Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:55:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524672.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_SRR10524672 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524672.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:55:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524672.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	975,706
Mapped reads	898,456 / 92.08%
Unmapped reads	77,250 / 7.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,624 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	23,858 / 2.45%
Duplication rate	1.96%
Clipped reads	899,322 / 92.17%

2.2. ACGT Content

Number/percentage of A's	13,708,115 / 25.94%
Number/percentage of C's	10,312,037 / 19.51%
Number/percentage of T's	16,491,207 / 31.2%
Number/percentage of G's	12,331,916 / 23.33%
Number/percentage of N's	7,354 / 0.01%
GC Percentage	42.85%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.1801

2.4. Mapping Quality

Mean Mapping Quality	45.54

2.5. Mismatches and indels

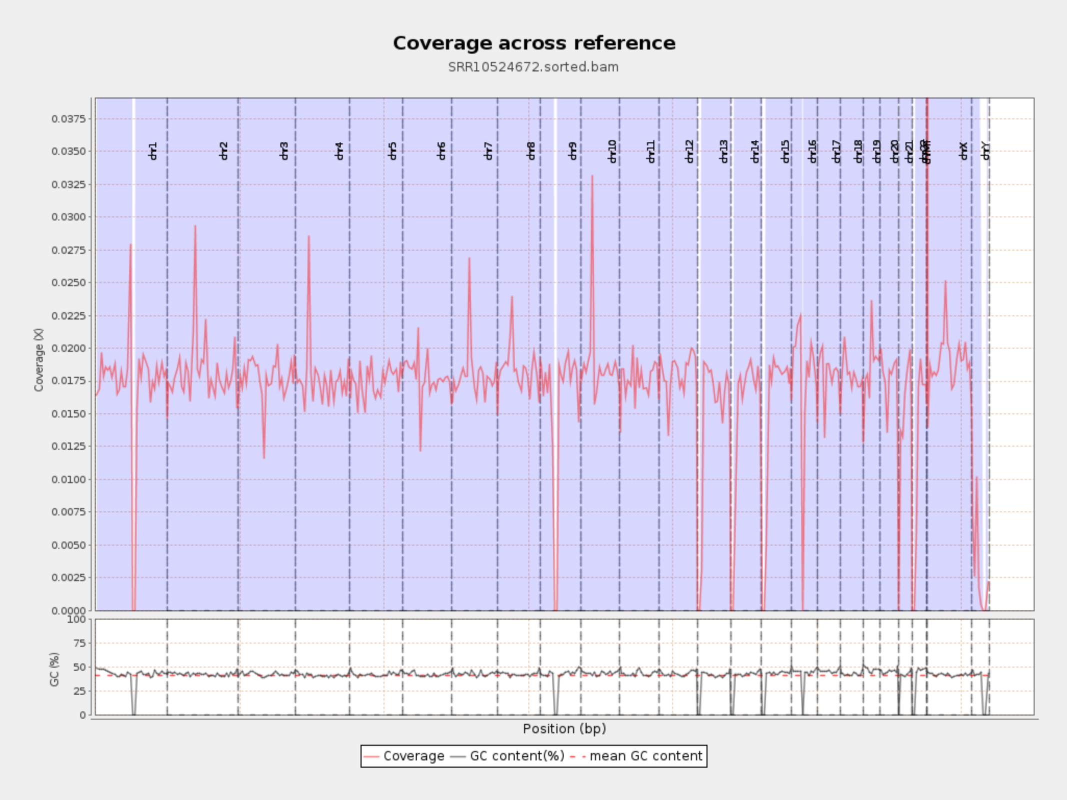
General error rate	0.52%
Mismatches	265,338
Insertions	4,298
Mapped reads with at least one insertion	0.48%
Deletions	9,949
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.05%

2.6. Chromosome stats

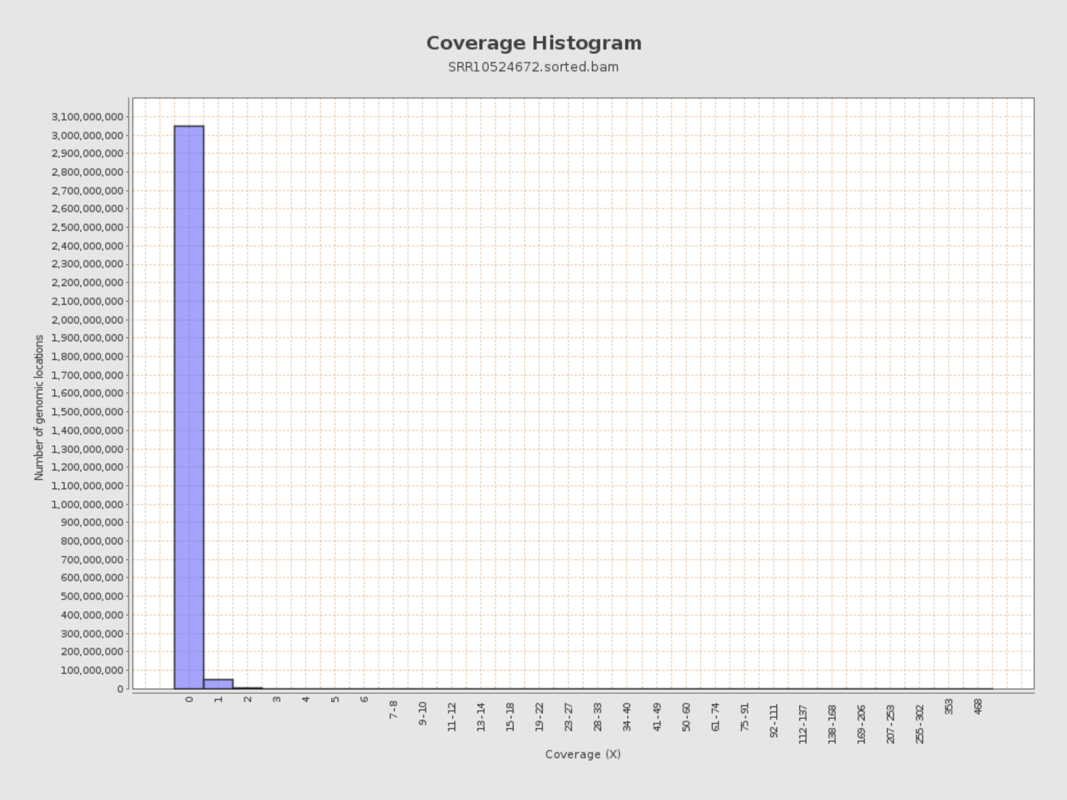
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4245442	0.017	0.2699
chr2	243199373	4456045	0.0183	0.2482
chr3	198022430	3505396	0.0177	0.14
chr4	191154276	3392168	0.0177	0.1509
chr5	180915260	3178475	0.0176	0.1394
chr6	171115067	3041356	0.0178	0.1514
chr7	159138663	2877623	0.0181	0.2056

chr8	146364022	2703696	0.0185	0.1967
chr9	141213431	2213894	0.0157	0.16
chr10	135534747	2571761	0.019	0.1892
chr11	135006516	2390771	0.0177	0.1603
chr12	133851895	2421534	0.0181	0.1423
chr13	115169878	1654814	0.0144	0.1264
chr14	107349540	1566412	0.0146	0.13
chr15	102531392	1509989	0.0147	0.1291
chr16	90354753	1579896	0.0175	0.1458
chr17	81195210	1462351	0.018	0.1455
chr18	78077248	1402464	0.018	0.2613
chr19	59128983	1107237	0.0187	0.2252
chr20	63025520	1111006	0.0176	0.1428
chr21	48129895	709509	0.0147	0.1407
chr22	51304566	623791	0.0122	0.1157
chrMT	16571	12300	0.7423	0.9608
chrX	155270560	2958059	0.0191	0.1527
chrY	59373566	170410	0.0029	0.1

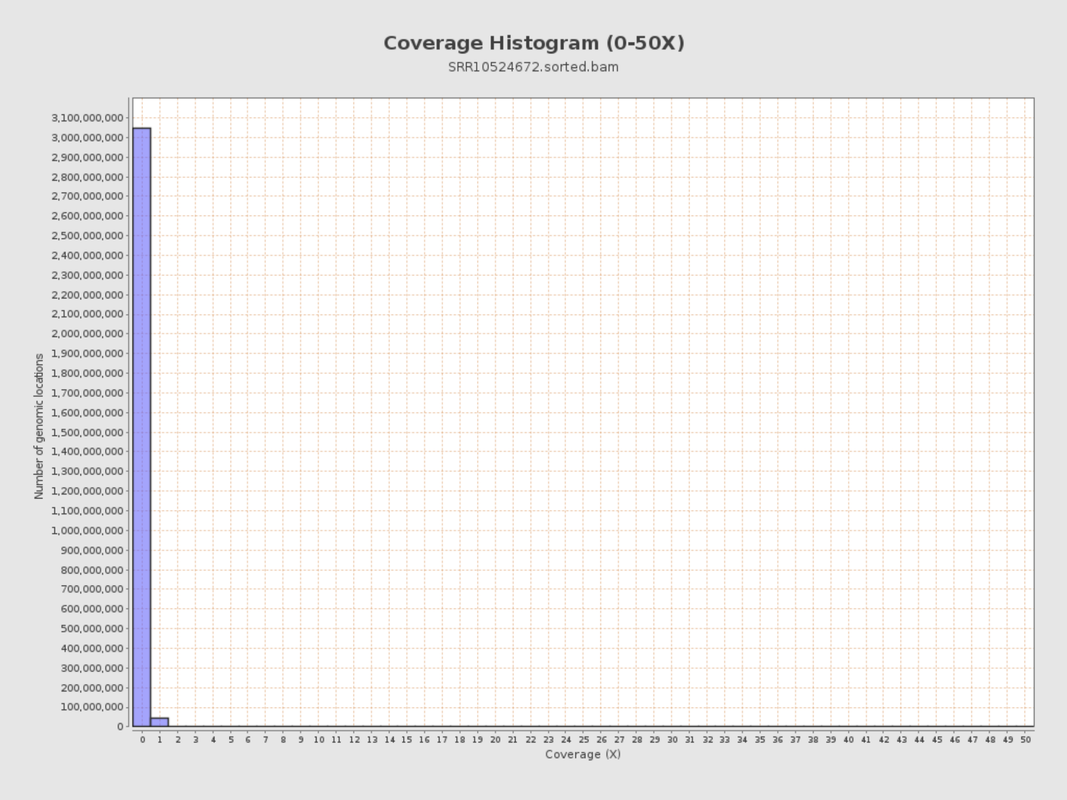
3. Results : Coverage across reference



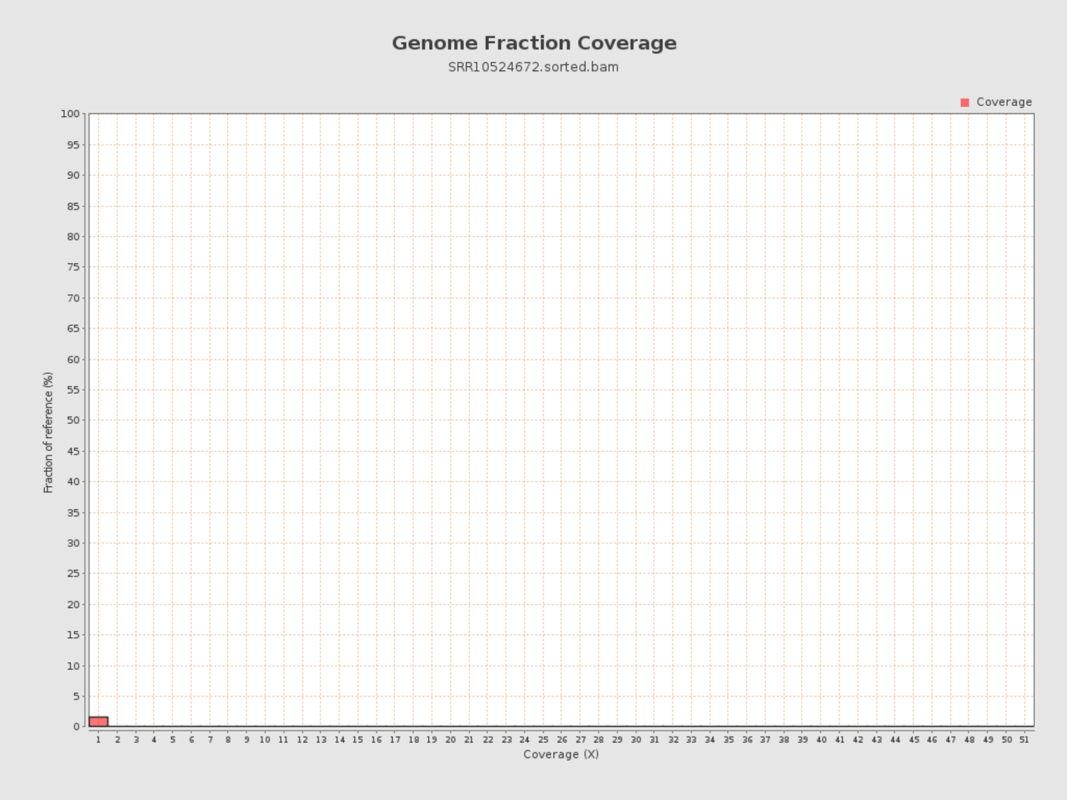
4. Results : Coverage Histogram



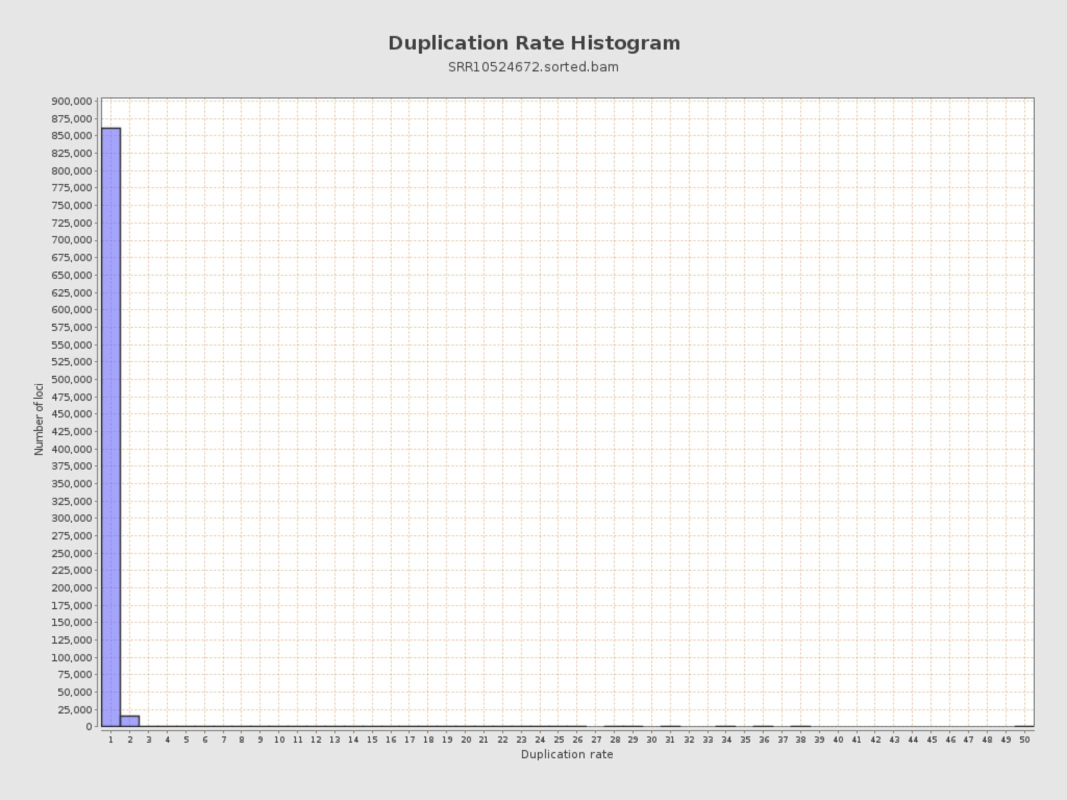
5. Results : Coverage Histogram (0-50X)



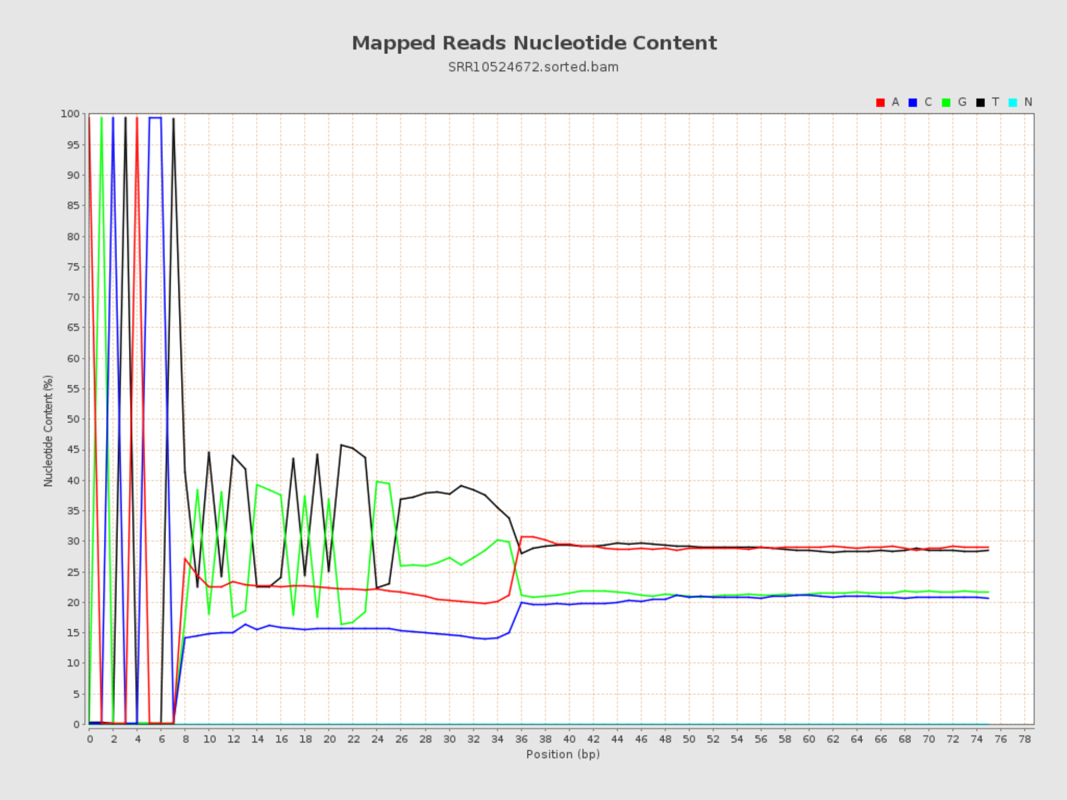
6. Results : Genome Fraction Coverage



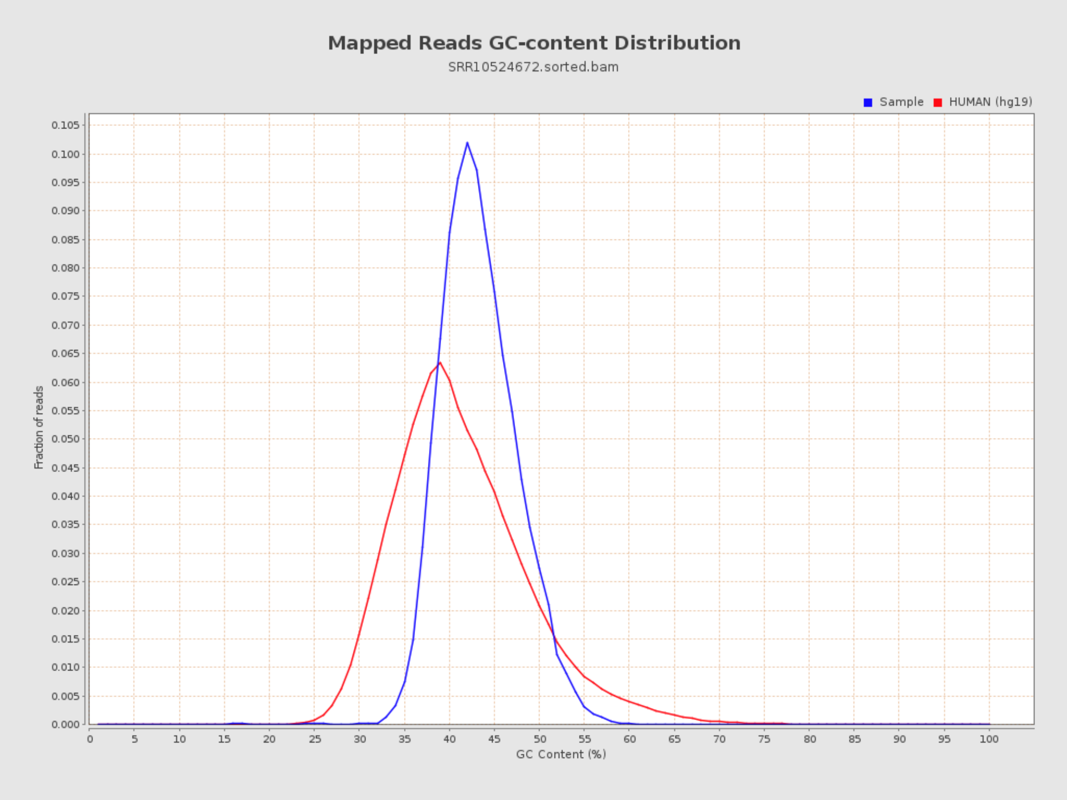
7. Results : Duplication Rate Histogram



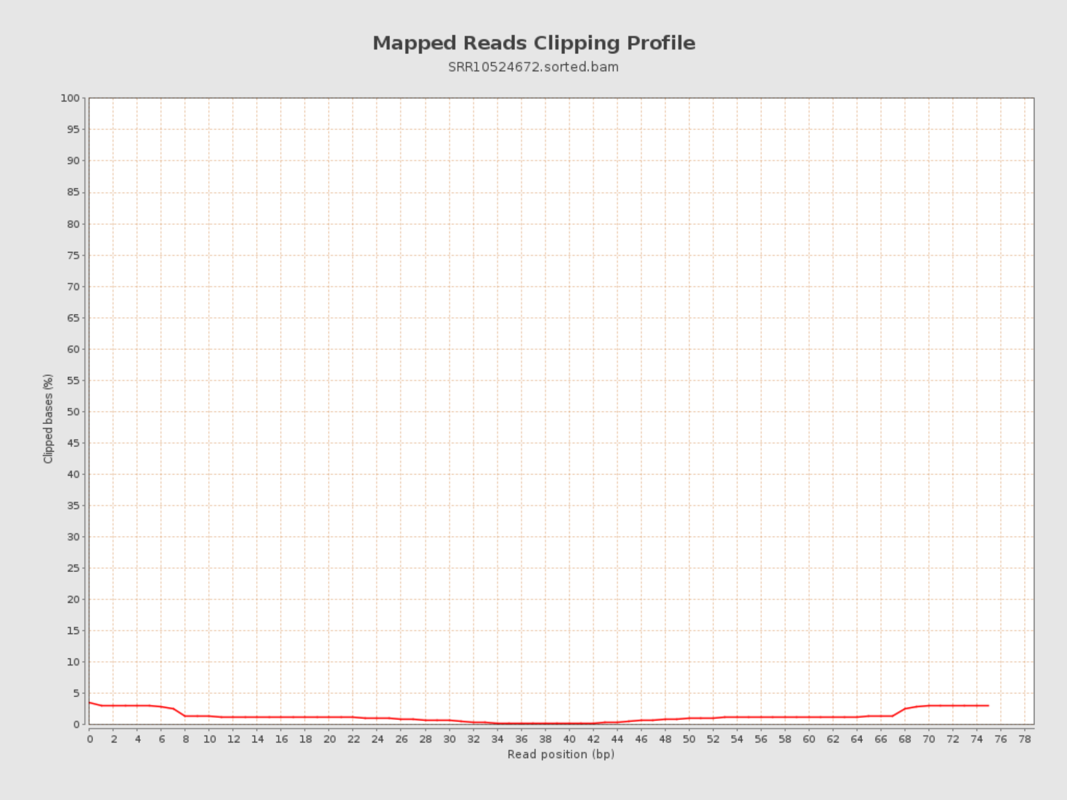
8. Results : Mapped Reads Nucleotide Content



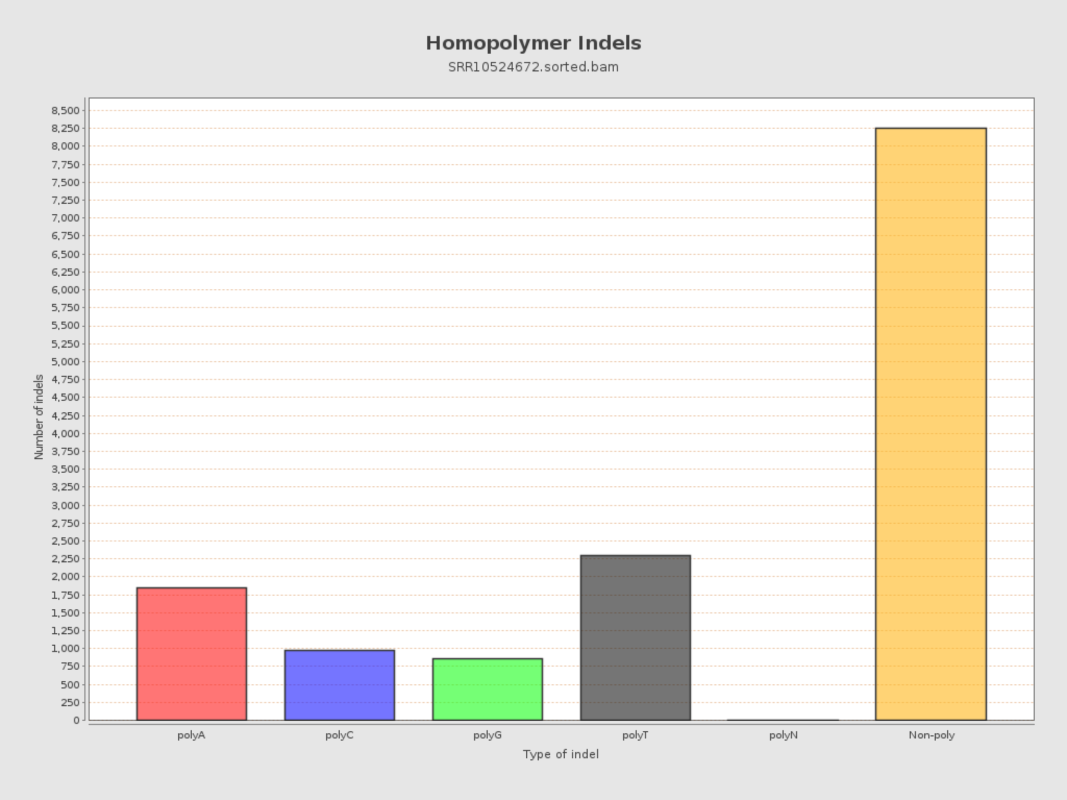
9. Results : Mapped Reads GC-content Distribution



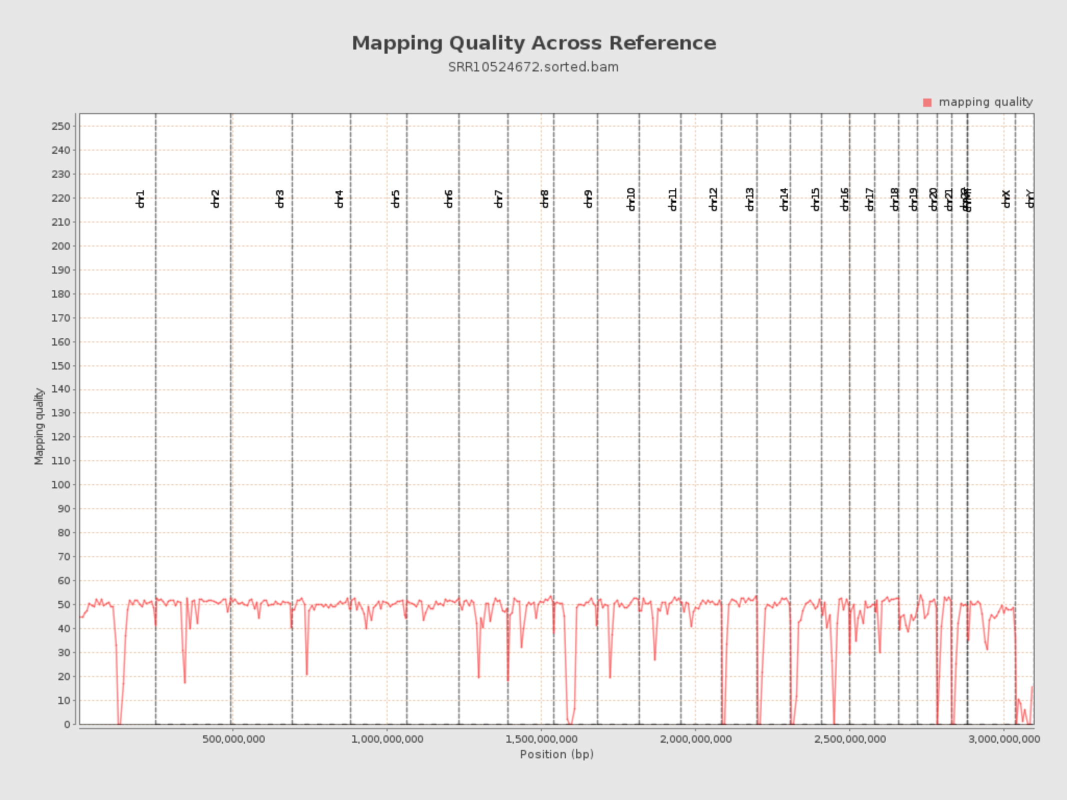
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram