

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2021/01/12 17:45:12

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/case3.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/case3.pair1.truncated.gz -2 /opt/tsinghua/zhangwei/Pipeline_test/o_WGBS-PE/intermediate_result/step_03_adapterremoval/case3.pair2.truncated.gz"
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	Bismark (v0.23.0)

Analysis date:	Tue Jan 12 17:45:10 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/case3.pair1_sorted.bam

2. Summary

2.1. Globals

Reference size	3,137,161,264
Number of reads	6,967,966
Mapped reads	6,967,966 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	6,967,966 / 100%
Mapped reads, first in pair	3,483,983 / 50%
Mapped reads, second in pair	3,483,983 / 50%
Mapped reads, both in pair	6,967,966 / 100%
Mapped reads, singletons	0 / 0%
Secondary alignments	0
Read min/max/mean length	16 / 150 / 147.77
Duplicated reads (estimated)	637,869 / 9.15%
Duplication rate	9.05%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	407,365,880 / 39.57%
Number/percentage of C's	107,531,610 / 10.45%
Number/percentage of T's	409,116,580 / 39.74%
Number/percentage of G's	105,366,081 / 10.24%
Number/percentage of N's	17,066 / 0%
GC Percentage	20.68%

2.3. Coverage

Mean	0.3282
Standard Deviation	2.002

2.4. Mapping Quality

Mean Mapping Quality	34.57
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2.5. Insert size

Mean	183.93
Standard Deviation	55.73
P25/Median/P75	159 / 169 / 183

2.6. Mismatches and indels

General error rate	14.8%
Mismatches	152,147,393
Insertions	164,500
Mapped reads with at least one insertion	2.32%
Deletions	169,325
Mapped reads with at least one deletion	2.39%
Homopolymer indels	80.57%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

chr1	249250621	80451118	0.3228	2.0751
chr2	243199373	90241857	0.3711	0.9159
chr3	198022430	75588424	0.3817	0.9263
chr4	191154276	78862986	0.4126	0.9616
chr5	180915260	68806466	0.3803	0.9142
chr6	171115067	64281675	0.3757	0.9749
chr7	159138663	57723661	0.3627	1.4128
chr8	146364022	54123222	0.3698	0.9107
chr9	141213431	40359366	0.2858	0.8122
chr10	135534747	49613776	0.3661	5.4646
chr11	135006516	46407027	0.3437	0.8714
chr12	133851895	48047946	0.359	0.8854
chr13	115169878	39592624	0.3438	0.8772
chr14	107349540	32572224	0.3034	0.8272
chr15	102531392	27894182	0.2721	0.7922
chr16	90354753	26812883	0.2968	4.3427
chr17	81195210	21993741	0.2709	0.7778
chr18	78077248	29041943	0.372	0.9064
chr19	59128983	13835214	0.234	0.9313
chr20	63025520	18128797	0.2876	0.8062
chr21	48129895	13891334	0.2886	0.8942
chr22	51304566	8286487	0.1615	0.613
chrX	155270560	29873275	0.1924	0.6306
chrY	59373566	5322124	0.0896	4.5199

chrM	16571	5910	0.3566	0.7373
chr1_gl00019 1_random	106433	4605	0.0433	0.276
chr1_gl00019 2_random	547496	101645	0.1857	0.6538
chr4_ctg9_ha p1	590426	13291	0.0225	0.2051
chr4_gl00019 3_random	189789	126521	0.6666	1.4762
chr4_gl00019 4_random	191469	73615	0.3845	1.0788
chr6_apd_ha p1	4622290	1791	0.0004	0.0299
chr6_cox_hap 2	4795371	23869	0.005	0.1024
chr6_dbb_ha p3	4610396	11552	0.0025	0.0715
chr6_mann_h ap4	4683263	14507	0.0031	0.0845
chr6_mcf_ha p5	4833398	12456	0.0026	0.0715
chr6_qbl_hap 6	4611984	11489	0.0025	0.0686
chr6_ssto_ha p7	4928567	15046	0.0031	0.0807
chr7_gl00019 5_random	182896	198934	1.0877	1.9981
chr8_gl00019 6_random	38914	900	0.0231	0.2615

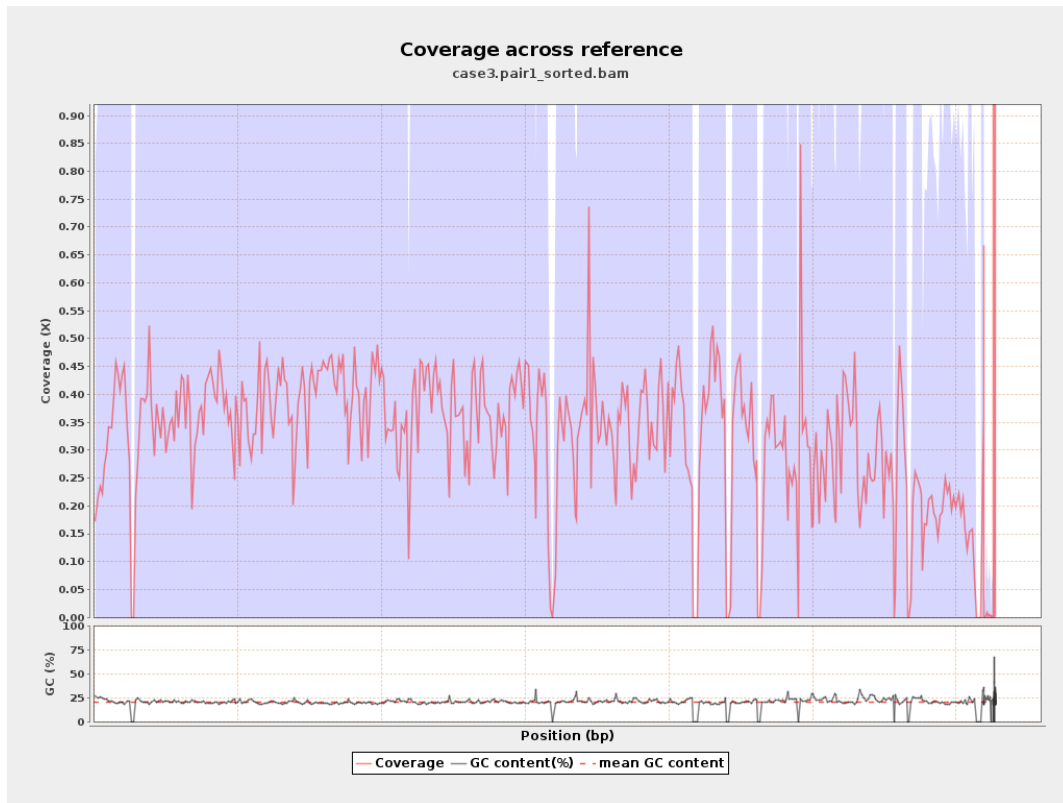
chr8_gl000197_random	37175	0	0	0
chr9_gl000198_random	90085	60455	0.6711	1.8004
chr9_gl000199_random	169874	158084	0.9306	3.5331
chr9_gl000200_random	187035	0	0	0
chr9_gl000201_random	36148	300	0.0083	0.1246
chr11_gl000202_random	40103	3543	0.0883	0.4567
chr17_ctg5_hap1	1680828	9798	0.0058	0.1104
chr17_gl000203_random	37498	7915	0.2111	0.756
chr17_gl000204_random	81310	7613	0.0936	0.4125
chr17_gl000205_random	174588	145235	0.8319	1.7938
chr17_gl000206_random	41001	1178	0.0287	0.2192
chr18_gl000207_random	4262	582	0.1366	0.4984
chr19_gl000208_random	92689	58911	0.6356	1.634
chr19_gl000209_random	159169	2698	0.017	0.177
chr21_gl000210_random	27682	0	0	0

chrUn_gl0002 11	166566	61791	0.371	0.889
chrUn_gl0002 12	186858	74844	0.4005	2.9007
chrUn_gl0002 13	164239	10658	0.0649	0.3465
chrUn_gl0002 14	137718	211190	1.5335	2.6132
chrUn_gl0002 15	172545	2408	0.014	0.1497
chrUn_gl0002 16	172294	186104	1.0802	1.799
chrUn_gl0002 17	172149	38260	0.2222	0.775
chrUn_gl0002 18	161147	130298	0.8086	1.5824
chrUn_gl0002 19	179198	189253	1.0561	2.0797
chrUn_gl0002 20	161802	5183257	32.0346	115.9875
chrUn_gl0002 21	155397	32757	0.2108	0.8536
chrUn_gl0002 22	186861	17018	0.0911	0.5089
chrUn_gl0002 23	180455	300	0.0017	0.0407
chrUn_gl0002 24	179693	178384	0.9927	4.6534
chrUn_gl0002 25	211173	74475	0.3527	1.1162

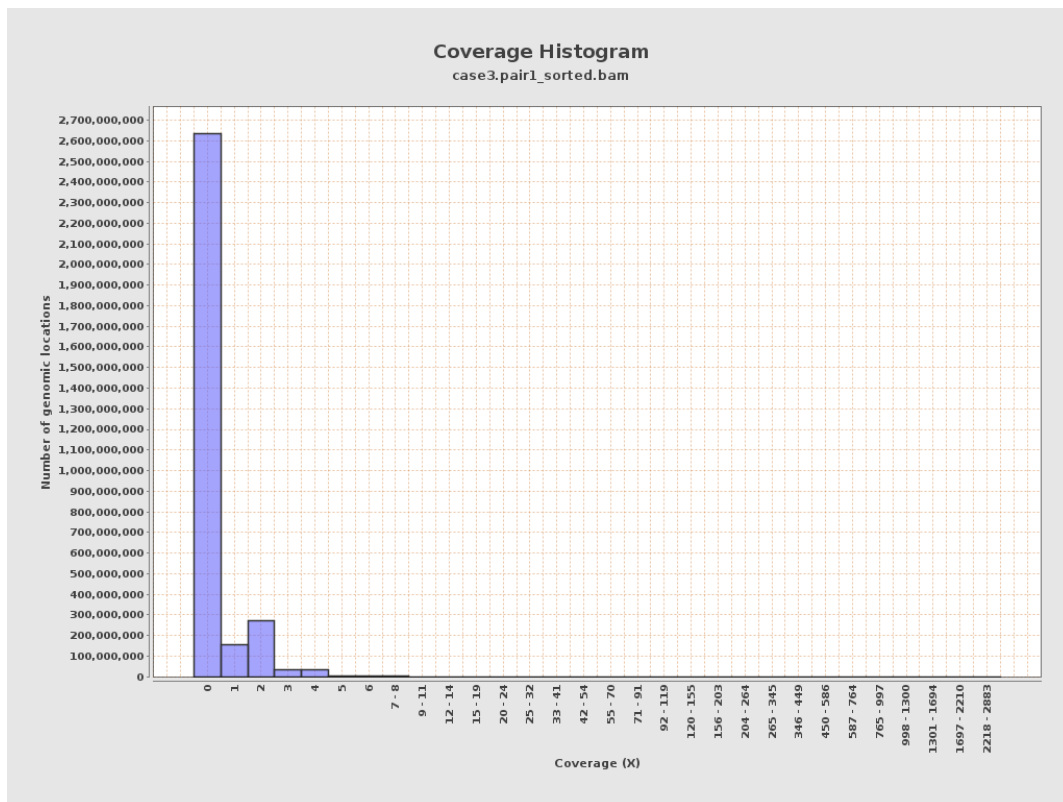
chrUn_gl0002 26	15008	107287	7.1487	22.2709
chrUn_gl0002 27	128374	3300	0.0257	0.2224
chrUn_gl0002 28	129120	9081	0.0703	0.4596
chrUn_gl0002 29	19913	23681	1.1892	2.058
chrUn_gl0002 30	43691	14939	0.3419	0.9045
chrUn_gl0002 31	27386	22489	0.8212	1.5024
chrUn_gl0002 32	40652	56214	1.3828	2.705
chrUn_gl0002 33	45941	16792	0.3655	0.9649
chrUn_gl0002 34	40531	49703	1.2263	2.1668
chrUn_gl0002 35	34474	33690	0.9773	1.862
chrUn_gl0002 36	41934	1784	0.0425	0.2843
chrUn_gl0002 37	45867	20153	0.4394	1.334
chrUn_gl0002 38	39939	1778	0.0445	0.2755
chrUn_gl0002 39	33824	3608	0.1067	0.8104
chrUn_gl0002 40	41933	12542	0.2991	0.8675

chrUn_gl0002 41	42152	73710	1.7487	2.2396
chrUn_gl0002 42	43523	1498	0.0344	0.291
chrUn_gl0002 43	43341	5701	0.1315	0.6094
chrUn_gl0002 44	39929	1500	0.0376	0.2764
chrUn_gl0002 45	36651	1810	0.0494	0.3935
chrUn_gl0002 46	38154	2993	0.0784	0.4198
chrUn_gl0002 47	36422	2091	0.0574	0.3934
chrUn_gl0002 48	39786	900	0.0226	0.2053
chrUn_gl0002 49	38502	300	0.0078	0.1203

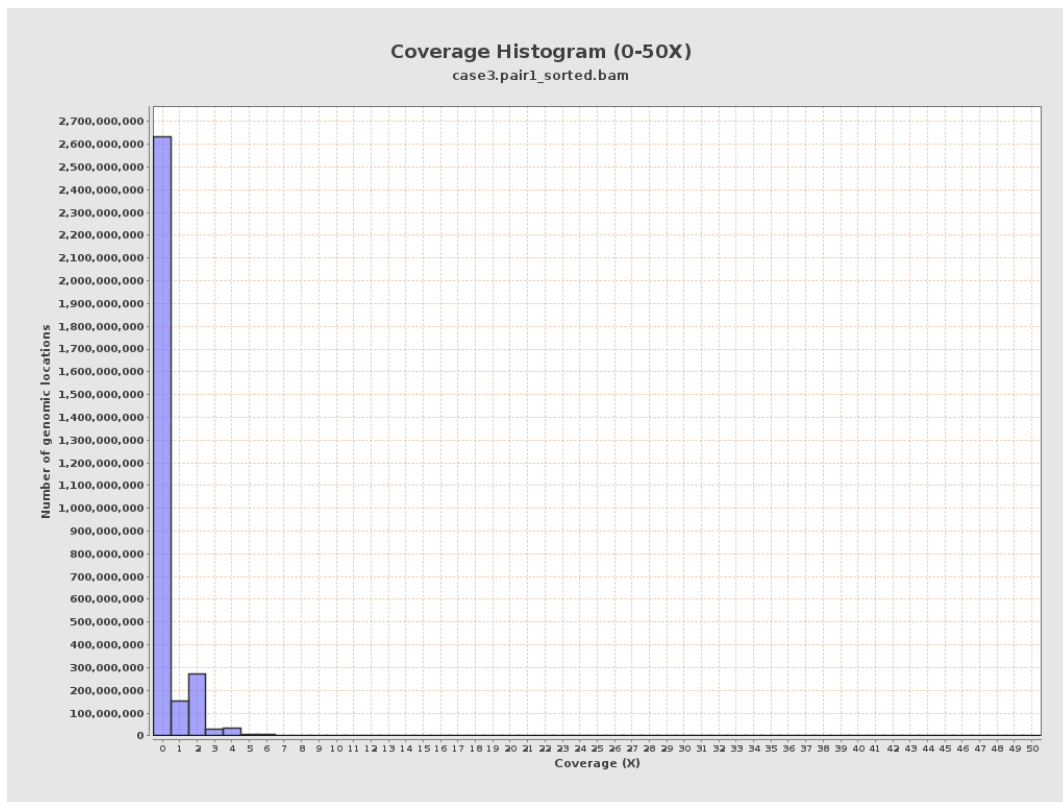
3. Results : Coverage across reference



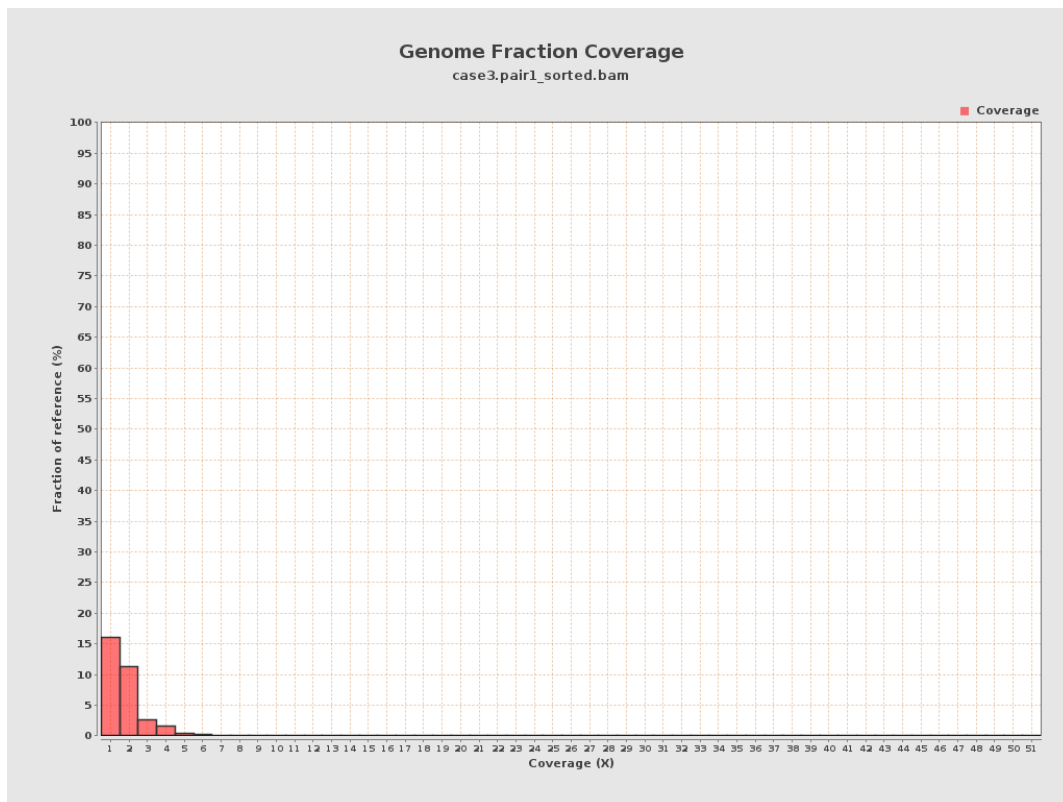
4. Results : Coverage Histogram



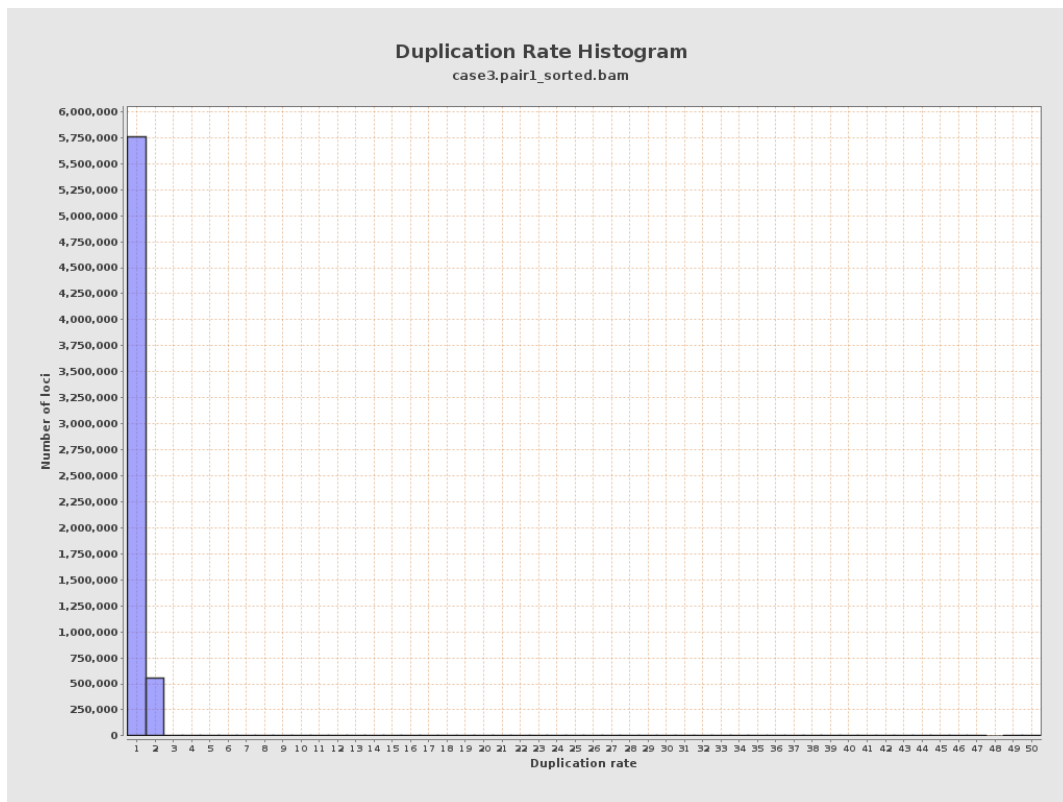
5. Results : Coverage Histogram (0-50X)



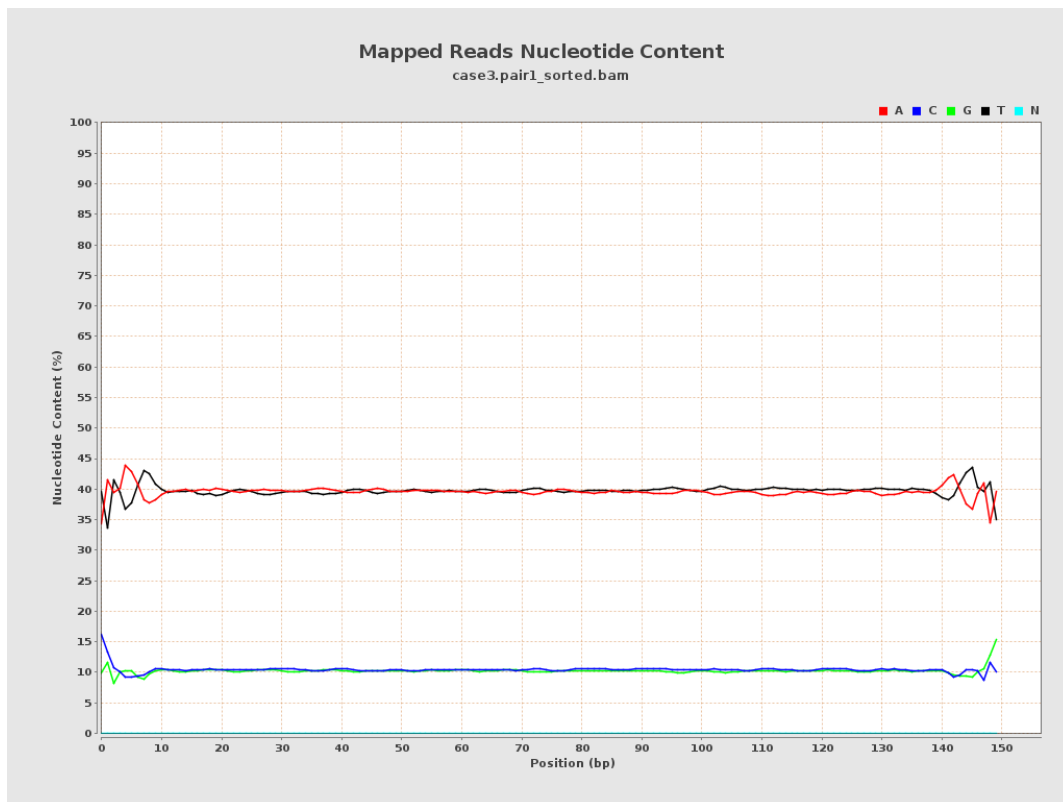
6. Results : Genome Fraction Coverage



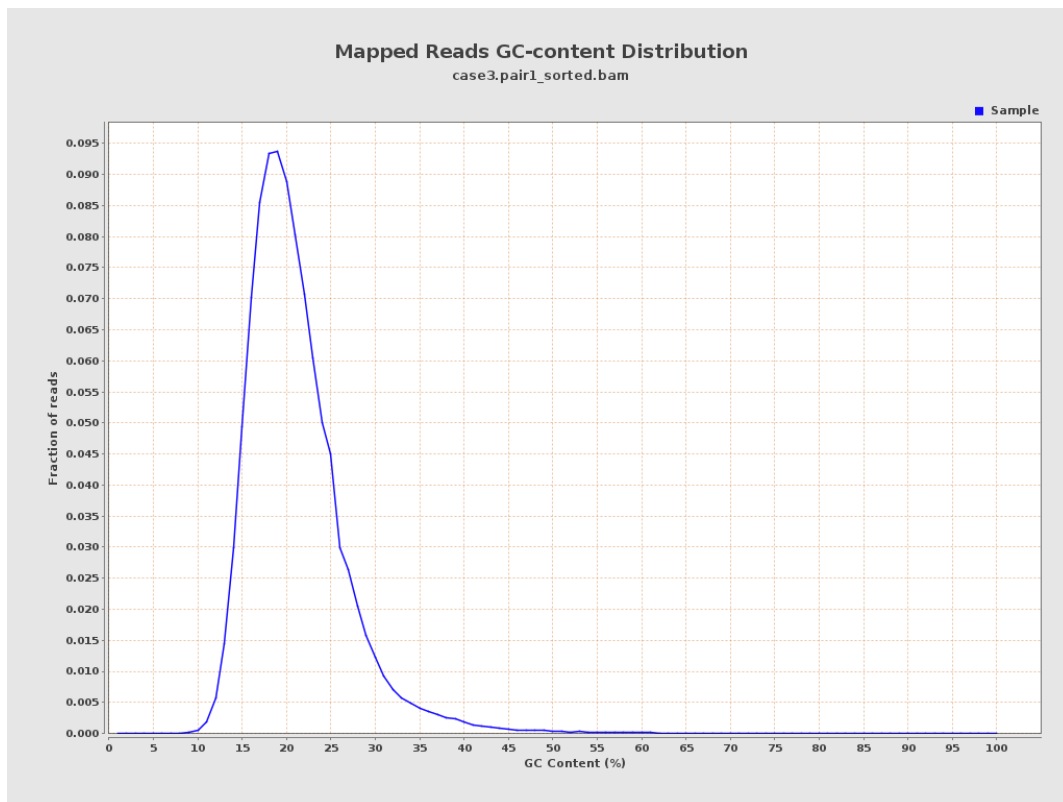
7. Results : Duplication Rate Histogram



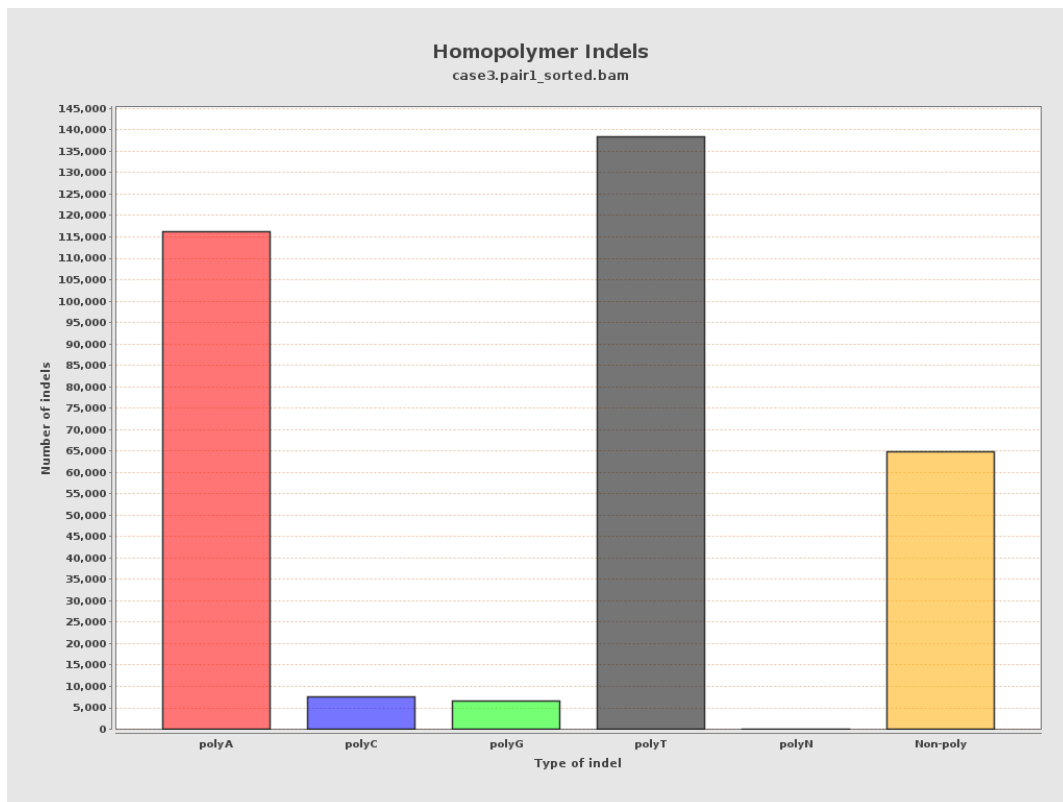
8. Results : Mapped Reads Nucleotide Content



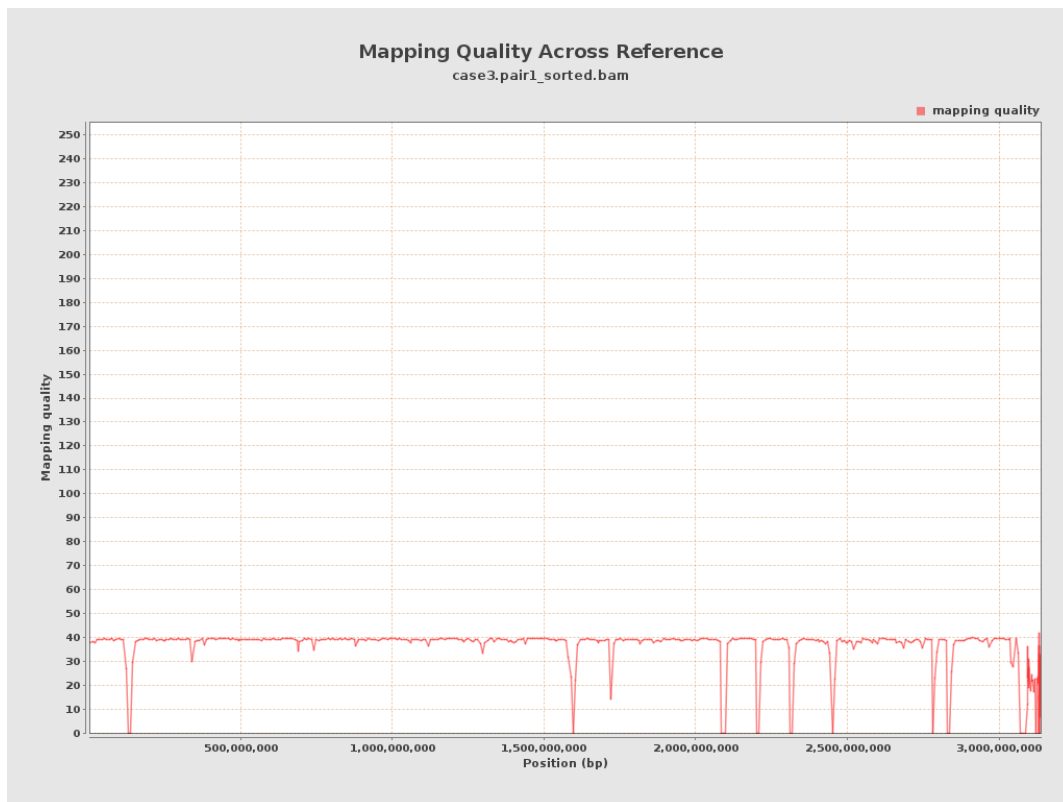
9. Results : Mapped Reads GC-content Distribution



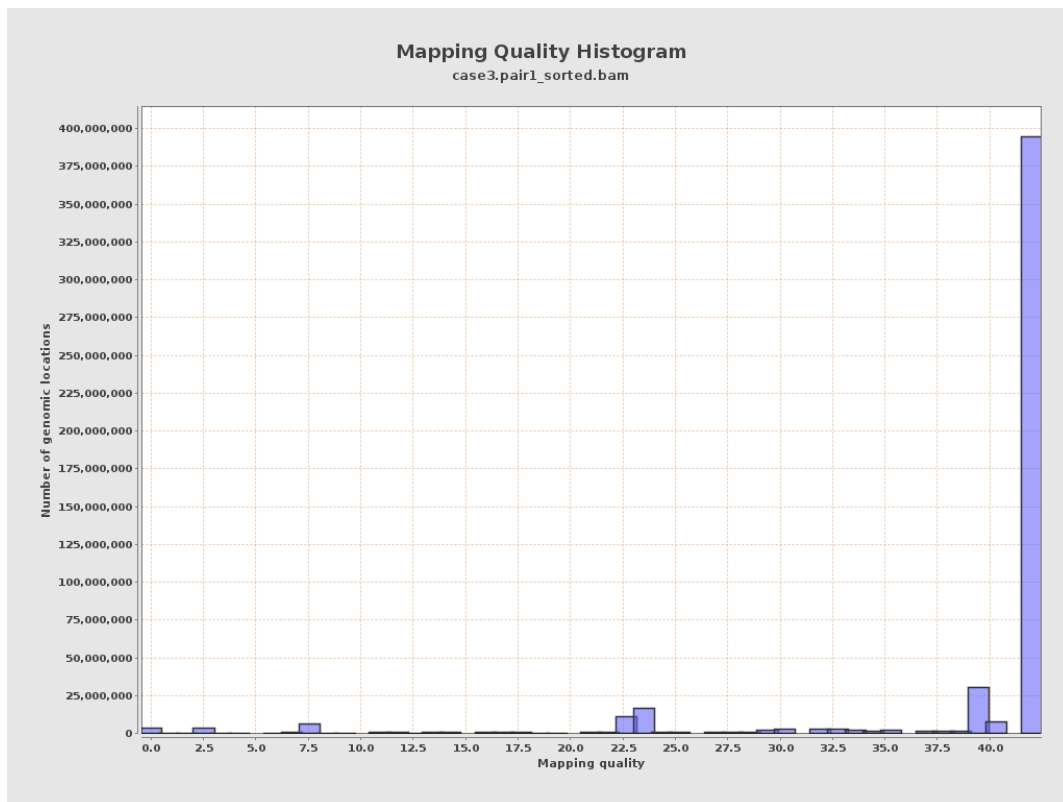
10. Results : Homopolymer Indels



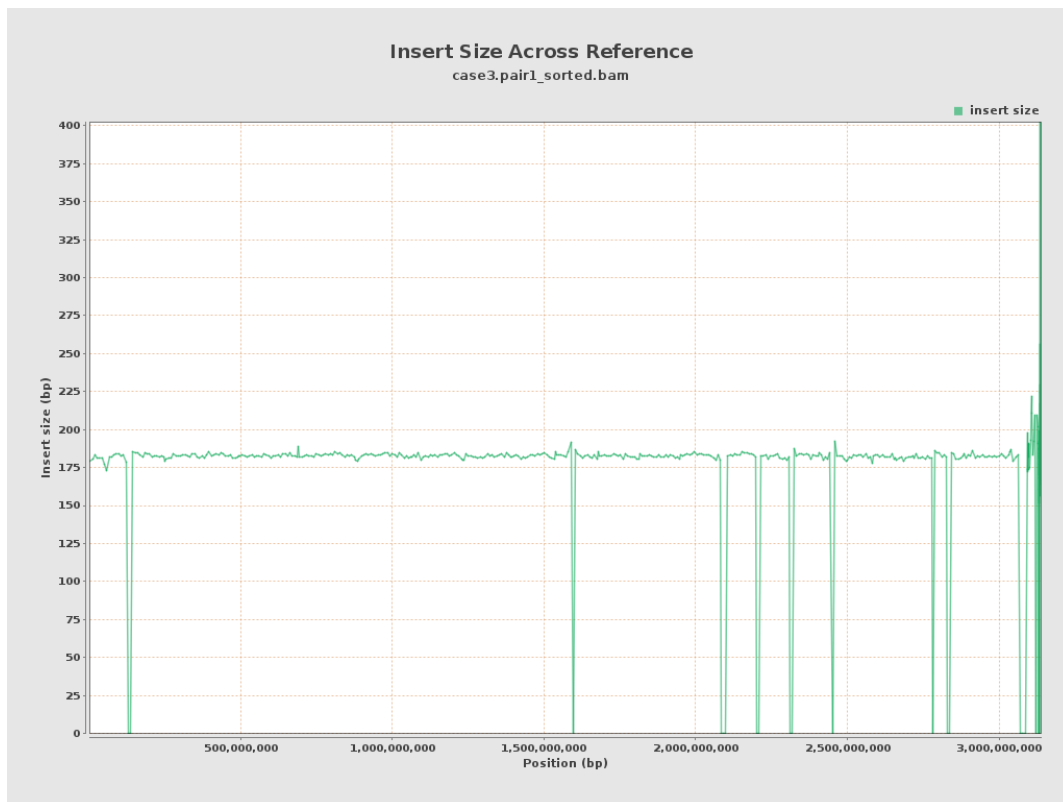
11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram



13. Results : Insert Size Across Reference



14. Results : Insert Size Histogram

