Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:04:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524799.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_SRR10524799 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524799.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:04:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524799.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,169,784
Mapped reads	1,069,057 / 91.39%
Unmapped reads	100,727 / 8.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,720 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	33,627 / 2.87%
Duplication rate	2.41%
Clipped reads	1,072,203 / 91.66%

2.2. ACGT Content

Number/percentage of A's	14,788,299 / 24.09%
Number/percentage of C's	11,934,321 / 19.44%
Number/percentage of T's	19,281,873 / 31.41%
Number/percentage of G's	15,378,337 / 25.05%
Number/percentage of N's	6,978 / 0.01%
GC Percentage	44.49%

2.3. Coverage

Mean	0.0198

Standard Deviation	0.1905

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

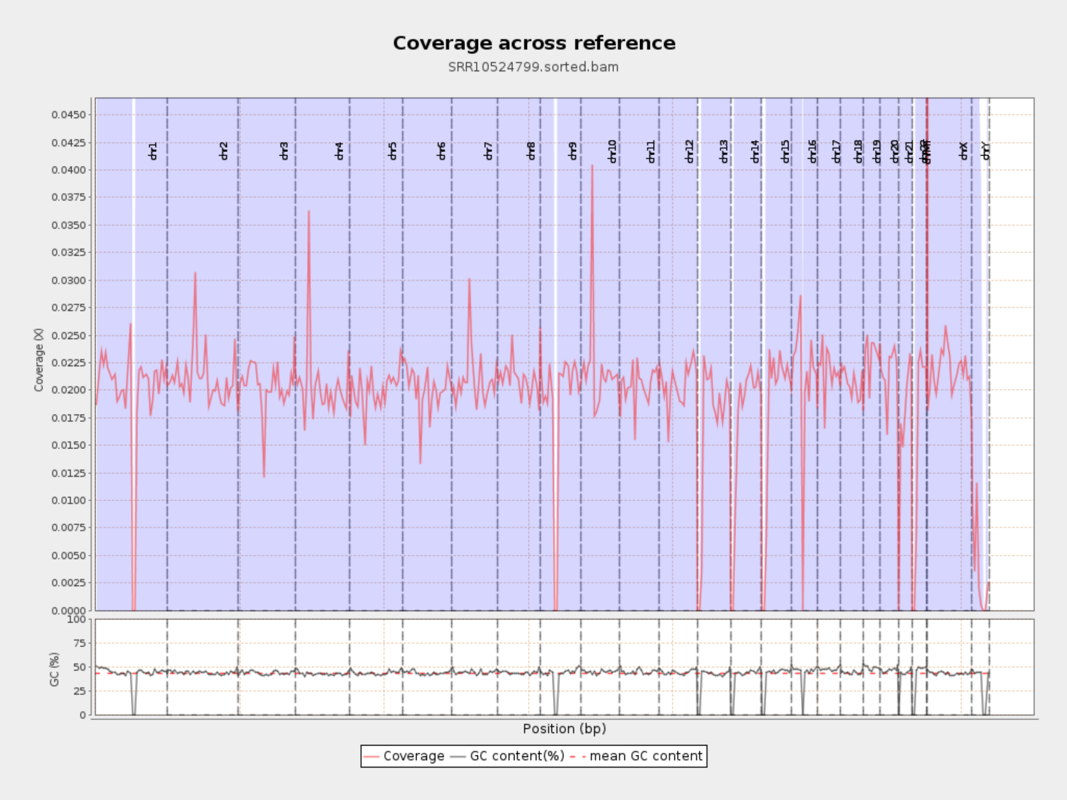
General error rate	0.51%
Mismatches	308,214
Insertions	3,754
Mapped reads with at least one insertion	0.35%
Deletions	12,138
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.7%

2.6. Chromosome stats

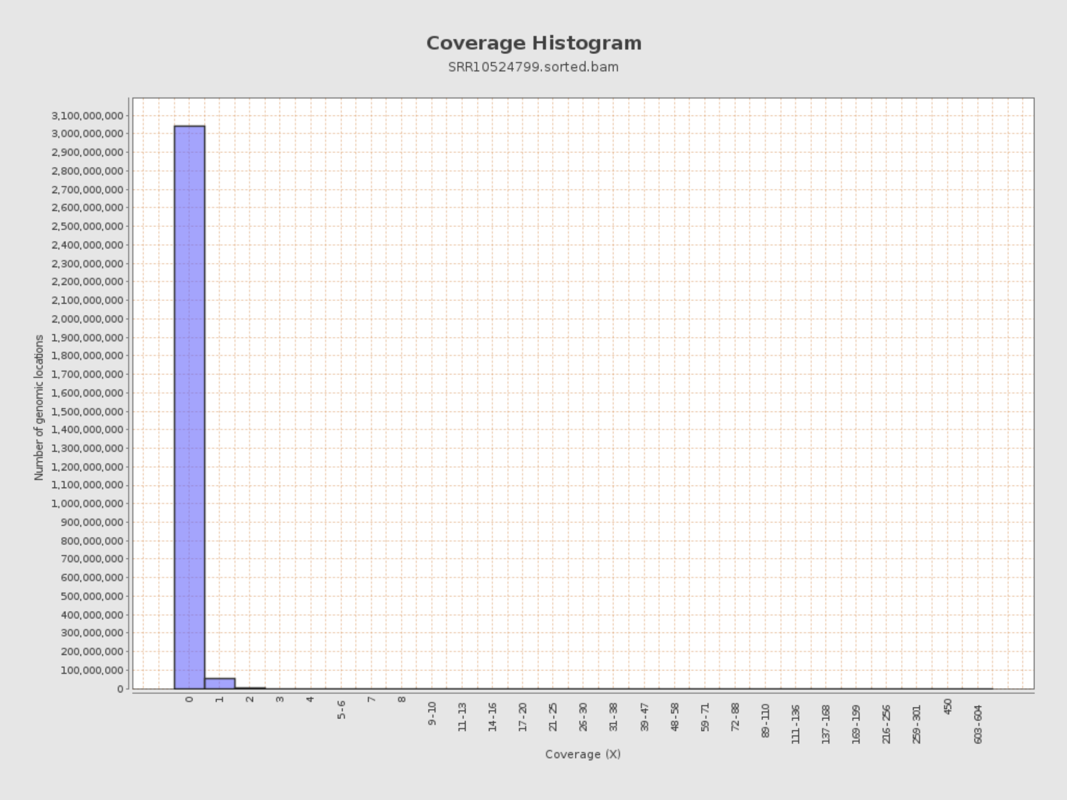
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4922058	0.0197	0.2431
chr2	243199373	5144652	0.0212	0.2967
chr3	198022430	4026042	0.0203	0.1539
chr4	191154276	3916513	0.0205	0.17
chr5	180915260	3646980	0.0202	0.1527
chr6	171115067	3456521	0.0202	0.1646
chr7	159138663	3342678	0.021	0.2201

chr8	146364022	3063009	0.0209	0.178
chr9	141213431	2636540	0.0187	0.1667
chr10	135534747	2987475	0.022	0.2233
chr11	135006516	2770791	0.0205	0.1719
chr12	133851895	2758192	0.0206	0.1556
chr13	115169878	1901228	0.0165	0.1386
chr14	107349540	1817302	0.0169	0.1427
chr15	102531392	1811461	0.0177	0.1435
chr16	90354753	1878656	0.0208	0.1705
chr17	81195210	1771501	0.0218	0.1628
chr18	78077248	1610159	0.0206	0.2374
chr19	59128983	1366468	0.0231	0.2053
chr20	63025520	1347628	0.0214	0.1609
chr21	48129895	832169	0.0173	0.1553
chr22	51304566	792894	0.0155	0.135
chrMT	16571	14496	0.8748	1.0903
chrX	155270560	3390110	0.0218	0.1666
chrY	59373566	204370	0.0034	0.1009

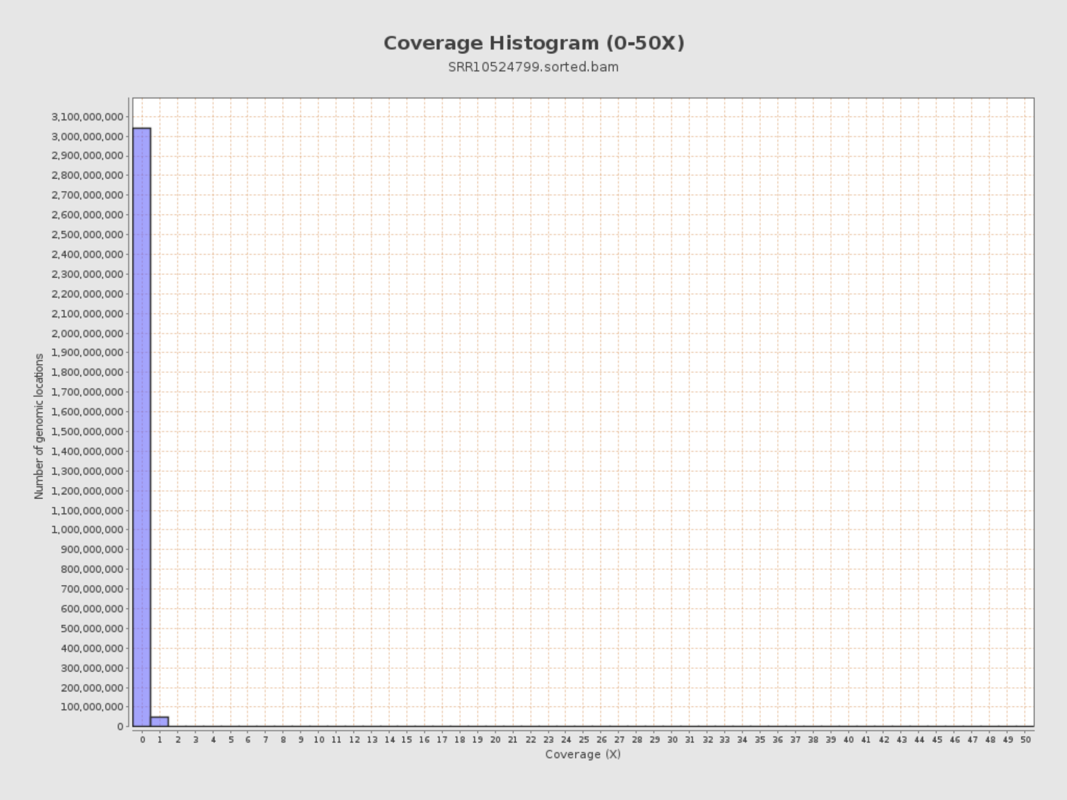
3. Results : Coverage across reference



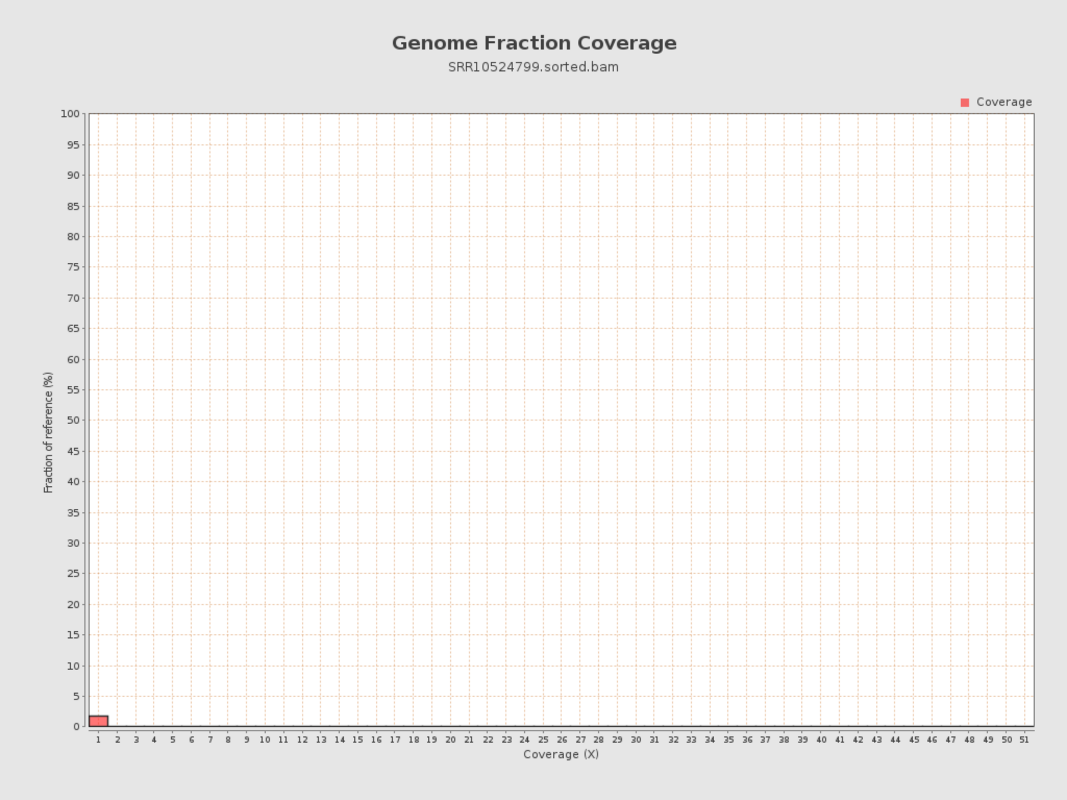
4. Results : Coverage Histogram



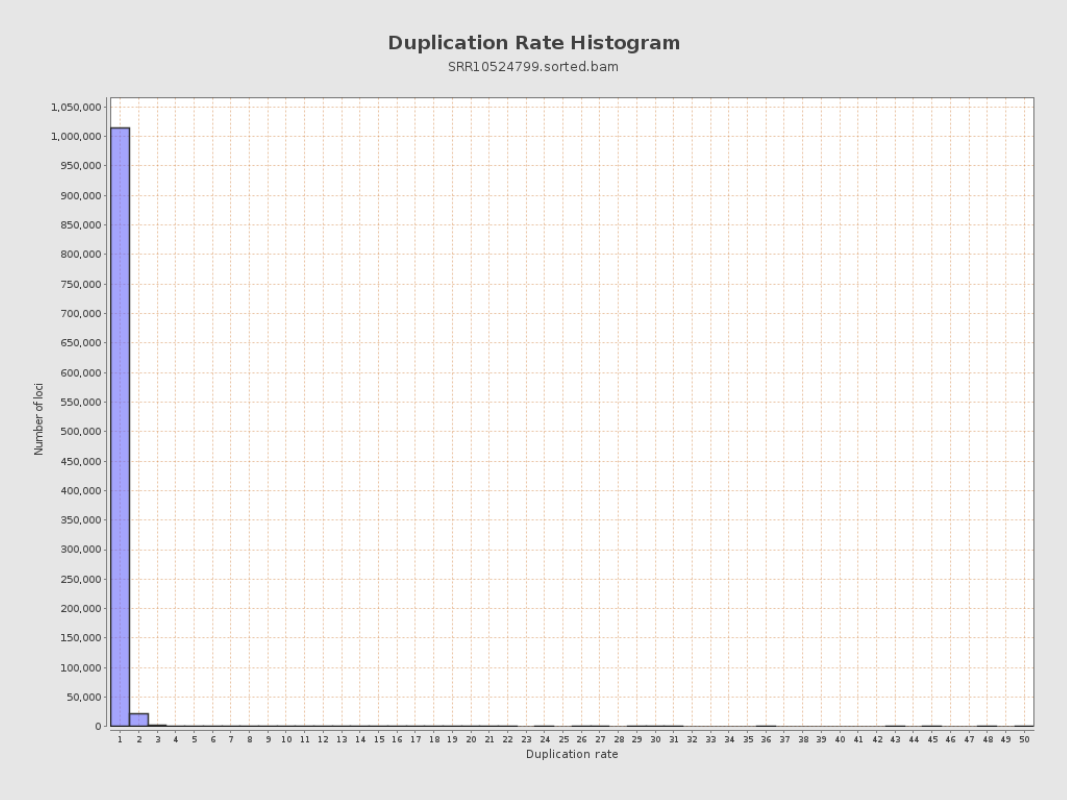
5. Results : Coverage Histogram (0-50X)



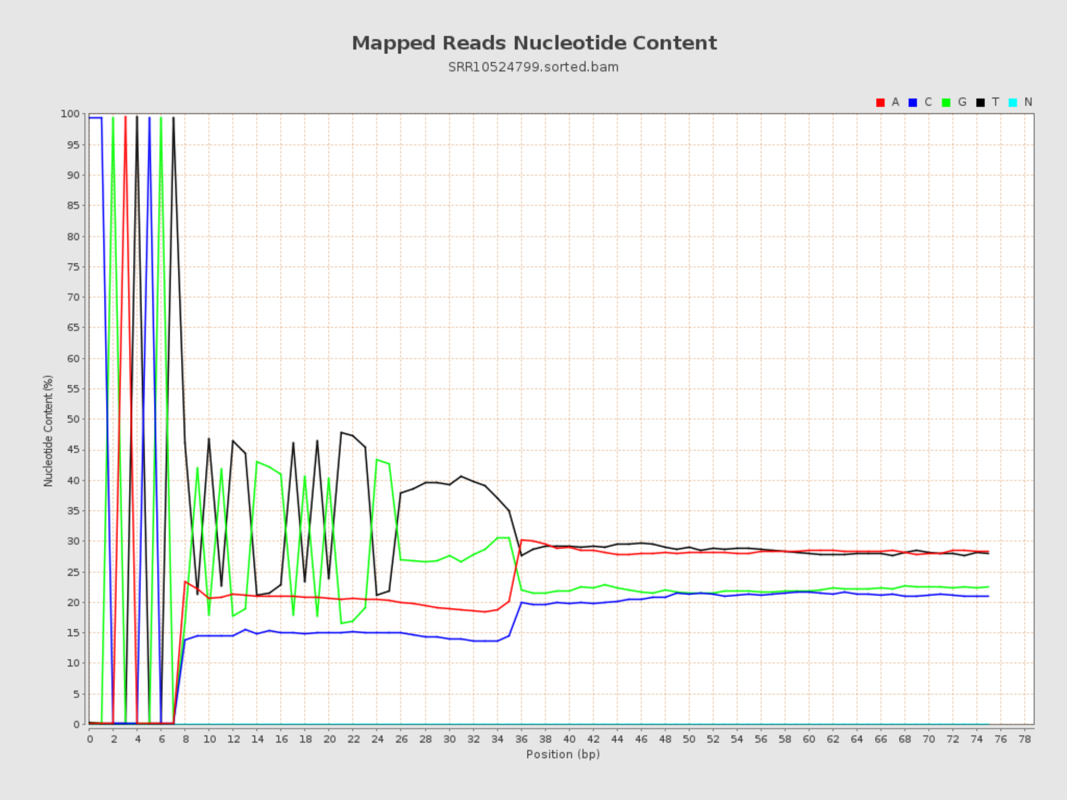
6. Results : Genome Fraction Coverage



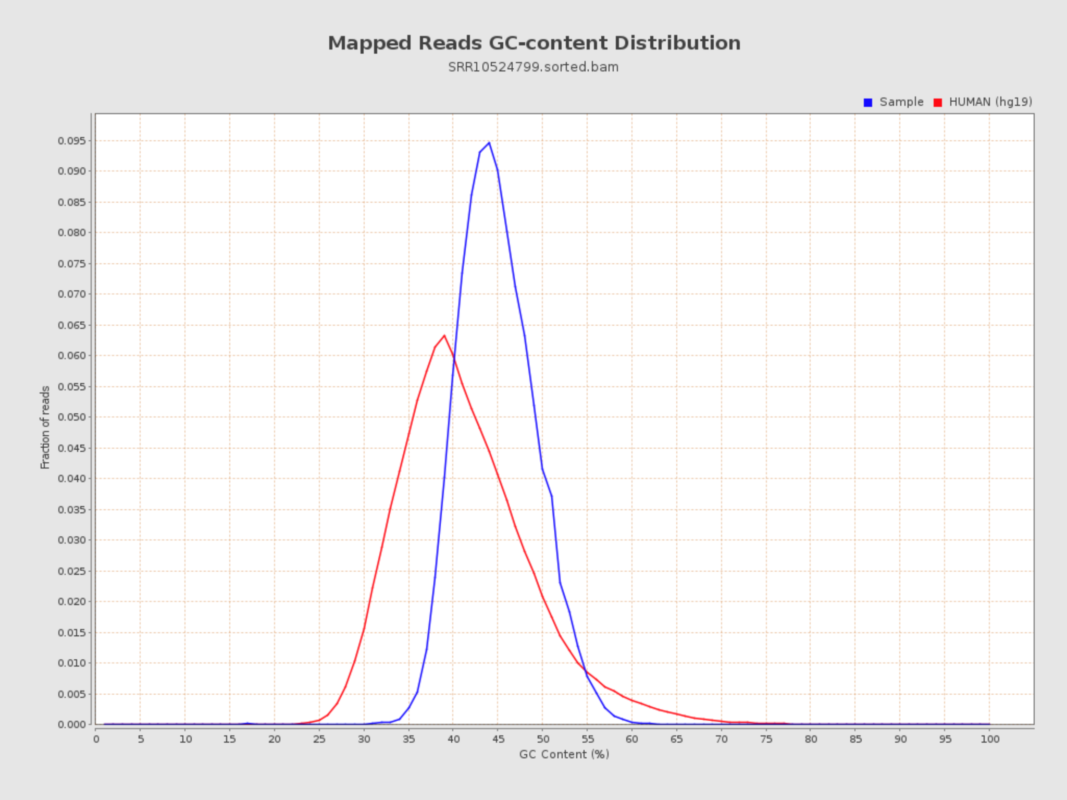
7. Results : Duplication Rate Histogram



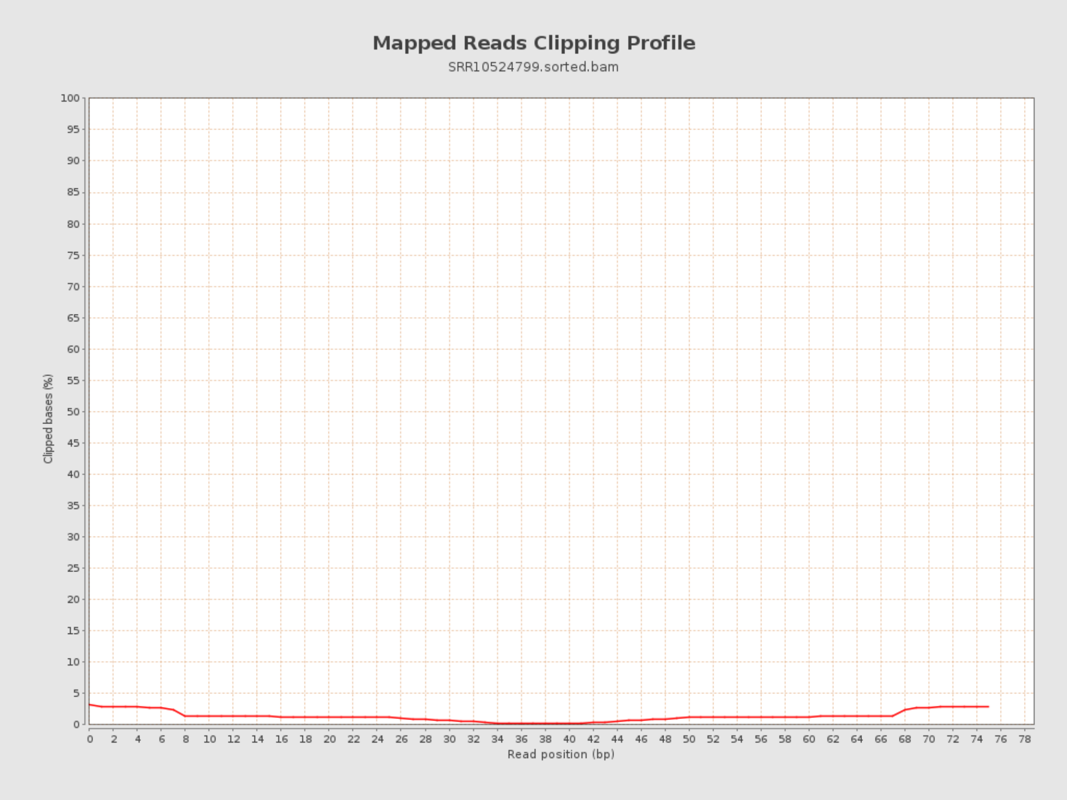
8. Results : Mapped Reads Nucleotide Content



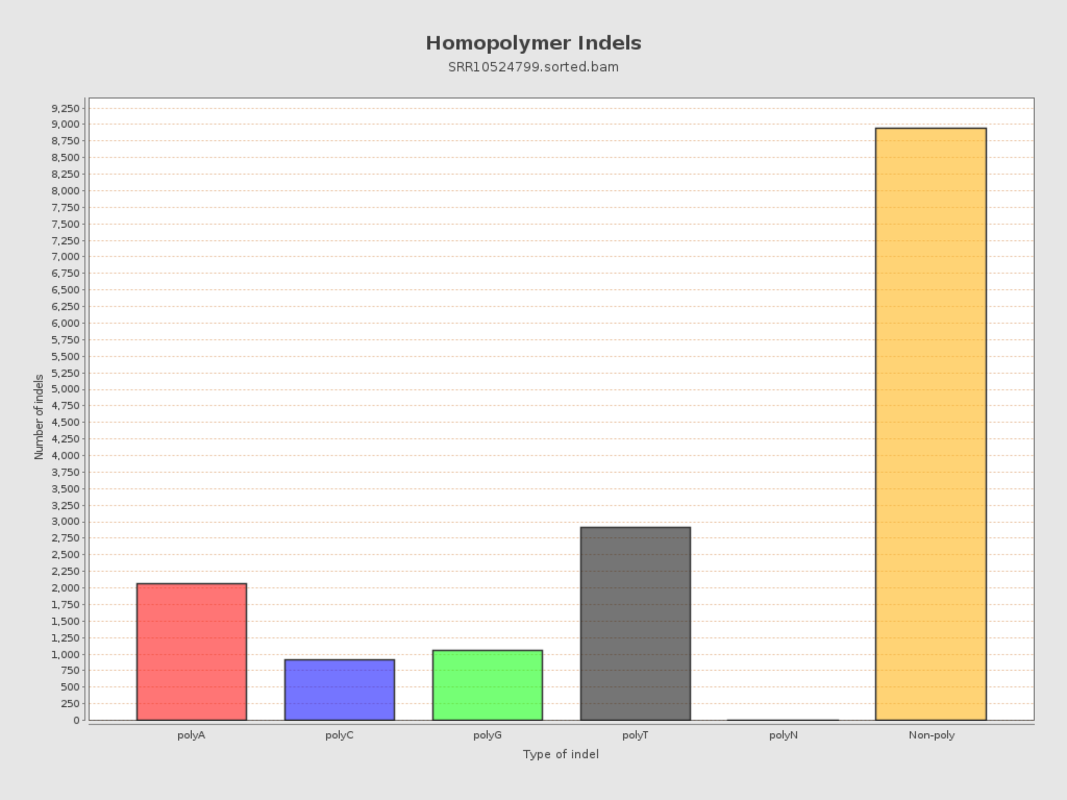
9. Results : Mapped Reads GC-content Distribution



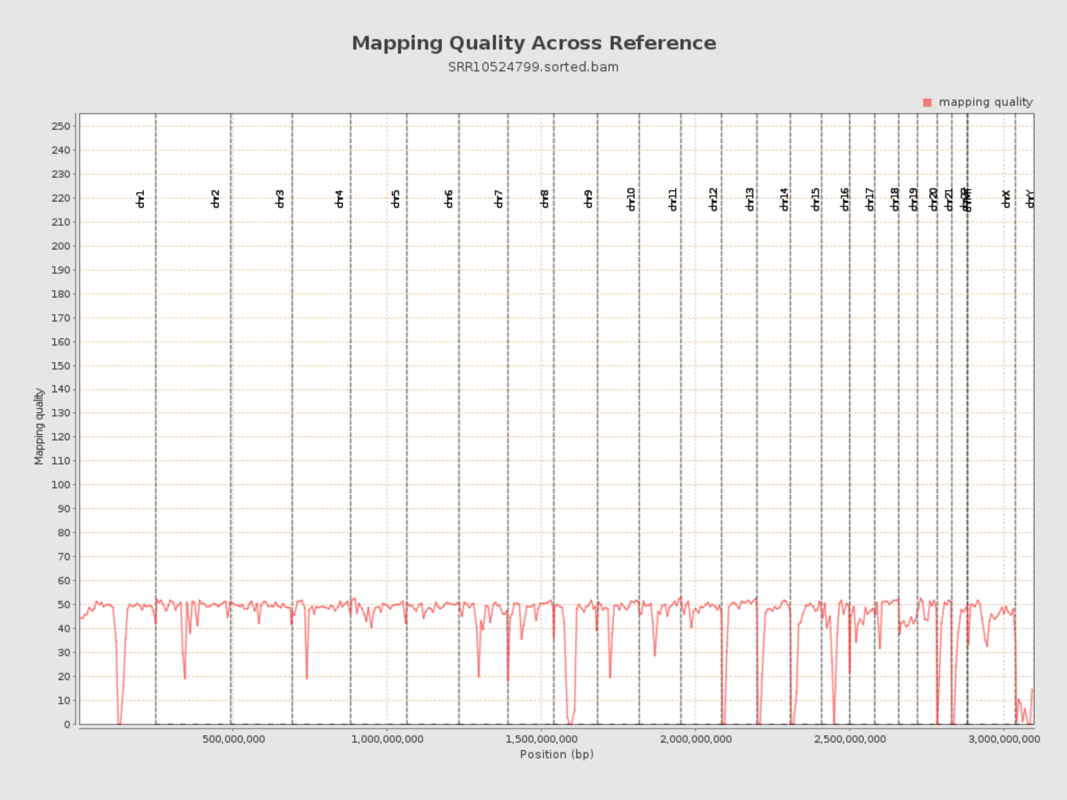
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram