Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 07:44:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094162.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_ERR2094162 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094162_1.fastq.gz ERR2094162_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 07:44:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	292,302
Mapped reads	267,369 / 91.47%
Unmapped reads	24,933 / 8.53%
Mapped paired reads	267,369 / 91.47%
Mapped reads, first in pair	134,556 / 46.03%
Mapped reads, second in pair	132,813 / 45.44%
Mapped reads, both in pair	264,450 / 90.47%
Mapped reads, singletons	2,919 / 1%
Secondary alignments	0
Supplementary alignments	10,627 / 3.64%
Read min/max/mean length	30 / 151 / 133.82
Duplicated reads (estimated)	265,722 / 90.91%
Duplication rate	51.42%
Clipped reads	145,876 / 49.91%

2.2. ACGT Content

Number/percentage of A's	9,196,296 / 28.8%
Number/percentage of C's	6,899,613 / 21.61%
Number/percentage of T's	8,869,585 / 27.78%
Number/percentage of G's	6,962,886 / 21.81%
Number/percentage of N's	303 / 0%

GC Percentage	43.42%

2.3. Coverage

Mean	0.0105
Standard Deviation	10.4257

2.4. Mapping Quality

Mean Mapping Quality	33.01

2.5. Insert size

Mean	151,058.14
Standard Deviation	3,978,350.9
P25/Median/P75	117 / 154 / 168

2.6. Mismatches and indels

General error rate	3.1%
Mismatches	951,494
Insertions	14,928
Mapped reads with at least one insertion	5.44%
Deletions	75,897
Mapped reads with at least one deletion	27.32%
Homopolymer indels	27.3%

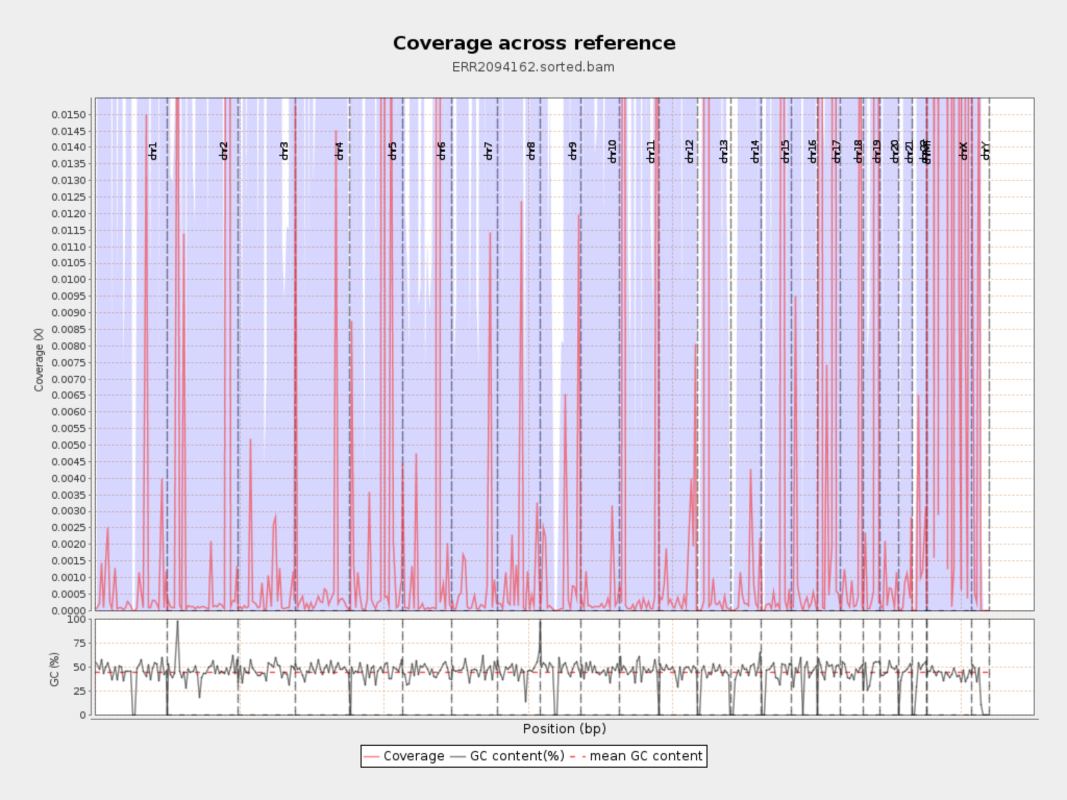
2.7. Chromosome stats

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

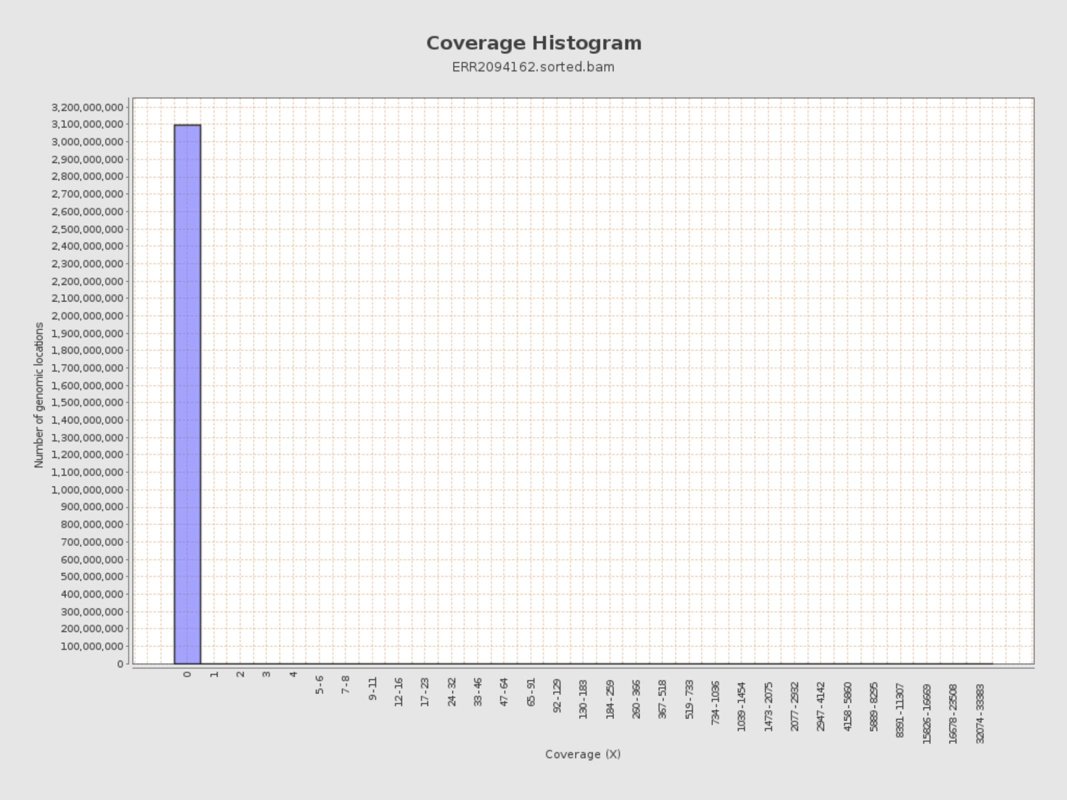
		bases	coverage	deviation
chr1	249250621	242749	0.001	0.5829
chr2	243199373	991247	0.0041	2.2529
chr3	198022430	136653	0.0007	0.175
chr4	191154276	252578	0.0013	0.6246
chr5	180915260	1694329	0.0094	8.6422
chr6	171115067	2073311	0.0121	13.0381
chr7	159138663	147652	0.0009	0.2491
chr8	146364022	189624	0.0013	0.7105
chr9	141213431	202436	0.0014	0.6419
chr10	135534747	55785	0.0004	0.1129
chr11	135006516	652036	0.0048	2.9611
chr12	133851895	163736	0.0012	0.4052
chr13	115169878	5037188	0.0437	36.9392
chr14	107349540	76878	0.0007	0.1725
chr15	102531392	384902	0.0038	2.7973
chr16	90354753	95243	0.0011	0.5527
chr17	81195210	2700379	0.0333	13.1378
chr18	78077248	257918	0.0033	1.9998
chr19	59128983	1354749	0.0229	11.0721
chr20	63025520	40801	0.0006	0.1255
chr21	48129895	33398	0.0007	0.1473
chr22	51304566	92082	0.0018	0.2721
chrMT	16571	2551	0.1539	0.7929
chrX	155270560	15350949	0.0989	26.7826

chrY	59373566	204571	0.0034	1.798

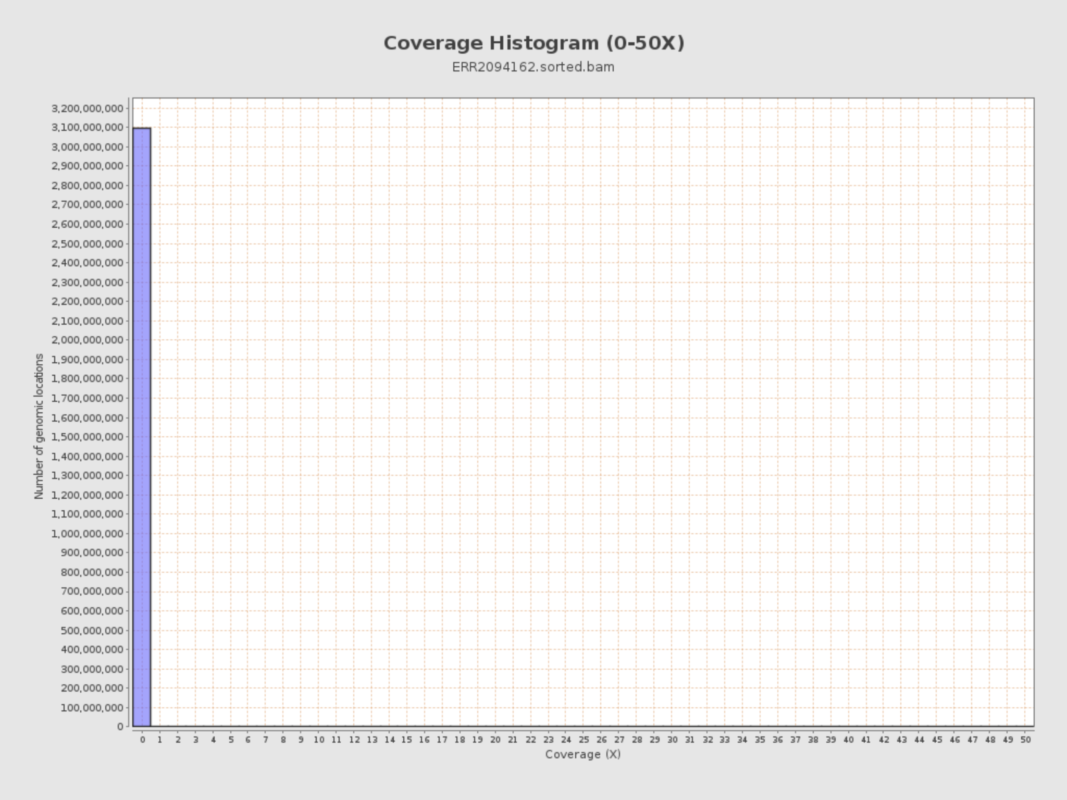
3. Results : Coverage across reference



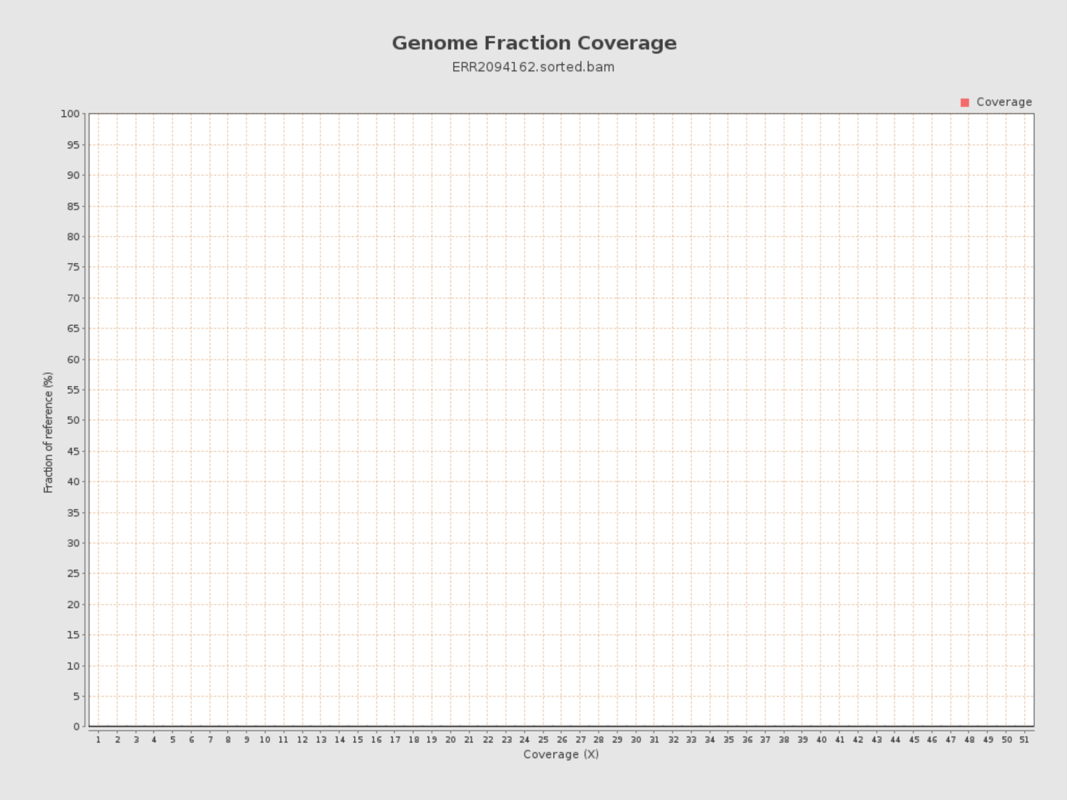
4. Results : Coverage Histogram



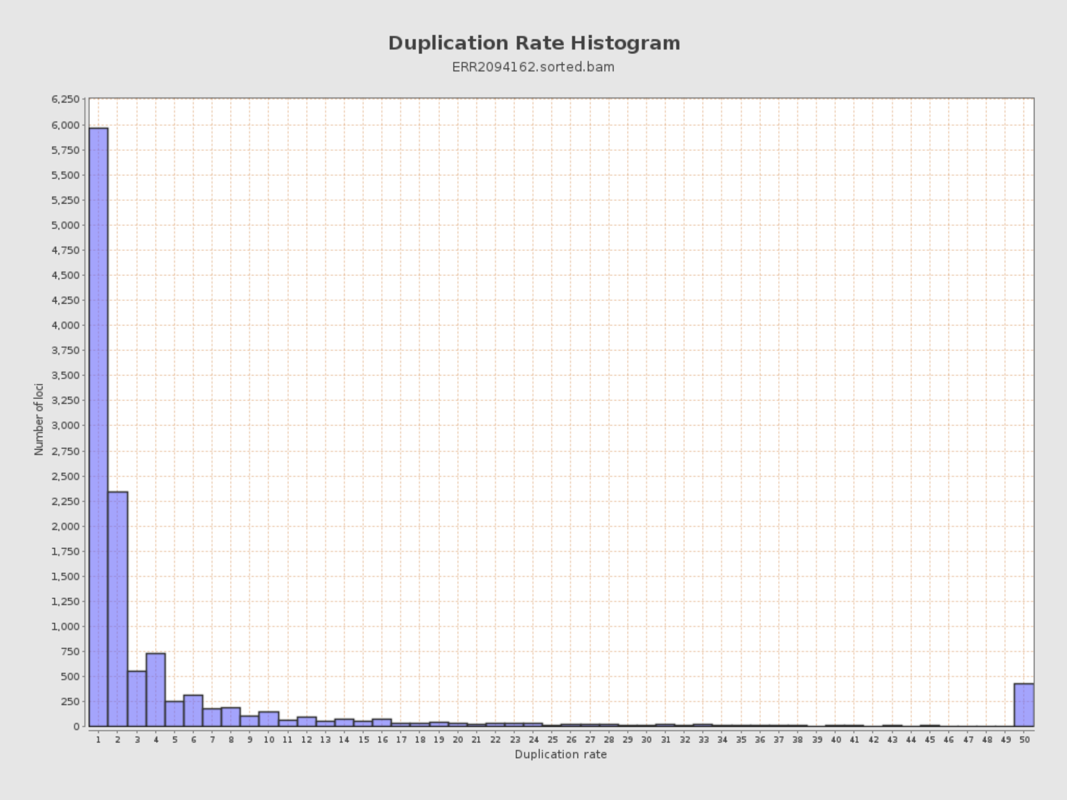
5. Results : Coverage Histogram (0-50X)



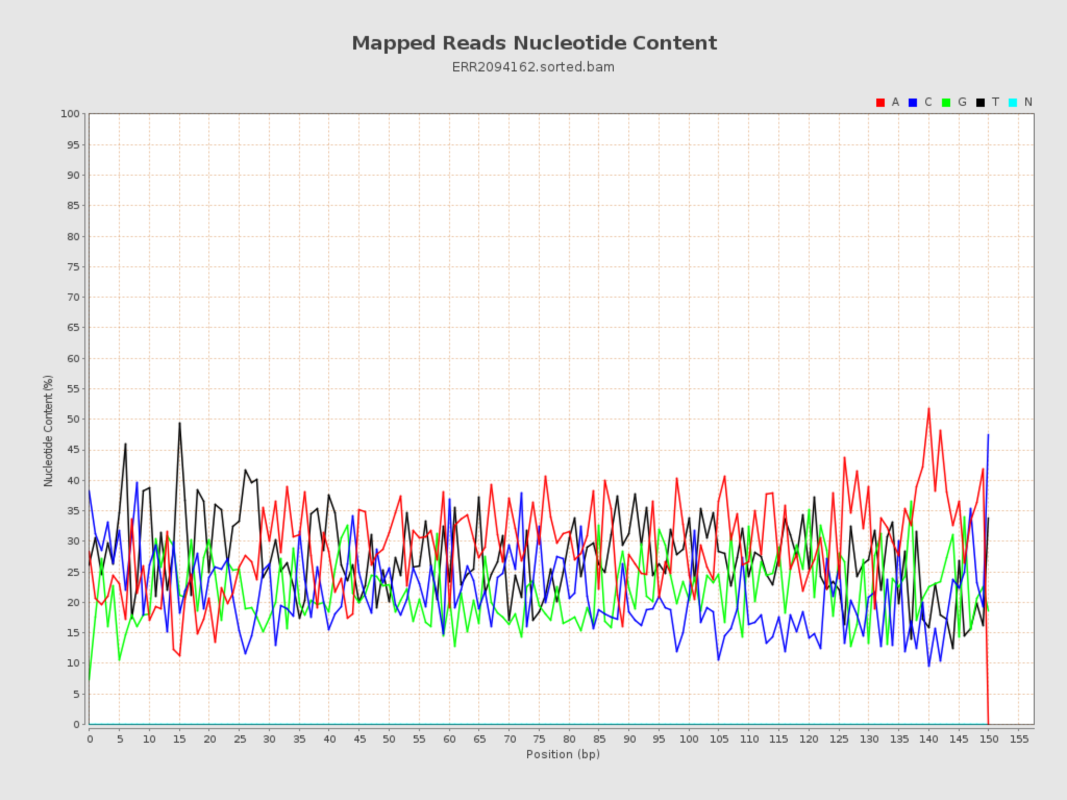
6. Results : Genome Fraction Coverage



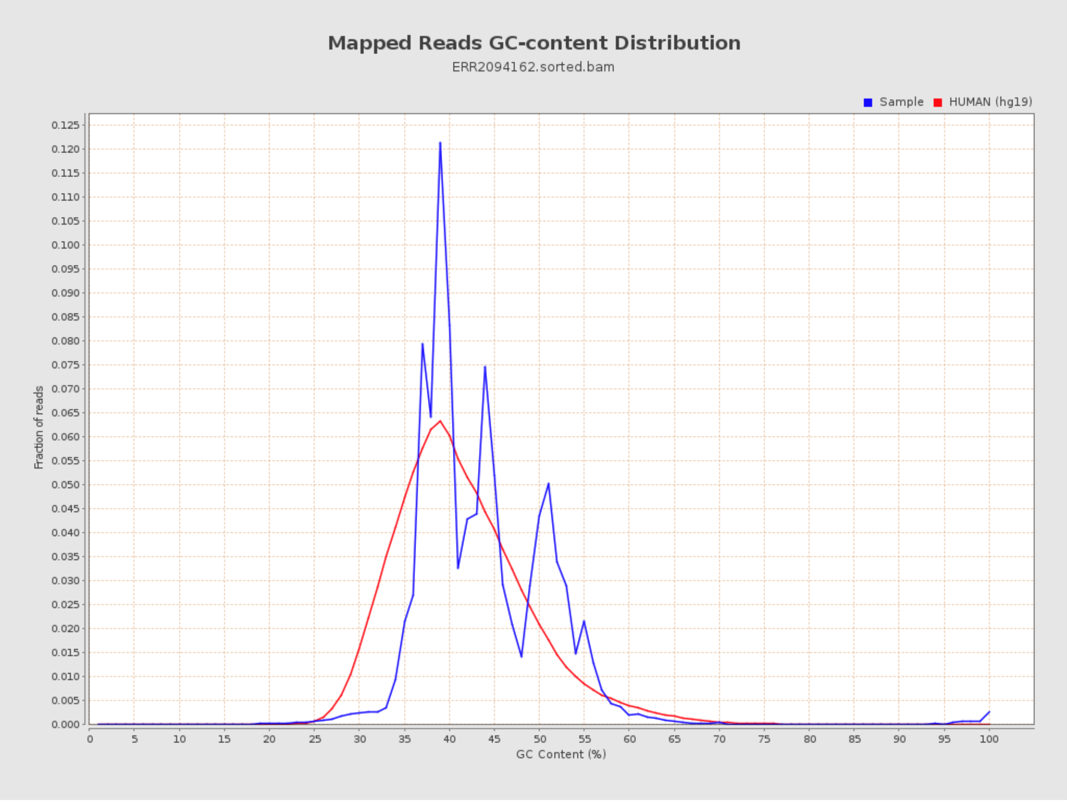
7. Results : Duplication Rate Histogram



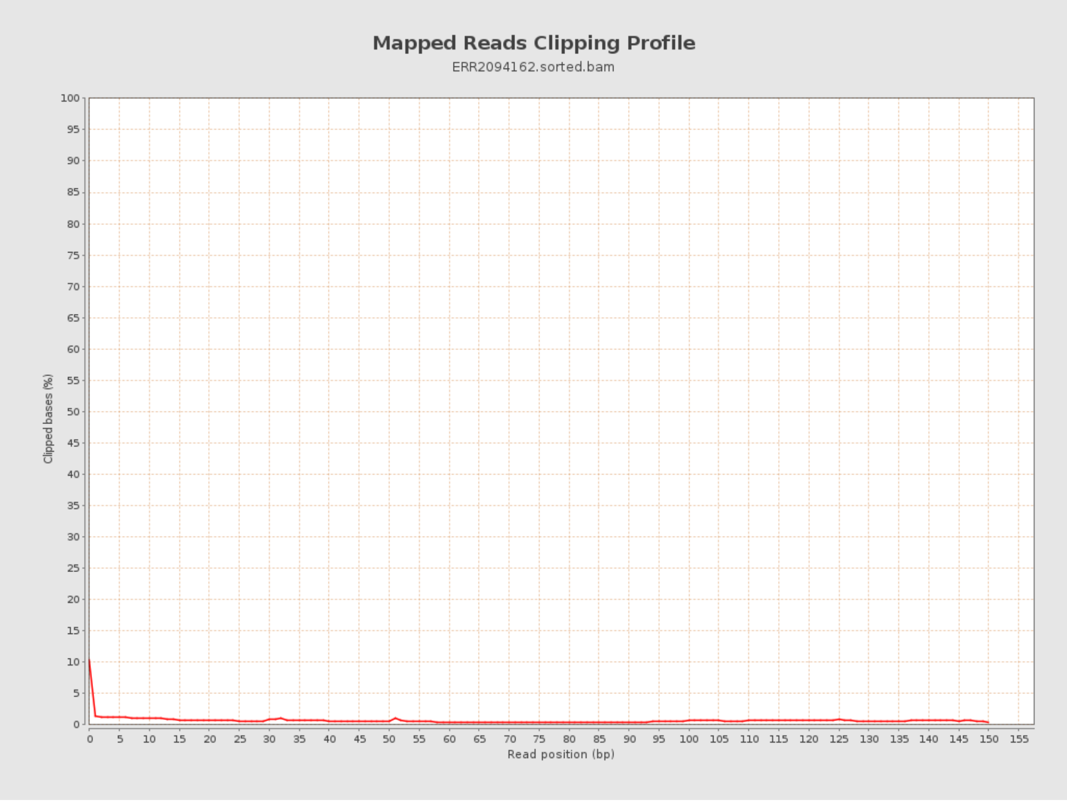
8. Results : Mapped Reads Nucleotide Content



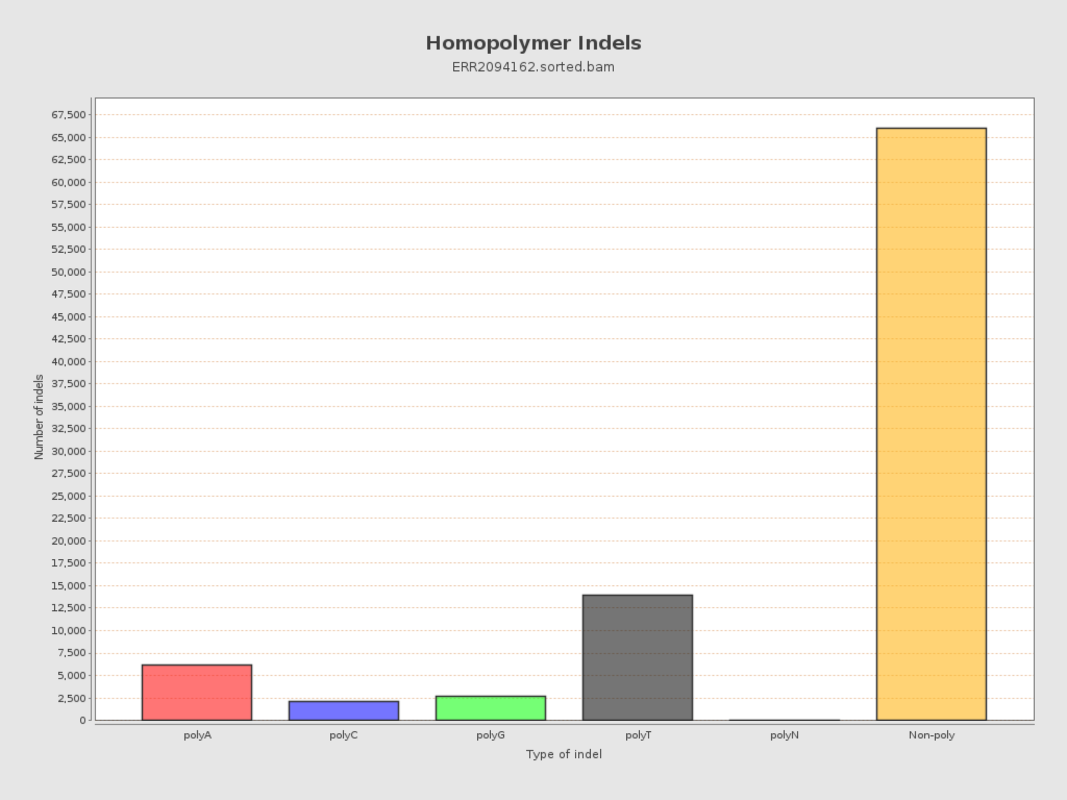
9. Results : Mapped Reads GC-content Distribution



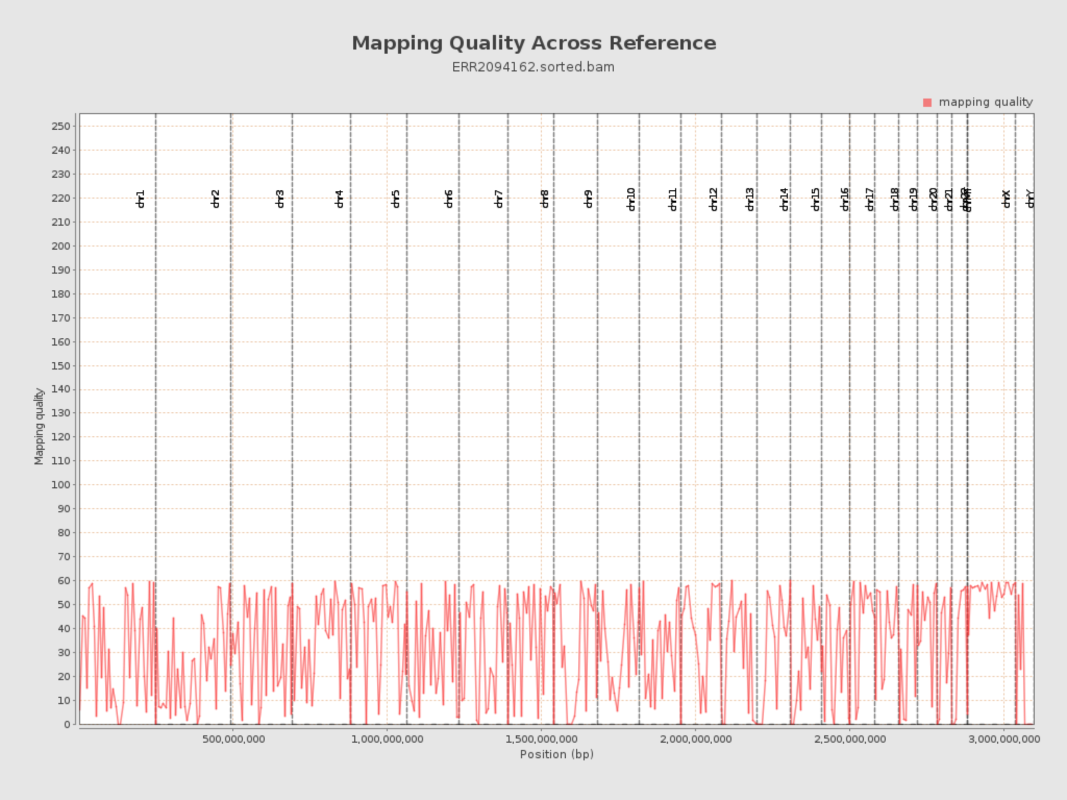
10. Results : Mapped Reads Clipping Profile



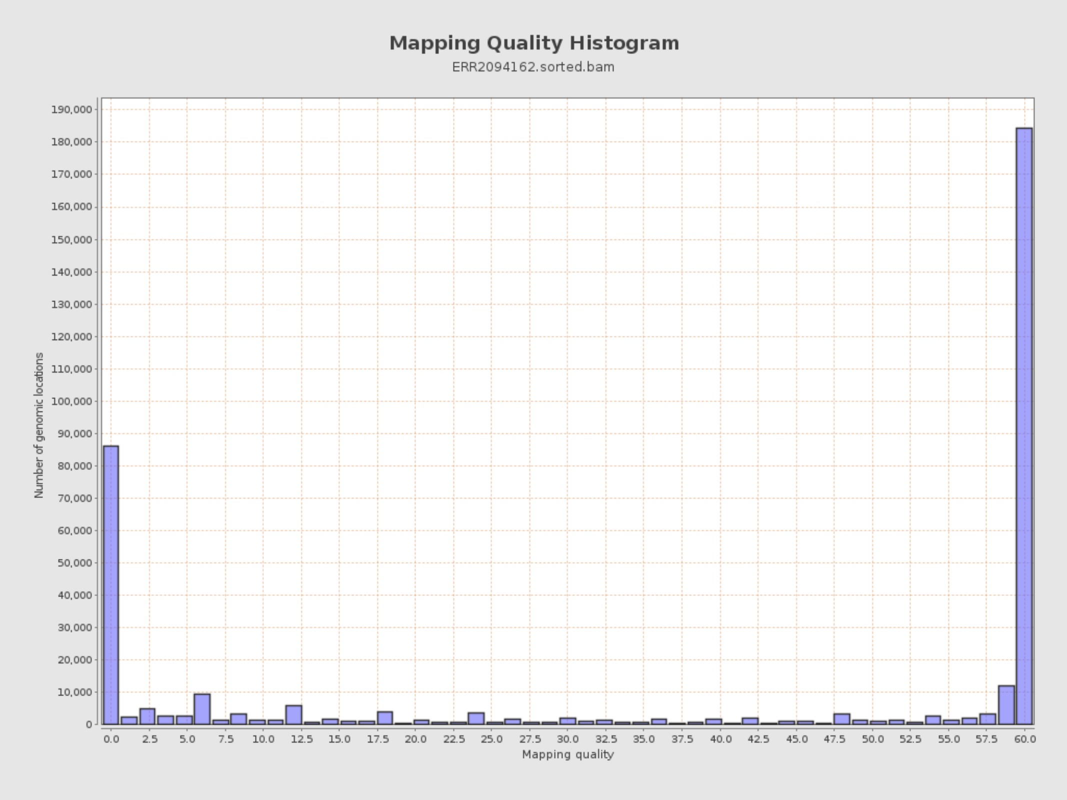
11. Results : Homopolymer Indels



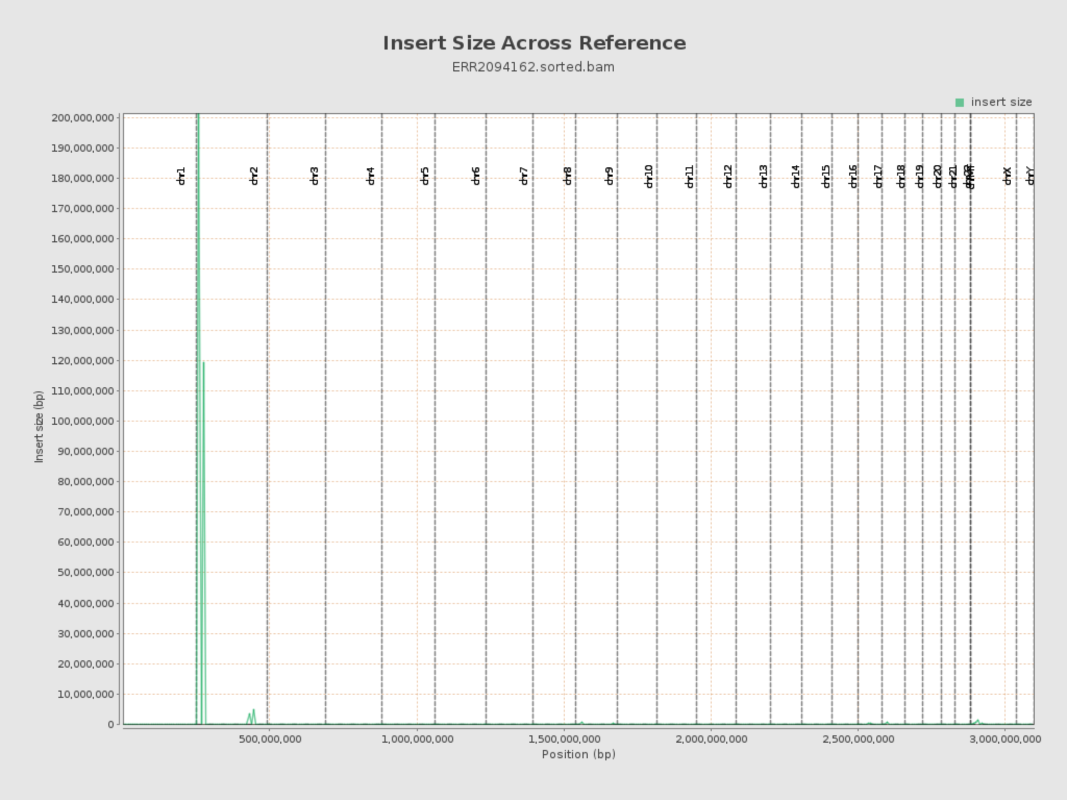
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram