

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 22:46:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174027.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_SRR10174027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174027_1.fastq.gz SRR10174027_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 22:46:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,910,938
Mapped reads	1,873,829 / 98.06%
Unmapped reads	37,109 / 1.94%
Mapped paired reads	1,873,829 / 98.06%
Mapped reads, first in pair	934,871 / 48.92%
Mapped reads, second in pair	938,958 / 49.14%
Mapped reads, both in pair	1,849,840 / 96.8%
Mapped reads, singletons	23,989 / 1.26%
Secondary alignments	0
Supplementary alignments	200,342 / 10.48%
Read min/max/mean length	30 / 133 / 128.56
Duplicated reads (estimated)	1,457,508 / 76.27%
Duplication rate	64.39%
Clipped reads	731,647 / 38.29%

2.2. ACGT Content

Number/percentage of A's	67,892,780 / 30.39%
Number/percentage of C's	43,167,322 / 19.33%
Number/percentage of T's	67,802,476 / 30.35%
Number/percentage of G's	44,506,510 / 19.92%
Number/percentage of N's	2,818 / 0%

GC Percentage	39.25%
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2.3. Coverage

Mean	0.0722
Standard Deviation	1.2482

2.4. Mapping Quality

Mean Mapping Quality	52.6
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2.5. Insert size

Mean	939,112.15
Standard Deviation	9,084,791.03
P25/Median/P75	144 / 197 / 282

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	2,121,950
Insertions	23,914
Mapped reads with at least one insertion	1.24%
Deletions	41,370
Mapped reads with at least one deletion	2.14%
Homopolymer indels	44.24%

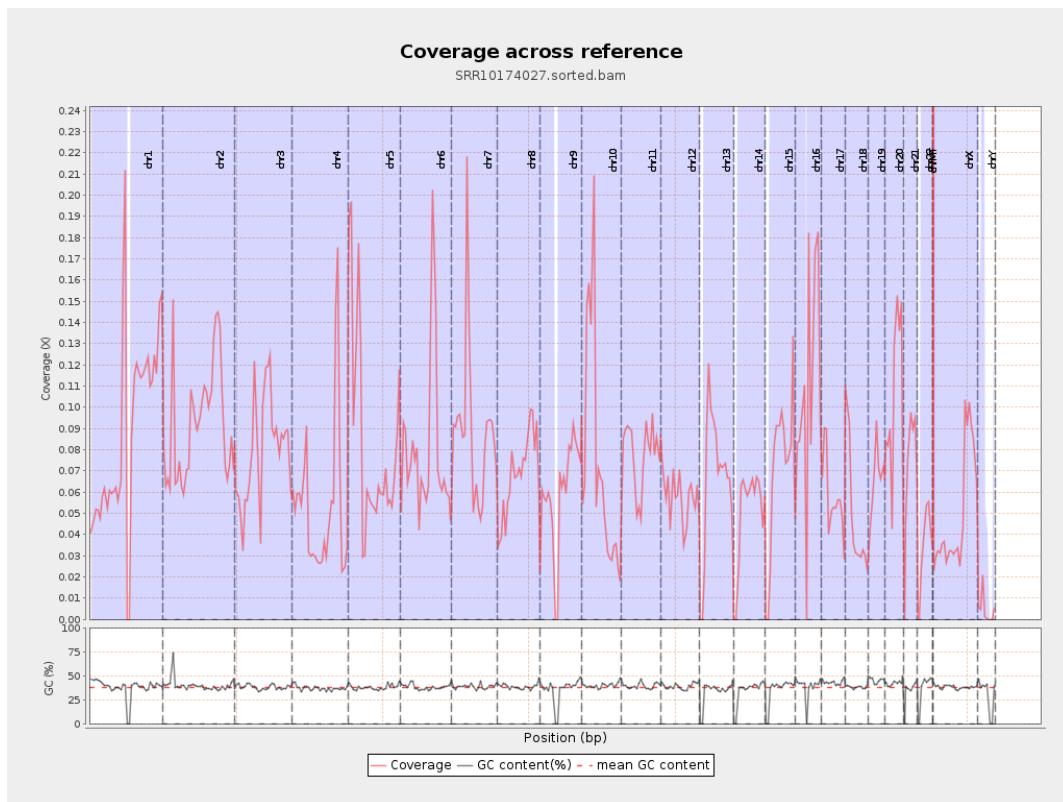
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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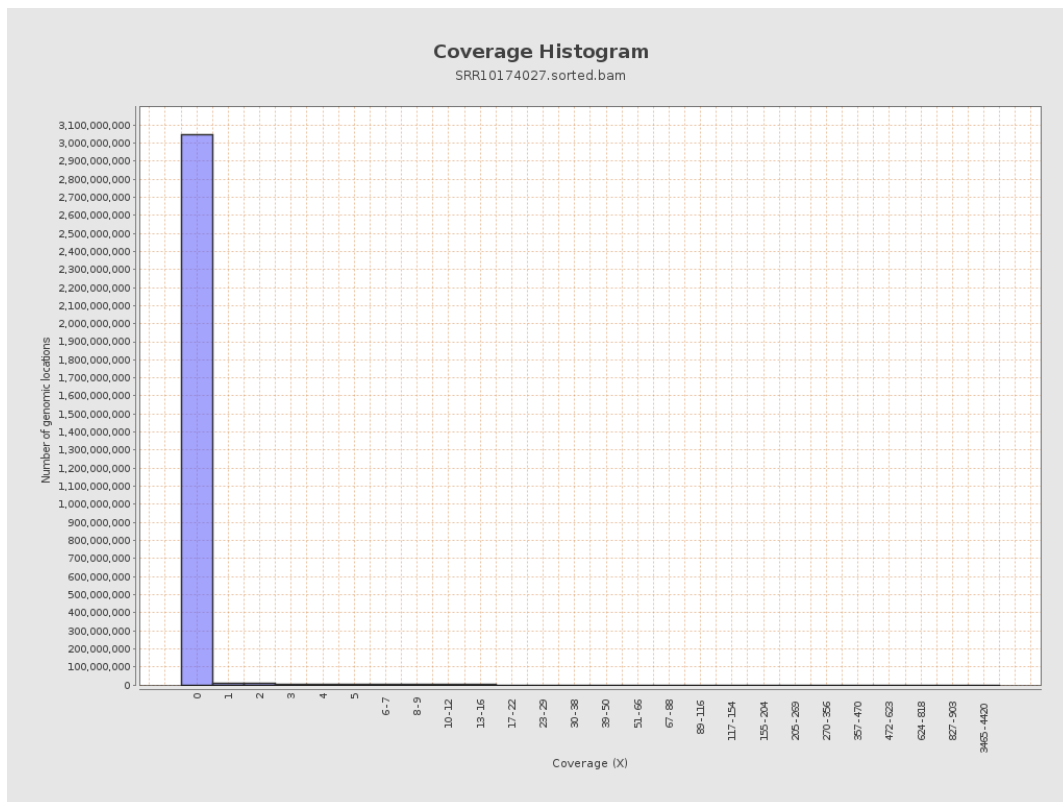
		bases	coverage	deviation
chr1	249250621	22107019	0.0887	1.1211
chr2	243199373	22441762	0.0923	3.1776
chr3	198022430	15783354	0.0797	0.8192
chr4	191154276	10298659	0.0539	0.7459
chr5	180915260	15272735	0.0844	0.8447
chr6	171115067	13690029	0.08	0.8337
chr7	159138663	14028094	0.0882	1.3399
chr8	146364022	10081581	0.0689	0.852
chr9	141213431	8538595	0.0605	0.7739
chr10	135534747	9802911	0.0723	1.3145
chr11	135006516	10417632	0.0772	0.8076
chr12	133851895	7795129	0.0582	0.6915
chr13	115169878	7736640	0.0672	0.766
chr14	107349540	5446992	0.0507	0.6487
chr15	102531392	7206050	0.0703	0.7519
chr16	90354753	9647001	0.1068	1.144
chr17	81195210	4781300	0.0589	0.7284
chr18	78077248	3863556	0.0495	0.9929
chr19	59128983	3888059	0.0658	1.134
chr20	63025520	6777183	0.1075	0.9382
chr21	48129895	3445111	0.0716	0.7796
chr22	51304566	1759247	0.0343	0.4991
chrMT	16571	688036	41.5205	38.4168
chrX	155270560	7702246	0.0496	0.6446

chrY	59373566	282839	0.0048	0.2402
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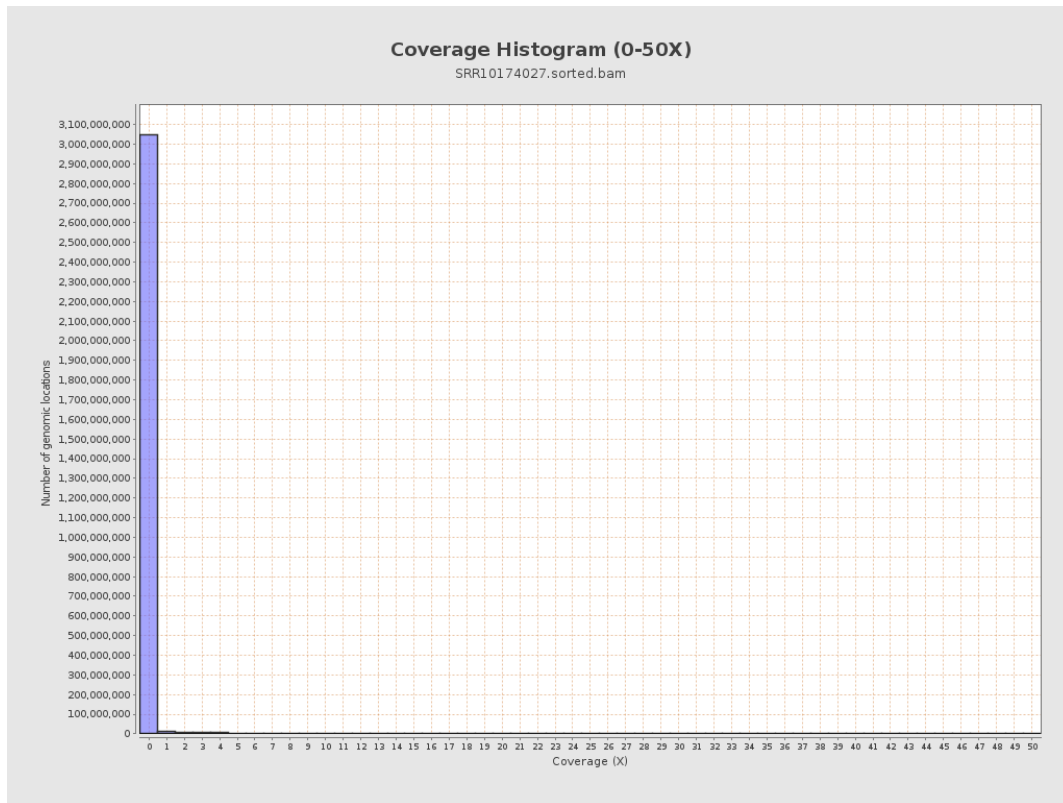
3. Results : Coverage across reference



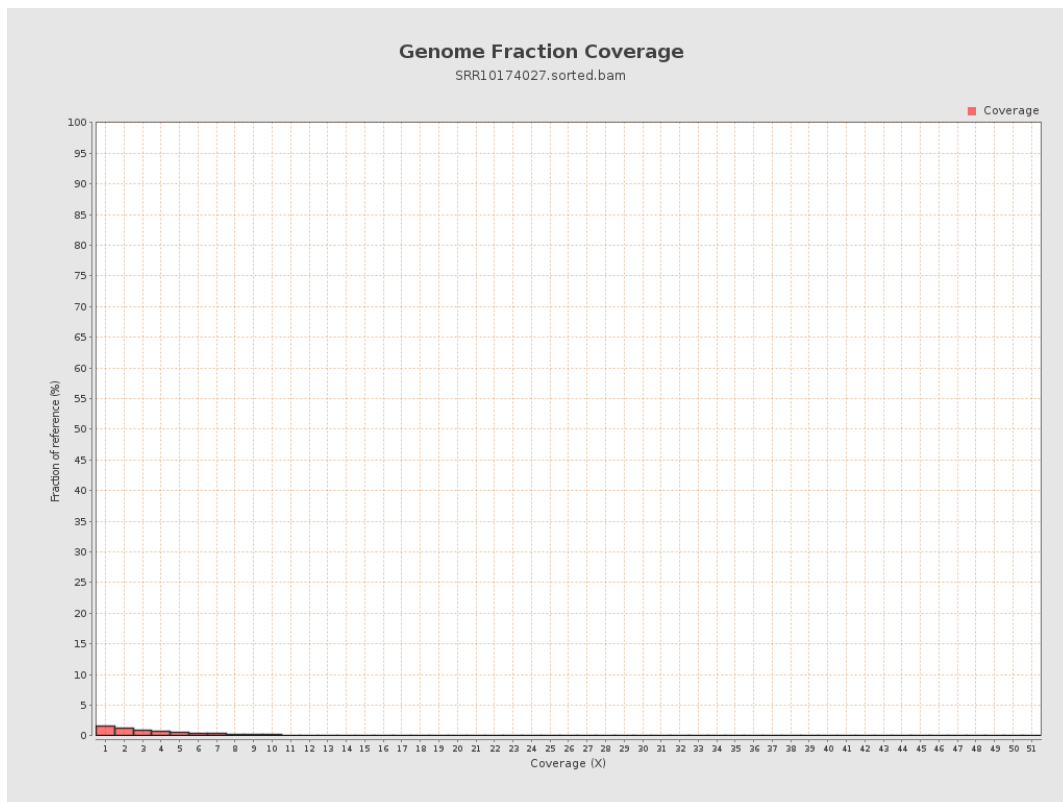
4. Results : Coverage Histogram



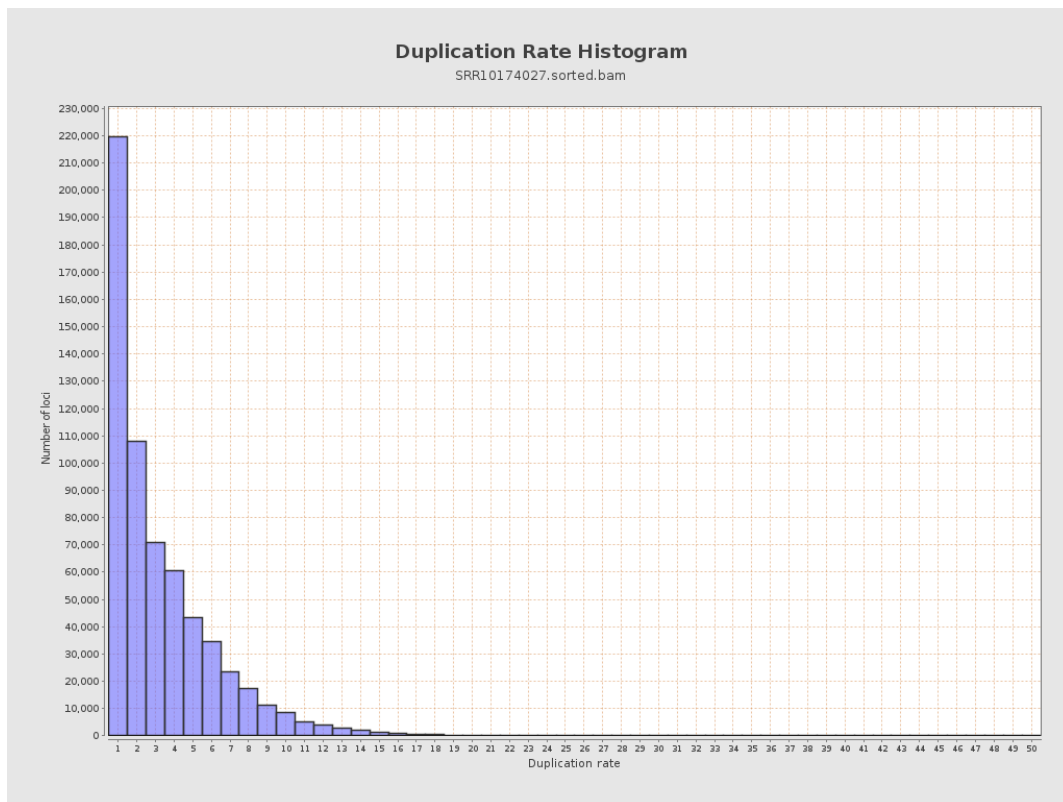
5. Results : Coverage Histogram (0-50X)



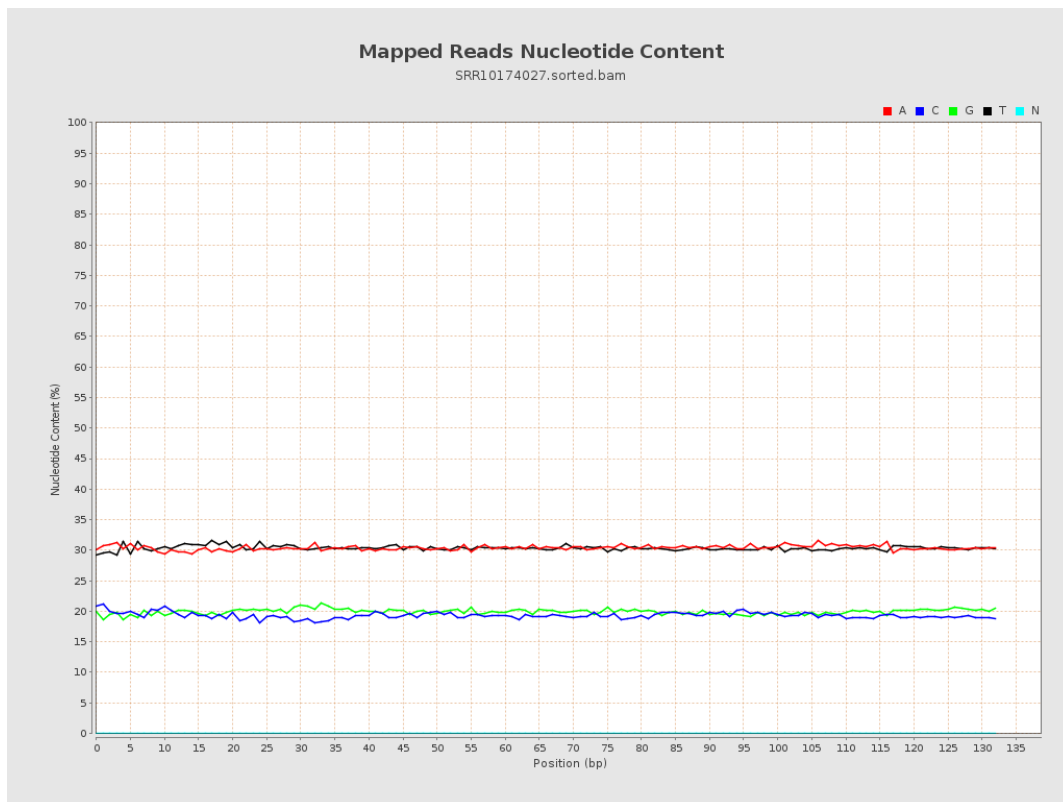
6. Results : Genome Fraction Coverage



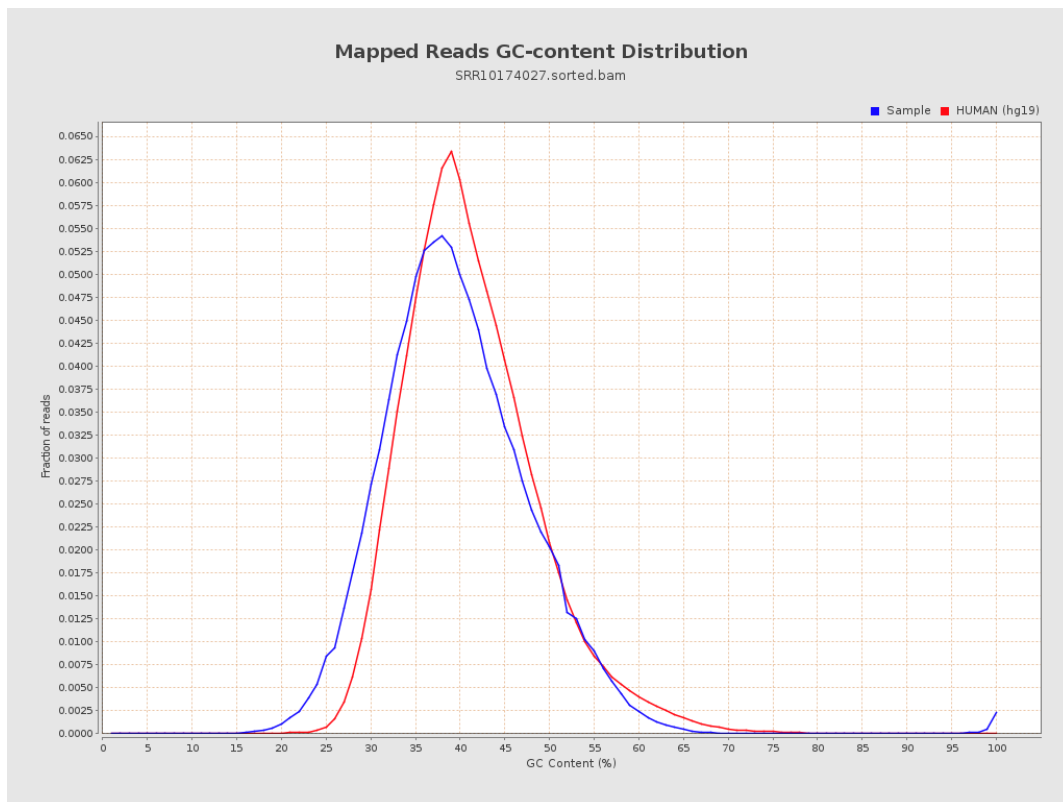
7. Results : Duplication Rate Histogram



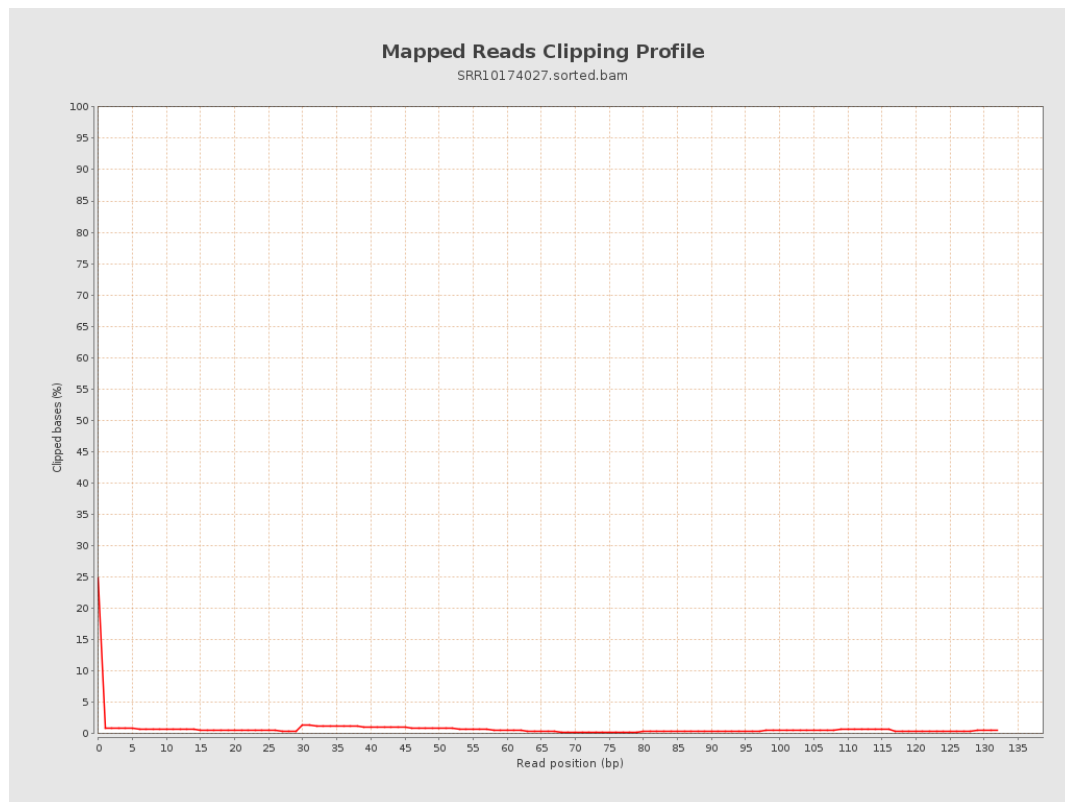
8. Results : Mapped Reads Nucleotide Content



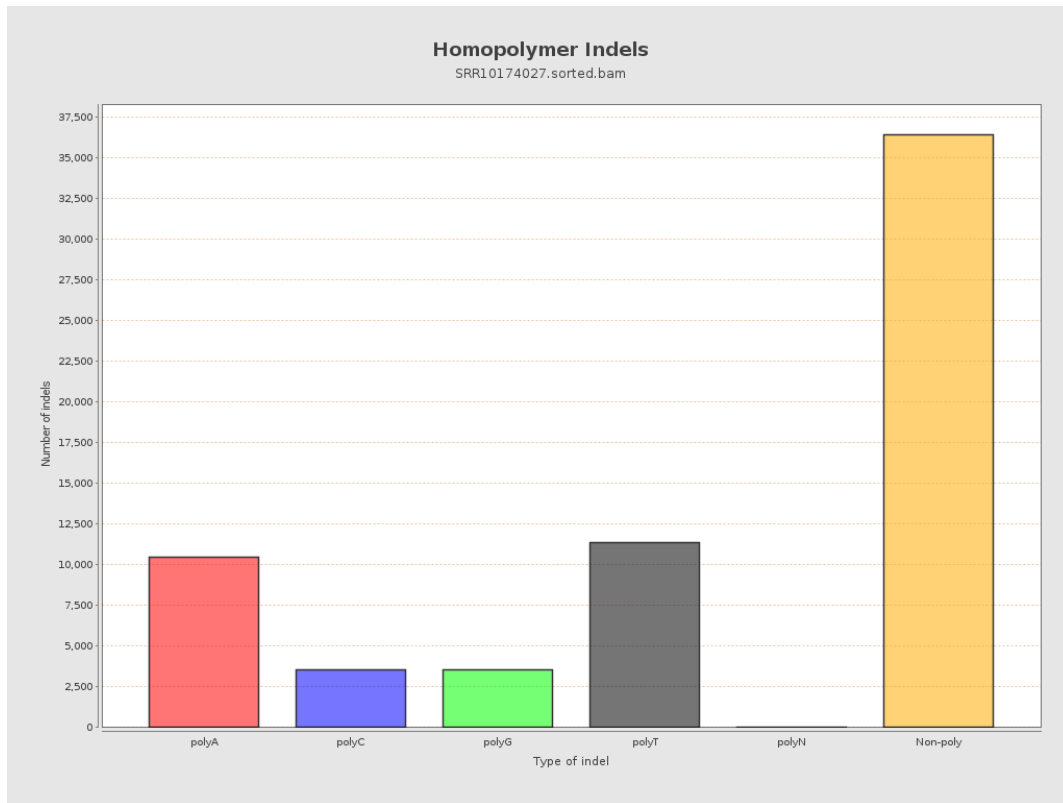
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



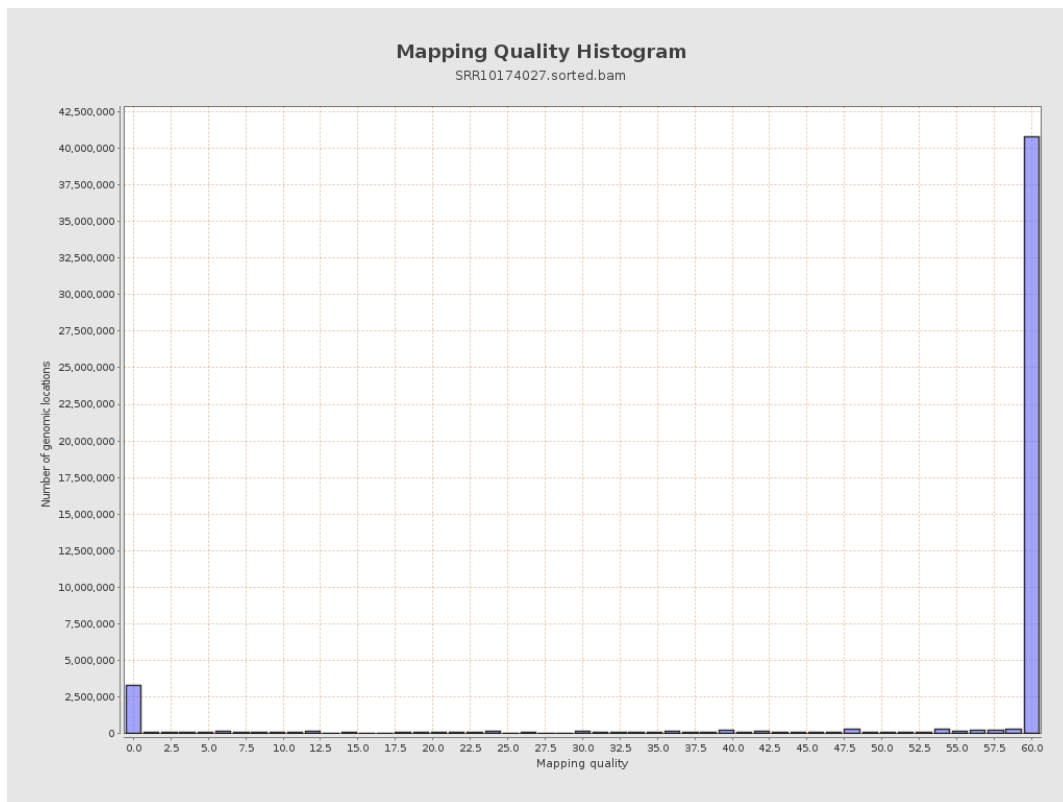
11. Results : Homopolymer Indels



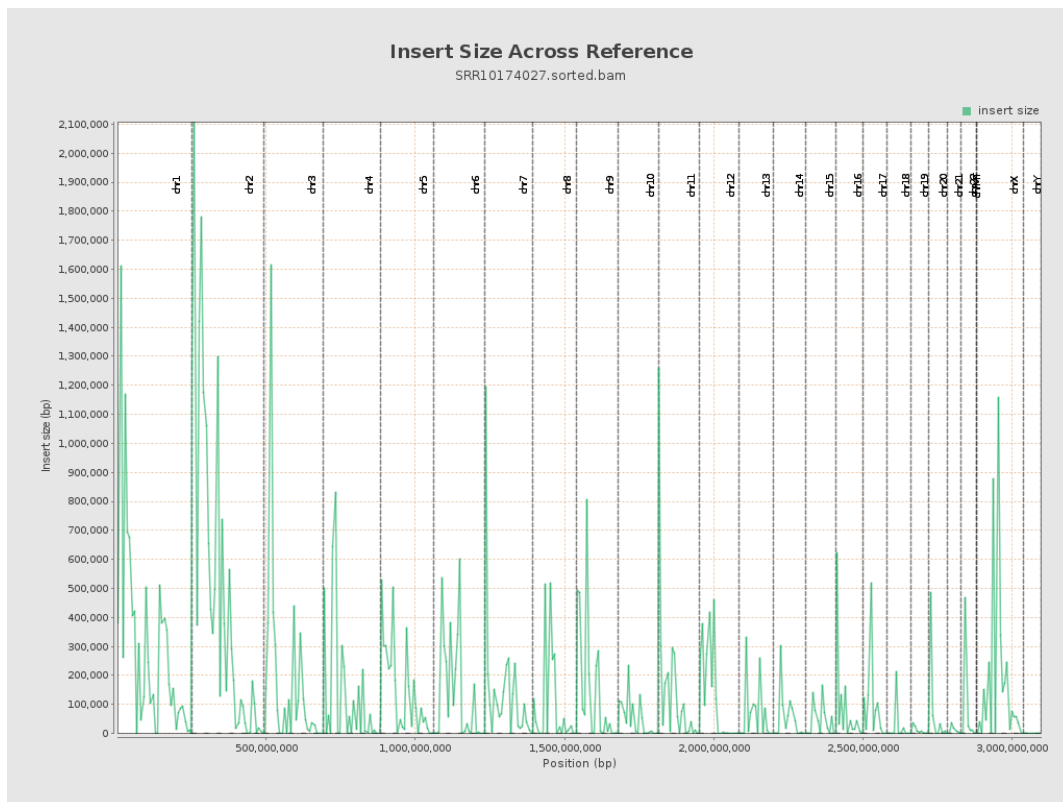
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

