Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:29:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094130.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_ERR2094130 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094130_1.fastq.gz ERR2094130_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:29:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094130.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	527,278
Mapped reads	506,263 / 96.01%
Unmapped reads	21,015 / 3.99%
Mapped paired reads	506,263 / 96.01%
Mapped reads, first in pair	254,032 / 48.18%
Mapped reads, second in pair	252,231 / 47.84%
Mapped reads, both in pair	503,426 / 95.48%
Mapped reads, singletons	2,837 / 0.54%
Secondary alignments	0
Supplementary alignments	3,178 / 0.6%
Read min/max/mean length	30 / 151 / 146.67
Duplicated reads (estimated)	502,068 / 95.22%
Duplication rate	44.19%
Clipped reads	130,477 / 24.75%

2.2. ACGT Content

Number/percentage of A's	19,865,929 / 27.46%
Number/percentage of C's	15,731,448 / 21.75%
Number/percentage of T's	20,720,462 / 28.64%
Number/percentage of G's	16,020,169 / 22.15%
Number/percentage of N's	828 / 0%

GC Percentage	43.89%

2.3. Coverage

Mean	0.0235
Standard Deviation	32.5518

2.4. Mapping Quality

Mean Mapping Quality	26.64

2.5. Insert size

Mean	21,717.19
Standard Deviation	1,367,101.38
P25/Median/P75	205 / 217 / 256

2.6. Mismatches and indels

General error rate	1.98%
Mismatches	1,373,761
Insertions	36,108
Mapped reads with at least one insertion	7.04%
Deletions	94,462
Mapped reads with at least one deletion	18.21%
Homopolymer indels	49.53%

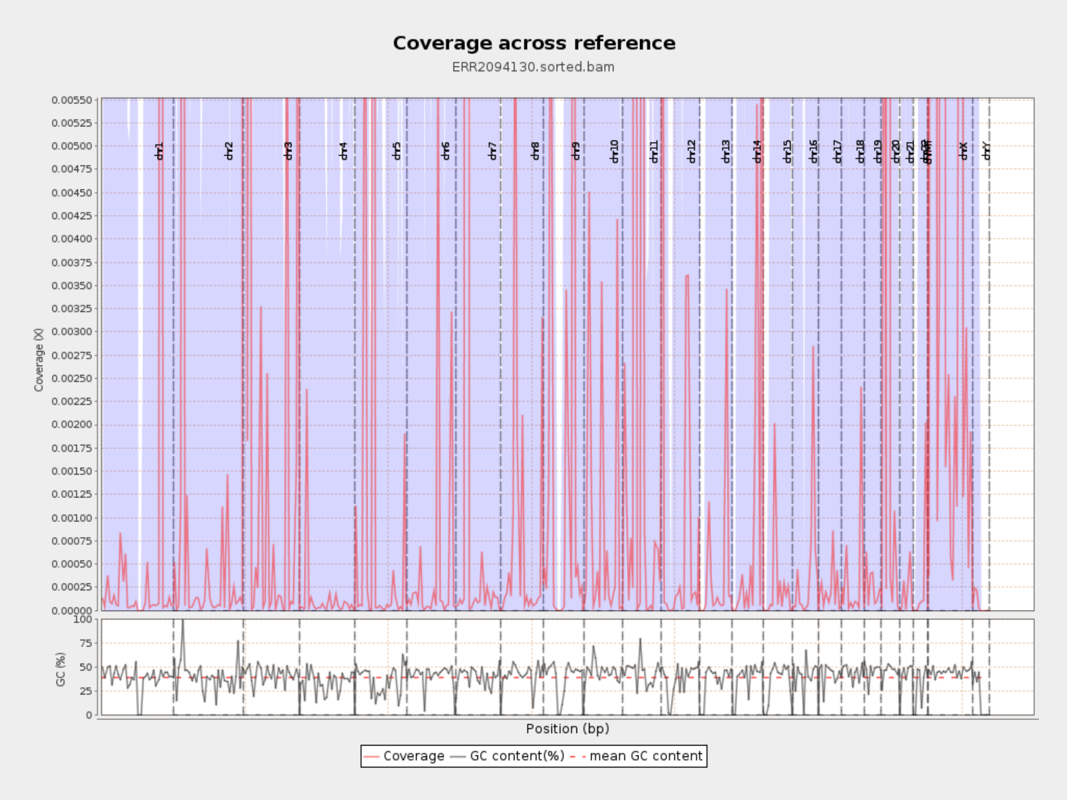
2.7. Chromosome stats

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

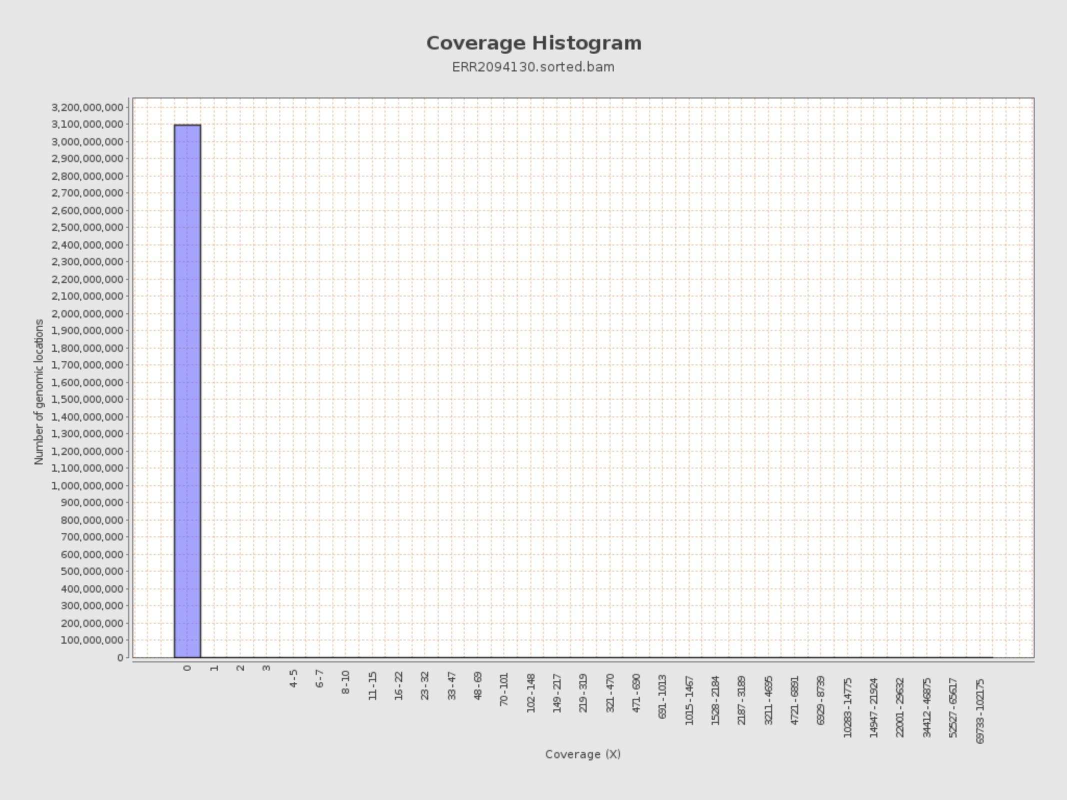
		bases	coverage	deviation
chr1	249250621	390978	0.0016	1.7753
chr2	243199373	280257	0.0012	0.928
chr3	198022430	6030435	0.0305	28.5288
chr4	191154276	28666	0.0001	0.0964
chr5	180915260	236561	0.0013	0.719
chr6	171115067	89131	0.0005	0.2706
chr7	159138663	2035423	0.0128	11.6616
chr8	146364022	132457	0.0009	0.4133
chr9	141213431	268686	0.0019	0.8964
chr10	135534747	124078	0.0009	0.3183
chr11	135006516	891022	0.0066	5.1874
chr12	133851895	166505	0.0012	0.7392
chr13	115169878	44841	0.0004	0.1314
chr14	107349540	170577	0.0016	0.6817
chr15	102531392	25518	0.0002	0.089
chr16	90354753	41608	0.0005	0.1553
chr17	81195210	18657	0.0002	0.0645
chr18	78077248	29592	0.0004	0.1585
chr19	59128983	15342	0.0003	0.0471
chr20	63025520	2098773	0.0333	19.9444
chr21	48129895	10233	0.0002	0.0442
chr22	51304566	17939	0.0003	0.1109
chrMT	16571	52645692	3,176.9774	13,084.9591
chrX	155270560	6906477	0.0445	20.1661

chrY	59373566	3955	0.0001	0.0154

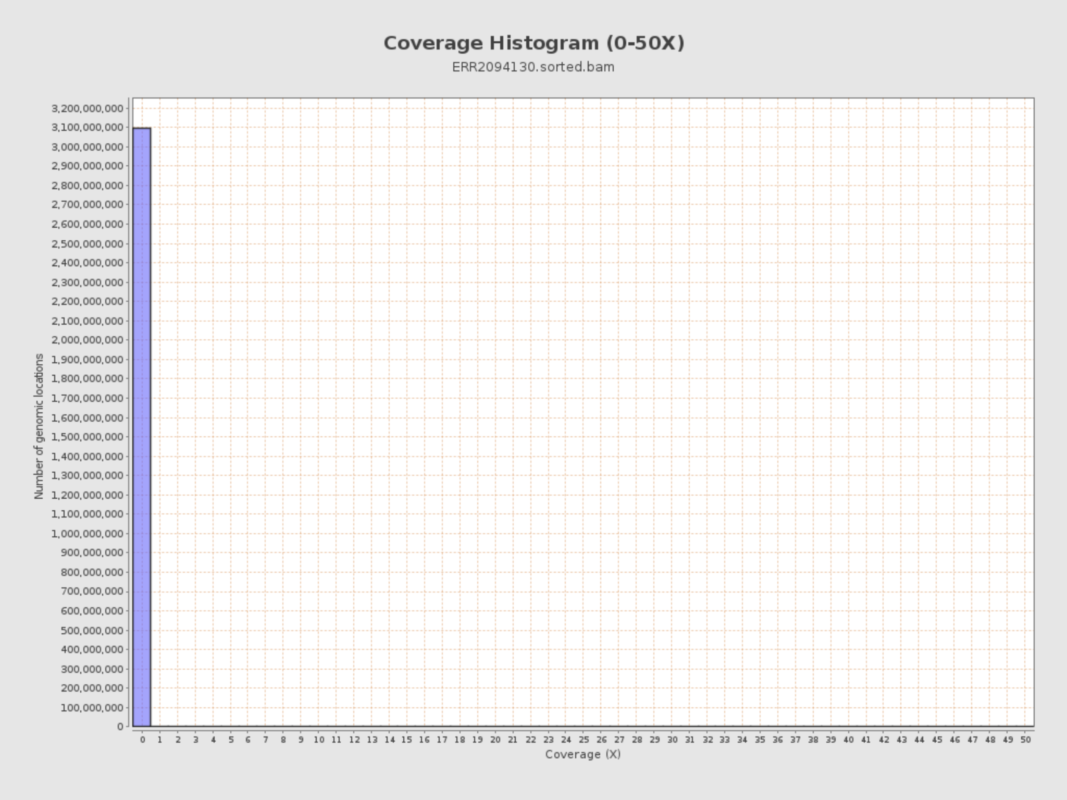
3. Results : Coverage across reference



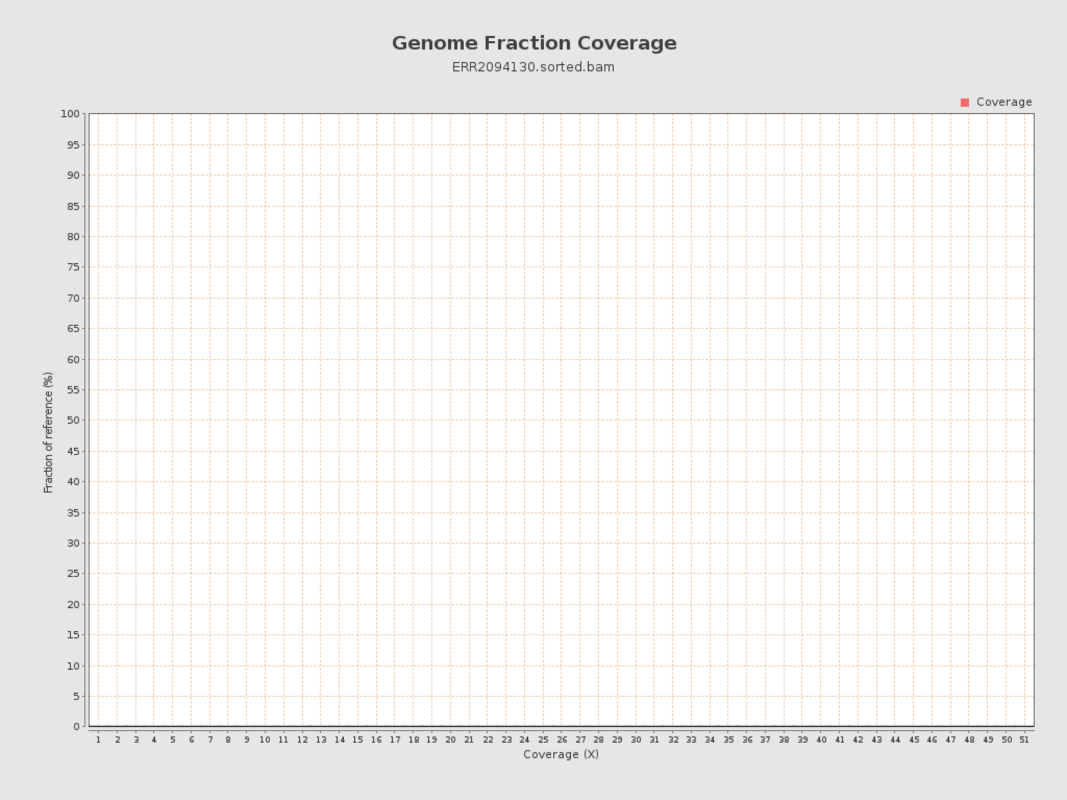
4. Results : Coverage Histogram



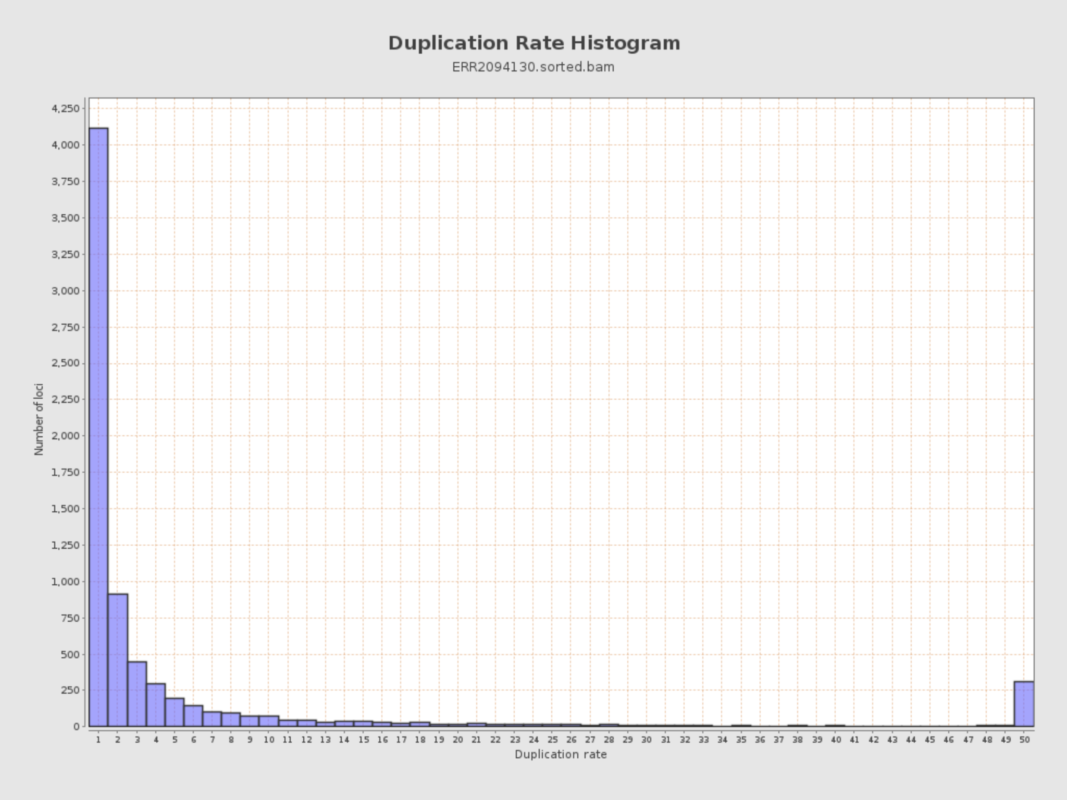
5. Results : Coverage Histogram (0-50X)



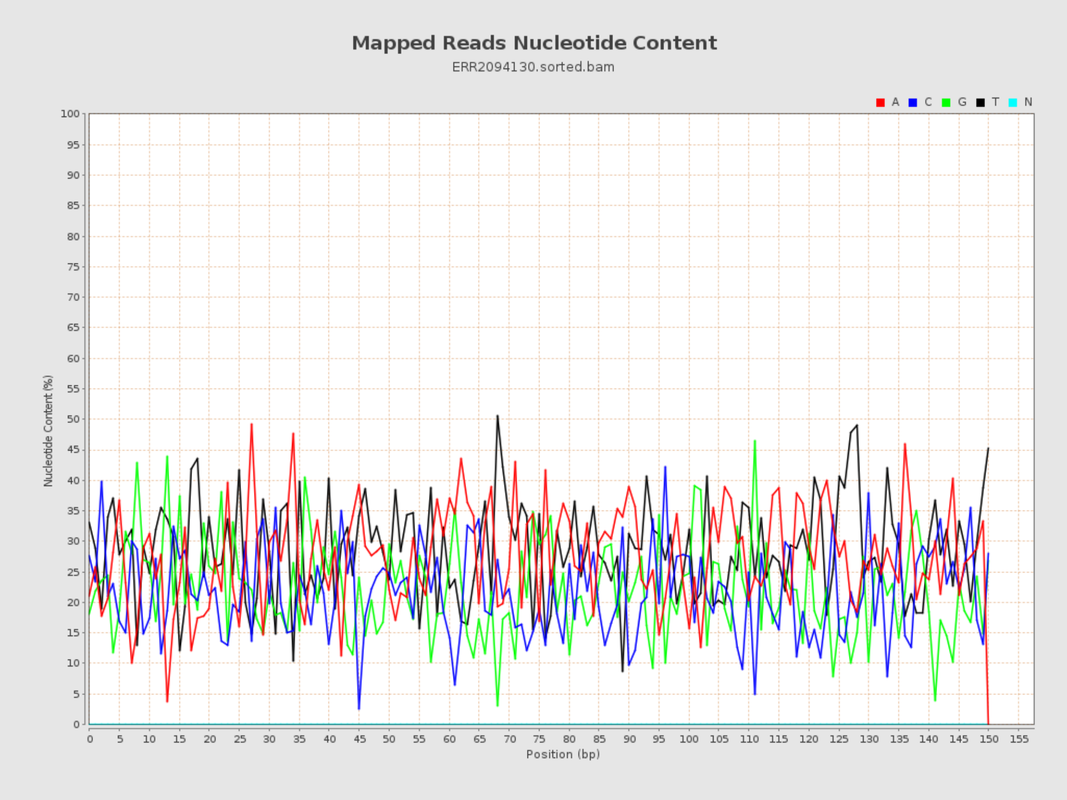
6. Results : Genome Fraction Coverage



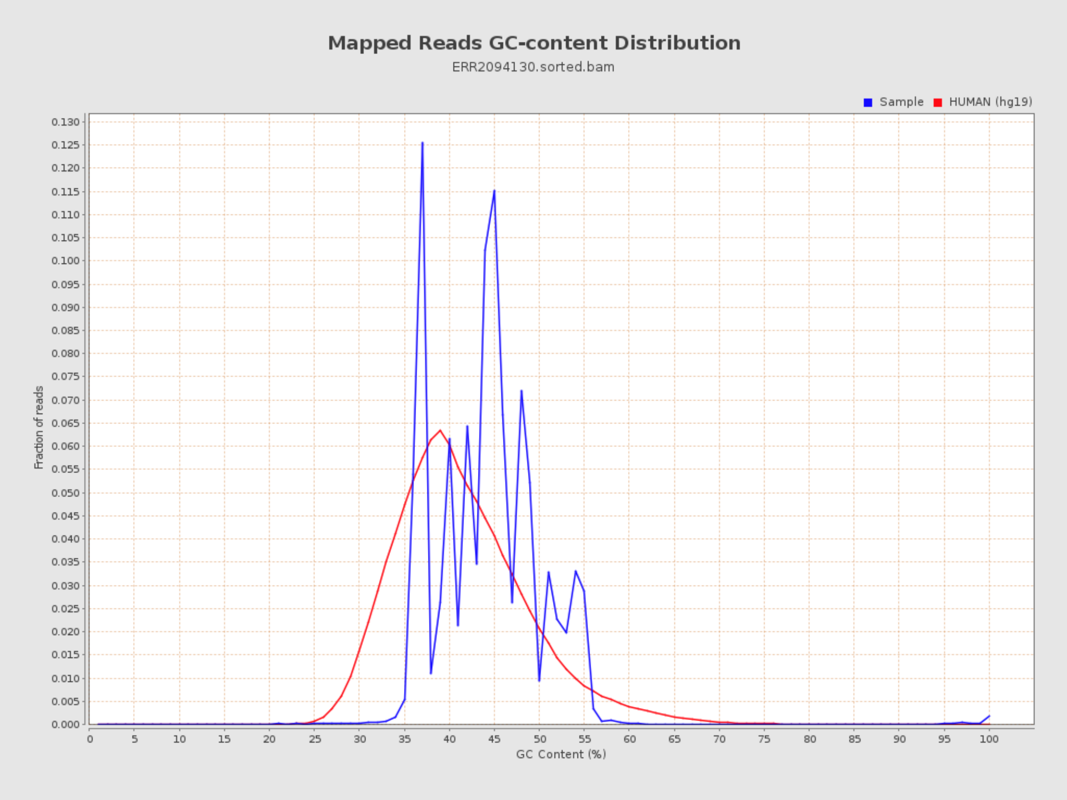
7. Results : Duplication Rate Histogram



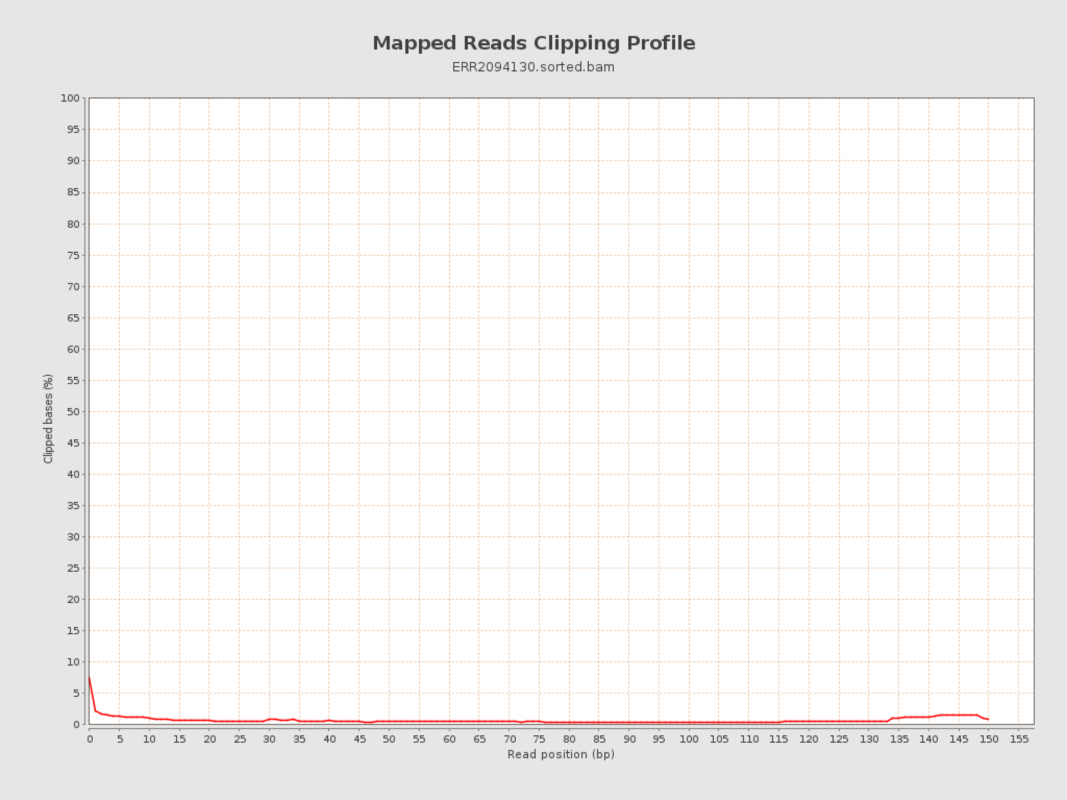
8. Results : Mapped Reads Nucleotide Content



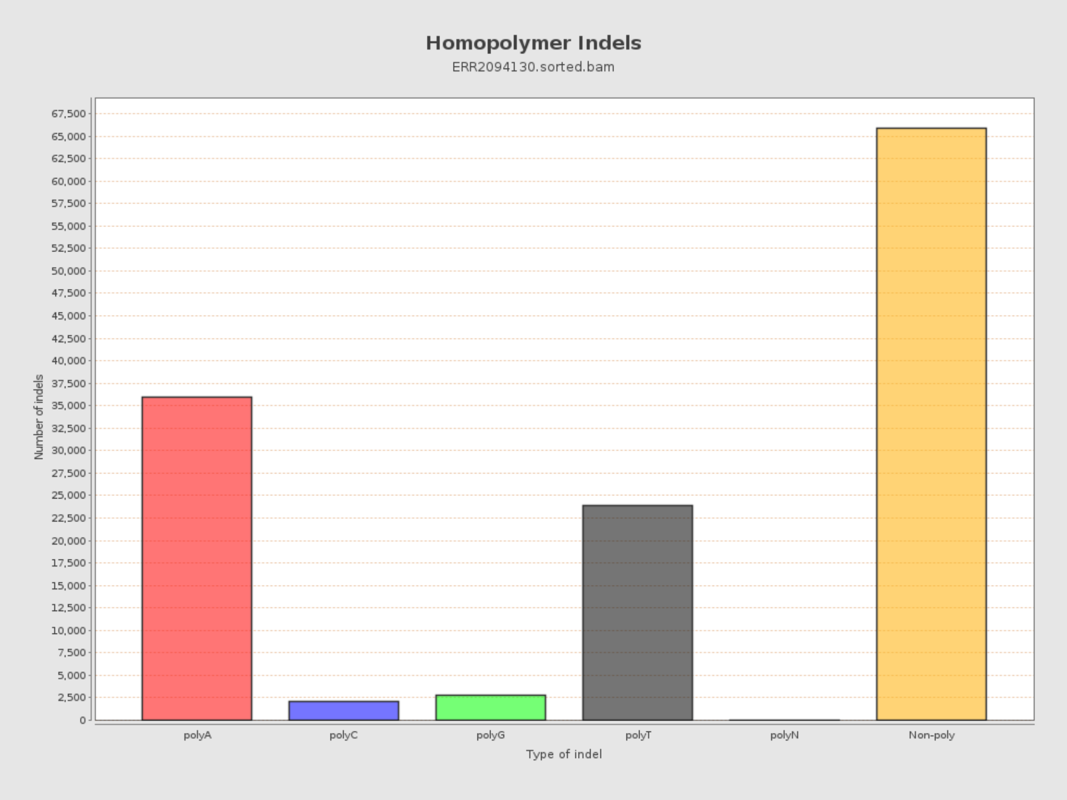
9. Results : Mapped Reads GC-content Distribution



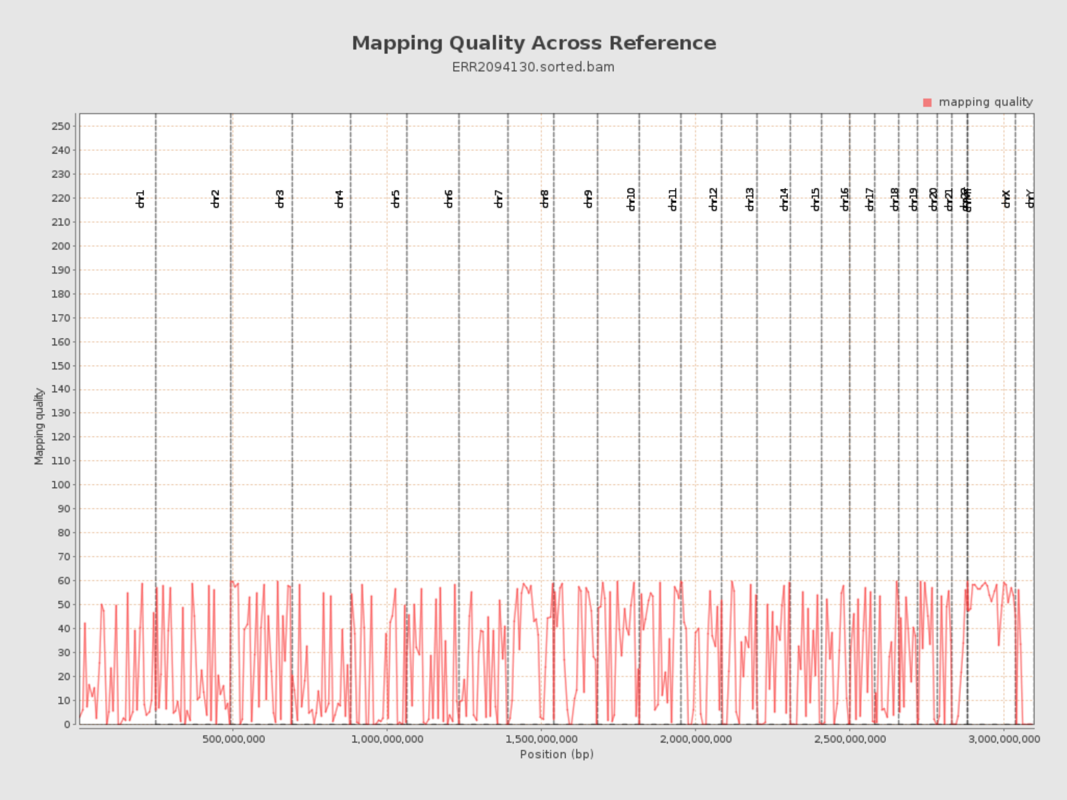
10. Results : Mapped Reads Clipping Profile



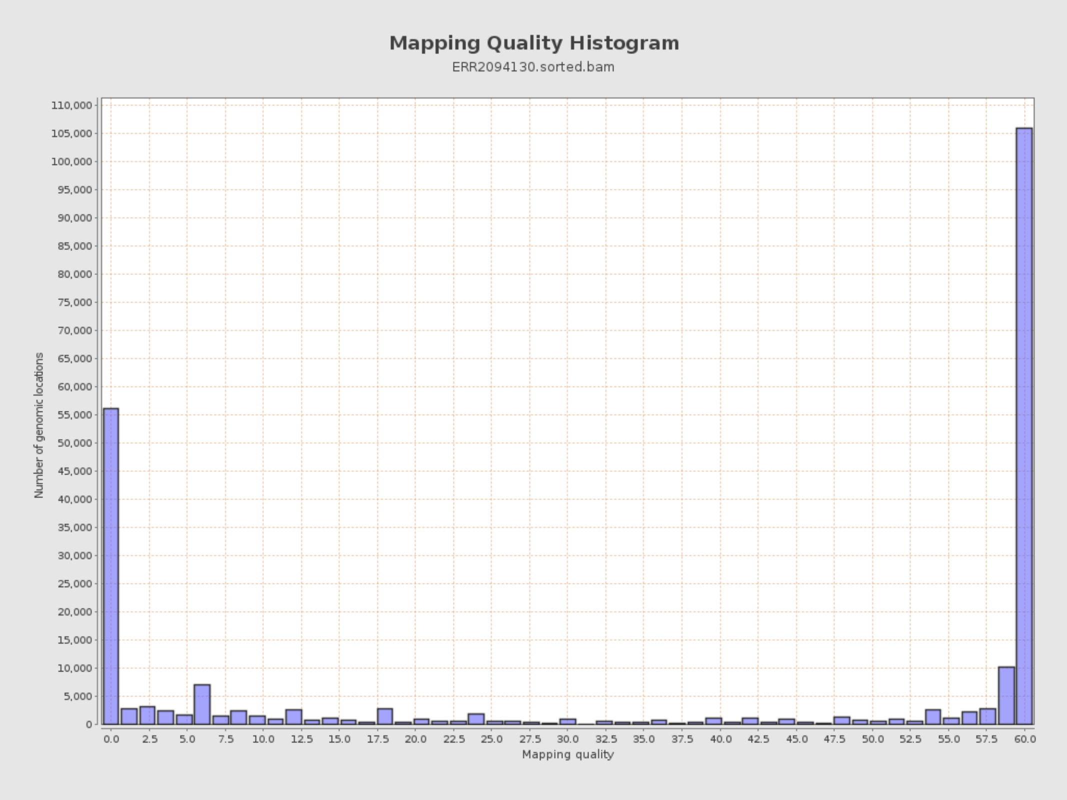
11. Results : Homopolymer Indels



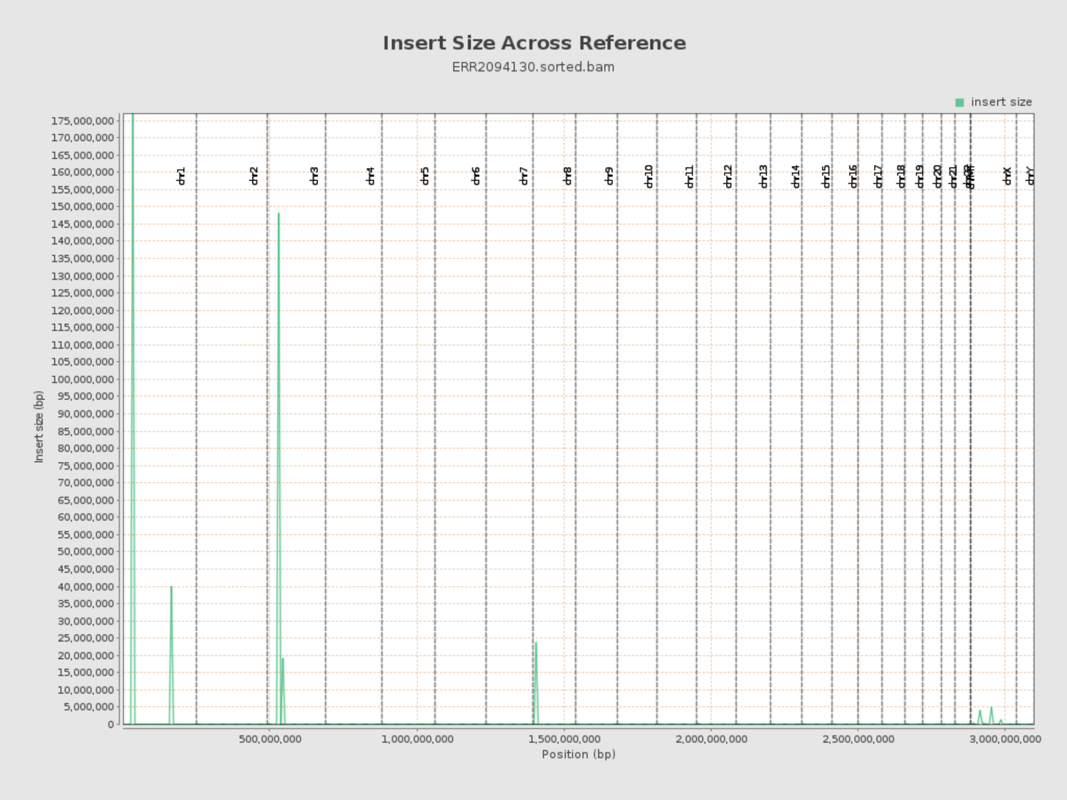
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram