Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:35:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708527.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_SRR1708527 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708527.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:35:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708527.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,086,424
Mapped reads	2,008,771 / 65.08%
Unmapped reads	1,077,653 / 34.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	799 / 0.03%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	83,336 / 2.7%
Duplication rate	2.88%
Clipped reads	482,398 / 15.63%

2.2. ACGT Content

Number/percentage of A's	26,878,297 / 28.25%
Number/percentage of C's	17,863,752 / 18.78%
Number/percentage of T's	30,041,075 / 31.58%
Number/percentage of G's	20,345,470 / 21.39%
Number/percentage of N's	1,298 / 0%
GC Percentage	40.17%

2.3. Coverage

Mean	0.0307

Standard Deviation	0.3112

2.4. Mapping Quality

Mean Mapping Quality	38.81

2.5. Mismatches and indels

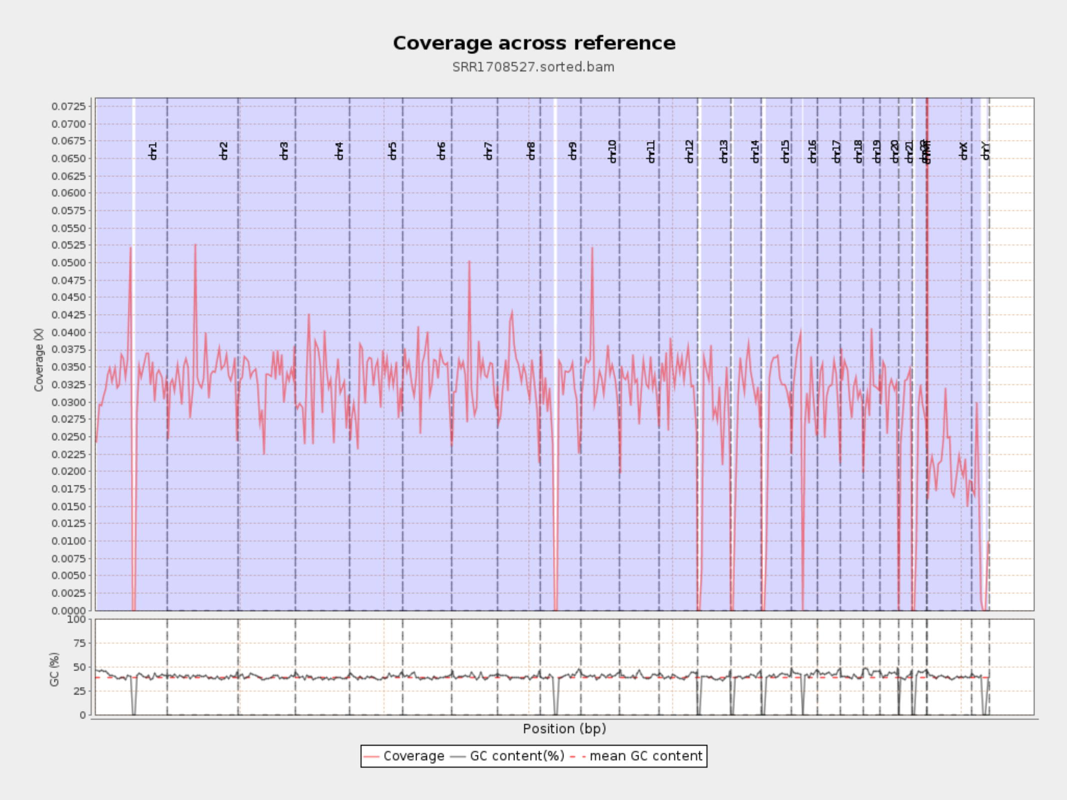
General error rate	0.55%
Mismatches	517,516
Insertions	5,738
Mapped reads with at least one insertion	0.28%
Deletions	15,157
Mapped reads with at least one deletion	0.75%
Homopolymer indels	46.83%

2.6. Chromosome stats

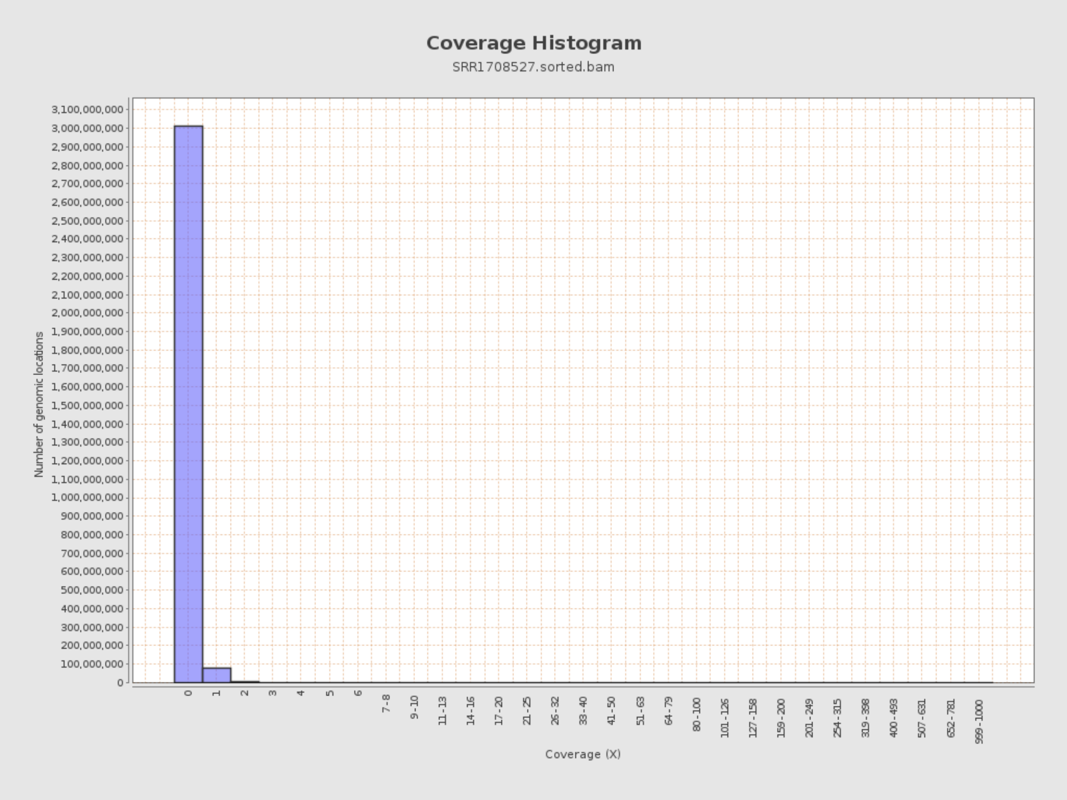
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7886987	0.0316	0.483
chr2	243199373	8301294	0.0341	0.4838
chr3	198022430	6599999	0.0333	0.2124
chr4	191154276	6151234	0.0322	0.2163
chr5	180915260	5940078	0.0328	0.2064
chr6	171115067	5868784	0.0343	0.3036
chr7	159138663	5350244	0.0336	0.3321

chr8	146364022	4885897	0.0334	0.4346
chr9	141213431	4014075	0.0284	0.2708
chr10	135534747	4662935	0.0344	0.265
chr11	135006516	4409248	0.0327	0.2971
chr12	133851895	4512874	0.0337	0.2132
chr13	115169878	2964108	0.0257	0.237
chr14	107349540	2938451	0.0274	0.2016
chr15	102531392	2774673	0.0271	0.1971
chr16	90354753	2615371	0.0289	0.2114
chr17	81195210	2546586	0.0314	0.241
chr18	78077248	2521003	0.0323	0.4297
chr19	59128983	1867880	0.0316	0.3563
chr20	63025520	1973331	0.0313	0.2095
chr21	48129895	1309485	0.0272	0.2062
chr22	51304566	1042304	0.0203	0.1672
chrMT	16571	111098	6.7044	4.5406
chrX	155270560	3233028	0.0208	0.2002
chrY	59373566	672132	0.0113	0.1408

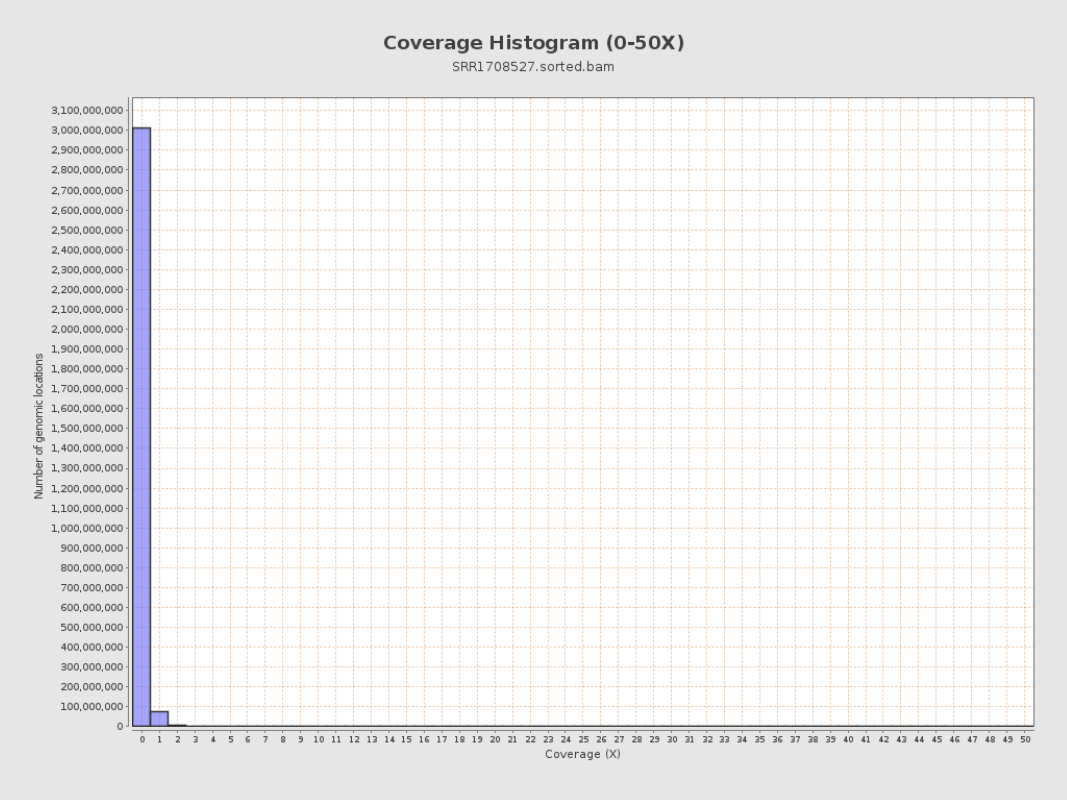
3. Results : Coverage across reference



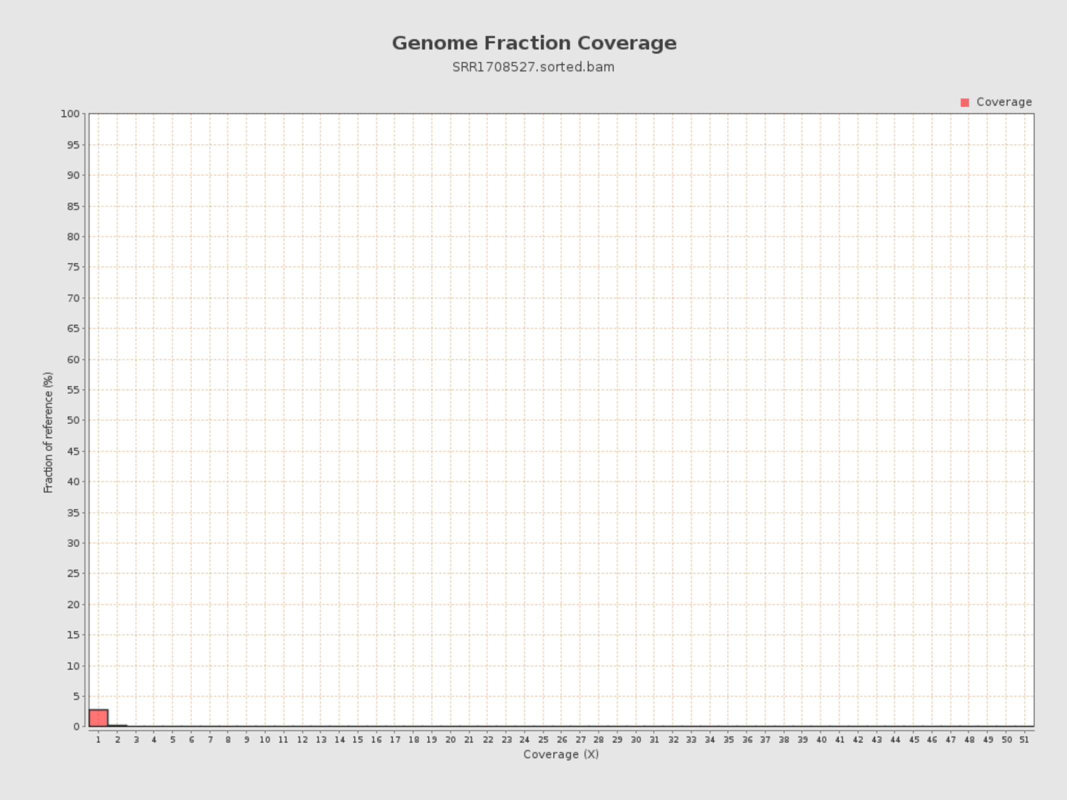
4. Results : Coverage Histogram



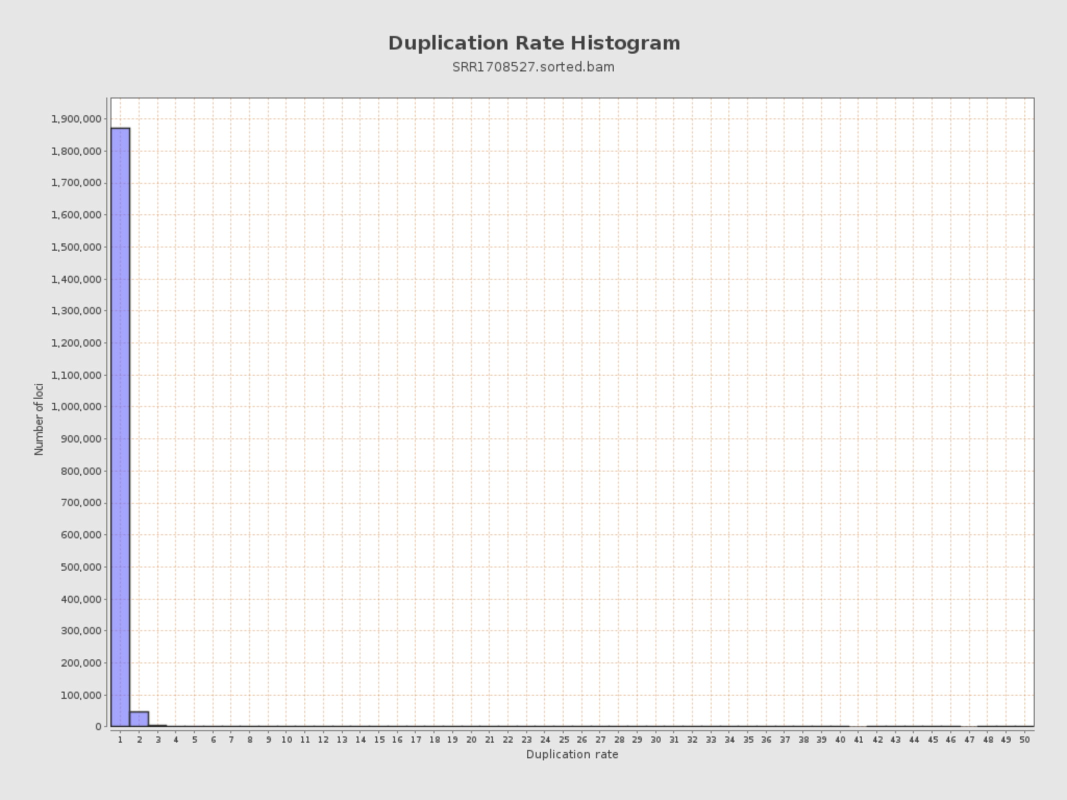
5. Results : Coverage Histogram (0-50X)



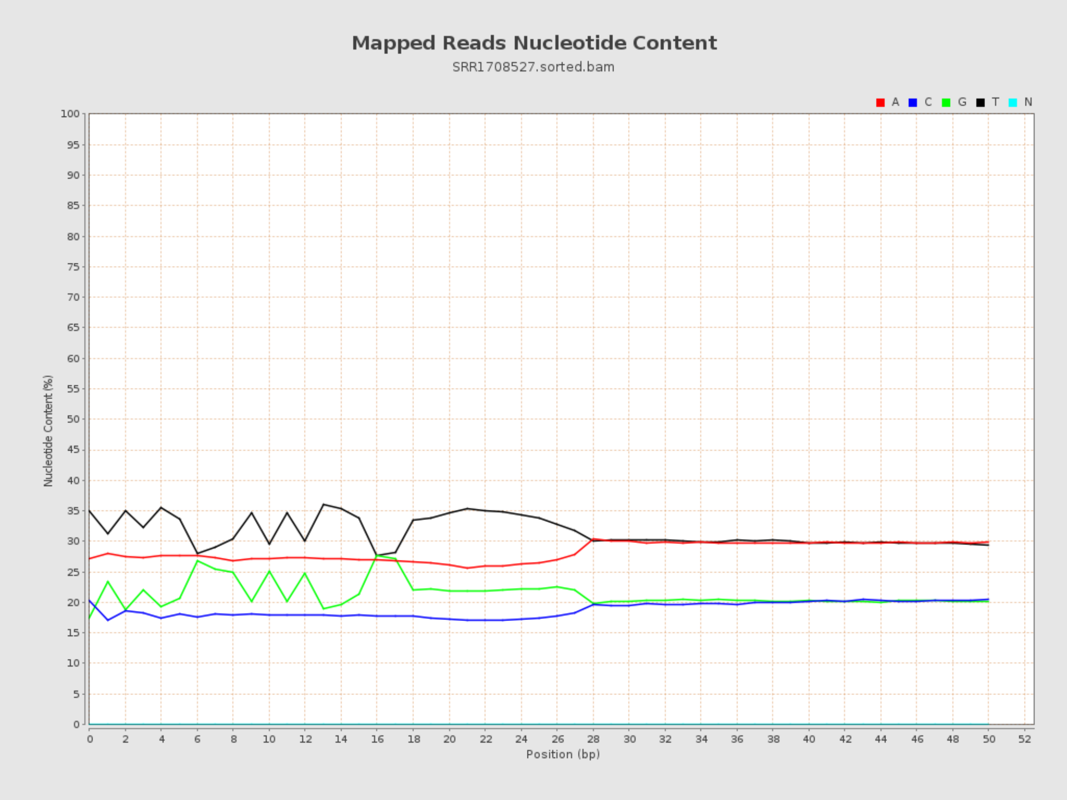
6. Results : Genome Fraction Coverage



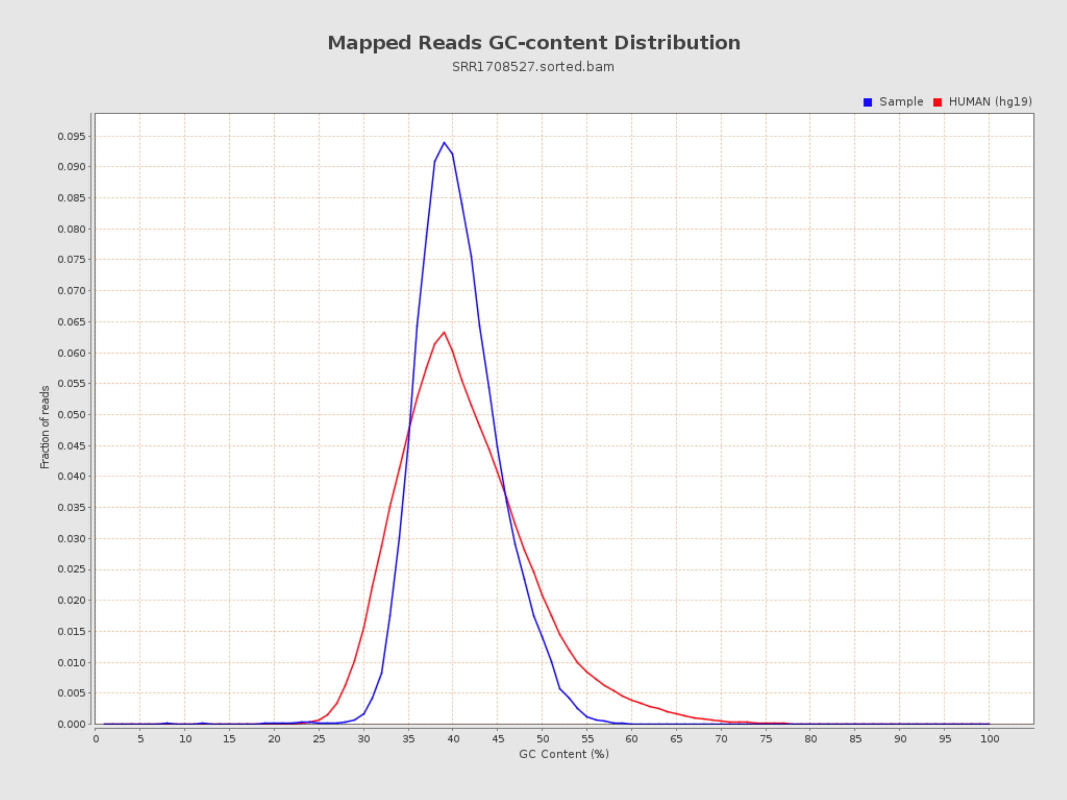
7. Results : Duplication Rate Histogram



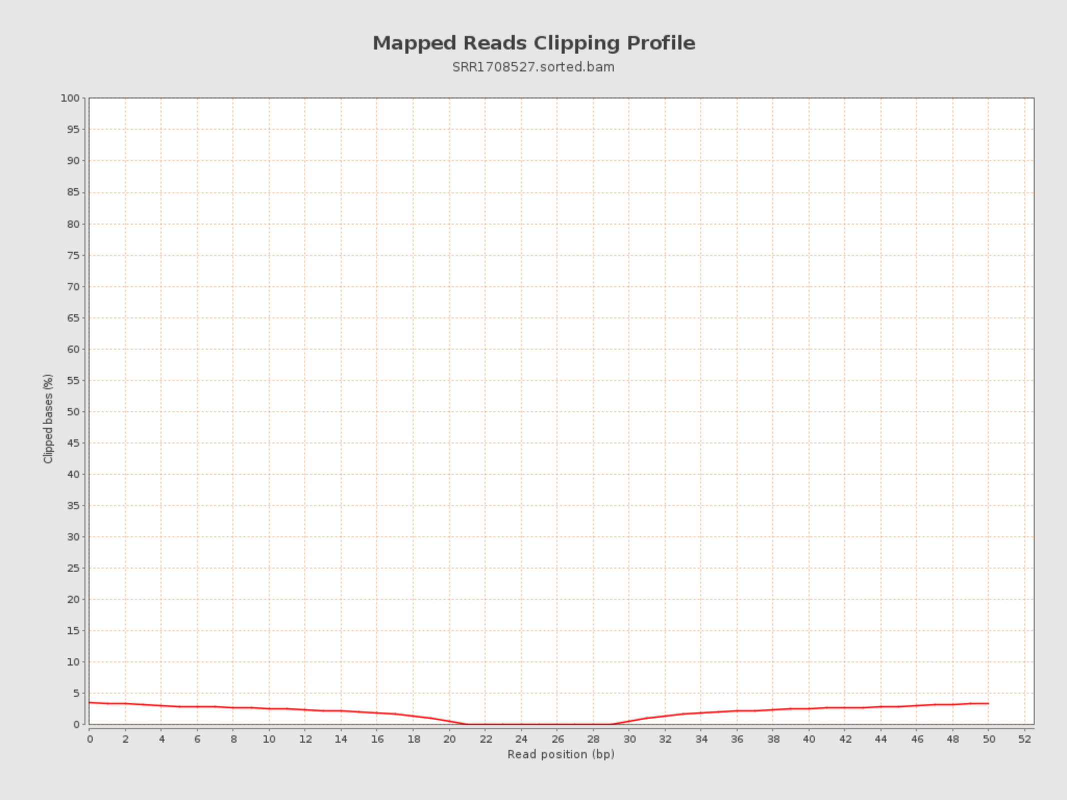
8. Results : Mapped Reads Nucleotide Content



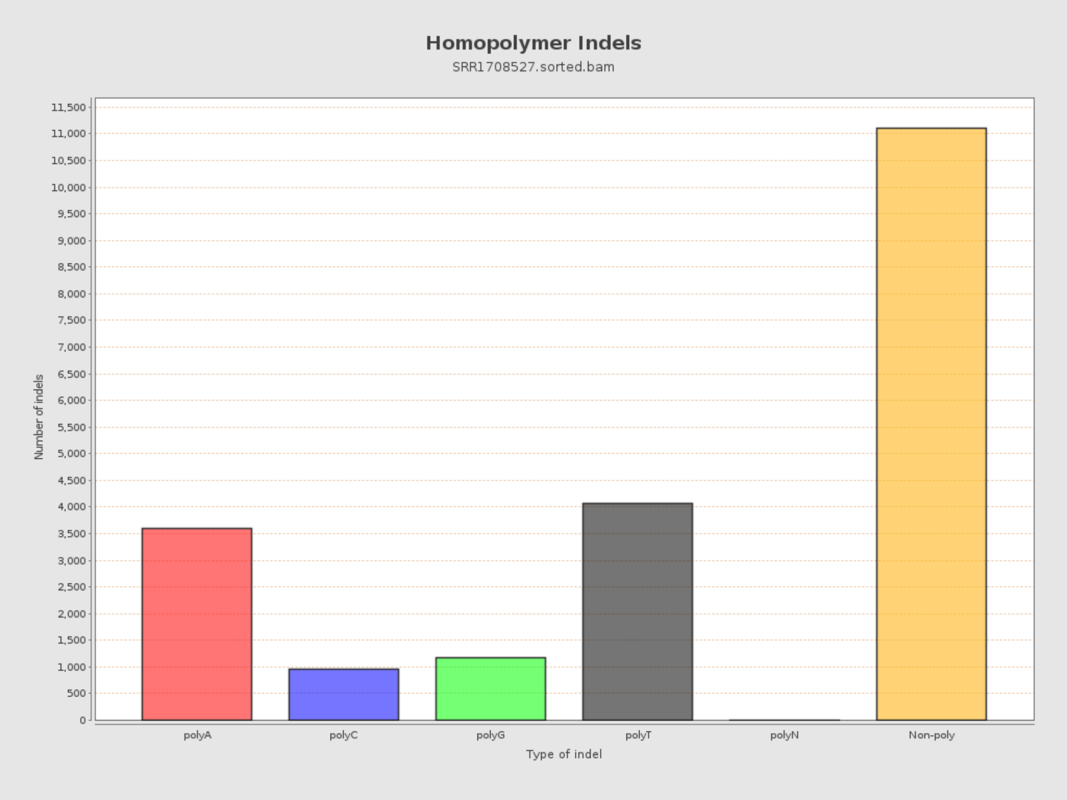
9. Results : Mapped Reads GC-content Distribution



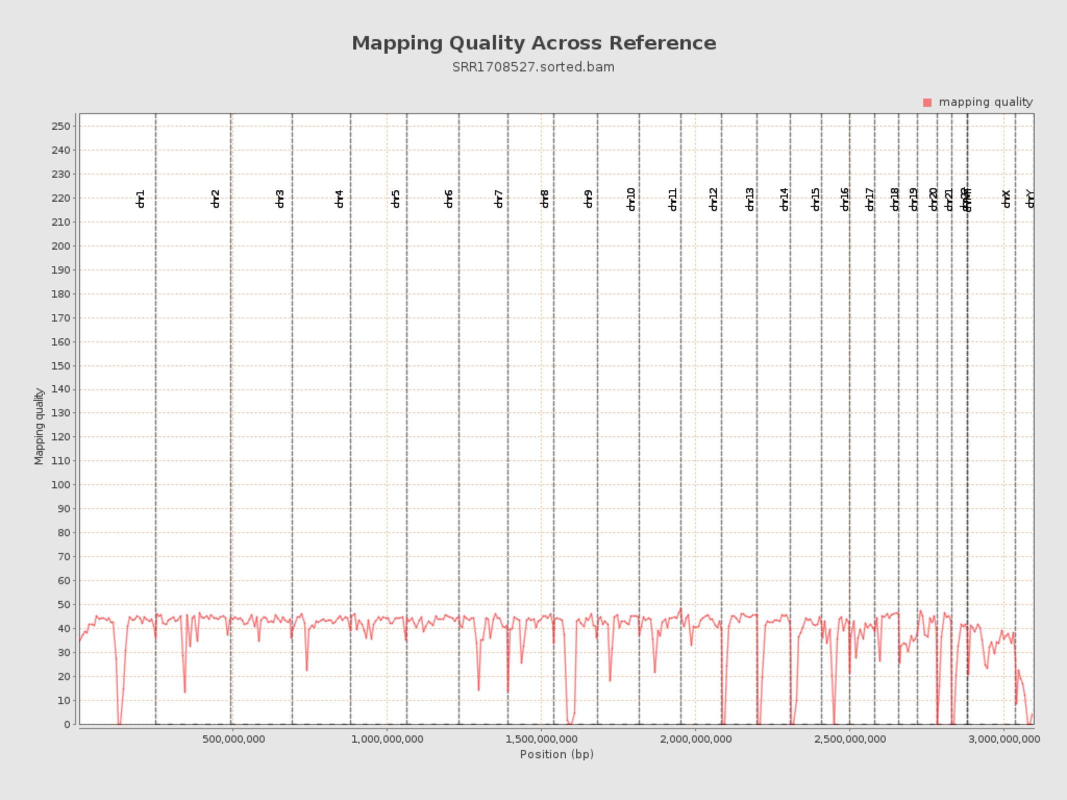
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram