Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2021/01/12 17:42:16

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/case1.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/case1.pair1.truncated.gz -2 /opt/tsinghua/zhangwei/Pipeline_test/o_WGBS-PE/intermediate_result/step_03_adapterremoval/case1.pair2.truncated.gz"
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	Bismark (v0.23.0)

PRINCIPE FELIPE
CENTRO DE INVESTIGACION

Analysis date:	Tue Jan 12 17:42:14 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_bamsort/case1.pair1_sorted.bam

2. Summary

2.1. Globals

Reference size	3,137,161,264
Number of reads	5,237,692
Mapped reads	5,237,692 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	5,237,692 / 100%
Mapped reads, first in pair	2,618,846 / 50%
Mapped reads, second in pair	2,618,846 / 50%
Mapped reads, both in pair	5,237,692 / 100%
Mapped reads, singletons	0 / 0%
Secondary alignments	0
Read min/max/mean length	21 / 150 / 149.09
Duplicated reads (estimated)	231,706 / 4.42%
Duplication rate	4.42%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	303,150,109 / 38.95%
Number/percentage of C's	86,063,977 / 11.06%
Number/percentage of T's	303,346,900 / 38.98%
Number/percentage of G's	85,730,601 / 11.02%
Number/percentage of N's	93,413 / 0.01%
GC Percentage	22.07%

2.3. Coverage

Mean	0.2485
Standard Deviation	0.9418

2.4. Mapping Quality

Mean Mapping Quality	23.66

2.5. Insert size

Mean	198.61
Standard Deviation	58.12
P25/Median/P75	166 / 180 / 204

2.6. Mismatches and indels

General error rate	20.18%
Mismatches	154,843,251
Insertions	757,703
Mapped reads with at least one insertion	14.4%
Deletions	455,014
Mapped reads with at least one deletion	8.35%
Homopolymer indels	59.36%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

chr1	249250621	63079022	0.2531	1.6469
chr2	243199373	68011573	0.2797	0.7143
chr3	198022430	56321635	0.2844	0.7028
chr4	191154276	54844170	0.2869	0.7065
chr5	180915260	50903218	0.2814	0.7011
chr6	171115067	47514029	0.2777	0.8517
chr7	159138663	43630040	0.2742	1.7885
chr8	146364022	40973990	0.2799	0.7337
chr9	141213431	31335761	0.2219	0.6314
chr10	135534747	37080081	0.2736	1.2317
chr11	135006516	36515552	0.2705	0.6876
chr12	133851895	36775475	0.2747	0.6924
chr13	115169878	27850649	0.2418	0.6553
chr14	107349540	24964450	0.2326	0.6449
chr15	102531392	22534280	0.2198	0.6282
chr16	90354753	21360309	0.2364	1.2164
chr17	81195210	19751299	0.2433	0.6571
chr18	78077248	21672839	0.2776	0.6971
chr19	59128983	12595180	0.213	0.7269
chr20	63025520	16256766	0.2579	0.6725
chr21	48129895	10107831	0.21	0.6231
chr22	51304566	8285038	0.1615	0.5427
chrX	155270560	21326524	0.1374	0.5162
chrY	59373566	2567109	0.0432	0.4257

chrM	16571	49748	3.0021	2.2917
chr1_gl000191_random	106433	5672	0.0533	0.331
chr1_gl000192_random	547496	65176	0.119	0.4745
chr4_ctg9_hap1	590426	8095	0.0137	0.1504
chr4_gl000193_random	189789	107935	0.5687	1.0747
chr4_gl000194_random	191469	53108	0.2774	0.7429
chr6_apd_hap1	4622290	1481	0.0003	0.0285
chr6_cox_hap2	4795371	18765	0.0039	0.0847
chr6_dbb_hap3	4610396	13415	0.0029	0.072
chr6_mann_hap4	4683263	10996	0.0023	0.0672
chr6_mcf_hap5	4833398	5531	0.0011	0.0448
chr6_qbl_hap6	4611984	10960	0.0024	0.0626
chr6_ssto_hap7	4928567	13081	0.0027	0.0707
chr7_gl000195_random	182896	144186	0.7883	1.2865
chr8_gl000196_random	38914	300	0.0077	0.1135

chr8_gl000197_random	37175	304	0.0082	0.1182
chr9_gl000198_random	90085	26260	0.2915	0.8459
chr9_gl000199_random	169874	242106	1.4252	4.8623
chr9_gl000200_random	187035	0	0	0
chr9_gl000201_random	36148	0	0	0
chr11_gl000202_random	40103	3589	0.0895	0.3888
chr17_ctg5_hap1	1680828	12575	0.0075	0.1148
chr17_gl000203_random	37498	2704	0.0721	0.3694
chr17_gl000204_random	81310	8949	0.1101	0.4656
chr17_gl000205_random	174588	113408	0.6496	1.1714
chr17_gl000206_random	41001	898	0.0219	0.1953
chr18_gl000207_random	4262	1190	0.2792	0.5565
chr19_gl000208_random	92689	68416	0.7381	1.8245
chr19_gl000209_random	159169	1195	0.0075	0.1097
chr21_gl000210_random	27682	300	0.0108	0.1385

chrUn_gl0002 11	166566	42077	0.2526	0.6847
chrUn_gl0002 12	186858	42462	0.2272	0.6394
chrUn_gl0002 13	164239	5973	0.0364	0.2474
chrUn_gl0002 14	137718	127903	0.9287	1.482
chrUn_gl0002 15	172545	1498	0.0087	0.141
chrUn_gl0002 16	172294	31332	0.1819	0.5663
chrUn_gl0002 17	172149	15817	0.0919	0.4019
chrUn_gl0002 18	161147	95654	0.5936	1.0464
chrUn_gl0002 19	179198	100114	0.5587	1.0149
chrUn_gl0002 20	161802	1160973	7.1753	18.5205
chrUn_gl0002 21	155397	21713	0.1397	0.5521
chrUn_gl0002 22	186861	13482	0.0721	0.3335
chrUn_gl0002 23	180455	2111	0.0117	0.1486
chrUn_gl0002 24	179693	162710	0.9055	2.535
chrUn_gl0002 25	211173	52923	0.2506	0.7773

chrUn_gl000226	15008	220299	14.6788	42.5859
chrUn_gl000227	128374	3565	0.0278	0.2166
chrUn_gl000228	129120	12864	0.0996	0.7747
chrUn_gl000229	19913	7172	0.3602	0.8901
chrUn_gl000230	43691	10993	0.2516	0.7841
chrUn_gl000231	27386	10968	0.4005	0.9214
chrUn_gl000232	40652	28366	0.6978	1.1725
chrUn_gl000233	45941	9527	0.2074	0.5932
chrUn_gl000234	40531	26200	0.6464	1.0674
chrUn_gl000235	34474	18165	0.5269	1.0015
chrUn_gl000236	41934	1500	0.0358	0.2701
chrUn_gl000237	45867	8384	0.1828	0.5742
chrUn_gl000238	39939	1196	0.0299	0.2121
chrUn_gl000239	33824	2398	0.0709	0.3757
chrUn_gl000240	41933	10142	0.2419	0.7259

chrUn_gl000241	42152	33193	0.7875	1.2854
chrUn_gl000242	43523	300	0.0069	0.0889
chrUn_gl000243	43341	7194	0.166	0.5601
chrUn_gl000244	39929	298	0.0075	0.1105
chrUn_gl000245	36651	602	0.0164	0.1728
chrUn_gl000246	38154	2999	0.0786	0.3505
chrUn_gl000247	36422	2397	0.0658	0.3467
chrUn_gl000248	39786	2998	0.0754	0.4061
chrUn_gl000249	38502	0	0	0

3. Results : Coverage across reference

4. Results : Coverage Histogram

Coverage Histogram
case1.pair1_sorted.bam

5. Results : Coverage Histogram (0-50X)
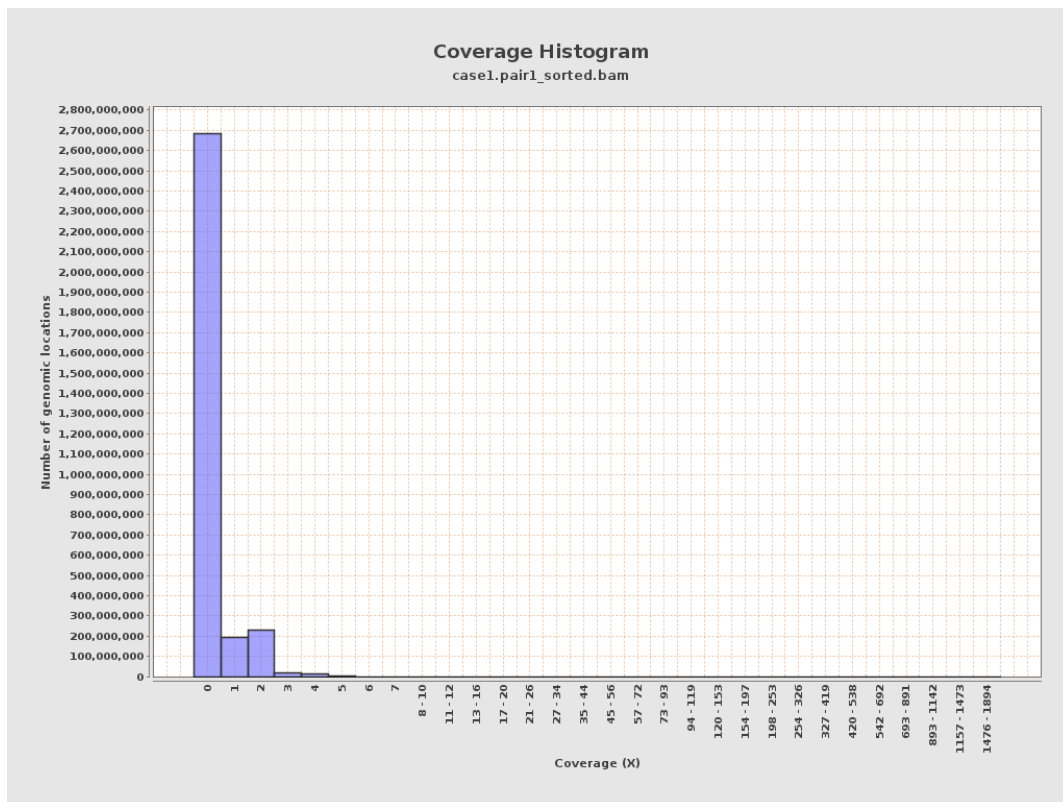
Coverage Histogram (0-50X)
case1.pair1_sorted.bam
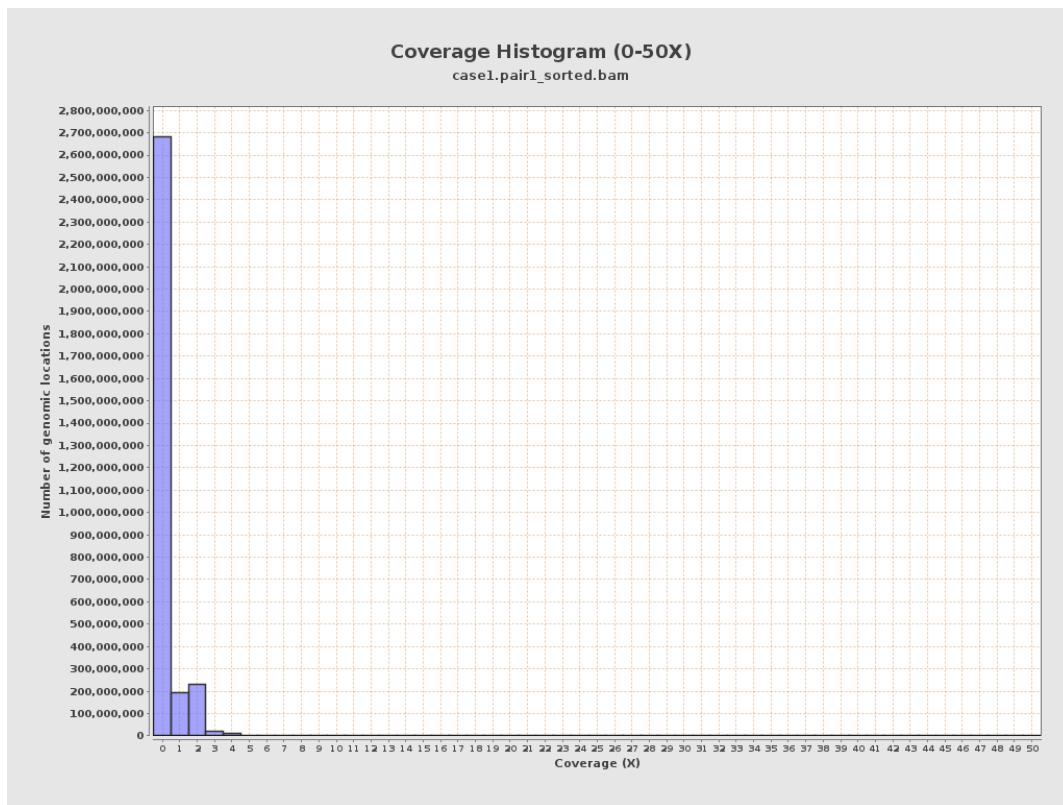
6. Results : Genome Fraction Coverage
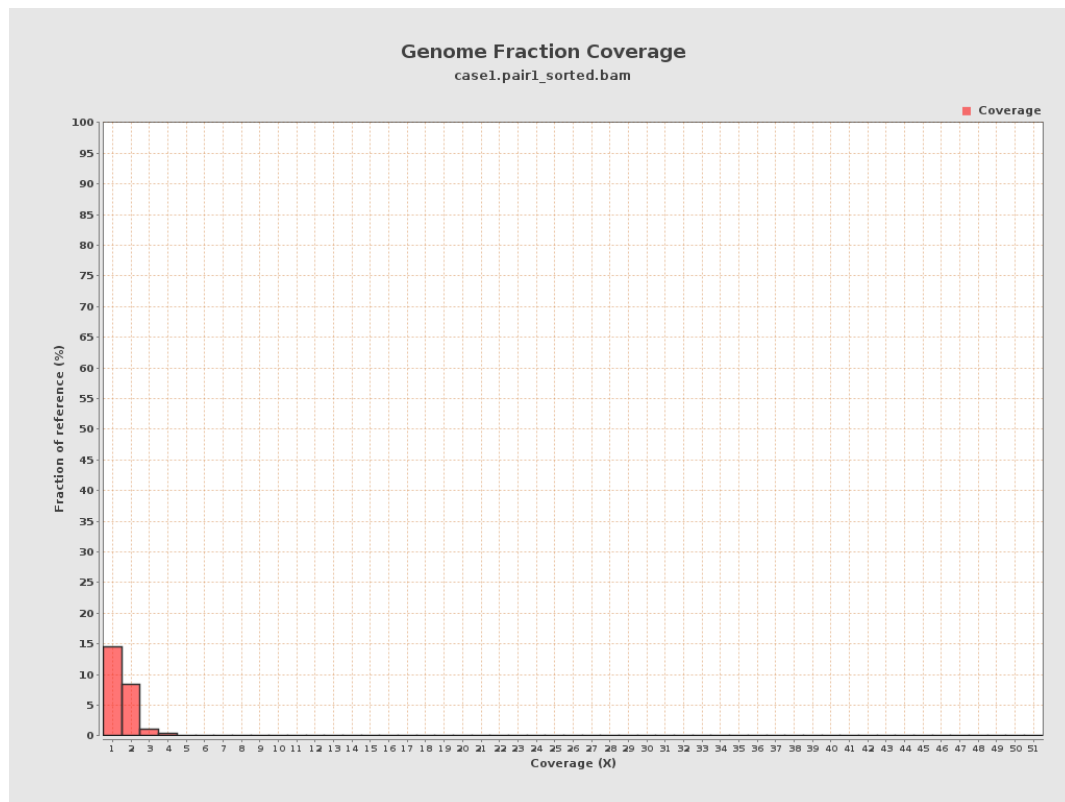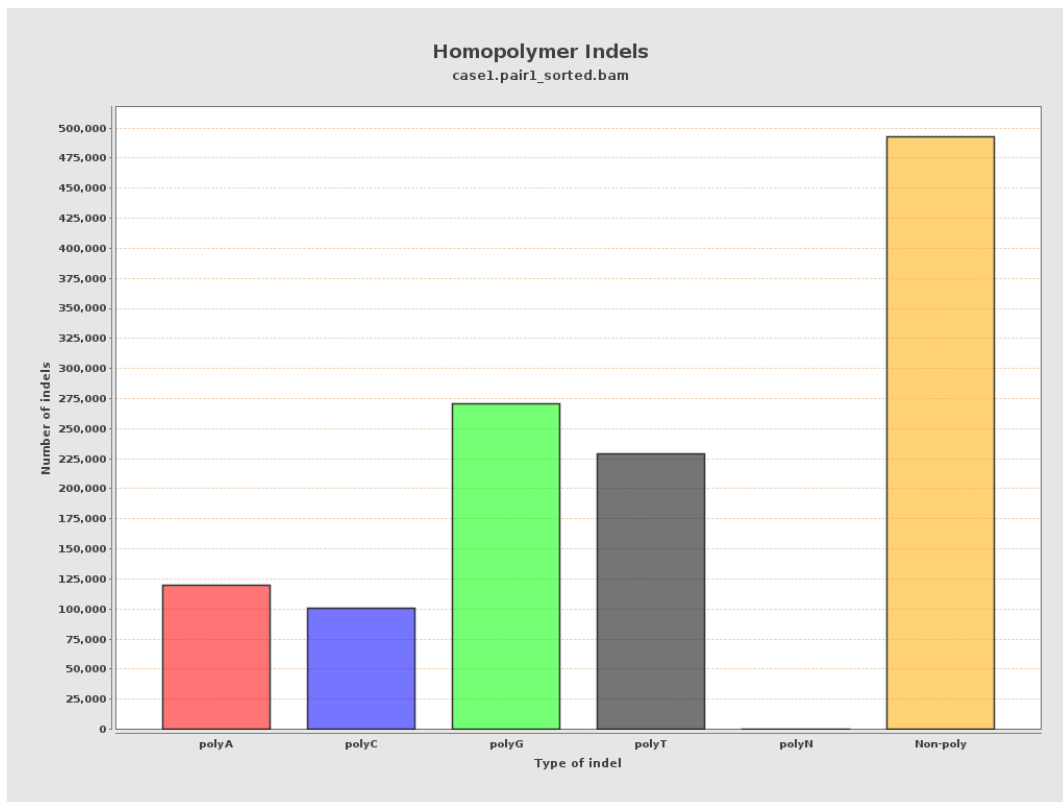
7. Results : Duplication Rate Histogram
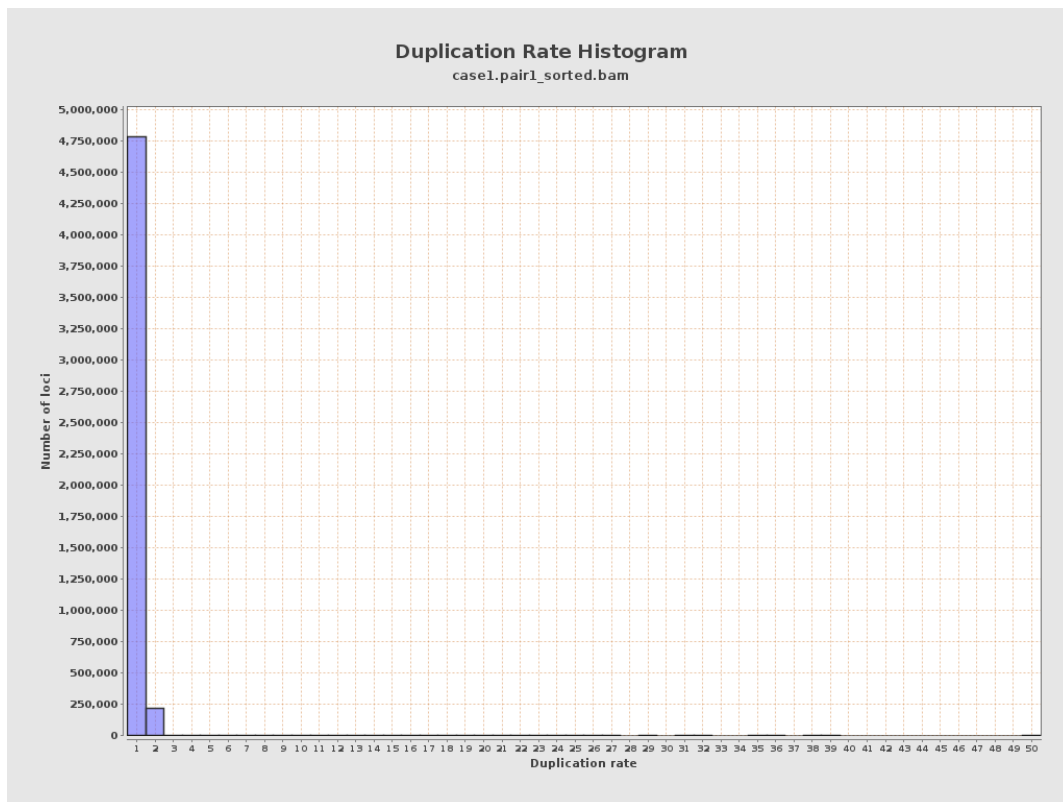
8. Results : Mapped Reads Nucleotide Content
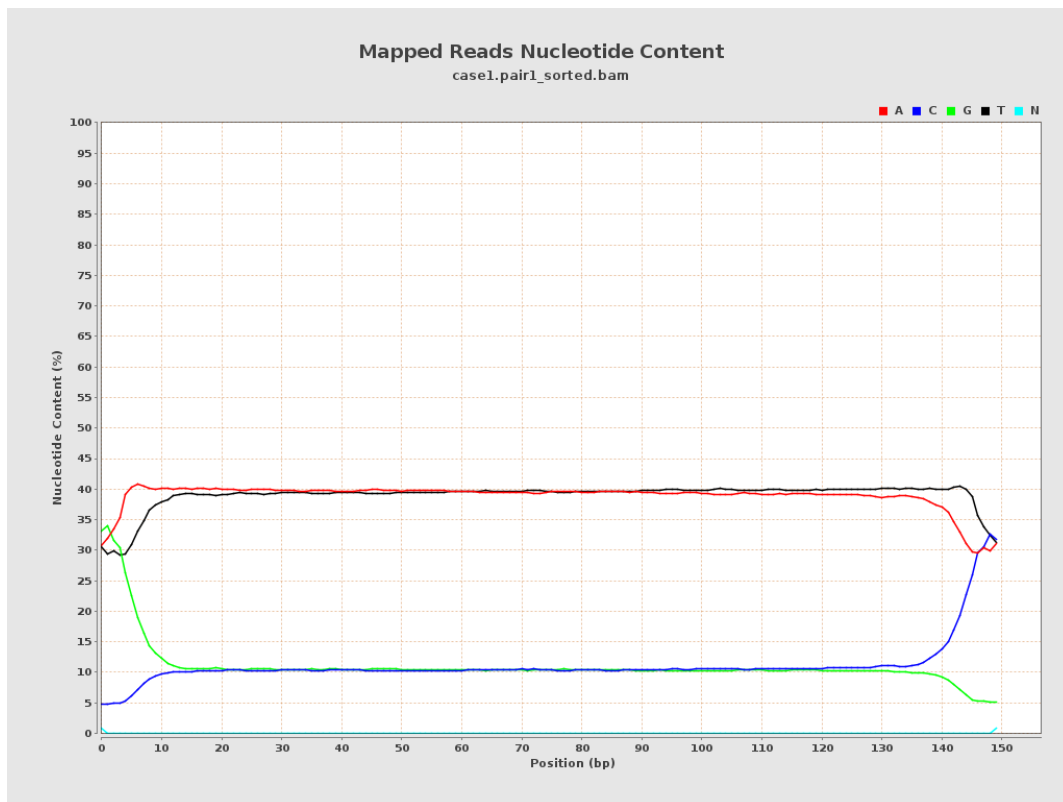
9. Results : Mapped Reads GC-content Distribution
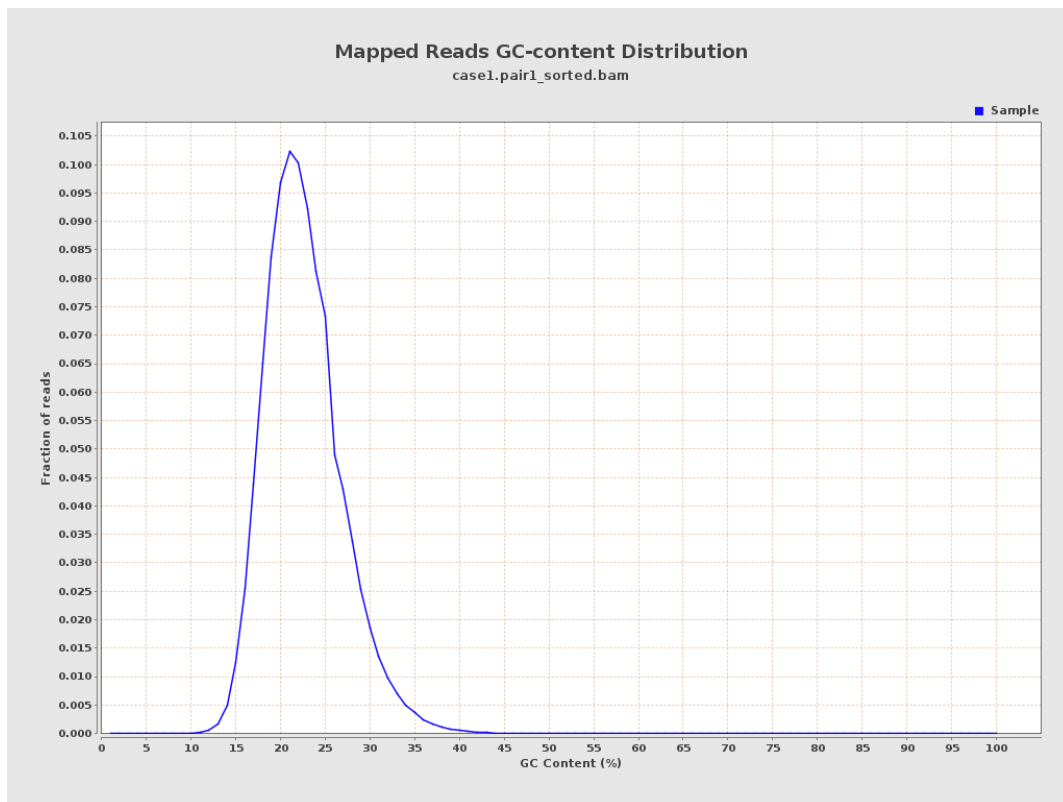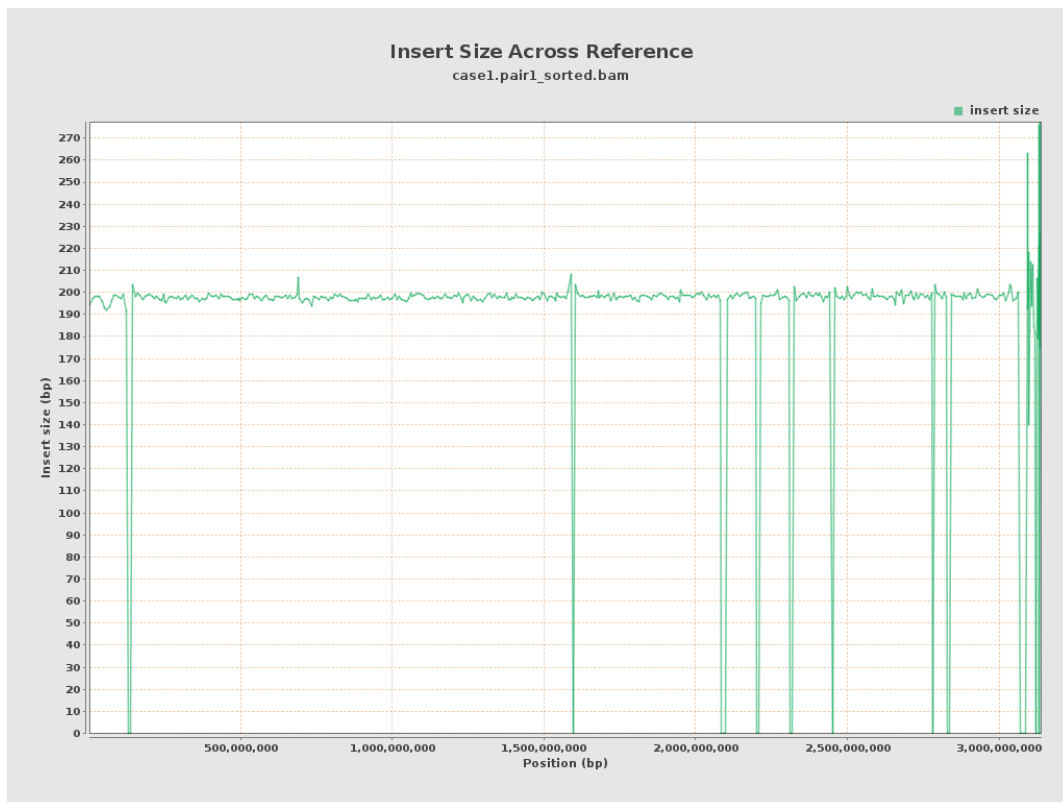
10. Results : Homopolymer Indels

11. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
case1.pair1_sorted.bam
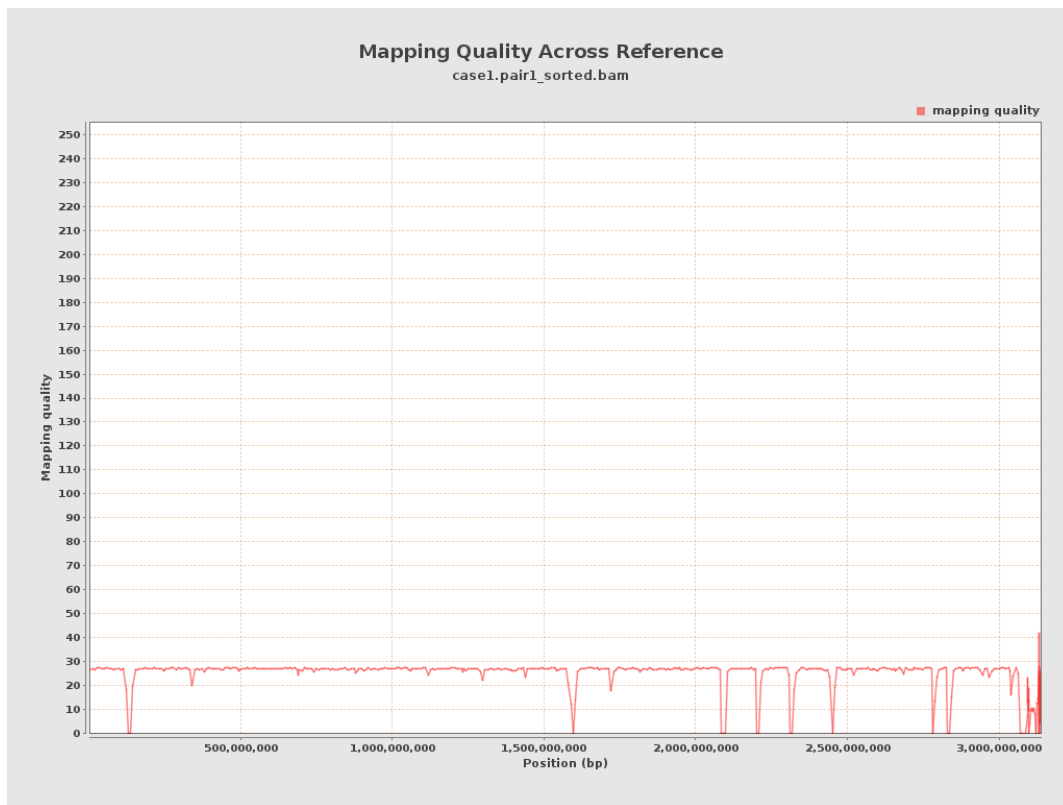
12. Results : Mapping Quality Histogram
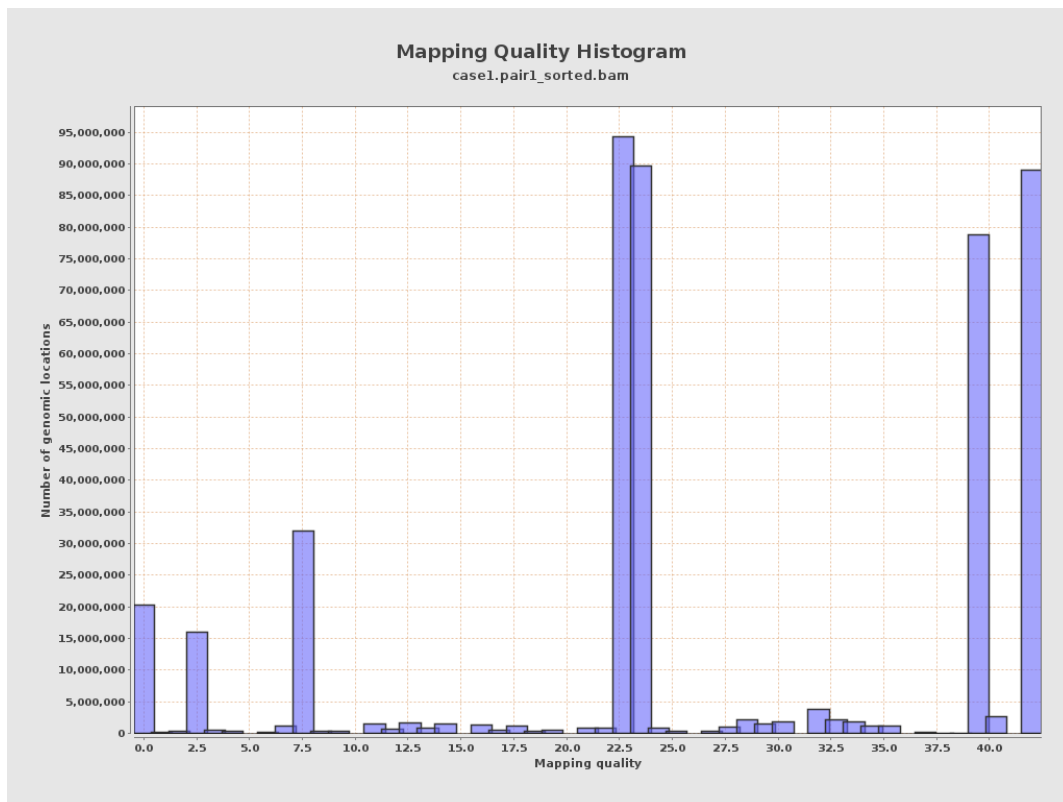
13. Results : Insert Size Across Reference

14. Results : Insert Size Histogram