

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 05:33:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174076.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_SRR10174076 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174076_1.fastq.gz SRR10174076_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 05:33:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,046,386
Mapped reads	2,976,091 / 97.69%
Unmapped reads	70,295 / 2.31%
Mapped paired reads	2,976,091 / 97.69%
Mapped reads, first in pair	1,489,246 / 48.89%
Mapped reads, second in pair	1,486,845 / 48.81%
Mapped reads, both in pair	2,931,166 / 96.22%
Mapped reads, singletons	44,925 / 1.47%
Secondary alignments	0
Supplementary alignments	281,713 / 9.25%
Read min/max/mean length	30 / 133 / 127.88
Duplicated reads (estimated)	2,297,632 / 75.42%
Duplication rate	65.11%
Clipped reads	1,124,727 / 36.92%

2.2. ACGT Content

Number/percentage of A's	106,728,120 / 30.22%
Number/percentage of C's	68,982,441 / 19.54%
Number/percentage of T's	106,210,284 / 30.08%
Number/percentage of G's	71,187,034 / 20.16%
Number/percentage of N's	4,680 / 0%

GC Percentage	39.7%
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2.3. Coverage

Mean	0.1141
Standard Deviation	1.7436

2.4. Mapping Quality

Mean Mapping Quality	52.8
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2.5. Insert size

Mean	821,584.37
Standard Deviation	8,476,970.07
P25/Median/P75	145 / 200 / 285

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	3,545,403
Insertions	36,869
Mapped reads with at least one insertion	1.2%
Deletions	77,491
Mapped reads with at least one deletion	2.54%
Homopolymer indels	42.66%

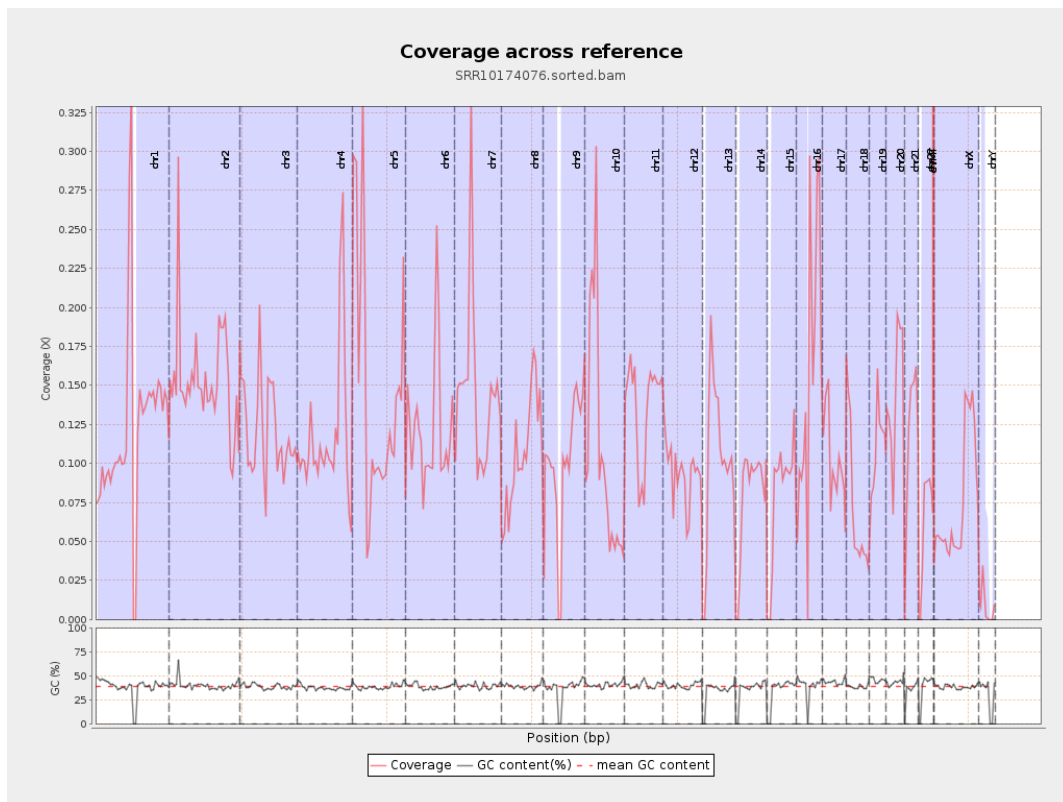
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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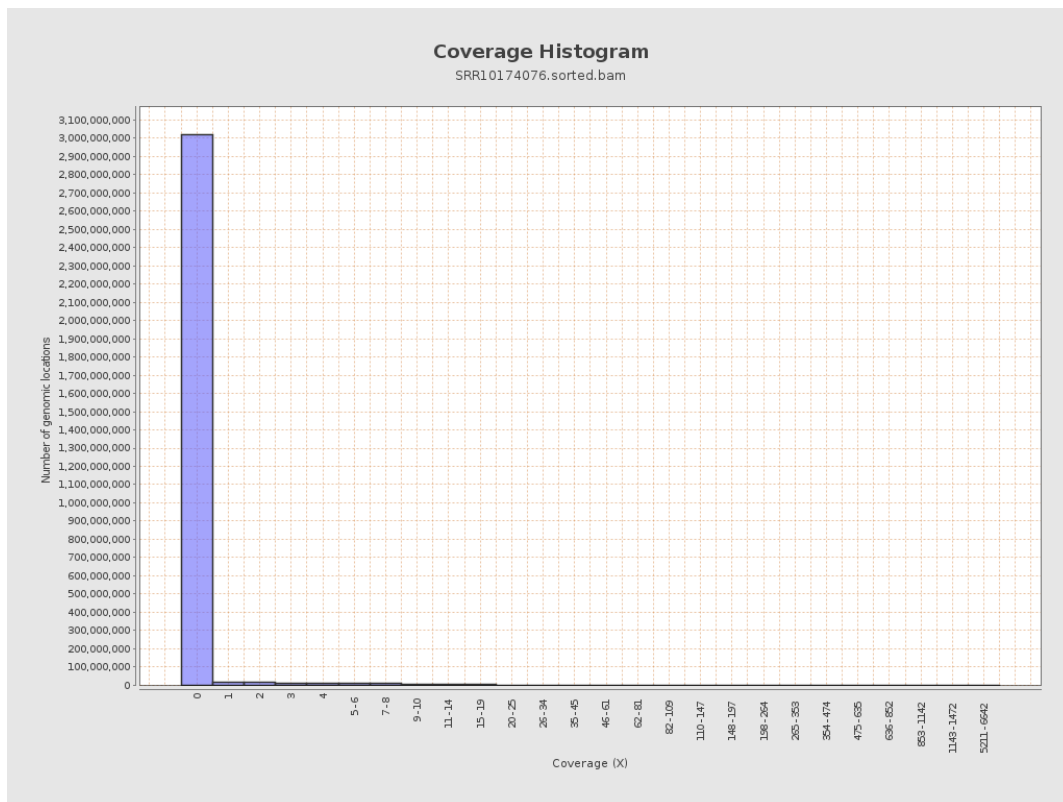
		bases	coverage	deviation
chr1	249250621	30484194	0.1223	1.4803
chr2	243199373	37236306	0.1531	4.749
chr3	198022430	23963576	0.121	1.003
chr4	191154276	21970122	0.1149	1.0824
chr5	180915260	26629539	0.1472	1.1174
chr6	171115067	21050744	0.123	1.0313
chr7	159138663	23208780	0.1458	1.6073
chr8	146364022	15774158	0.1078	1.0559
chr9	141213431	14300722	0.1013	1.0102
chr10	135534747	14575472	0.1075	1.8406
chr11	135006516	18372022	0.1361	1.0703
chr12	133851895	12514009	0.0935	0.8755
chr13	115169878	11623938	0.1009	0.9219
chr14	107349540	8399672	0.0782	0.8064
chr15	102531392	8197610	0.08	0.7948
chr16	90354753	14204387	0.1572	1.4674
chr17	81195210	8155758	0.1004	0.9747
chr18	78077248	5511741	0.0706	1.3449
chr19	59128983	6471743	0.1095	1.4935
chr20	63025520	8982099	0.1425	1.0822
chr21	48129895	5647351	0.1173	1.0036
chr22	51304566	3075646	0.0599	0.6604
chrMT	16571	899990	54.3111	46.7699
chrX	155270560	11589347	0.0746	0.7853

chrY	59373566	463923	0.0078	0.3839
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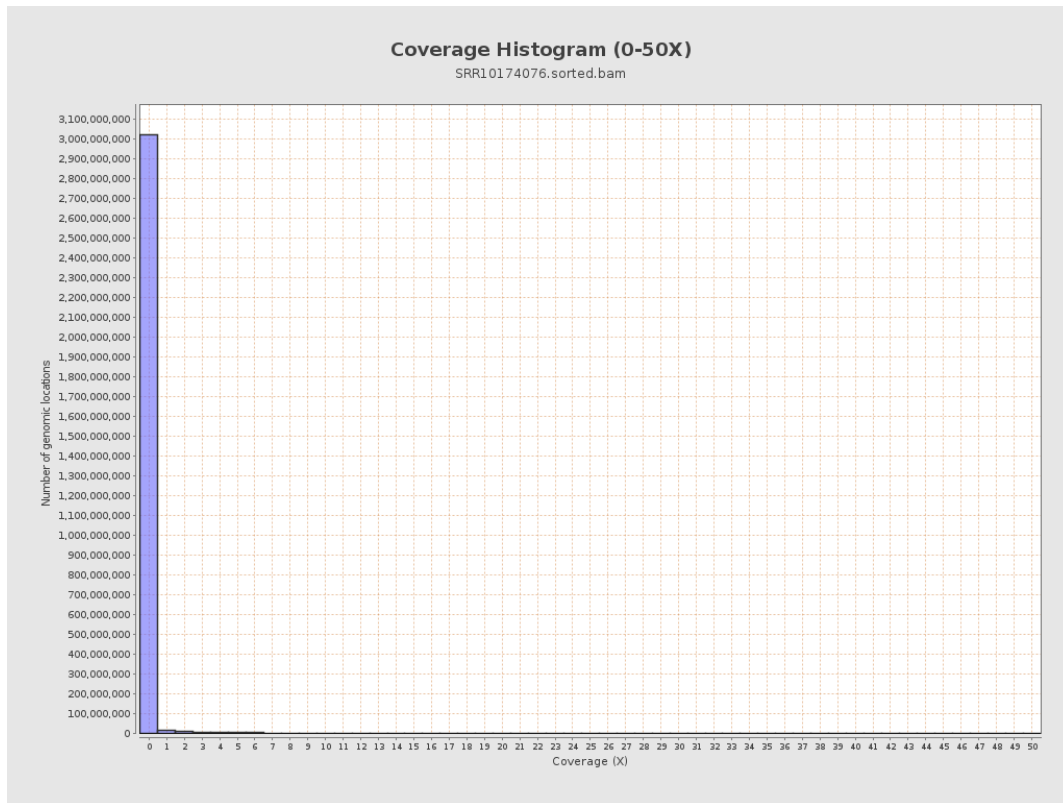
3. Results : Coverage across reference



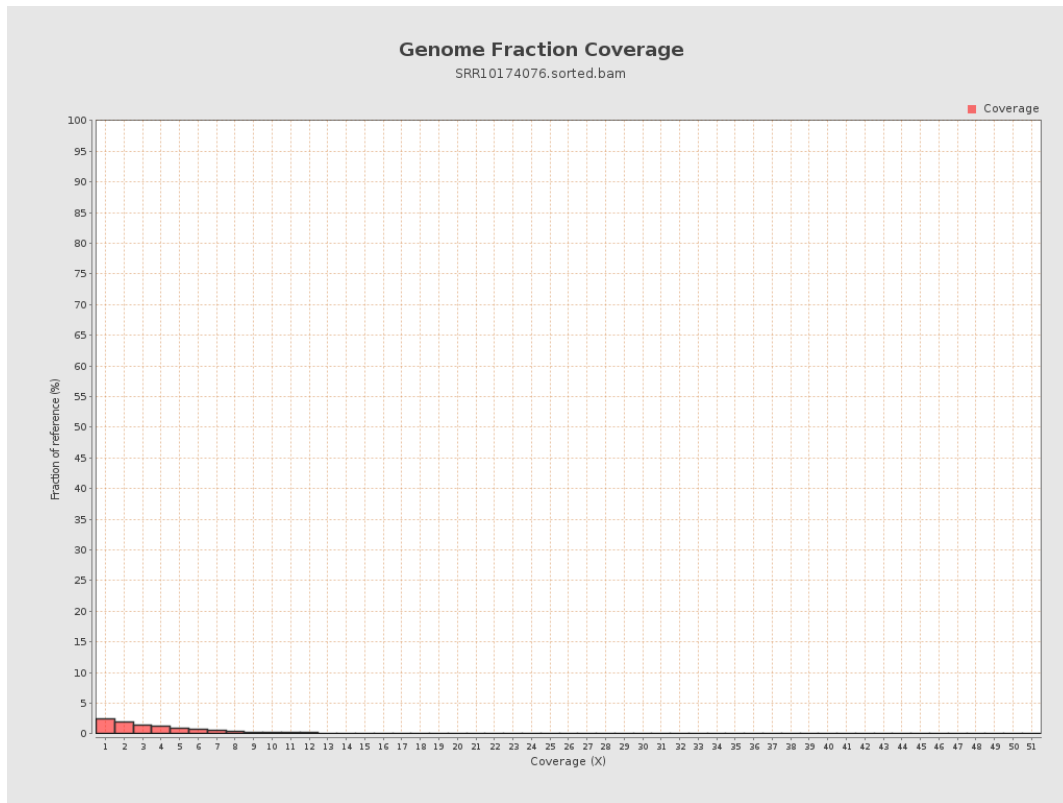
4. Results : Coverage Histogram



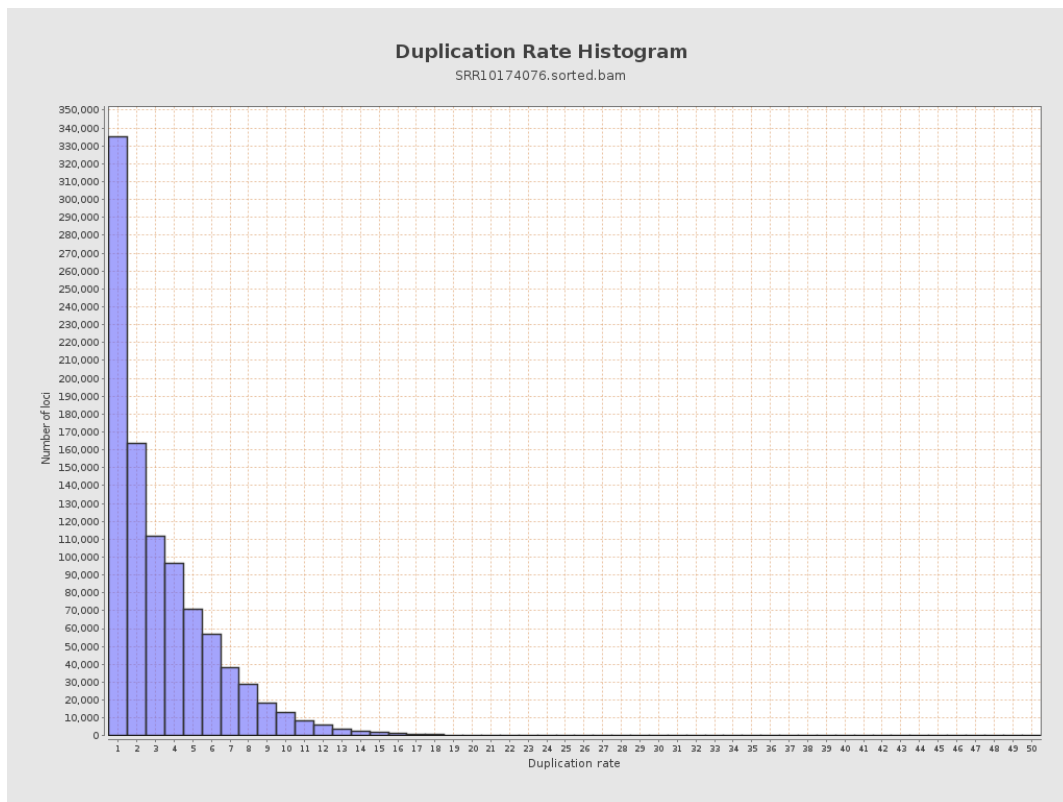
5. Results : Coverage Histogram (0-50X)



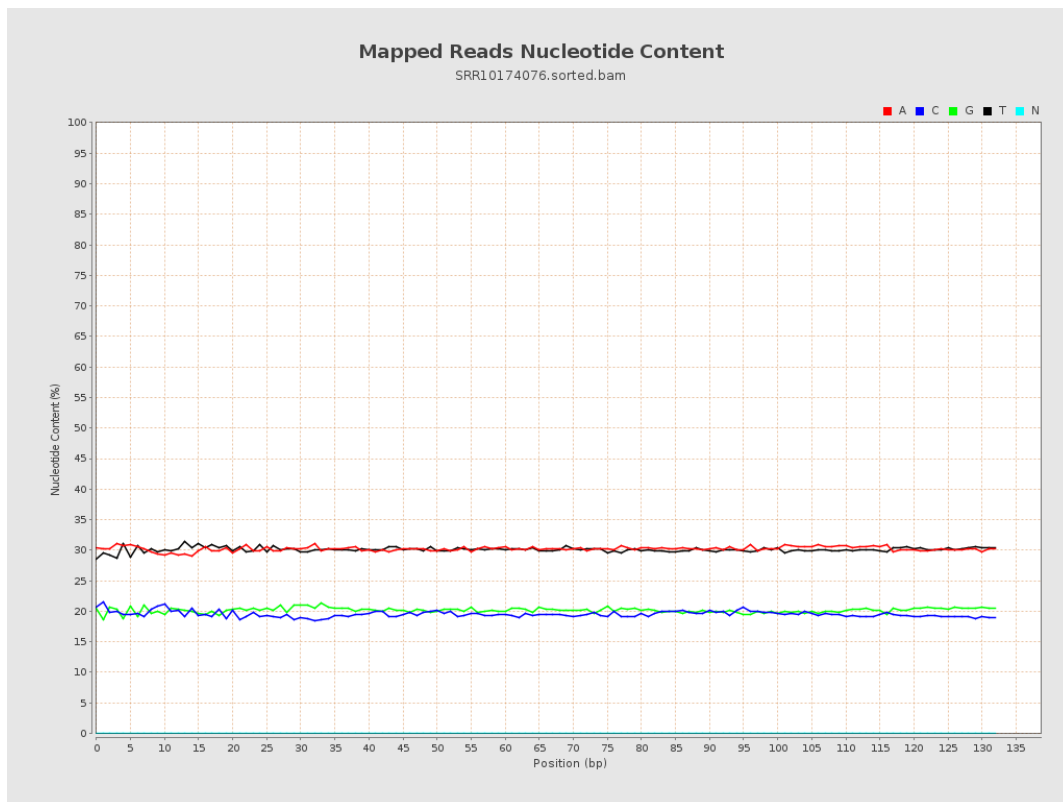
6. Results : Genome Fraction Coverage



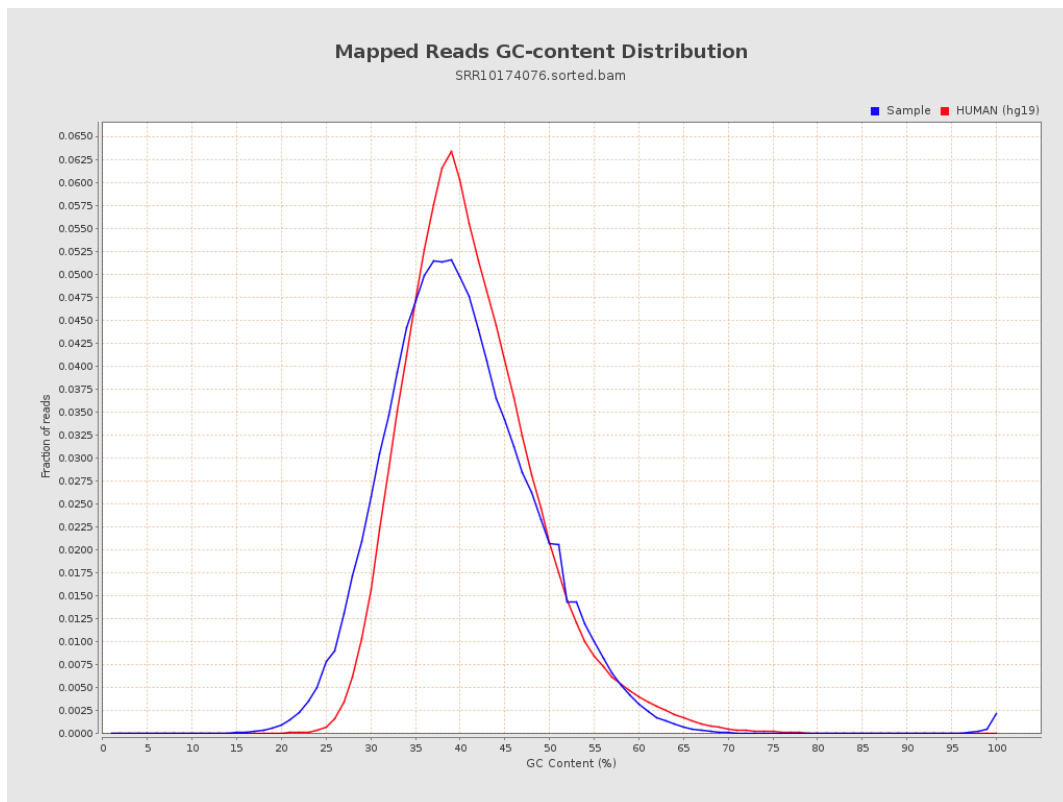
7. Results : Duplication Rate Histogram



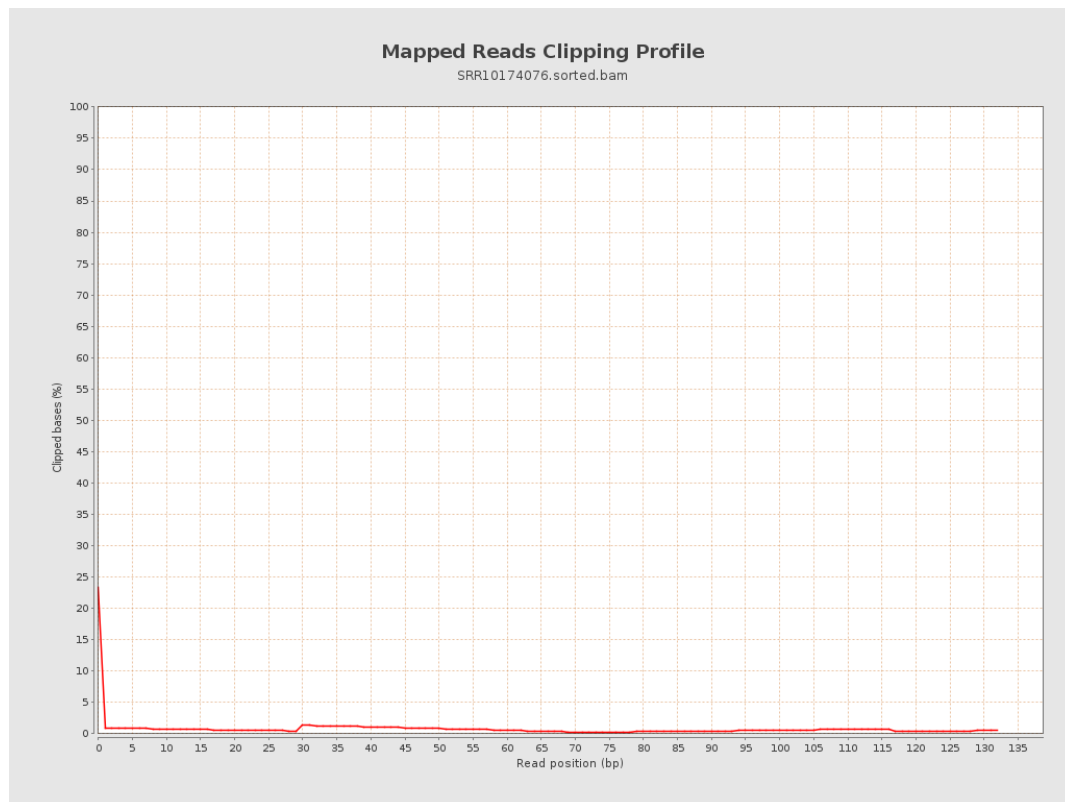
8. Results : Mapped Reads Nucleotide Content



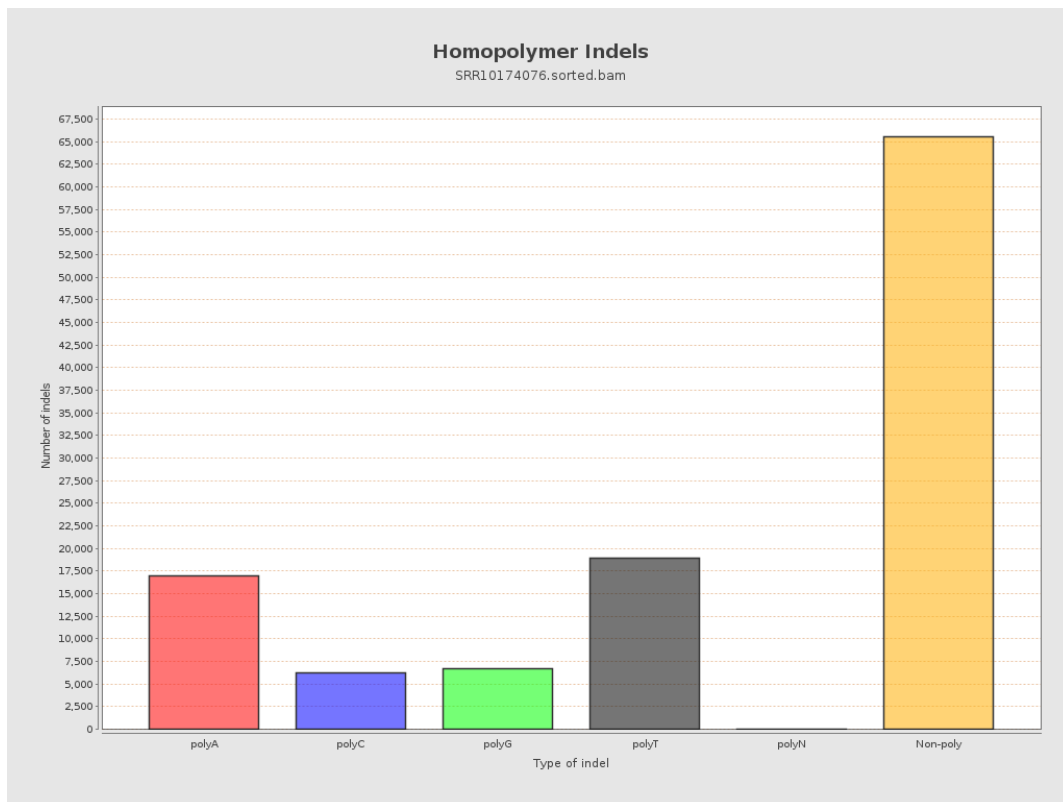
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



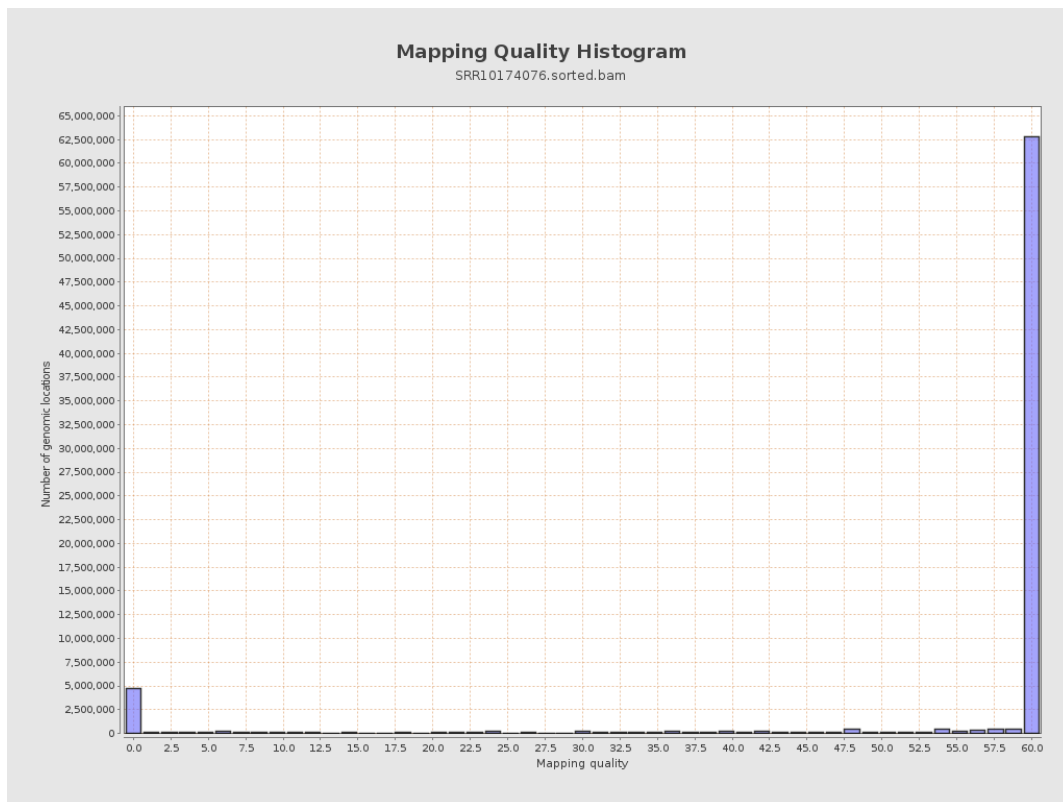
11. Results : Homopolymer Indels



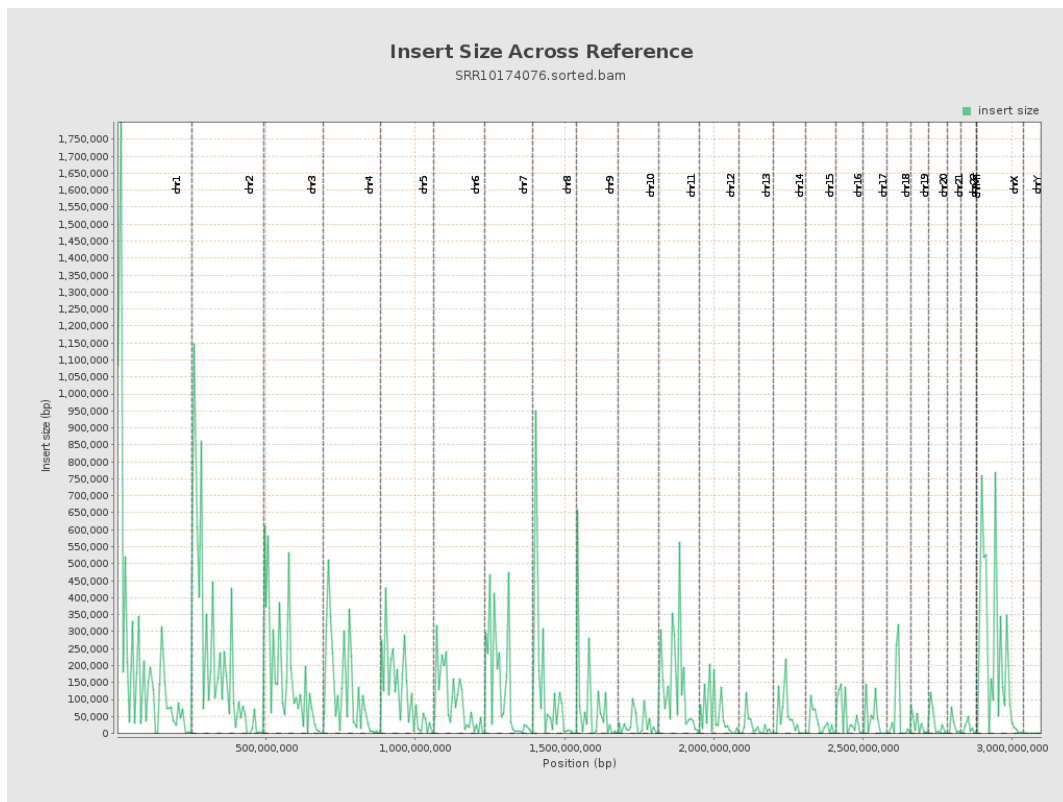
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

