Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:21:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524706.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_SRR10524706 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524706.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:21:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524706.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	769,709
Mapped reads	708,900 / 92.1%
Unmapped reads	60,809 / 7.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,740 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	18,806 / 2.44%
Duplication rate	1.95%
Clipped reads	709,408 / 92.17%

2.2. ACGT Content

Number/percentage of A's	11,086,804 / 26.32%
Number/percentage of C's	7,889,499 / 18.73%
Number/percentage of T's	13,532,040 / 32.12%
Number/percentage of G's	9,614,343 / 22.82%
Number/percentage of N's	6,027 / 0.01%
GC Percentage	41.55%

2.3. Coverage

Mean	0.0136

Standard Deviation	0.1585

2.4. Mapping Quality

Mean Mapping Quality	46.05

2.5. Mismatches and indels

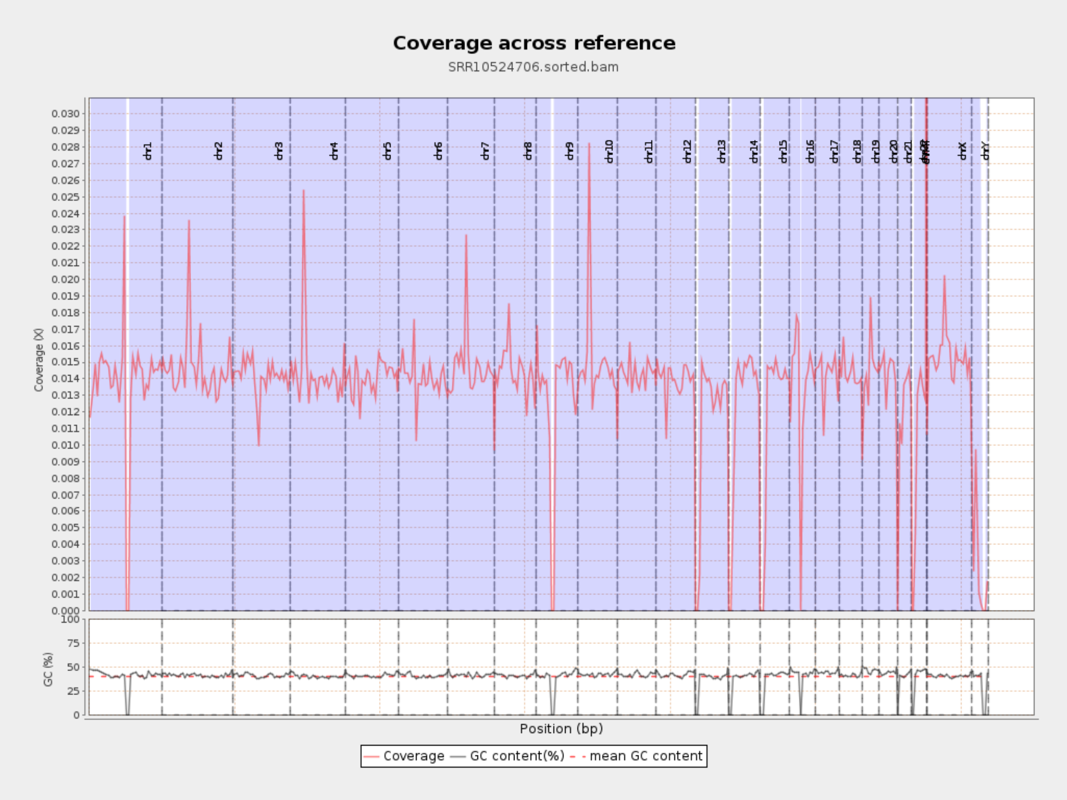
General error rate	0.52%
Mismatches	212,897
Insertions	3,122
Mapped reads with at least one insertion	0.44%
Deletions	8,303
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.33%

2.6. Chromosome stats

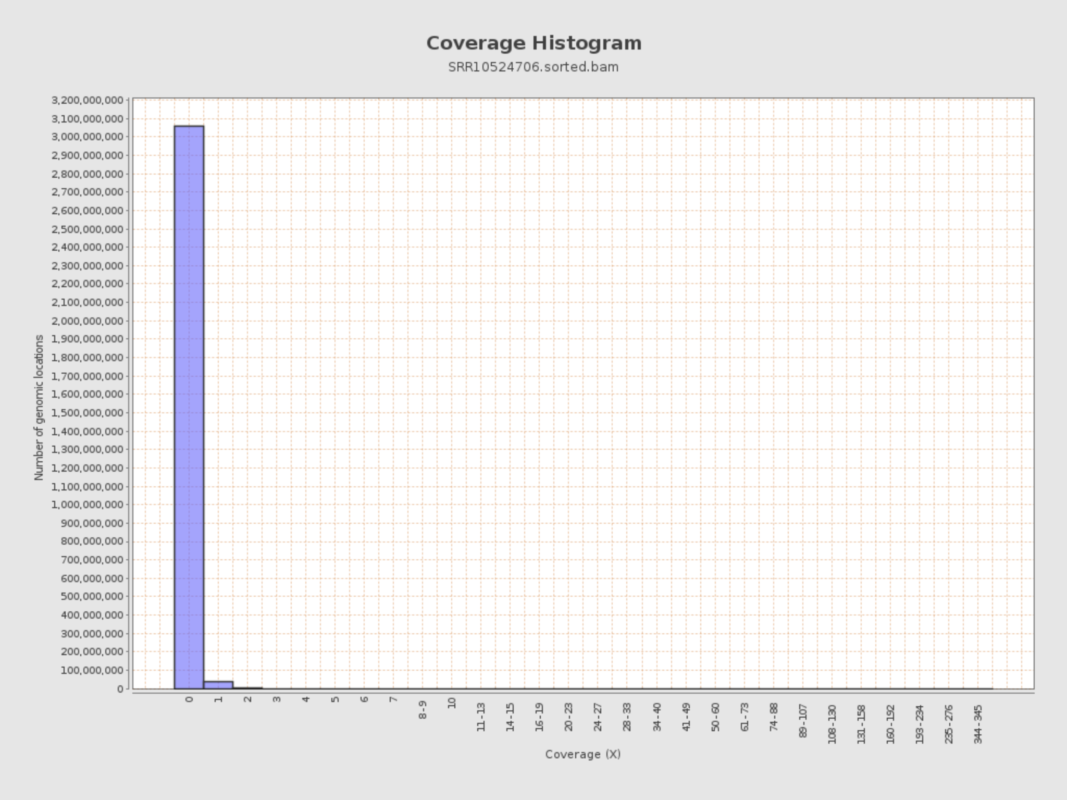
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3404190	0.0137	0.2473
chr2	243199373	3573042	0.0147	0.2024
chr3	198022430	2799202	0.0141	0.1244
chr4	191154276	2751745	0.0144	0.1392
chr5	180915260	2549134	0.0141	0.1254
chr6	171115067	2415906	0.0141	0.1332
chr7	159138663	2352390	0.0148	0.184

chr8	146364022	2110632	0.0144	0.1685
chr9	141213431	1758767	0.0125	0.1365
chr10	135534747	2041987	0.0151	0.1702
chr11	135006516	1925398	0.0143	0.1445
chr12	133851895	1868441	0.014	0.1239
chr13	115169878	1295887	0.0113	0.1118
chr14	107349540	1291923	0.012	0.1163
chr15	102531392	1189304	0.0116	0.1125
chr16	90354753	1219112	0.0135	0.1264
chr17	81195210	1149416	0.0142	0.1288
chr18	78077248	1125288	0.0144	0.2175
chr19	59128983	857521	0.0145	0.2033
chr20	63025520	899284	0.0143	0.1277
chr21	48129895	556296	0.0116	0.124
chr22	51304566	479432	0.0093	0.1016
chrMT	16571	3442	0.2077	0.4794
chrX	155270560	2375015	0.0153	0.1349
chrY	59373566	149245	0.0025	0.1073

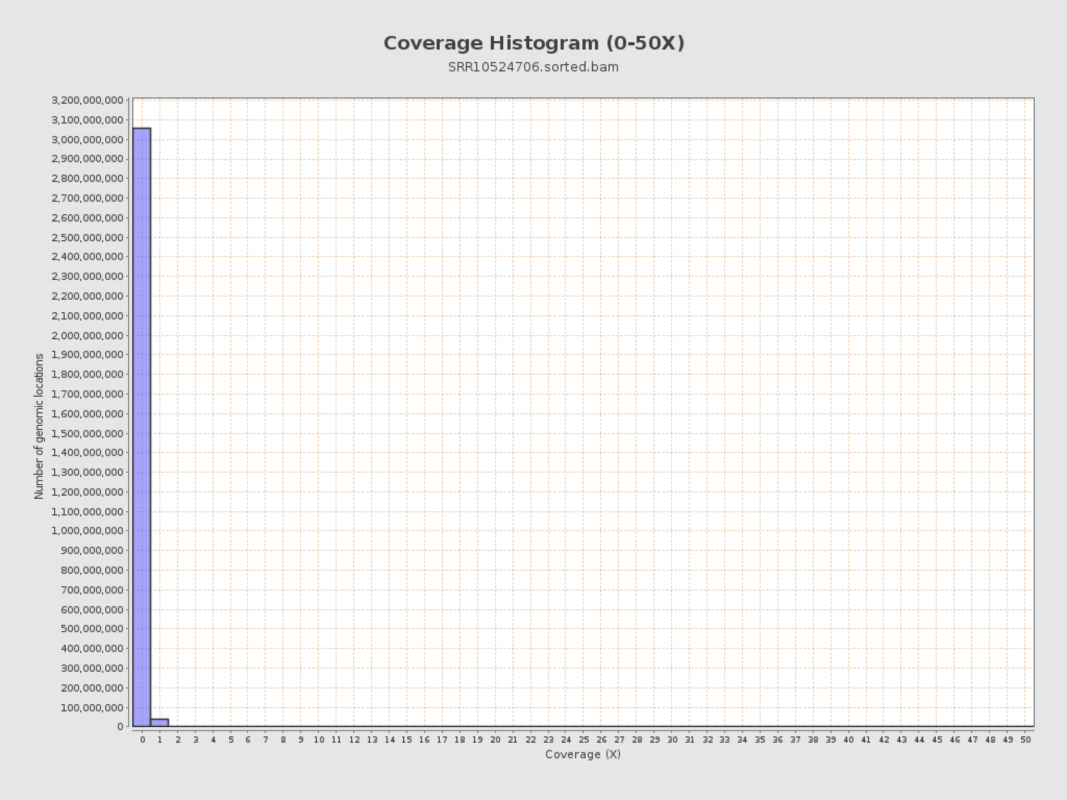
3. Results : Coverage across reference



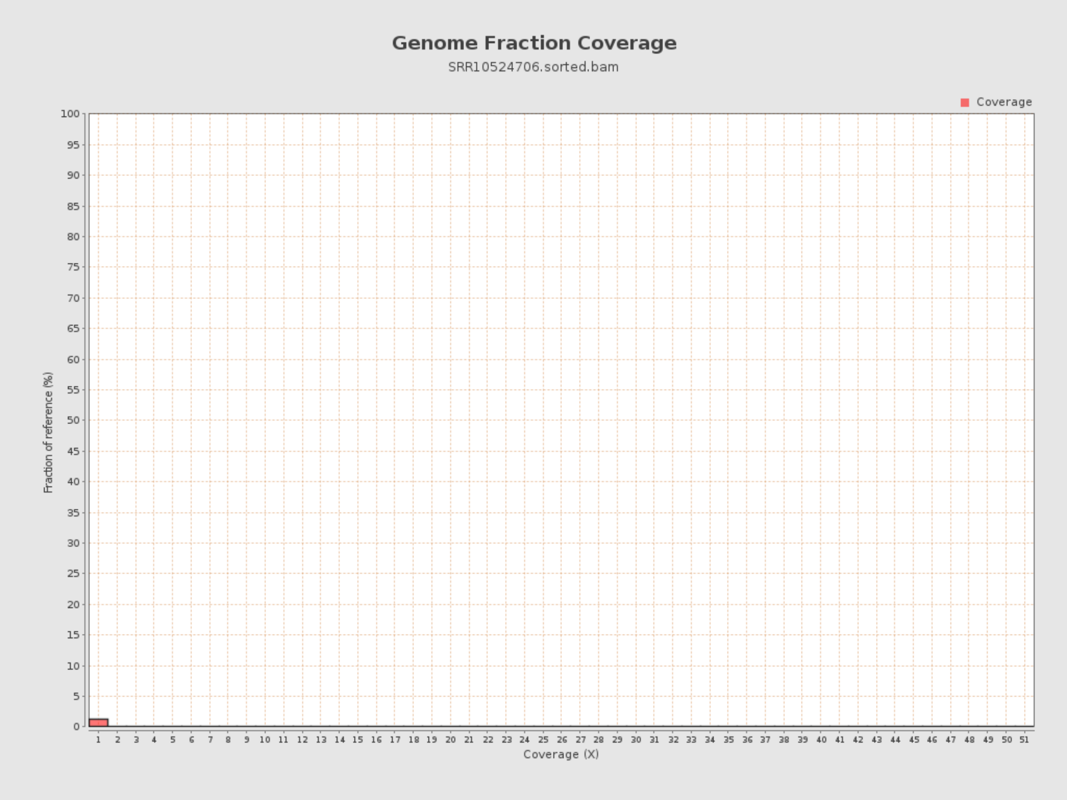
4. Results : Coverage Histogram



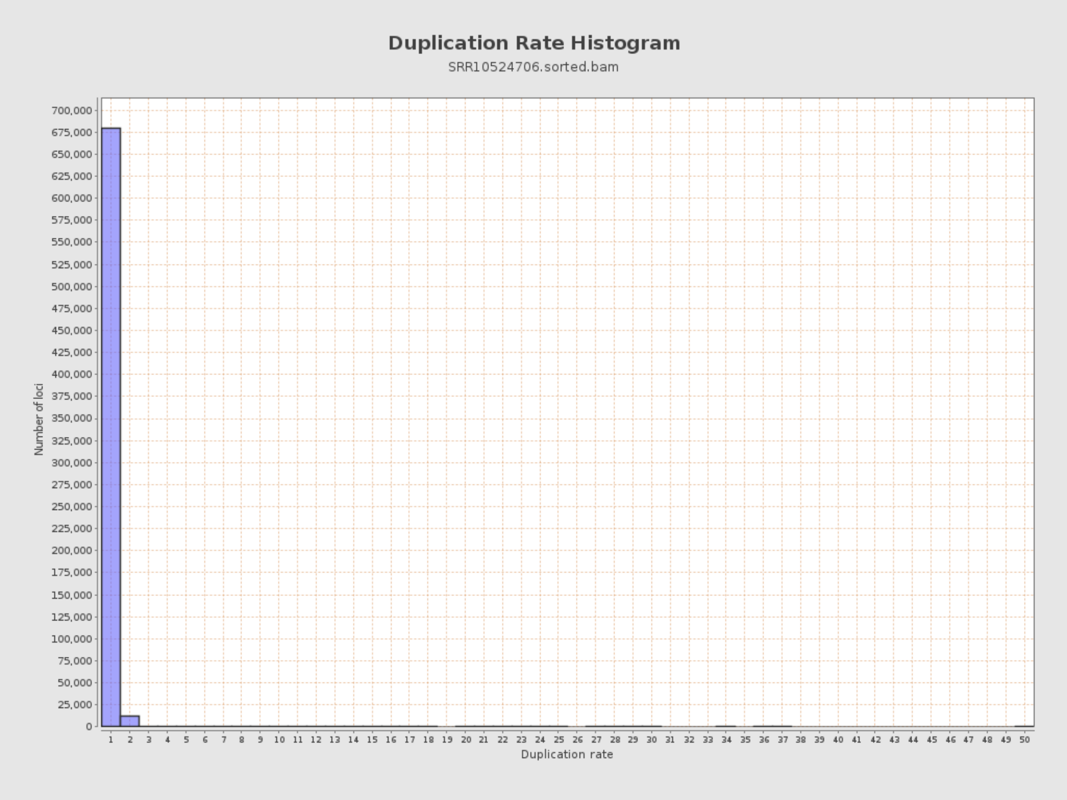
5. Results : Coverage Histogram (0-50X)



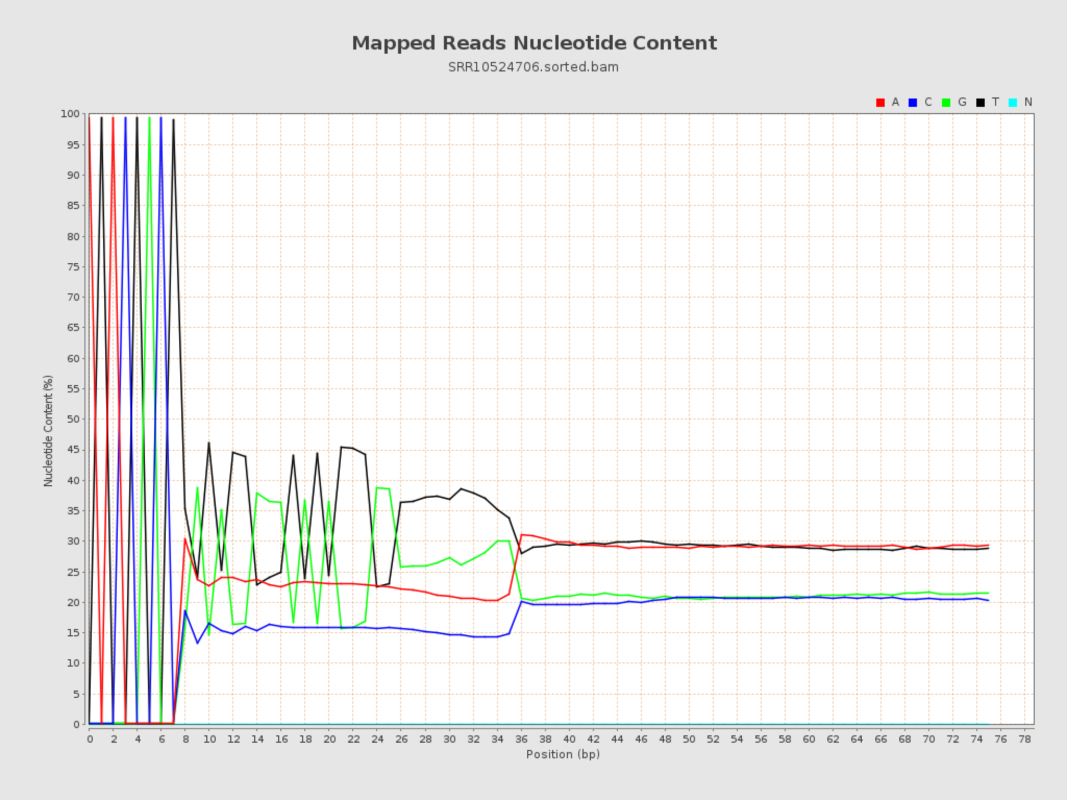
6. Results : Genome Fraction Coverage



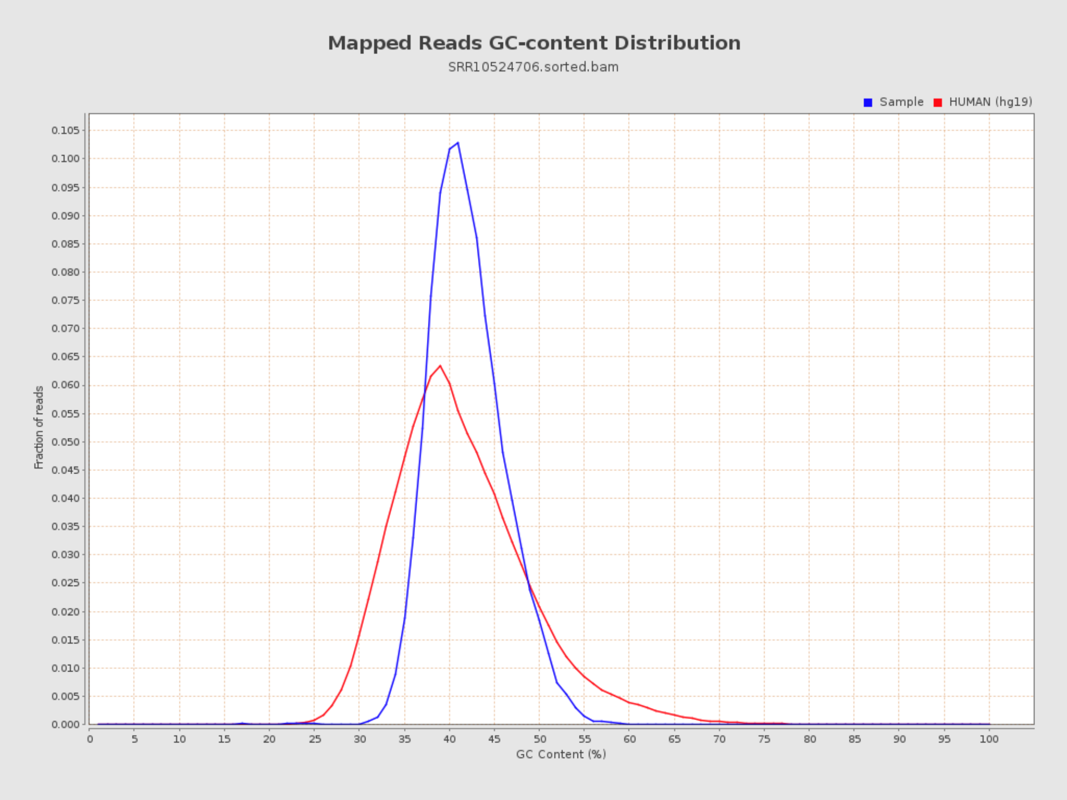
7. Results : Duplication Rate Histogram



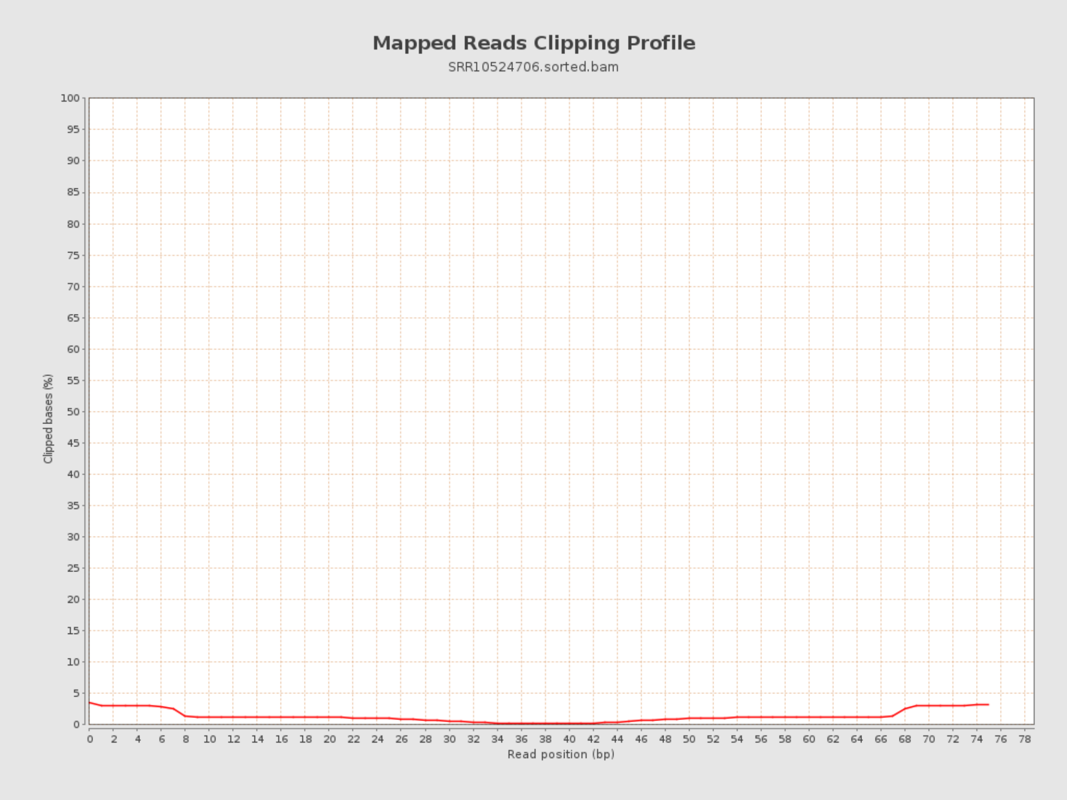
8. Results : Mapped Reads Nucleotide Content



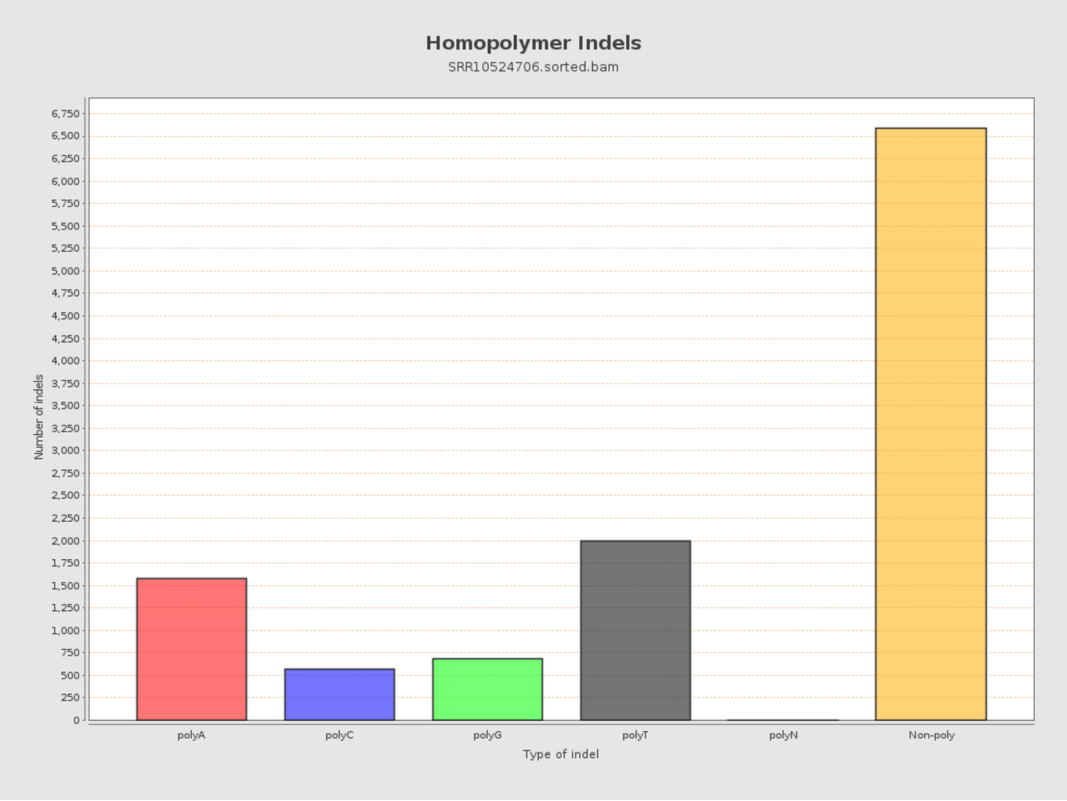
9. Results : Mapped Reads GC-content Distribution



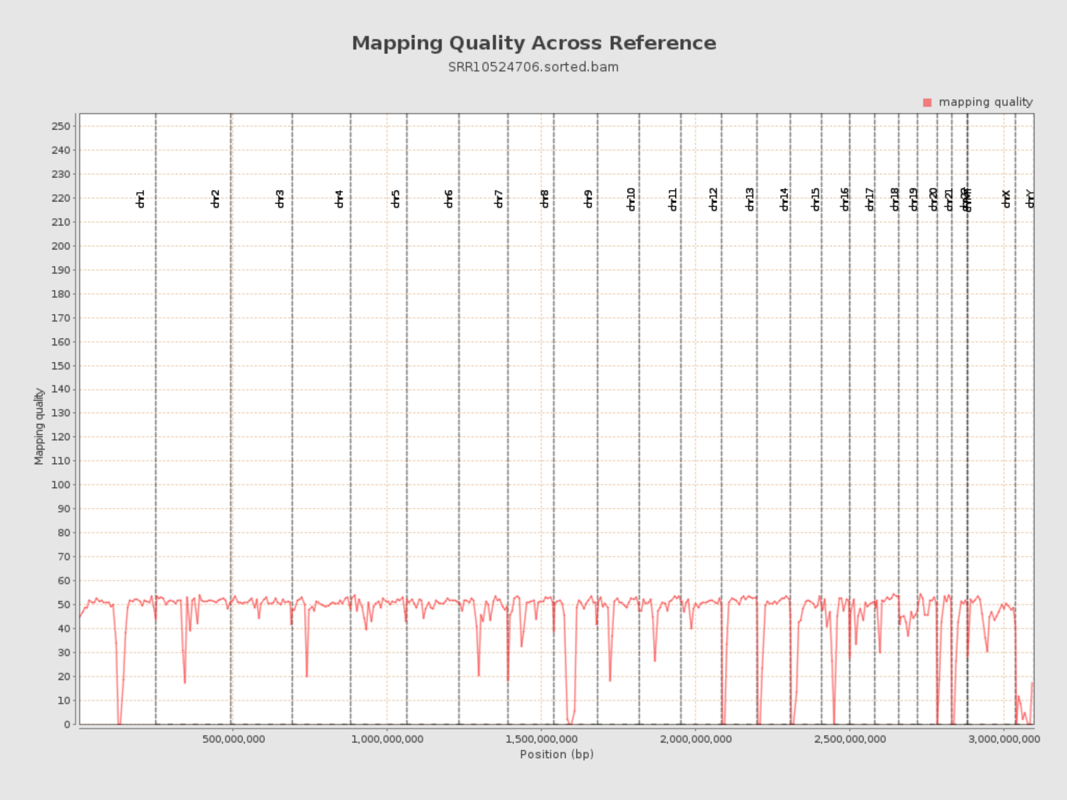
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram