Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:03:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524329.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_SRR10524329 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524329.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:03:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524329.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	495,186
Mapped reads	450,018 / 90.88%
Unmapped reads	45,168 / 9.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,127 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	8,301 / 1.68%
Duplication rate	1.26%
Clipped reads	451,005 / 91.08%

2.2. ACGT Content

Number/percentage of A's	6,541,716 / 25.06%
Number/percentage of C's	5,170,204 / 19.8%
Number/percentage of T's	8,135,473 / 31.16%
Number/percentage of G's	6,254,343 / 23.96%
Number/percentage of N's	3,865 / 0.01%
GC Percentage	43.76%

2.3. Coverage

Mean	0.0084

Standard Deviation	0.1173

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Mismatches and indels

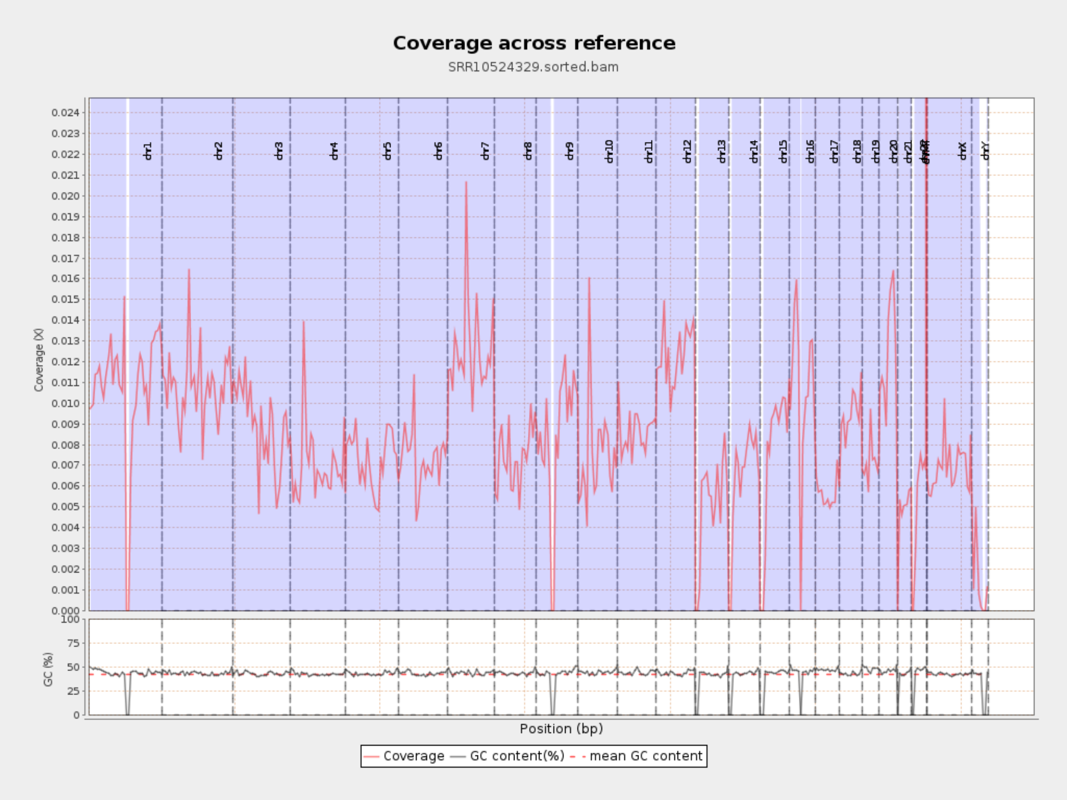
General error rate	0.54%
Mismatches	137,024
Insertions	1,743
Mapped reads with at least one insertion	0.39%
Deletions	4,389
Mapped reads with at least one deletion	0.97%
Homopolymer indels	41.94%

2.6. Chromosome stats

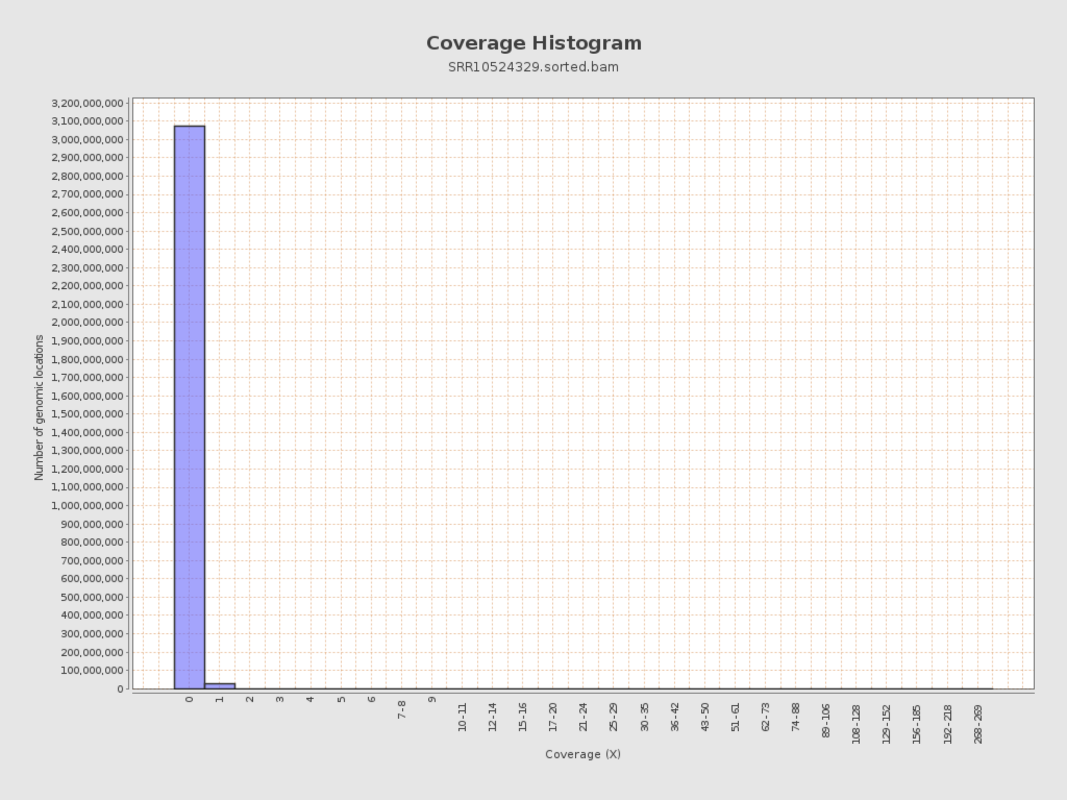
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2670619	0.0107	0.1805
chr2	243199373	2631408	0.0108	0.1534
chr3	198022430	1768210	0.0089	0.0974
chr4	191154276	1334517	0.007	0.092
chr5	180915260	1328033	0.0073	0.0883
chr6	171115067	1252982	0.0073	0.0917
chr7	159138663	2009999	0.0126	0.1766

chr8	146364022	1085638	0.0074	0.098
chr9	141213431	1167581	0.0083	0.1043
chr10	135534747	1004072	0.0074	0.1151
chr11	135006516	1163522	0.0086	0.1045
chr12	133851895	1647583	0.0123	0.1149
chr13	115169878	582786	0.0051	0.0729
chr14	107349540	680833	0.0063	0.084
chr15	102531392	767301	0.0075	0.0891
chr16	90354753	975256	0.0108	0.1108
chr17	81195210	461378	0.0057	0.0799
chr18	78077248	730121	0.0094	0.1507
chr19	59128983	424493	0.0072	0.1324
chr20	63025520	783004	0.0124	0.1151
chr21	48129895	230206	0.0048	0.0752
chr22	51304566	248162	0.0048	0.0713
chrMT	16571	16009	0.9661	1.0976
chrX	155270560	1067524	0.0069	0.0905
chrY	59373566	81379	0.0014	0.0519

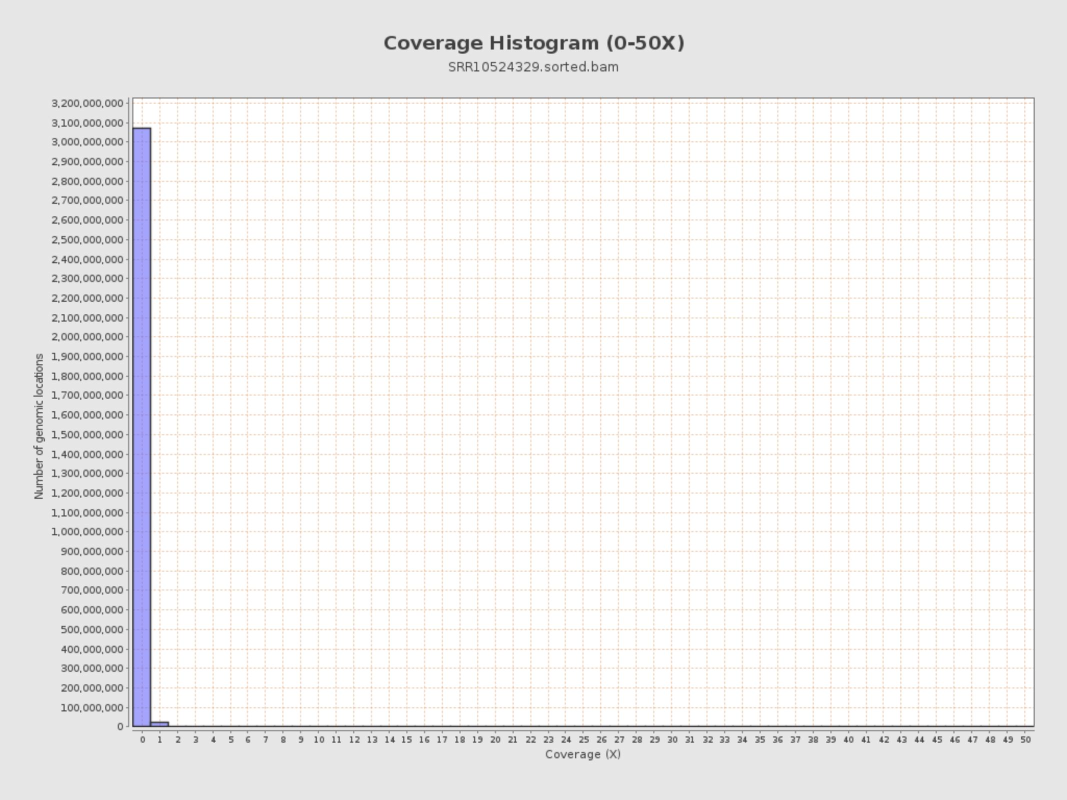
3. Results : Coverage across reference



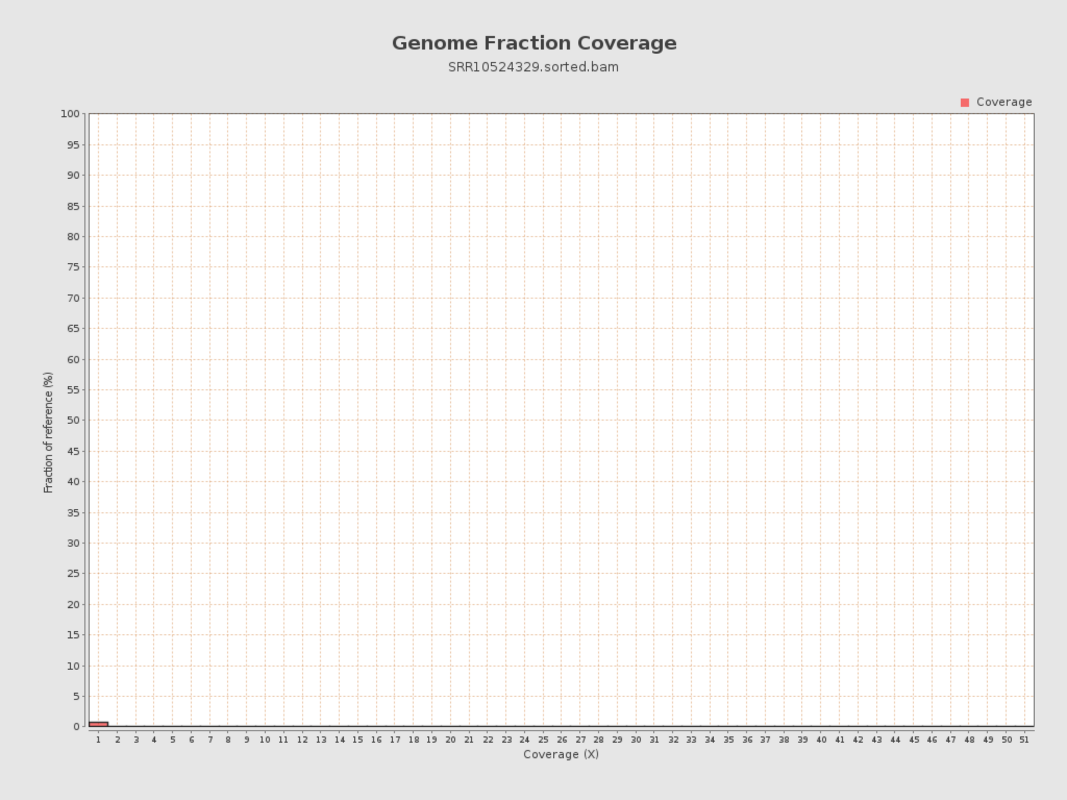
4. Results : Coverage Histogram



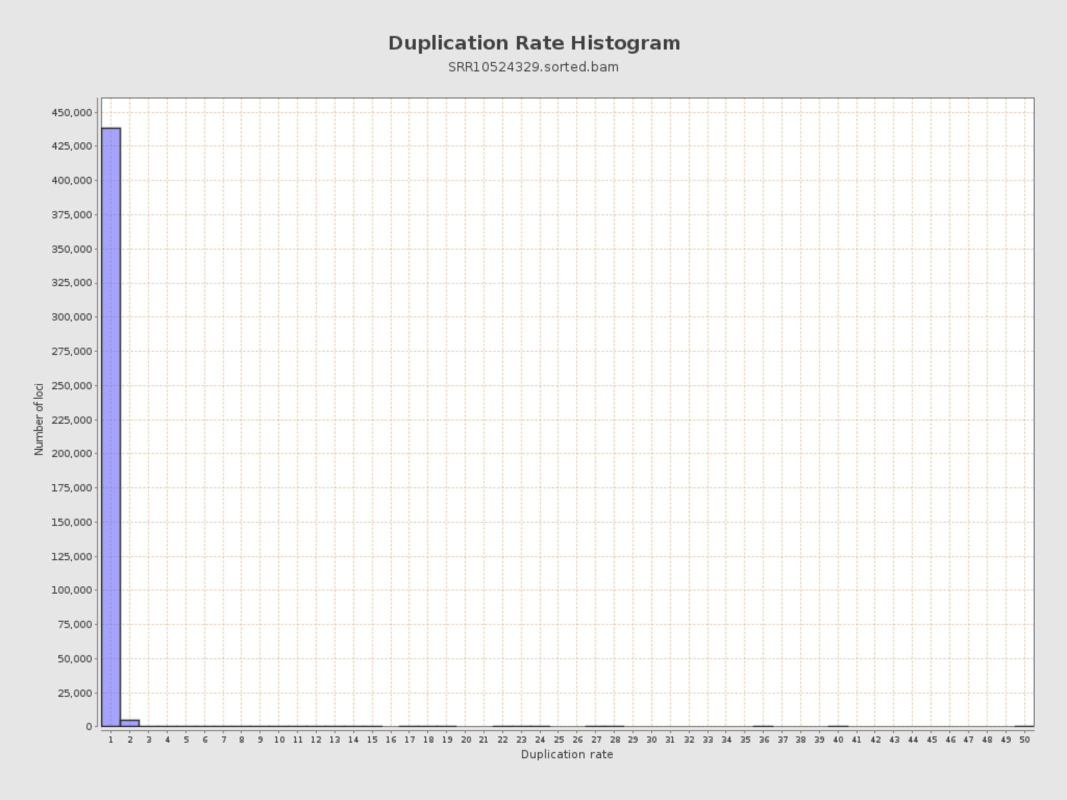
5. Results : Coverage Histogram (0-50X)



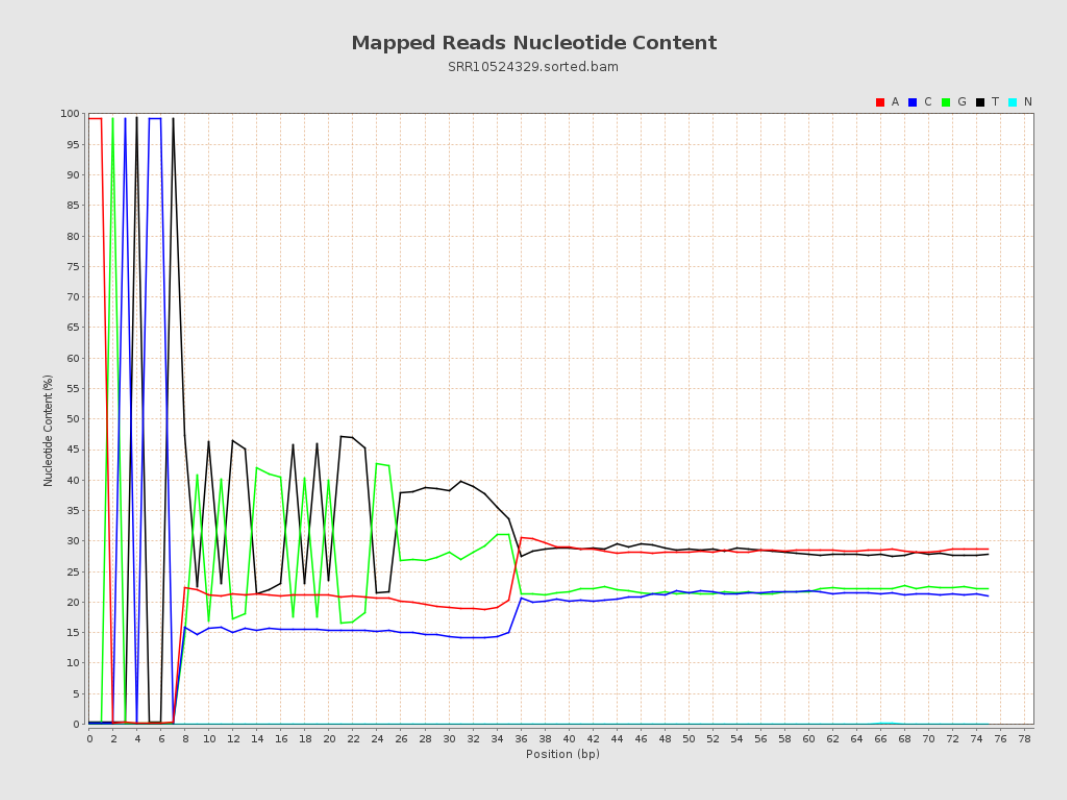
6. Results : Genome Fraction Coverage



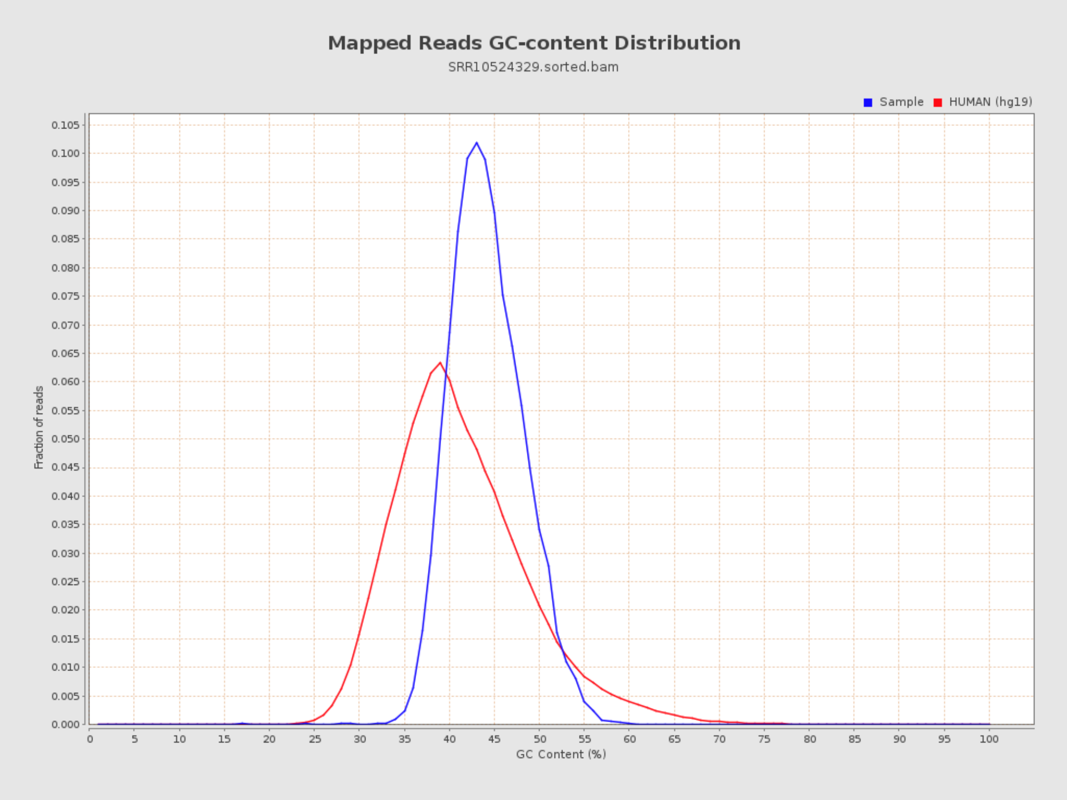
7. Results : Duplication Rate Histogram



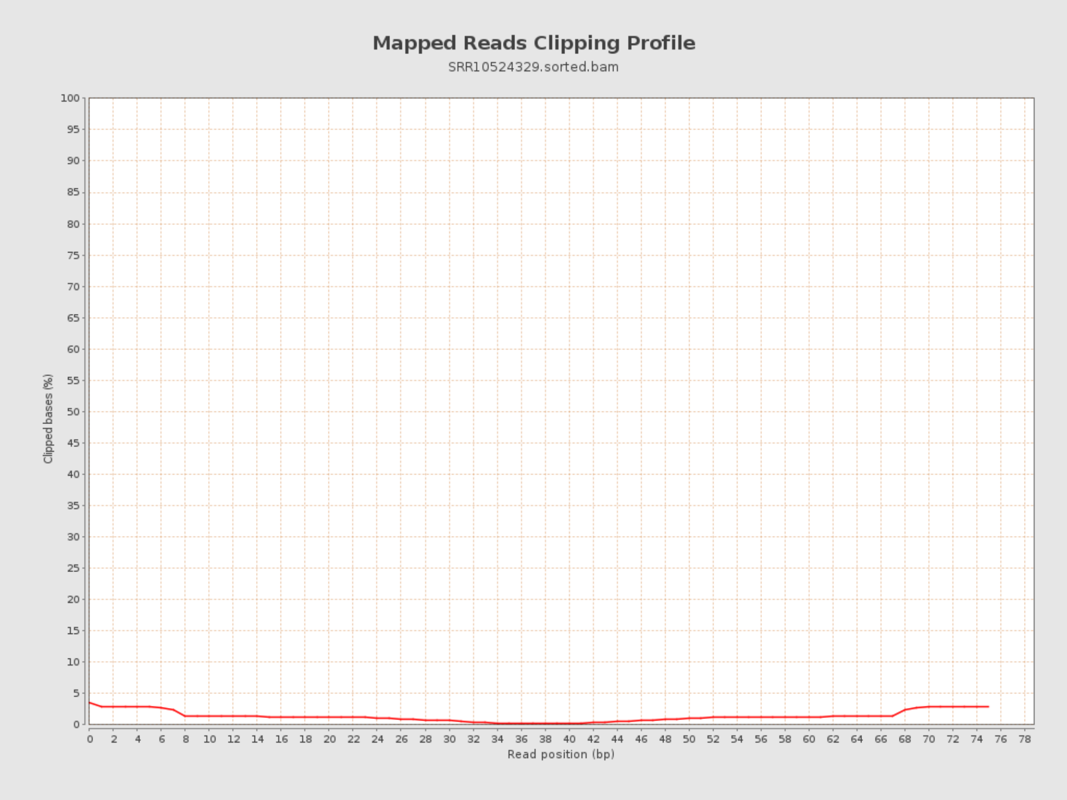
8. Results : Mapped Reads Nucleotide Content



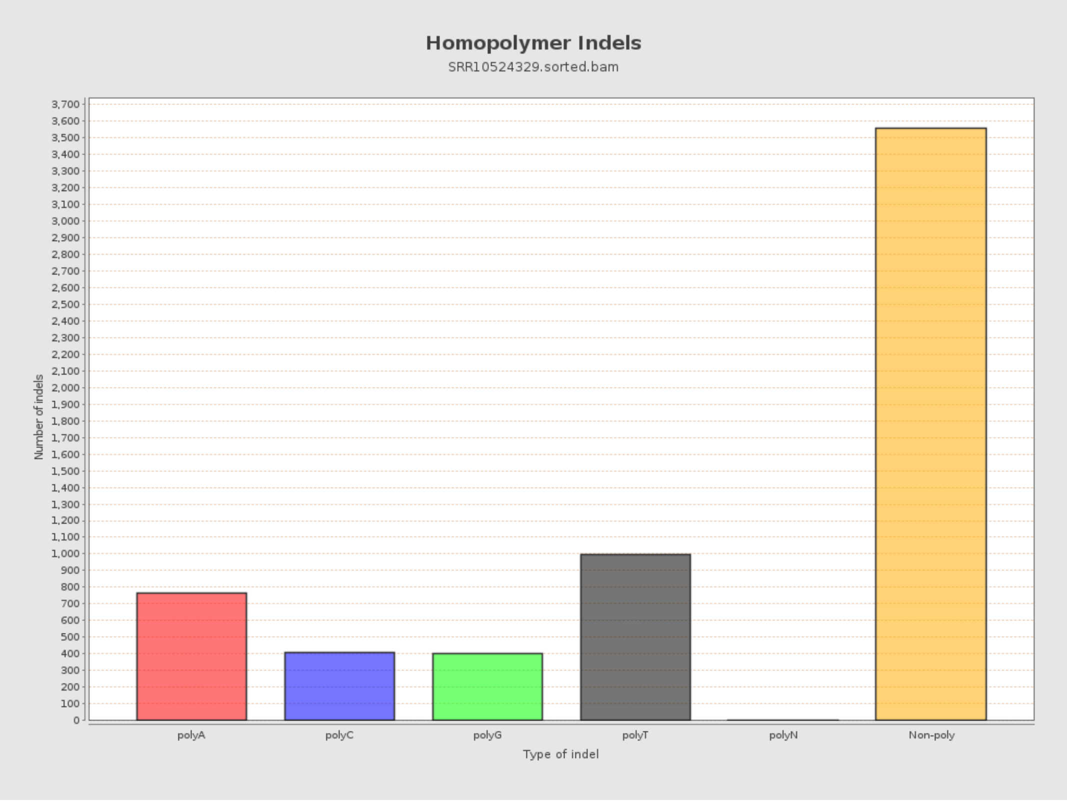
9. Results : Mapped Reads GC-content Distribution



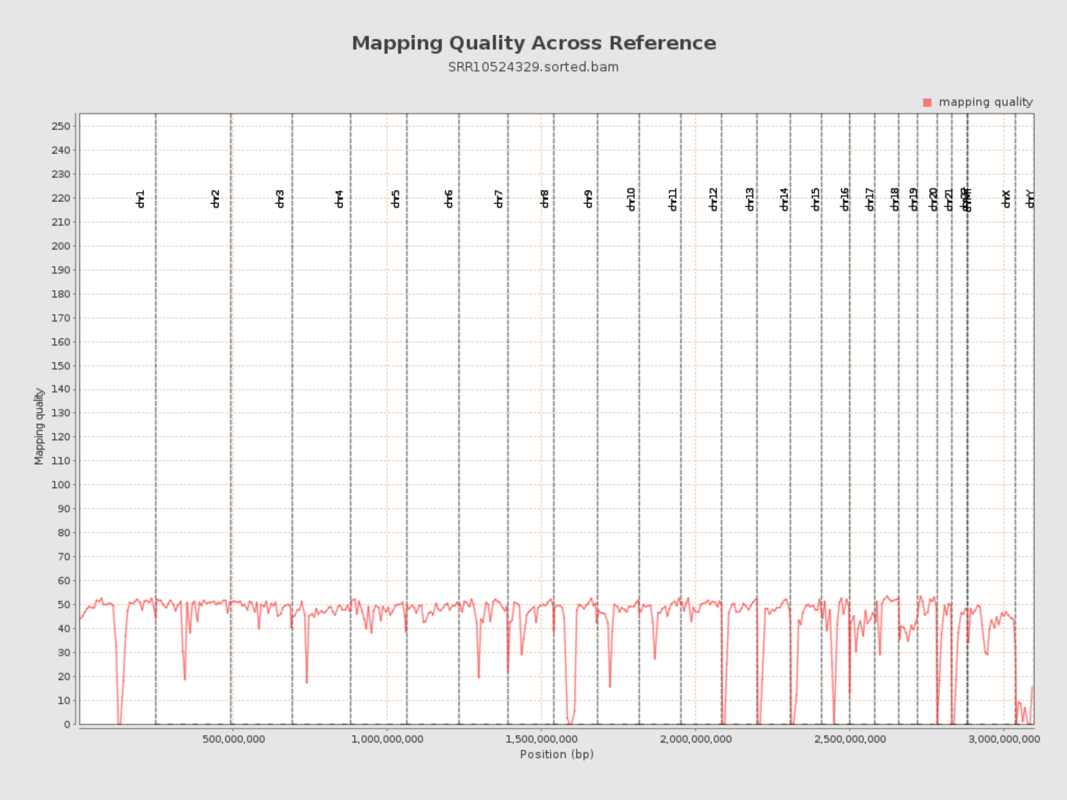
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram