Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:28:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094087.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_ERR2094087 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094087_1.fastq.gz ERR2094087_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:28:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	400,164
Mapped reads	389,330 / 97.29%
Unmapped reads	10,834 / 2.71%
Mapped paired reads	389,330 / 97.29%
Mapped reads, first in pair	195,558 / 48.87%
Mapped reads, second in pair	193,772 / 48.42%
Mapped reads, both in pair	386,804 / 96.66%
Mapped reads, singletons	2,526 / 0.63%
Secondary alignments	0
Supplementary alignments	13,633 / 3.41%
Read min/max/mean length	30 / 151 / 143.22
Duplicated reads (estimated)	372,433 / 93.07%
Duplication rate	51.18%
Clipped reads	150,064 / 37.5%

2.2. ACGT Content

Number/percentage of A's	13,232,925 / 26.01%
Number/percentage of C's	12,260,949 / 24.1%
Number/percentage of T's	12,647,299 / 24.86%
Number/percentage of G's	12,727,763 / 25.02%
Number/percentage of N's	699 / 0%

GC Percentage	49.12%

2.3. Coverage

Mean	0.0168
Standard Deviation	4.8989

2.4. Mapping Quality

Mean Mapping Quality	37.66

2.5. Insert size

Mean	461,824.42
Standard Deviation	6,160,640.73
P25/Median/P75	140 / 169 / 199

2.6. Mismatches and indels

General error rate	4.1%
Mismatches	2,006,975
Insertions	31,008
Mapped reads with at least one insertion	7.86%
Deletions	153,384
Mapped reads with at least one deletion	37.73%
Homopolymer indels	26.68%

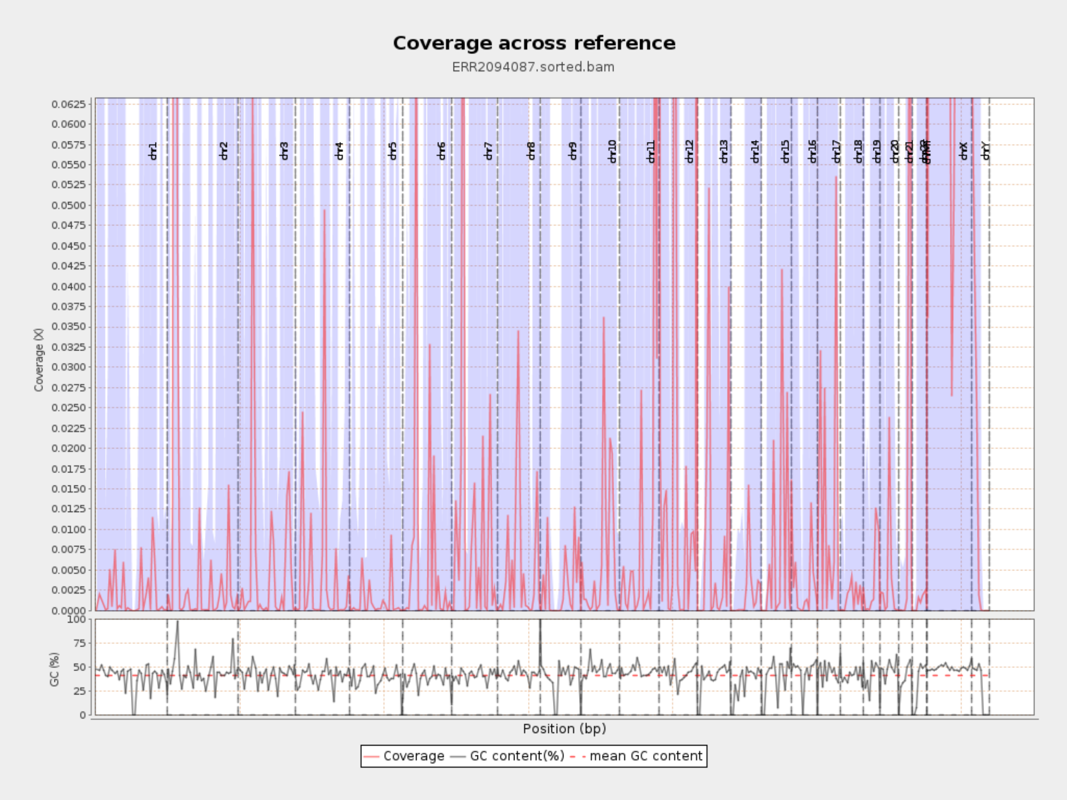
2.7. Chromosome stats

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

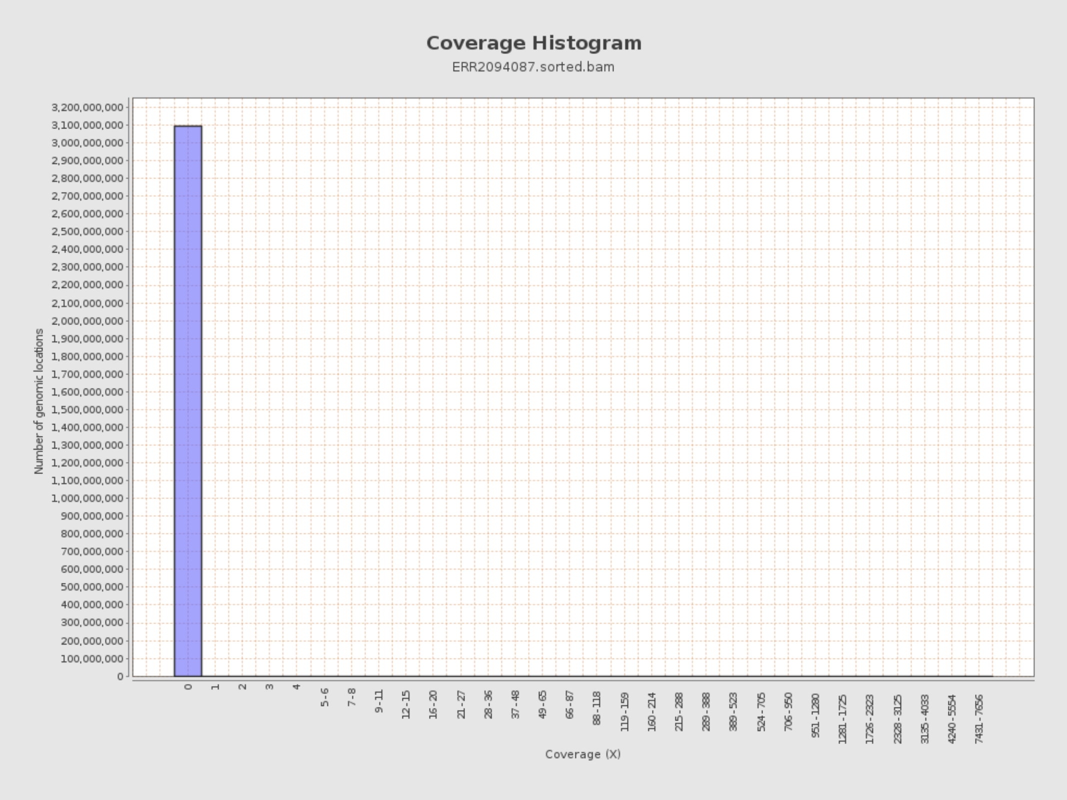
		bases	coverage	deviation
chr1	249250621	453792	0.0018	0.6968
chr2	243199373	2368261	0.0097	4.5923
chr3	198022430	1065809	0.0054	2.1814
chr4	191154276	881361	0.0046	1.7038
chr5	180915260	196406	0.0011	0.5487
chr6	171115067	1206435	0.0071	3.8593
chr7	159138663	1746643	0.011	4.1948
chr8	146364022	796050	0.0054	1.7733
chr9	141213431	424810	0.003	0.9797
chr10	135534747	854573	0.0063	2.3286
chr11	135006516	1682205	0.0125	3.8113
chr12	133851895	1967047	0.0147	5.8776
chr13	115169878	1011307	0.0088	3.1603
chr14	107349540	248092	0.0023	0.9365
chr15	102531392	773392	0.0075	2.3979
chr16	90354753	323239	0.0036	1.1073
chr17	81195210	1088607	0.0134	4.2585
chr18	78077248	130437	0.0017	0.491
chr19	59128983	204106	0.0035	0.9757
chr20	63025520	252364	0.004	1.2833
chr21	48129895	853730	0.0177	8.1926
chr22	51304566	54940	0.0011	0.2793
chrMT	16571	1947642	117.5332	581.1723
chrX	155270560	30633241	0.1973	16.1525

chrY	59373566	855600	0.0144	4.2197

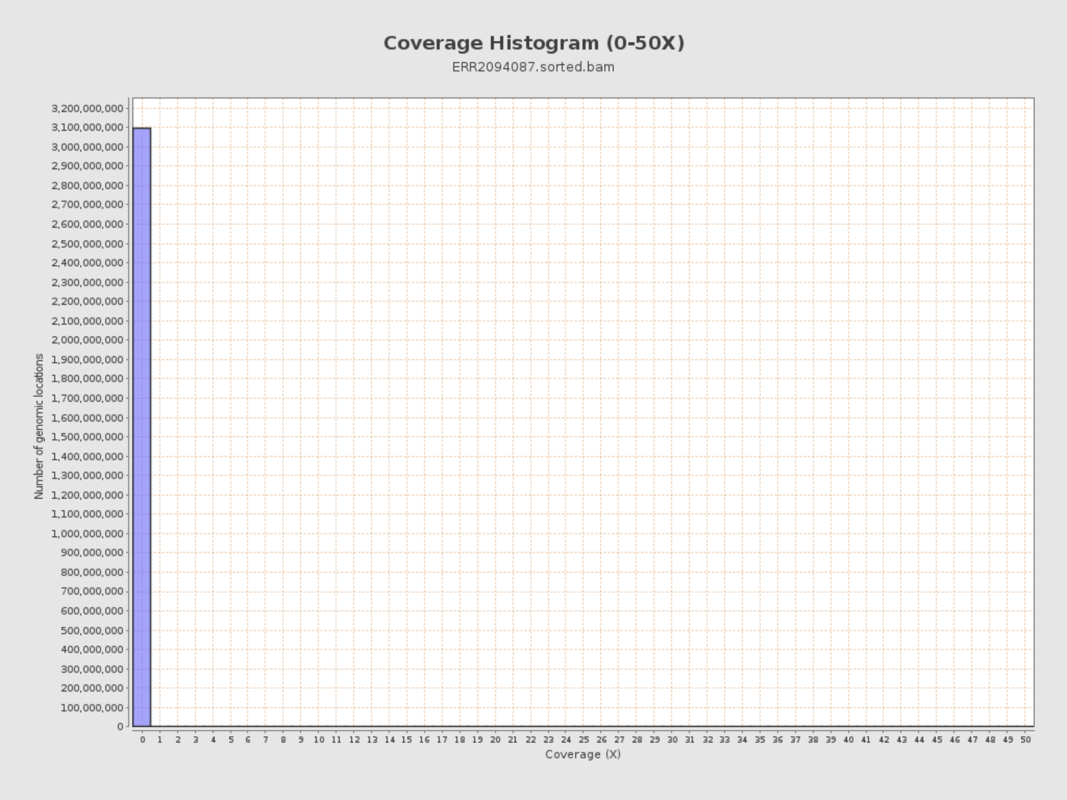
3. Results : Coverage across reference



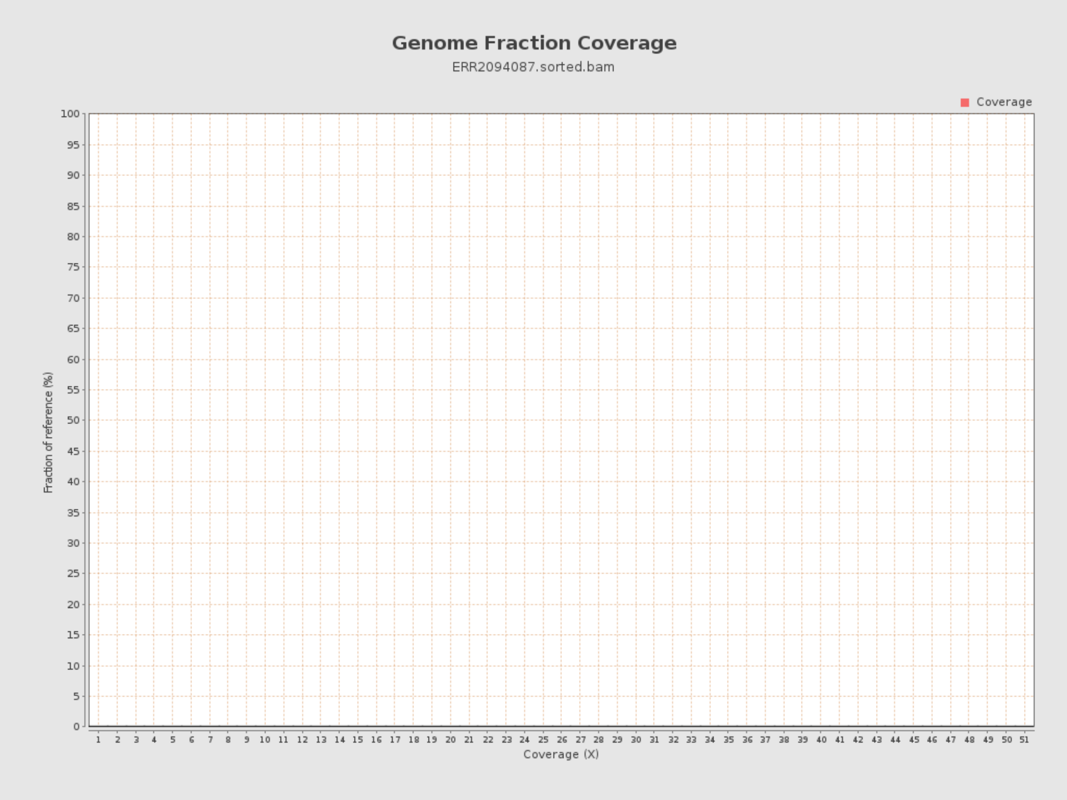
4. Results : Coverage Histogram



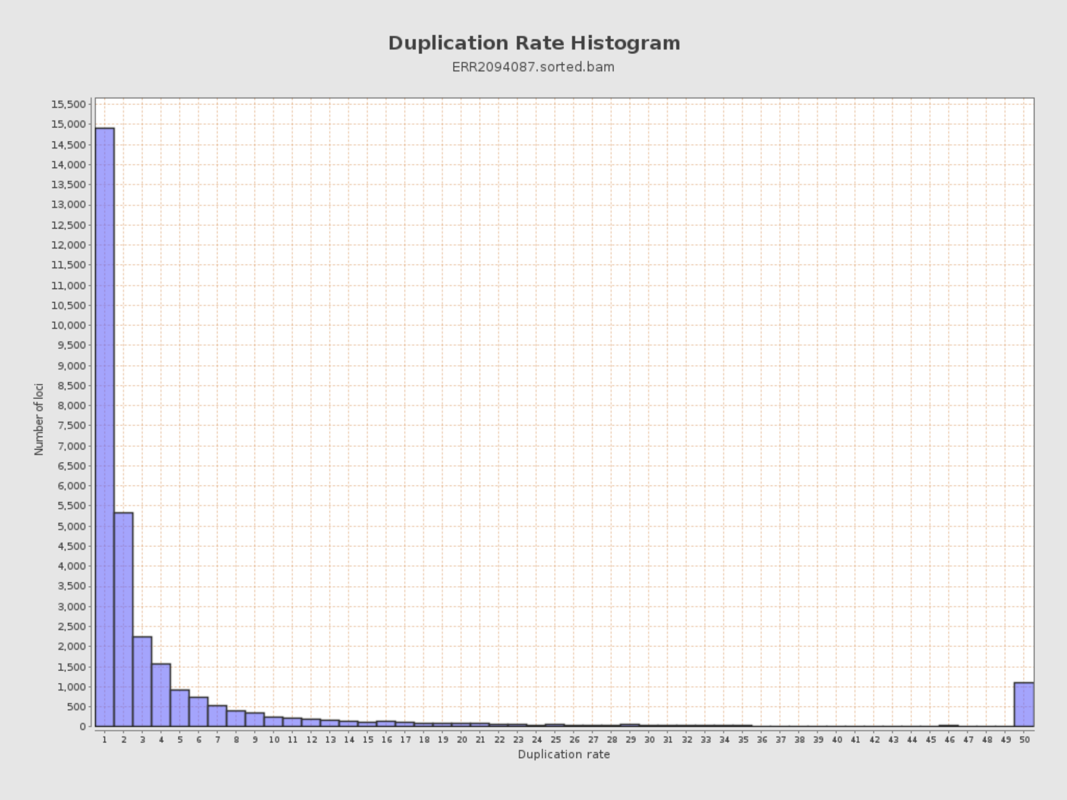
5. Results : Coverage Histogram (0-50X)



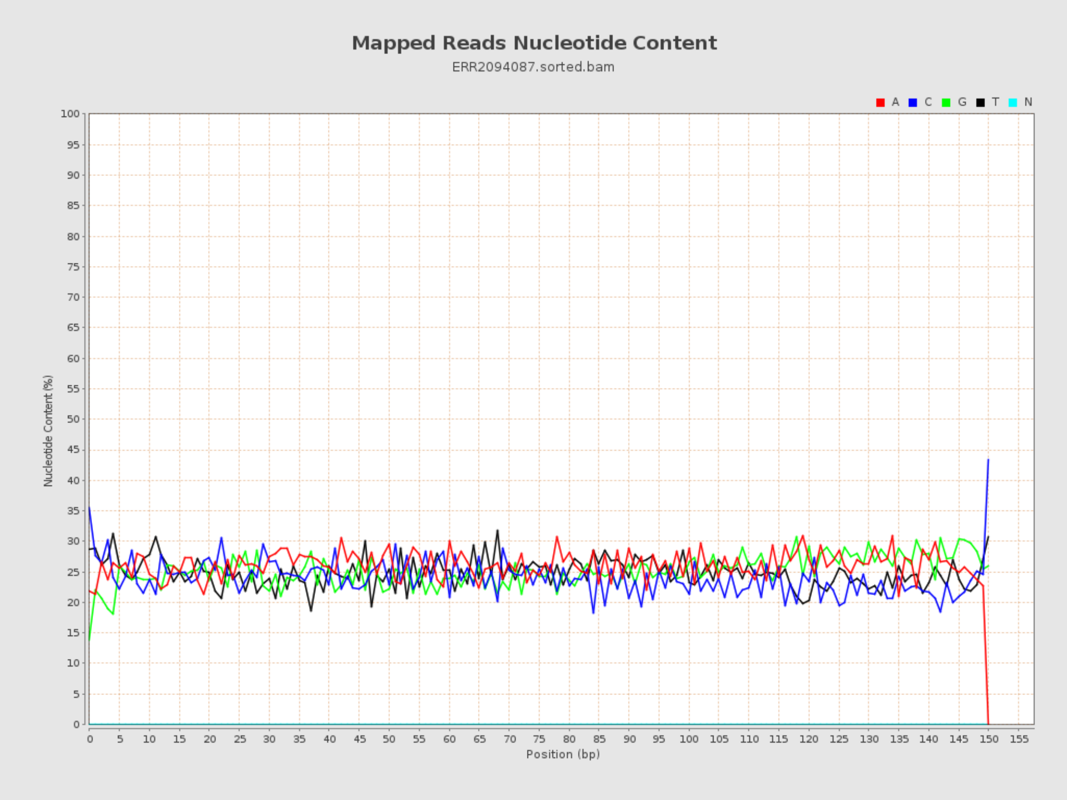
6. Results : Genome Fraction Coverage



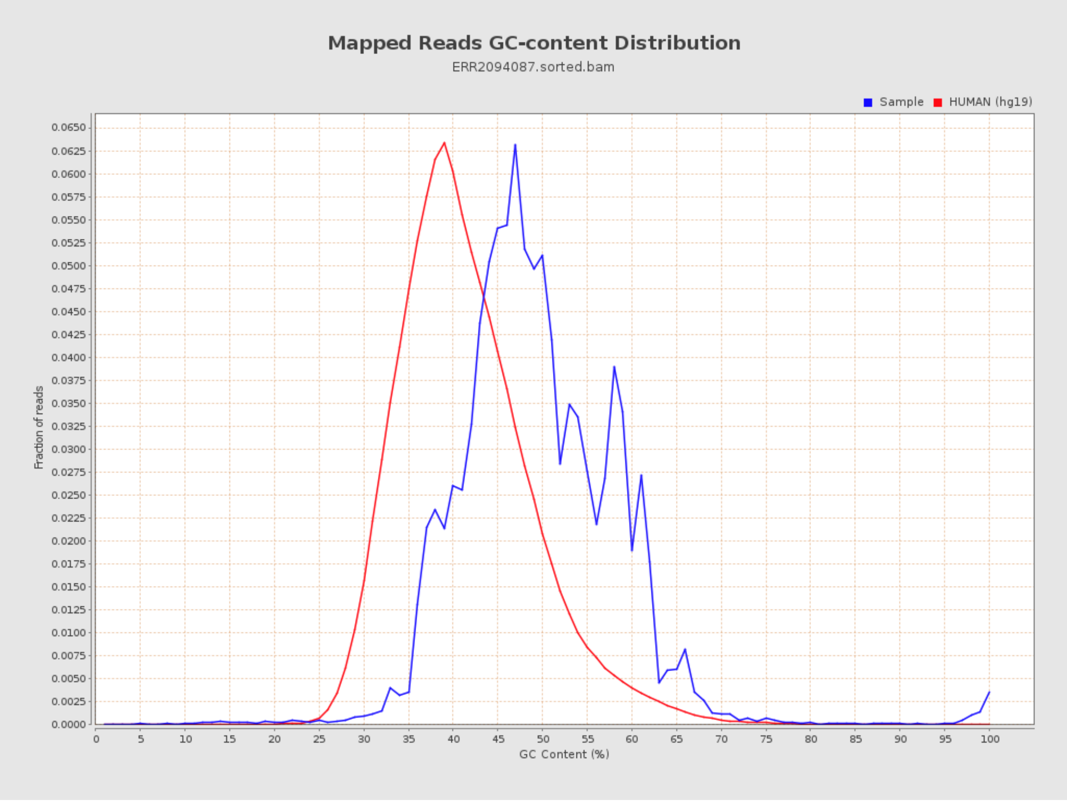
7. Results : Duplication Rate Histogram



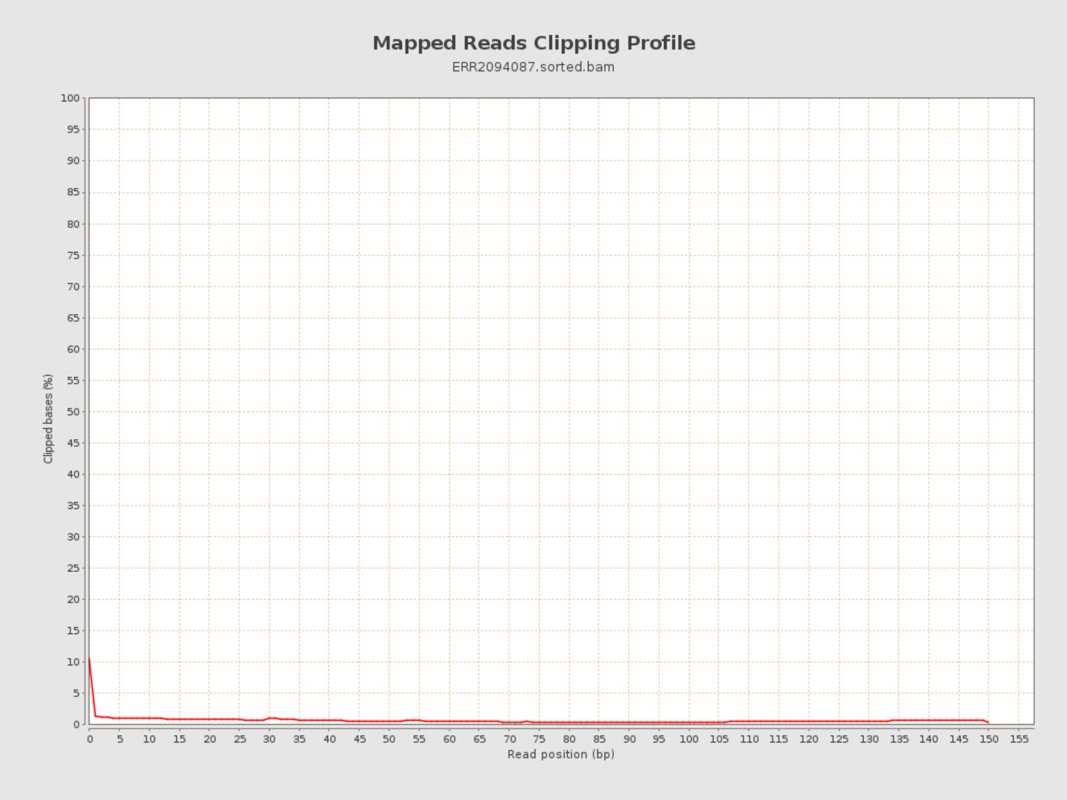
8. Results : Mapped Reads Nucleotide Content



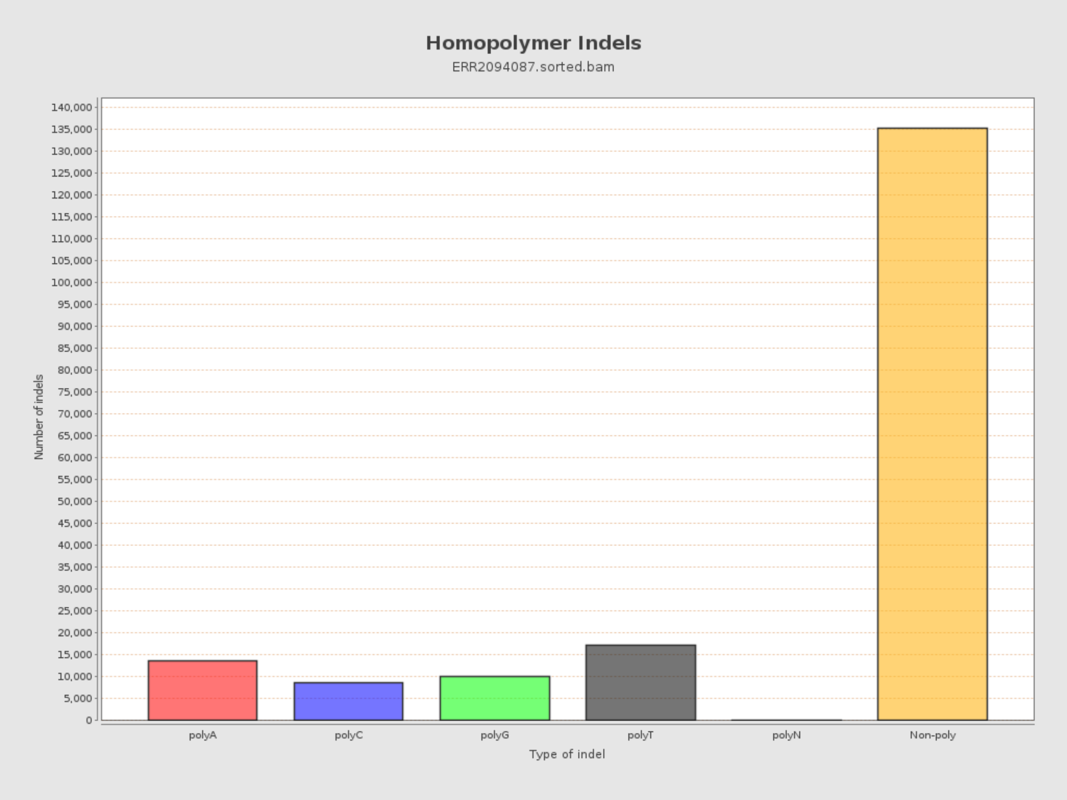
9. Results : Mapped Reads GC-content Distribution



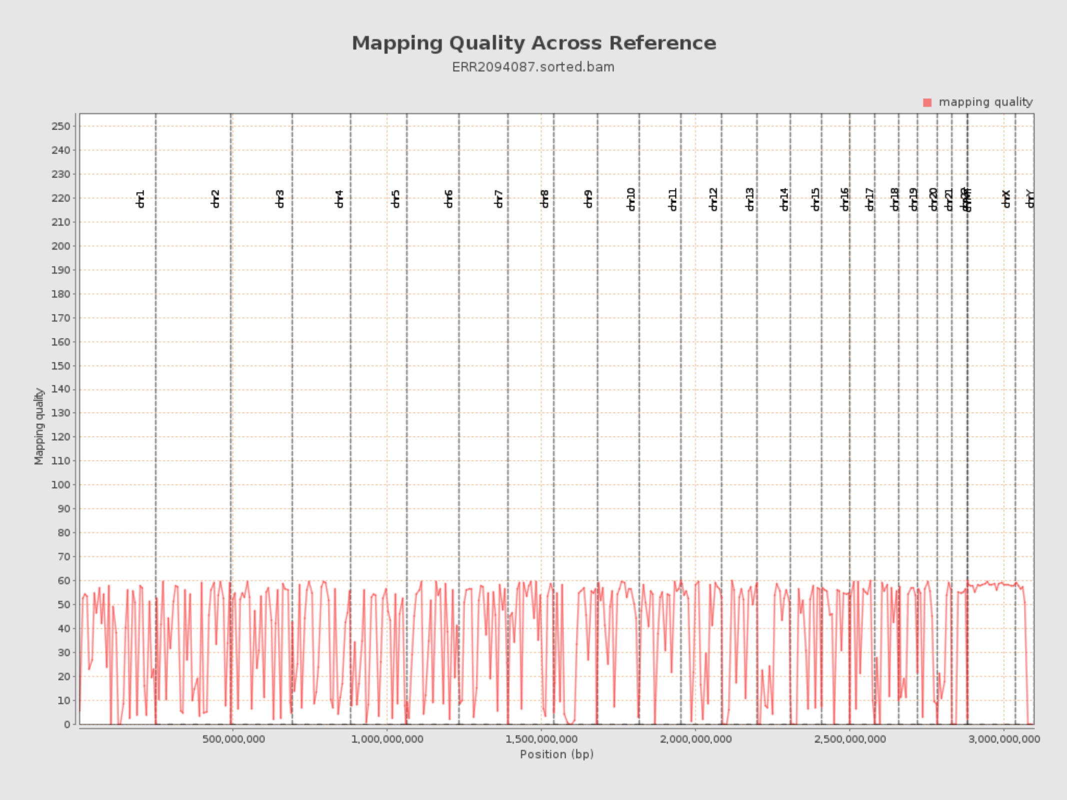
10. Results : Mapped Reads Clipping Profile



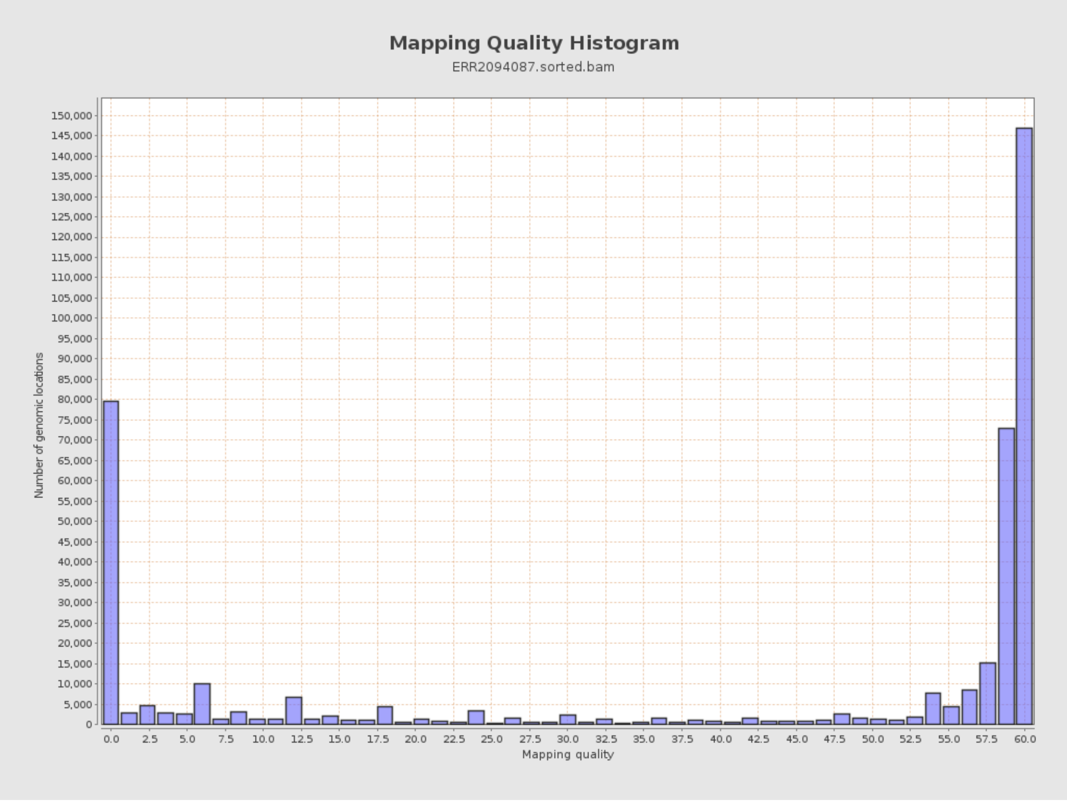
11. Results : Homopolymer Indels



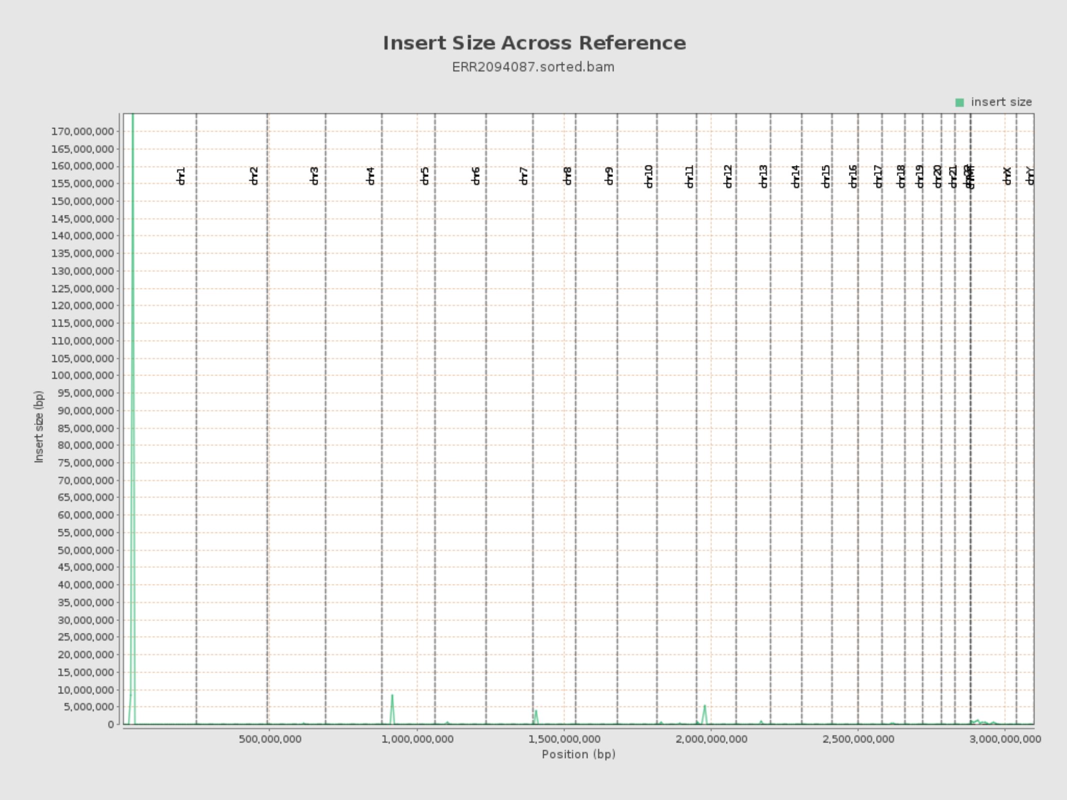
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram