Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:57:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094041.sorted.bam -c -nw 400 -hm 3
```

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_ERR2094041 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094041_1.fastq.gz ERR2094041_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:57:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	358,778
Mapped reads	344,315 / 95.97%
Unmapped reads	14,463 / 4.03%
Mapped paired reads	344,315 / 95.97%
Mapped reads, first in pair	172,950 / 48.21%
Mapped reads, second in pair	171,365 / 47.76%
Mapped reads, both in pair	341,700 / 95.24%
Mapped reads, singletons	2,615 / 0.73%
Secondary alignments	0
Supplementary alignments	15,543 / 4.33%
Read min/max/mean length	30 / 151 / 141.28
Duplicated reads (estimated)	319,665 / 89.1%
Duplication rate	49.76%
Clipped reads	147,443 / 41.1%

2.2. ACGT Content

Number/percentage of A's	12,179,072 / 27.47%
Number/percentage of C's	10,039,111 / 22.64%
Number/percentage of T's	11,719,196 / 26.43%
Number/percentage of G's	10,401,333 / 23.46%
Number/percentage of N's	422 / 0%

GC Percentage	46.1%

2.3. Coverage

Mean	0.0147
Standard Deviation	3.0381

2.4. Mapping Quality

Mean Mapping Quality	43.6

2.5. Insert size

Mean	796,838
Standard Deviation	8,009,607.04
P25/Median/P75	131 / 166 / 198

2.6. Mismatches and indels

General error rate	4.22%
Mismatches	1,820,793
Insertions	28,954
Mapped reads with at least one insertion	8.27%
Deletions	149,457
Mapped reads with at least one deletion	40.58%
Homopolymer indels	29.8%

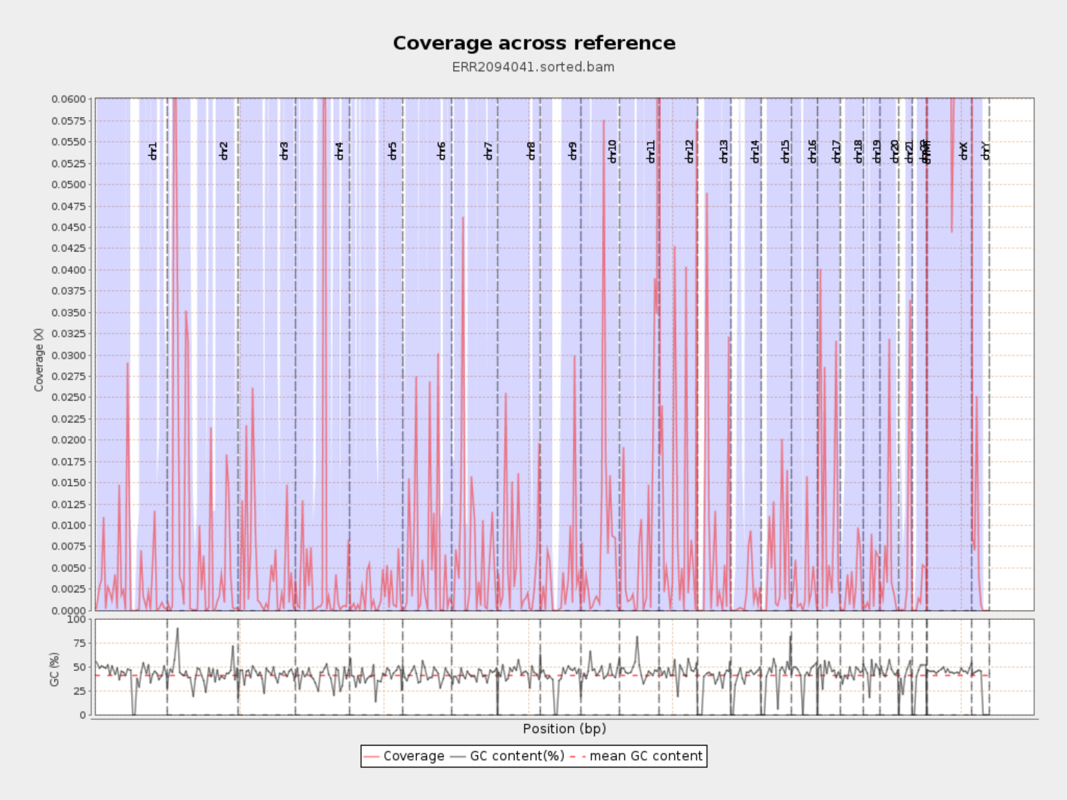
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

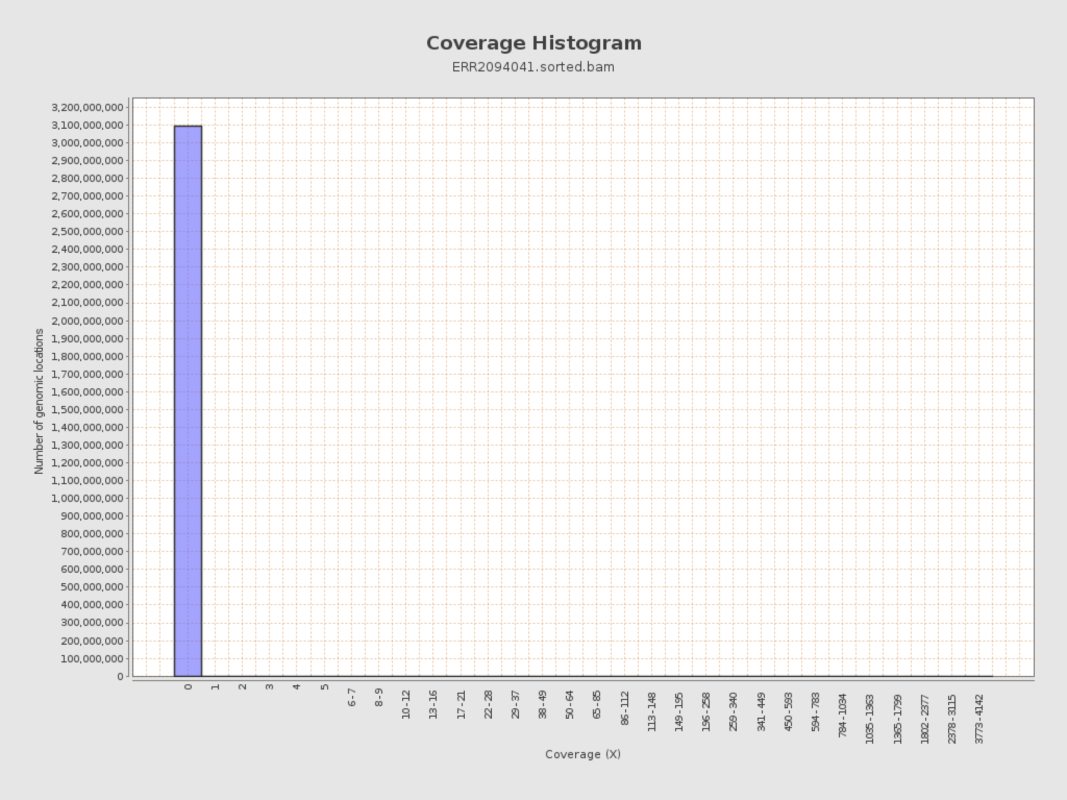
		bases	coverage	deviation
chr1	249250621	824344	0.0033	1.2984
chr2	243199373	2171883	0.0089	2.3511
chr3	198022430	932291	0.0047	1.4342
chr4	191154276	1318781	0.0069	2.6258
chr5	180915260	342910	0.0019	0.5117
chr6	171115067	1134582	0.0066	2.387
chr7	159138663	1084566	0.0068	1.7643
chr8	146364022	831806	0.0057	1.7023
chr9	141213431	571234	0.004	1.4585
chr10	135534747	1143536	0.0084	2.5523
chr11	135006516	1401300	0.0104	2.5018
chr12	133851895	1454049	0.0109	2.9851
chr13	115169878	919889	0.008	2.0434
chr14	107349540	206023	0.0019	0.7439
chr15	102531392	558387	0.0054	1.2704
chr16	90354753	279635	0.0031	1.1058
chr17	81195210	1099314	0.0135	2.9297
chr18	78077248	232623	0.003	0.845
chr19	59128983	187444	0.0032	0.8137
chr20	63025520	398667	0.0063	1.5796
chr21	48129895	364496	0.0076	2.9421
chr22	51304566	97984	0.0019	0.4193
chrMT	16571	1951510	117.7666	491.8503
chrX	155270560	25558067	0.1646	9.2892

chrY	59373566	328530	0.0055	1.231

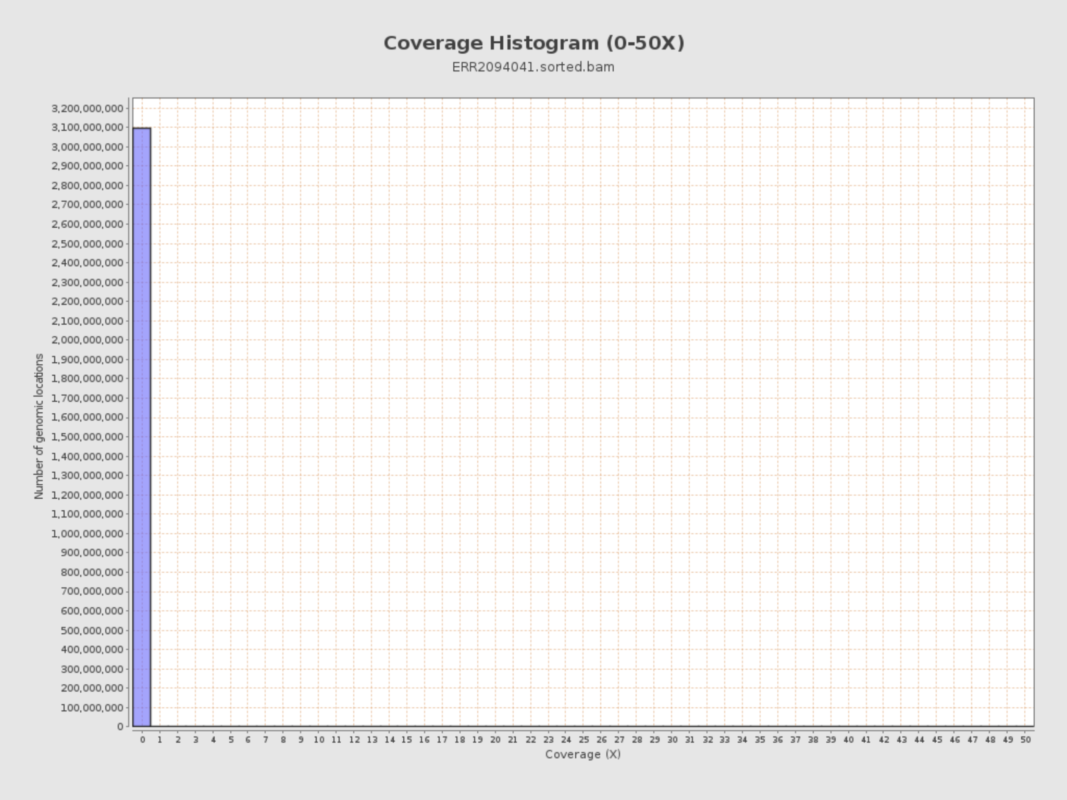
3. Results : Coverage across reference



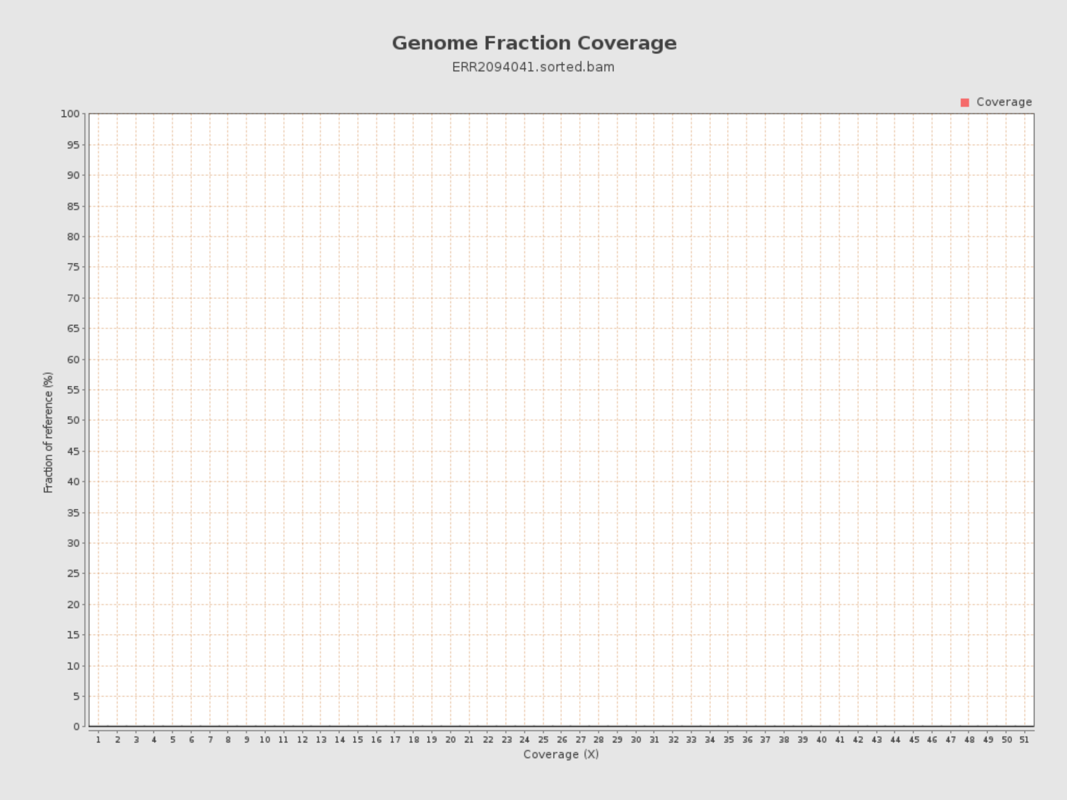
4. Results : Coverage Histogram



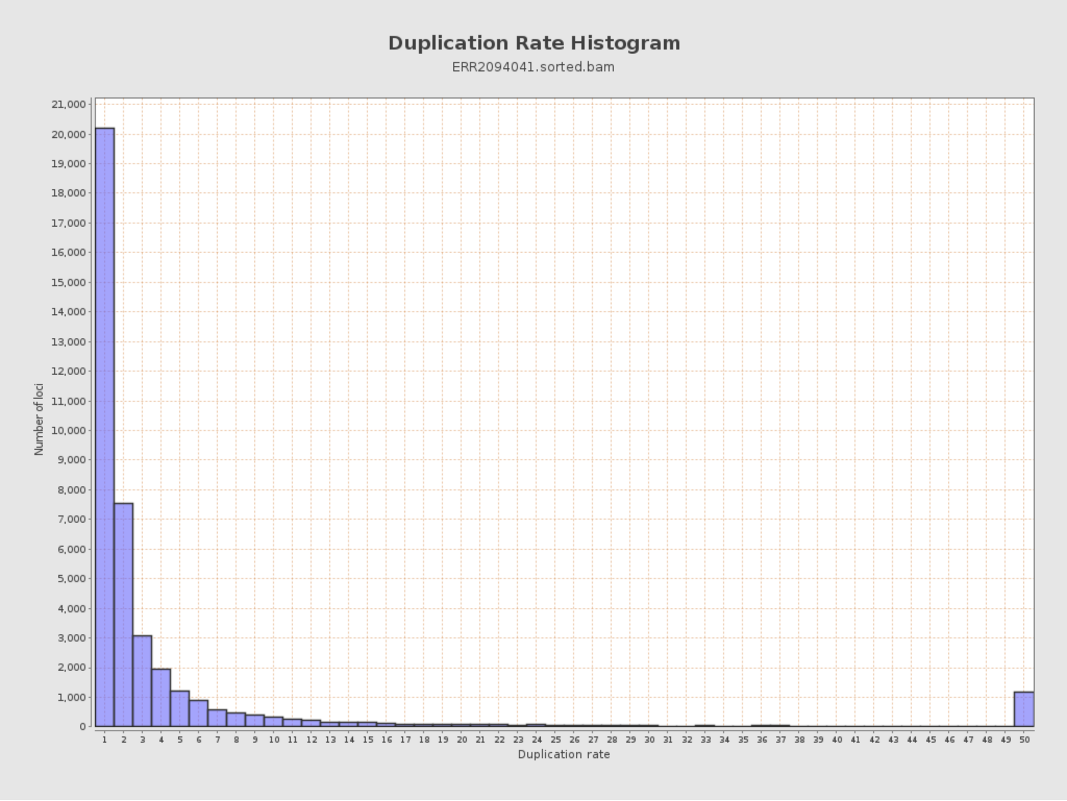
5. Results : Coverage Histogram (0-50X)



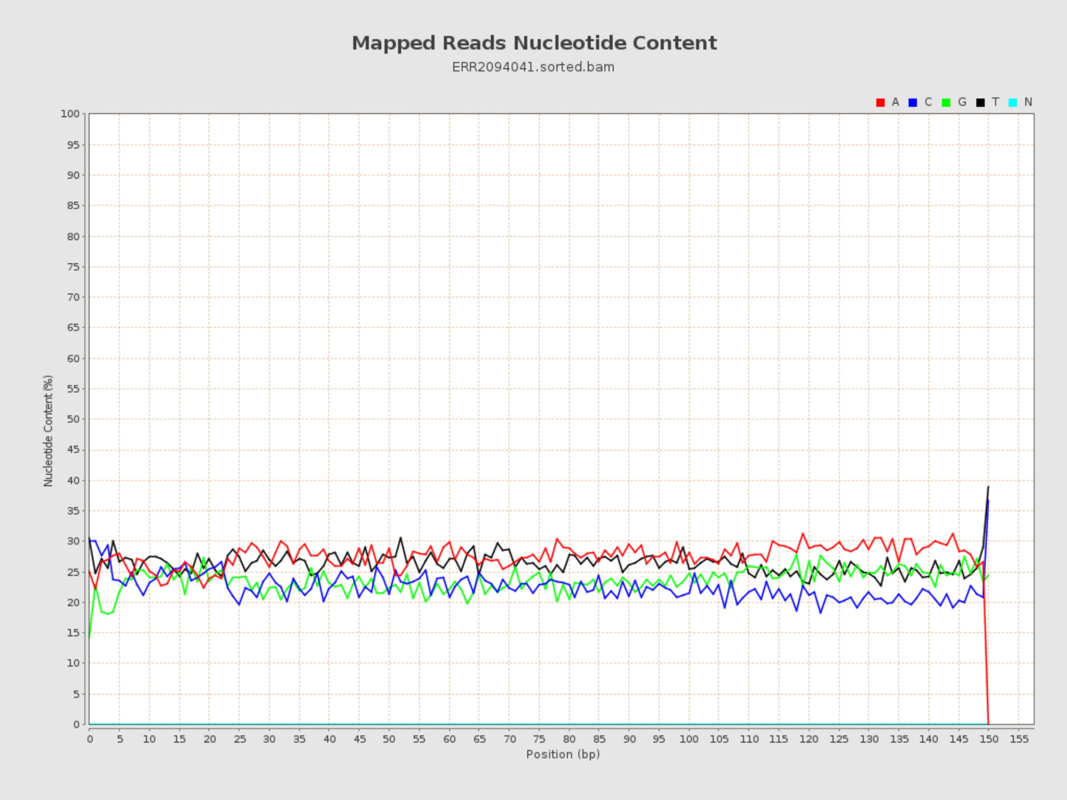
6. Results : Genome Fraction Coverage



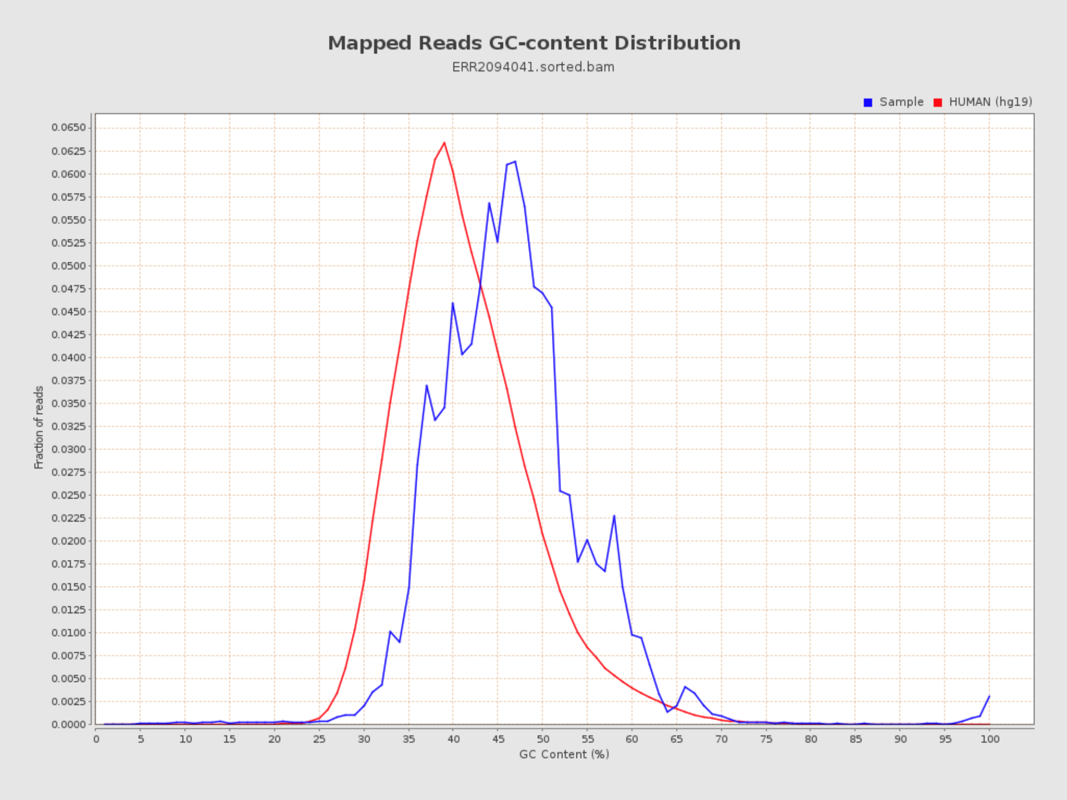
7. Results : Duplication Rate Histogram



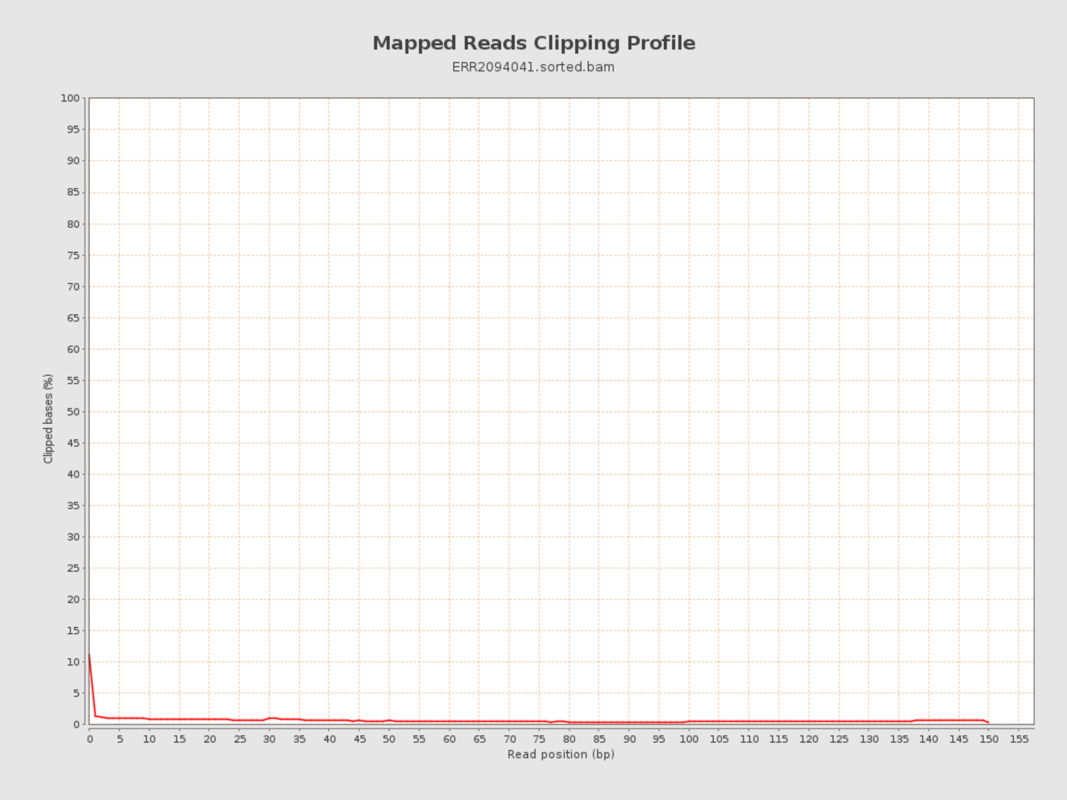
8. Results : Mapped Reads Nucleotide Content



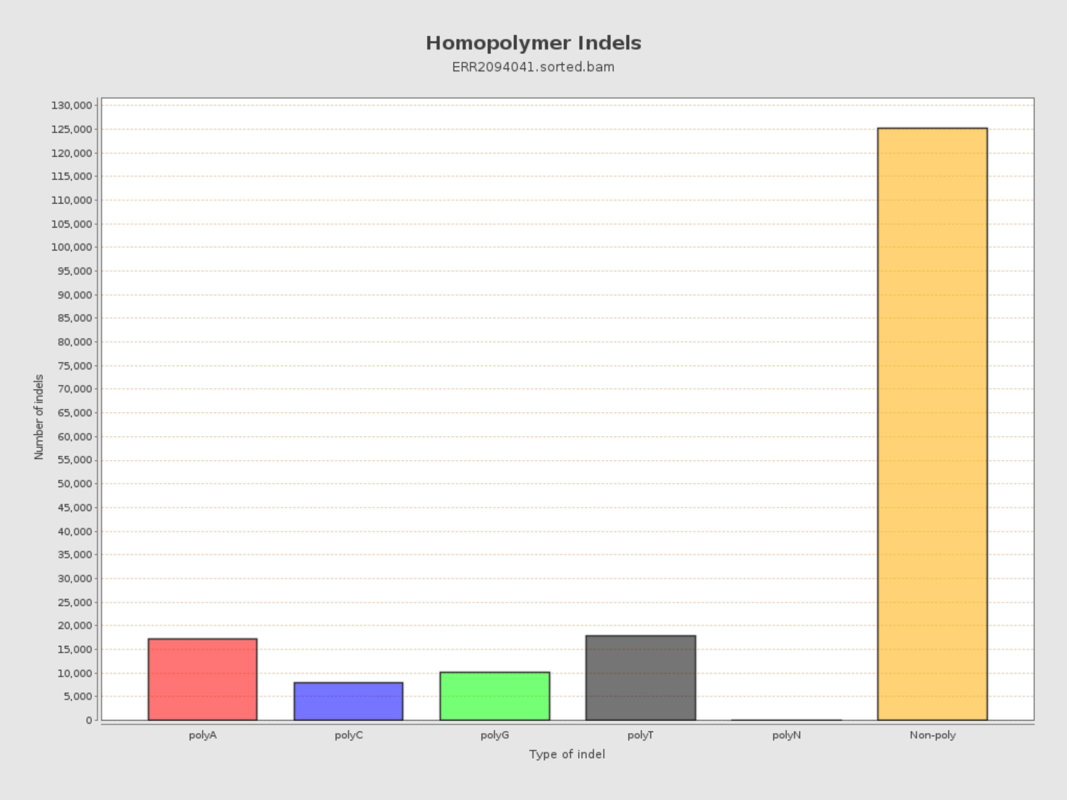
9. Results : Mapped Reads GC-content Distribution



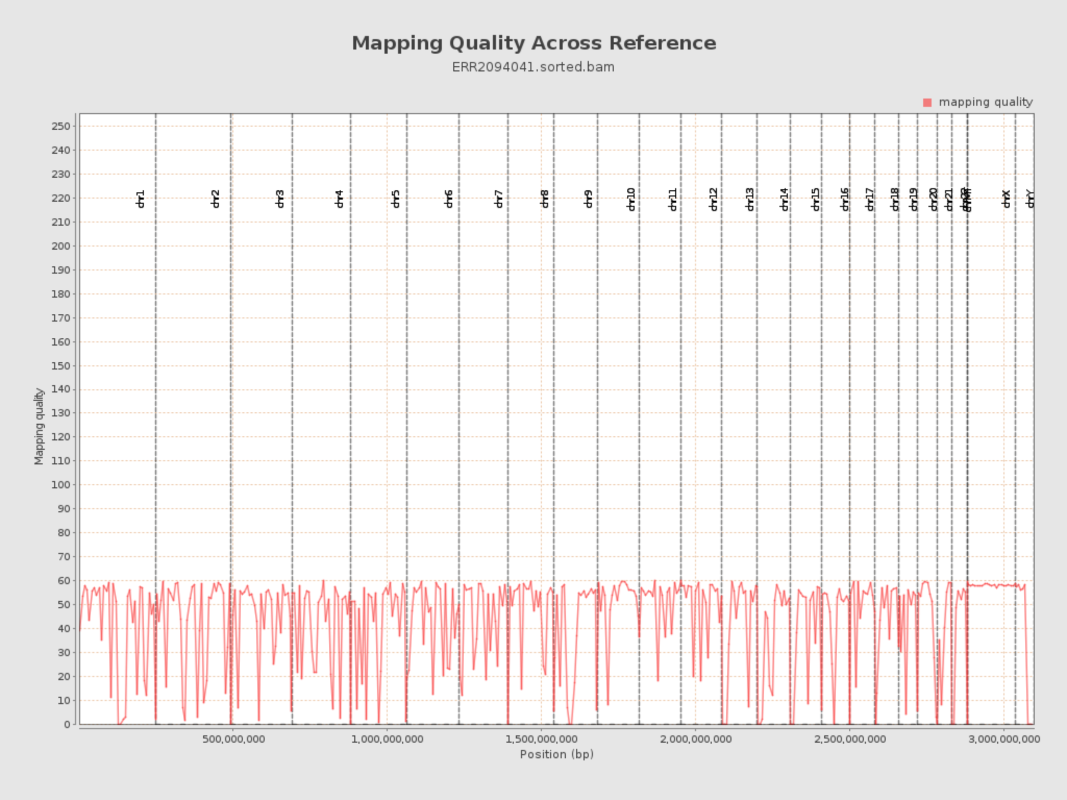
10. Results : Mapped Reads Clipping Profile



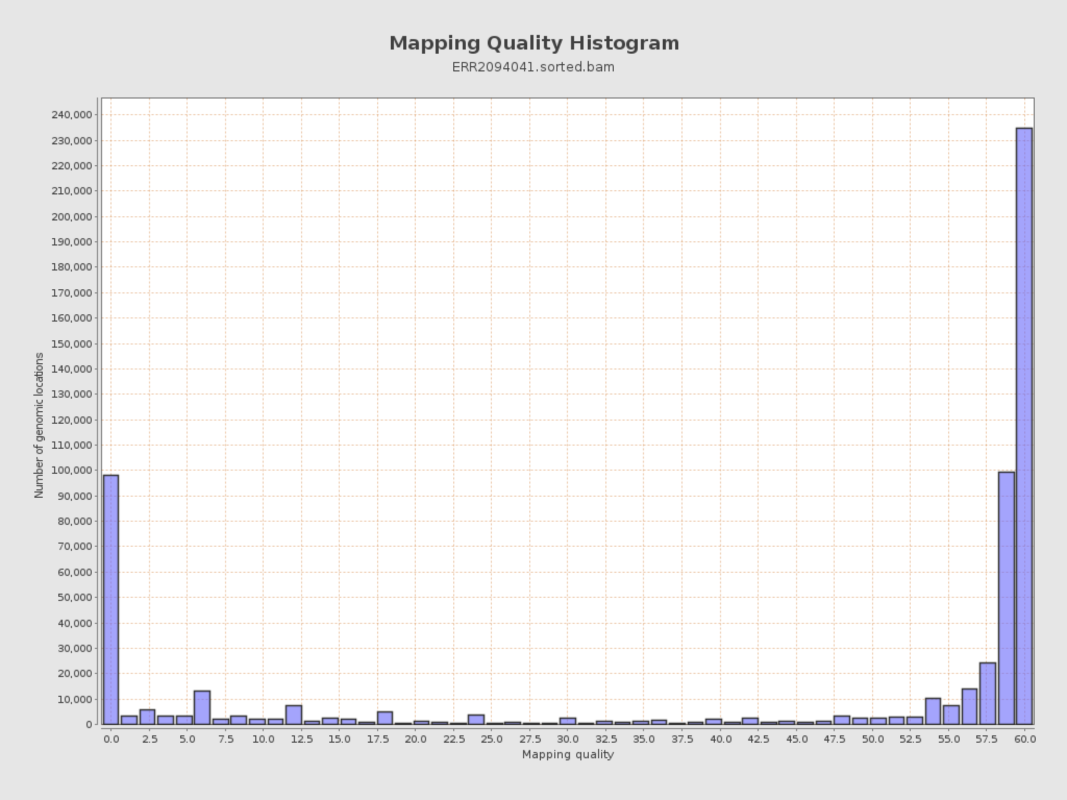
11. Results : Homopolymer Indels



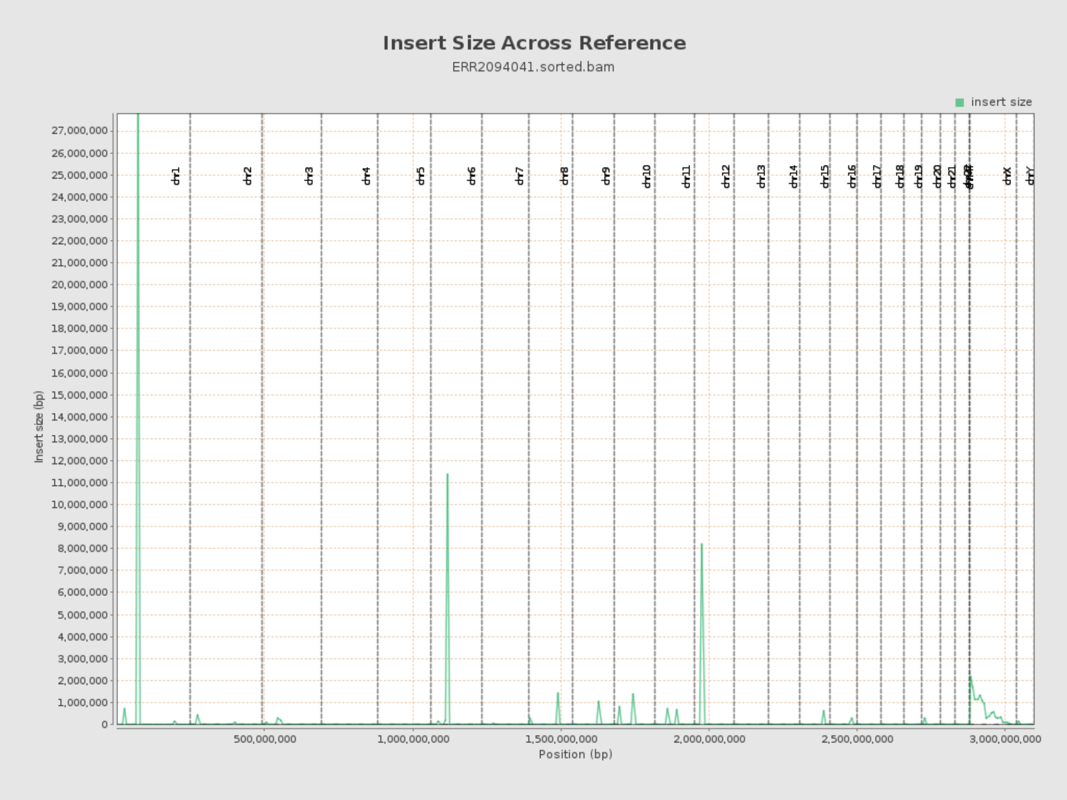
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram