

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 08:41:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173932.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_SRR10173932 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173932_1.fastq.gz SRR10173932_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 08:41:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173932.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,810,592
Mapped reads	3,724,565 / 97.74%
Unmapped reads	86,027 / 2.26%
Mapped paired reads	3,724,565 / 97.74%
Mapped reads, first in pair	1,864,863 / 48.94%
Mapped reads, second in pair	1,859,702 / 48.8%
Mapped reads, both in pair	3,671,486 / 96.35%
Mapped reads, singletons	53,079 / 1.39%
Secondary alignments	0
Supplementary alignments	472,294 / 12.39%
Read min/max/mean length	30 / 133 / 125.06
Duplicated reads (estimated)	2,926,926 / 76.81%
Duplication rate	63.82%
Clipped reads	1,833,787 / 48.12%

2.2. ACGT Content

Number/percentage of A's	126,487,433 / 29.97%
Number/percentage of C's	83,508,744 / 19.78%
Number/percentage of T's	125,293,382 / 29.68%
Number/percentage of G's	86,818,960 / 20.57%
Number/percentage of N's	3,459 / 0%

GC Percentage	40.35%
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2.3. Coverage

Mean	0.1364
Standard Deviation	2.6539

2.4. Mapping Quality

Mean Mapping Quality	52.63
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2.5. Insert size

Mean	1,322,463.28
Standard Deviation	10,692,641.46
P25/Median/P75	105 / 154 / 235

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	3,669,370
Insertions	45,664
Mapped reads with at least one insertion	1.18%
Deletions	123,618
Mapped reads with at least one deletion	3.24%
Homopolymer indels	40.71%

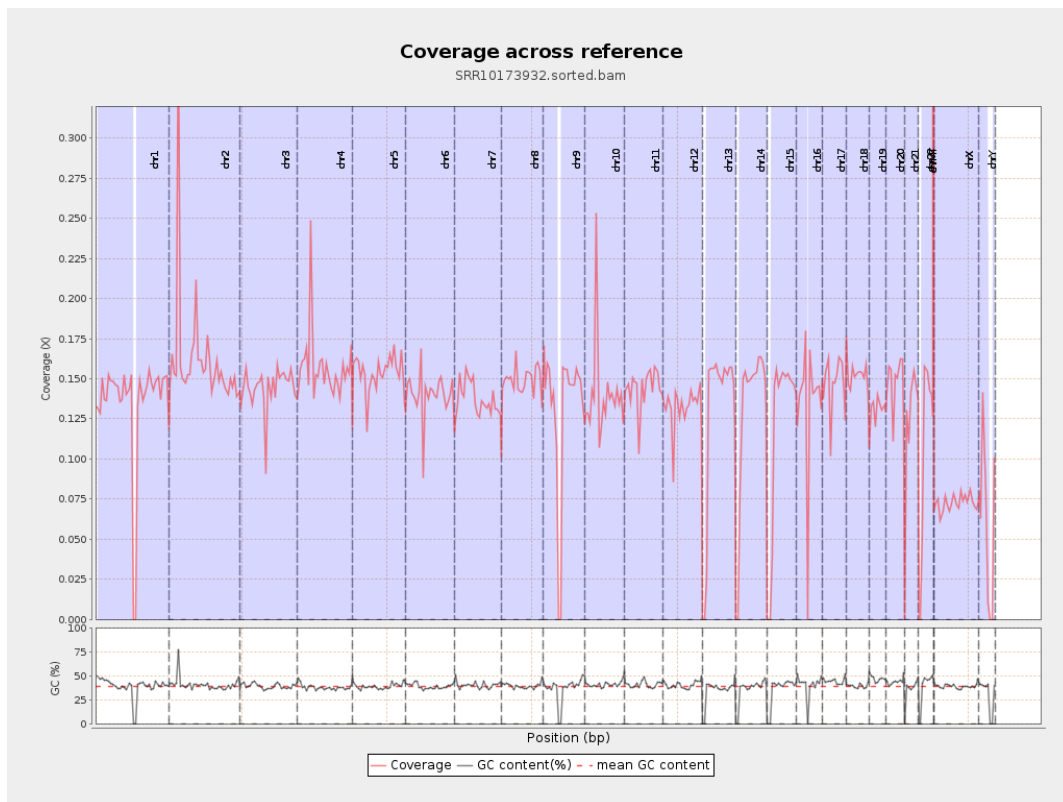
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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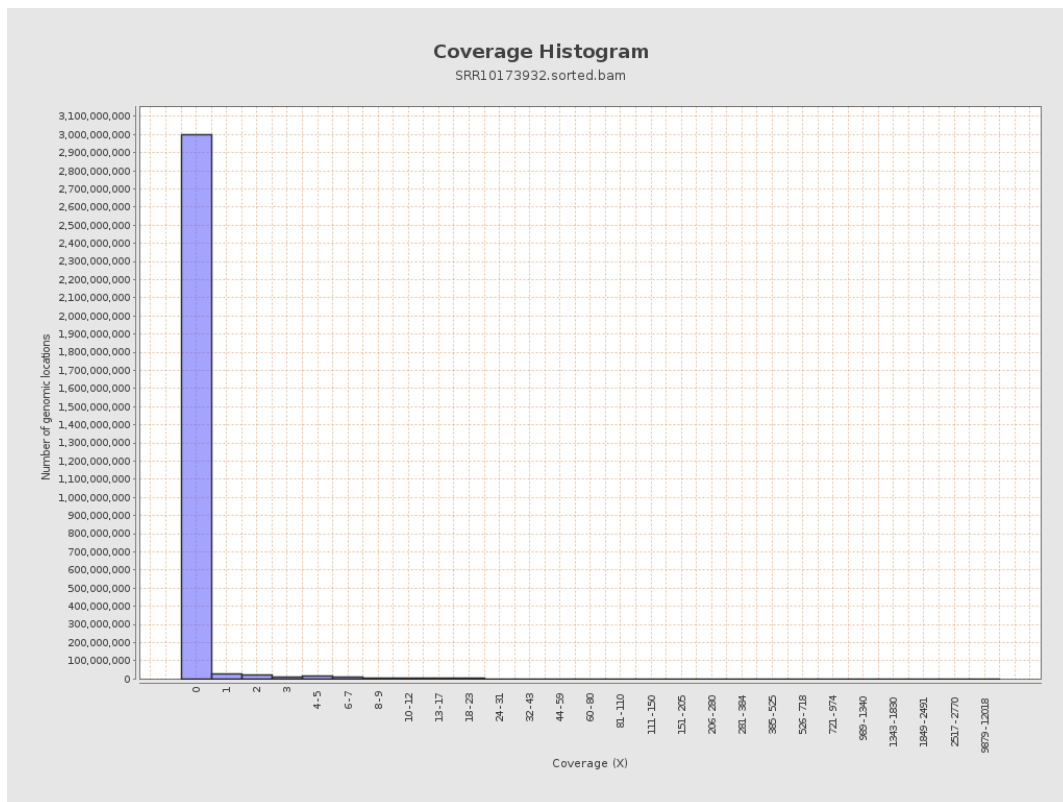
		bases	coverage	deviation
chr1	249250621	33707965	0.1352	1.2938
chr2	243199373	39607704	0.1629	8.4631
chr3	198022430	28610409	0.1445	1.1256
chr4	191154276	29979475	0.1568	1.4143
chr5	180915260	27883263	0.1541	1.1773
chr6	171115067	23938288	0.1399	1.2225
chr7	159138663	21922064	0.1378	1.2793
chr8	146364022	21835969	0.1492	1.5958
chr9	141213431	18428577	0.1305	1.3266
chr10	135534747	18923137	0.1396	1.5524
chr11	135006516	19483301	0.1443	1.1318
chr12	133851895	17712607	0.1323	1.1033
chr13	115169878	14746461	0.128	1.065
chr14	107349540	13885387	0.1293	1.0739
chr15	102531392	12324221	0.1202	1.0388
chr16	90354753	12139459	0.1344	1.1999
chr17	81195210	11833273	0.1457	1.1855
chr18	78077248	11913497	0.1526	1.6363
chr19	59128983	7764166	0.1313	1.1285
chr20	63025520	9352969	0.1484	1.1651
chr21	48129895	5959424	0.1238	1.2174
chr22	51304566	5282363	0.103	1.0103
chrMT	16571	444784	26.8411	25.7182
chrX	155270560	11272521	0.0726	0.792

chrY	59373566	3451842	0.0581	0.9904
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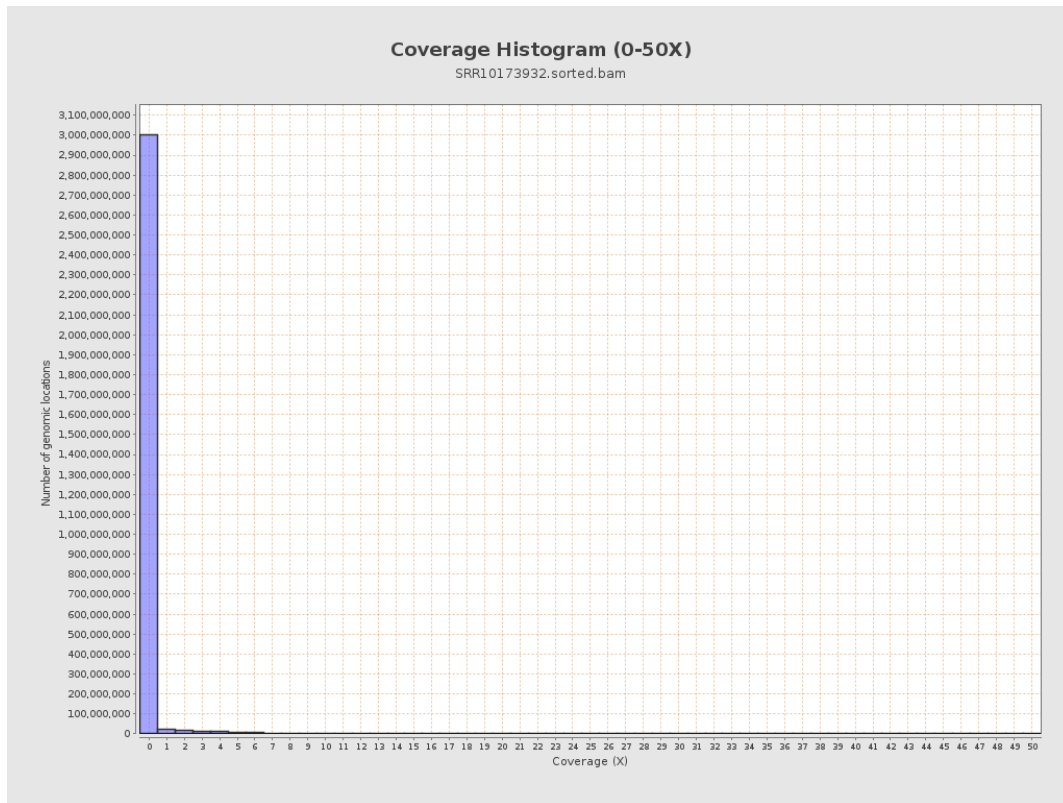
3. Results : Coverage across reference



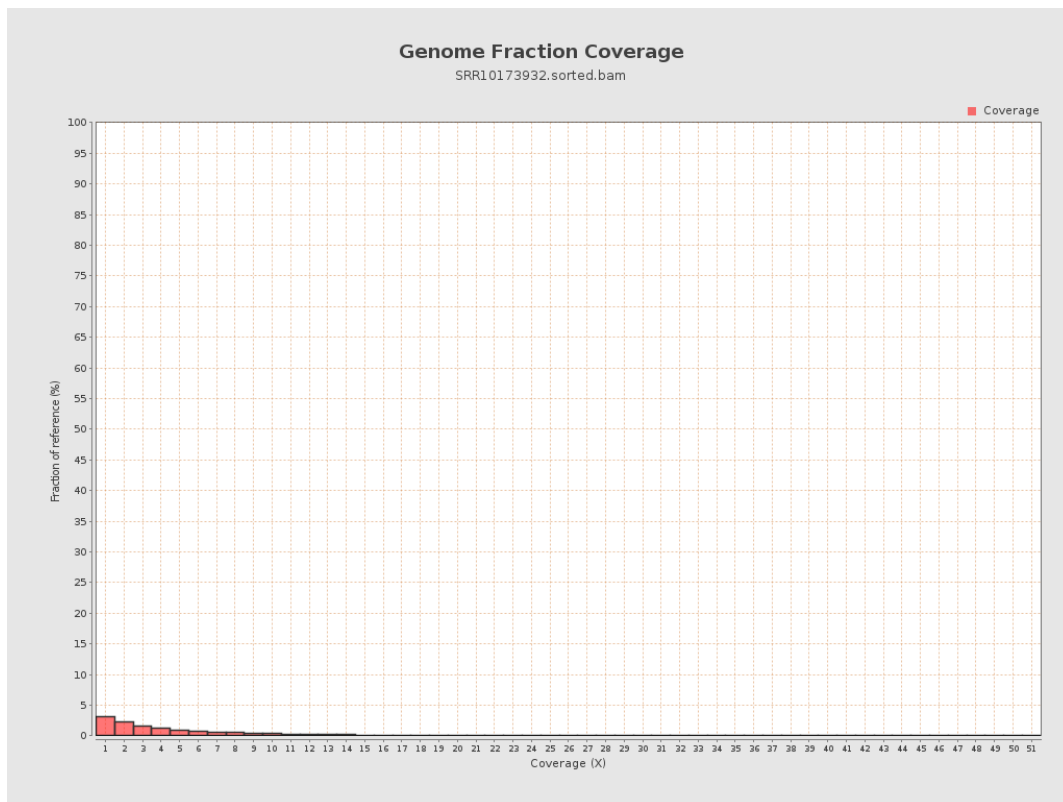
4. Results : Coverage Histogram



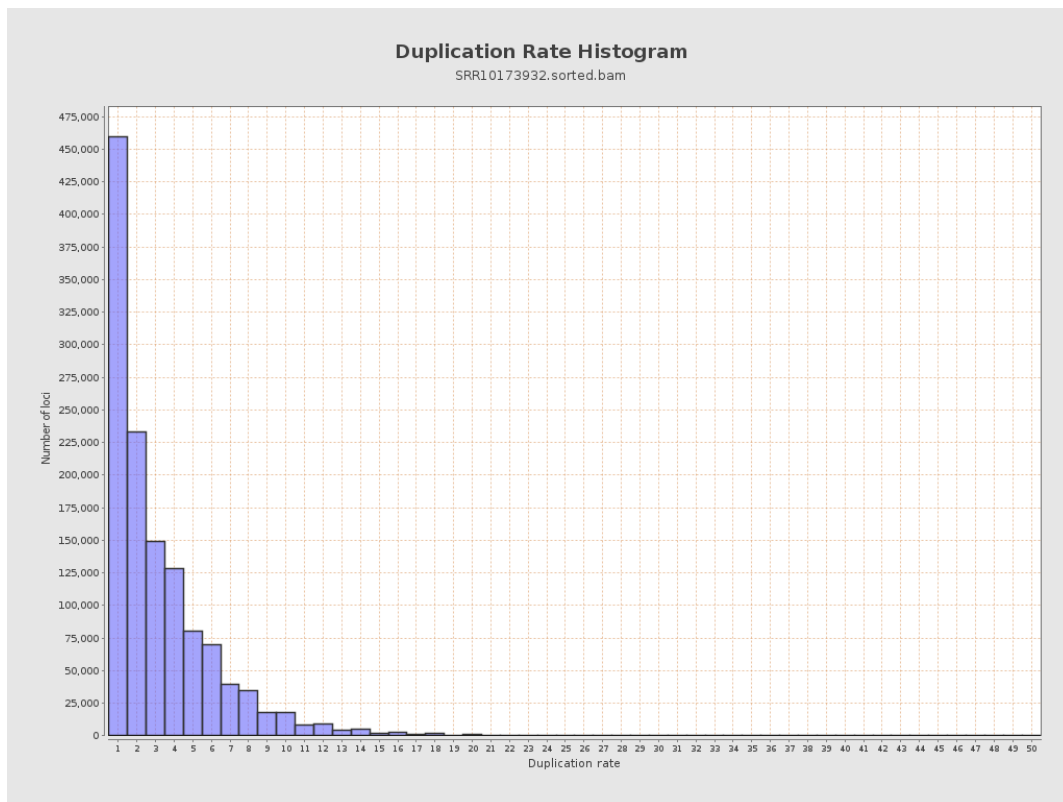
5. Results : Coverage Histogram (0-50X)



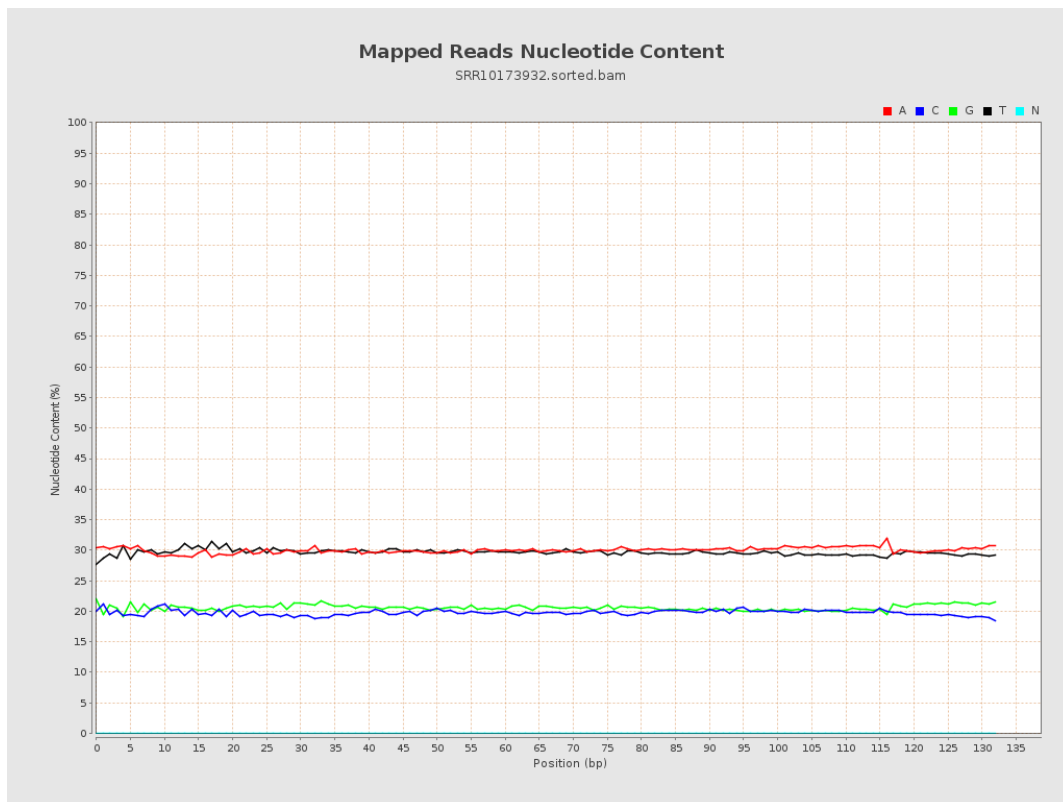
6. Results : Genome Fraction Coverage



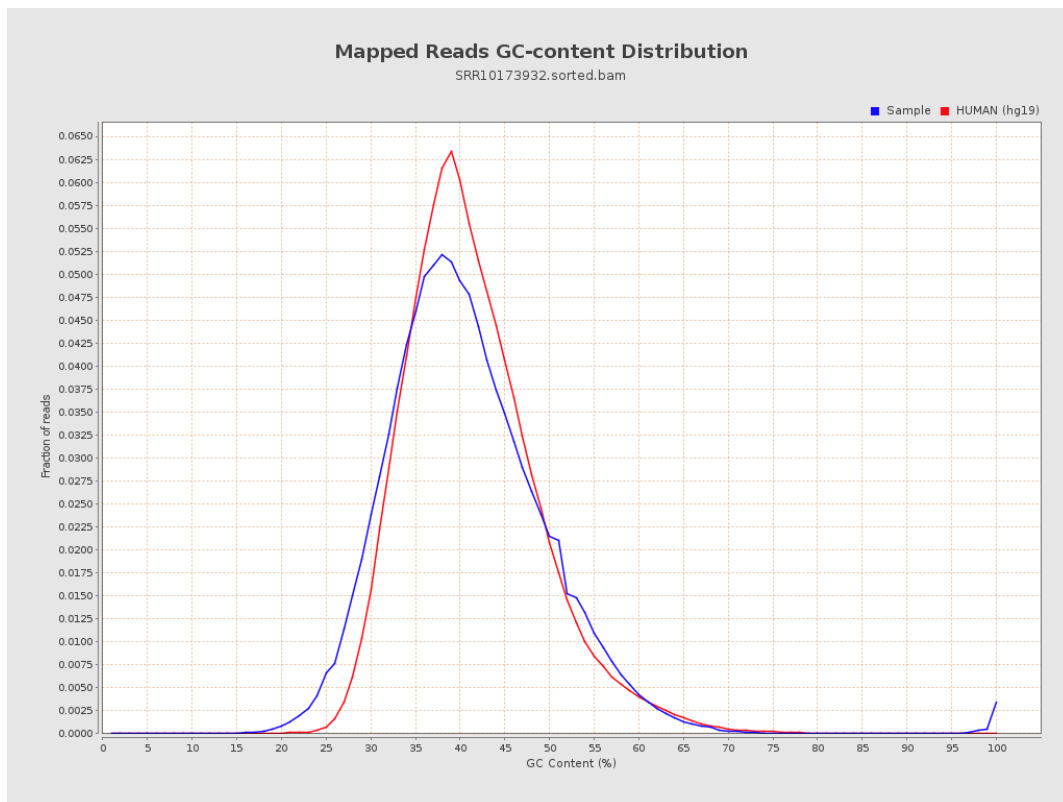
7. Results : Duplication Rate Histogram



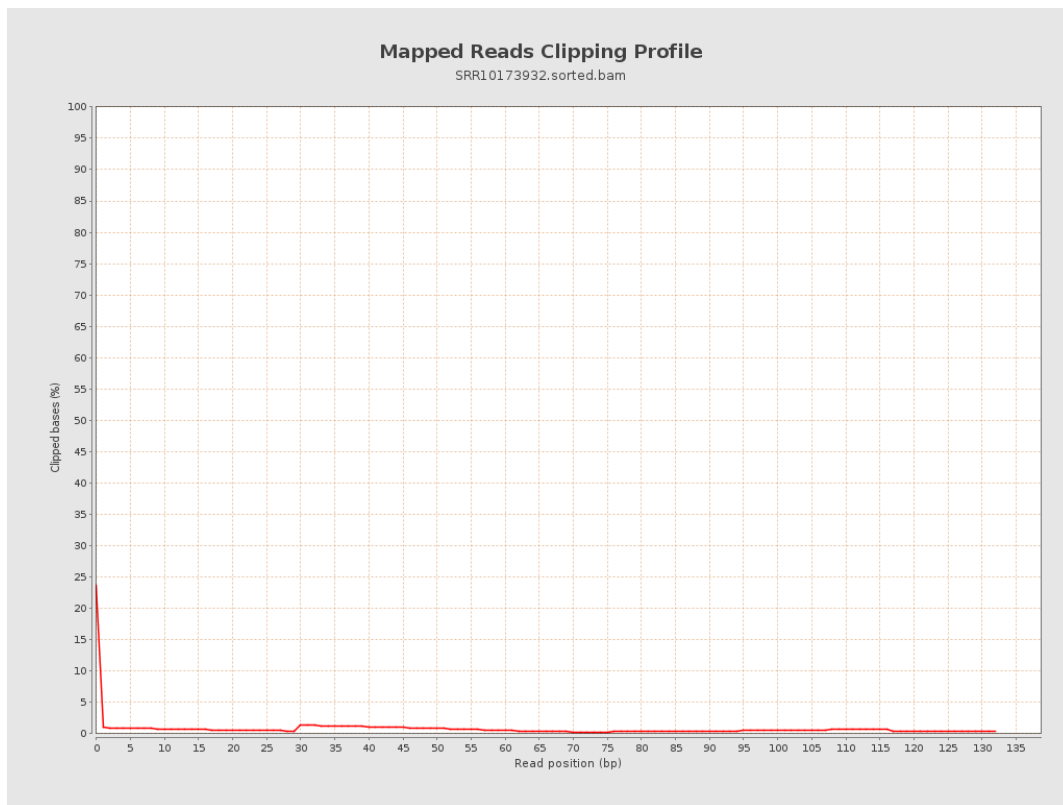
8. Results : Mapped Reads Nucleotide Content



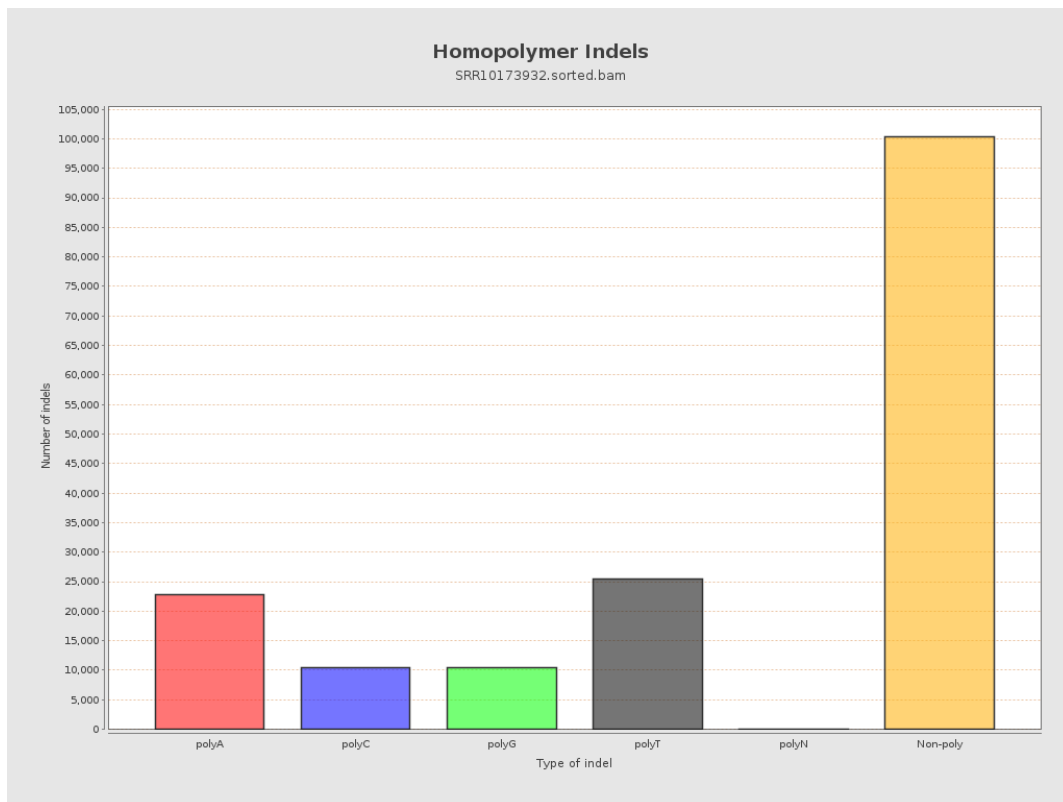
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



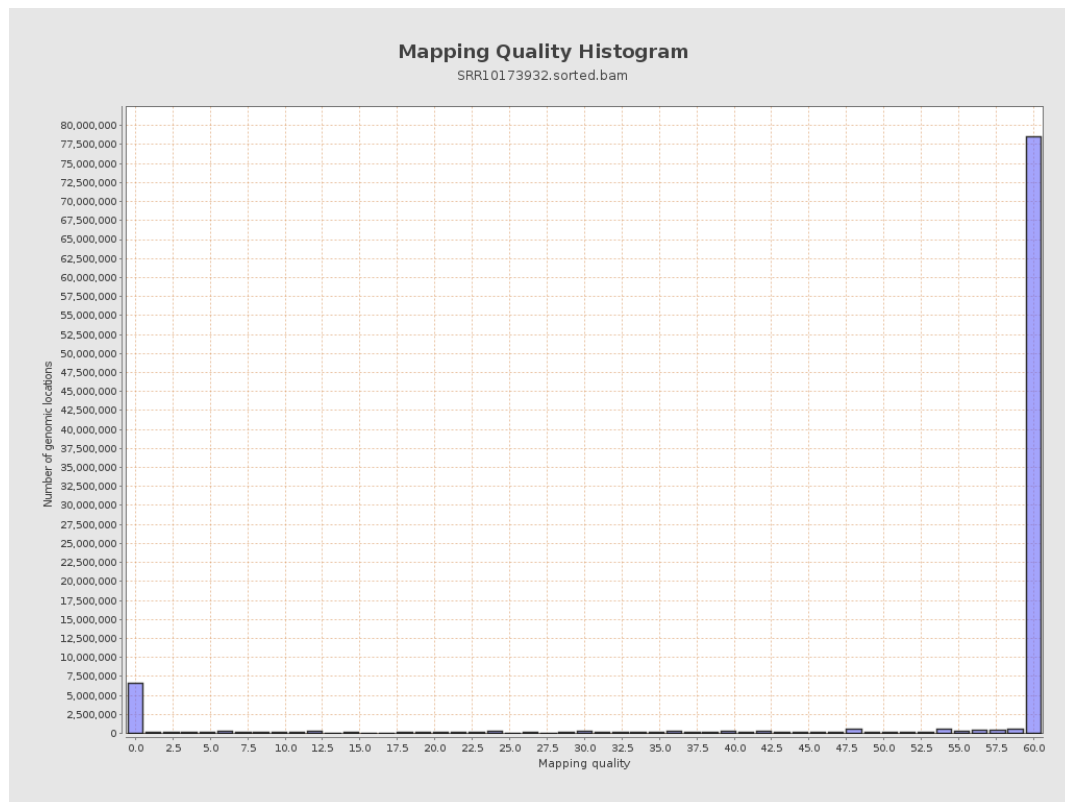
11. Results : Homopolymer Indels



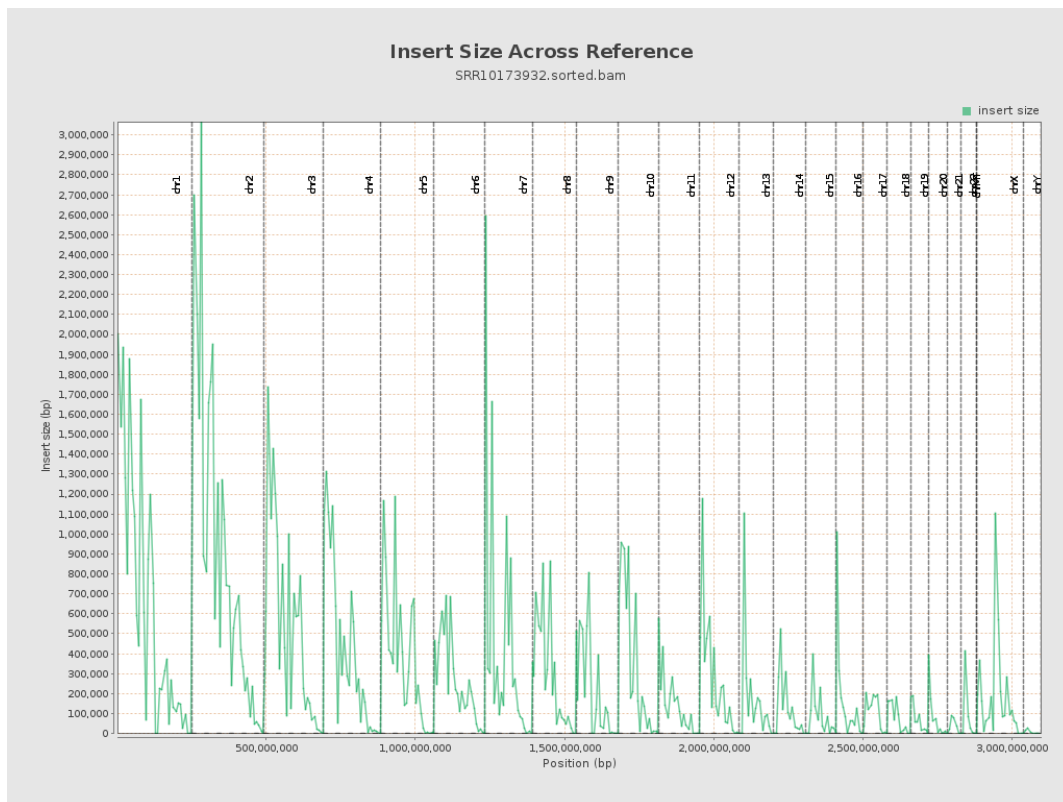
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

