

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:37:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173872.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_SRR10173872 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173872_1.fastq.gz SRR10173872_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:37:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173872.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,457,416
Mapped reads	11,130,995 / 97.15%
Unmapped reads	326,421 / 2.85%
Mapped paired reads	11,130,995 / 97.15%
Mapped reads, first in pair	5,583,664 / 48.73%
Mapped reads, second in pair	5,547,331 / 48.42%
Mapped reads, both in pair	10,910,054 / 95.22%
Mapped reads, singletons	220,941 / 1.93%
Secondary alignments	0
Supplementary alignments	1,166,393 / 10.18%
Read min/max/mean length	30 / 133 / 127.92
Duplicated reads (estimated)	8,744,643 / 76.32%
Duplication rate	65.56%
Clipped reads	4,845,522 / 42.29%

2.2. ACGT Content

Number/percentage of A's	392,571,199 / 30.14%
Number/percentage of C's	254,677,109 / 19.55%
Number/percentage of T's	391,900,296 / 30.09%
Number/percentage of G's	263,406,277 / 20.22%
Number/percentage of N's	15,846 / 0%

GC Percentage	39.77%
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2.3. Coverage

Mean	0.421
Standard Deviation	6.1568

2.4. Mapping Quality

Mean Mapping Quality	52.66
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2.5. Insert size

Mean	760,985.35
Standard Deviation	7,830,273.72
P25/Median/P75	138 / 195 / 283

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	13,369,661
Insertions	138,572
Mapped reads with at least one insertion	1.2%
Deletions	293,048
Mapped reads with at least one deletion	2.57%
Homopolymer indels	42.5%

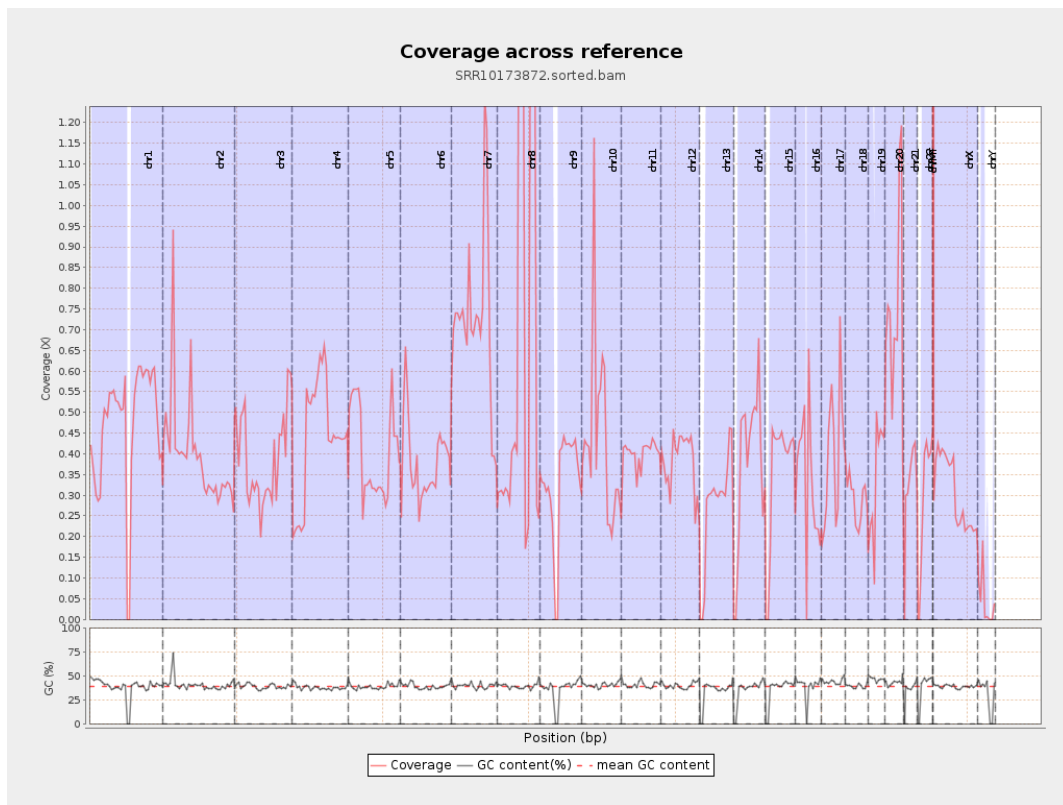
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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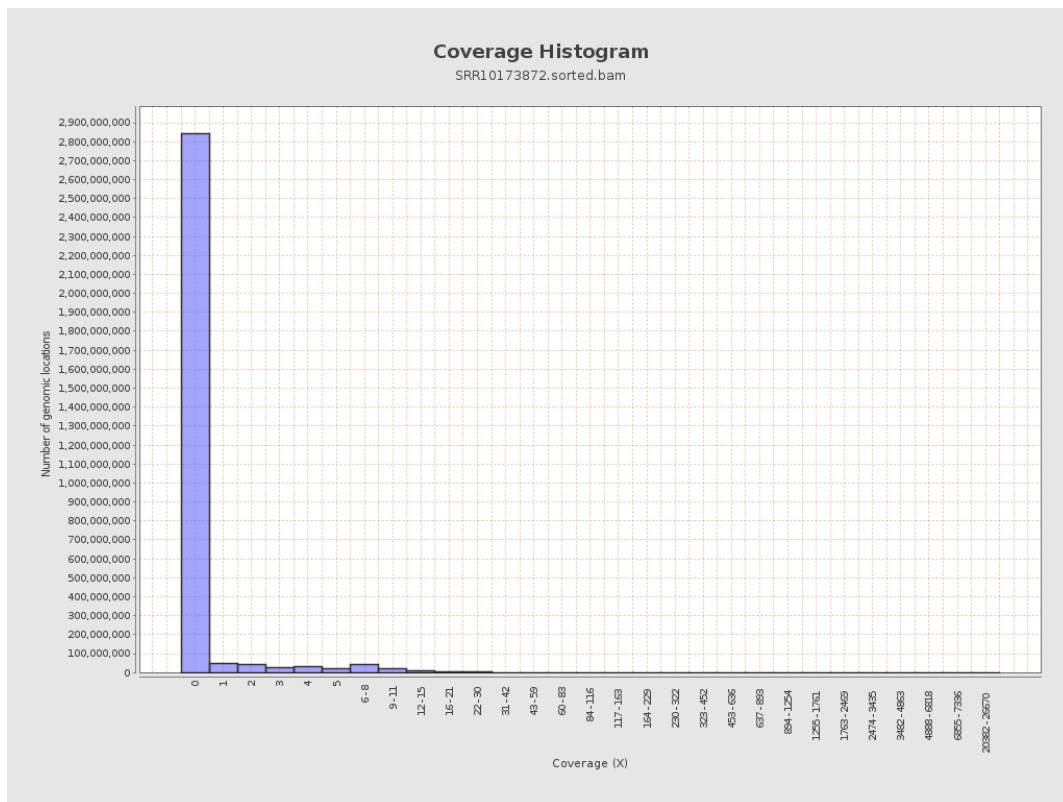
		bases	coverage	deviation
chr1	249250621	116883475	0.4689	3.3598
chr2	243199373	96042658	0.3949	18.6527
chr3	198022430	77264683	0.3902	1.8735
chr4	191154276	85080852	0.4451	3.0972
chr5	180915260	72712169	0.4019	1.8478
chr6	171115067	65243219	0.3813	2.0187
chr7	159138663	114353835	0.7186	6.9959
chr8	146364022	118842242	0.812	3.7459
chr9	141213431	46335175	0.3281	2.7017
chr10	135534747	58305704	0.4302	7.6346
chr11	135006516	53946693	0.3996	2.038
chr12	133851895	51239193	0.3828	1.8383
chr13	115169878	32126247	0.2789	1.5479
chr14	107349540	41558797	0.3871	1.8726
chr15	102531392	35939674	0.3505	1.7376
chr16	90354753	30147913	0.3337	3.0988
chr17	81195210	31807712	0.3917	2.3559
chr18	78077248	23060960	0.2954	3.9241
chr19	59128983	19936476	0.3372	2.5441
chr20	63025520	48940714	0.7765	2.7301
chr21	48129895	15585802	0.3238	2.0622
chr22	51304566	14631265	0.2852	1.5151
chrMT	16571	3291763	198.646	129.0012
chrX	155270560	47371765	0.3051	1.6695

chrY	59373566	2652844	0.0447	1.8733
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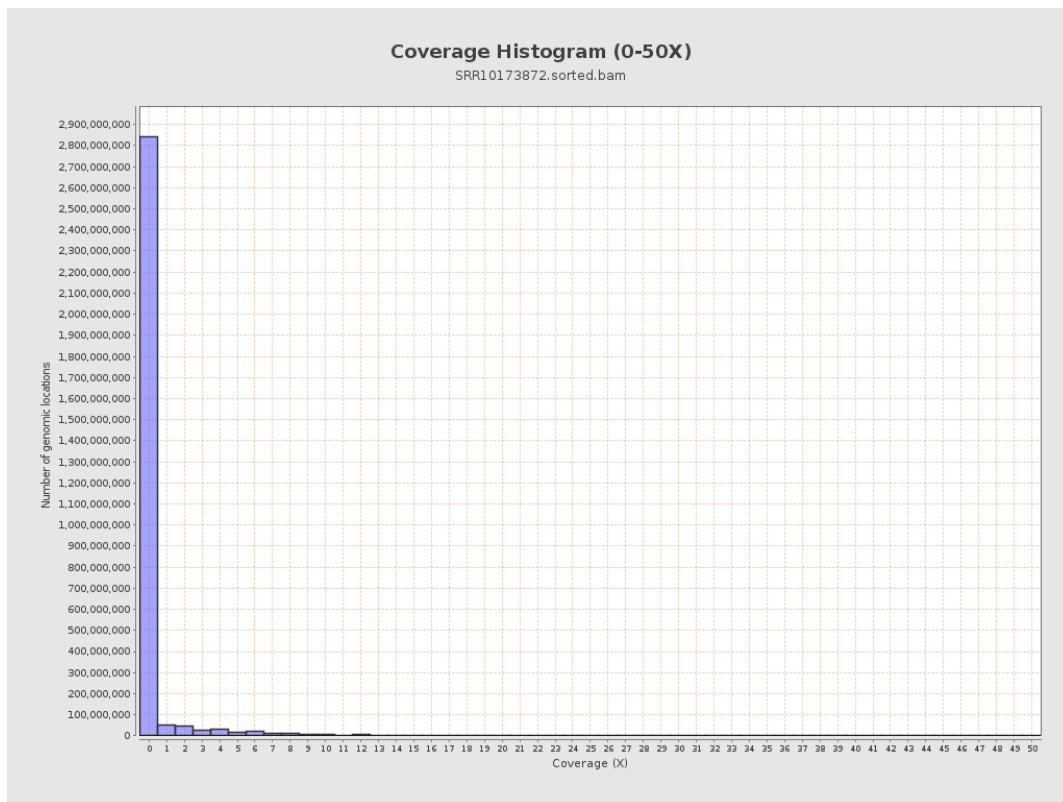
3. Results : Coverage across reference



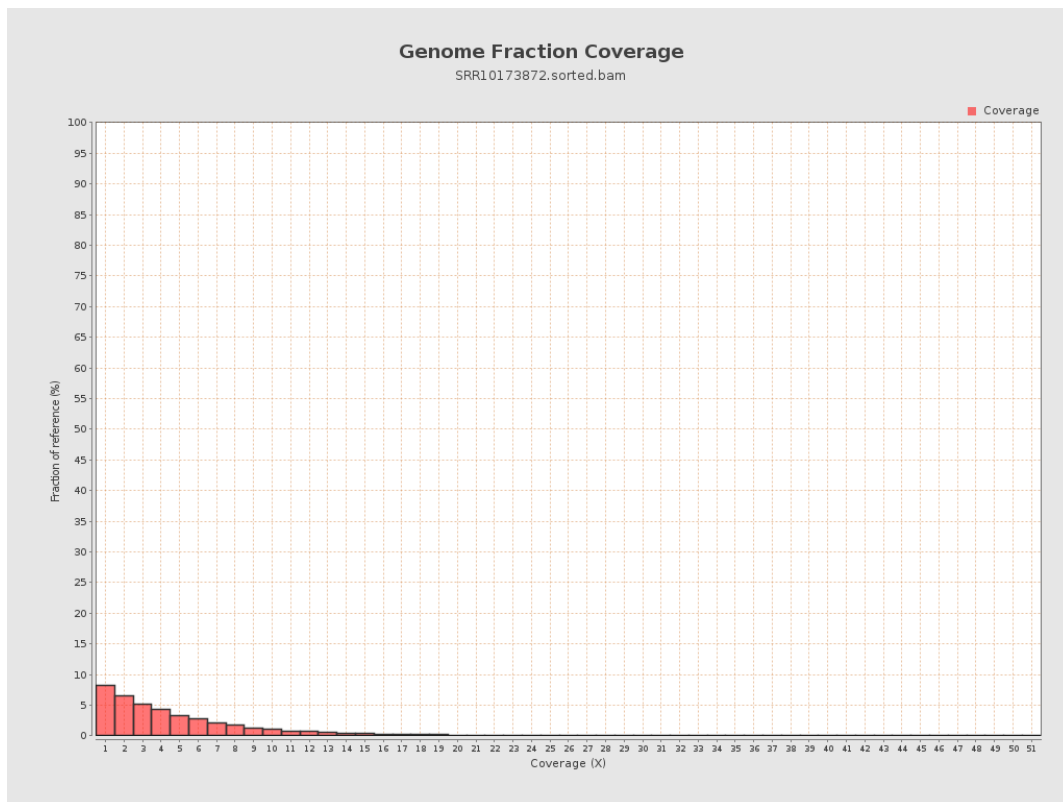
4. Results : Coverage Histogram



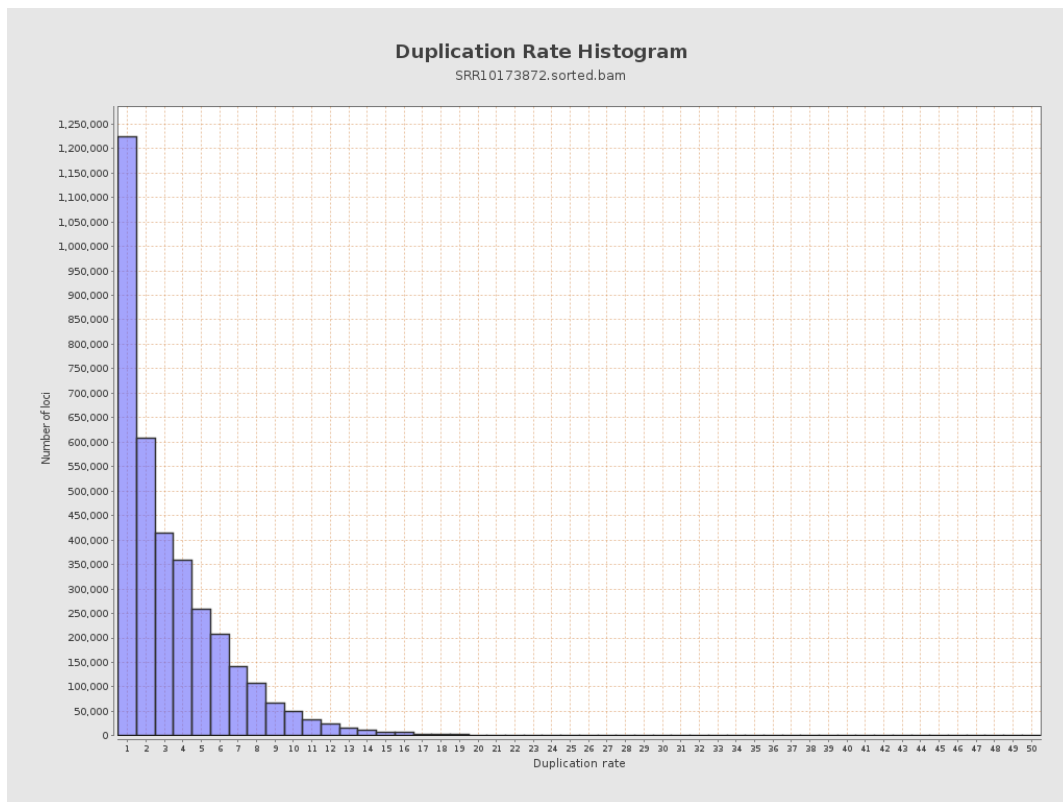
5. Results : Coverage Histogram (0-50X)



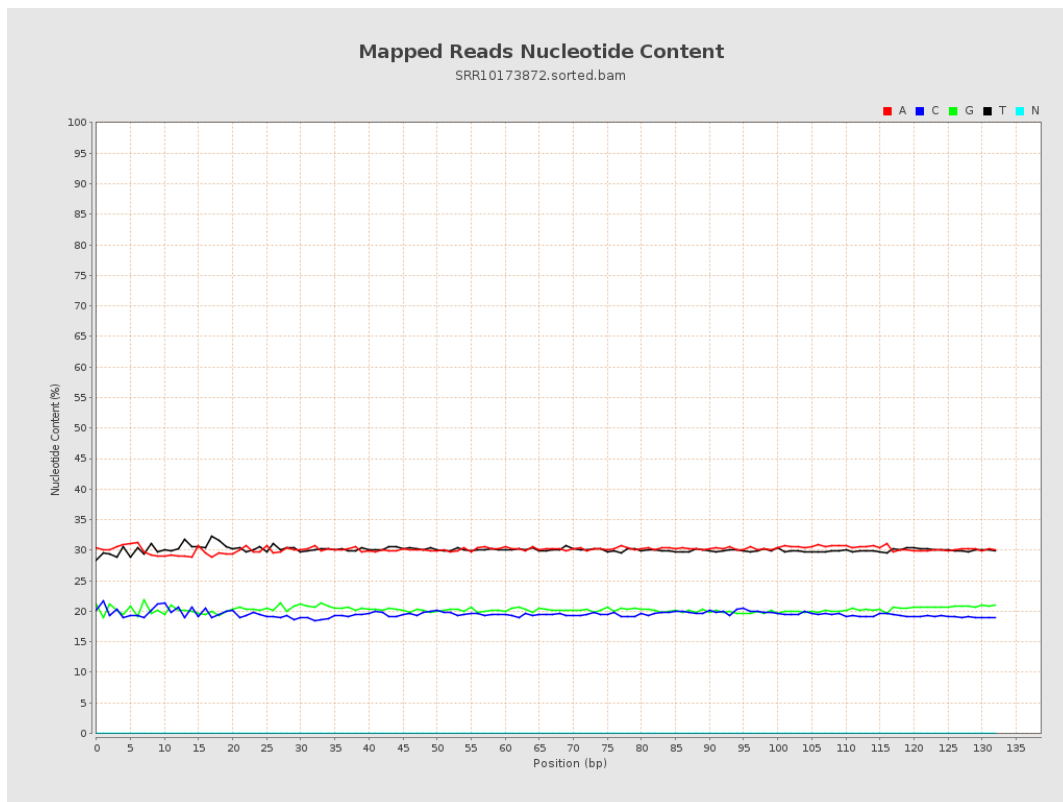
6. Results : Genome Fraction Coverage



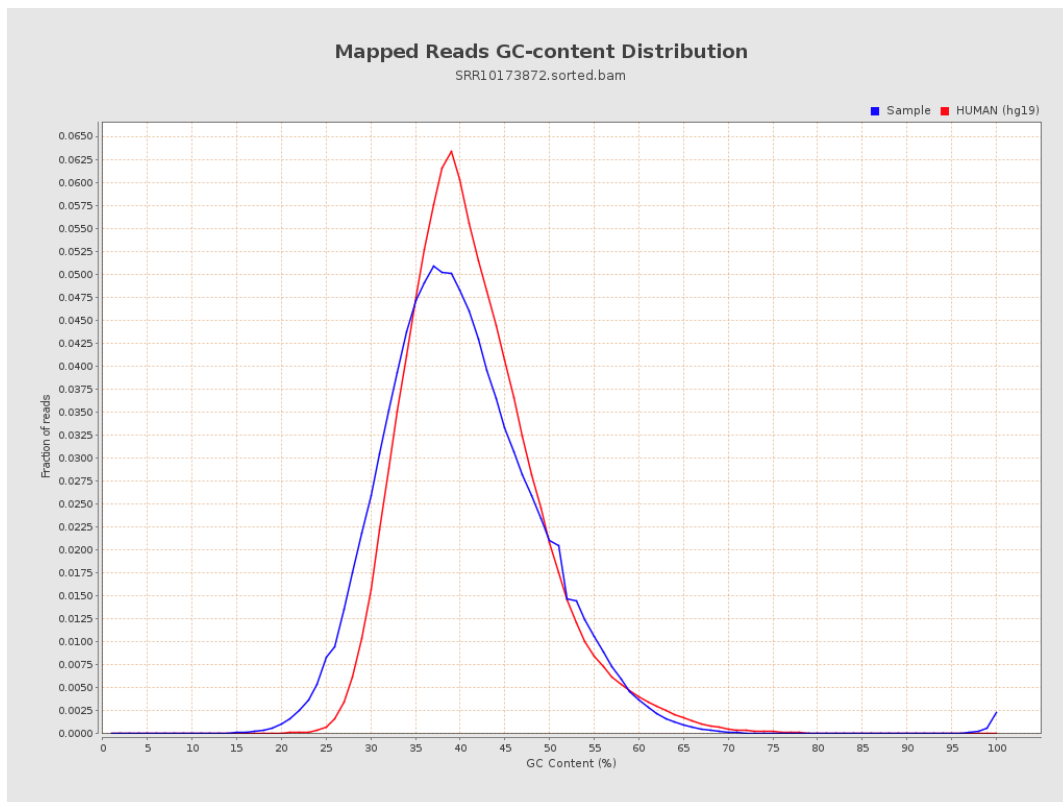
7. Results : Duplication Rate Histogram



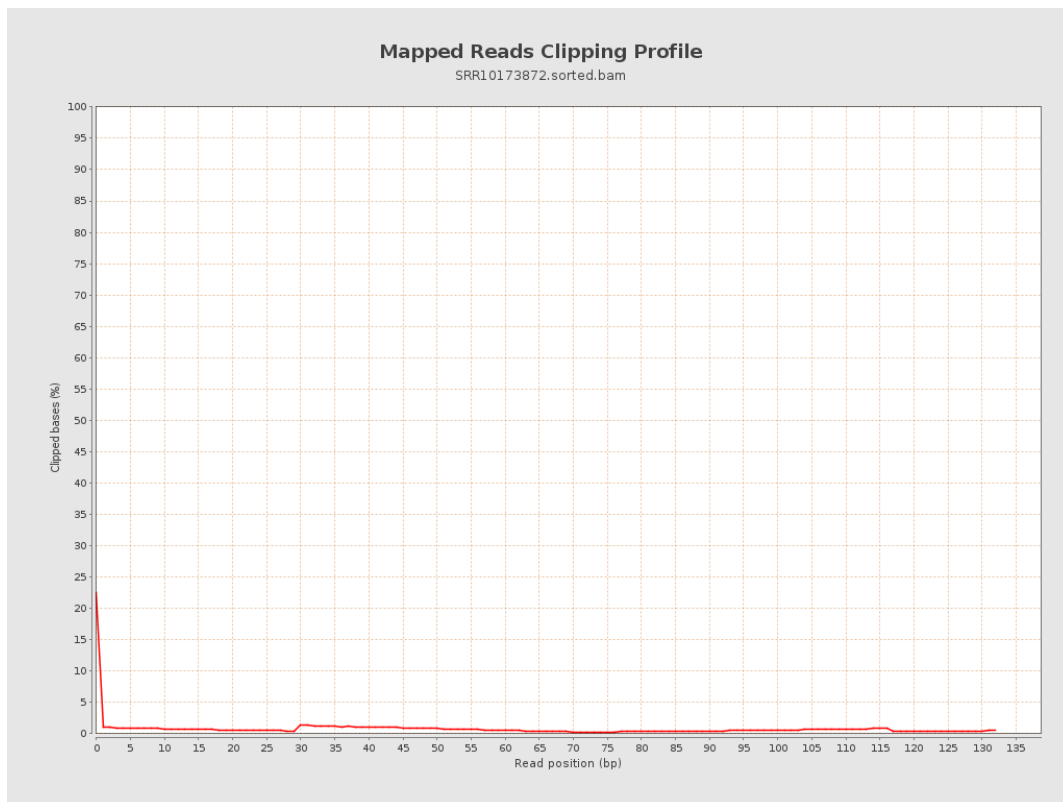
8. Results : Mapped Reads Nucleotide Content



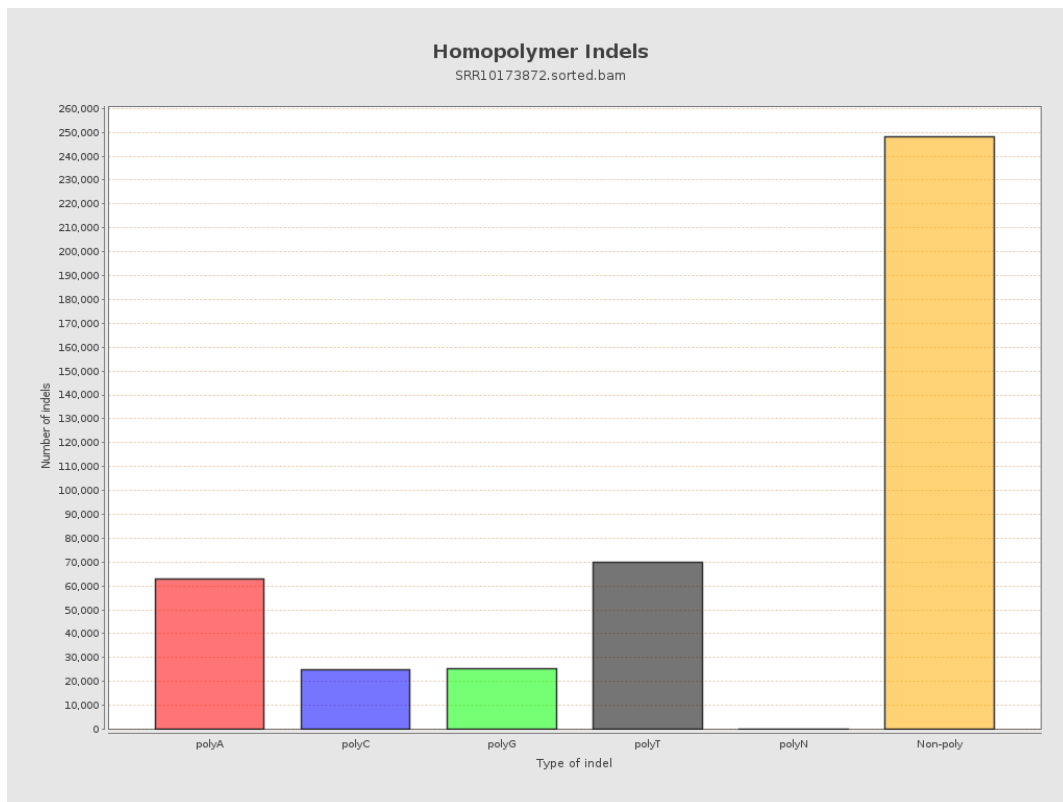
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



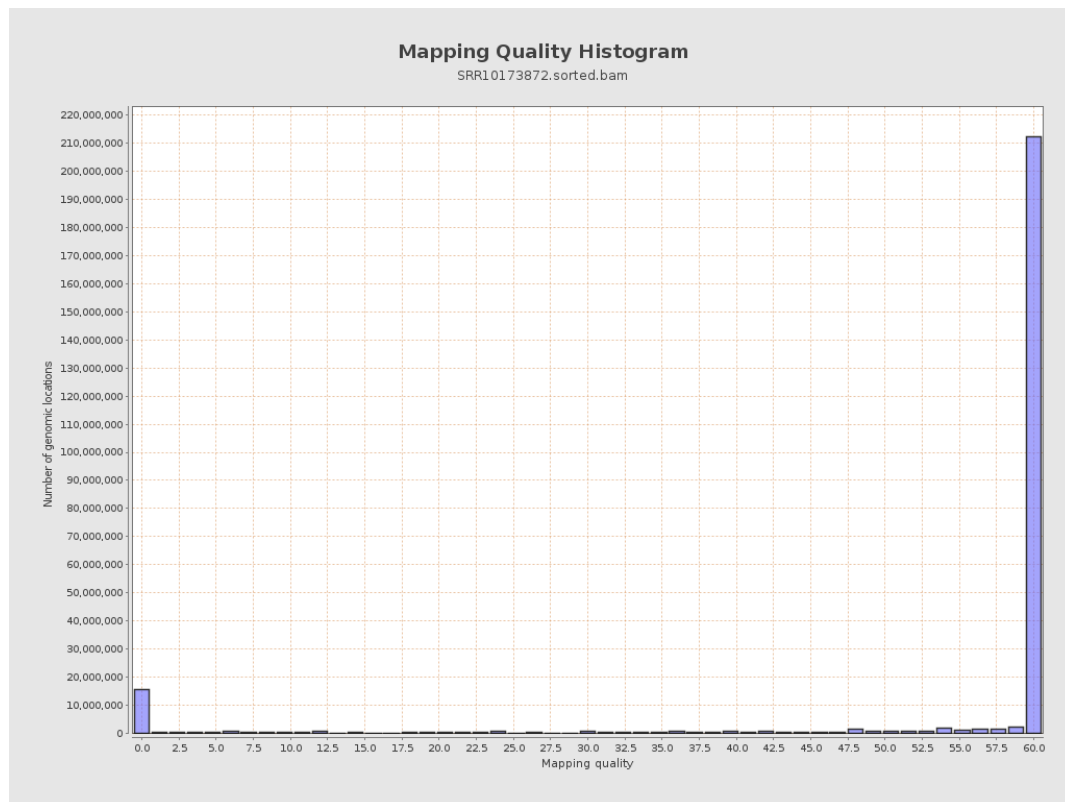
11. Results : Homopolymer Indels



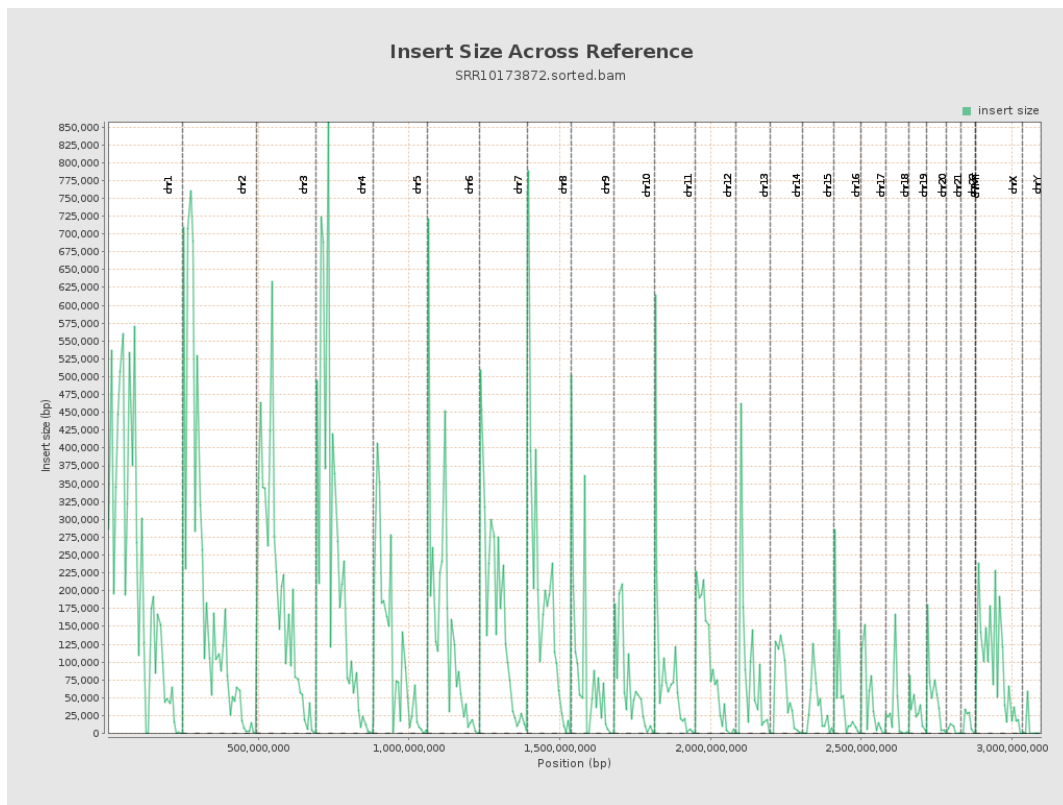
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

