

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:37:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094067.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_ERR2094067 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094067_1.fastq.gz ERR2094067_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:37:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094067.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	325,858
Mapped reads	314,425 / 96.49%
Unmapped reads	11,433 / 3.51%
Mapped paired reads	314,425 / 96.49%
Mapped reads, first in pair	157,899 / 48.46%
Mapped reads, second in pair	156,526 / 48.04%
Mapped reads, both in pair	312,426 / 95.88%
Mapped reads, singletons	1,999 / 0.61%
Secondary alignments	0
Supplementary alignments	10,701 / 3.28%
Read min/max/mean length	30 / 151 / 143.63
Duplicated reads (estimated)	297,225 / 91.21%
Duplication rate	50.09%
Clipped reads	120,692 / 37.04%

2.2. ACGT Content

Number/percentage of A's	10,976,031 / 26.36%
Number/percentage of C's	9,803,866 / 23.54%
Number/percentage of T's	10,580,347 / 25.41%
Number/percentage of G's	10,278,187 / 24.68%
Number/percentage of N's	479 / 0%

GC Percentage	48.23%
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2.3. Coverage

Mean	0.0137
Standard Deviation	3.733

2.4. Mapping Quality

Mean Mapping Quality	37.36
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2.5. Insert size

Mean	440,787.93
Standard Deviation	6,094,499.15
P25/Median/P75	147 / 172 / 204

2.6. Mismatches and indels

General error rate	3.84%
Mismatches	1,547,907
Insertions	23,763
Mapped reads with at least one insertion	7.42%
Deletions	124,434
Mapped reads with at least one deletion	37.57%
Homopolymer indels	26.03%

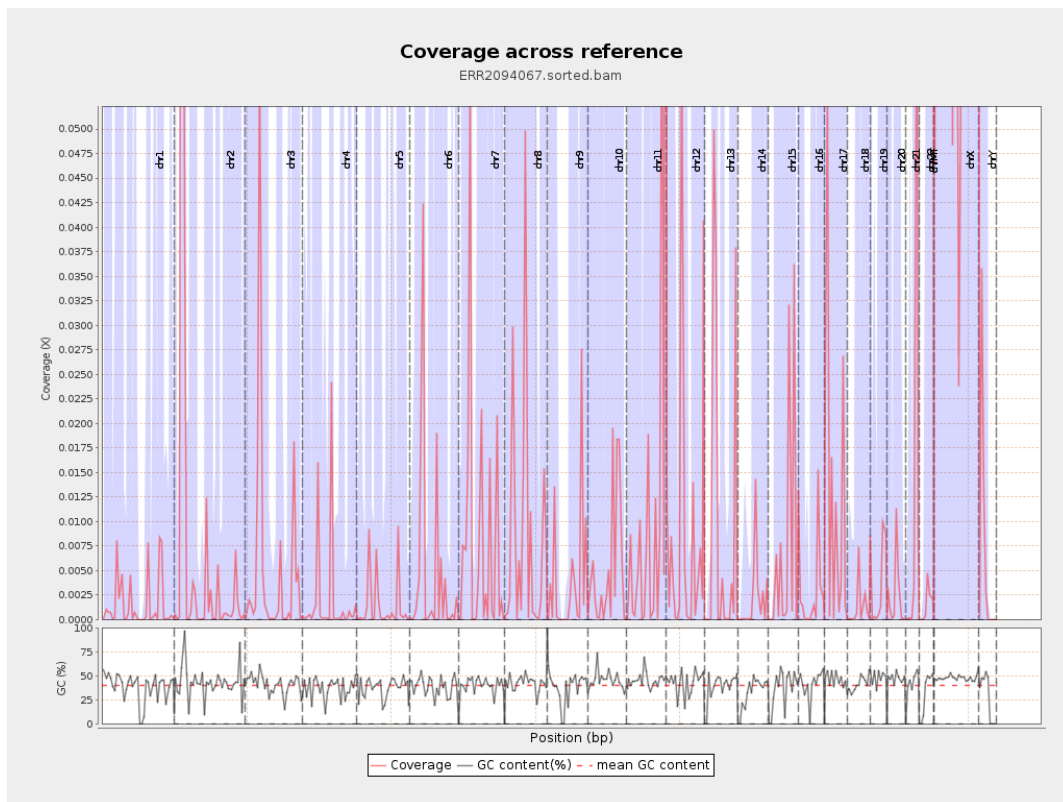
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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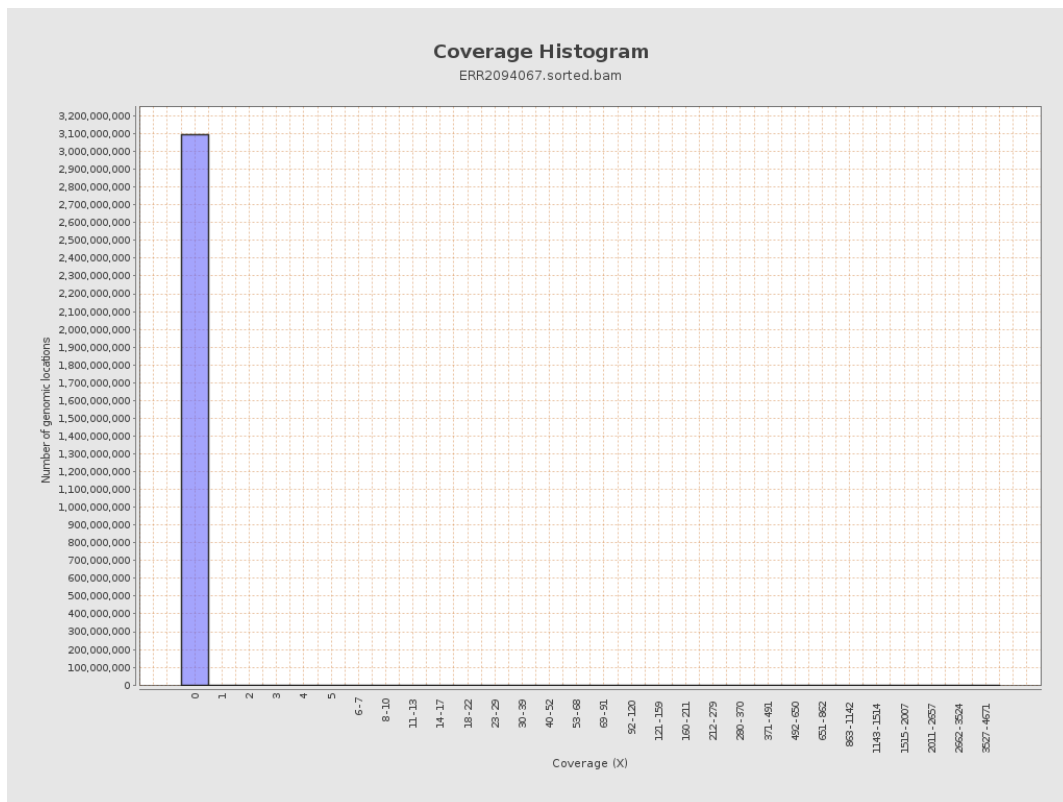
		bases	coverage	deviation
chr1	249250621	387823	0.0016	0.5998
chr2	243199373	1839999	0.0076	3.2269
chr3	198022430	955525	0.0048	2.1557
chr4	191154276	373655	0.002	0.9034
chr5	180915260	255428	0.0014	0.6333
chr6	171115067	804763	0.0047	2.2294
chr7	159138663	1210185	0.0076	2.6937
chr8	146364022	1185363	0.0081	2.5333
chr9	141213431	534641	0.0038	1.4542
chr10	135534747	681256	0.005	1.6044
chr11	135006516	1316291	0.0097	2.6258
chr12	133851895	1029971	0.0077	2.9456
chr13	115169878	1037043	0.009	2.9058
chr14	107349540	232677	0.0022	0.9116
chr15	102531392	663376	0.0065	2.198
chr16	90354753	268921	0.003	1.0298
chr17	81195210	1084227	0.0134	3.4933
chr18	78077248	100396	0.0013	0.5596
chr19	59128983	186204	0.0031	0.8535
chr20	63025520	153499	0.0024	0.6894
chr21	48129895	663957	0.0138	6.1605
chr22	51304566	75161	0.0015	0.3335
chrMT	16571	1332118	80.3885	387.9406
chrX	155270560	25714058	0.1656	13.0069

chrY	59373566	401080	0.0068	2.0046
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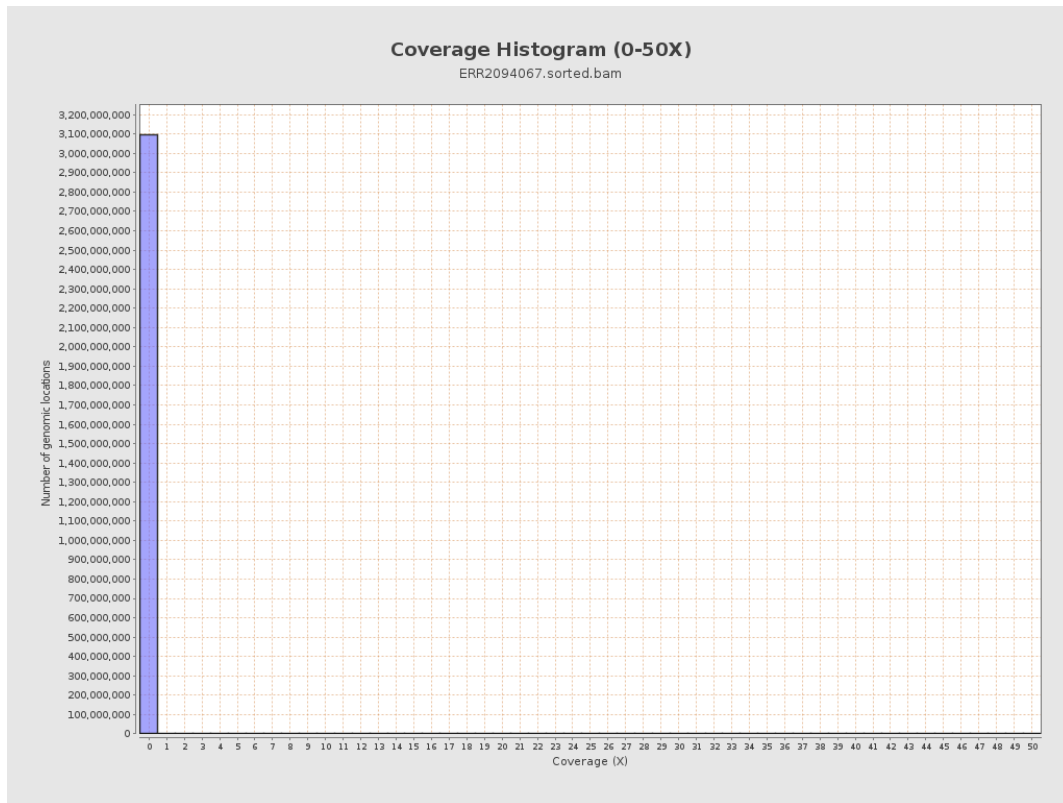
3. Results : Coverage across reference



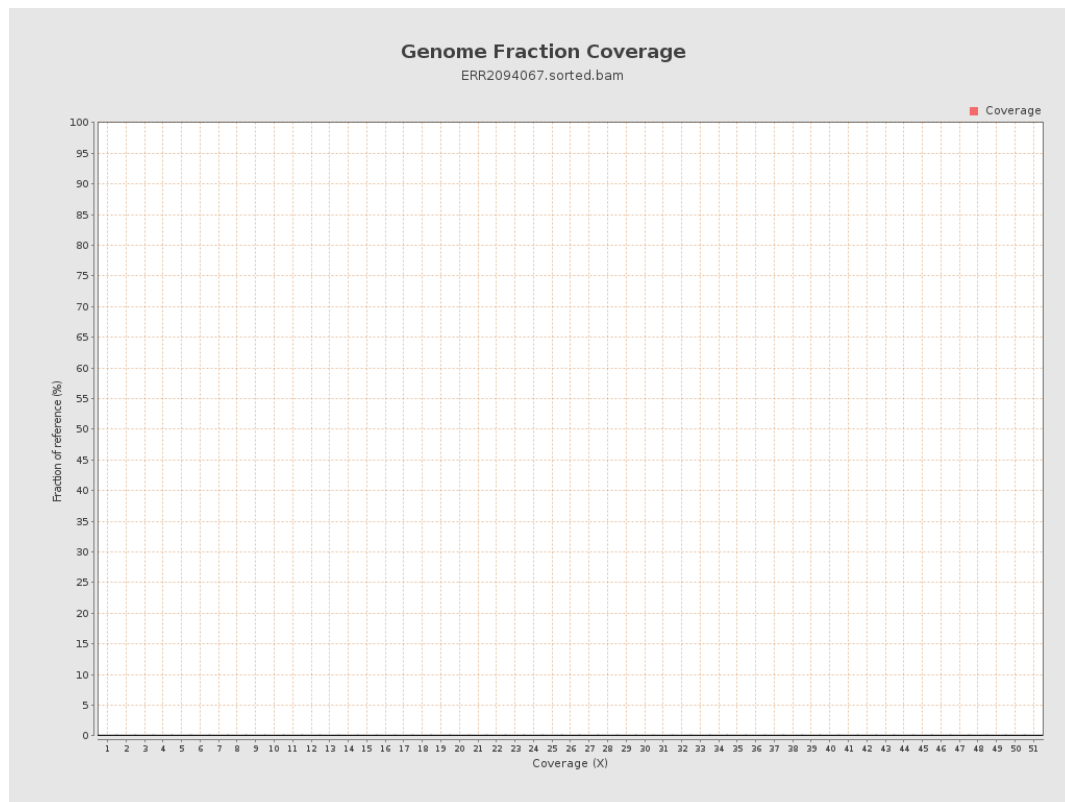
4. Results : Coverage Histogram



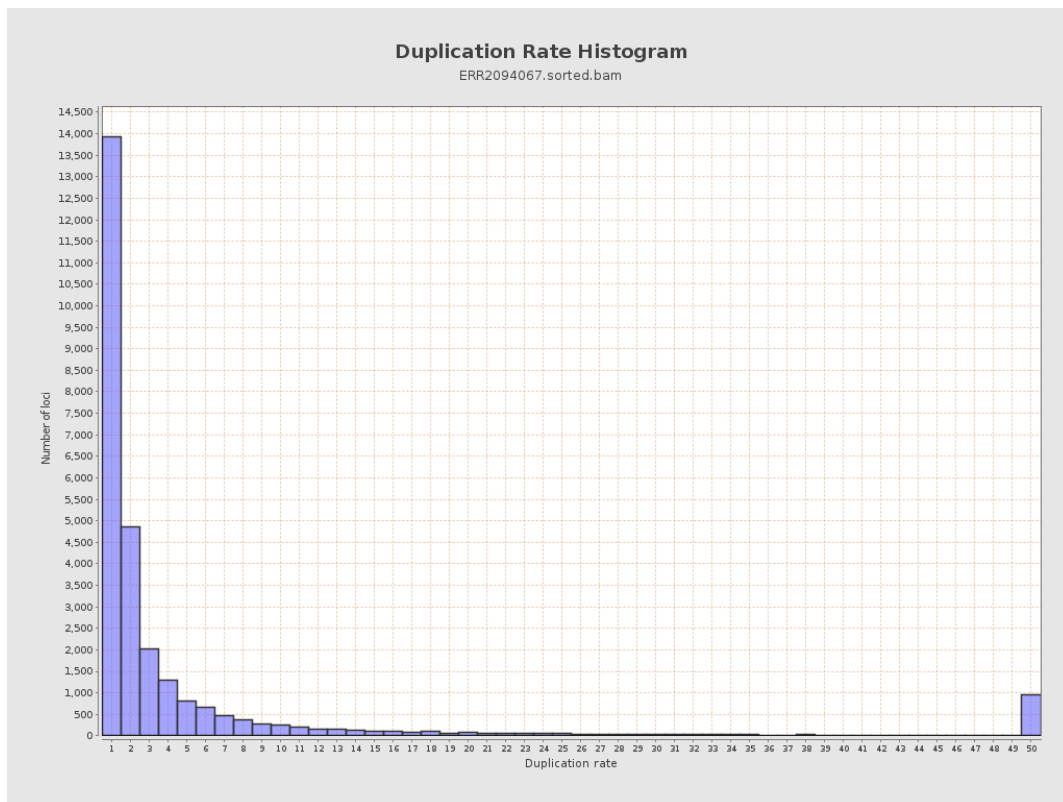
5. Results : Coverage Histogram (0-50X)



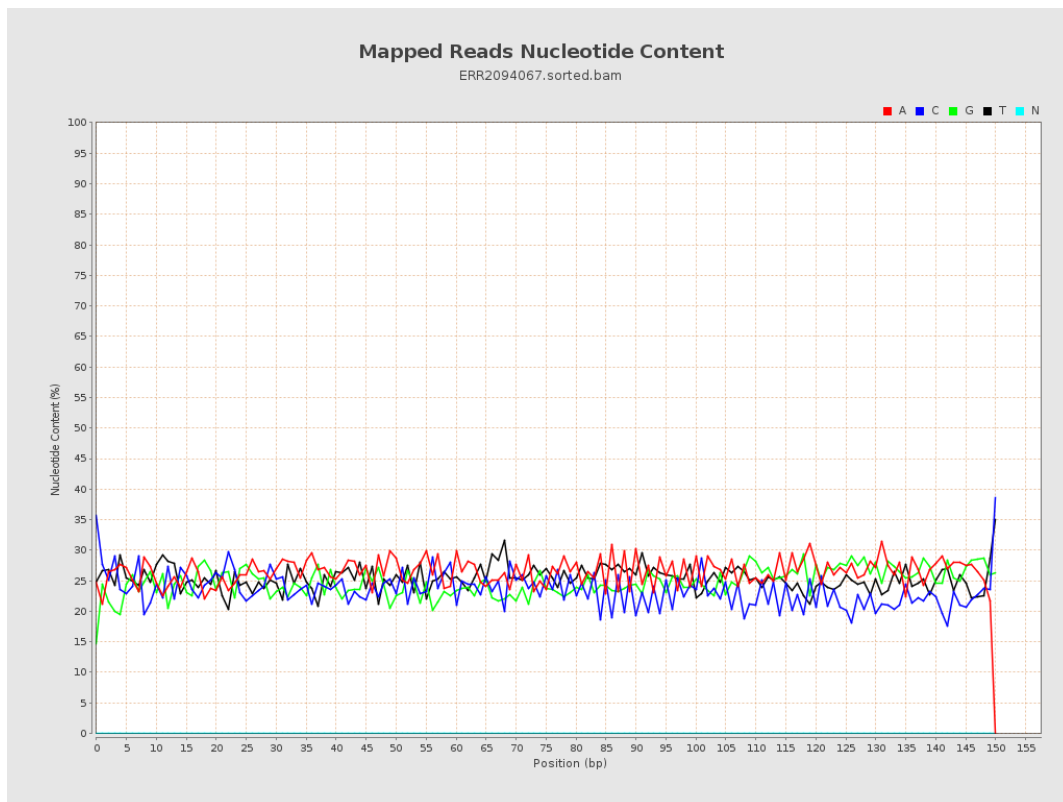
6. Results : Genome Fraction Coverage



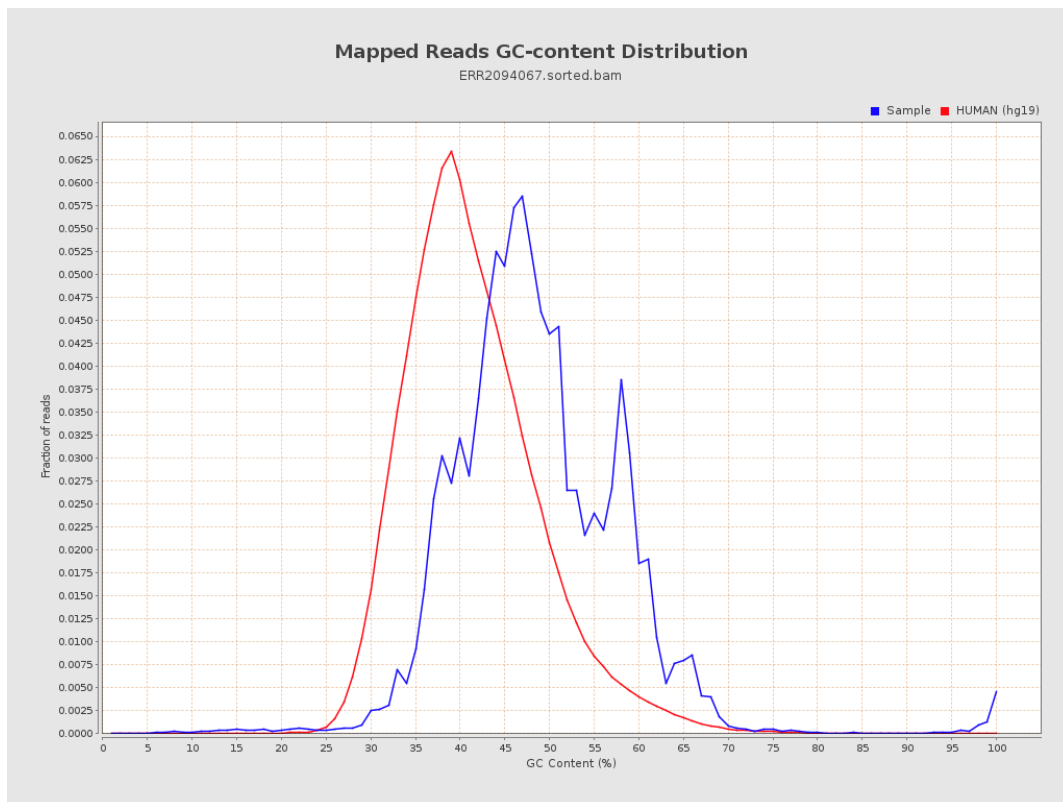
7. Results : Duplication Rate Histogram



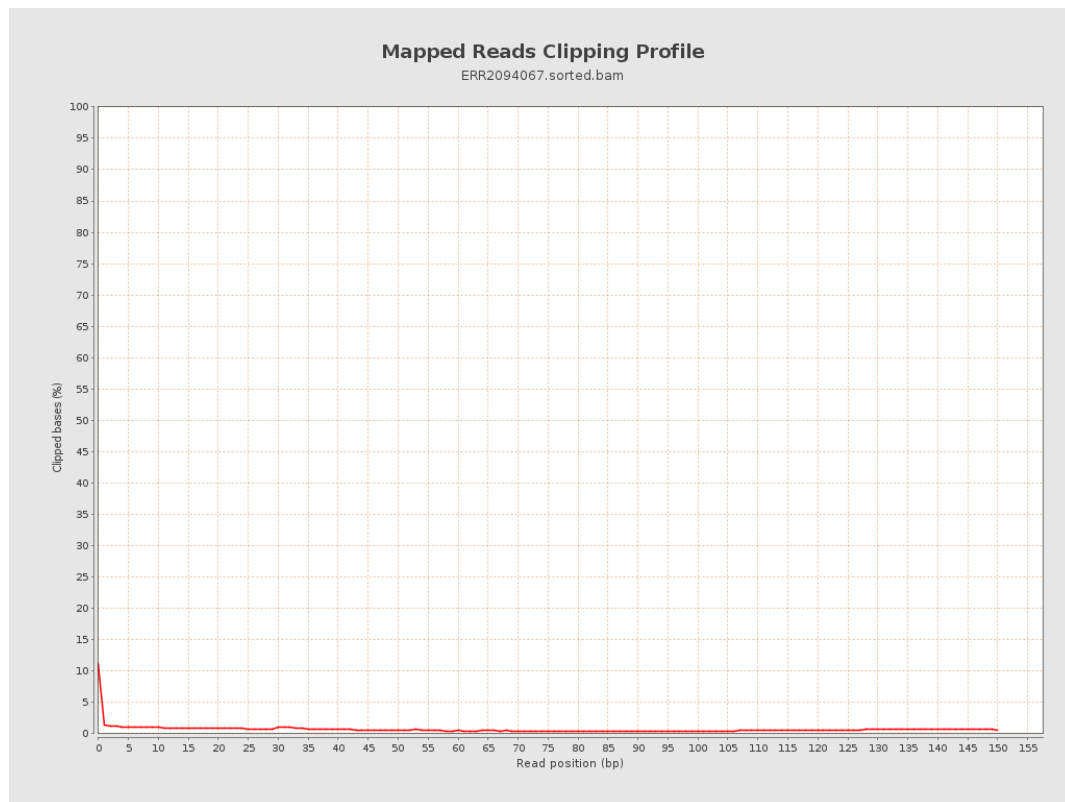
8. Results : Mapped Reads Nucleotide Content



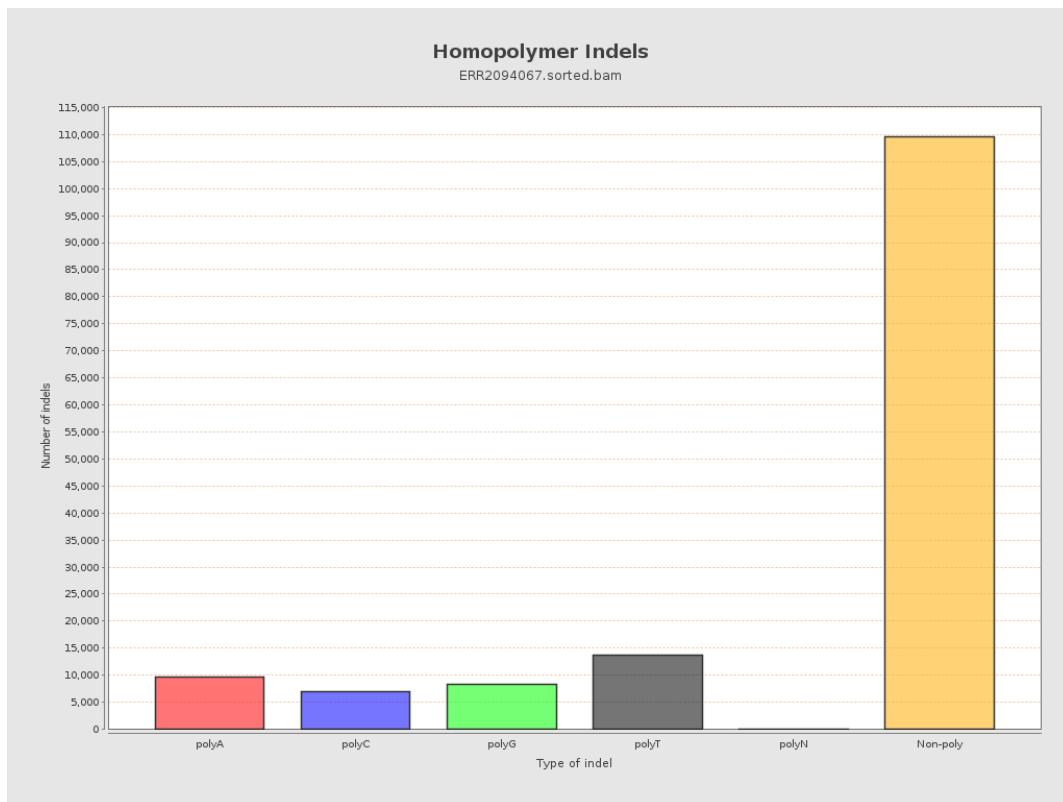
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



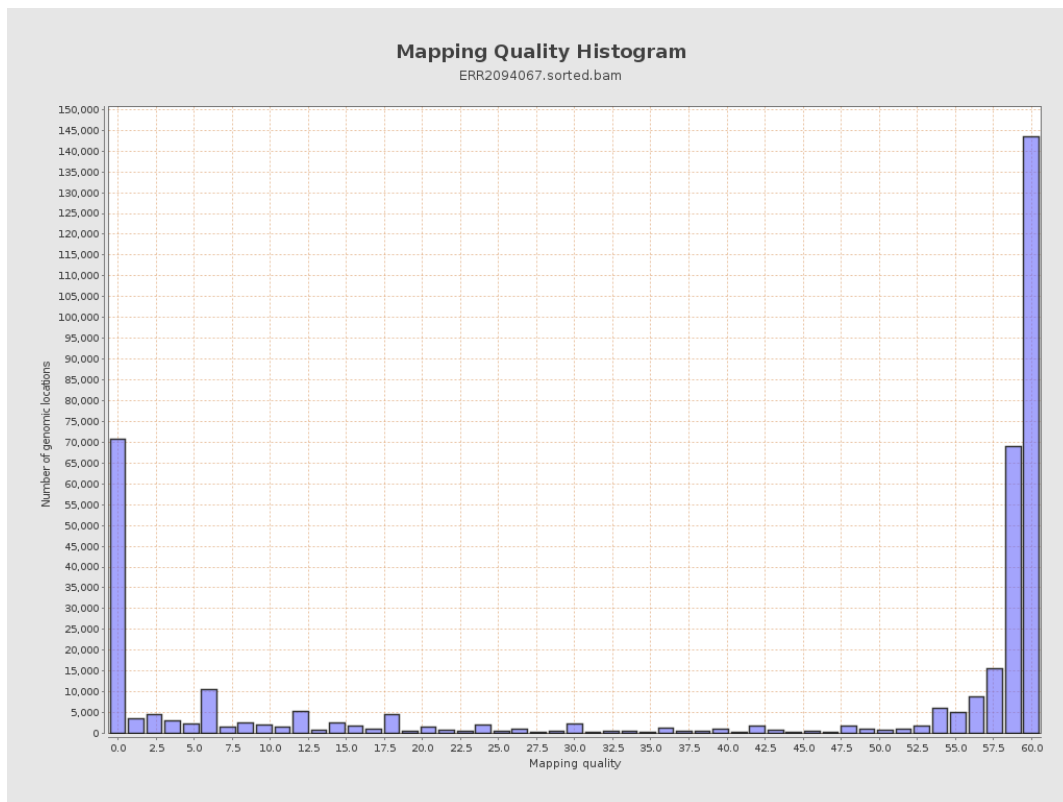
11. Results : Homopolymer Indels



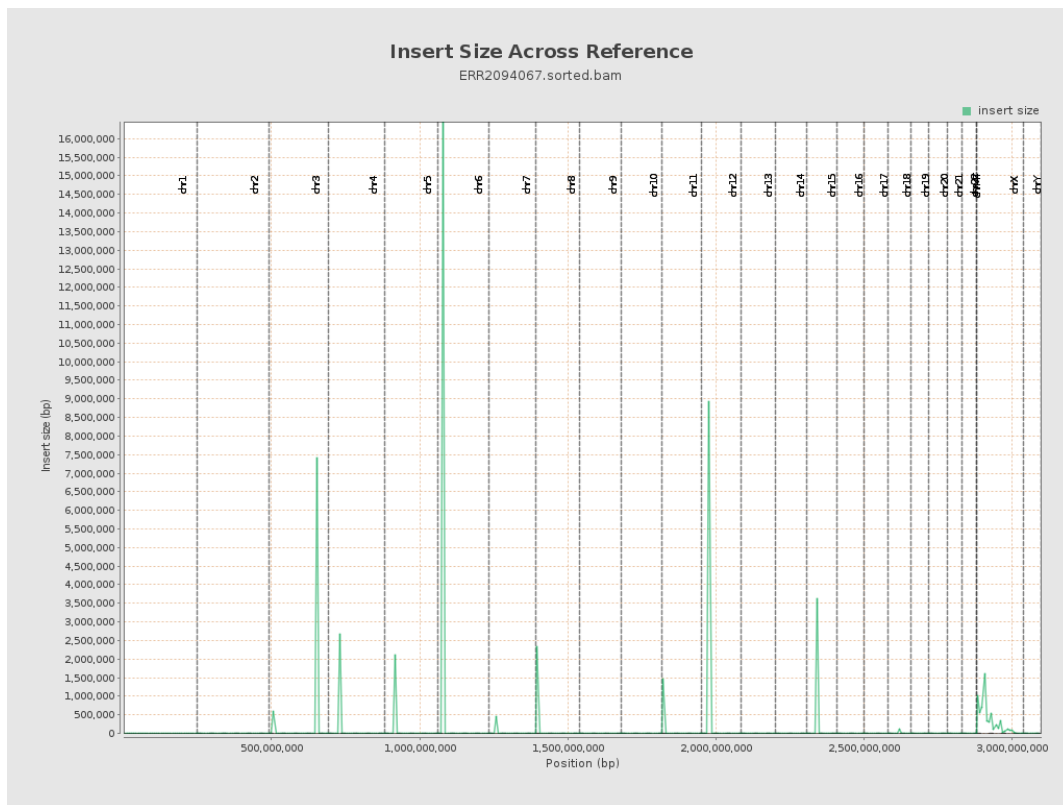
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

