Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:56:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708619.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_SRR1708619 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708619.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:56:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708619.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,400,589
Mapped reads	2,447,260 / 71.97%
Unmapped reads	953,329 / 28.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	863 / 0.03%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	84,724 / 2.49%
Duplication rate	2.37%
Clipped reads	386,209 / 11.36%

2.2. ACGT Content

Number/percentage of A's	34,894,791 / 29.31%
Number/percentage of C's	22,565,261 / 18.96%
Number/percentage of T's	37,436,851 / 31.45%
Number/percentage of G's	24,127,357 / 20.27%
Number/percentage of N's	10,427 / 0.01%
GC Percentage	39.23%

2.3. Coverage

Mean	0.0385

Standard Deviation	0.3816

2.4. Mapping Quality

Mean Mapping Quality	42.61

2.5. Mismatches and indels

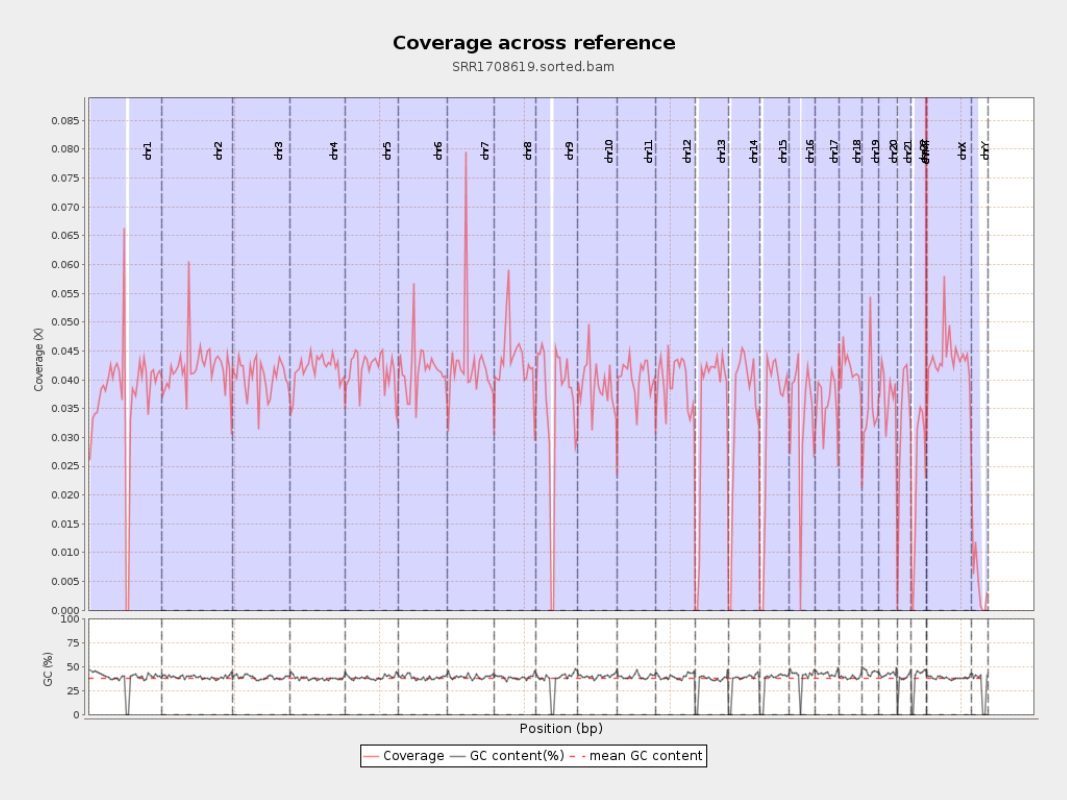
General error rate	0.64%
Mismatches	757,567
Insertions	5,711
Mapped reads with at least one insertion	0.23%
Deletions	15,244
Mapped reads with at least one deletion	0.62%
Homopolymer indels	48.12%

2.6. Chromosome stats

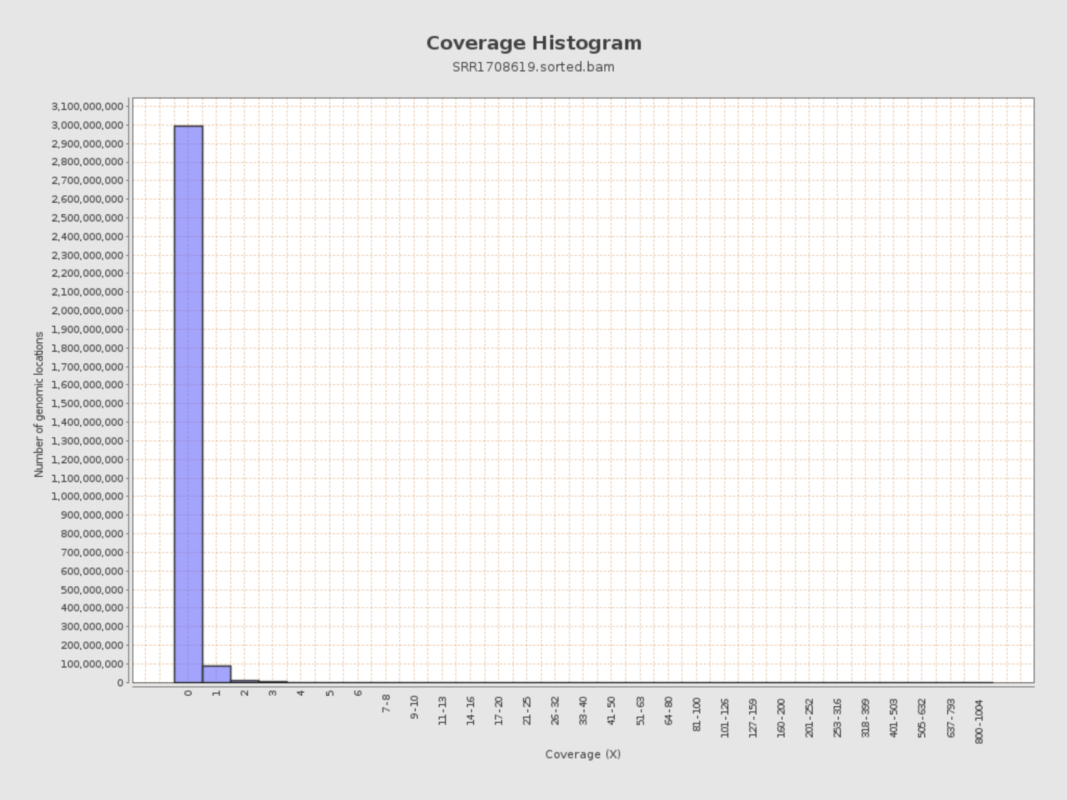
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9275986	0.0372	0.6969
chr2	243199373	10248741	0.0421	0.4123
chr3	198022430	8029042	0.0405	0.2302
chr4	191154276	7997931	0.0418	0.2366
chr5	180915260	7550211	0.0417	0.2349
chr6	171115067	7143550	0.0417	0.3239
chr7	159138663	6846238	0.043	0.5696

chr8	146364022	6355114	0.0434	0.6133
chr9	141213431	5054061	0.0358	0.3043
chr10	135534747	5300853	0.0391	0.3009
chr11	135006516	5431519	0.0402	0.306
chr12	133851895	5299834	0.0396	0.2347
chr13	115169878	4012647	0.0348	0.2162
chr14	107349540	3678142	0.0343	0.23
chr15	102531392	3388888	0.0331	0.2073
chr16	90354753	3054793	0.0338	0.2233
chr17	81195210	2889821	0.0356	0.2513
chr18	78077248	3274064	0.0419	0.5918
chr19	59128983	2093367	0.0354	0.5195
chr20	63025520	2342853	0.0372	0.2273
chr21	48129895	1556349	0.0323	0.2229
chr22	51304566	1166609	0.0227	0.17
chrMT	16571	5184	0.3128	0.6478
chrX	155270560	6774650	0.0436	0.2662
chrY	59373566	287656	0.0048	0.0868

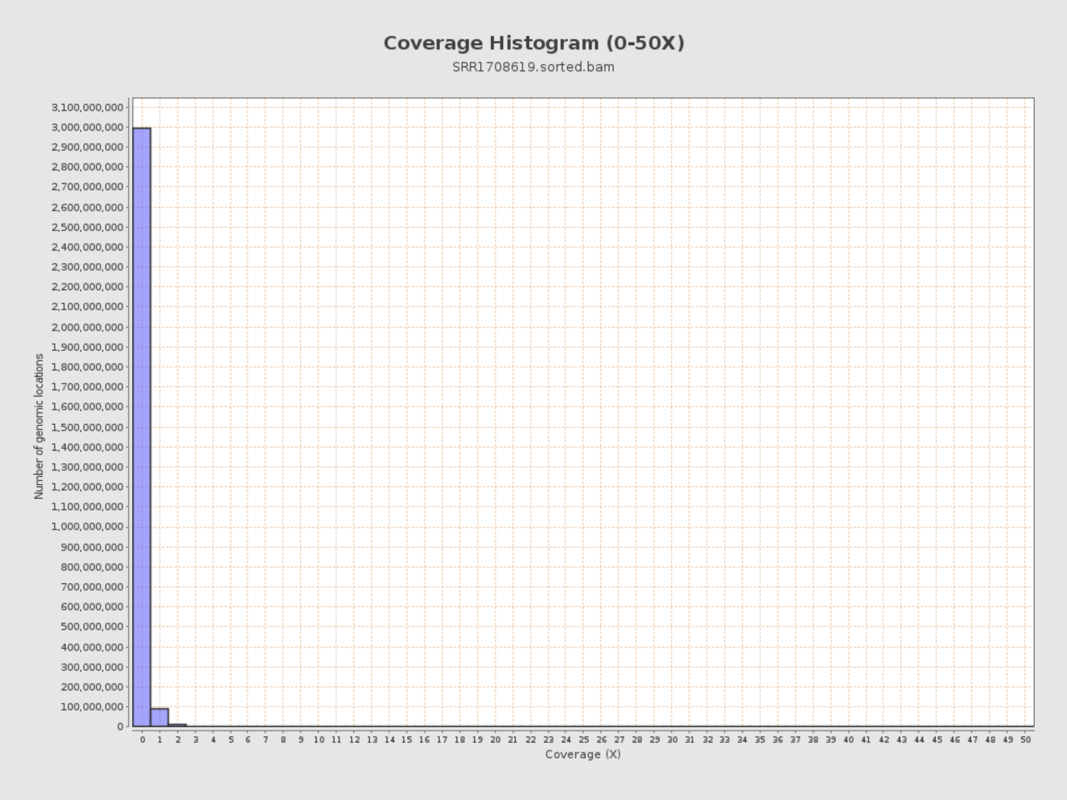
3. Results : Coverage across reference



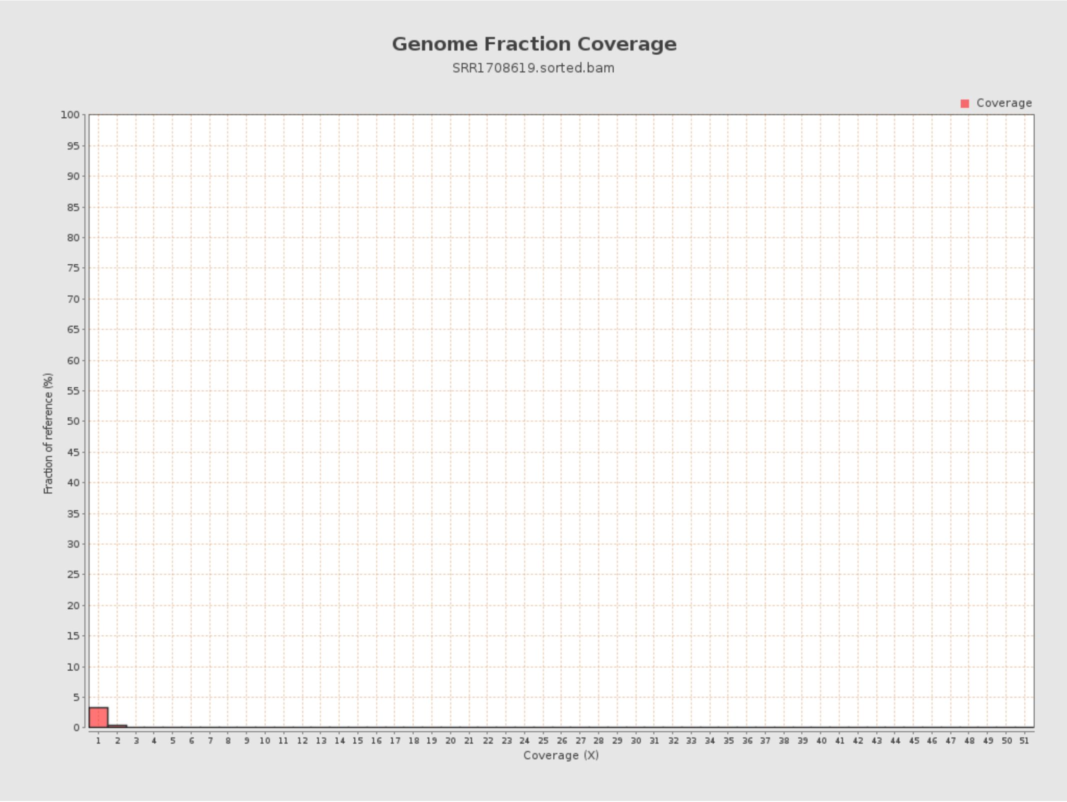
4. Results : Coverage Histogram



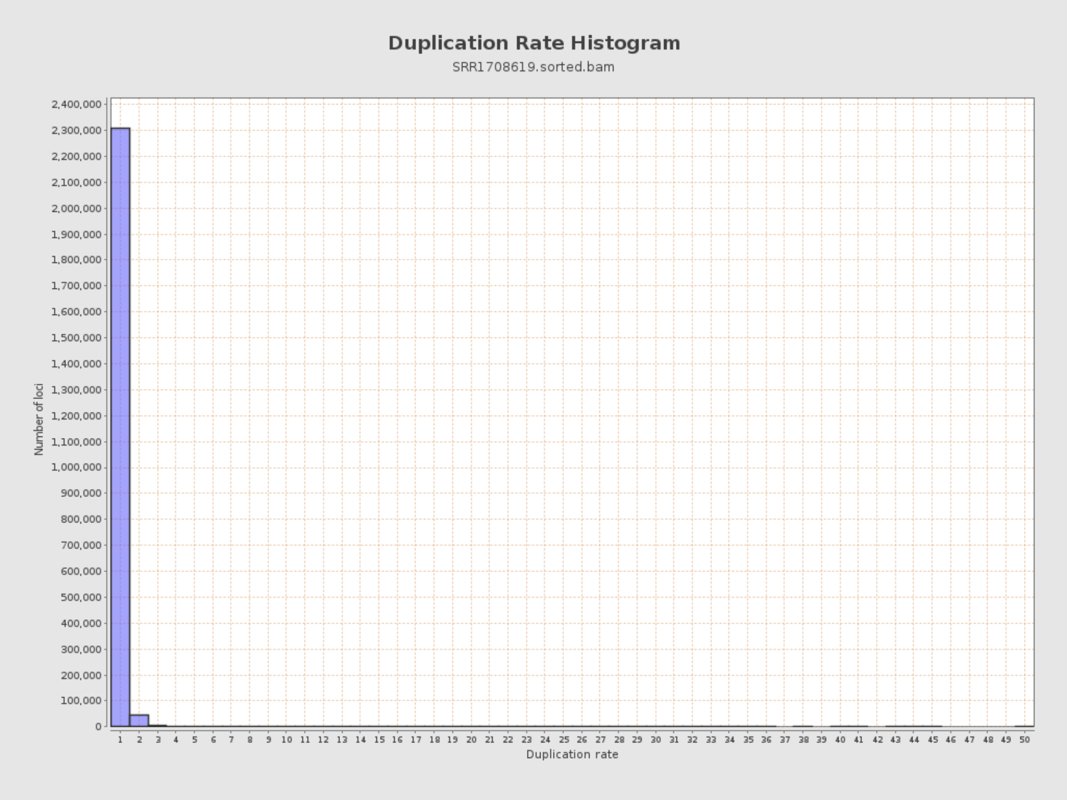
5. Results : Coverage Histogram (0-50X)



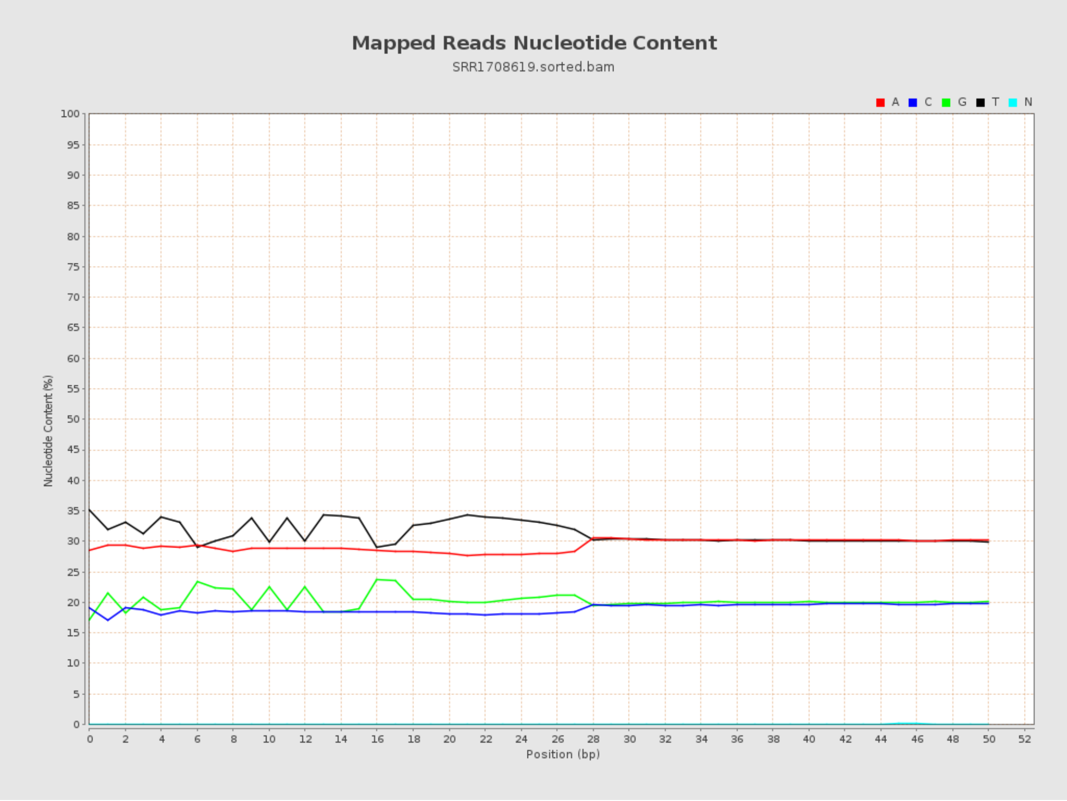
6. Results : Genome Fraction Coverage



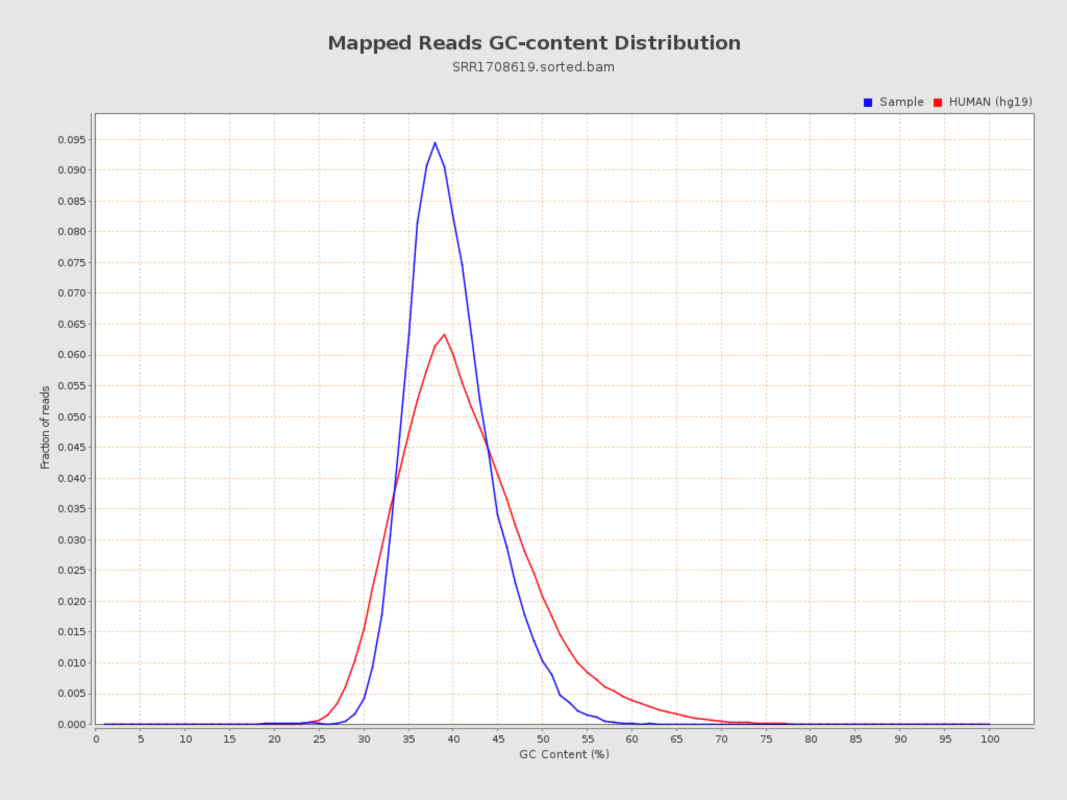
7. Results : Duplication Rate Histogram



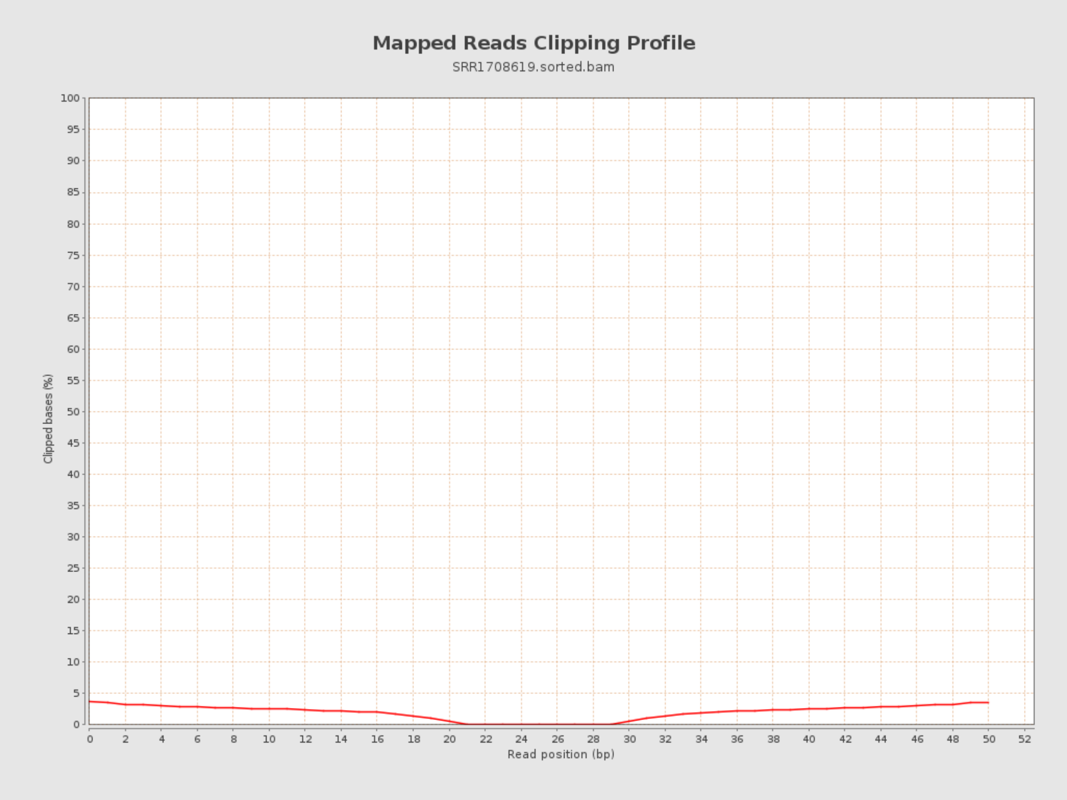
8. Results : Mapped Reads Nucleotide Content



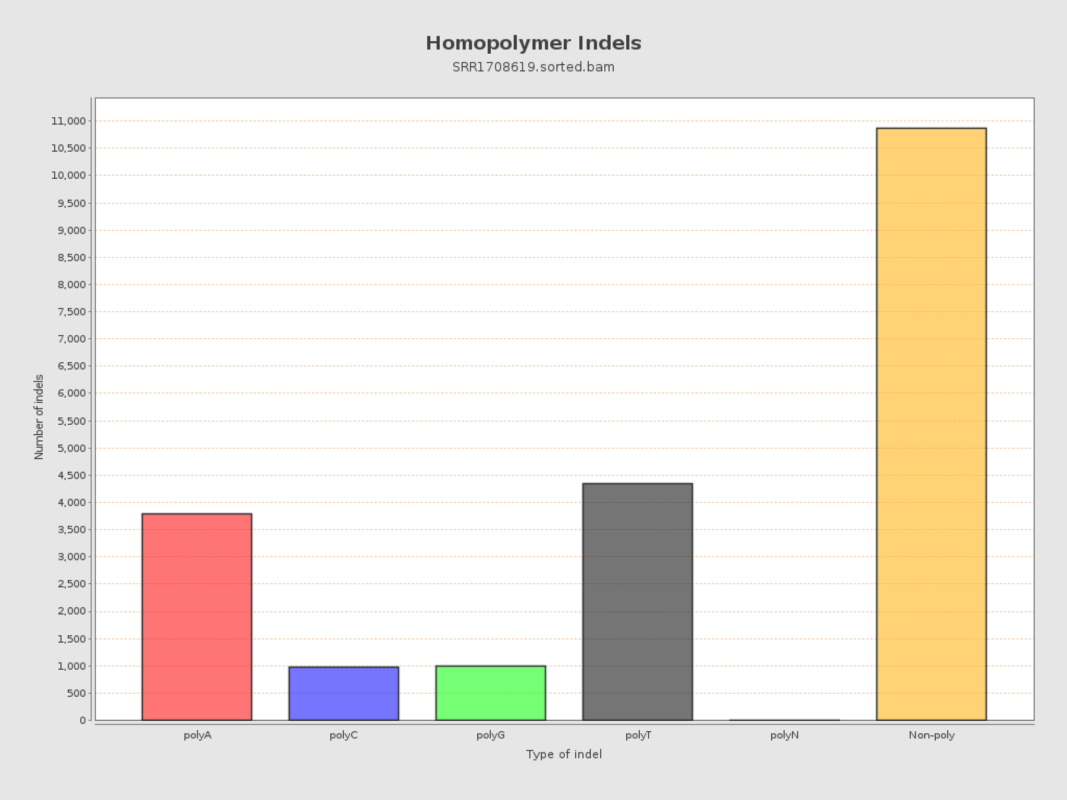
9. Results : Mapped Reads GC-content Distribution



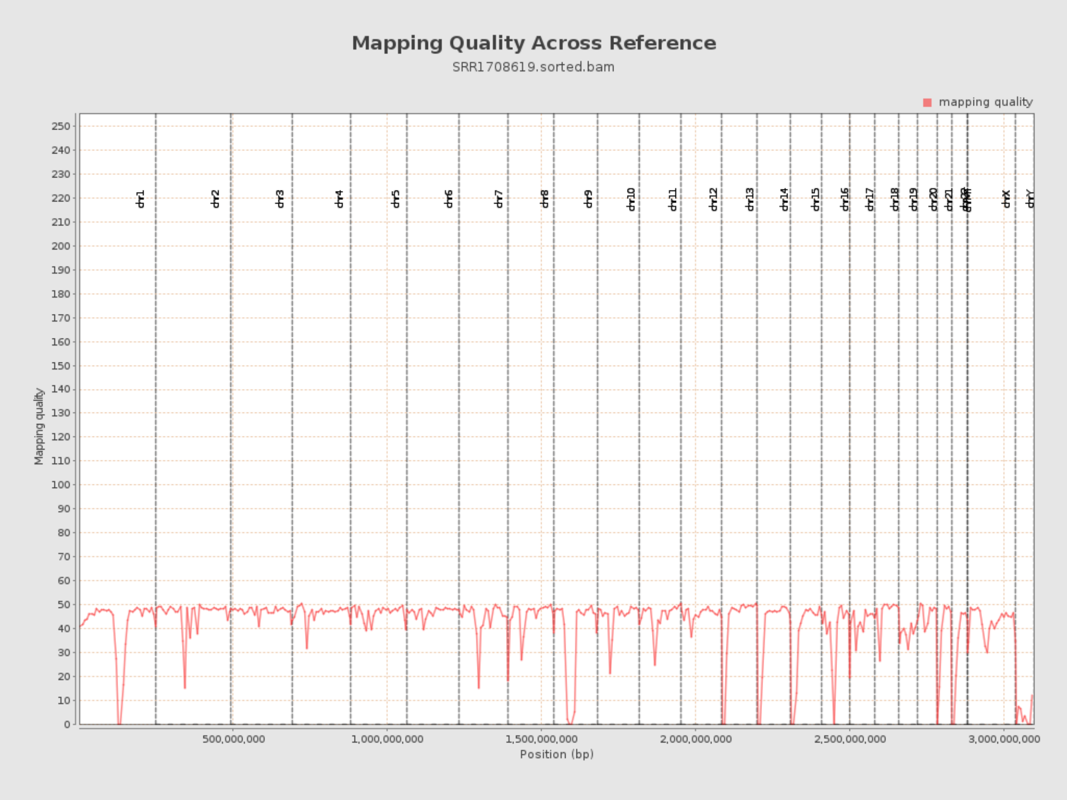
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram