

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:48:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094037.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_ERR2094037 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094037_1.fastq.gz ERR2094037_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:47:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	349,286
Mapped reads	309,049 / 88.48%
Unmapped reads	40,237 / 11.52%
Mapped paired reads	309,049 / 88.48%
Mapped reads, first in pair	155,073 / 44.4%
Mapped reads, second in pair	153,976 / 44.08%
Mapped reads, both in pair	306,686 / 87.8%
Mapped reads, singletons	2,363 / 0.68%
Secondary alignments	0
Supplementary alignments	11,053 / 3.16%
Read min/max/mean length	30 / 151 / 129.71
Duplicated reads (estimated)	290,828 / 83.26%
Duplication rate	51.06%
Clipped reads	128,884 / 36.9%

2.2. ACGT Content

Number/percentage of A's	10,554,686 / 27.51%
Number/percentage of C's	8,607,170 / 22.43%
Number/percentage of T's	10,177,953 / 26.53%
Number/percentage of G's	9,026,008 / 23.53%
Number/percentage of N's	362 / 0%

GC Percentage	45.96%
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2.3. Coverage

Mean	0.0127
Standard Deviation	3.5161

2.4. Mapping Quality

Mean Mapping Quality	41.8
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2.5. Insert size

Mean	505,178.56
Standard Deviation	6,431,823.54
P25/Median/P75	121 / 154 / 184

2.6. Mismatches and indels

General error rate	4.61%
Mismatches	1,716,097
Insertions	28,203
Mapped reads with at least one insertion	8.96%
Deletions	147,078
Mapped reads with at least one deletion	44.28%
Homopolymer indels	26.55%

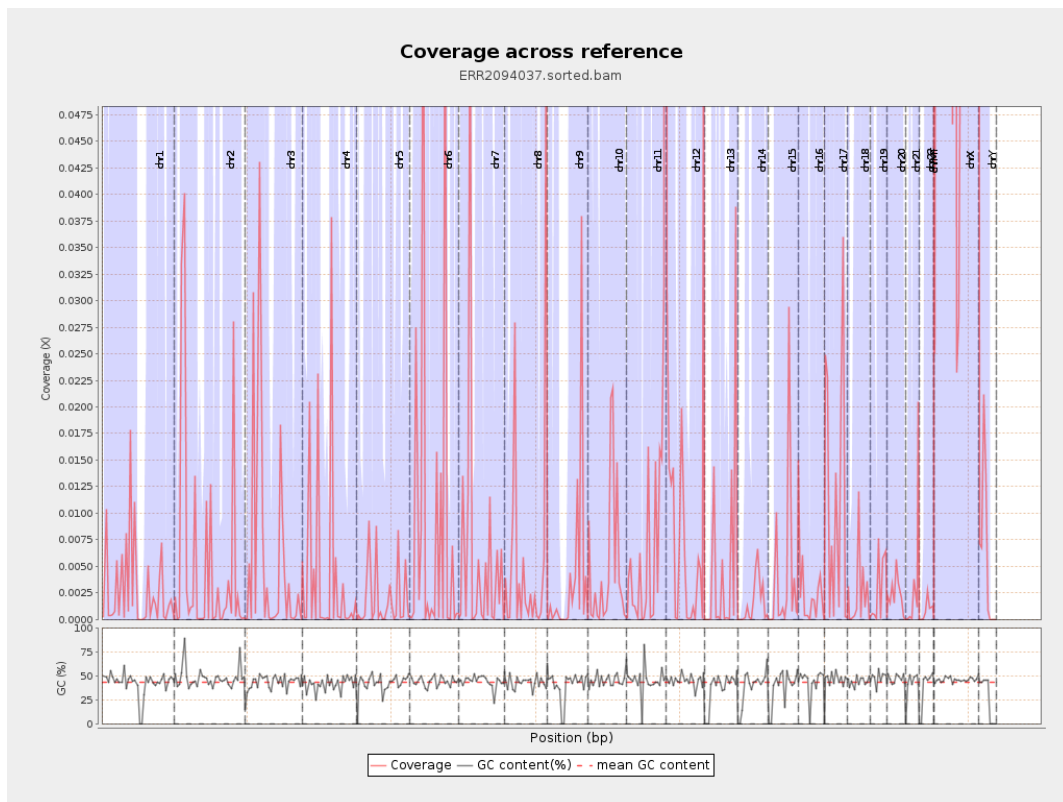
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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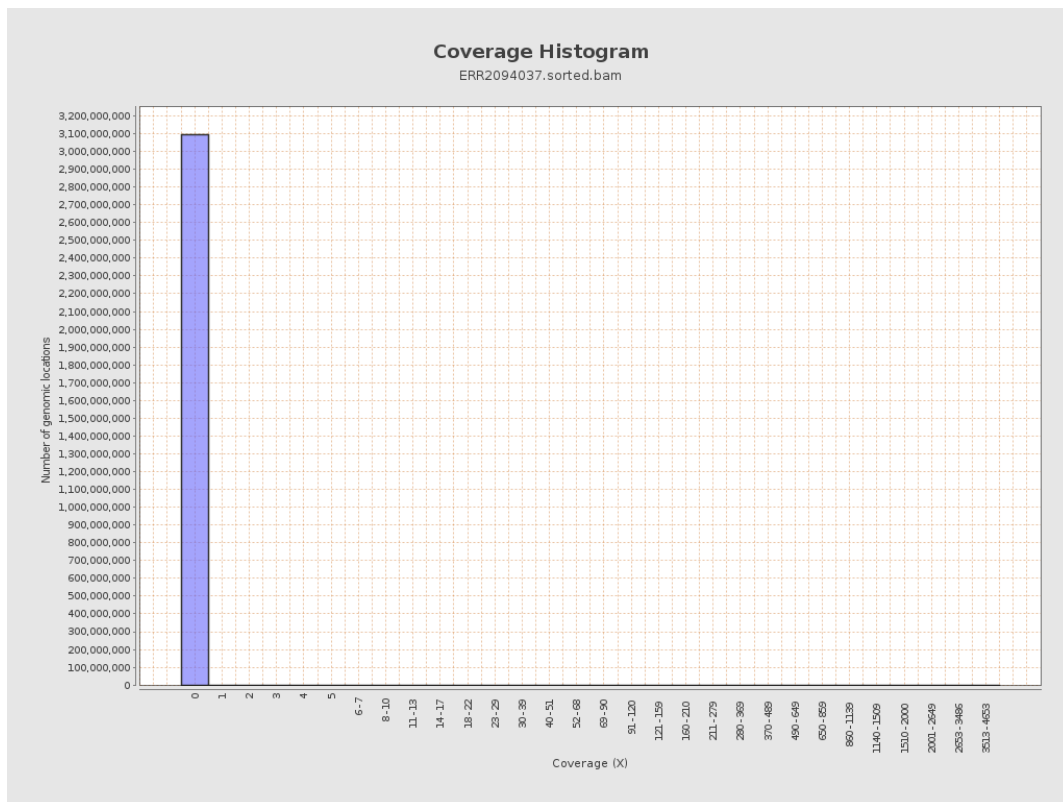
		bases	coverage	deviation
chr1	249250621	685424	0.0027	0.9668
chr2	243199373	1234678	0.0051	1.7544
chr3	198022430	1169828	0.0059	1.99
chr4	191154276	804715	0.0042	1.6519
chr5	180915260	366765	0.002	0.6474
chr6	171115067	1677386	0.0098	5.0928
chr7	159138663	980089	0.0062	2.6493
chr8	146364022	889476	0.0061	2.7843
chr9	141213431	540924	0.0038	1.5612
chr10	135534747	672850	0.005	1.7087
chr11	135006516	1180184	0.0087	2.9797
chr12	133851895	1062526	0.0079	2.0014
chr13	115169878	586251	0.0051	2.0157
chr14	107349540	163221	0.0015	0.5459
chr15	102531392	381096	0.0037	1.1277
chr16	90354753	230155	0.0025	0.8093
chr17	81195210	977335	0.012	2.9374
chr18	78077248	192589	0.0025	0.934
chr19	59128983	163546	0.0028	0.767
chr20	63025520	150531	0.0024	0.5271
chr21	48129895	142263	0.003	0.8486
chr22	51304566	44599	0.0009	0.2181
chrMT	16571	2355676	142.1565	584.0003
chrX	155270560	22384763	0.1442	11.0726

chrY	59373566	365785	0.0062	1.6953
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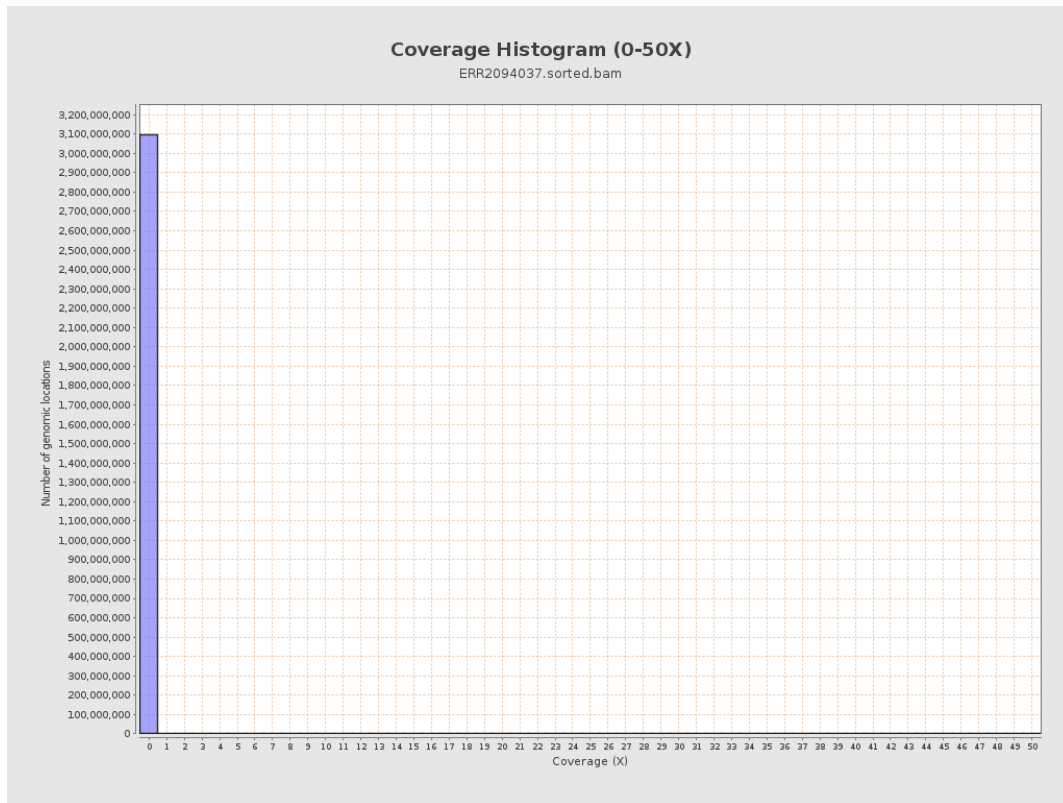
3. Results : Coverage across reference



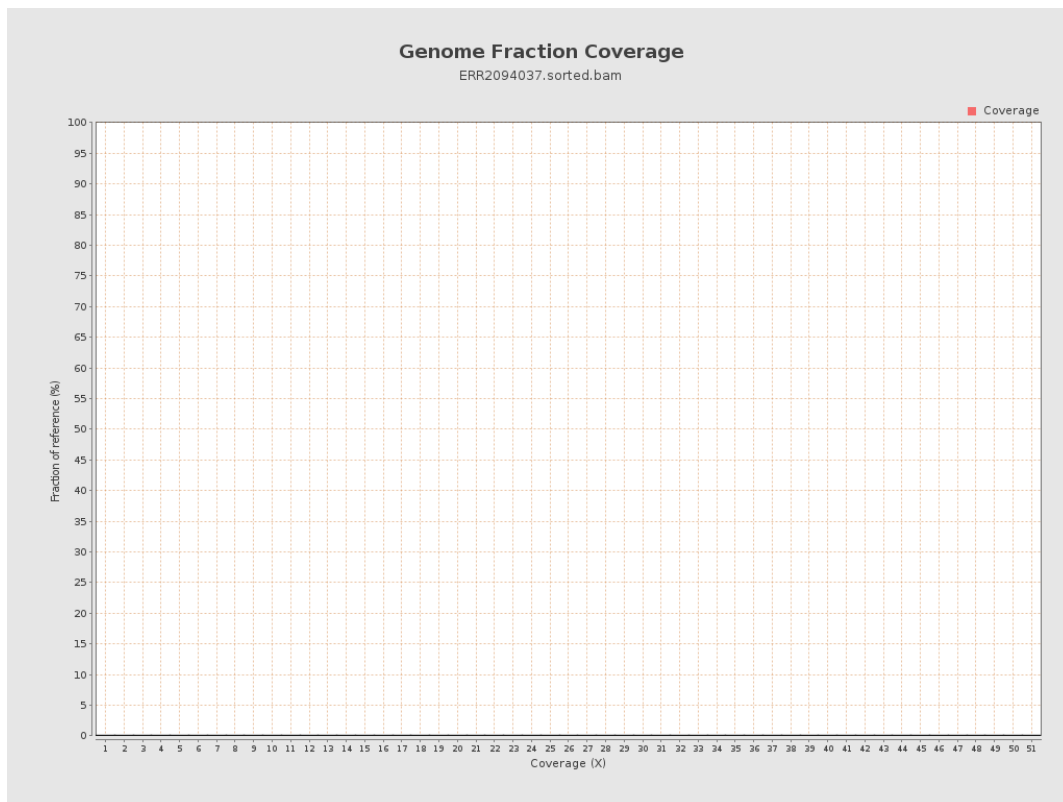
4. Results : Coverage Histogram



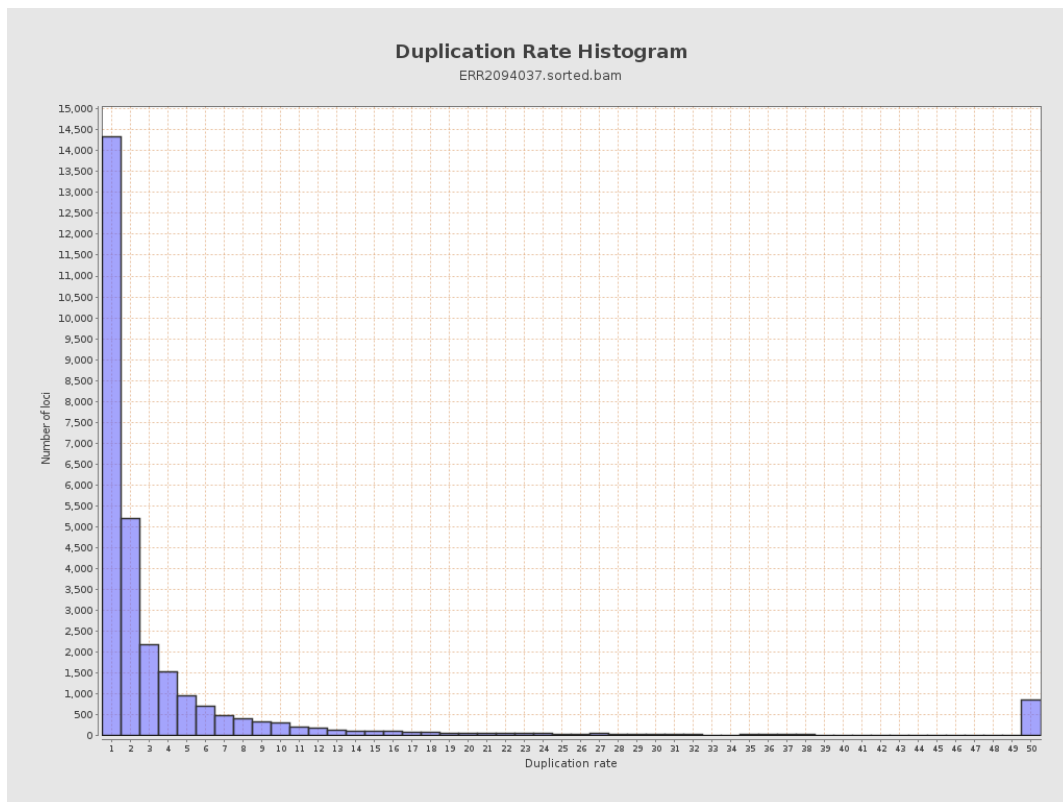
5. Results : Coverage Histogram (0-50X)



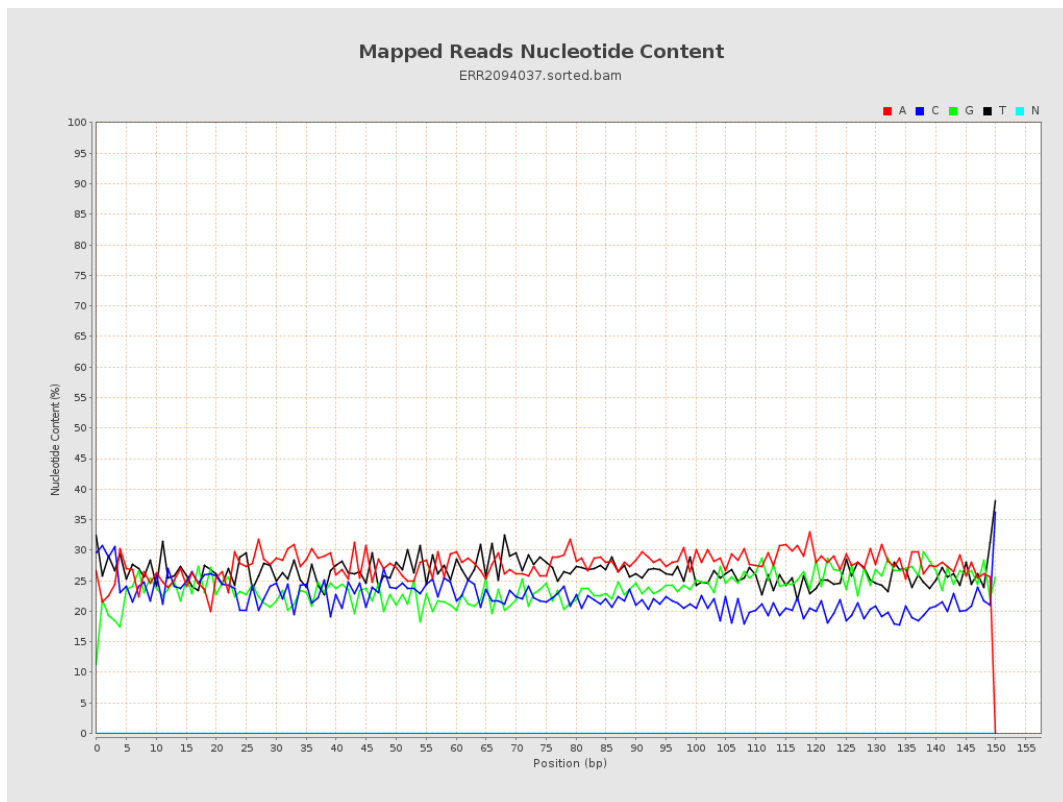
6. Results : Genome Fraction Coverage



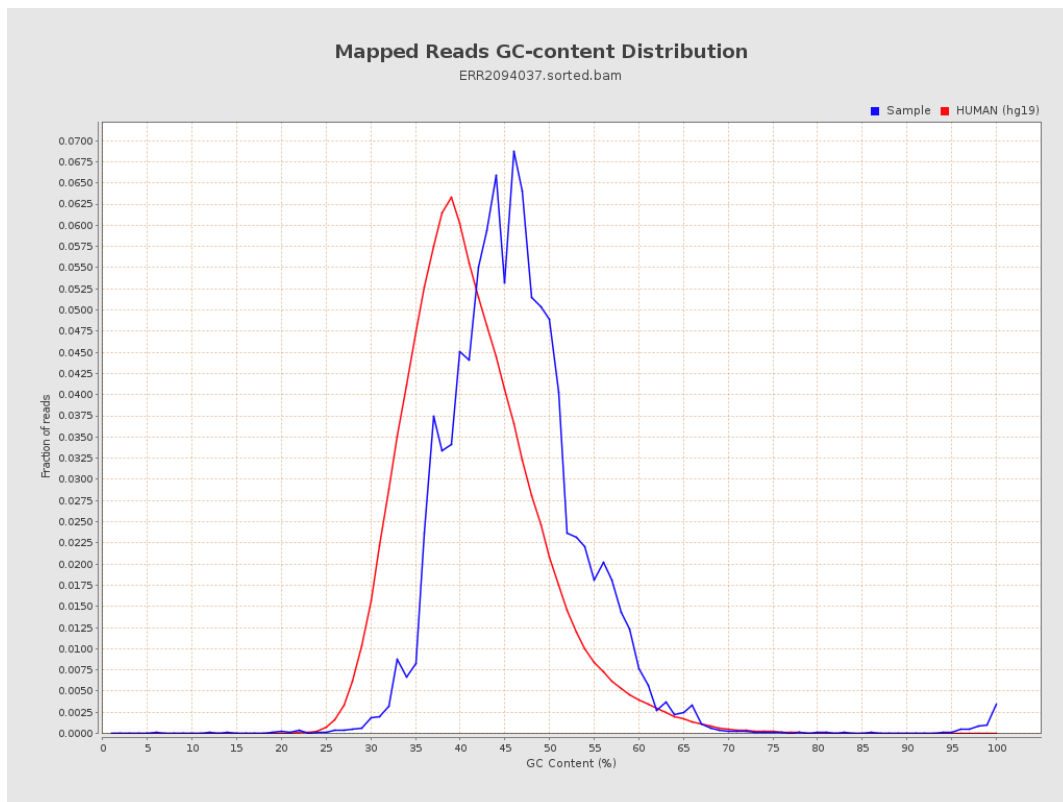
7. Results : Duplication Rate Histogram



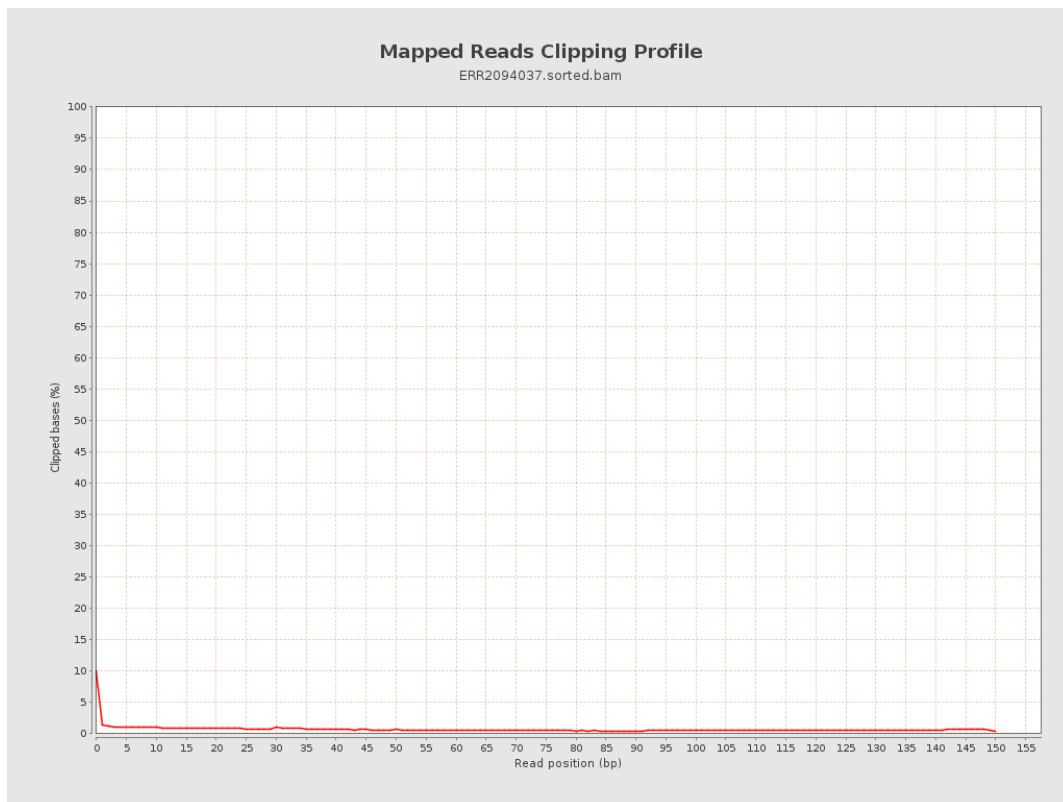
8. Results : Mapped Reads Nucleotide Content



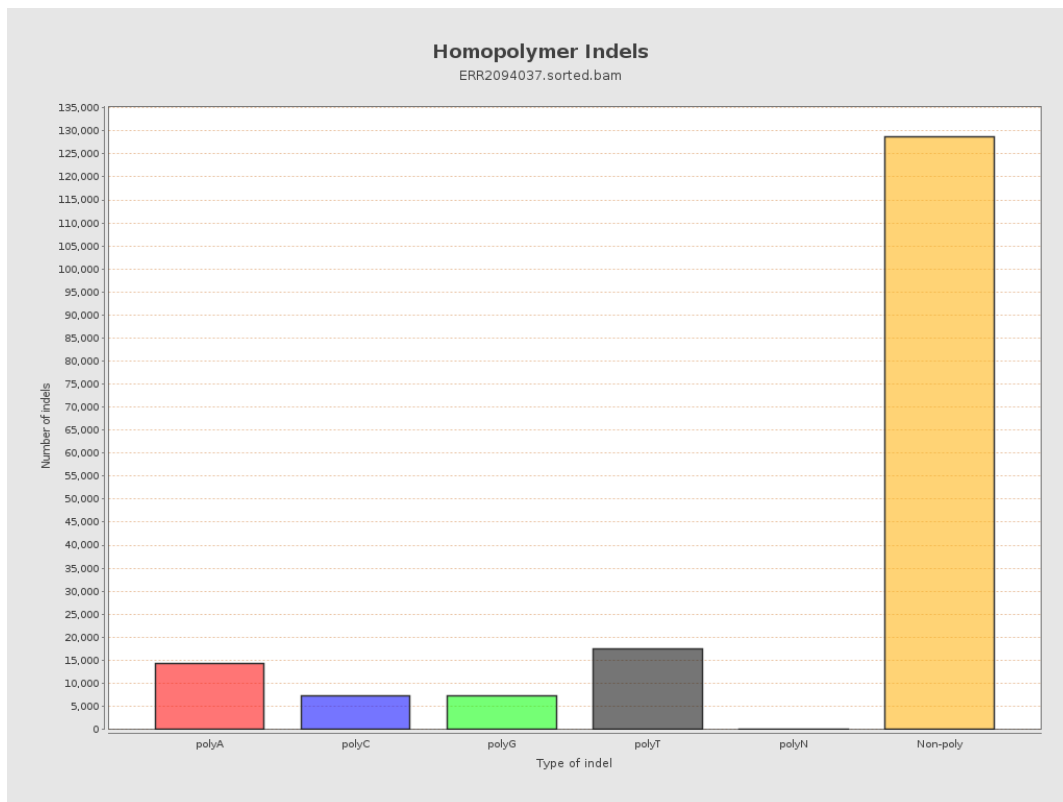
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



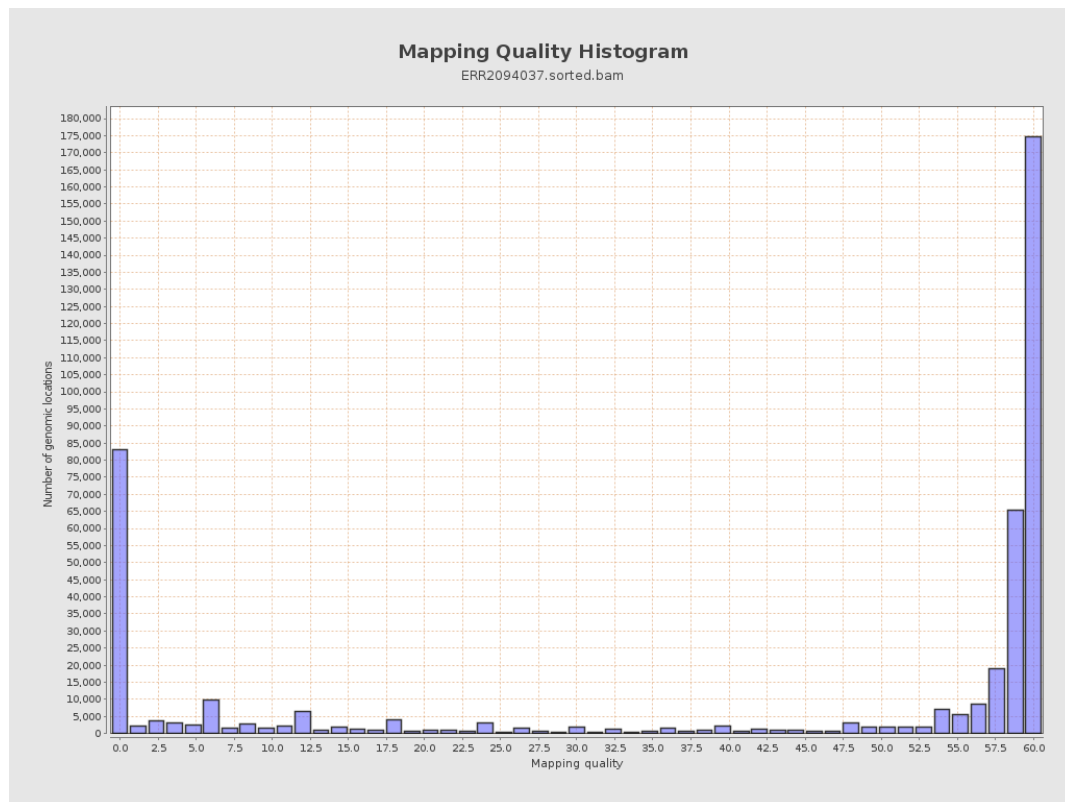
11. Results : Homopolymer Indels



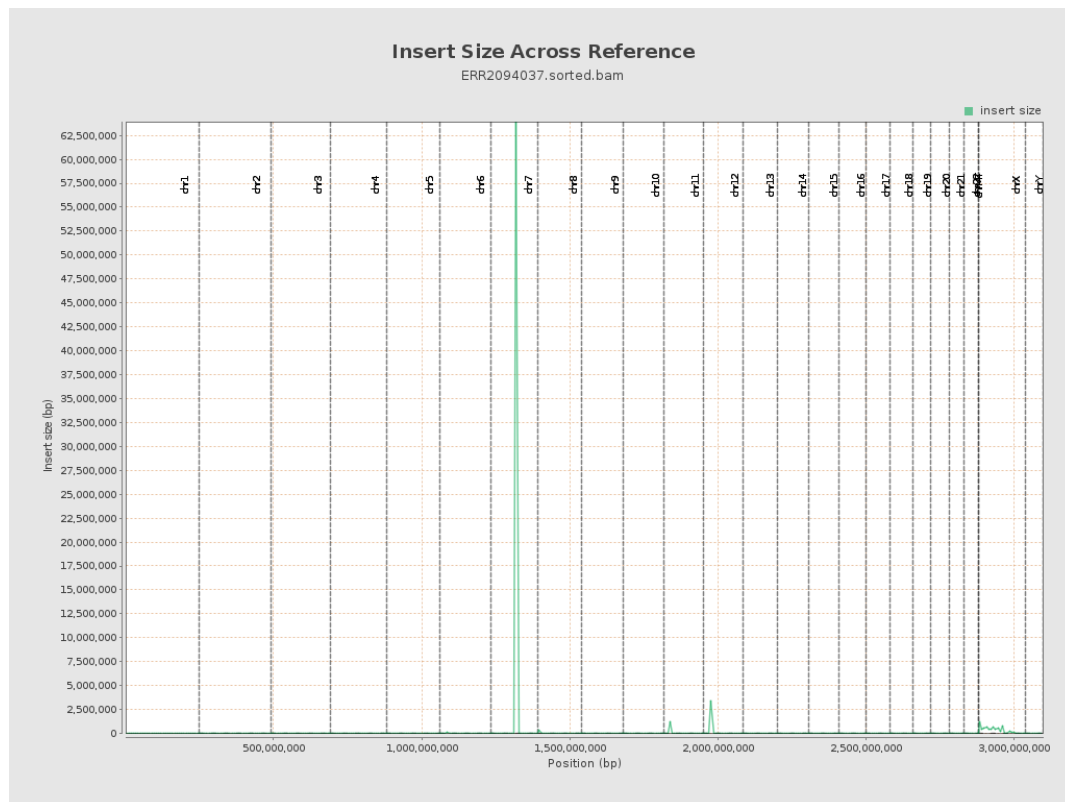
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

