Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:32:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524389.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_SRR10524389 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524389.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:31:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524389.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,086,631
Mapped reads	995,595 / 91.62%
Unmapped reads	91,036 / 8.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,358 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	31,626 / 2.91%
Duplication rate	2.4%
Clipped reads	996,400 / 91.7%

2.2. ACGT Content

Number/percentage of A's	14,831,849 / 25.75%
Number/percentage of C's	10,932,515 / 18.98%
Number/percentage of T's	18,403,695 / 31.95%
Number/percentage of G's	13,436,085 / 23.32%
Number/percentage of N's	1,176 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.198

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

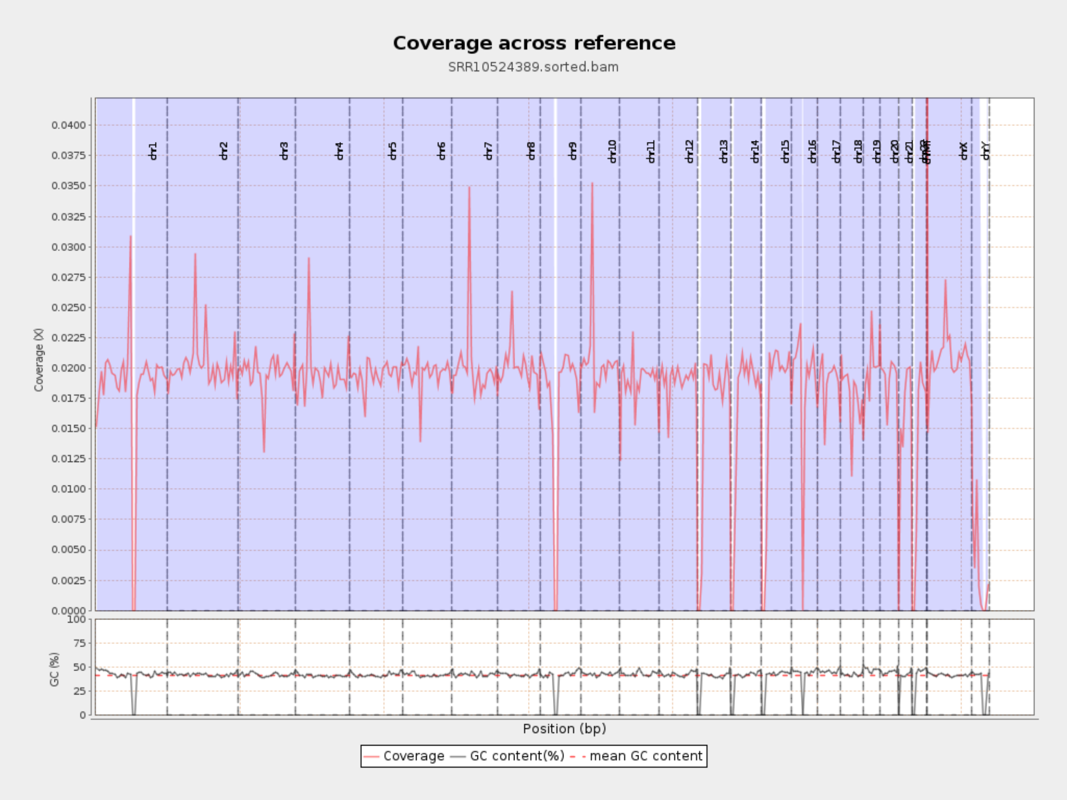
General error rate	0.51%
Mismatches	285,753
Insertions	4,324
Mapped reads with at least one insertion	0.43%
Deletions	11,425
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.77%

2.6. Chromosome stats

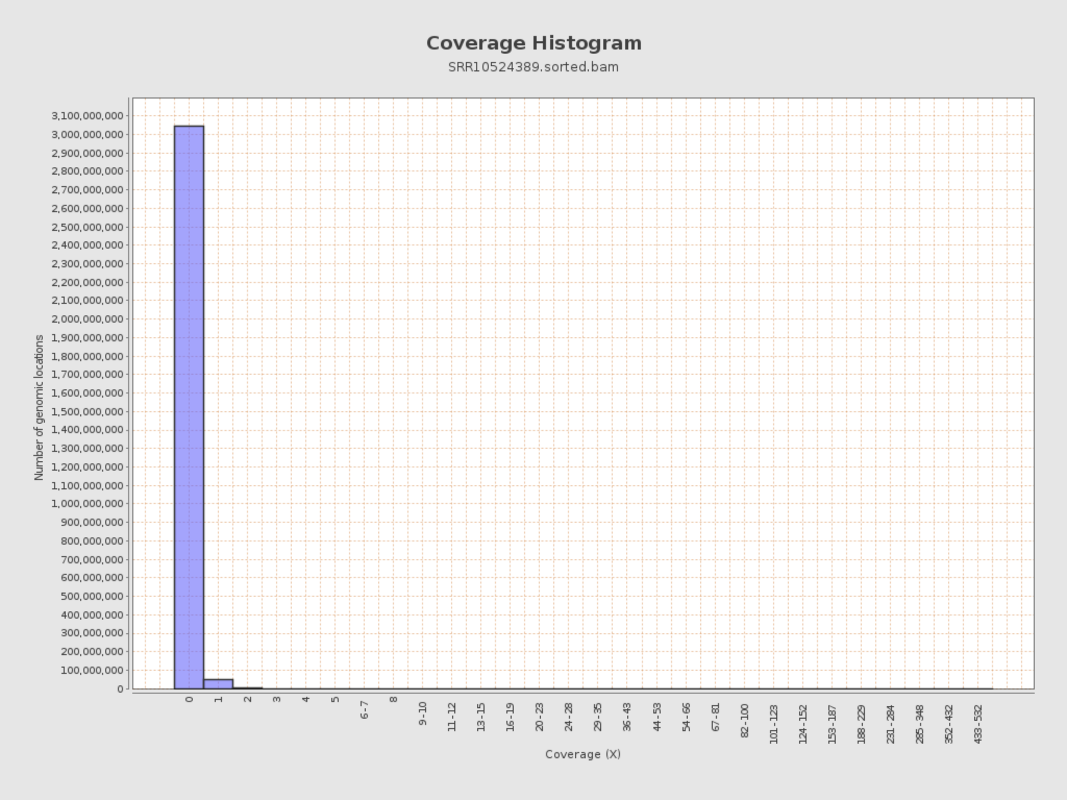
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4581019	0.0184	0.3189
chr2	243199373	4938191	0.0203	0.2672
chr3	198022430	3869739	0.0195	0.149
chr4	191154276	3750826	0.0196	0.1566
chr5	180915260	3522608	0.0195	0.1482
chr6	171115067	3355510	0.0196	0.1606
chr7	159138663	3214594	0.0202	0.274

chr8	146364022	2948420	0.0201	0.2129
chr9	141213431	2438960	0.0173	0.1669
chr10	135534747	2806879	0.0207	0.1987
chr11	135006516	2574691	0.0191	0.1672
chr12	133851895	2545793	0.019	0.148
chr13	115169878	1851370	0.0161	0.1352
chr14	107349540	1747191	0.0163	0.1372
chr15	102531392	1688887	0.0165	0.1386
chr16	90354753	1661710	0.0184	0.1539
chr17	81195210	1525079	0.0188	0.151
chr18	78077248	1374291	0.0176	0.2659
chr19	59128983	1179387	0.0199	0.2353
chr20	63025520	1195301	0.019	0.1469
chr21	48129895	751544	0.0156	0.1391
chr22	51304566	665812	0.013	0.1214
chrMT	16571	2730	0.1647	0.4205
chrX	155270560	3246591	0.0209	0.1639
chrY	59373566	186553	0.0031	0.0929

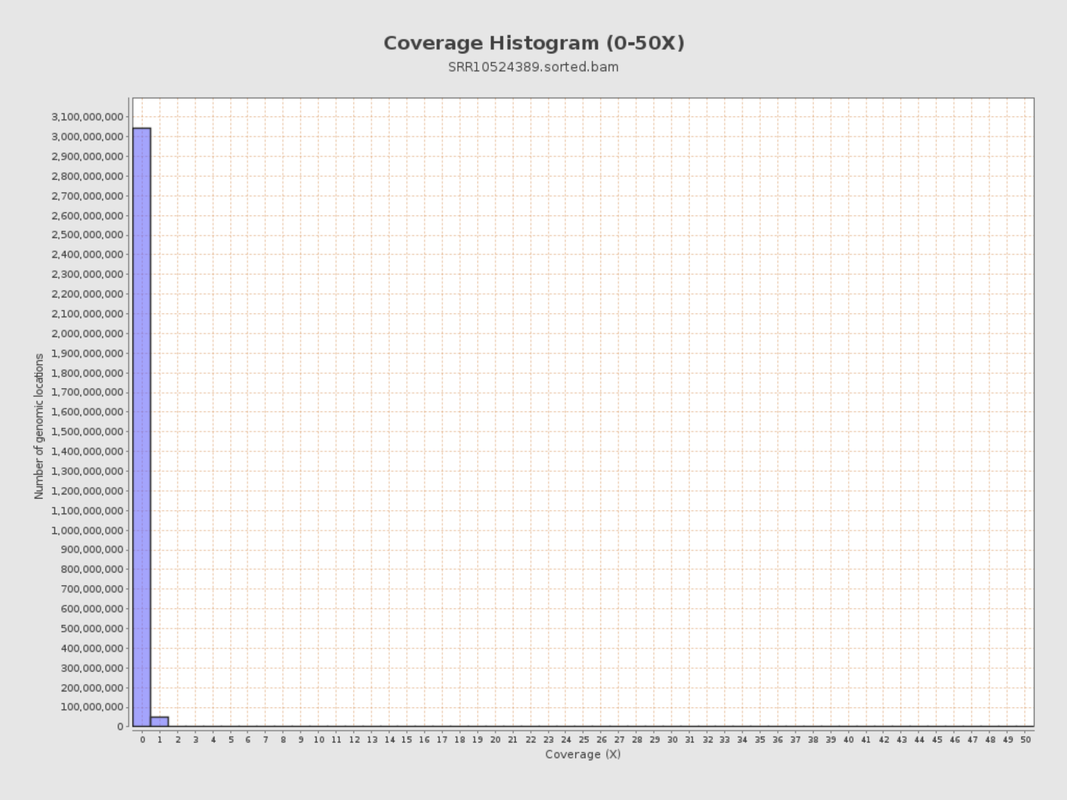
3. Results : Coverage across reference



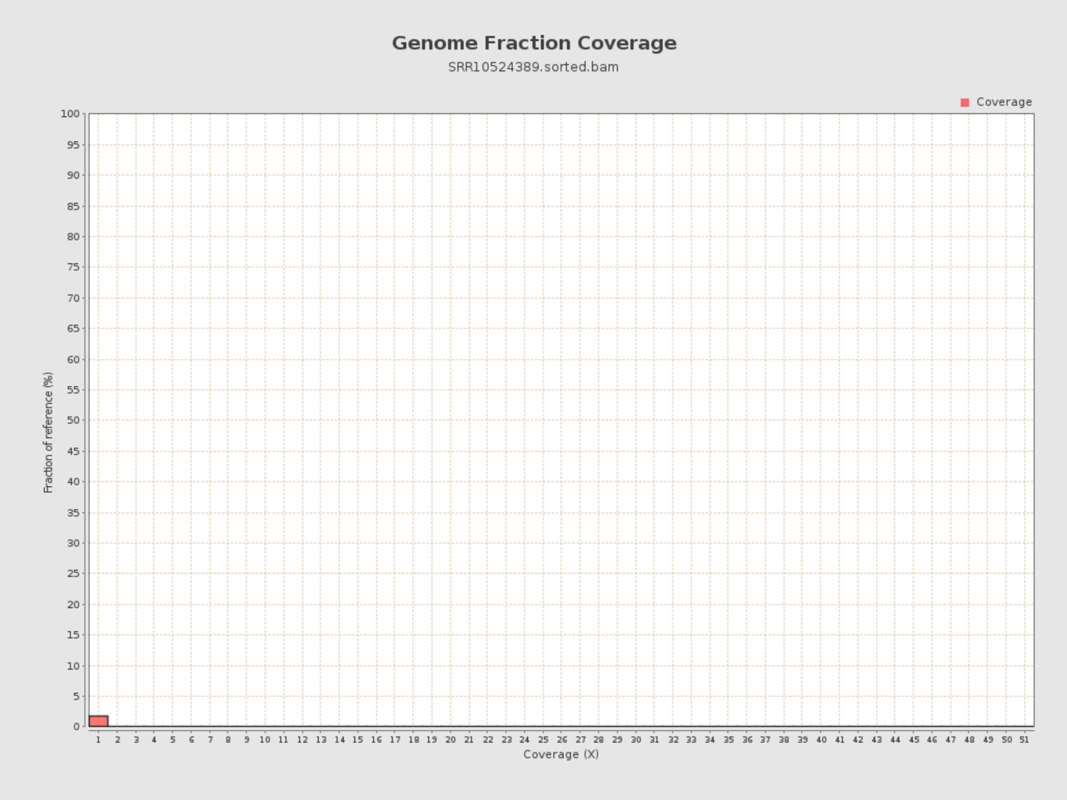
4. Results : Coverage Histogram



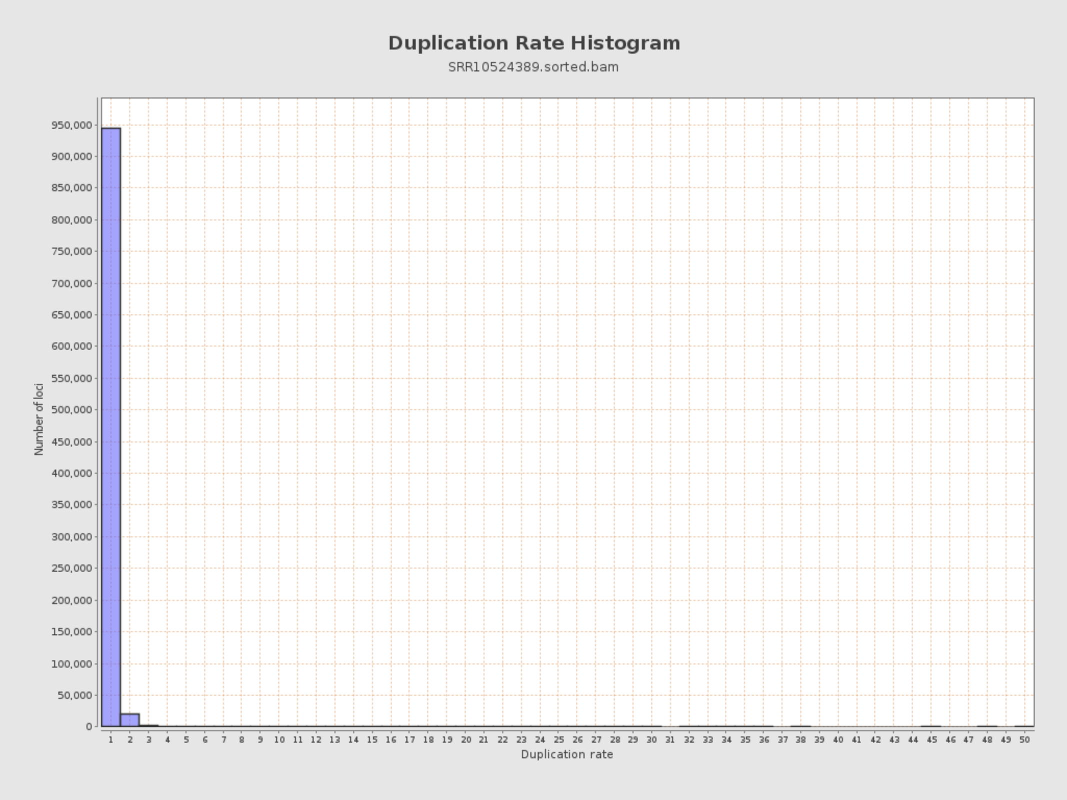
5. Results : Coverage Histogram (0-50X)



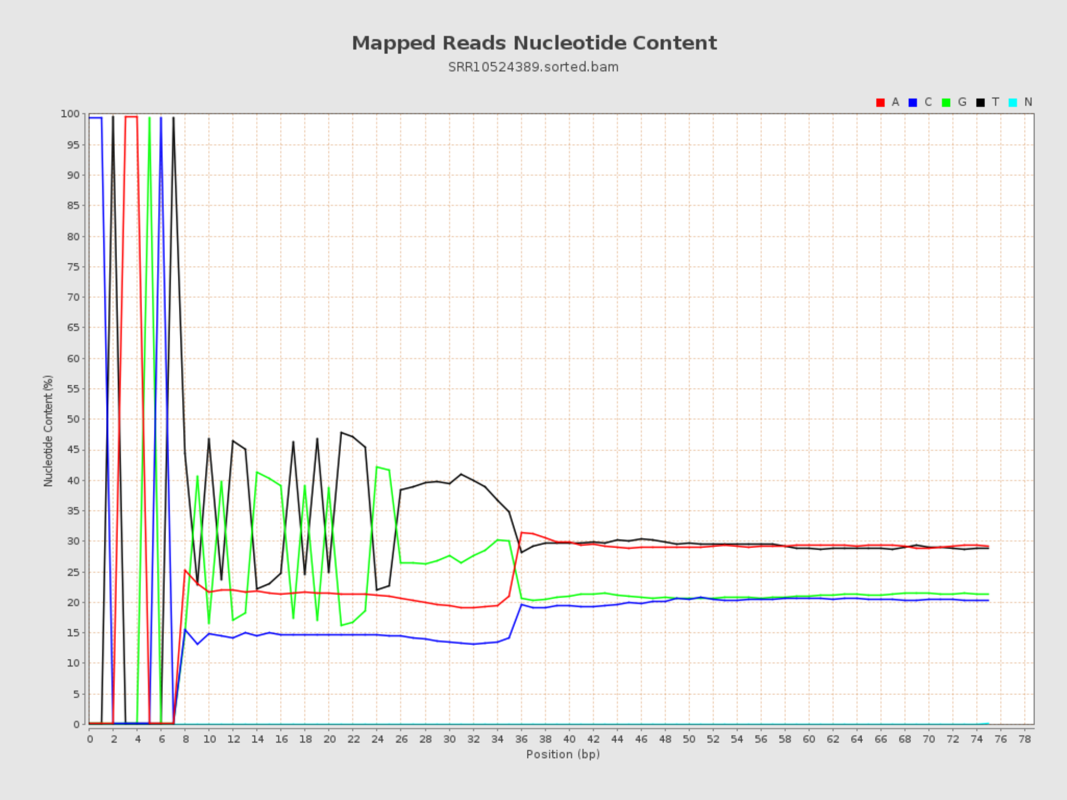
6. Results : Genome Fraction Coverage



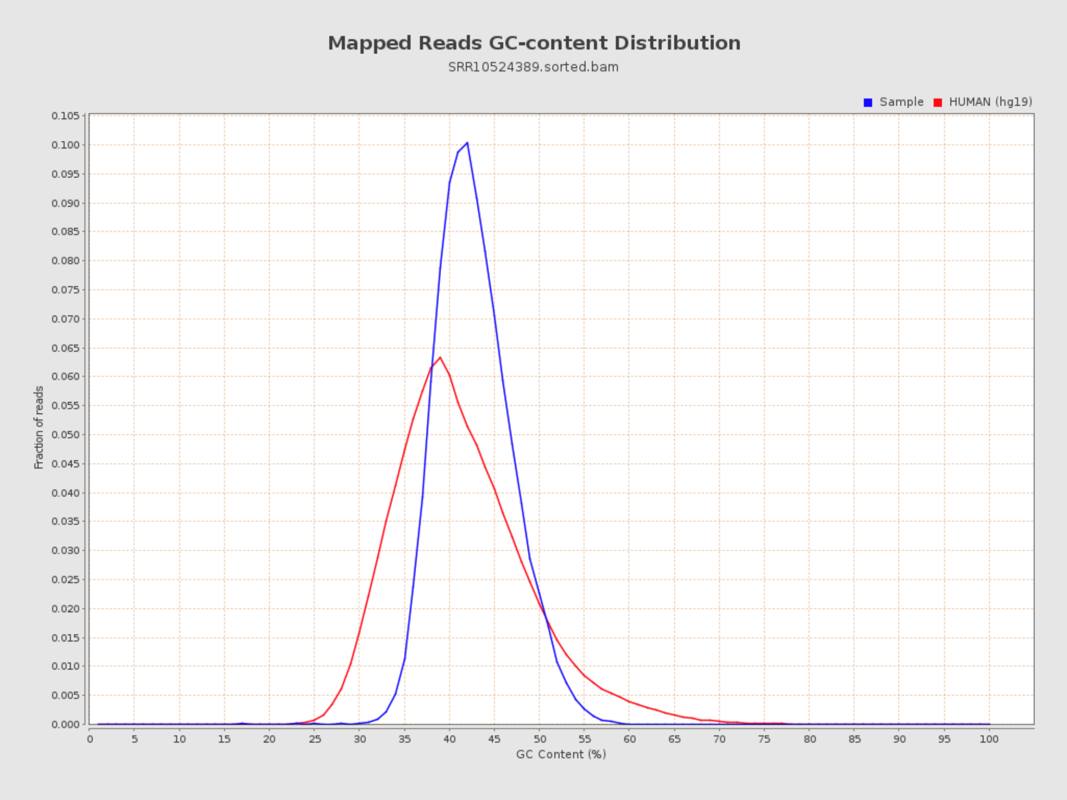
7. Results : Duplication Rate Histogram



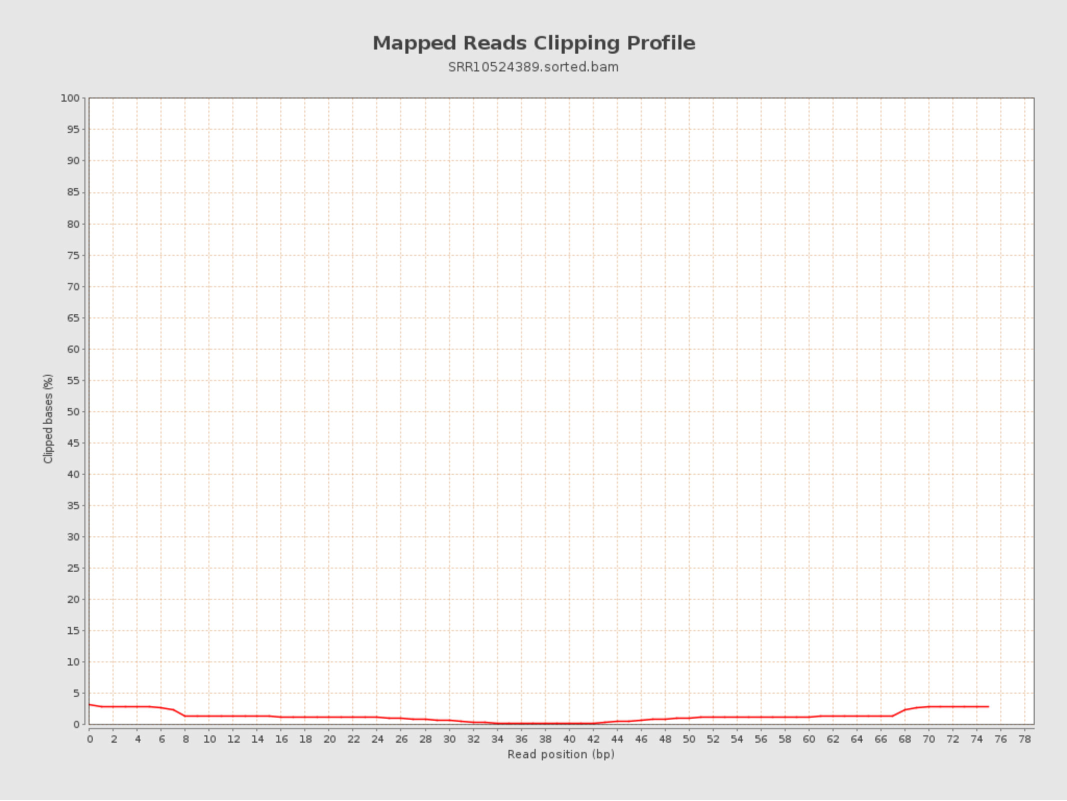
8. Results : Mapped Reads Nucleotide Content



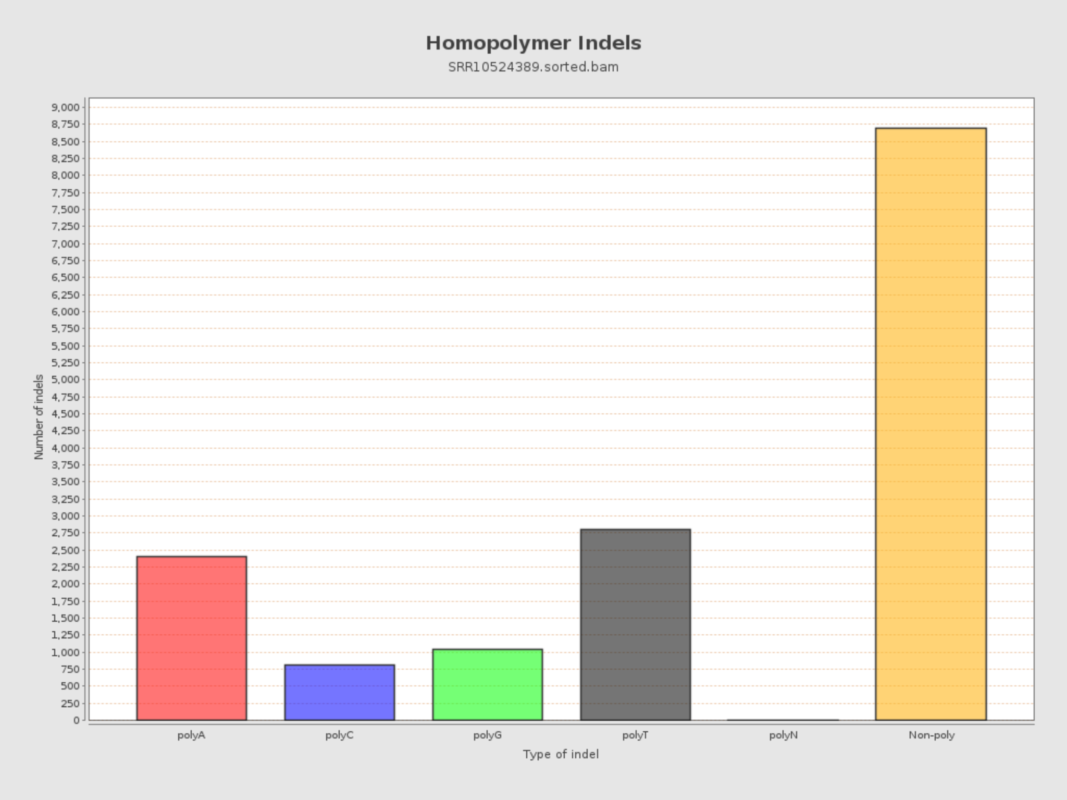
9. Results : Mapped Reads GC-content Distribution



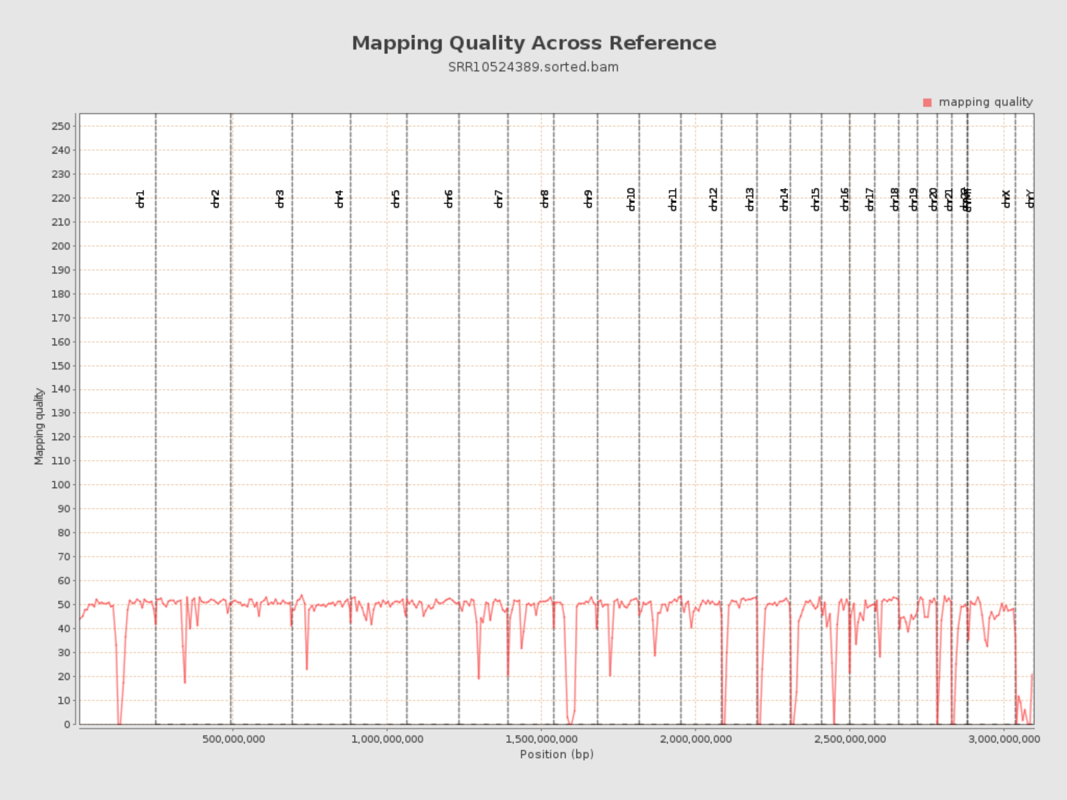
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram