

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 06:59:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094155.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_ERR2094155 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094155_1.fastq.gz ERR2094155_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 06:59:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094155.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	336,238
Mapped reads	299,958 / 89.21%
Unmapped reads	36,280 / 10.79%
Mapped paired reads	299,958 / 89.21%
Mapped reads, first in pair	150,539 / 44.77%
Mapped reads, second in pair	149,419 / 44.44%
Mapped reads, both in pair	297,932 / 88.61%
Mapped reads, singletons	2,026 / 0.6%
Secondary alignments	0
Supplementary alignments	2,504 / 0.74%
Read min/max/mean length	30 / 151 / 133.32
Duplicated reads (estimated)	294,817 / 87.68%
Duplication rate	43.01%
Clipped reads	131,226 / 39.03%

2.2. ACGT Content

Number/percentage of A's	10,706,400 / 27.75%
Number/percentage of C's	8,352,591 / 21.65%
Number/percentage of T's	10,744,369 / 27.85%
Number/percentage of G's	8,776,181 / 22.75%
Number/percentage of N's	308 / 0%

GC Percentage	44.4%
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2.3. Coverage

Mean	0.0129
Standard Deviation	12.9387

2.4. Mapping Quality

Mean Mapping Quality	29.75
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2.5. Insert size

Mean	118,797.68
Standard Deviation	3,151,491.21
P25/Median/P75	129 / 164 / 223

2.6. Mismatches and indels

General error rate	4.87%
Mismatches	1,910,825
Insertions	13,677
Mapped reads with at least one insertion	4.48%
Deletions	170,040
Mapped reads with at least one deletion	52.05%
Homopolymer indels	19.99%

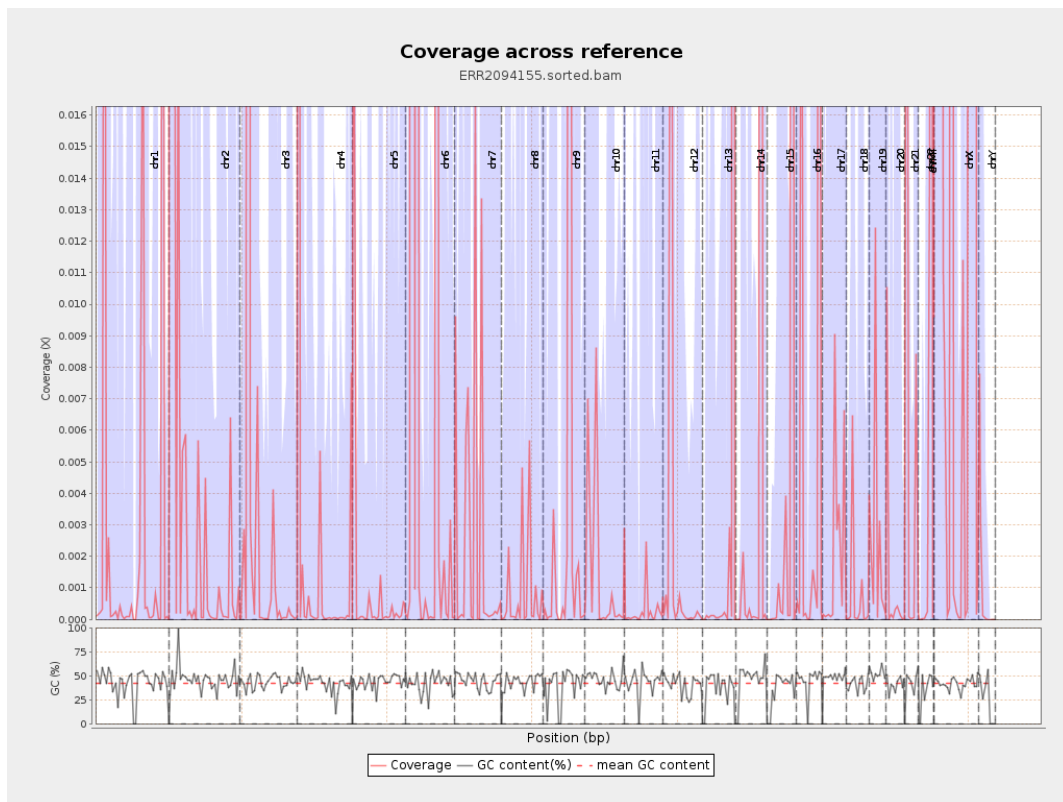
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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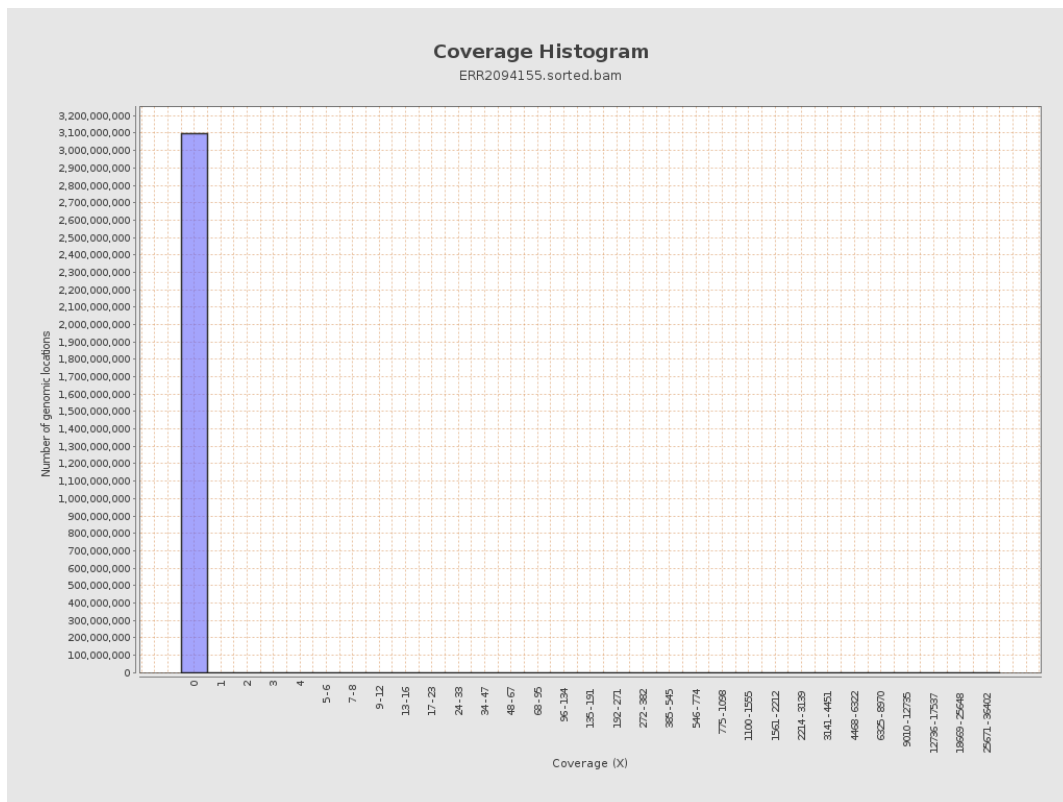
		bases	coverage	deviation
chr1	249250621	812235	0.0033	2.053
chr2	243199373	1866800	0.0077	4.9509
chr3	198022430	1837811	0.0093	8.4201
chr4	191154276	745464	0.0039	3.5407
chr5	180915260	225040	0.0012	0.9758
chr6	171115067	7997218	0.0467	34.4632
chr7	159138663	395198	0.0025	1.1478
chr8	146364022	125669	0.0009	0.3632
chr9	141213431	615690	0.0044	2.6665
chr10	135534747	198228	0.0015	0.5426
chr11	135006516	42376	0.0003	0.1572
chr12	133851895	294165	0.0022	1.8464
chr13	115169878	2928368	0.0254	22.9164
chr14	107349540	925266	0.0086	5.0029
chr15	102531392	983879	0.0096	7.3002
chr16	90354753	696498	0.0077	3.6994
chr17	81195210	188326	0.0023	0.5649
chr18	78077248	64585	0.0008	0.3919
chr19	59128983	158807	0.0027	1.0089
chr20	63025520	68120	0.0011	0.5458
chr21	48129895	347027	0.0072	2.4774
chr22	51304566	575870	0.0112	4.6894
chrMT	16571	5580888	336.7864	2,159.7685
chrX	155270560	12058728	0.0777	29.9273

chrY	59373566	65011	0.0011	0.4758
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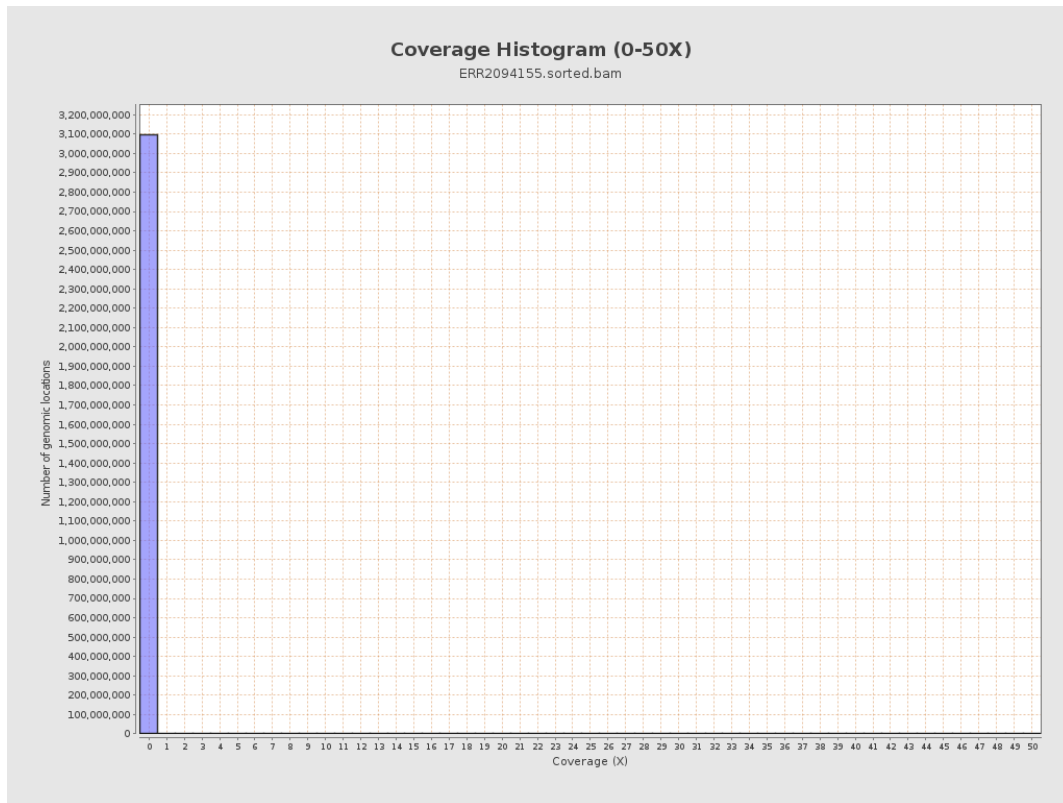
3. Results : Coverage across reference



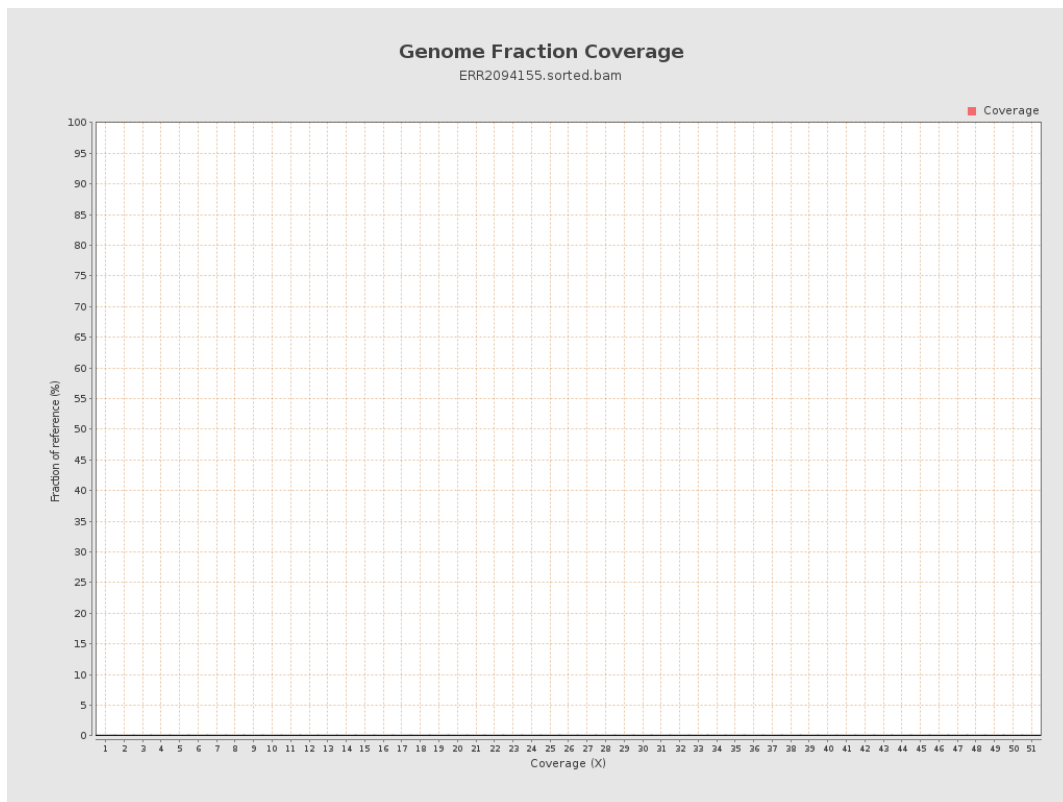
4. Results : Coverage Histogram



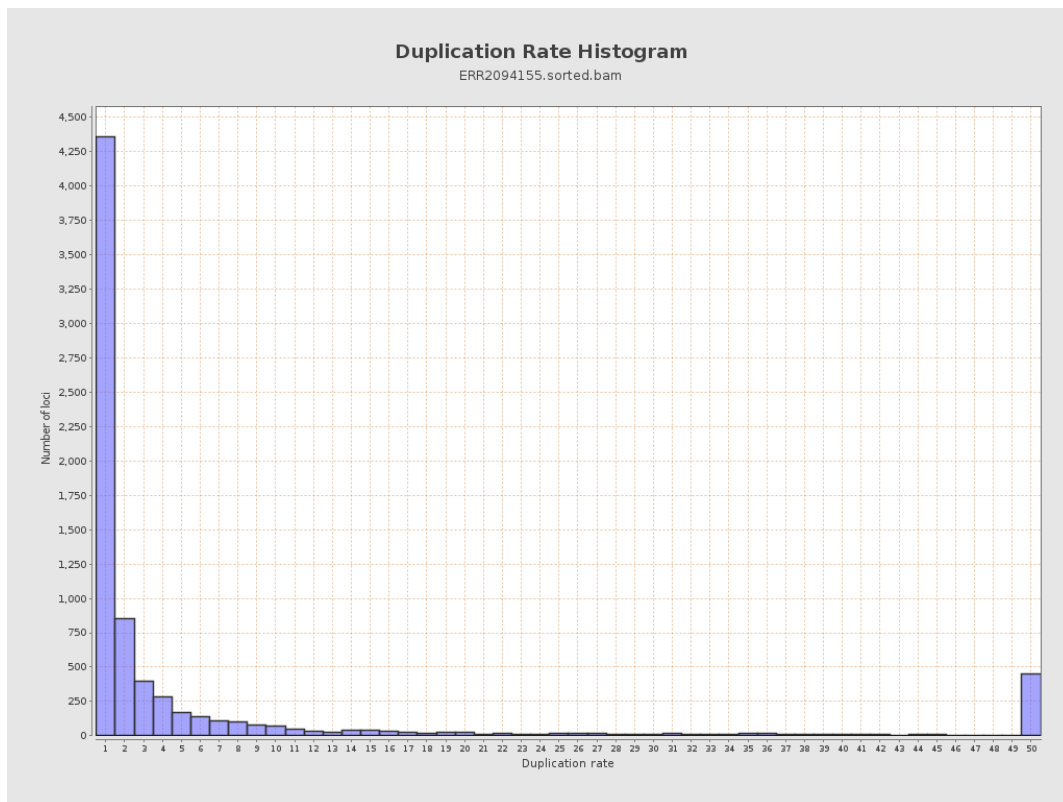
5. Results : Coverage Histogram (0-50X)



