Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:10:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094080.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_ERR2094080 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094080_1.fastq.gz ERR2094080_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:10:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	391,518
Mapped reads	354,390 / 90.52%
Unmapped reads	37,128 / 9.48%
Mapped paired reads	354,390 / 90.52%
Mapped reads, first in pair	177,939 / 45.45%
Mapped reads, second in pair	176,451 / 45.07%
Mapped reads, both in pair	351,686 / 89.83%
Mapped reads, singletons	2,704 / 0.69%
Secondary alignments	0
Supplementary alignments	11,224 / 2.87%
Read min/max/mean length	30 / 151 / 133.89
Duplicated reads (estimated)	334,952 / 85.55%
Duplication rate	49.14%
Clipped reads	141,851 / 36.23%

2.2. ACGT Content

Number/percentage of A's	12,111,630 / 26.92%
Number/percentage of C's	10,365,544 / 23.04%
Number/percentage of T's	11,529,930 / 25.62%
Number/percentage of G's	10,990,979 / 24.43%
Number/percentage of N's	531 / 0%

GC Percentage	47.46%

2.3. Coverage

Mean	0.0149
Standard Deviation	3.8235

2.4. Mapping Quality

Mean Mapping Quality	40.46

2.5. Insert size

Mean	316,219.66
Standard Deviation	5,219,403.93
P25/Median/P75	129 / 164 / 191

2.6. Mismatches and indels

General error rate	4.29%
Mismatches	1,881,499
Insertions	28,383
Mapped reads with at least one insertion	7.83%
Deletions	155,083
Mapped reads with at least one deletion	41.26%
Homopolymer indels	28.39%

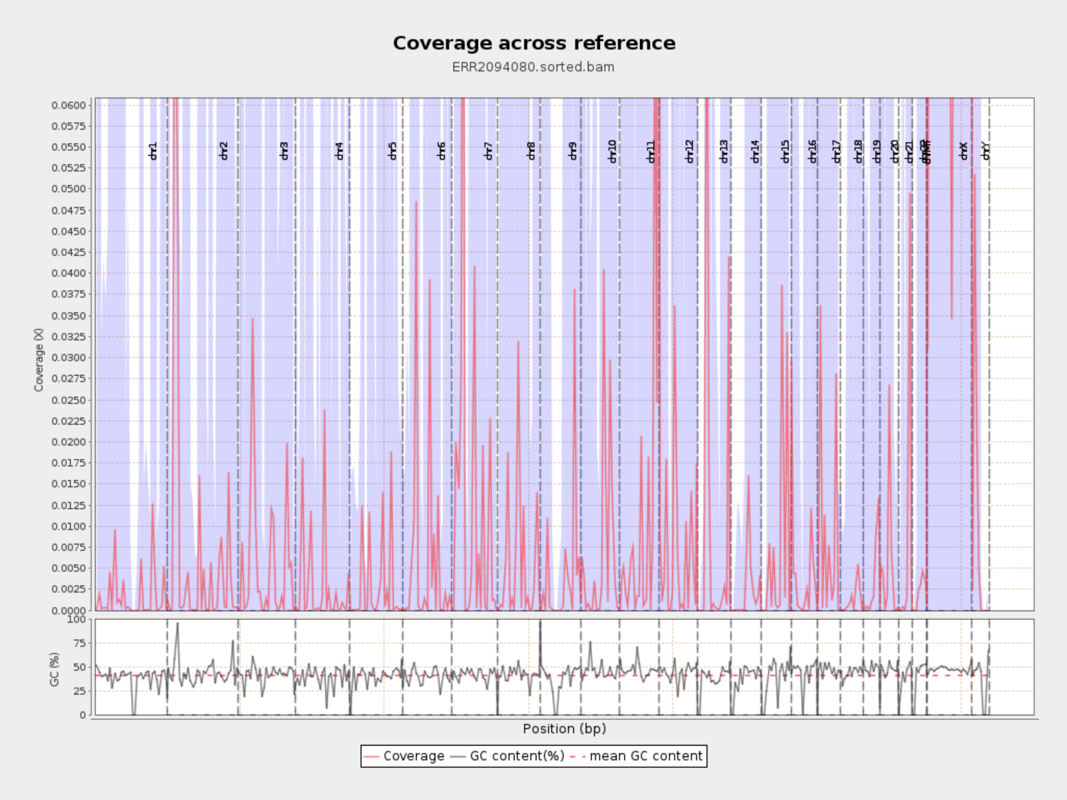
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

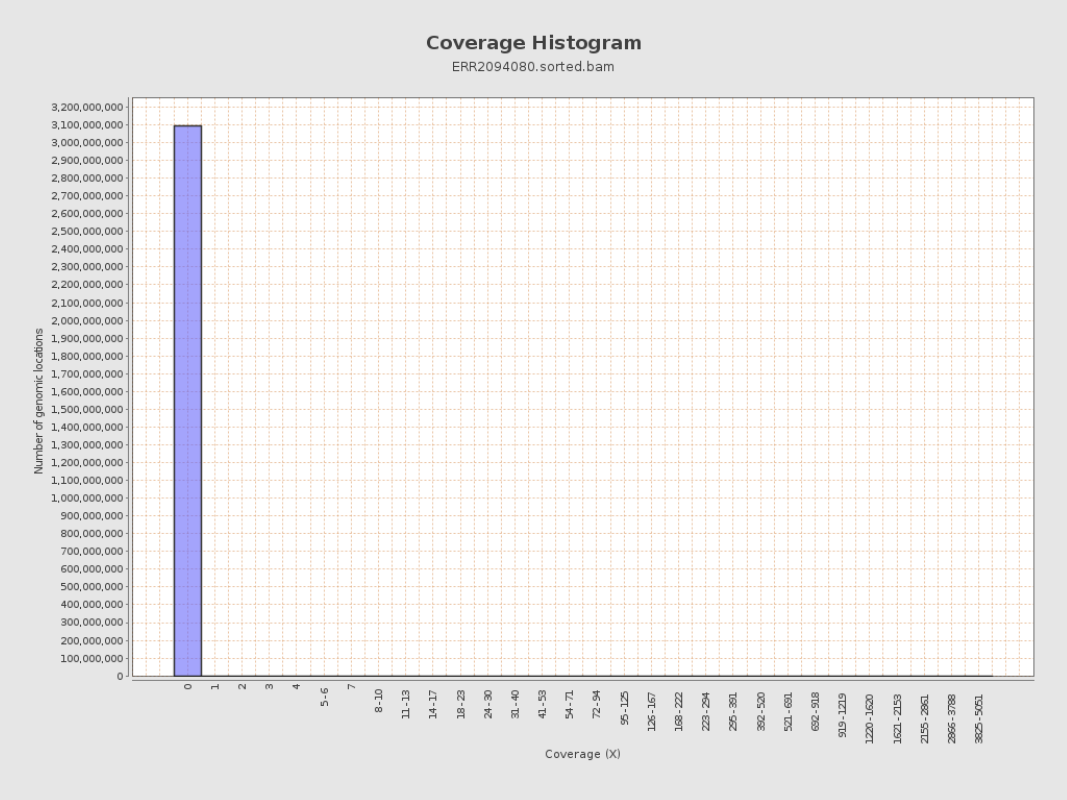
		bases	**coverage**	**deviation**
chr1	249250621	431190	0.0017	0.7034
chr2	243199373	1665253	0.0068	2.4531
chr3	198022430	1035545	0.0052	1.621
chr4	191154276	567694	0.003	1.1014
chr5	180915260	520350	0.0029	1.3355
chr6	171115067	1070695	0.0063	2.7888
chr7	159138663	2039669	0.0128	4.4787
chr8	146364022	800747	0.0055	1.7132
chr9	141213431	593335	0.0042	1.8725
chr10	135534747	942768	0.007	2.5654
chr11	135006516	1529249	0.0113	3.2911
chr12	133851895	886057	0.0066	2.0124
chr13	115169878	1134084	0.0098	2.9553
chr14	107349540	284334	0.0026	1.0518
chr15	102531392	706645	0.0069	2.3671
chr16	90354753	396121	0.0044	1.5583
chr17	81195210	703743	0.0087	2.5575
chr18	78077248	112675	0.0014	0.3622
chr19	59128983	201444	0.0034	1.0214
chr20	63025520	344457	0.0055	1.7077
chr21	48129895	420062	0.0087	3.4313
chr22	51304566	106248	0.0021	0.4897
chrMT	16571	864844	52.1902	234.3418
chrX	155270560	28138935	0.1812	13.7725

chrY	59373566	617948	0.0104	3.06

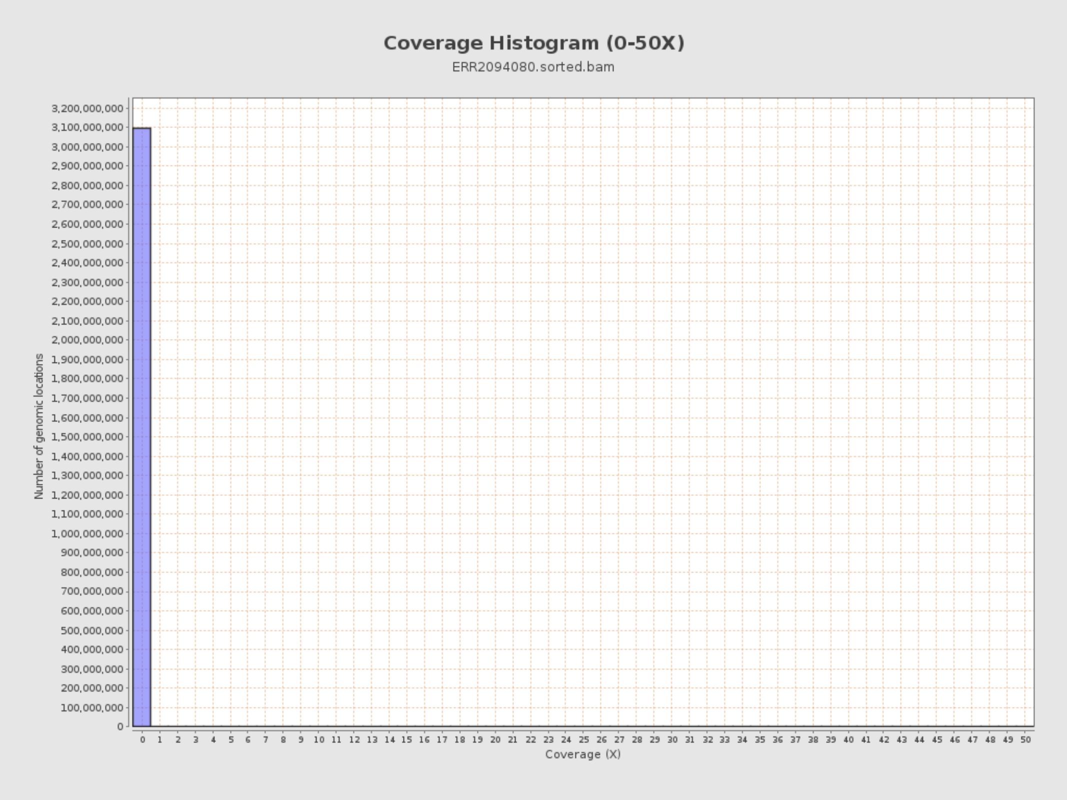
3. Results : Coverage across reference



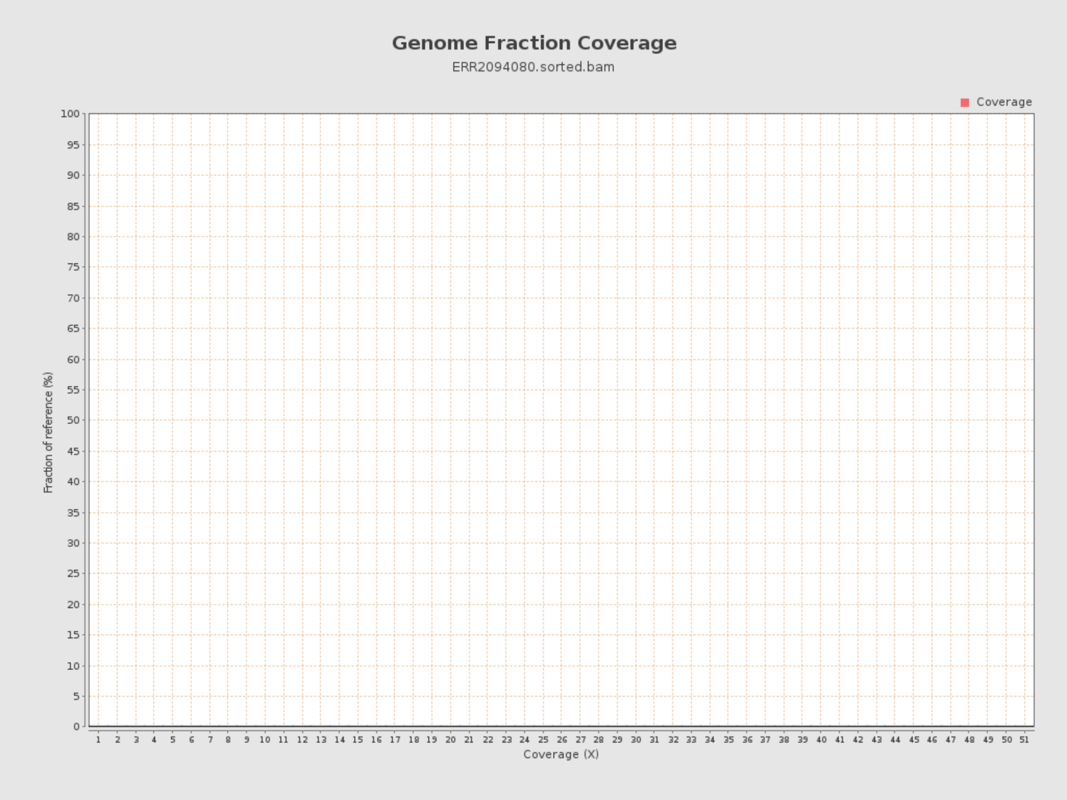
4. Results : Coverage Histogram



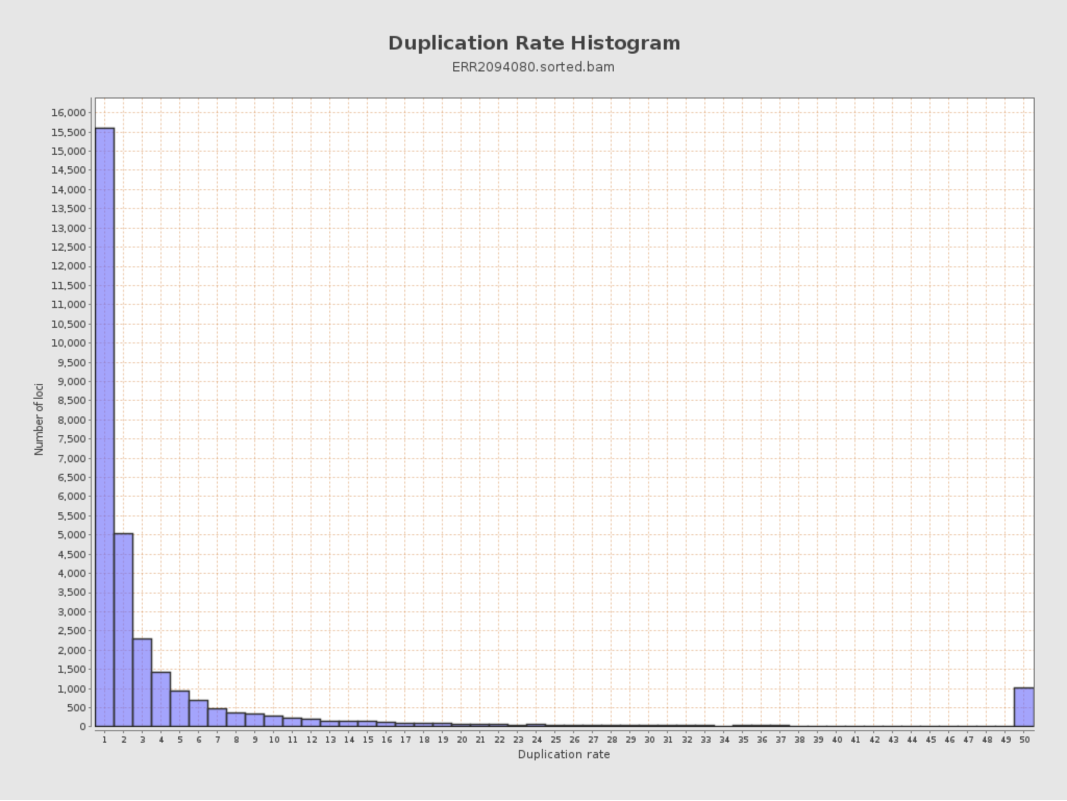
5. Results : Coverage Histogram (0-50X)



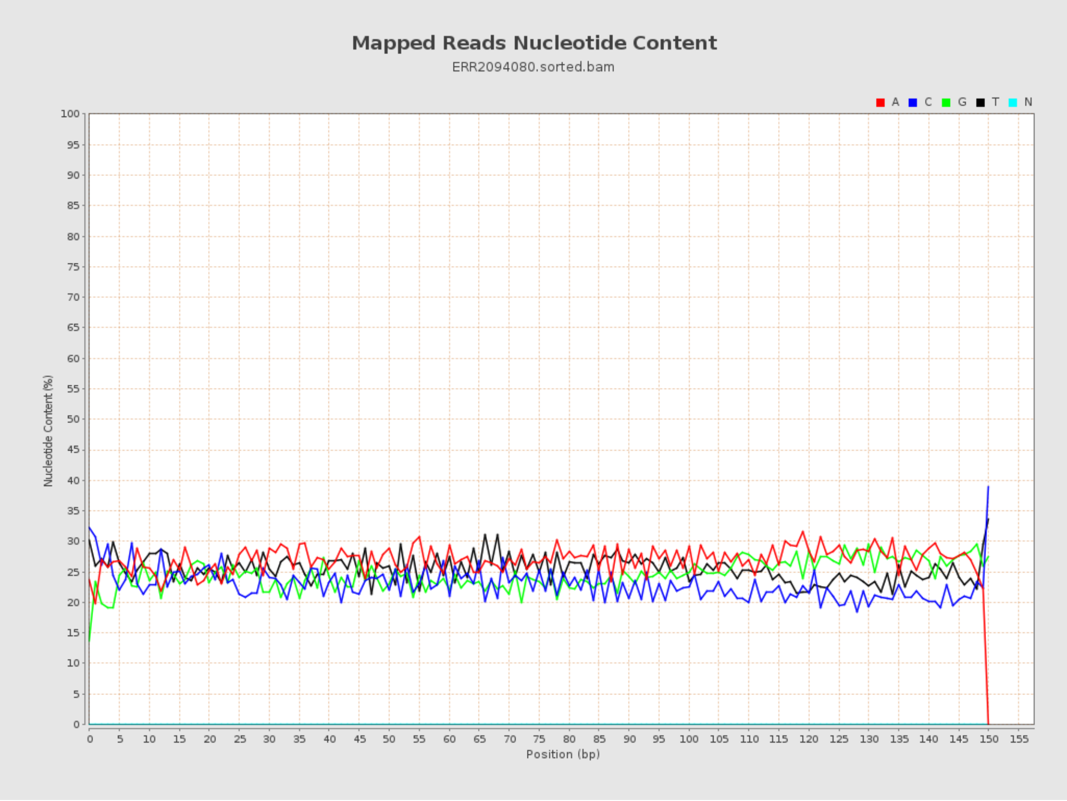
6. Results : Genome Fraction Coverage



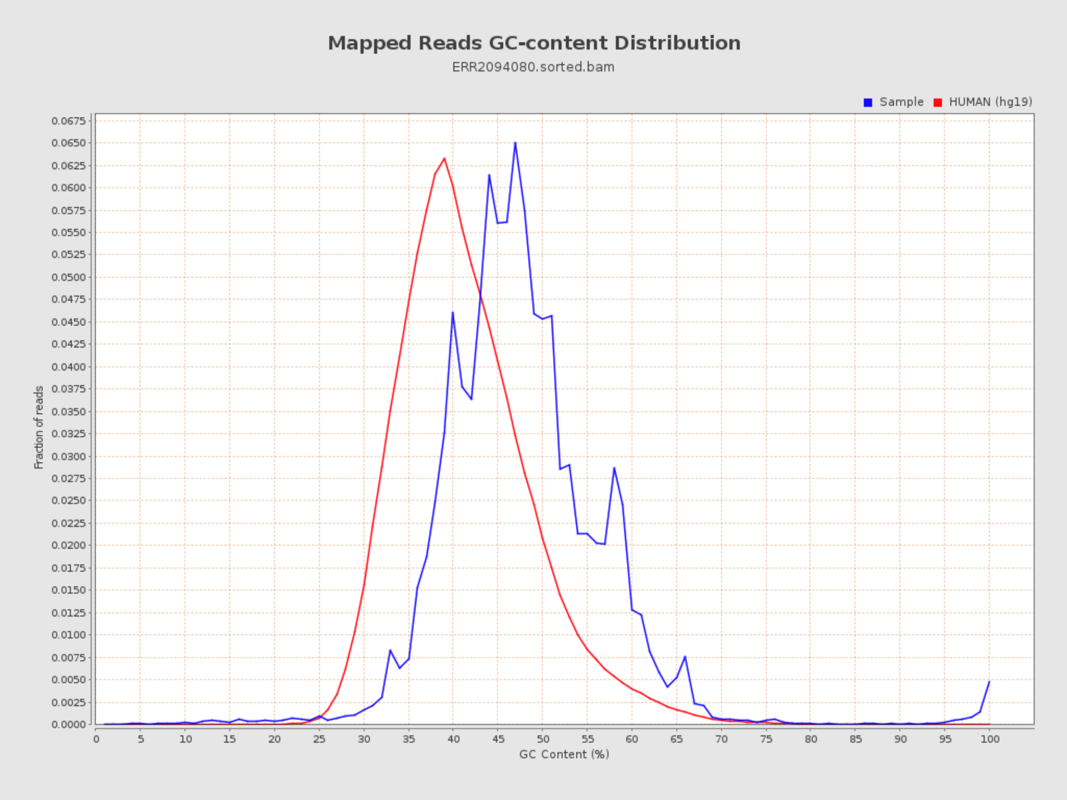
7. Results : Duplication Rate Histogram



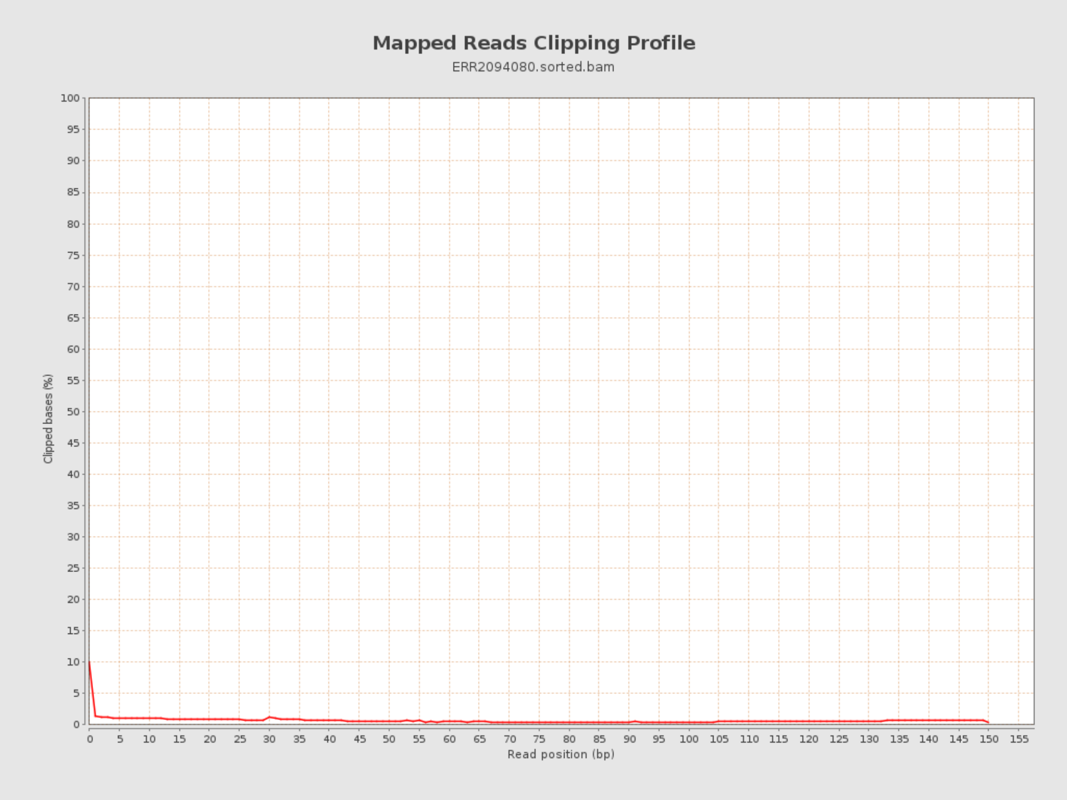
8. Results : Mapped Reads Nucleotide Content



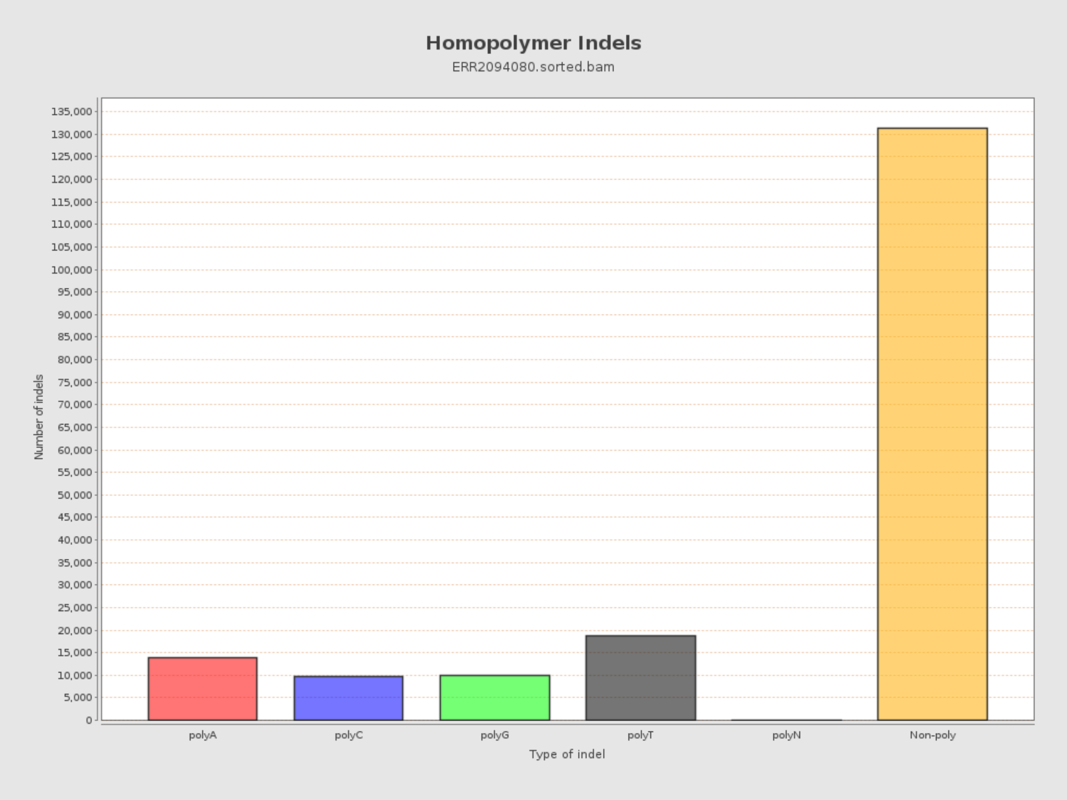
9. Results : Mapped Reads GC-content Distribution



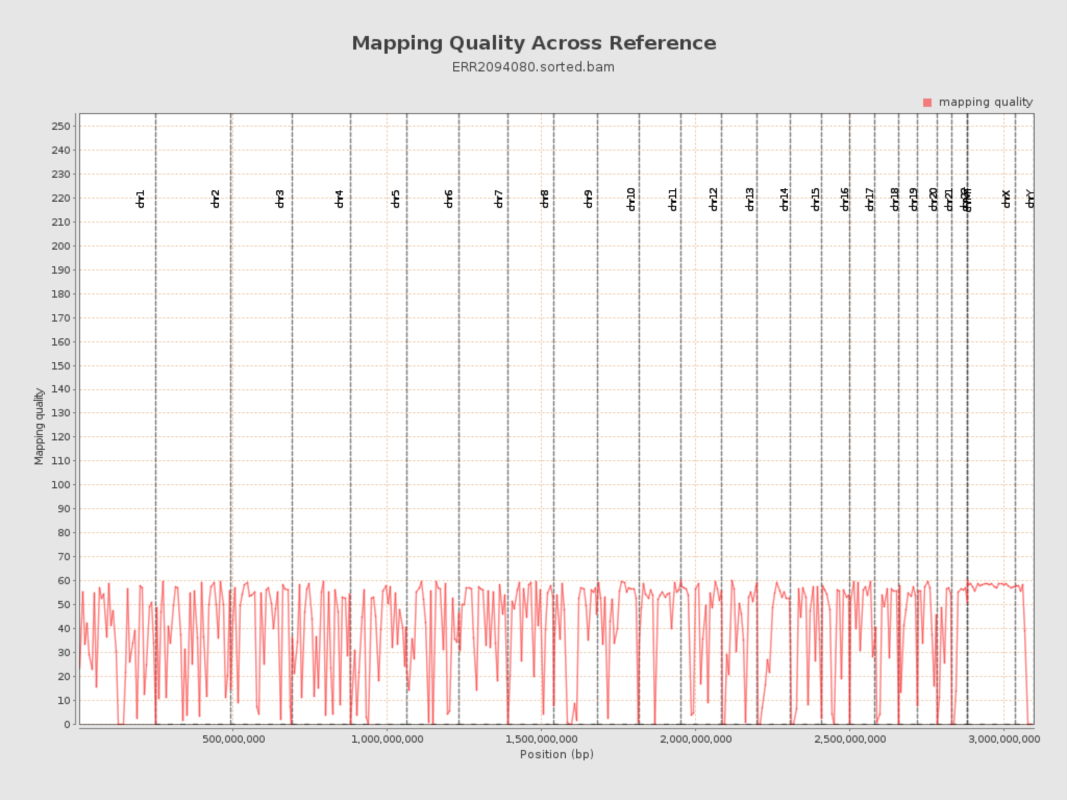
10. Results : Mapped Reads Clipping Profile



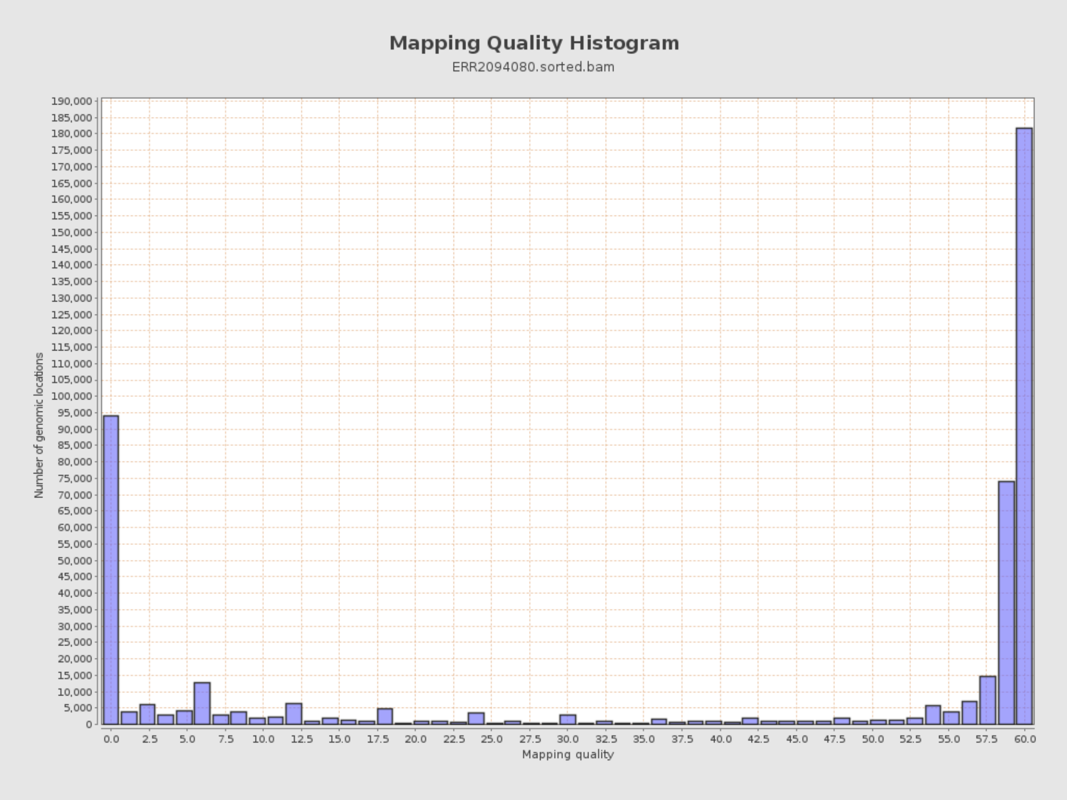
11. Results : Homopolymer Indels



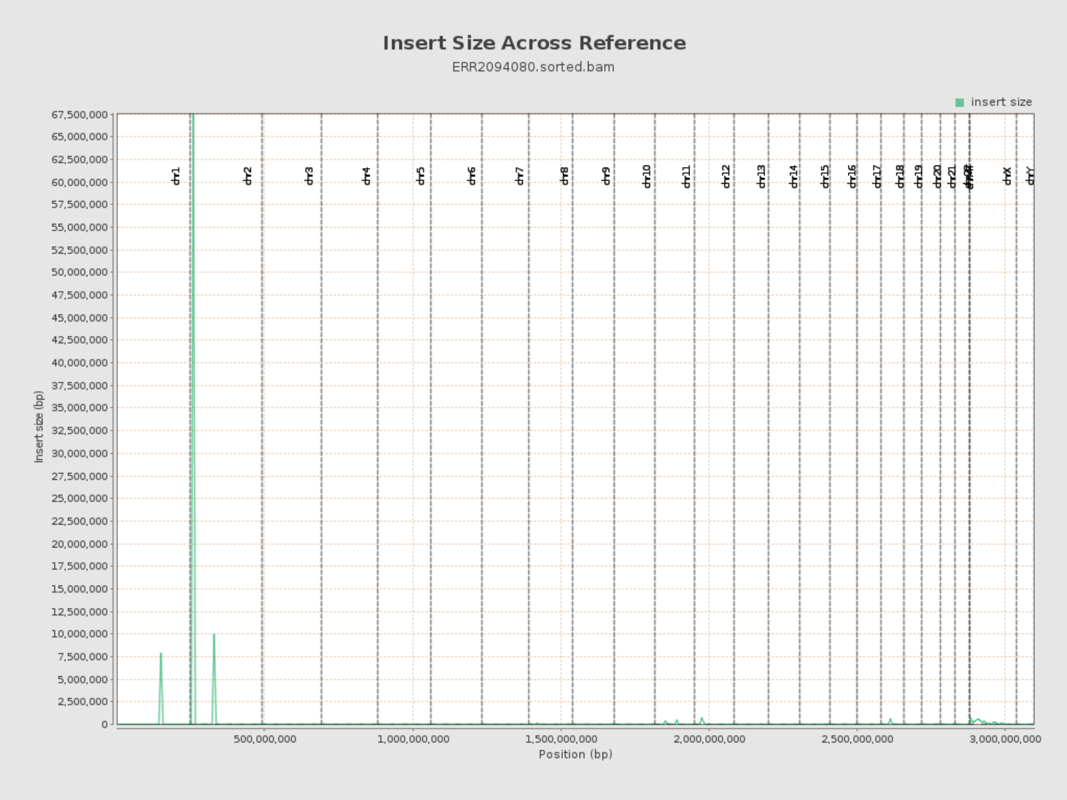
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram