Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:38:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708629.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_SRR1708629 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708629.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:38:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708629.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,631,112
Mapped reads	2,659,742 / 73.25%
Unmapped reads	971,370 / 26.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,017 / 0.03%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	89,508 / 2.47%
Duplication rate	2.29%
Clipped reads	409,958 / 11.29%

2.2. ACGT Content

Number/percentage of A's	38,297,186 / 29.54%
Number/percentage of C's	24,575,947 / 18.96%
Number/percentage of T's	40,707,804 / 31.4%
Number/percentage of G's	26,041,176 / 20.09%
Number/percentage of N's	11,424 / 0.01%
GC Percentage	39.05%

2.3. Coverage

Mean	0.0419

Standard Deviation	0.4024

2.4. Mapping Quality

Mean Mapping Quality	43.38

2.5. Mismatches and indels

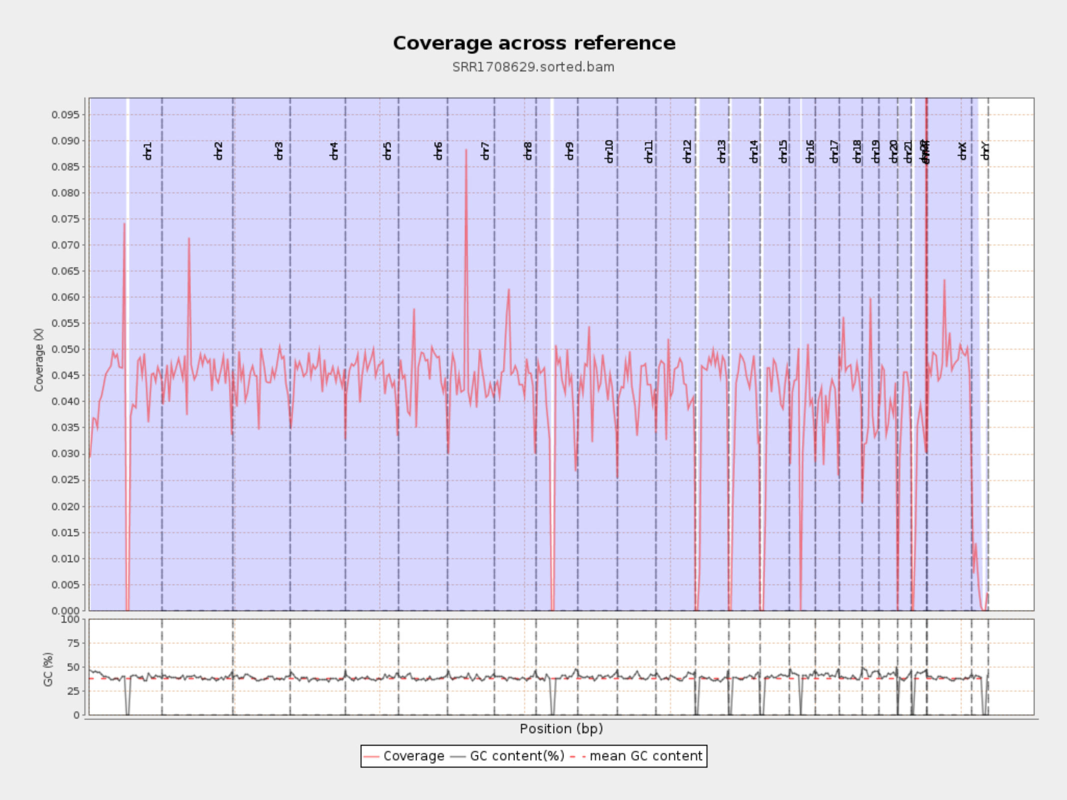
General error rate	0.64%
Mismatches	825,247
Insertions	6,245
Mapped reads with at least one insertion	0.23%
Deletions	16,218
Mapped reads with at least one deletion	0.61%
Homopolymer indels	48.16%

2.6. Chromosome stats

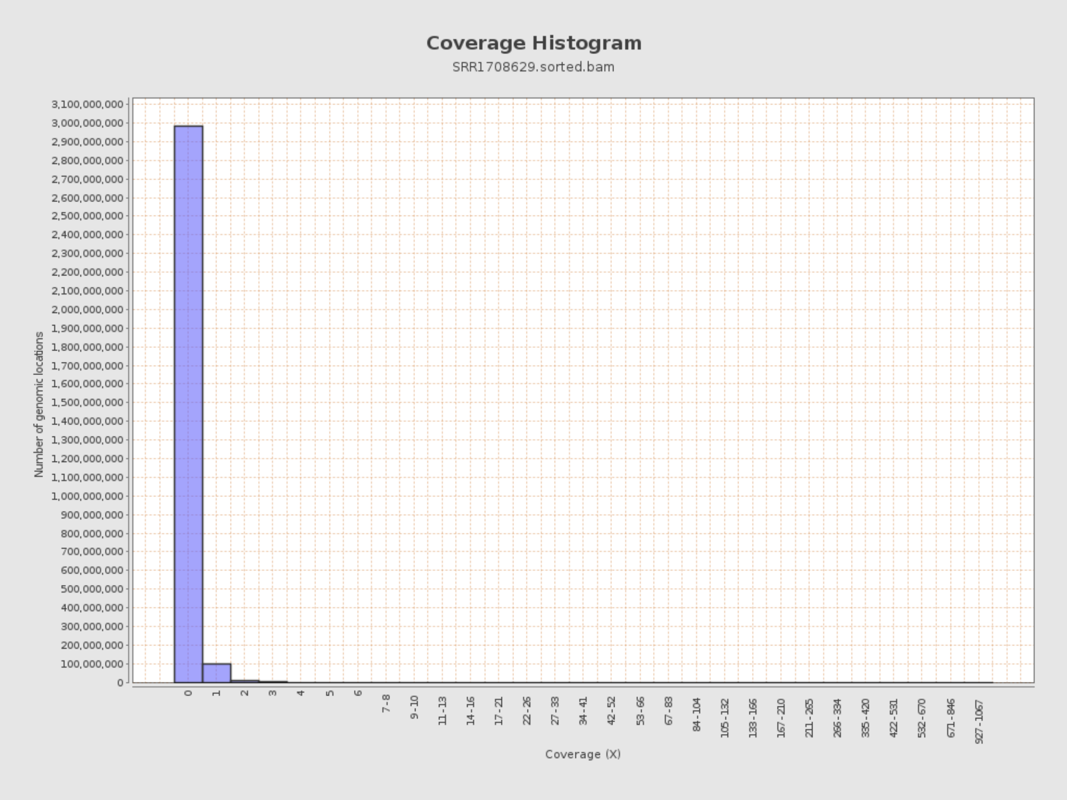
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10348844	0.0415	0.731
chr2	243199373	11235209	0.0462	0.4172
chr3	198022430	8861699	0.0448	0.2383
chr4	191154276	8682366	0.0454	0.243
chr5	180915260	8211344	0.0454	0.2436
chr6	171115067	7812622	0.0457	0.2991
chr7	159138663	7220710	0.0454	0.6218

chr8	146364022	6654148	0.0455	0.6434
chr9	141213431	5428262	0.0384	0.3257
chr10	135534747	5929817	0.0438	0.3195
chr11	135006516	5763063	0.0427	0.3237
chr12	133851895	5825870	0.0435	0.2432
chr13	115169878	4502993	0.0391	0.2232
chr14	107349540	4011738	0.0374	0.2389
chr15	102531392	3677381	0.0359	0.212
chr16	90354753	3384880	0.0375	0.2344
chr17	81195210	3083241	0.038	0.2645
chr18	78077248	3624261	0.0464	0.6918
chr19	59128983	2191742	0.0371	0.571
chr20	63025520	2498833	0.0396	0.2397
chr21	48129895	1712706	0.0356	0.2295
chr22	51304566	1274881	0.0248	0.1748
chrMT	16571	6763	0.4081	0.7036
chrX	155270560	7413336	0.0477	0.2788
chrY	59373566	301672	0.0051	0.0958

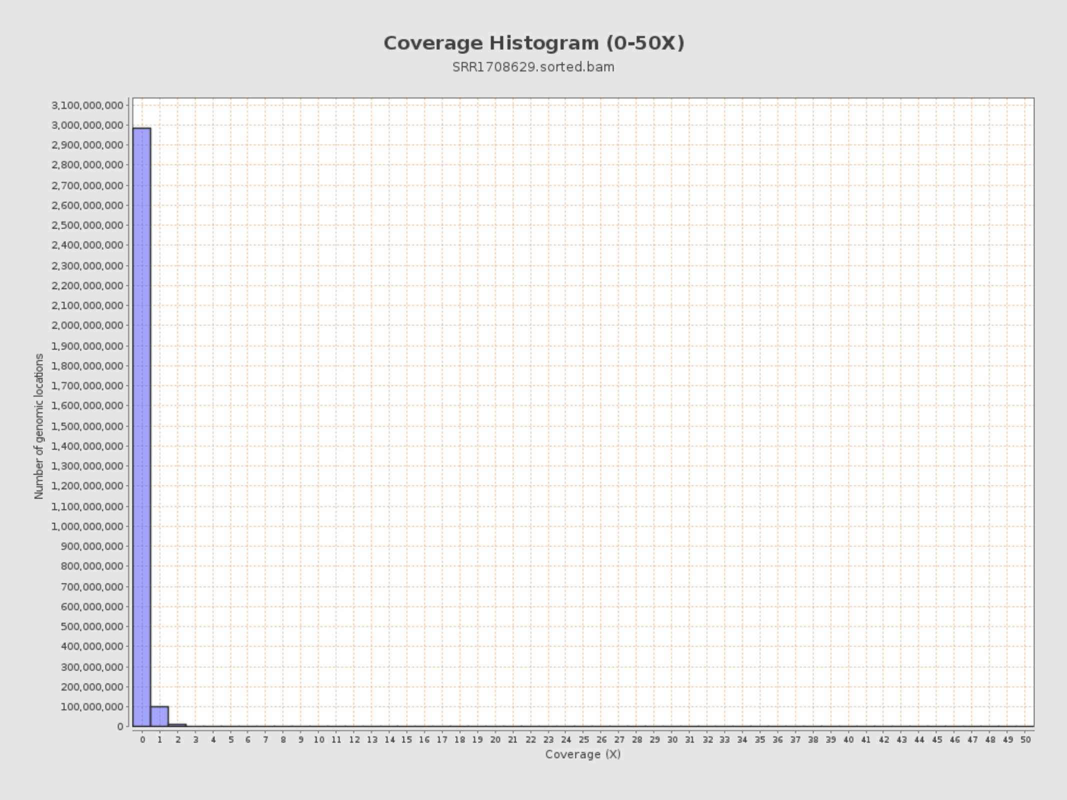
3. Results : Coverage across reference



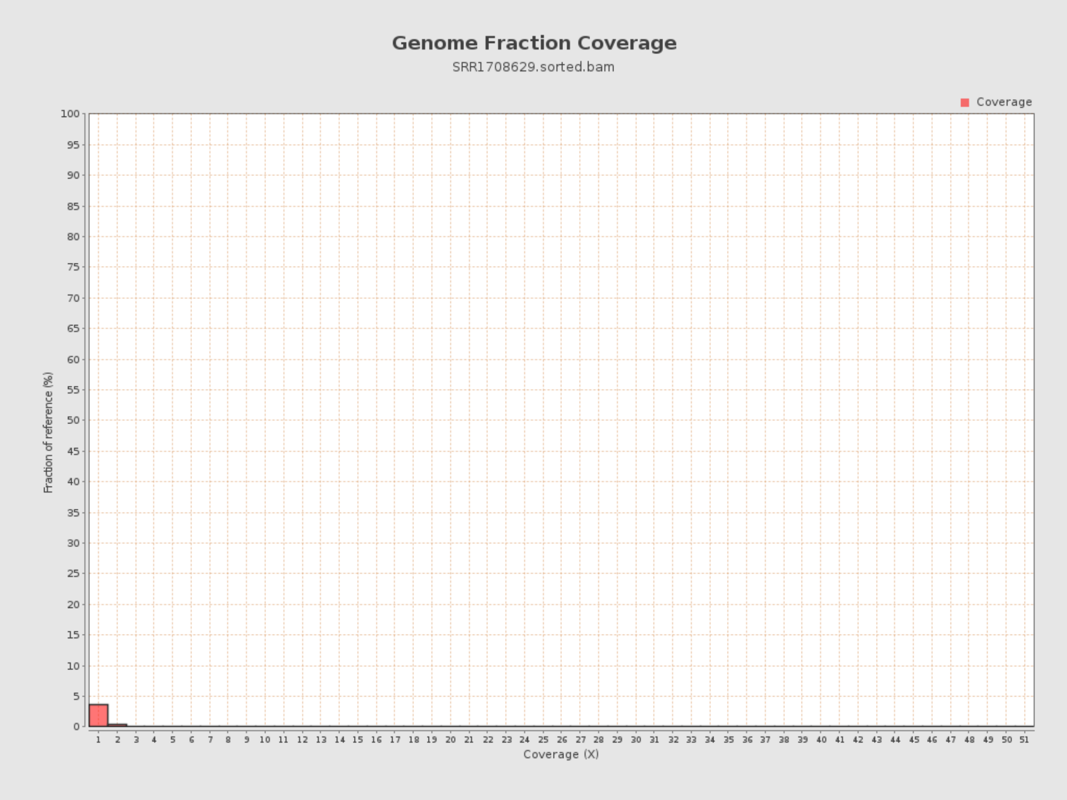
4. Results : Coverage Histogram



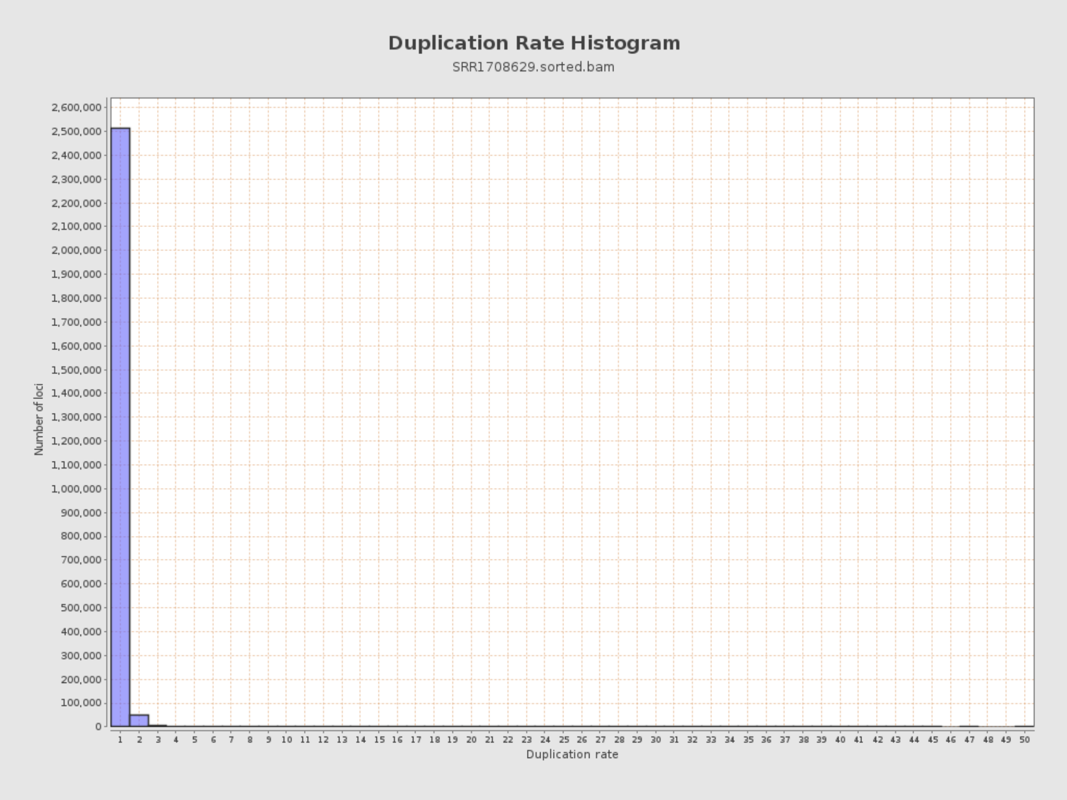
5. Results : Coverage Histogram (0-50X)



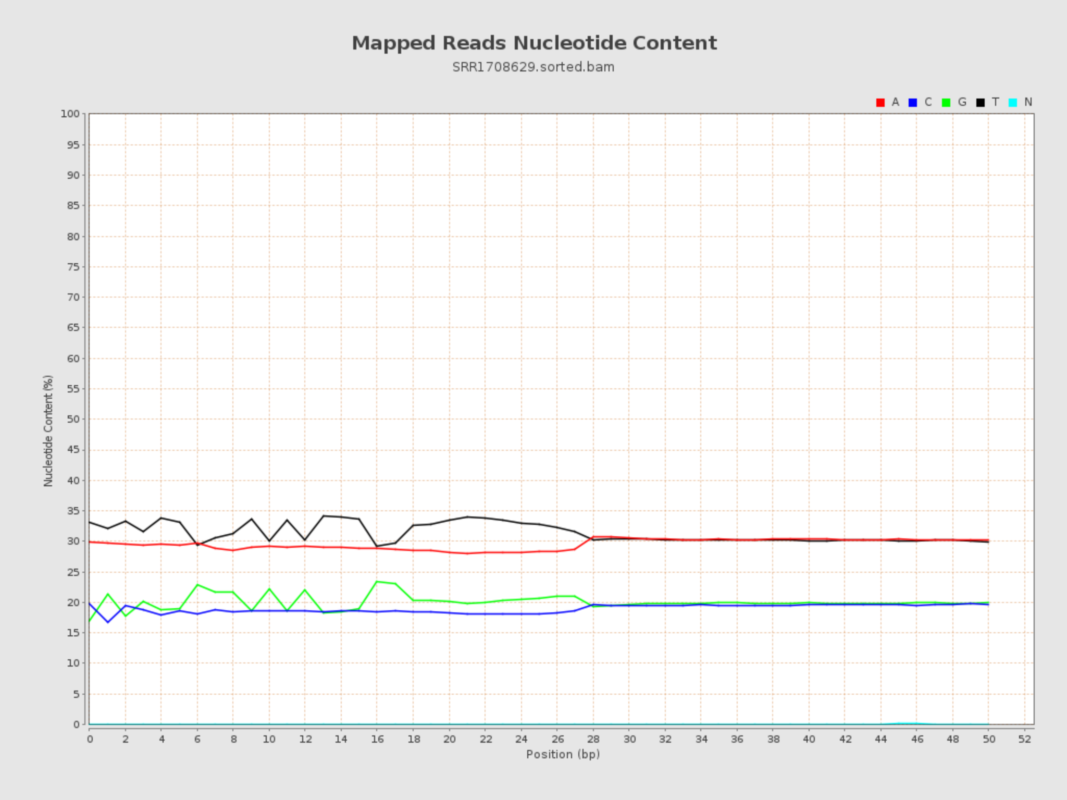
6. Results : Genome Fraction Coverage



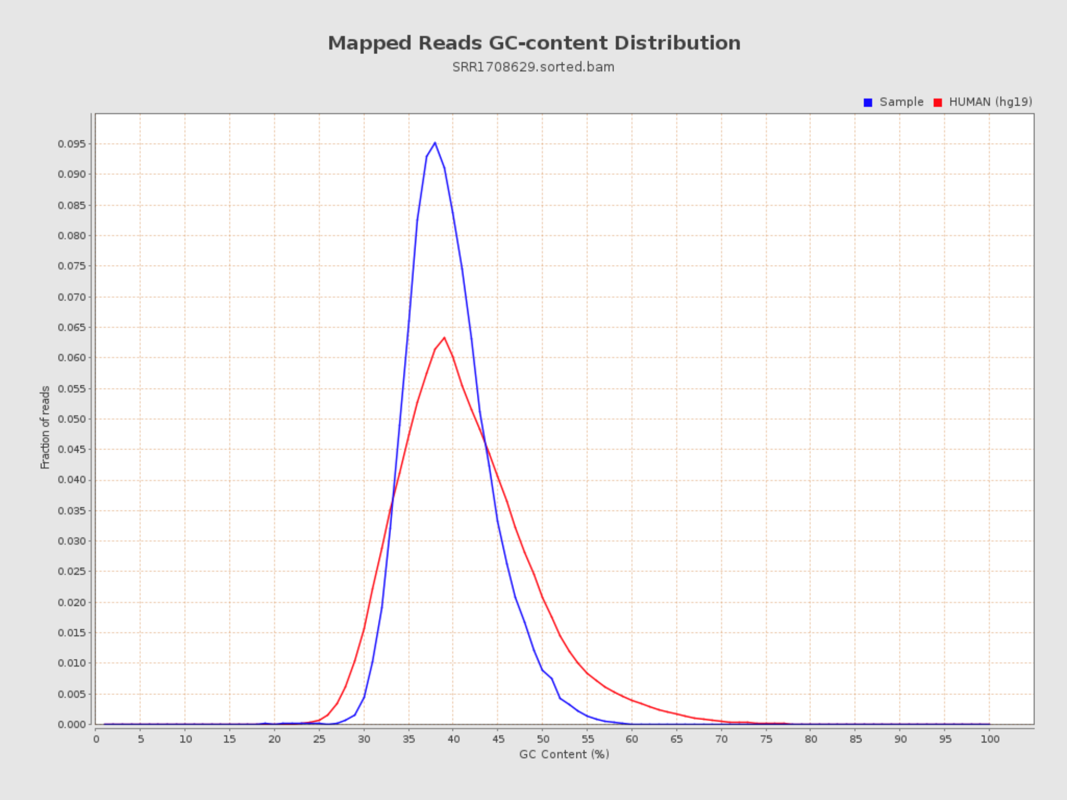
7. Results : Duplication Rate Histogram



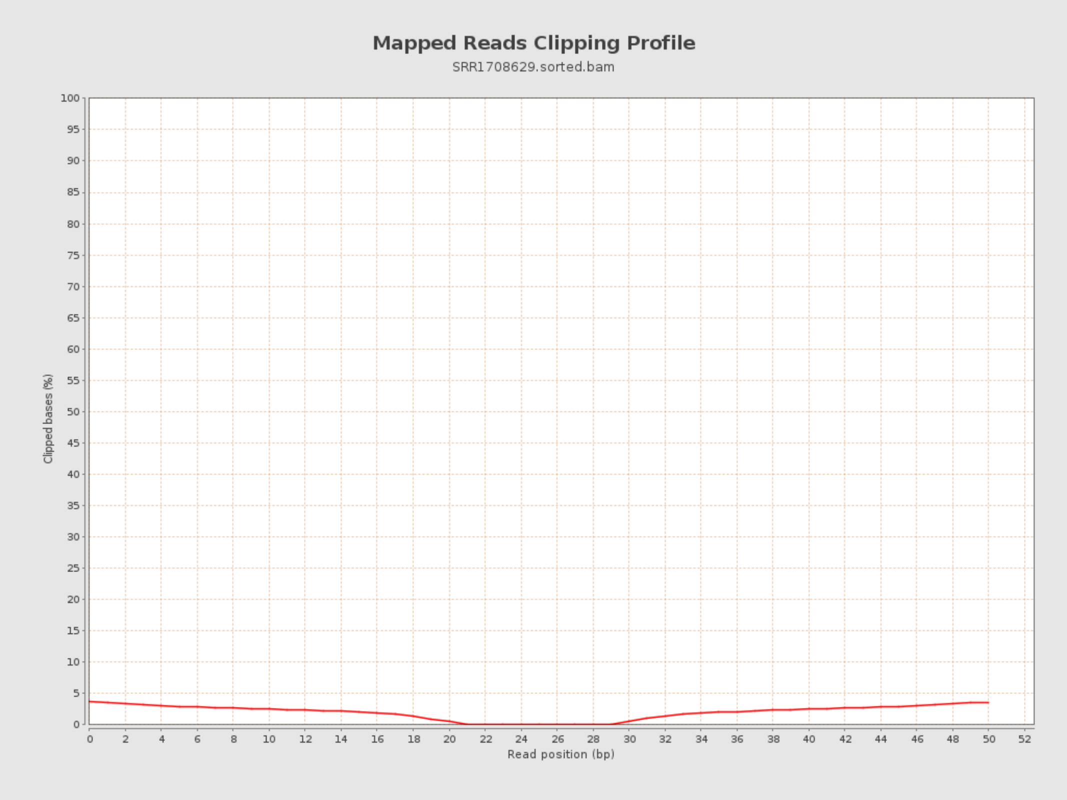
8. Results : Mapped Reads Nucleotide Content



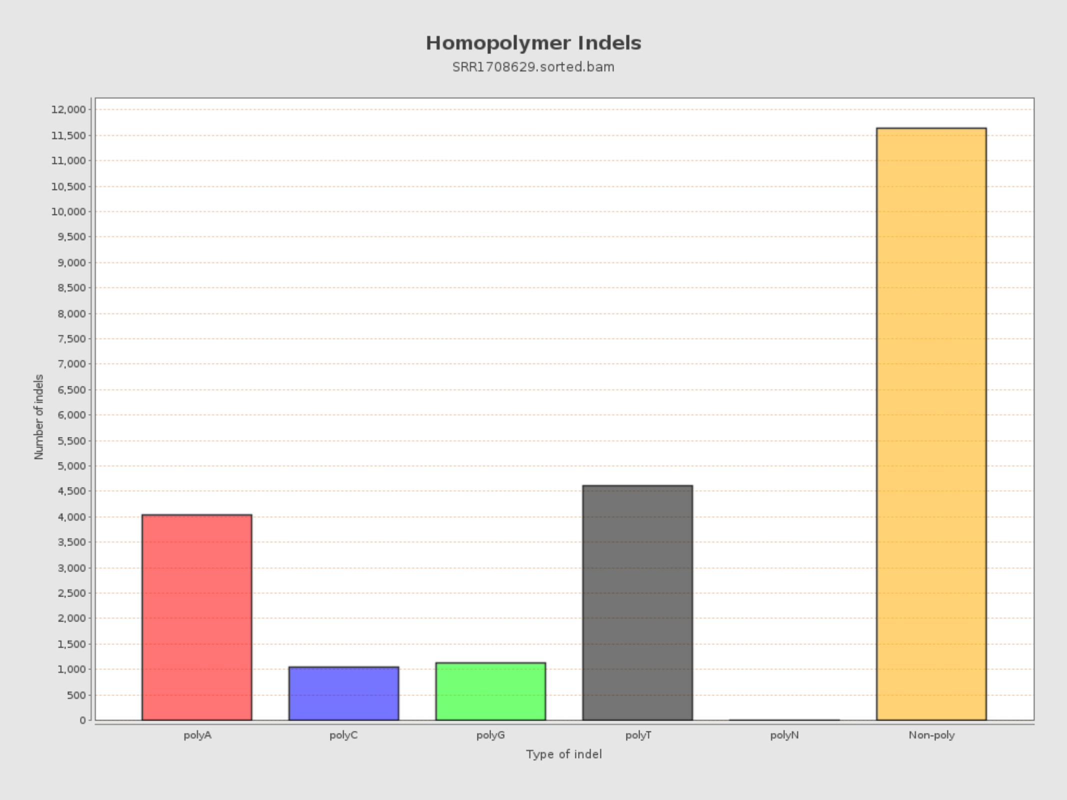
9. Results : Mapped Reads GC-content Distribution



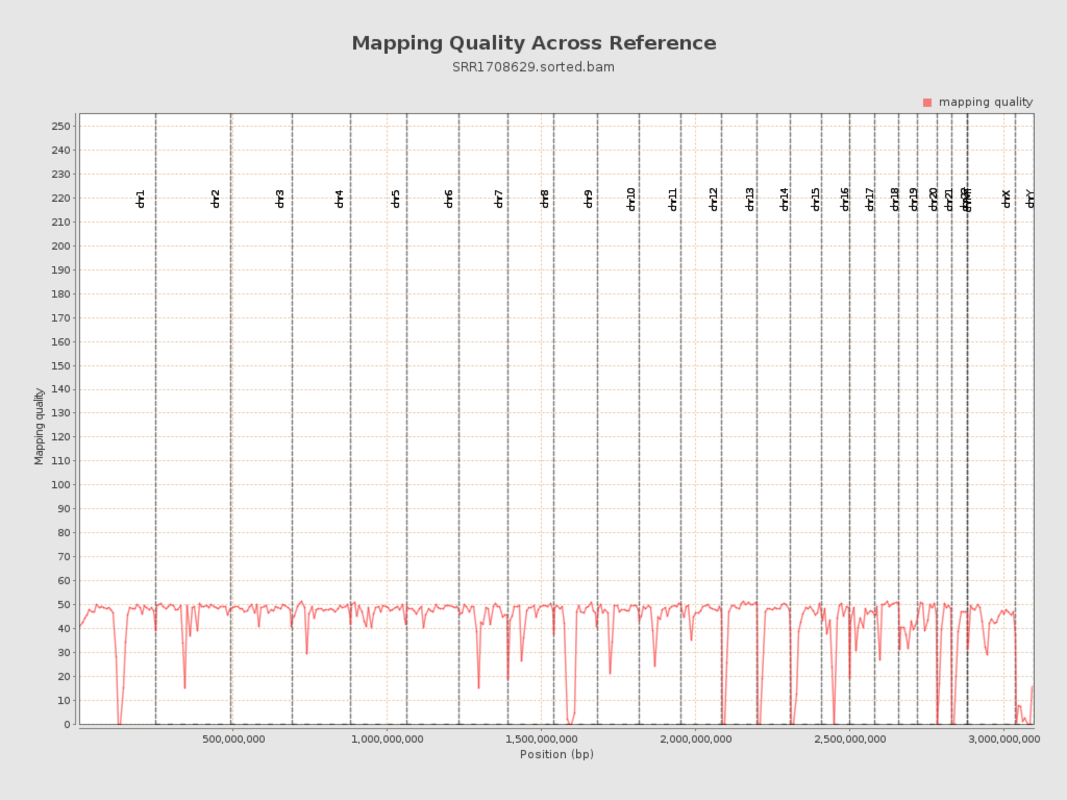
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram