Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:23:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708610.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_SRR1708610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708610.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:23:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,374,715
Mapped reads	1,480,690 / 62.35%
Unmapped reads	894,025 / 37.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	406 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	58,590 / 2.47%
Duplication rate	3.21%
Clipped reads	274,346 / 11.55%

2.2. ACGT Content

Number/percentage of A's	20,579,771 / 28.85%
Number/percentage of C's	13,652,953 / 19.14%
Number/percentage of T's	22,296,237 / 31.26%
Number/percentage of G's	14,794,569 / 20.74%
Number/percentage of N's	5,924 / 0.01%
GC Percentage	39.88%

2.3. Coverage

Mean	0.023

Standard Deviation	0.2288

2.4. Mapping Quality

Mean Mapping Quality	41.62

2.5. Mismatches and indels

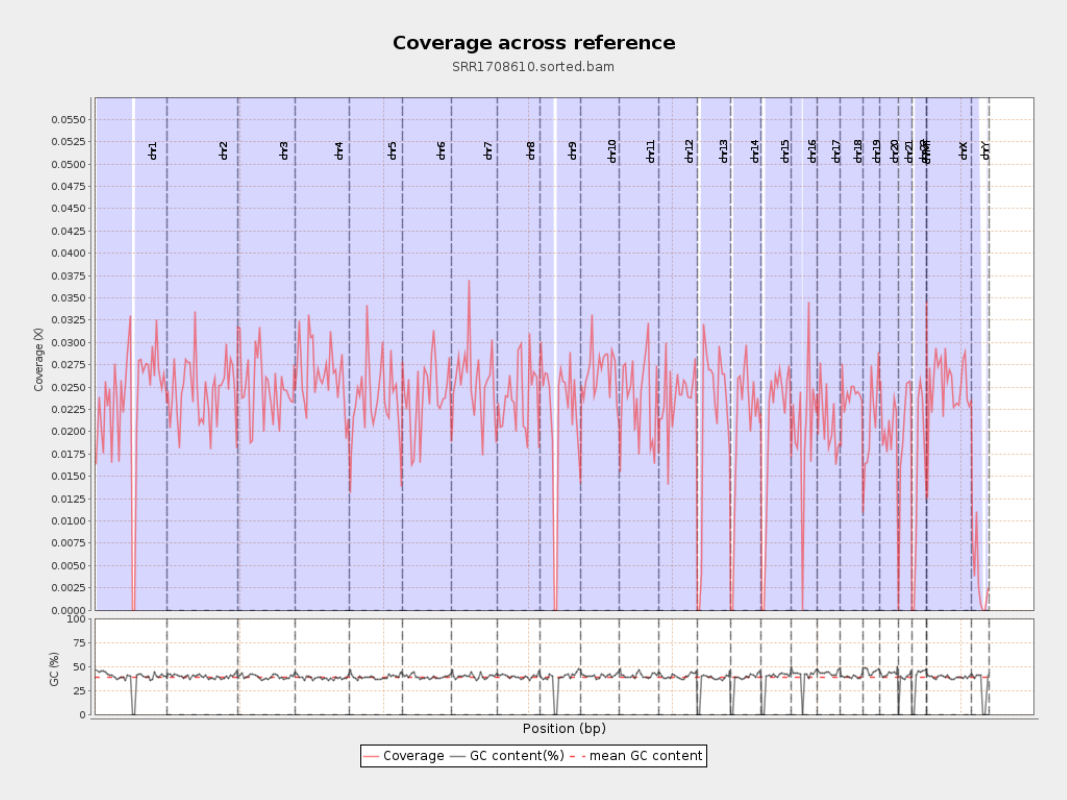
General error rate	0.69%
Mismatches	489,452
Insertions	3,518
Mapped reads with at least one insertion	0.24%
Deletions	12,214
Mapped reads with at least one deletion	0.82%
Homopolymer indels	49.39%

2.6. Chromosome stats

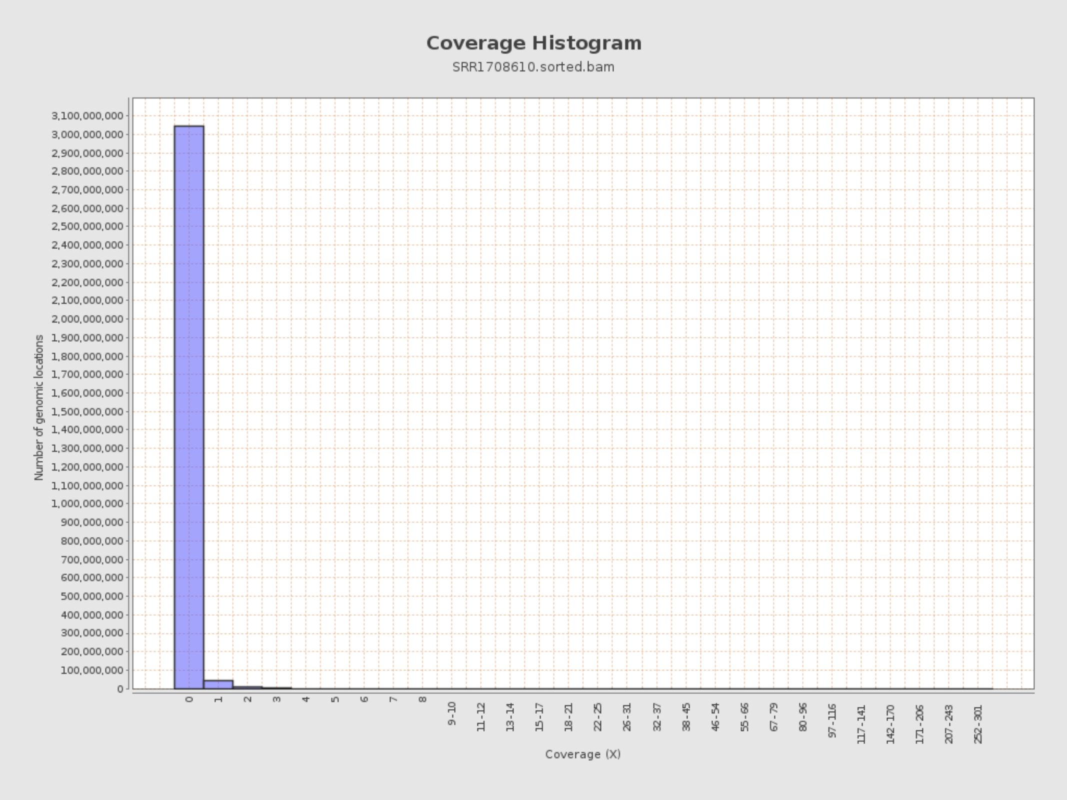
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5811891	0.0233	0.2685
chr2	243199373	5964282	0.0245	0.2563
chr3	198022430	4933264	0.0249	0.205
chr4	191154276	5039879	0.0264	0.2185
chr5	180915260	4298448	0.0238	0.1995
chr6	171115067	4118004	0.0241	0.2332
chr7	159138663	4066862	0.0256	0.2864

chr8	146364022	3477970	0.0238	0.2489
chr9	141213431	3083696	0.0218	0.2158
chr10	135534747	3602742	0.0266	0.235
chr11	135006516	3217108	0.0238	0.2401
chr12	133851895	3205913	0.024	0.2027
chr13	115169878	2471715	0.0215	0.1909
chr14	107349540	2197106	0.0205	0.1934
chr15	102531392	2087360	0.0204	0.1851
chr16	90354753	1818754	0.0201	0.1888
chr17	81195210	1703916	0.021	0.2104
chr18	78077248	1886627	0.0242	0.3325
chr19	59128983	1252920	0.0212	0.279
chr20	63025520	1273975	0.0202	0.1913
chr21	48129895	952898	0.0198	0.1914
chr22	51304566	772131	0.015	0.1578
chrMT	16571	574	0.0346	0.1925
chrX	155270560	3909802	0.0252	0.2147
chrY	59373566	200417	0.0034	0.0871

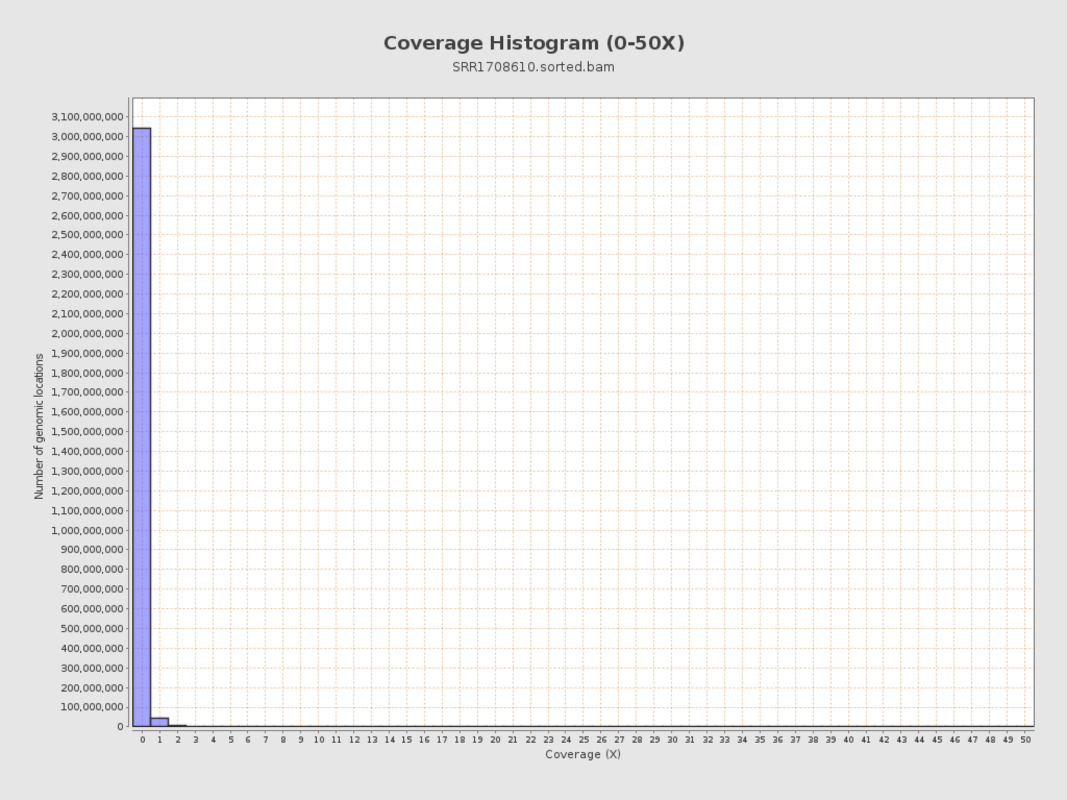
3. Results : Coverage across reference



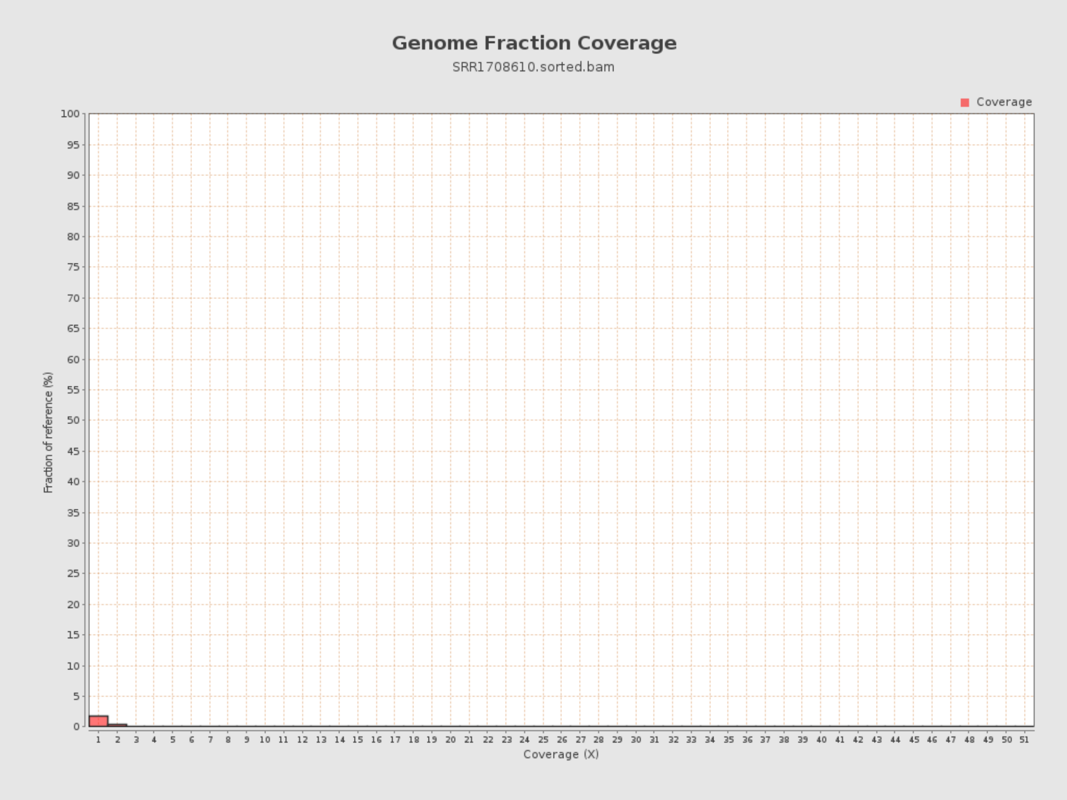
4. Results : Coverage Histogram



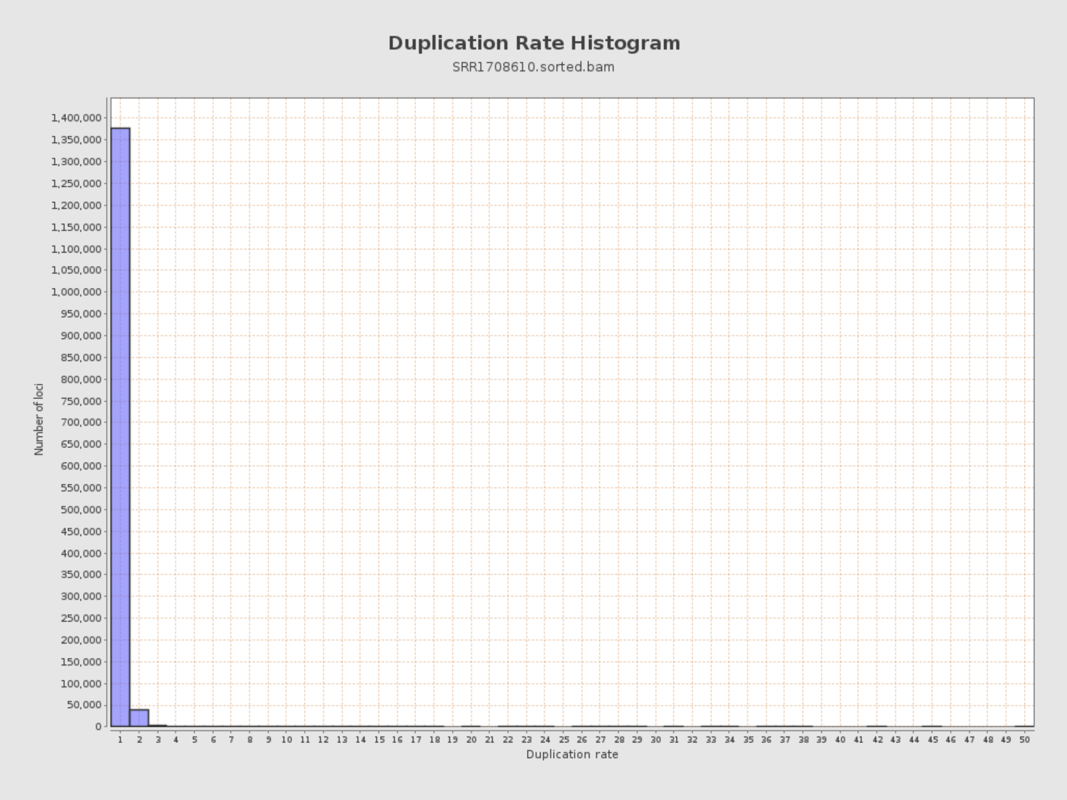
5. Results : Coverage Histogram (0-50X)



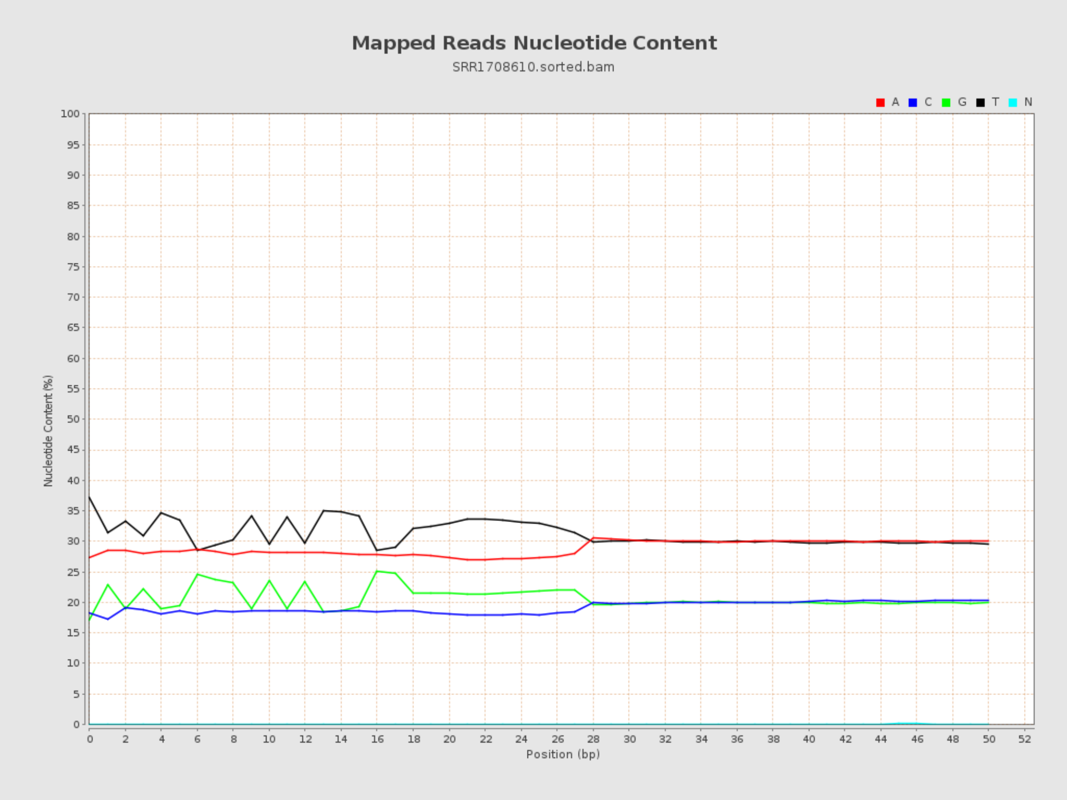
6. Results : Genome Fraction Coverage



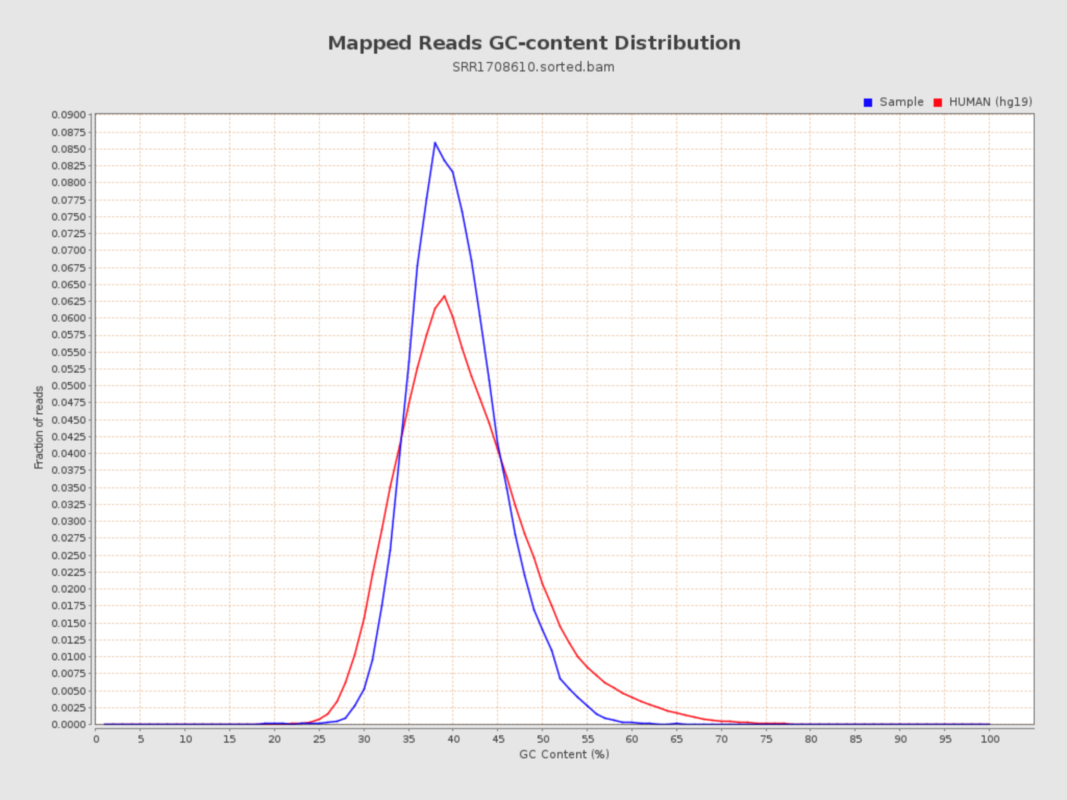
7. Results : Duplication Rate Histogram



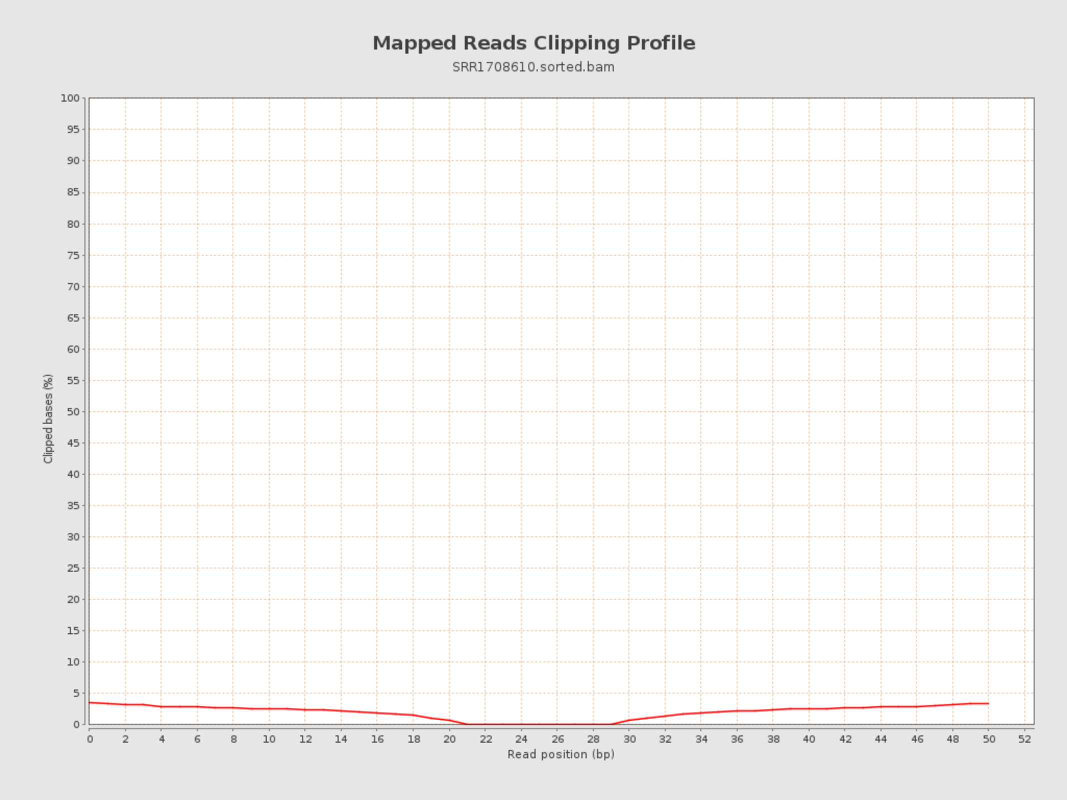
8. Results : Mapped Reads Nucleotide Content



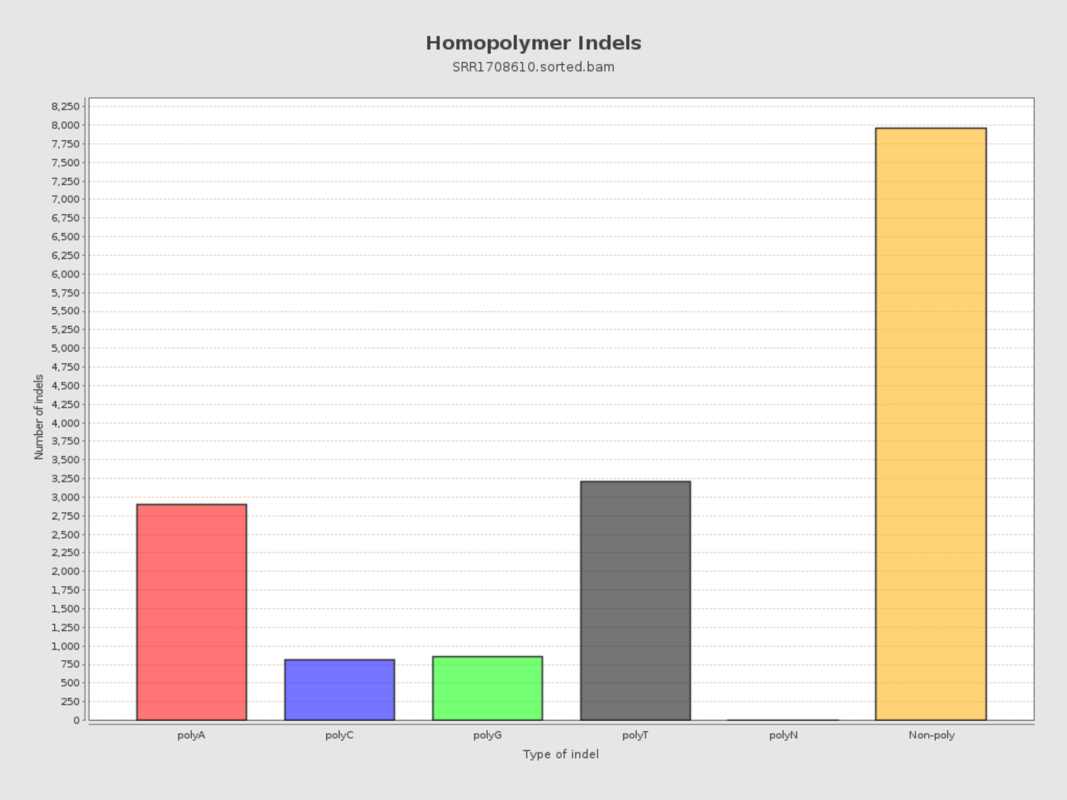
9. Results : Mapped Reads GC-content Distribution



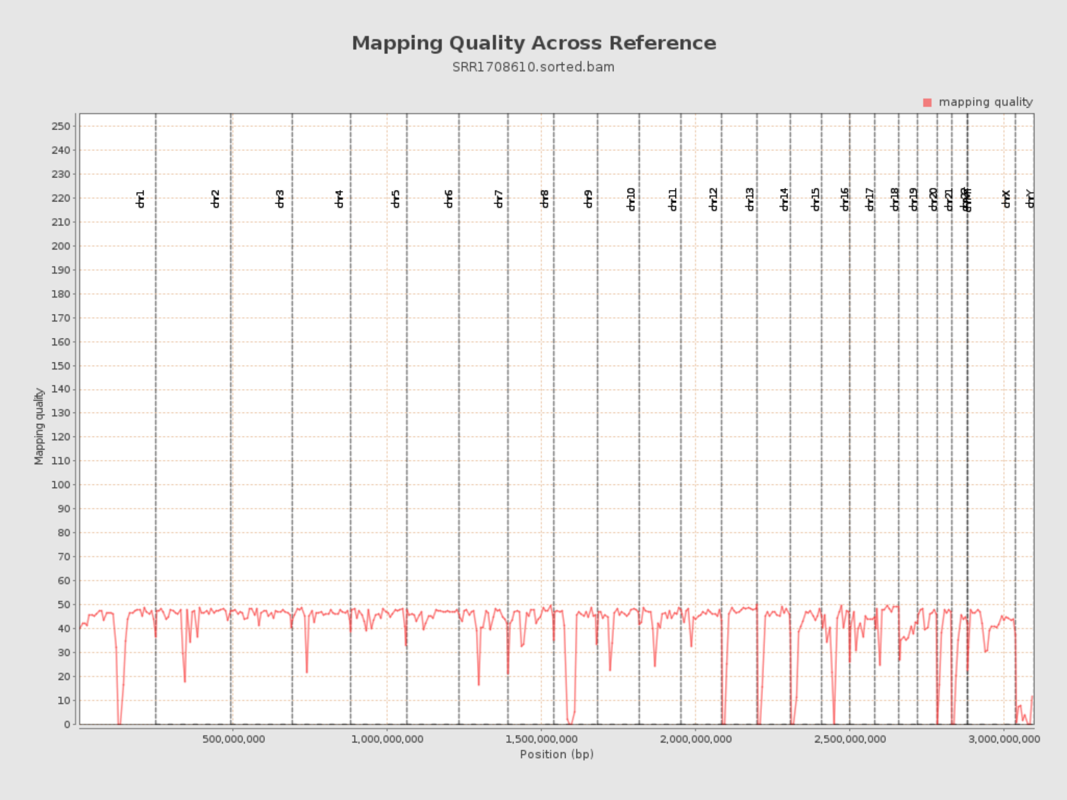
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram