Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 20:10:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089695.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_SRR089695 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089695.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 20:10:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089695.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,811,324
Mapped reads	14,382,590 / 72.6%
Unmapped reads	5,428,734 / 27.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	595 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,124,725 / 5.68%
Duplication rate	5.94%
Clipped reads	2,558,277 / 12.91%

2.2. ACGT Content

Number/percentage of A's	208,414,289 / 31.3%
Number/percentage of C's	136,538,602 / 20.51%
Number/percentage of T's	179,643,918 / 26.98%
Number/percentage of G's	140,918,120 / 21.17%
Number/percentage of N's	291,862 / 0.04%
GC Percentage	41.67%

2.3. Coverage

Mean	0.2151

Standard Deviation	1.146

2.4. Mapping Quality

Mean Mapping Quality	41.72

2.5. Mismatches and indels

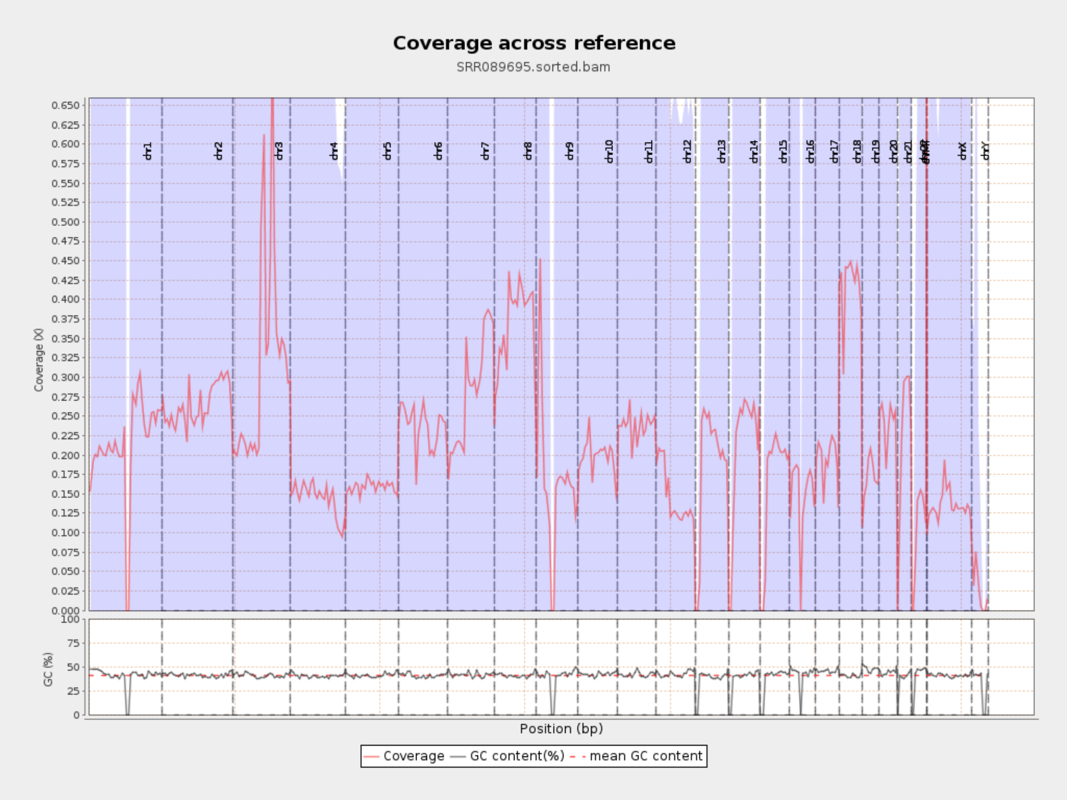
General error rate	0.79%
Mismatches	5,190,346
Insertions	32,513
Mapped reads with at least one insertion	0.23%
Deletions	91,993
Mapped reads with at least one deletion	0.64%
Homopolymer indels	42.96%

2.6. Chromosome stats

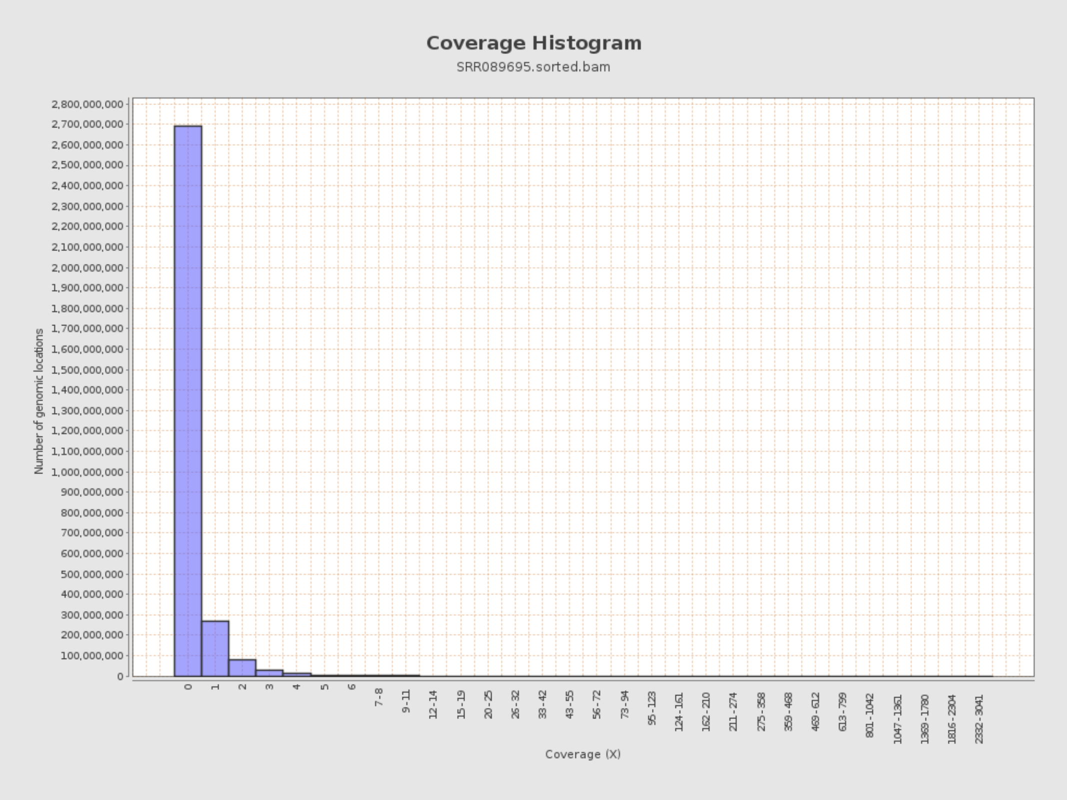
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	53005221	0.2127	1.3077
chr2	243199373	64534542	0.2654	1.7489
chr3	198022430	62781806	0.317	0.9618
chr4	191154276	27467289	0.1437	0.6
chr5	180915260	28792642	0.1591	0.6195
chr6	171115067	40702730	0.2379	0.9256
chr7	159138663	45426500	0.2855	1.8814

chr8	146364022	54440864	0.372	2.0807
chr9	141213431	24024613	0.1701	1.0121
chr10	135534747	27087389	0.1999	1.0233
chr11	135006516	31965889	0.2368	1.0244
chr12	133851895	19345751	0.1445	0.6155
chr13	115169878	21474924	0.1865	0.6818
chr14	107349540	22317299	0.2079	0.7964
chr15	102531392	16866476	0.1645	0.6268
chr16	90354753	13503355	0.1494	0.666
chr17	81195210	15760219	0.1941	0.7759
chr18	78077248	32744867	0.4194	1.5568
chr19	59128983	10240649	0.1732	1.2644
chr20	63025520	15052053	0.2388	0.8071
chr21	48129895	10733424	0.223	0.8327
chr22	51304566	5134722	0.1001	0.4797
chrMT	16571	15306	0.9237	2.2773
chrX	155270560	21003349	0.1353	0.8249
chrY	59373566	1519936	0.0256	0.3494

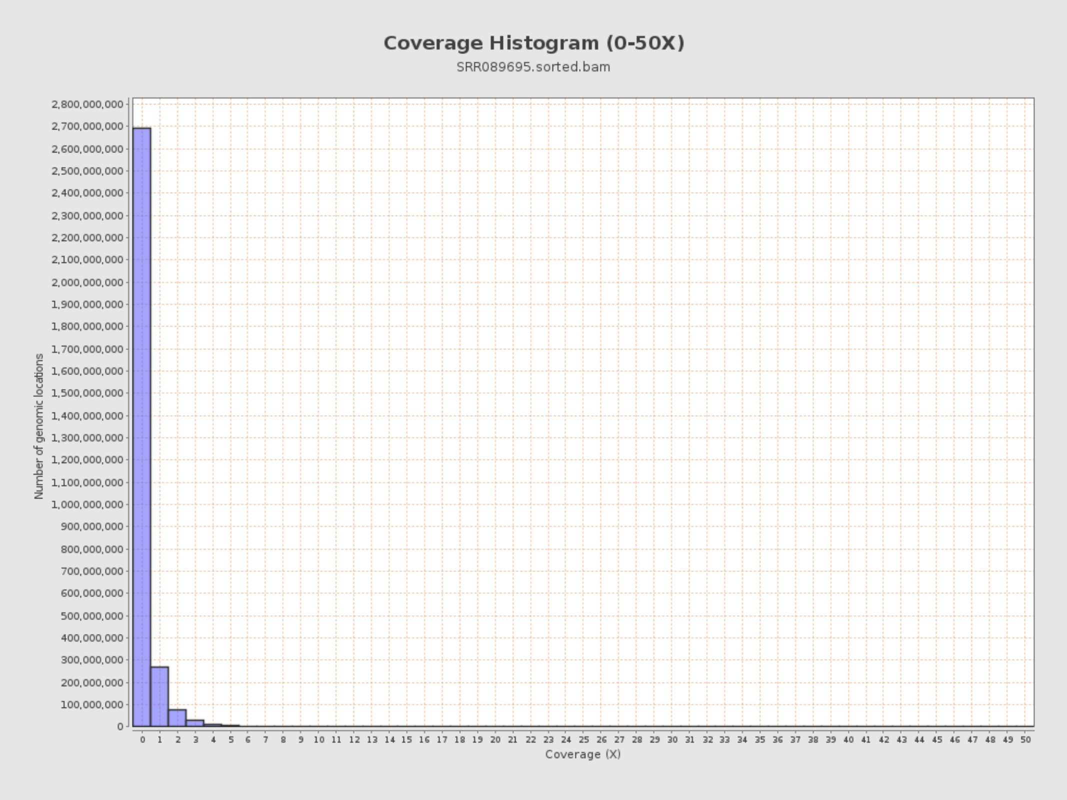
3. Results : Coverage across reference



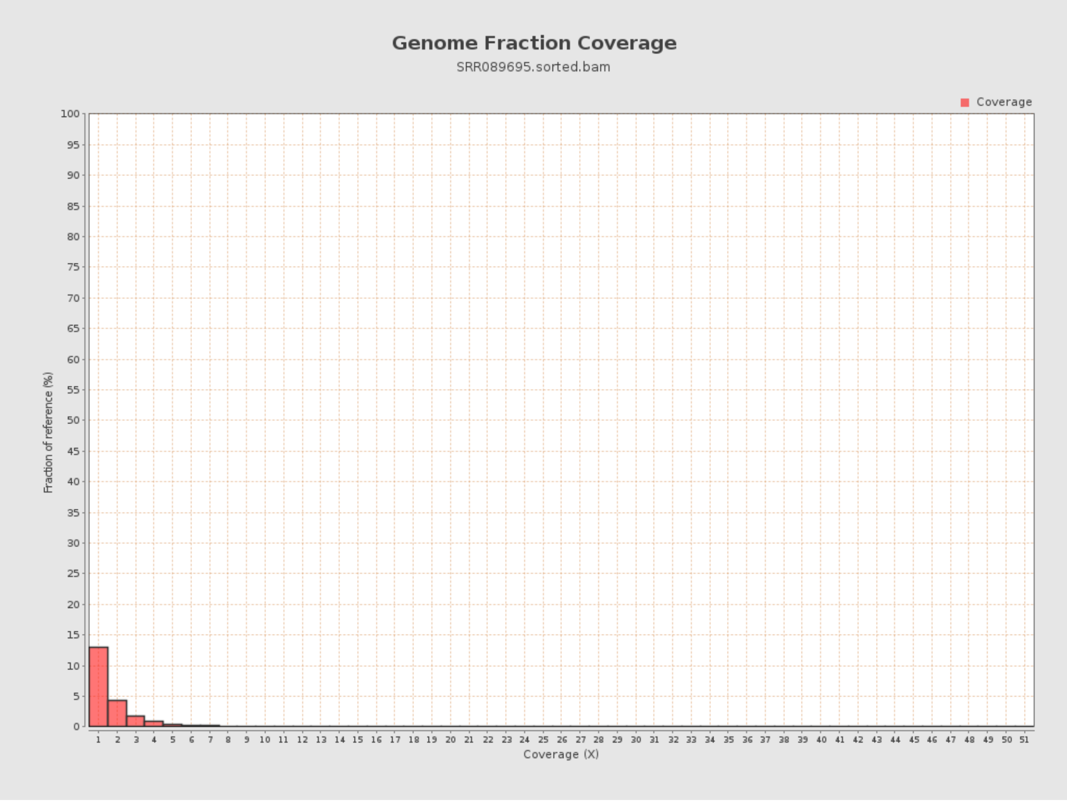
4. Results : Coverage Histogram



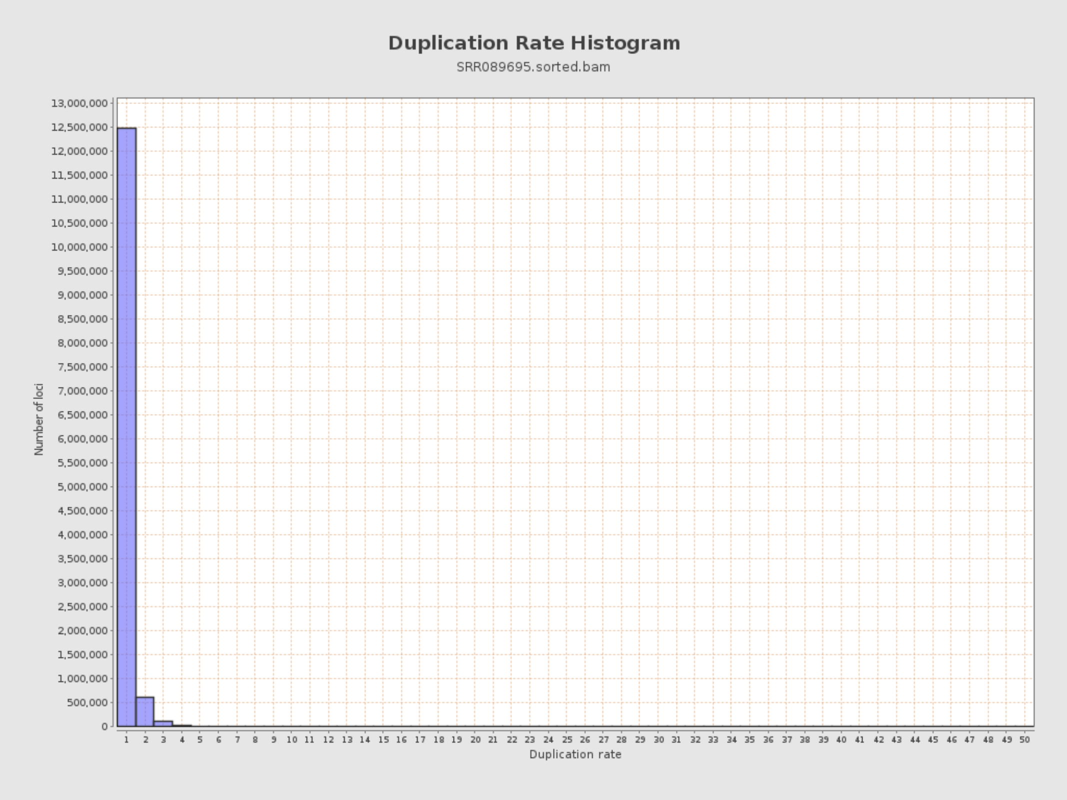
5. Results : Coverage Histogram (0-50X)



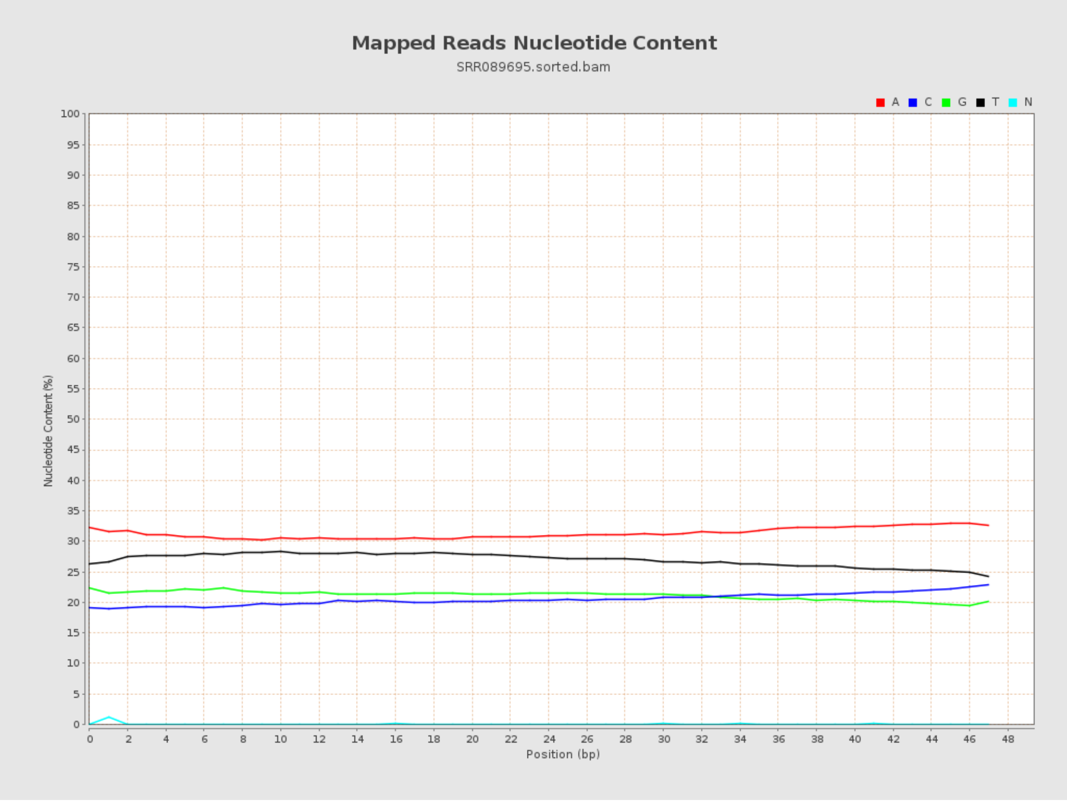
6. Results : Genome Fraction Coverage



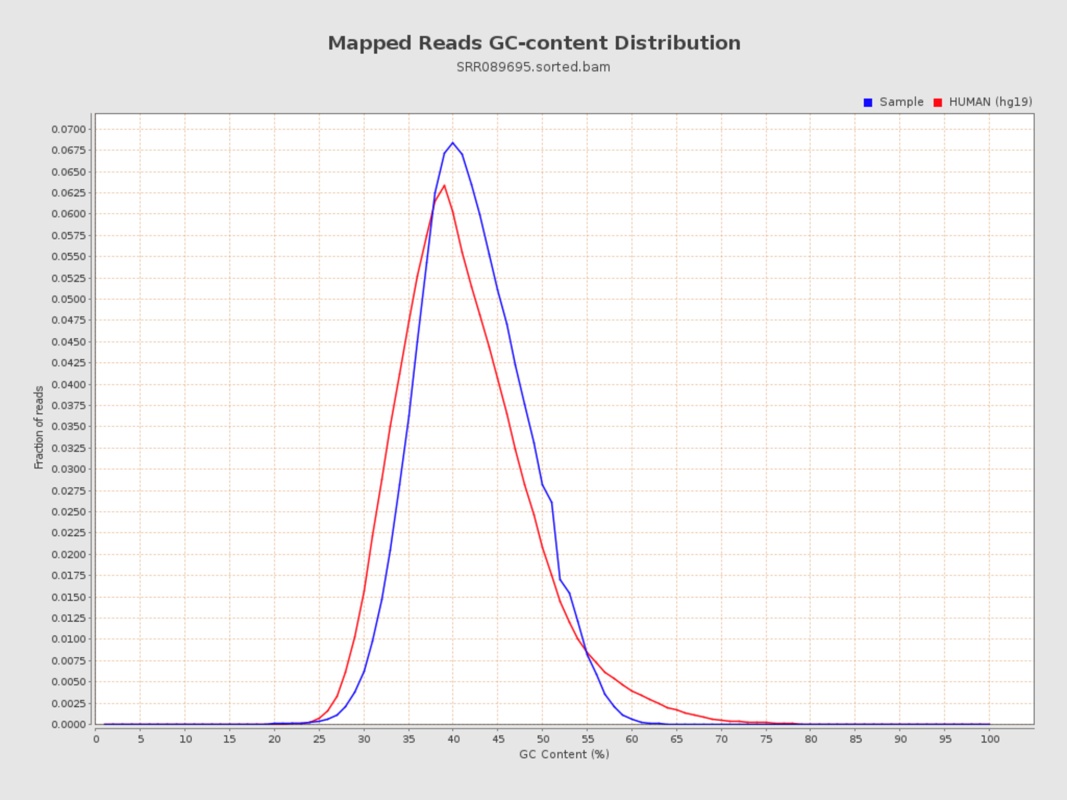
7. Results : Duplication Rate Histogram



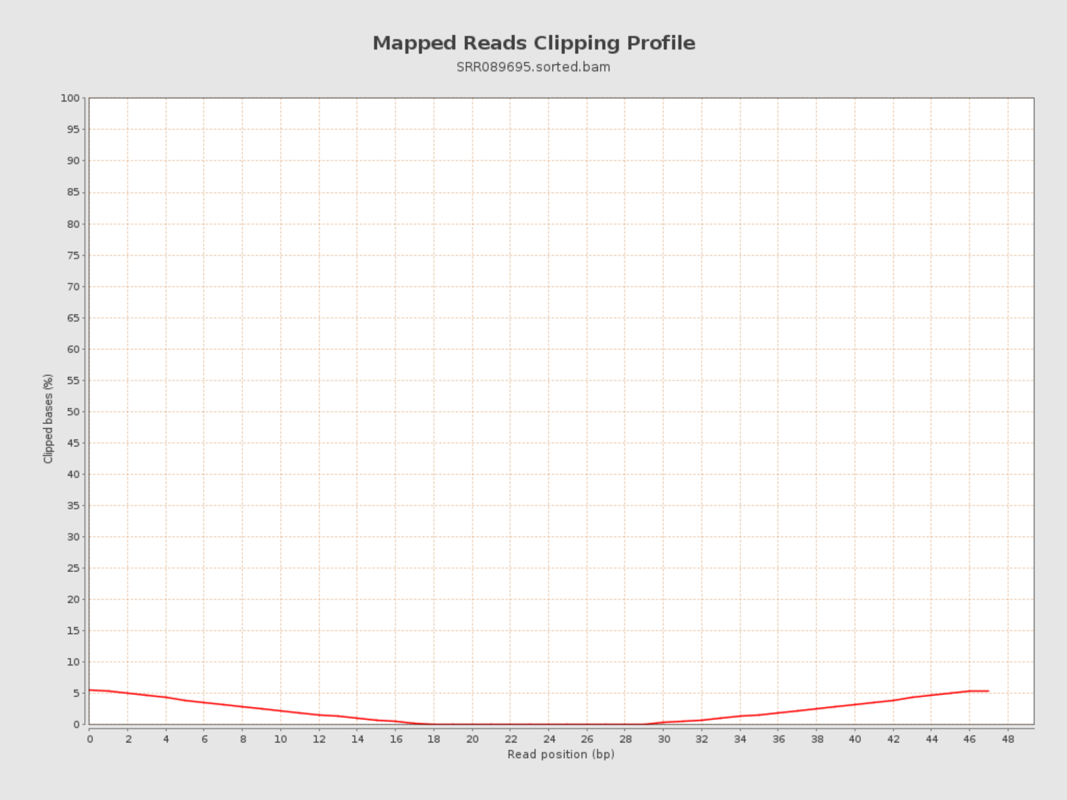
8. Results : Mapped Reads Nucleotide Content



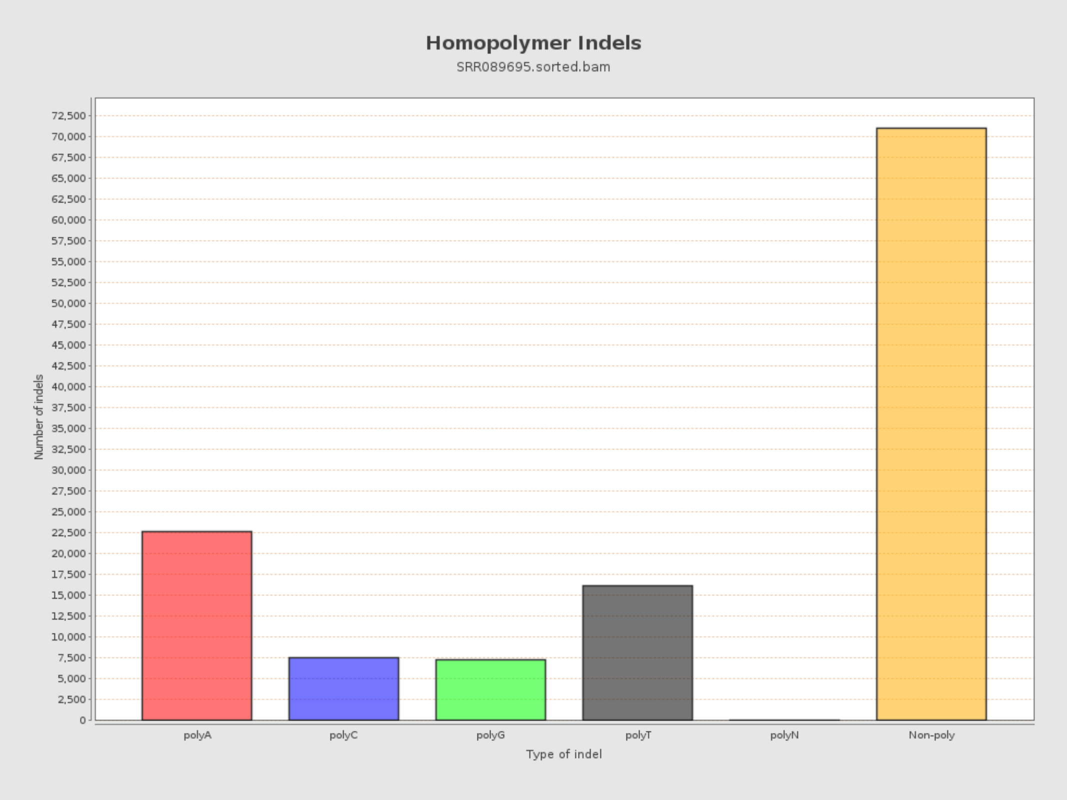
9. Results : Mapped Reads GC-content Distribution



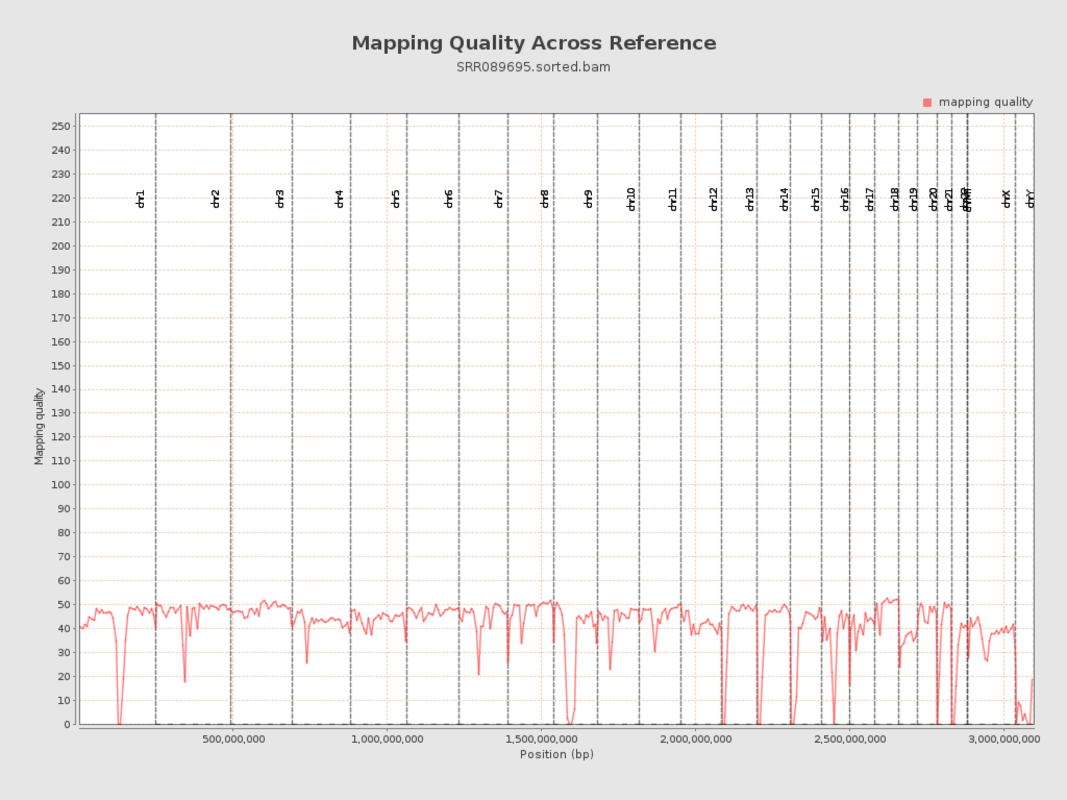
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram