Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:13:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708623.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_SRR1708623 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708623.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:13:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708623.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,964,676
Mapped reads	2,873,155 / 72.47%
Unmapped reads	1,091,521 / 27.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	949 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	118,187 / 2.98%
Duplication rate	2.83%
Clipped reads	455,006 / 11.48%

2.2. ACGT Content

Number/percentage of A's	41,071,934 / 29.4%
Number/percentage of C's	26,210,038 / 18.76%
Number/percentage of T's	44,330,631 / 31.73%
Number/percentage of G's	28,069,896 / 20.09%
Number/percentage of N's	11,931 / 0.01%
GC Percentage	38.86%

2.3. Coverage

Mean	0.0451

Standard Deviation	0.4566

2.4. Mapping Quality

Mean Mapping Quality	43.04

2.5. Mismatches and indels

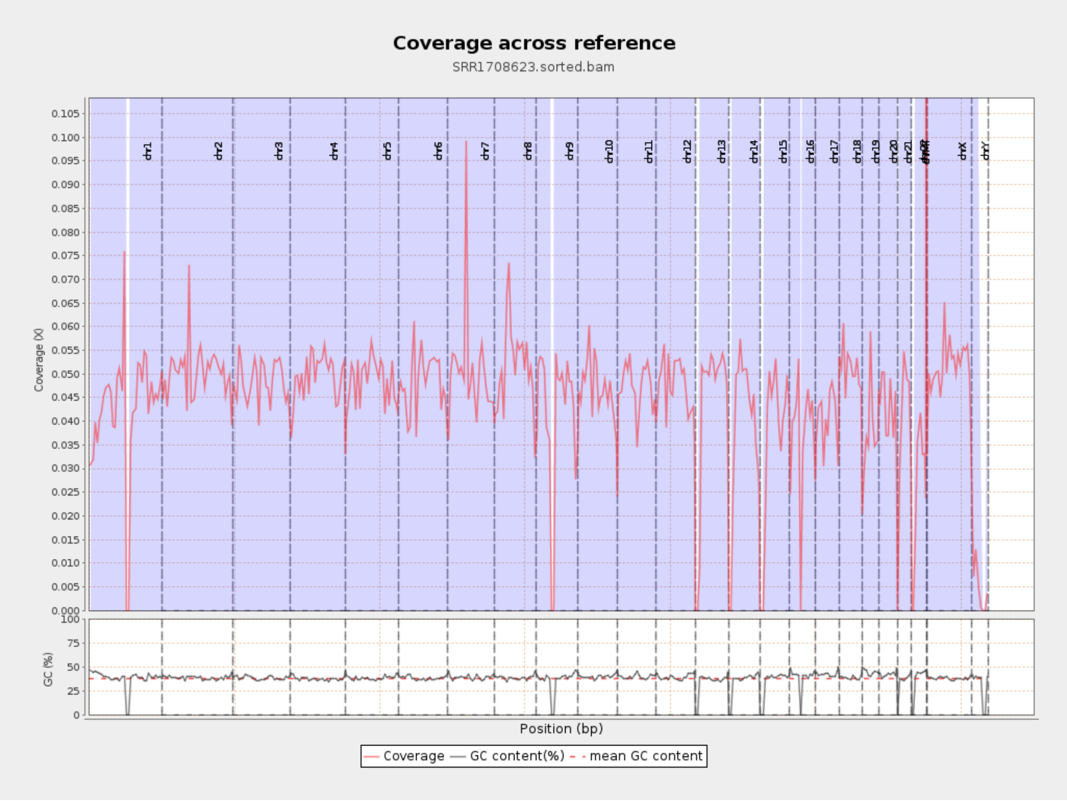
General error rate	0.64%
Mismatches	891,355
Insertions	6,492
Mapped reads with at least one insertion	0.23%
Deletions	17,641
Mapped reads with at least one deletion	0.61%
Homopolymer indels	48.1%

2.6. Chromosome stats

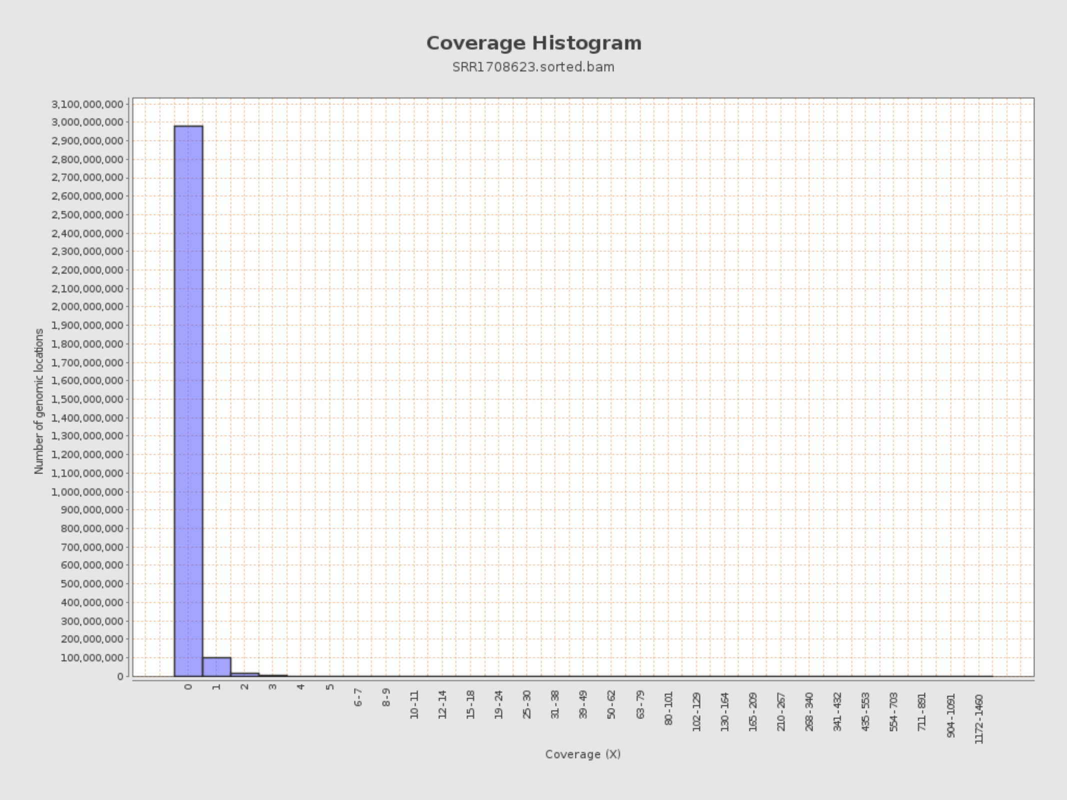
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10606159	0.0426	0.7847
chr2	243199373	12304656	0.0506	0.4804
chr3	198022430	9598747	0.0485	0.2624
chr4	191154276	9491432	0.0497	0.2677
chr5	180915260	8805985	0.0487	0.2675
chr6	171115067	8293379	0.0485	0.351
chr7	159138663	8135284	0.0511	0.7408

chr8	146364022	7576353	0.0518	0.8408
chr9	141213431	5883493	0.0417	0.3585
chr10	135534747	6407343	0.0473	0.3578
chr11	135006516	6347501	0.047	0.3772
chr12	133851895	6376906	0.0476	0.2702
chr13	115169878	4916477	0.0427	0.2518
chr14	107349540	4135623	0.0385	0.2601
chr15	102531392	3731273	0.0364	0.2248
chr16	90354753	3391498	0.0375	0.2478
chr17	81195210	3264663	0.0402	0.2831
chr18	78077248	4011334	0.0514	0.7331
chr19	59128983	2260489	0.0382	0.5957
chr20	63025520	2711233	0.043	0.2509
chr21	48129895	1879224	0.039	0.2496
chr22	51304566	1281618	0.025	0.1834
chrMT	16571	11942	0.7207	1.1436
chrX	155270560	7988124	0.0514	0.3115
chrY	59373566	310617	0.0052	0.095

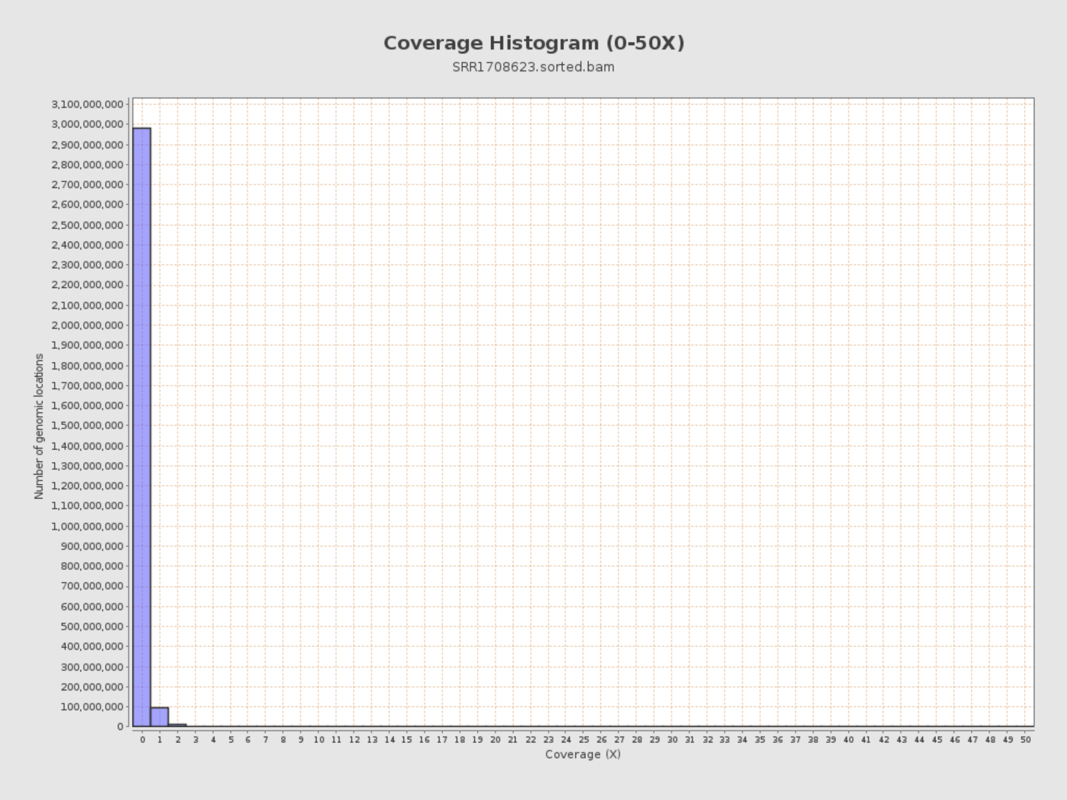
3. Results : Coverage across reference



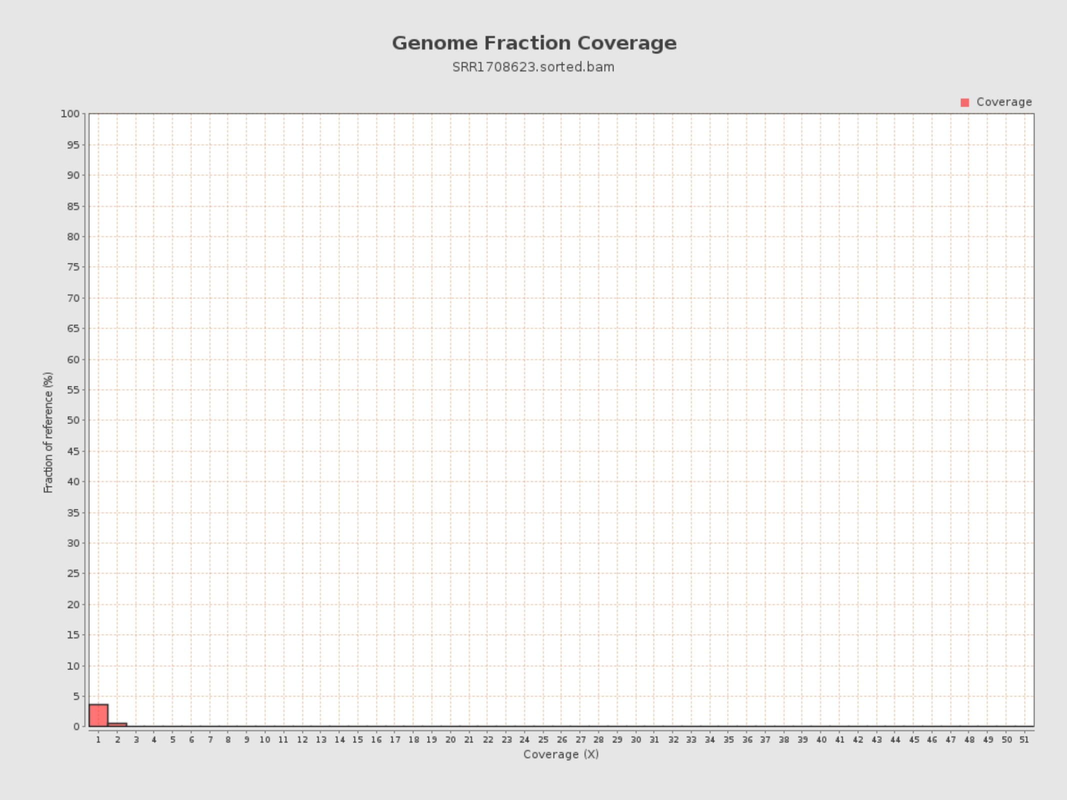
4. Results : Coverage Histogram



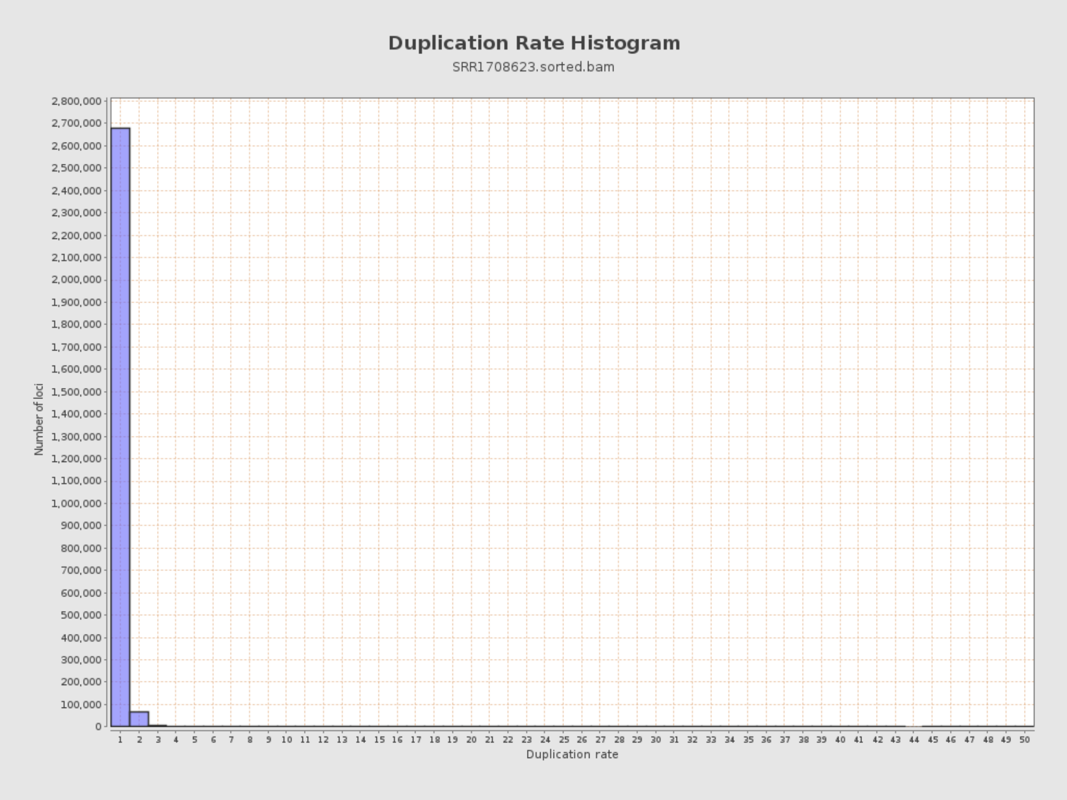
5. Results : Coverage Histogram (0-50X)



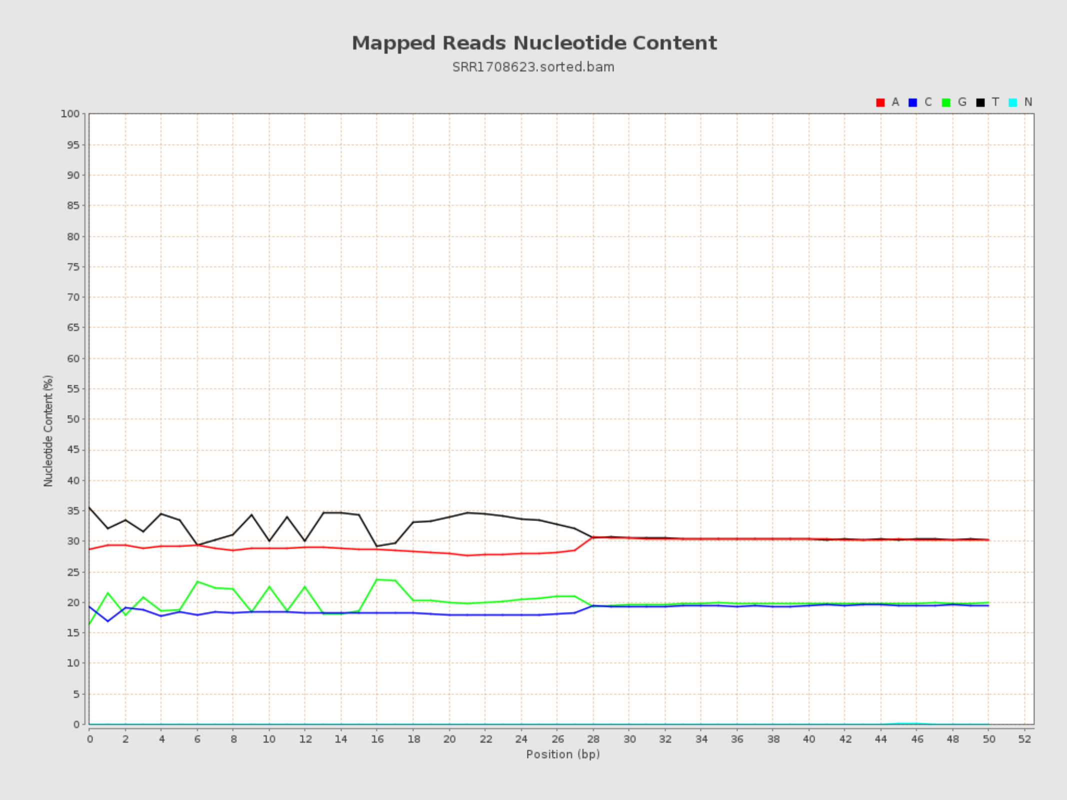
6. Results : Genome Fraction Coverage



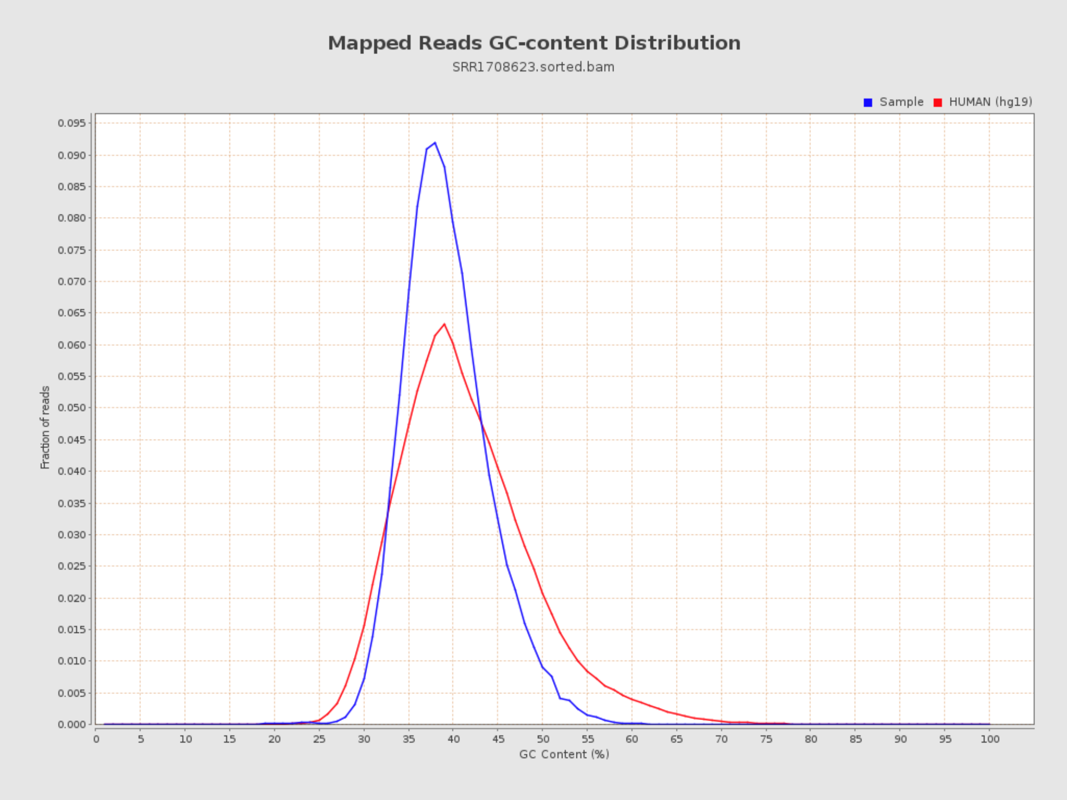
7. Results : Duplication Rate Histogram



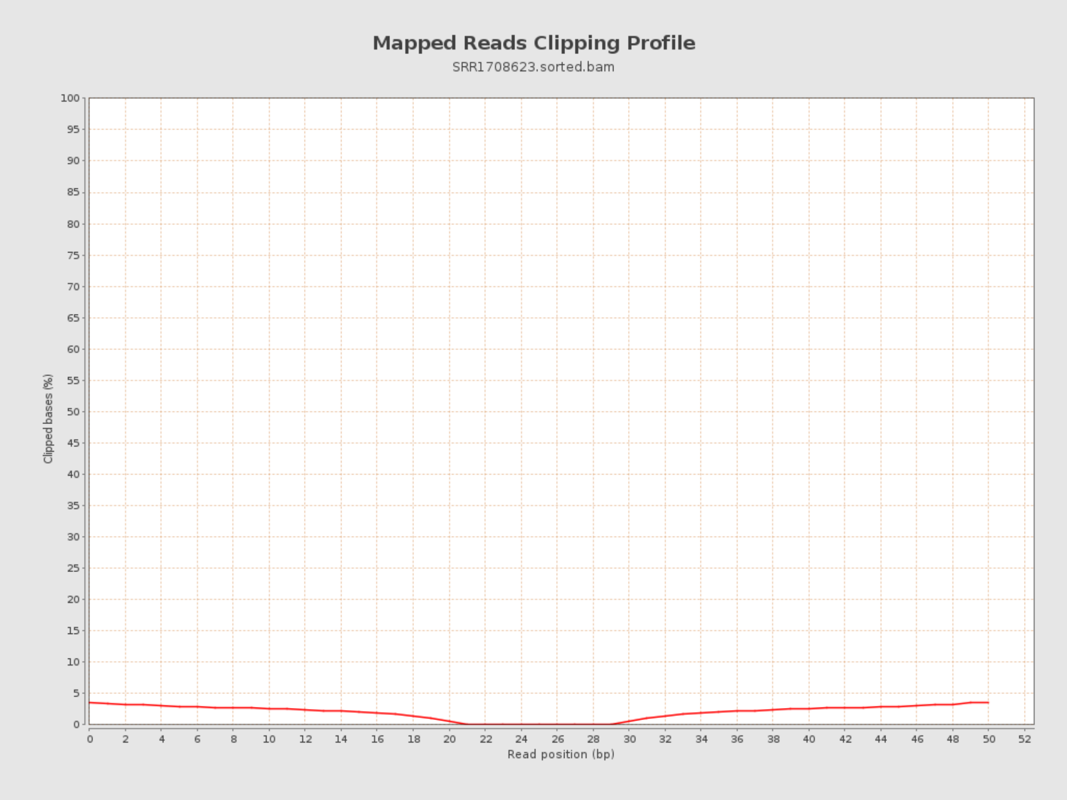
8. Results : Mapped Reads Nucleotide Content



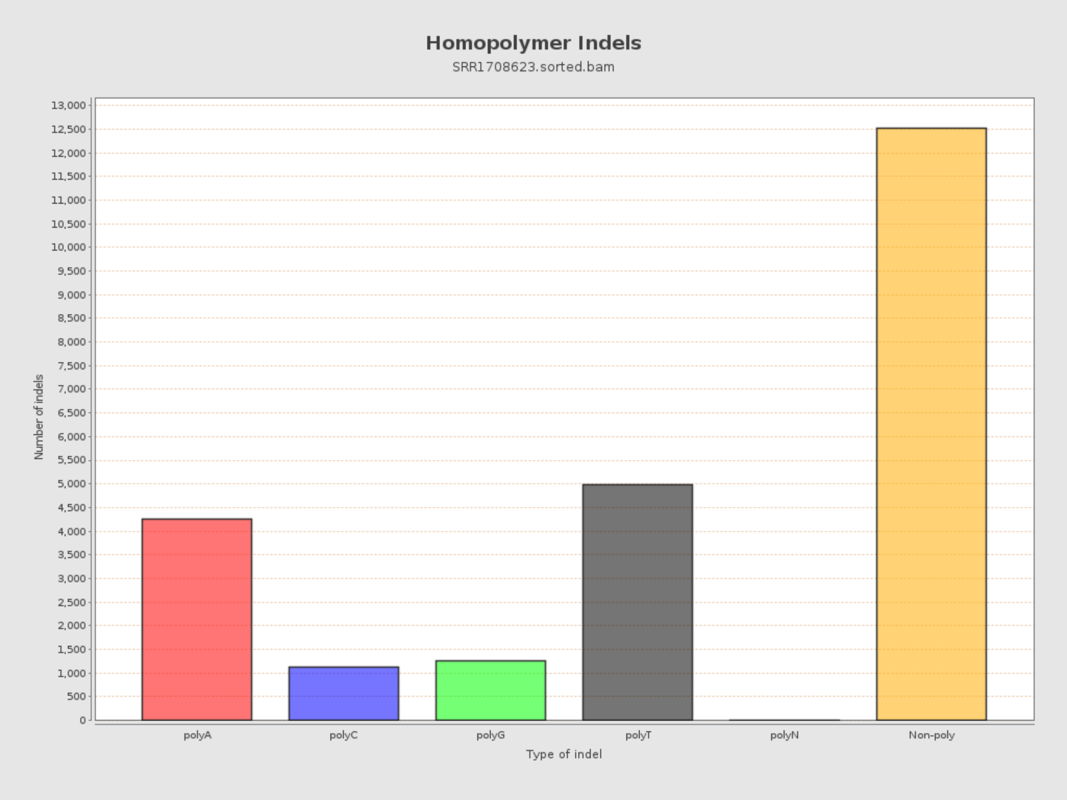
9. Results : Mapped Reads GC-content Distribution



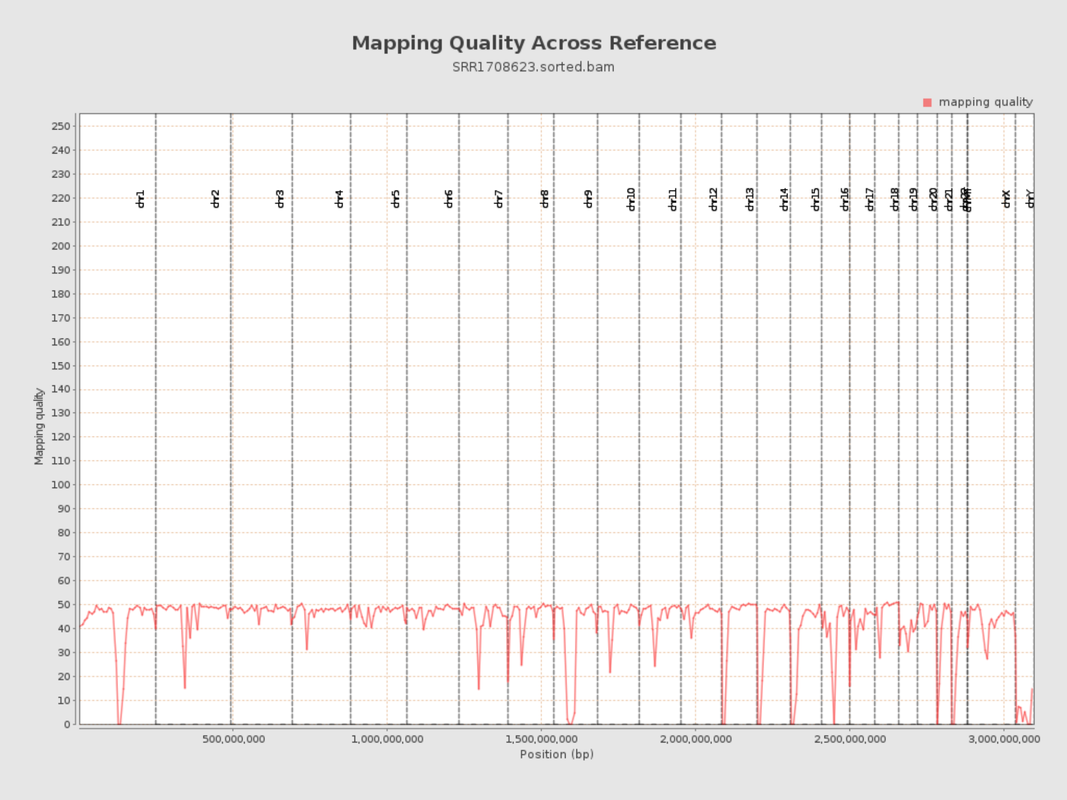
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram