Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:44:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524366.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_SRR10524366 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524366.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:44:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524366.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,240,568
Mapped reads	1,138,076 / 91.74%
Unmapped reads	102,492 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,474 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	38,262 / 3.08%
Duplication rate	2.53%
Clipped reads	1,139,308 / 91.84%

2.2. ACGT Content

Number/percentage of A's	16,491,746 / 24.96%
Number/percentage of C's	12,081,247 / 18.29%
Number/percentage of T's	21,507,024 / 32.55%
Number/percentage of G's	15,984,722 / 24.2%
Number/percentage of N's	1,408 / 0%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.22

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

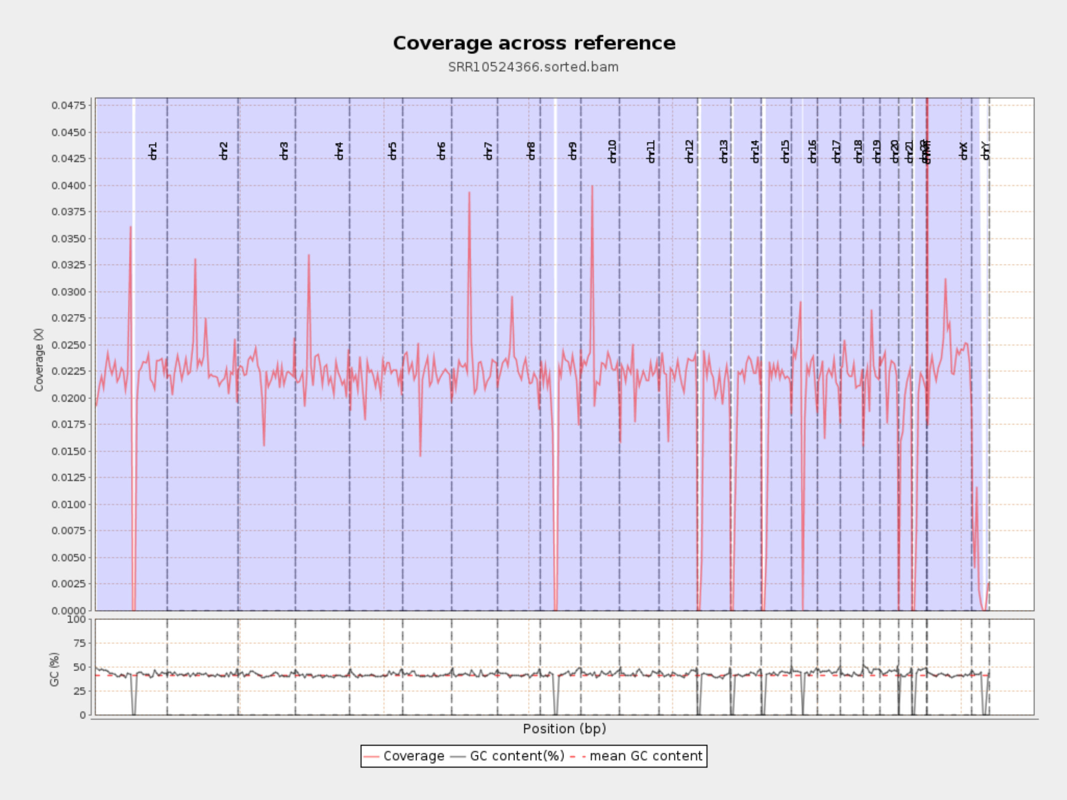
General error rate	0.52%
Mismatches	335,778
Insertions	4,699
Mapped reads with at least one insertion	0.41%
Deletions	14,104
Mapped reads with at least one deletion	1.23%
Homopolymer indels	44.36%

2.6. Chromosome stats

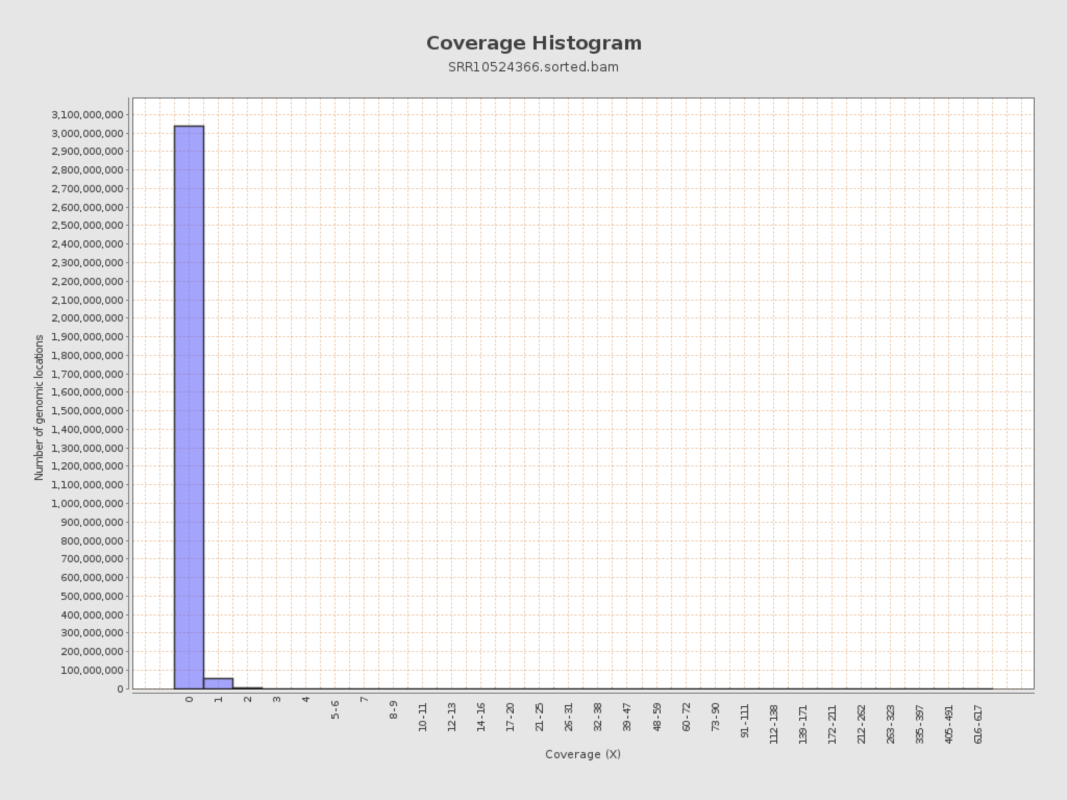
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5328382	0.0214	0.3696
chr2	243199373	5588320	0.023	0.3019
chr3	198022430	4398405	0.0222	0.1599
chr4	191154276	4309280	0.0225	0.1701
chr5	180915260	3994662	0.0221	0.1597
chr6	171115067	3809699	0.0223	0.1727
chr7	159138663	3716306	0.0234	0.298

chr8	146364022	3352483	0.0229	0.2273
chr9	141213431	2774612	0.0196	0.1849
chr10	135534747	3211904	0.0237	0.2101
chr11	135006516	2985811	0.0221	0.1847
chr12	133851895	2979352	0.0223	0.1612
chr13	115169878	2110638	0.0183	0.1452
chr14	107349540	2031408	0.0189	0.1494
chr15	102531392	1834762	0.0179	0.1443
chr16	90354753	1898744	0.021	0.1709
chr17	81195210	1741452	0.0214	0.1607
chr18	78077248	1749519	0.0224	0.3026
chr19	59128983	1319629	0.0223	0.2776
chr20	63025520	1400710	0.0222	0.1625
chr21	48129895	849739	0.0177	0.1502
chr22	51304566	754507	0.0147	0.1296
chrMT	16571	10448	0.6305	0.8994
chrX	155270560	3732397	0.024	0.1794
chrY	59373566	205501	0.0035	0.0997

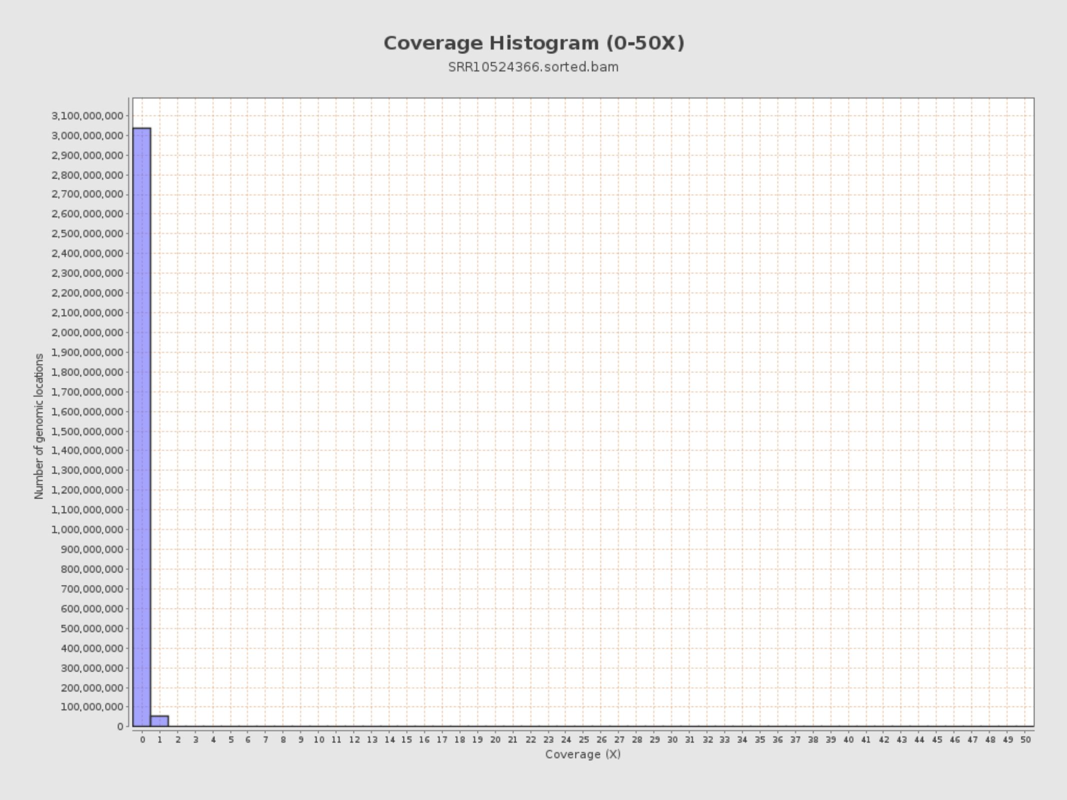
3. Results : Coverage across reference



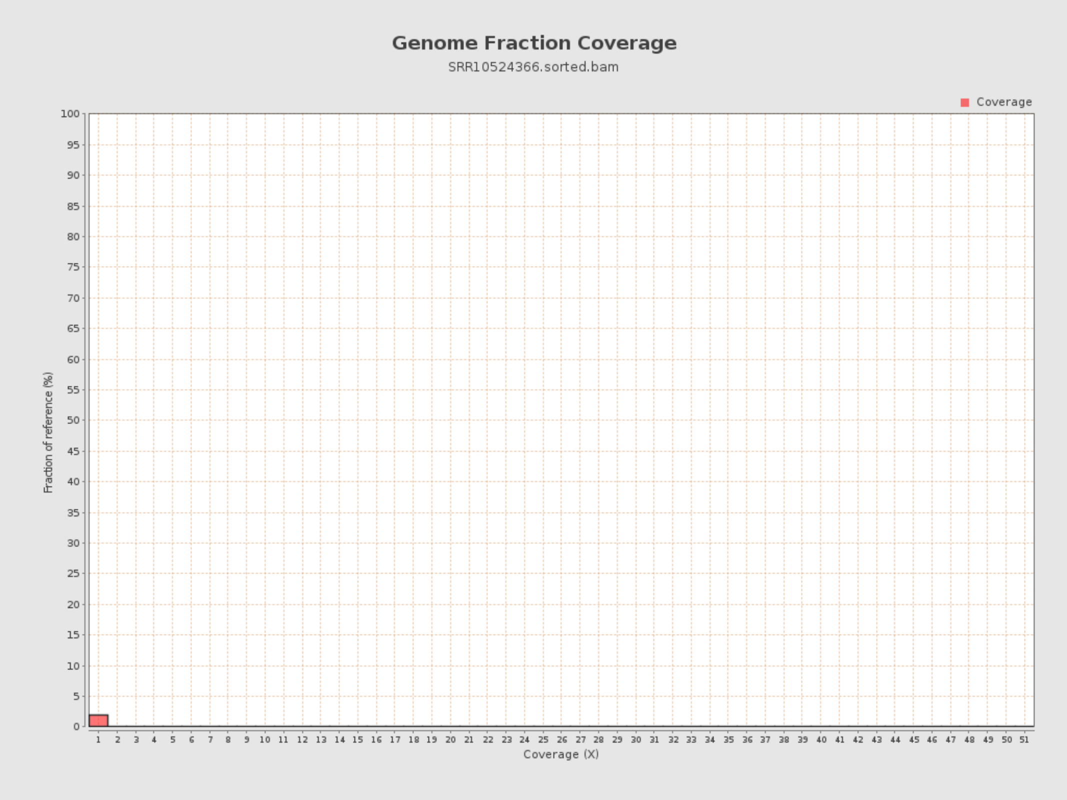
4. Results : Coverage Histogram



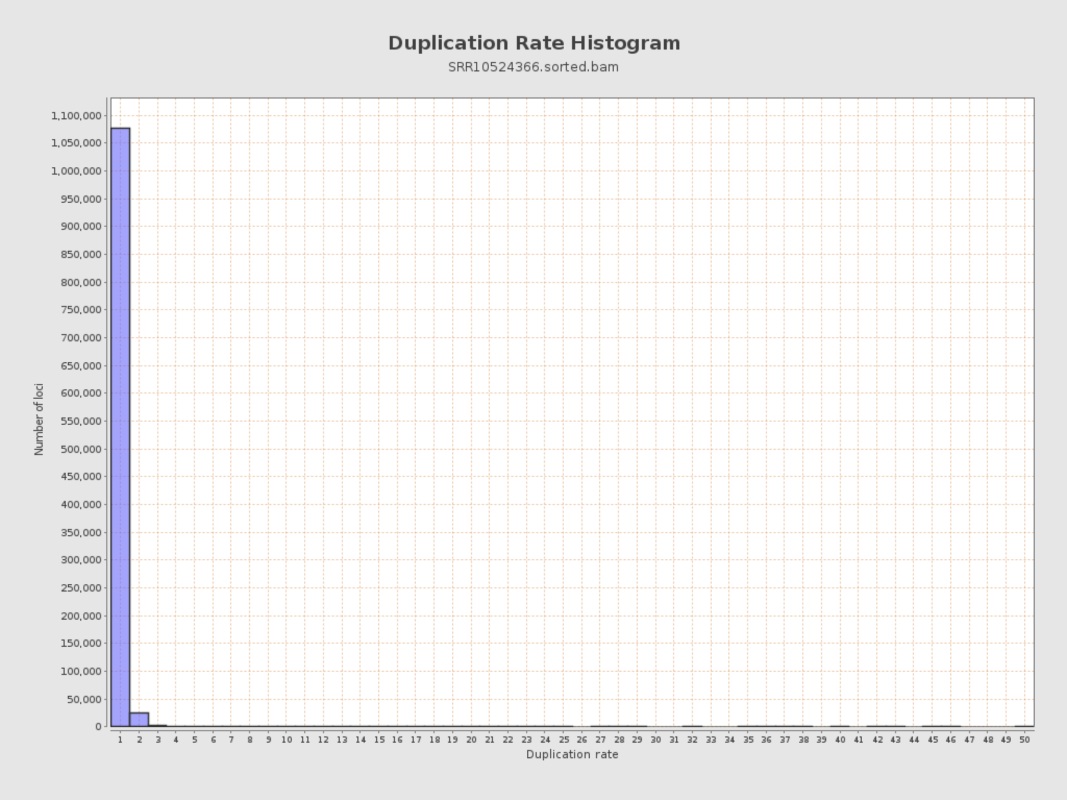
5. Results : Coverage Histogram (0-50X)



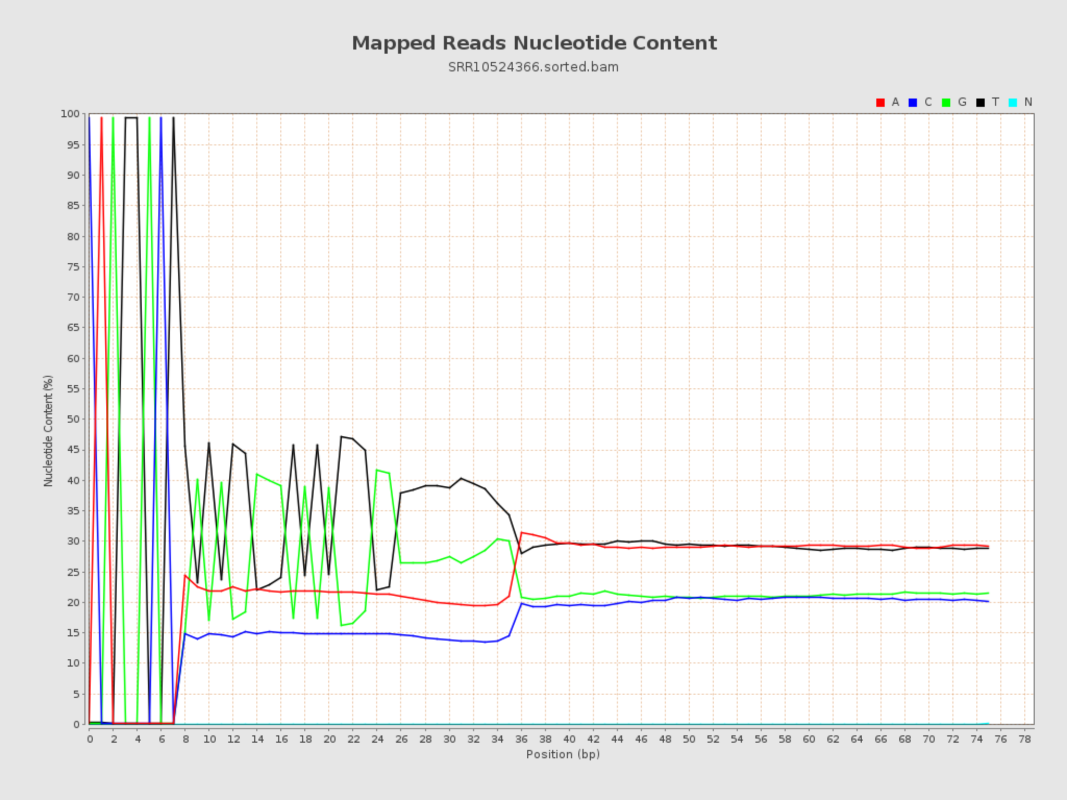
6. Results : Genome Fraction Coverage



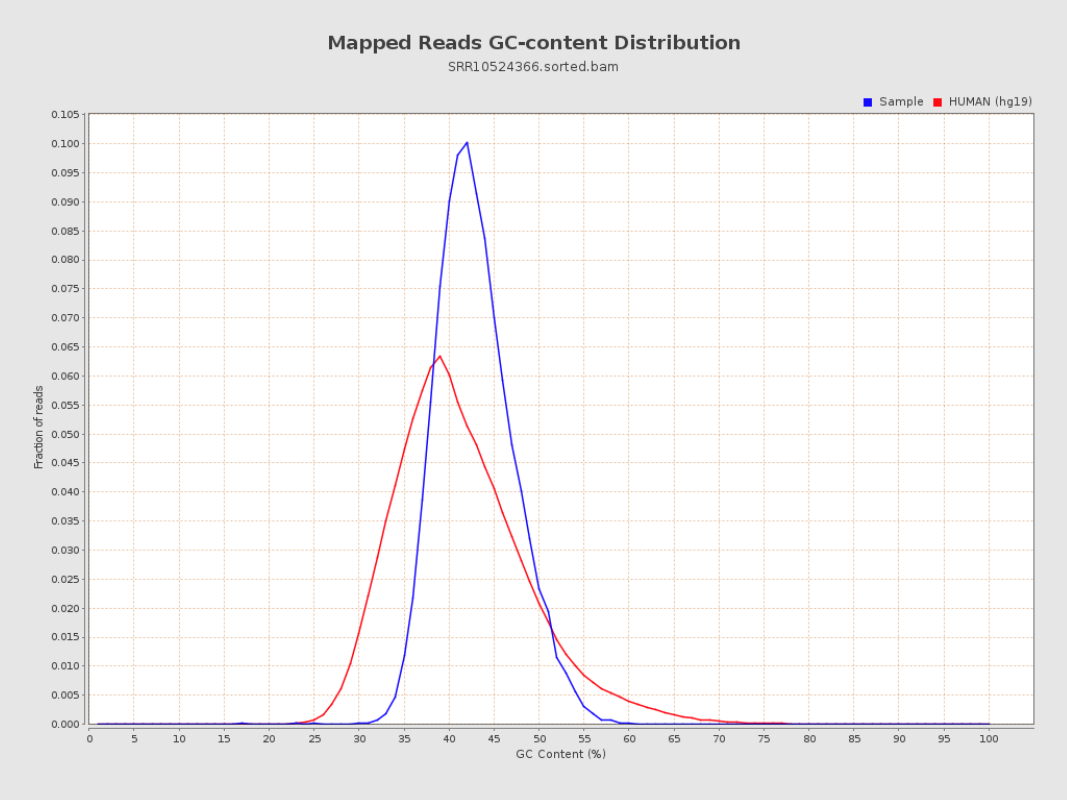
7. Results : Duplication Rate Histogram



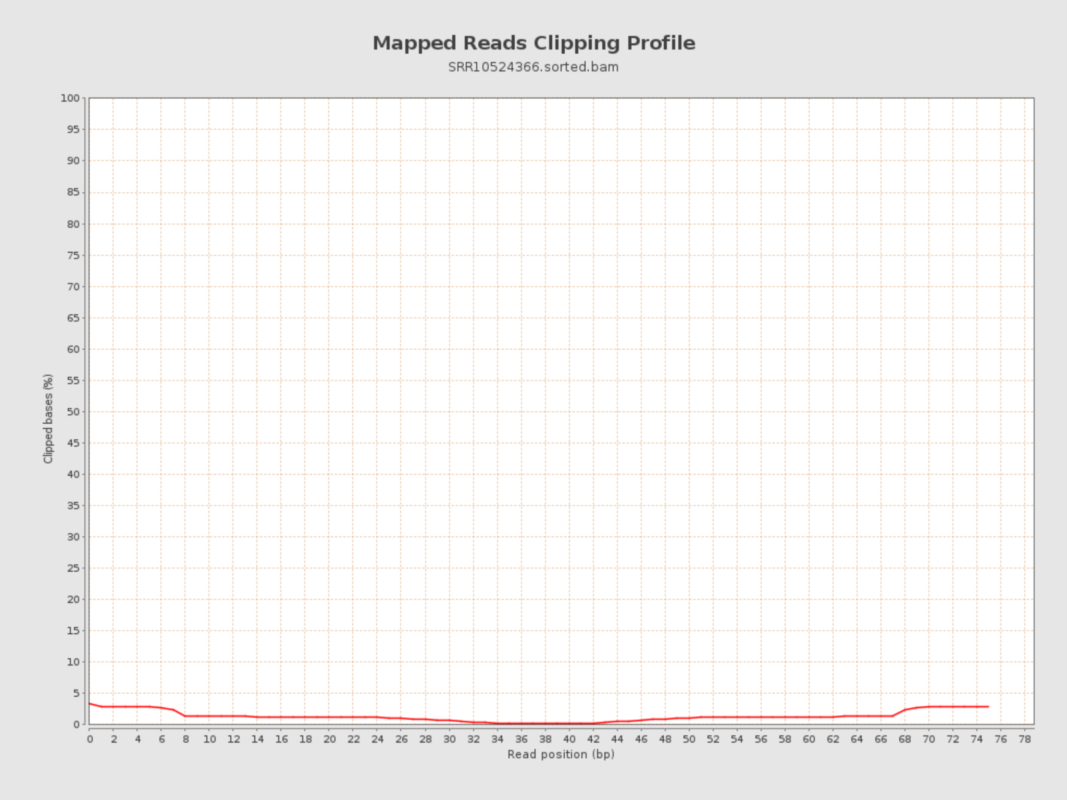
8. Results : Mapped Reads Nucleotide Content



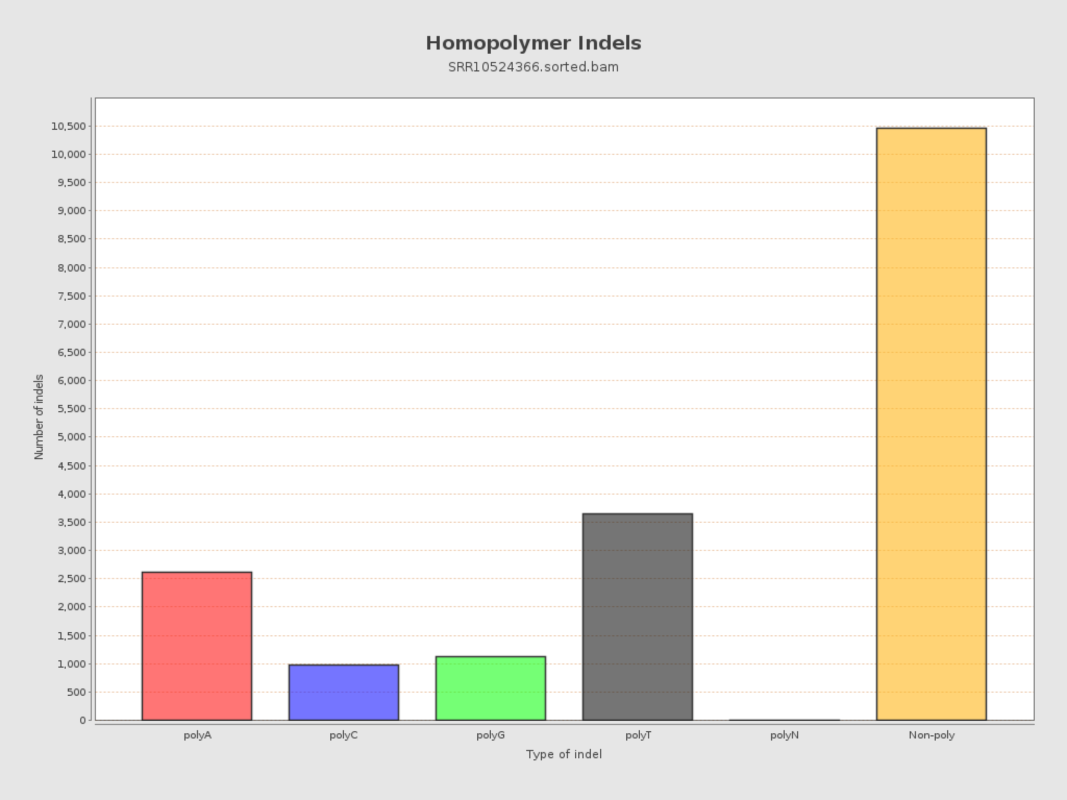
9. Results : Mapped Reads GC-content Distribution



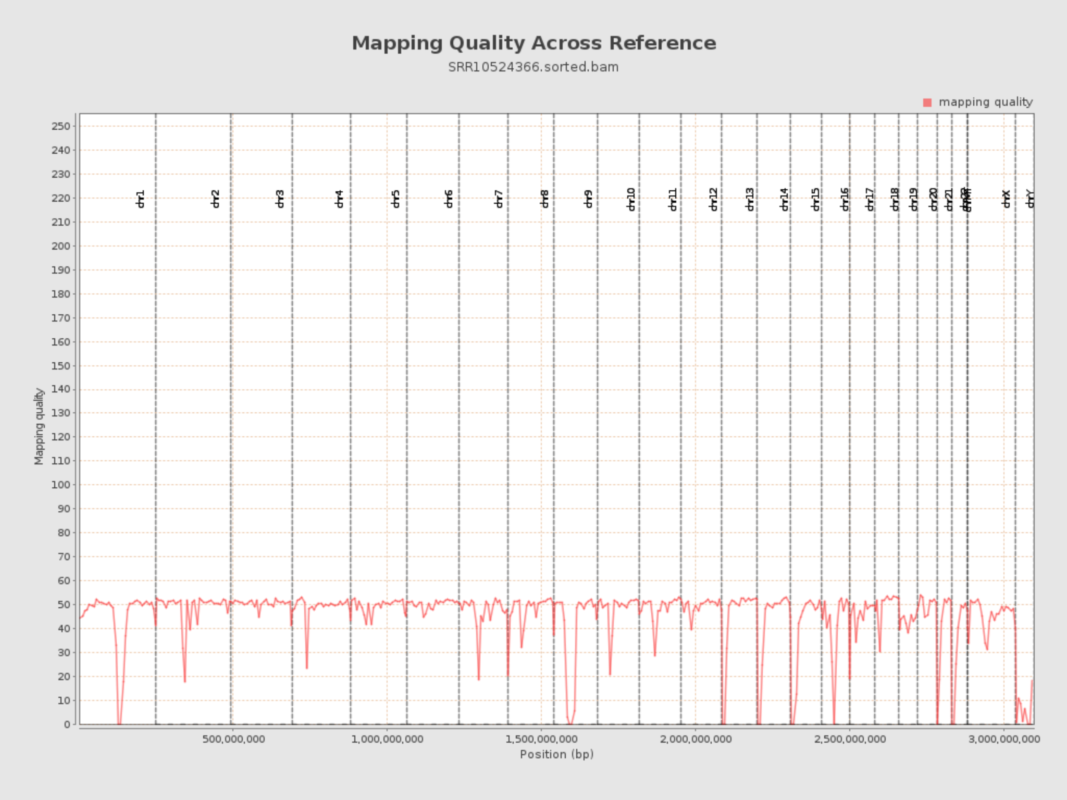
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram