Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:03:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708525.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_SRR1708525 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708525.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:03:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708525.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,364,858
Mapped reads	2,345,116 / 69.69%
Unmapped reads	1,019,742 / 30.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	526 / 0.02%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	101,465 / 3.02%
Duplication rate	3.47%
Clipped reads	450,235 / 13.38%

2.2. ACGT Content

Number/percentage of A's	32,550,626 / 28.9%
Number/percentage of C's	21,042,520 / 18.69%
Number/percentage of T's	35,866,717 / 31.85%
Number/percentage of G's	23,154,435 / 20.56%
Number/percentage of N's	1,692 / 0%
GC Percentage	39.25%

2.3. Coverage

Mean	0.0364

Standard Deviation	0.3194

2.4. Mapping Quality

Mean Mapping Quality	43.04

2.5. Mismatches and indels

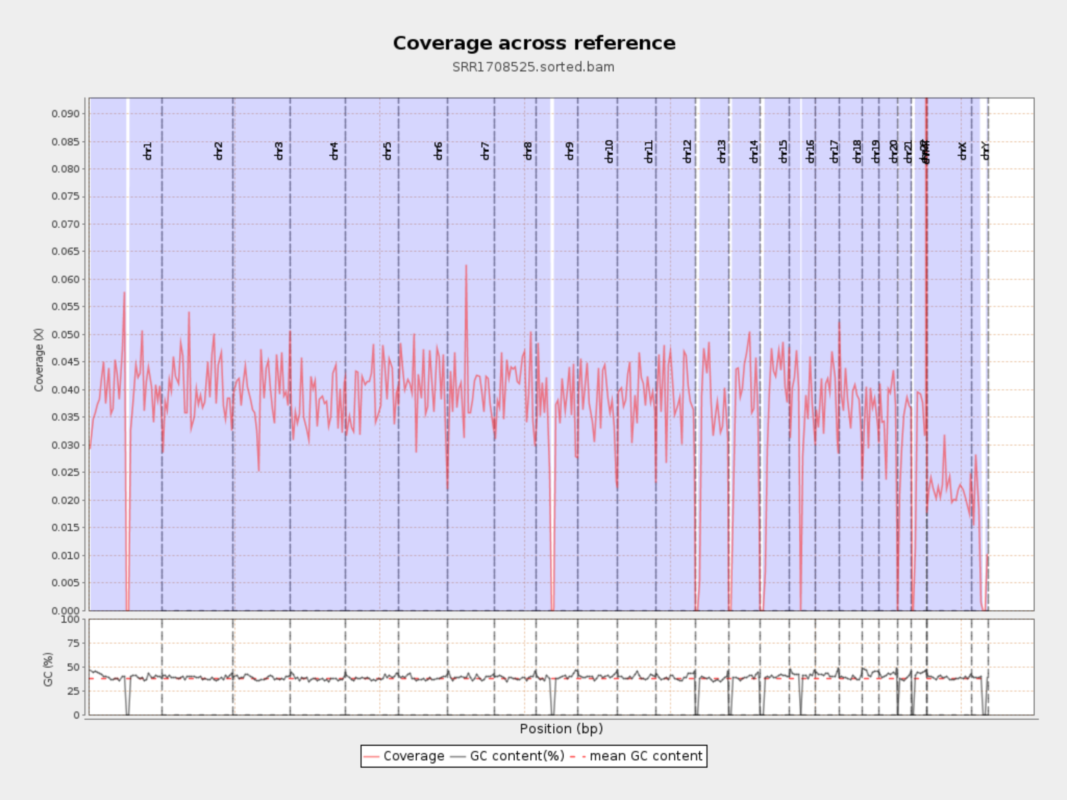
General error rate	0.48%
Mismatches	536,583
Insertions	5,332
Mapped reads with at least one insertion	0.23%
Deletions	13,827
Mapped reads with at least one deletion	0.59%
Homopolymer indels	48.29%

2.6. Chromosome stats

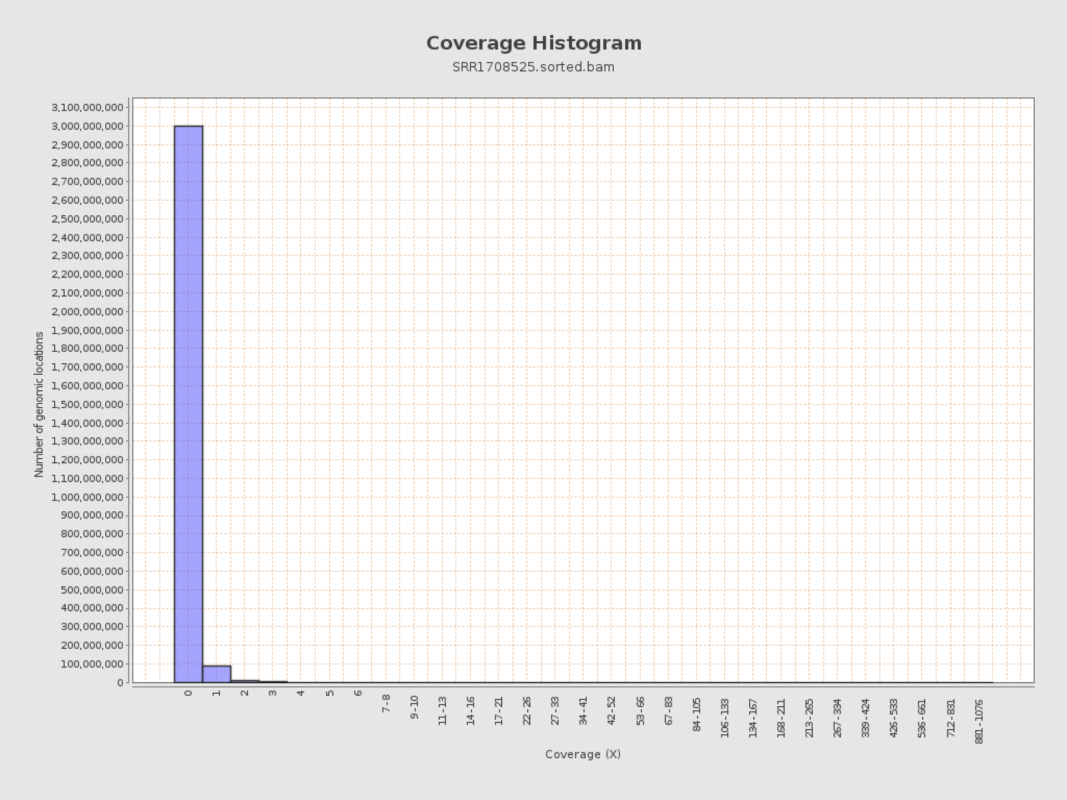
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9452775	0.0379	0.5536
chr2	243199373	9799784	0.0403	0.2999
chr3	198022430	7845550	0.0396	0.2261
chr4	191154276	7118988	0.0372	0.2223
chr5	180915260	7150586	0.0395	0.2269
chr6	171115067	7015118	0.041	0.2782
chr7	159138663	6364163	0.04	0.4076

chr8	146364022	5945472	0.0406	0.6132
chr9	141213431	4770138	0.0338	0.2384
chr10	135534747	5160955	0.0381	0.2627
chr11	135006516	5260132	0.039	0.2744
chr12	133851895	5313386	0.0397	0.229
chr13	115169878	3671039	0.0319	0.203
chr14	107349540	3730012	0.0347	0.2158
chr15	102531392	3448447	0.0336	0.2084
chr16	90354753	3165135	0.035	0.2162
chr17	81195210	3098525	0.0382	0.2508
chr18	78077248	3040366	0.0389	0.3642
chr19	59128983	2085279	0.0353	0.4075
chr20	63025520	2255118	0.0358	0.2138
chr21	48129895	1435291	0.0298	0.2177
chr22	51304566	1300459	0.0253	0.1907
chrMT	16571	153570	9.2674	6.5705
chrX	155270560	3380230	0.0218	0.1851
chrY	59373566	676875	0.0114	0.1299

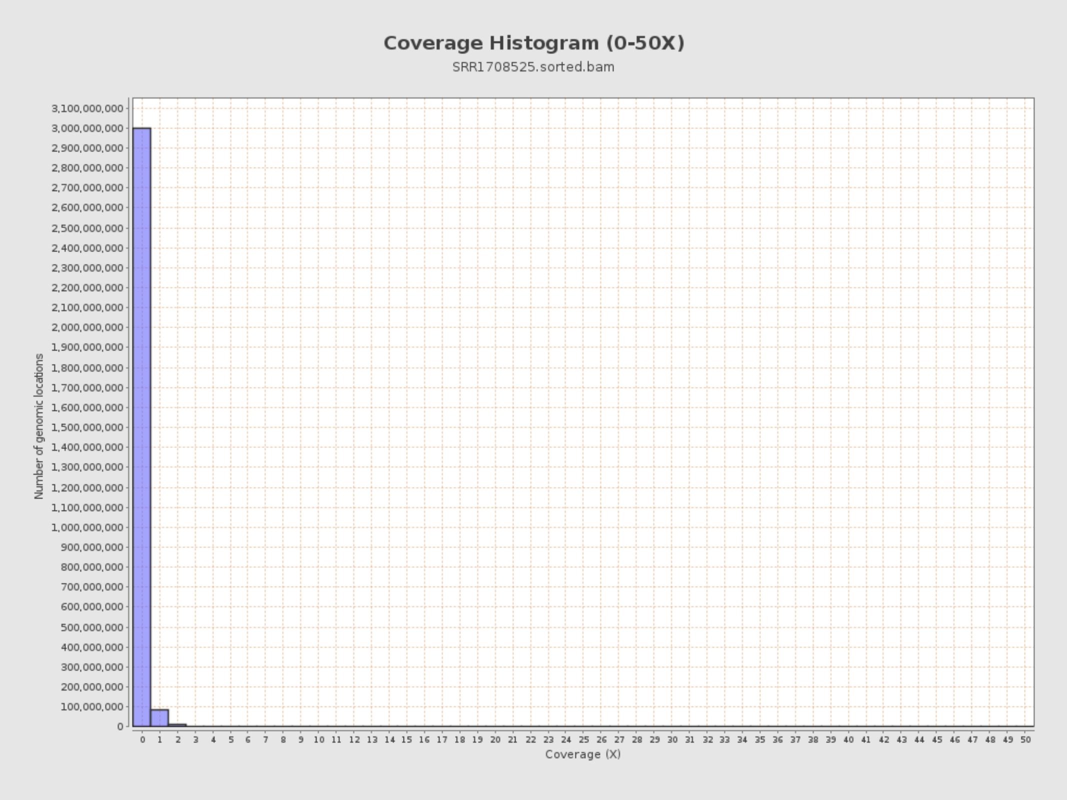
3. Results : Coverage across reference



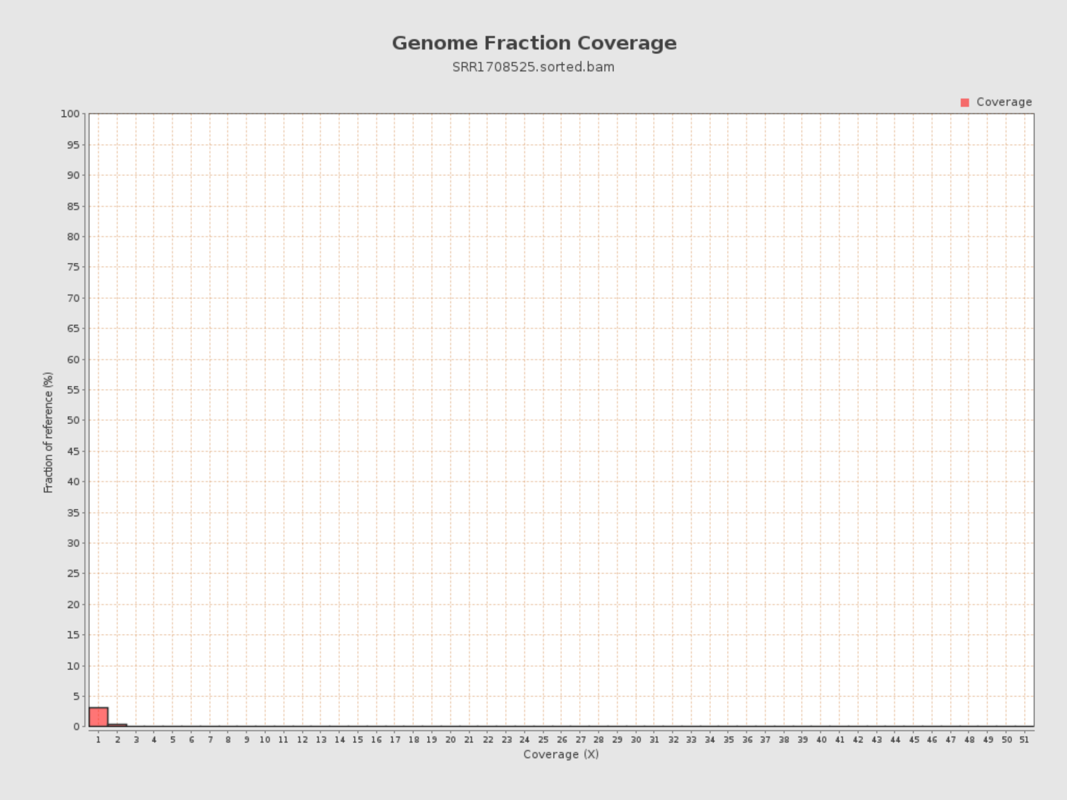
4. Results : Coverage Histogram



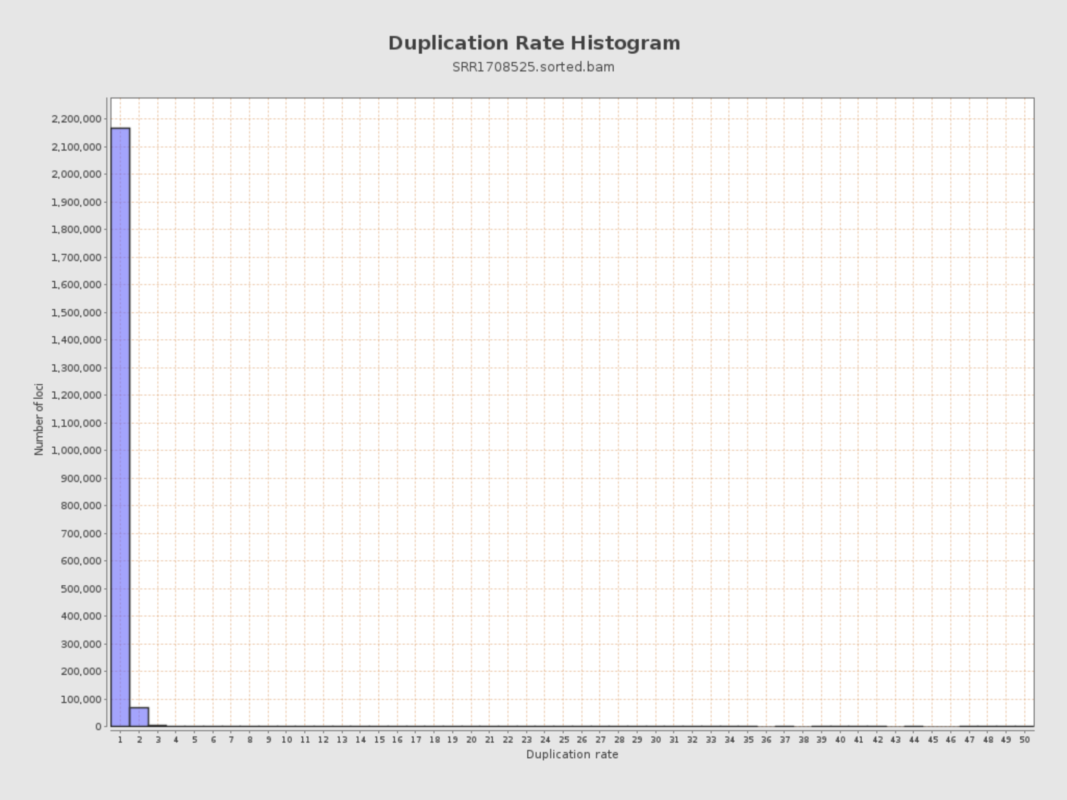
5. Results : Coverage Histogram (0-50X)



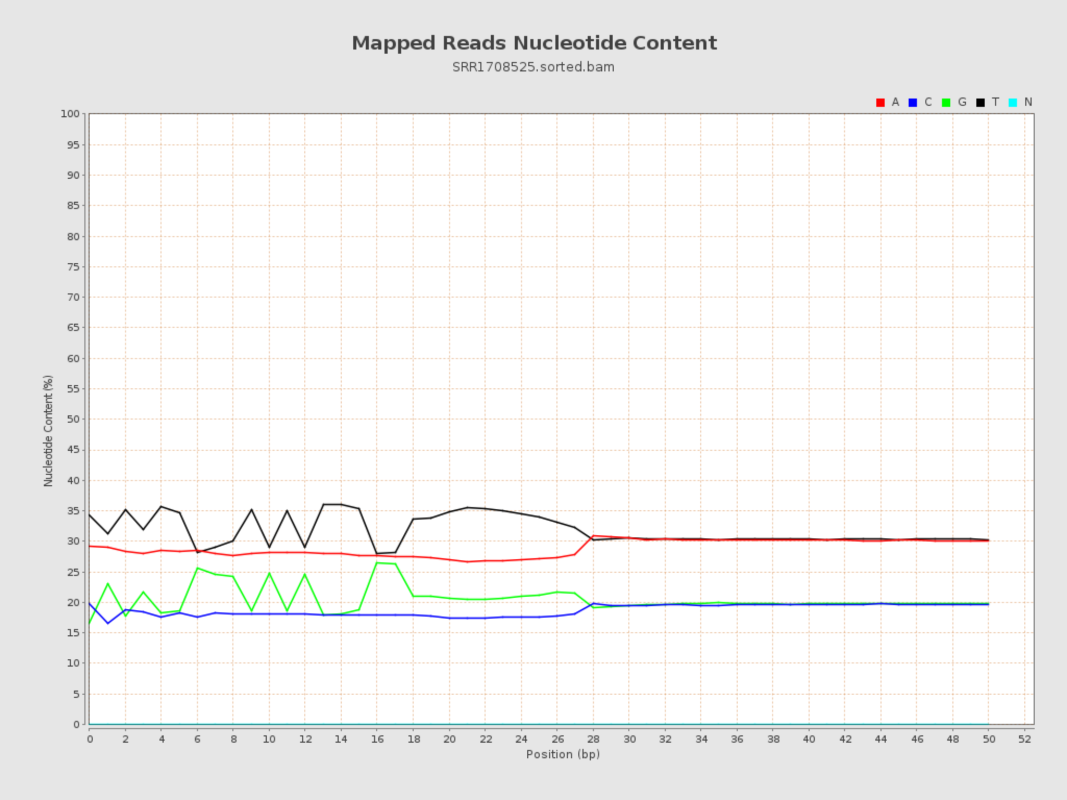
6. Results : Genome Fraction Coverage



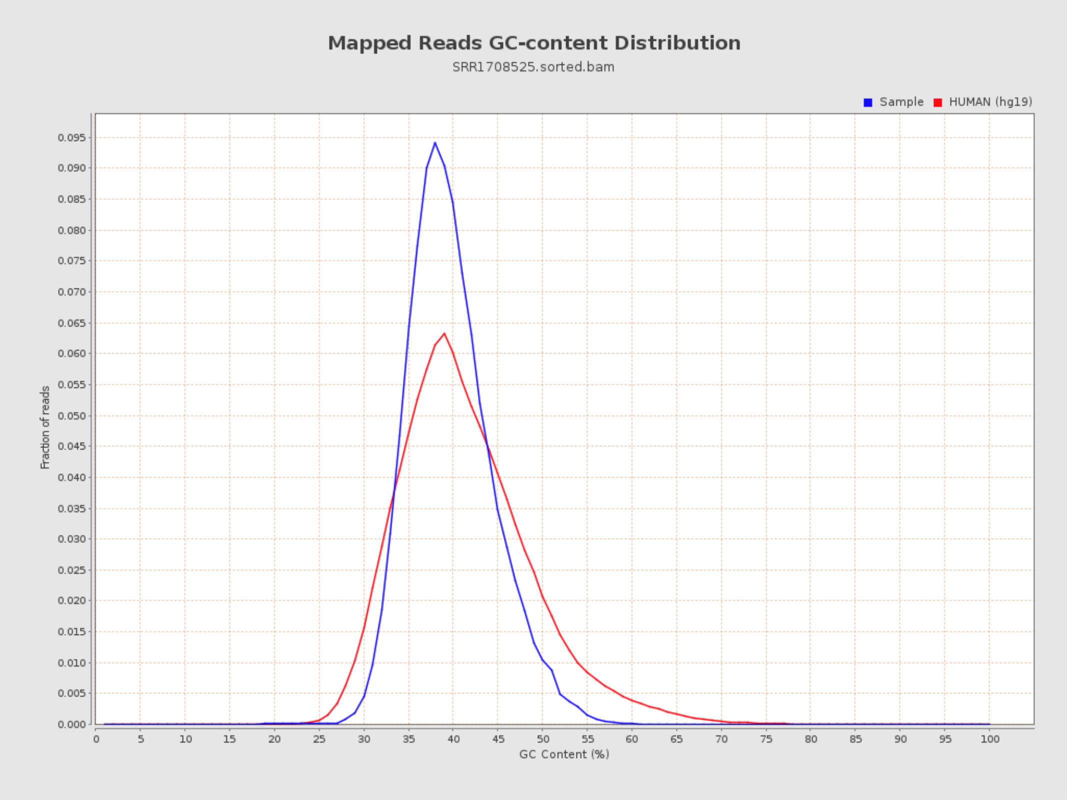
7. Results : Duplication Rate Histogram



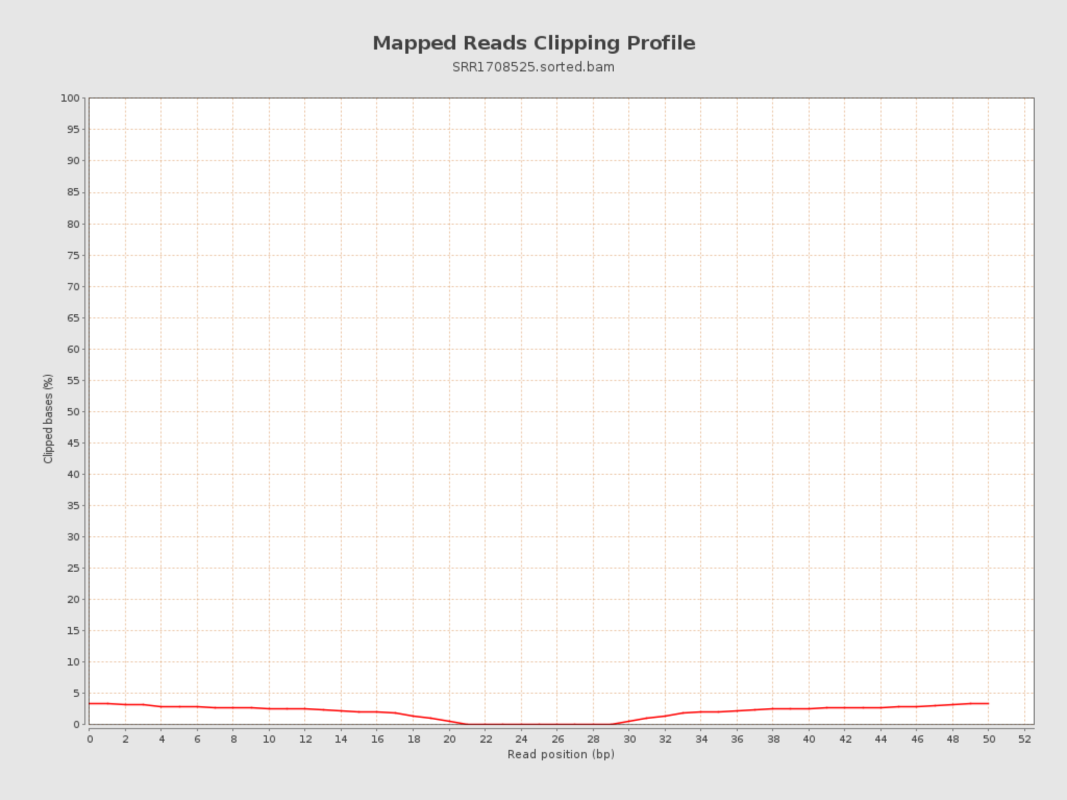
8. Results : Mapped Reads Nucleotide Content



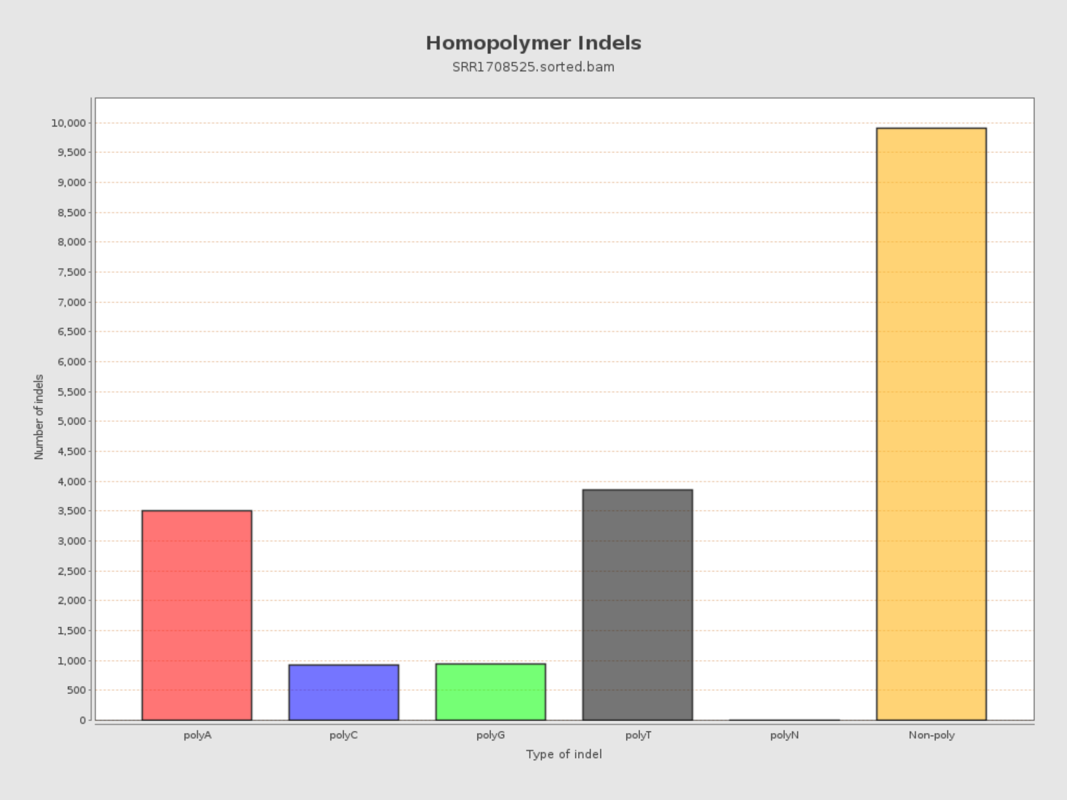
9. Results : Mapped Reads GC-content Distribution



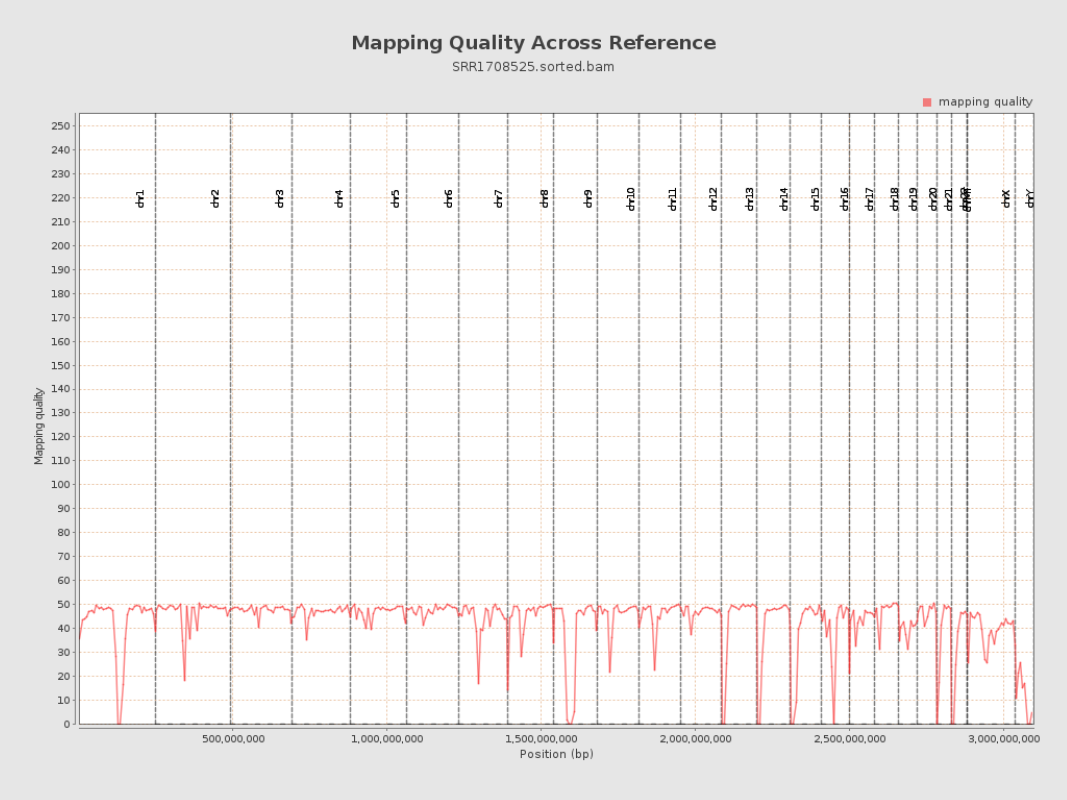
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram