

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 16:28:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173981.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_SRR10173981 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173981_1.fastq.gz SRR10173981_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 16:28:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173981.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,438,454
Mapped reads	3,371,525 / 98.05%
Unmapped reads	66,929 / 1.95%
Mapped paired reads	3,371,525 / 98.05%
Mapped reads, first in pair	1,686,403 / 49.05%
Mapped reads, second in pair	1,685,122 / 49.01%
Mapped reads, both in pair	3,330,622 / 96.86%
Mapped reads, singletons	40,903 / 1.19%
Secondary alignments	0
Supplementary alignments	454,404 / 13.22%
Read min/max/mean length	30 / 133 / 125.26
Duplicated reads (estimated)	2,718,426 / 79.06%
Duplication rate	65.29%
Clipped reads	1,709,671 / 49.72%

2.2. ACGT Content

Number/percentage of A's	114,005,618 / 29.86%
Number/percentage of C's	75,850,329 / 19.86%
Number/percentage of T's	113,324,321 / 29.68%
Number/percentage of G's	78,662,495 / 20.6%
Number/percentage of N's	2,908 / 0%

GC Percentage	40.46%
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2.3. Coverage

Mean	0.1234
Standard Deviation	2.2163

2.4. Mapping Quality

Mean Mapping Quality	52.43
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2.5. Insert size

Mean	955,446.14
Standard Deviation	9,178,971.85
P25/Median/P75	104 / 151 / 228

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	3,261,902
Insertions	46,285
Mapped reads with at least one insertion	1.32%
Deletions	120,473
Mapped reads with at least one deletion	3.49%
Homopolymer indels	40.99%

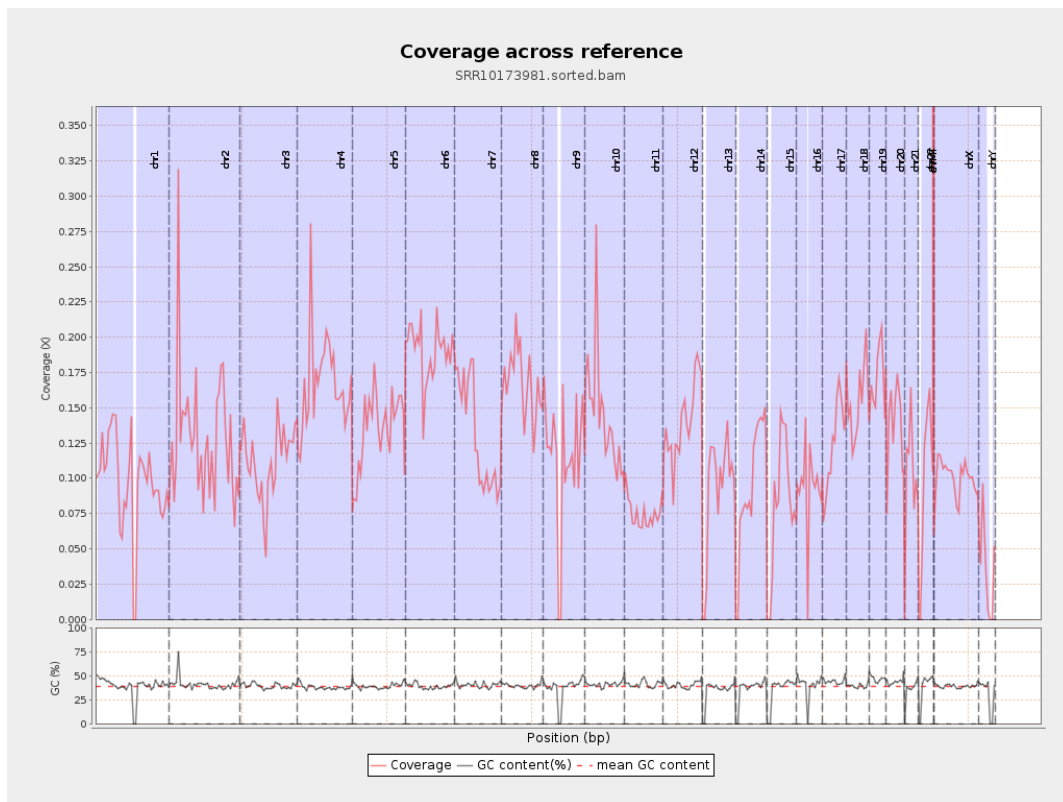
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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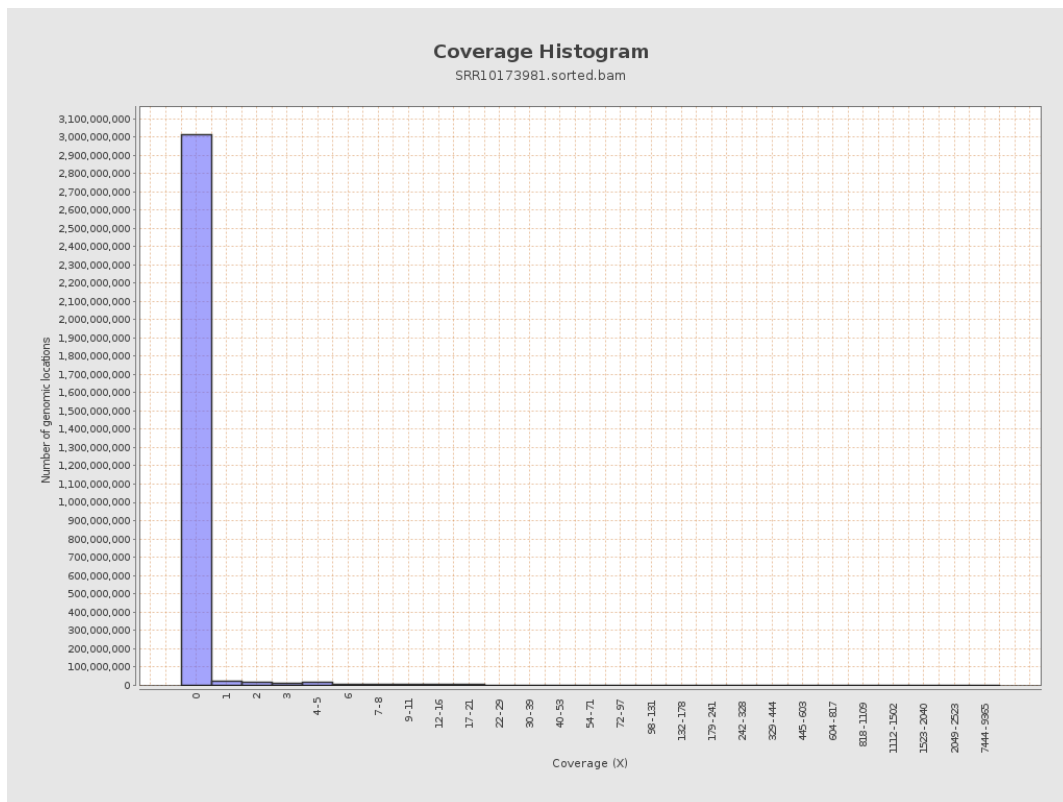
		bases	coverage	deviation
chr1	249250621	24108859	0.0967	1.3303
chr2	243199373	31351333	0.1289	6.6034
chr3	198022430	22201673	0.1121	1.0136
chr4	191154276	31815639	0.1664	1.653
chr5	180915260	24644844	0.1362	1.1269
chr6	171115067	32573626	0.1904	1.478
chr7	159138663	20605966	0.1295	1.4361
chr8	146364022	24430644	0.1669	1.57
chr9	141213431	15895048	0.1126	1.3347
chr10	135534747	19588261	0.1445	1.7503
chr11	135006516	10186733	0.0755	0.8981
chr12	133851895	18662372	0.1394	1.1424
chr13	115169878	10417656	0.0905	0.9171
chr14	107349540	10180565	0.0948	0.9469
chr15	102531392	8325047	0.0812	0.8753
chr16	90354753	8411654	0.0931	1.0457
chr17	81195210	10065357	0.124	1.1253
chr18	78077248	12199827	0.1563	1.6475
chr19	59128983	10122641	0.1712	1.3167
chr20	63025520	8656715	0.1374	1.1809
chr21	48129895	4890408	0.1016	1.1152
chr22	51304566	4919502	0.0959	0.9104
chrMT	16571	363409	21.9304	23.6672
chrX	155270560	15488454	0.0998	0.9643

chrY	59373566	2013390	0.0339	0.9108
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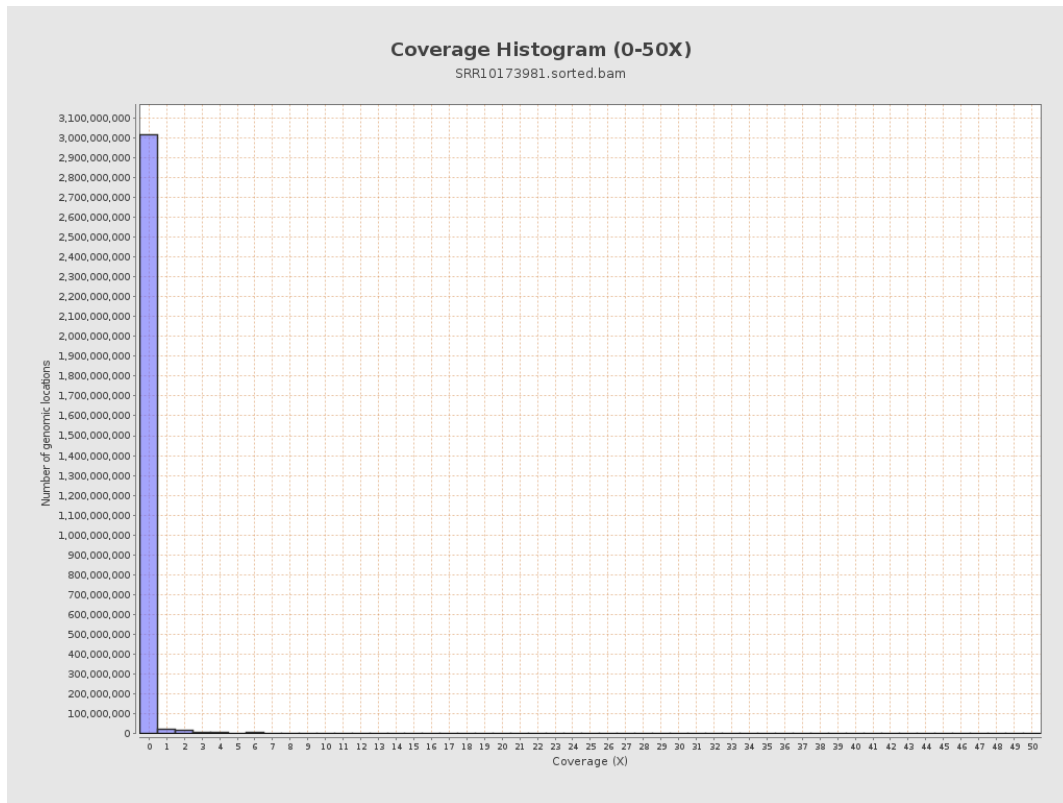
3. Results : Coverage across reference



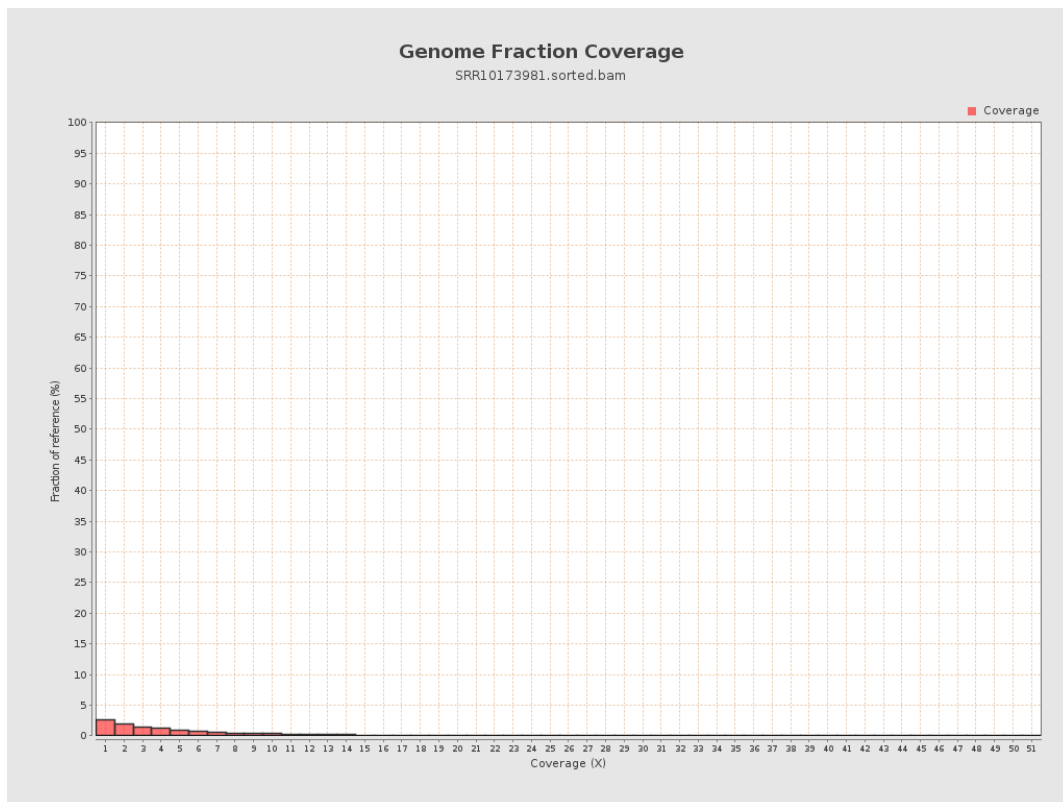
4. Results : Coverage Histogram



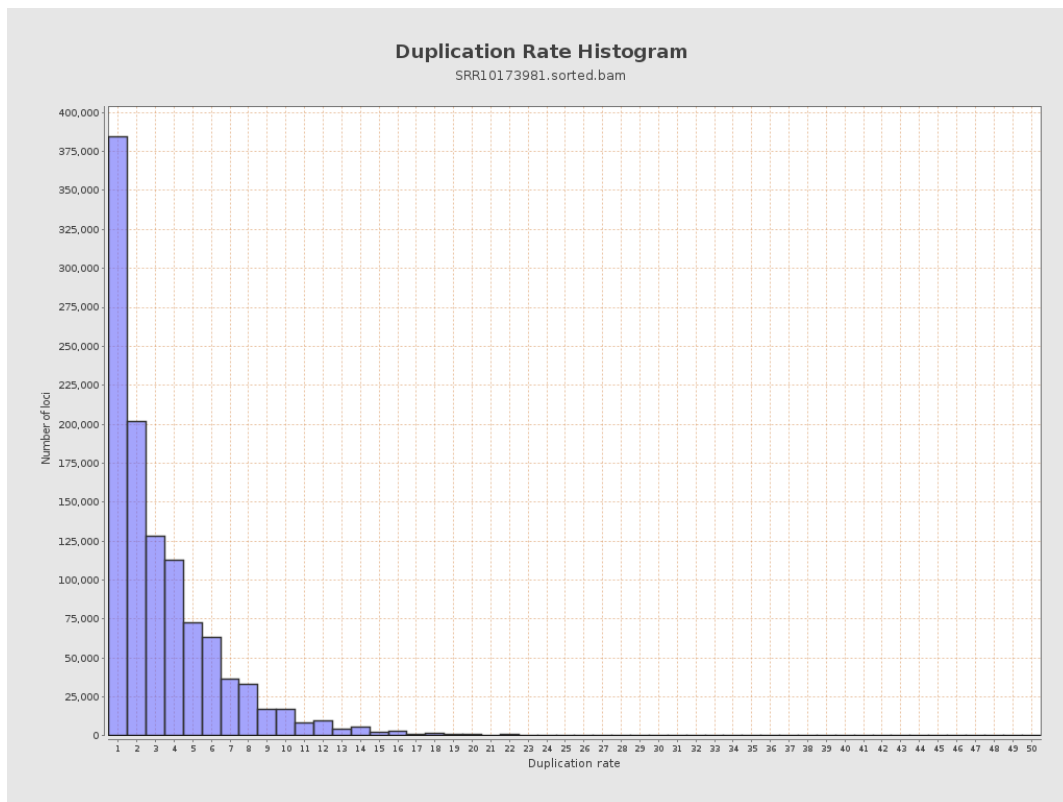
5. Results : Coverage Histogram (0-50X)



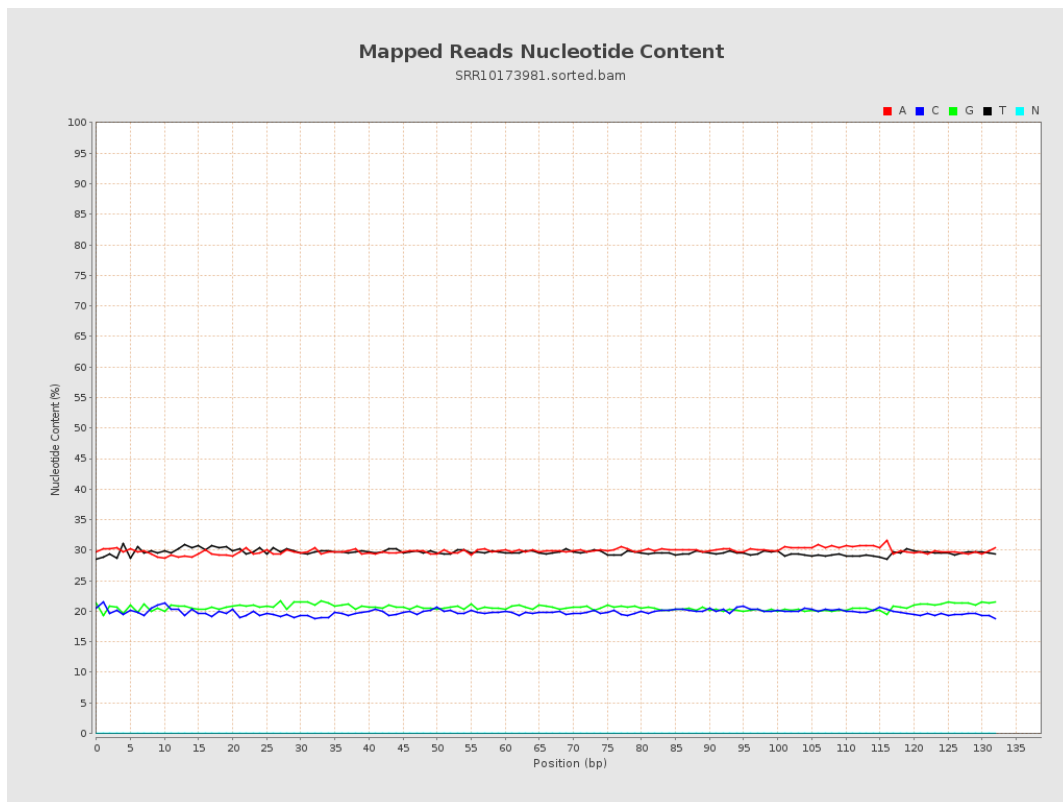
6. Results : Genome Fraction Coverage



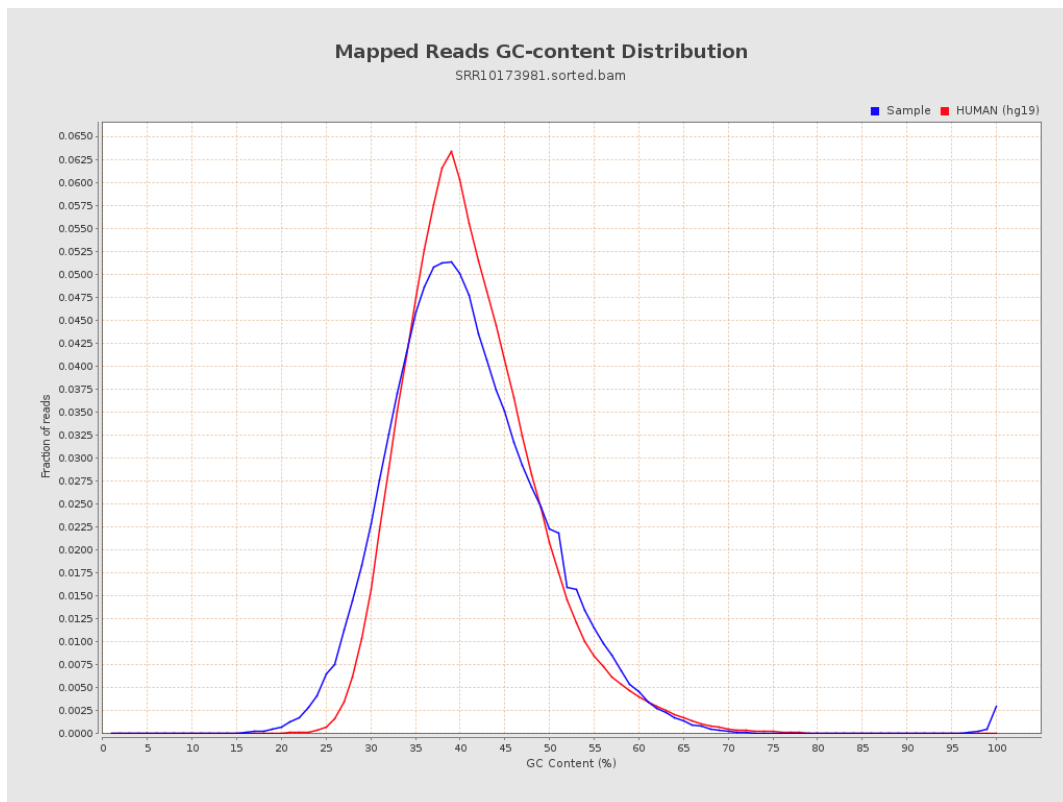
7. Results : Duplication Rate Histogram



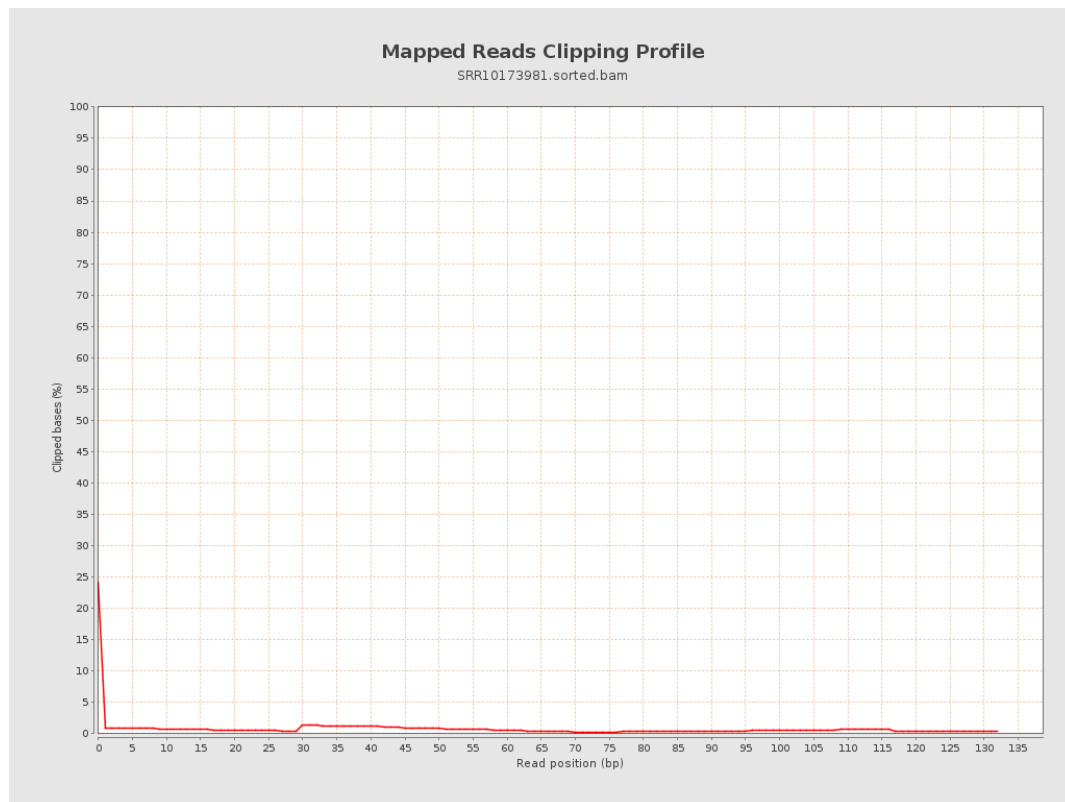
8. Results : Mapped Reads Nucleotide Content



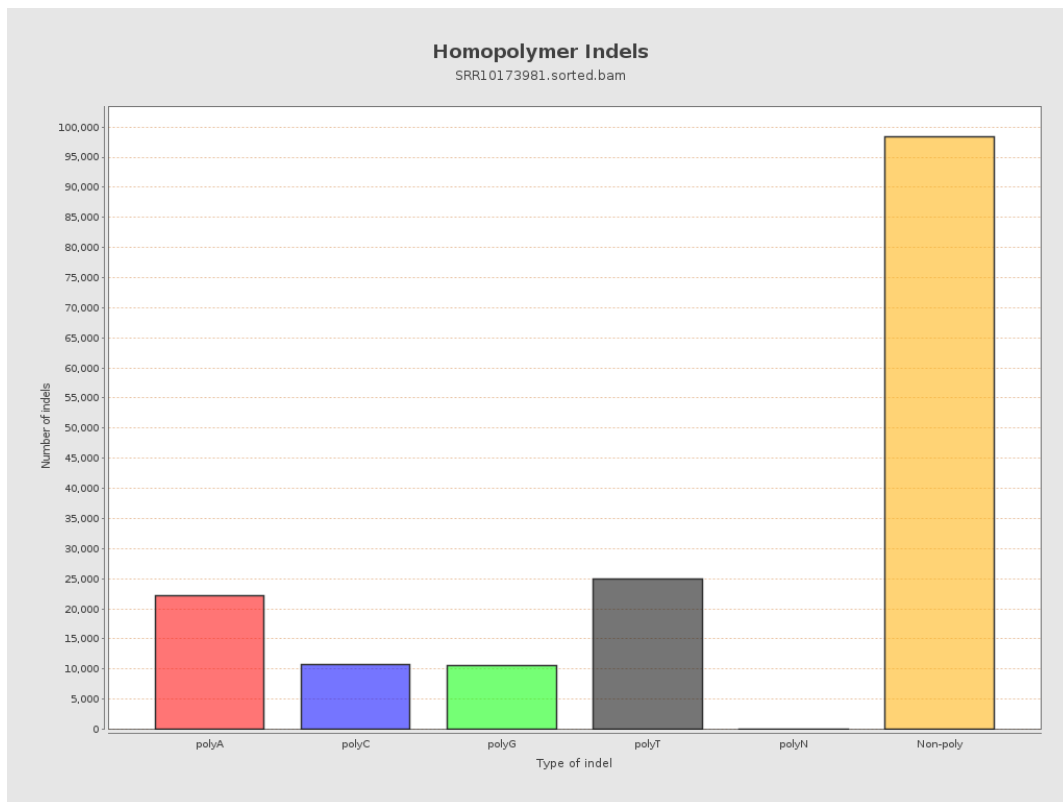
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



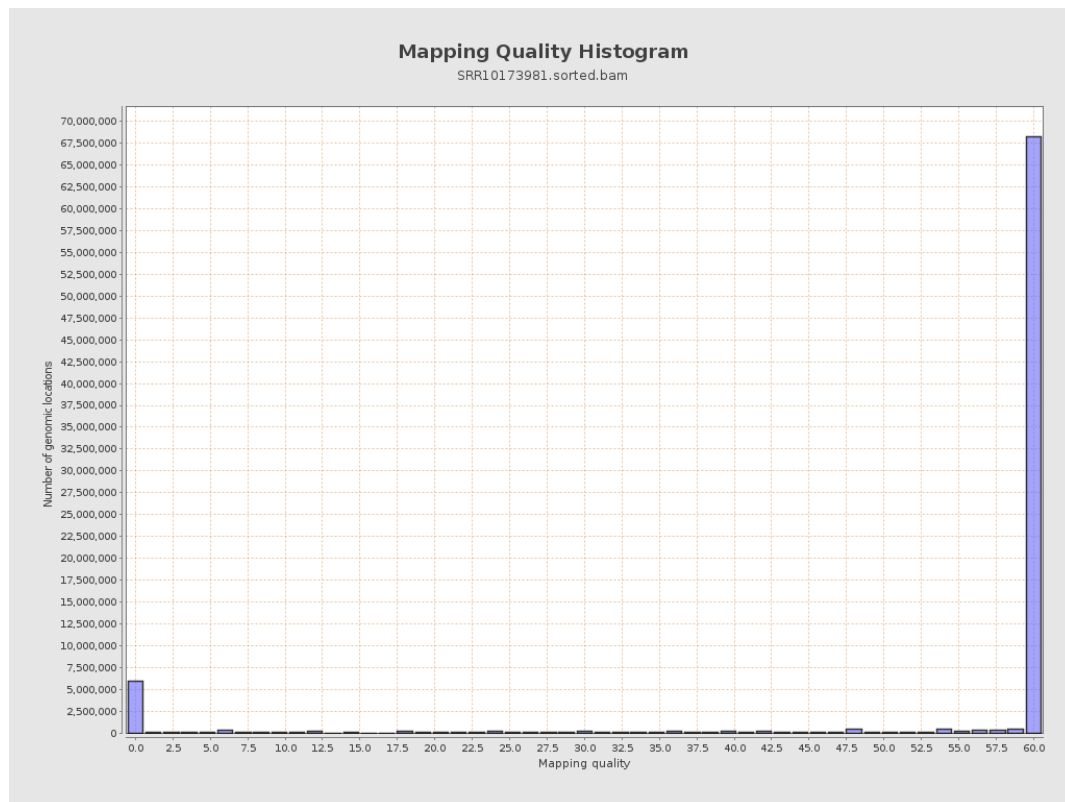
11. Results : Homopolymer Indels



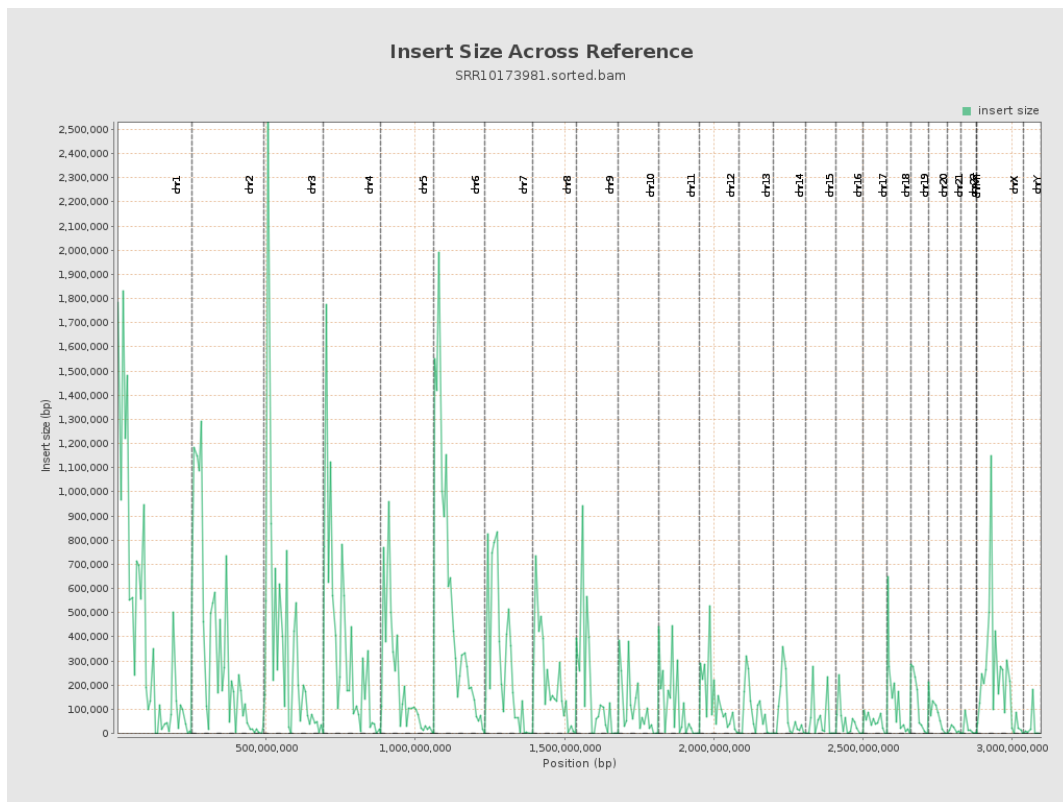
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

