Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:41:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083639.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_SRR3083639 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083639.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:41:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083639.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,062,558
Mapped reads	1,696,412 / 82.25%
Unmapped reads	366,146 / 17.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,511 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	58,913 / 2.86%
Duplication rate	3.01%
Clipped reads	1,208,672 / 58.6%

2.2. ACGT Content

Number/percentage of A's	29,576,717 / 29.51%
Number/percentage of C's	19,520,897 / 19.48%
Number/percentage of T's	29,554,356 / 29.49%
Number/percentage of G's	21,557,568 / 21.51%
Number/percentage of N's	12,850 / 0.01%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0324

Standard Deviation	0.244

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

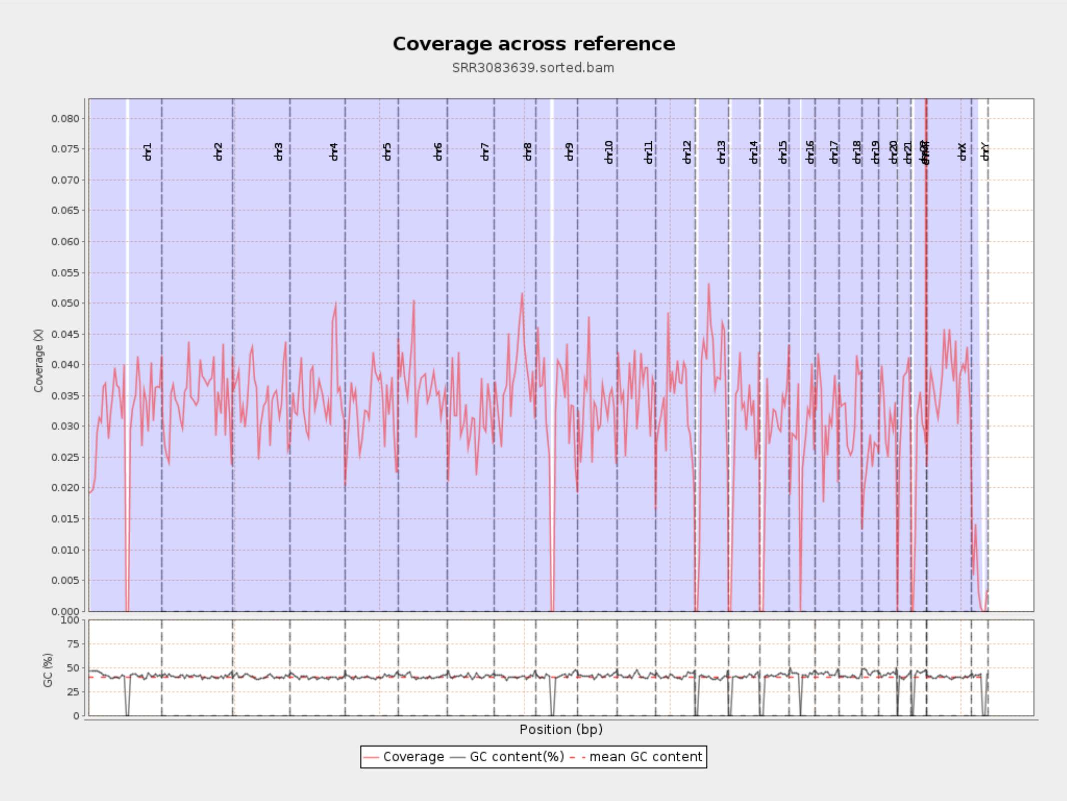
General error rate	0.82%
Mismatches	809,428
Insertions	6,689
Mapped reads with at least one insertion	0.39%
Deletions	19,117
Mapped reads with at least one deletion	1.12%
Homopolymer indels	45.72%

2.6. Chromosome stats

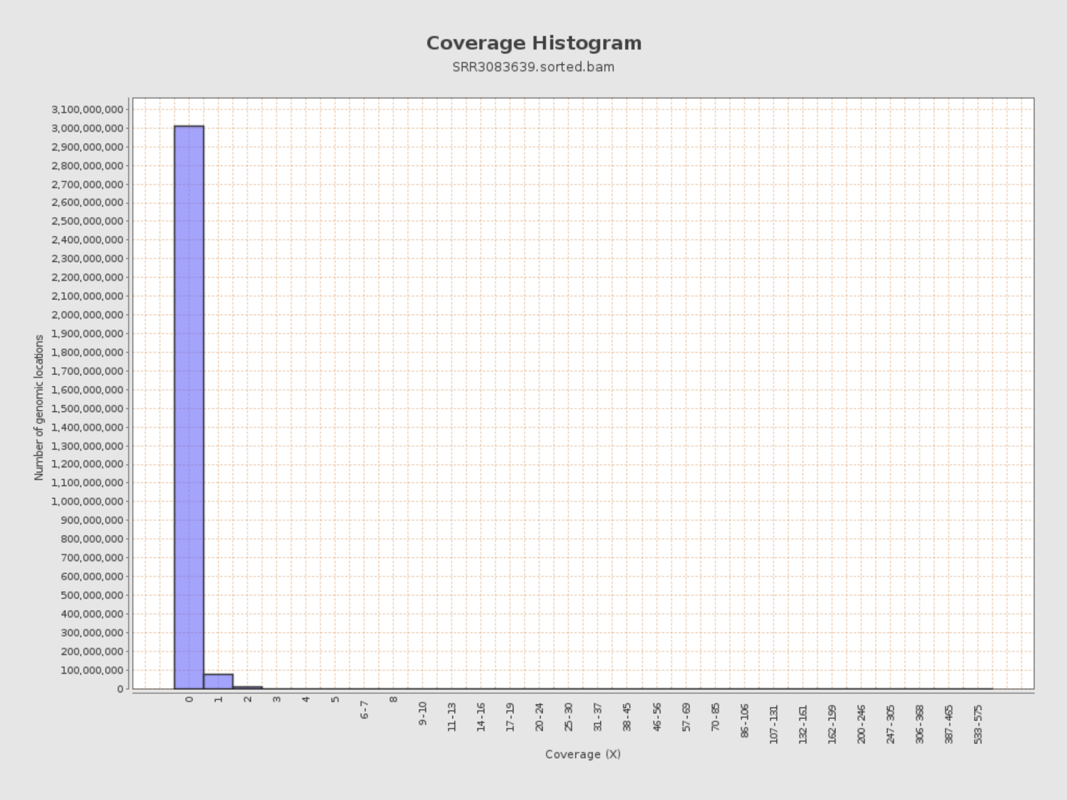
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7710426	0.0309	0.3233
chr2	243199373	8335333	0.0343	0.2412
chr3	198022430	6862747	0.0347	0.2063
chr4	191154276	6724690	0.0352	0.2129
chr5	180915260	5917834	0.0327	0.2014
chr6	171115067	6378158	0.0373	0.2383
chr7	159138663	5013796	0.0315	0.2427

chr8	146364022	5532855	0.0378	0.405
chr9	141213431	4424632	0.0313	0.2243
chr10	135534747	4470205	0.033	0.2498
chr11	135006516	4825129	0.0357	0.2287
chr12	133851895	4562306	0.0341	0.207
chr13	115169878	4005137	0.0348	0.2071
chr14	107349540	2985133	0.0278	0.1898
chr15	102531392	2772677	0.027	0.1835
chr16	90354753	2467816	0.0273	0.1911
chr17	81195210	2518020	0.031	0.2026
chr18	78077248	2556299	0.0327	0.3696
chr19	59128983	1439422	0.0243	0.2481
chr20	63025520	1980439	0.0314	0.2032
chr21	48129895	1479844	0.0307	0.2016
chr22	51304566	1123121	0.0219	0.1631
chrMT	16571	69957	4.2217	2.9606
chrX	155270560	5835296	0.0376	0.2254
chrY	59373566	261428	0.0044	0.1093

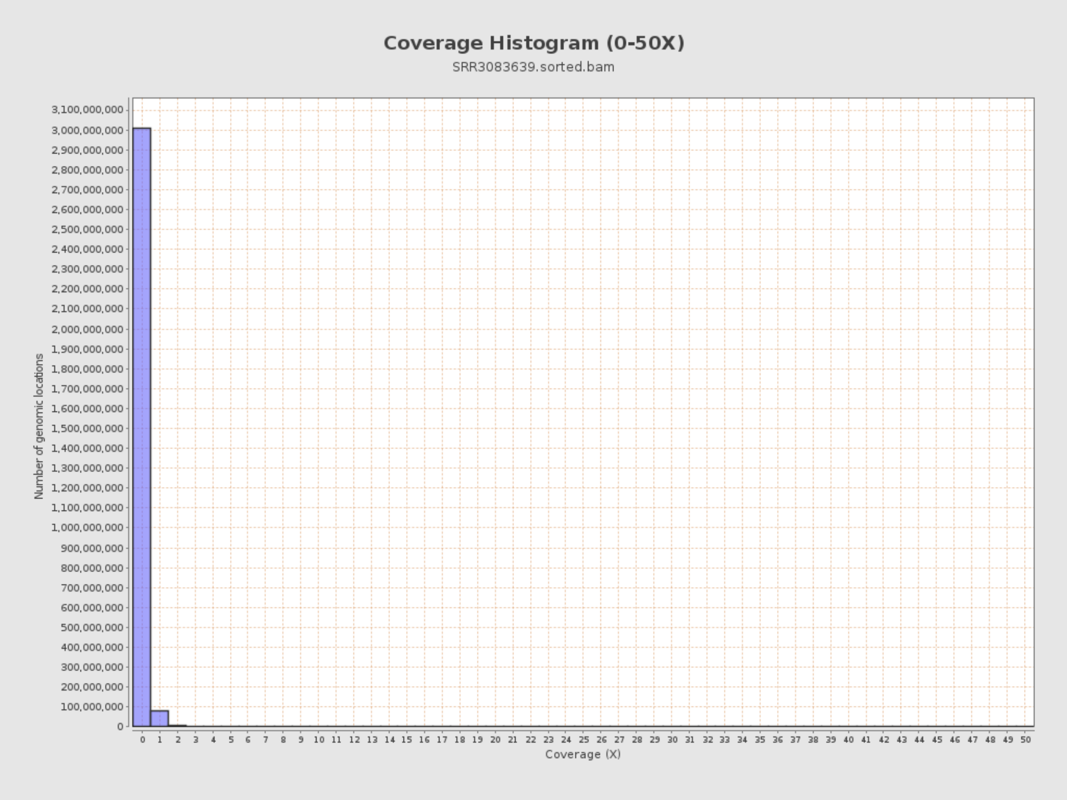
3. Results : Coverage across reference



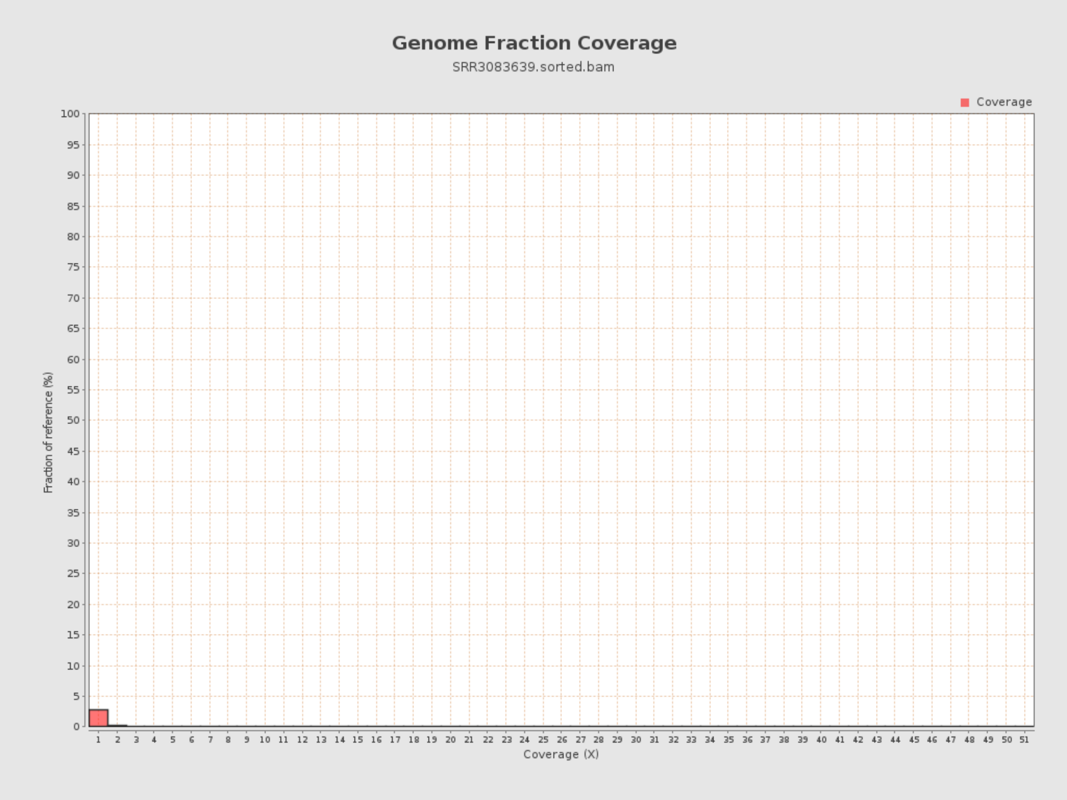
4. Results : Coverage Histogram



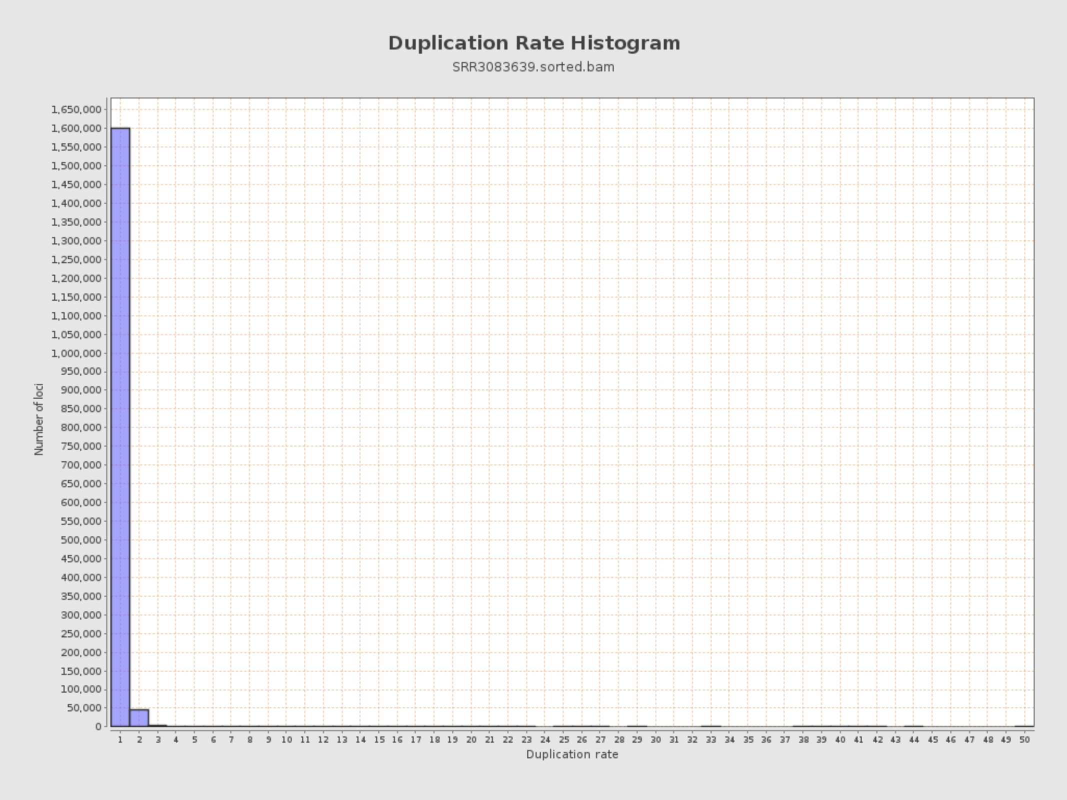
5. Results : Coverage Histogram (0-50X)



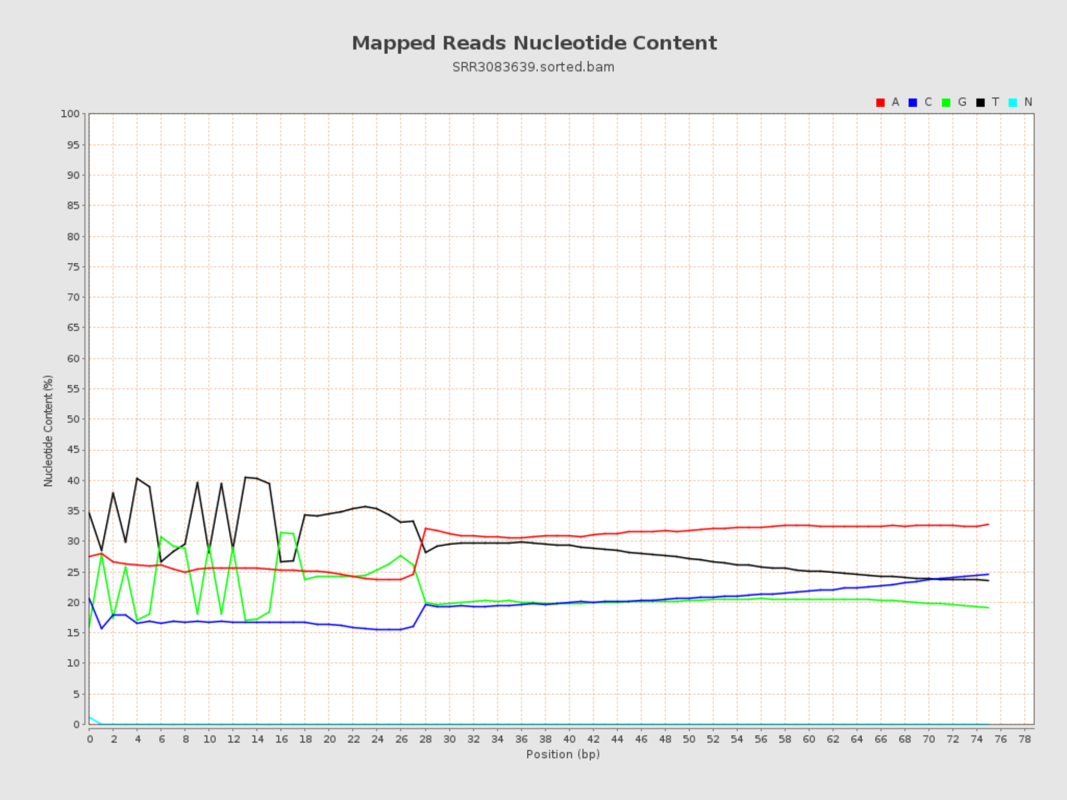
6. Results : Genome Fraction Coverage



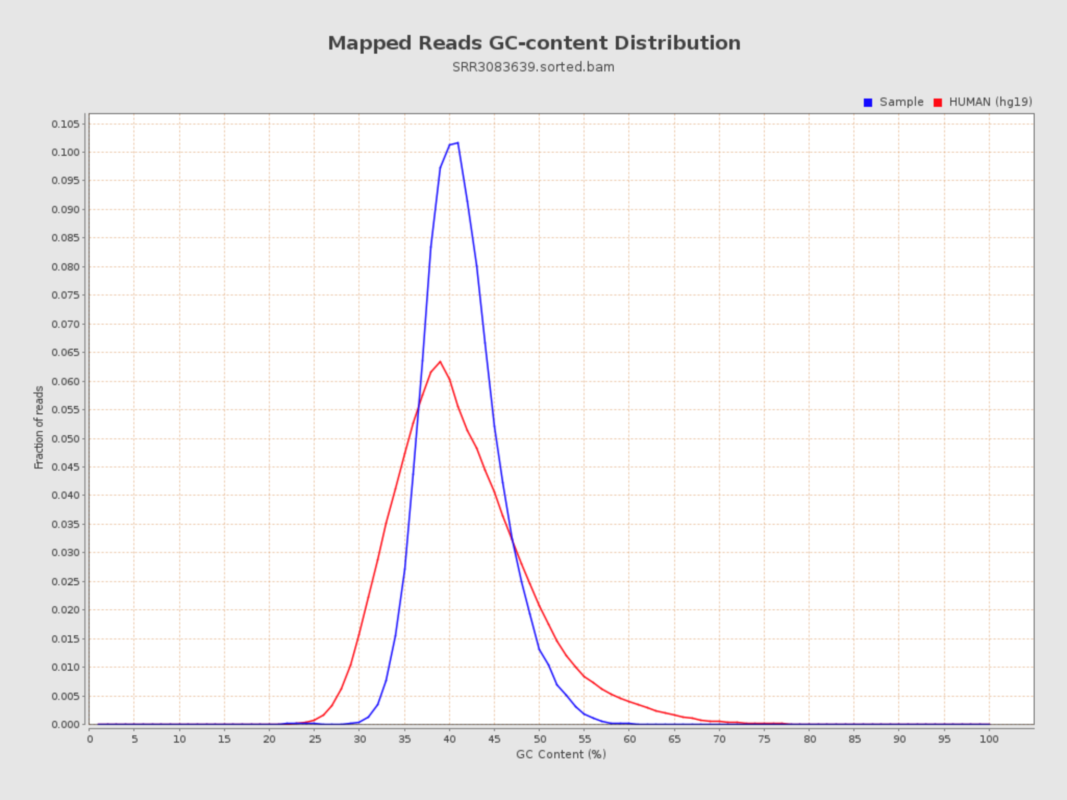
7. Results : Duplication Rate Histogram



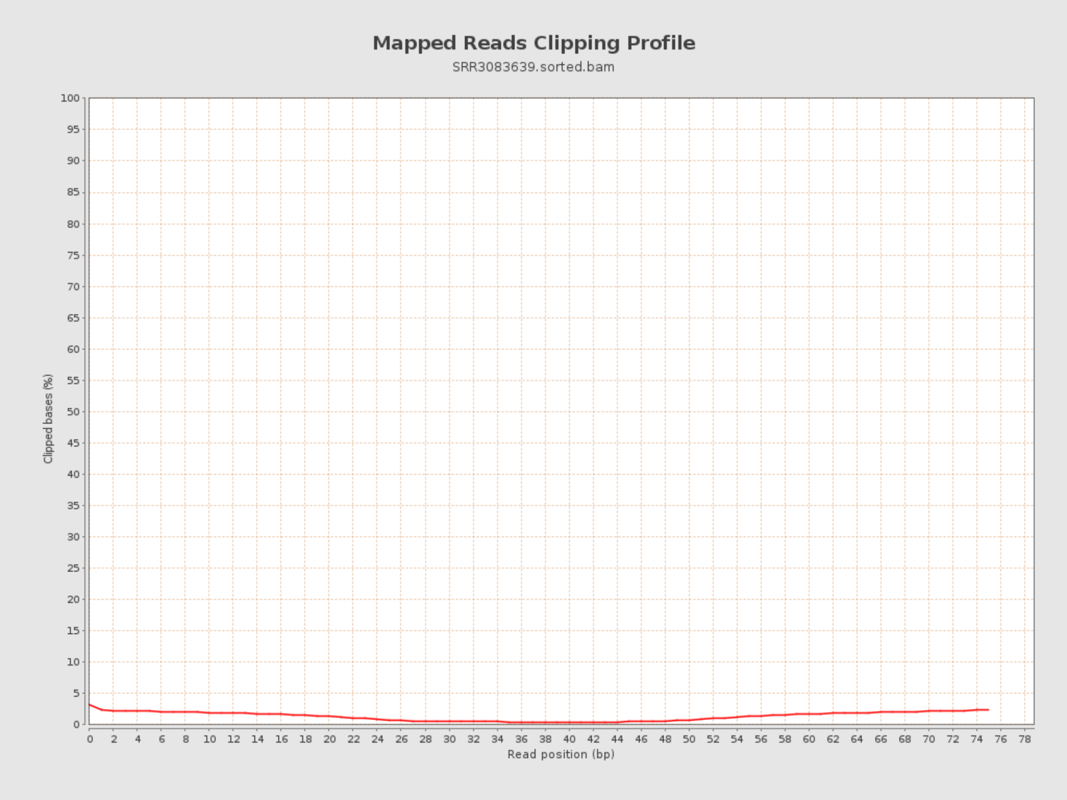
8. Results : Mapped Reads Nucleotide Content



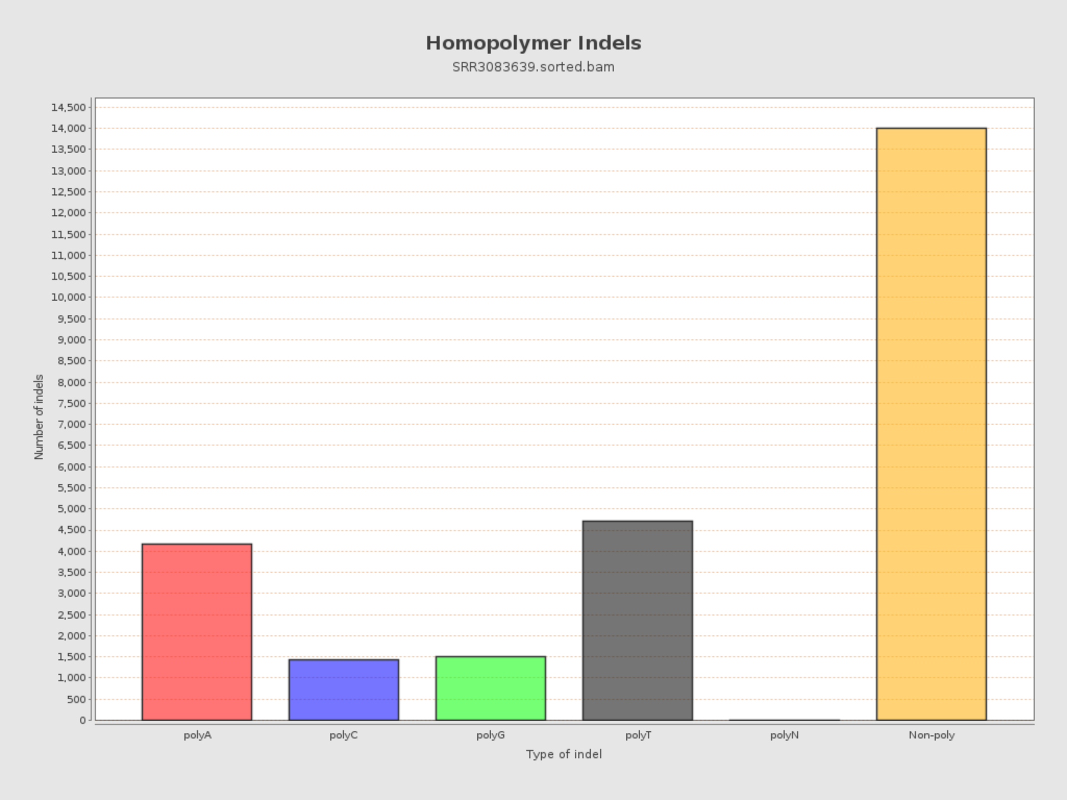
9. Results : Mapped Reads GC-content Distribution



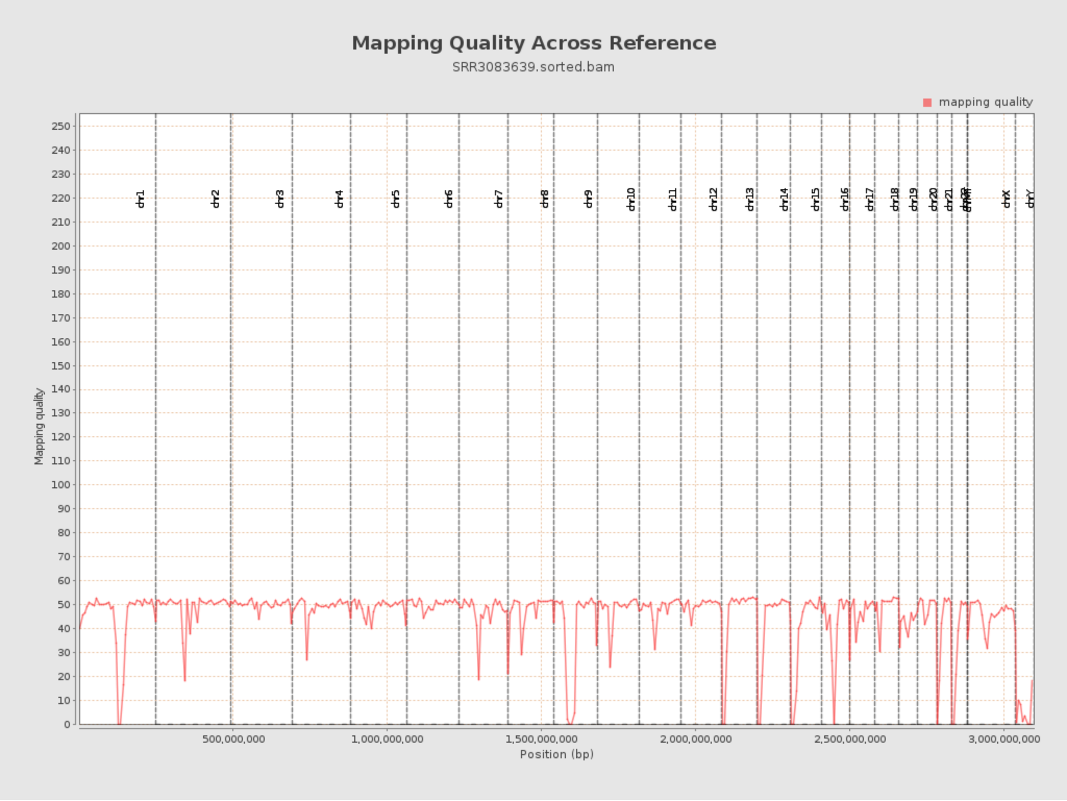
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram