Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:17:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094025.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_ERR2094025 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094025_1.fastq.gz ERR2094025_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:17:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	408,534
Mapped reads	379,102 / 92.8%
Unmapped reads	29,432 / 7.2%
Mapped paired reads	379,102 / 92.8%
Mapped reads, first in pair	190,664 / 46.67%
Mapped reads, second in pair	188,438 / 46.13%
Mapped reads, both in pair	372,786 / 91.25%
Mapped reads, singletons	6,316 / 1.55%
Secondary alignments	0
Supplementary alignments	20,050 / 4.91%
Read min/max/mean length	30 / 151 / 143.04
Duplicated reads (estimated)	350,146 / 85.71%
Duplication rate	43.17%
Clipped reads	180,815 / 44.26%

2.2. ACGT Content

Number/percentage of A's	13,423,816 / 28.04%
Number/percentage of C's	10,527,878 / 21.99%
Number/percentage of T's	12,937,408 / 27.02%
Number/percentage of G's	10,985,629 / 22.95%
Number/percentage of N's	335 / 0%

GC Percentage	44.94%

2.3. Coverage

Mean	0.0157
Standard Deviation	6.2926

2.4. Mapping Quality

Mean Mapping Quality	43.33

2.5. Insert size

Mean	515,346.67
Standard Deviation	6,652,520.62
P25/Median/P75	135 / 174 / 217

2.6. Mismatches and indels

General error rate	3.25%
Mismatches	1,496,731
Insertions	27,039
Mapped reads with at least one insertion	7%
Deletions	112,391
Mapped reads with at least one deletion	28.55%
Homopolymer indels	28.09%

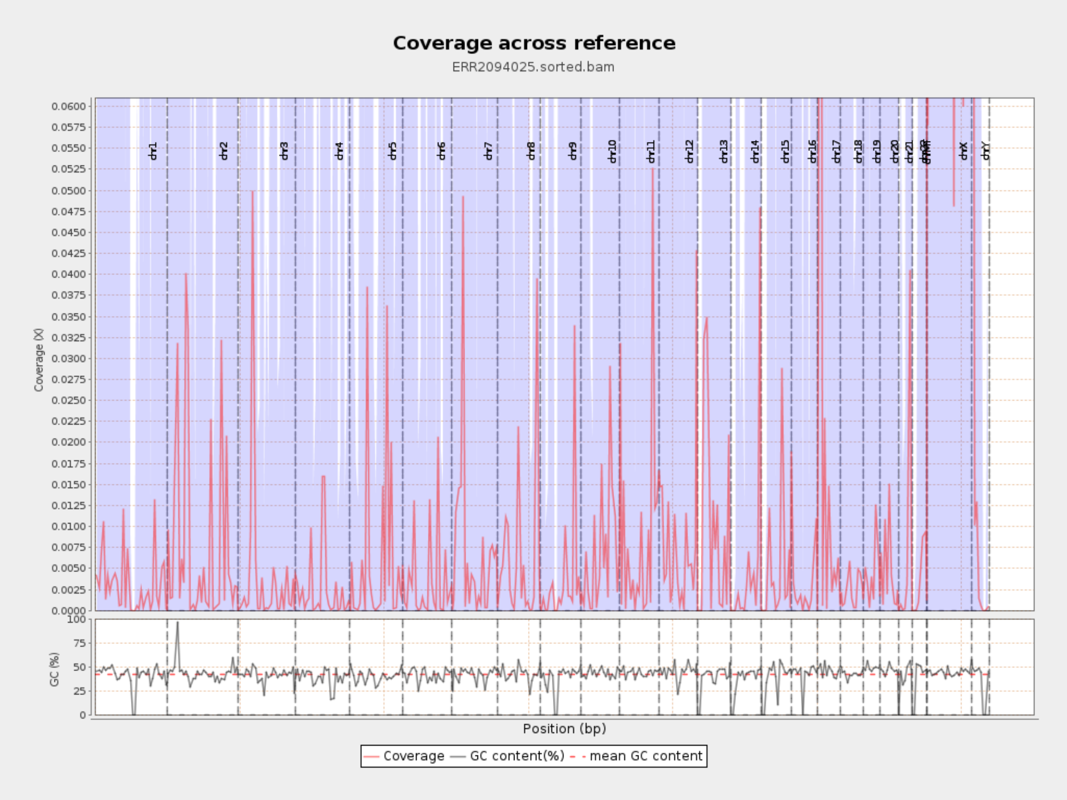
2.7. Chromosome stats

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

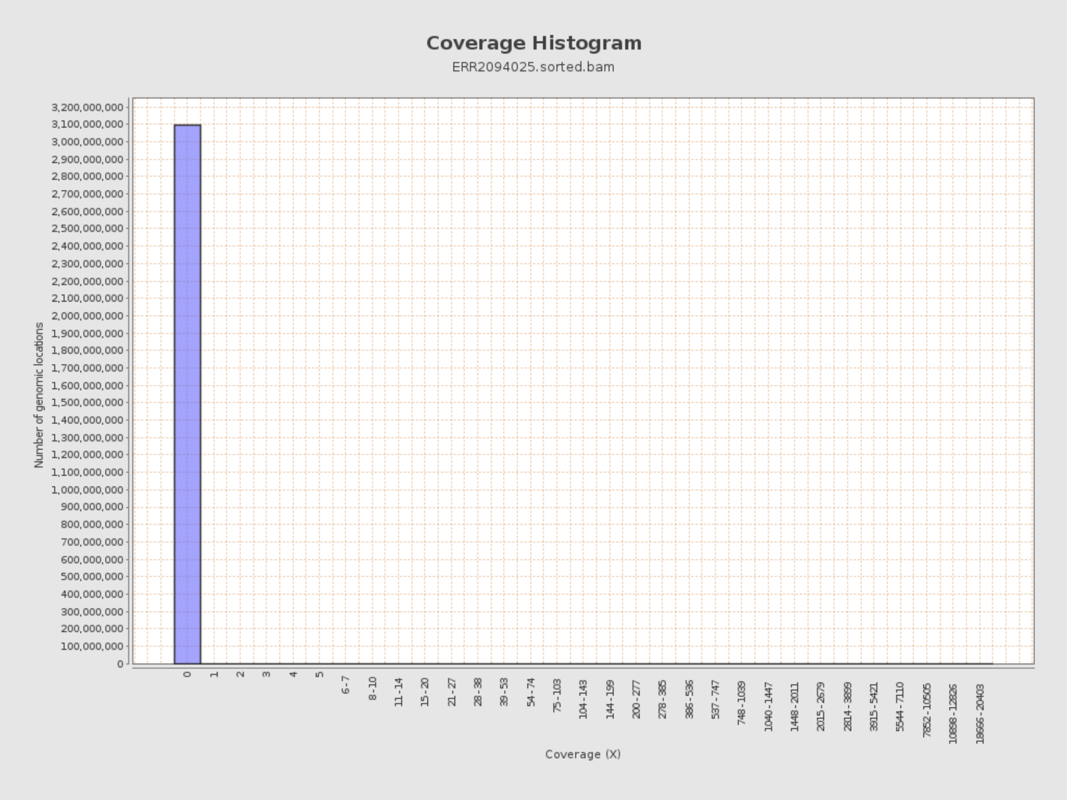
		bases	**coverage**	**deviation**
chr1	249250621	778683	0.0031	0.8151
chr2	243199373	1924180	0.0079	2.1707
chr3	198022430	752563	0.0038	1.4185
chr4	191154276	519623	0.0027	0.772
chr5	180915260	1108914	0.0061	2.726
chr6	171115067	608575	0.0036	1.2411
chr7	159138663	1138870	0.0072	2.0176
chr8	146364022	904077	0.0062	1.851
chr9	141213431	512367	0.0036	1.403
chr10	135534747	949485	0.007	1.6301
chr11	135006516	1144655	0.0085	2.3072
chr12	133851895	921508	0.0069	1.5492
chr13	115169878	1182966	0.0103	2.2875
chr14	107349540	575085	0.0054	0.8753
chr15	102531392	469185	0.0046	1.5261
chr16	90354753	305792	0.0034	0.9905
chr17	81195210	2120810	0.0261	6.3795
chr18	78077248	197782	0.0025	0.5598
chr19	59128983	260965	0.0044	0.6489
chr20	63025520	313718	0.005	1.2256
chr21	48129895	399315	0.0083	3.0952
chr22	51304566	185876	0.0036	0.356
chrMT	16571	8770310	529.2565	2,256.5318
chrX	155270560	21581003	0.139	11.065

chrY	59373566	993420	0.0167	7.5272

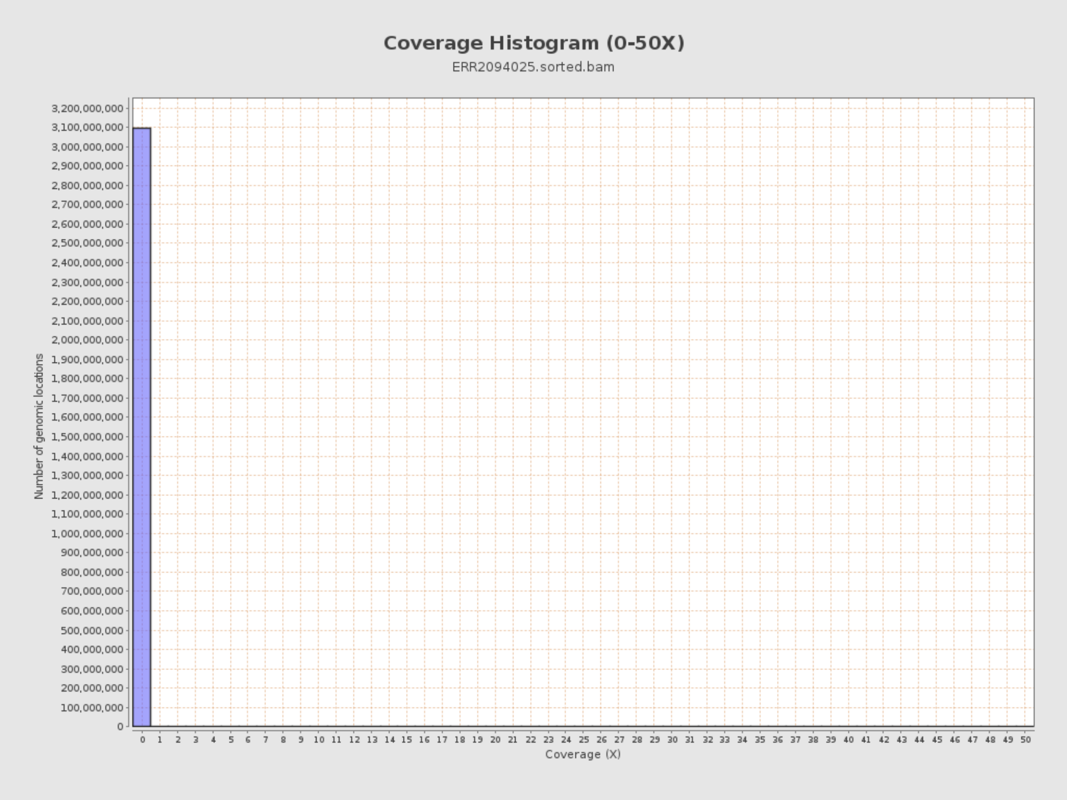
3. Results : Coverage across reference



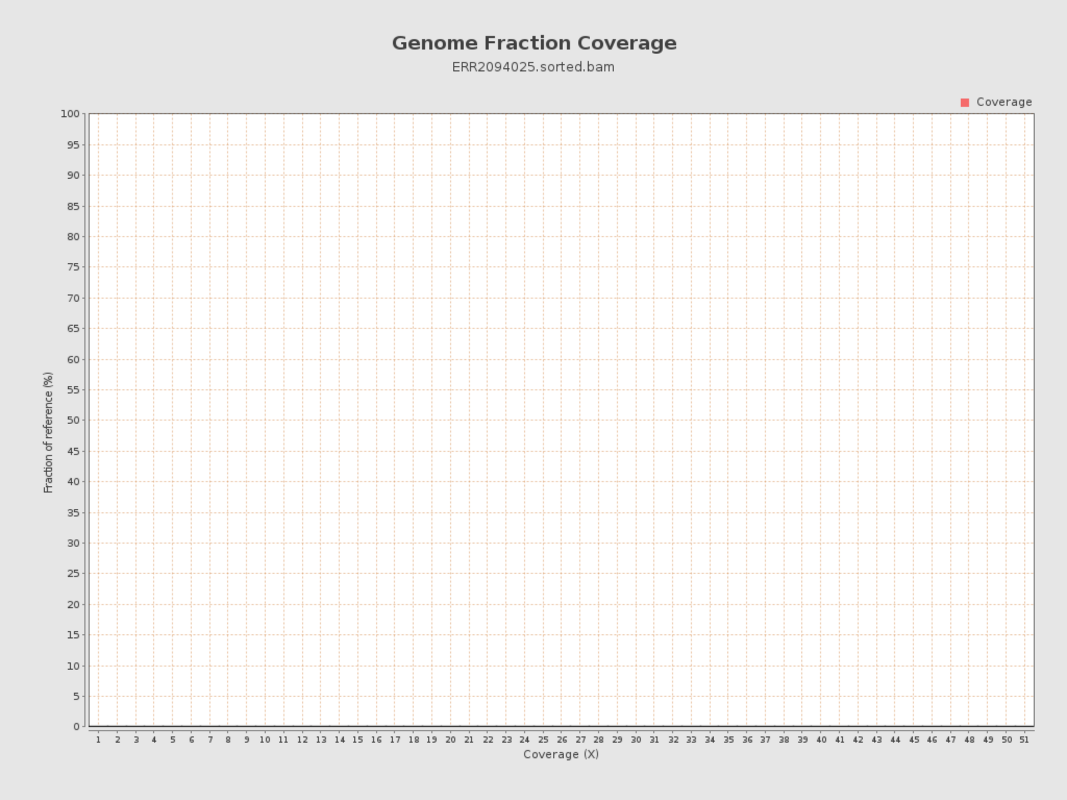
4. Results : Coverage Histogram



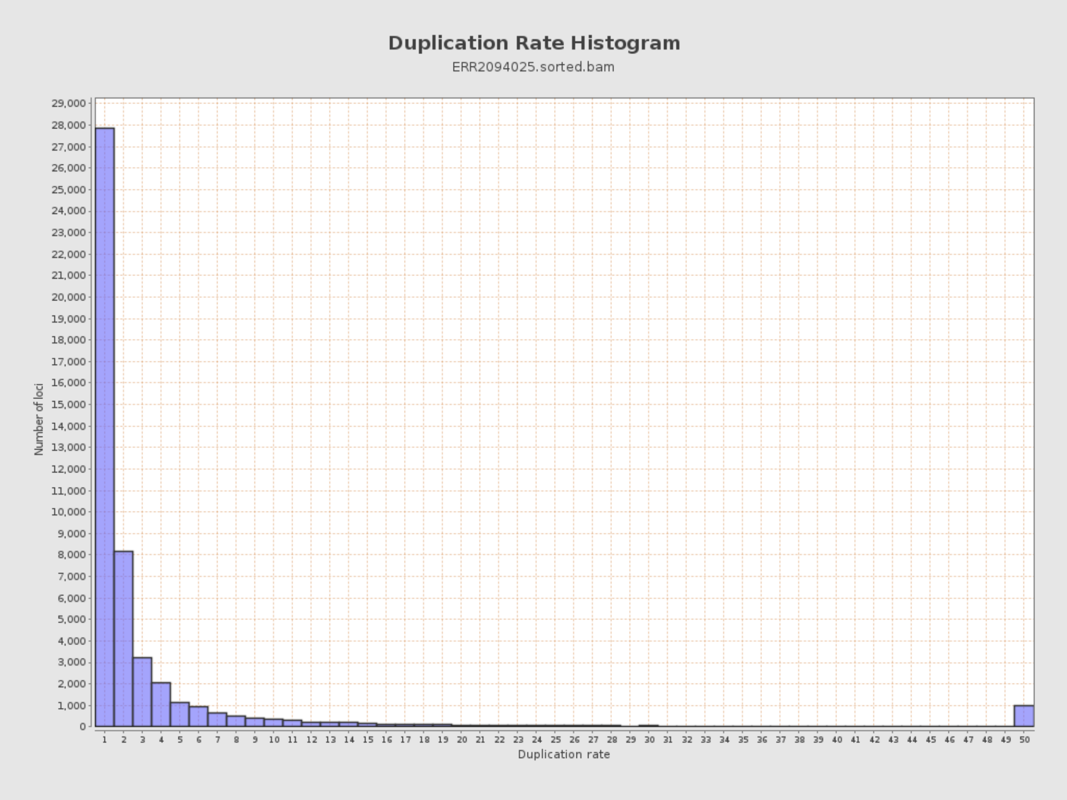
5. Results : Coverage Histogram (0-50X)



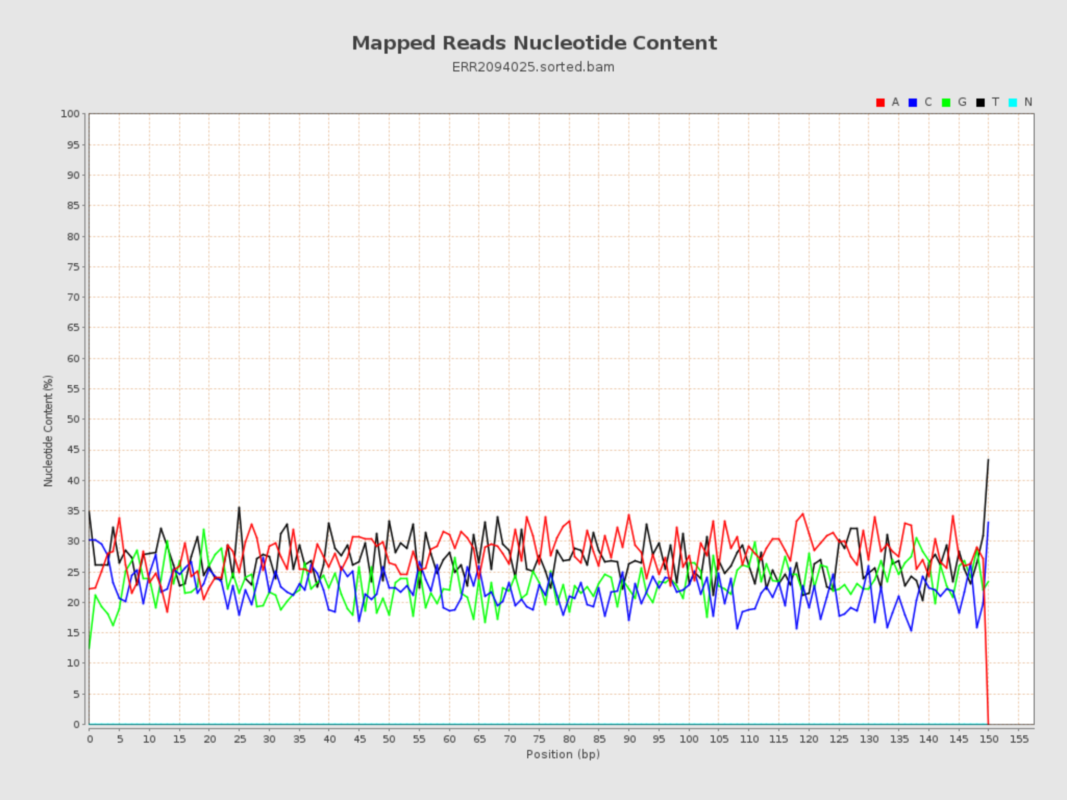
6. Results : Genome Fraction Coverage



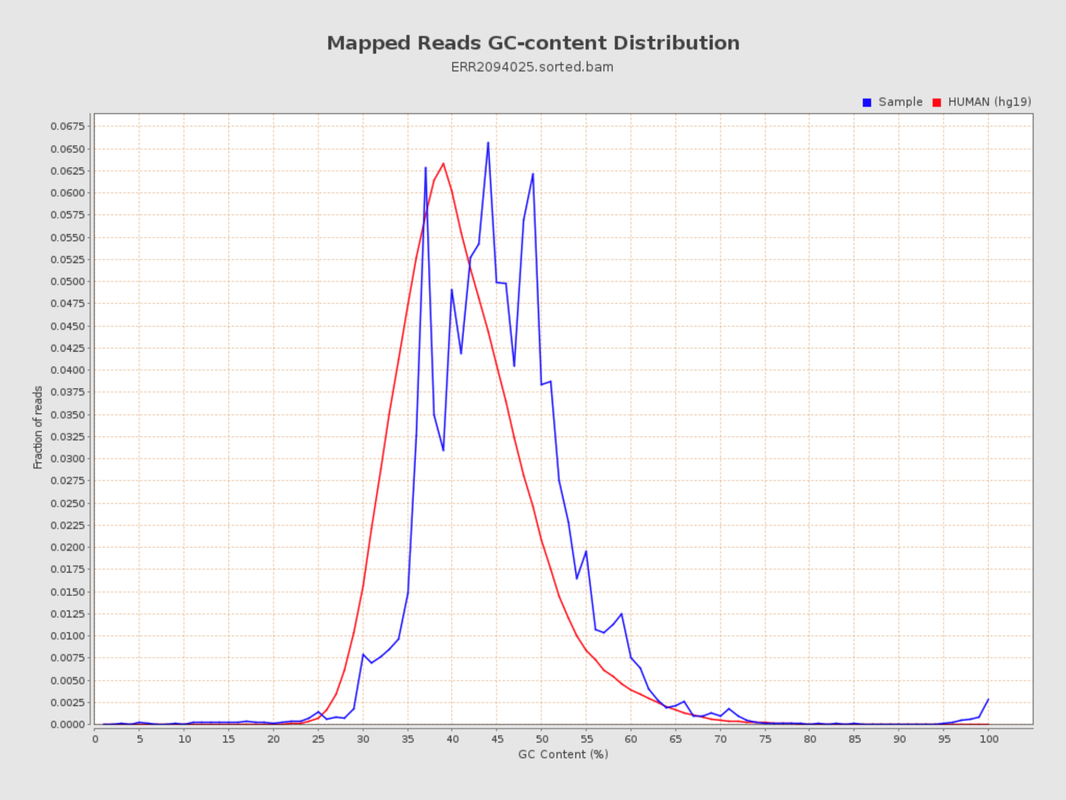
7. Results : Duplication Rate Histogram



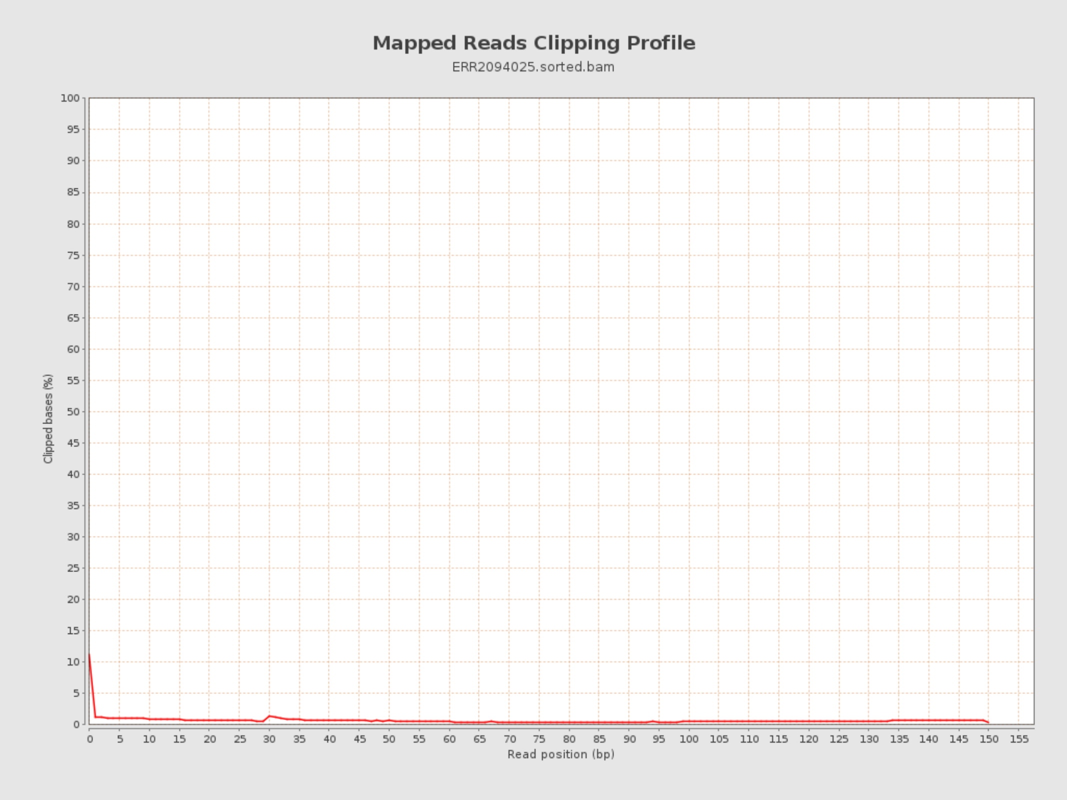
8. Results : Mapped Reads Nucleotide Content



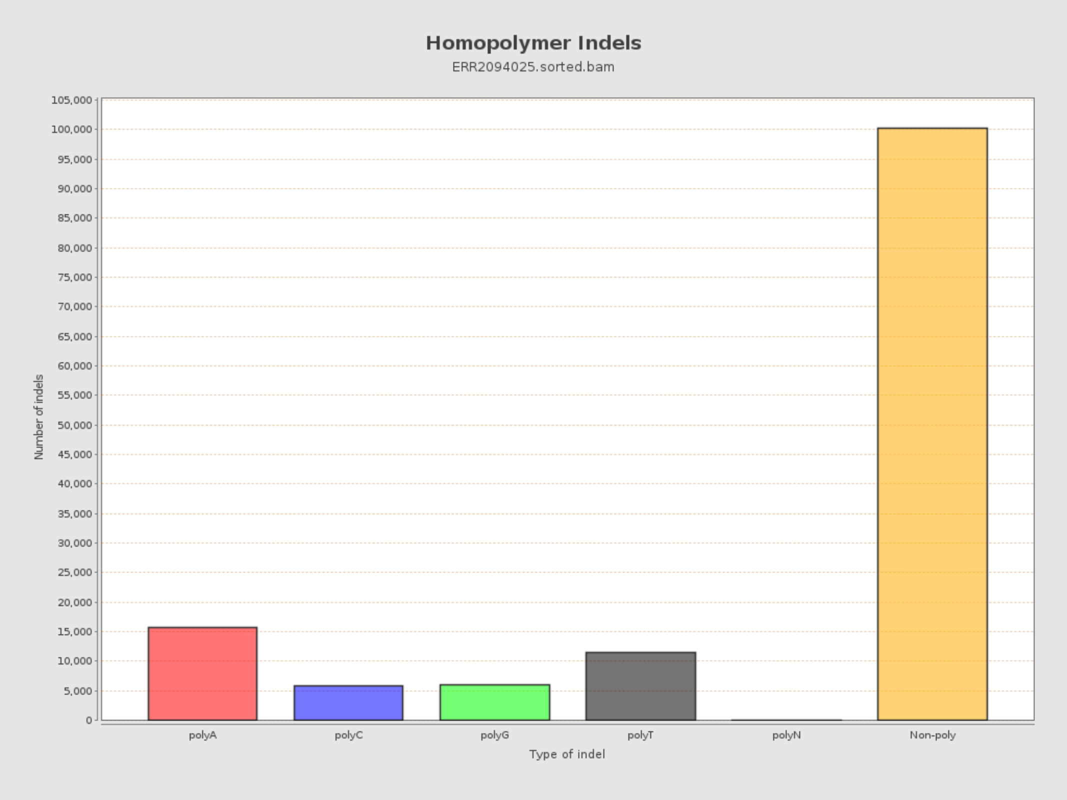
9. Results : Mapped Reads GC-content Distribution



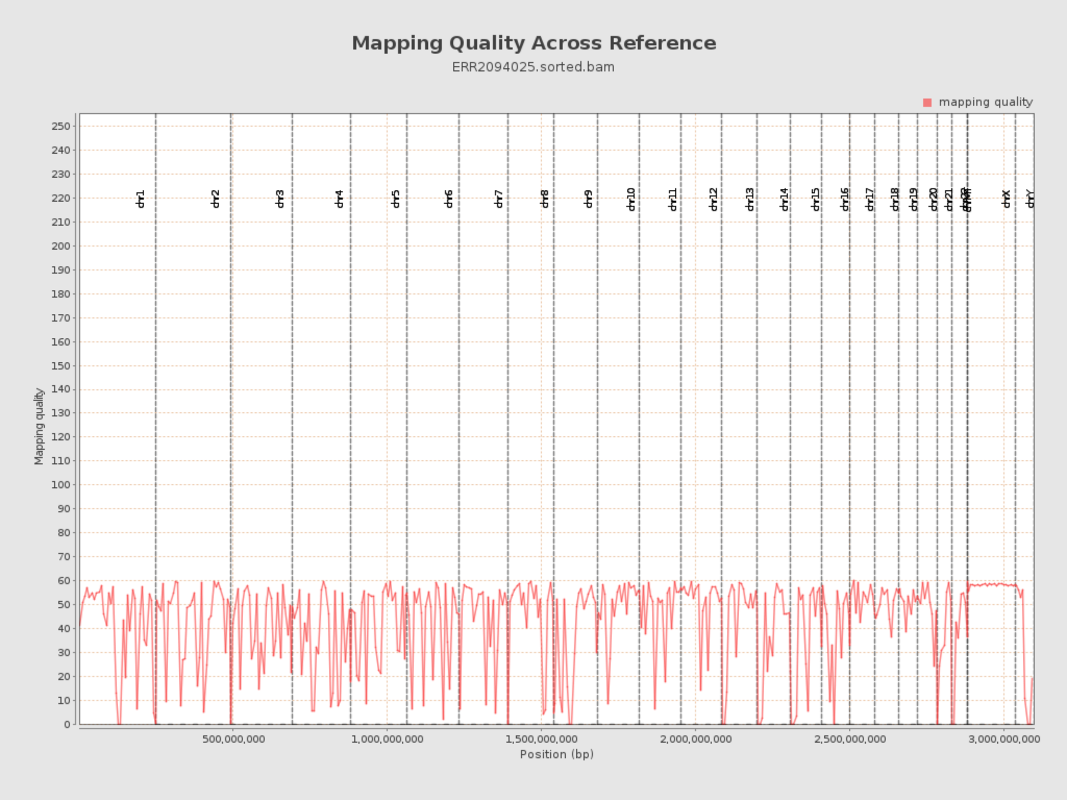
10. Results : Mapped Reads Clipping Profile



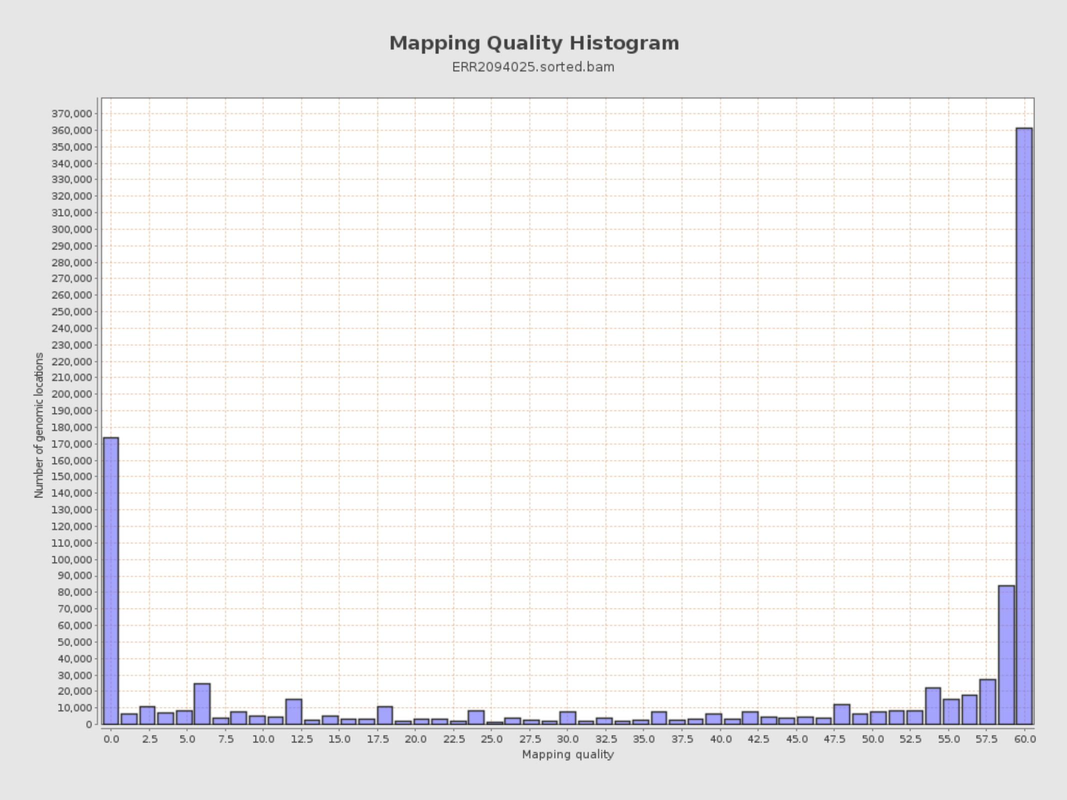
11. Results : Homopolymer Indels



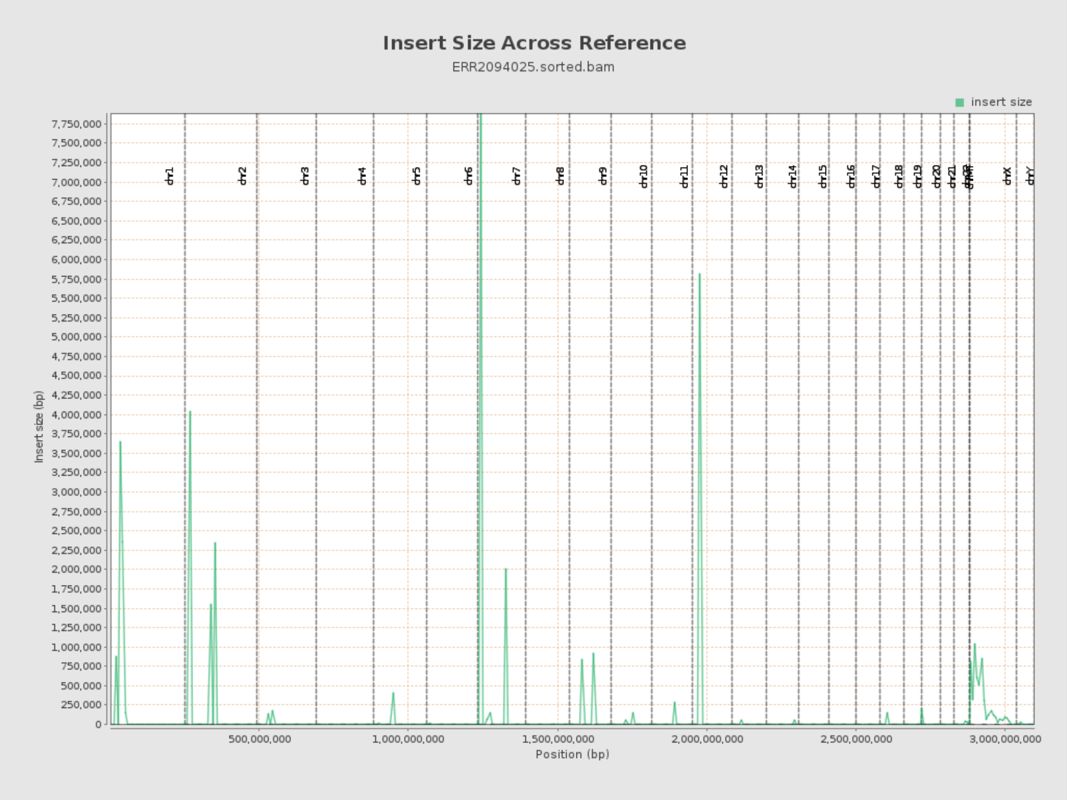
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram