

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:26:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094086.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_ERR2094086 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094086_1.fastq.gz ERR2094086_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:26:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	316,718
Mapped reads	301,882 / 95.32%
Unmapped reads	14,836 / 4.68%
Mapped paired reads	301,882 / 95.32%
Mapped reads, first in pair	151,759 / 47.92%
Mapped reads, second in pair	150,123 / 47.4%
Mapped reads, both in pair	299,492 / 94.56%
Mapped reads, singletons	2,390 / 0.75%
Secondary alignments	0
Supplementary alignments	10,793 / 3.41%
Read min/max/mean length	30 / 151 / 141.01
Duplicated reads (estimated)	284,408 / 89.8%
Duplication rate	49.01%
Clipped reads	114,340 / 36.1%

2.2. ACGT Content

Number/percentage of A's	10,349,893 / 26.29%
Number/percentage of C's	9,375,717 / 23.81%
Number/percentage of T's	9,932,963 / 25.23%
Number/percentage of G's	9,713,816 / 24.67%
Number/percentage of N's	327 / 0%

GC Percentage	48.48%
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2.3. Coverage

Mean	0.013
Standard Deviation	3.6322

2.4. Mapping Quality

Mean Mapping Quality	39.95
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2.5. Insert size

Mean	482,219.29
Standard Deviation	6,212,200.74
P25/Median/P75	137 / 168 / 201

2.6. Mismatches and indels

General error rate	3.86%
Mismatches	1,464,962
Insertions	23,262
Mapped reads with at least one insertion	7.57%
Deletions	118,716
Mapped reads with at least one deletion	37.49%
Homopolymer indels	28.04%

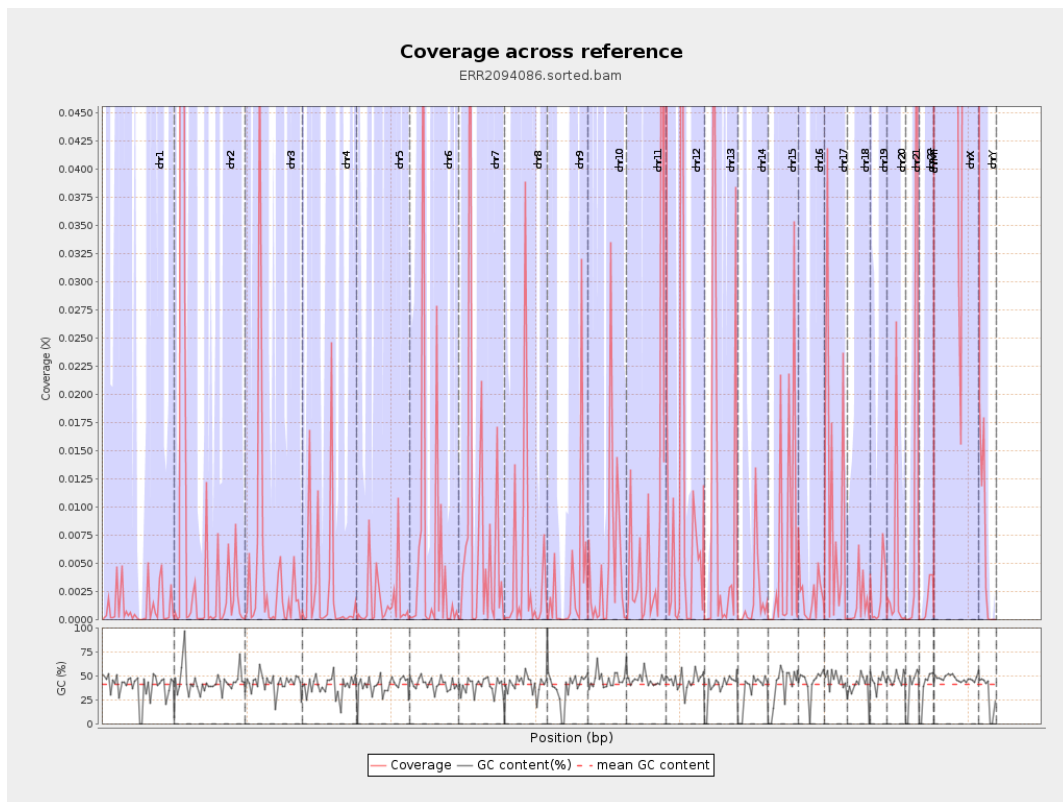
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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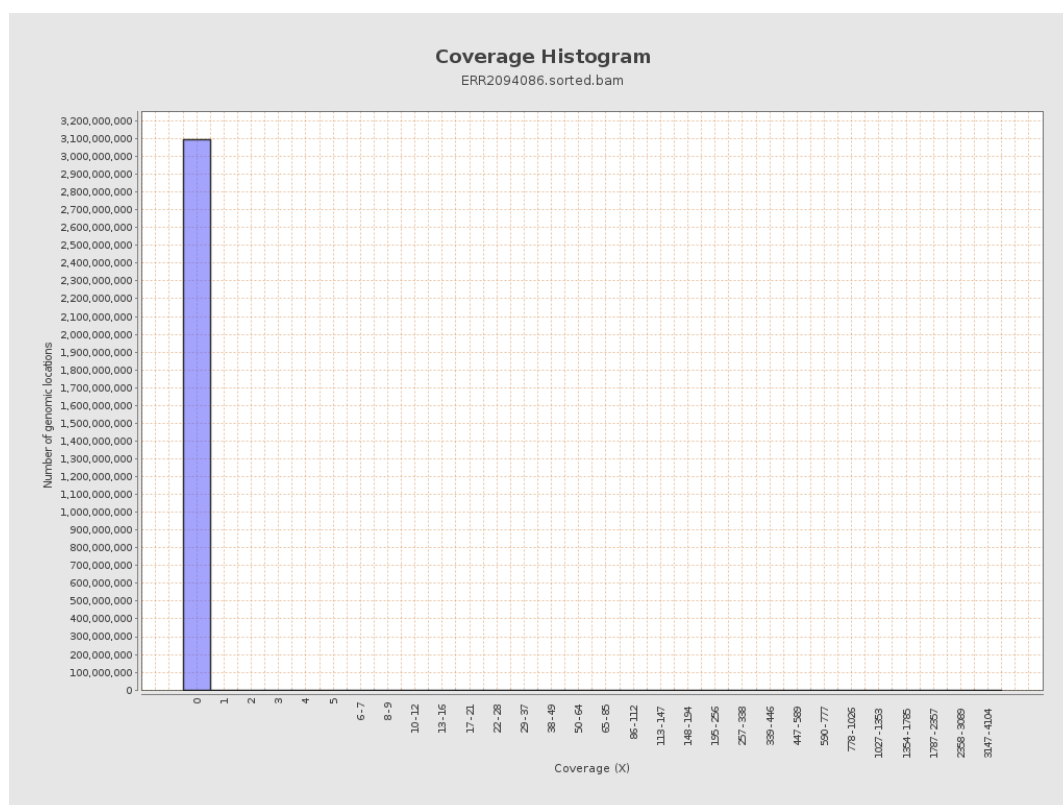
		bases	coverage	deviation
chr1	249250621	269232	0.0011	0.3896
chr2	243199373	2097504	0.0086	3.8717
chr3	198022430	768741	0.0039	1.7815
chr4	191154276	515538	0.0027	1.1107
chr5	180915260	301768	0.0017	0.7207
chr6	171115067	948597	0.0055	2.9941
chr7	159138663	1197803	0.0075	2.9081
chr8	146364022	608872	0.0042	1.7851
chr9	141213431	453789	0.0032	1.5054
chr10	135534747	699203	0.0052	1.937
chr11	135006516	1241024	0.0092	2.482
chr12	133851895	1193725	0.0089	4.0419
chr13	115169878	1077893	0.0094	2.6251
chr14	107349540	198357	0.0018	0.8329
chr15	102531392	647915	0.0063	2.2069
chr16	90354753	197380	0.0022	0.5451
chr17	81195210	868084	0.0107	3.0031
chr18	78077248	117485	0.0015	0.5603
chr19	59128983	120387	0.002	0.5407
chr20	63025520	242504	0.0038	1.2412
chr21	48129895	616536	0.0128	5.3861
chr22	51304566	77171	0.0015	0.4448
chrMT	16571	1340285	80.8814	387.1688
chrX	155270560	24045368	0.1549	12.0668

chrY	59373566	352093	0.0059	1.4779
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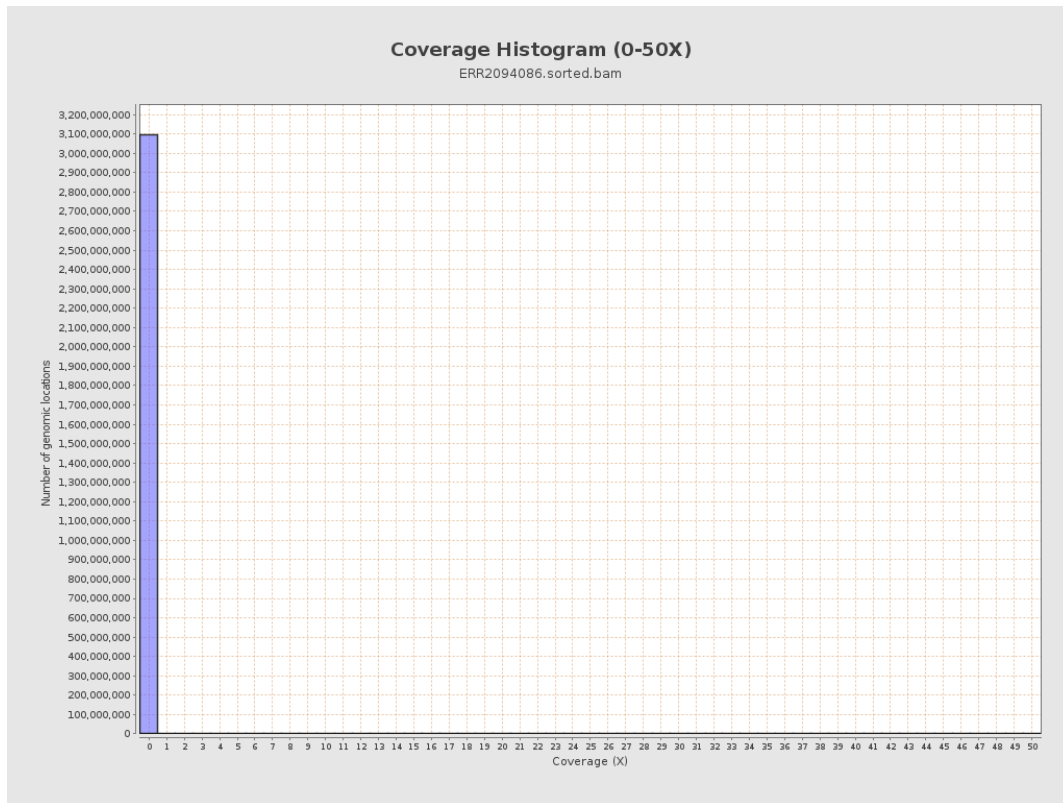
3. Results : Coverage across reference



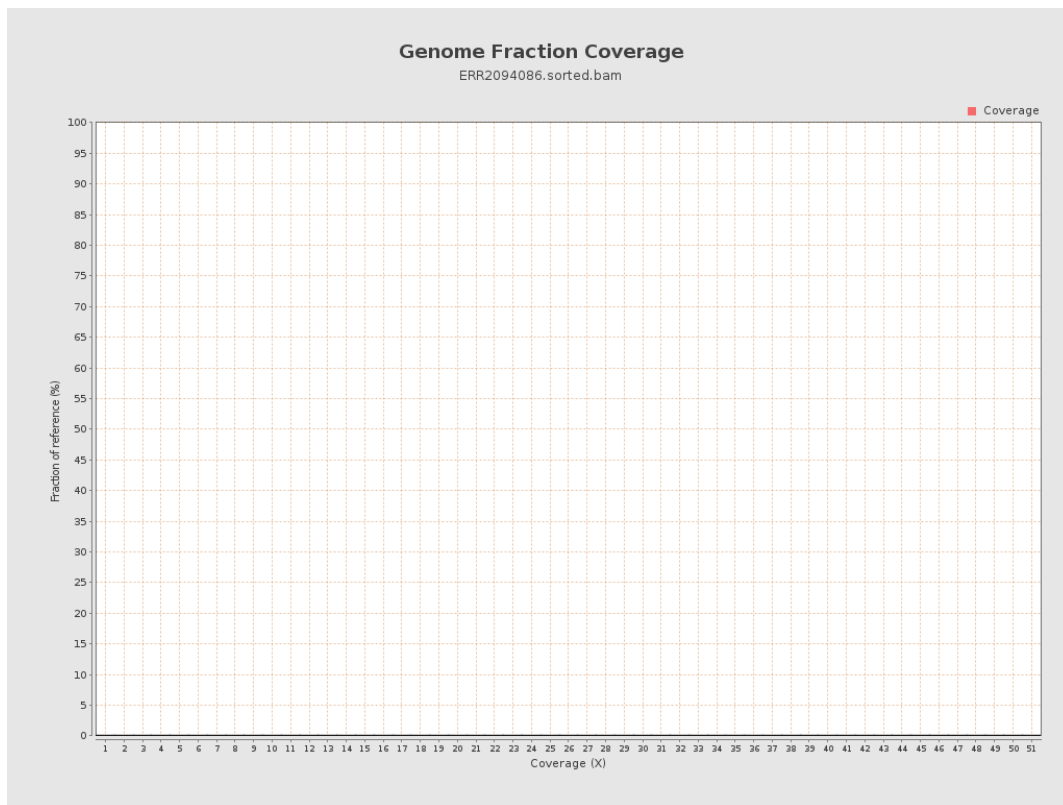
4. Results : Coverage Histogram



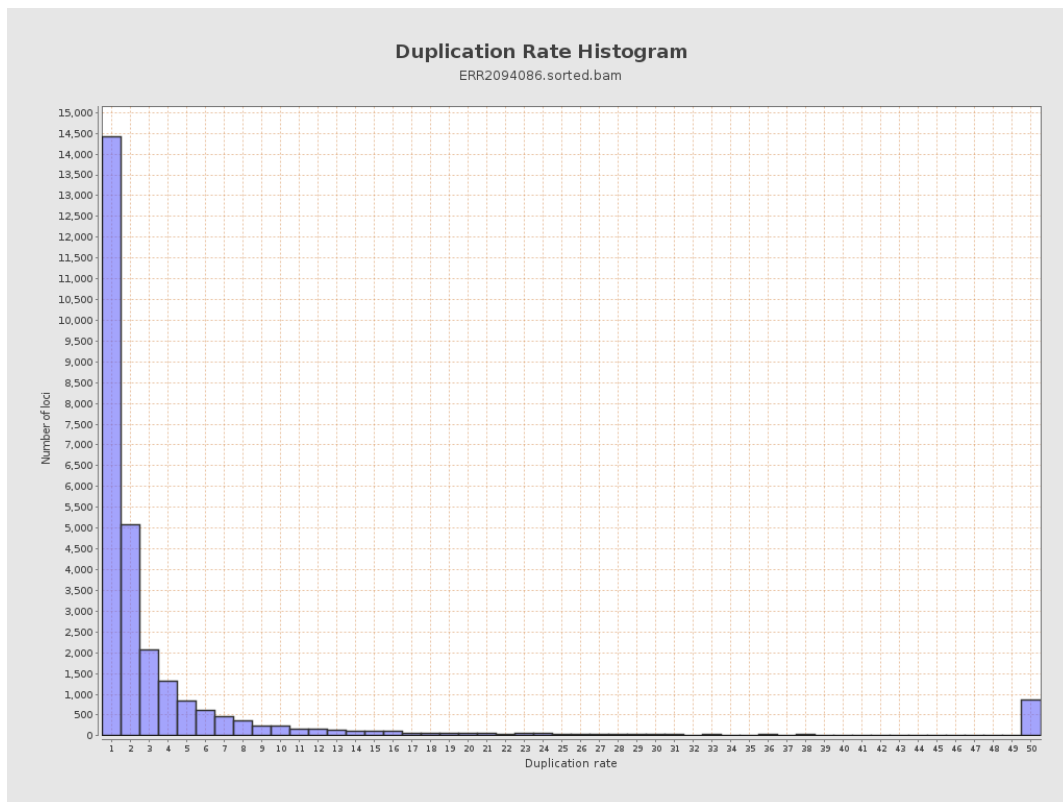
5. Results : Coverage Histogram (0-50X)



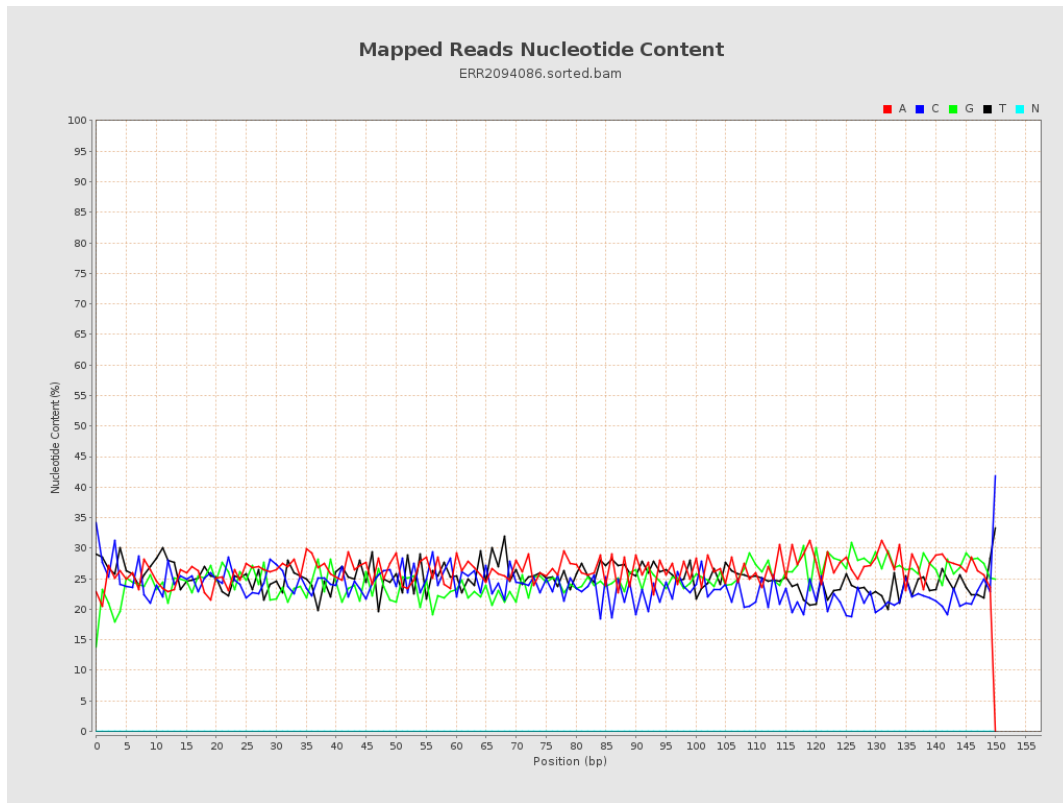
6. Results : Genome Fraction Coverage



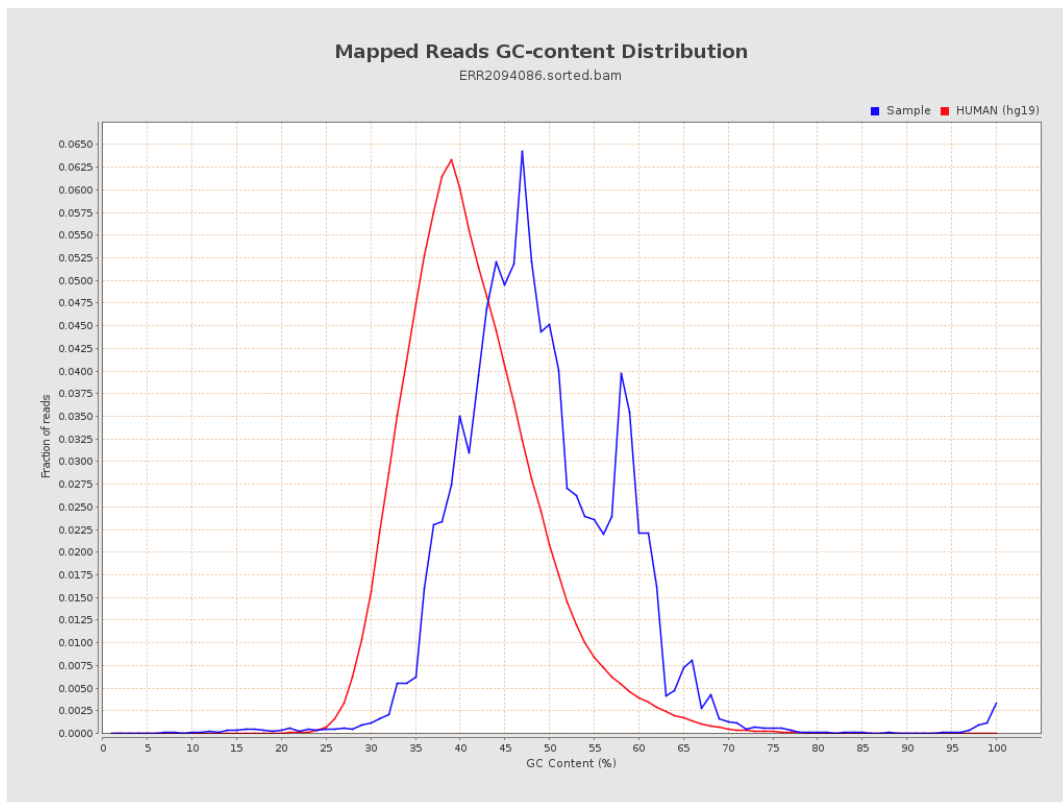
7. Results : Duplication Rate Histogram



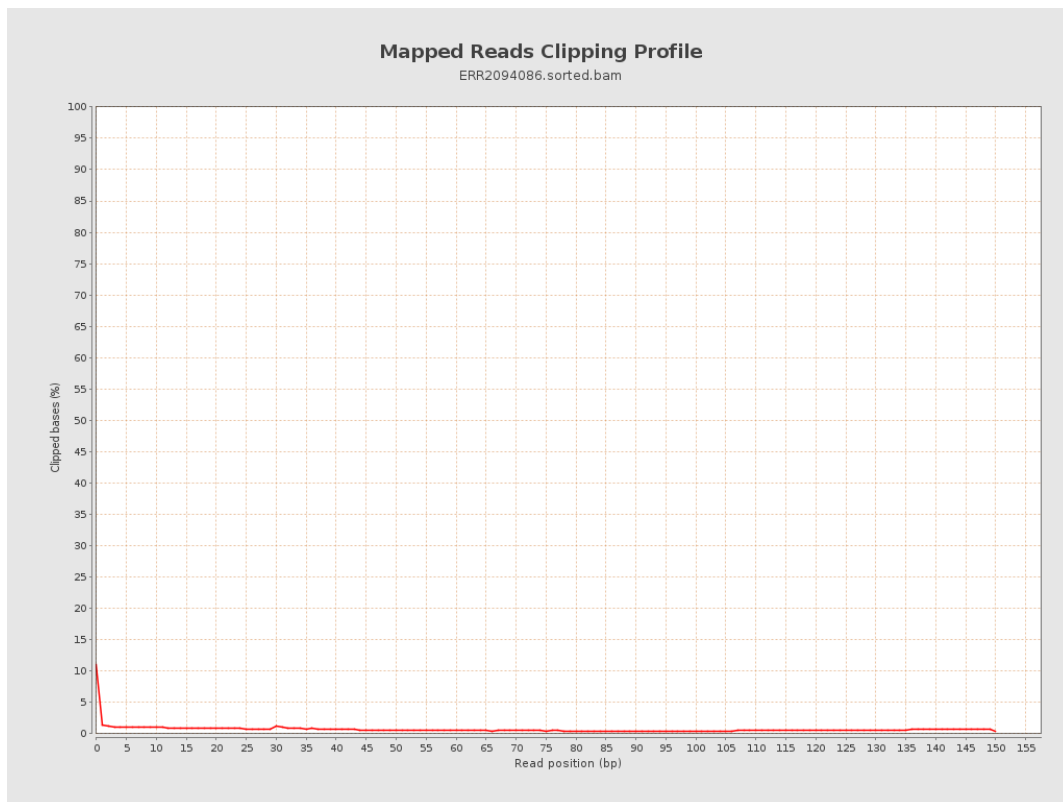
8. Results : Mapped Reads Nucleotide Content



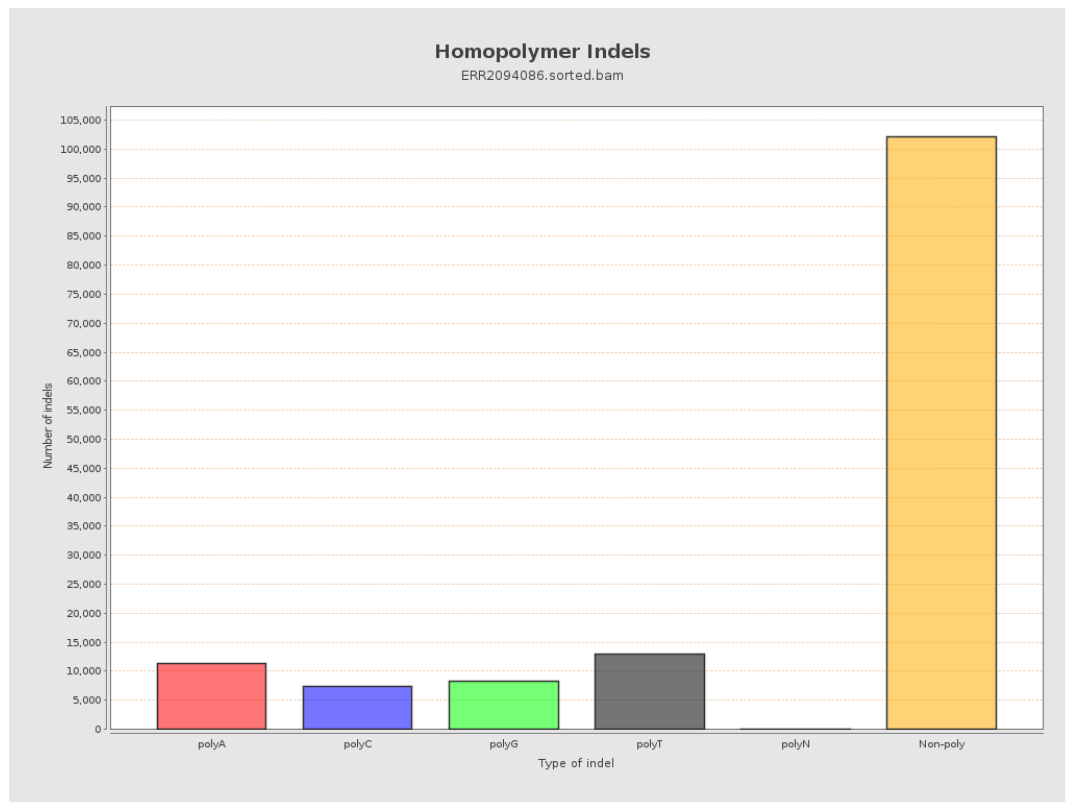
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



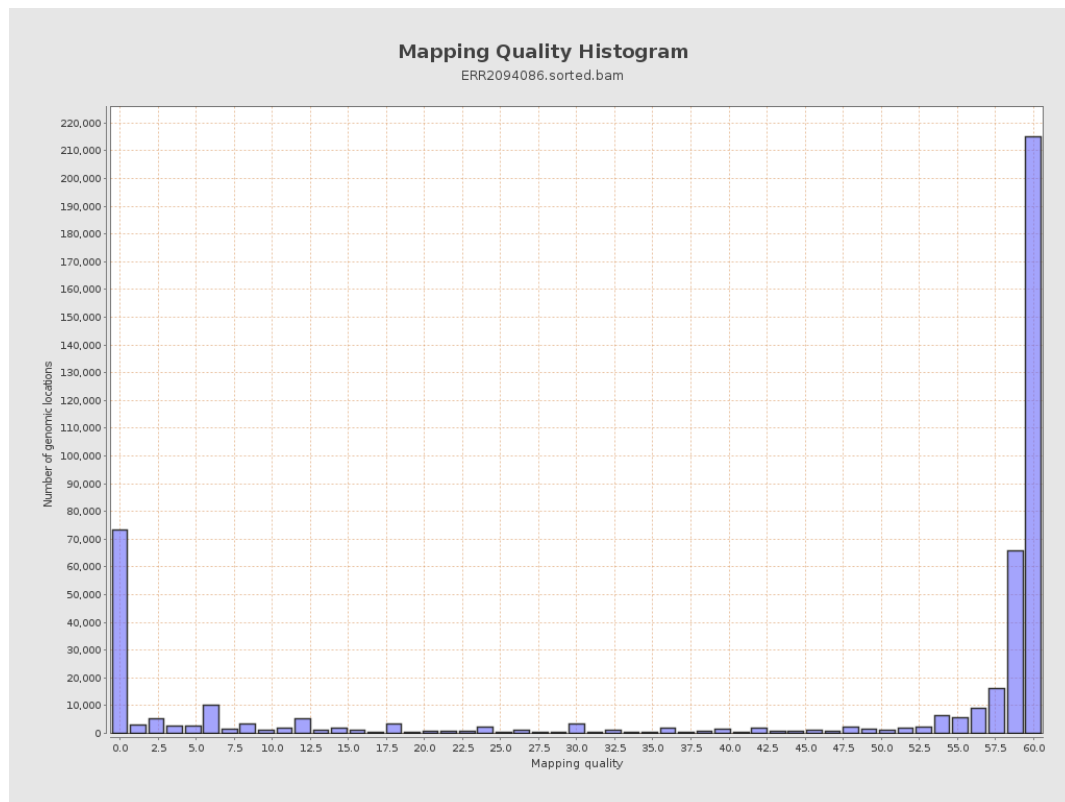
11. Results : Homopolymer Indels



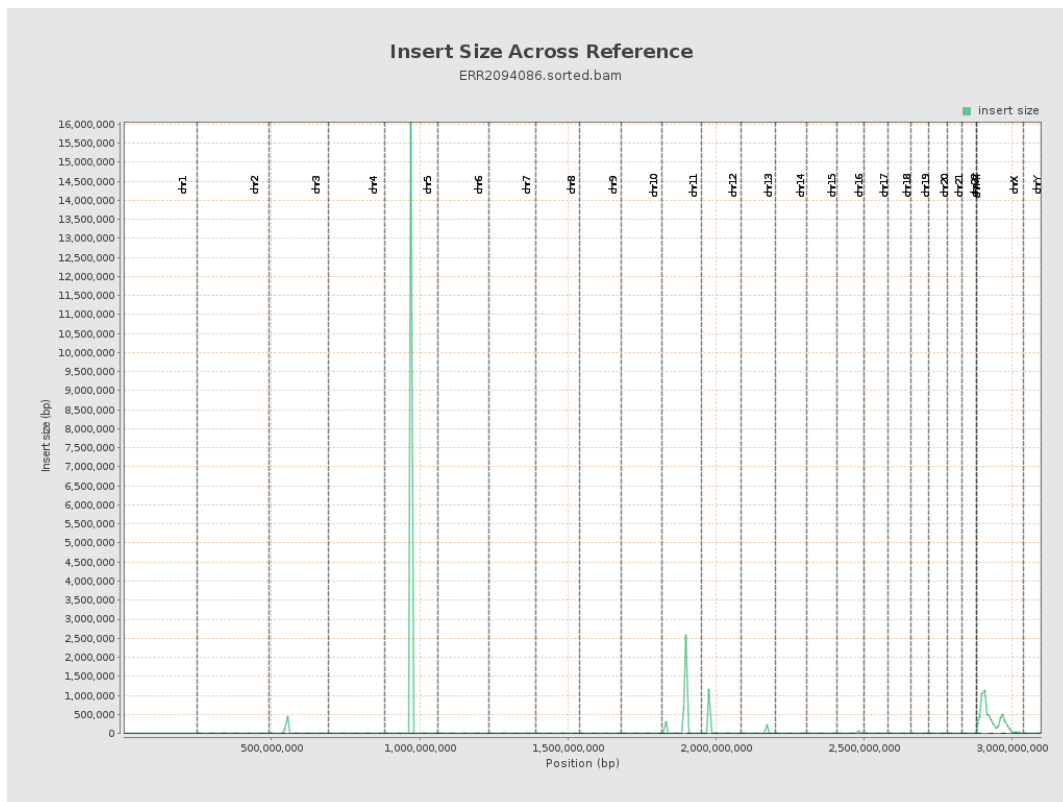
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