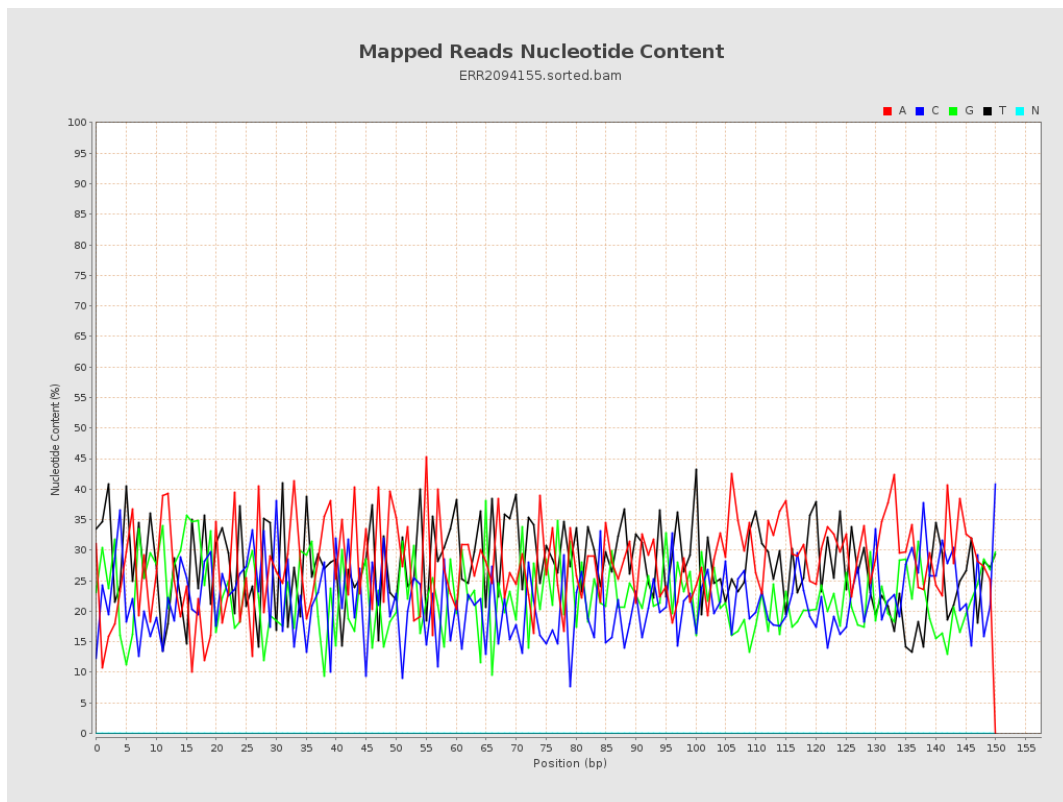
6. Results : Genome Fraction Coverage



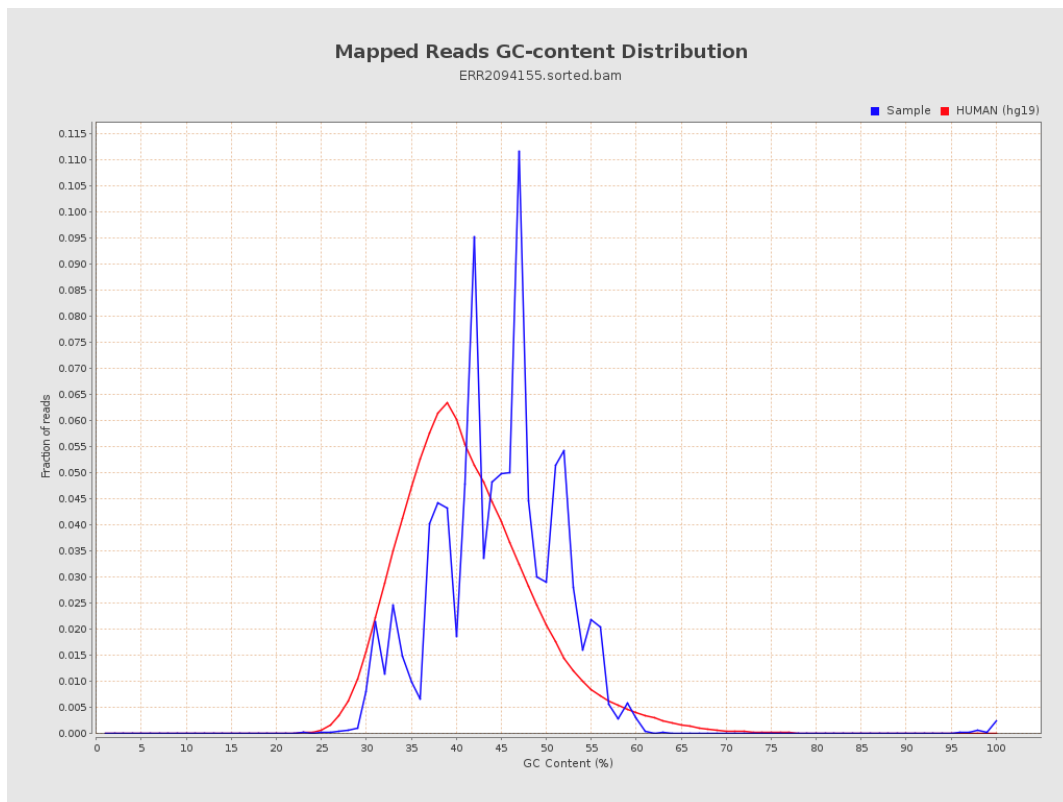
7. Results : Duplication Rate Histogram



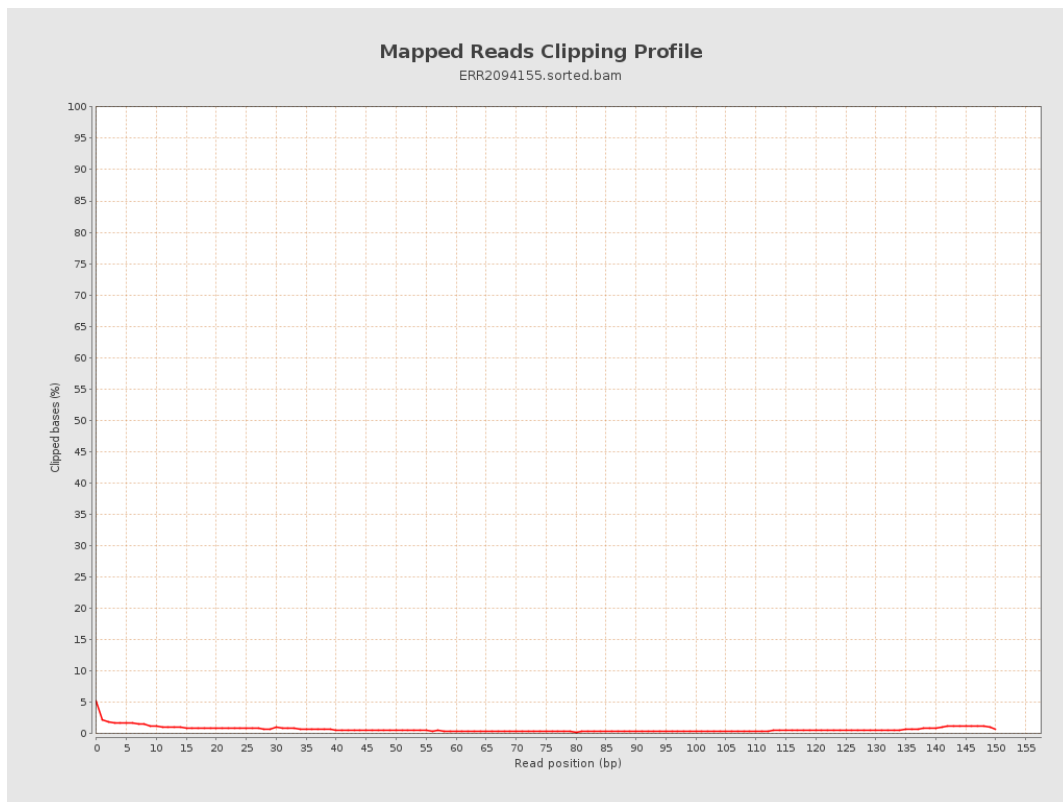
8. Results : Mapped Reads Nucleotide Content



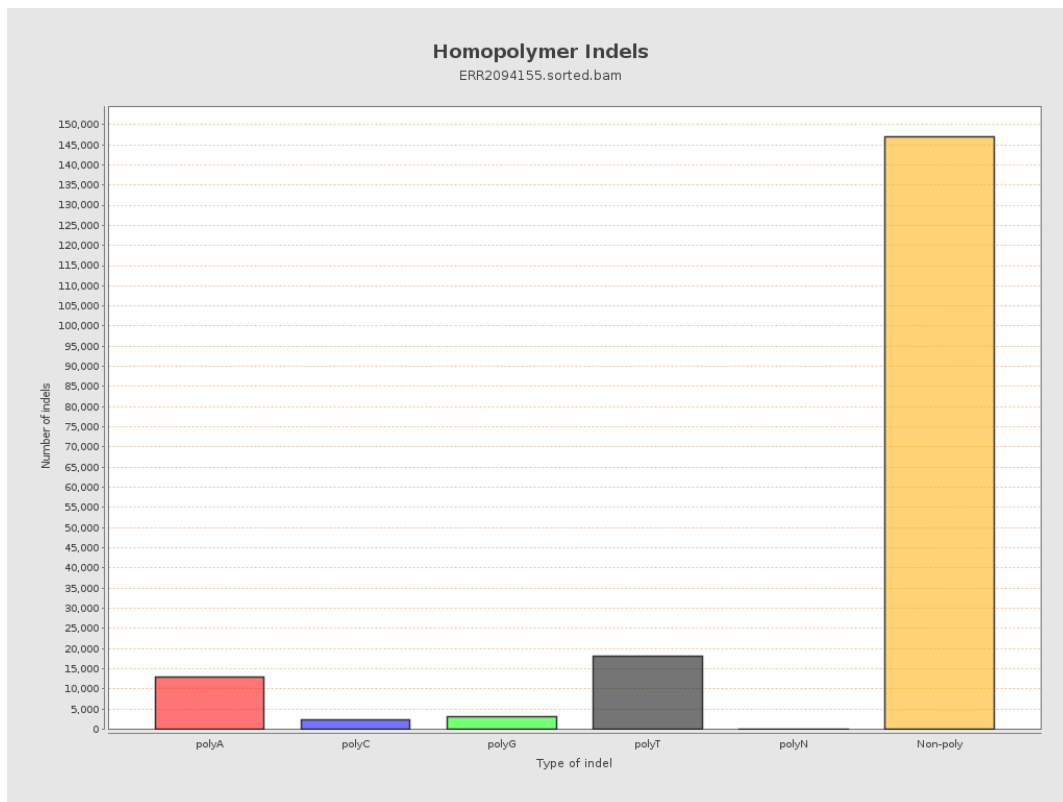
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



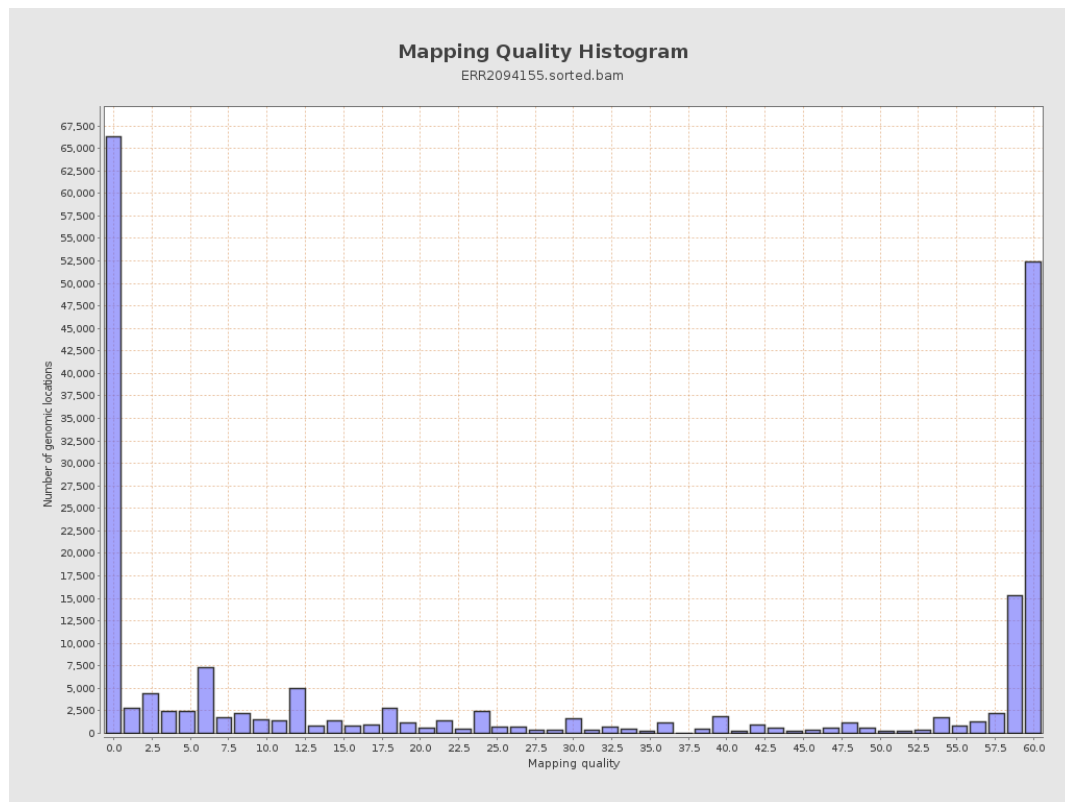
11. Results : Homopolymer Indels



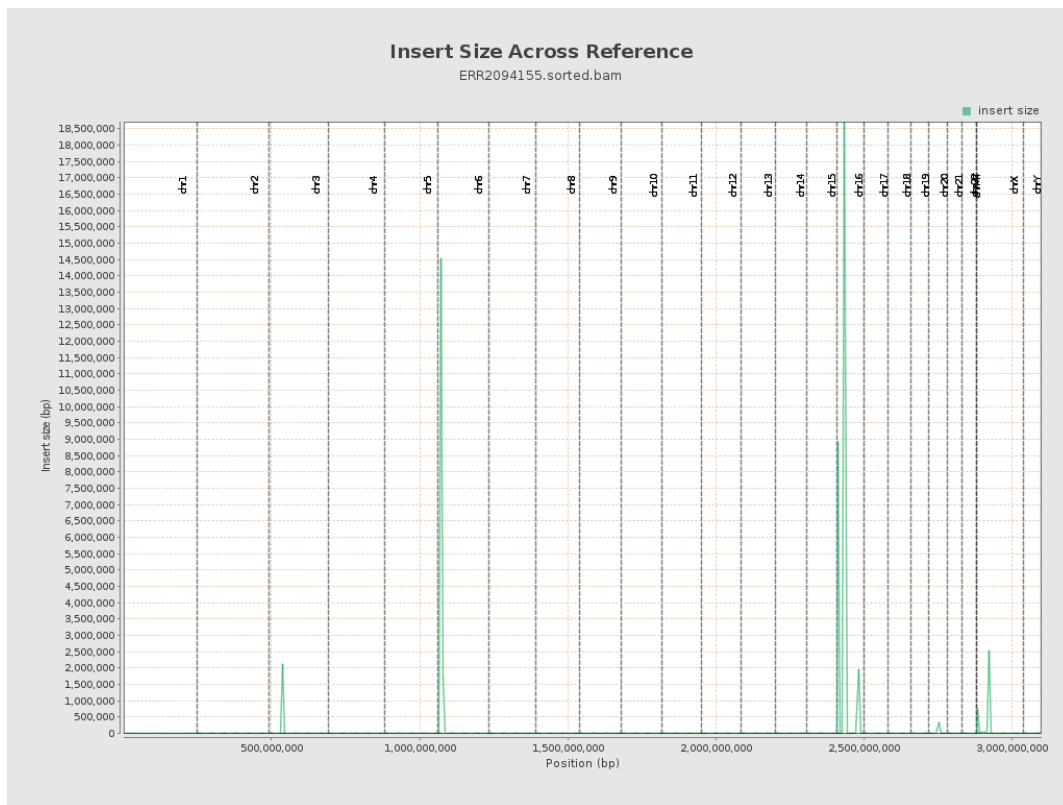
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

