

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:57:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094015.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_ERR2094015 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094015_1.fastq.gz ERR2094015_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:57:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,496
Mapped reads	12,642 / 45.98%
Unmapped reads	14,854 / 54.02%
Mapped paired reads	12,642 / 45.98%
Mapped reads, first in pair	6,269 / 22.8%
Mapped reads, second in pair	6,373 / 23.18%
Mapped reads, both in pair	12,388 / 45.05%
Mapped reads, singletons	254 / 0.92%
Secondary alignments	0
Supplementary alignments	36 / 0.13%
Read min/max/mean length	30 / 151 / 98.4
Duplicated reads (estimated)	12,049 / 43.82%
Duplication rate	29.41%
Clipped reads	1,075 / 3.91%

2.2. ACGT Content

Number/percentage of A's	550,421 / 29.79%
Number/percentage of C's	360,325 / 19.5%
Number/percentage of T's	542,890 / 29.39%
Number/percentage of G's	393,768 / 21.31%
Number/percentage of N's	7 / 0%

GC Percentage	40.82%
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2.3. Coverage

Mean	0.0006
Standard Deviation	1.8864

2.4. Mapping Quality

Mean Mapping Quality	12.39
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2.5. Insert size

Mean	30,614.94
Standard Deviation	1,398,690.16
P25/Median/P75	217 / 217 / 217

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	21,851
Insertions	120
Mapped reads with at least one insertion	0.89%
Deletions	809
Mapped reads with at least one deletion	5.88%
Homopolymer indels	37.14%

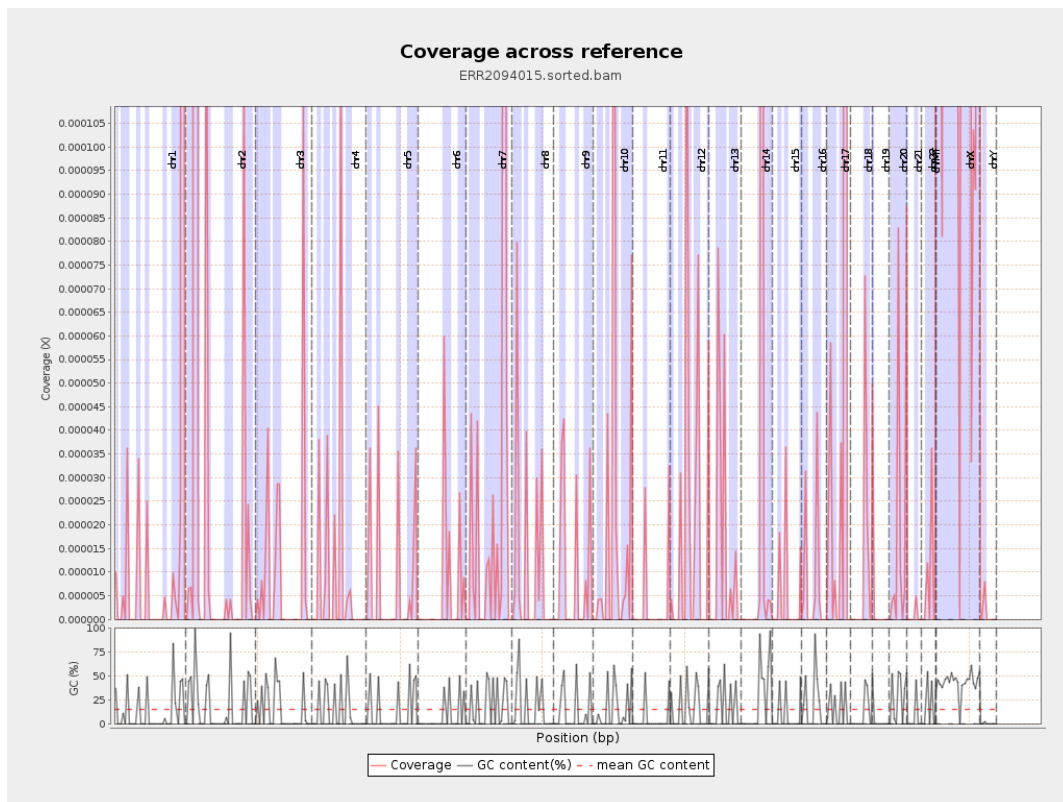
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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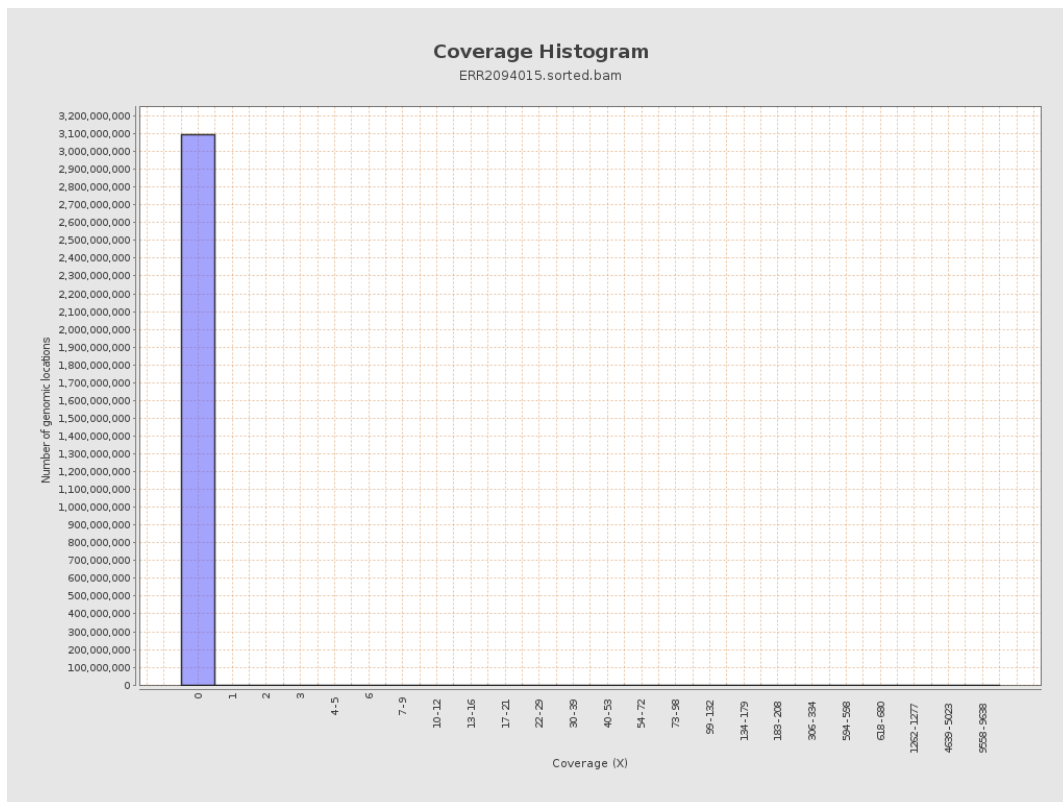
		bases	coverage	deviation
chr1	249250621	11068	0	0.0442
chr2	243199373	29381	0.0001	0.1094
chr3	198022430	1955	0	0.0056
chr4	191154276	1849	0	0.0039
chr5	180915260	1358	0	0.0037
chr6	171115067	886	0	0.003
chr7	159138663	4031	0	0.015
chr8	146364022	1544	0	0.0049
chr9	141213431	1203	0	0.0036
chr10	135534747	2942	0	0.0126
chr11	135006516	470	0	0.0025
chr12	133851895	2766	0	0.0094
chr13	115169878	1578	0	0.0056
chr14	107349540	2785	0	0.022
chr15	102531392	471	0	0.0027
chr16	90354753	674	0	0.0034
chr17	81195210	6943	0.0001	0.0399
chr18	78077248	731	0	0.0054
chr19	59128983	142	0	0.0015
chr20	63025520	1113	0	0.0066
chr21	48129895	38	0	0.0009
chr22	51304566	375	0	0.0032
chrMT	16571	1733451	104.6075	808.4663
chrX	155270560	43136	0.0003	0.0538

chrY	59373566	62	0	0.001
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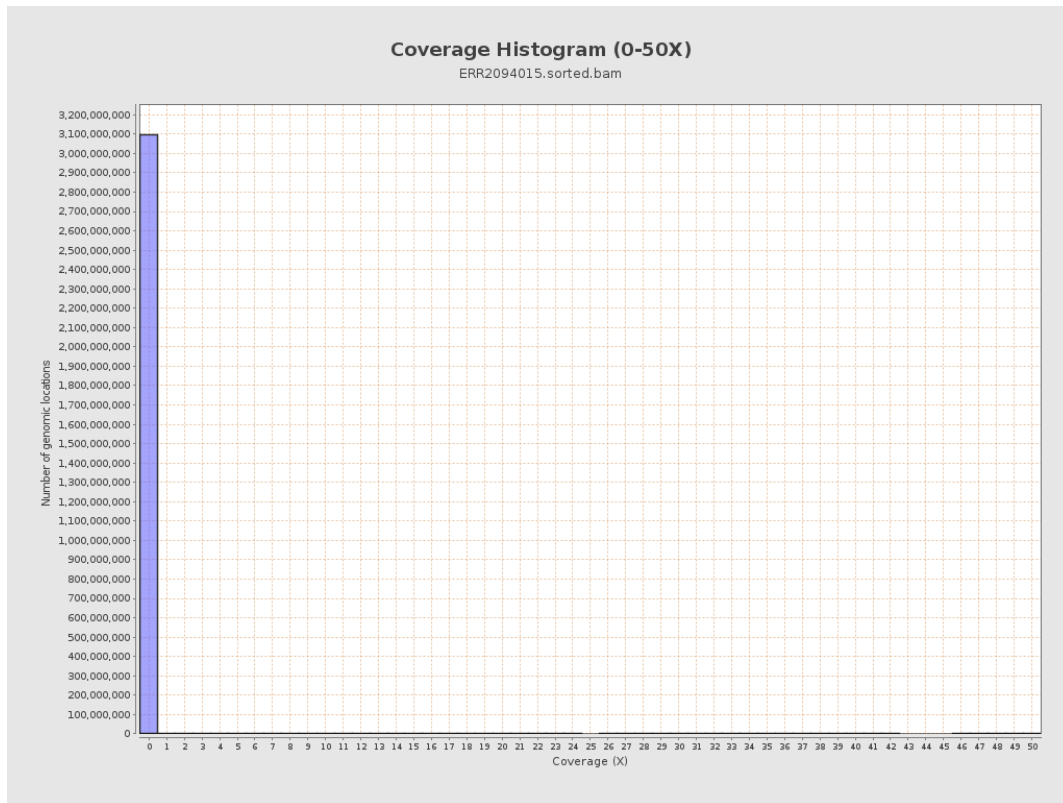
3. Results : Coverage across reference



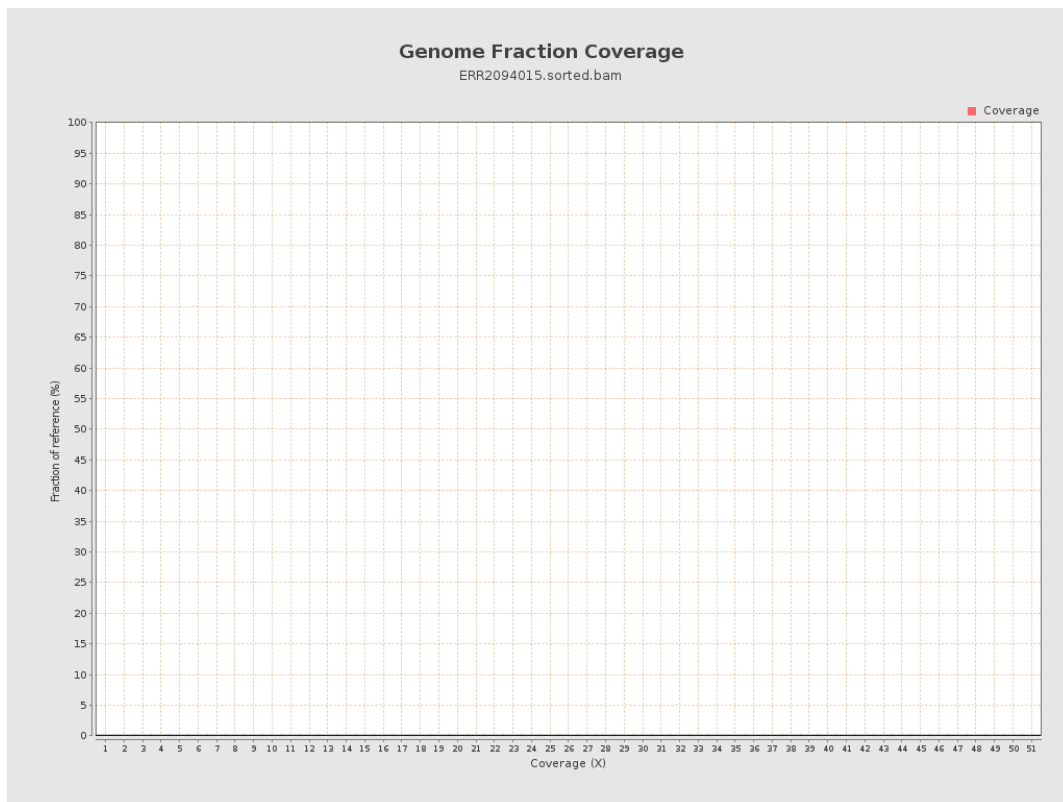
4. Results : Coverage Histogram



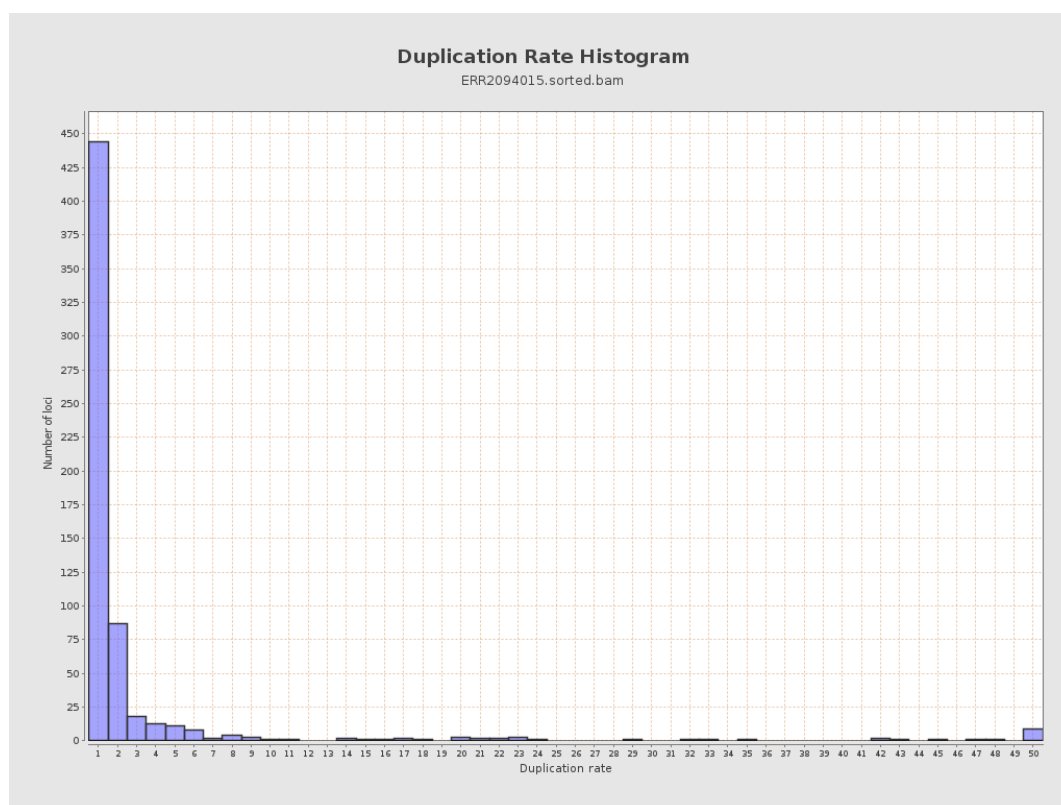
5. Results : Coverage Histogram (0-50X)



6. Results : Genome Fraction Coverage



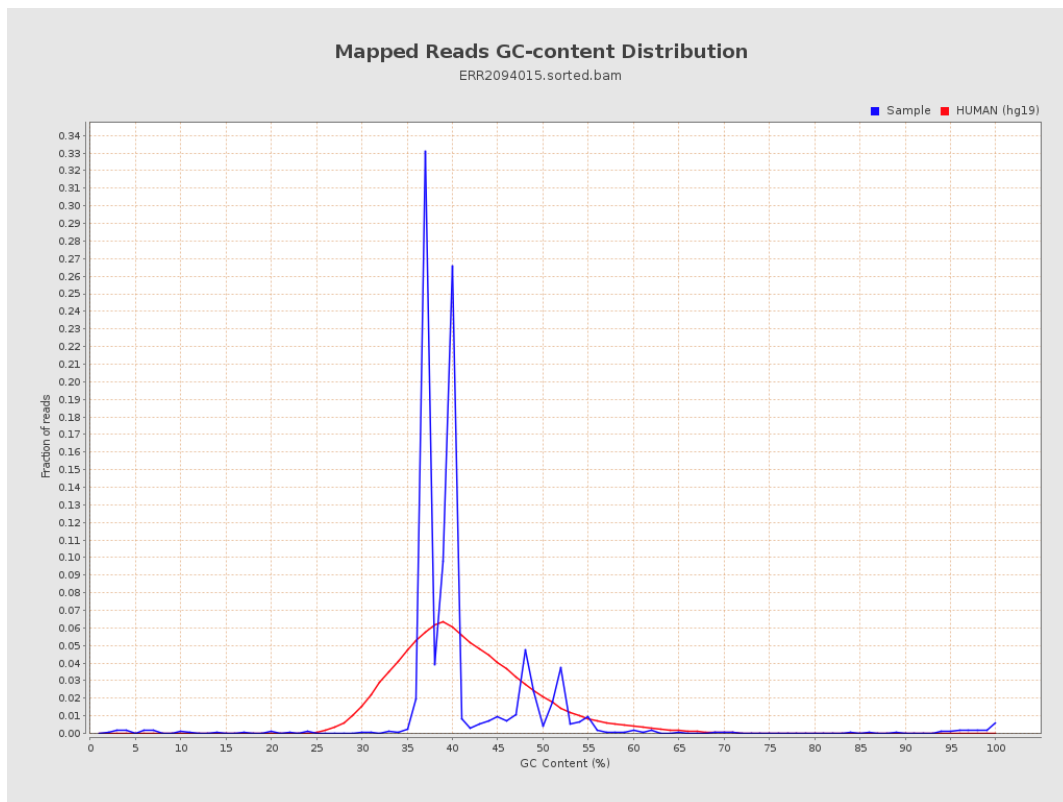
7. Results : Duplication Rate Histogram



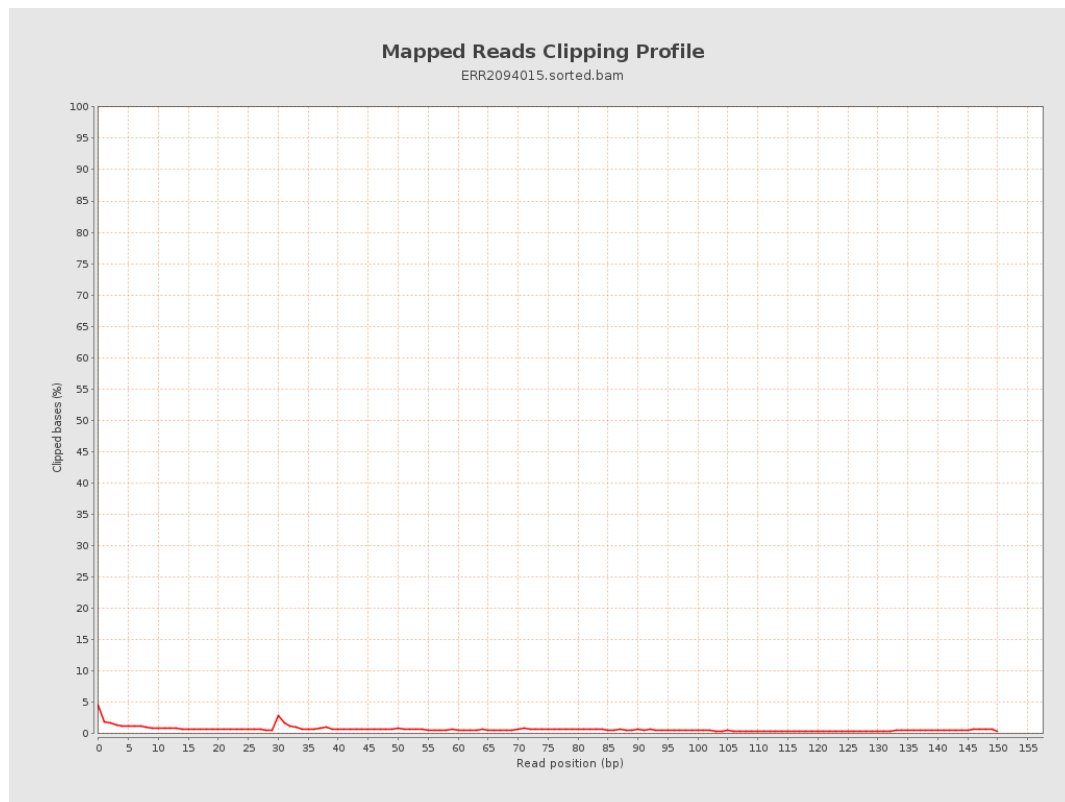
8. Results : Mapped Reads Nucleotide Content



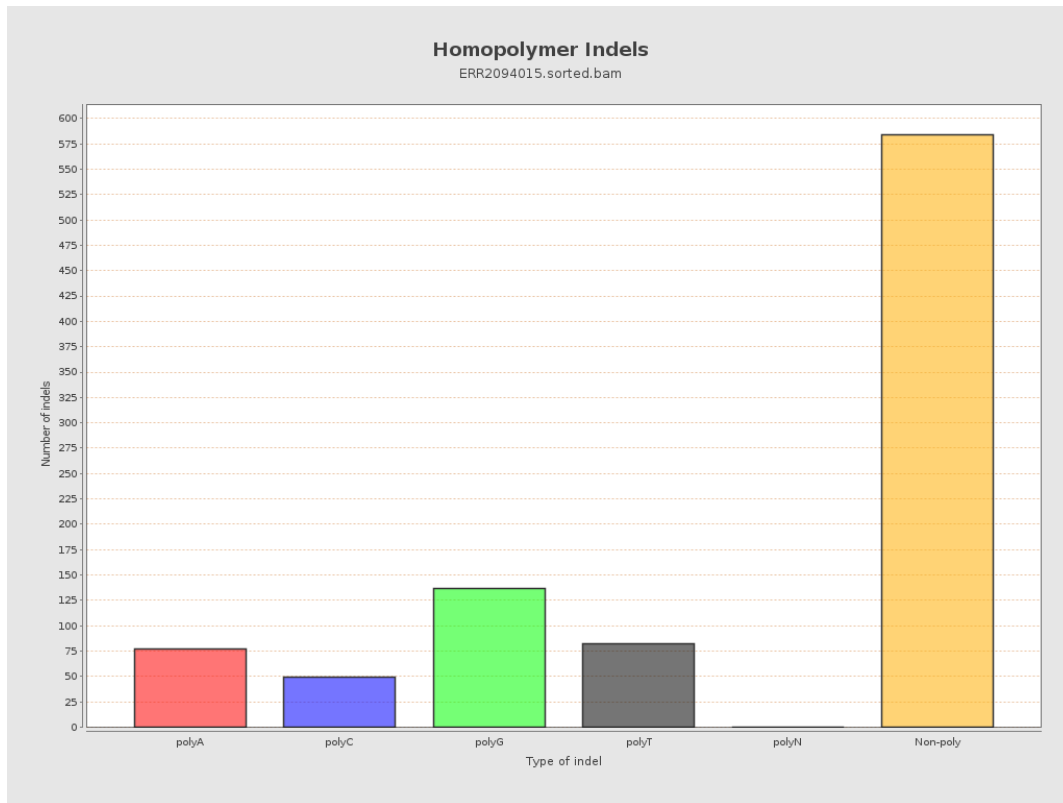
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



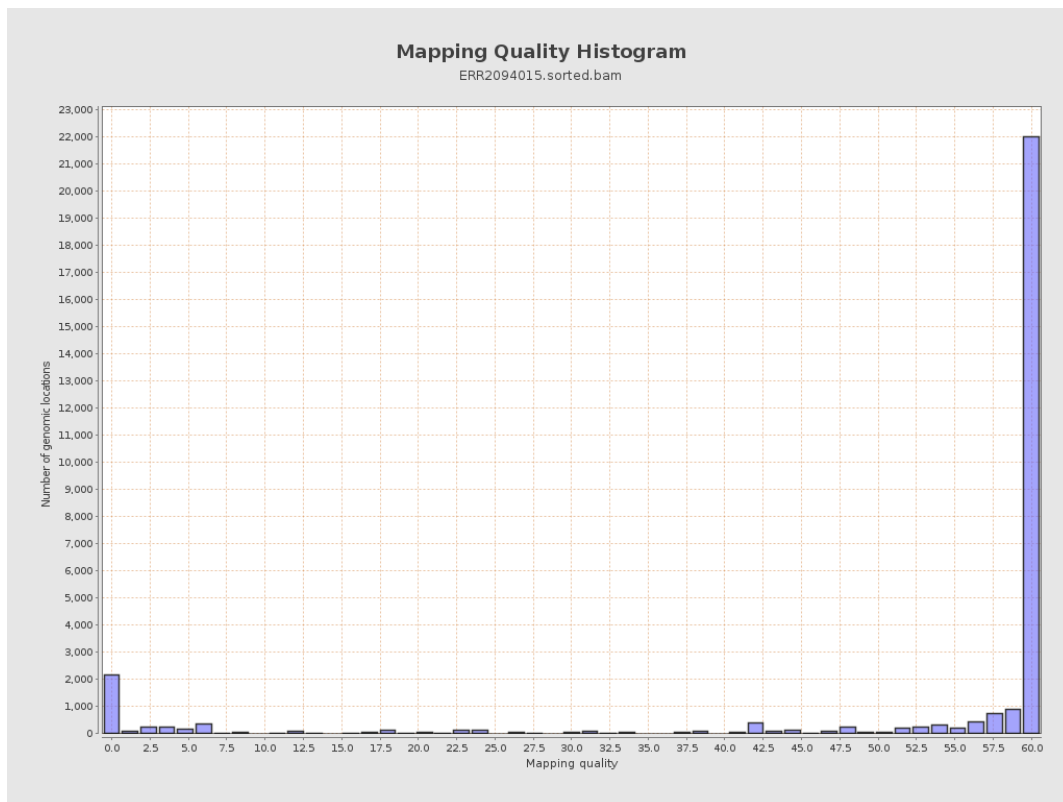
11. Results : Homopolymer Indels



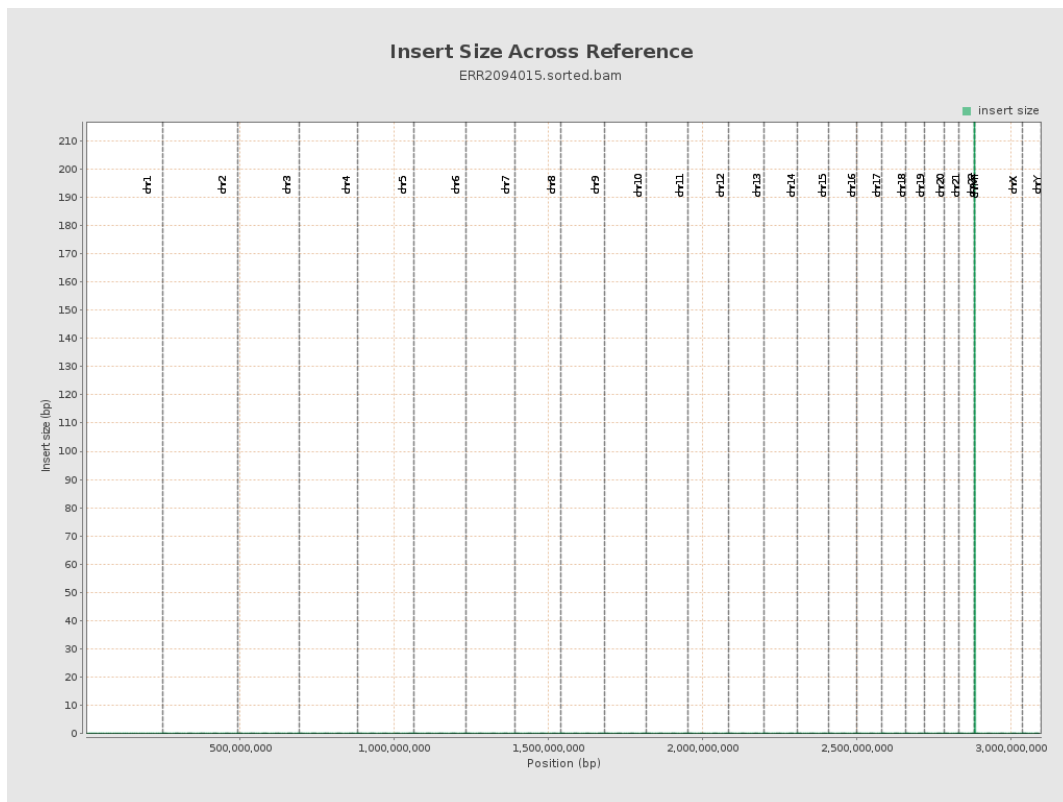
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

