Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:53:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524869.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_SRR10524869 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524869.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:53:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524869.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,411,124
Mapped reads	1,299,996 / 92.12%
Unmapped reads	111,128 / 7.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,349 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	37,291 / 2.64%
Duplication rate	1.96%
Clipped reads	1,301,494 / 92.23%

2.2. ACGT Content

Number/percentage of A's	20,031,609 / 26.42%
Number/percentage of C's	13,647,312 / 18%
Number/percentage of T's	24,784,785 / 32.68%
Number/percentage of G's	17,355,970 / 22.89%
Number/percentage of N's	10,048 / 0.01%
GC Percentage	40.89%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2571

2.4. Mapping Quality

Mean Mapping Quality	45.58

2.5. Mismatches and indels

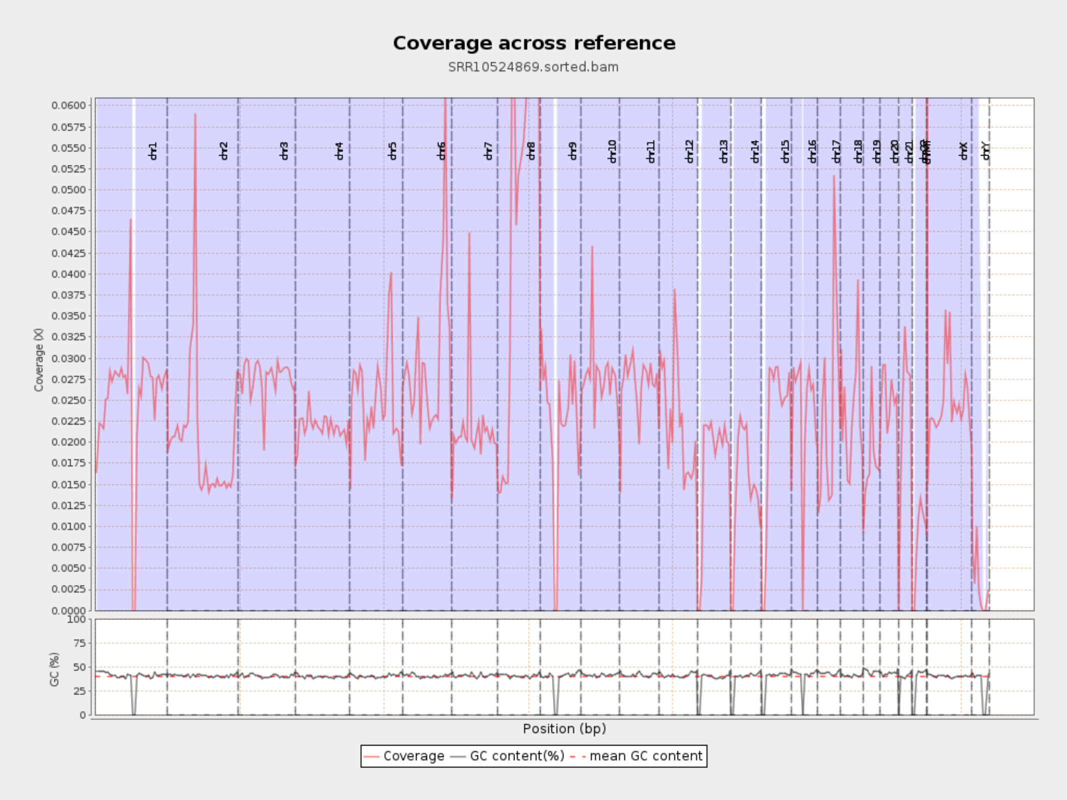
General error rate	0.49%
Mismatches	362,150
Insertions	6,034
Mapped reads with at least one insertion	0.46%
Deletions	13,952
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.76%

2.6. Chromosome stats

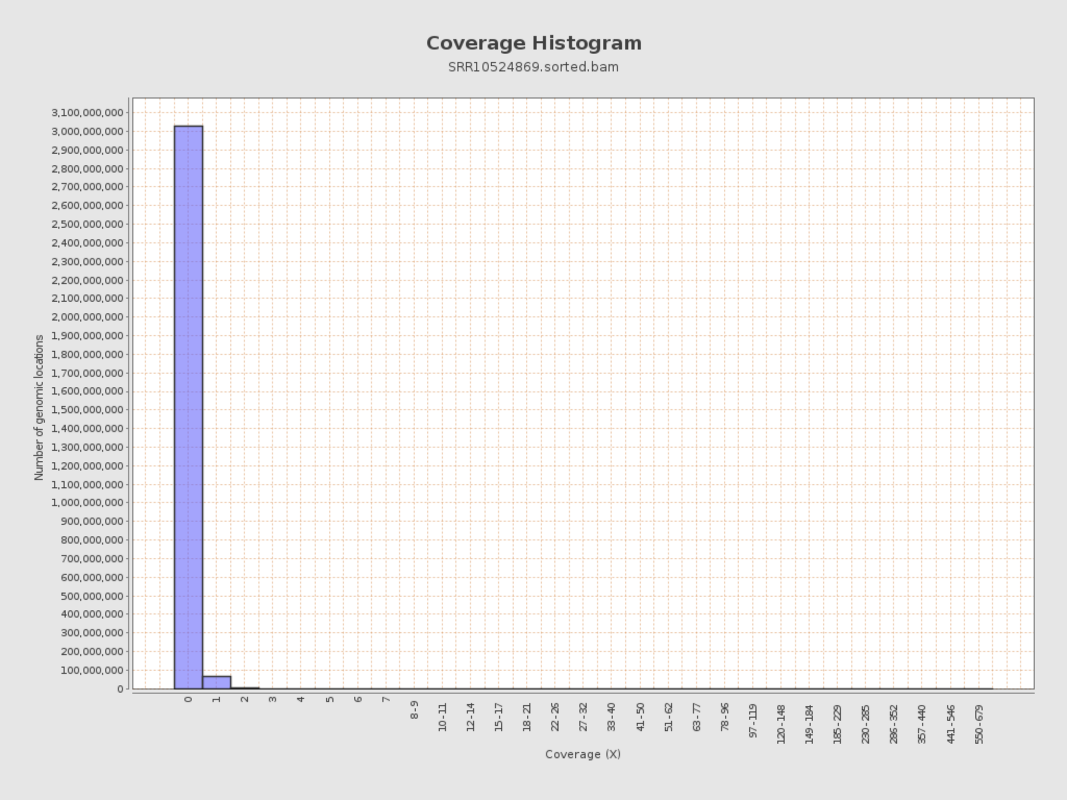
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6295964	0.0253	0.5008
chr2	243199373	4914305	0.0202	0.2467
chr3	198022430	5485957	0.0277	0.1751
chr4	191154276	4149197	0.0217	0.1657
chr5	180915260	4628023	0.0256	0.1707
chr6	171115067	5060198	0.0296	0.2018
chr7	159138663	3461625	0.0218	0.3551

chr8	146364022	8323524	0.0569	0.3539
chr9	141213431	3130961	0.0222	0.2126
chr10	135534747	3768361	0.0278	0.2363
chr11	135006516	3663824	0.0271	0.2324
chr12	133851895	3005747	0.0225	0.1628
chr13	115169878	1990682	0.0173	0.1399
chr14	107349540	1581593	0.0147	0.1381
chr15	102531392	2239614	0.0218	0.157
chr16	90354753	2104141	0.0233	0.175
chr17	81195210	1988731	0.0245	0.1837
chr18	78077248	1855743	0.0238	0.3758
chr19	59128983	1057021	0.0179	0.35
chr20	63025520	1577128	0.025	0.1697
chr21	48129895	1110058	0.0231	0.1683
chr22	51304566	428319	0.0083	0.0958
chrMT	16571	1697	0.1024	0.3631
chrX	155270560	3849078	0.0248	0.1912
chrY	59373566	179825	0.003	0.0847

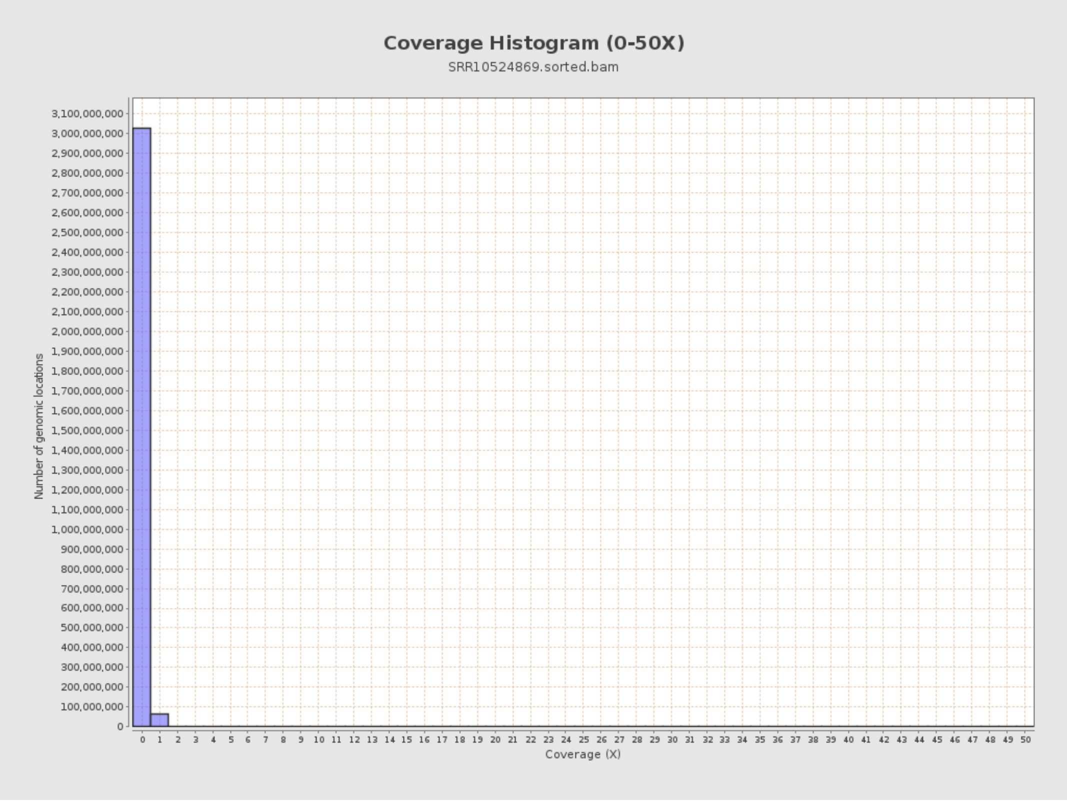
3. Results : Coverage across reference



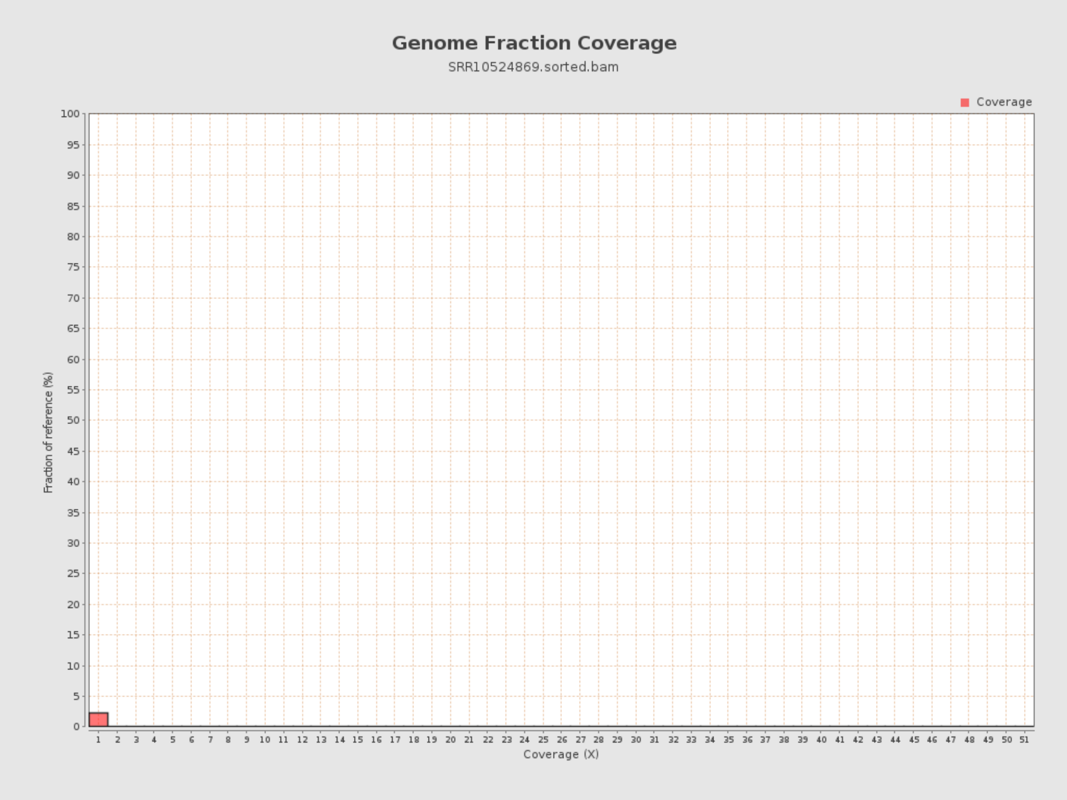
4. Results : Coverage Histogram



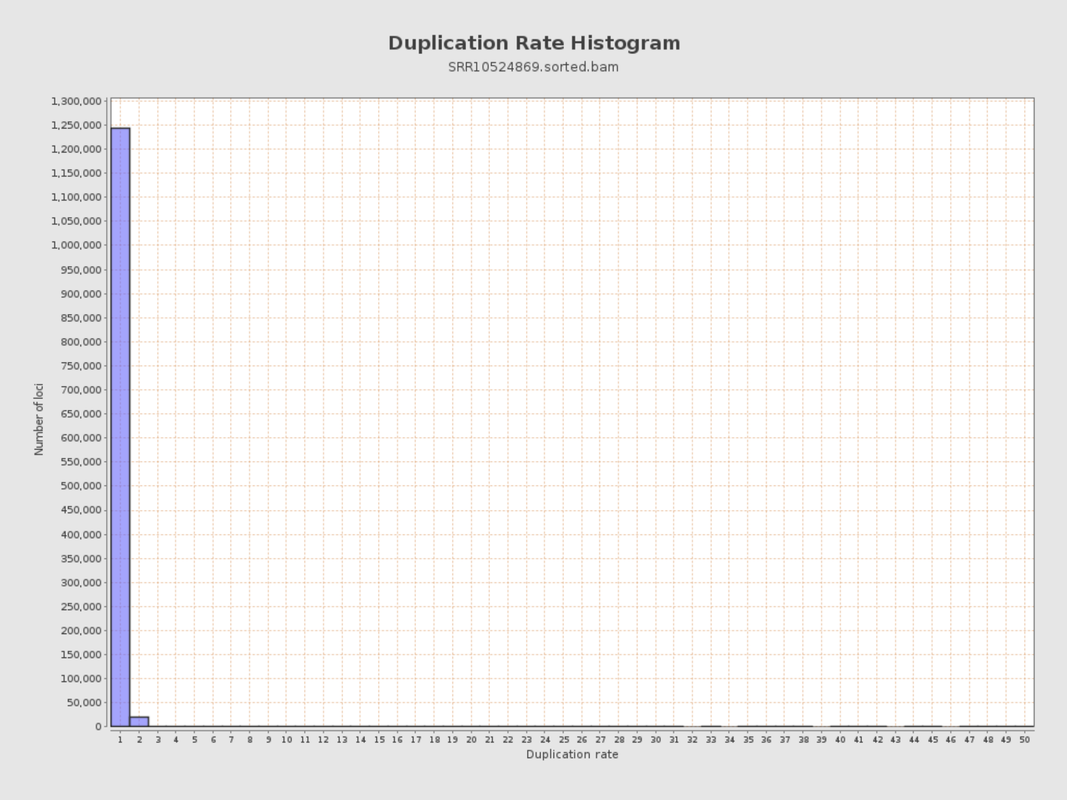
5. Results : Coverage Histogram (0-50X)



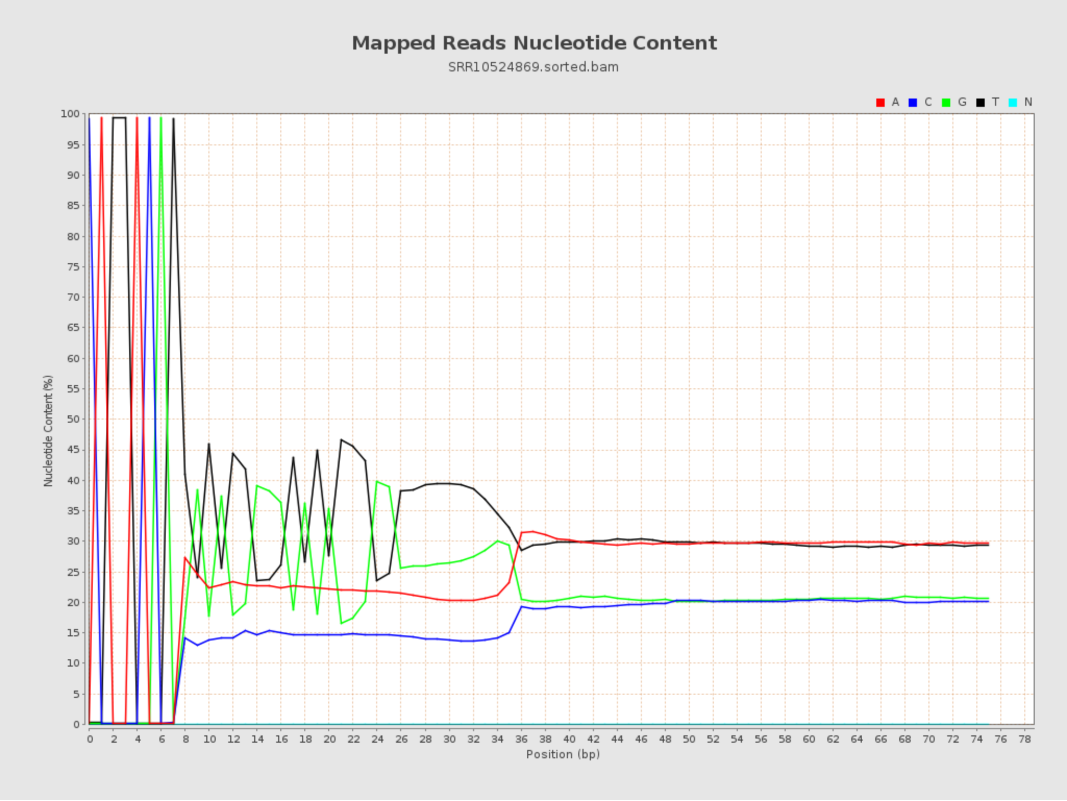
6. Results : Genome Fraction Coverage



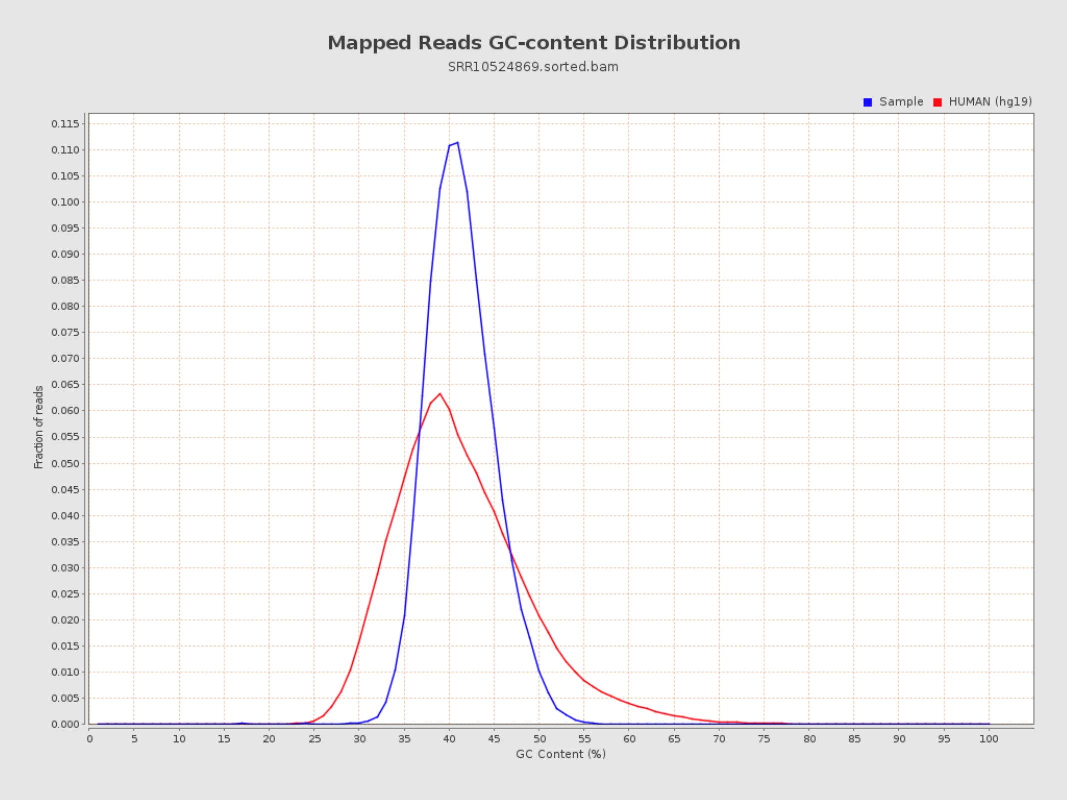
7. Results : Duplication Rate Histogram



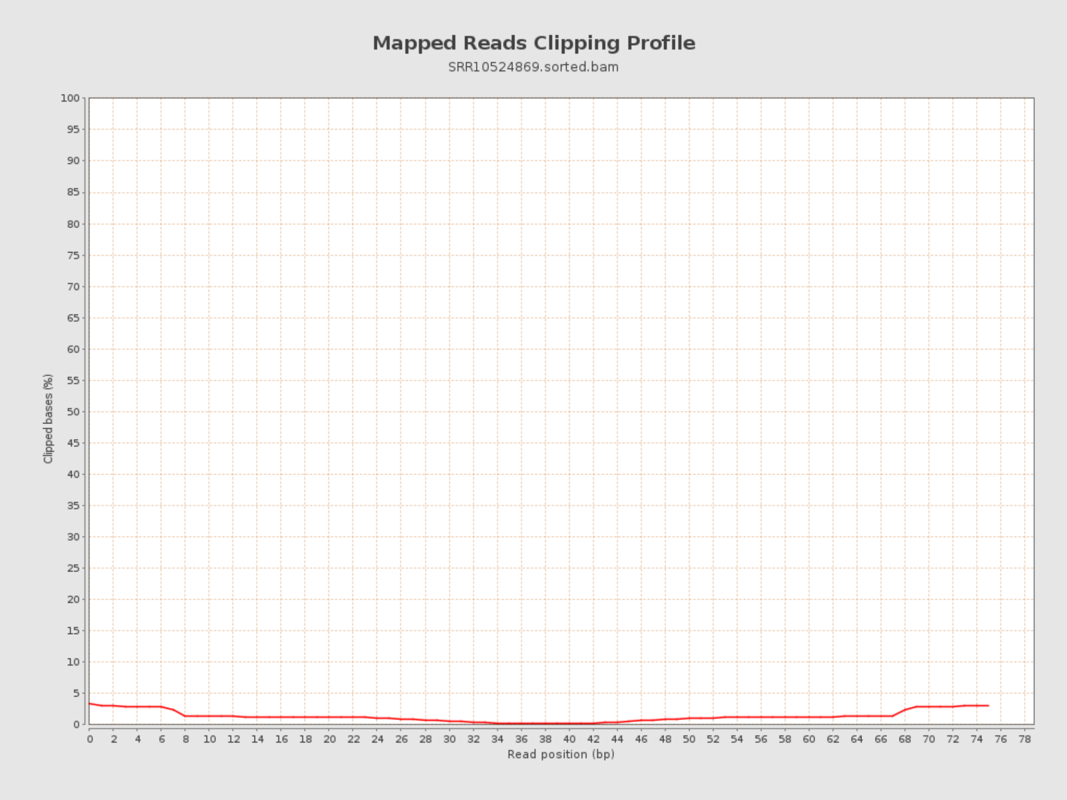
8. Results : Mapped Reads Nucleotide Content



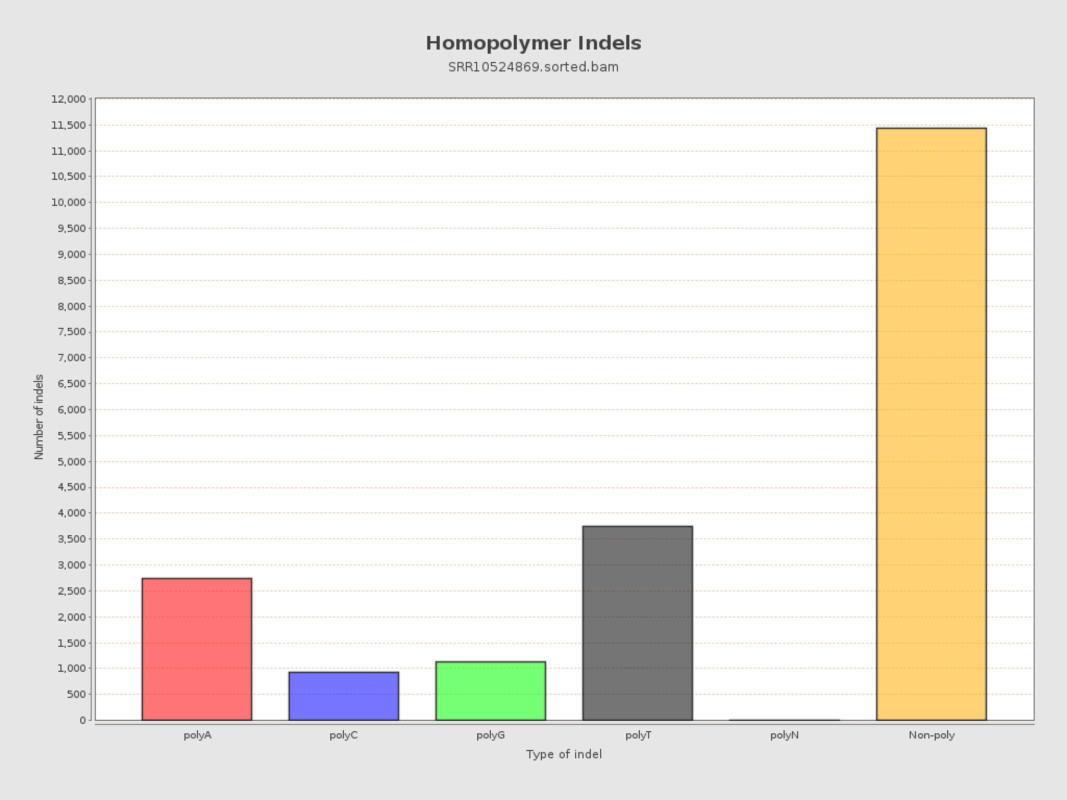
9. Results : Mapped Reads GC-content Distribution



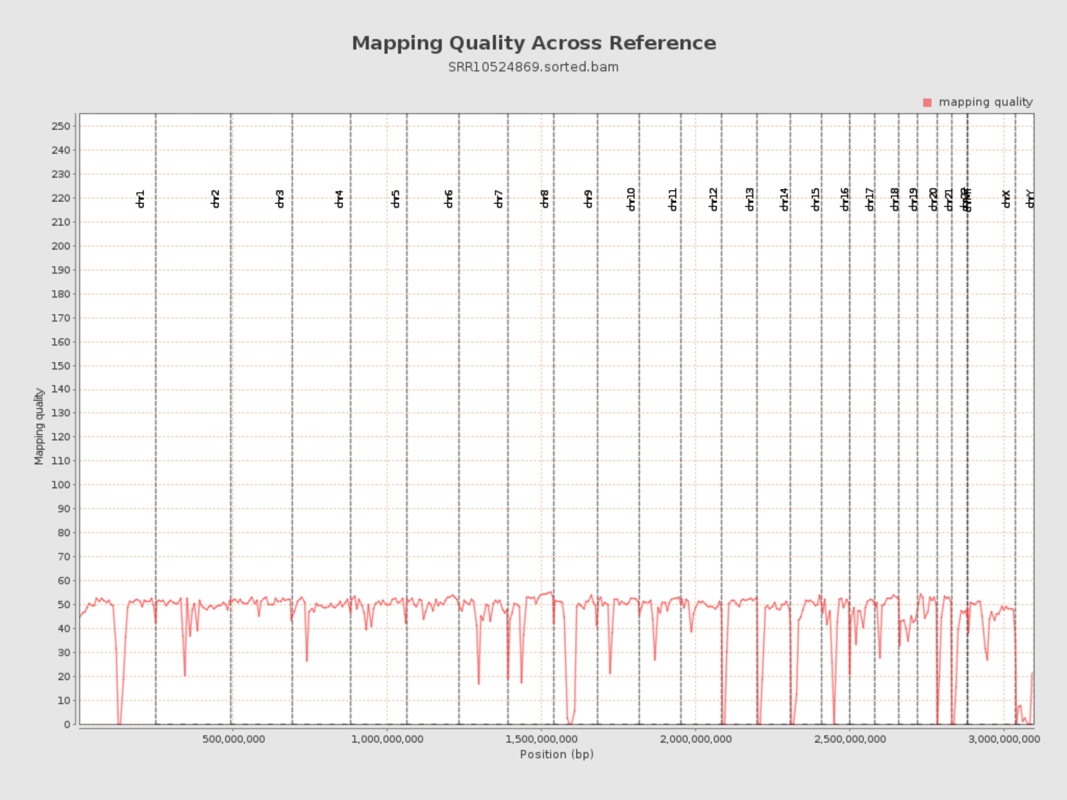
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram