Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:28:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094053.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_ERR2094053 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094053_1.fastq.gz ERR2094053_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:28:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	383,550
Mapped reads	352,712 / 91.96%
Unmapped reads	30,838 / 8.04%
Mapped paired reads	352,712 / 91.96%
Mapped reads, first in pair	177,131 / 46.18%
Mapped reads, second in pair	175,581 / 45.78%
Mapped reads, both in pair	349,856 / 91.22%
Mapped reads, singletons	2,856 / 0.74%
Secondary alignments	0
Supplementary alignments	11,471 / 2.99%
Read min/max/mean length	30 / 151 / 134.99
Duplicated reads (estimated)	329,261 / 85.85%
Duplication rate	49.92%
Clipped reads	142,304 / 37.1%

2.2. ACGT Content

Number/percentage of A's	12,431,036 / 27.7%
Number/percentage of C's	10,013,138 / 22.32%
Number/percentage of T's	11,963,090 / 26.66%
Number/percentage of G's	10,463,619 / 23.32%
Number/percentage of N's	674 / 0%

GC Percentage	45.63%

2.3. Coverage

Mean	0.0149
Standard Deviation	3.2963

2.4. Mapping Quality

Mean Mapping Quality	43.7

2.5. Insert size

Mean	488,176.94
Standard Deviation	6,255,494.56
P25/Median/P75	128 / 166 / 197

2.6. Mismatches and indels

General error rate	4.63%
Mismatches	2,027,640
Insertions	32,645
Mapped reads with at least one insertion	9.05%
Deletions	163,067
Mapped reads with at least one deletion	42.89%
Homopolymer indels	29.84%

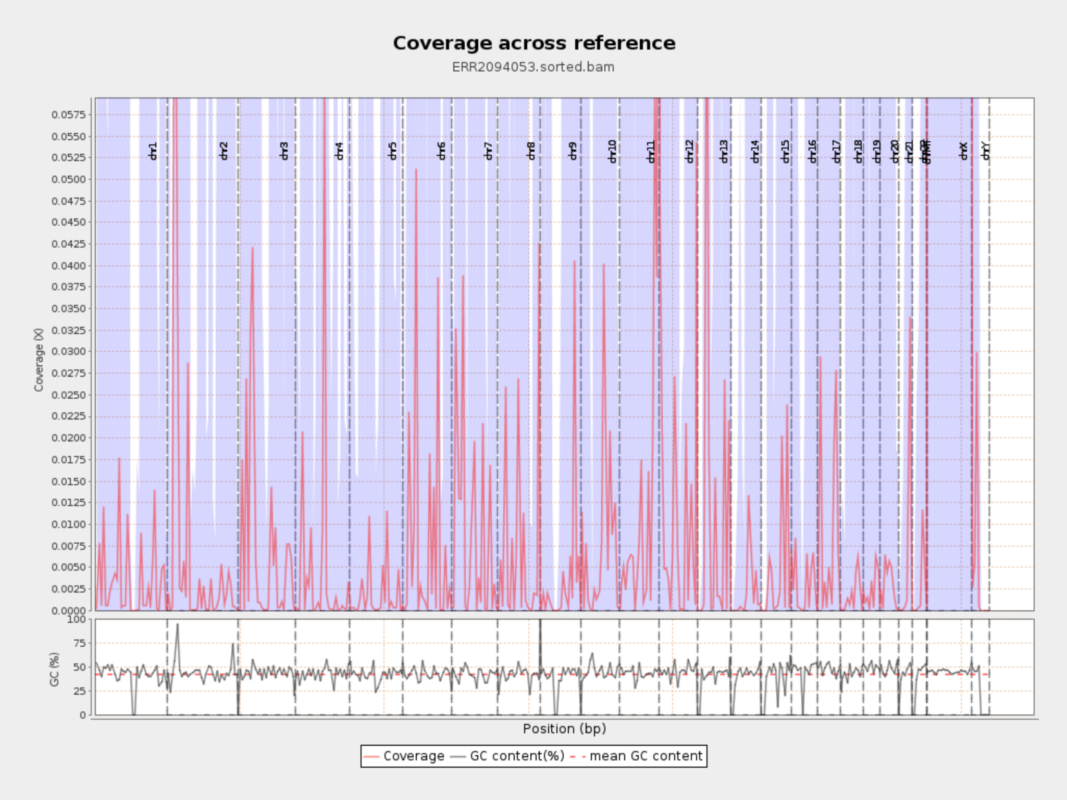
2.7. Chromosome stats

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

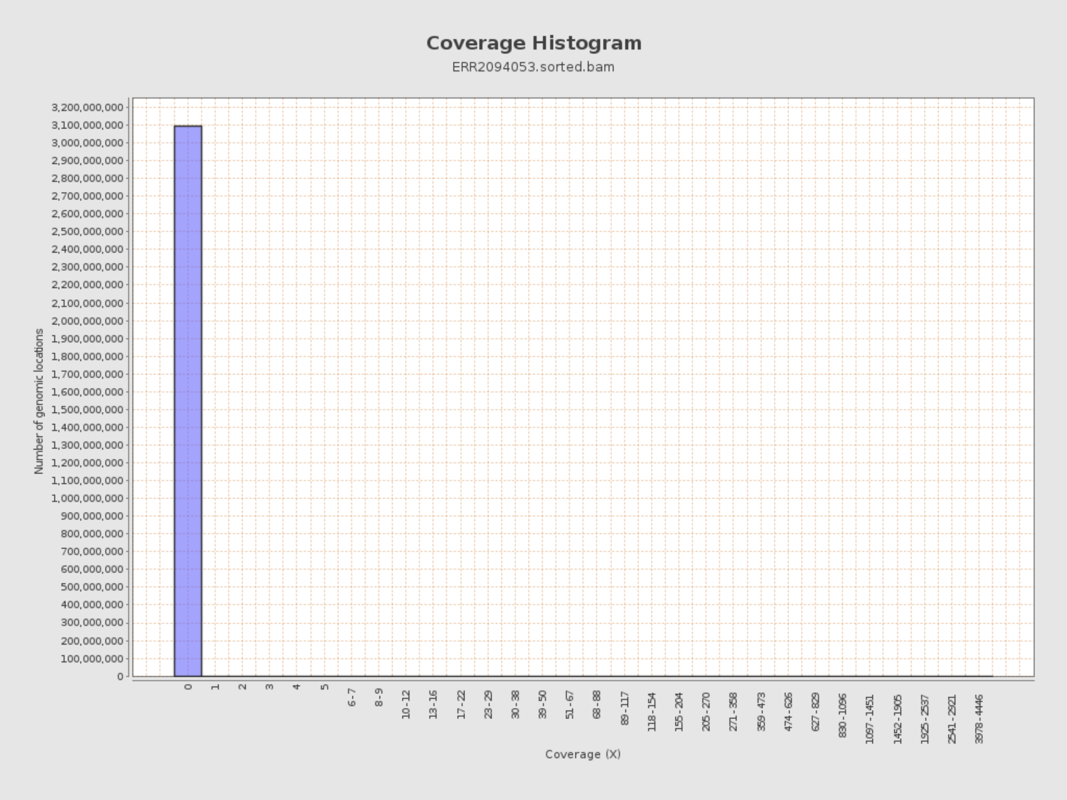
		bases	coverage	deviation
chr1	249250621	843583	0.0034	1.1622
chr2	243199373	1646915	0.0068	2.2117
chr3	198022430	1409750	0.0071	2.0747
chr4	191154276	920918	0.0048	2.2697
chr5	180915260	349097	0.0019	0.7076
chr6	171115067	1371732	0.008	3.4803
chr7	159138663	1378280	0.0087	2.6597
chr8	146364022	999872	0.0068	2.3464
chr9	141213431	548893	0.0039	1.635
chr10	135534747	1088456	0.008	2.4405
chr11	135006516	1730662	0.0128	3.121
chr12	133851895	1394423	0.0104	2.6978
chr13	115169878	1317774	0.0114	3.0117
chr14	107349540	242156	0.0023	0.9357
chr15	102531392	457056	0.0045	1.7154
chr16	90354753	274252	0.003	0.8142
chr17	81195210	739243	0.0091	2.6393
chr18	78077248	142969	0.0018	0.52
chr19	59128983	140879	0.0024	0.4907
chr20	63025520	197342	0.0031	0.7719
chr21	48129895	327512	0.0068	2.2395
chr22	51304566	116507	0.0023	0.887
chrMT	16571	2057520	124.1639	518.4308
chrX	155270560	26125441	0.1683	9.9703

chrY	59373566	290801	0.0049	1.5197

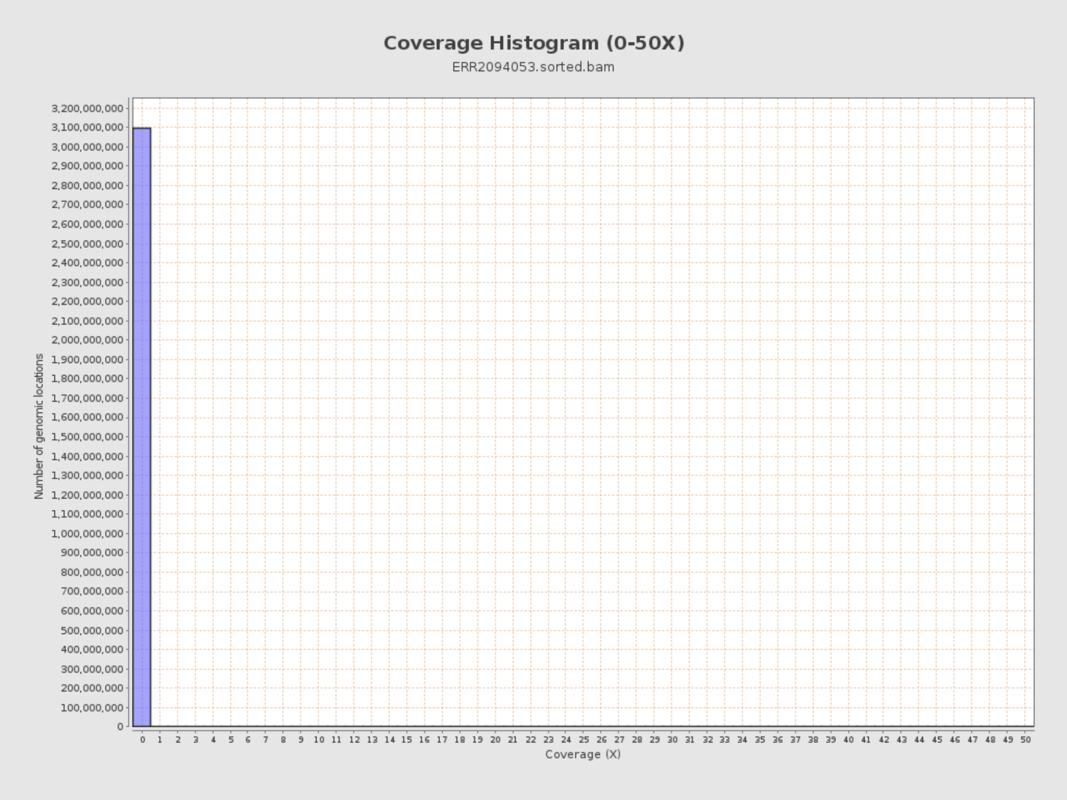
3. Results : Coverage across reference



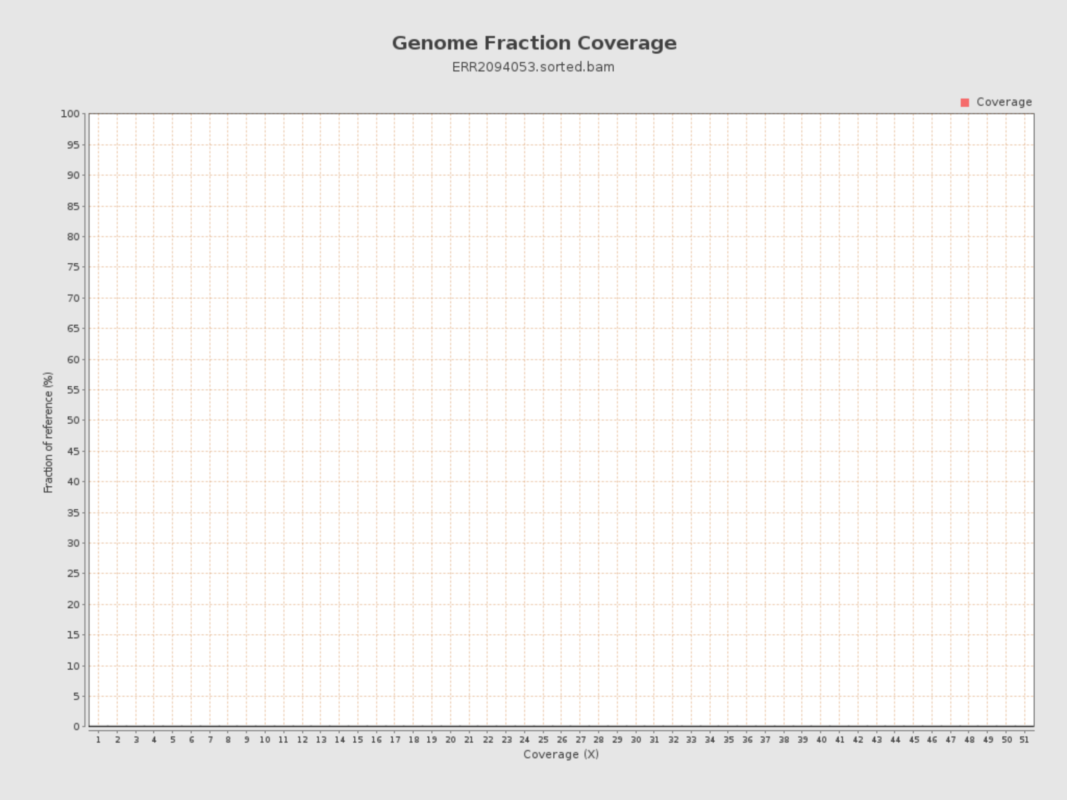
4. Results : Coverage Histogram



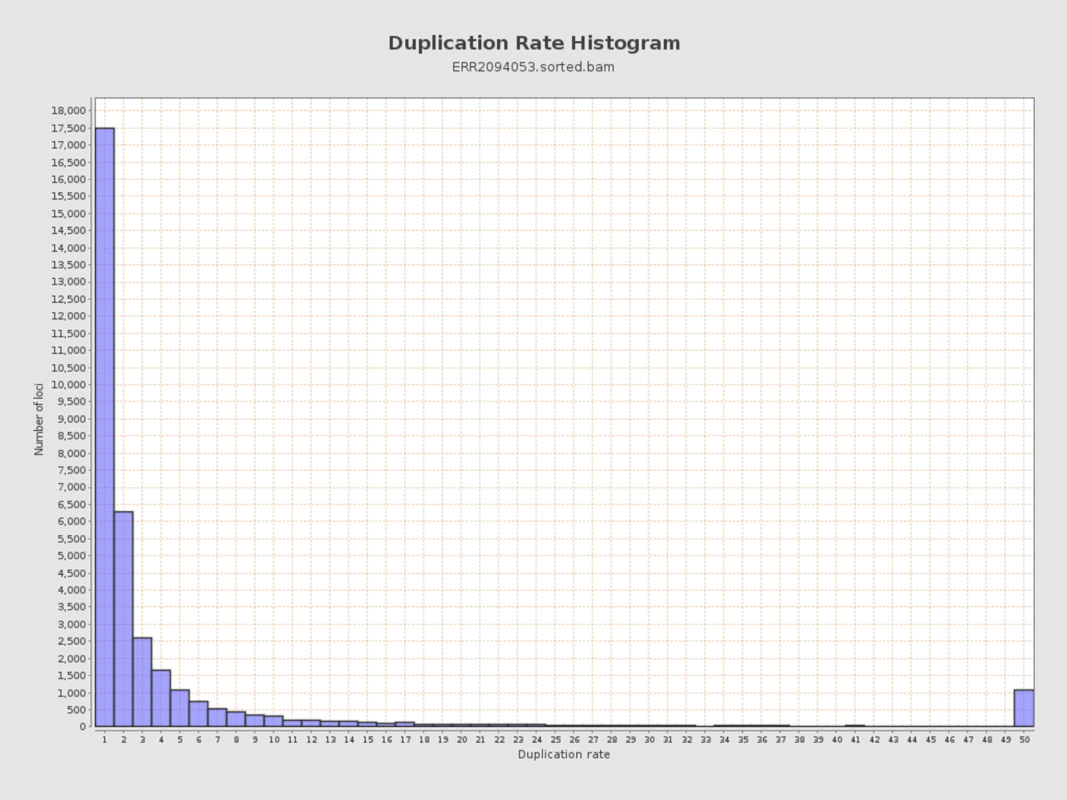
5. Results : Coverage Histogram (0-50X)



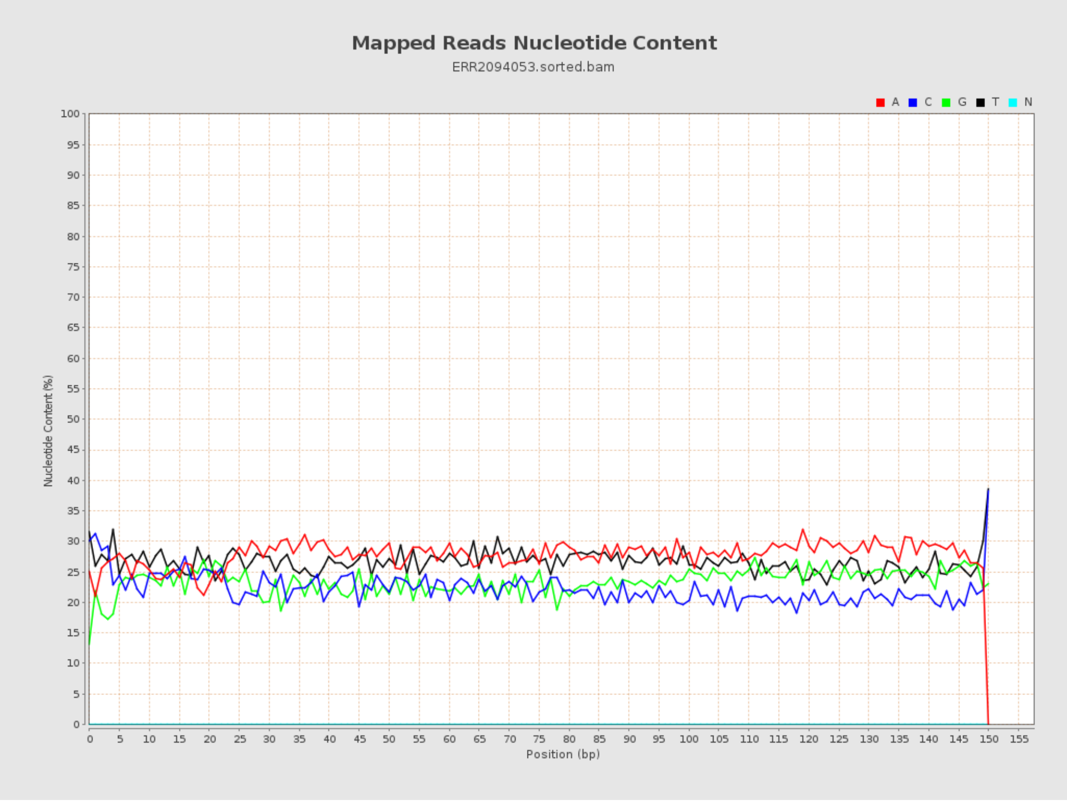
6. Results : Genome Fraction Coverage



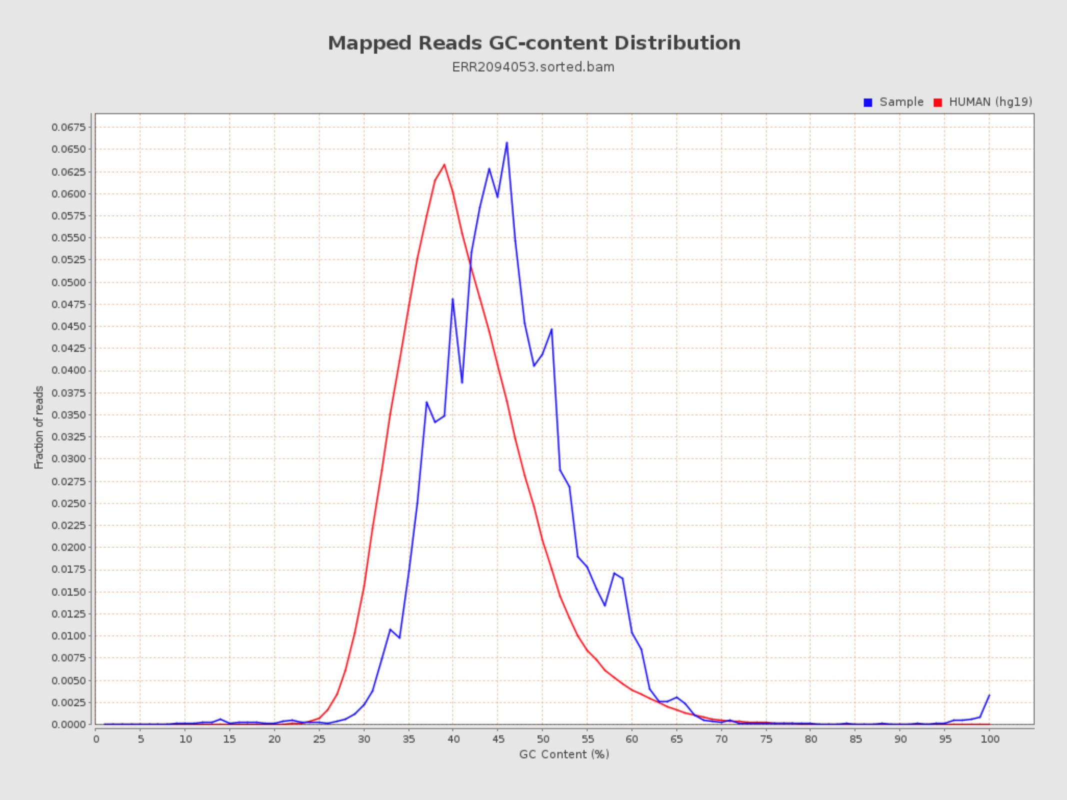
7. Results : Duplication Rate Histogram



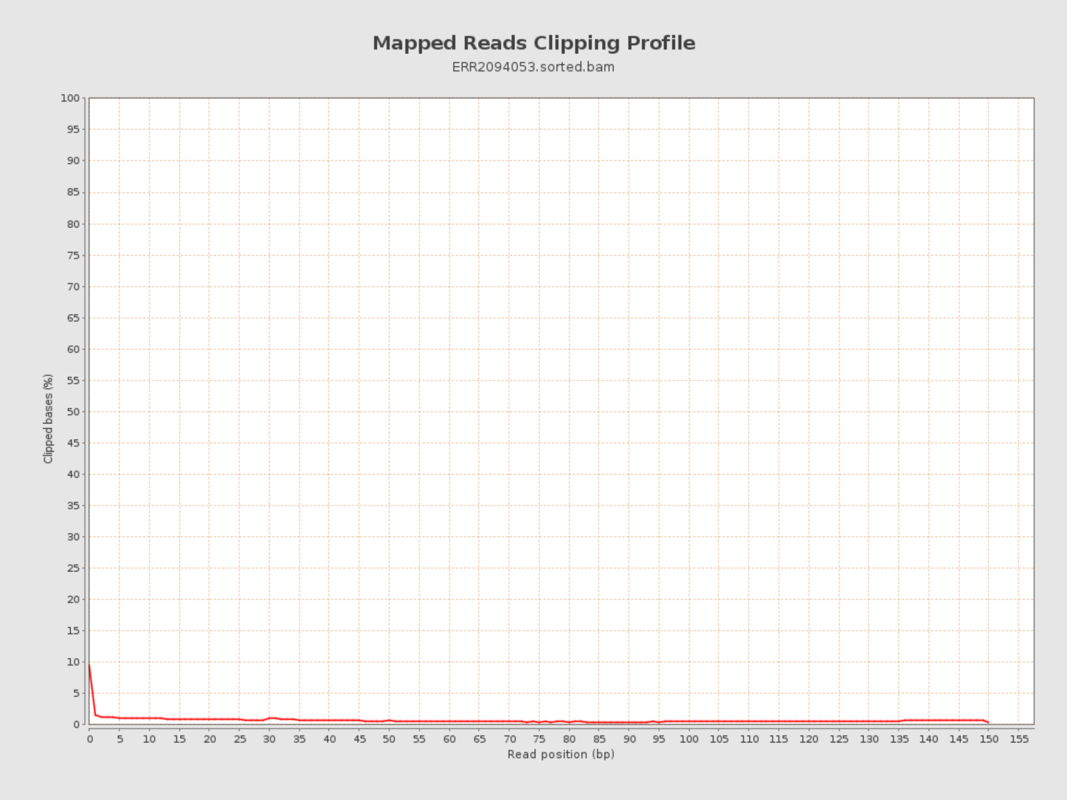
8. Results : Mapped Reads Nucleotide Content



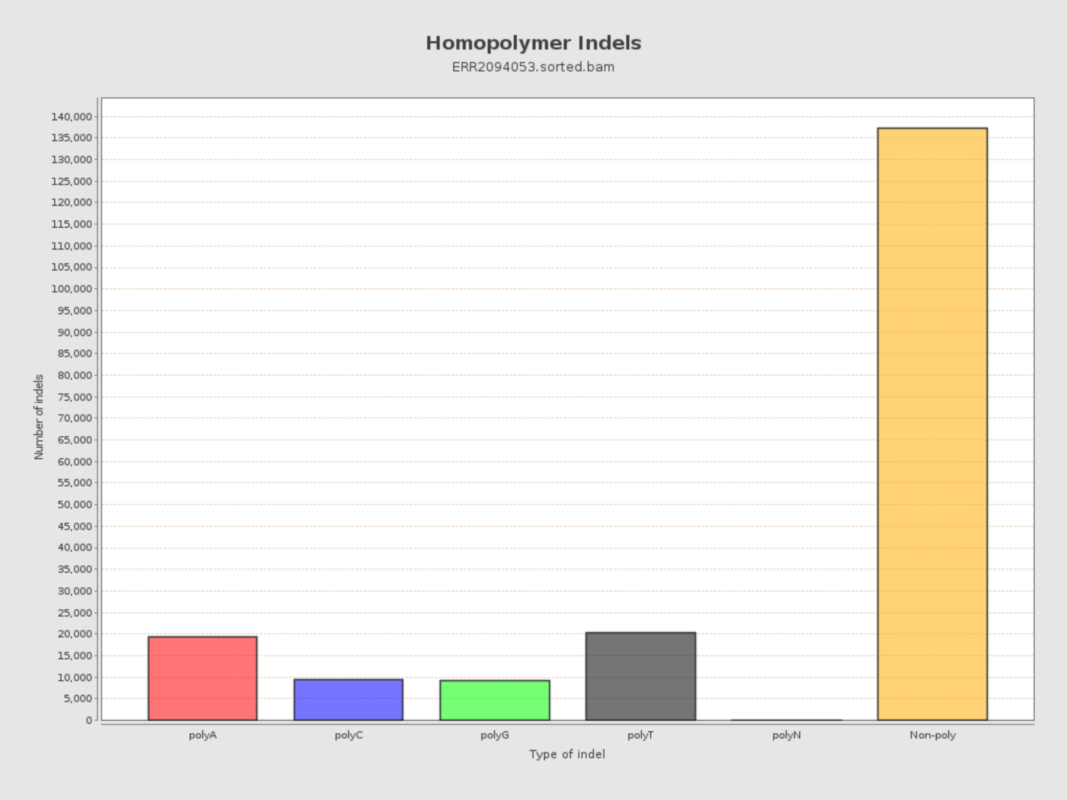
9. Results : Mapped Reads GC-content Distribution



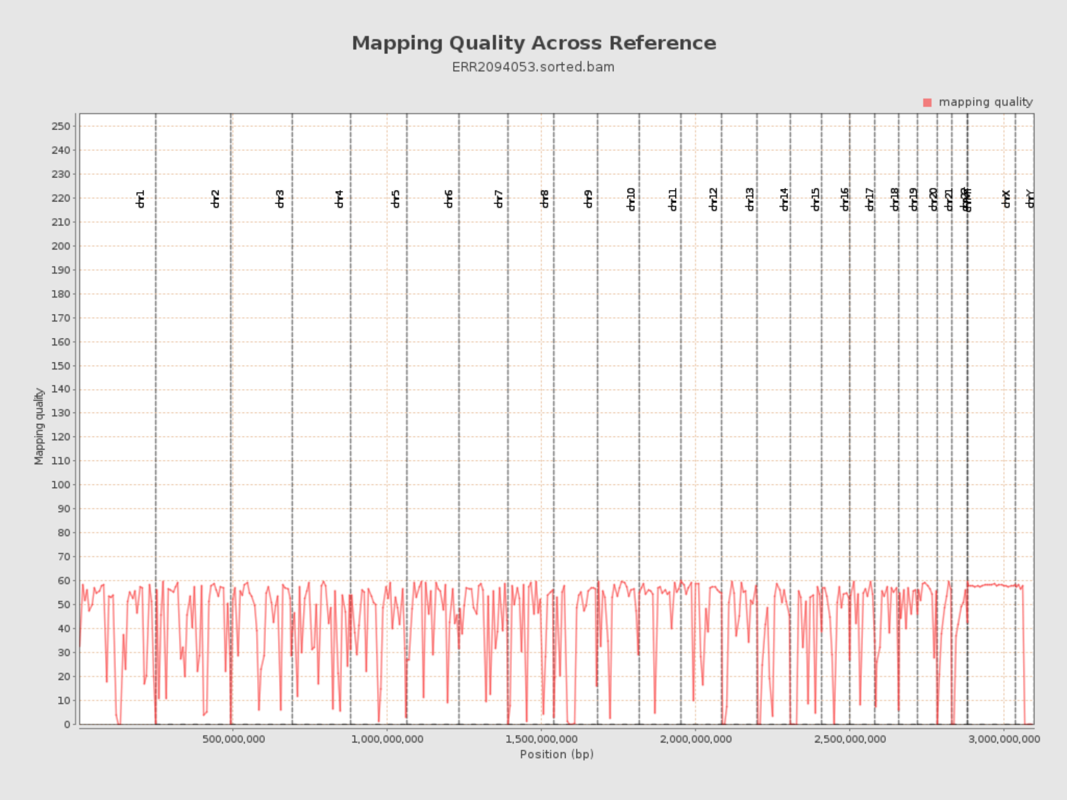
10. Results : Mapped Reads Clipping Profile



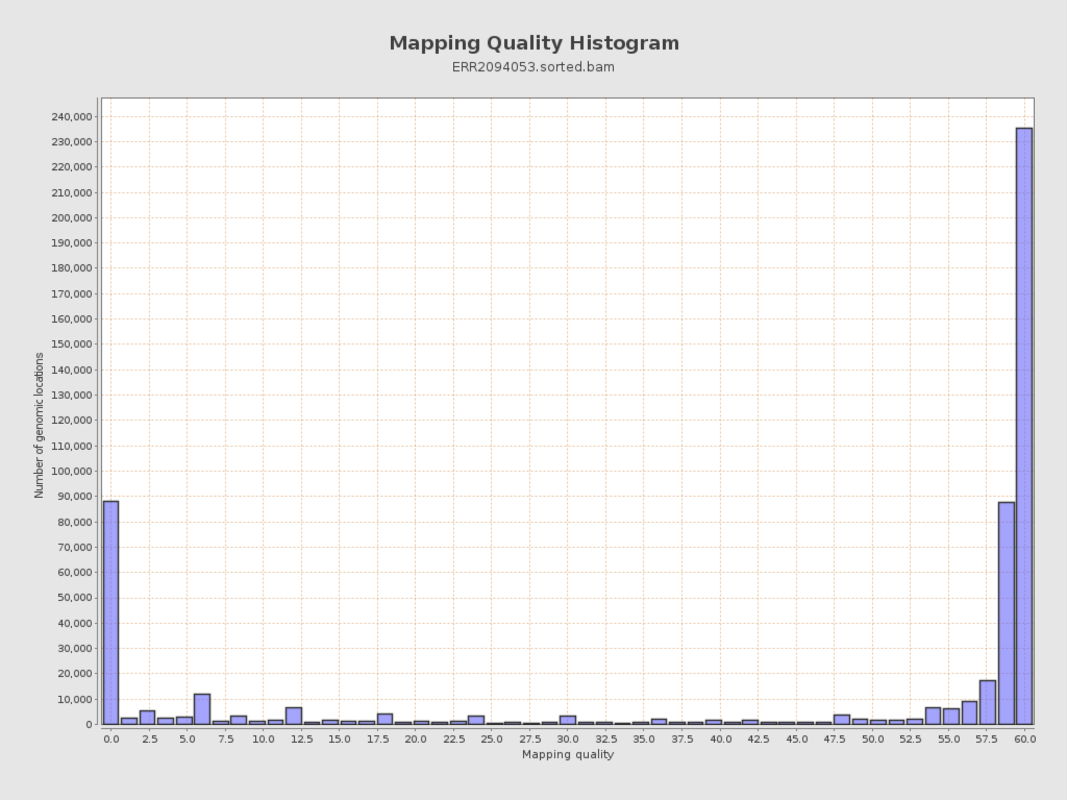
11. Results : Homopolymer Indels



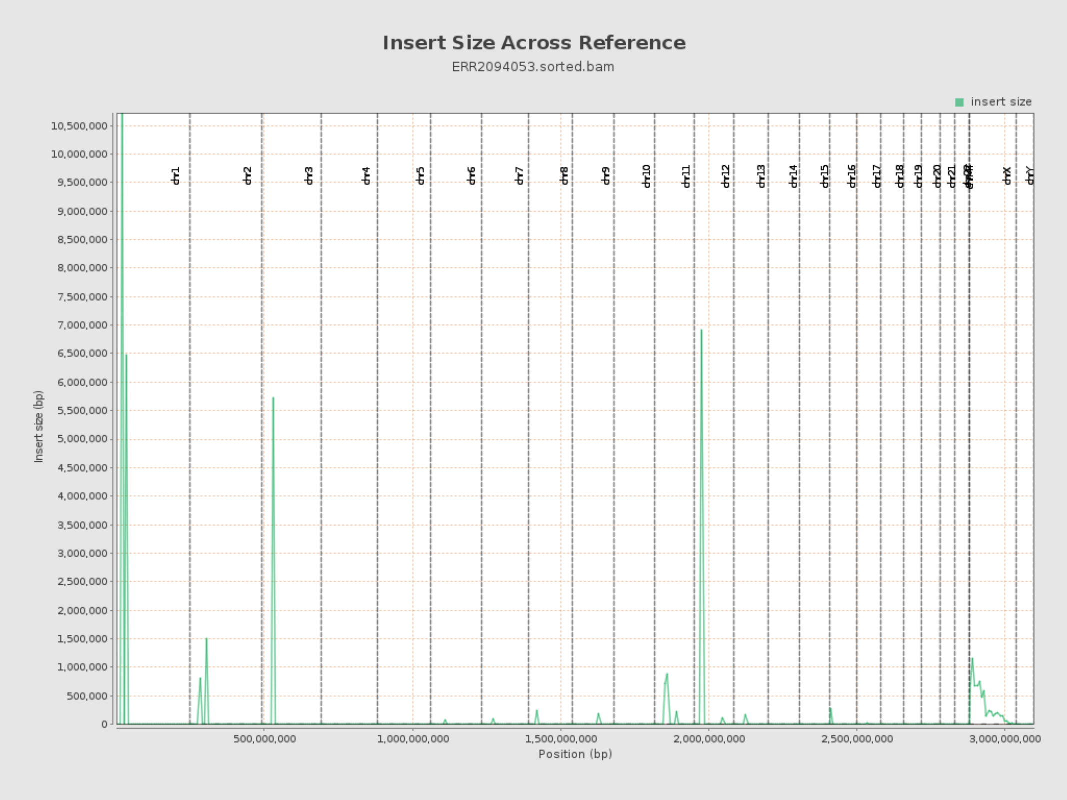
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram