Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:47:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524612.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_SRR10524612 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524612.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:47:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524612.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,899,292
Mapped reads	1,767,857 / 93.08%
Unmapped reads	131,435 / 6.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,843 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	85,767 / 4.52%
Duplication rate	3.82%
Clipped reads	1,767,363 / 93.05%

2.2. ACGT Content

Number/percentage of A's	26,262,746 / 25.48%
Number/percentage of C's	19,967,799 / 19.37%
Number/percentage of T's	32,366,977 / 31.4%
Number/percentage of G's	24,465,354 / 23.74%
Number/percentage of N's	695 / 0%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.282

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

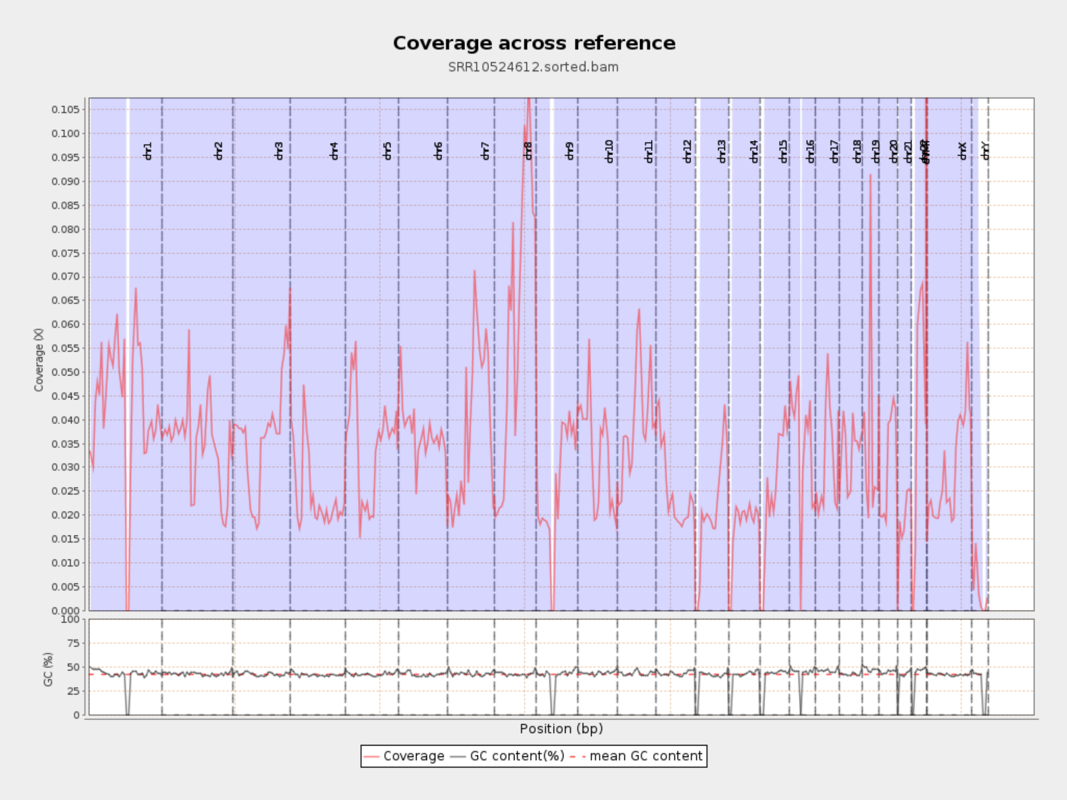
General error rate	0.49%
Mismatches	486,846
Insertions	6,927
Mapped reads with at least one insertion	0.39%
Deletions	19,754
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.63%

2.6. Chromosome stats

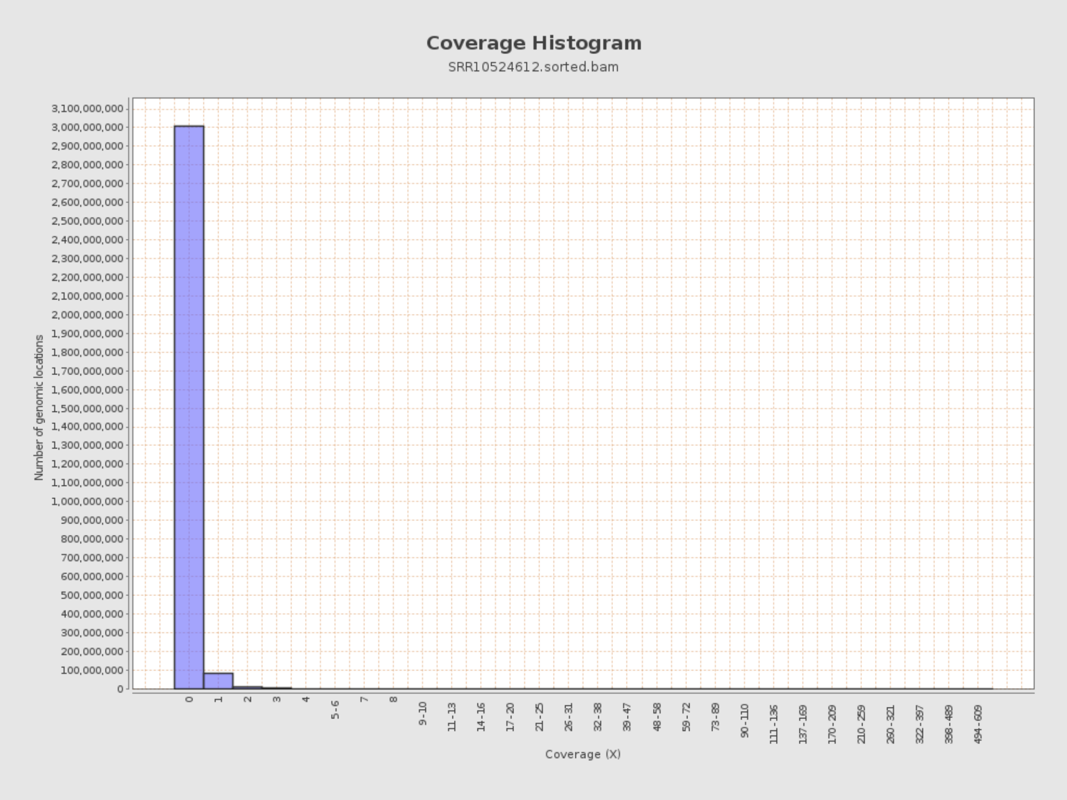
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10775659	0.0432	0.4829
chr2	243199373	8563143	0.0352	0.3304
chr3	198022430	7305925	0.0369	0.2165
chr4	191154276	4646480	0.0243	0.199
chr5	180915260	6262700	0.0346	0.209
chr6	171115067	6378257	0.0373	0.2309
chr7	159138663	6215518	0.0391	0.3602

chr8	146364022	9024533	0.0617	0.3785
chr9	141213431	3599691	0.0255	0.2515
chr10	135534747	4469438	0.033	0.2788
chr11	135006516	5362900	0.0397	0.277
chr12	133851895	3369934	0.0252	0.1839
chr13	115169878	2421603	0.021	0.1659
chr14	107349540	1865666	0.0174	0.1565
chr15	102531392	2615512	0.0255	0.1915
chr16	90354753	3140497	0.0348	0.2202
chr17	81195210	2587475	0.0319	0.2066
chr18	78077248	2635757	0.0338	0.385
chr19	59128983	2145557	0.0363	0.3653
chr20	63025520	1949680	0.0309	0.2013
chr21	48129895	903769	0.0188	0.1669
chr22	51304566	2063019	0.0402	0.2264
chrMT	16571	10217	0.6166	0.9542
chrX	155270560	4551228	0.0293	0.2155
chrY	59373566	233090	0.0039	0.1124

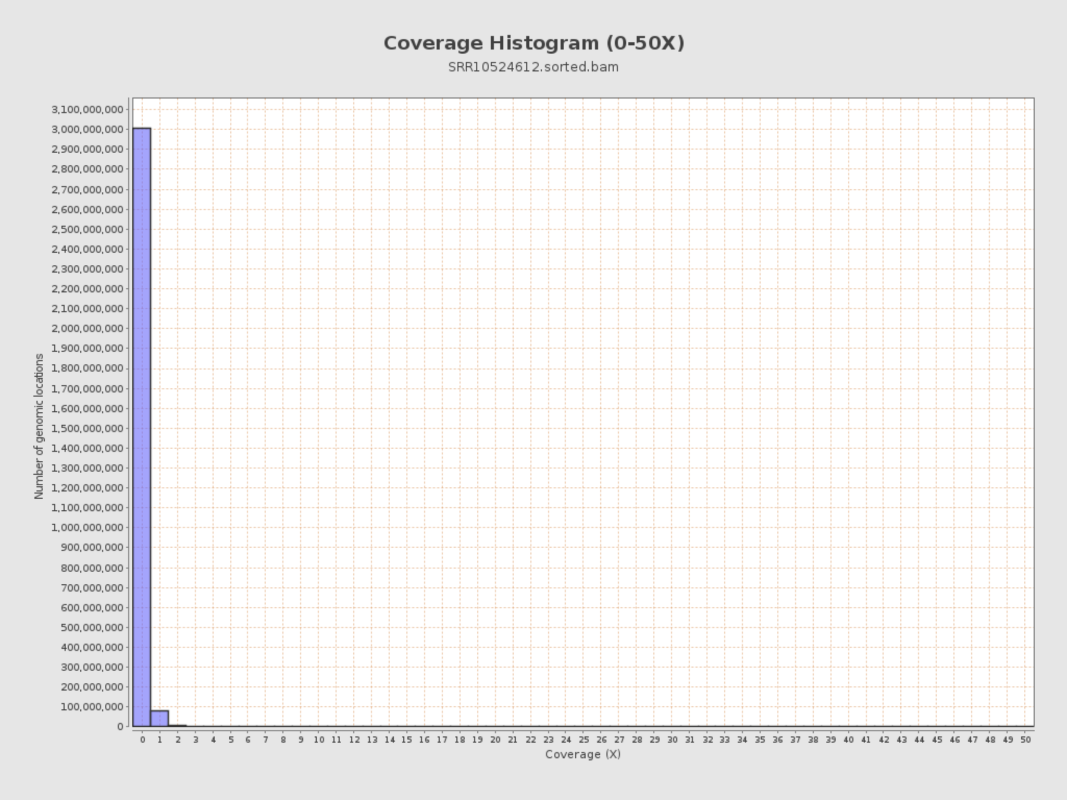
3. Results : Coverage across reference



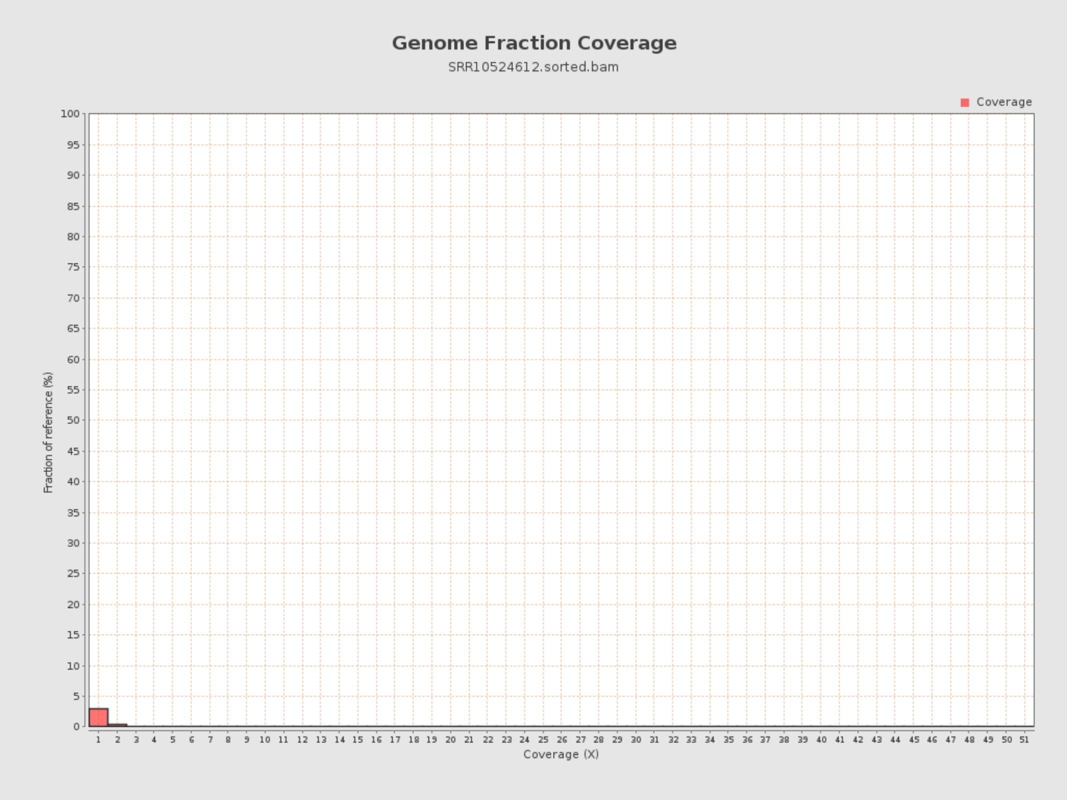
4. Results : Coverage Histogram



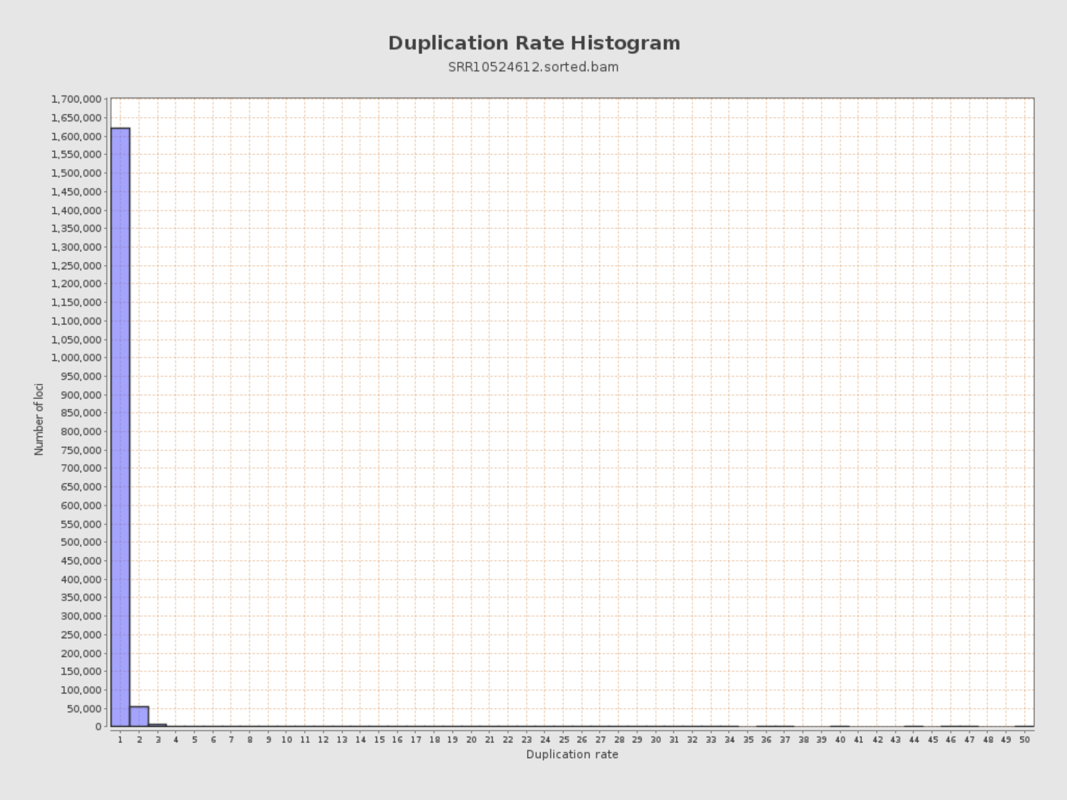
5. Results : Coverage Histogram (0-50X)



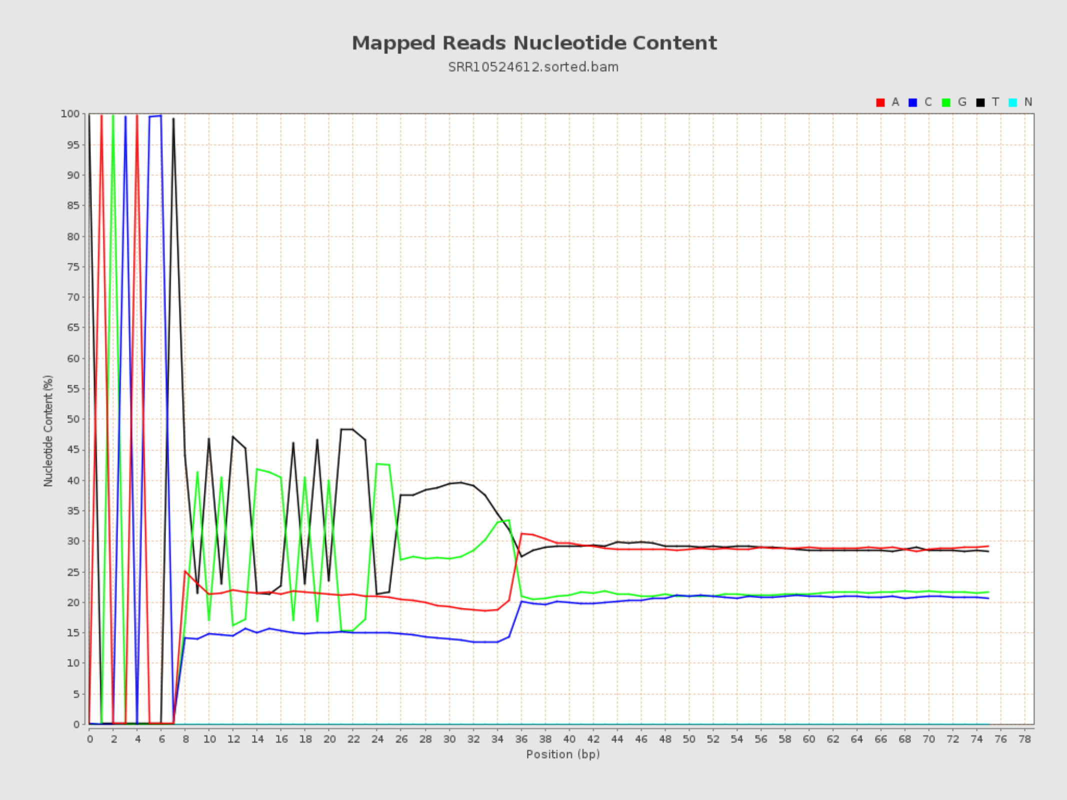
6. Results : Genome Fraction Coverage



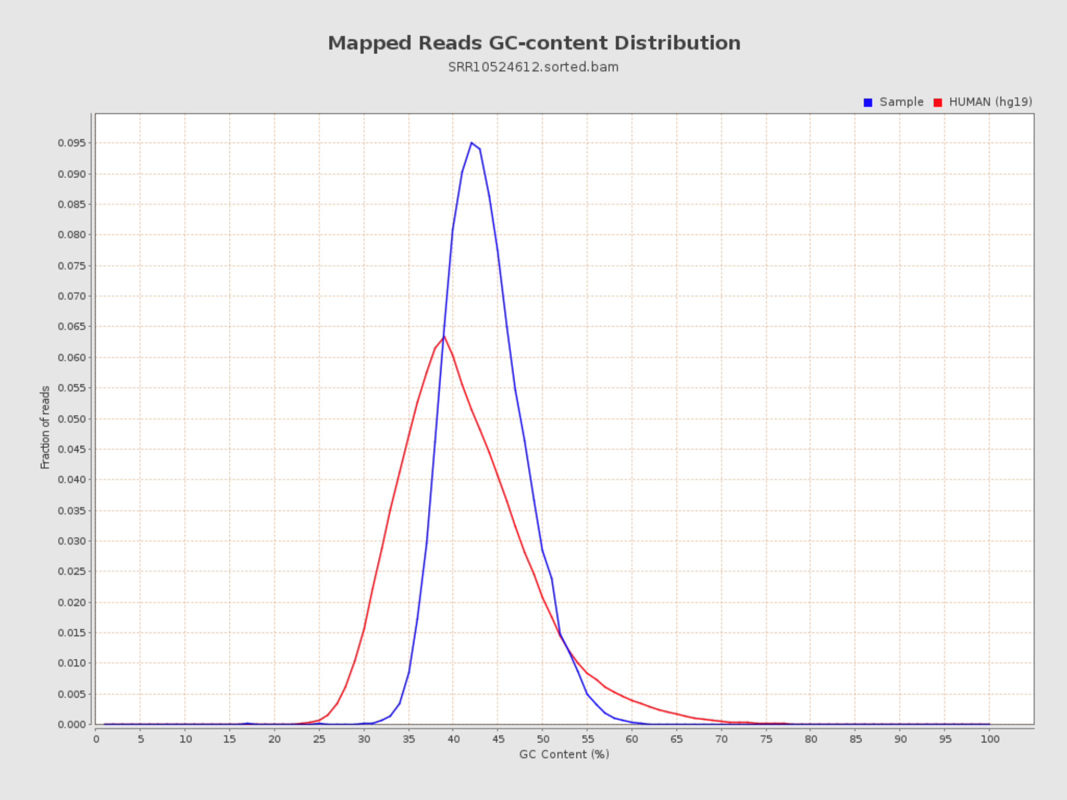
7. Results : Duplication Rate Histogram



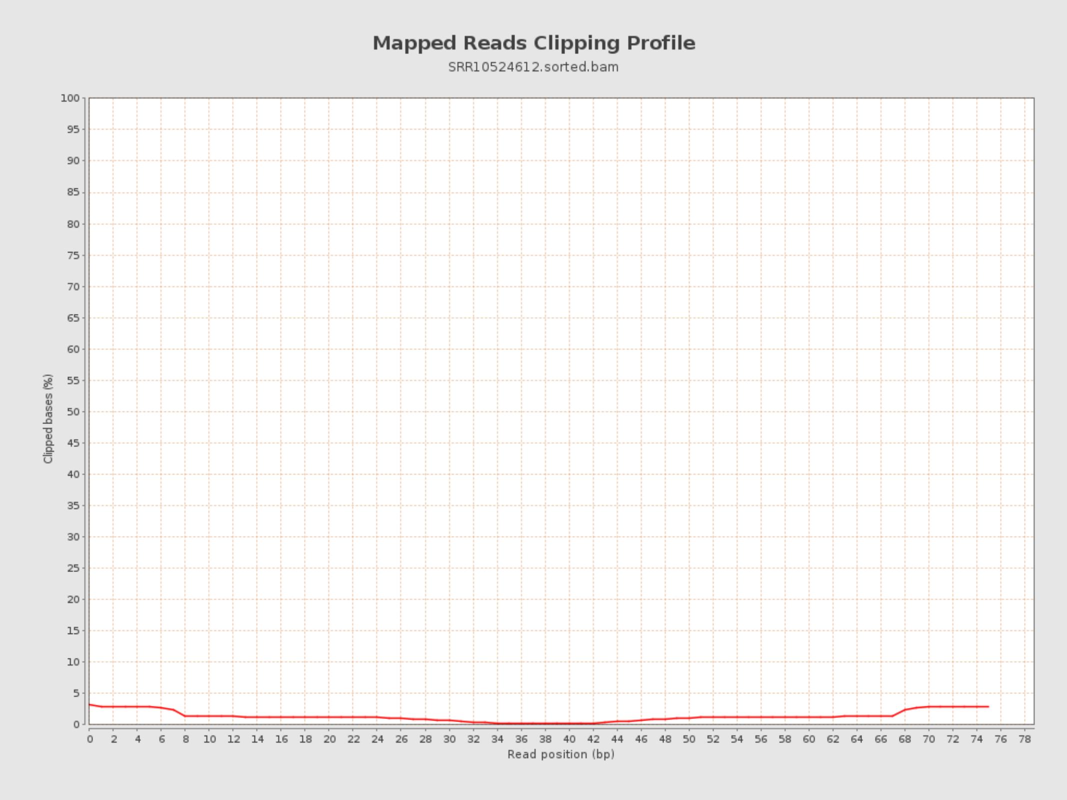
8. Results : Mapped Reads Nucleotide Content



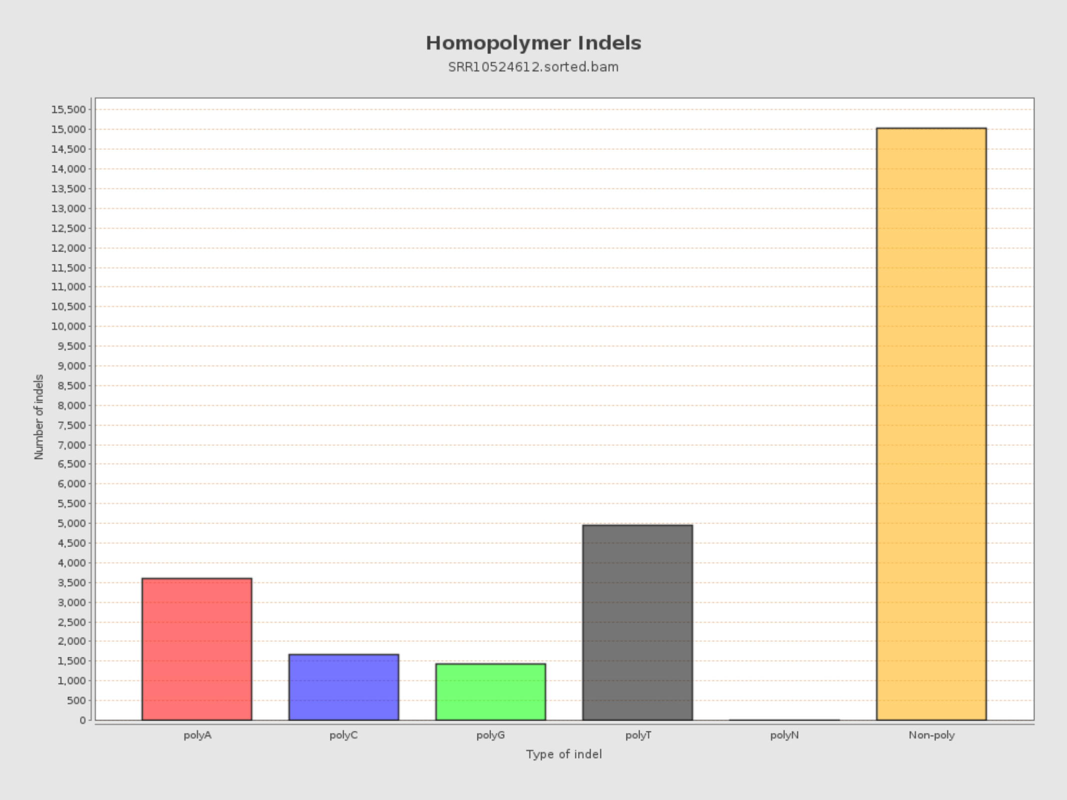
9. Results : Mapped Reads GC-content Distribution



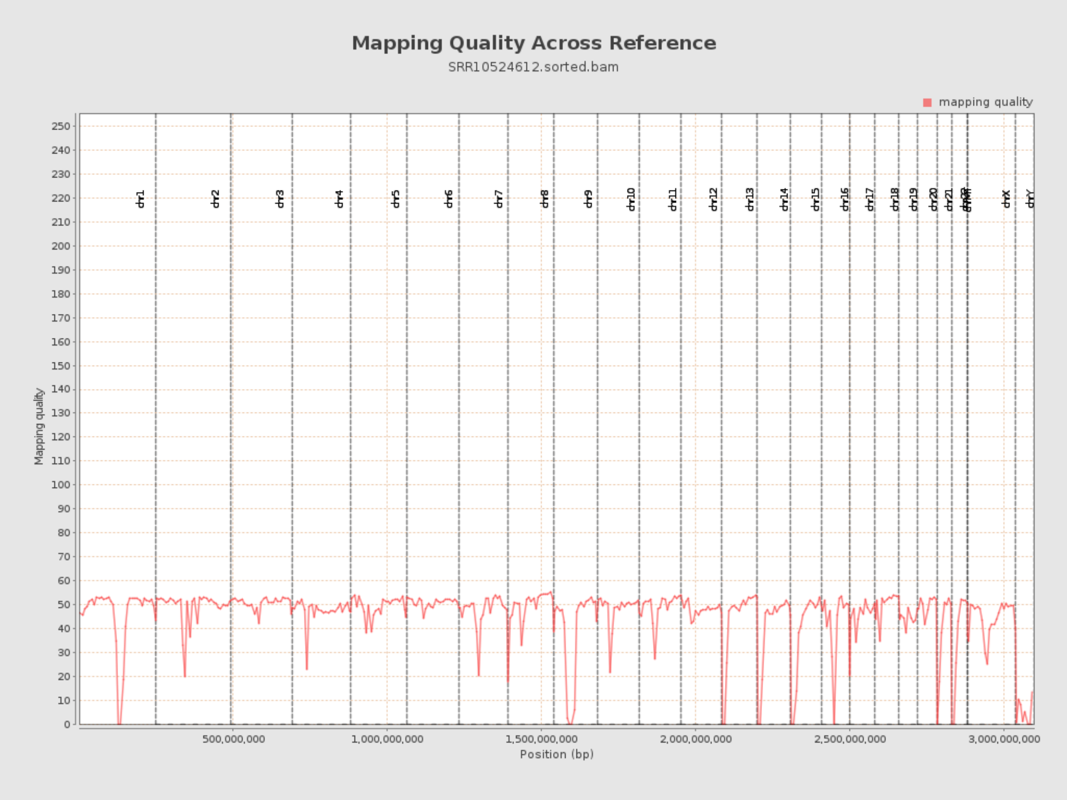
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram