Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:25:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524832.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_SRR10524832 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524832.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:25:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524832.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,183,465
Mapped reads	1,090,999 / 92.19%
Unmapped reads	92,466 / 7.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,651 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	27,486 / 2.32%
Duplication rate	1.71%
Clipped reads	1,093,102 / 92.36%

2.2. ACGT Content

Number/percentage of A's	15,754,541 / 24.76%
Number/percentage of C's	10,960,479 / 17.23%
Number/percentage of T's	21,266,340 / 33.43%
Number/percentage of G's	15,628,599 / 24.57%
Number/percentage of N's	8,669 / 0.01%
GC Percentage	41.79%

2.3. Coverage

Mean	0.0206

Standard Deviation	0.2189

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

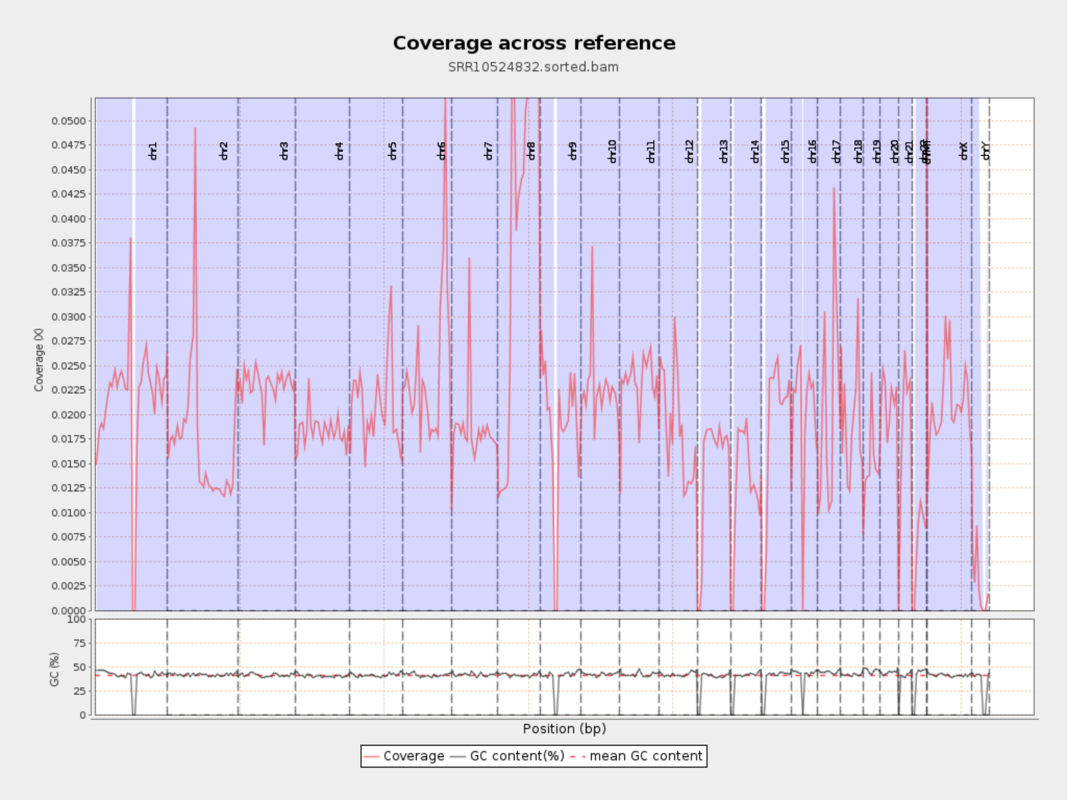
General error rate	0.49%
Mismatches	306,510
Insertions	4,600
Mapped reads with at least one insertion	0.42%
Deletions	11,674
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.28%

2.6. Chromosome stats

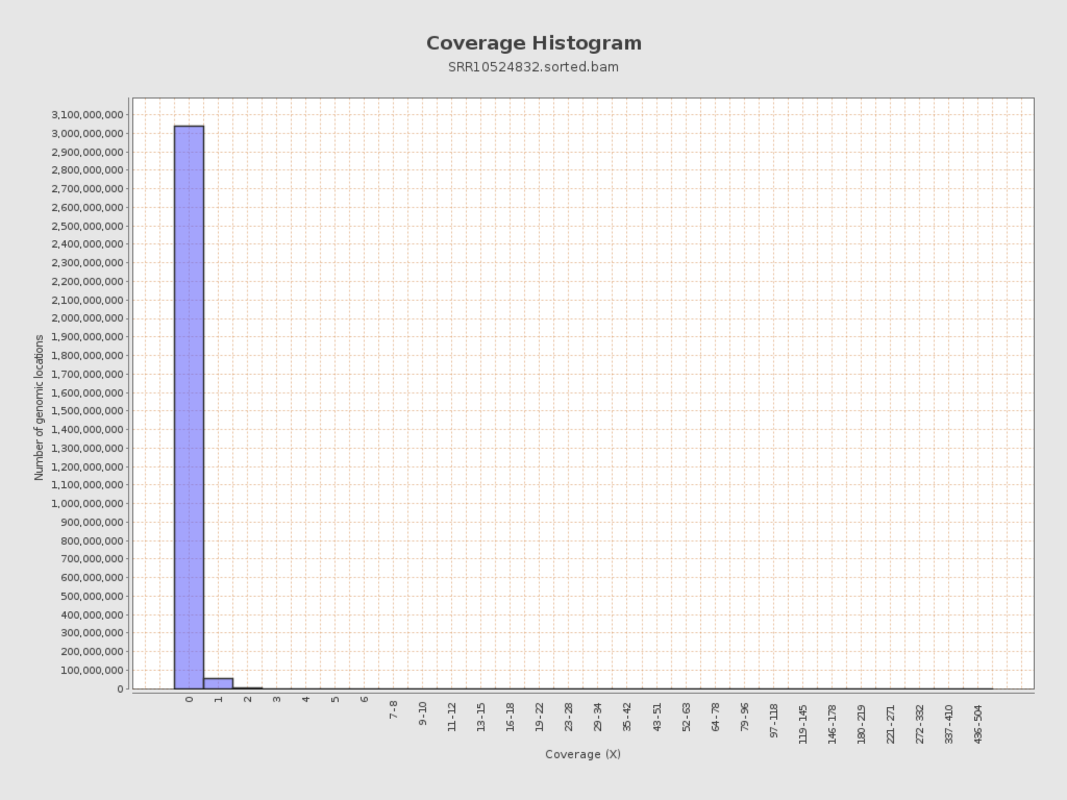
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5345270	0.0214	0.3964
chr2	243199373	4158298	0.0171	0.2086
chr3	198022430	4565984	0.0231	0.1597
chr4	191154276	3500873	0.0183	0.1503
chr5	180915260	3832379	0.0212	0.1543
chr6	171115067	4164732	0.0243	0.1791
chr7	159138663	2961925	0.0186	0.299

chr8	146364022	6857798	0.0469	0.3062
chr9	141213431	2626535	0.0186	0.1919
chr10	135534747	3068036	0.0226	0.2118
chr11	135006516	3156573	0.0234	0.204
chr12	133851895	2466332	0.0184	0.1451
chr13	115169878	1686969	0.0146	0.1282
chr14	107349540	1379177	0.0128	0.1251
chr15	102531392	1901206	0.0185	0.1441
chr16	90354753	1803522	0.02	0.159
chr17	81195210	1720607	0.0212	0.1687
chr18	78077248	1510479	0.0193	0.3414
chr19	59128983	902754	0.0153	0.2735
chr20	63025520	1322223	0.021	0.1541
chr21	48129895	896863	0.0186	0.1498
chr22	51304566	357381	0.007	0.0866
chrMT	16571	955	0.0576	0.2586
chrX	155270560	3297095	0.0212	0.1716
chrY	59373566	153028	0.0026	0.0709

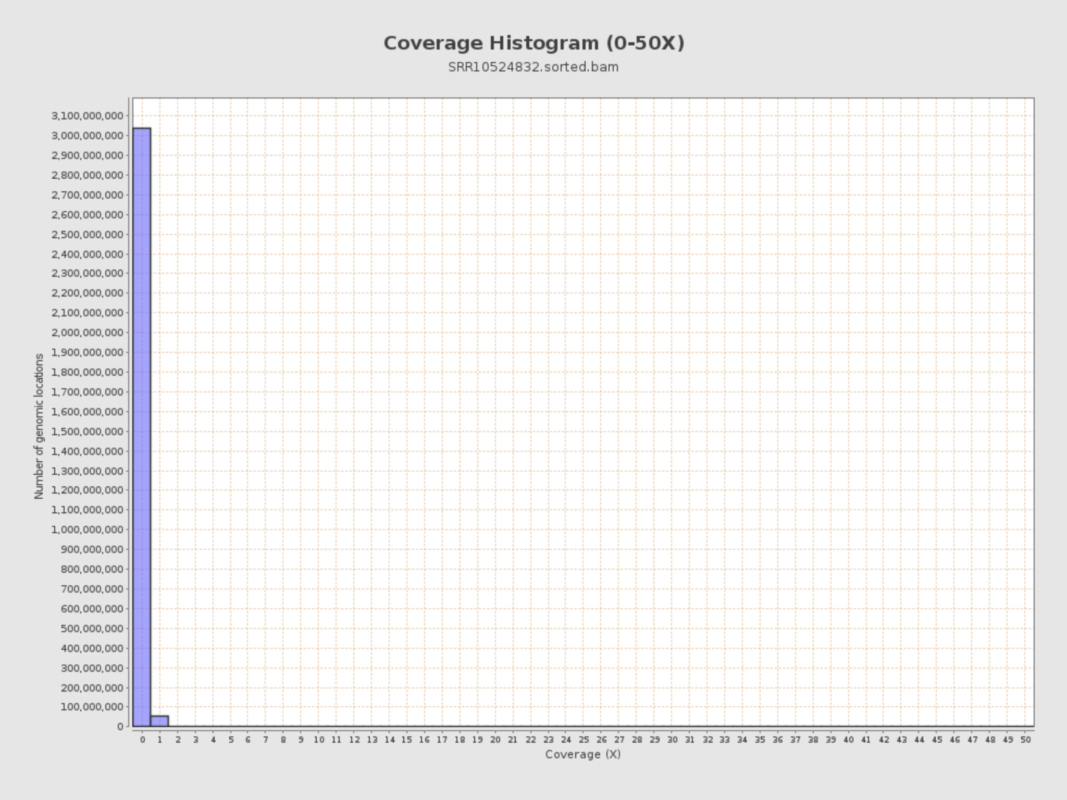
3. Results : Coverage across reference



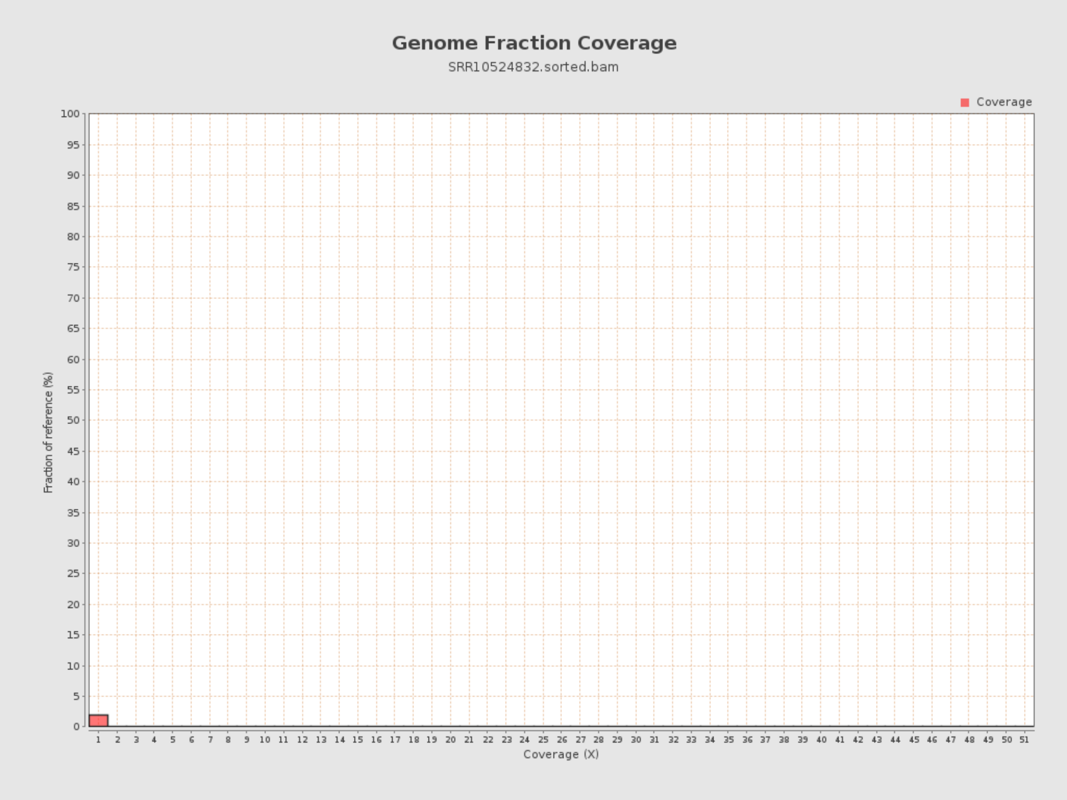
4. Results : Coverage Histogram



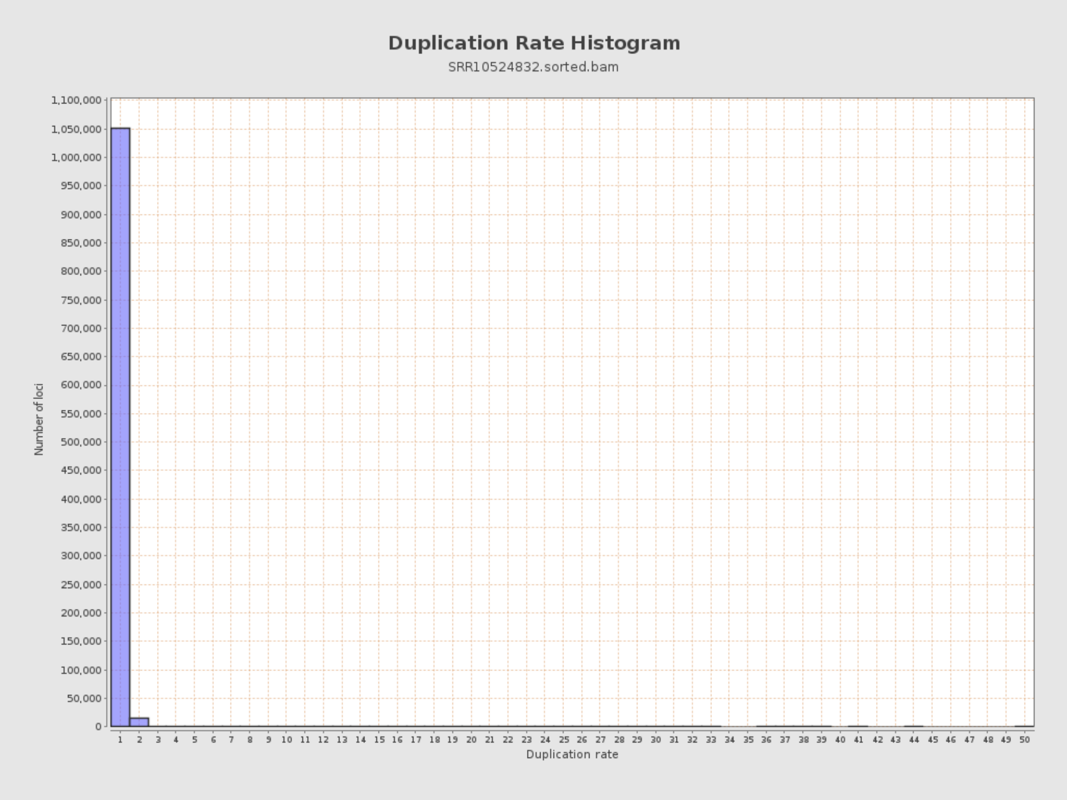
5. Results : Coverage Histogram (0-50X)



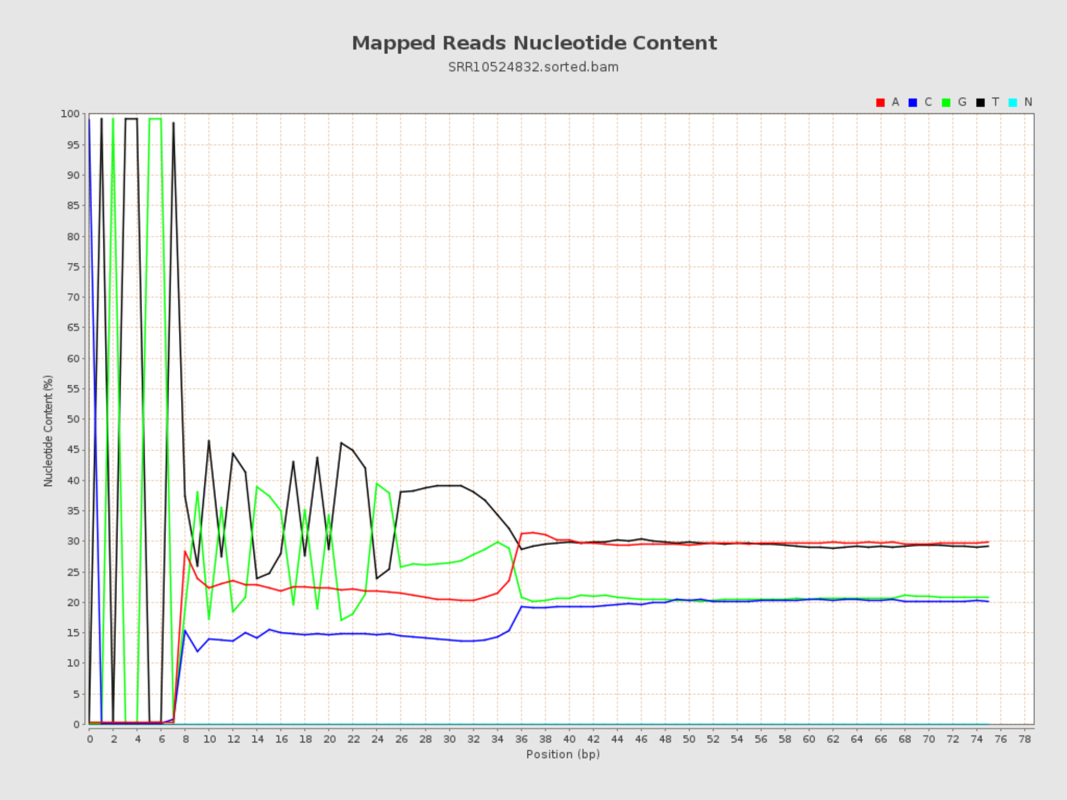
6. Results : Genome Fraction Coverage



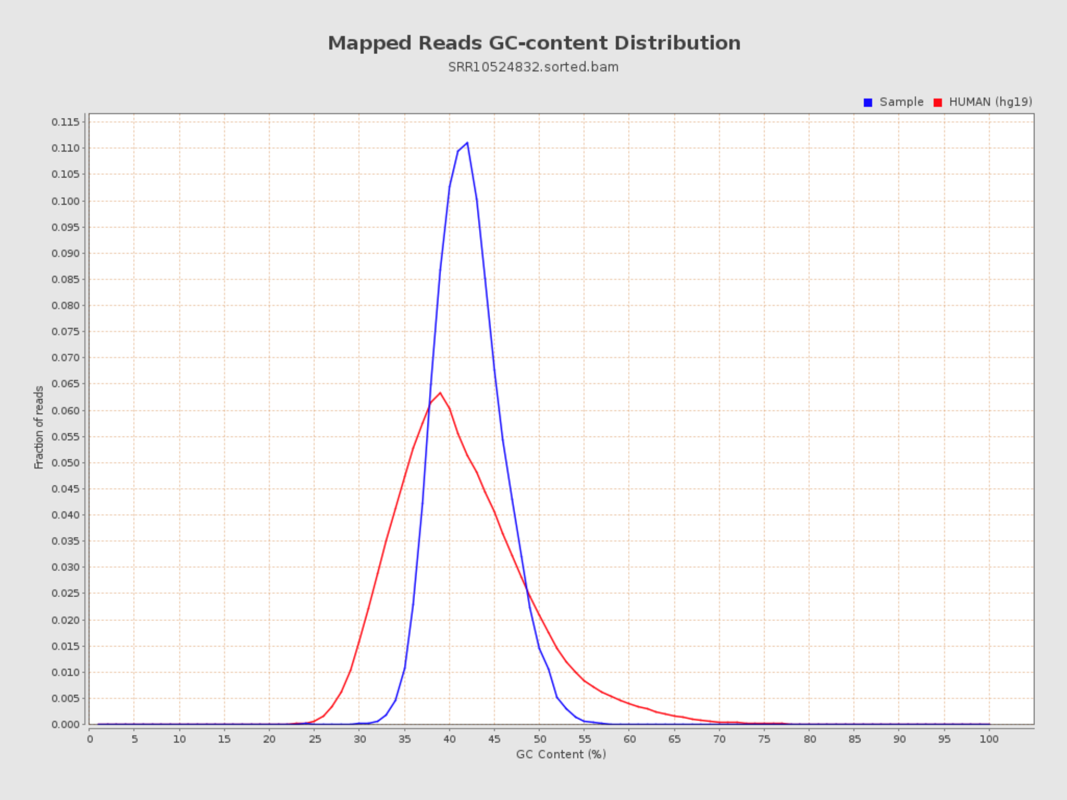
7. Results : Duplication Rate Histogram



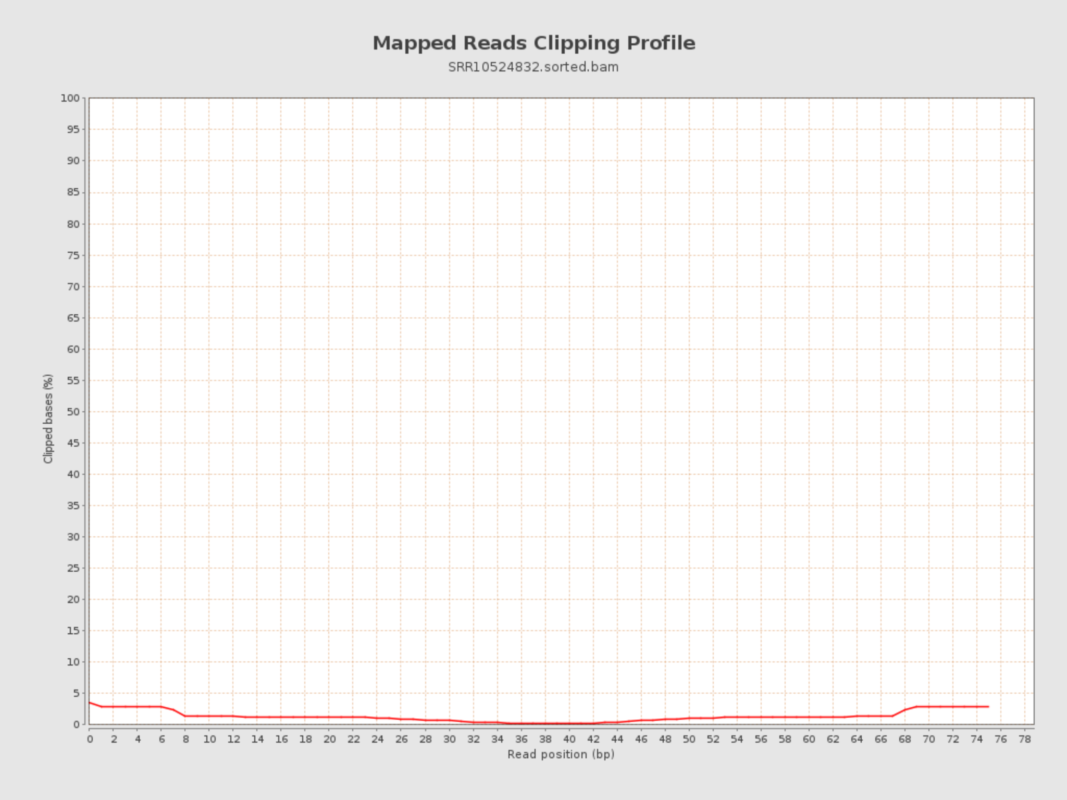
8. Results : Mapped Reads Nucleotide Content



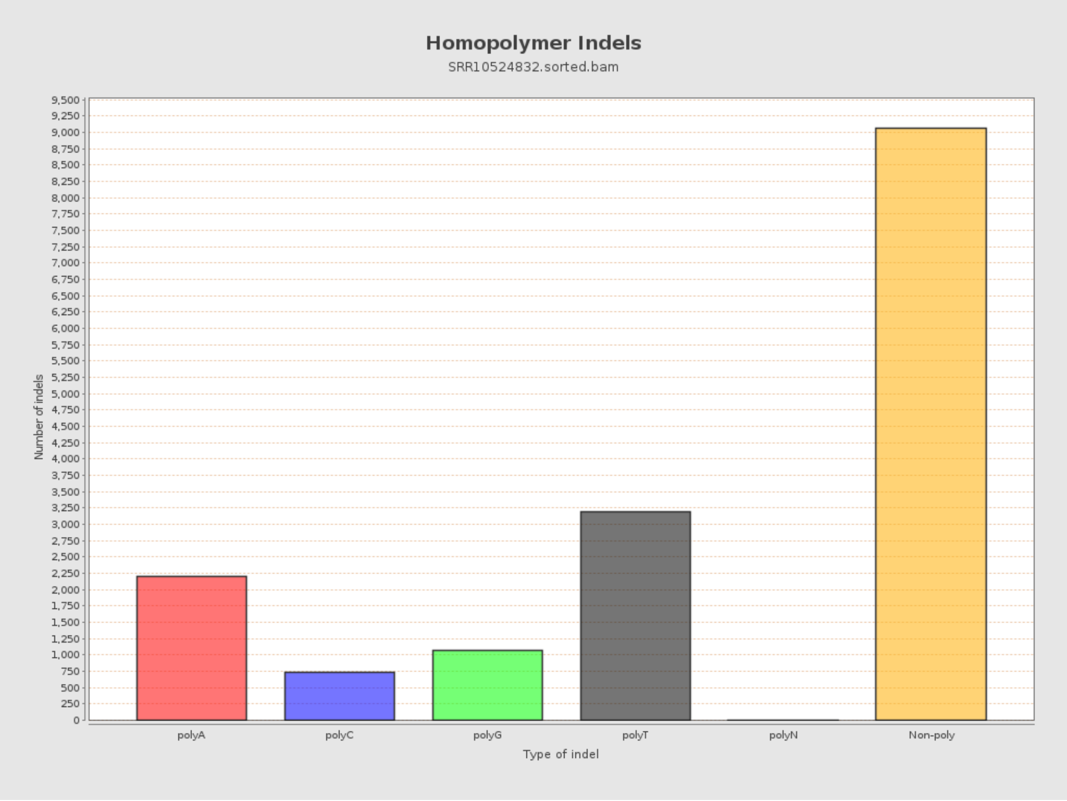
9. Results : Mapped Reads GC-content Distribution



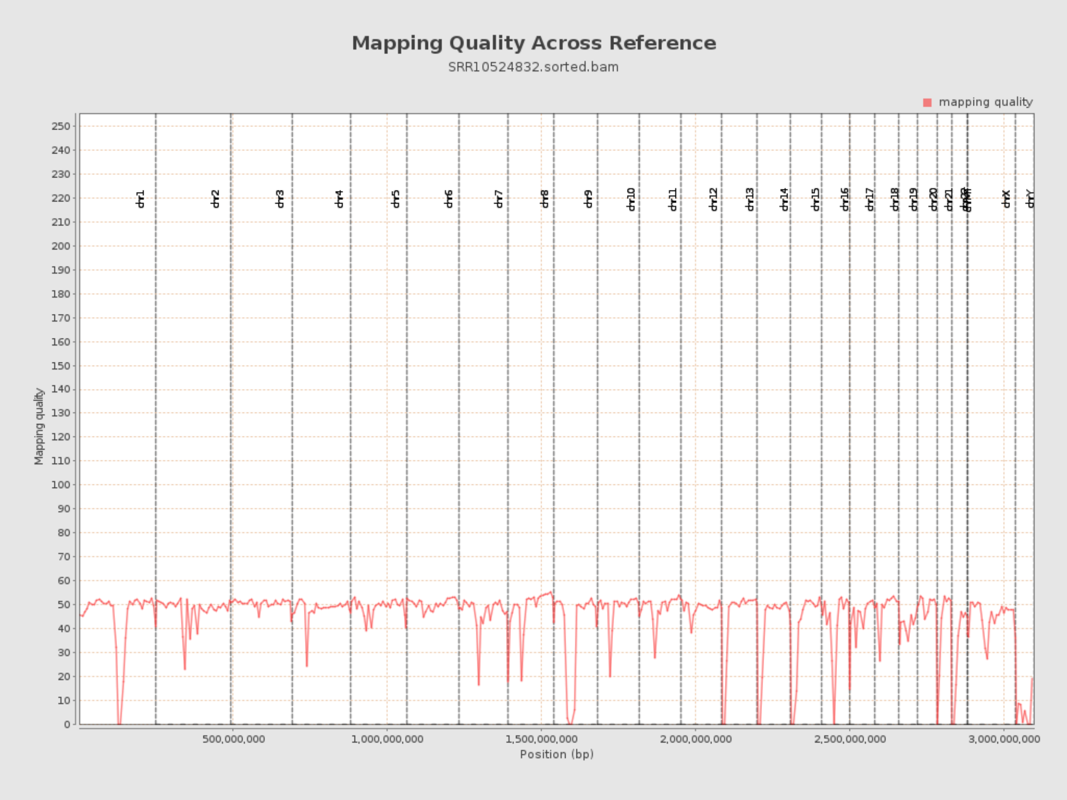
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram