Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:14:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094125.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_ERR2094125 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094125_1.fastq.gz ERR2094125_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:14:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094125.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,726
Mapped reads	1,112 / 5.64%
Unmapped reads	18,614 / 94.36%
Mapped paired reads	1,112 / 5.64%
Mapped reads, first in pair	491 / 2.49%
Mapped reads, second in pair	621 / 3.15%
Mapped reads, both in pair	888 / 4.5%
Mapped reads, singletons	224 / 1.14%
Secondary alignments	0
Supplementary alignments	53 / 0.27%
Read min/max/mean length	30 / 151 / 56.44
Duplicated reads (estimated)	503 / 2.55%
Duplication rate	25.98%
Clipped reads	730 / 3.7%

2.2. ACGT Content

Number/percentage of A's	27,121 / 25.12%
Number/percentage of C's	19,213 / 17.79%
Number/percentage of T's	23,725 / 21.97%
Number/percentage of G's	37,914 / 35.11%
Number/percentage of N's	0 / 0%

GC Percentage	52.91%

2.3. Coverage

Mean	0
Standard Deviation	0.0242

2.4. Mapping Quality

Mean Mapping Quality	15.4

2.5. Insert size

Mean	1,025,216.5
Standard Deviation	8,254,894.39
P25/Median/P75	72 / 131 / 166

2.6. Mismatches and indels

General error rate	3.96%
Mismatches	3,880
Insertions	93
Mapped reads with at least one insertion	6.56%
Deletions	273
Mapped reads with at least one deletion	23.56%
Homopolymer indels	36.61%

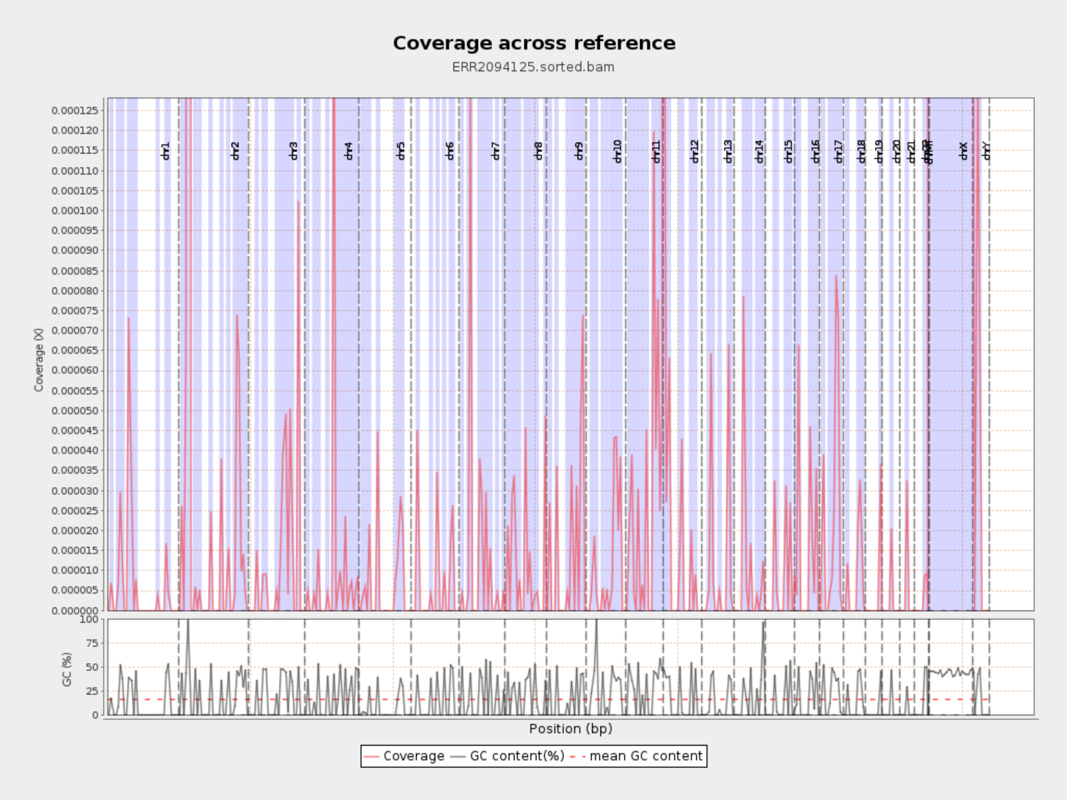
2.7. Chromosome stats

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

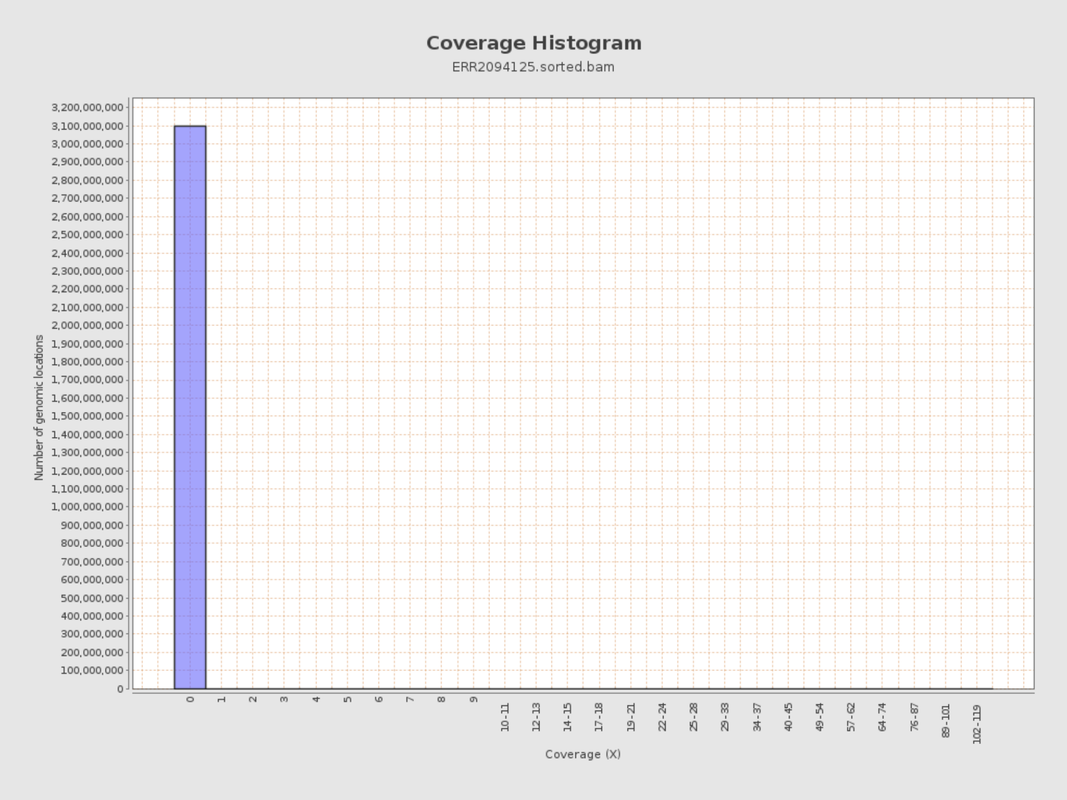
		bases	coverage	deviation
chr1	249250621	1467	0	0.0036
chr2	243199373	21620	0.0001	0.0762
chr3	198022430	2499	0	0.0061
chr4	191154276	2051	0	0.0046
chr5	180915260	1135	0	0.003
chr6	171115067	1063	0	0.0036
chr7	159138663	2054	0	0.006
chr8	146364022	1604	0	0.0041
chr9	141213431	2005	0	0.0053
chr10	135534747	1456	0	0.0041
chr11	135006516	4277	0	0.0102
chr12	133851895	2815	0	0.0095
chr13	115169878	1172	0	0.0047
chr14	107349540	939	0	0.0054
chr15	102531392	736	0	0.0035
chr16	90354753	1387	0	0.0056
chr17	81195210	1838	0	0.0085
chr18	78077248	554	0	0.0034
chr19	59128983	283	0	0.0029
chr20	63025520	158	0	0.0022
chr21	48129895	252	0	0.0029
chr22	51304566	140	0	0.0017
chrMT	16571	2249	0.1357	0.9058
chrX	155270560	54020	0.0003	0.0438

chrY	59373566	2186	0	0.0098

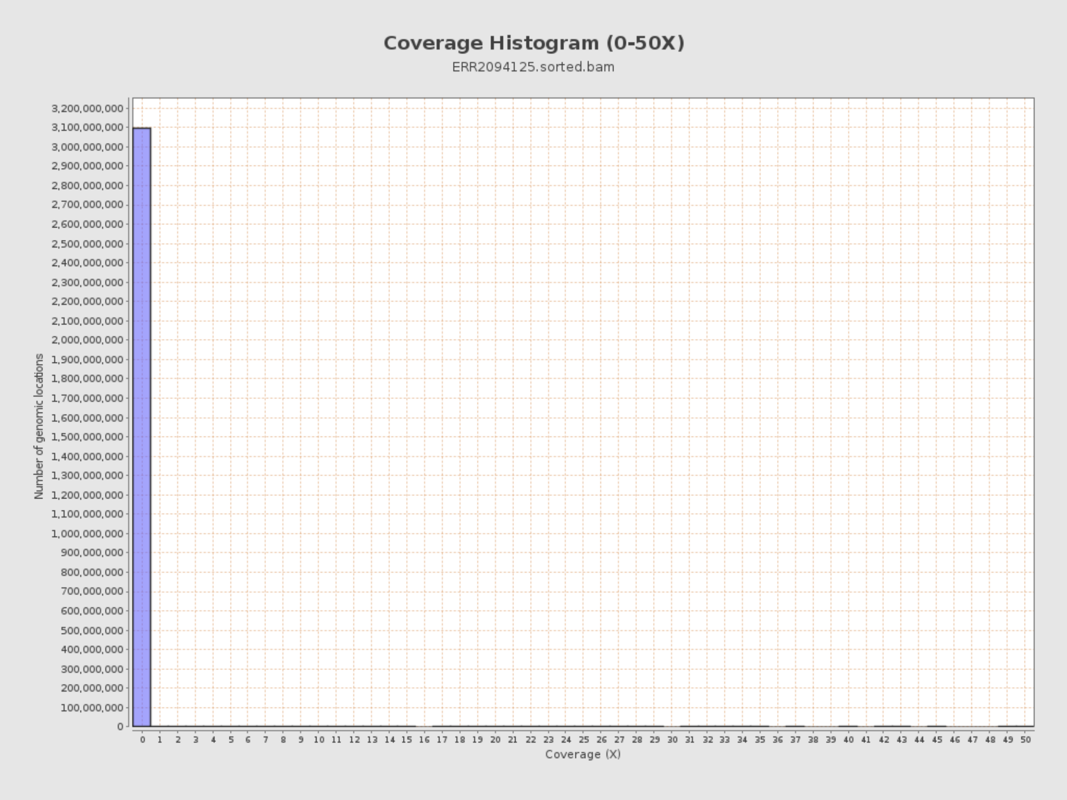
3. Results : Coverage across reference



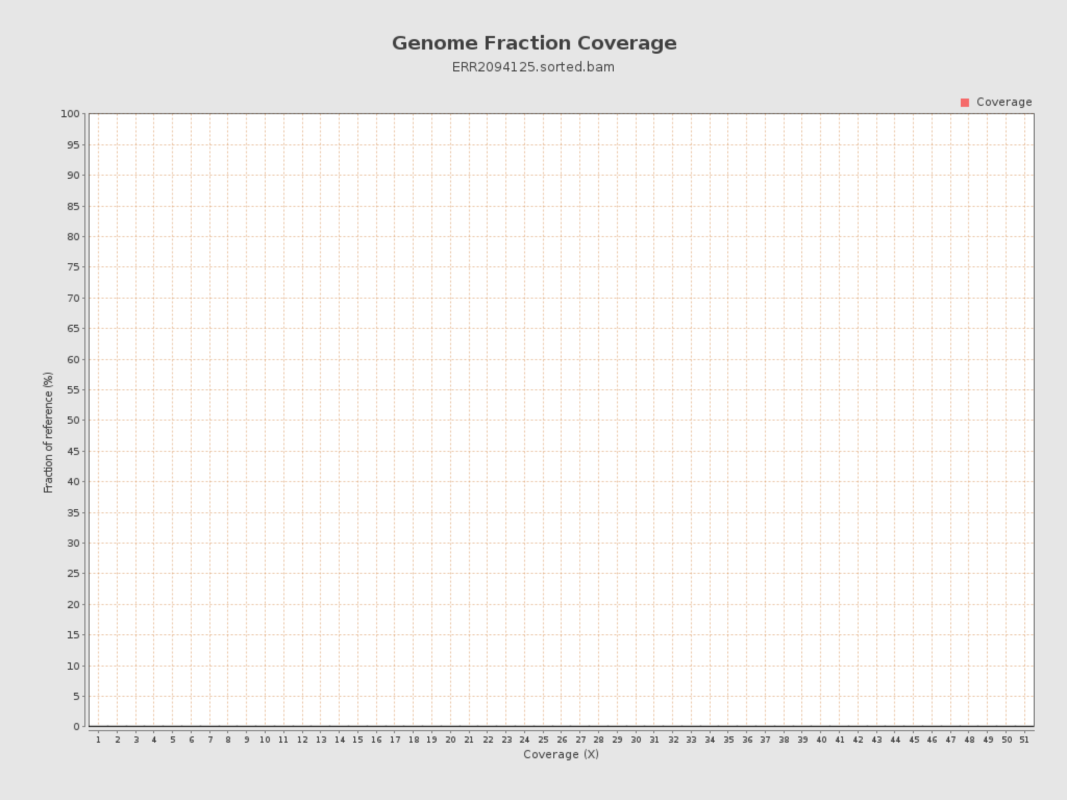
4. Results : Coverage Histogram



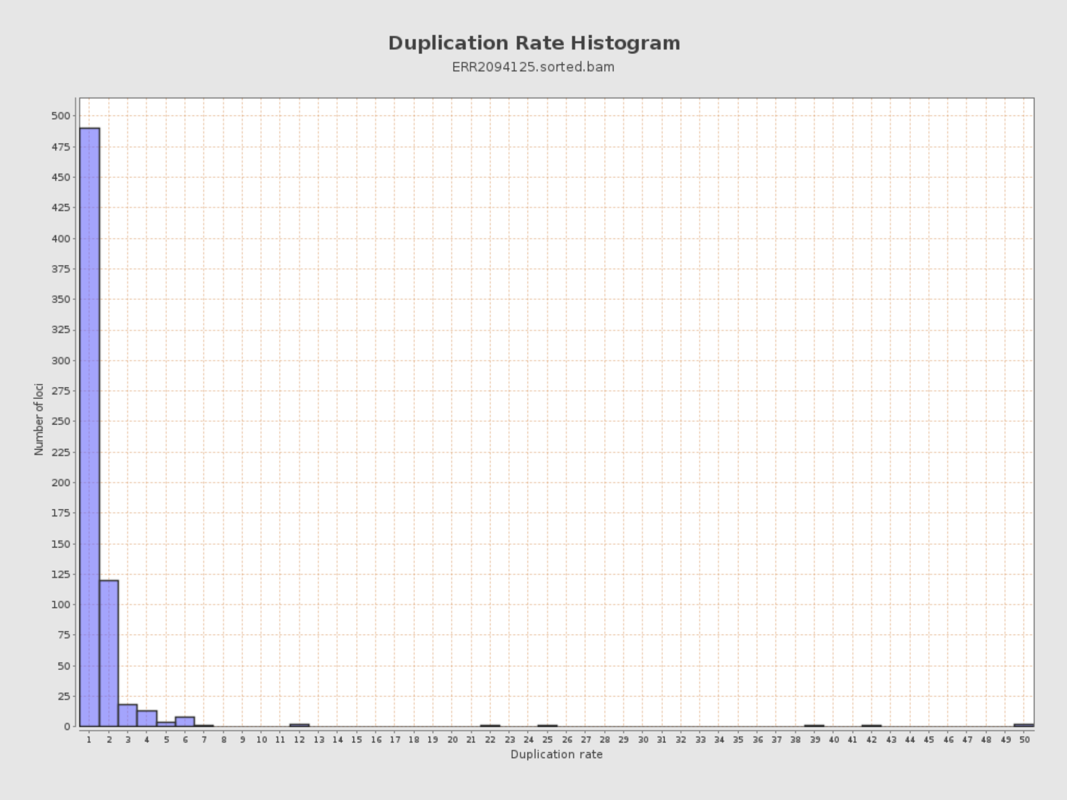
5. Results : Coverage Histogram (0-50X)



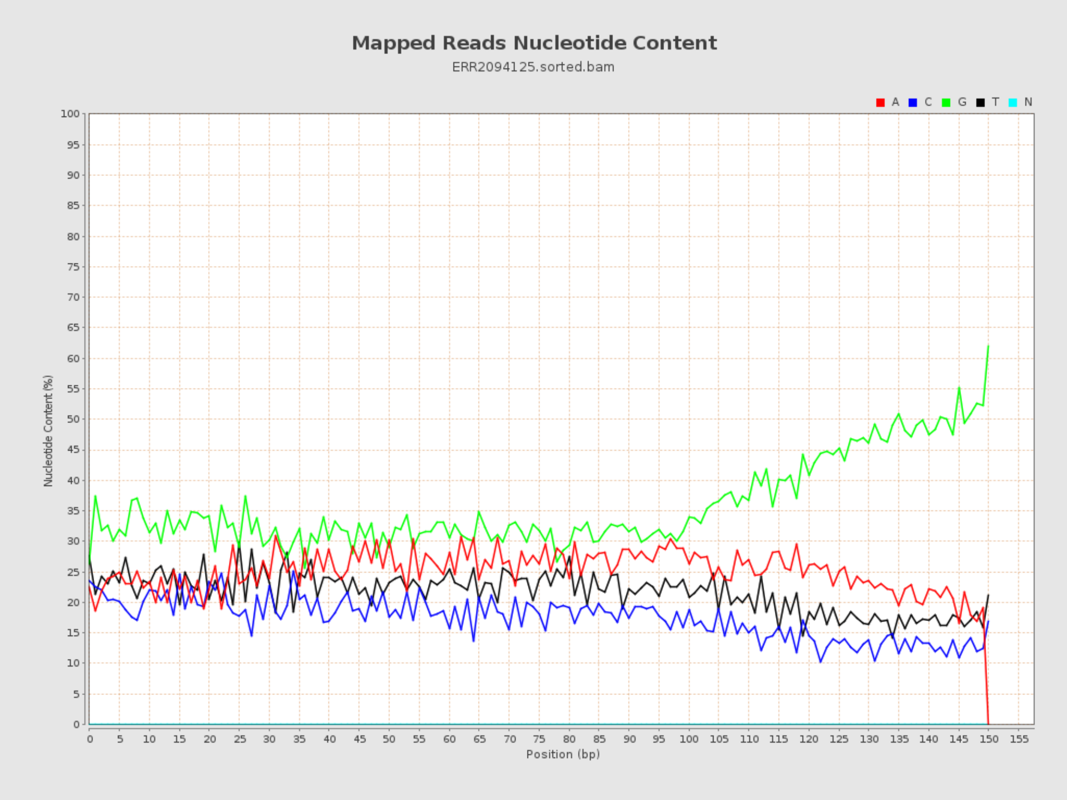
6. Results : Genome Fraction Coverage



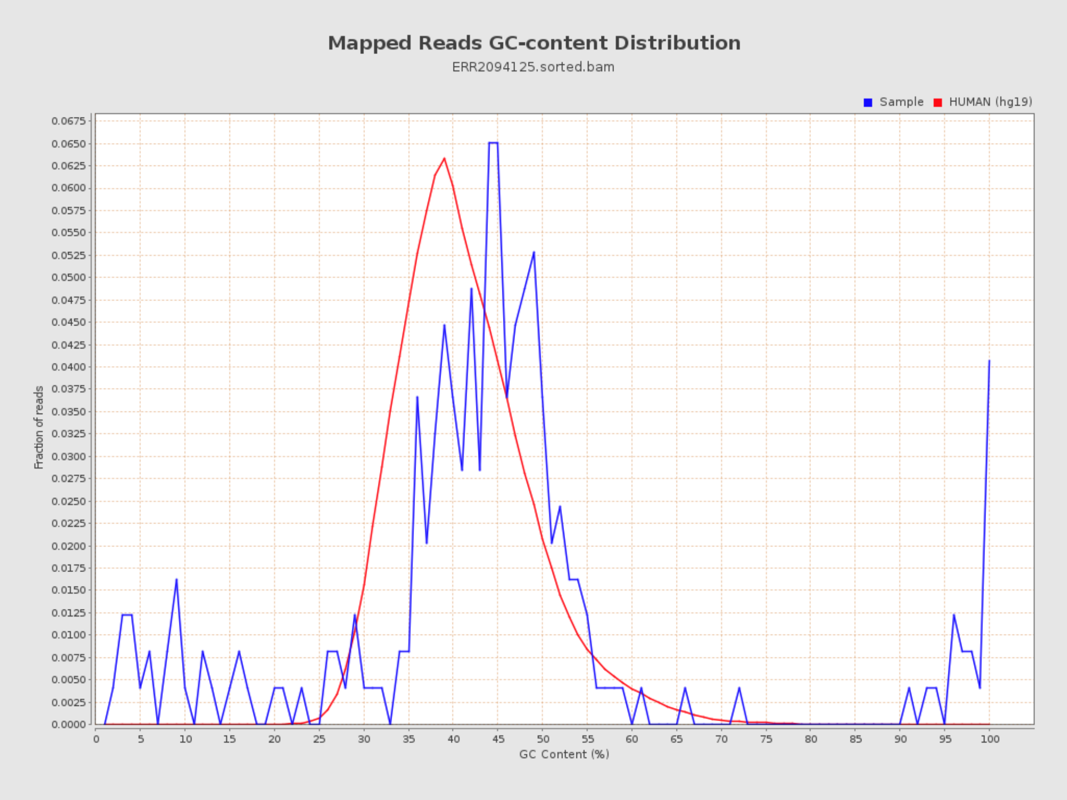
7. Results : Duplication Rate Histogram



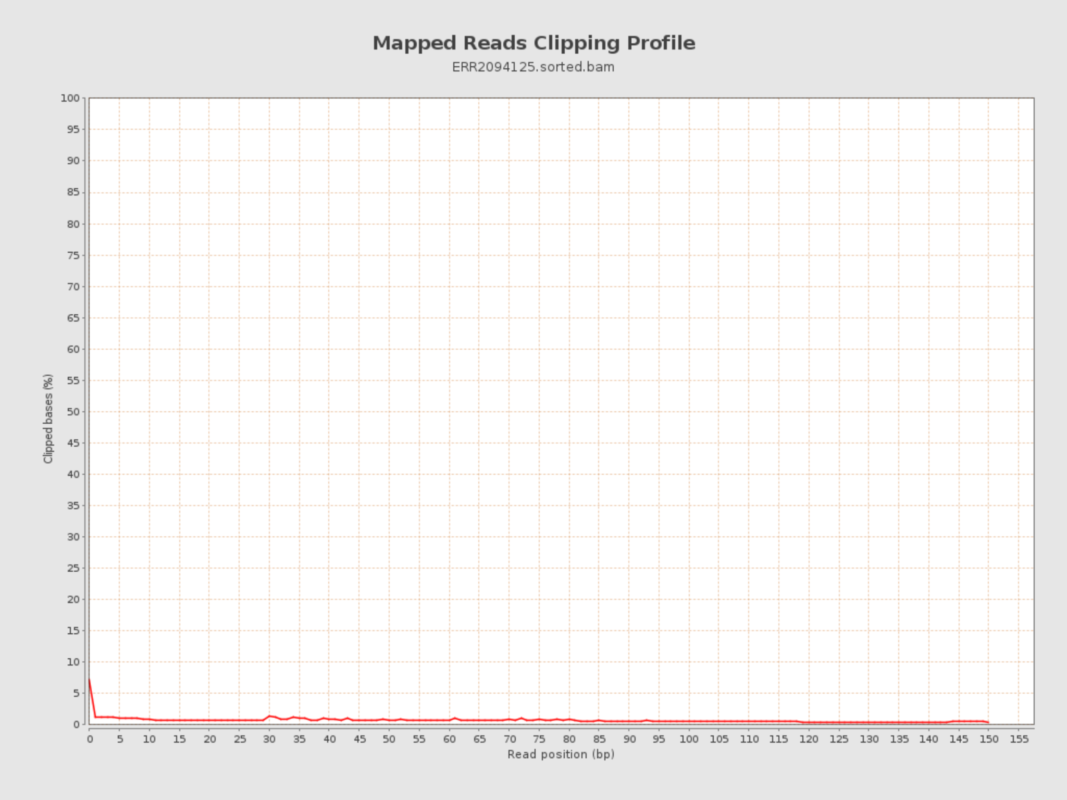
8. Results : Mapped Reads Nucleotide Content



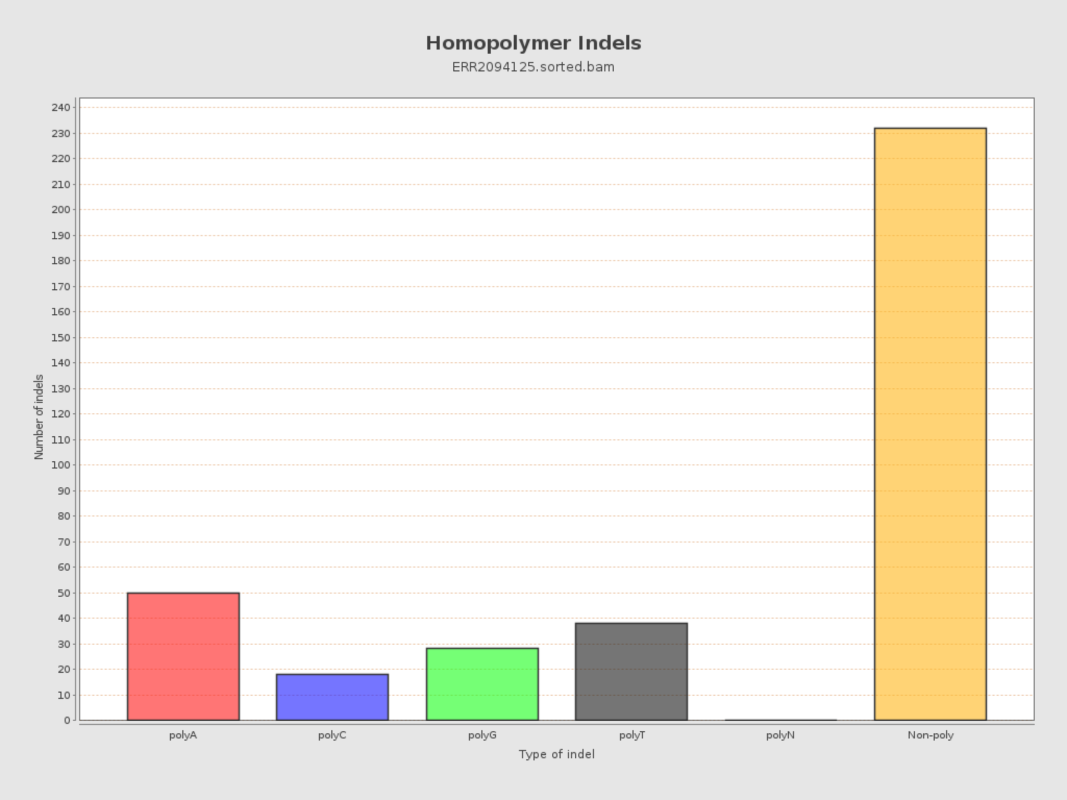
9. Results : Mapped Reads GC-content Distribution



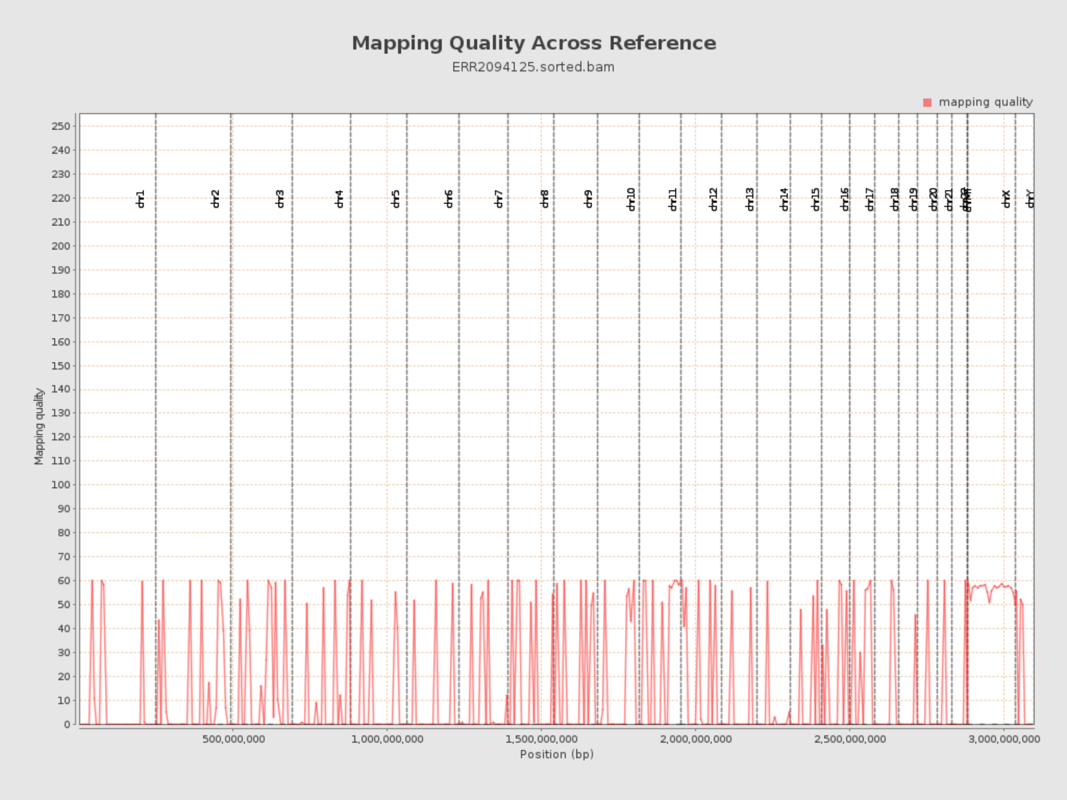
10. Results : Mapped Reads Clipping Profile



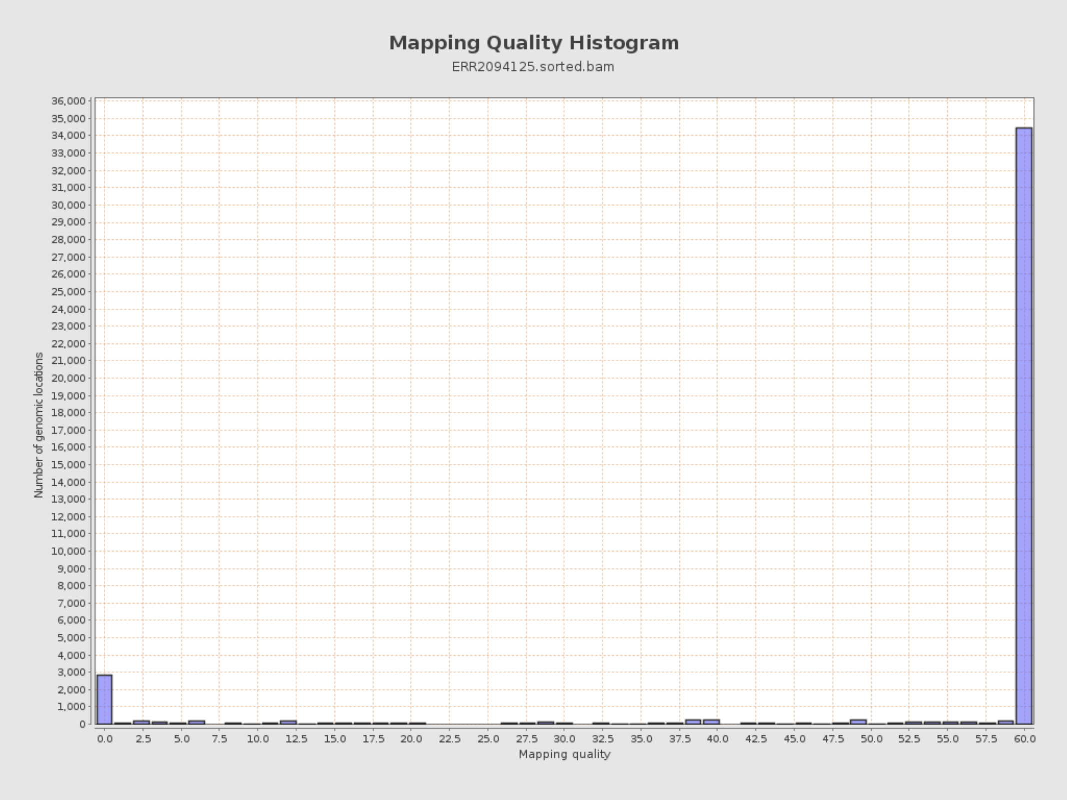
11. Results : Homopolymer Indels



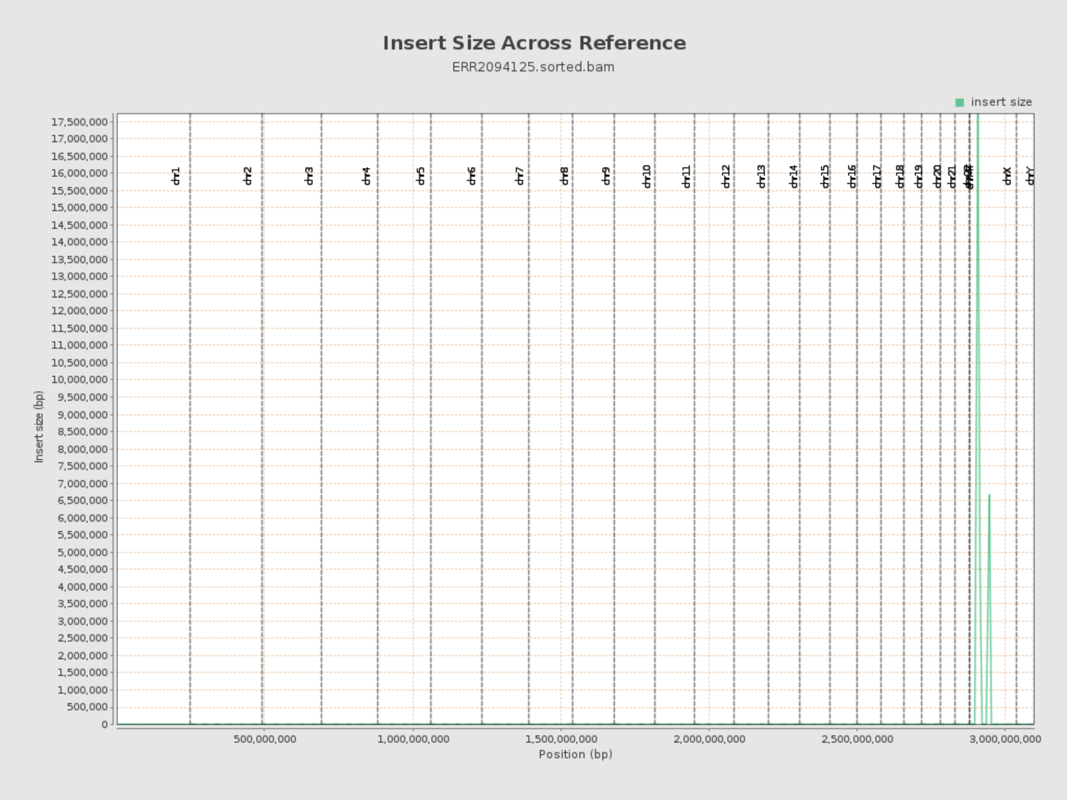
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram