Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:33:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524411.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_SRR10524411 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524411.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:33:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524411.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,124,488
Mapped reads	1,021,048 / 90.8%
Unmapped reads	103,440 / 9.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,739 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	33,634 / 2.99%
Duplication rate	2.51%
Clipped reads	1,022,046 / 90.89%

2.2. ACGT Content

Number/percentage of A's	15,687,777 / 26.53%
Number/percentage of C's	10,302,706 / 17.42%
Number/percentage of T's	18,788,114 / 31.77%
Number/percentage of G's	14,361,248 / 24.28%
Number/percentage of N's	1,238 / 0%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0191

Standard Deviation	0.2022

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

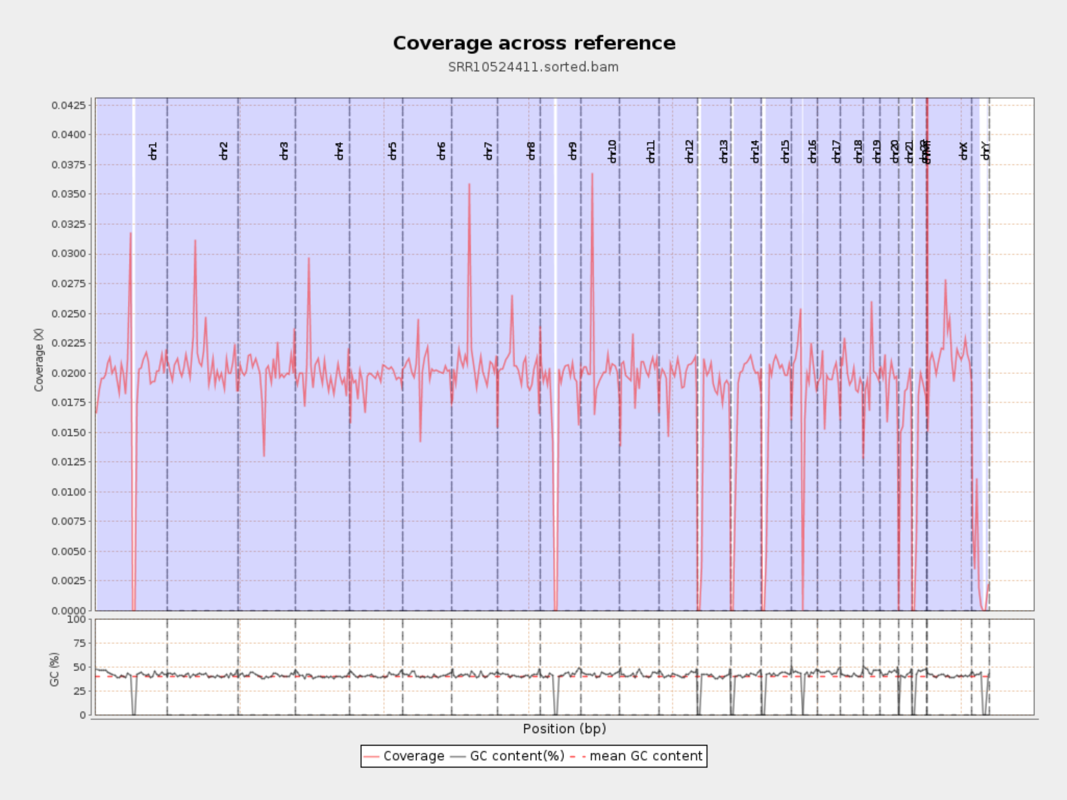
General error rate	0.53%
Mismatches	304,561
Insertions	4,024
Mapped reads with at least one insertion	0.39%
Deletions	12,188
Mapped reads with at least one deletion	1.18%
Homopolymer indels	43.25%

2.6. Chromosome stats

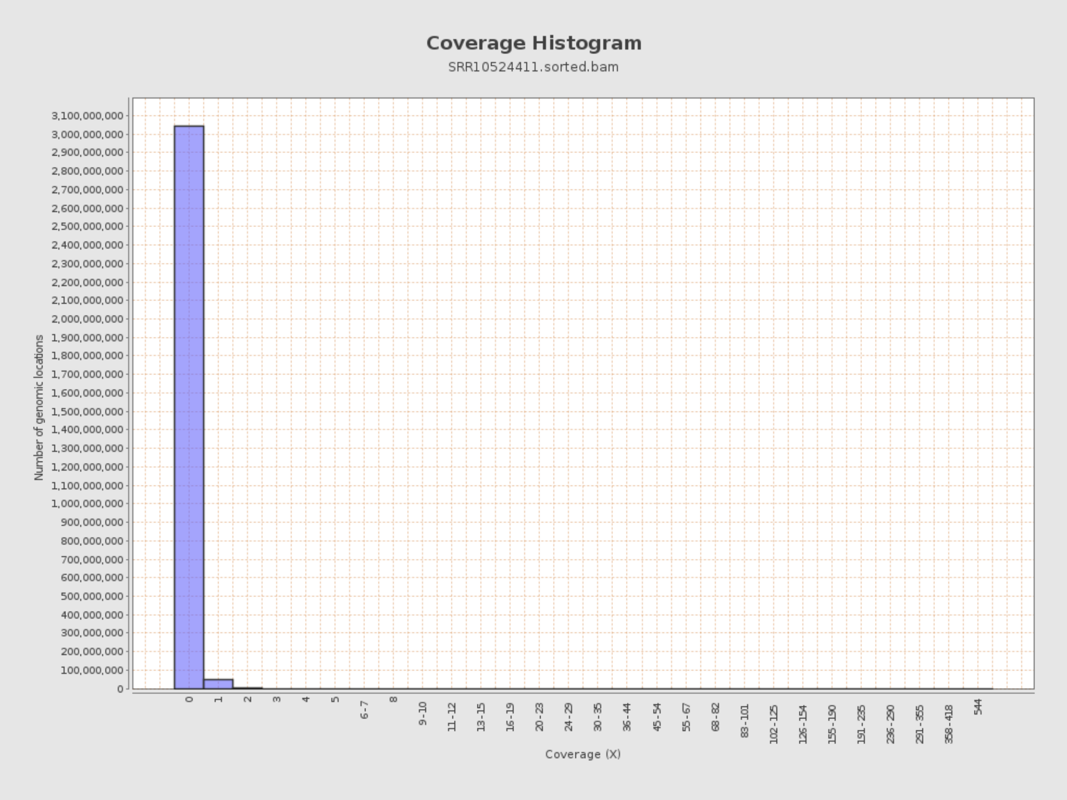
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4750671	0.0191	0.3295
chr2	243199373	5084325	0.0209	0.2783
chr3	198022430	3964414	0.02	0.1515
chr4	191154276	3836051	0.0201	0.1595
chr5	180915260	3552261	0.0196	0.1492
chr6	171115067	3465660	0.0203	0.1632
chr7	159138663	3365790	0.0212	0.2798

chr8	146364022	2994709	0.0205	0.201
chr9	141213431	2438894	0.0173	0.1699
chr10	135534747	2812607	0.0208	0.1982
chr11	135006516	2720342	0.0201	0.1726
chr12	133851895	2653367	0.0198	0.1511
chr13	115169878	1856064	0.0161	0.1352
chr14	107349540	1807641	0.0168	0.1406
chr15	102531392	1685074	0.0164	0.1383
chr16	90354753	1685484	0.0187	0.1549
chr17	81195210	1568941	0.0193	0.1519
chr18	78077248	1550370	0.0199	0.2716
chr19	59128983	1164694	0.0197	0.2564
chr20	63025520	1221240	0.0194	0.1493
chr21	48129895	768496	0.016	0.1451
chr22	51304566	662738	0.0129	0.121
chrMT	16571	12777	0.771	1.0299
chrX	155270560	3352936	0.0216	0.1652
chrY	59373566	185091	0.0031	0.0918

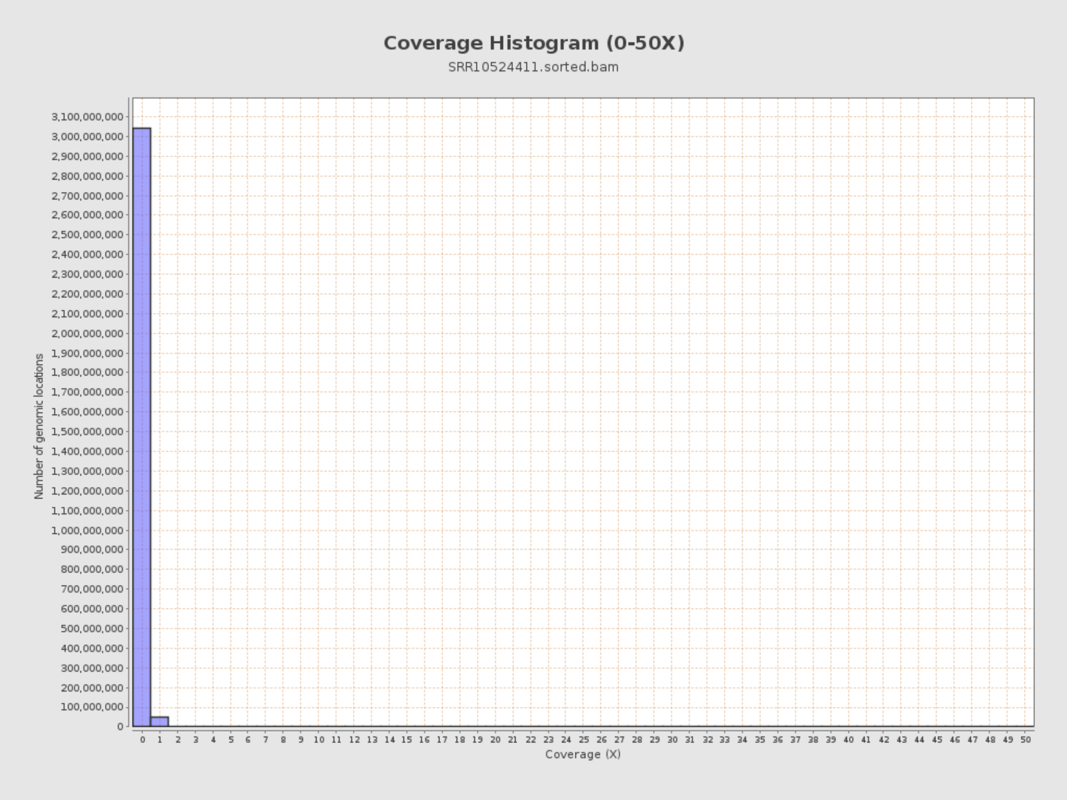
3. Results : Coverage across reference



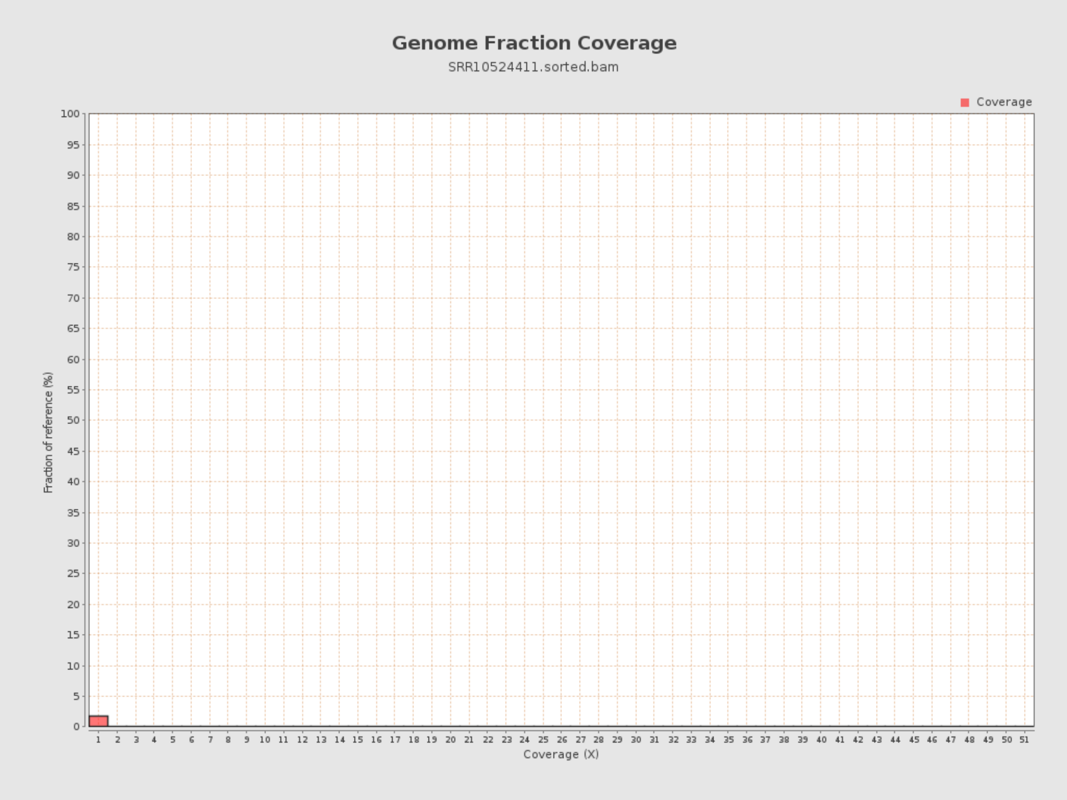
4. Results : Coverage Histogram



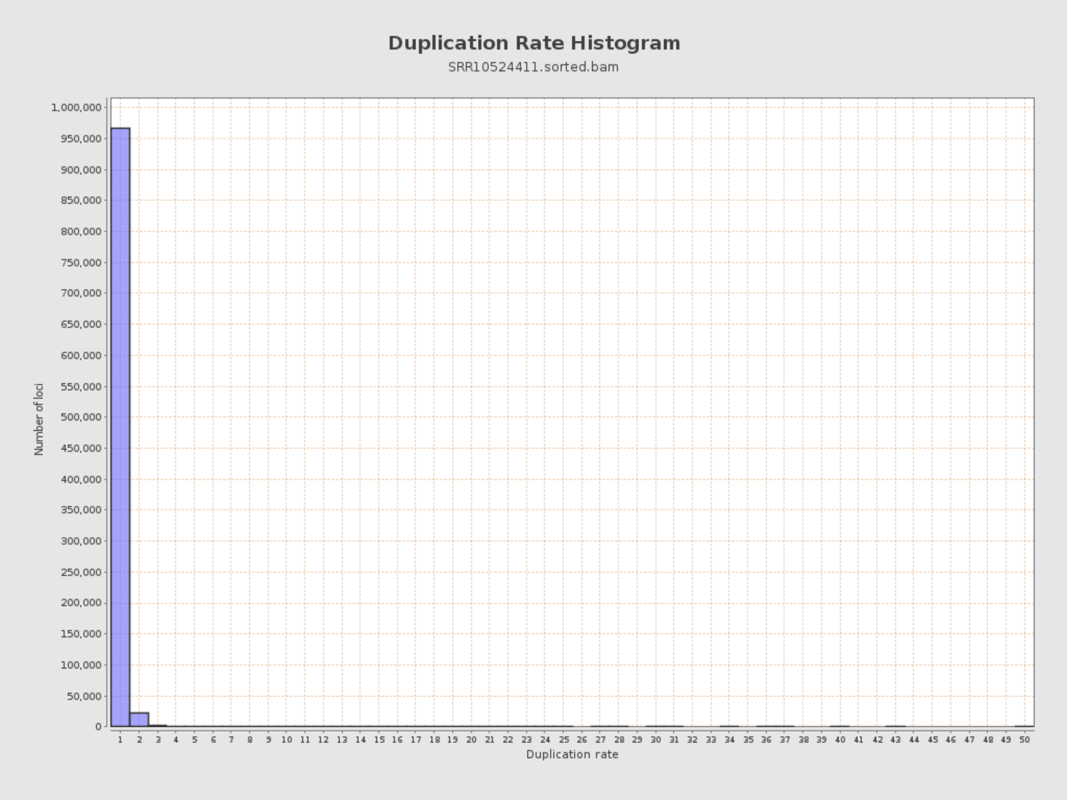
5. Results : Coverage Histogram (0-50X)



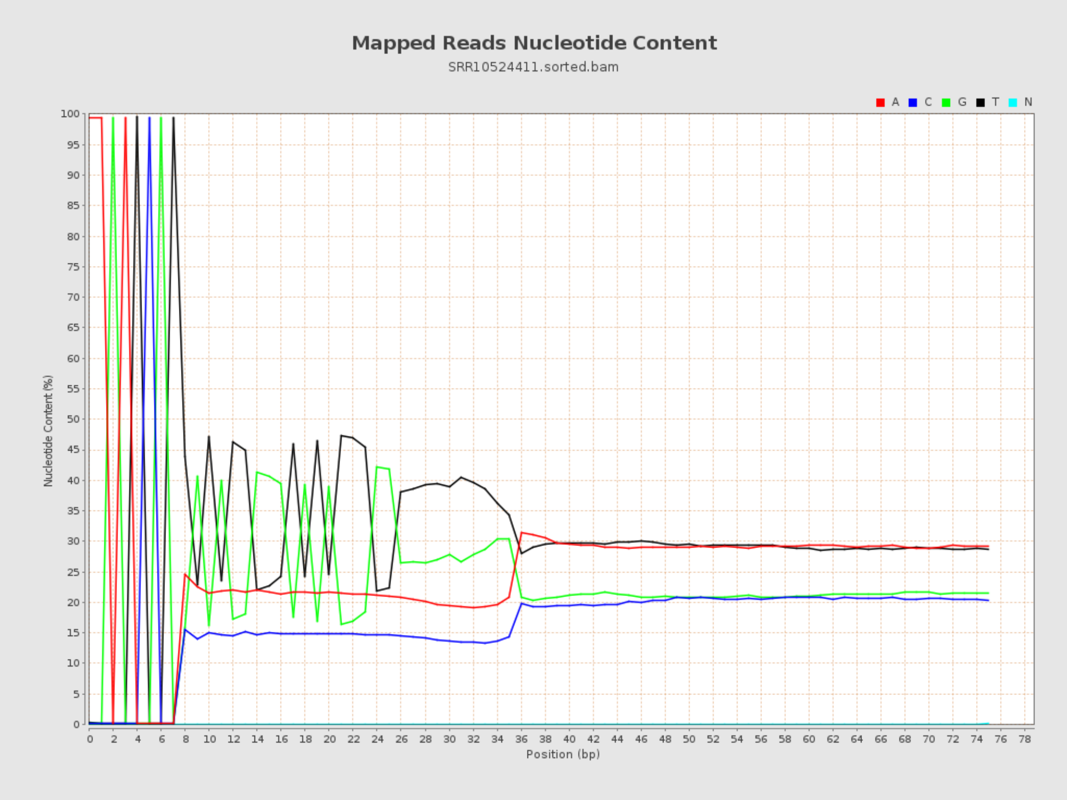
6. Results : Genome Fraction Coverage



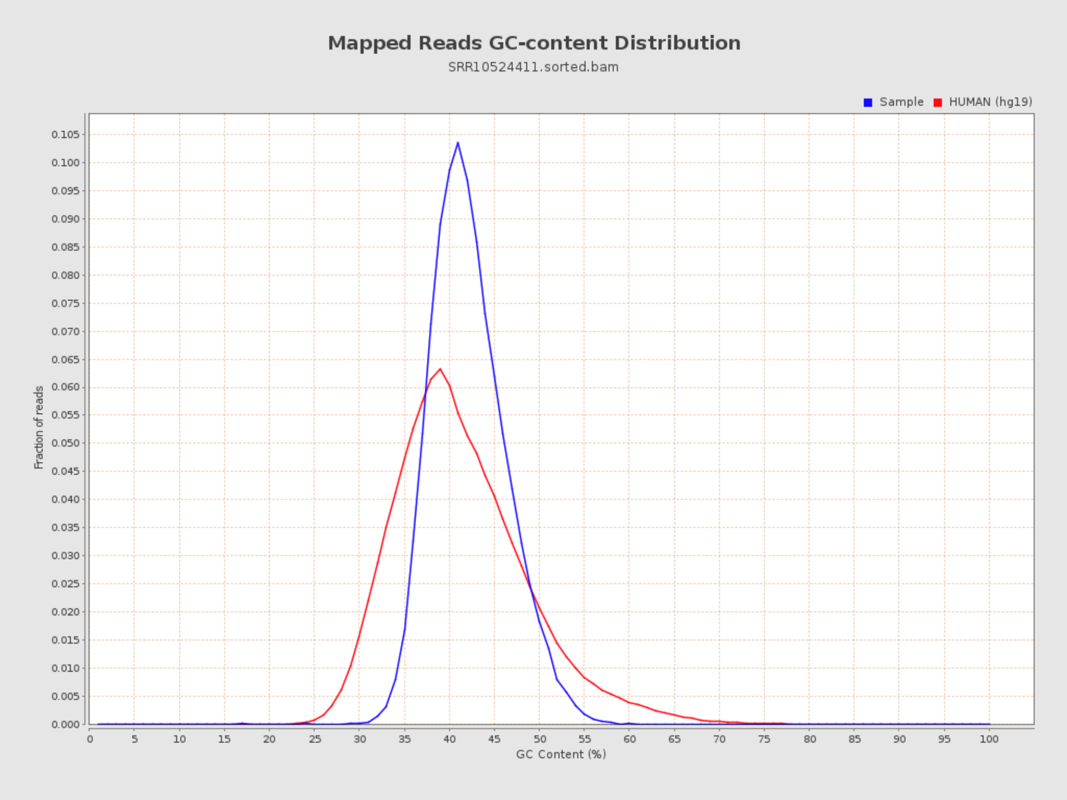
7. Results : Duplication Rate Histogram



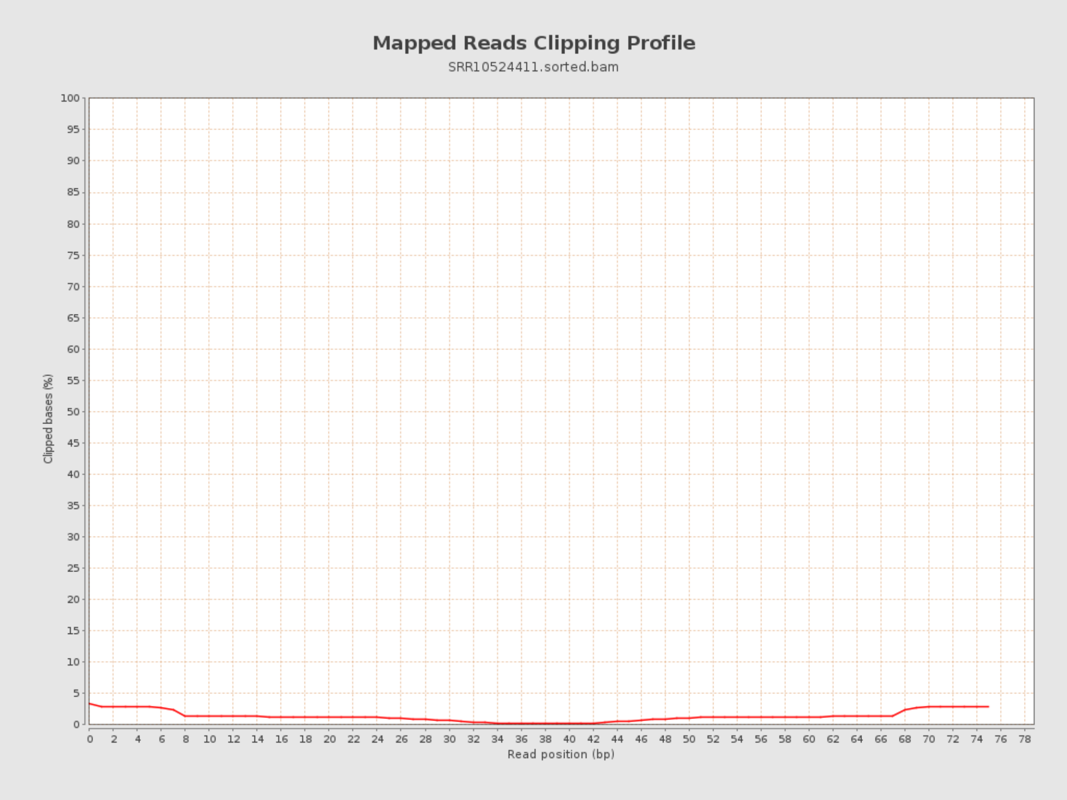
8. Results : Mapped Reads Nucleotide Content



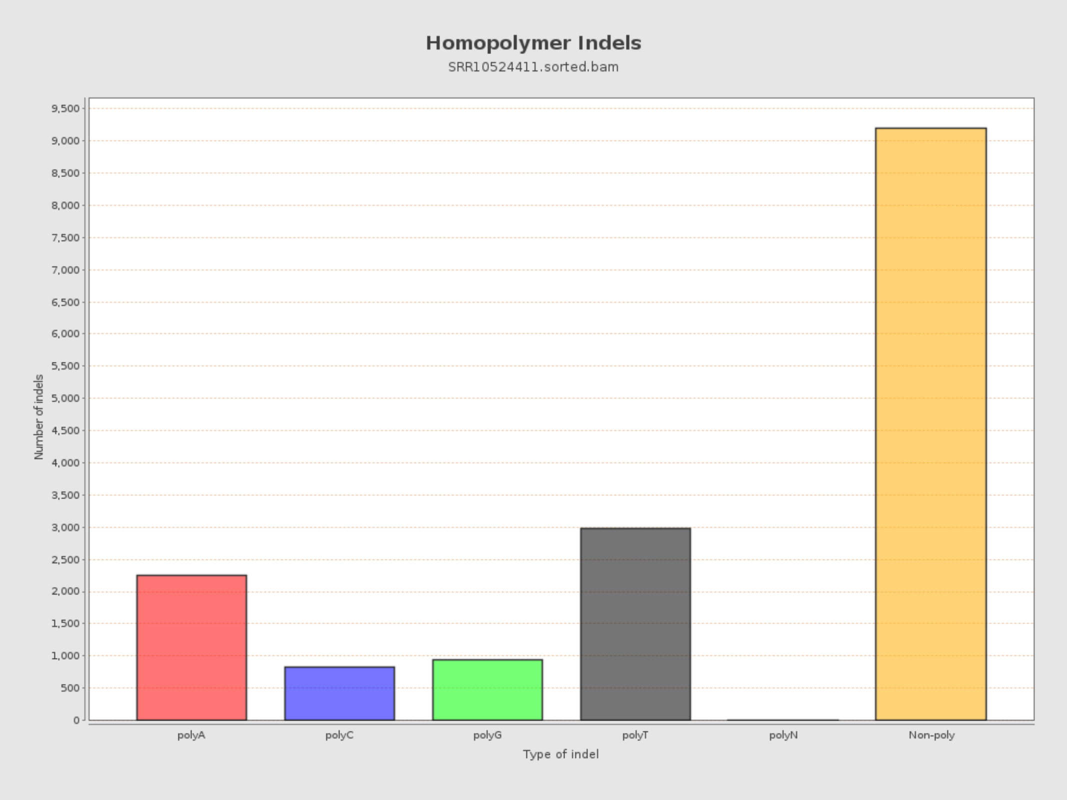
9. Results : Mapped Reads GC-content Distribution



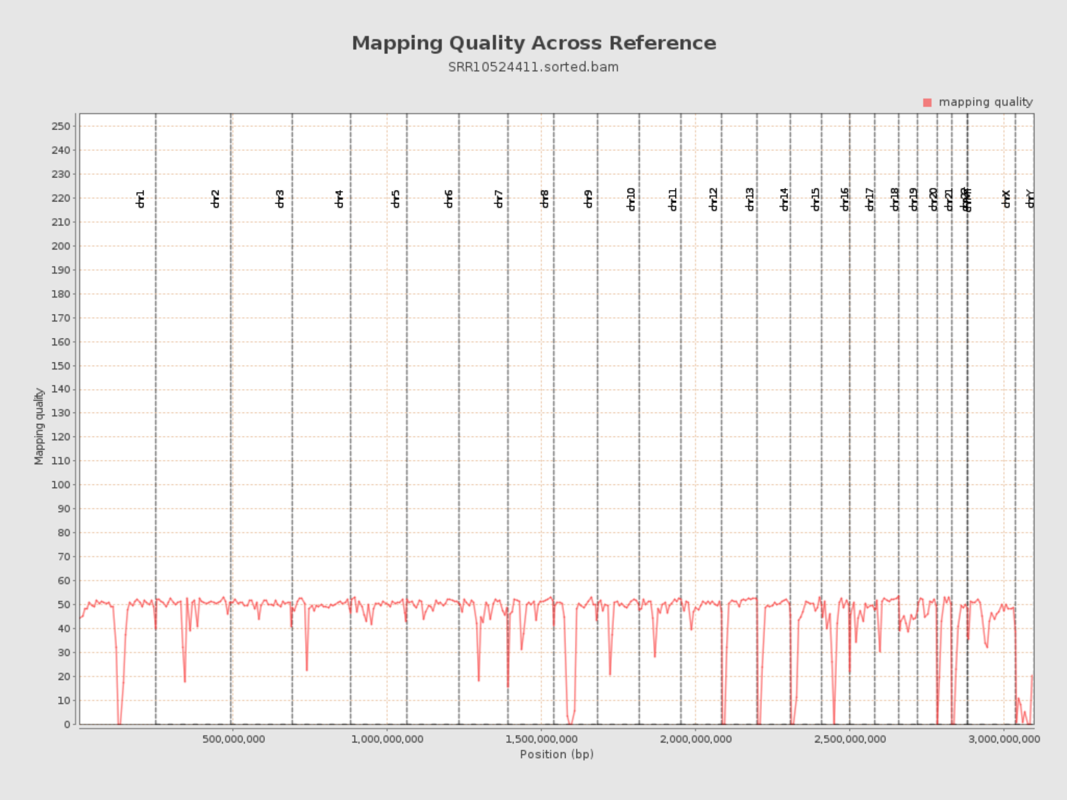
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram