Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:50:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524649.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_SRR10524649 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524649.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:50:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524649.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	832,521
Mapped reads	769,495 / 92.43%
Unmapped reads	63,026 / 7.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,008 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	25,662 / 3.08%
Duplication rate	2.62%
Clipped reads	771,649 / 92.69%

2.2. ACGT Content

Number/percentage of A's	10,967,888 / 24.5%
Number/percentage of C's	8,385,163 / 18.73%
Number/percentage of T's	14,432,801 / 32.24%
Number/percentage of G's	10,981,291 / 24.53%
Number/percentage of N's	386 / 0%
GC Percentage	43.26%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1612

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

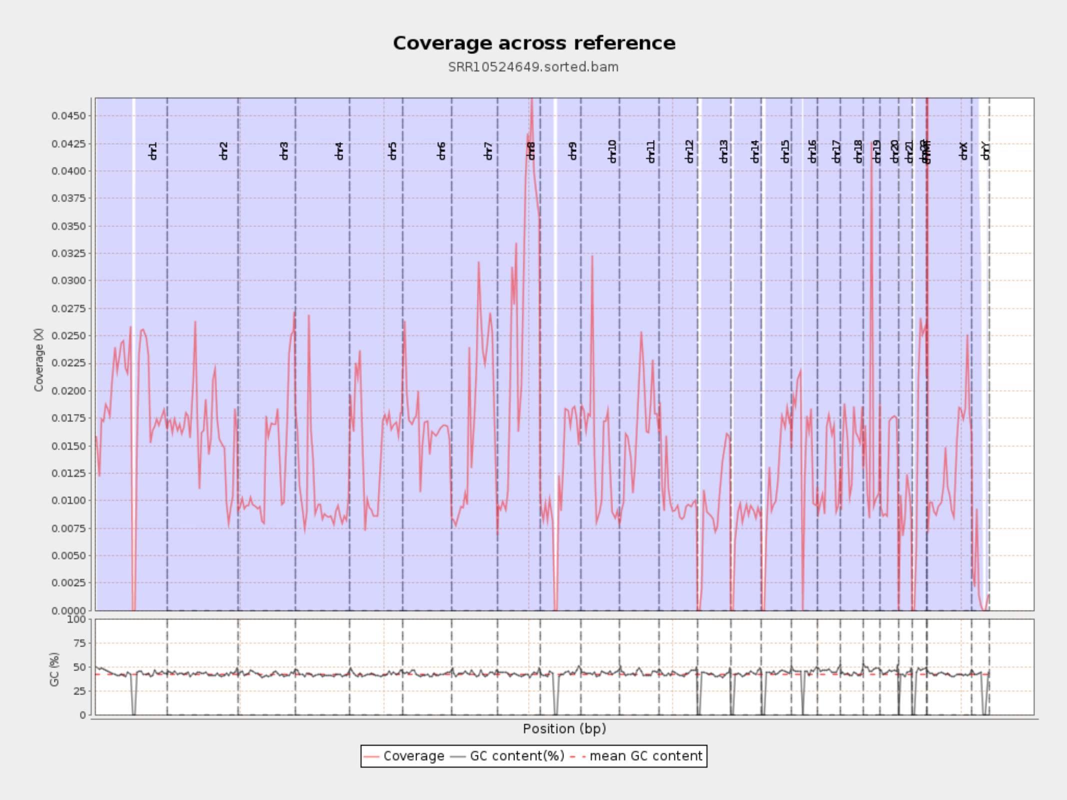
General error rate	0.51%
Mismatches	223,937
Insertions	2,603
Mapped reads with at least one insertion	0.34%
Deletions	8,617
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.84%

2.6. Chromosome stats

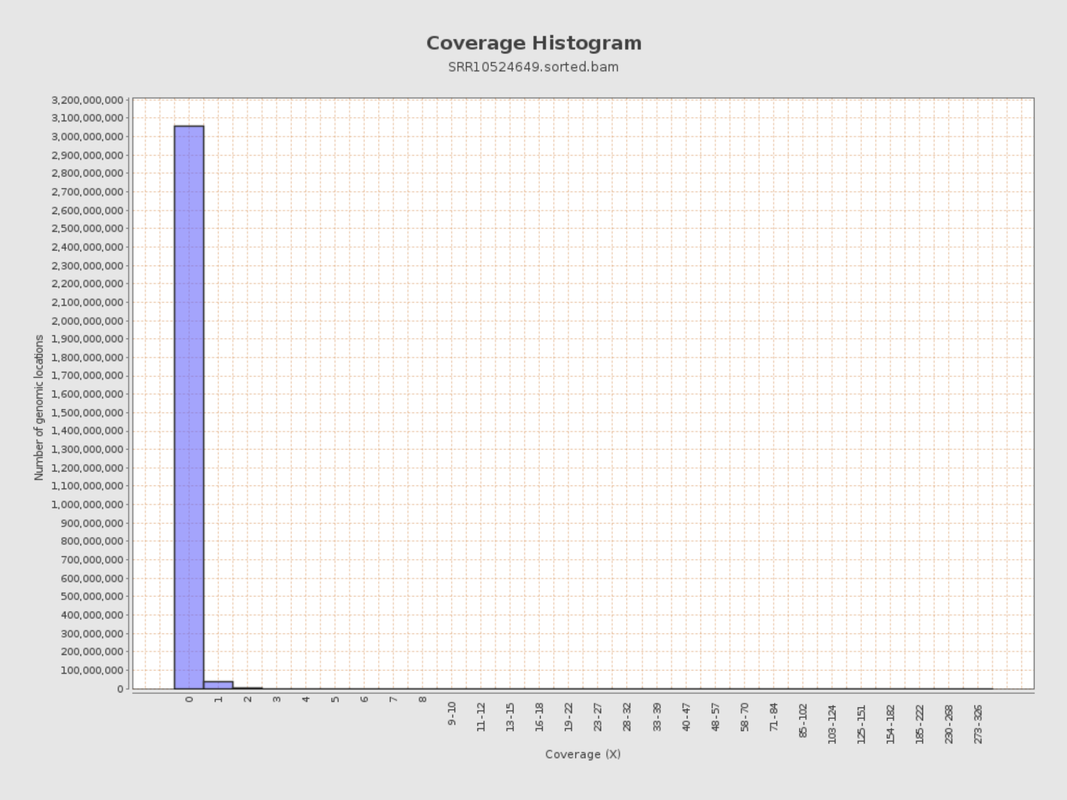
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4655713	0.0187	0.2648
chr2	243199373	3960119	0.0163	0.1909
chr3	198022430	2696747	0.0136	0.1253
chr4	191154276	2050286	0.0107	0.1299
chr5	180915260	2750384	0.0152	0.1311
chr6	171115067	2906065	0.017	0.143
chr7	159138663	2749369	0.0173	0.1956

chr8	146364022	3923890	0.0268	0.2094
chr9	141213431	1658328	0.0117	0.1316
chr10	135534747	1992896	0.0147	0.18
chr11	135006516	2235591	0.0166	0.1492
chr12	133851895	1388514	0.0104	0.11
chr13	115169878	1064178	0.0092	0.1021
chr14	107349540	828108	0.0077	0.0957
chr15	102531392	1174541	0.0115	0.1144
chr16	90354753	1352006	0.015	0.1345
chr17	81195210	1011045	0.0125	0.1213
chr18	78077248	1178130	0.0151	0.1975
chr19	59128983	918454	0.0155	0.1862
chr20	63025520	840624	0.0133	0.1245
chr21	48129895	412785	0.0086	0.1138
chr22	51304566	852803	0.0166	0.137
chrMT	16571	6262	0.3779	0.6758
chrX	155270560	2042639	0.0132	0.1296
chrY	59373566	132707	0.0022	0.0912

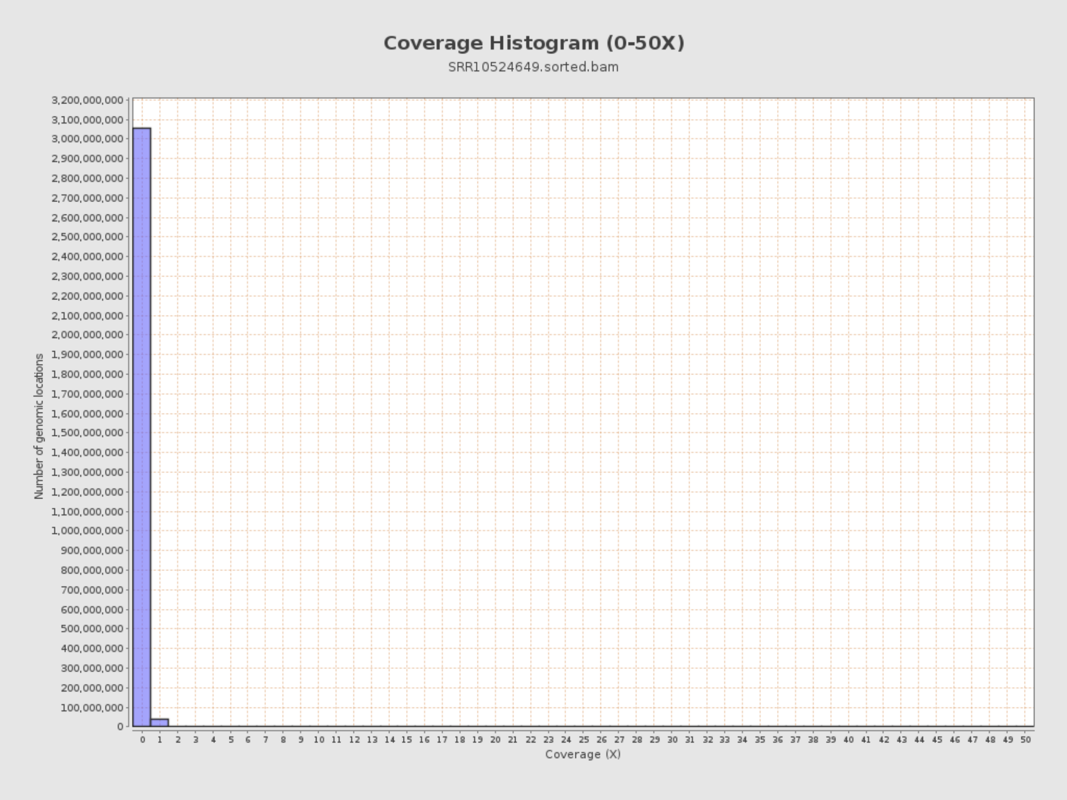
3. Results : Coverage across reference



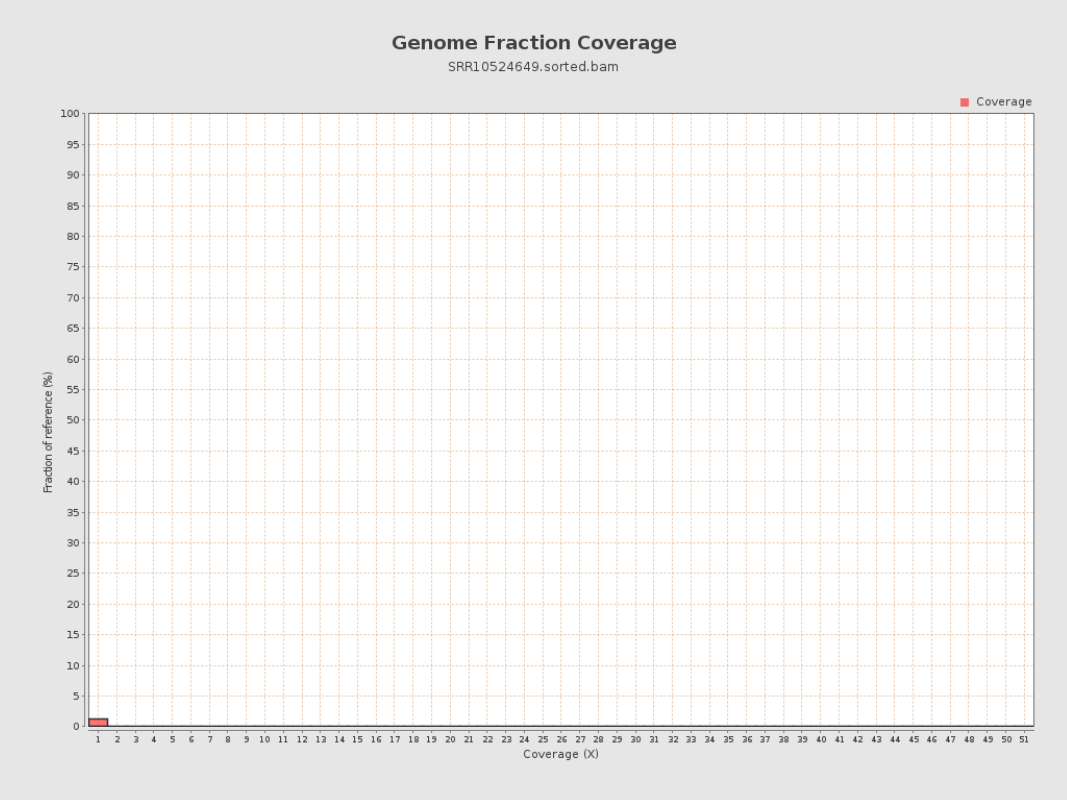
4. Results : Coverage Histogram



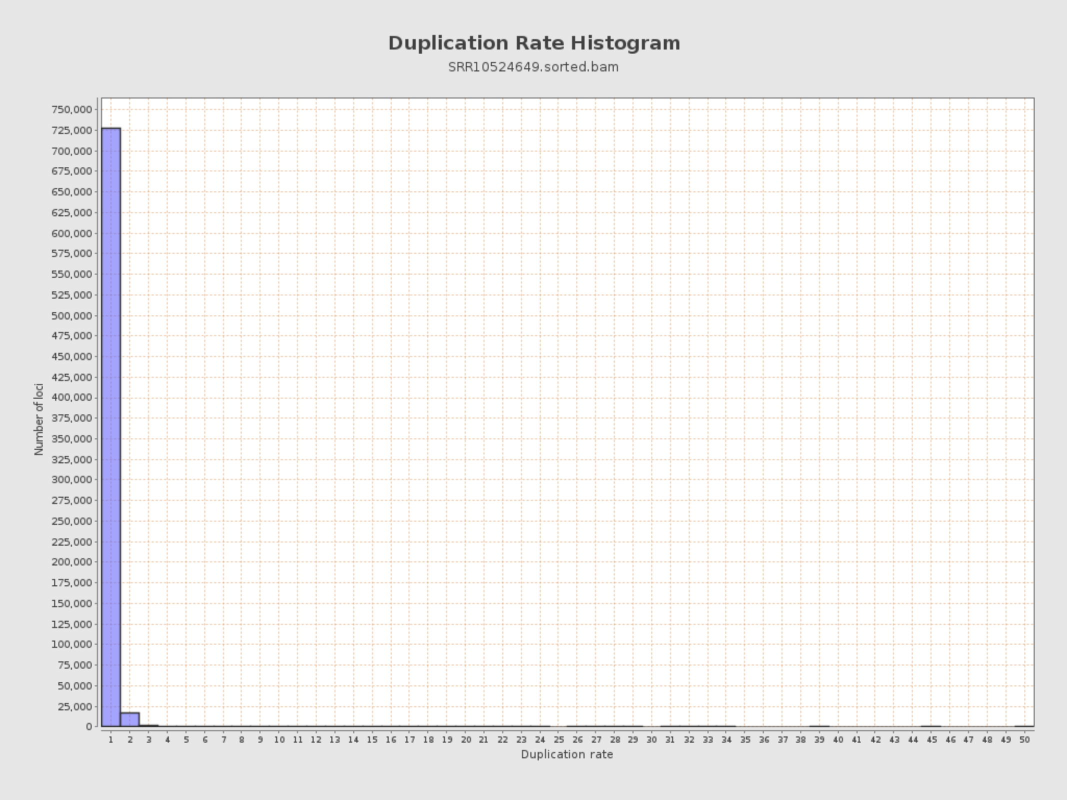
5. Results : Coverage Histogram (0-50X)



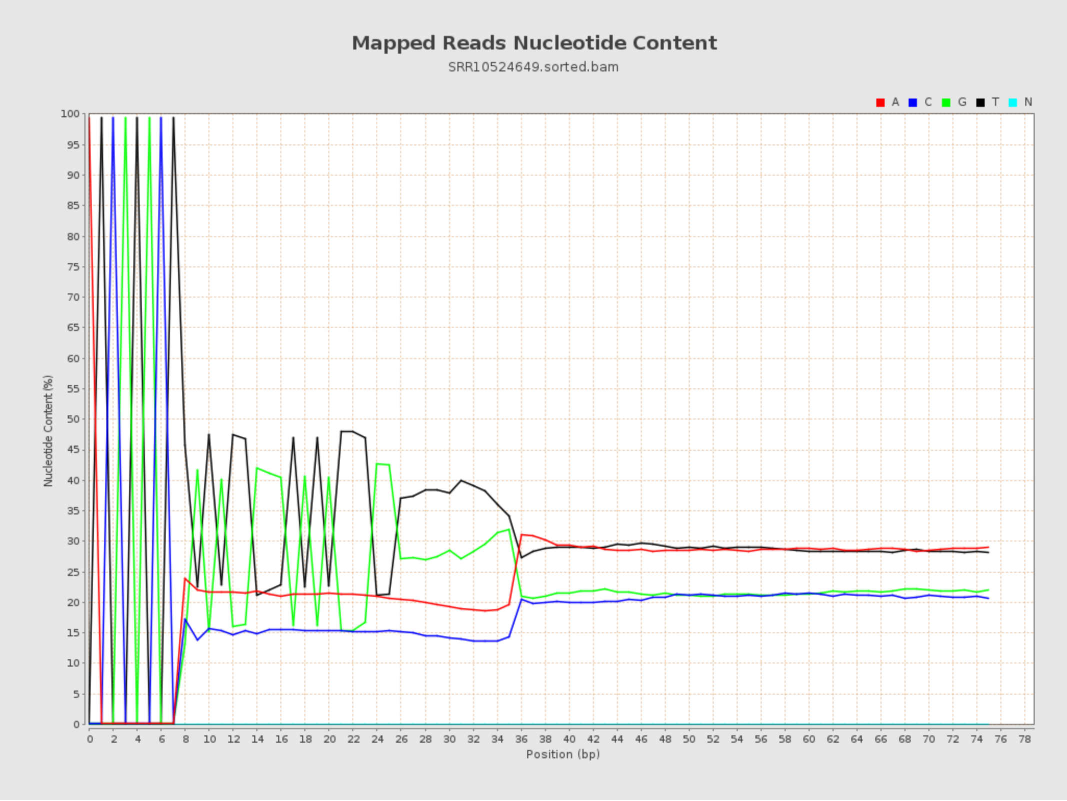
6. Results : Genome Fraction Coverage



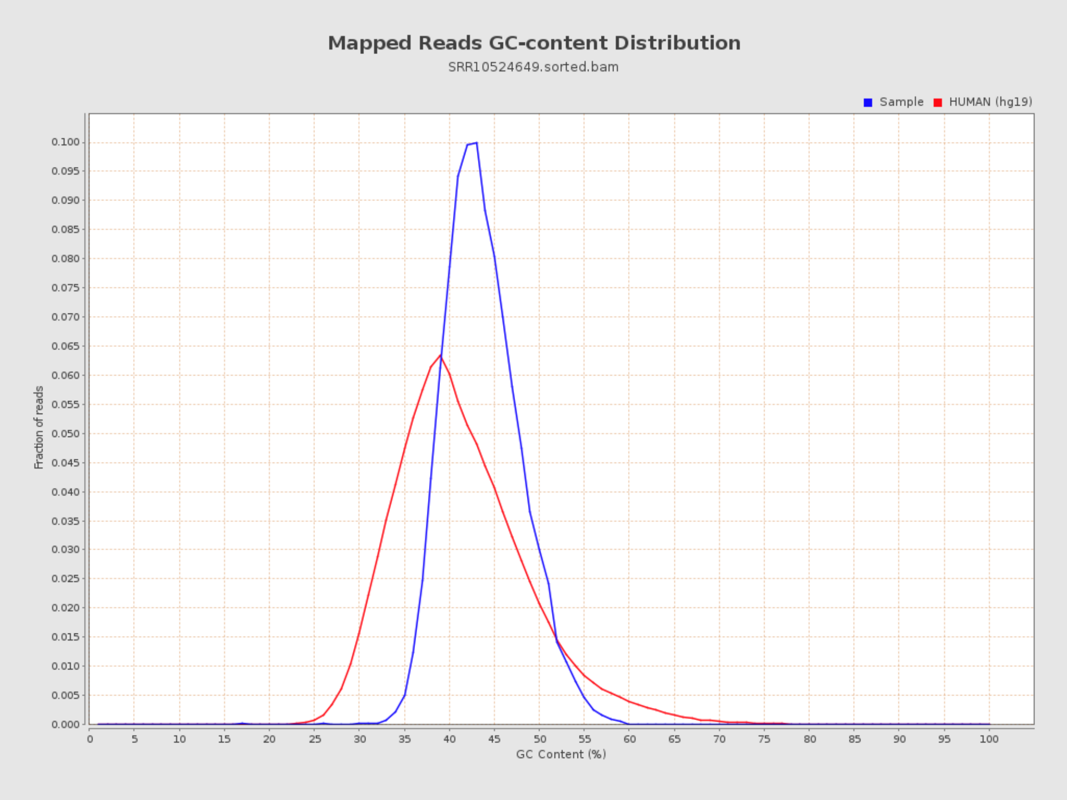
7. Results : Duplication Rate Histogram



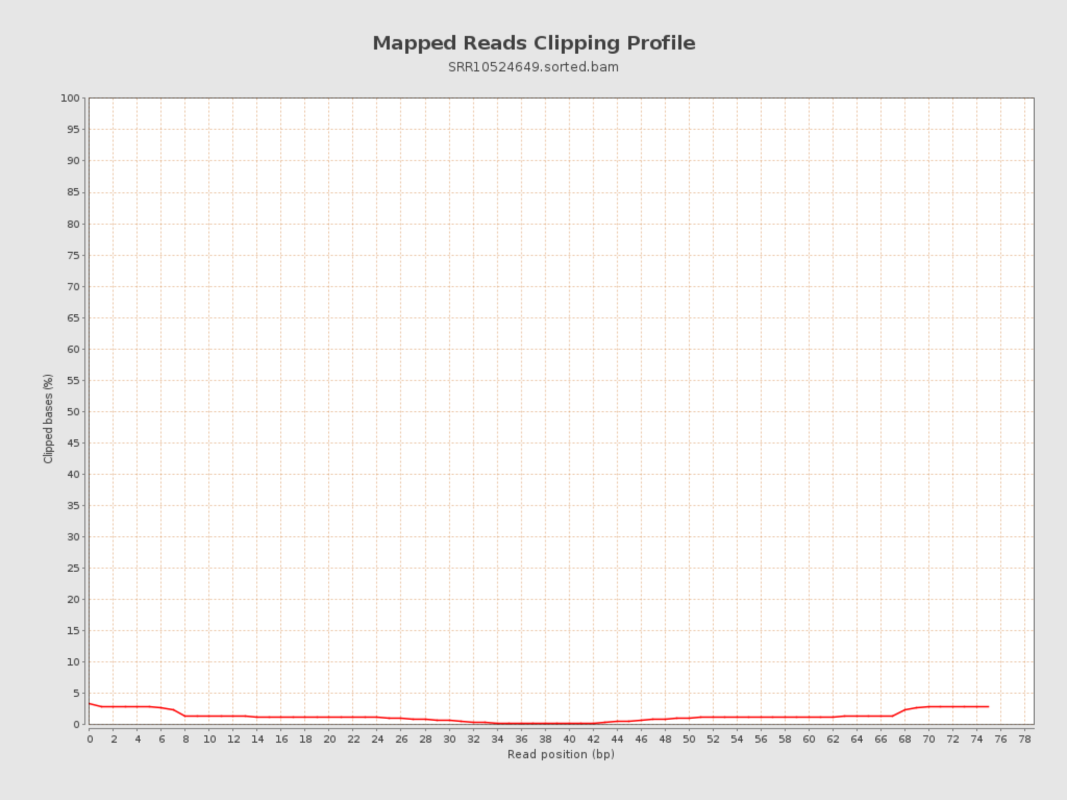
8. Results : Mapped Reads Nucleotide Content



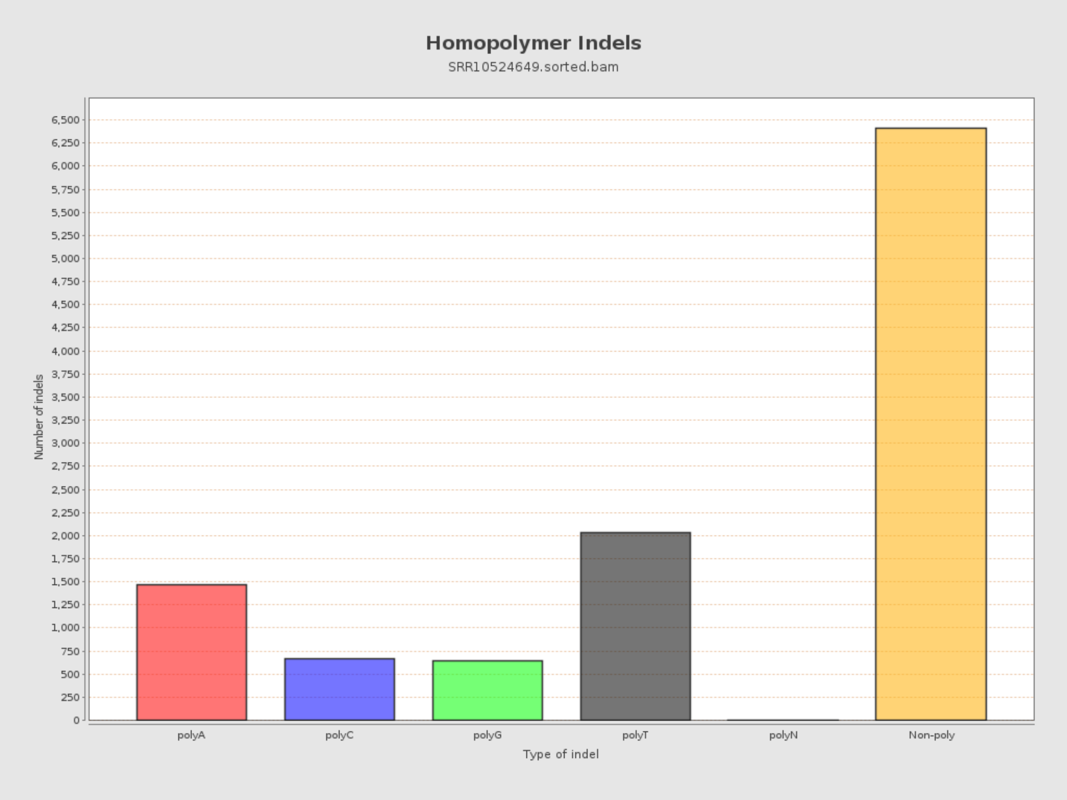
9. Results : Mapped Reads GC-content Distribution



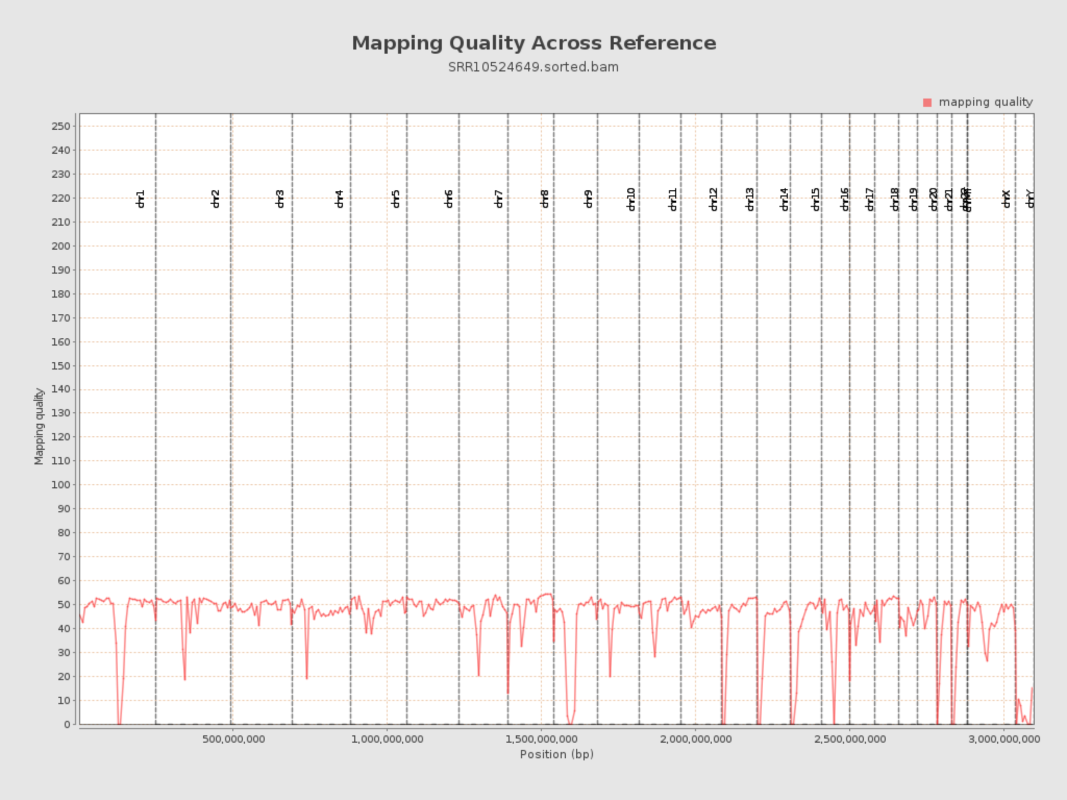
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram