Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 05:05:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094147.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_ERR2094147 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094147_1.fastq.gz ERR2094147_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 05:05:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094147.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	419,294
Mapped reads	383,327 / 91.42%
Unmapped reads	35,967 / 8.58%
Mapped paired reads	383,327 / 91.42%
Mapped reads, first in pair	192,487 / 45.91%
Mapped reads, second in pair	190,840 / 45.51%
Mapped reads, both in pair	380,158 / 90.67%
Mapped reads, singletons	3,169 / 0.76%
Secondary alignments	0
Supplementary alignments	23,796 / 5.68%
Read min/max/mean length	30 / 151 / 134.11
Duplicated reads (estimated)	354,911 / 84.64%
Duplication rate	48.6%
Clipped reads	191,196 / 45.6%

2.2. ACGT Content

Number/percentage of A's	12,931,881 / 27.55%
Number/percentage of C's	10,482,528 / 22.34%
Number/percentage of T's	12,272,091 / 26.15%
Number/percentage of G's	11,244,725 / 23.96%
Number/percentage of N's	464 / 0%

GC Percentage	46.3%

2.3. Coverage

Mean	0.0155
Standard Deviation	2.5344

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Insert size

Mean	1,298,383.74
Standard Deviation	10,279,100.48
P25/Median/P75	117 / 151 / 184

2.6. Mismatches and indels

General error rate	4.05%
Mismatches	1,839,580
Insertions	30,794
Mapped reads with at least one insertion	7.91%
Deletions	148,323
Mapped reads with at least one deletion	37.49%
Homopolymer indels	28.51%

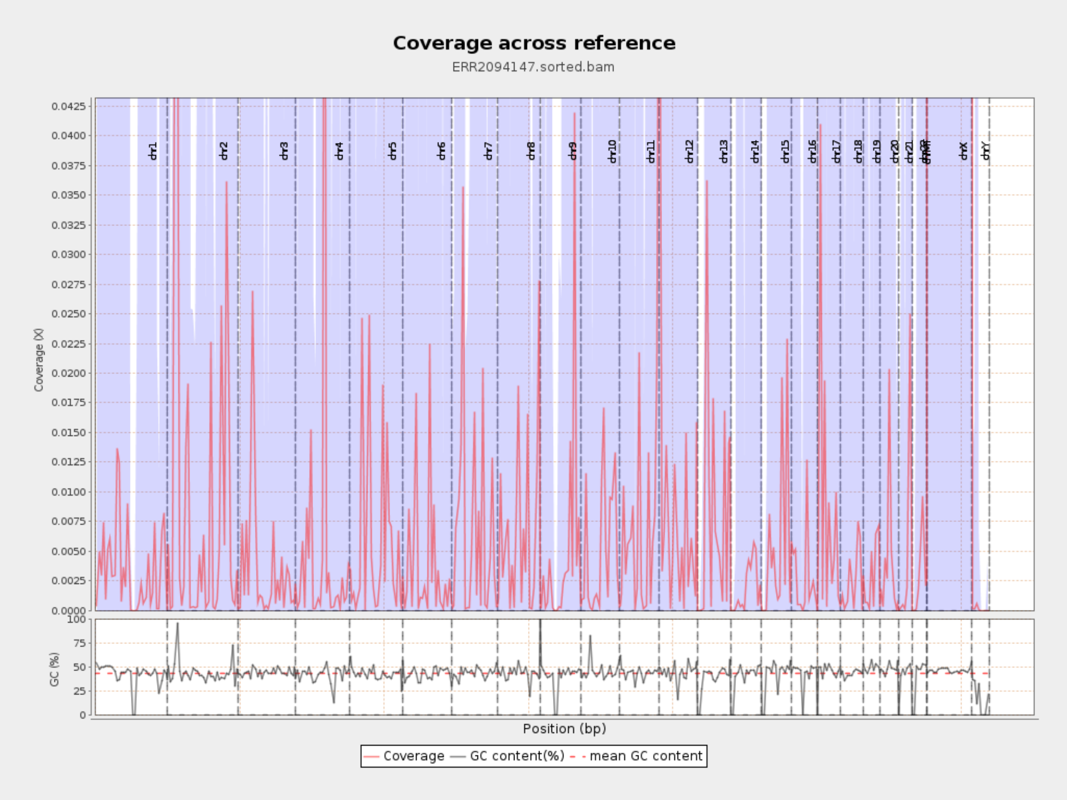
2.7. Chromosome stats

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

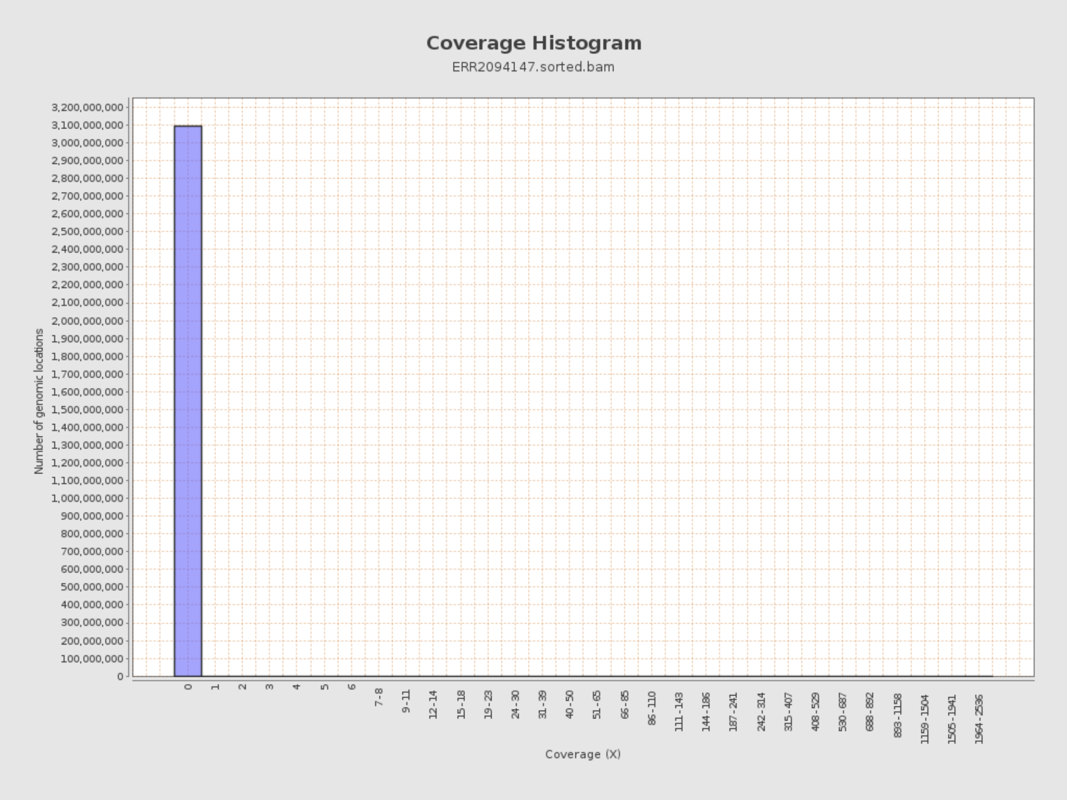
		bases	coverage	deviation
chr1	249250621	866610	0.0035	1.0833
chr2	243199373	2184756	0.009	2.5206
chr3	198022430	726960	0.0037	0.9775
chr4	191154276	1101231	0.0058	1.4661
chr5	180915260	1081313	0.006	1.8497
chr6	171115067	670689	0.0039	1.195
chr7	159138663	1084056	0.0068	1.6851
chr8	146364022	981767	0.0067	1.9238
chr9	141213431	688912	0.0049	1.6559
chr10	135534747	678805	0.005	1.1326
chr11	135006516	893768	0.0066	1.4892
chr12	133851895	1092488	0.0082	1.8596
chr13	115169878	920485	0.008	1.5196
chr14	107349540	204482	0.0019	0.5669
chr15	102531392	543210	0.0053	1.221
chr16	90354753	260074	0.0029	0.8168
chr17	81195210	729057	0.009	1.7678
chr18	78077248	205993	0.0026	0.6301
chr19	59128983	167729	0.0028	0.7165
chr20	63025520	276039	0.0044	1.3514
chr21	48129895	271625	0.0056	1.5161
chr22	51304566	152908	0.003	0.6068
chrMT	16571	1353222	81.6621	327.9132
chrX	155270560	30919634	0.1991	8.5292

chrY	59373566	6575	0.0001	0.0447

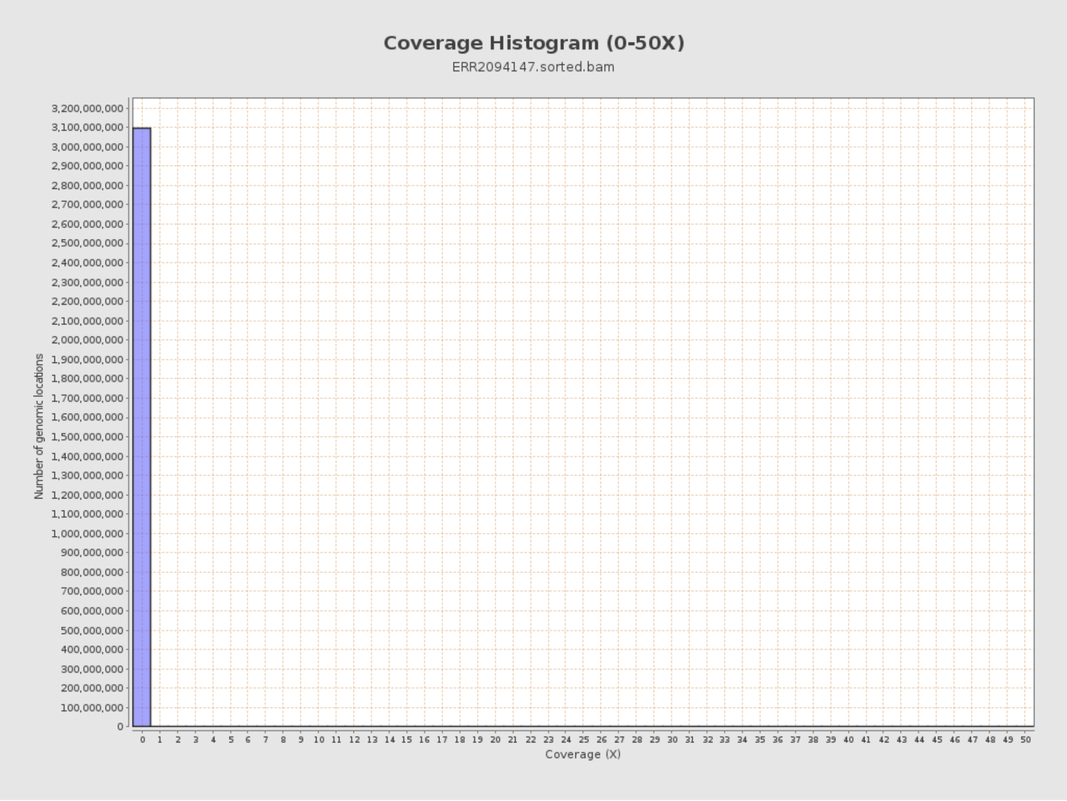
3. Results : Coverage across reference



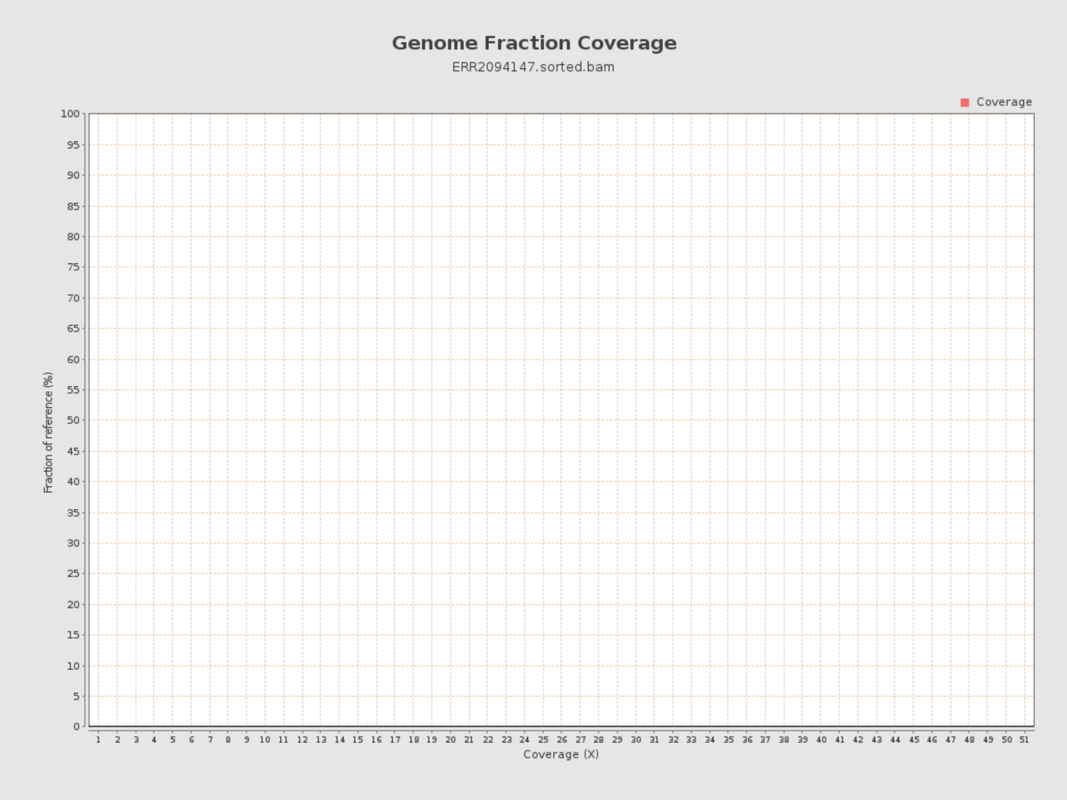
4. Results : Coverage Histogram



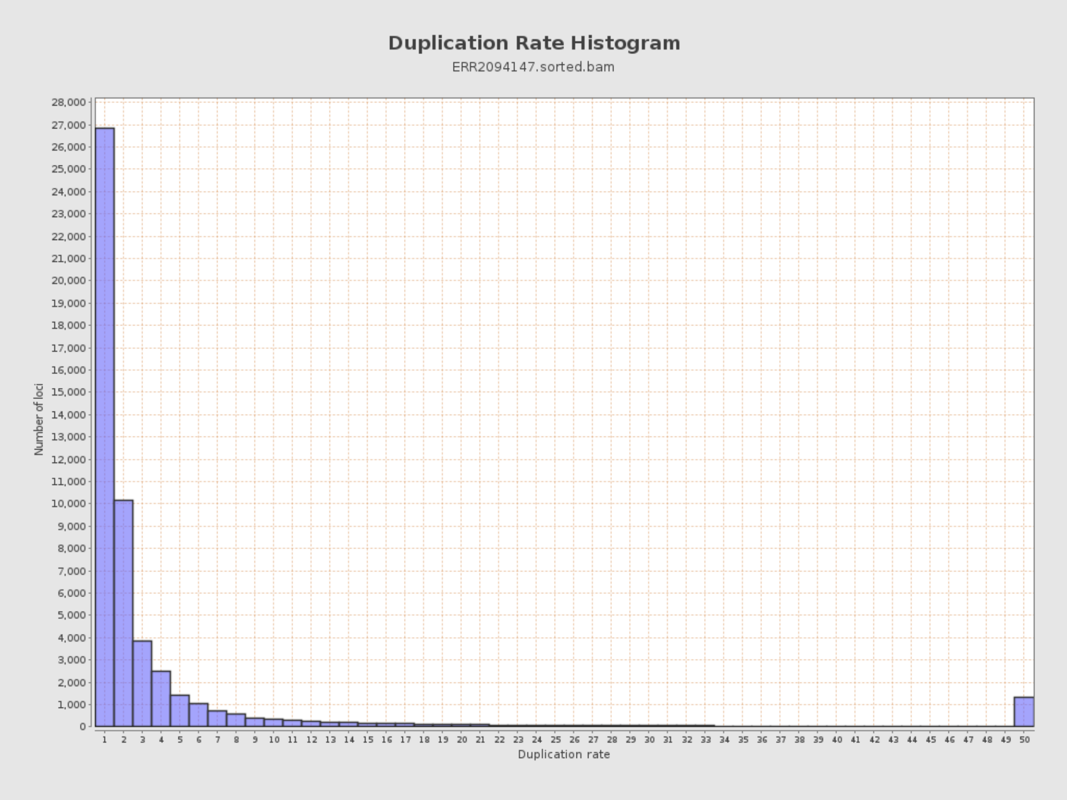
5. Results : Coverage Histogram (0-50X)



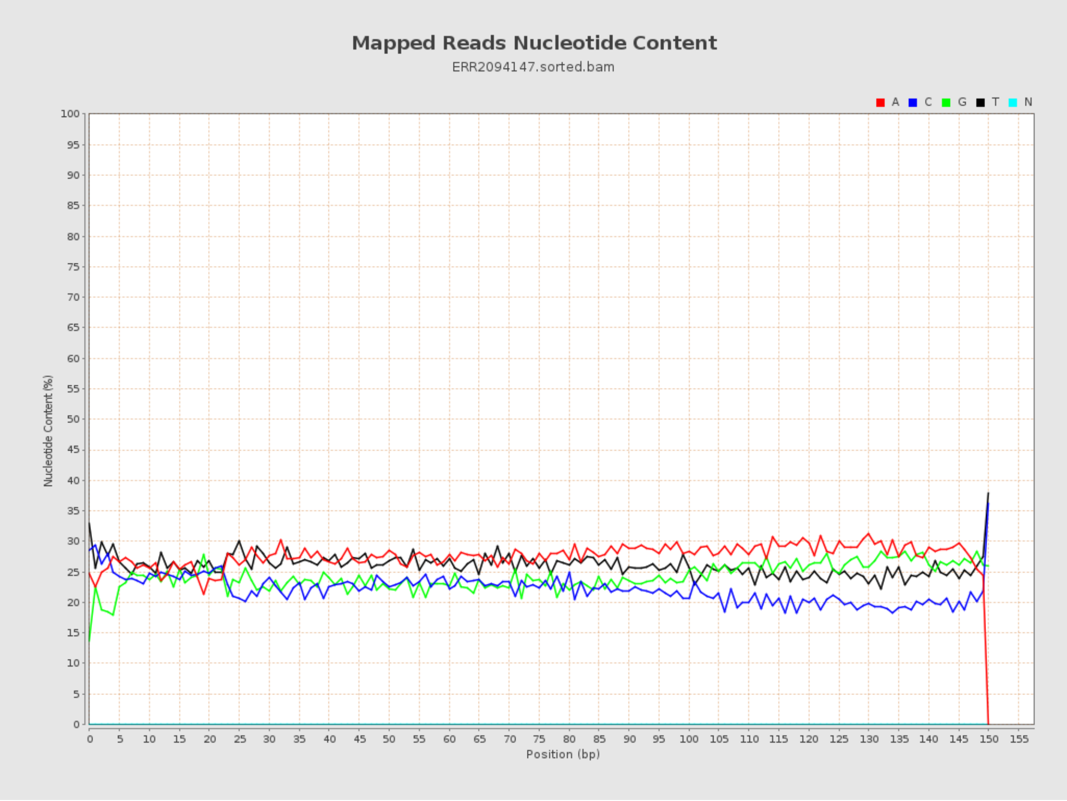
6. Results : Genome Fraction Coverage



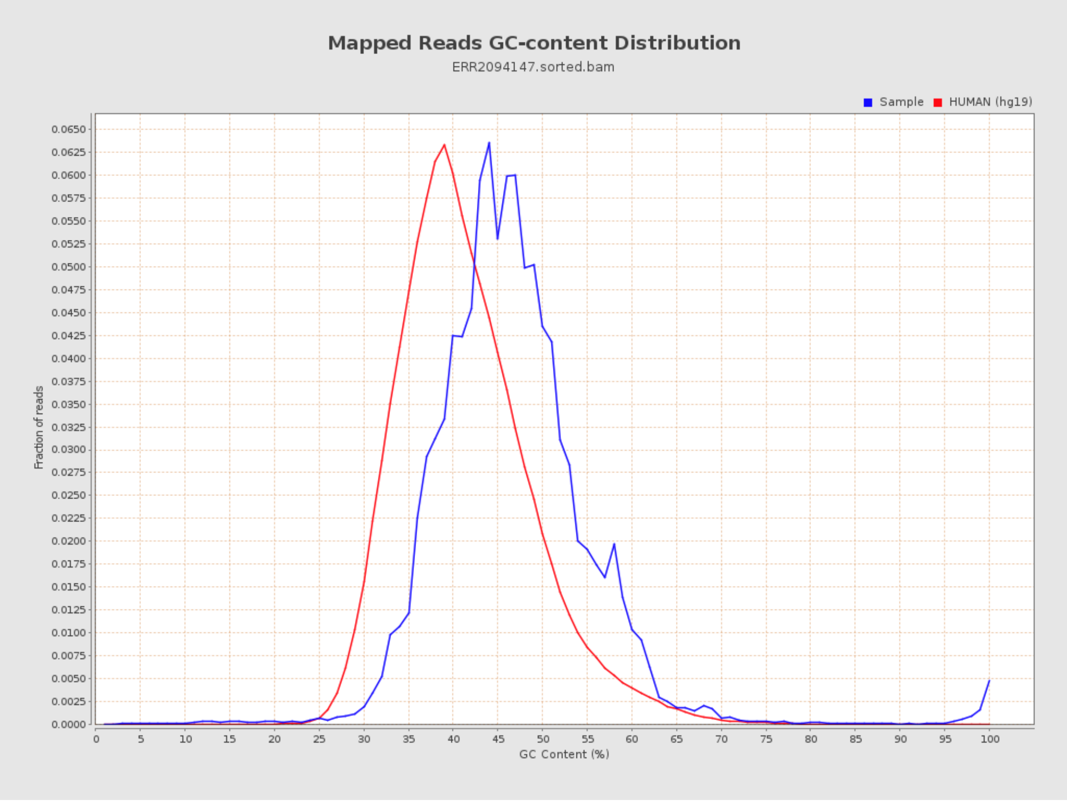
7. Results : Duplication Rate Histogram



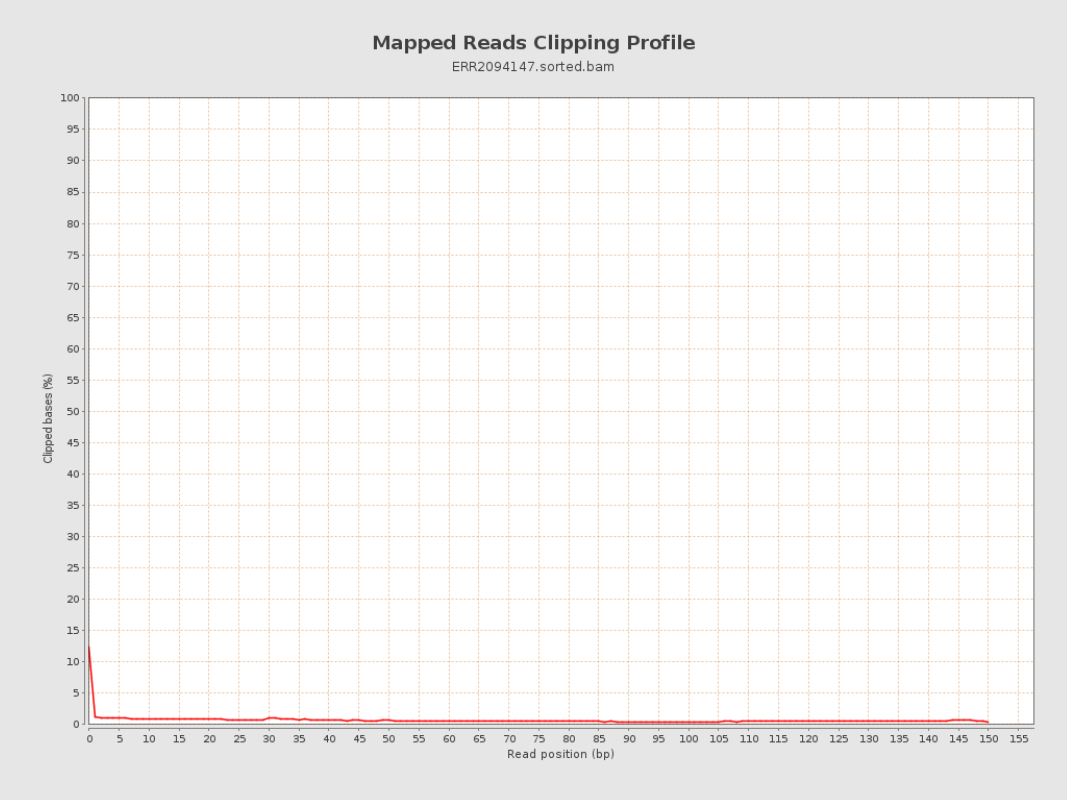
8. Results : Mapped Reads Nucleotide Content



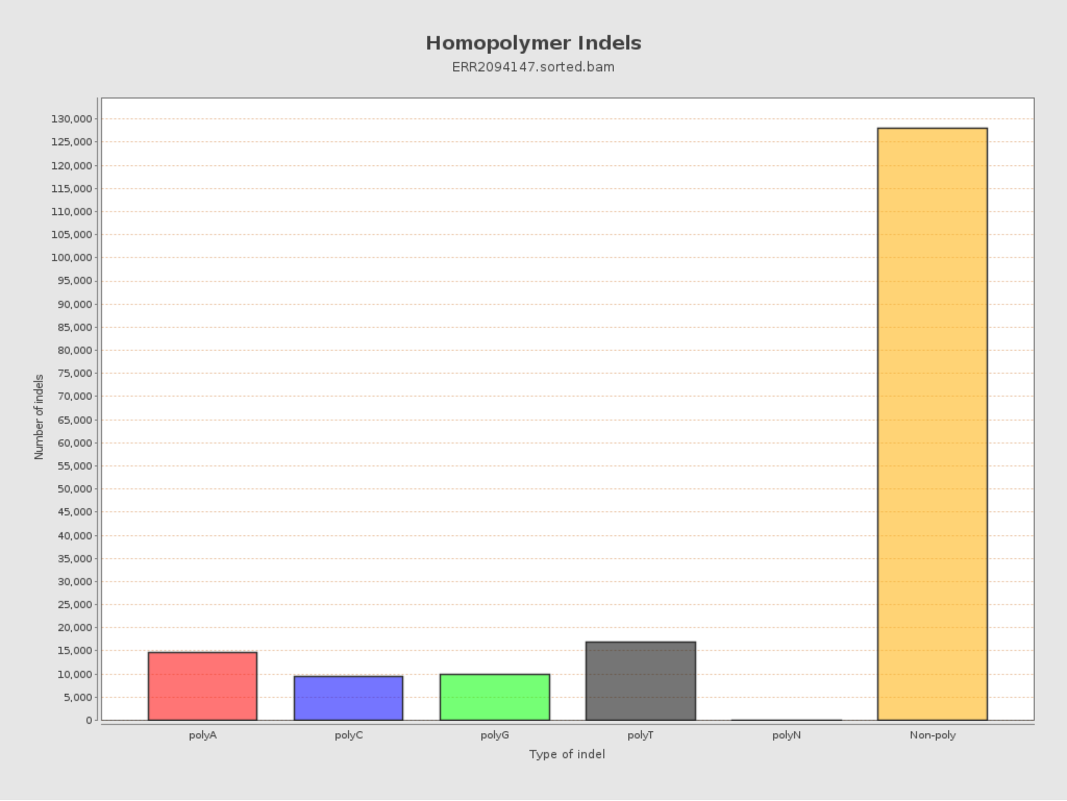
9. Results : Mapped Reads GC-content Distribution



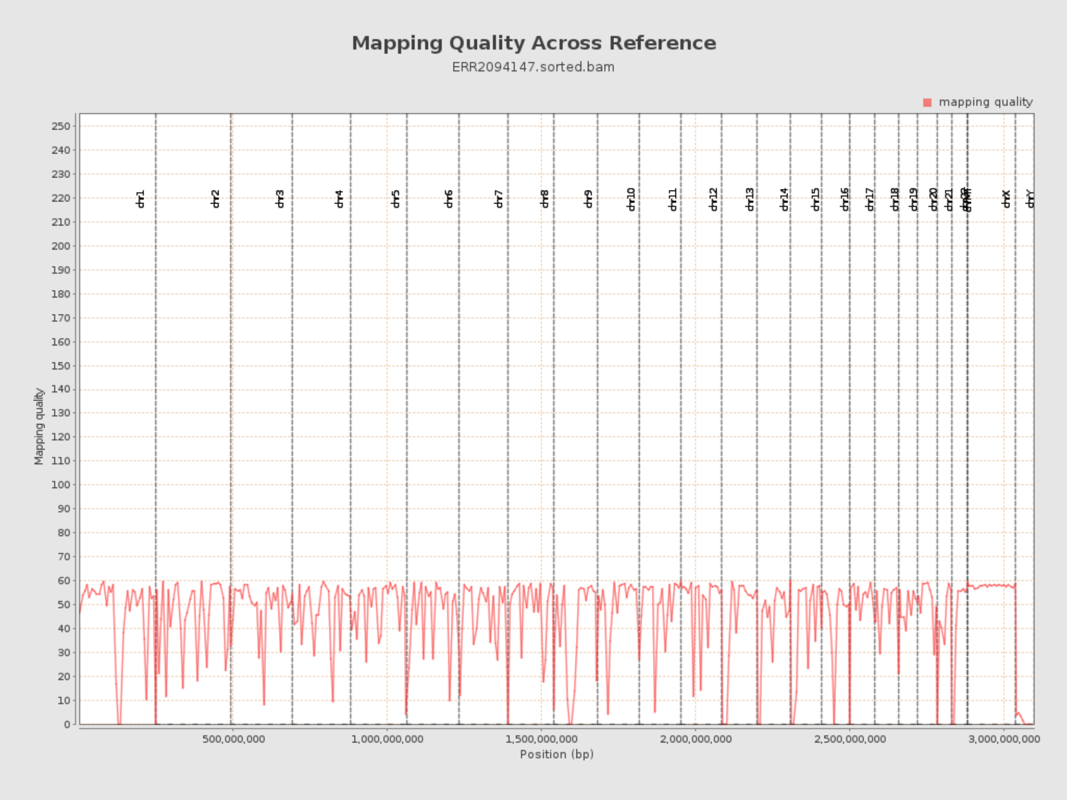
10. Results : Mapped Reads Clipping Profile



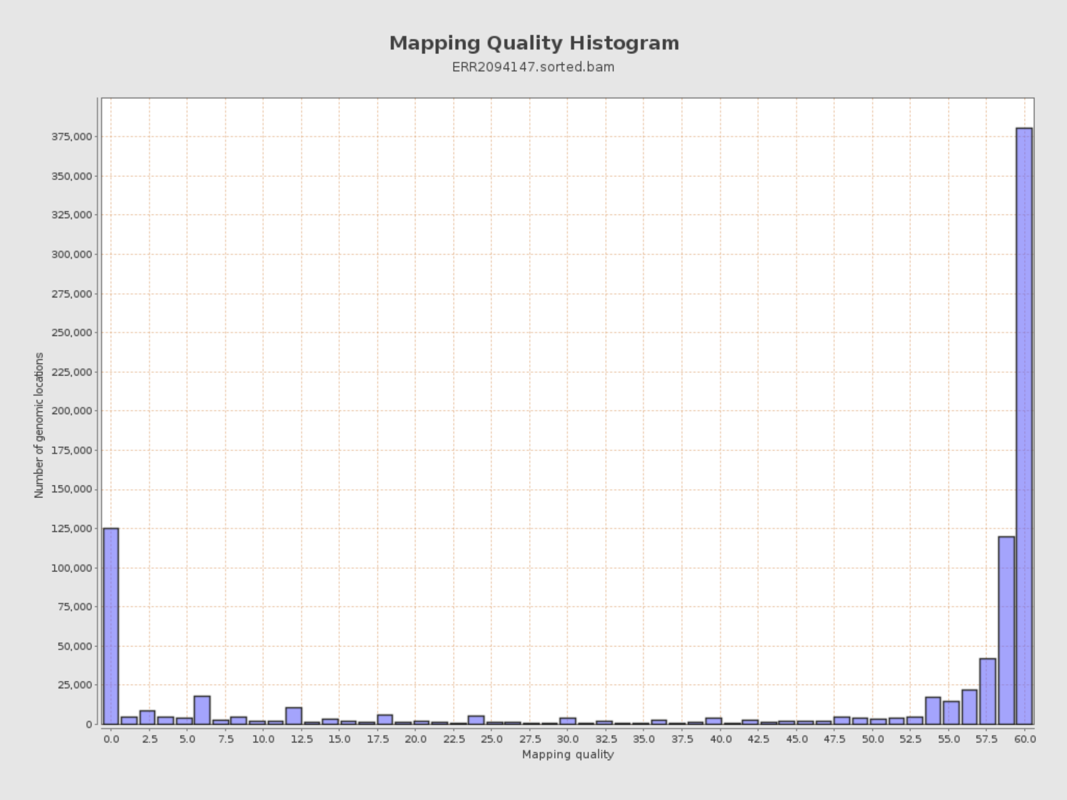
11. Results : Homopolymer Indels



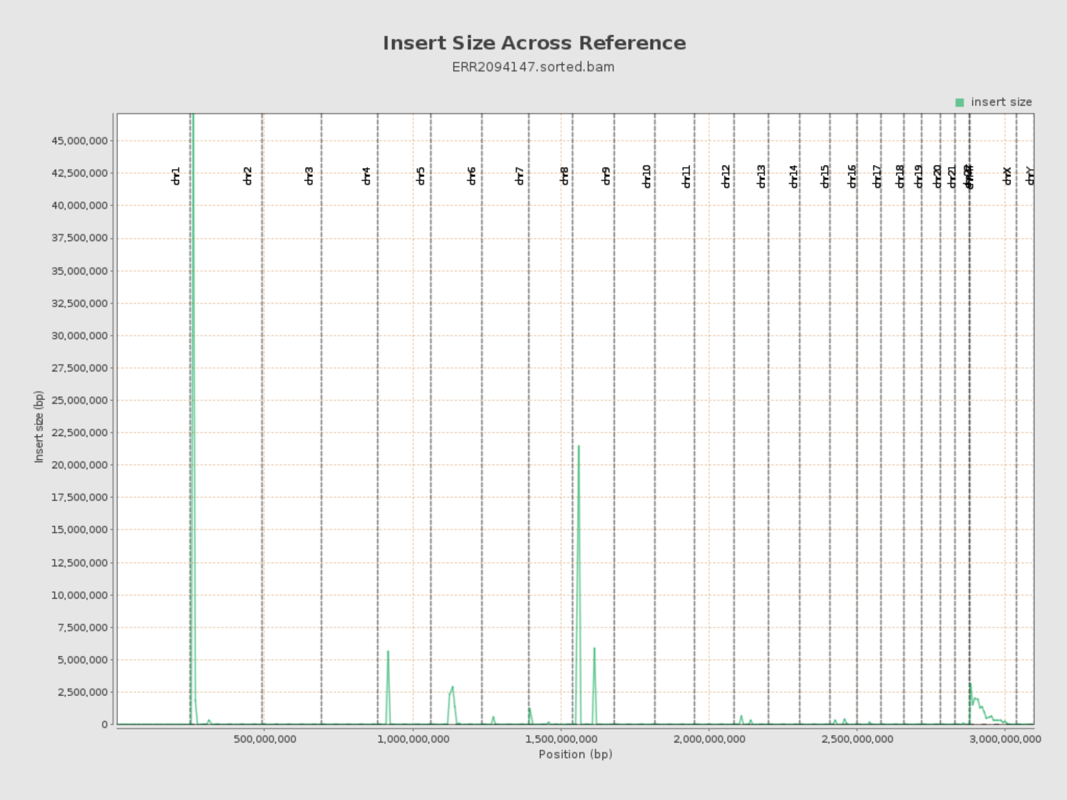
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram