Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:52:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094073.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_ERR2094073 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094073_1.fastq.gz ERR2094073_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:52:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	423,956
Mapped reads	405,945 / 95.75%
Unmapped reads	18,011 / 4.25%
Mapped paired reads	405,945 / 95.75%
Mapped reads, first in pair	203,826 / 48.08%
Mapped reads, second in pair	202,119 / 47.67%
Mapped reads, both in pair	403,262 / 95.12%
Mapped reads, singletons	2,683 / 0.63%
Secondary alignments	0
Supplementary alignments	12,800 / 3.02%
Read min/max/mean length	30 / 151 / 140.67
Duplicated reads (estimated)	386,571 / 91.18%
Duplication rate	49.58%
Clipped reads	154,971 / 36.55%

2.2. ACGT Content

Number/percentage of A's	14,001,329 / 26.62%
Number/percentage of C's	12,339,481 / 23.46%
Number/percentage of T's	13,342,895 / 25.37%
Number/percentage of G's	12,903,755 / 24.54%
Number/percentage of N's	497 / 0%

GC Percentage	48%

2.3. Coverage

Mean	0.0174
Standard Deviation	4.7952

2.4. Mapping Quality

Mean Mapping Quality	38.48

2.5. Insert size

Mean	397,090.81
Standard Deviation	5,638,341.28
P25/Median/P75	135 / 166 / 196

2.6. Mismatches and indels

General error rate	4.08%
Mismatches	2,057,017
Insertions	34,491
Mapped reads with at least one insertion	8.32%
Deletions	167,325
Mapped reads with at least one deletion	39.34%
Homopolymer indels	26.75%

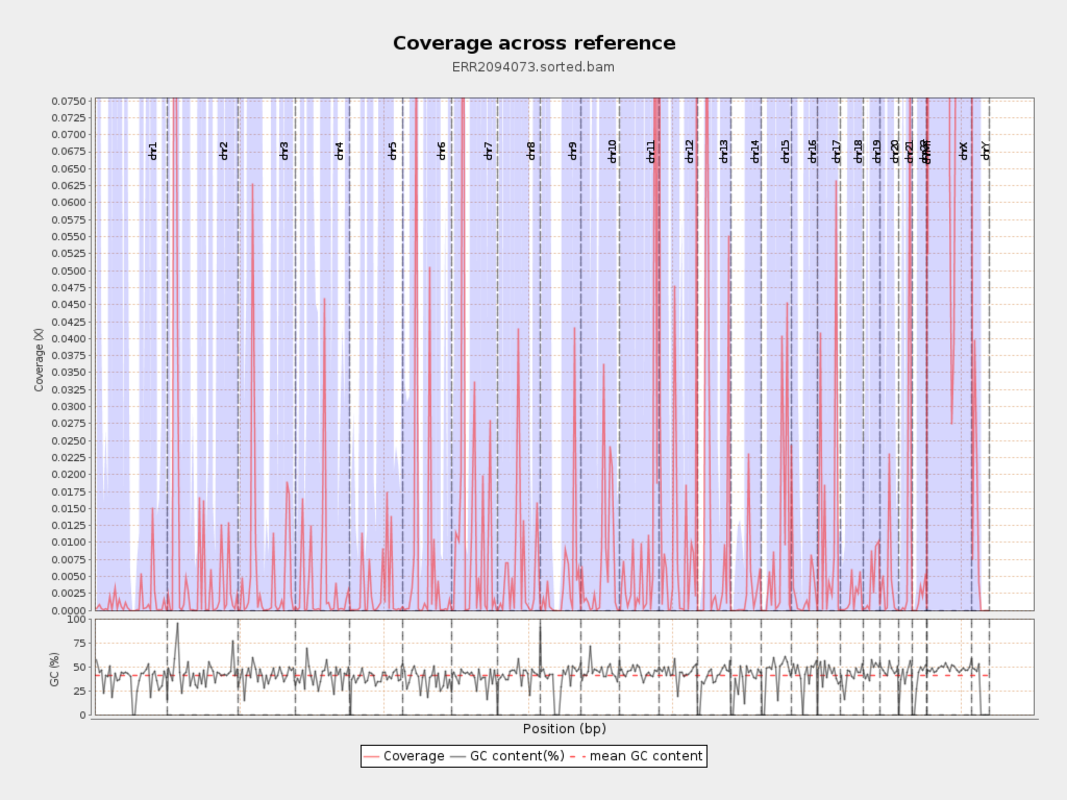
2.7. Chromosome stats

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

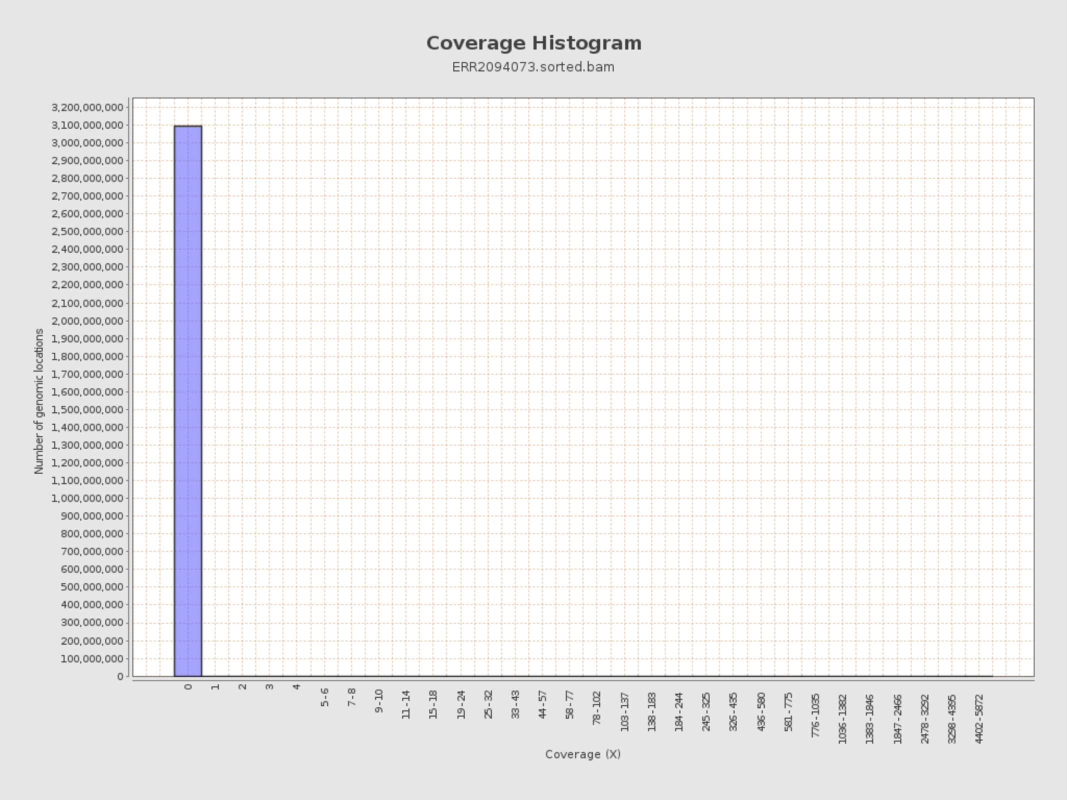
		bases	coverage	deviation
chr1	249250621	301091	0.0012	0.6383
chr2	243199373	2042807	0.0084	3.1132
chr3	198022430	1085080	0.0055	2.0269
chr4	191154276	819778	0.0043	1.4331
chr5	180915260	516536	0.0029	1.2959
chr6	171115067	1329082	0.0078	4.4874
chr7	159138663	2110819	0.0133	5.0581
chr8	146364022	881598	0.006	2.1286
chr9	141213431	620918	0.0044	1.9704
chr10	135534747	918712	0.0068	2.4331
chr11	135006516	1494336	0.0111	3.7349
chr12	133851895	1324543	0.0099	2.9404
chr13	115169878	1590521	0.0138	3.9285
chr14	107349540	341912	0.0032	1.4438
chr15	102531392	879938	0.0086	3.077
chr16	90354753	302846	0.0034	1.2913
chr17	81195210	1101163	0.0136	4.9187
chr18	78077248	150811	0.0019	0.5722
chr19	59128983	251382	0.0043	1.0573
chr20	63025520	278435	0.0044	1.3717
chr21	48129895	685039	0.0142	6.1309
chr22	51304566	95581	0.0019	0.4572
chrMT	16571	1426222	86.0673	397.8294
chrX	155270560	32659832	0.2103	16.904

chrY	59373566	556131	0.0094	2.6169

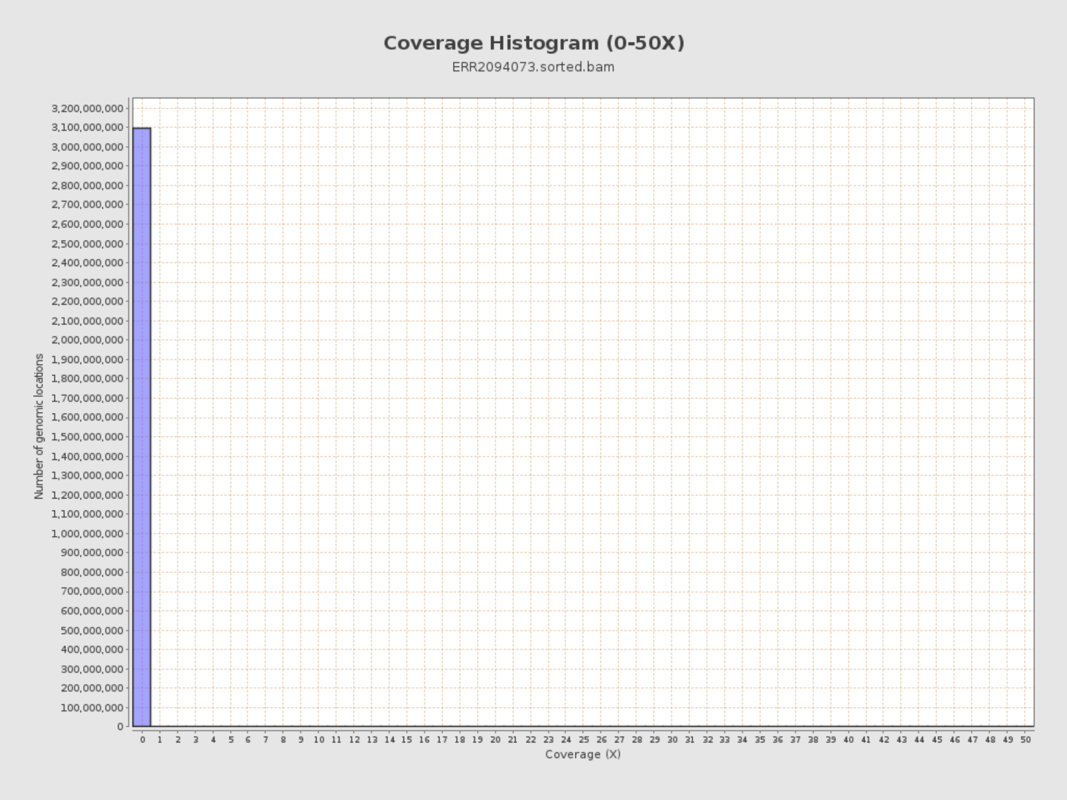
3. Results : Coverage across reference



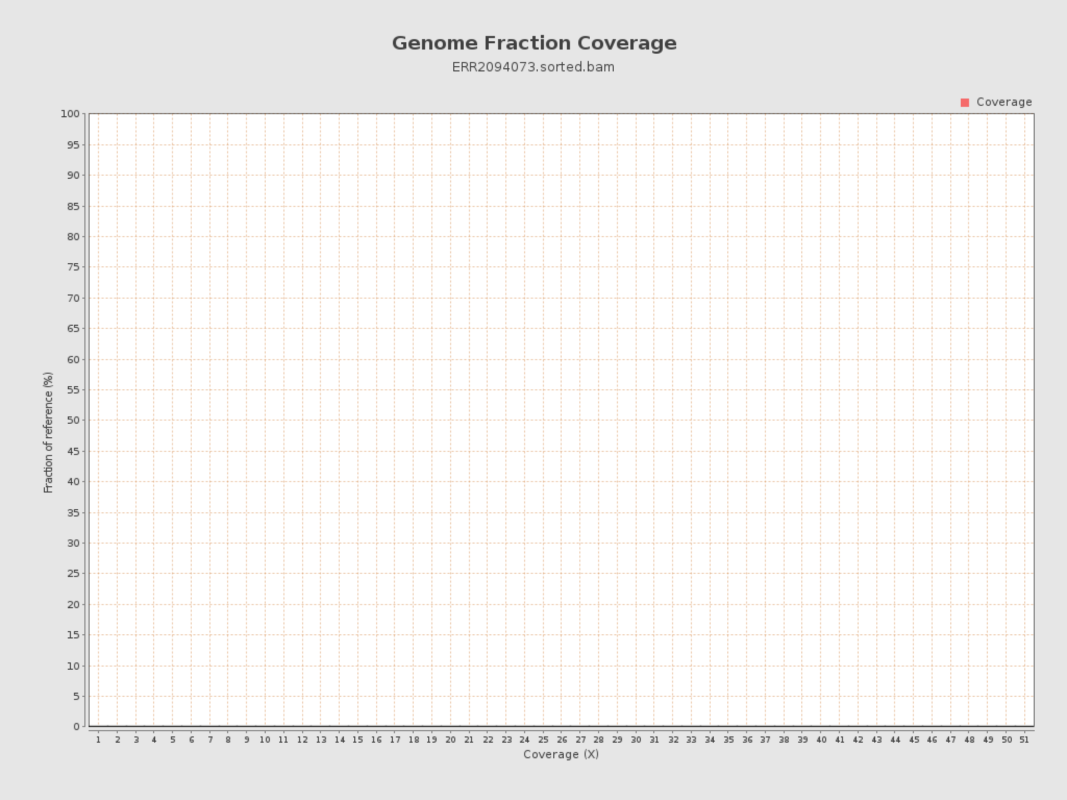
4. Results : Coverage Histogram



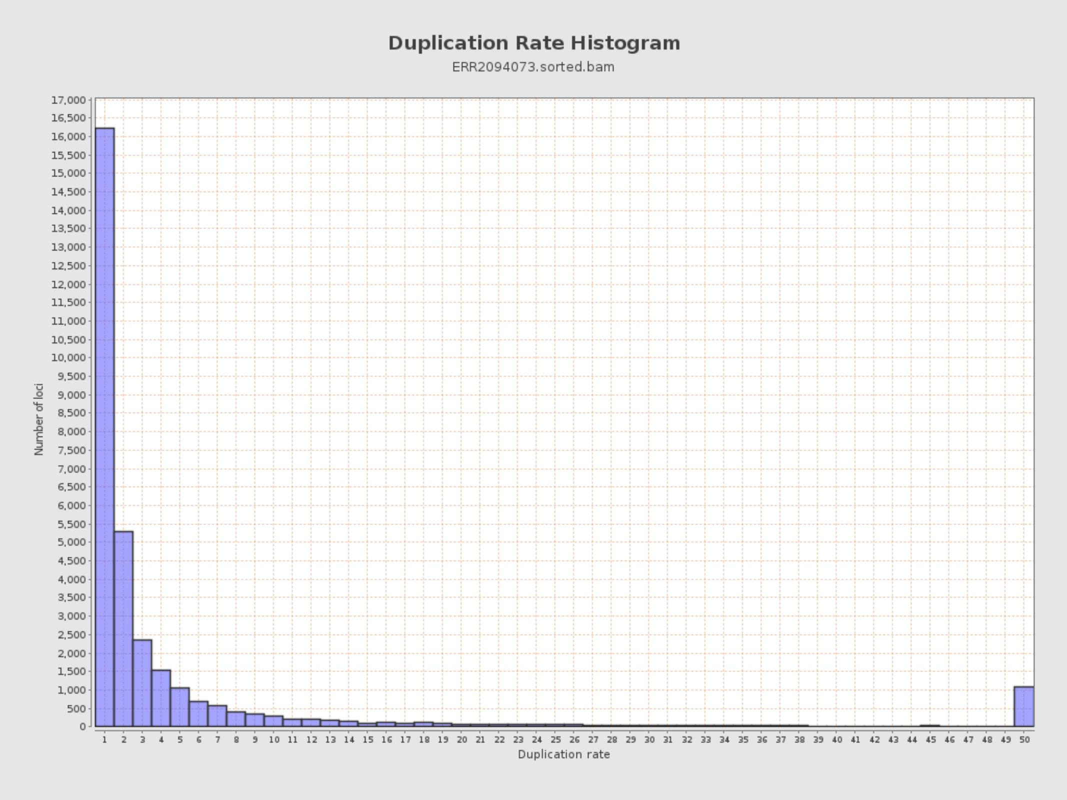
5. Results : Coverage Histogram (0-50X)



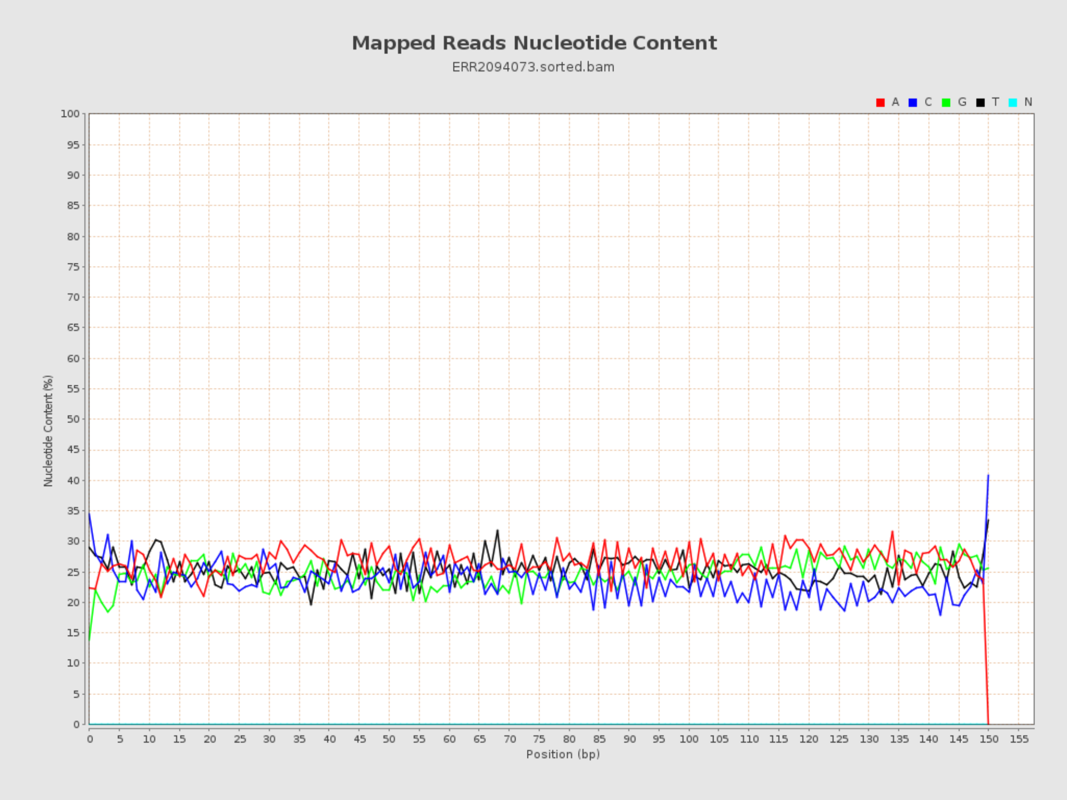
6. Results : Genome Fraction Coverage



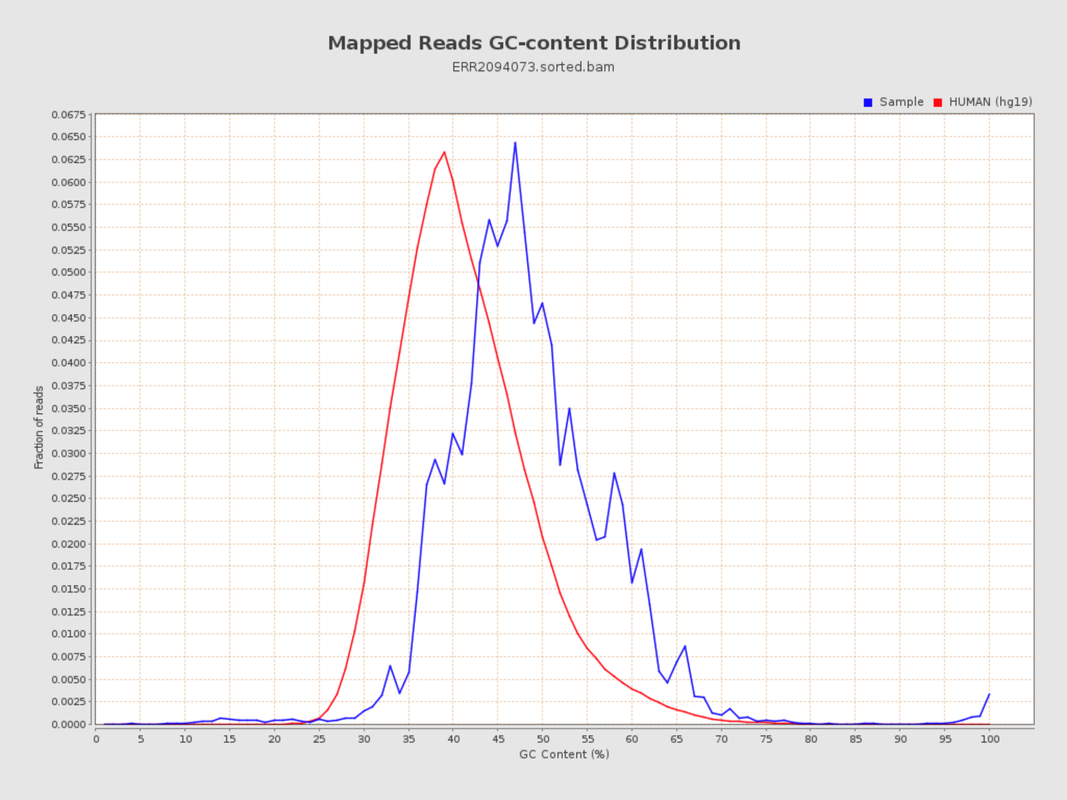
7. Results : Duplication Rate Histogram



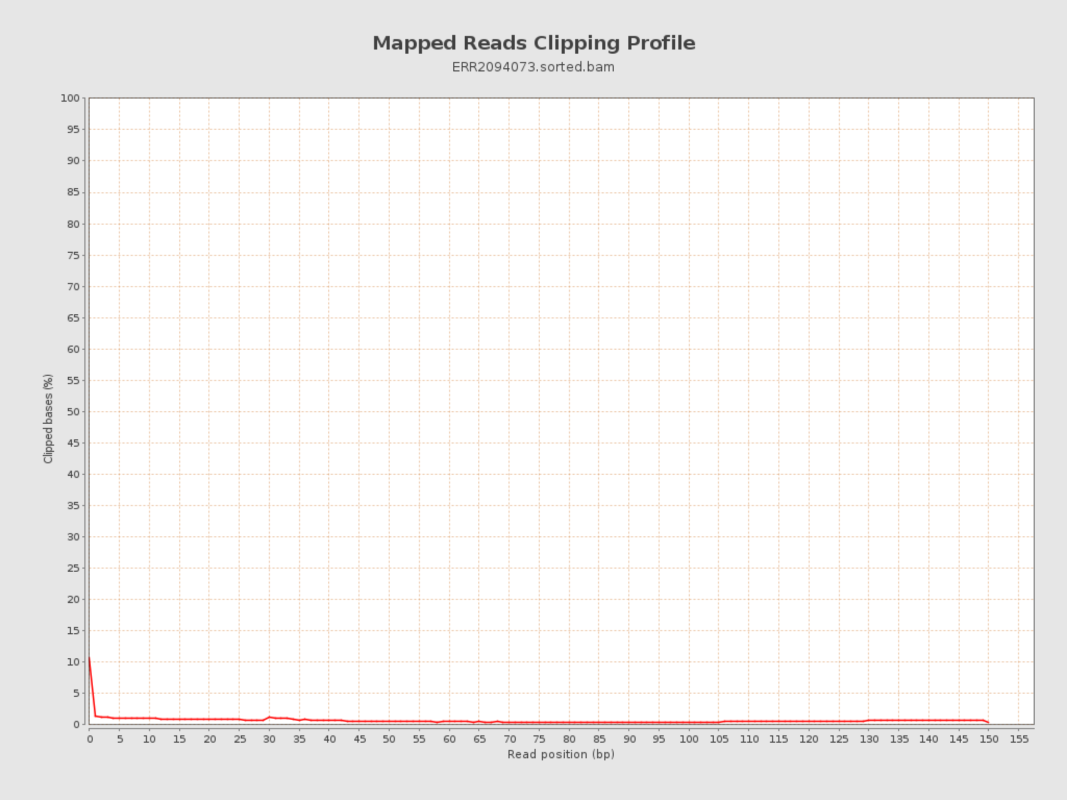
8. Results : Mapped Reads Nucleotide Content



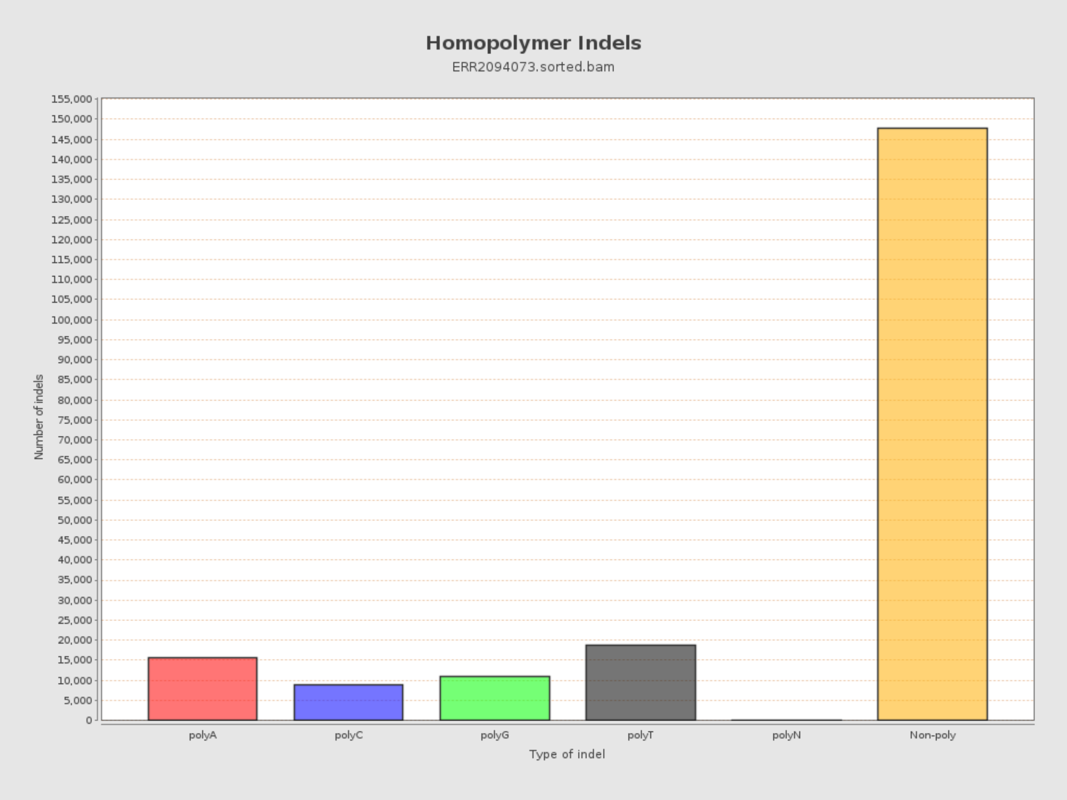
9. Results : Mapped Reads GC-content Distribution



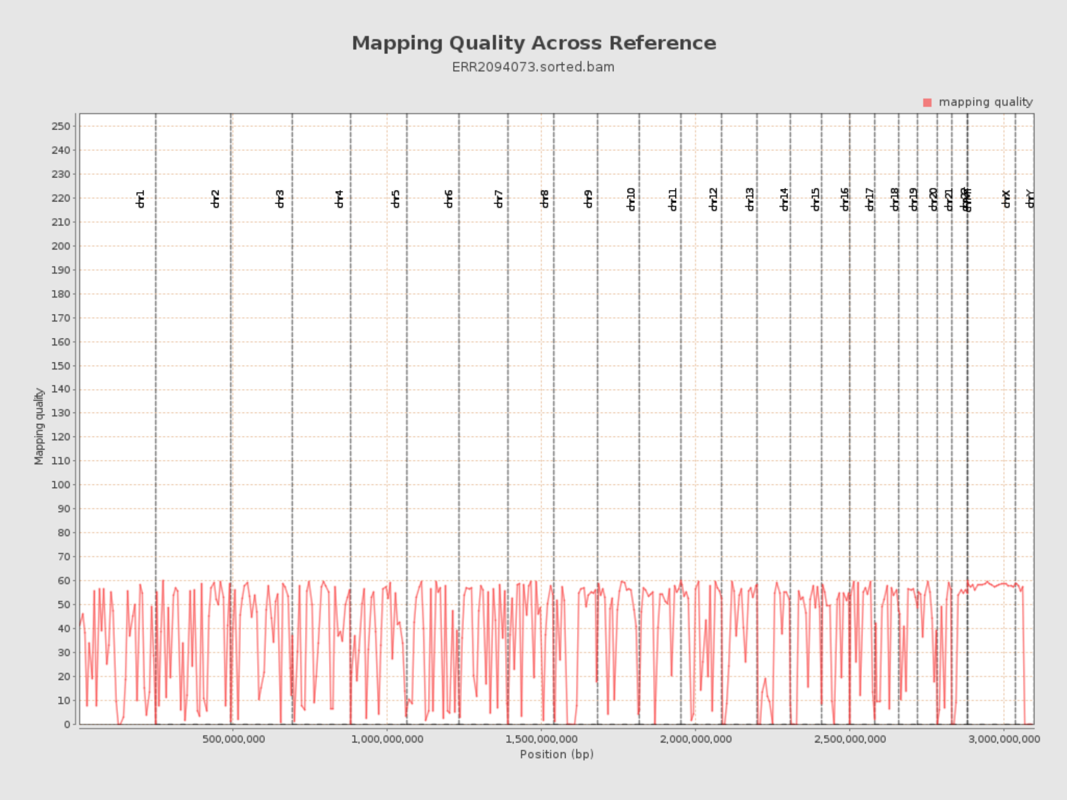
10. Results : Mapped Reads Clipping Profile



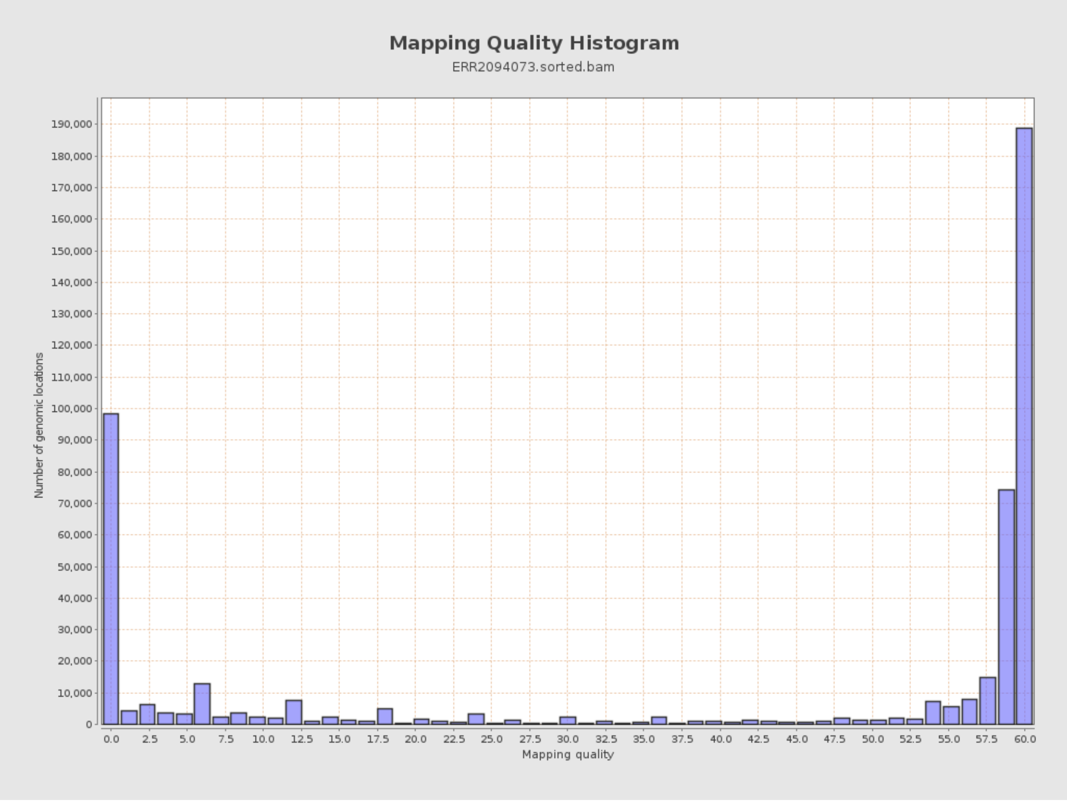
11. Results : Homopolymer Indels



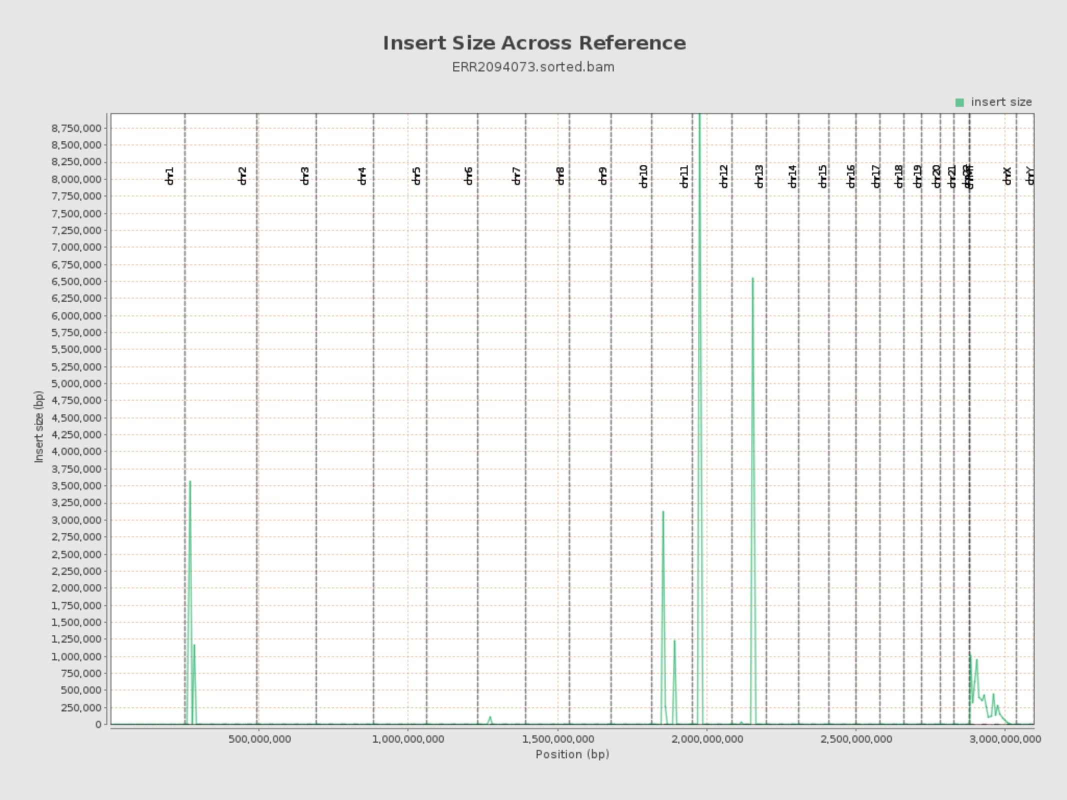
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram