

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:54:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094119.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_ERR2094119 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094119_1.fastq.gz ERR2094119_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:54:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094119.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	398,342
Mapped reads	343,704 / 86.28%
Unmapped reads	54,638 / 13.72%
Mapped paired reads	343,704 / 86.28%
Mapped reads, first in pair	172,407 / 43.28%
Mapped reads, second in pair	171,297 / 43%
Mapped reads, both in pair	341,008 / 85.61%
Mapped reads, singletons	2,696 / 0.68%
Secondary alignments	0
Supplementary alignments	3,668 / 0.92%
Read min/max/mean length	30 / 151 / 137.38
Duplicated reads (estimated)	343,550 / 86.24%
Duplication rate	44.77%
Clipped reads	80,927 / 20.32%

2.2. ACGT Content

Number/percentage of A's	13,539,813 / 27.09%
Number/percentage of C's	10,776,407 / 21.56%
Number/percentage of T's	14,313,978 / 28.64%
Number/percentage of G's	11,352,476 / 22.71%
Number/percentage of N's	597 / 0%

GC Percentage	44.27%
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2.3. Coverage

Mean	0.0162
Standard Deviation	27.3774

2.4. Mapping Quality

Mean Mapping Quality	16.06
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2.5. Insert size

Mean	18,099.79
Standard Deviation	1,323,225.25
P25/Median/P75	212 / 231 / 256

2.6. Mismatches and indels

General error rate	1.6%
Mismatches	762,962
Insertions	24,673
Mapped reads with at least one insertion	7.08%
Deletions	31,881
Mapped reads with at least one deletion	9.07%
Homopolymer indels	62.76%

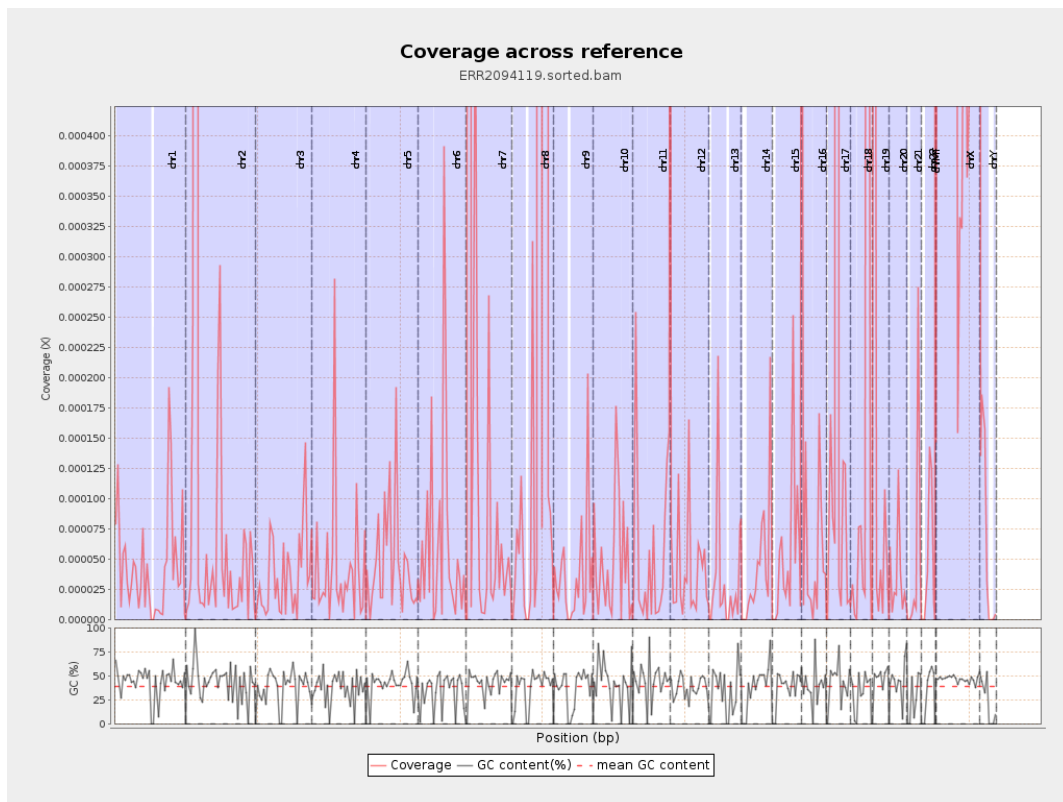
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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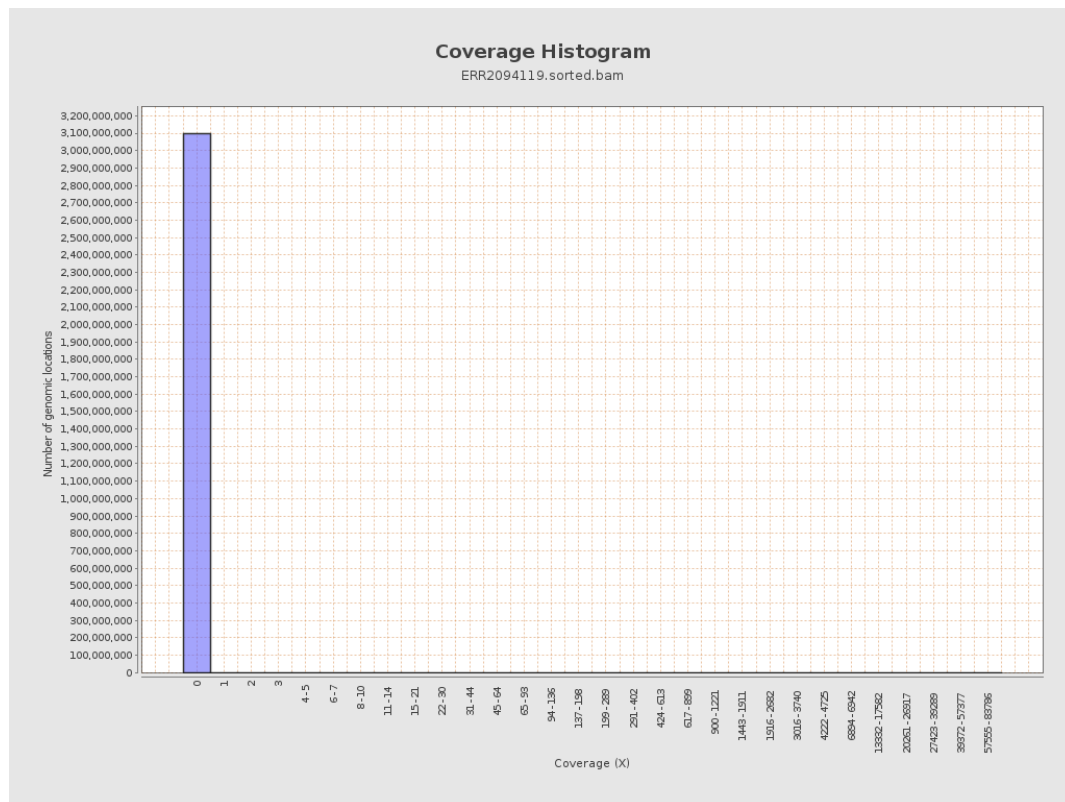
		bases	coverage	deviation
chr1	249250621	10964	0	0.0236
chr2	243199373	224951	0.0009	0.873
chr3	198022430	7132	0	0.0135
chr4	191154276	8110	0	0.0158
chr5	180915260	8478	0	0.0198
chr6	171115067	9984	0.0001	0.0301
chr7	159138663	63948	0.0004	0.5933
chr8	146364022	3831390	0.0262	9.0572
chr9	141213431	5091	0	0.0093
chr10	135534747	6493	0	0.0135
chr11	135006516	7509	0.0001	0.0293
chr12	133851895	5804	0	0.0123
chr13	115169878	3687	0	0.0102
chr14	107349540	4678	0	0.0238
chr15	102531392	5426	0.0001	0.0147
chr16	90354753	9550	0.0001	0.043
chr17	81195210	67173	0.0008	0.2075
chr18	78077248	18129	0.0002	0.1039
chr19	59128983	12499	0.0002	0.1977
chr20	63025520	2237	0	0.0072
chr21	48129895	2555	0.0001	0.0172
chr22	51304566	2473	0	0.0271
chrMT	16571	45596026	2,751.5555	11,477.008
chrX	155270560	105398	0.0007	0.0907

chrY	59373566	3633	0.0001	0.015
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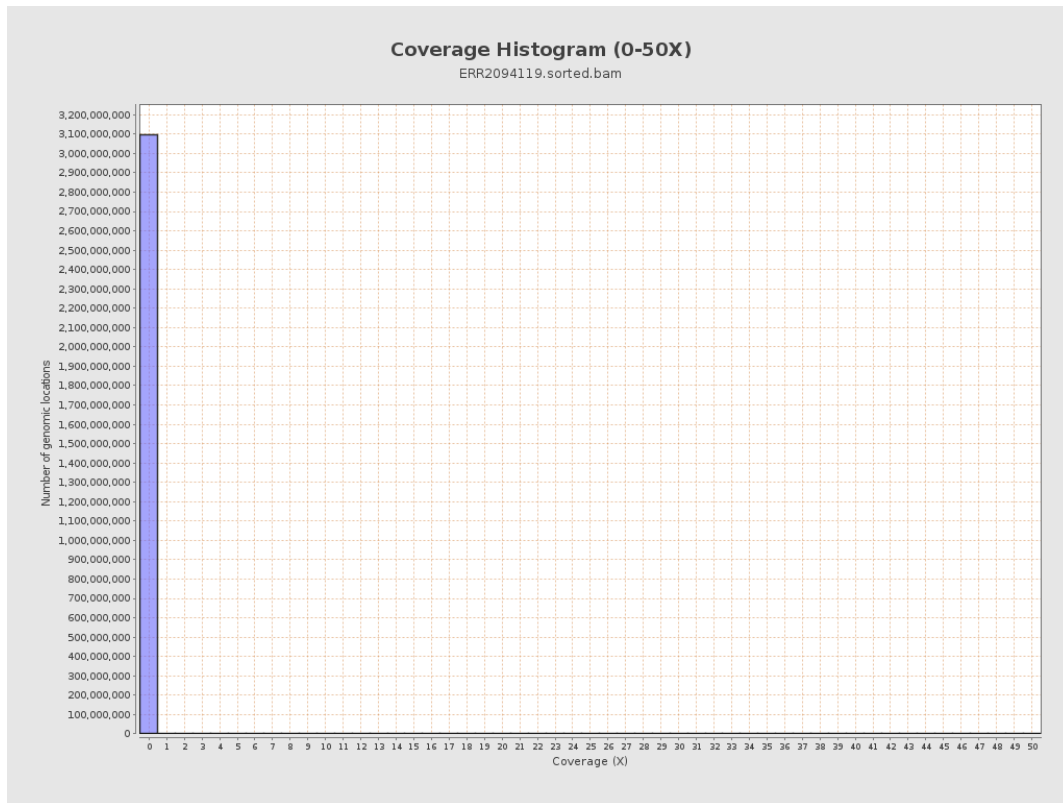
3. Results : Coverage across reference



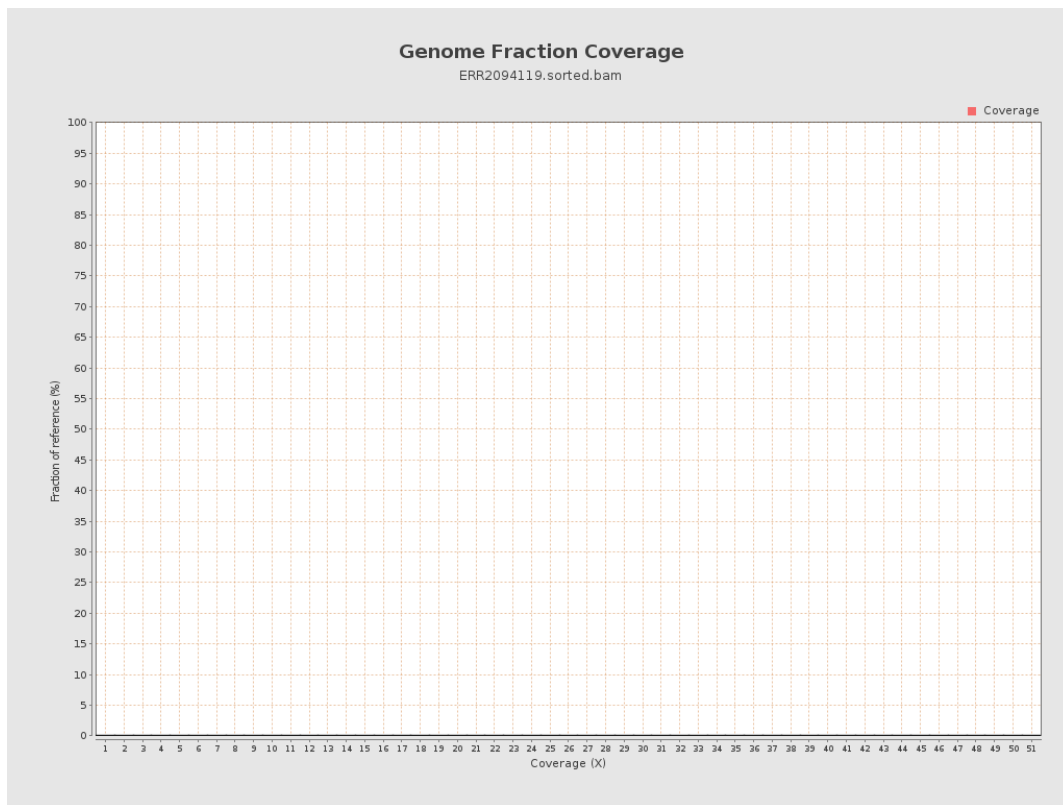
4. Results : Coverage Histogram



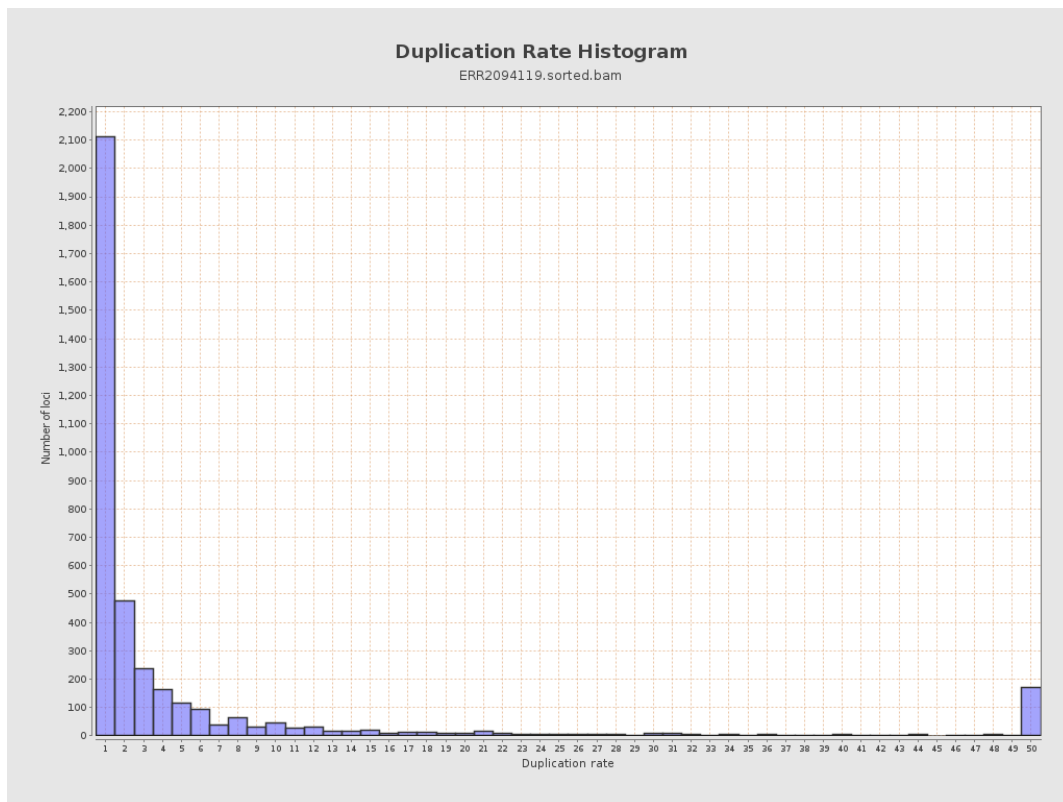
5. Results : Coverage Histogram (0-50X)



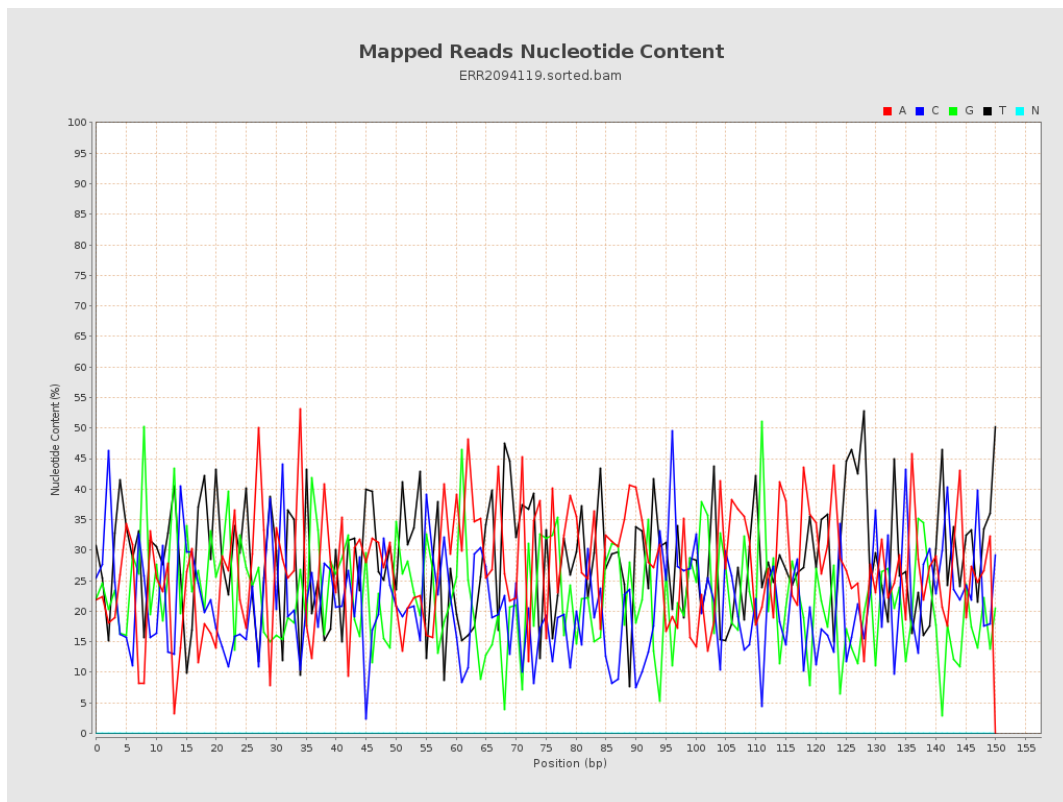
6. Results : Genome Fraction Coverage



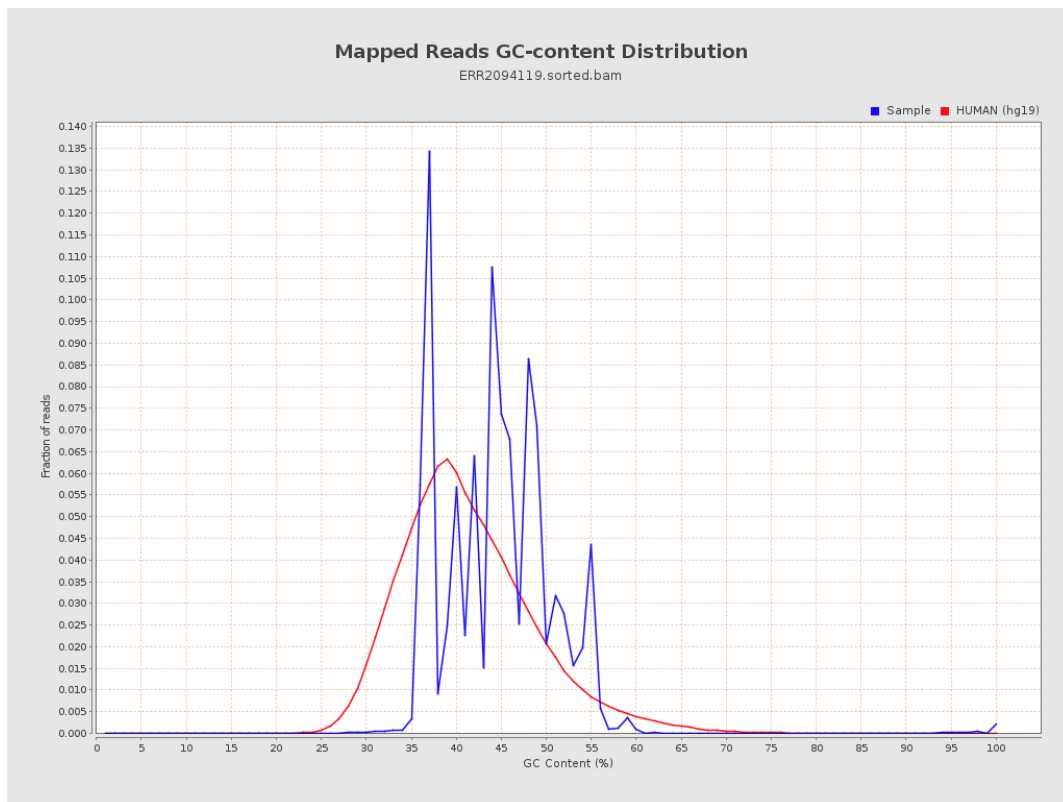
7. Results : Duplication Rate Histogram



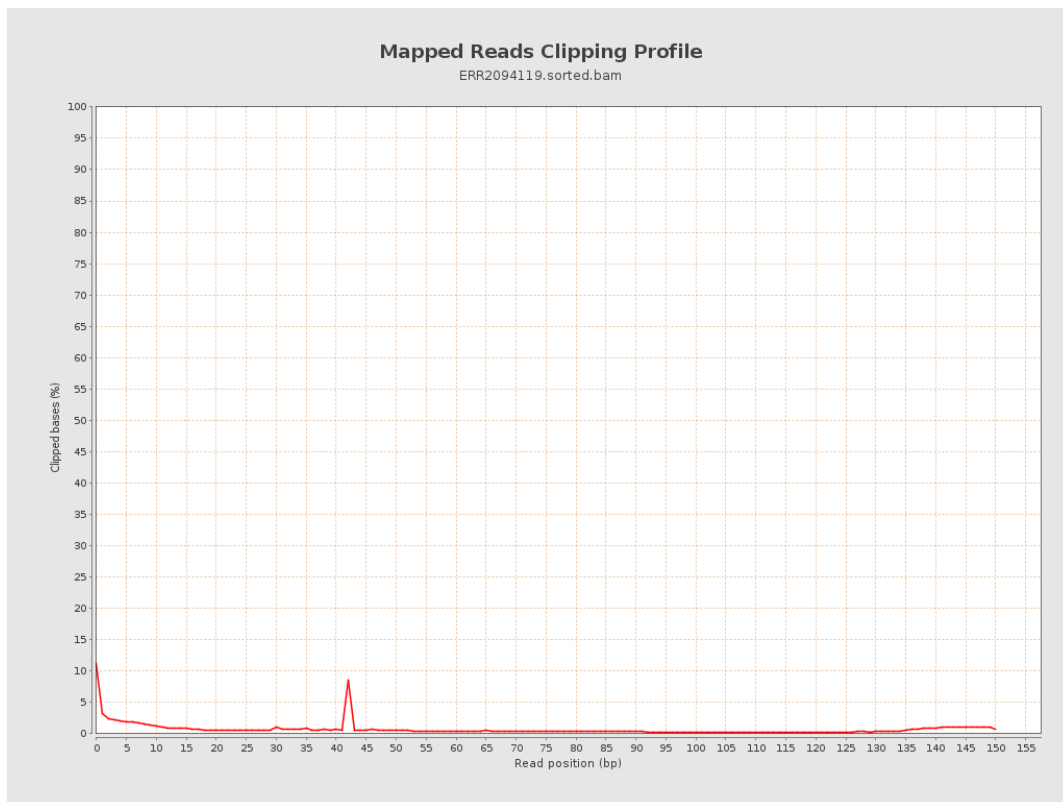
8. Results : Mapped Reads Nucleotide Content



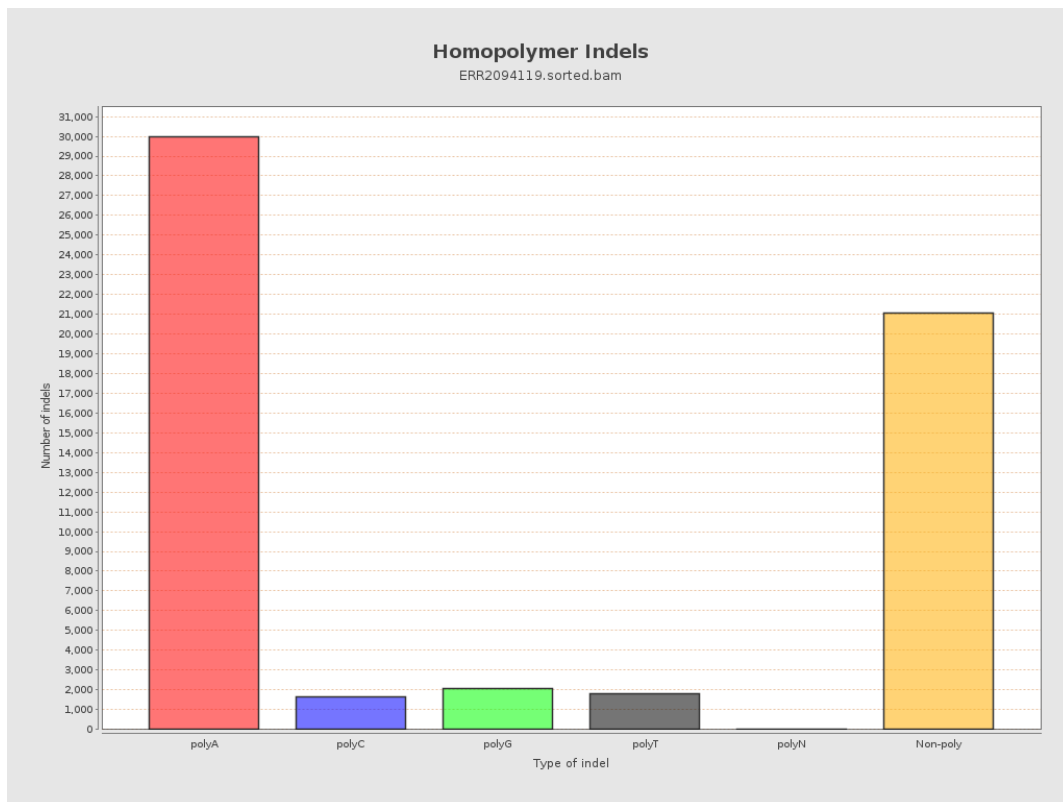
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



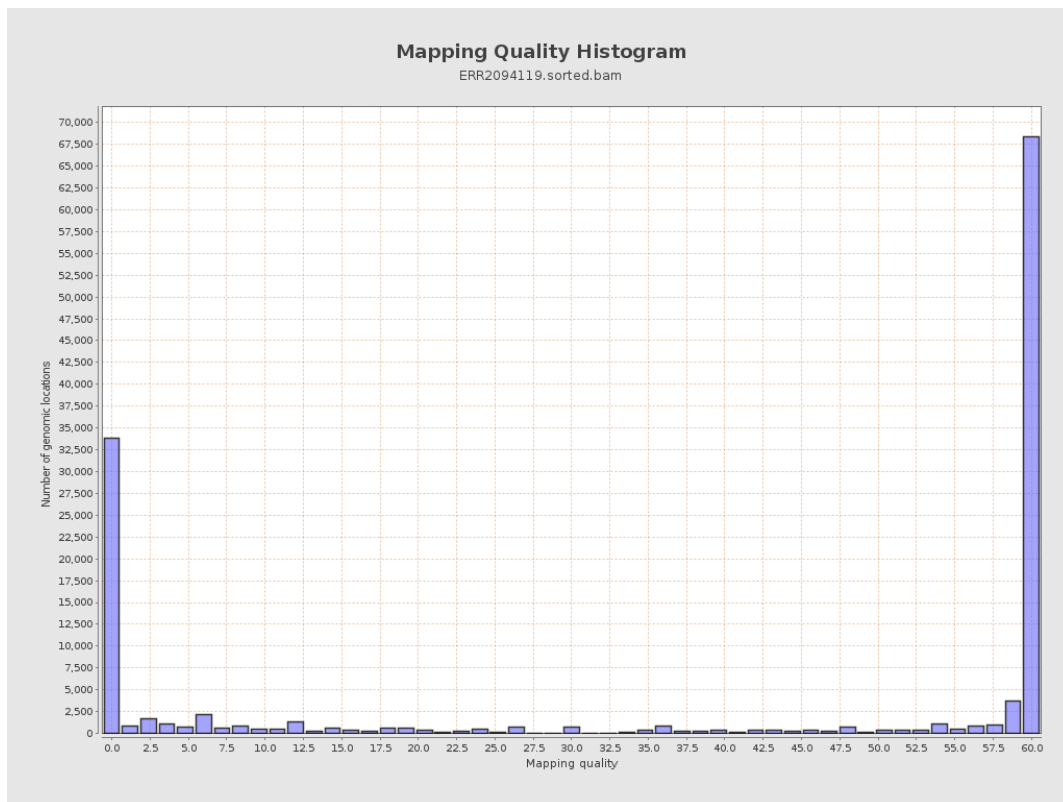
11. Results : Homopolymer Indels



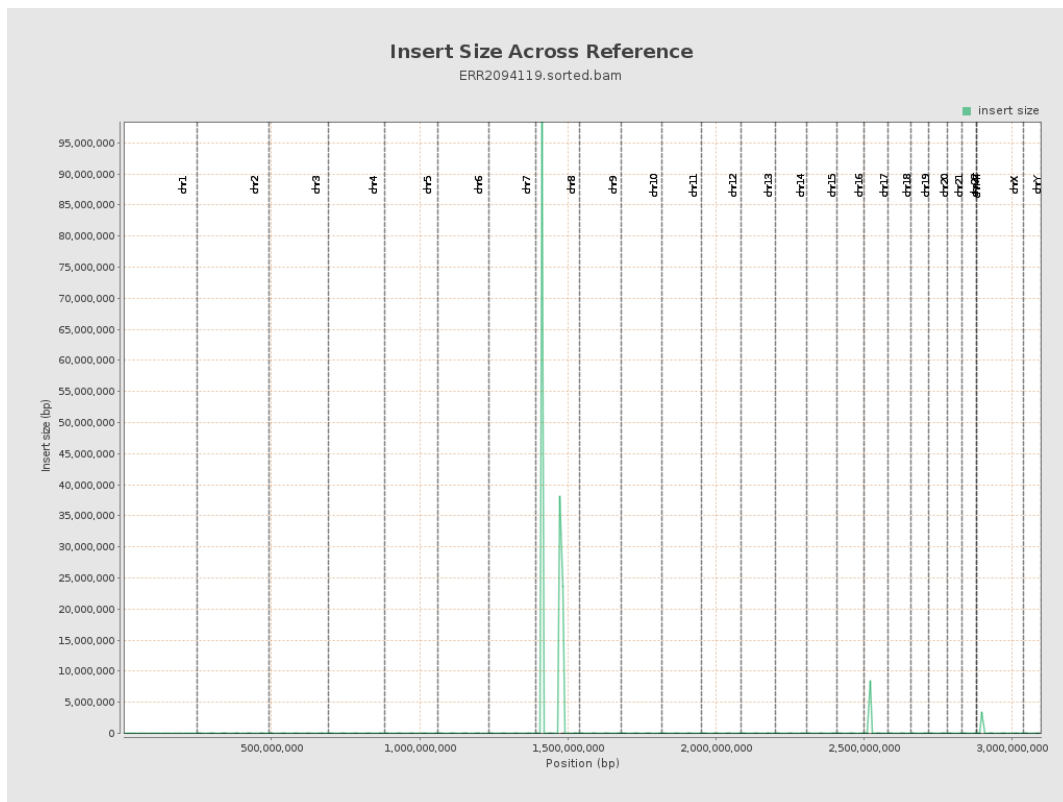
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

