Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:59:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094017.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_ERR2094017 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094017_1.fastq.gz ERR2094017_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:59:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,038
Mapped reads	1,024 / 3.2%
Unmapped reads	31,014 / 96.8%
Mapped paired reads	1,024 / 3.2%
Mapped reads, first in pair	404 / 1.26%
Mapped reads, second in pair	620 / 1.94%
Mapped reads, both in pair	698 / 2.18%
Mapped reads, singletons	326 / 1.02%
Secondary alignments	0
Supplementary alignments	35 / 0.11%
Read min/max/mean length	30 / 151 / 59.54
Duplicated reads (estimated)	655 / 2.04%
Duplication rate	23.27%
Clipped reads	781 / 2.44%

2.2. ACGT Content

Number/percentage of A's	14,903 / 19.56%
Number/percentage of C's	12,463 / 16.36%
Number/percentage of T's	13,338 / 17.51%
Number/percentage of G's	35,486 / 46.58%
Number/percentage of N's	0 / 0%

GC Percentage	62.93%

2.3. Coverage

Mean	0
Standard Deviation	0.032

2.4. Mapping Quality

Mean Mapping Quality	7.51

2.5. Insert size

Mean	298,489.36
Standard Deviation	5,453,409.62
P25/Median/P75	31 / 36 / 167

2.6. Mismatches and indels

General error rate	4.04%
Mismatches	2,804
Insertions	59
Mapped reads with at least one insertion	4.3%
Deletions	131
Mapped reads with at least one deletion	12.5%
Homopolymer indels	31.58%

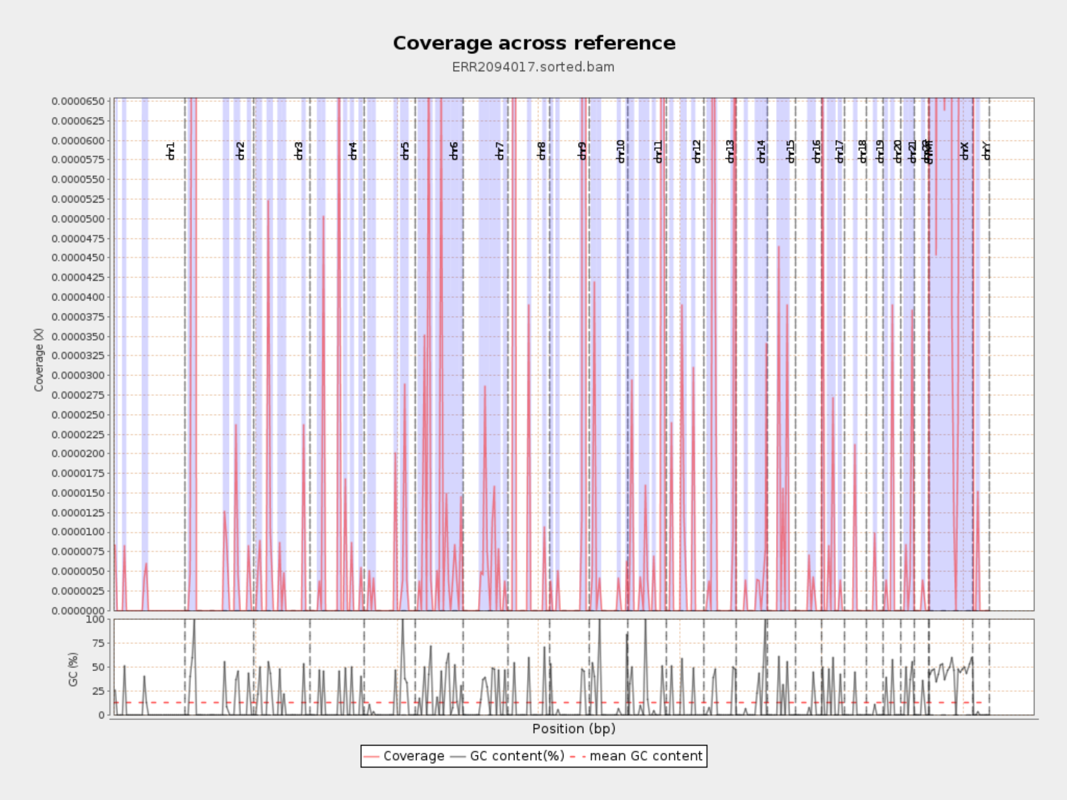
2.7. Chromosome stats

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

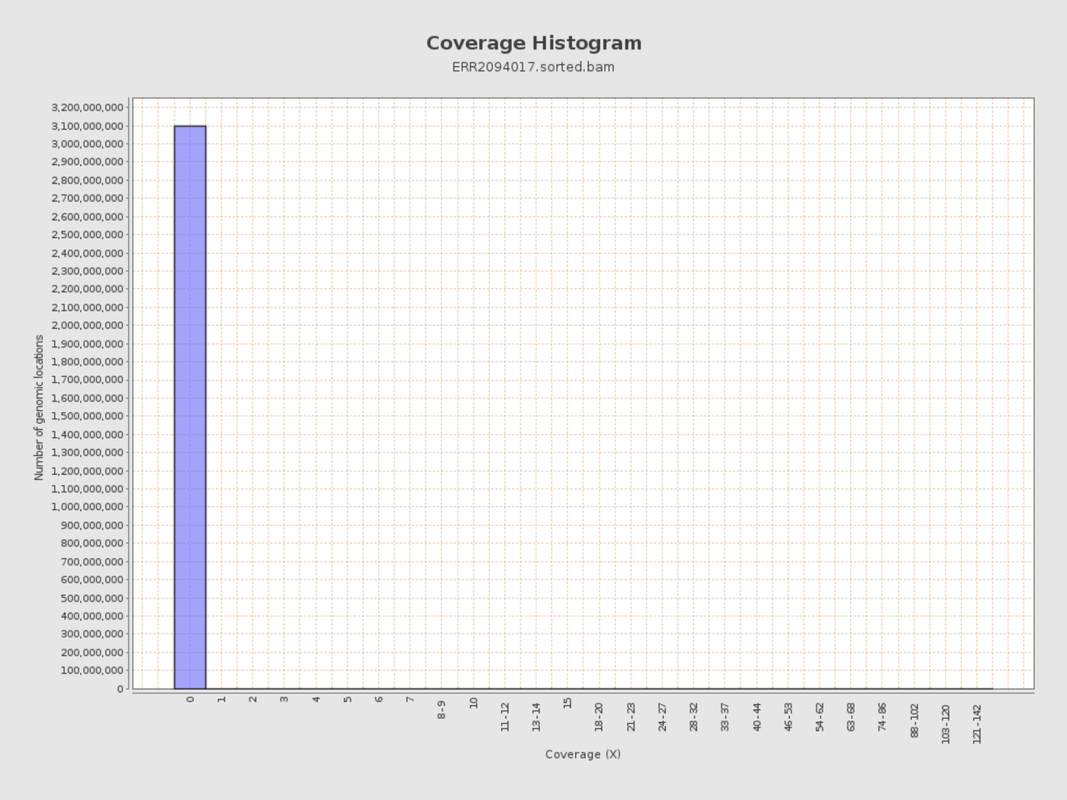
		bases	coverage	deviation
chr1	249250621	210	0	0.001
chr2	243199373	24147	0.0001	0.0939
chr3	198022430	879	0	0.0026
chr4	191154276	1261	0	0.0056
chr5	180915260	513	0	0.0022
chr6	171115067	1894	0	0.0056
chr7	159138663	657	0	0.0026
chr8	146364022	2257	0	0.026
chr9	141213431	5895	0	0.0307
chr10	135534747	457	0	0.0024
chr11	135006516	1747	0	0.0063
chr12	133851895	819	0	0.0032
chr13	115169878	2228	0	0.0074
chr14	107349540	216	0	0.0016
chr15	102531392	783	0	0.0039
chr16	90354753	89	0	0.001
chr17	81195210	842	0	0.0047
chr18	78077248	164	0	0.0014
chr19	59128983	77	0	0.0011
chr20	63025520	333	0	0.0029
chr21	48129895	396	0	0.0037
chr22	51304566	31	0	0.0008
chrMT	16571	1507	0.0909	0.4292
chrX	155270560	30321	0.0002	0.0695

chrY	59373566	118	0	0.002

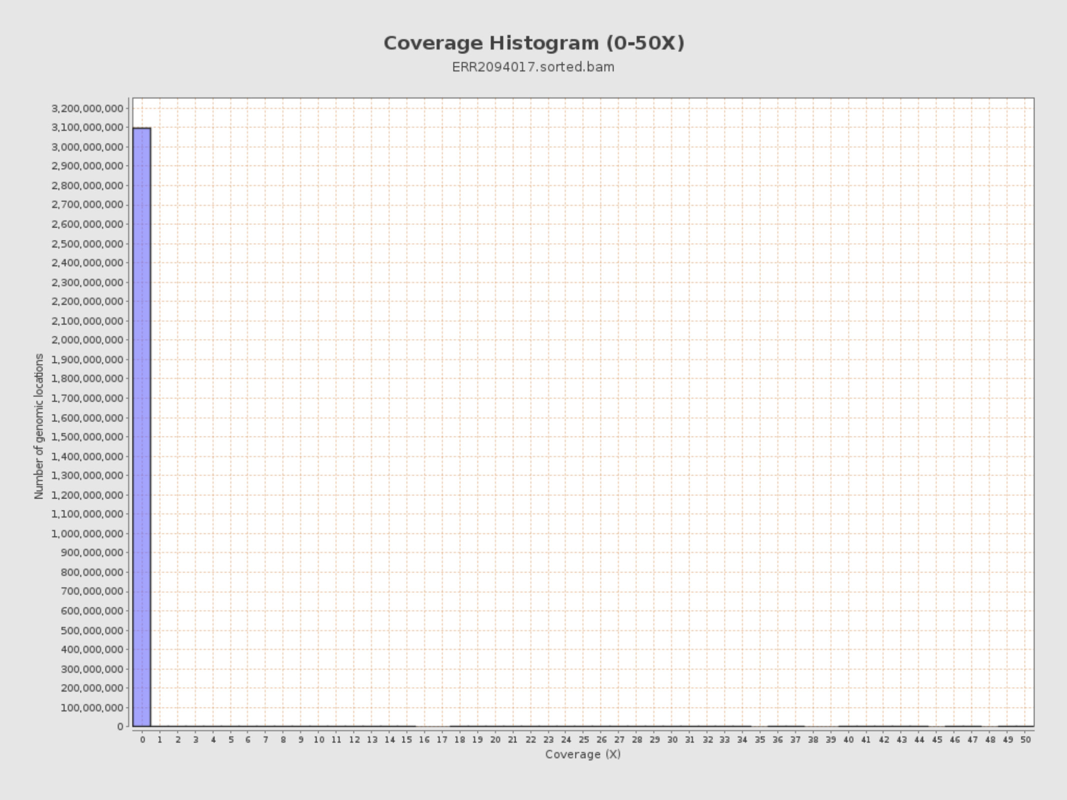
3. Results : Coverage across reference



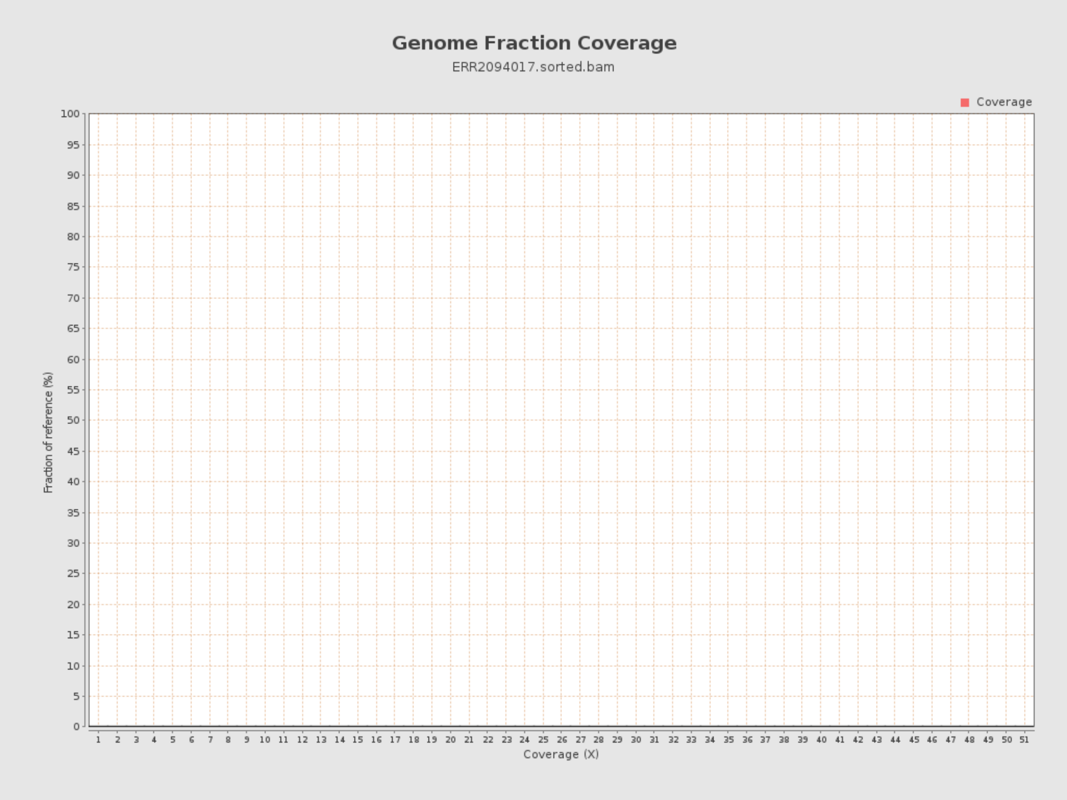
4. Results : Coverage Histogram



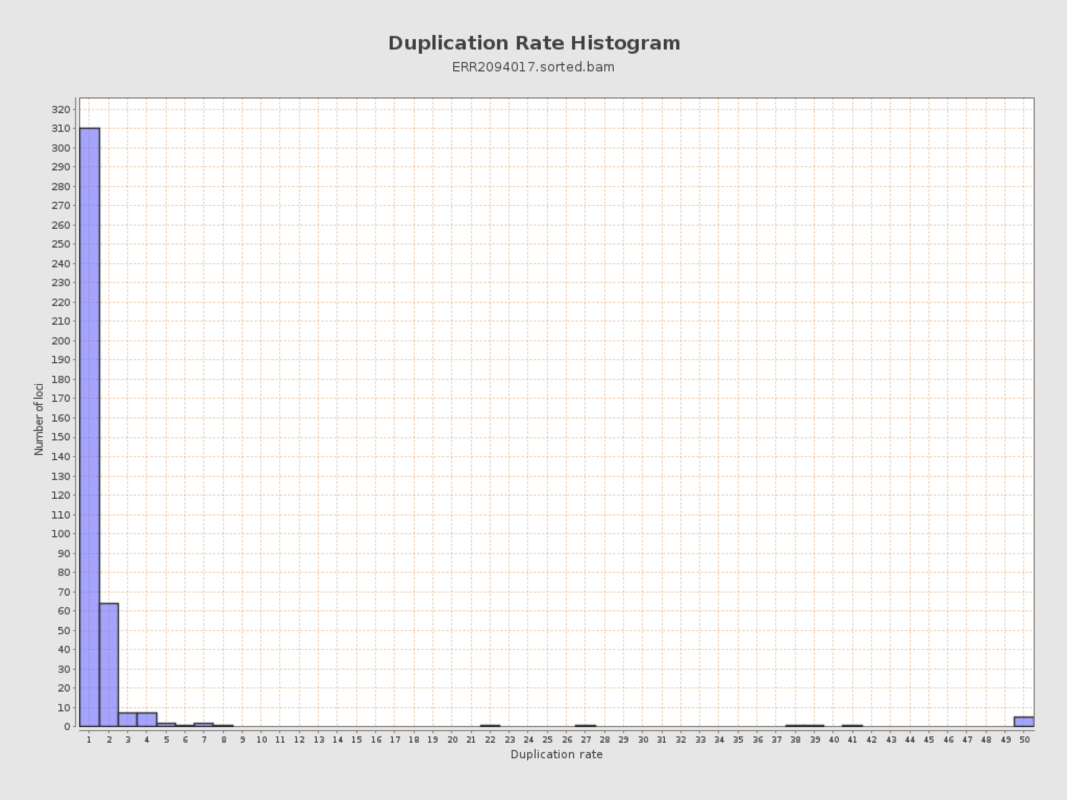
5. Results : Coverage Histogram (0-50X)



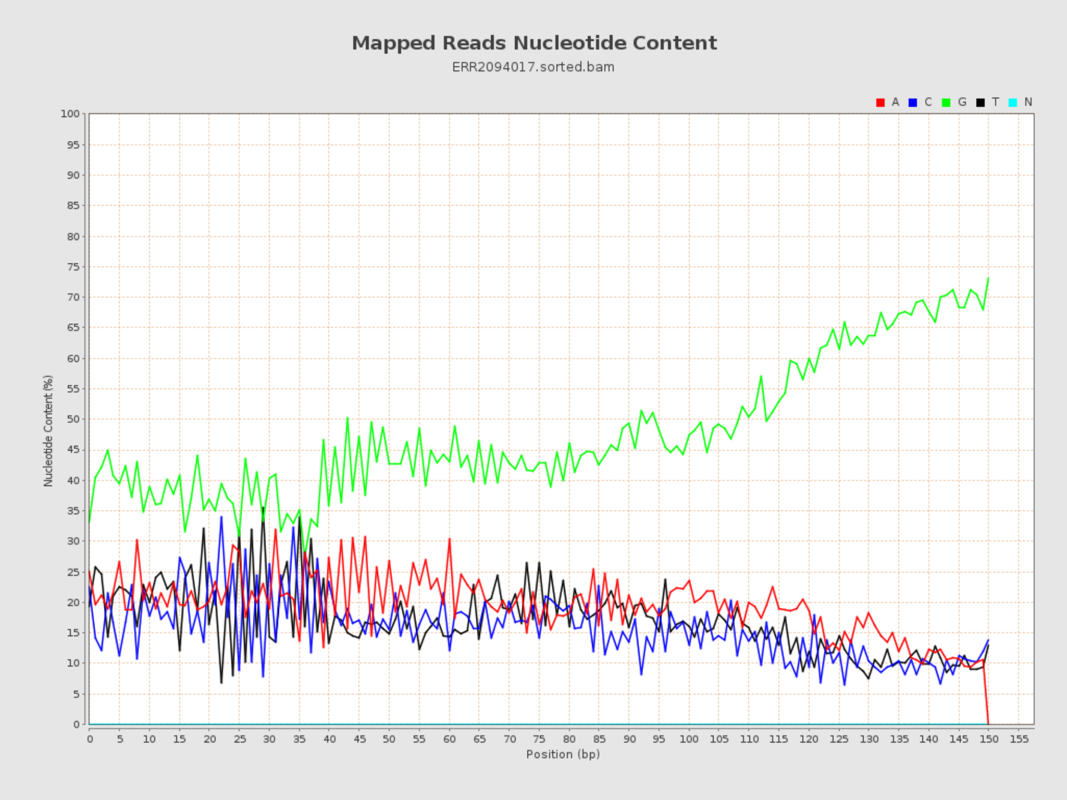
6. Results : Genome Fraction Coverage



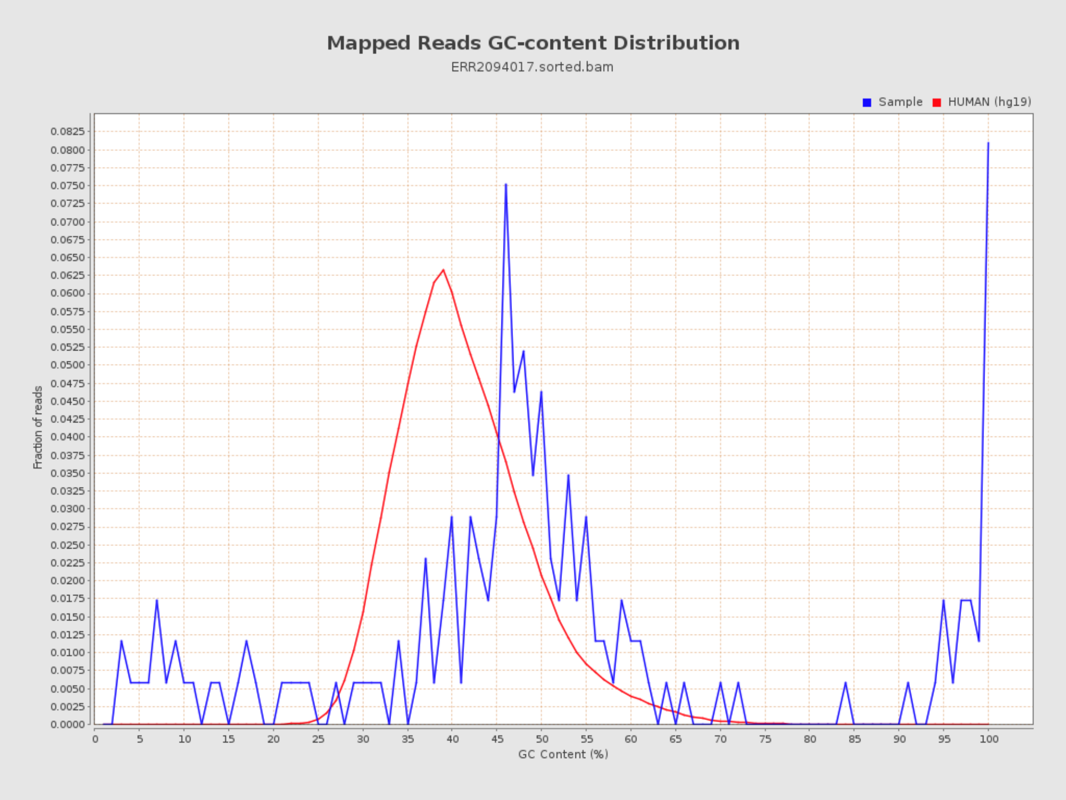
7. Results : Duplication Rate Histogram



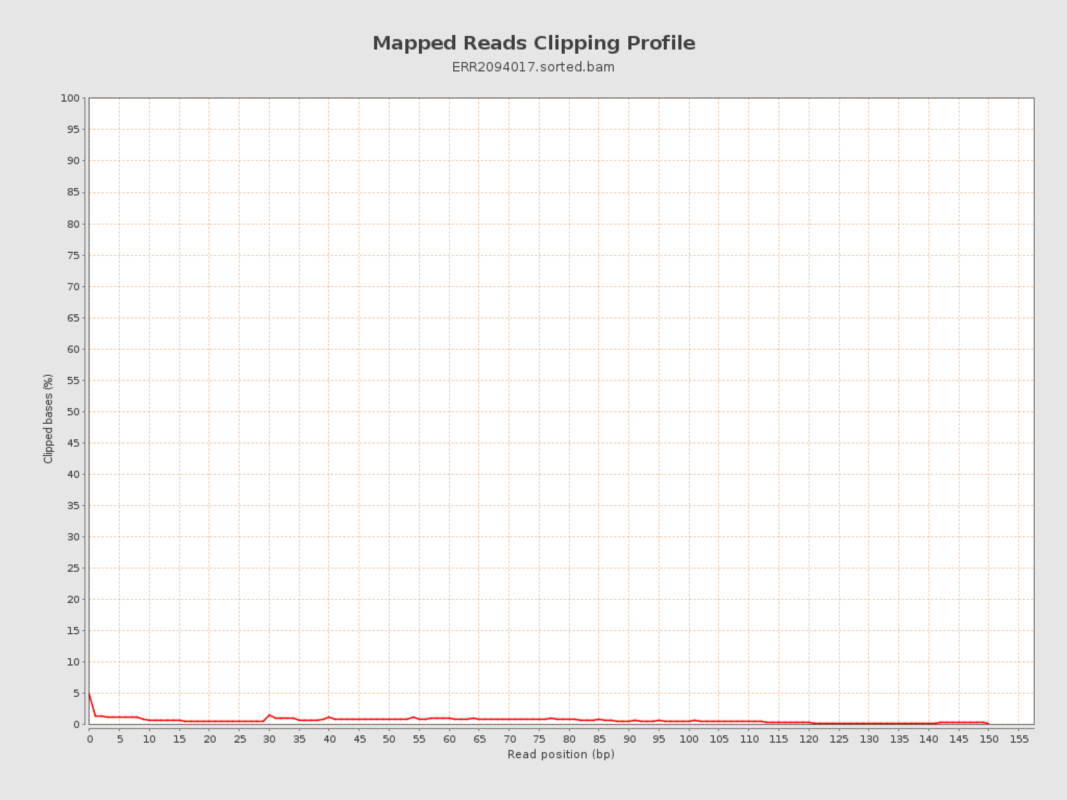
8. Results : Mapped Reads Nucleotide Content



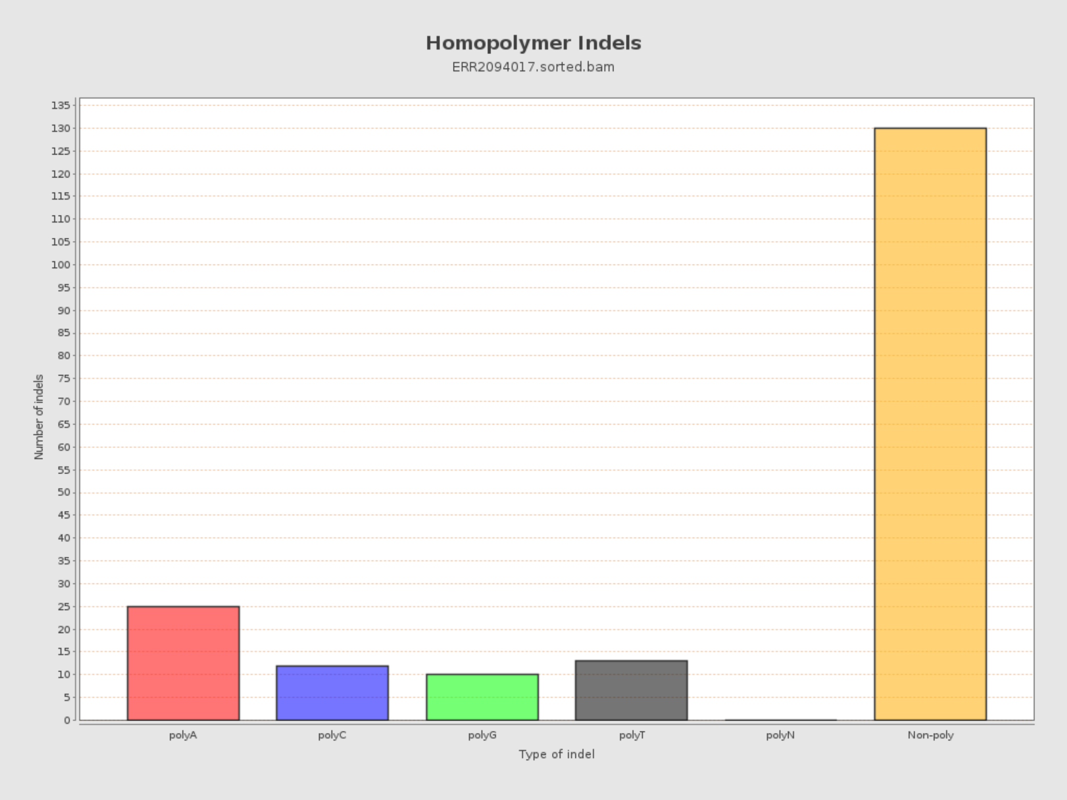
9. Results : Mapped Reads GC-content Distribution



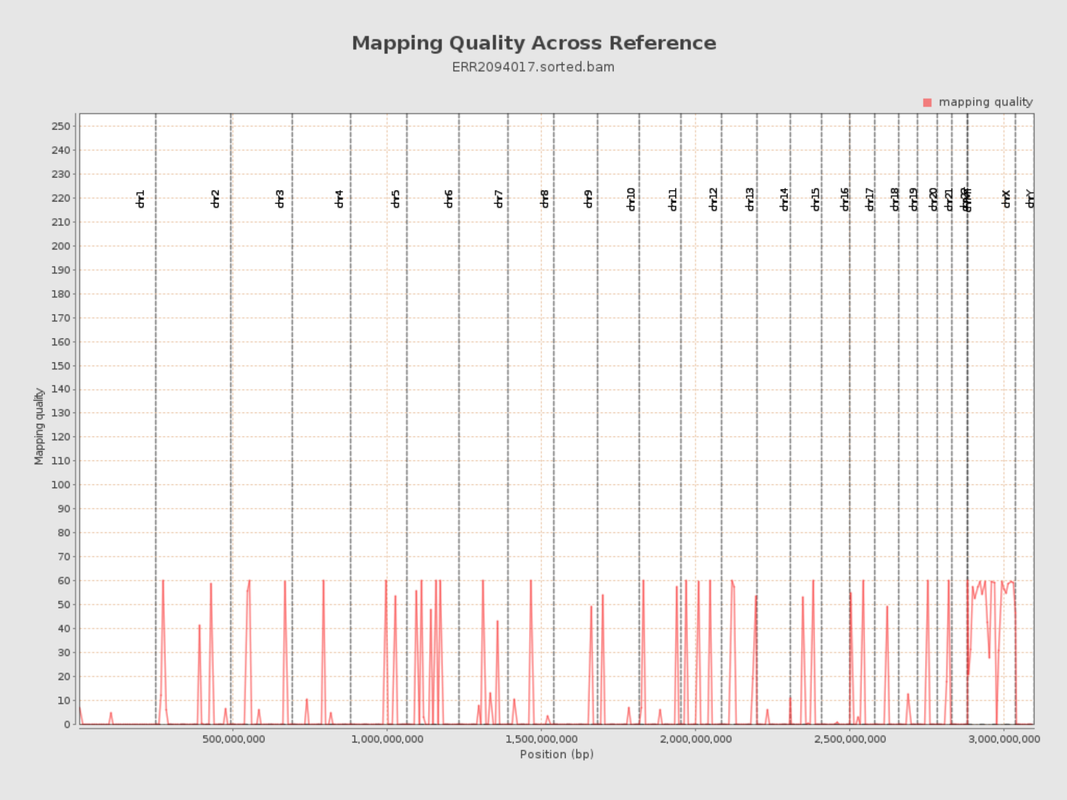
10. Results : Mapped Reads Clipping Profile



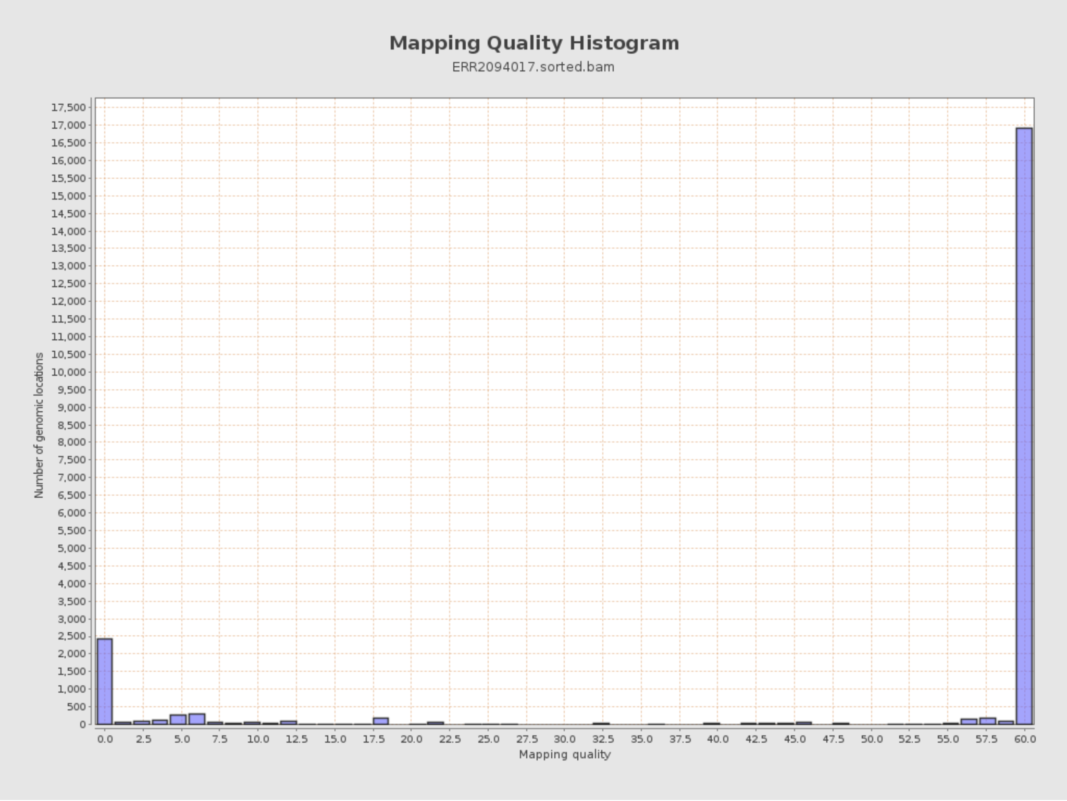
11. Results : Homopolymer Indels



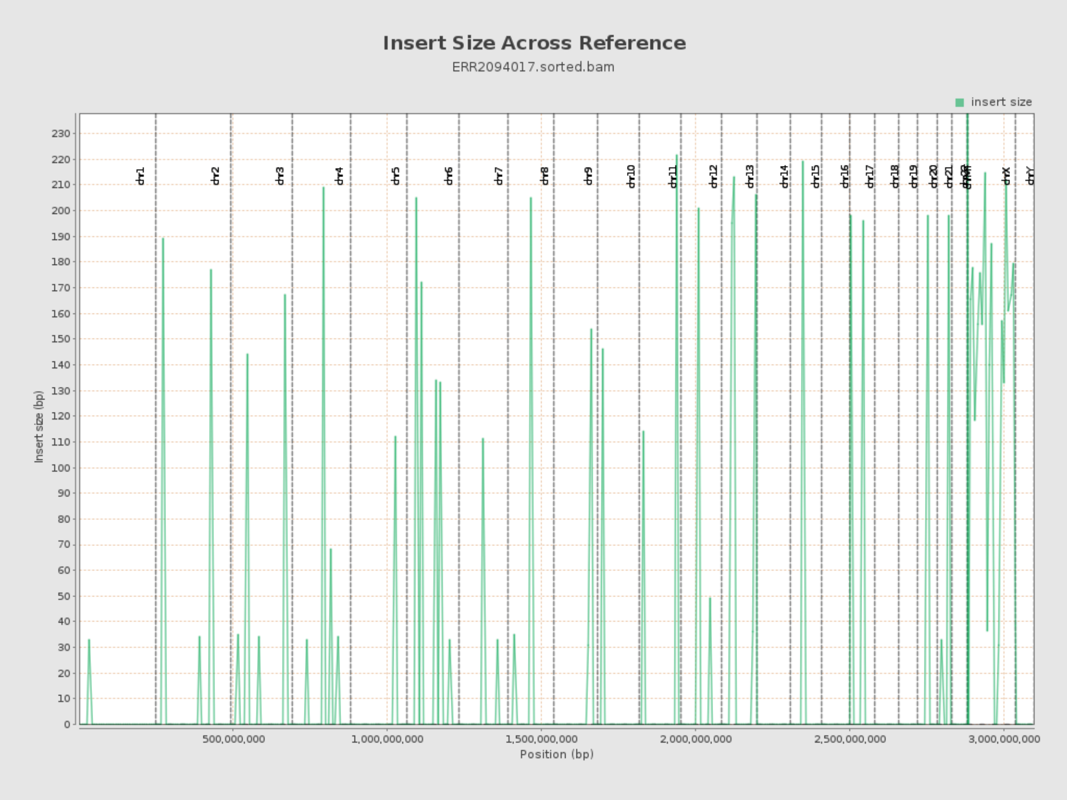
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram