

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 15:06:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173971.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_SRR10173971 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173971_1.fastq.gz SRR10173971_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 15:06:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173971.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,545,830
Mapped reads	2,497,700 / 98.11%
Unmapped reads	48,130 / 1.89%
Mapped paired reads	2,497,700 / 98.11%
Mapped reads, first in pair	1,248,618 / 49.05%
Mapped reads, second in pair	1,249,082 / 49.06%
Mapped reads, both in pair	2,469,610 / 97.01%
Mapped reads, singletons	28,090 / 1.1%
Secondary alignments	0
Supplementary alignments	320,862 / 12.6%
Read min/max/mean length	30 / 133 / 123.51
Duplicated reads (estimated)	1,940,348 / 76.22%
Duplication rate	61.13%
Clipped reads	1,252,933 / 49.22%

2.2. ACGT Content

Number/percentage of A's	83,969,608 / 30.05%
Number/percentage of C's	55,184,200 / 19.75%
Number/percentage of T's	83,204,932 / 29.78%
Number/percentage of G's	57,049,359 / 20.42%
Number/percentage of N's	2,203 / 0%

GC Percentage	40.17%
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2.3. Coverage

Mean	0.0903
Standard Deviation	1.7371

2.4. Mapping Quality

Mean Mapping Quality	52.58
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2.5. Insert size

Mean	823,776.06
Standard Deviation	8,322,982.69
P25/Median/P75	98 / 141 / 214

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	2,297,326
Insertions	31,079
Mapped reads with at least one insertion	1.2%
Deletions	84,031
Mapped reads with at least one deletion	3.28%
Homopolymer indels	40.89%

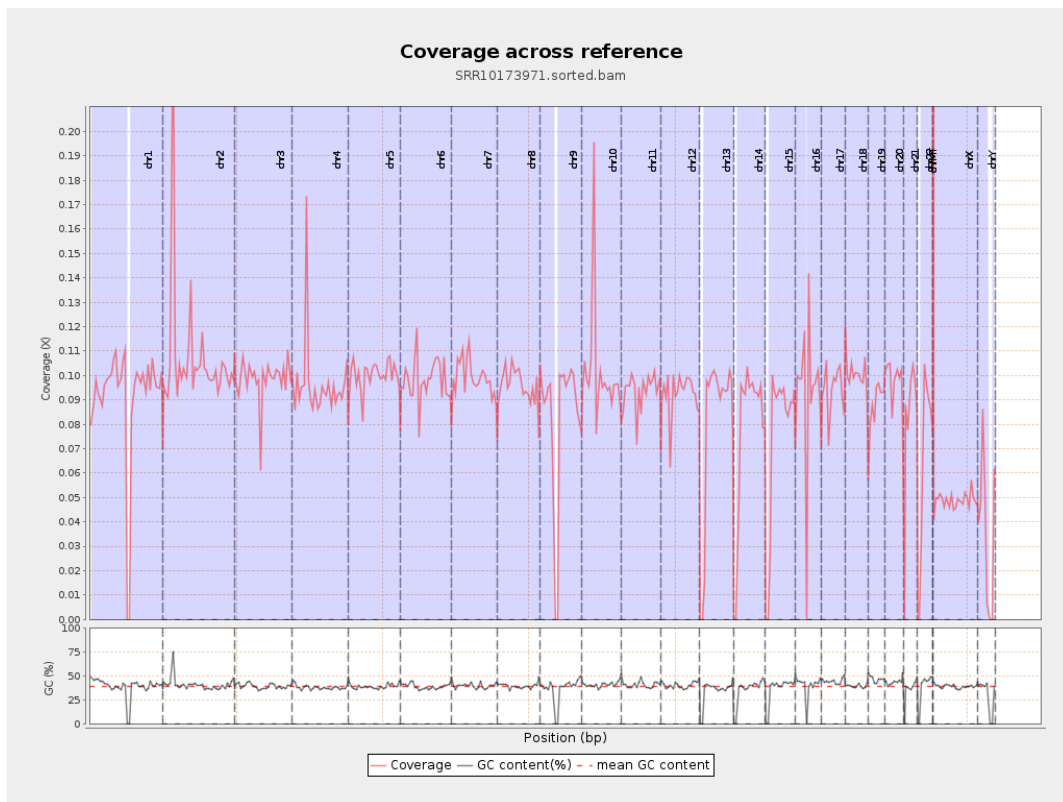
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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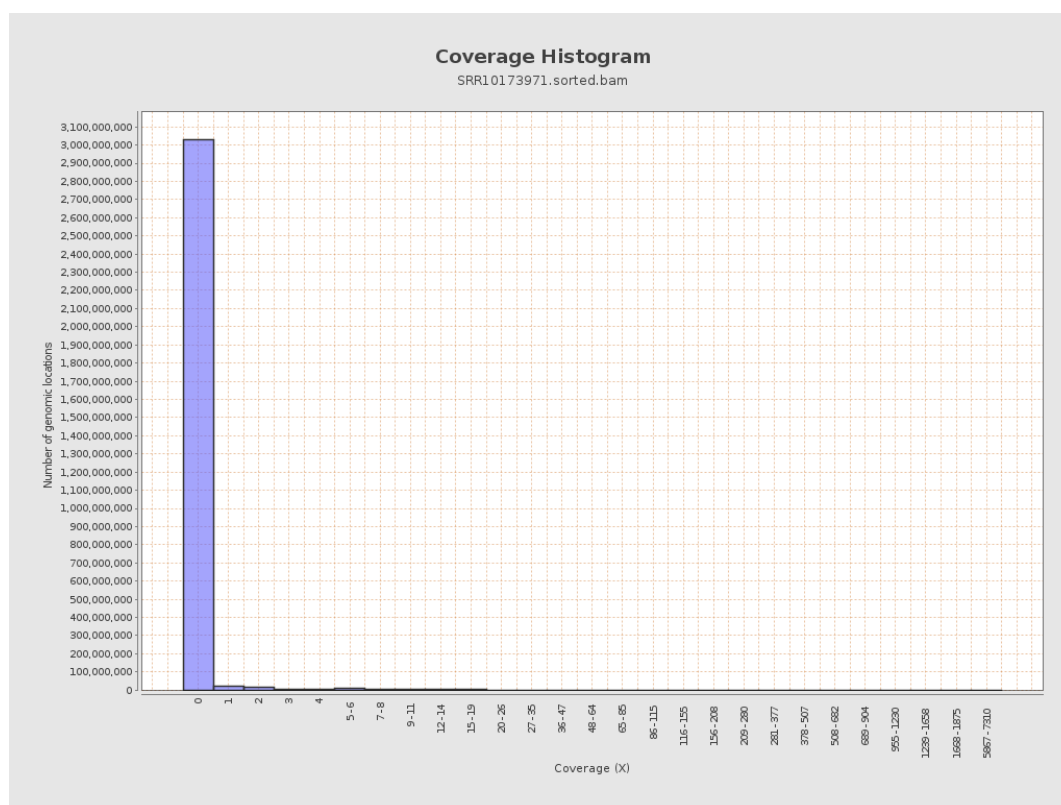
		bases	coverage	deviation
chr1	249250621	22780796	0.0914	1.0773
chr2	243199373	25876466	0.1064	5.1593
chr3	198022430	19521437	0.0986	0.9486
chr4	191154276	18427124	0.0964	1.0833
chr5	180915260	18031454	0.0997	0.9557
chr6	171115067	16853057	0.0985	0.9966
chr7	159138663	15725732	0.0988	1.0932
chr8	146364022	14011656	0.0957	1.2231
chr9	141213431	11694107	0.0828	1.0004
chr10	135534747	13705776	0.1011	1.307
chr11	135006516	12637418	0.0936	0.9395
chr12	133851895	12429836	0.0929	0.9221
chr13	115169878	9269266	0.0805	0.8582
chr14	107349540	8419350	0.0784	0.8307
chr15	102531392	7552371	0.0737	0.8042
chr16	90354753	8309897	0.092	1.0436
chr17	81195210	7707572	0.0949	0.9651
chr18	78077248	7863156	0.1007	1.2621
chr19	59128983	5239456	0.0886	0.9681
chr20	63025520	6200795	0.0984	0.9547
chr21	48129895	4015373	0.0834	0.9644
chr22	51304566	3325990	0.0648	0.8299
chrMT	16571	260396	15.714	19.3776
chrX	155270560	7558313	0.0487	0.6656

chrY	59373566	2192269	0.0369	0.7038
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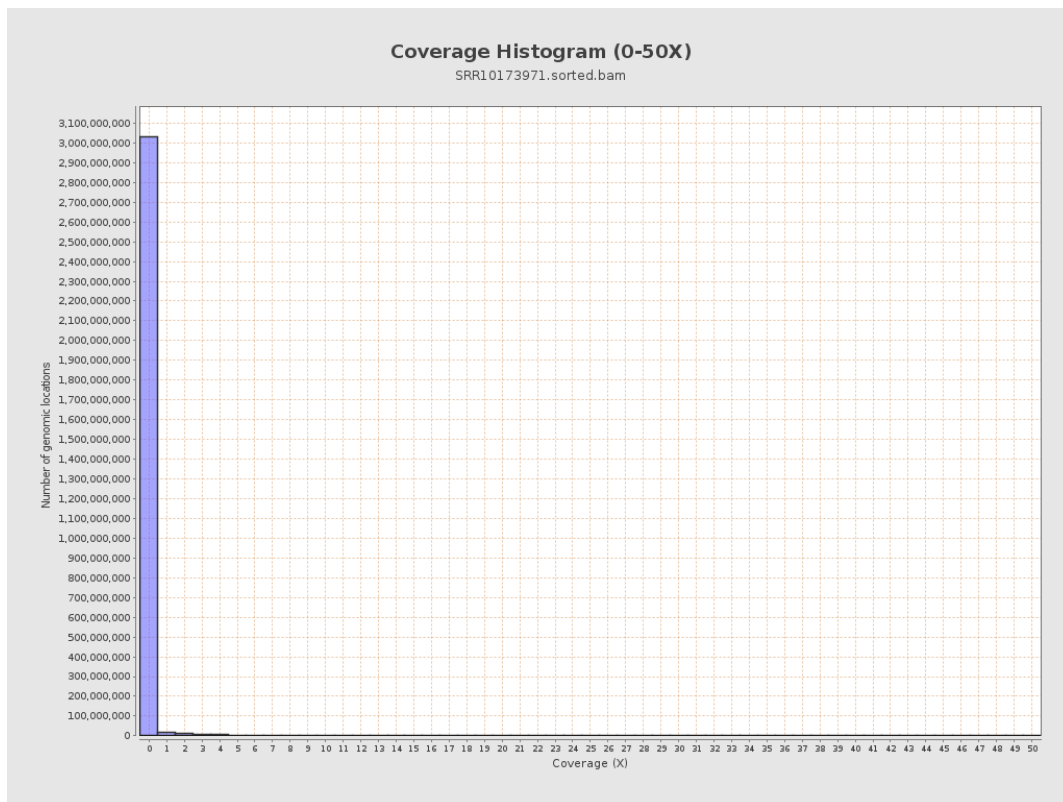
3. Results : Coverage across reference



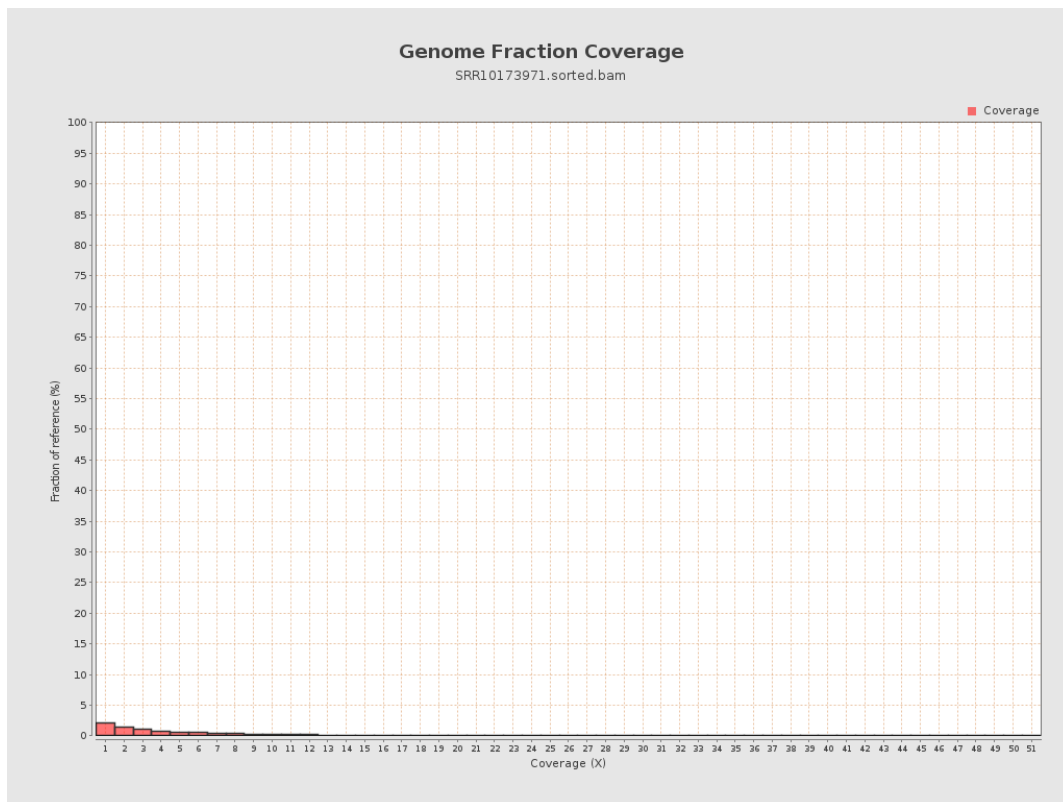
4. Results : Coverage Histogram



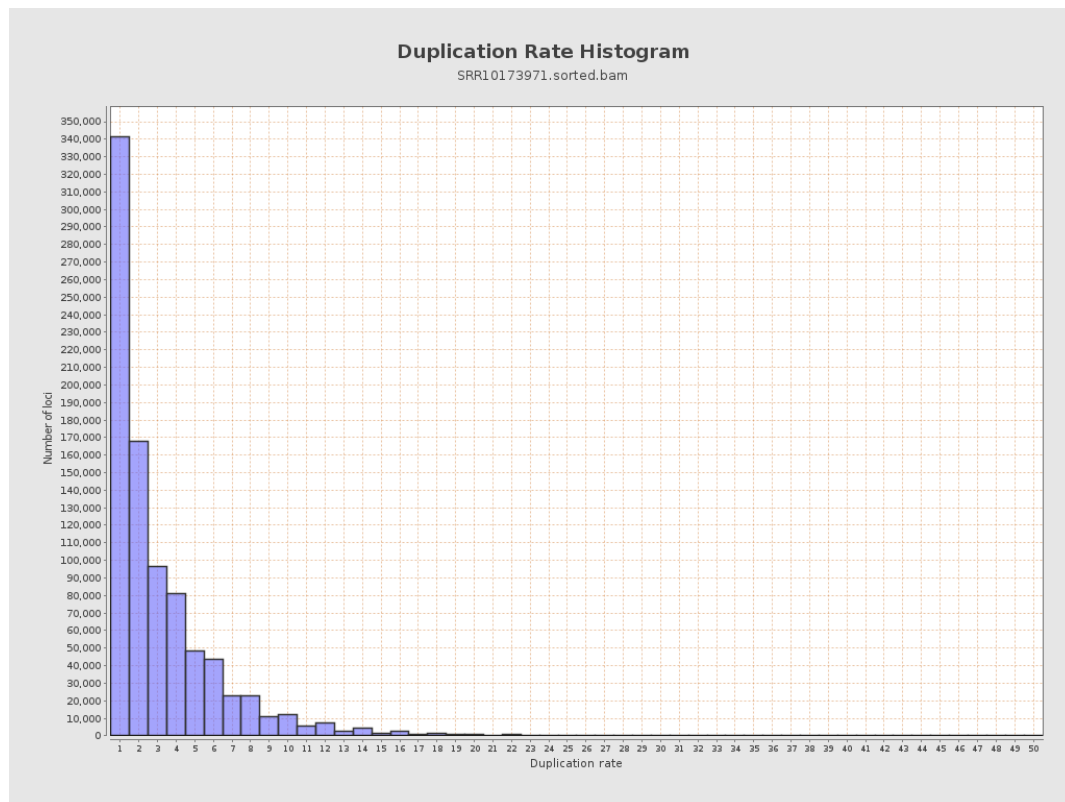
5. Results : Coverage Histogram (0-50X)



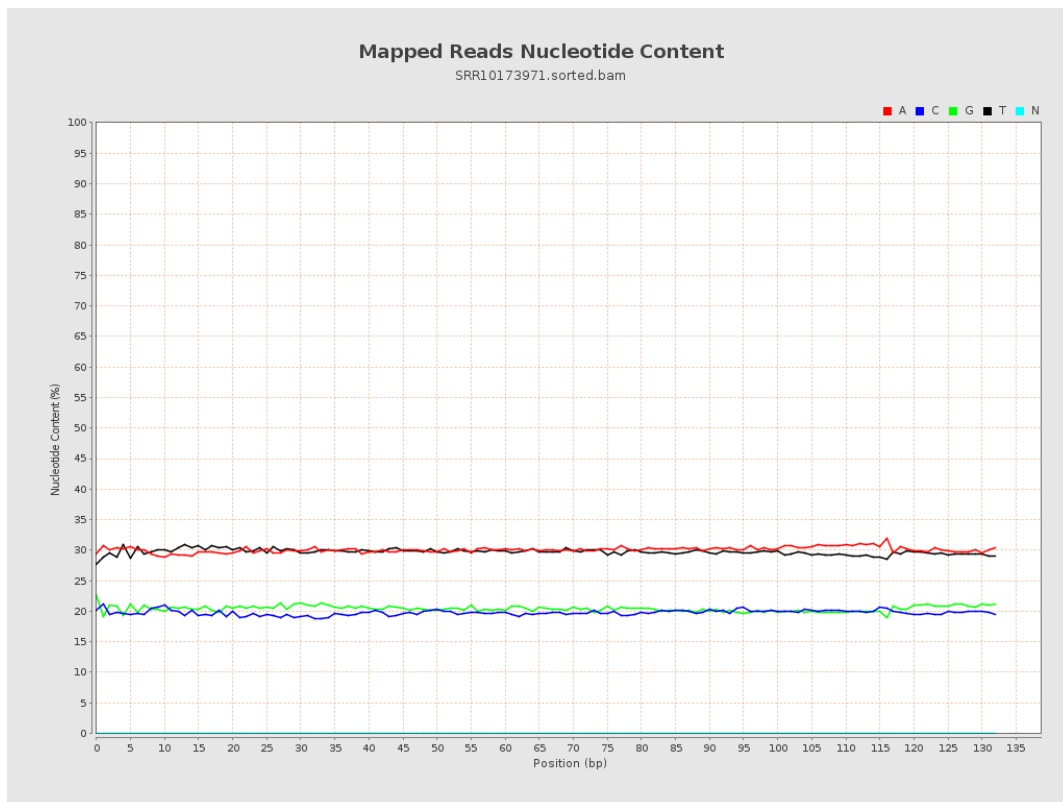
6. Results : Genome Fraction Coverage



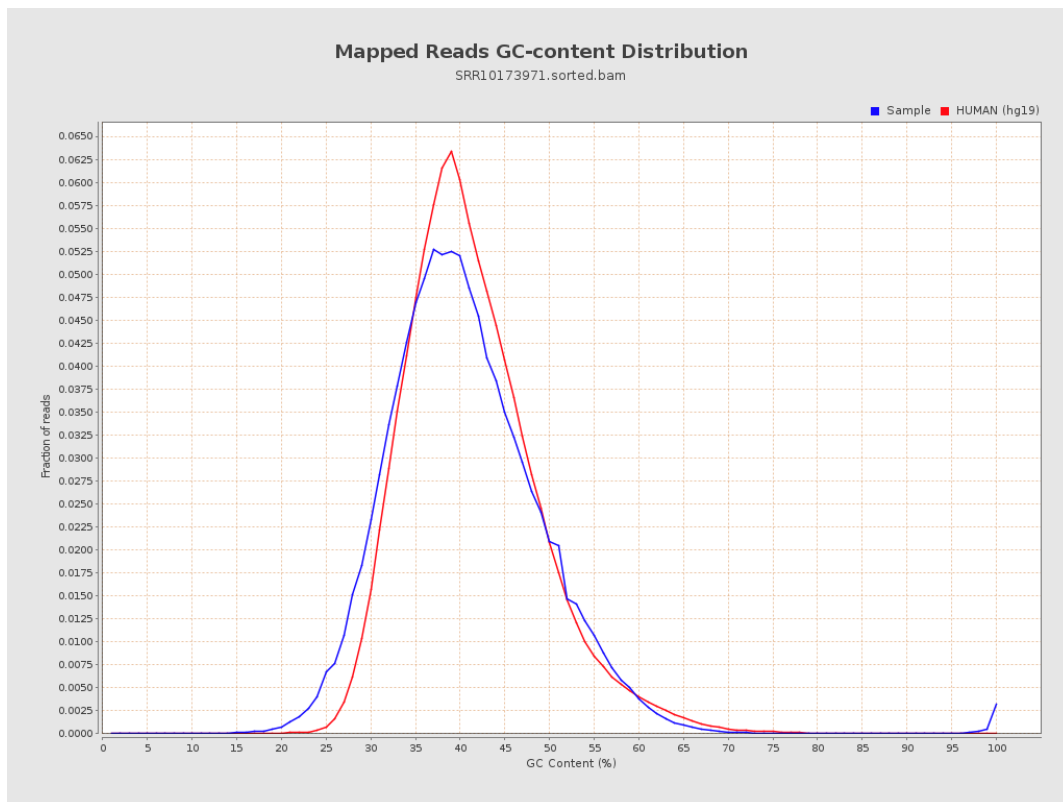
7. Results : Duplication Rate Histogram



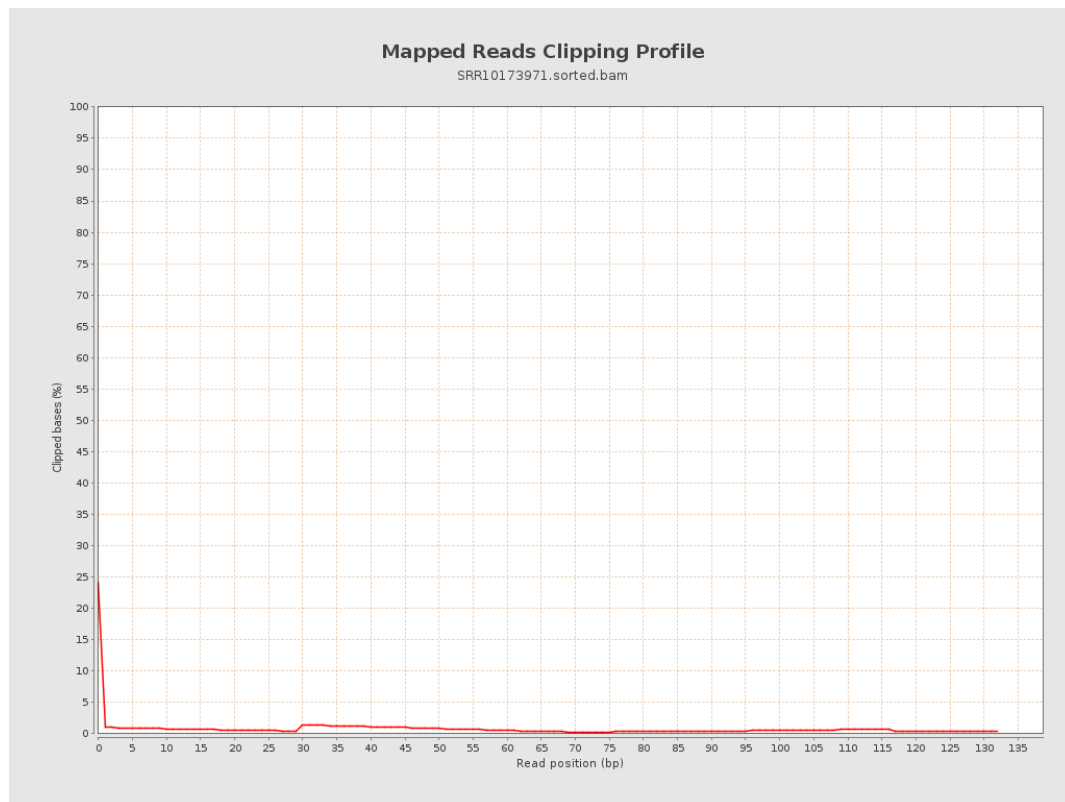
8. Results : Mapped Reads Nucleotide Content



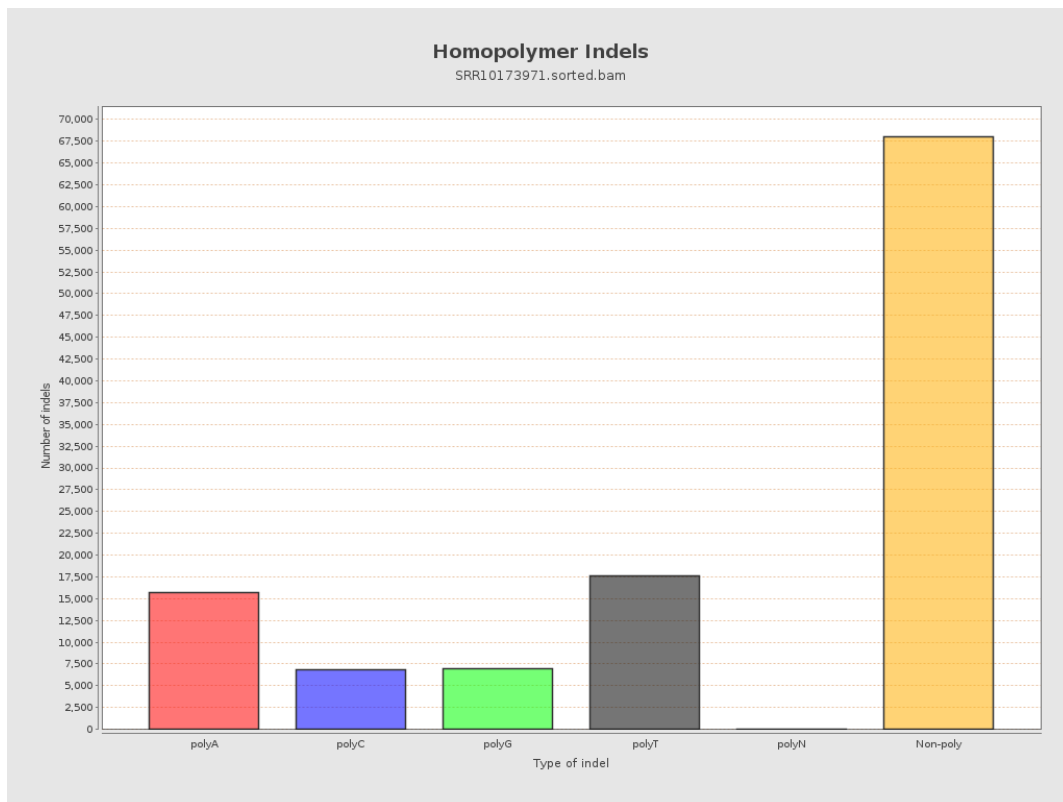
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



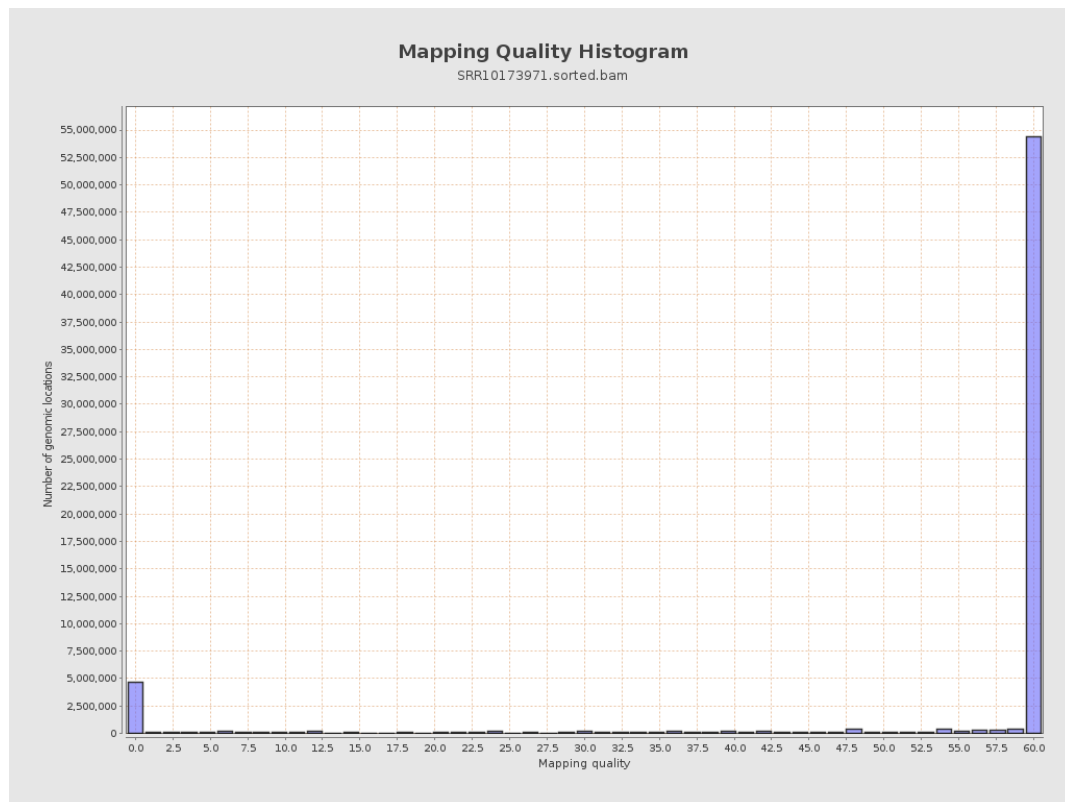
11. Results : Homopolymer Indels



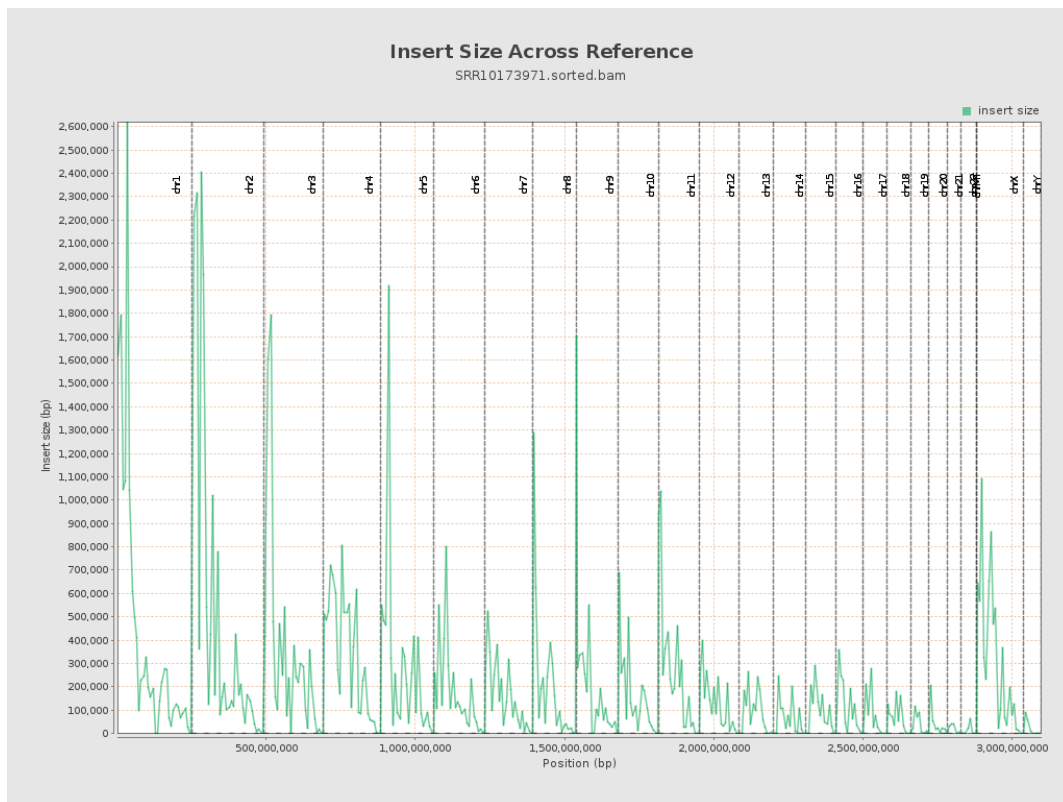
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

