

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 07:51:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617389.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_SRR617389 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617389_1.fastq.gz SRR617389_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 07:51:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617389.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,242,246 / 94.51%
Unmapped reads	1,757,754 / 5.49%
Mapped paired reads	30,242,246 / 94.51%
Mapped reads, first in pair	15,205,925 / 47.52%
Mapped reads, second in pair	15,036,321 / 46.99%
Mapped reads, both in pair	29,677,310 / 92.74%
Mapped reads, singletons	564,936 / 1.77%
Secondary alignments	0
Supplementary alignments	91,831 / 0.29%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	1,607,714 / 5.02%
Duplication rate	1.52%
Clipped reads	2,540,822 / 7.94%

2.2. ACGT Content

Number/percentage of A's	898,831,506 / 30.34%
Number/percentage of C's	586,927,353 / 19.81%
Number/percentage of T's	886,790,765 / 29.94%
Number/percentage of G's	588,838,059 / 19.88%
Number/percentage of N's	764,626 / 0.03%

GC Percentage	39.69%
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2.3. Coverage

Mean	0.9571
Standard Deviation	9.8574

2.4. Mapping Quality

Mean Mapping Quality	53.41
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2.5. Insert size

Mean	62,703.87
Standard Deviation	2,385,757.11
P25/Median/P75	170 / 210 / 271

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	30,220,693
Insertions	299,900
Mapped reads with at least one insertion	0.96%
Deletions	361,883
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.41%

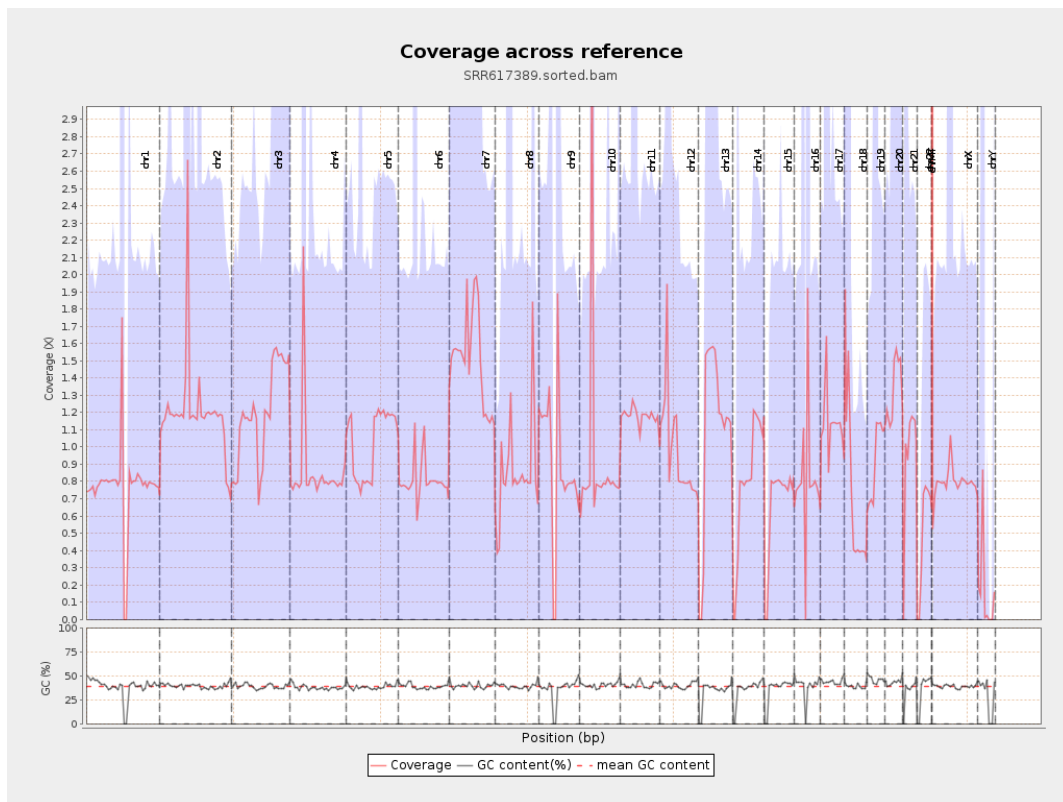
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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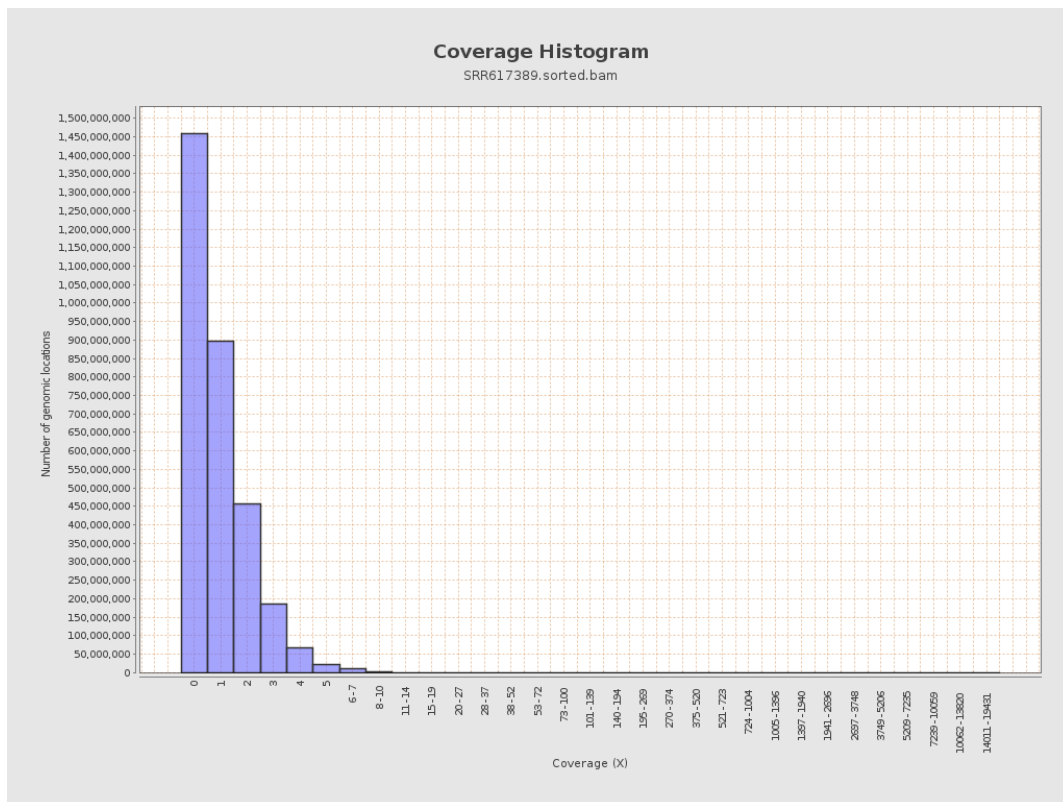
		bases	coverage	deviation
chr1	249250621	192261608	0.7714	19.9121
chr2	243199373	292818702	1.204	8.9254
chr3	198022430	236091222	1.1922	1.5234
chr4	191154276	162677651	0.851	9.4012
chr5	180915260	185847511	1.0273	1.48
chr6	171115067	139062189	0.8127	3.6948
chr7	159138663	240250454	1.5097	10.9711
chr8	146364022	124735979	0.8522	7.8124
chr9	141213431	124774803	0.8836	14.9962
chr10	135534747	124880254	0.9214	20.3682
chr11	135006516	158998755	1.1777	5.7712
chr12	133851895	130714587	0.9766	1.3939
chr13	115169878	129314834	1.1228	1.3192
chr14	107349540	85810641	0.7994	1.3878
chr15	102531392	66671869	0.6503	1.0872
chr16	90354753	74276268	0.8221	8.0429
chr17	81195210	91925001	1.1321	7.1468
chr18	78077248	53662613	0.6873	15.5056
chr19	59128983	54762776	0.9262	9.6268
chr20	63025520	84614421	1.3425	2.4235
chr21	48129895	47063654	0.9778	3.3213
chr22	51304566	26260957	0.5119	0.9302
chrMT	16571	2047237	123.5434	18.5817
chrX	155270560	123350909	0.7944	3.0363

chrY	59373566	10149420	0.1709	8.3101
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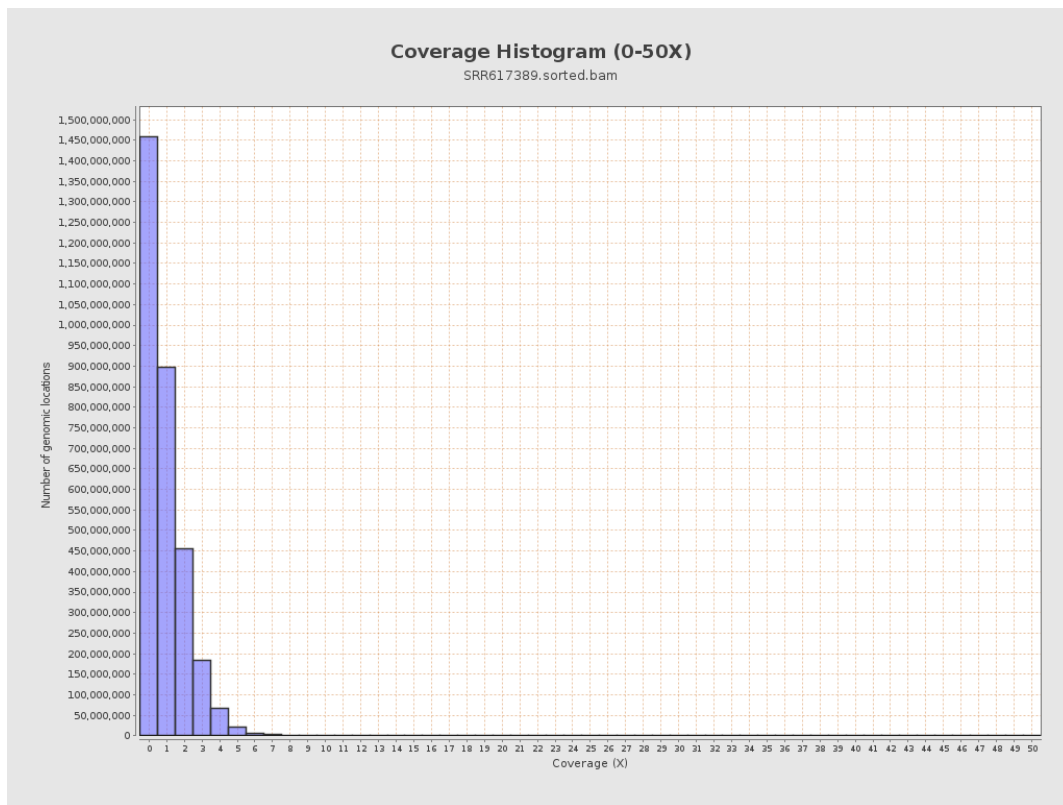
3. Results : Coverage across reference



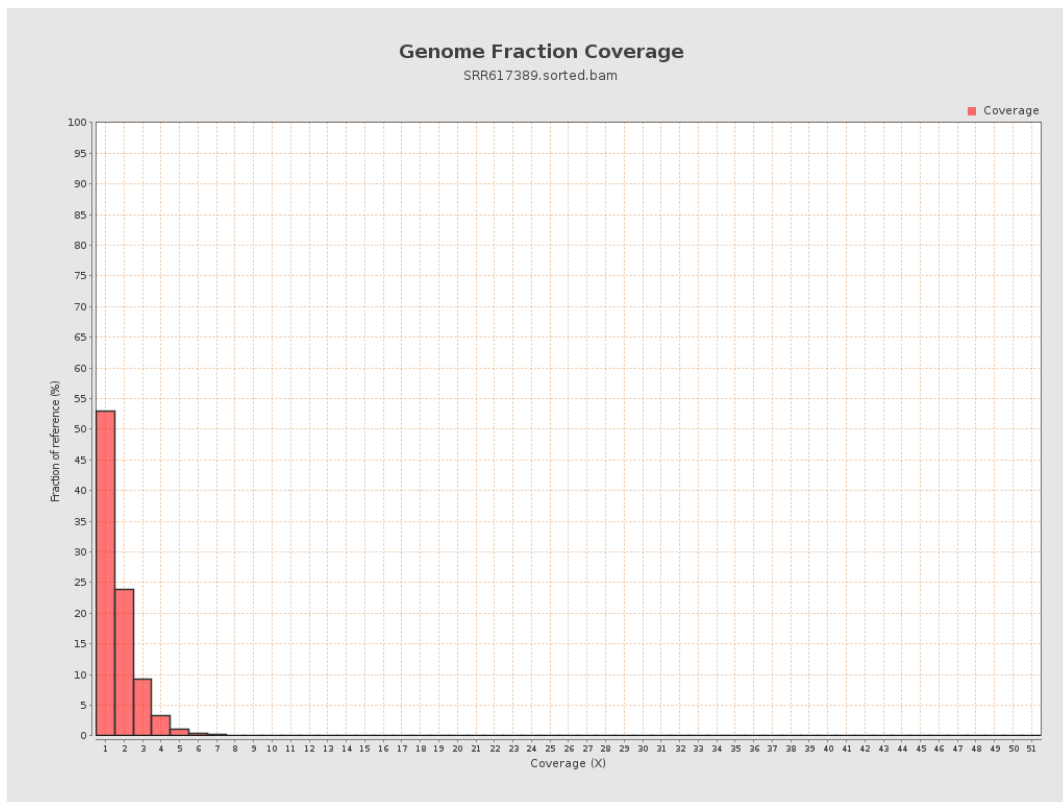
4. Results : Coverage Histogram



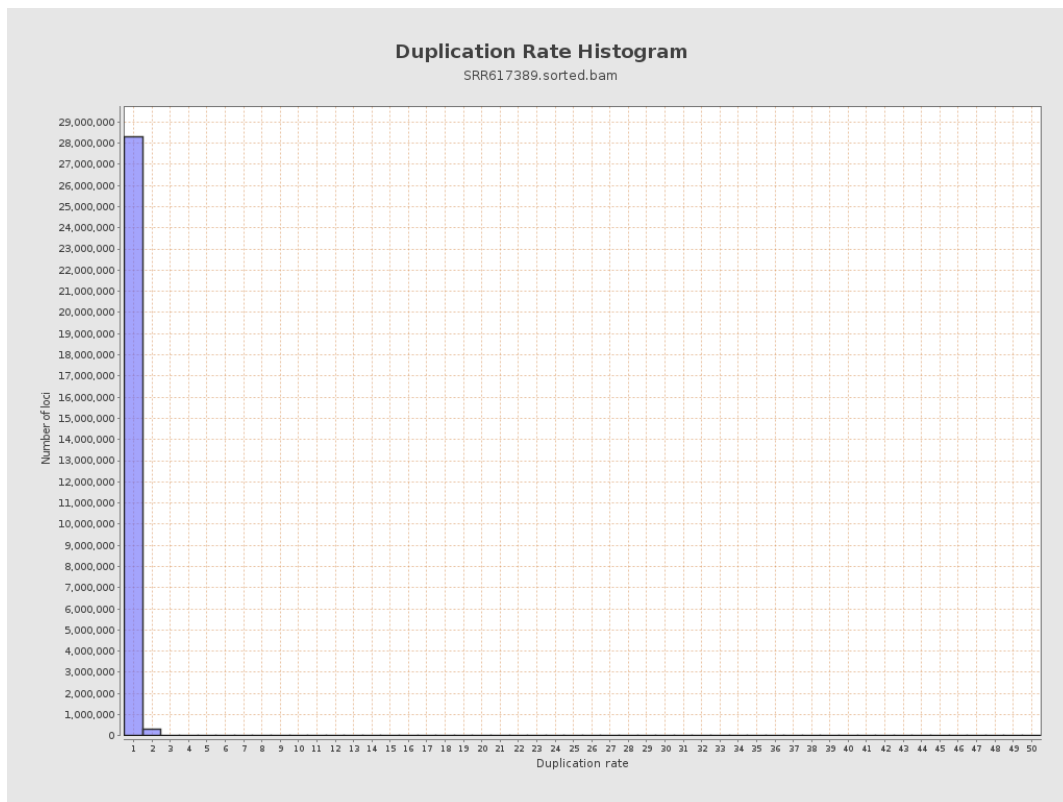
5. Results : Coverage Histogram (0-50X)



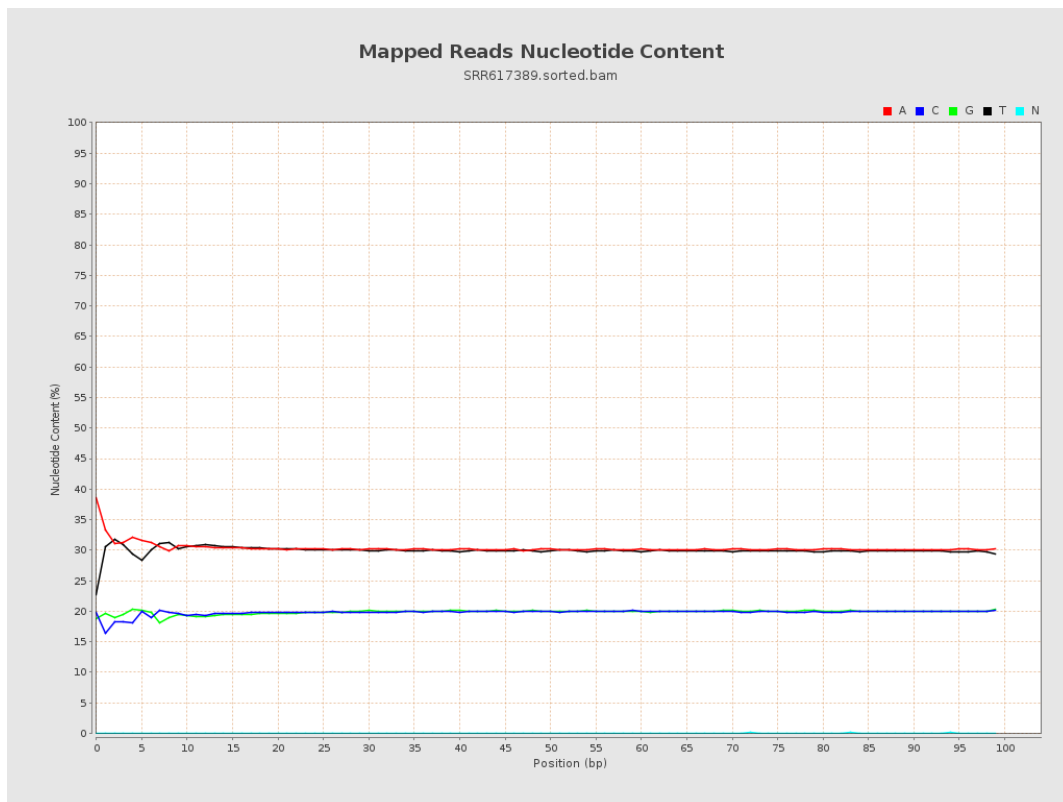
6. Results : Genome Fraction Coverage



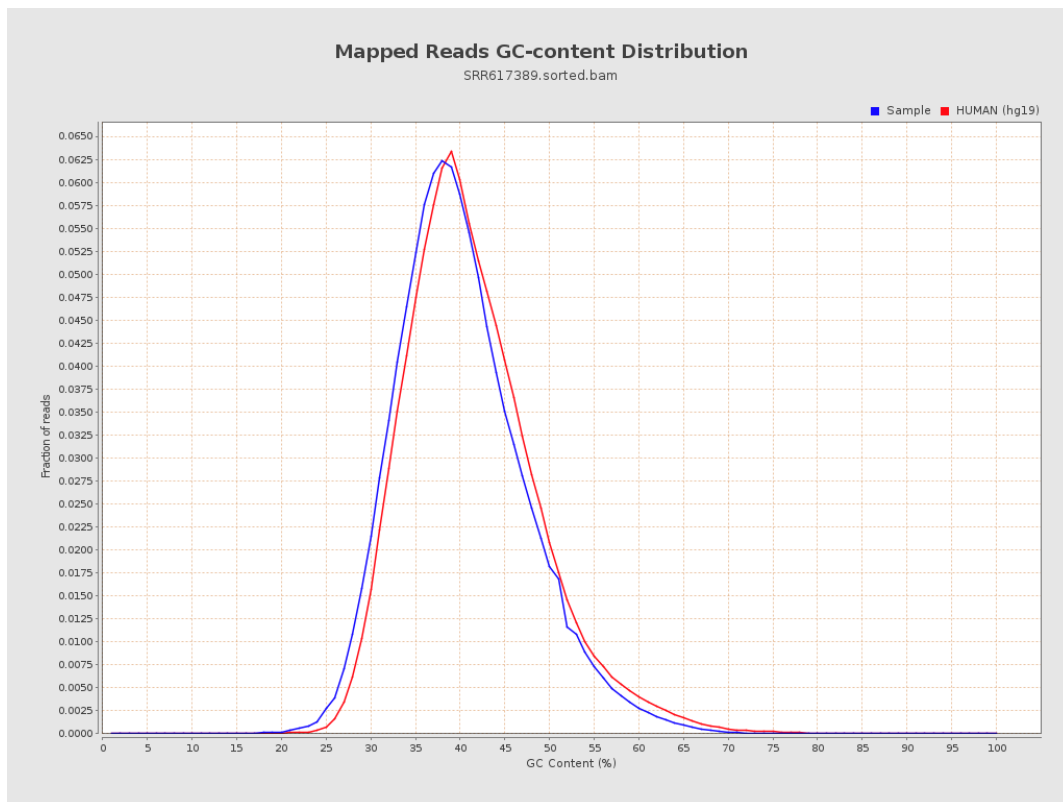
7. Results : Duplication Rate Histogram



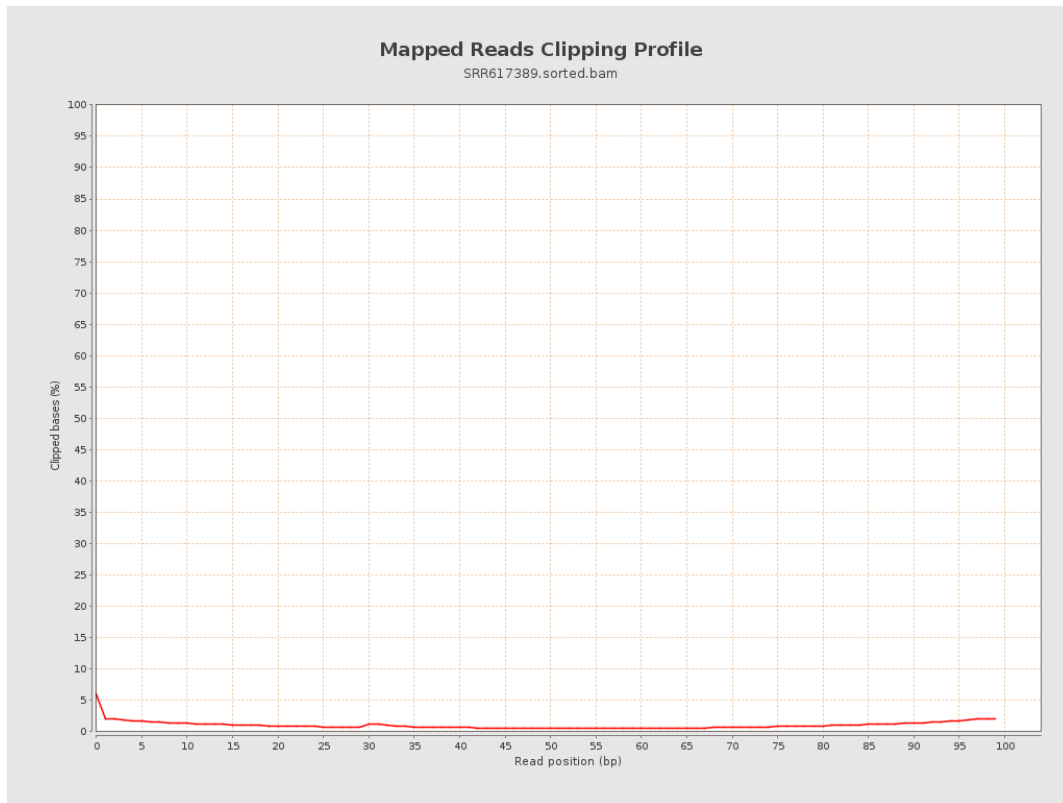
8. Results : Mapped Reads Nucleotide Content



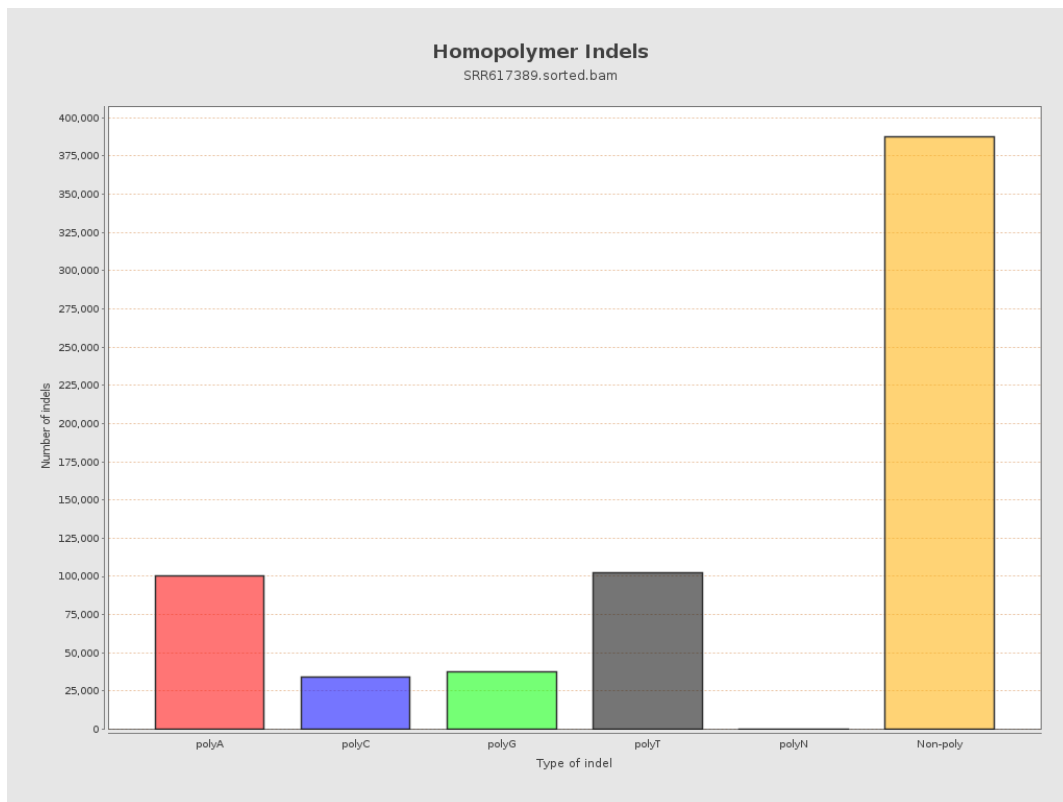
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



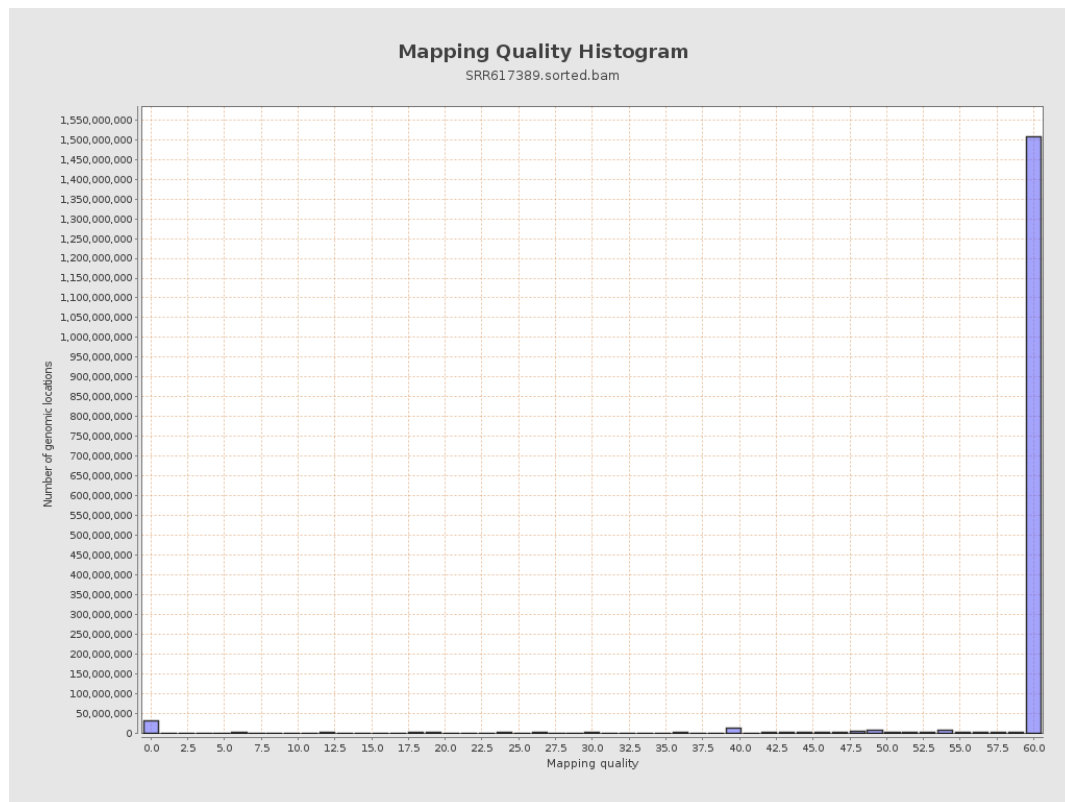
11. Results : Homopolymer Indels



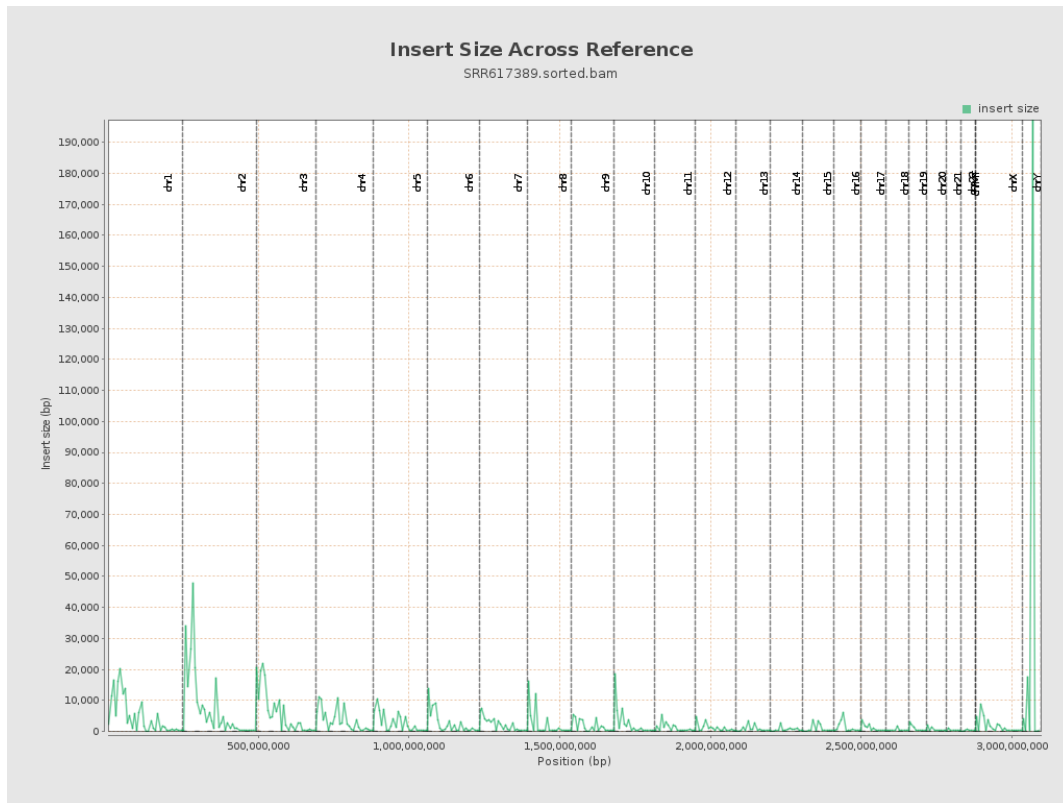
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

