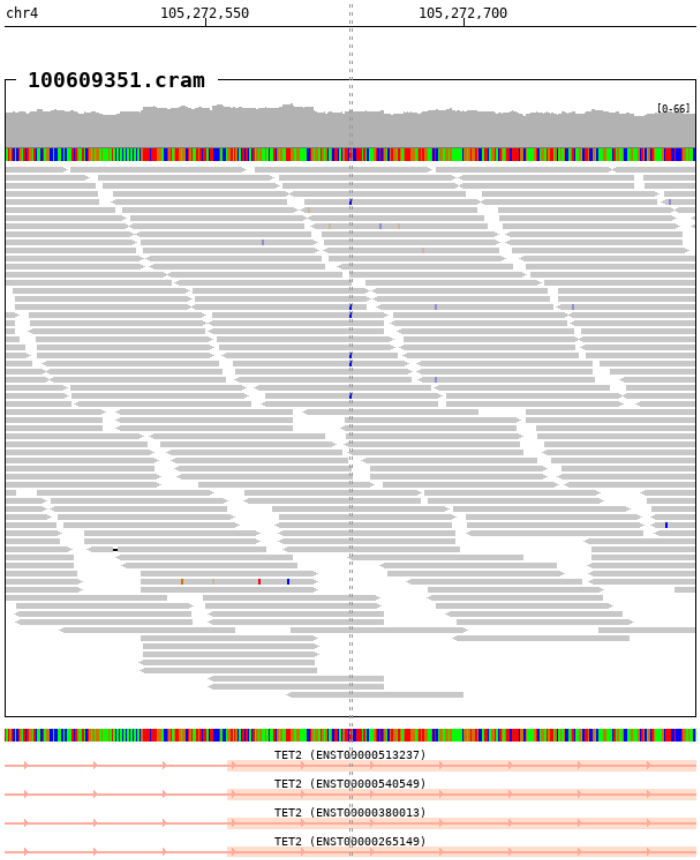
34.79. chr4_105272629_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100602519	chr4_105272629_C/G	41	5	*TET2*	missense_variant



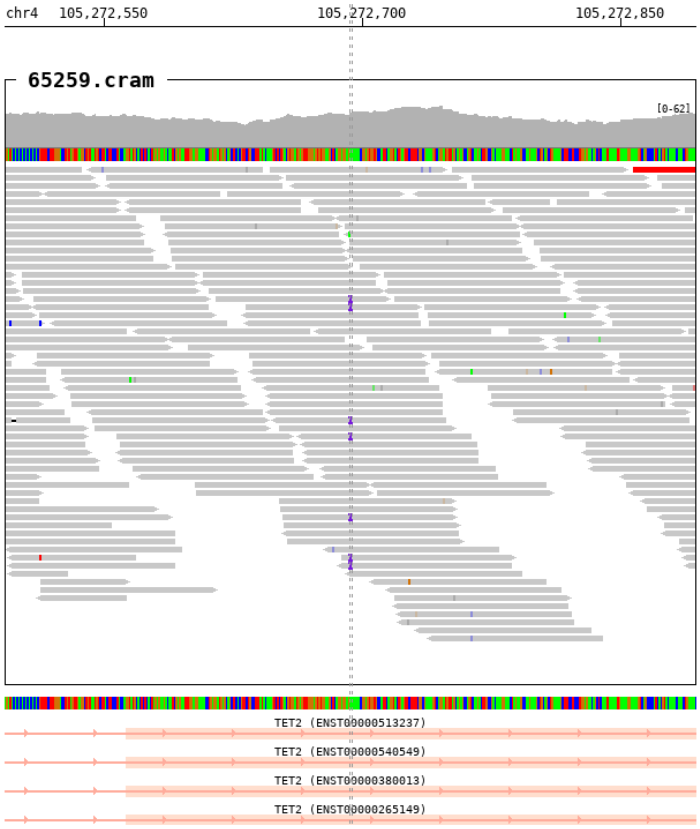
34.80. chr4_105272634_T/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100609351	chr4_105272634_T/C	44	6	*TET2*	missense_variant



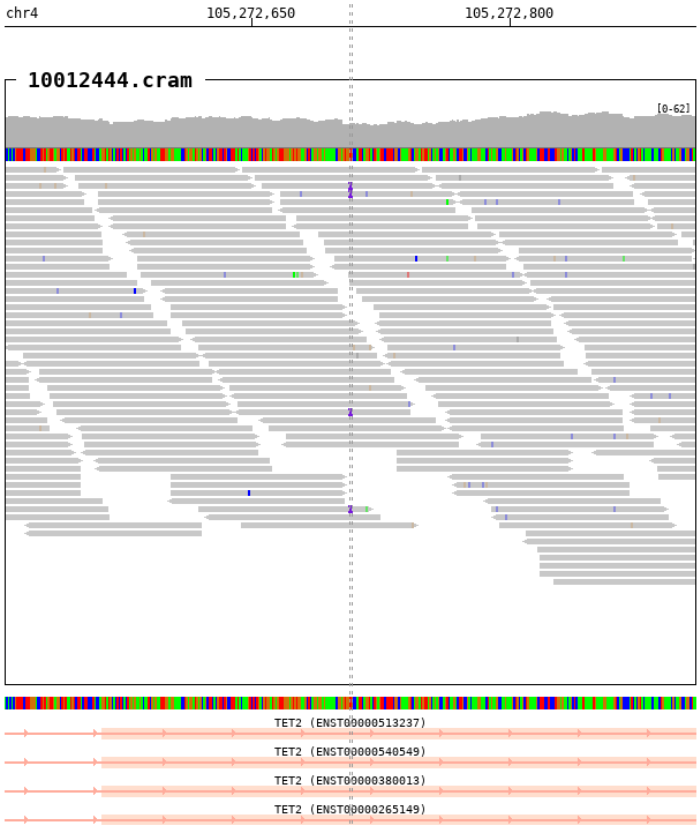
34.81. chr4_105272693_-/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
65259	chr4_105272693_-/A	35	9	*TET2*	frameshift_variant



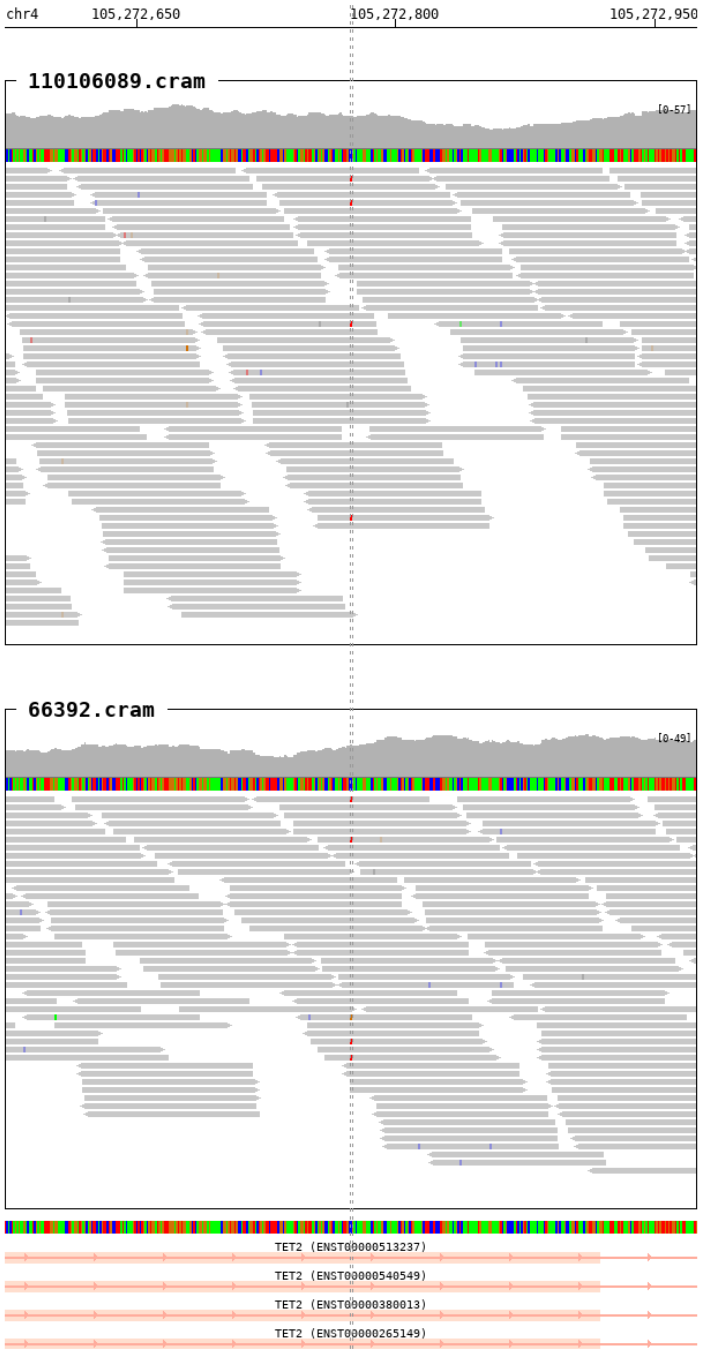
34.82. chr4_105272707_-/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10012444	chr4_105272707_-/T	28	4	*TET2*	frameshift_variant



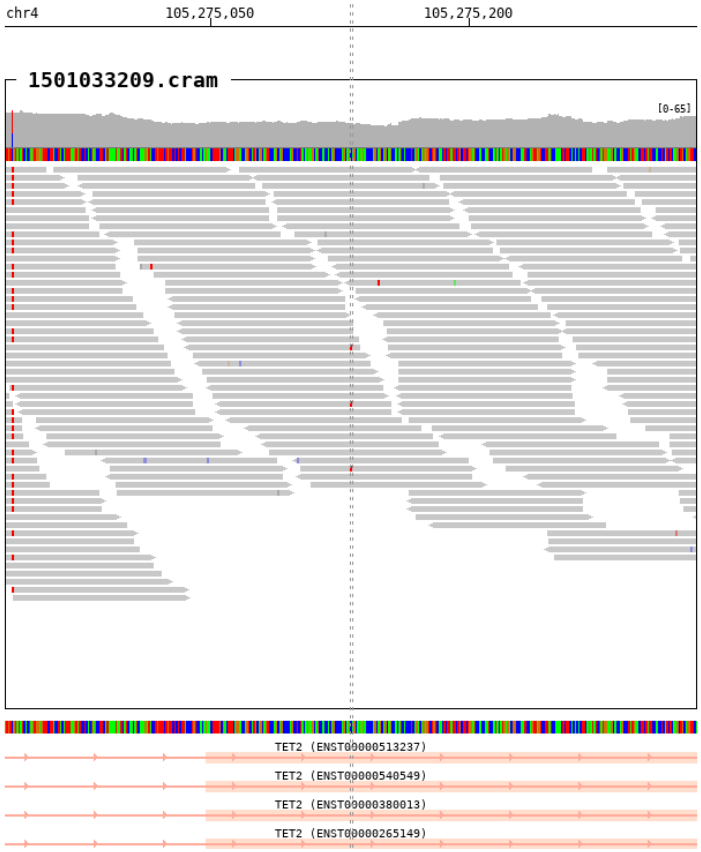
34.83. chr4_105272774_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110106089	chr4_105272774_C/T	36	4	*TET2*	stop_gained
66392	chr4_105272774_C/T	30	4	*TET2*	stop_gained



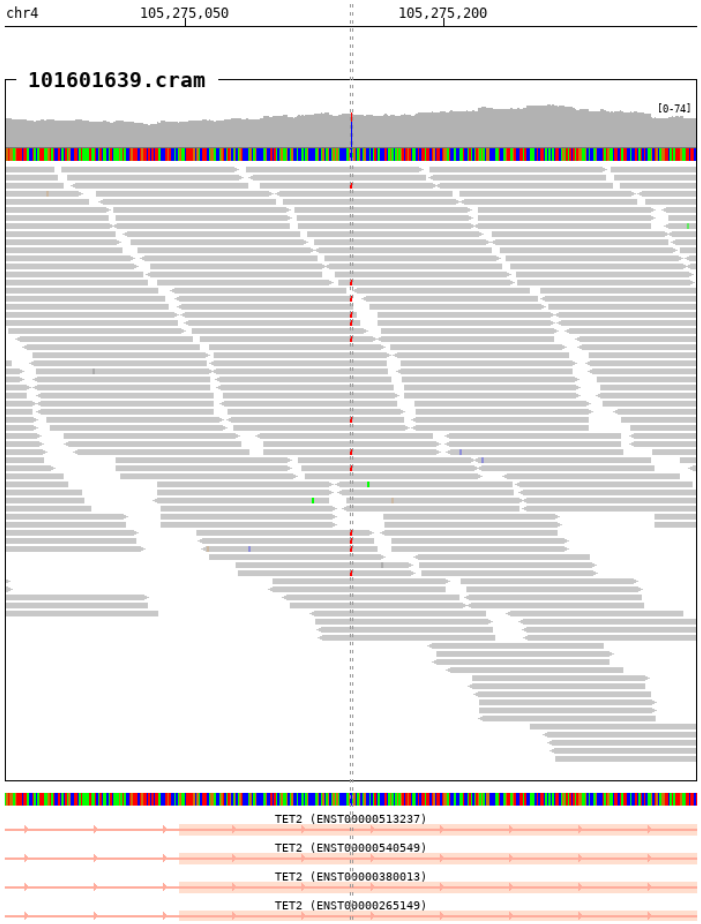
34.84. chr4_105275131_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
1501033209	chr4_105275131_C/T	32	3	*TET2*	stop_gained



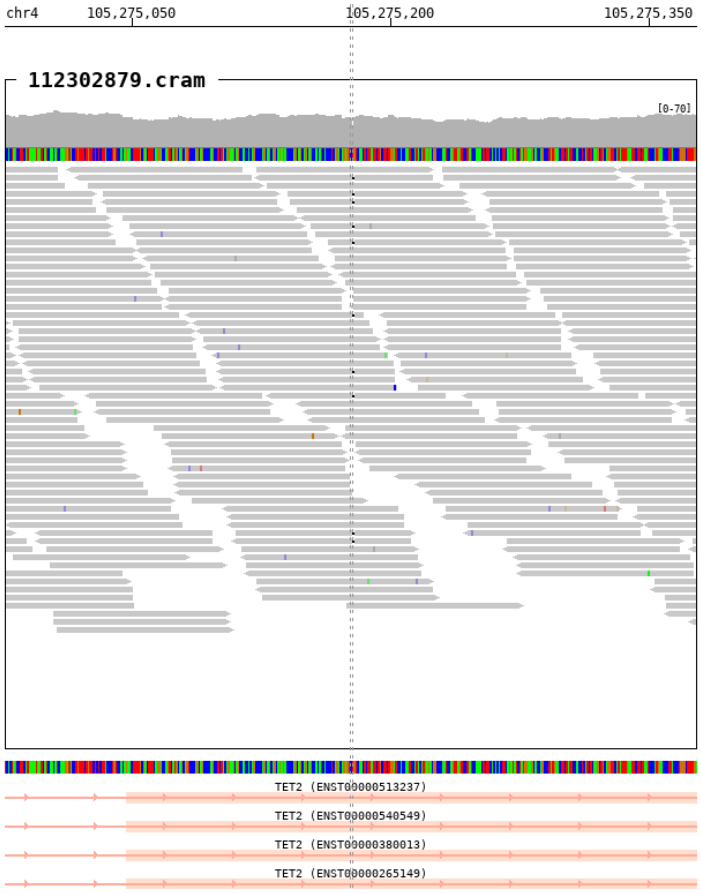
34.85. chr4_105275146_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101601639	chr4_105275146_C/T	44	13	*TET2*	stop_gained



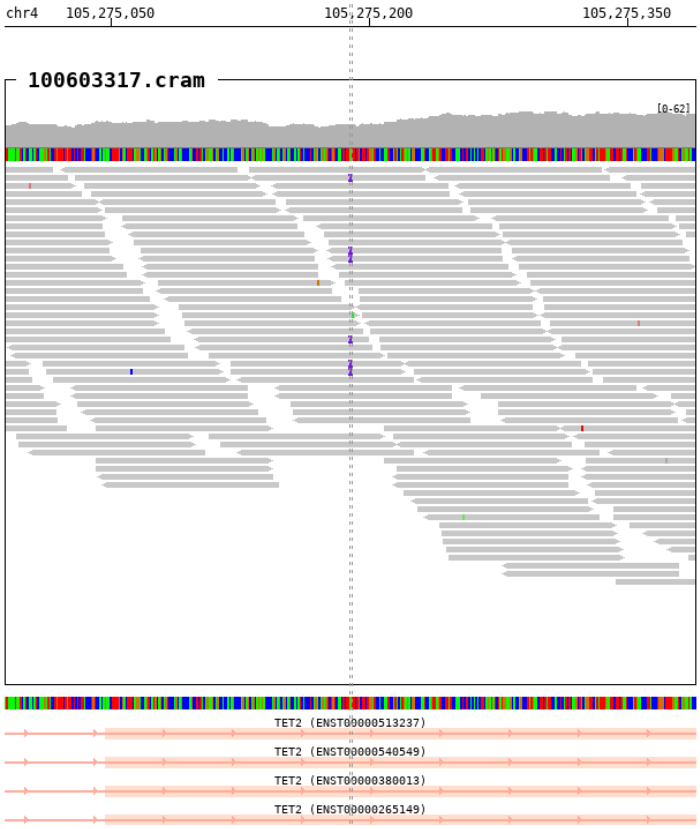
34.86. chr4_105275177_T/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112302879	chr4_105275177_T/-	34	10	*TET2*	frameshift_variant



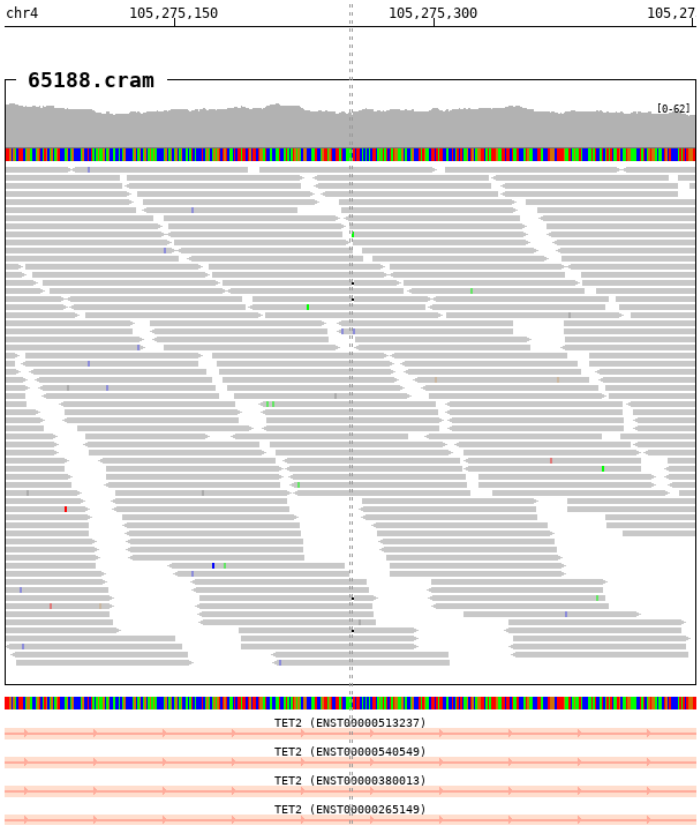
34.87. chr4_105275189_-/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
100603317	chr4_105275189_-/A	25	6	*TET2*	stop_gained



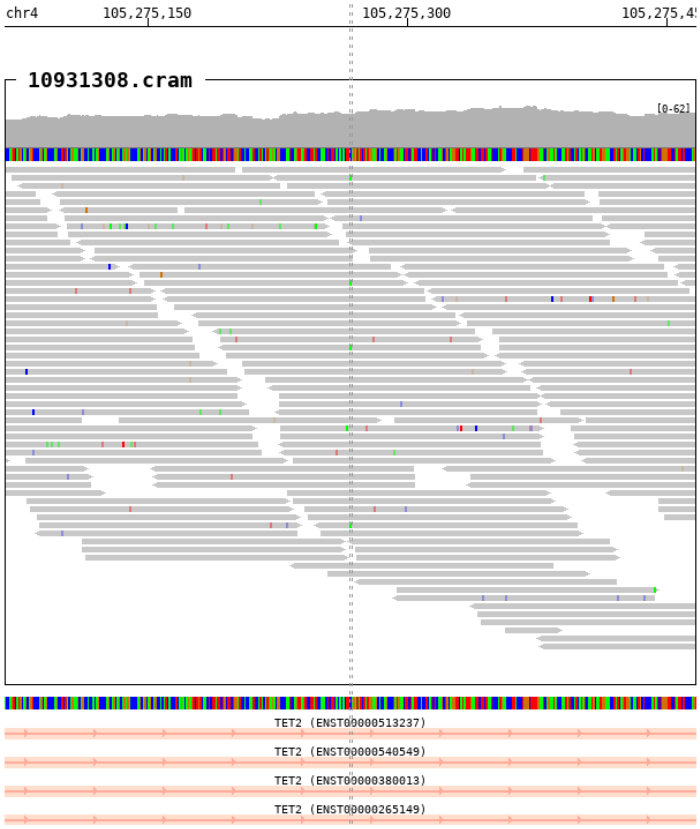
34.88. chr4_105275252_C/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
65188	chr4_105275252_C/-	43	5	*TET2*	frameshift_variant



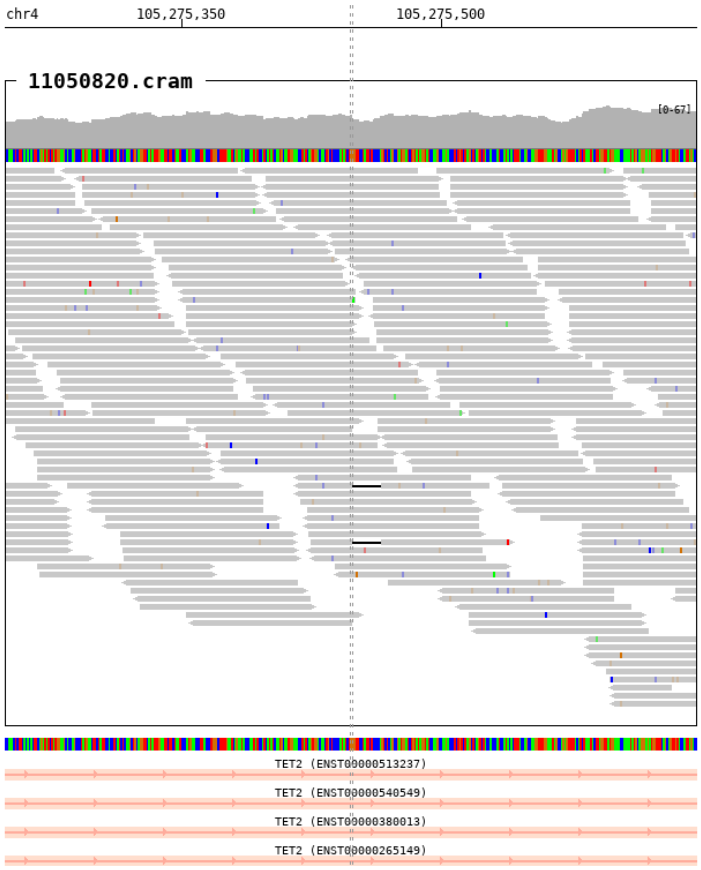
34.89. chr4_105275267_C/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10931308	chr4_105275267_C/A	42	4	*TET2*	stop_gained



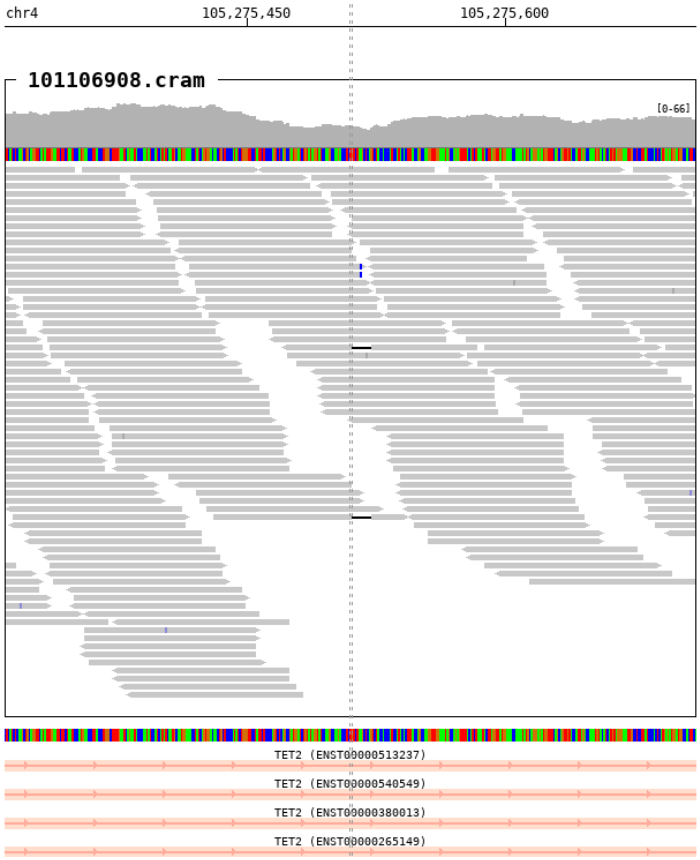
34.90. chr4_105275448_GGTTCCTATTCTCCCC/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11050820	chr4_105275448_GGTTCCTATTCTCCCC/-	53	6	*TET2*	frameshift_variant



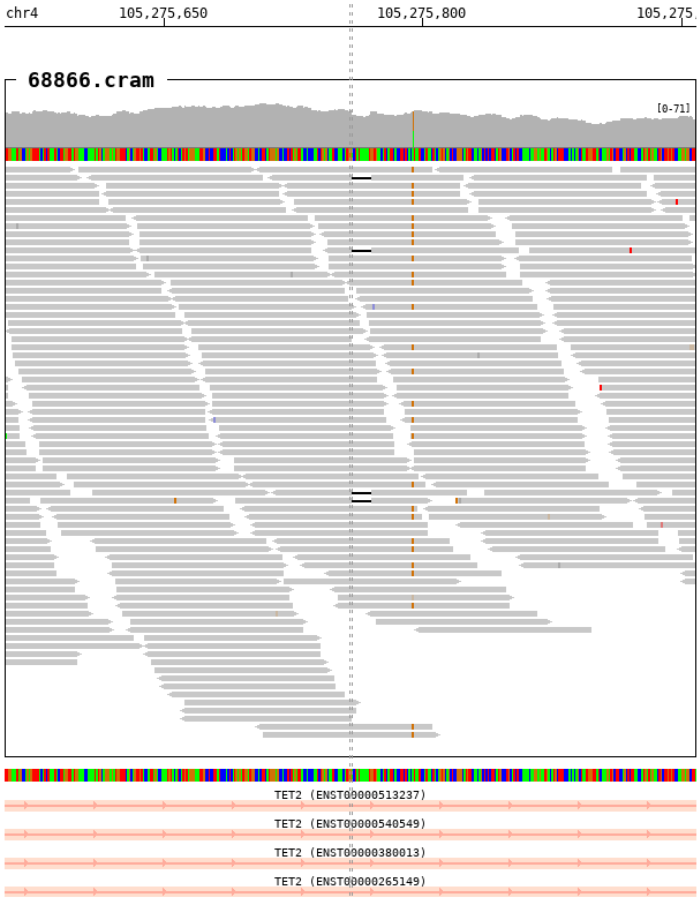
34.91. chr4_105275510_GTCTAAGCTCA/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101106908	chr4_105275510_GTCTAAGCTCA/-	28	8	*TET2*	frameshift_variant



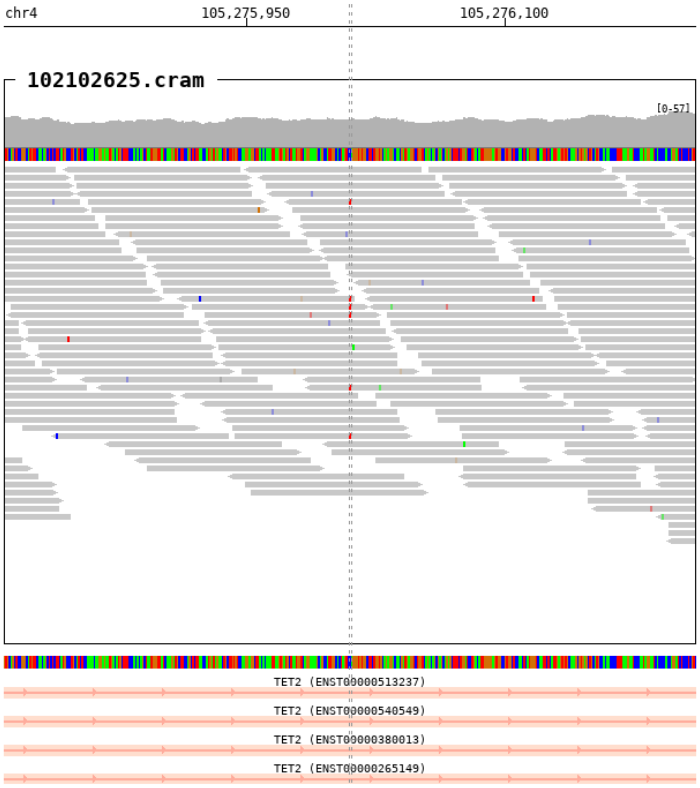
34.92. chr4_105275758_ACTATAAAAAT/-

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
68866	chr4_105275758_ACTATAAAAAT/-	56	7	*TET2*	frameshift_variant



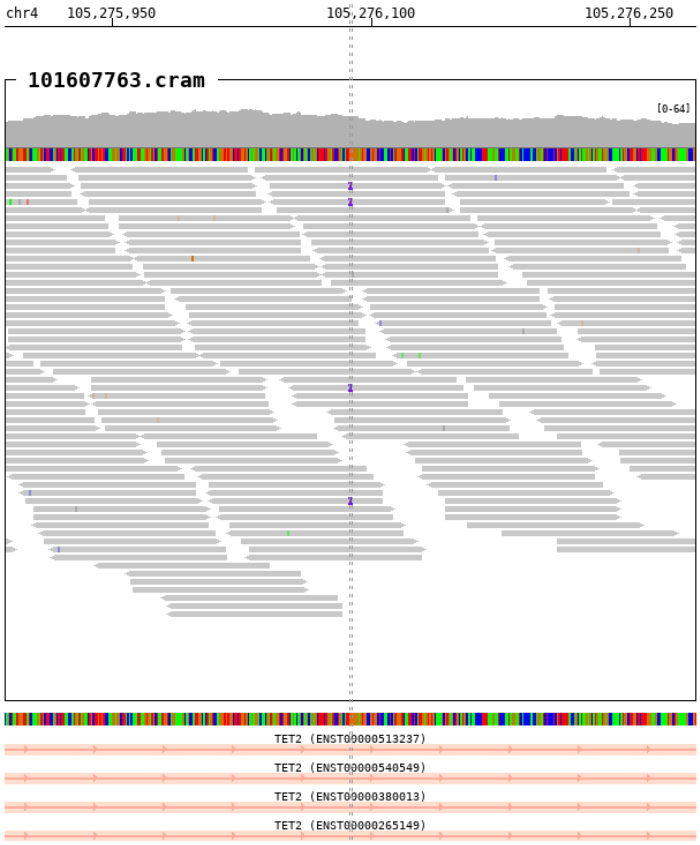
34.93. chr4_105276010_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102102625	chr4_105276010_C/T	29	6	*TET2*	stop_gained



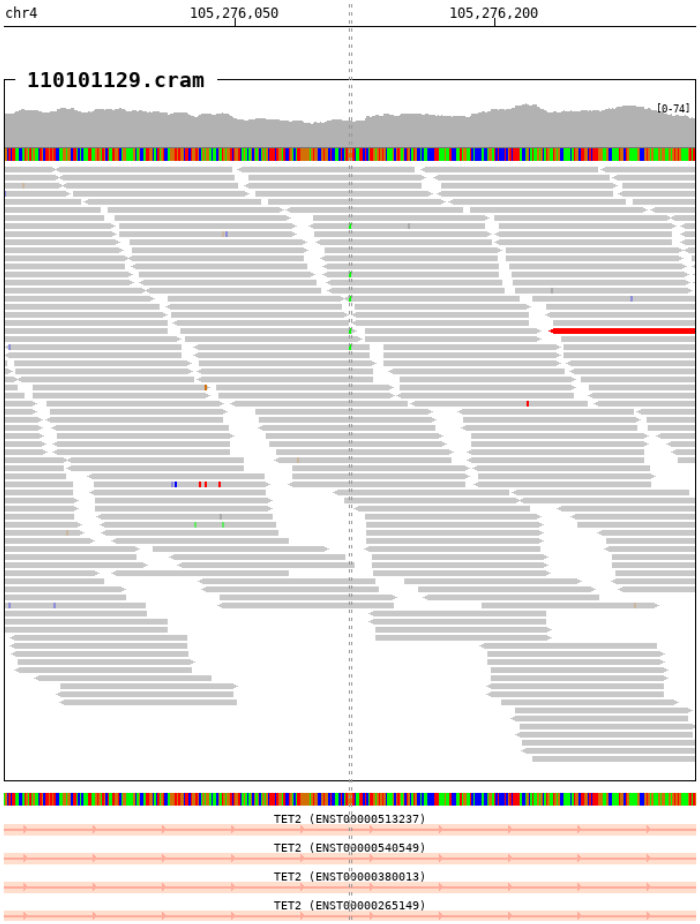
34.94. chr4_105276088_-/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101607763	chr4_105276088_-/G	38	5	*TET2*	frameshift_variant



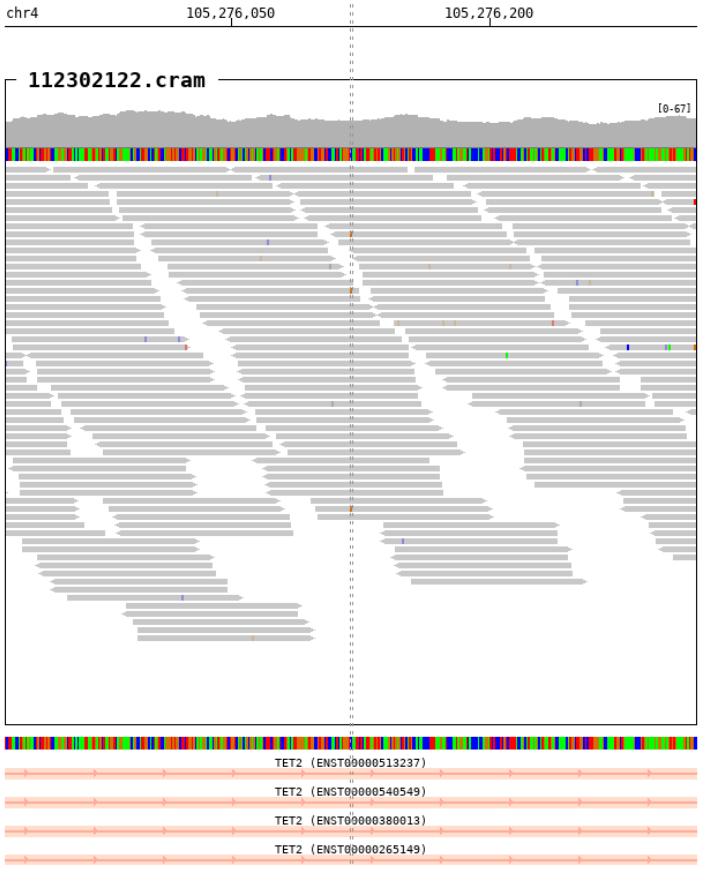
34.95. chr4_105276116_G/A

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
110101129	chr4_105276116_G/A	39	5	*TET2*	missense_variant



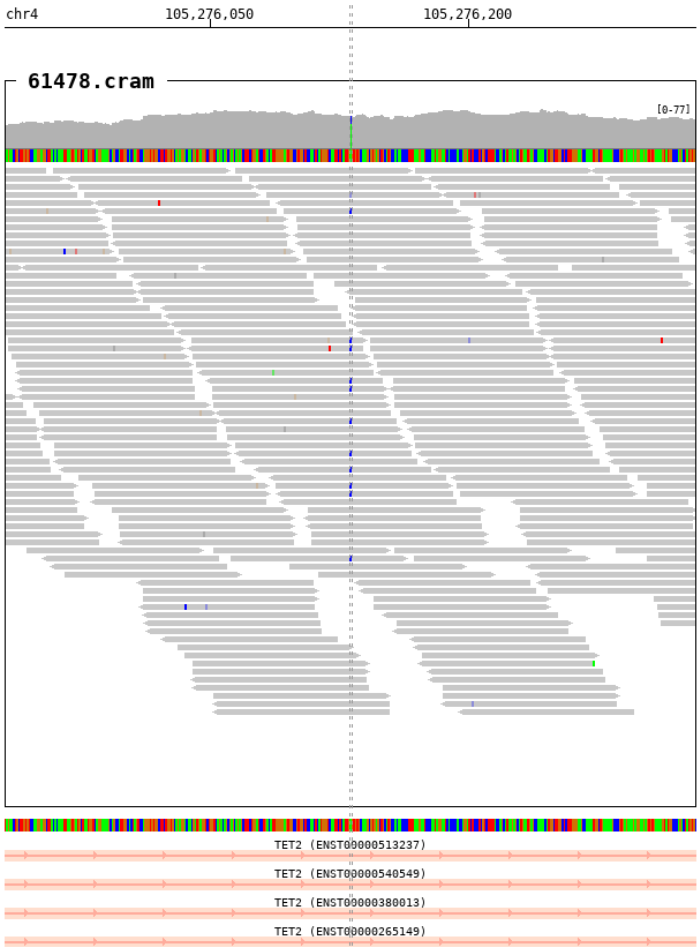
34.96. chr4_105276119_C/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
112302122	chr4_105276119_C/G	35	3	*TET2*	stop_gained



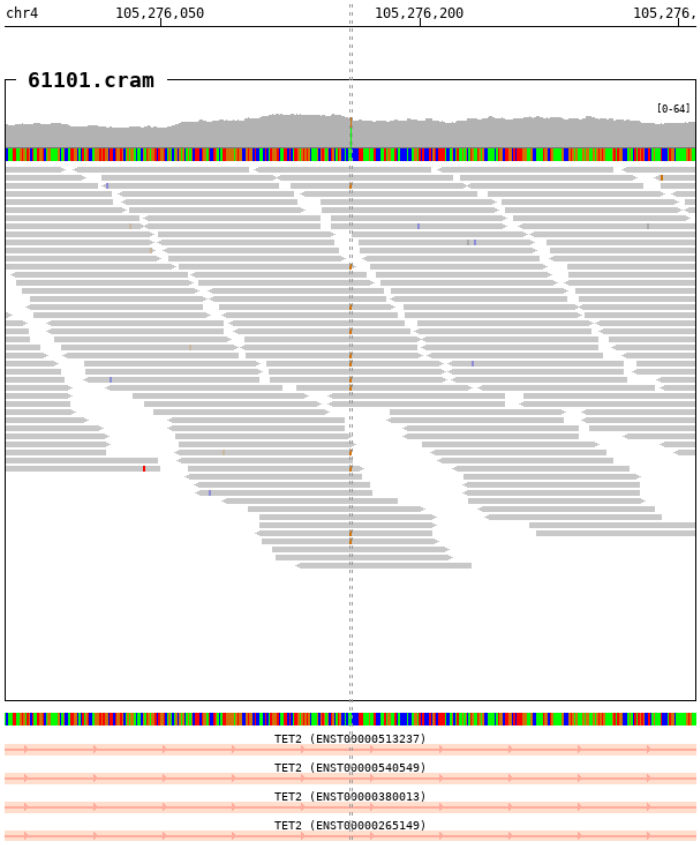
34.97. chr4_105276131_A/C

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
61478	chr4_105276131_A/C	41	10	*TET2*	missense_variant



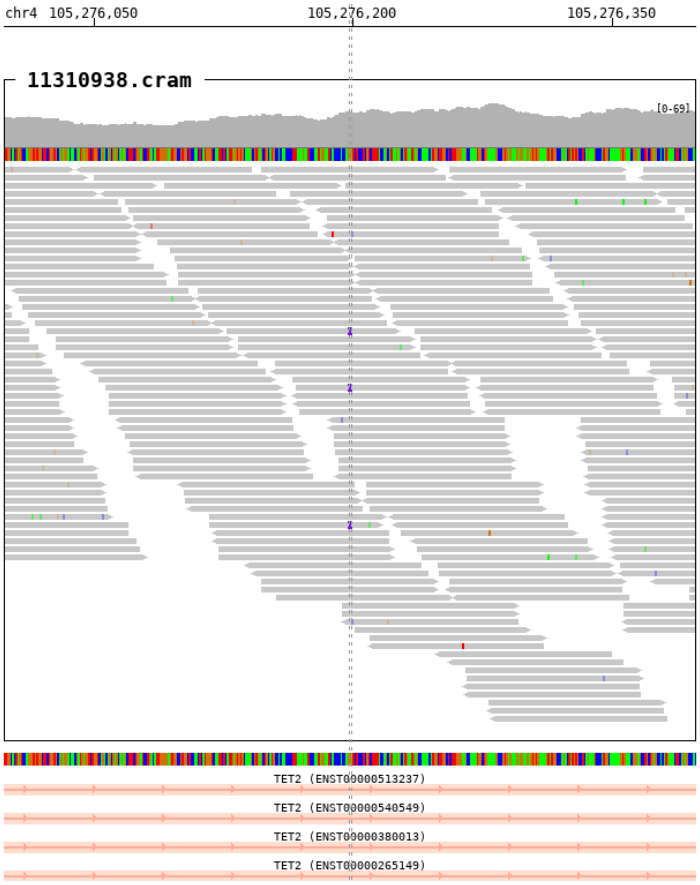
34.98. chr4_105276160_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
61101	chr4_105276160_A/G	30	11	*TET2*	missense_variant



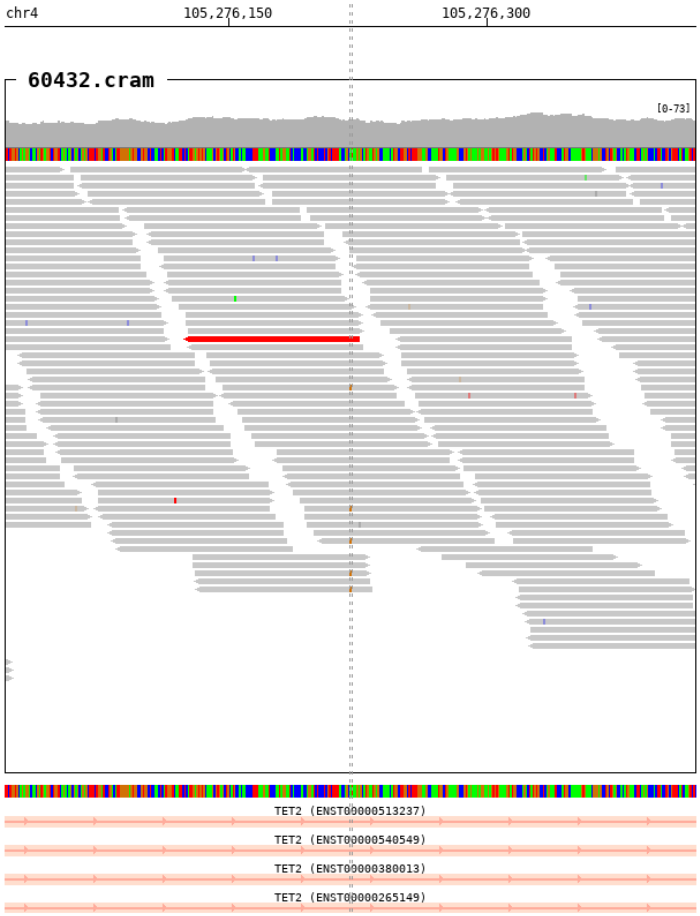
34.99. chr4_105276198_-/GA

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
11310938	chr4_105276198_-/GA	47	3	*TET2*	frameshift_variant



34.100. chr4_105276221_A/G

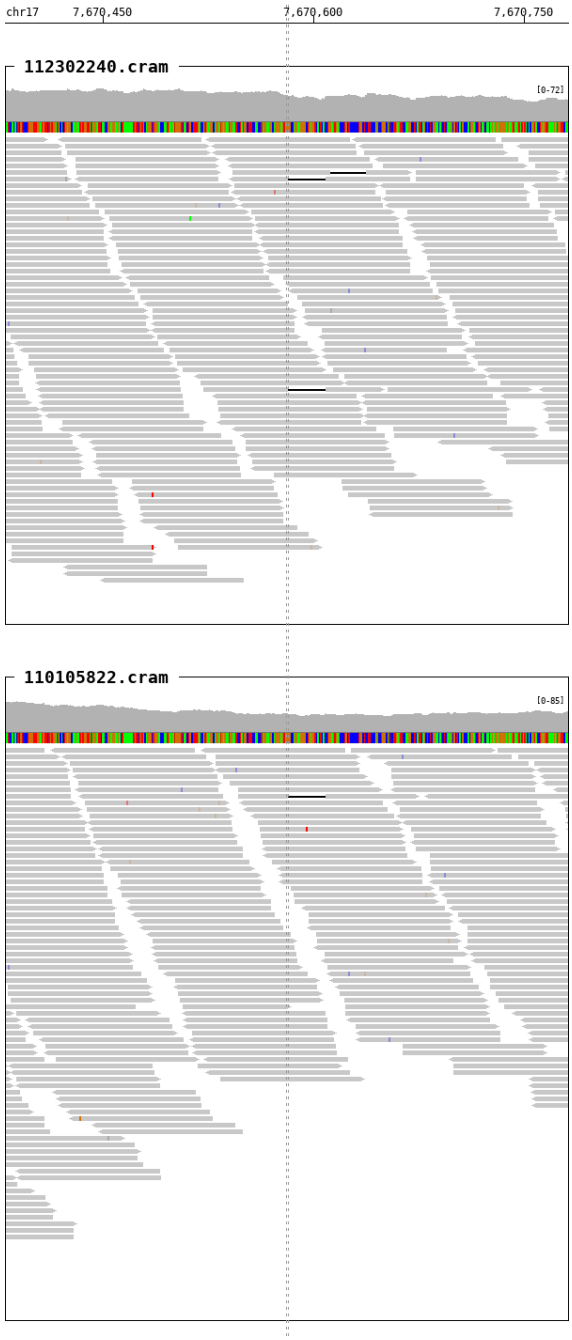
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
60432	chr4_105276221_A/G	41	5	*TET2*	missense_variant

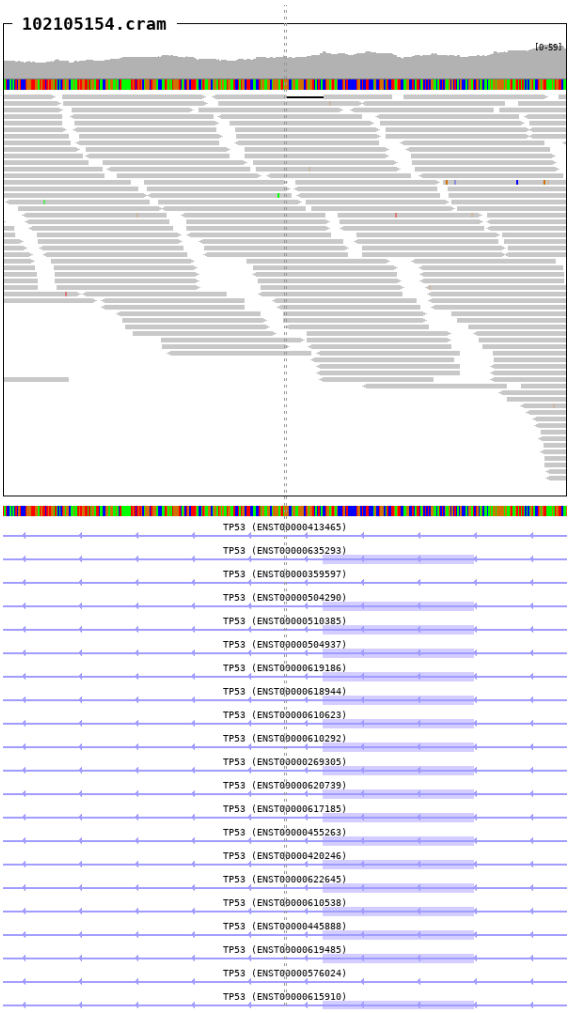


35. *TP53*

35.1. chr17_7670581_GGCCAGGAAGGGGCTGAGGTCACTCA/-

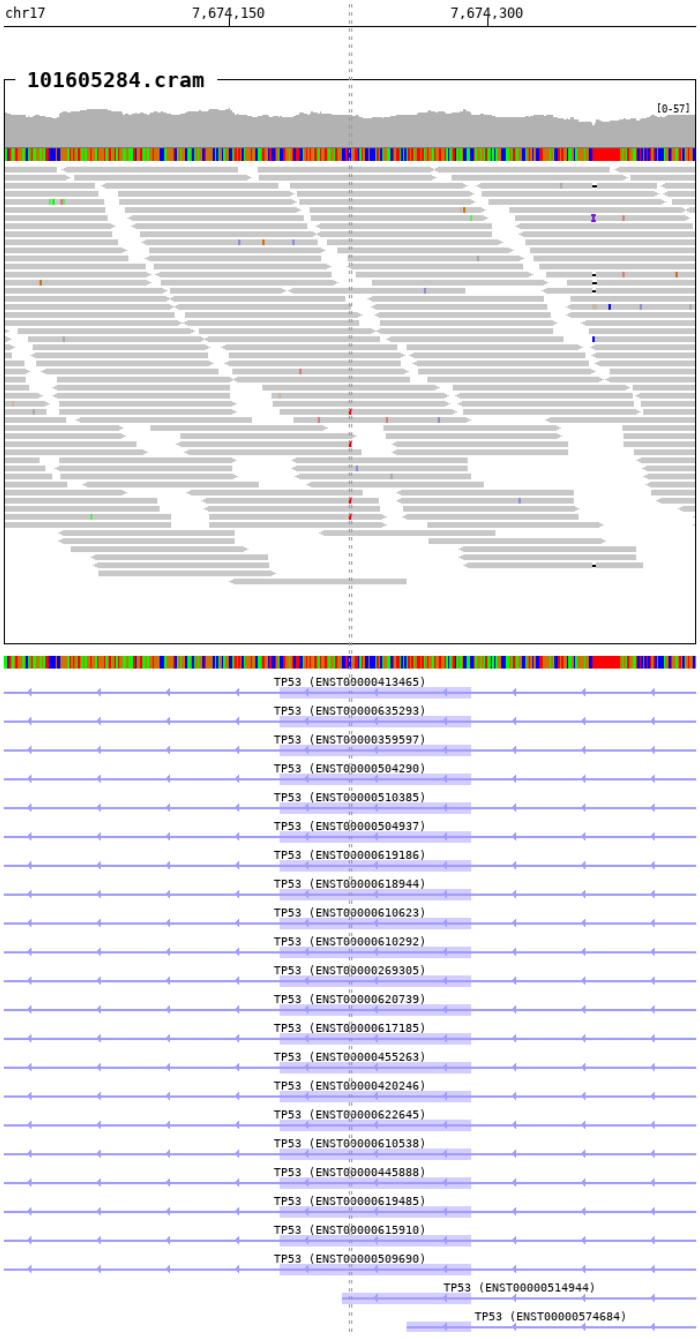
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
102105154	chr17_7670581_GGCCAGGAAGGGGCTGAGGTCACTCA/-	45	3	*TP53*	splice_donor_variant
110105822	chr17_7670581_GGCCAGGAAGGGGCTGAGGTCACTCA/-	52	3	*TP53*	splice_donor_variant
112302240	chr17_7670581_GGCCAGGAAGGGGCTGAGGTCACTCA/-	60	3	*TP53*	splice_donor_variant




102105154.cram
[0-55]
TP53 (ENST00000413465)
TP53 (ENST00000635293)
TP53 (ENST00000359597)
TP53 (ENST00000504290)
TP53 (ENST00000510385)
TP53 (ENST00000504937)
TP53 (ENST00000619186)
TP53 (ENST00000618944)
TP53 (ENST00000610623)
TP53 (ENST00000610292)
TP53 (ENST00000269305)
TP53 (ENST00000620739)
TP53 (ENST00000617185)
TP53 (ENST00000455263)
TP53 (ENST00000420246)
TP53 (ENST00000622645)
TP53 (ENST00000610538)
TP53 (ENST00000445888)
TP53 (ENST00000619485)
TP53 (ENST00000576024)
TP53 (ENST00000615910)

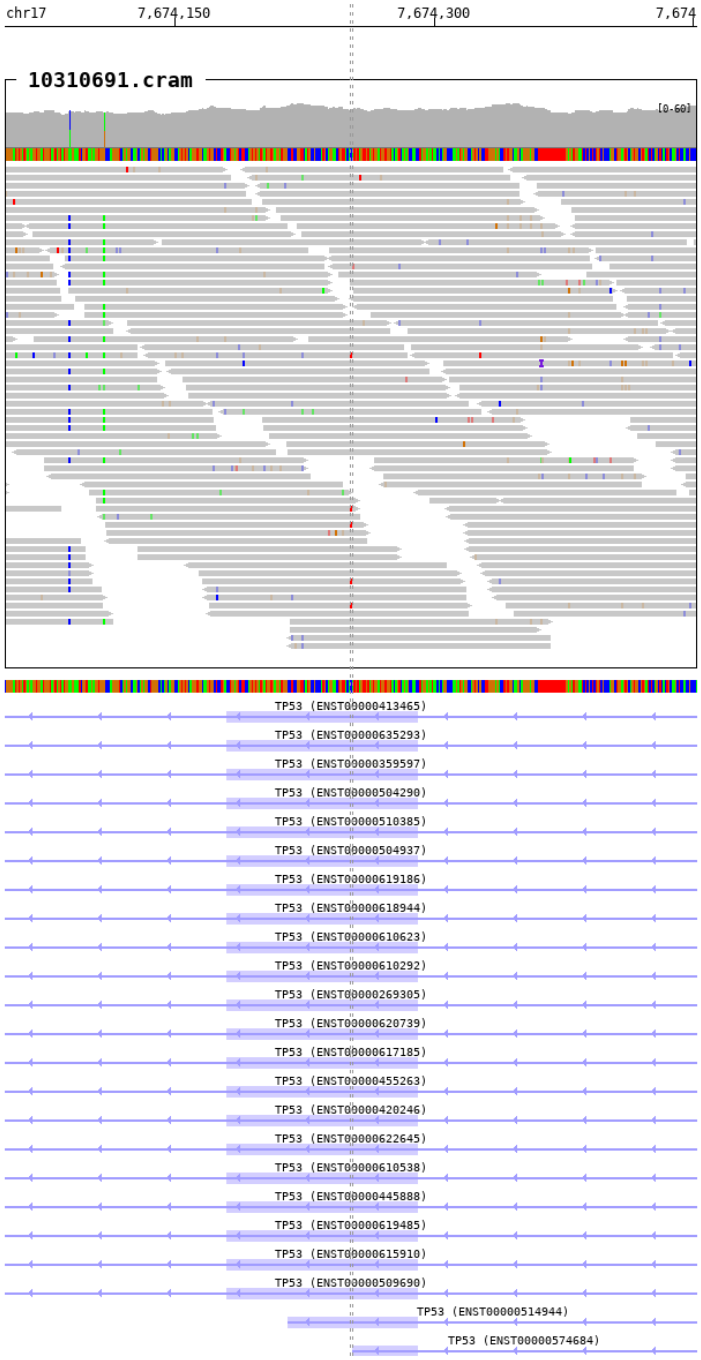
35.2. chr17_7674220_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
101605284	chr17_7674220_C/T	38	4	*TP53*	missense_variant



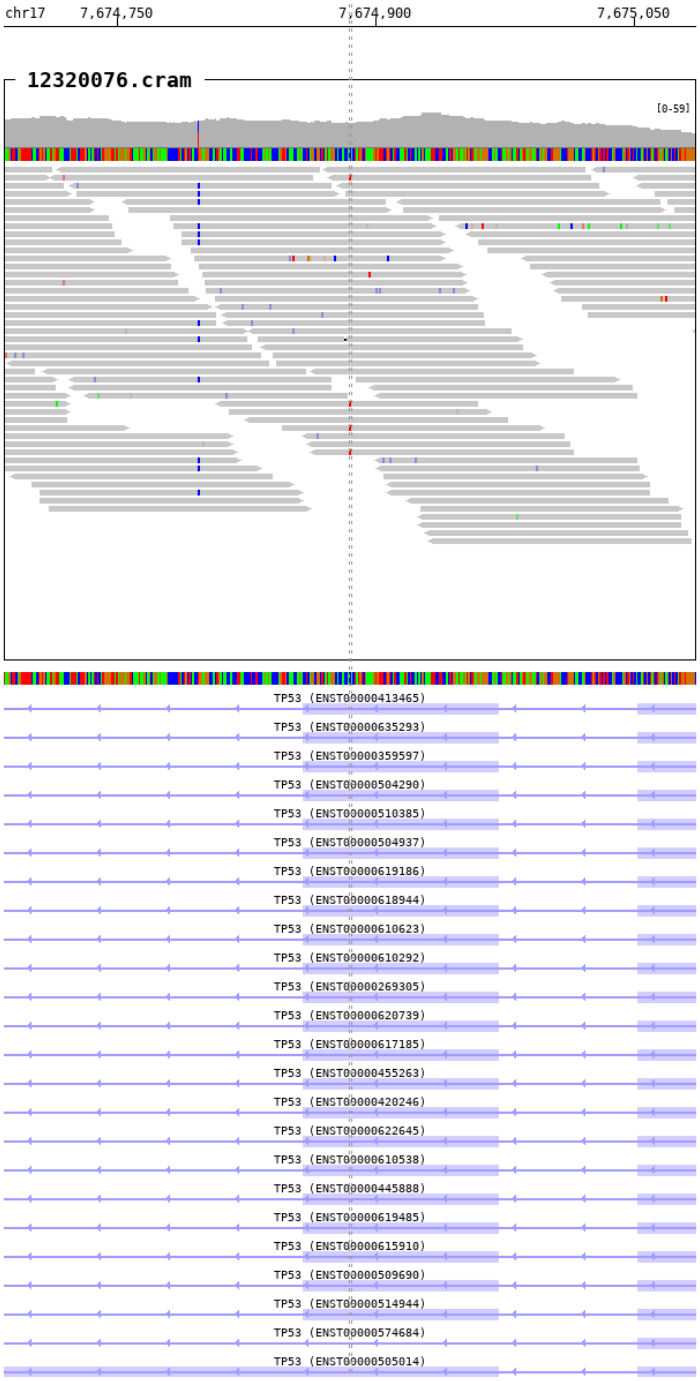
35.3. chr17_7674252_C/T

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10310691	chr17_7674252_C/T	44	5	*TP53*	missense_variant



35.4. chr17_7674885_C/T

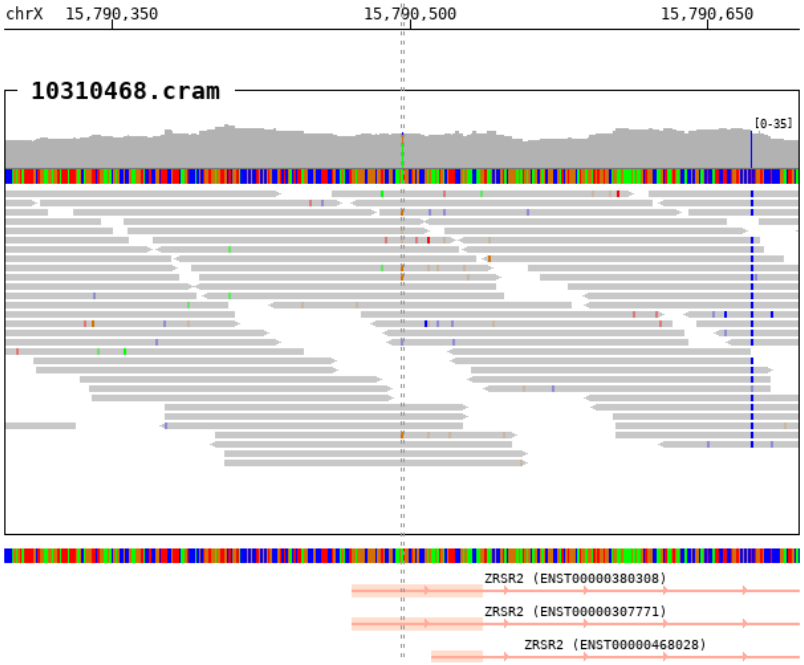
SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
12320076	chr17_7674885_C/T	25	4	*TP53*	missense_variant



36. *ZRSR2*

36.1. chrX_15790496_A/G

SampleID	Variants (GRCh38)	Ref_depth	Alt_depth	Gene	Consequence
10310468	chrX_15790496_A/G	16	5	*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.