Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:39:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094006.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_ERR2094006 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094006_1.fastq.gz ERR2094006_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:39:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	485,424
Mapped reads	296,211 / 61.02%
Unmapped reads	189,213 / 38.98%
Mapped paired reads	296,211 / 61.02%
Mapped reads, first in pair	147,752 / 30.44%
Mapped reads, second in pair	148,459 / 30.58%
Mapped reads, both in pair	292,410 / 60.24%
Mapped reads, singletons	3,801 / 0.78%
Secondary alignments	0
Supplementary alignments	2,434 / 0.5%
Read min/max/mean length	30 / 151 / 111.36
Duplicated reads (estimated)	291,369 / 60.02%
Duplication rate	40.42%
Clipped reads	85,741 / 17.66%

2.2. ACGT Content

Number/percentage of A's	11,679,746 / 28.31%
Number/percentage of C's	8,630,004 / 20.92%
Number/percentage of T's	11,757,578 / 28.5%
Number/percentage of G's	9,189,005 / 22.27%
Number/percentage of N's	531 / 0%

GC Percentage	43.19%

2.3. Coverage

Mean	0.0135
Standard Deviation	14.9499

2.4. Mapping Quality

Mean Mapping Quality	22.57

2.5. Insert size

Mean	49,303.73
Standard Deviation	2,193,860.08
P25/Median/P75	165 / 182 / 237

2.6. Mismatches and indels

General error rate	2.86%
Mismatches	1,172,096
Insertions	7,979
Mapped reads with at least one insertion	2.62%
Deletions	71,166
Mapped reads with at least one deletion	23.09%
Homopolymer indels	39.5%

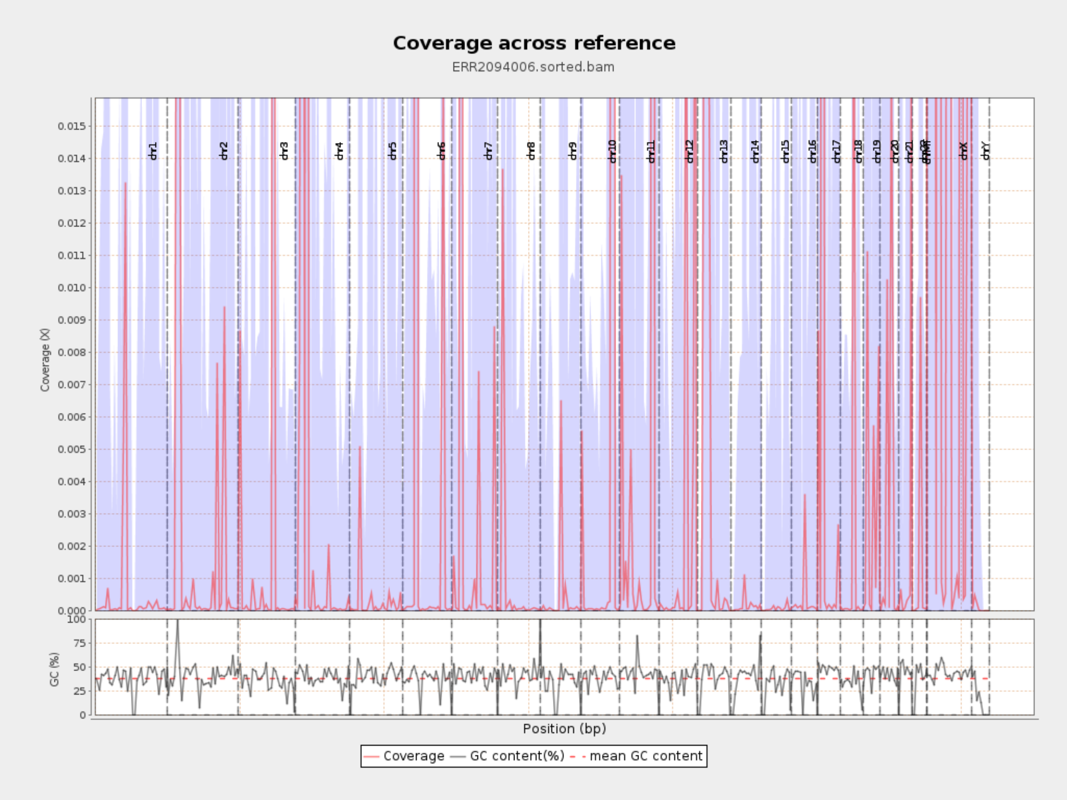
2.7. Chromosome stats

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

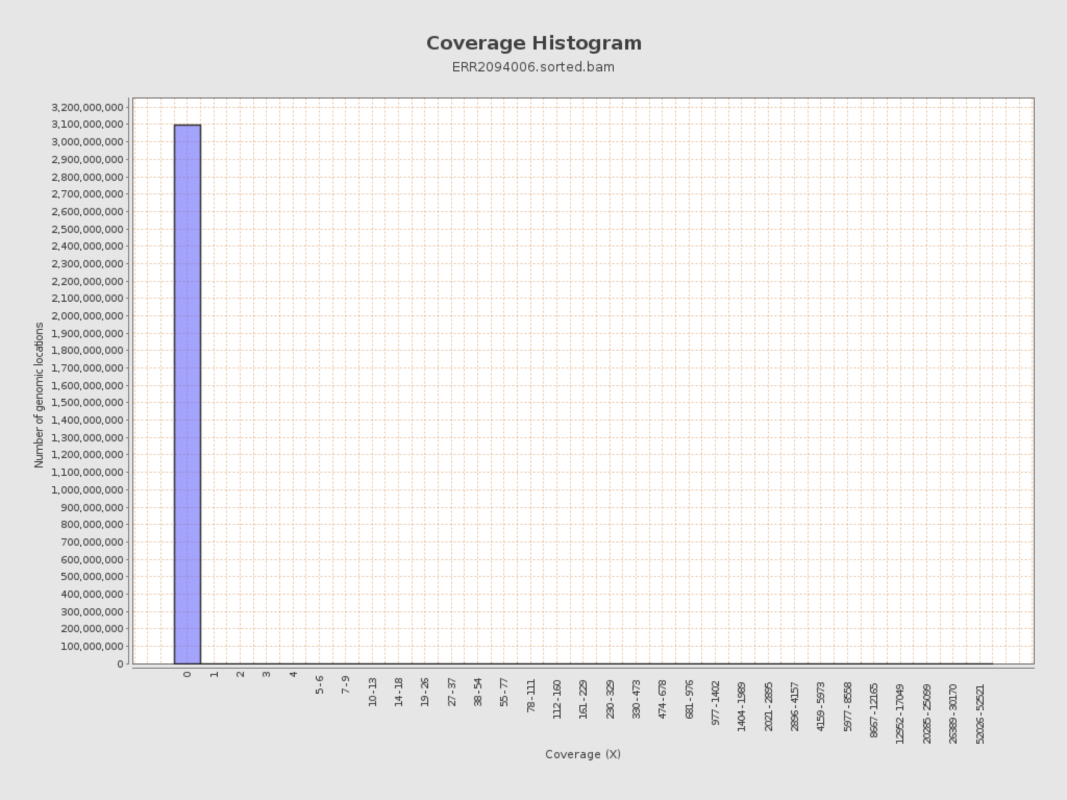
		bases	**coverage**	**deviation**
chr1	249250621	166822	0.0007	0.5573
chr2	243199373	608264	0.0025	1.4735
chr3	198022430	523309	0.0026	2.548
chr4	191154276	1531904	0.008	6.0056
chr5	180915260	64731	0.0004	0.2313
chr6	171115067	4333644	0.0253	25.0927
chr7	159138663	693585	0.0044	3.5401
chr8	146364022	116010	0.0008	0.6646
chr9	141213431	63100	0.0004	0.3126
chr10	135534747	1383434	0.0102	7.8807
chr11	135006516	1216541	0.009	6.9396
chr12	133851895	465035	0.0035	1.9399
chr13	115169878	734007	0.0064	3.5959
chr14	107349540	16820	0.0002	0.0717
chr15	102531392	7496	0.0001	0.0223
chr16	90354753	36018	0.0004	0.2086
chr17	81195210	849215	0.0105	6.6532
chr18	78077248	167916	0.0022	1.488
chr19	59128983	203653	0.0034	1.1067
chr20	63025520	219617	0.0035	1.8209
chr21	48129895	96891	0.002	0.9964
chr22	51304566	77195	0.0015	0.8249
chrMT	16571	18505255	1,116.7253	5,188.5662
chrX	155270560	9611954	0.0619	23.4642

chrY	59373566	6127	0.0001	0.0377

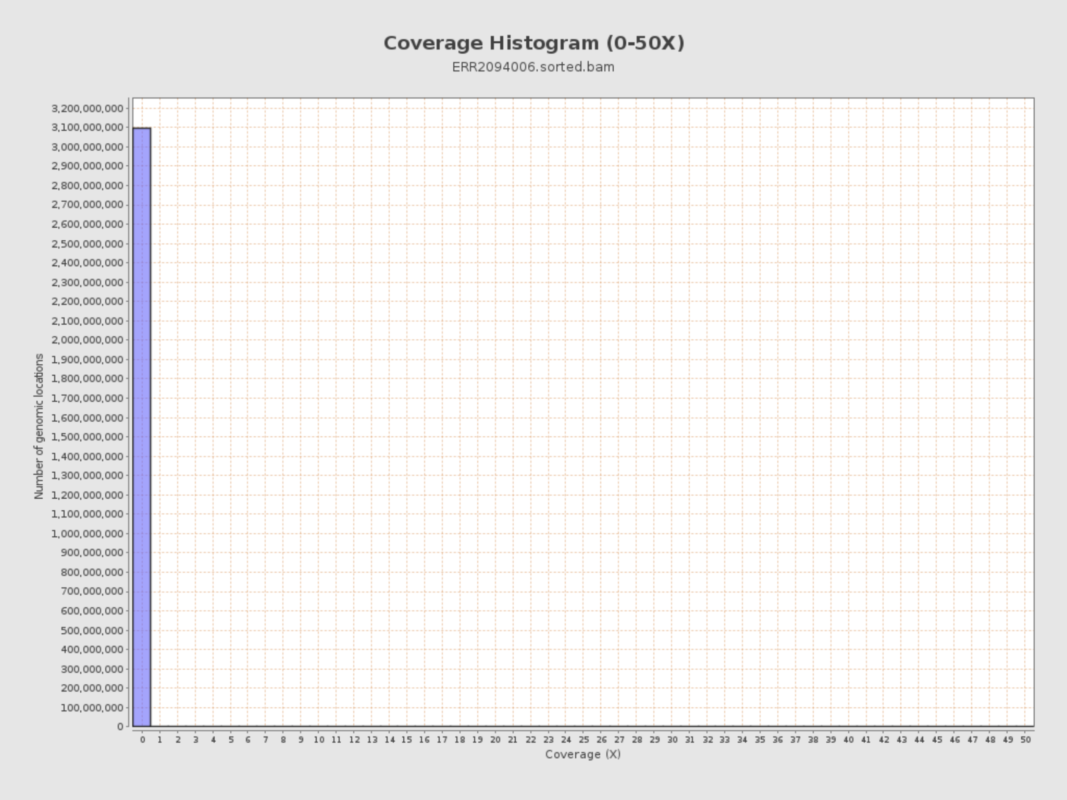
3. Results : Coverage across reference



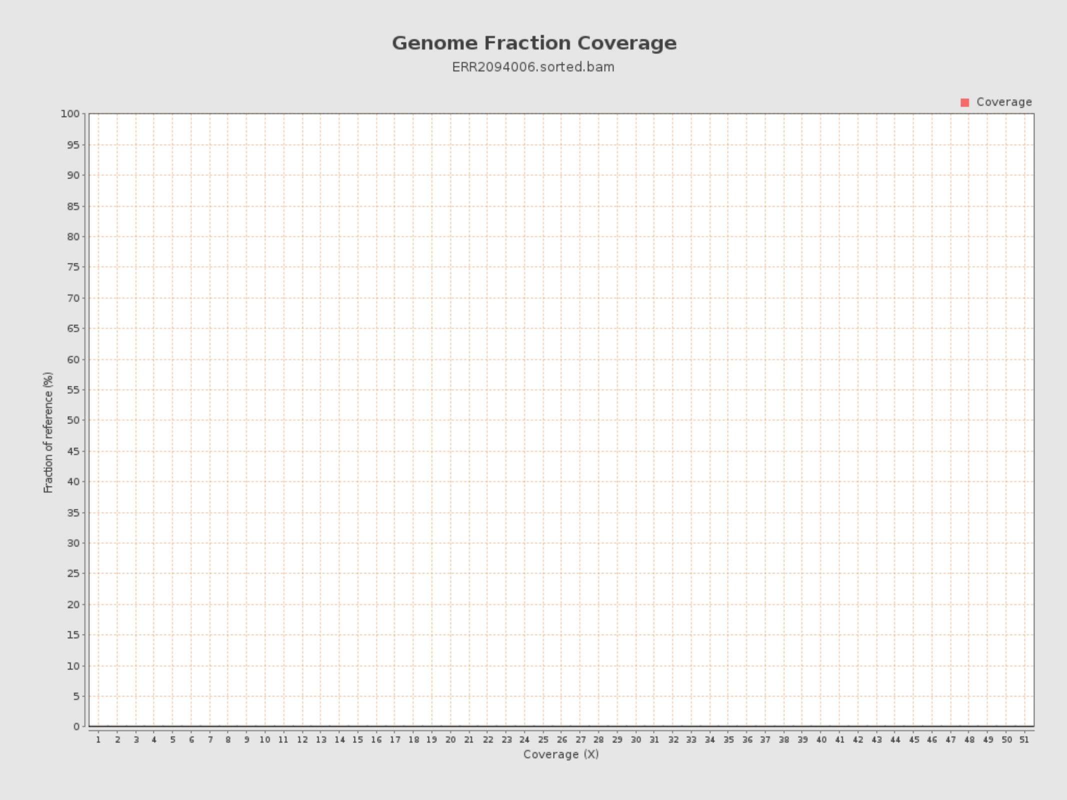
4. Results : Coverage Histogram



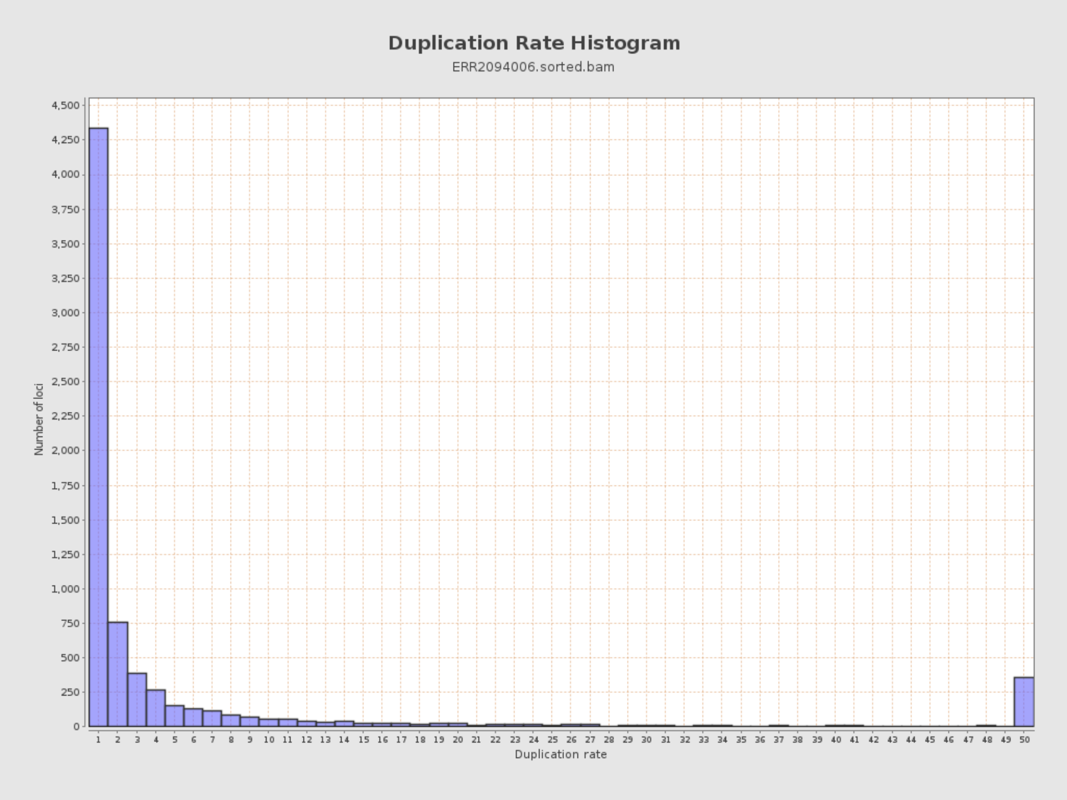
5. Results : Coverage Histogram (0-50X)



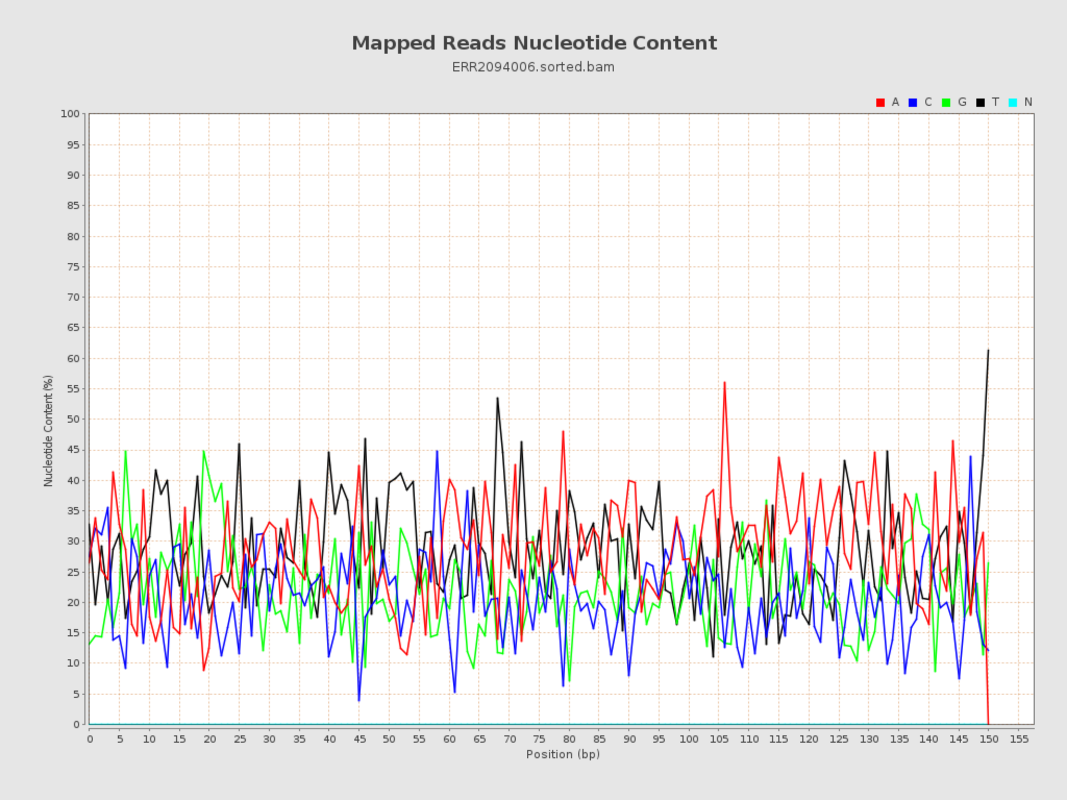
6. Results : Genome Fraction Coverage



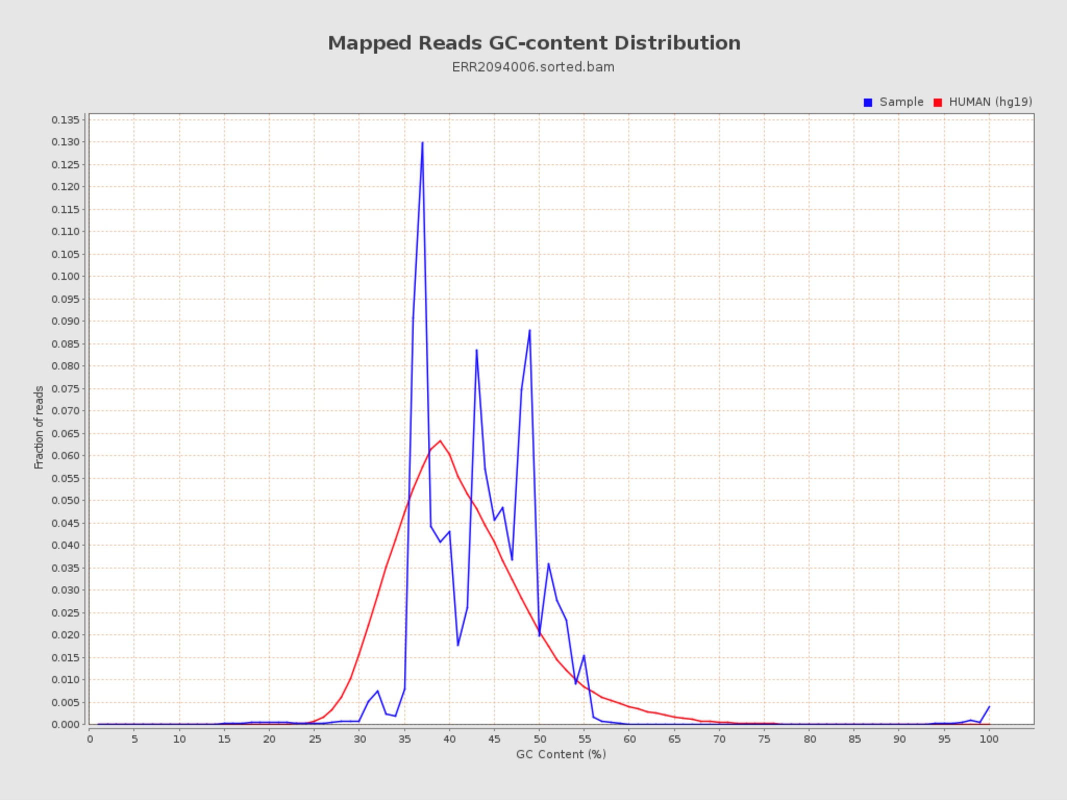
7. Results : Duplication Rate Histogram



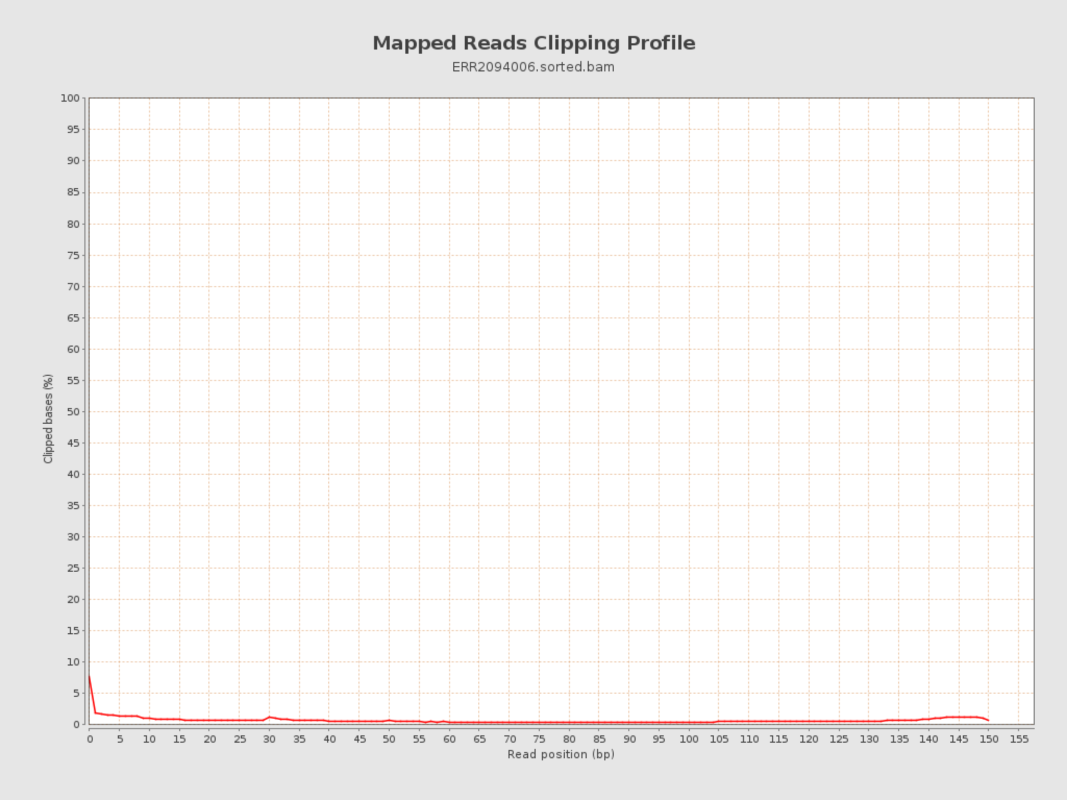
8. Results : Mapped Reads Nucleotide Content



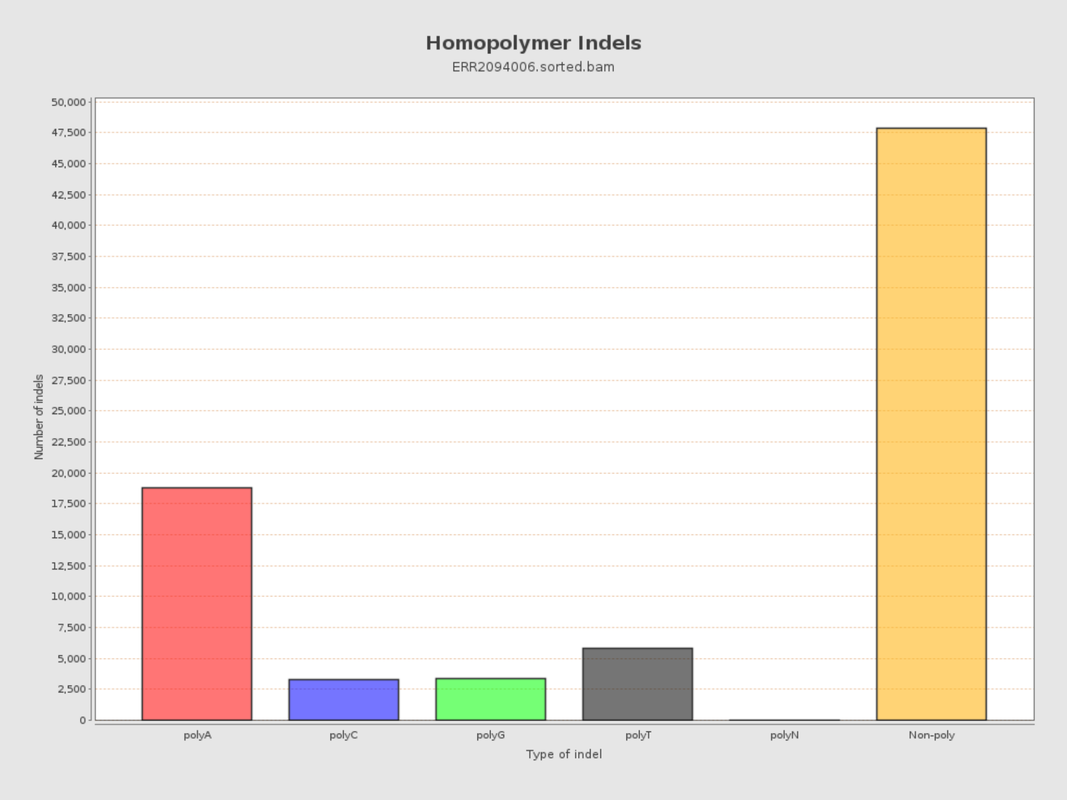
9. Results : Mapped Reads GC-content Distribution



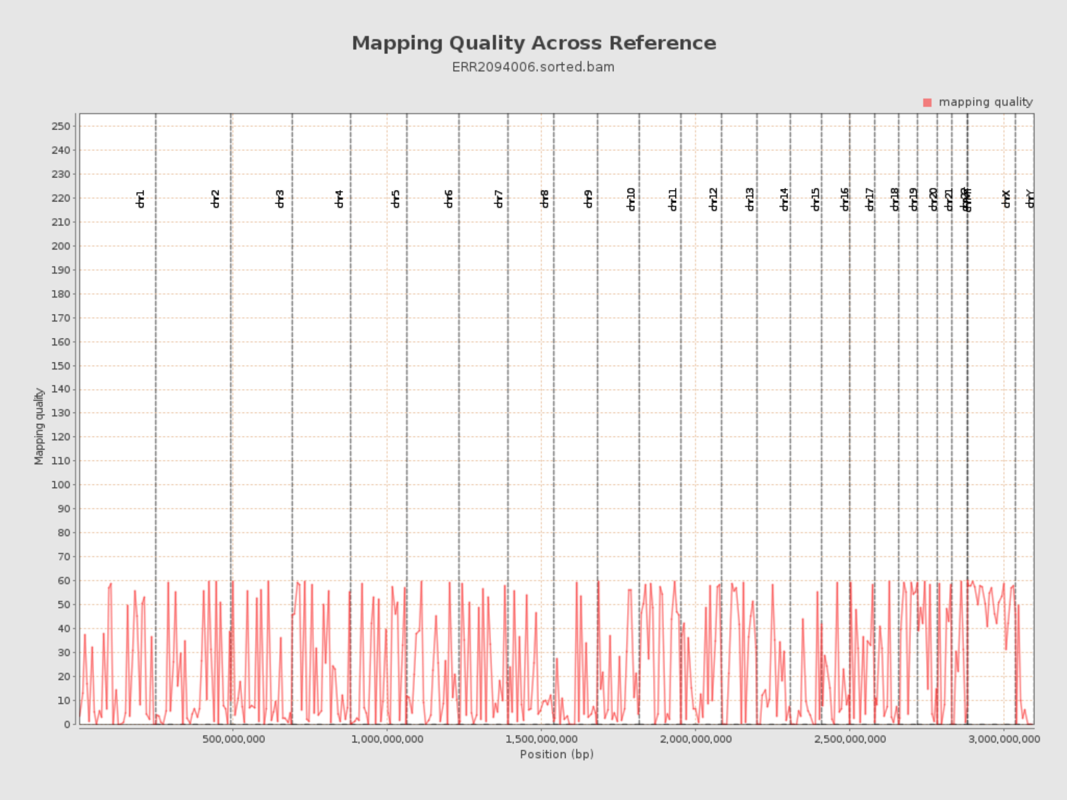
10. Results : Mapped Reads Clipping Profile



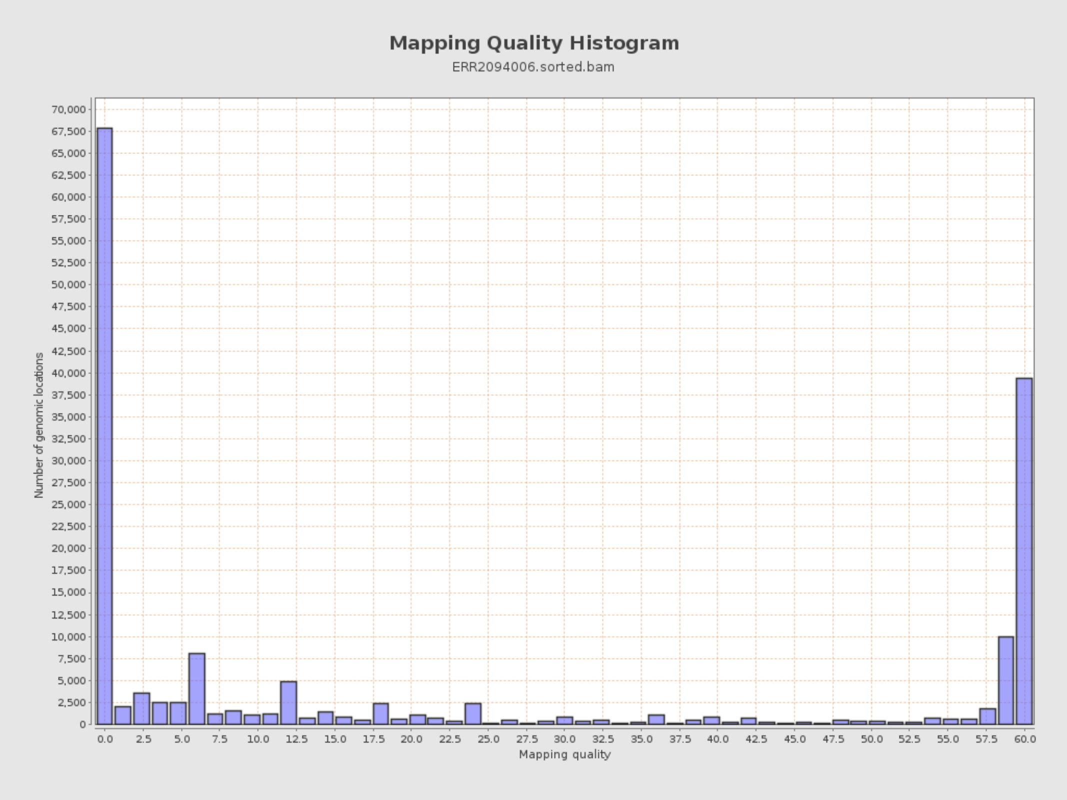
11. Results : Homopolymer Indels



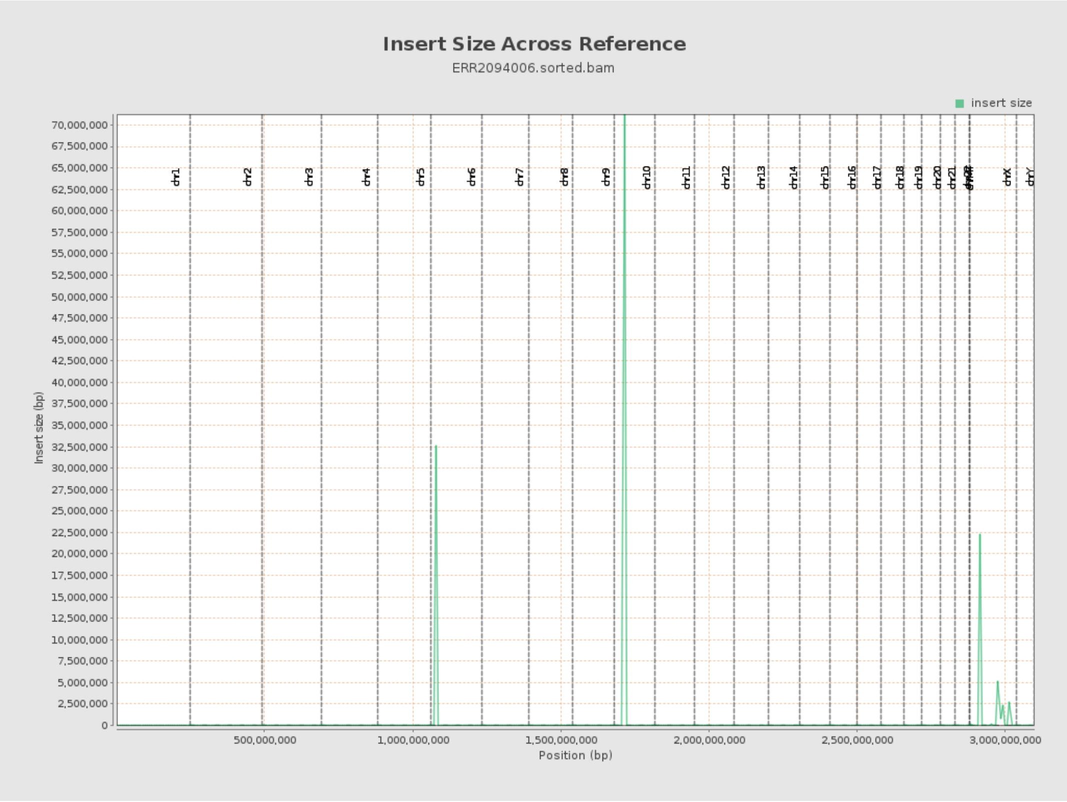
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram