

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2025/01/08 02:20:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam output/samtools/anc.sorted.dedup.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa mem data/assembly/scaffolds.fasta data/trimmed/anc_R1.fastq.gz data/trimmed/anc_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Wed Jan 08 02:20:55 PST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/samtools/anc.sorted.dedup.bam

2. Summary

2.1. Globals

Reference size	4,561,556
Number of reads	528,116
Mapped reads	524,874 / 99.39%
Unmapped reads	3,242 / 0.61%
Mapped paired reads	524,874 / 99.39%
Mapped reads, first in pair	262,705 / 49.74%
Mapped reads, second in pair	262,169 / 49.64%
Mapped reads, both in pair	523,084 / 99.05%
Mapped reads, singletons	1,790 / 0.34%
Secondary alignments	0
Supplementary alignments	228 / 0.04%
Read min/max/mean length	15 / 150 / 125.87
Duplicated reads (estimated)	137,299 / 26%
Duplication rate	27.34%
Clipped reads	3,982 / 0.75%

2.2. ACGT Content

Number/percentage of A's	16,320,943 / 24.6%
Number/percentage of C's	16,755,376 / 25.26%
Number/percentage of T's	16,325,641 / 24.61%
Number/percentage of G's	16,938,449 / 25.53%
Number/percentage of N's	102 / 0%

GC Percentage	50.79%
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2.3. Coverage

Mean	14.5438
Standard Deviation	7.6481

2.4. Mapping Quality

Mean Mapping Quality	54.38
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2.5. Insert size

Mean	233.7
Standard Deviation	450.41
P25/Median/P75	128 / 206 / 312

2.6. Mismatches and indels

General error rate	0.14%
Mismatches	89,444
Insertions	337
Mapped reads with at least one insertion	0.06%
Deletions	1,457
Mapped reads with at least one deletion	0.28%
Homopolymer indels	44.15%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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		bases	coverage	deviation
NODE_1_len gth_348724_ cov_30.41061 3	348724	5081370	14.5713	5.3673
NODE_2_len gth_327290_ cov_30.82832 6	327290	4877758	14.9035	10.4418
NODE_3_len gth_312063_ cov_30.52320 9	312063	4546632	14.5696	5.3329
NODE_4_len gth_202800_ cov_31.50077 7	202800	3034830	14.9646	16.1981
NODE_5_len gth_164027_ cov_28.93517 5	164027	2308685	14.075	5.0109
NODE_6_len gth_144088_ cov_29.90798 6	144088	2108065	14.6304	5.3189
NODE_7_len gth_140177_ cov_30.44111 3	140177	2059065	14.689	5.1831
NODE_8_len gth_127776_ cov_30.97688 3	127776	1877480	14.6935	6.7192

NODE_9_length_123571_cov_29.288152	123571	1753639	14.1913	5.0499
NODE_10_length_118944_cov_29.338572	118944	1669533	14.0363	4.8723
NODE_11_length_116005_cov_30.127036	116005	1637149	14.1127	5.1533
NODE_12_length_115292_cov_29.218192	115292	1597621	13.8572	4.8274
NODE_13_length_115019_cov_29.129970	115019	1600113	13.9117	4.964
NODE_14_length_105066_cov_31.022726	105066	1534748	14.6075	5.1833
NODE_15_length_101045_cov_29.964256	101045	1424334	14.096	5.0193
NODE_16_length_97665_cov_30.761641	97665	1446914	14.8151	5.6541
NODE_17_length_96980	96980	1432309	14.7691	5.1509

ngth_96980_ cov_30.80702 4				
NODE_18_le ngth_93668_ cov_29.87807 6	93668	1340490	14.3111	4.8813
NODE_19_le ngth_93657_ cov_27.89973 3	93657	1288382	13.7564	5.5388
NODE_20_le ngth_90130_ cov_29.10029 6	90130	1248863	13.8562	5.2764
NODE_21_le ngth_89111_ cov_29.73411 3	89111	1251203	14.0409	5.1864
NODE_22_le ngth_87915_ cov_29.48871 8	87915	1225670	13.9415	5.1646
NODE_23_le ngth_82281_ cov_29.59817 0	82281	1178272	14.3201	5.7231
NODE_24_le ngth_64635_ cov_29.57611 8	64635	893787	13.8282	5.3508
NODE_25_le ngth_60439_ cov_30.11018	60439	877417	14.5174	5.1305

5				
NODE_26_length_59685_cov_30.383304	59685	881002	14.7609	5.1176
NODE_27_length_55232_cov_30.200073	55232	779091	14.1058	5.5112
NODE_28_length_54771_cov_30.970326	54771	800444	14.6144	5.3457
NODE_29_length_52138_cov_30.092833	52138	754496	14.4711	5.1616
NODE_30_length_48196_cov_29.149151	48196	646176	13.4073	5.1321
NODE_31_length_46922_cov_30.386978	46922	676039	14.4077	5.1525
NODE_32_length_46460_cov_30.242309	46460	655657	14.1123	4.9384
NODE_33_length_46046_cov_31.315495	46046	692413	15.0374	10.518

NODE_34_le ngth_45753_ cov_30.42611 0	45753	691321	15.1099	5.2627
NODE_35_le ngth_44700_ cov_29.78121 1	44700	637274	14.2567	4.8626
NODE_36_le ngth_41536_ cov_32.62753 6	41536	658694	15.8584	5.5663
NODE_37_le ngth_41086_ cov_30.47816 3	41086	588765	14.3301	5.6452
NODE_38_le ngth_40828_ cov_28.52327 6	40828	557434	13.6532	5.3662
NODE_39_le ngth_40801_ cov_30.67262 5	40801	595333	14.5911	5.9433
NODE_40_le ngth_39502_ cov_30.75832 6	39502	565347	14.3119	5.5537
NODE_41_le ngth_34862_ cov_30.07687 2	34862	480947	13.7957	4.9986
NODE_42_le	30861	436115	14.1316	4.7813

ngth_30861_ cov_31.04898 6				
NODE_43_le ngth_30094_ cov_30.29653 2	30094	442427	14.7015	5.8085
NODE_44_le ngth_29959_ cov_29.45422 0	29959	434215	14.4936	5.4093
NODE_45_le ngth_28922_ cov_30.89249 4	28922	430970	14.9011	5.1187
NODE_46_le ngth_28491_ cov_30.23301 9	28491	404526	14.1984	5.1483
NODE_47_le ngth_27211_ cov_27.97328 1	27211	354984	13.0456	5.0663
NODE_48_le ngth_22868_ cov_29.98275 6	22868	330882	14.4692	5.3844
NODE_49_le ngth_20918_ cov_28.86512 2	20918	298255	14.2583	5.6303
NODE_50_le ngth_16506_ cov_29.38766	16506	228405	13.8377	4.9592

8				
NODE_51_length_16418_cov_30.461600	16418	240178	14.6289	4.7209
NODE_52_length_15612_cov_31.586353	15612	236949	15.1774	5.901
NODE_53_length_15148_cov_27.490611	15148	195073	12.8778	4.9371
NODE_54_length_14242_cov_29.450124	14242	201516	14.1494	5.2809
NODE_55_length_14021_cov_28.407702	14021	191508	13.6587	5.384
NODE_56_length_13692_cov_30.550512	13692	199197	14.5484	4.7702
NODE_57_length_9478_cov_29.379534	9478	135408	14.2866	5.3523
NODE_58_length_6711_cov_27.390865	6711	96762	14.4184	5.5316

NODE_59_length_6446_cov_27.963574	6446	91118	14.1356	5.9685
NODE_60_length_5807_cov_27.397382	5807	72478	12.4811	4.8212
NODE_61_length_4414_cov_35.839059	4414	72242	16.3666	5.9479
NODE_62_length_3105_cov_33.928666	3105	46392	14.9411	6.1437
NODE_63_length_2900_cov_61.188452	2900	76765	26.4707	8.3406
NODE_64_length_2654_cov_224.861855	2654	268746	101.2607	18.8007
NODE_65_length_2372_cov_24.938126	2372	32069	13.5198	5.8399
NODE_66_length_1662_cov_26.001893	1662	19277	11.5987	4.6984
NODE_67_length_1518	1518	22030	14.5125	5.7213

ngth_1518_c ov_32.67383 8				
NODE_68_le ngth_1343_c ov_129.1990 52	1343	77499	57.7059	12.4372
NODE_69_le ngth_1317_c ov_64.51612 9	1317	40609	30.8345	7.6711
NODE_70_le ngth_1211_c ov_45.51675 5	1211	22713	18.7556	5.6822
NODE_71_le ngth_1061_c ov_260.1260 16	1061	109378	103.0895	21.8667
NODE_72_le ngth_1042_c ov_27.84766 8	1042	15750	15.1152	6.05
NODE_73_le ngth_1013_c ov_151.5438 03	1013	63185	62.3741	15.227
NODE_74_le ngth_869_cov _74.214646	869	23656	27.2221	10.0584
NODE_75_le ngth_869_cov _35.061869	869	11054	12.7204	3.4195

NODE_76_le ngth_791_cov _244.456583	791	81216	102.6751	25.976
NODE_77_le ngth_719_cov _161.823988	719	50349	70.0264	27.2824
NODE_78_le ngth_556_cov _61.807933	556	14160	25.4676	9.7494
NODE_79_le ngth_548_cov _263.447983	548	56046	102.2737	31.2386
NODE_80_le ngth_470_cov _65.119593	470	11030	23.4681	10.2079
NODE_81_le ngth_470_cov _24.284987	470	6606	14.0553	6.2872
NODE_82_le ngth_426_cov _31.286533	426	6409	15.0446	9.0684
NODE_83_le ngth_417_cov _27.391176	417	4485	10.7554	6.4516
NODE_84_le ngth_396_cov _38.962382	396	5761	14.548	5.4477
NODE_85_le ngth_391_cov _40.996815	391	6251	15.9872	6.875
NODE_86_le ngth_387_cov	387	4648	12.0103	5.6951

_29.245161				
NODE_87_le ngth_372_cov _120.583051	372	16442	44.1989	13.3098
NODE_88_le ngth_337_cov _32.100000	337	4027	11.9496	4.777
NODE_89_le ngth_334_cov _27.634241	334	4201	12.5778	3.9856
NODE_90_le ngth_323_cov _96.585366	323	10761	33.3158	14.9055
NODE_91_le ngth_299_cov _24.261261	299	2463	8.2375	2.0497
NODE_92_le ngth_293_cov _57.958333	293	6088	20.7782	7.7944
NODE_93_le ngth_286_cov _30.990431	286	2599	9.0874	2.46
NODE_94_le ngth_273_cov _35.244898	273	2958	10.8352	8.1379
NODE_95_le ngth_259_cov _41.192308	259	3048	11.7683	6.7269
NODE_96_le ngth_259_cov _29.428571	259	2301	8.8842	4.6426
NODE_97_le	258	1772	6.8682	1.9995

ngth_258_cov _28.475138				
NODE_98_le ngth_258_cov _27.718232	258	2244	8.6977	4.6939
NODE_99_le ngth_235_cov _25.575949	235	2458	10.4596	2.5718
NODE_100_I ength_227_c ov_103.2800 00	227	7584	33.4097	14.4345
NODE_101_I ength_227_c ov_30.23333 3	227	1761	7.7577	3.285
NODE_102_I ength_224_c ov_26.95918 4	224	1327	5.9241	3.3804
NODE_103_I ength_224_c ov_18.30612 2	224	365	1.6295	0.9596
NODE_104_I ength_219_c ov_14.65493 0	219	598	2.7306	2.3767
NODE_105_I ength_215_c ov_43.78985 5	215	3187	14.8233	6.2711
NODE_106_I	214	2738	12.7944	4.0677

ength_214_c ov_37.68613 1				
NODE_107_I ength_214_c ov_18.32116 8	214	1176	5.4953	3.1634
NODE_108_I ength_213_c ov_31.33823 5	213	1084	5.0892	1.925
NODE_109_I ength_212_c ov_15.55555 6	212	1001	4.7217	2.867
NODE_110_I ength_206_c ov_14.14728 7	206	1379	6.6942	2.9327
NODE_111_I ength_205_c ov_46.59375 0	205	1852	9.0341	3.5646
NODE_112_I ength_205_c ov_24.89062 5	205	2491	12.1512	5.1629
NODE_113_I ength_204_c ov_31.00000 0	204	1476	7.2353	3.097
NODE_114_I ength_203_c ov_31.30952	203	2264	11.1527	6.1877

4				
NODE_115_I ength_199_c ov_51.83606 6	199	3881	19.5025	8.4763
NODE_116_I ength_196_c ov_70.23529 4	196	2972	15.1633	5.3865
NODE_117_I ength_195_c ov_30.99152 5	195	1877	9.6256	3.7469
NODE_118_I ength_191_c ov_124.6140 35	191	6016	31.4974	10.7015
NODE_119_I ength_191_c ov_103.0175 44	191	5136	26.8901	10.6645
NODE_120_I ength_188_c ov_13.04504 5	188	368	1.9574	1.8817
NODE_121_I ength_187_c ov_96.21818 2	187	5787	30.9465	11.5873
NODE_122_I ength_183_c ov_19.81132 1	183	260	1.4208	1.8326

NODE_123_I ength_181_c ov_823.0865 38	181	37219	205.6298	75.6214
NODE_124_I ength_174_c ov_32.54639 2	174	1652	9.4943	3.3763
NODE_125_I ength_167_c ov_36.64444 4	167	1010	6.0479	1.4593
NODE_126_I ength_166_c ov_118.7078 65	166	1262	7.6024	3.7879
NODE_127_I ength_160_c ov_30.08433 7	160	1392	8.7	3.2245
NODE_128_I ength_160_c ov_19.10843 4	160	513	3.2062	1.6167
NODE_129_I ength_158_c ov_45.82716 0	158	1507	9.538	3.3425
NODE_130_I ength_158_c ov_38.28395 1	158	2782	17.6076	4.6071
NODE_131_I	155	7360	47.4839	16.9848

ength_155_c ov_574.2051 28				
NODE_132_I ength_155_c ov_361.5256 41	155	6532	42.1419	15.3717
NODE_133_I ength_155_c ov_120.8974 36	155	1506	9.7161	3.3519
NODE_134_I ength_155_c ov_107.5512 82	155	3560	22.9677	6.7513
NODE_135_I ength_155_c ov_79.55128 2	155	2845	18.3548	5.1151
NODE_136_I ength_155_c ov_53.97435 9	155	2594	16.7355	4.6657
NODE_137_I ength_155_c ov_44.34615 4	155	492	3.1742	1.1976
NODE_138_I ength_155_c ov_44.32051 3	155	1031	6.6516	2.1719
NODE_139_I ength_155_c ov_42.56410	155	88	0.5677	0.9017

3				
NODE_140_I ength_155_c ov_41.98717 9	155	1303	8.4065	1.8929
NODE_141_I ength_155_c ov_39.03846 2	155	194	1.2516	0.9678
NODE_142_I ength_155_c ov_36.66666 7	155	306	1.9742	1.6302
NODE_143_I ength_155_c ov_33.03846 2	155	264	1.7032	0.6737
NODE_144_I ength_155_c ov_32.65384 6	155	2609	16.8323	2.7797
NODE_145_I ength_155_c ov_30.98717 9	155	443	2.8581	1.2414
NODE_146_I ength_155_c ov_29.79487 2	155	149	0.9613	0.1929
NODE_147_I ength_155_c ov_27.19230 8	155	480	3.0968	1.7219

NODE_148_I ength_155_c ov_25.53846 2	155	298	1.9226	0.2904
NODE_149_I ength_155_c ov_25.06410 3	155	264	1.7032	0.711
NODE_150_I ength_155_c ov_21.67948 7	155	753	4.8581	1.7244
NODE_151_I ength_155_c ov_20.34615 4	155	136	0.8774	0.328
NODE_152_I ength_155_c ov_20.00000 0	155	150	0.9677	0.1767
NODE_153_I ength_155_c ov_17.93589 7	155	147	0.9484	0.2212
NODE_154_I ength_155_c ov_13.11538 5	155	247	1.5935	0.9066
NODE_155_I ength_154_c ov_36.49350 6	154	1983	12.8766	5.121
NODE_156_I	154	1817	11.7987	2.9374

ength_154_c ov_29.67532 5				
NODE_157_I ength_154_c ov_21.85714 3	154	1489	9.6688	2.856
NODE_158_I ength_154_c ov_18.40259 7	154	97	0.6299	0.4828
NODE_159_I ength_153_c ov_28.75000 0	153	609	3.9804	0.918
NODE_160_I ength_153_c ov_25.34210 5	153	0	0	0
NODE_161_I ength_152_c ov_42.16000 0	152	1064	7	1.9668
NODE_162_I ength_152_c ov_24.77333 3	152	1372	9.0263	2.9955
NODE_163_I ength_151_c ov_30.81081 1	151	1074	7.1126	2.6559
NODE_164_I ength_151_c ov_21.70270	151	349	2.3113	1.0684

3				
NODE_165_I ength_142_c ov_20.49230 8	142	414	2.9155	1.7218
NODE_166_I ength_133_c ov_55.87500 0	133	1164	8.7519	2.195
NODE_167_I ength_130_c ov_126.6981 13	130	2814	21.6462	3.6729
NODE_168_I ength_129_c ov_32.51923 1	129	338	2.6202	1.1627
NODE_169_I ength_129_c ov_27.98076 9	129	771	5.9767	0.1507
NODE_170_I ength_125_c ov_53.60416 7	125	748	5.984	1.4366
NODE_171_I ength_123_c ov_56.82608 7	123	1267	10.3008	1.0196
NODE_172_I ength_122_c ov_29.26666 7	122	0	0	0

NODE_173_I ength_121_c ov_32.90909 1	121	92	0.7603	0.9709
NODE_174_I ength_117_c ov_28.35000 0	117	0	0	0
NODE_175_I ength_115_c ov_67.65789 5	115	619	5.3826	1.0761
NODE_176_I ength_112_c ov_80.91428 6	112	224	2	0
NODE_177_I ength_109_c ov_26.46875 0	109	212	1.945	0.3272
NODE_178_I ength_107_c ov_20.80000 0	107	0	0	0
NODE_179_I ength_105_c ov_63.85714 3	105	105	1	0
NODE_180_I ength_104_c ov_22.51851 9	104	126	1.2115	0.9774
NODE_181_I	99	92	0.9293	0.9975

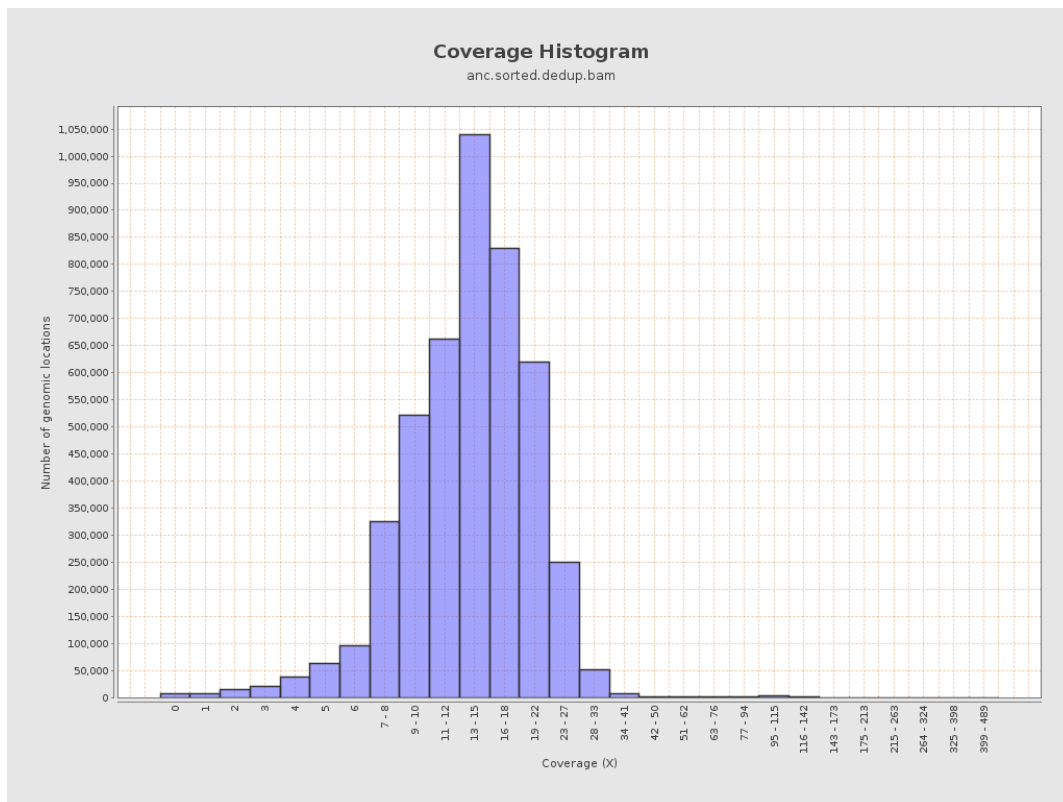
ength_99_cov _17.772727				
NODE_182_I ength_93_cov _18.750000	93	73	0.7849	0.4109
NODE_183_I ength_92_cov _38.000000	92	0	0	0
NODE_184_I ength_86_cov _36.222222	86	0	0	0
NODE_185_I ength_85_cov _90.125000	85	0	0	0
NODE_186_I ength_81_cov _41.000000	81	0	0	0
NODE_187_I ength_79_cov _132.500000	79	0	0	0
NODE_188_I ength_79_cov _92.500000	79	0	0	0
NODE_189_I ength_79_cov _54.500000	79	102	1.2911	0.9567
NODE_190_I ength_79_cov _39.000000	79	0	0	0
NODE_191_I ength_79_cov _38.000000	79	0	0	0

NODE_192_I ength_78_cov _77.000000	78	0	0	0
NODE_193_I ength_78_cov _70.000000	78	424	5.4359	2.9508
NODE_194_I ength_78_cov _69.000000	78	0	0	0
NODE_195_I ength_78_cov _64.000000	78	0	0	0
NODE_196_I ength_78_cov _48.000000	78	27	0.3462	0.4757

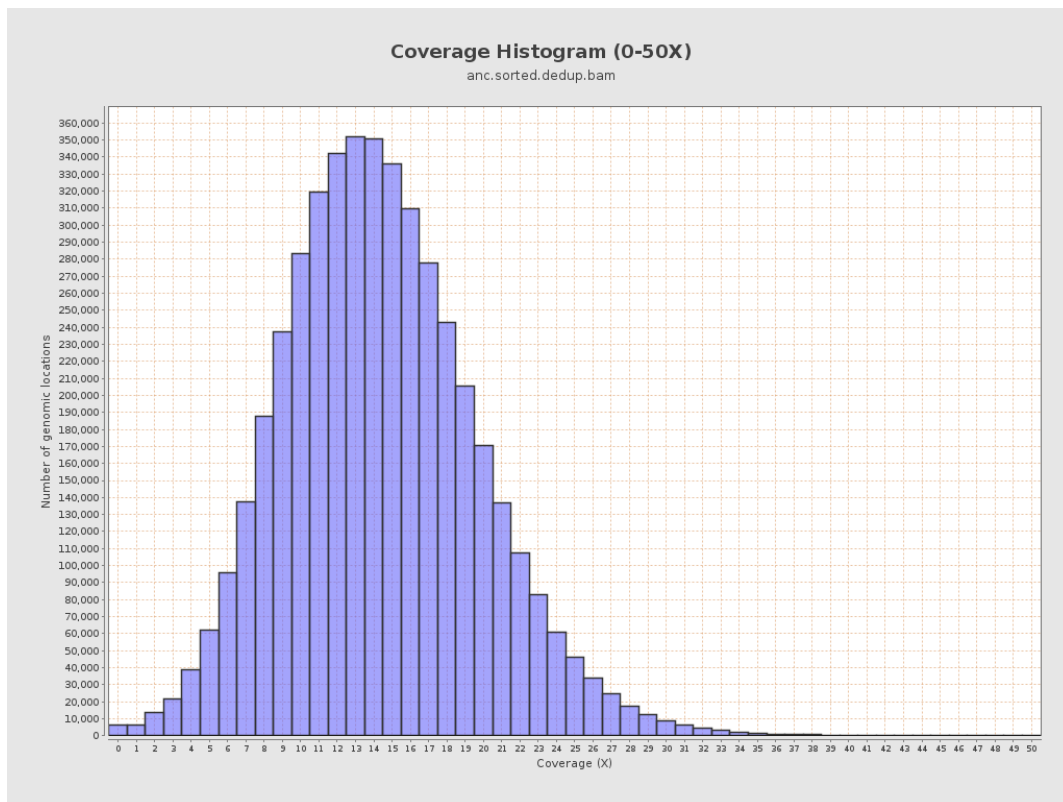
3. Results : Coverage across reference



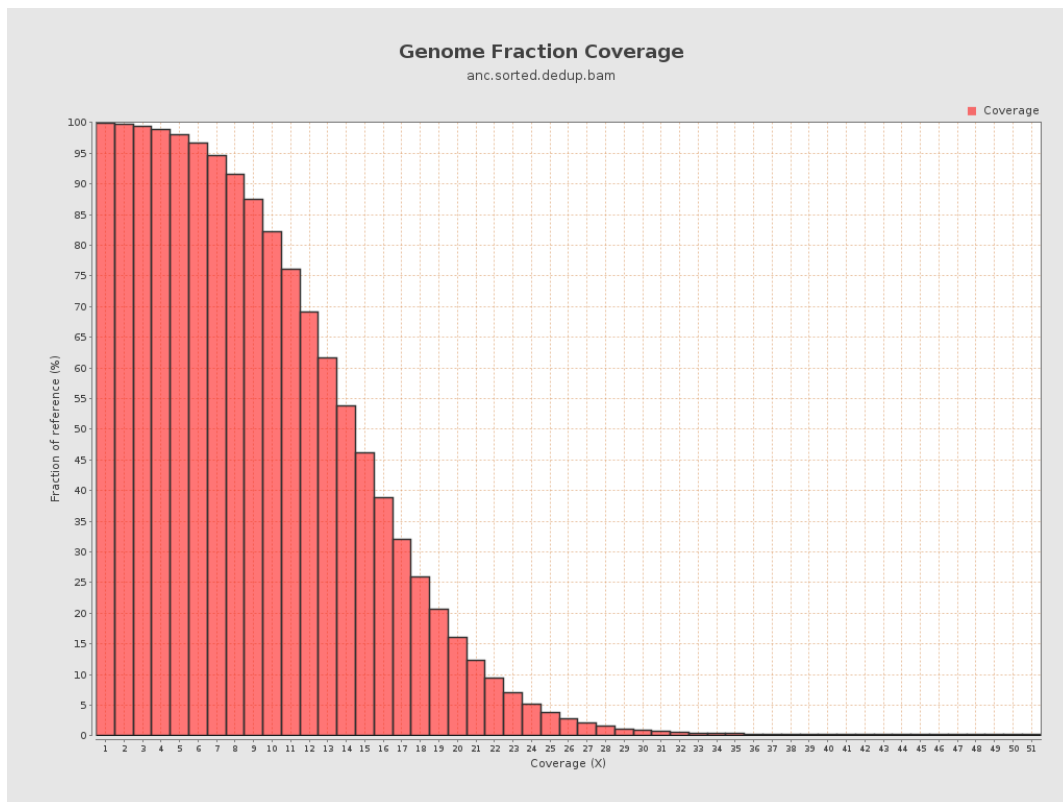
4. Results : Coverage Histogram



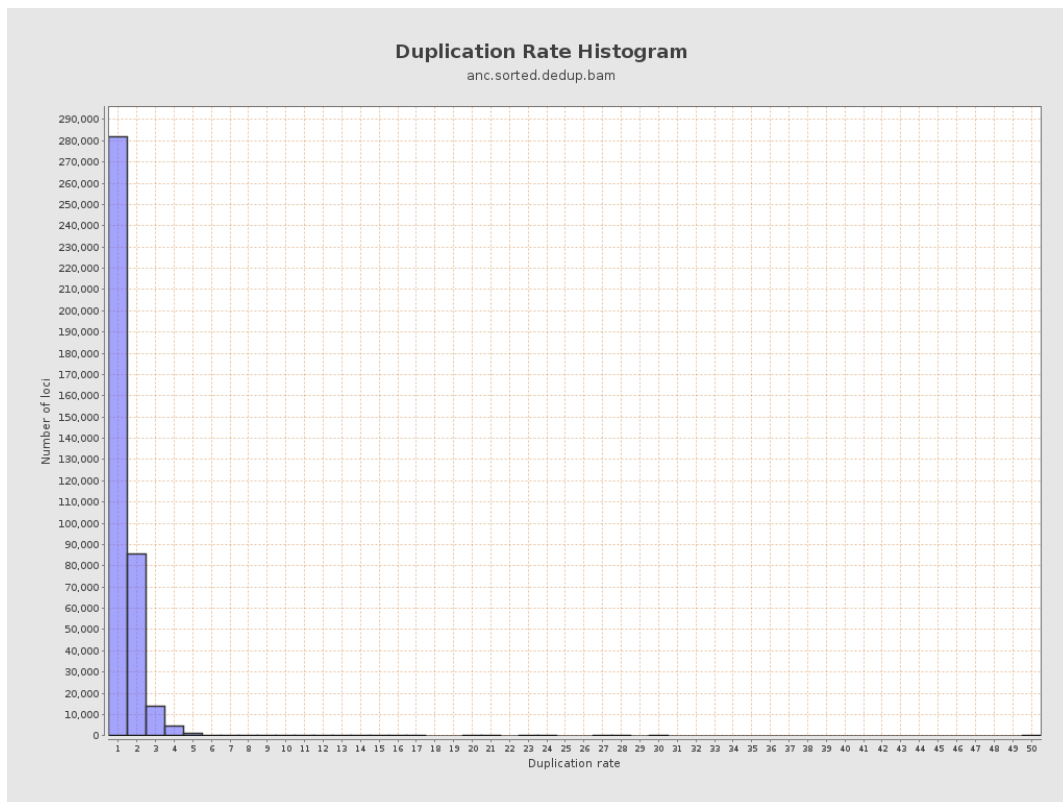
5. Results : Coverage Histogram (0-50X)



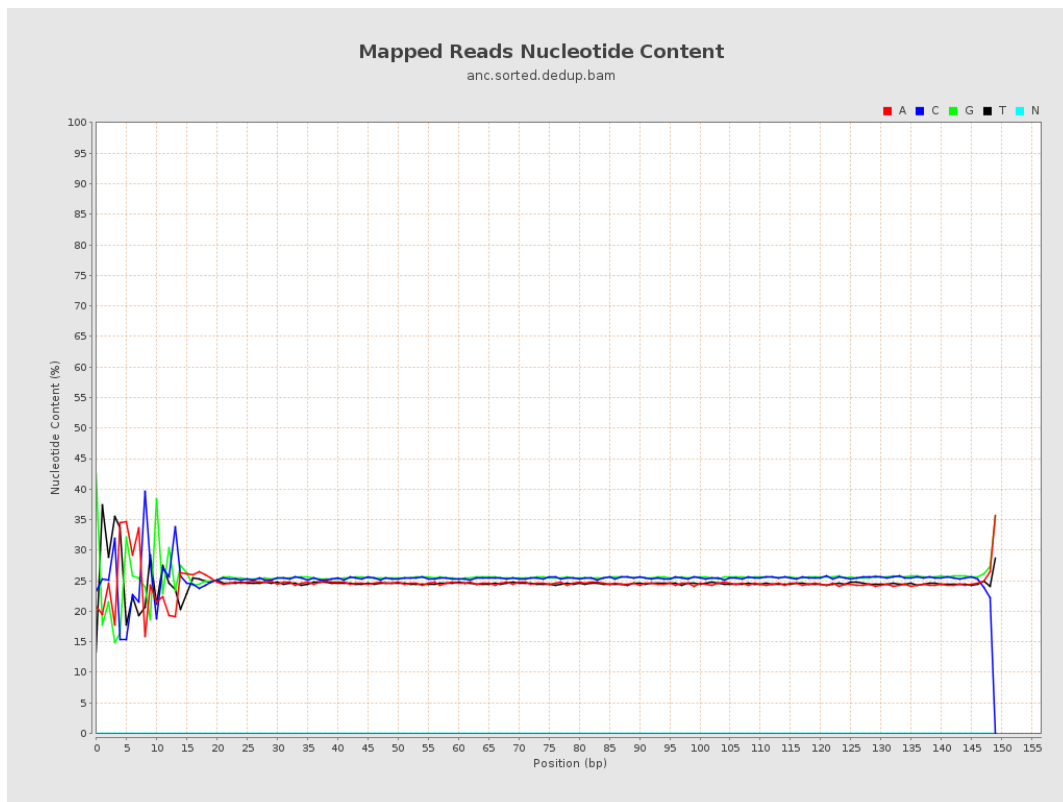
6. Results : Genome Fraction Coverage



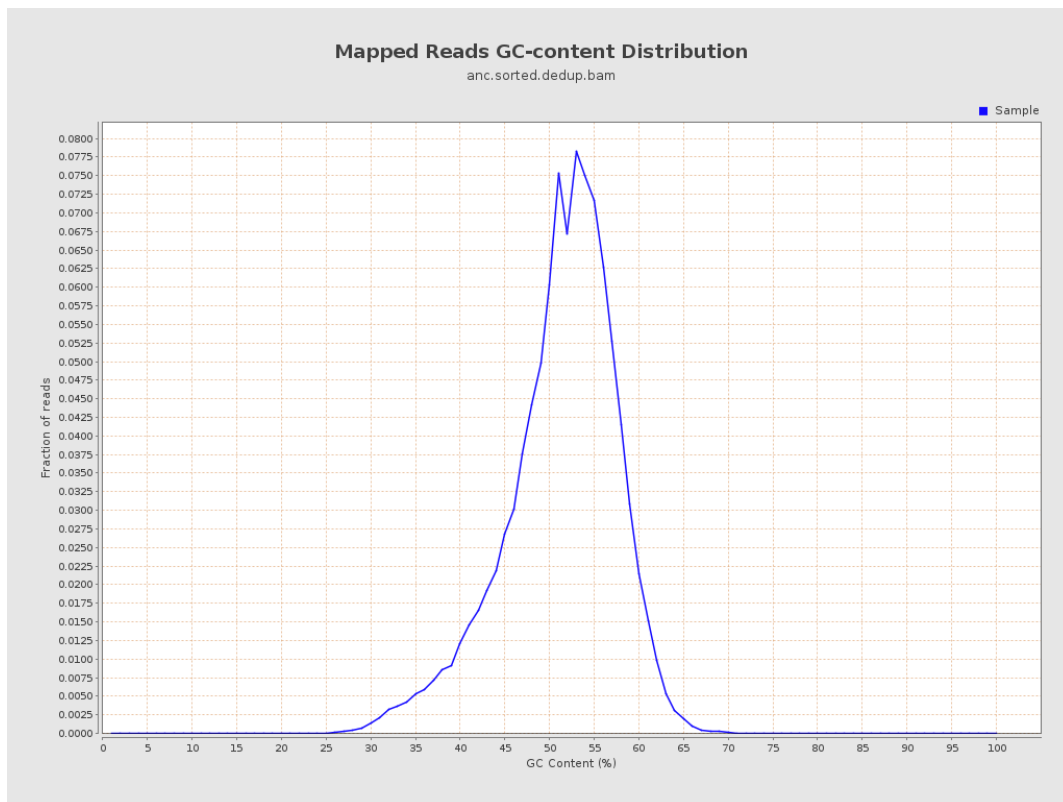
7. Results : Duplication Rate Histogram



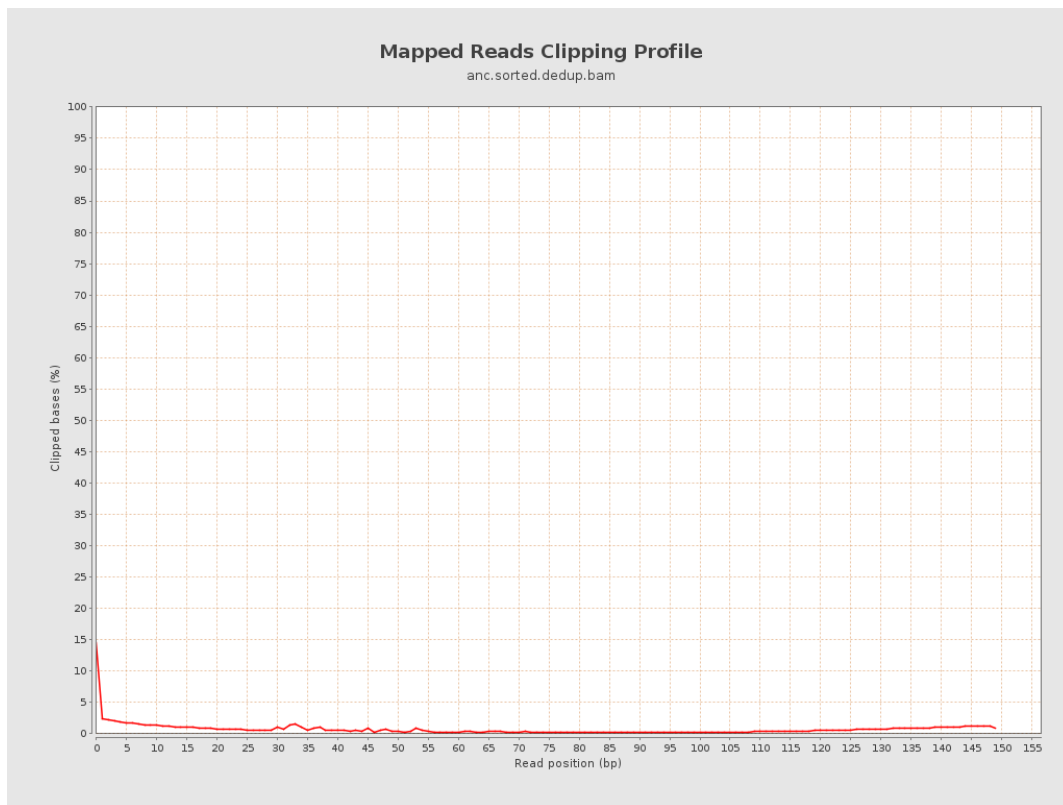
8. Results : Mapped Reads Nucleotide Content



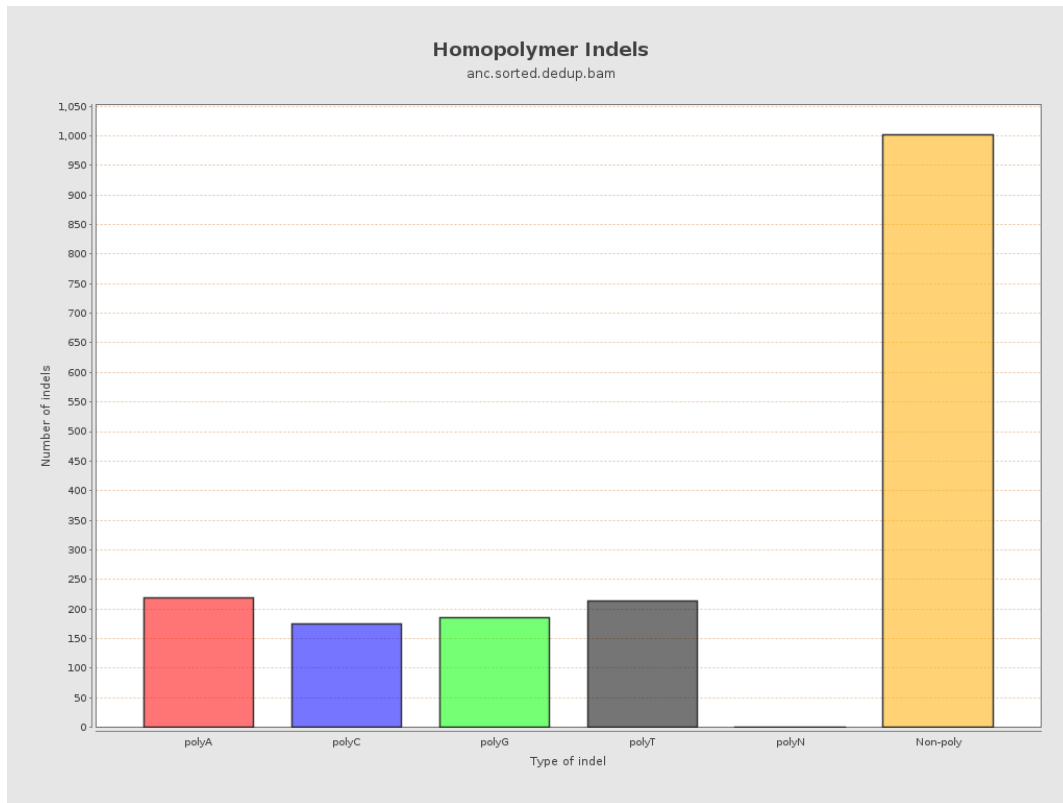
9. Results : Mapped Reads GC-content Distribution



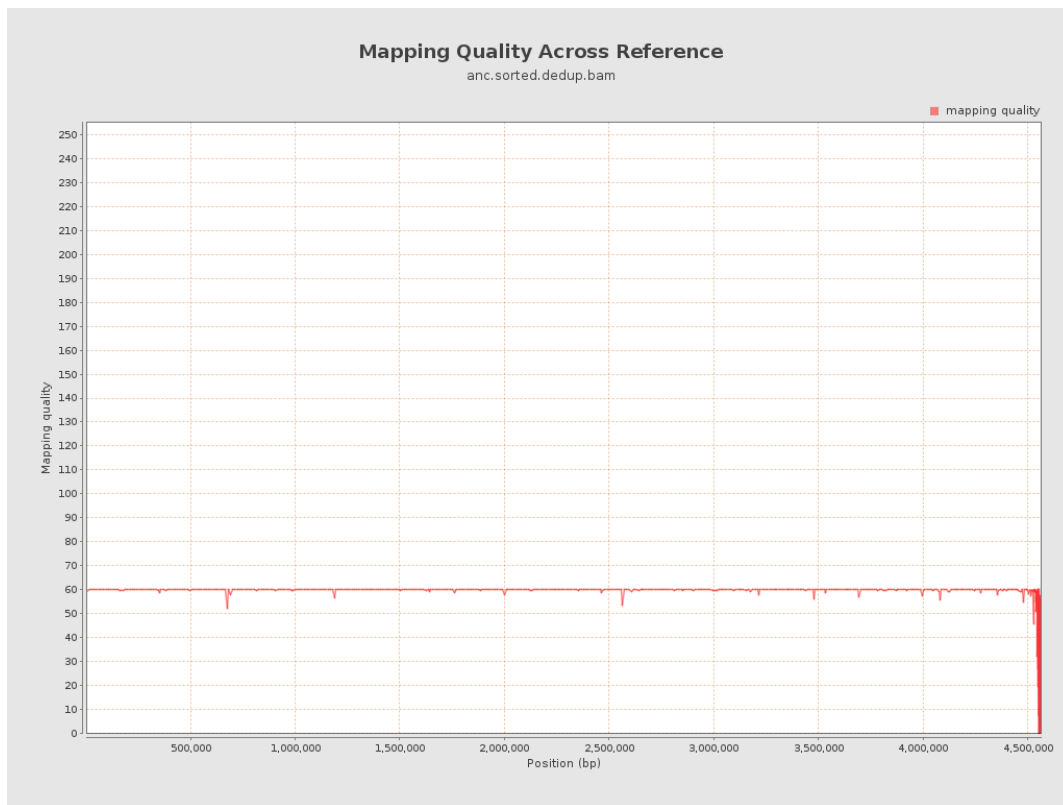
10. Results : Mapped Reads Clipping Profile



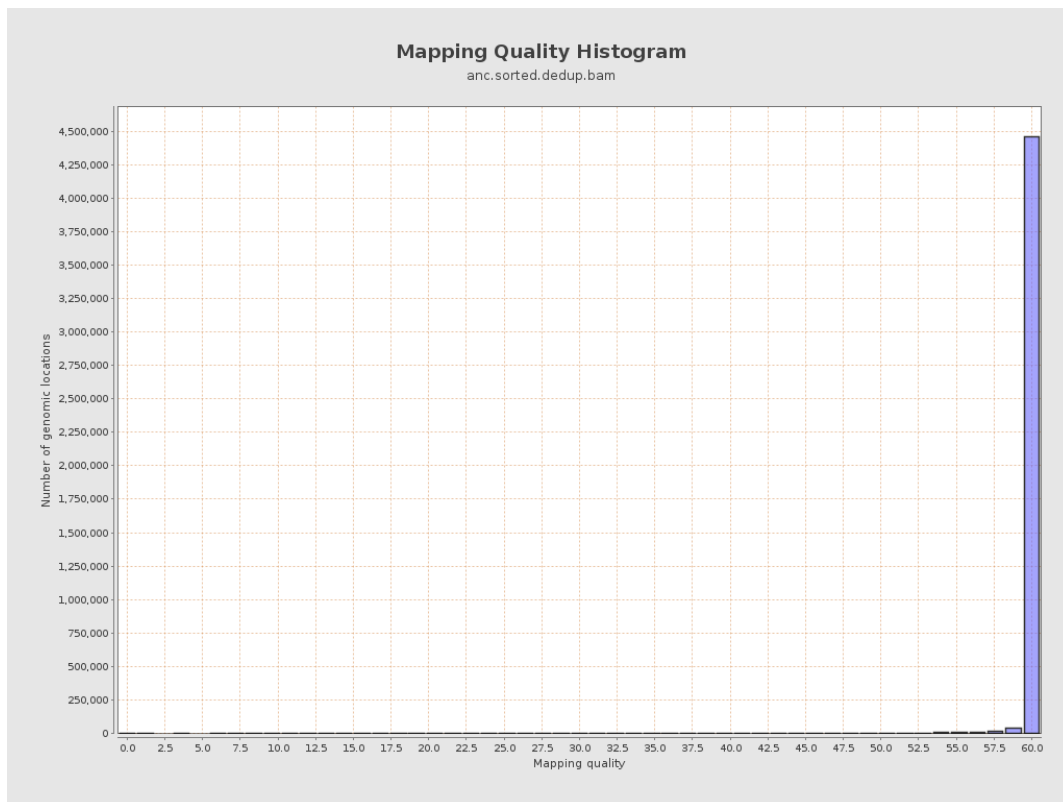
11. Results : Homopolymer Indels



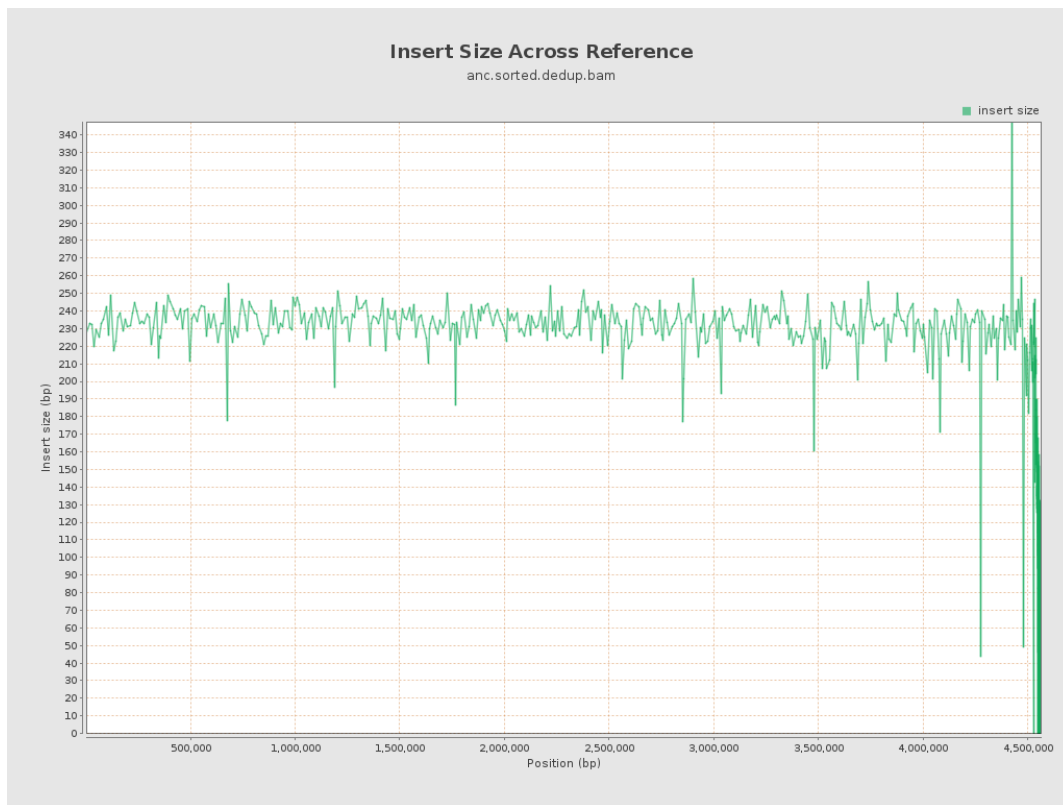
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

