

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:49:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094117.sorted.bam -c -nw 400 -hm 3
```

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_ERR2094117 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094117_1.fastq.gz ERR2094117_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:49:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	507,654
Mapped reads	404,641 / 79.71%
Unmapped reads	103,013 / 20.29%
Mapped paired reads	404,641 / 79.71%
Mapped reads, first in pair	202,681 / 39.93%
Mapped reads, second in pair	201,960 / 39.78%
Mapped reads, both in pair	401,780 / 79.14%
Mapped reads, singletons	2,861 / 0.56%
Secondary alignments	0
Supplementary alignments	632 / 0.12%
Read min/max/mean length	30 / 151 / 129.79
Duplicated reads (estimated)	403,743 / 79.53%
Duplication rate	54.84%
Clipped reads	50,418 / 9.93%

2.2. ACGT Content

Number/percentage of A's	16,536,742 / 27.53%
Number/percentage of C's	12,611,228 / 21%
Number/percentage of T's	17,413,194 / 28.99%
Number/percentage of G's	13,504,306 / 22.48%
Number/percentage of N's	896 / 0%

GC Percentage	43.48%
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2.3. Coverage

Mean	0.0194
Standard Deviation	35.5413

2.4. Mapping Quality

Mean Mapping Quality	6.37
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2.5. Insert size

Mean	418.97
Standard Deviation	65,765.29
P25/Median/P75	217 / 233 / 266

2.6. Mismatches and indels

General error rate	1.74%
Mismatches	1,018,896
Insertions	21,732
Mapped reads with at least one insertion	5.3%
Deletions	44,768
Mapped reads with at least one deletion	10.84%
Homopolymer indels	62.69%

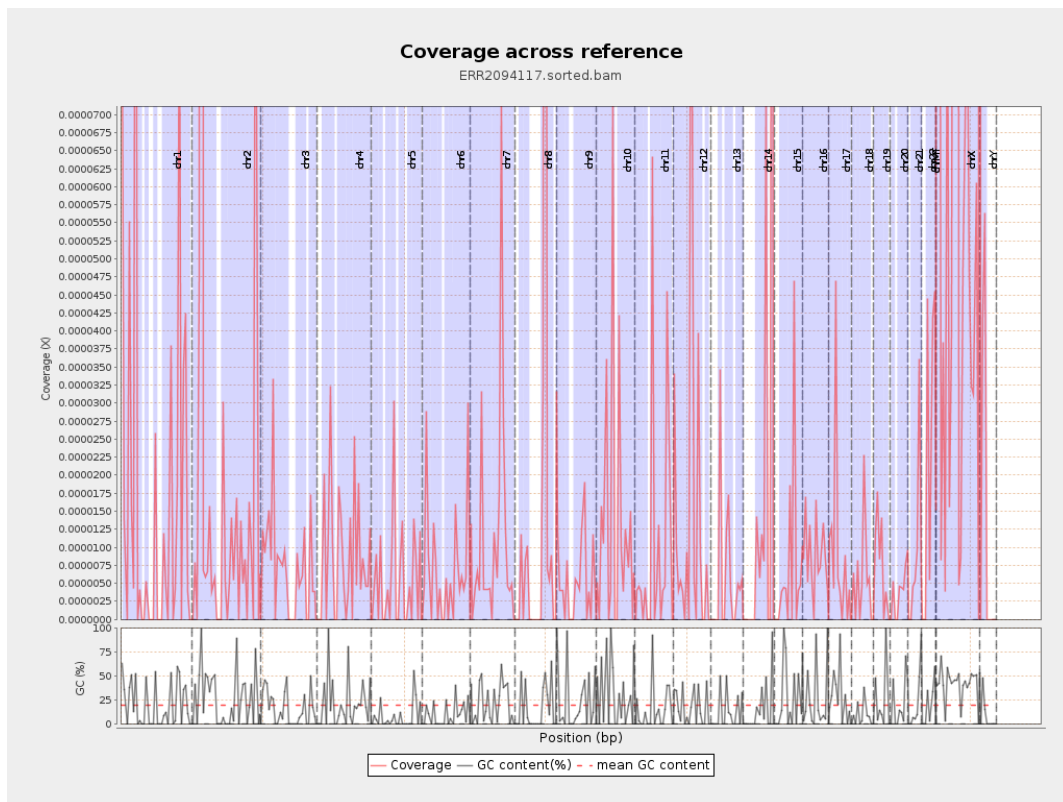
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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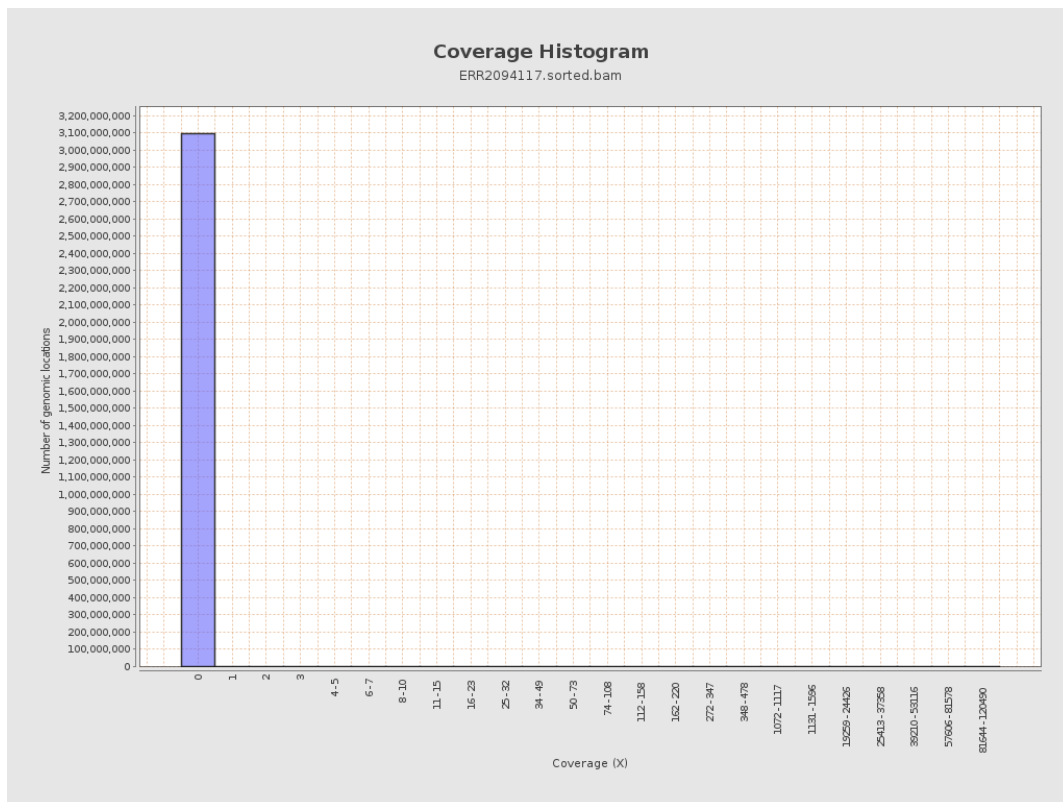
		bases	coverage	deviation
chr1	249250621	4738	0	0.0089
chr2	243199373	279840	0.0012	1.1399
chr3	198022430	1453	0	0.0029
chr4	191154276	1652	0	0.0037
chr5	180915260	1021	0	0.0031
chr6	171115067	1192	0	0.0033
chr7	159138663	1798	0	0.007
chr8	146364022	3157	0	0.0166
chr9	141213431	763	0	0.0027
chr10	135534747	1843	0	0.0081
chr11	135006516	1374	0	0.0068
chr12	133851895	1876	0	0.0088
chr13	115169878	641	0	0.0028
chr14	107349540	2575	0	0.0293
chr15	102531392	703	0	0.0034
chr16	90354753	791	0	0.0037
chr17	81195210	754	0	0.0066
chr18	78077248	405	0	0.0023
chr19	59128983	432	0	0.0029
chr20	63025520	234	0	0.0022
chr21	48129895	459	0	0.0038
chr22	51304566	1094	0	0.0052
chrMT	16571	59780006	3,607.5075	14,932.1006
chrX	155270560	25272	0.0002	0.1572

chrY	59373566	760	0	0.0056
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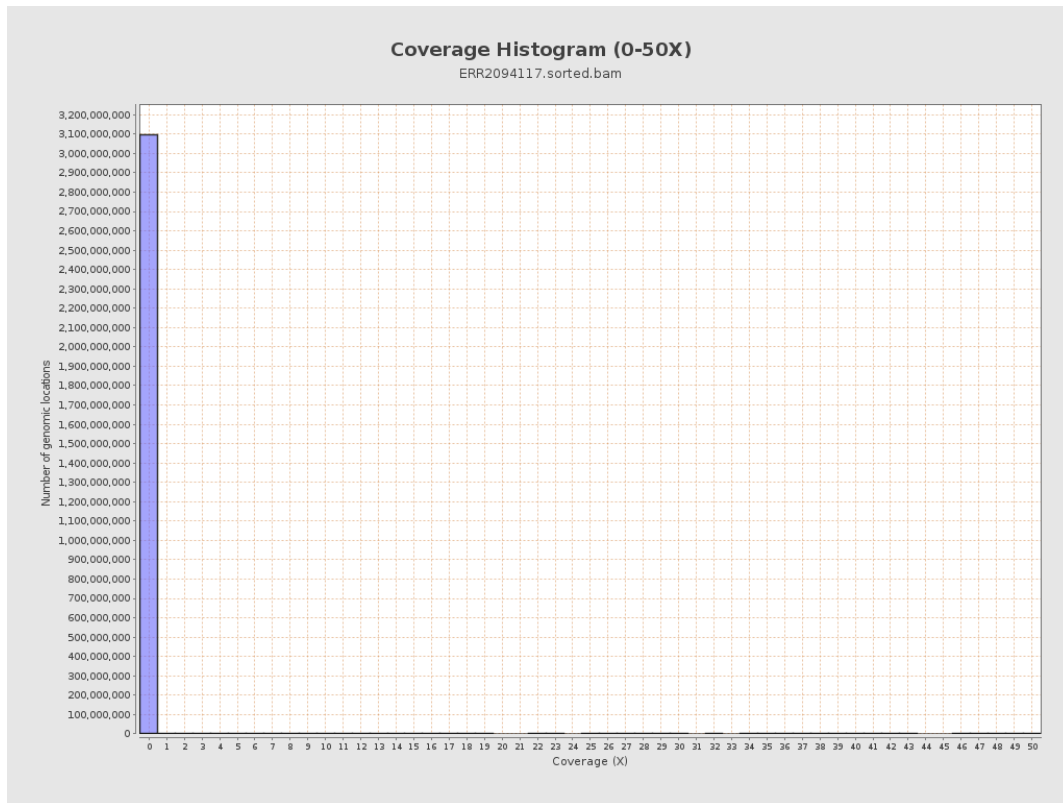
3. Results : Coverage across reference



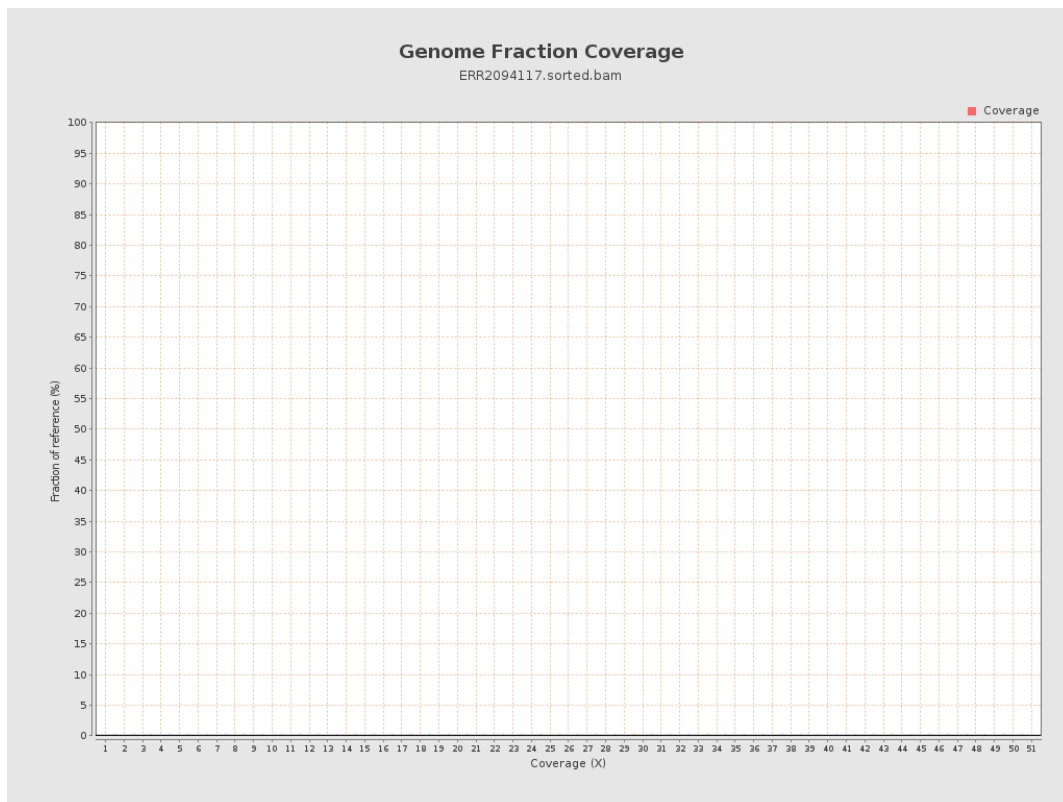
4. Results : Coverage Histogram



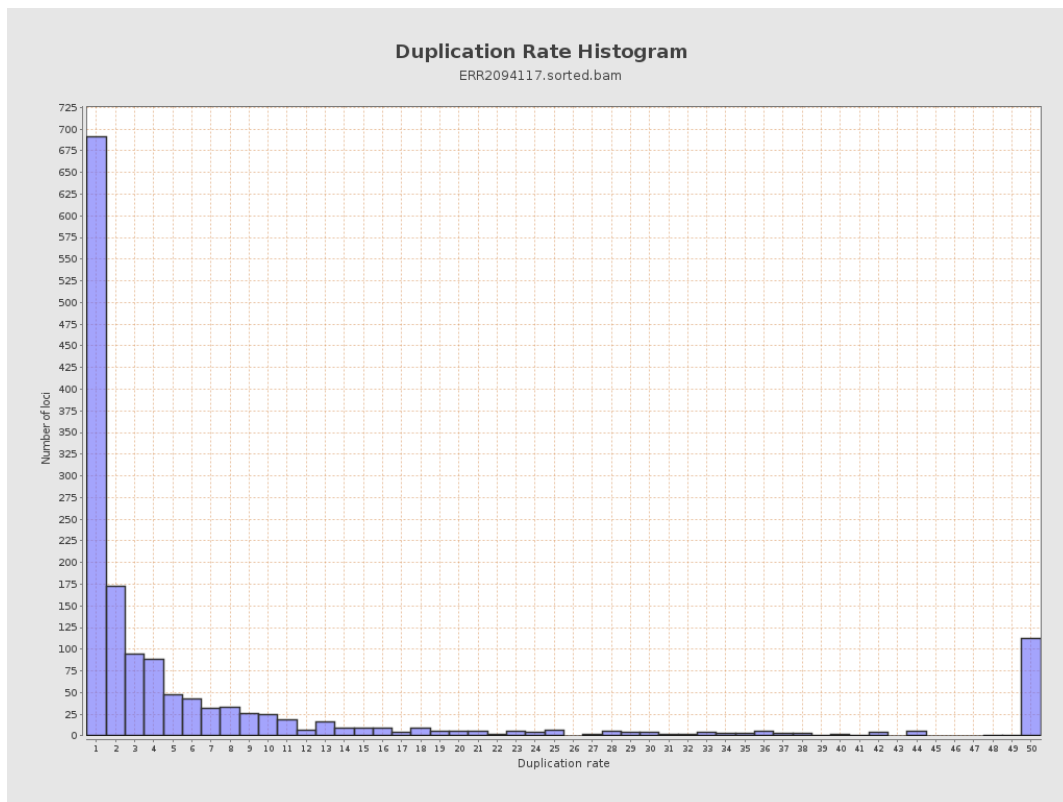
5. Results : Coverage Histogram (0-50X)



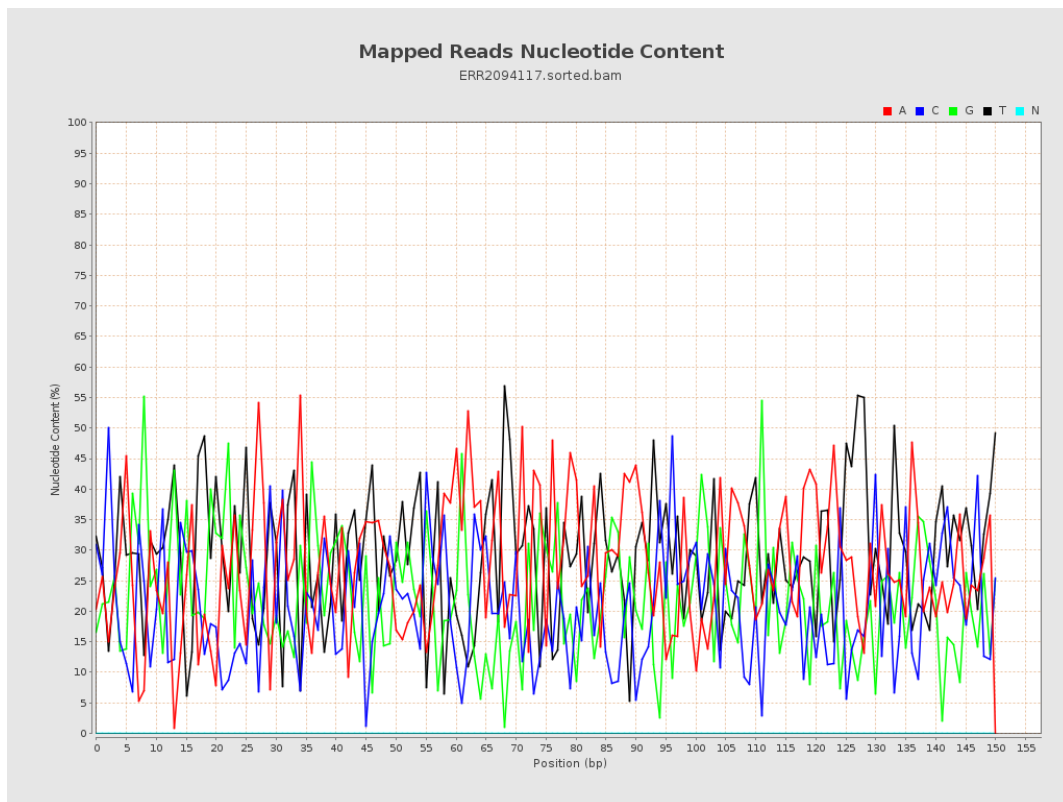
6. Results : Genome Fraction Coverage



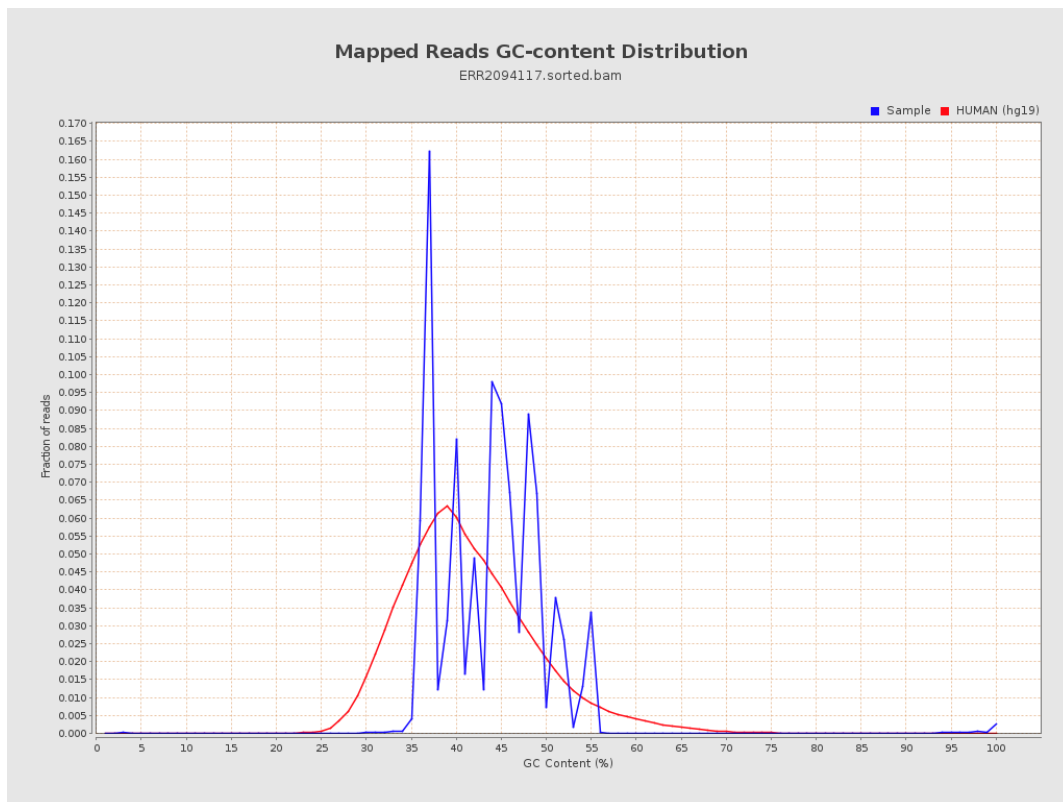
7. Results : Duplication Rate Histogram



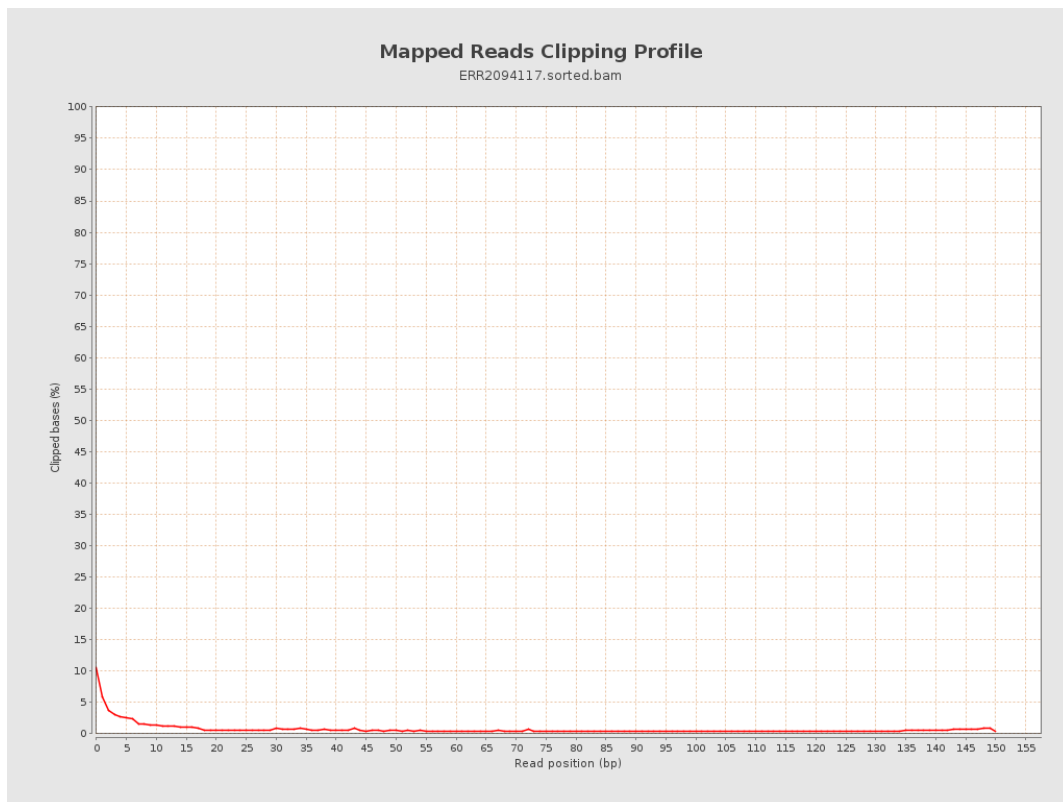
8. Results : Mapped Reads Nucleotide Content



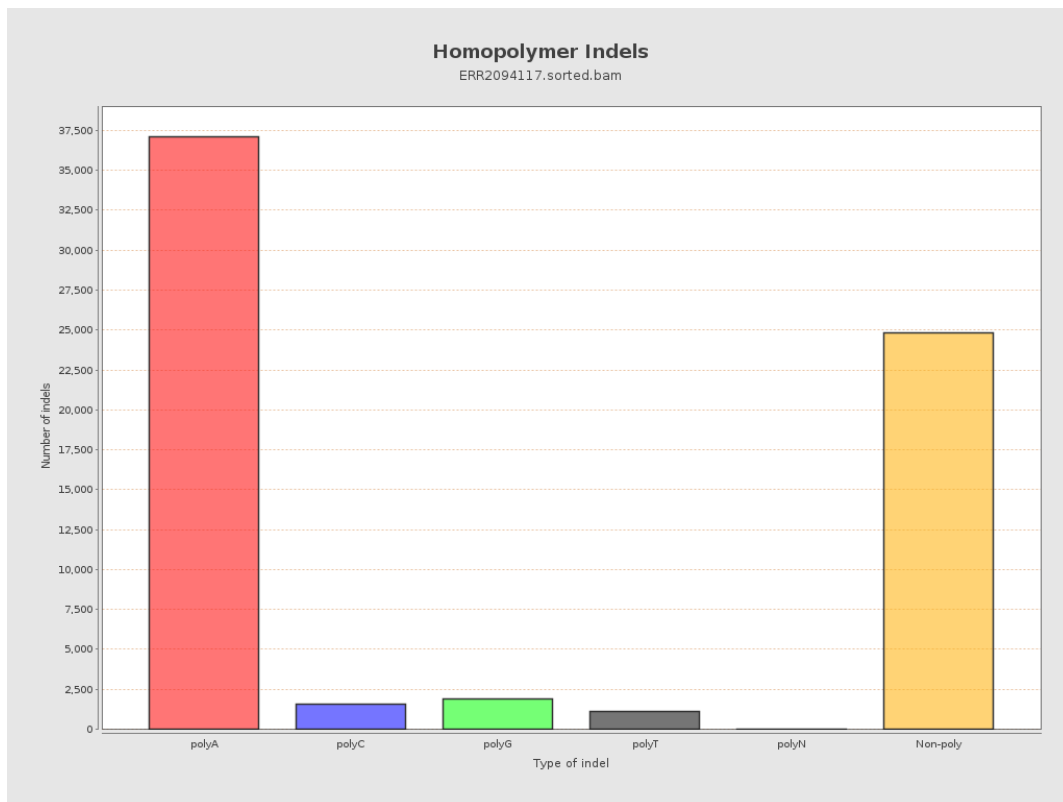
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



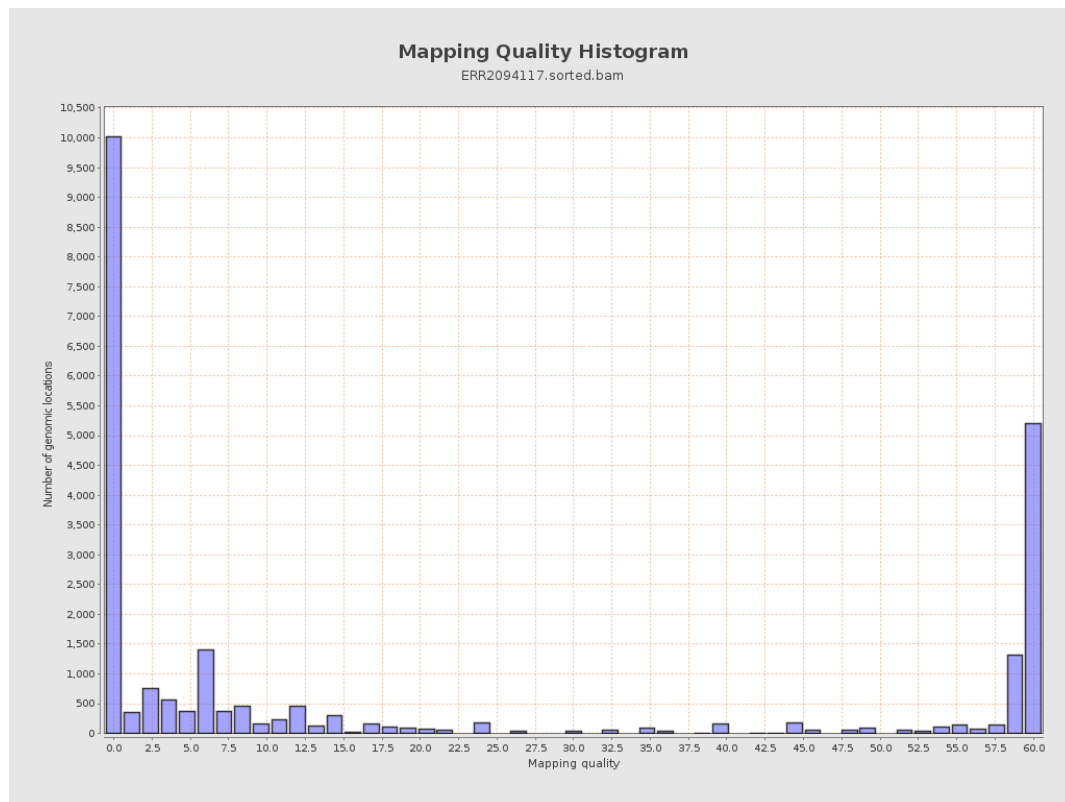
11. Results : Homopolymer Indels



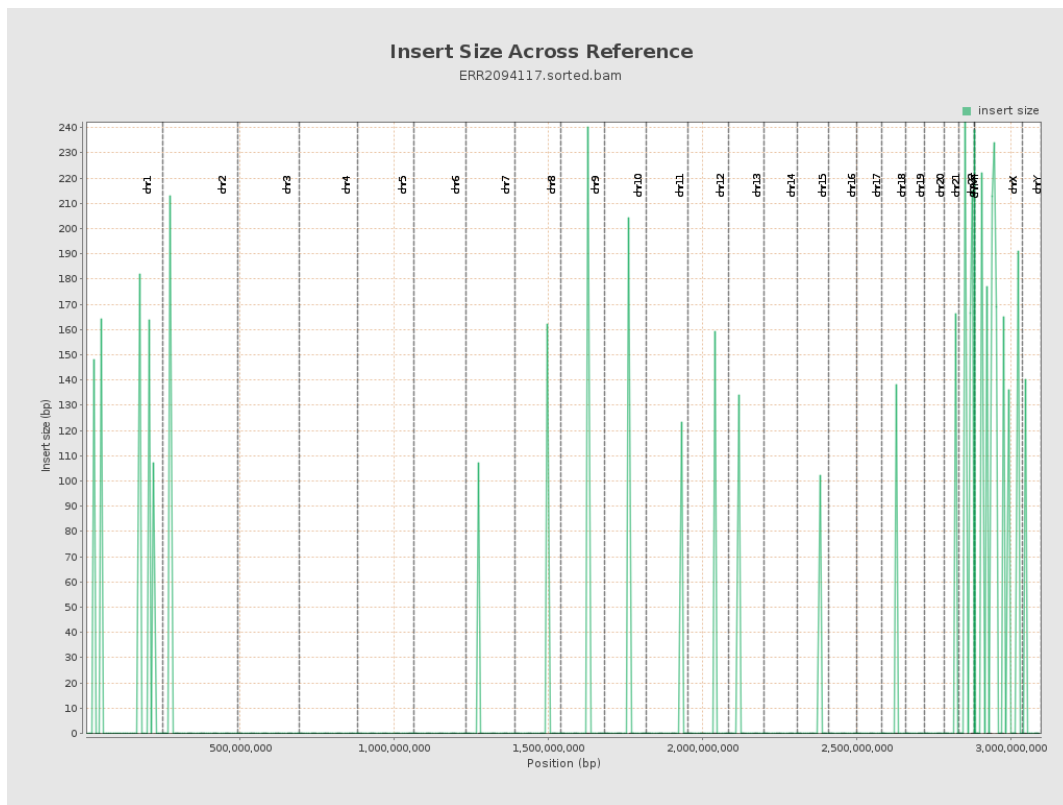
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

