Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:37:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524947.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_SRR10524947 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524947.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:37:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524947.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,430,845
Mapped reads	1,334,221 / 93.25%
Unmapped reads	96,624 / 6.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,883 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	34,964 / 2.44%
Duplication rate	1.82%
Clipped reads	1,332,720 / 93.14%

2.2. ACGT Content

Number/percentage of A's	20,243,161 / 25.59%
Number/percentage of C's	14,804,047 / 18.71%
Number/percentage of T's	25,088,464 / 31.71%
Number/percentage of G's	18,971,035 / 23.98%
Number/percentage of N's	863 / 0%
GC Percentage	42.7%

2.3. Coverage

Mean	0.0256

Standard Deviation	0.2433

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

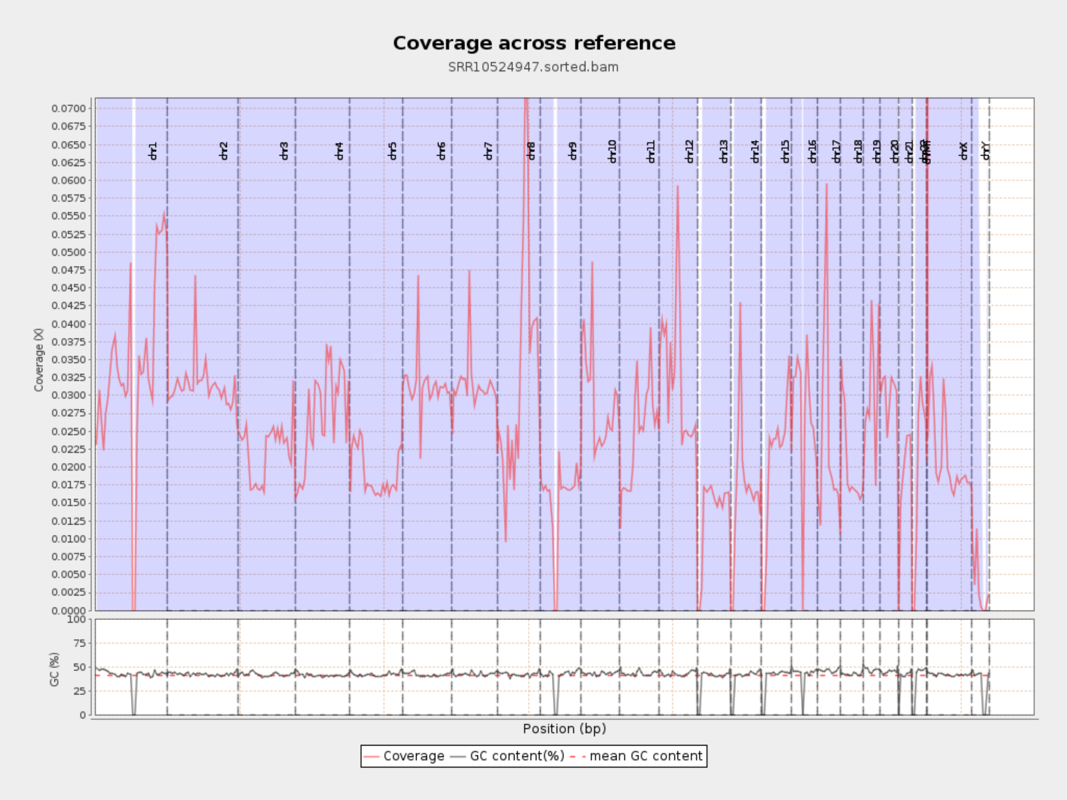
General error rate	0.49%
Mismatches	379,229
Insertions	6,227
Mapped reads with at least one insertion	0.46%
Deletions	15,751
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.37%

2.6. Chromosome stats

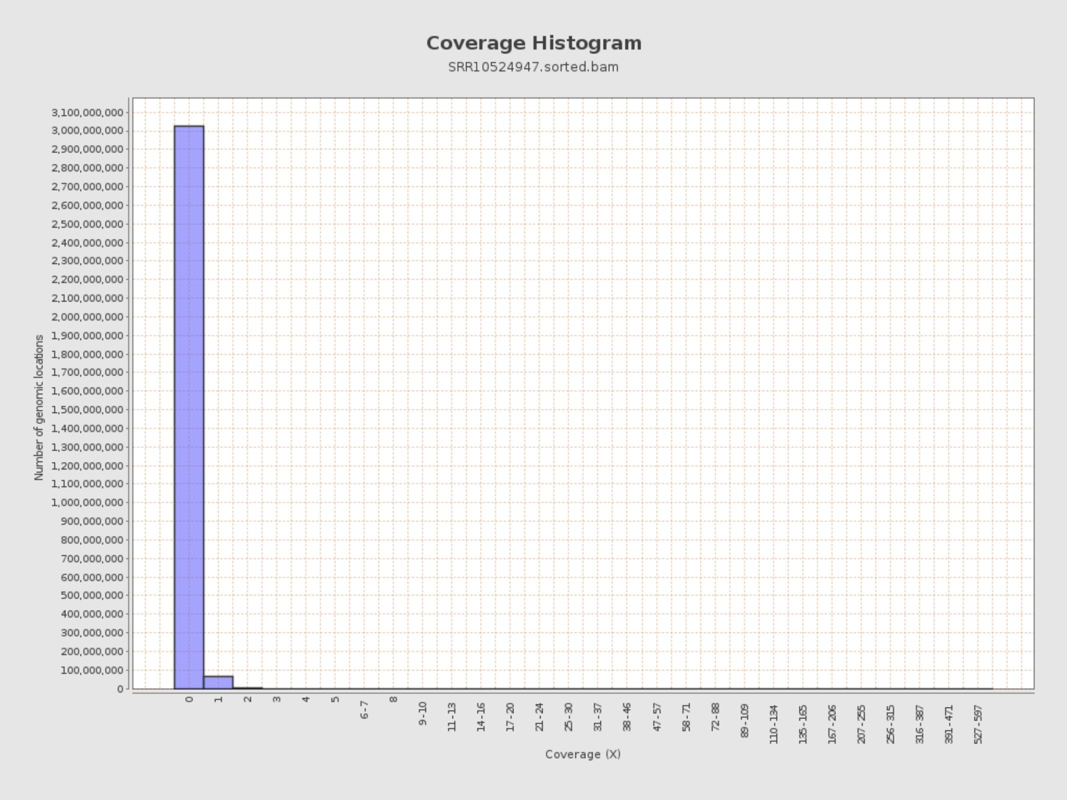
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8407569	0.0337	0.4595
chr2	243199373	7635749	0.0314	0.2701
chr3	198022430	4435493	0.0224	0.1599
chr4	191154276	5229215	0.0274	0.186
chr5	180915260	3476802	0.0192	0.1507
chr6	171115067	5361127	0.0313	0.2575
chr7	159138663	5027739	0.0316	0.328

chr8	146364022	4935085	0.0337	0.2517
chr9	141213431	2183814	0.0155	0.1838
chr10	135534747	3983568	0.0294	0.2371
chr11	135006516	3357751	0.0249	0.2184
chr12	133851895	4360439	0.0326	0.1931
chr13	115169878	1543566	0.0134	0.1234
chr14	107349540	1809411	0.0169	0.1425
chr15	102531392	2135792	0.0208	0.1619
chr16	90354753	2462168	0.0273	0.1847
chr17	81195210	1980195	0.0244	0.2186
chr18	78077248	1583186	0.0203	0.2859
chr19	59128983	1819741	0.0308	0.2973
chr20	63025520	1879522	0.0298	0.1867
chr21	48129895	904311	0.0188	0.155
chr22	51304566	1011329	0.0197	0.148
chrMT	16571	48170	2.9069	2.3698
chrX	155270560	3360580	0.0216	0.1788
chrY	59373566	202228	0.0034	0.0913

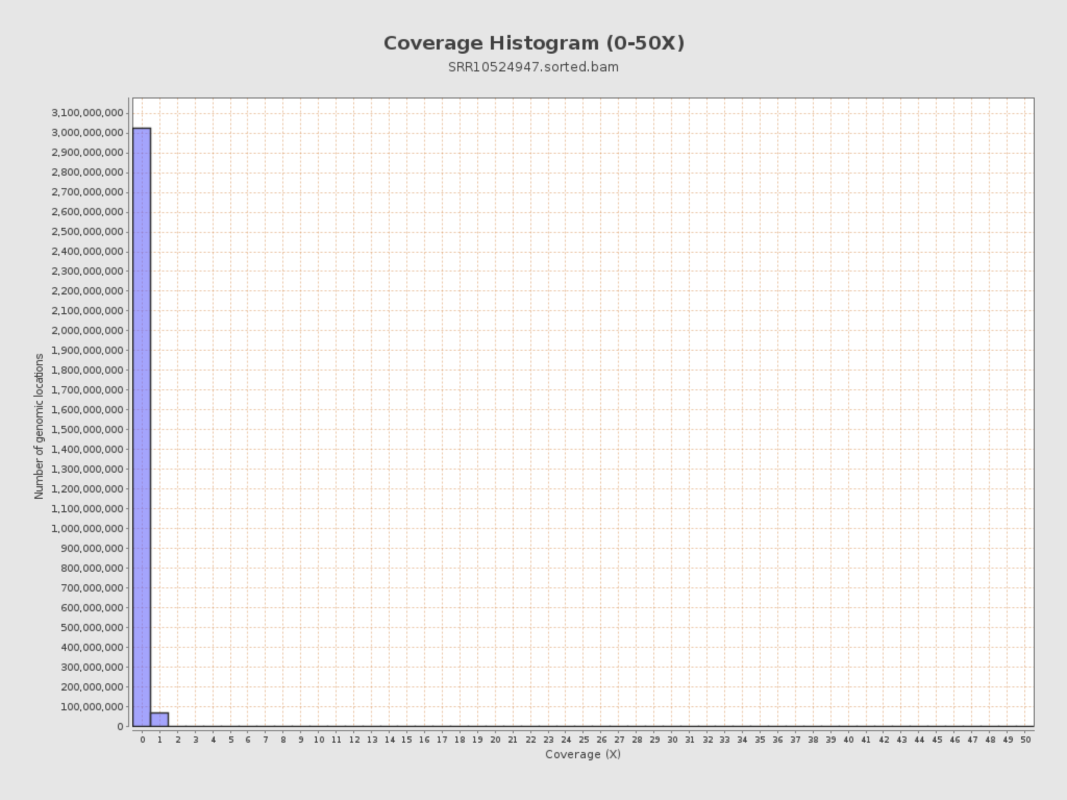
3. Results : Coverage across reference



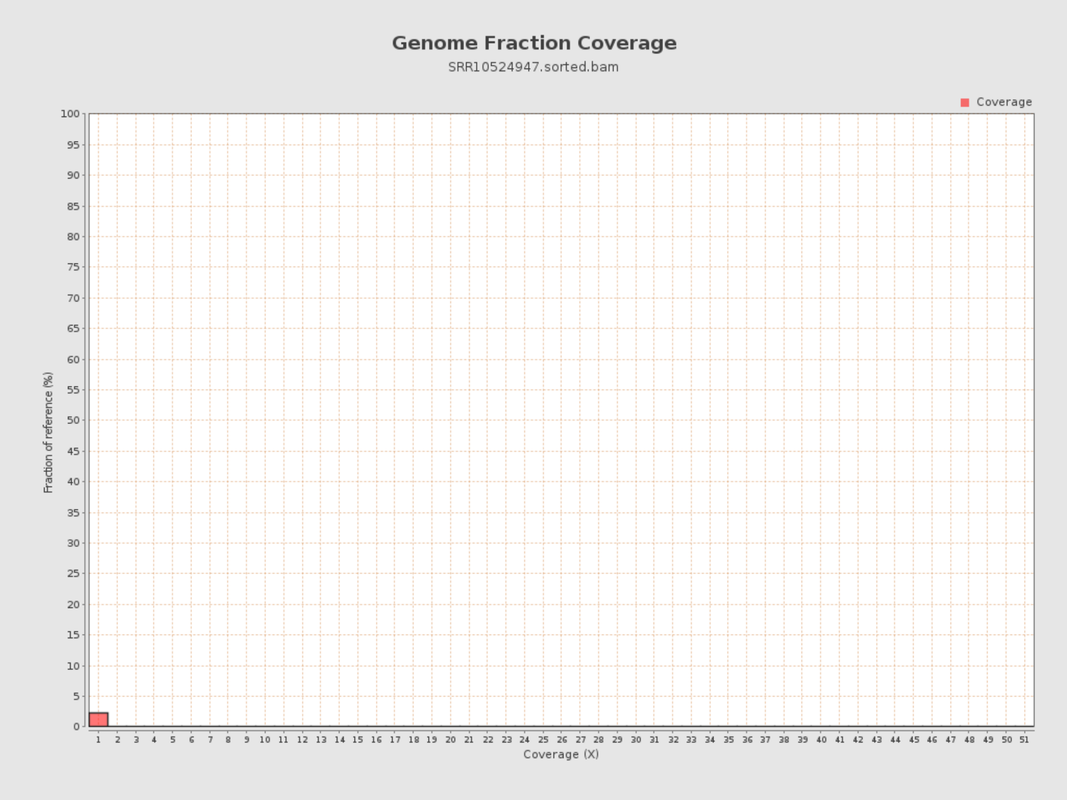
4. Results : Coverage Histogram



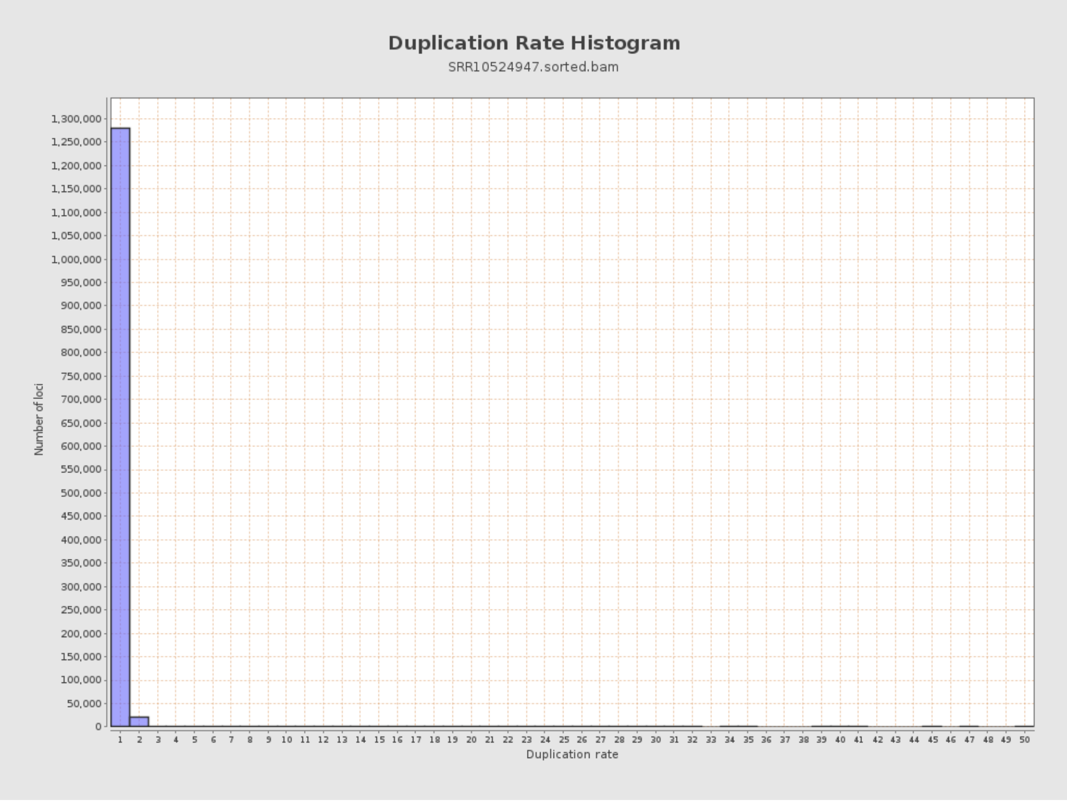
5. Results : Coverage Histogram (0-50X)



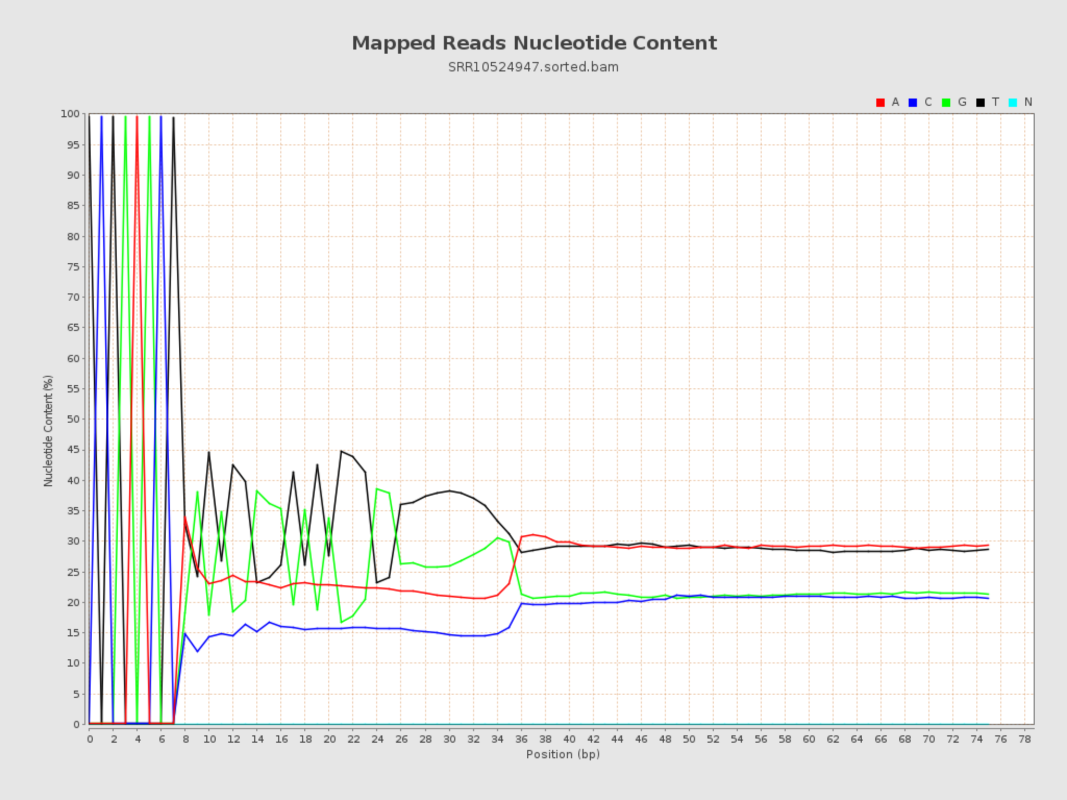
6. Results : Genome Fraction Coverage



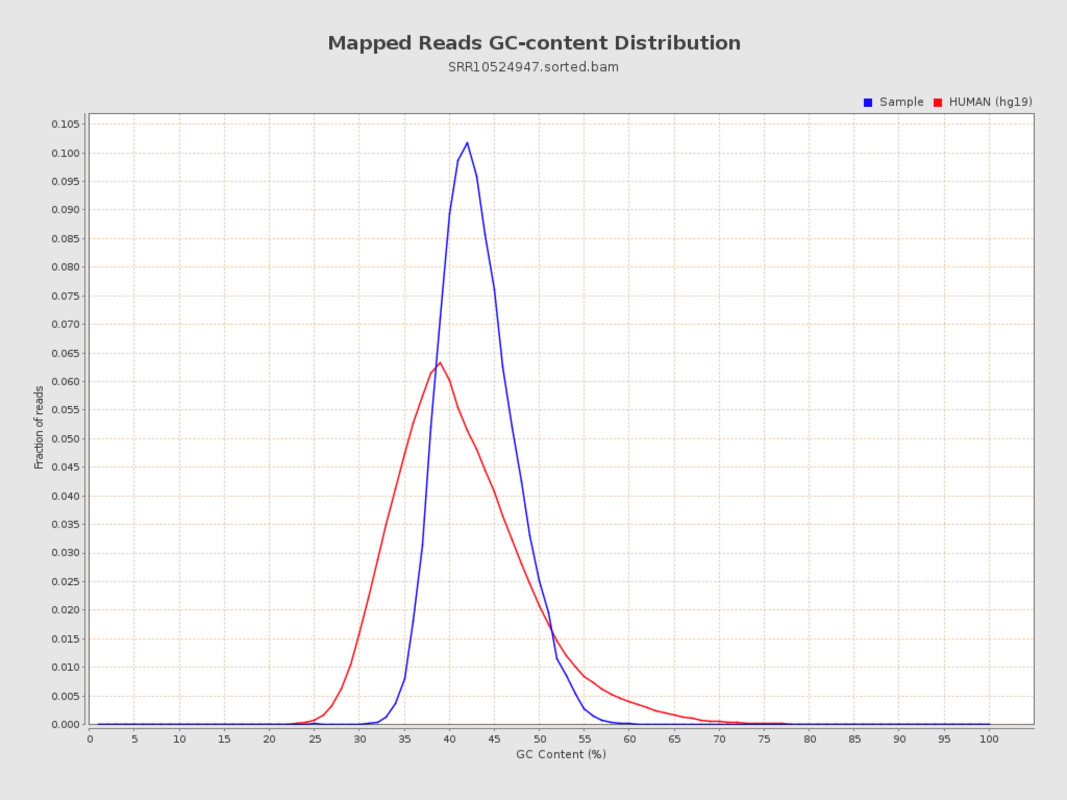
7. Results : Duplication Rate Histogram



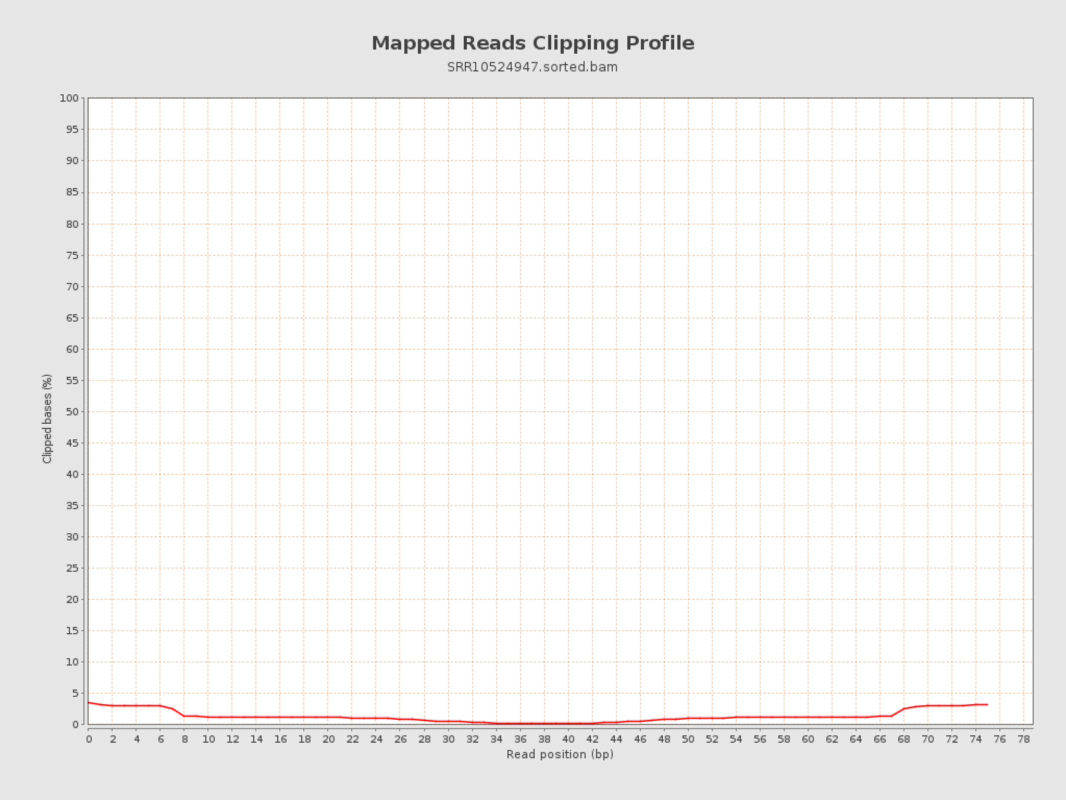
8. Results : Mapped Reads Nucleotide Content



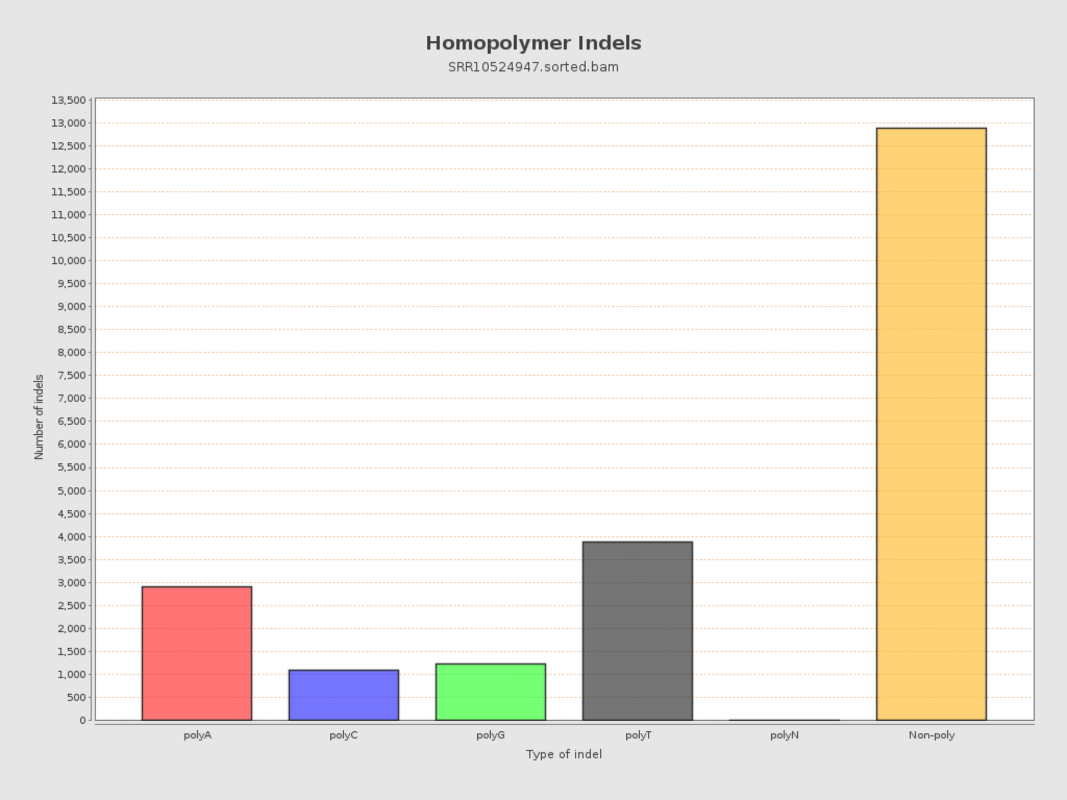
9. Results : Mapped Reads GC-content Distribution



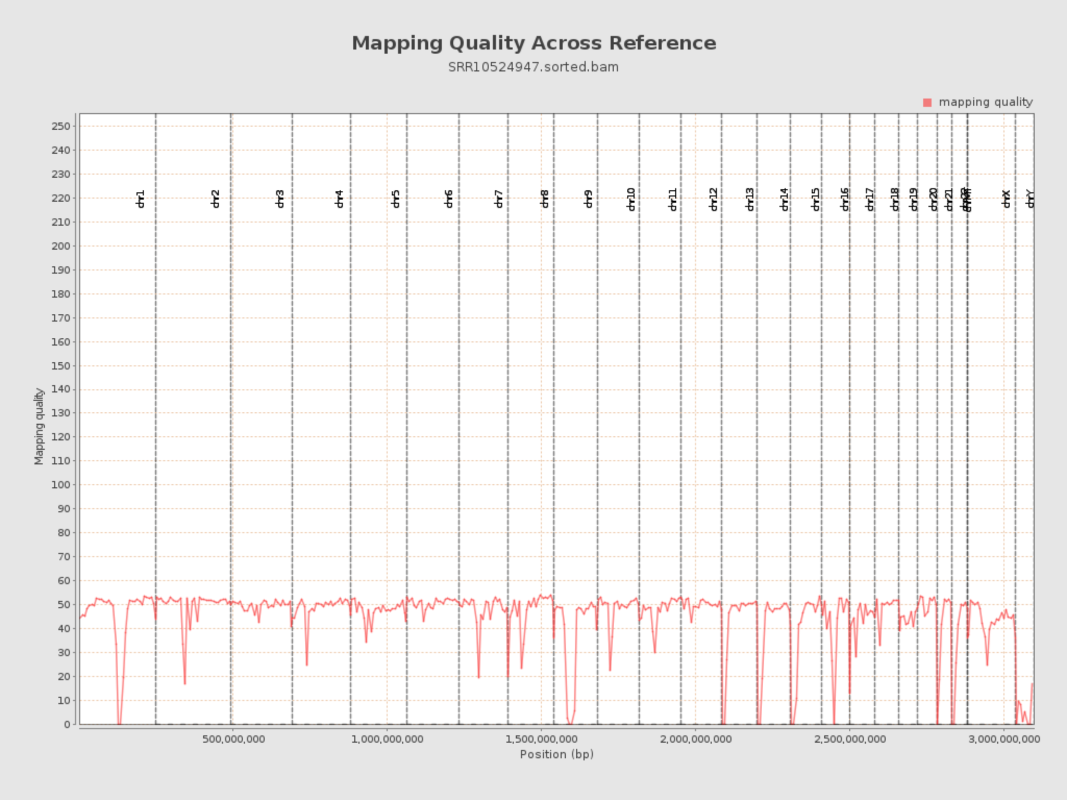
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram