Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:28:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525261.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_SRR10525261 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525261.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:28:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525261.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	583,027
Mapped reads	531,862 / 91.22%
Unmapped reads	51,165 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,448 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	10,735 / 1.84%
Duplication rate	1.44%
Clipped reads	532,421 / 91.32%

2.2. ACGT Content

Number/percentage of A's	8,053,653 / 26.08%
Number/percentage of C's	5,843,479 / 18.92%
Number/percentage of T's	9,886,936 / 32.02%
Number/percentage of G's	7,094,173 / 22.97%
Number/percentage of N's	755 / 0%
GC Percentage	41.9%

2.3. Coverage

Mean	0.01

Standard Deviation	0.1334

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

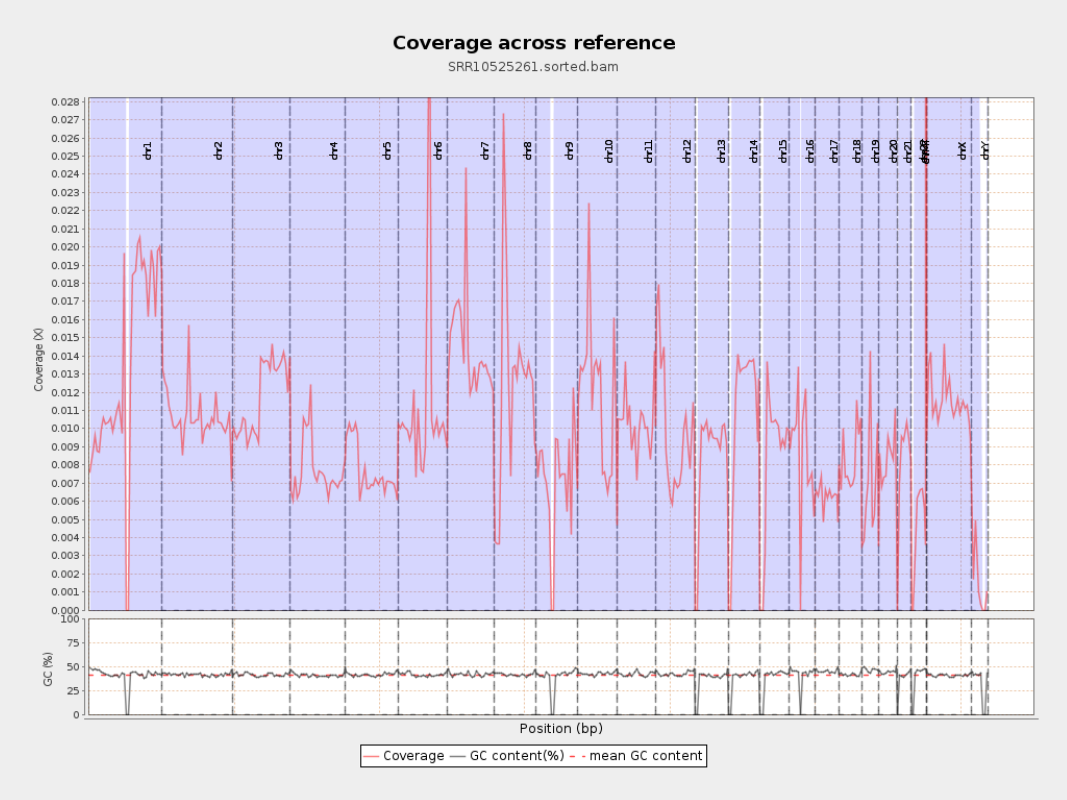
General error rate	0.51%
Mismatches	152,782
Insertions	2,419
Mapped reads with at least one insertion	0.45%
Deletions	6,028
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.6%

2.6. Chromosome stats

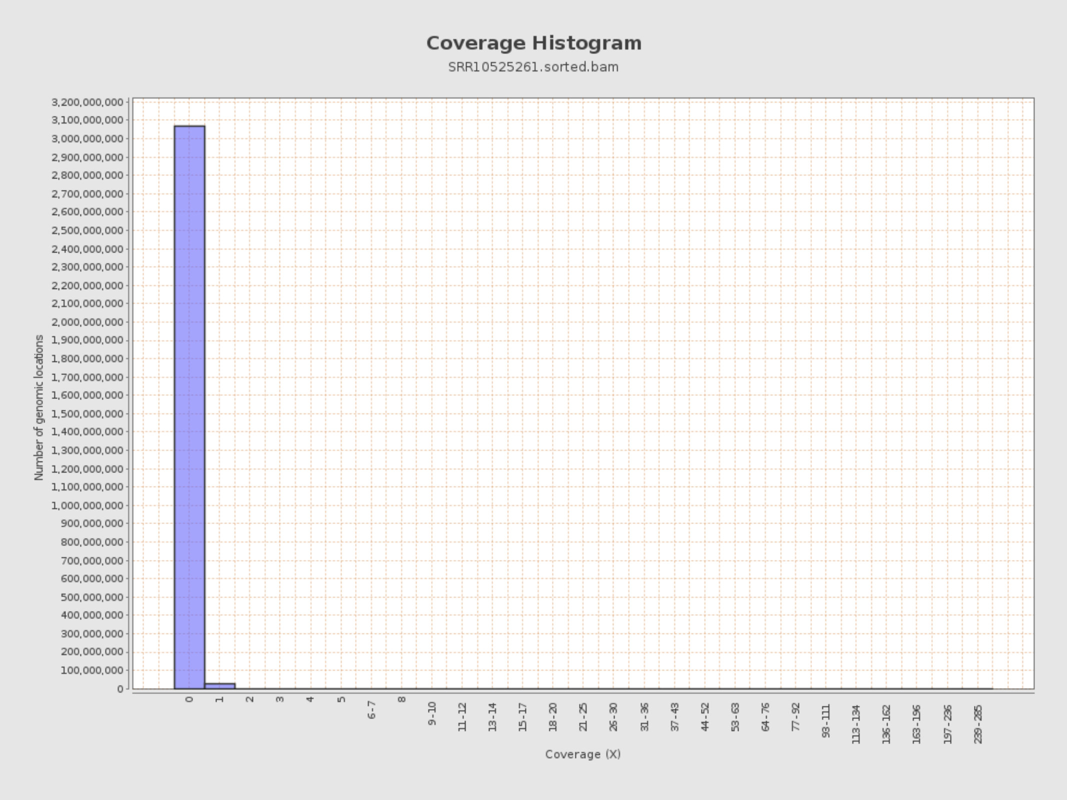
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3322317	0.0133	0.2364
chr2	243199373	2598344	0.0107	0.1456
chr3	198022430	2327288	0.0118	0.1124
chr4	191154276	1466224	0.0077	0.0922
chr5	180915260	1391863	0.0077	0.0906
chr6	171115067	1956919	0.0114	0.1157
chr7	159138663	2317175	0.0146	0.207

chr8	146364022	1776117	0.0121	0.1382
chr9	141213431	997211	0.0071	0.0968
chr10	135534747	1632993	0.012	0.1428
chr11	135006516	1388510	0.0103	0.1121
chr12	133851895	1322261	0.0099	0.1029
chr13	115169878	966302	0.0084	0.0942
chr14	107349540	1158439	0.0108	0.108
chr15	102531392	858082	0.0084	0.0949
chr16	90354753	765491	0.0085	0.1003
chr17	81195210	509342	0.0063	0.0839
chr18	78077248	650907	0.0083	0.1506
chr19	59128983	413111	0.007	0.1442
chr20	63025520	527976	0.0084	0.0945
chr21	48129895	393942	0.0082	0.0948
chr22	51304566	224269	0.0044	0.0677
chrMT	16571	36224	2.186	1.8425
chrX	155270560	1793675	0.0116	0.1148
chrY	59373566	93367	0.0016	0.0565

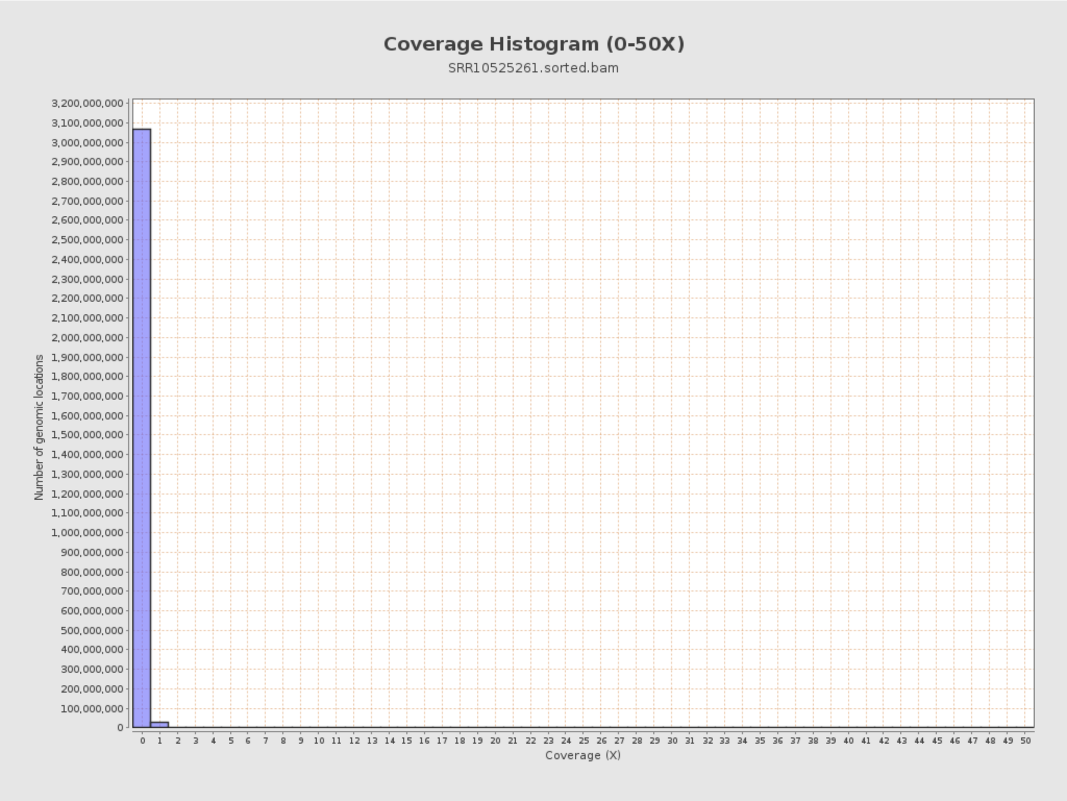
3. Results : Coverage across reference



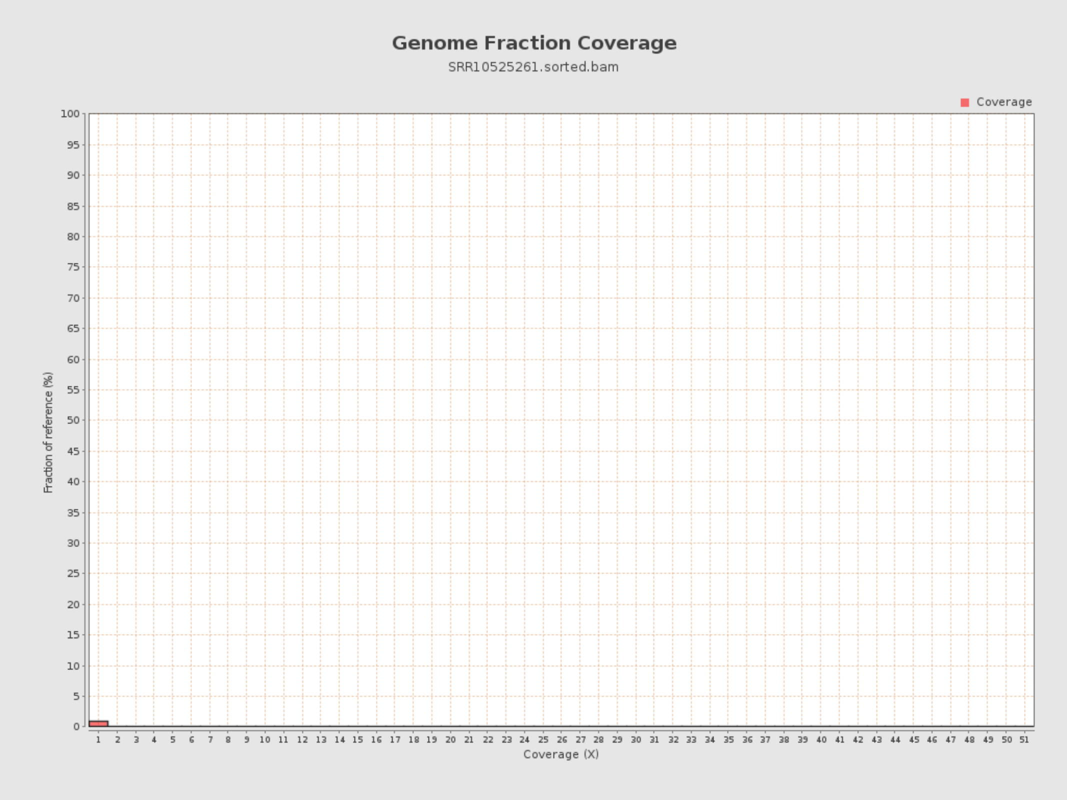
4. Results : Coverage Histogram



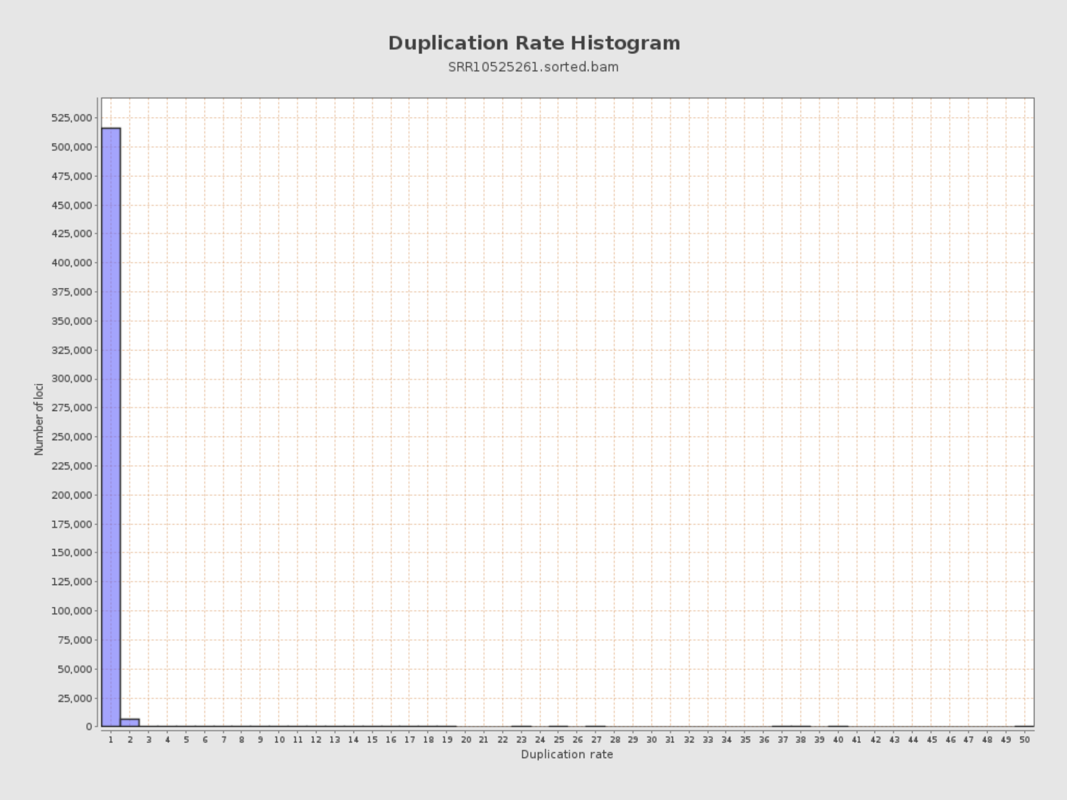
5. Results : Coverage Histogram (0-50X)



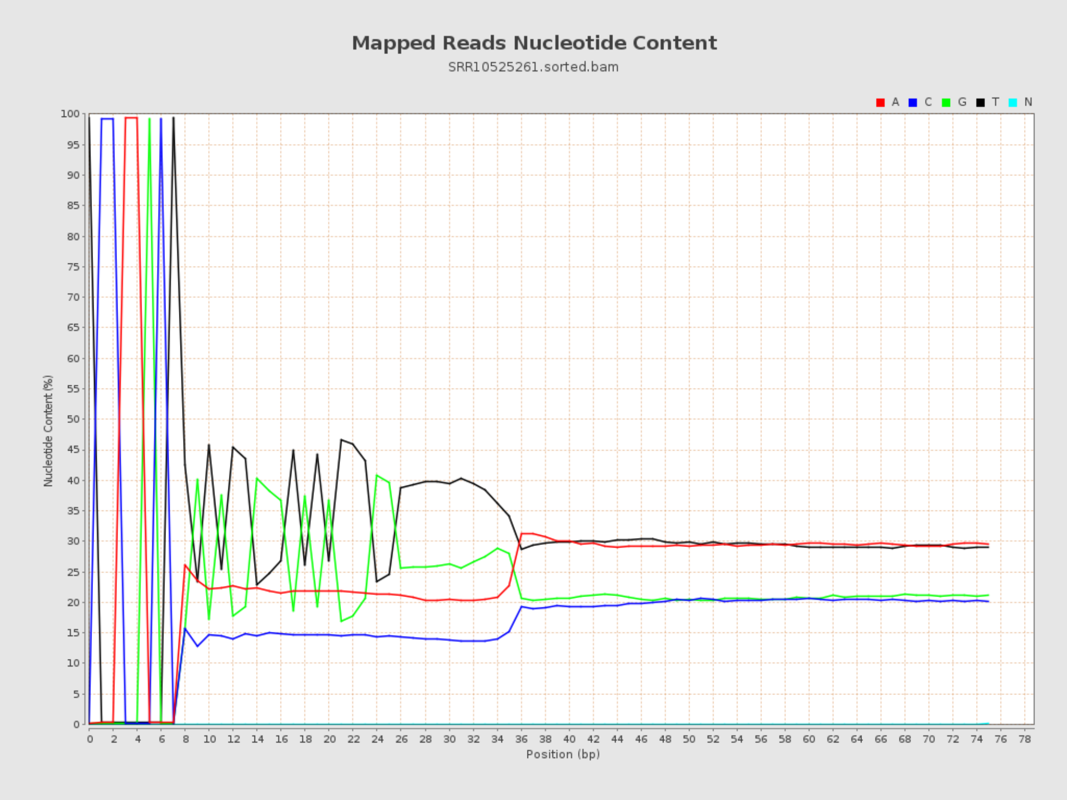
6. Results : Genome Fraction Coverage



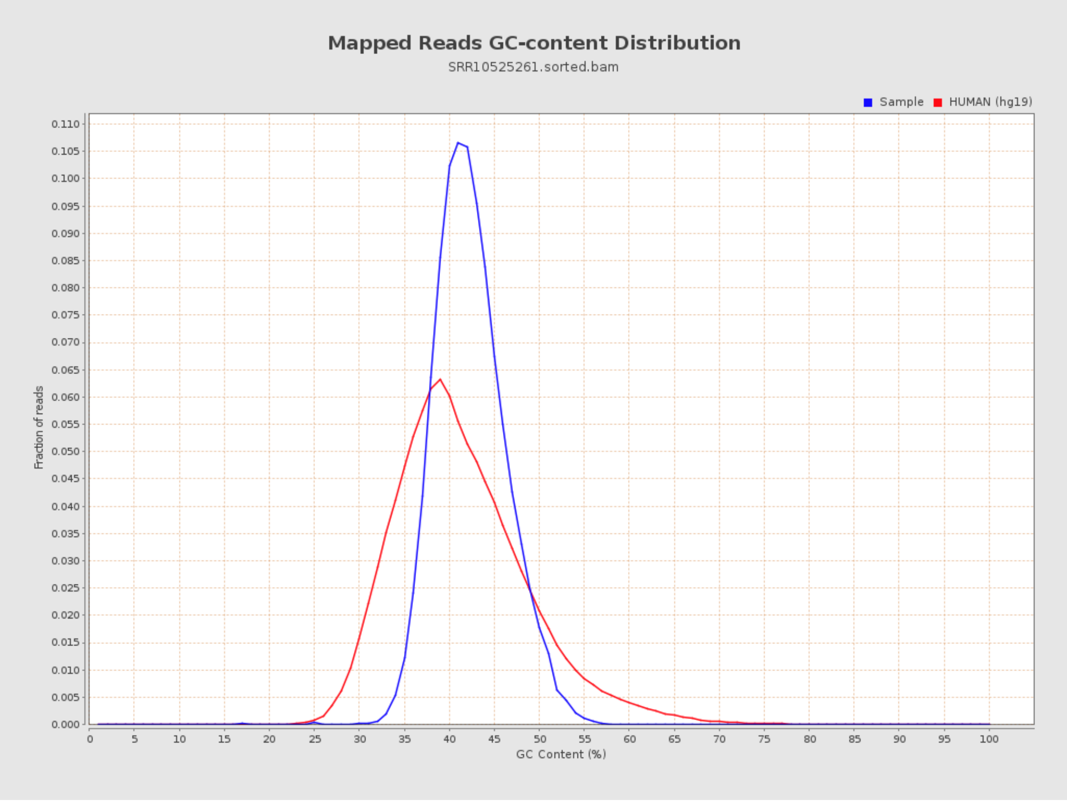
7. Results : Duplication Rate Histogram



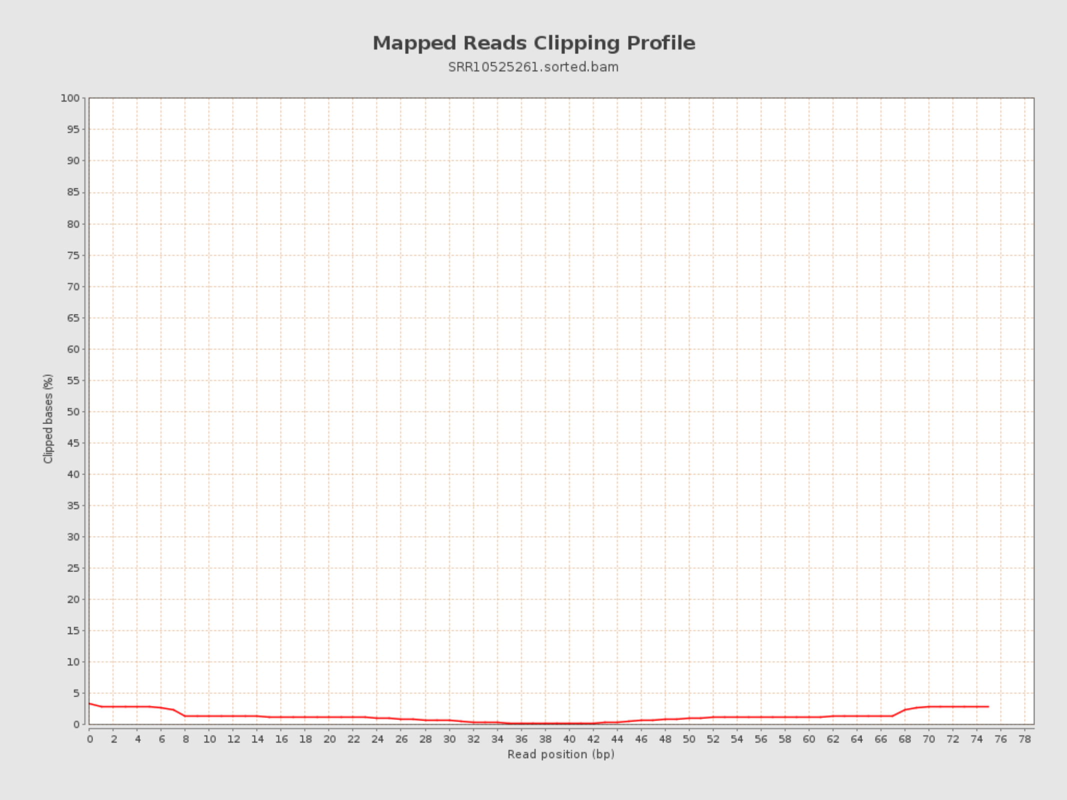
8. Results : Mapped Reads Nucleotide Content



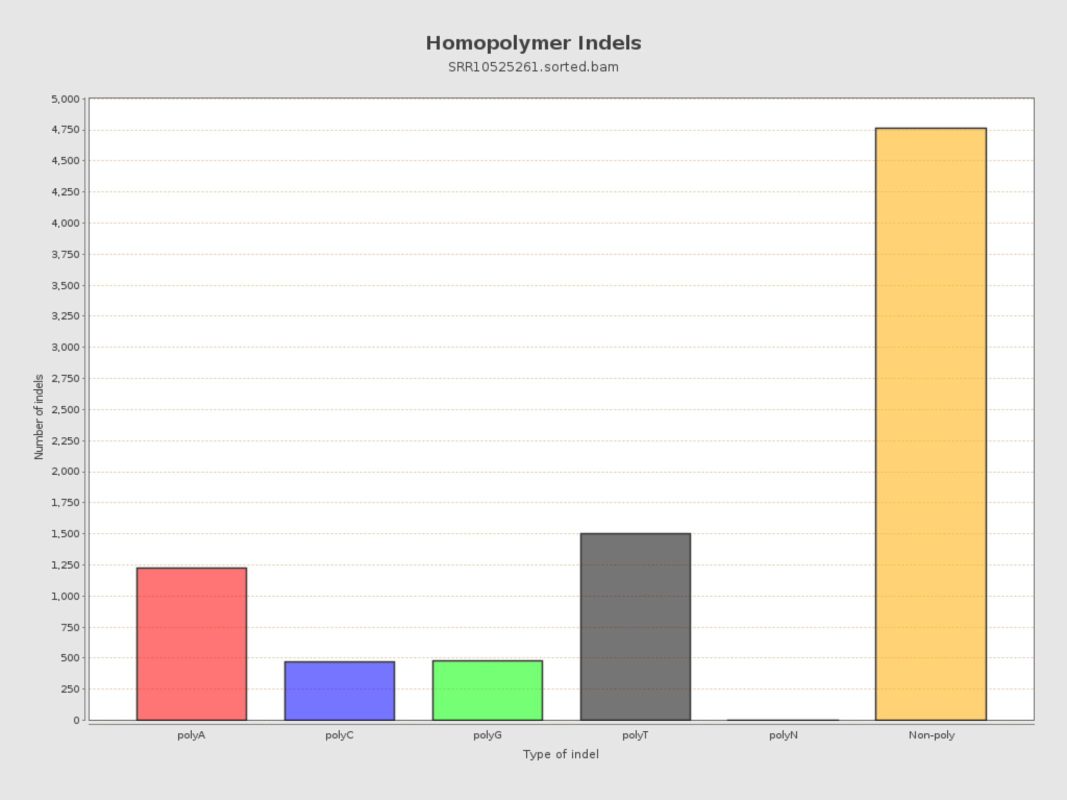
9. Results : Mapped Reads GC-content Distribution



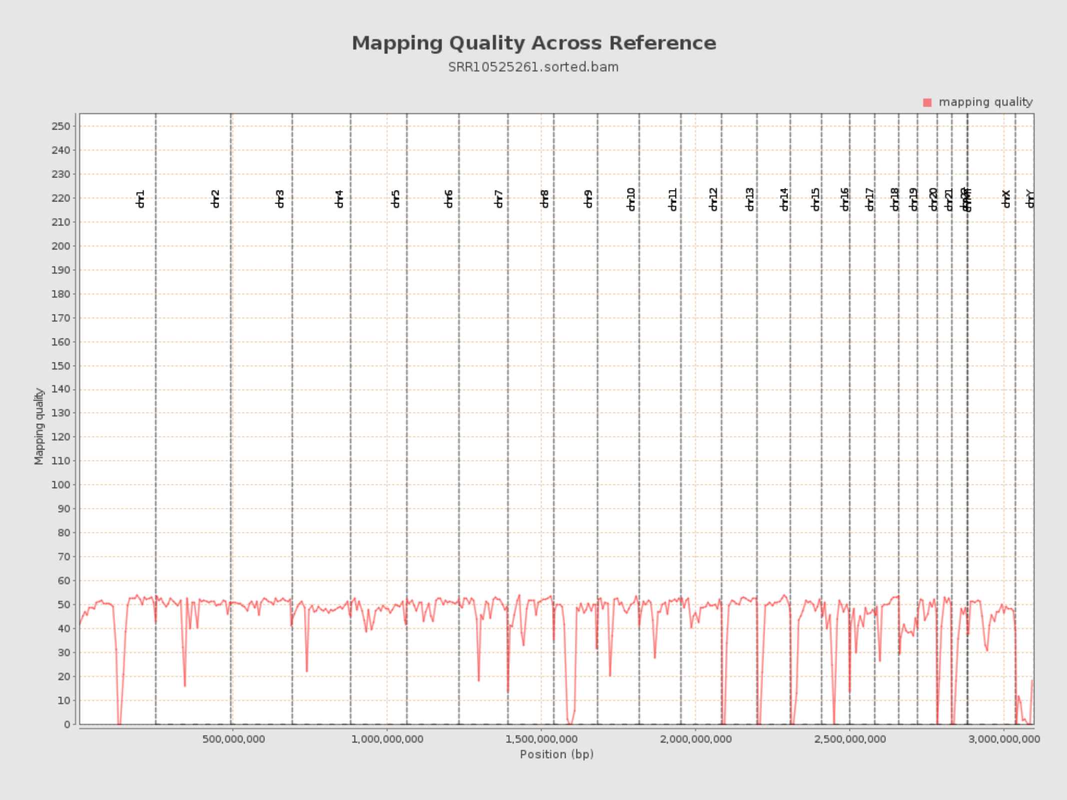
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram