Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:11:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524993.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_SRR10524993 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524993.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:11:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524993.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	828,698
Mapped reads	767,559 / 92.62%
Unmapped reads	61,139 / 7.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,756 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	18,752 / 2.26%
Duplication rate	1.84%
Clipped reads	766,454 / 92.49%

2.2. ACGT Content

Number/percentage of A's	11,545,063 / 25.85%
Number/percentage of C's	8,230,152 / 18.42%
Number/percentage of T's	14,360,119 / 32.15%
Number/percentage of G's	10,533,442 / 23.58%
Number/percentage of N's	466 / 0%
GC Percentage	42.01%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1545

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

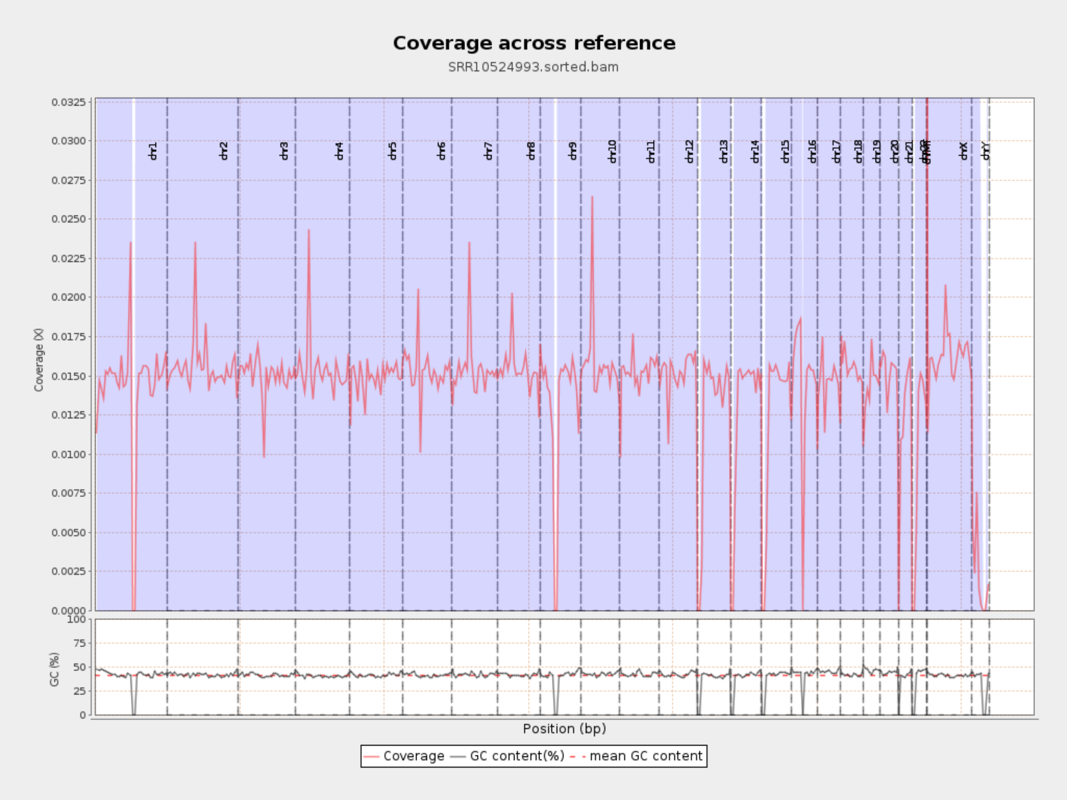
General error rate	0.5%
Mismatches	215,936
Insertions	3,416
Mapped reads with at least one insertion	0.44%
Deletions	8,471
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.92%

2.6. Chromosome stats

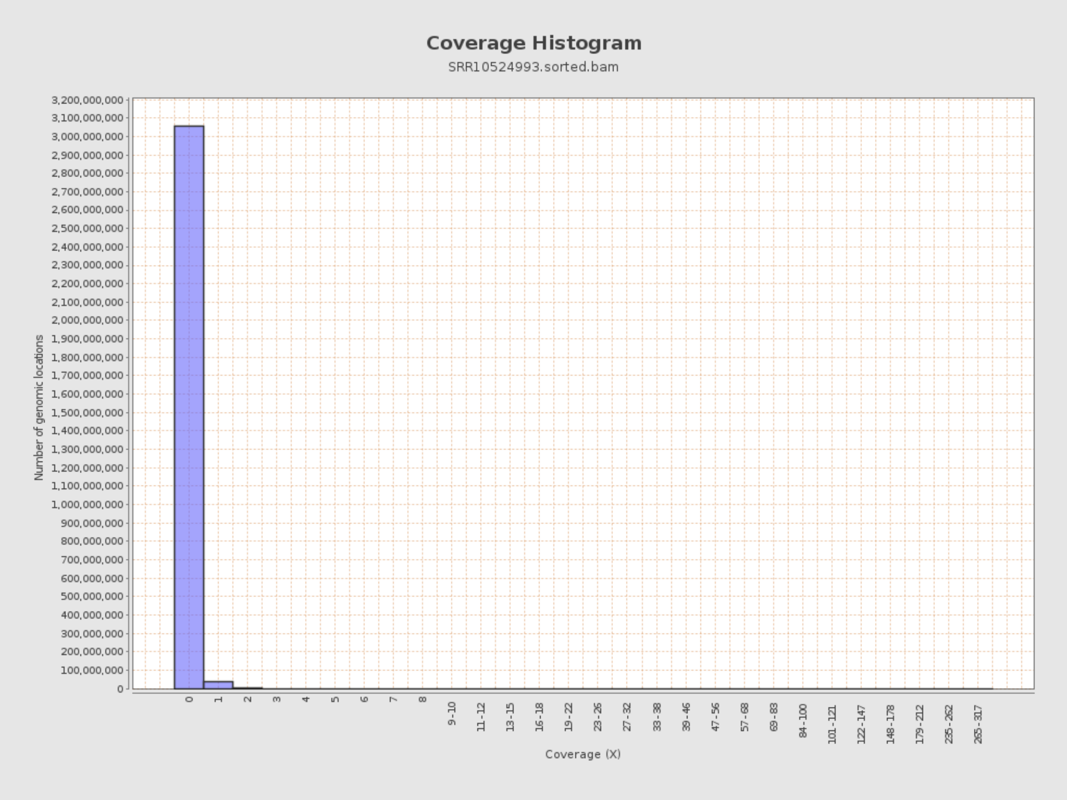
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3531459	0.0142	0.2395
chr2	243199373	3798411	0.0156	0.169
chr3	198022430	2978228	0.015	0.1289
chr4	191154276	2949903	0.0154	0.1382
chr5	180915260	2709373	0.015	0.1285
chr6	171115067	2619874	0.0153	0.1471
chr7	159138663	2463532	0.0155	0.1806

chr8	146364022	2258102	0.0154	0.1665
chr9	141213431	1839157	0.013	0.1365
chr10	135534747	2157041	0.0159	0.1624
chr11	135006516	2065683	0.0153	0.1506
chr12	133851895	2034643	0.0152	0.1306
chr13	115169878	1419612	0.0123	0.1173
chr14	107349540	1349457	0.0126	0.1191
chr15	102531392	1246996	0.0122	0.1186
chr16	90354753	1292836	0.0143	0.1289
chr17	81195210	1185672	0.0146	0.1338
chr18	78077248	1217411	0.0156	0.2052
chr19	59128983	857282	0.0145	0.1679
chr20	63025520	957008	0.0152	0.131
chr21	48129895	584000	0.0121	0.1216
chr22	51304566	507297	0.0099	0.1035
chrMT	16571	1251	0.0755	0.2747
chrX	155270560	2528055	0.0163	0.1414
chrY	59373566	131253	0.0022	0.0706

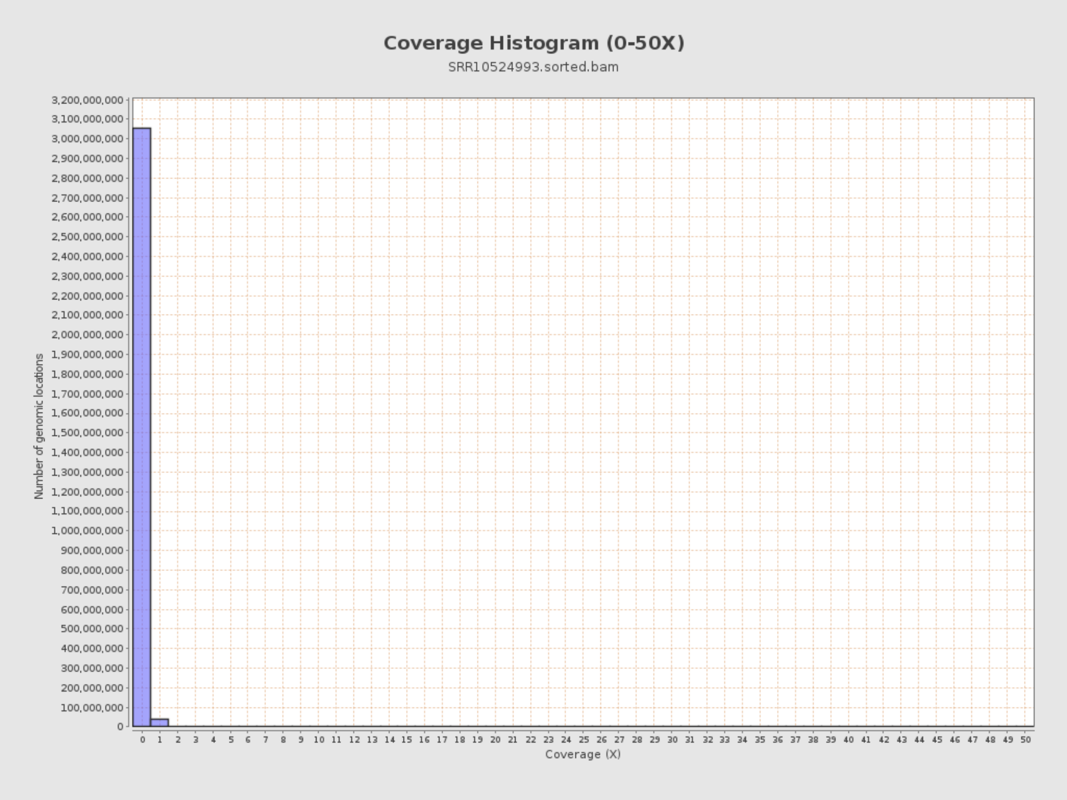
3. Results : Coverage across reference



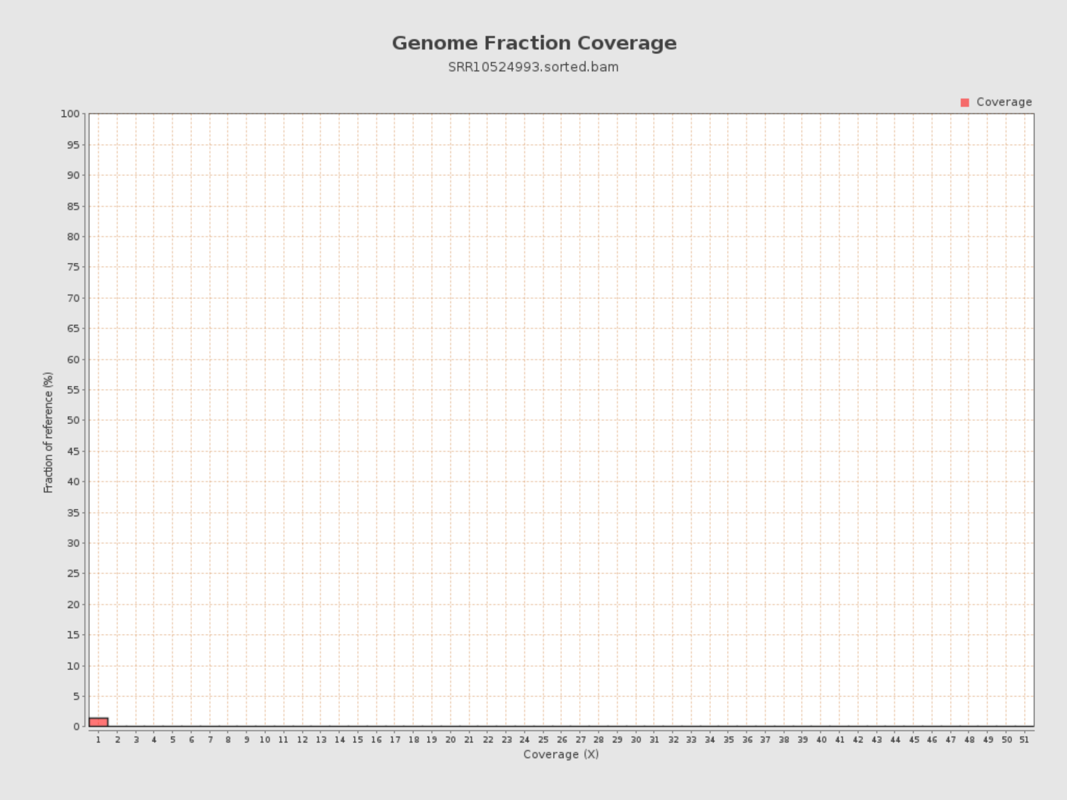
4. Results : Coverage Histogram



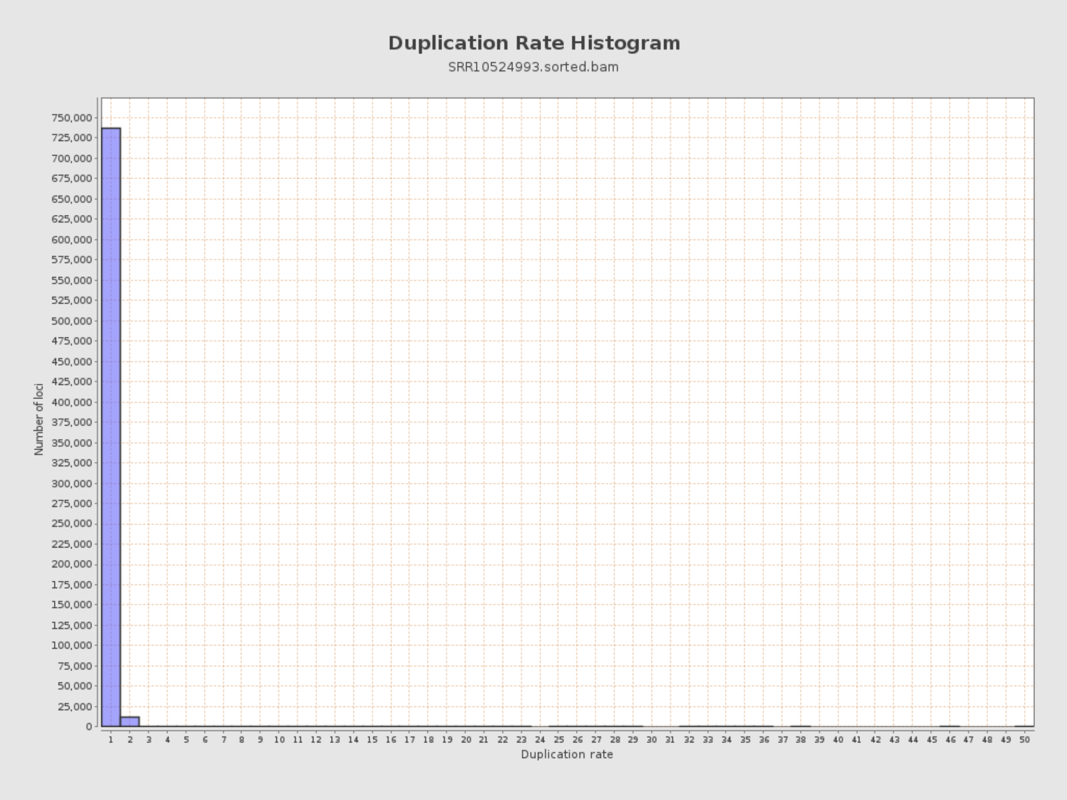
5. Results : Coverage Histogram (0-50X)



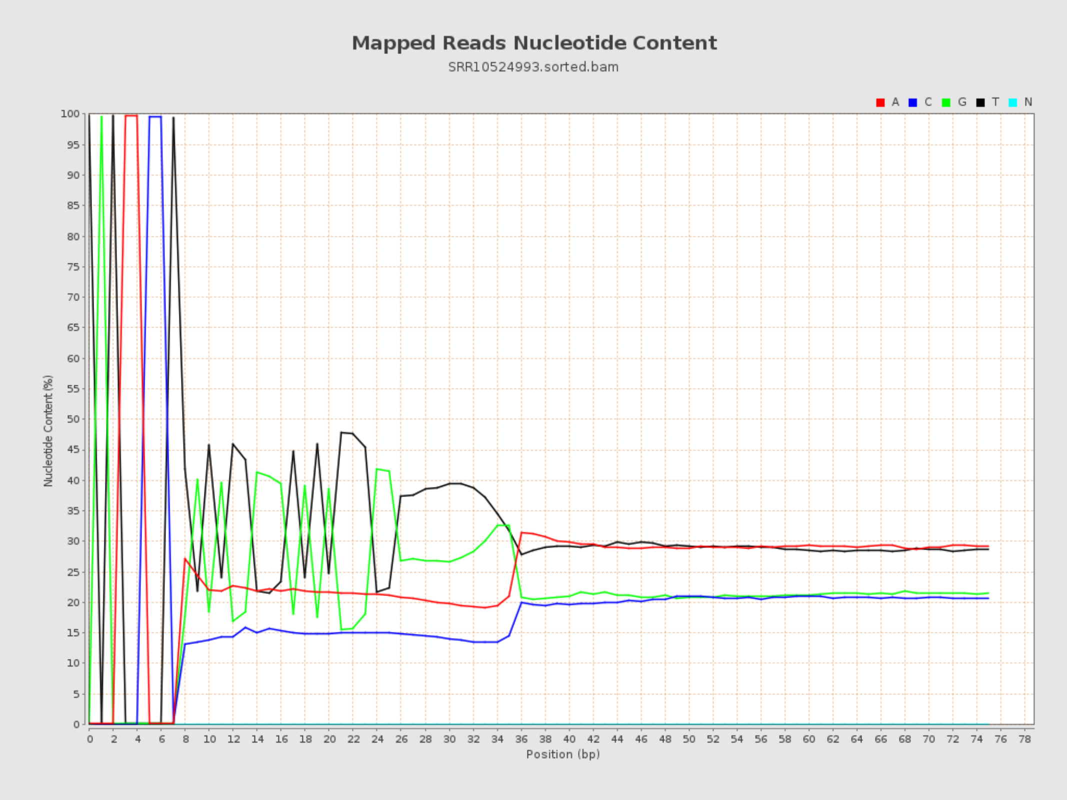
6. Results : Genome Fraction Coverage



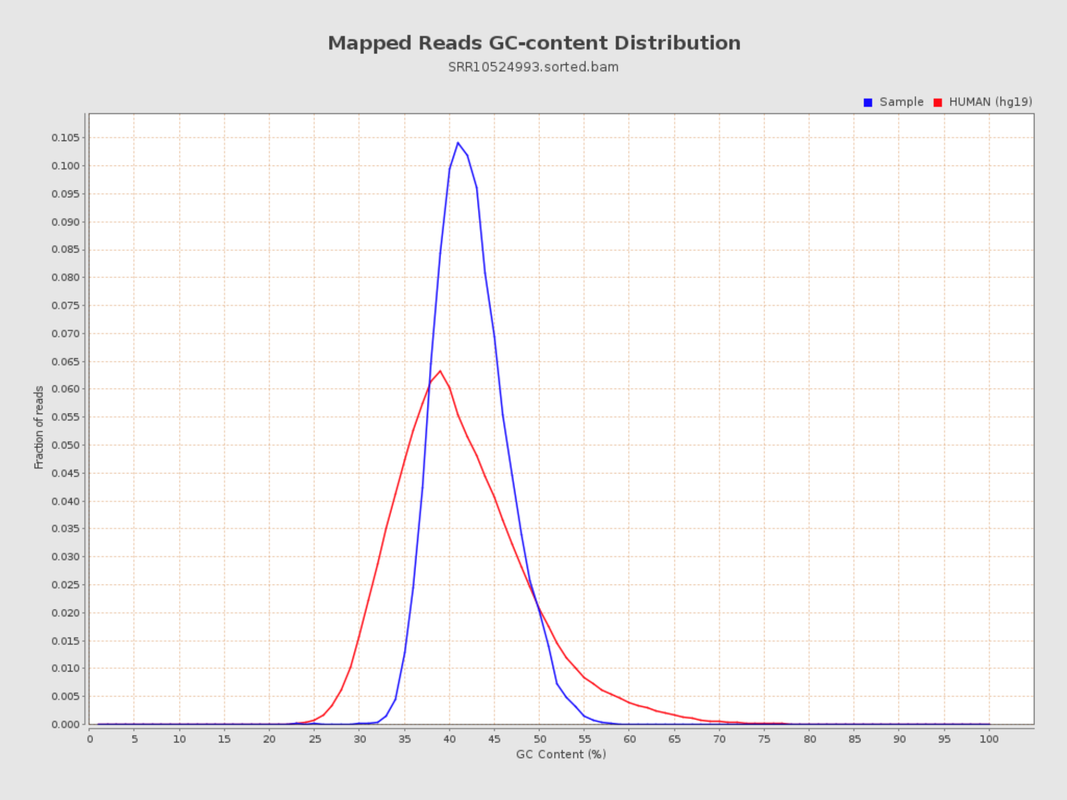
7. Results : Duplication Rate Histogram



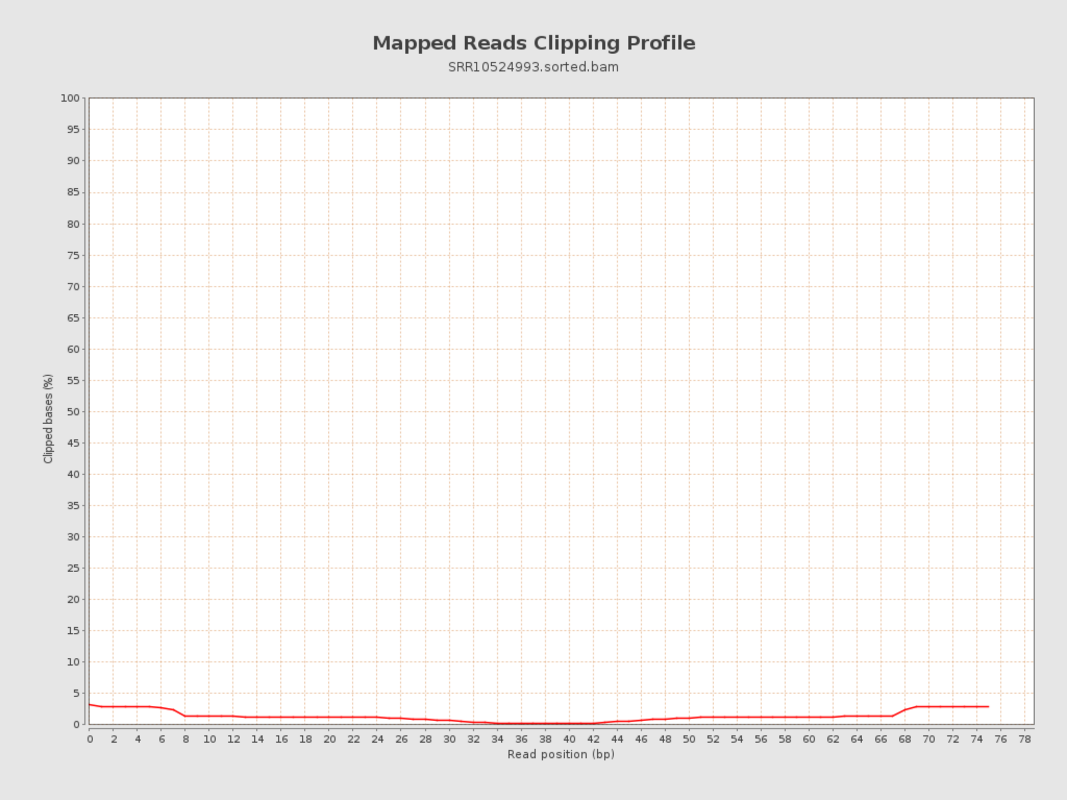
8. Results : Mapped Reads Nucleotide Content



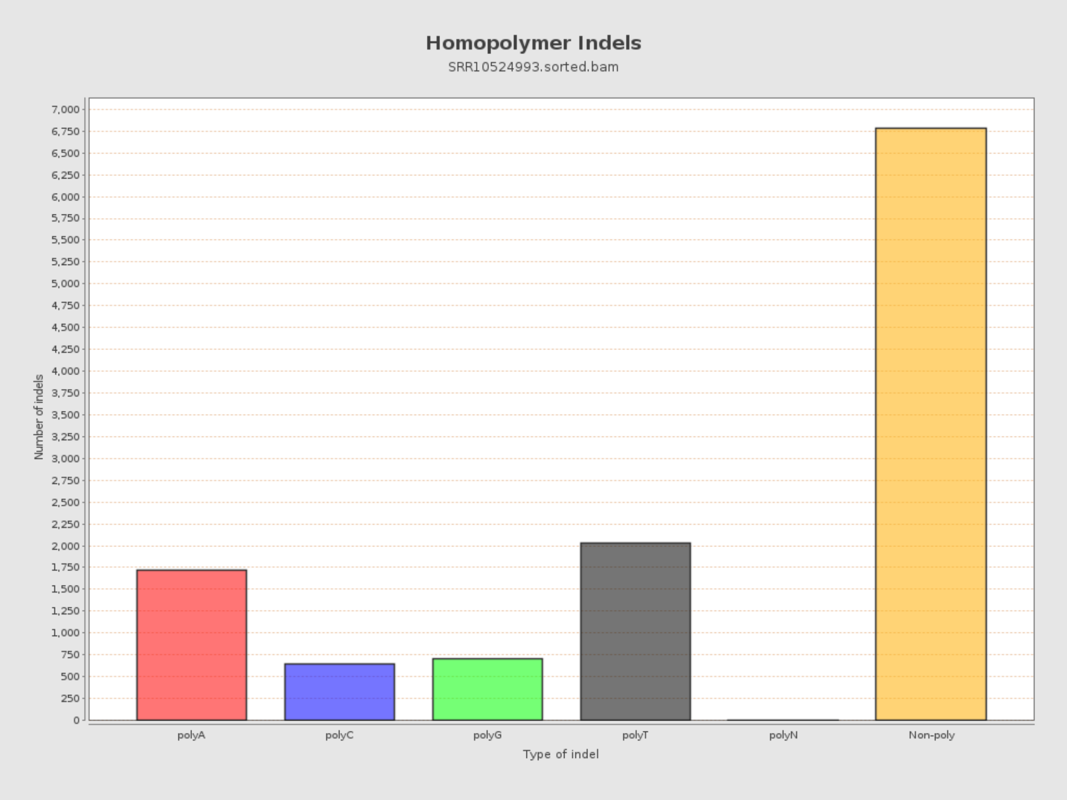
9. Results : Mapped Reads GC-content Distribution



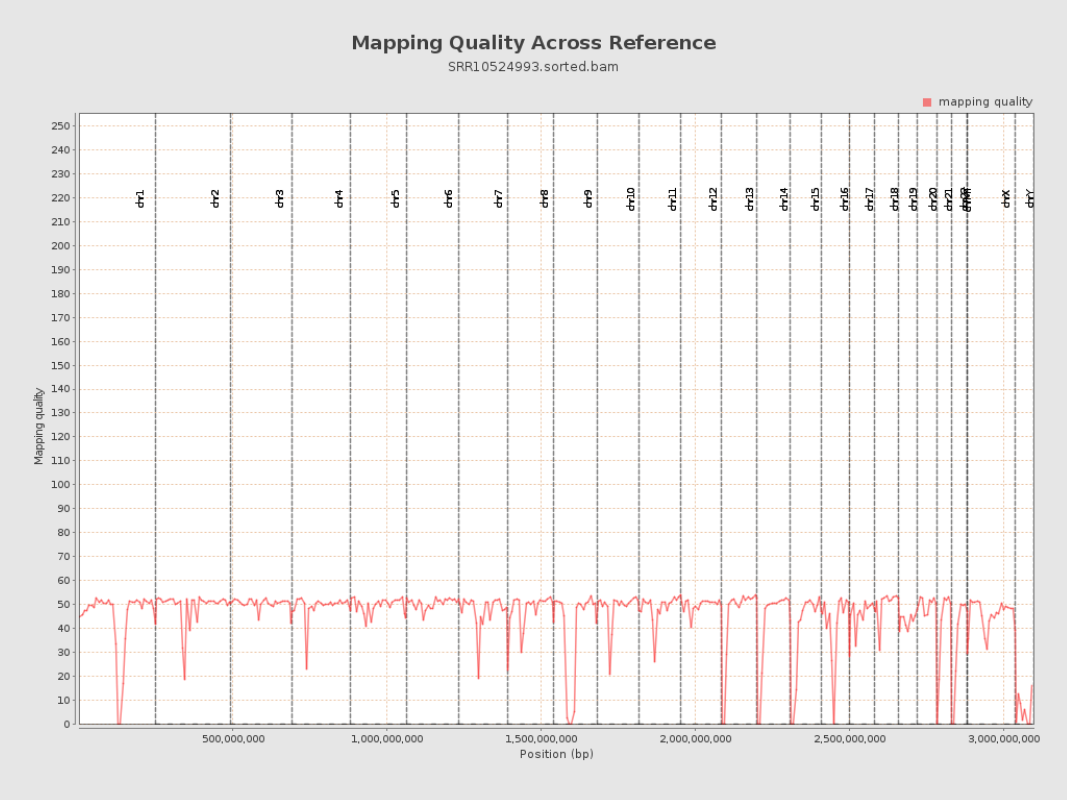
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram