Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:05:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094100.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_ERR2094100 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094100_1.fastq.gz ERR2094100_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:05:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	379,056
Mapped reads	355,390 / 93.76%
Unmapped reads	23,666 / 6.24%
Mapped paired reads	355,390 / 93.76%
Mapped reads, first in pair	178,479 / 47.09%
Mapped reads, second in pair	176,911 / 46.67%
Mapped reads, both in pair	352,568 / 93.01%
Mapped reads, singletons	2,822 / 0.74%
Secondary alignments	0
Supplementary alignments	25,204 / 6.65%
Read min/max/mean length	30 / 151 / 138.65
Duplicated reads (estimated)	335,149 / 88.42%
Duplication rate	50.16%
Clipped reads	187,110 / 49.36%

2.2. ACGT Content

Number/percentage of A's	13,031,089 / 29.53%
Number/percentage of C's	9,170,020 / 20.78%
Number/percentage of T's	12,197,898 / 27.64%
Number/percentage of G's	9,735,420 / 22.06%
Number/percentage of N's	442 / 0%

GC Percentage	42.84%

2.3. Coverage

Mean	0.0145
Standard Deviation	2.7755

2.4. Mapping Quality

Mean Mapping Quality	41.3

2.5. Insert size

Mean	1,629,509.03
Standard Deviation	11,208,662.4
P25/Median/P75	121 / 155 / 184

2.6. Mismatches and indels

General error rate	3.66%
Mismatches	1,549,759
Insertions	30,427
Mapped reads with at least one insertion	8.41%
Deletions	126,382
Mapped reads with at least one deletion	34.2%
Homopolymer indels	28.42%

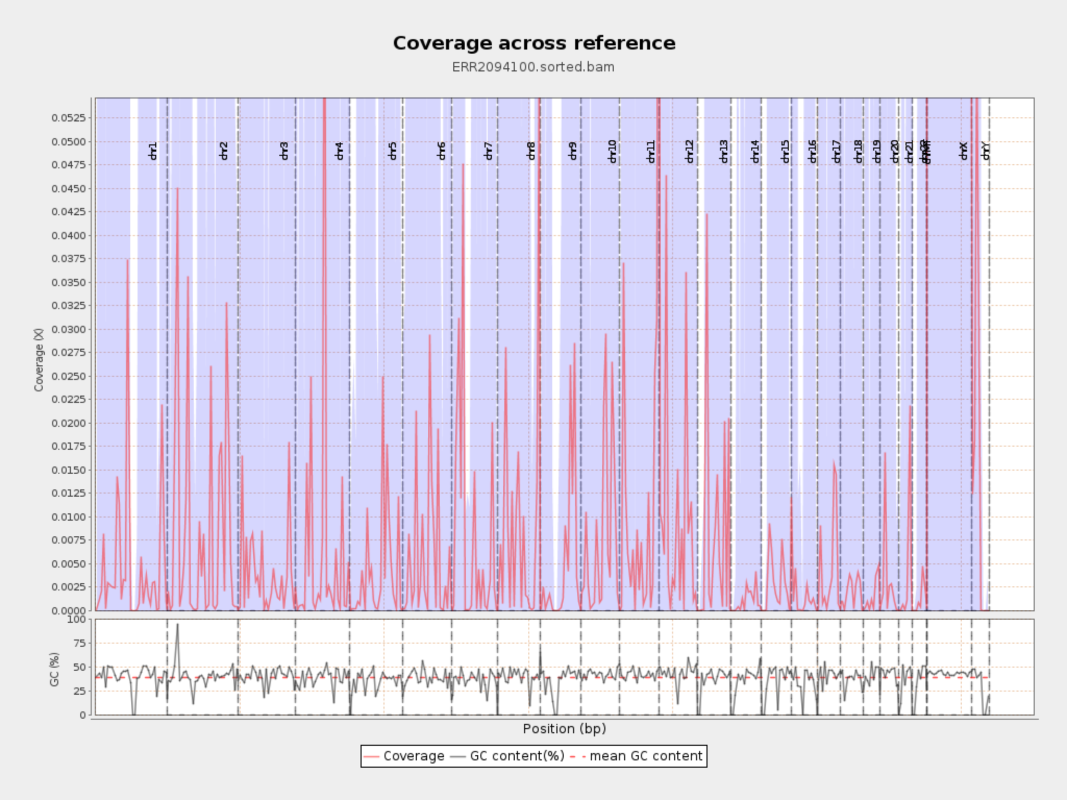
2.7. Chromosome stats

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

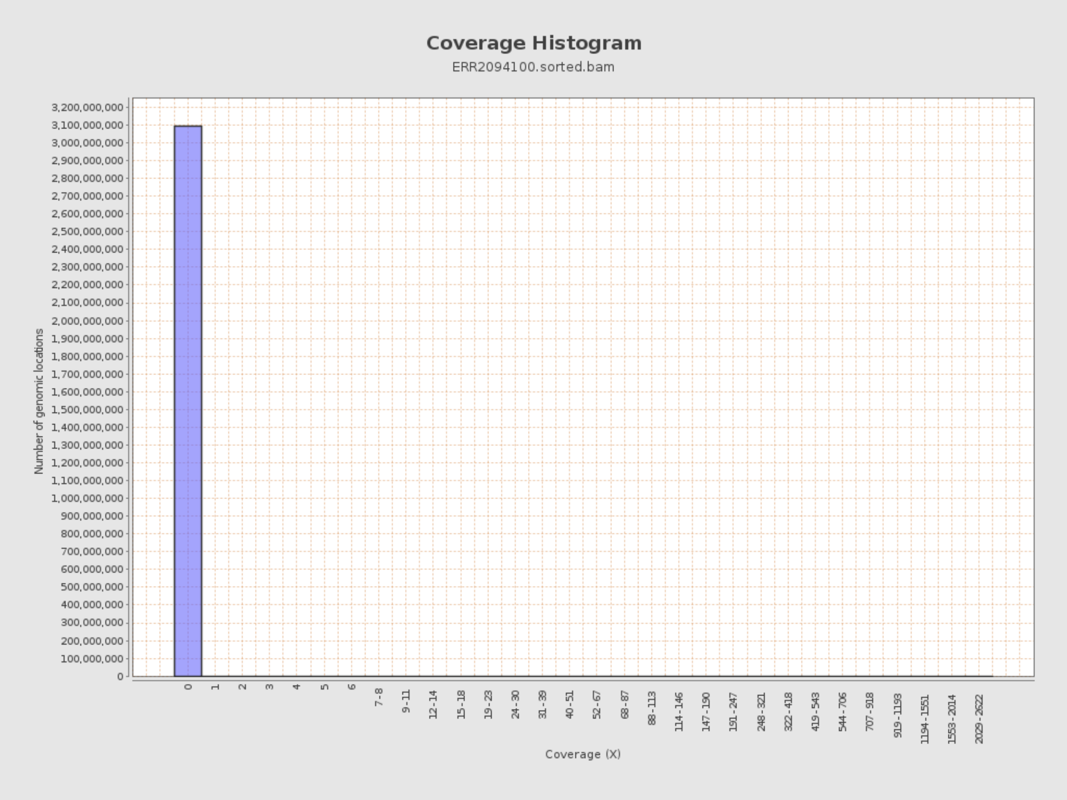
		bases	coverage	deviation
chr1	249250621	1112835	0.0045	1.6341
chr2	243199373	2048536	0.0084	2.3373
chr3	198022430	790036	0.004	1.1499
chr4	191154276	1365209	0.0071	1.9305
chr5	180915260	806148	0.0045	1.6539
chr6	171115067	1008508	0.0059	1.5982
chr7	159138663	1236042	0.0078	2.3337
chr8	146364022	1284620	0.0088	2.8767
chr9	141213431	714290	0.0051	1.5026
chr10	135534747	1024097	0.0076	2.1328
chr11	135006516	1323889	0.0098	2.3091
chr12	133851895	1272706	0.0095	2.5639
chr13	115169878	930292	0.0081	1.9914
chr14	107349540	117084	0.0011	0.3044
chr15	102531392	272795	0.0027	0.5938
chr16	90354753	153433	0.0017	0.6588
chr17	81195210	369129	0.0045	1.2018
chr18	78077248	165065	0.0021	0.4773
chr19	59128983	89189	0.0015	0.4111
chr20	63025520	199859	0.0032	1.3155
chr21	48129895	201240	0.0042	1.236
chr22	51304566	60670	0.0012	0.3049
chrMT	16571	838230	50.5842	241.4306
chrX	155270560	26731748	0.1722	9.0932

chrY	59373566	908674	0.0153	3.2033

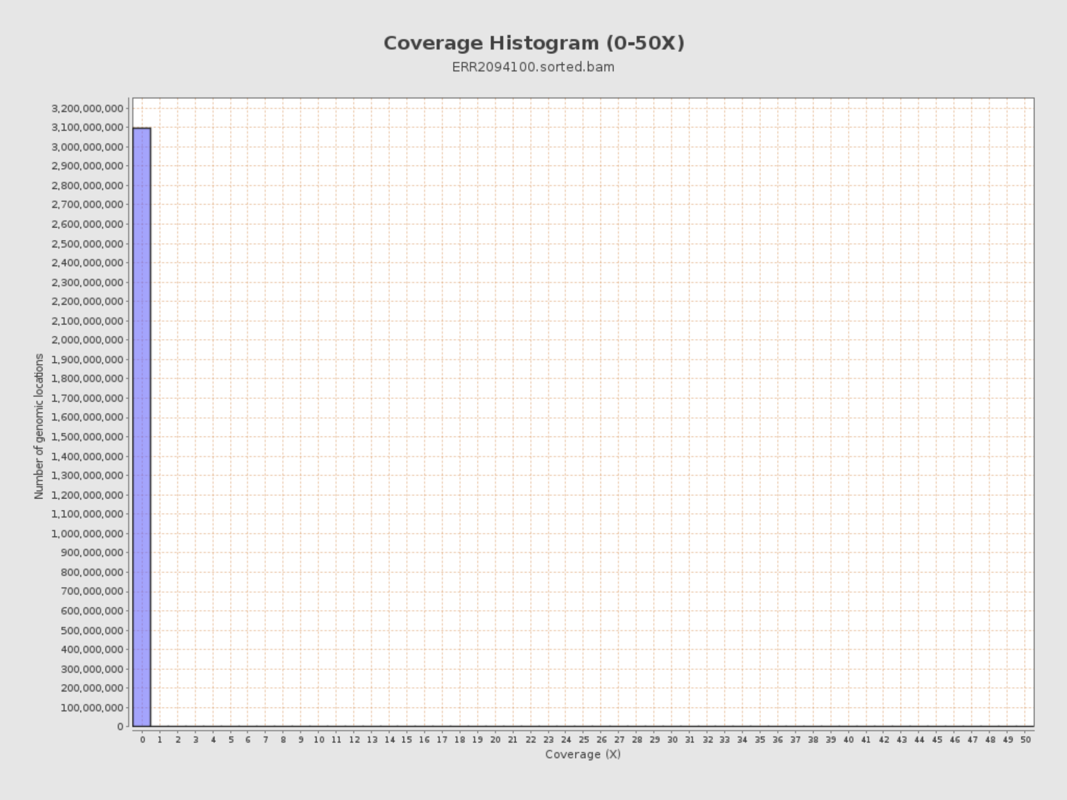
3. Results : Coverage across reference



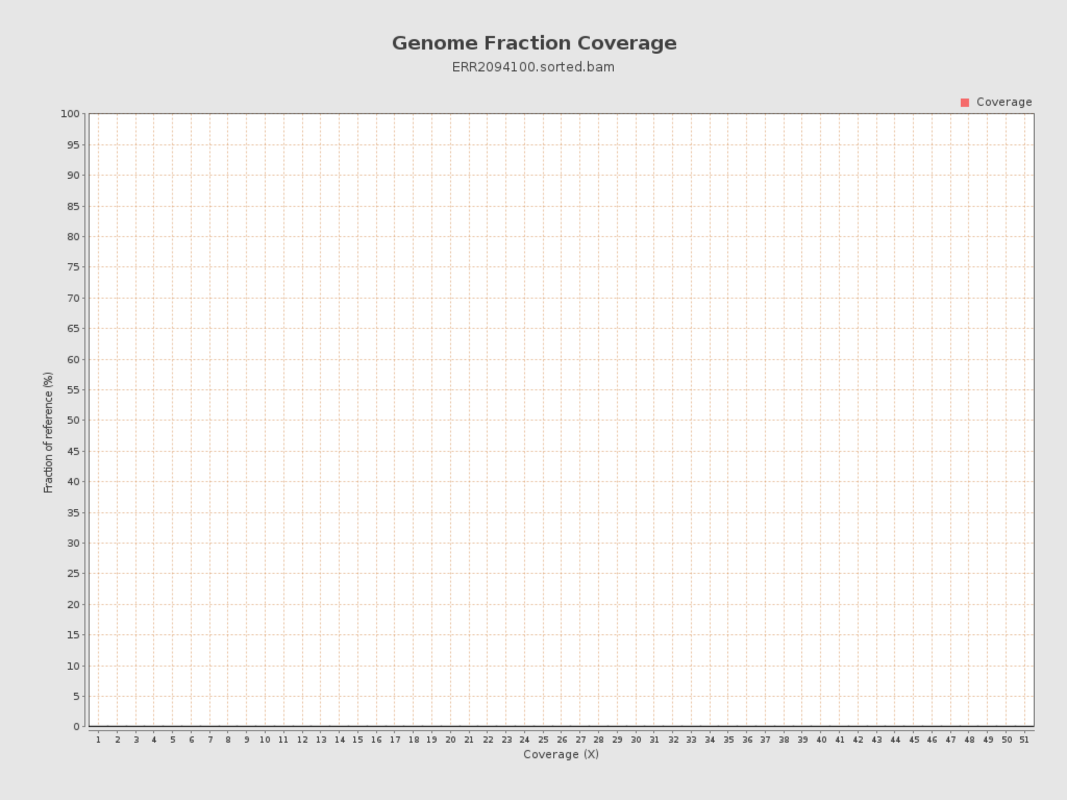
4. Results : Coverage Histogram



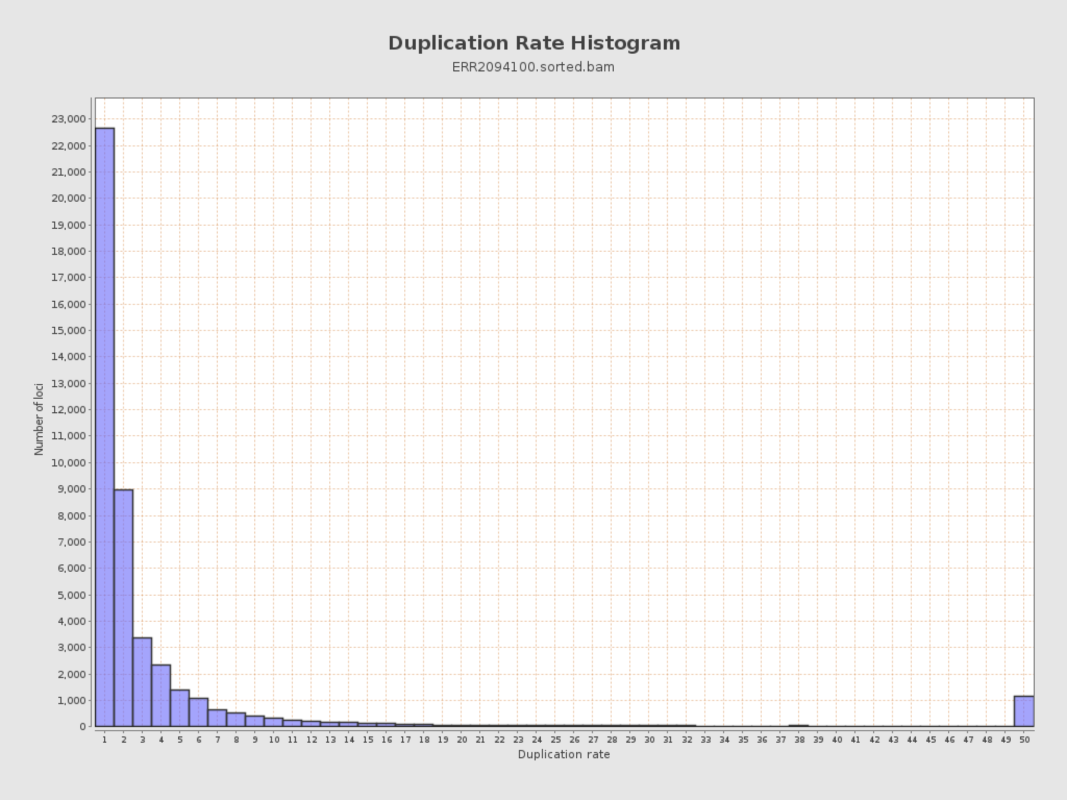
5. Results : Coverage Histogram (0-50X)



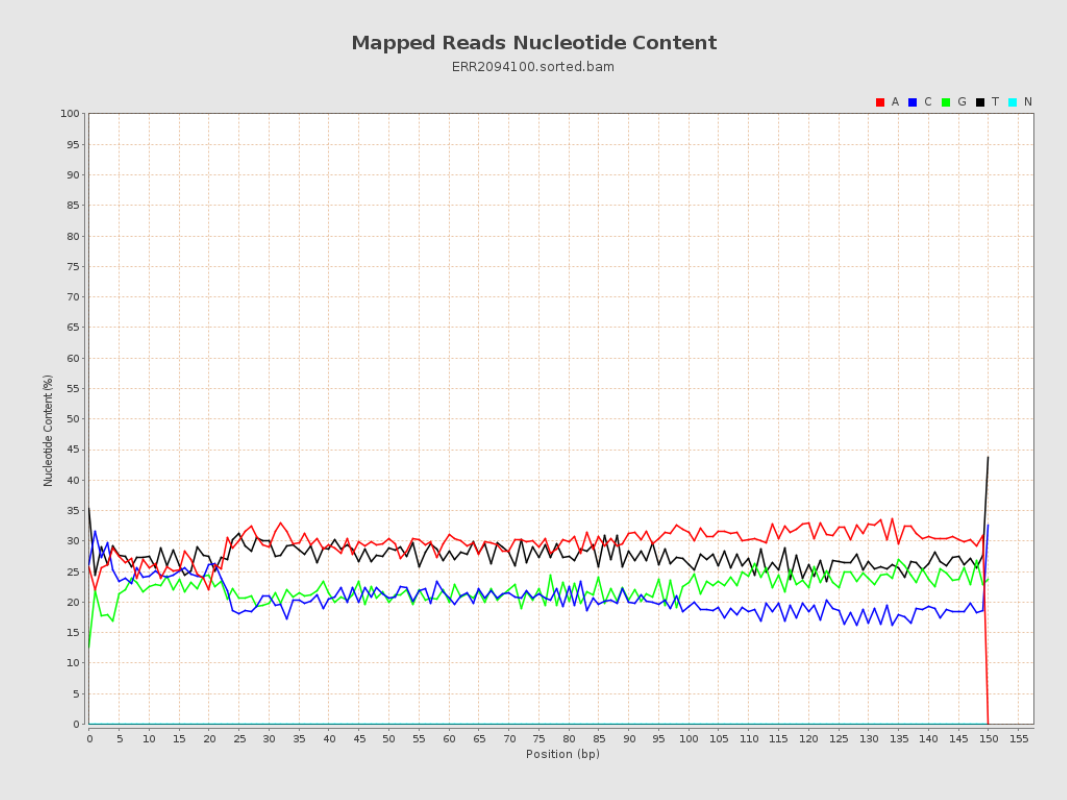
6. Results : Genome Fraction Coverage



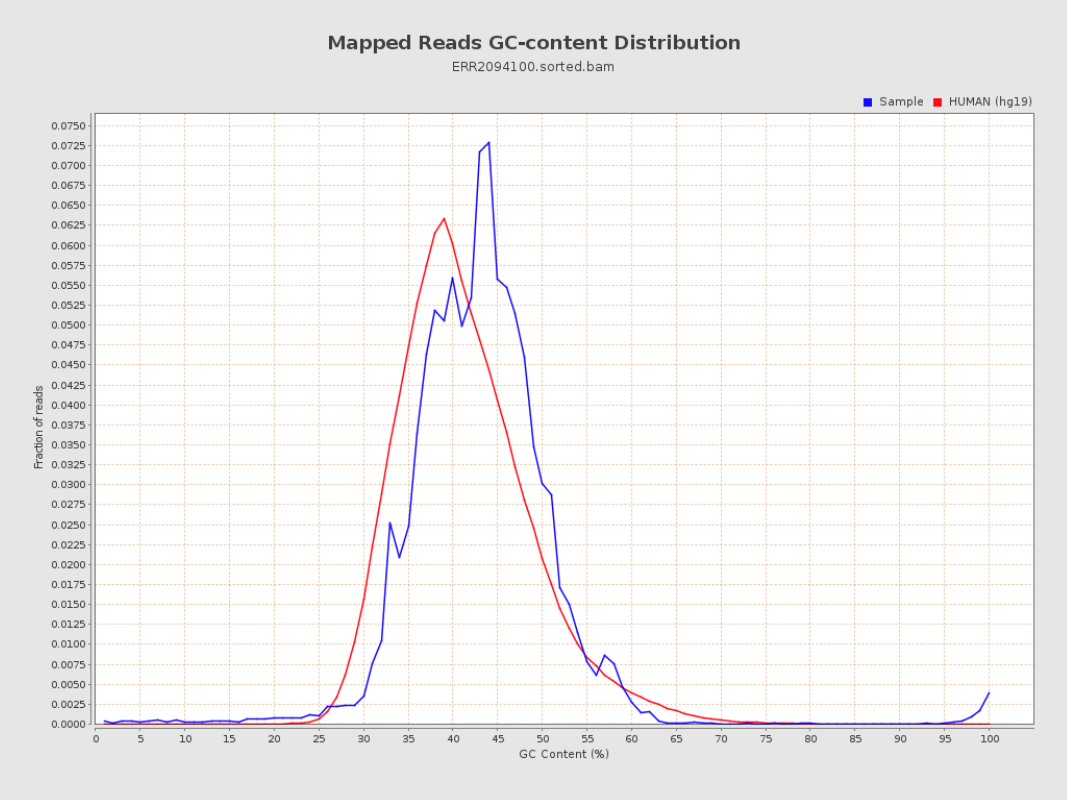
7. Results : Duplication Rate Histogram



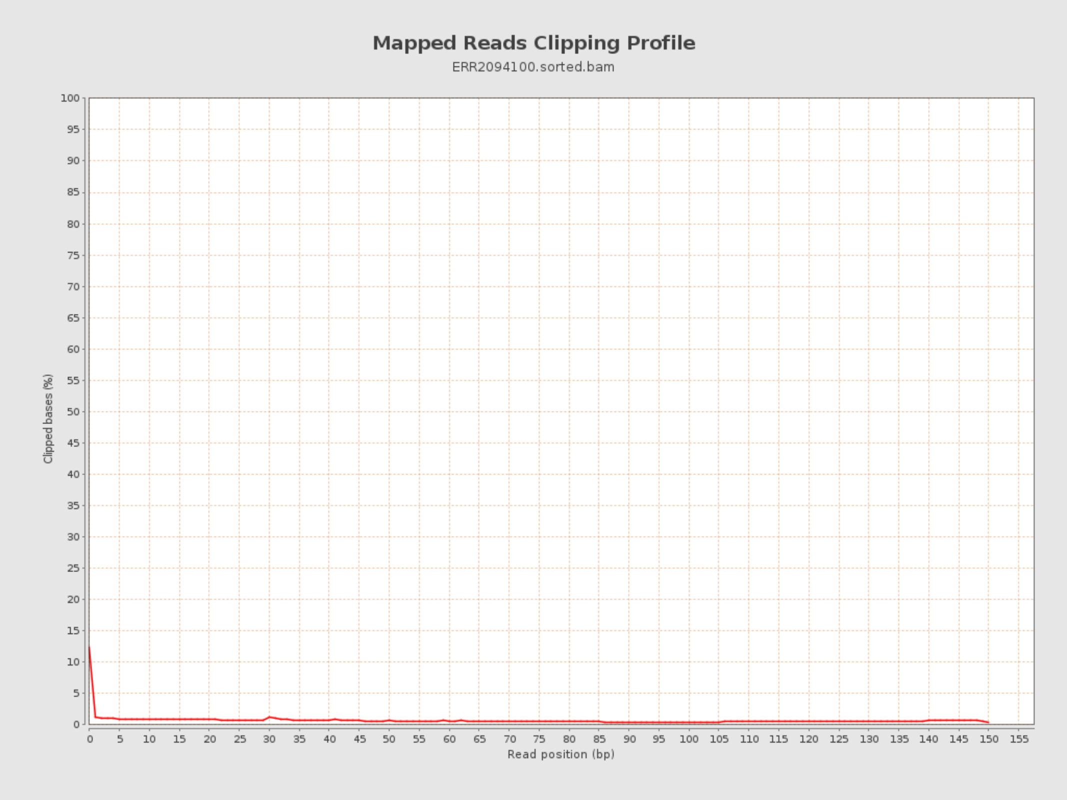
8. Results : Mapped Reads Nucleotide Content



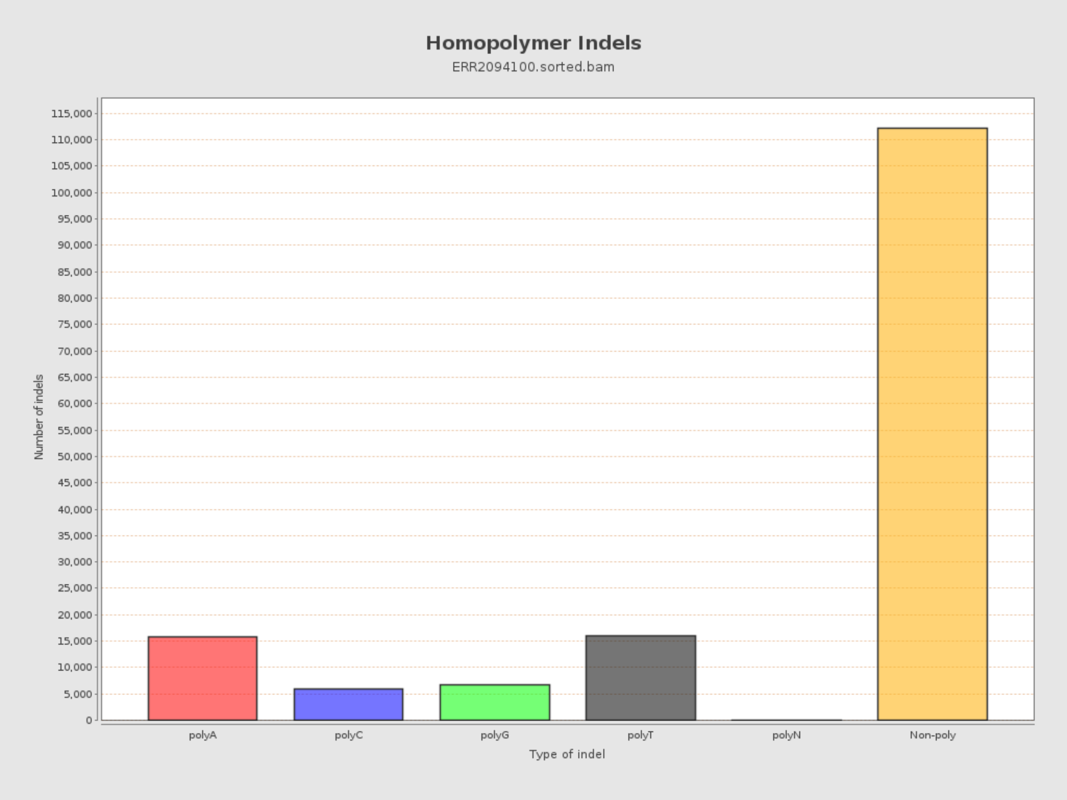
9. Results : Mapped Reads GC-content Distribution



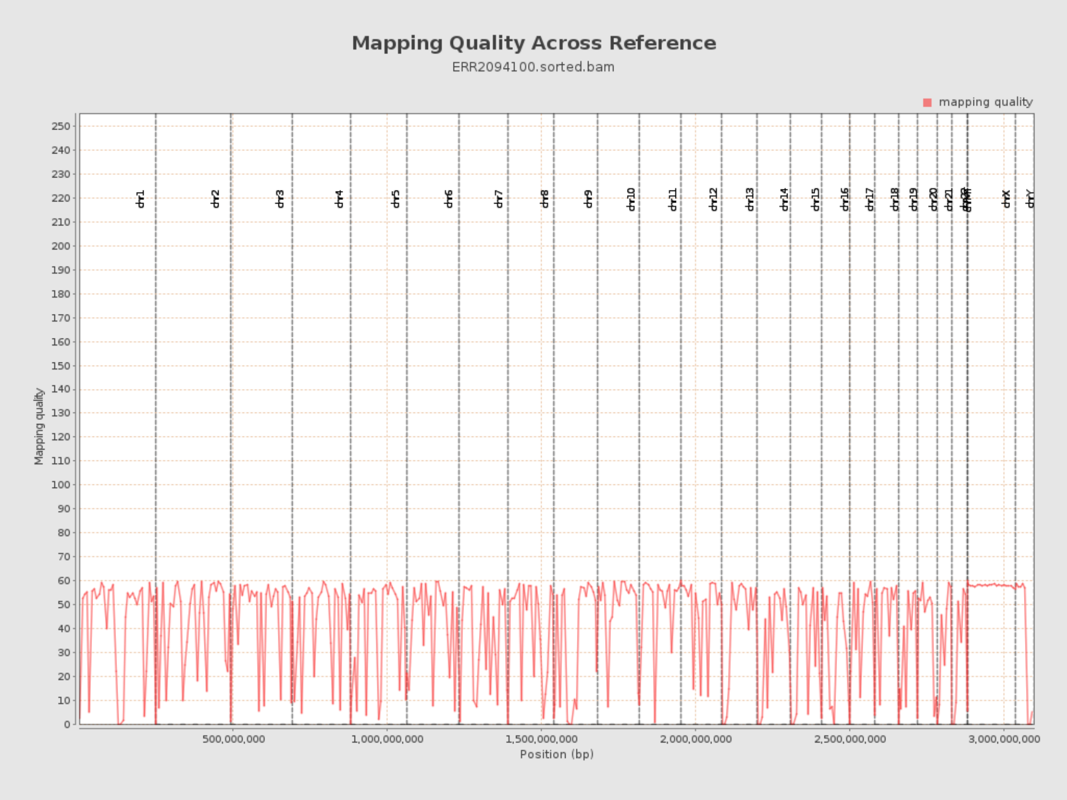
10. Results : Mapped Reads Clipping Profile



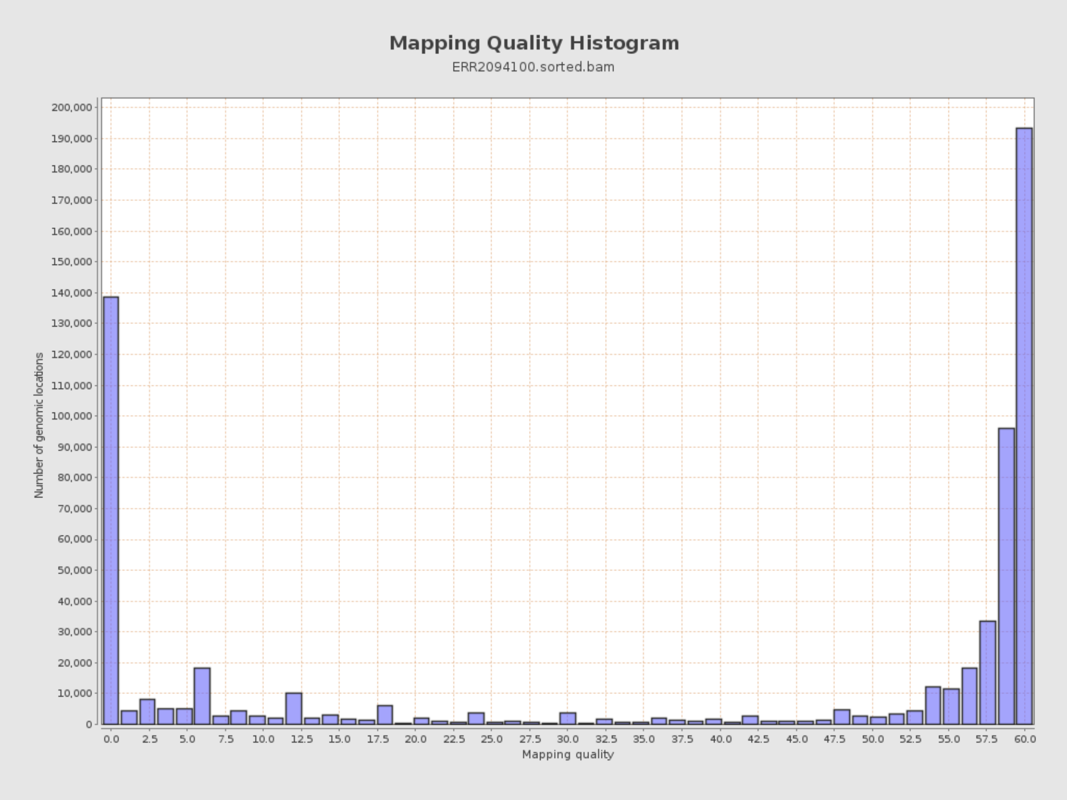
11. Results : Homopolymer Indels



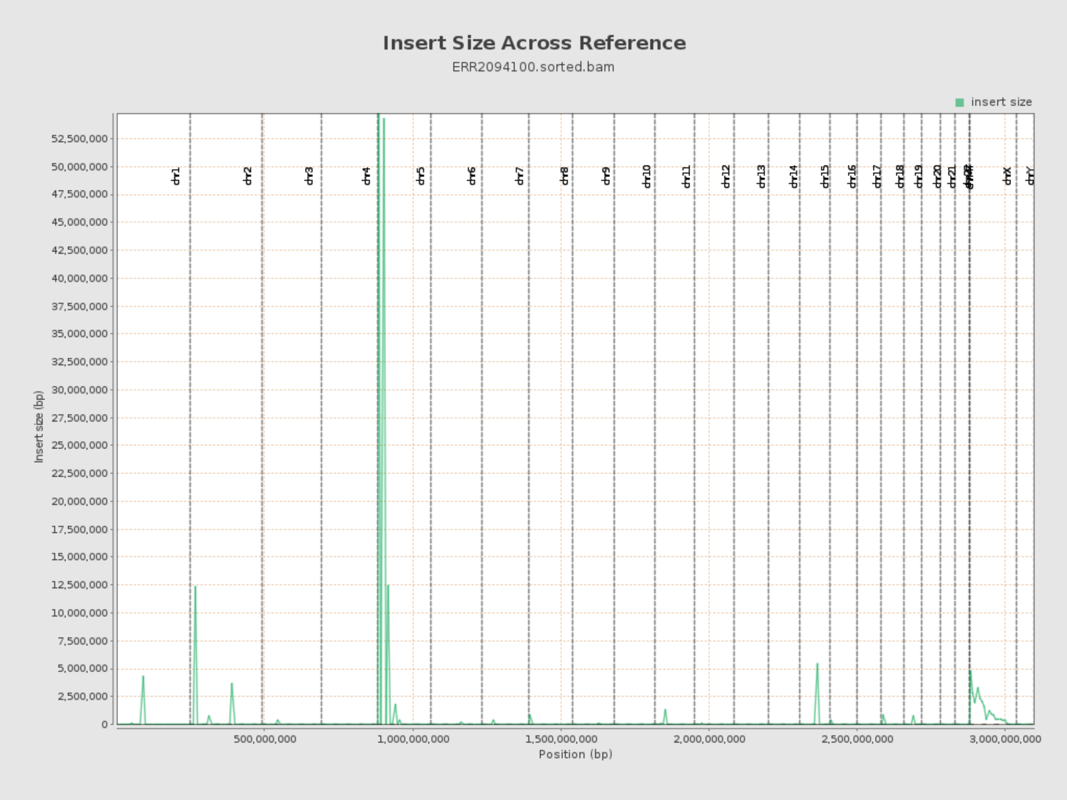
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram