

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:20:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094084.sorted.bam -c -nw 400 -hm 3
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1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_ERR2094084 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094084_1.fastq.gz ERR2094084_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:20:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	395,466
Mapped reads	381,003 / 96.34%
Unmapped reads	14,463 / 3.66%
Mapped paired reads	381,003 / 96.34%
Mapped reads, first in pair	191,456 / 48.41%
Mapped reads, second in pair	189,547 / 47.93%
Mapped reads, both in pair	378,326 / 95.67%
Mapped reads, singletons	2,677 / 0.68%
Secondary alignments	0
Supplementary alignments	11,049 / 2.79%
Read min/max/mean length	30 / 151 / 142.38
Duplicated reads (estimated)	363,400 / 91.89%
Duplication rate	48.23%
Clipped reads	136,781 / 34.59%

2.2. ACGT Content

Number/percentage of A's	13,251,617 / 26.47%
Number/percentage of C's	11,928,610 / 23.82%
Number/percentage of T's	12,655,758 / 25.28%
Number/percentage of G's	12,232,324 / 24.43%
Number/percentage of N's	699 / 0%

GC Percentage	48.26%
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2.3. Coverage

Mean	0.0165
Standard Deviation	4.8098

2.4. Mapping Quality

Mean Mapping Quality	38.12
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2.5. Insert size

Mean	255,837.97
Standard Deviation	4,586,258.77
P25/Median/P75	144 / 172 / 203

2.6. Mismatches and indels

General error rate	3.98%
Mismatches	1,919,638
Insertions	27,848
Mapped reads with at least one insertion	7.2%
Deletions	152,832
Mapped reads with at least one deletion	38.27%
Homopolymer indels	30.03%

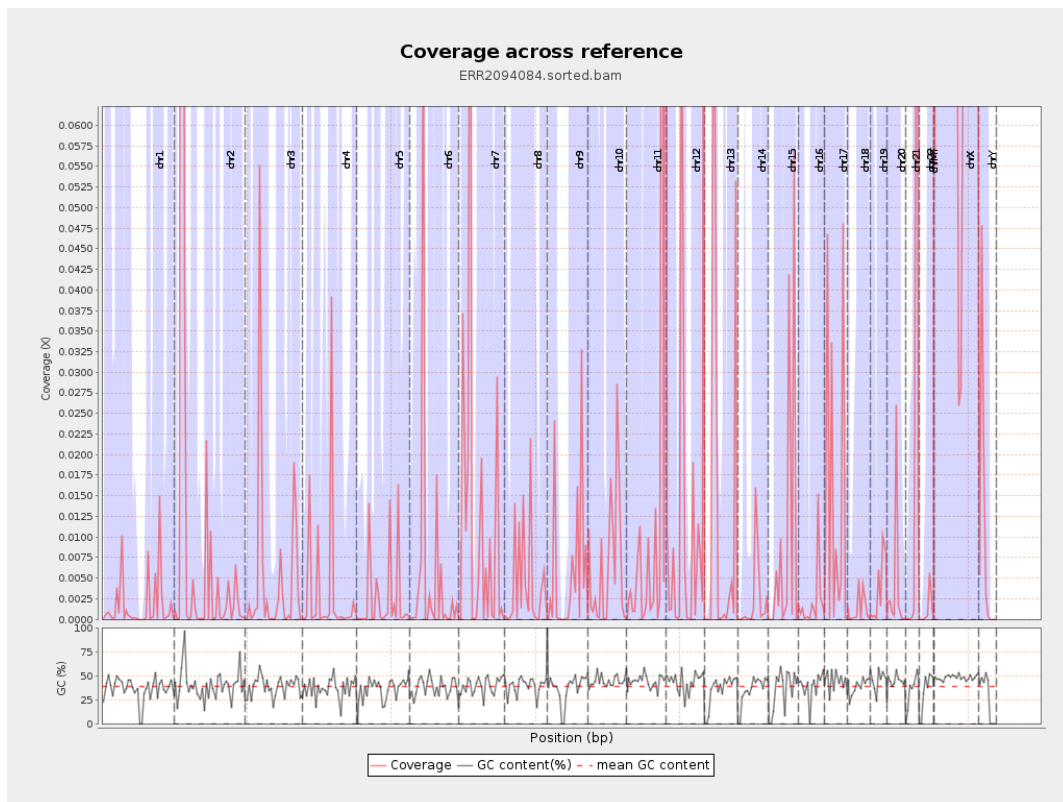
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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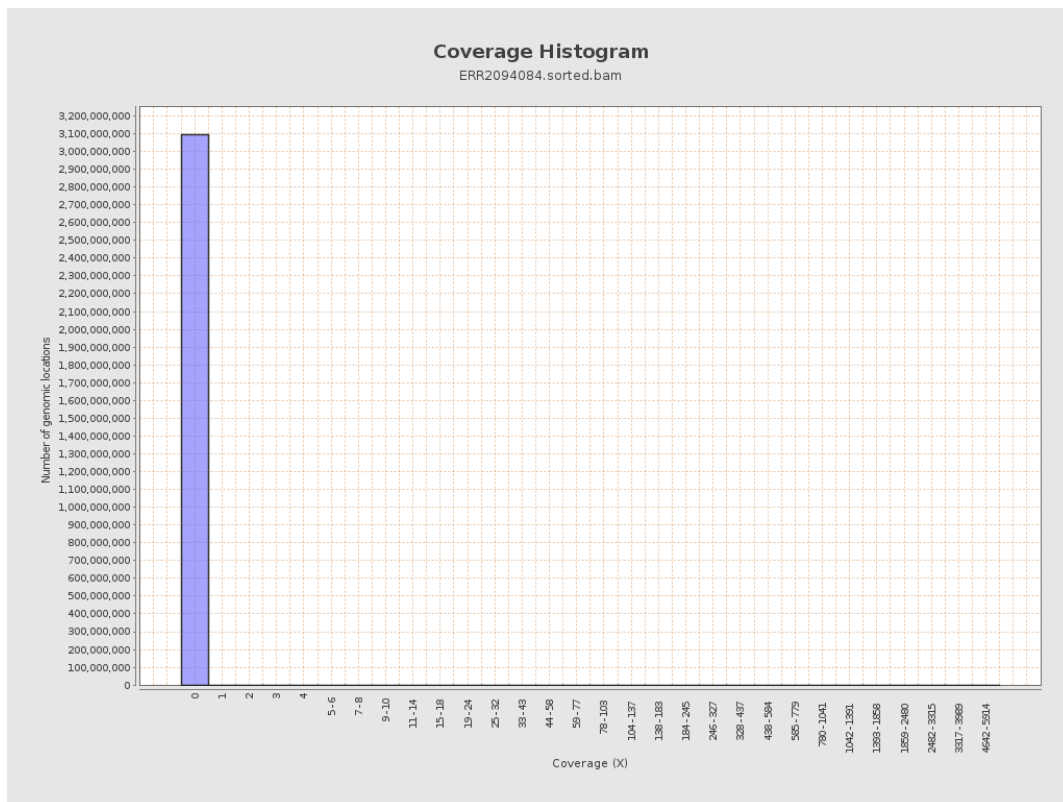
		bases	coverage	deviation
chr1	249250621	430352	0.0017	0.7894
chr2	243199373	2950869	0.0121	5.3086
chr3	198022430	924407	0.0047	1.937
chr4	191154276	594248	0.0031	1.4175
chr5	180915260	458103	0.0025	1.2428
chr6	171115067	949883	0.0056	3.6276
chr7	159138663	1938218	0.0122	4.4993
chr8	146364022	647945	0.0044	1.3953
chr9	141213431	792168	0.0056	2.0726
chr10	135534747	887114	0.0065	1.9699
chr11	135006516	1700999	0.0126	4.1804
chr12	133851895	1457173	0.0109	4.3487
chr13	115169878	1457788	0.0127	3.8881
chr14	107349540	248858	0.0023	1.0733
chr15	102531392	928695	0.0091	2.7183
chr16	90354753	205062	0.0023	0.7995
chr17	81195210	1177873	0.0145	4.6481
chr18	78077248	106042	0.0014	0.4777
chr19	59128983	210406	0.0036	0.9134
chr20	63025520	256195	0.0041	1.2827
chr21	48129895	957939	0.0199	8.7131
chr22	51304566	55414	0.0011	0.3641
chrMT	16571	2583789	155.9223	729.492
chrX	155270560	28664453	0.1846	14.6799

chrY	59373566	577379	0.0097	2.8078
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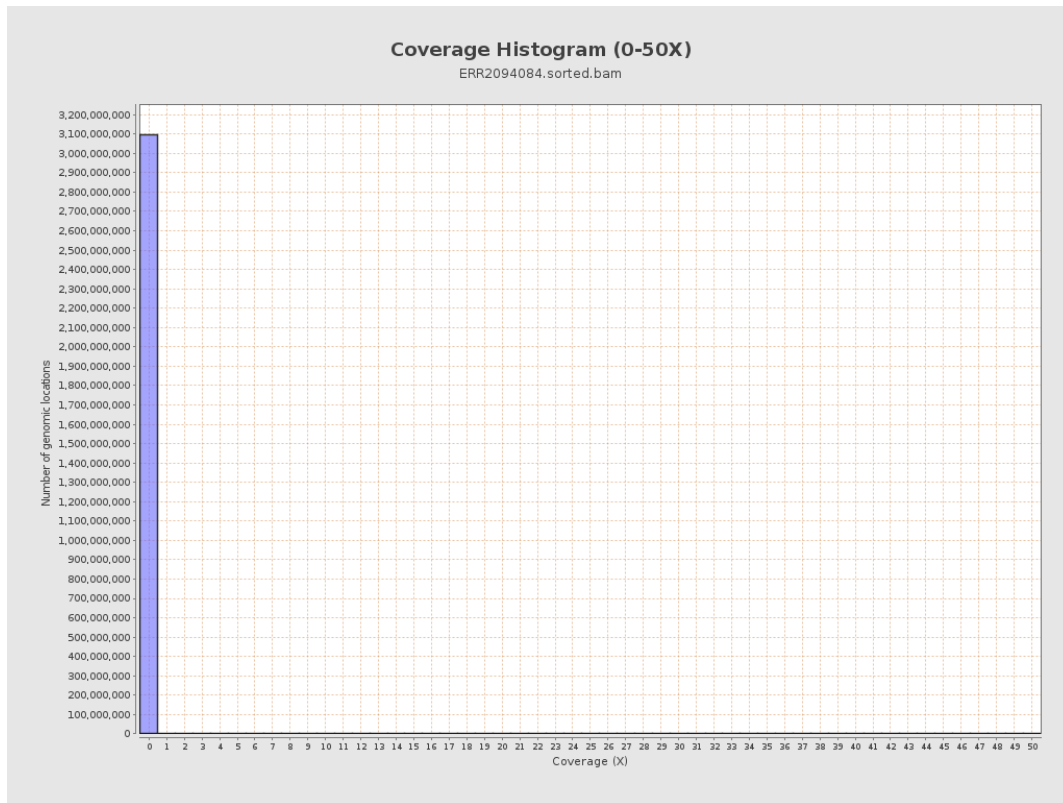
3. Results : Coverage across reference



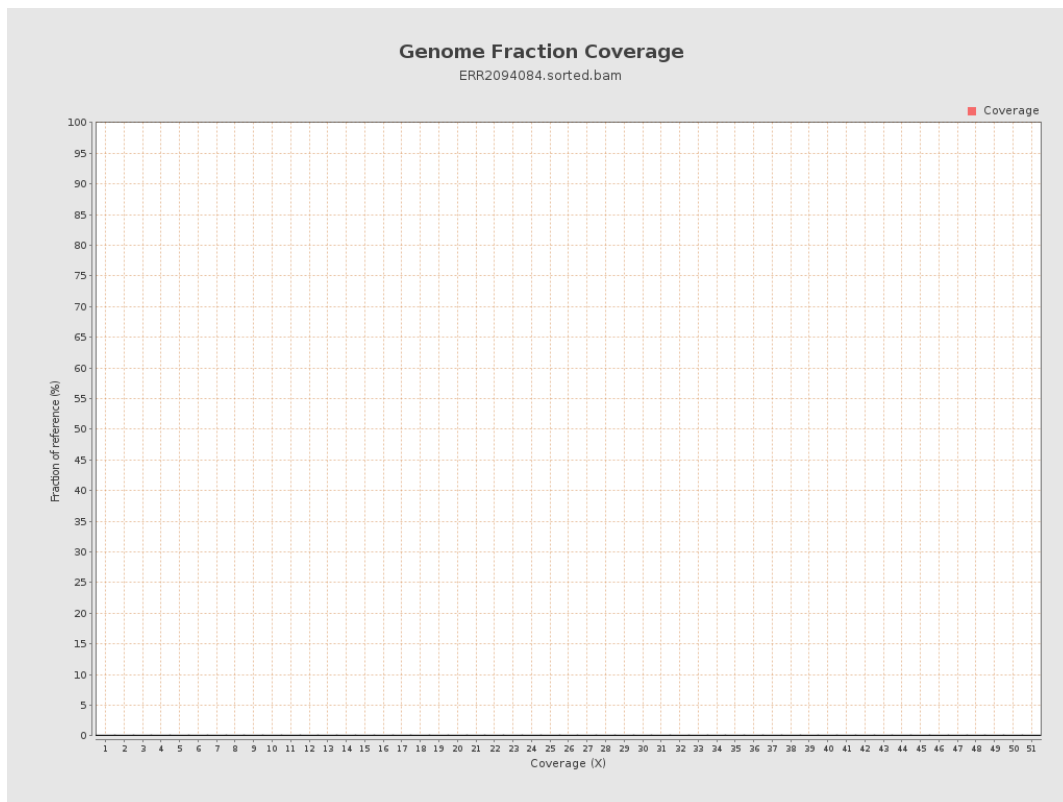
4. Results : Coverage Histogram



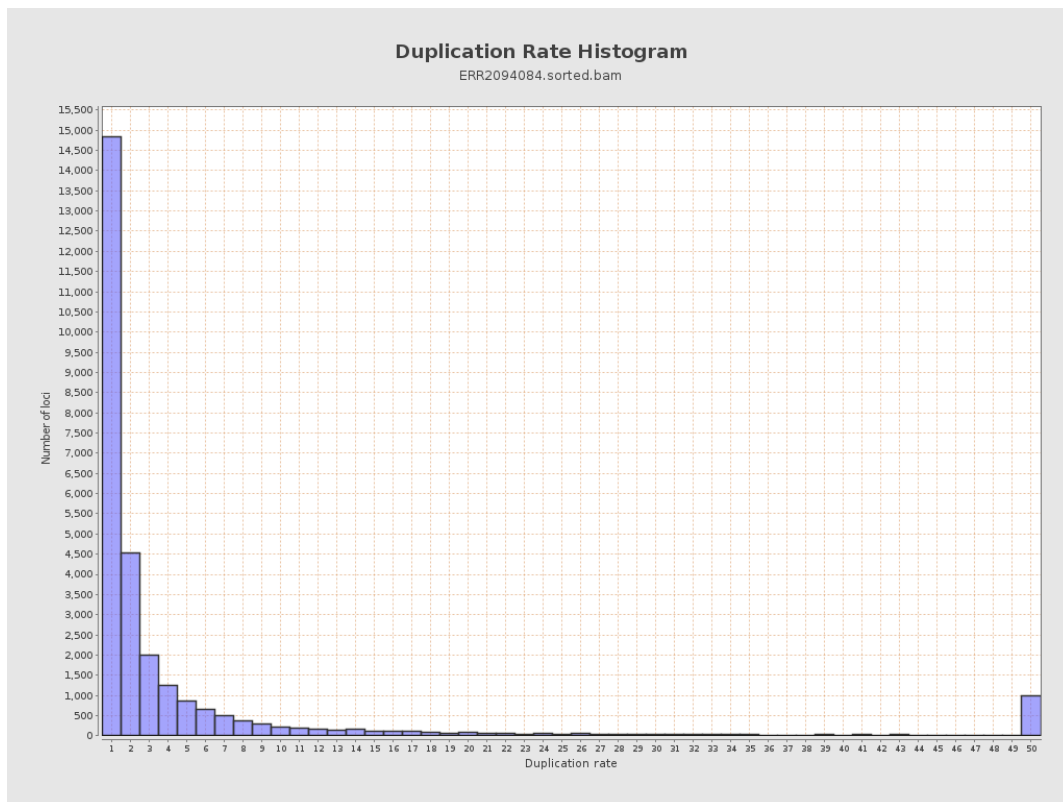
5. Results : Coverage Histogram (0-50X)



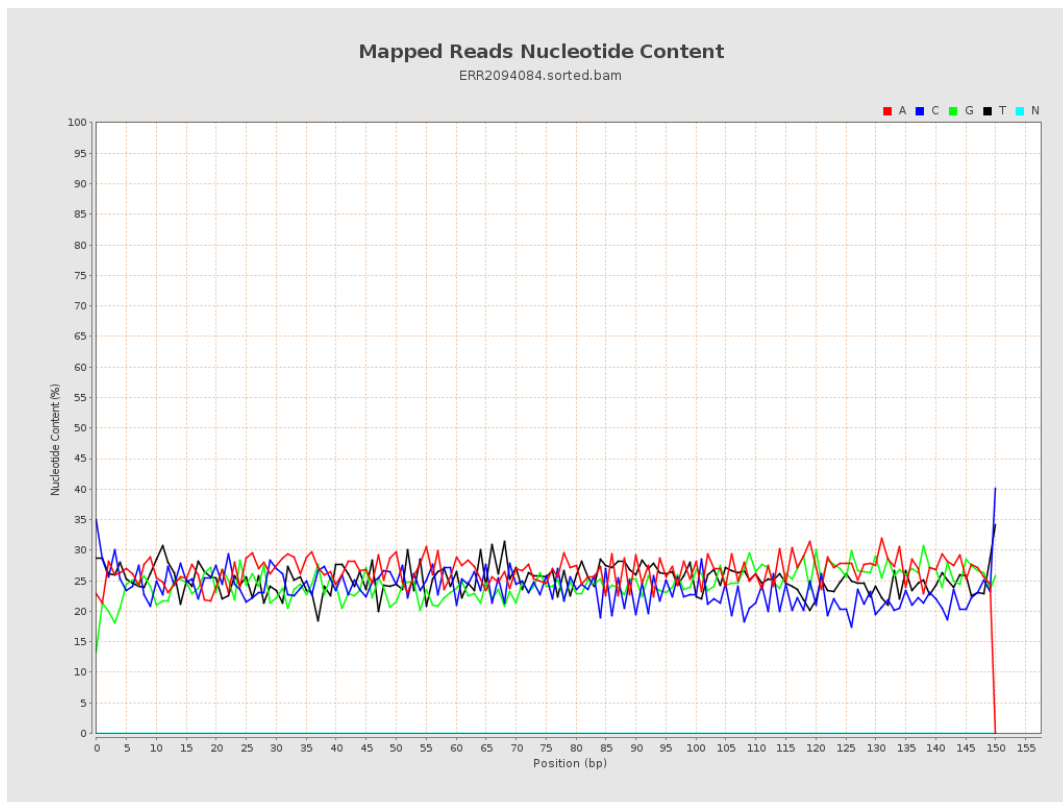
6. Results : Genome Fraction Coverage



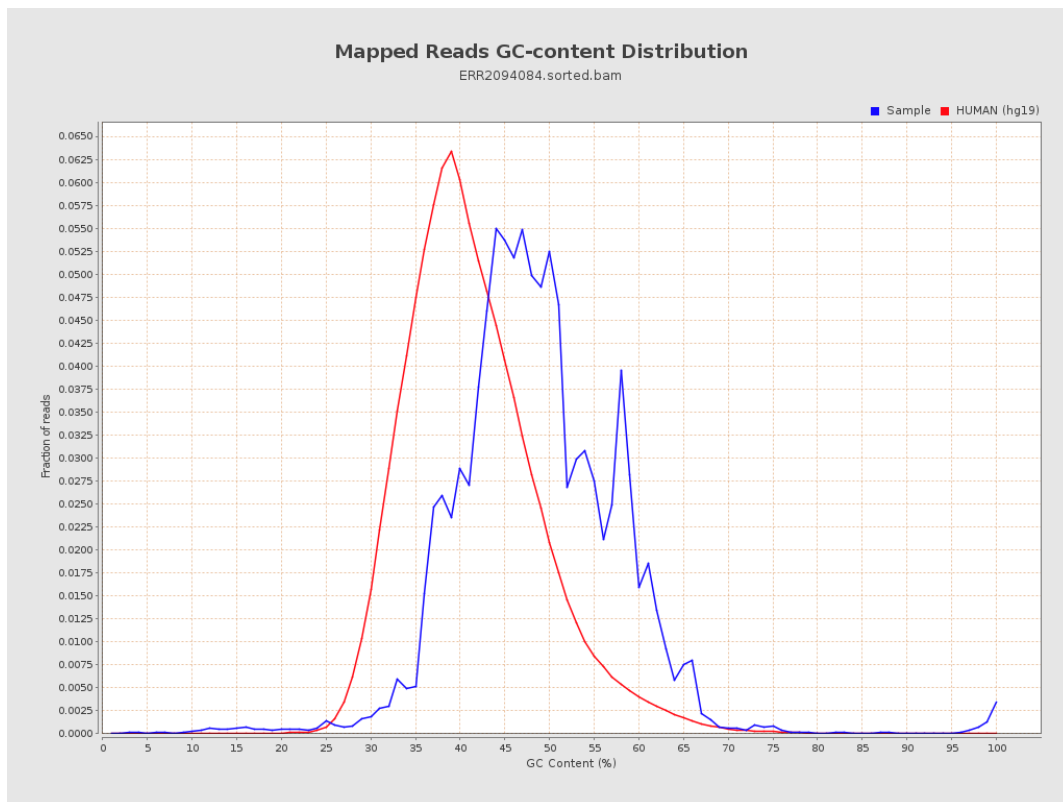
7. Results : Duplication Rate Histogram



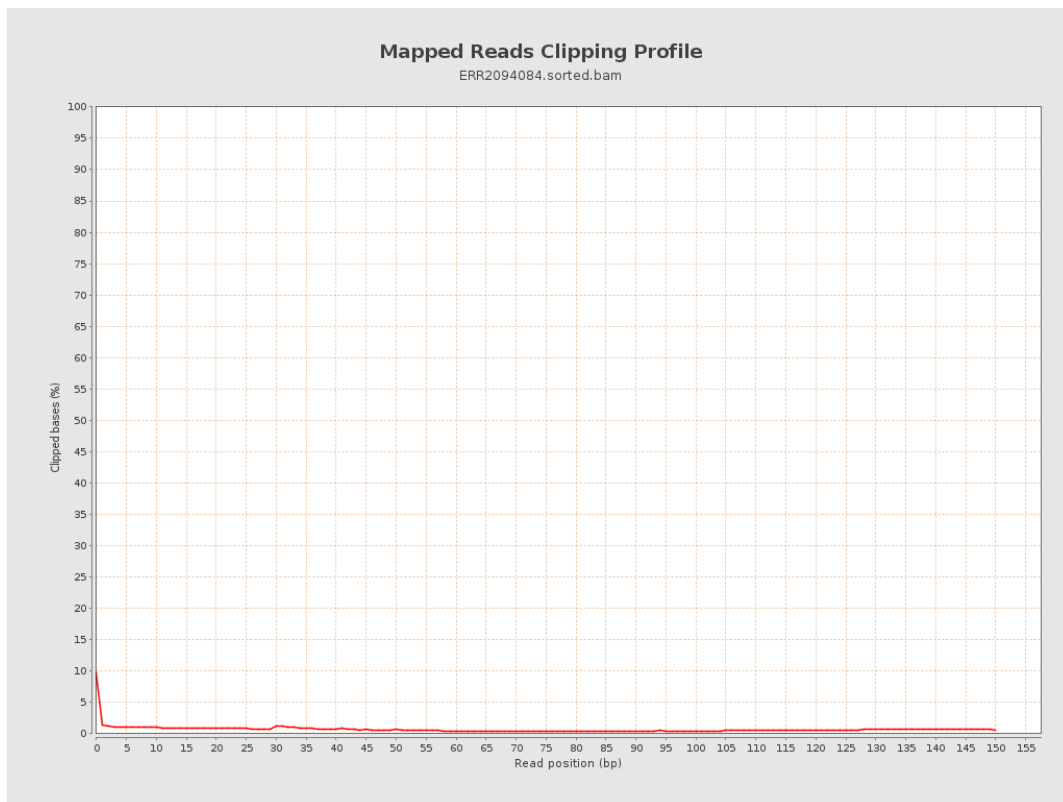
8. Results : Mapped Reads Nucleotide Content



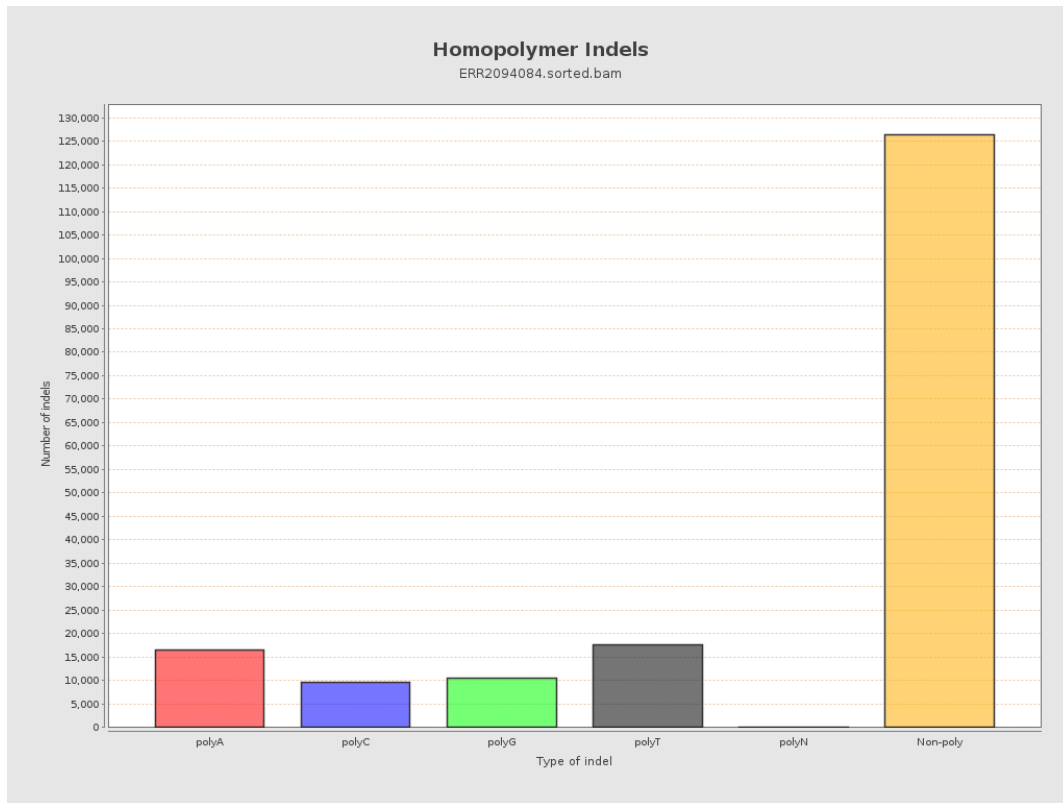
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



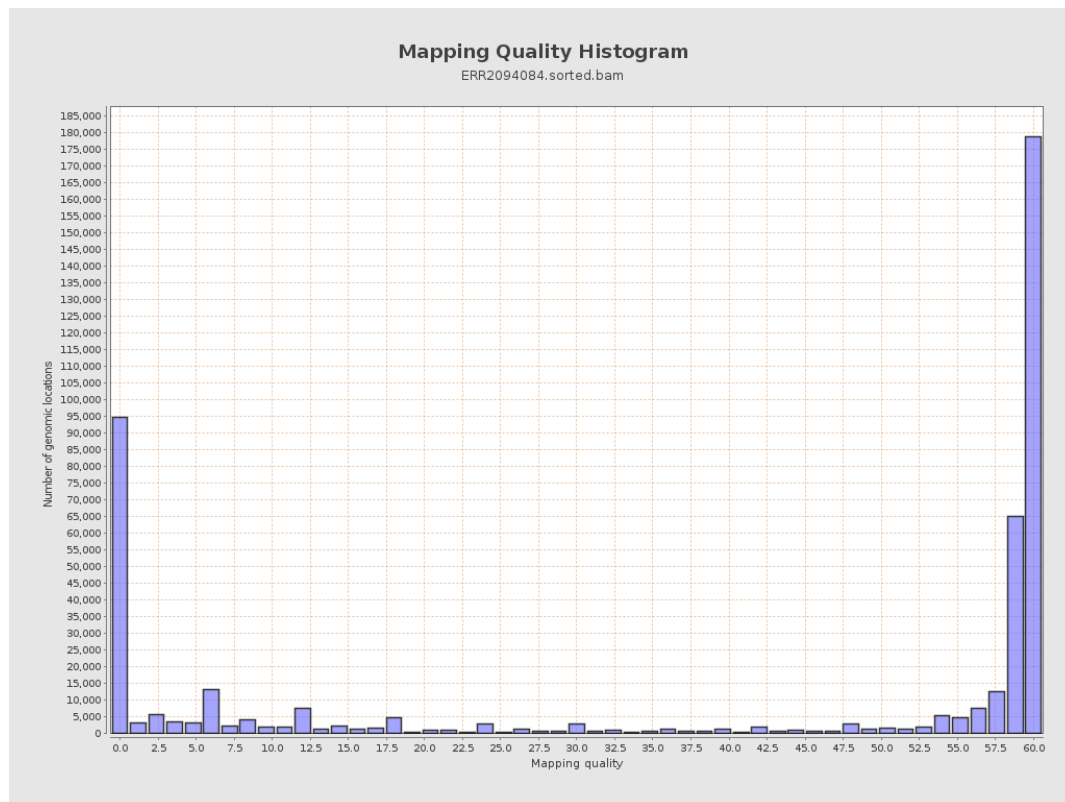
11. Results : Homopolymer Indels



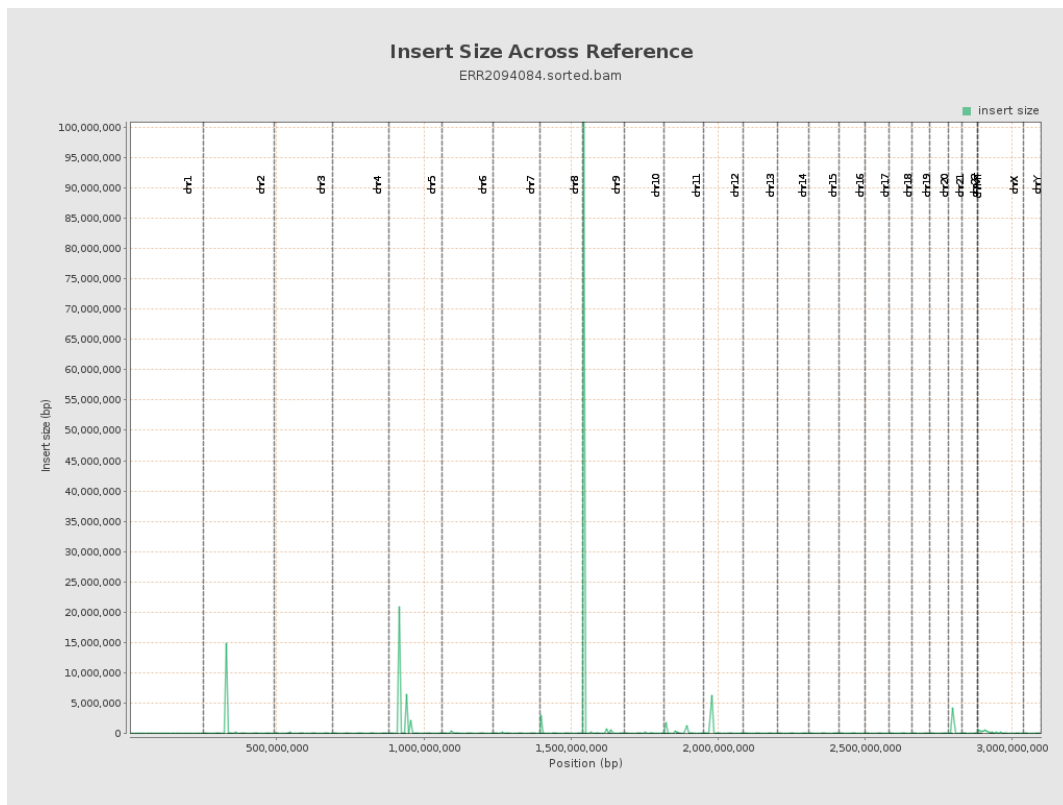
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

