Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:35:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524473.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_SRR10524473 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524473.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:35:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524473.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	584,386
Mapped reads	539,569 / 92.33%
Unmapped reads	44,817 / 7.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,209 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	12,237 / 2.09%
Duplication rate	1.78%
Clipped reads	540,371 / 92.47%

2.2. ACGT Content

Number/percentage of A's	8,071,989 / 25.69%
Number/percentage of C's	5,570,006 / 17.73%
Number/percentage of T's	9,810,579 / 31.22%
Number/percentage of G's	7,970,561 / 25.36%
Number/percentage of N's	643 / 0%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0102

Standard Deviation	0.1232

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

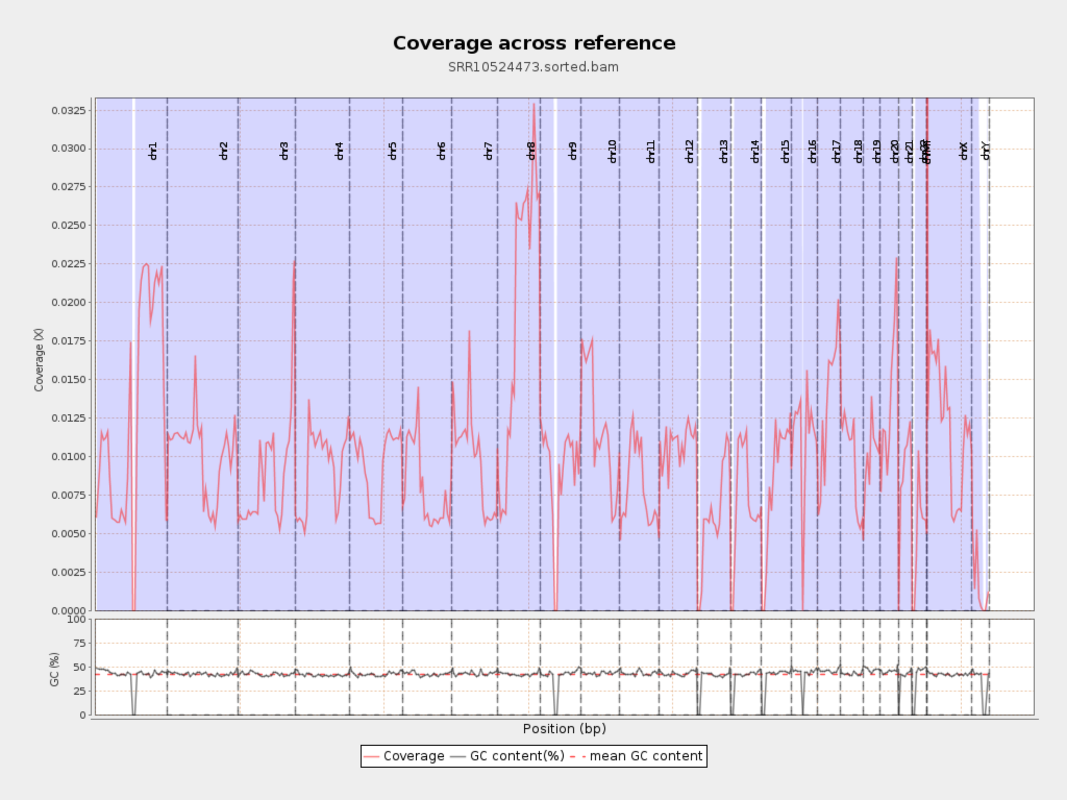
General error rate	0.47%
Mismatches	143,683
Insertions	1,660
Mapped reads with at least one insertion	0.31%
Deletions	5,775
Mapped reads with at least one deletion	1.07%
Homopolymer indels	44.92%

2.6. Chromosome stats

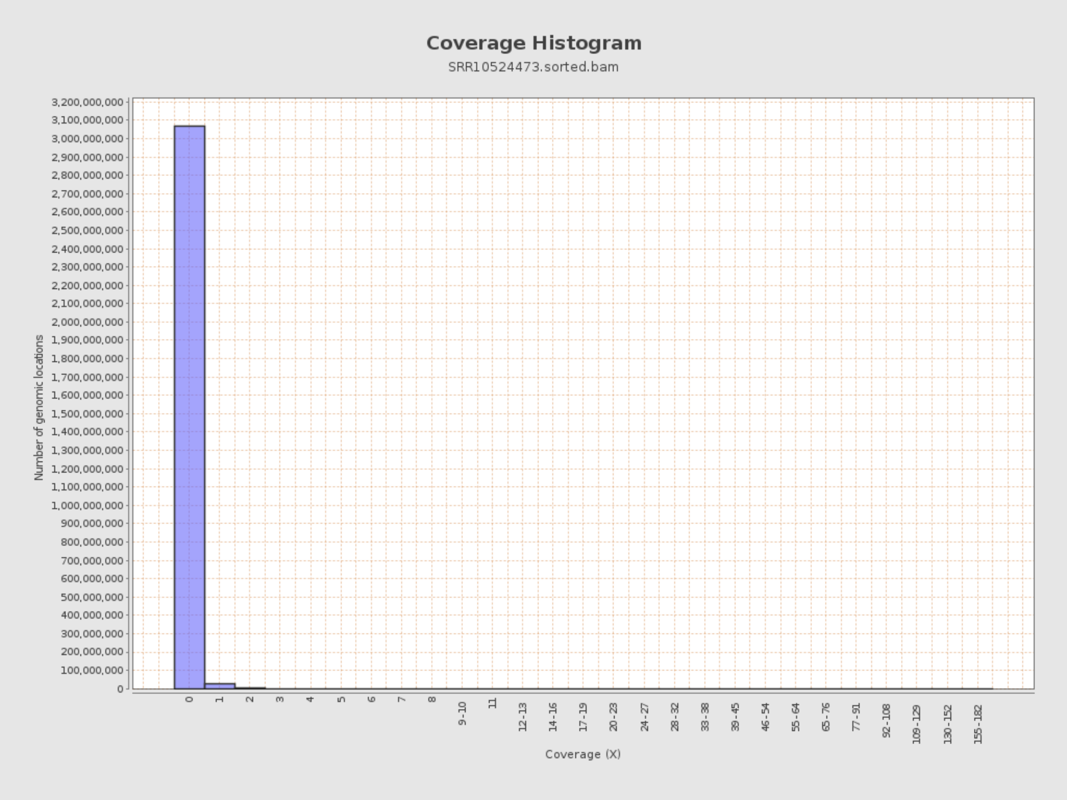
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3112413	0.0125	0.1802
chr2	243199373	2479313	0.0102	0.1334
chr3	198022430	1730418	0.0087	0.0978
chr4	191154276	1779105	0.0093	0.104
chr5	180915260	1715293	0.0095	0.1014
chr6	171115067	1363802	0.008	0.1025
chr7	159138663	1581199	0.0099	0.1477

chr8	146364022	2872086	0.0196	0.155
chr9	141213431	1262985	0.0089	0.111
chr10	135534747	1646057	0.0121	0.1289
chr11	135006516	1085223	0.008	0.1128
chr12	133851895	1446652	0.0108	0.1085
chr13	115169878	709684	0.0062	0.0823
chr14	107349540	757749	0.0071	0.0882
chr15	102531392	853085	0.0083	0.0957
chr16	90354753	998548	0.0111	0.1125
chr17	81195210	1095144	0.0135	0.1228
chr18	78077248	759727	0.0097	0.1721
chr19	59128983	603342	0.0102	0.143
chr20	63025520	876668	0.0139	0.123
chr21	48129895	435706	0.0091	0.1018
chr22	51304566	261038	0.0051	0.0744
chrMT	16571	28560	1.7235	1.6759
chrX	155270560	1884077	0.0121	0.1197
chrY	59373566	95754	0.0016	0.0537

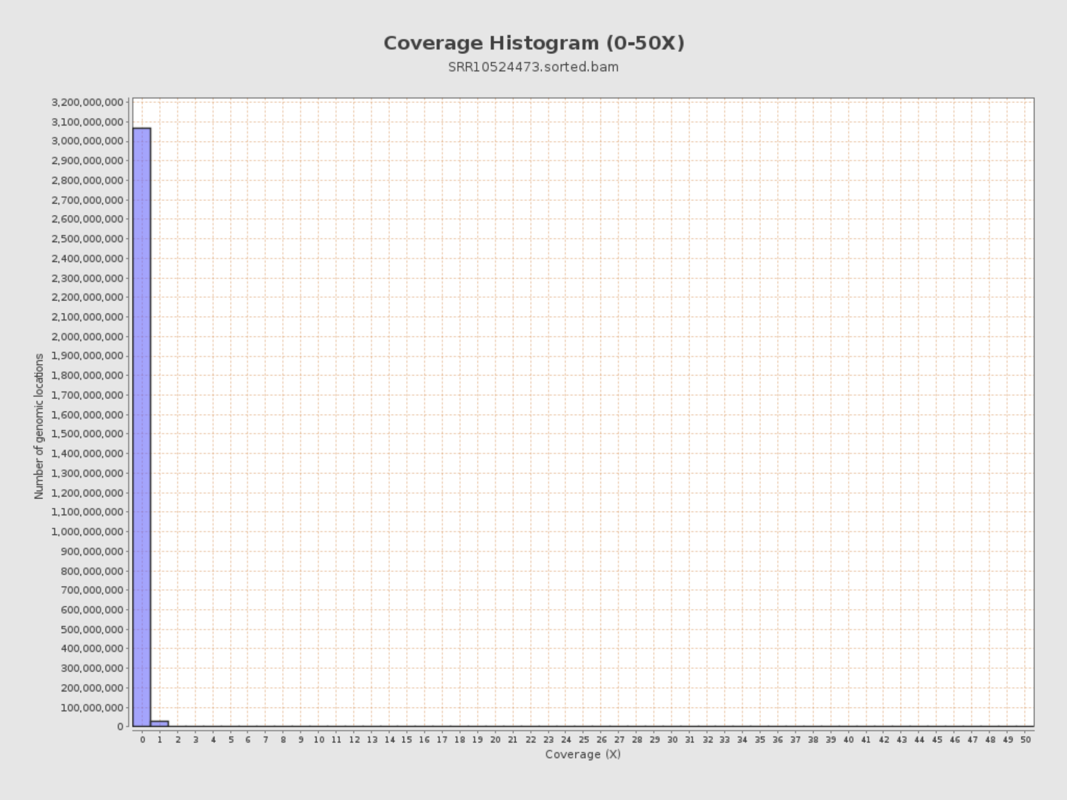
3. Results : Coverage across reference



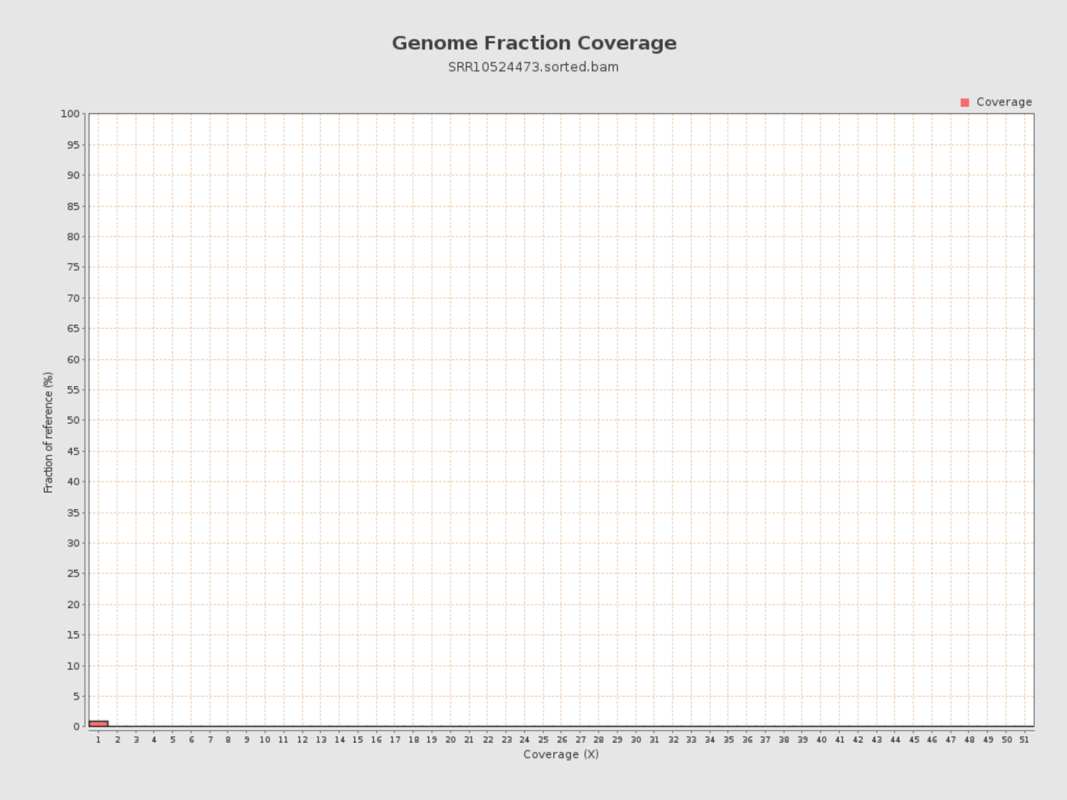
4. Results : Coverage Histogram



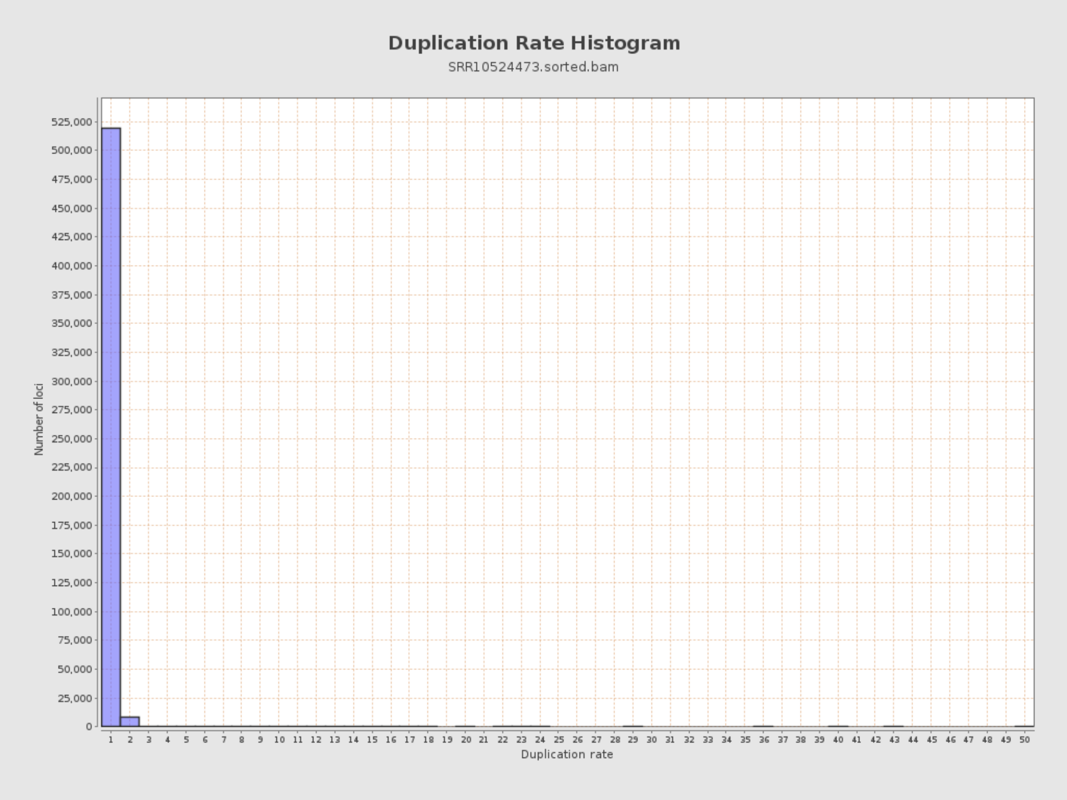
5. Results : Coverage Histogram (0-50X)



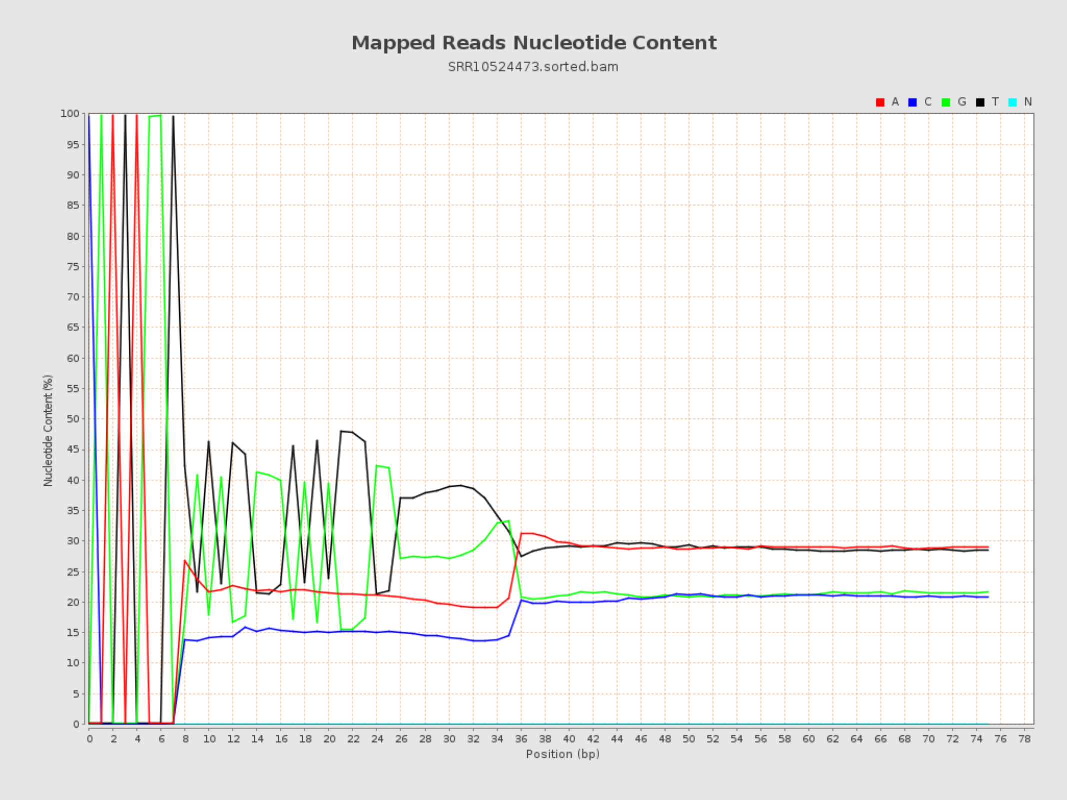
6. Results : Genome Fraction Coverage



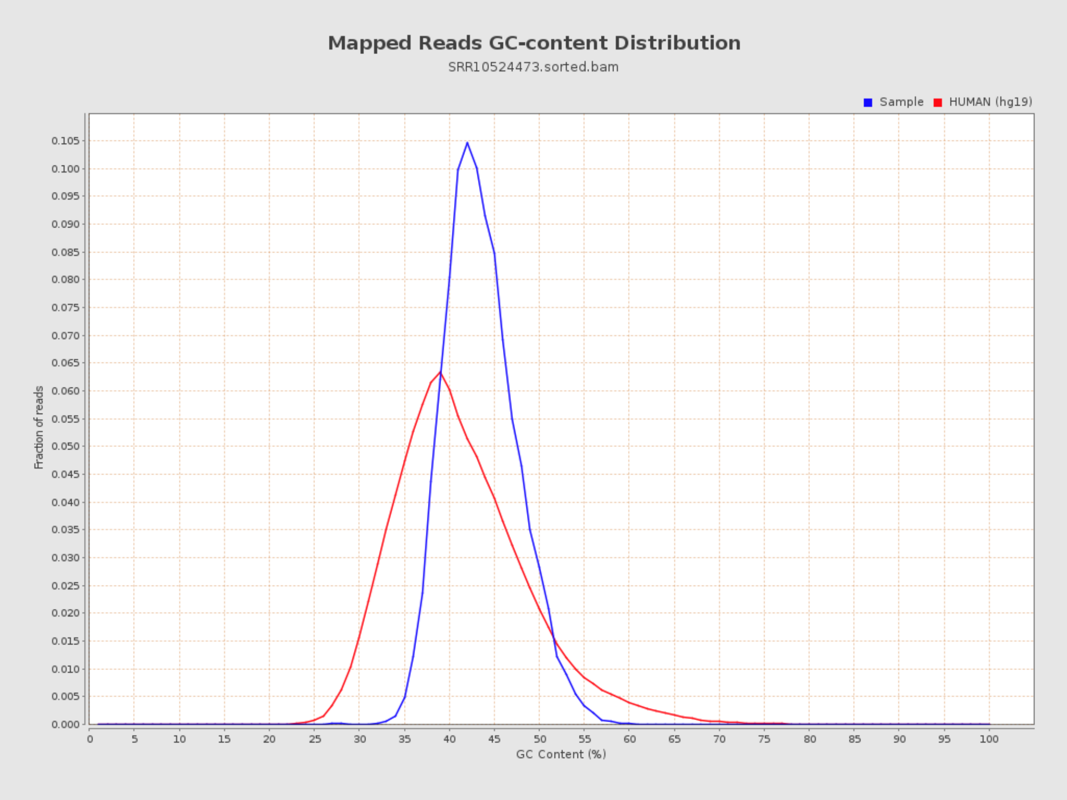
7. Results : Duplication Rate Histogram



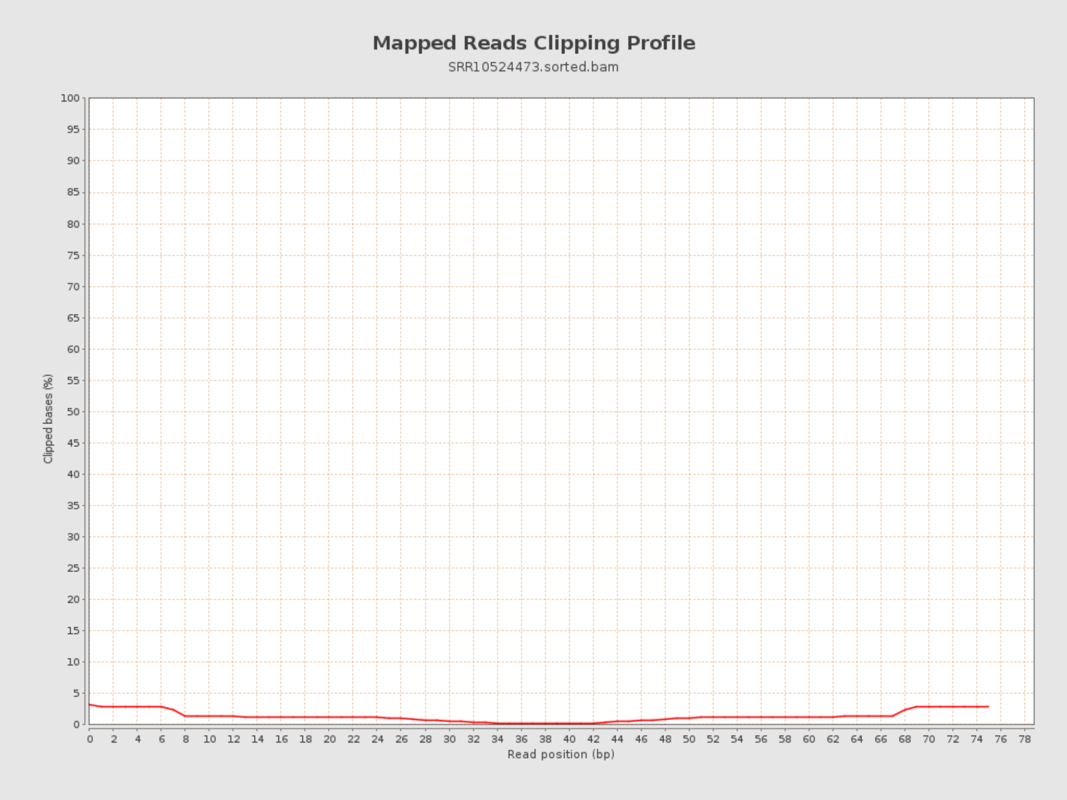
8. Results : Mapped Reads Nucleotide Content



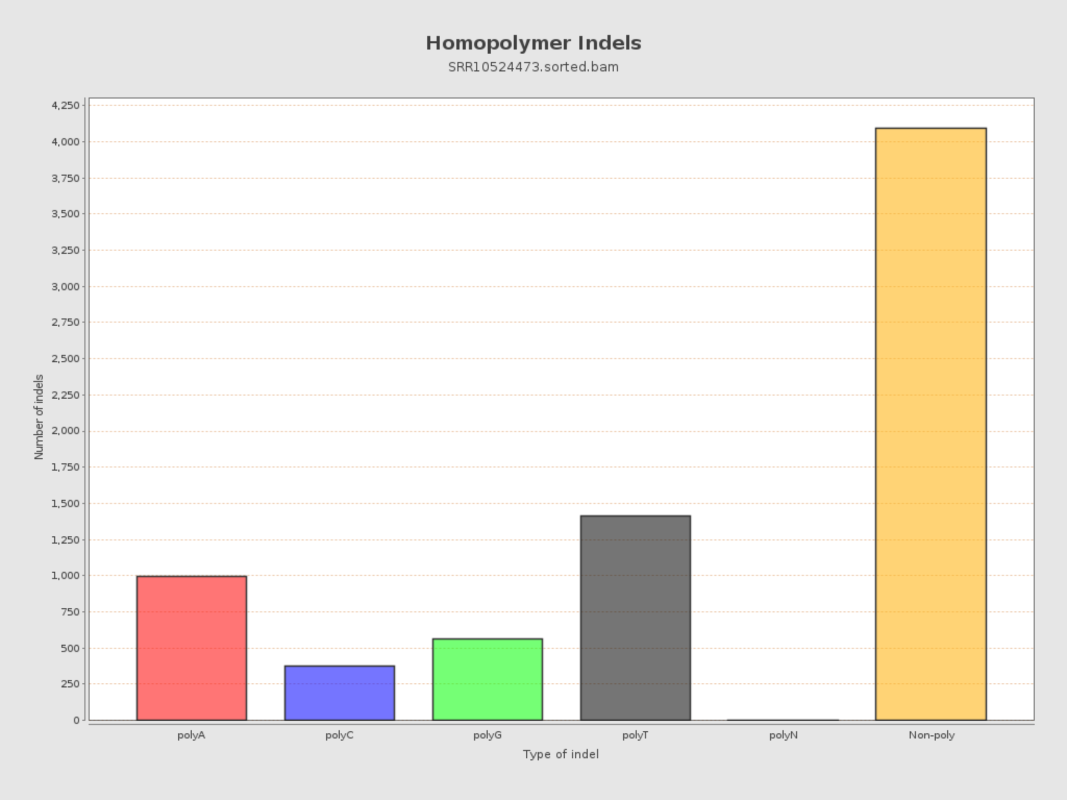
9. Results : Mapped Reads GC-content Distribution



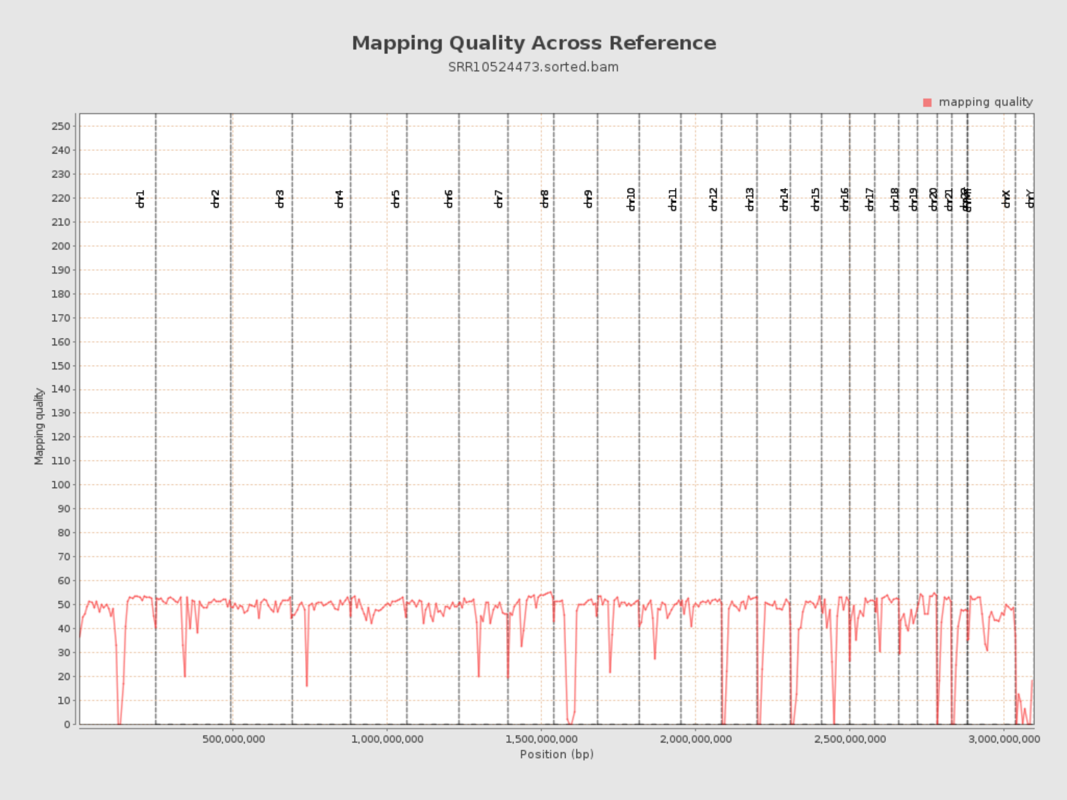
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram