Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:29:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708523.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_SRR1708523 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708523.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:29:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708523.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,471,990
Mapped reads	2,424,995 / 69.84%
Unmapped reads	1,046,995 / 30.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	520 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	117,259 / 3.38%
Duplication rate	3.68%
Clipped reads	453,452 / 13.06%

2.2. ACGT Content

Number/percentage of A's	34,063,267 / 29.2%
Number/percentage of C's	21,532,025 / 18.46%
Number/percentage of T's	37,380,307 / 32.05%
Number/percentage of G's	23,665,148 / 20.29%
Number/percentage of N's	1,690 / 0%
GC Percentage	38.75%

2.3. Coverage

Mean	0.0377

Standard Deviation	0.3917

2.4. Mapping Quality

Mean Mapping Quality	43.19

2.5. Mismatches and indels

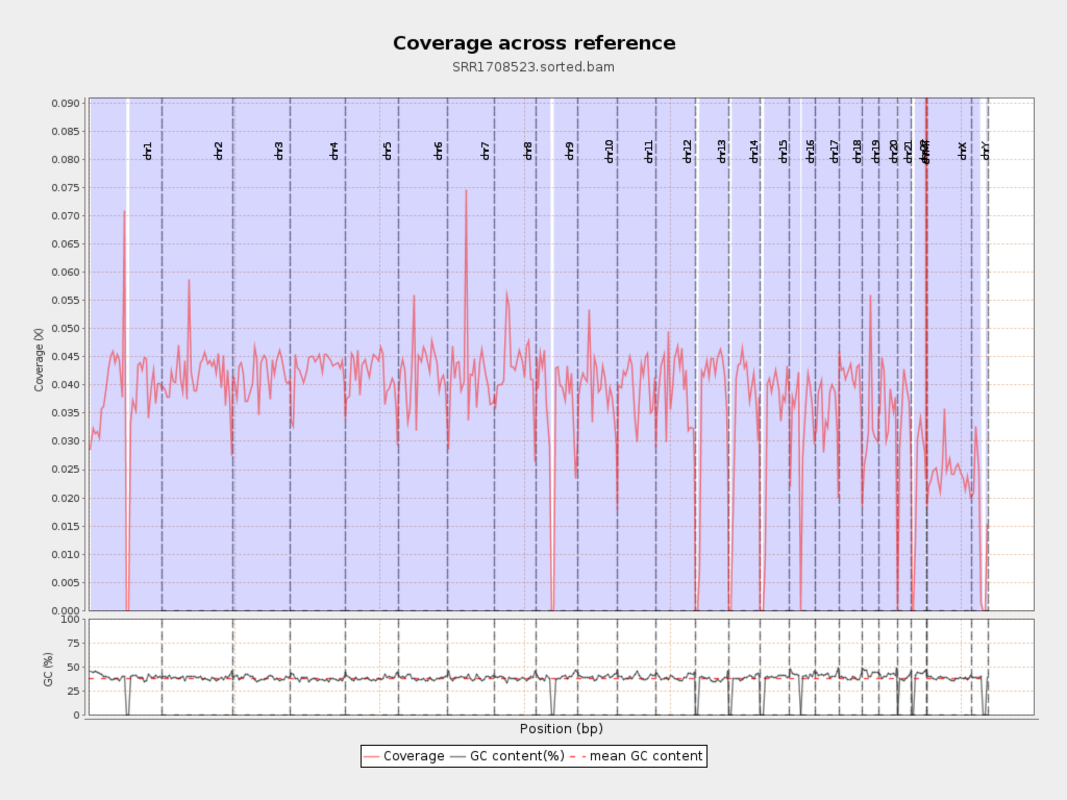
General error rate	0.49%
Mismatches	566,473
Insertions	5,562
Mapped reads with at least one insertion	0.23%
Deletions	13,921
Mapped reads with at least one deletion	0.57%
Homopolymer indels	48.2%

2.6. Chromosome stats

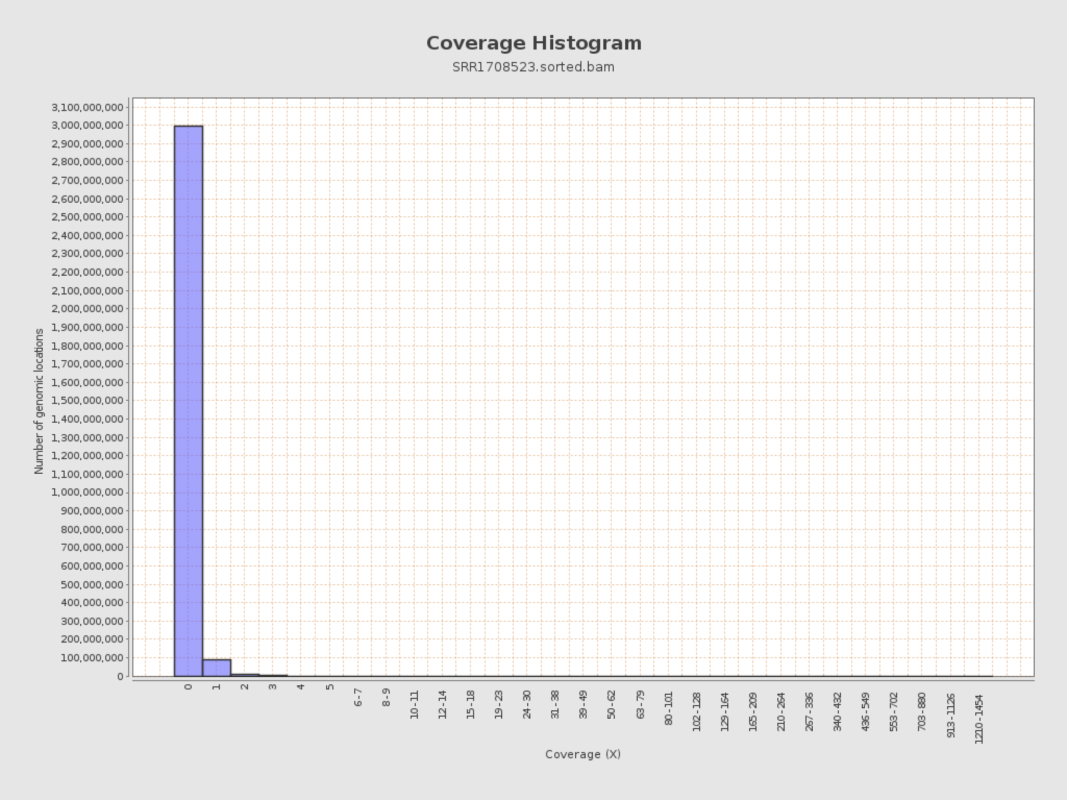
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9375319	0.0376	0.7593
chr2	243199373	10182884	0.0419	0.3246
chr3	198022430	8281168	0.0418	0.2356
chr4	191154276	8214554	0.043	0.2427
chr5	180915260	7564905	0.0418	0.2367
chr6	171115067	7270664	0.0425	0.2927
chr7	159138663	6758540	0.0425	0.5024

chr8	146364022	6291933	0.043	0.8096
chr9	141213431	4896847	0.0347	0.2657
chr10	135534747	5438333	0.0401	0.3099
chr11	135006516	5368199	0.0398	0.3232
chr12	133851895	5297955	0.0396	0.2345
chr13	115169878	4092383	0.0355	0.2181
chr14	107349540	3643501	0.0339	0.2176
chr15	102531392	3239676	0.0316	0.2022
chr16	90354753	2965516	0.0328	0.2173
chr17	81195210	2816439	0.0347	0.2734
chr18	78077248	3274361	0.0419	0.4688
chr19	59128983	1941626	0.0328	0.5247
chr20	63025520	2283735	0.0362	0.219
chr21	48129895	1548957	0.0322	0.2567
chr22	51304566	1091987	0.0213	0.19
chrMT	16571	203392	12.274	8
chrX	155270560	3772597	0.0243	0.2046
chrY	59373566	847659	0.0143	0.1519

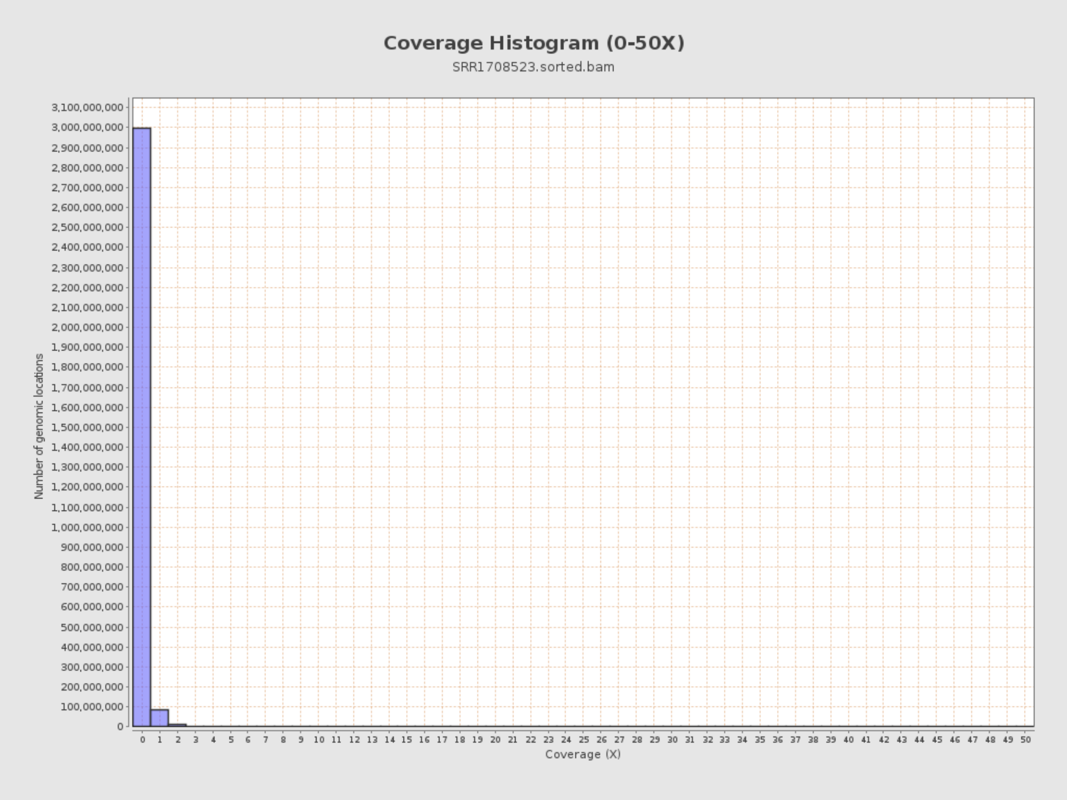
3. Results : Coverage across reference



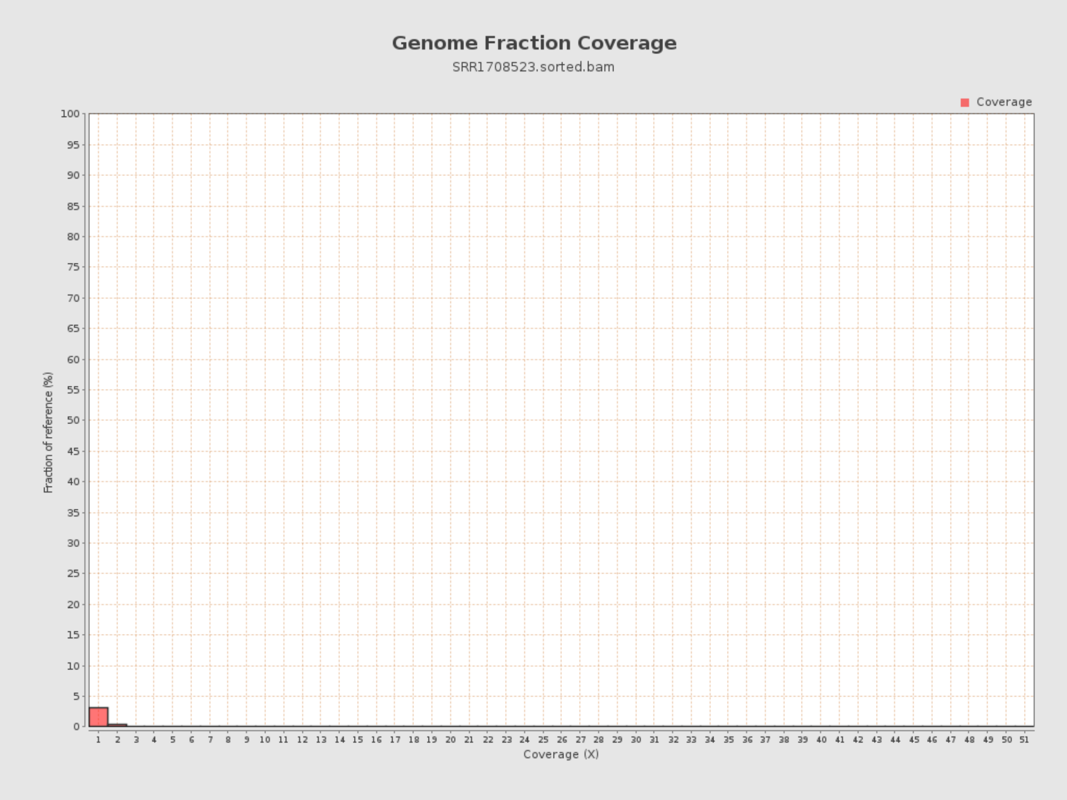
4. Results : Coverage Histogram



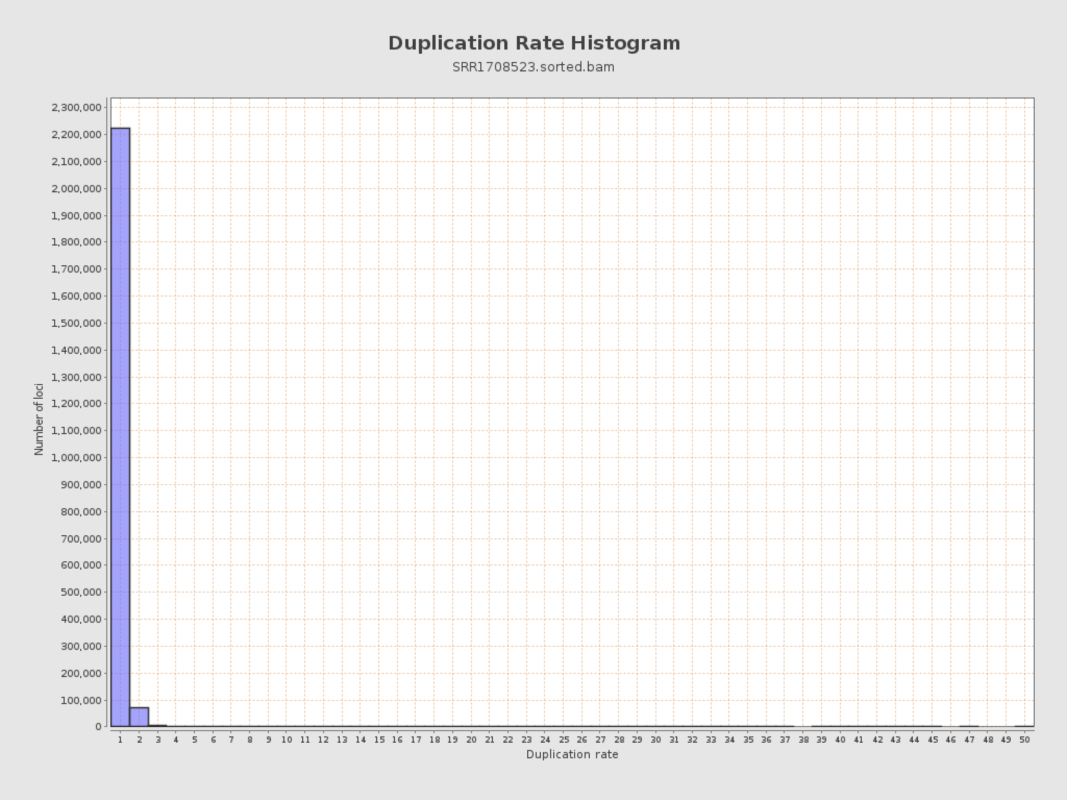
5. Results : Coverage Histogram (0-50X)



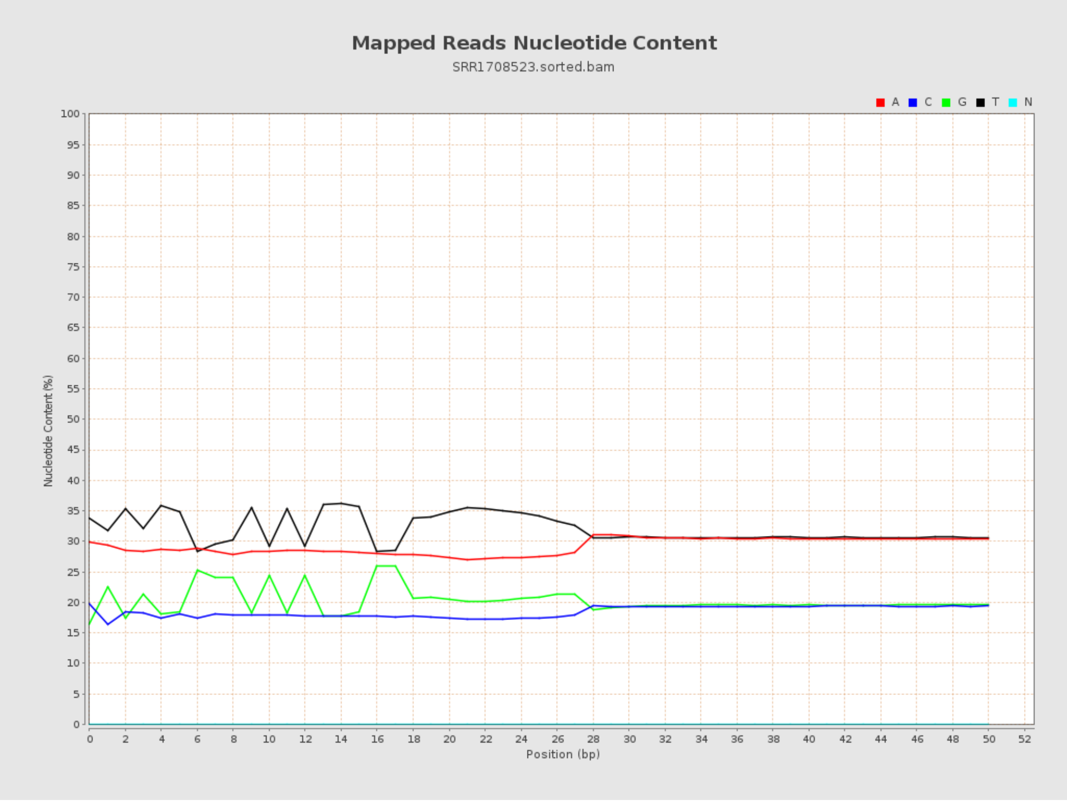
6. Results : Genome Fraction Coverage



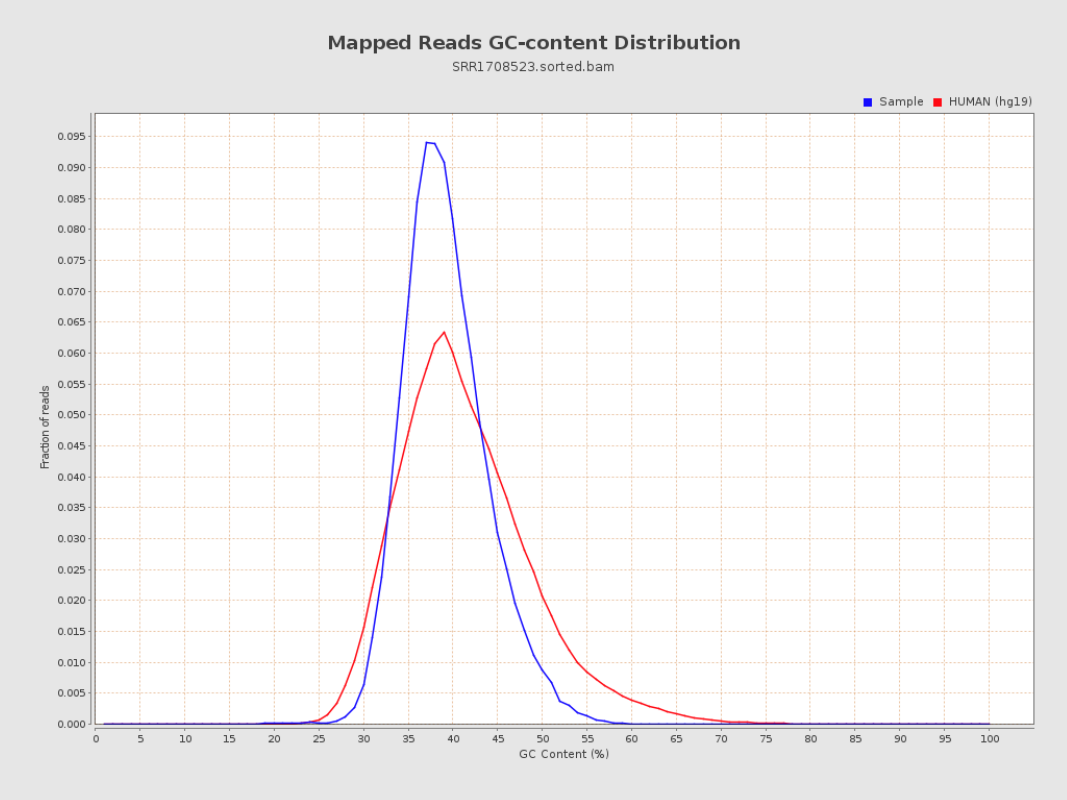
7. Results : Duplication Rate Histogram



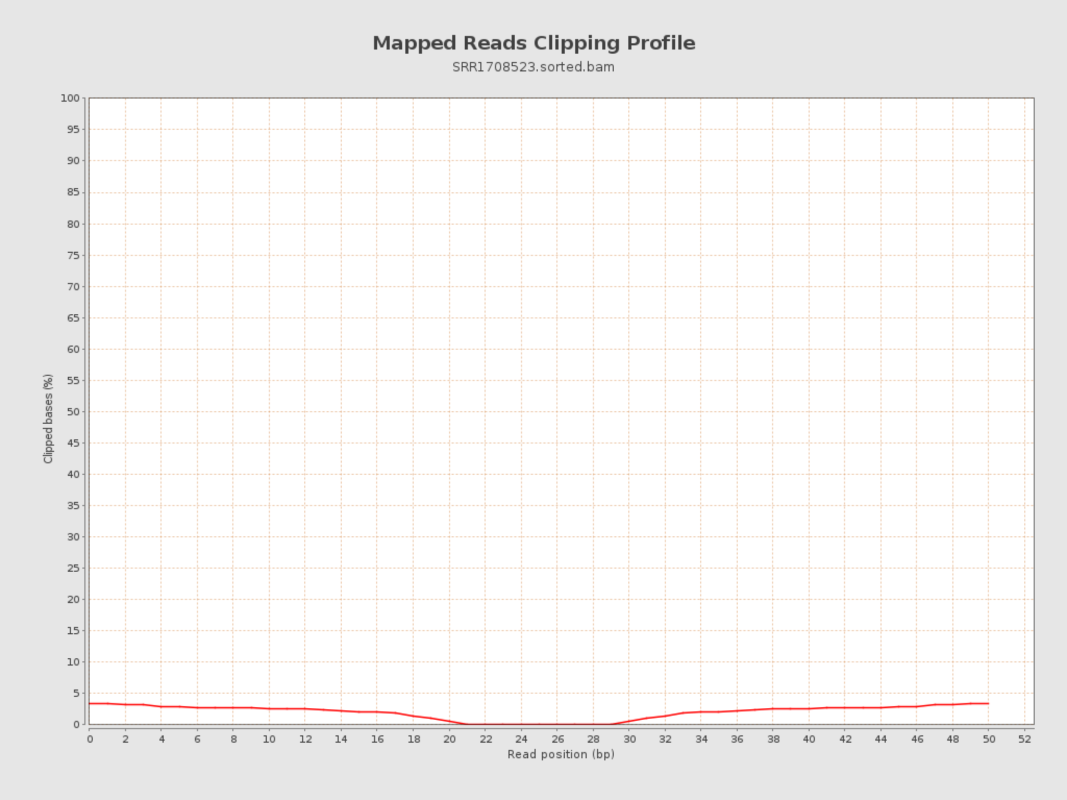
8. Results : Mapped Reads Nucleotide Content



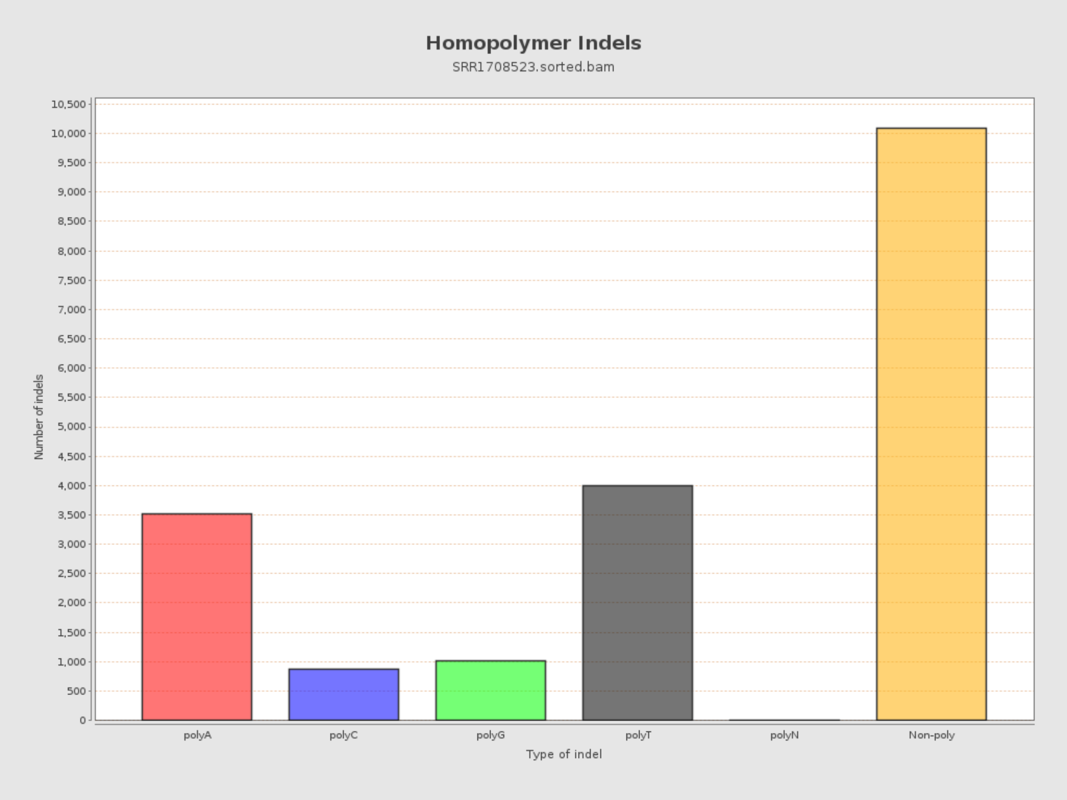
9. Results : Mapped Reads GC-content Distribution



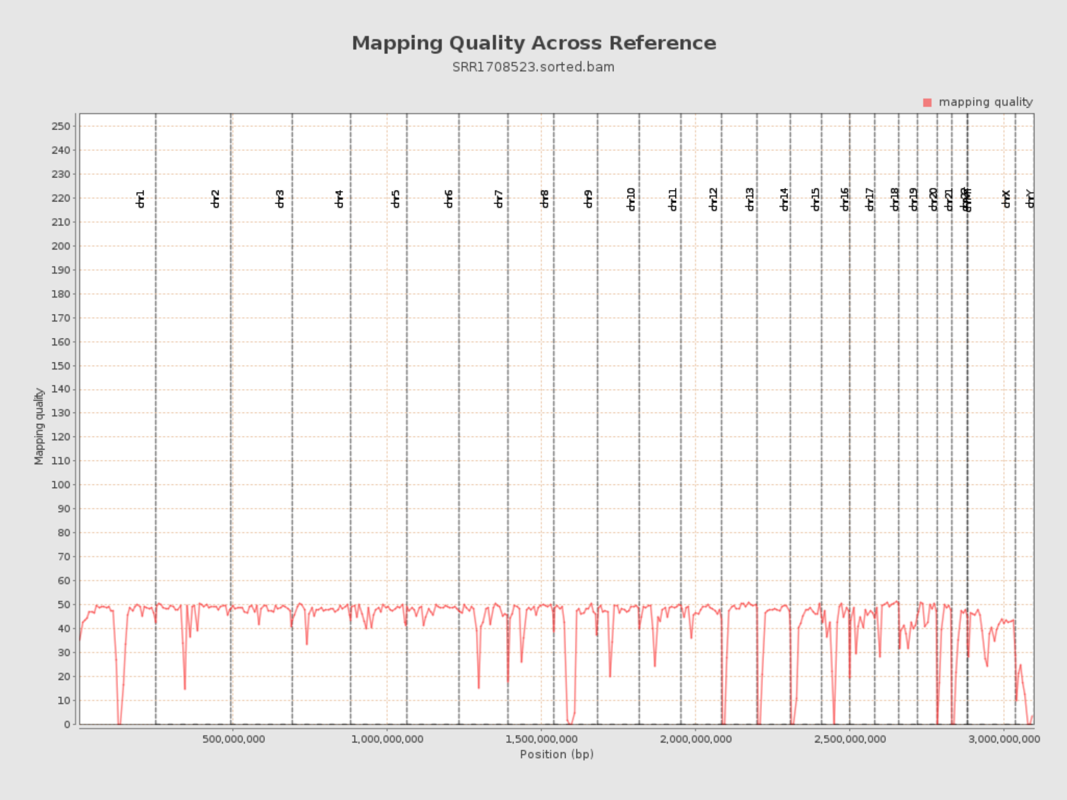
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram