Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:06:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708653.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_SRR1708653 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708653.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:06:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708653.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,223,508
Mapped reads	20,717,106 / 97.61%
Unmapped reads	506,402 / 2.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	519 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	211,668 / 1%
Duplication rate	1.01%
Clipped reads	257,966 / 1.22%

2.2. ACGT Content

Number/percentage of A's	314,518,521 / 30.43%
Number/percentage of C's	200,195,188 / 19.37%
Number/percentage of T's	313,959,491 / 30.38%
Number/percentage of G's	204,751,613 / 19.81%
Number/percentage of N's	36,578 / 0%
GC Percentage	39.18%

2.3. Coverage

Mean	0.3339

Standard Deviation	0.6745

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

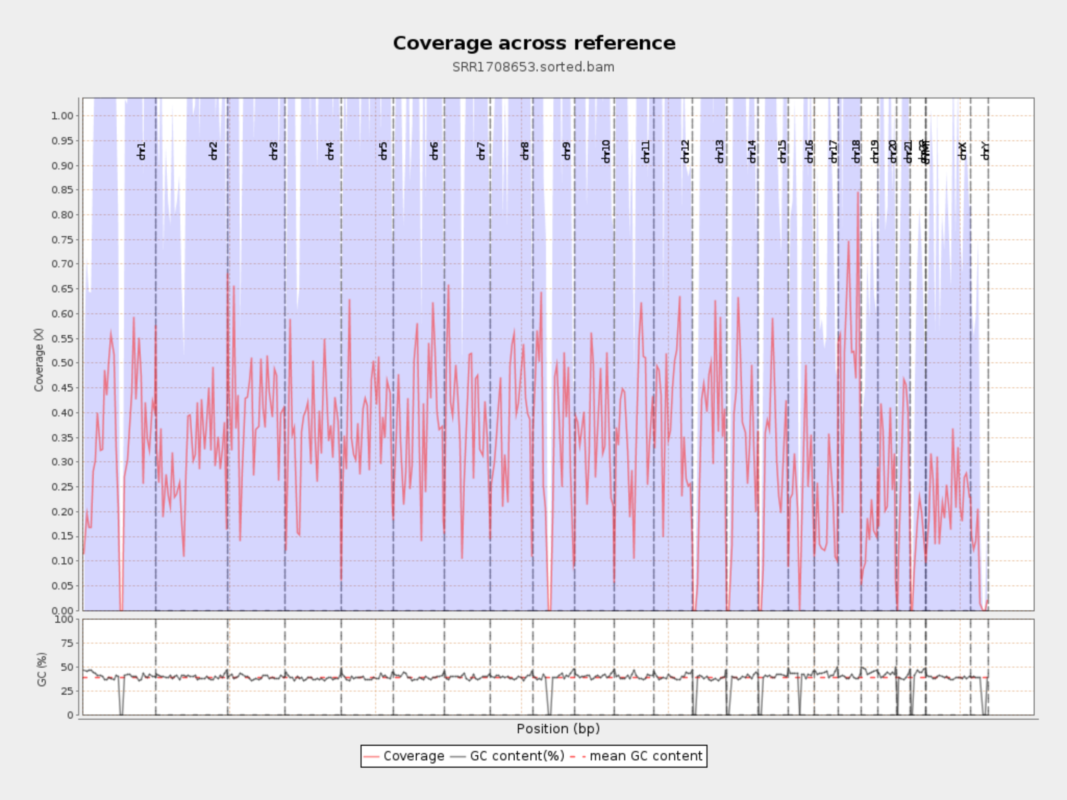
General error rate	0.21%
Mismatches	2,111,590
Insertions	64,789
Mapped reads with at least one insertion	0.31%
Deletions	57,270
Mapped reads with at least one deletion	0.28%
Homopolymer indels	48.88%

2.6. Chromosome stats

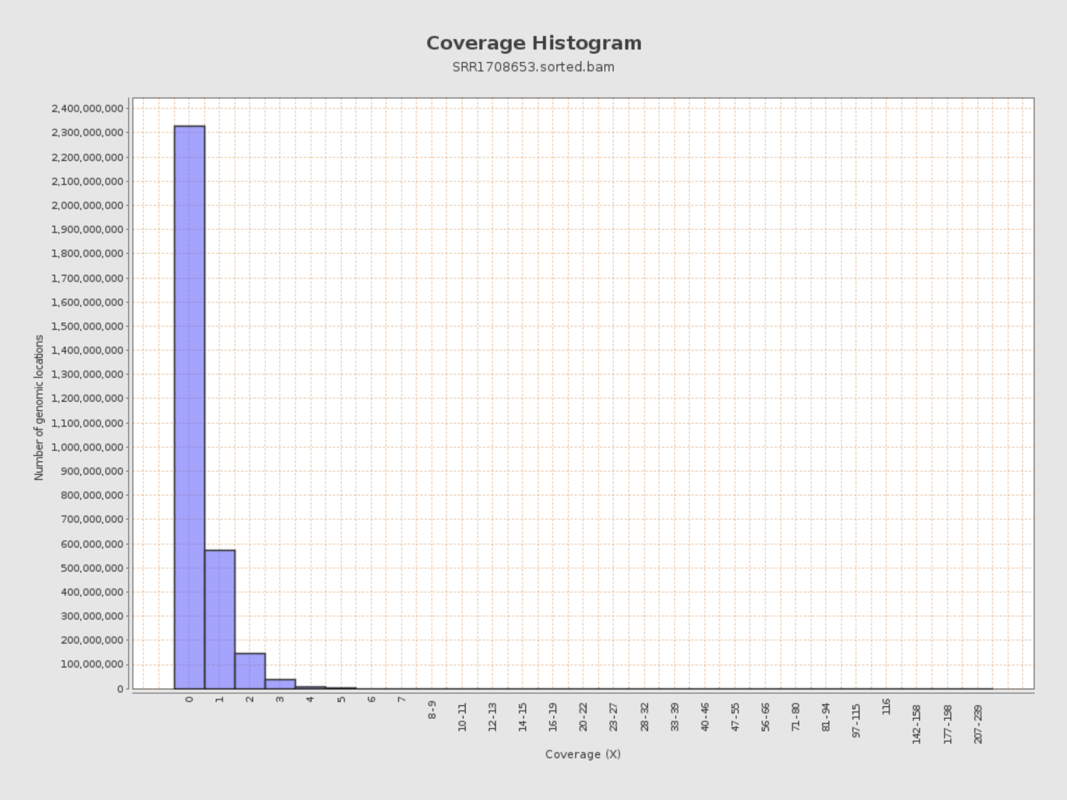
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	85541855	0.3432	0.6922
chr2	243199373	74675039	0.3071	0.6345
chr3	198022430	81373808	0.4109	0.7374
chr4	191154276	68409498	0.3579	0.6825
chr5	180915260	67725657	0.3744	0.6993
chr6	171115067	64782852	0.3786	0.7083
chr7	159138663	61502489	0.3865	0.7257

chr8	146364022	56372600	0.3852	0.7137
chr9	141213431	48566502	0.3439	0.6977
chr10	135534747	49880506	0.368	0.6943
chr11	135006516	50543122	0.3744	0.722
chr12	133851895	51243741	0.3828	0.7177
chr13	115169878	40649493	0.353	0.6927
chr14	107349540	35079226	0.3268	0.6725
chr15	102531392	29732622	0.29	0.6321
chr16	90354753	22062287	0.2442	0.5695
chr17	81195210	15057518	0.1854	0.4974
chr18	78077248	42676653	0.5466	0.8622
chr19	59128983	8855407	0.1498	0.4337
chr20	63025520	17885168	0.2838	0.6139
chr21	48129895	13787052	0.2865	0.648
chr22	51304566	6719628	0.131	0.414
chrMT	16571	1596	0.0963	0.3209
chrX	155270560	35753396	0.2303	0.5425
chrY	59373566	4680122	0.0788	0.3301

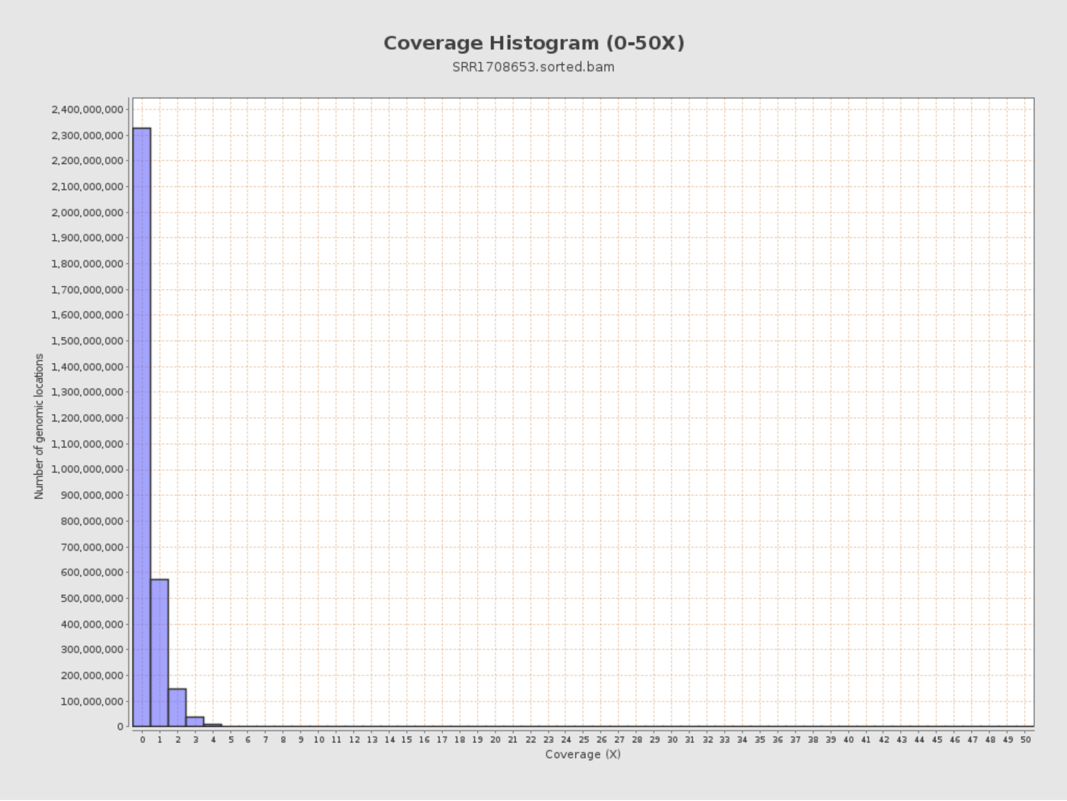
3. Results : Coverage across reference



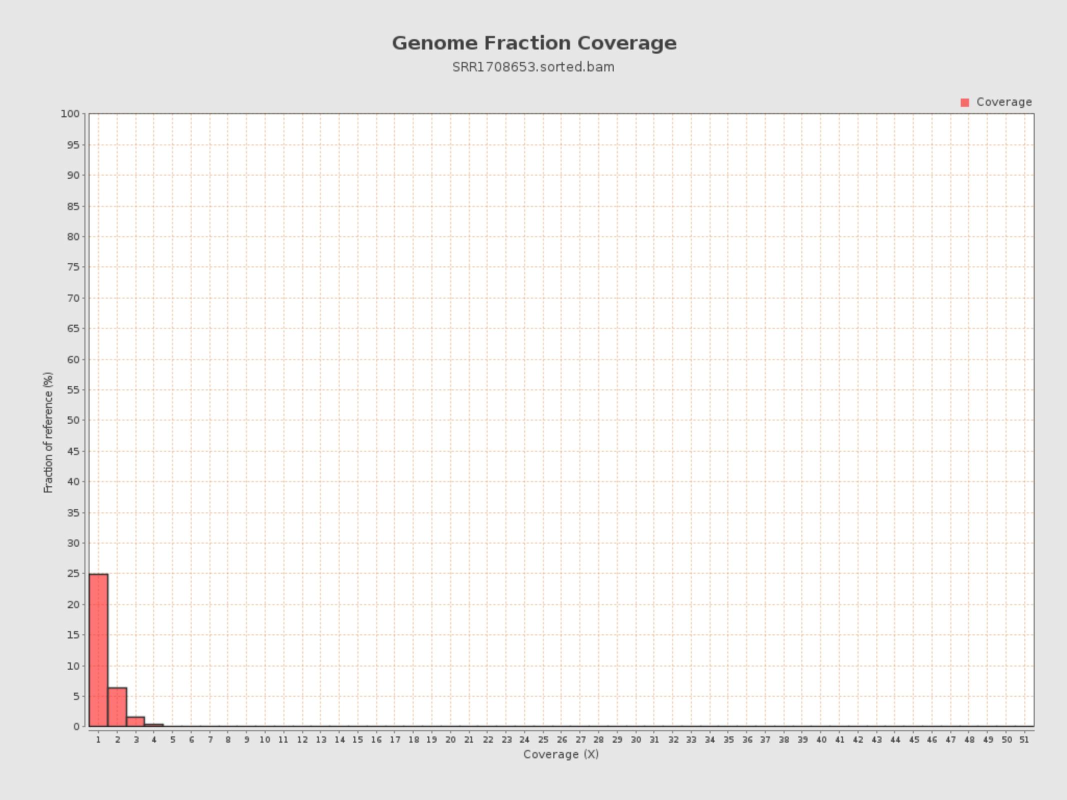
4. Results : Coverage Histogram



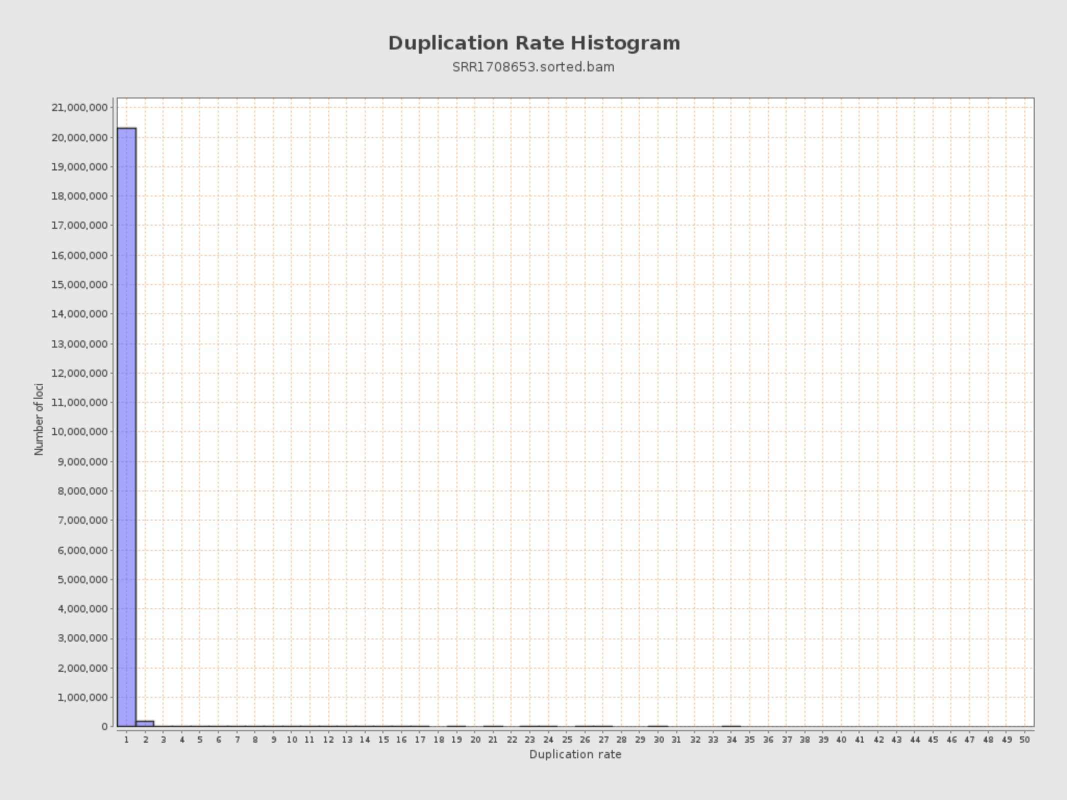
5. Results : Coverage Histogram (0-50X)



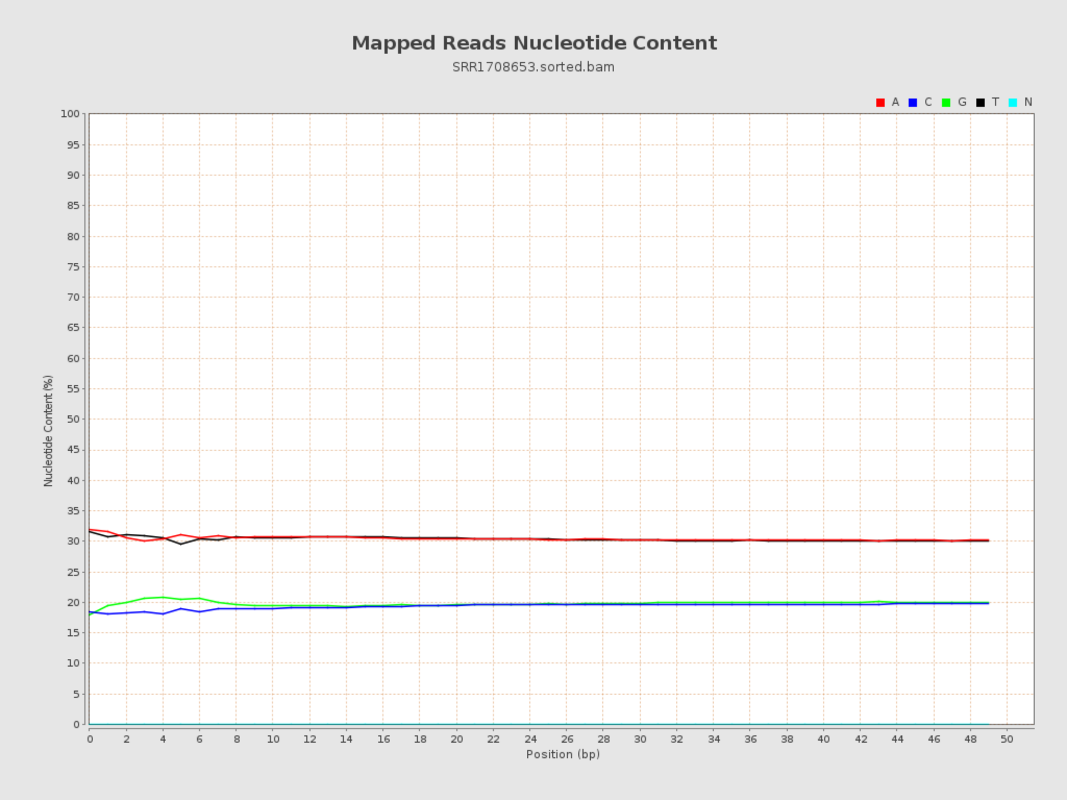
6. Results : Genome Fraction Coverage



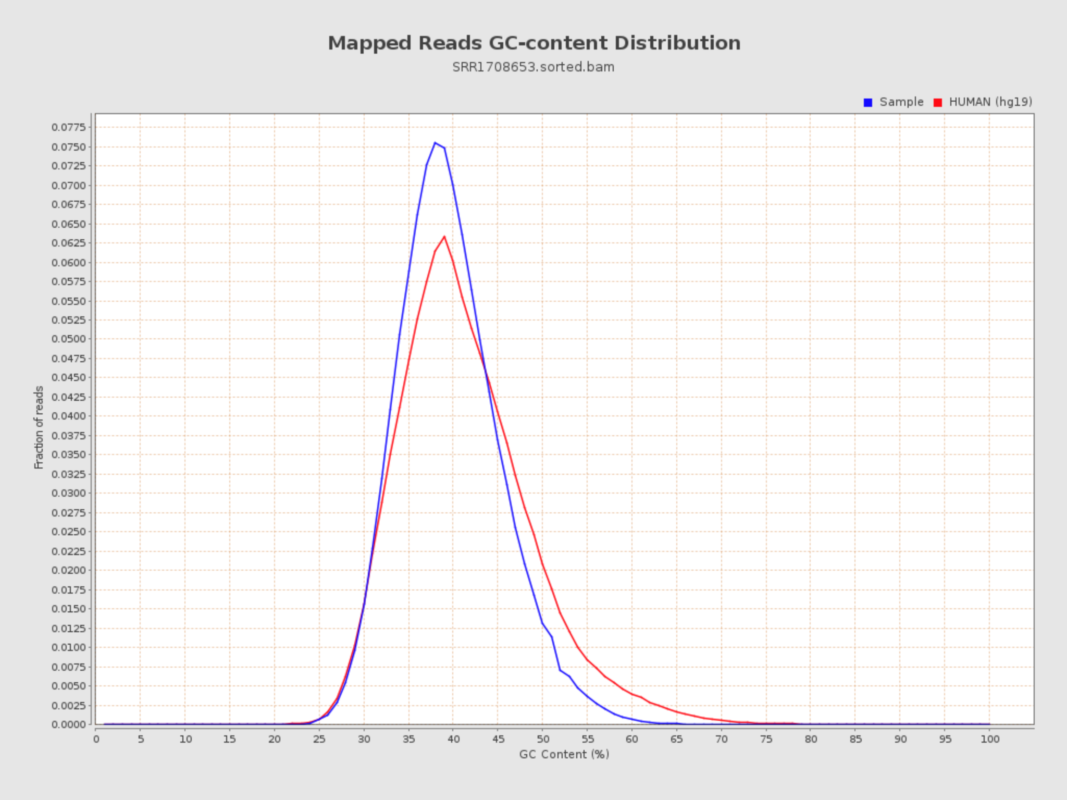
7. Results : Duplication Rate Histogram



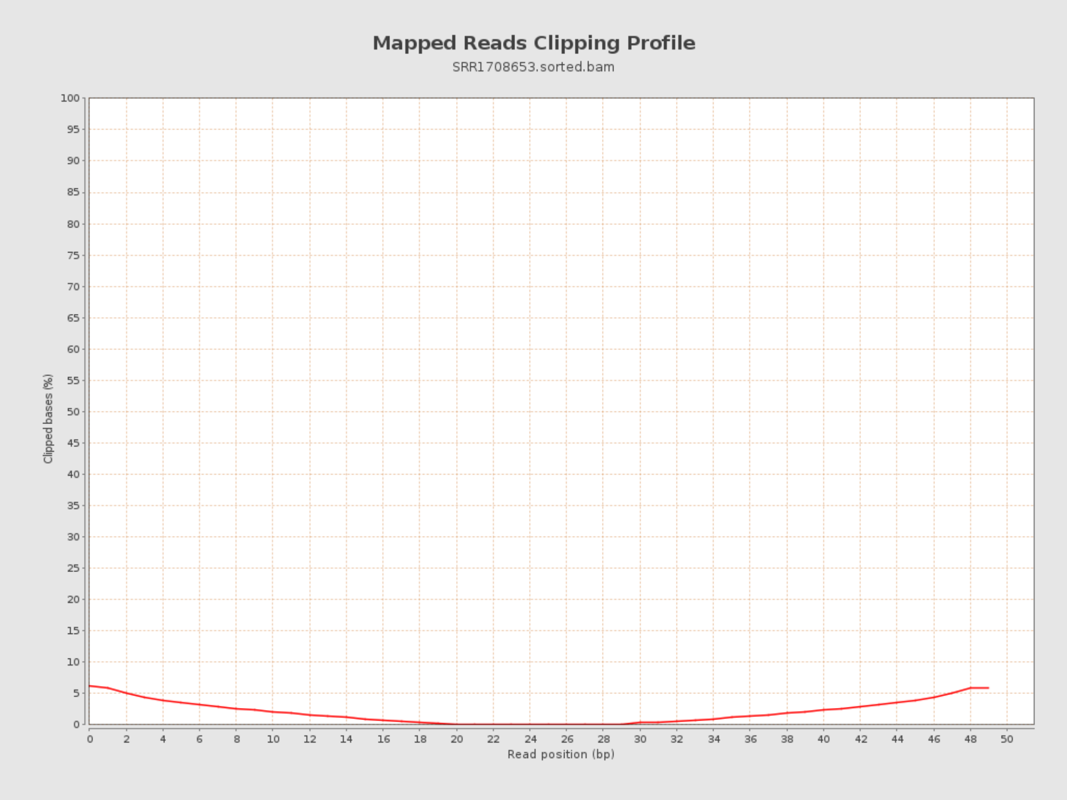
8. Results : Mapped Reads Nucleotide Content



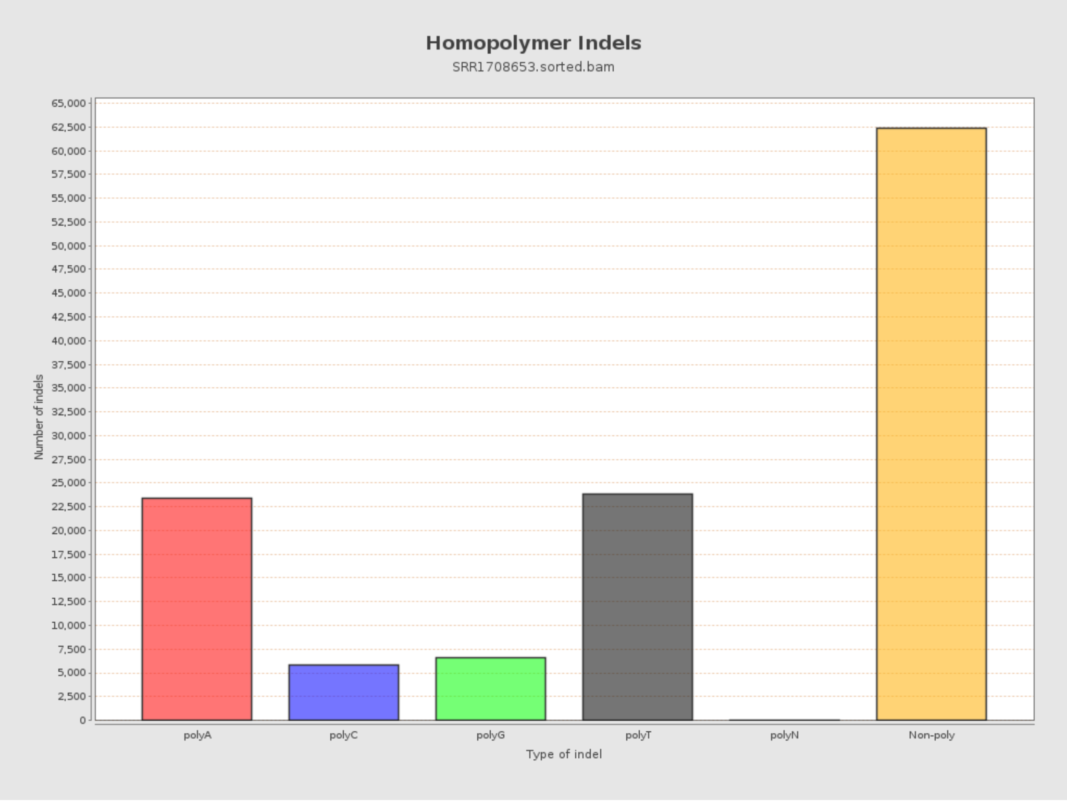
9. Results : Mapped Reads GC-content Distribution



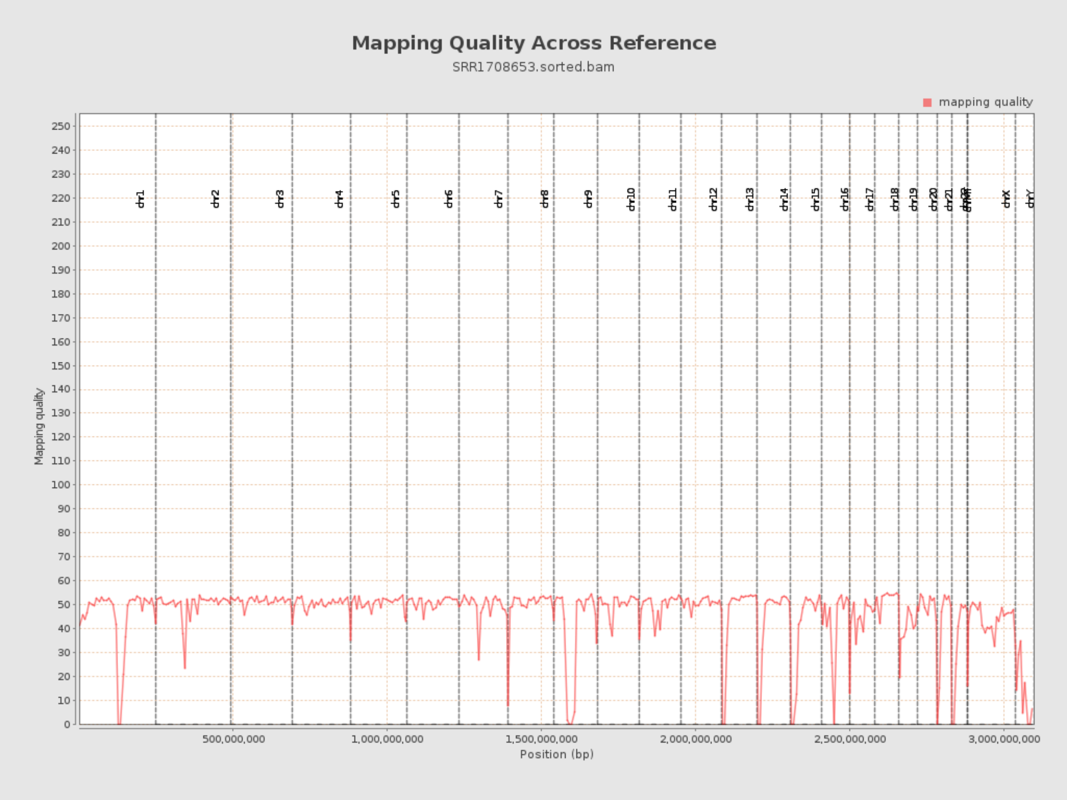
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram