Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:02:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094077.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_ERR2094077 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094077_1.fastq.gz ERR2094077_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:02:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	431,474
Mapped reads	419,905 / 97.32%
Unmapped reads	11,569 / 2.68%
Mapped paired reads	419,905 / 97.32%
Mapped reads, first in pair	211,068 / 48.92%
Mapped reads, second in pair	208,837 / 48.4%
Mapped reads, both in pair	416,930 / 96.63%
Mapped reads, singletons	2,975 / 0.69%
Secondary alignments	0
Supplementary alignments	14,913 / 3.46%
Read min/max/mean length	30 / 151 / 144
Duplicated reads (estimated)	401,203 / 92.98%
Duplication rate	49.68%
Clipped reads	160,513 / 37.2%

2.2. ACGT Content

Number/percentage of A's	14,567,064 / 26.33%
Number/percentage of C's	13,055,690 / 23.59%
Number/percentage of T's	13,984,109 / 25.27%
Number/percentage of G's	13,726,650 / 24.81%
Number/percentage of N's	592 / 0%

GC Percentage	48.4%

2.3. Coverage

Mean	0.0183
Standard Deviation	4.9485

2.4. Mapping Quality

Mean Mapping Quality	38.4

2.5. Insert size

Mean	469,009.55
Standard Deviation	6,199,017.58
P25/Median/P75	143 / 172 / 201

2.6. Mismatches and indels

General error rate	3.95%
Mismatches	2,106,035
Insertions	34,224
Mapped reads with at least one insertion	8.05%
Deletions	166,408
Mapped reads with at least one deletion	37.85%
Homopolymer indels	29.25%

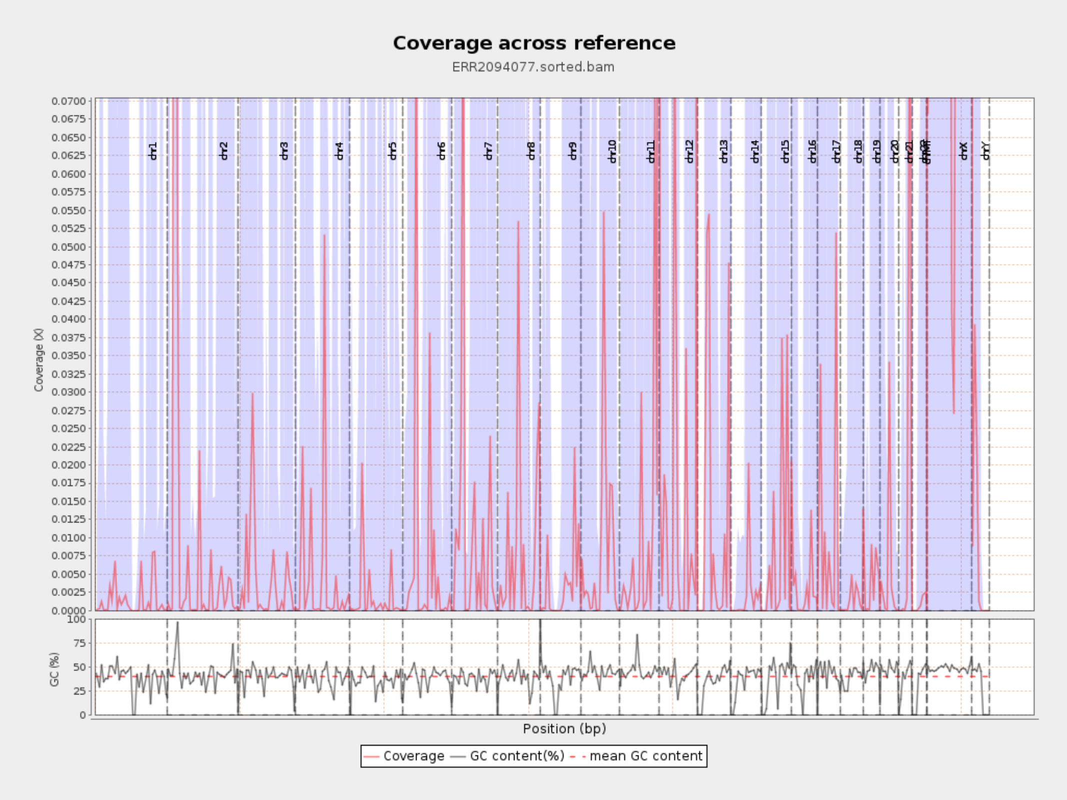
2.7. Chromosome stats

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

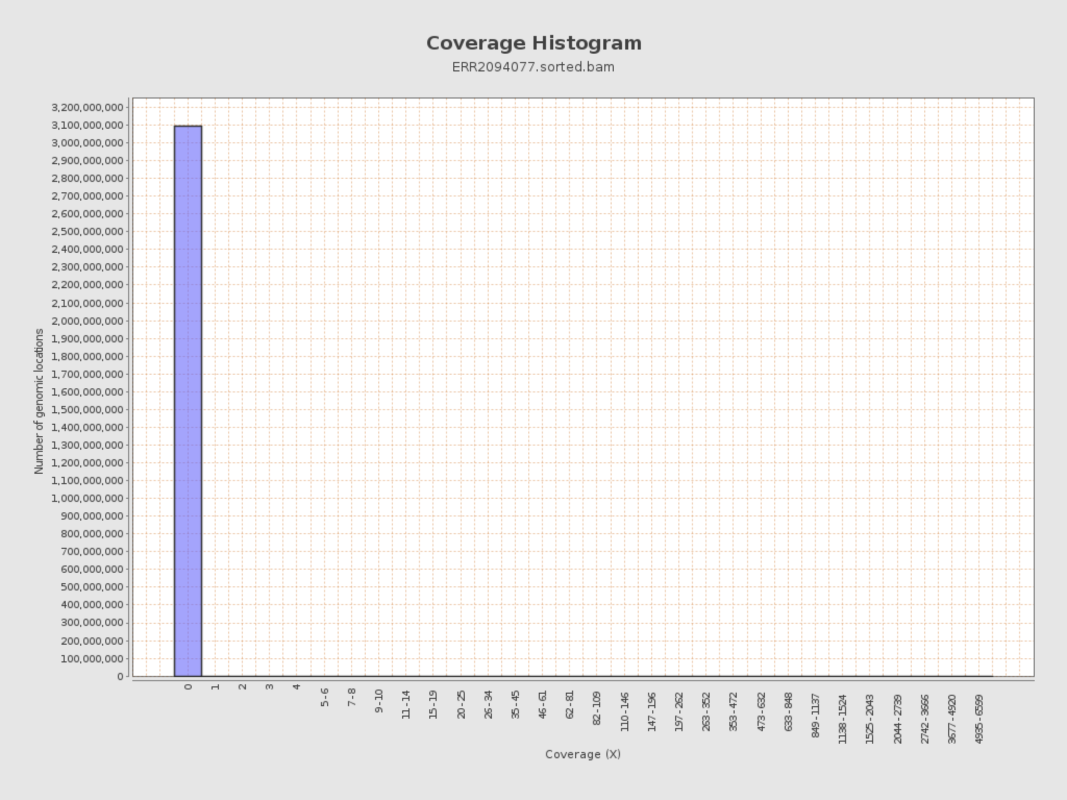
		bases	coverage	deviation
chr1	249250621	359131	0.0014	0.5716
chr2	243199373	2783224	0.0114	5.0189
chr3	198022430	800726	0.004	1.2606
chr4	191154276	897810	0.0047	1.6467
chr5	180915260	322762	0.0018	0.9289
chr6	171115067	1235274	0.0072	4.3019
chr7	159138663	1617039	0.0102	3.7717
chr8	146364022	1201523	0.0082	2.7926
chr9	141213431	496977	0.0035	1.207
chr10	135534747	1145328	0.0085	3.1797
chr11	135006516	1516388	0.0112	3.2331
chr12	133851895	1747677	0.0131	4.571
chr13	115169878	1379008	0.012	3.7415
chr14	107349540	262297	0.0024	1.2018
chr15	102531392	792284	0.0077	2.6066
chr16	90354753	335768	0.0037	1.2244
chr17	81195210	886205	0.0109	4.0399
chr18	78077248	110670	0.0014	0.4558
chr19	59128983	230265	0.0039	0.9614
chr20	63025520	335867	0.0053	2.0079
chr21	48129895	872468	0.0181	8.0102
chr22	51304566	44402	0.0009	0.2471
chrMT	16571	1773089	106.9995	496.7605
chrX	155270560	34825175	0.2243	16.8819

chrY	59373566	536797	0.009	2.5115

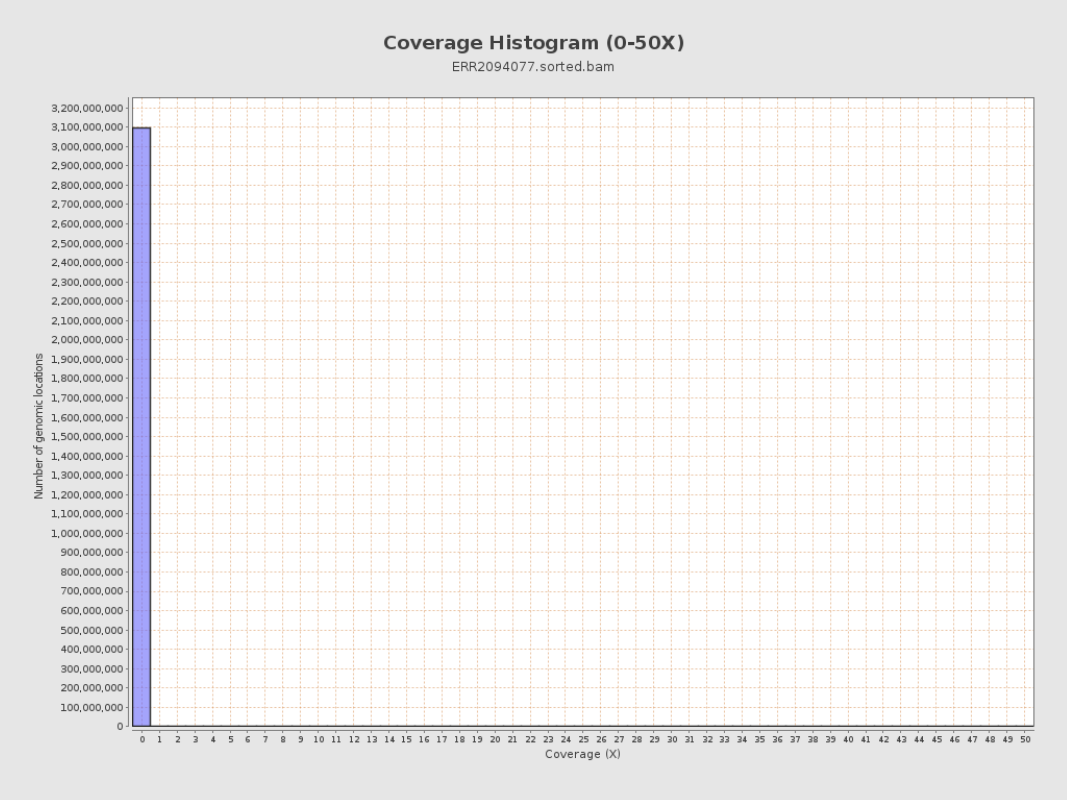
3. Results : Coverage across reference



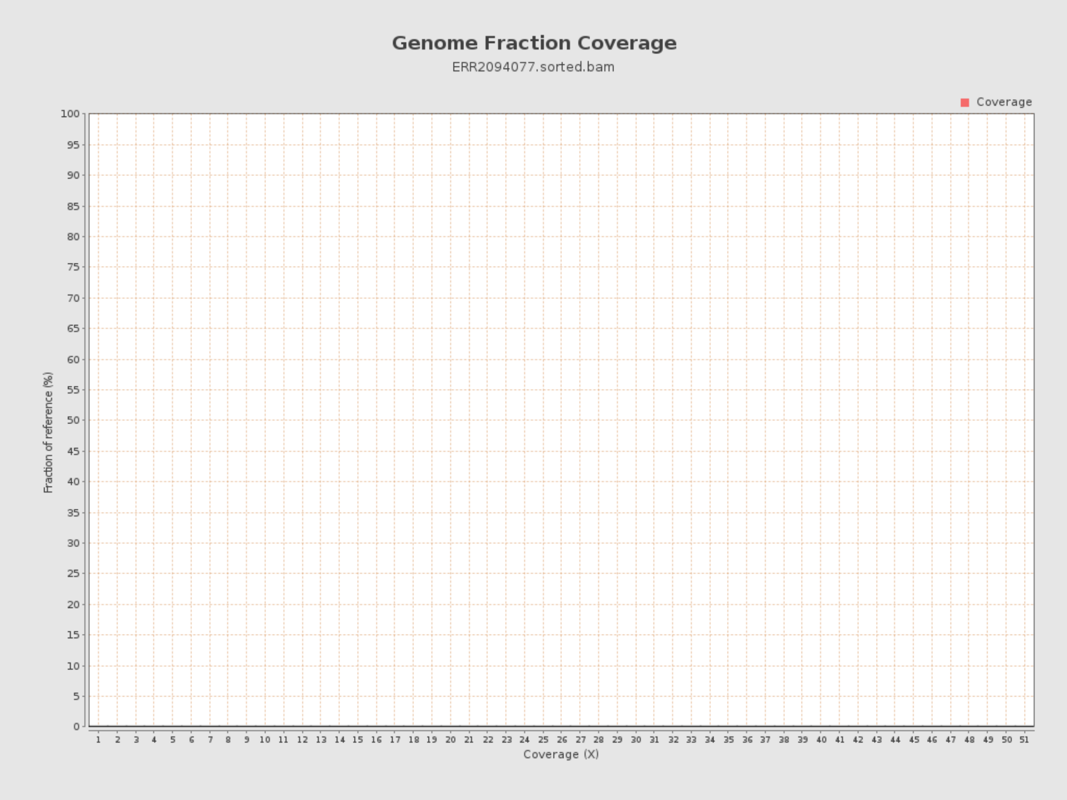
4. Results : Coverage Histogram



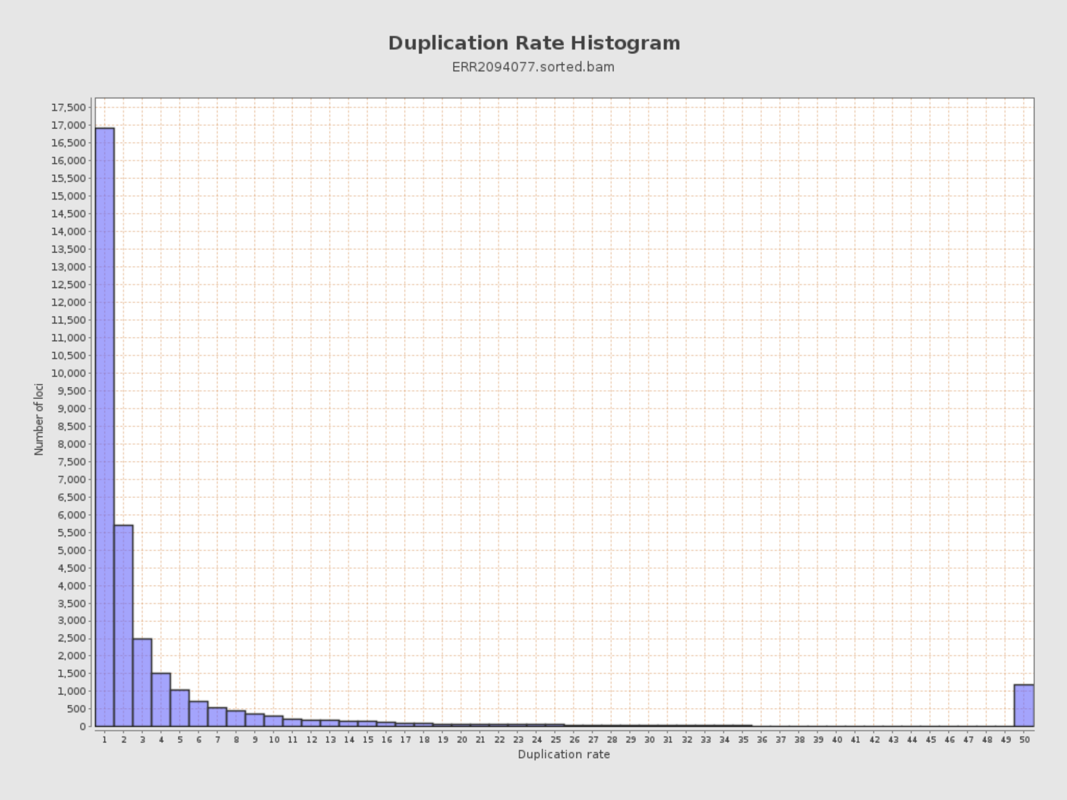
5. Results : Coverage Histogram (0-50X)



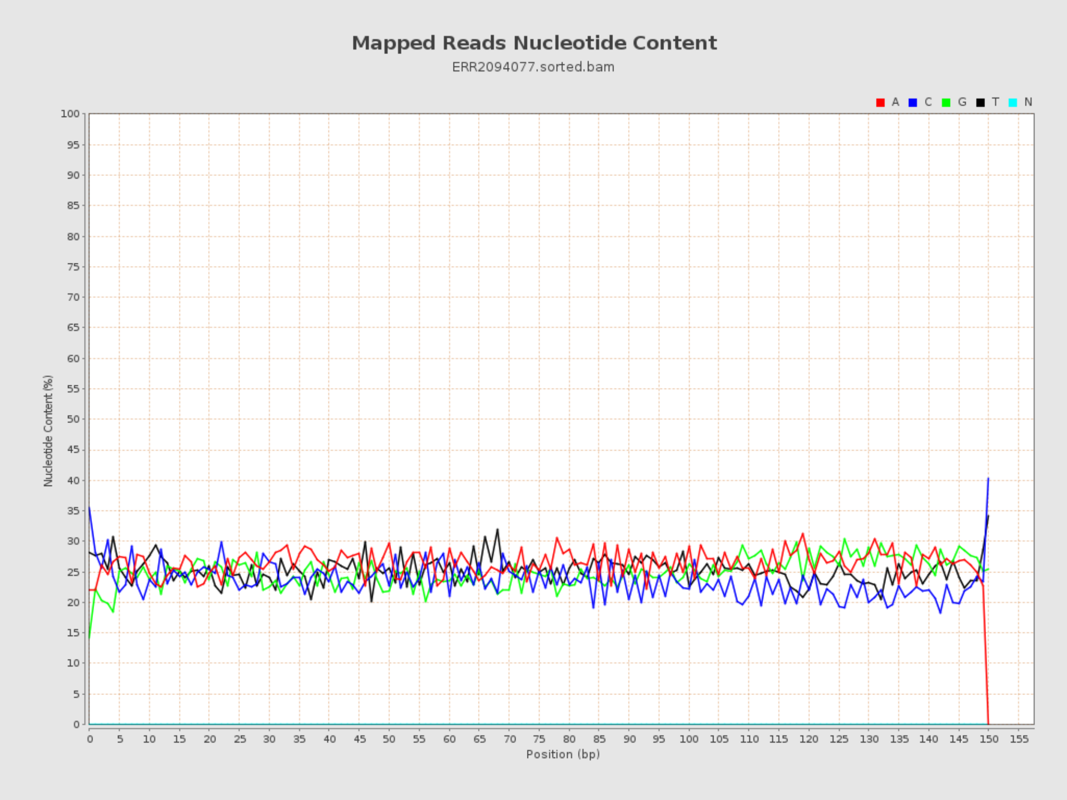
6. Results : Genome Fraction Coverage



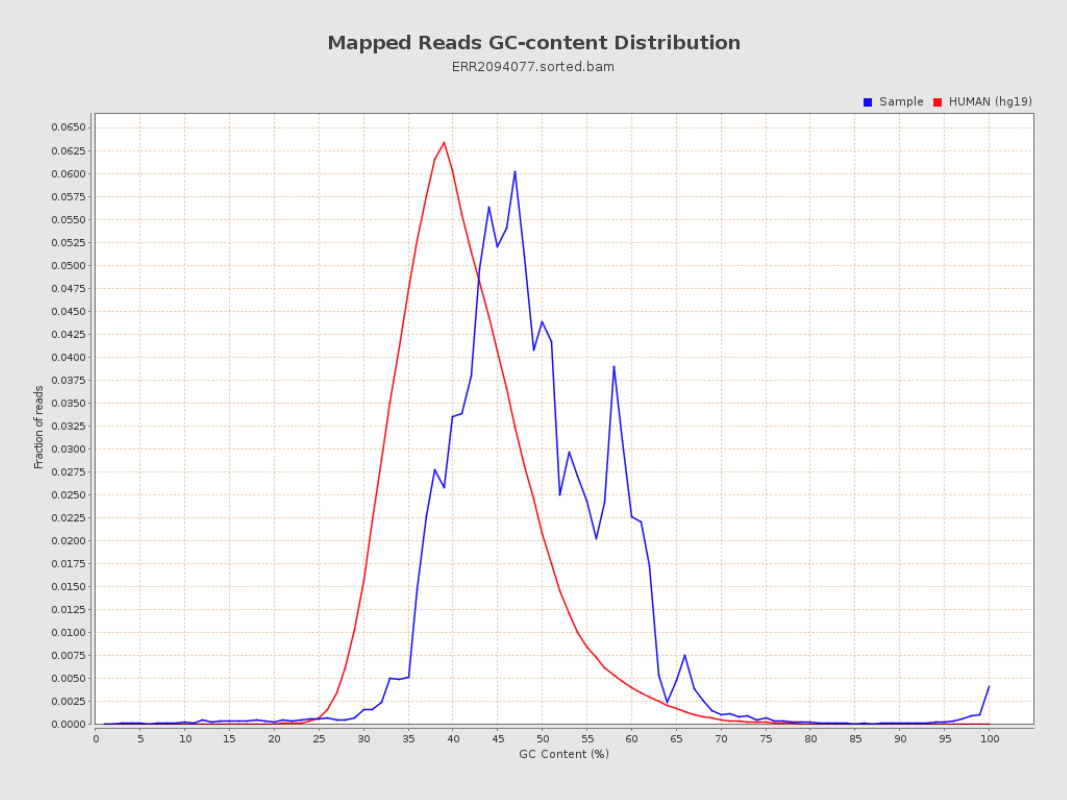
7. Results : Duplication Rate Histogram



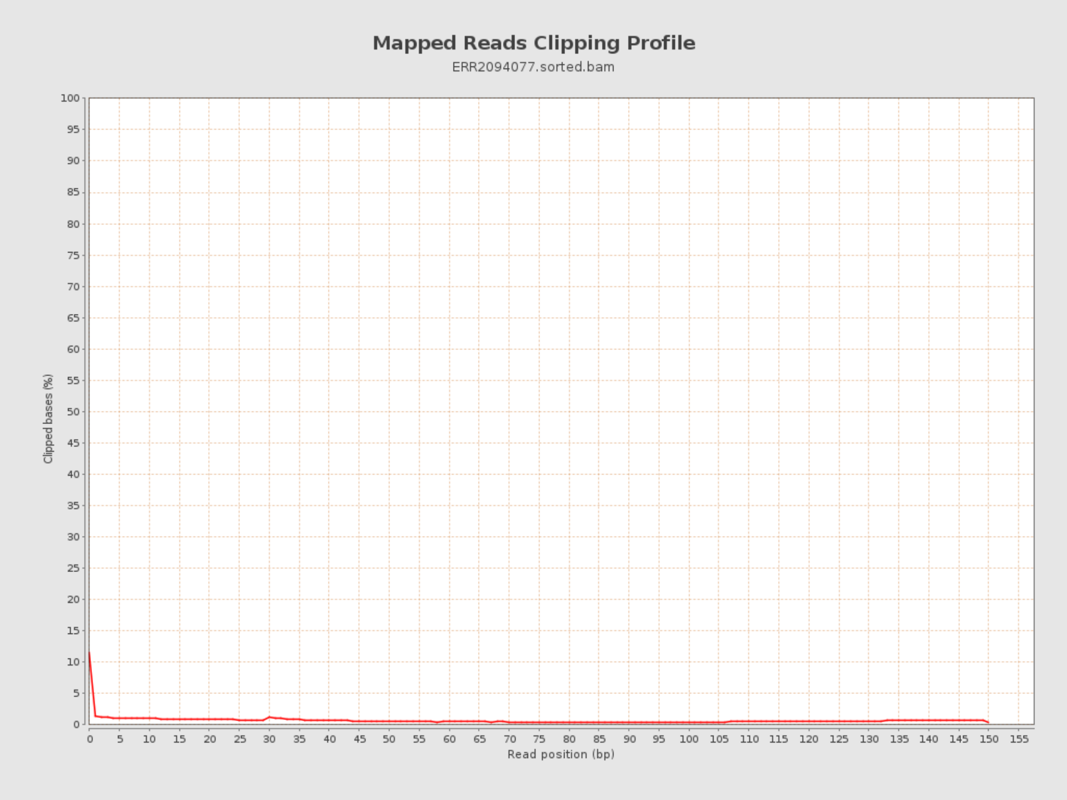
8. Results : Mapped Reads Nucleotide Content



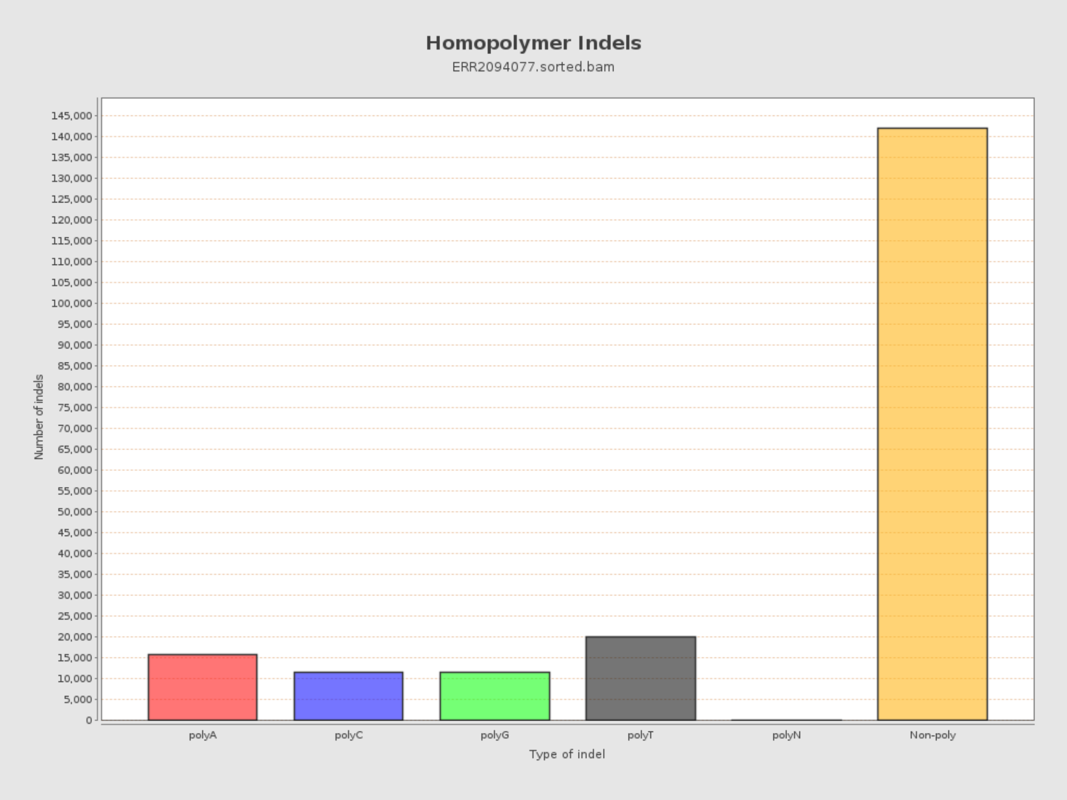
9. Results : Mapped Reads GC-content Distribution



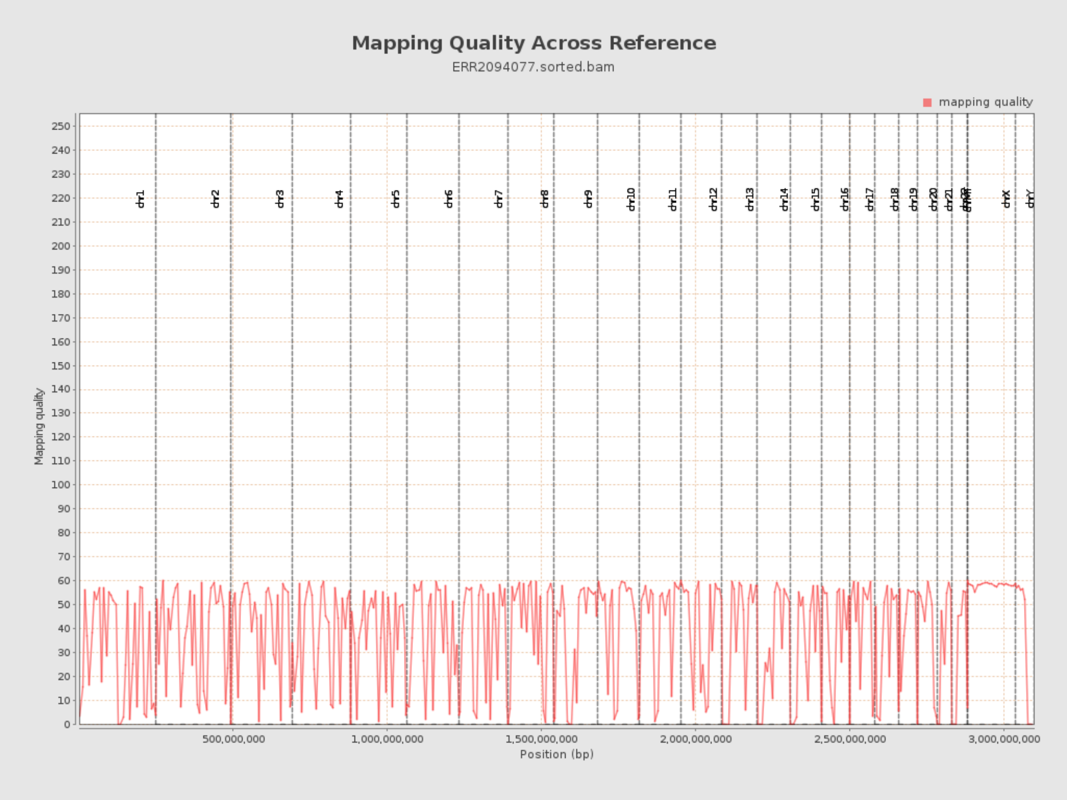
10. Results : Mapped Reads Clipping Profile



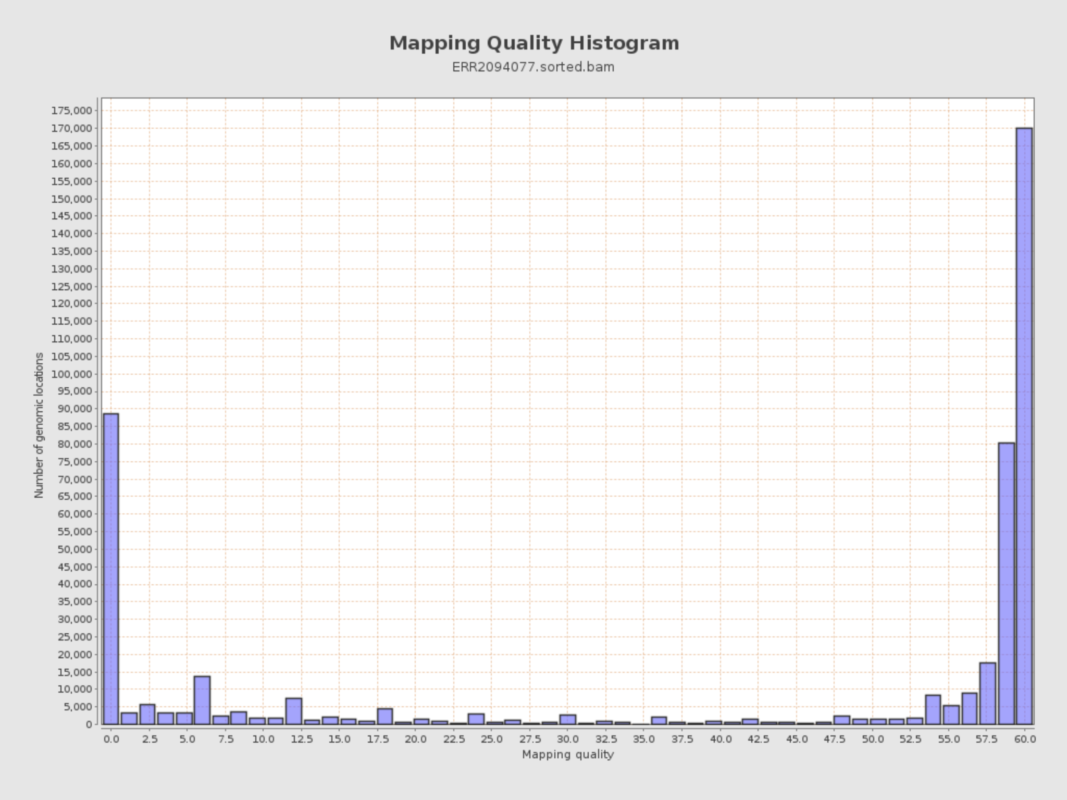
11. Results : Homopolymer Indels



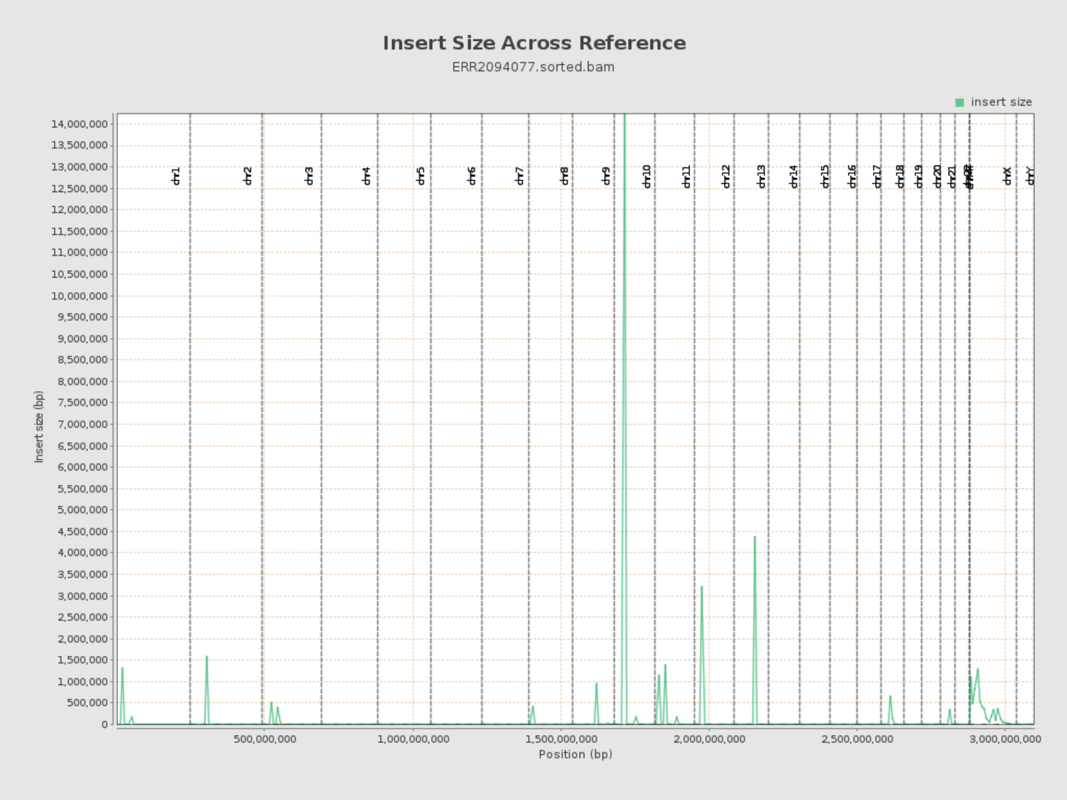
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram