

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:46:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094071.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_ERR2094071 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094071_1.fastq.gz ERR2094071_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:46:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	496,818
Mapped reads	477,307 / 96.07%
Unmapped reads	19,511 / 3.93%
Mapped paired reads	477,307 / 96.07%
Mapped reads, first in pair	239,786 / 48.26%
Mapped reads, second in pair	237,521 / 47.81%
Mapped reads, both in pair	473,950 / 95.4%
Mapped reads, singletons	3,357 / 0.68%
Secondary alignments	0
Supplementary alignments	15,655 / 3.15%
Read min/max/mean length	30 / 151 / 141.11
Duplicated reads (estimated)	459,610 / 92.51%
Duplication rate	49.28%
Clipped reads	185,901 / 37.42%

2.2. ACGT Content

Number/percentage of A's	16,955,767 / 27.5%
Number/percentage of C's	14,061,117 / 22.8%
Number/percentage of T's	15,999,794 / 25.95%
Number/percentage of G's	14,640,953 / 23.75%
Number/percentage of N's	710 / 0%

GC Percentage	46.55%
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2.3. Coverage

Mean	0.0204
Standard Deviation	6.0378

2.4. Mapping Quality

Mean Mapping Quality	36.69
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2.5. Insert size

Mean	387,120.57
Standard Deviation	5,688,845.93
P25/Median/P75	134 / 168 / 197

2.6. Mismatches and indels

General error rate	4.38%
Mismatches	2,611,522
Insertions	45,120
Mapped reads with at least one insertion	9.26%
Deletions	208,323
Mapped reads with at least one deletion	41.6%
Homopolymer indels	27.15%

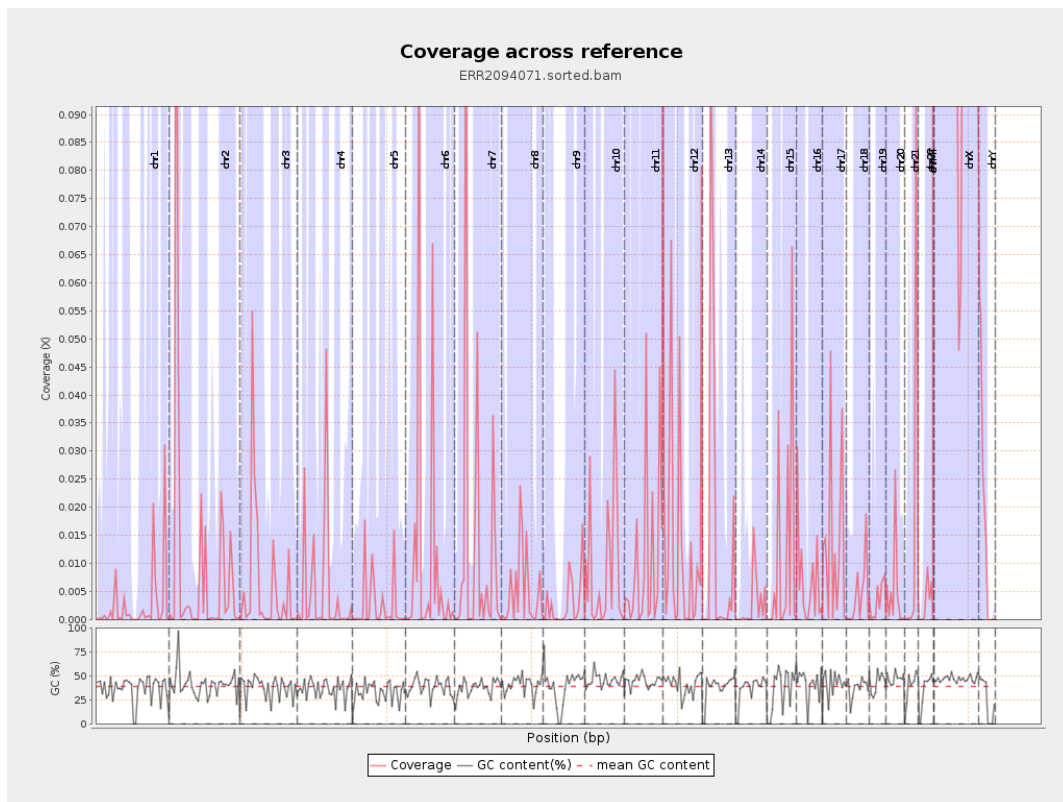
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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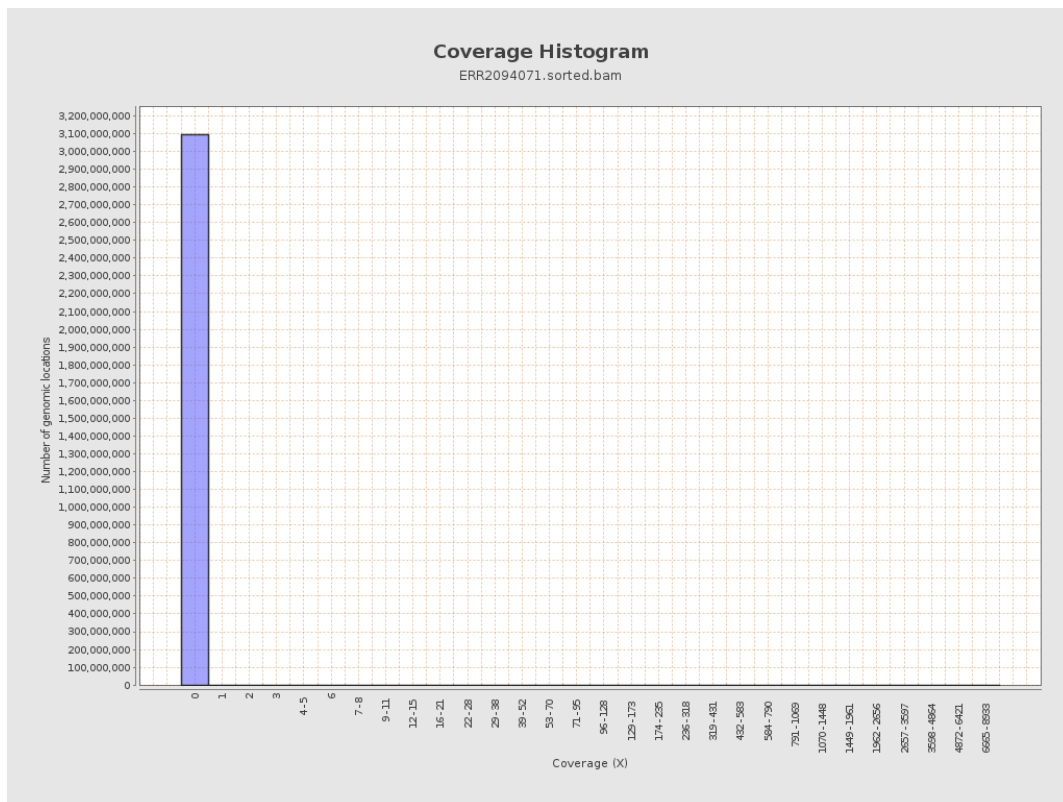
		bases	coverage	deviation
chr1	249250621	641342	0.0026	1.3881
chr2	243199373	2325307	0.0096	3.3629
chr3	198022430	1151574	0.0058	2.6326
chr4	191154276	944791	0.0049	1.9812
chr5	180915260	461514	0.0026	1.115
chr6	171115067	1797170	0.0105	6.0544
chr7	159138663	2128385	0.0134	5.2645
chr8	146364022	728659	0.005	1.3781
chr9	141213431	416954	0.003	1.0912
chr10	135534747	1218685	0.009	2.822
chr11	135006516	1511455	0.0112	3.0253
chr12	133851895	1790364	0.0134	3.8454
chr13	115169878	1425777	0.0124	4.103
chr14	107349540	277994	0.0026	1.1101
chr15	102531392	1115390	0.0109	4.0784
chr16	90354753	555927	0.0062	1.9644
chr17	81195210	1057042	0.013	3.8838
chr18	78077248	326186	0.0042	1.6122
chr19	59128983	191858	0.0032	0.6985
chr20	63025520	327242	0.0052	1.6721
chr21	48129895	759136	0.0158	6.4055
chr22	51304566	154893	0.003	0.8052
chrMT	16571	2190677	132.1994	599.1964
chrX	155270560	38661763	0.249	22.2197

chrY	59373566	1043247	0.0176	4.46
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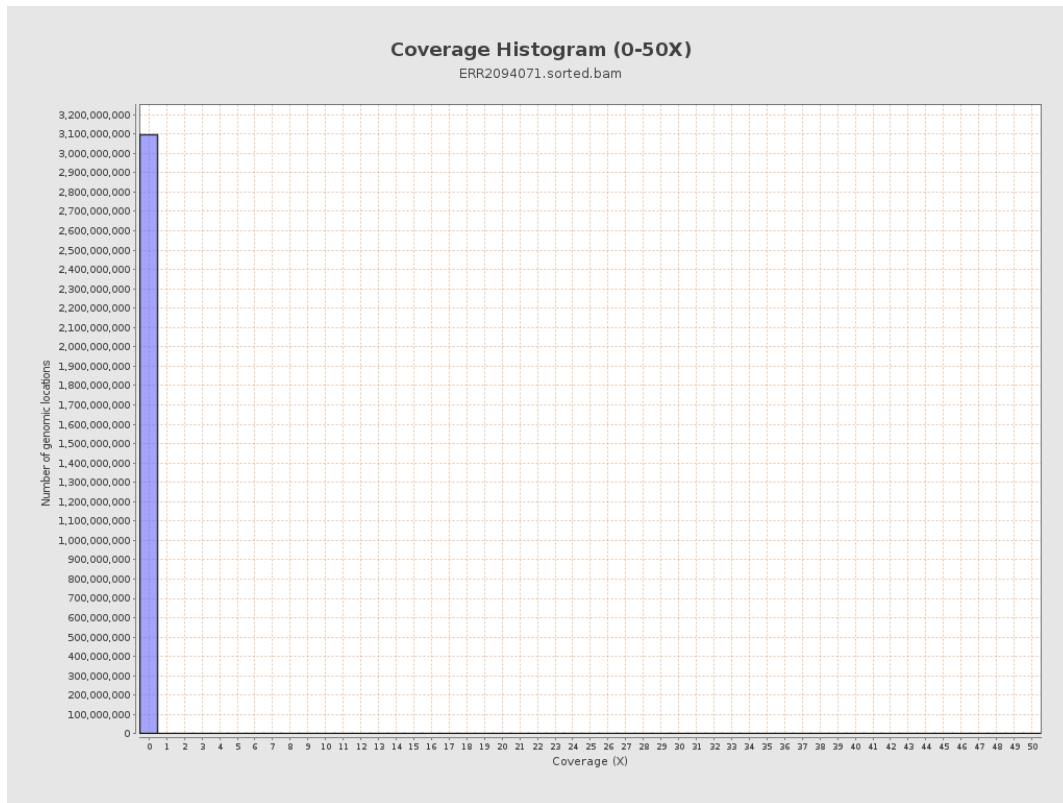
3. Results : Coverage across reference



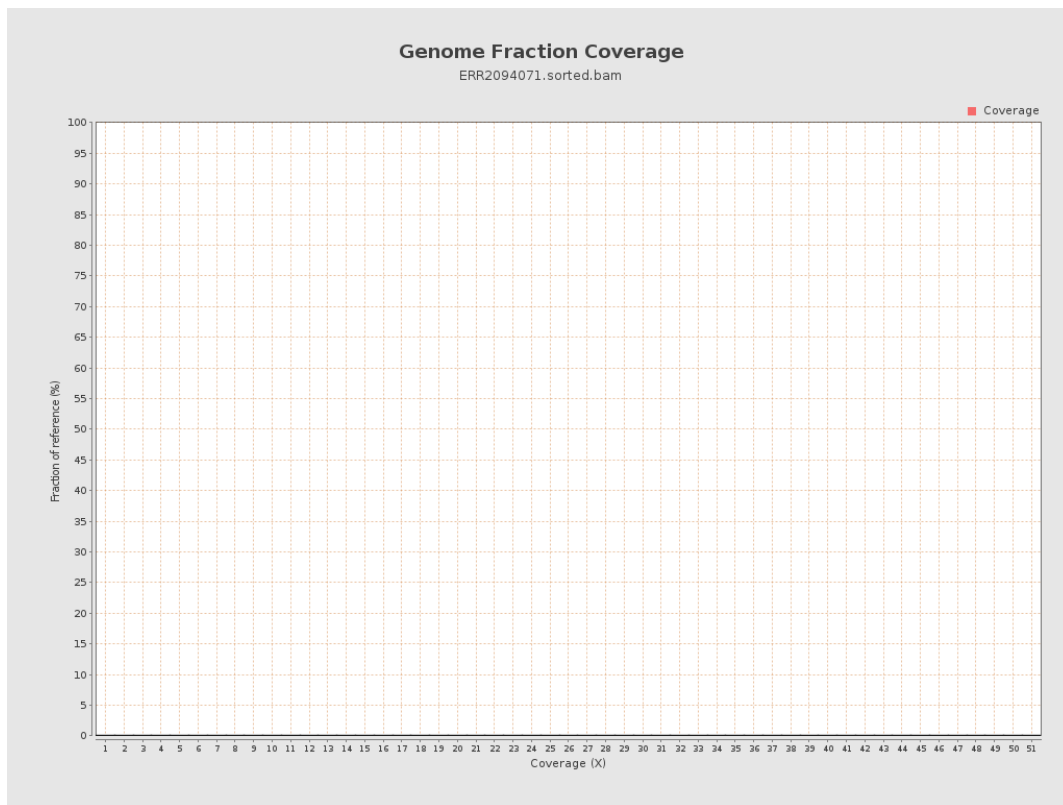
4. Results : Coverage Histogram



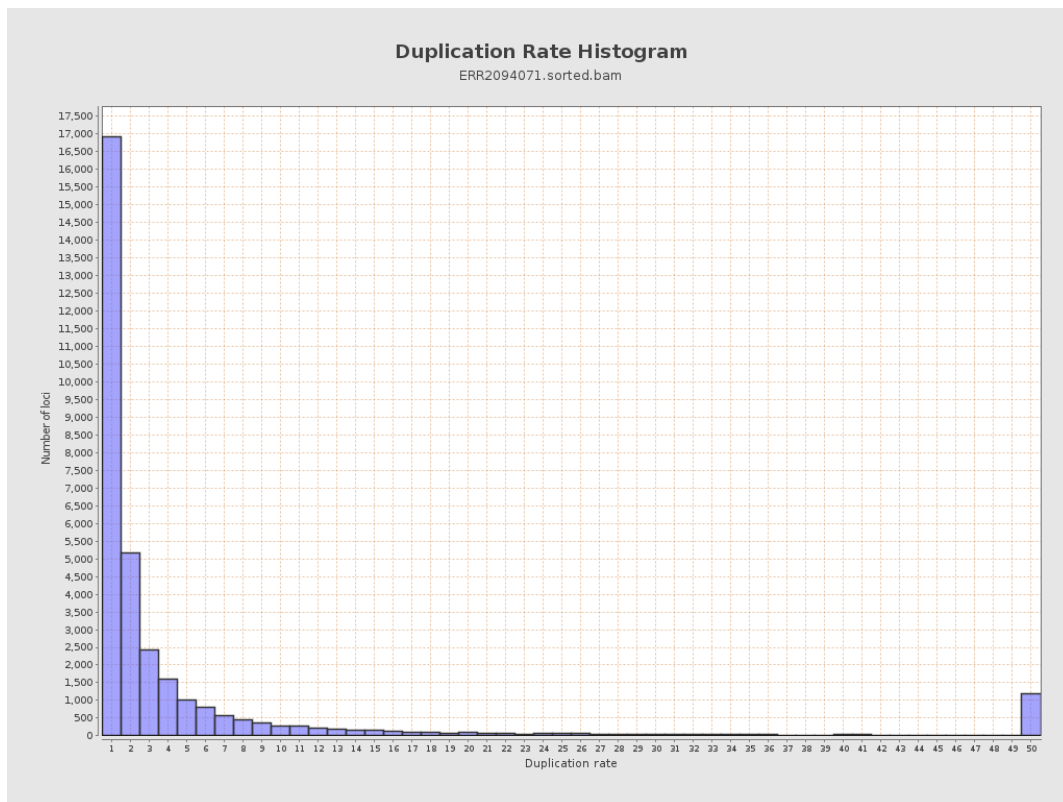
5. Results : Coverage Histogram (0-50X)



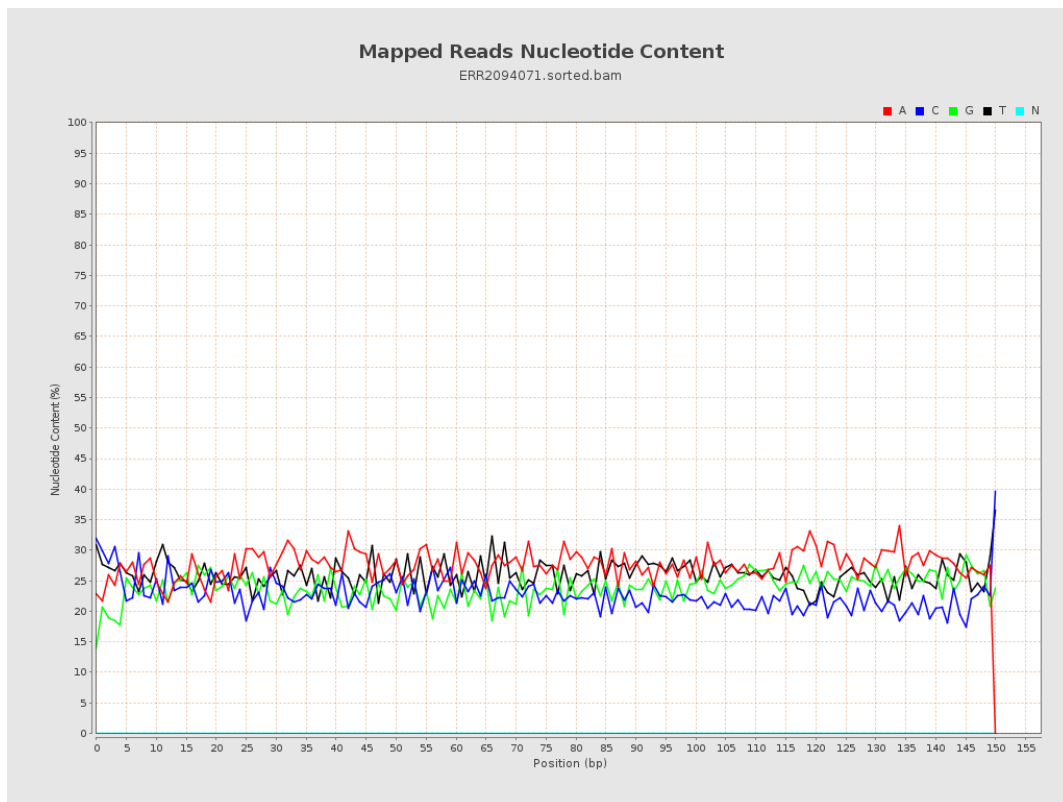
6. Results : Genome Fraction Coverage



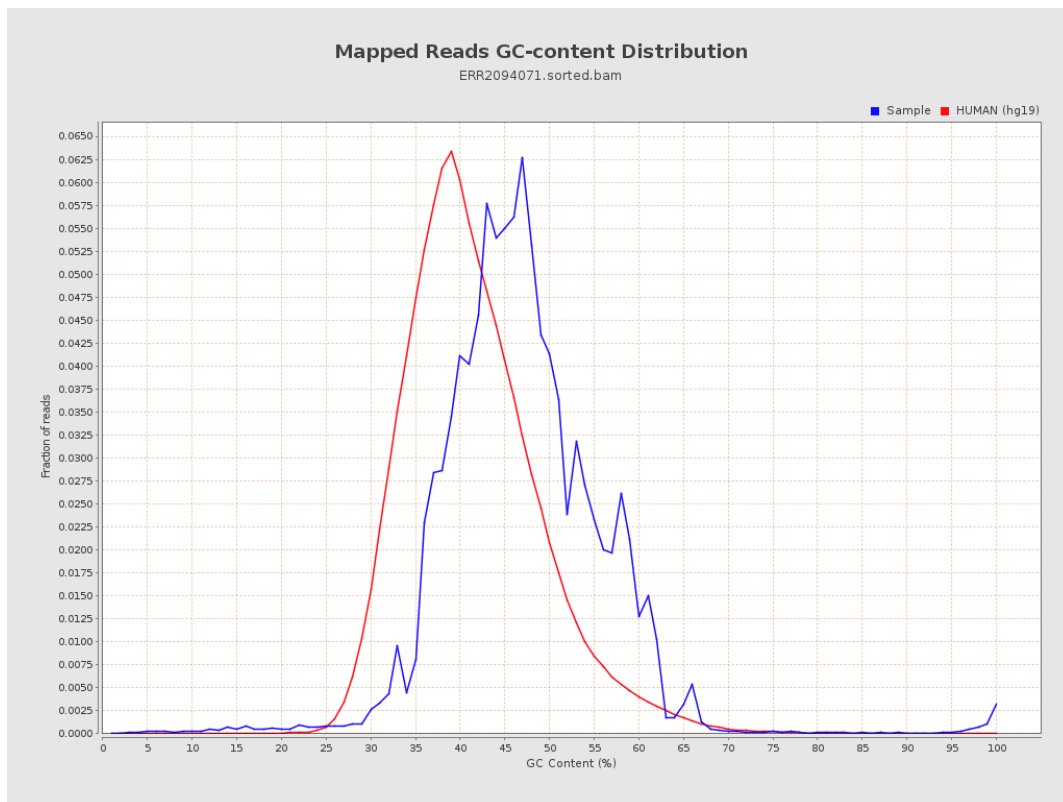
7. Results : Duplication Rate Histogram



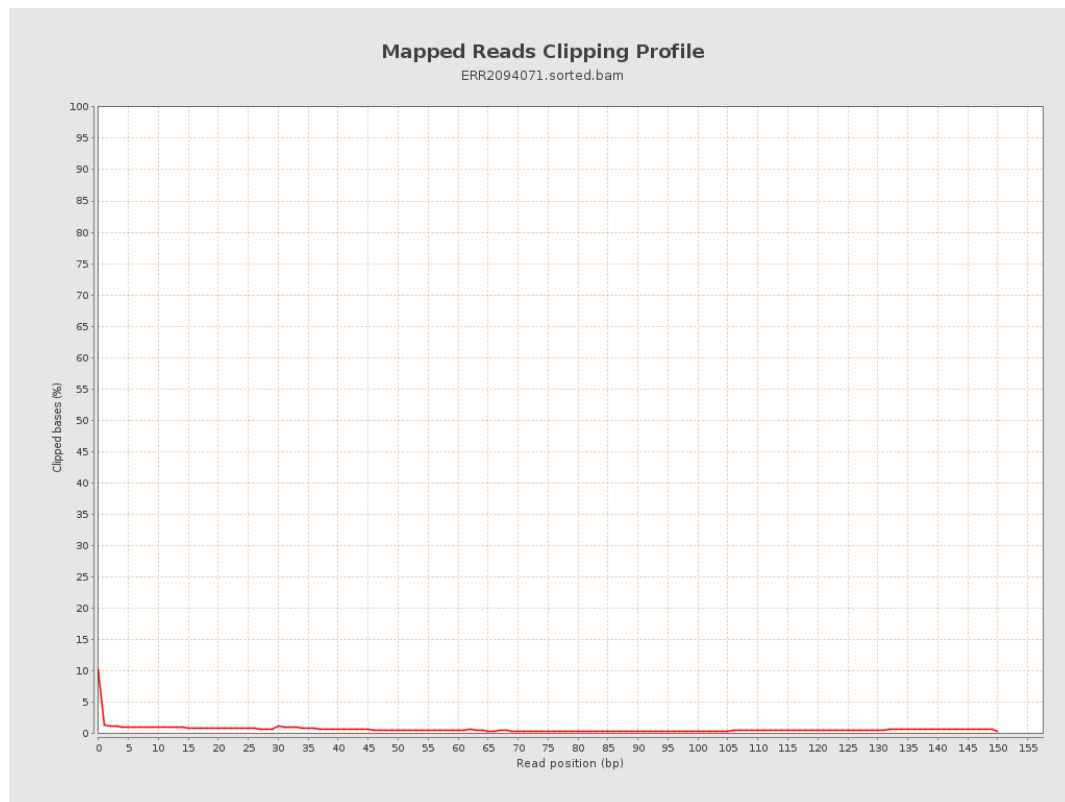
8. Results : Mapped Reads Nucleotide Content



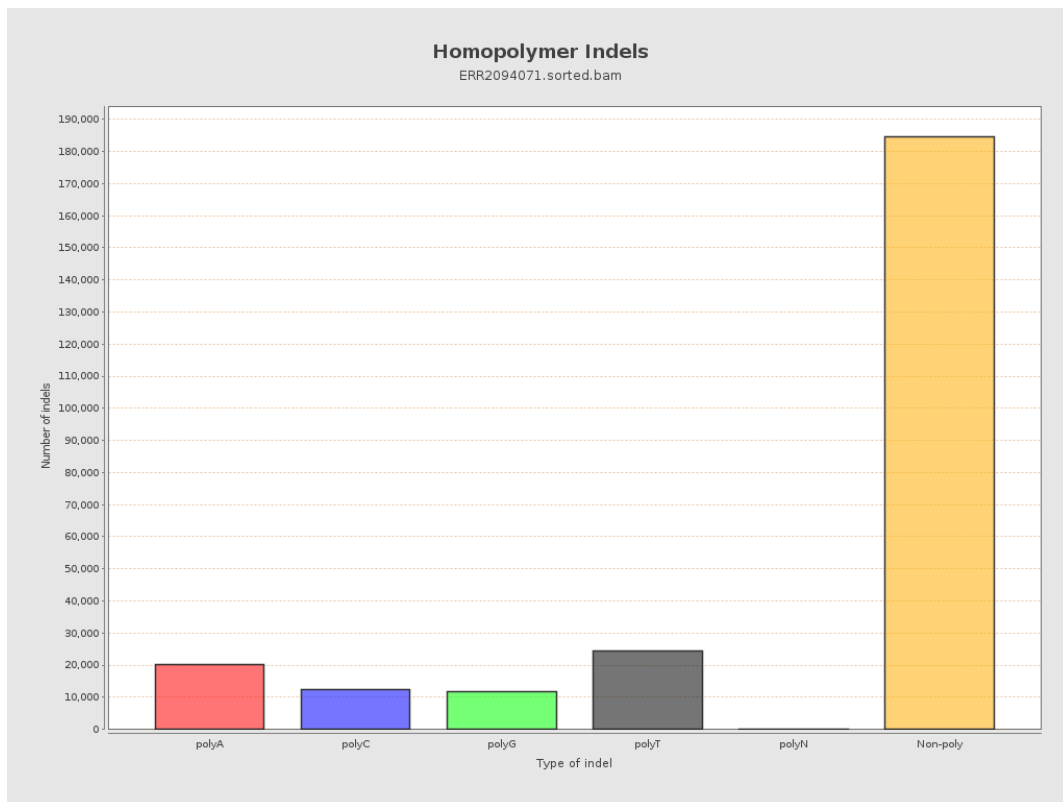
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



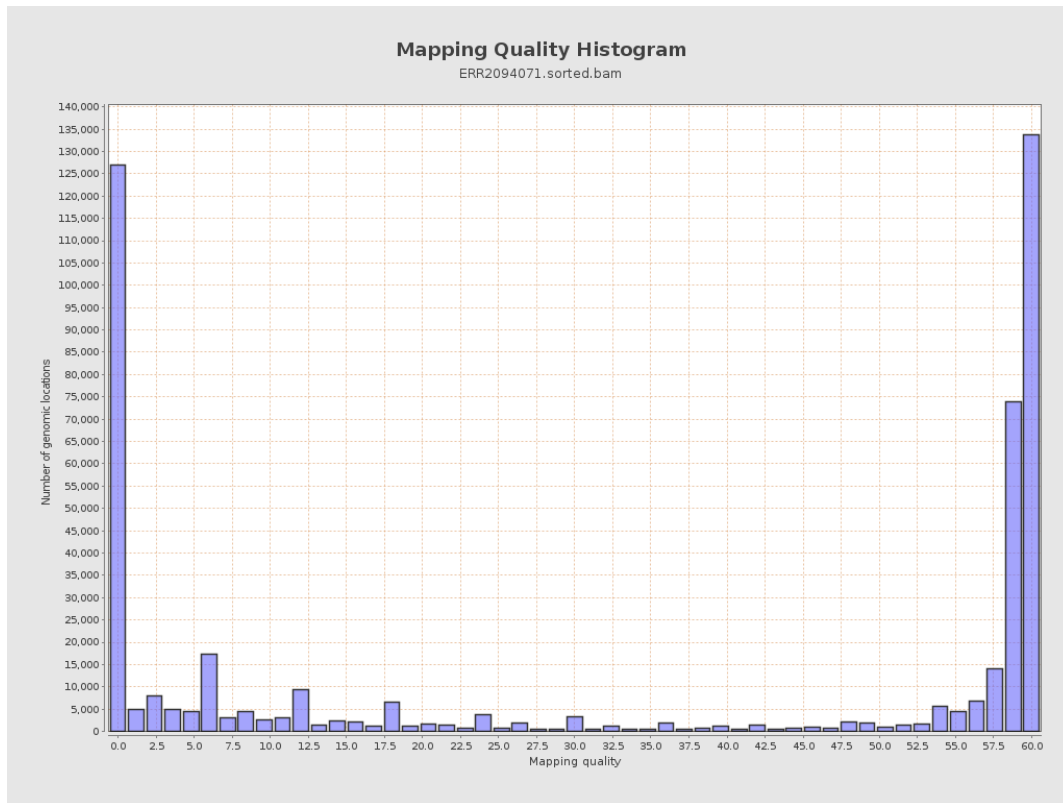
11. Results : Homopolymer Indels



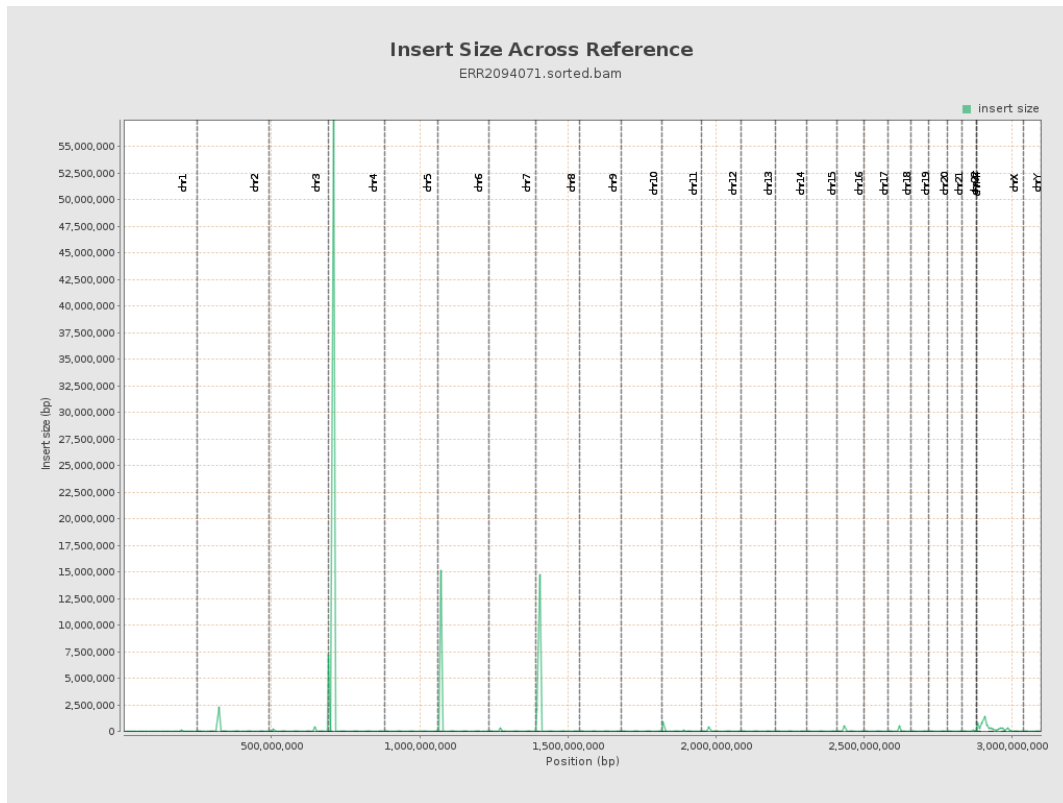
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

