Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:27:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094063.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_ERR2094063 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094063_1.fastq.gz ERR2094063_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:27:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	890,272
Mapped reads	848,955 / 95.36%
Unmapped reads	41,317 / 4.64%
Mapped paired reads	848,955 / 95.36%
Mapped reads, first in pair	426,333 / 47.89%
Mapped reads, second in pair	422,622 / 47.47%
Mapped reads, both in pair	843,152 / 94.71%
Mapped reads, singletons	5,803 / 0.65%
Secondary alignments	0
Supplementary alignments	26,903 / 3.02%
Read min/max/mean length	30 / 151 / 140.28
Duplicated reads (estimated)	828,903 / 93.11%
Duplication rate	50.37%
Clipped reads	321,924 / 36.16%

2.2. ACGT Content

Number/percentage of A's	29,019,034 / 26.4%
Number/percentage of C's	25,990,134 / 23.64%
Number/percentage of T's	27,594,454 / 25.1%
Number/percentage of G's	27,336,435 / 24.86%
Number/percentage of N's	1,269 / 0%

GC Percentage	48.5%

2.3. Coverage

Mean	0.0363
Standard Deviation	10.3541

2.4. Mapping Quality

Mean Mapping Quality	38.33

2.5. Insert size

Mean	330,098.38
Standard Deviation	5,217,357.44
P25/Median/P75	136 / 168 / 198

2.6. Mismatches and indels

General error rate	4.1%
Mismatches	4,378,320
Insertions	66,049
Mapped reads with at least one insertion	7.68%
Deletions	351,952
Mapped reads with at least one deletion	39.58%
Homopolymer indels	27.58%

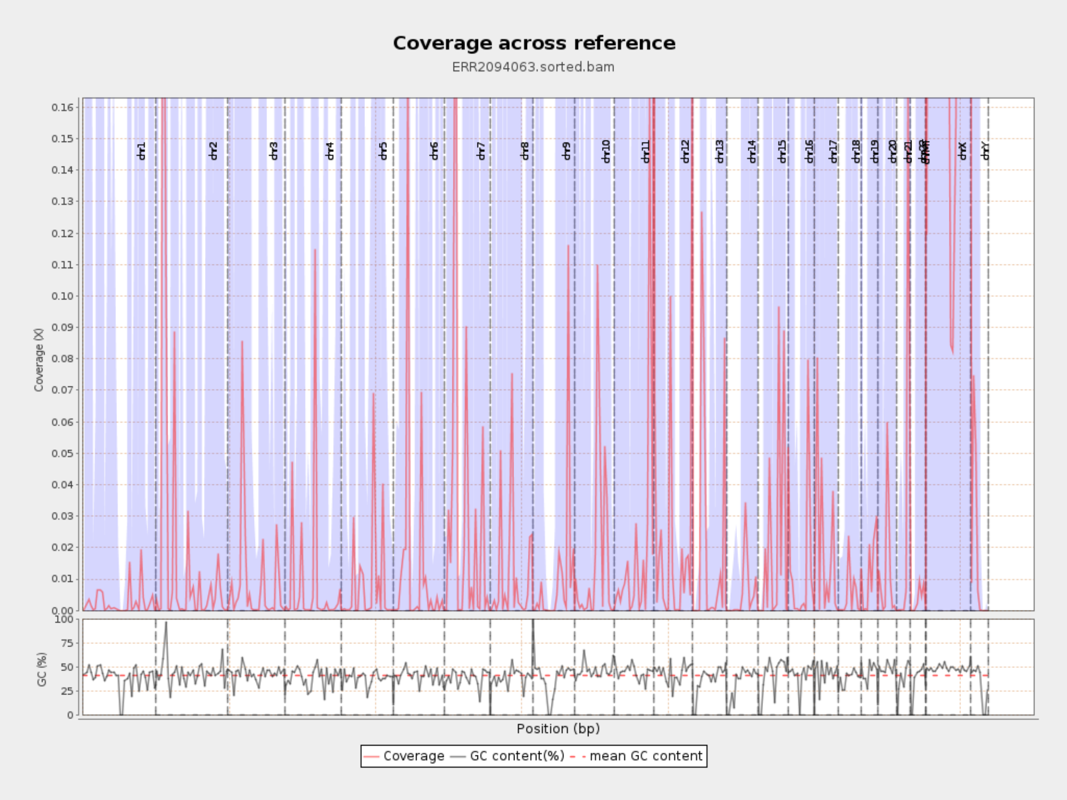
2.7. Chromosome stats

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

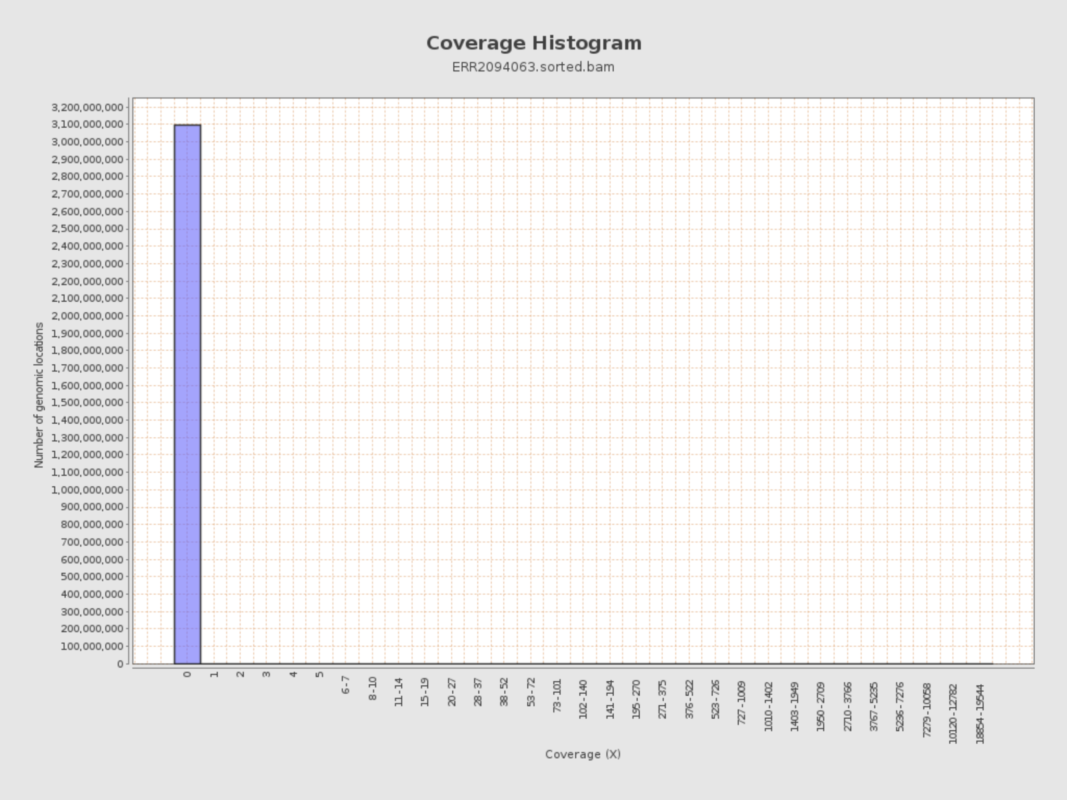
		bases	**coverage**	**deviation**
chr1	249250621	646327	0.0026	1.0604
chr2	243199373	4441514	0.0183	6.6972
chr3	198022430	1699512	0.0086	2.9724
chr4	191154276	1676818	0.0088	3.7163
chr5	180915260	1434806	0.0079	4.1577
chr6	171115067	2532152	0.0148	8.381
chr7	159138663	4369596	0.0275	10.749
chr8	146364022	1818646	0.0124	4.4582
chr9	141213431	1512194	0.0107	5.4989
chr10	135534747	2227037	0.0164	6.6954
chr11	135006516	2614747	0.0194	6.1404
chr12	133851895	2794626	0.0209	6.2061
chr13	115169878	2492850	0.0216	6.6489
chr14	107349540	585296	0.0055	2.2191
chr15	102531392	2090201	0.0204	7.1215
chr16	90354753	1186308	0.0131	4.7904
chr17	81195210	1690686	0.0208	5.5779
chr18	78077248	346678	0.0044	1.8629
chr19	59128983	665458	0.0113	2.6461
chr20	63025520	688390	0.0109	3.6601
chr21	48129895	1522717	0.0316	11.9823
chr22	51304566	192995	0.0038	1.0161
chrMT	16571	2181618	131.6528	615.4426
chrX	155270560	69994232	0.4508	38.2637

chrY	59373566	1085542	0.0183	4.9112

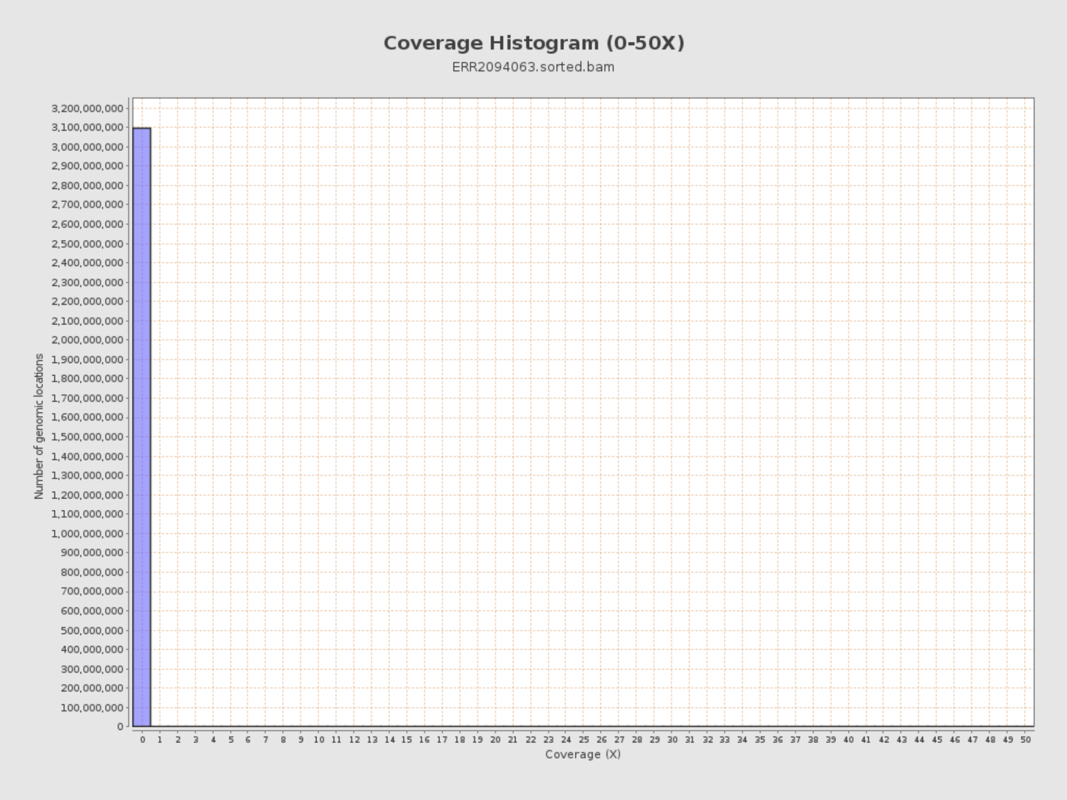
3. Results : Coverage across reference



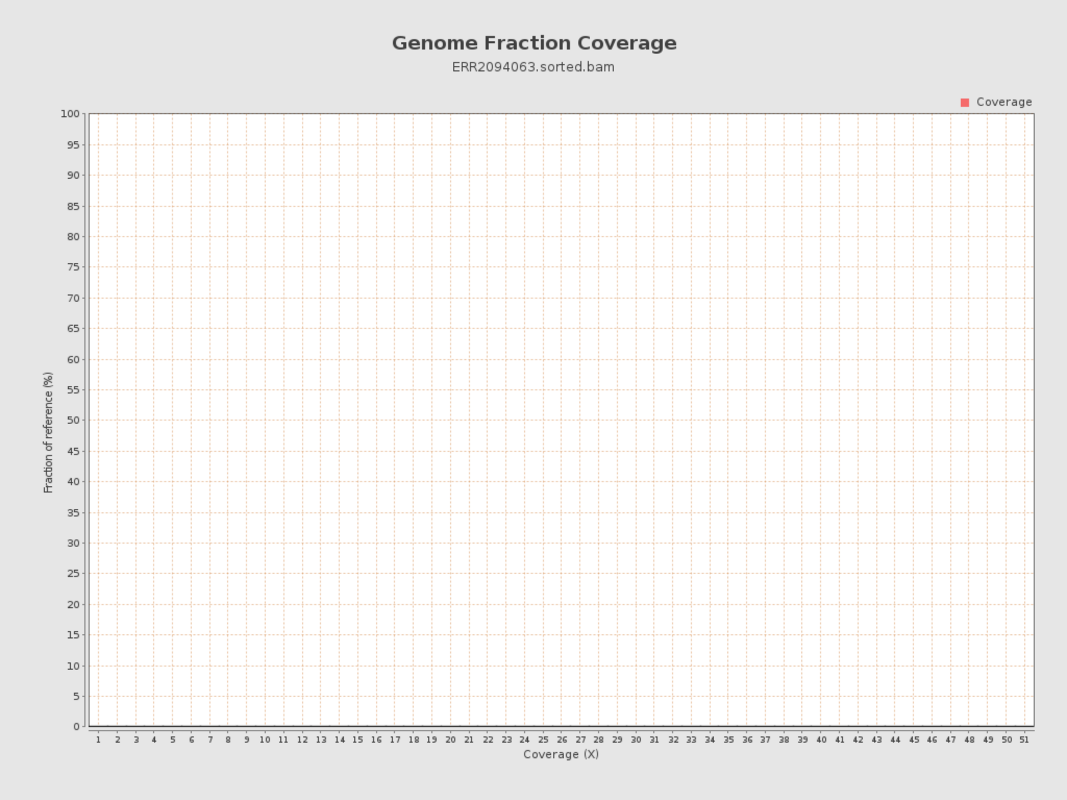
4. Results : Coverage Histogram



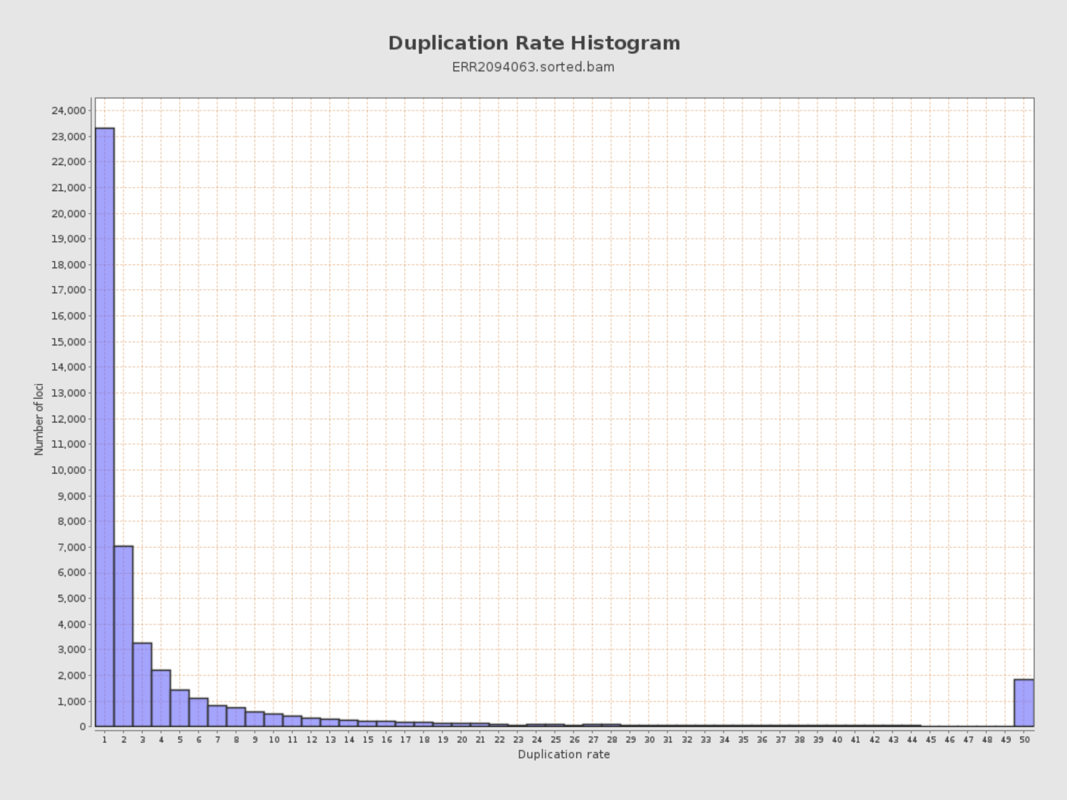
5. Results : Coverage Histogram (0-50X)



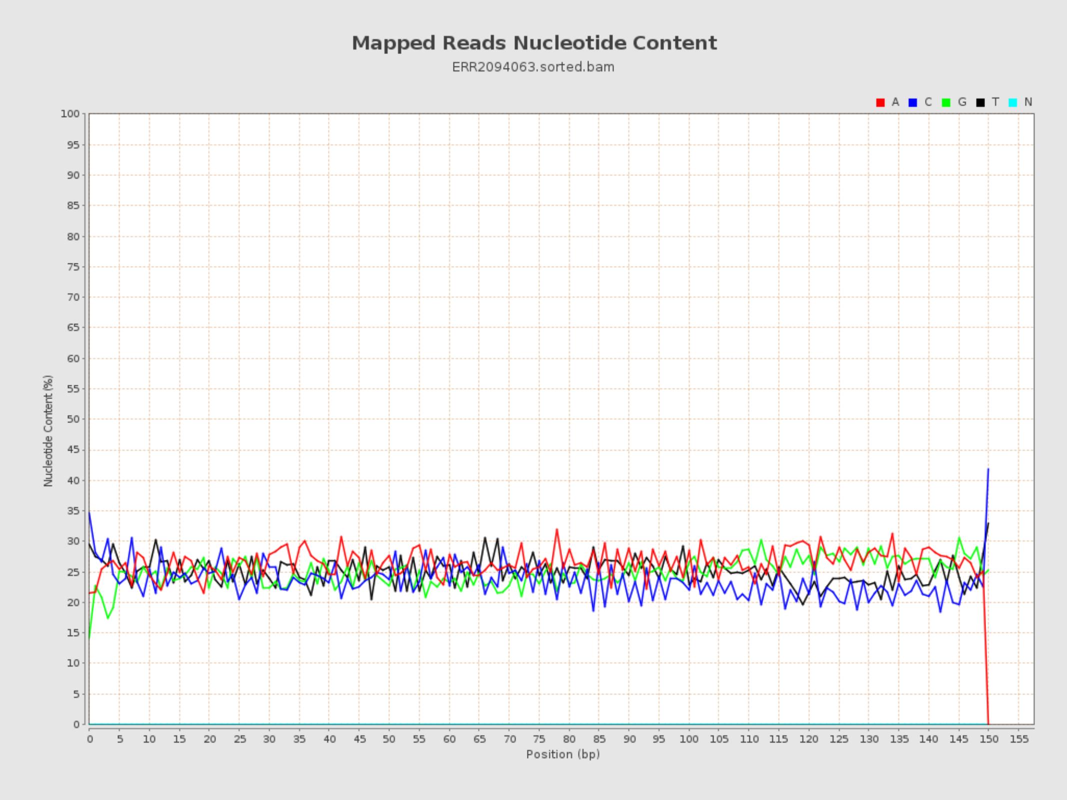
6. Results : Genome Fraction Coverage



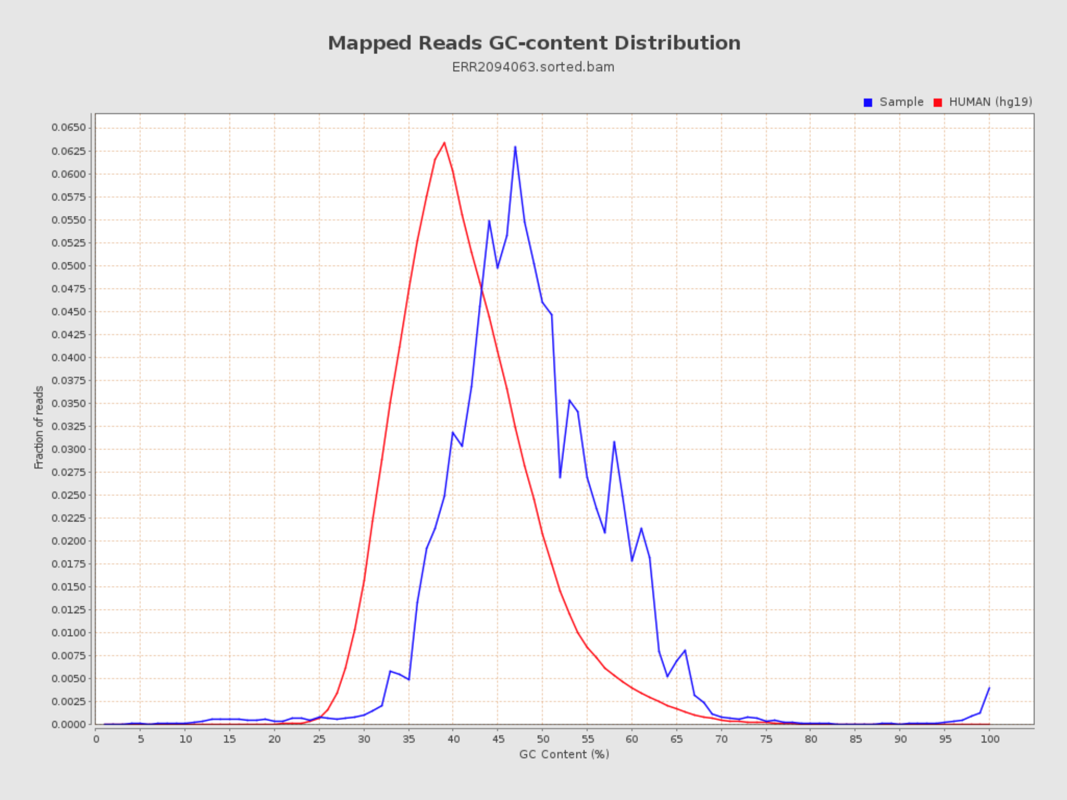
7. Results : Duplication Rate Histogram



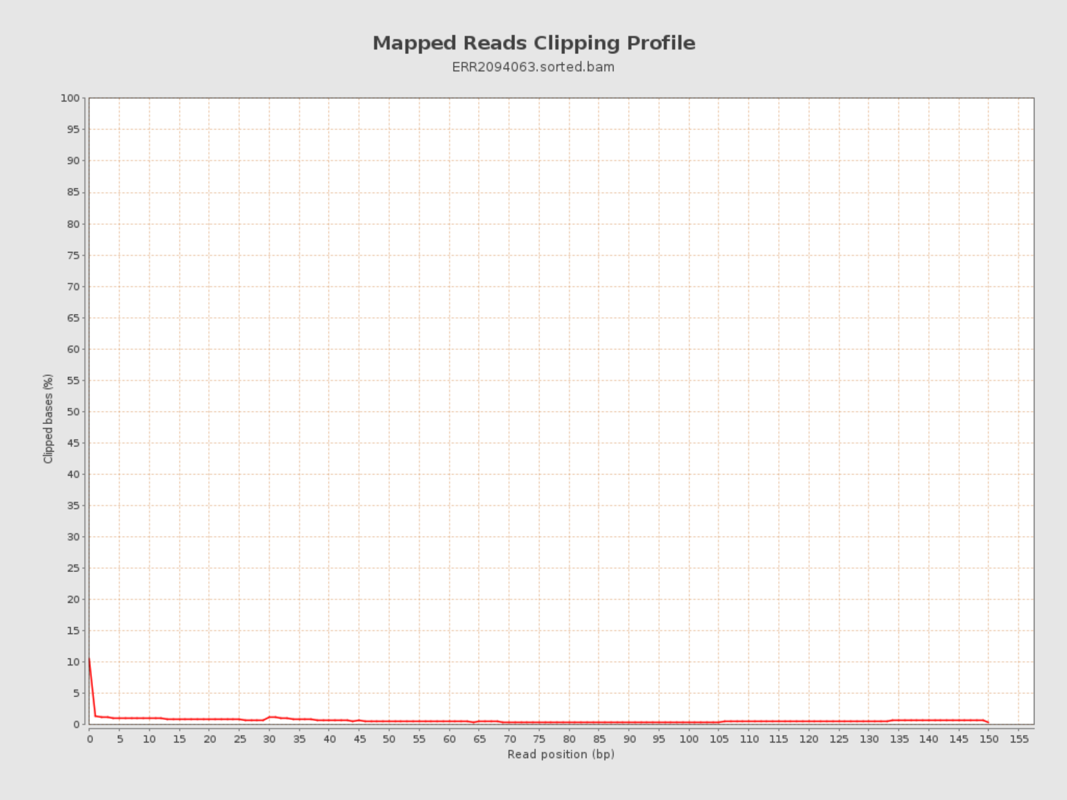
8. Results : Mapped Reads Nucleotide Content



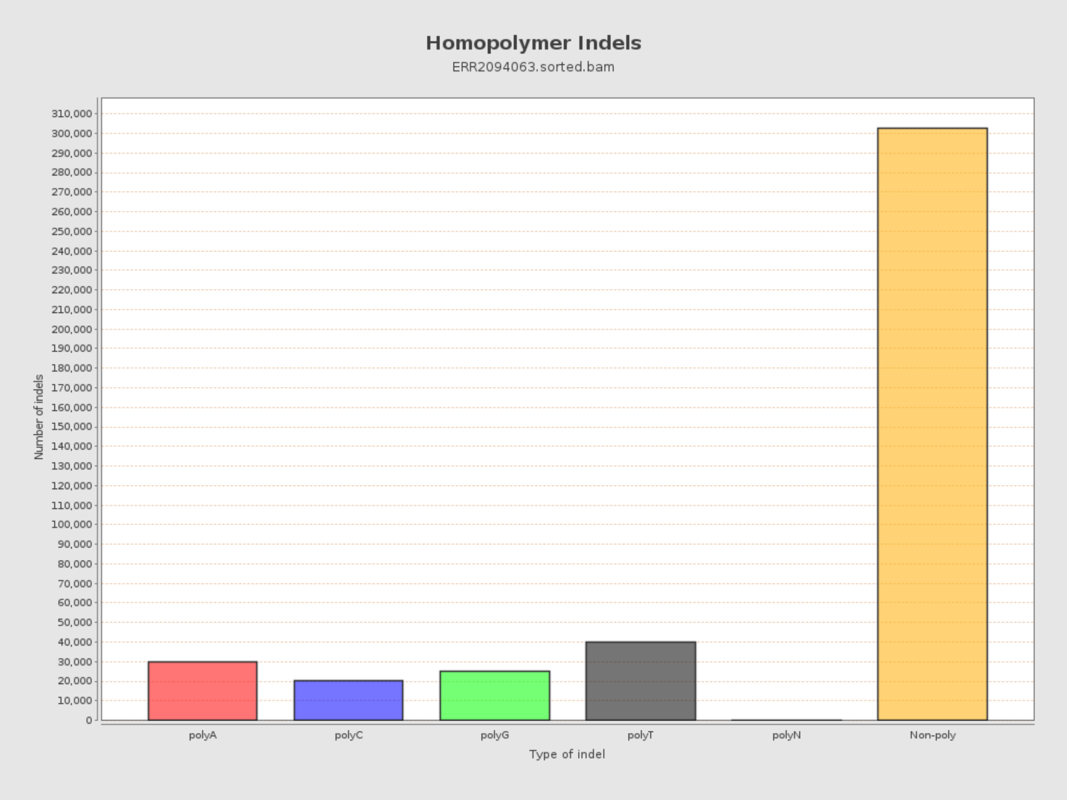
9. Results : Mapped Reads GC-content Distribution



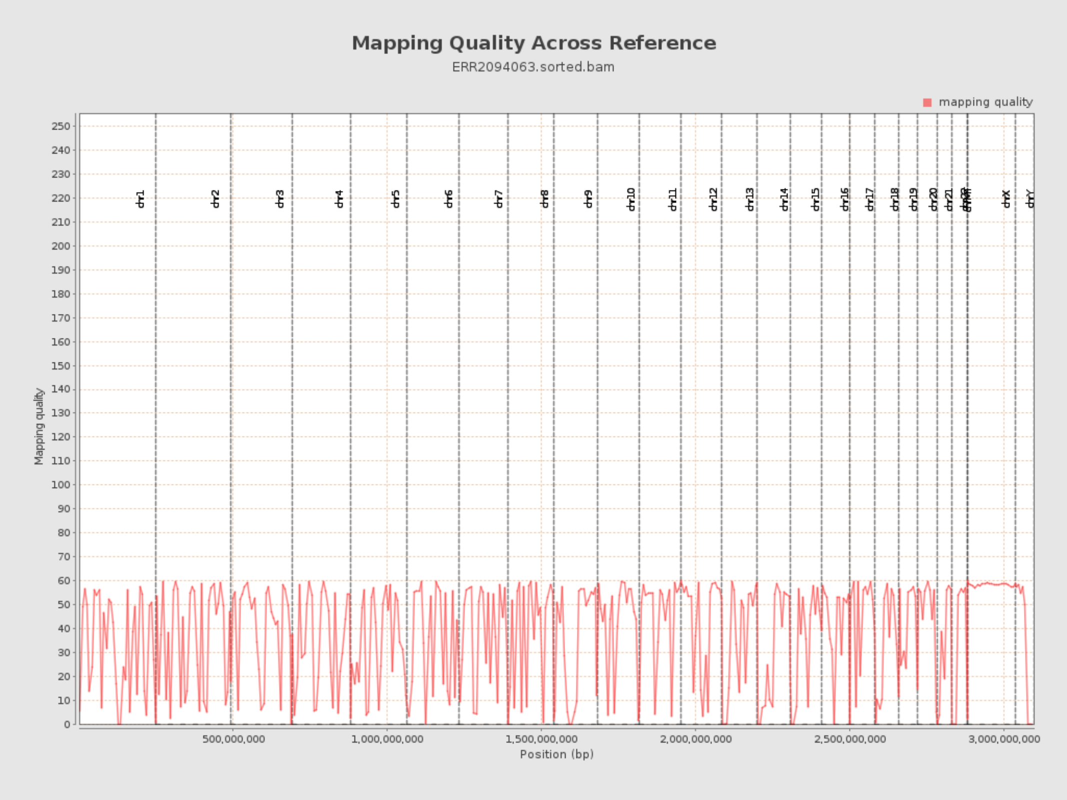
10. Results : Mapped Reads Clipping Profile



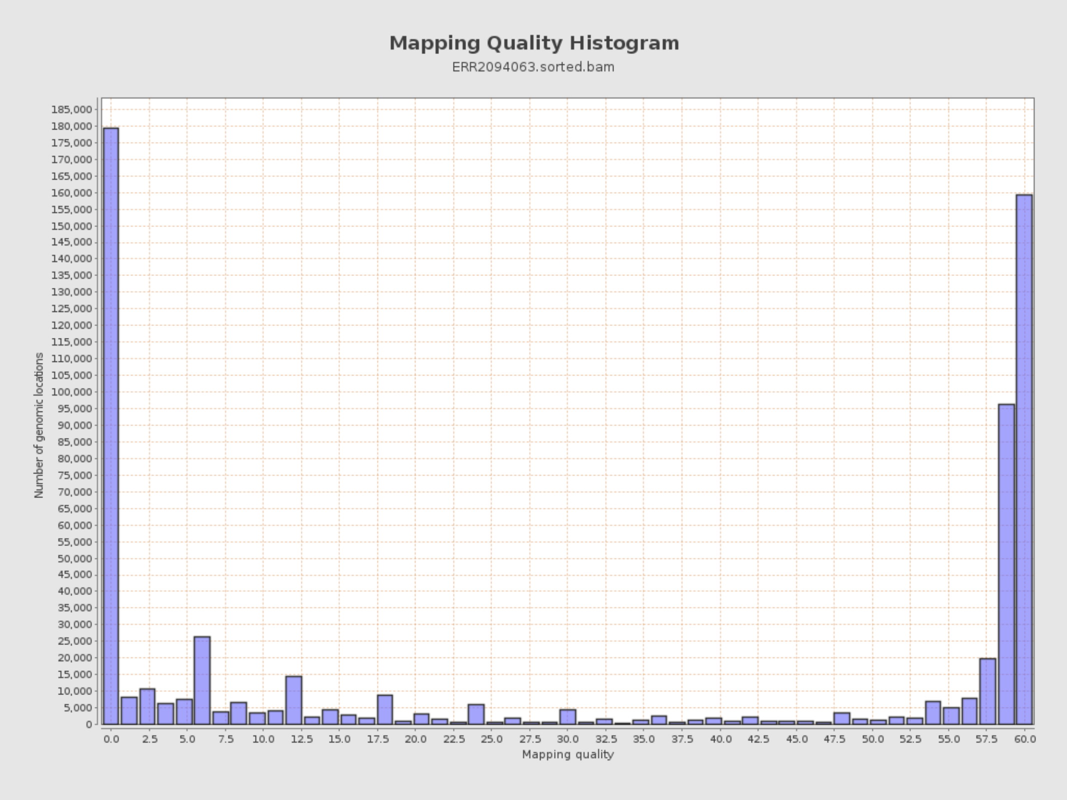
11. Results : Homopolymer Indels



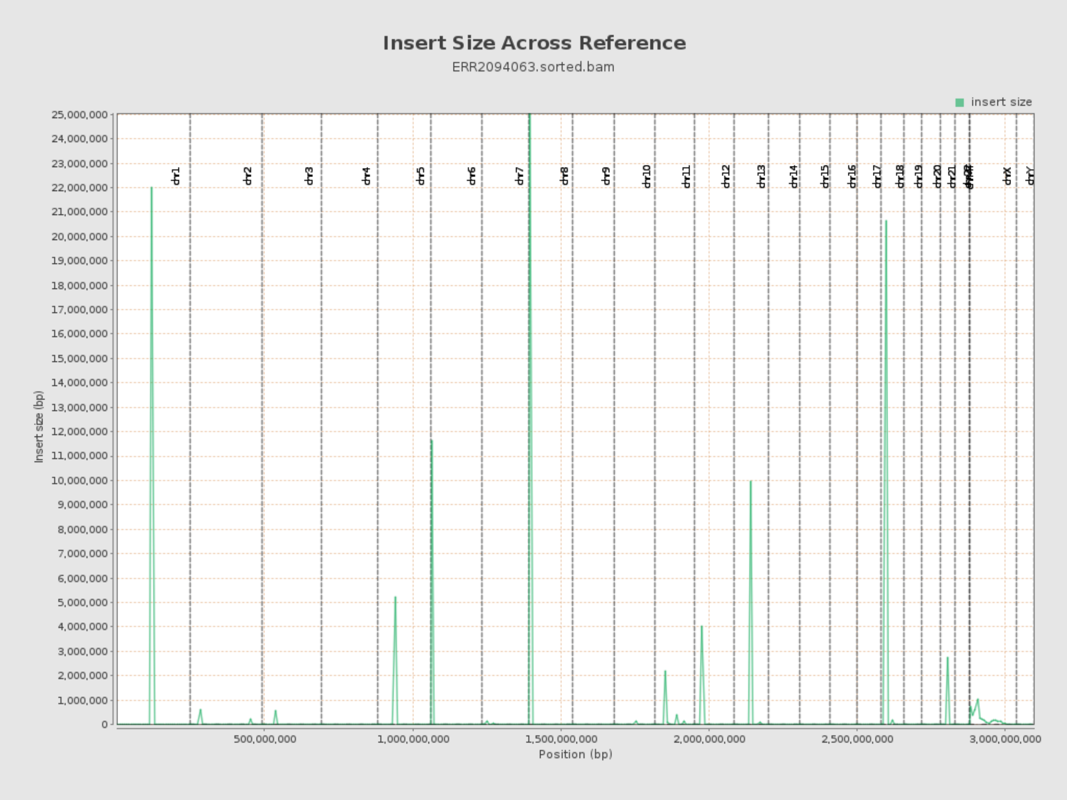
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram