

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 07:34:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173923.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_SRR10173923 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173923_1.fastq.gz SRR10173923_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 07:34:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,864,898
Mapped reads	2,799,921 / 97.73%
Unmapped reads	64,977 / 2.27%
Mapped paired reads	2,799,921 / 97.73%
Mapped reads, first in pair	1,399,649 / 48.86%
Mapped reads, second in pair	1,400,272 / 48.88%
Mapped reads, both in pair	2,756,680 / 96.22%
Mapped reads, singletons	43,241 / 1.51%
Secondary alignments	0
Supplementary alignments	256,412 / 8.95%
Read min/max/mean length	30 / 133 / 127.57
Duplicated reads (estimated)	2,084,274 / 72.75%
Duplication rate	64.15%
Clipped reads	1,043,681 / 36.43%

2.2. ACGT Content

Number/percentage of A's	99,940,261 / 30.15%
Number/percentage of C's	65,026,275 / 19.62%
Number/percentage of T's	99,510,977 / 30.02%
Number/percentage of G's	66,963,784 / 20.2%
Number/percentage of N's	3,769 / 0%

GC Percentage	39.82%
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2.3. Coverage

Mean	0.1071
Standard Deviation	1.6533

2.4. Mapping Quality

Mean Mapping Quality	52.86
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2.5. Insert size

Mean	801,772.3
Standard Deviation	8,400,720.64
P25/Median/P75	144 / 201 / 287

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	3,290,461
Insertions	33,901
Mapped reads with at least one insertion	1.17%
Deletions	66,915
Mapped reads with at least one deletion	2.33%
Homopolymer indels	44.11%

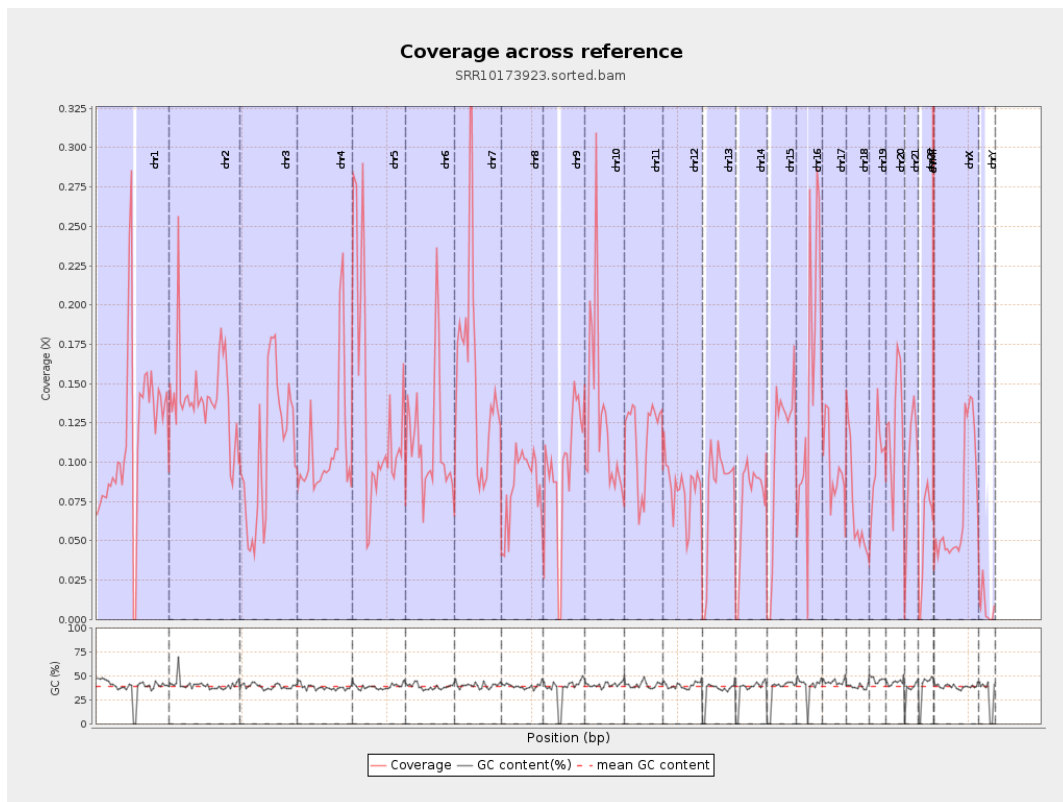
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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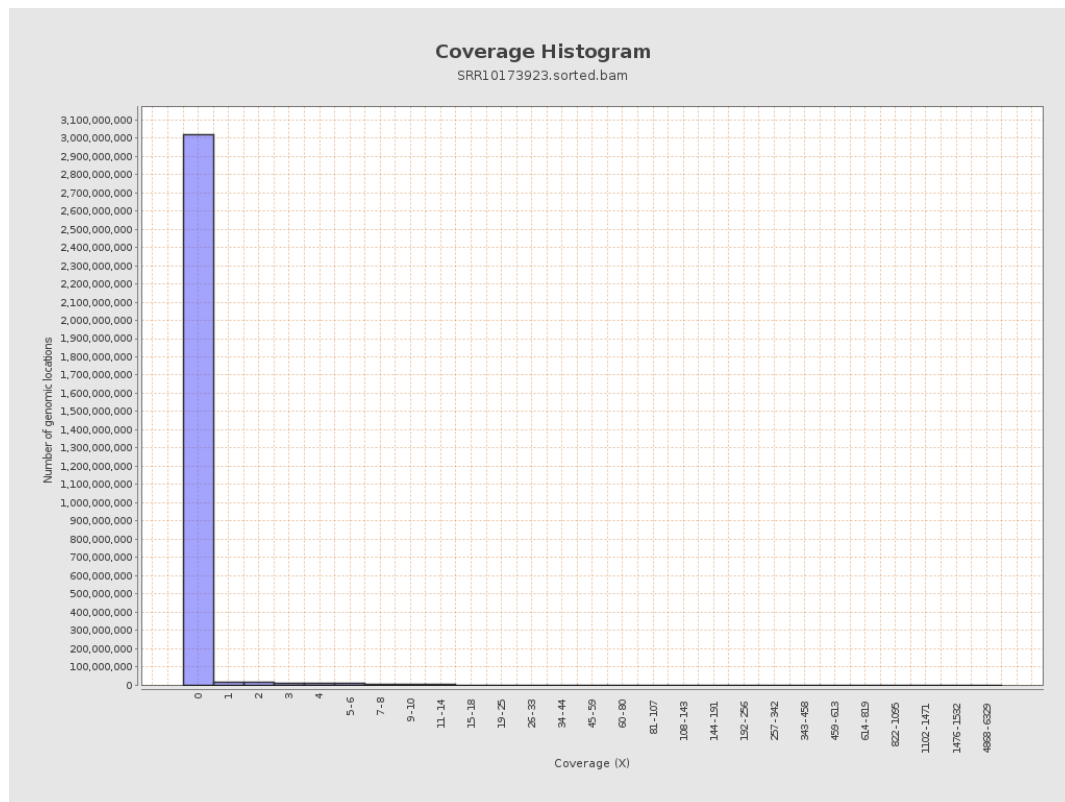
		bases	coverage	deviation
chr1	249250621	28836925	0.1157	1.3535
chr2	243199373	34396062	0.1414	4.4974
chr3	198022430	21419235	0.1082	0.8968
chr4	191154276	20361037	0.1065	1.0285
chr5	180915260	24208725	0.1338	1.0023
chr6	171115067	19399847	0.1134	0.9318
chr7	159138663	24248921	0.1524	1.7091
chr8	146364022	12413197	0.0848	0.9148
chr9	141213431	13954274	0.0988	0.9497
chr10	135534747	17290887	0.1276	1.8369
chr11	135006516	15689004	0.1162	0.9318
chr12	133851895	11108156	0.083	0.7827
chr13	115169878	9227353	0.0801	0.7776
chr14	107349540	7961963	0.0742	0.7369
chr15	102531392	10898525	0.1063	0.8804
chr16	90354753	13287499	0.1471	1.3608
chr17	81195210	7650985	0.0942	0.9031
chr18	78077248	5557343	0.0712	1.0918
chr19	59128983	5867669	0.0992	1.3884
chr20	63025520	7706599	0.1223	0.9435
chr21	48129895	4665142	0.0969	0.8677
chr22	51304566	2733491	0.0533	0.5908
chrMT	16571	1292222	77.9809	66.2414
chrX	155270560	11005987	0.0709	0.7188

chrY	59373566	433653	0.0073	0.3783
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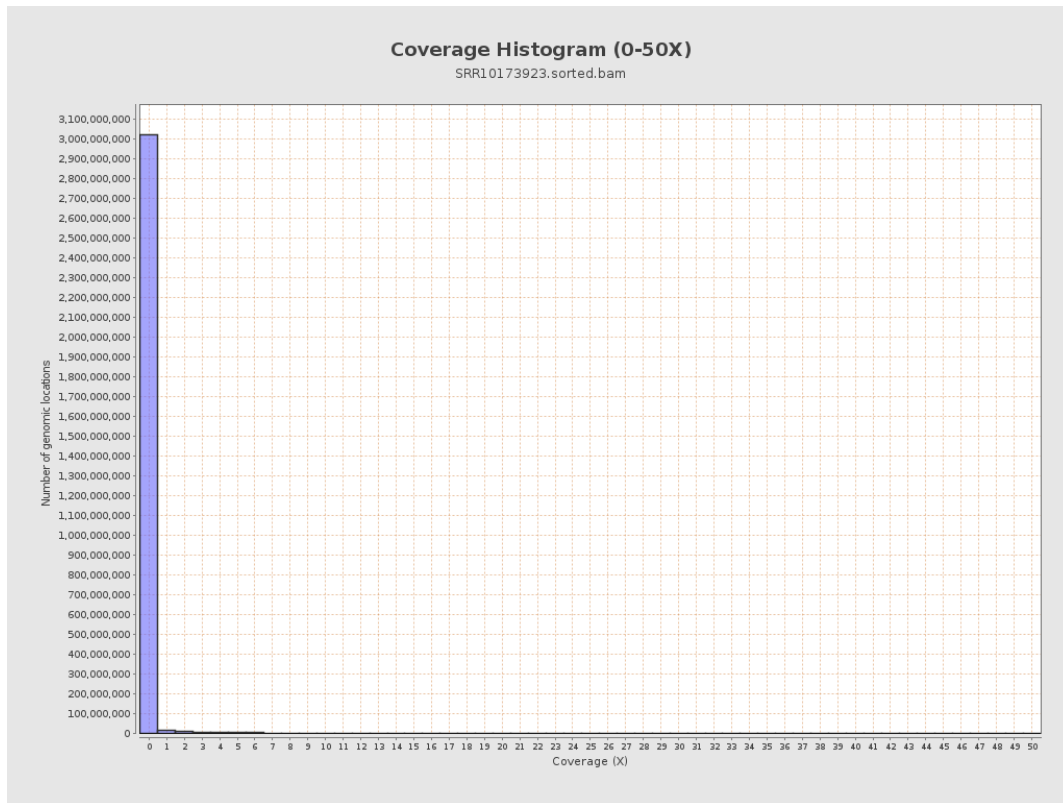
3. Results : Coverage across reference



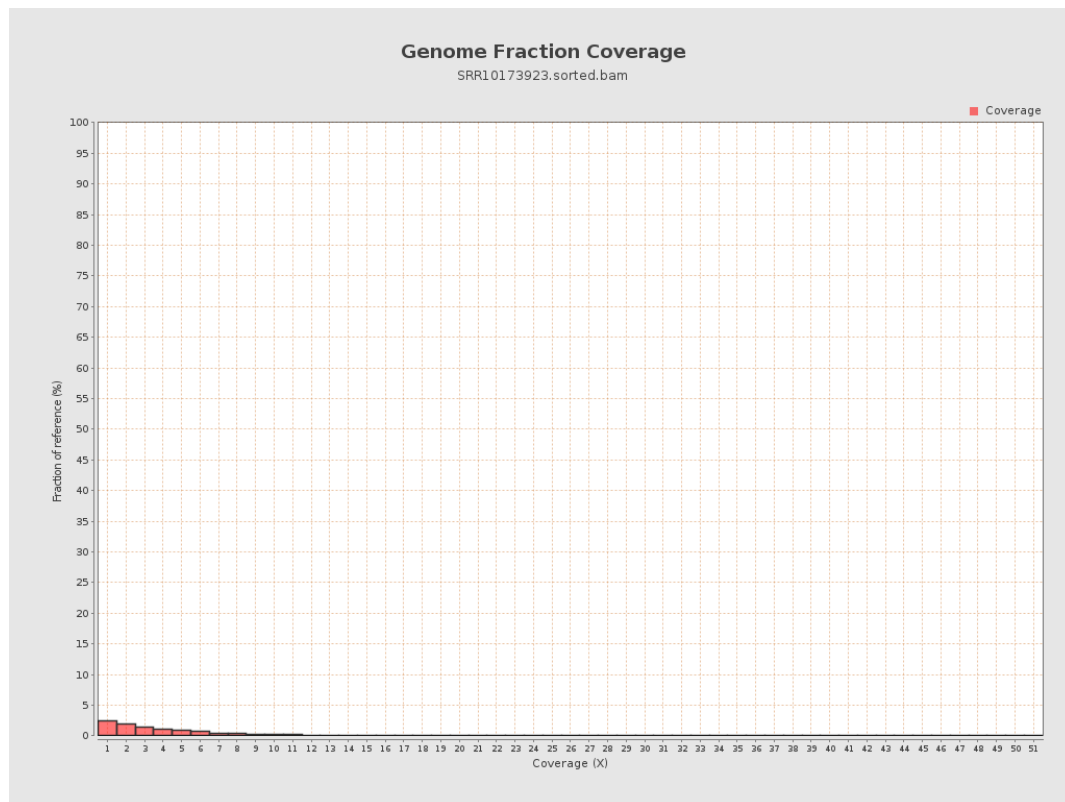
4. Results : Coverage Histogram



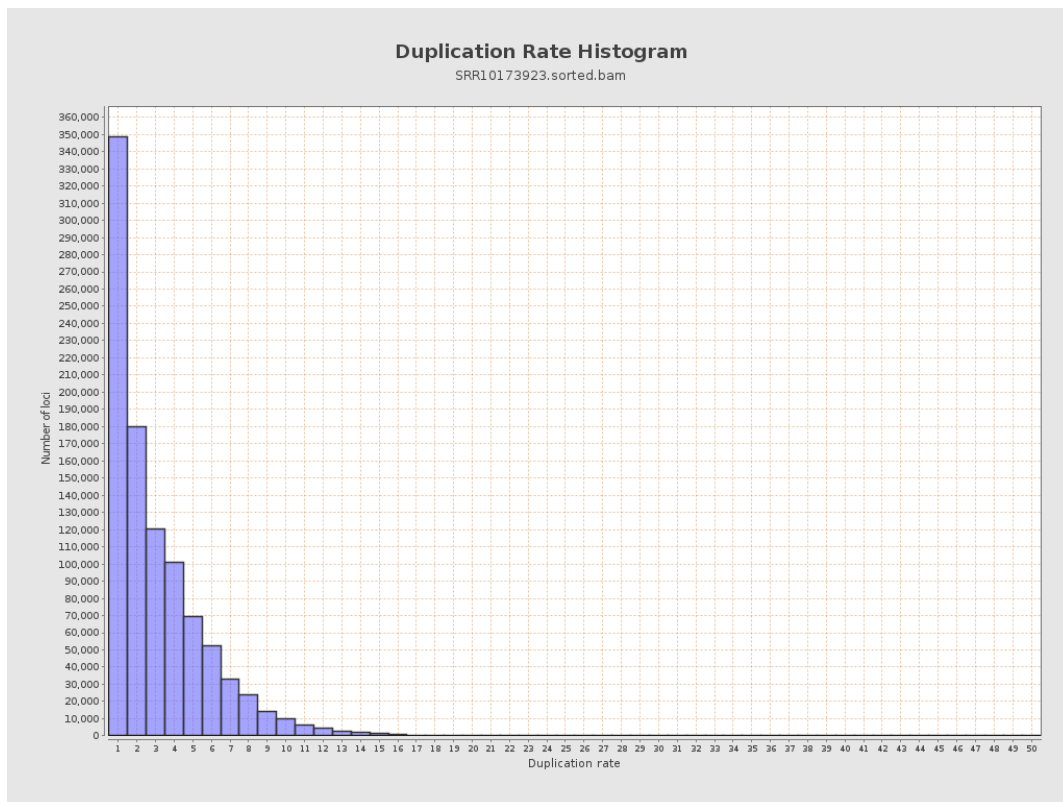
5. Results : Coverage Histogram (0-50X)



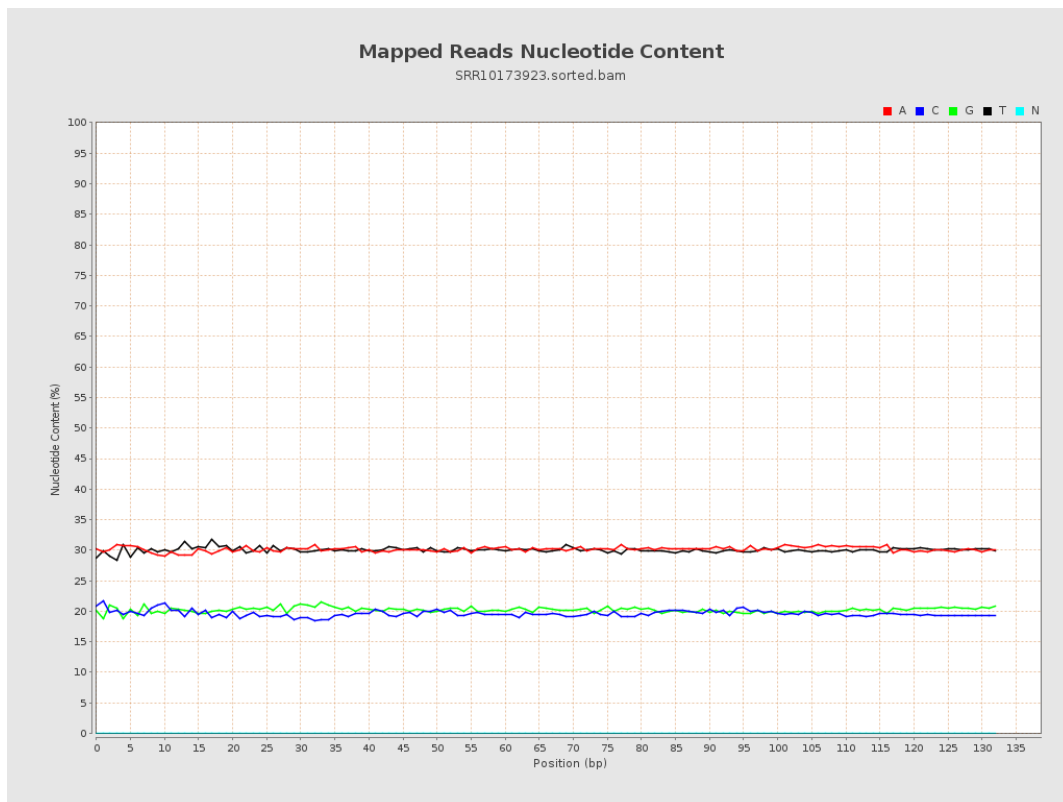
6. Results : Genome Fraction Coverage



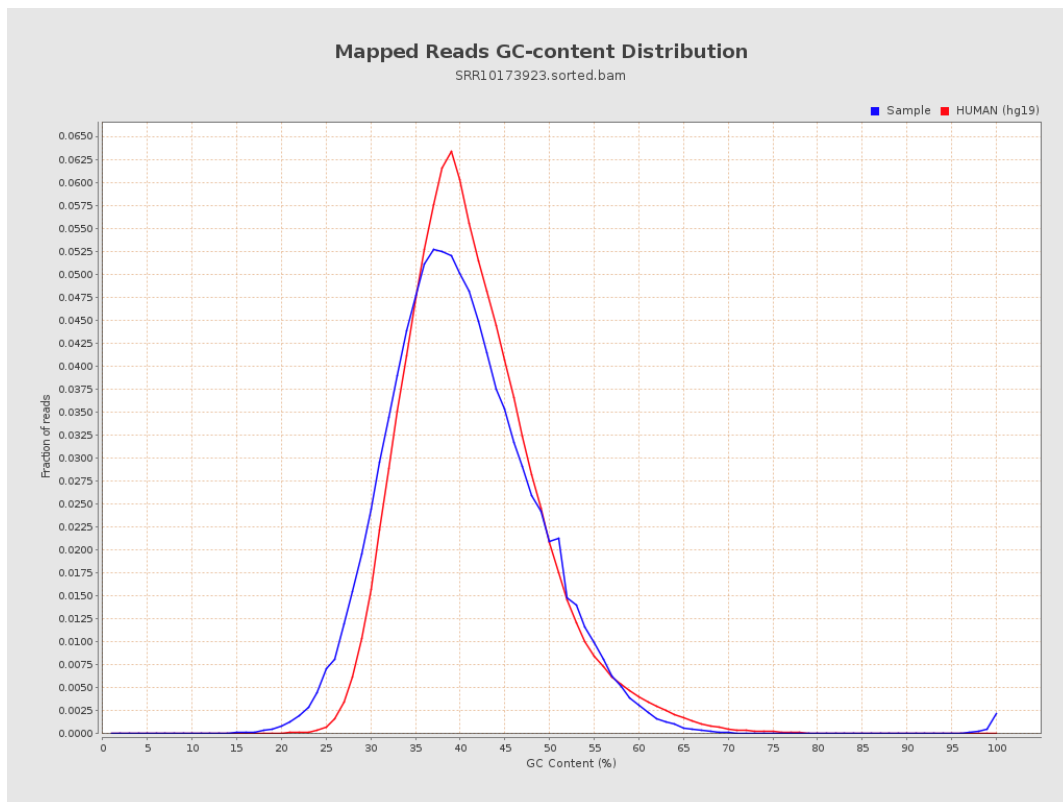
7. Results : Duplication Rate Histogram



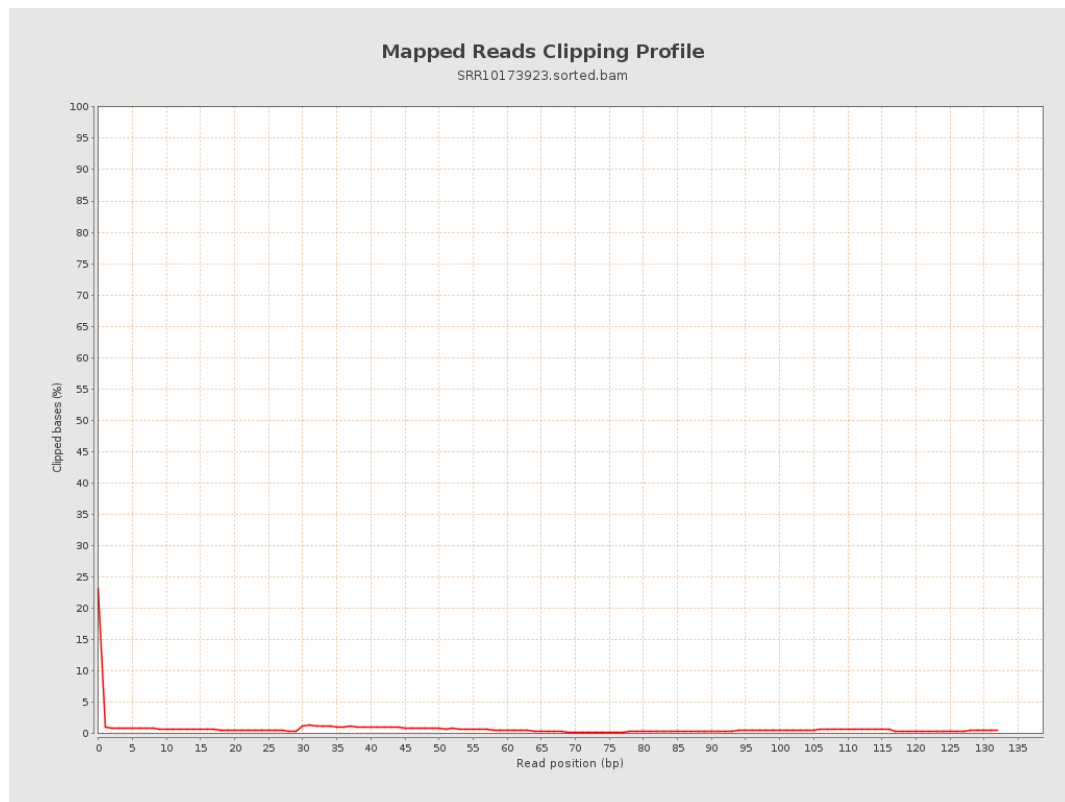
8. Results : Mapped Reads Nucleotide Content



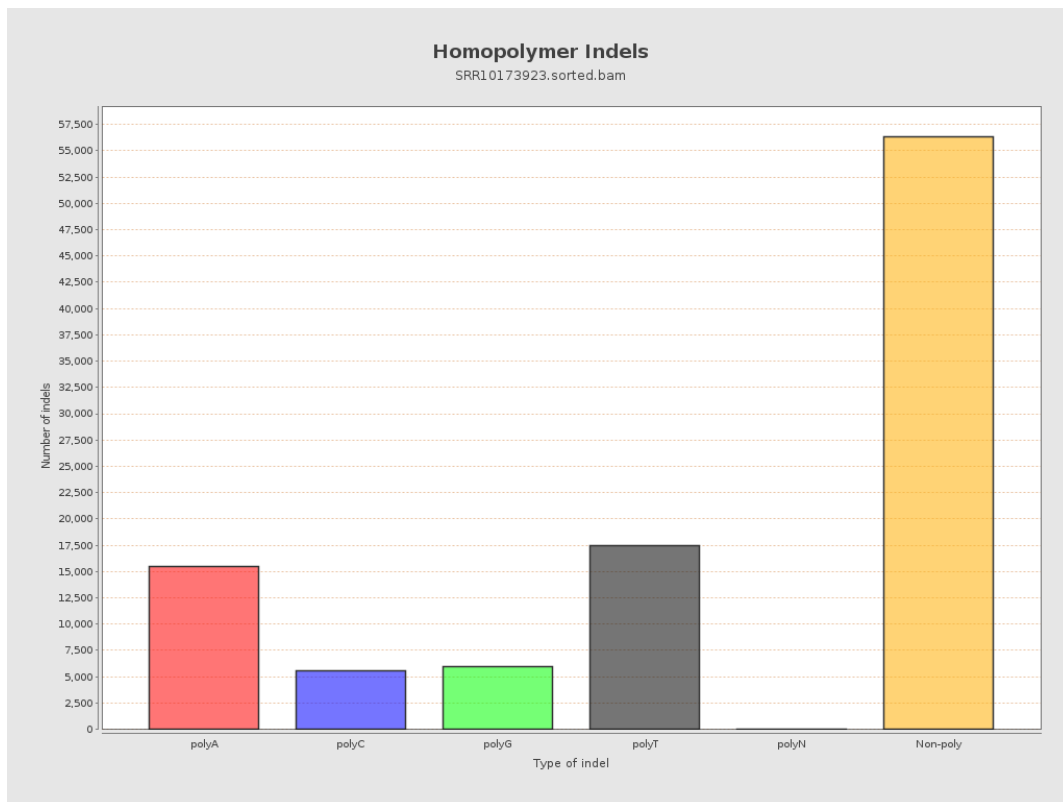
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



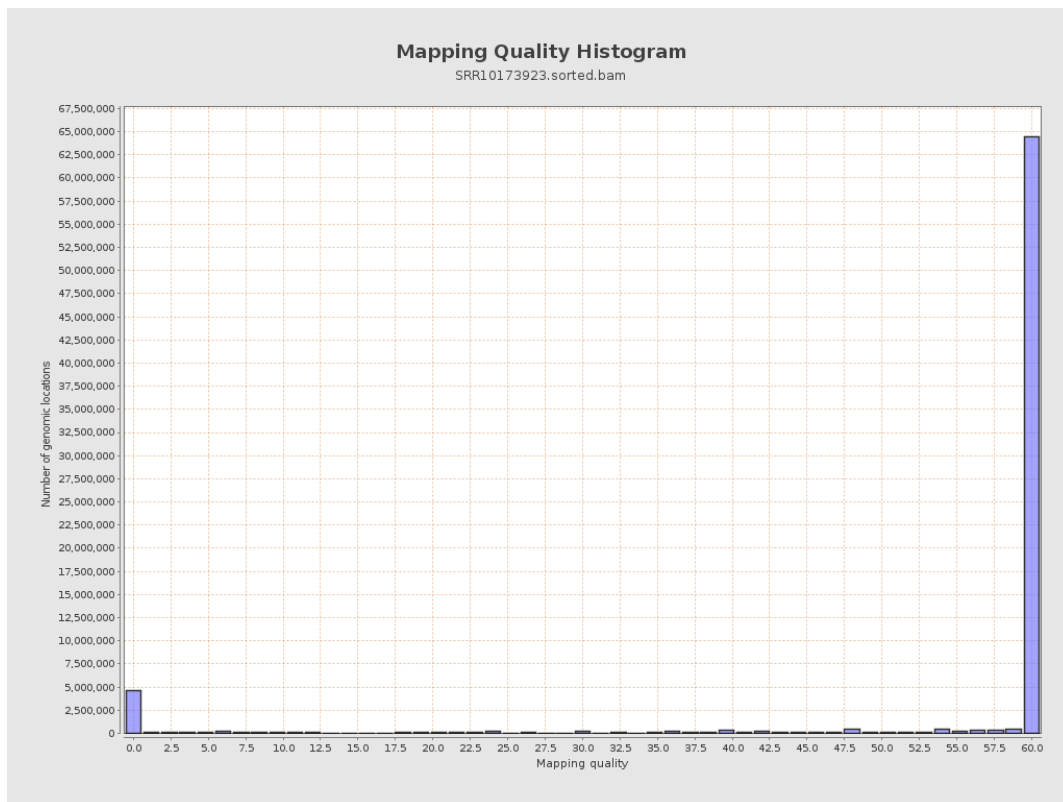
11. Results : Homopolymer Indels



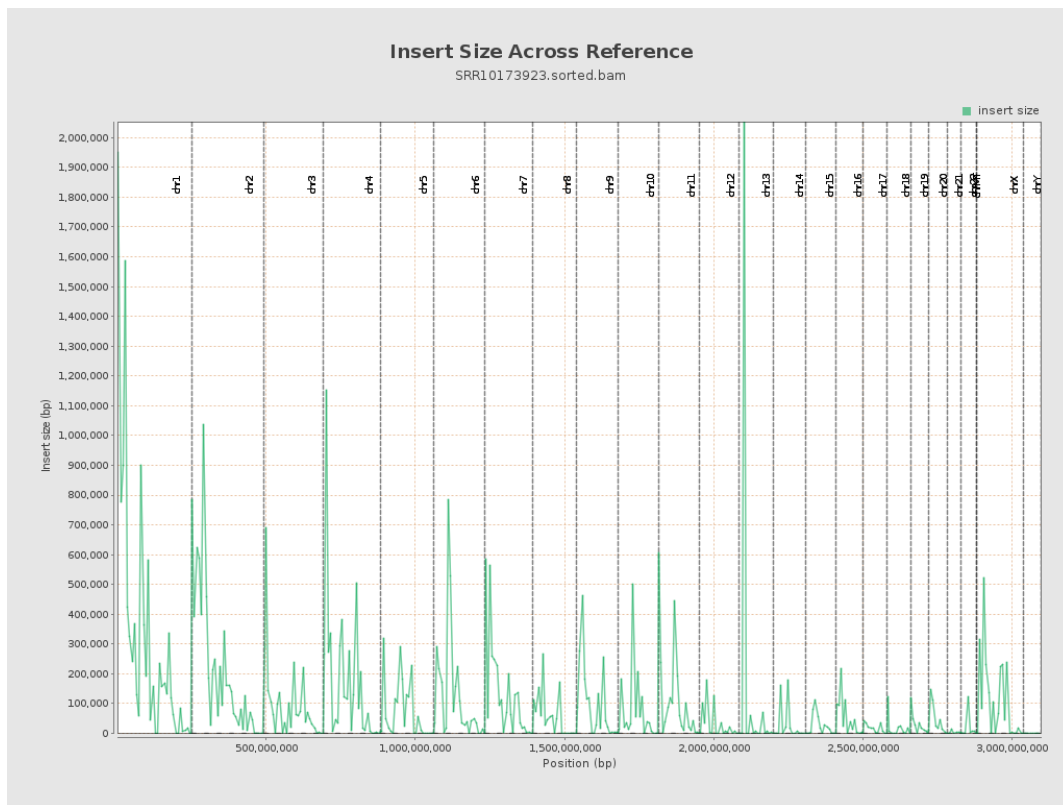
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

