Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:38:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094090.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_ERR2094090 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094090_1.fastq.gz ERR2094090_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:38:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094090.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	431,074
Mapped reads	413,768 / 95.99%
Unmapped reads	17,306 / 4.01%
Mapped paired reads	413,768 / 95.99%
Mapped reads, first in pair	207,905 / 48.23%
Mapped reads, second in pair	205,863 / 47.76%
Mapped reads, both in pair	410,384 / 95.2%
Mapped reads, singletons	3,384 / 0.79%
Secondary alignments	0
Supplementary alignments	23,971 / 5.56%
Read min/max/mean length	30 / 151 / 134.76
Duplicated reads (estimated)	401,792 / 93.21%
Duplication rate	53.84%
Clipped reads	208,420 / 48.35%

2.2. ACGT Content

Number/percentage of A's	13,869,490 / 28.6%
Number/percentage of C's	10,446,821 / 21.54%
Number/percentage of T's	13,048,071 / 26.91%
Number/percentage of G's	11,126,066 / 22.94%
Number/percentage of N's	413 / 0%

GC Percentage	44.49%

2.3. Coverage

Mean	0.016
Standard Deviation	4.1517

2.4. Mapping Quality

Mean Mapping Quality	38.58

2.5. Insert size

Mean	1,348,639.11
Standard Deviation	10,360,852.63
P25/Median/P75	110 / 134 / 162

2.6. Mismatches and indels

General error rate	3.69%
Mismatches	1,732,695
Insertions	33,918
Mapped reads with at least one insertion	8.12%
Deletions	143,595
Mapped reads with at least one deletion	33.6%
Homopolymer indels	26.83%

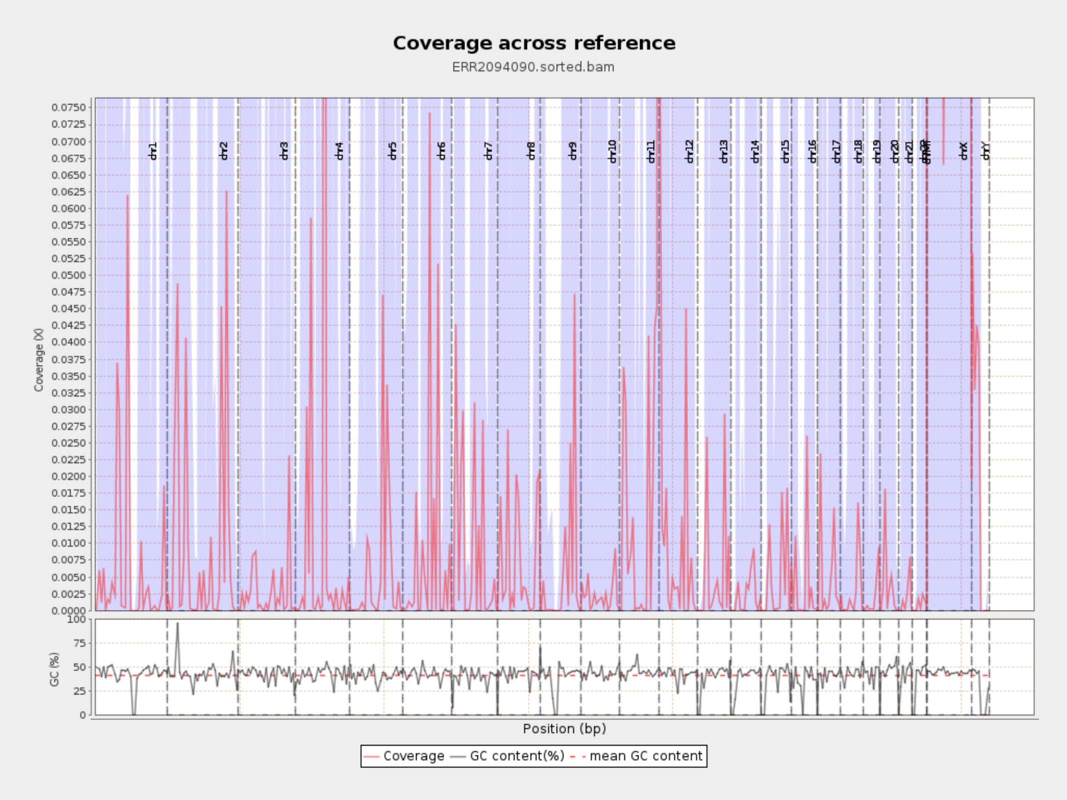
2.7. Chromosome stats

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

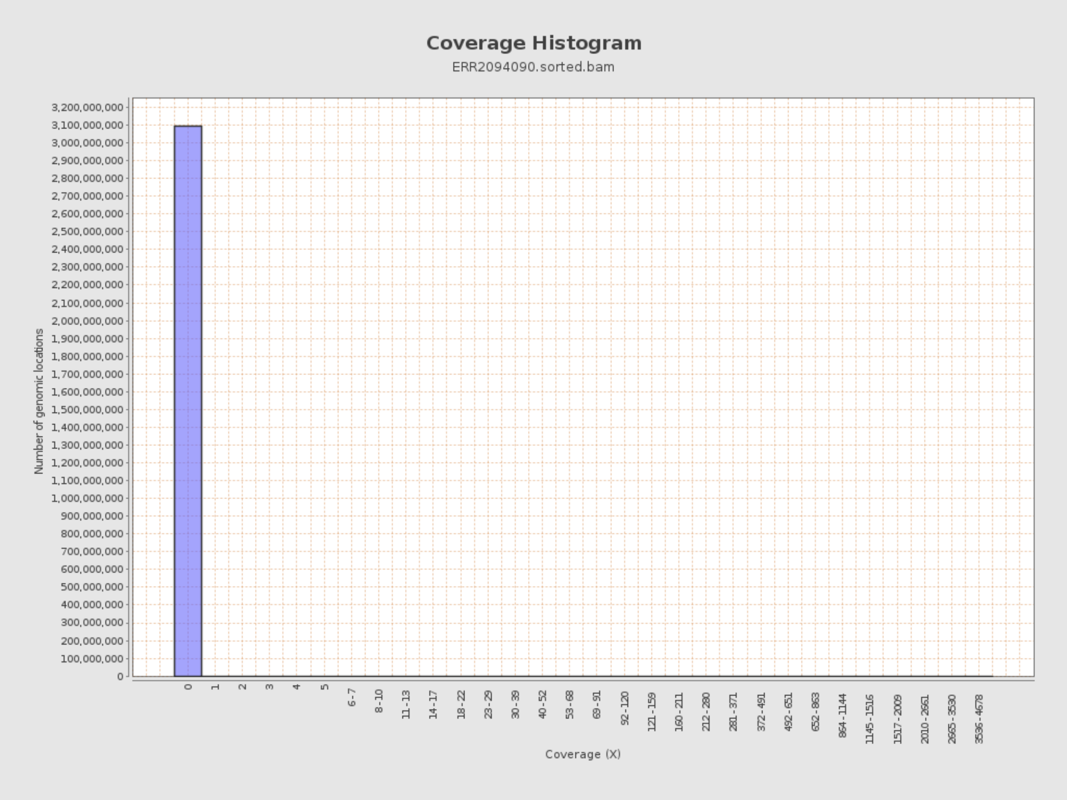
		bases	coverage	deviation
chr1	249250621	1502716	0.006	3.1559
chr2	243199373	2294156	0.0094	3.6895
chr3	198022430	565217	0.0029	1.1638
chr4	191154276	2654132	0.0139	4.7617
chr5	180915260	1121371	0.0062	3.0432
chr6	171115067	1521466	0.0089	3.6752
chr7	159138663	1384075	0.0087	2.9781
chr8	146364022	1096883	0.0075	2.4046
chr9	141213431	785570	0.0056	2.1049
chr10	135534747	302105	0.0022	0.5892
chr11	135006516	2200526	0.0163	4.7196
chr12	133851895	1537582	0.0115	3.7121
chr13	115169878	610251	0.0053	1.638
chr14	107349540	235389	0.0022	0.9066
chr15	102531392	432642	0.0042	1.4945
chr16	90354753	358942	0.004	1.9097
chr17	81195210	401046	0.0049	1.6961
chr18	78077248	242660	0.0031	1.2828
chr19	59128983	108055	0.0018	0.7446
chr20	63025520	240077	0.0038	1.4606
chr21	48129895	95814	0.002	0.5516
chr22	51304566	45723	0.0009	0.2162
chrMT	16571	6264	0.378	2.6796
chrX	155270560	28606459	0.1842	13.5672

chrY	59373566	1165207	0.0196	4.3188

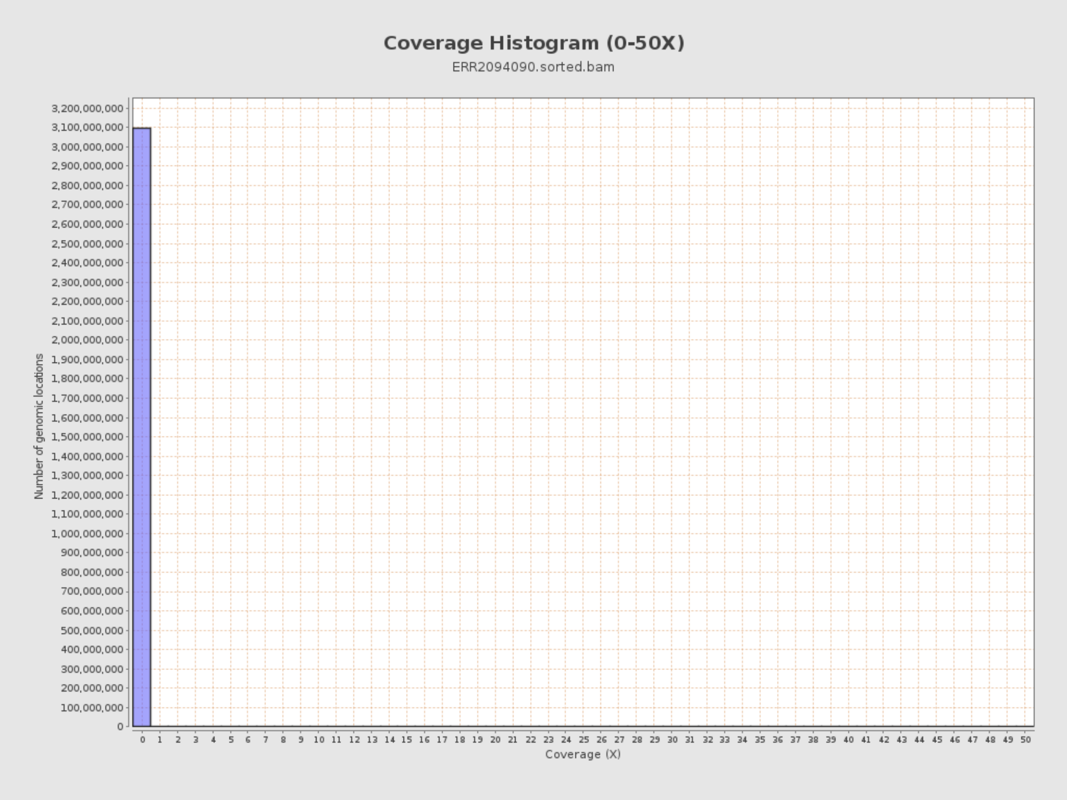
3. Results : Coverage across reference



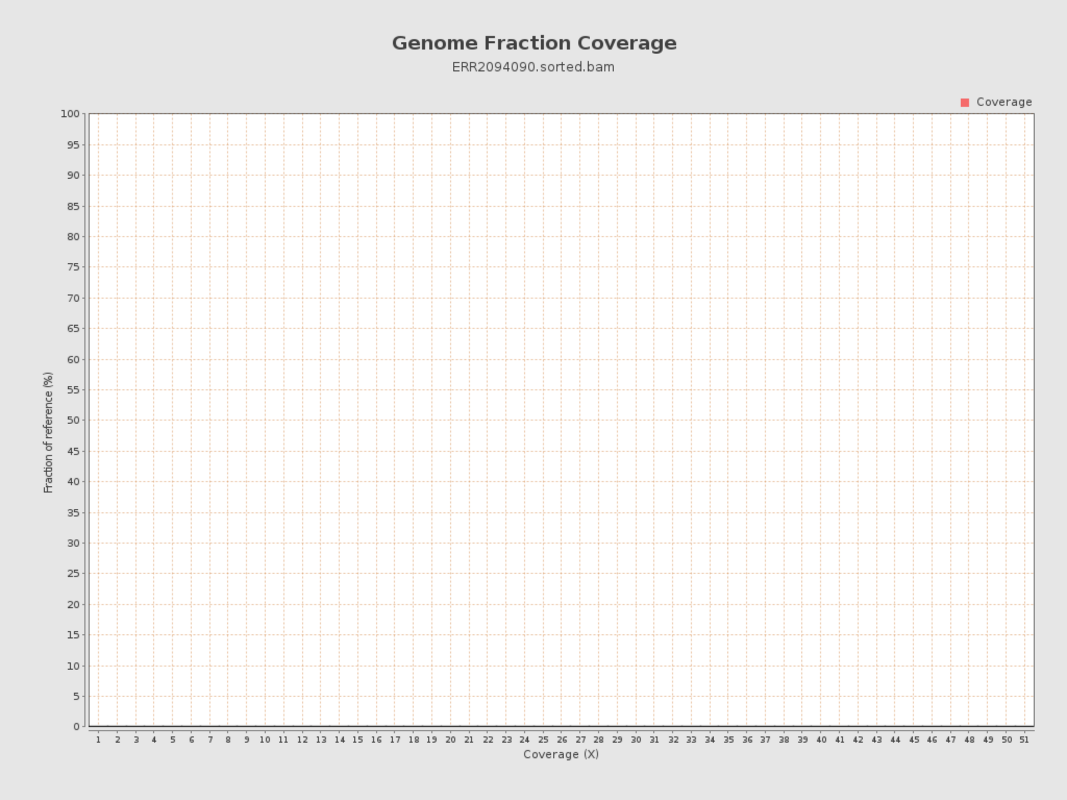
4. Results : Coverage Histogram



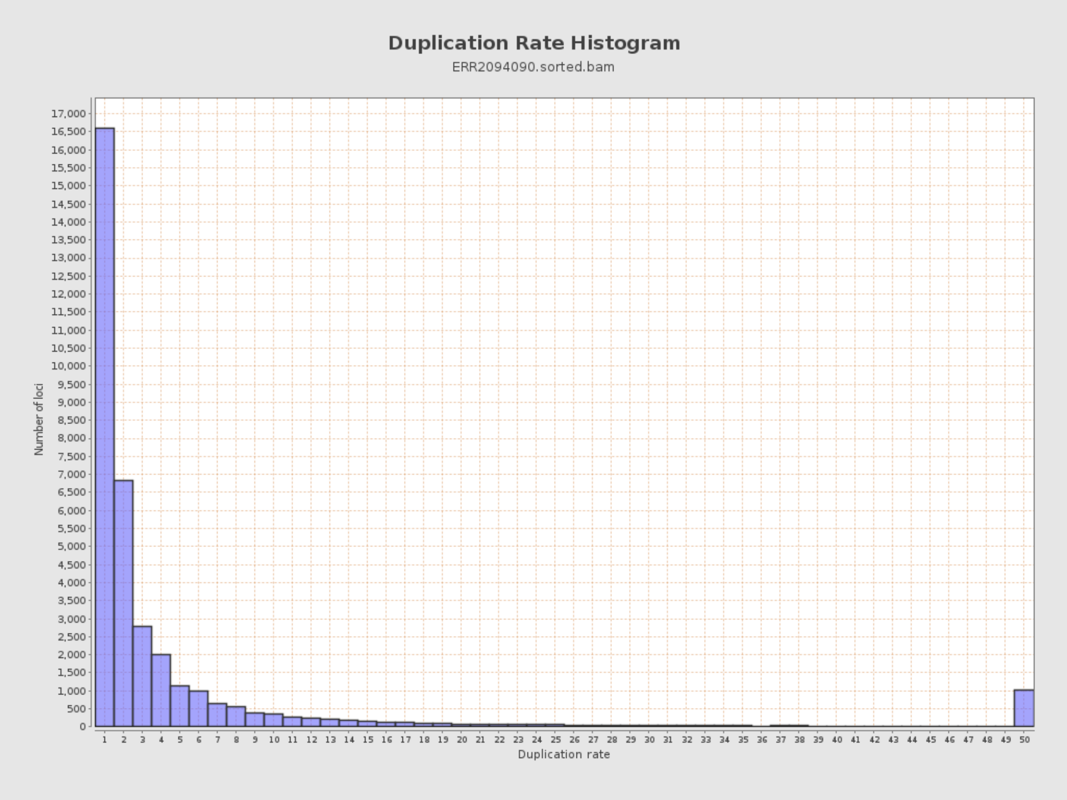
5. Results : Coverage Histogram (0-50X)



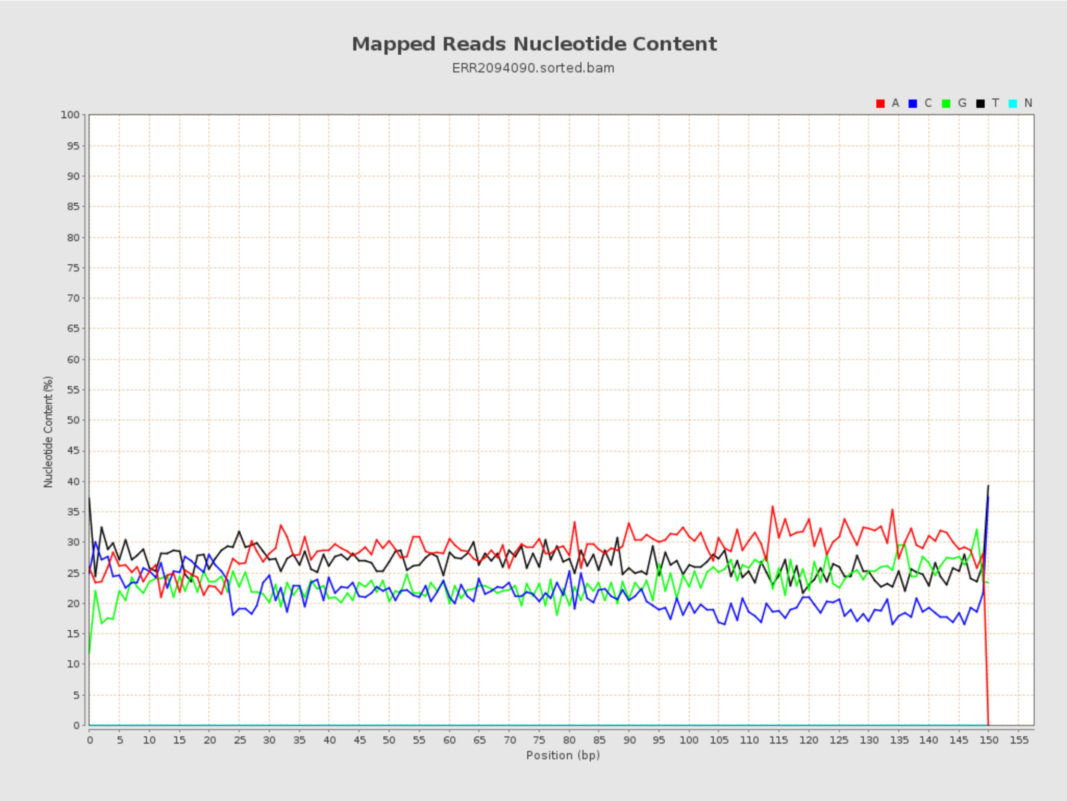
6. Results : Genome Fraction Coverage



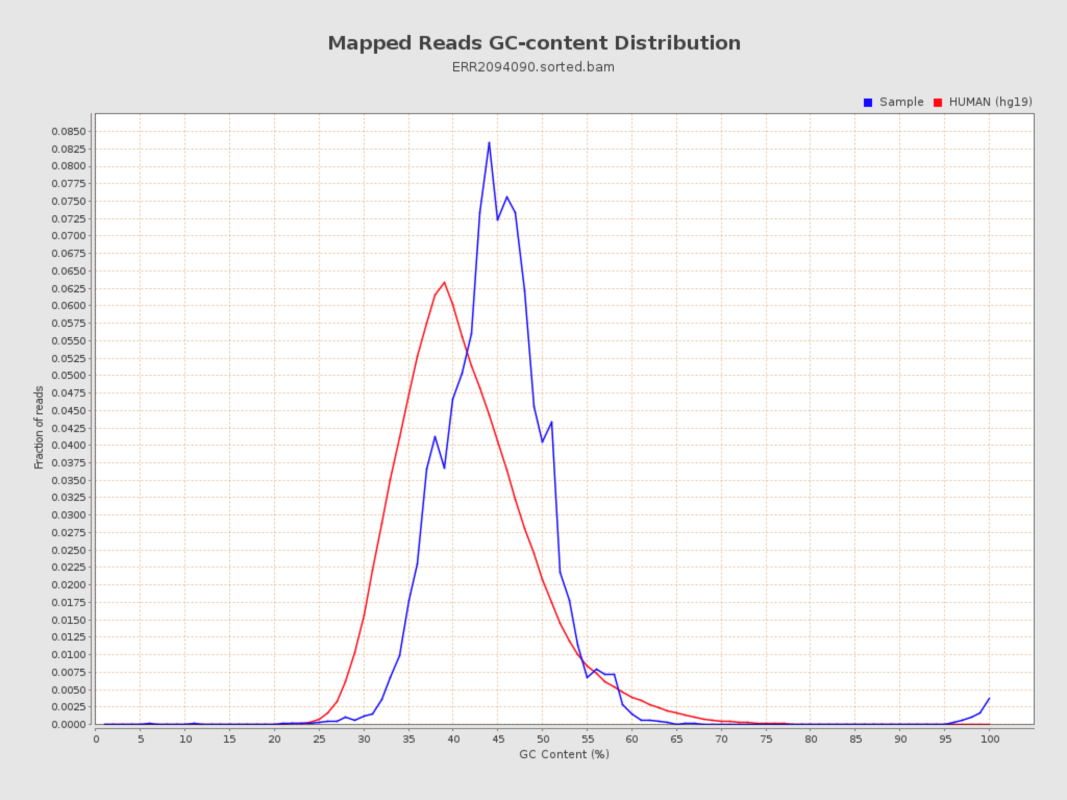
7. Results : Duplication Rate Histogram



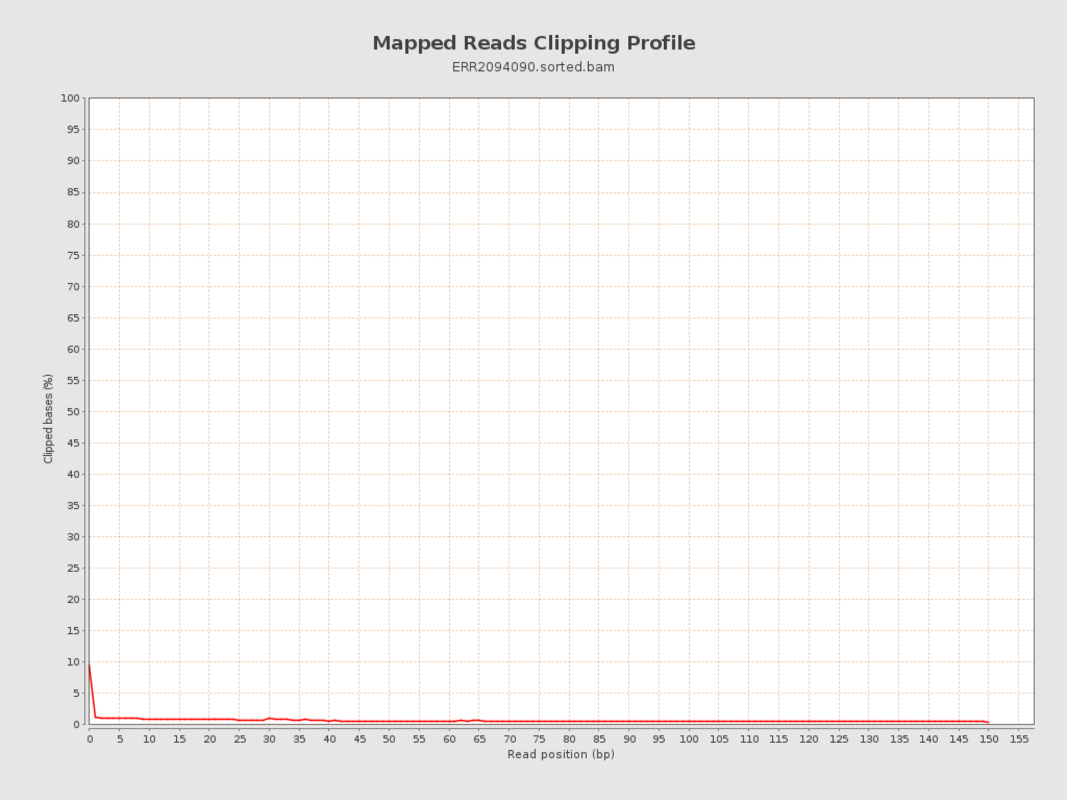
8. Results : Mapped Reads Nucleotide Content



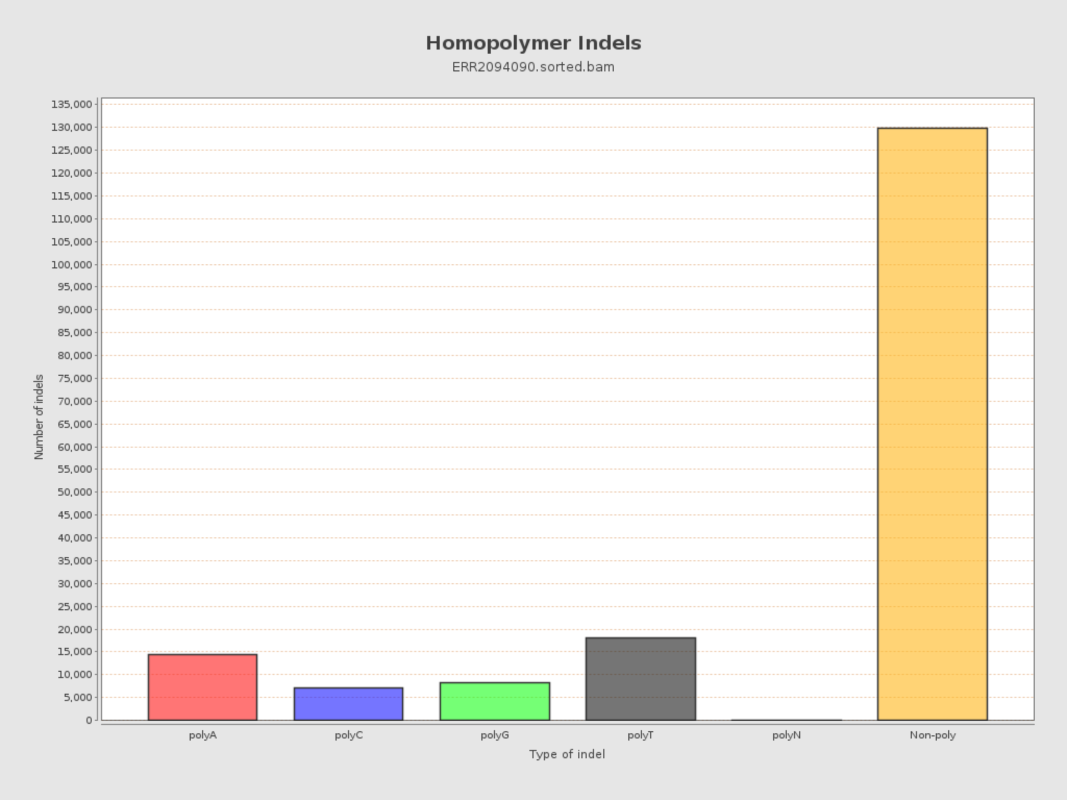
9. Results : Mapped Reads GC-content Distribution



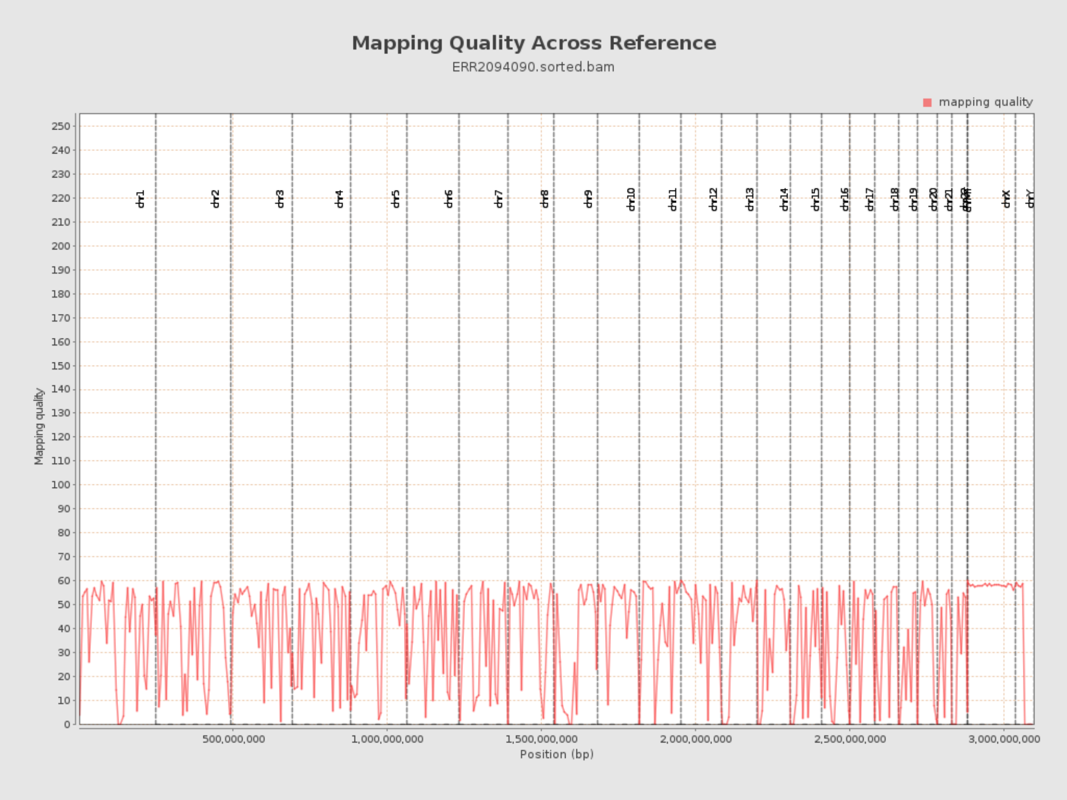
10. Results : Mapped Reads Clipping Profile



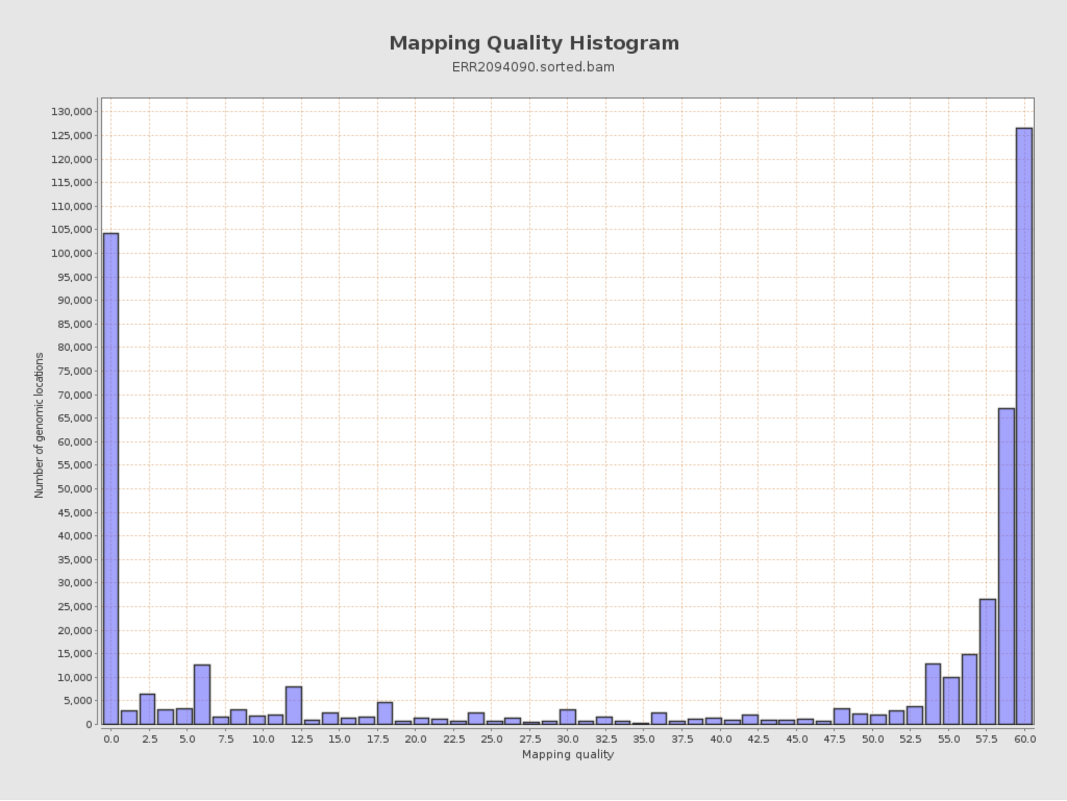
11. Results : Homopolymer Indels



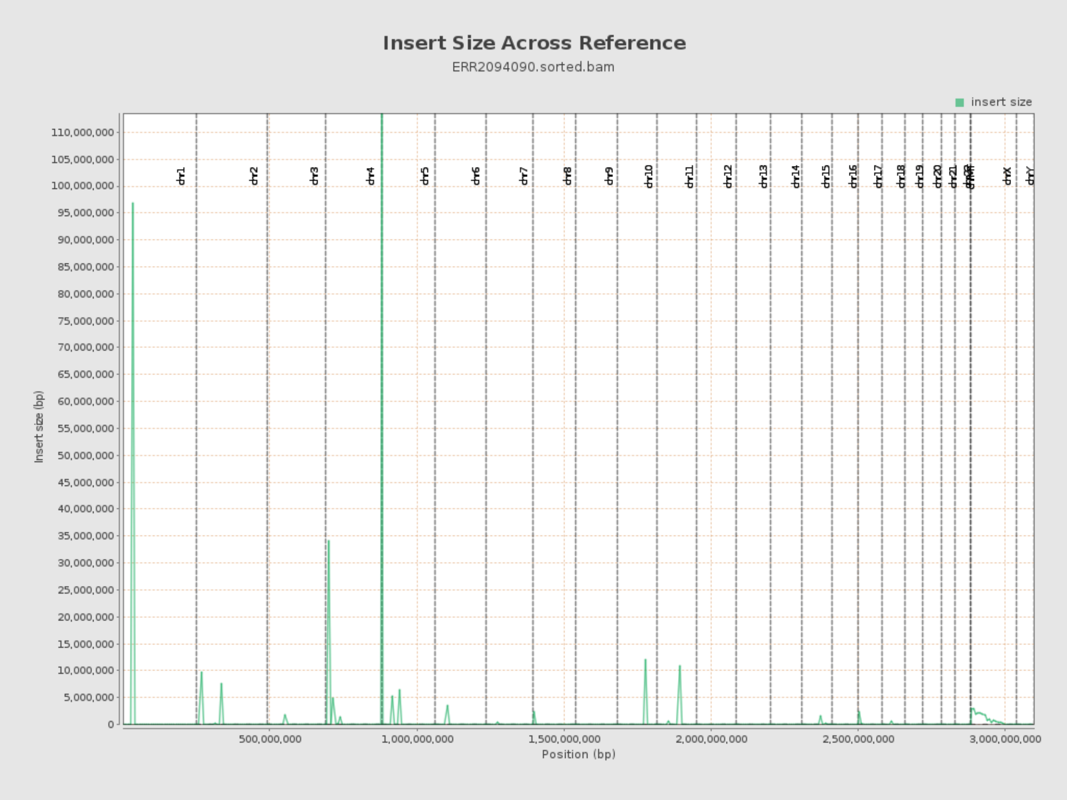
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram