Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:08:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524899.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_SRR10524899 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524899.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:08:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524899.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	685,355
Mapped reads	633,171 / 92.39%
Unmapped reads	52,184 / 7.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,266 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	13,490 / 1.97%
Duplication rate	1.53%
Clipped reads	632,954 / 92.35%

2.2. ACGT Content

Number/percentage of A's	10,068,068 / 27.03%
Number/percentage of C's	6,916,356 / 18.57%
Number/percentage of T's	11,355,668 / 30.49%
Number/percentage of G's	8,898,288 / 23.89%
Number/percentage of N's	5,235 / 0.01%
GC Percentage	42.46%

2.3. Coverage

Mean	0.012

Standard Deviation	0.1461

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

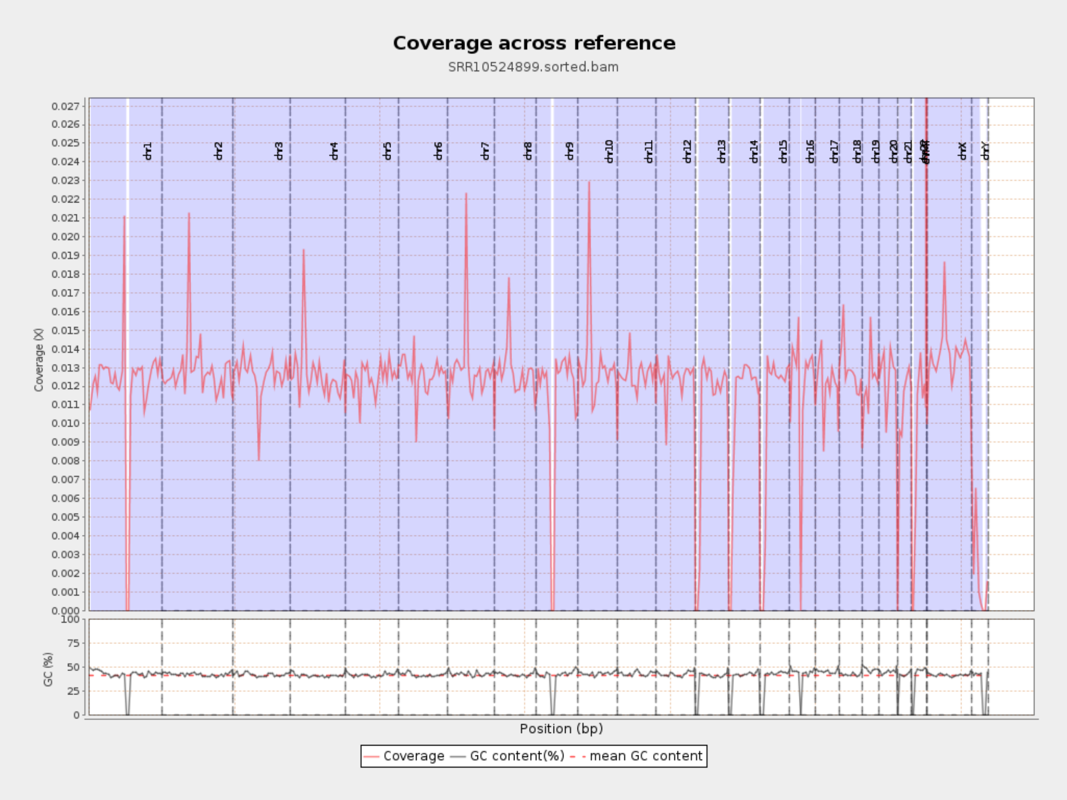
General error rate	0.51%
Mismatches	181,737
Insertions	3,238
Mapped reads with at least one insertion	0.51%
Deletions	7,241
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.45%

2.6. Chromosome stats

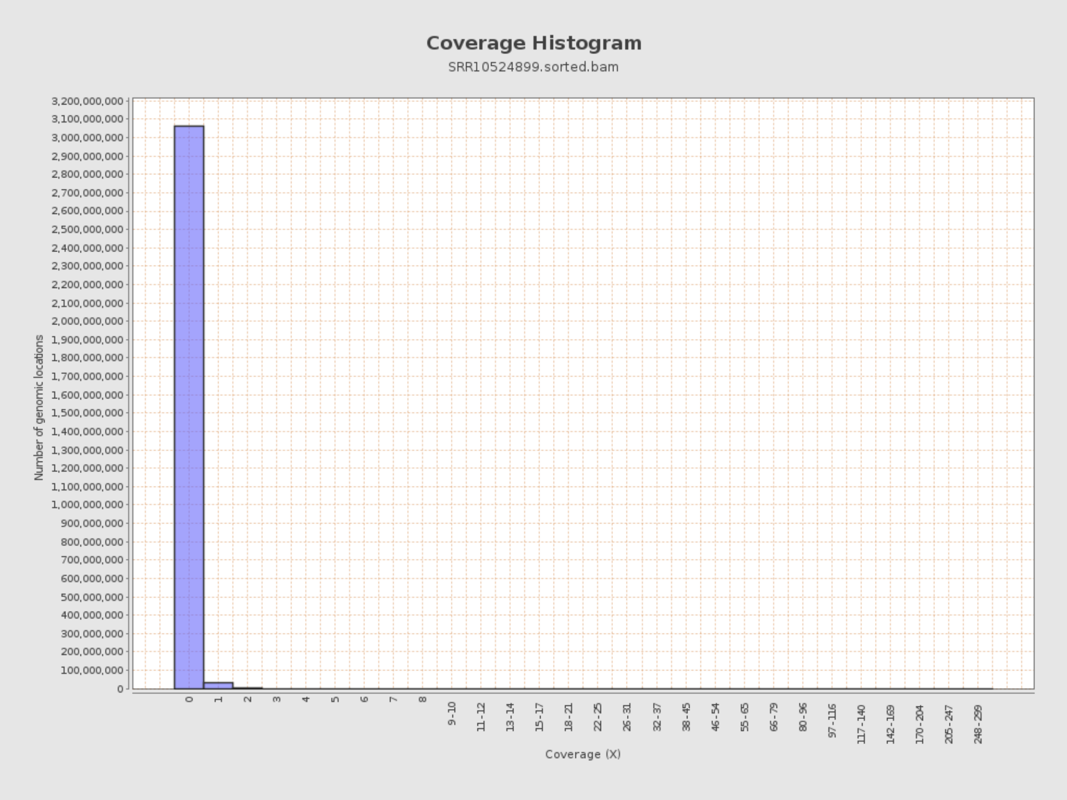
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2981389	0.012	0.2461
chr2	243199373	3143398	0.0129	0.1553
chr3	198022430	2489639	0.0126	0.1159
chr4	191154276	2415807	0.0126	0.1212
chr5	180915260	2249808	0.0124	0.1155
chr6	171115067	2158603	0.0126	0.1212
chr7	159138663	2076468	0.013	0.1843

chr8	146364022	1877517	0.0128	0.1405
chr9	141213431	1573034	0.0111	0.132
chr10	135534747	1786861	0.0132	0.1431
chr11	135006516	1700415	0.0126	0.1406
chr12	133851895	1664748	0.0124	0.1165
chr13	115169878	1193180	0.0104	0.1053
chr14	107349540	1132460	0.0105	0.1079
chr15	102531392	1052349	0.0103	0.1048
chr16	90354753	1082015	0.012	0.1193
chr17	81195210	974721	0.012	0.1173
chr18	78077248	1012200	0.013	0.2308
chr19	59128983	726327	0.0123	0.1738
chr20	63025520	785594	0.0125	0.1161
chr21	48129895	495017	0.0103	0.1107
chr22	51304566	437047	0.0085	0.0957
chrMT	16571	5830	0.3518	0.5863
chrX	155270560	2127026	0.0137	0.1292
chrY	59373566	113723	0.0019	0.0607

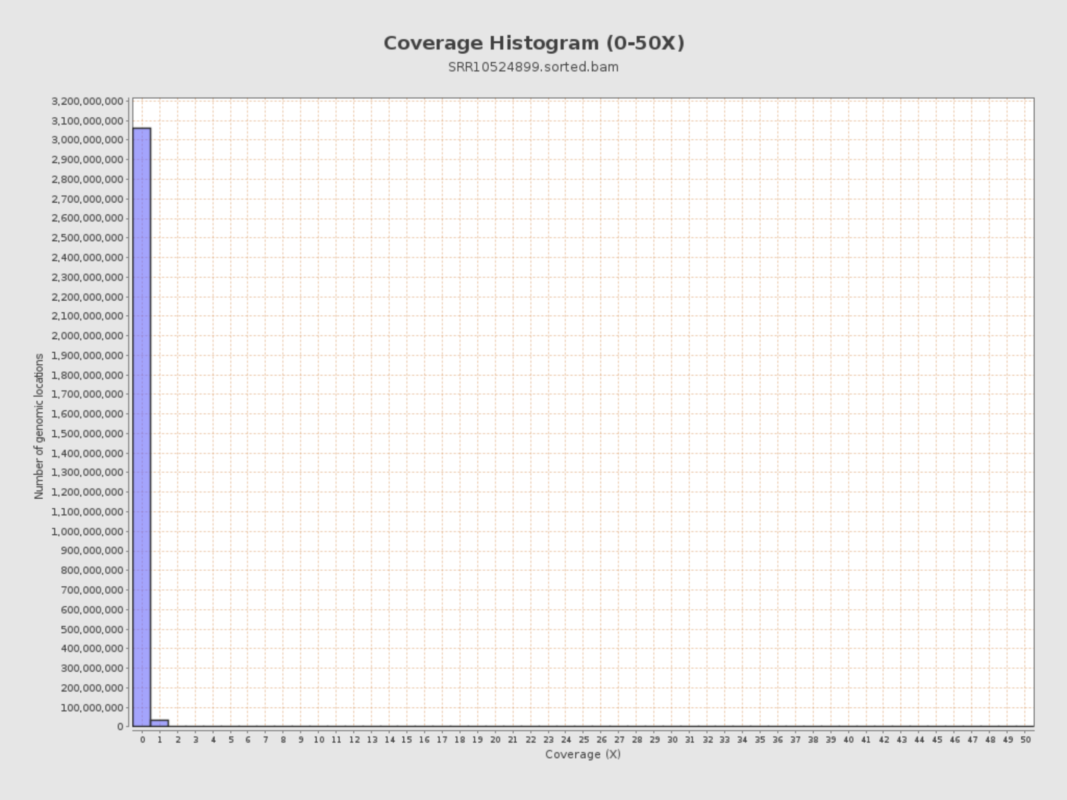
3. Results : Coverage across reference



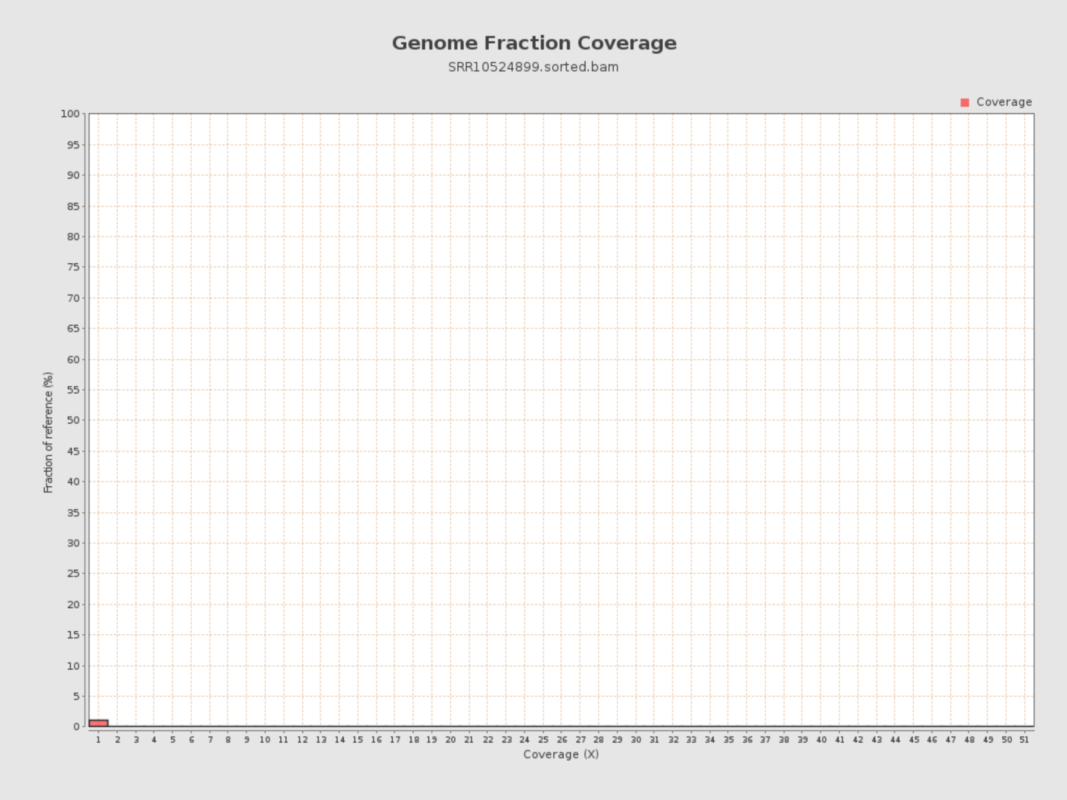
4. Results : Coverage Histogram



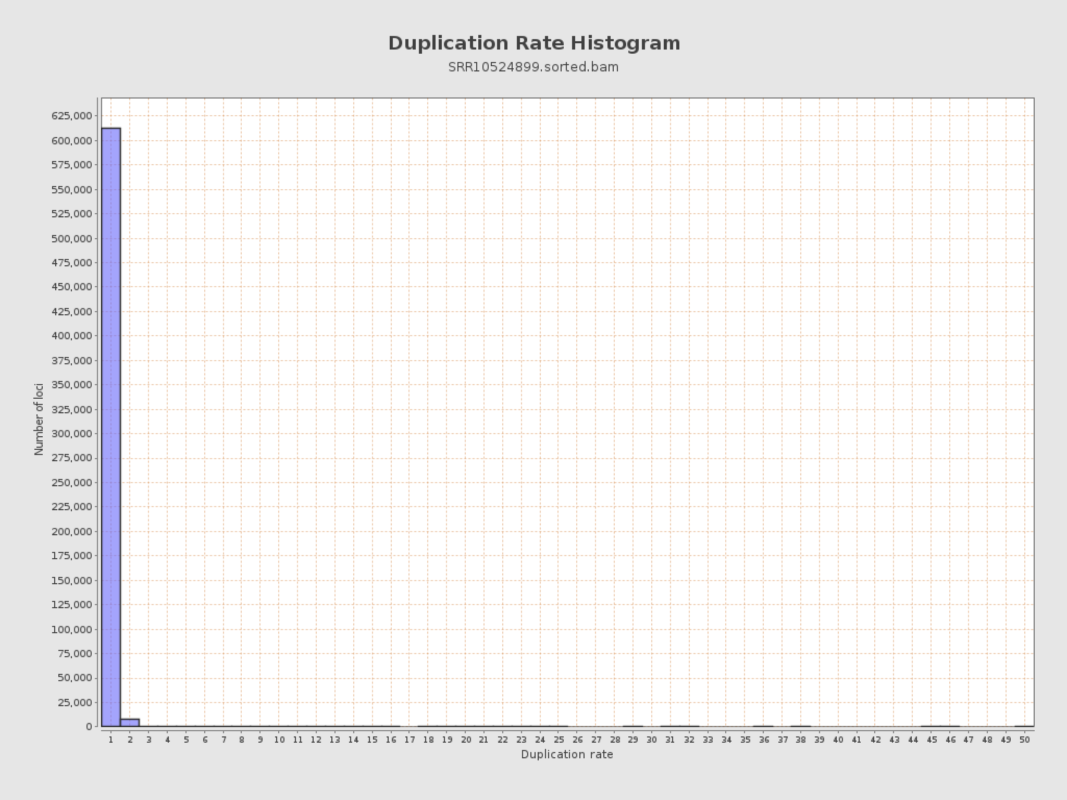
5. Results : Coverage Histogram (0-50X)



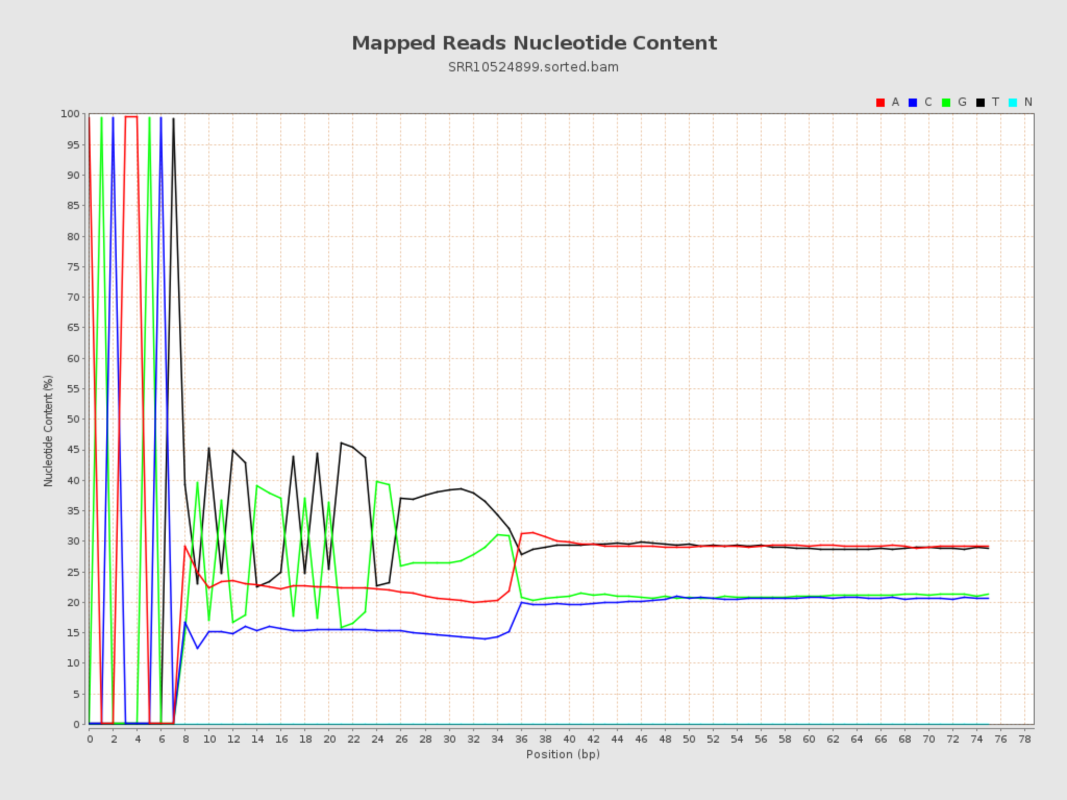
6. Results : Genome Fraction Coverage



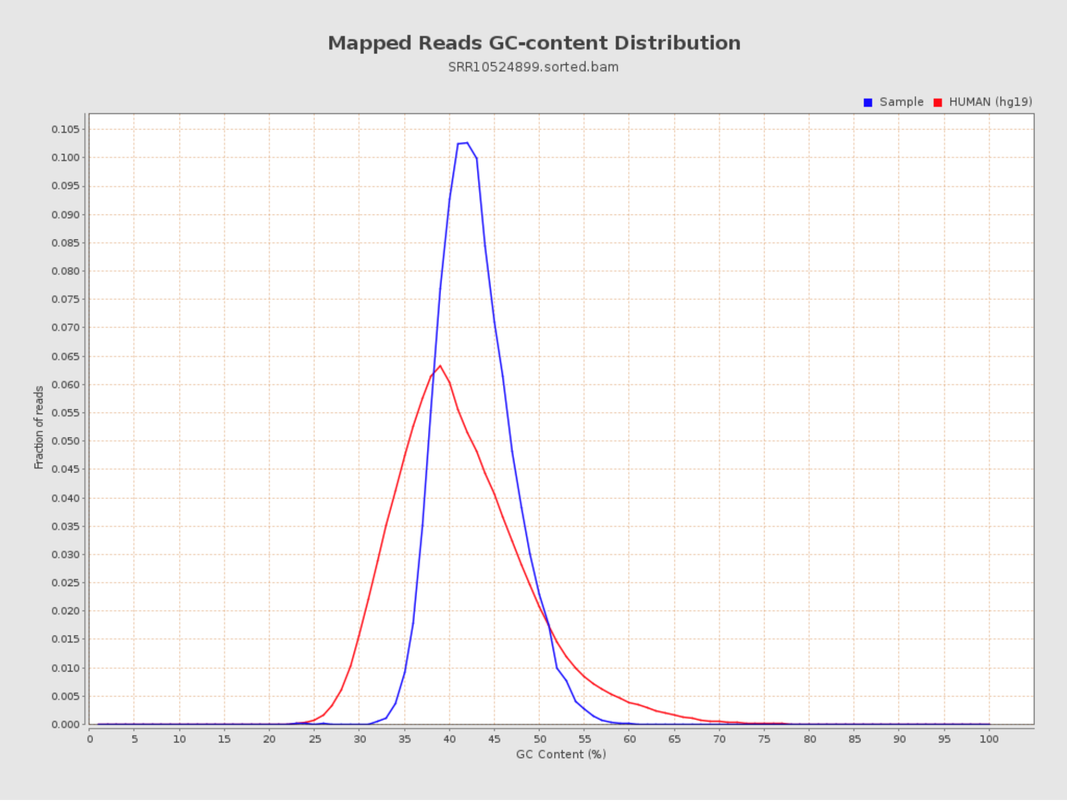
7. Results : Duplication Rate Histogram



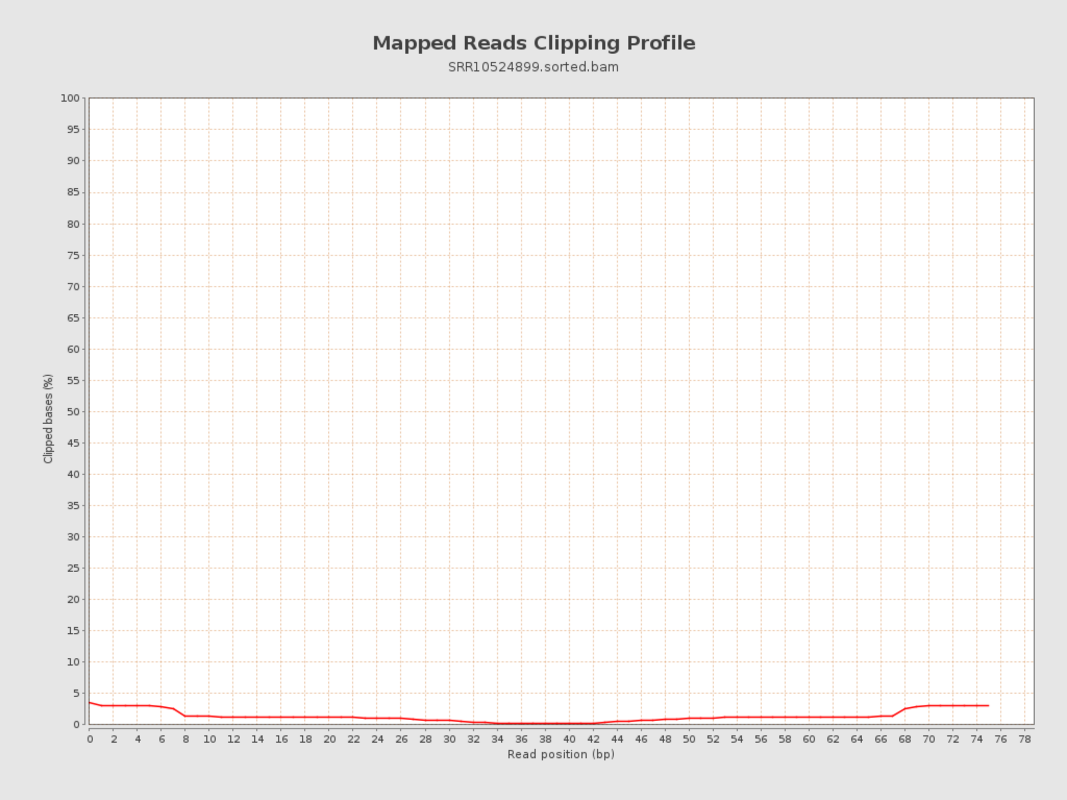
8. Results : Mapped Reads Nucleotide Content



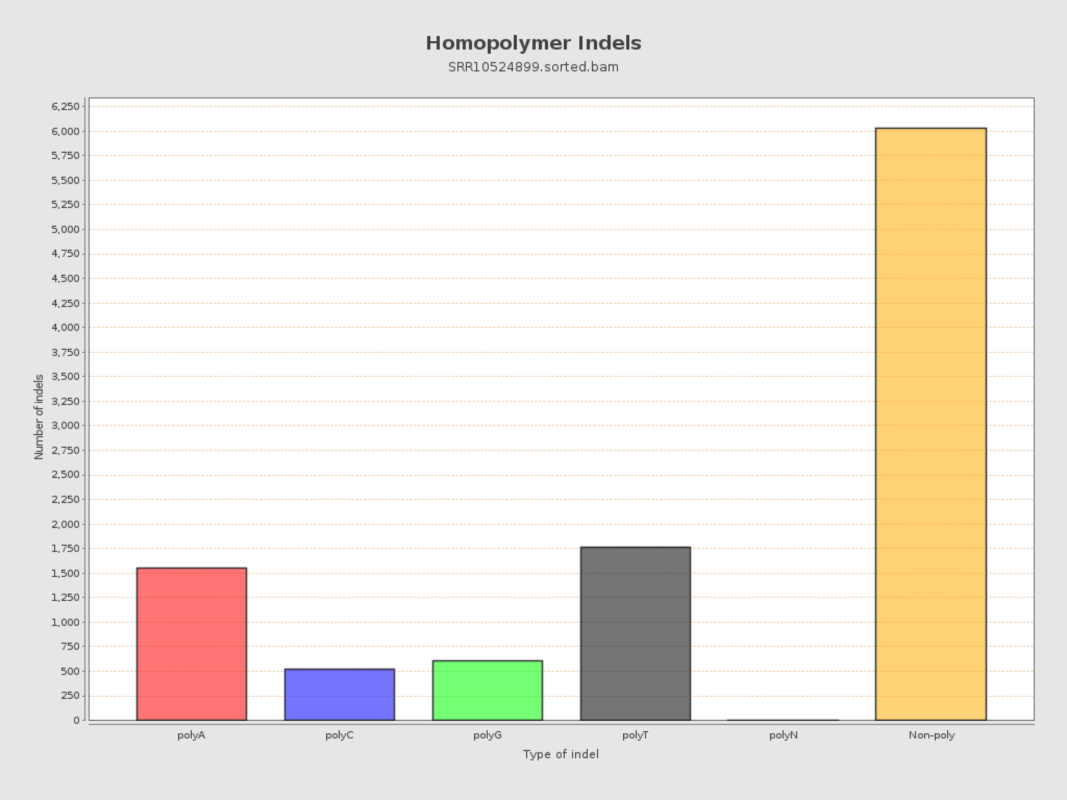
9. Results : Mapped Reads GC-content Distribution



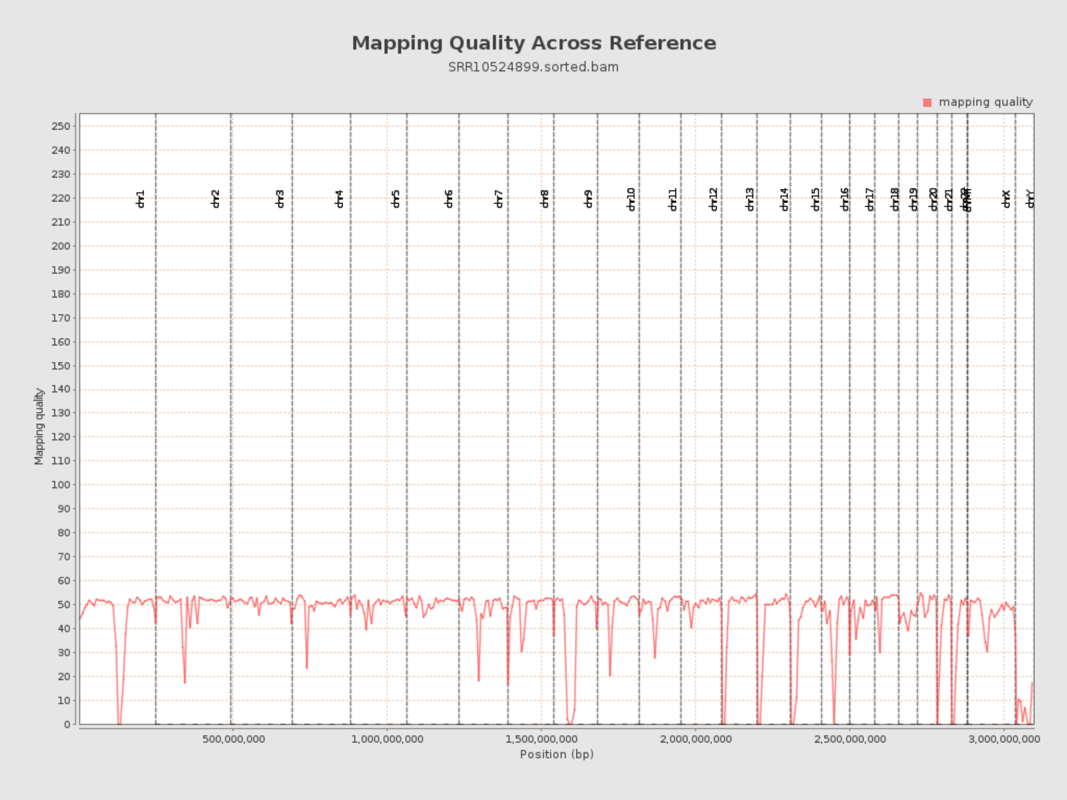
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram