Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 00:55:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053631.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_SRR053631 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053631.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 00:55:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053631.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,905,178
Mapped reads	9,384,536 / 78.83%
Unmapped reads	2,520,642 / 21.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	270 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,237,164 / 18.79%
Duplication rate	16.77%
Clipped reads	659,602 / 5.54%

2.2. ACGT Content

Number/percentage of A's	130,179,147 / 29.29%
Number/percentage of C's	85,977,244 / 19.34%
Number/percentage of T's	130,466,825 / 29.35%
Number/percentage of G's	97,882,402 / 22.02%
Number/percentage of N's	8,357 / 0%
GC Percentage	41.36%

2.3. Coverage

Mean	0.1436

Standard Deviation	1.0418

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

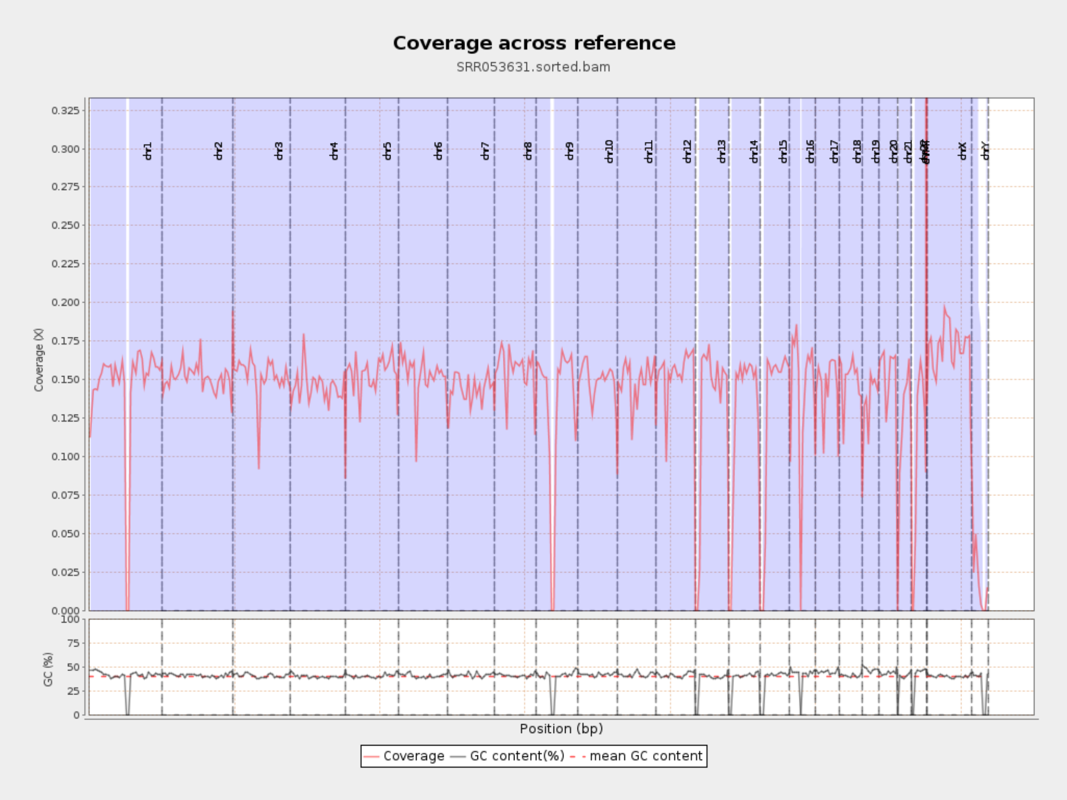
General error rate	0.55%
Mismatches	2,429,836
Insertions	16,971
Mapped reads with at least one insertion	0.18%
Deletions	54,290
Mapped reads with at least one deletion	0.58%
Homopolymer indels	46.98%

2.6. Chromosome stats

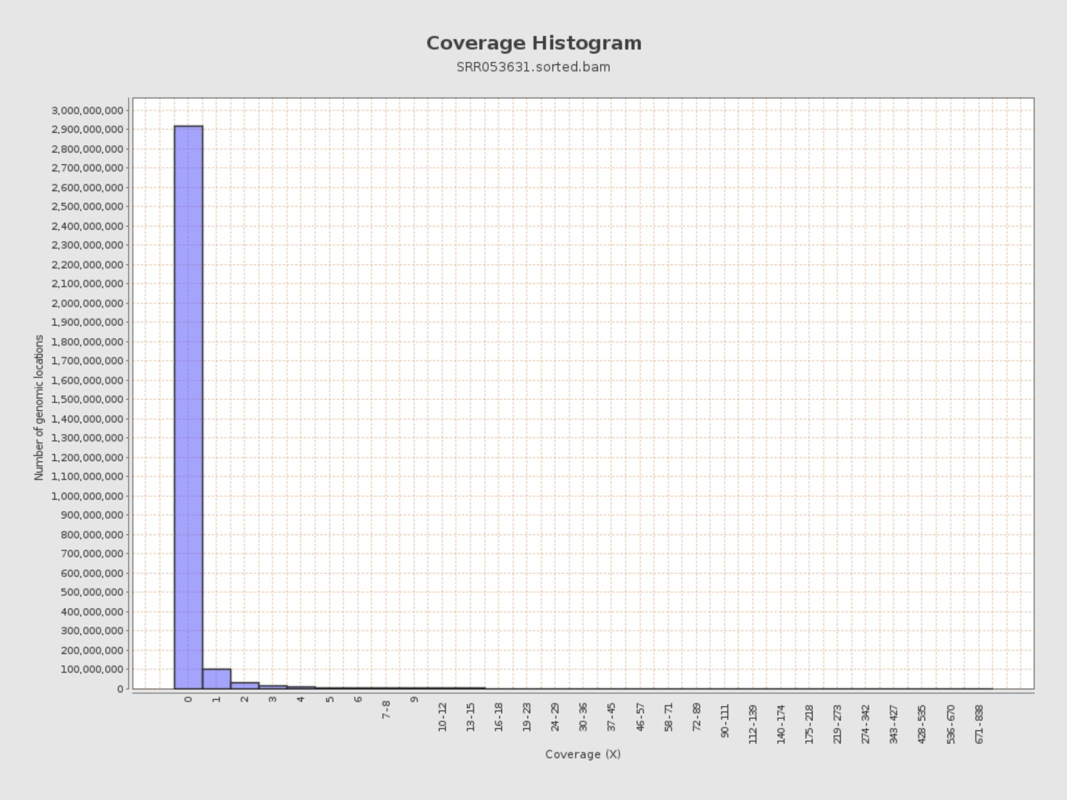
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36001367	0.1444	1.0859
chr2	243199373	36803520	0.1513	1.1987
chr3	198022430	30308117	0.1531	1.0456
chr4	191154276	27772484	0.1453	1.0187
chr5	180915260	27862463	0.154	0.9912
chr6	171115067	26177872	0.153	1.0291
chr7	159138663	22959677	0.1443	1.1357

chr8	146364022	22915926	0.1566	1.0634
chr9	141213431	18608950	0.1318	1.0138
chr10	135534747	20411513	0.1506	1.0907
chr11	135006516	20073837	0.1487	1.0786
chr12	133851895	20559500	0.1536	1.015
chr13	115169878	14879937	0.1292	0.9324
chr14	107349540	13625905	0.1269	1.0502
chr15	102531392	13087859	0.1276	0.8883
chr16	90354753	12881145	0.1426	0.9872
chr17	81195210	11778201	0.1451	0.9559
chr18	78077248	11711204	0.15	1.0868
chr19	59128983	8069974	0.1365	1.0294
chr20	63025520	9639679	0.1529	1.0297
chr21	48129895	5629513	0.117	0.9557
chr22	51304566	5027304	0.098	0.7823
chrMT	16571	33320	2.0107	3.9504
chrX	155270560	26589731	0.1712	1.1336
chrY	59373566	1185784	0.02	0.4204

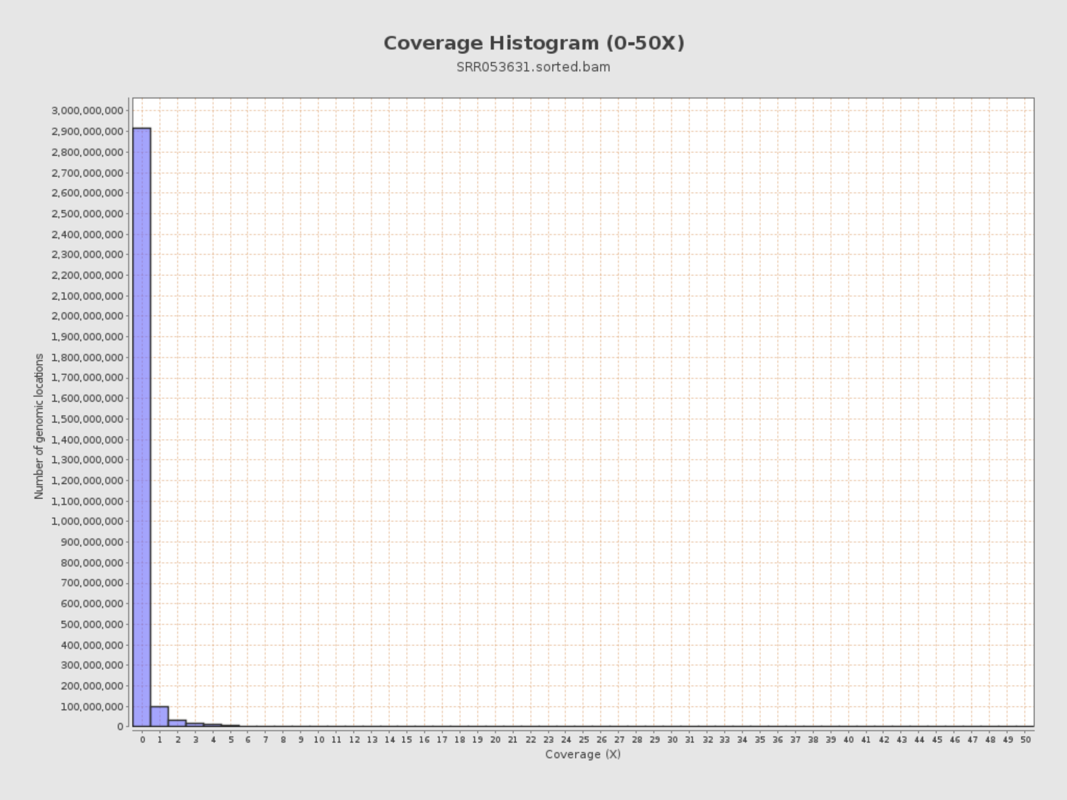
3. Results : Coverage across reference



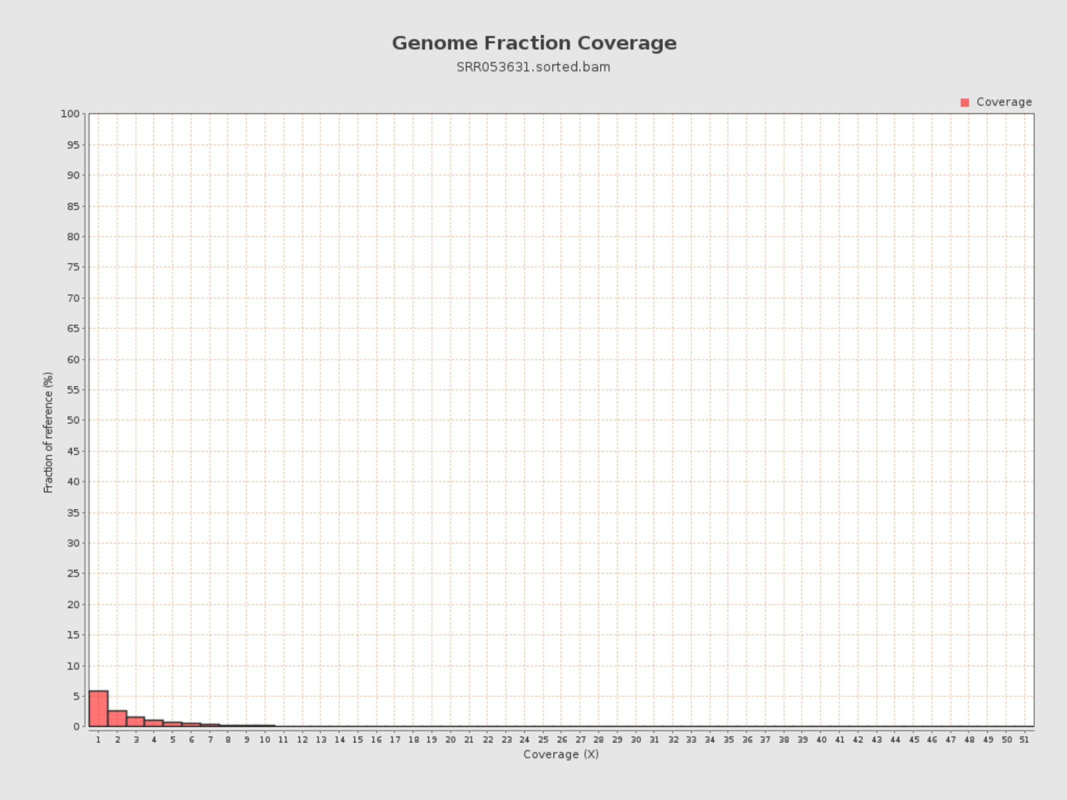
4. Results : Coverage Histogram



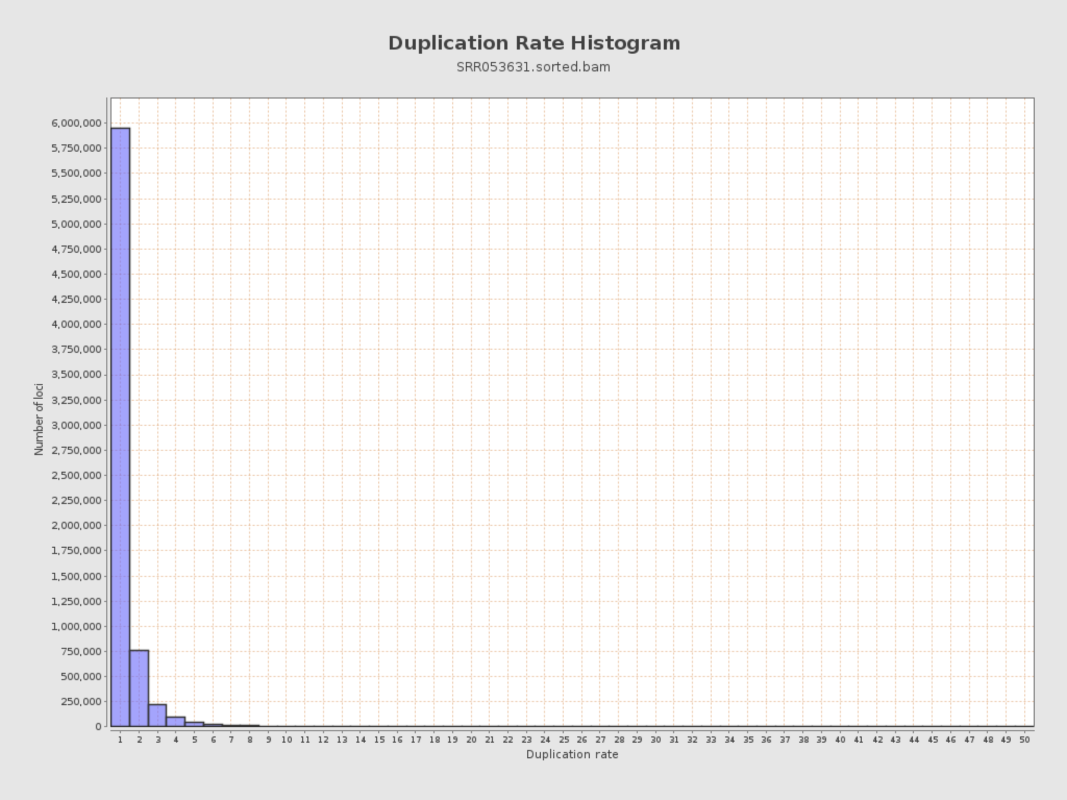
5. Results : Coverage Histogram (0-50X)



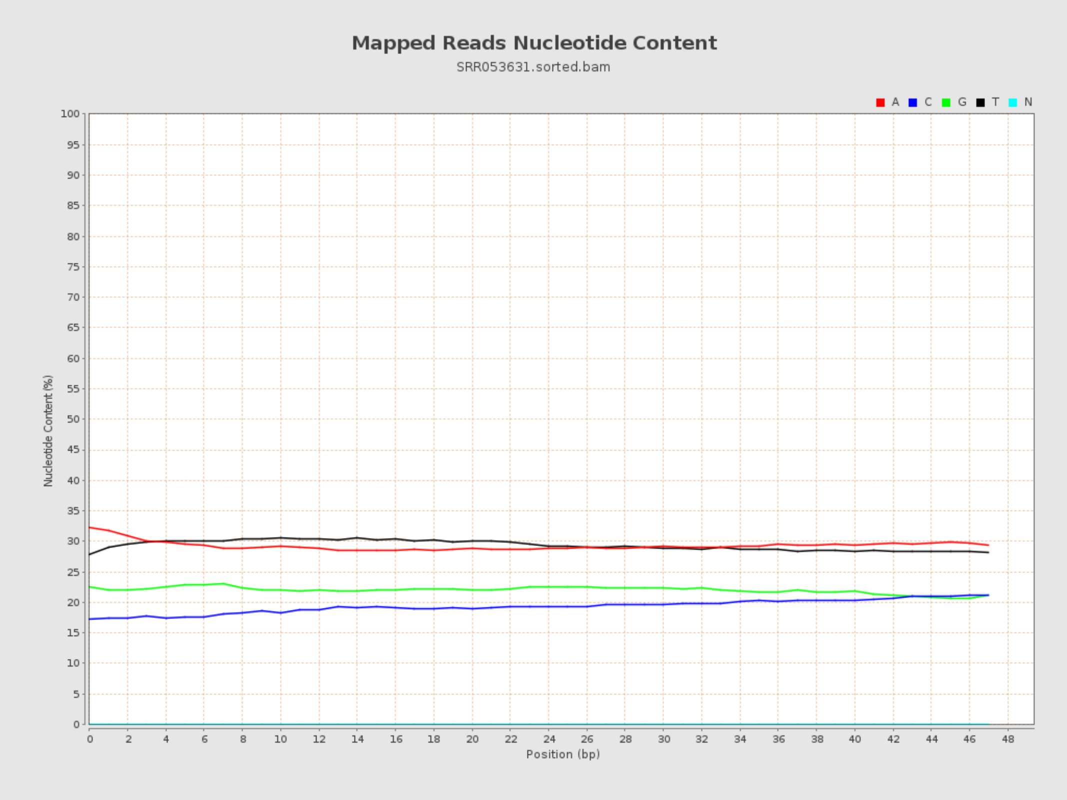
6. Results : Genome Fraction Coverage



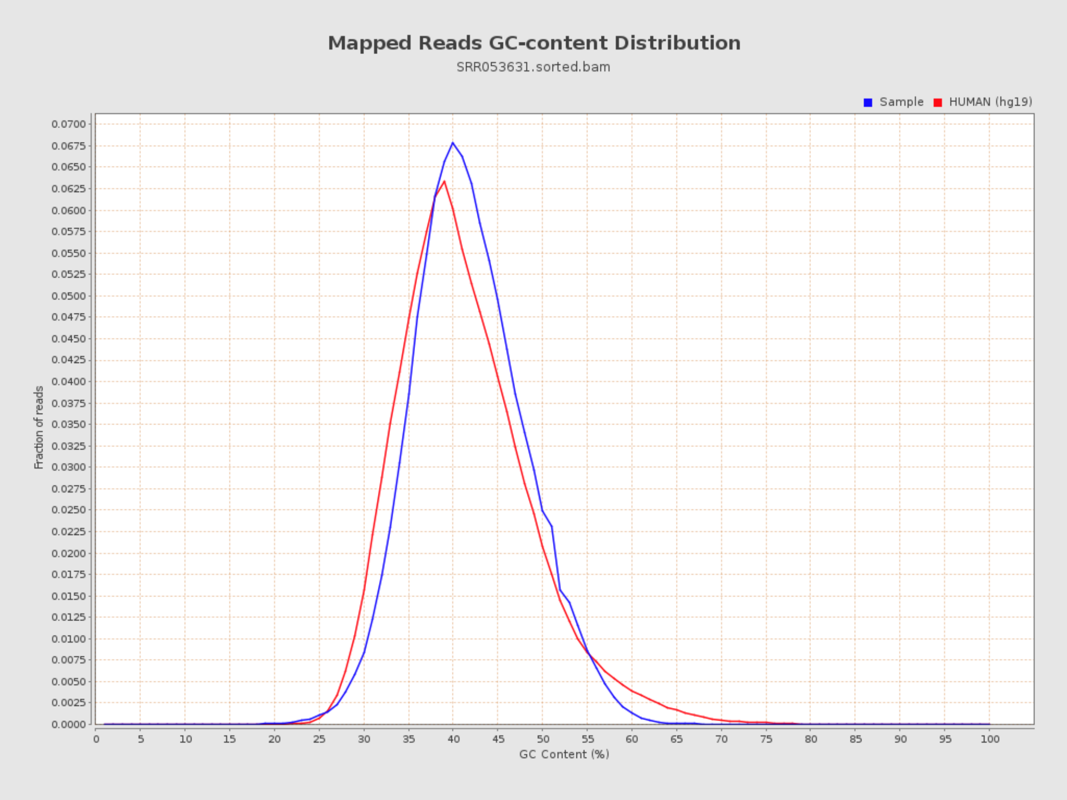
7. Results : Duplication Rate Histogram



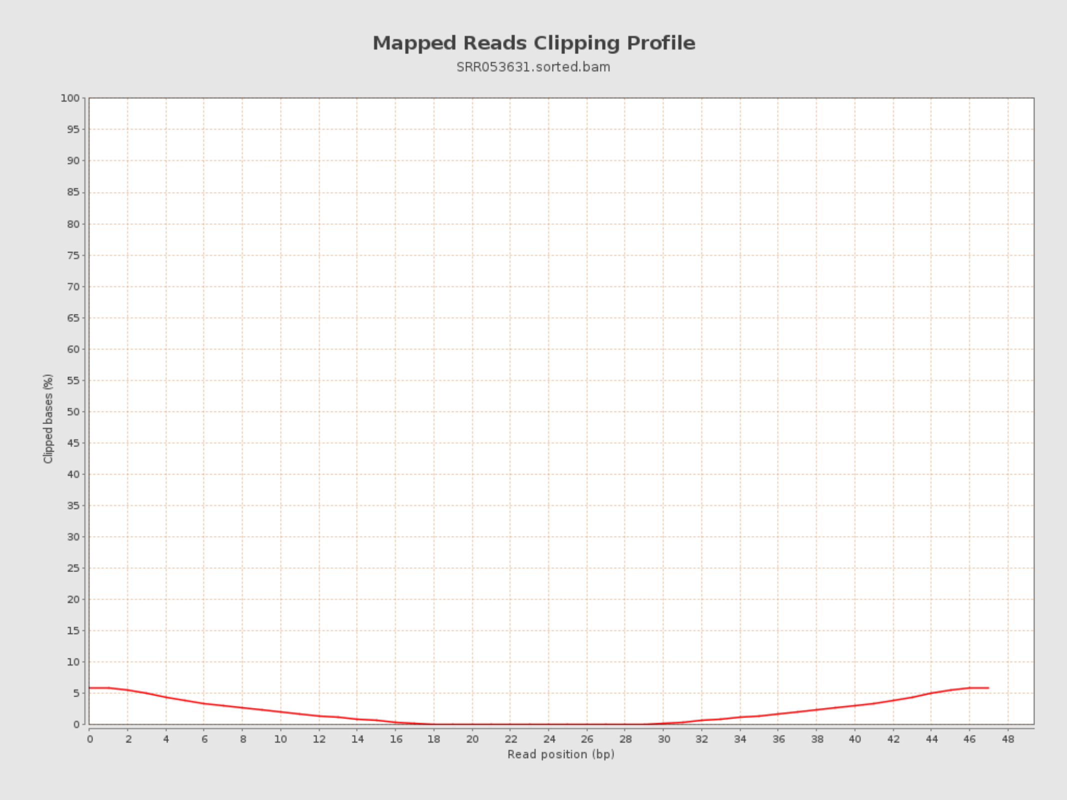
8. Results : Mapped Reads Nucleotide Content



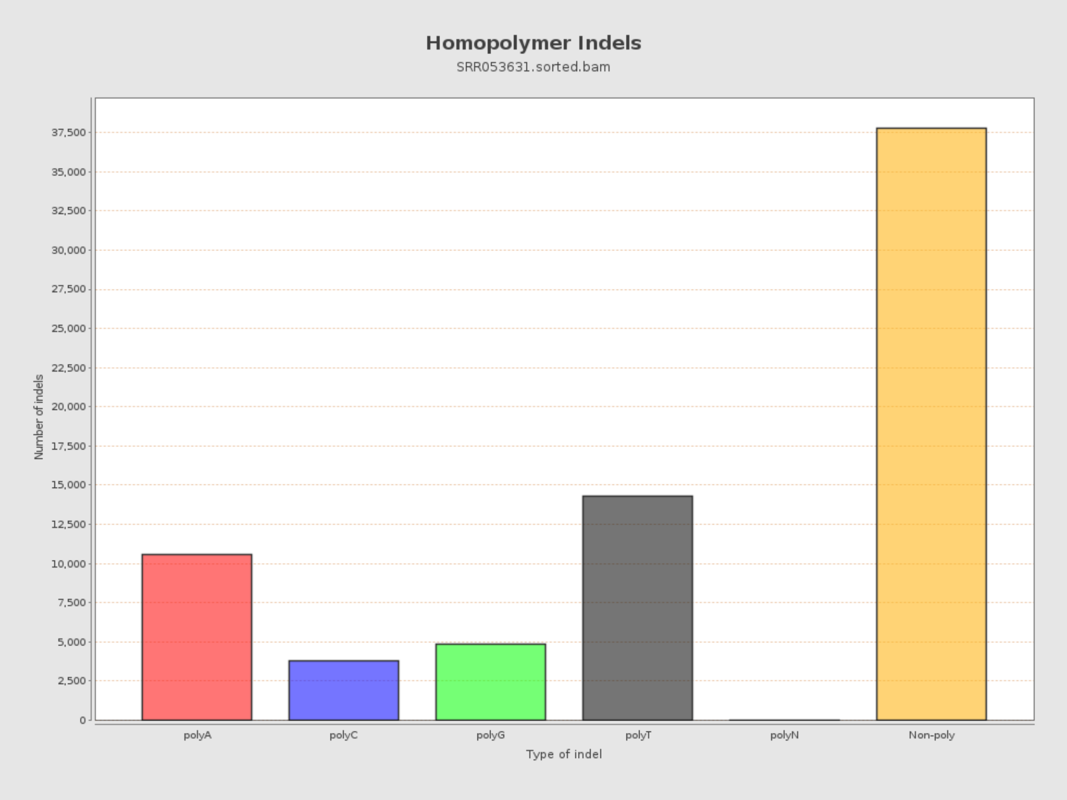
9. Results : Mapped Reads GC-content Distribution



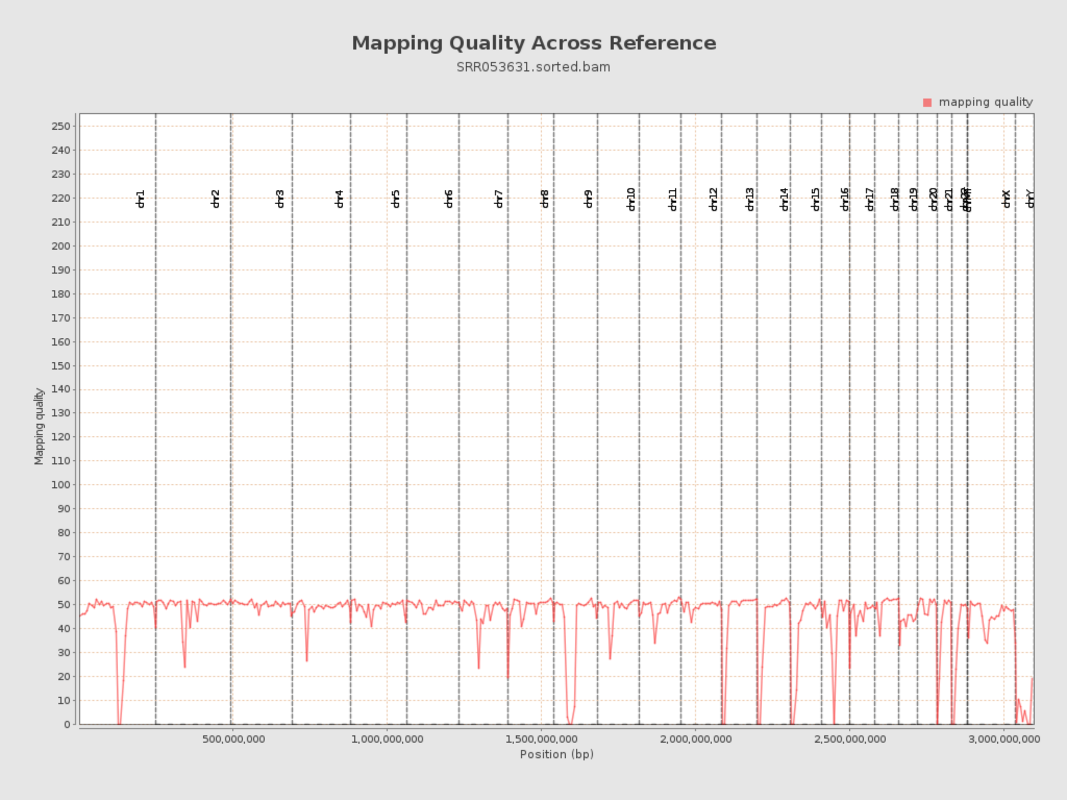
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram