

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:23:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008673.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_SRR6008673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008673.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:23:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,634,916
Mapped reads	1,468,744 / 89.84%
Unmapped reads	166,172 / 10.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,673 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	56,262 / 3.44%
Duplication rate	2.81%
Clipped reads	669,280 / 40.94%

2.2. ACGT Content

Number/percentage of A's	27,128,250 / 27.9%
Number/percentage of C's	18,009,854 / 18.52%
Number/percentage of T's	30,702,484 / 31.58%
Number/percentage of G's	21,250,975 / 21.86%
Number/percentage of N's	139,930 / 0.14%
GC Percentage	40.38%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.3499
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.15
----------------------	-------

2.5. Mismatches and indels

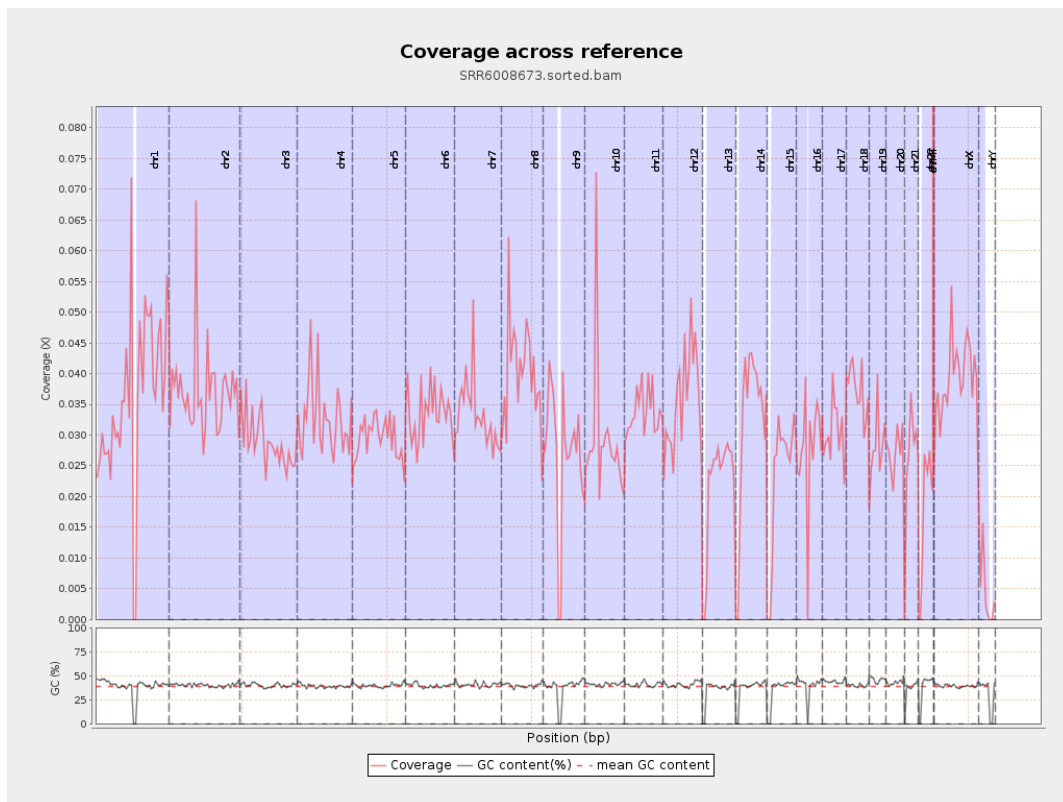
General error rate	0.85%
Mismatches	812,533
Insertions	7,134
Mapped reads with at least one insertion	0.48%
Deletions	27,743
Mapped reads with at least one deletion	1.87%
Homopolymer indels	46.35%

2.6. Chromosome stats

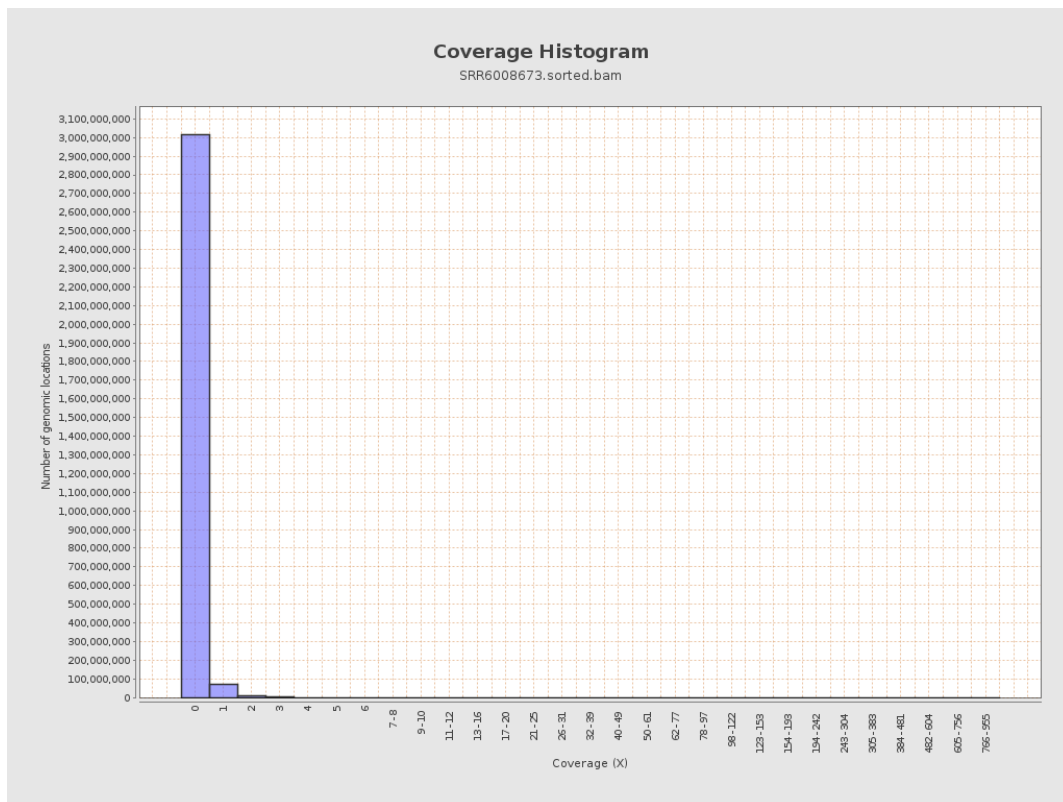
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8959624	0.0359	0.7133
chr2	243199373	8989362	0.037	0.3571
chr3	198022430	5727164	0.0289	0.2008
chr4	191154276	6228028	0.0326	0.214
chr5	180915260	5342944	0.0295	0.1961
chr6	171115067	5729899	0.0335	0.2388
chr7	159138663	5320306	0.0334	0.3418

chr8	146364022	5836184	0.0399	0.6056
chr9	141213431	3861804	0.0273	0.2681
chr10	135534747	3943142	0.0291	0.4144
chr11	135006516	4544509	0.0337	0.2602
chr12	133851895	4799362	0.0359	0.2184
chr13	115169878	2477934	0.0215	0.1657
chr14	107349540	3418886	0.0318	0.2156
chr15	102531392	2389969	0.0233	0.1736
chr16	90354753	2495062	0.0276	0.2253
chr17	81195210	2430836	0.0299	0.2172
chr18	78077248	2920317	0.0374	0.4849
chr19	59128983	1680309	0.0284	0.467
chr20	63025520	1686096	0.0268	0.1931
chr21	48129895	1264255	0.0263	0.1965
chr22	51304566	889990	0.0173	0.1466
chrMT	16571	5949	0.359	0.6507
chrX	155270560	6071943	0.0391	0.2438
chrY	59373566	266333	0.0045	0.1249

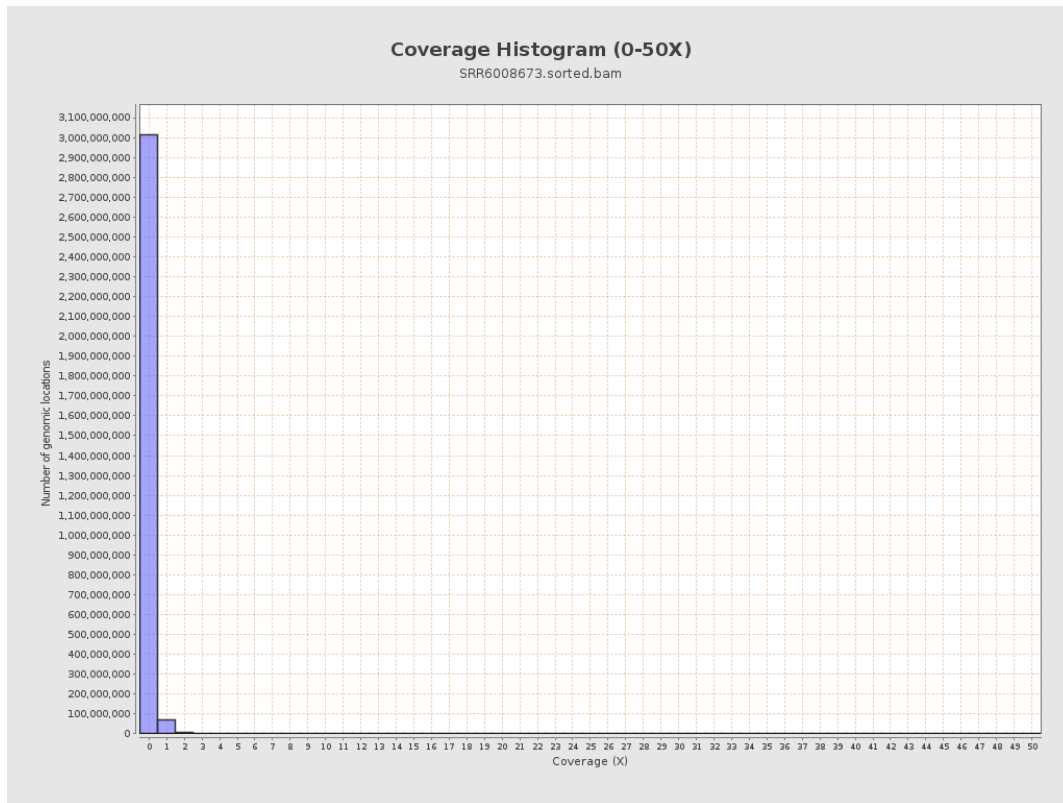
3. Results : Coverage across reference



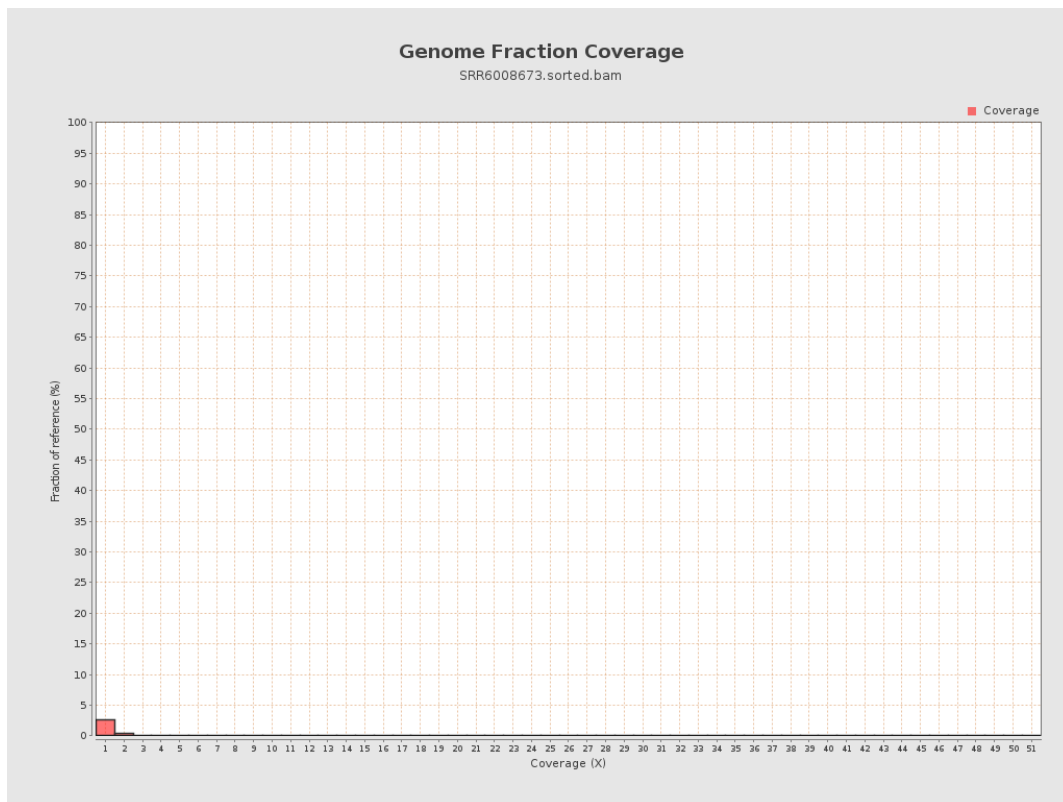
4. Results : Coverage Histogram



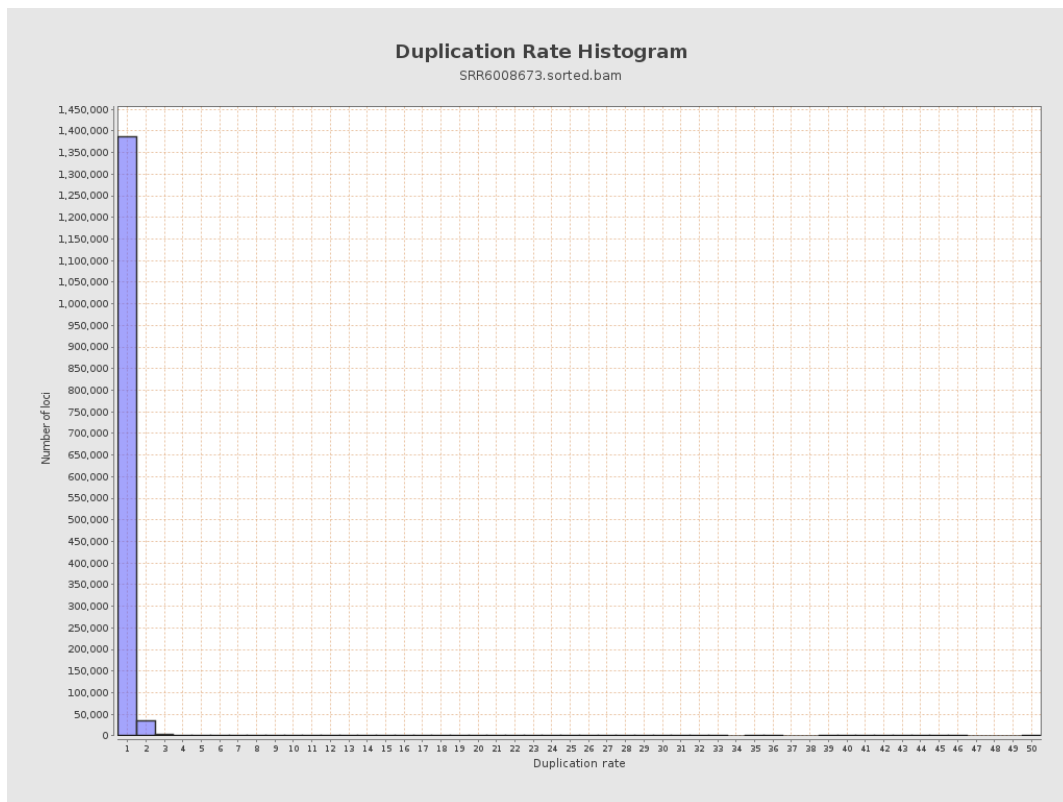
5. Results : Coverage Histogram (0-50X)



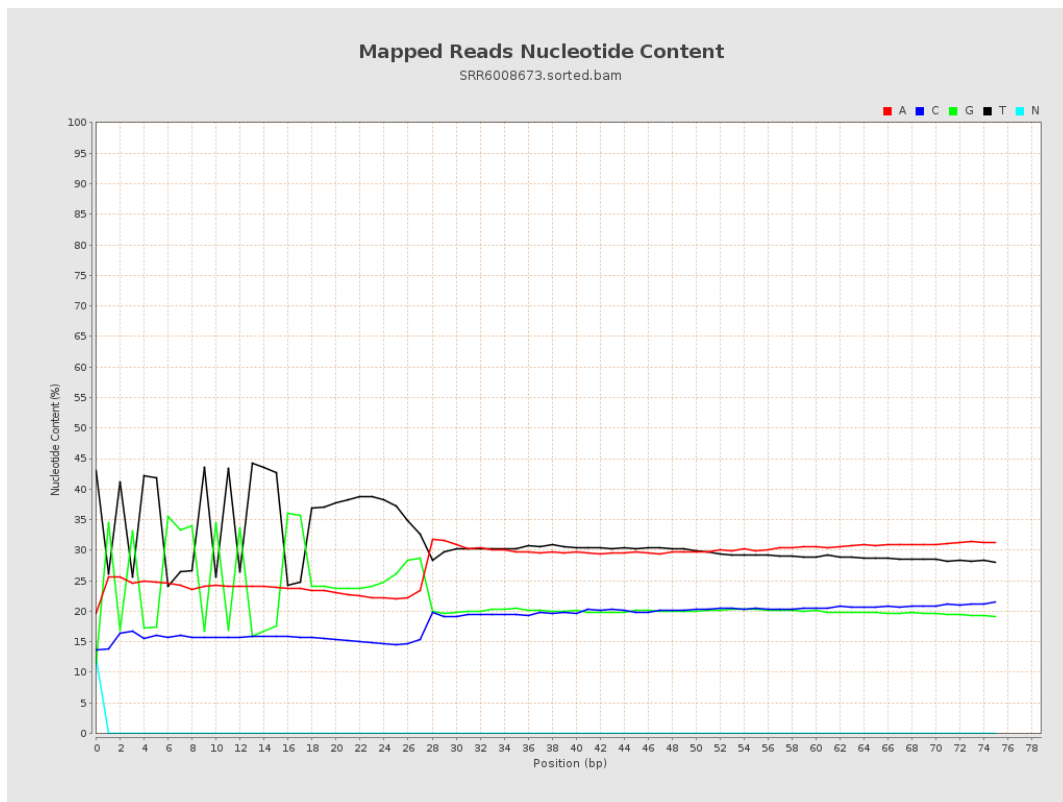
6. Results : Genome Fraction Coverage



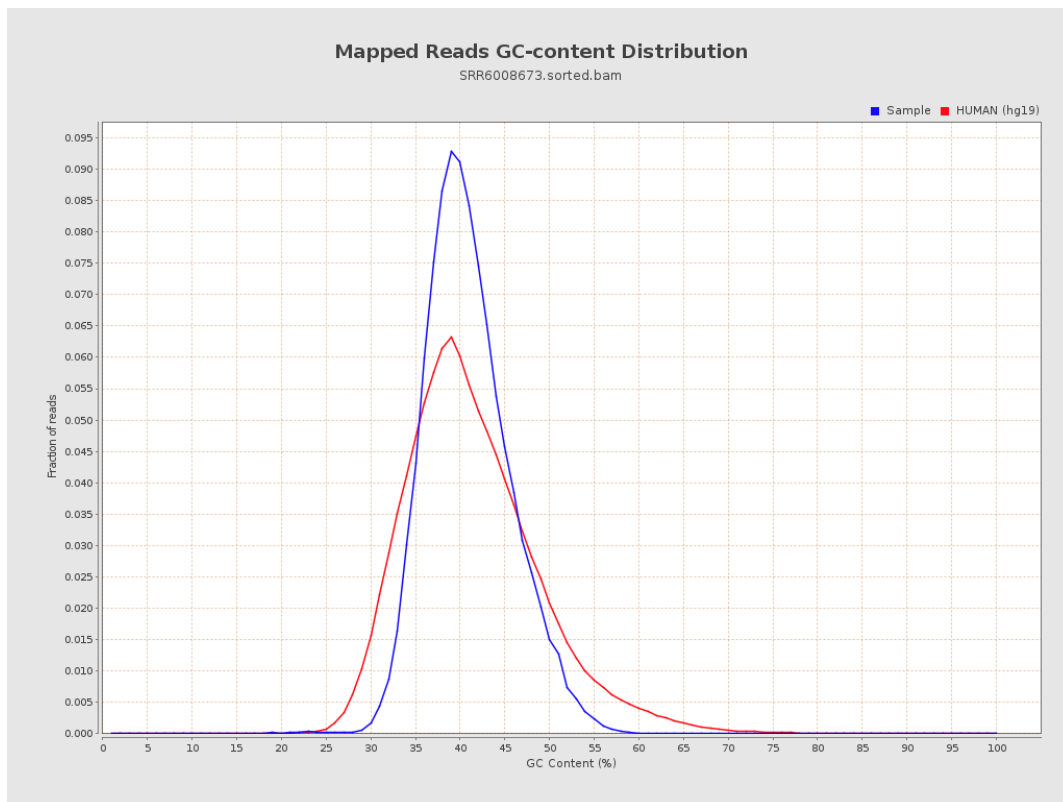
7. Results : Duplication Rate Histogram



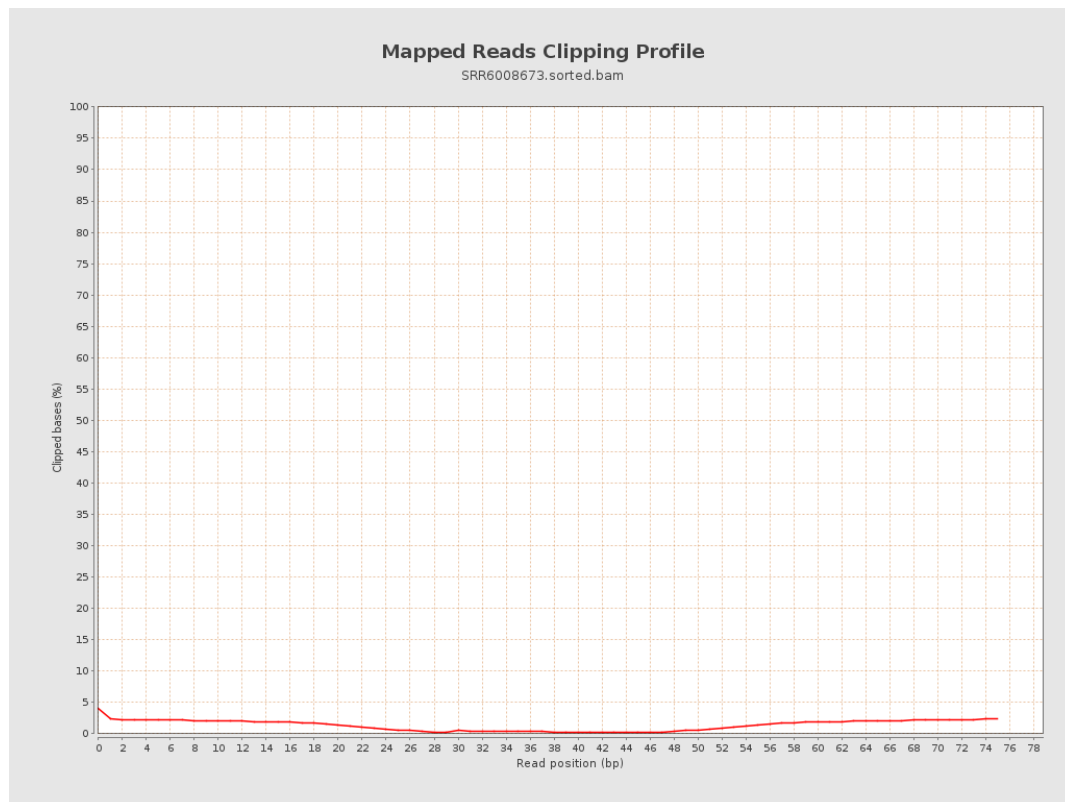
8. Results : Mapped Reads Nucleotide Content



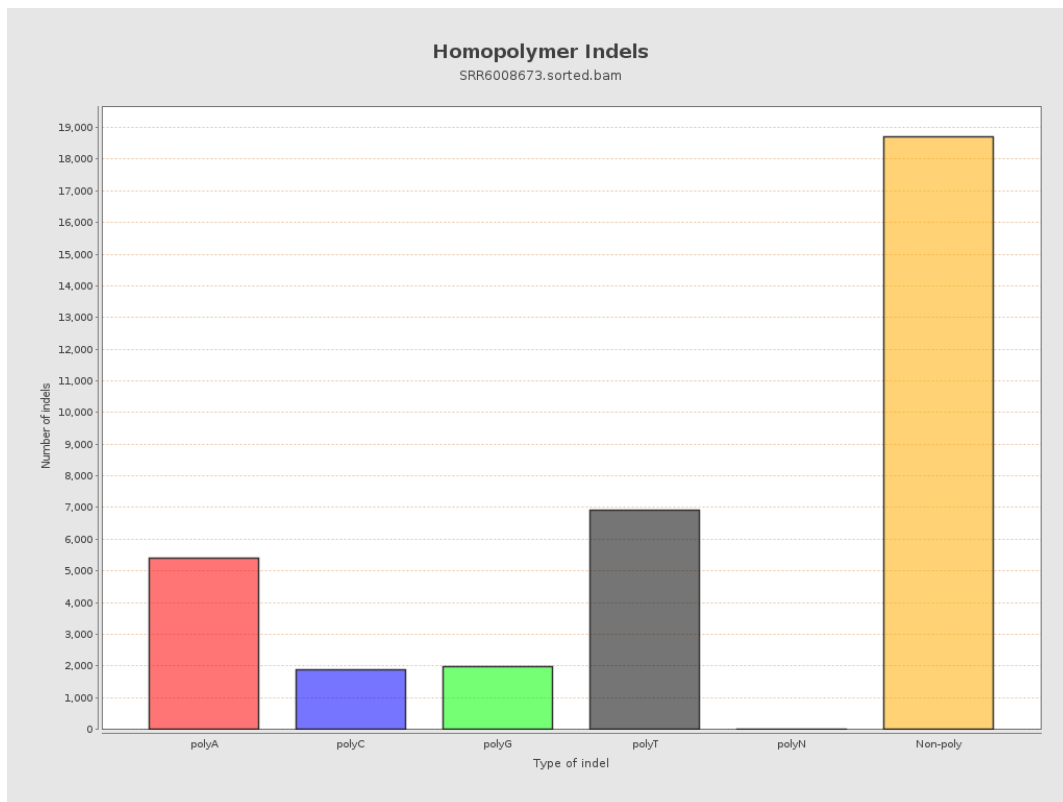
9. Results : Mapped Reads GC-content Distribution



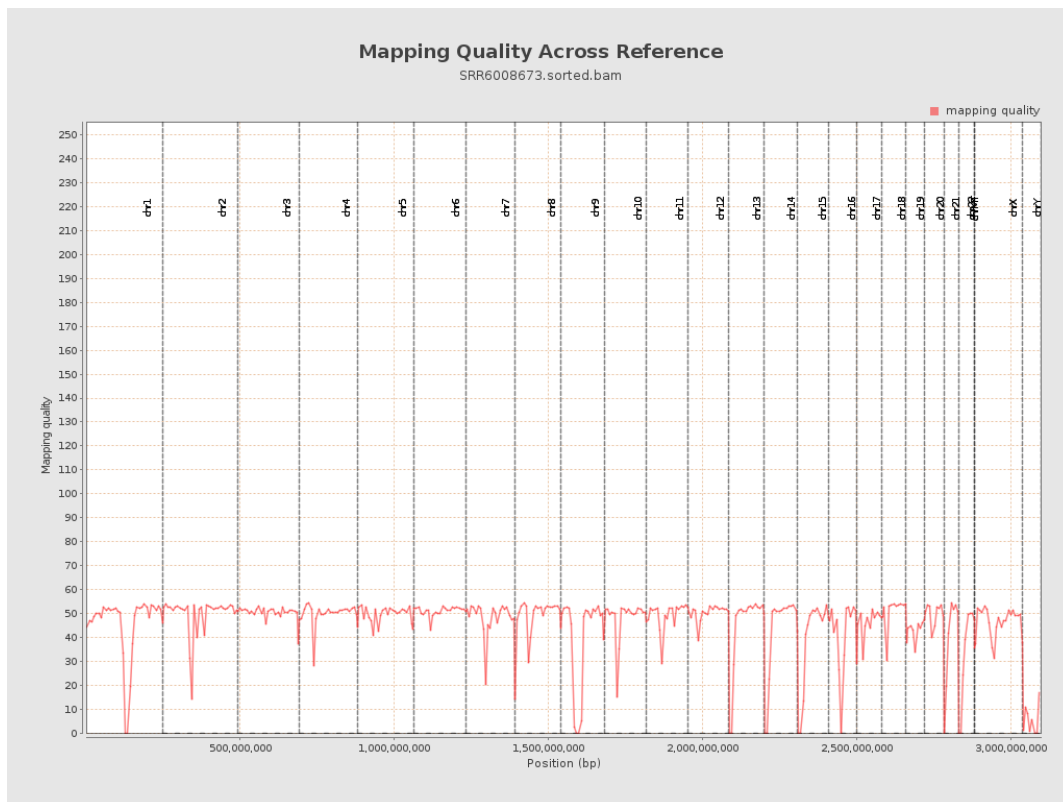
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

