Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:12:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524826.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_SRR10524826 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524826.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:12:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524826.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	655,025
Mapped reads	590,898 / 90.21%
Unmapped reads	64,127 / 9.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,065 / 0.32%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	13,453 / 2.05%
Duplication rate	1.77%
Clipped reads	591,515 / 90.3%

2.2. ACGT Content

Number/percentage of A's	8,028,923 / 24.03%
Number/percentage of C's	6,064,212 / 18.15%
Number/percentage of T's	10,942,328 / 32.75%
Number/percentage of G's	8,374,348 / 25.06%
Number/percentage of N's	4,059 / 0.01%
GC Percentage	43.21%

2.3. Coverage

Mean	0.0108

Standard Deviation	0.1248

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

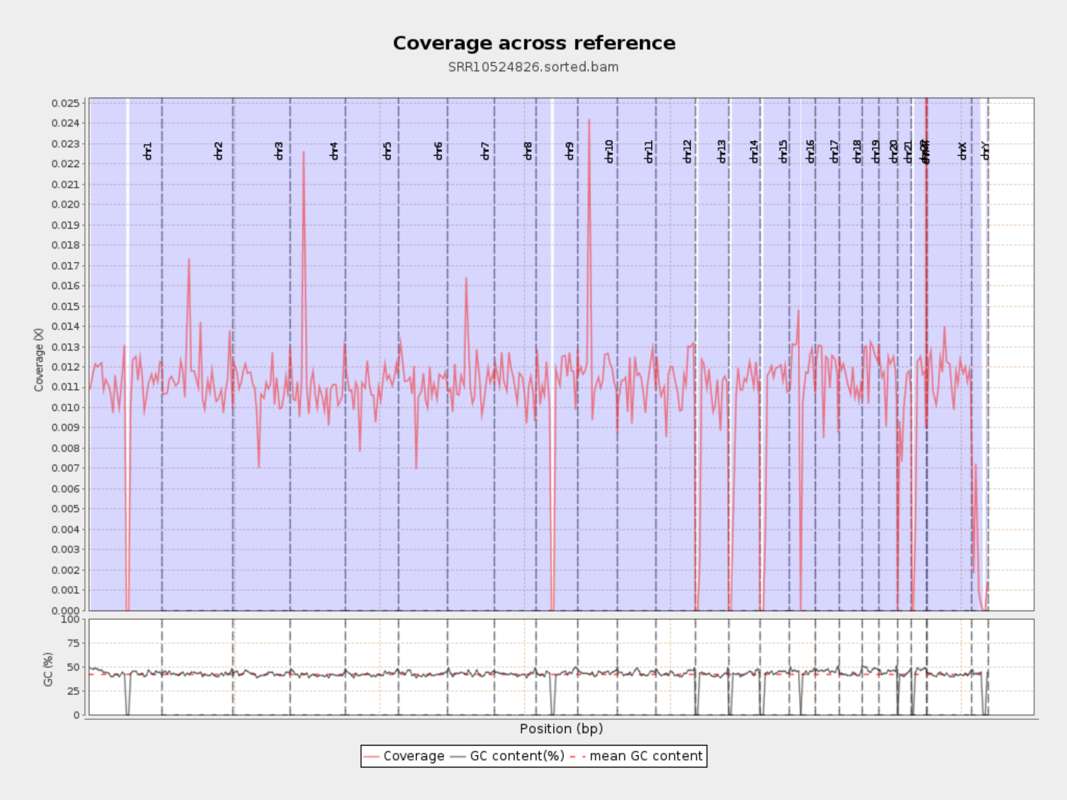
General error rate	0.52%
Mismatches	170,385
Insertions	2,313
Mapped reads with at least one insertion	0.39%
Deletions	6,497
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.61%

2.6. Chromosome stats

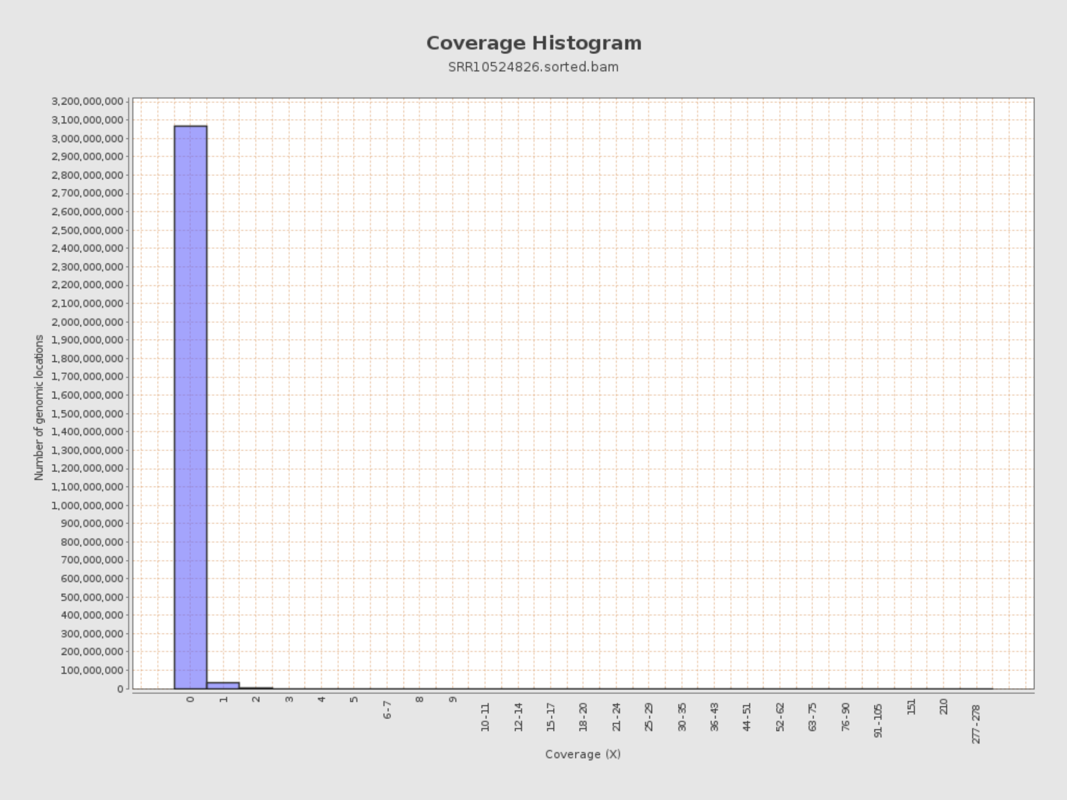
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2664026	0.0107	0.1372
chr2	243199373	2801915	0.0115	0.1704
chr3	198022430	2169275	0.011	0.1106
chr4	191154276	2143871	0.0112	0.1212
chr5	180915260	1985078	0.011	0.1098
chr6	171115067	1906857	0.0111	0.1177
chr7	159138663	1817088	0.0114	0.1383

chr8	146364022	1642419	0.0112	0.1211
chr9	141213431	1444087	0.0102	0.1166
chr10	135534747	1662114	0.0123	0.1482
chr11	135006516	1512937	0.0112	0.1195
chr12	133851895	1519761	0.0114	0.1122
chr13	115169878	1060130	0.0092	0.1008
chr14	107349540	1012738	0.0094	0.1034
chr15	102531392	964560	0.0094	0.1016
chr16	90354753	1022326	0.0113	0.1175
chr17	81195210	956411	0.0118	0.1159
chr18	78077248	884124	0.0113	0.1529
chr19	59128983	733507	0.0124	0.1368
chr20	63025520	731655	0.0116	0.1159
chr21	48129895	440818	0.0092	0.107
chr22	51304566	420969	0.0082	0.0957
chrMT	16571	8495	0.5126	0.7588
chrX	155270560	1802903	0.0116	0.117
chrY	59373566	116253	0.002	0.069

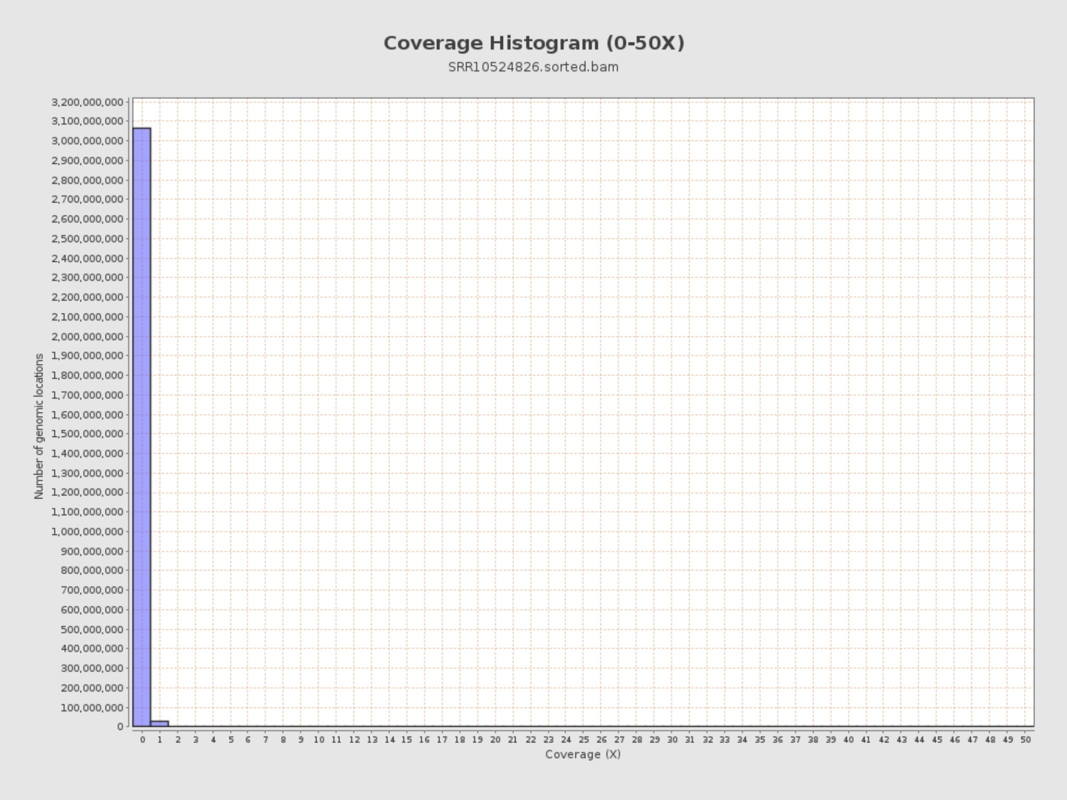
3. Results : Coverage across reference



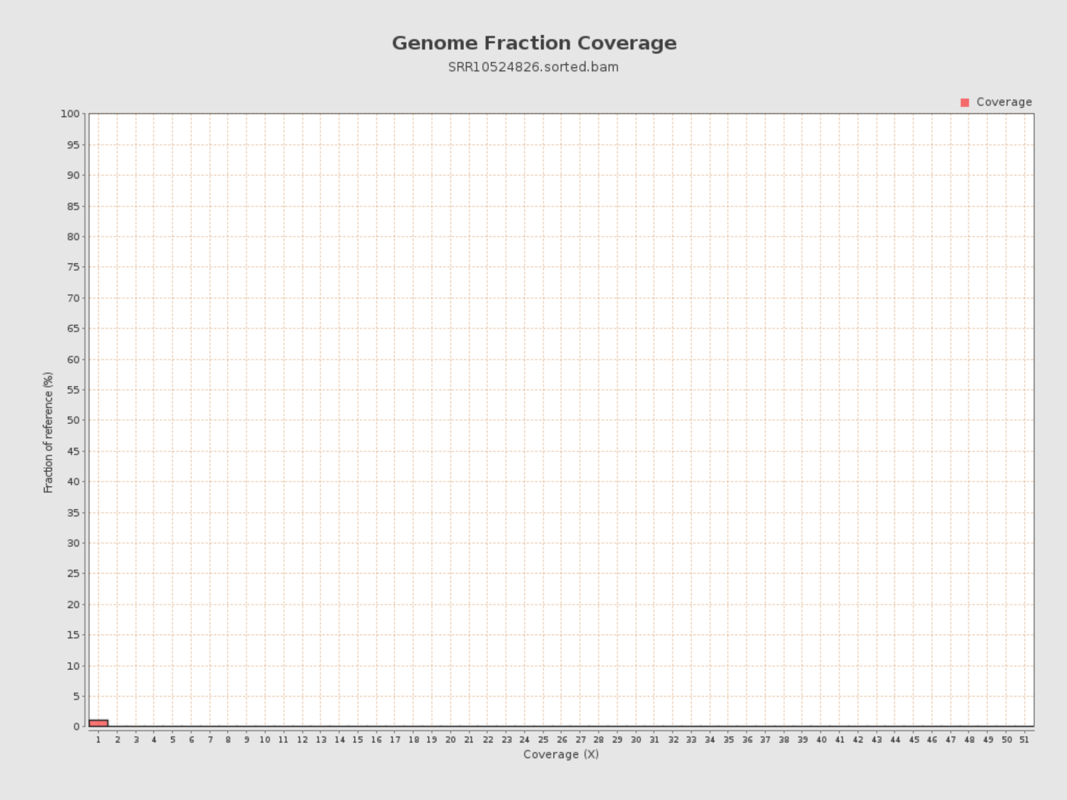
4. Results : Coverage Histogram



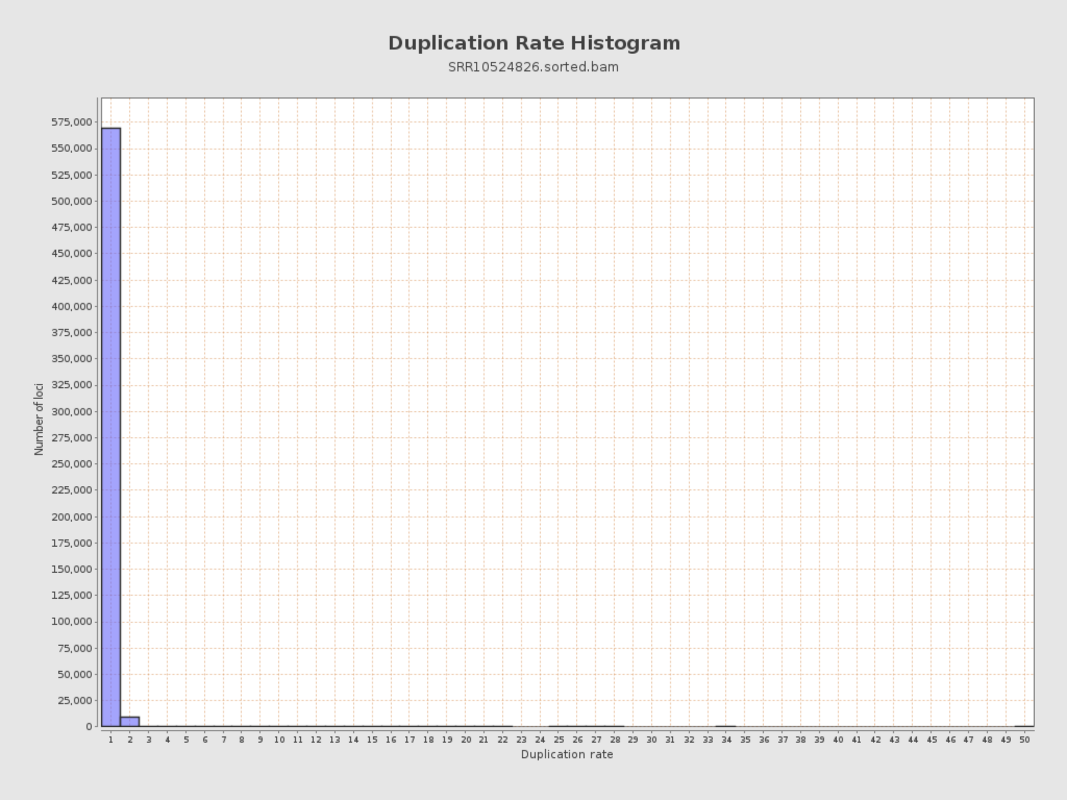
5. Results : Coverage Histogram (0-50X)



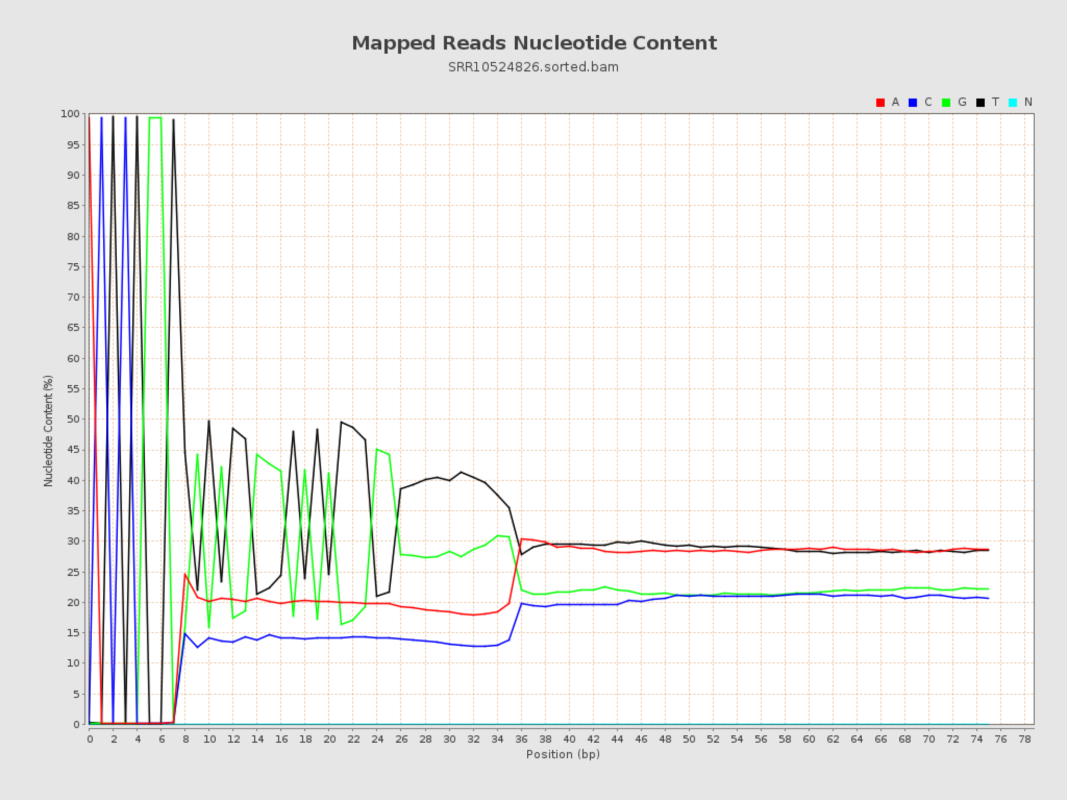
6. Results : Genome Fraction Coverage



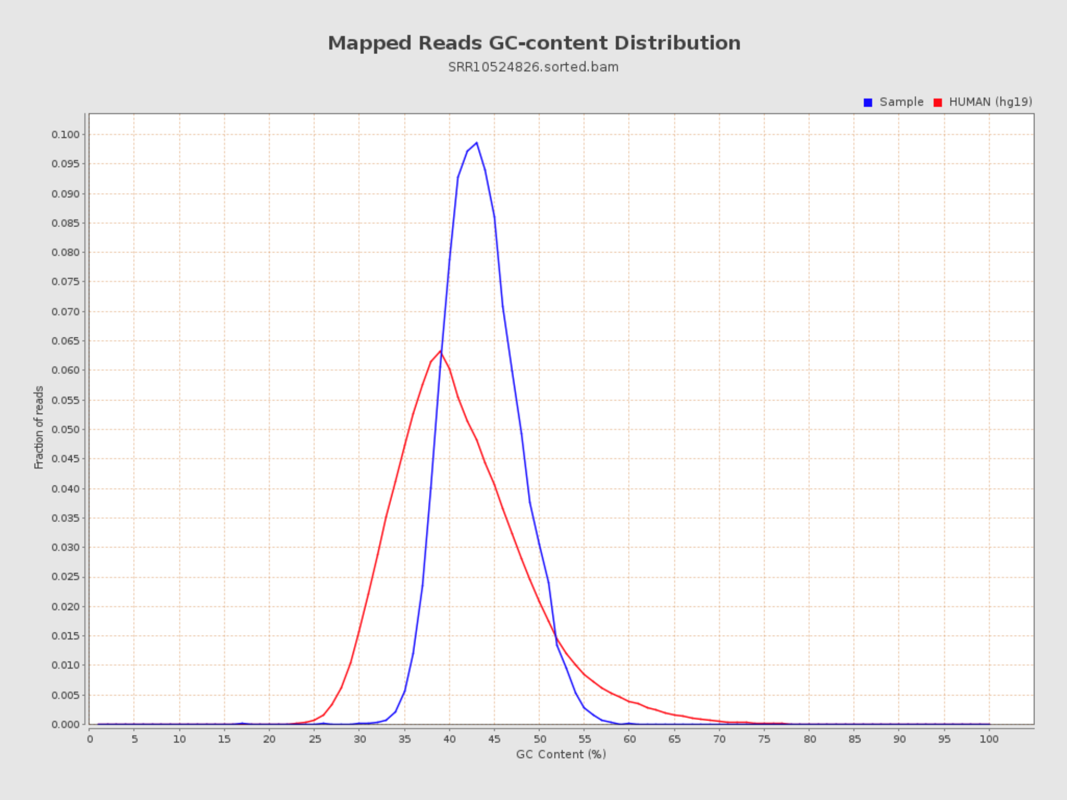
7. Results : Duplication Rate Histogram



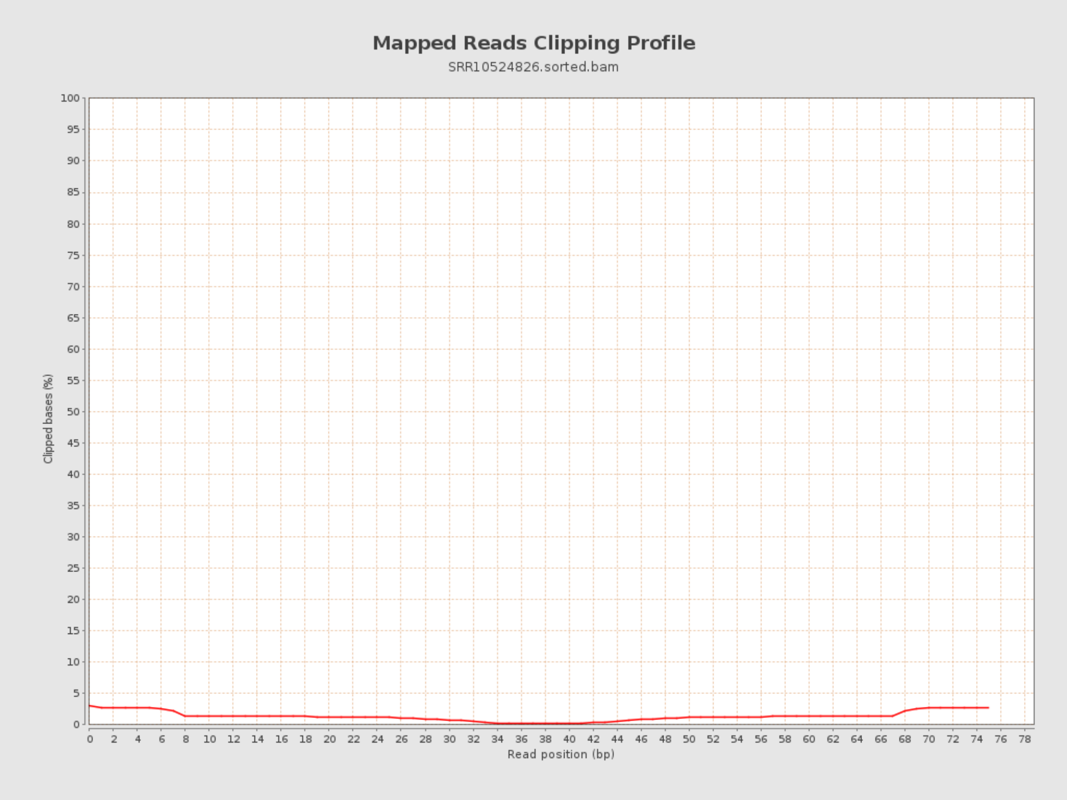
8. Results : Mapped Reads Nucleotide Content



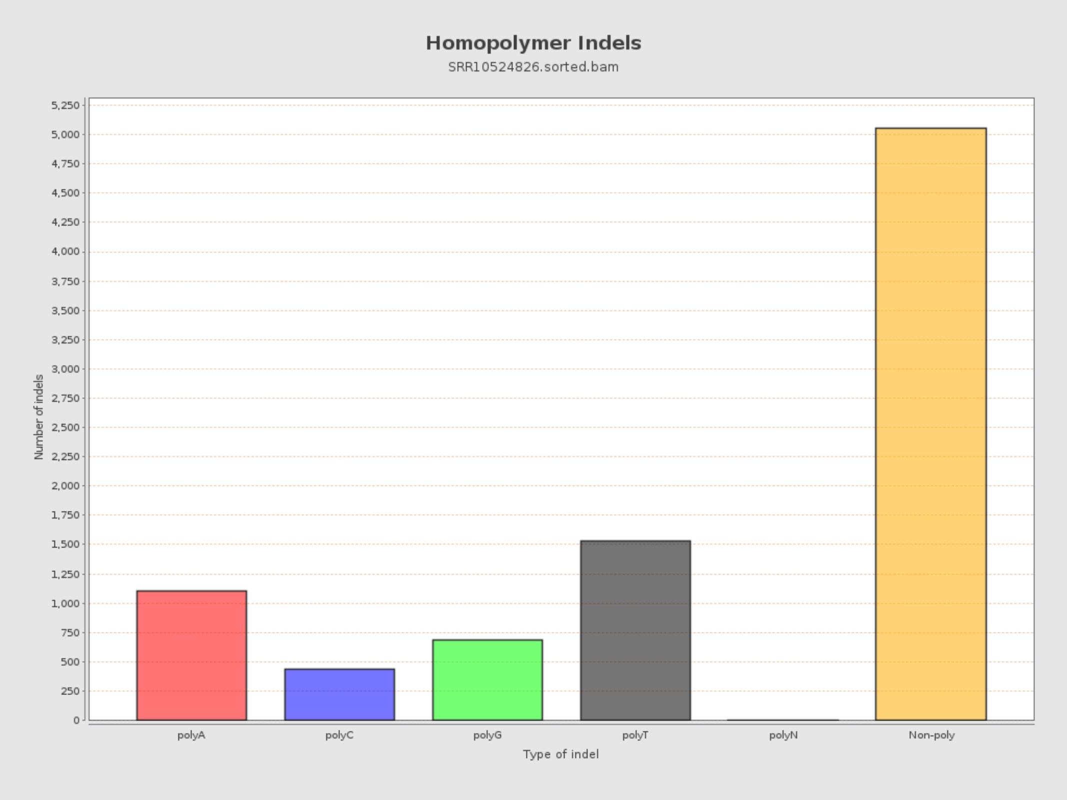
9. Results : Mapped Reads GC-content Distribution



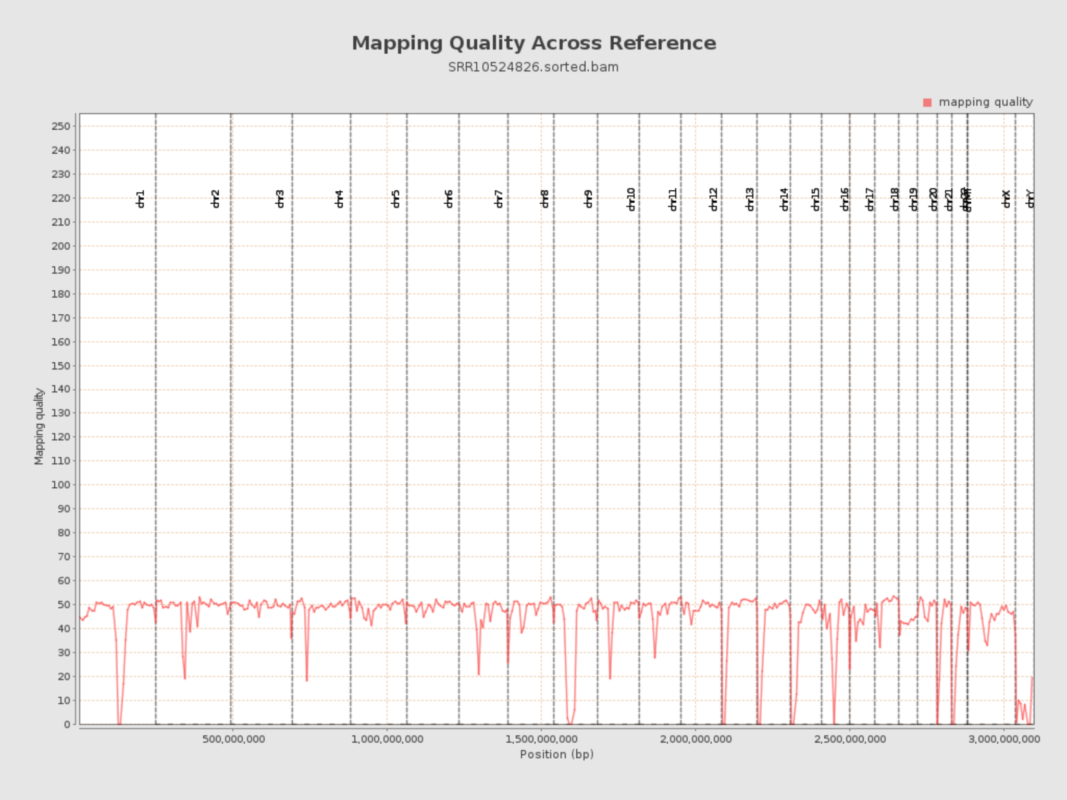
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram