Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:53:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524671.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_SRR10524671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524671.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:53:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524671.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	560,596
Mapped reads	511,696 / 91.28%
Unmapped reads	48,900 / 8.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,982 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	10,139 / 1.81%
Duplication rate	1.46%
Clipped reads	512,695 / 91.46%

2.2. ACGT Content

Number/percentage of A's	7,838,065 / 26.01%
Number/percentage of C's	5,615,779 / 18.64%
Number/percentage of T's	9,673,550 / 32.1%
Number/percentage of G's	7,001,340 / 23.24%
Number/percentage of N's	3,753 / 0.01%
GC Percentage	41.87%

2.3. Coverage

Mean	0.0097

Standard Deviation	0.1247

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

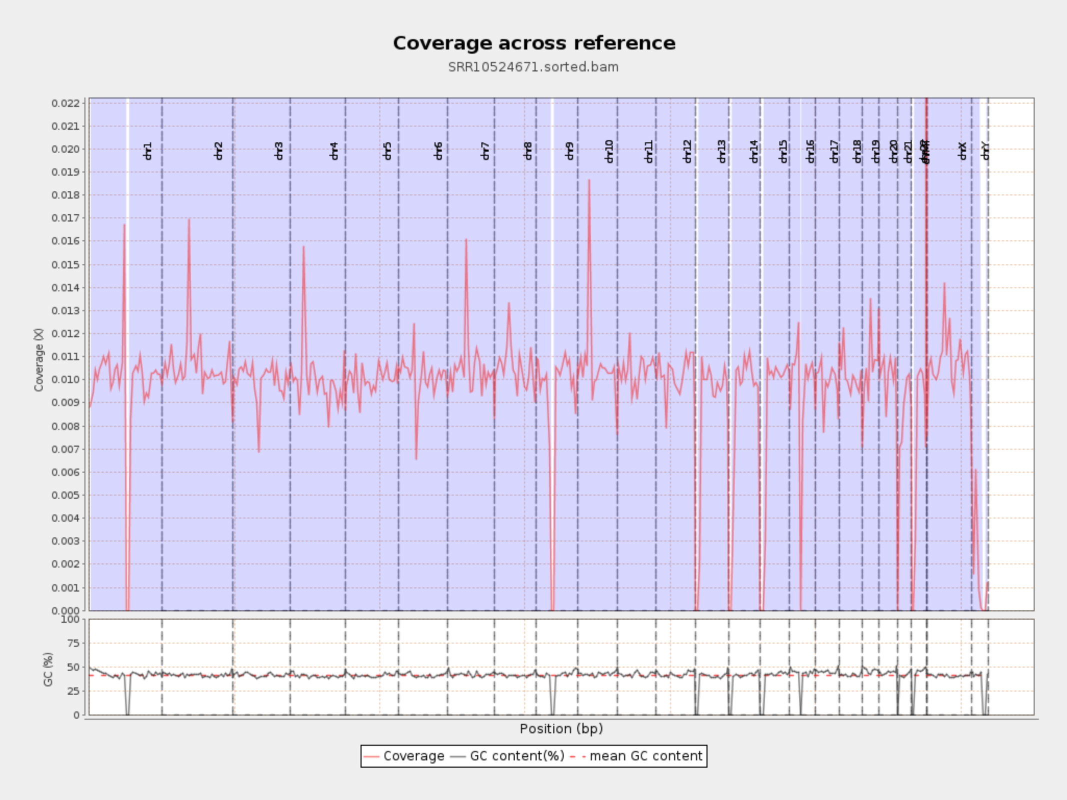
General error rate	0.52%
Mismatches	152,451
Insertions	2,014
Mapped reads with at least one insertion	0.39%
Deletions	5,565
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.94%

2.6. Chromosome stats

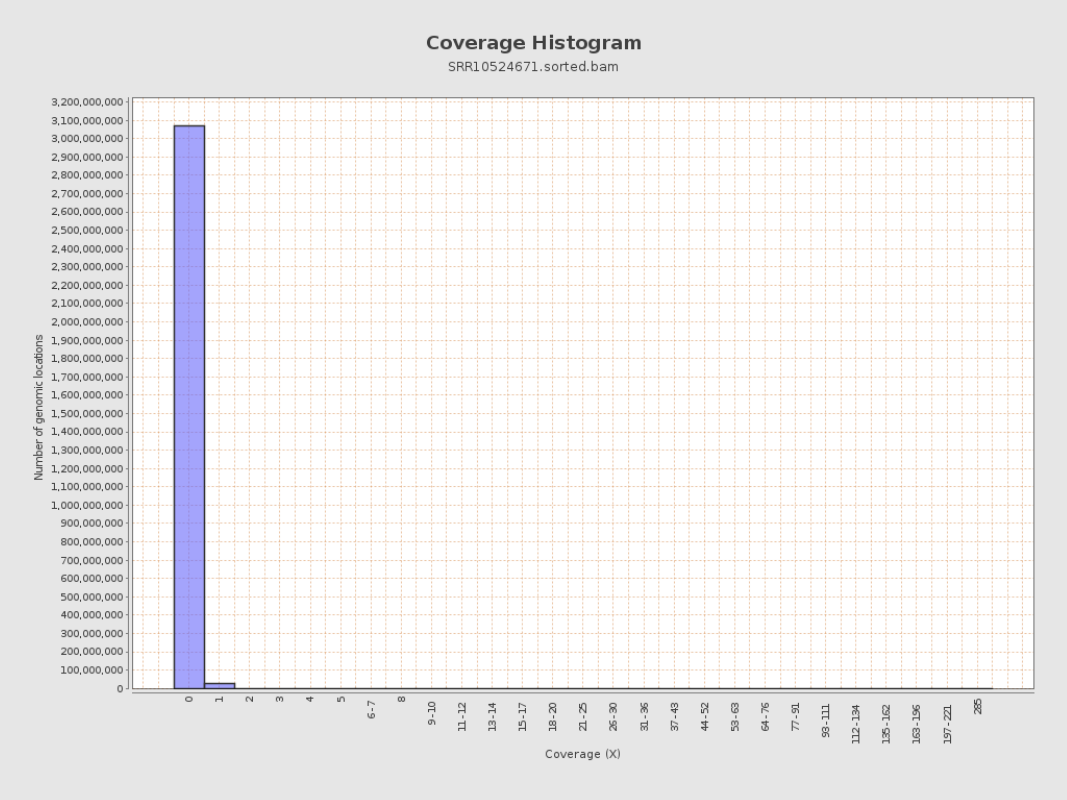
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2420477	0.0097	0.1891
chr2	243199373	2600329	0.0107	0.1619
chr3	198022430	1973164	0.01	0.1028
chr4	191154276	1914698	0.01	0.1075
chr5	180915260	1812864	0.01	0.1032
chr6	171115067	1738410	0.0102	0.1096
chr7	159138663	1685362	0.0106	0.1365

chr8	146364022	1543178	0.0105	0.1263
chr9	141213431	1263154	0.0089	0.1096
chr10	135534747	1458089	0.0108	0.1272
chr11	135006516	1397528	0.0104	0.1149
chr12	133851895	1369850	0.0102	0.1046
chr13	115169878	960509	0.0083	0.0941
chr14	107349540	911013	0.0085	0.0963
chr15	102531392	856854	0.0084	0.0941
chr16	90354753	858988	0.0095	0.1038
chr17	81195210	798592	0.0098	0.1047
chr18	78077248	799369	0.0102	0.1659
chr19	59128983	626925	0.0106	0.1601
chr20	63025520	641034	0.0102	0.1045
chr21	48129895	381946	0.0079	0.0948
chr22	51304566	350158	0.0068	0.0854
chrMT	16571	7279	0.4393	0.7222
chrX	155270560	1673480	0.0108	0.111
chrY	59373566	98188	0.0017	0.0665

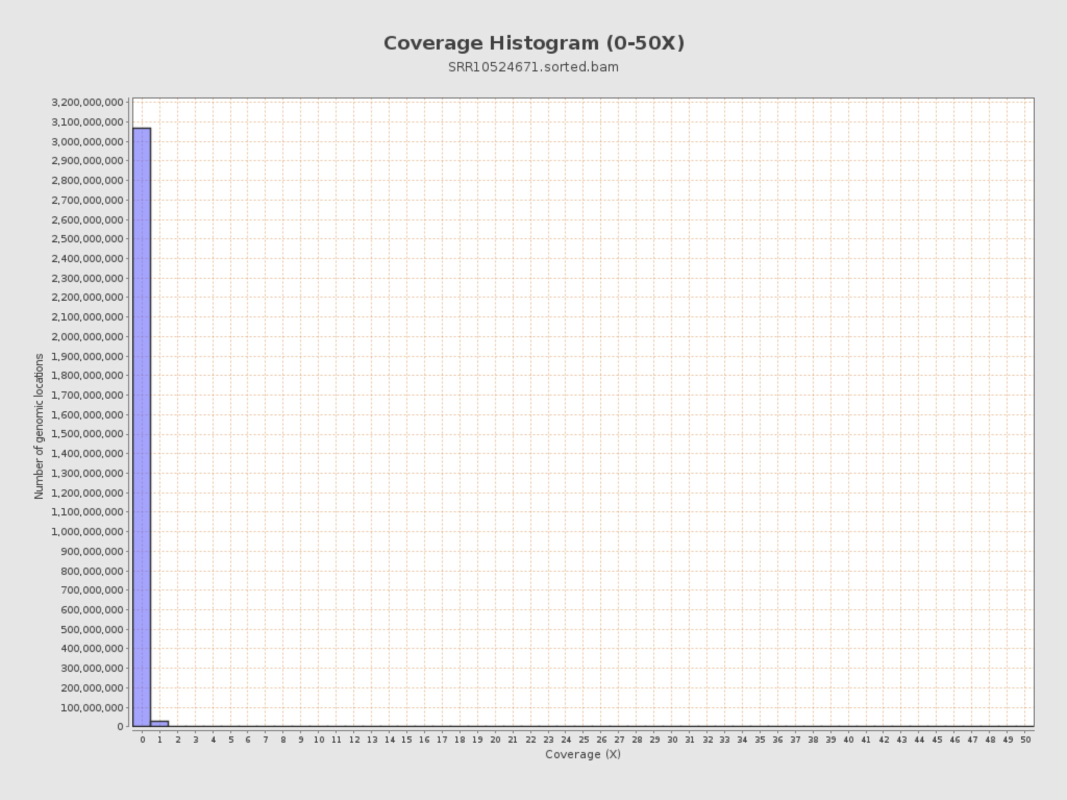
3. Results : Coverage across reference



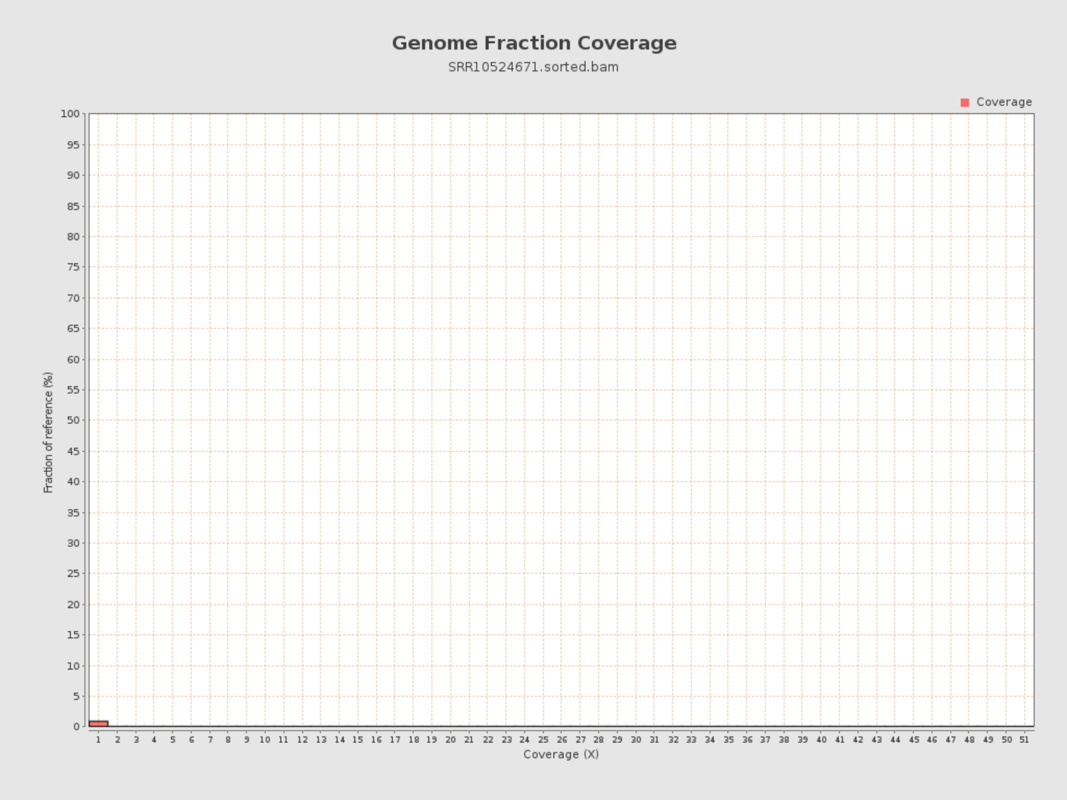
4. Results : Coverage Histogram



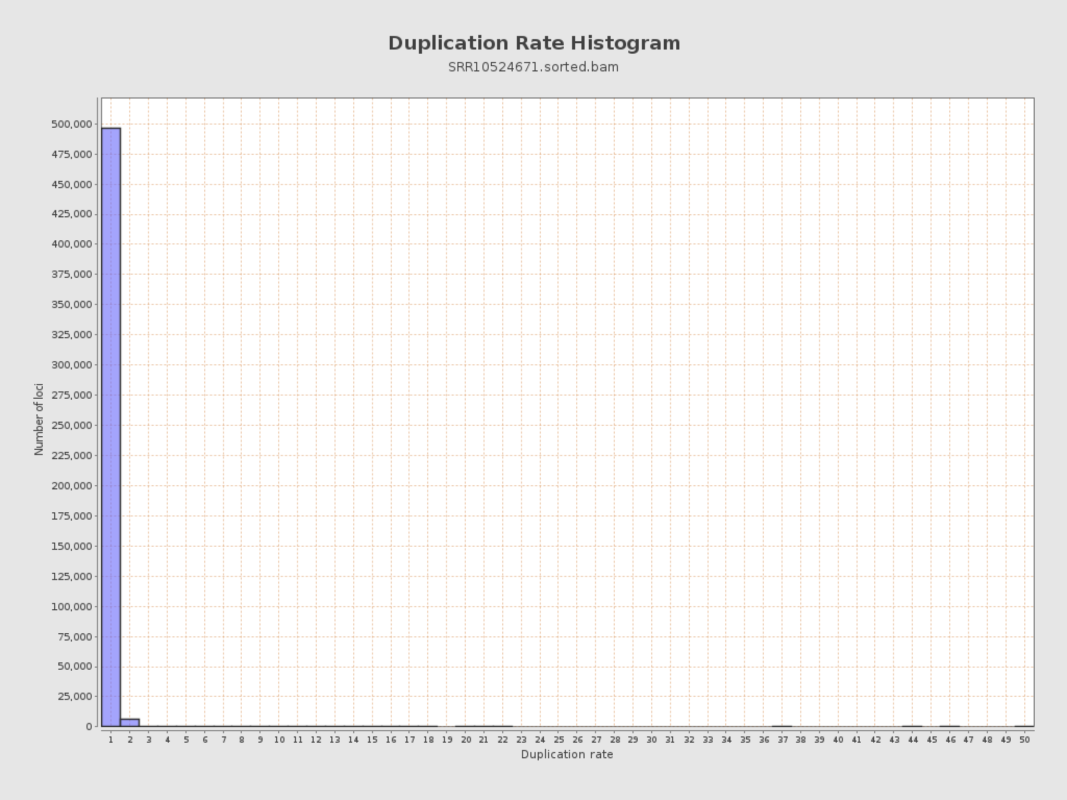
5. Results : Coverage Histogram (0-50X)



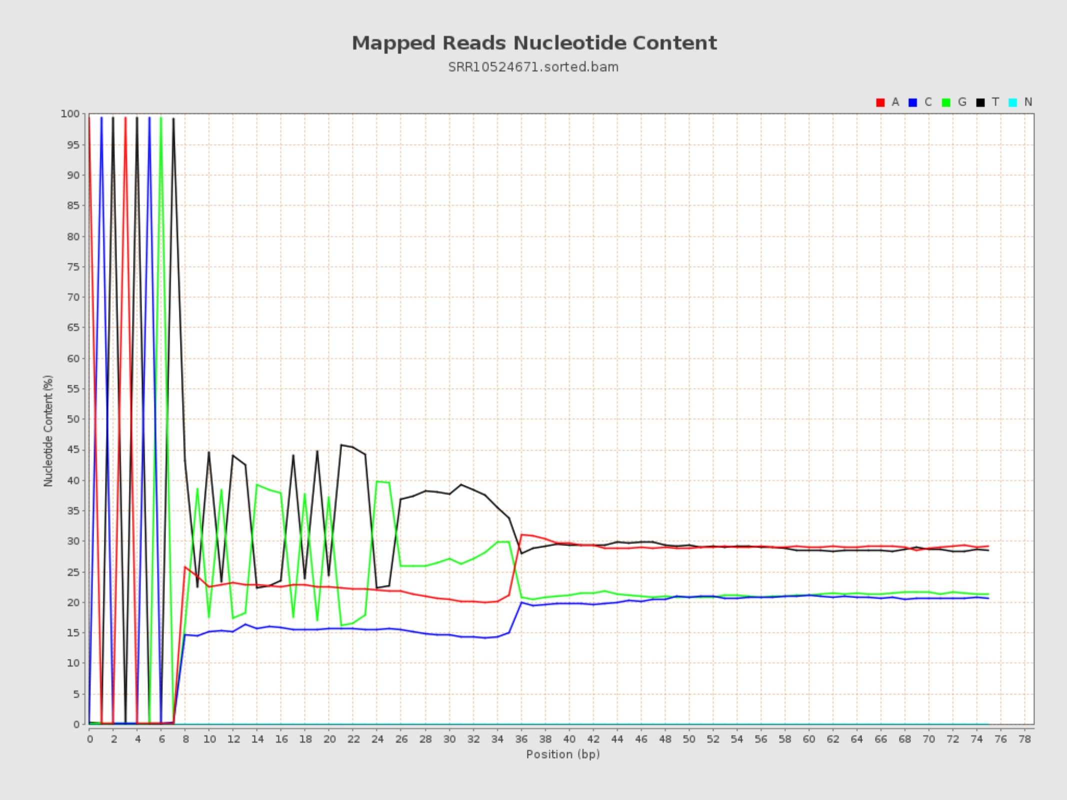
6. Results : Genome Fraction Coverage



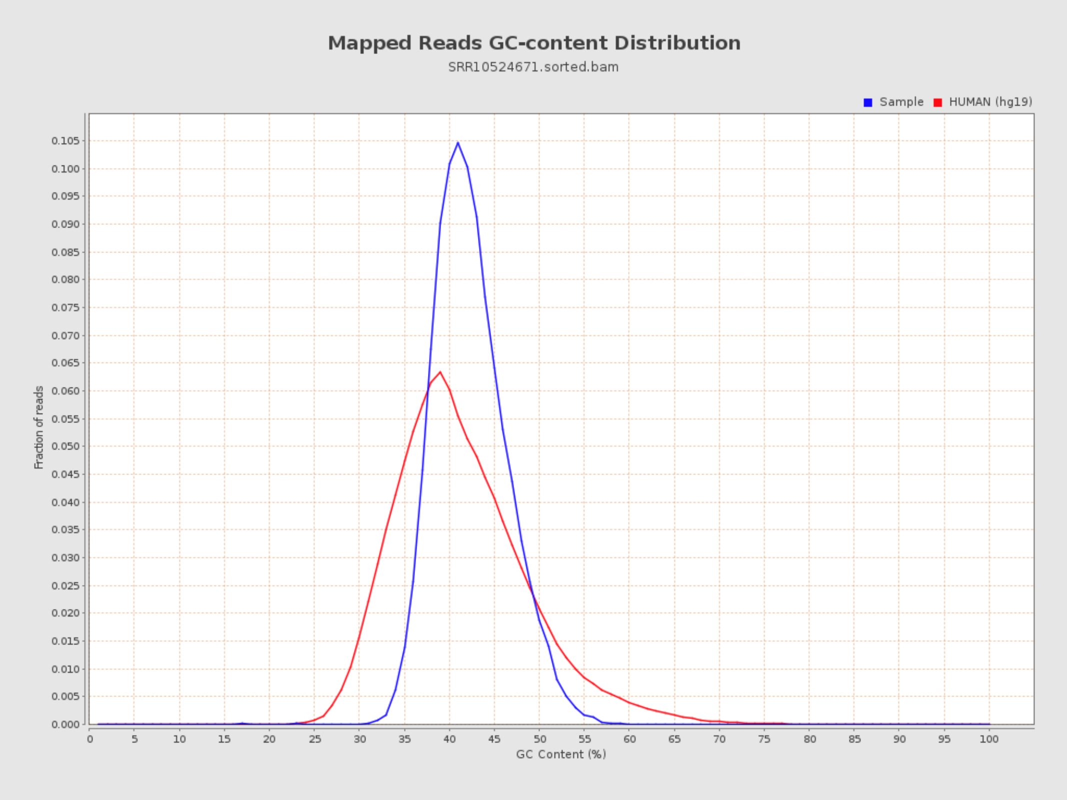
7. Results : Duplication Rate Histogram



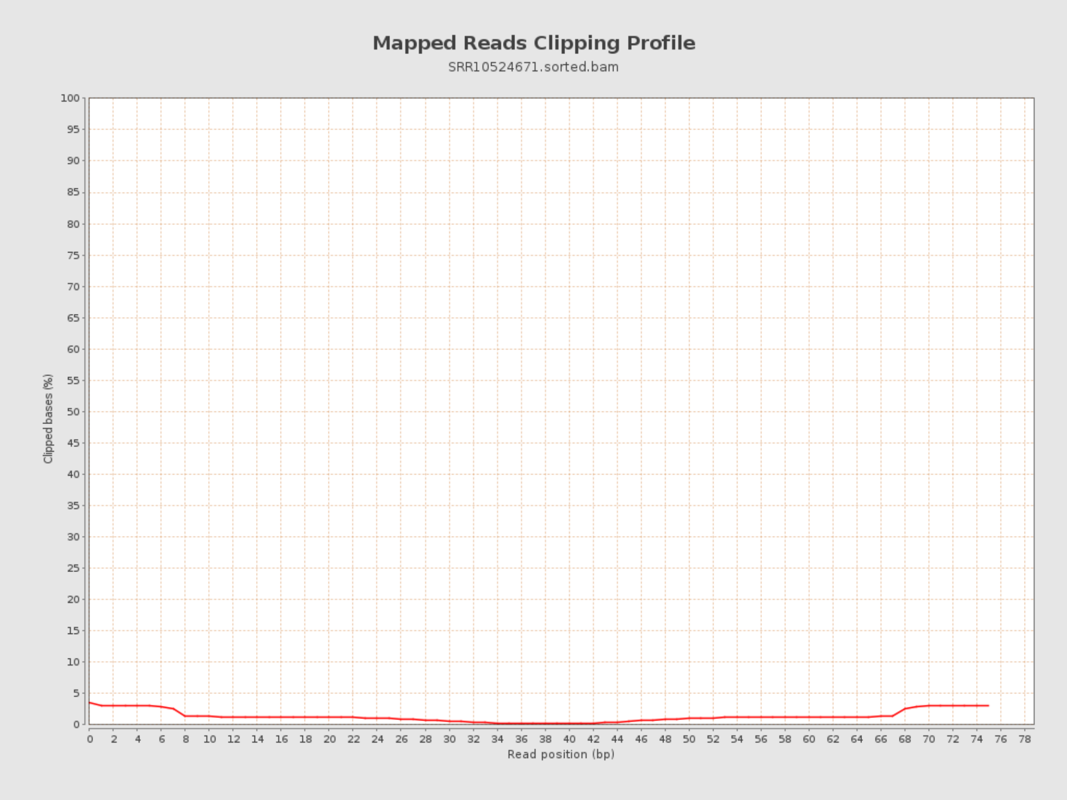
8. Results : Mapped Reads Nucleotide Content



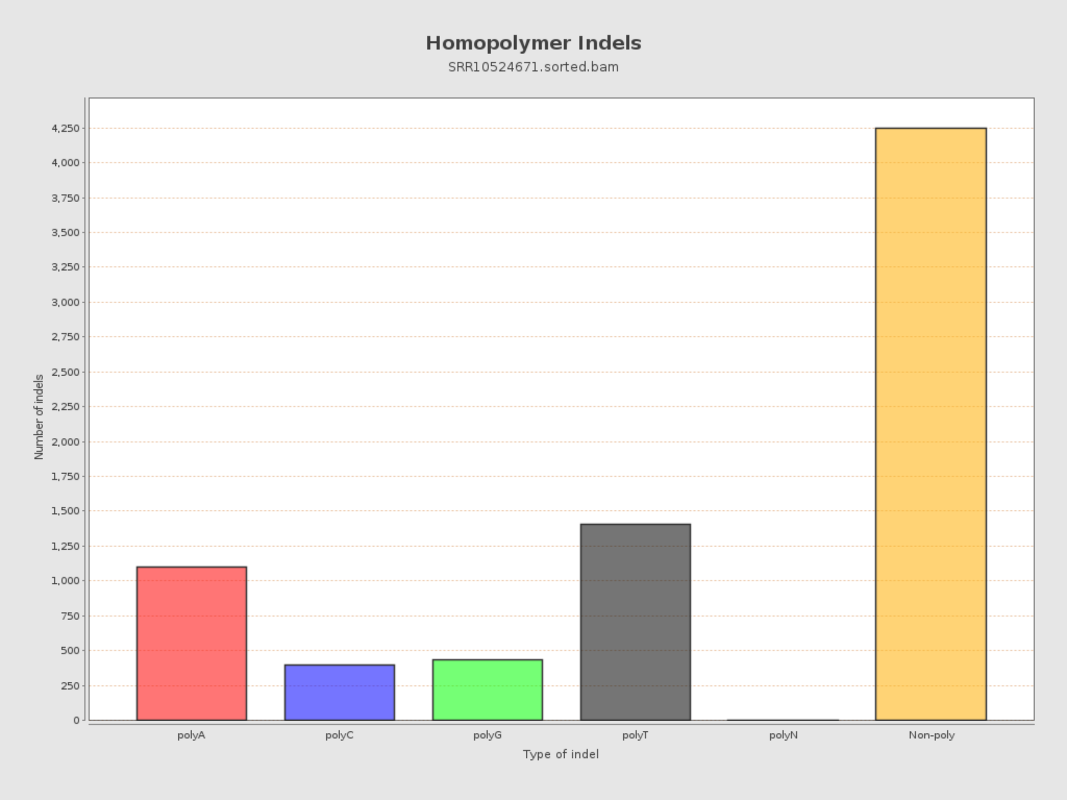
9. Results : Mapped Reads GC-content Distribution



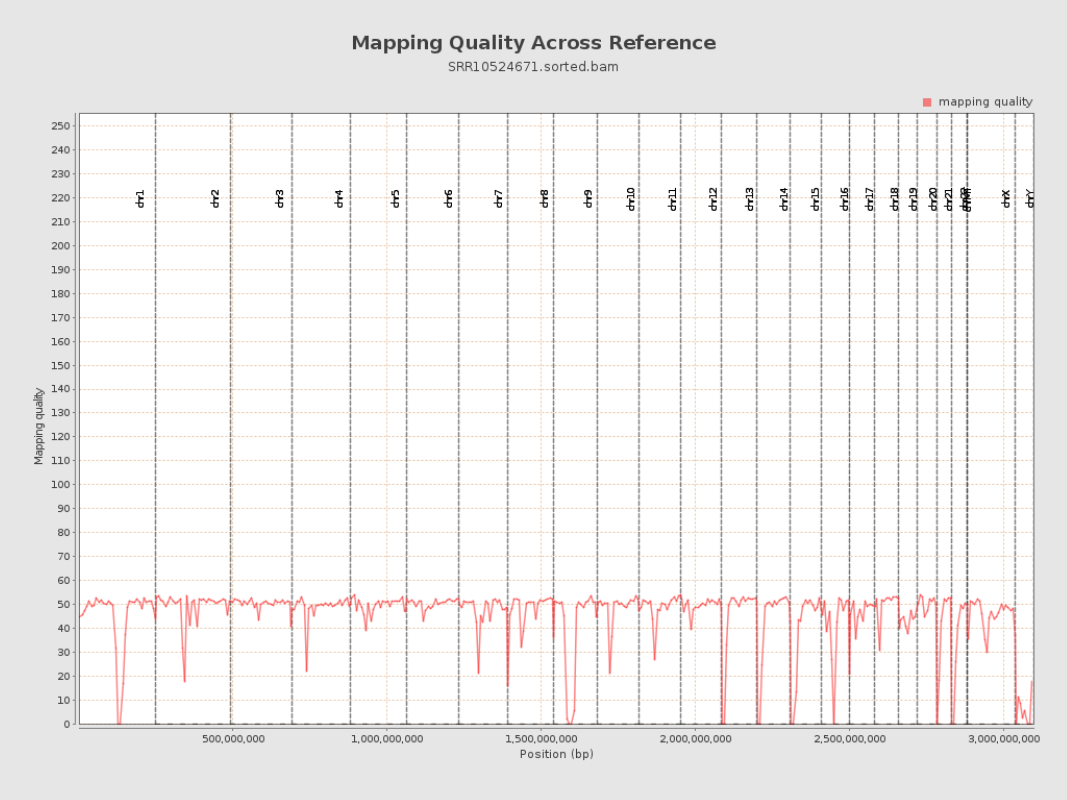
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram