

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2021/01/12 17:43:31

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/case2.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/case2.pair1.truncated.gz -2 /opt/tsinghua/zhangwei/Pipeline_test/o_WGBS-PE/intermediate_result/step_03_adapterremoval/case2.pair2.truncated.gz"
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	Bismark (v0.23.0)

Analysis date:	Tue Jan 12 17:43:29 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/case2.pair1_sorted.bam

2. Summary

2.1. Globals

Reference size	3,137,161,264
Number of reads	5,105,250
Mapped reads	5,105,250 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	5,105,250 / 100%
Mapped reads, first in pair	2,552,625 / 50%
Mapped reads, second in pair	2,552,625 / 50%
Mapped reads, both in pair	5,105,250 / 100%
Mapped reads, singletons	0 / 0%
Secondary alignments	0
Read min/max/mean length	20 / 150 / 149.14
Duplicated reads (estimated)	214,402 / 4.2%
Duplication rate	4.17%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	296,076,478 / 39.02%
Number/percentage of C's	83,505,437 / 11%
Number/percentage of T's	296,160,353 / 39.03%
Number/percentage of G's	83,116,949 / 10.95%
Number/percentage of N's	91,233 / 0.01%
GC Percentage	21.96%

2.3. Coverage

Mean	0.2423
Standard Deviation	0.9439

2.4. Mapping Quality

Mean Mapping Quality	23.59
----------------------	-------

2.5. Insert size

Mean	198.61
Standard Deviation	57.36
P25/Median/P75	167 / 180 / 204

2.6. Mismatches and indels

General error rate	19.68%
Mismatches	147,109,330
Insertions	743,996
Mapped reads with at least one insertion	14.51%
Deletions	442,194
Mapped reads with at least one deletion	8.32%
Homopolymer indels	59.39%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

chr1	249250621	61093747	0.2451	1.7199
chr2	243199373	66783452	0.2746	0.7159
chr3	198022430	55578115	0.2807	0.6996
chr4	191154276	54161013	0.2833	0.7043
chr5	180915260	50215841	0.2776	0.6982
chr6	171115067	46837526	0.2737	0.8487
chr7	159138663	42687102	0.2682	1.8202
chr8	146364022	40079652	0.2738	0.7358
chr9	141213431	30606444	0.2167	0.6249
chr10	135534747	35857045	0.2646	1.155
chr11	135006516	35256521	0.2611	0.6762
chr12	133851895	36002152	0.269	0.686
chr13	115169878	27608771	0.2397	0.6533
chr14	107349540	24370420	0.227	0.638
chr15	102531392	21686845	0.2115	0.6181
chr16	90354753	20271023	0.2243	1.1292
chr17	81195210	18642664	0.2296	0.6398
chr18	78077248	21452223	0.2748	0.6949
chr19	59128983	11503775	0.1946	0.6893
chr20	63025520	15384207	0.2441	0.6539
chr21	48129895	9838490	0.2044	0.6171
chr22	51304566	7528211	0.1467	0.5139
chrX	155270560	20943808	0.1349	0.5198
chrY	59373566	2492592	0.042	0.3929

chrM	16571	72837	4.3954	2.3182
chr1_gl00019 1_random	106433	5090	0.0478	0.2929
chr1_gl00019 2_random	547496	68355	0.1249	0.4751
chr4_ctg9_ha p1	590426	7992	0.0135	0.161
chr4_gl00019 3_random	189789	100544	0.5298	1.0222
chr4_gl00019 4_random	191469	53850	0.2812	0.7131
chr6_apd_ha p1	4622290	1800	0.0004	0.0278
chr6_cox_hap 2	4795371	18386	0.0038	0.0808
chr6_dbb_ha p3	4610396	8368	0.0018	0.0561
chr6_mann_h ap4	4683263	10473	0.0022	0.0613
chr6_mcf_ha p5	4833398	6849	0.0014	0.0478
chr6_qbl_hap 6	4611984	8688	0.0019	0.0578
chr6_ssto_ha p7	4928567	15481	0.0031	0.0759
chr7_gl00019 5_random	182896	127366	0.6964	1.2305
chr8_gl00019 6_random	38914	1200	0.0308	0.2307

chr8_gl00019 7_random	37175	302	0.0081	0.0895
chr9_gl00019 8_random	90085	30464	0.3382	0.9629
chr9_gl00019 9_random	169874	264718	1.5583	4.8811
chr9_gl00020 0_random	187035	0	0	0
chr9_gl00020 1_random	36148	0	0	0
chr11_gl0002 02_random	40103	2995	0.0747	0.3441
chr17_ctg5_h ap1	1680828	10787	0.0064	0.1099
chr17_gl0002 03_random	37498	4469	0.1192	0.5068
chr17_gl0002 04_random	81310	8653	0.1064	0.4359
chr17_gl0002 05_random	174588	103397	0.5922	1.1472
chr17_gl0002 06_random	41001	1198	0.0292	0.2133
chr18_gl0002 07_random	4262	891	0.2091	0.5798
chr19_gl0002 08_random	92689	63835	0.6887	1.5372
chr19_gl0002 09_random	159169	2397	0.0151	0.1467
chr21_gl0002 10_random	27682	0	0	0

chrUn_gl0002 11	166566	48961	0.2939	0.7182
chrUn_gl0002 12	186858	49403	0.2644	0.7052
chrUn_gl0002 13	164239	5049	0.0307	0.2231
chrUn_gl0002 14	137718	128148	0.9305	1.566
chrUn_gl0002 15	172545	2699	0.0156	0.1749
chrUn_gl0002 16	172294	28016	0.1626	0.567
chrUn_gl0002 17	172149	16456	0.0956	0.4006
chrUn_gl0002 18	161147	91195	0.5659	1.014
chrUn_gl0002 19	179198	88392	0.4933	0.9392
chrUn_gl0002 20	161802	1112967	6.8786	18.1671
chrUn_gl0002 21	155397	19432	0.125	0.5045
chrUn_gl0002 22	186861	12464	0.0667	0.3302
chrUn_gl0002 23	180455	1491	0.0083	0.1138
chrUn_gl0002 24	179693	151768	0.8446	2.0539
chrUn_gl0002 25	211173	43190	0.2045	0.6718

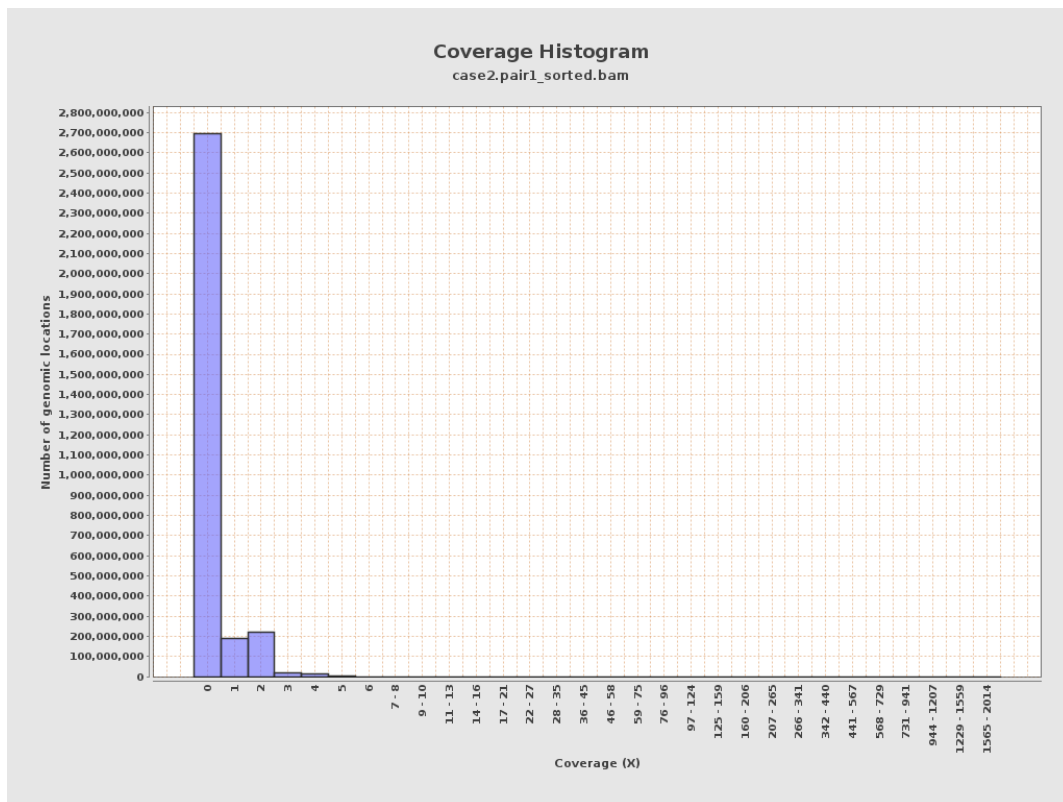
chrUn_gl0002 26	15008	209046	13.929	41.2561
chrUn_gl0002 27	128374	3007	0.0234	0.1956
chrUn_gl0002 28	129120	6285	0.0487	0.3418
chrUn_gl0002 29	19913	9238	0.4639	1.1162
chrUn_gl0002 30	43691	10370	0.2373	0.6925
chrUn_gl0002 31	27386	9825	0.3588	0.8998
chrUn_gl0002 32	40652	23241	0.5717	1.048
chrUn_gl0002 33	45941	9584	0.2086	0.6921
chrUn_gl0002 34	40531	22071	0.5445	0.9736
chrUn_gl0002 35	34474	22146	0.6424	1.1116
chrUn_gl0002 36	41934	298	0.0071	0.1126
chrUn_gl0002 37	45867	8698	0.1896	0.6248
chrUn_gl0002 38	39939	598	0.015	0.1642
chrUn_gl0002 39	33824	1457	0.0431	0.3234
chrUn_gl0002 40	41933	10966	0.2615	0.7015

chrUn_gl0002 41	42152	36339	0.8621	1.3039
chrUn_gl0002 42	43523	1206	0.0277	0.213
chrUn_gl0002 43	43341	4790	0.1105	0.4277
chrUn_gl0002 44	39929	604	0.0151	0.1629
chrUn_gl0002 45	36651	896	0.0244	0.2243
chrUn_gl0002 46	38154	3577	0.0938	0.4585
chrUn_gl0002 47	36422	1726	0.0474	0.2901
chrUn_gl0002 48	39786	1500	0.0377	0.2548
chrUn_gl0002 49	38502	300	0.0078	0.1184

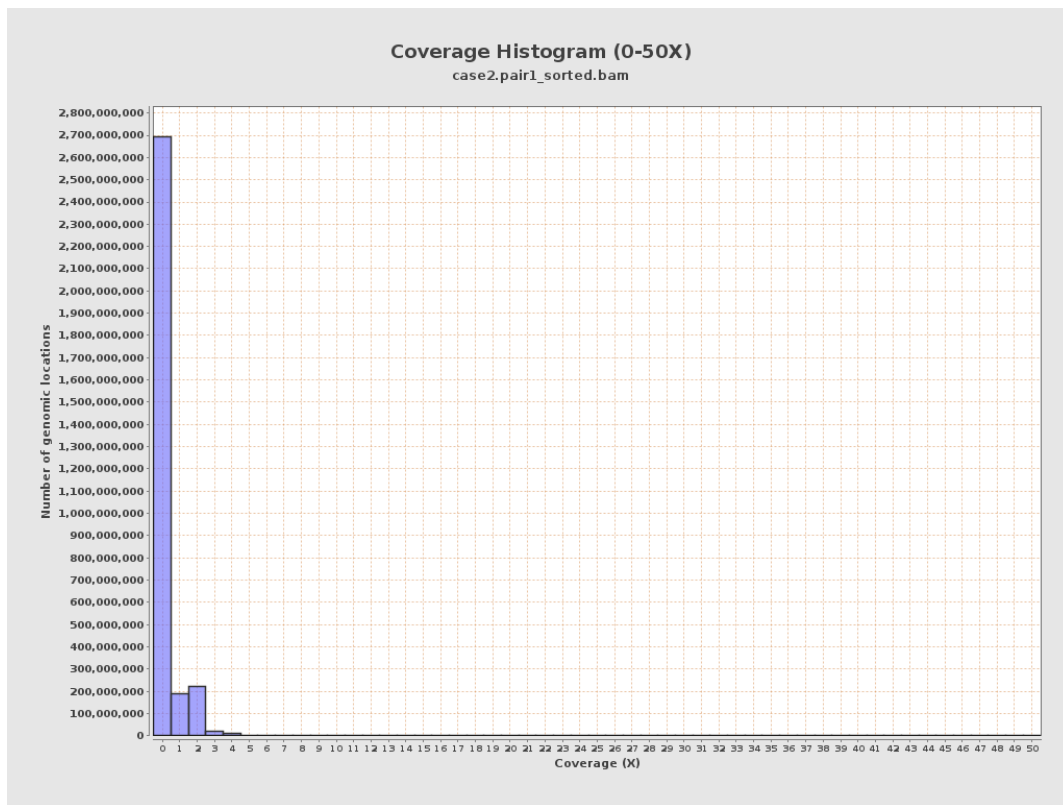
3. Results : Coverage across reference



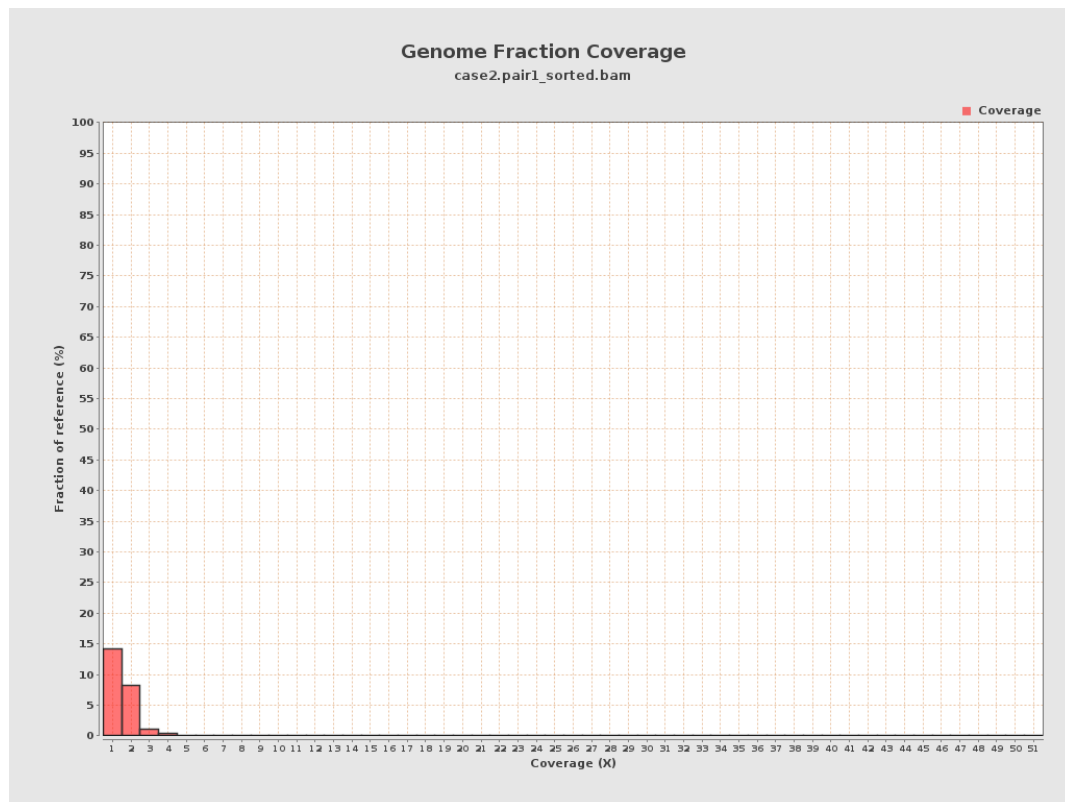
4. Results : Coverage Histogram



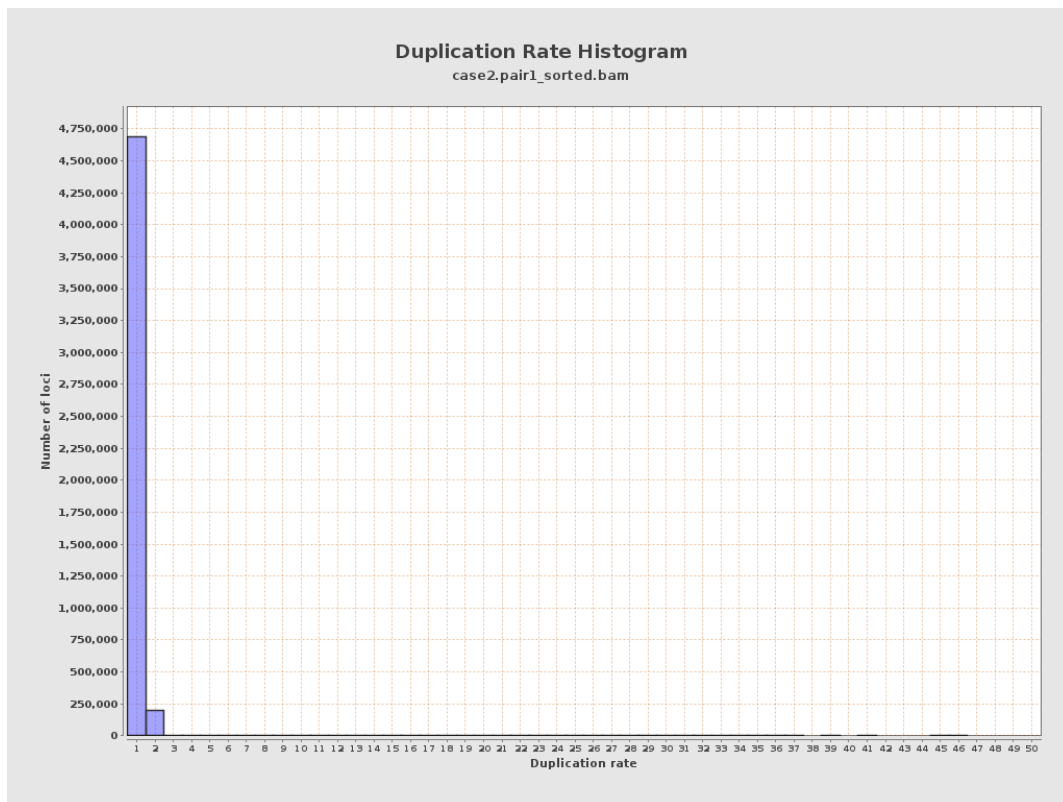
5. Results : Coverage Histogram (0-50X)



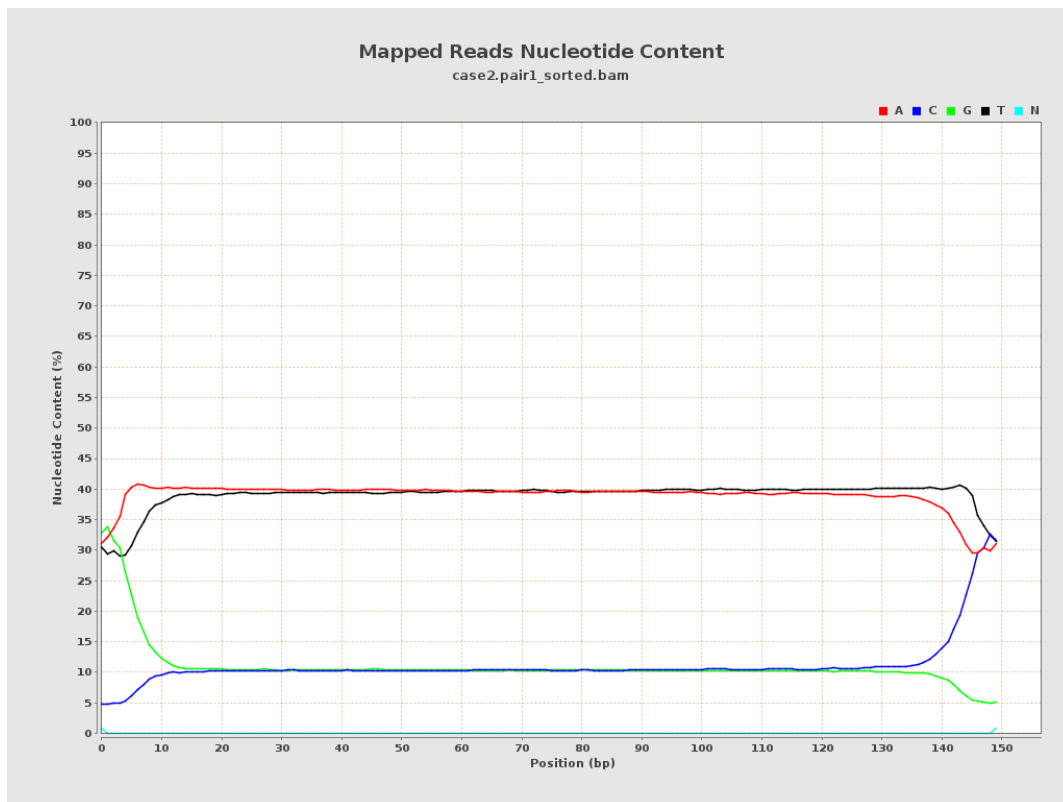
6. Results : Genome Fraction Coverage



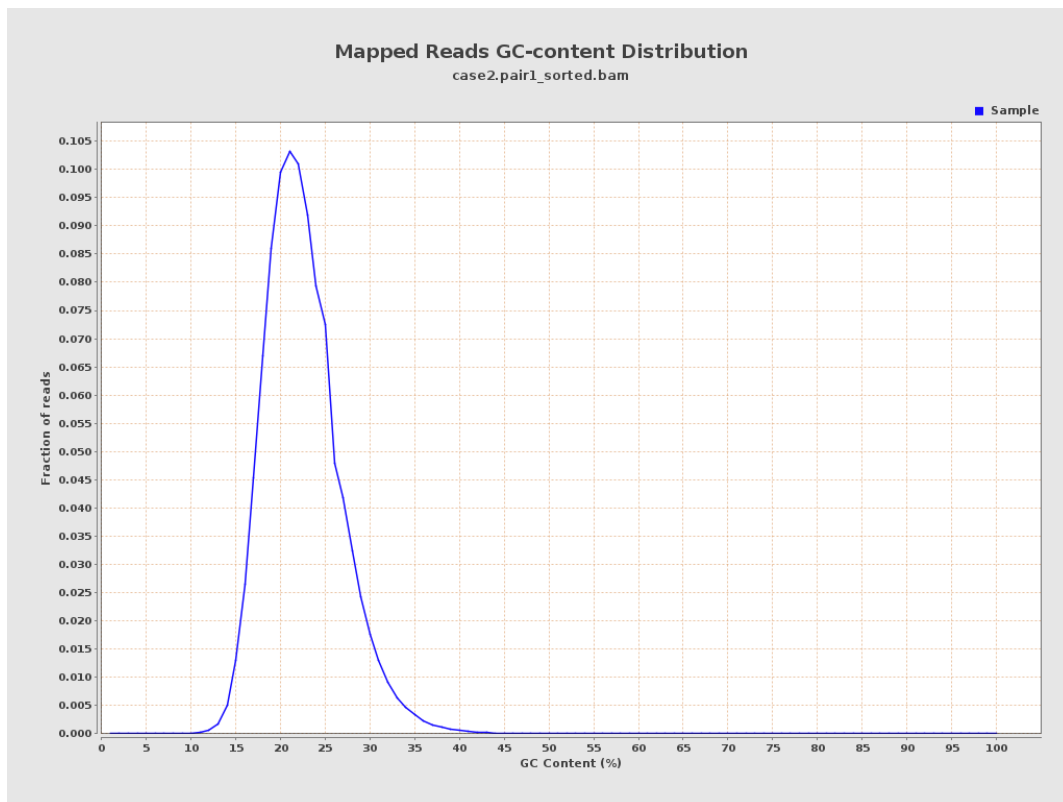
7. Results : Duplication Rate Histogram



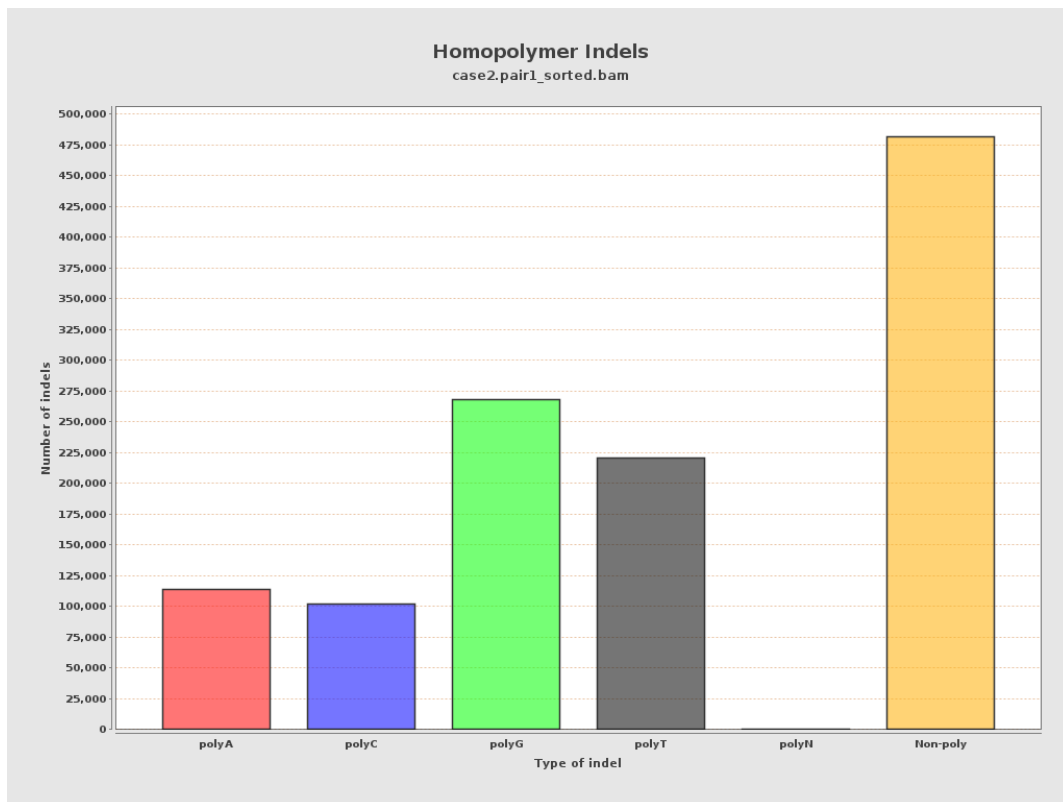
8. Results : Mapped Reads Nucleotide Content



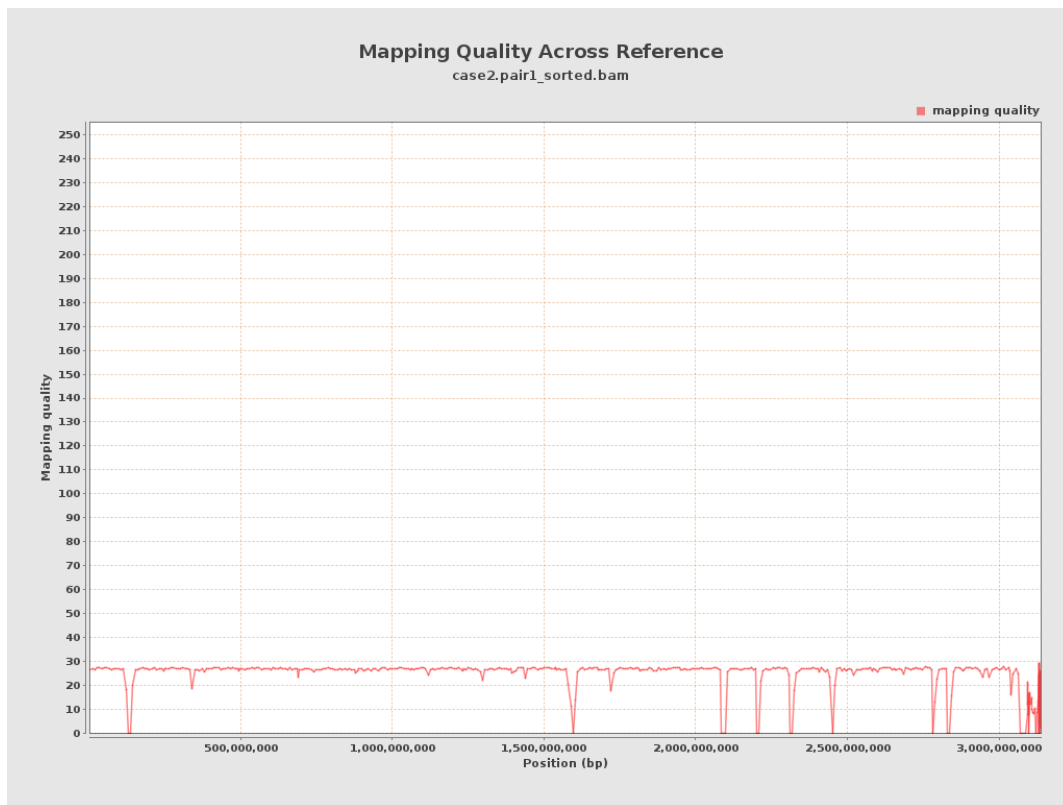
9. Results : Mapped Reads GC-content Distribution



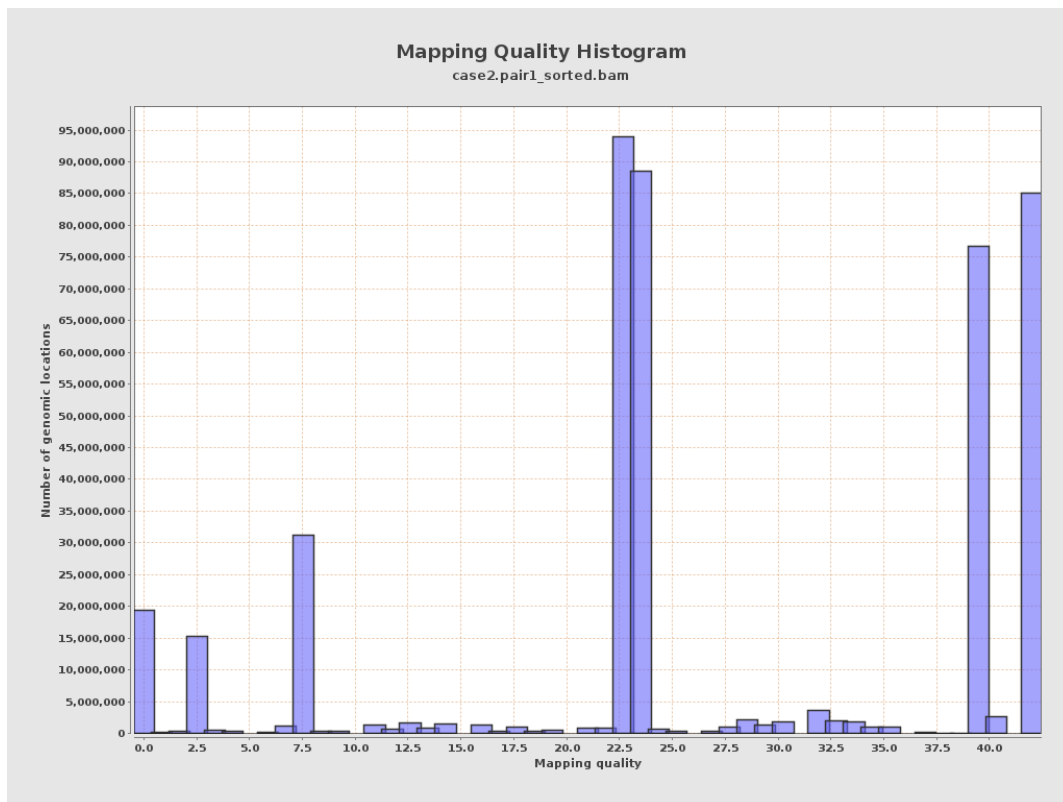
10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram



13. Results : Insert Size Across Reference



14. Results : Insert Size Histogram

