Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:36:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708614.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_SRR1708614 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708614.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:36:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708614.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,156,093
Mapped reads	951,027 / 44.11%
Unmapped reads	1,205,066 / 55.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	260 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	35,682 / 1.65%
Duplication rate	2.99%
Clipped reads	189,860 / 8.81%

2.2. ACGT Content

Number/percentage of A's	13,222,813 / 28.99%
Number/percentage of C's	8,696,769 / 19.06%
Number/percentage of T's	14,259,830 / 31.26%
Number/percentage of G's	9,435,192 / 20.68%
Number/percentage of N's	3,834 / 0.01%
GC Percentage	39.75%

2.3. Coverage

Mean	0.0147

Standard Deviation	0.1762

2.4. Mapping Quality

Mean Mapping Quality	41.4

2.5. Mismatches and indels

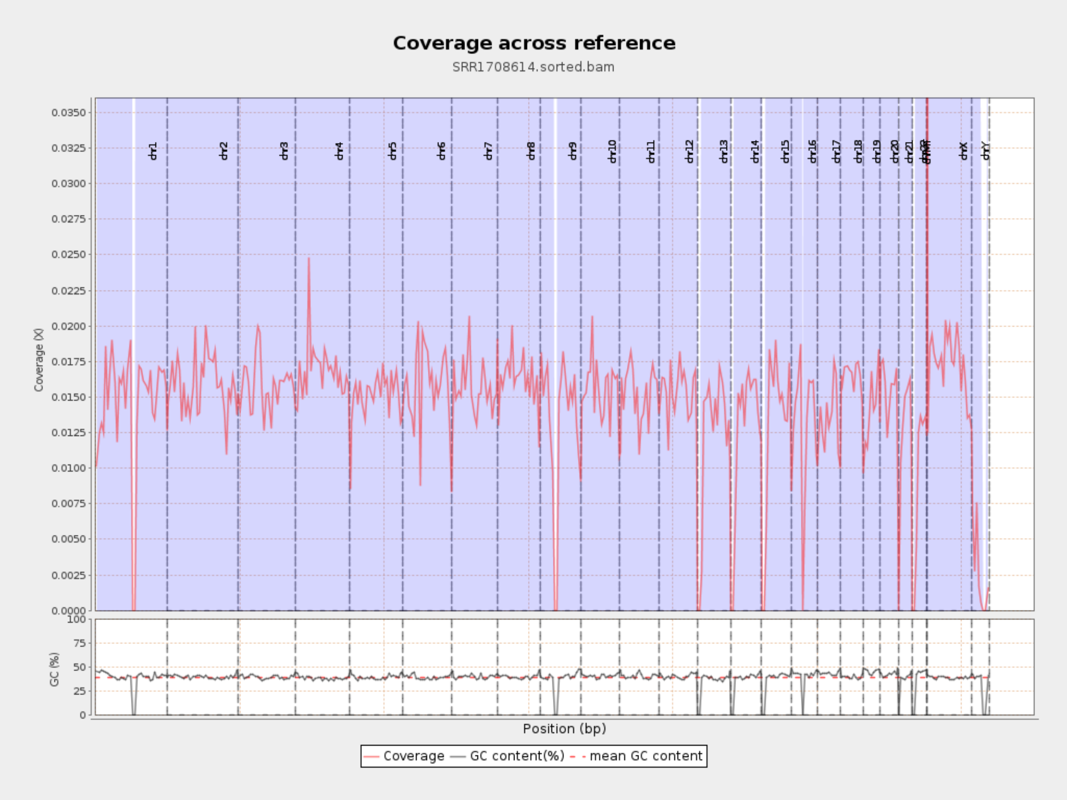
General error rate	0.7%
Mismatches	314,192
Insertions	2,449
Mapped reads with at least one insertion	0.26%
Deletions	7,904
Mapped reads with at least one deletion	0.82%
Homopolymer indels	47.38%

2.6. Chromosome stats

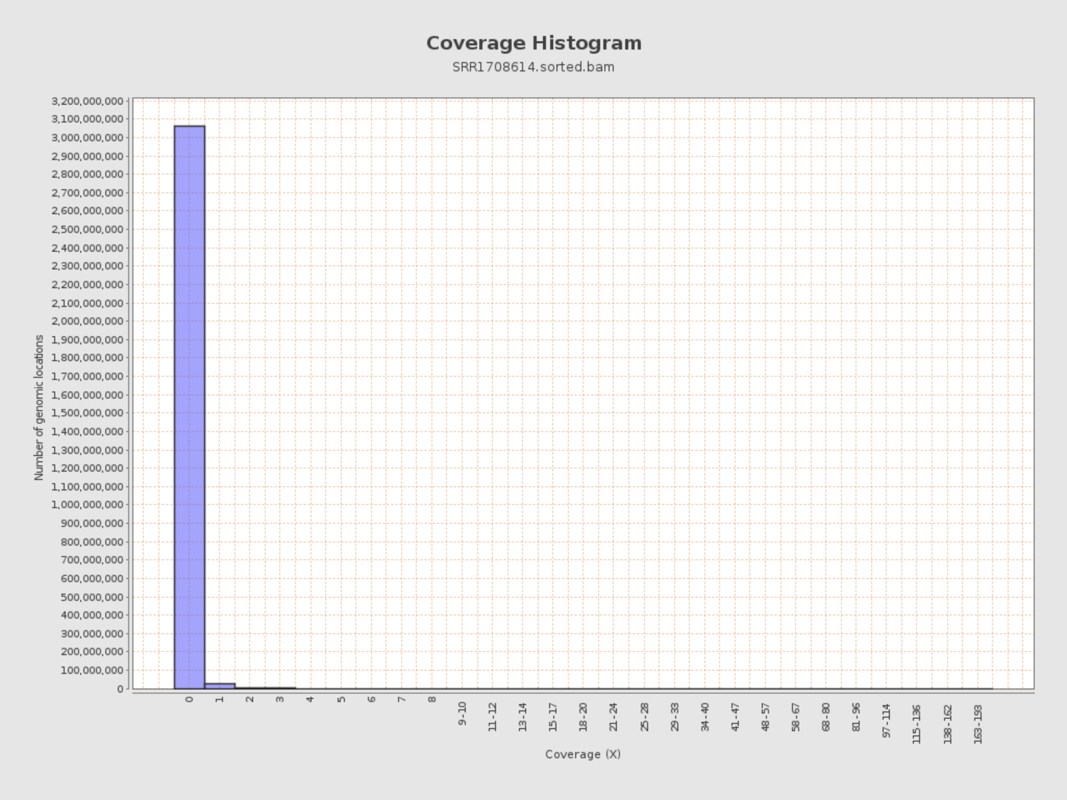
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3616862	0.0145	0.2073
chr2	243199373	3860623	0.0159	0.2109
chr3	198022430	3144456	0.0159	0.1602
chr4	191154276	3223474	0.0169	0.1716
chr5	180915260	2768011	0.0153	0.1809
chr6	171115067	2705614	0.0158	0.187
chr7	159138663	2495190	0.0157	0.1874

chr8	146364022	2376425	0.0162	0.1935
chr9	141213431	1887817	0.0134	0.1653
chr10	135534747	2107670	0.0156	0.1695
chr11	135006516	2063128	0.0153	0.179
chr12	133851895	2072426	0.0155	0.1576
chr13	115169878	1380558	0.012	0.1392
chr14	107349540	1342710	0.0125	0.148
chr15	102531392	1330337	0.013	0.144
chr16	90354753	1145036	0.0127	0.1416
chr17	81195210	1092012	0.0134	0.1567
chr18	78077248	1295667	0.0166	0.2325
chr19	59128983	834418	0.0141	0.1987
chr20	63025520	973127	0.0154	0.1633
chr21	48129895	606615	0.0126	0.1523
chr22	51304566	468773	0.0091	0.1185
chrMT	16571	7243	0.4371	0.8211
chrX	155270560	2687970	0.0173	0.1709
chrY	59373566	144749	0.0024	0.0691

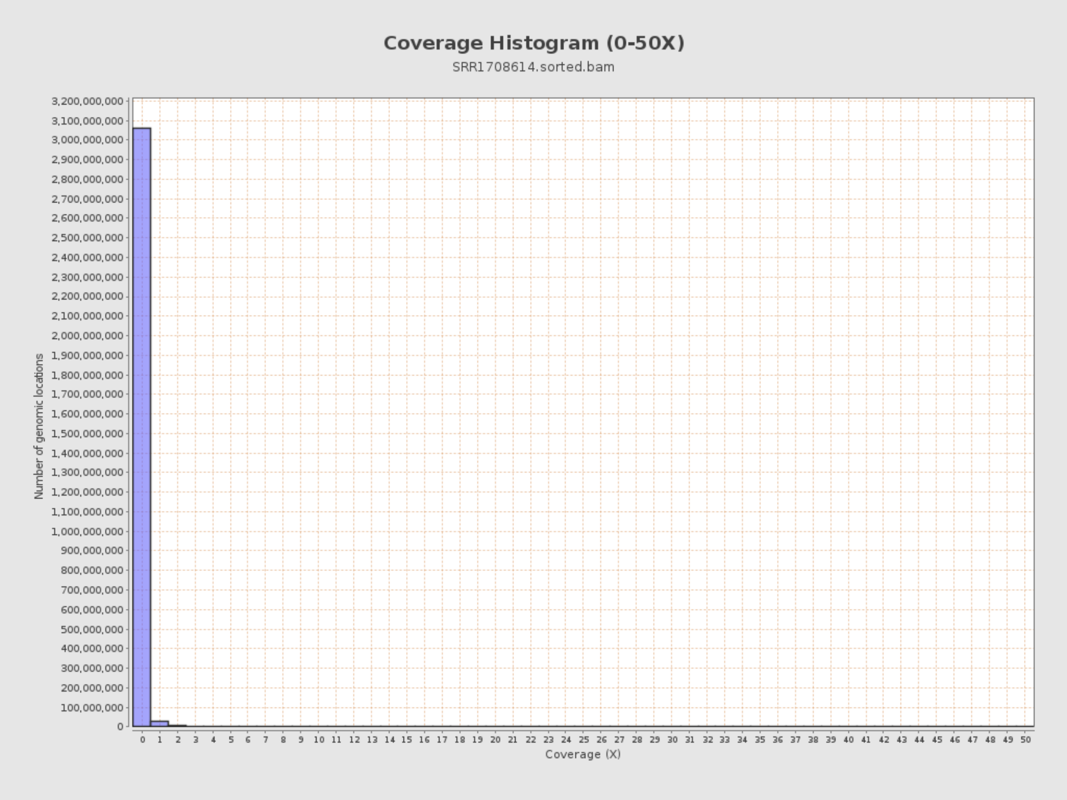
3. Results : Coverage across reference



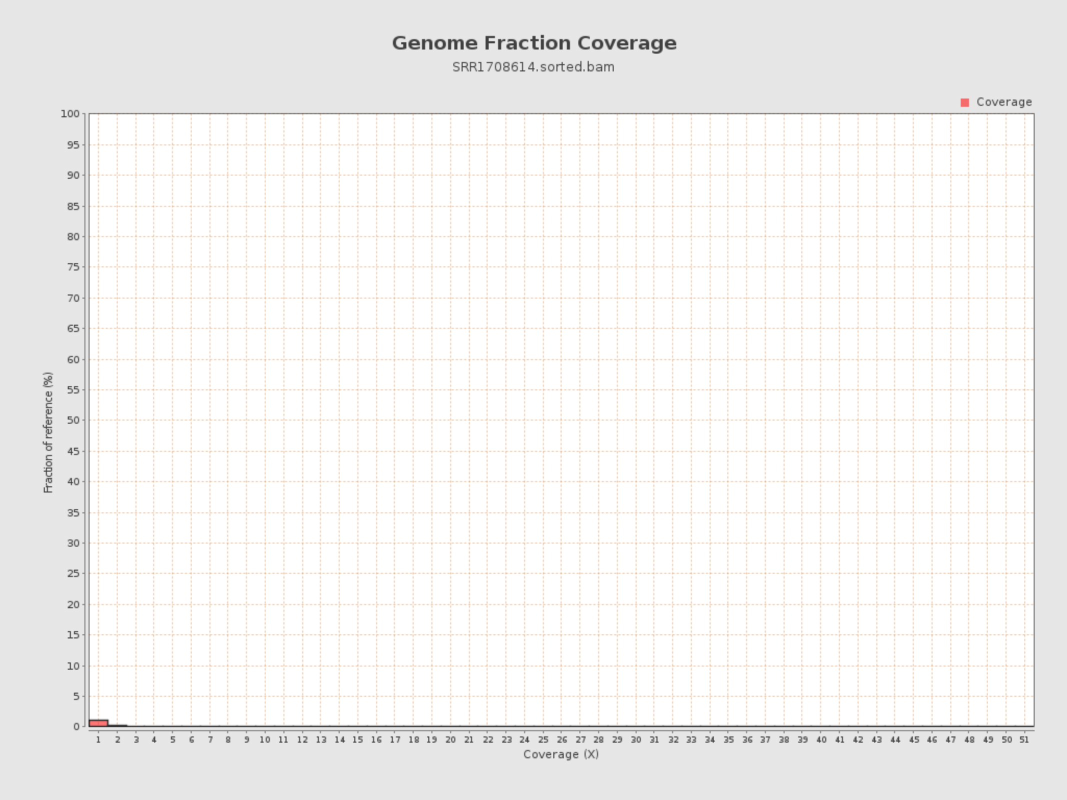
4. Results : Coverage Histogram



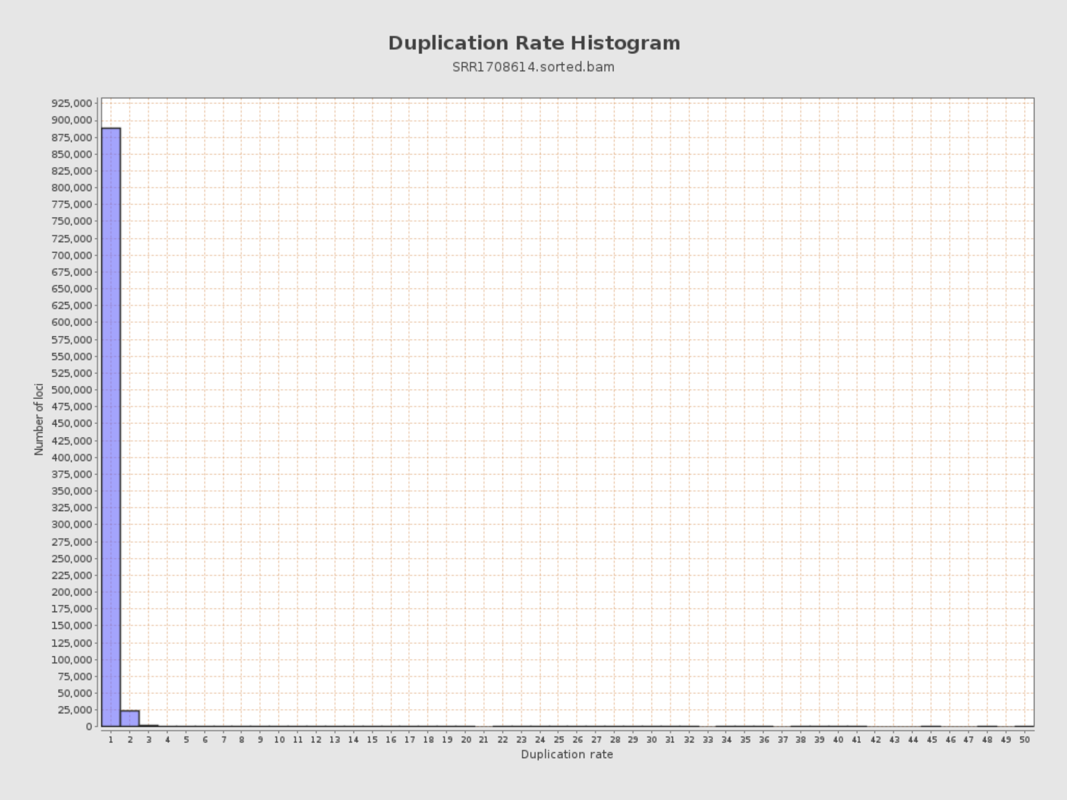
5. Results : Coverage Histogram (0-50X)



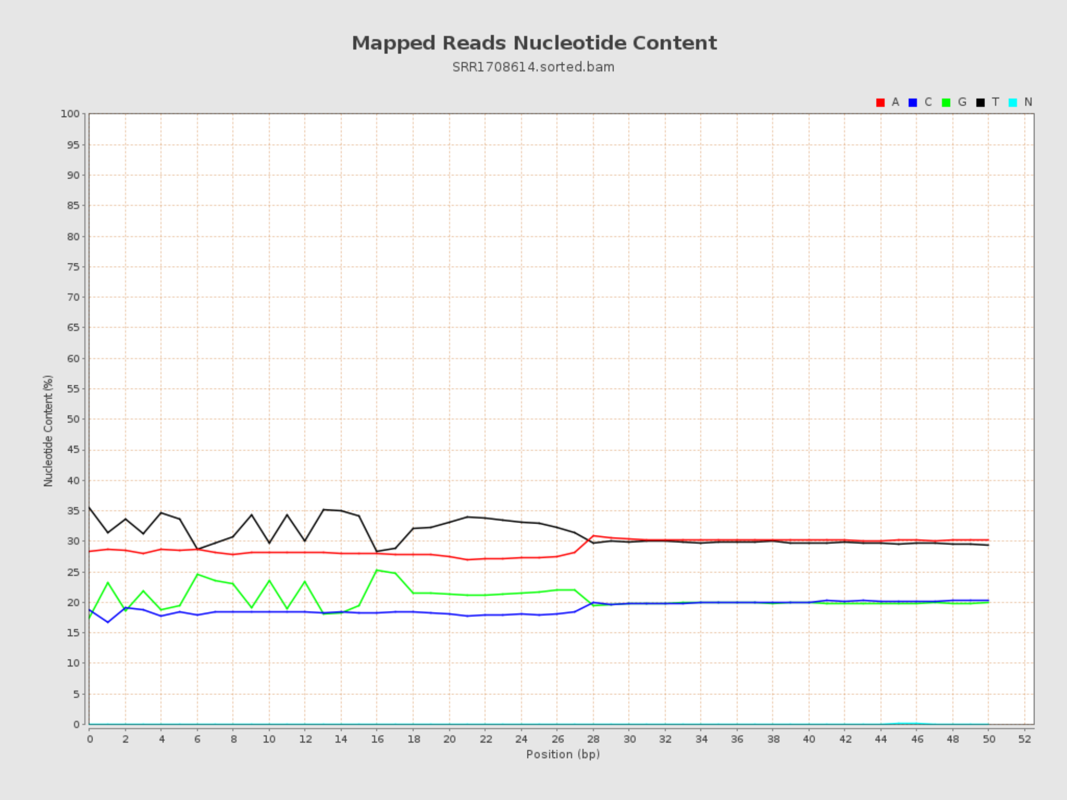
6. Results : Genome Fraction Coverage



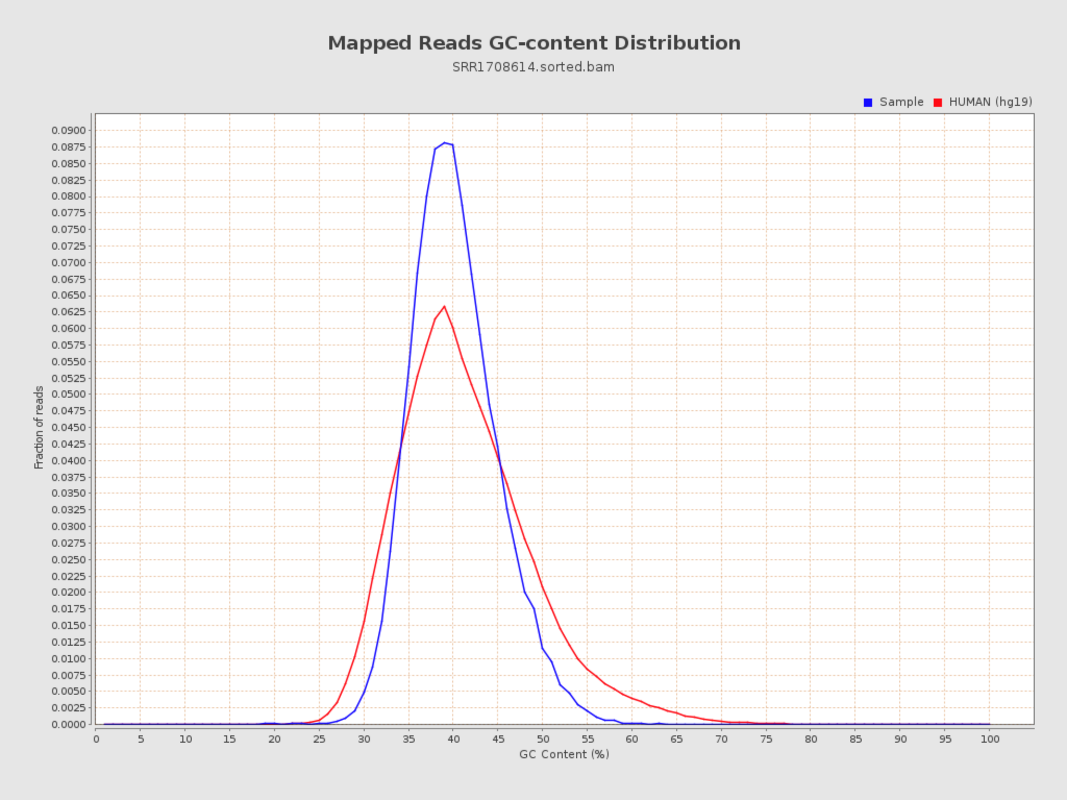
7. Results : Duplication Rate Histogram



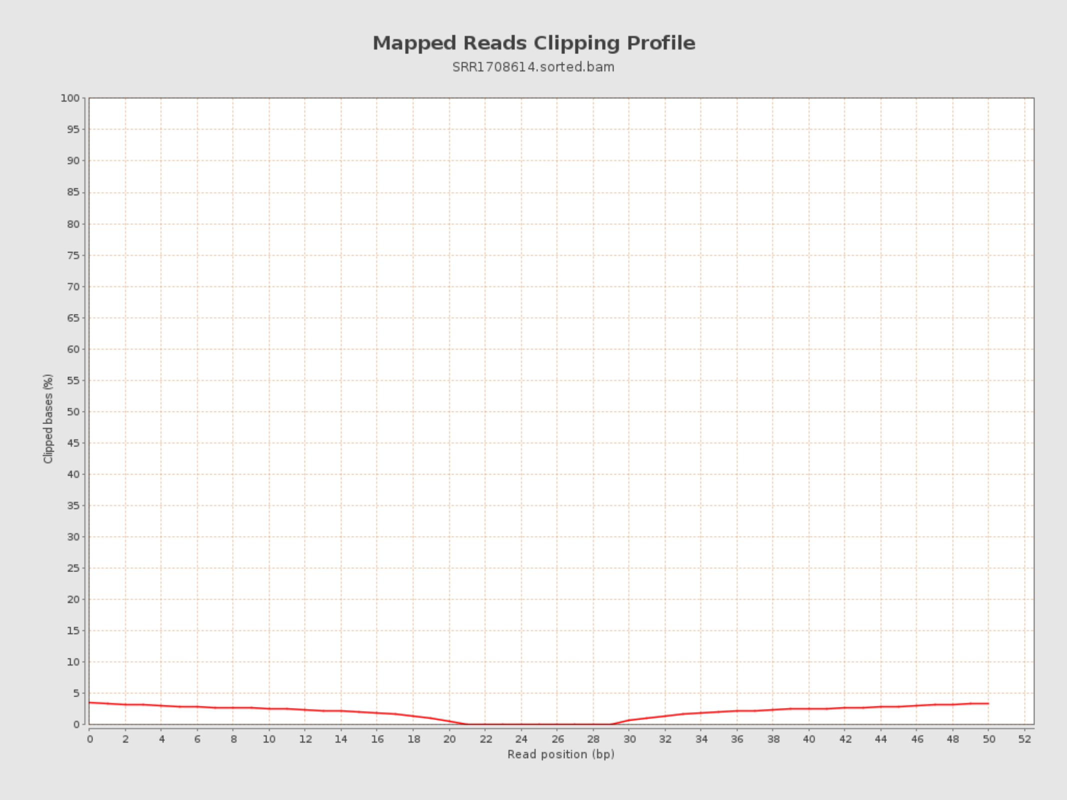
8. Results : Mapped Reads Nucleotide Content



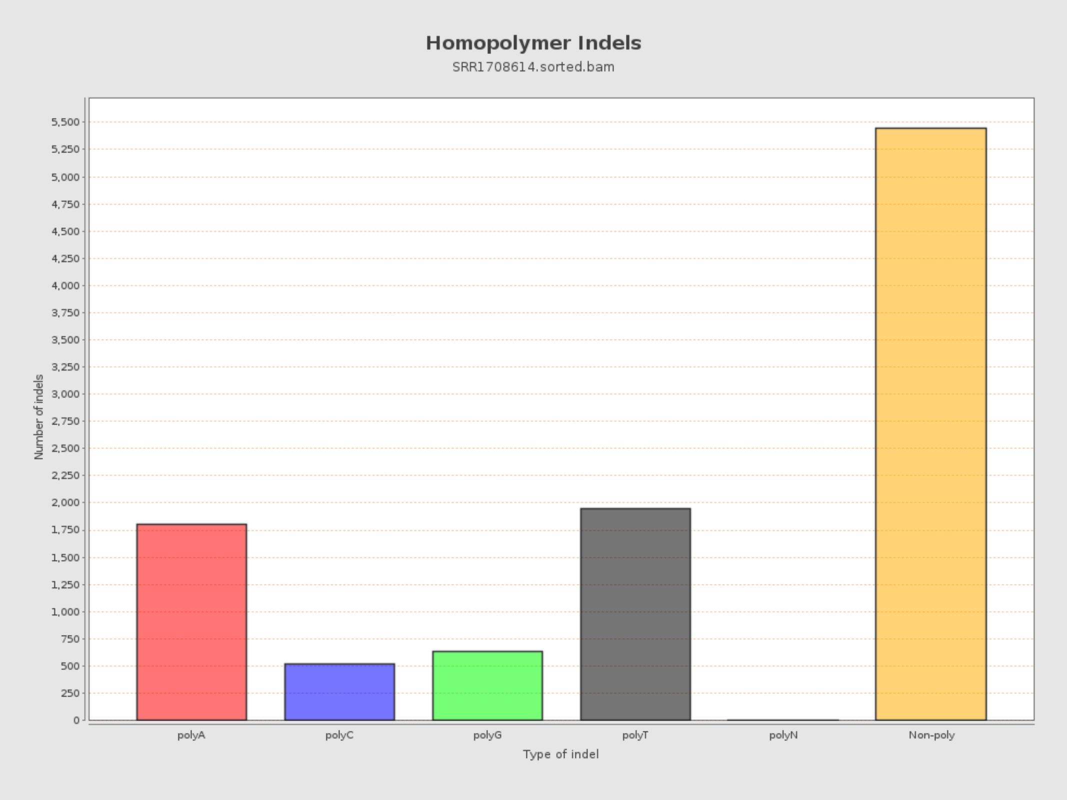
9. Results : Mapped Reads GC-content Distribution



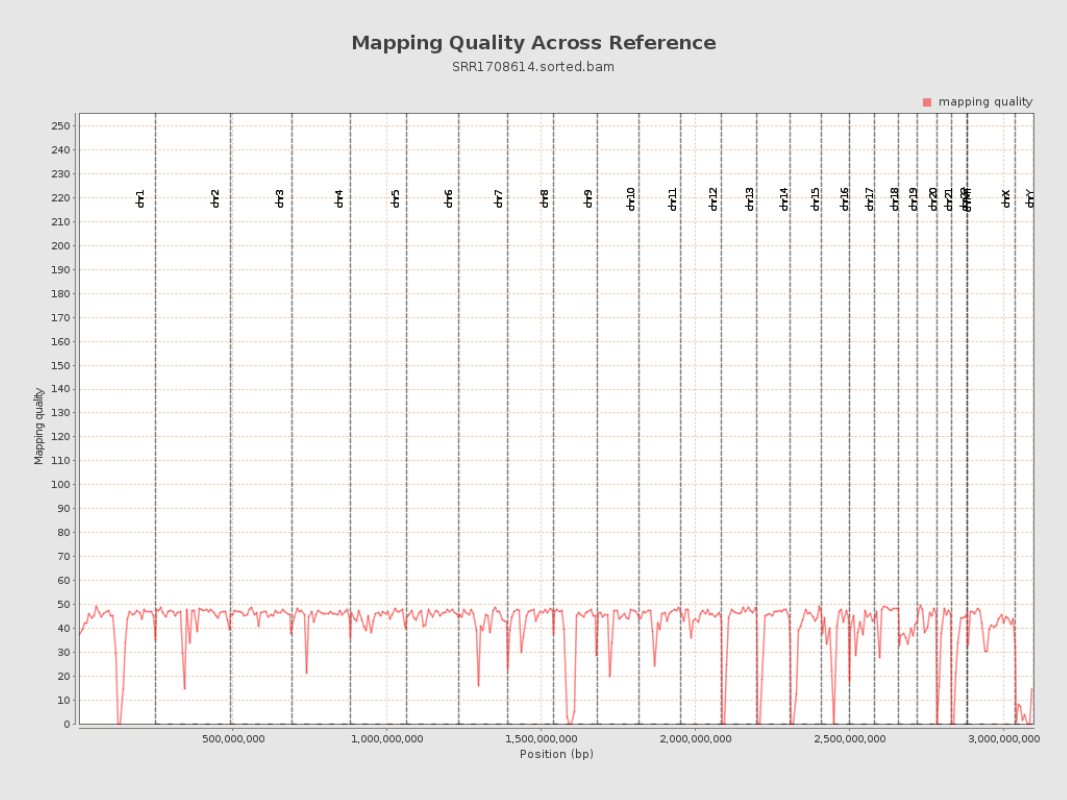
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram