Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:03:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524653.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_SRR10524653 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524653.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:03:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524653.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,189,758
Mapped reads	1,099,808 / 92.44%
Unmapped reads	89,950 / 7.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,183 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	43,109 / 3.62%
Duplication rate	3.07%
Clipped reads	1,101,606 / 92.59%

2.2. ACGT Content

Number/percentage of A's	15,702,078 / 24.53%
Number/percentage of C's	11,966,785 / 18.7%
Number/percentage of T's	20,618,510 / 32.22%
Number/percentage of G's	15,712,625 / 24.55%
Number/percentage of N's	599 / 0%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2047

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

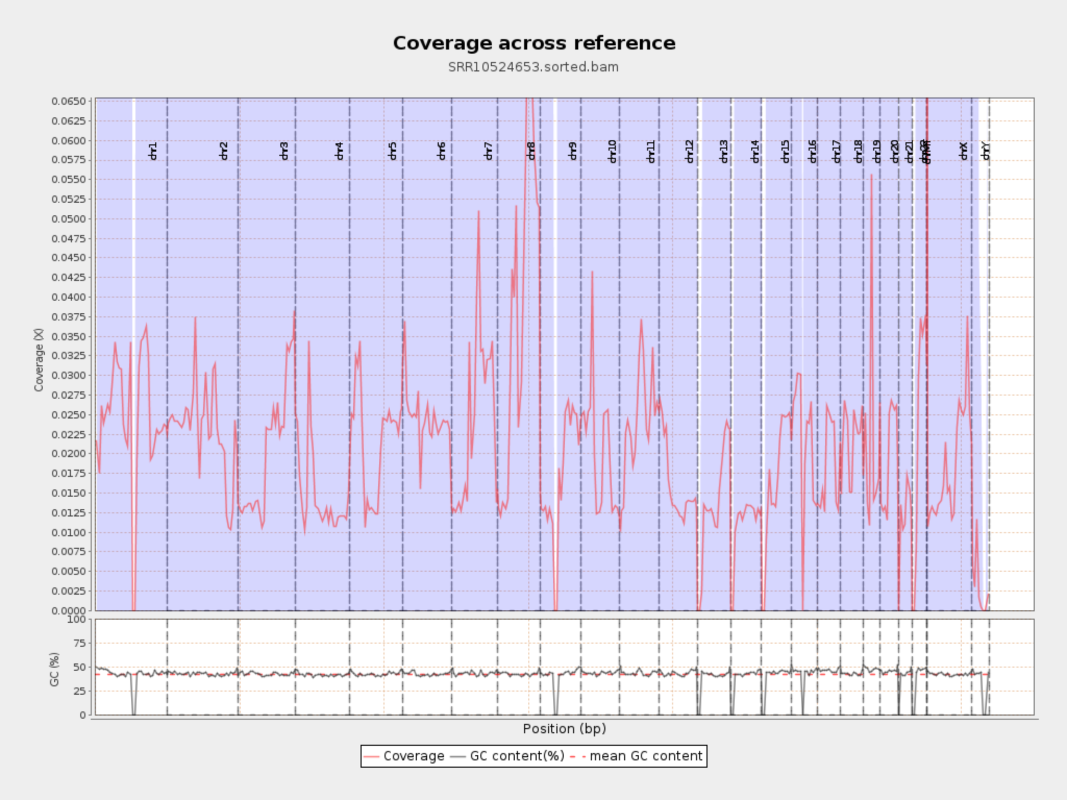
General error rate	0.52%
Mismatches	324,616
Insertions	4,152
Mapped reads with at least one insertion	0.38%
Deletions	12,156
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.65%

2.6. Chromosome stats

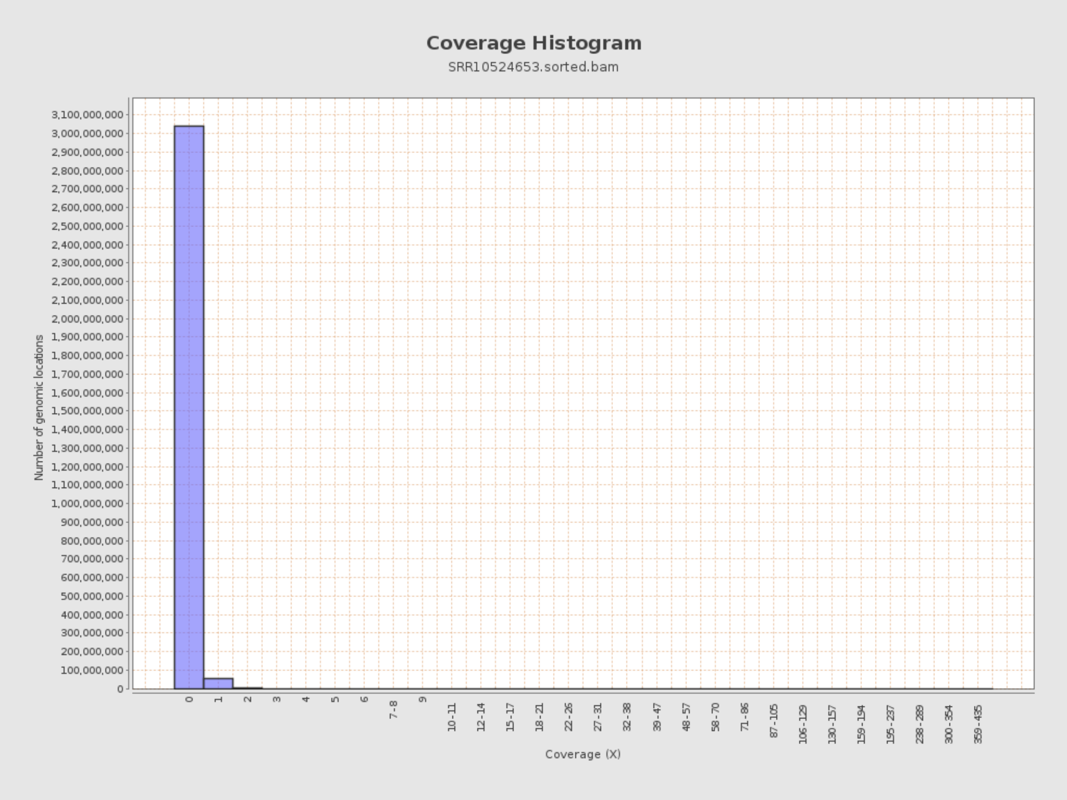
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6139949	0.0246	0.3391
chr2	243199373	5614374	0.0231	0.2452
chr3	198022430	4015922	0.0203	0.1552
chr4	191154276	2860984	0.015	0.1534
chr5	180915260	3938492	0.0218	0.1598
chr6	171115067	4209164	0.0246	0.1805
chr7	159138663	3913798	0.0246	0.2538

chr8	146364022	5831334	0.0398	0.2768
chr9	141213431	2354510	0.0167	0.1738
chr10	135534747	2824044	0.0208	0.224
chr11	135006516	3284801	0.0243	0.1891
chr12	133851895	2145146	0.016	0.1404
chr13	115169878	1541163	0.0134	0.1257
chr14	107349540	1166928	0.0109	0.1162
chr15	102531392	1667426	0.0163	0.1386
chr16	90354753	1937176	0.0214	0.1667
chr17	81195210	1485971	0.0183	0.1503
chr18	78077248	1701106	0.0218	0.255
chr19	59128983	1276353	0.0216	0.2528
chr20	63025520	1234430	0.0196	0.1556
chr21	48129895	582193	0.0121	0.1392
chr22	51304566	1210812	0.0236	0.1673
chrMT	16571	3194	0.1927	0.4773
chrX	155270560	2903382	0.0187	0.1586
chrY	59373566	178299	0.003	0.1049

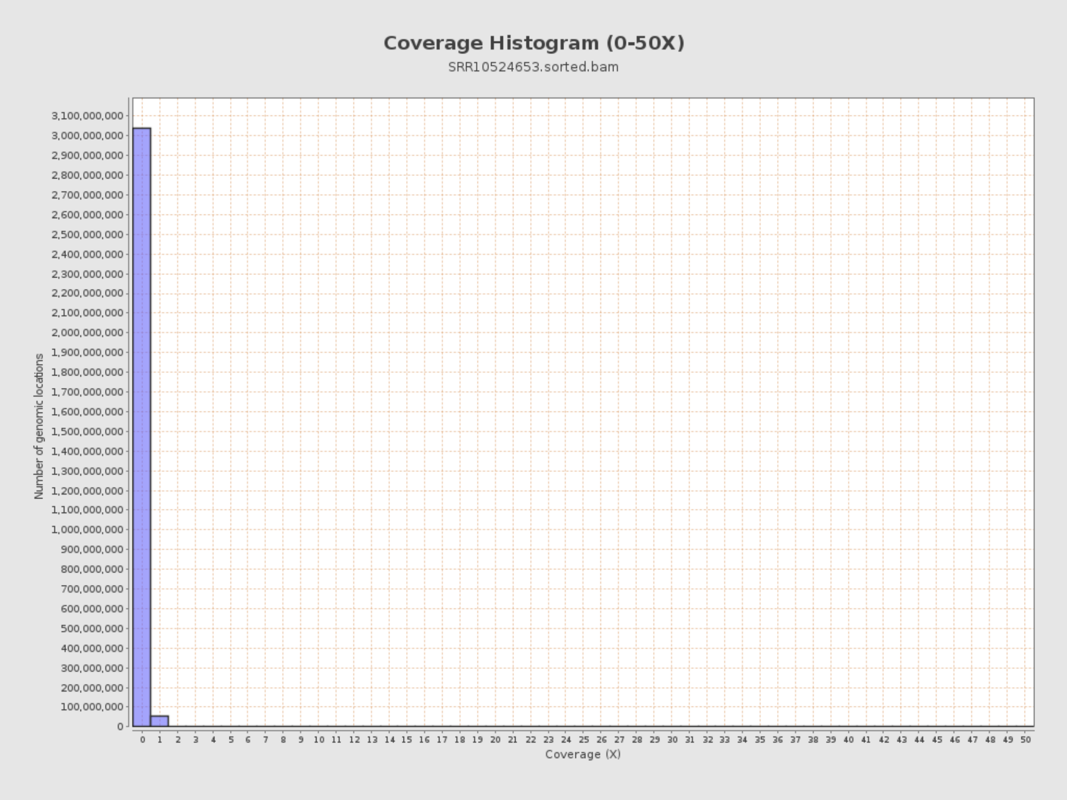
3. Results : Coverage across reference



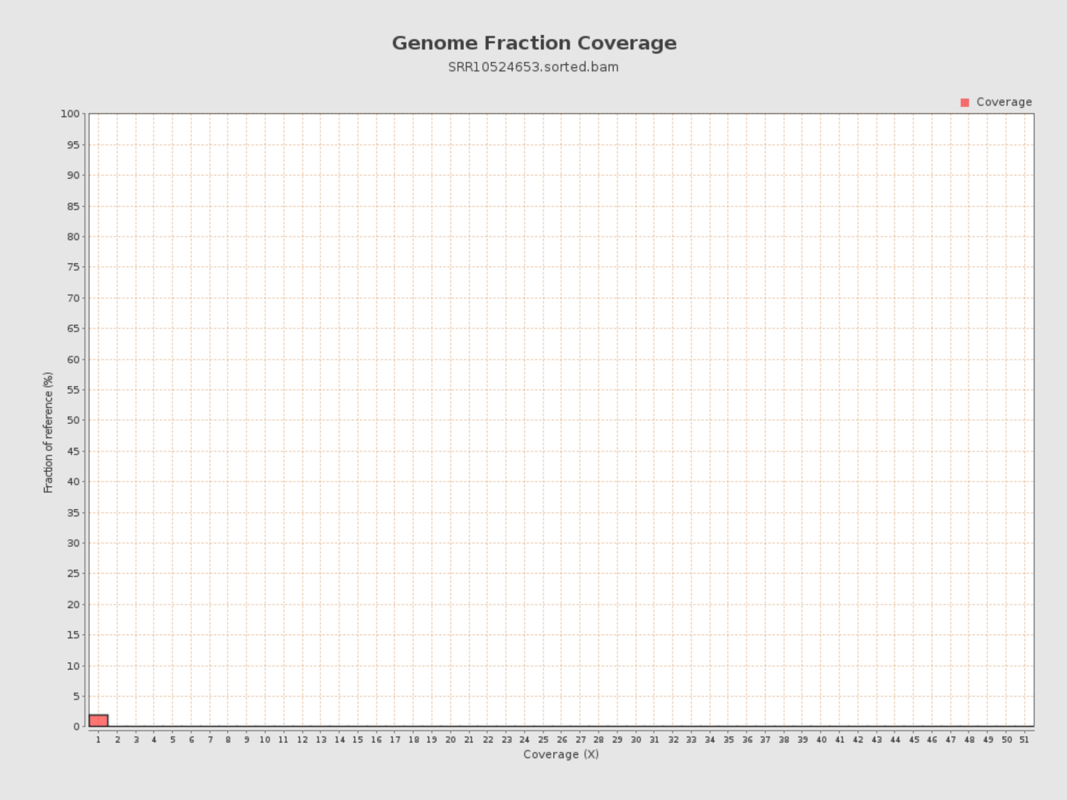
4. Results : Coverage Histogram



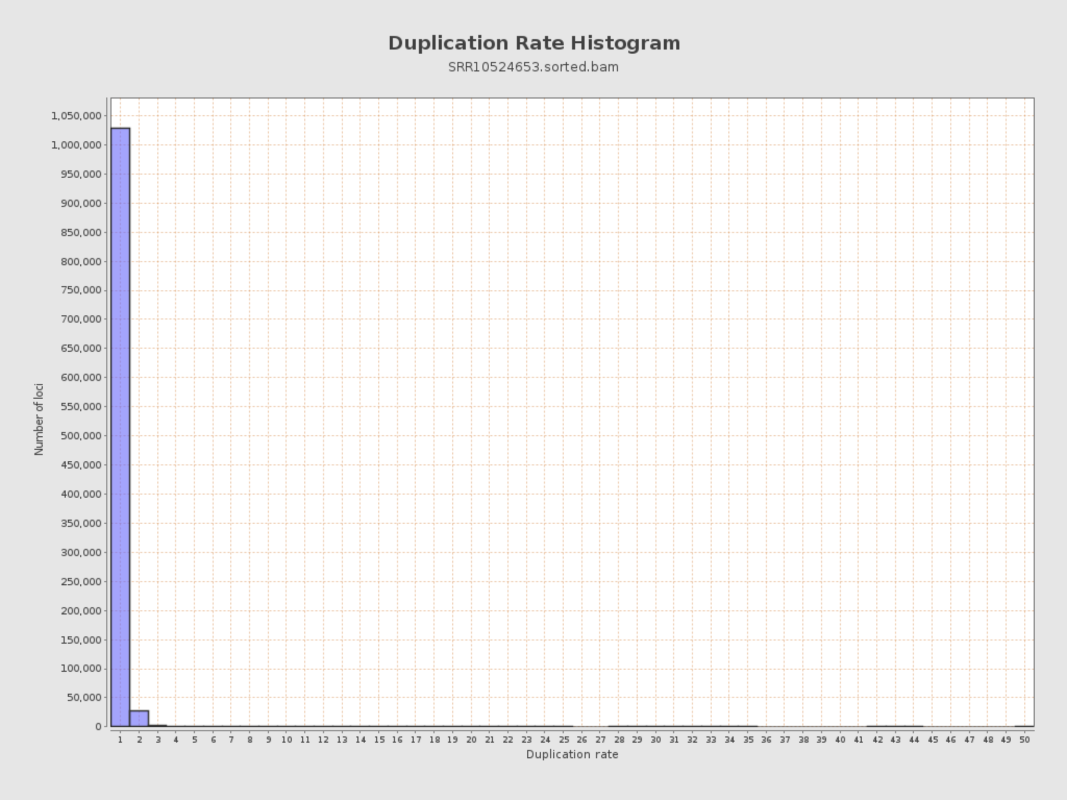
5. Results : Coverage Histogram (0-50X)



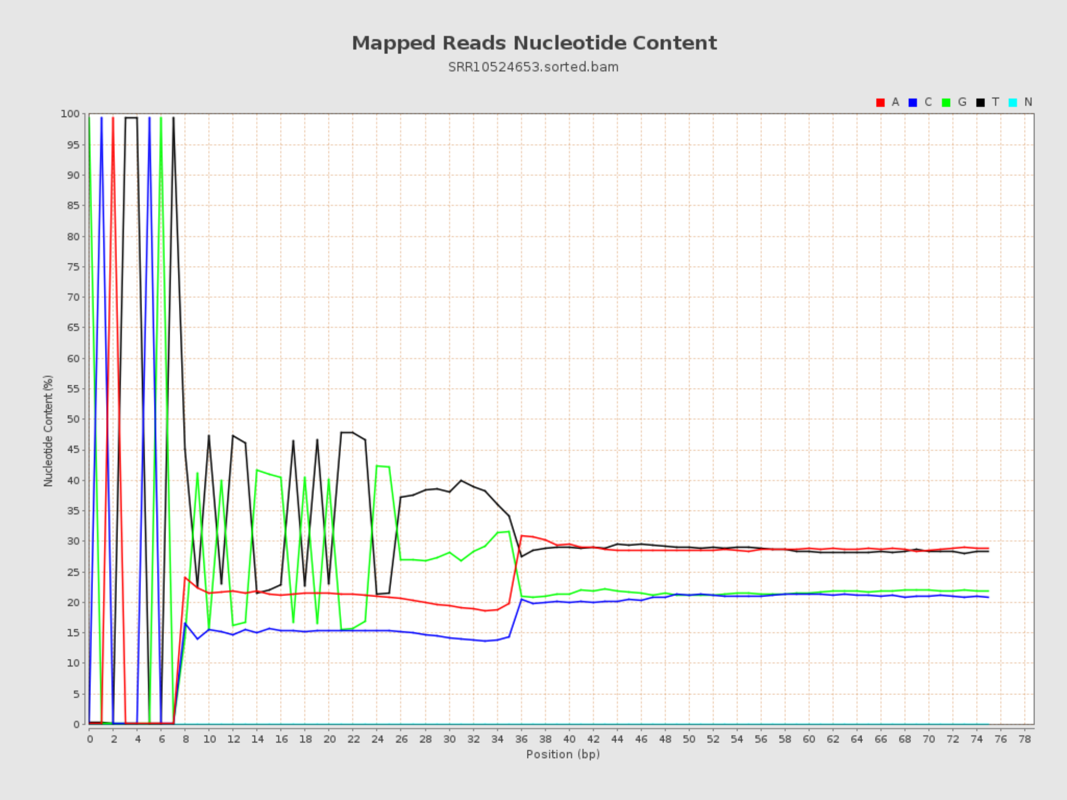
6. Results : Genome Fraction Coverage



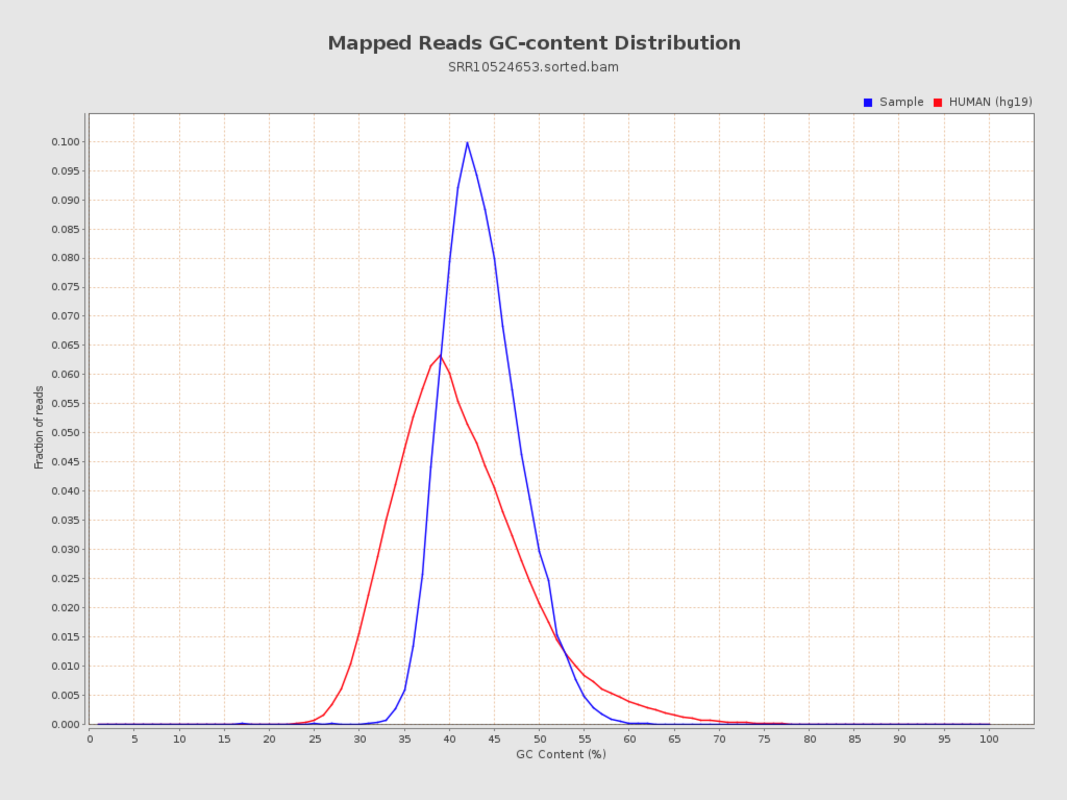
7. Results : Duplication Rate Histogram



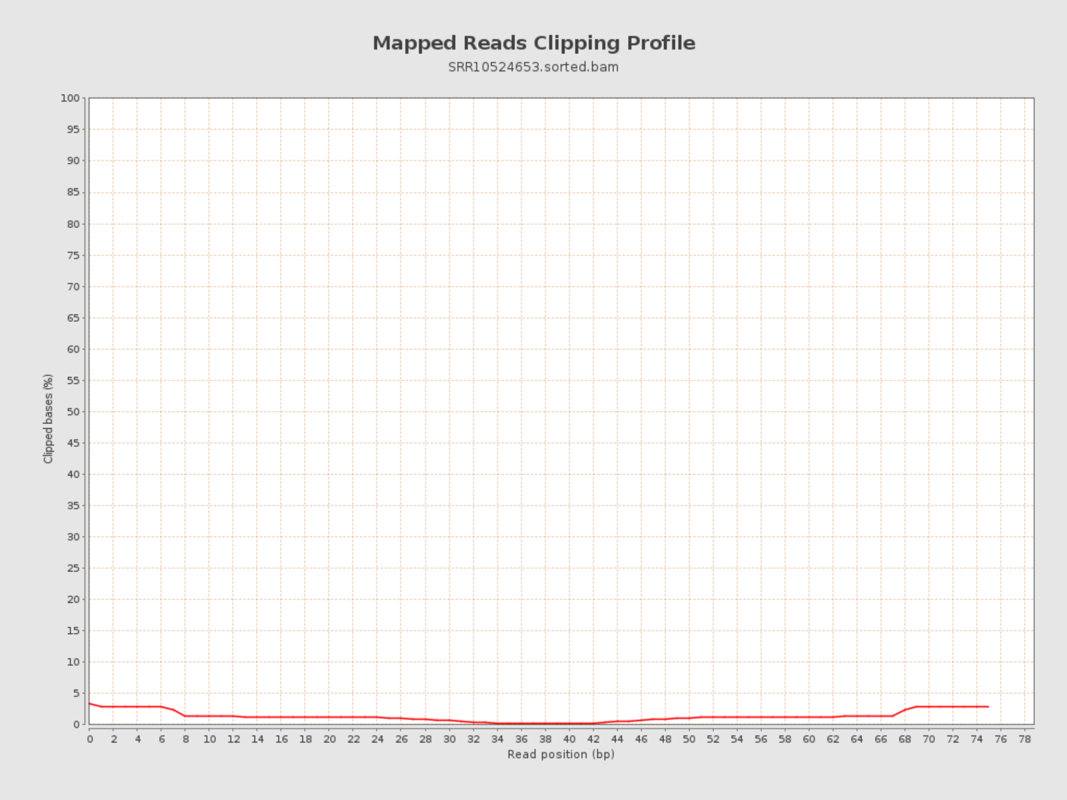
8. Results : Mapped Reads Nucleotide Content



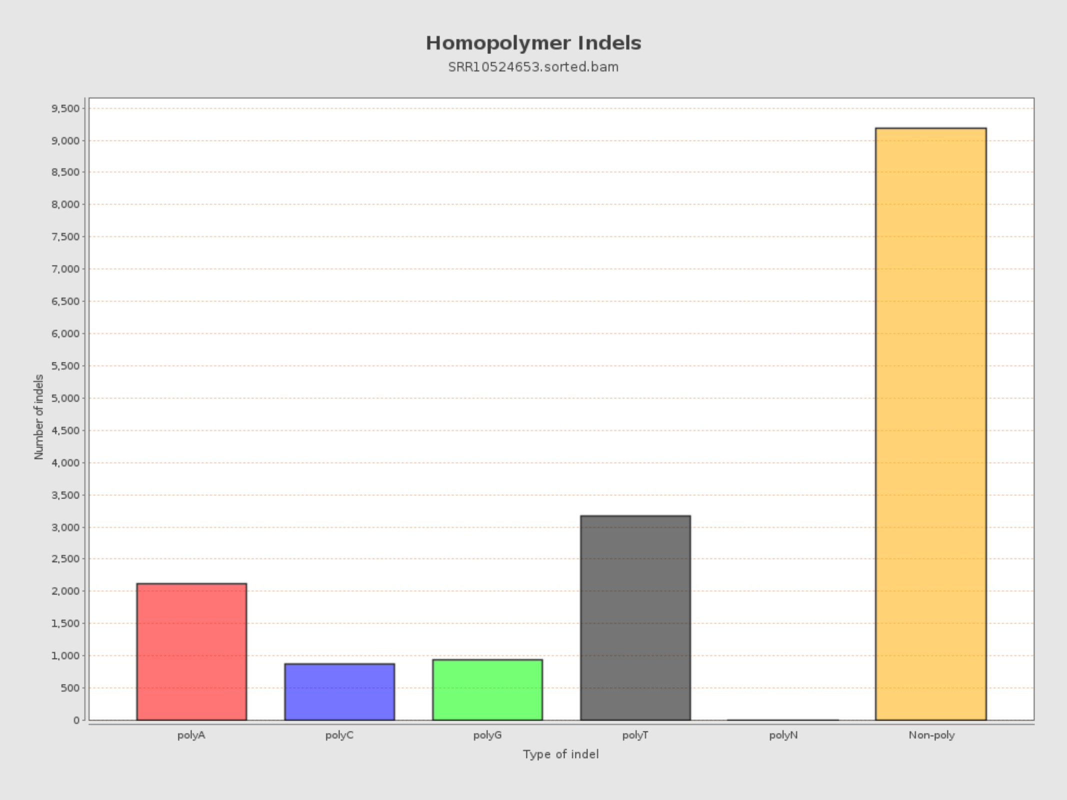
9. Results : Mapped Reads GC-content Distribution



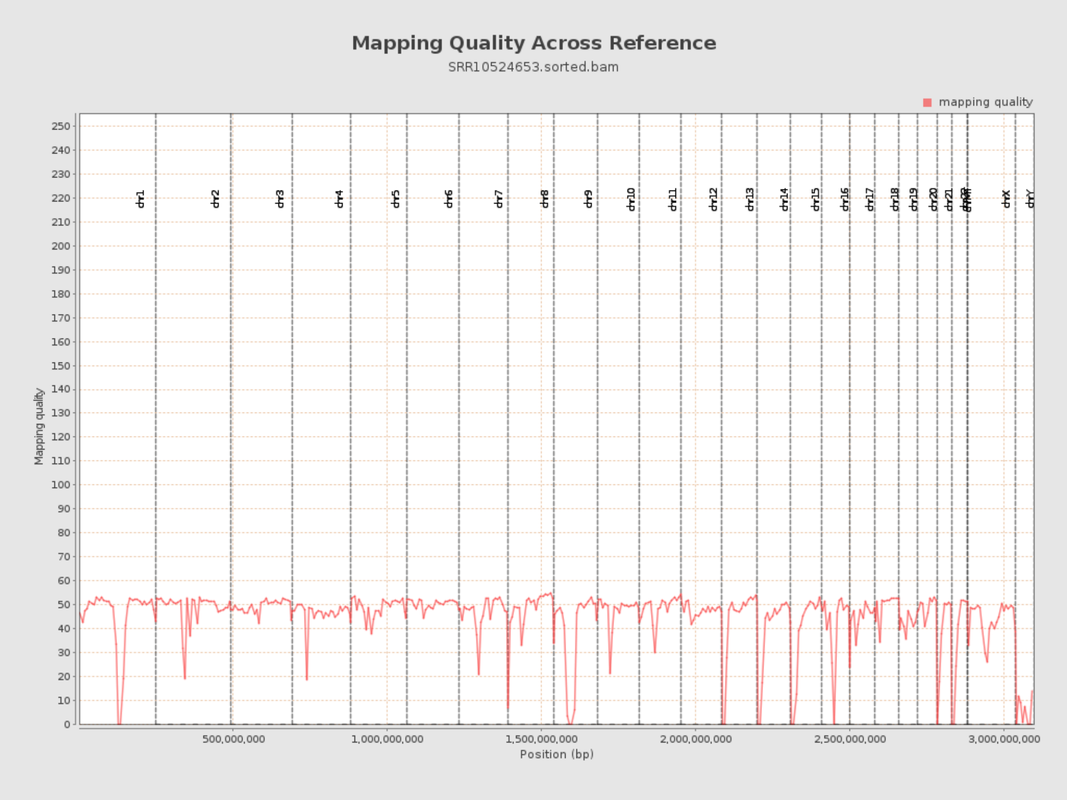
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram