Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:02:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094043.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_ERR2094043 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094043_1.fastq.gz ERR2094043_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:02:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094043.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	374,300
Mapped reads	355,064 / 94.86%
Unmapped reads	19,236 / 5.14%
Mapped paired reads	355,064 / 94.86%
Mapped reads, first in pair	178,418 / 47.67%
Mapped reads, second in pair	176,646 / 47.19%
Mapped reads, both in pair	352,498 / 94.18%
Mapped reads, singletons	2,566 / 0.69%
Secondary alignments	0
Supplementary alignments	12,608 / 3.37%
Read min/max/mean length	30 / 151 / 142.49
Duplicated reads (estimated)	335,595 / 89.66%
Duplication rate	49.05%
Clipped reads	138,456 / 36.99%

2.2. ACGT Content

Number/percentage of A's	12,942,371 / 27.45%
Number/percentage of C's	10,547,467 / 22.37%
Number/percentage of T's	12,536,546 / 26.59%
Number/percentage of G's	11,125,140 / 23.59%
Number/percentage of N's	538 / 0%

GC Percentage	45.96%

2.3. Coverage

Mean	0.0156
Standard Deviation	4.4344

2.4. Mapping Quality

Mean Mapping Quality	41.18

2.5. Insert size

Mean	485,825.34
Standard Deviation	6,352,963.72
P25/Median/P75	149 / 176 / 210

2.6. Mismatches and indels

General error rate	4.19%
Mismatches	1,922,600
Insertions	32,195
Mapped reads with at least one insertion	8.84%
Deletions	150,648
Mapped reads with at least one deletion	39.29%
Homopolymer indels	31.18%

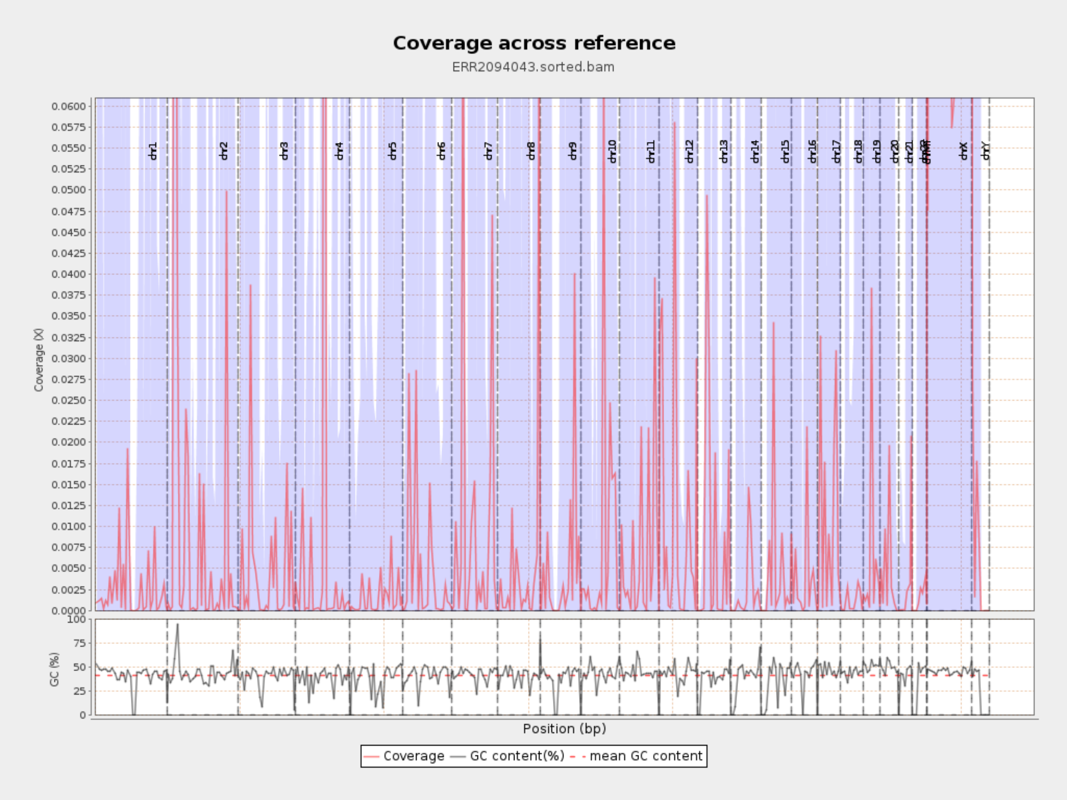
2.7. Chromosome stats

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

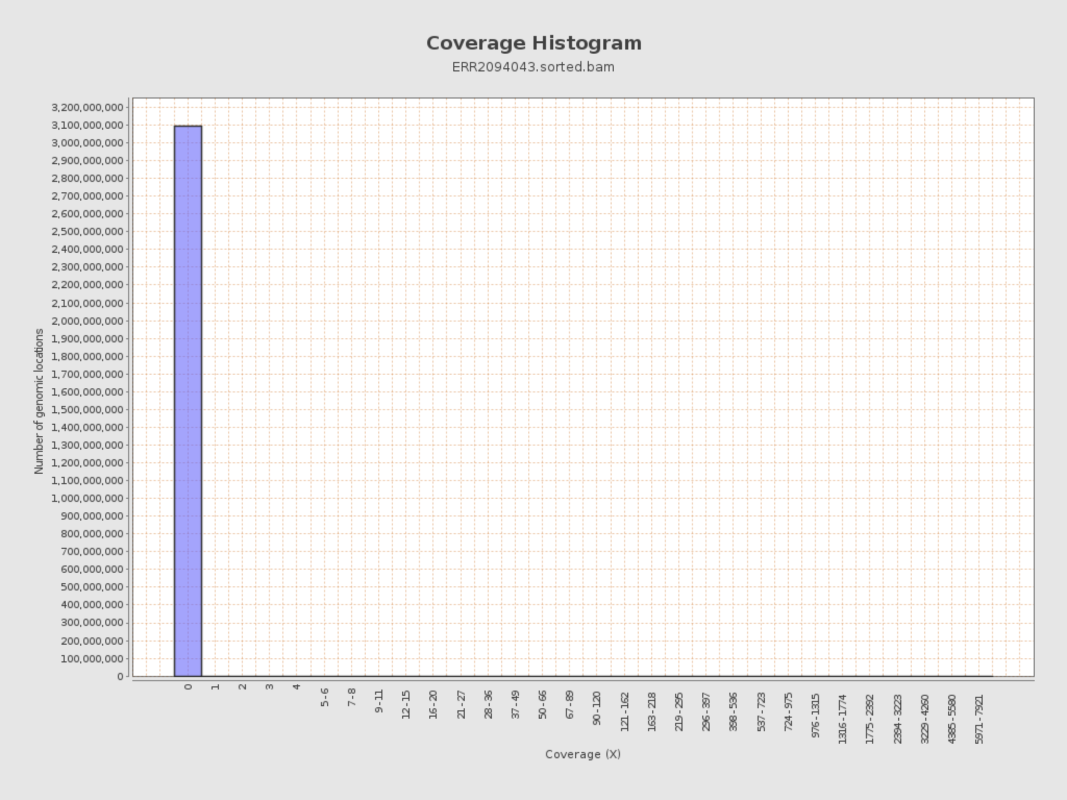
		bases	coverage	deviation
chr1	249250621	649601	0.0026	0.8787
chr2	243199373	2487538	0.0102	3.5609
chr3	198022430	927054	0.0047	1.7339
chr4	191154276	1670703	0.0087	3.2524
chr5	180915260	289902	0.0016	0.4941
chr6	171115067	837915	0.0049	1.9651
chr7	159138663	1552121	0.0098	3.2615
chr8	146364022	825265	0.0056	2.7541
chr9	141213431	705599	0.005	2.0274
chr10	135534747	1077366	0.0079	3.368
chr11	135006516	1041529	0.0077	2.0682
chr12	133851895	1451283	0.0108	3.7027
chr13	115169878	1012218	0.0088	2.3818
chr14	107349540	258828	0.0024	1.0991
chr15	102531392	460605	0.0045	1.7302
chr16	90354753	372358	0.0041	1.6531
chr17	81195210	905899	0.0112	2.6262
chr18	78077248	88552	0.0011	0.2539
chr19	59128983	409172	0.0069	2.674
chr20	63025520	294932	0.0047	1.0216
chr21	48129895	146962	0.0031	0.8055
chr22	51304566	76926	0.0015	0.3208
chrMT	16571	4207248	253.8922	1,024.0575
chrX	155270560	26134055	0.1683	12.9002

chrY	59373566	365343	0.0062	1.9594

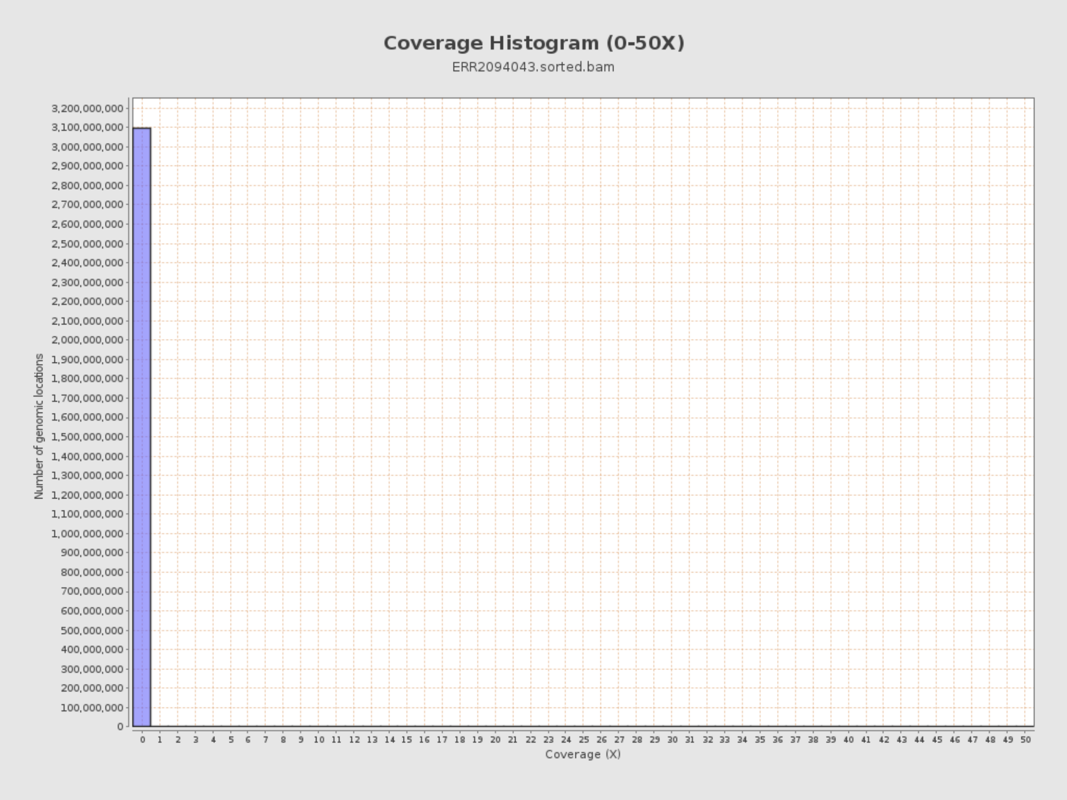
3. Results : Coverage across reference



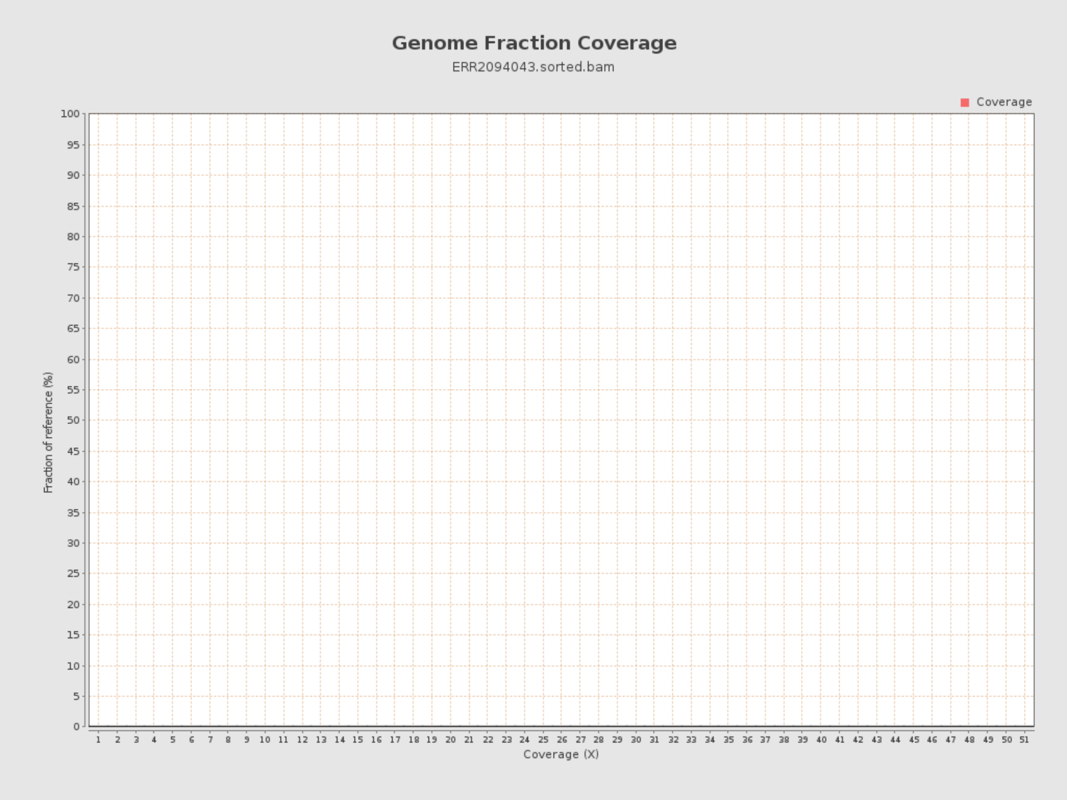
4. Results : Coverage Histogram



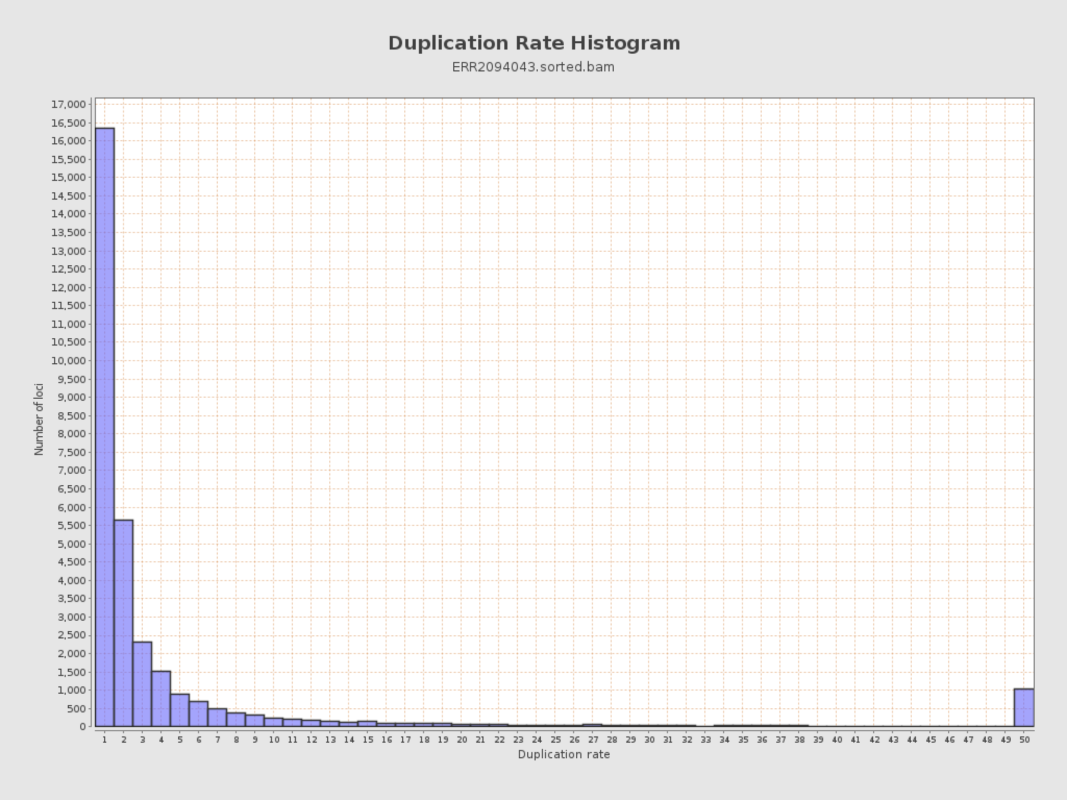
5. Results : Coverage Histogram (0-50X)



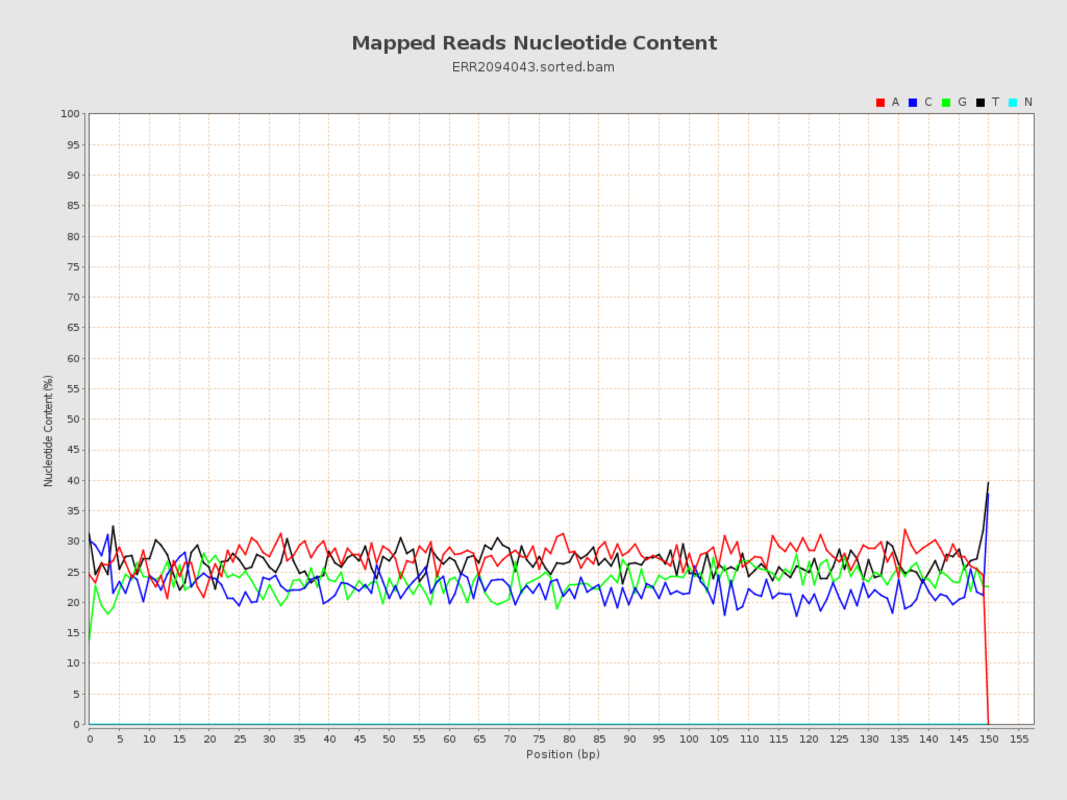
6. Results : Genome Fraction Coverage



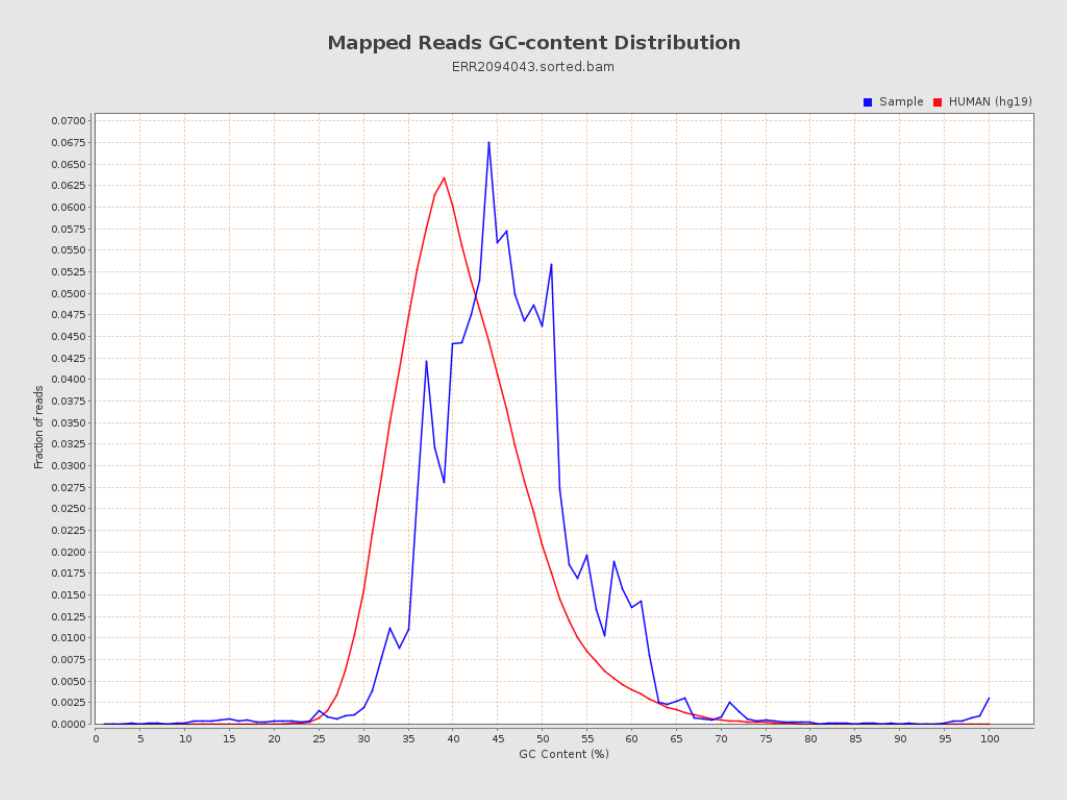
7. Results : Duplication Rate Histogram



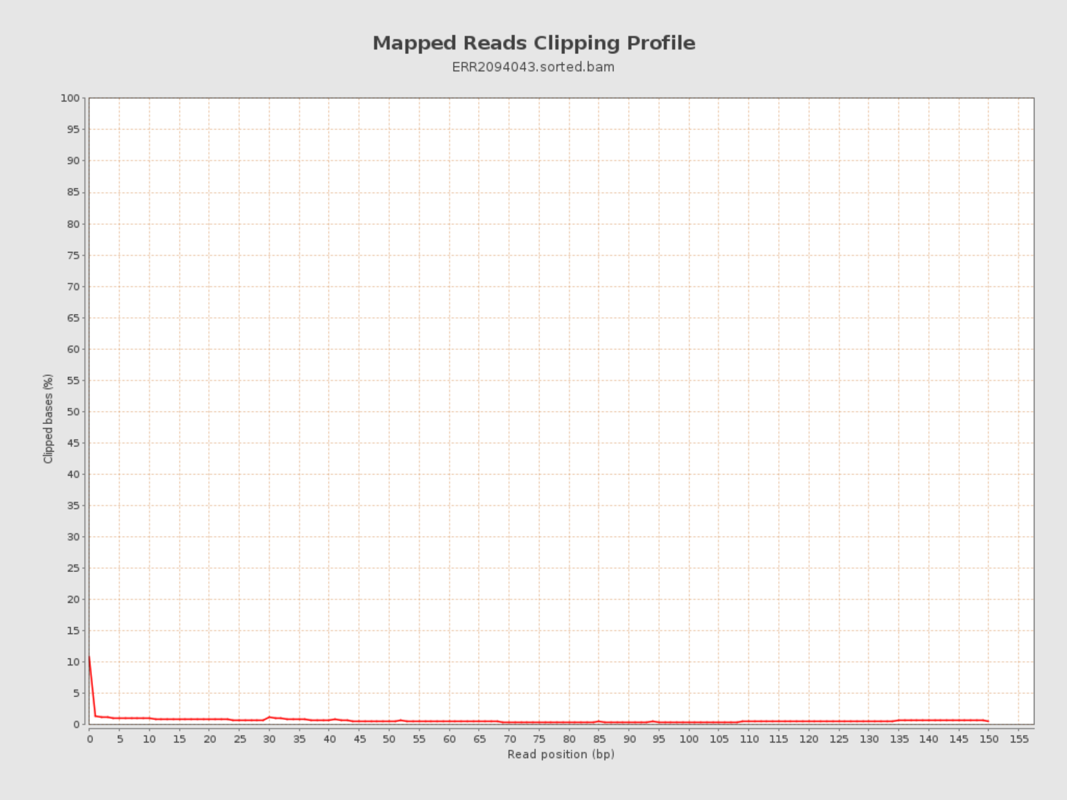
8. Results : Mapped Reads Nucleotide Content



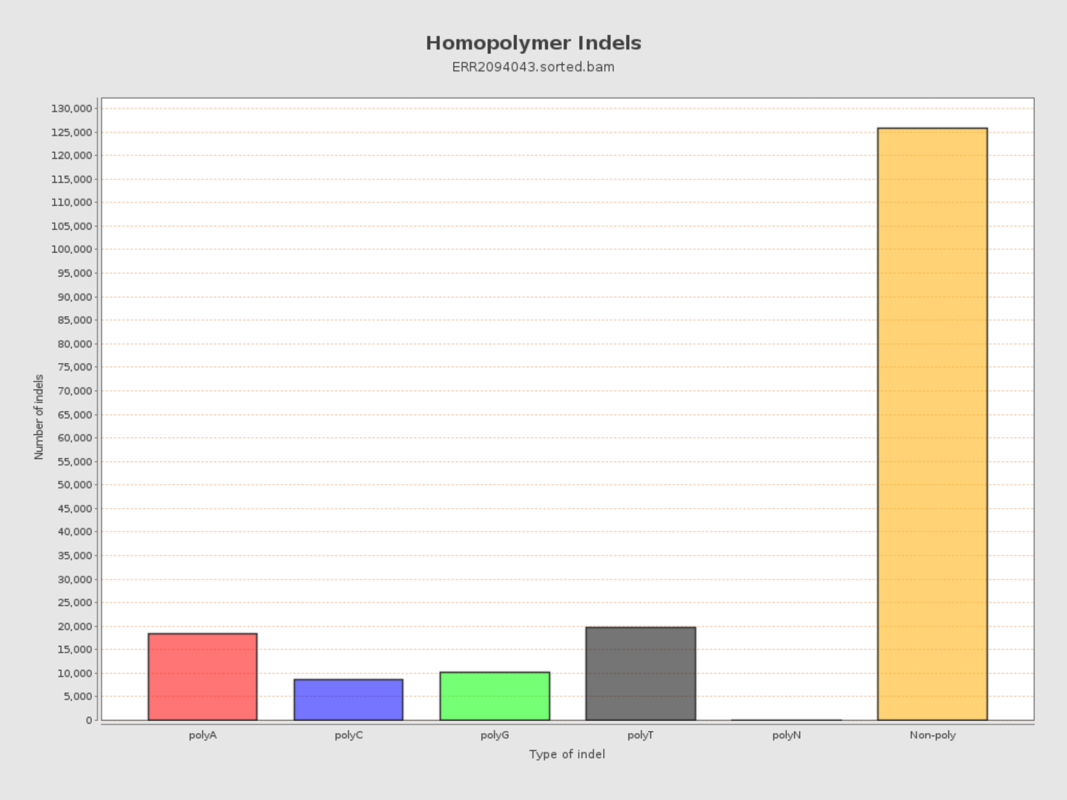
9. Results : Mapped Reads GC-content Distribution



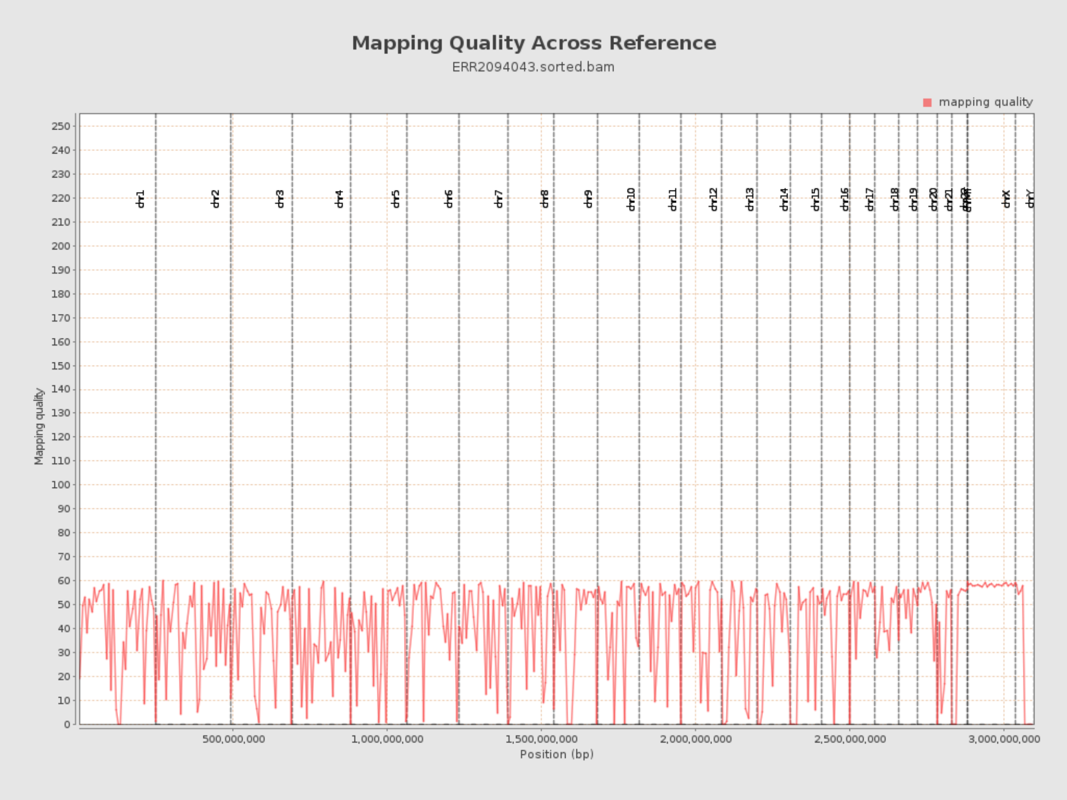
10. Results : Mapped Reads Clipping Profile



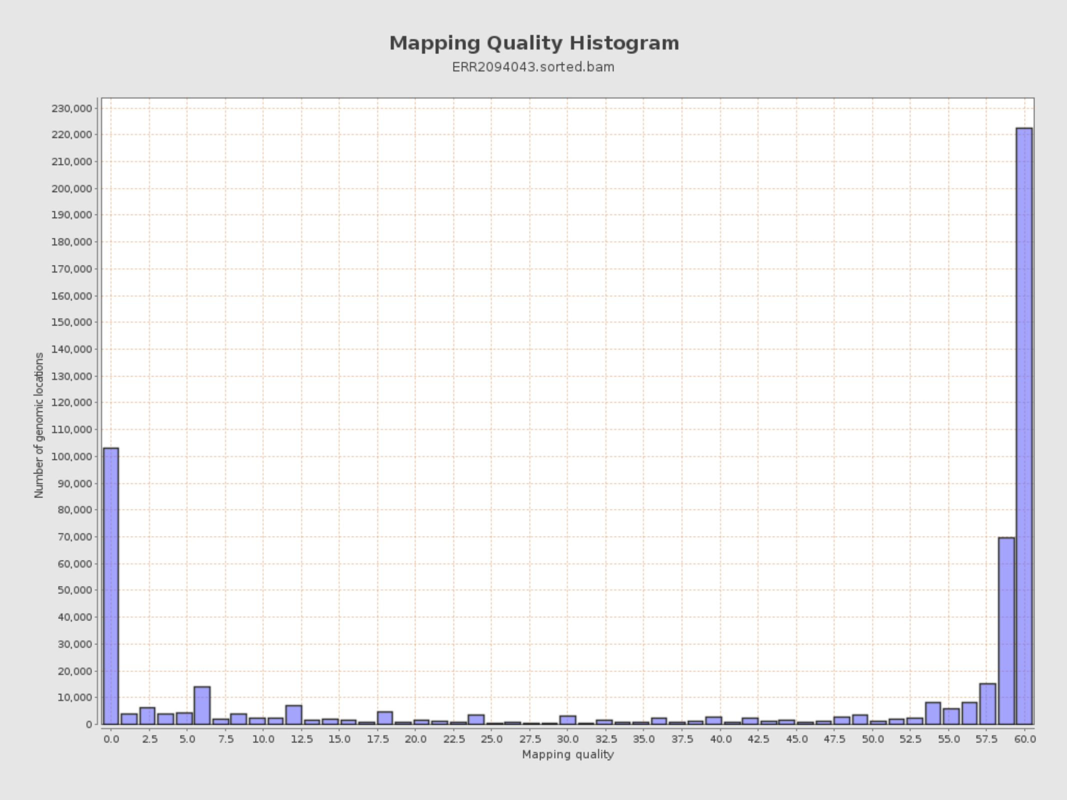
11. Results : Homopolymer Indels



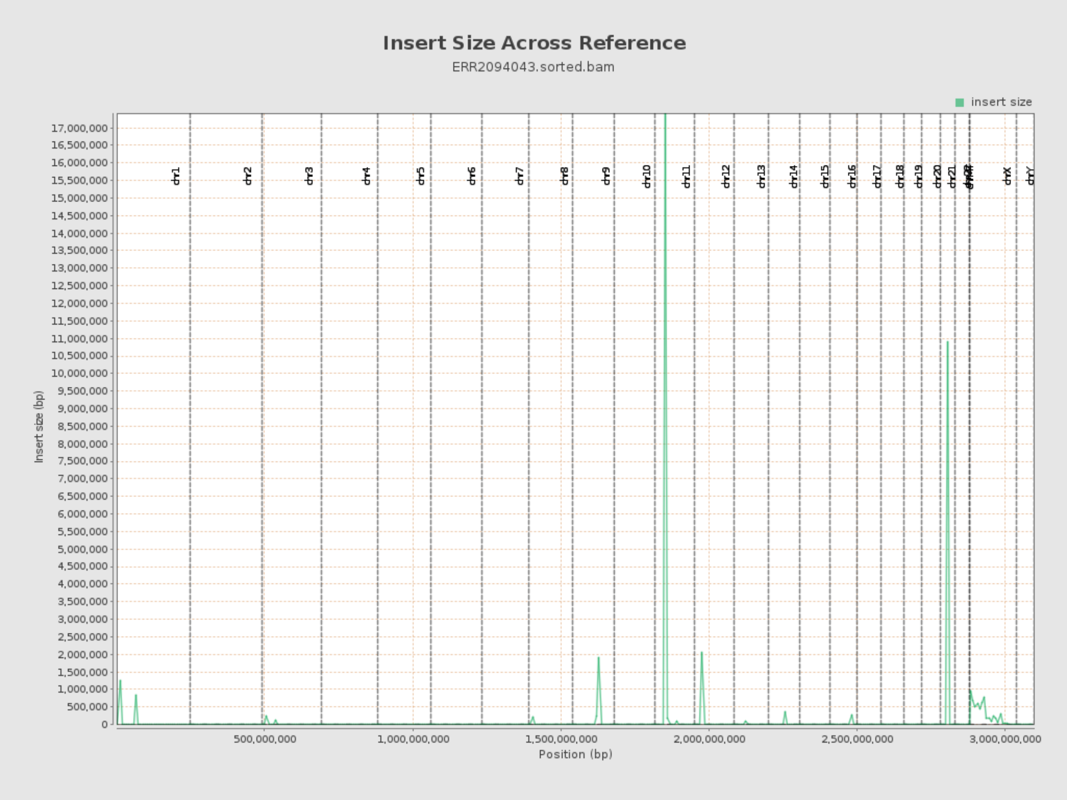
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram