Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:47:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093985.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_ERR2093985 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093985_1.fastq.gz ERR2093985_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:47:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	360,064
Mapped reads	343,151 / 95.3%
Unmapped reads	16,913 / 4.7%
Mapped paired reads	343,151 / 95.3%
Mapped reads, first in pair	172,576 / 47.93%
Mapped reads, second in pair	170,575 / 47.37%
Mapped reads, both in pair	339,800 / 94.37%
Mapped reads, singletons	3,351 / 0.93%
Secondary alignments	0
Supplementary alignments	21,095 / 5.86%
Read min/max/mean length	30 / 151 / 141.07
Duplicated reads (estimated)	323,021 / 89.71%
Duplication rate	49.44%
Clipped reads	165,647 / 46%

2.2. ACGT Content

Number/percentage of A's	11,297,824 / 26.19%
Number/percentage of C's	10,284,784 / 23.84%
Number/percentage of T's	10,601,846 / 24.57%
Number/percentage of G's	10,958,632 / 25.4%
Number/percentage of N's	517 / 0%

GC Percentage	49.24%

2.3. Coverage

Mean	0.0142
Standard Deviation	2.847

2.4. Mapping Quality

Mean Mapping Quality	40.51

2.5. Insert size

Mean	1,030,877.31
Standard Deviation	9,162,734.35
P25/Median/P75	126 / 163 / 201

2.6. Mismatches and indels

General error rate	3.37%
Mismatches	1,400,062
Insertions	23,269
Mapped reads with at least one insertion	6.67%
Deletions	112,956
Mapped reads with at least one deletion	31.6%
Homopolymer indels	29.83%

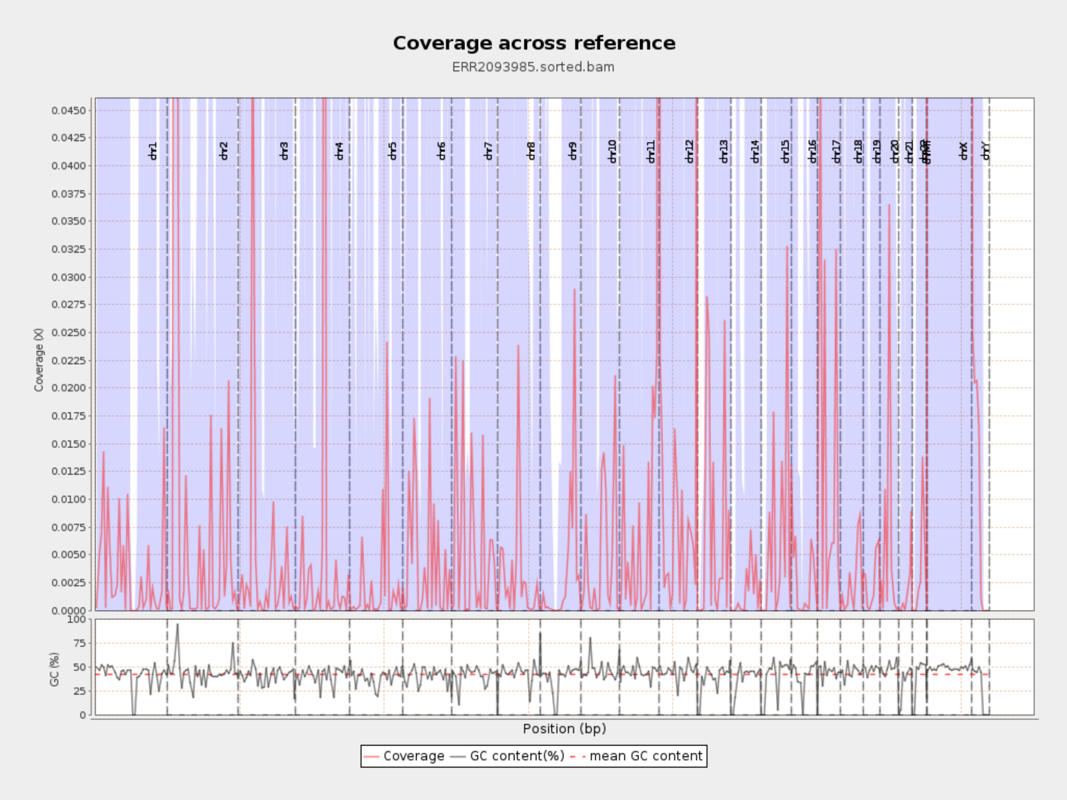
2.7. Chromosome stats

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

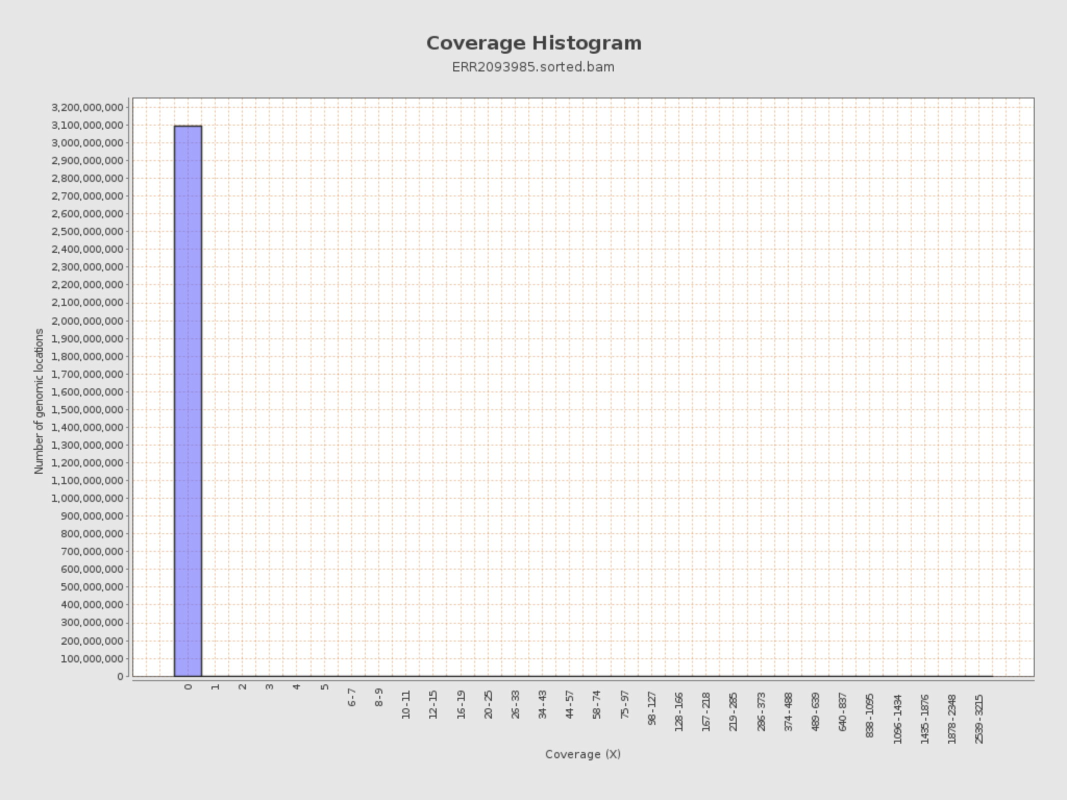
		bases	**coverage**	**deviation**
chr1	249250621	843581	0.0034	1.1319
chr2	243199373	2419411	0.0099	3.2213
chr3	198022430	810215	0.0041	1.461
chr4	191154276	1117611	0.0058	2.0352
chr5	180915260	419396	0.0023	1.3298
chr6	171115067	782155	0.0046	1.3588
chr7	159138663	847988	0.0053	1.5184
chr8	146364022	446747	0.0031	0.9764
chr9	141213431	504915	0.0036	1.0825
chr10	135534747	631657	0.0047	1.3578
chr11	135006516	1119156	0.0083	2.1881
chr12	133851895	1011383	0.0076	1.8294
chr13	115169878	860285	0.0075	2.2475
chr14	107349540	179711	0.0017	0.568
chr15	102531392	658229	0.0064	1.7092
chr16	90354753	260148	0.0029	0.8499
chr17	81195210	1211666	0.0149	3.5244
chr18	78077248	208163	0.0027	0.7065
chr19	59128983	146769	0.0025	0.6762
chr20	63025520	426459	0.0068	2.4612
chr21	48129895	87566	0.0018	0.3409
chr22	51304566	163654	0.0032	0.9457
chrMT	16571	1274325	76.9009	355.6989
chrX	155270560	26869704	0.1731	9.347

chrY	59373566	586411	0.0099	1.4818

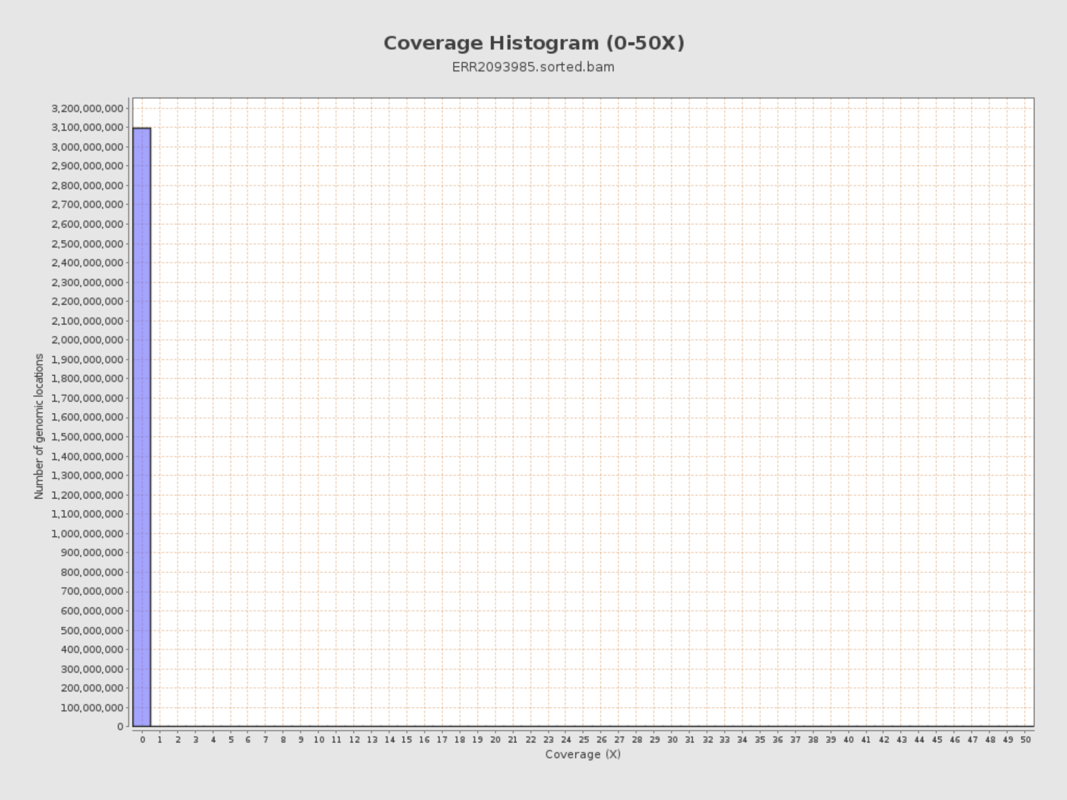
3. Results : Coverage across reference



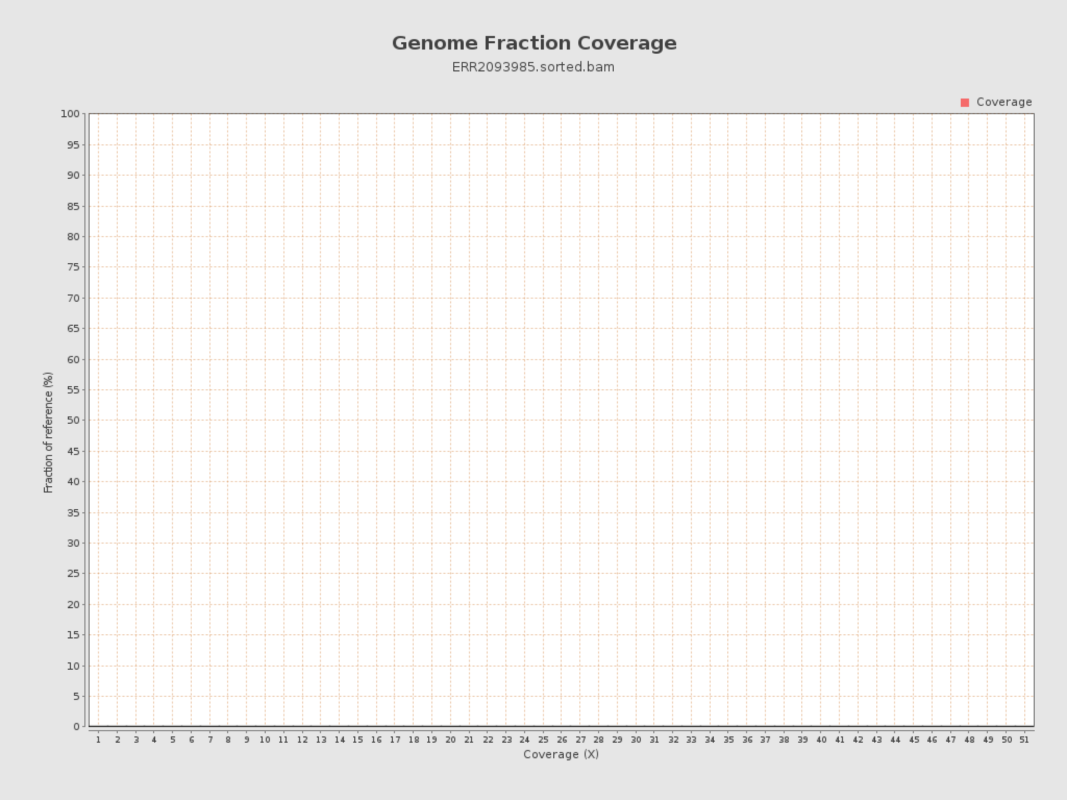
4. Results : Coverage Histogram



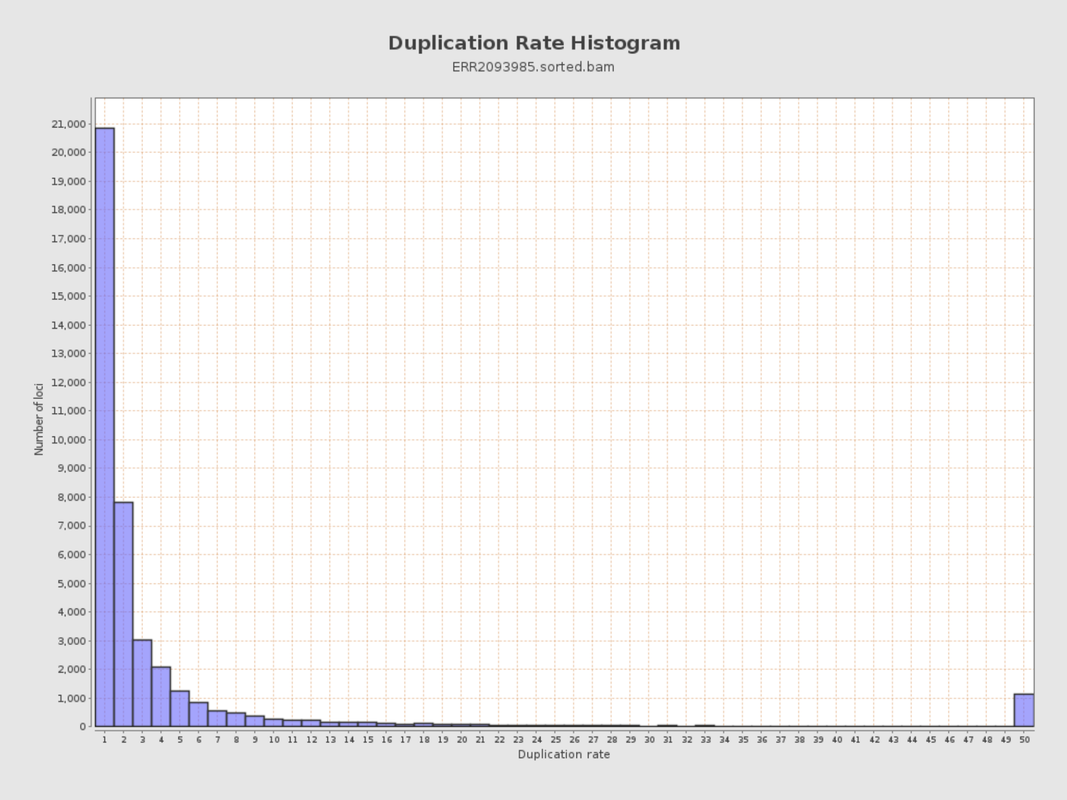
5. Results : Coverage Histogram (0-50X)



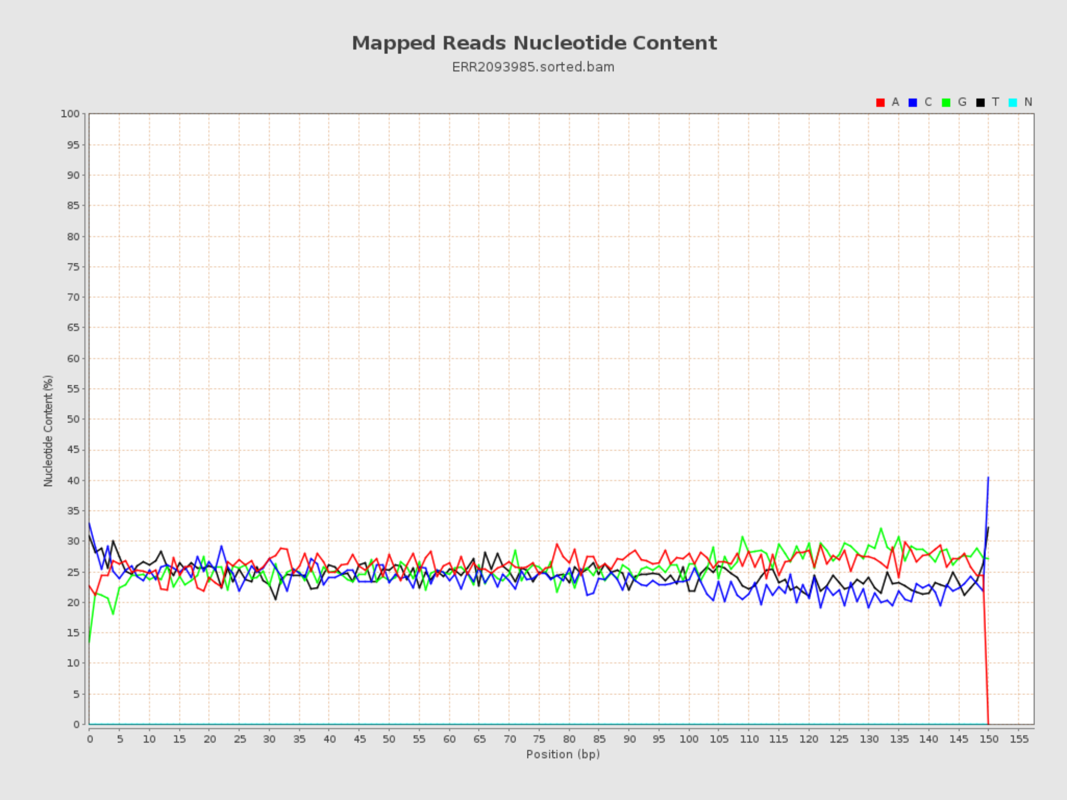
6. Results : Genome Fraction Coverage



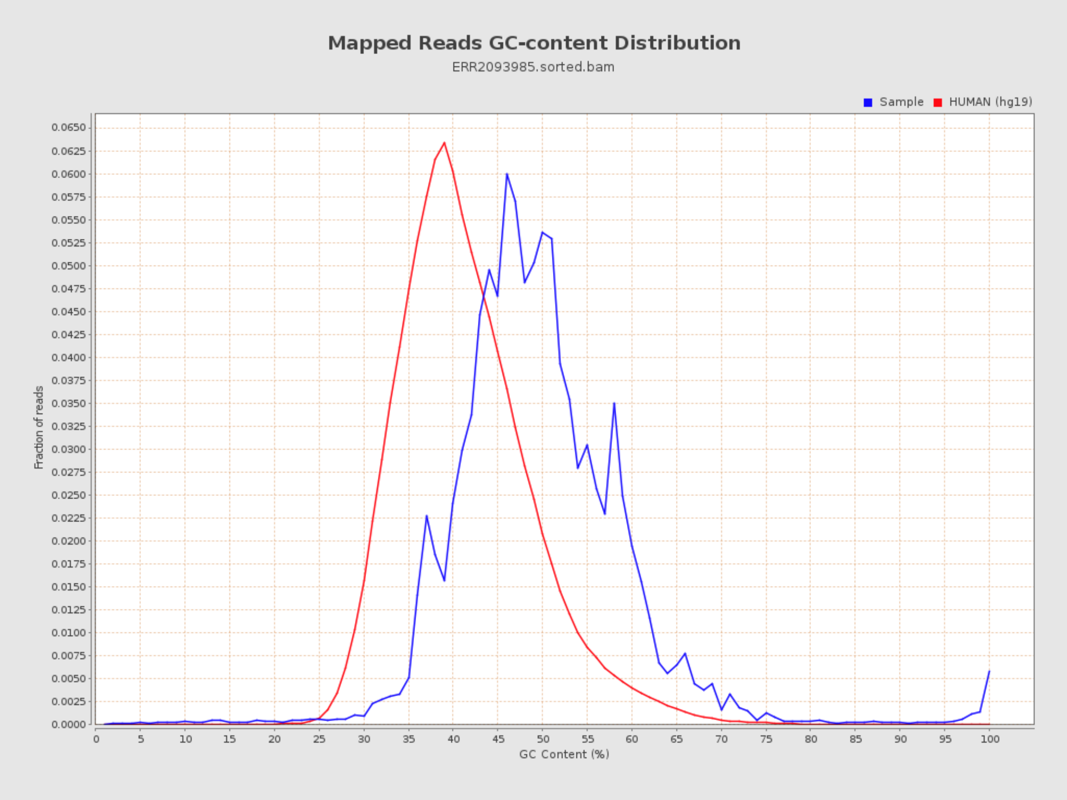
7. Results : Duplication Rate Histogram



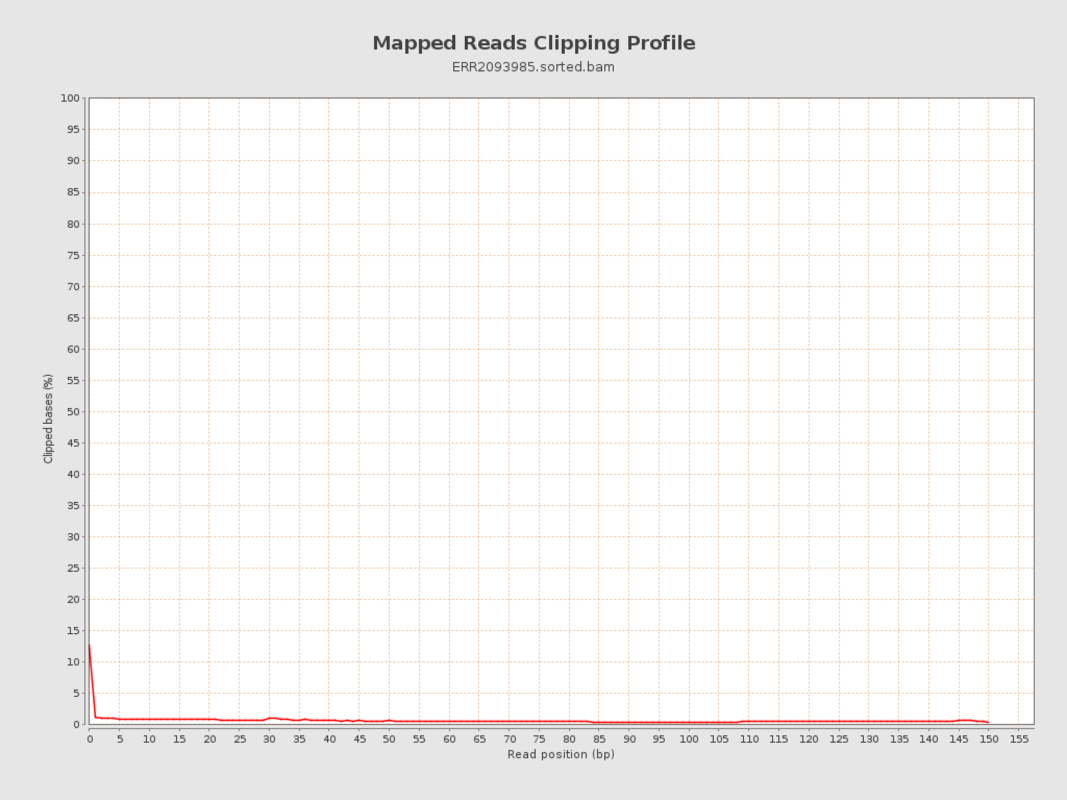
8. Results : Mapped Reads Nucleotide Content



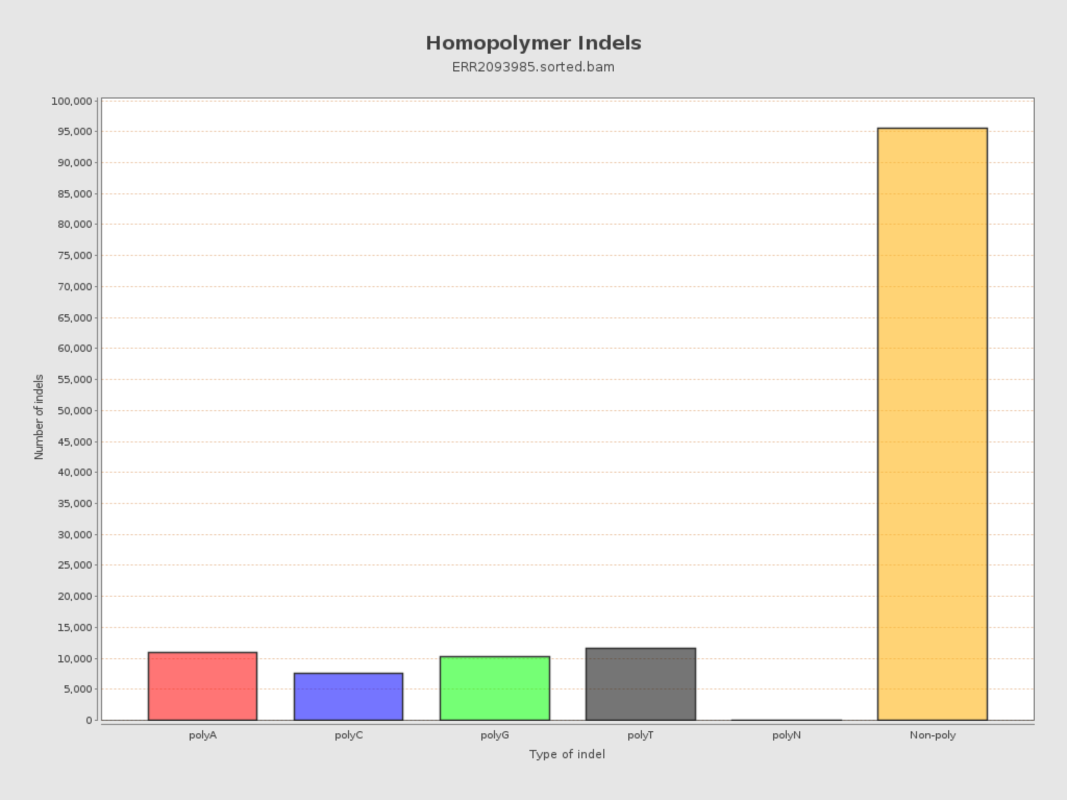
9. Results : Mapped Reads GC-content Distribution



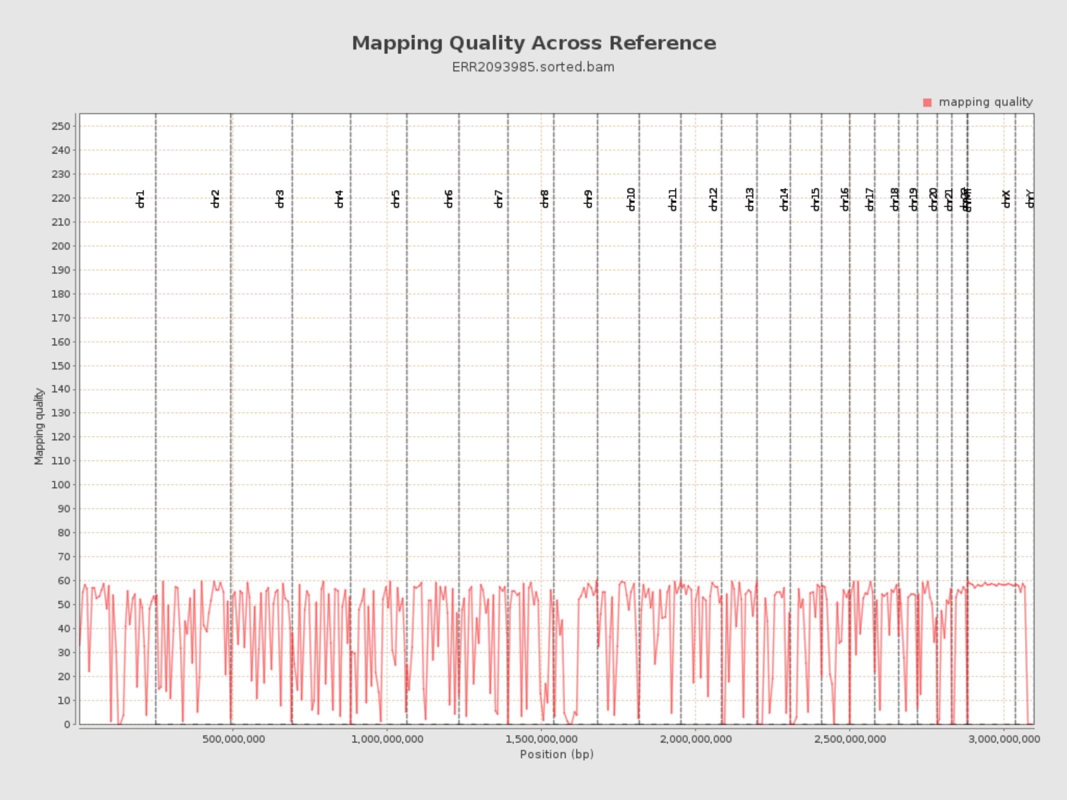
10. Results : Mapped Reads Clipping Profile



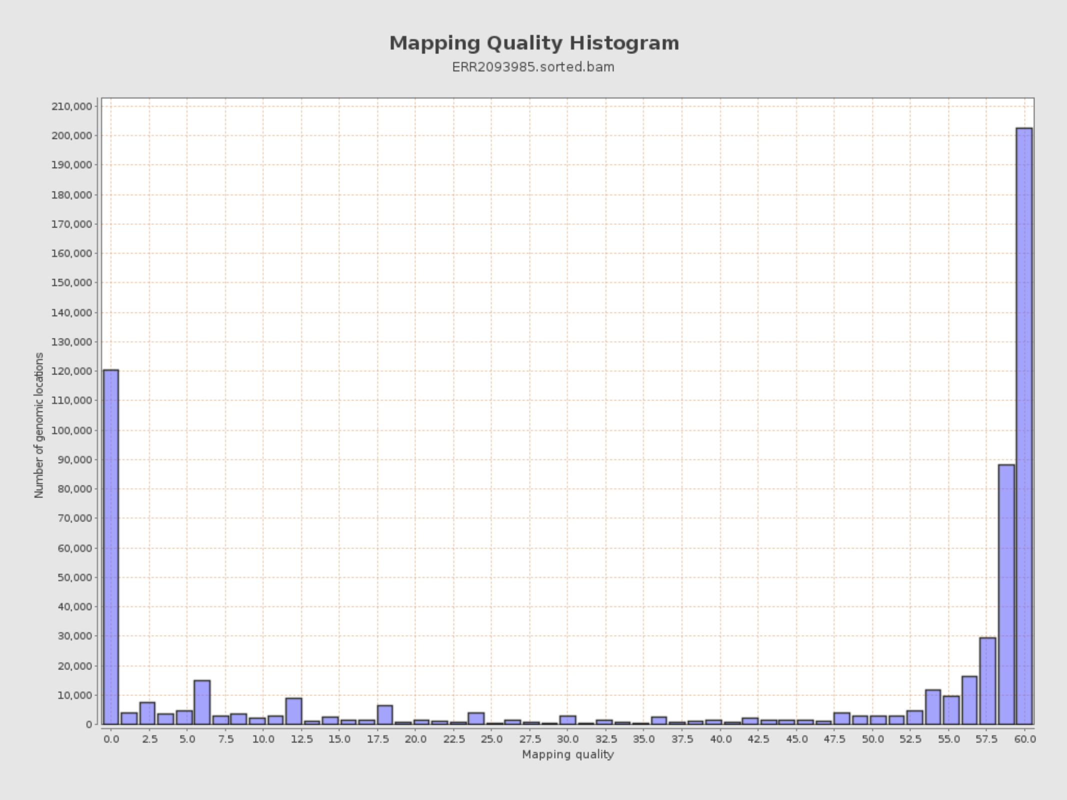
11. Results : Homopolymer Indels



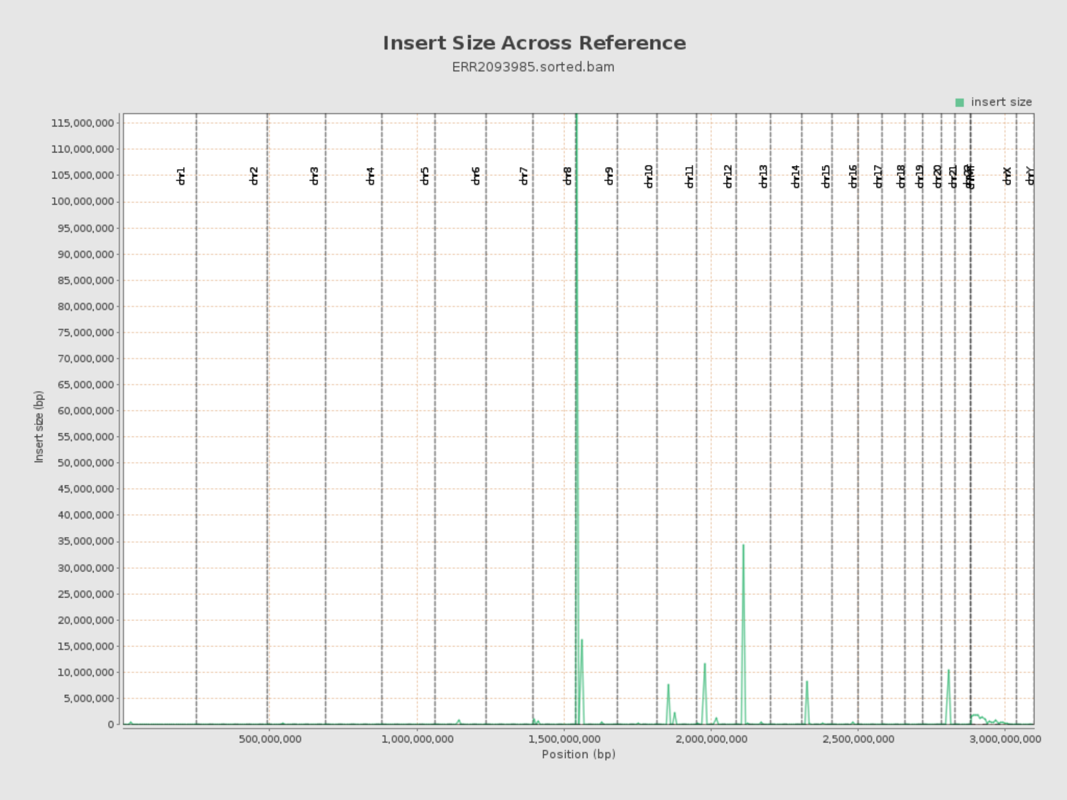
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram