

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 02:51:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174059.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_SRR10174059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174059_1.fastq.gz SRR10174059_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 02:51:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,686,314
Mapped reads	3,577,050 / 97.04%
Unmapped reads	109,264 / 2.96%
Mapped paired reads	3,577,050 / 97.04%
Mapped reads, first in pair	1,794,471 / 48.68%
Mapped reads, second in pair	1,782,579 / 48.36%
Mapped reads, both in pair	3,502,842 / 95.02%
Mapped reads, singletons	74,208 / 2.01%
Secondary alignments	0
Supplementary alignments	369,804 / 10.03%
Read min/max/mean length	30 / 133 / 128.3
Duplicated reads (estimated)	2,804,077 / 76.07%
Duplication rate	64.35%
Clipped reads	1,536,586 / 41.68%

2.2. ACGT Content

Number/percentage of A's	126,047,889 / 30%
Number/percentage of C's	82,740,696 / 19.69%
Number/percentage of T's	125,715,175 / 29.92%
Number/percentage of G's	85,714,641 / 20.4%
Number/percentage of N's	5,433 / 0%

GC Percentage	40.09%
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2.3. Coverage

Mean	0.1358
Standard Deviation	2.155

2.4. Mapping Quality

Mean Mapping Quality	52.54
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2.5. Insert size

Mean	964,593.36
Standard Deviation	9,157,144.13
P25/Median/P75	144 / 201 / 291

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	4,503,314
Insertions	47,288
Mapped reads with at least one insertion	1.27%
Deletions	102,242
Mapped reads with at least one deletion	2.78%
Homopolymer indels	42.23%

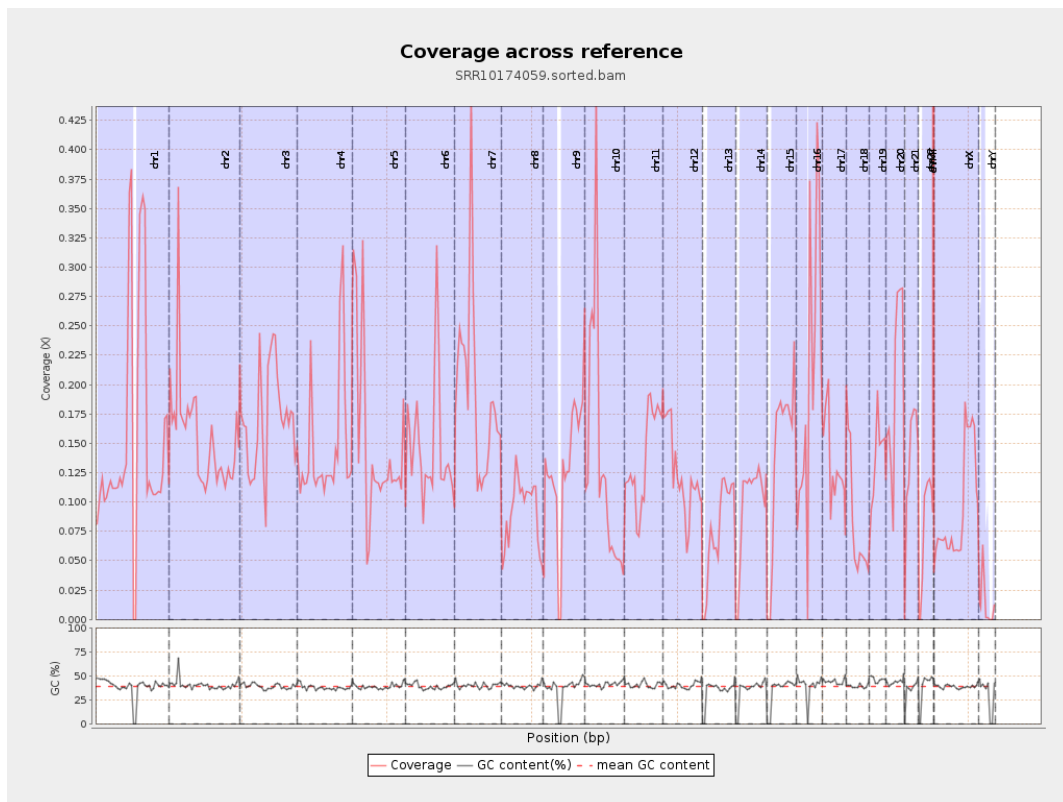
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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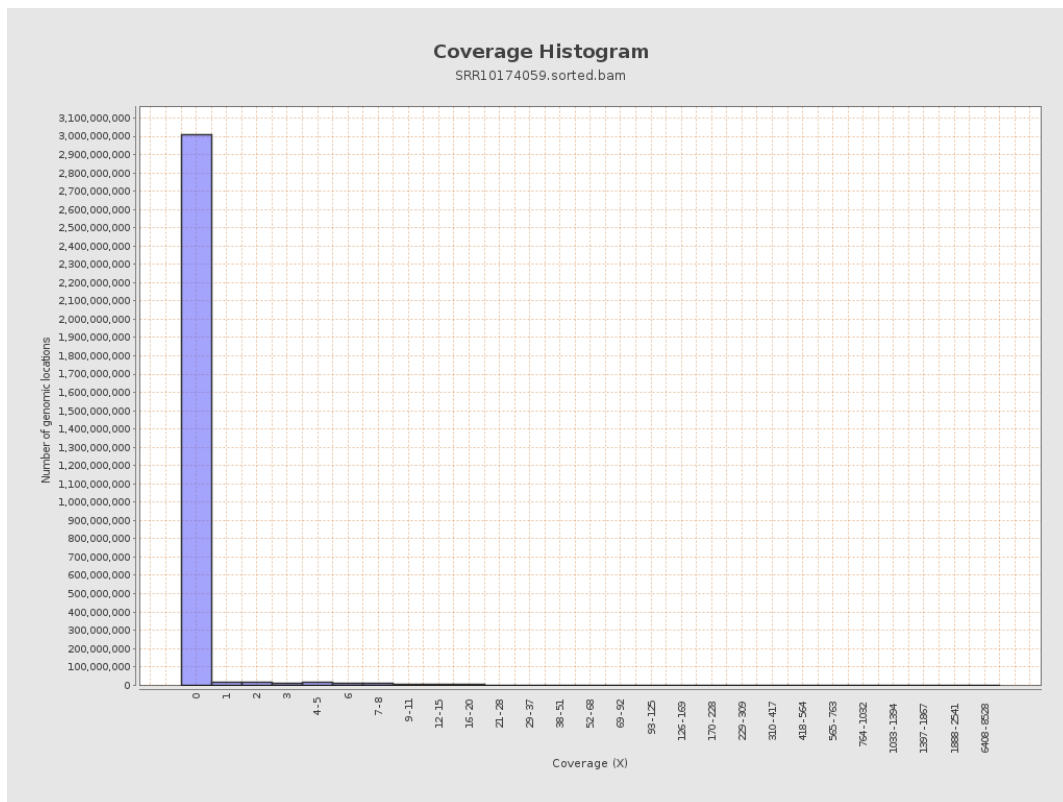
		bases	coverage	deviation
chr1	249250621	37526648	0.1506	1.591
chr2	243199373	37691247	0.155	6.0013
chr3	198022430	33853620	0.171	1.2171
chr4	191154276	27417755	0.1434	1.474
chr5	180915260	27059629	0.1496	1.1373
chr6	171115067	25349017	0.1481	1.1607
chr7	159138663	30657974	0.1926	2.1095
chr8	146364022	13399048	0.0915	1.0486
chr9	141213431	18063935	0.1279	1.1738
chr10	135534747	17974493	0.1326	2.5804
chr11	135006516	18617954	0.1379	1.0972
chr12	133851895	16391080	0.1225	1.019
chr13	115169878	8697881	0.0755	0.8068
chr14	107349540	10374736	0.0966	0.9228
chr15	102531392	14550292	0.1419	1.094
chr16	90354753	18435605	0.204	1.874
chr17	81195210	10549089	0.1299	1.1534
chr18	78077248	6403225	0.082	1.5407
chr19	59128983	8069827	0.1365	1.6474
chr20	63025520	12682833	0.2012	1.3377
chr21	48129895	6491466	0.1349	1.1759
chr22	51304566	3954564	0.0771	0.7664
chrMT	16571	1062338	64.1083	50.8174
chrX	155270560	14440837	0.093	0.8905

chrY	59373566	767317	0.0129	0.7967
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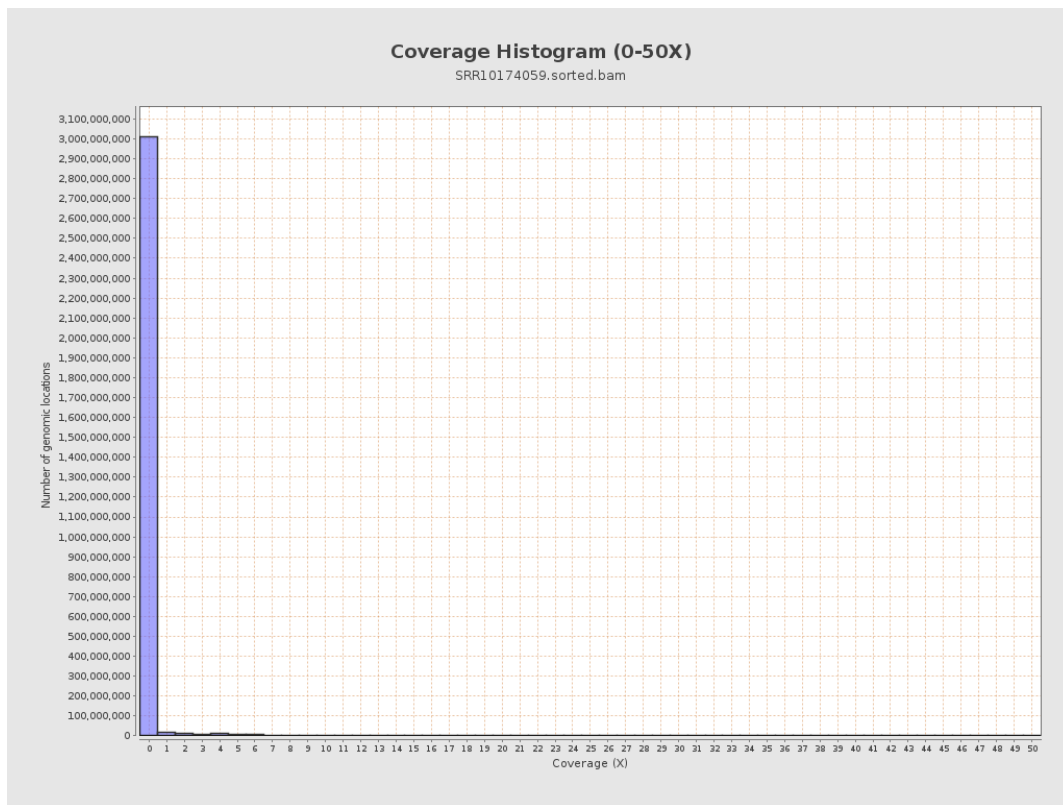
3. Results : Coverage across reference



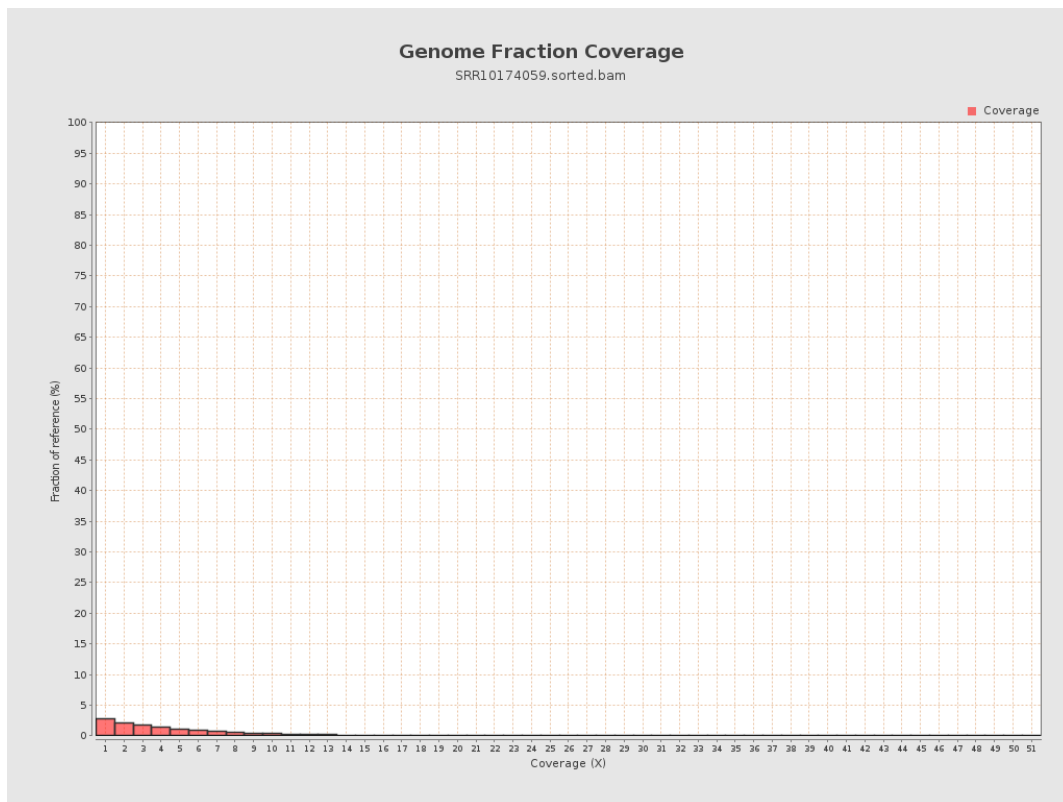
4. Results : Coverage Histogram



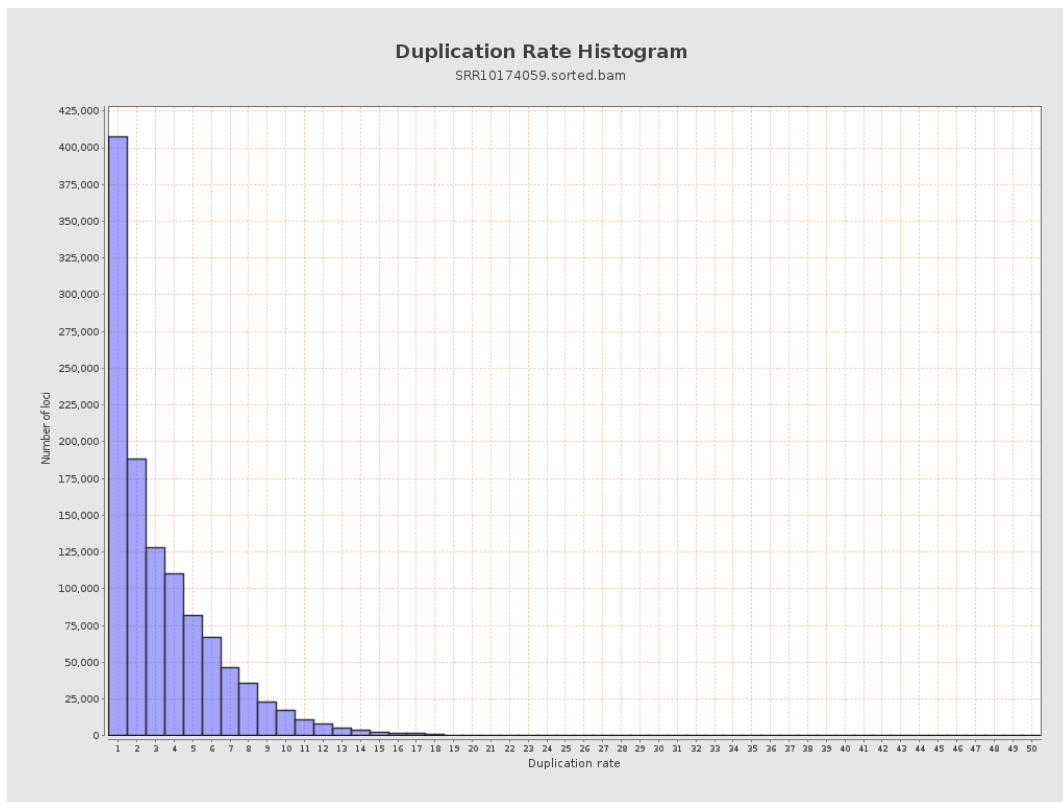
5. Results : Coverage Histogram (0-50X)



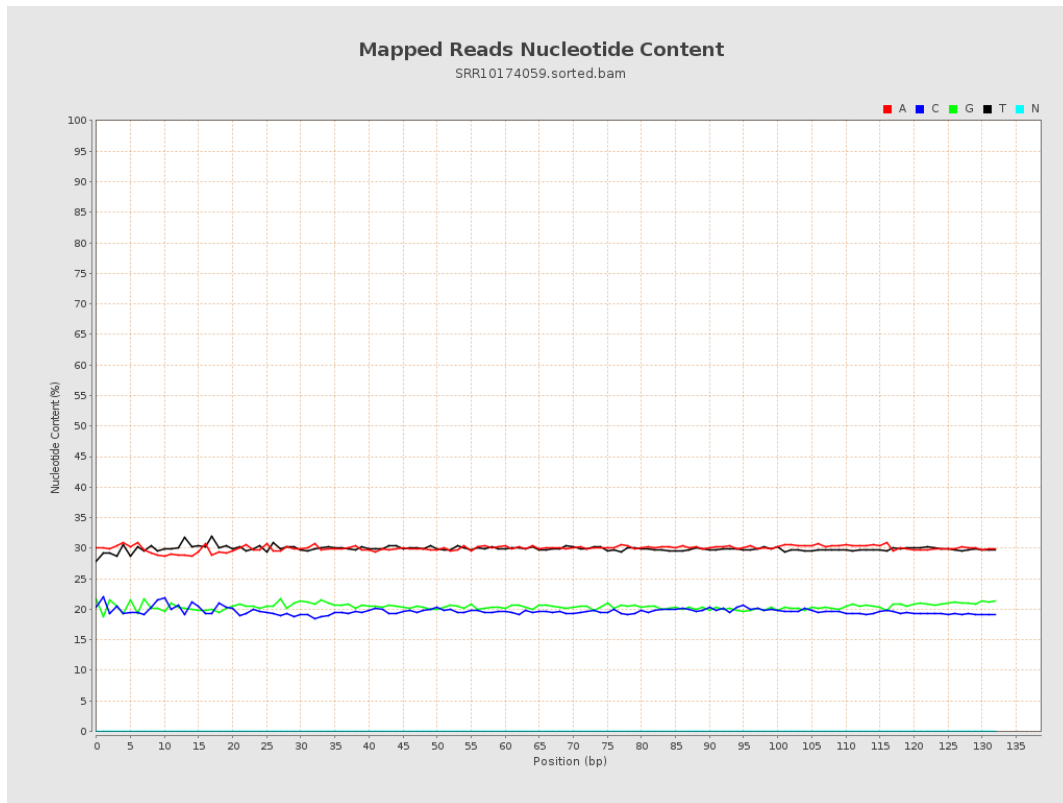
6. Results : Genome Fraction Coverage



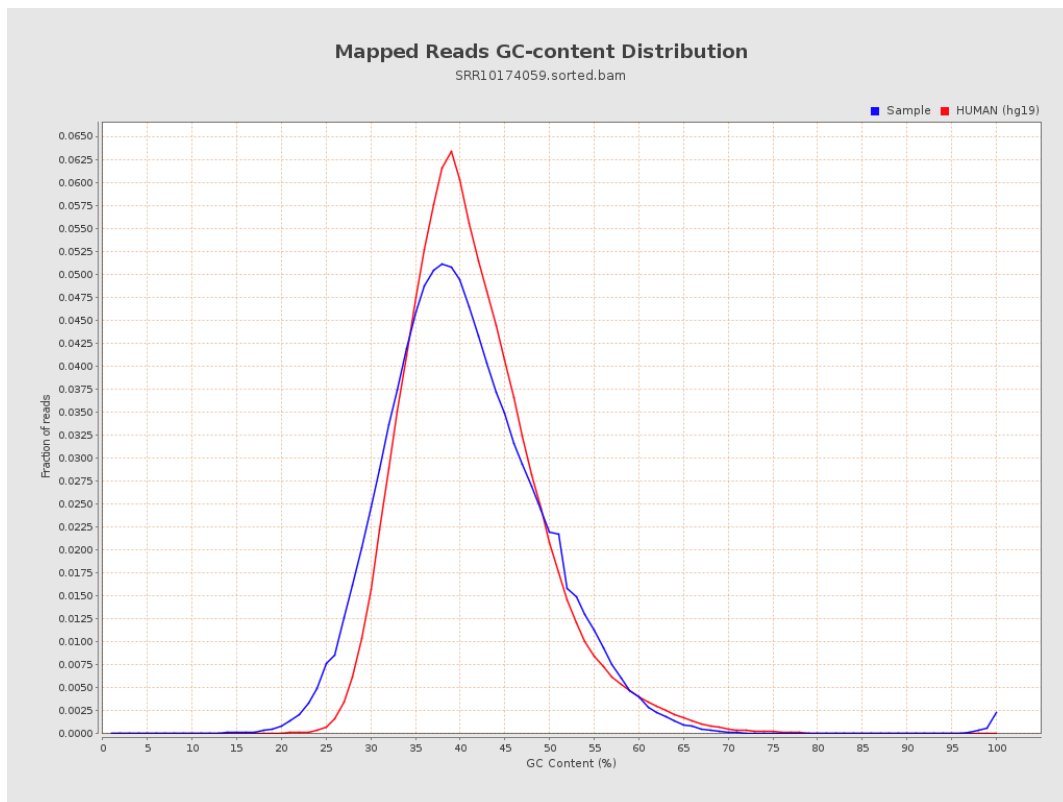
7. Results : Duplication Rate Histogram



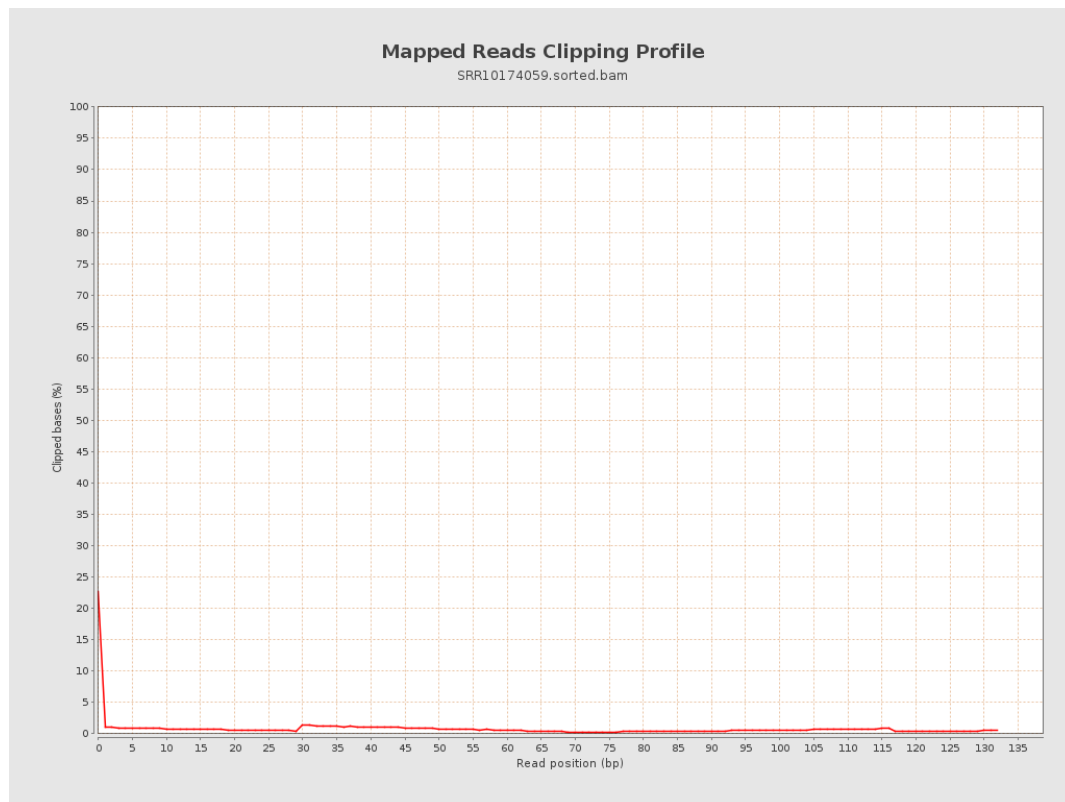
8. Results : Mapped Reads Nucleotide Content



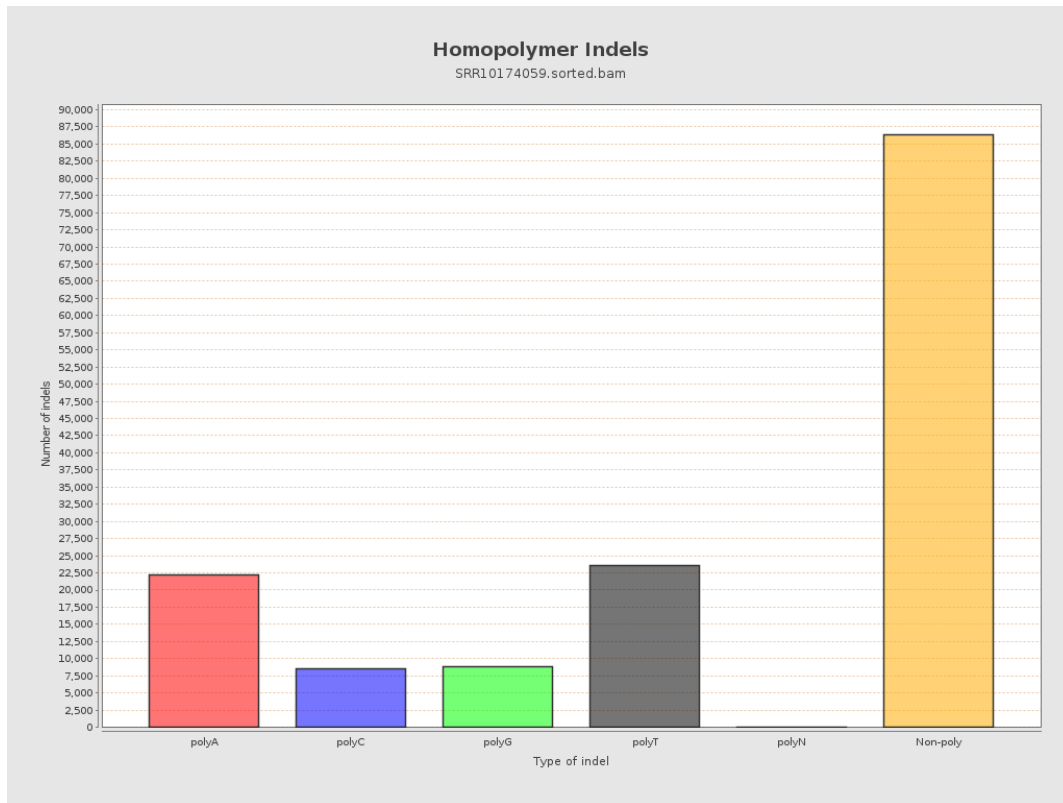
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



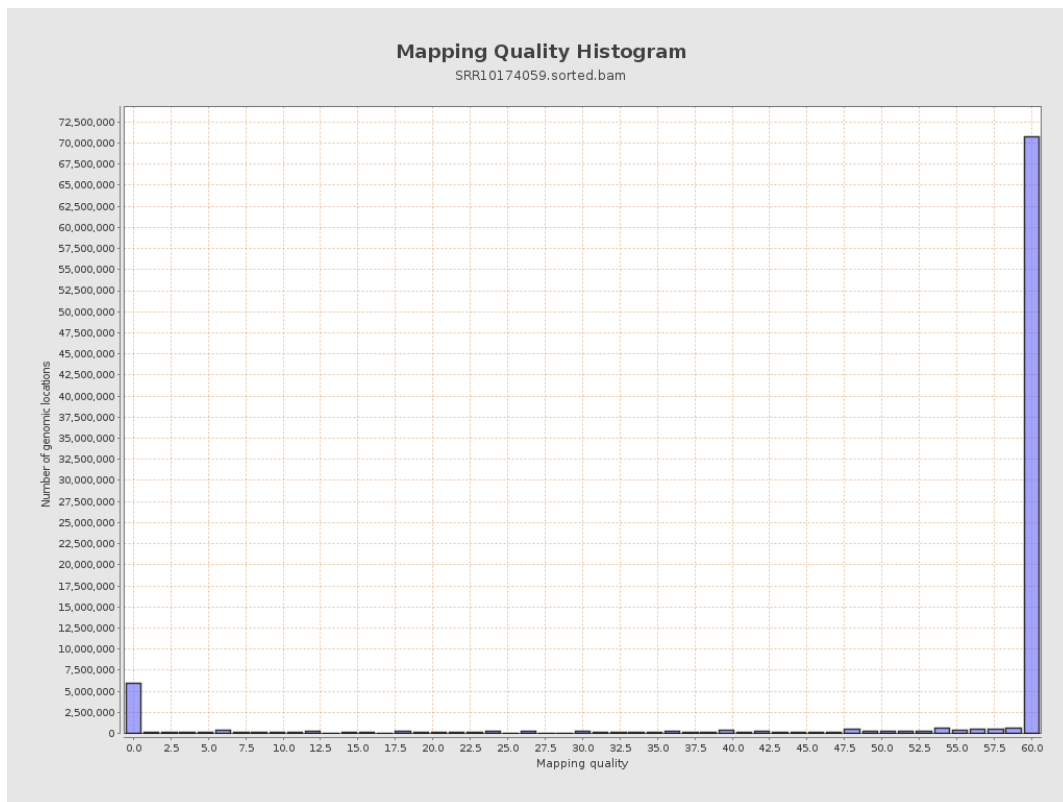
11. Results : Homopolymer Indels



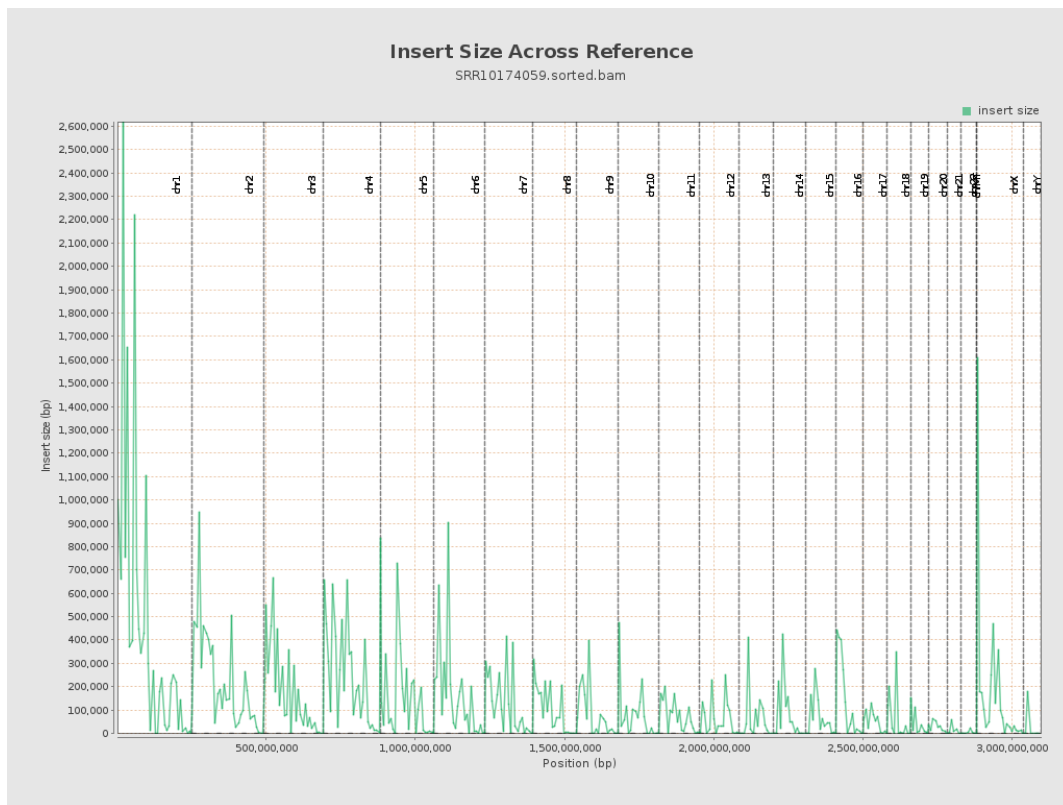
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

