

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:26:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472404.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_SRR3472404 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472404_1.fastq.gz SRR3472404_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:26:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472404.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,766,244
Mapped reads	20,577,120 / 99.09%
Unmapped reads	189,124 / 0.91%
Mapped paired reads	20,577,120 / 99.09%
Mapped reads, first in pair	10,321,730 / 49.7%
Mapped reads, second in pair	10,255,390 / 49.38%
Mapped reads, both in pair	20,460,926 / 98.53%
Mapped reads, singletons	116,194 / 0.56%
Secondary alignments	0
Supplementary alignments	79,108 / 0.38%
Read min/max/mean length	30 / 100 / 99.47
Duplicated reads (estimated)	13,071,314 / 62.95%
Duplication rate	47.78%
Clipped reads	1,410,477 / 6.79%

2.2. ACGT Content

Number/percentage of A's	547,611,420 / 27.11%
Number/percentage of C's	463,791,579 / 22.96%
Number/percentage of T's	548,187,482 / 27.13%
Number/percentage of G's	460,410,496 / 22.79%
Number/percentage of N's	254,927 / 0.01%

GC Percentage	45.75%
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2.3. Coverage

Mean	0.6527
Standard Deviation	19.1702

2.4. Mapping Quality

Mean Mapping Quality	55.04
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2.5. Insert size

Mean	20,342.61
Standard Deviation	1,382,584.56
P25/Median/P75	158 / 219 / 295

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	11,413,253
Insertions	114,207
Mapped reads with at least one insertion	0.55%
Deletions	99,724
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.65%

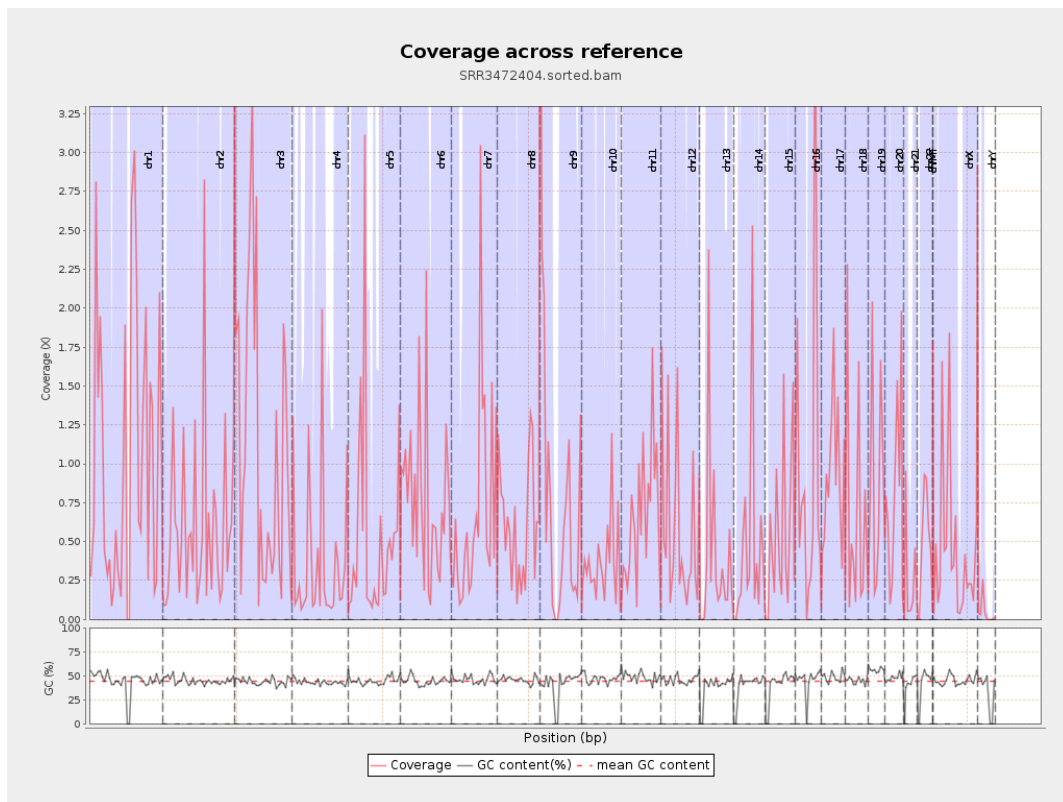
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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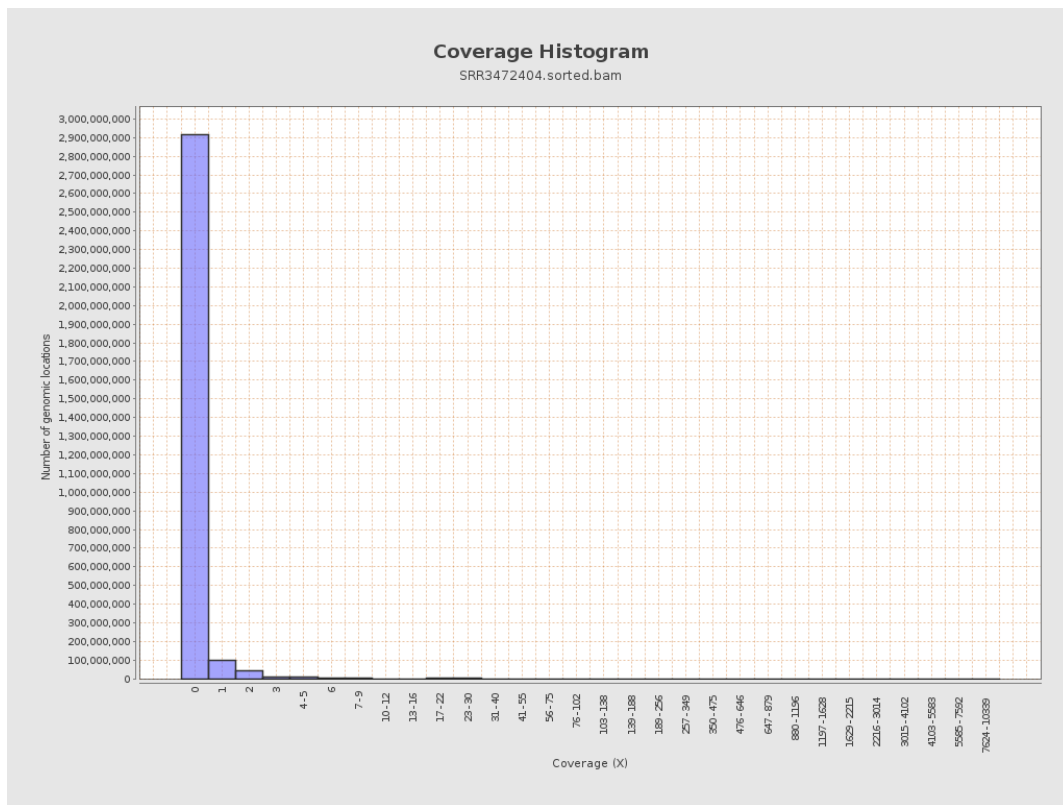
		bases	coverage	deviation
chr1	249250621	254196667	1.0198	27.4543
chr2	243199373	143125833	0.5885	16.8827
chr3	198022430	223937395	1.1309	26.353
chr4	191154276	72997285	0.3819	15.7805
chr5	180915260	97543928	0.5392	15.1117
chr6	171115067	131677937	0.7695	16.9288
chr7	159138663	112430590	0.7065	21.1675
chr8	146364022	89373495	0.6106	14.643
chr9	141213431	97335318	0.6893	17.4911
chr10	135534747	50824209	0.375	11.2355
chr11	135006516	89196591	0.6607	18.7914
chr12	133851895	80269843	0.5997	17.5813
chr13	115169878	45126653	0.3918	13.8808
chr14	107349540	49400795	0.4602	13.3213
chr15	102531392	56717273	0.5532	21.394
chr16	90354753	83003134	0.9186	23.8939
chr17	81195210	76323849	0.94	21.5581
chr18	78077248	49985214	0.6402	25.5519
chr19	59128983	49943162	0.8446	18.7617
chr20	63025520	51928892	0.8239	25.0665
chr21	48129895	13188401	0.274	17.0236
chr22	51304566	25407956	0.4952	15.0492
chrMT	16571	29769	1.7965	1.8213
chrX	155270560	73698142	0.4746	15.6245

chrY	59373566	2832359	0.0477	2.6516
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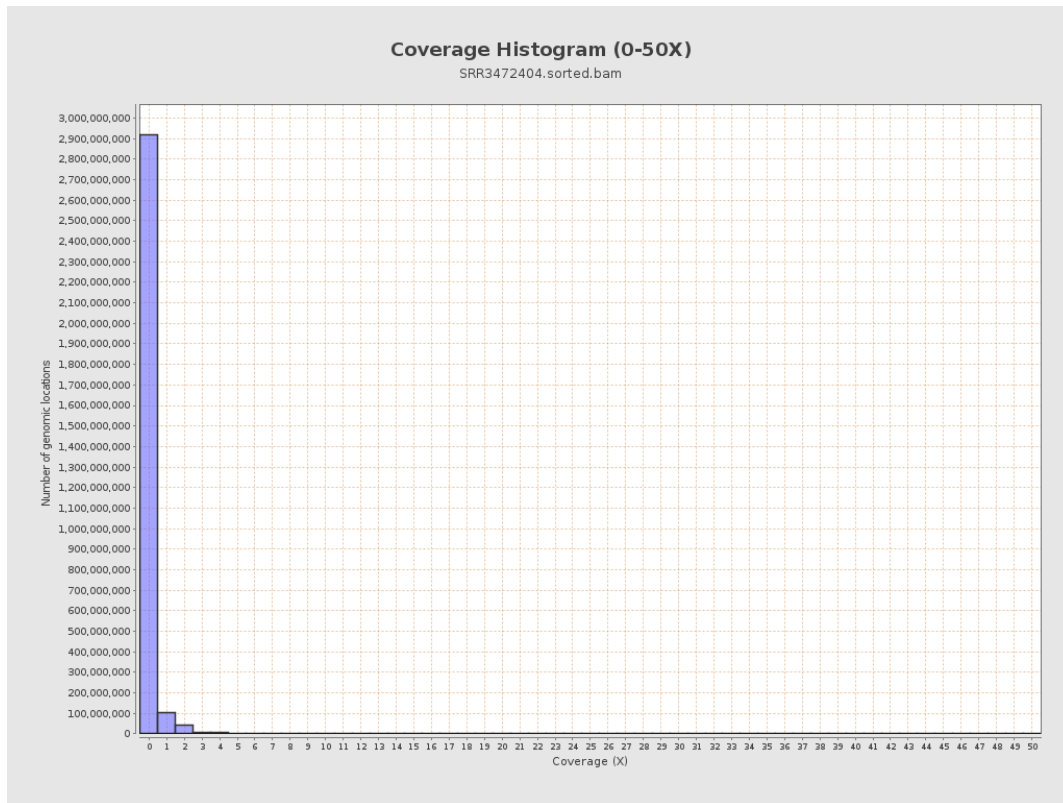
3. Results : Coverage across reference



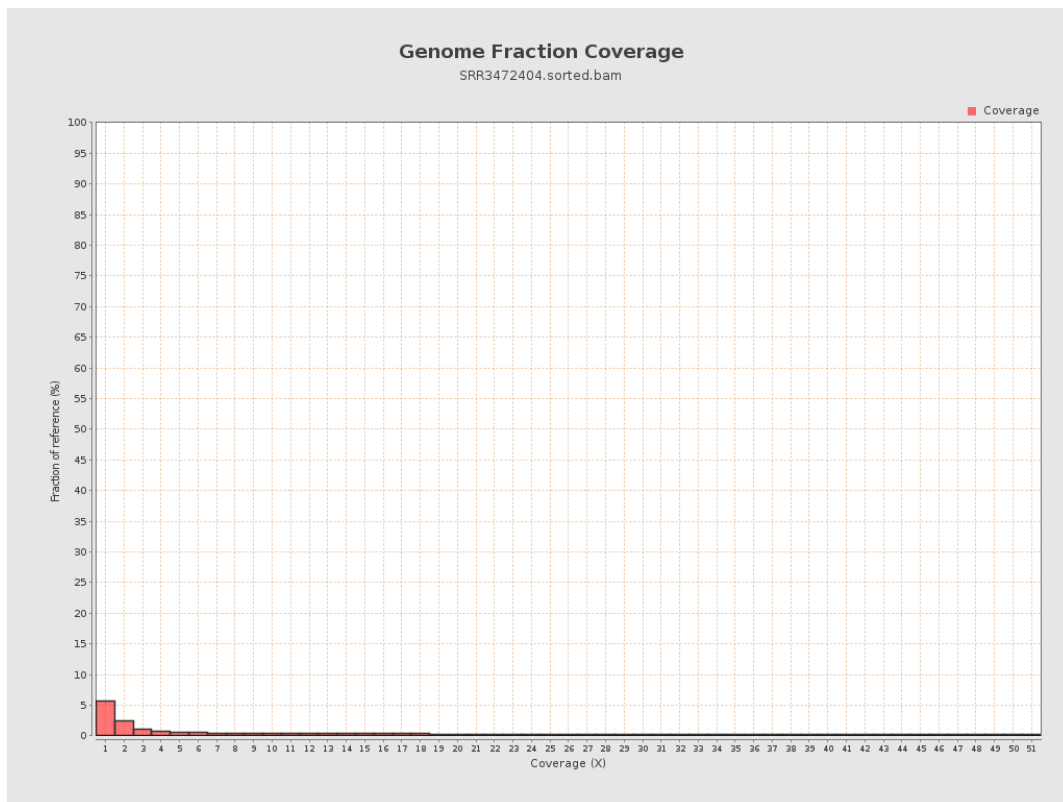
4. Results : Coverage Histogram



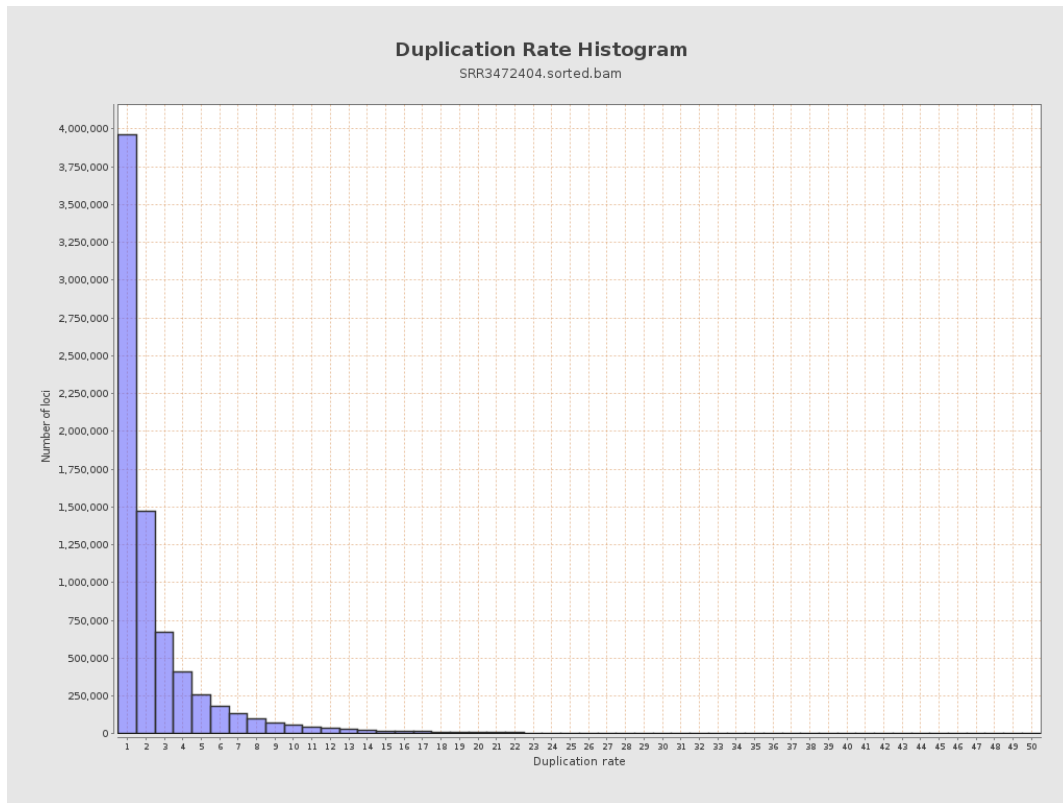
5. Results : Coverage Histogram (0-50X)



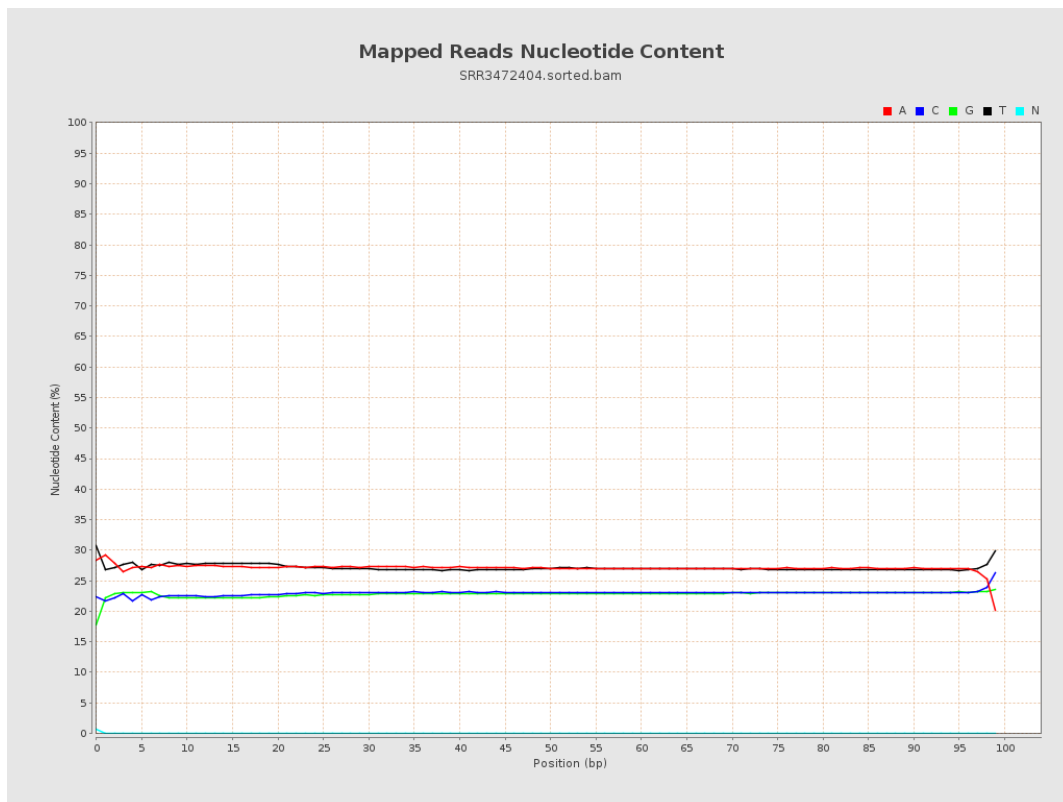
6. Results : Genome Fraction Coverage



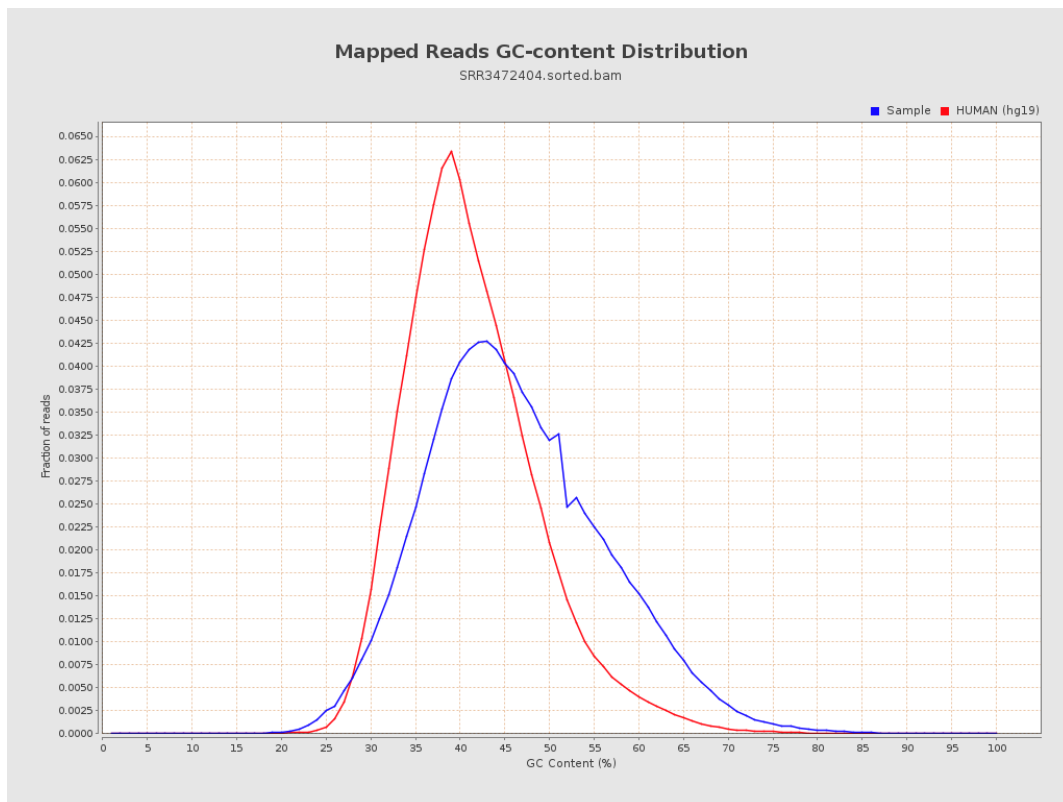
7. Results : Duplication Rate Histogram



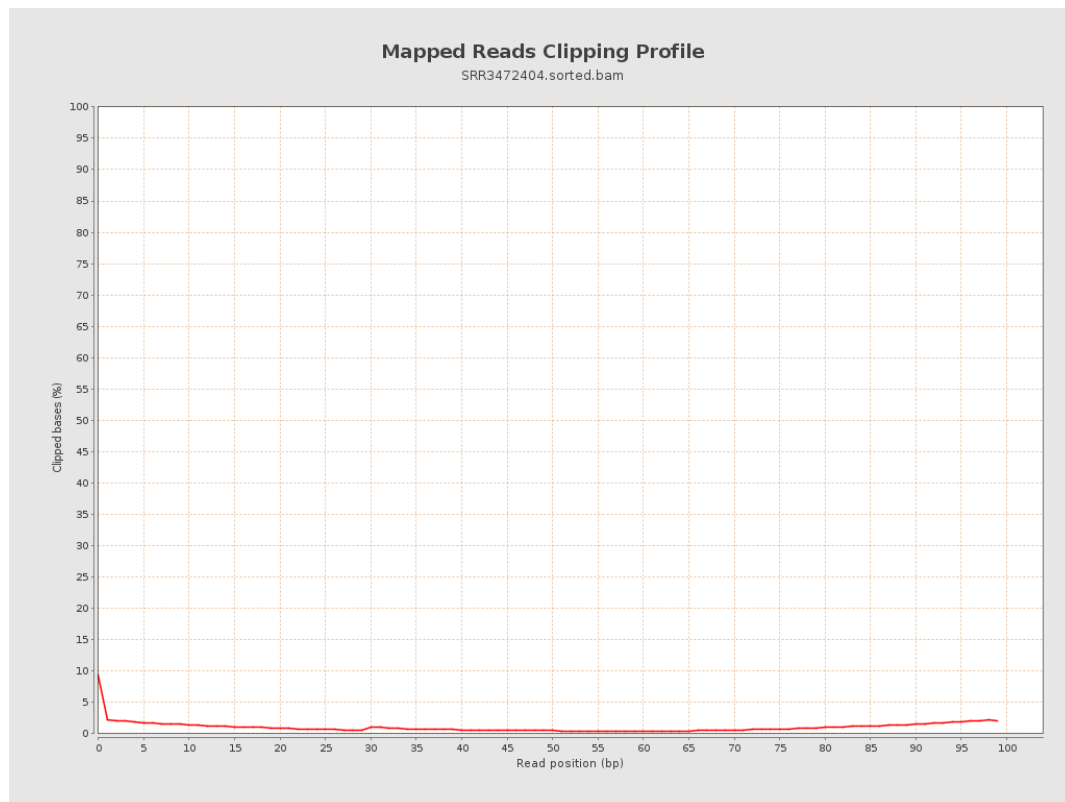
8. Results : Mapped Reads Nucleotide Content



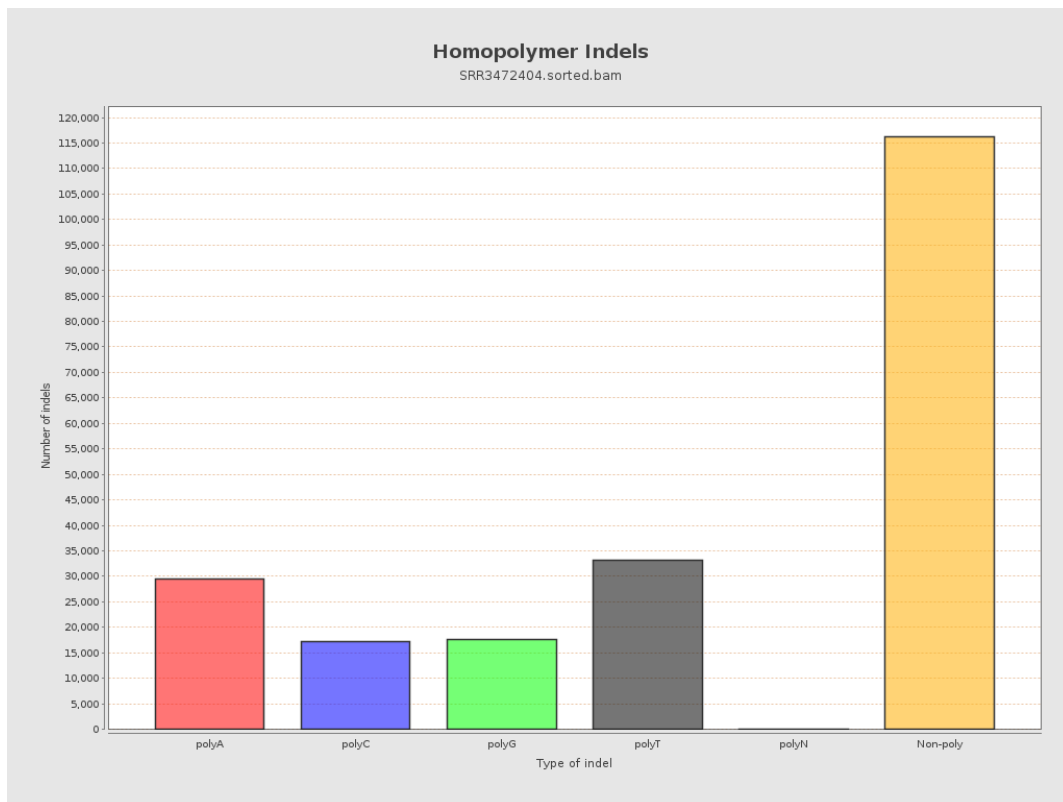
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



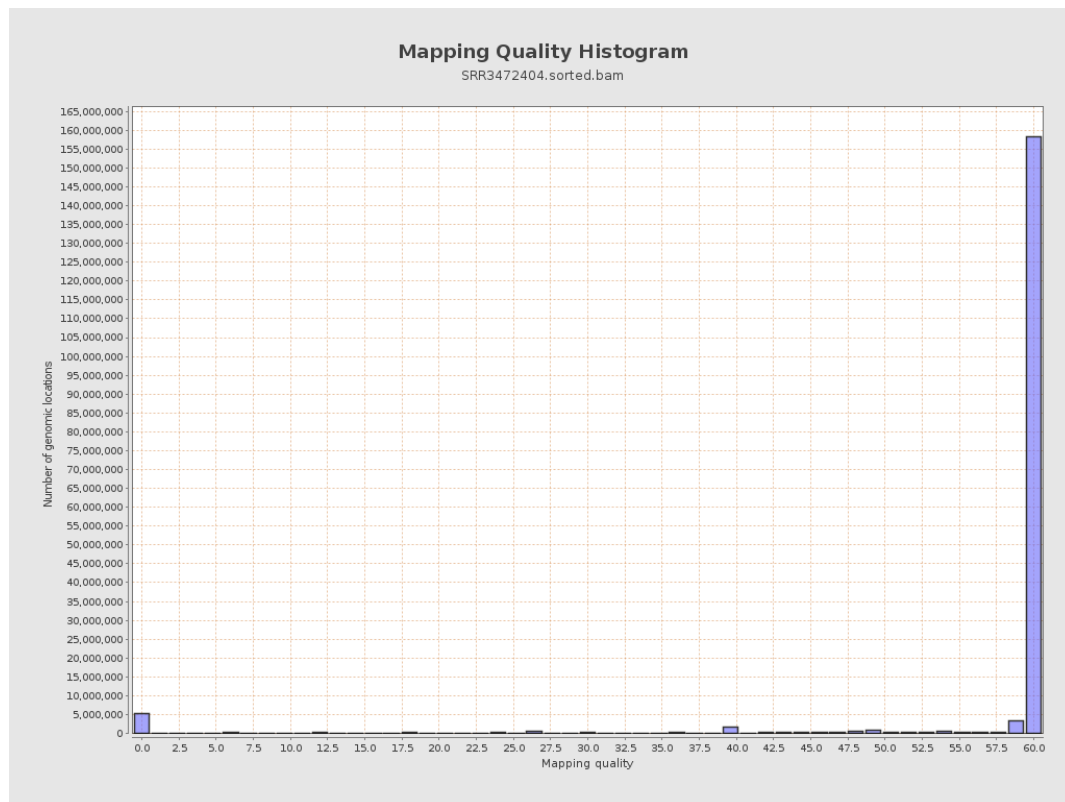
11. Results : Homopolymer Indels



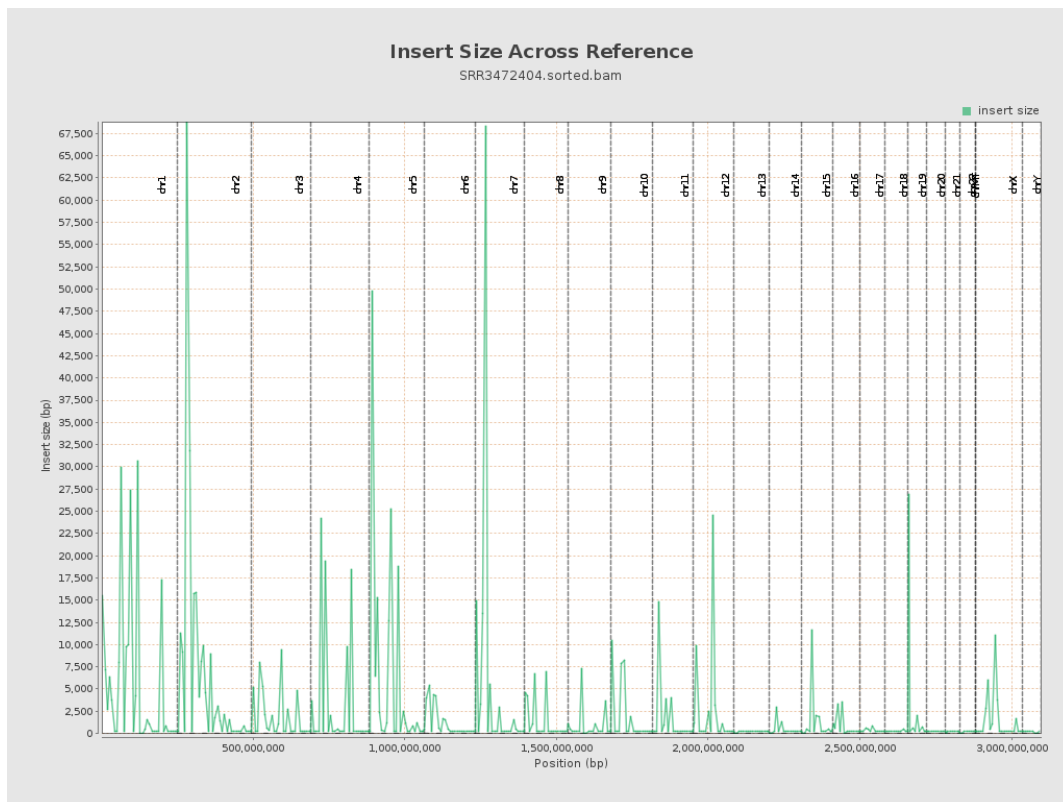
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

