Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:07:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094101.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_ERR2094101 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094101_1.fastq.gz ERR2094101_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:07:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	353,754
Mapped reads	331,717 / 93.77%
Unmapped reads	22,037 / 6.23%
Mapped paired reads	331,717 / 93.77%
Mapped reads, first in pair	166,860 / 47.17%
Mapped reads, second in pair	164,857 / 46.6%
Mapped reads, both in pair	328,278 / 92.8%
Mapped reads, singletons	3,439 / 0.97%
Secondary alignments	0
Supplementary alignments	22,761 / 6.43%
Read min/max/mean length	30 / 151 / 135.64
Duplicated reads (estimated)	313,238 / 88.55%
Duplication rate	50.26%
Clipped reads	175,673 / 49.66%

2.2. ACGT Content

Number/percentage of A's	11,472,328 / 28.93%
Number/percentage of C's	8,456,819 / 21.33%
Number/percentage of T's	10,712,643 / 27.02%
Number/percentage of G's	9,008,698 / 22.72%
Number/percentage of N's	402 / 0%

GC Percentage	44.05%

2.3. Coverage

Mean	0.0131
Standard Deviation	2.7035

2.4. Mapping Quality

Mean Mapping Quality	40.09

2.5. Insert size

Mean	1,610,631.39
Standard Deviation	11,325,693.11
P25/Median/P75	112 / 143 / 171

2.6. Mismatches and indels

General error rate	3.68%
Mismatches	1,408,576
Insertions	26,005
Mapped reads with at least one insertion	7.72%
Deletions	112,988
Mapped reads with at least one deletion	32.77%
Homopolymer indels	28.22%

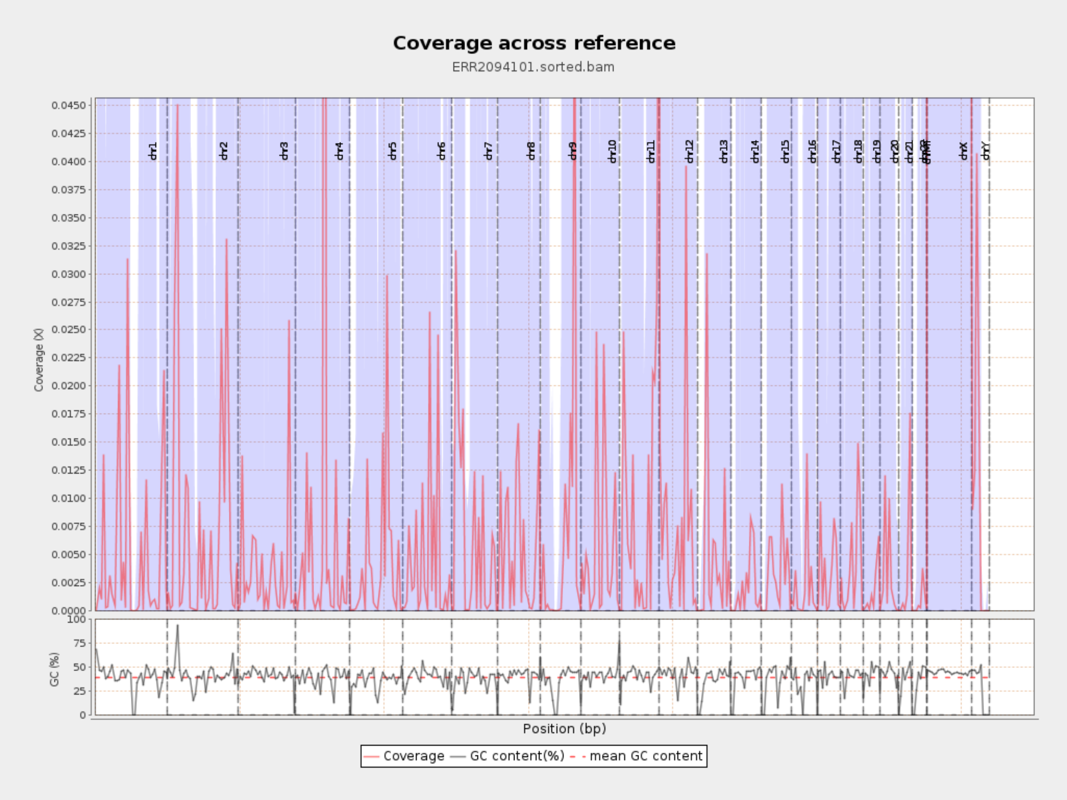
2.7. Chromosome stats

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

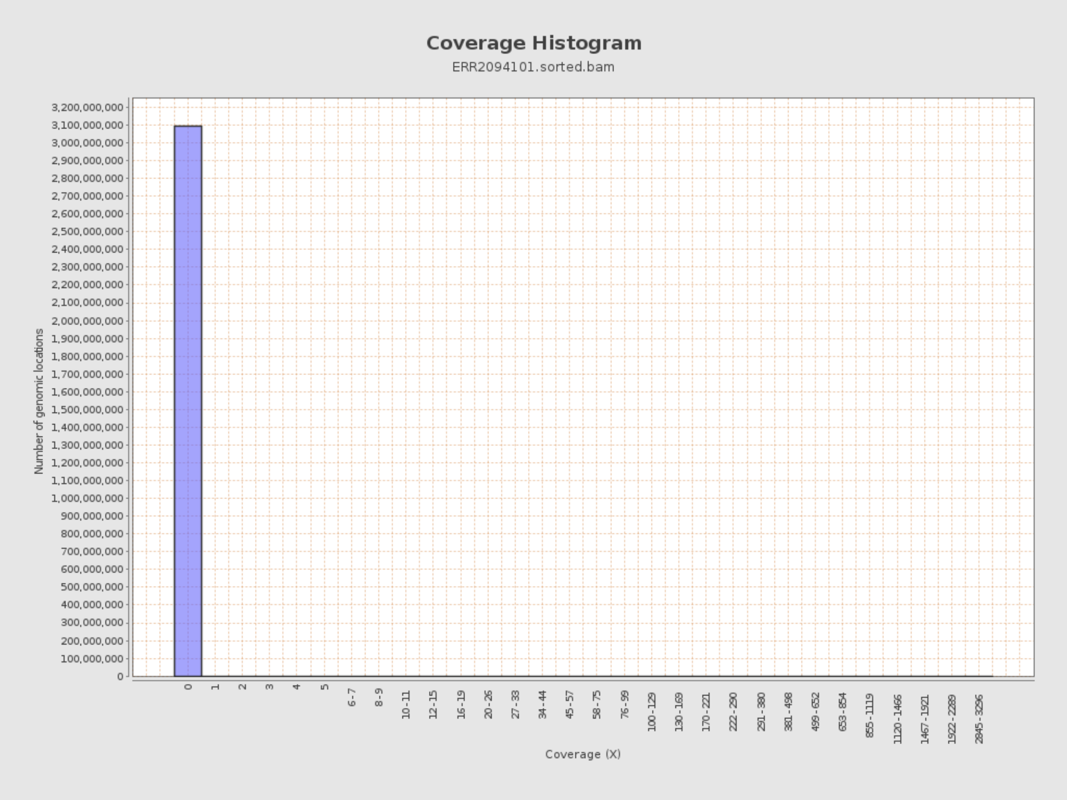
		bases	coverage	deviation
chr1	249250621	1187323	0.0048	1.8361
chr2	243199373	1778704	0.0073	2.1631
chr3	198022430	712264	0.0036	1.2871
chr4	191154276	1652402	0.0086	2.3467
chr5	180915260	795116	0.0044	1.8587
chr6	171115067	812134	0.0047	1.4307
chr7	159138663	996309	0.0063	1.8711
chr8	146364022	821428	0.0056	1.4707
chr9	141213431	933311	0.0066	2.9309
chr10	135534747	762200	0.0056	1.8343
chr11	135006516	1221497	0.009	2.2556
chr12	133851895	942818	0.007	1.7154
chr13	115169878	539769	0.0047	1.1314
chr14	107349540	205455	0.0019	0.741
chr15	102531392	340389	0.0033	0.702
chr16	90354753	199566	0.0022	0.9469
chr17	81195210	272811	0.0034	0.7849
chr18	78077248	327177	0.0042	1.1736
chr19	59128983	99335	0.0017	0.5638
chr20	63025520	211897	0.0034	1.0765
chr21	48129895	167149	0.0035	1.3001
chr22	51304566	39893	0.0008	0.2403
chrMT	16571	200599	12.1054	65.5986
chrX	155270560	24640557	0.1587	9.3767

chrY	59373566	607839	0.0102	2.1265

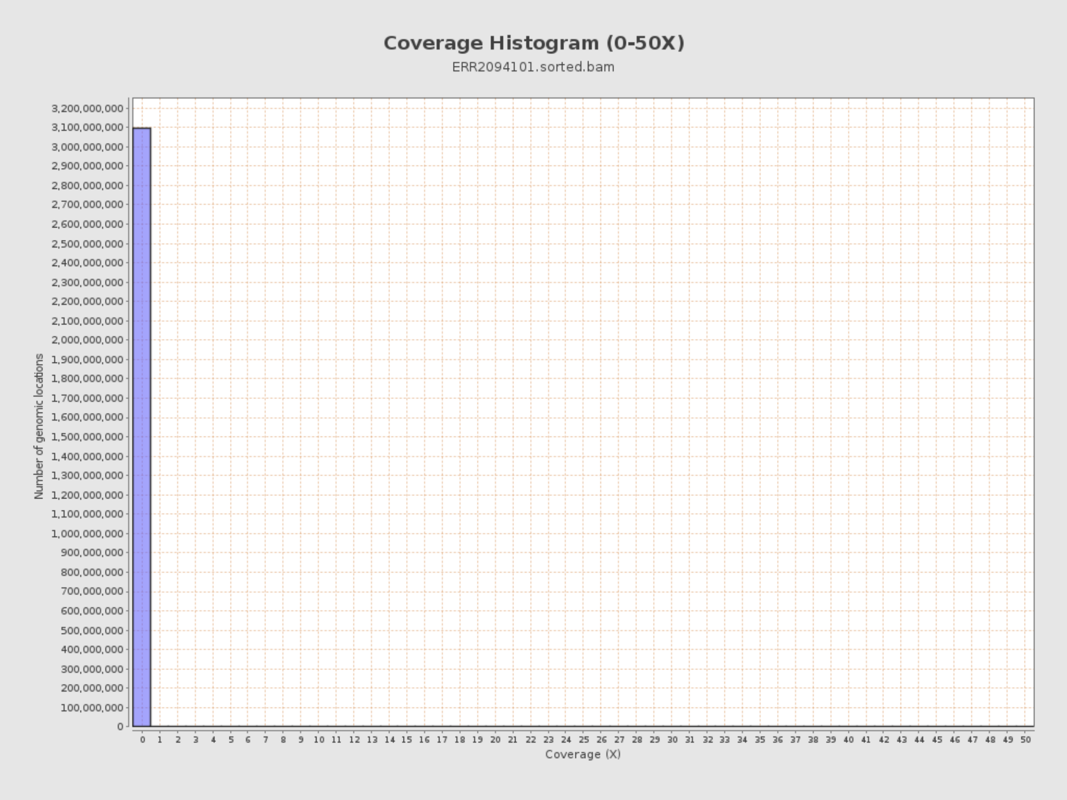
3. Results : Coverage across reference



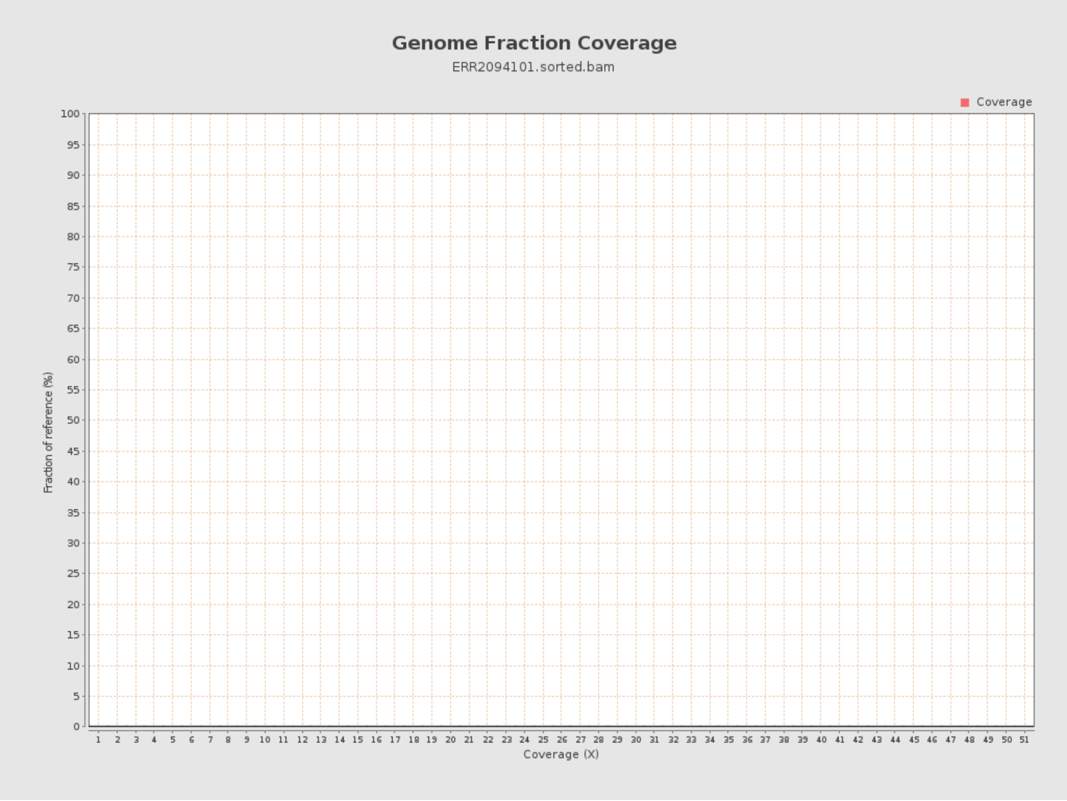
4. Results : Coverage Histogram



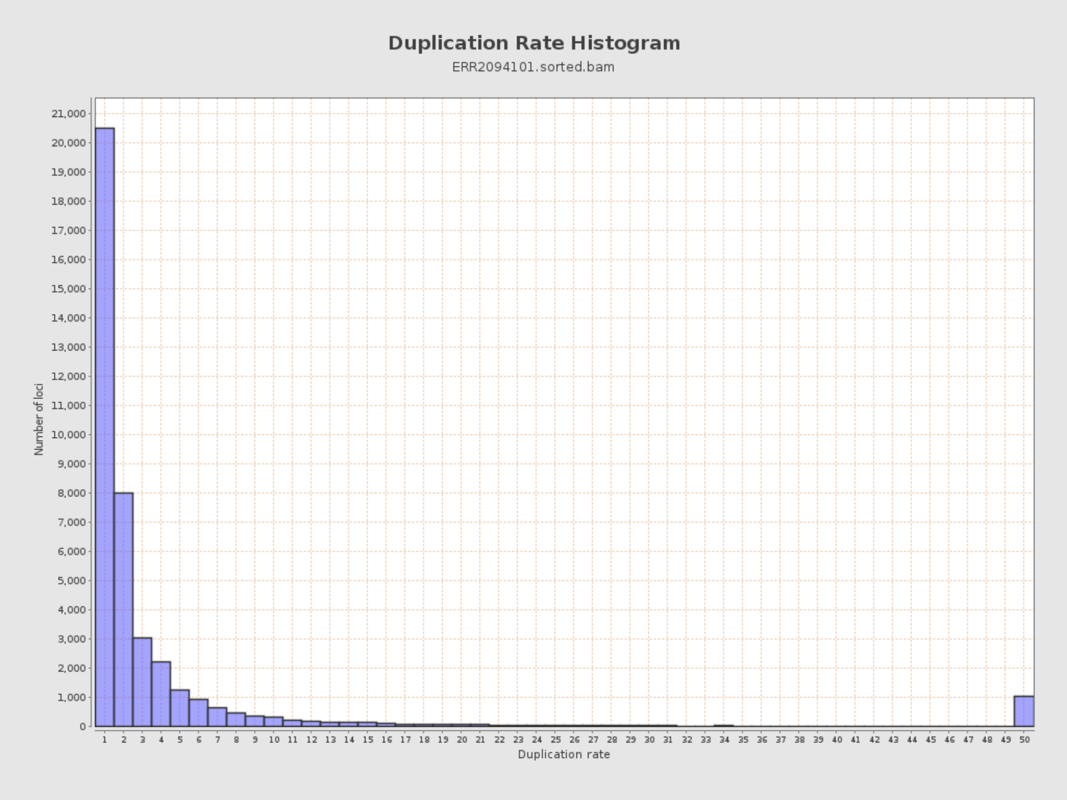
5. Results : Coverage Histogram (0-50X)



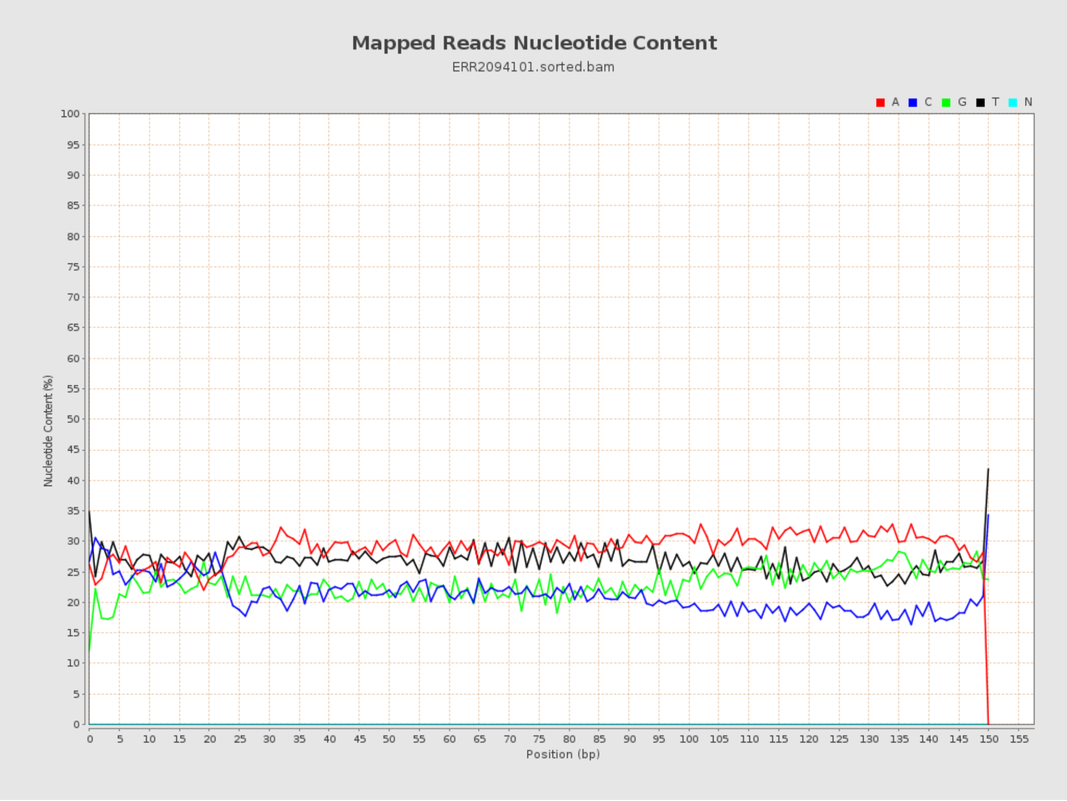
6. Results : Genome Fraction Coverage



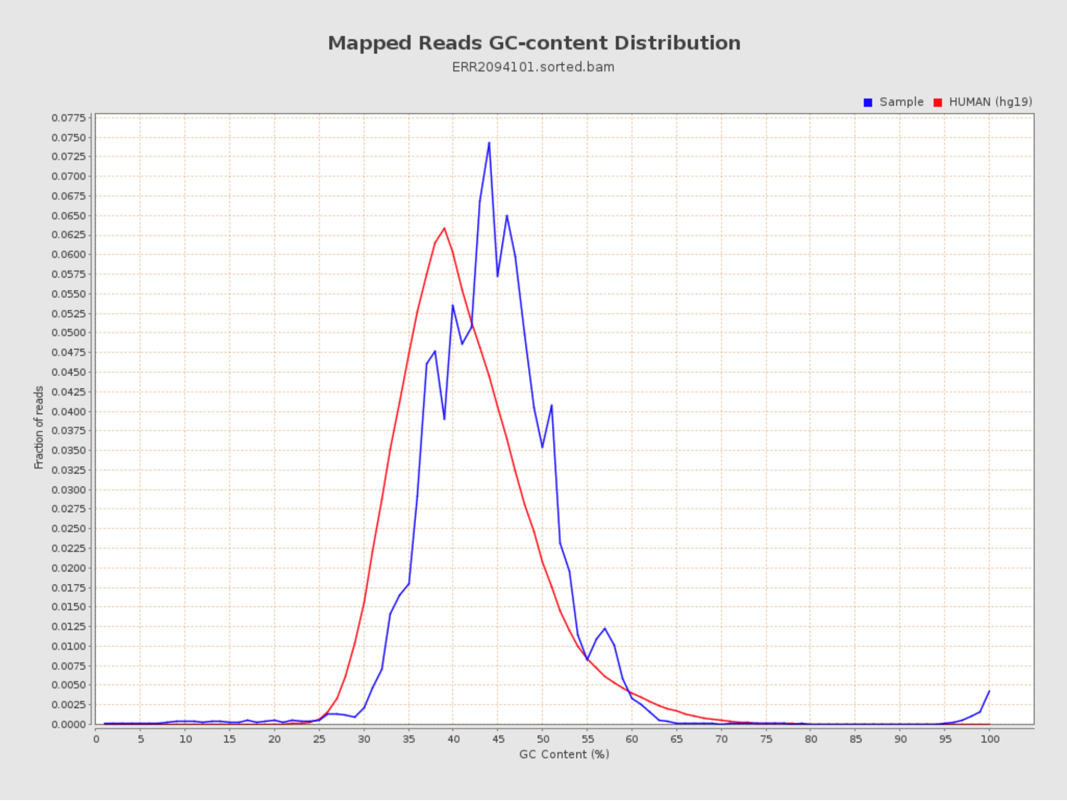
7. Results : Duplication Rate Histogram



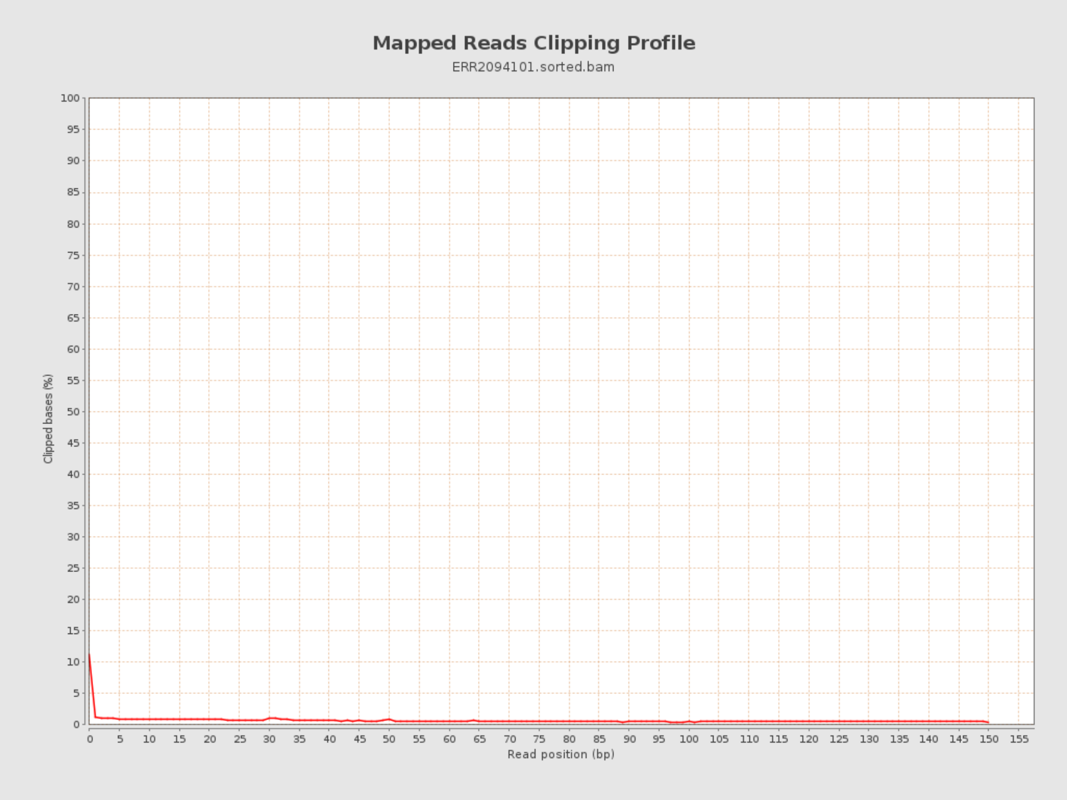
8. Results : Mapped Reads Nucleotide Content



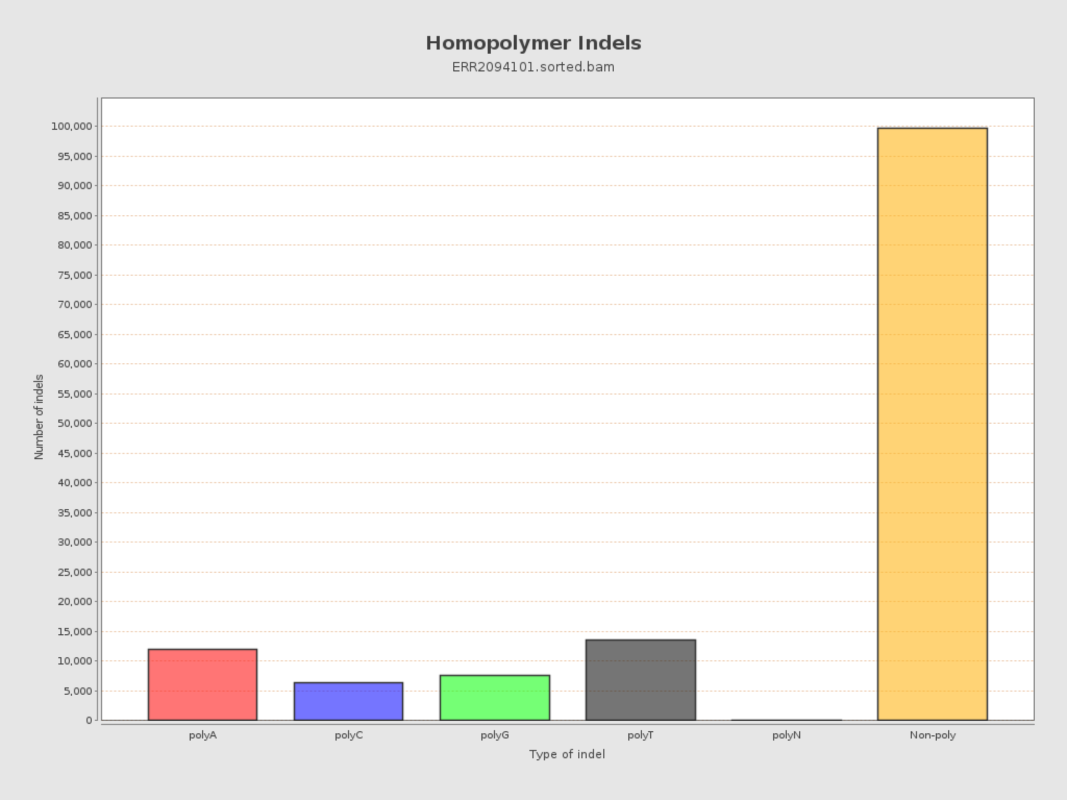
9. Results : Mapped Reads GC-content Distribution



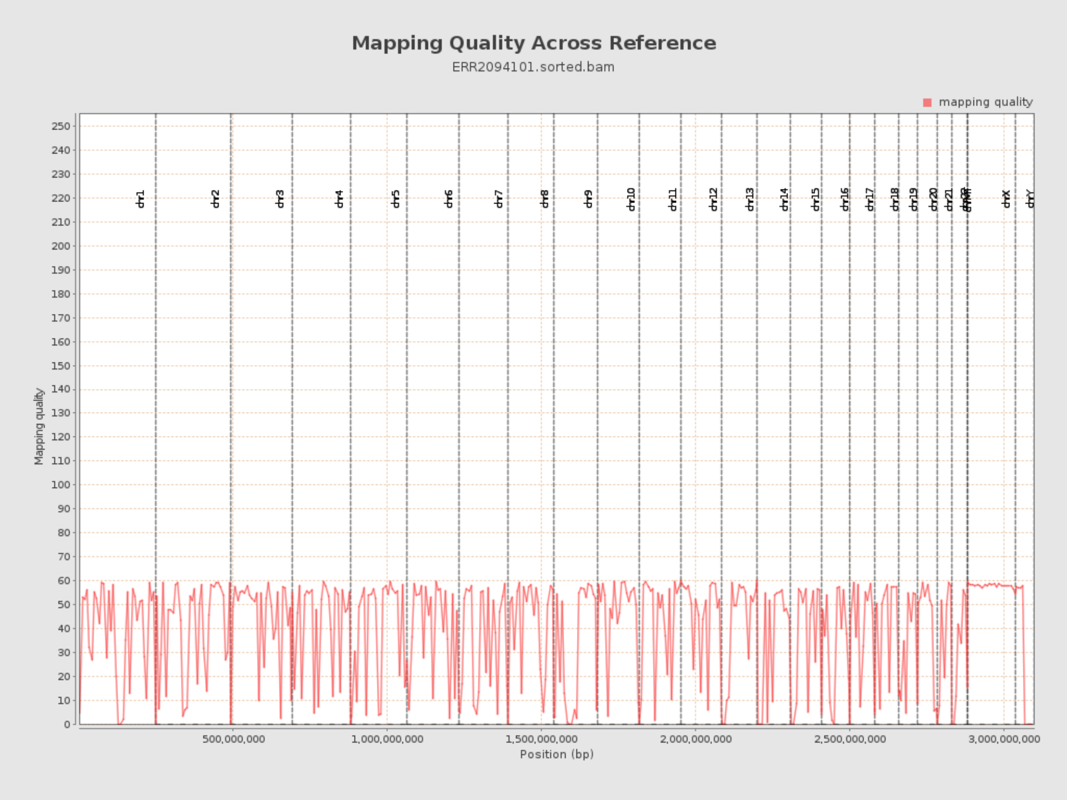
10. Results : Mapped Reads Clipping Profile



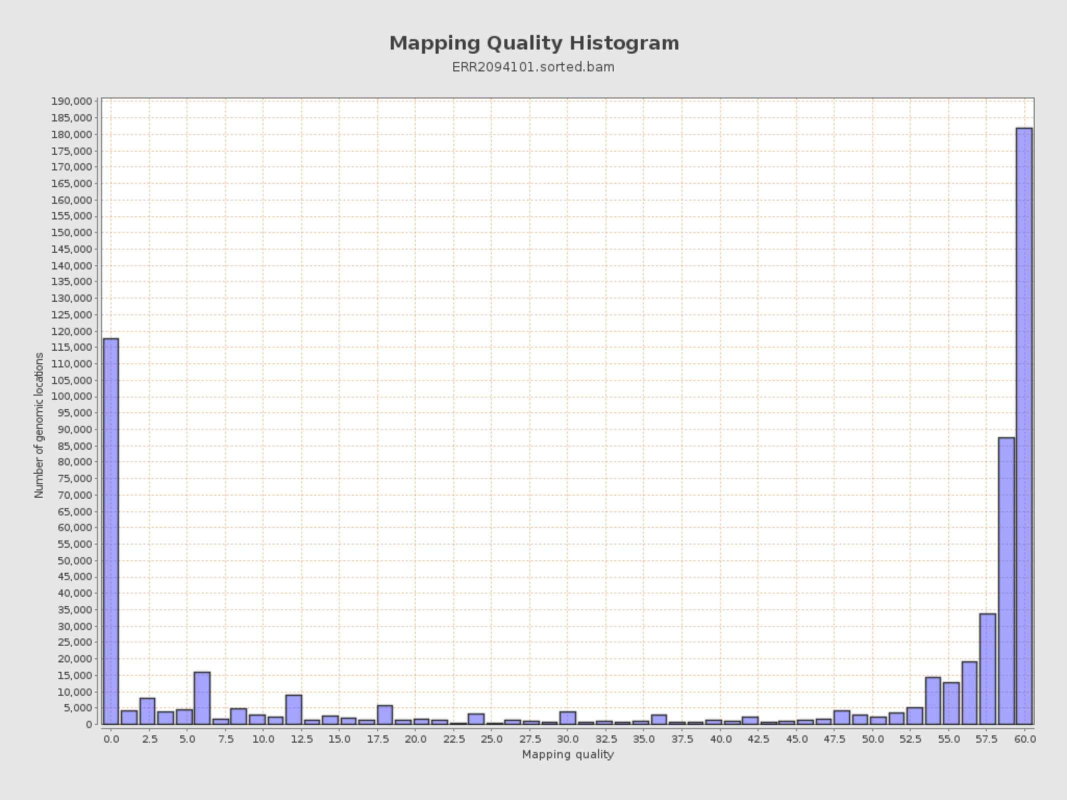
11. Results : Homopolymer Indels



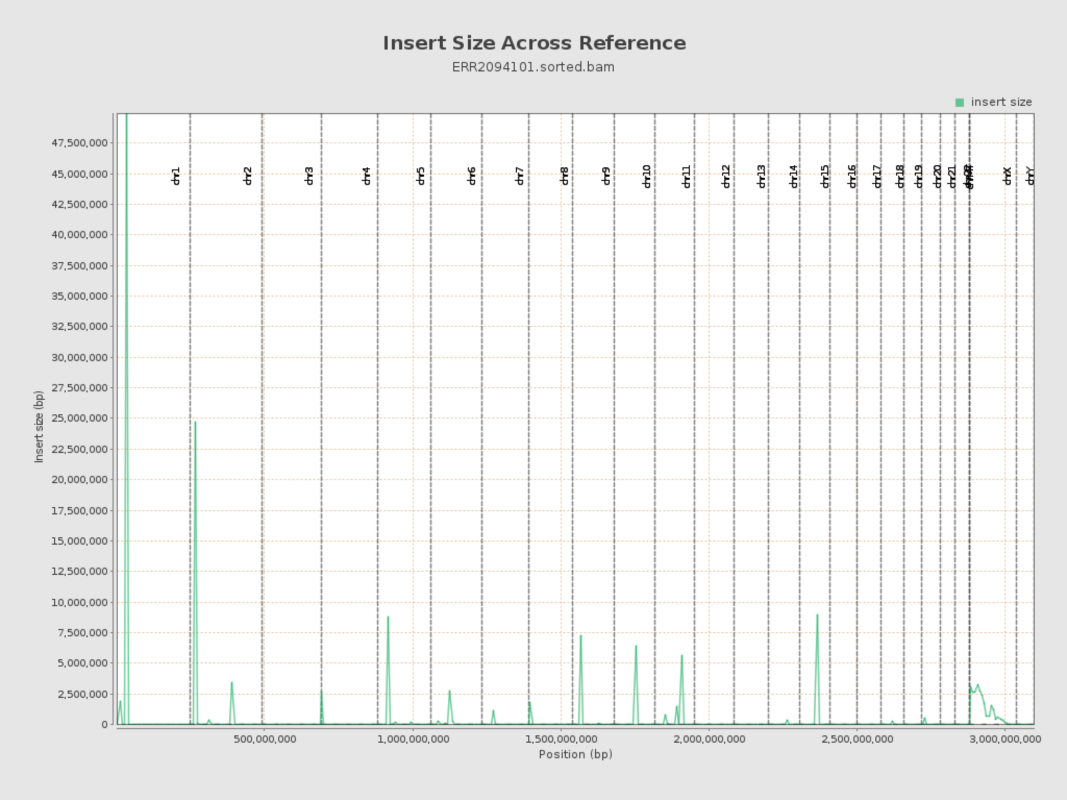
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram