

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:46:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094009.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_ERR2094009 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094009_1.fastq.gz ERR2094009_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:46:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094009.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	518,730
Mapped reads	403,090 / 77.71%
Unmapped reads	115,640 / 22.29%
Mapped paired reads	403,090 / 77.71%
Mapped reads, first in pair	202,028 / 38.95%
Mapped reads, second in pair	201,062 / 38.76%
Mapped reads, both in pair	399,292 / 76.97%
Mapped reads, singletons	3,798 / 0.73%
Secondary alignments	0
Supplementary alignments	12,067 / 2.33%
Read min/max/mean length	30 / 151 / 124.72
Duplicated reads (estimated)	397,630 / 76.65%
Duplication rate	46.39%
Clipped reads	153,155 / 29.52%

2.2. ACGT Content

Number/percentage of A's	15,127,581 / 28.56%
Number/percentage of C's	11,201,096 / 21.14%
Number/percentage of T's	14,602,186 / 27.56%
Number/percentage of G's	12,045,224 / 22.74%
Number/percentage of N's	540 / 0%

GC Percentage	43.88%
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2.3. Coverage

Mean	0.0174
Standard Deviation	16.1746

2.4. Mapping Quality

Mean Mapping Quality	36.14
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2.5. Insert size

Mean	271,980.33
Standard Deviation	4,918,453.08
P25/Median/P75	141 / 186 / 217

2.6. Mismatches and indels

General error rate	3.04%
Mismatches	1,572,381
Insertions	17,726
Mapped reads with at least one insertion	4.32%
Deletions	107,453
Mapped reads with at least one deletion	25.67%
Homopolymer indels	32.21%

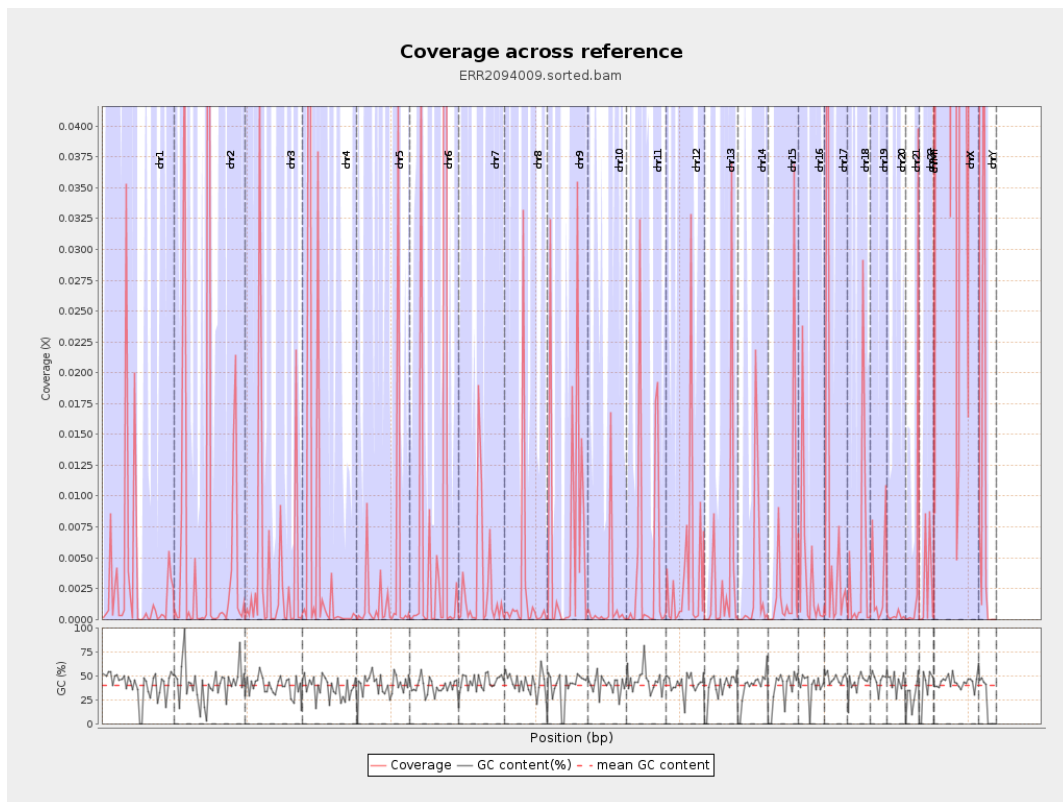
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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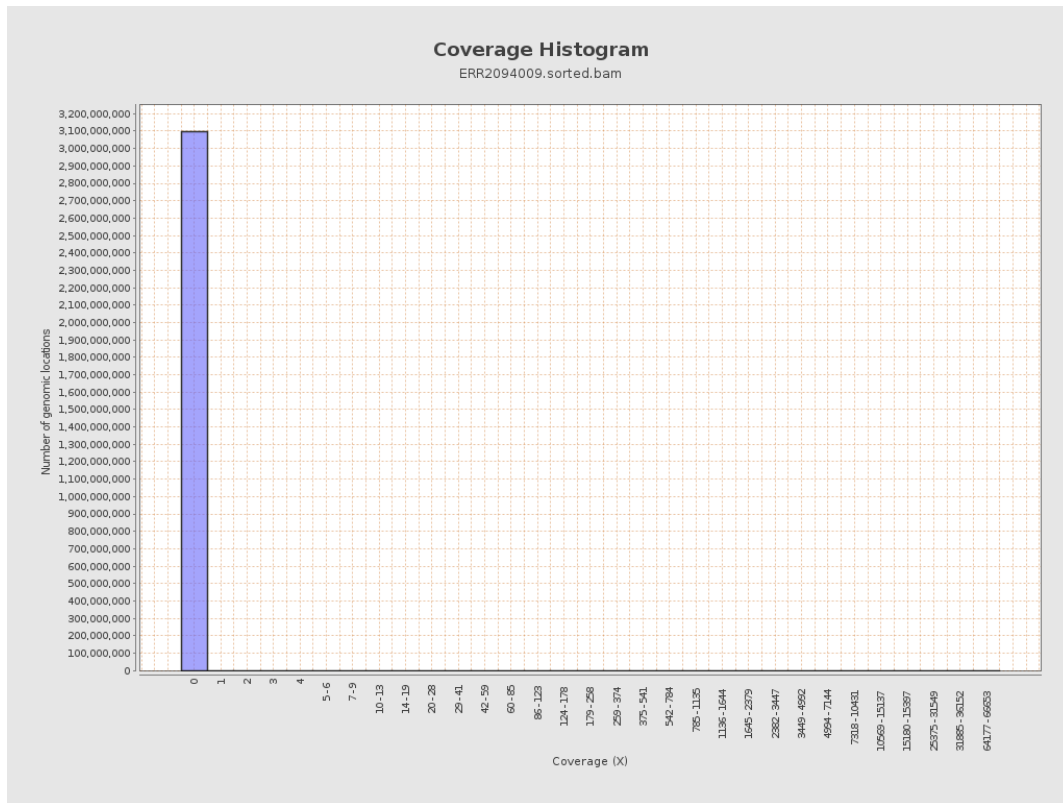
		bases	coverage	deviation
chr1	249250621	733068	0.0029	1.6134
chr2	243199373	1656248	0.0068	4.0777
chr3	198022430	750341	0.0038	1.5354
chr4	191154276	1036189	0.0054	4.3506
chr5	180915260	482824	0.0027	2.2239
chr6	171115067	2185101	0.0128	9.5894
chr7	159138663	393552	0.0025	1.0394
chr8	146364022	329230	0.0022	1.7528
chr9	141213431	909586	0.0064	2.7208
chr10	135534747	159394	0.0012	0.8741
chr11	135006516	601097	0.0045	2.3501
chr12	133851895	528274	0.0039	1.8243
chr13	115169878	431717	0.0037	2.0051
chr14	107349540	305851	0.0028	1.1001
chr15	102531392	415682	0.0041	2.3975
chr16	90354753	347129	0.0038	1.7786
chr17	81195210	763838	0.0094	4.665
chr18	78077248	372516	0.0048	1.7586
chr19	59128983	173772	0.0029	0.8908
chr20	63025520	15253	0.0002	0.0752
chr21	48129895	213051	0.0044	1.9681
chr22	51304566	137894	0.0027	0.6889
chrMT	16571	17918045	1,081.2893	6,064.1774
chrX	155270560	22323415	0.1438	30.9149

chrY	59373566	549725	0.0093	3.2937
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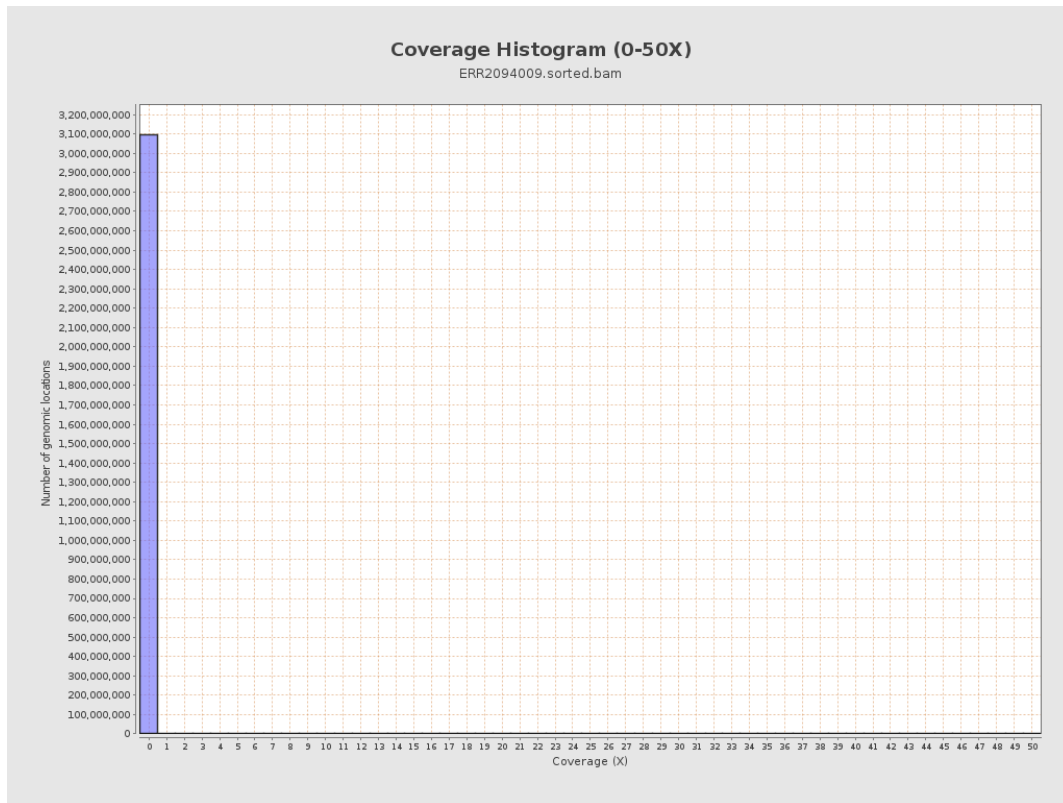
3. Results : Coverage across reference



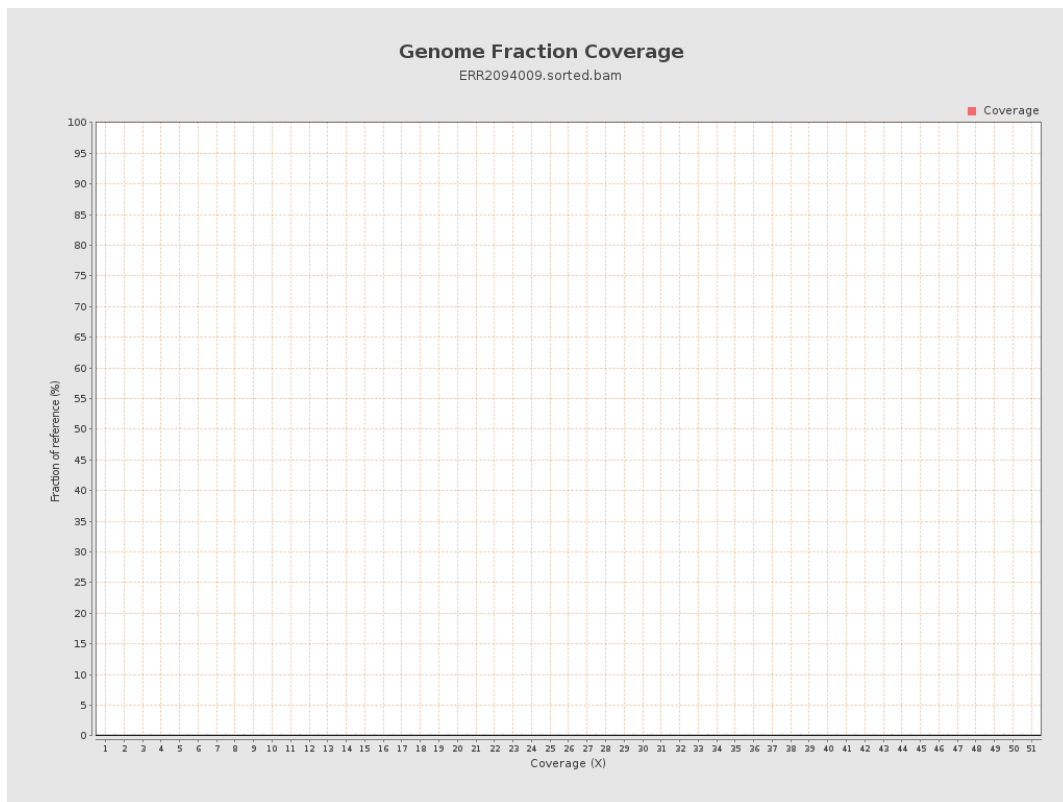
4. Results : Coverage Histogram



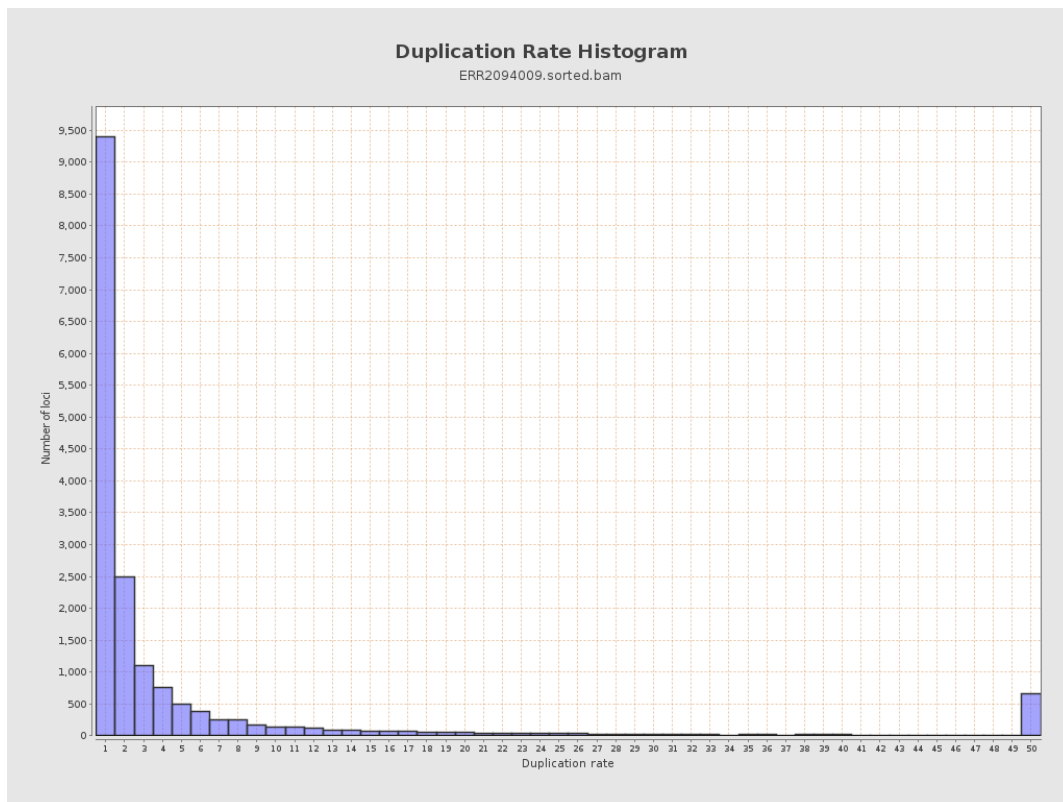
5. Results : Coverage Histogram (0-50X)



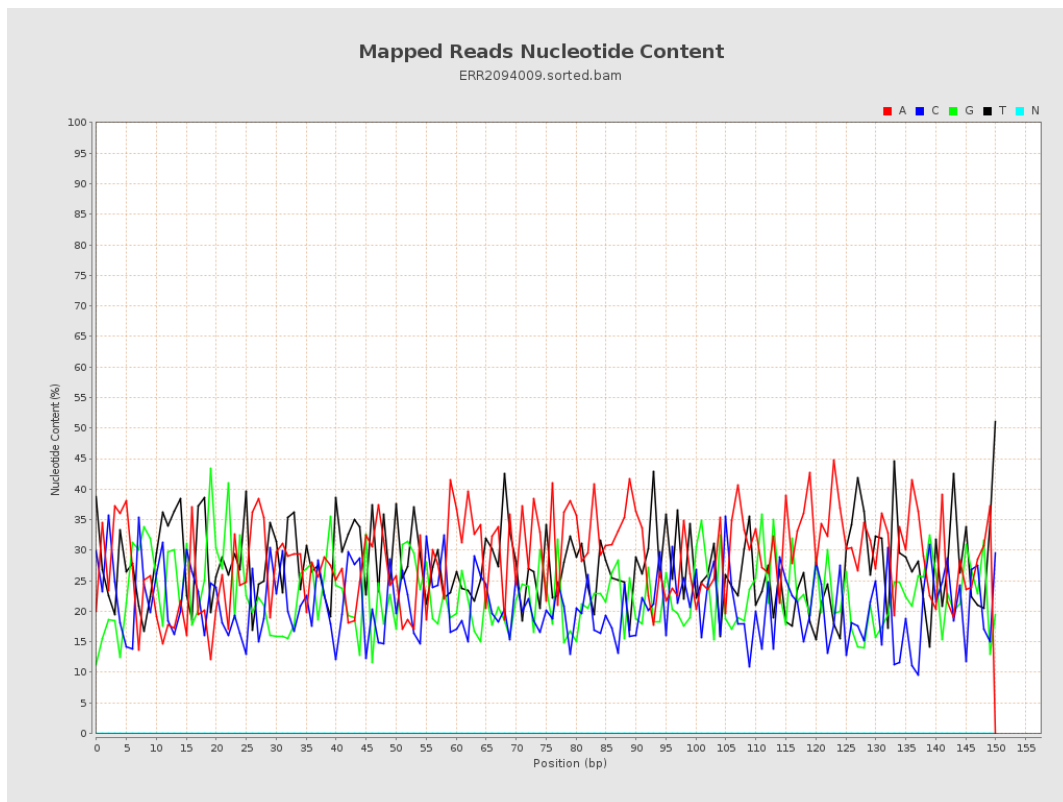
6. Results : Genome Fraction Coverage



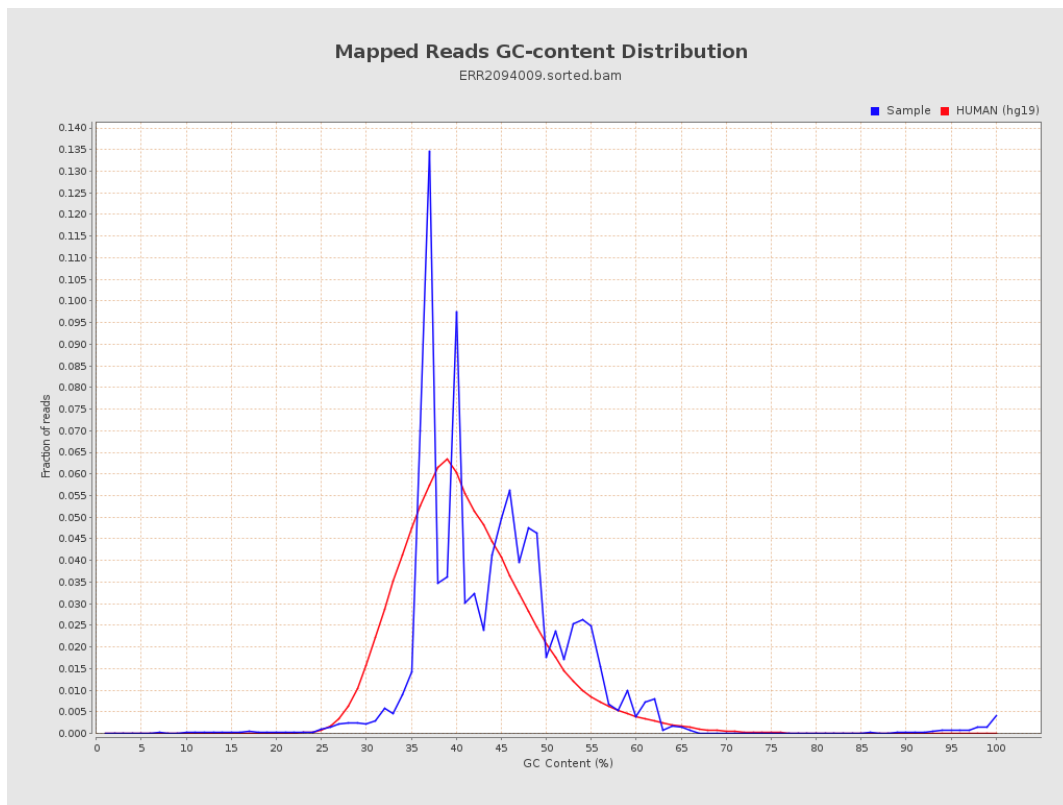
7. Results : Duplication Rate Histogram



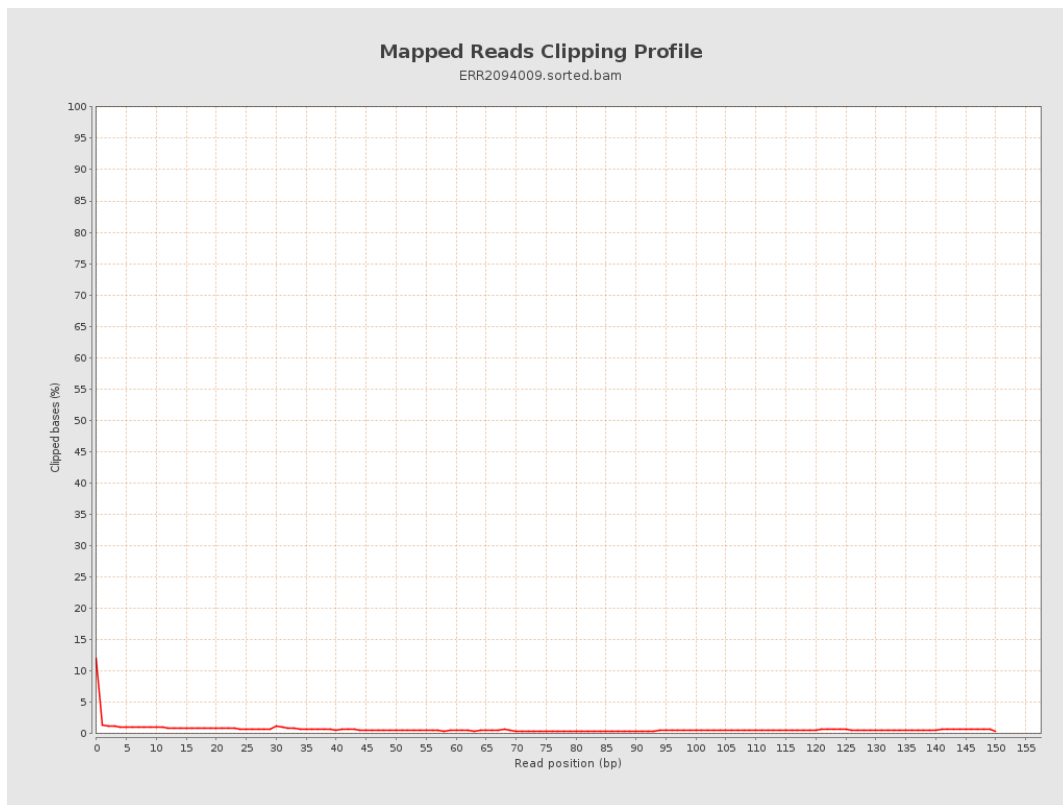
8. Results : Mapped Reads Nucleotide Content



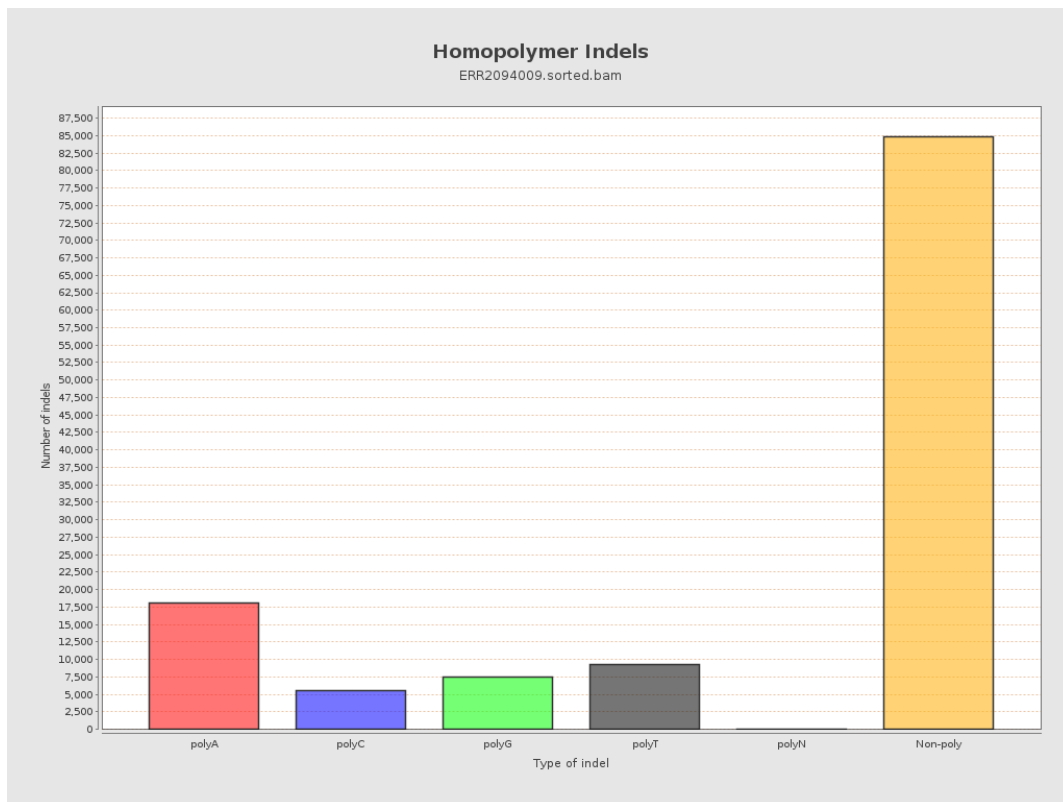
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



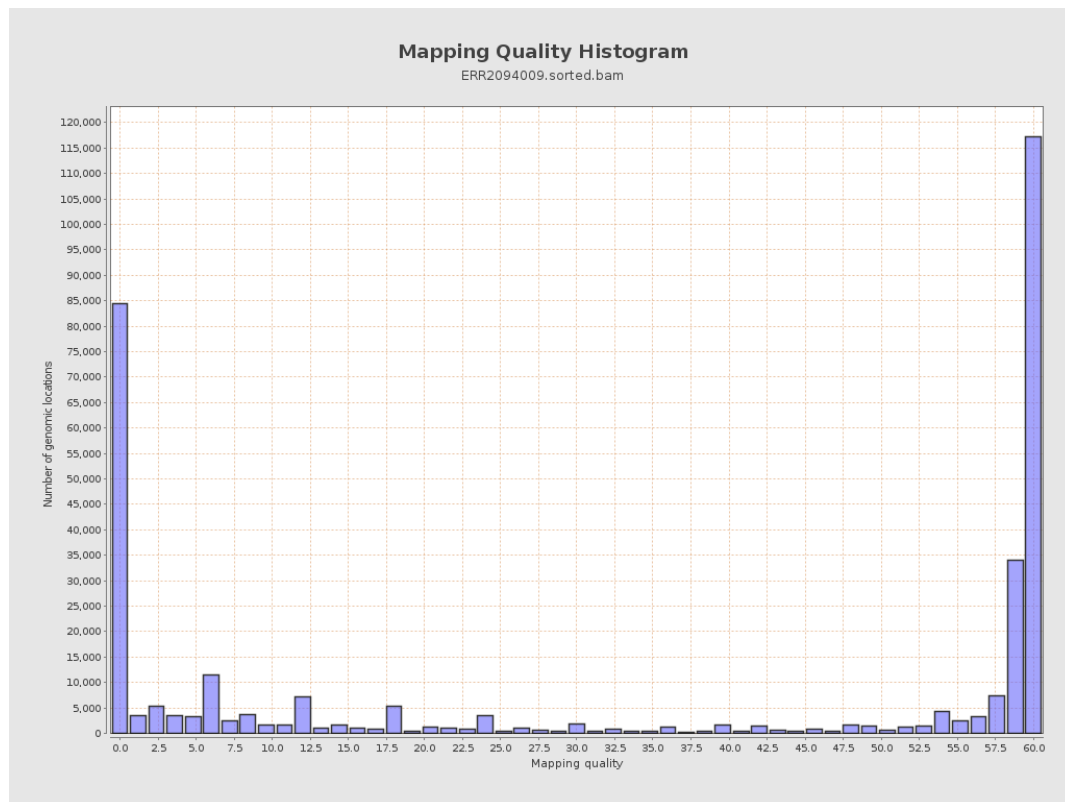
11. Results : Homopolymer Indels



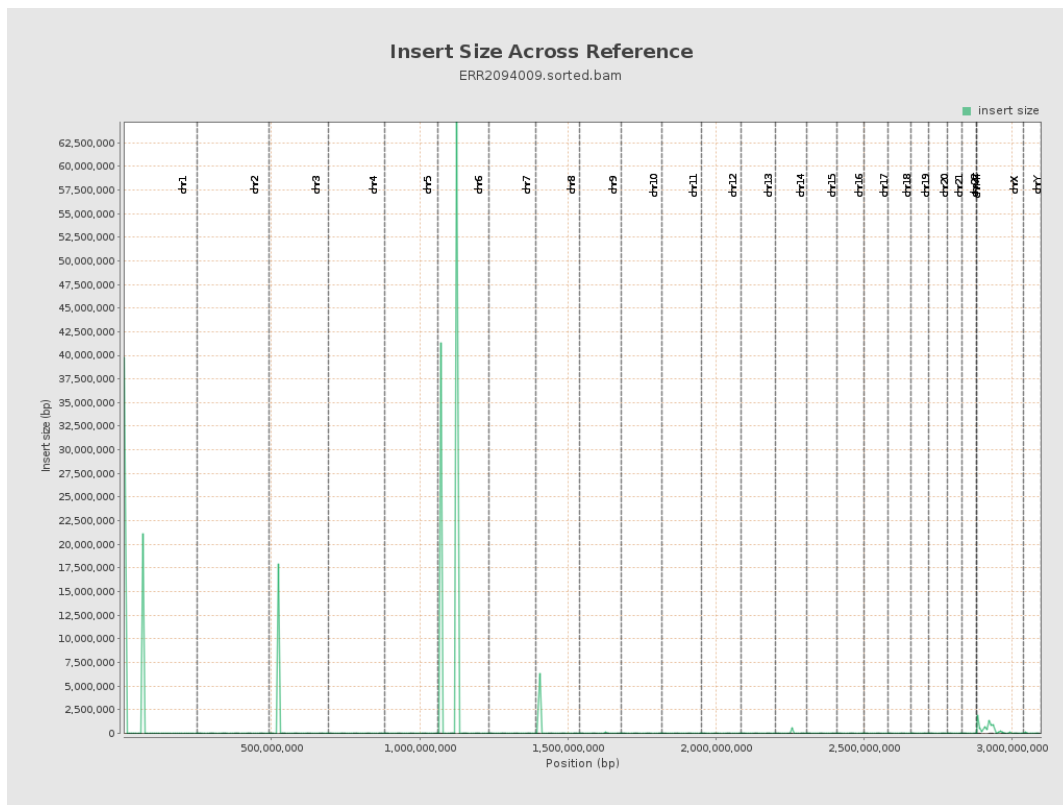
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

