

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 10:27:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173945.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_SRR10173945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173945_1.fastq.gz SRR10173945_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 10:27:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,330,950
Mapped reads	4,234,768 / 97.78%
Unmapped reads	96,182 / 2.22%
Mapped paired reads	4,234,768 / 97.78%
Mapped reads, first in pair	2,118,345 / 48.91%
Mapped reads, second in pair	2,116,423 / 48.87%
Mapped reads, both in pair	4,173,562 / 96.37%
Mapped reads, singletons	61,206 / 1.41%
Secondary alignments	0
Supplementary alignments	512,022 / 11.82%
Read min/max/mean length	30 / 133 / 124.99
Duplicated reads (estimated)	3,441,044 / 79.45%
Duplication rate	66.18%
Clipped reads	1,987,735 / 45.9%

2.2. ACGT Content

Number/percentage of A's	143,604,083 / 29.81%
Number/percentage of C's	95,930,056 / 19.92%
Number/percentage of T's	142,258,796 / 29.53%
Number/percentage of G's	99,865,529 / 20.73%
Number/percentage of N's	3,618 / 0%

GC Percentage	40.65%
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2.3. Coverage

Mean	0.1557
Standard Deviation	3.0288

2.4. Mapping Quality

Mean Mapping Quality	52.66
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2.5. Insert size

Mean	1,073,893.16
Standard Deviation	9,723,228.49
P25/Median/P75	107 / 158 / 242

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	4,037,727
Insertions	52,407
Mapped reads with at least one insertion	1.19%
Deletions	124,290
Mapped reads with at least one deletion	2.86%
Homopolymer indels	41.43%

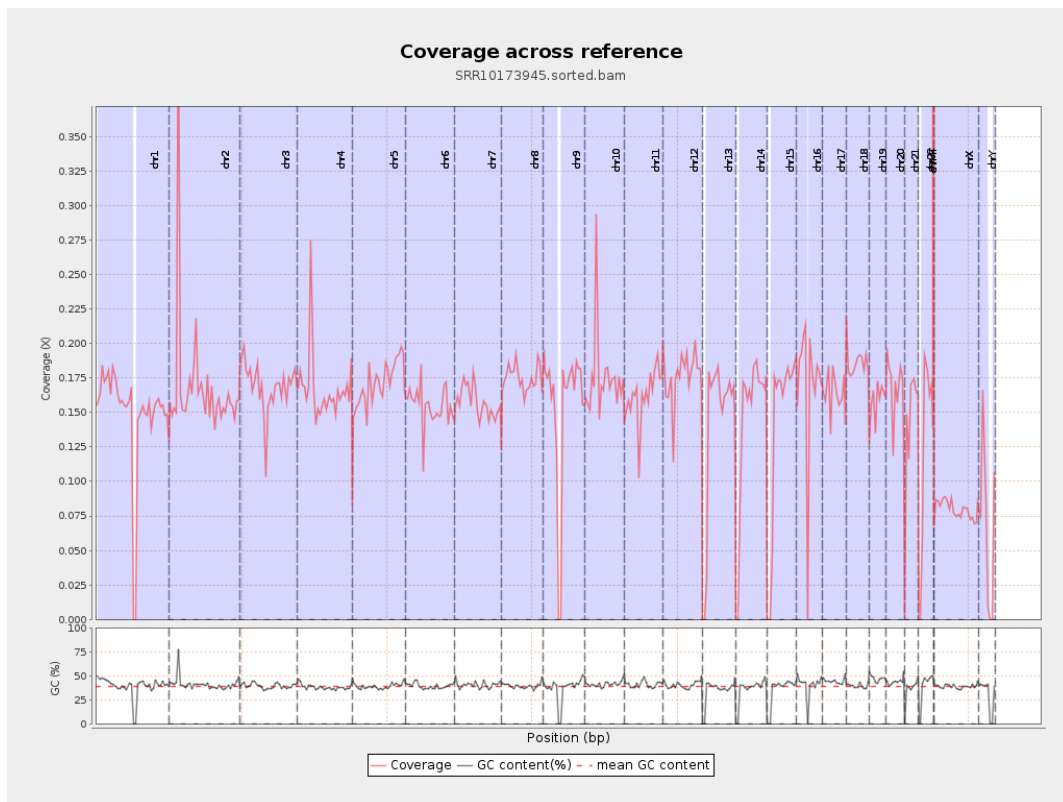
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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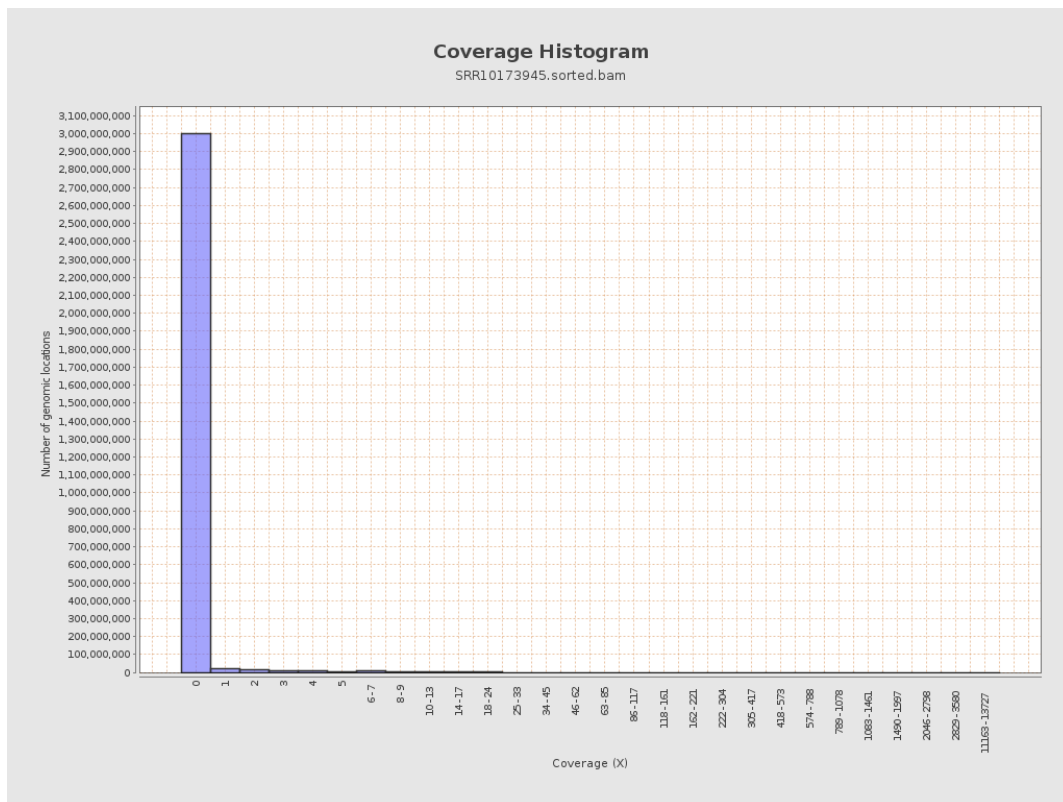
		bases	coverage	deviation
chr1	249250621	37206204	0.1493	1.4235
chr2	243199373	41131780	0.1691	9.6527
chr3	198022430	33462969	0.169	1.291
chr4	191154276	31833578	0.1665	1.5253
chr5	180915260	31011887	0.1714	1.2985
chr6	171115067	26475243	0.1547	1.3205
chr7	159138663	25090829	0.1577	1.4592
chr8	146364022	25633390	0.1751	1.8339
chr9	141213431	21533626	0.1525	1.5235
chr10	135534747	23664502	0.1746	1.8341
chr11	135006516	21948698	0.1626	1.2846
chr12	133851895	23602012	0.1763	1.352
chr13	115169878	16162087	0.1403	1.1742
chr14	107349540	15334191	0.1428	1.1908
chr15	102531392	14455280	0.141	1.1737
chr16	90354753	15346677	0.1698	1.4628
chr17	81195210	13344100	0.1643	1.3366
chr18	78077248	14524054	0.186	1.8621
chr19	59128983	9389225	0.1588	1.3768
chr20	63025520	10580513	0.1679	1.2954
chr21	48129895	6802044	0.1413	1.4383
chr22	51304566	6182887	0.1205	1.3351
chrMT	16571	1087654	65.636	55.1064
chrX	155270560	12329242	0.0794	0.867

chrY	59373566	3821210	0.0644	1.0321
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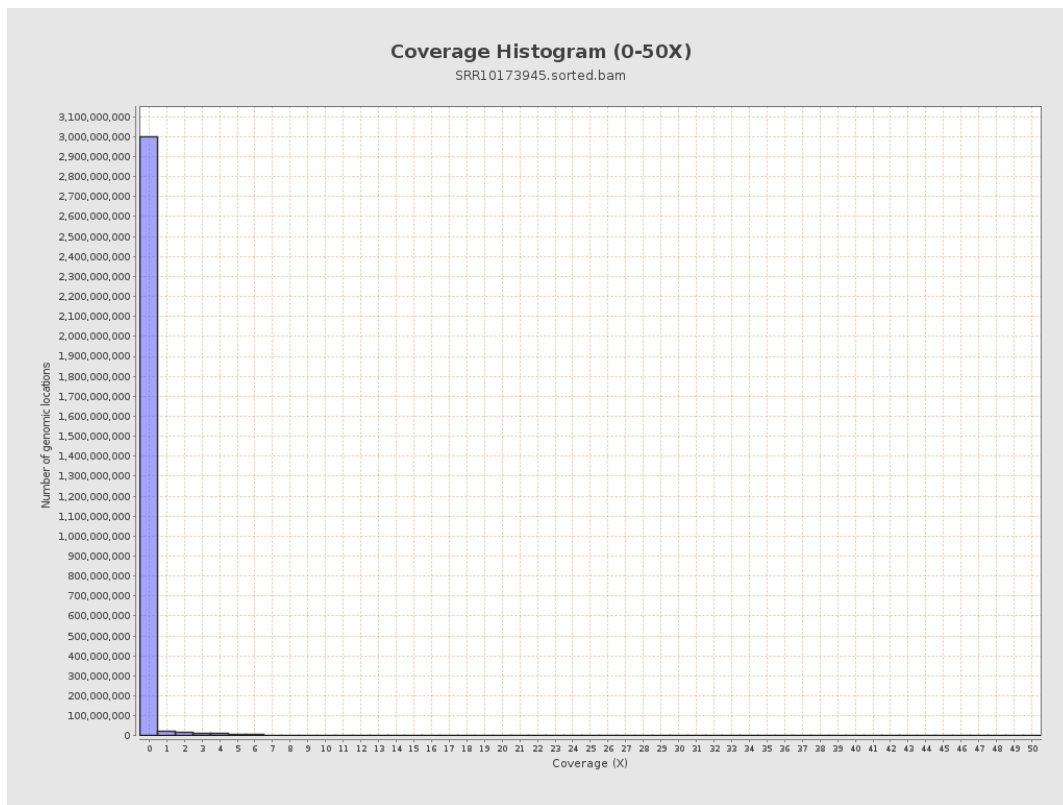
3. Results : Coverage across reference



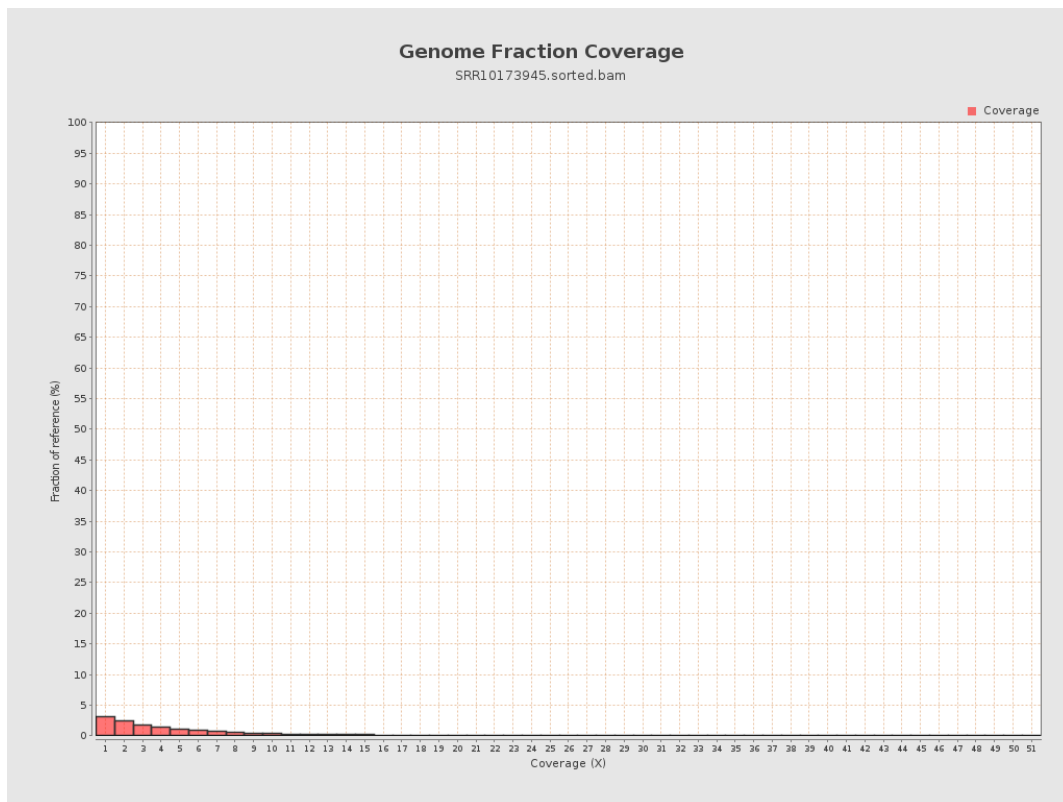
4. Results : Coverage Histogram



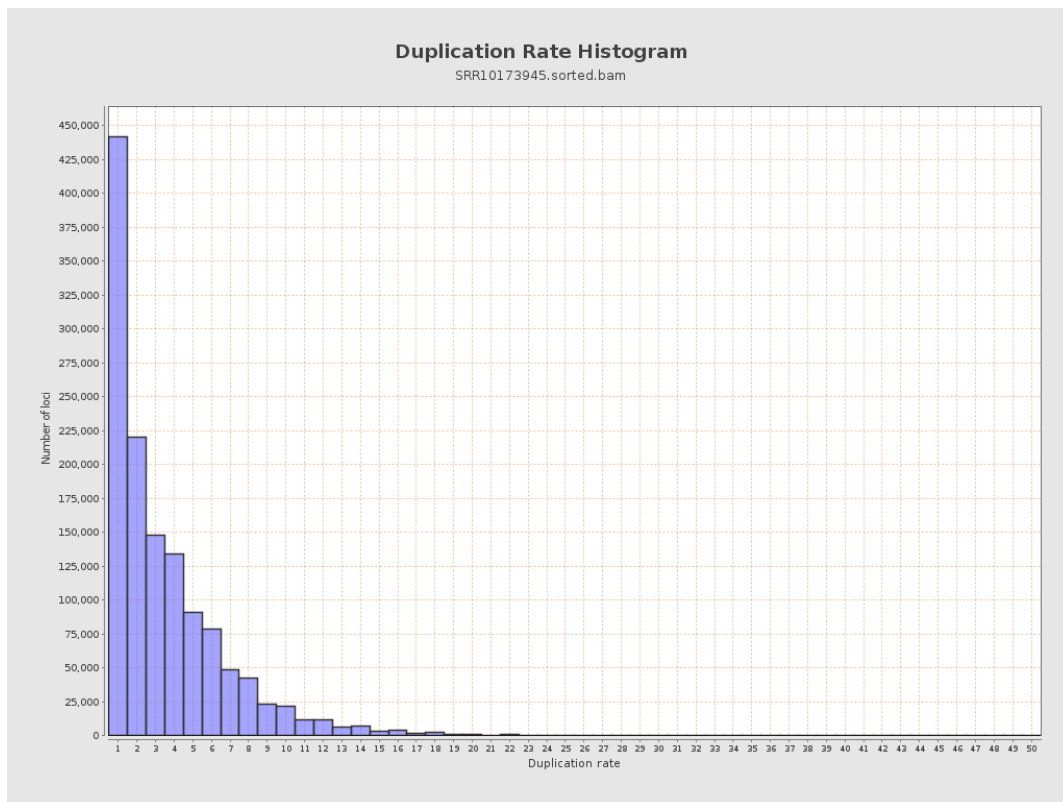
5. Results : Coverage Histogram (0-50X)



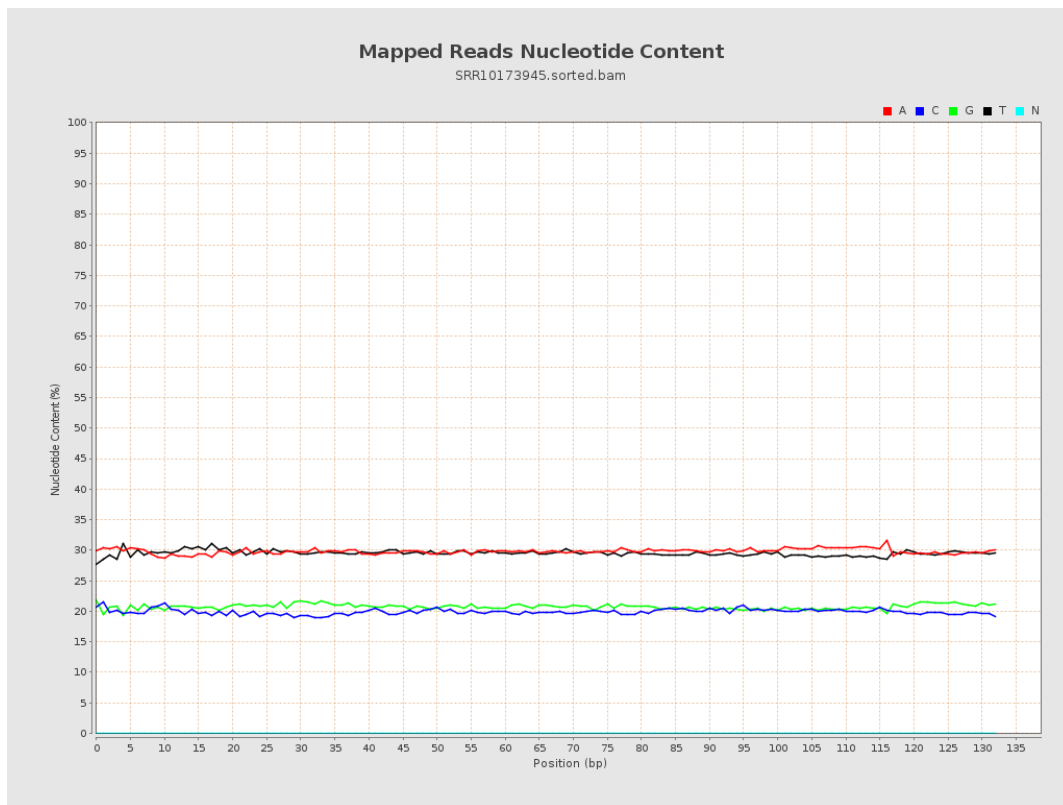
6. Results : Genome Fraction Coverage



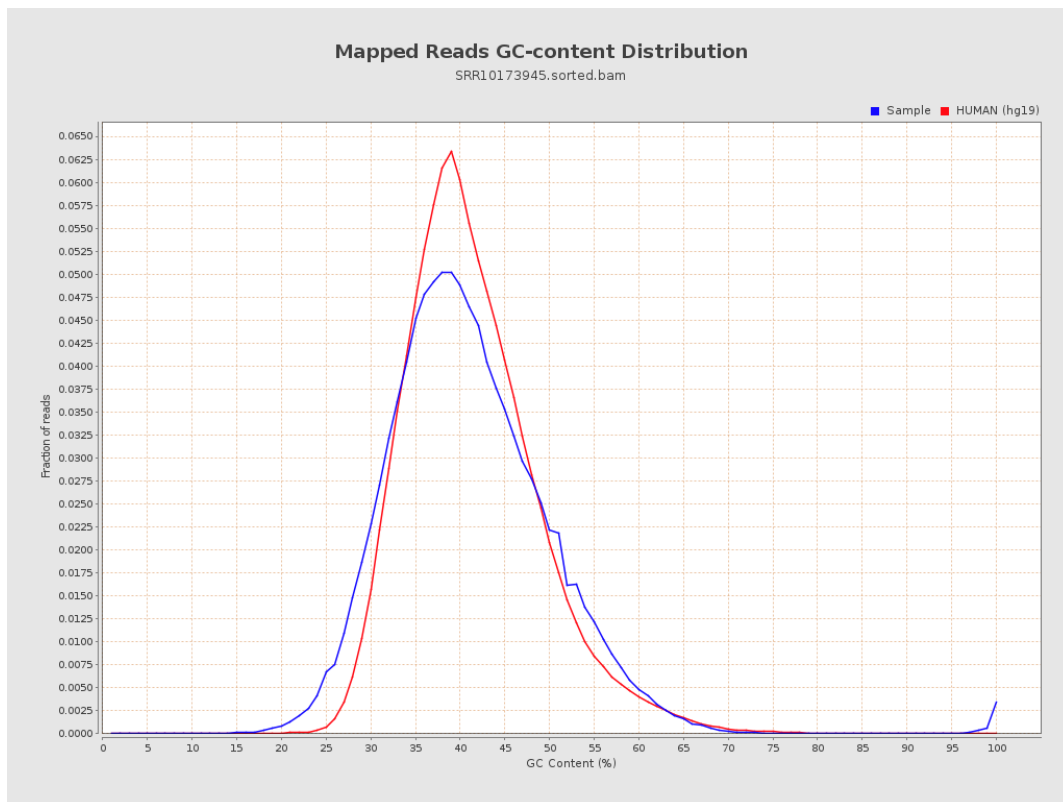
7. Results : Duplication Rate Histogram



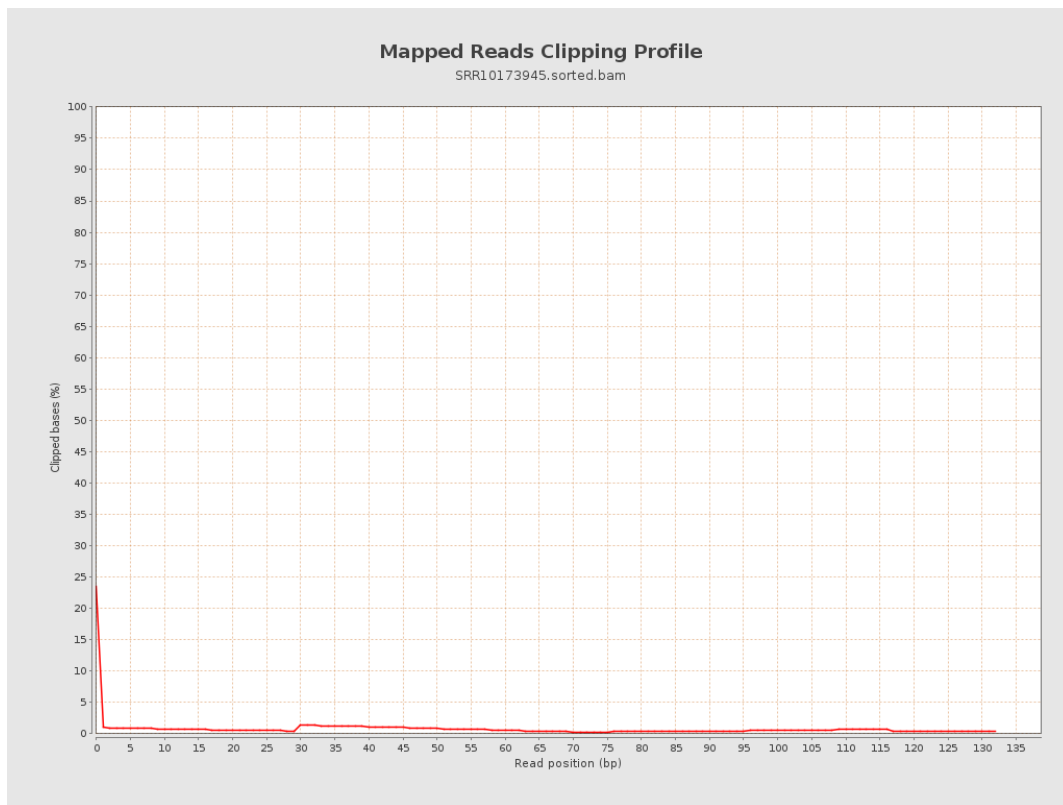
8. Results : Mapped Reads Nucleotide Content



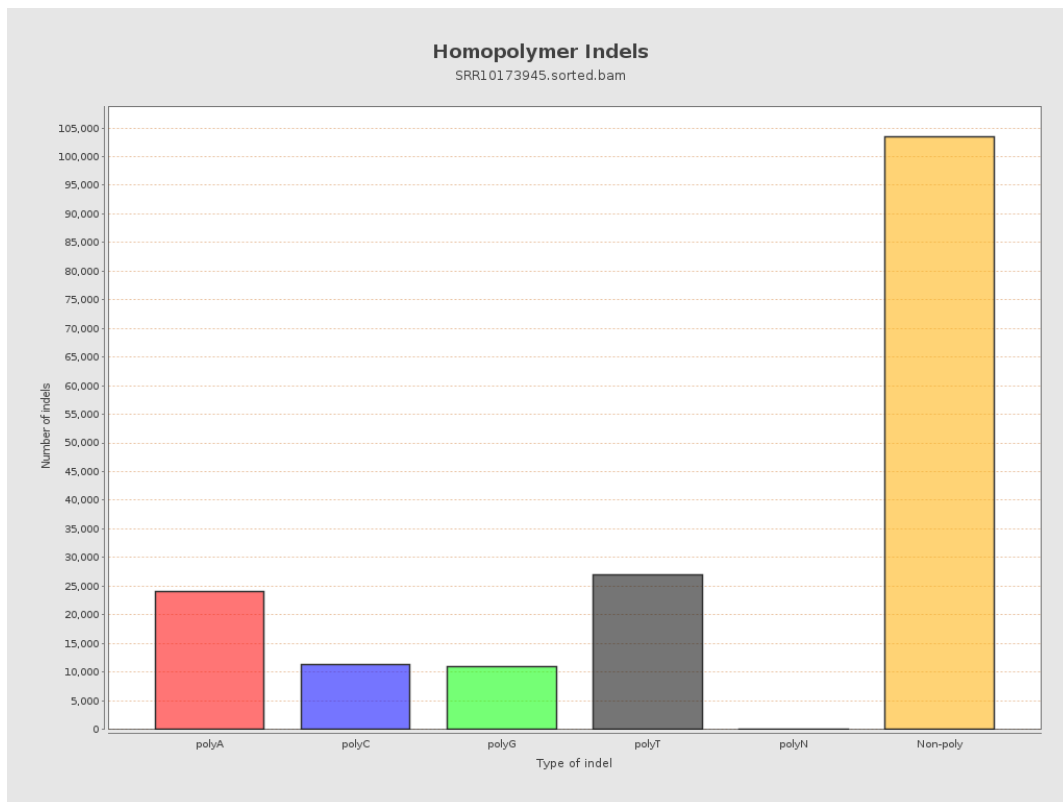
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



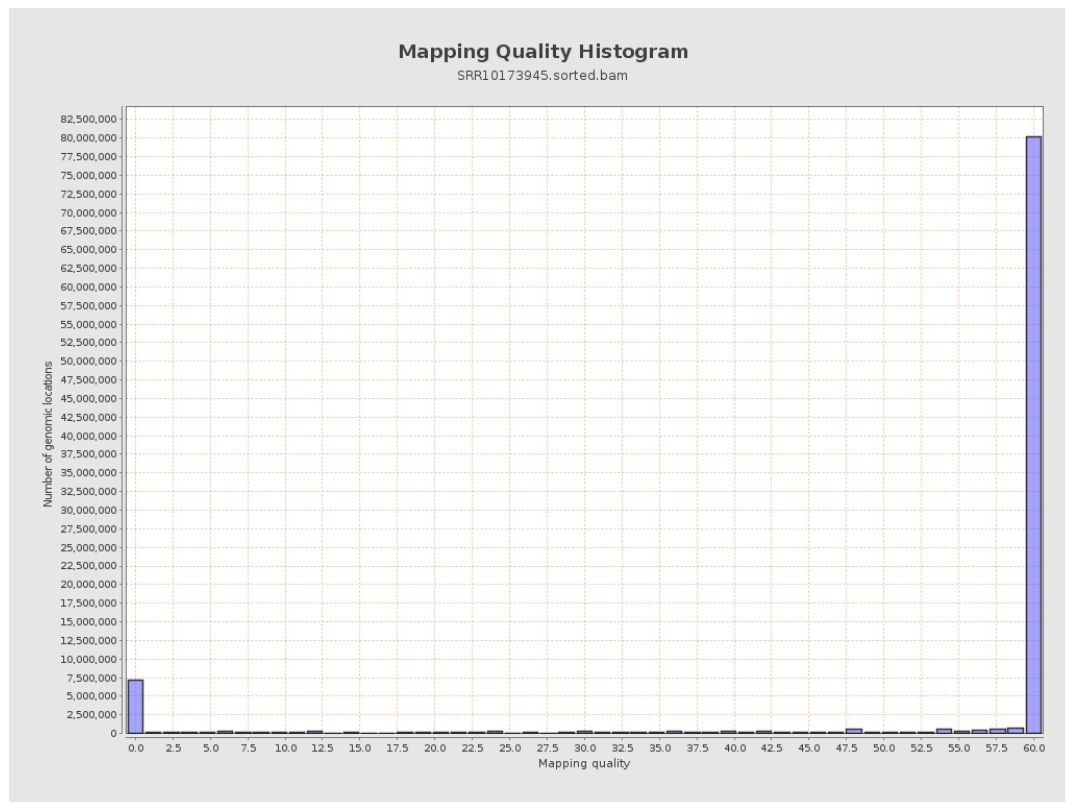
11. Results : Homopolymer Indels



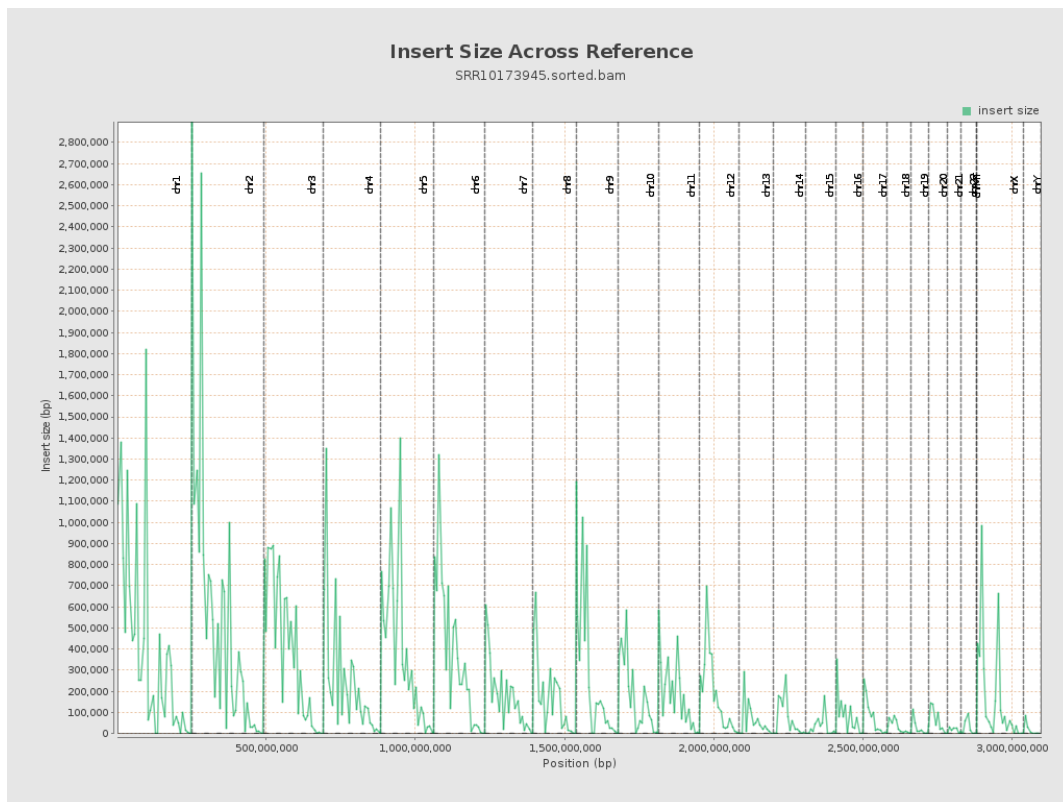
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

