Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:43:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524344.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_SRR10524344 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524344.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:43:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524344.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,515,123
Mapped reads	1,375,277 / 90.77%
Unmapped reads	139,846 / 9.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,426 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	55,689 / 3.68%
Duplication rate	3.06%
Clipped reads	1,376,208 / 90.83%

2.2. ACGT Content

Number/percentage of A's	19,638,008 / 24.78%
Number/percentage of C's	14,960,494 / 18.88%
Number/percentage of T's	26,710,018 / 33.71%
Number/percentage of G's	17,926,106 / 22.62%
Number/percentage of N's	1,606 / 0%
GC Percentage	41.5%

2.3. Coverage

Mean	0.0256

Standard Deviation	0.2564

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

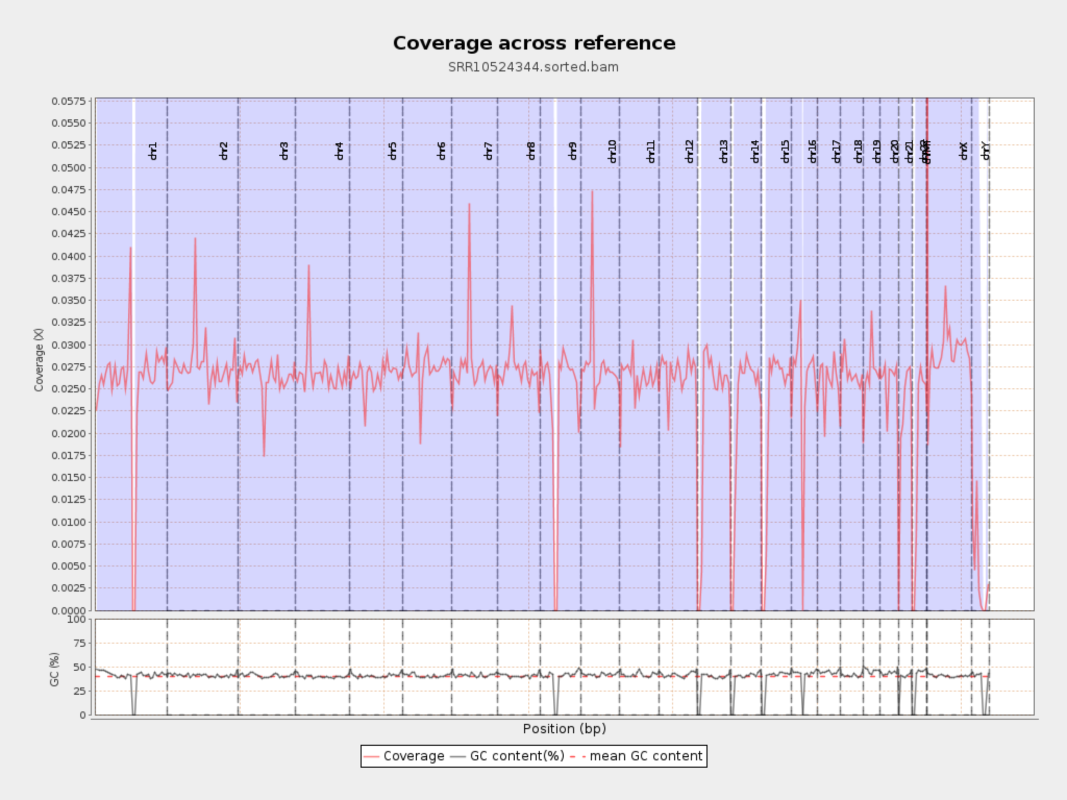
General error rate	0.53%
Mismatches	411,540
Insertions	5,484
Mapped reads with at least one insertion	0.4%
Deletions	16,706
Mapped reads with at least one deletion	1.2%
Homopolymer indels	43.22%

2.6. Chromosome stats

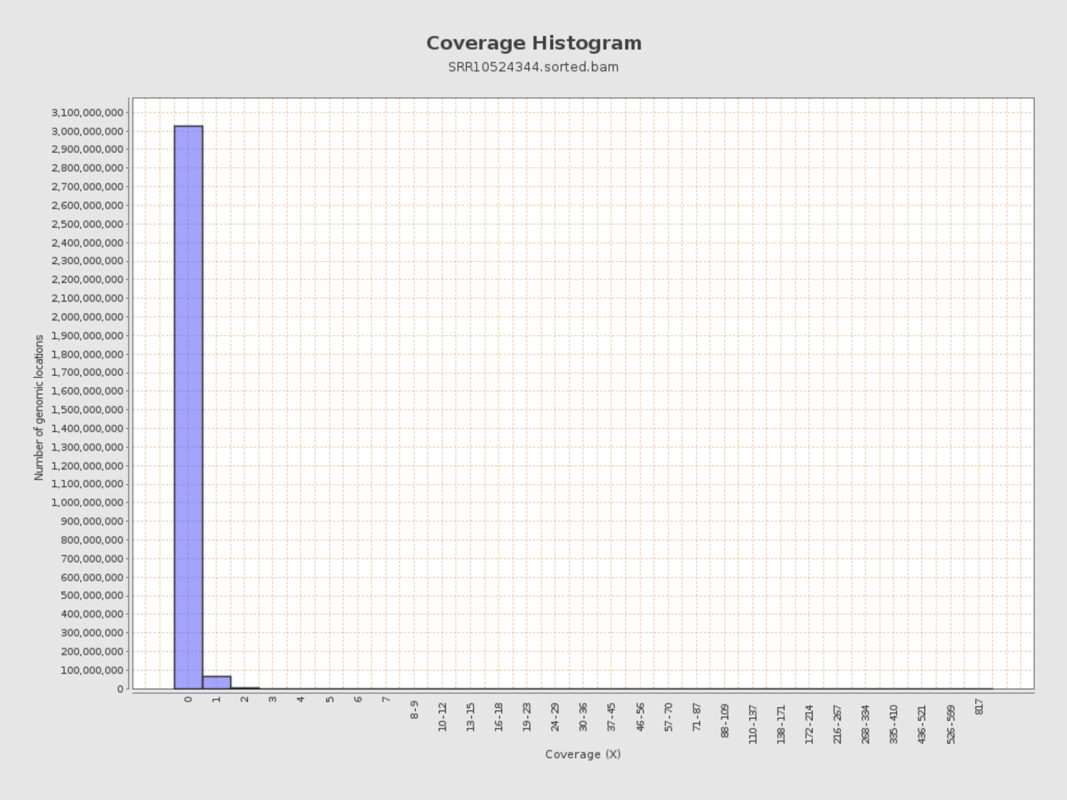
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6335253	0.0254	0.418
chr2	243199373	6704994	0.0276	0.3808
chr3	198022430	5236179	0.0264	0.1765
chr4	191154276	5158394	0.027	0.19
chr5	180915260	4796402	0.0265	0.1771
chr6	171115067	4675702	0.0273	0.1976
chr7	159138663	4432276	0.0279	0.3491

chr8	146364022	3987846	0.0272	0.2843
chr9	141213431	3337528	0.0236	0.2133
chr10	135534747	3779845	0.0279	0.2456
chr11	135006516	3559864	0.0264	0.2143
chr12	133851895	3588288	0.0268	0.1794
chr13	115169878	2581327	0.0224	0.1629
chr14	107349540	2398334	0.0223	0.1676
chr15	102531392	2249905	0.0219	0.1627
chr16	90354753	2280549	0.0252	0.187
chr17	81195210	2086935	0.0257	0.1803
chr18	78077248	2095623	0.0268	0.3692
chr19	59128983	1602723	0.0271	0.3199
chr20	63025520	1629156	0.0258	0.1773
chr21	48129895	1050648	0.0218	0.1726
chr22	51304566	923307	0.018	0.1452
chrMT	16571	4660	0.2812	0.5847
chrX	155270560	4521749	0.0291	0.2005
chrY	59373566	245552	0.0041	0.1199

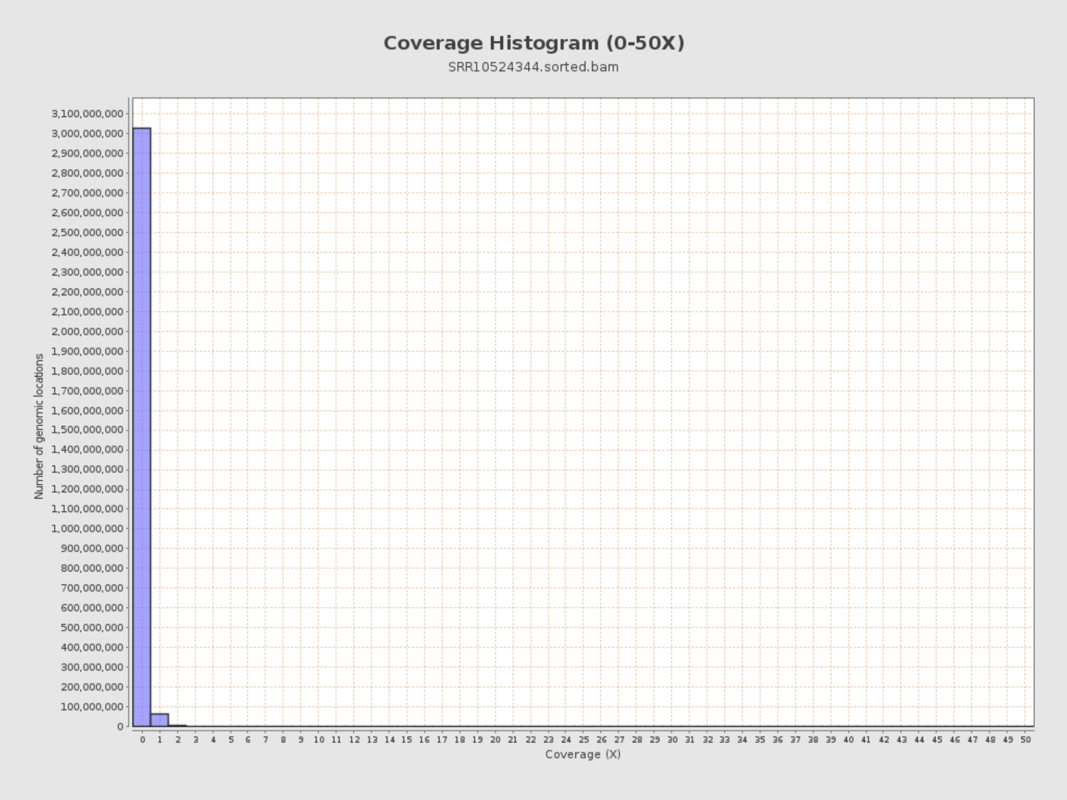
3. Results : Coverage across reference



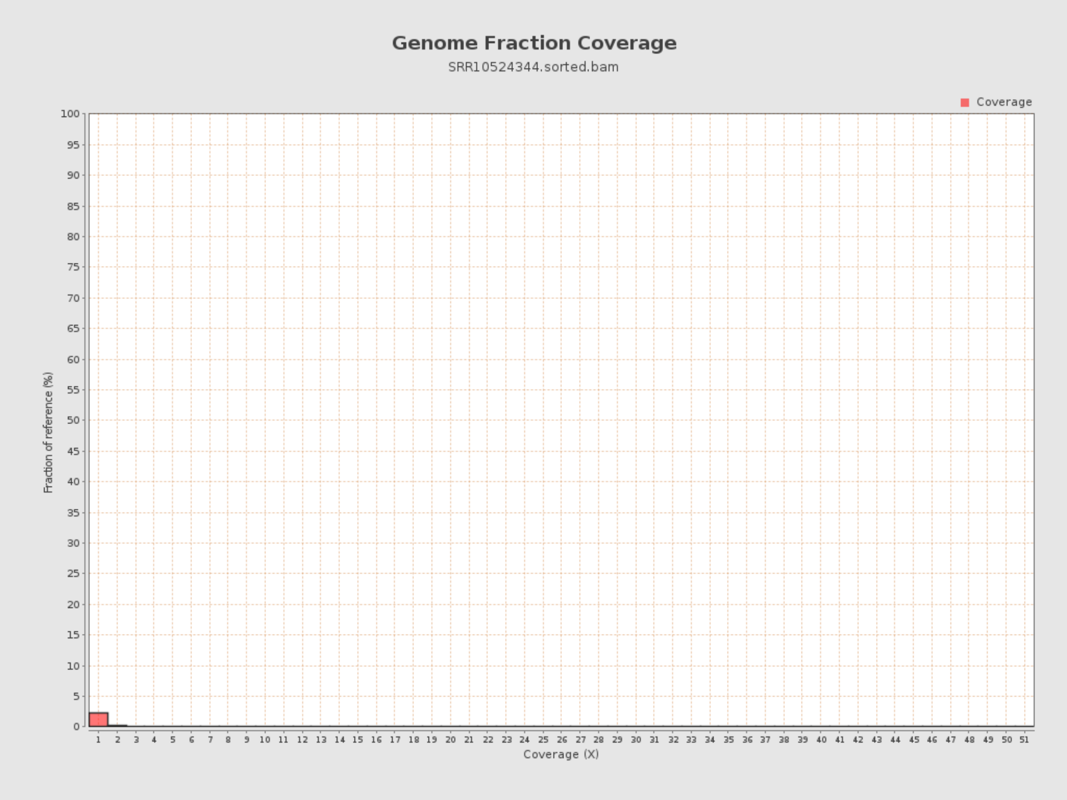
4. Results : Coverage Histogram



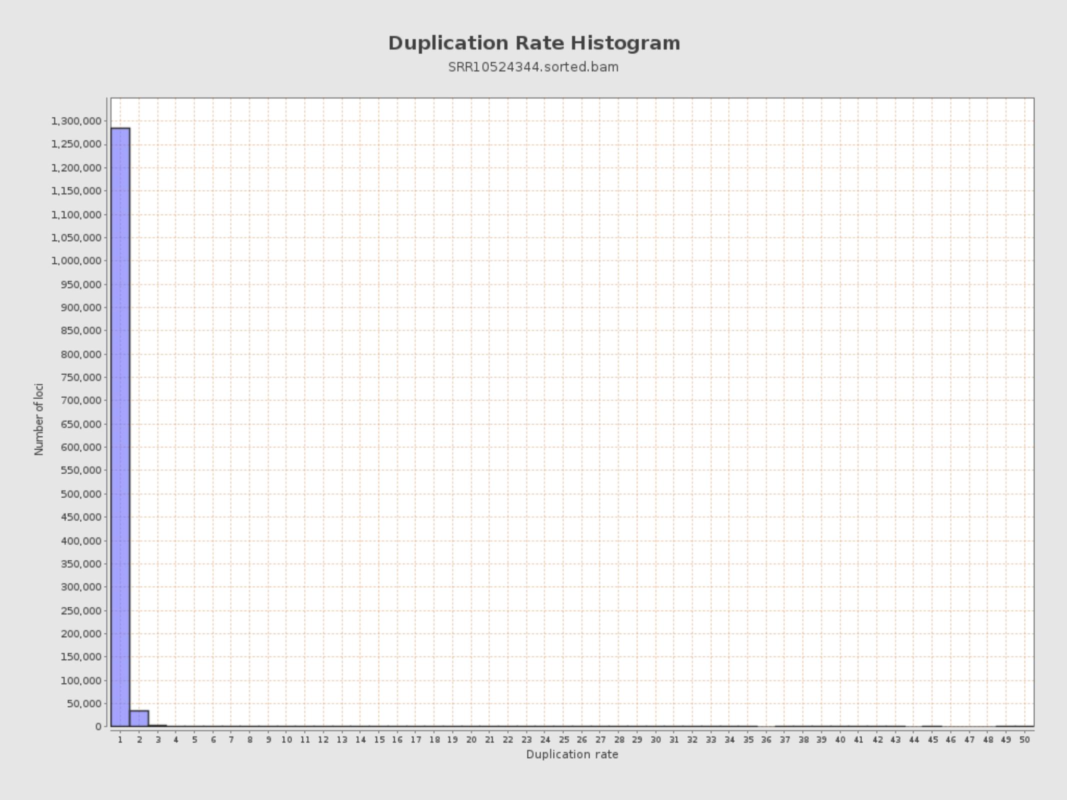
5. Results : Coverage Histogram (0-50X)



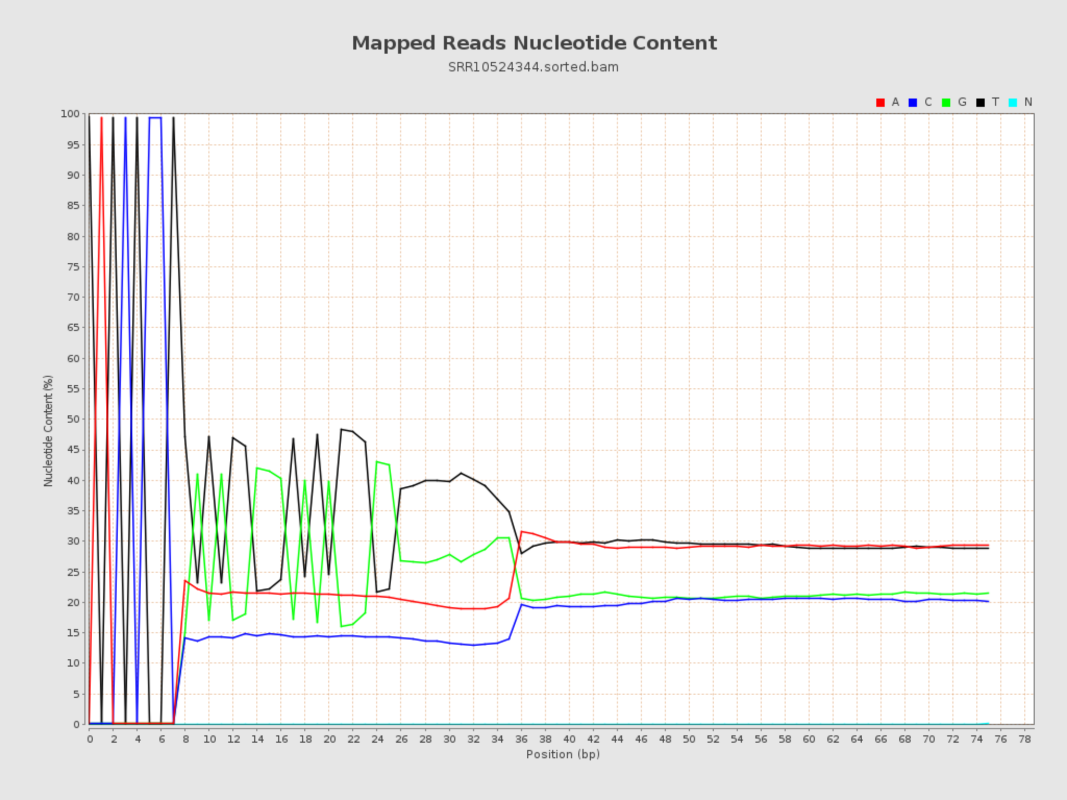
6. Results : Genome Fraction Coverage



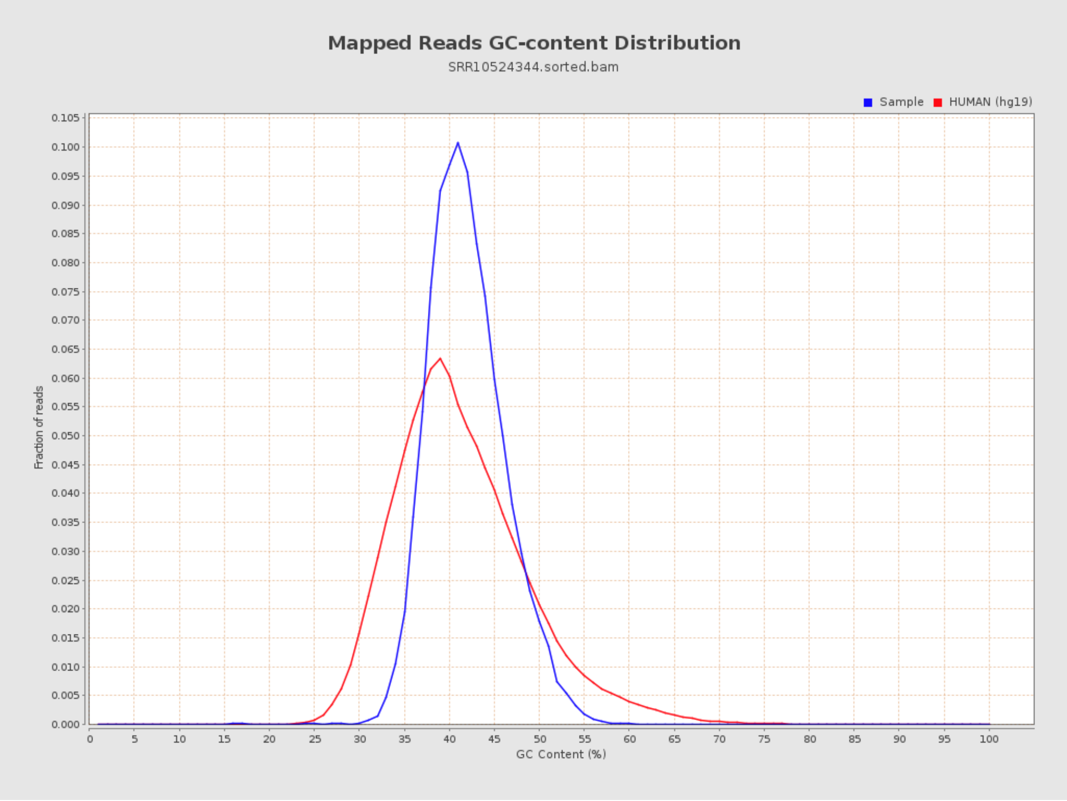
7. Results : Duplication Rate Histogram



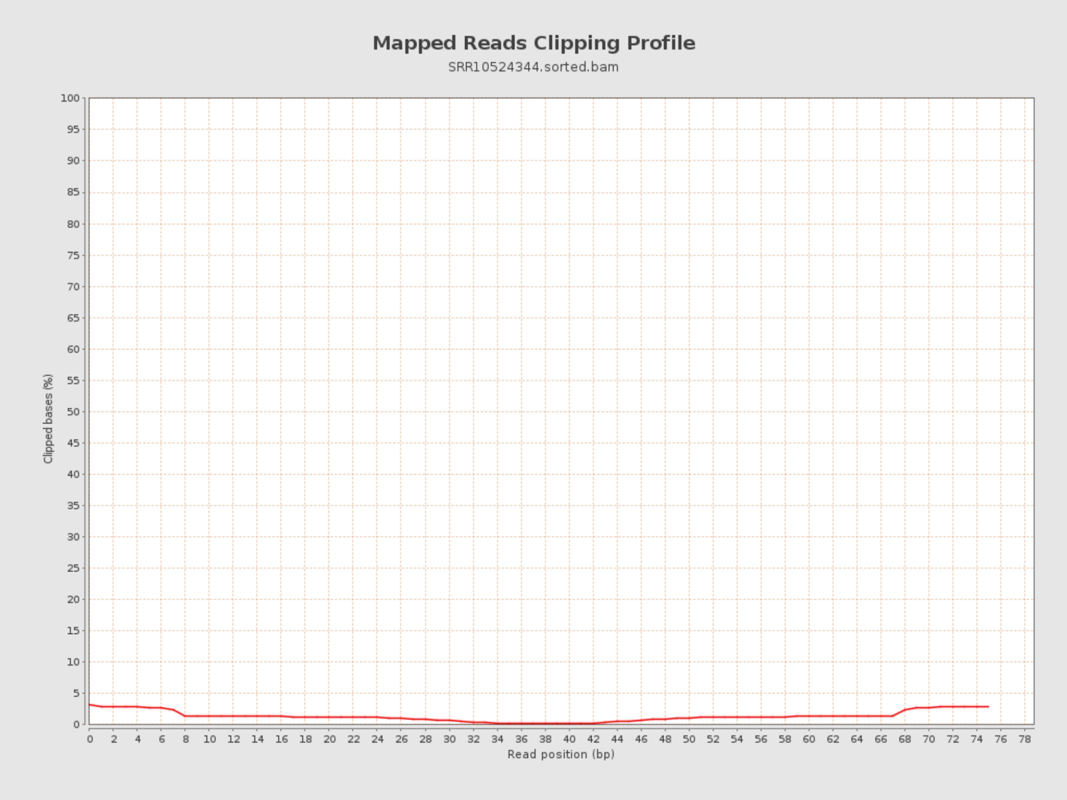
8. Results : Mapped Reads Nucleotide Content



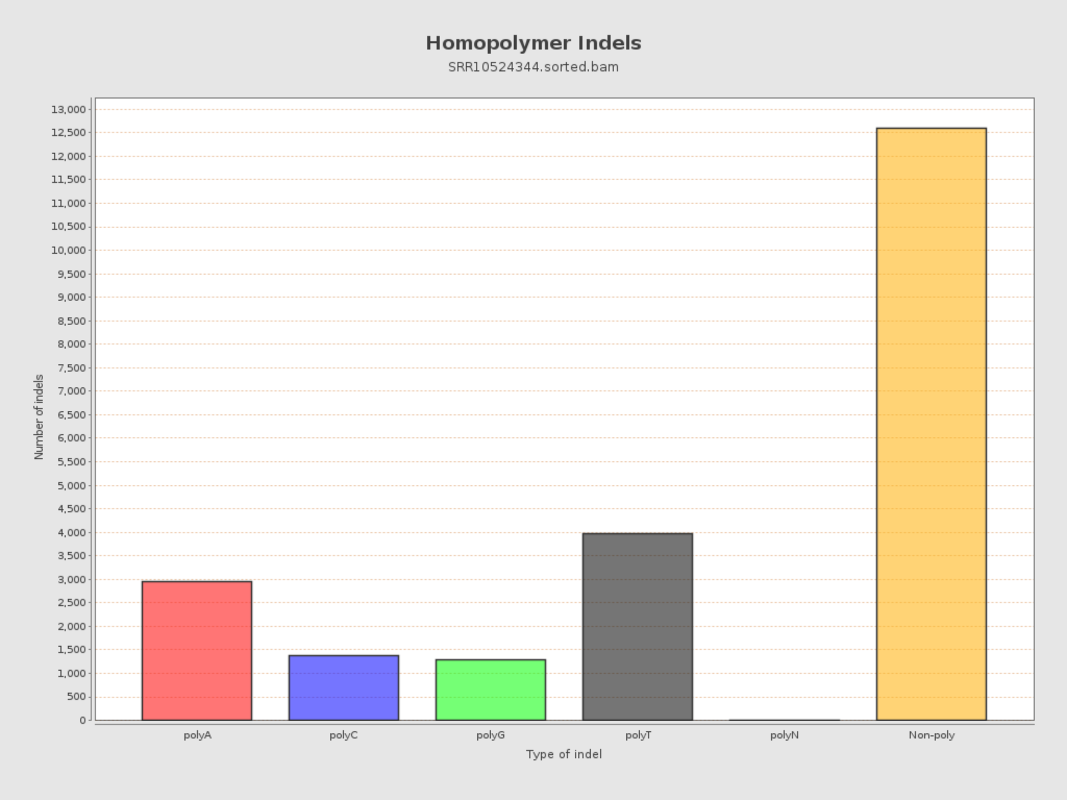
9. Results : Mapped Reads GC-content Distribution



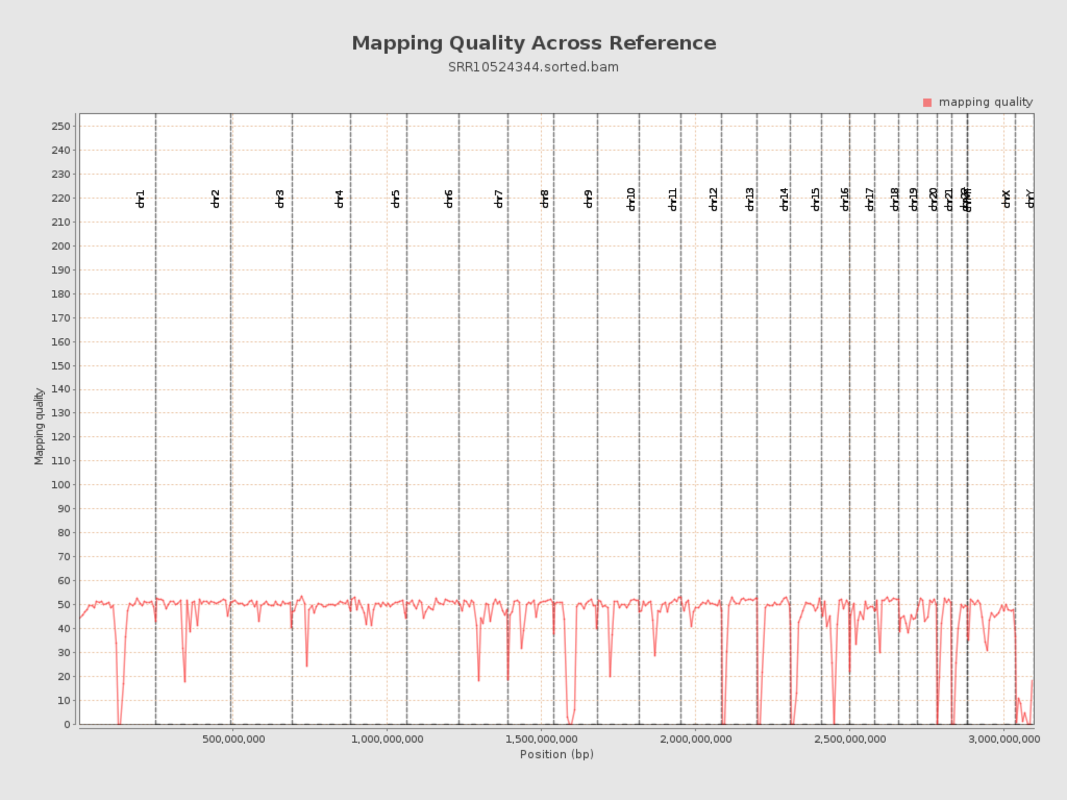
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram