

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 18:16:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751195.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_SRR8751195 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751195.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 18:16:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751195.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,572,050
Mapped reads	4,496,240 / 98.34%
Unmapped reads	75,810 / 1.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	83,660 / 1.83%
Read min/max/mean length	30 / 101 / 101.76
Duplicated reads (estimated)	62,965 / 1.38%
Duplication rate	1.24%
Clipped reads	569,490 / 12.46%

2.2. ACGT Content

Number/percentage of A's	131,181,693 / 29.48%
Number/percentage of C's	91,434,179 / 20.55%
Number/percentage of T's	132,039,952 / 29.68%
Number/percentage of G's	90,260,990 / 20.29%
Number/percentage of N's	2,508 / 0%
GC Percentage	40.84%

2.3. Coverage

Mean	0.1438

Standard Deviation	0.5055
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	51.77
----------------------	-------

2.5. Mismatches and indels

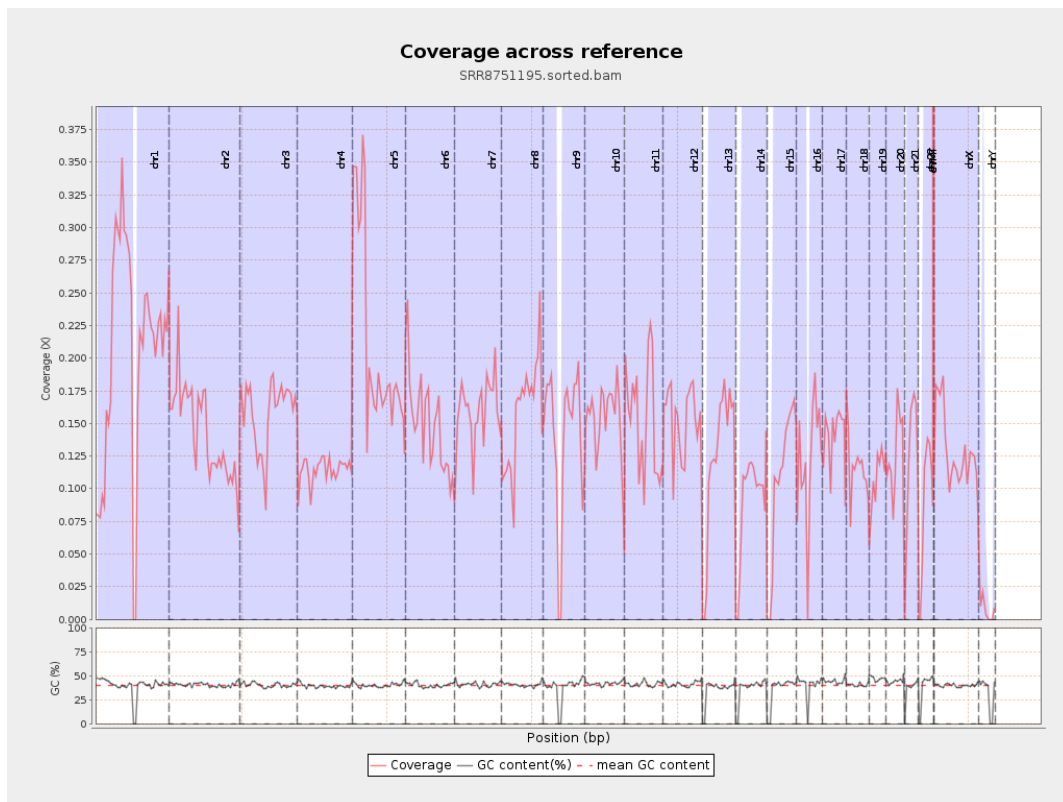
General error rate	0.28%
Mismatches	1,176,792
Insertions	46,822
Mapped reads with at least one insertion	1.03%
Deletions	50,675
Mapped reads with at least one deletion	1.11%
Homopolymer indels	46.19%

2.6. Chromosome stats

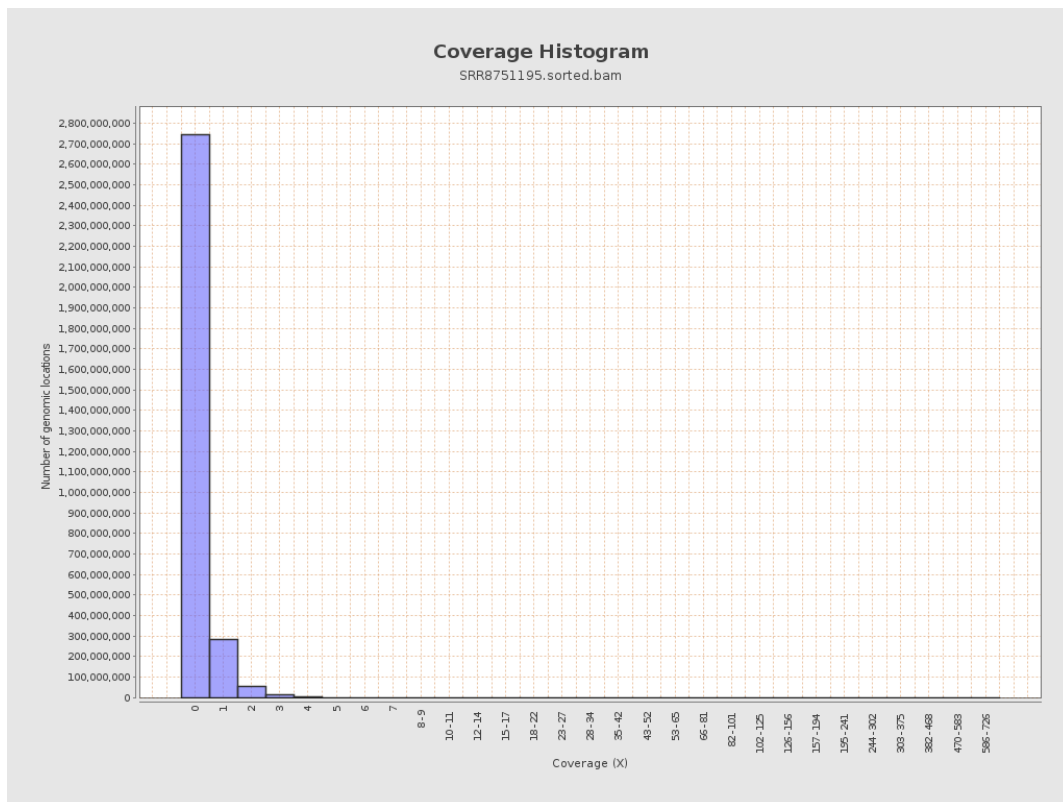
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	51034393	0.2048	0.8511
chr2	243199373	34705196	0.1427	0.4421
chr3	198022430	31298775	0.1581	0.4614
chr4	191154276	21875677	0.1144	0.3912
chr5	180915260	38248346	0.2114	0.5419
chr6	171115067	25533153	0.1492	0.4886
chr7	159138663	25600629	0.1609	0.4708

chr8	146364022	23034068	0.1574	0.4641
chr9	141213431	19854363	0.1406	0.4449
chr10	135534747	21195645	0.1564	0.5355
chr11	135006516	20549920	0.1522	0.4708
chr12	133851895	20477177	0.153	0.4569
chr13	115169878	14103764	0.1225	0.4073
chr14	107349540	9560585	0.0891	0.3463
chr15	102531392	10955637	0.1069	0.3831
chr16	90354753	11048054	0.1223	0.4112
chr17	81195210	11319450	0.1394	0.4713
chr18	78077248	9059199	0.116	0.4509
chr19	59128983	6372469	0.1078	0.5937
chr20	63025520	7835962	0.1243	0.4131
chr21	48129895	5775762	0.12	0.4135
chr22	51304566	4420638	0.0862	0.3466
chrMT	16571	625132	37.7245	19.8334
chrX	155270560	20039125	0.1291	0.4218
chrY	59373566	507236	0.0085	0.1881

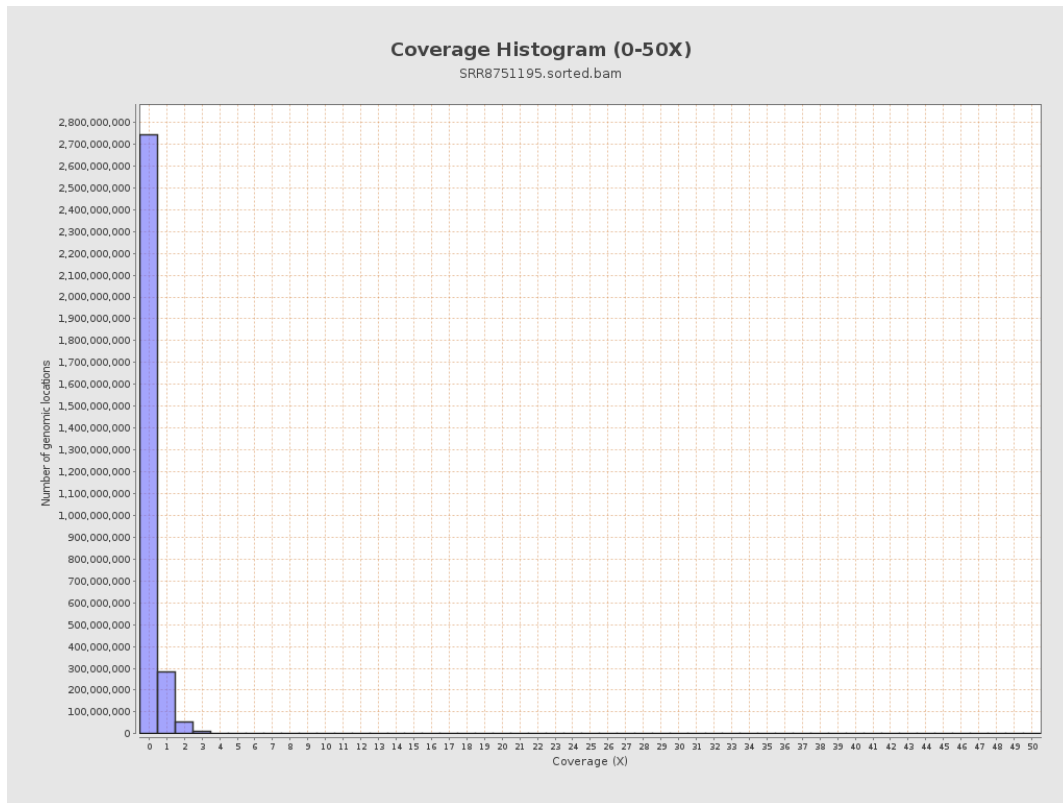
3. Results : Coverage across reference



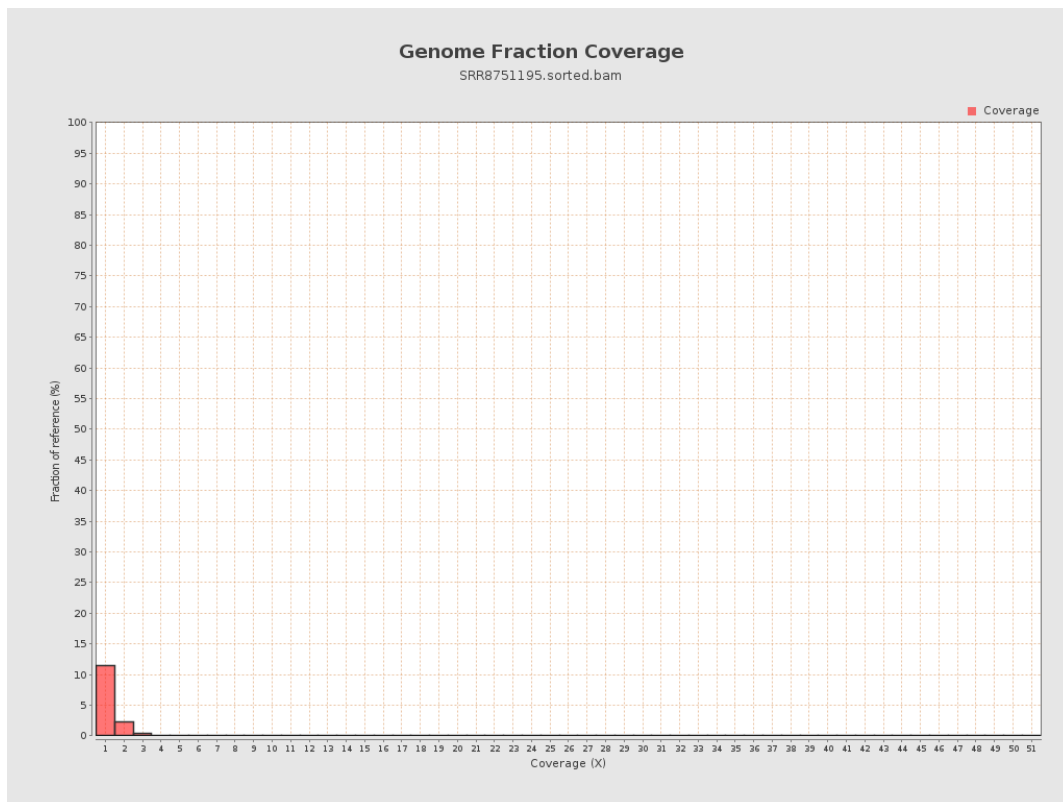
4. Results : Coverage Histogram



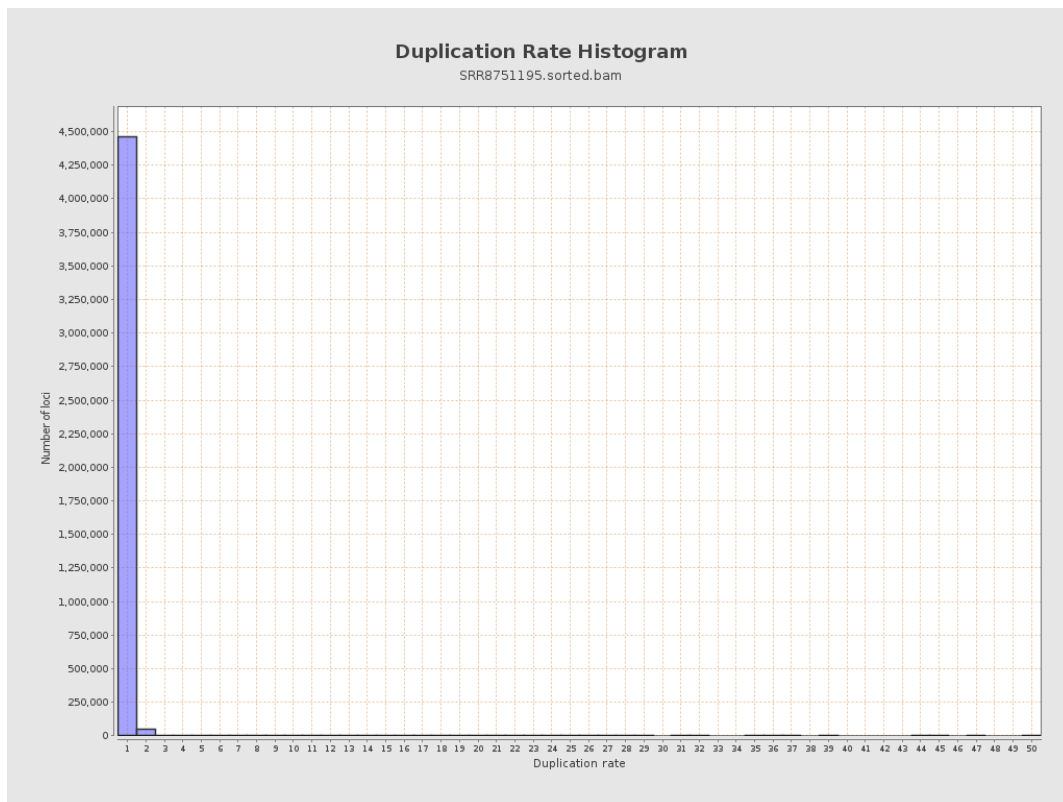
5. Results : Coverage Histogram (0-50X)



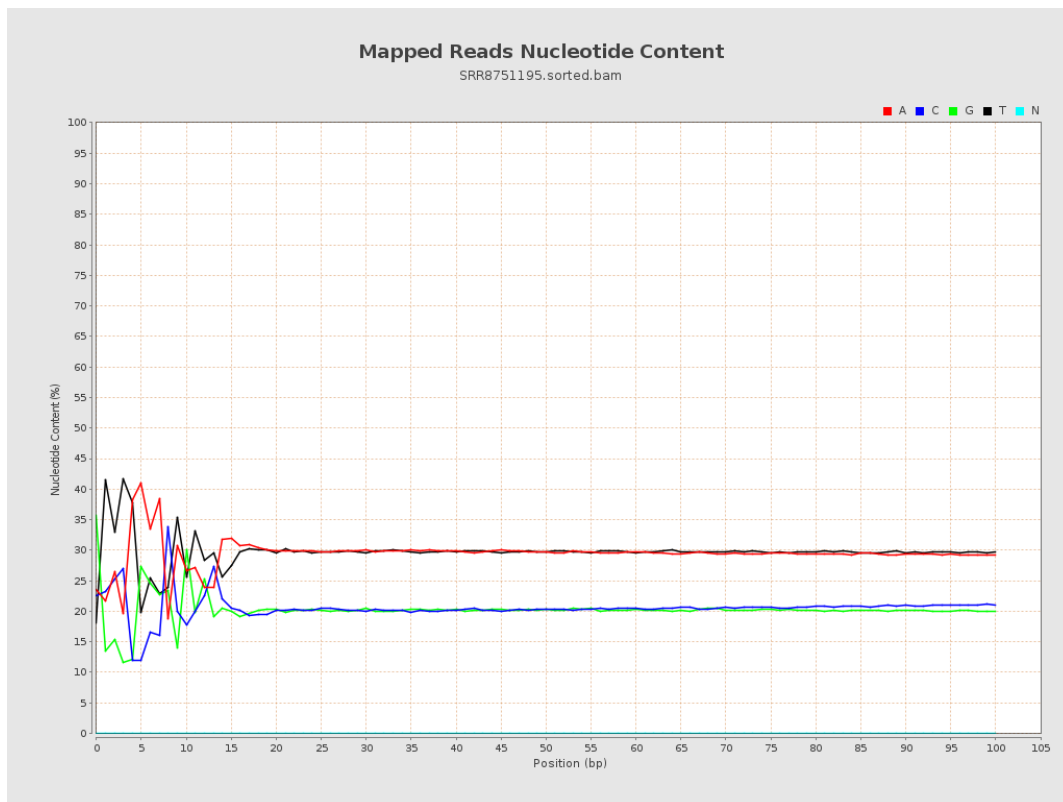
6. Results : Genome Fraction Coverage



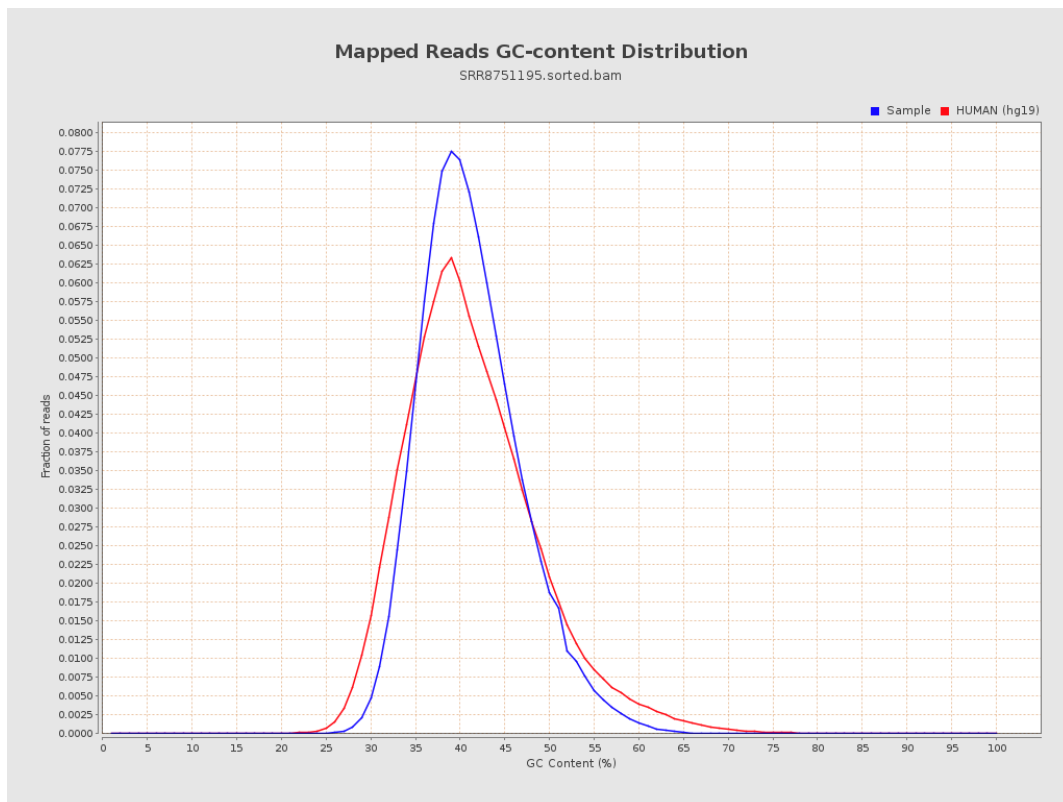
7. Results : Duplication Rate Histogram



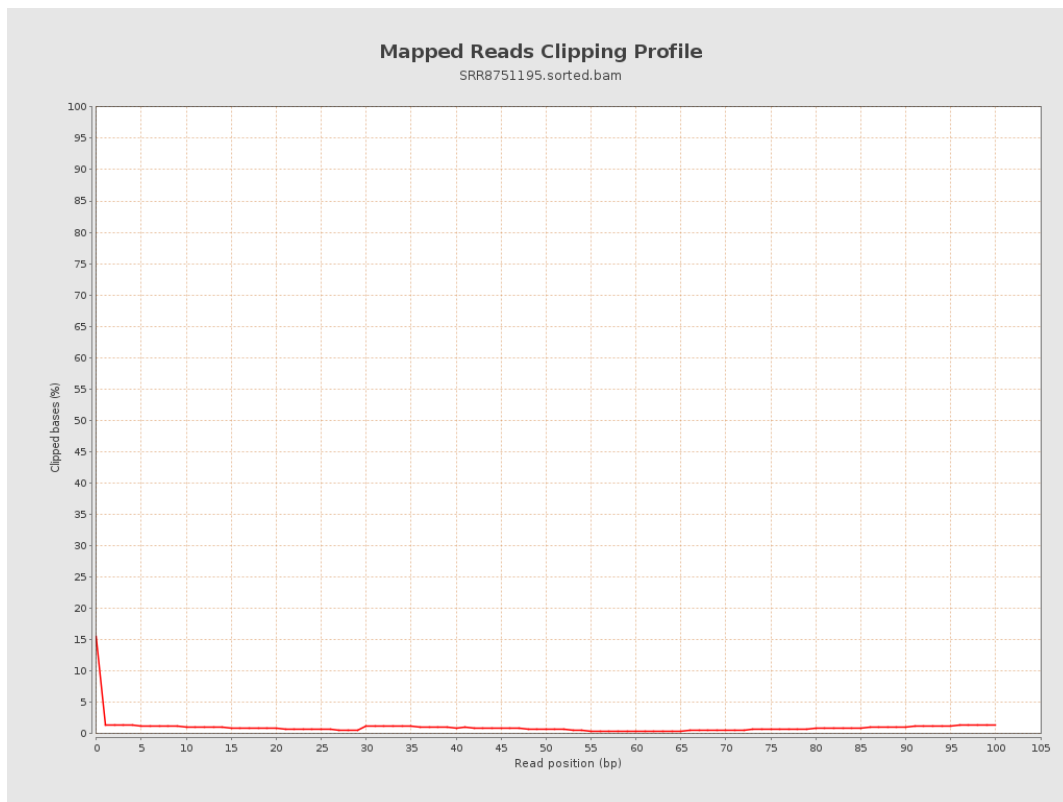
8. Results : Mapped Reads Nucleotide Content



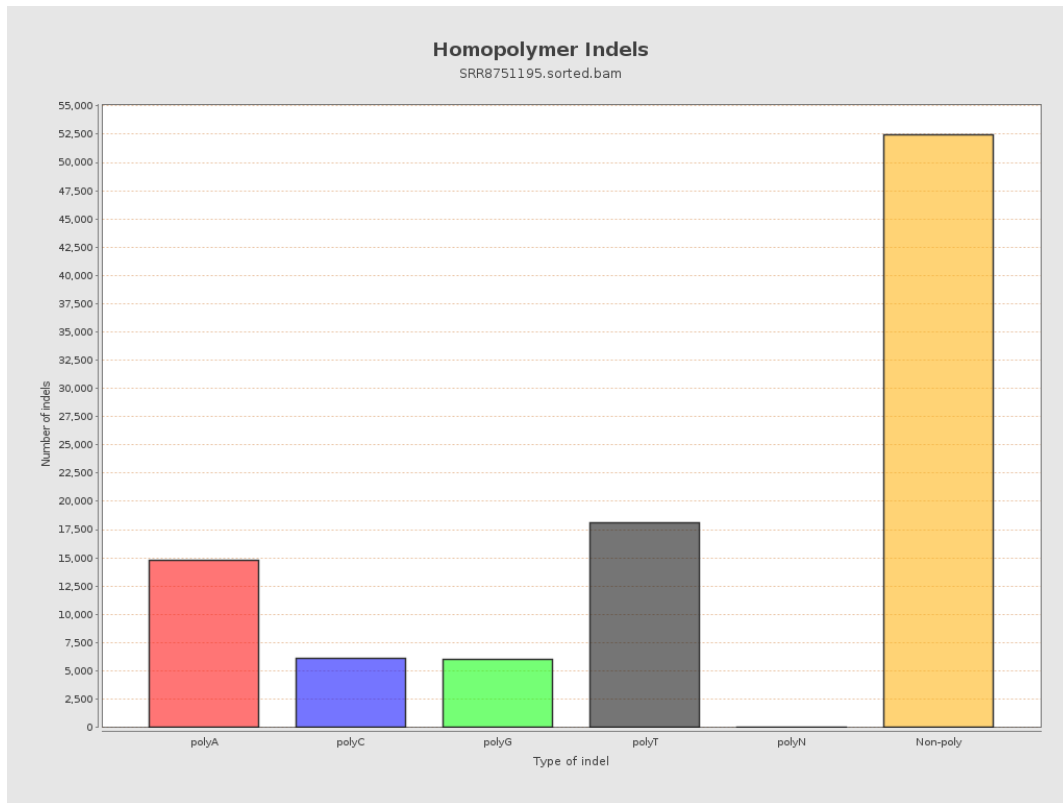
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

