Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:33:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524812.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_SRR10524812 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524812.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:33:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524812.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,851,110
Mapped reads	1,665,952 / 90%
Unmapped reads	185,158 / 10%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,445 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	74,209 / 4.01%
Duplication rate	3.43%
Clipped reads	1,667,168 / 90.06%

2.2. ACGT Content

Number/percentage of A's	22,648,569 / 23.94%
Number/percentage of C's	18,097,083 / 19.13%
Number/percentage of T's	31,683,234 / 33.49%
Number/percentage of G's	22,162,418 / 23.43%
Number/percentage of N's	11,698 / 0.01%
GC Percentage	42.56%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.2681

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

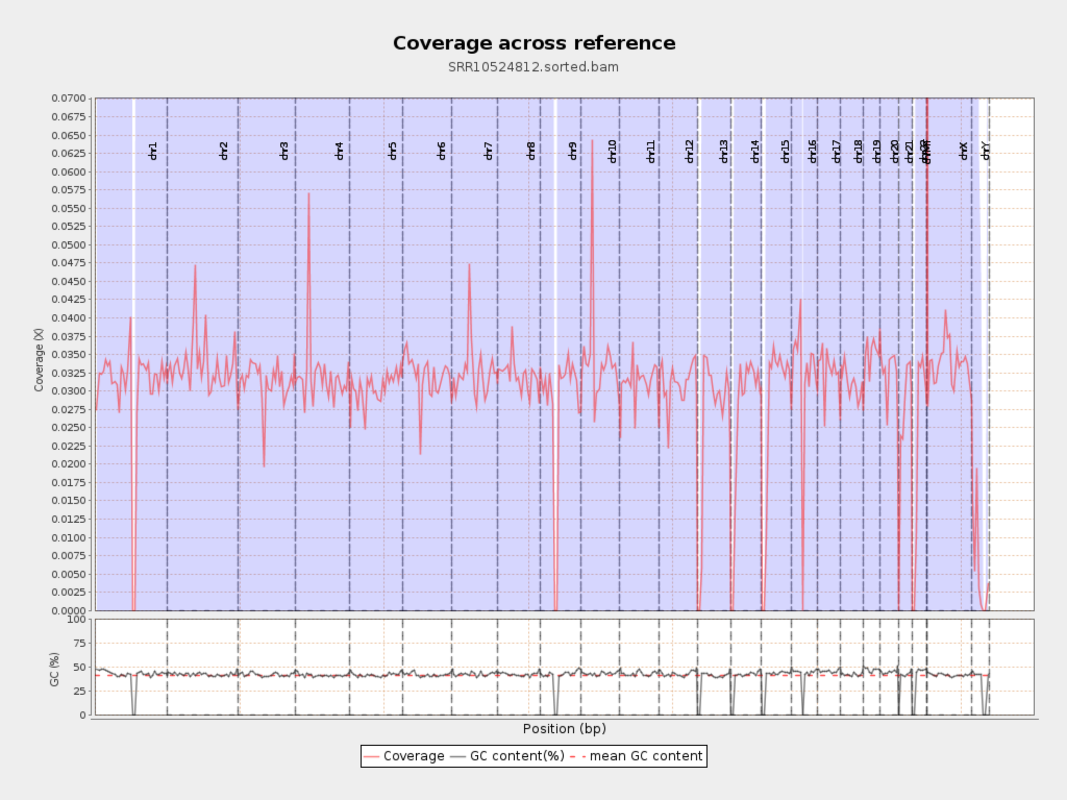
General error rate	0.53%
Mismatches	487,622
Insertions	6,469
Mapped reads with at least one insertion	0.39%
Deletions	18,552
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.13%

2.6. Chromosome stats

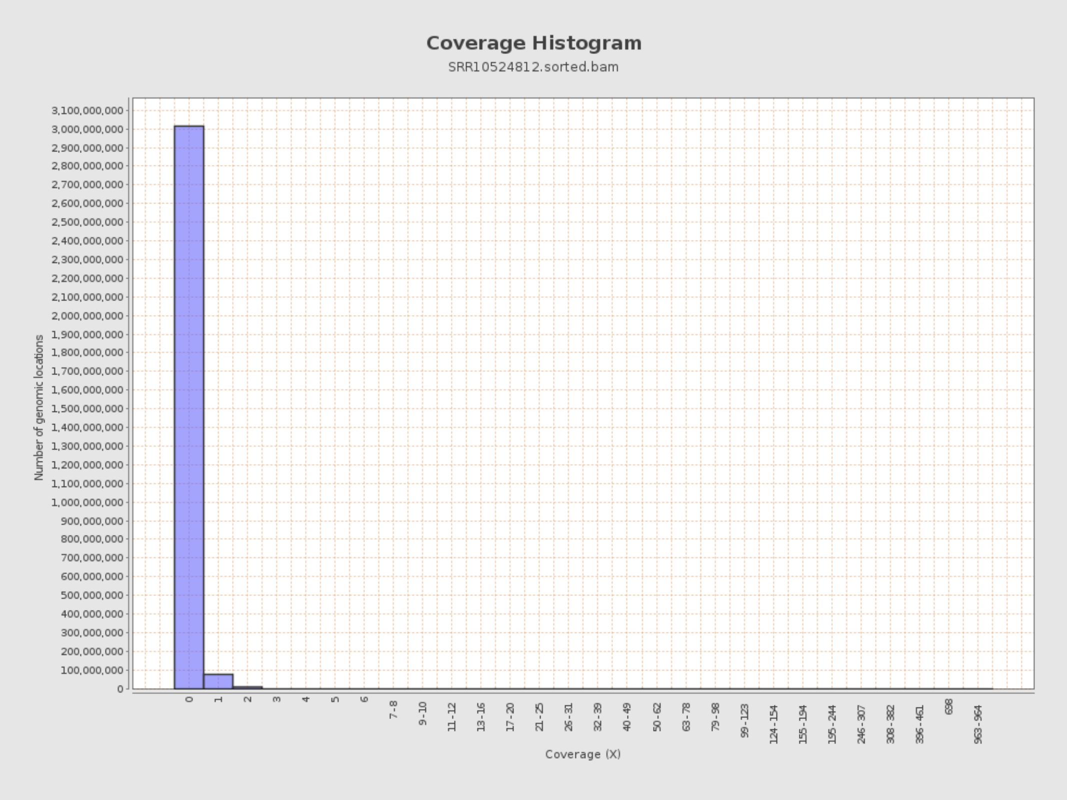
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7514365	0.0301	0.3525
chr2	243199373	8163815	0.0336	0.4545
chr3	198022430	6181848	0.0312	0.201
chr4	191154276	6169596	0.0323	0.231
chr5	180915260	5540651	0.0306	0.1956
chr6	171115067	5480184	0.032	0.2273
chr7	159138663	5204840	0.0327	0.3124

chr8	146364022	4711146	0.0322	0.2502
chr9	141213431	3953106	0.028	0.2266
chr10	135534747	4680438	0.0345	0.315
chr11	135006516	4248303	0.0315	0.2337
chr12	133851895	4161089	0.0311	0.2003
chr13	115169878	2954511	0.0257	0.1798
chr14	107349540	2831619	0.0264	0.188
chr15	102531392	2783965	0.0272	0.1857
chr16	90354753	2834871	0.0314	0.2223
chr17	81195210	2658241	0.0327	0.214
chr18	78077248	2421218	0.031	0.3449
chr19	59128983	2075149	0.0351	0.2948
chr20	63025520	2038966	0.0324	0.2105
chr21	48129895	1264777	0.0263	0.2013
chr22	51304566	1160605	0.0226	0.1695
chrMT	16571	20077	1.2116	1.3639
chrX	155270560	5250129	0.0338	0.2234
chrY	59373566	328933	0.0055	0.1546

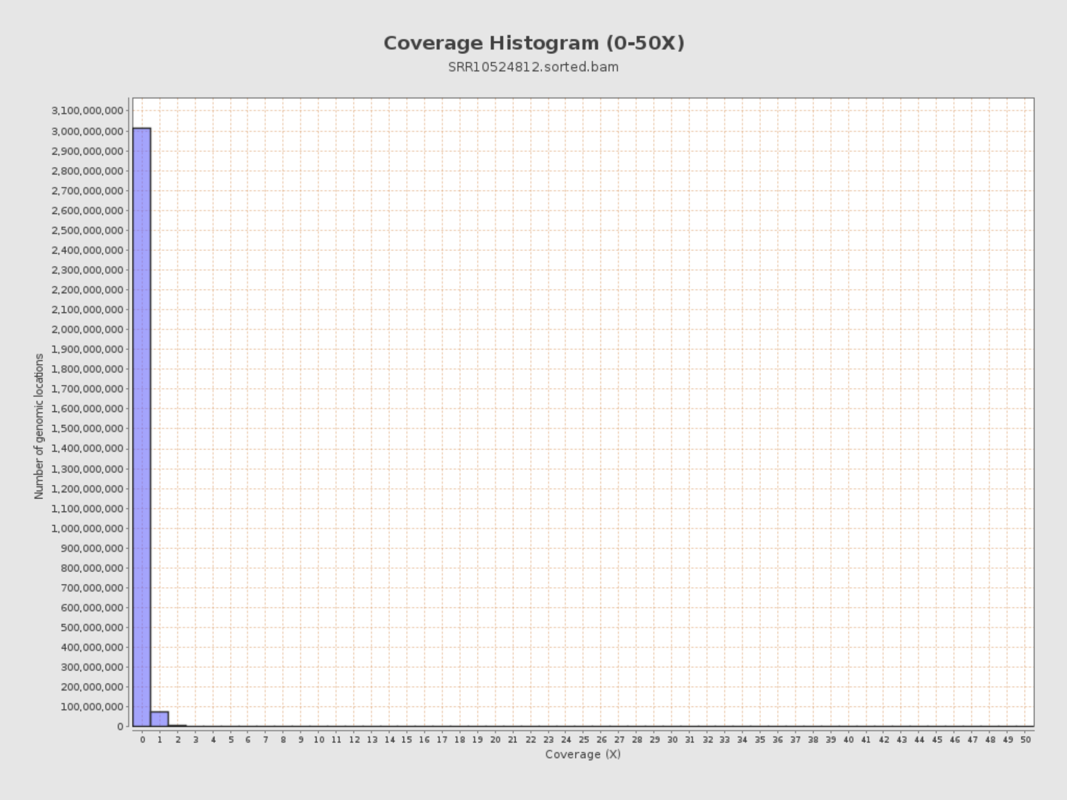
3. Results : Coverage across reference



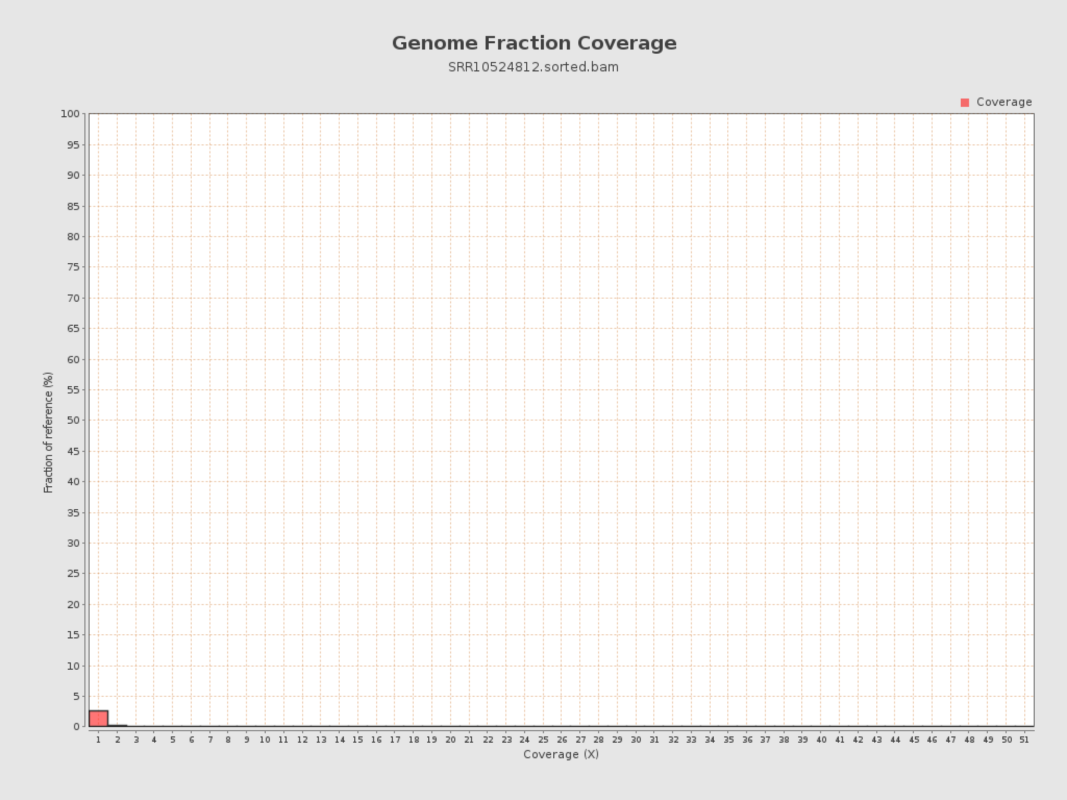
4. Results : Coverage Histogram



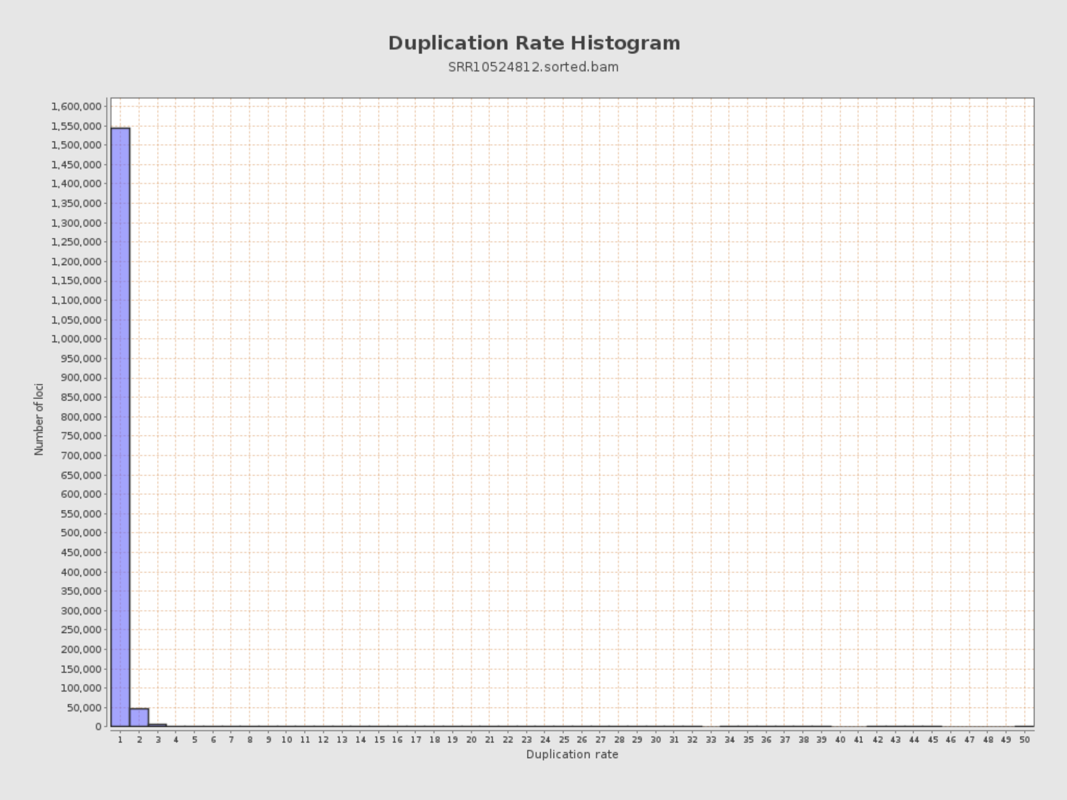
5. Results : Coverage Histogram (0-50X)



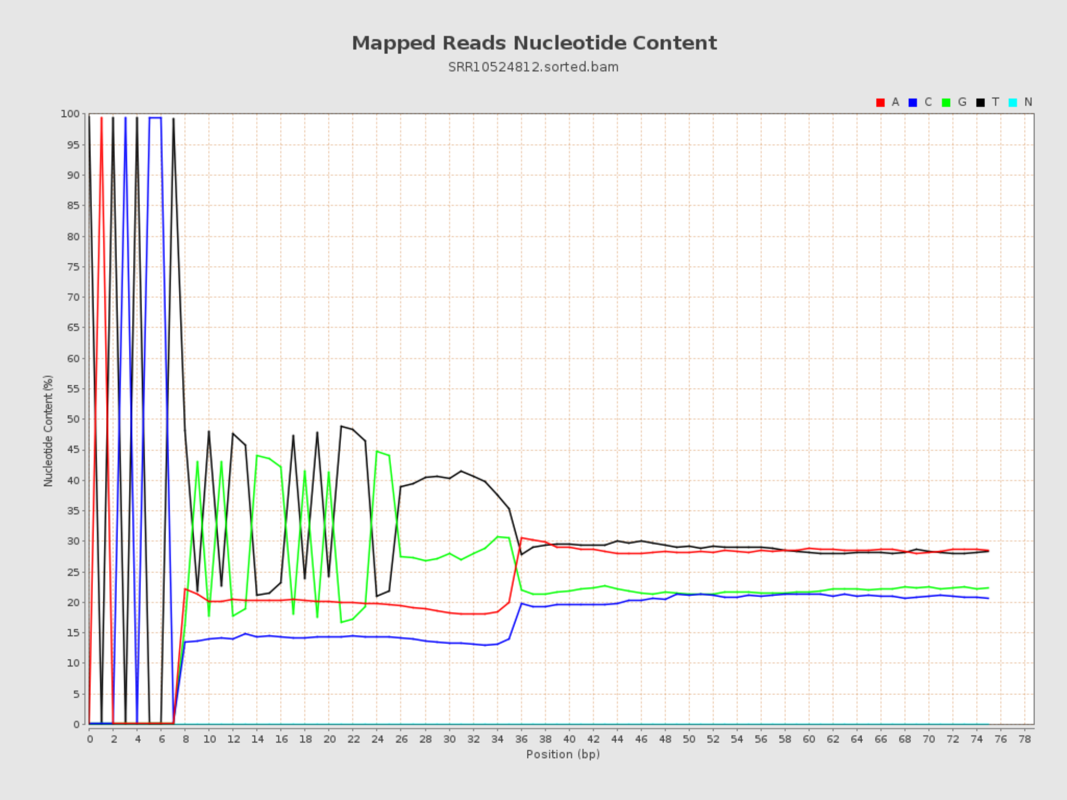
6. Results : Genome Fraction Coverage



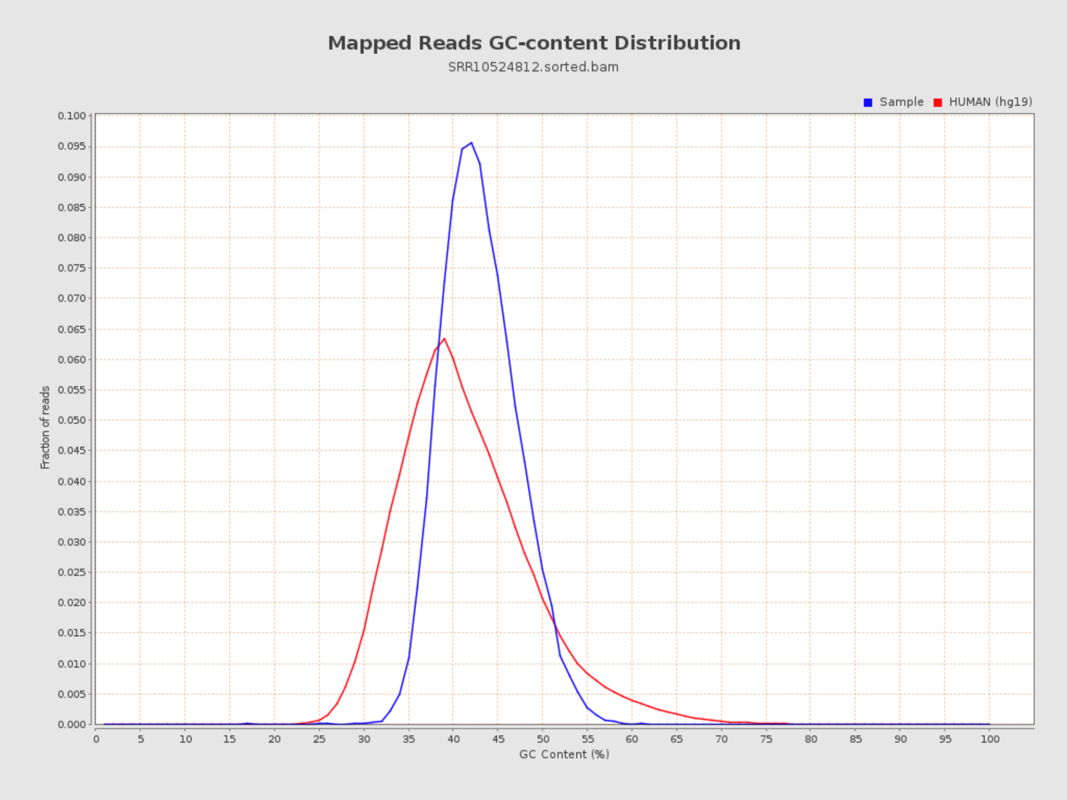
7. Results : Duplication Rate Histogram



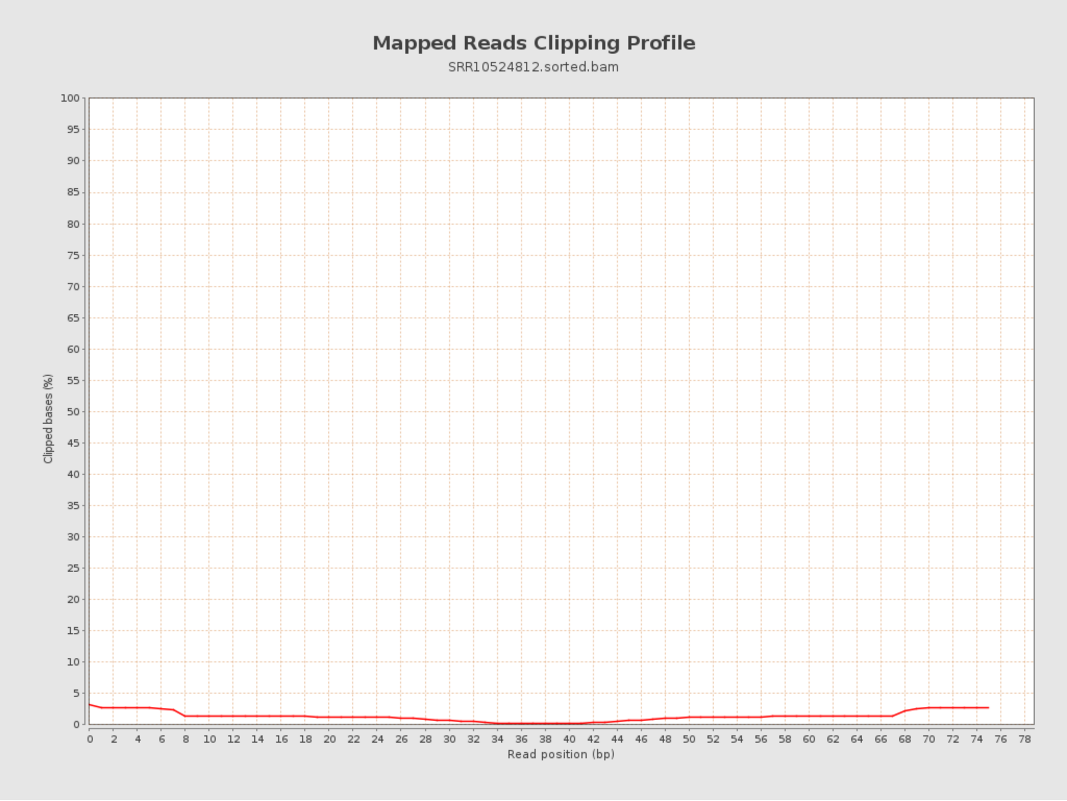
8. Results : Mapped Reads Nucleotide Content



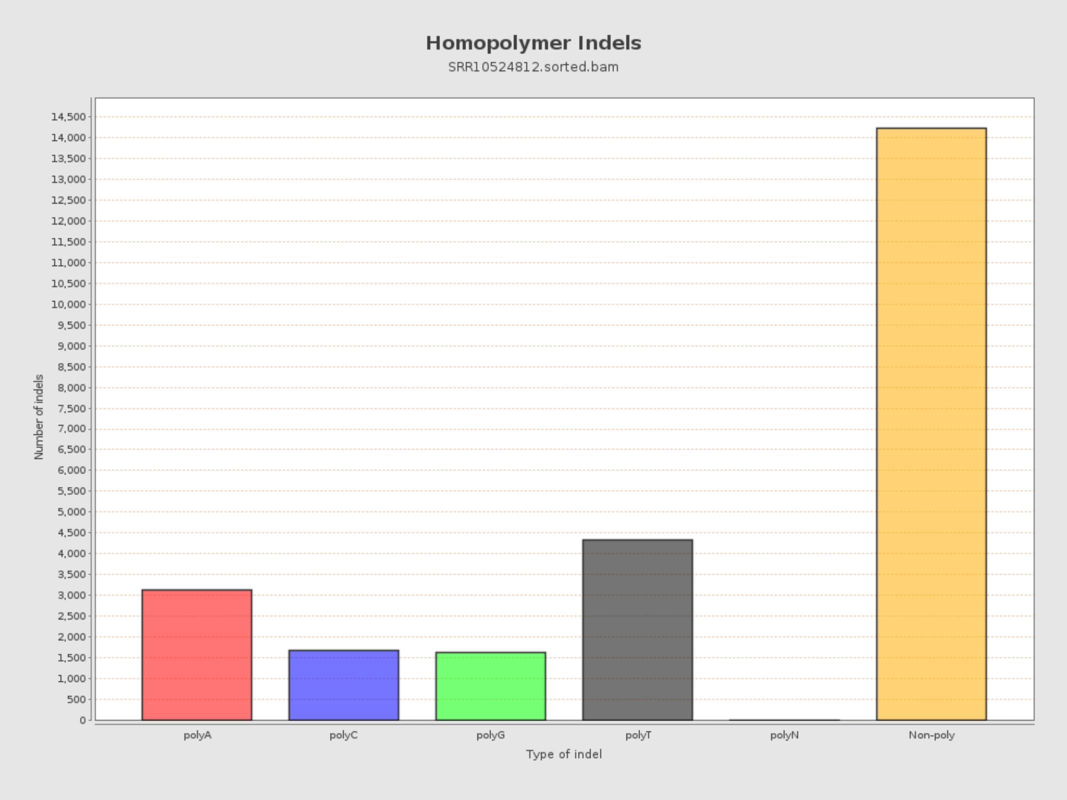
9. Results : Mapped Reads GC-content Distribution



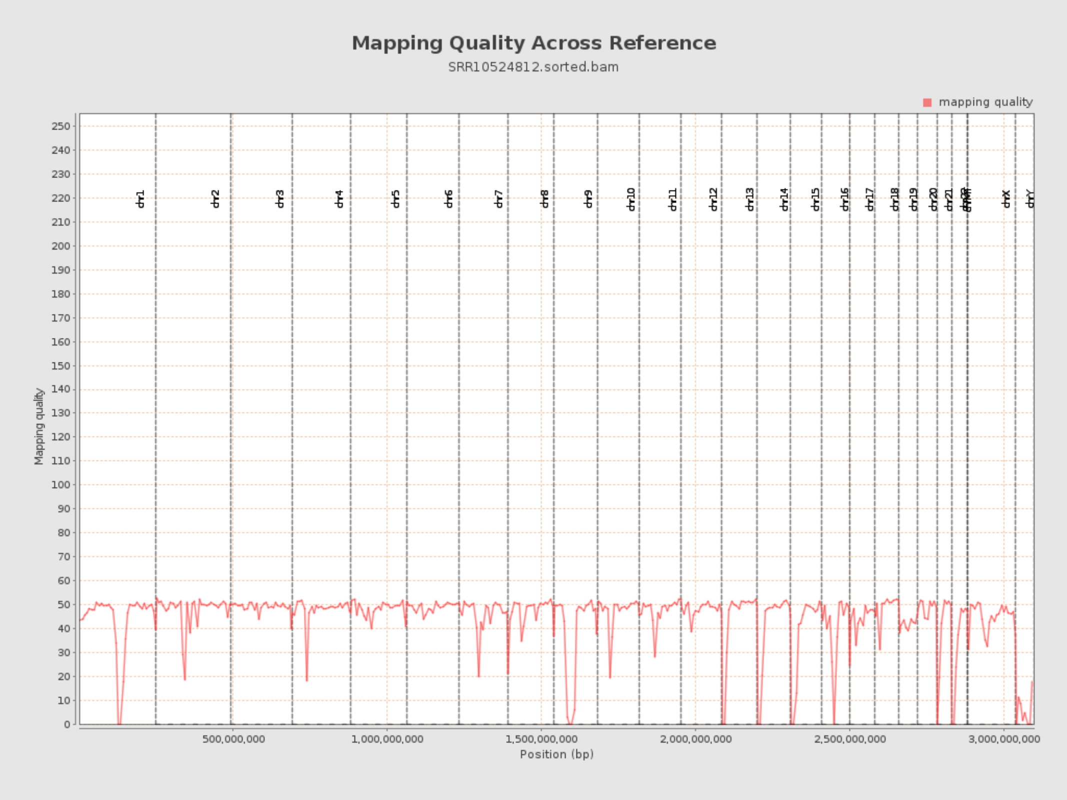
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram