Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:15:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094126.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_ERR2094126 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094126_1.fastq.gz ERR2094126_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:15:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	474,174
Mapped reads	444,762 / 93.8%
Unmapped reads	29,412 / 6.2%
Mapped paired reads	444,762 / 93.8%
Mapped reads, first in pair	223,055 / 47.04%
Mapped reads, second in pair	221,707 / 46.76%
Mapped reads, both in pair	442,782 / 93.38%
Mapped reads, singletons	1,980 / 0.42%
Secondary alignments	0
Supplementary alignments	832 / 0.18%
Read min/max/mean length	30 / 151 / 144.83
Duplicated reads (estimated)	442,229 / 93.26%
Duplication rate	50.73%
Clipped reads	71,357 / 15.05%

2.2. ACGT Content

Number/percentage of A's	18,049,084 / 27.53%
Number/percentage of C's	14,009,297 / 21.37%
Number/percentage of T's	18,833,254 / 28.73%
Number/percentage of G's	14,663,393 / 22.37%
Number/percentage of N's	734 / 0%

GC Percentage	43.74%

2.3. Coverage

Mean	0.0212
Standard Deviation	36.8209

2.4. Mapping Quality

Mean Mapping Quality	20.05

2.5. Insert size

Mean	4,467.92
Standard Deviation	572,725.82
P25/Median/P75	217 / 233 / 266

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	1,043,993
Insertions	18,591
Mapped reads with at least one insertion	4.14%
Deletions	44,885
Mapped reads with at least one deletion	9.89%
Homopolymer indels	64.9%

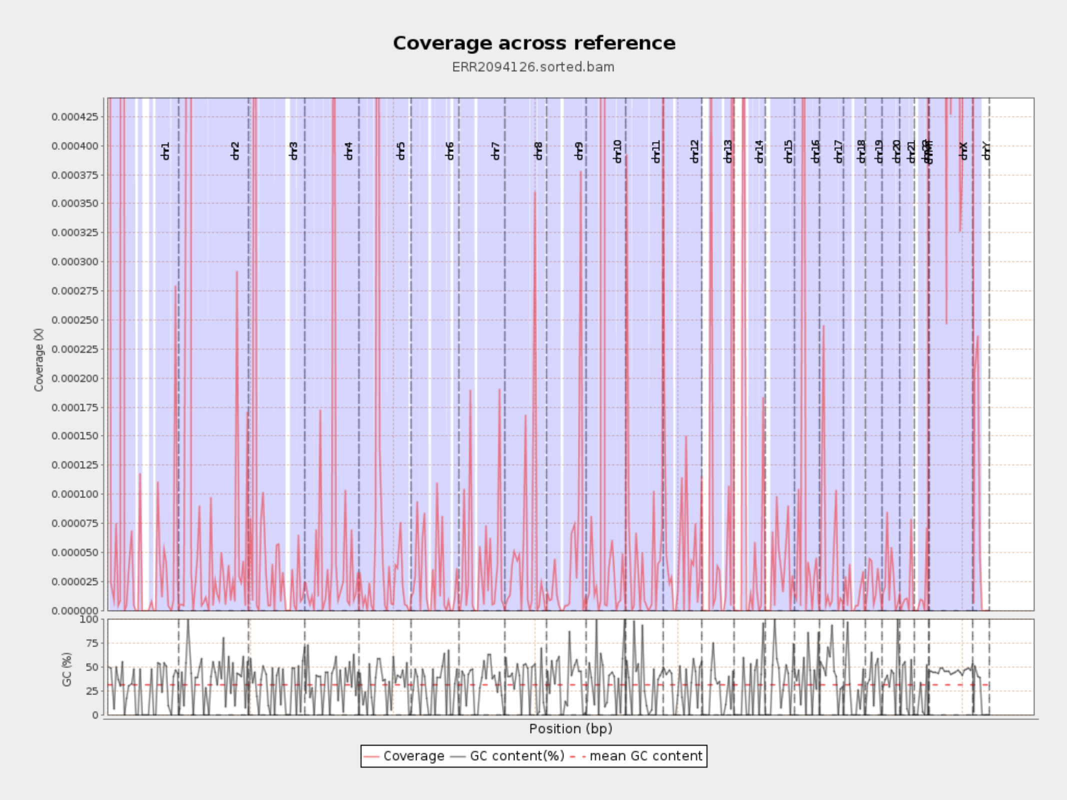
2.7. Chromosome stats

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

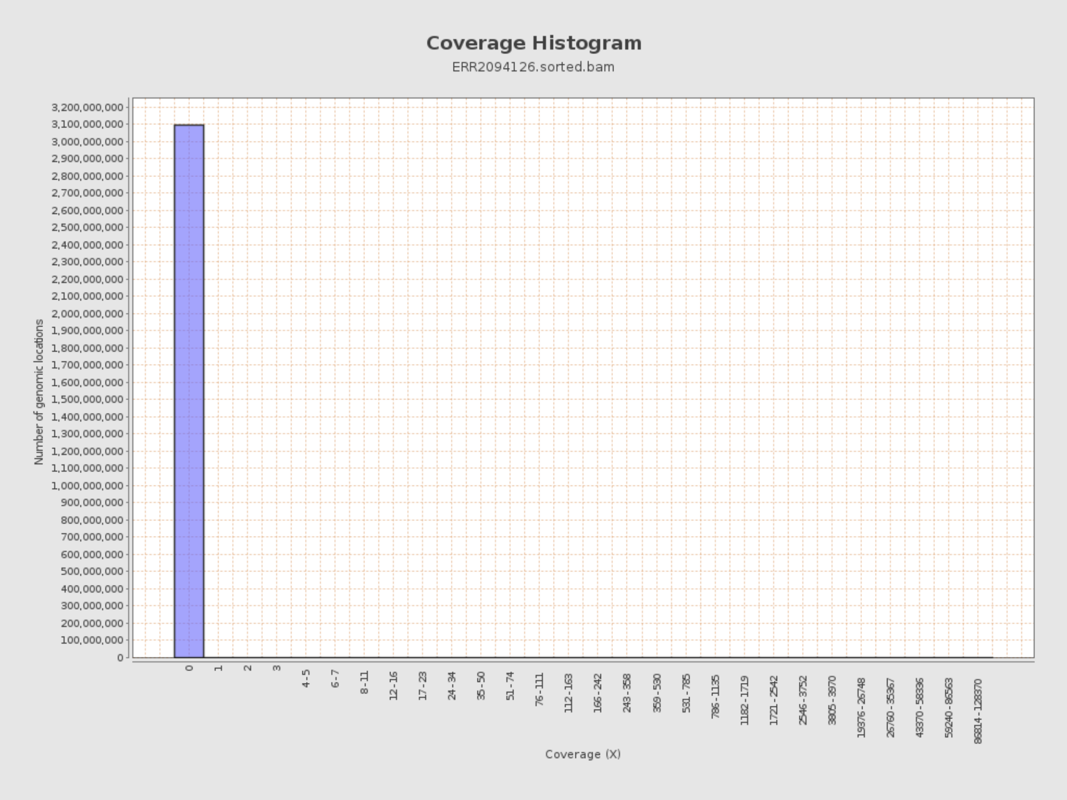
		bases	**coverage**	**deviation**
chr1	249250621	57736	0.0002	0.1549
chr2	243199373	191023	0.0008	0.7318
chr3	198022430	12480	0.0001	0.0443
chr4	191154276	11334	0.0001	0.0163
chr5	180915260	11460	0.0001	0.0177
chr6	171115067	4662	0	0.008
chr7	159138663	6485	0	0.0114
chr8	146364022	6637	0	0.0202
chr9	141213431	5825	0	0.0147
chr10	135534747	1244913	0.0092	3.9926
chr11	135006516	7300	0.0001	0.0228
chr12	133851895	6650	0	0.0142
chr13	115169878	15137	0.0001	0.0938
chr14	107349540	7035	0.0001	0.0581
chr15	102531392	3580	0	0.009
chr16	90354753	7635	0.0001	0.0649
chr17	81195210	3699	0	0.0111
chr18	78077248	1030	0	0.0052
chr19	59128983	1292	0	0.0072
chr20	63025520	1716	0	0.0078
chr21	48129895	804	0	0.0068
chr22	51304566	698	0	0.0074
chrMT	16571	63880690	3,854.9689	15,437.0195
chrX	155270560	114456	0.0007	0.0692

chrY	59373566	3790	0.0001	0.0231

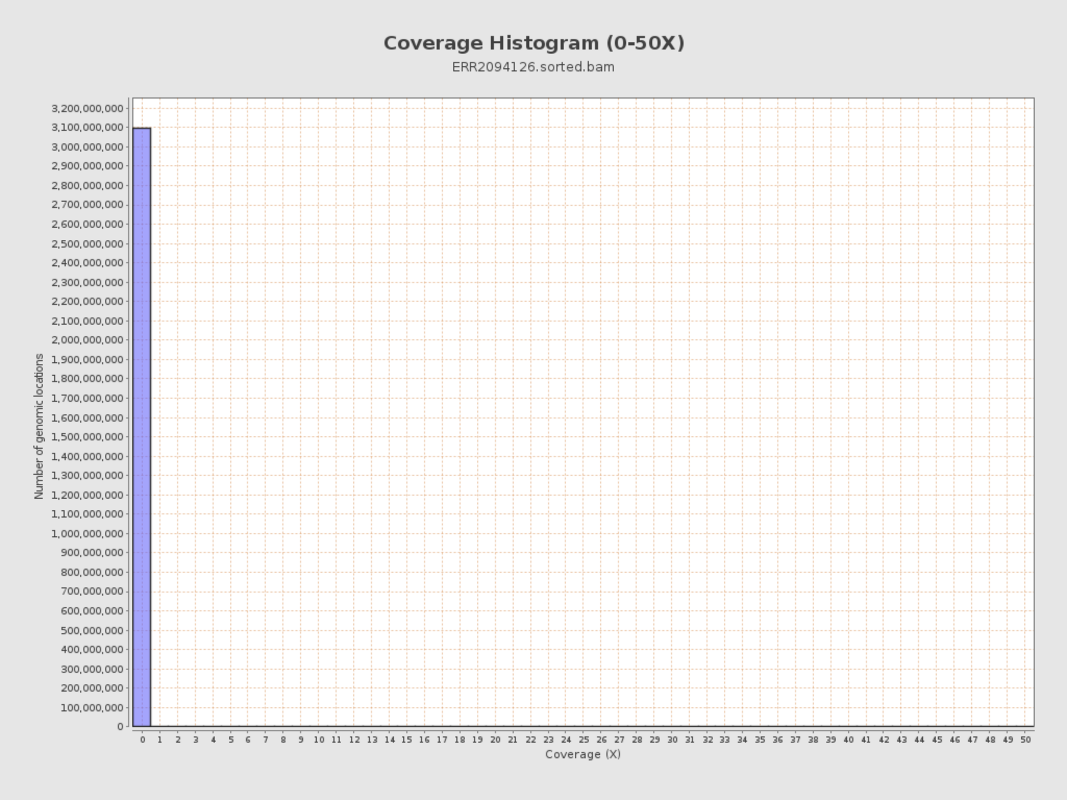
3. Results : Coverage across reference



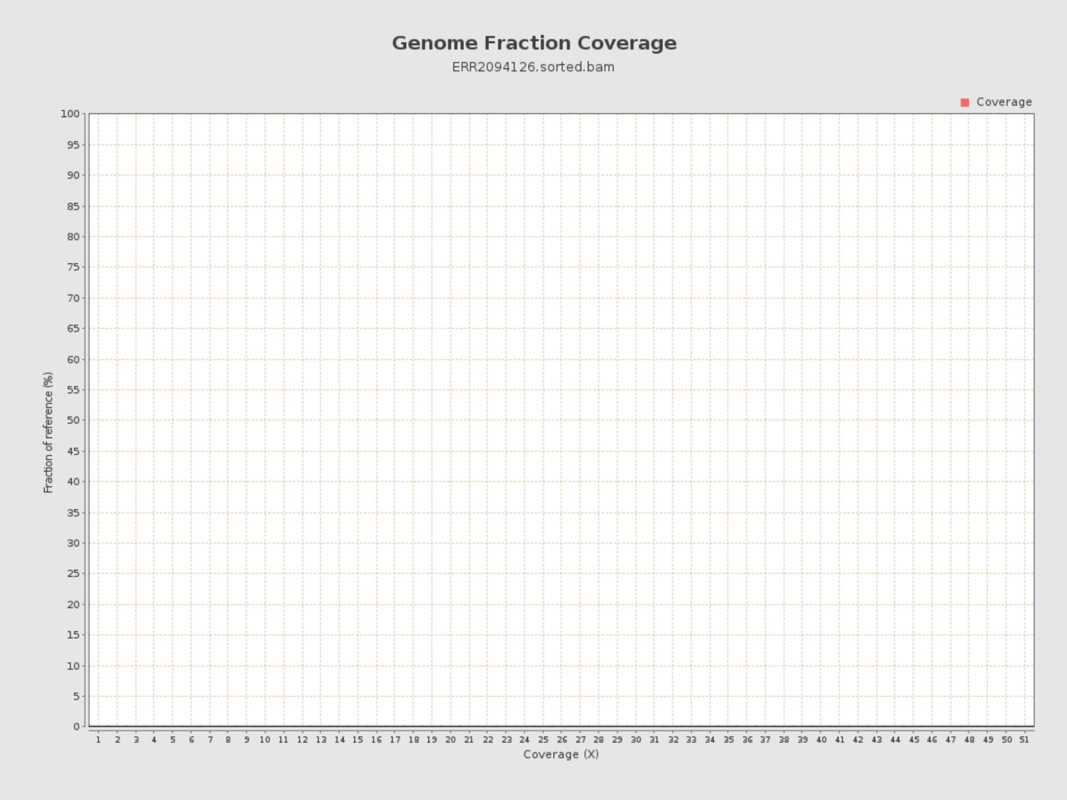
4. Results : Coverage Histogram



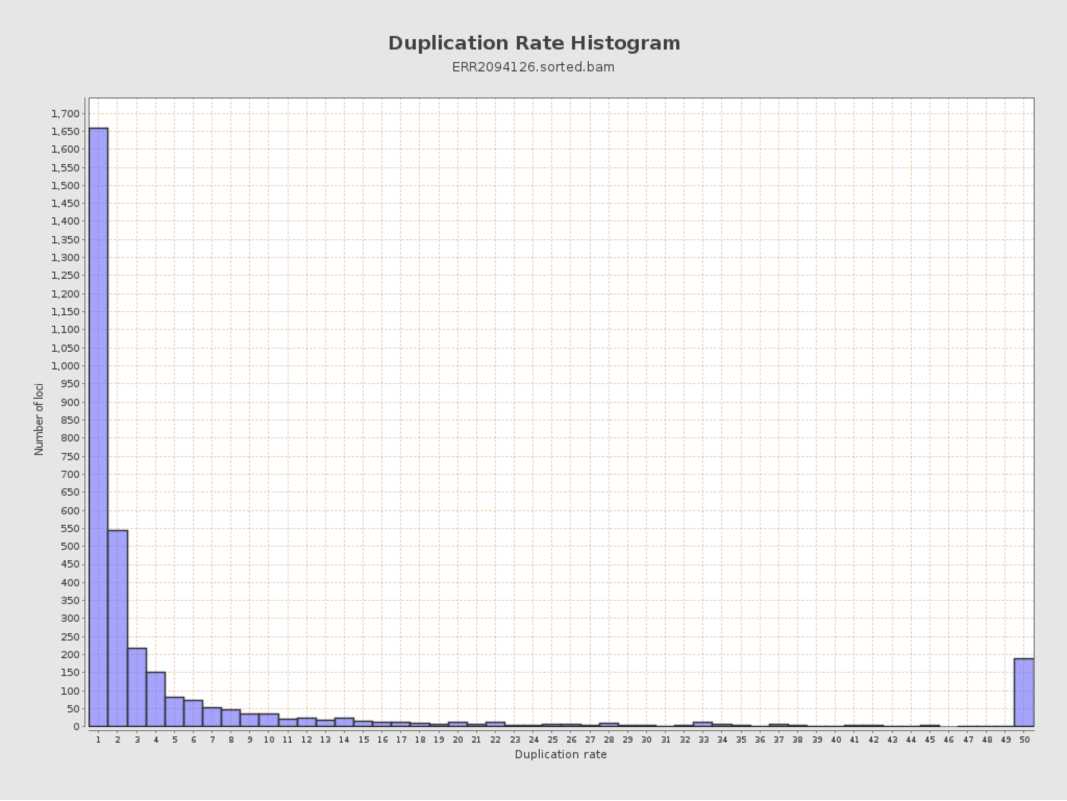
5. Results : Coverage Histogram (0-50X)



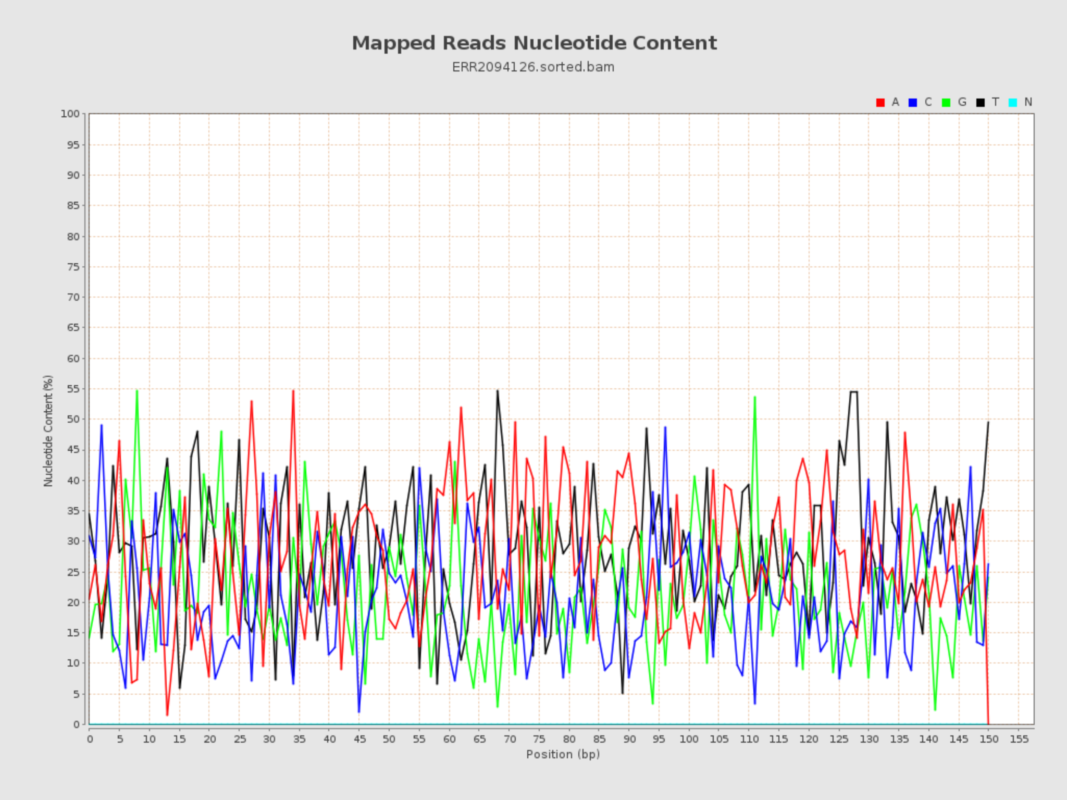
6. Results : Genome Fraction Coverage



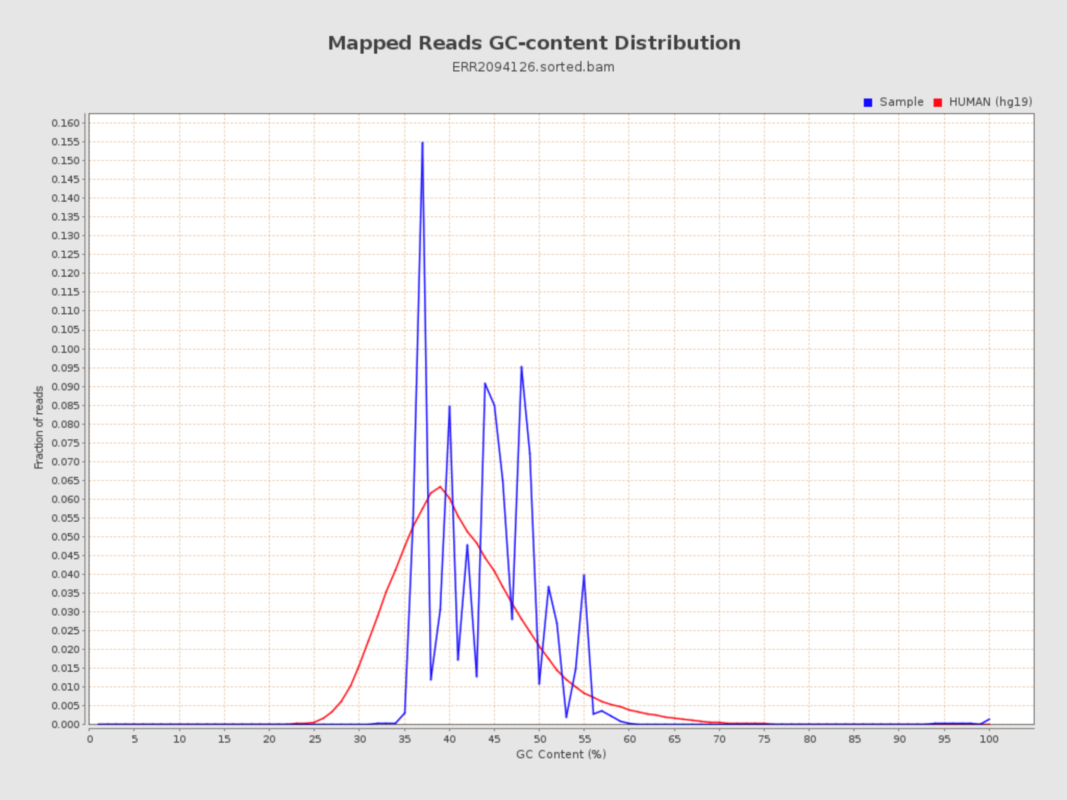
7. Results : Duplication Rate Histogram



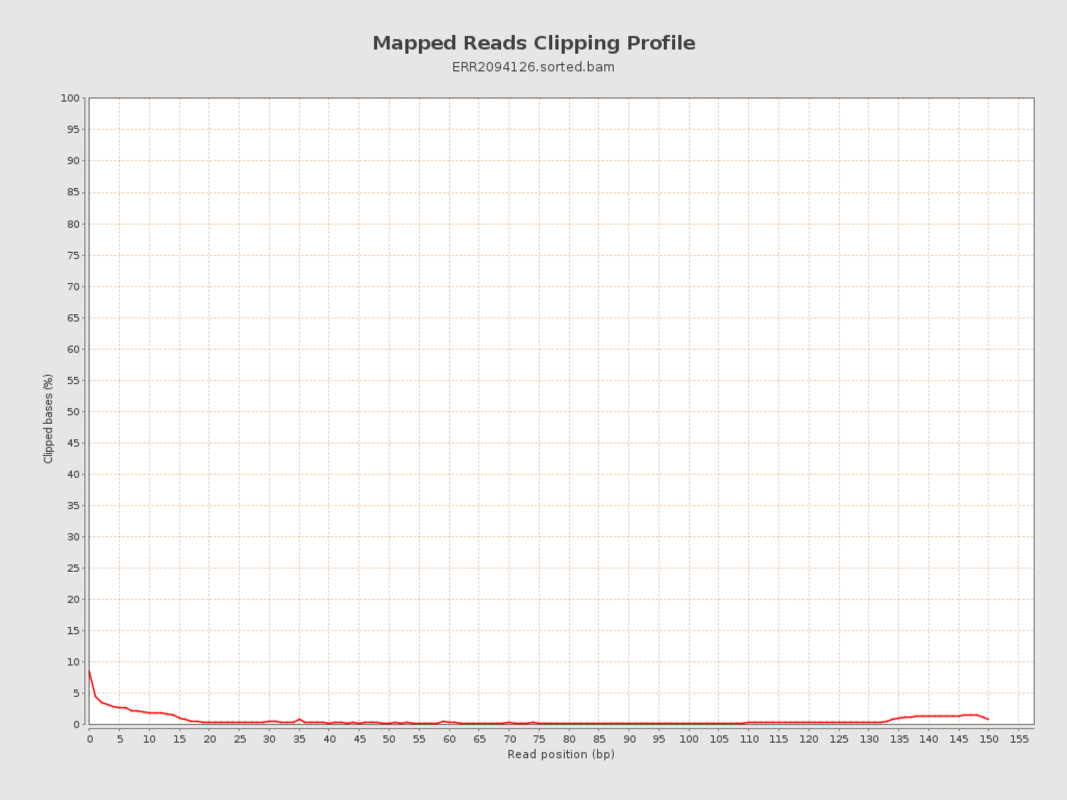
8. Results : Mapped Reads Nucleotide Content



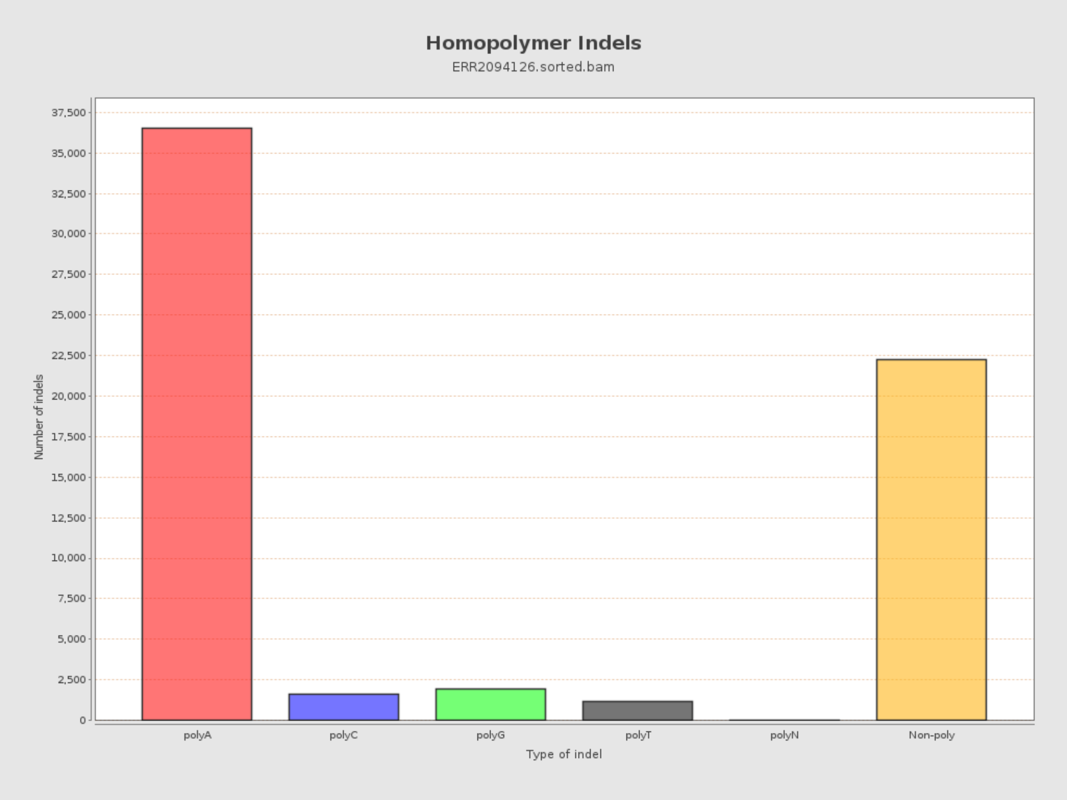
9. Results : Mapped Reads GC-content Distribution



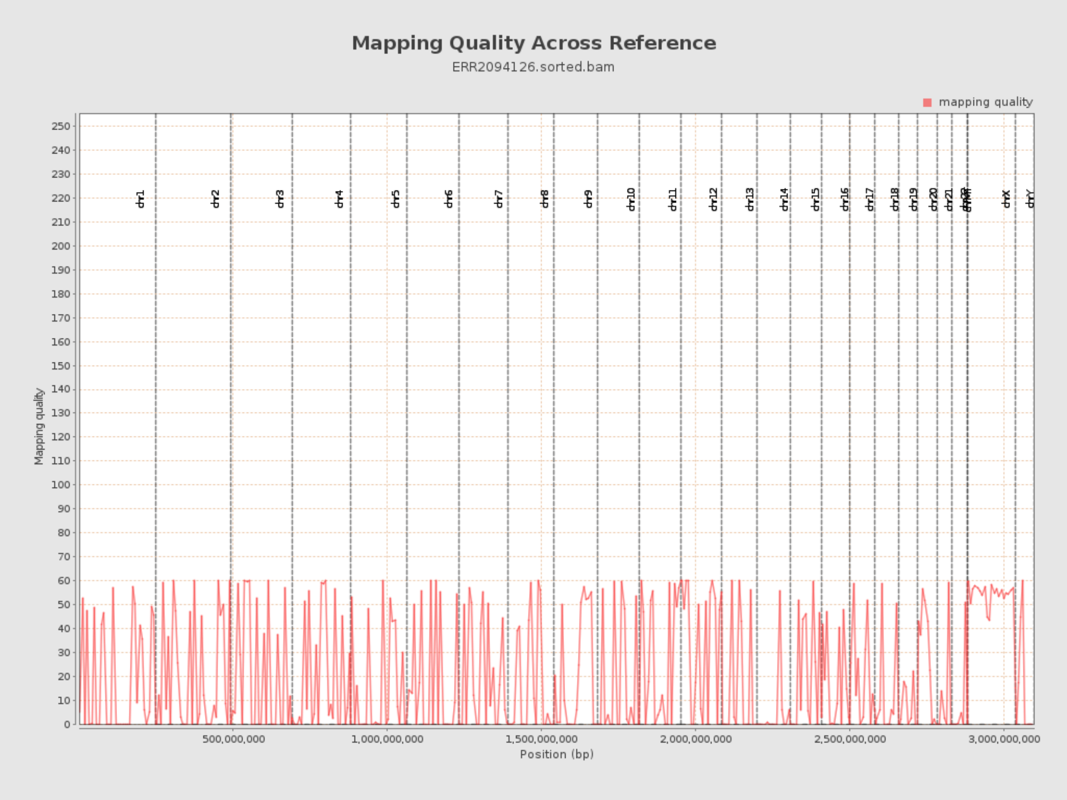
10. Results : Mapped Reads Clipping Profile



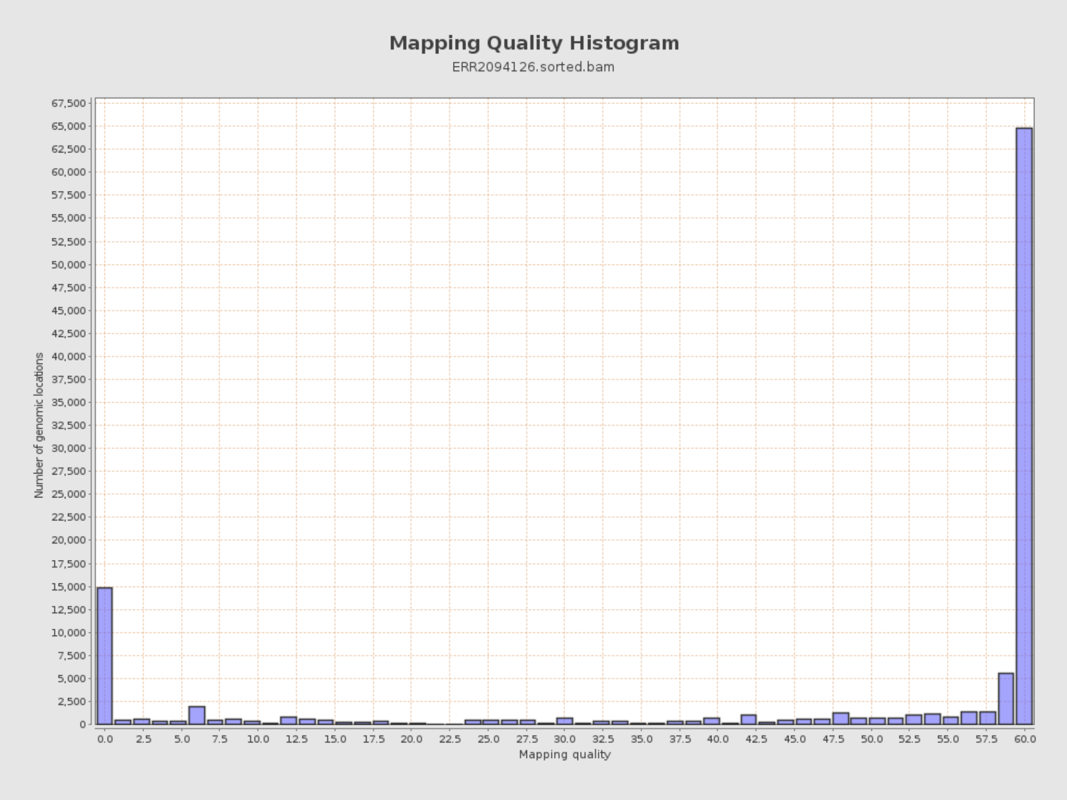
11. Results : Homopolymer Indels



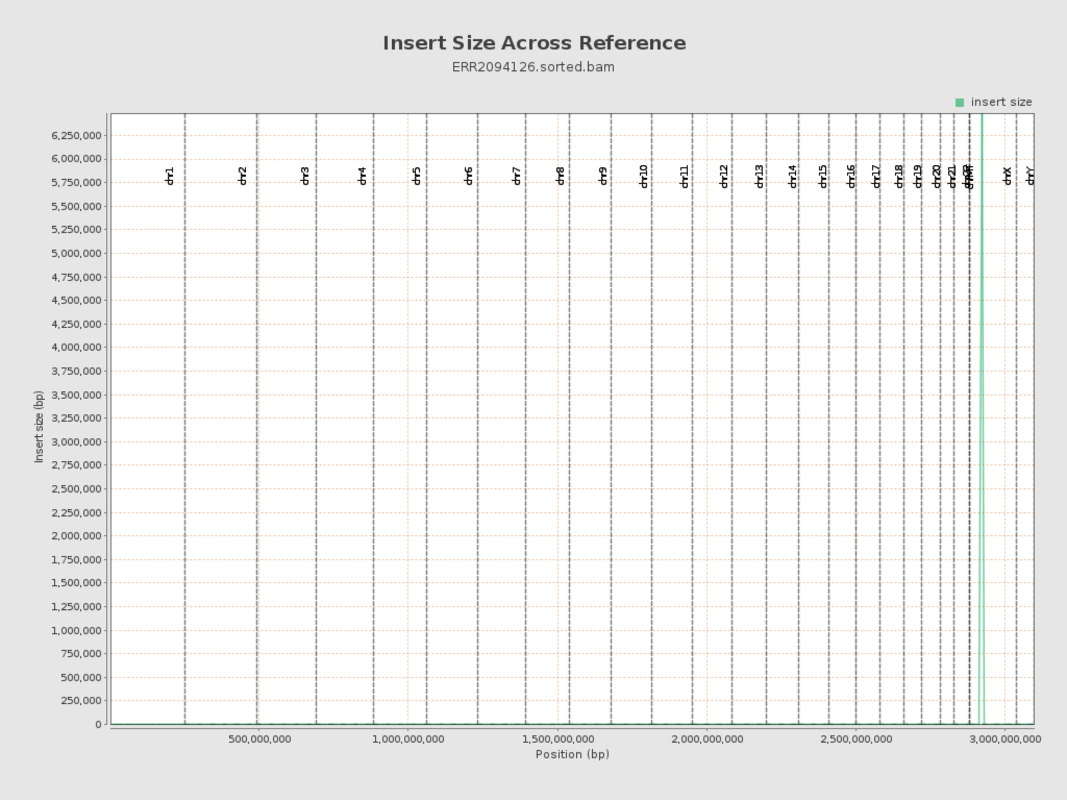
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram