Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2021/01/12 17:46:53

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /opt/tsinghua/zhangwei/Pipeline_test/o_WGBS-PE/intermediate_result/step_06_bamsort/case4.pair1_sorted.bam -nw 400 -hm 3

1.2. Alignment

Command line:	"bismark -q --phred33-quals --bowtie2 --un --multicore 12 --output_dir /opt/tsinghua/zhangwei/Pipeline_test/o_WGBS-PE/intermediate_result/step_04_bismark --temp_dir /opt/tsinghua/zhangwei/Pipeline_test/o_WGBS-PE/intermediate_result/step_04_bismark --genome_folder /home/zhangwei/Genome/hg19_bismark -1 /opt/tsinghua/zhangwei/Pipeline_test/o_WGBS-PE/intermediate_result/step_03_adapterremoval/case4.pair1.truncated.gz -2 /opt/tsinghua/zhangwei/Pipeline_test/o_WGBS-PE/intermediate_result/step_03_adapterremoval/case4.pair2.truncated.gz"
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	Bismark (v0.23.0)

Analysis date:	Tue Jan 12 17:46:51 CST 2021
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/opt/tsinghua/zhangwei/Pipeline_test/o_WGBS-PE/intermediate_result/step_06_bam sort/case4.pair1_sorted.bam

2. Summary

2.1. Globals

Reference size	3,137,161,264
Number of reads	7,180,310
Mapped reads	7,180,310 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	7,180,310 / 100%
Mapped reads, first in pair	3,590,155 / 50%
Mapped reads, second in pair	3,590,155 / 50%
Mapped reads, both in pair	7,180,310 / 100%
Mapped reads, singletons	0 / 0%
Secondary alignments	0
Read min/max/mean length	16 / 150 / 147.54
Duplicated reads (estimated)	673,620 / 9.38%
Duplication rate	9.45%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	418,083,805 / 39.48%
Number/percentage of C's	111,302,197 / 10.51%
Number/percentage of T's	419,905,744 / 39.65%
Number/percentage of G's	109,783,667 / 10.37%
Number/percentage of N's	17,881 / 0%
GC Percentage	20.88%

2.3. Coverage

Mean	0.3377
Standard Deviation	1.8975

2.4. Mapping Quality

Mean Mapping Quality	34.92

2.5. Insert size

Mean	182.34
Standard Deviation	54.74
P25/Median/P75	158 / 169 / 183

2.6. Mismatches and indels

General error rate	14.91%
Mismatches	157,677,516
Insertions	167,683
Mapped reads with at least one insertion	2.29%
Deletions	172,794
Mapped reads with at least one deletion	2.36%
Homopolymer indels	80.7%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

chr1	249250621	82708989	0.3318	2.348
chr2	243199373	93147946	0.383	0.9216
chr3	198022430	77755495	0.3927	0.928
chr4	191154276	81029254	0.4239	0.9707
chr5	180915260	70594912	0.3902	0.9127
chr6	171115067	66200416	0.3869	0.9917
chr7	159138663	59211422	0.3721	1.5036
chr8	146364022	56084269	0.3832	0.9173
chr9	141213431	41902810	0.2967	0.8155
chr10	135534747	51075345	0.3768	5.0073
chr11	135006516	48024725	0.3557	0.877
chr12	133851895	49059753	0.3665	0.8837
chr13	115169878	40733232	0.3537	0.8811
chr14	107349540	33609095	0.3131	0.8313
chr15	102531392	28694379	0.2799	0.7952
chr16	90354753	27392809	0.3032	3.9129
chr17	81195210	22706273	0.2797	0.7802
chr18	78077248	29949009	0.3836	0.9082
chr19	59128983	14071019	0.238	1.0294
chr20	63025520	18964618	0.3009	0.8127
chr21	48129895	14474045	0.3007	0.9143
chr22	51304566	8762906	0.1708	0.6226
chrX	155270560	30275478	0.195	0.6324
chrY	59373566	5247285	0.0884	4.0606

chrM	16571	2748	0.1658	0.6314
chr1_gl000191_random	106433	7433	0.0698	0.356
chr1_gl000192_random	547496	102178	0.1866	0.6603
chr4_ctg9_hap1	590426	13428	0.0227	0.2159
chr4_gl000193_random	189789	140584	0.7407	1.4786
chr4_gl000194_random	191469	68455	0.3575	1.0348
chr6_apd_hap1	4622290	1200	0.0003	0.0212
chr6_cox_hap2	4795371	23170	0.0048	0.105
chr6_dbb_hap3	4610396	13014	0.0028	0.0724
chr6_mann_hap4	4683263	13128	0.0028	0.0738
chr6_mcf_hap5	4833398	8926	0.0018	0.0613
chr6_qbl_hap6	4611984	10849	0.0024	0.0644
chr6_ssto_hap7	4928567	17725	0.0036	0.0846
chr7_gl000195_random	182896	211322	1.1554	2.1149
chr8_gl000196_random	38914	600	0.0154	0.2371

chr8_gl000197_random	37175	0	0	0
chr9_gl000198_random	90085	56551	0.6278	1.5303
chr9_gl000199_random	169874	166165	0.9782	3.7259
chr9_gl000200_random	187035	0	0	0
chr9_gl000201_random	36148	294	0.0081	0.1208
chr11_gl000202_random	40103	2288	0.0571	0.3588
chr17_ctg5_hap1	1680828	9154	0.0054	0.1007
chr17_gl000203_random	37498	10716	0.2858	1.0071
chr17_gl000204_random	81310	7624	0.0938	0.4271
chr17_gl000205_random	174588	152571	0.8739	1.8398
chr17_gl000206_random	41001	600	0.0146	0.1584
chr18_gl000207_random	4262	300	0.0704	0.3442
chr19_gl000208_random	92689	62104	0.67	2.1238
chr19_gl000209_random	159169	2100	0.0132	0.1629
chr21_gl000210_random	27682	294	0.0106	0.1406

chrUn_gl000211	166566	68006	0.4083	0.9978
chrUn_gl000212	186858	79615	0.4261	3.1371
chrUn_gl000213	164239	10386	0.0632	0.3362
chrUn_gl000214	137718	208623	1.5149	2.4996
chrUn_gl000215	172545	1496	0.0087	0.1352
chrUn_gl000216	172294	178567	1.0364	1.6282
chrUn_gl000217	172149	35017	0.2034	0.7228
chrUn_gl000218	161147	117137	0.7269	1.357
chrUn_gl000219	179198	191885	1.0708	1.9586
chrUn_gl000220	161802	4862354	30.0513	103.747
chrUn_gl000221	155397	40609	0.2613	0.9233
chrUn_gl000222	186861	15296	0.0819	0.447
chrUn_gl000223	180455	900	0.005	0.097
chrUn_gl000224	179693	208724	1.1616	5.1366
chrUn_gl000225	211173	88133	0.4173	1.2805

chrUn_gl000226	15008	118369	7.8871	25.2155
chrUn_gl000227	128374	3594	0.028	0.2264
chrUn_gl000228	129120	17276	0.1338	1.0428
chrUn_gl000229	19913	24775	1.2442	2.3606
chrUn_gl000230	43691	13886	0.3178	0.9228
chrUn_gl000231	27386	25943	0.9473	1.5865
chrUn_gl000232	40652	70198	1.7268	2.4637
chrUn_gl000233	45941	19606	0.4268	1.1493
chrUn_gl000234	40531	47119	1.1625	2.1154
chrUn_gl000235	34474	37093	1.076	2.008
chrUn_gl000236	41934	1200	0.0286	0.2182
chrUn_gl000237	45867	15950	0.3477	1.1857
chrUn_gl000238	39939	890	0.0223	0.2063
chrUn_gl000239	33824	3268	0.0966	0.892
chrUn_gl000240	41933	11823	0.2819	0.7743

chrUn_gl000241	42152	61955	1.4698	2.1272
chrUn_gl000242	43523	300	0.0069	0.1148
chrUn_gl000243	43341	8297	0.1914	0.8839
chrUn_gl000244	39929	900	0.0225	0.1819
chrUn_gl000245	36651	2070	0.0565	0.3591
chrUn_gl000246	38154	3546	0.0929	0.4204
chrUn_gl000247	36422	4174	0.1146	0.6707
chrUn_gl000248	39786	1198	0.0301	0.2244
chrUn_gl000249	38502	286	0.0074	0.1217

3. Results : Coverage across reference

Coverage across reference
case4.pair1_sorted.bam

4. Results : Coverage Histogram

Coverage Histogram
case4.pair1_sorted.bam
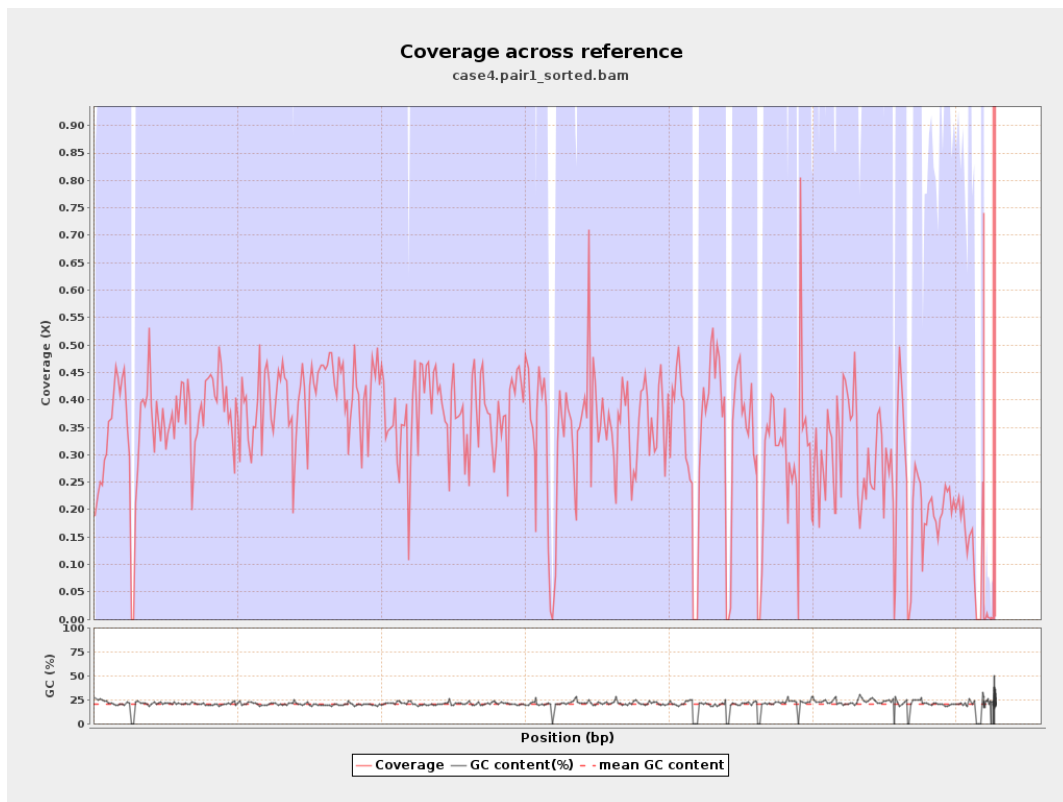
5. Results : Coverage Histogram (0-50X)
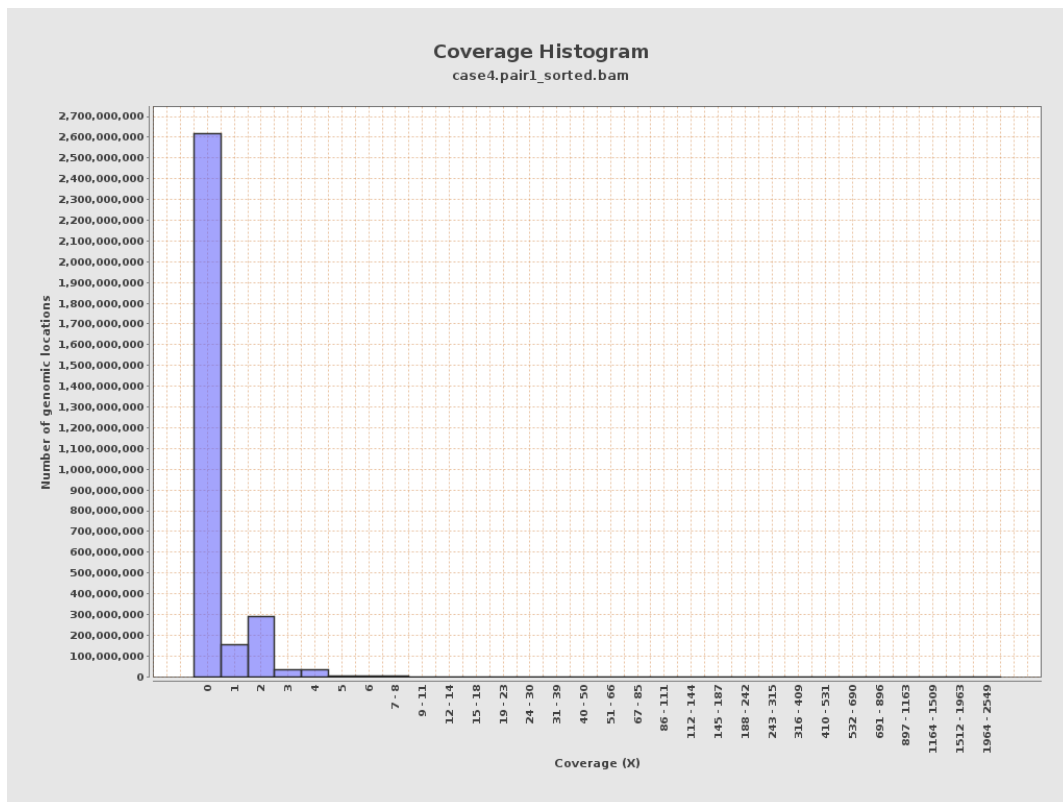
Coverage Histogram (0-50X)
case4.pair1_sorted.bam
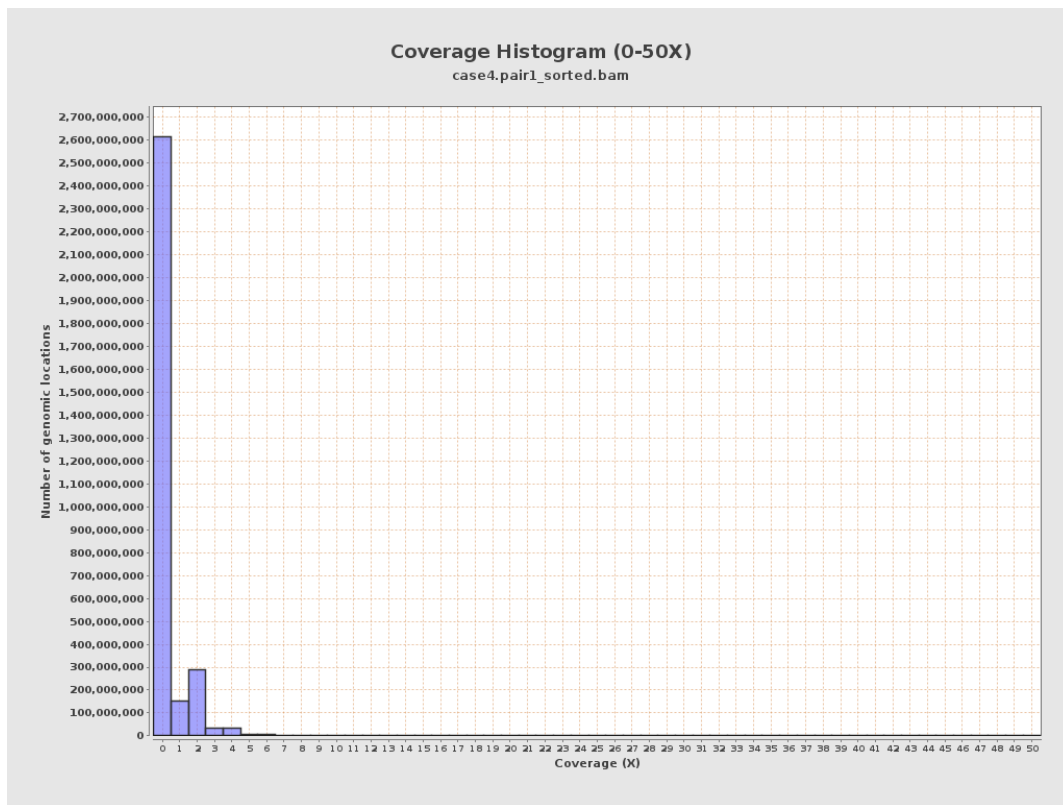
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
case4.pair1_sorted.bam
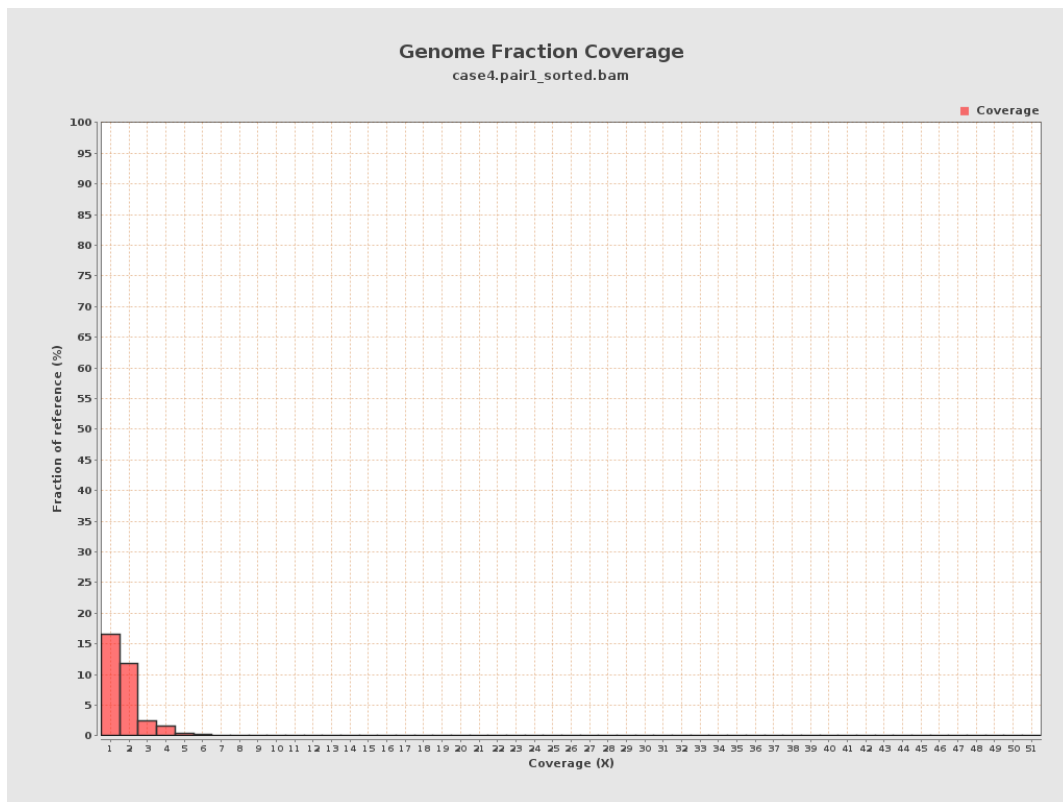
7. Results : Duplication Rate Histogram
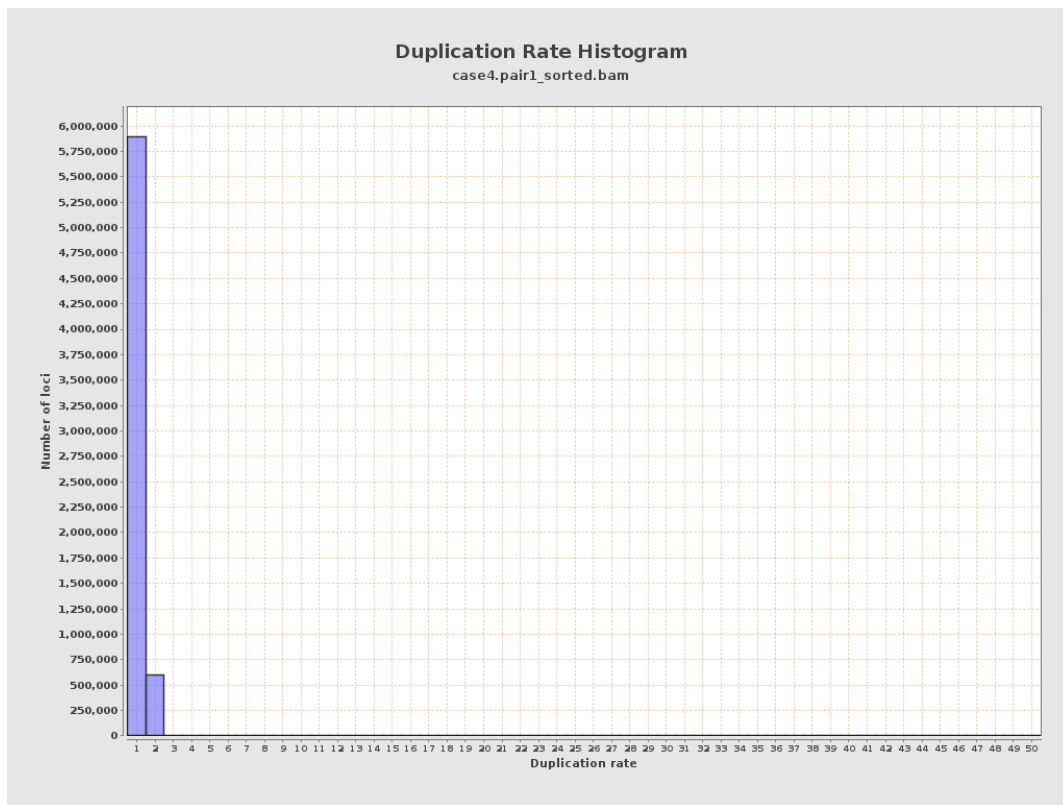
8. Results : Mapped Reads Nucleotide Content
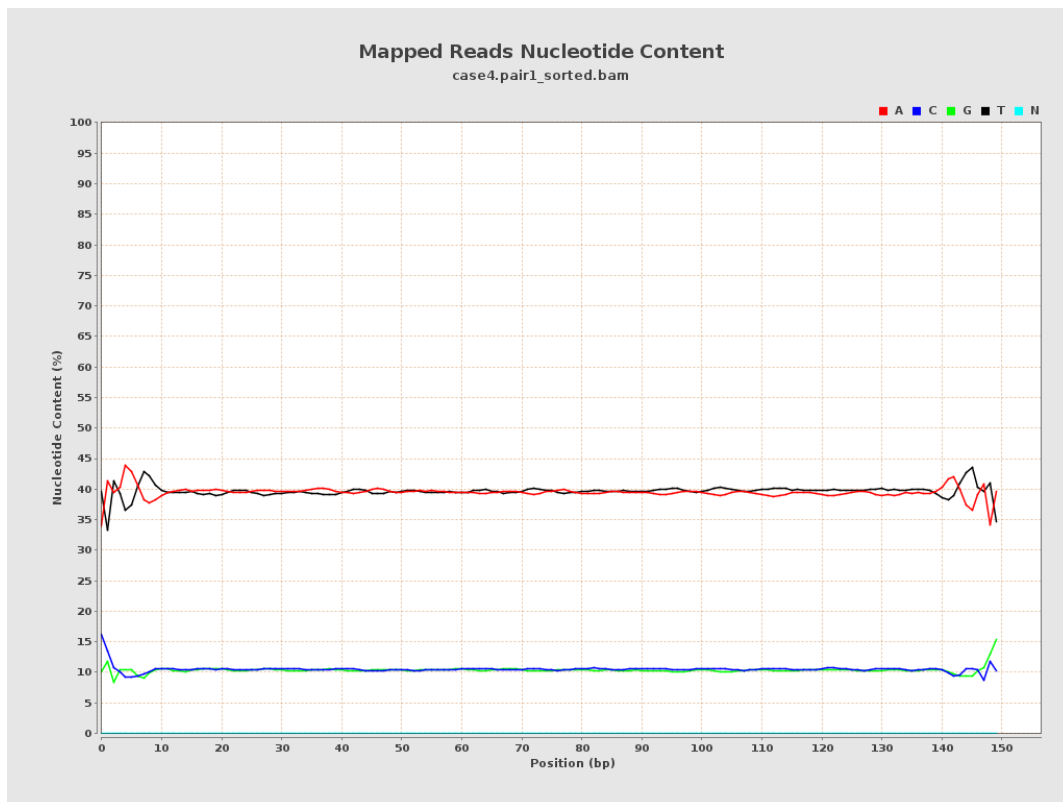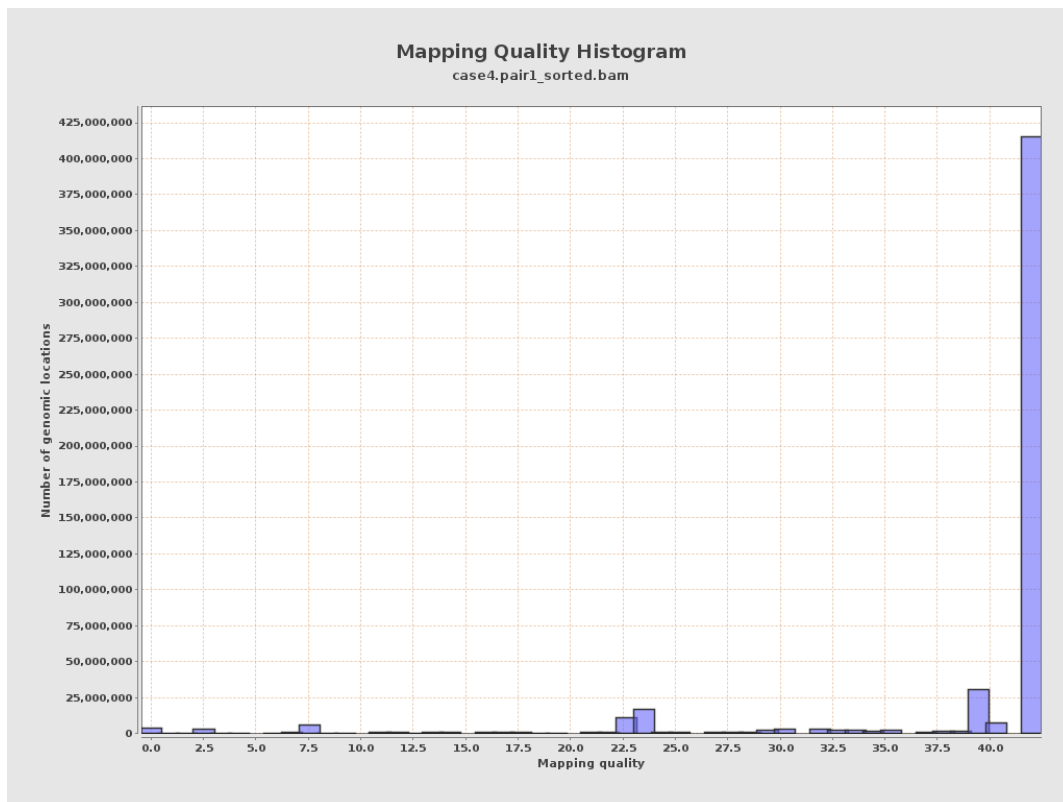
9. Results : Mapped Reads GC-content Distribution
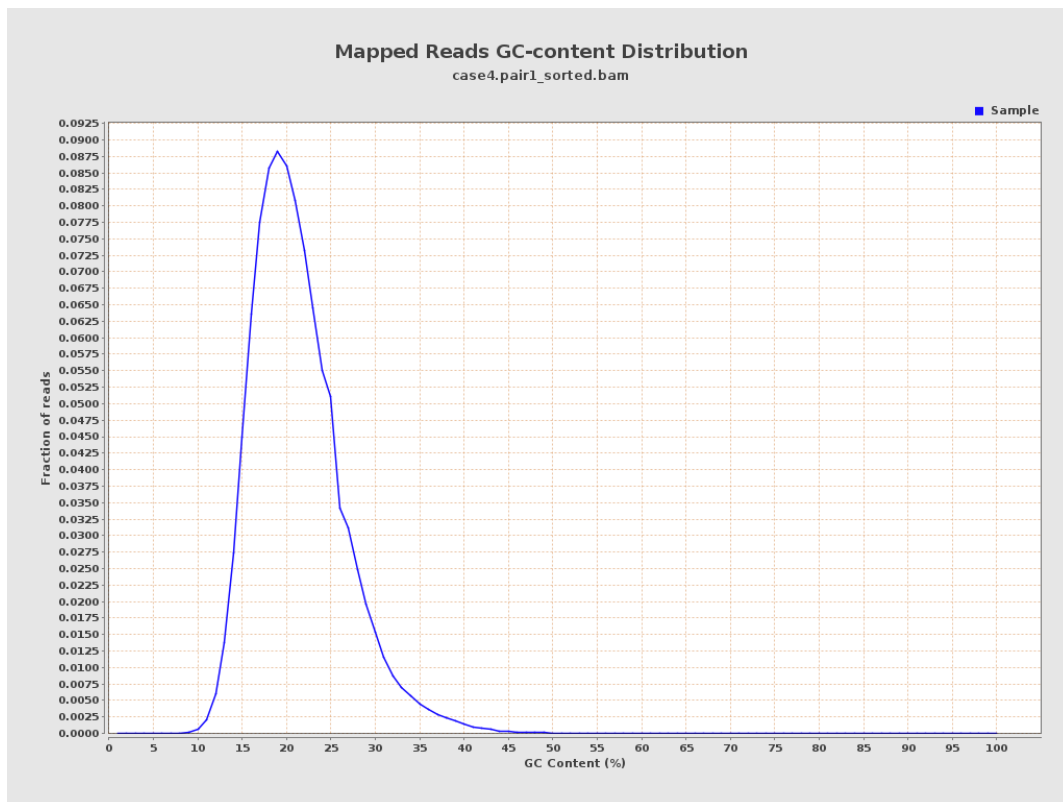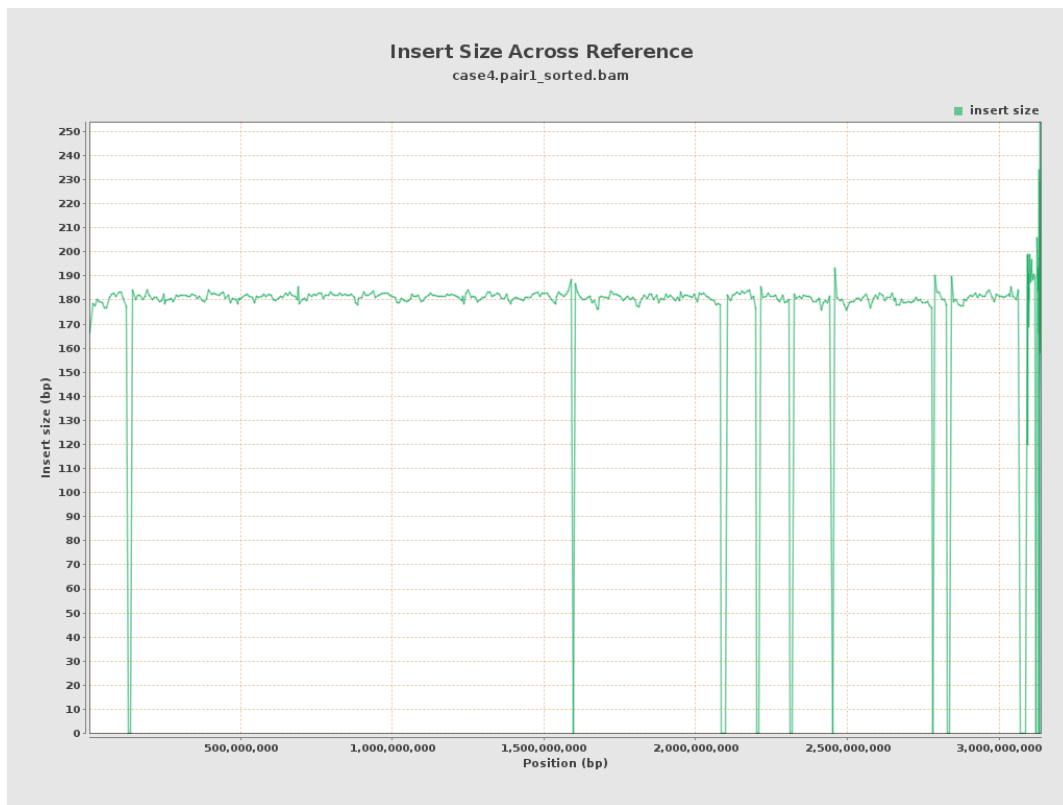
10. Results : Homopolymer Indels

Homopolymer Indels
case4.pair1_sorted.bam

11. Results : Mapping Quality Across Reference
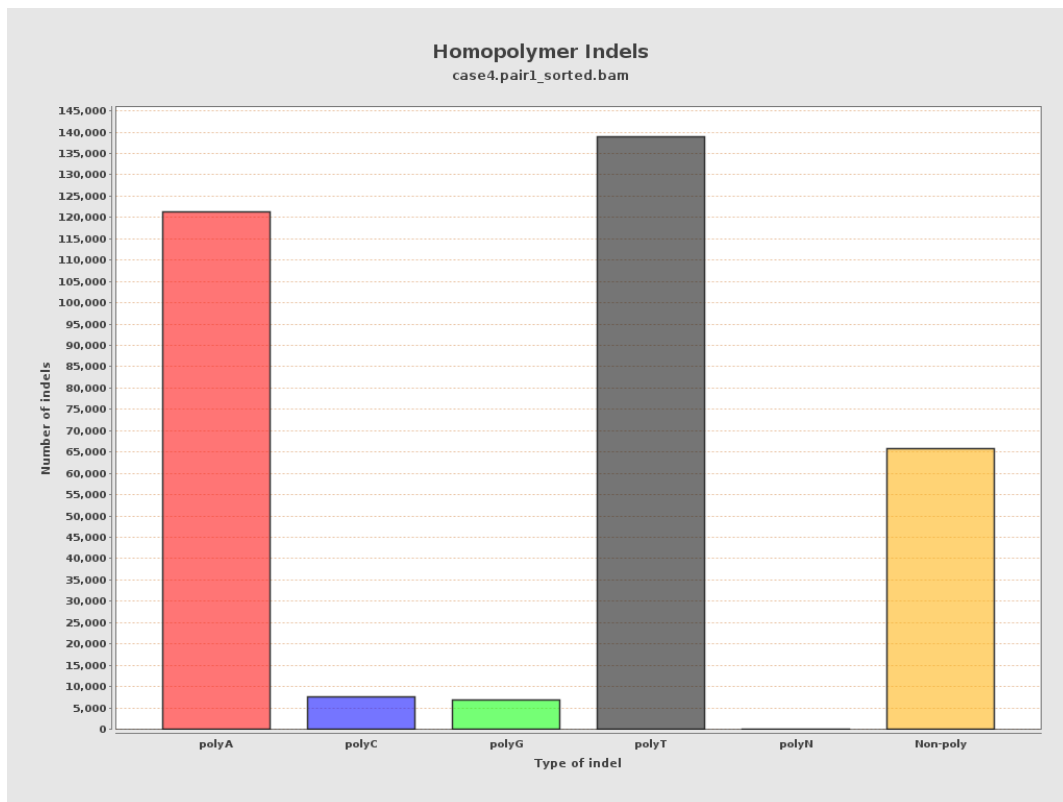
Mapping Quality Across Reference
case4.pair1_sorted.bam
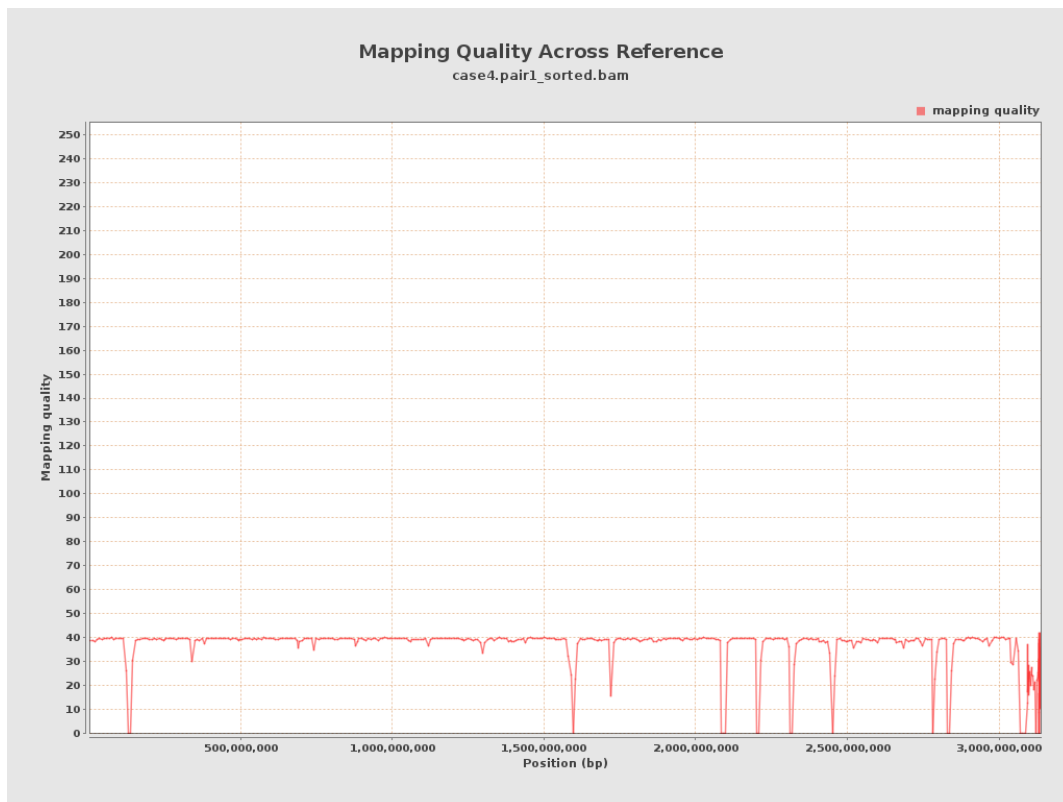
12. Results : Mapping Quality Histogram

13. Results : Insert Size Across Reference

14. Results : Insert Size Histogram