Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:35:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524412.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_SRR10524412 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524412.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:35:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524412.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,084,969
Mapped reads	999,141 / 92.09%
Unmapped reads	85,828 / 7.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,037 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	42,332 / 3.9%
Duplication rate	3.27%
Clipped reads	1,000,406 / 92.21%

2.2. ACGT Content

Number/percentage of A's	15,604,357 / 26.54%
Number/percentage of C's	10,578,973 / 17.99%
Number/percentage of T's	18,274,767 / 31.08%
Number/percentage of G's	14,325,024 / 24.37%
Number/percentage of N's	7,357 / 0.01%
GC Percentage	42.36%

2.3. Coverage

Mean	0.019

Standard Deviation	0.2206

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

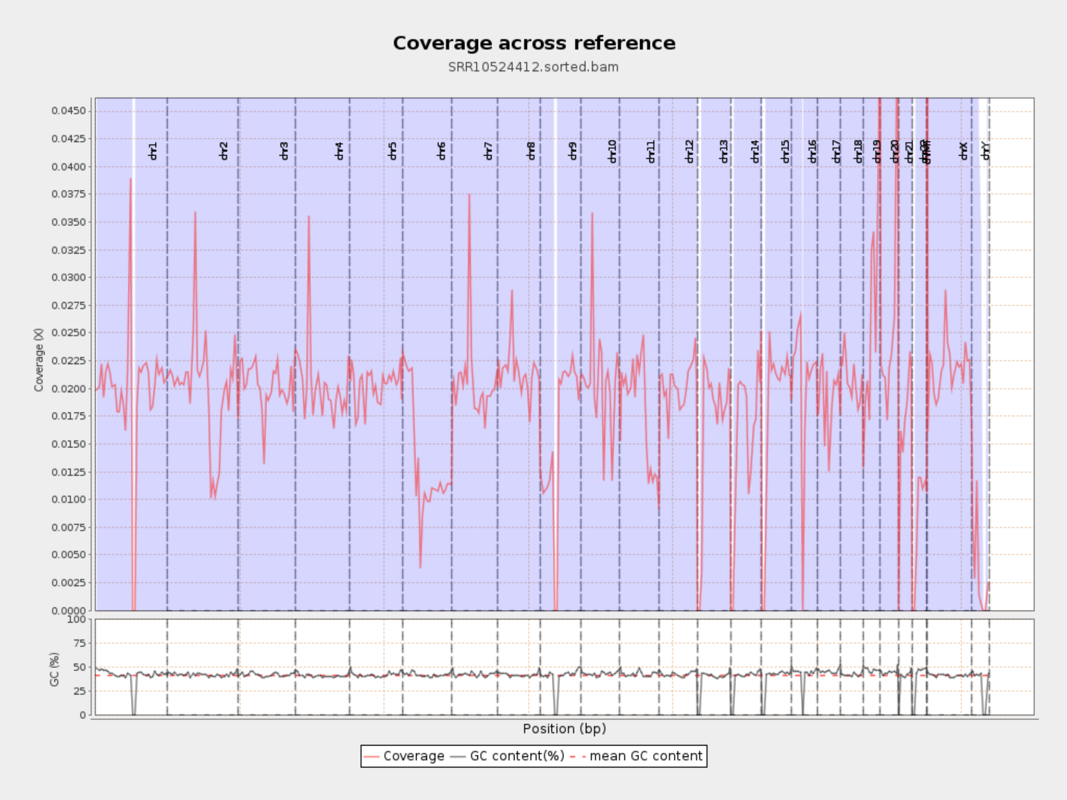
General error rate	0.51%
Mismatches	290,130
Insertions	4,209
Mapped reads with at least one insertion	0.42%
Deletions	10,468
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.35%

2.6. Chromosome stats

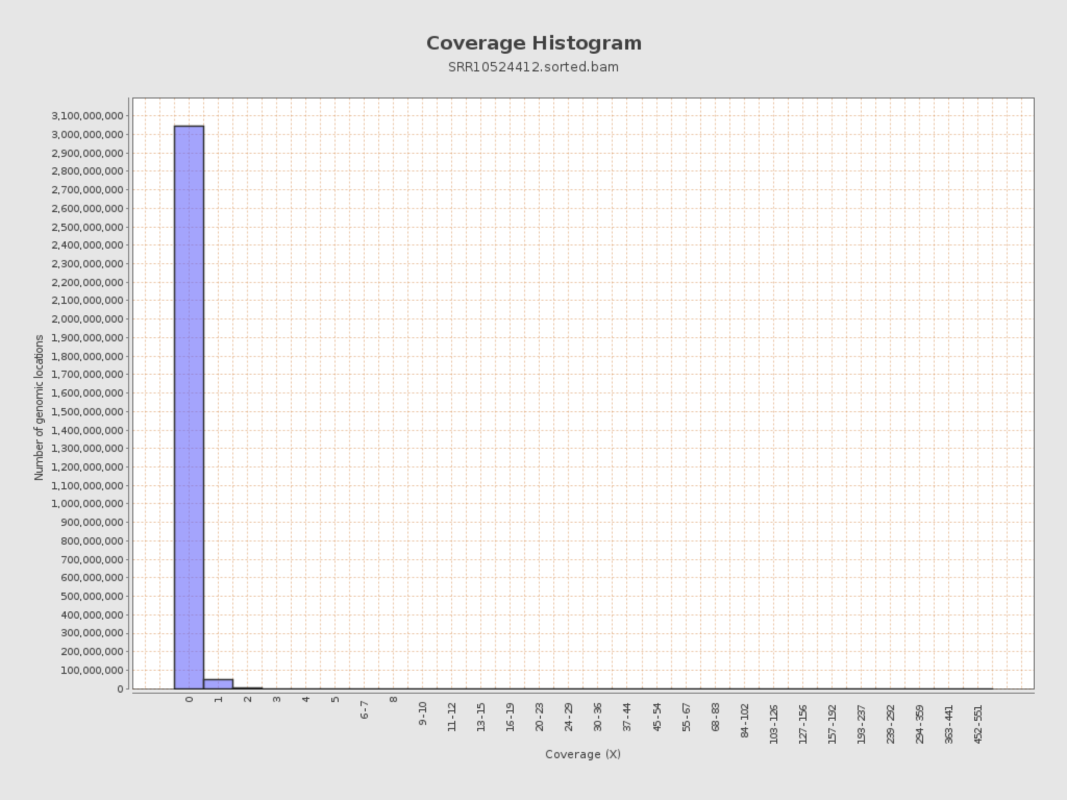
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4904230	0.0197	0.4409
chr2	243199373	4860597	0.02	0.2376
chr3	198022430	4005020	0.0202	0.1535
chr4	191154276	3900792	0.0204	0.1755
chr5	180915260	3675750	0.0203	0.154
chr6	171115067	2254472	0.0132	0.1311
chr7	159138663	3292009	0.0207	0.2952

chr8	146364022	3166043	0.0216	0.2278
chr9	141213431	2213279	0.0157	0.1688
chr10	135534747	2808564	0.0207	0.2106
chr11	135006516	2465083	0.0183	0.1721
chr12	133851895	2719962	0.0203	0.1578
chr13	115169878	1892117	0.0164	0.1379
chr14	107349540	1652987	0.0154	0.136
chr15	102531392	1836333	0.0179	0.1441
chr16	90354753	1831493	0.0203	0.1586
chr17	81195210	1558317	0.0192	0.1607
chr18	78077248	1624705	0.0208	0.2874
chr19	59128983	1653543	0.028	0.3101
chr20	63025520	1691360	0.0268	0.1821
chr21	48129895	801561	0.0167	0.1549
chr22	51304566	420922	0.0082	0.0975
chrMT	16571	5238	0.3161	0.5969
chrX	155270560	3384528	0.0218	0.172
chrY	59373566	188349	0.0032	0.1011

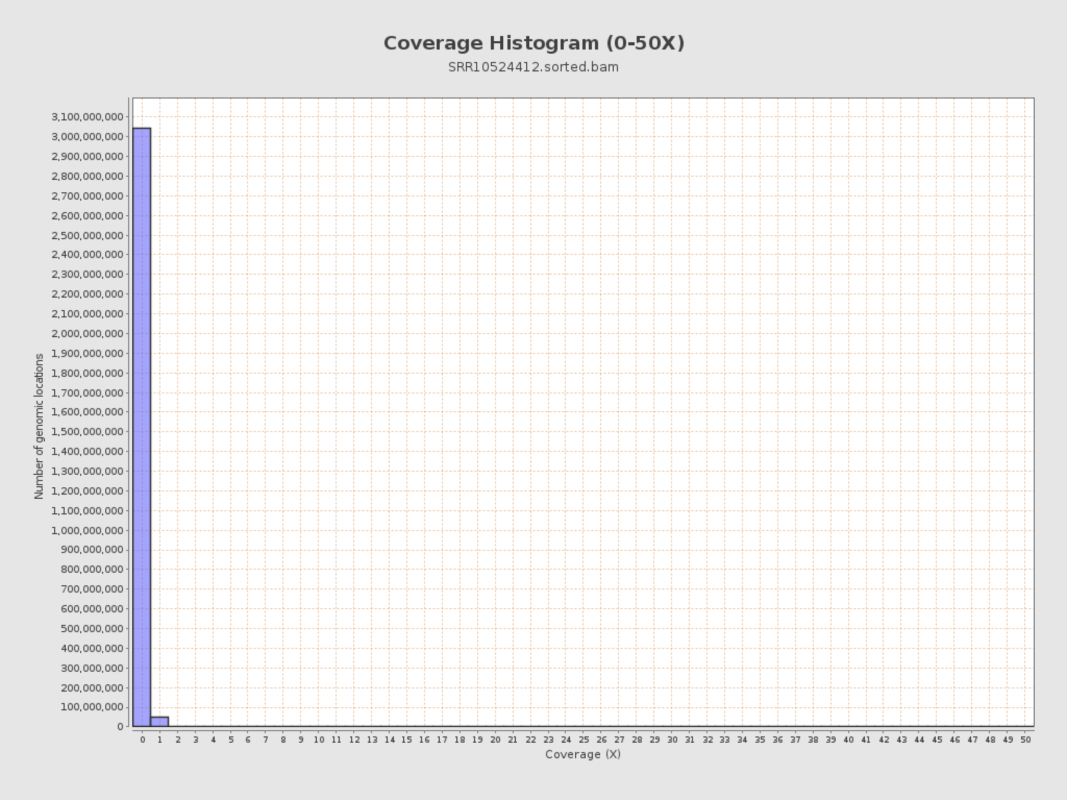
3. Results : Coverage across reference



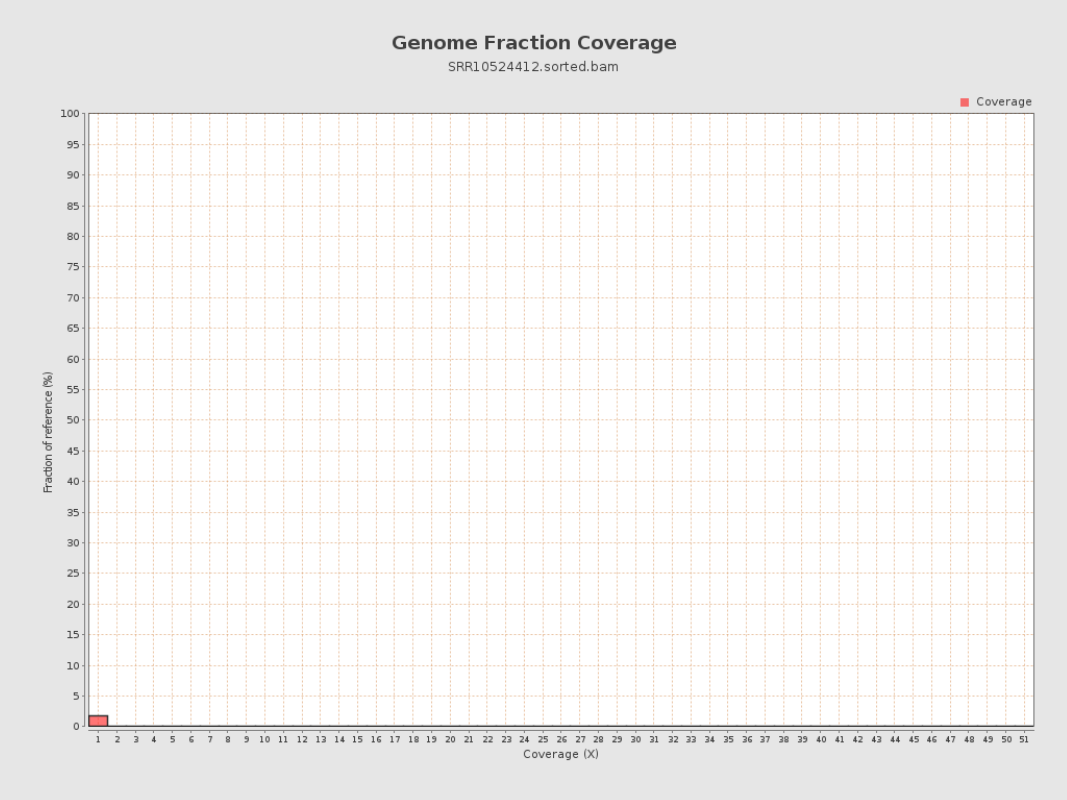
4. Results : Coverage Histogram



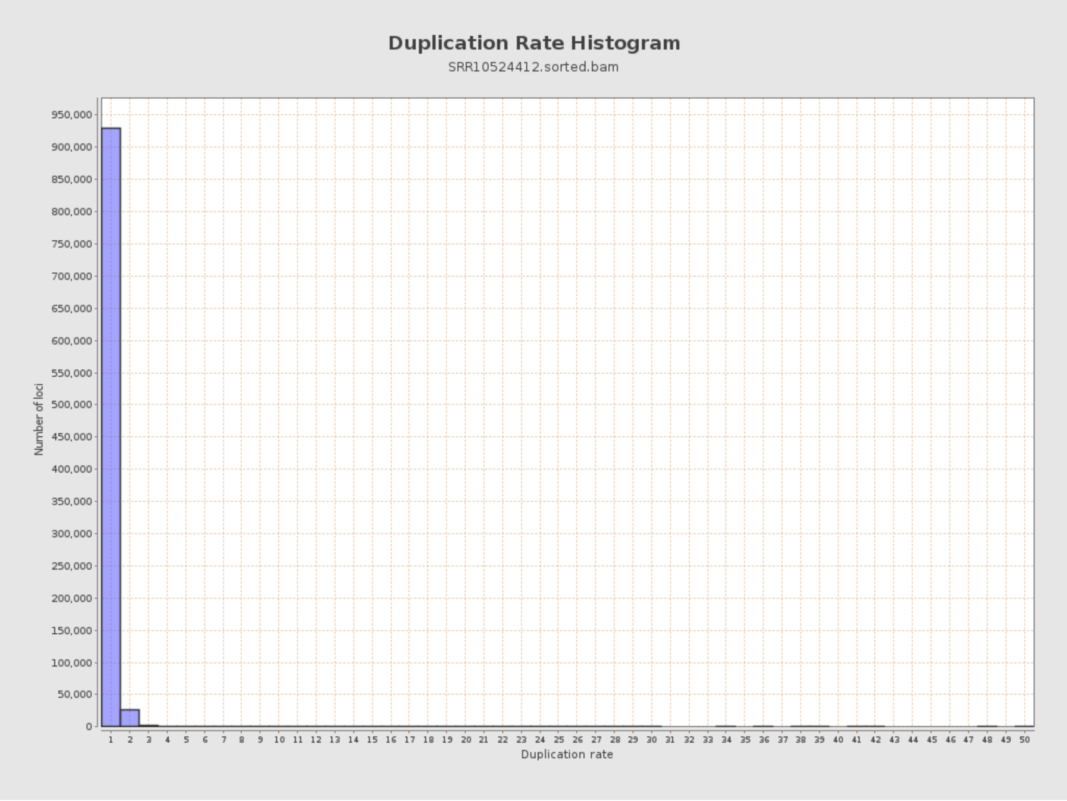
5. Results : Coverage Histogram (0-50X)



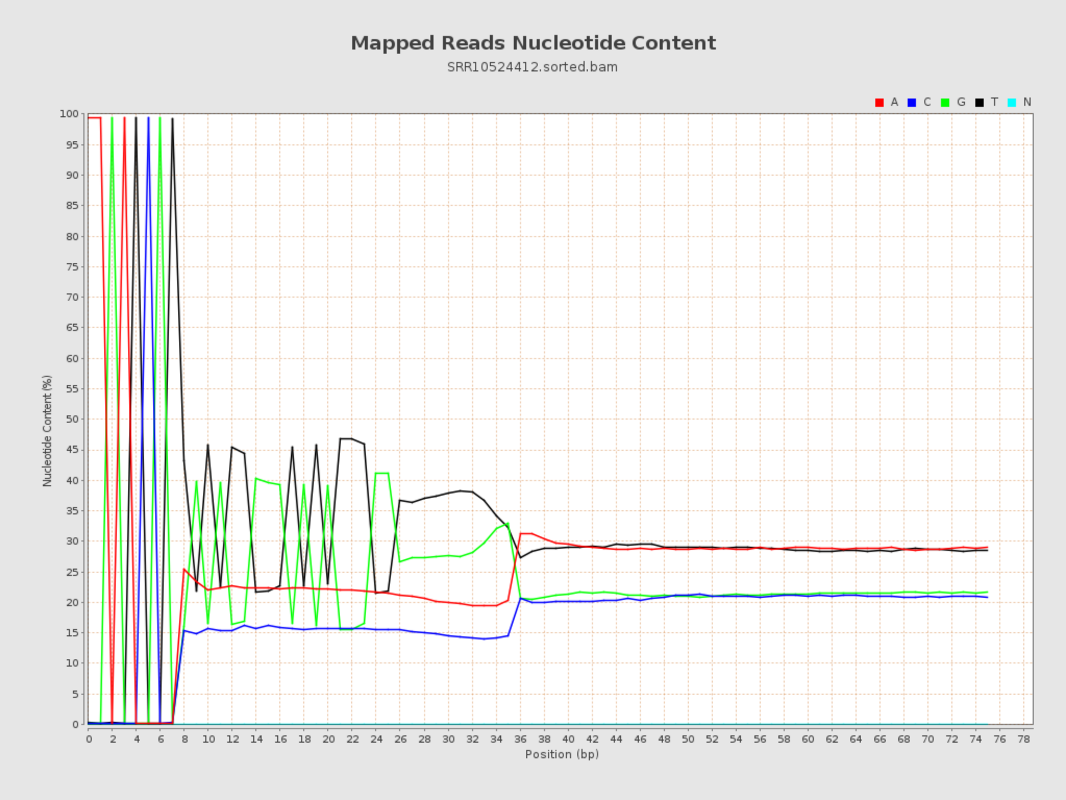
6. Results : Genome Fraction Coverage



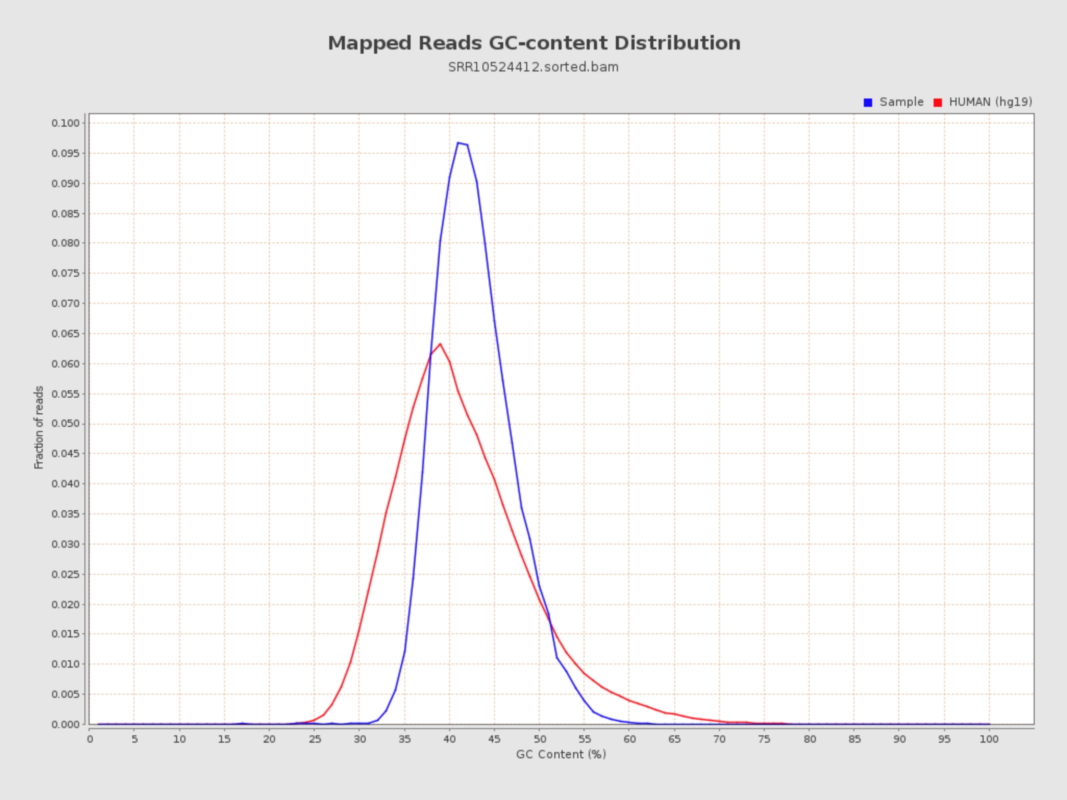
7. Results : Duplication Rate Histogram



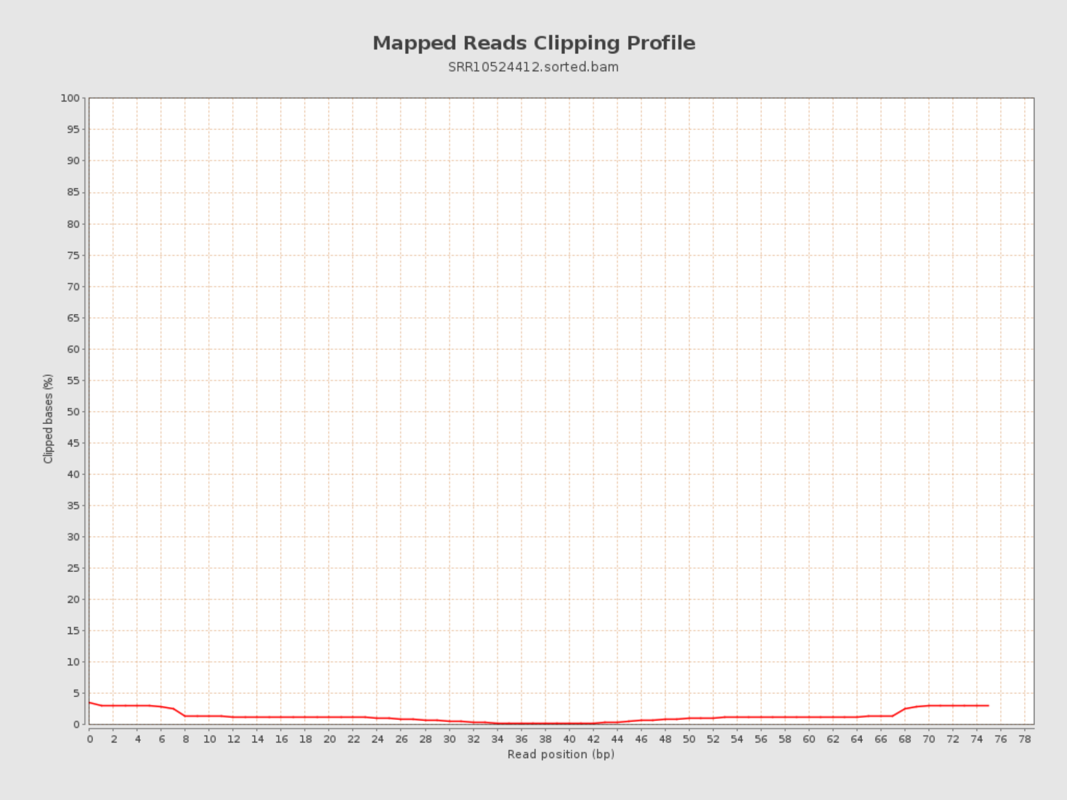
8. Results : Mapped Reads Nucleotide Content



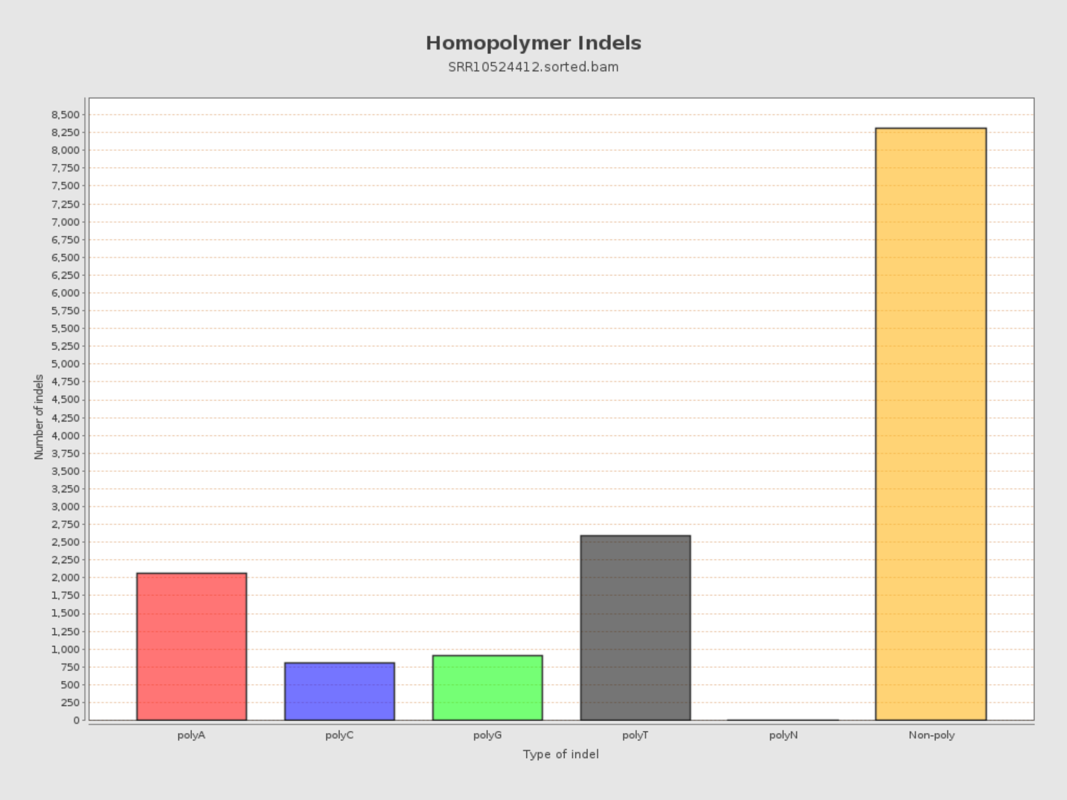
9. Results : Mapped Reads GC-content Distribution



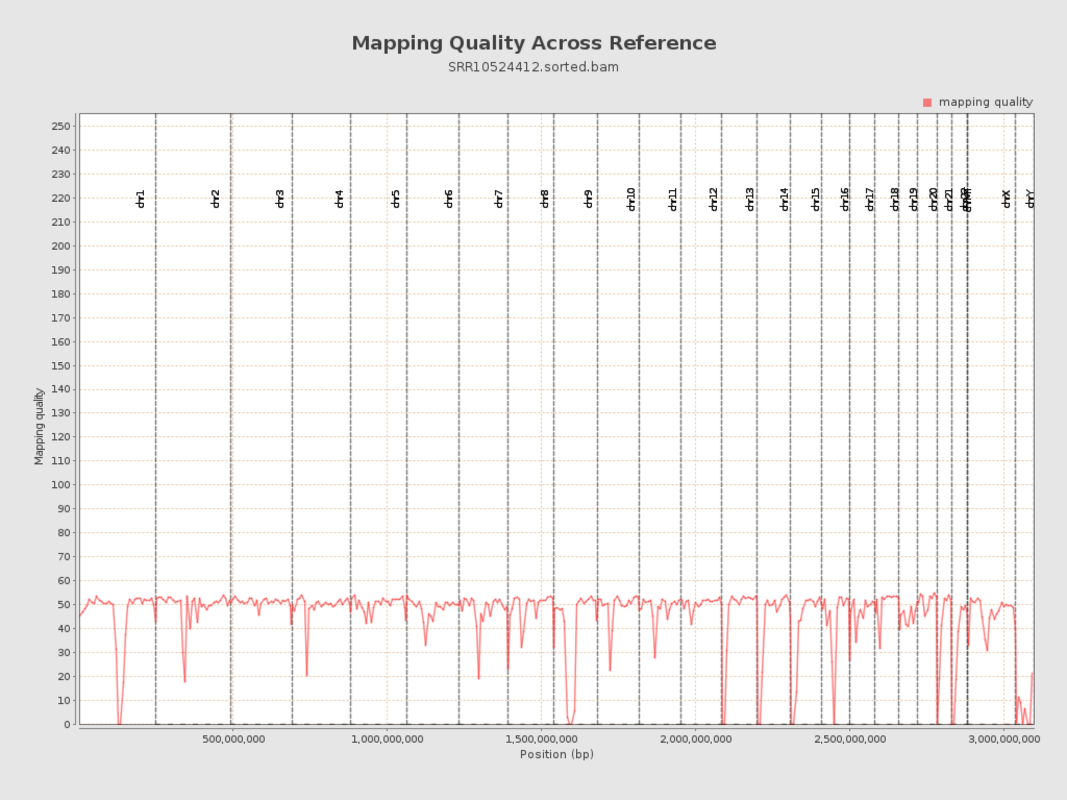
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram