

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:19:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093998.sorted.bam -c -nw 400 -hm 3
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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_ERR2093998 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093998_1.fastq.gz ERR2093998_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:19:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093998.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	345,044
Mapped reads	332,251 / 96.29%
Unmapped reads	12,793 / 3.71%
Mapped paired reads	332,251 / 96.29%
Mapped reads, first in pair	167,170 / 48.45%
Mapped reads, second in pair	165,081 / 47.84%
Mapped reads, both in pair	329,020 / 95.36%
Mapped reads, singletons	3,231 / 0.94%
Secondary alignments	0
Supplementary alignments	23,296 / 6.75%
Read min/max/mean length	30 / 151 / 142.85
Duplicated reads (estimated)	315,310 / 91.38%
Duplication rate	51.66%
Clipped reads	165,033 / 47.83%

2.2. ACGT Content

Number/percentage of A's	10,985,545 / 26.09%
Number/percentage of C's	9,980,421 / 23.71%
Number/percentage of T's	10,415,409 / 24.74%
Number/percentage of G's	10,717,681 / 25.46%
Number/percentage of N's	469 / 0%

GC Percentage	49.16%
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2.3. Coverage

Mean	0.0138
Standard Deviation	2.7937

2.4. Mapping Quality

Mean Mapping Quality	40.21
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2.5. Insert size

Mean	1,288,154.64
Standard Deviation	10,319,230.72
P25/Median/P75	126 / 164 / 202

2.6. Mismatches and indels

General error rate	3.37%
Mismatches	1,367,986
Insertions	22,628
Mapped reads with at least one insertion	6.68%
Deletions	110,977
Mapped reads with at least one deletion	32.09%
Homopolymer indels	30.6%

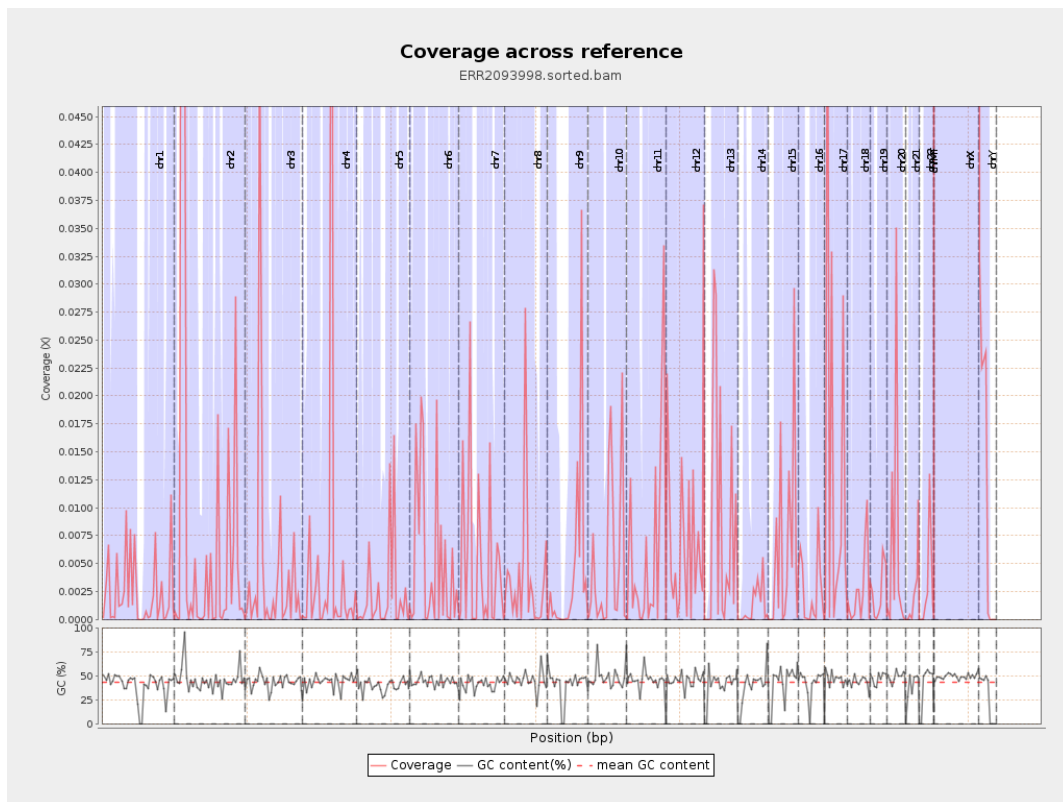
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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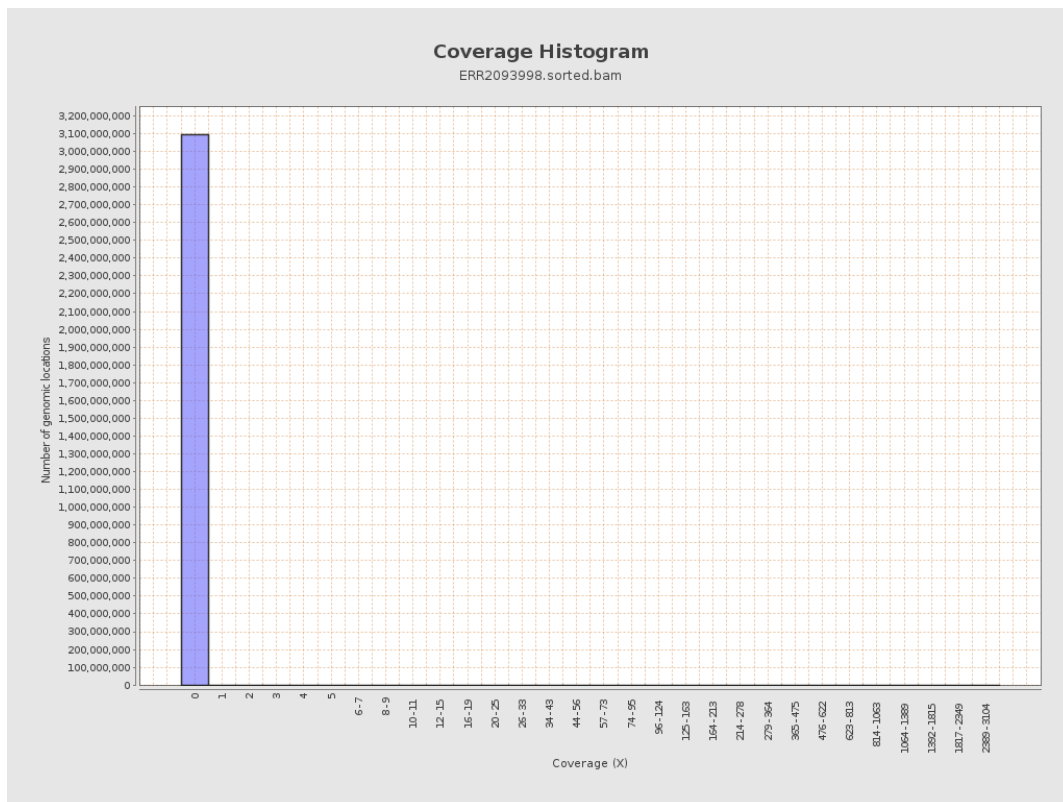
		bases	coverage	deviation
chr1	249250621	611969	0.0025	0.7724
chr2	243199373	1942816	0.008	2.5639
chr3	198022430	788045	0.004	1.4124
chr4	191154276	1041311	0.0054	1.785
chr5	180915260	413248	0.0023	1.0952
chr6	171115067	885445	0.0052	1.5769
chr7	159138663	786113	0.0049	1.3834
chr8	146364022	535074	0.0037	1.2721
chr9	141213431	581040	0.0041	1.2982
chr10	135534747	682368	0.005	1.4508
chr11	135006516	892362	0.0066	1.8356
chr12	133851895	936986	0.007	1.6547
chr13	115169878	935644	0.0081	2.3448
chr14	107349540	132156	0.0012	0.42
chr15	102531392	637037	0.0062	1.666
chr16	90354753	243545	0.0027	0.6934
chr17	81195210	1127985	0.0139	3.5338
chr18	78077248	215135	0.0028	0.7343
chr19	59128983	133949	0.0023	0.5971
chr20	63025520	421004	0.0067	2.4482
chr21	48129895	101622	0.0021	0.3803
chr22	51304566	140152	0.0027	0.8466
chrMT	16571	1358432	81.9765	340.7926
chrX	155270560	26564944	0.1711	9.5482

chrY	59373566	711012	0.012	1.8683
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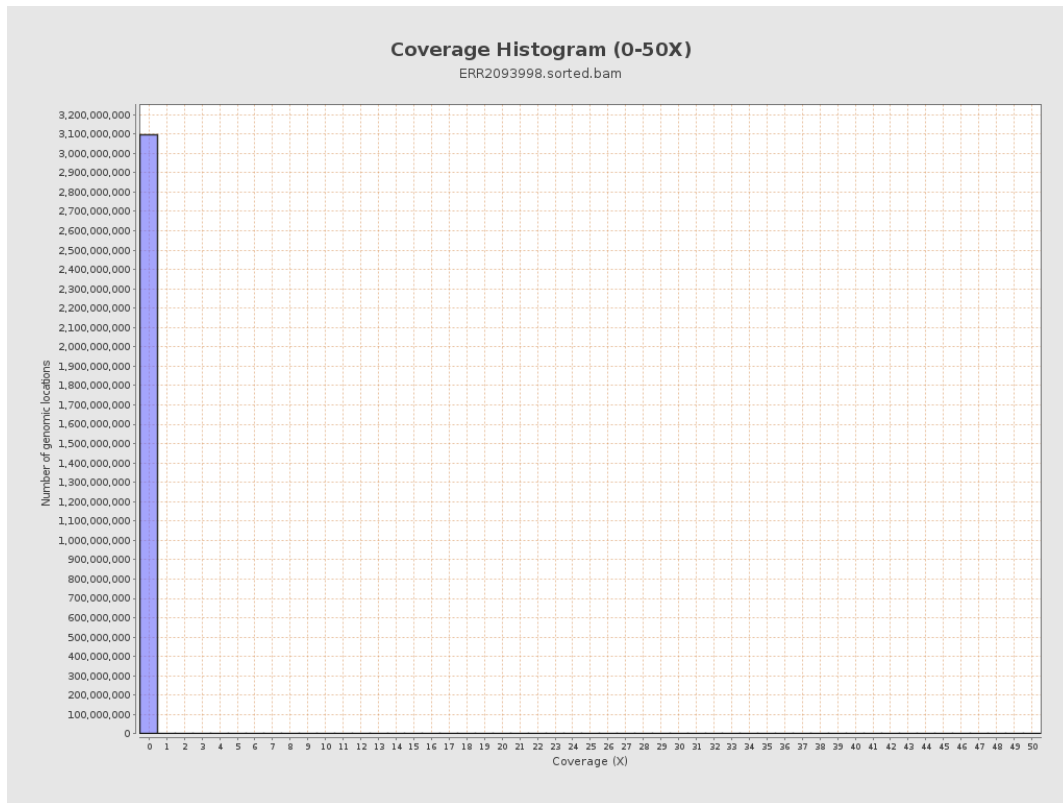
3. Results : Coverage across reference



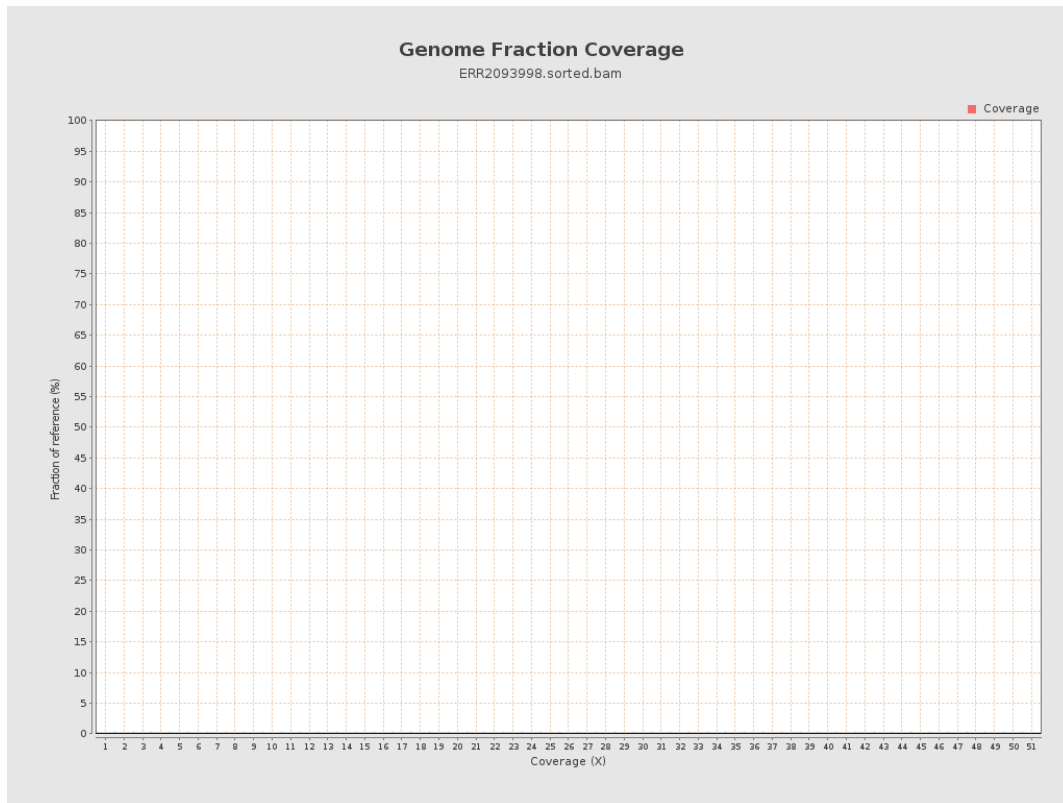
4. Results : Coverage Histogram



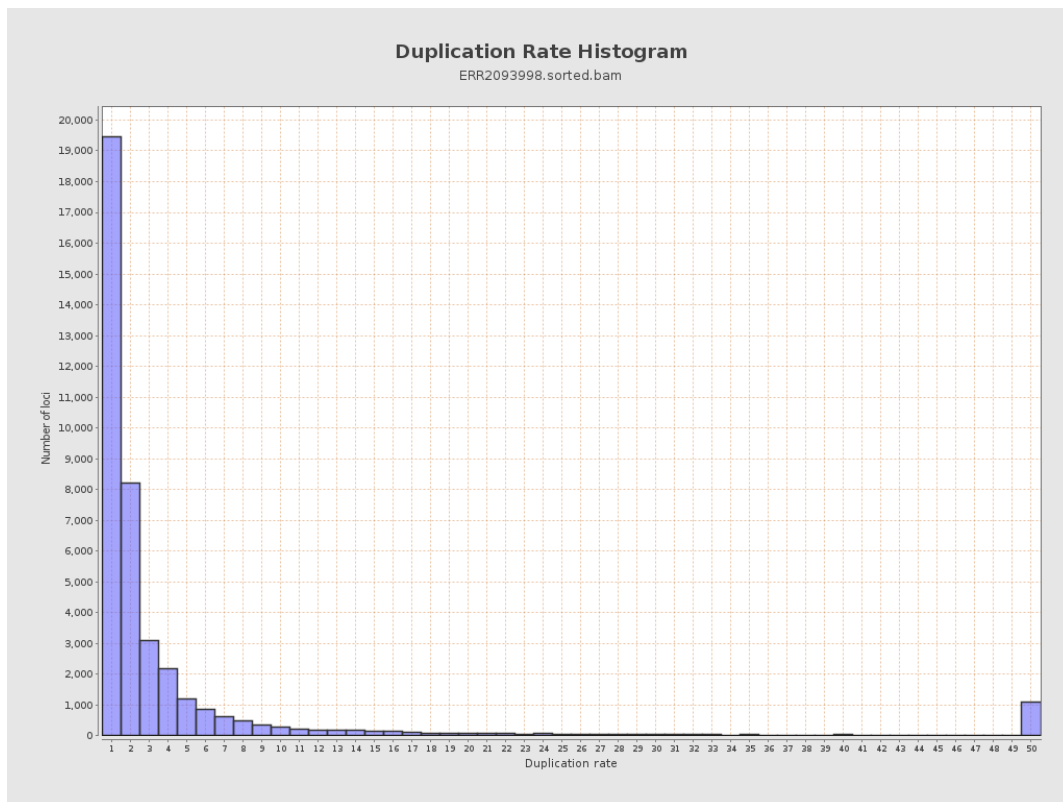
5. Results : Coverage Histogram (0-50X)



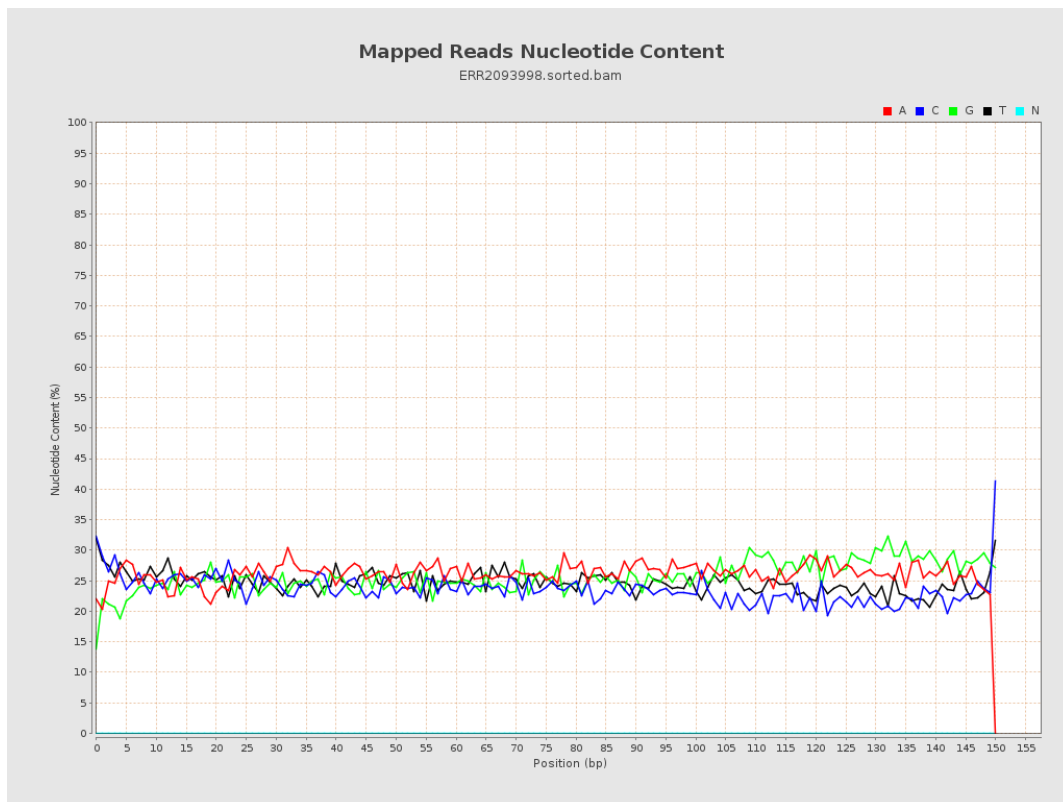
6. Results : Genome Fraction Coverage



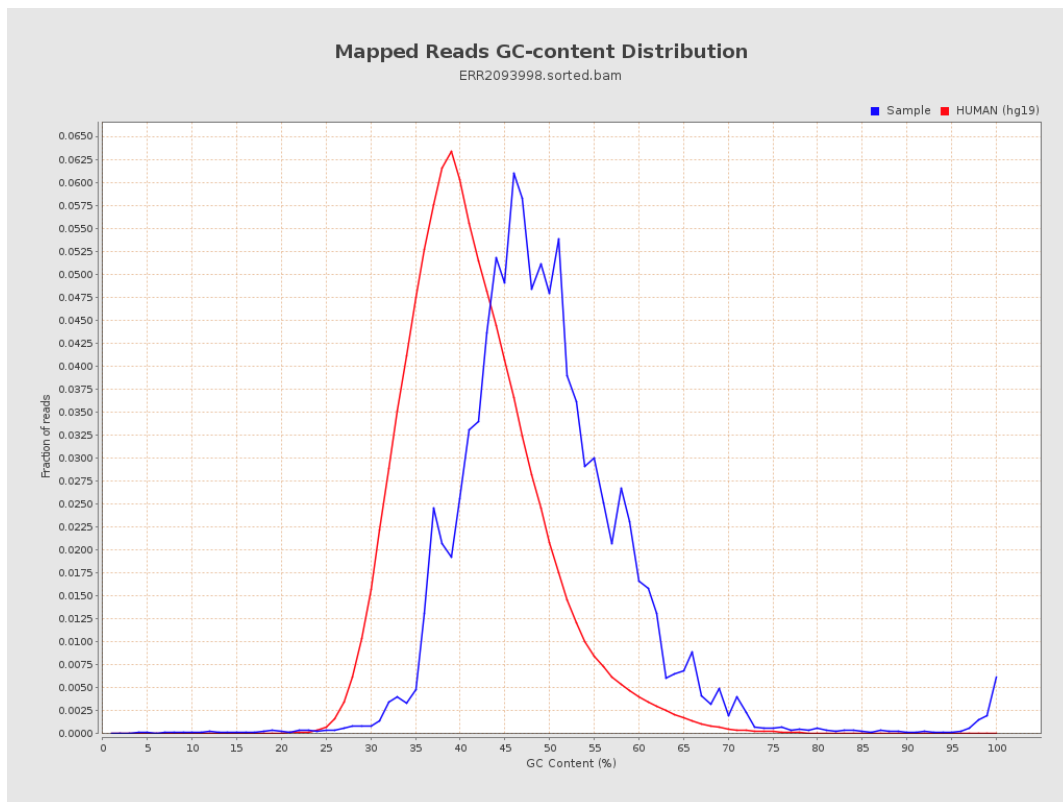
7. Results : Duplication Rate Histogram



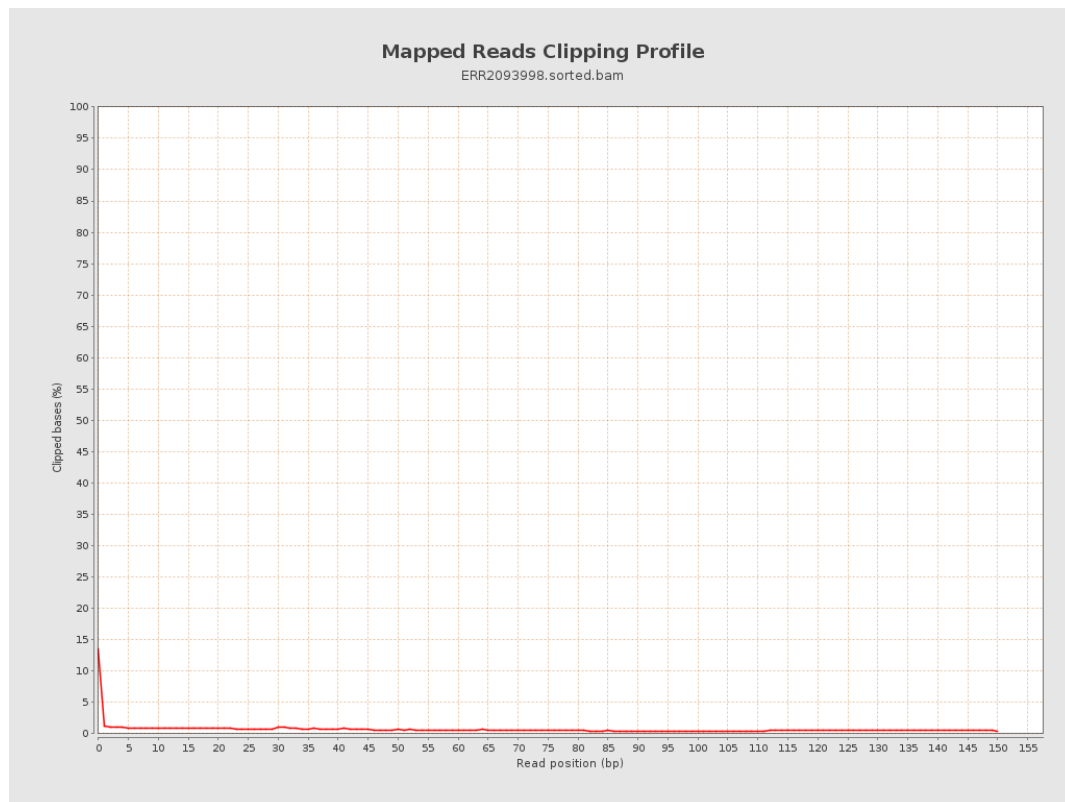
8. Results : Mapped Reads Nucleotide Content



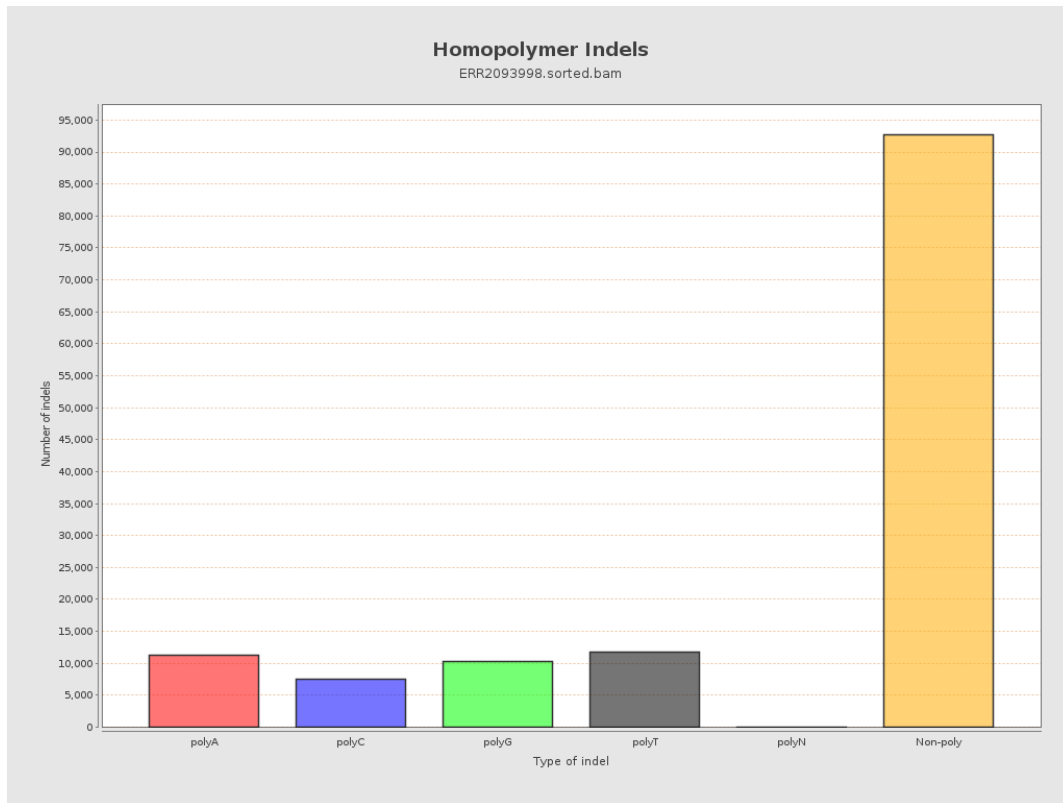
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



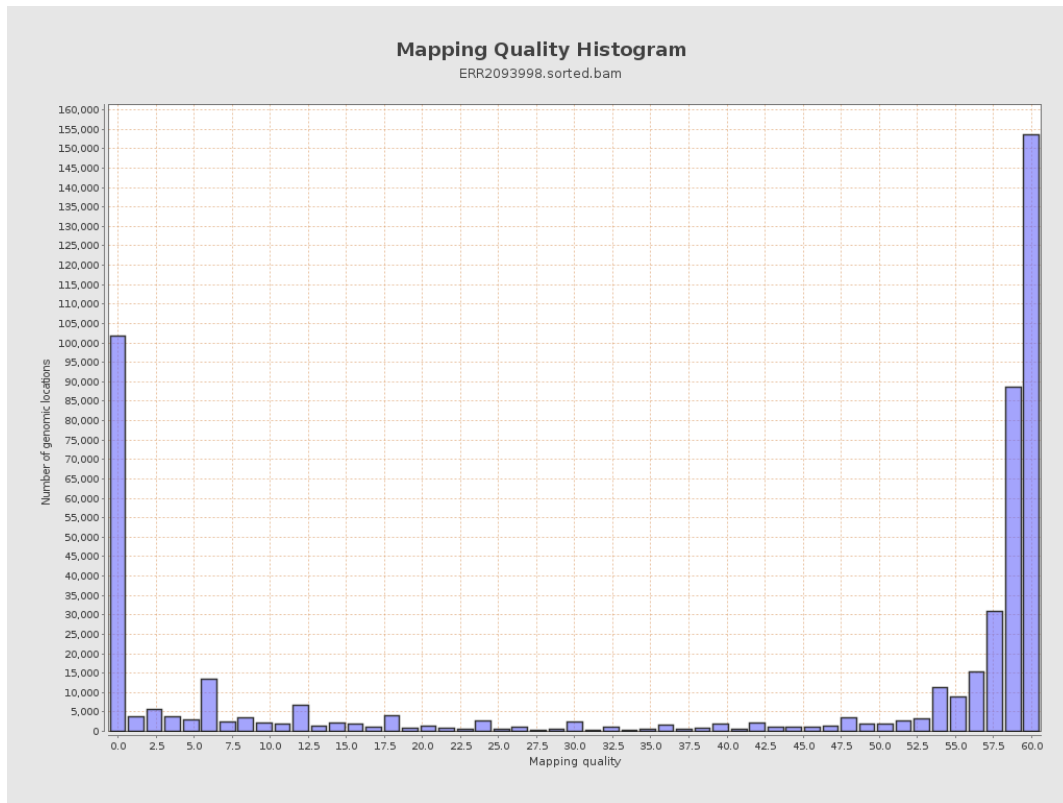
11. Results : Homopolymer Indels



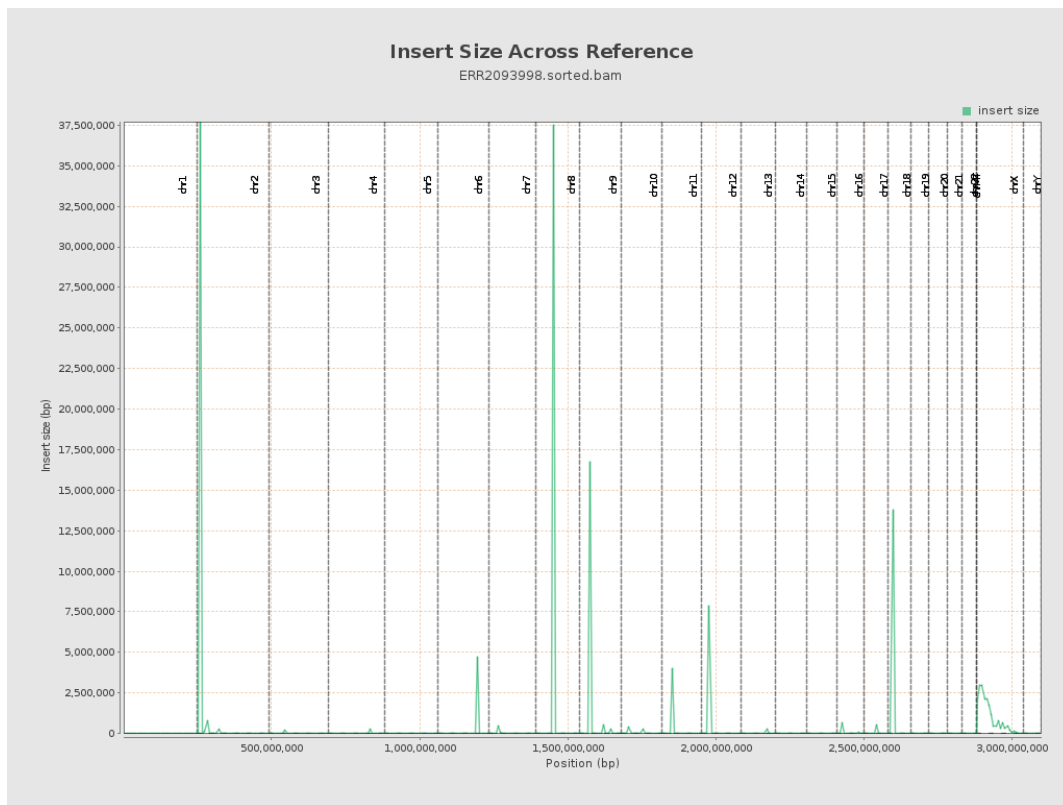
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

