Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 03:40:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083676.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_SRR3083676 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083676.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 03:40:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083676.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,314,846
Mapped reads	1,843,180 / 79.62%
Unmapped reads	471,666 / 20.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,816 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	57,984 / 2.5%
Duplication rate	2.63%
Clipped reads	1,318,257 / 56.95%

2.2. ACGT Content

Number/percentage of A's	32,558,354 / 29.73%
Number/percentage of C's	21,218,668 / 19.38%
Number/percentage of T's	32,043,250 / 29.26%
Number/percentage of G's	23,663,198 / 21.61%
Number/percentage of N's	14,952 / 0.01%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0354

Standard Deviation	0.2875

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

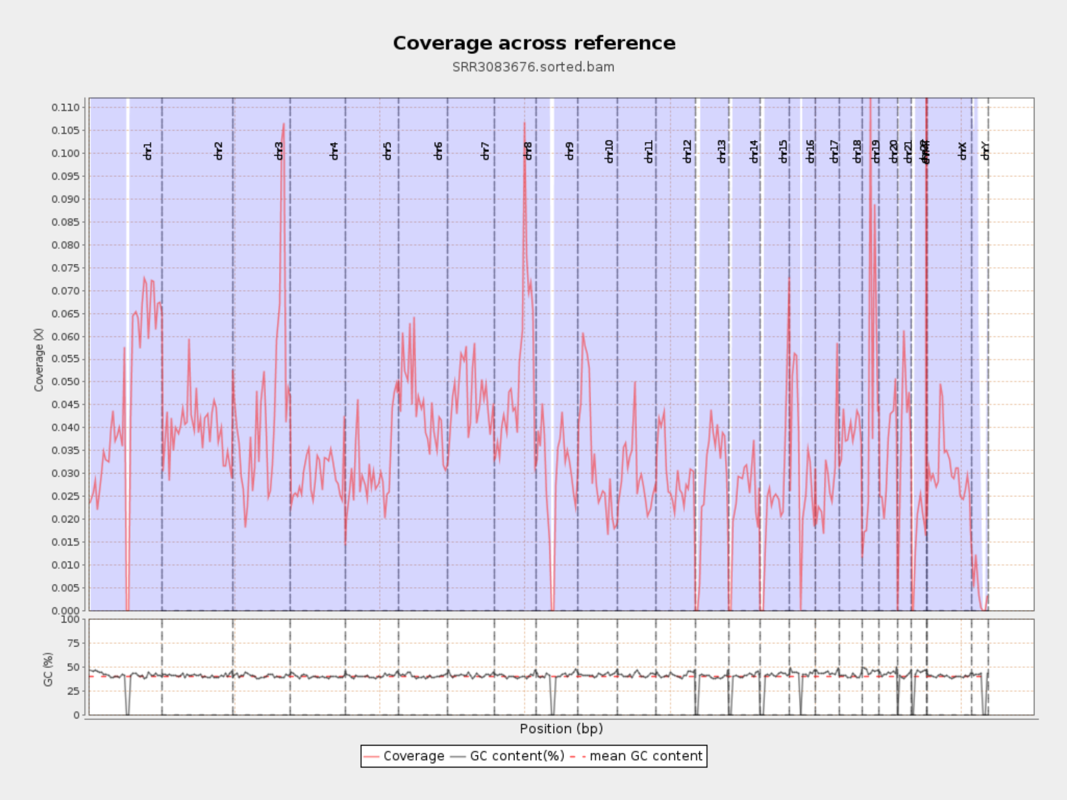
General error rate	0.85%
Mismatches	919,520
Insertions	7,380
Mapped reads with at least one insertion	0.4%
Deletions	21,412
Mapped reads with at least one deletion	1.15%
Homopolymer indels	45.77%

2.6. Chromosome stats

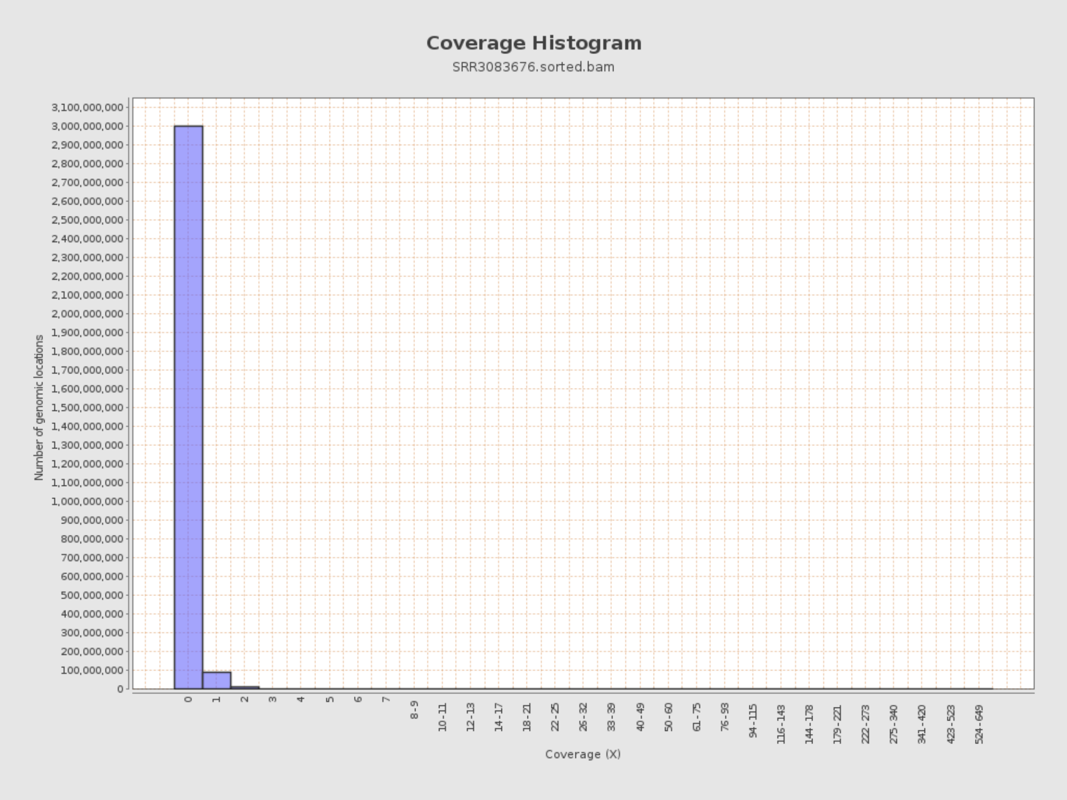
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11353371	0.0456	0.582
chr2	243199373	9626570	0.0396	0.258
chr3	198022430	8629807	0.0436	0.2298
chr4	191154276	5653530	0.0296	0.192
chr5	180915260	5597645	0.0309	0.1929
chr6	171115067	7617545	0.0445	0.2604
chr7	159138663	7492778	0.0471	0.3709

chr8	146364022	7617773	0.052	0.3917
chr9	141213431	4101385	0.029	0.2138
chr10	135534747	4603654	0.034	0.2496
chr11	135006516	3976528	0.0295	0.2163
chr12	133851895	3975409	0.0297	0.1881
chr13	115169878	3305996	0.0287	0.1839
chr14	107349540	2562760	0.0239	0.1696
chr15	102531392	2509623	0.0245	0.1716
chr16	90354753	2917397	0.0323	0.2027
chr17	81195210	2340626	0.0288	0.1918
chr18	78077248	3047062	0.039	0.3584
chr19	59128983	2769041	0.0468	0.4028
chr20	63025520	2168098	0.0344	0.2072
chr21	48129895	1852696	0.0385	0.2167
chr22	51304566	804765	0.0157	0.1343
chrMT	16571	5316	0.3208	0.6199
chrX	155270560	4765013	0.0307	0.1996
chrY	59373566	237755	0.004	0.0932

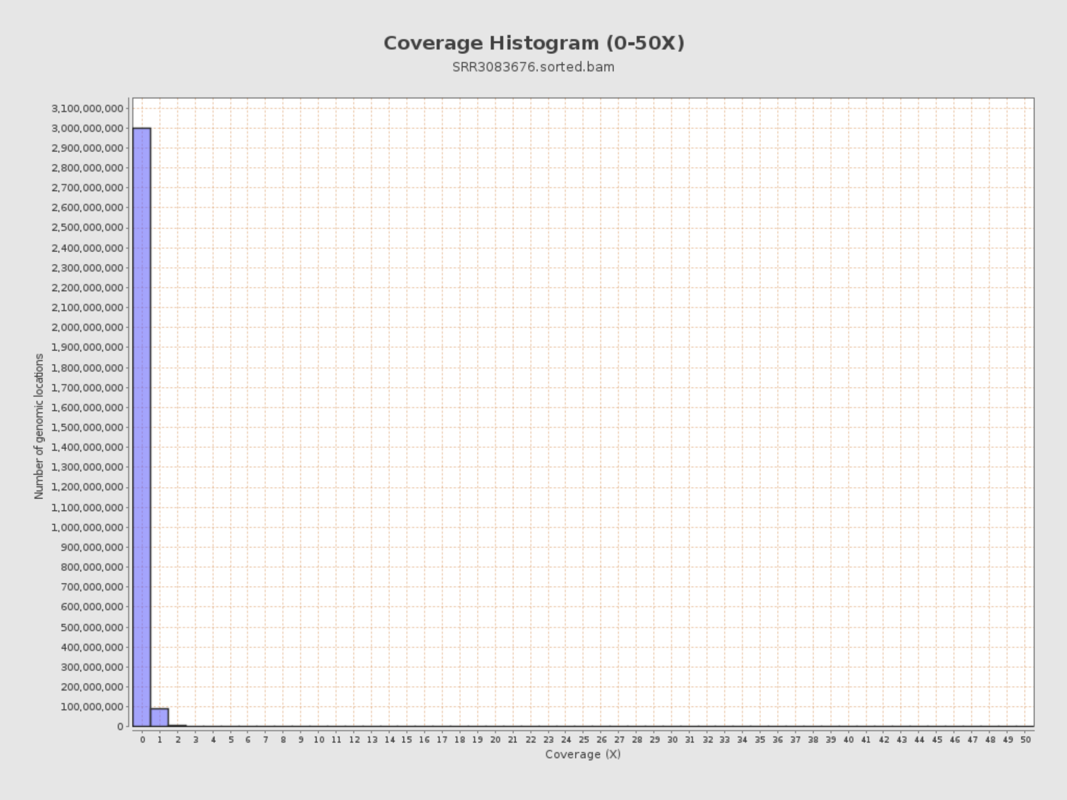
3. Results : Coverage across reference



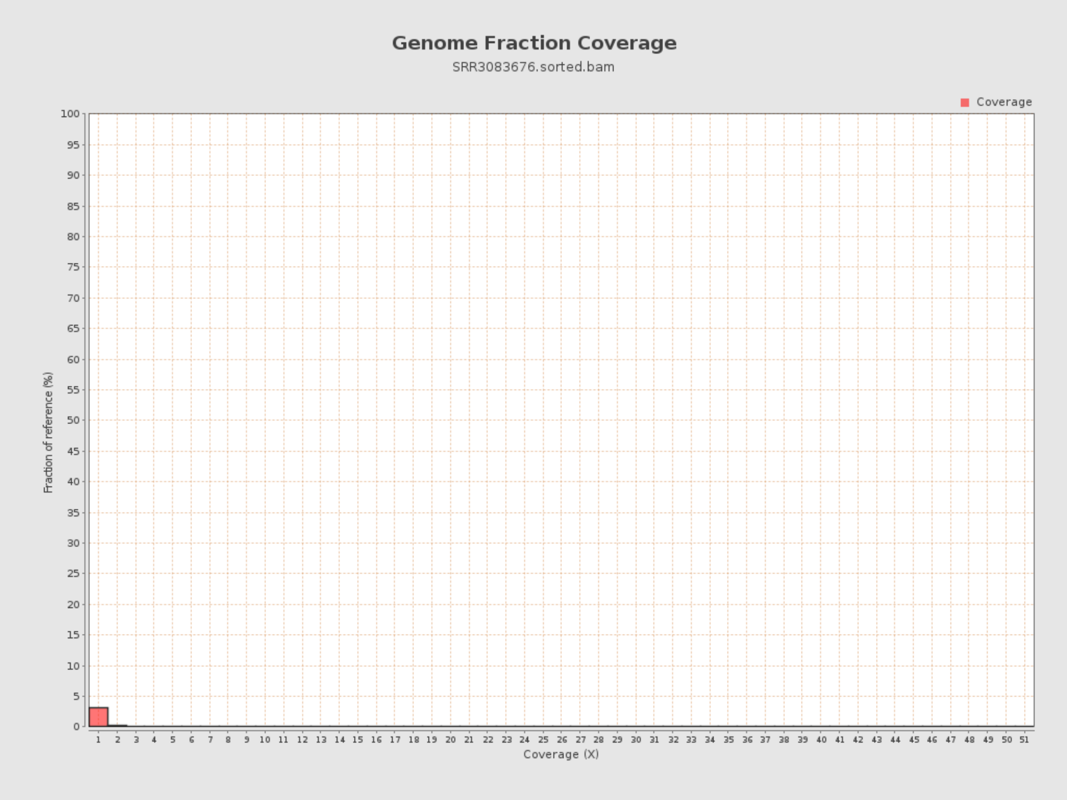
4. Results : Coverage Histogram



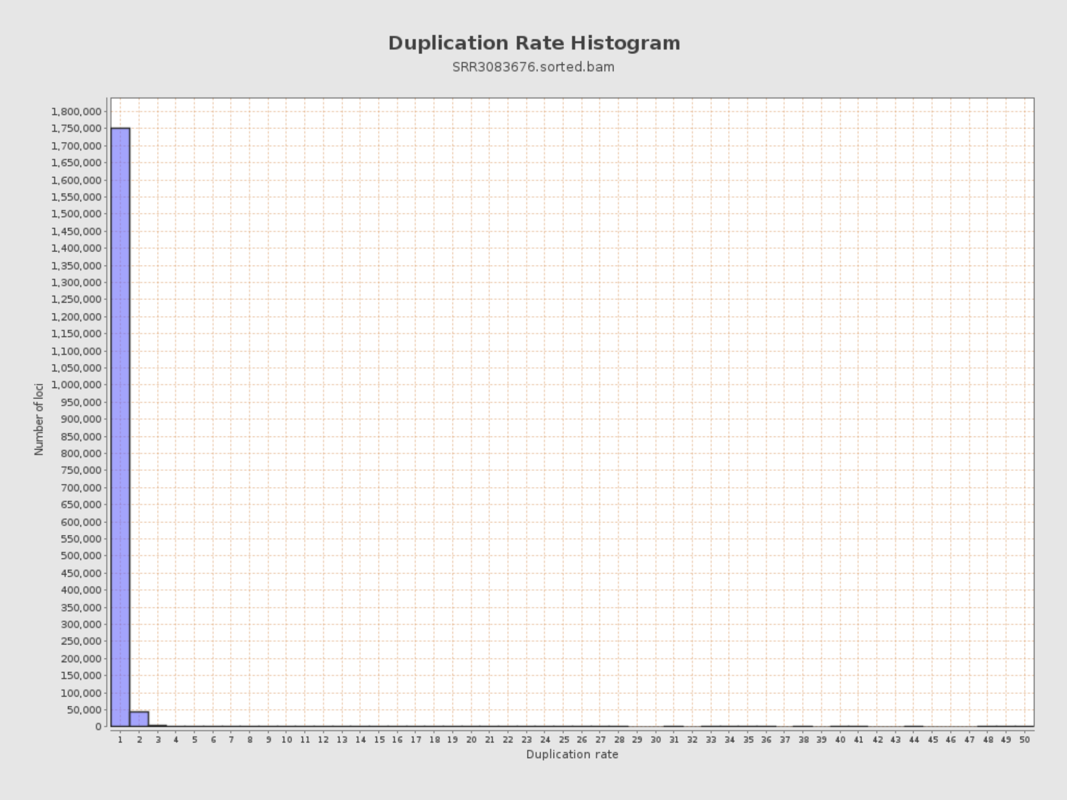
5. Results : Coverage Histogram (0-50X)



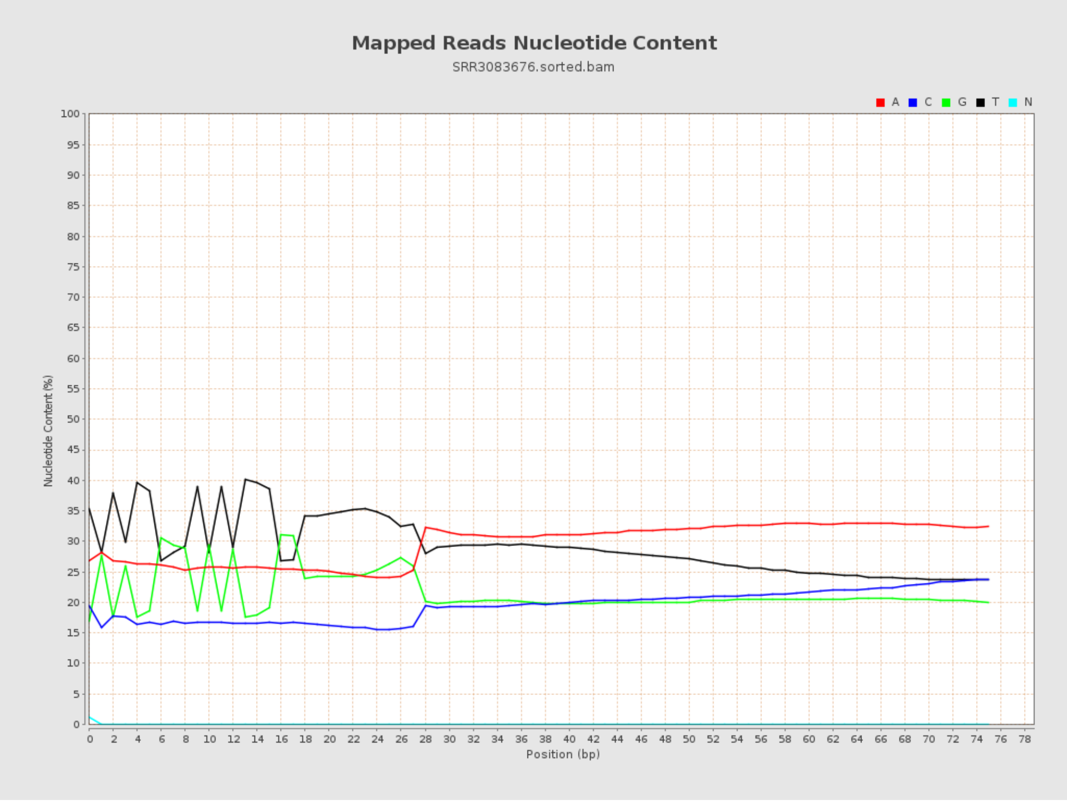
6. Results : Genome Fraction Coverage



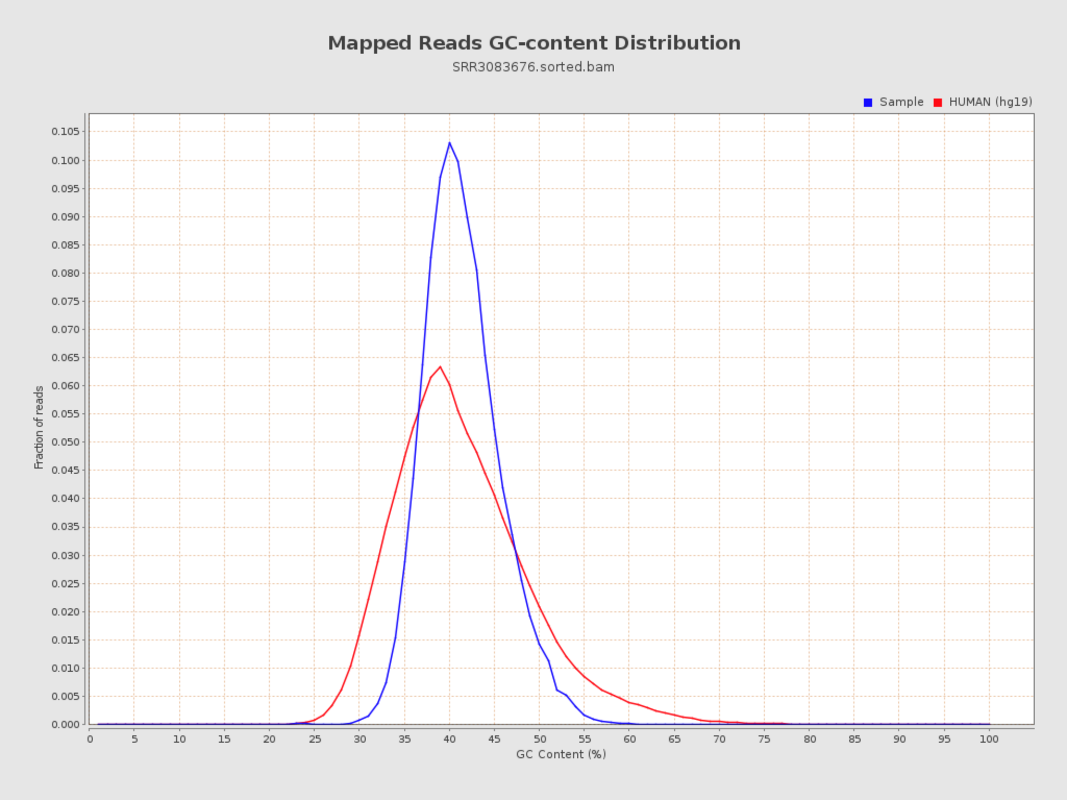
7. Results : Duplication Rate Histogram



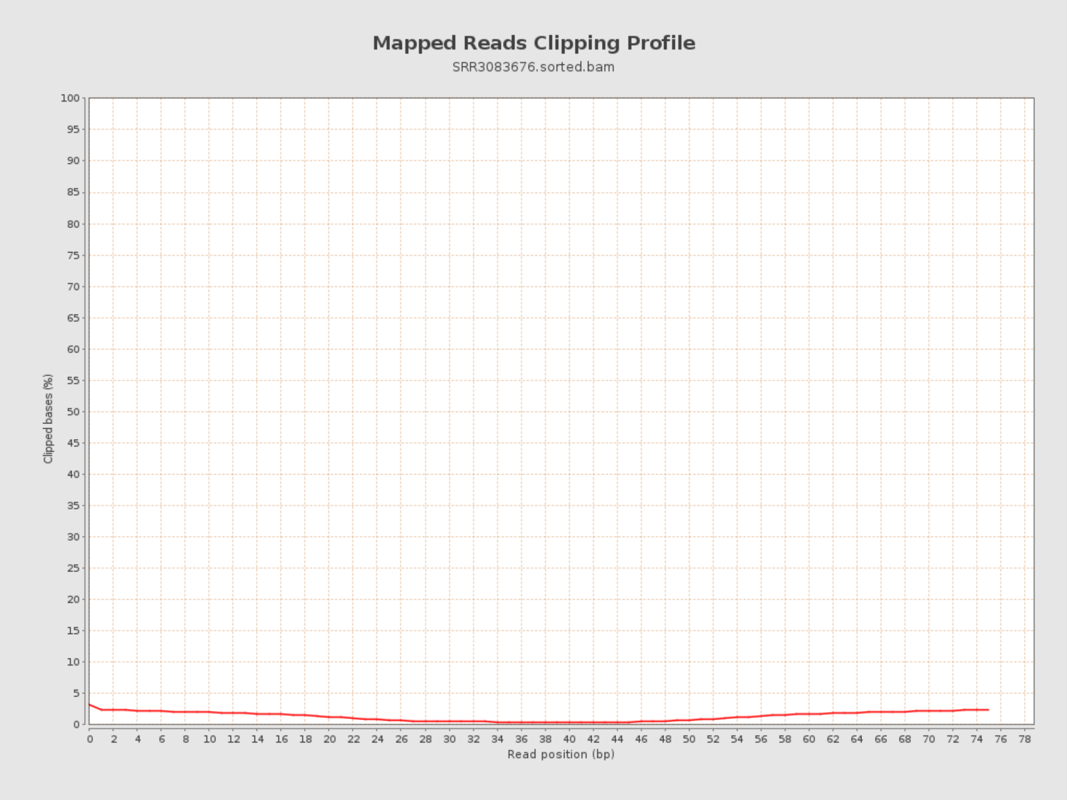
8. Results : Mapped Reads Nucleotide Content



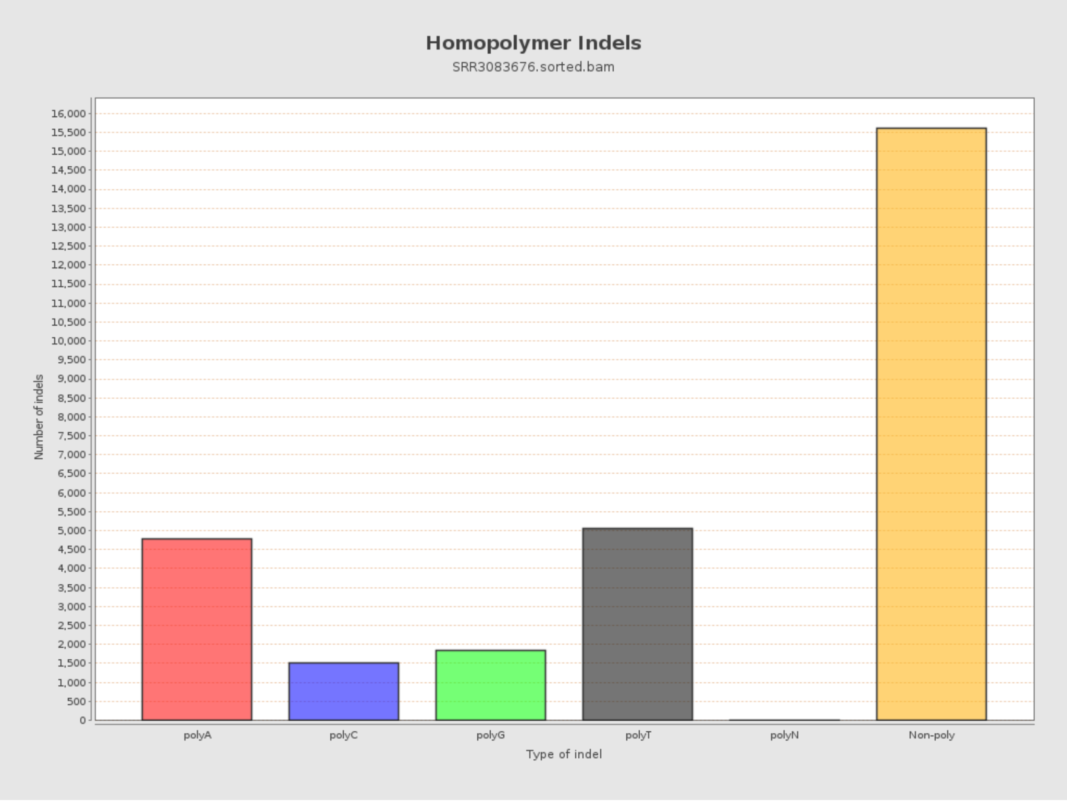
9. Results : Mapped Reads GC-content Distribution



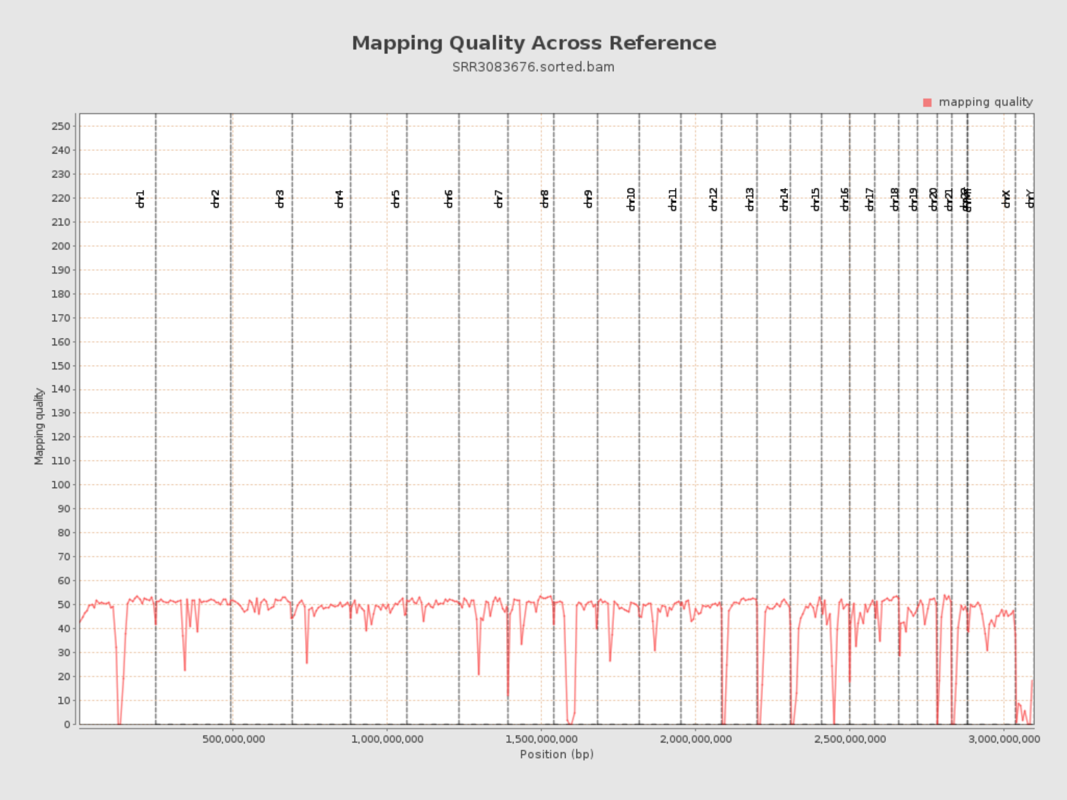
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram