Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:53:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094012.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_ERR2094012 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094012_1.fastq.gz ERR2094012_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:53:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	449,254
Mapped reads	400,384 / 89.12%
Unmapped reads	48,870 / 10.88%
Mapped paired reads	400,384 / 89.12%
Mapped reads, first in pair	200,809 / 44.7%
Mapped reads, second in pair	199,575 / 44.42%
Mapped reads, both in pair	397,852 / 88.56%
Mapped reads, singletons	2,532 / 0.56%
Secondary alignments	0
Supplementary alignments	3,633 / 0.81%
Read min/max/mean length	30 / 151 / 134.4
Duplicated reads (estimated)	391,613 / 87.17%
Duplication rate	46.11%
Clipped reads	115,418 / 25.69%

2.2. ACGT Content

Number/percentage of A's	15,091,905 / 28.24%
Number/percentage of C's	11,578,258 / 21.67%
Number/percentage of T's	14,799,189 / 27.69%
Number/percentage of G's	11,969,676 / 22.4%
Number/percentage of N's	625 / 0%

GC Percentage	44.06%

2.3. Coverage

Mean	0.0176
Standard Deviation	15.9876

2.4. Mapping Quality

Mean Mapping Quality	34.74

2.5. Insert size

Mean	76,458.39
Standard Deviation	2,556,108.27
P25/Median/P75	149 / 180 / 217

2.6. Mismatches and indels

General error rate	3.49%
Mismatches	1,844,428
Insertions	19,156
Mapped reads with at least one insertion	4.67%
Deletions	138,285
Mapped reads with at least one deletion	33.13%
Homopolymer indels	29.12%

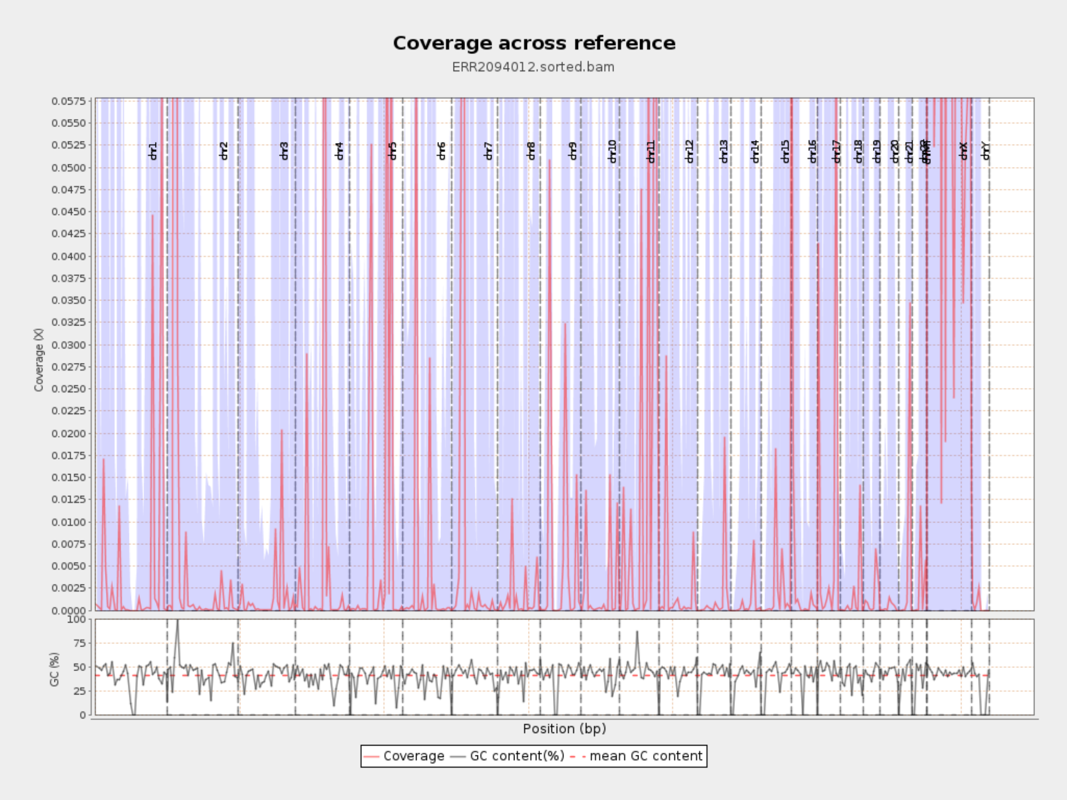
2.7. Chromosome stats

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

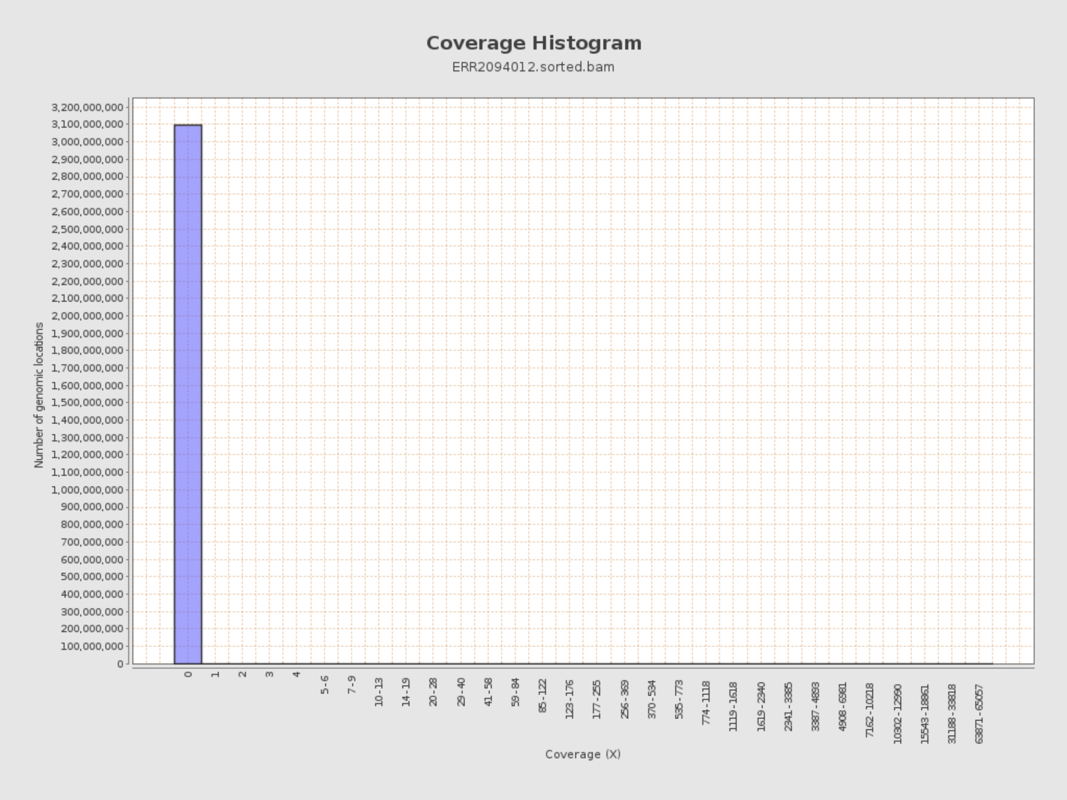
		bases	coverage	deviation
chr1	249250621	1166846	0.0047	2.8181
chr2	243199373	3021604	0.0124	12.3699
chr3	198022430	337001	0.0017	1.0819
chr4	191154276	1313843	0.0069	3.6736
chr5	180915260	1961634	0.0108	5.9517
chr6	171115067	822534	0.0048	3.3295
chr7	159138663	1716875	0.0108	6.4121
chr8	146364022	235394	0.0016	0.71
chr9	141213431	859066	0.0061	3.0473
chr10	135534747	356572	0.0026	1.4274
chr11	135006516	2413323	0.0179	6.681
chr12	133851895	338755	0.0025	1.4127
chr13	115169878	195999	0.0017	1.0485
chr14	107349540	85885	0.0008	0.3251
chr15	102531392	231180	0.0023	1.1217
chr16	90354753	561087	0.0062	4.2322
chr17	81195210	895807	0.011	4.8414
chr18	78077248	141800	0.0018	1.0085
chr19	59128983	96772	0.0016	0.4829
chr20	63025520	25363	0.0004	0.1065
chr21	48129895	277418	0.0058	2.7413
chr22	51304566	137681	0.0027	0.8693
chrMT	16571	18711894	1,129.1952	6,117.6292
chrX	155270560	18503813	0.1192	22.825

chrY	59373566	33015	0.0006	0.2674

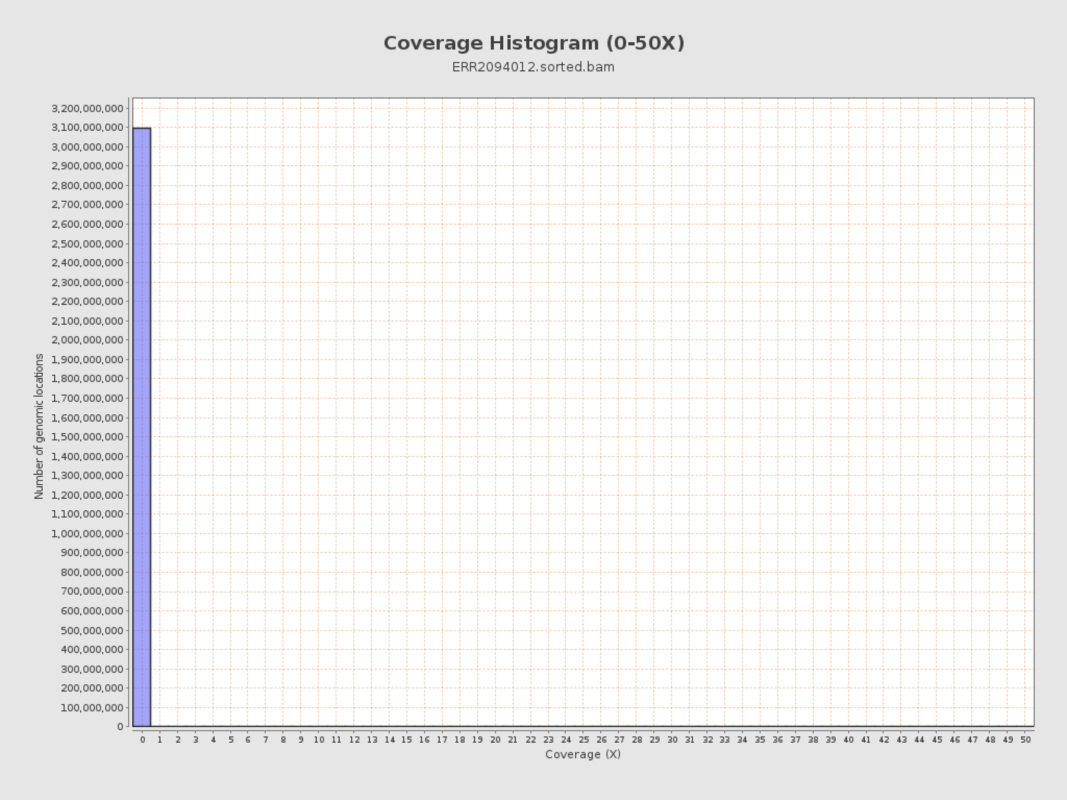
3. Results : Coverage across reference



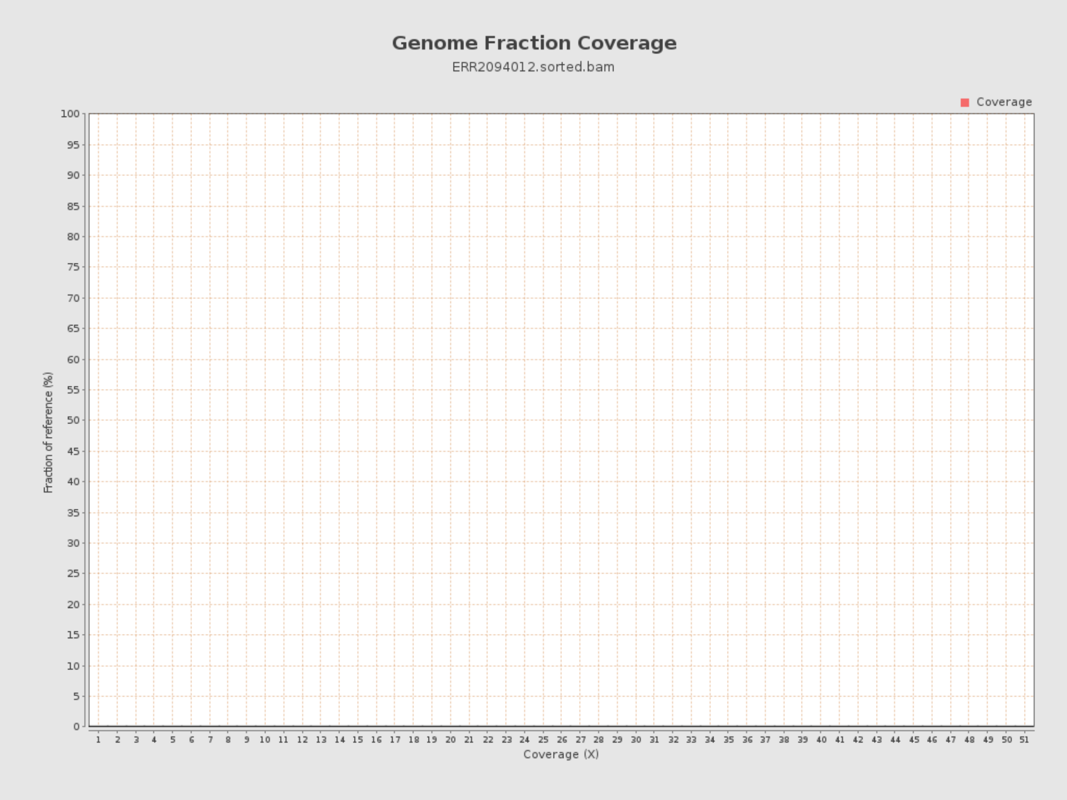
4. Results : Coverage Histogram



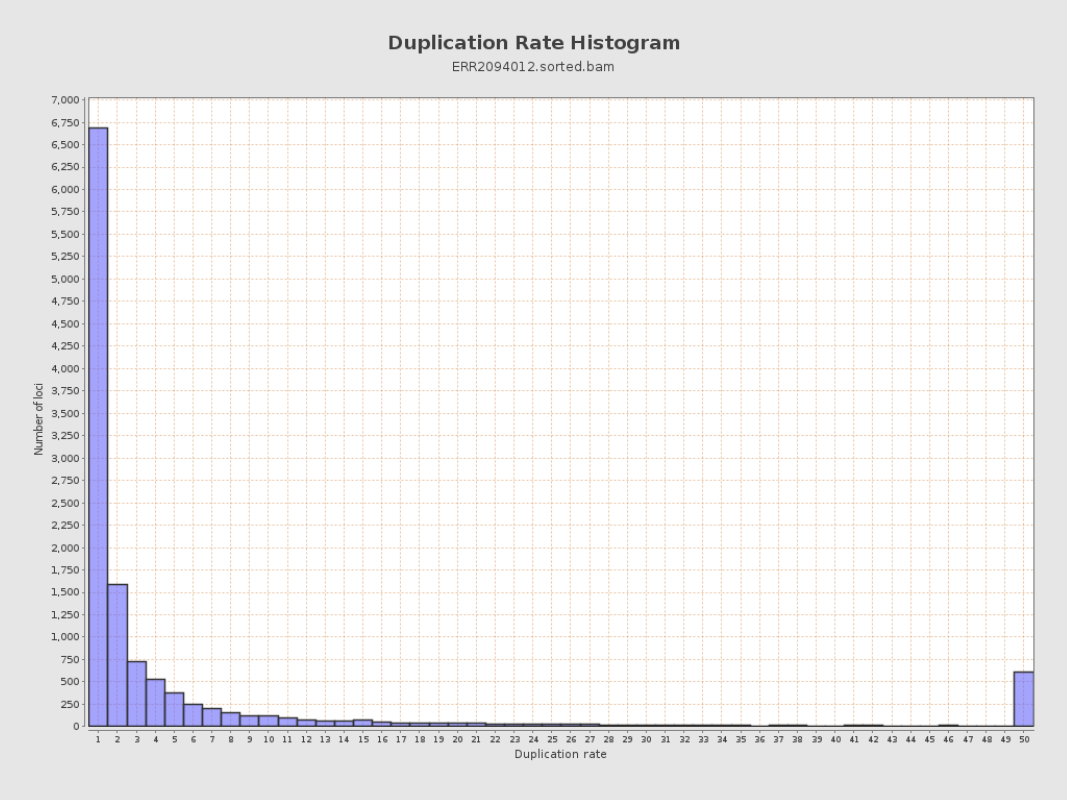
5. Results : Coverage Histogram (0-50X)



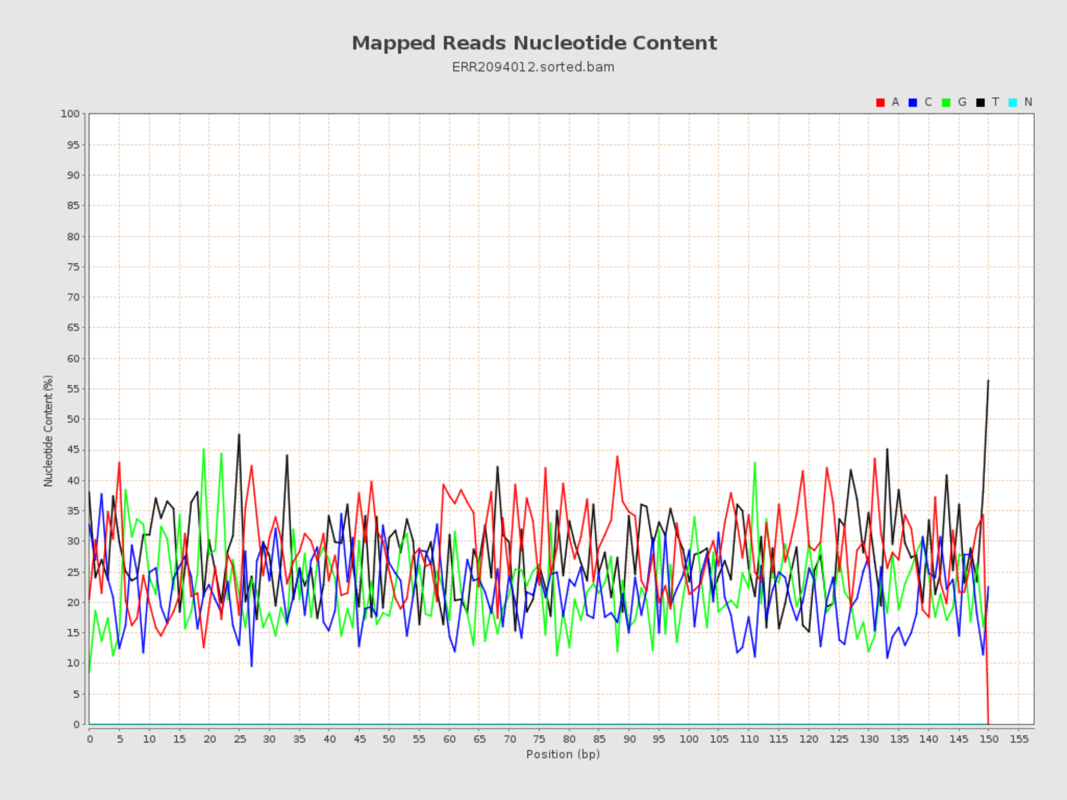
6. Results : Genome Fraction Coverage



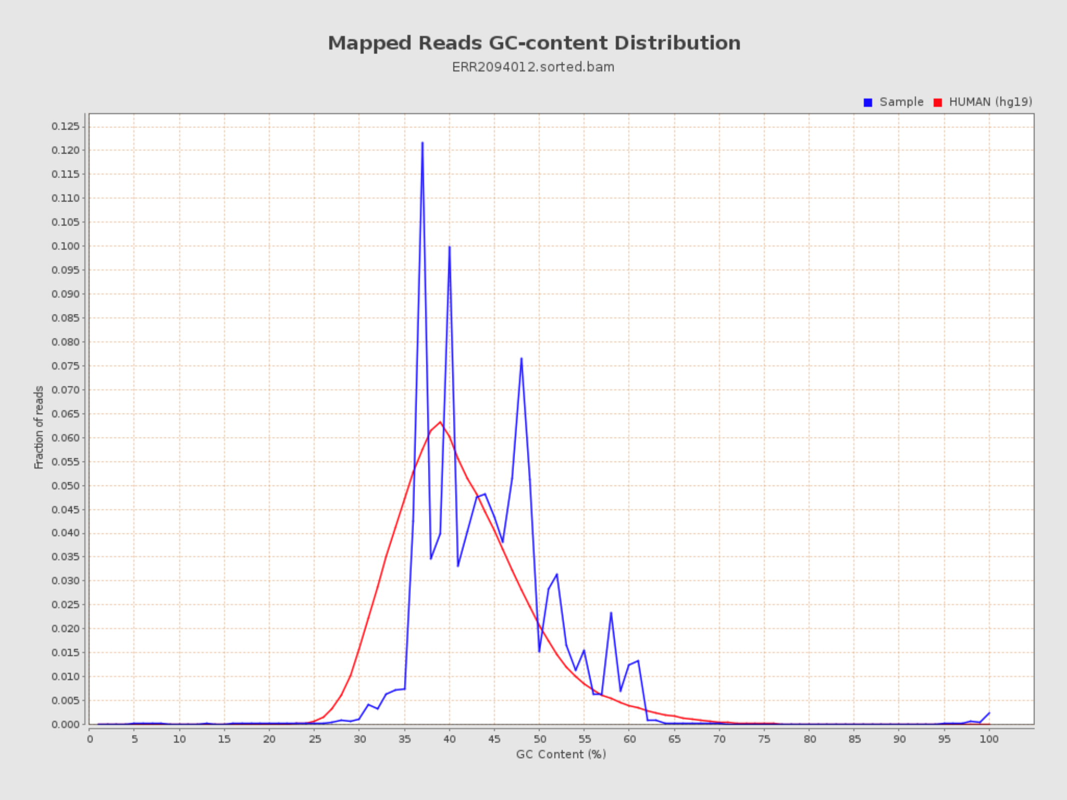
7. Results : Duplication Rate Histogram



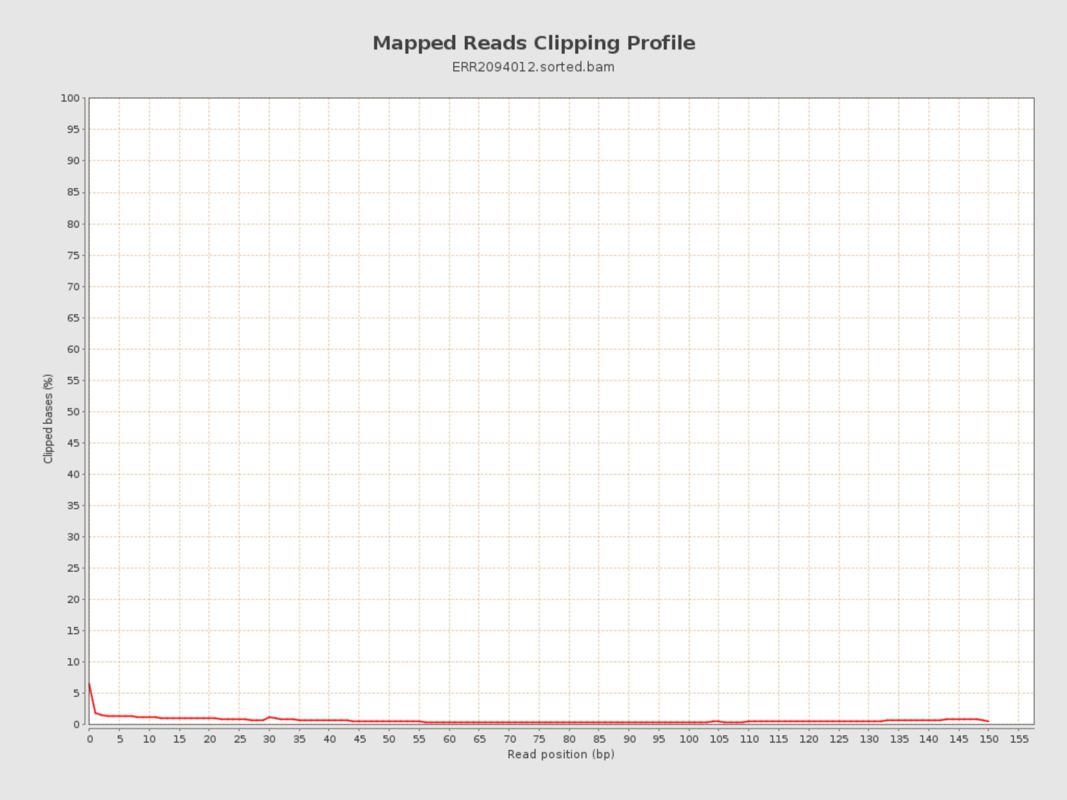
8. Results : Mapped Reads Nucleotide Content



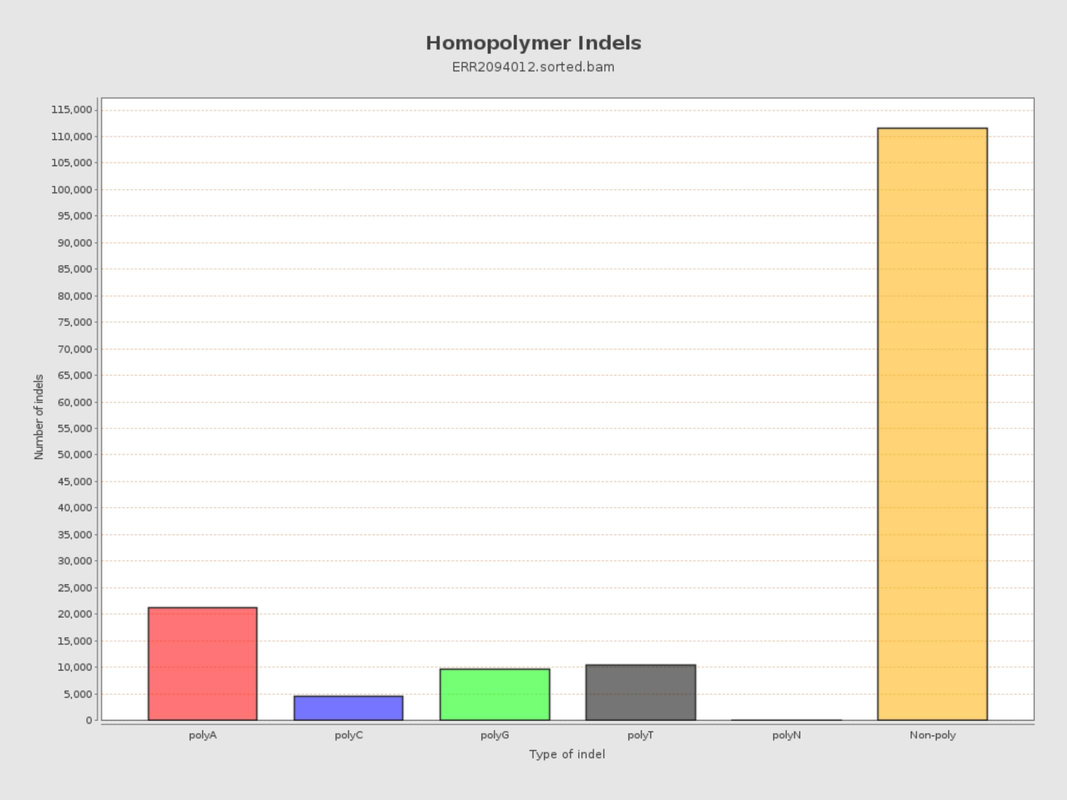
9. Results : Mapped Reads GC-content Distribution



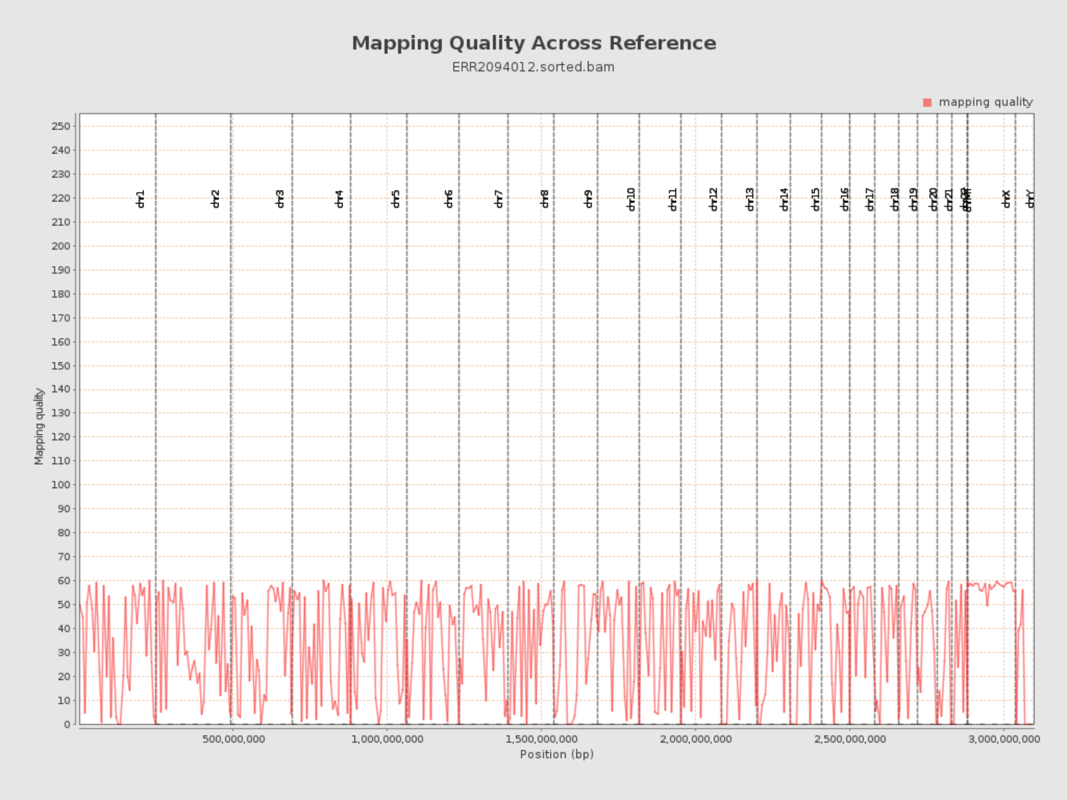
10. Results : Mapped Reads Clipping Profile



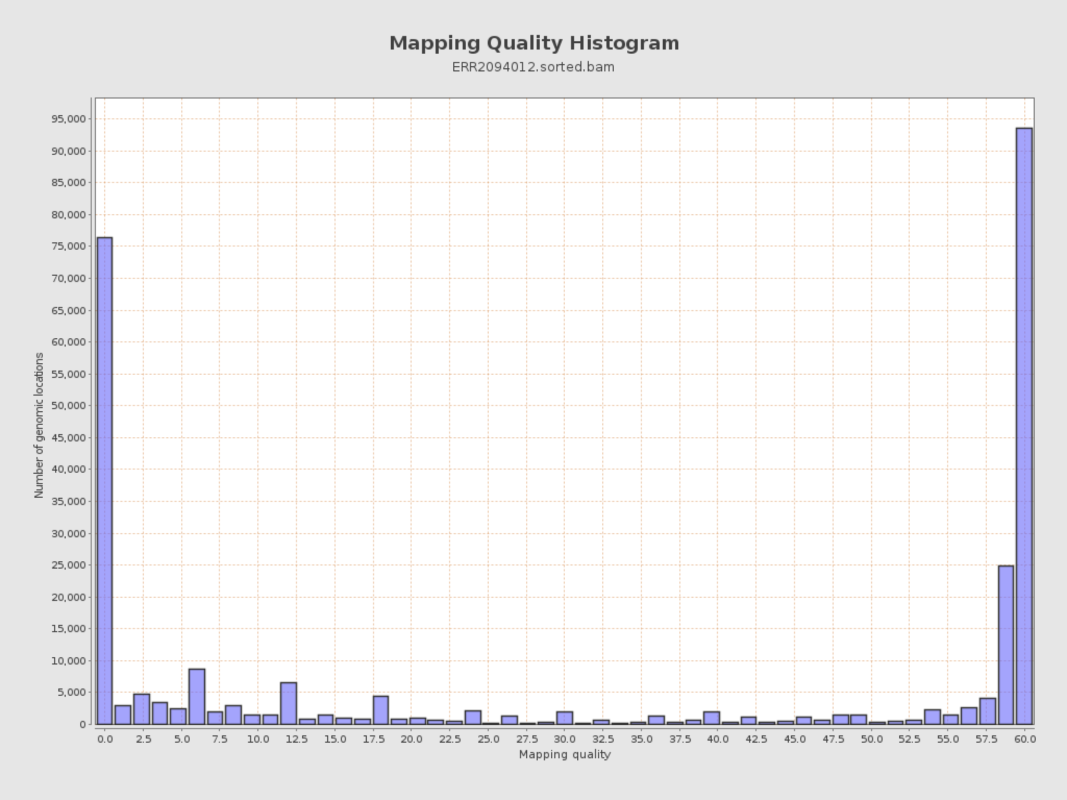
11. Results : Homopolymer Indels



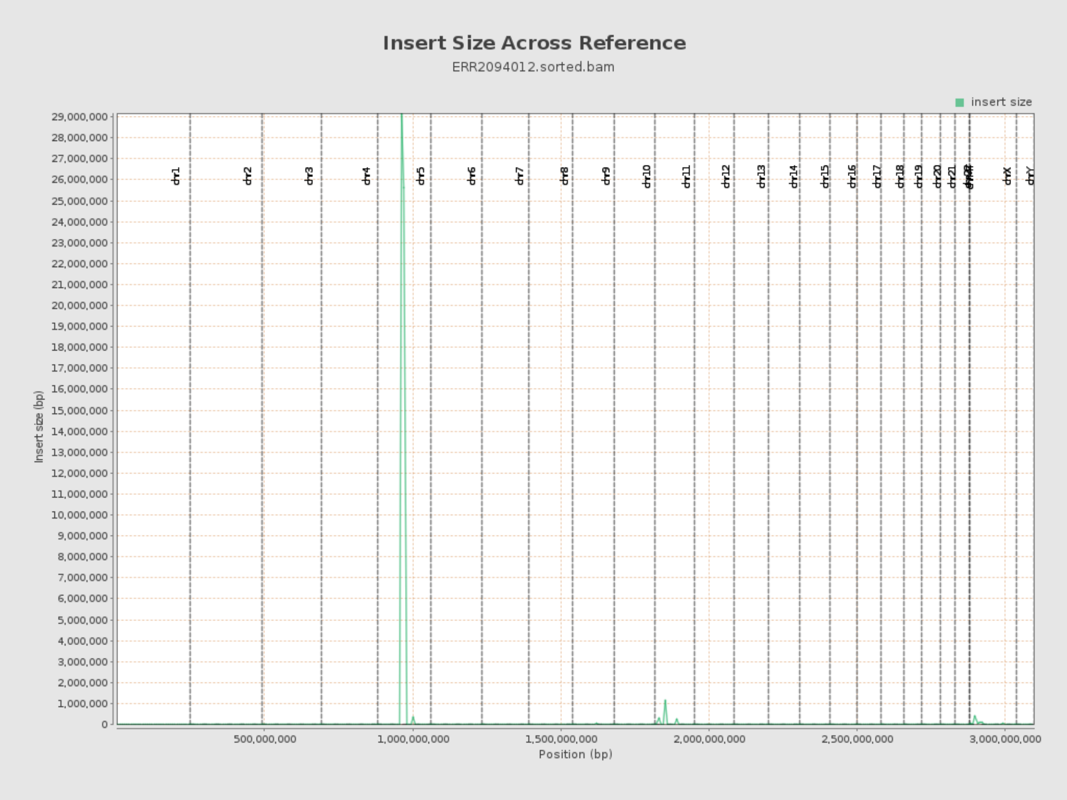
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram