Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:36:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524999.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_SRR10524999 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524999.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:36:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524999.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,434,634
Mapped reads	1,304,140 / 90.9%
Unmapped reads	130,494 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,093 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	40,187 / 2.8%
Duplication rate	2.22%
Clipped reads	1,304,380 / 90.92%

2.2. ACGT Content

Number/percentage of A's	18,917,920 / 25.2%
Number/percentage of C's	13,874,854 / 18.48%
Number/percentage of T's	24,274,227 / 32.34%
Number/percentage of G's	17,996,130 / 23.97%
Number/percentage of N's	715 / 0%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2349

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

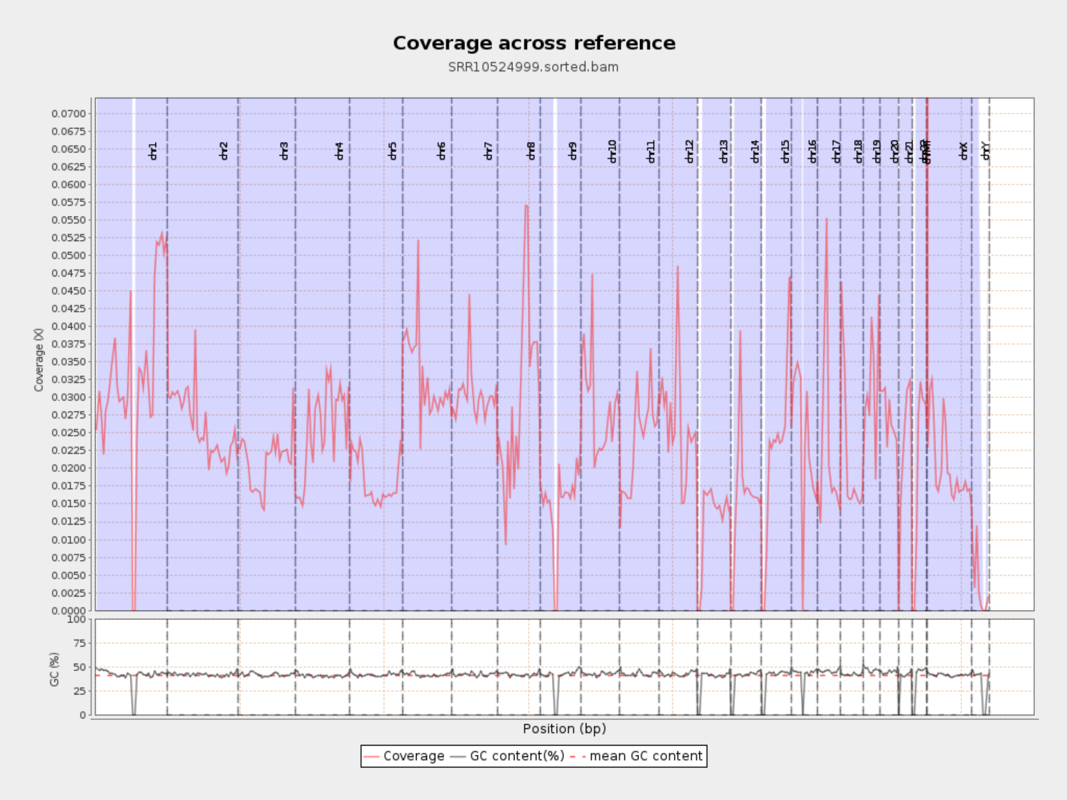
General error rate	0.52%
Mismatches	375,926
Insertions	5,647
Mapped reads with at least one insertion	0.43%
Deletions	14,802
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.96%

2.6. Chromosome stats

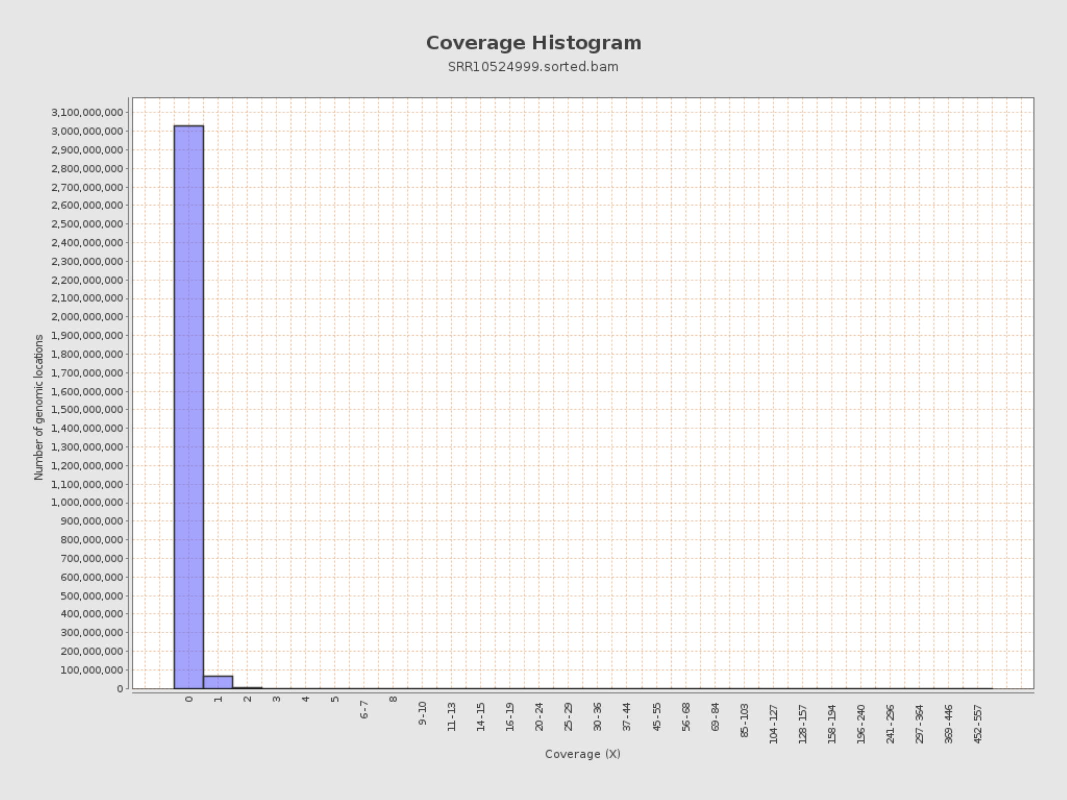
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8168486	0.0328	0.44
chr2	243199373	6304841	0.0259	0.2711
chr3	198022430	4185032	0.0211	0.1565
chr4	191154276	4892407	0.0256	0.1827
chr5	180915260	3317827	0.0183	0.1473
chr6	171115067	5646942	0.033	0.2629
chr7	159138663	4836136	0.0304	0.3042

chr8	146364022	4462880	0.0305	0.2296
chr9	141213431	2106772	0.0149	0.1701
chr10	135534747	3910165	0.0288	0.2335
chr11	135006516	3242612	0.024	0.2069
chr12	133851895	3538146	0.0264	0.1759
chr13	115169878	1473897	0.0128	0.1217
chr14	107349540	1735308	0.0162	0.1397
chr15	102531392	2325845	0.0227	0.1672
chr16	90354753	2156705	0.0239	0.1725
chr17	81195210	1901436	0.0234	0.204
chr18	78077248	1703594	0.0218	0.2922
chr19	59128983	1877221	0.0317	0.2711
chr20	63025520	1705605	0.0271	0.1778
chr21	48129895	1112909	0.0231	0.1685
chr22	51304566	1045760	0.0204	0.1519
chrMT	16571	29448	1.7771	1.6466
chrX	155270560	3203106	0.0206	0.1741
chrY	59373566	204874	0.0035	0.1039

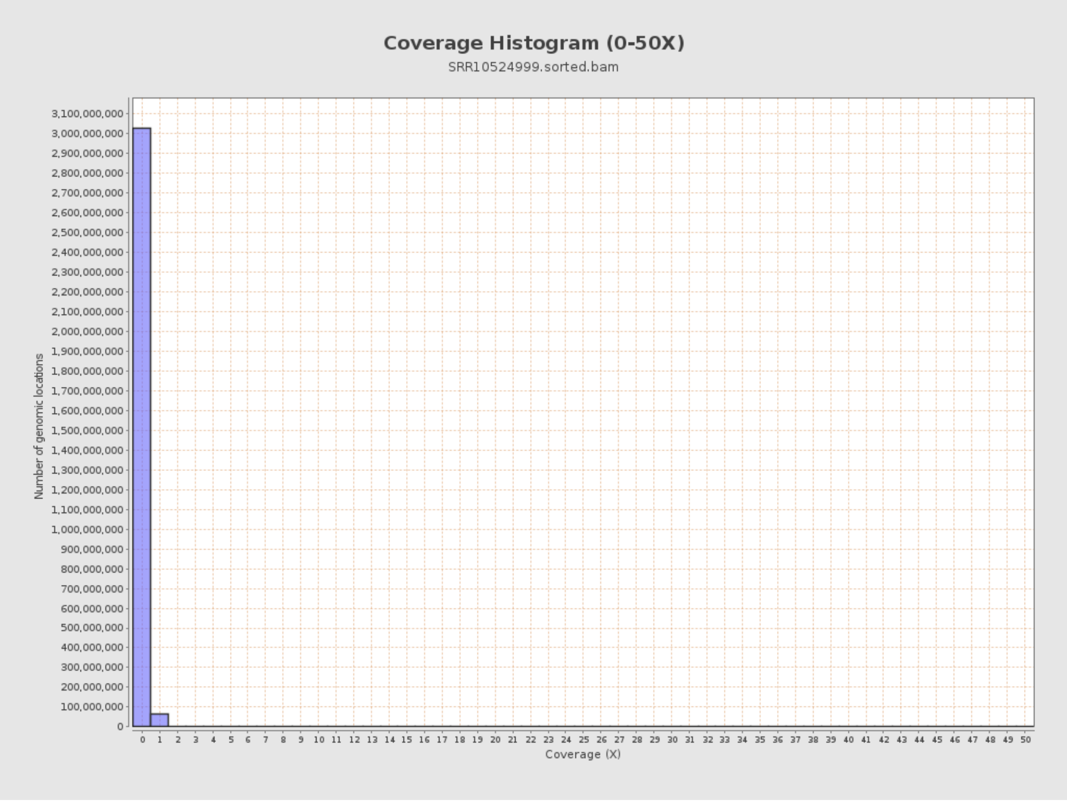
3. Results : Coverage across reference



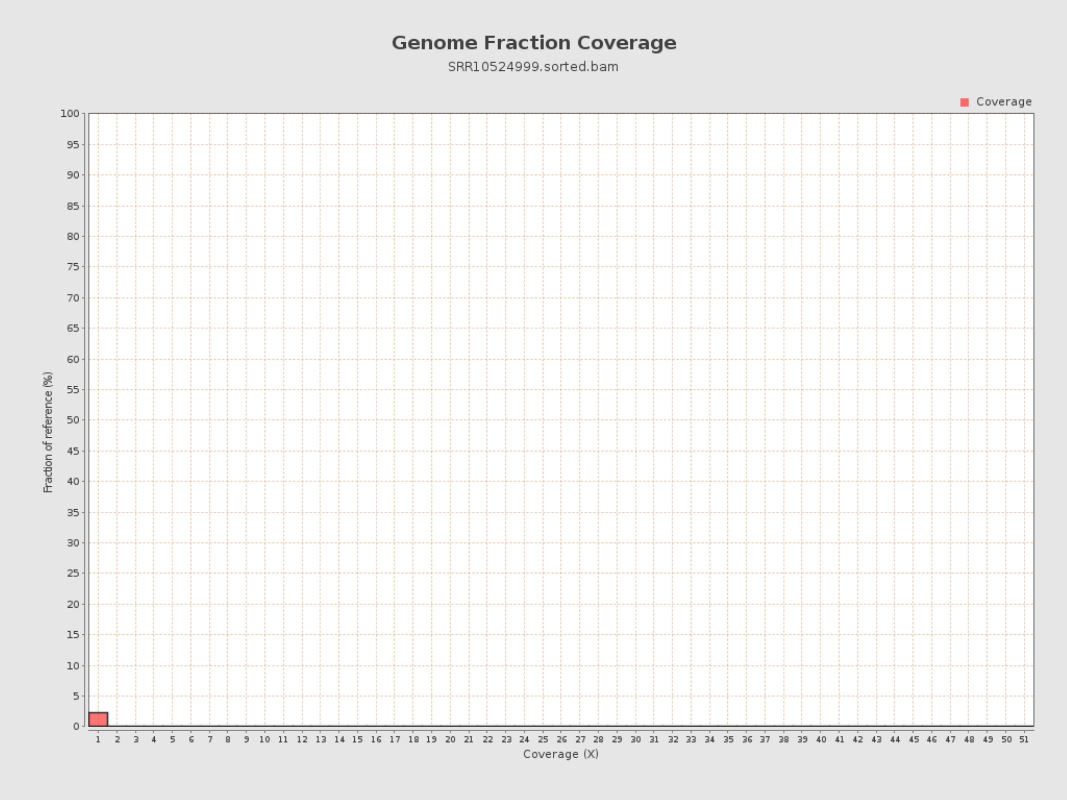
4. Results : Coverage Histogram



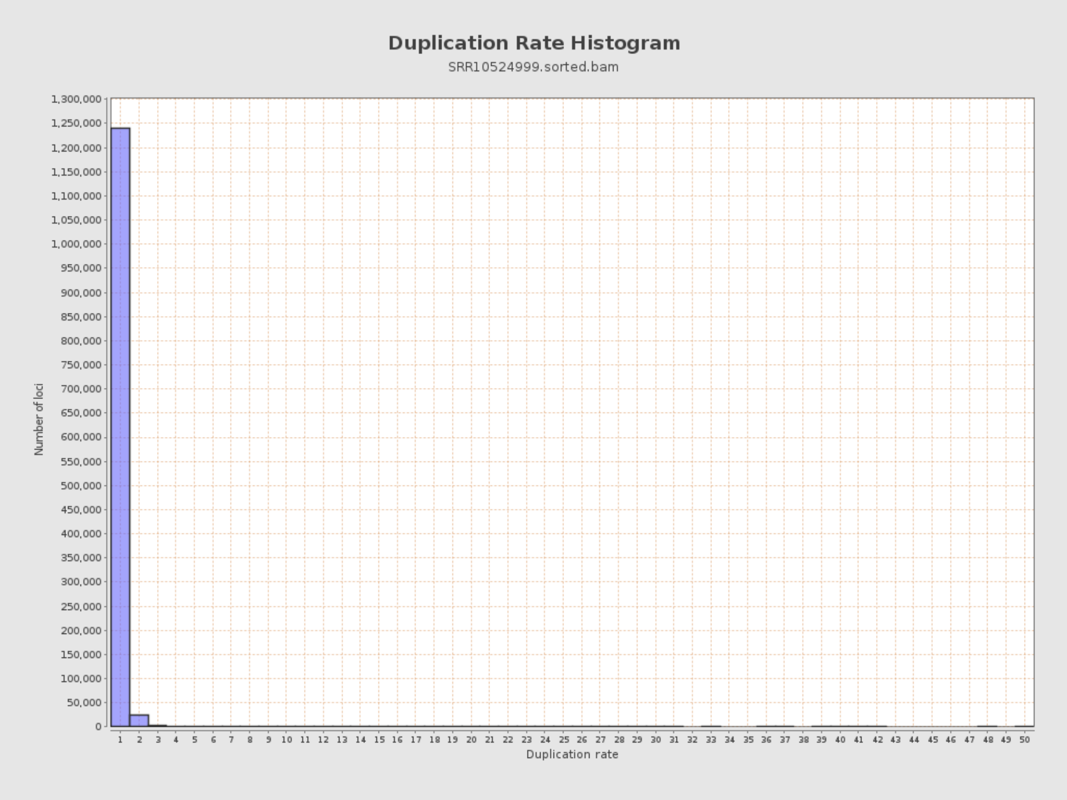
5. Results : Coverage Histogram (0-50X)



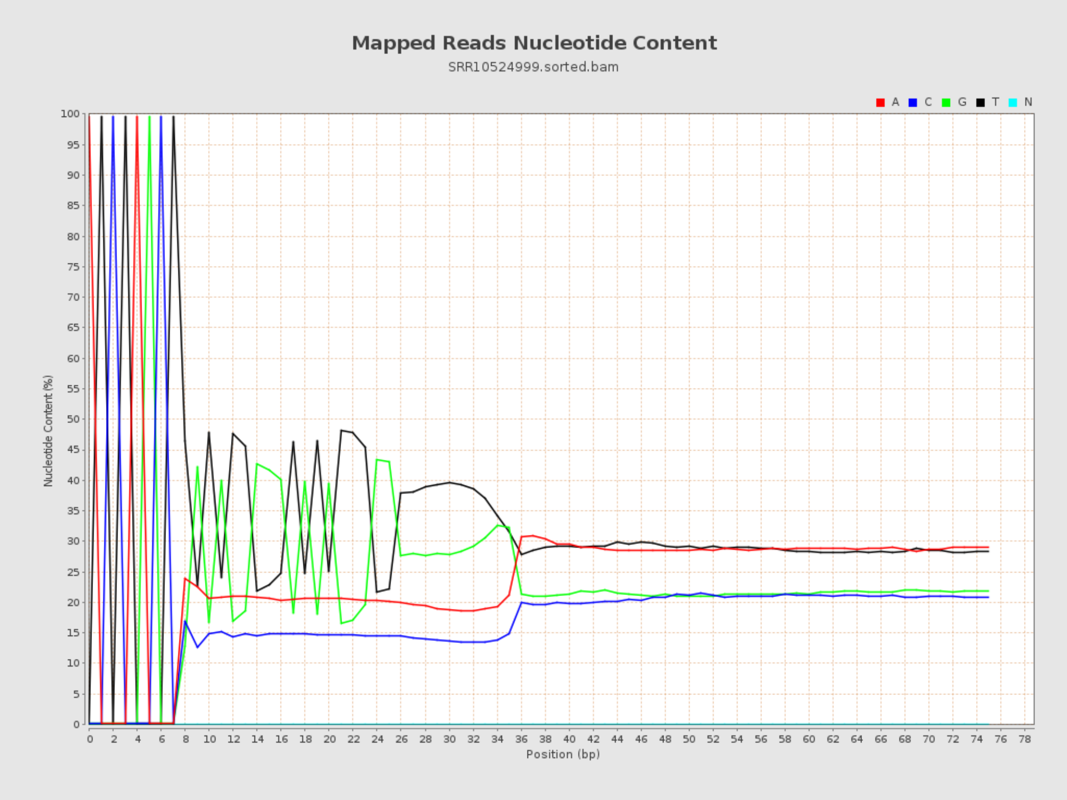
6. Results : Genome Fraction Coverage



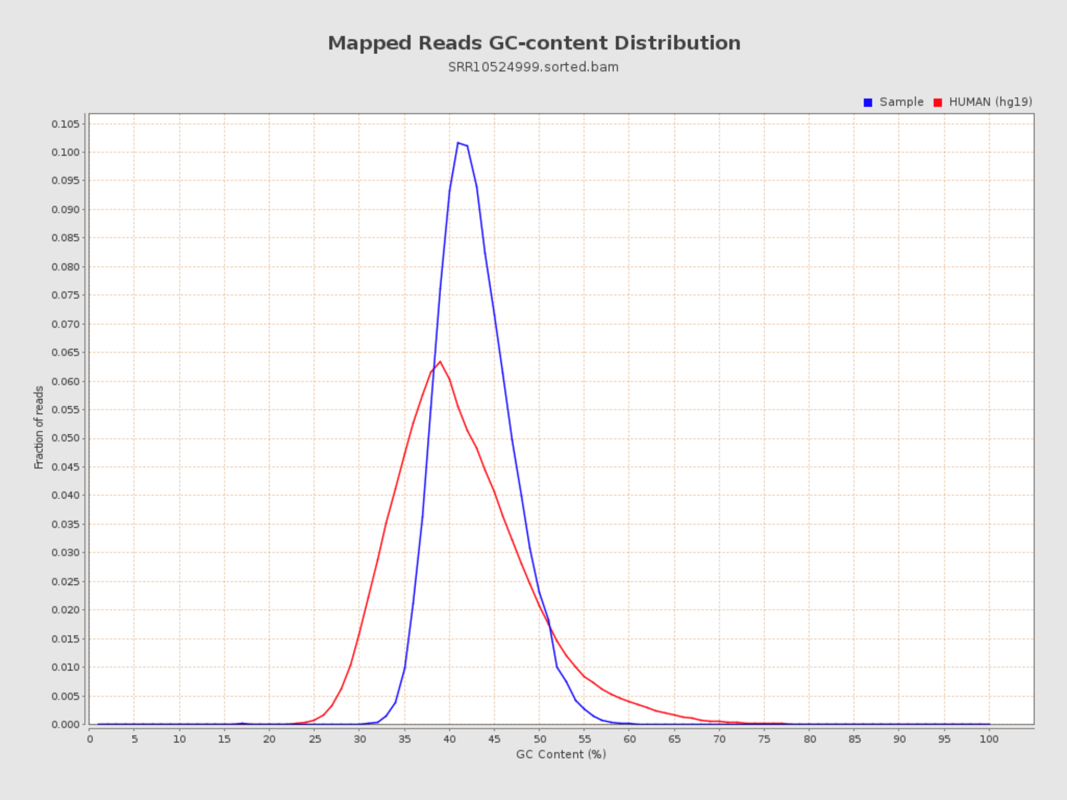
7. Results : Duplication Rate Histogram



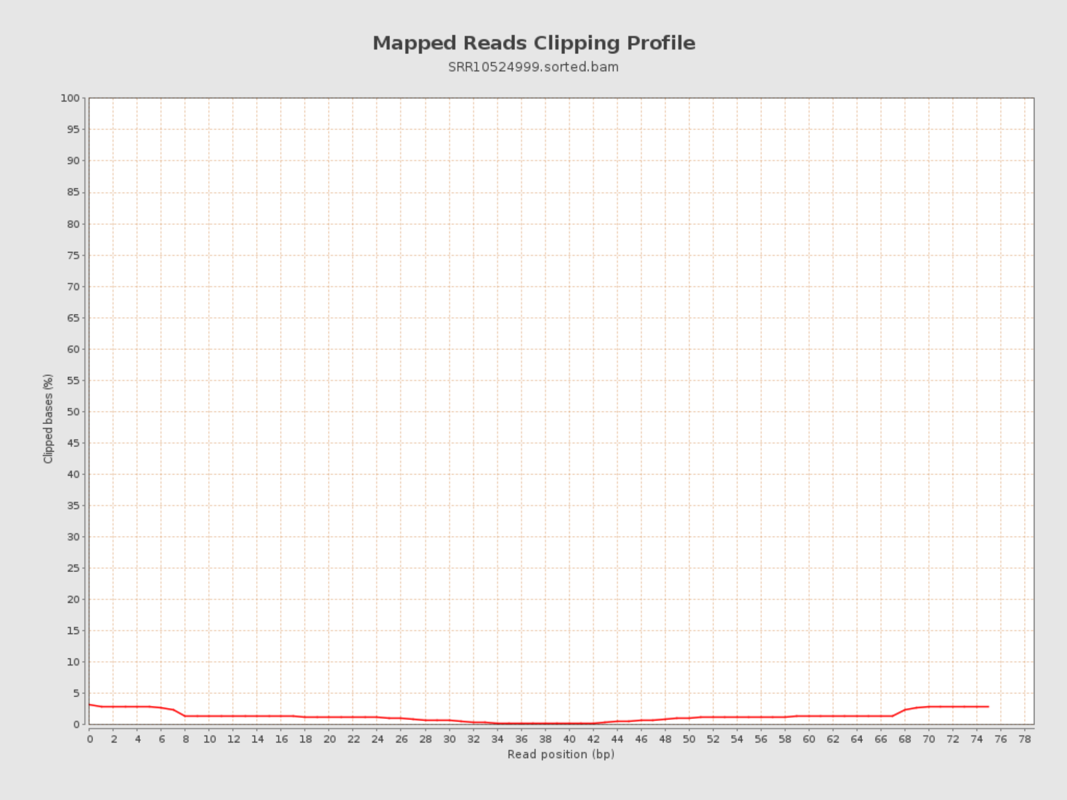
8. Results : Mapped Reads Nucleotide Content



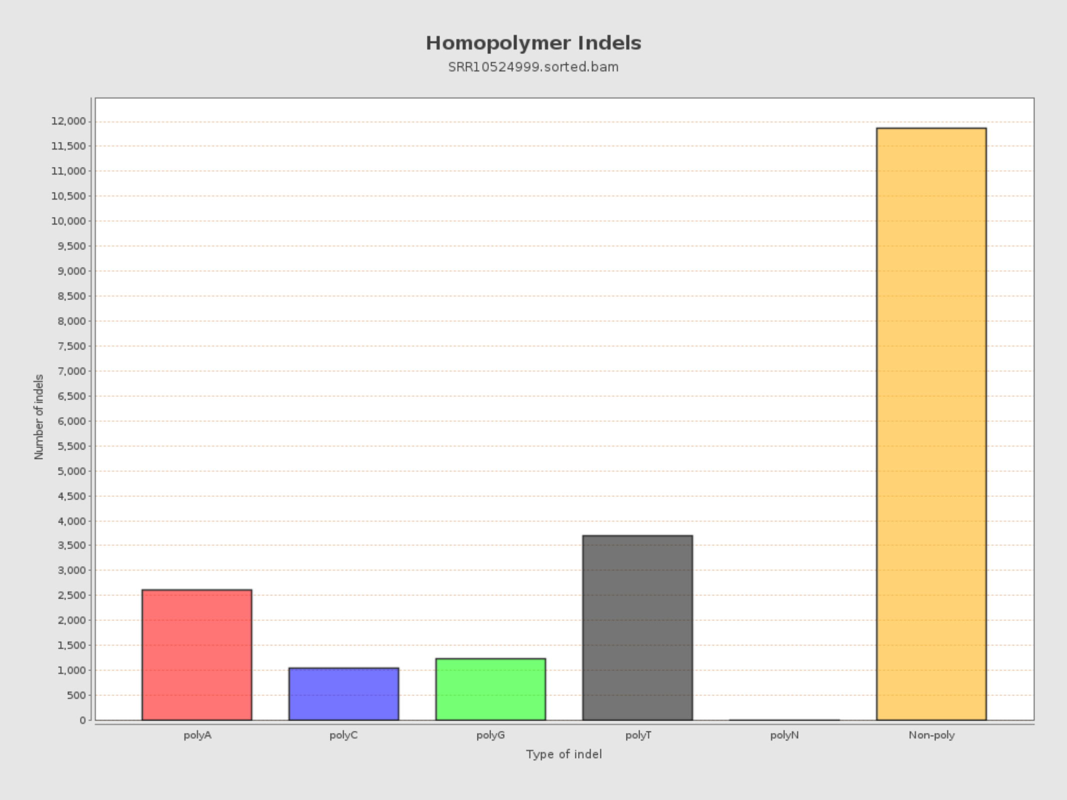
9. Results : Mapped Reads GC-content Distribution



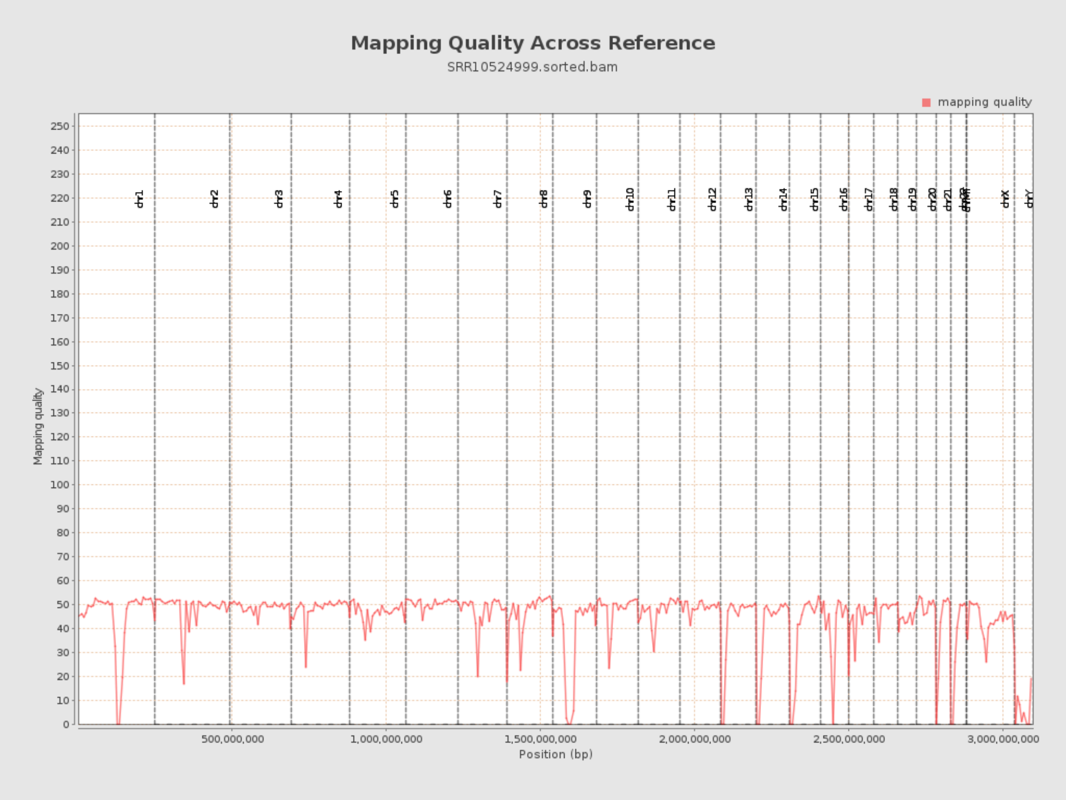
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram