Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:12:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524379.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_SRR10524379 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524379.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:12:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524379.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	681,424
Mapped reads	629,735 / 92.41%
Unmapped reads	51,689 / 7.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,460 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	12,036 / 1.77%
Duplication rate	1.34%
Clipped reads	630,260 / 92.49%

2.2. ACGT Content

Number/percentage of A's	9,612,638 / 25.98%
Number/percentage of C's	7,264,859 / 19.64%
Number/percentage of T's	11,454,389 / 30.96%
Number/percentage of G's	8,662,880 / 23.41%
Number/percentage of N's	4,690 / 0.01%
GC Percentage	43.05%

2.3. Coverage

Mean	0.012

Standard Deviation	0.1458

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

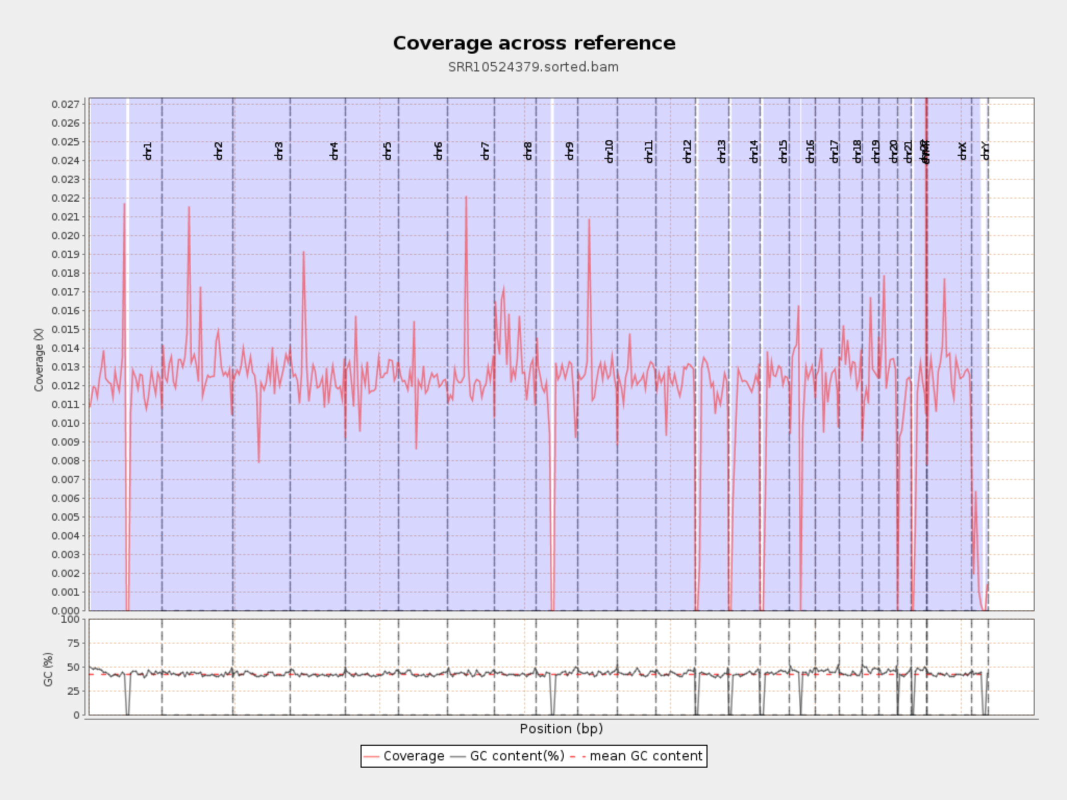
General error rate	0.5%
Mismatches	178,655
Insertions	2,513
Mapped reads with at least one insertion	0.4%
Deletions	6,596
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.97%

2.6. Chromosome stats

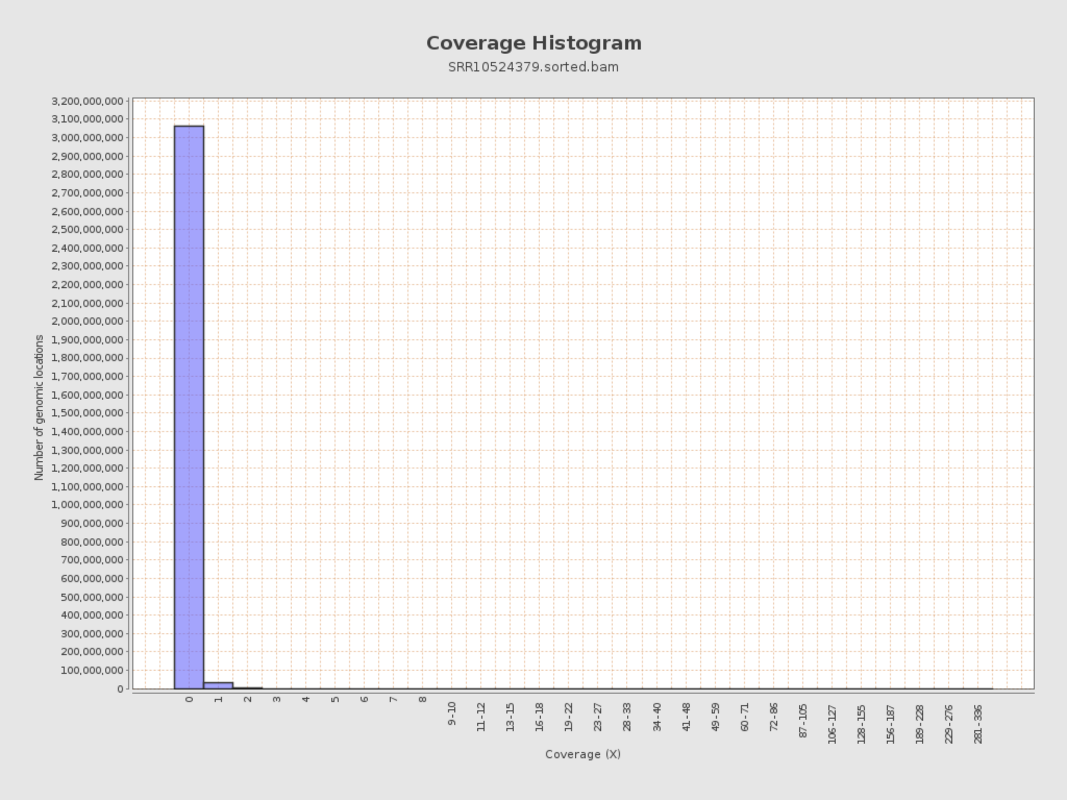
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2902977	0.0116	0.2558
chr2	243199373	3240063	0.0133	0.1583
chr3	198022430	2486631	0.0126	0.1157
chr4	191154276	2387064	0.0125	0.12
chr5	180915260	2256759	0.0125	0.1154
chr6	171115067	2095149	0.0122	0.1205
chr7	159138663	2010204	0.0126	0.1862

chr8	146364022	2008487	0.0137	0.1391
chr9	141213431	1529750	0.0108	0.1262
chr10	135534747	1761099	0.013	0.1372
chr11	135006516	1682584	0.0125	0.1363
chr12	133851895	1641663	0.0123	0.1161
chr13	115169878	1172429	0.0102	0.104
chr14	107349540	1086273	0.0101	0.1079
chr15	102531392	1063130	0.0104	0.1051
chr16	90354753	1064139	0.0118	0.1156
chr17	81195210	980274	0.0121	0.1182
chr18	78077248	1040242	0.0133	0.199
chr19	59128983	743771	0.0126	0.1875
chr20	63025520	846877	0.0134	0.1215
chr21	48129895	478805	0.0099	0.1065
chr22	51304566	432545	0.0084	0.0949
chrMT	16571	9316	0.5622	0.8423
chrX	155270560	1982096	0.0128	0.1231
chrY	59373566	107663	0.0018	0.0588

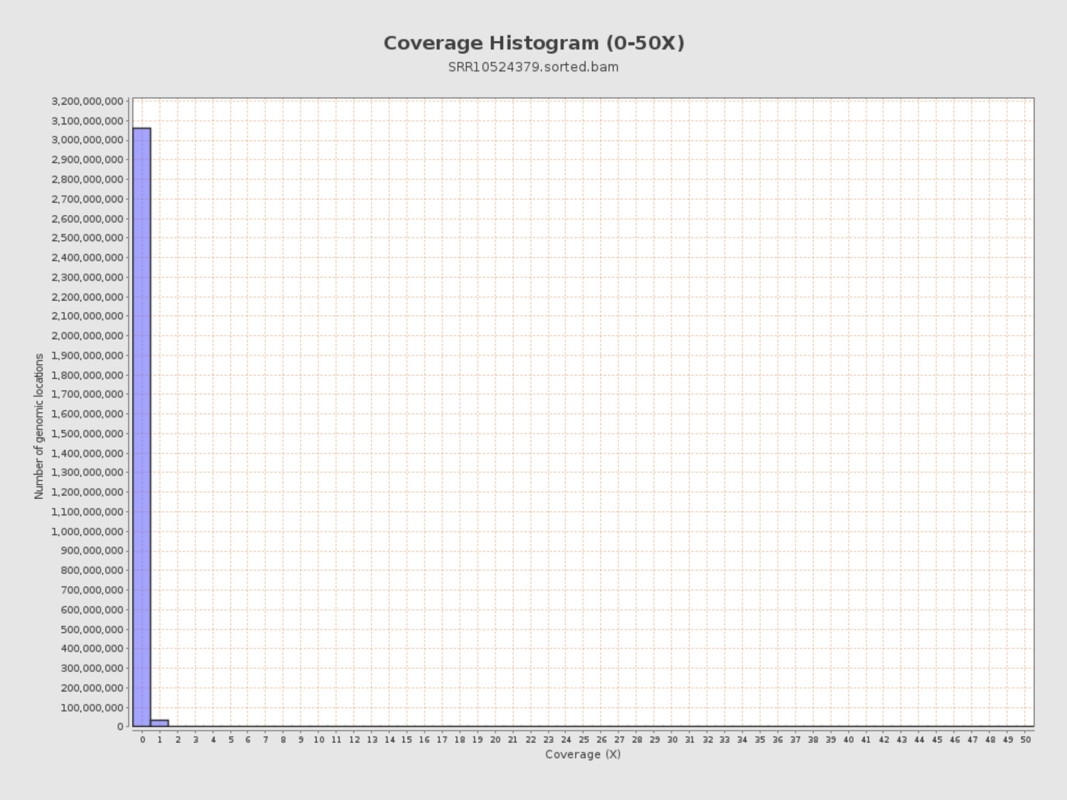
3. Results : Coverage across reference



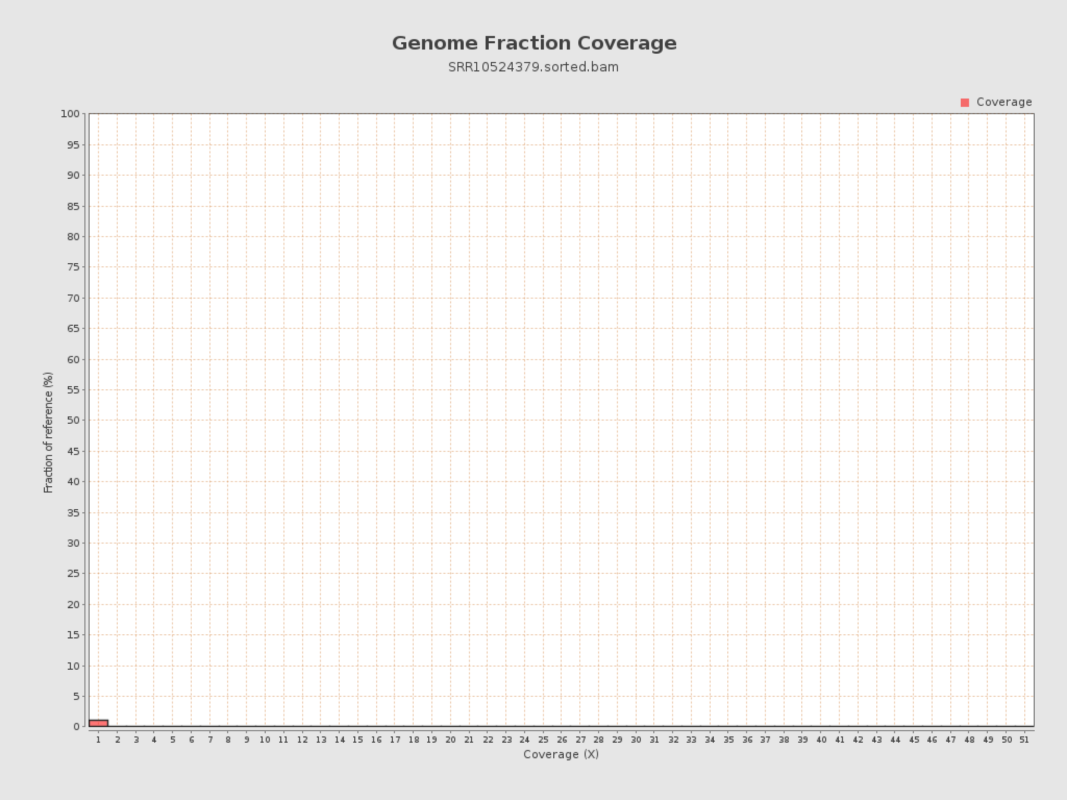
4. Results : Coverage Histogram



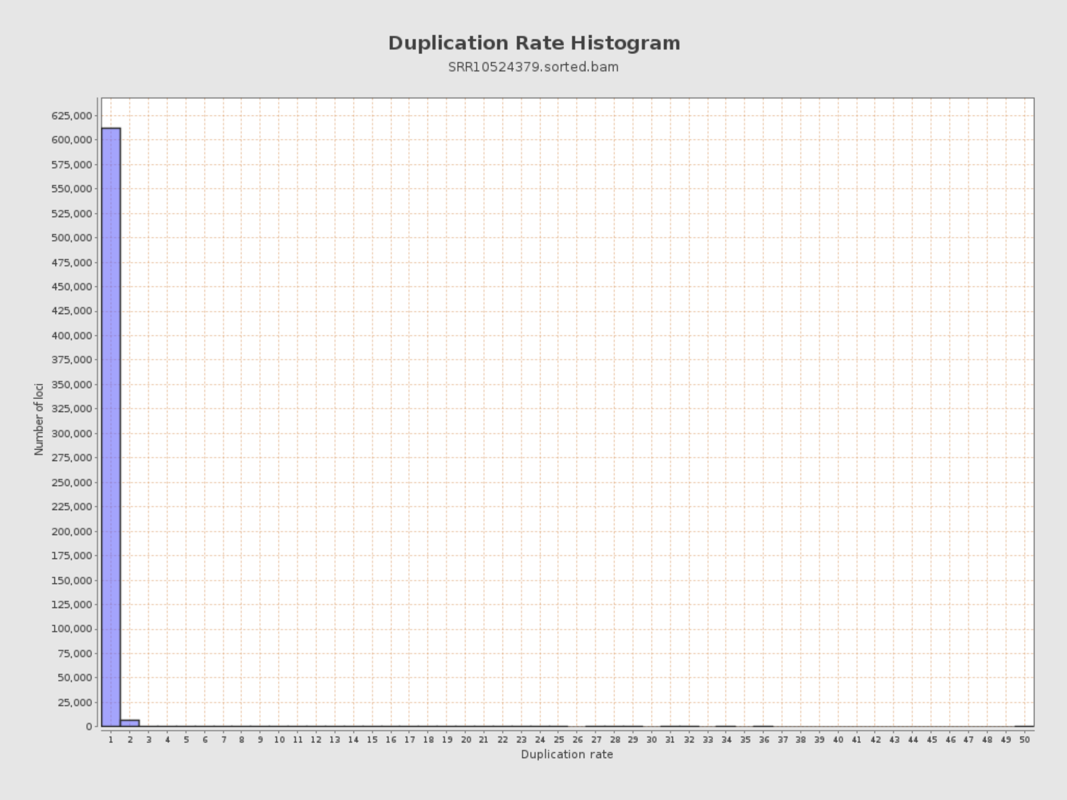
5. Results : Coverage Histogram (0-50X)



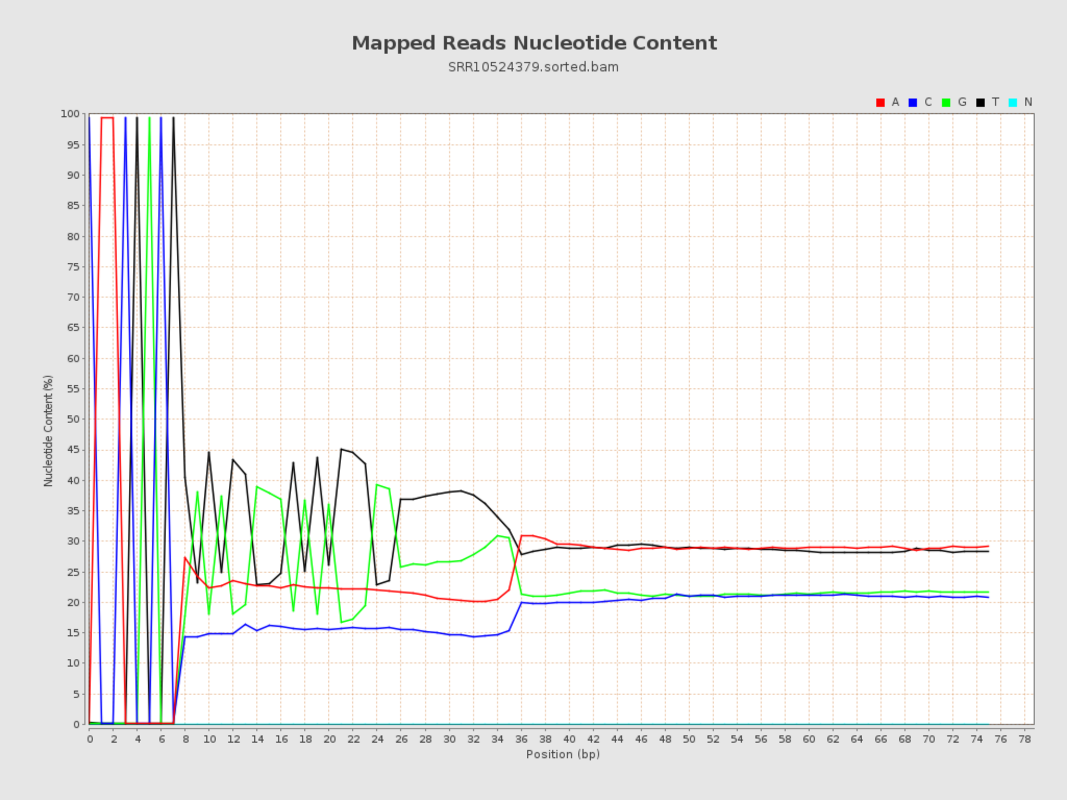
6. Results : Genome Fraction Coverage



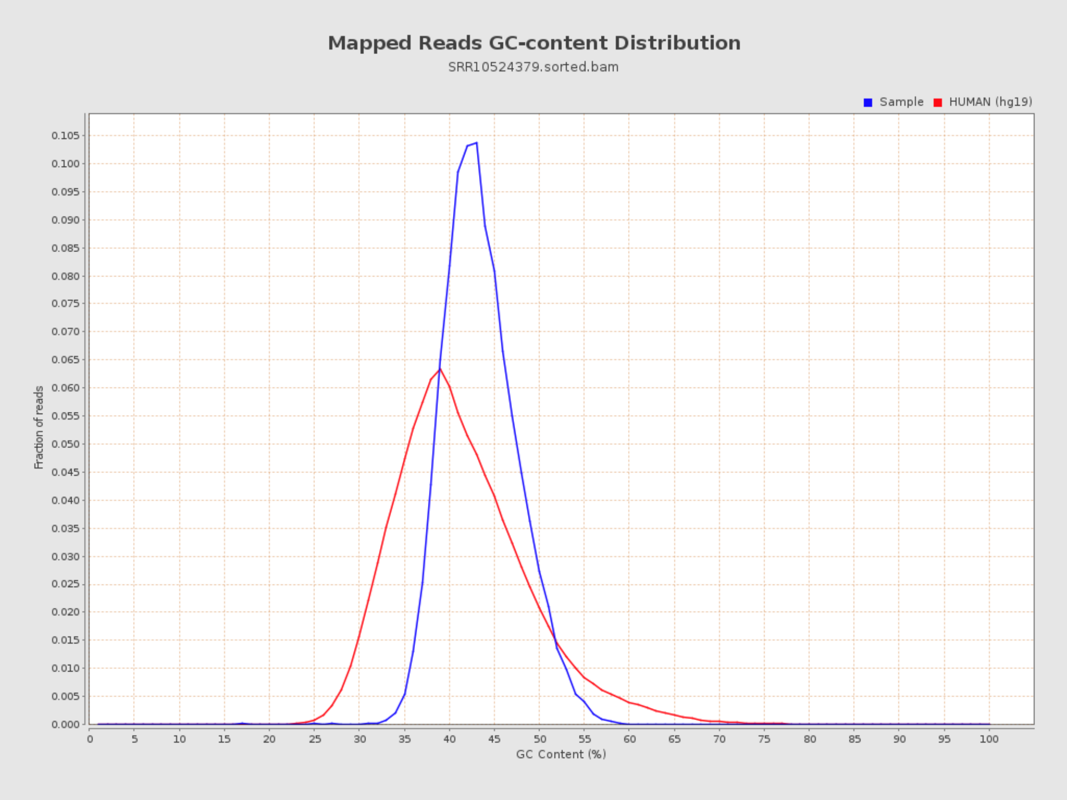
7. Results : Duplication Rate Histogram



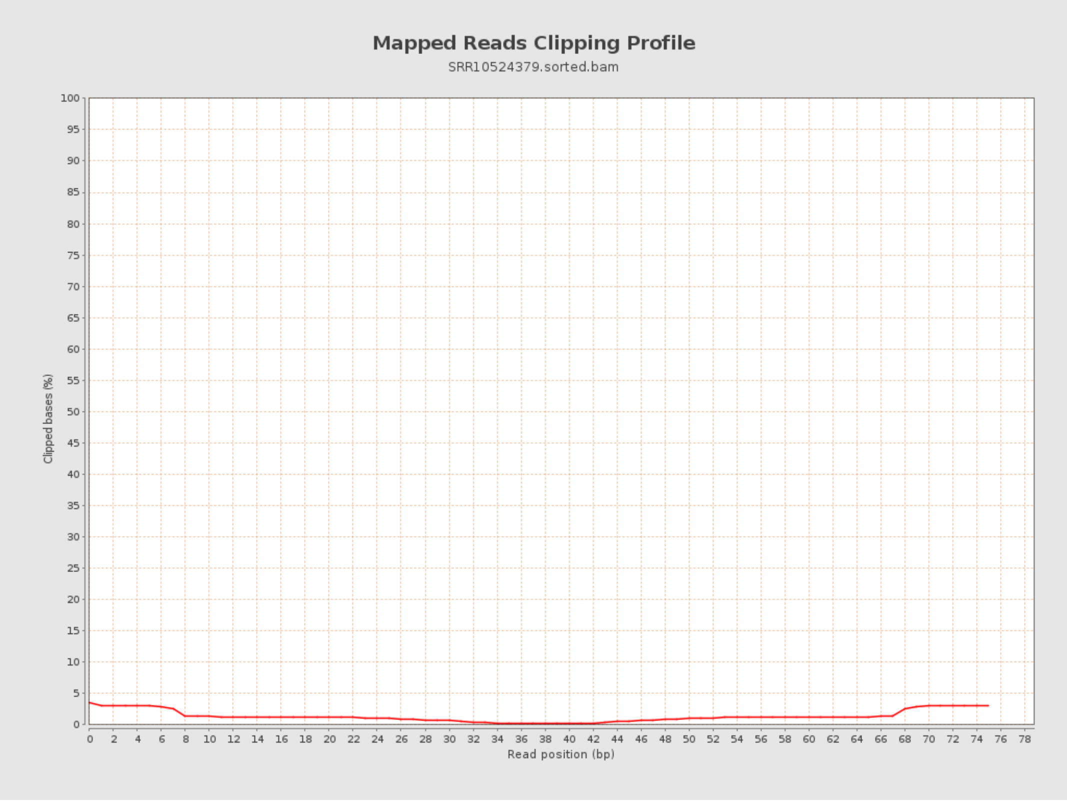
8. Results : Mapped Reads Nucleotide Content



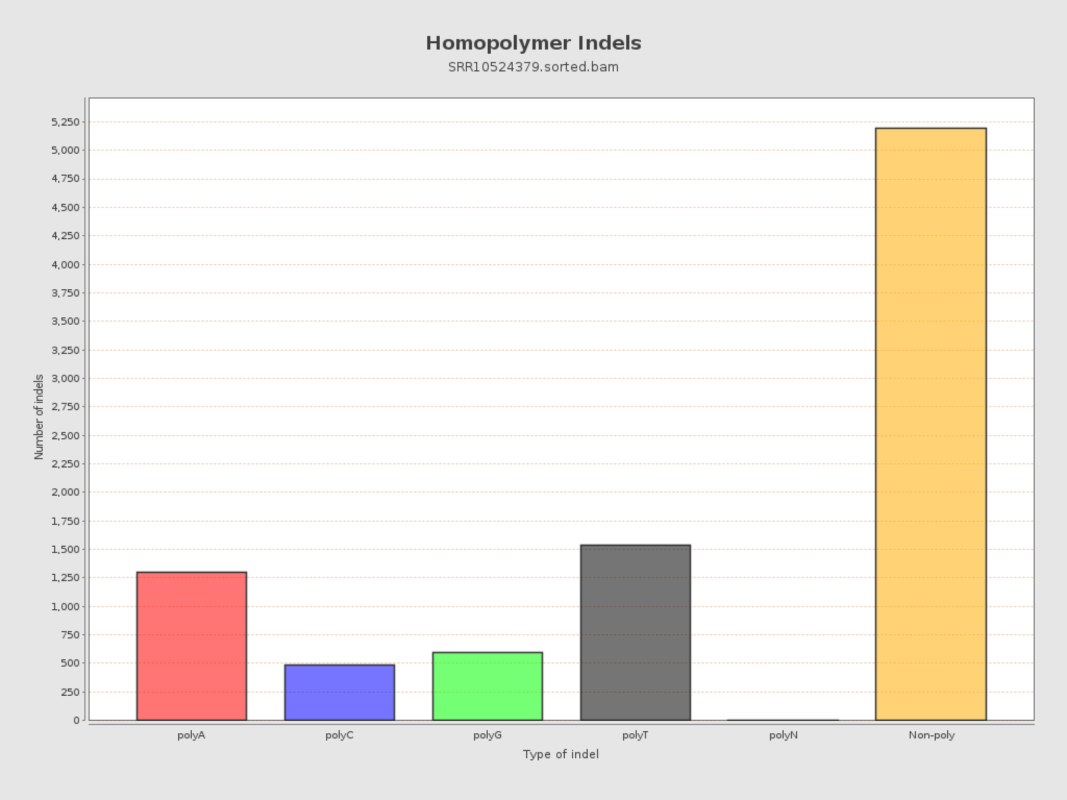
9. Results : Mapped Reads GC-content Distribution



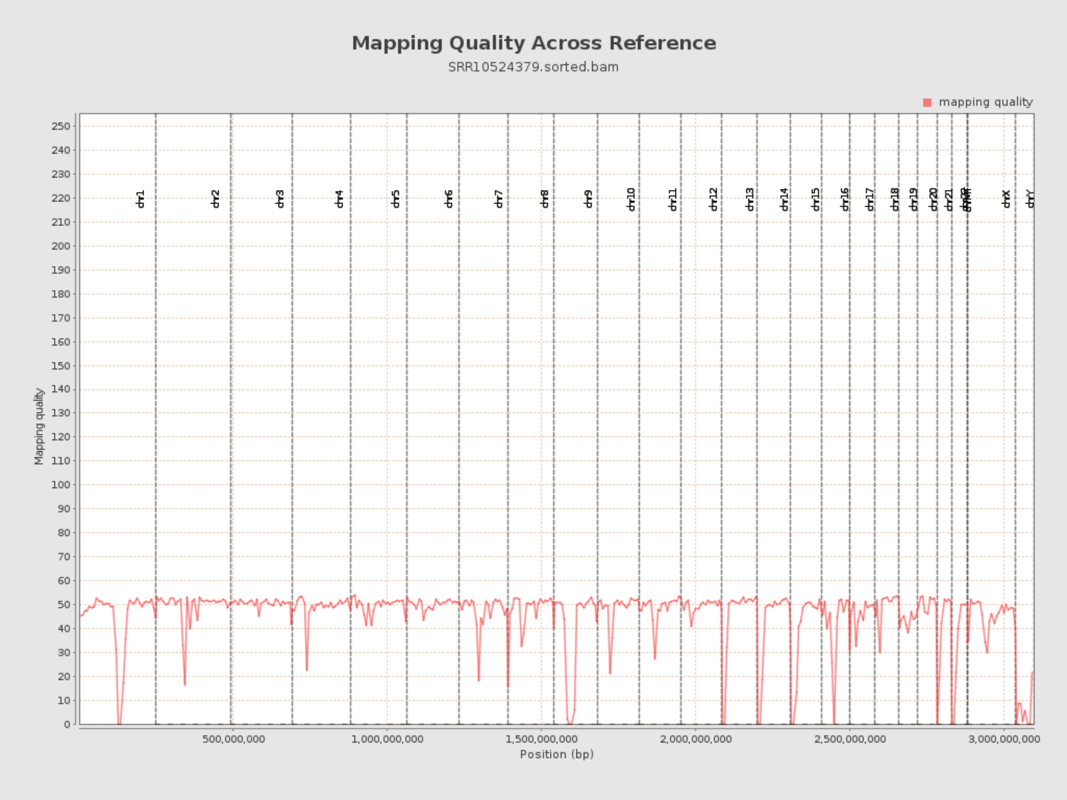
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram