Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:12:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708522.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_SRR1708522 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708522.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:12:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708522.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,302,302
Mapped reads	2,280,402 / 69.05%
Unmapped reads	1,021,900 / 30.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	499 / 0.02%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	109,350 / 3.31%
Duplication rate	3.64%
Clipped reads	436,665 / 13.22%

2.2. ACGT Content

Number/percentage of A's	31,893,841 / 29.13%
Number/percentage of C's	20,186,775 / 18.44%
Number/percentage of T's	35,183,928 / 32.13%
Number/percentage of G's	22,223,333 / 20.3%
Number/percentage of N's	1,645 / 0%
GC Percentage	38.73%

2.3. Coverage

Mean	0.0354

Standard Deviation	0.3763

2.4. Mapping Quality

Mean Mapping Quality	43.08

2.5. Mismatches and indels

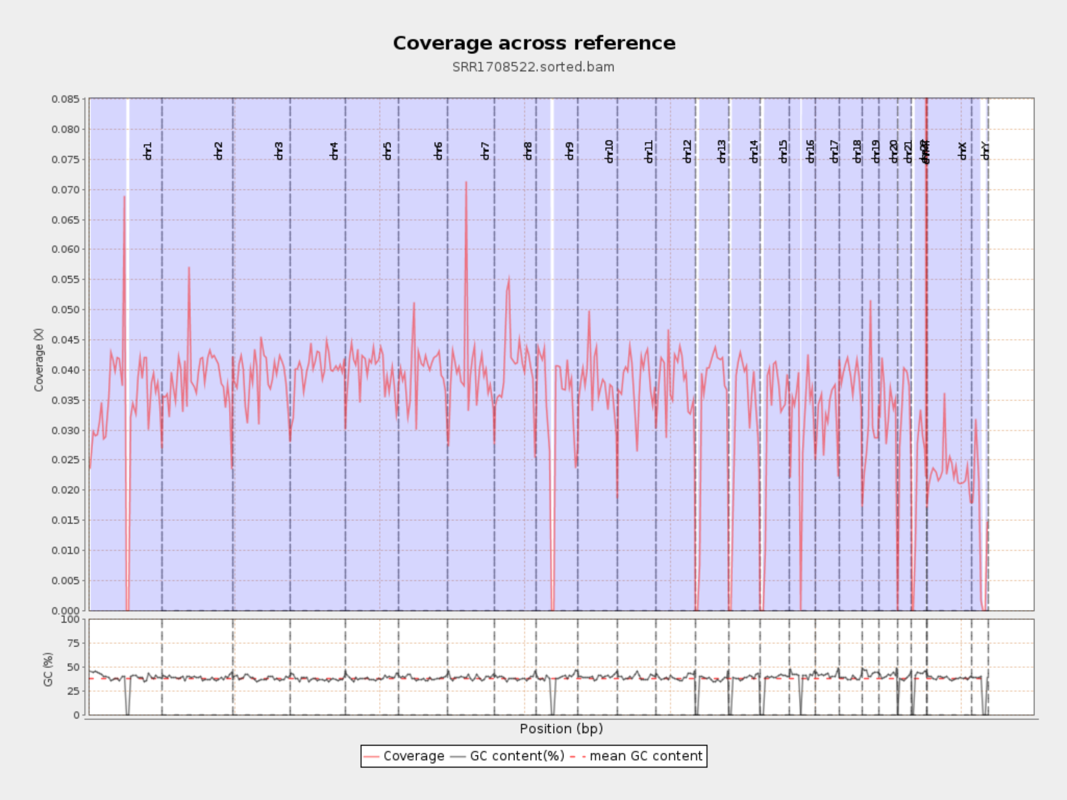
General error rate	0.49%
Mismatches	530,158
Insertions	5,252
Mapped reads with at least one insertion	0.23%
Deletions	13,116
Mapped reads with at least one deletion	0.57%
Homopolymer indels	48.75%

2.6. Chromosome stats

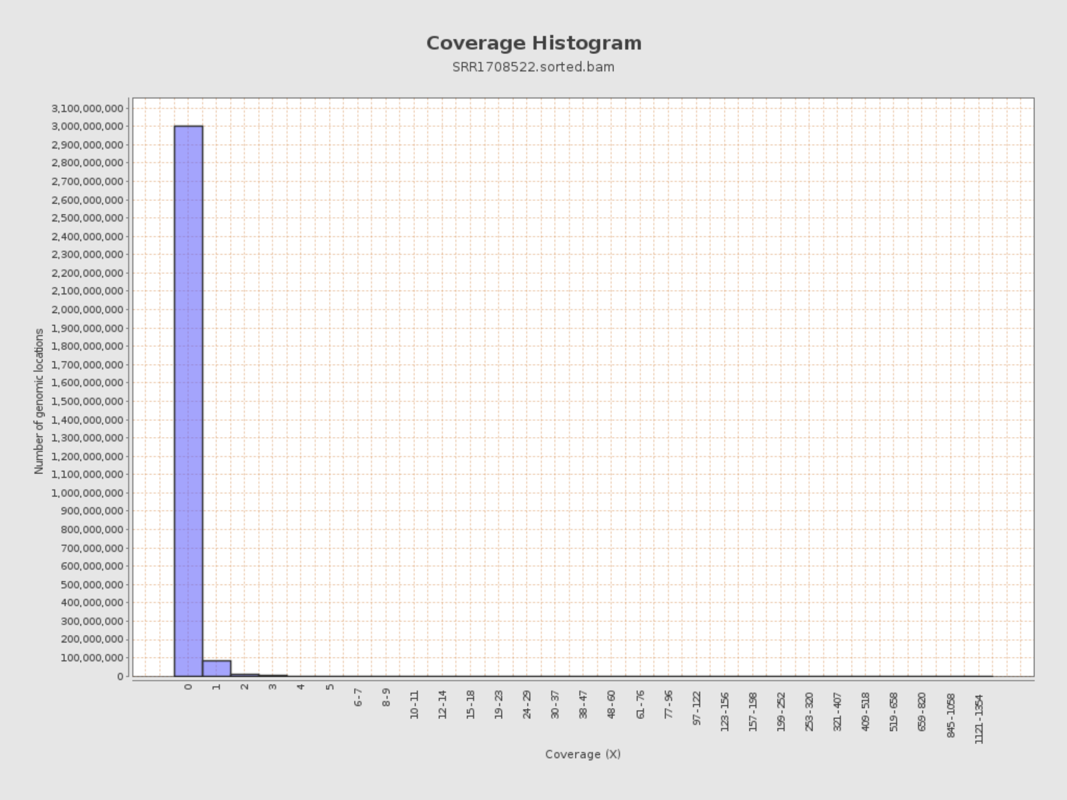
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8584390	0.0344	0.7373
chr2	243199373	9380471	0.0386	0.3048
chr3	198022430	7723370	0.039	0.2274
chr4	191154276	7677829	0.0402	0.2351
chr5	180915260	7230532	0.04	0.2324
chr6	171115067	6806552	0.0398	0.2812
chr7	159138663	6392764	0.0402	0.476

chr8	146364022	5934271	0.0405	0.7667
chr9	141213431	4699187	0.0333	0.2571
chr10	135534747	5144766	0.038	0.2926
chr11	135006516	5097605	0.0378	0.3312
chr12	133851895	5082024	0.038	0.2265
chr13	115169878	3848174	0.0334	0.2096
chr14	107349540	3352500	0.0312	0.2103
chr15	102531392	3071234	0.03	0.1968
chr16	90354753	2837503	0.0314	0.2115
chr17	81195210	2597966	0.032	0.2693
chr18	78077248	3061551	0.0392	0.4406
chr19	59128983	1817157	0.0307	0.5105
chr20	63025520	2125779	0.0337	0.2111
chr21	48129895	1497310	0.0311	0.2441
chr22	51304566	1032837	0.0201	0.1763
chrMT	16571	166663	10.0575	7.1074
chrX	155270560	3555327	0.0229	0.1984
chrY	59373566	791760	0.0133	0.1462

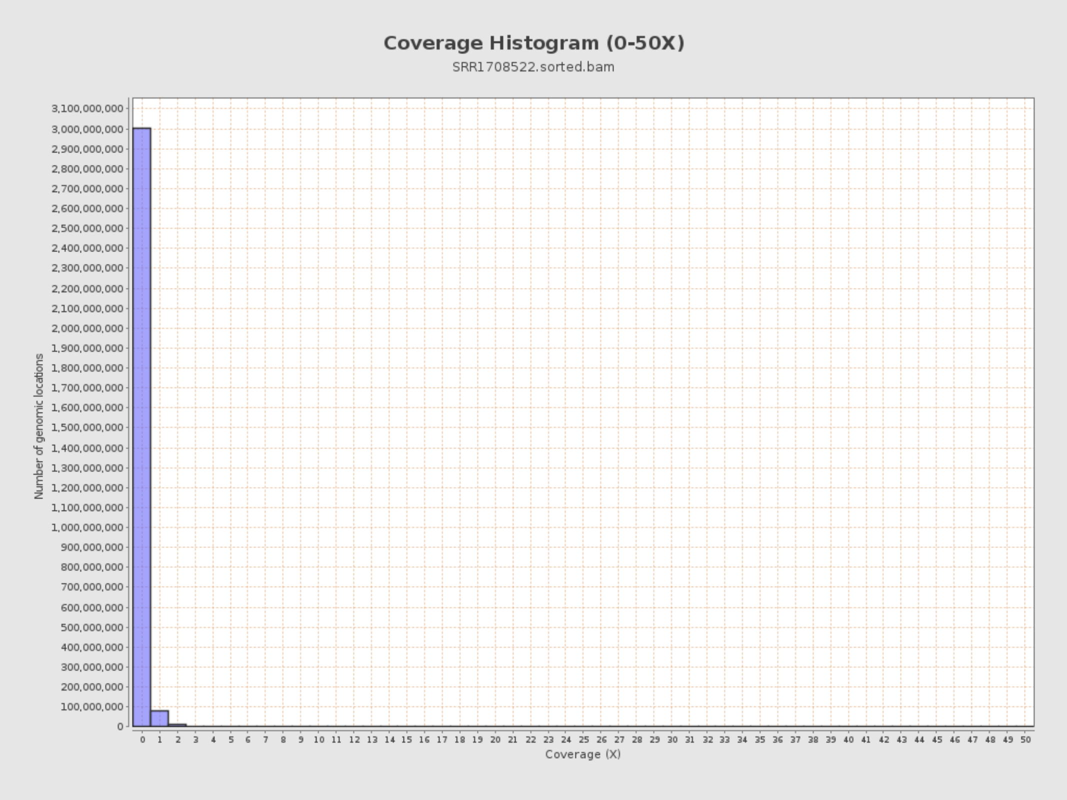
3. Results : Coverage across reference



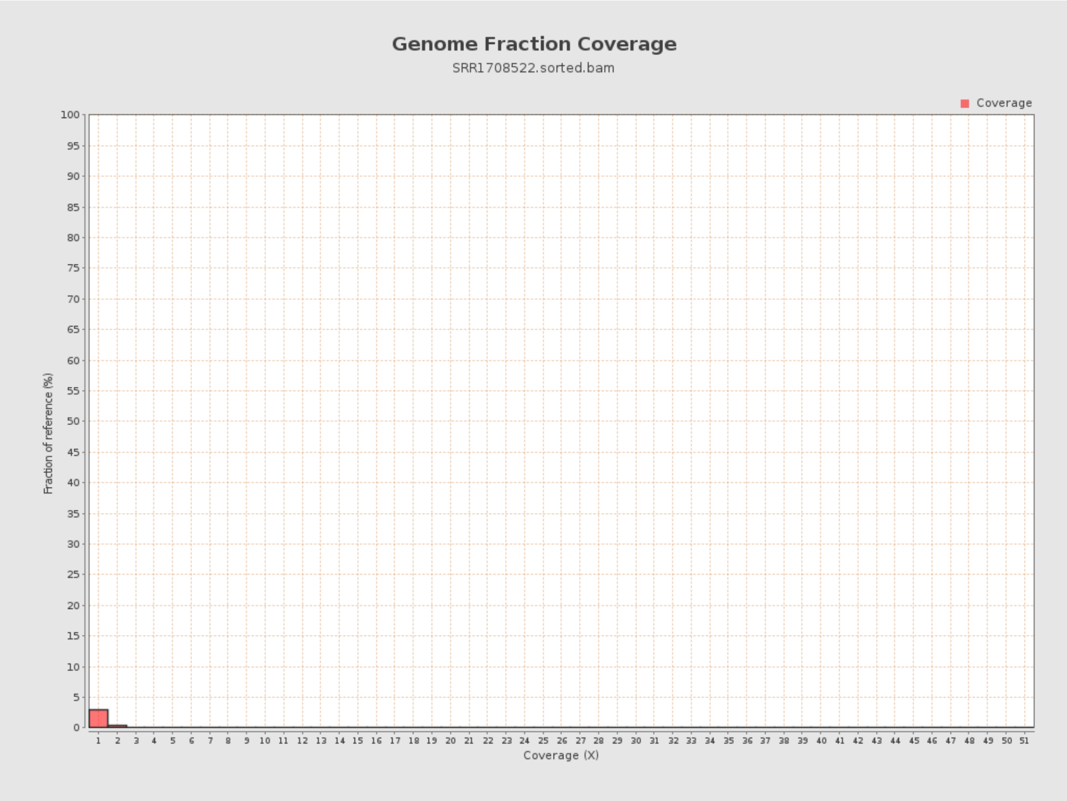
4. Results : Coverage Histogram



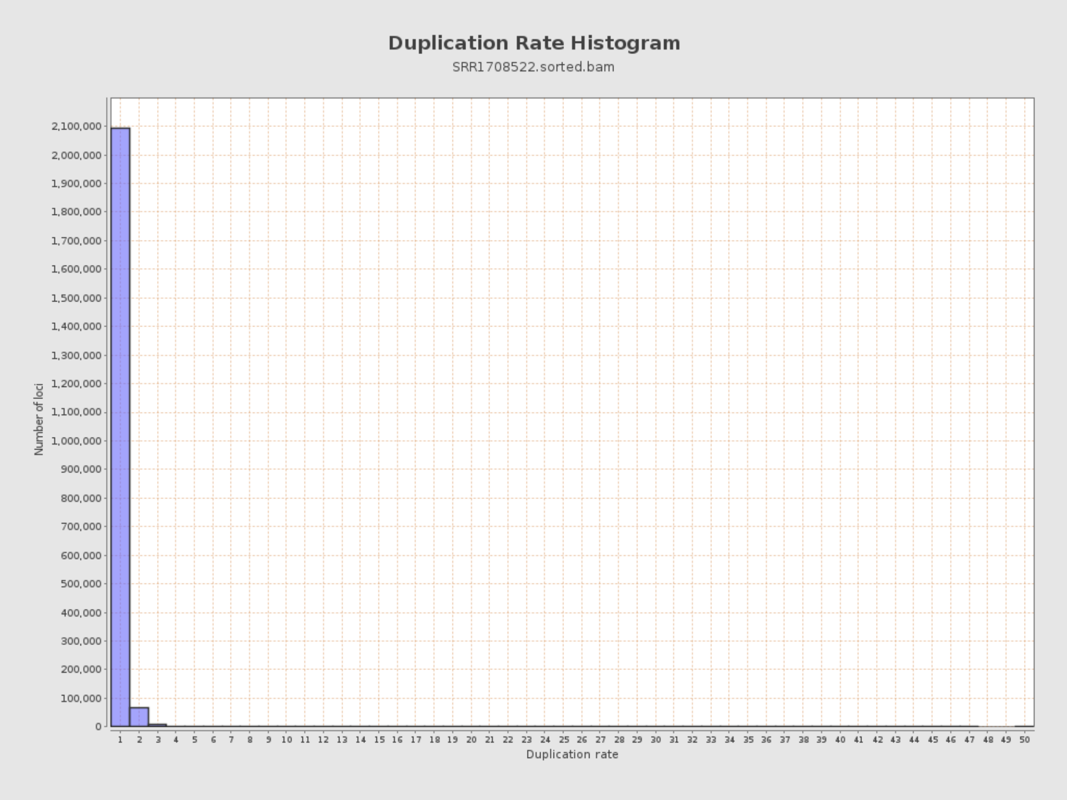
5. Results : Coverage Histogram (0-50X)



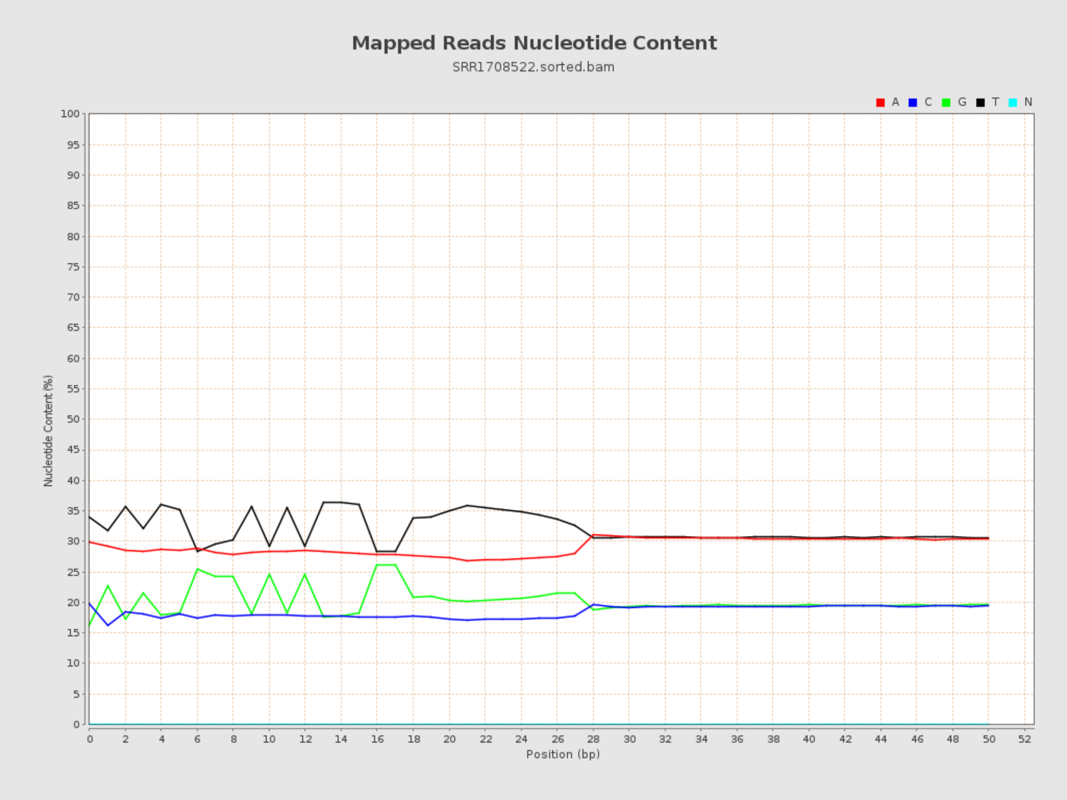
6. Results : Genome Fraction Coverage



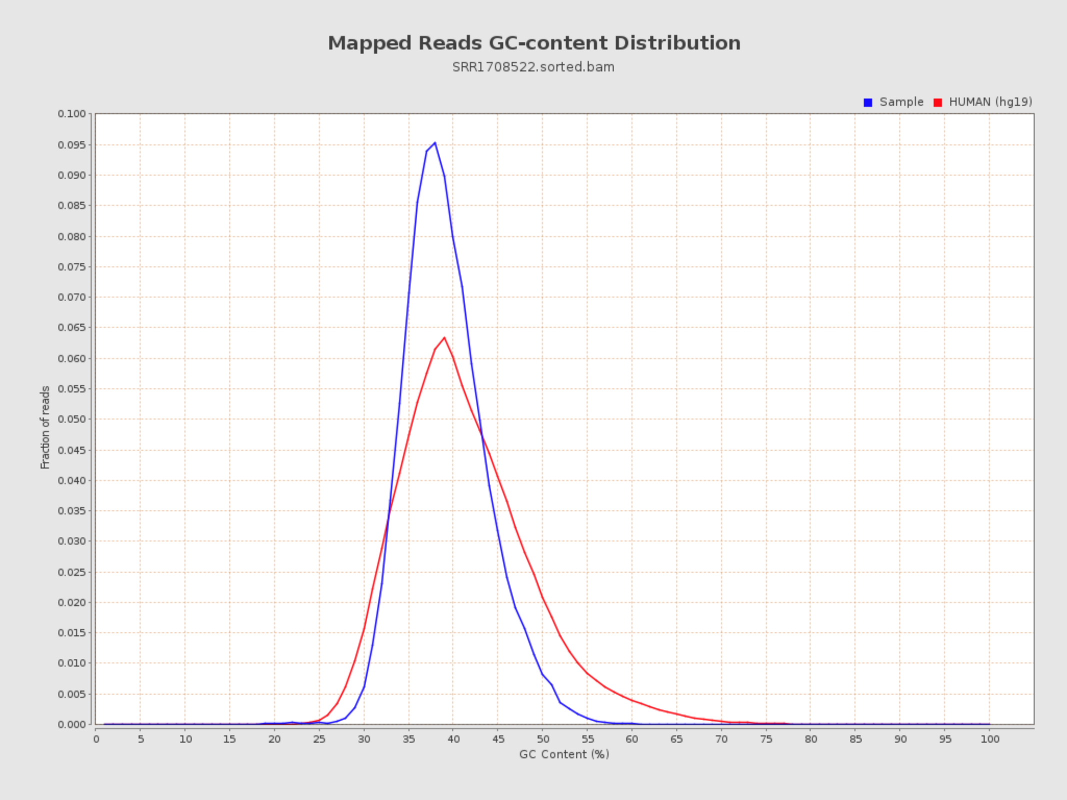
7. Results : Duplication Rate Histogram



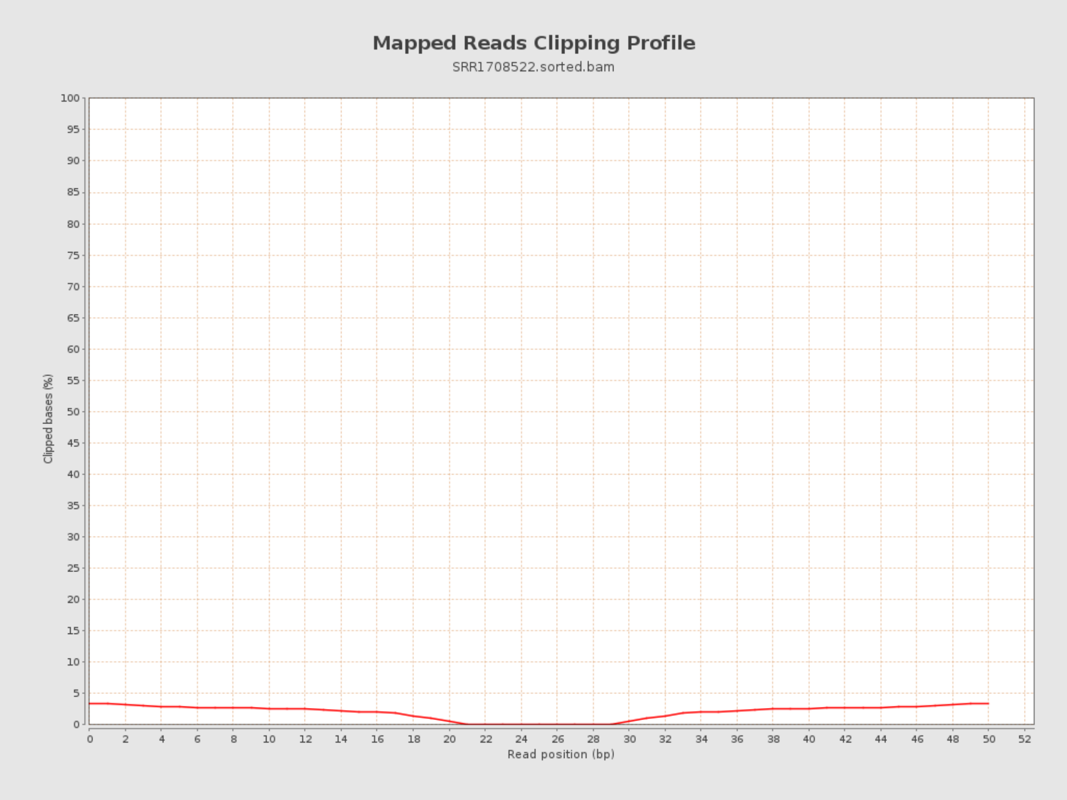
8. Results : Mapped Reads Nucleotide Content



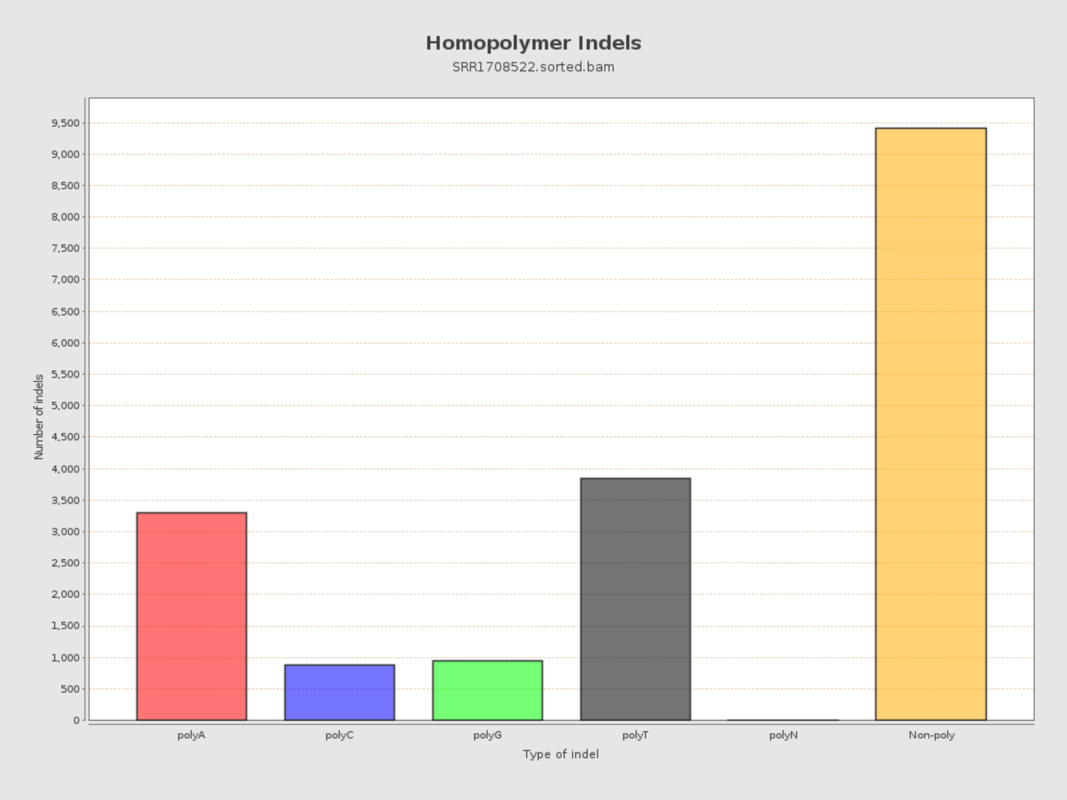
9. Results : Mapped Reads GC-content Distribution



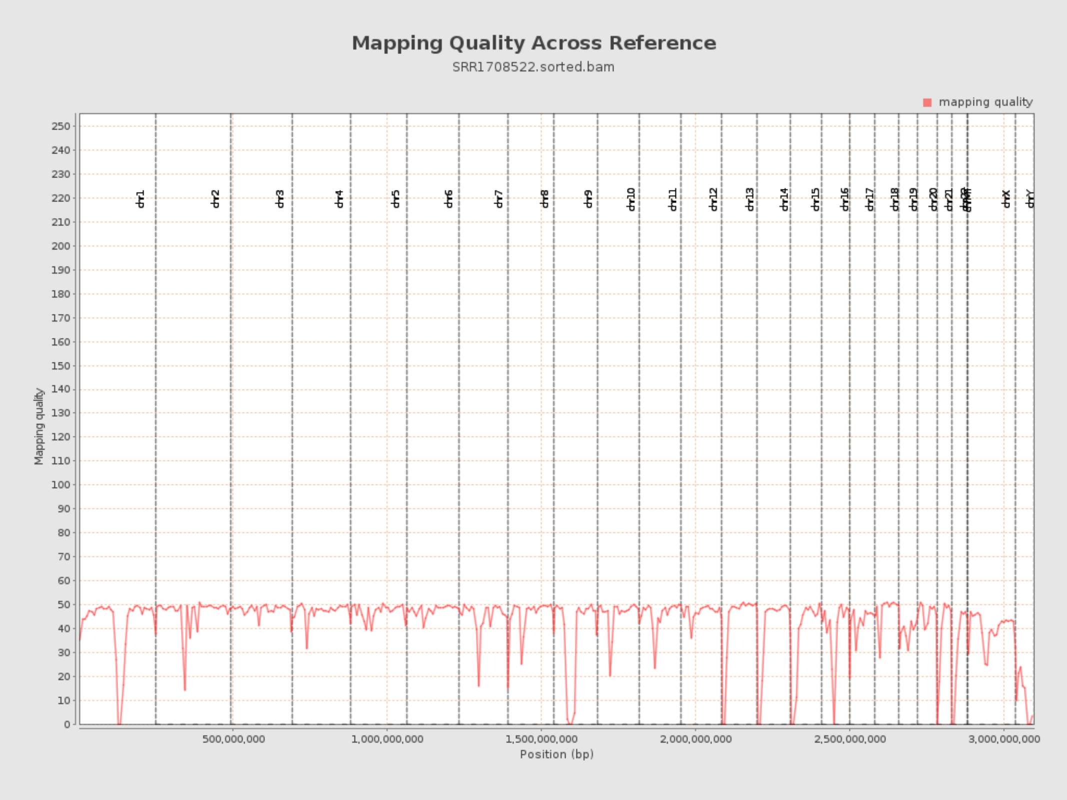
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram