Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:40:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093982.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_ERR2093982 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093982_1.fastq.gz ERR2093982_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:40:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	366,446
Mapped reads	352,425 / 96.17%
Unmapped reads	14,021 / 3.83%
Mapped paired reads	352,425 / 96.17%
Mapped reads, first in pair	177,194 / 48.35%
Mapped reads, second in pair	175,231 / 47.82%
Mapped reads, both in pair	349,158 / 95.28%
Mapped reads, singletons	3,267 / 0.89%
Secondary alignments	0
Supplementary alignments	22,058 / 6.02%
Read min/max/mean length	30 / 151 / 142.73
Duplicated reads (estimated)	333,070 / 90.89%
Duplication rate	50.21%
Clipped reads	178,305 / 48.66%

2.2. ACGT Content

Number/percentage of A's	11,699,594 / 26.36%
Number/percentage of C's	10,444,154 / 23.53%
Number/percentage of T's	11,062,229 / 24.92%
Number/percentage of G's	11,178,009 / 25.18%
Number/percentage of N's	605 / 0%

GC Percentage	48.72%

2.3. Coverage

Mean	0.0146
Standard Deviation	2.9512

2.4. Mapping Quality

Mean Mapping Quality	40.82

2.5. Insert size

Mean	1,094,611.63
Standard Deviation	9,538,011.29
P25/Median/P75	128 / 164 / 203

2.6. Mismatches and indels

General error rate	3.54%
Mismatches	1,515,210
Insertions	24,386
Mapped reads with at least one insertion	6.79%
Deletions	118,623
Mapped reads with at least one deletion	32.31%
Homopolymer indels	28.9%

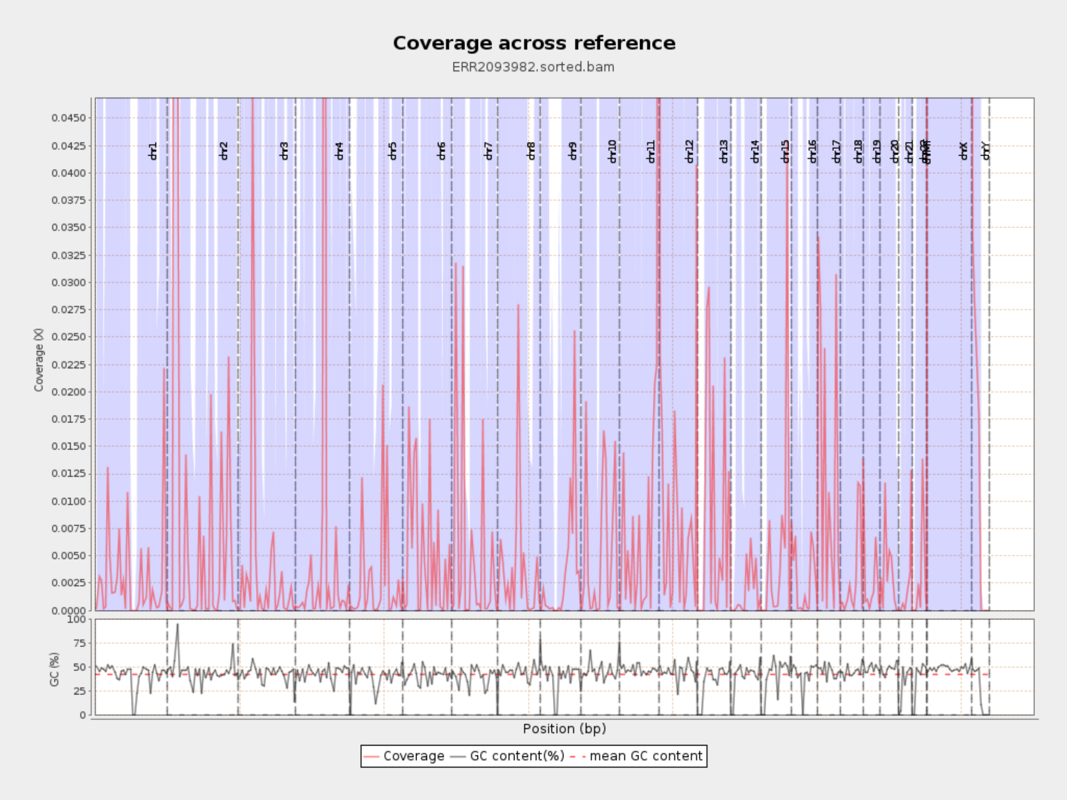
2.7. Chromosome stats

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

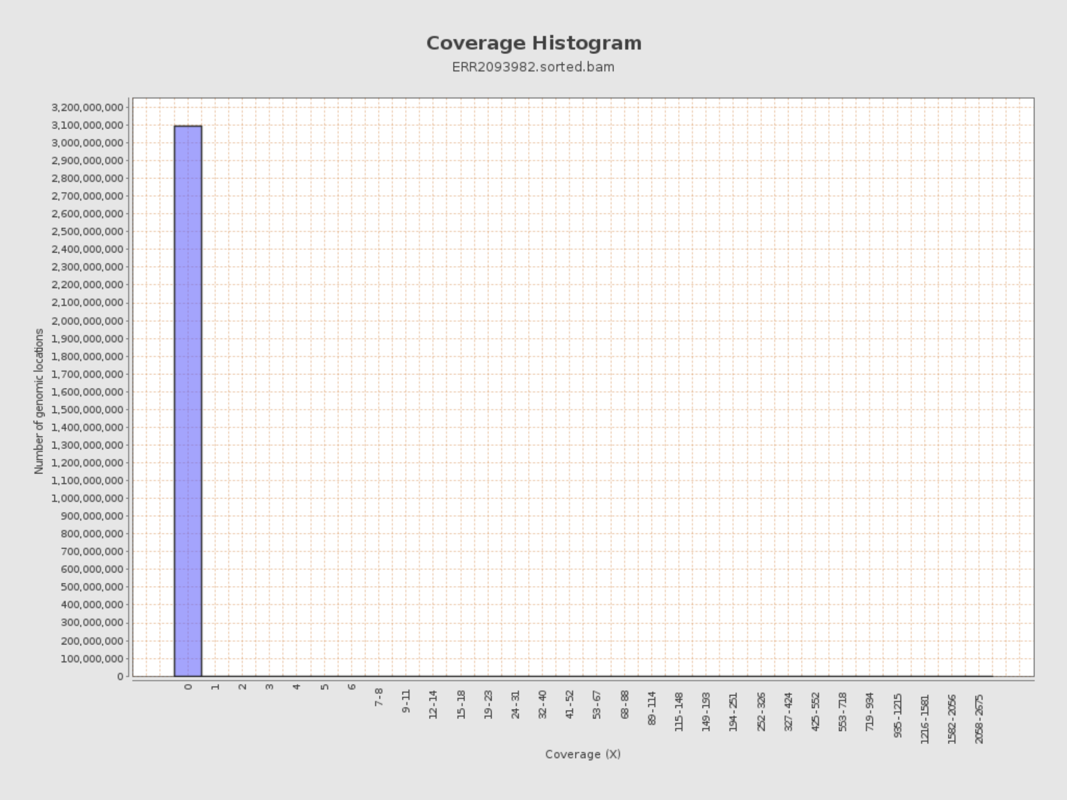
		bases	coverage	deviation
chr1	249250621	742939	0.003	1.0677
chr2	243199373	2268198	0.0093	2.9273
chr3	198022430	699945	0.0035	1.2445
chr4	191154276	1207696	0.0063	2.1936
chr5	180915260	523358	0.0029	1.3381
chr6	171115067	905703	0.0053	1.5107
chr7	159138663	833487	0.0052	1.7234
chr8	146364022	556392	0.0038	1.166
chr9	141213431	510255	0.0036	1.0362
chr10	135534747	702653	0.0052	1.5963
chr11	135006516	1093666	0.0081	2.0262
chr12	133851895	996178	0.0074	1.8061
chr13	115169878	970479	0.0084	2.2837
chr14	107349540	174490	0.0016	0.5443
chr15	102531392	558907	0.0055	1.6237
chr16	90354753	259586	0.0029	0.7214
chr17	81195210	1050506	0.0129	3.2834
chr18	78077248	241902	0.0031	0.934
chr19	59128983	134913	0.0023	0.5134
chr20	63025520	219108	0.0035	1.0616
chr21	48129895	107286	0.0022	0.4008
chr22	51304566	138639	0.0027	0.8729
chrMT	16571	1127676	68.0512	297.2362
chrX	155270560	28453033	0.1832	10.3757

chrY	59373566	710990	0.012	1.8643

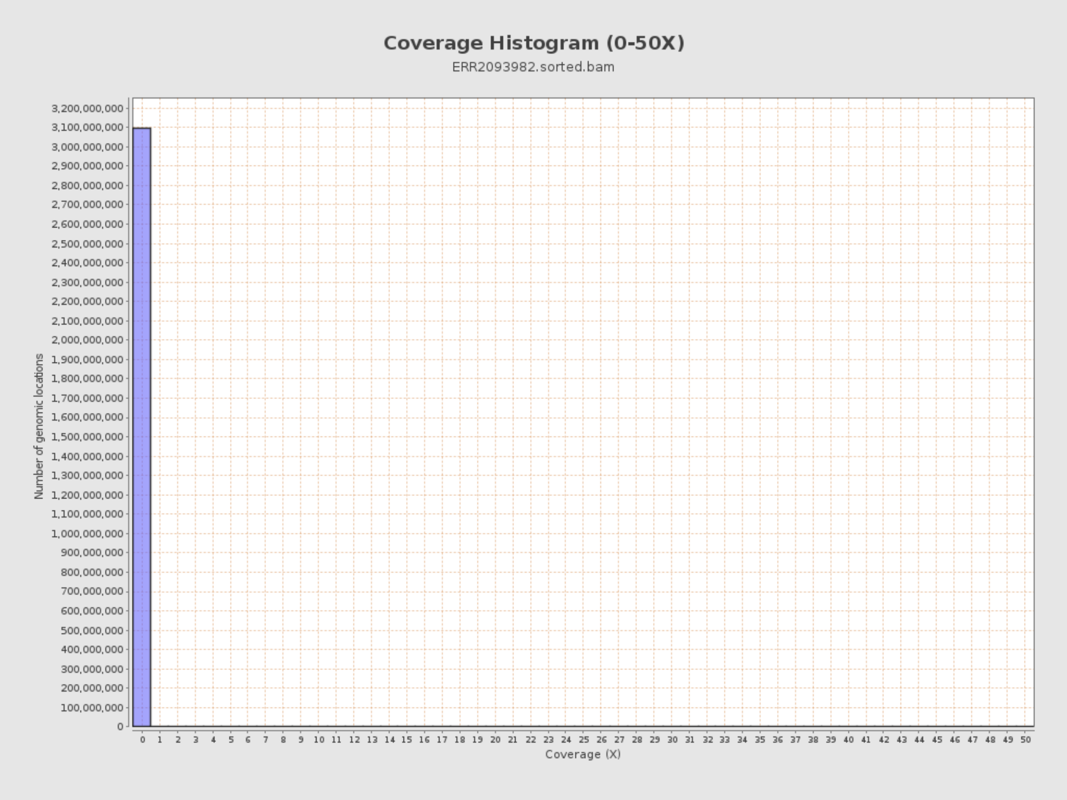
3. Results : Coverage across reference



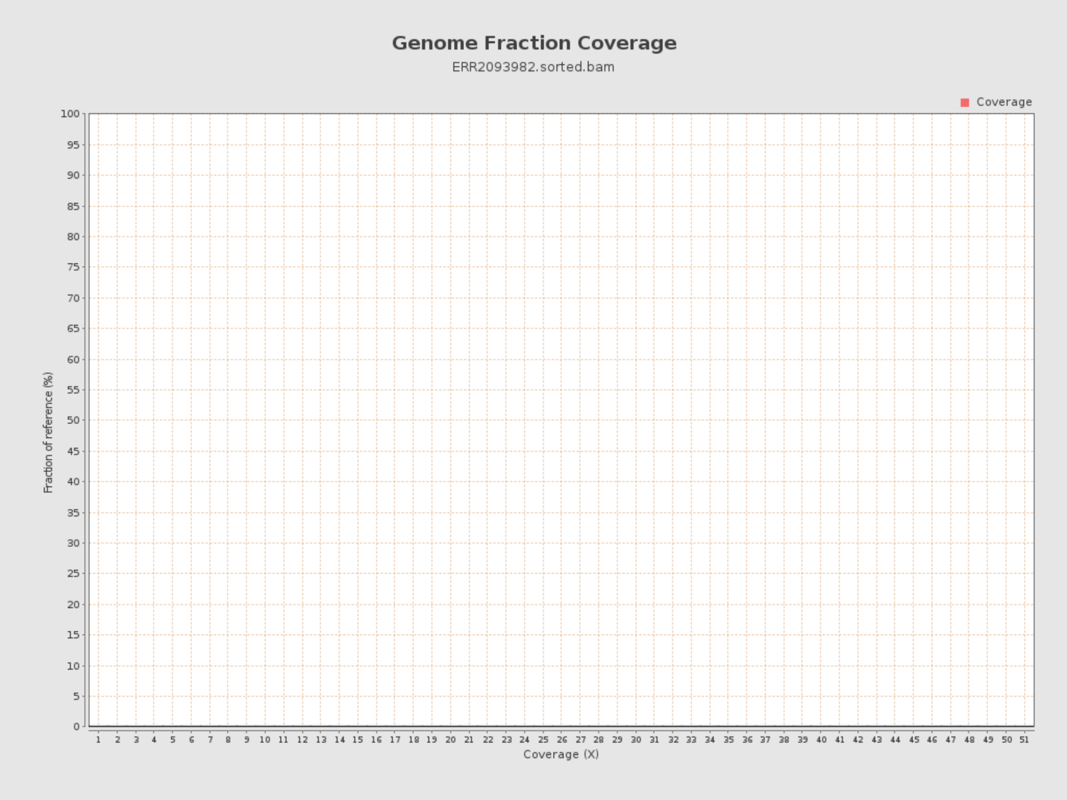
4. Results : Coverage Histogram



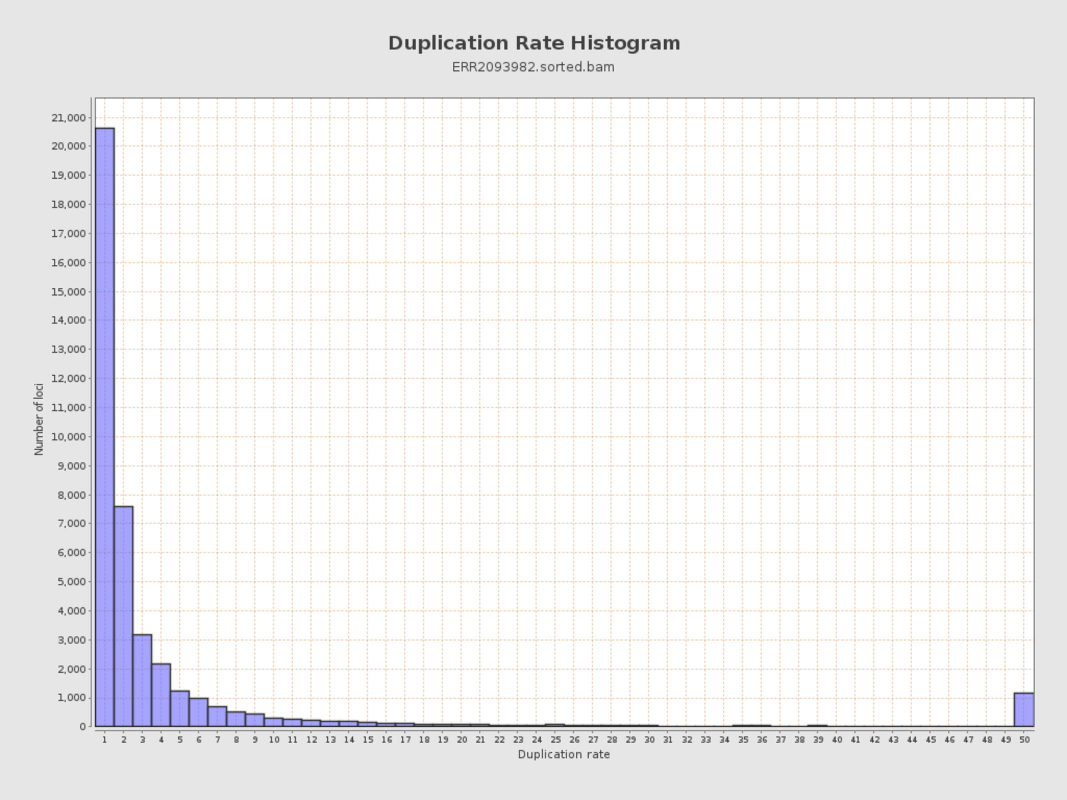
5. Results : Coverage Histogram (0-50X)



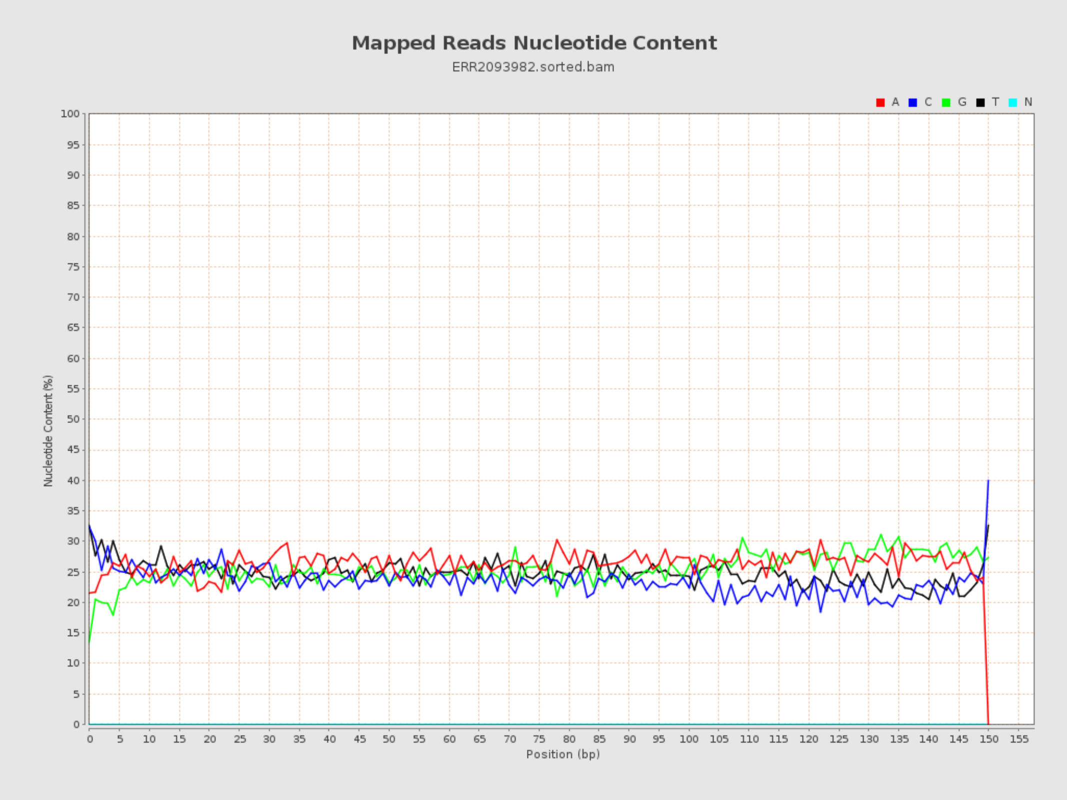
6. Results : Genome Fraction Coverage



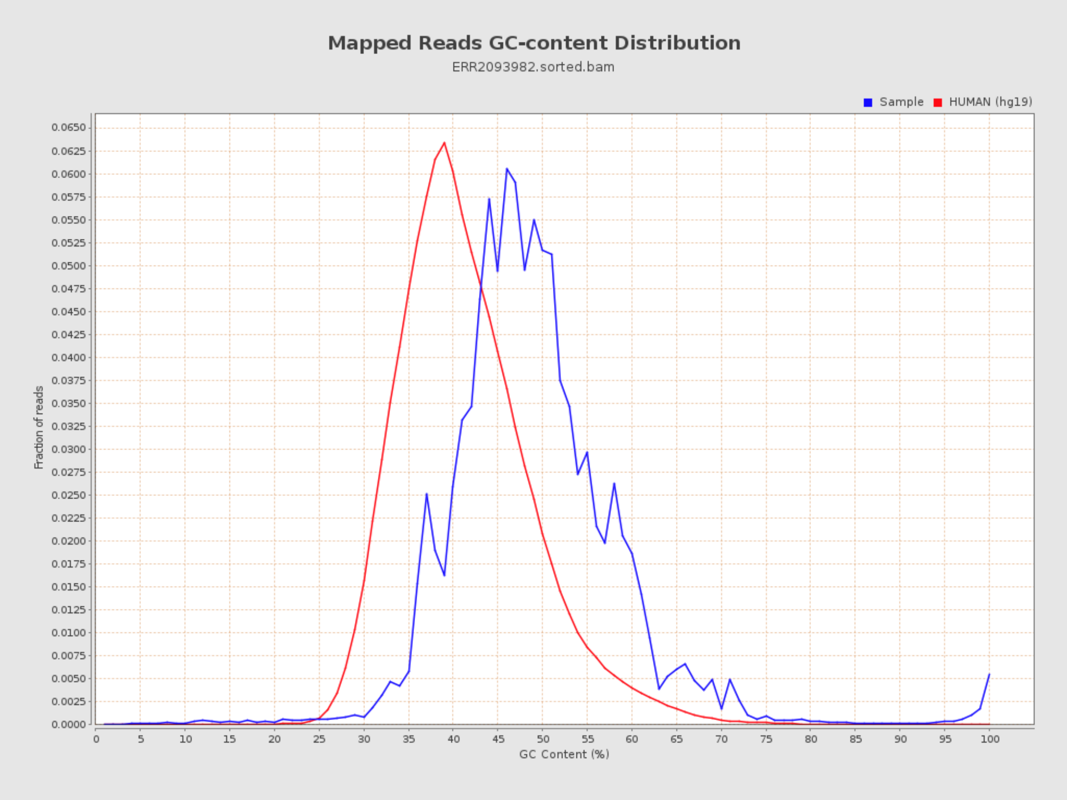
7. Results : Duplication Rate Histogram



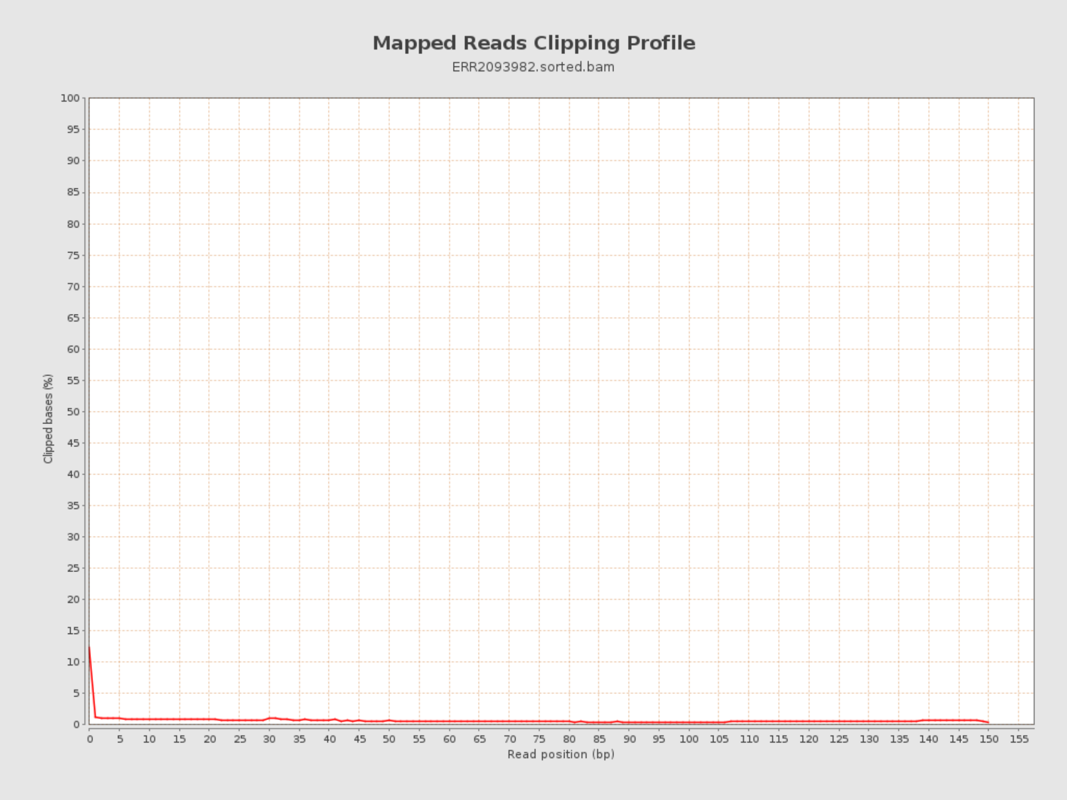
8. Results : Mapped Reads Nucleotide Content



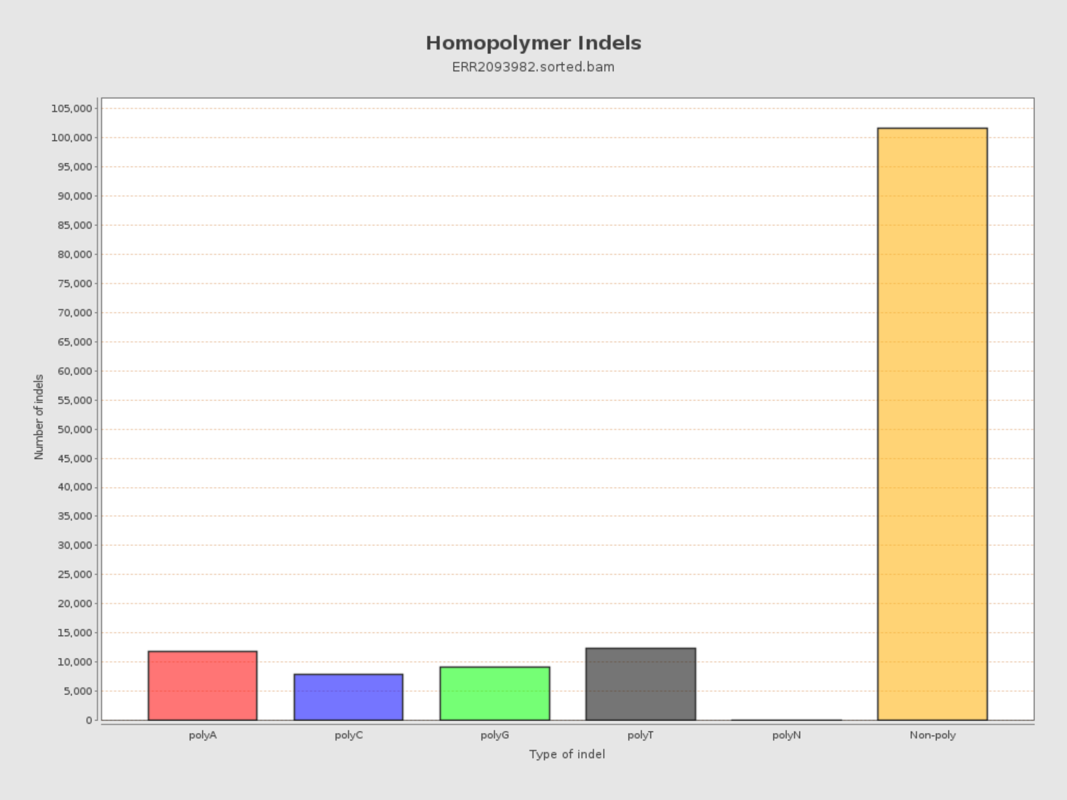
9. Results : Mapped Reads GC-content Distribution



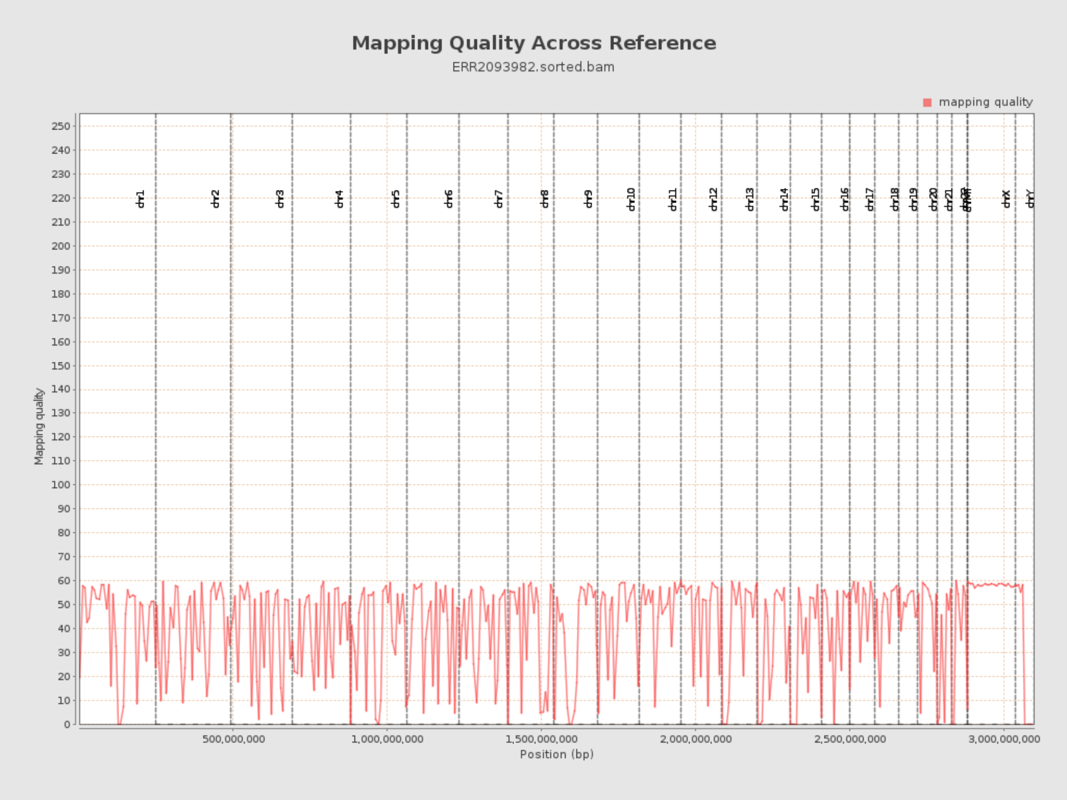
10. Results : Mapped Reads Clipping Profile



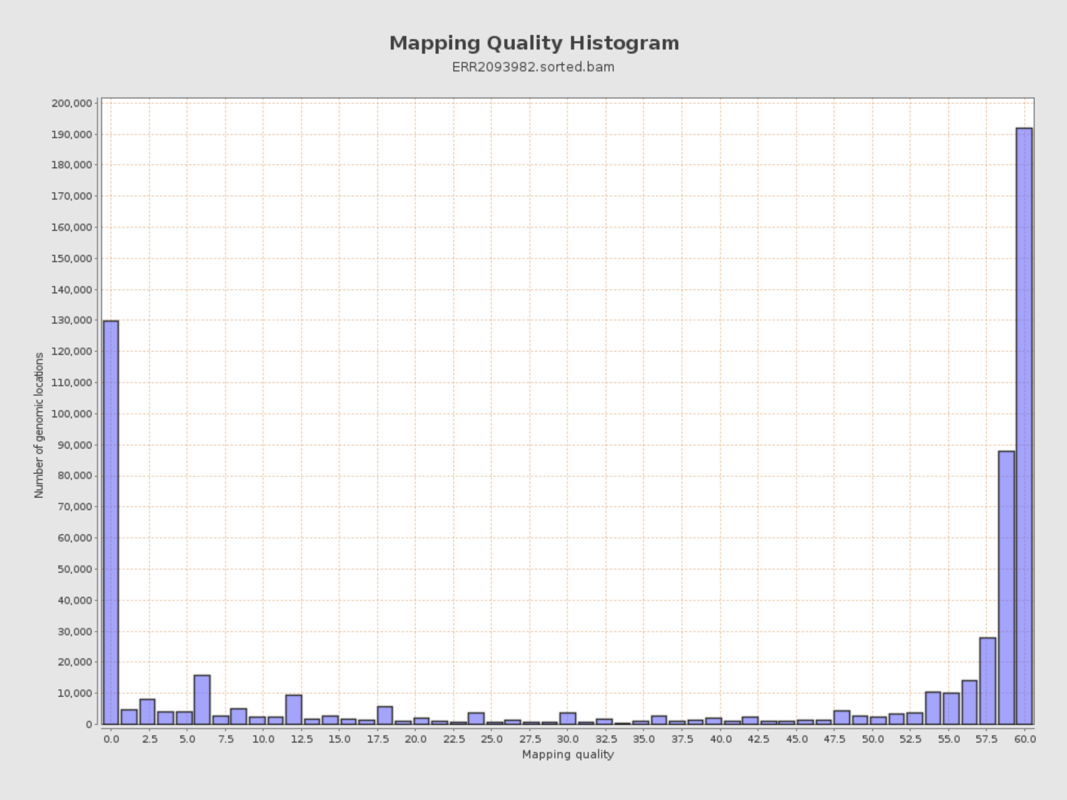
11. Results : Homopolymer Indels



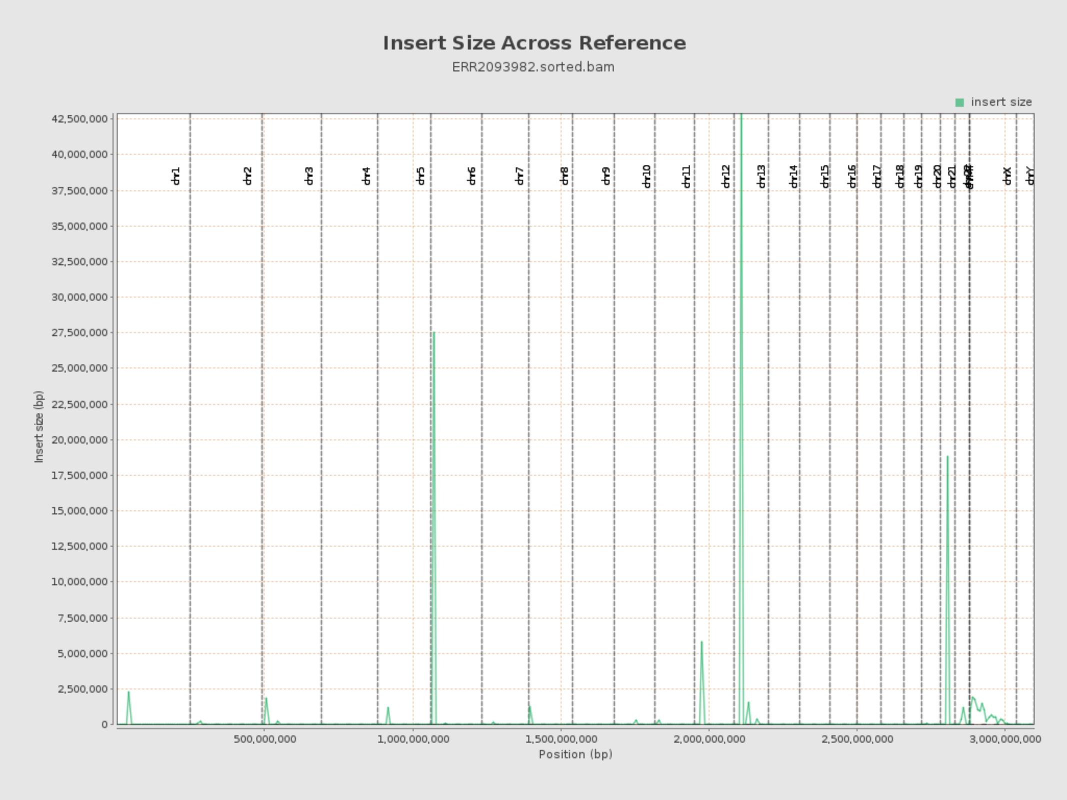
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram