Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:16:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094049.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_ERR2094049 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094049_1.fastq.gz ERR2094049_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:16:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	402,962
Mapped reads	383,919 / 95.27%
Unmapped reads	19,043 / 4.73%
Mapped paired reads	383,919 / 95.27%
Mapped reads, first in pair	192,805 / 47.85%
Mapped reads, second in pair	191,114 / 47.43%
Mapped reads, both in pair	381,466 / 94.67%
Mapped reads, singletons	2,453 / 0.61%
Secondary alignments	0
Supplementary alignments	9,221 / 2.29%
Read min/max/mean length	30 / 151 / 141.22
Duplicated reads (estimated)	365,780 / 90.77%
Duplication rate	50.24%
Clipped reads	142,043 / 35.25%

2.2. ACGT Content

Number/percentage of A's	13,895,701 / 27.51%
Number/percentage of C's	11,274,570 / 22.32%
Number/percentage of T's	13,578,116 / 26.88%
Number/percentage of G's	11,764,545 / 23.29%
Number/percentage of N's	721 / 0%

GC Percentage	45.61%

2.3. Coverage

Mean	0.0167
Standard Deviation	5.8895

2.4. Mapping Quality

Mean Mapping Quality	41.93

2.5. Insert size

Mean	314,559.74
Standard Deviation	5,078,406.79
P25/Median/P75	143 / 173 / 206

2.6. Mismatches and indels

General error rate	4.38%
Mismatches	2,105,243
Insertions	44,452
Mapped reads with at least one insertion	11.3%
Deletions	169,594
Mapped reads with at least one deletion	41.05%
Homopolymer indels	32.13%

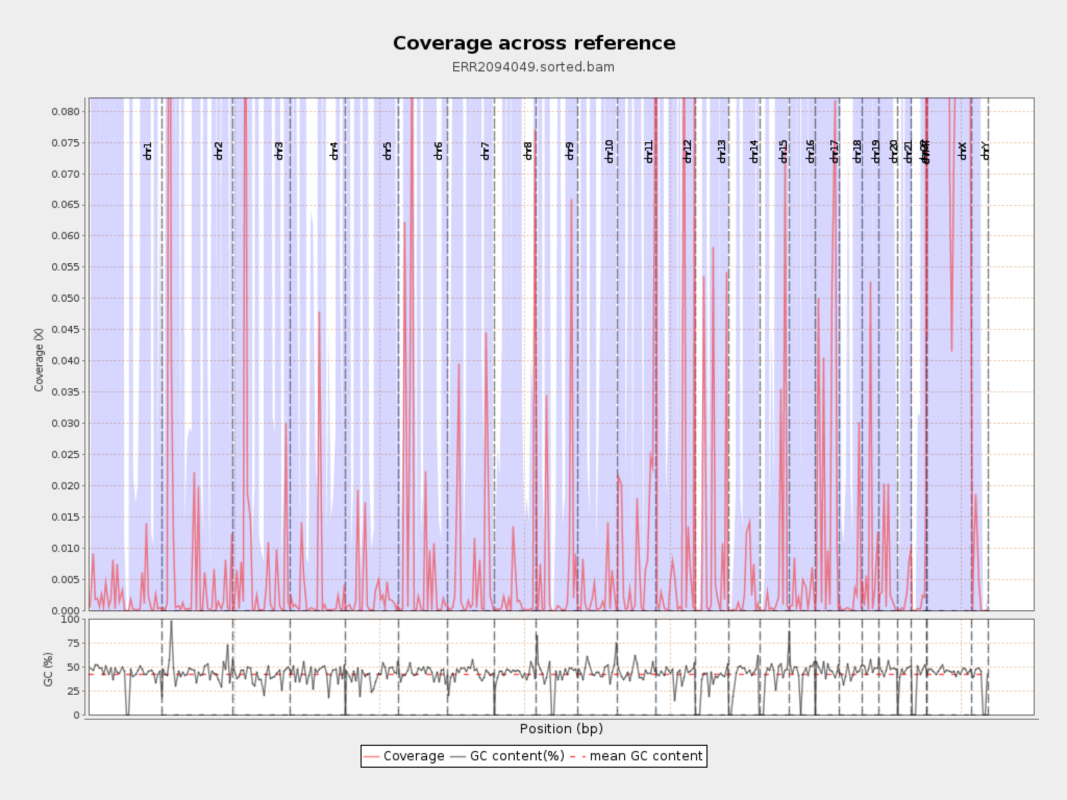
2.7. Chromosome stats

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

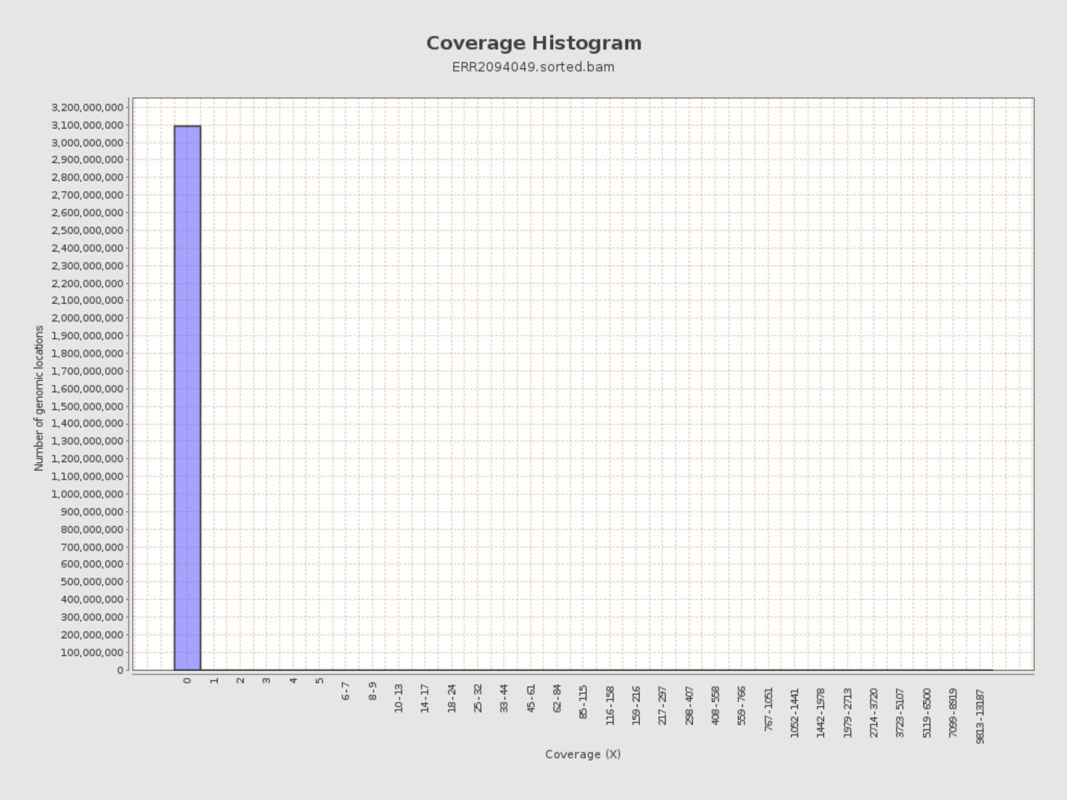
		bases	coverage	deviation
chr1	249250621	578707	0.0023	0.8766
chr2	243199373	2214626	0.0091	3.3248
chr3	198022430	1816572	0.0092	4.8026
chr4	191154276	627135	0.0033	1.5626
chr5	180915260	492024	0.0027	1.0904
chr6	171115067	1876581	0.011	5.5041
chr7	159138663	1205962	0.0076	2.6159
chr8	146364022	756148	0.0052	3.2537
chr9	141213431	1025410	0.0073	3.4998
chr10	135534747	335960	0.0025	0.8103
chr11	135006516	1965340	0.0146	4.08
chr12	133851895	1408602	0.0105	5.6569
chr13	115169878	1443746	0.0125	4.7709
chr14	107349540	325065	0.003	1.2087
chr15	102531392	918121	0.009	3.4915
chr16	90354753	257580	0.0029	0.6506
chr17	81195210	1922675	0.0237	6.2515
chr18	78077248	293076	0.0038	1.4546
chr19	59128983	595071	0.0101	3.7607
chr20	63025520	389677	0.0062	1.7368
chr21	48129895	138307	0.0029	0.5977
chr22	51304566	75379	0.0015	0.4107
chrMT	16571	6404517	386.4895	1,604.3653
chrX	155270560	24397381	0.1571	13.7441

chrY	59373566	248763	0.0042	1.6429

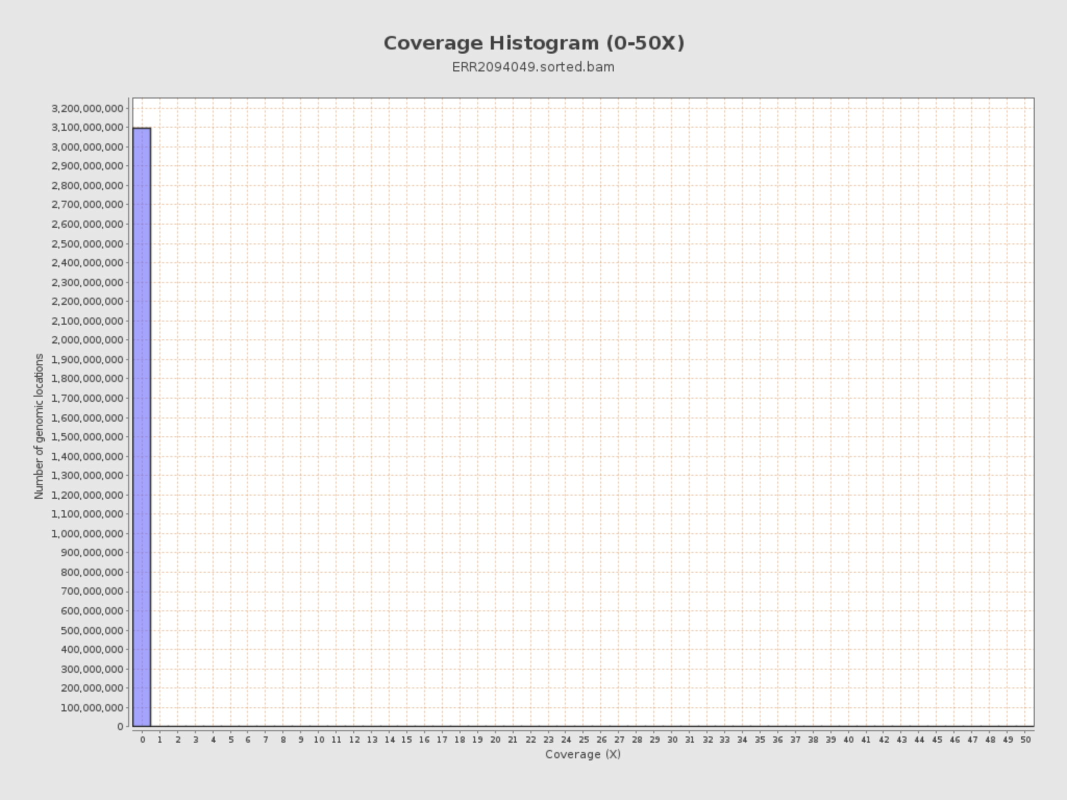
3. Results : Coverage across reference



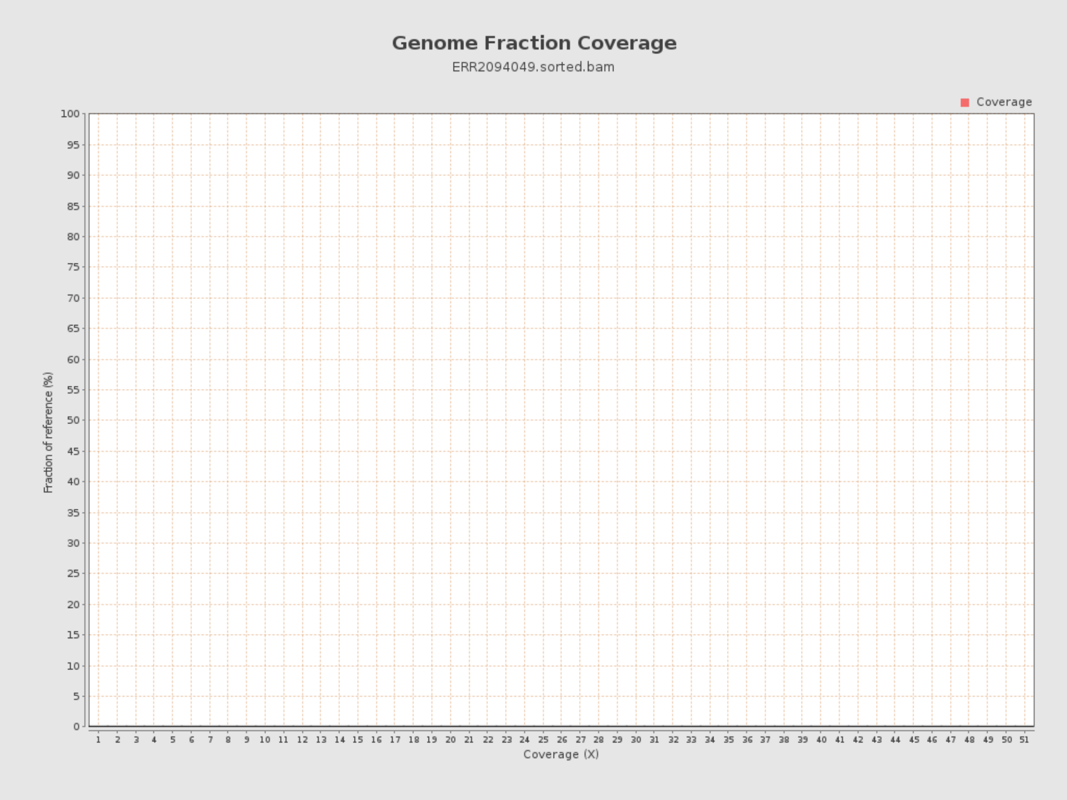
4. Results : Coverage Histogram



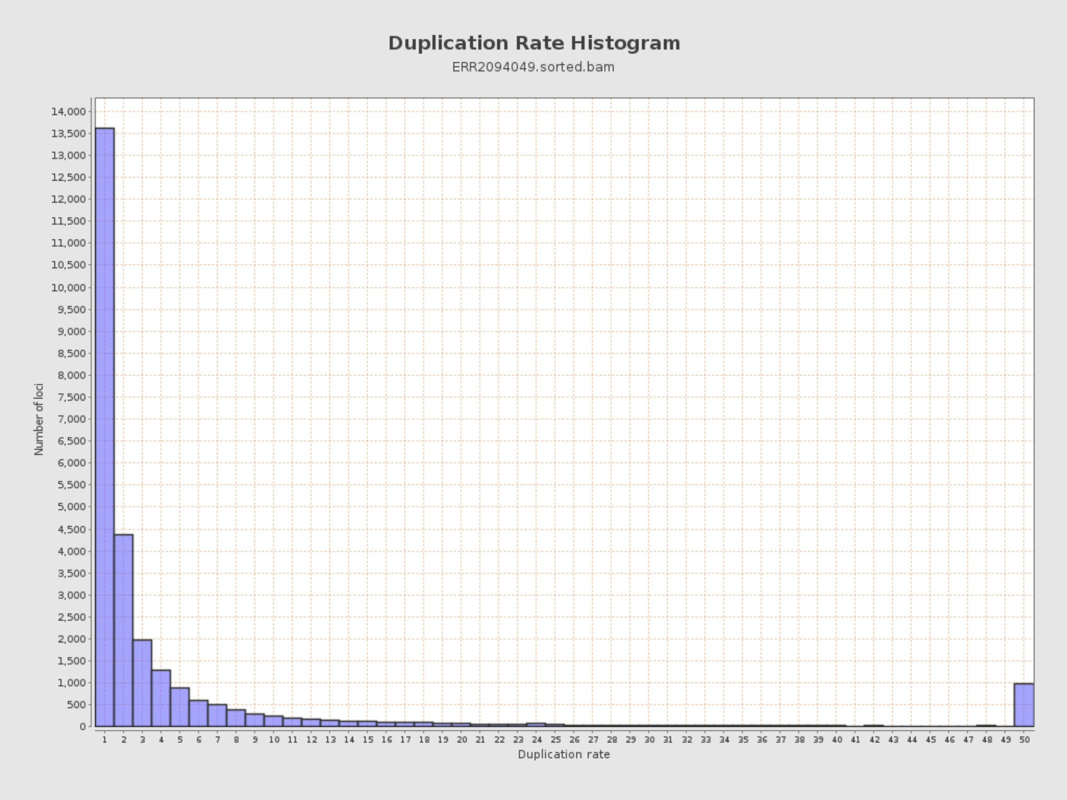
5. Results : Coverage Histogram (0-50X)



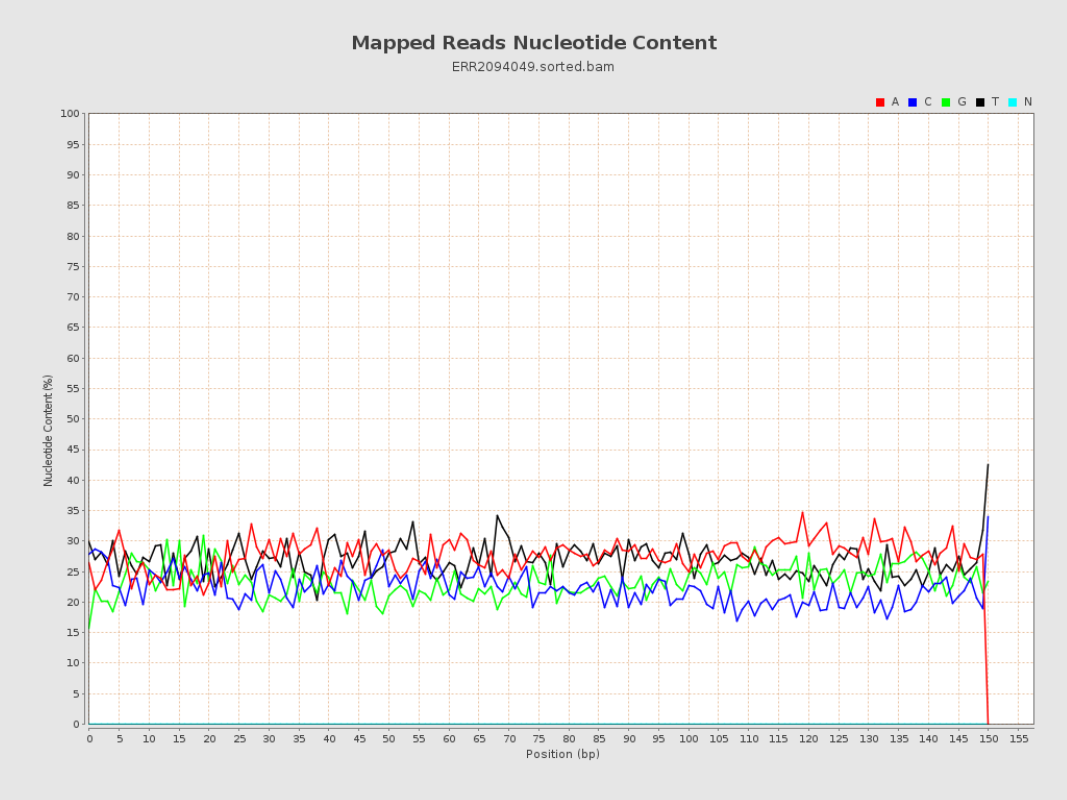
6. Results : Genome Fraction Coverage



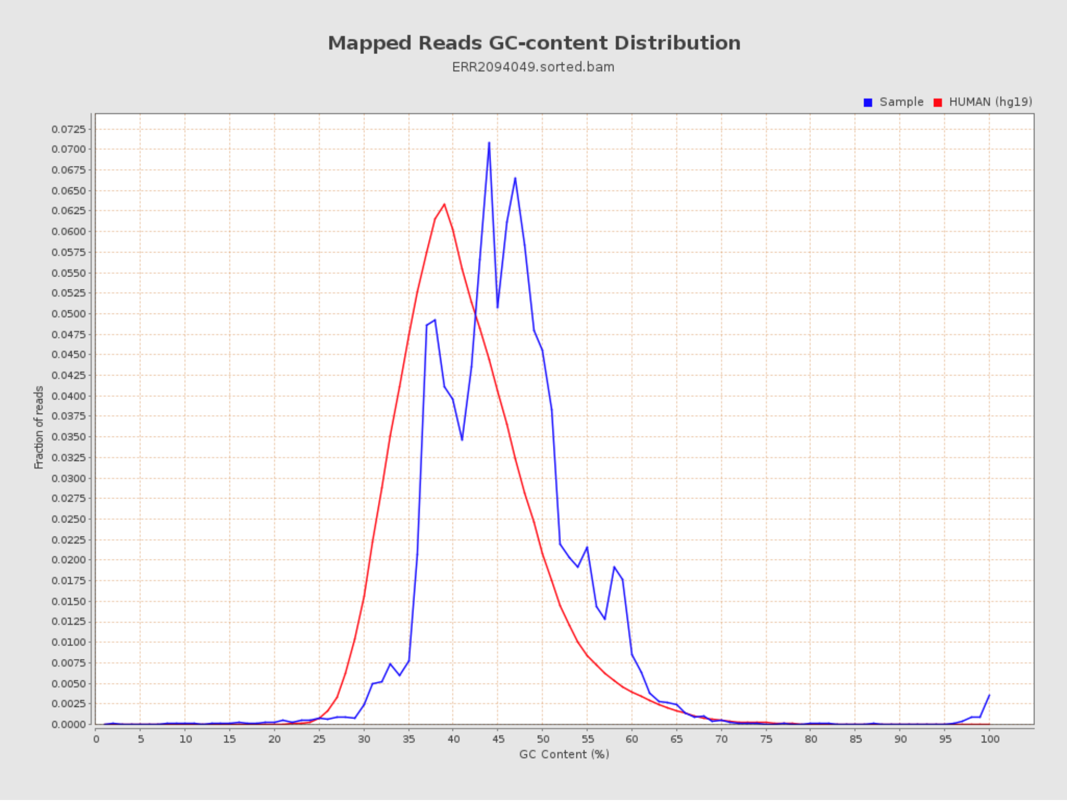
7. Results : Duplication Rate Histogram



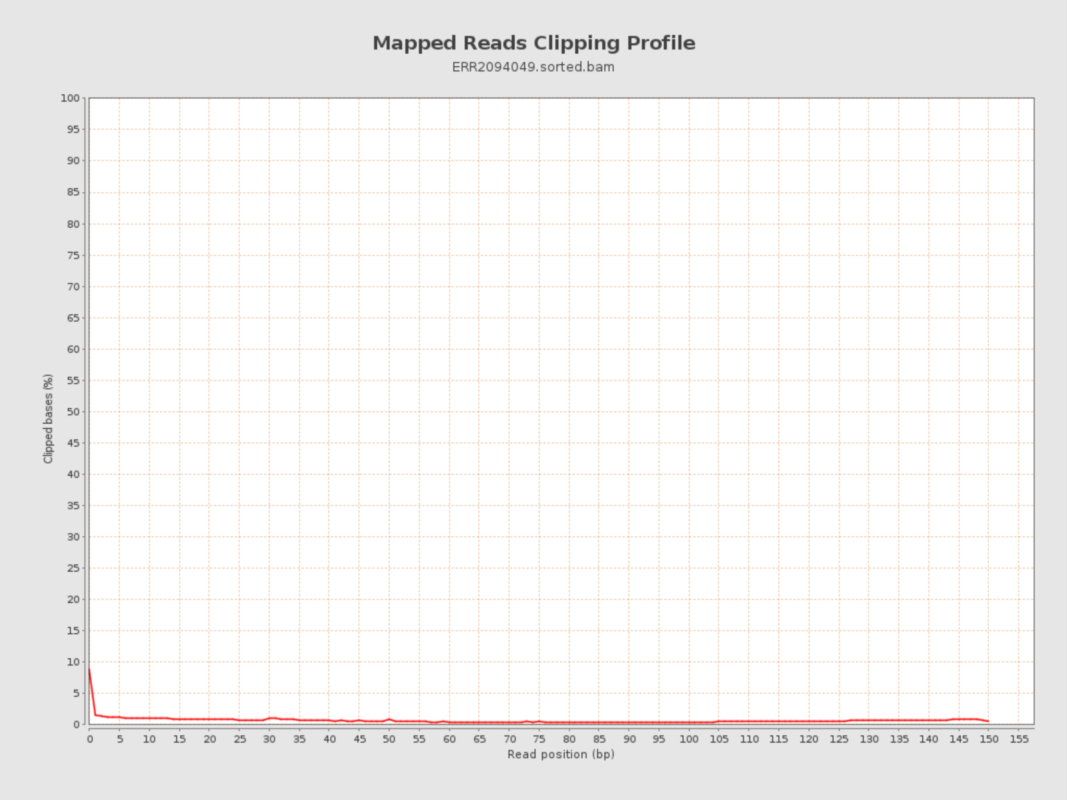
8. Results : Mapped Reads Nucleotide Content



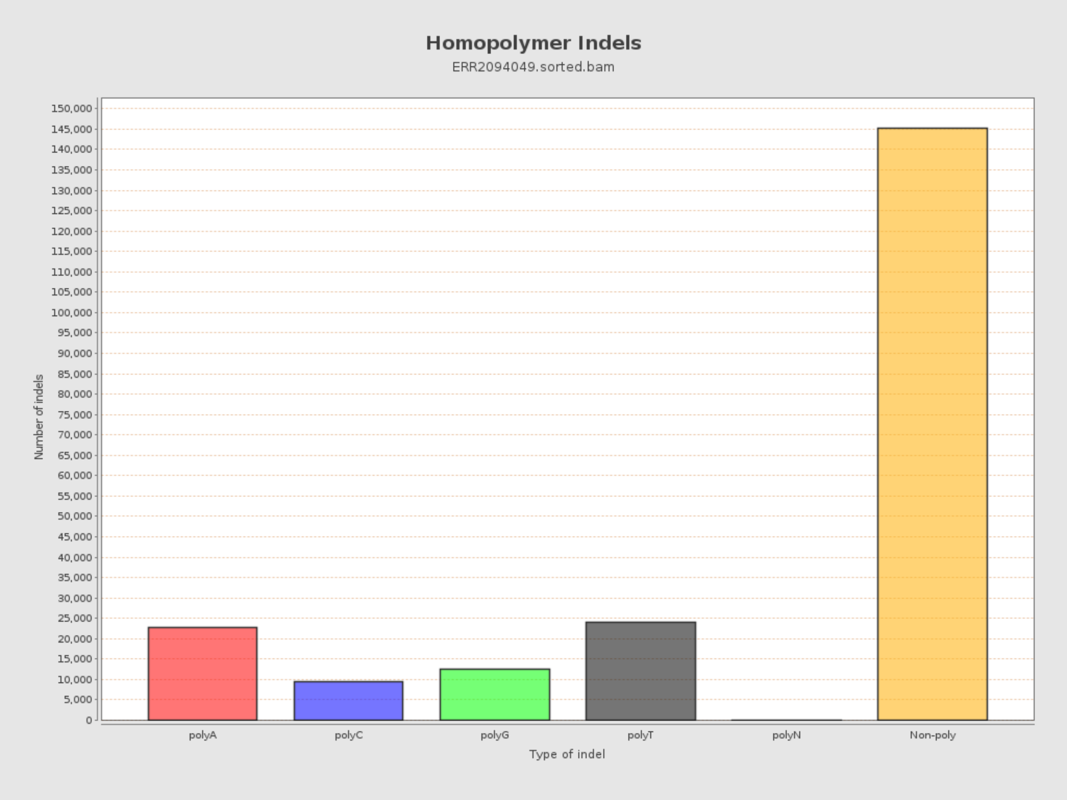
9. Results : Mapped Reads GC-content Distribution



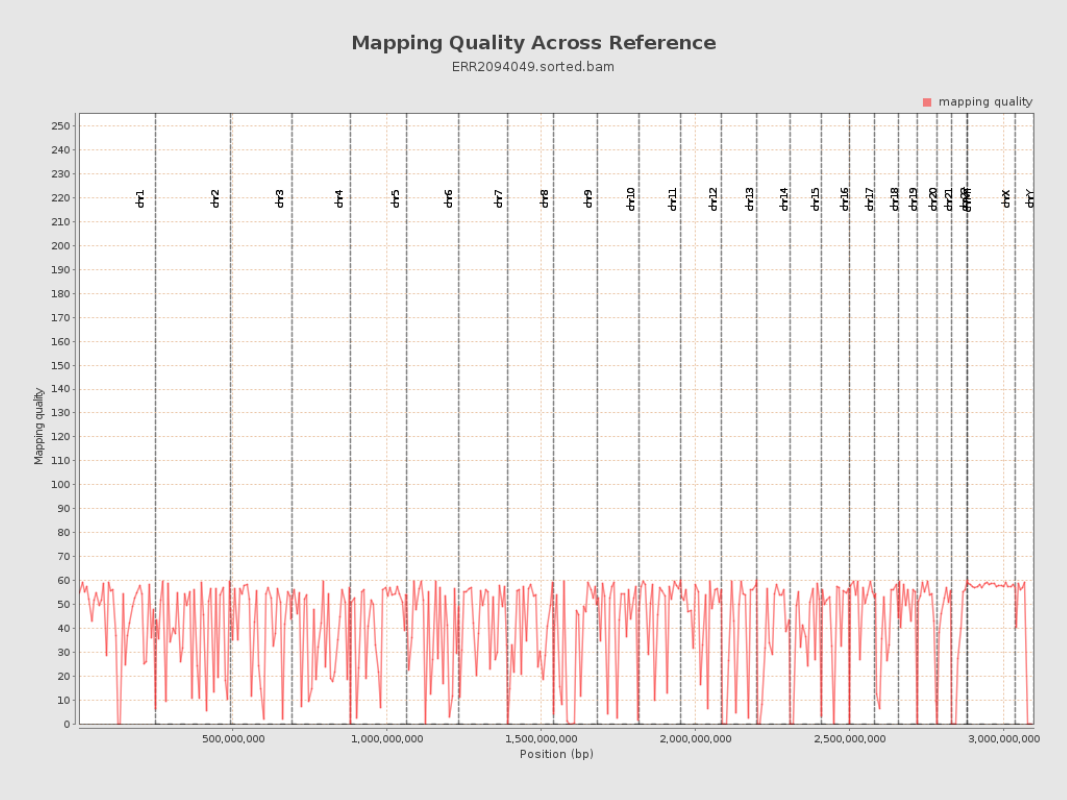
10. Results : Mapped Reads Clipping Profile



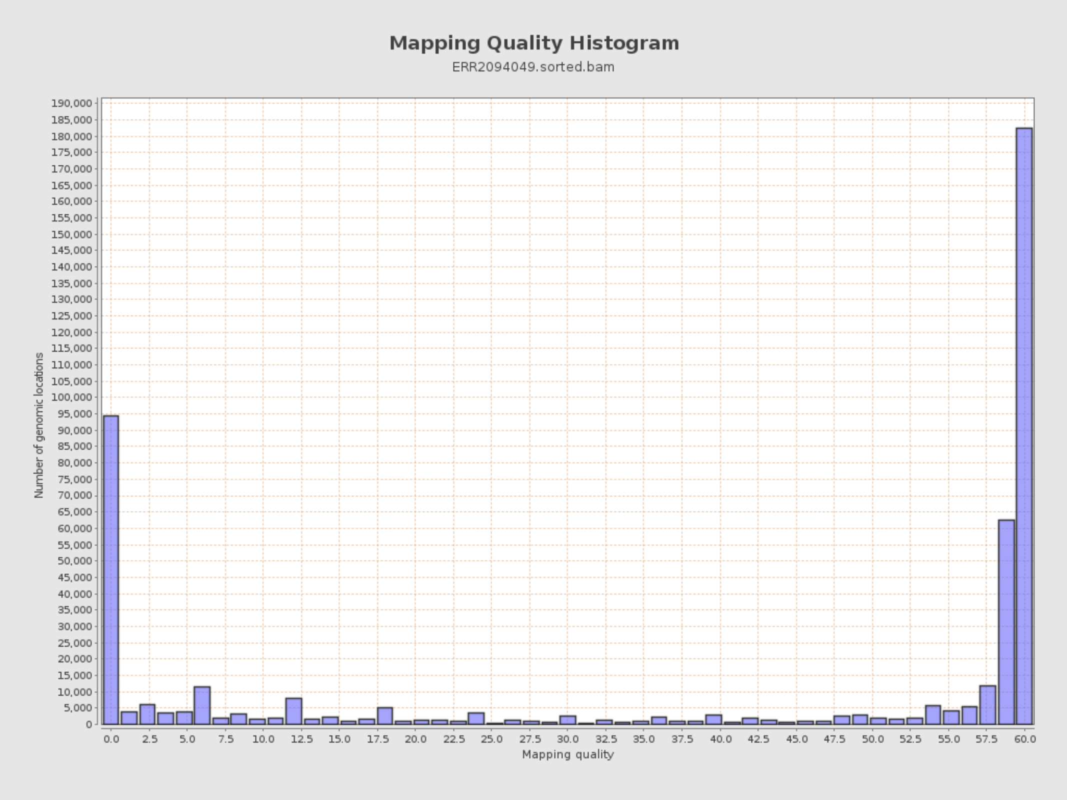
11. Results : Homopolymer Indels



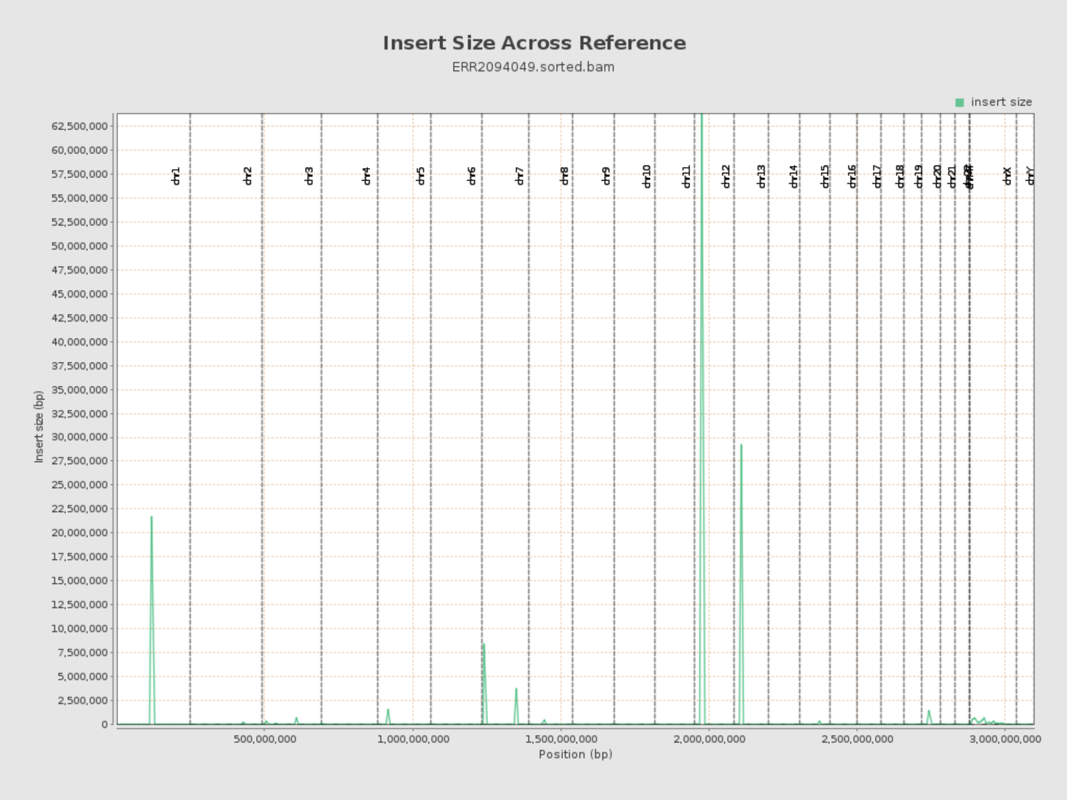
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram