Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:39:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708615.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_SRR1708615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708615.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:39:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708615.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,806,086
Mapped reads	2,789,306 / 73.29%
Unmapped reads	1,016,780 / 26.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	848 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	112,003 / 2.94%
Duplication rate	2.71%
Clipped reads	428,765 / 11.27%

2.2. ACGT Content

Number/percentage of A's	39,974,623 / 29.43%
Number/percentage of C's	25,594,541 / 18.85%
Number/percentage of T's	42,907,388 / 31.59%
Number/percentage of G's	27,326,623 / 20.12%
Number/percentage of N's	11,951 / 0.01%
GC Percentage	38.97%

2.3. Coverage

Mean	0.0439

Standard Deviation	0.4624

2.4. Mapping Quality

Mean Mapping Quality	43.31

2.5. Mismatches and indels

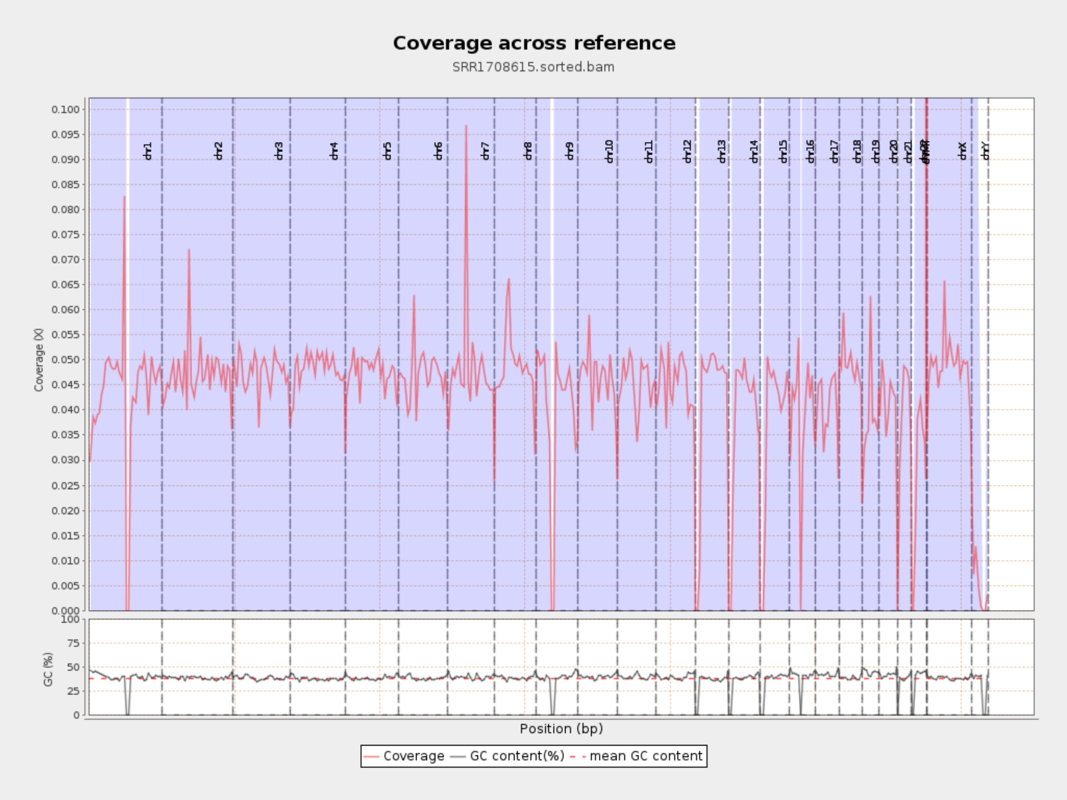
General error rate	0.63%
Mismatches	843,429
Insertions	6,432
Mapped reads with at least one insertion	0.23%
Deletions	17,141
Mapped reads with at least one deletion	0.61%
Homopolymer indels	48.53%

2.6. Chromosome stats

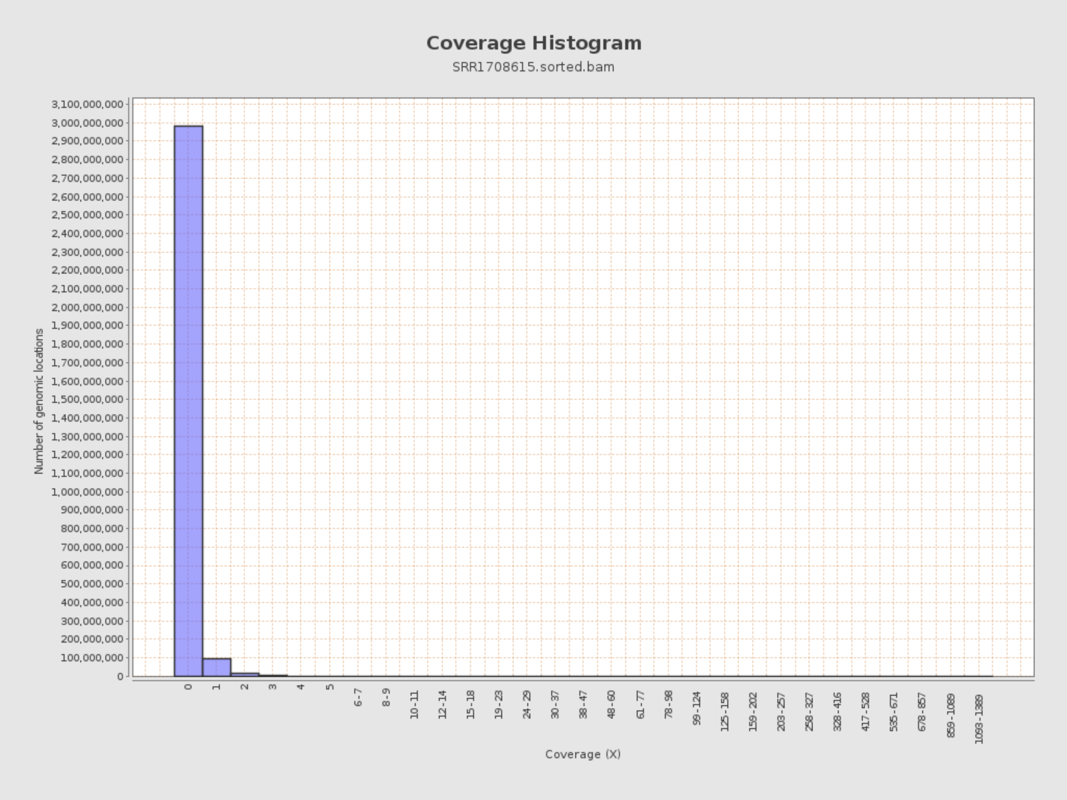
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10807015	0.0434	0.8785
chr2	243199373	11515057	0.0473	0.4623
chr3	198022430	9415183	0.0475	0.2577
chr4	191154276	9222536	0.0482	0.2648
chr5	180915260	8616369	0.0476	0.262
chr6	171115067	8068291	0.0472	0.3458
chr7	159138663	7788141	0.0489	0.6775

chr8	146364022	7122827	0.0487	0.8072
chr9	141213431	5677401	0.0402	0.3636
chr10	135534747	6328017	0.0467	0.36
chr11	135006516	6094179	0.0451	0.3962
chr12	133851895	6067728	0.0453	0.2643
chr13	115169878	4672885	0.0406	0.2402
chr14	107349540	4065326	0.0379	0.252
chr15	102531392	3778061	0.0368	0.2241
chr16	90354753	3518497	0.0389	0.2546
chr17	81195210	3265663	0.0402	0.2844
chr18	78077248	3851122	0.0493	0.7448
chr19	59128983	2303754	0.039	0.6456
chr20	63025520	2628952	0.0417	0.2539
chr21	48129895	1781487	0.037	0.2487
chr22	51304566	1332022	0.026	0.1847
chrMT	16571	20722	1.2505	1.4911
chrX	155270560	7595212	0.0489	0.3038
chrY	59373566	304599	0.0051	0.0957

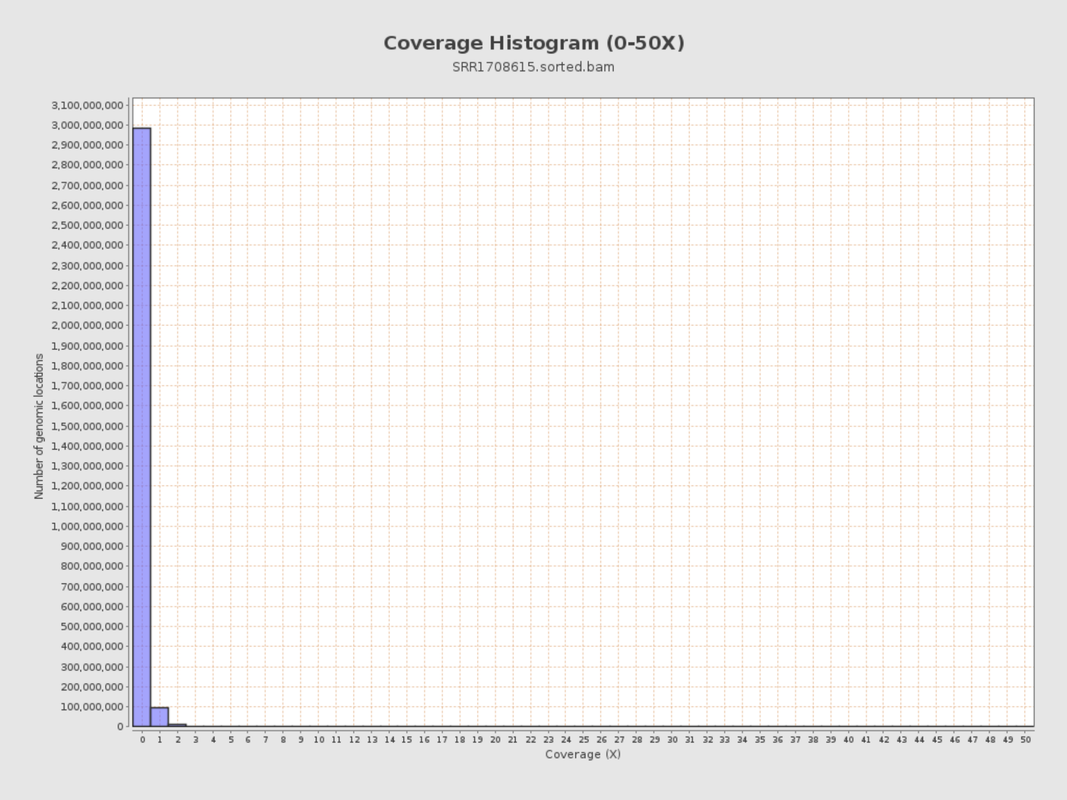
3. Results : Coverage across reference



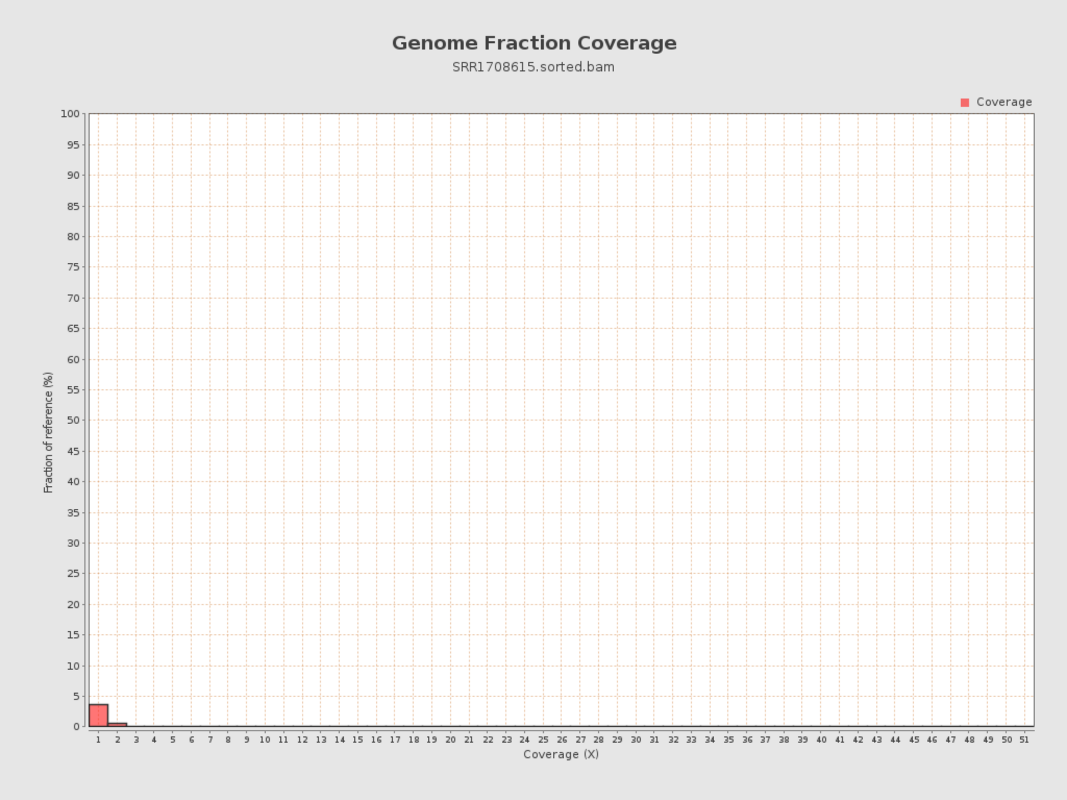
4. Results : Coverage Histogram



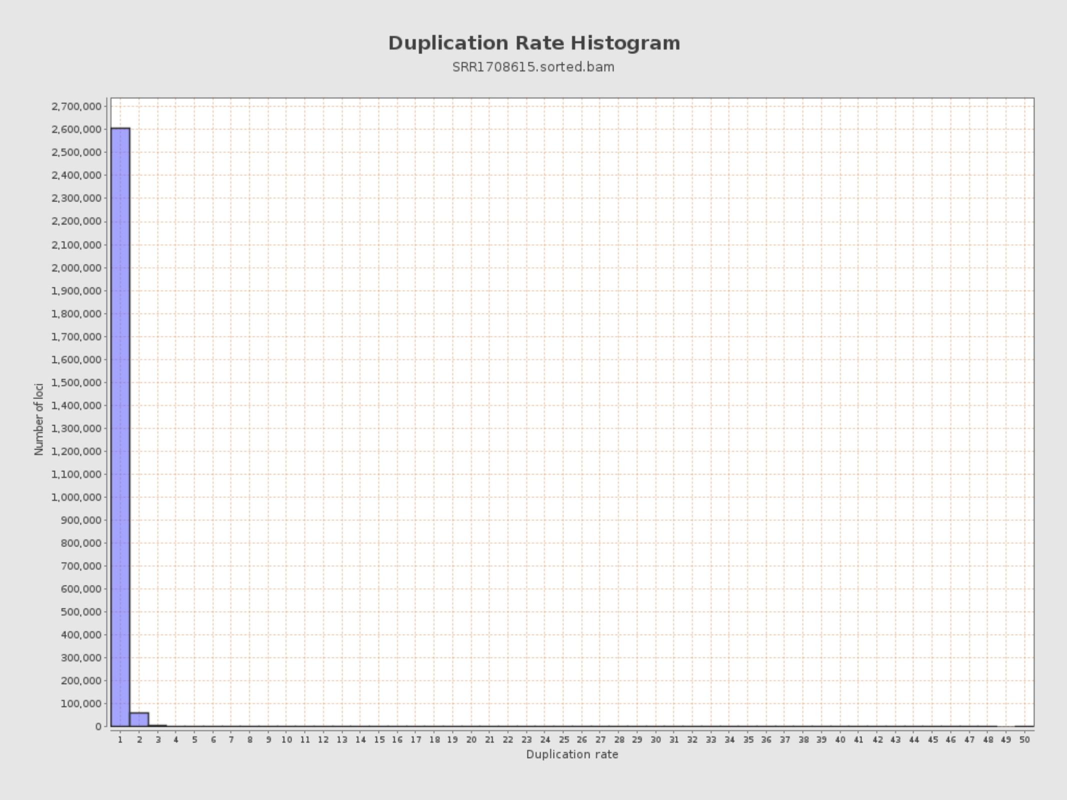
5. Results : Coverage Histogram (0-50X)



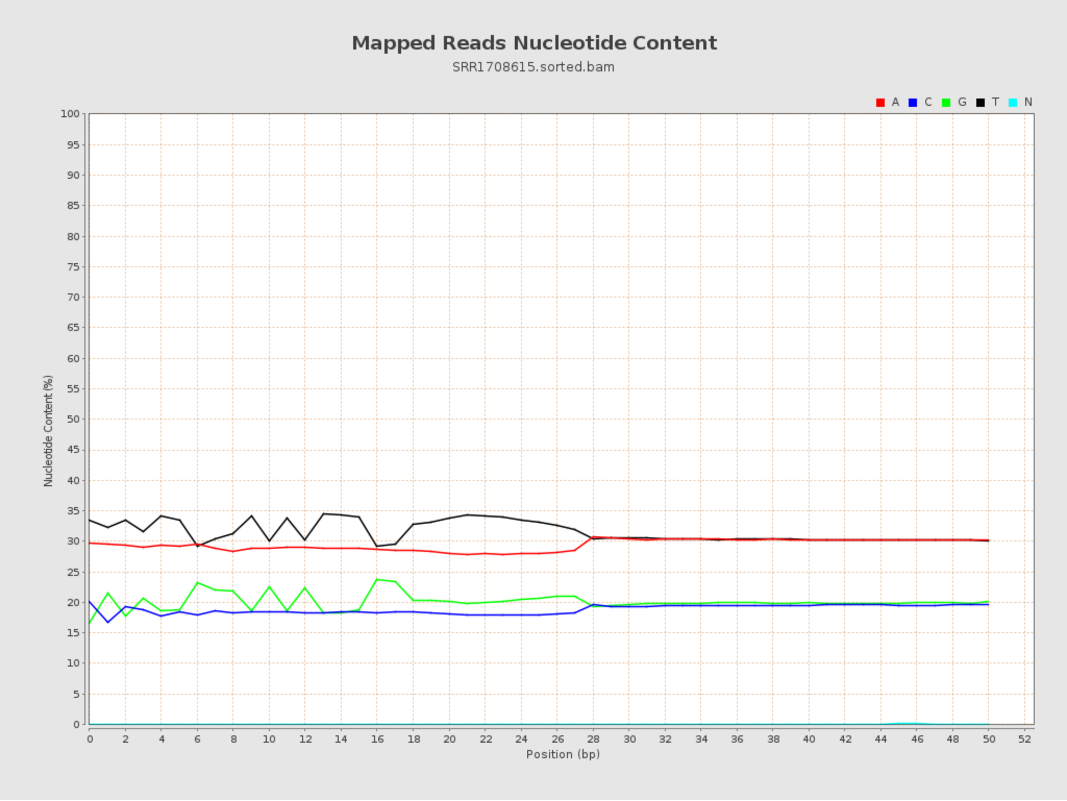
6. Results : Genome Fraction Coverage



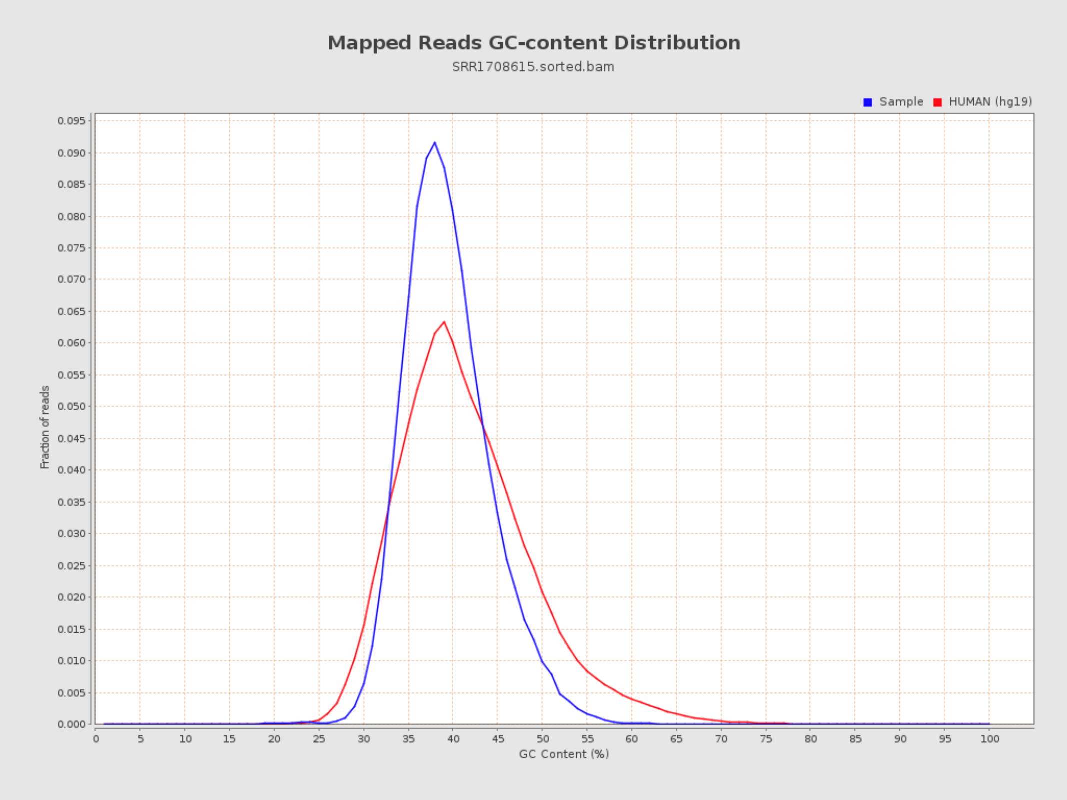
7. Results : Duplication Rate Histogram



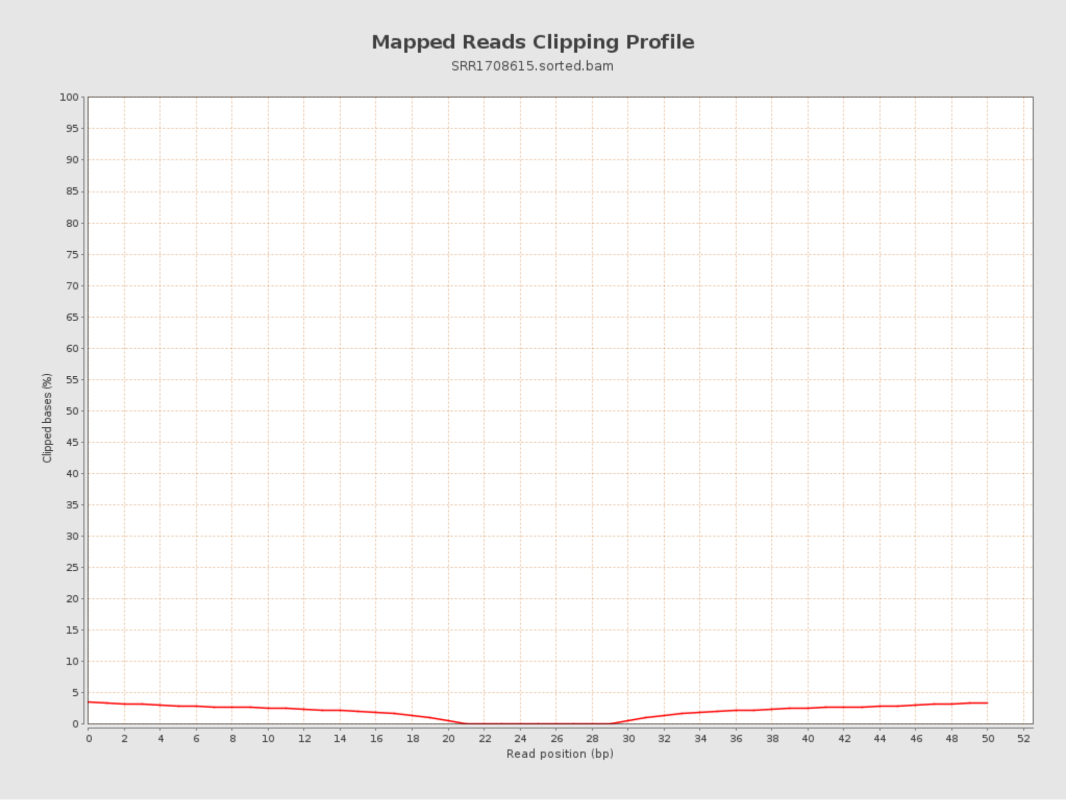
8. Results : Mapped Reads Nucleotide Content



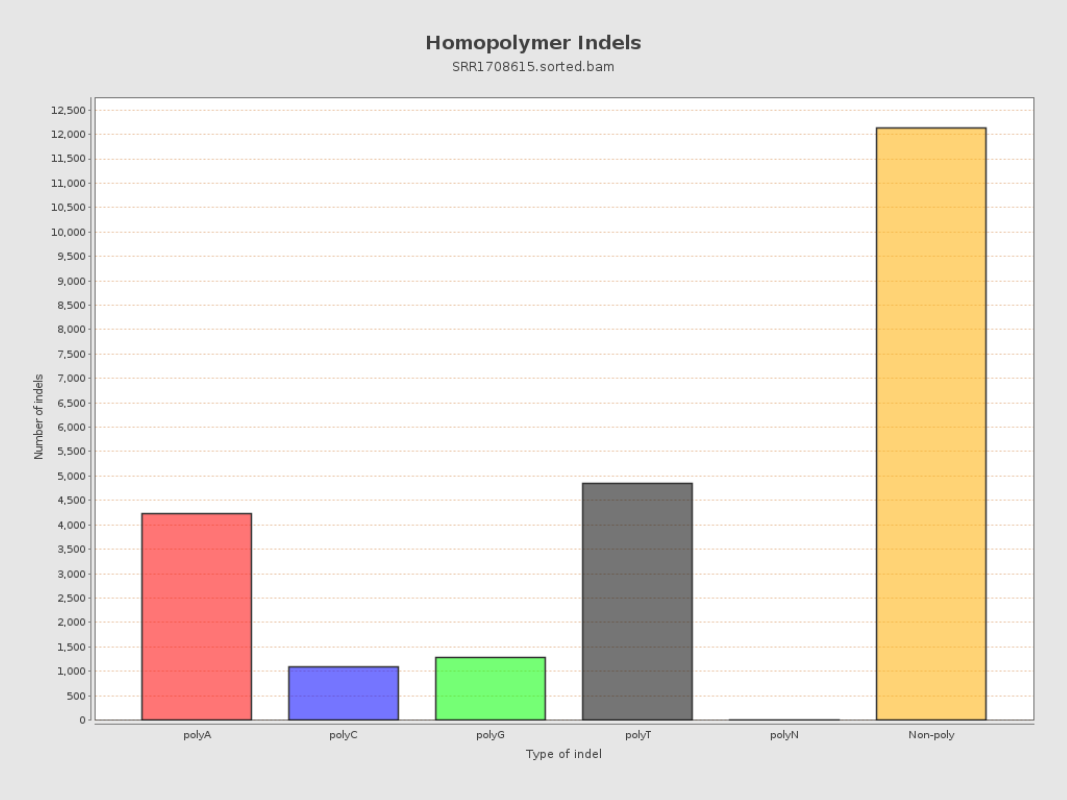
9. Results : Mapped Reads GC-content Distribution



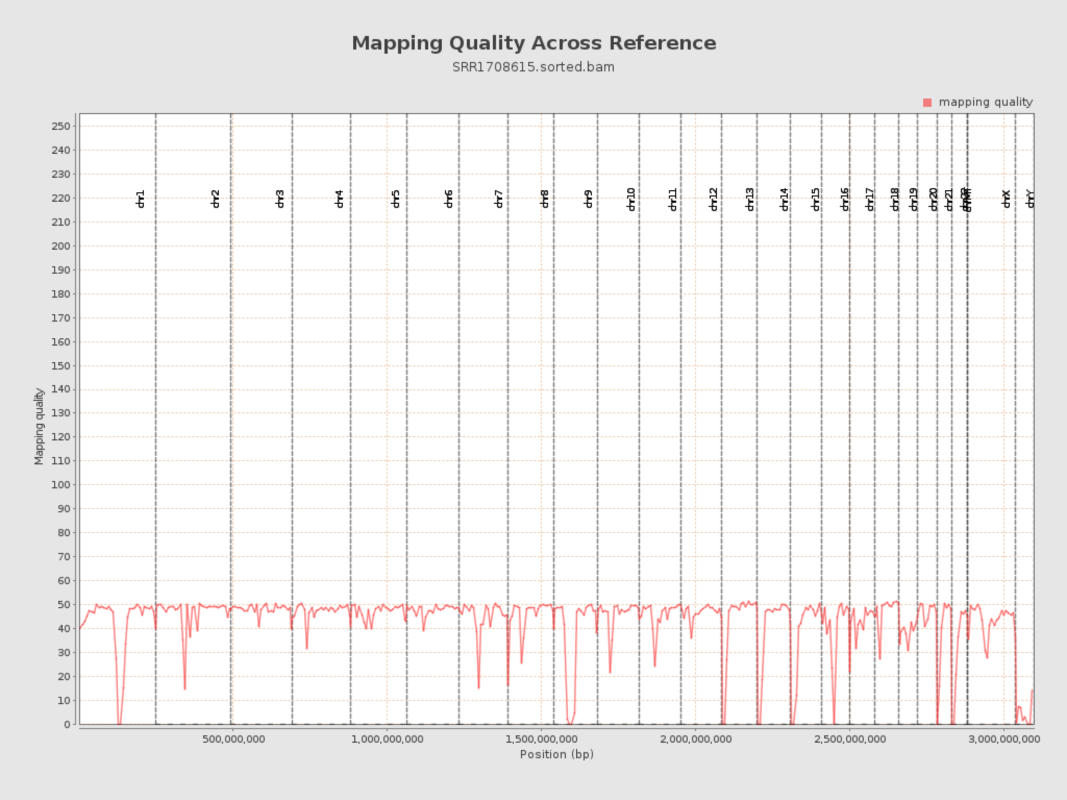
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram