

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:57:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093989.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_ERR2093989 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093989_1.fastq.gz ERR2093989_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:57:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	273,378
Mapped reads	259,461 / 94.91%
Unmapped reads	13,917 / 5.09%
Mapped paired reads	259,461 / 94.91%
Mapped reads, first in pair	130,411 / 47.7%
Mapped reads, second in pair	129,050 / 47.21%
Mapped reads, both in pair	257,256 / 94.1%
Mapped reads, singletons	2,205 / 0.81%
Secondary alignments	0
Supplementary alignments	14,930 / 5.46%
Read min/max/mean length	30 / 151 / 139.9
Duplicated reads (estimated)	241,156 / 88.21%
Duplication rate	49.54%
Clipped reads	124,049 / 45.38%

2.2. ACGT Content

Number/percentage of A's	8,674,339 / 26.63%
Number/percentage of C's	7,618,524 / 23.39%
Number/percentage of T's	8,183,904 / 25.12%
Number/percentage of G's	8,098,468 / 24.86%
Number/percentage of N's	395 / 0%

GC Percentage	48.25%
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2.3. Coverage

Mean	0.0107
Standard Deviation	2.2324

2.4. Mapping Quality

Mean Mapping Quality	39.69
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2.5. Insert size

Mean	979,949.44
Standard Deviation	9,117,961.61
P25/Median/P75	125 / 159 / 201

2.6. Mismatches and indels

General error rate	3.45%
Mismatches	1,082,578
Insertions	18,061
Mapped reads with at least one insertion	6.85%
Deletions	89,614
Mapped reads with at least one deletion	33.17%
Homopolymer indels	29.43%

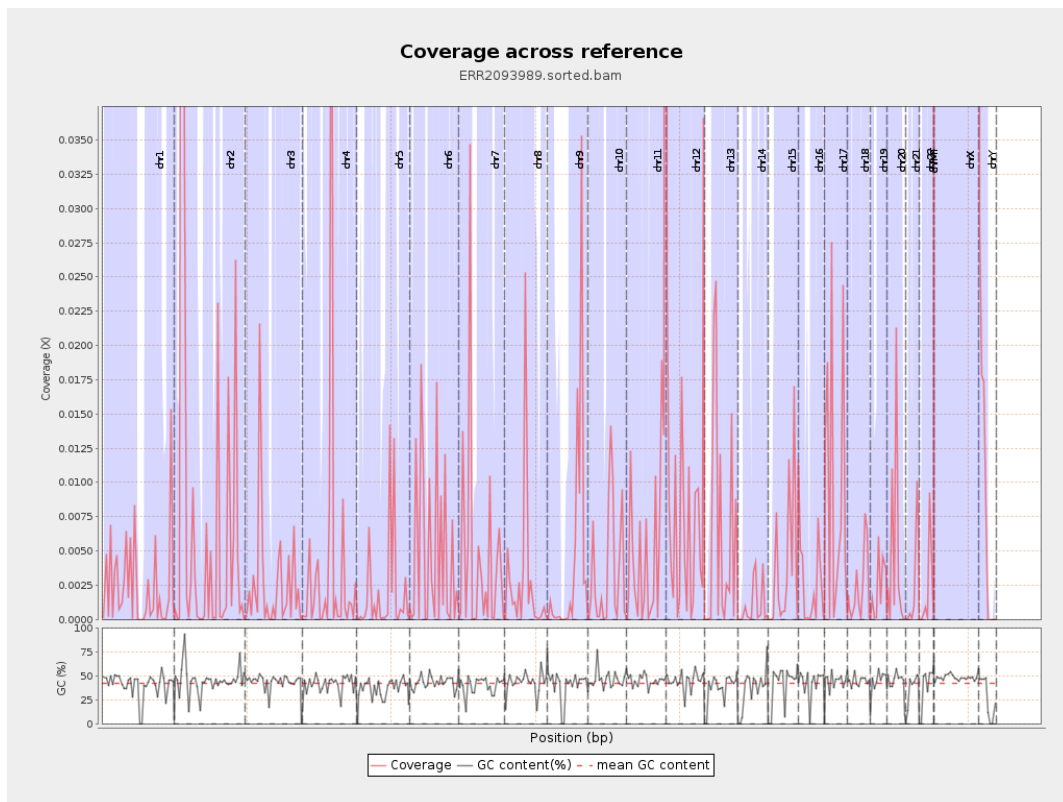
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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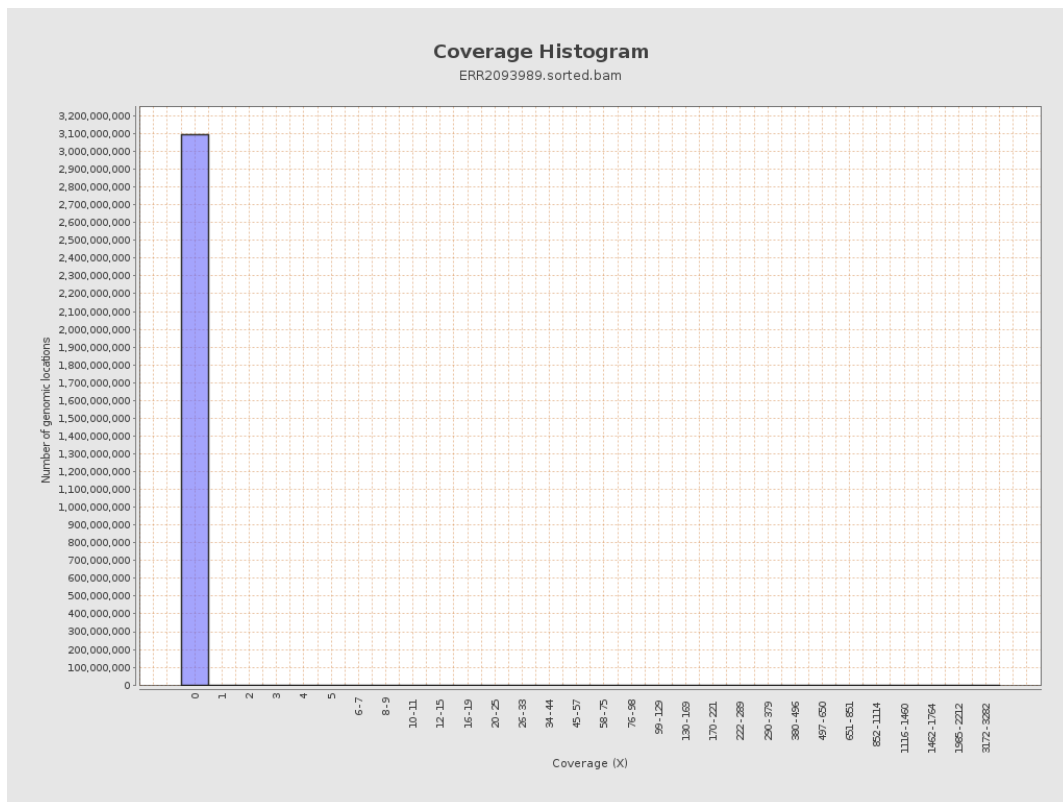
		bases	coverage	deviation
chr1	249250621	606567	0.0024	0.8243
chr2	243199373	1927217	0.0079	2.5615
chr3	198022430	490773	0.0025	0.8165
chr4	191154276	806850	0.0042	1.3742
chr5	180915260	360383	0.002	0.973
chr6	171115067	836019	0.0049	1.4665
chr7	159138663	702881	0.0044	1.4168
chr8	146364022	383949	0.0026	1.0724
chr9	141213431	591220	0.0042	1.3612
chr10	135534747	477297	0.0035	0.941
chr11	135006516	854421	0.0063	1.7033
chr12	133851895	959196	0.0072	1.6818
chr13	115169878	702665	0.0061	1.813
chr14	107349540	107798	0.001	0.3476
chr15	102531392	374413	0.0037	0.9434
chr16	90354753	244830	0.0027	0.7578
chr17	81195210	786615	0.0097	2.5264
chr18	78077248	192056	0.0025	0.6741
chr19	59128983	134254	0.0023	0.5852
chr20	63025520	295230	0.0047	1.668
chr21	48129895	125661	0.0026	0.4852
chr22	51304566	95362	0.0019	0.6027
chrMT	16571	1296568	78.2432	337.6994
chrX	155270560	19320171	0.1244	6.9626

chrY	59373566	486844	0.0082	1.6268
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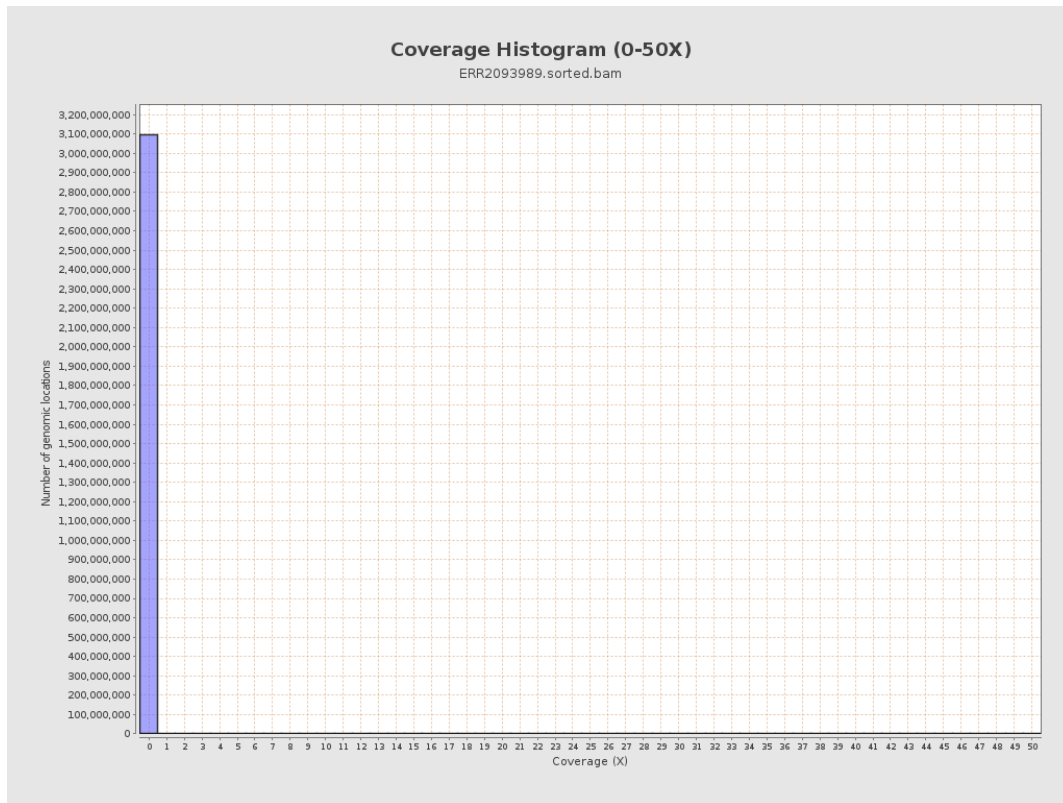
3. Results : Coverage across reference



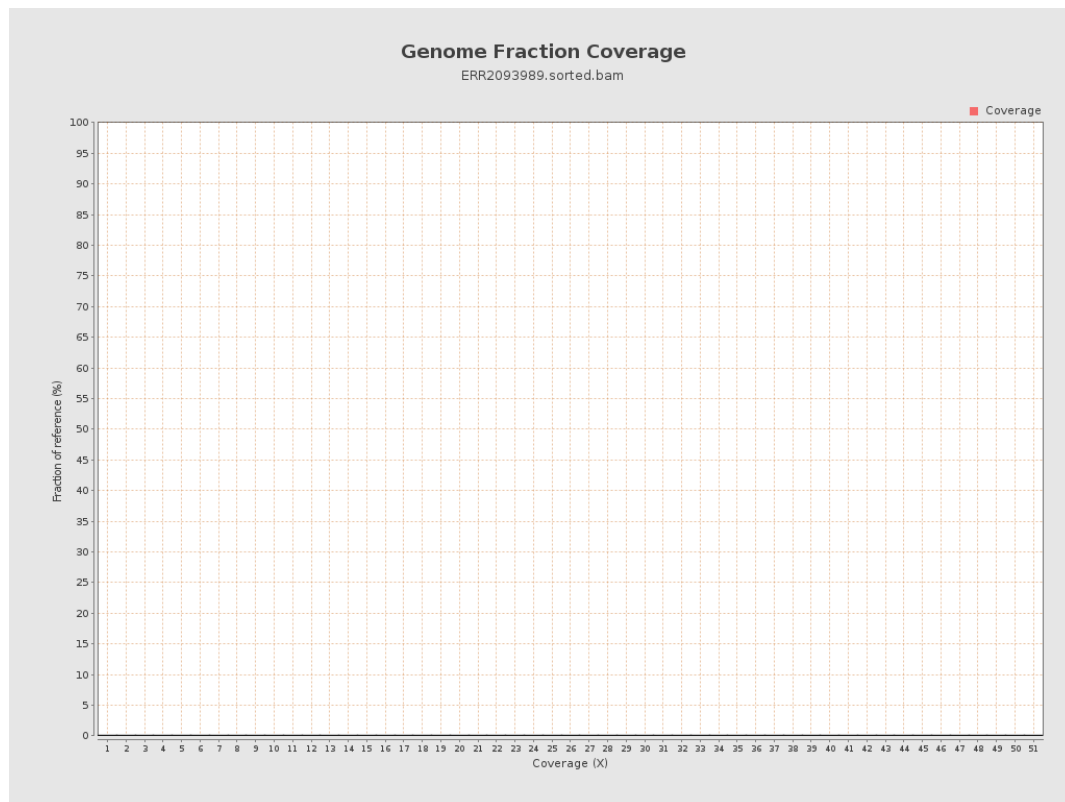
4. Results : Coverage Histogram



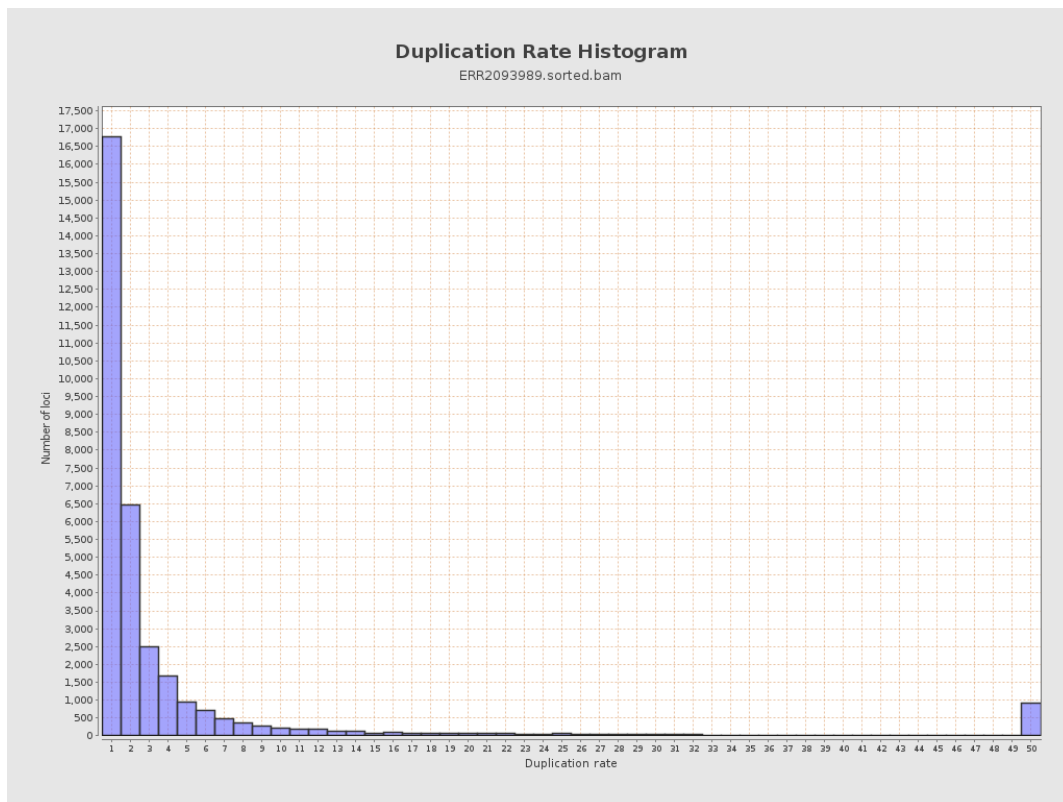
5. Results : Coverage Histogram (0-50X)



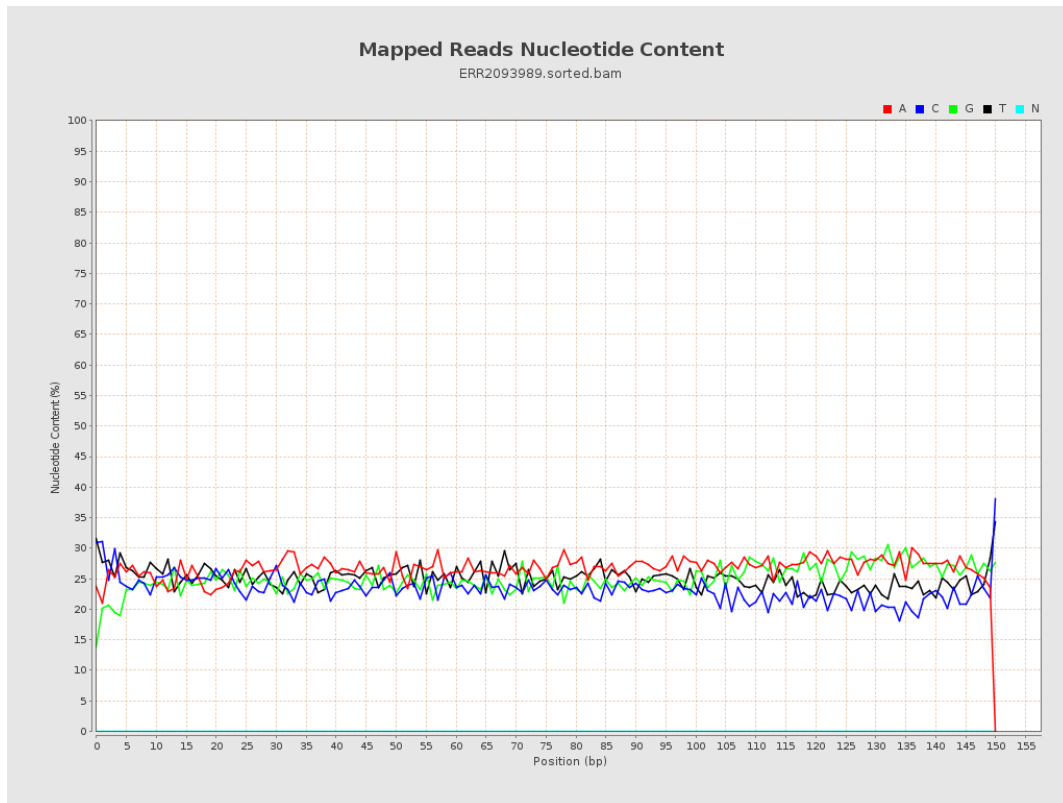
6. Results : Genome Fraction Coverage



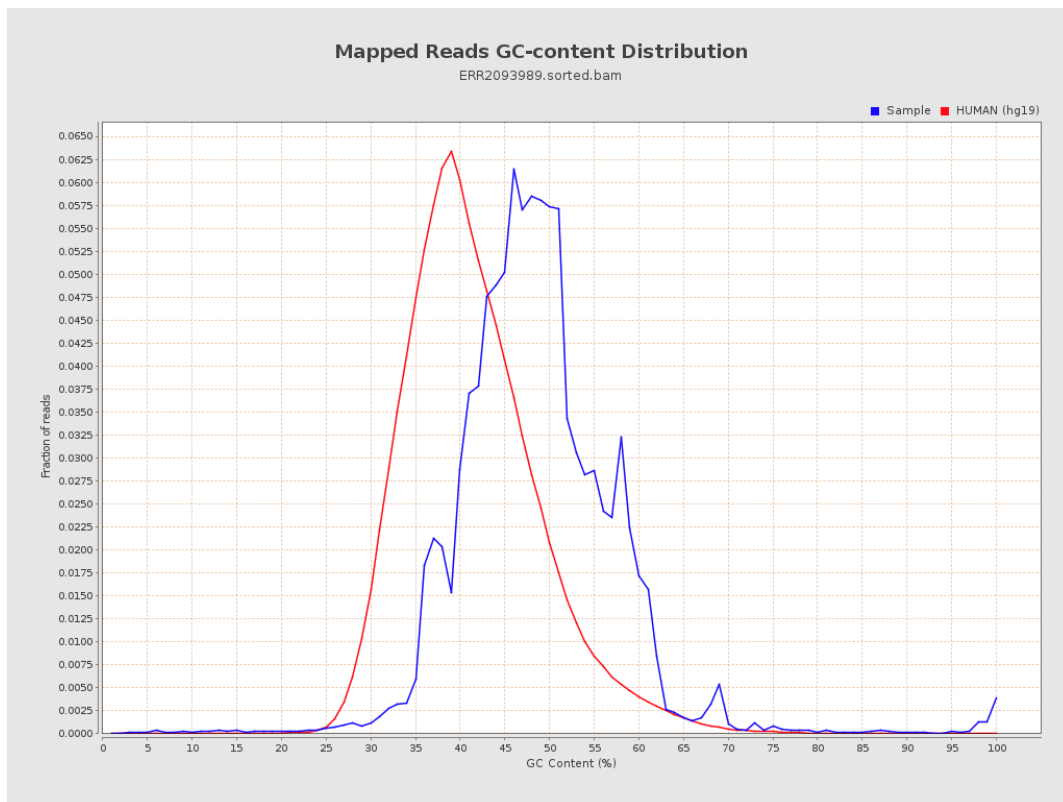
7. Results : Duplication Rate Histogram



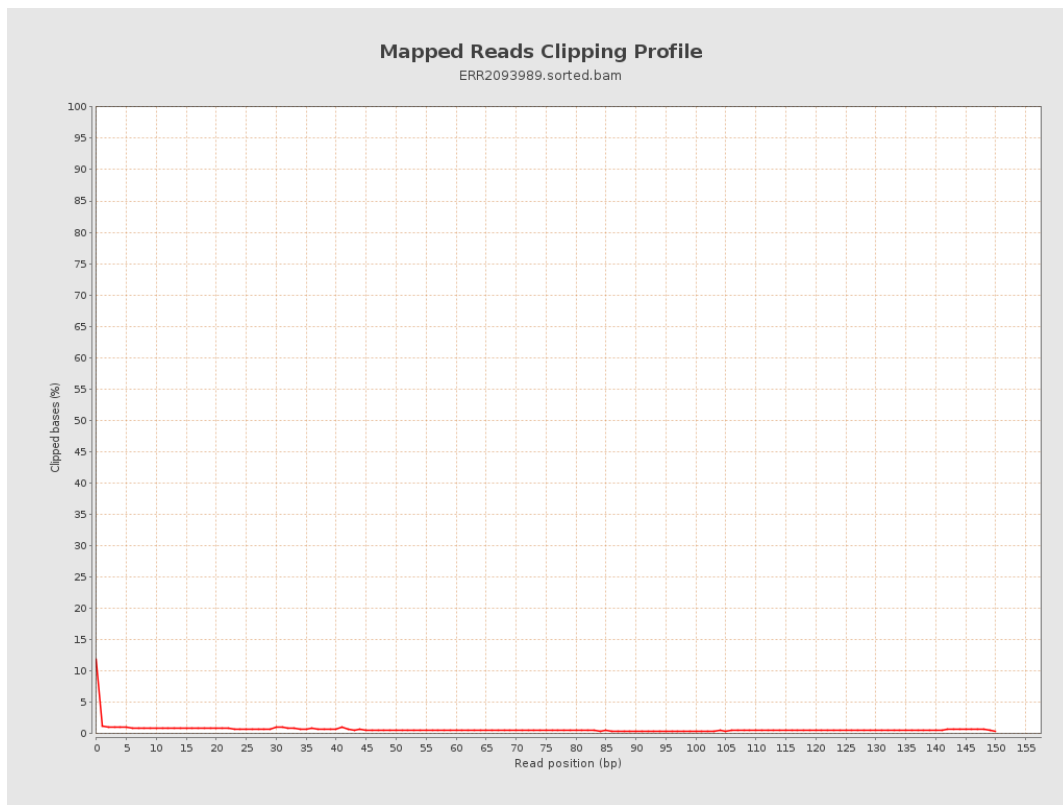
8. Results : Mapped Reads Nucleotide Content



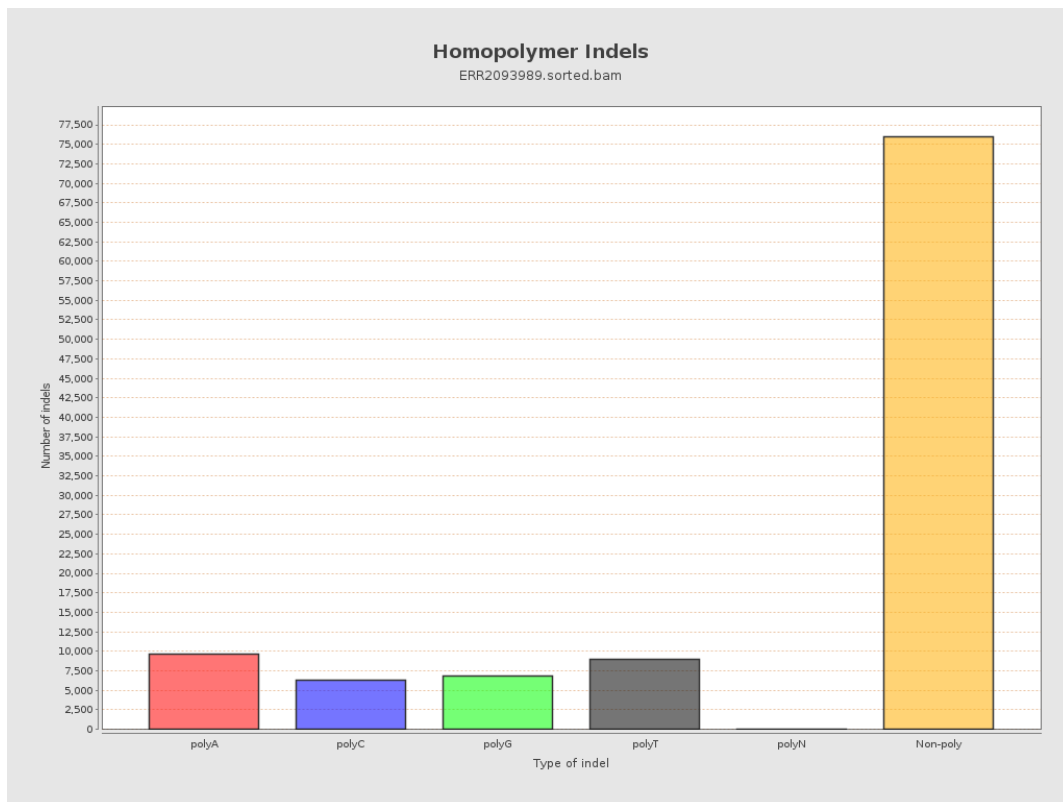
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



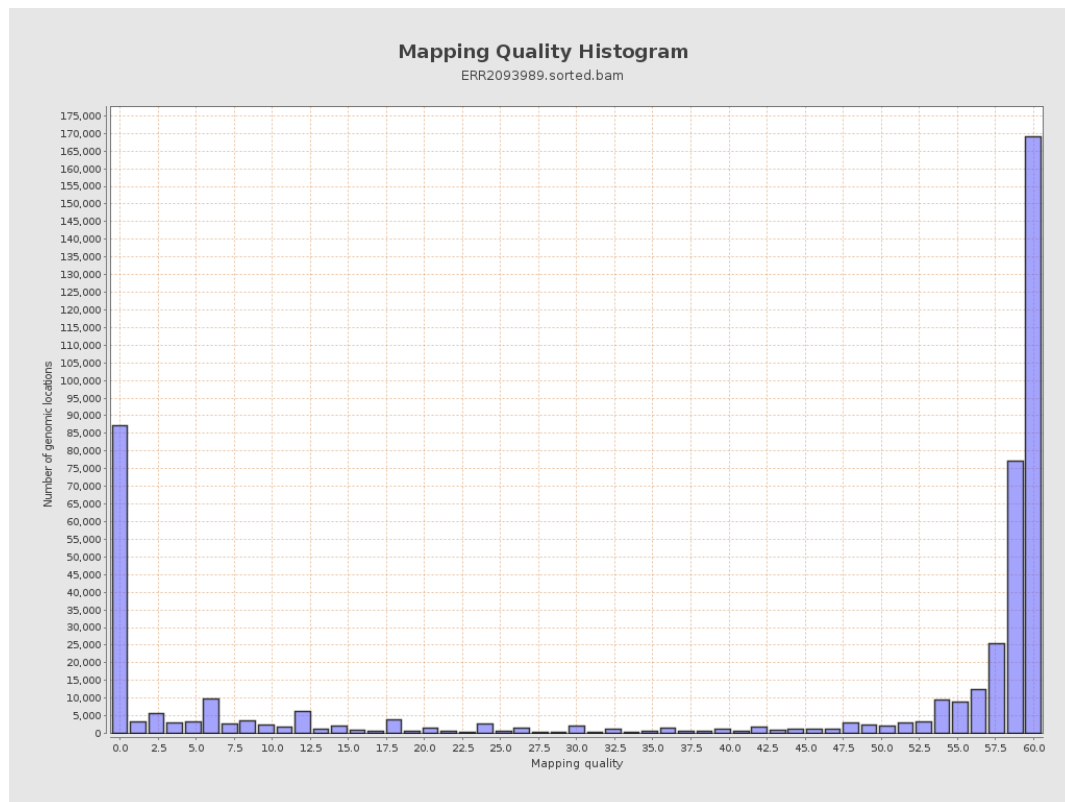
11. Results : Homopolymer Indels



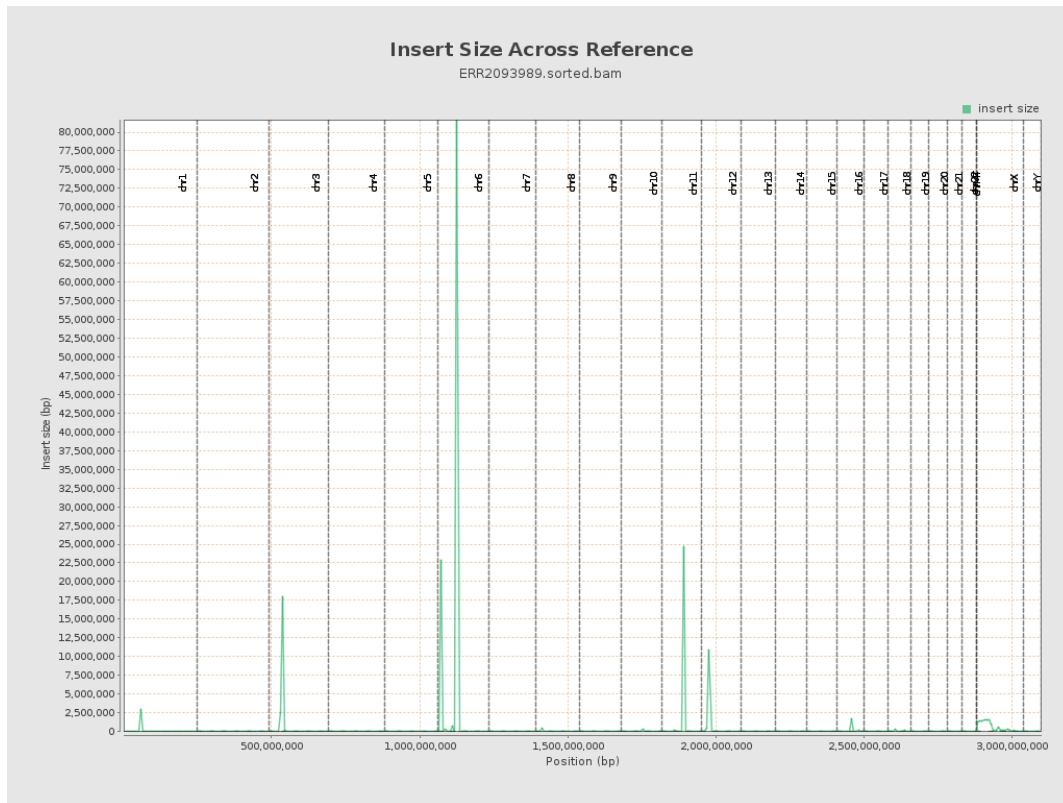
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

