

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 15:13:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173972.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_SRR10173972 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173972_1.fastq.gz SRR10173972_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 15:13:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173972.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,888,900
Mapped reads	5,758,572 / 97.79%
Unmapped reads	130,328 / 2.21%
Mapped paired reads	5,758,572 / 97.79%
Mapped reads, first in pair	2,882,559 / 48.95%
Mapped reads, second in pair	2,876,013 / 48.84%
Mapped reads, both in pair	5,681,448 / 96.48%
Mapped reads, singletons	77,124 / 1.31%
Secondary alignments	0
Supplementary alignments	735,001 / 12.48%
Read min/max/mean length	30 / 133 / 124.73
Duplicated reads (estimated)	4,527,626 / 76.88%
Duplication rate	63.65%
Clipped reads	3,105,698 / 52.74%

2.2. ACGT Content

Number/percentage of A's	193,667,512 / 30.02%
Number/percentage of C's	127,346,015 / 19.74%
Number/percentage of T's	191,959,733 / 29.76%
Number/percentage of G's	132,045,052 / 20.47%
Number/percentage of N's	4,960 / 0%

GC Percentage	40.21%
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2.3. Coverage

Mean	0.2085
Standard Deviation	3.6083

2.4. Mapping Quality

Mean Mapping Quality	52.6
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2.5. Insert size

Mean	1,049,005.91
Standard Deviation	9,536,650.57
P25/Median/P75	102 / 149 / 227

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	5,495,812
Insertions	71,709
Mapped reads with at least one insertion	1.2%
Deletions	187,469
Mapped reads with at least one deletion	3.18%
Homopolymer indels	40.7%

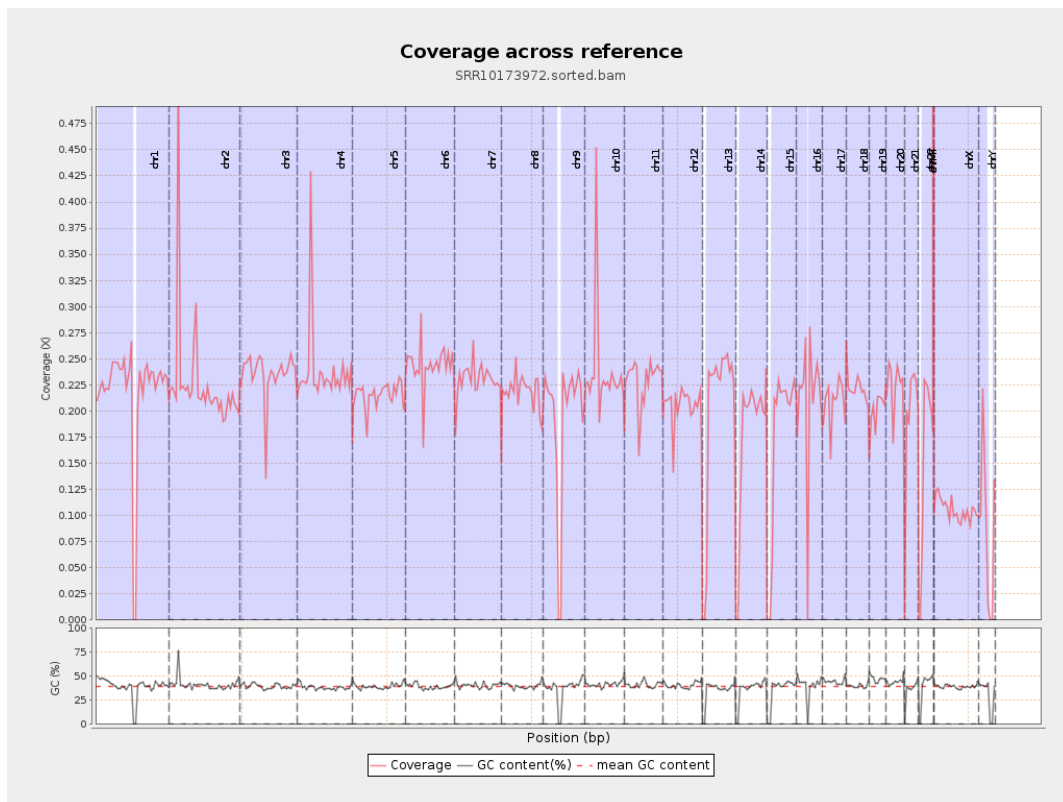
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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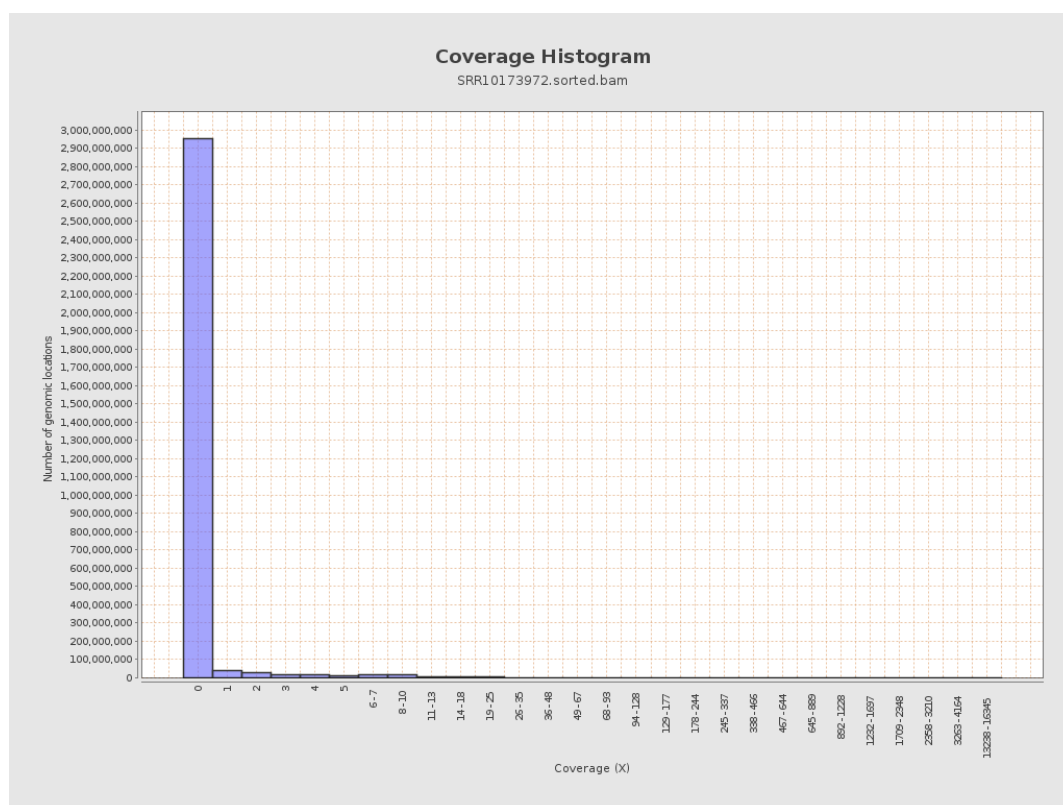
		bases	coverage	deviation
chr1	249250621	54299399	0.2179	1.9561
chr2	243199373	55220359	0.2271	11.4611
chr3	198022430	46639650	0.2355	1.448
chr4	191154276	45428086	0.2377	2.0617
chr5	180915260	38858142	0.2148	1.3795
chr6	171115067	41603912	0.2431	1.6551
chr7	159138663	36729258	0.2308	2.0294
chr8	146364022	31997876	0.2186	2.2898
chr9	141213431	27175536	0.1924	1.715
chr10	135534747	32101592	0.2369	2.4643
chr11	135006516	30949370	0.2292	1.4782
chr12	133851895	27411261	0.2048	1.3875
chr13	115169878	22849522	0.1984	1.3387
chr14	107349540	18617008	0.1734	1.2362
chr15	102531392	17830675	0.1739	1.2524
chr16	90354753	18993530	0.2102	1.6539
chr17	81195210	16790001	0.2068	1.4041
chr18	78077248	17280748	0.2213	2.2491
chr19	59128983	11904353	0.2013	1.5653
chr20	63025520	14016536	0.2224	1.5035
chr21	48129895	9367866	0.1946	1.6529
chr22	51304566	7610867	0.1483	1.3795
chrMT	16571	508704	30.6984	29.4927
chrX	155270560	16311834	0.1051	0.9636

chrY	59373566	4970784	0.0837	1.4435
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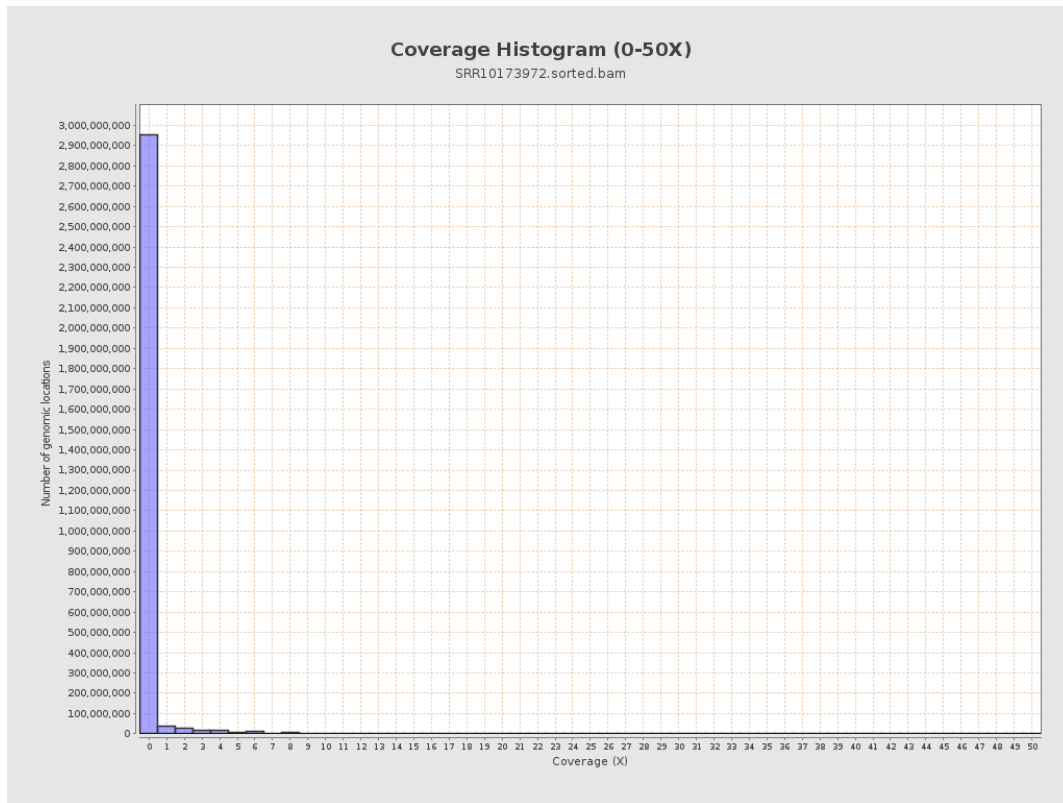
3. Results : Coverage across reference



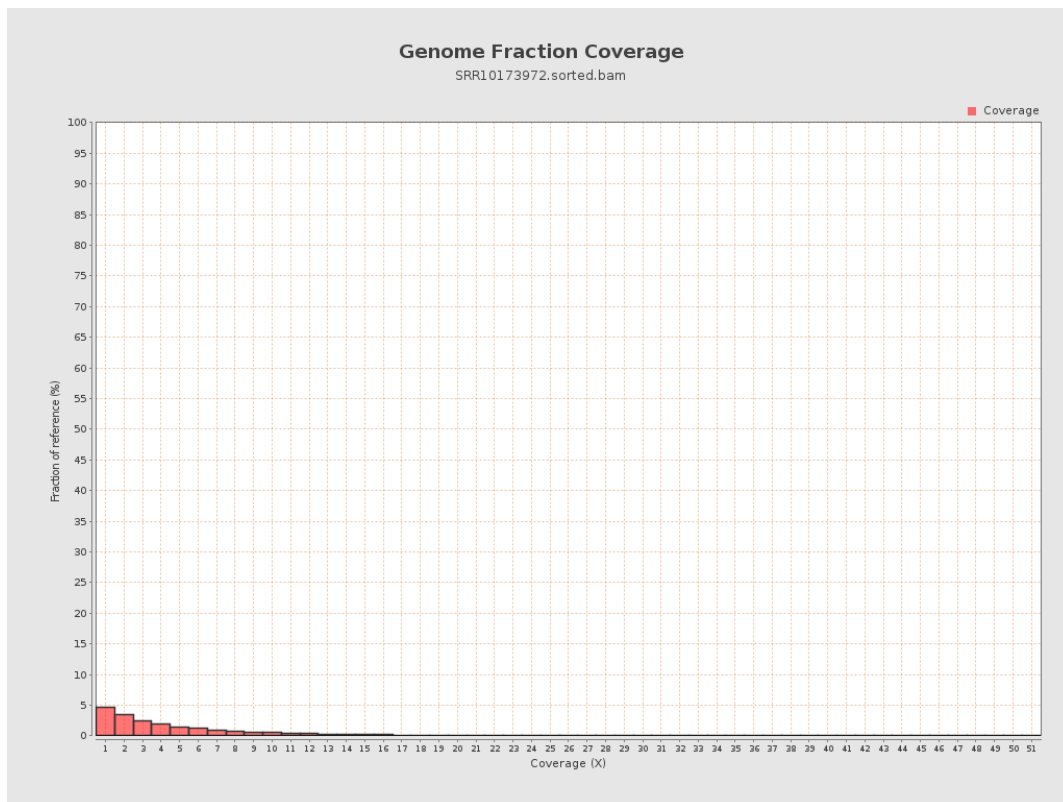
4. Results : Coverage Histogram



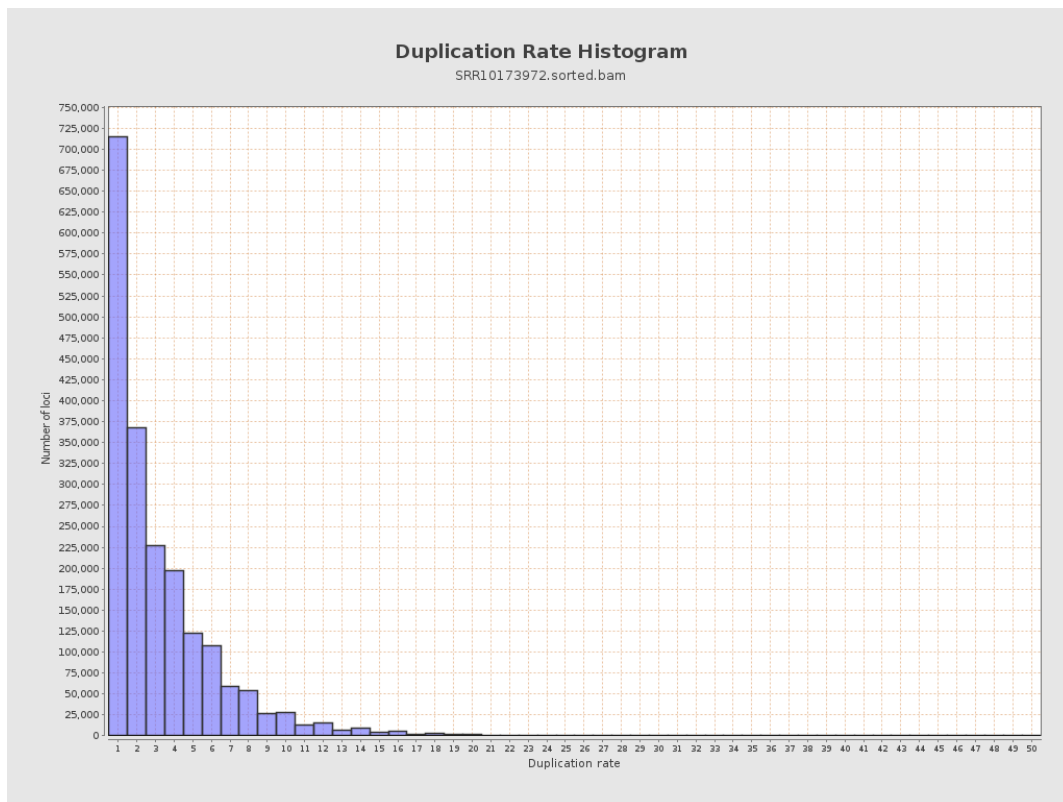
5. Results : Coverage Histogram (0-50X)



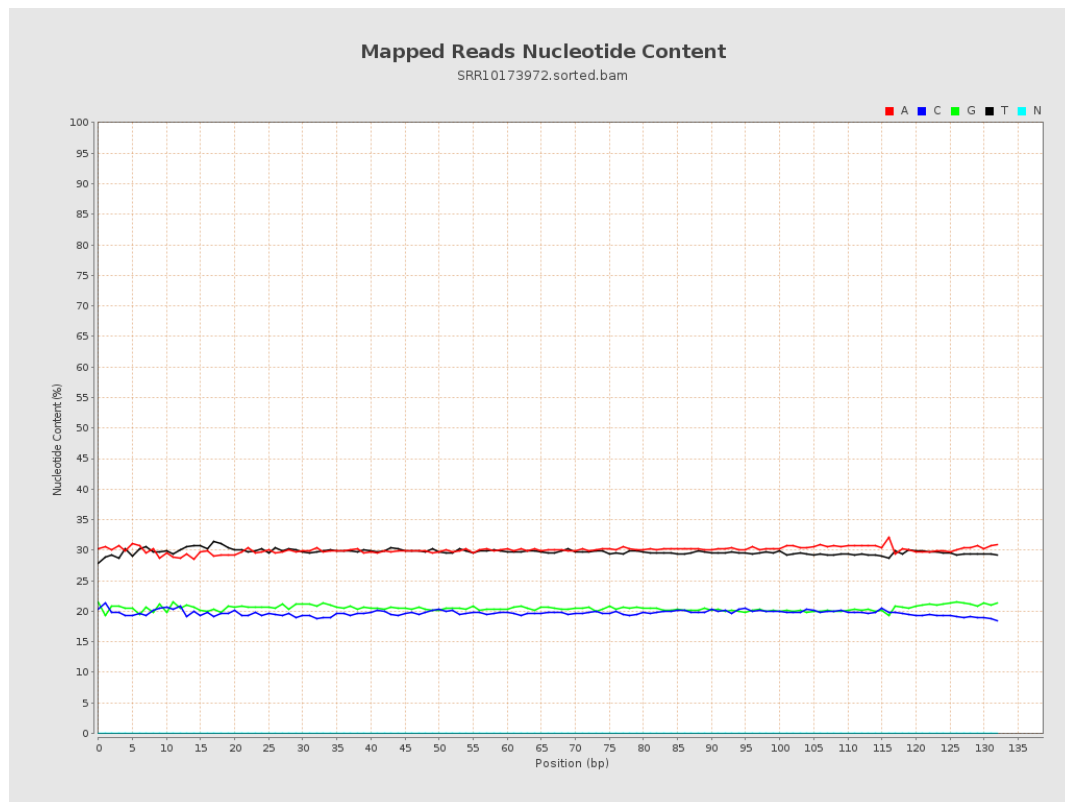
6. Results : Genome Fraction Coverage



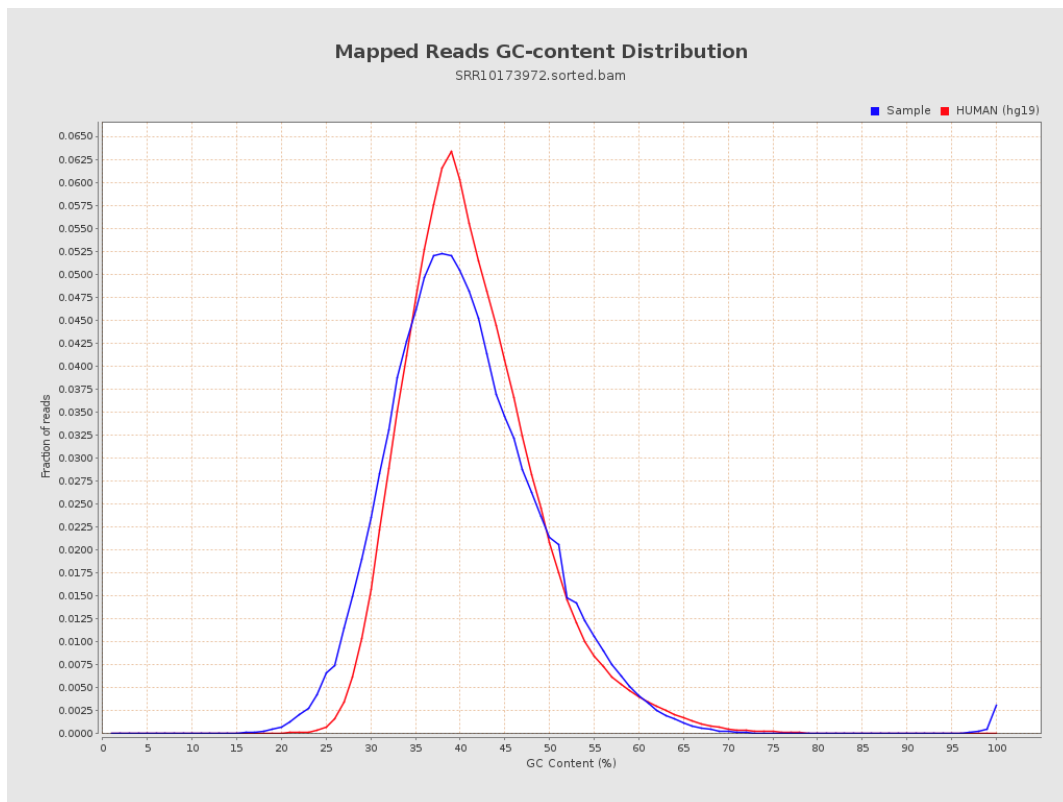
7. Results : Duplication Rate Histogram



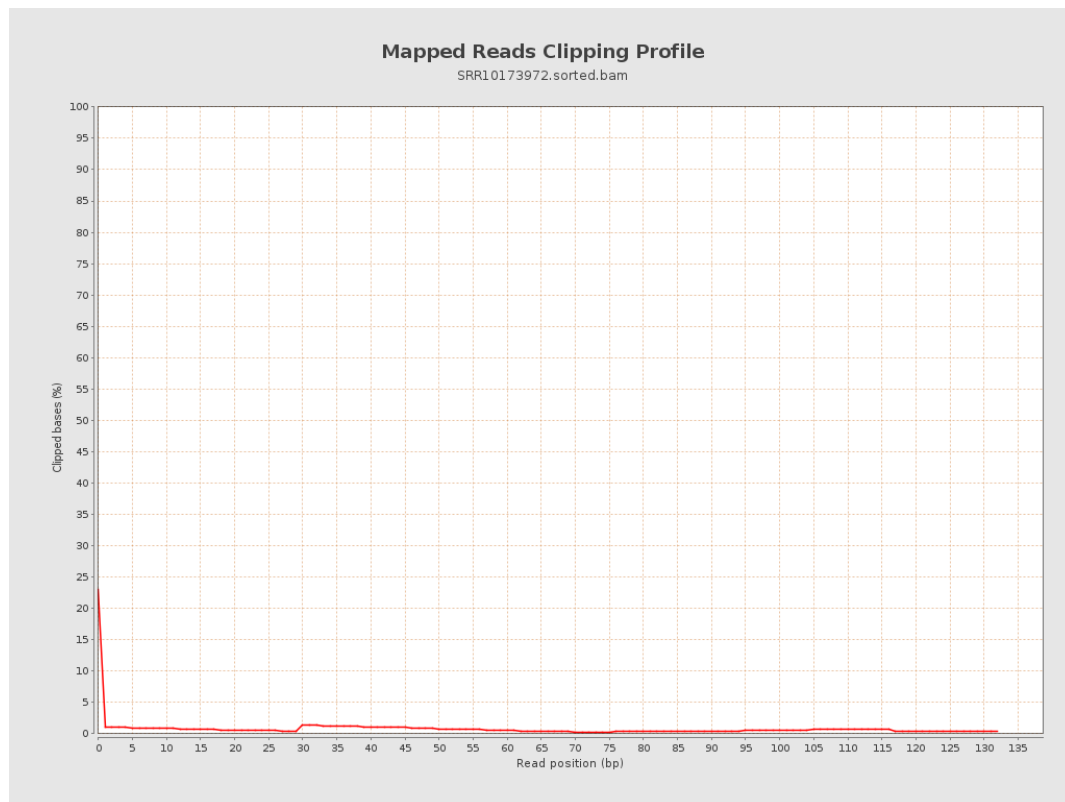
8. Results : Mapped Reads Nucleotide Content



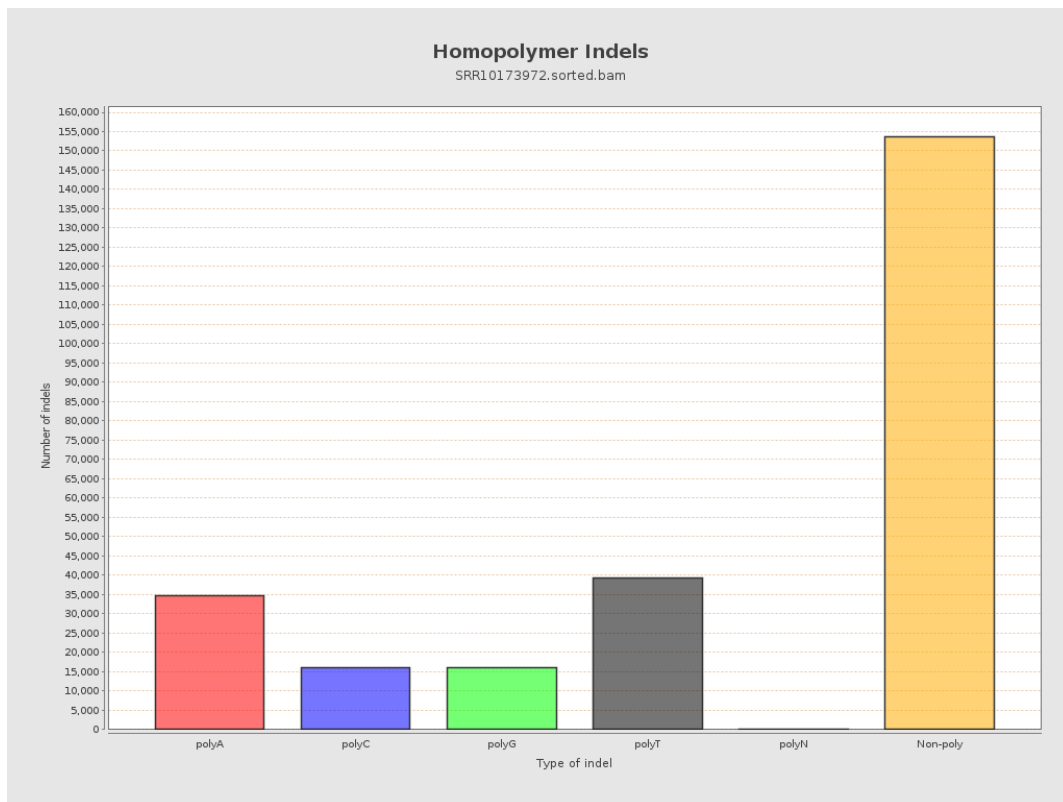
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



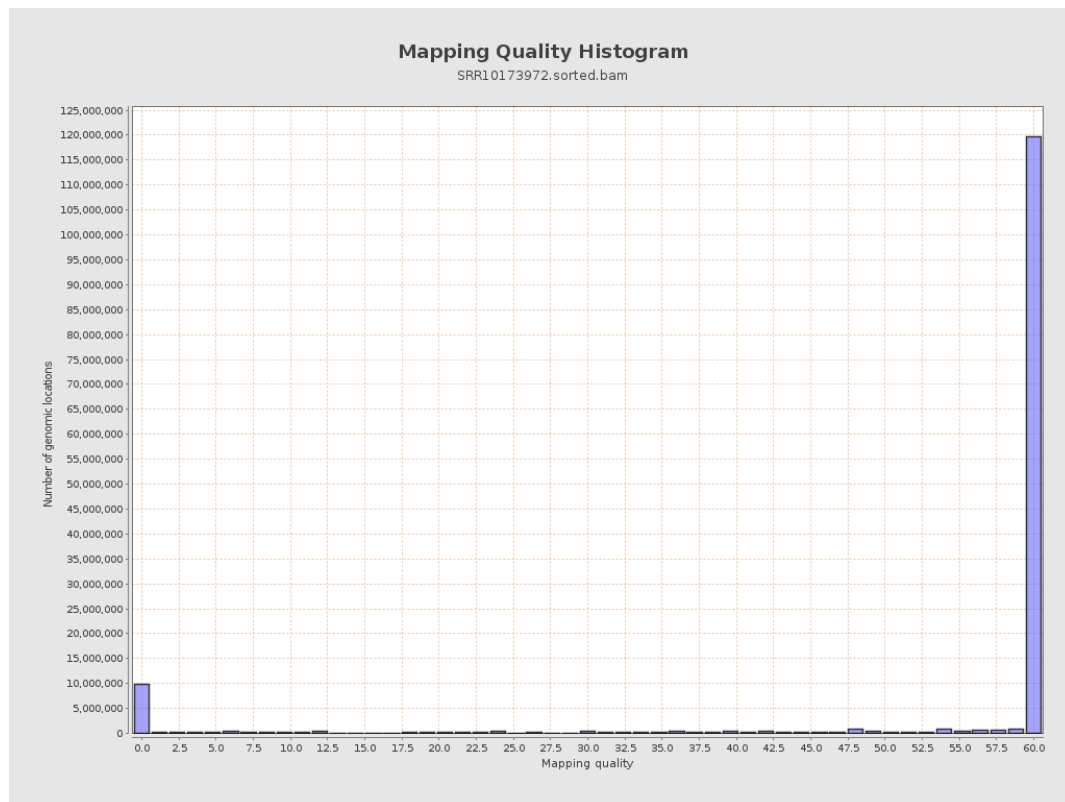
11. Results : Homopolymer Indels



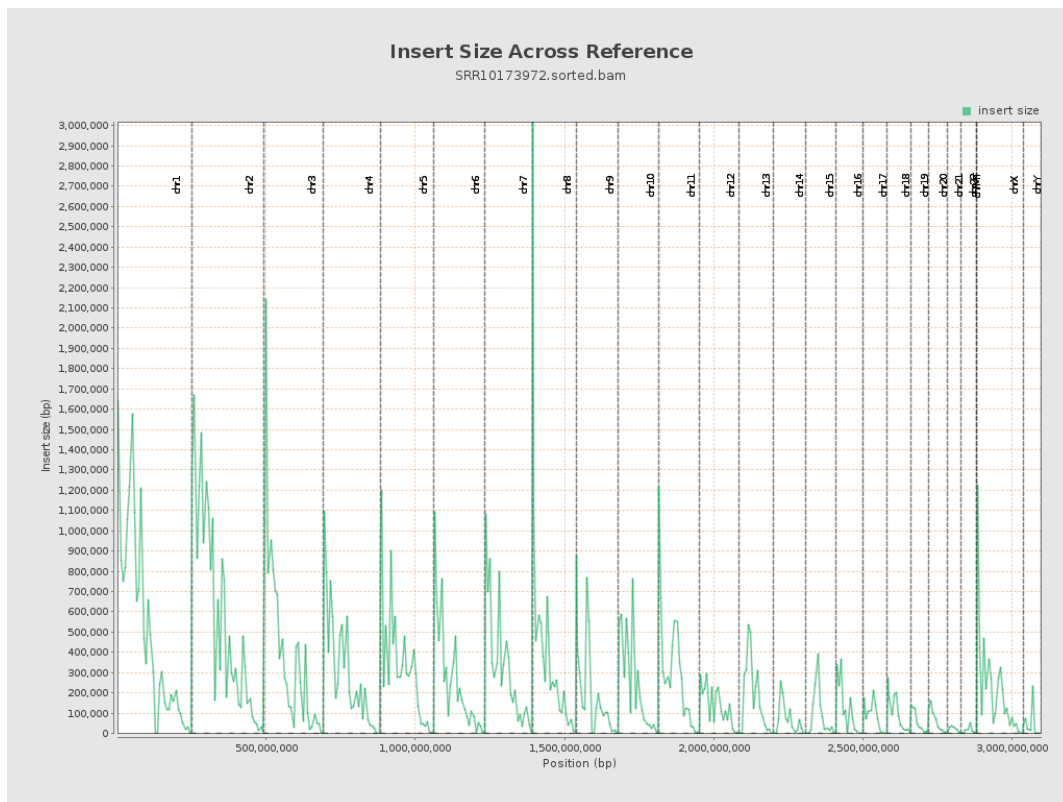
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

