Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:42:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093983.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_ERR2093983 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093983_1.fastq.gz ERR2093983_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:42:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	489,974
Mapped reads	481,983 / 98.37%
Unmapped reads	7,991 / 1.63%
Mapped paired reads	481,983 / 98.37%
Mapped reads, first in pair	242,504 / 49.49%
Mapped reads, second in pair	239,479 / 48.88%
Mapped reads, both in pair	477,774 / 97.51%
Mapped reads, singletons	4,209 / 0.86%
Secondary alignments	0
Supplementary alignments	29,134 / 5.95%
Read min/max/mean length	30 / 151 / 148.25
Duplicated reads (estimated)	497,875 / 101.61%
Duplication rate	47.36%
Clipped reads	202,507 / 41.33%

2.2. ACGT Content

Number/percentage of A's	17,998,580 / 28.07%
Number/percentage of C's	13,618,530 / 21.24%
Number/percentage of T's	17,077,727 / 26.64%
Number/percentage of G's	15,417,387 / 24.05%
Number/percentage of N's	739 / 0%

GC Percentage	45.29%

2.3. Coverage

Mean	0.0209
Standard Deviation	14.1549

2.4. Mapping Quality

Mean Mapping Quality	19.08

2.5. Insert size

Mean	430,867.93
Standard Deviation	5,347,853.25
P25/Median/P75	147 / 184 / 218

2.6. Mismatches and indels

General error rate	2.63%
Mismatches	1,610,668
Insertions	32,899
Mapped reads with at least one insertion	6.74%
Deletions	127,168
Mapped reads with at least one deletion	25.63%
Homopolymer indels	33.52%

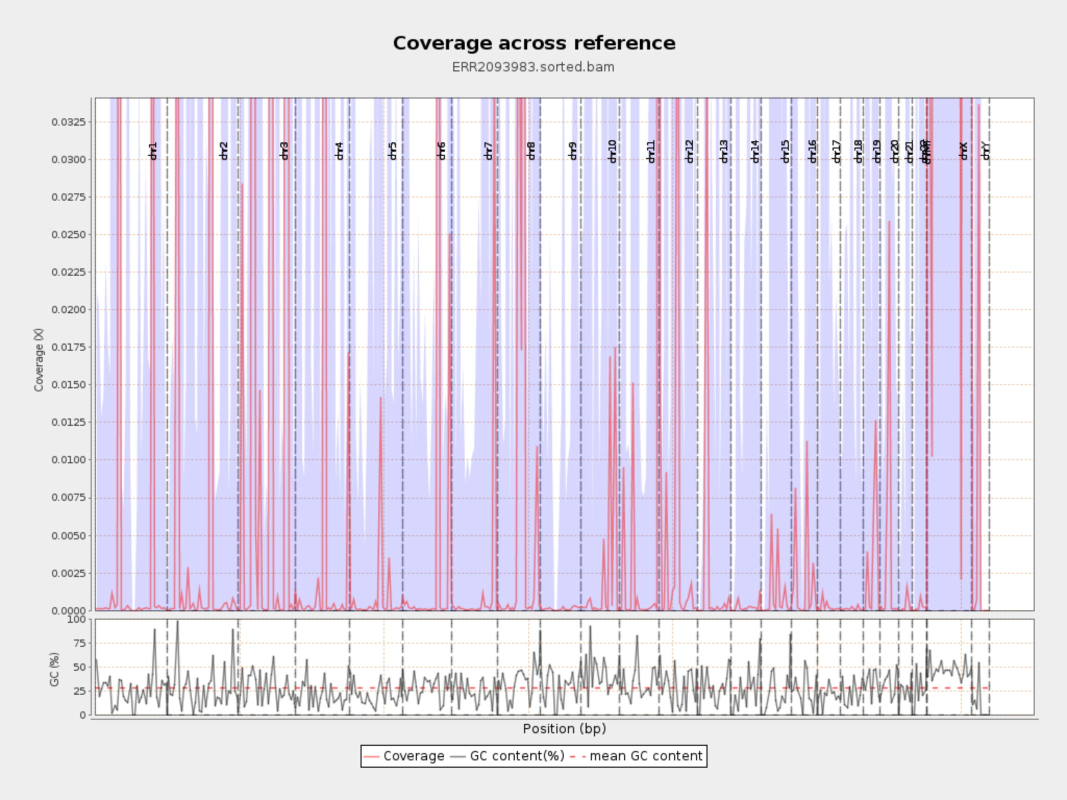
2.7. Chromosome stats

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

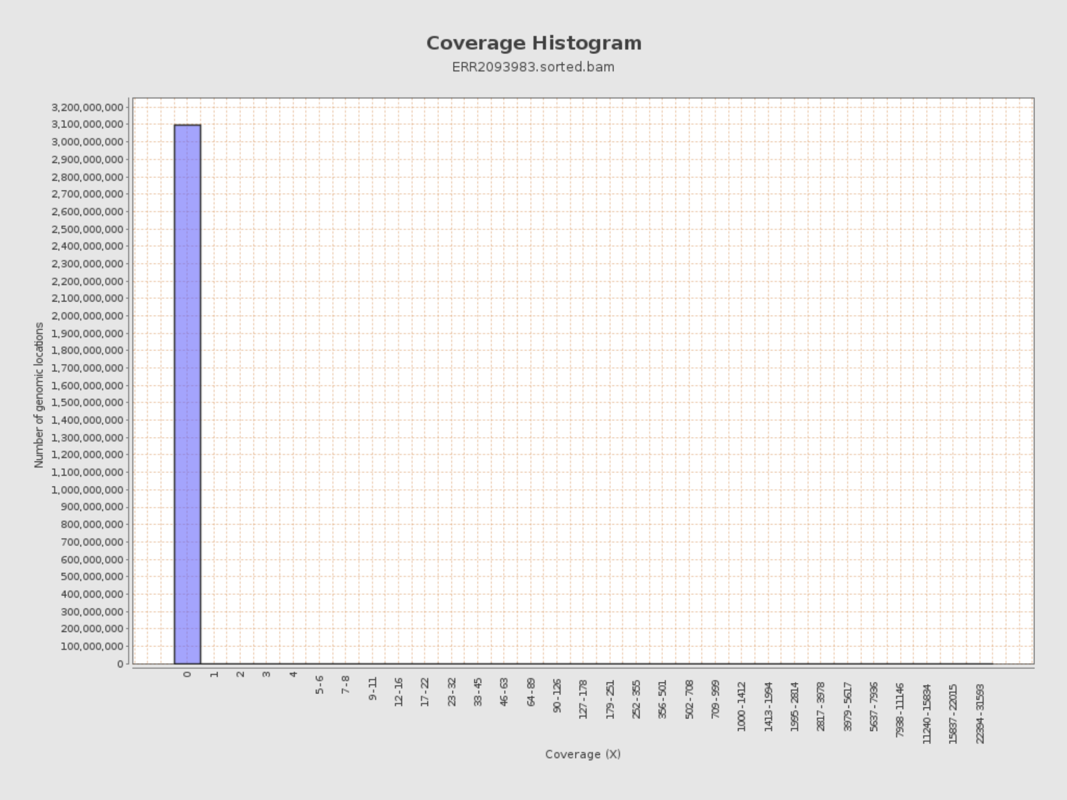
		bases	**coverage**	**deviation**
chr1	249250621	1282487	0.0051	4.9386
chr2	243199373	2887743	0.0119	12.3949
chr3	198022430	5074621	0.0256	14.9966
chr4	191154276	2185395	0.0114	8.2175
chr5	180915260	165452	0.0009	0.6621
chr6	171115067	1214592	0.0071	6.8816
chr7	159138663	316152	0.002	1.2986
chr8	146364022	1661526	0.0114	6.4965
chr9	141213431	16914	0.0001	0.0232
chr10	135534747	328419	0.0024	1.1426
chr11	135006516	599513	0.0044	2.8626
chr12	133851895	663301	0.005	3.9018
chr13	115169878	307603	0.0027	2.3014
chr14	107349540	27003	0.0003	0.1277
chr15	102531392	115260	0.0011	0.6738
chr16	90354753	196457	0.0022	0.8988
chr17	81195210	22242	0.0003	0.1324
chr18	78077248	10255	0.0001	0.0438
chr19	59128983	186099	0.0031	1.2299
chr20	63025520	271245	0.0043	2.1821
chr21	48129895	14792	0.0003	0.1269
chr22	51304566	12295	0.0002	0.0804
chrMT	16571	7603078	458.8183	2,453.0007
chrX	155270560	39222442	0.2526	50.5398

chrY	59373566	267344	0.0045	2.8957

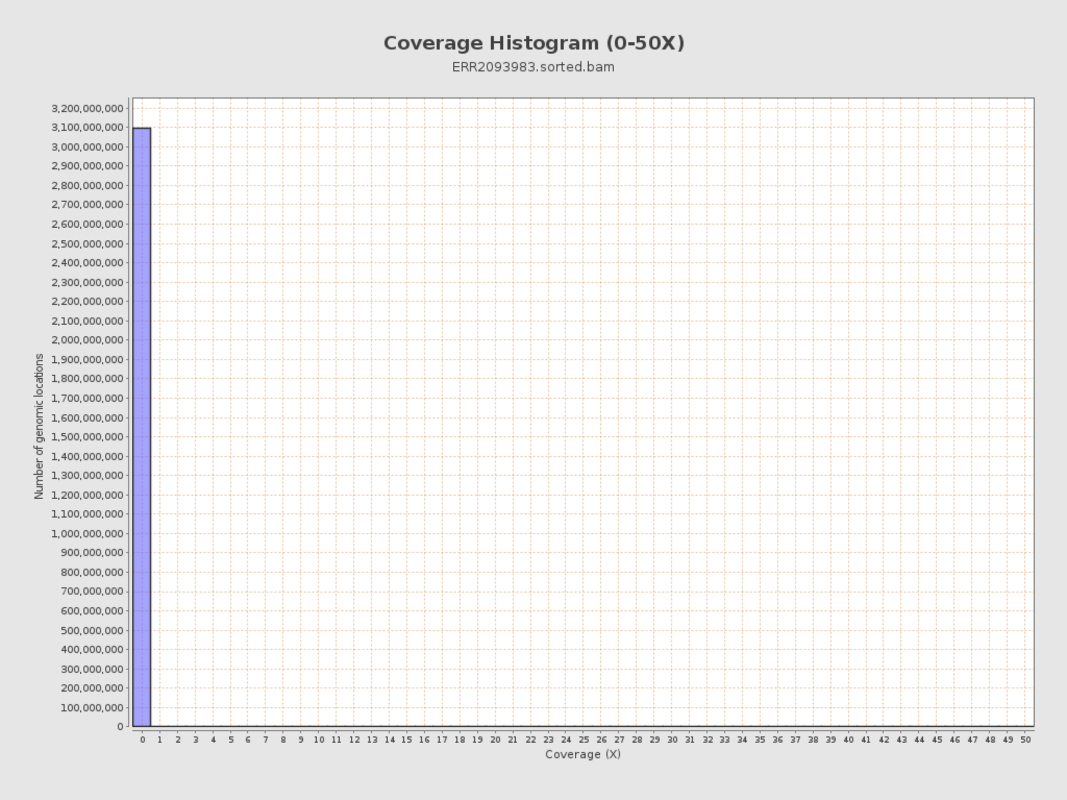
3. Results : Coverage across reference



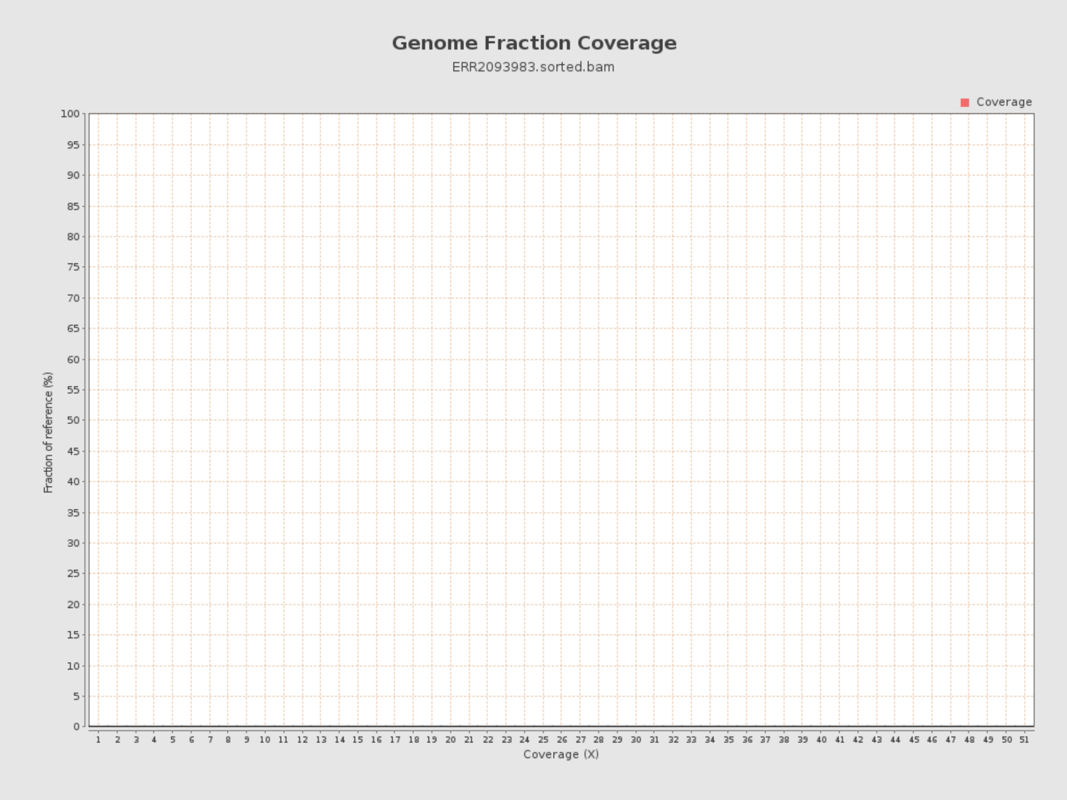
4. Results : Coverage Histogram



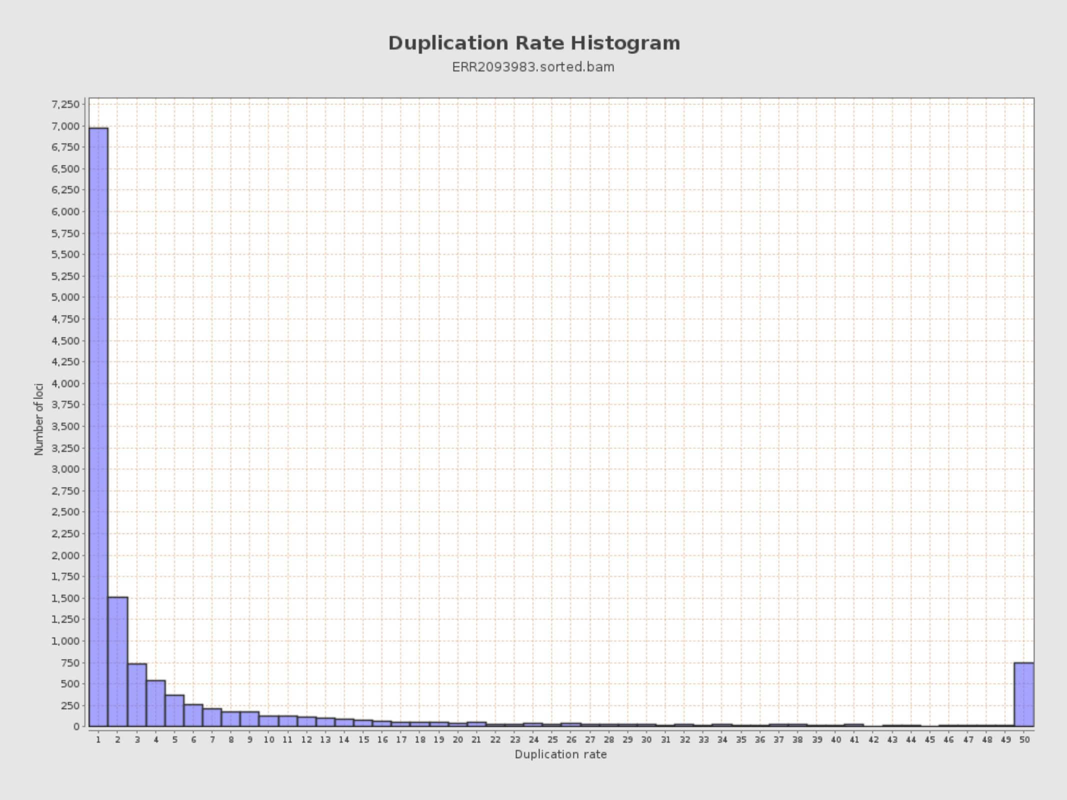
5. Results : Coverage Histogram (0-50X)



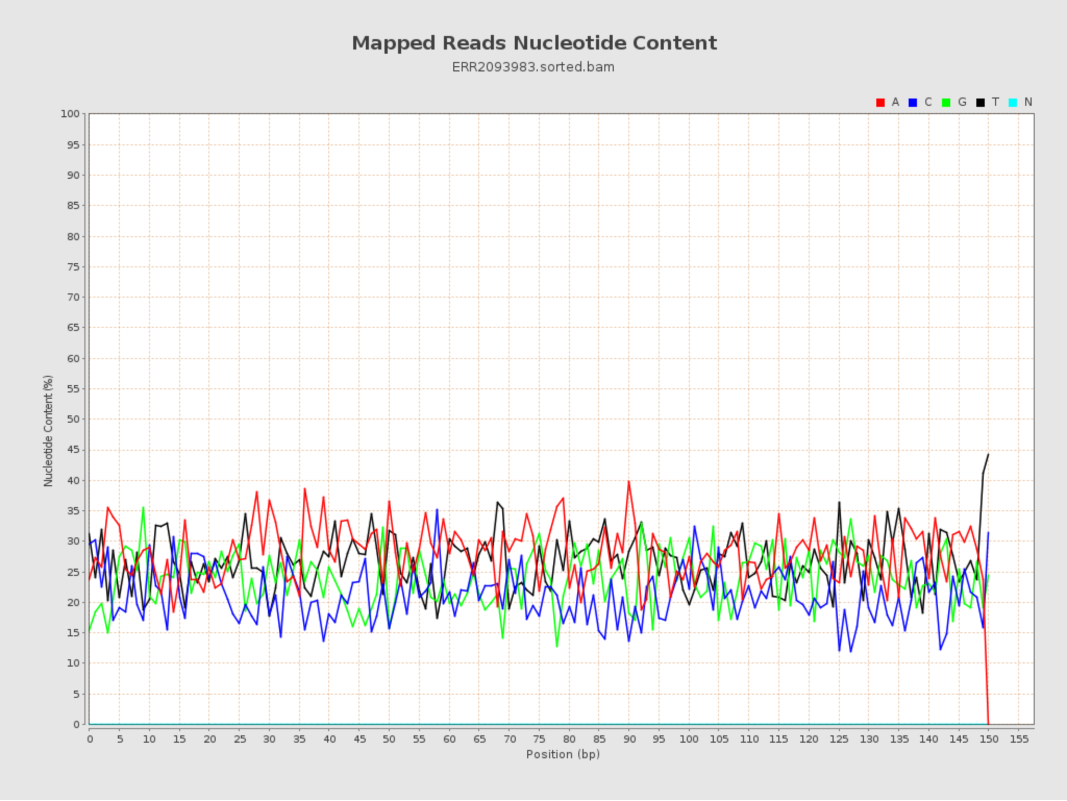
6. Results : Genome Fraction Coverage



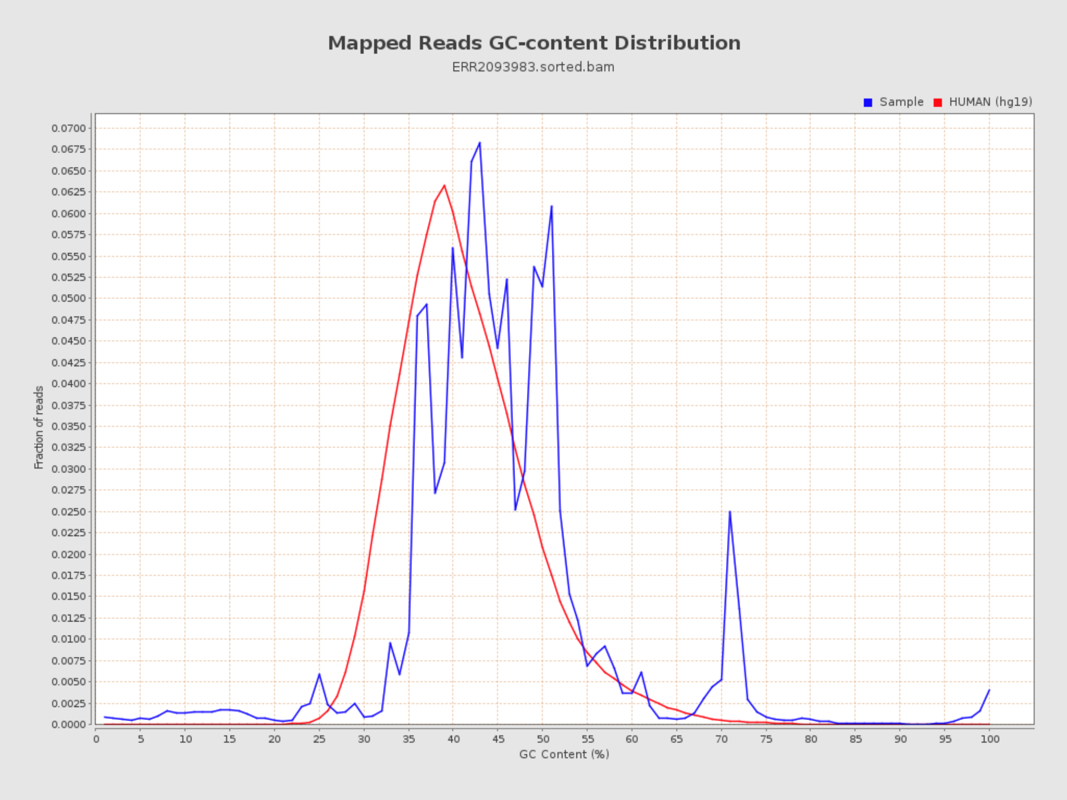
7. Results : Duplication Rate Histogram



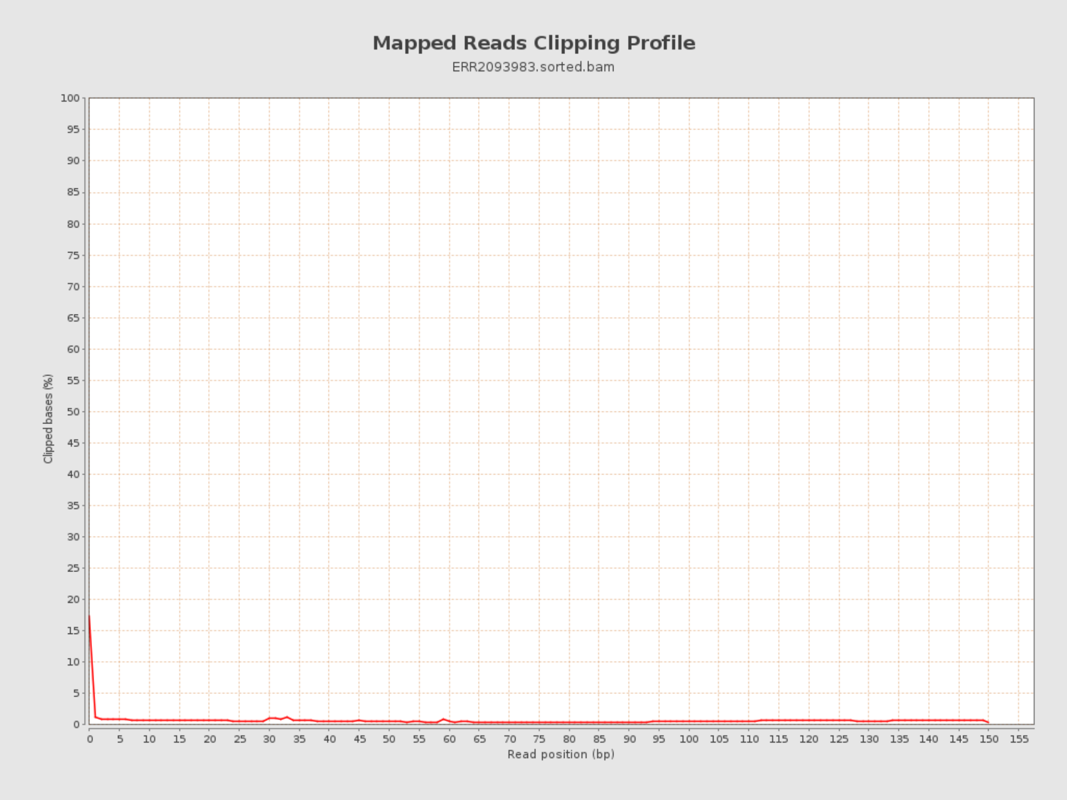
8. Results : Mapped Reads Nucleotide Content



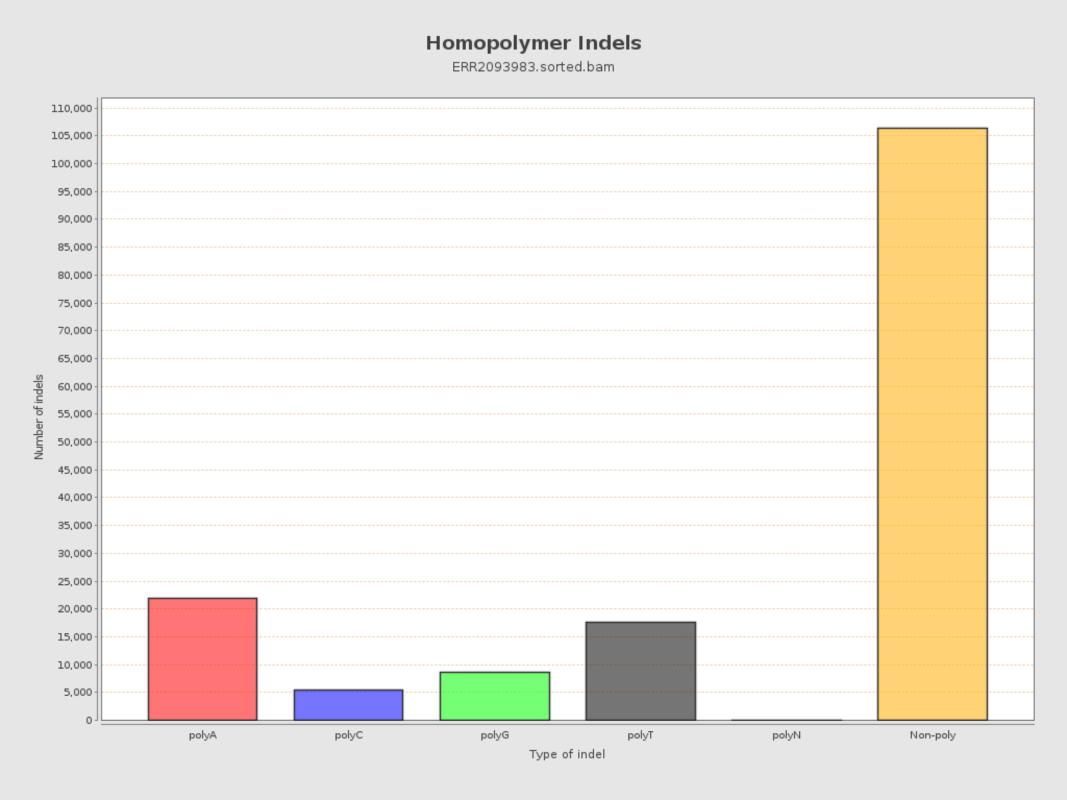
9. Results : Mapped Reads GC-content Distribution



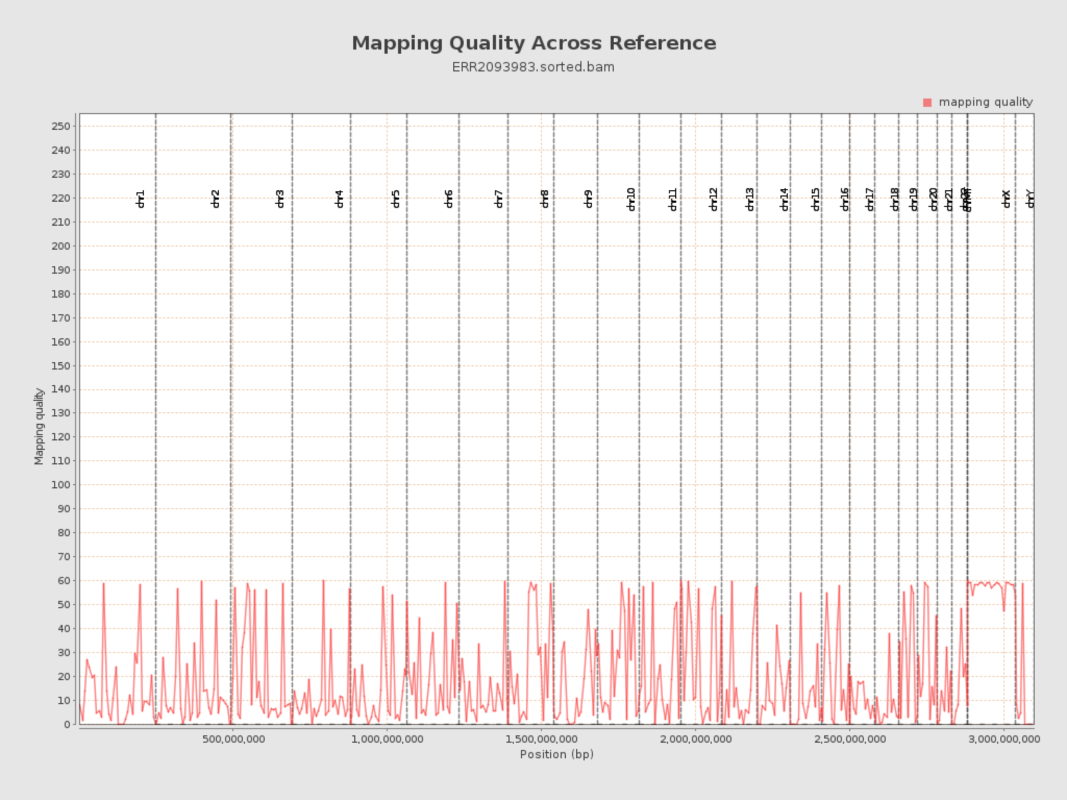
10. Results : Mapped Reads Clipping Profile



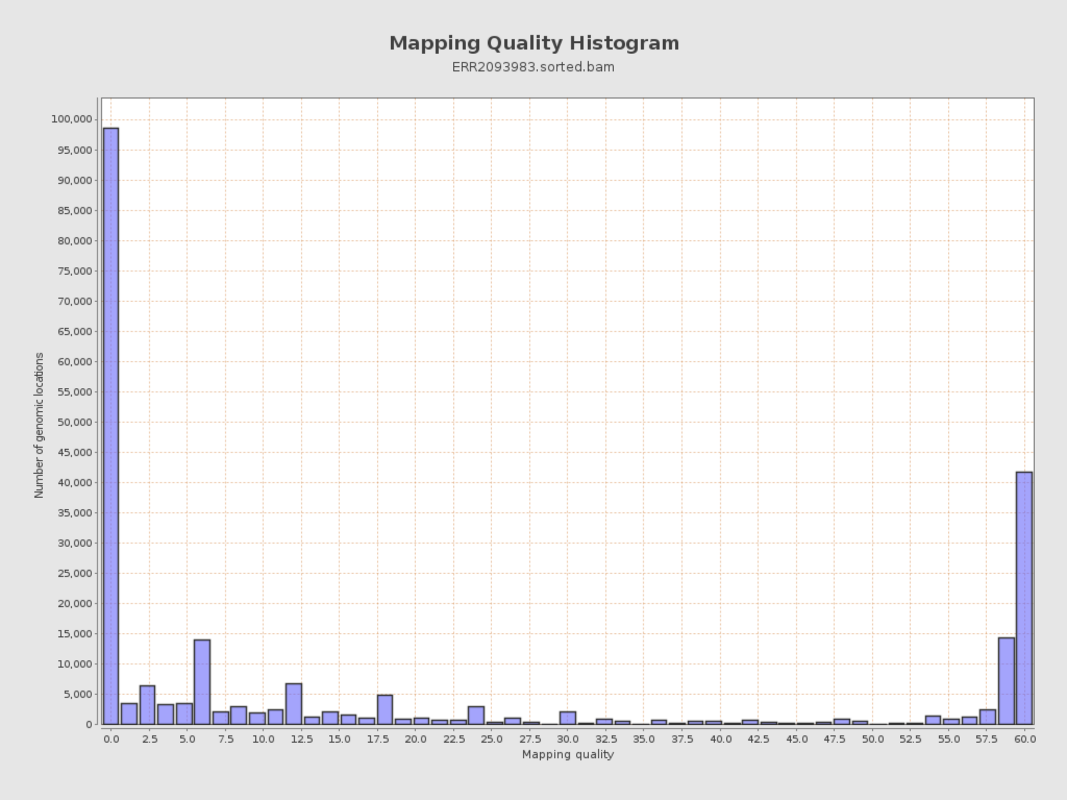
11. Results : Homopolymer Indels



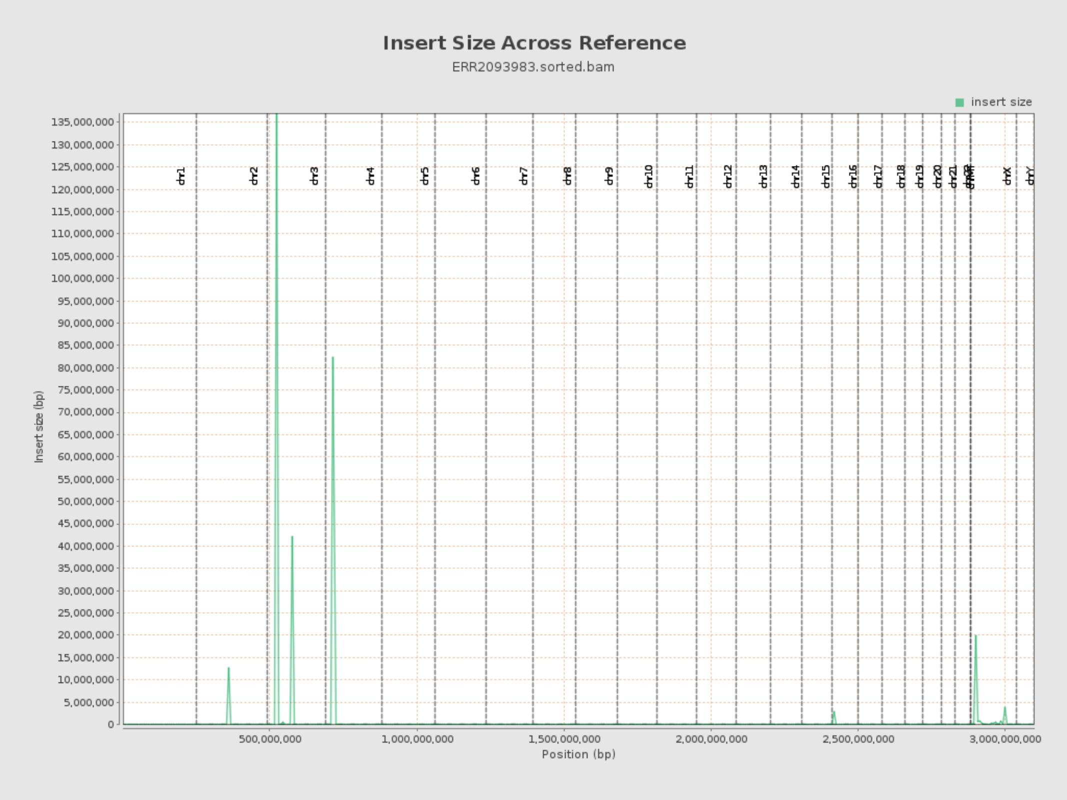
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram