Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:28:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708627.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_SRR1708627 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708627.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:28:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708627.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,301,249
Mapped reads	2,435,209 / 73.77%
Unmapped reads	866,040 / 26.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	818 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	93,359 / 2.83%
Duplication rate	2.59%
Clipped reads	380,059 / 11.51%

2.2. ACGT Content

Number/percentage of A's	34,885,332 / 29.42%
Number/percentage of C's	22,374,947 / 18.87%
Number/percentage of T's	37,367,325 / 31.52%
Number/percentage of G's	23,919,711 / 20.18%
Number/percentage of N's	10,272 / 0.01%
GC Percentage	39.05%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.4223

2.4. Mapping Quality

Mean Mapping Quality	43.79

2.5. Mismatches and indels

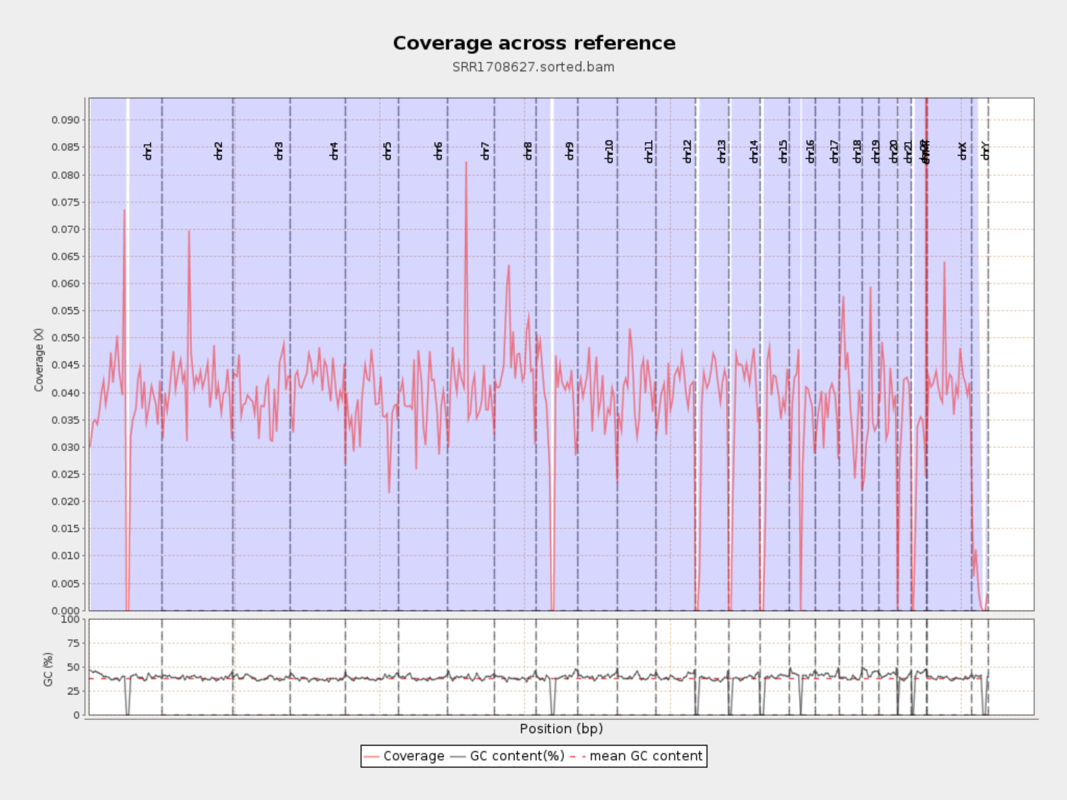
General error rate	0.64%
Mismatches	751,995
Insertions	5,441
Mapped reads with at least one insertion	0.22%
Deletions	14,125
Mapped reads with at least one deletion	0.58%
Homopolymer indels	48.23%

2.6. Chromosome stats

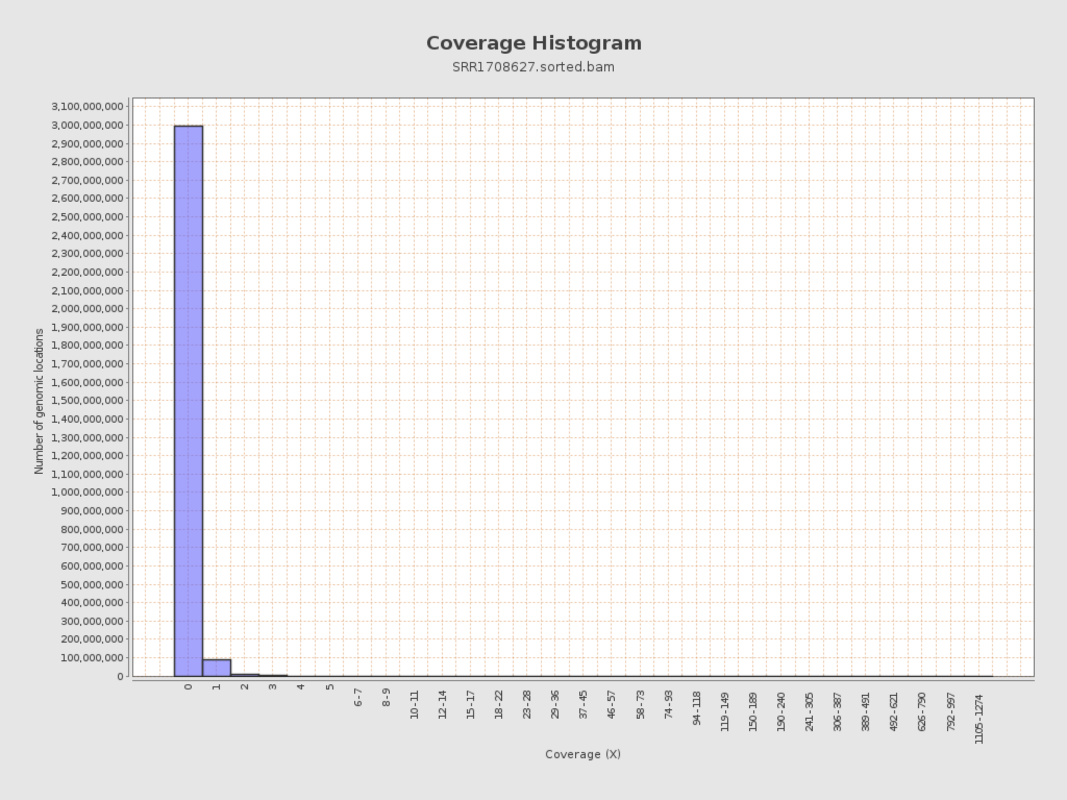
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9435810	0.0379	0.7874
chr2	243199373	10236937	0.0421	0.3941
chr3	198022430	7860708	0.0397	0.231
chr4	191154276	8064368	0.0422	0.2393
chr5	180915260	6780164	0.0375	0.2288
chr6	171115067	6582420	0.0385	0.2832
chr7	159138663	6678788	0.042	0.6339

chr8	146364022	6764493	0.0462	0.7516
chr9	141213431	5135869	0.0364	0.3397
chr10	135534747	5355706	0.0395	0.312
chr11	135006516	5451752	0.0404	0.3936
chr12	133851895	5368480	0.0401	0.239
chr13	115169878	4067822	0.0353	0.2164
chr14	107349540	3938789	0.0367	0.2433
chr15	102531392	3453870	0.0337	0.2105
chr16	90354753	3120104	0.0345	0.2379
chr17	81195210	2973116	0.0366	0.2922
chr18	78077248	3141435	0.0402	0.7394
chr19	59128983	2084888	0.0353	0.5582
chr20	63025520	2462825	0.0391	0.241
chr21	48129895	1609704	0.0334	0.2288
chr22	51304566	1202425	0.0234	0.1714
chrMT	16571	15270	0.9215	1.2048
chrX	155270560	6524904	0.042	0.2853
chrY	59373566	268720	0.0045	0.0907

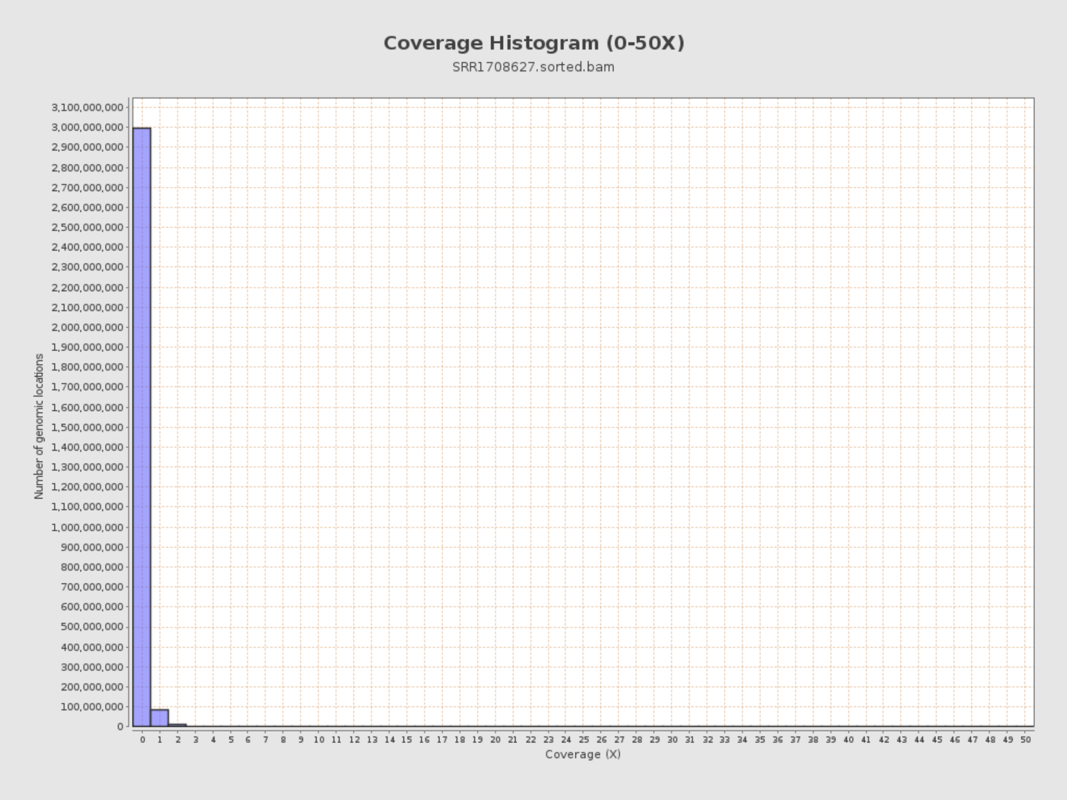
3. Results : Coverage across reference



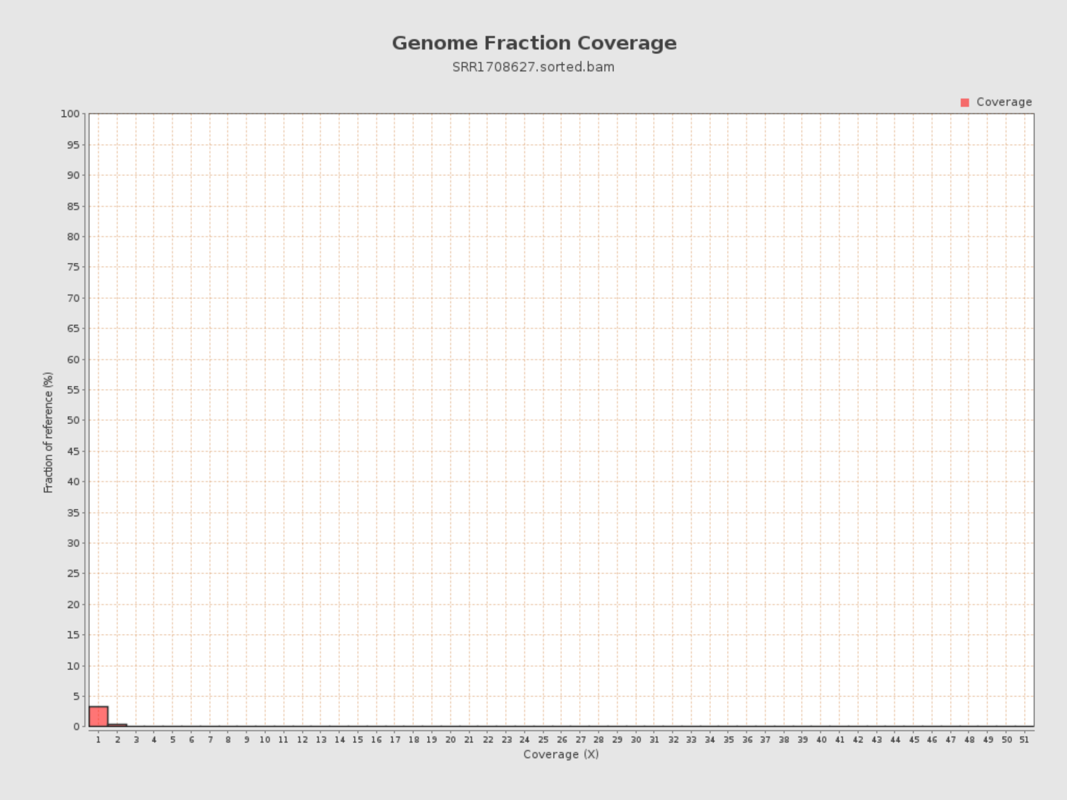
4. Results : Coverage Histogram



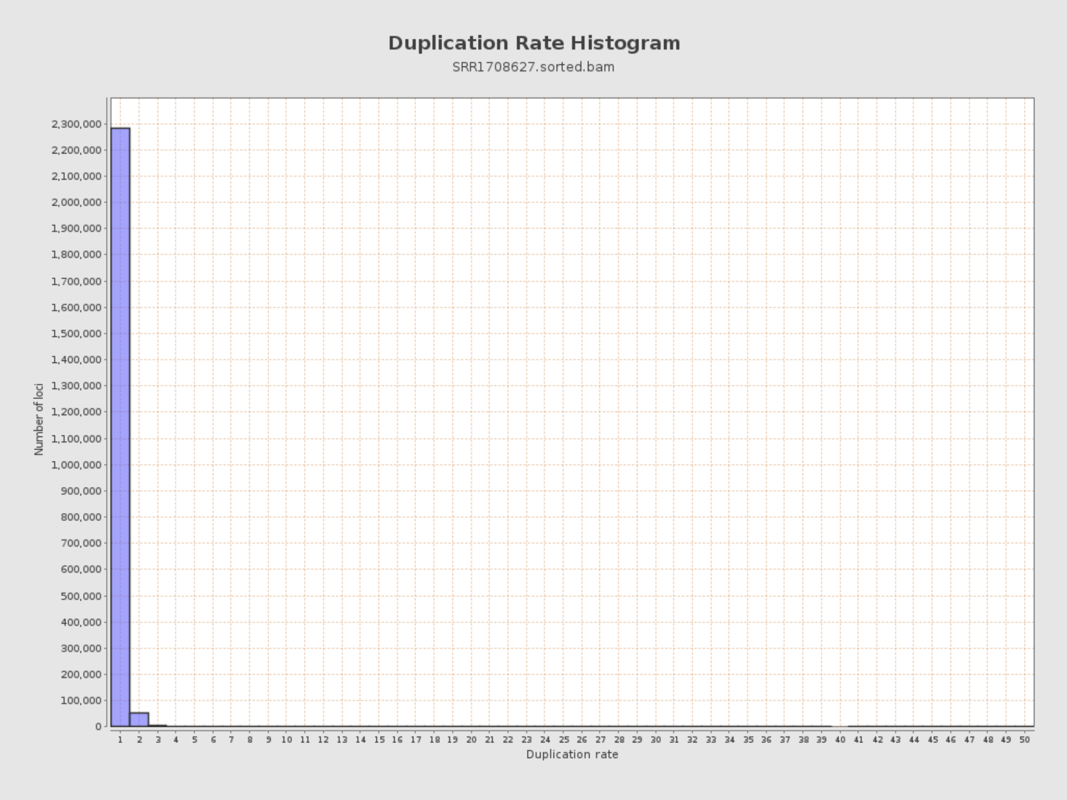
5. Results : Coverage Histogram (0-50X)



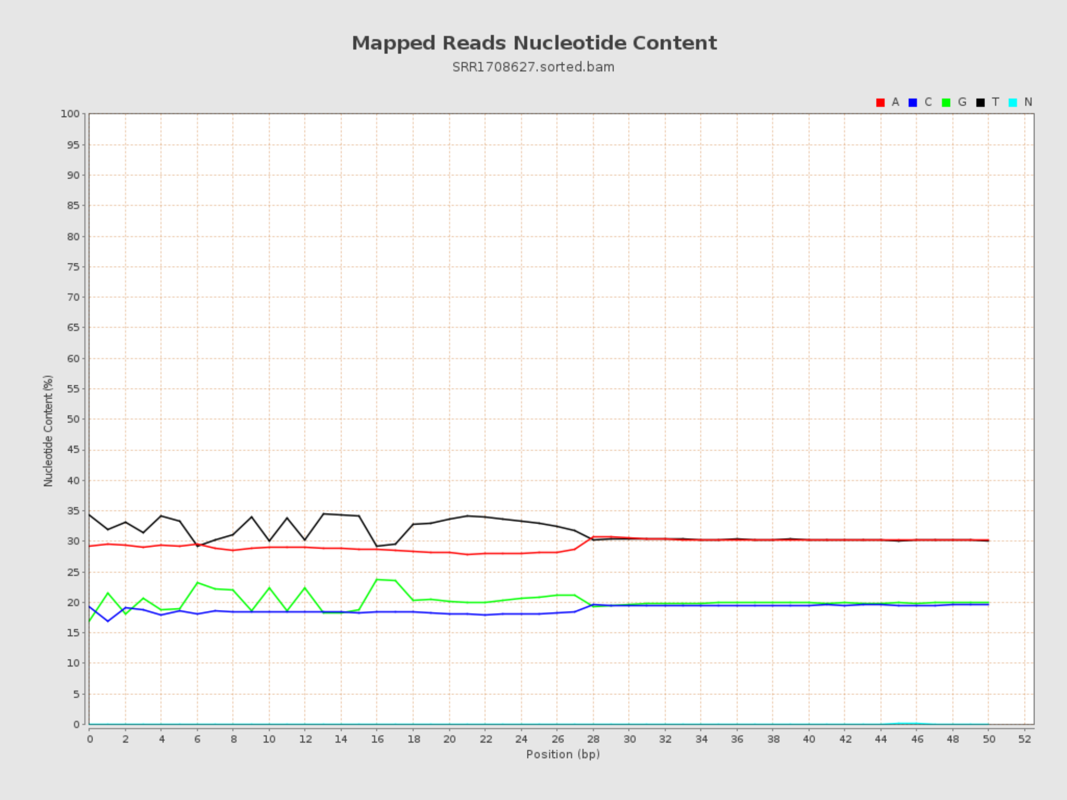
6. Results : Genome Fraction Coverage



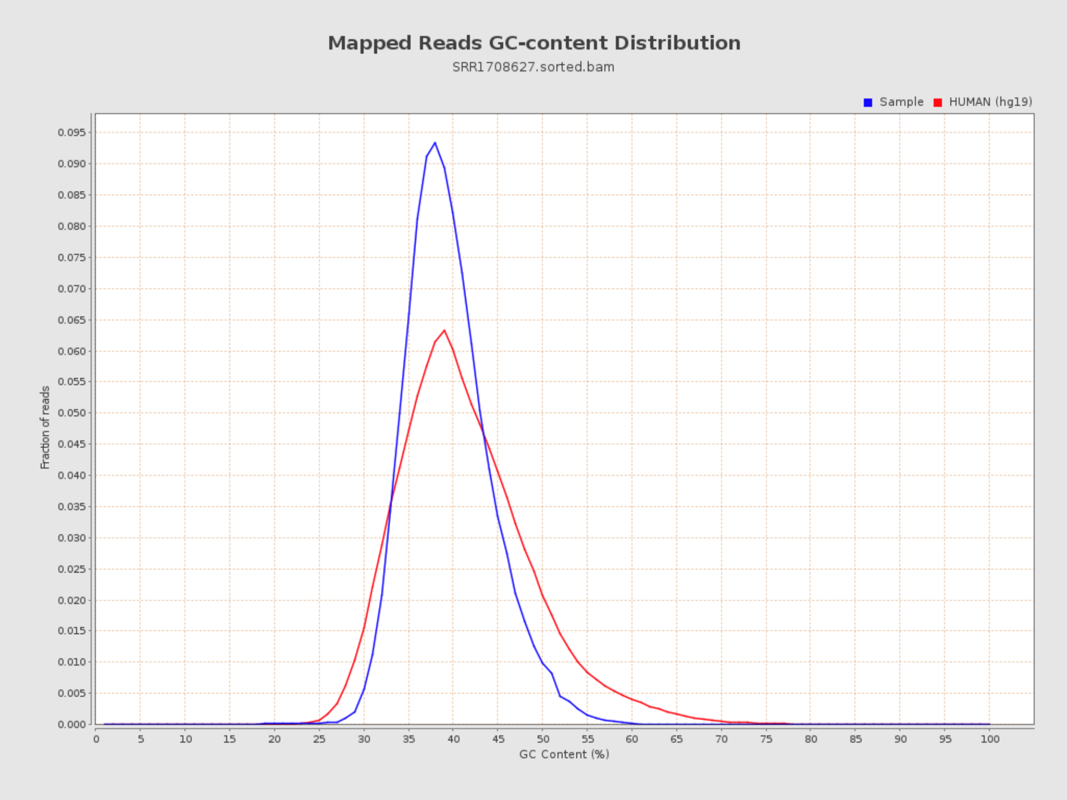
7. Results : Duplication Rate Histogram



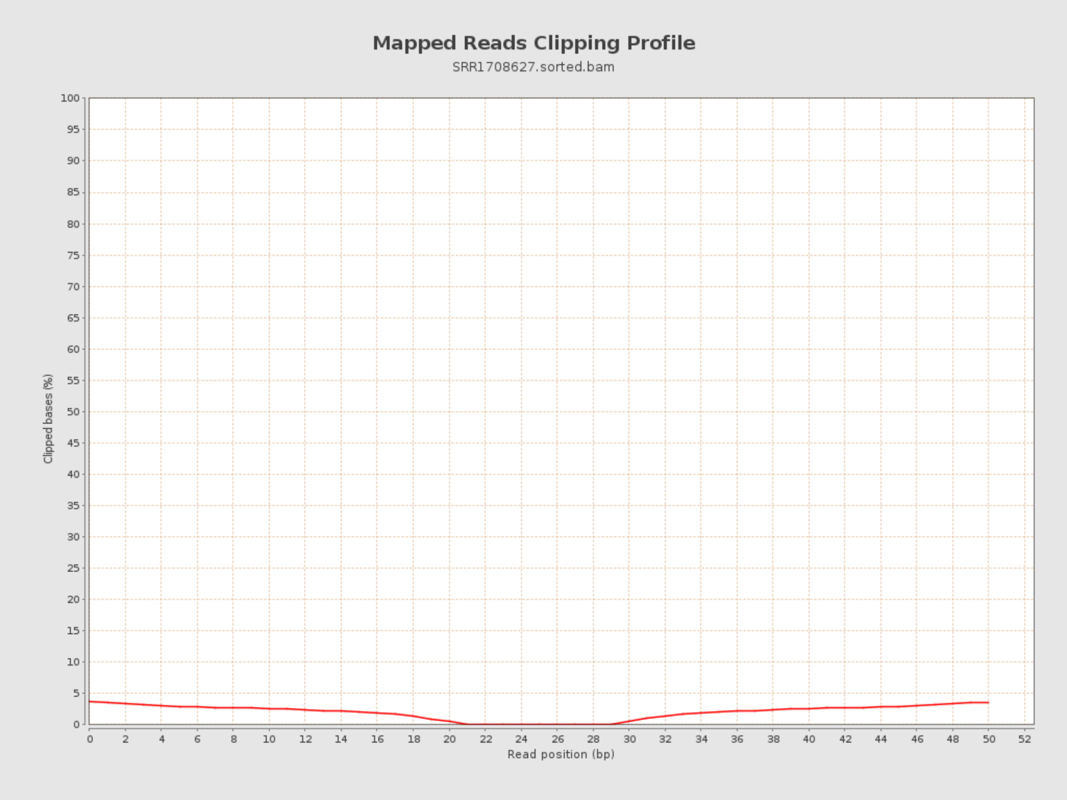
8. Results : Mapped Reads Nucleotide Content



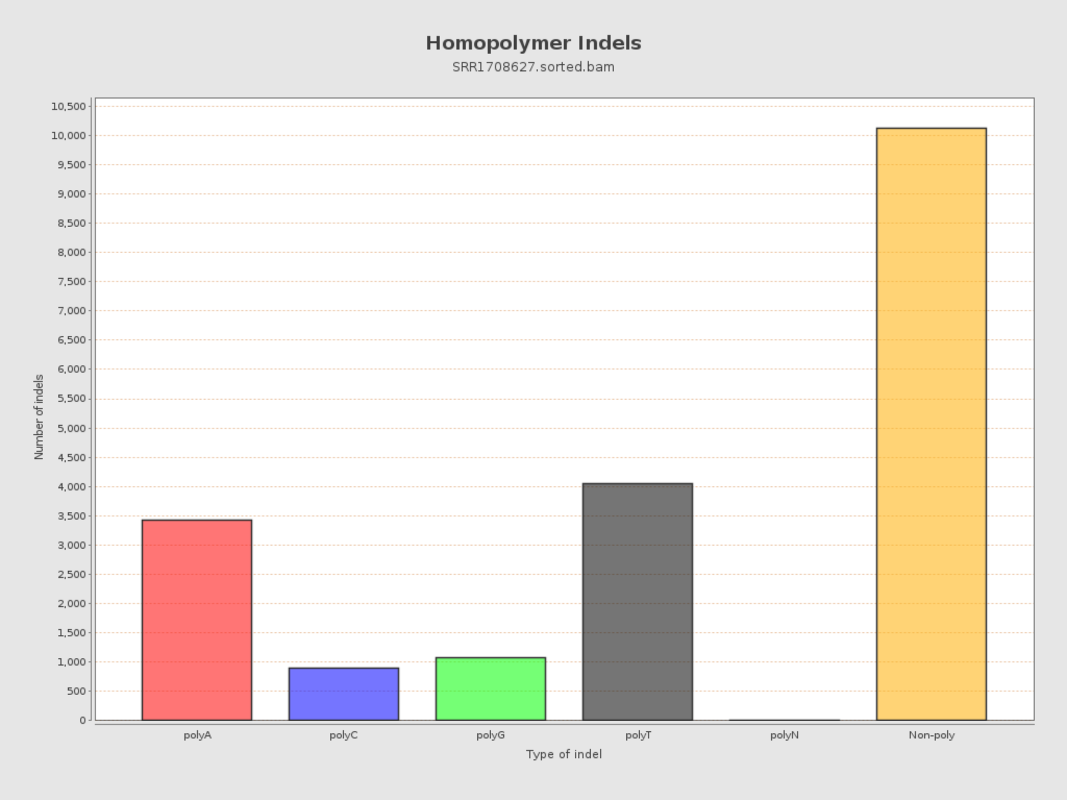
9. Results : Mapped Reads GC-content Distribution



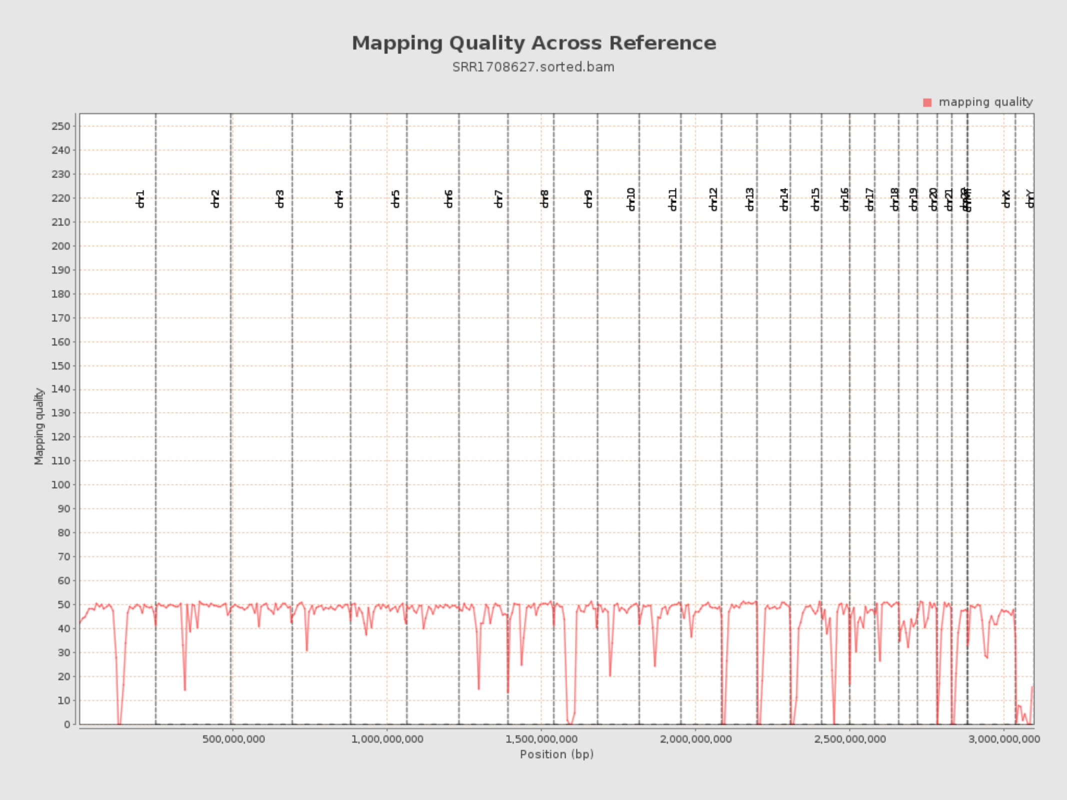
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram