Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:34:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524632.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_SRR10524632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524632.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:34:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,441,070
Mapped reads	1,340,660 / 93.03%
Unmapped reads	100,410 / 6.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,919 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	54,051 / 3.75%
Duplication rate	3.16%
Clipped reads	1,342,207 / 93.14%

2.2. ACGT Content

Number/percentage of A's	20,154,574 / 25.75%
Number/percentage of C's	15,080,631 / 19.27%
Number/percentage of T's	24,596,435 / 31.43%
Number/percentage of G's	18,425,027 / 23.54%
Number/percentage of N's	454 / 0%
GC Percentage	42.81%

2.3. Coverage

Mean	0.0253

Standard Deviation	0.2299

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

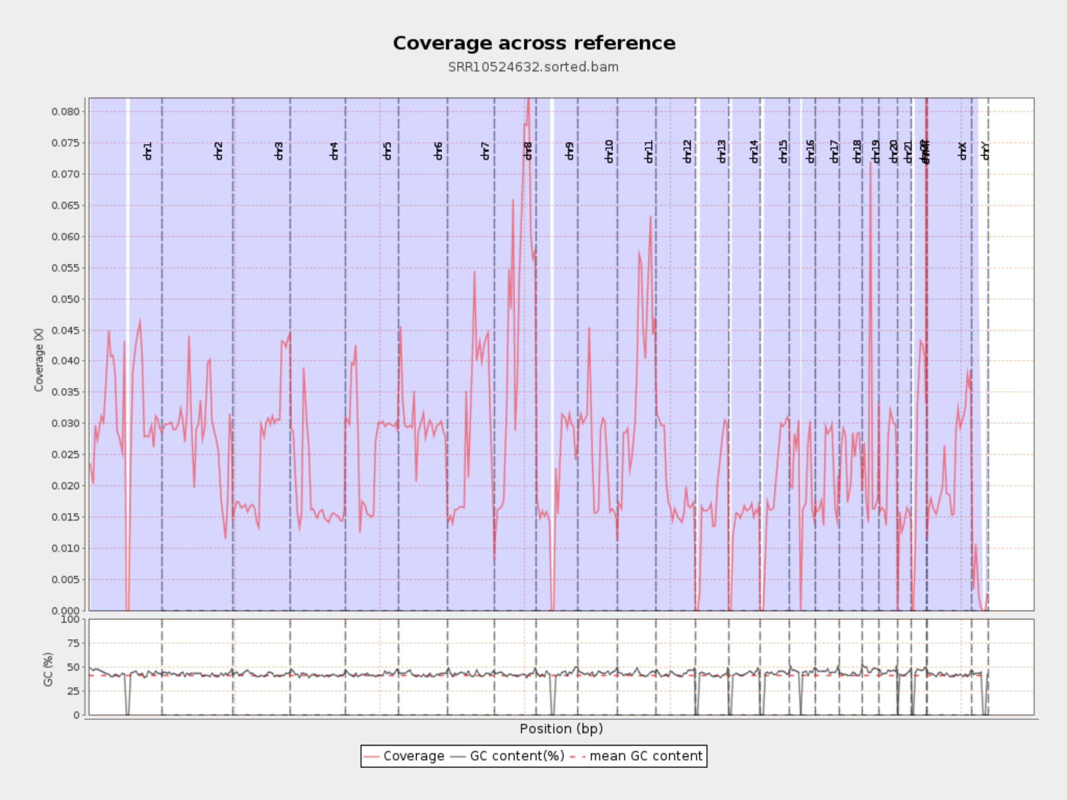
General error rate	0.48%
Mismatches	367,395
Insertions	4,350
Mapped reads with at least one insertion	0.32%
Deletions	14,856
Mapped reads with at least one deletion	1.1%
Homopolymer indels	45.22%

2.6. Chromosome stats

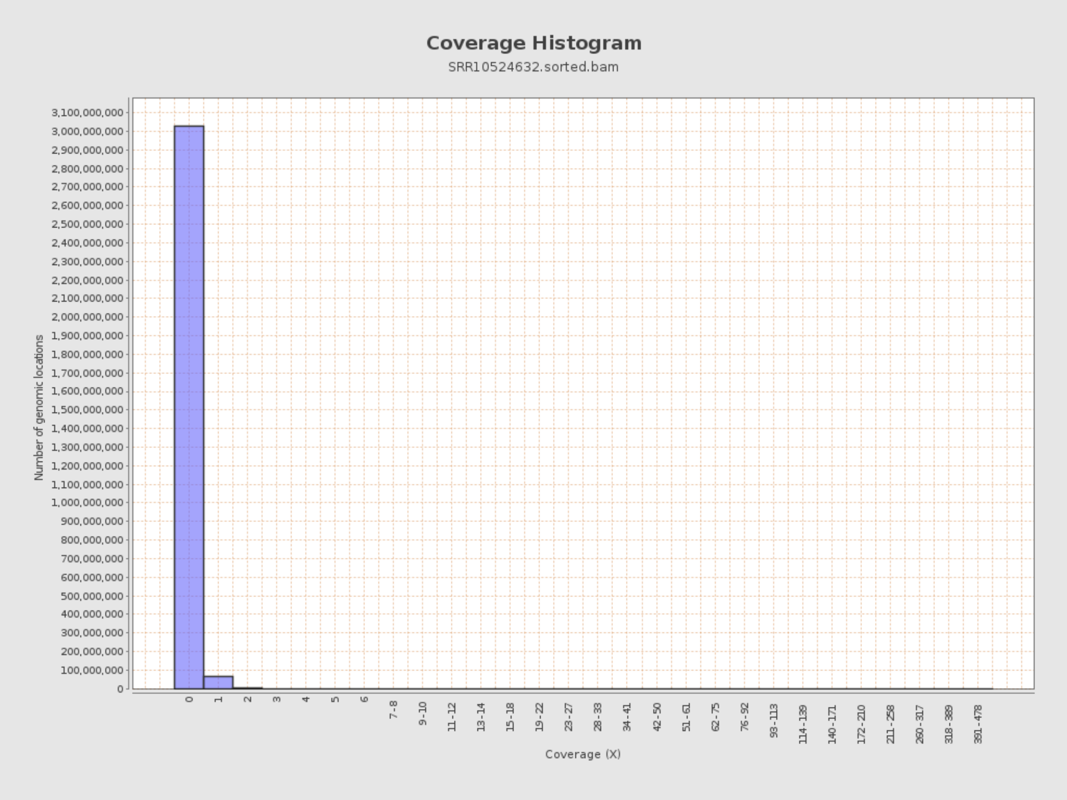
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7671815	0.0308	0.391
chr2	243199373	6967281	0.0286	0.2648
chr3	198022430	5051024	0.0255	0.1749
chr4	191154276	3530556	0.0185	0.169
chr5	180915260	4864606	0.0269	0.1793
chr6	171115067	5165966	0.0302	0.2047
chr7	159138663	4670581	0.0293	0.2469

chr8	146364022	6781479	0.0463	0.3101
chr9	141213431	2848781	0.0202	0.2052
chr10	135534747	3381949	0.025	0.2269
chr11	135006516	5006218	0.0371	0.2551
chr12	133851895	2630228	0.0197	0.1595
chr13	115169878	1951874	0.0169	0.1465
chr14	107349540	1461429	0.0136	0.133
chr15	102531392	1959866	0.0191	0.16
chr16	90354753	1854103	0.0205	0.1658
chr17	81195210	1715198	0.0211	0.163
chr18	78077248	1971876	0.0253	0.3157
chr19	59128983	1527764	0.0258	0.2939
chr20	63025520	1456358	0.0231	0.1693
chr21	48129895	647300	0.0134	0.1418
chr22	51304566	1376771	0.0268	0.1799
chrMT	16571	6547	0.3951	0.6901
chrX	155270560	3597778	0.0232	0.187
chrY	59373566	185022	0.0031	0.0869

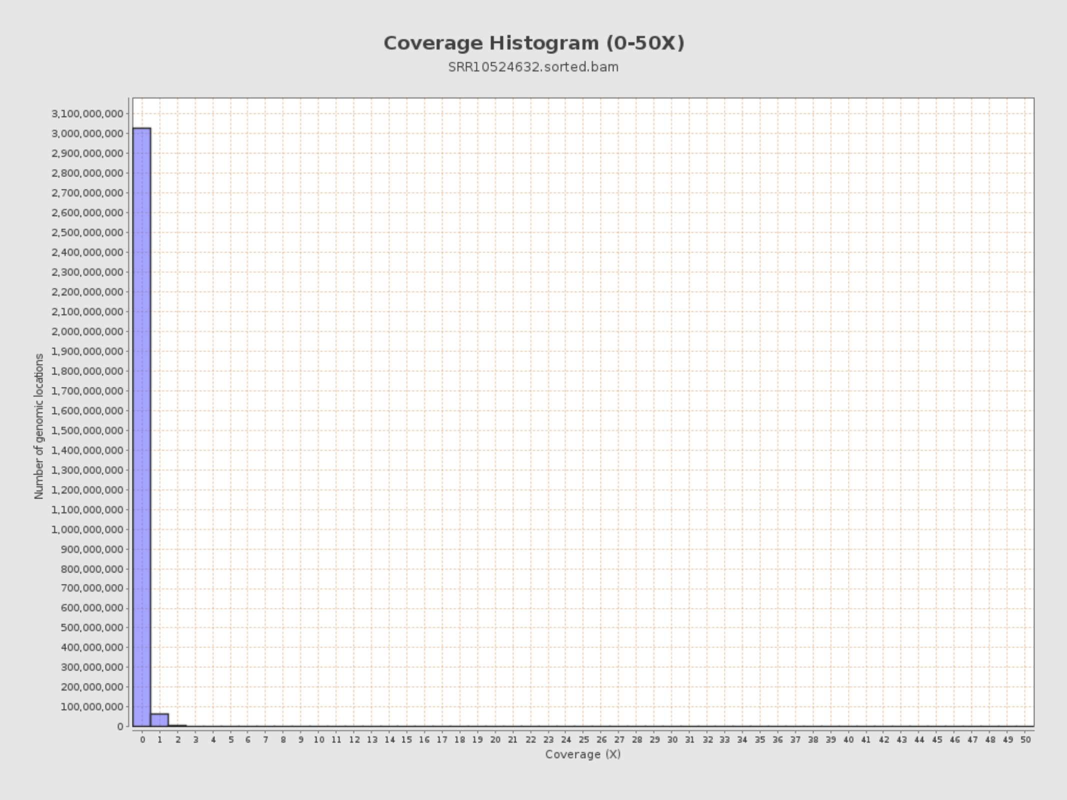
3. Results : Coverage across reference



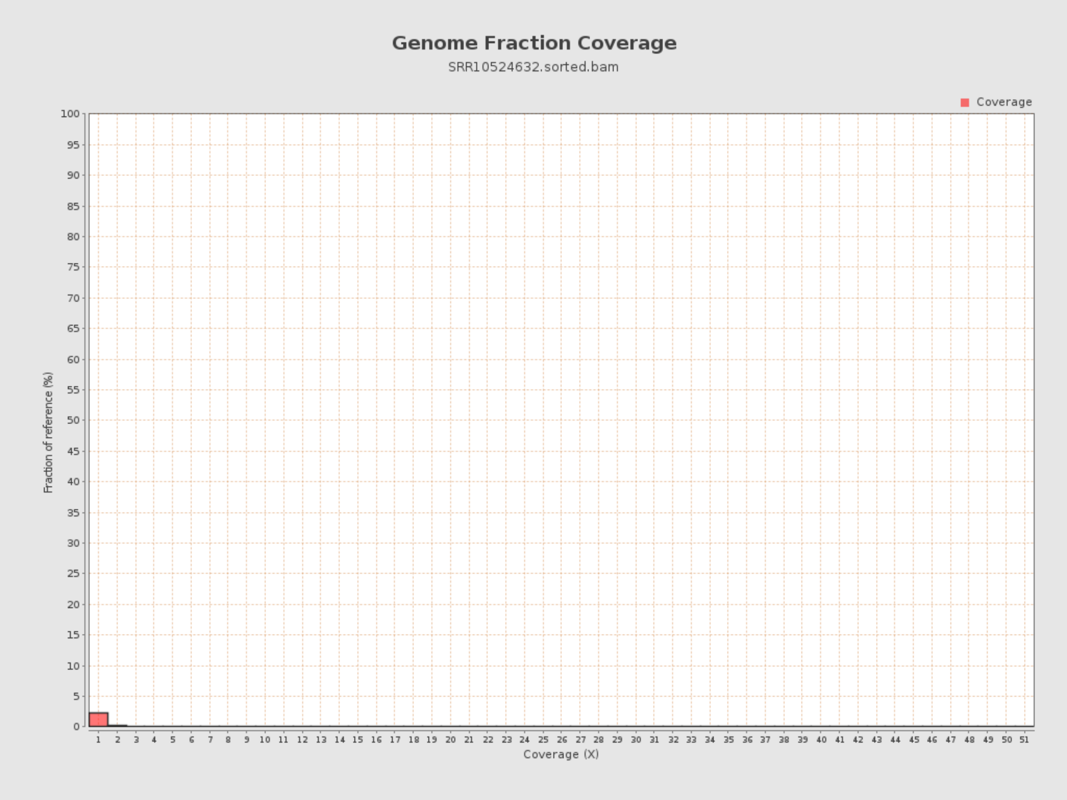
4. Results : Coverage Histogram



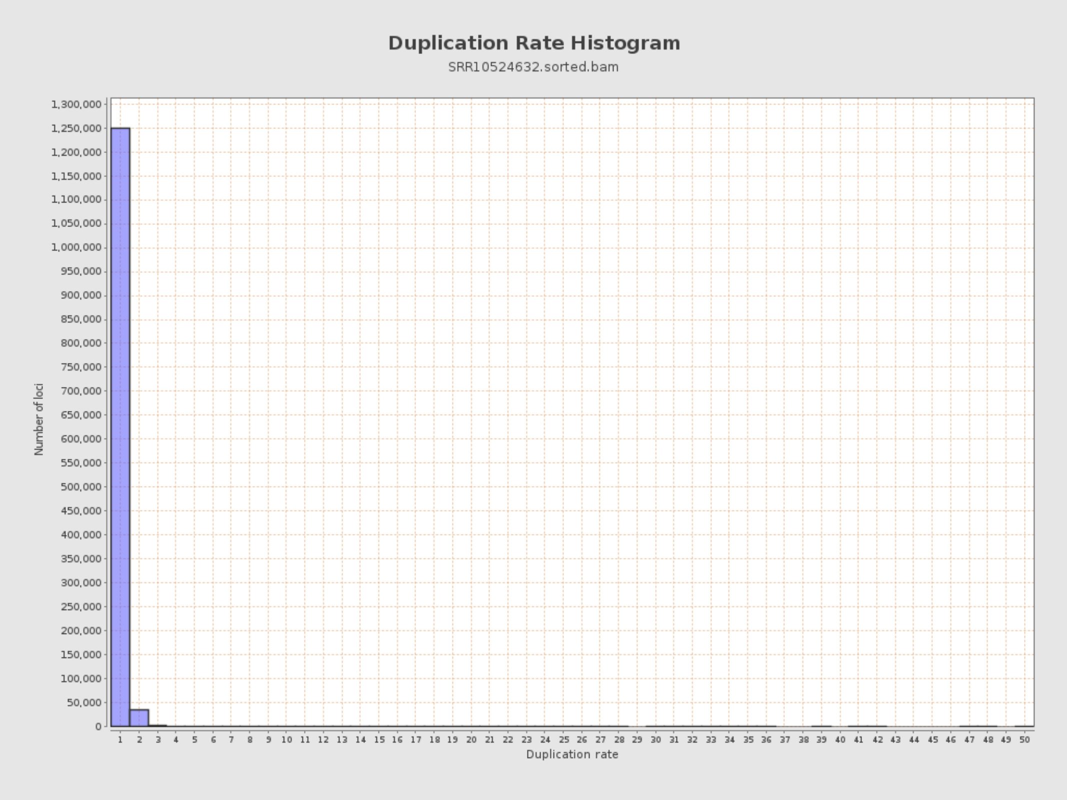
5. Results : Coverage Histogram (0-50X)



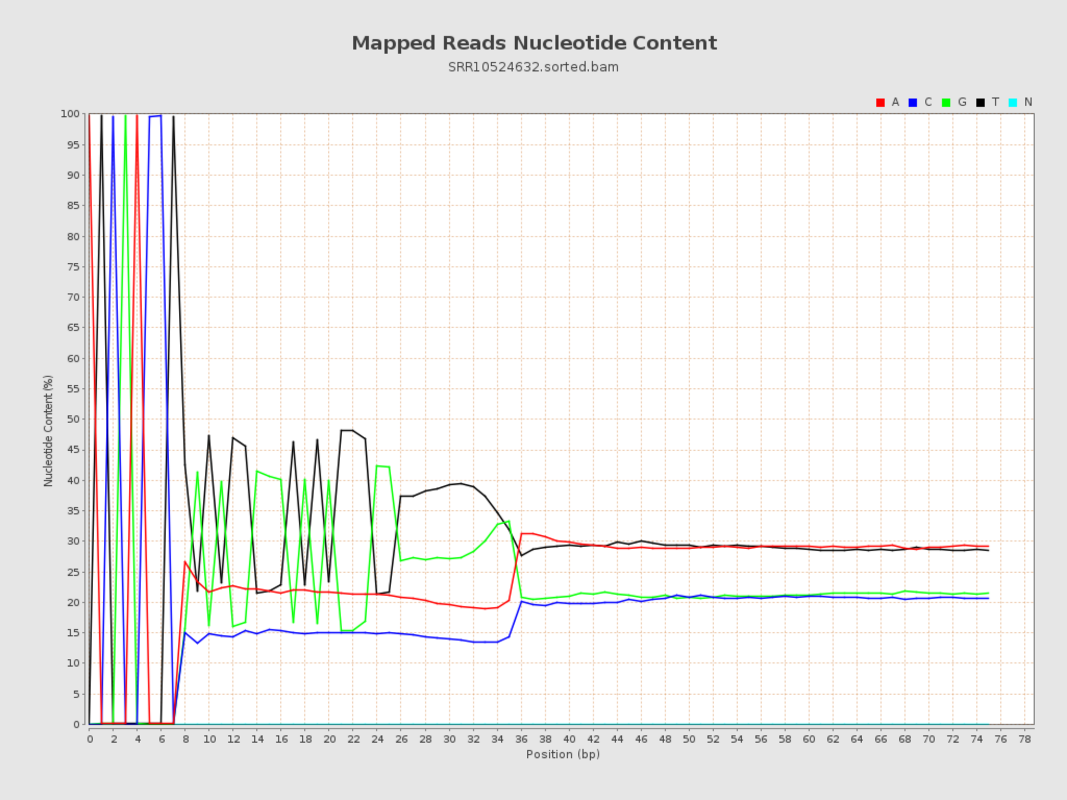
6. Results : Genome Fraction Coverage



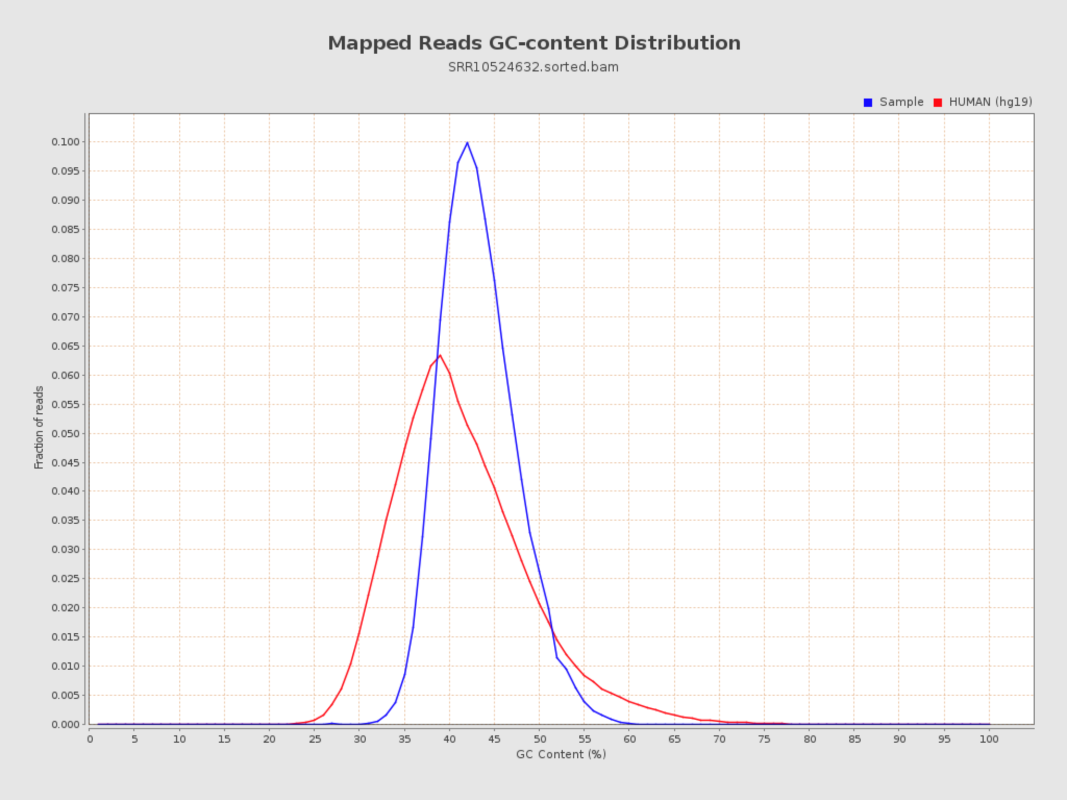
7. Results : Duplication Rate Histogram



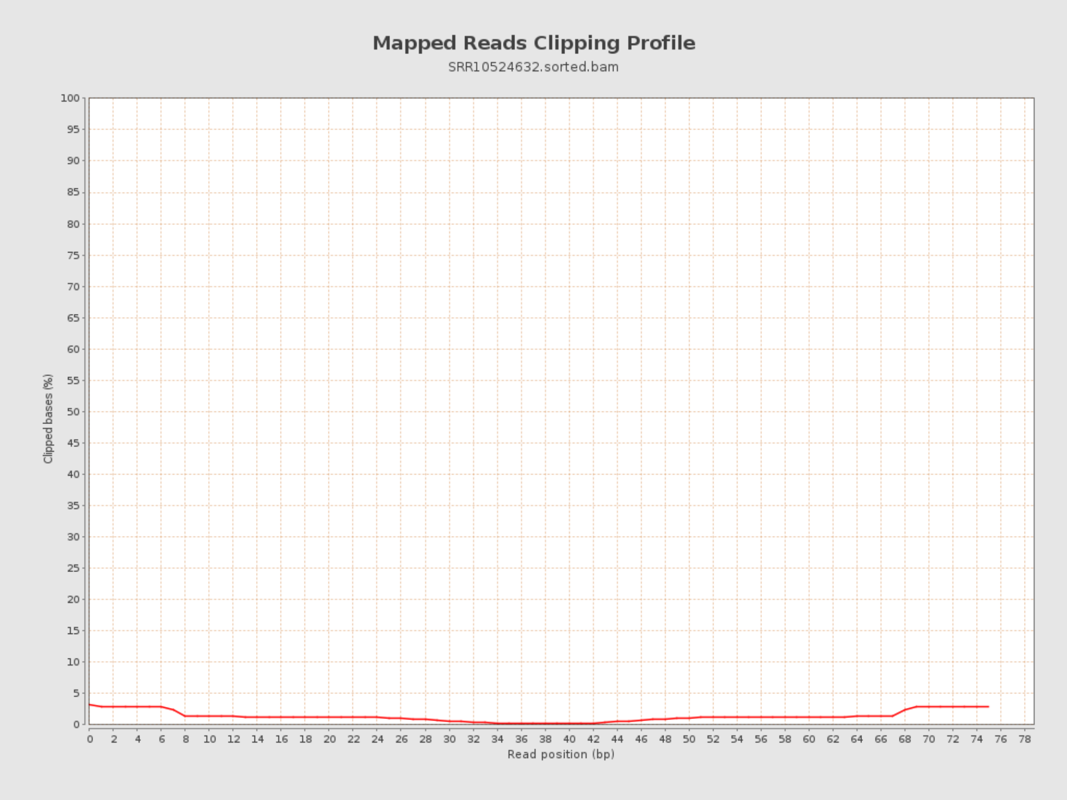
8. Results : Mapped Reads Nucleotide Content



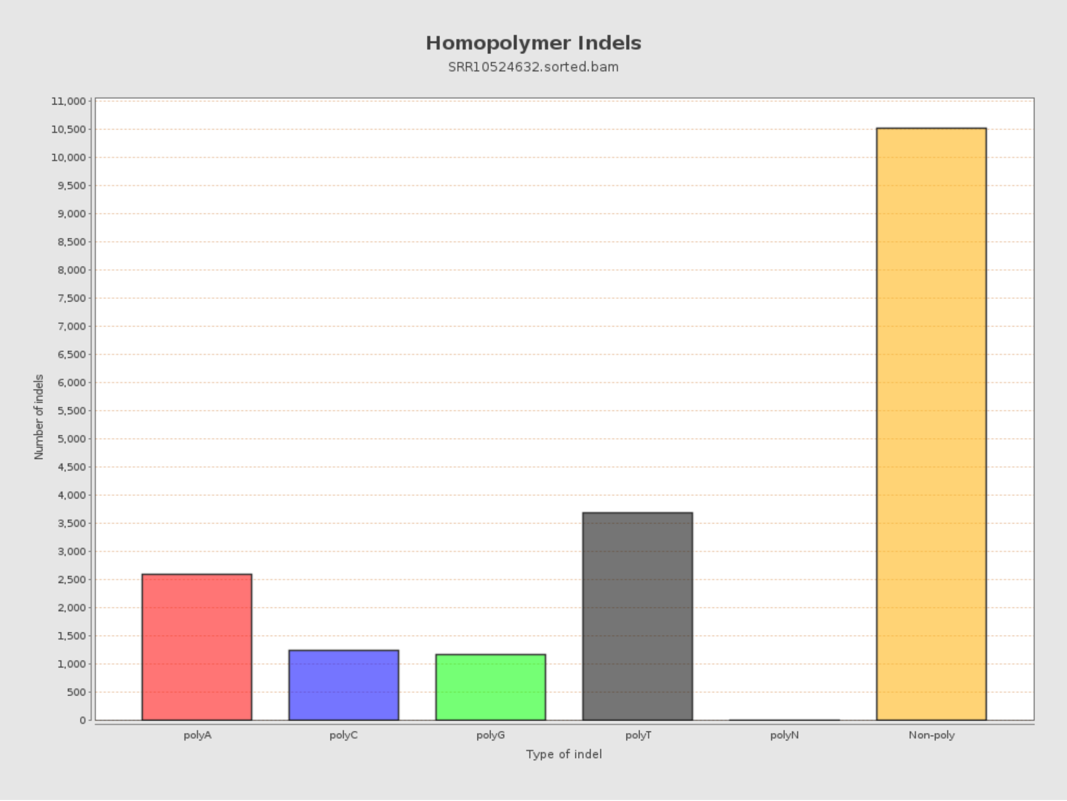
9. Results : Mapped Reads GC-content Distribution



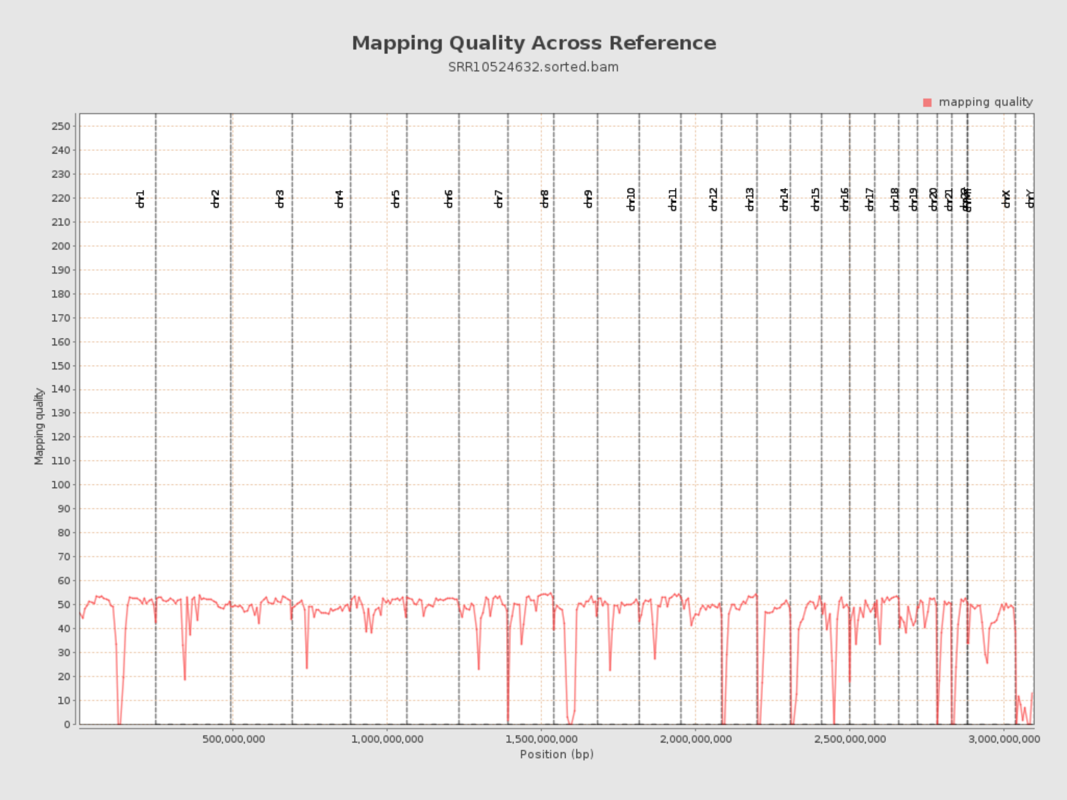
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram