Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:18:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524829.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_SRR10524829 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524829.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:18:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524829.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	983,937
Mapped reads	886,353 / 90.08%
Unmapped reads	97,584 / 9.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,939 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	18,076 / 1.84%
Duplication rate	1.41%
Clipped reads	888,306 / 90.28%

2.2. ACGT Content

Number/percentage of A's	12,717,453 / 25.17%
Number/percentage of C's	9,347,517 / 18.5%
Number/percentage of T's	16,200,783 / 32.06%
Number/percentage of G's	12,259,942 / 24.26%
Number/percentage of N's	6,084 / 0.01%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0163

Standard Deviation	0.1656

2.4. Mapping Quality

Mean Mapping Quality	43.81

2.5. Mismatches and indels

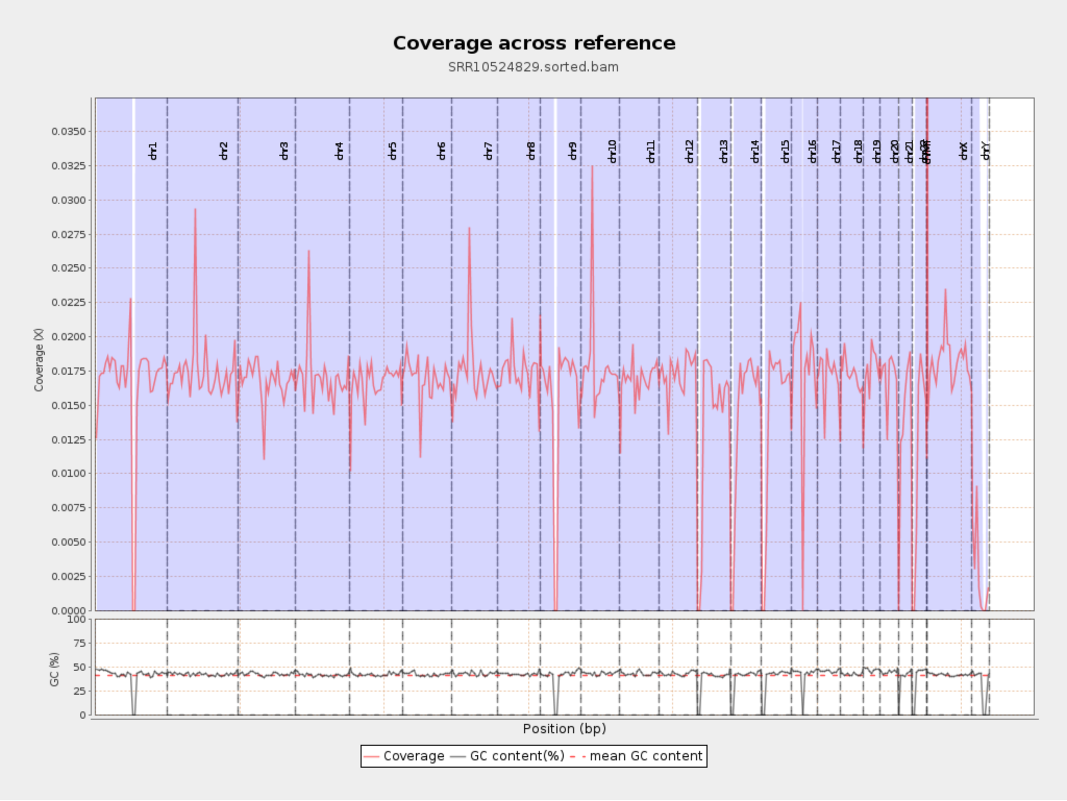
General error rate	0.52%
Mismatches	256,710
Insertions	4,063
Mapped reads with at least one insertion	0.46%
Deletions	9,375
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.37%

2.6. Chromosome stats

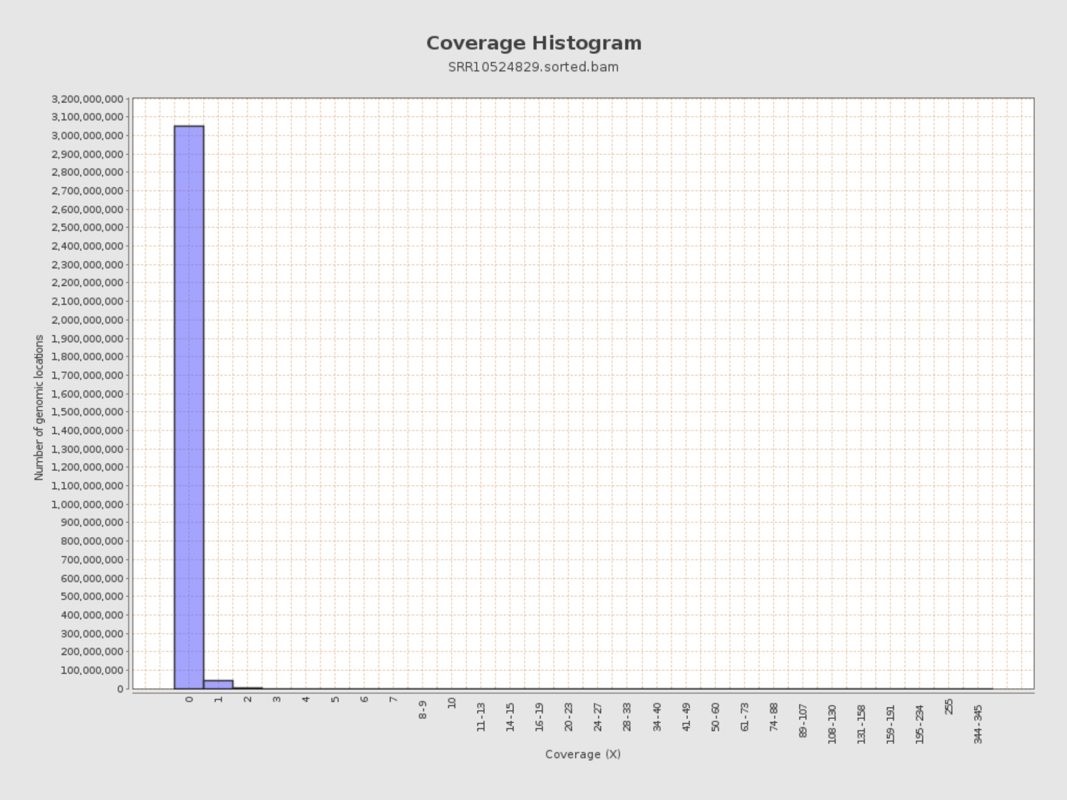
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4088467	0.0164	0.2104
chr2	243199373	4245417	0.0175	0.2224
chr3	198022430	3321515	0.0168	0.1368
chr4	191154276	3266327	0.0171	0.1471
chr5	180915260	3045745	0.0168	0.1369
chr6	171115067	2889946	0.0169	0.1406
chr7	159138663	2798668	0.0176	0.2113

chr8	146364022	2541660	0.0174	0.1576
chr9	141213431	2174173	0.0154	0.1586
chr10	135534747	2413251	0.0178	0.189
chr11	135006516	2284552	0.0169	0.1622
chr12	133851895	2305608	0.0172	0.139
chr13	115169878	1573190	0.0137	0.1221
chr14	107349540	1518554	0.0141	0.1301
chr15	102531392	1458572	0.0142	0.128
chr16	90354753	1541377	0.0171	0.1483
chr17	81195210	1382020	0.017	0.143
chr18	78077248	1351356	0.0173	0.2397
chr19	59128983	1040185	0.0176	0.1744
chr20	63025520	1058660	0.0168	0.1395
chr21	48129895	665581	0.0138	0.1301
chr22	51304566	592169	0.0115	0.1124
chrMT	16571	7946	0.4795	0.8043
chrX	155270560	2826306	0.0182	0.1539
chrY	59373566	155194	0.0026	0.0779

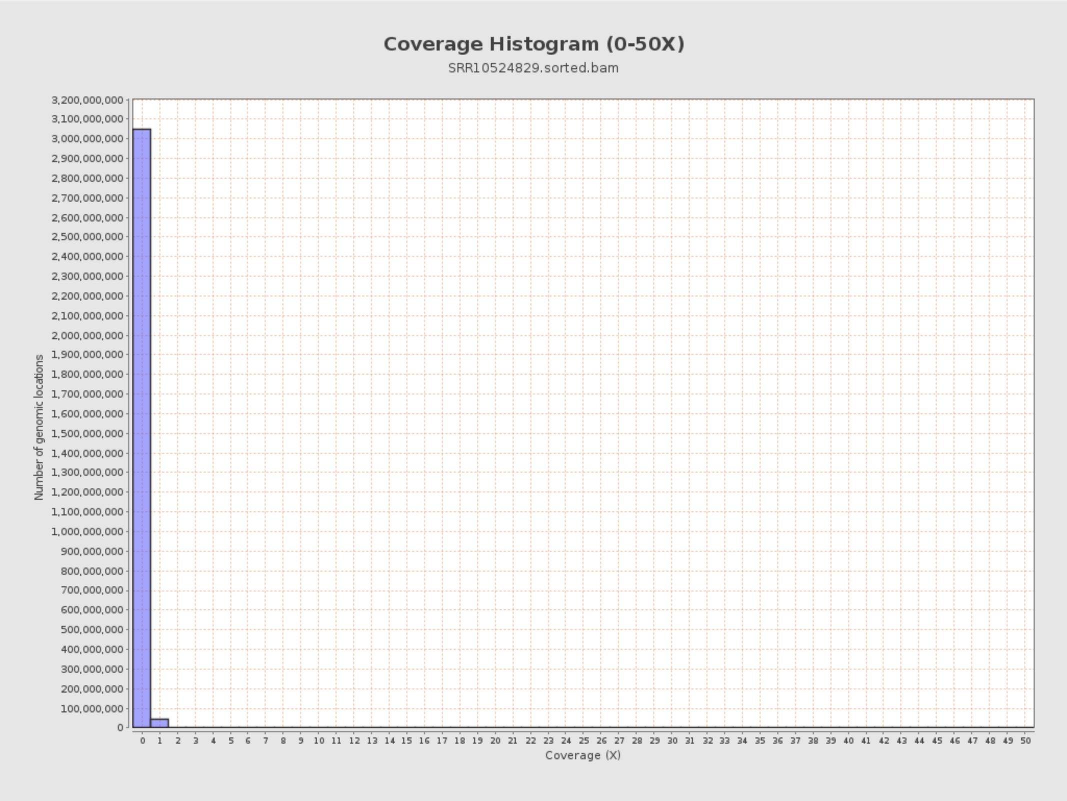
3. Results : Coverage across reference



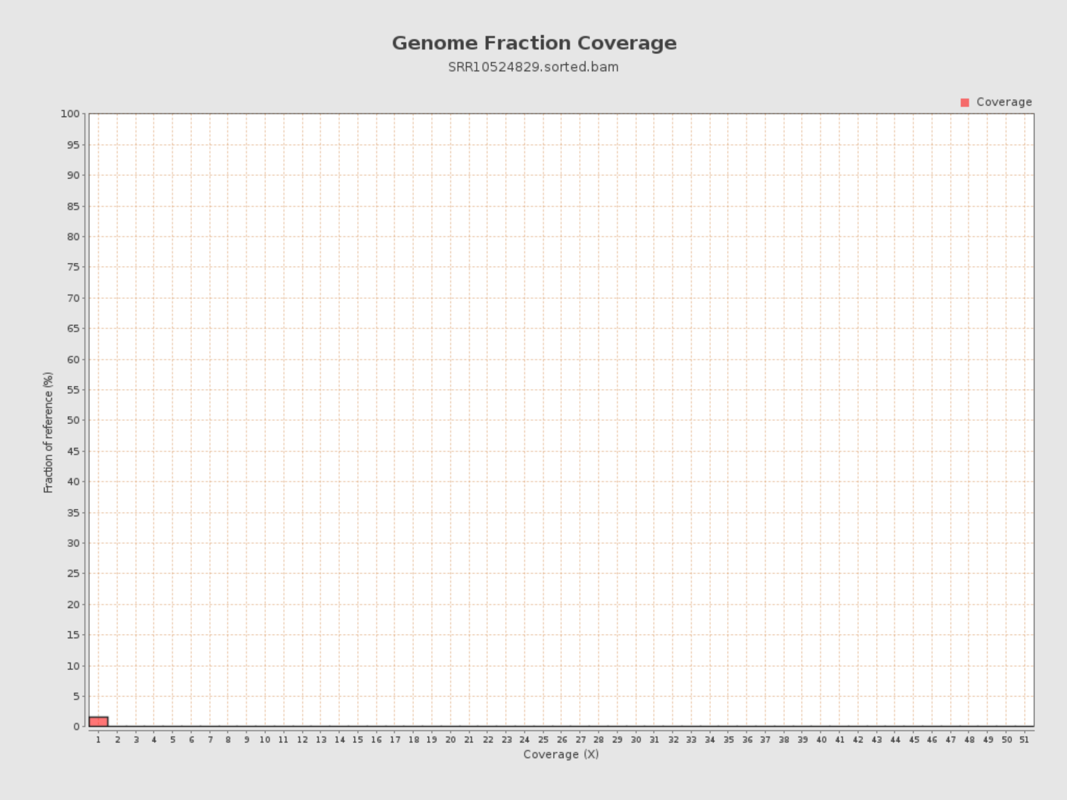
4. Results : Coverage Histogram



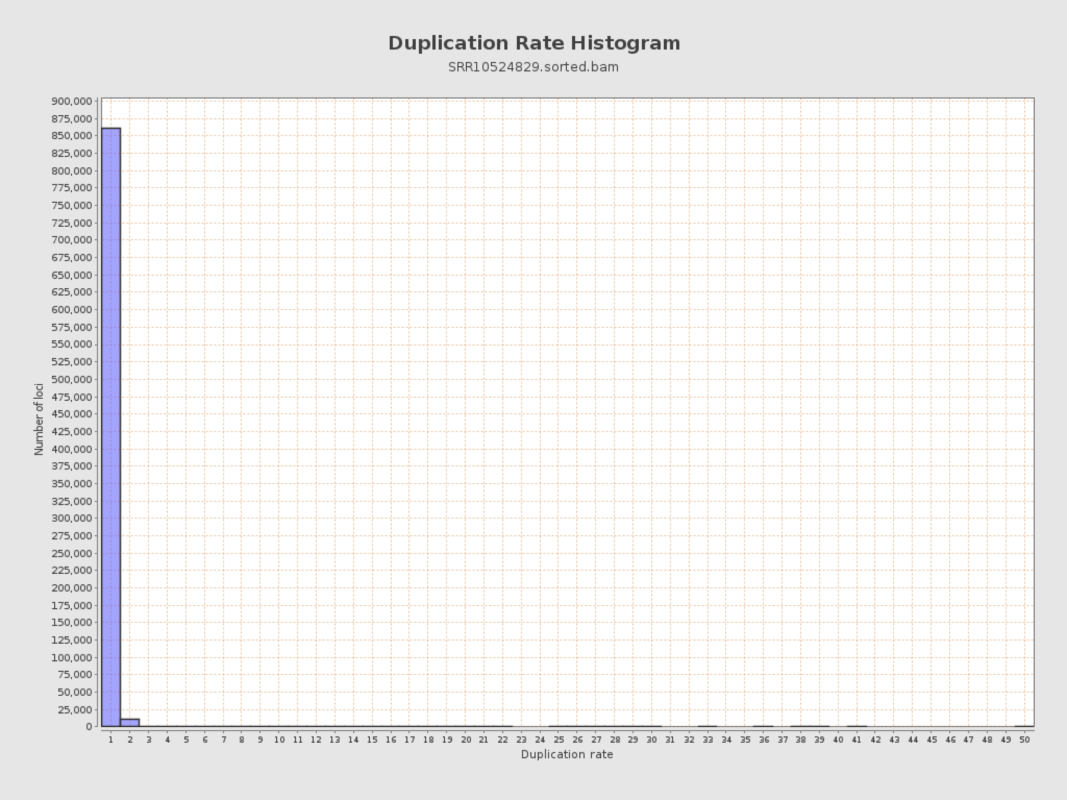
5. Results : Coverage Histogram (0-50X)



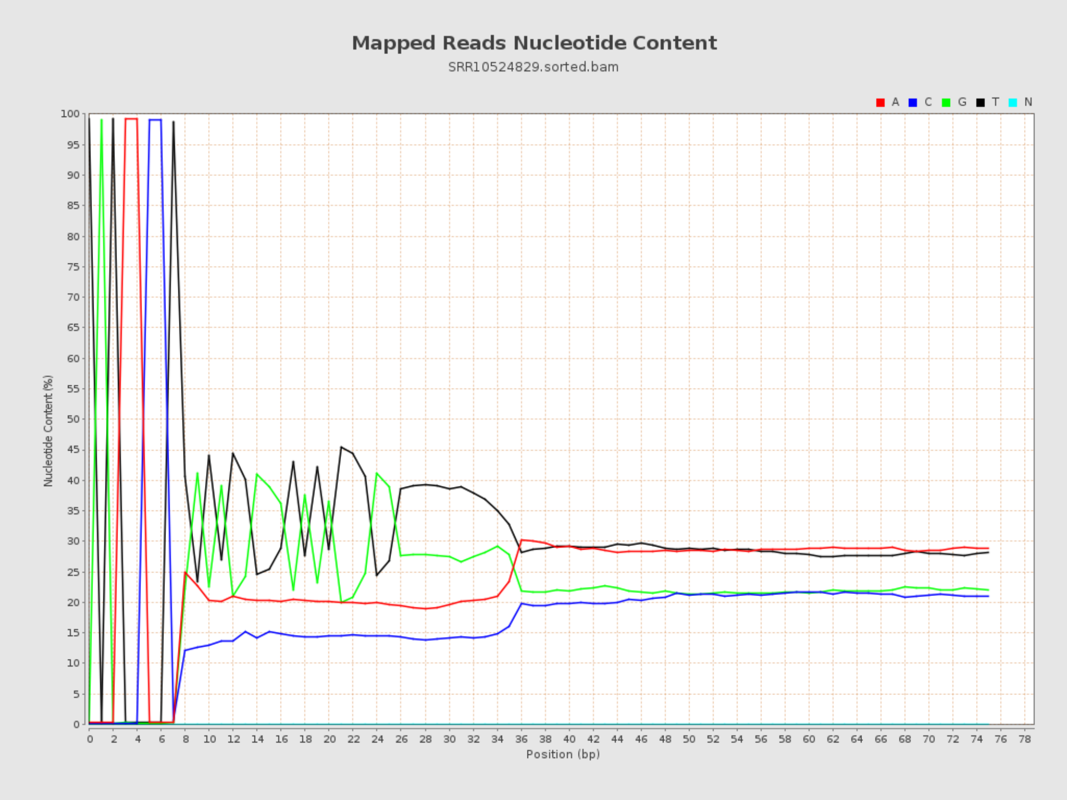
6. Results : Genome Fraction Coverage



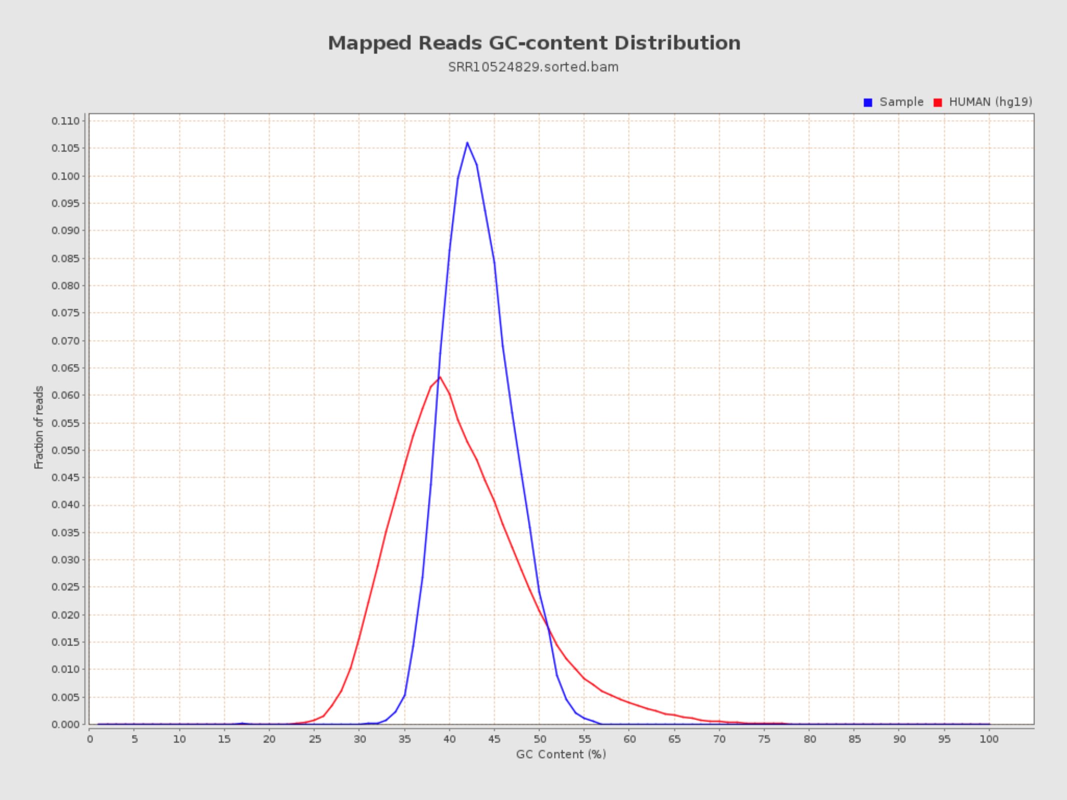
7. Results : Duplication Rate Histogram



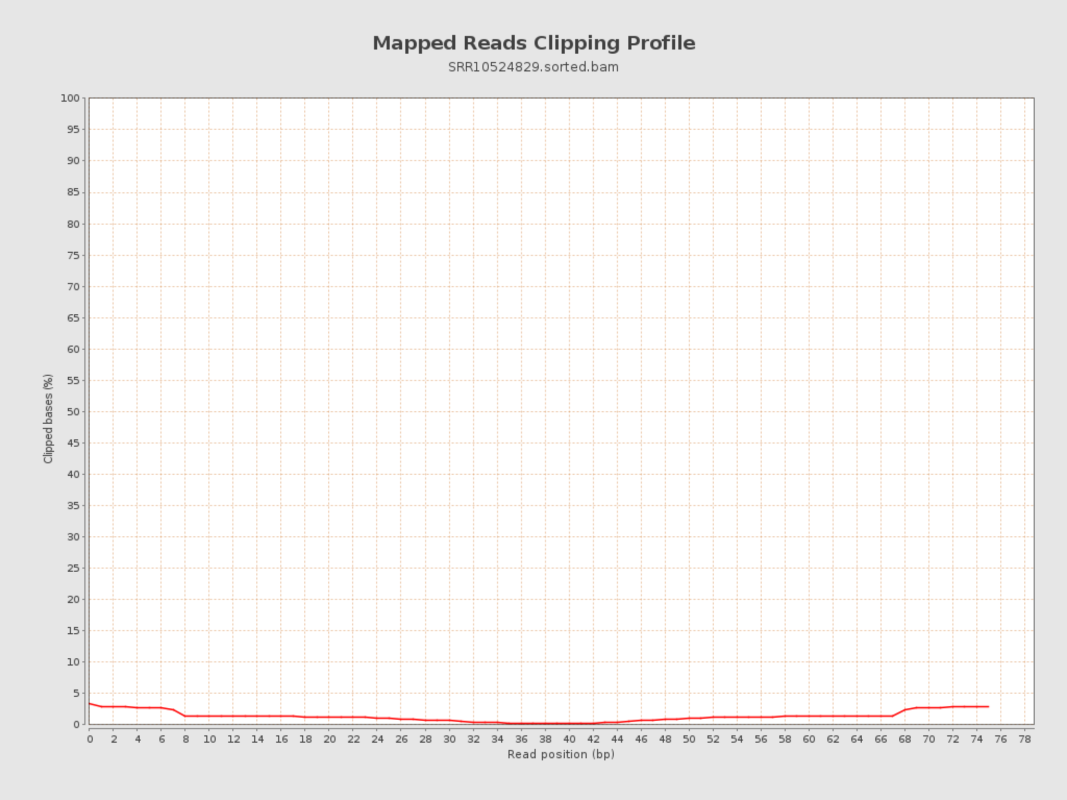
8. Results : Mapped Reads Nucleotide Content



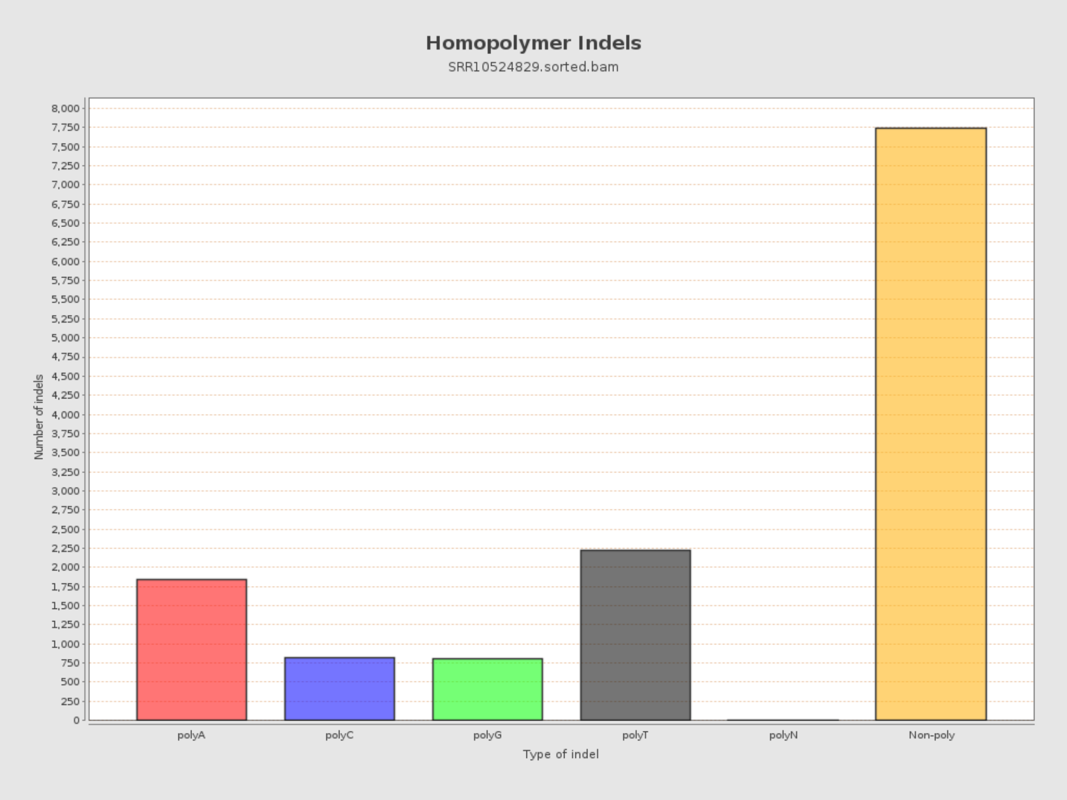
9. Results : Mapped Reads GC-content Distribution



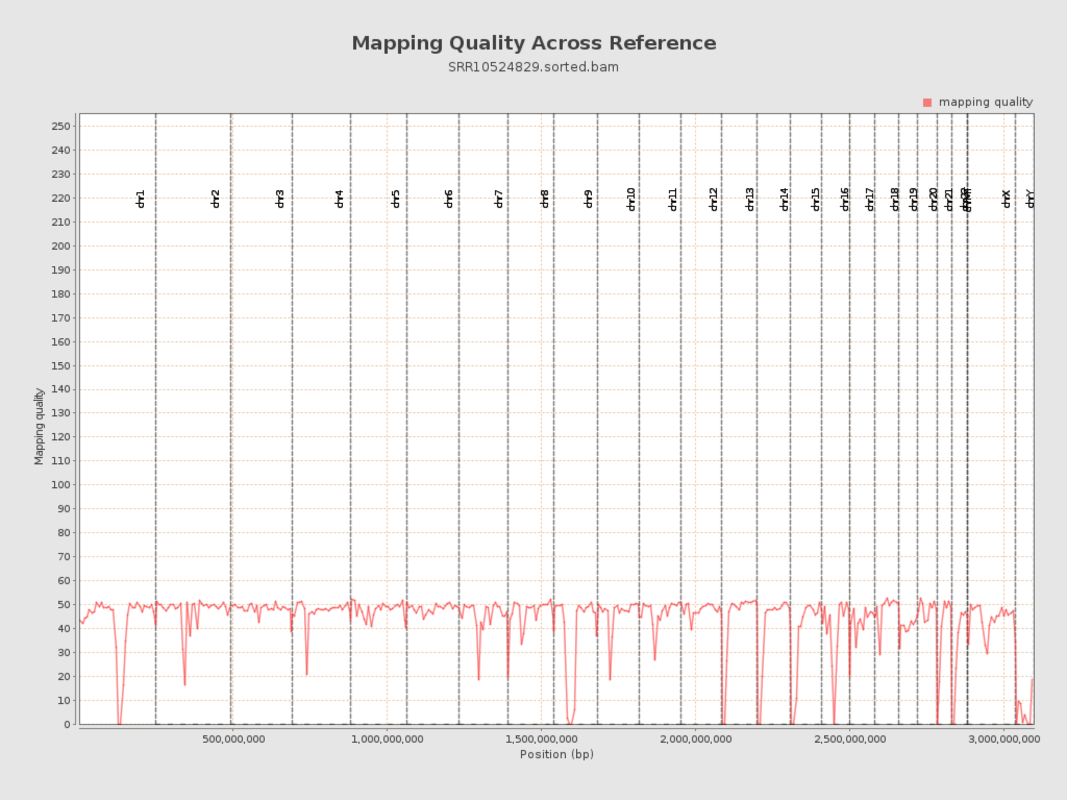
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram