

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 14:13:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006021.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_SRR1006021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006021_1.fastq.gz SRR1006021_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 14:13:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,777,998
Mapped reads	6,445,306 / 73.43%
Unmapped reads	2,332,692 / 26.57%
Mapped paired reads	6,445,306 / 73.43%
Mapped reads, first in pair	3,247,568 / 37%
Mapped reads, second in pair	3,197,738 / 36.43%
Mapped reads, both in pair	5,742,188 / 65.42%
Mapped reads, singletons	703,118 / 8.01%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	189,724 / 2.16%
Duplication rate	2.42%
Clipped reads	506,889 / 5.77%

2.2. ACGT Content

Number/percentage of A's	72,743,591 / 29.21%
Number/percentage of C's	51,310,191 / 20.61%
Number/percentage of T's	72,791,186 / 29.23%
Number/percentage of G's	52,123,222 / 20.93%
Number/percentage of N's	32,098 / 0.01%
GC Percentage	41.54%

2.3. Coverage

Mean	0.0804
Standard Deviation	0.4531

2.4. Mapping Quality

Mean Mapping Quality	47.25
----------------------	-------

2.5. Insert size

Mean	65,943.75
Standard Deviation	2,451,003.89
P25/Median/P75	64 / 90 / 131

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	1,528,791
Insertions	7,607
Mapped reads with at least one insertion	0.12%
Deletions	22,382
Mapped reads with at least one deletion	0.35%
Homopolymer indels	45.73%

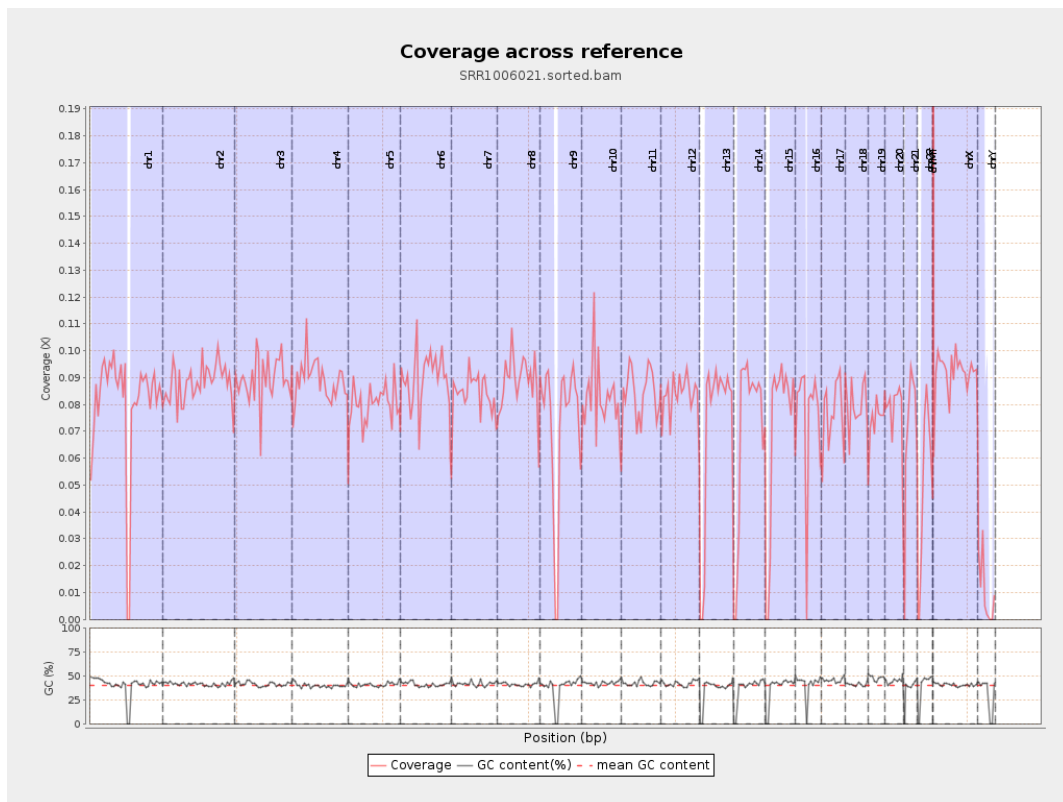
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

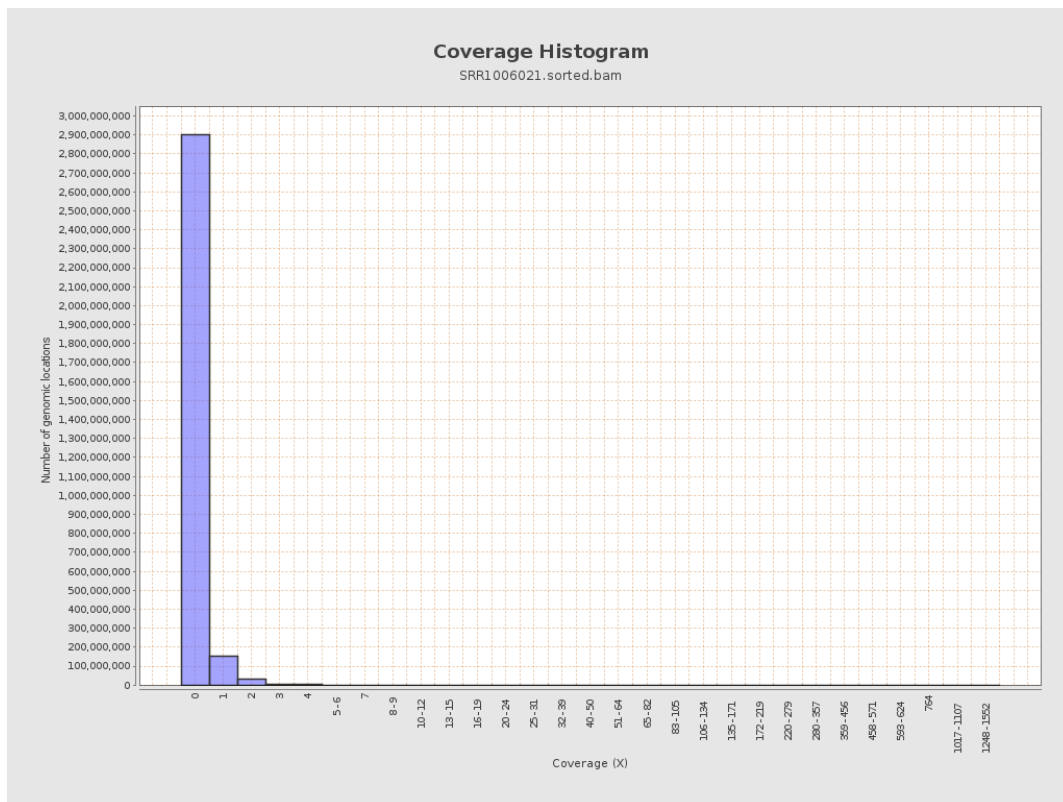
chr1	249250621	20090731	0.0806	0.6142
chr2	243199373	21439261	0.0882	0.4436
chr3	198022430	17704785	0.0894	0.3644
chr4	191154276	16989121	0.0889	0.3879
chr5	180915260	14486299	0.0801	0.343
chr6	171115067	15401719	0.09	0.4685
chr7	159138663	13340183	0.0838	0.4894
chr8	146364022	12957873	0.0885	0.8492
chr9	141213431	10259176	0.0727	0.3754
chr10	135534747	11195762	0.0826	0.5019
chr11	135006516	11358834	0.0841	0.4053
chr12	133851895	11159474	0.0834	0.3526
chr13	115169878	8316137	0.0722	0.3262
chr14	107349540	7720162	0.0719	0.3434
chr15	102531392	7184536	0.0701	0.3222
chr16	90354753	6703285	0.0742	0.3817
chr17	81195210	6242290	0.0769	0.357
chr18	78077248	6229695	0.0798	0.5386
chr19	59128983	4420416	0.0748	0.514
chr20	63025520	4968054	0.0788	0.3523
chr21	48129895	3391877	0.0705	0.3521
chr22	51304566	2608922	0.0509	0.2775
chrMT	16571	17186	1.0371	1.2795
chrX	155270560	14240243	0.0917	0.3997

chrY	59373566	602638	0.0101	0.2171
------	----------	--------	--------	--------

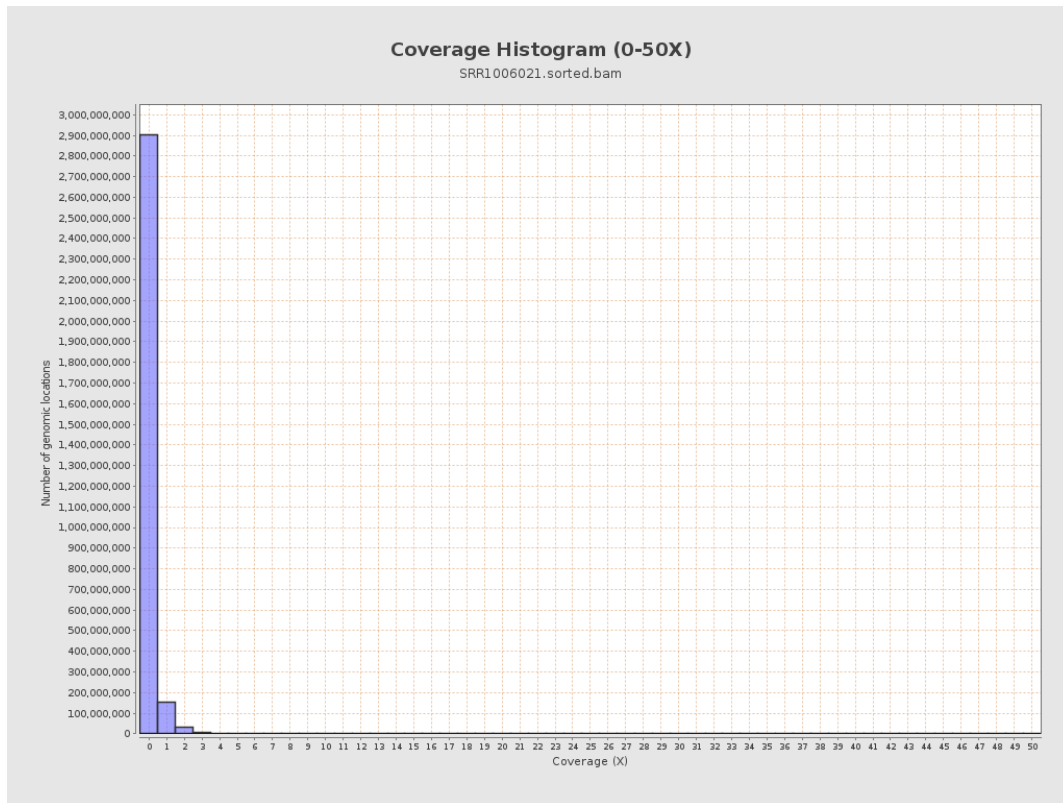
3. Results : Coverage across reference



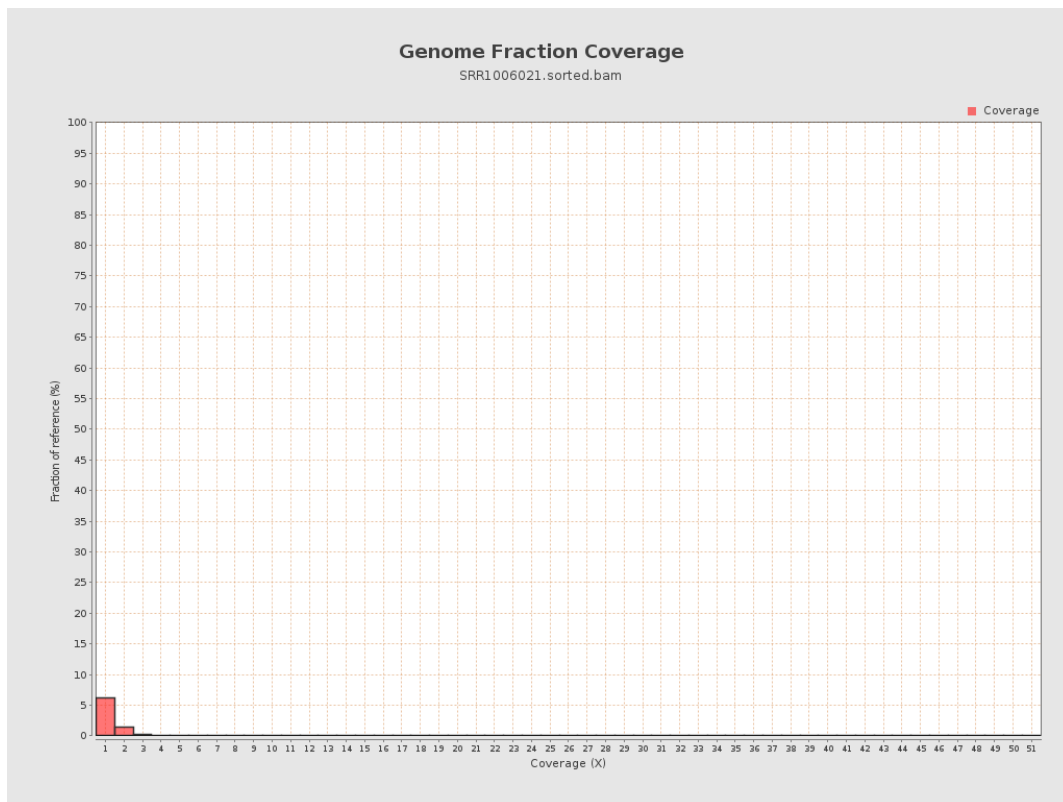
4. Results : Coverage Histogram



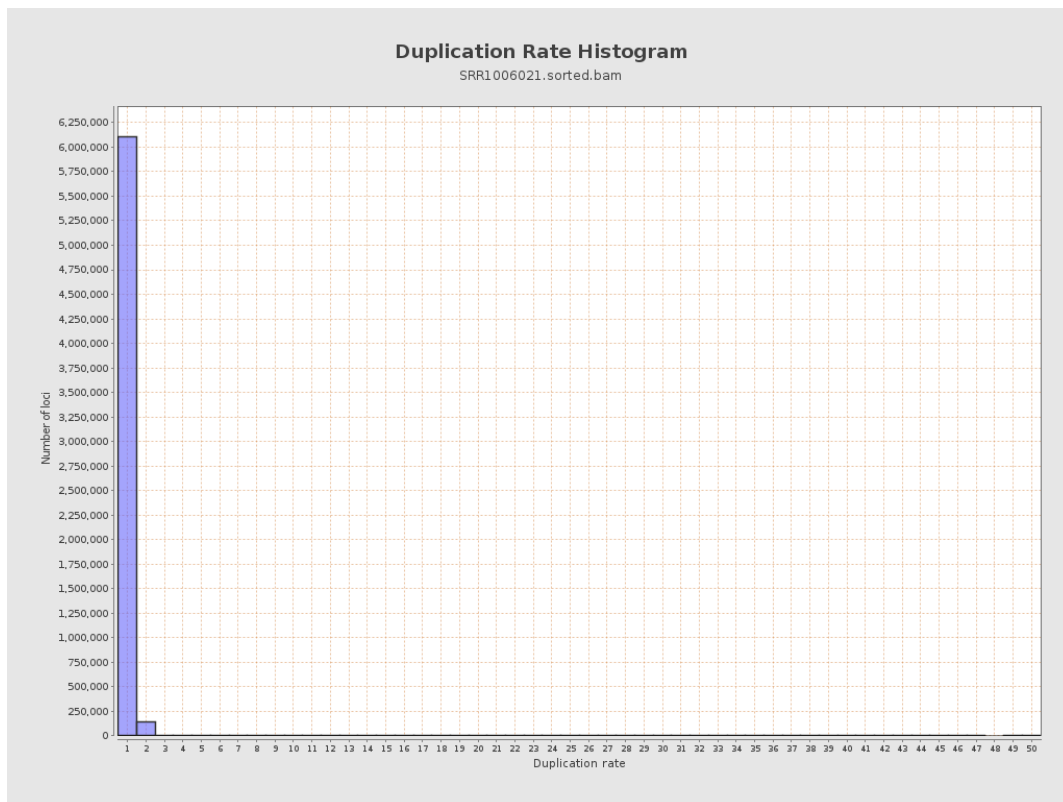
5. Results : Coverage Histogram (0-50X)



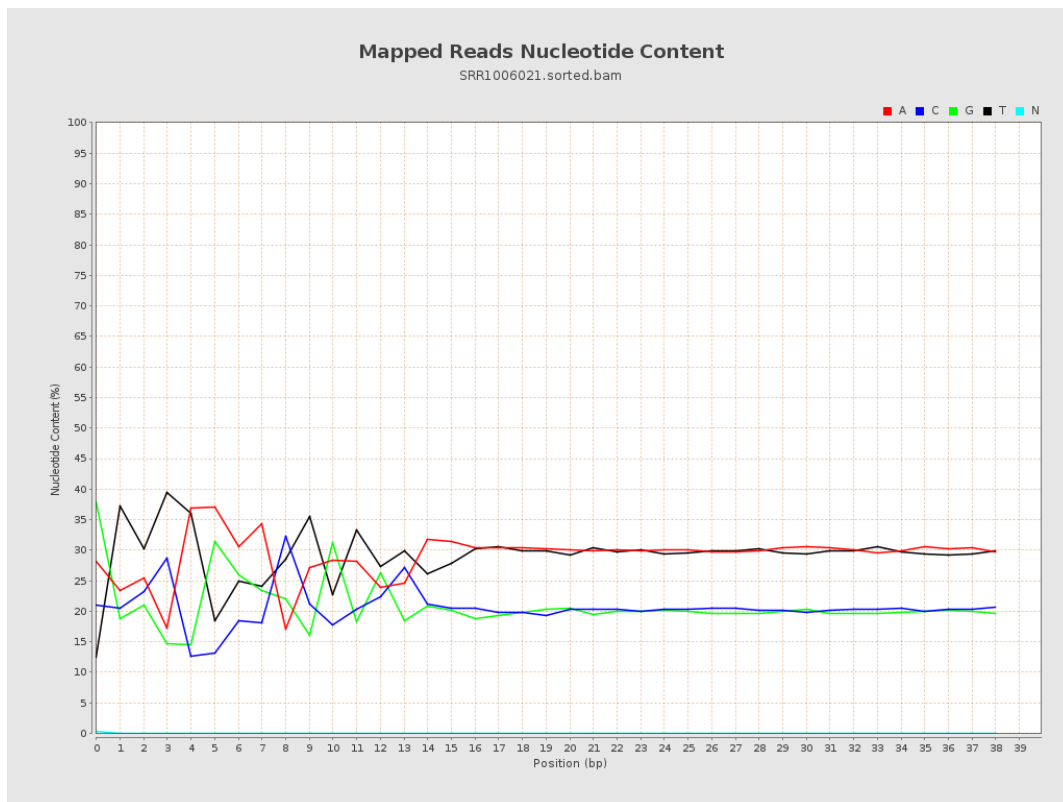
6. Results : Genome Fraction Coverage



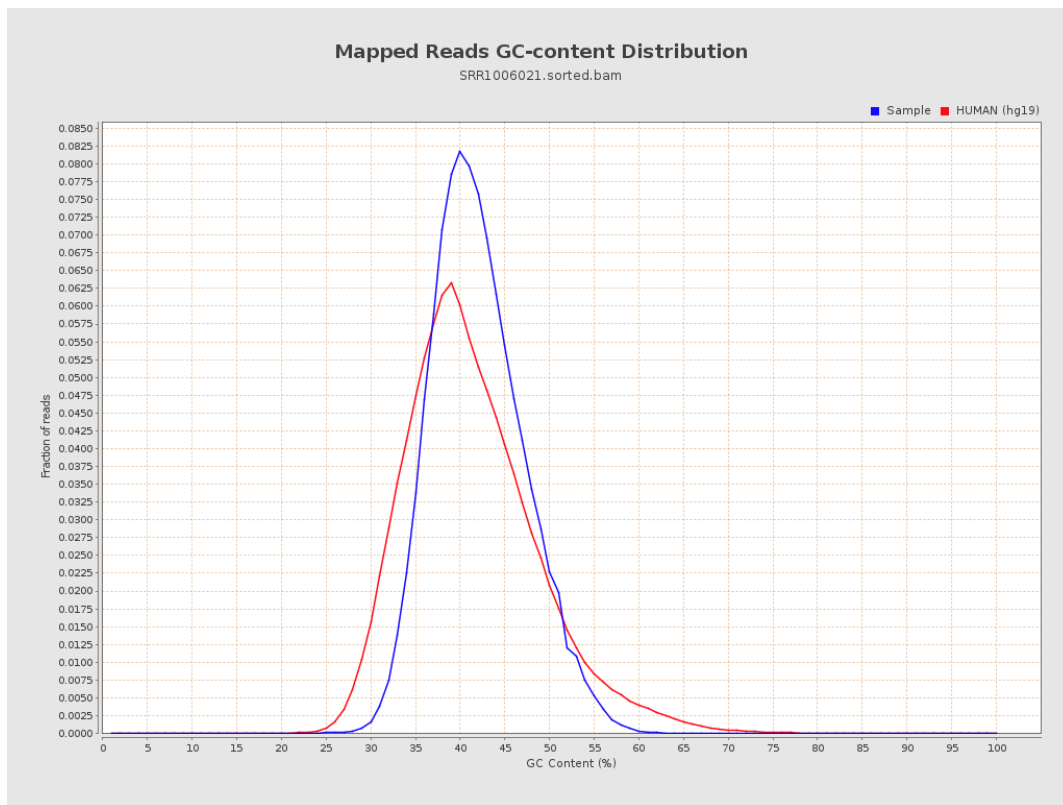
7. Results : Duplication Rate Histogram



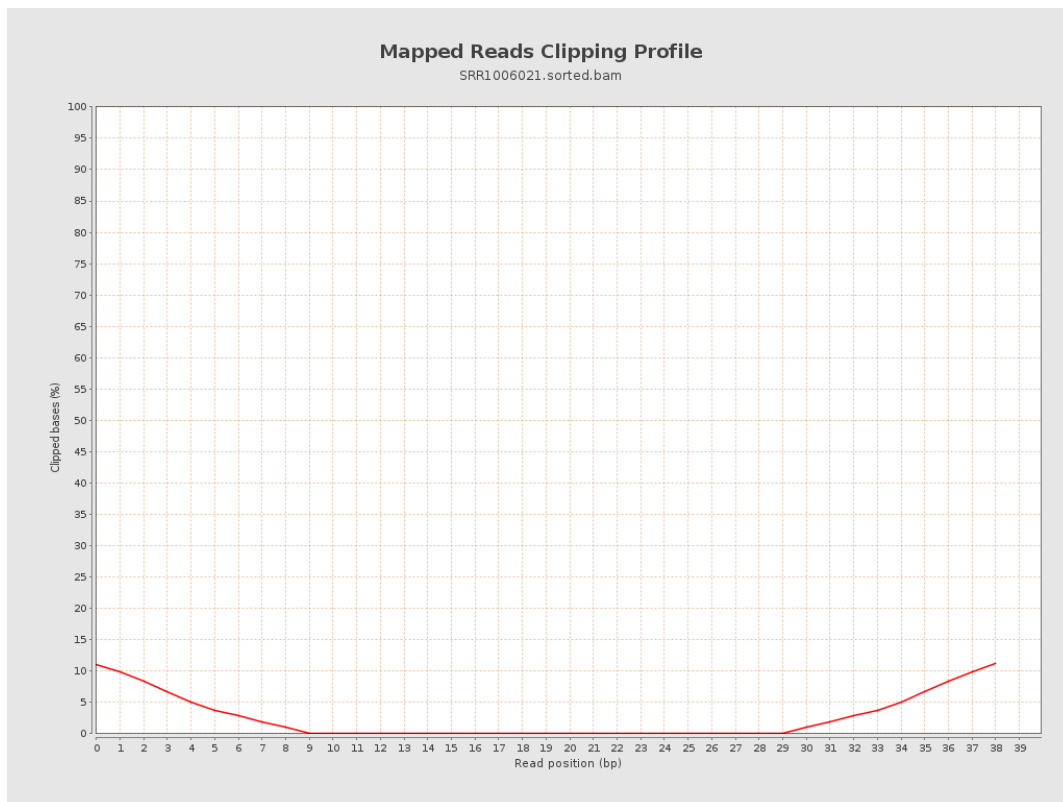
8. Results : Mapped Reads Nucleotide Content



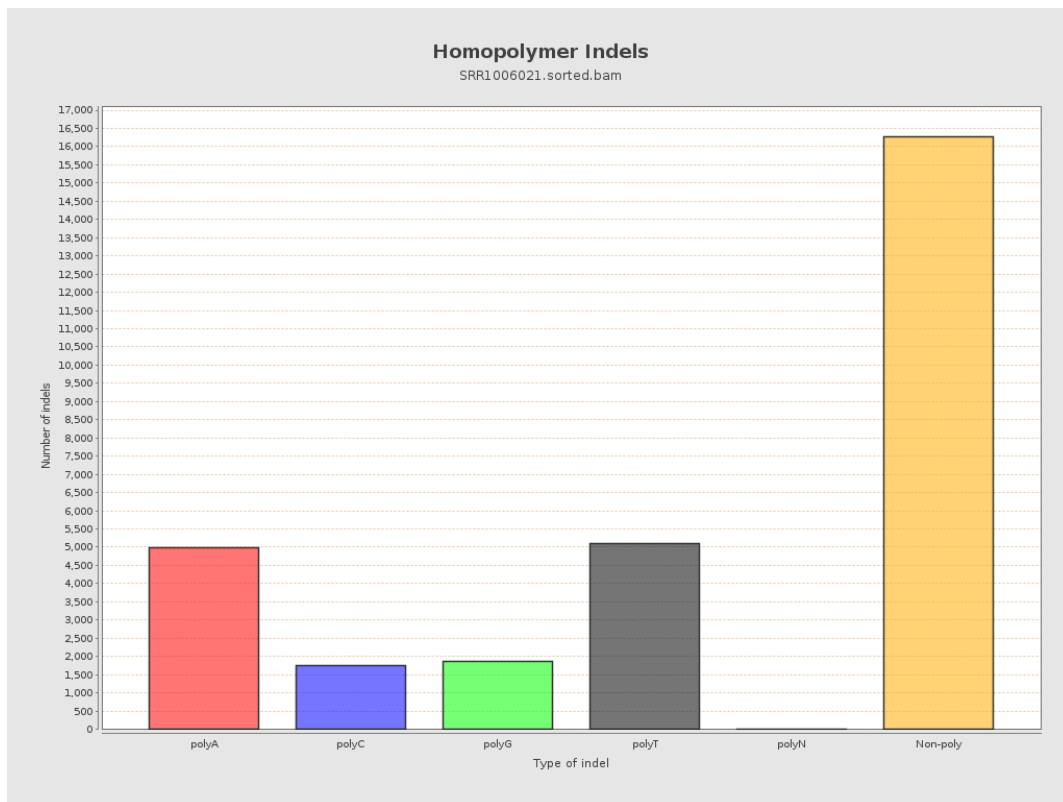
9. Results : Mapped Reads GC-content Distribution



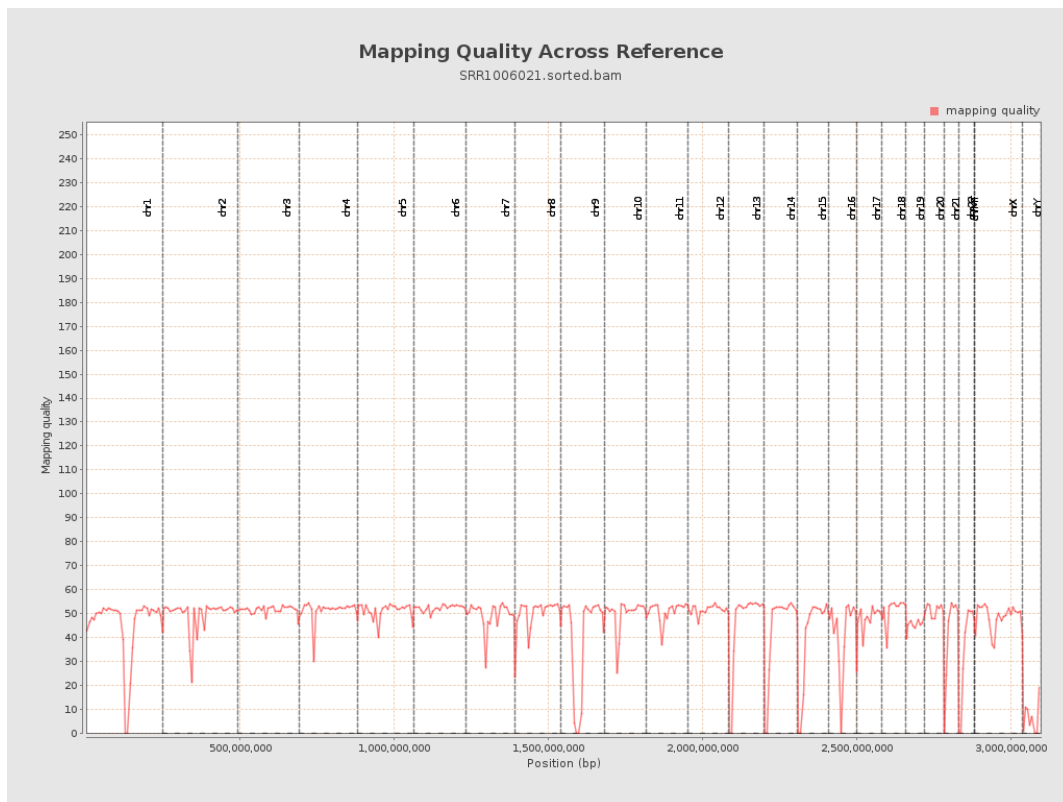
10. Results : Mapped Reads Clipping Profile



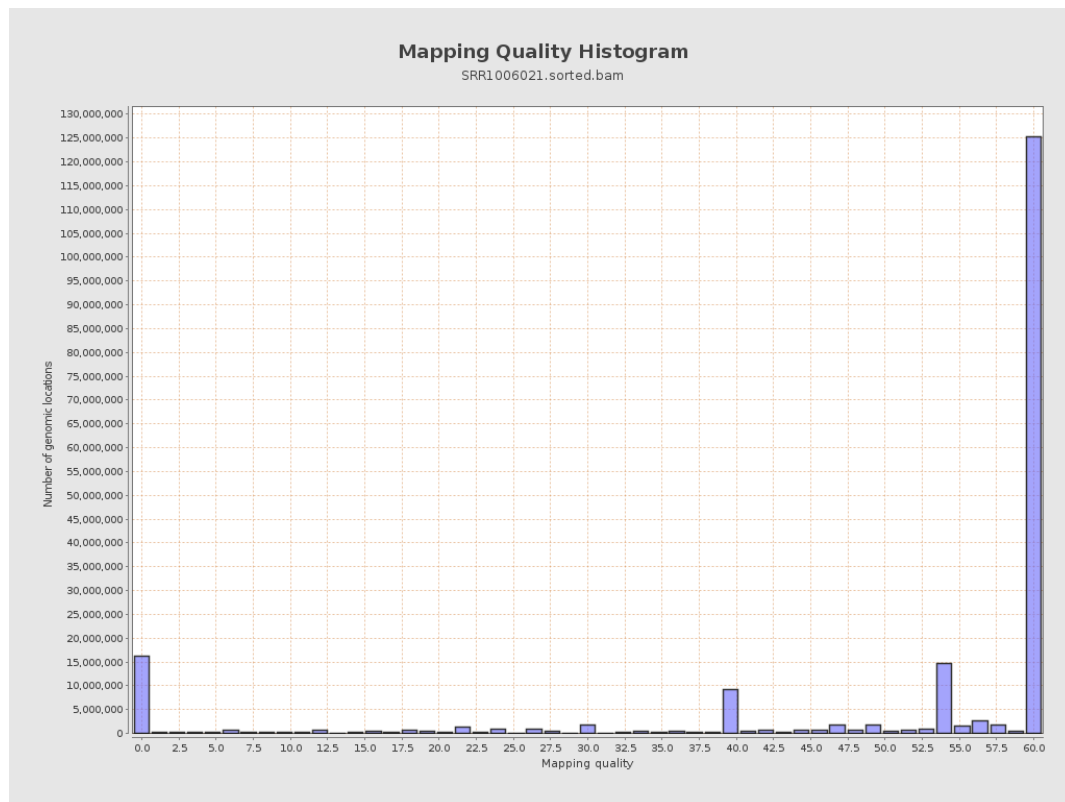
11. Results : Homopolymer Indels



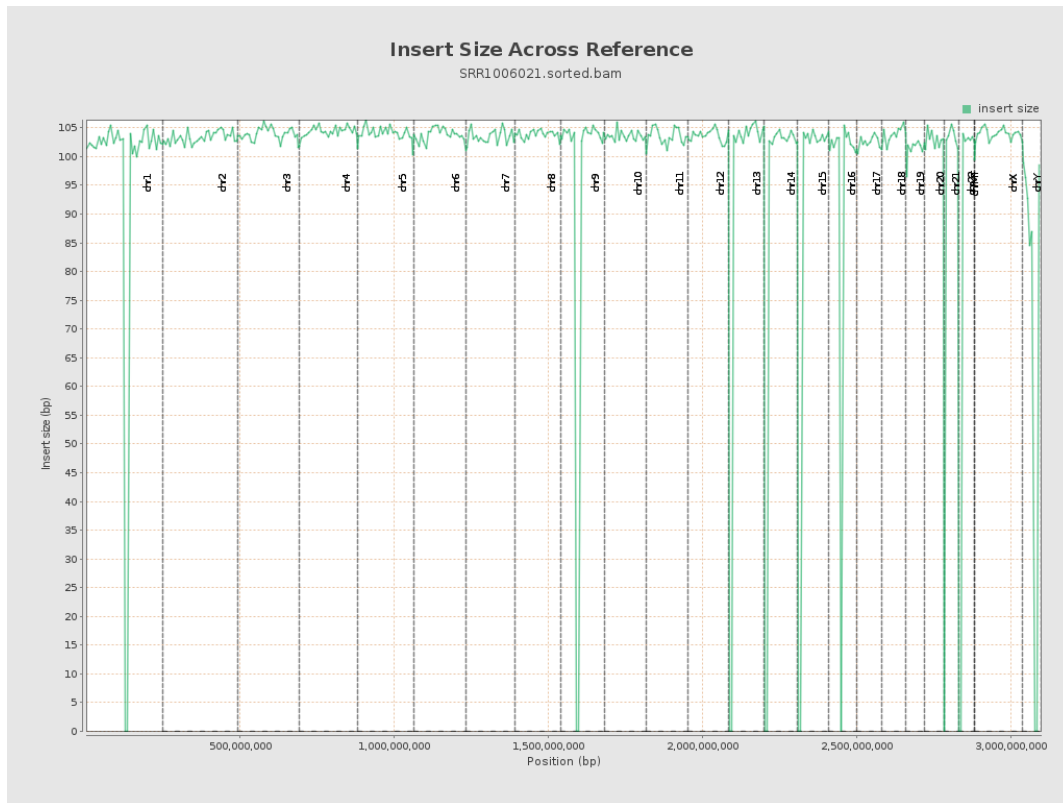
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

