

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 04:04:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094137.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_ERR2094137 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094137_1.fastq.gz ERR2094137_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 04:04:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	442,756
Mapped reads	430,876 / 97.32%
Unmapped reads	11,880 / 2.68%
Mapped paired reads	430,876 / 97.32%
Mapped reads, first in pair	216,143 / 48.82%
Mapped reads, second in pair	214,733 / 48.5%
Mapped reads, both in pair	428,886 / 96.87%
Mapped reads, singletons	1,990 / 0.45%
Secondary alignments	0
Supplementary alignments	5,620 / 1.27%
Read min/max/mean length	30 / 151 / 148.37
Duplicated reads (estimated)	430,247 / 97.17%
Duplication rate	40.61%
Clipped reads	78,783 / 17.79%

2.2. ACGT Content

Number/percentage of A's	17,853,602 / 28.19%
Number/percentage of C's	13,464,191 / 21.26%
Number/percentage of T's	18,150,767 / 28.66%
Number/percentage of G's	13,870,193 / 21.9%
Number/percentage of N's	766 / 0%

GC Percentage	43.16%
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2.3. Coverage

Mean	0.0205
Standard Deviation	32.5601

2.4. Mapping Quality

Mean Mapping Quality	25.07
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2.5. Insert size

Mean	105,414.05
Standard Deviation	3,857,221.62
P25/Median/P75	217 / 233 / 266

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	949,587
Insertions	22,043
Mapped reads with at least one insertion	5.06%
Deletions	41,217
Mapped reads with at least one deletion	9.33%
Homopolymer indels	61.28%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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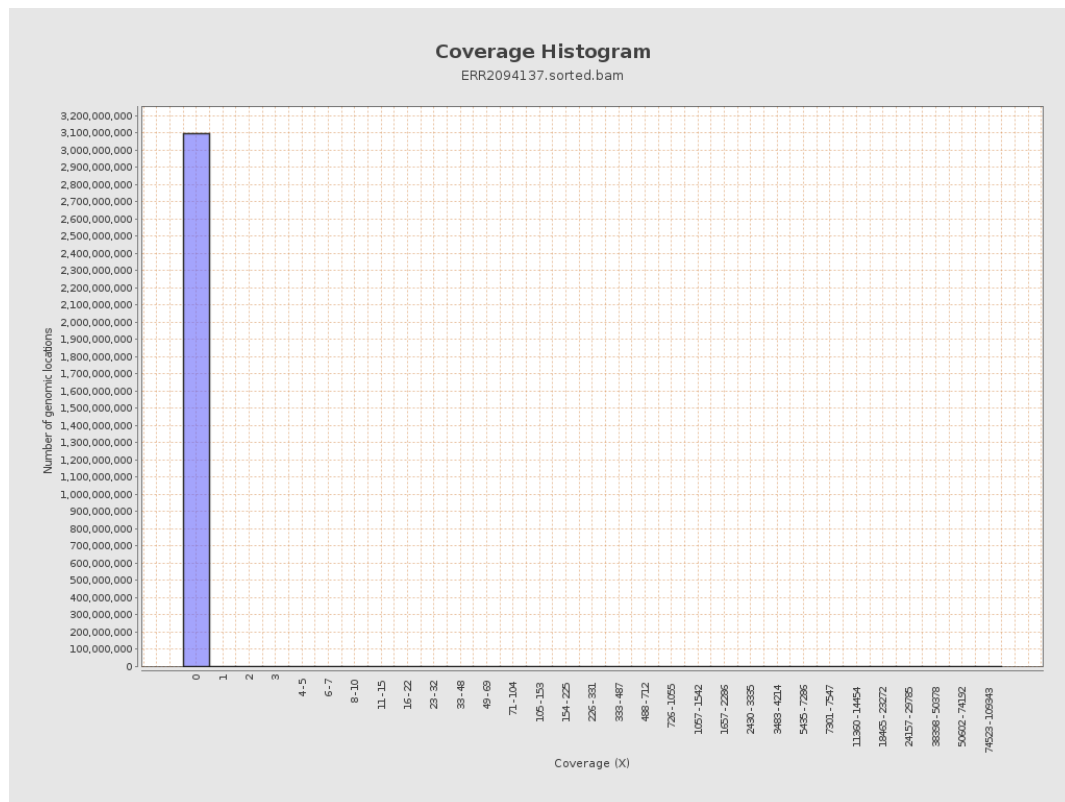
		bases	coverage	deviation
chr1	249250621	861759	0.0035	4.1707
chr2	243199373	4580461	0.0188	15.2251
chr3	198022430	256723	0.0013	0.8307
chr4	191154276	178452	0.0009	0.519
chr5	180915260	86936	0.0005	0.2932
chr6	171115067	155488	0.0009	0.4378
chr7	159138663	51470	0.0003	0.1299
chr8	146364022	18746	0.0001	0.0328
chr9	141213431	54712	0.0004	0.1548
chr10	135534747	66037	0.0005	0.2141
chr11	135006516	30234	0.0002	0.0688
chr12	133851895	203204	0.0015	0.7996
chr13	115169878	265126	0.0023	1.3068
chr14	107349540	29334	0.0003	0.0956
chr15	102531392	544483	0.0053	3.7526
chr16	90354753	97858	0.0011	0.502
chr17	81195210	307291	0.0038	1.9247
chr18	78077248	28757	0.0004	0.209
chr19	59128983	14149	0.0002	0.0883
chr20	63025520	10307	0.0002	0.0297
chr21	48129895	4015	0.0001	0.0165
chr22	51304566	6464	0.0001	0.0414
chrMT	16571	54126178	3,266.3194	13,544.1436
chrX	155270560	1409846	0.0091	4.0498

chrY	59373566	10459	0.0002	0.053
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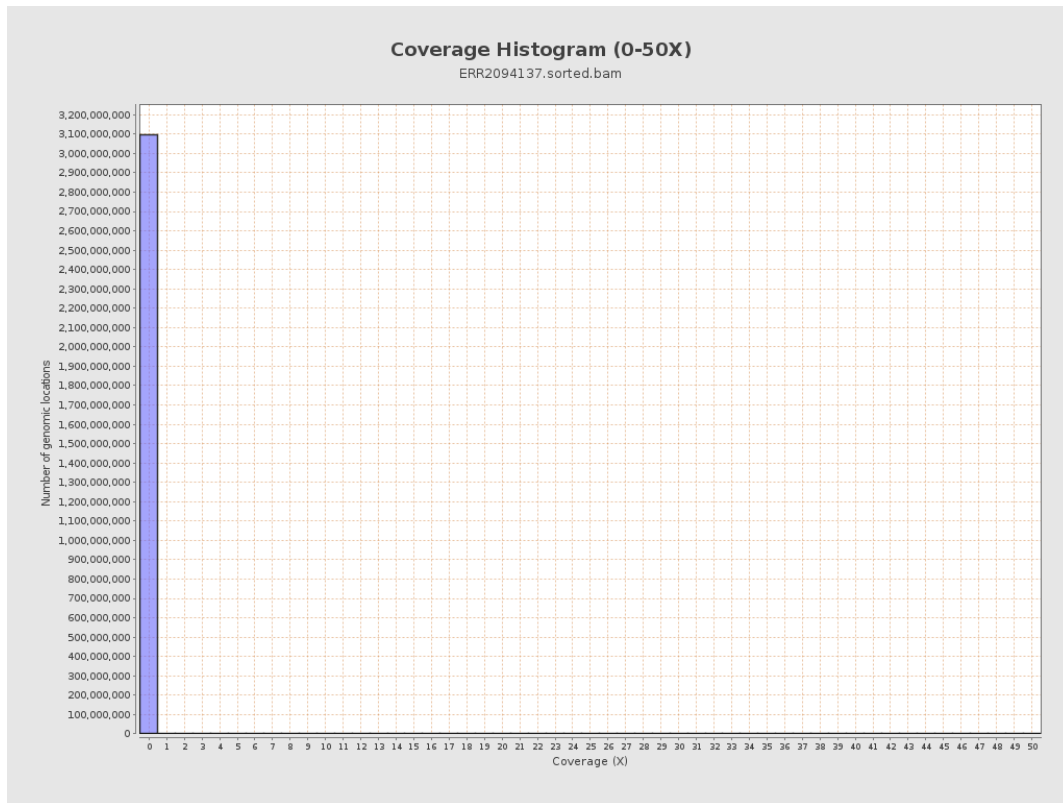
3. Results : Coverage across reference



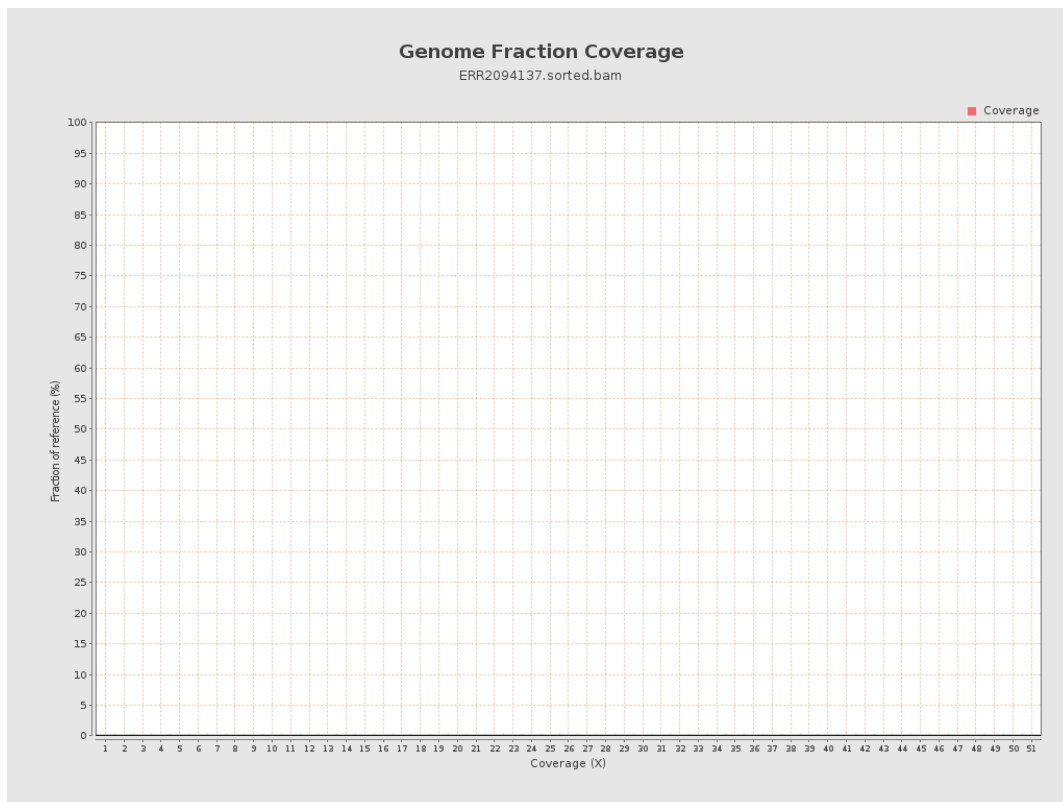
4. Results : Coverage Histogram



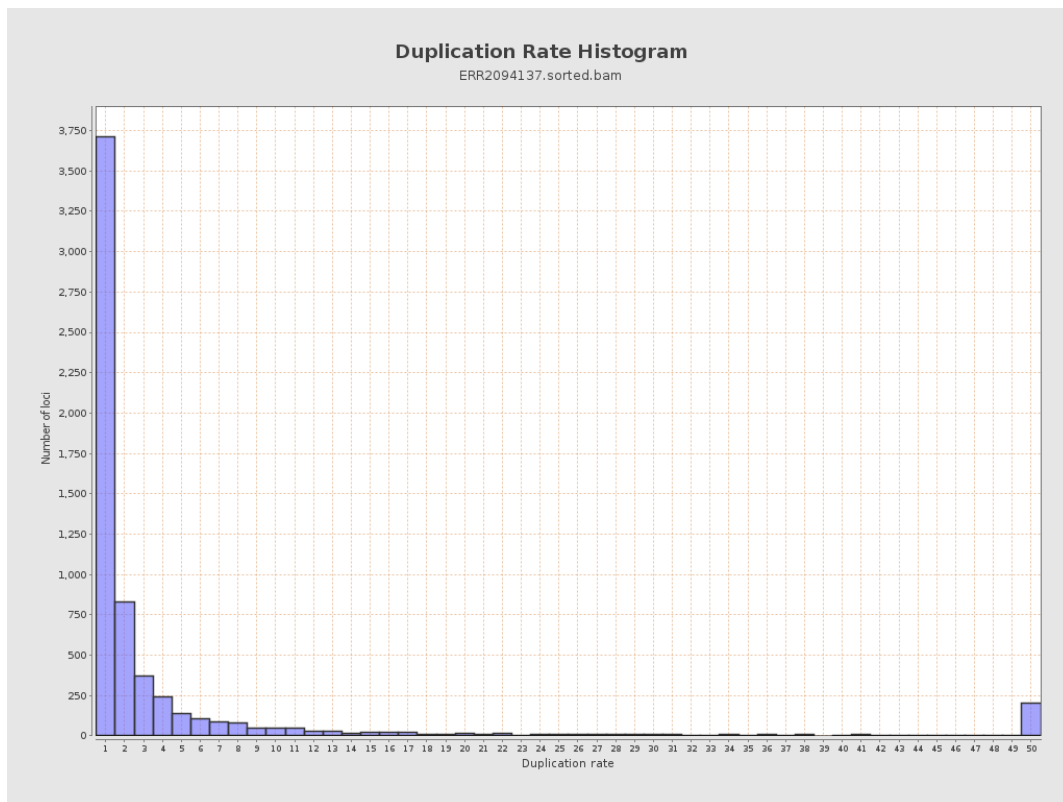
5. Results : Coverage Histogram (0-50X)



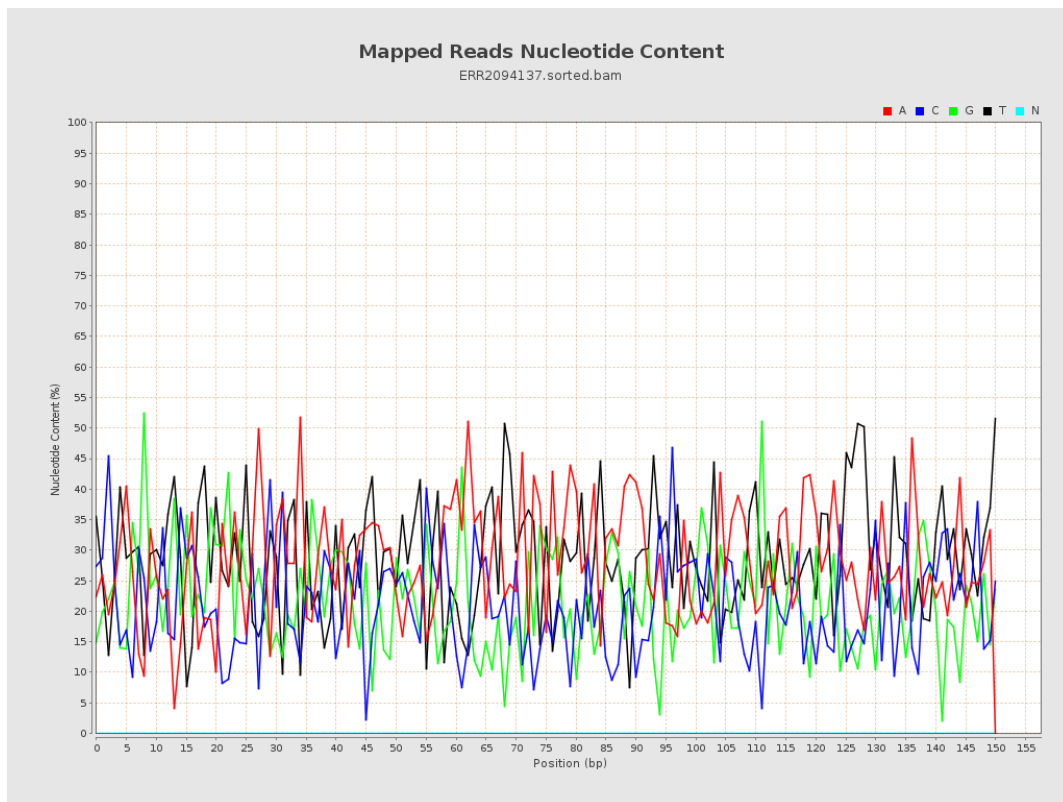
6. Results : Genome Fraction Coverage



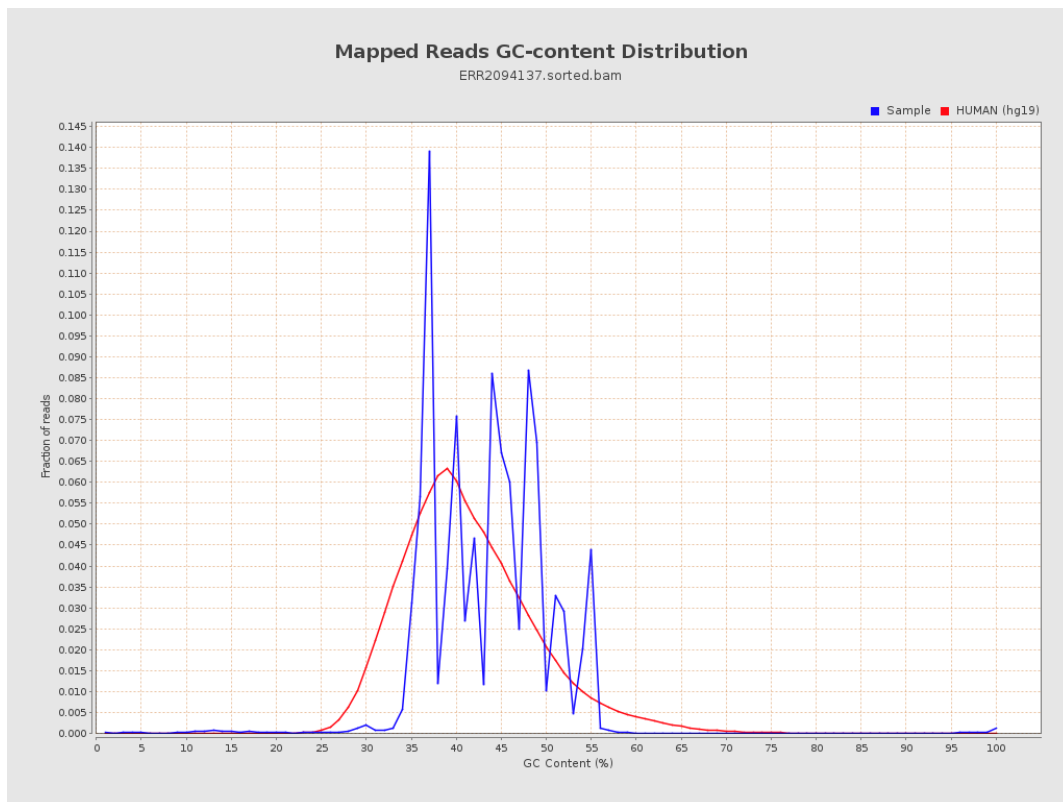
7. Results : Duplication Rate Histogram



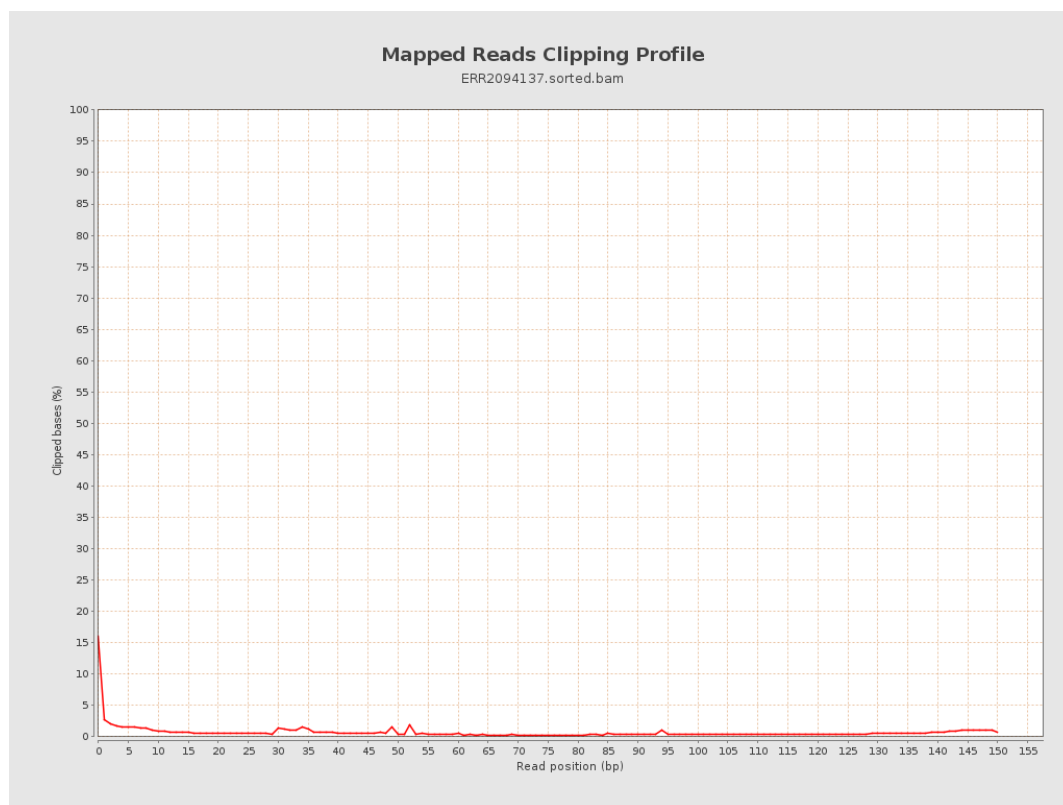
8. Results : Mapped Reads Nucleotide Content



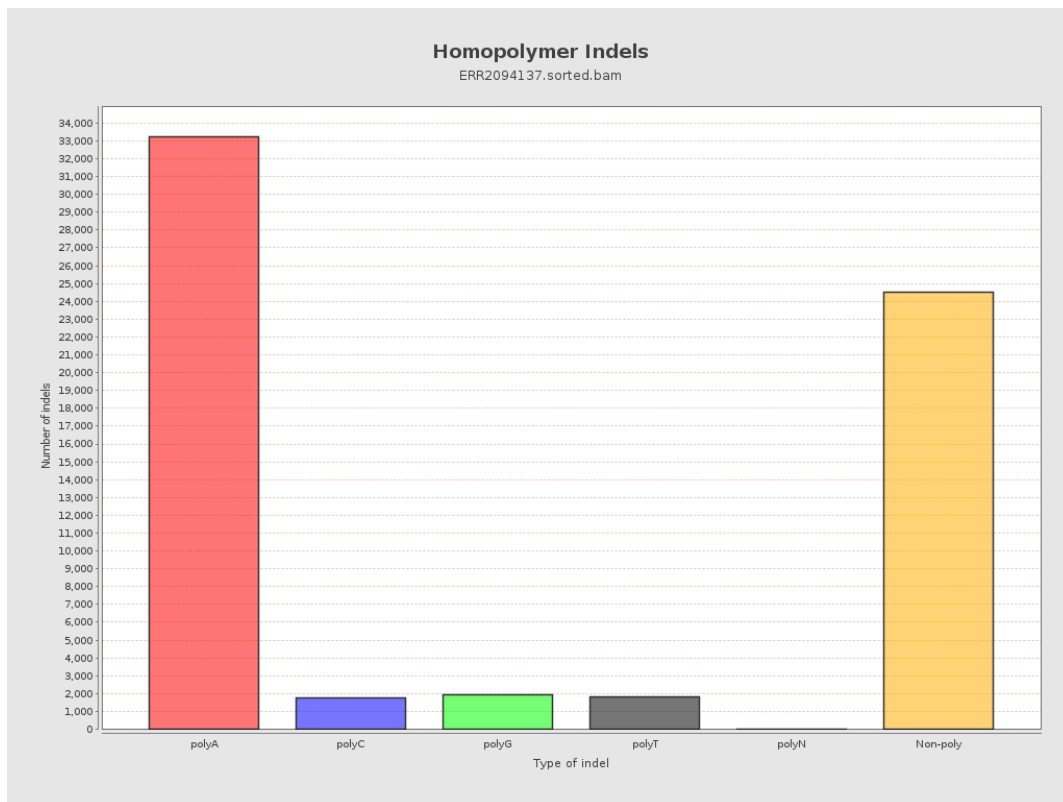
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



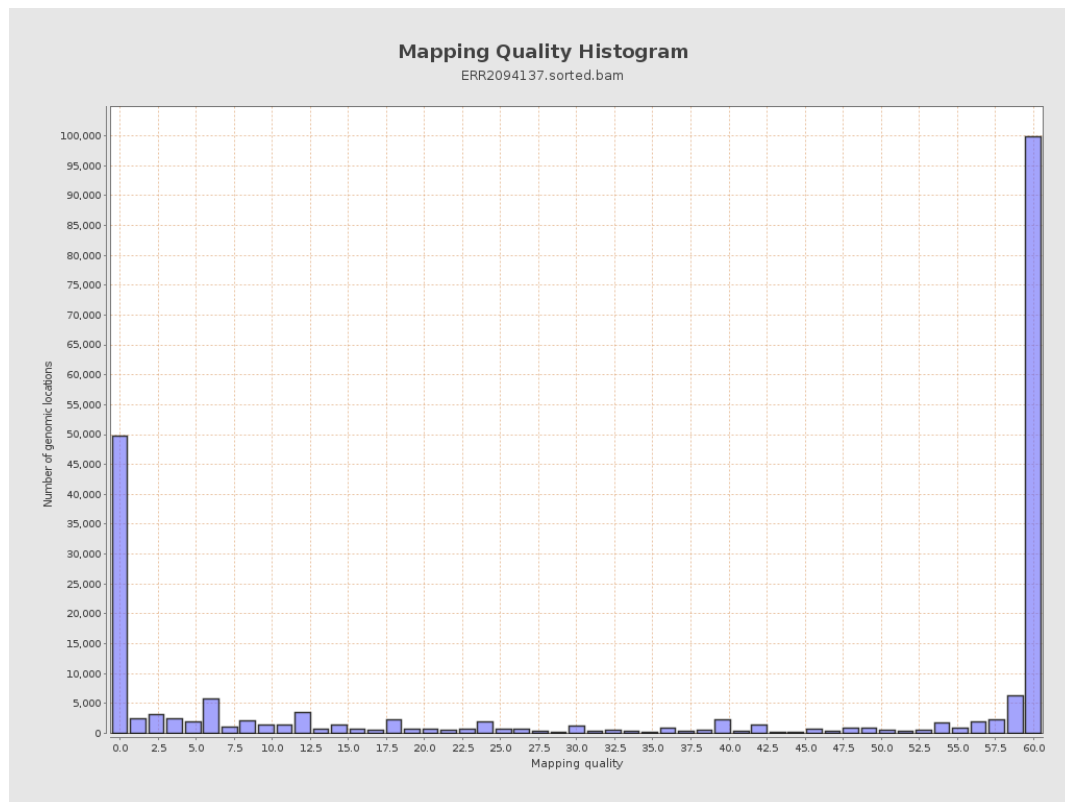
11. Results : Homopolymer Indels



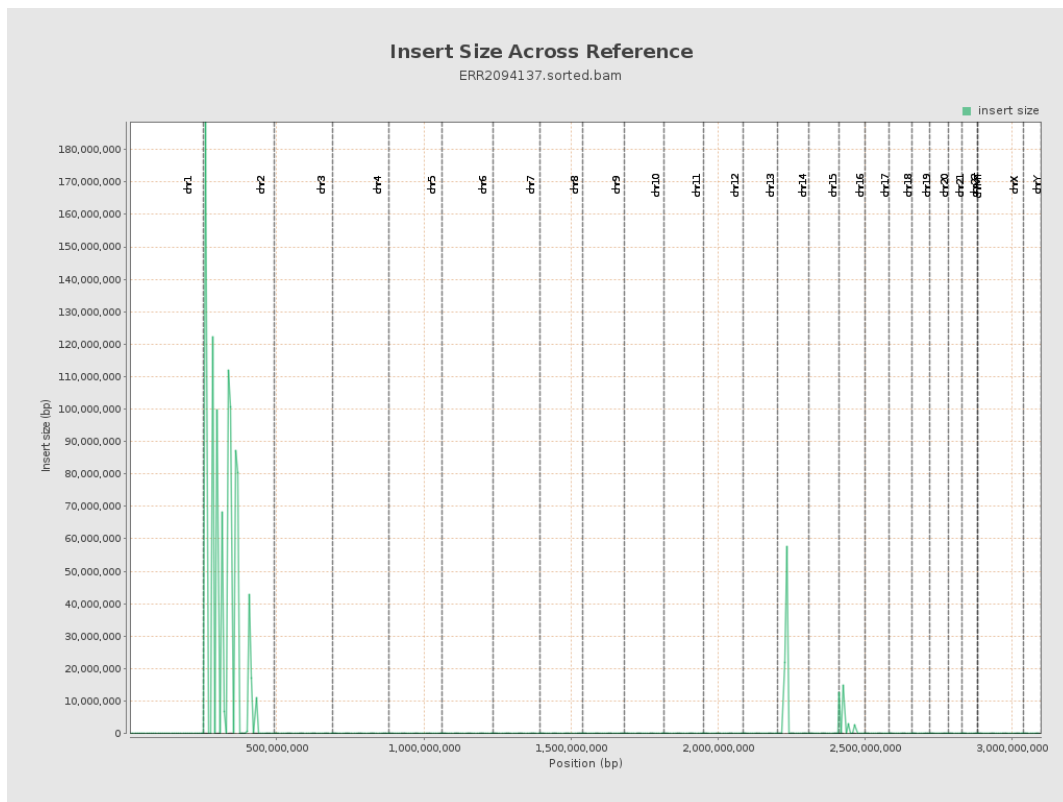
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

