Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:40:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708535.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_SRR1708535 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708535.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:40:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708535.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,342,018
Mapped reads	22,806,735 / 97.71%
Unmapped reads	535,283 / 2.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	617 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	255,197 / 1.09%
Duplication rate	1.11%
Clipped reads	278,394 / 1.19%

2.2. ACGT Content

Number/percentage of A's	353,469,416 / 31.07%
Number/percentage of C's	213,798,316 / 18.79%
Number/percentage of T's	353,125,373 / 31.04%
Number/percentage of G's	217,180,643 / 19.09%
Number/percentage of N's	39,440 / 0%
GC Percentage	37.88%

2.3. Coverage

Mean	0.3675

Standard Deviation	0.7071

2.4. Mapping Quality

Mean Mapping Quality	46.66

2.5. Mismatches and indels

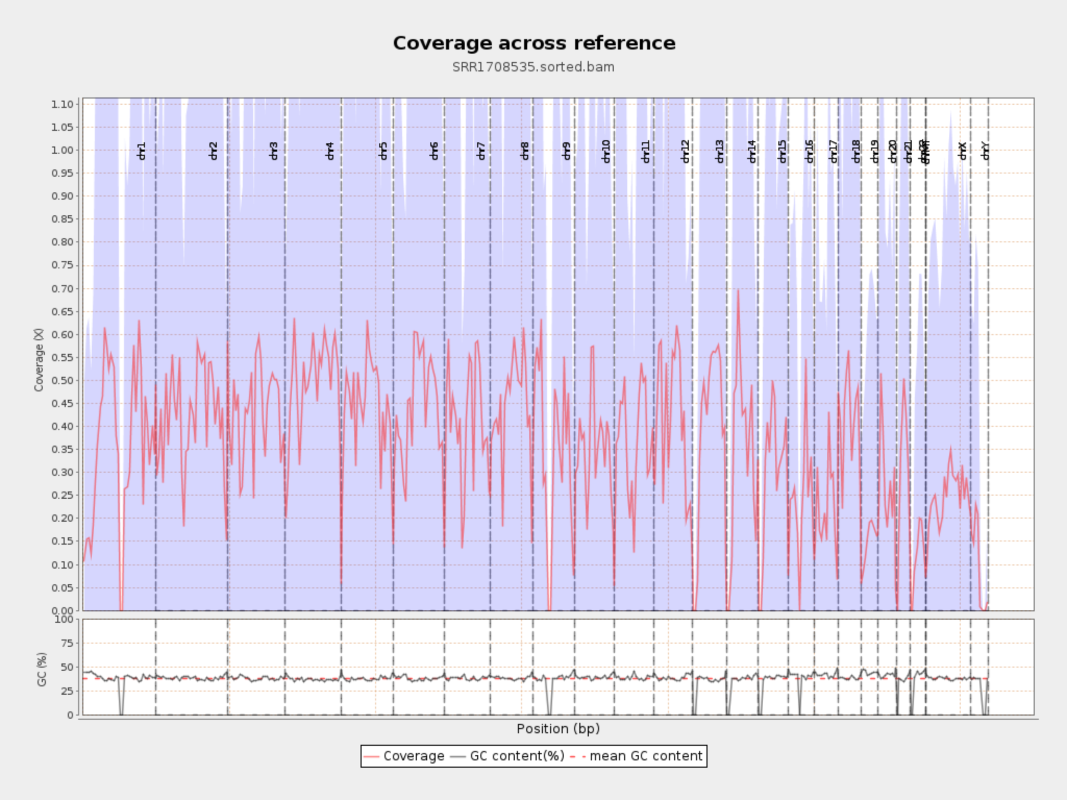
General error rate	0.2%
Mismatches	2,139,921
Insertions	67,512
Mapped reads with at least one insertion	0.3%
Deletions	61,482
Mapped reads with at least one deletion	0.27%
Homopolymer indels	49.27%

2.6. Chromosome stats

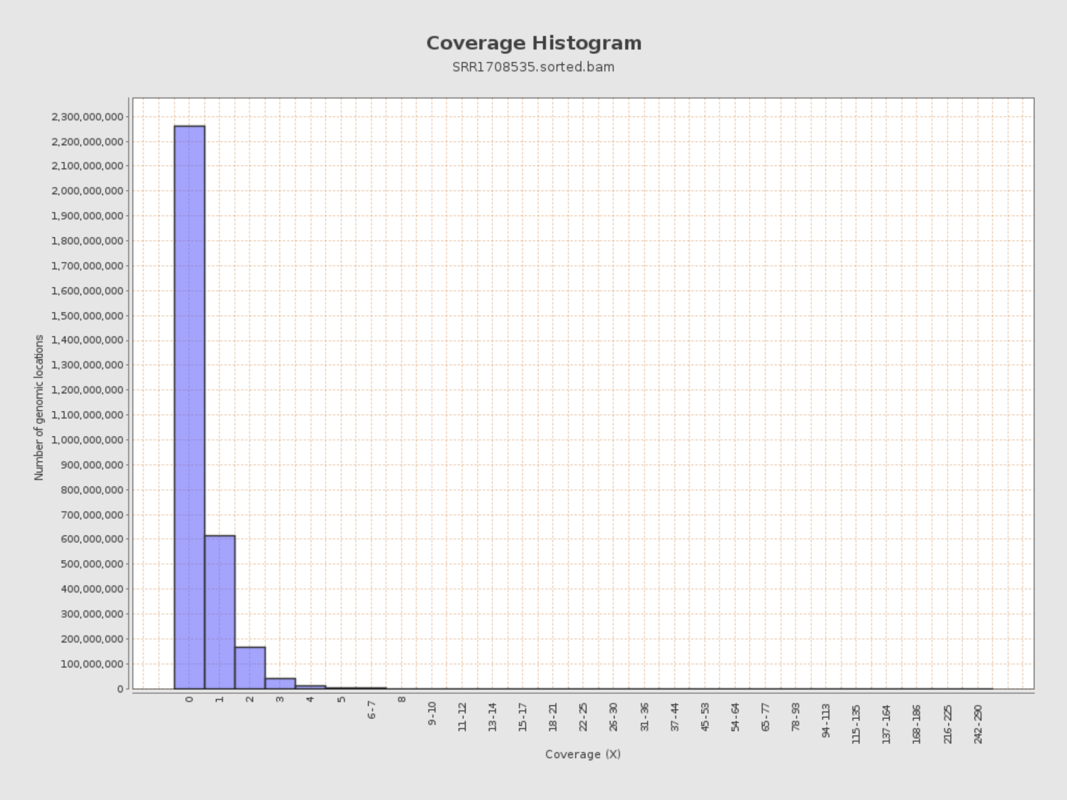
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	89204740	0.3579	0.712
chr2	243199373	102683000	0.4222	0.7473
chr3	198022430	85898110	0.4338	0.7489
chr4	191154276	94346067	0.4936	0.8004
chr5	180915260	79228040	0.4379	0.754
chr6	171115067	76584085	0.4476	0.7674
chr7	159138663	64653684	0.4063	0.7412

chr8	146364022	65319905	0.4463	0.7624
chr9	141213431	49694685	0.3519	0.7006
chr10	135534747	48626312	0.3588	0.6859
chr11	135006516	49514207	0.3668	0.7108
chr12	133851895	55149657	0.412	0.7482
chr13	115169878	45479921	0.3949	0.7308
chr14	107349540	37151147	0.3461	0.6972
chr15	102531392	30466928	0.2971	0.6508
chr16	90354753	21396920	0.2368	0.564
chr17	81195210	18355360	0.2261	0.557
chr18	78077248	32774014	0.4198	0.7419
chr19	59128983	8952185	0.1514	0.439
chr20	63025520	17777403	0.2821	0.6238
chr21	48129895	14142686	0.2938	0.6551
chr22	51304566	6016805	0.1173	0.3903
chrMT	16571	1299	0.0784	0.2806
chrX	155270560	38701046	0.2492	0.5566
chrY	59373566	5597645	0.0943	0.3601

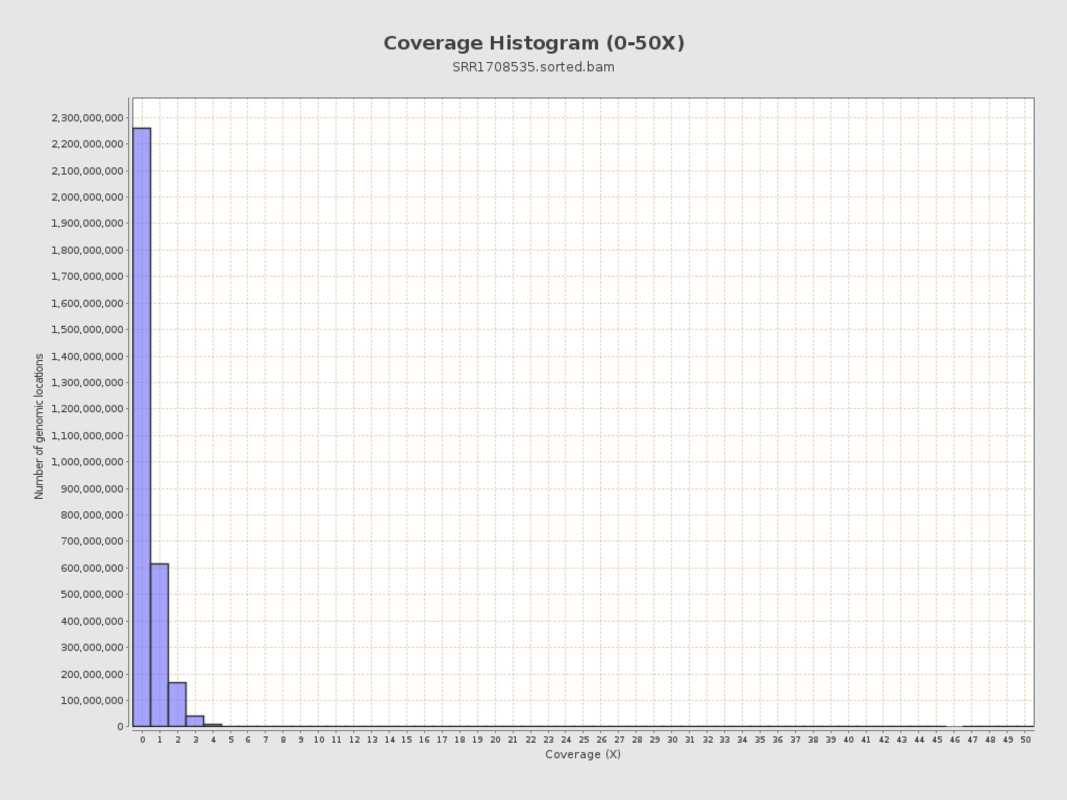
3. Results : Coverage across reference



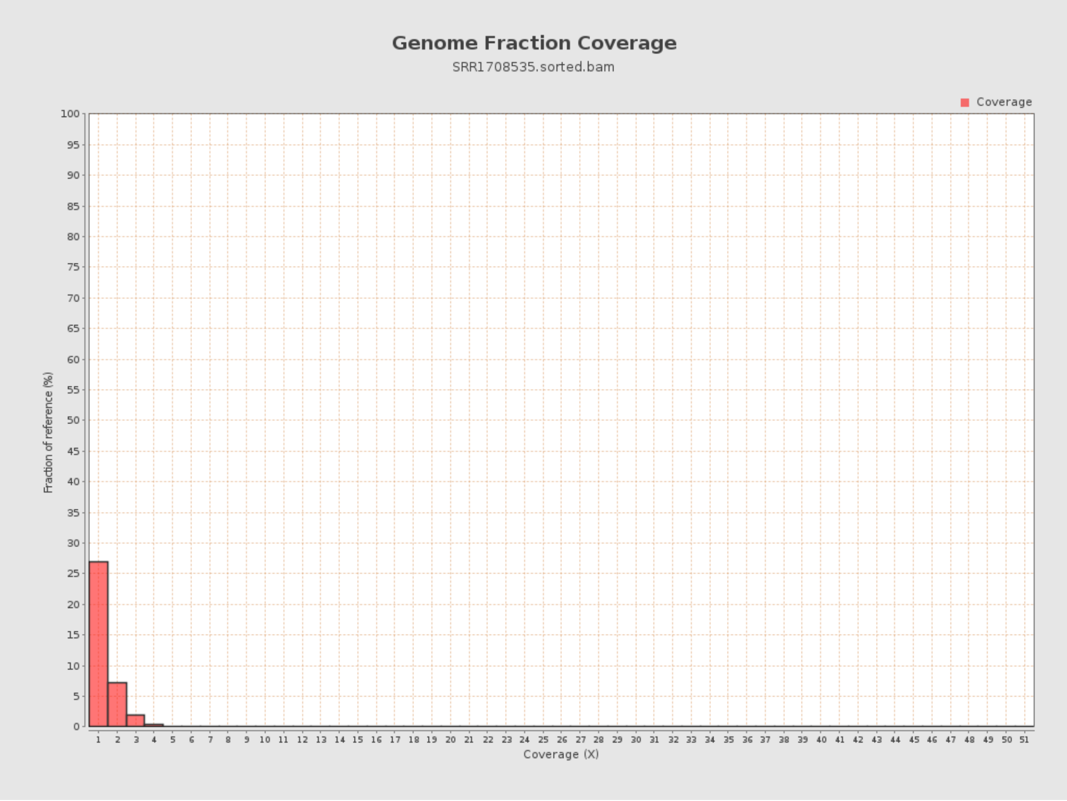
4. Results : Coverage Histogram



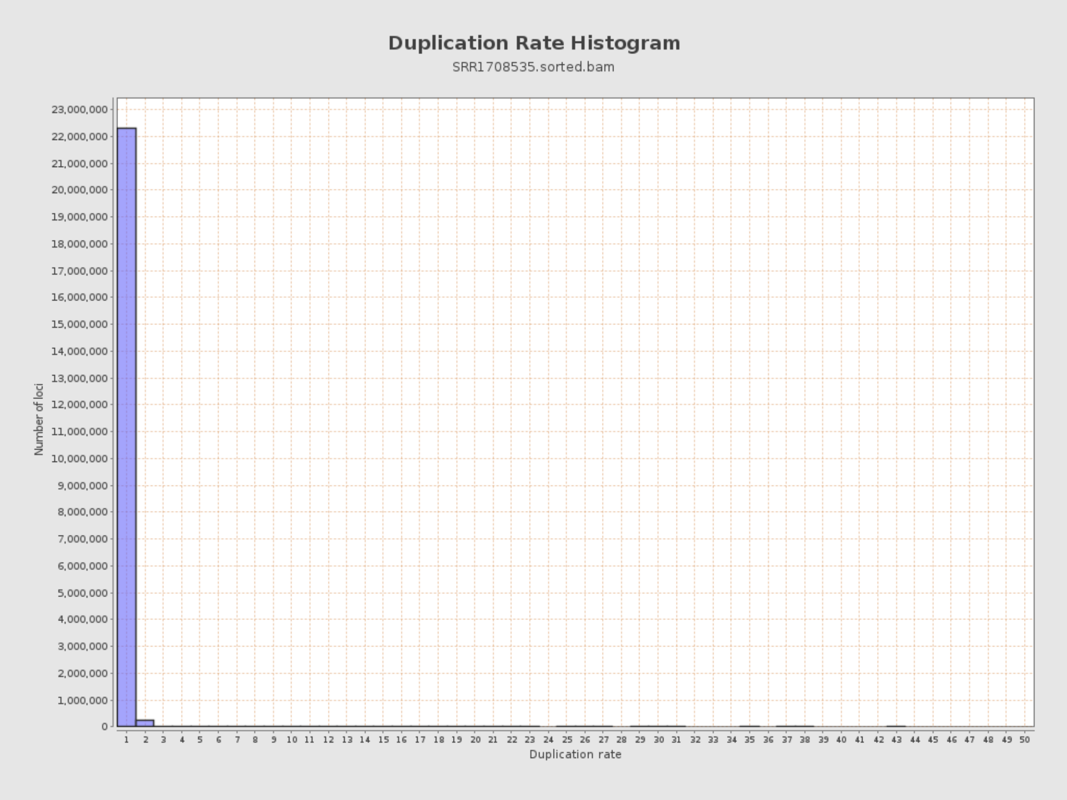
5. Results : Coverage Histogram (0-50X)



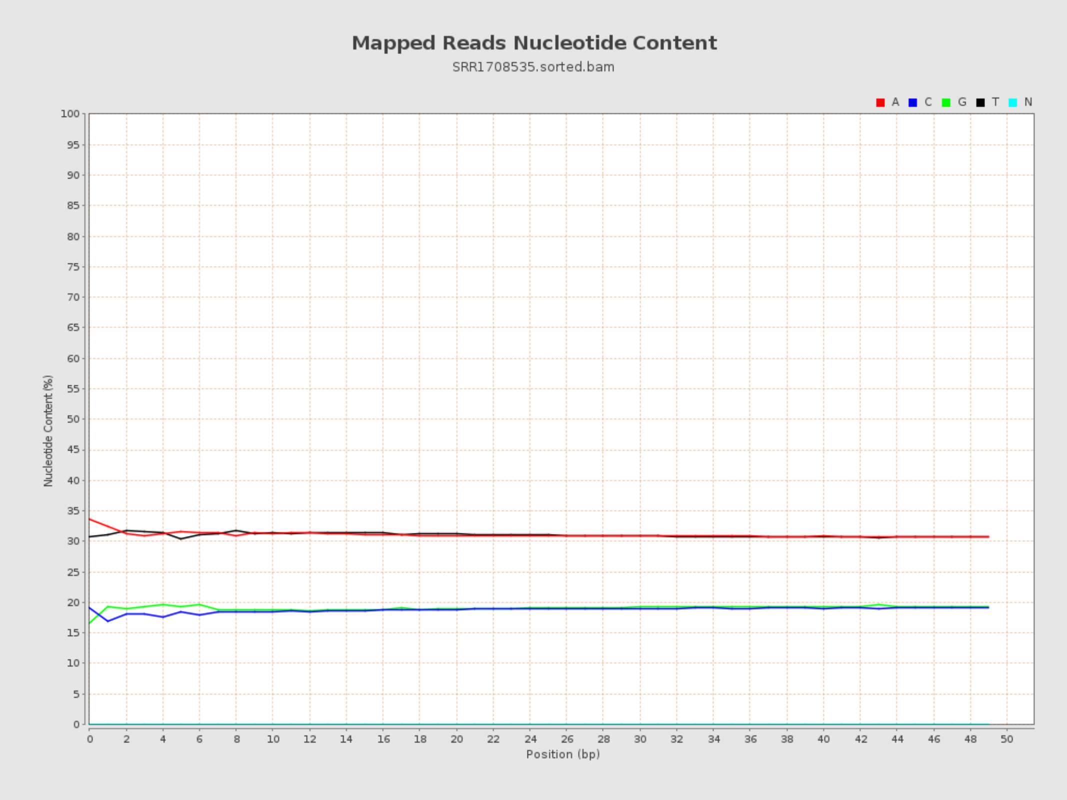
6. Results : Genome Fraction Coverage



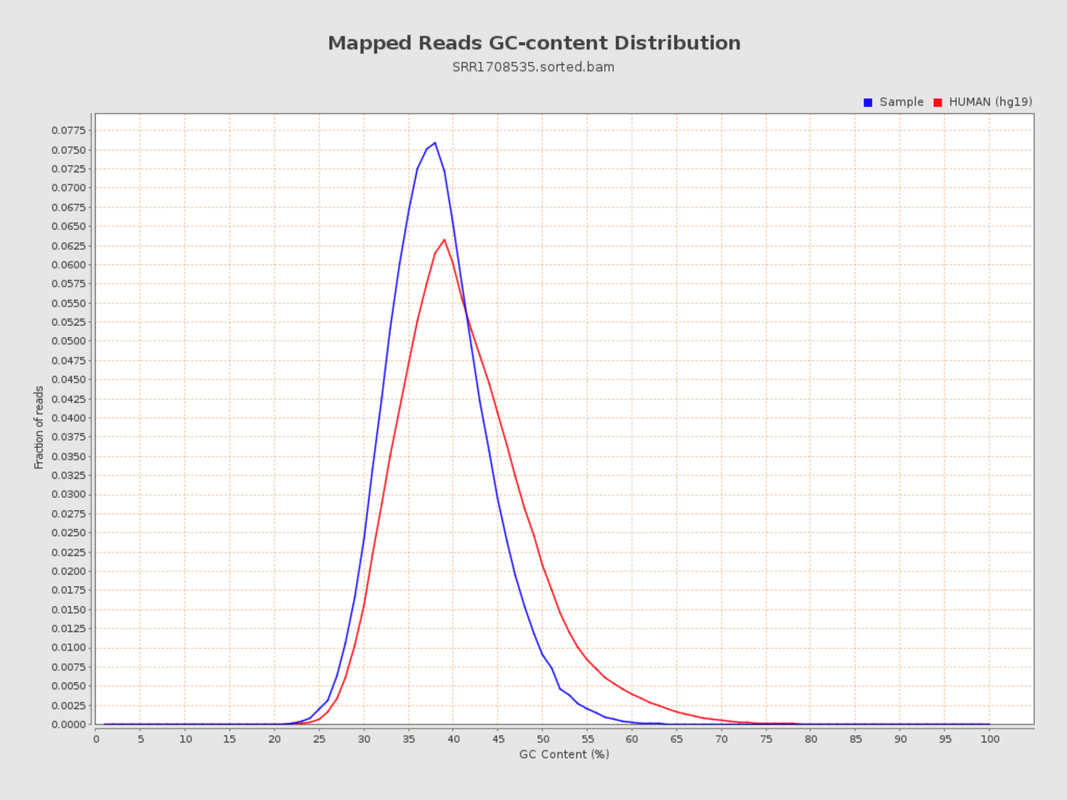
7. Results : Duplication Rate Histogram



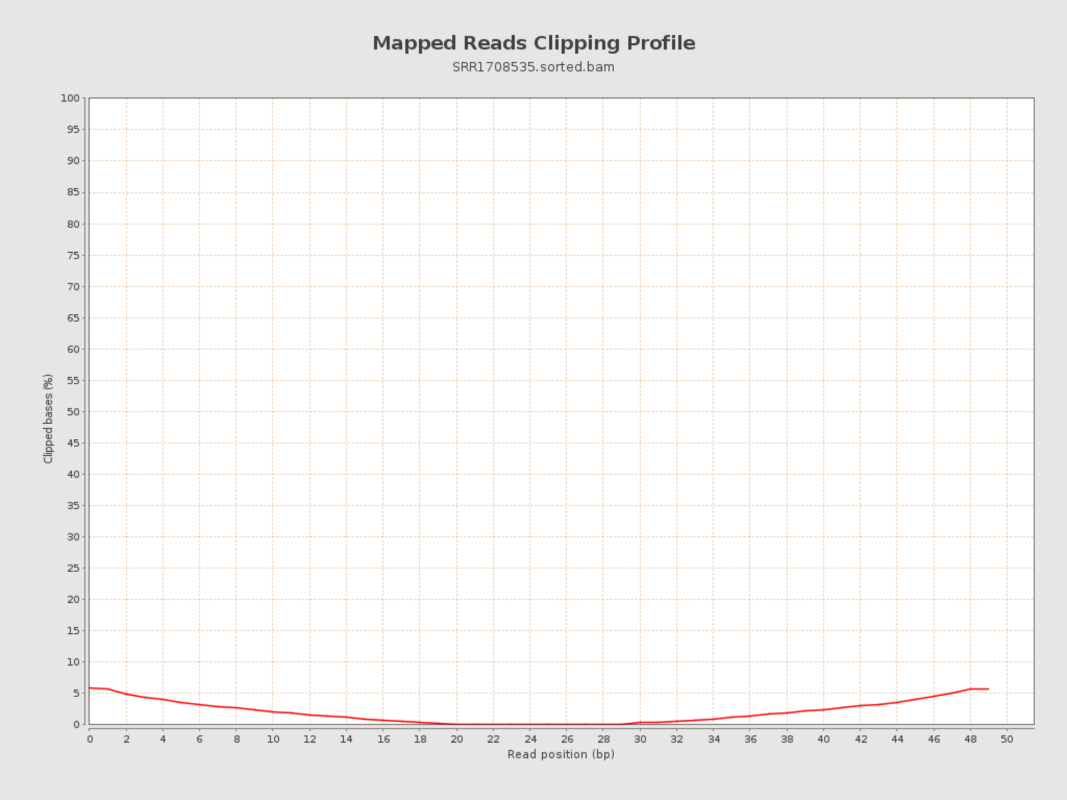
8. Results : Mapped Reads Nucleotide Content



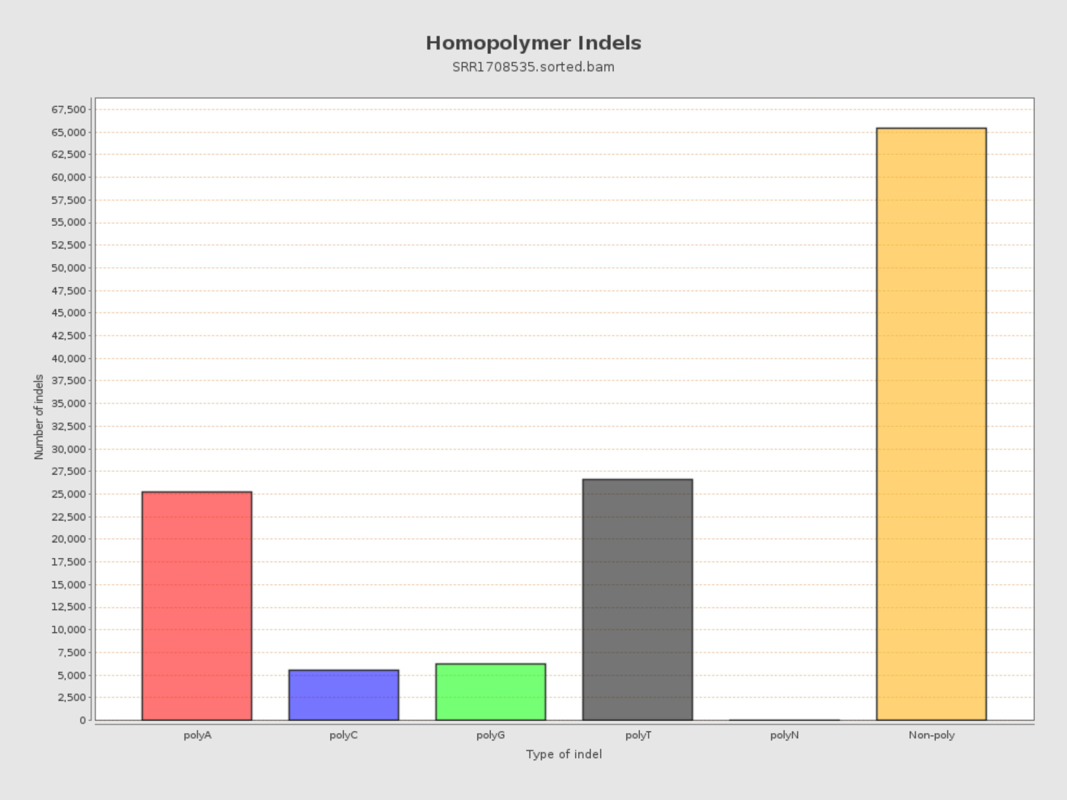
9. Results : Mapped Reads GC-content Distribution



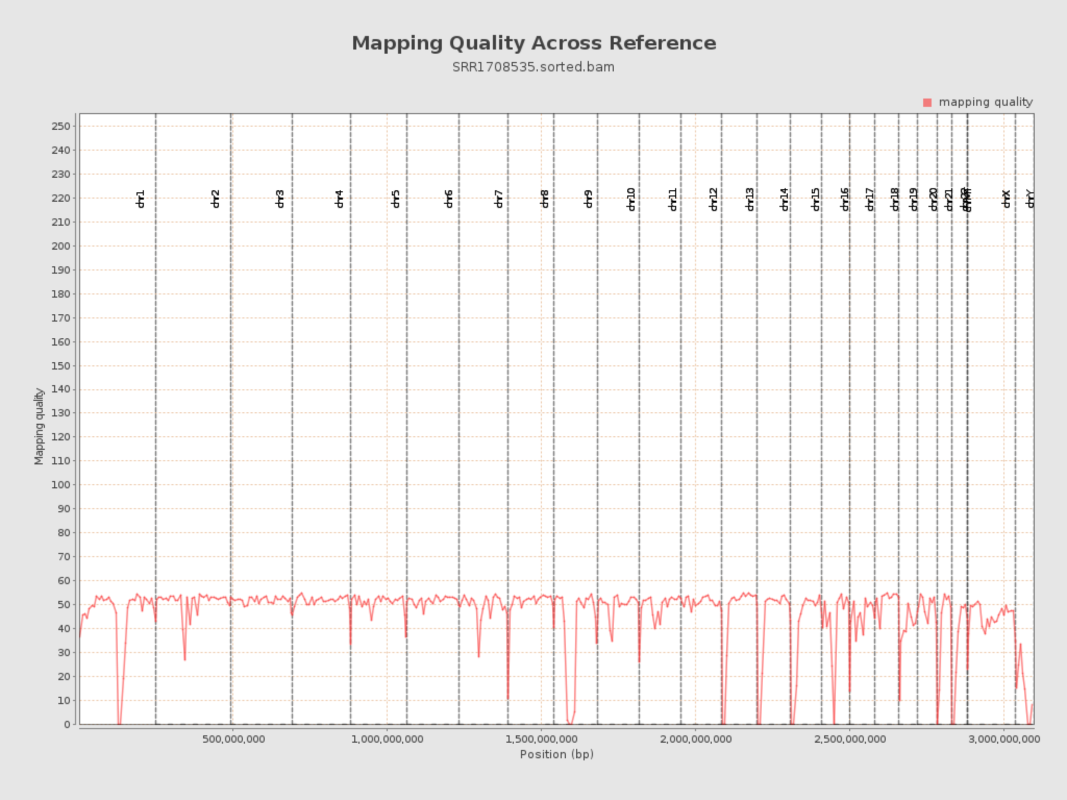
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram