Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:42:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094069.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_ERR2094069 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094069_1.fastq.gz ERR2094069_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:42:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	361,632
Mapped reads	341,950 / 94.56%
Unmapped reads	19,682 / 5.44%
Mapped paired reads	341,950 / 94.56%
Mapped reads, first in pair	171,717 / 47.48%
Mapped reads, second in pair	170,233 / 47.07%
Mapped reads, both in pair	339,590 / 93.9%
Mapped reads, singletons	2,360 / 0.65%
Secondary alignments	0
Supplementary alignments	12,441 / 3.44%
Read min/max/mean length	30 / 151 / 139.06
Duplicated reads (estimated)	323,929 / 89.57%
Duplication rate	49.36%
Clipped reads	140,610 / 38.88%

2.2. ACGT Content

Number/percentage of A's	11,685,558 / 26.71%
Number/percentage of C's	10,151,005 / 23.2%
Number/percentage of T's	11,172,839 / 25.53%
Number/percentage of G's	10,747,899 / 24.56%
Number/percentage of N's	501 / 0%

GC Percentage	47.76%

2.3. Coverage

Mean	0.0145
Standard Deviation	3.7634

2.4. Mapping Quality

Mean Mapping Quality	38.17

2.5. Insert size

Mean	415,204.77
Standard Deviation	5,814,391
P25/Median/P75	131 / 166 / 193

2.6. Mismatches and indels

General error rate	4.38%
Mismatches	1,862,325
Insertions	28,897
Mapped reads with at least one insertion	8.25%
Deletions	146,802
Mapped reads with at least one deletion	40.75%
Homopolymer indels	26.49%

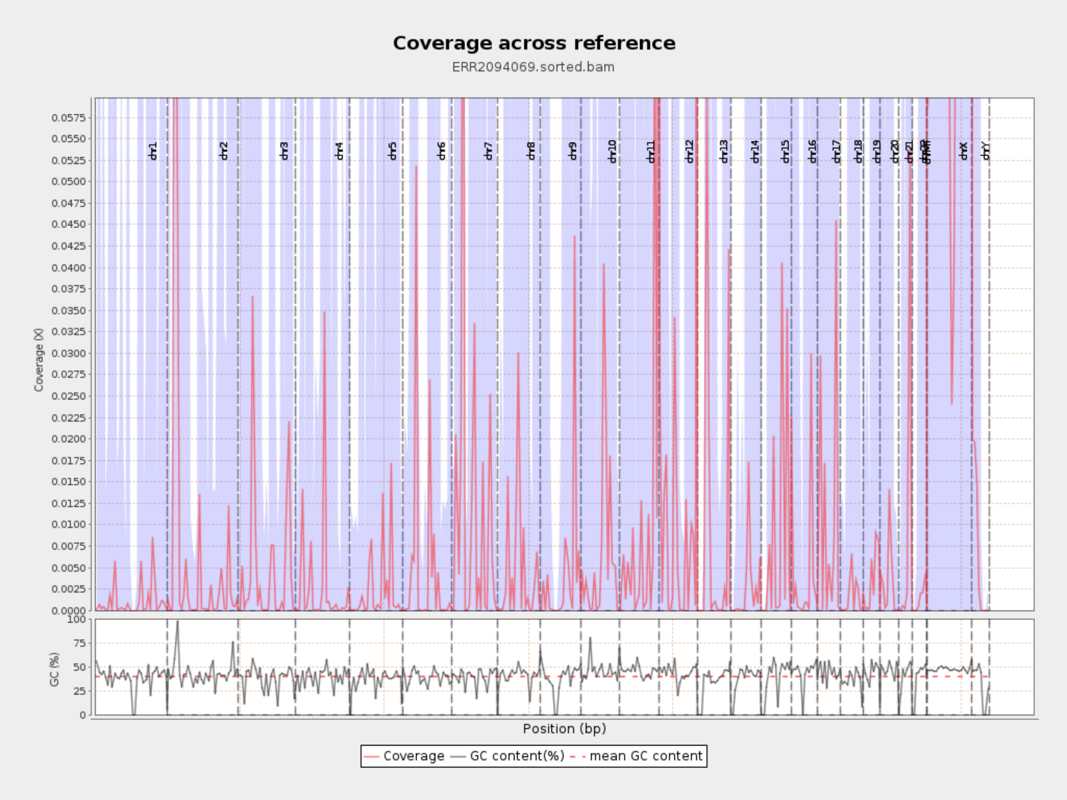
2.7. Chromosome stats

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

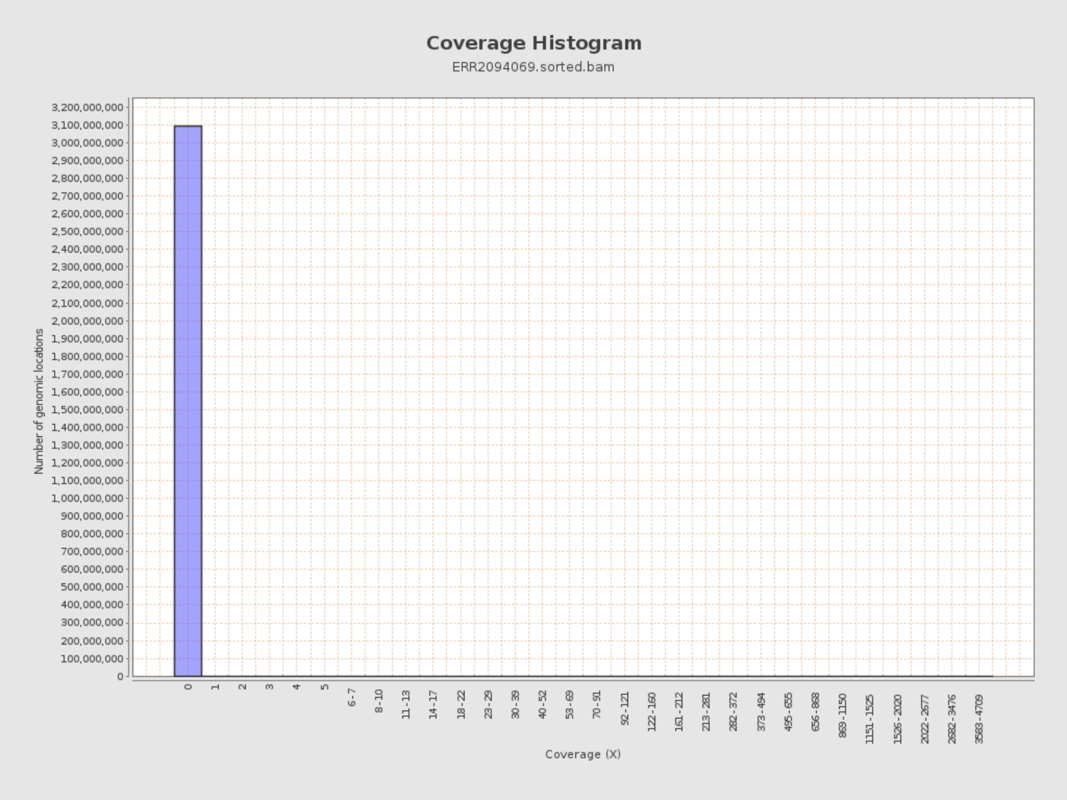
		bases	coverage	deviation
chr1	249250621	277156	0.0011	0.4659
chr2	243199373	1561825	0.0064	2.3426
chr3	198022430	904008	0.0046	1.5831
chr4	191154276	543084	0.0028	1.1073
chr5	180915260	433816	0.0024	1.179
chr6	171115067	856396	0.005	2.628
chr7	159138663	1893027	0.0119	4.2811
chr8	146364022	671540	0.0046	1.4631
chr9	141213431	610823	0.0043	1.9909
chr10	135534747	942776	0.007	2.4967
chr11	135006516	1234723	0.0091	2.7853
chr12	133851895	1338772	0.01	2.8212
chr13	115169878	999997	0.0087	2.5272
chr14	107349540	289354	0.0027	1.1112
chr15	102531392	856192	0.0084	2.8222
chr16	90354753	428970	0.0047	1.8586
chr17	81195210	890428	0.011	3.6508
chr18	78077248	133060	0.0017	0.5851
chr19	59128983	203063	0.0034	0.8225
chr20	63025520	221190	0.0035	0.9202
chr21	48129895	505721	0.0105	3.8605
chr22	51304566	70664	0.0014	0.3913
chrMT	16571	927153	55.9503	260.8232
chrX	155270560	27680155	0.1783	13.5074

chrY	59373566	392862	0.0066	1.3541

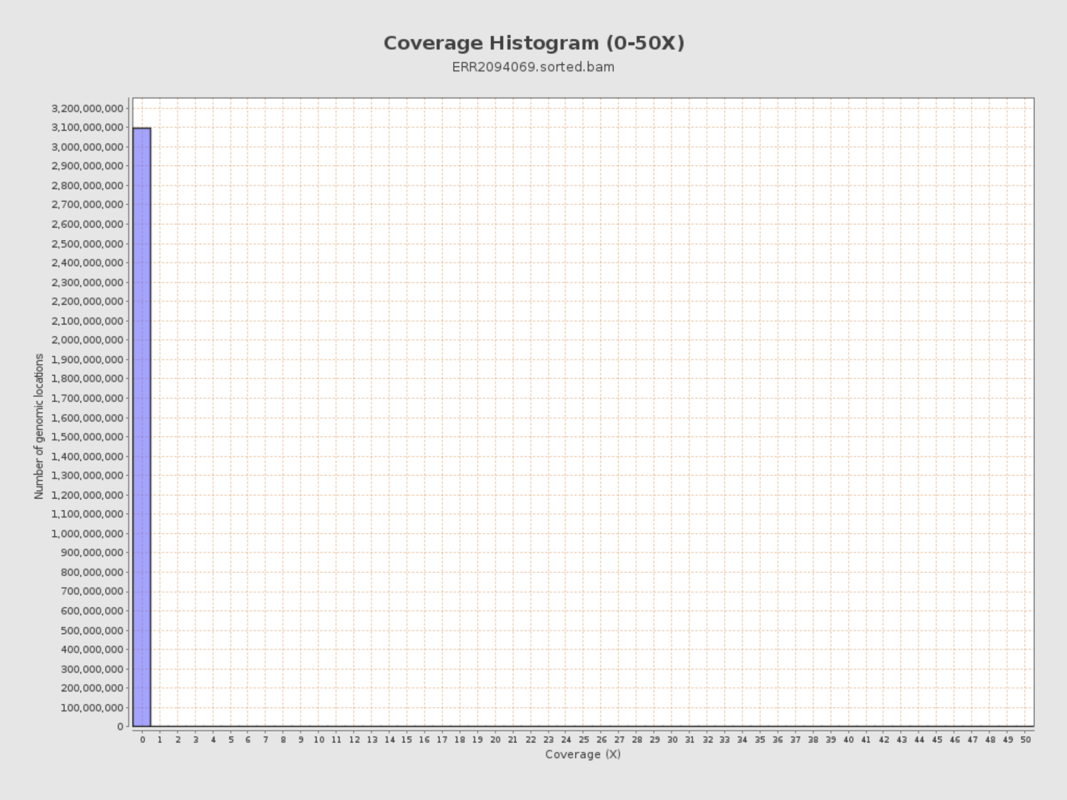
3. Results : Coverage across reference



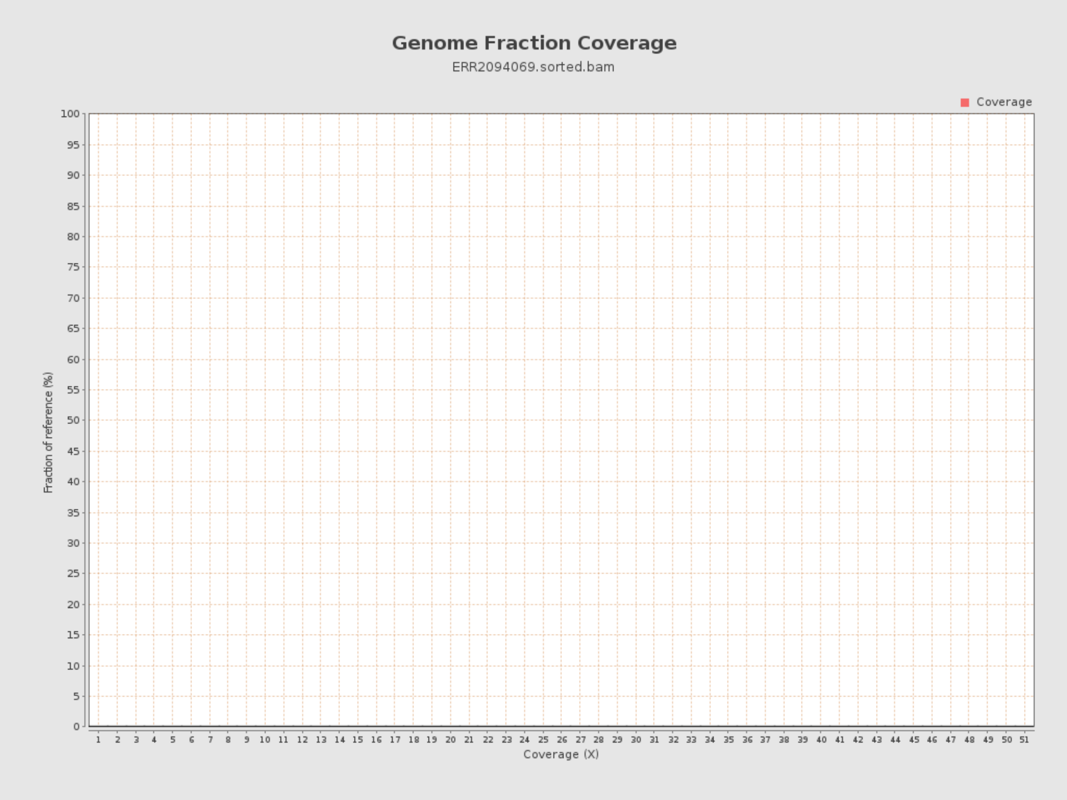
4. Results : Coverage Histogram



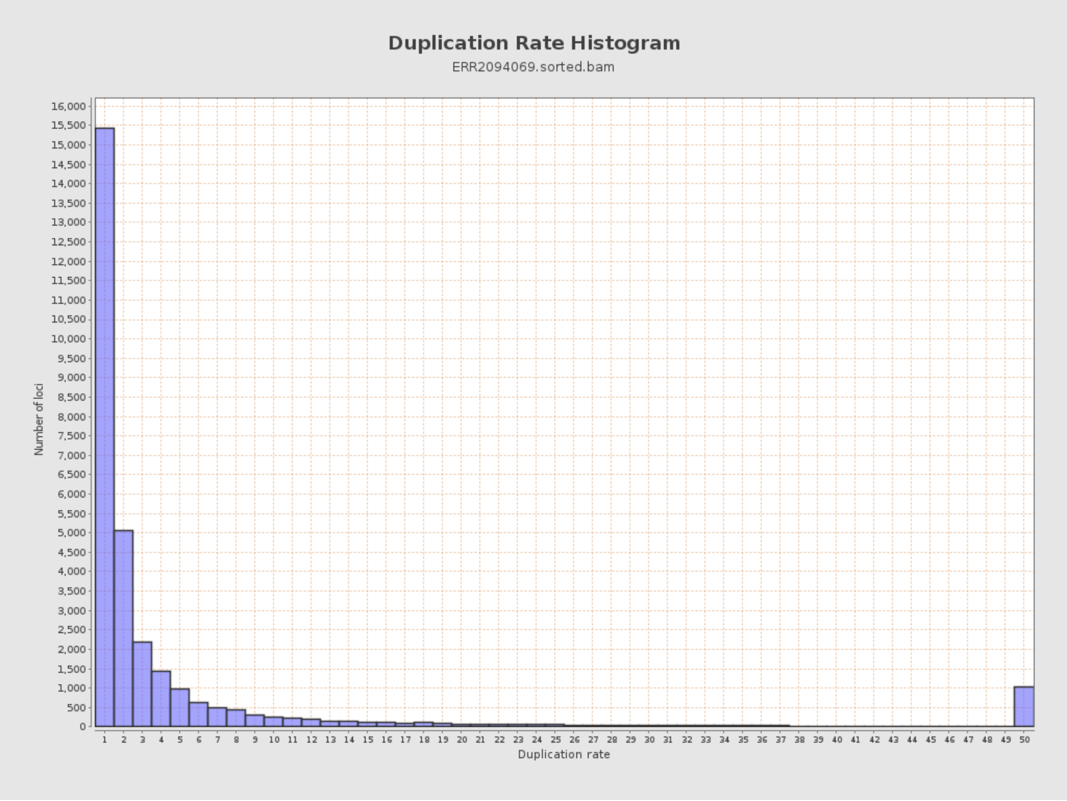
5. Results : Coverage Histogram (0-50X)



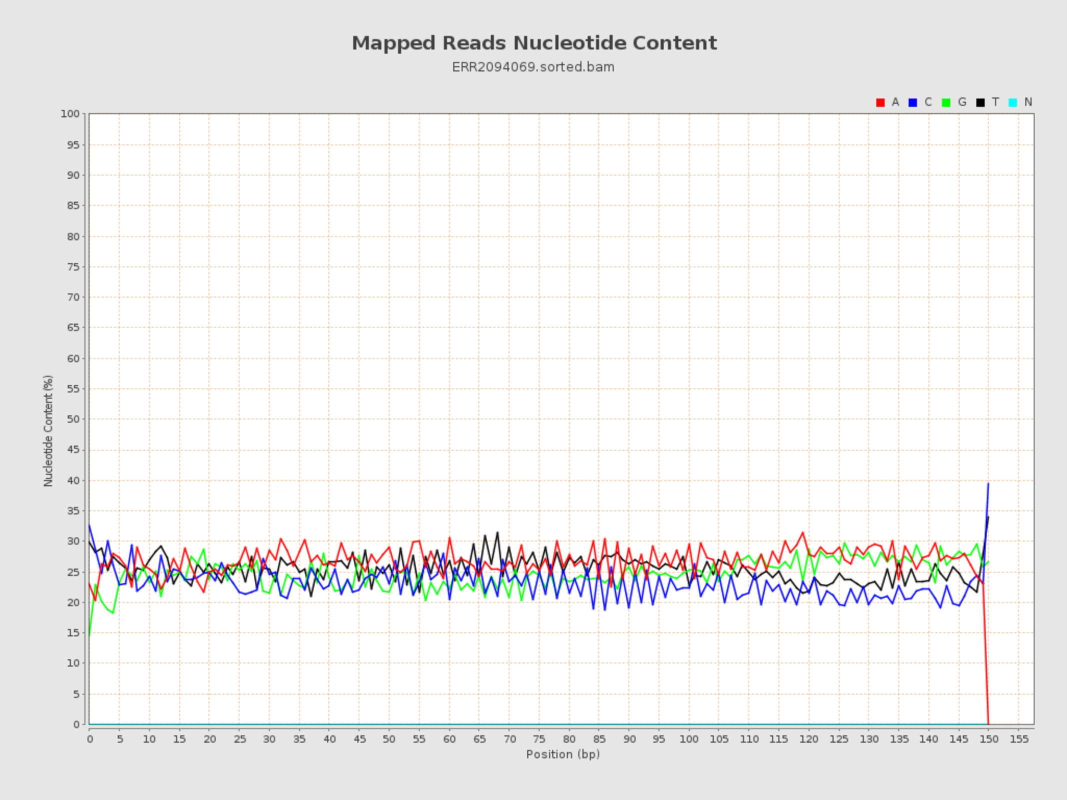
6. Results : Genome Fraction Coverage



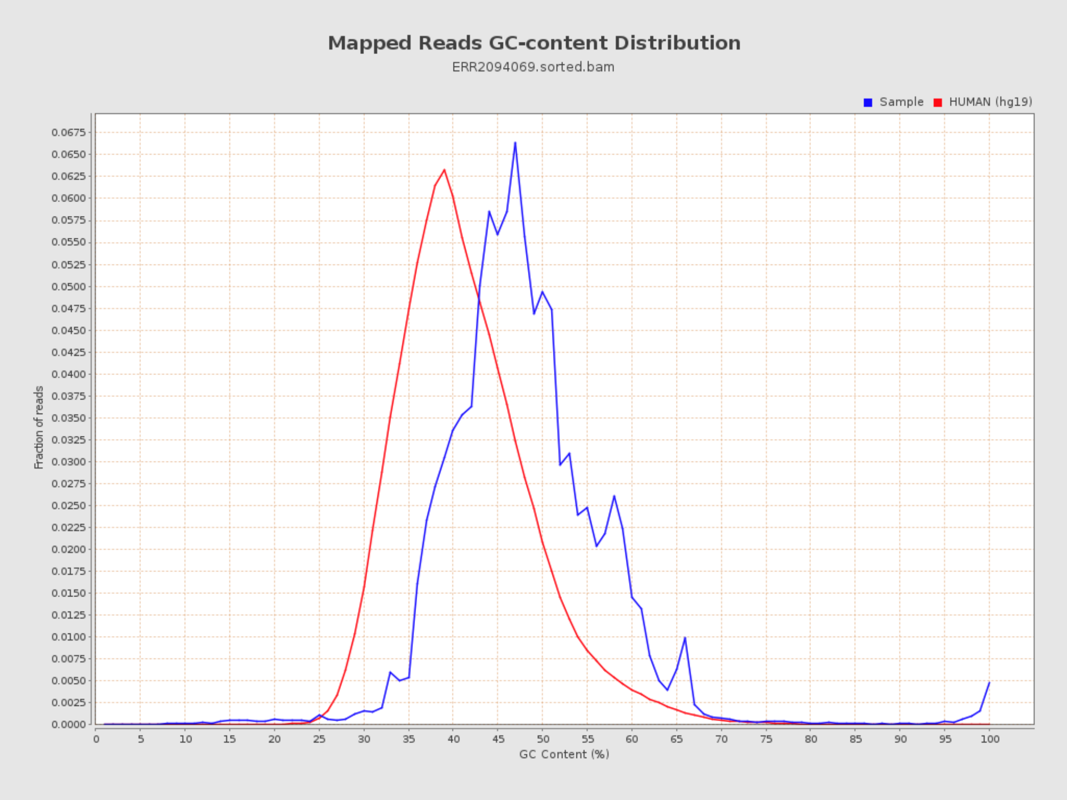
7. Results : Duplication Rate Histogram



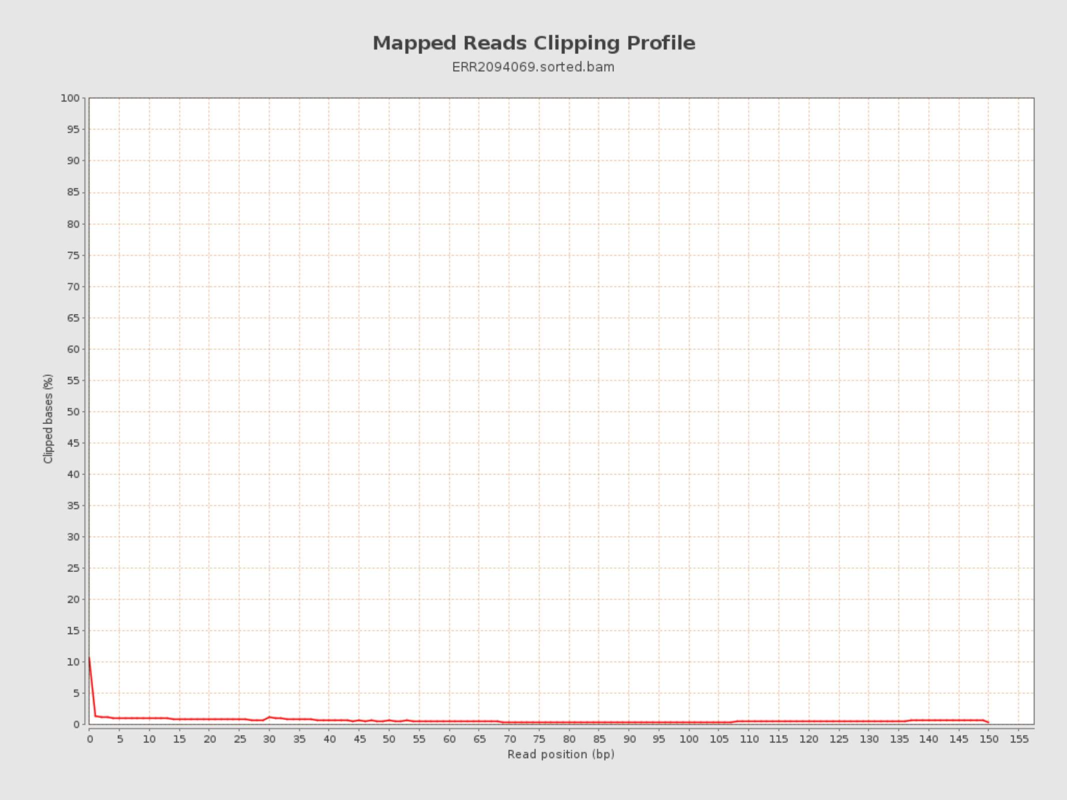
8. Results : Mapped Reads Nucleotide Content



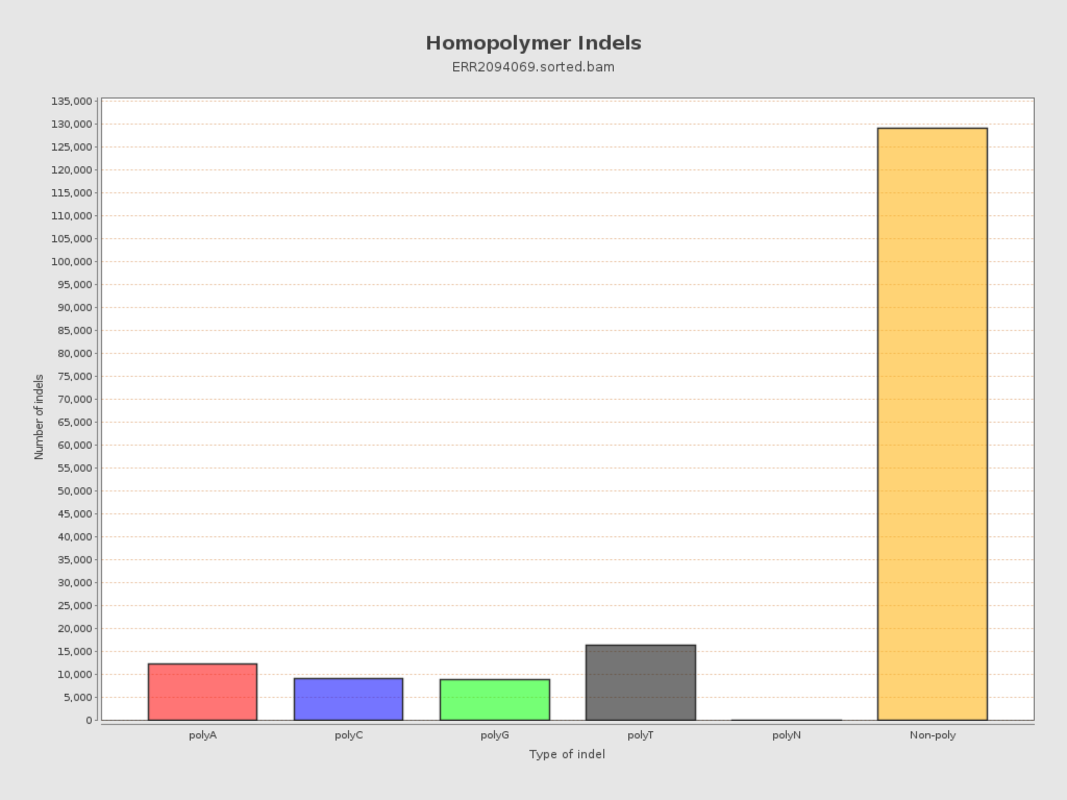
9. Results : Mapped Reads GC-content Distribution



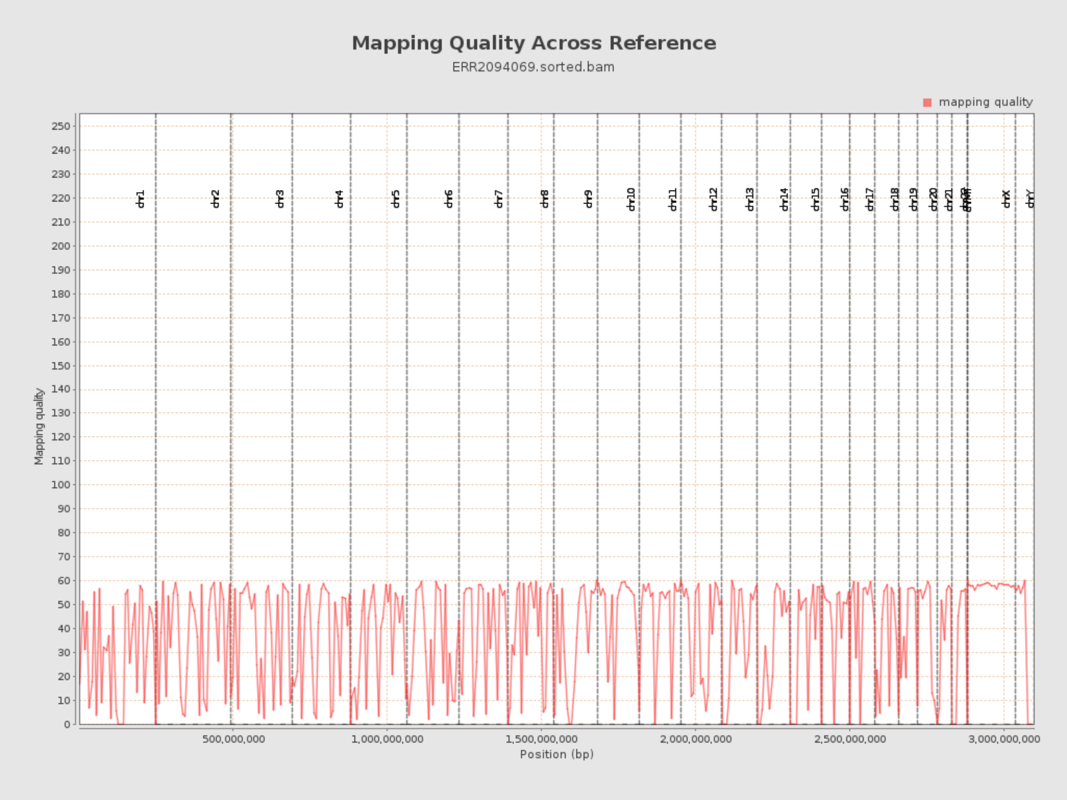
10. Results : Mapped Reads Clipping Profile



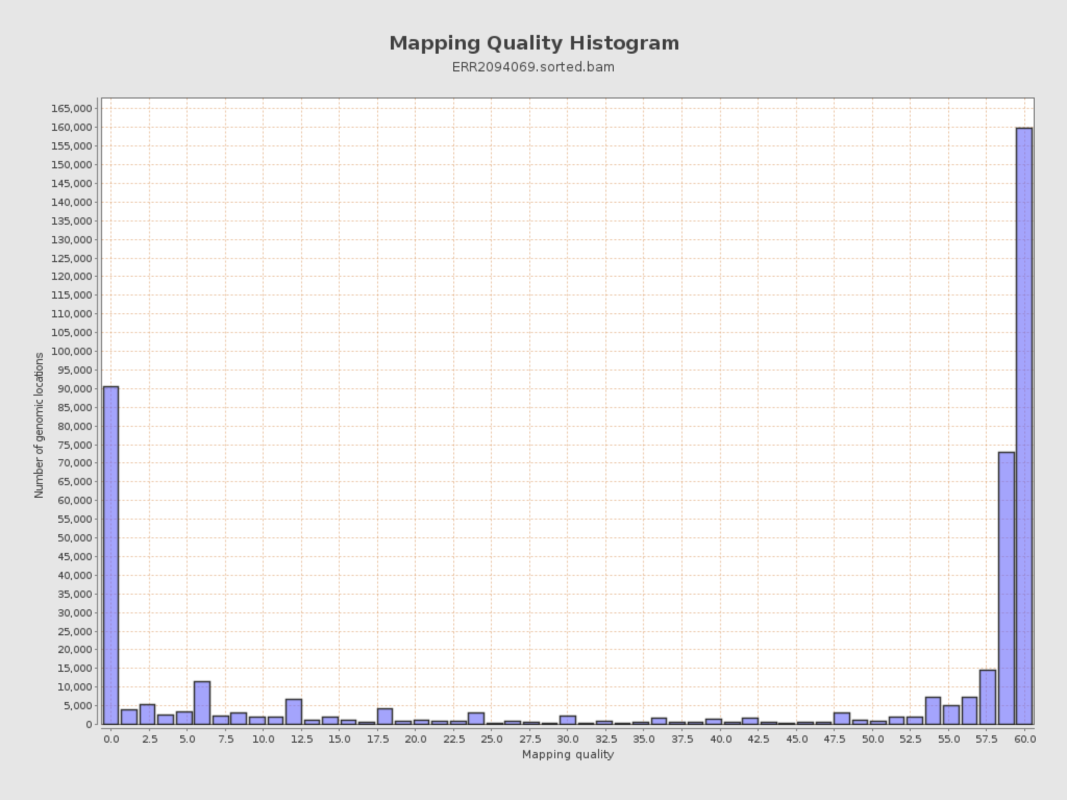
11. Results : Homopolymer Indels



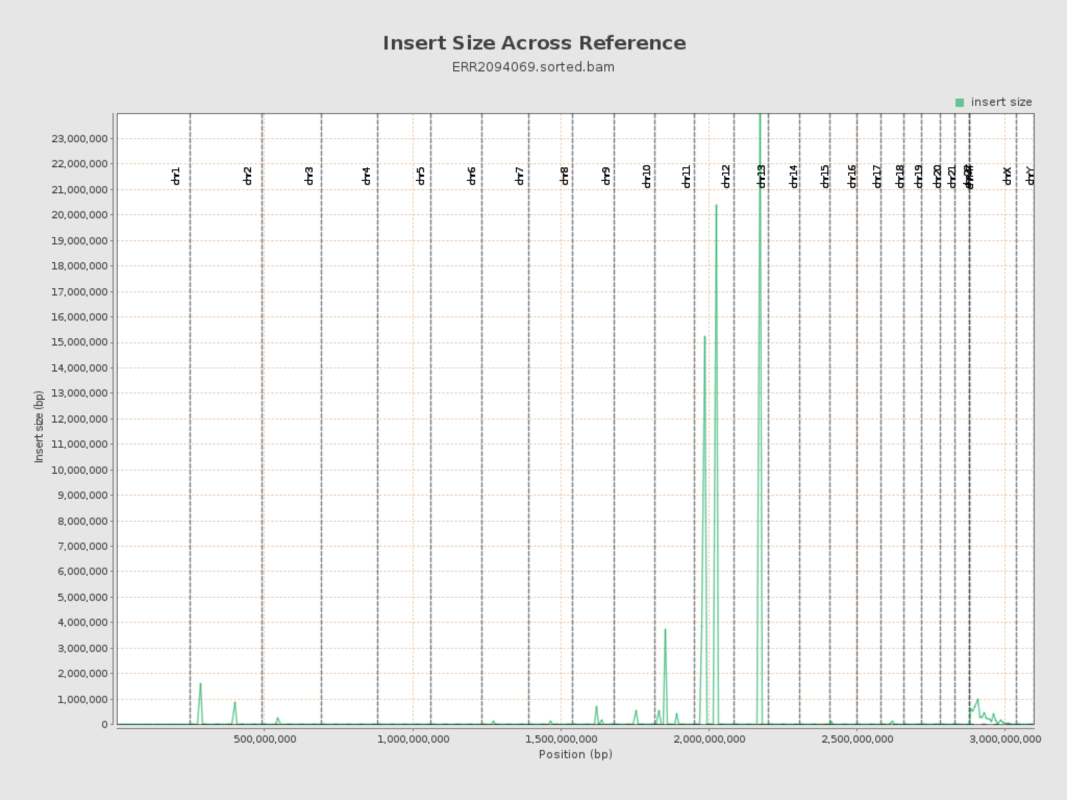
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram