Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:27:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524338.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_SRR10524338 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524338.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:27:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524338.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	590,298
Mapped reads	527,838 / 89.42%
Unmapped reads	62,460 / 10.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,277 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	8,913 / 1.51%
Duplication rate	1.21%
Clipped reads	529,262 / 89.66%

2.2. ACGT Content

Number/percentage of A's	7,471,147 / 24.75%
Number/percentage of C's	5,661,869 / 18.76%
Number/percentage of T's	9,695,387 / 32.12%
Number/percentage of G's	7,351,334 / 24.36%
Number/percentage of N's	4,286 / 0.01%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0098

Standard Deviation	0.1211

2.4. Mapping Quality

Mean Mapping Quality	43.33

2.5. Mismatches and indels

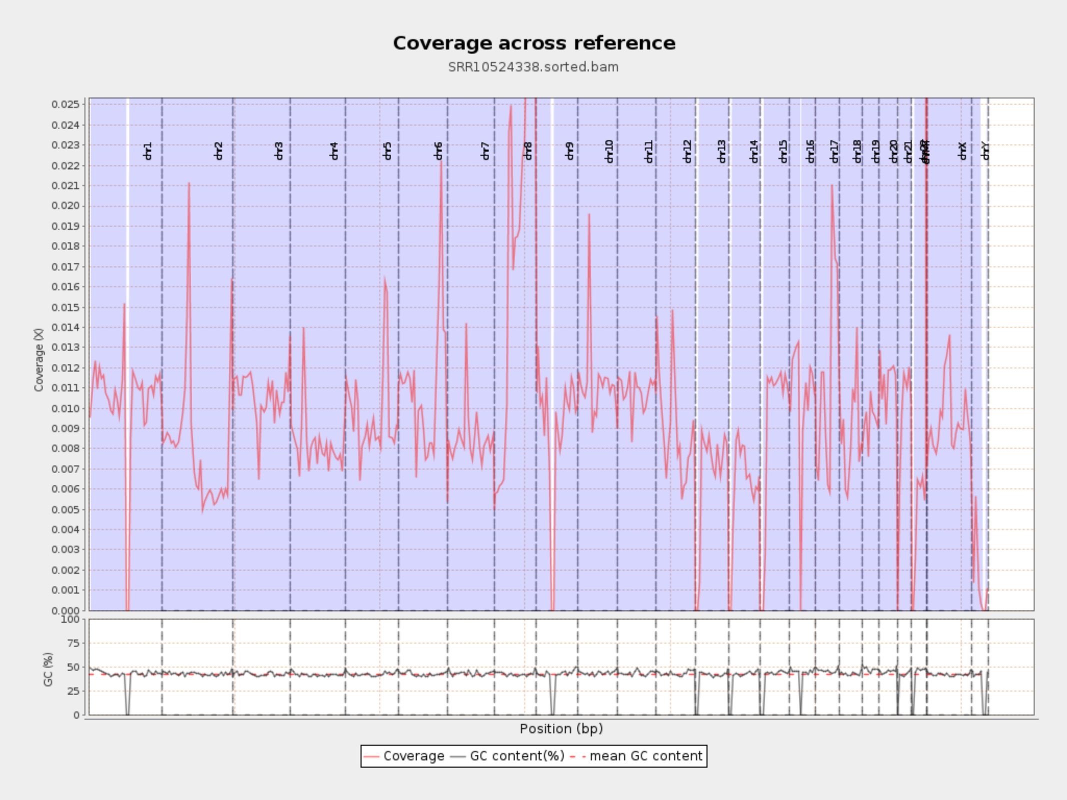
General error rate	0.53%
Mismatches	157,721
Insertions	1,838
Mapped reads with at least one insertion	0.35%
Deletions	4,843
Mapped reads with at least one deletion	0.91%
Homopolymer indels	42.33%

2.6. Chromosome stats

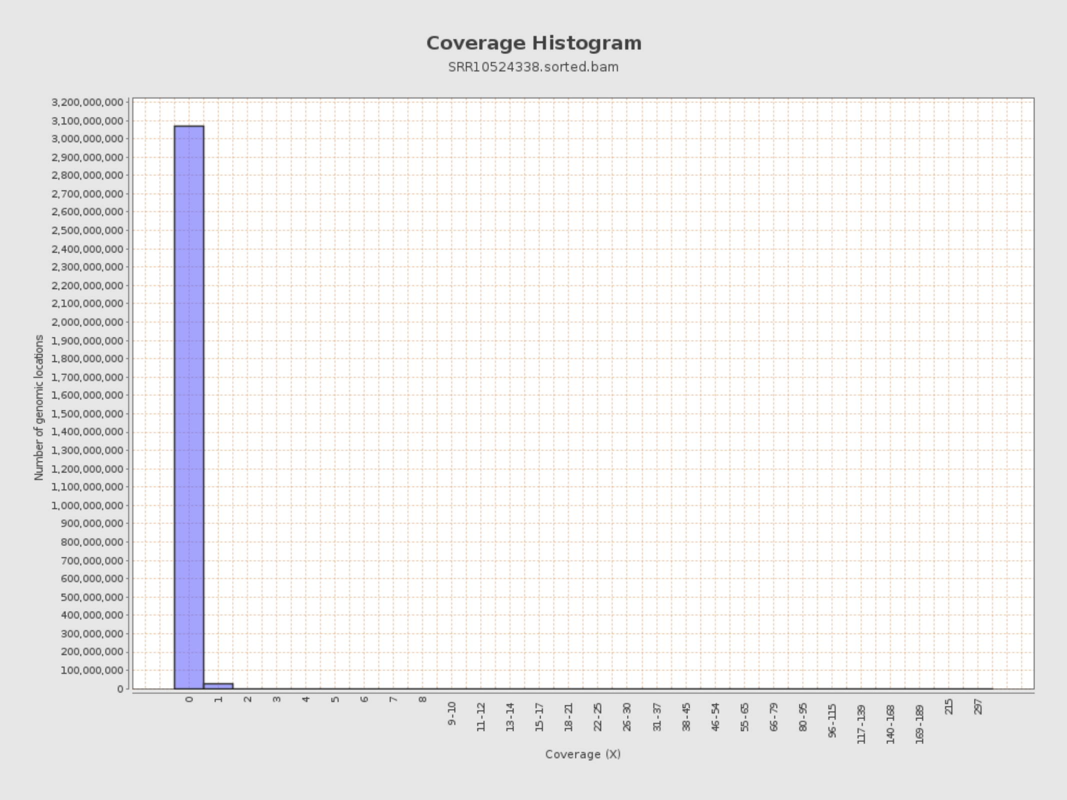
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2557467	0.0103	0.1707
chr2	243199373	1976131	0.0081	0.1498
chr3	198022430	2095138	0.0106	0.1062
chr4	191154276	1569157	0.0082	0.098
chr5	180915260	1766076	0.0098	0.102
chr6	171115067	1885524	0.011	0.1131
chr7	159138663	1366505	0.0086	0.1323

chr8	146364022	3110756	0.0213	0.1663
chr9	141213431	1256330	0.0089	0.1054
chr10	135534747	1536938	0.0113	0.1275
chr11	135006516	1456052	0.0108	0.1169
chr12	133851895	1208286	0.009	0.0987
chr13	115169878	756992	0.0066	0.0844
chr14	107349540	642701	0.006	0.0814
chr15	102531392	932435	0.0091	0.0996
chr16	90354753	950534	0.0105	0.1079
chr17	81195210	933133	0.0115	0.1132
chr18	78077248	697563	0.0089	0.1442
chr19	59128983	555025	0.0094	0.1331
chr20	63025520	713682	0.0113	0.1115
chr21	48129895	442282	0.0092	0.1026
chr22	51304566	222590	0.0043	0.0674
chrMT	16571	4363	0.2633	0.5417
chrX	155270560	1462680	0.0094	0.1046
chrY	59373566	93468	0.0016	0.0557

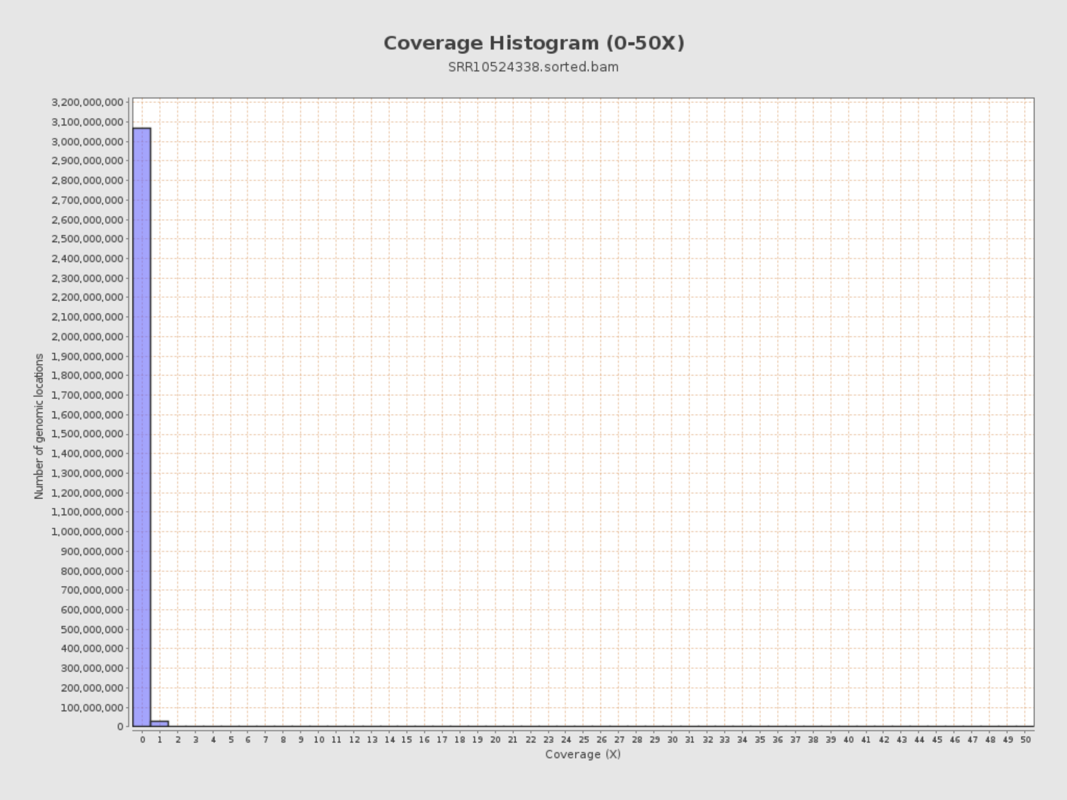
3. Results : Coverage across reference



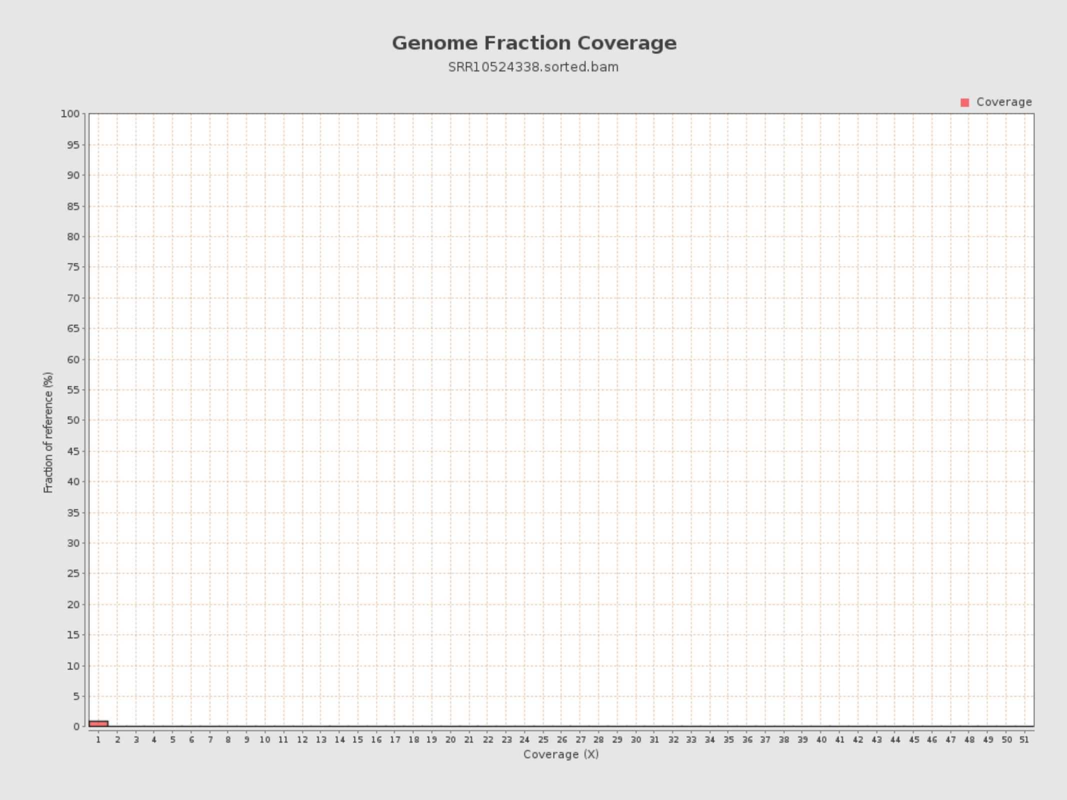
4. Results : Coverage Histogram



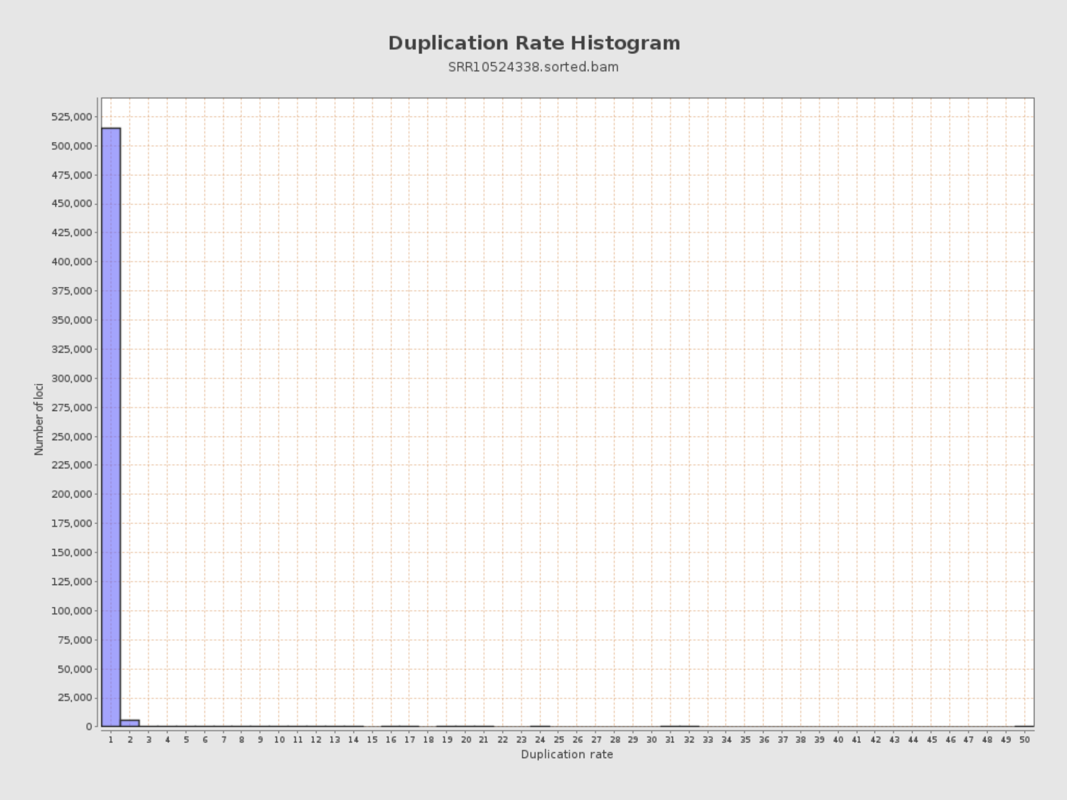
5. Results : Coverage Histogram (0-50X)



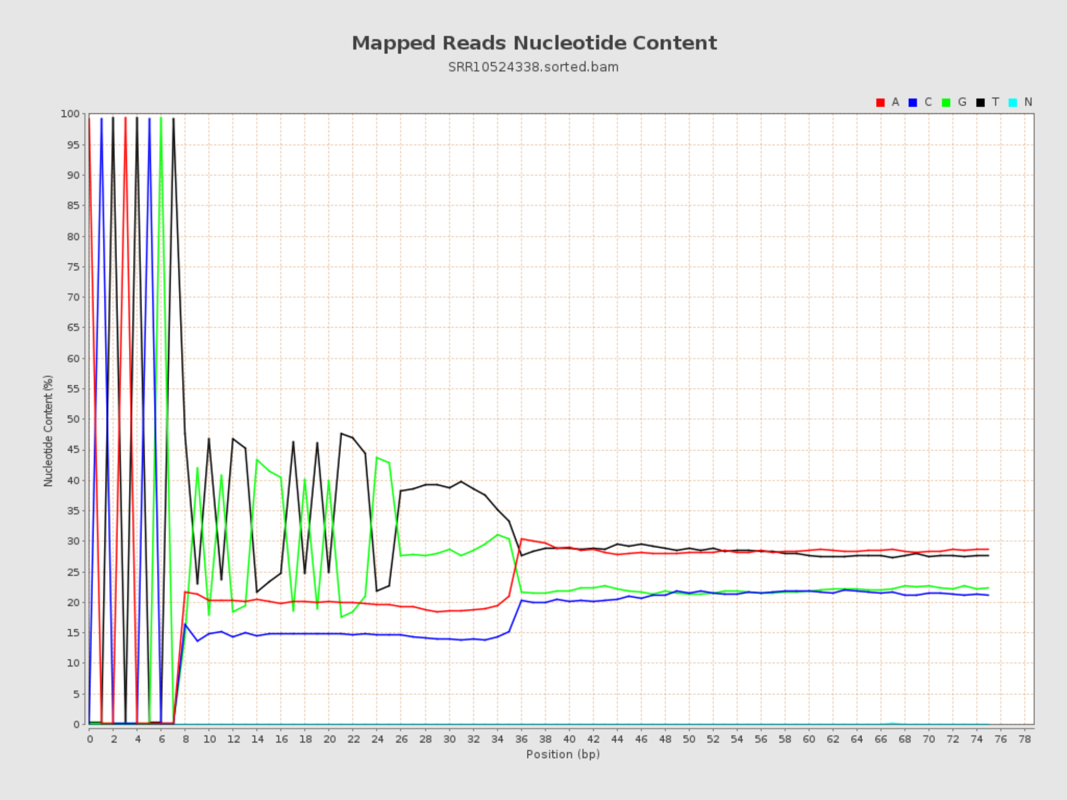
6. Results : Genome Fraction Coverage



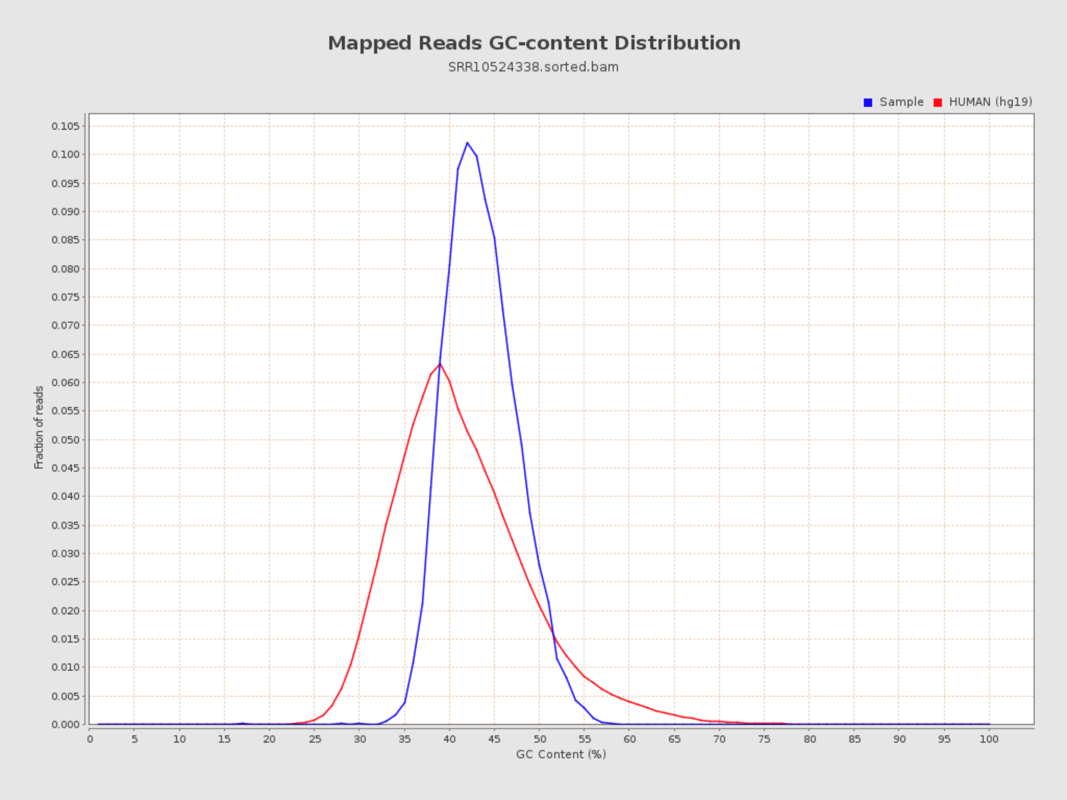
7. Results : Duplication Rate Histogram



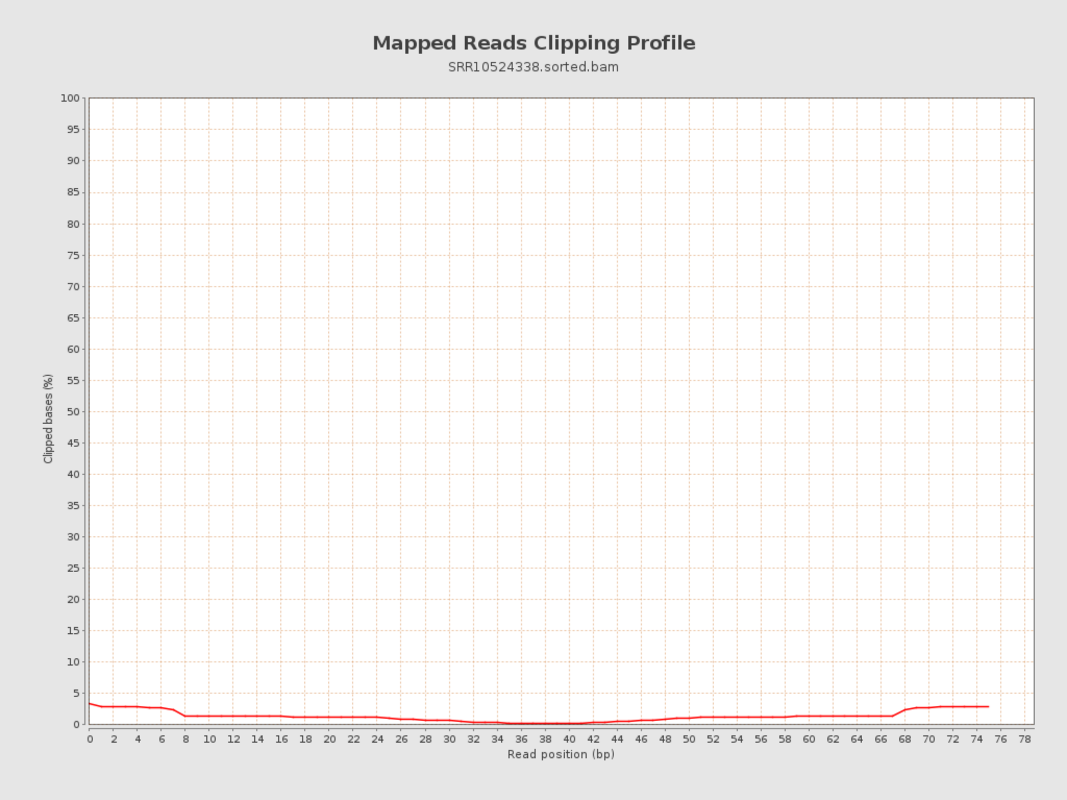
8. Results : Mapped Reads Nucleotide Content



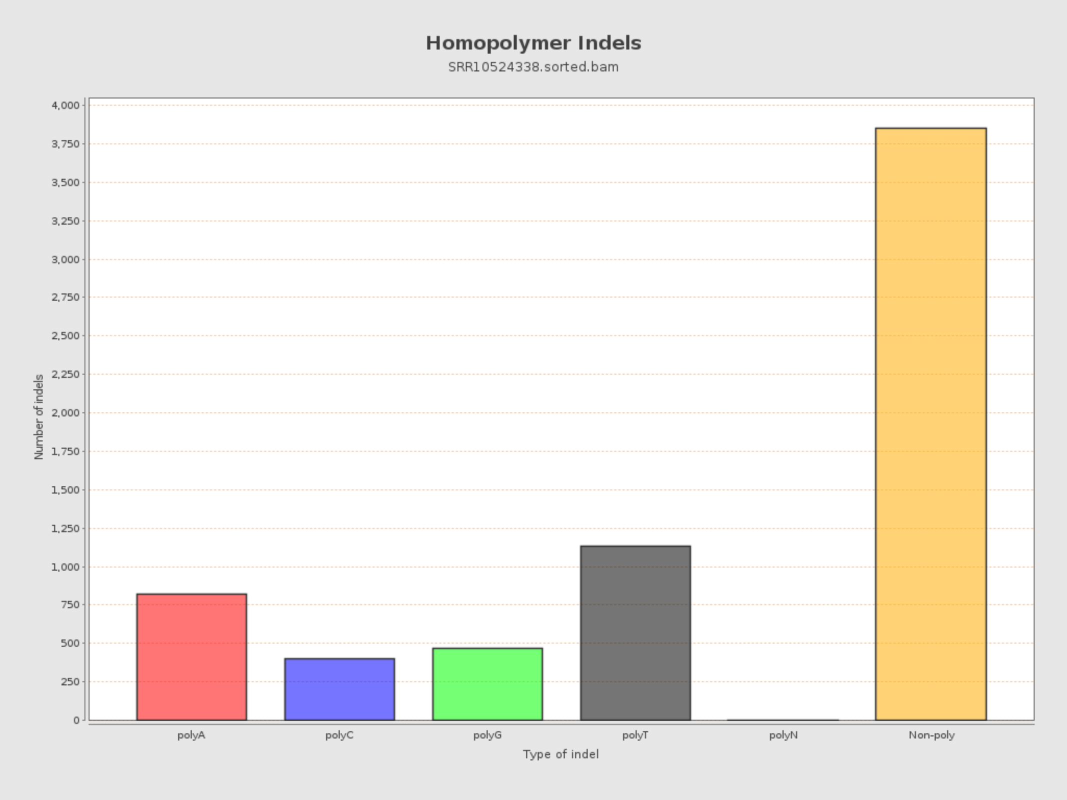
9. Results : Mapped Reads GC-content Distribution



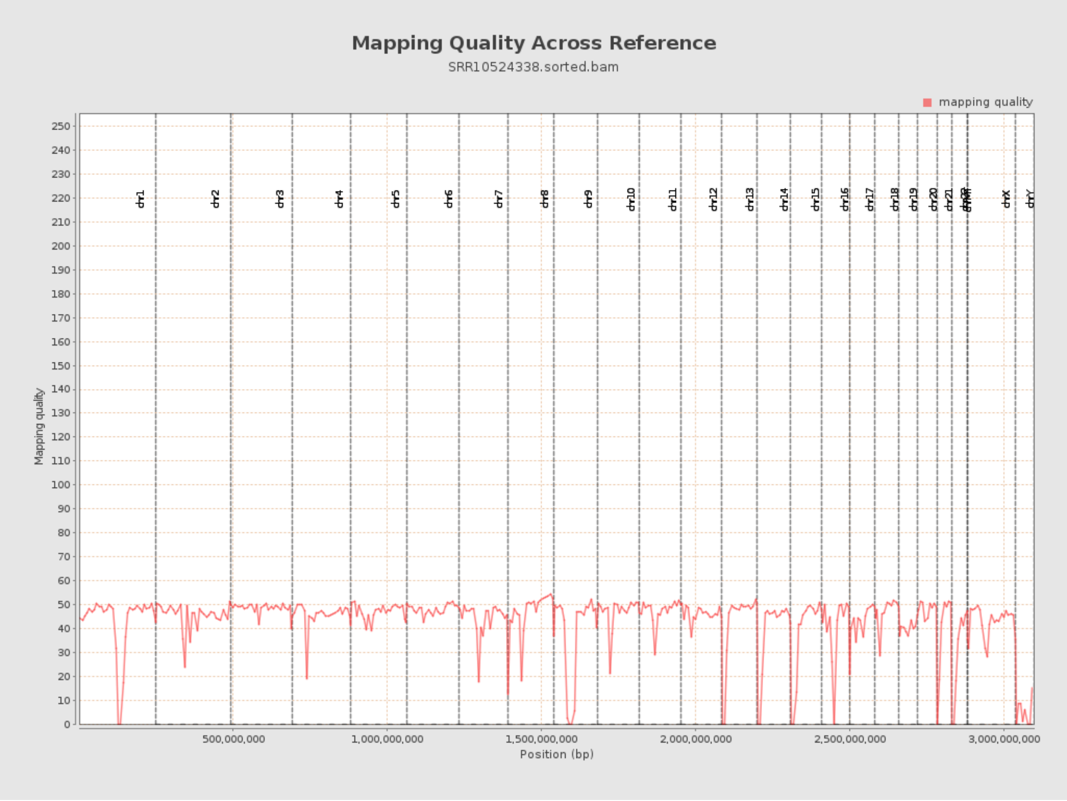
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram