Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 06:38:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094154.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_ERR2094154 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094154_1.fastq.gz ERR2094154_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 06:38:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094154.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	50,566
Mapped reads	4,662 / 9.22%
Unmapped reads	45,904 / 90.78%
Mapped paired reads	4,662 / 9.22%
Mapped reads, first in pair	2,161 / 4.27%
Mapped reads, second in pair	2,501 / 4.95%
Mapped reads, both in pair	4,020 / 7.95%
Mapped reads, singletons	642 / 1.27%
Secondary alignments	0
Supplementary alignments	167 / 0.33%
Read min/max/mean length	30 / 151 / 69.21
Duplicated reads (estimated)	3,999 / 7.91%
Duplication rate	18.55%
Clipped reads	2,589 / 5.12%

2.2. ACGT Content

Number/percentage of A's	158,292 / 29.44%
Number/percentage of C's	94,868 / 17.65%
Number/percentage of T's	143,685 / 26.73%
Number/percentage of G's	140,755 / 26.18%
Number/percentage of N's	4 / 0%

GC Percentage	43.83%

2.3. Coverage

Mean	0.0002
Standard Deviation	0.5847

2.4. Mapping Quality

Mean Mapping Quality	9.2

2.5. Insert size

Mean	265,022.47
Standard Deviation	5,357,158.96
P25/Median/P75	149 / 149 / 149

2.6. Mismatches and indels

General error rate	3.02%
Mismatches	15,603
Insertions	233
Mapped reads with at least one insertion	4.48%
Deletions	1,487
Mapped reads with at least one deletion	31.19%
Homopolymer indels	35.87%

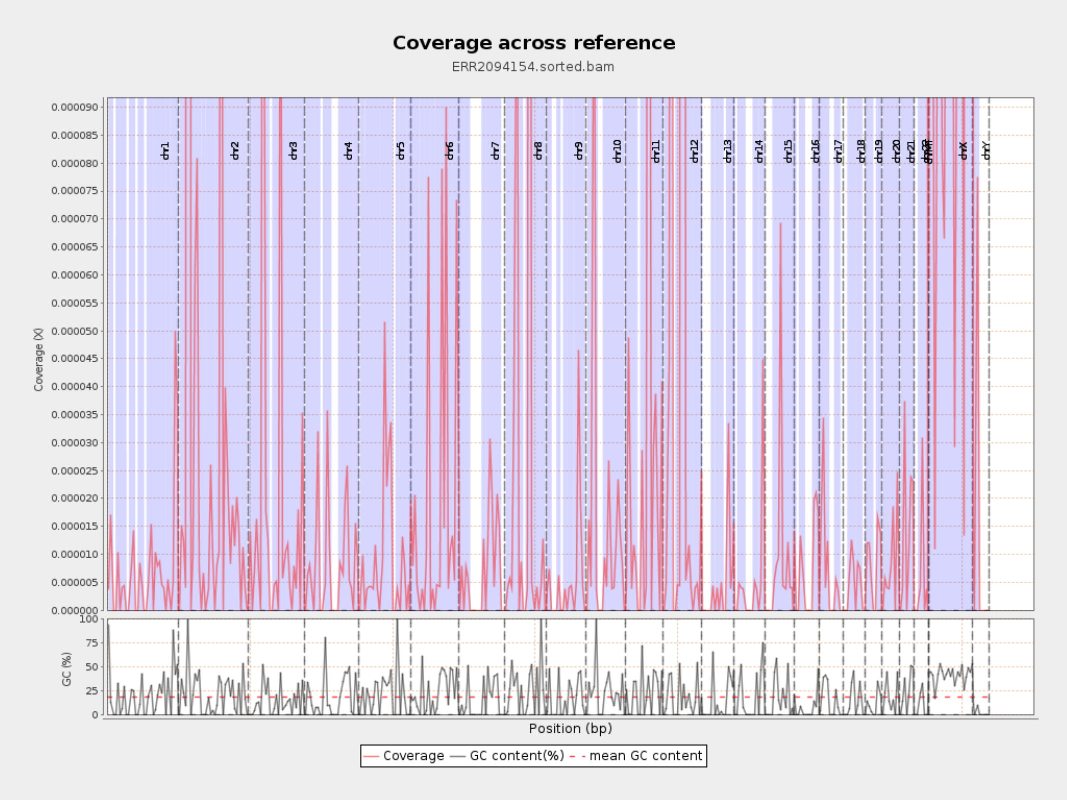
2.7. Chromosome stats

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

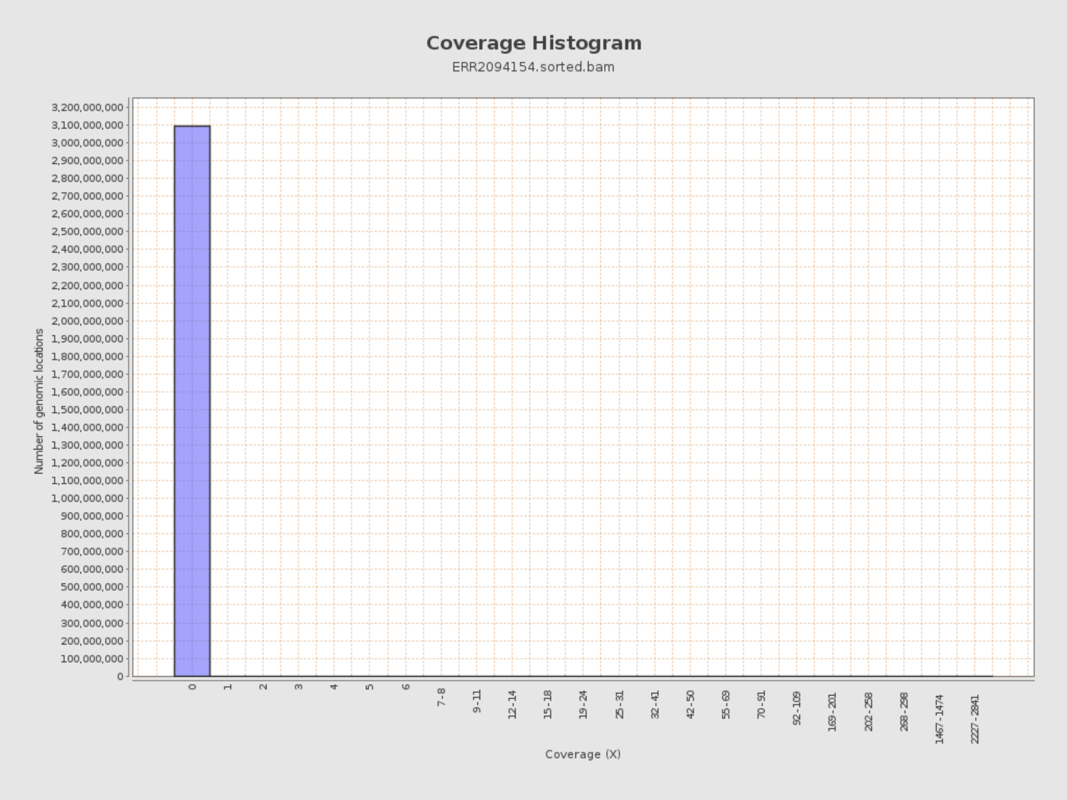
		bases	coverage	deviation
chr1	249250621	1765	0	0.0031
chr2	243199373	48576	0.0002	0.1894
chr3	198022430	3970	0	0.009
chr4	191154276	1618	0	0.0038
chr5	180915260	1680	0	0.0035
chr6	171115067	3502	0	0.0071
chr7	159138663	1072	0	0.0032
chr8	146364022	5024	0	0.022
chr9	141213431	817	0	0.0029
chr10	135534747	2063	0	0.0085
chr11	135006516	4082	0	0.0115
chr12	133851895	14161	0.0001	0.0617
chr13	115169878	488	0	0.0024
chr14	107349540	548	0	0.004
chr15	102531392	937	0	0.0075
chr16	90354753	667	0	0.003
chr17	81195210	538	0	0.0034
chr18	78077248	342	0	0.0021
chr19	59128983	465	0	0.0028
chr20	63025520	506	0	0.0031
chr21	48129895	696	0	0.0048
chr22	51304566	300	0	0.0029
chrMT	16571	14931	0.901	4.2764
chrX	155270560	433335	0.0028	2.5989

chrY	59373566	630	0	0.0067

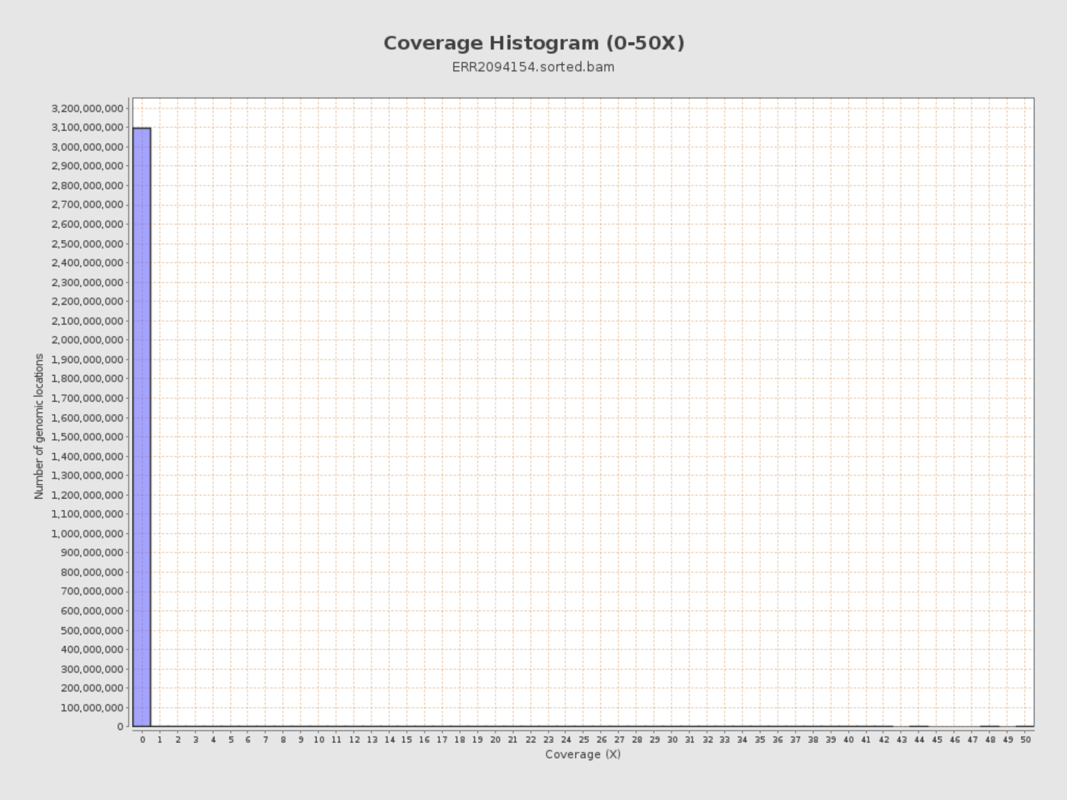
3. Results : Coverage across reference



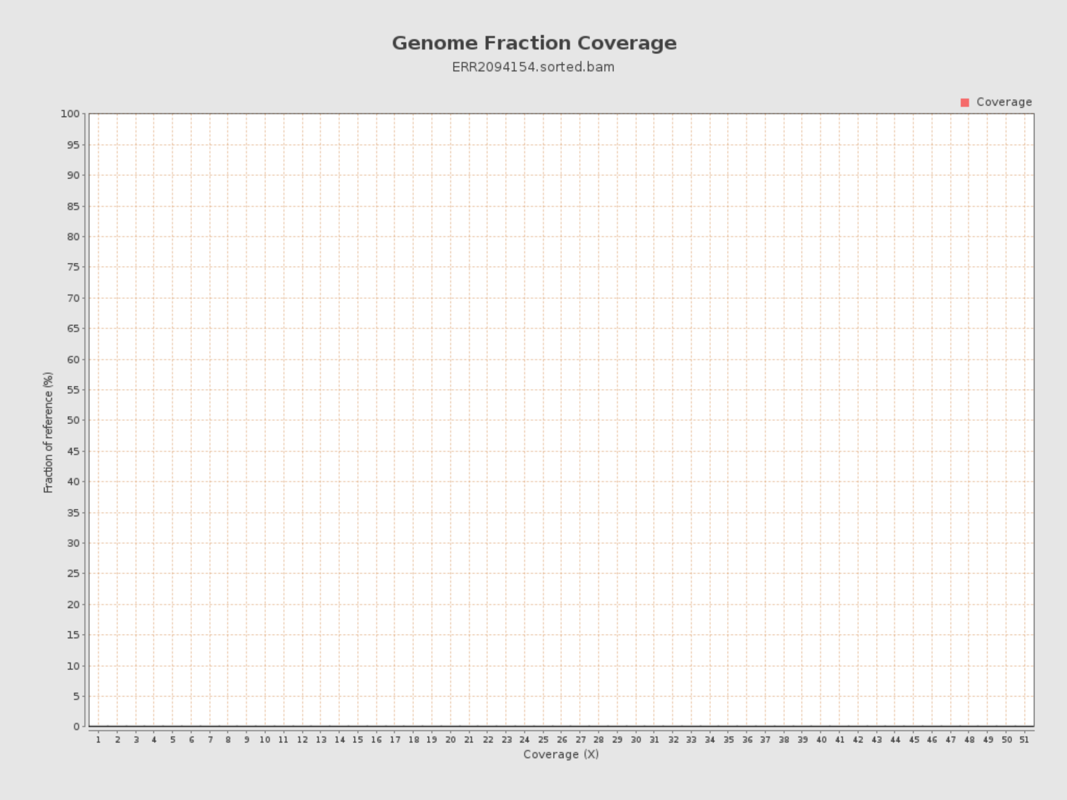
4. Results : Coverage Histogram



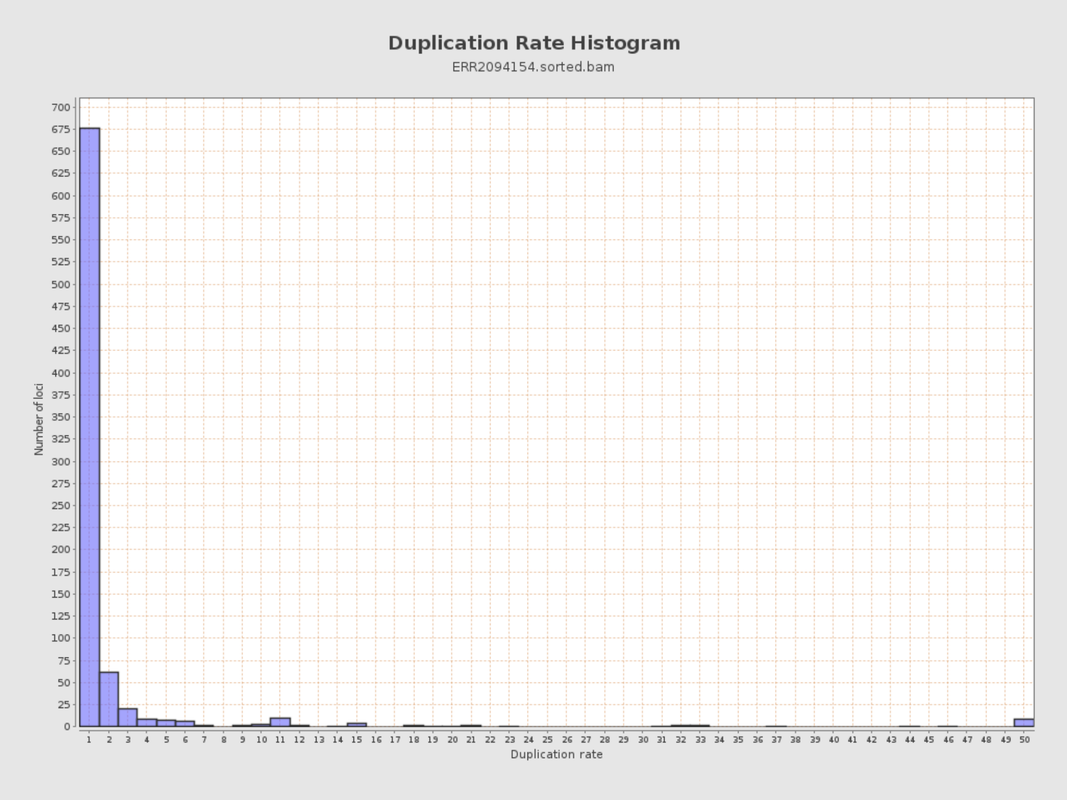
5. Results : Coverage Histogram (0-50X)



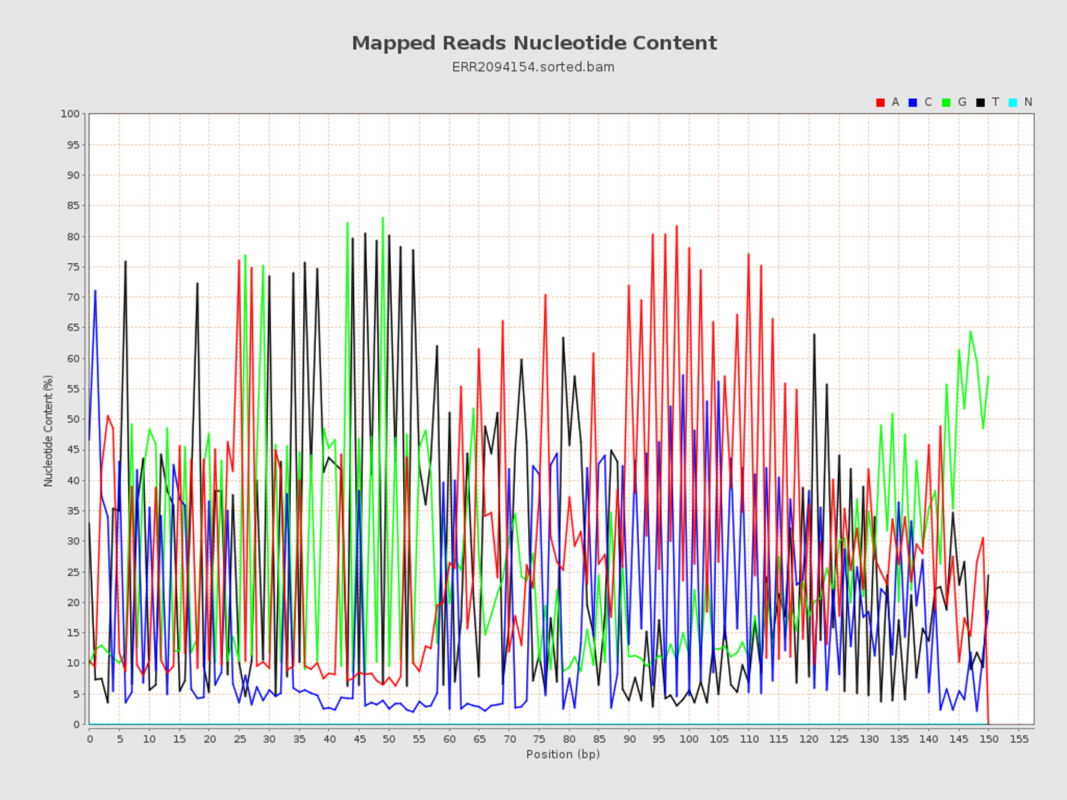
6. Results : Genome Fraction Coverage



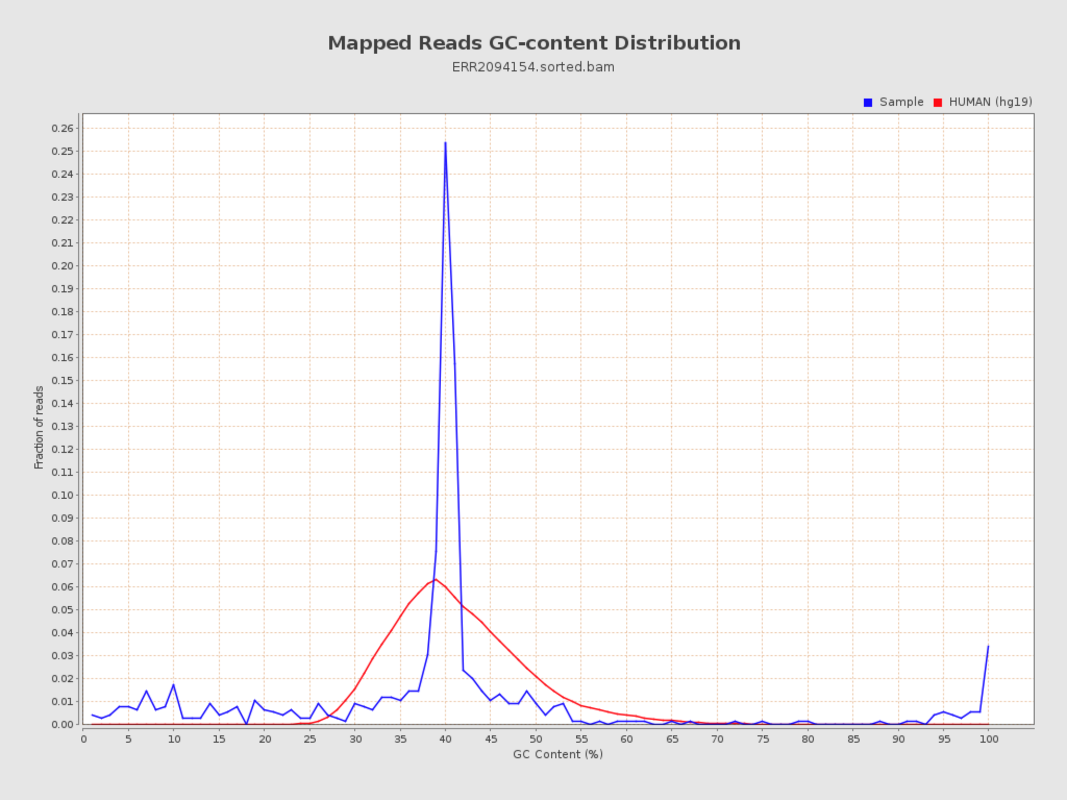
7. Results : Duplication Rate Histogram



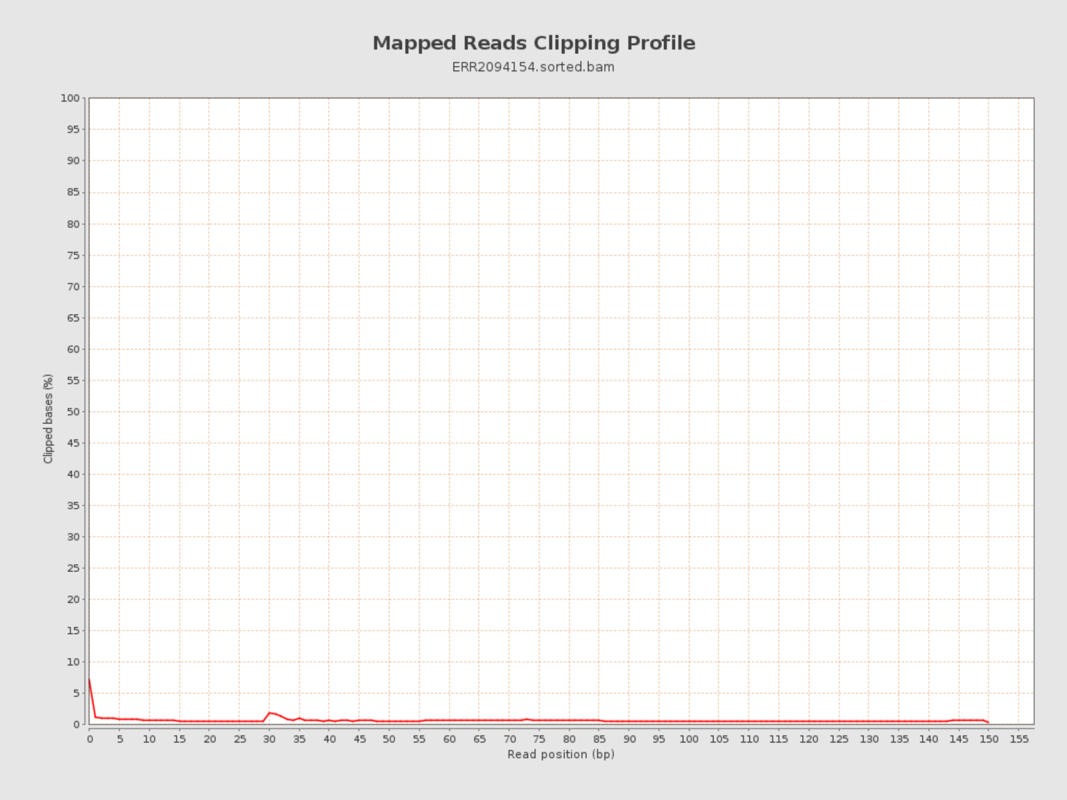
8. Results : Mapped Reads Nucleotide Content



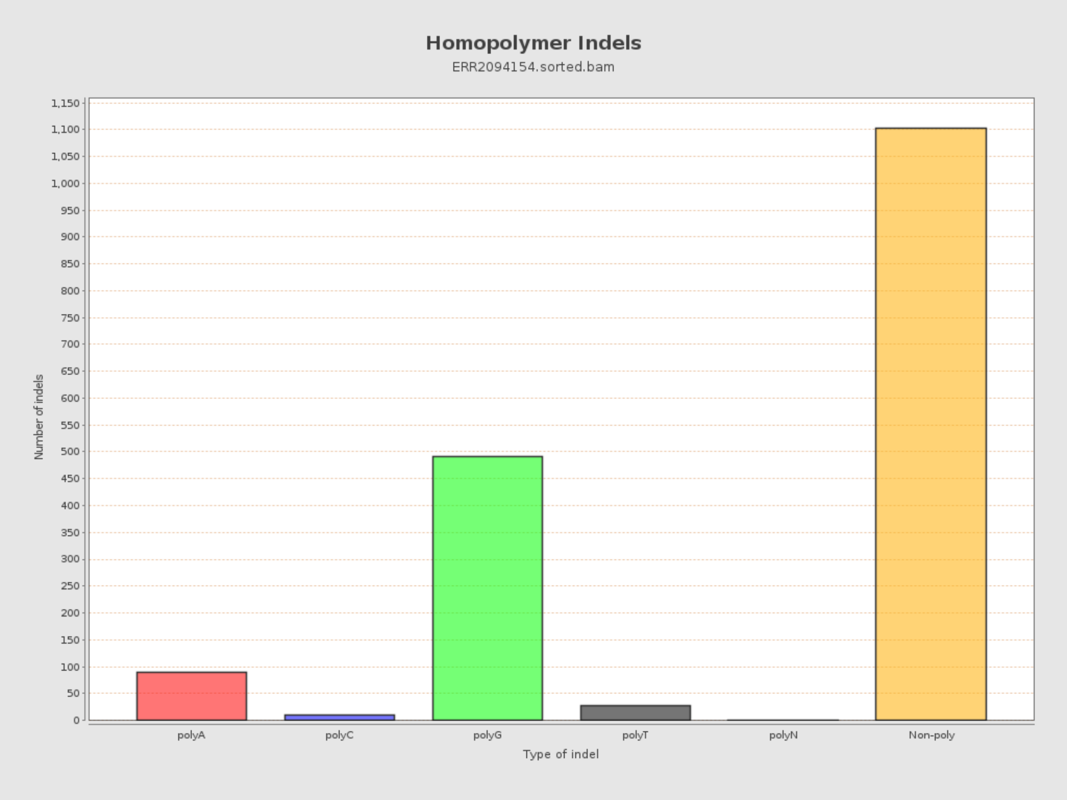
9. Results : Mapped Reads GC-content Distribution



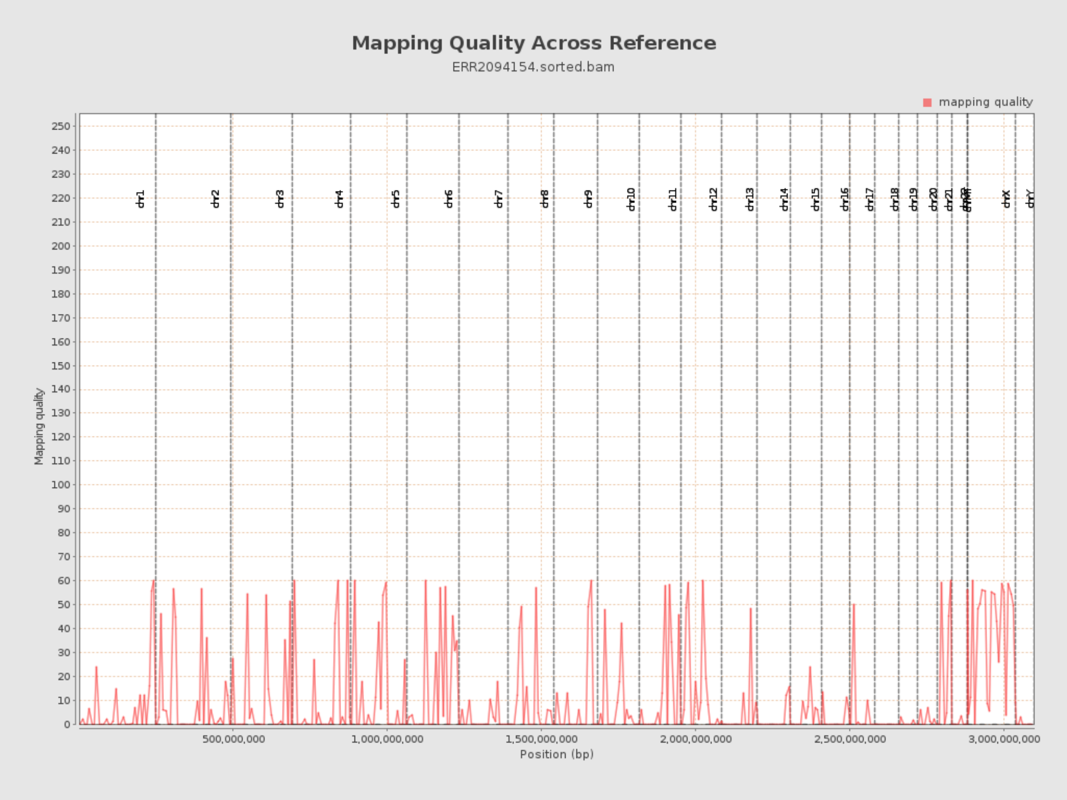
10. Results : Mapped Reads Clipping Profile



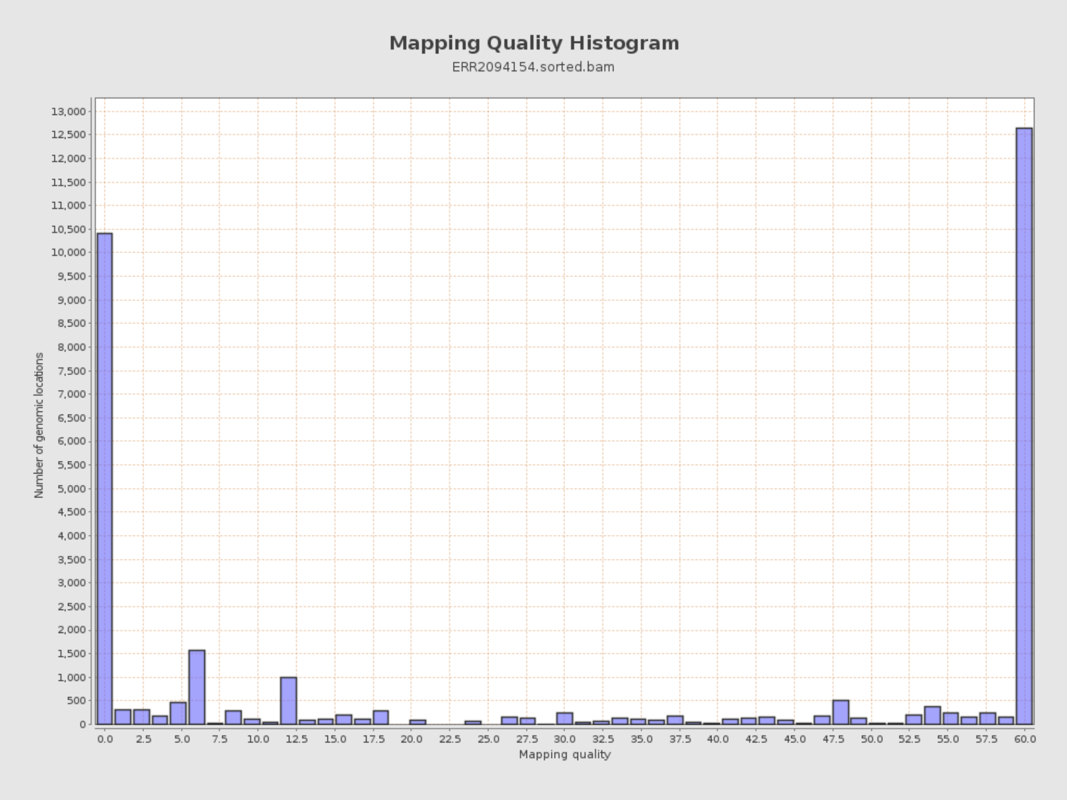
11. Results : Homopolymer Indels



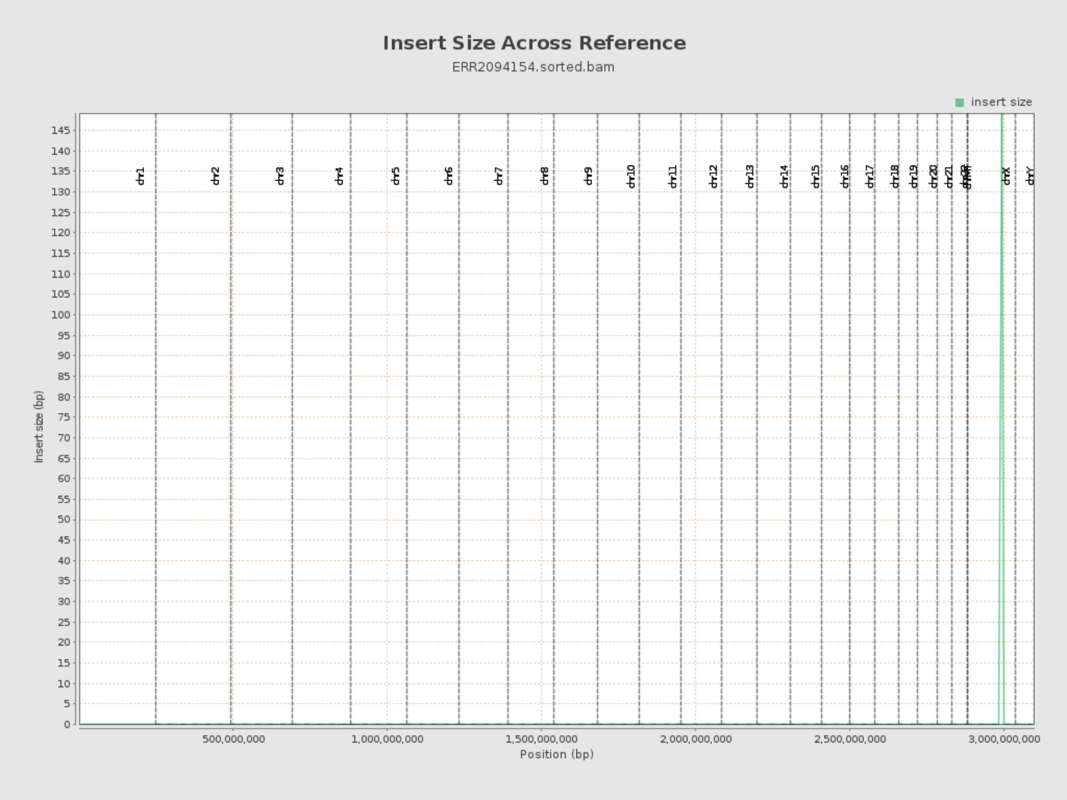
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram