

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 16:16:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173979.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_SRR10173979 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173979_1.fastq.gz SRR10173979_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 16:16:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173979.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,521,090
Mapped reads	3,444,889 / 97.84%
Unmapped reads	76,201 / 2.16%
Mapped paired reads	3,444,889 / 97.84%
Mapped reads, first in pair	1,724,015 / 48.96%
Mapped reads, second in pair	1,720,874 / 48.87%
Mapped reads, both in pair	3,397,622 / 96.49%
Mapped reads, singletons	47,267 / 1.34%
Secondary alignments	0
Supplementary alignments	422,998 / 12.01%
Read min/max/mean length	30 / 133 / 124.66
Duplicated reads (estimated)	2,752,506 / 78.17%
Duplication rate	64.94%
Clipped reads	1,813,342 / 51.5%

2.2. ACGT Content

Number/percentage of A's	115,926,540 / 30%
Number/percentage of C's	76,349,761 / 19.76%
Number/percentage of T's	114,944,820 / 29.75%
Number/percentage of G's	79,157,088 / 20.49%
Number/percentage of N's	3,012 / 0%

GC Percentage	40.25%
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2.3. Coverage

Mean	0.1249
Standard Deviation	2.3095

2.4. Mapping Quality

Mean Mapping Quality	52.65
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2.5. Insert size

Mean	938,824.62
Standard Deviation	9,176,476.37
P25/Median/P75	103 / 151 / 229

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	3,248,180
Insertions	44,168
Mapped reads with at least one insertion	1.23%
Deletions	110,098
Mapped reads with at least one deletion	3.12%
Homopolymer indels	41.45%

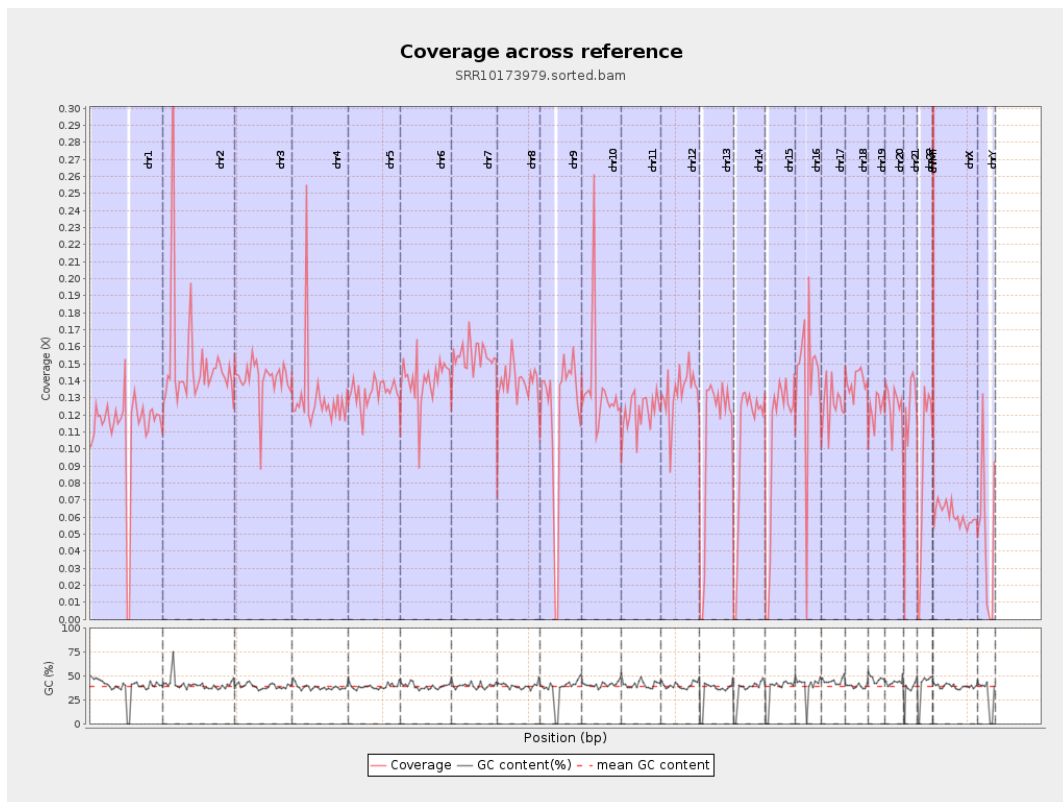
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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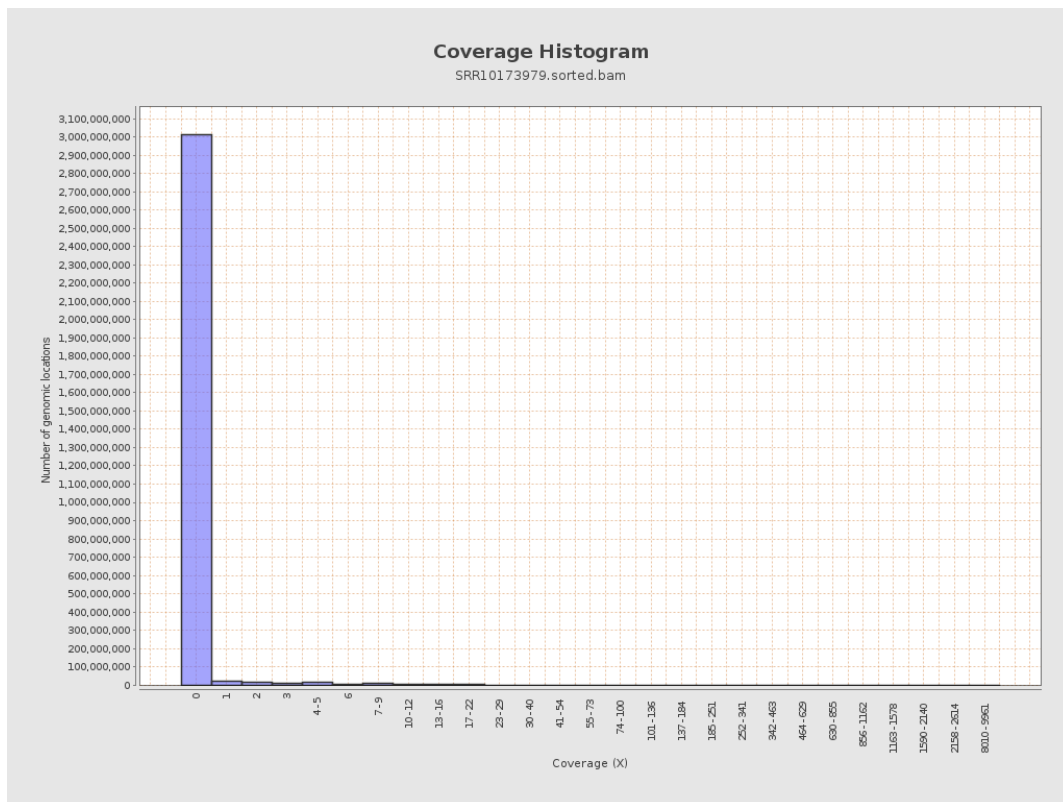
		bases	coverage	deviation
chr1	249250621	27824398	0.1116	1.3403
chr2	243199373	36540035	0.1502	7.0336
chr3	198022430	28033278	0.1416	1.1474
chr4	191154276	24862707	0.1301	1.4255
chr5	180915260	24026884	0.1328	1.1067
chr6	171115067	24017279	0.1404	1.2203
chr7	159138663	24582186	0.1545	1.5462
chr8	146364022	20477468	0.1399	1.6126
chr9	141213431	17242857	0.1221	1.25
chr10	135534747	18204956	0.1343	1.6534
chr11	135006516	16383827	0.1214	1.0804
chr12	133851895	17937117	0.134	1.1363
chr13	115169878	12406061	0.1077	0.9902
chr14	107349540	11418264	0.1064	0.9949
chr15	102531392	10671585	0.1041	0.9785
chr16	90354753	12561198	0.139	1.3247
chr17	81195210	10283155	0.1266	1.124
chr18	78077248	10908867	0.1397	1.4634
chr19	59128983	7288691	0.1233	1.2279
chr20	63025520	7891047	0.1252	1.1382
chr21	48129895	5608271	0.1165	1.3051
chr22	51304566	4591518	0.0895	1.0141
chrMT	16571	418591	25.2605	23.1896
chrX	155270560	9452338	0.0609	0.7454

chrY	59373566	3018904	0.0508	1.0494
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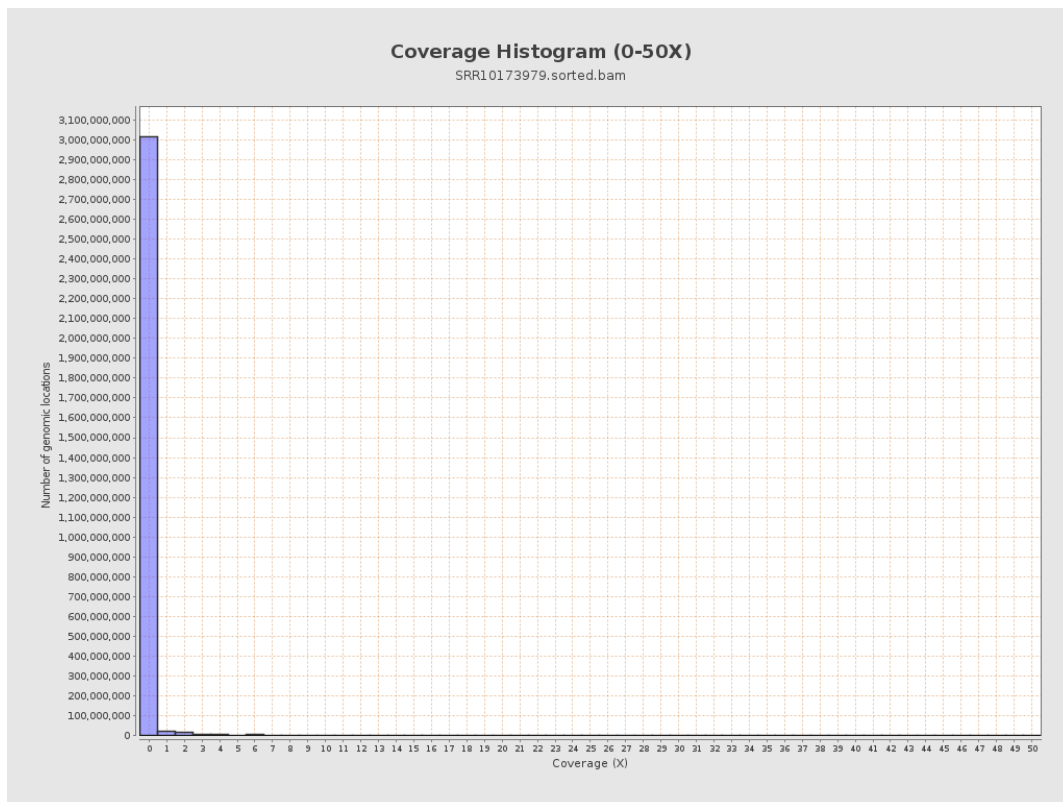
3. Results : Coverage across reference



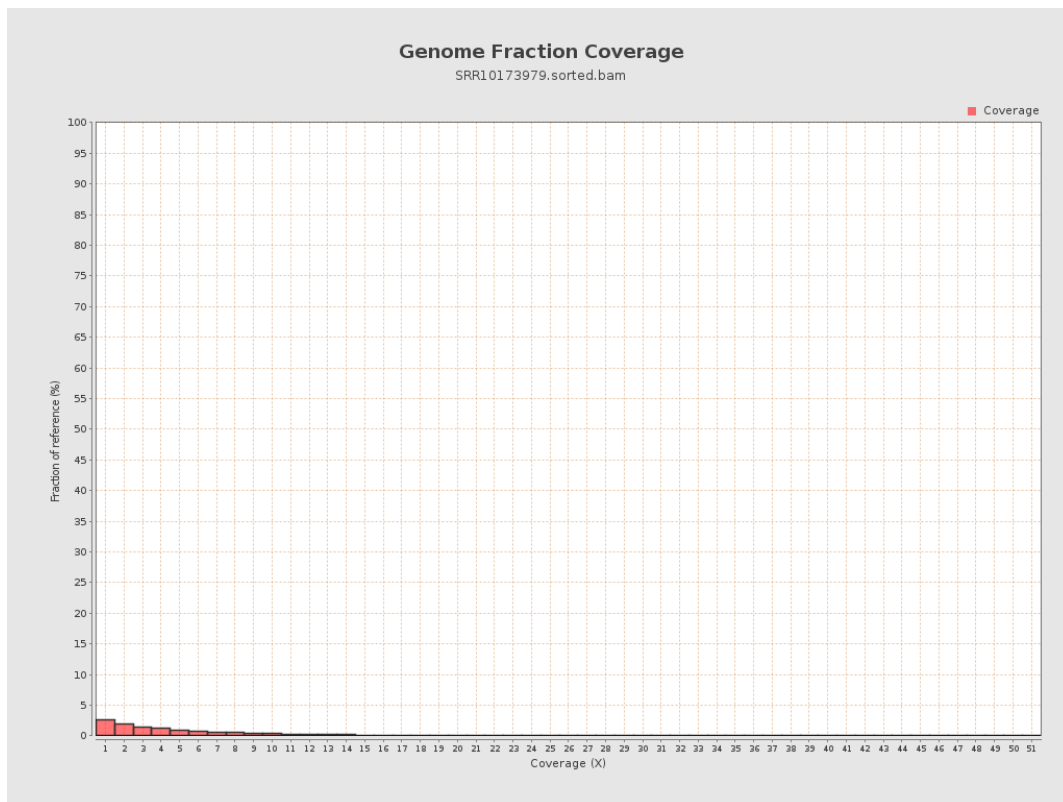
4. Results : Coverage Histogram



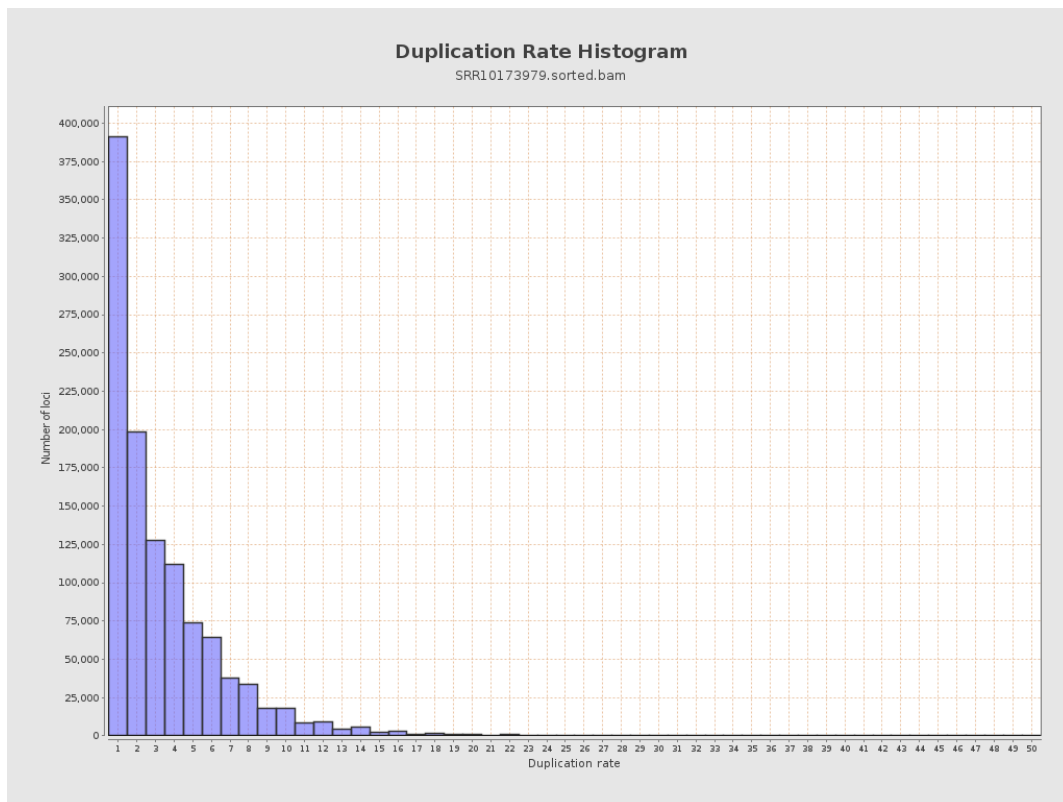
5. Results : Coverage Histogram (0-50X)



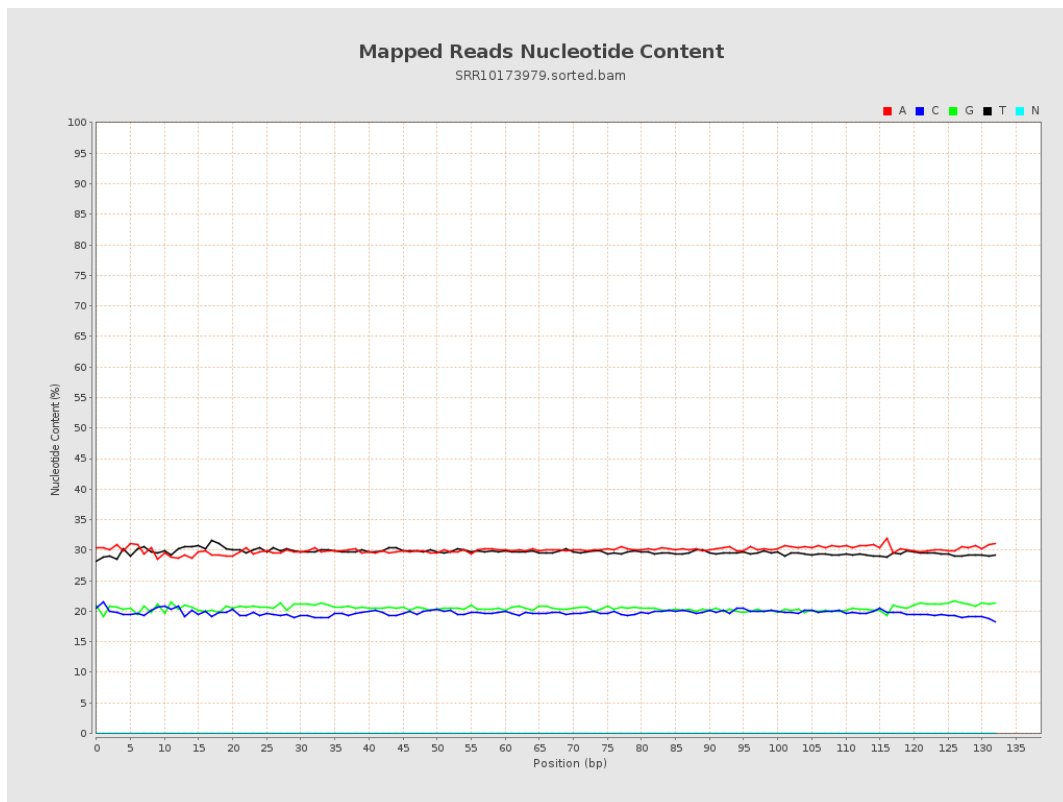
6. Results : Genome Fraction Coverage



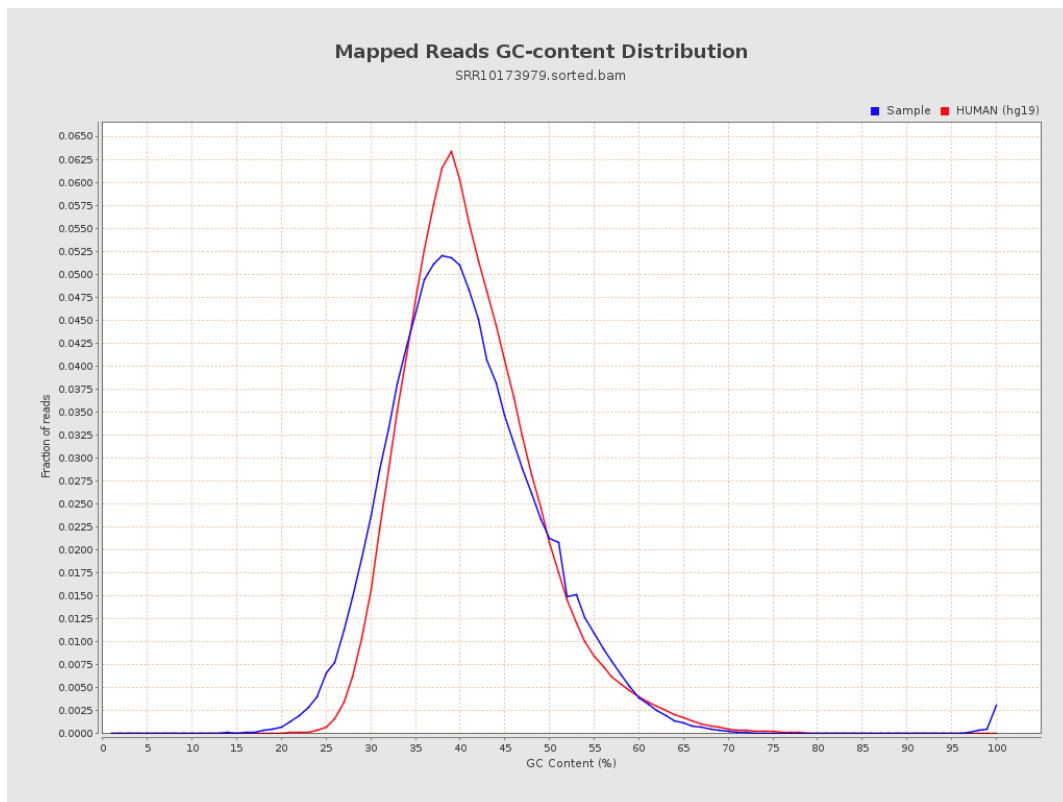
7. Results : Duplication Rate Histogram



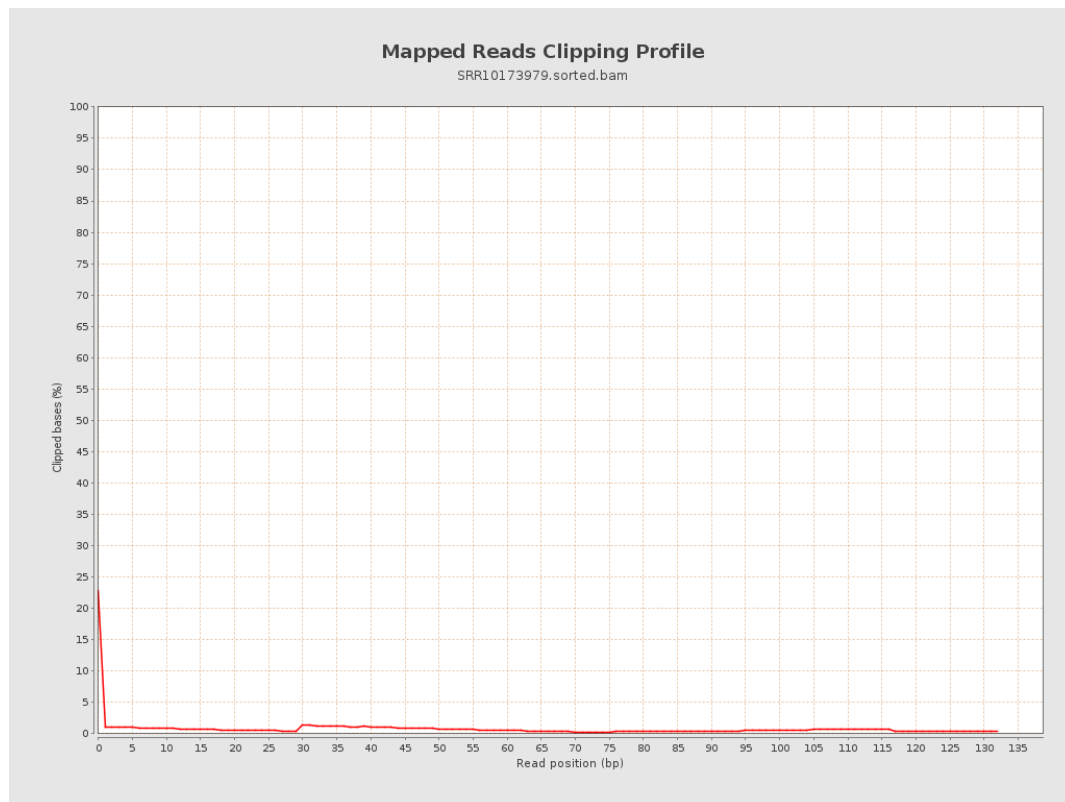
8. Results : Mapped Reads Nucleotide Content



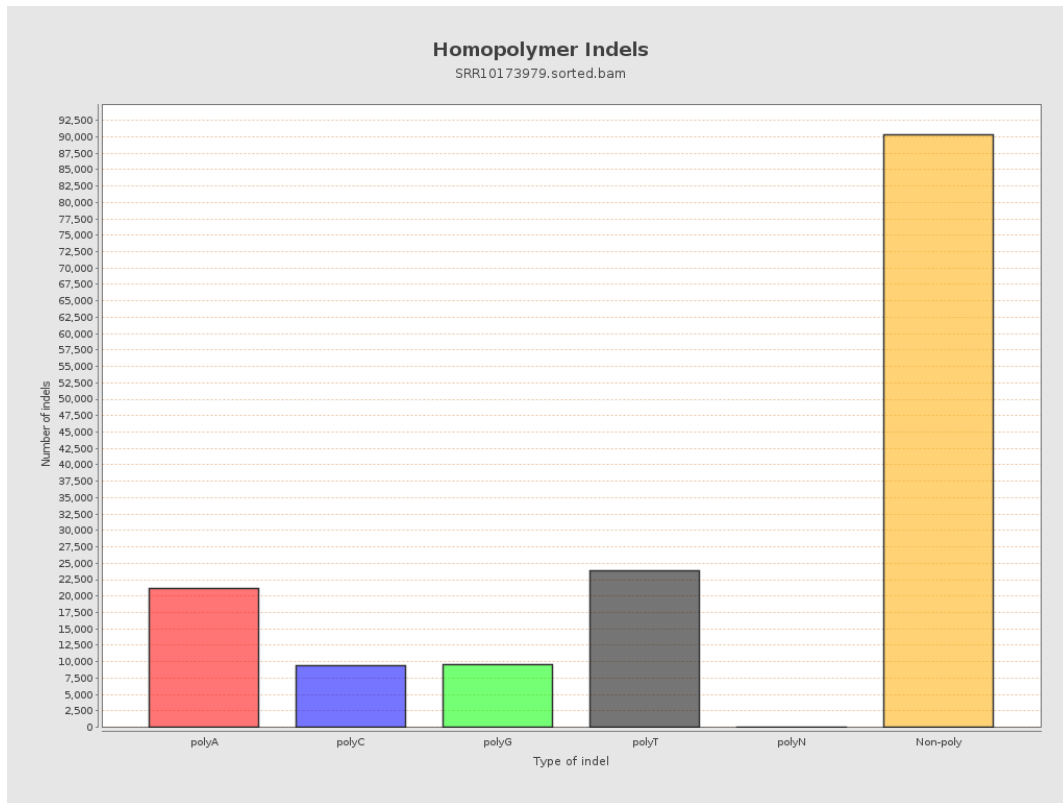
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



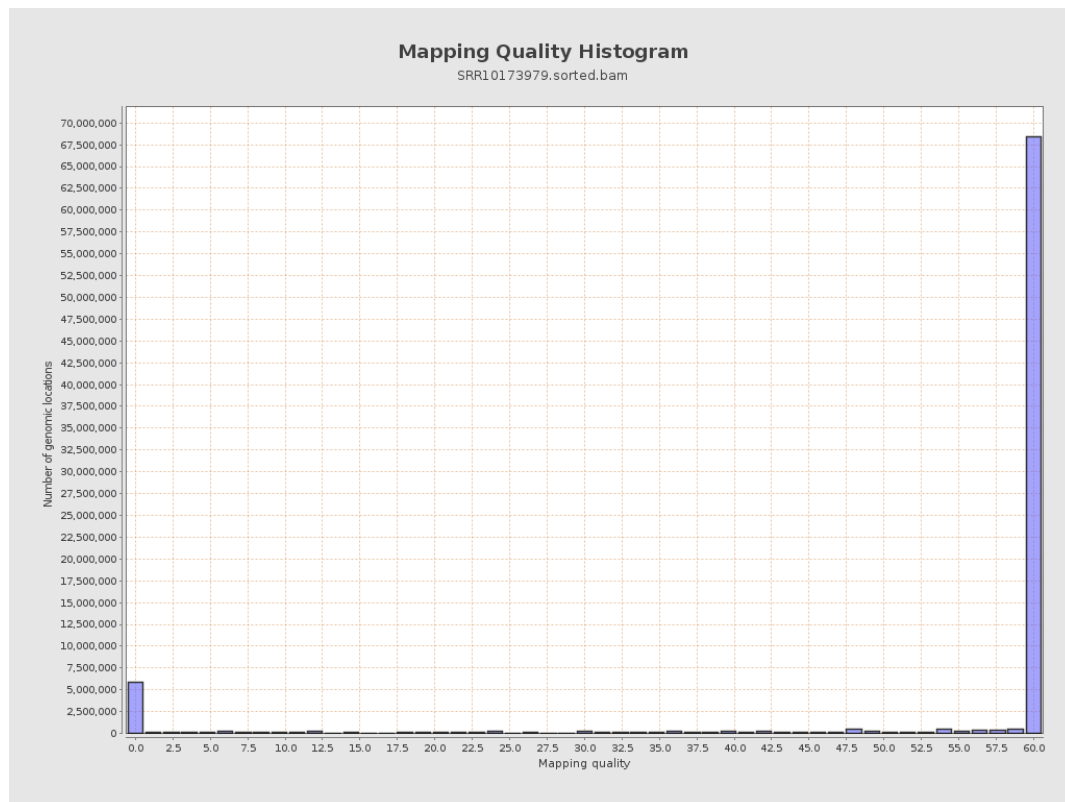
11. Results : Homopolymer Indels



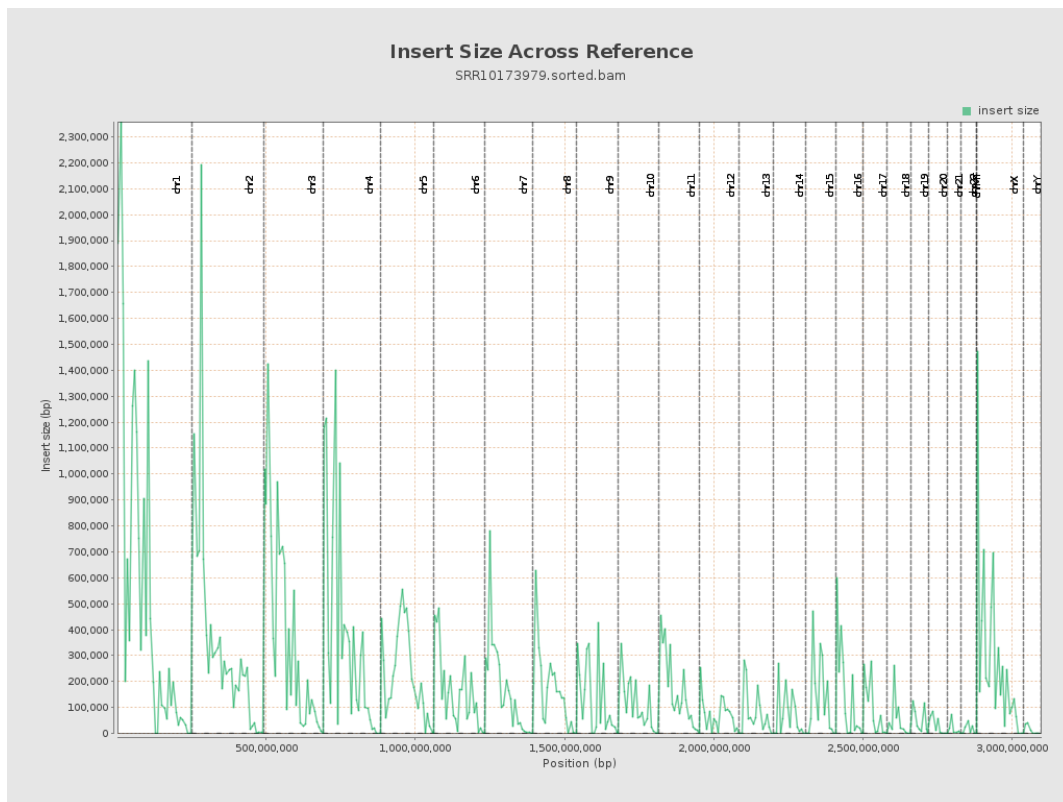
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

