

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 16:22:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173980.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_SRR10173980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173980_1.fastq.gz SRR10173980_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 16:22:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,082,356
Mapped reads	3,996,893 / 97.91%
Unmapped reads	85,463 / 2.09%
Mapped paired reads	3,996,893 / 97.91%
Mapped reads, first in pair	1,997,426 / 48.93%
Mapped reads, second in pair	1,999,467 / 48.98%
Mapped reads, both in pair	3,941,366 / 96.55%
Mapped reads, singletons	55,527 / 1.36%
Secondary alignments	0
Supplementary alignments	553,269 / 13.55%
Read min/max/mean length	30 / 133 / 125.52
Duplicated reads (estimated)	3,222,674 / 78.94%
Duplication rate	64.4%
Clipped reads	2,079,449 / 50.94%

2.2. ACGT Content

Number/percentage of A's	135,340,967 / 29.92%
Number/percentage of C's	89,701,490 / 19.83%
Number/percentage of T's	134,157,349 / 29.66%
Number/percentage of G's	93,125,666 / 20.59%
Number/percentage of N's	3,282 / 0%

GC Percentage	40.42%
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2.3. Coverage

Mean	0.1462
Standard Deviation	2.6292

2.4. Mapping Quality

Mean Mapping Quality	52.47
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2.5. Insert size

Mean	1,063,446.11
Standard Deviation	9,582,040.36
P25/Median/P75	104 / 151 / 232

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	3,769,401
Insertions	49,634
Mapped reads with at least one insertion	1.2%
Deletions	131,060
Mapped reads with at least one deletion	3.2%
Homopolymer indels	41.26%

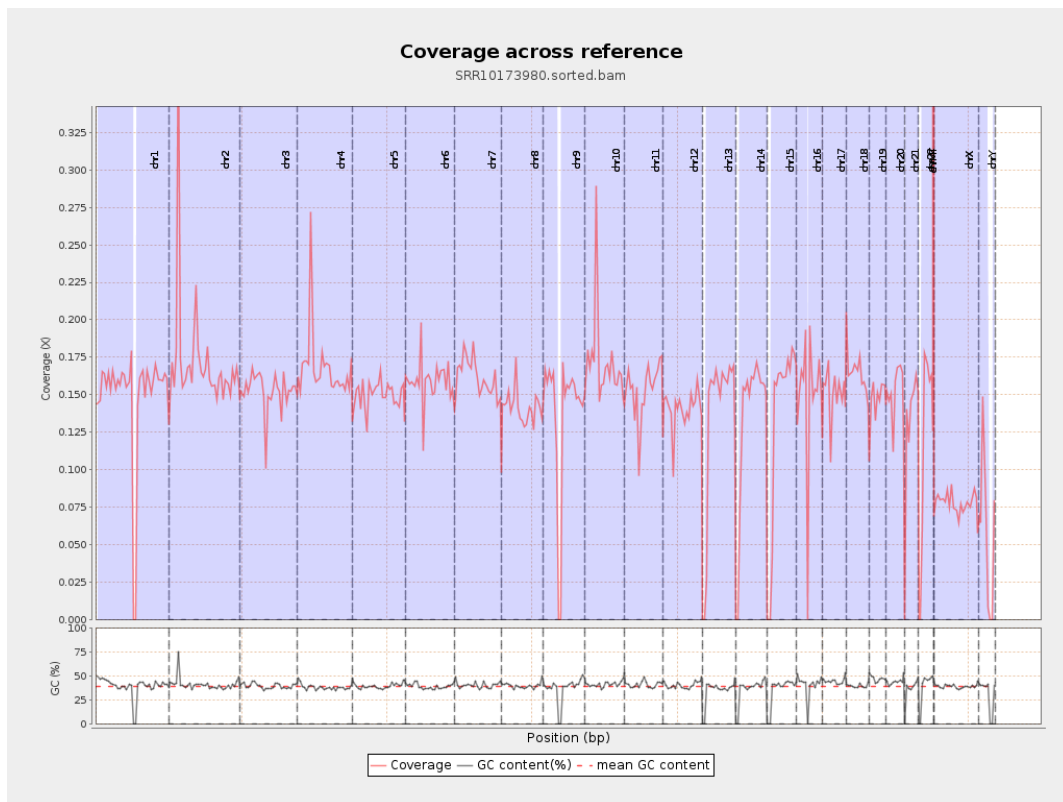
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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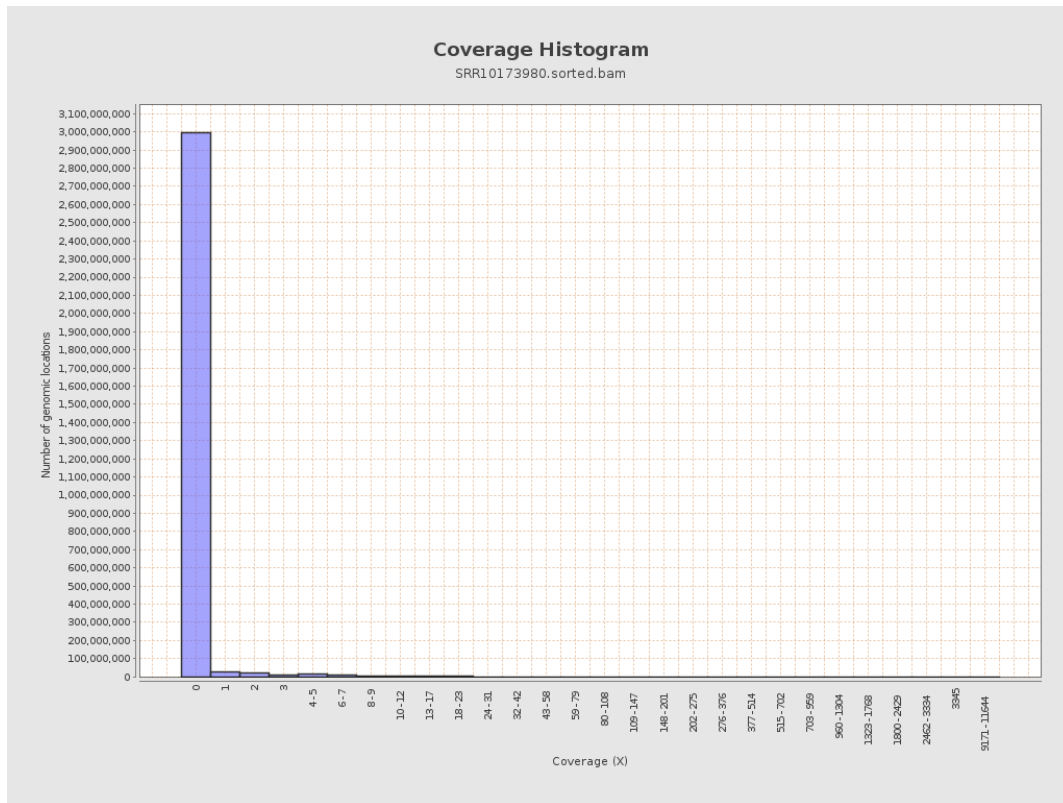
		bases	coverage	deviation
chr1	249250621	37205936	0.1493	1.4886
chr2	243199373	42000479	0.1727	8.1586
chr3	198022430	30208985	0.1526	1.1863
chr4	191154276	32055262	0.1677	1.5298
chr5	180915260	27170440	0.1502	1.1728
chr6	171115067	27129980	0.1585	1.3222
chr7	159138663	25835986	0.1623	1.531
chr8	146364022	20728837	0.1416	1.7589
chr9	141213431	19341638	0.137	1.3757
chr10	135534747	23224678	0.1714	1.7758
chr11	135006516	20740818	0.1536	1.2154
chr12	133851895	18807628	0.1405	1.1695
chr13	115169878	15398856	0.1337	1.1154
chr14	107349540	14258354	0.1328	1.1161
chr15	102531392	13728379	0.1339	1.1275
chr16	90354753	13406878	0.1484	1.3253
chr17	81195210	12227949	0.1506	1.216
chr18	78077248	12826123	0.1643	1.7917
chr19	59128983	8733875	0.1477	1.2582
chr20	63025520	9531682	0.1512	1.1944
chr21	48129895	6325849	0.1314	1.3504
chr22	51304566	5930168	0.1156	1.1728
chrMT	16571	453762	27.3829	26.9709
chrX	155270560	12091018	0.0779	0.8441

chrY	59373566	3277164	0.0552	1.0632
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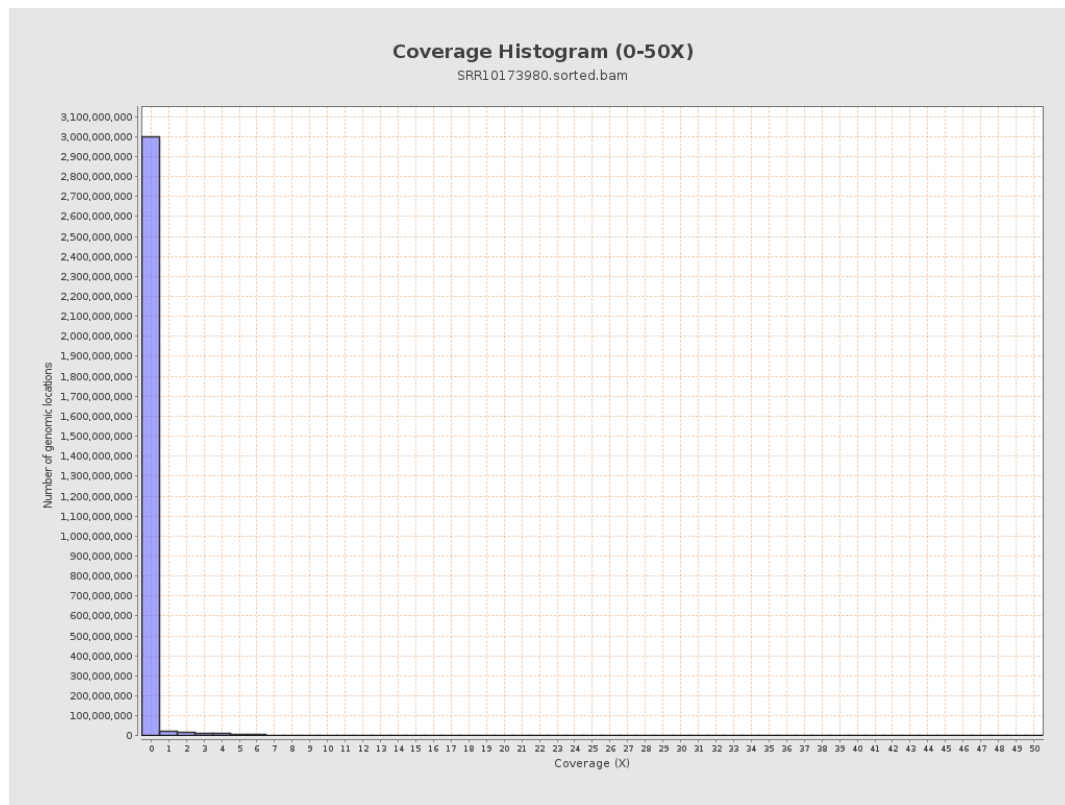
3. Results : Coverage across reference



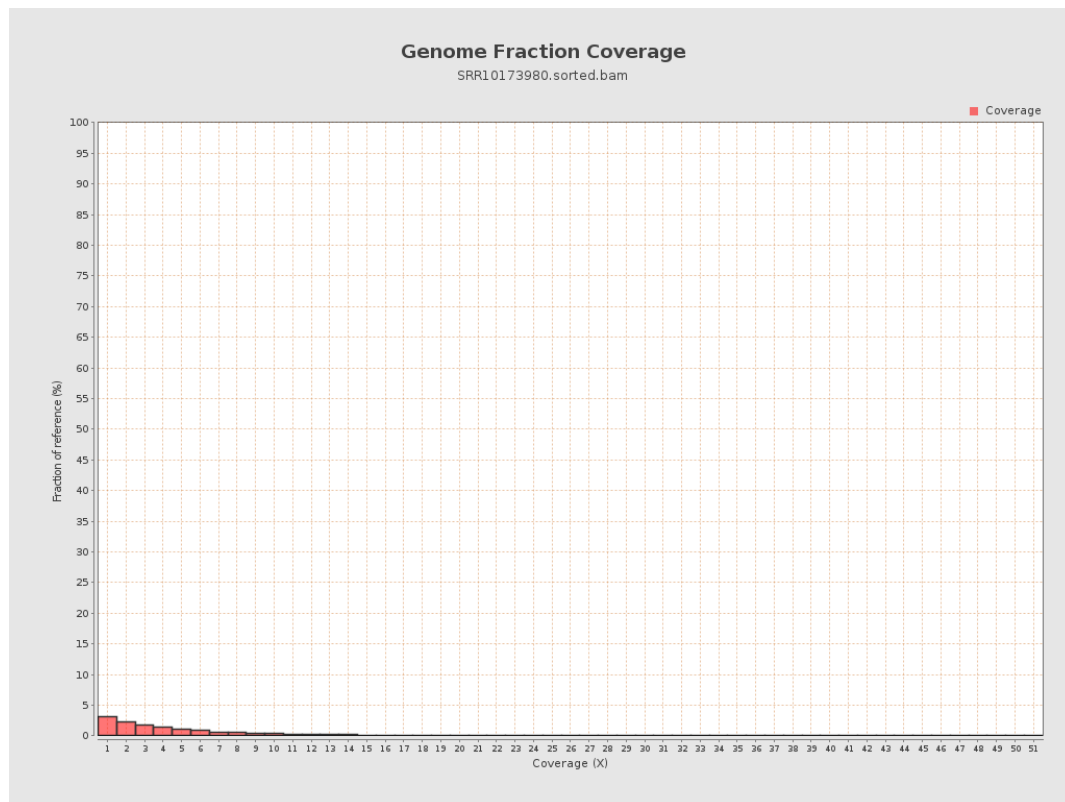
4. Results : Coverage Histogram



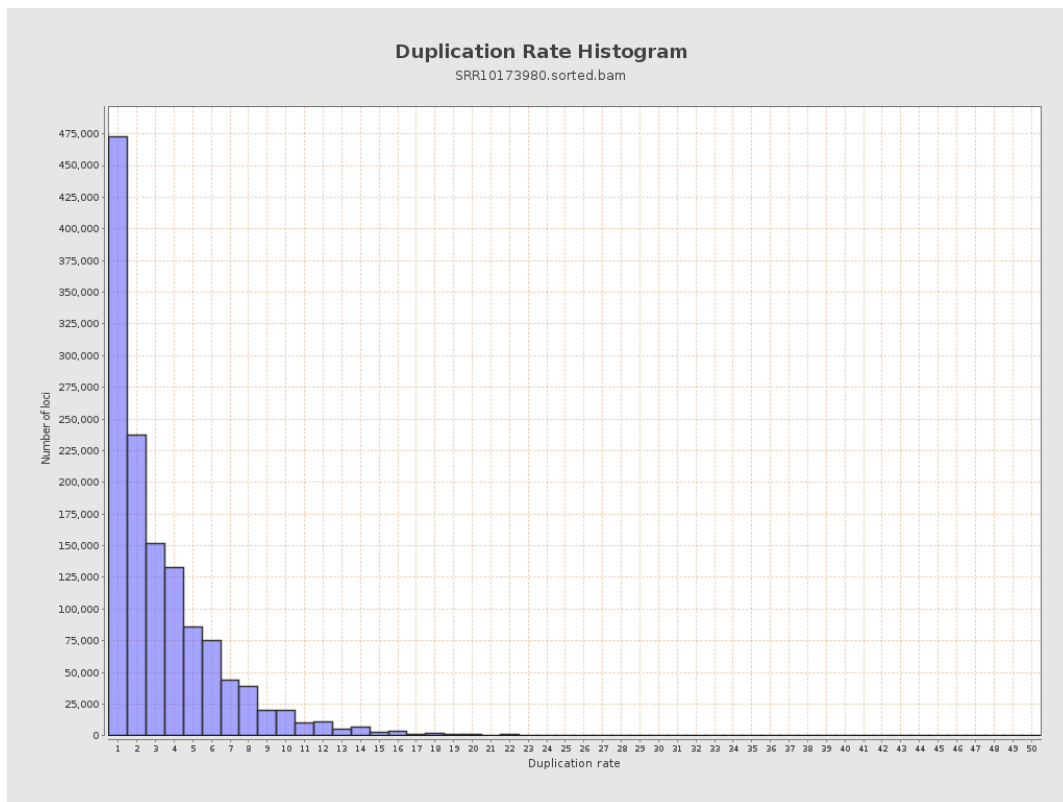
5. Results : Coverage Histogram (0-50X)



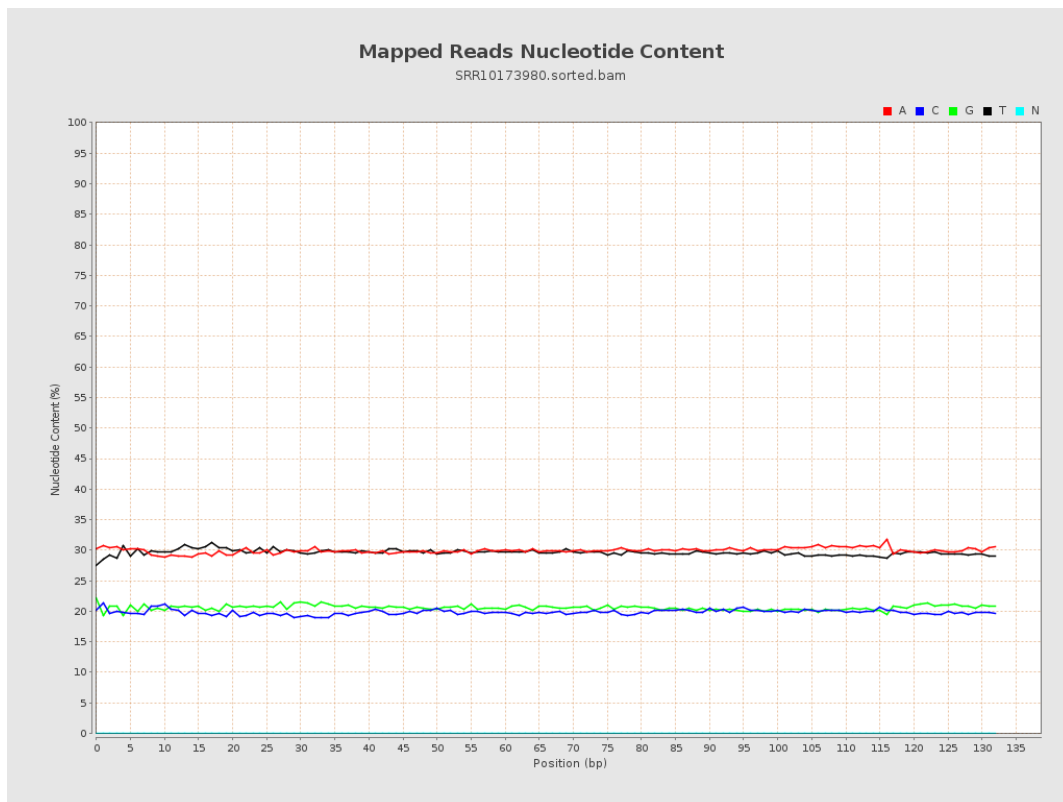
6. Results : Genome Fraction Coverage



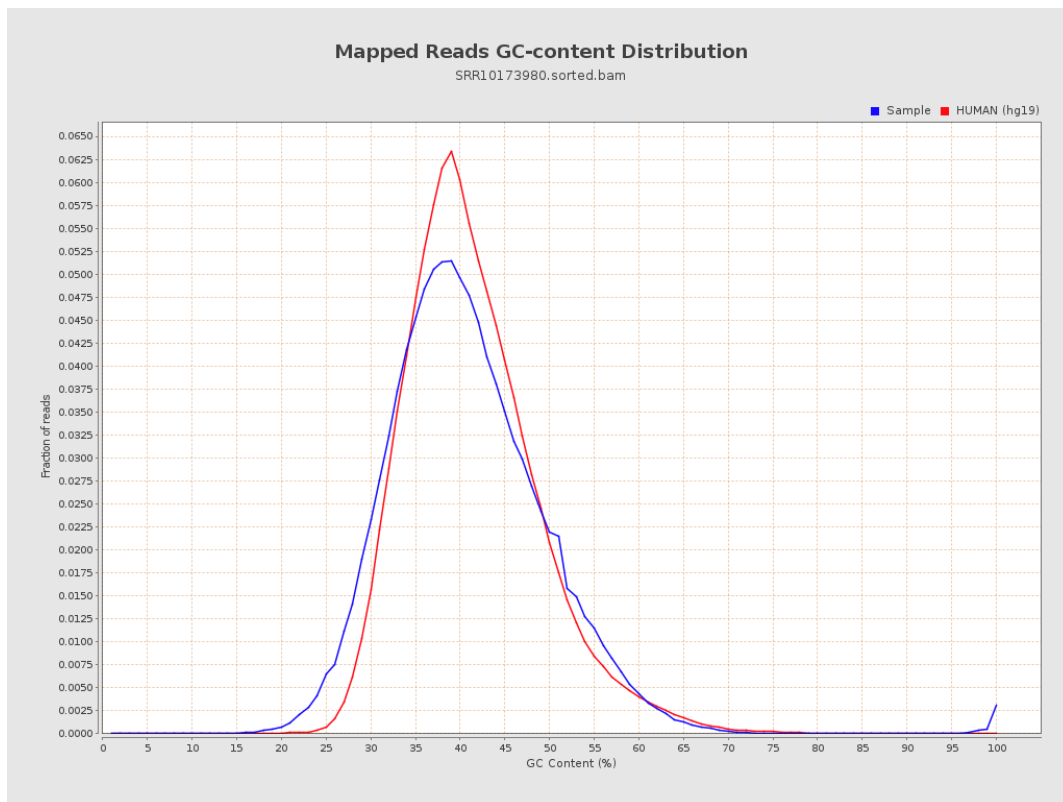
7. Results : Duplication Rate Histogram



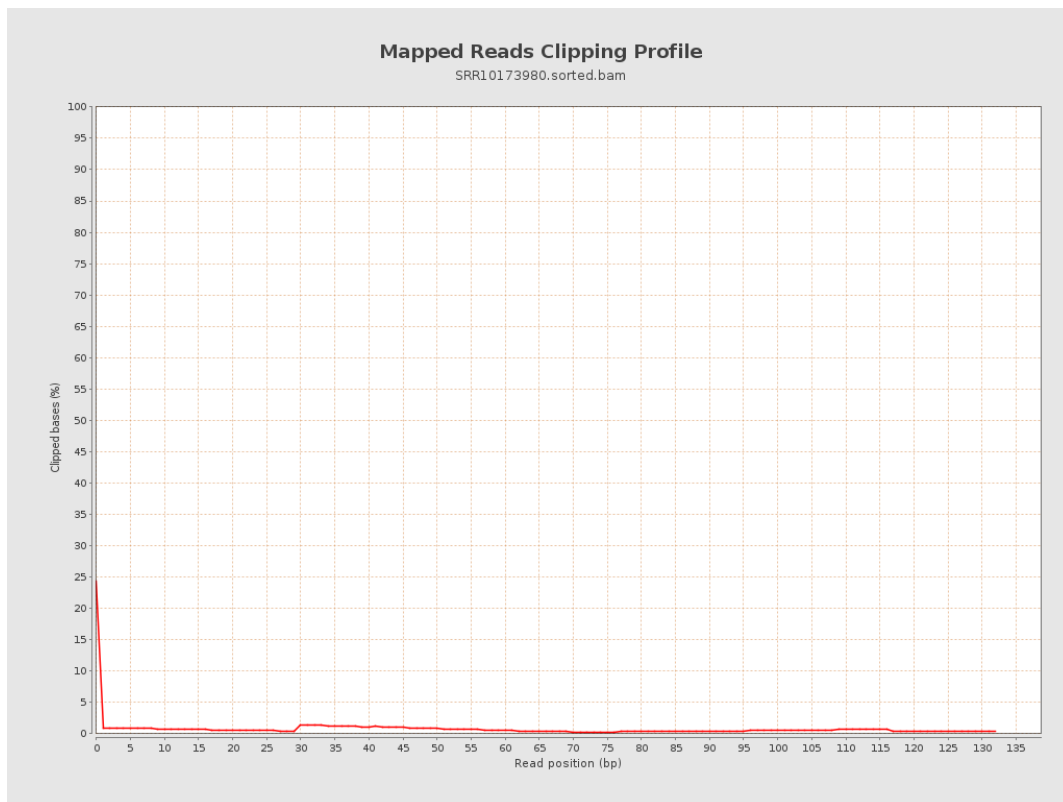
8. Results : Mapped Reads Nucleotide Content



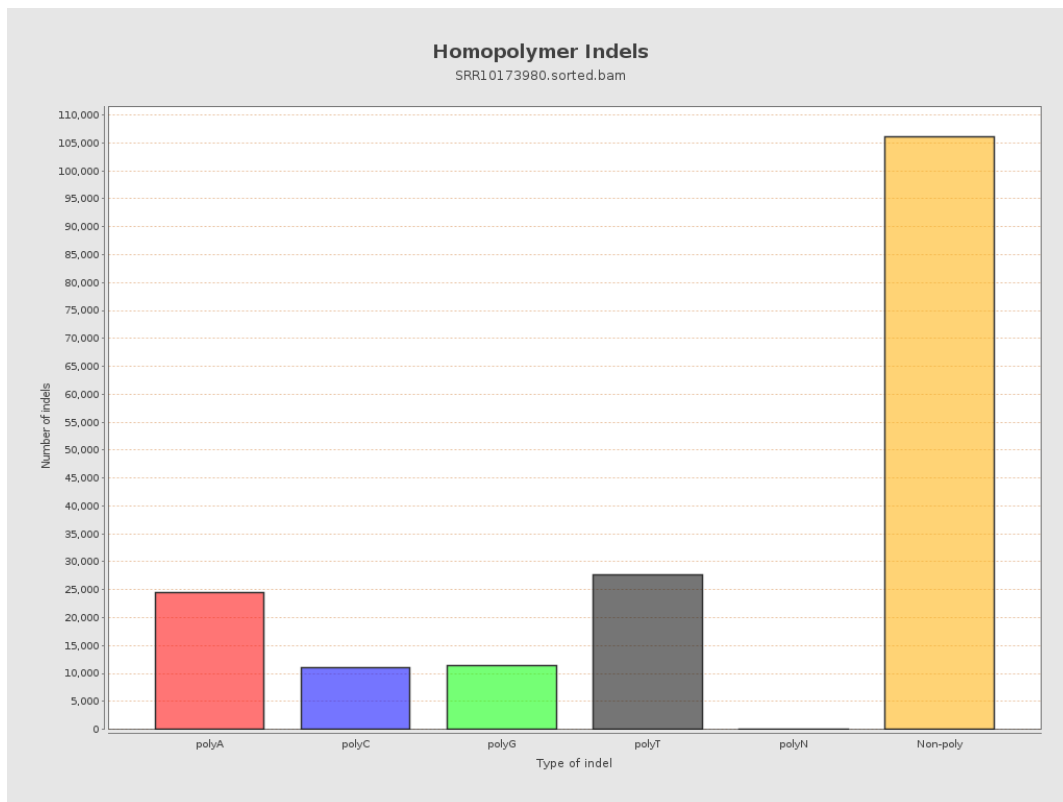
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



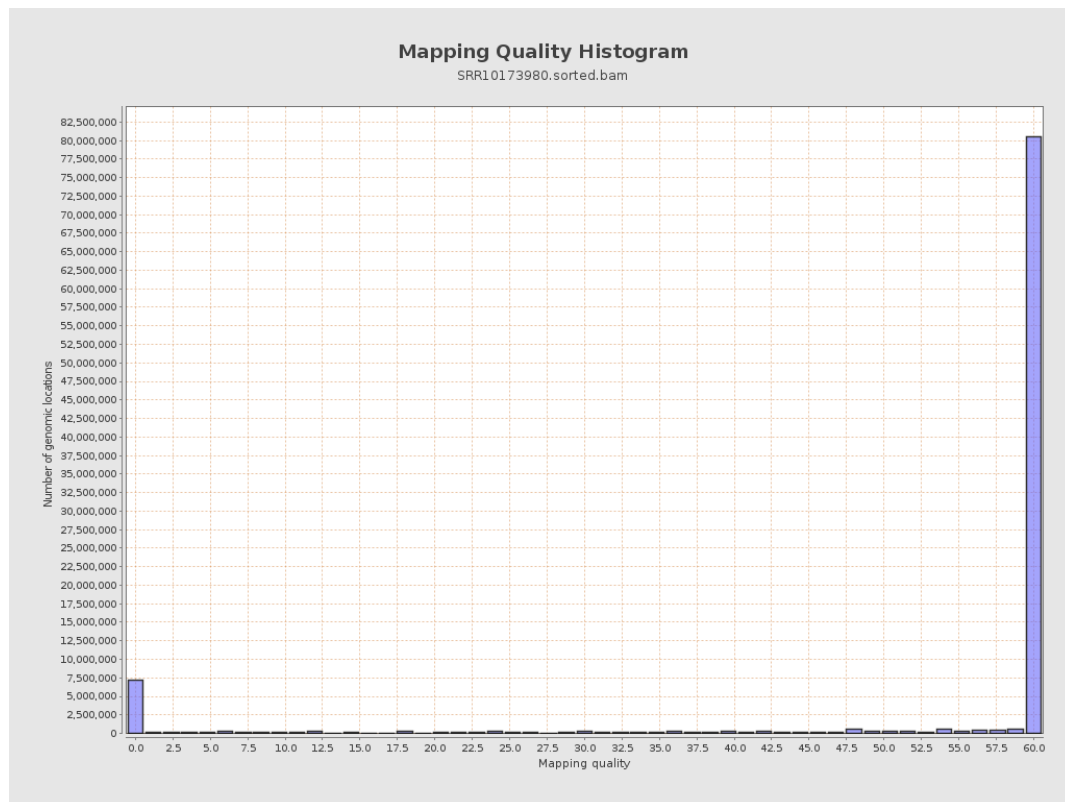
11. Results : Homopolymer Indels



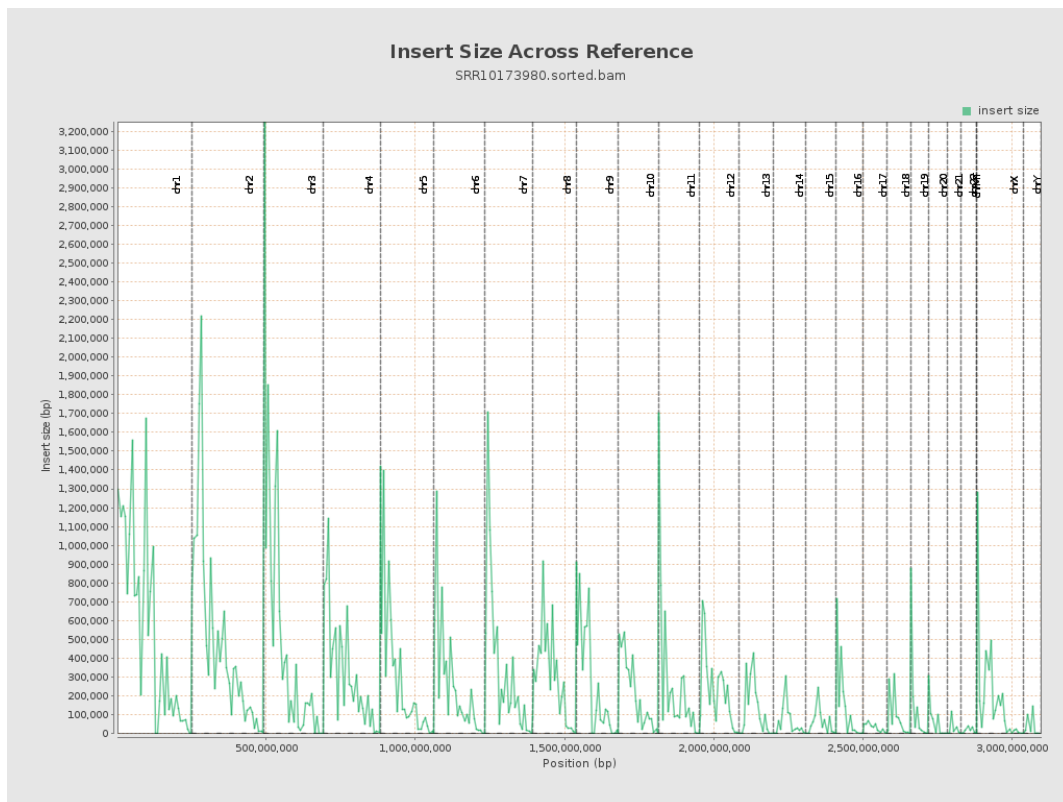
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

