Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:50:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524793.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_SRR10524793 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524793.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:50:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524793.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	992,017
Mapped reads	901,380 / 90.86%
Unmapped reads	90,637 / 9.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,435 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	28,977 / 2.92%
Duplication rate	2.49%
Clipped reads	902,678 / 90.99%

2.2. ACGT Content

Number/percentage of A's	12,784,531 / 24.9%
Number/percentage of C's	9,863,231 / 19.21%
Number/percentage of T's	16,298,700 / 31.74%
Number/percentage of G's	12,393,819 / 24.14%
Number/percentage of N's	6,118 / 0.01%
GC Percentage	43.35%

2.3. Coverage

Mean	0.0166

Standard Deviation	0.1722

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

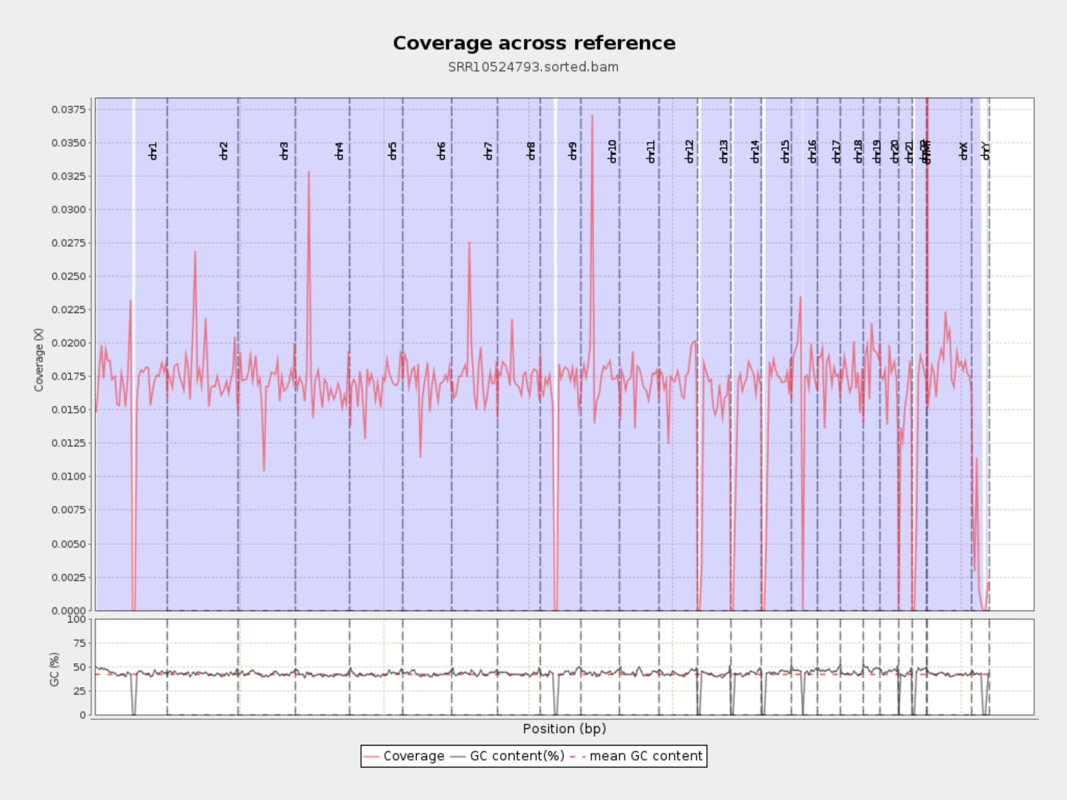
General error rate	0.51%
Mismatches	256,554
Insertions	3,822
Mapped reads with at least one insertion	0.42%
Deletions	9,794
Mapped reads with at least one deletion	1.08%
Homopolymer indels	40.47%

2.6. Chromosome stats

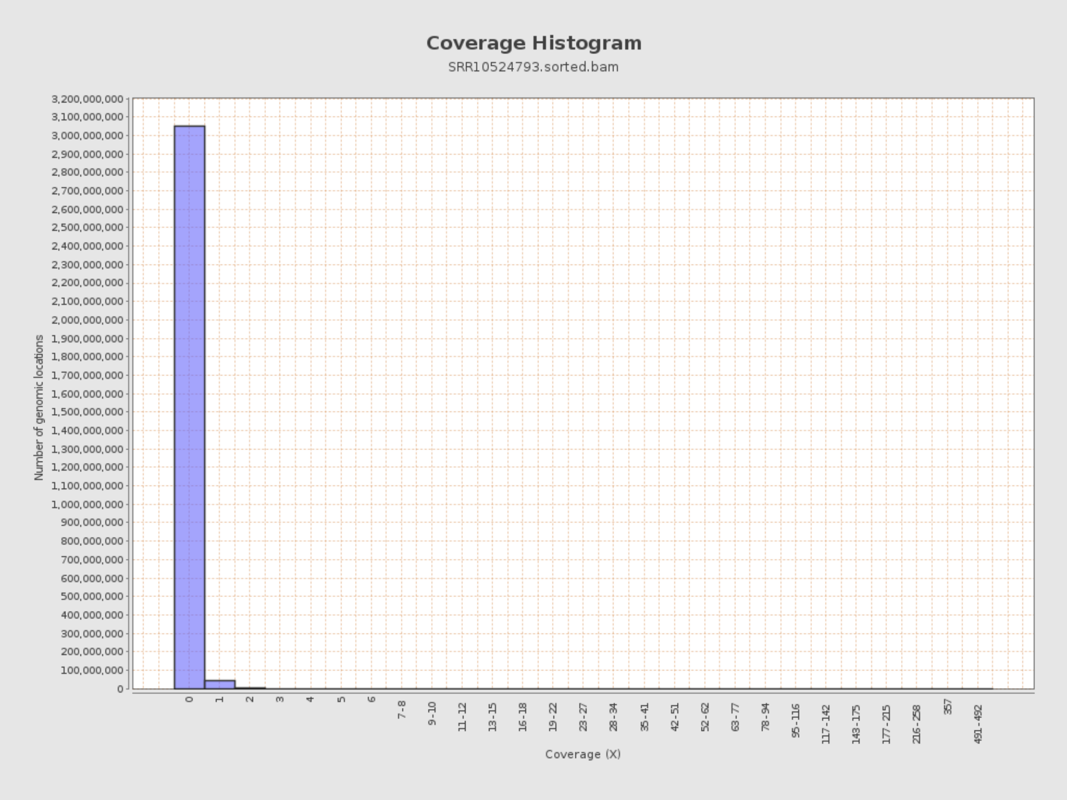
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4108964	0.0165	0.2238
chr2	243199373	4349831	0.0179	0.2566
chr3	198022430	3388302	0.0171	0.1415
chr4	191154276	3303066	0.0173	0.1566
chr5	180915260	3072838	0.017	0.1389
chr6	171115067	2916159	0.017	0.1492
chr7	159138663	2827967	0.0178	0.1998

chr8	146364022	2568797	0.0176	0.1649
chr9	141213431	2163893	0.0153	0.1505
chr10	135534747	2522113	0.0186	0.2038
chr11	135006516	2313656	0.0171	0.1556
chr12	133851895	2329433	0.0174	0.1425
chr13	115169878	1574079	0.0137	0.1247
chr14	107349540	1547276	0.0144	0.1313
chr15	102531392	1461364	0.0143	0.1274
chr16	90354753	1540132	0.017	0.1519
chr17	81195210	1445421	0.0178	0.1471
chr18	78077248	1362537	0.0175	0.219
chr19	59128983	1118500	0.0189	0.1963
chr20	63025520	1093076	0.0173	0.1464
chr21	48129895	673256	0.014	0.1352
chr22	51304566	639534	0.0125	0.1201
chrMT	16571	10733	0.6477	0.8934
chrX	155270560	2845852	0.0183	0.1507
chrY	59373566	185315	0.0031	0.0947

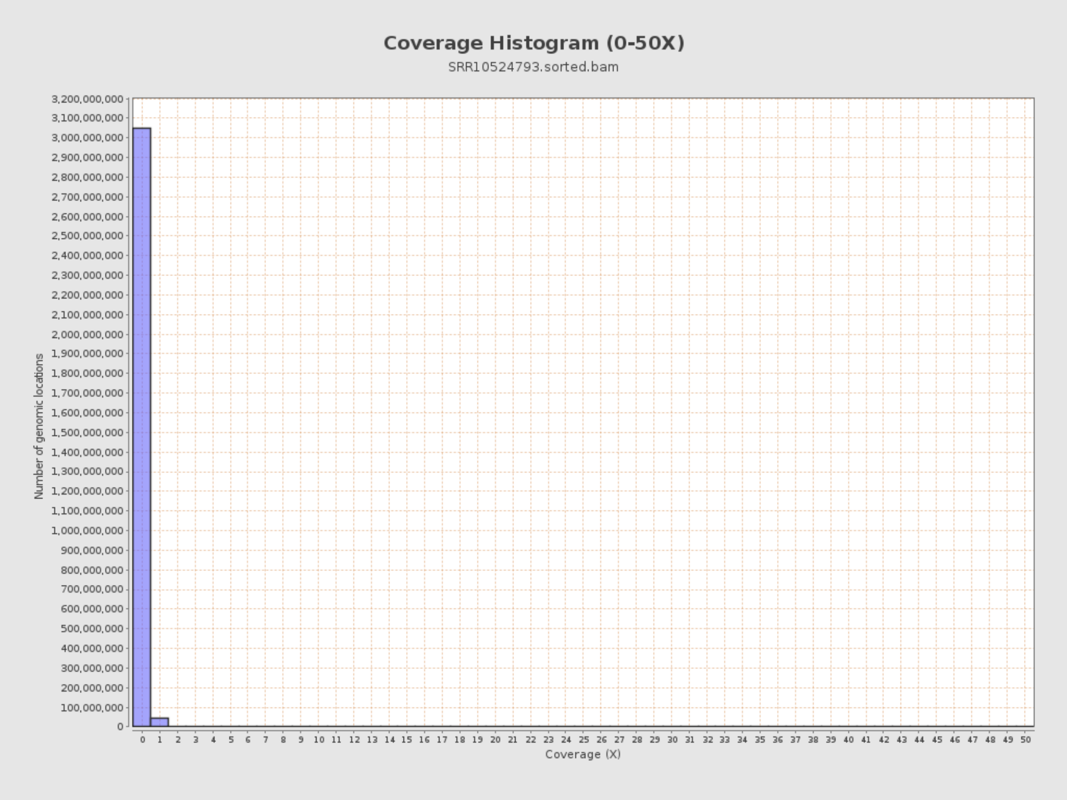
3. Results : Coverage across reference



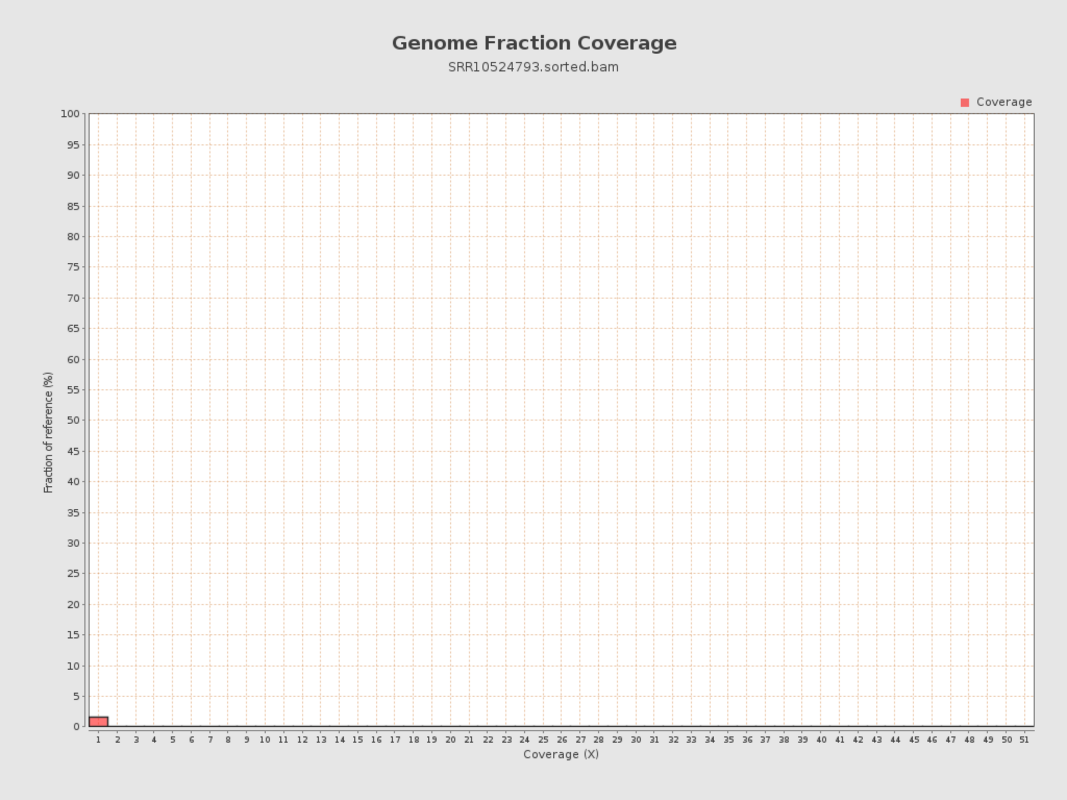
4. Results : Coverage Histogram



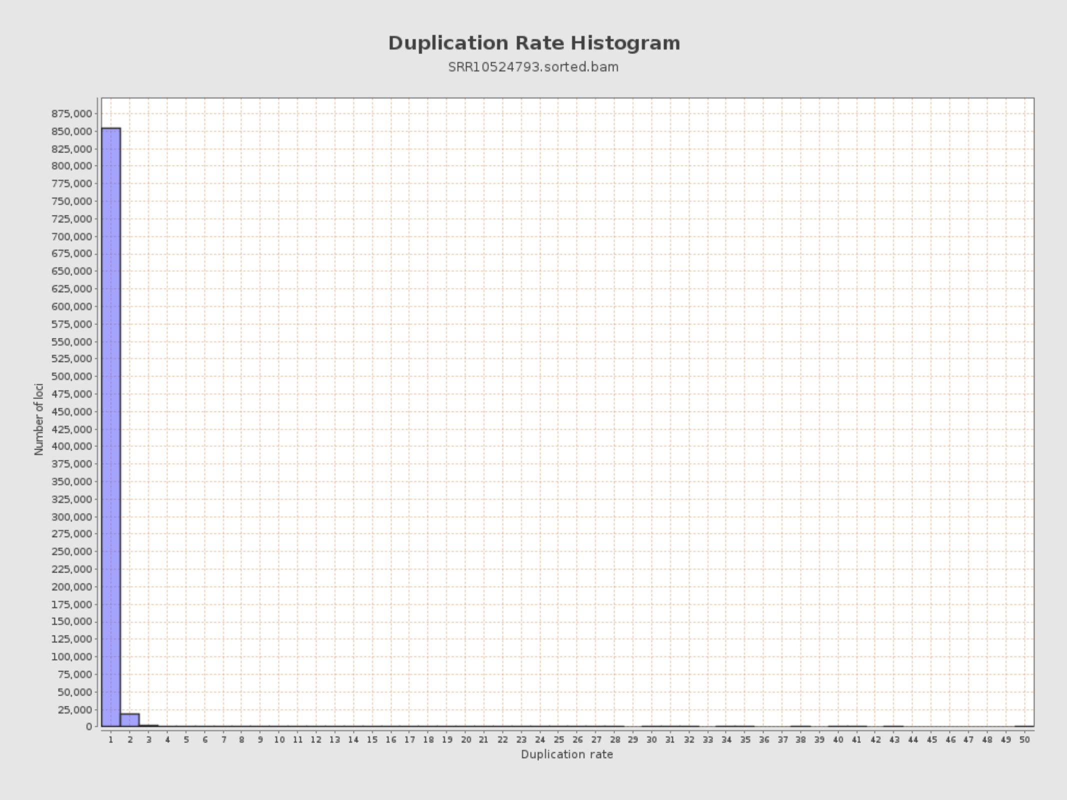
5. Results : Coverage Histogram (0-50X)



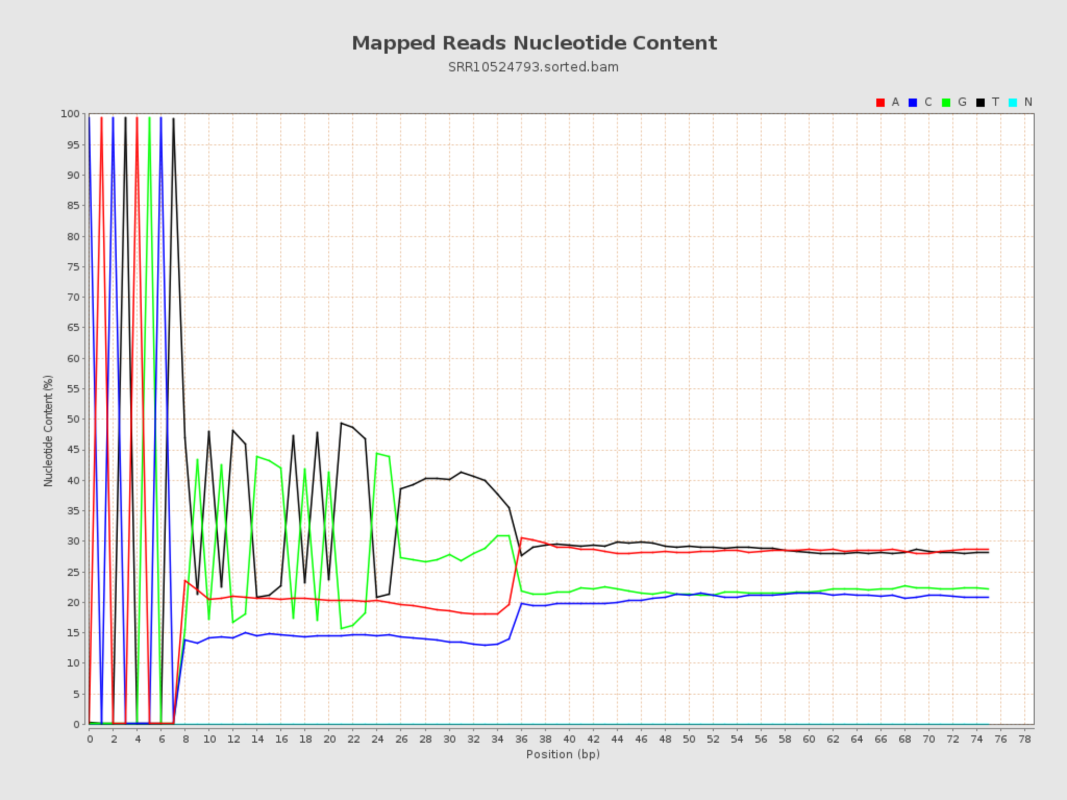
6. Results : Genome Fraction Coverage



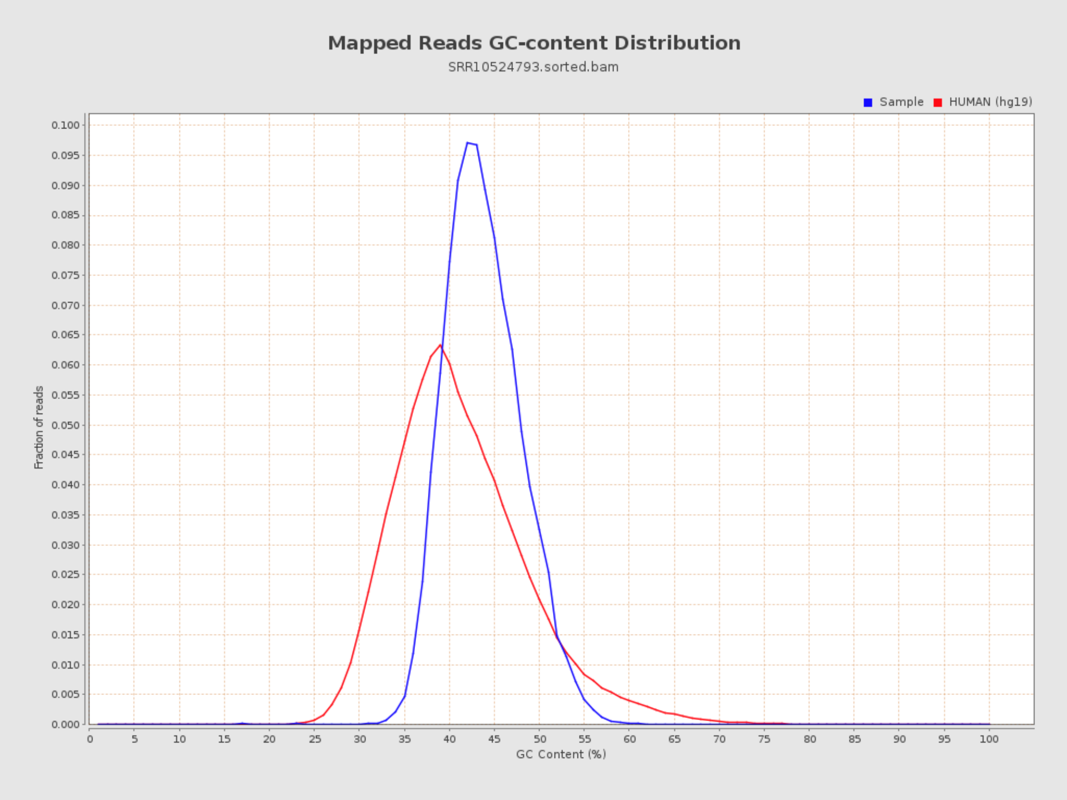
7. Results : Duplication Rate Histogram



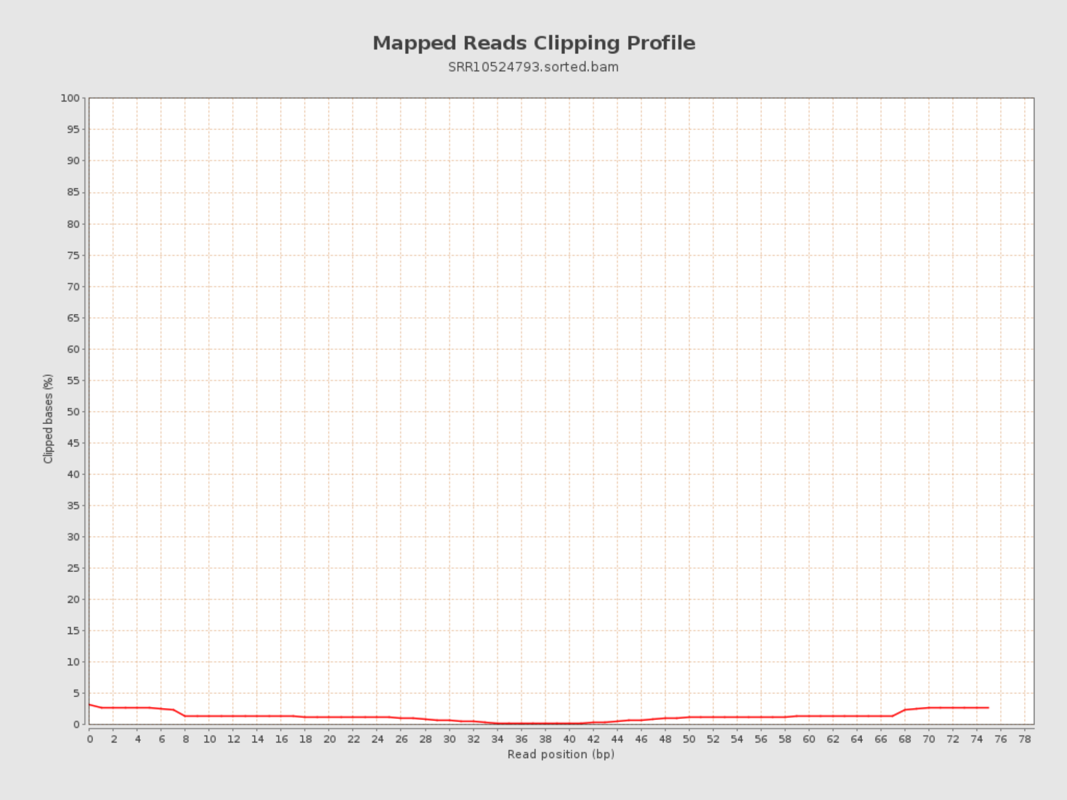
8. Results : Mapped Reads Nucleotide Content



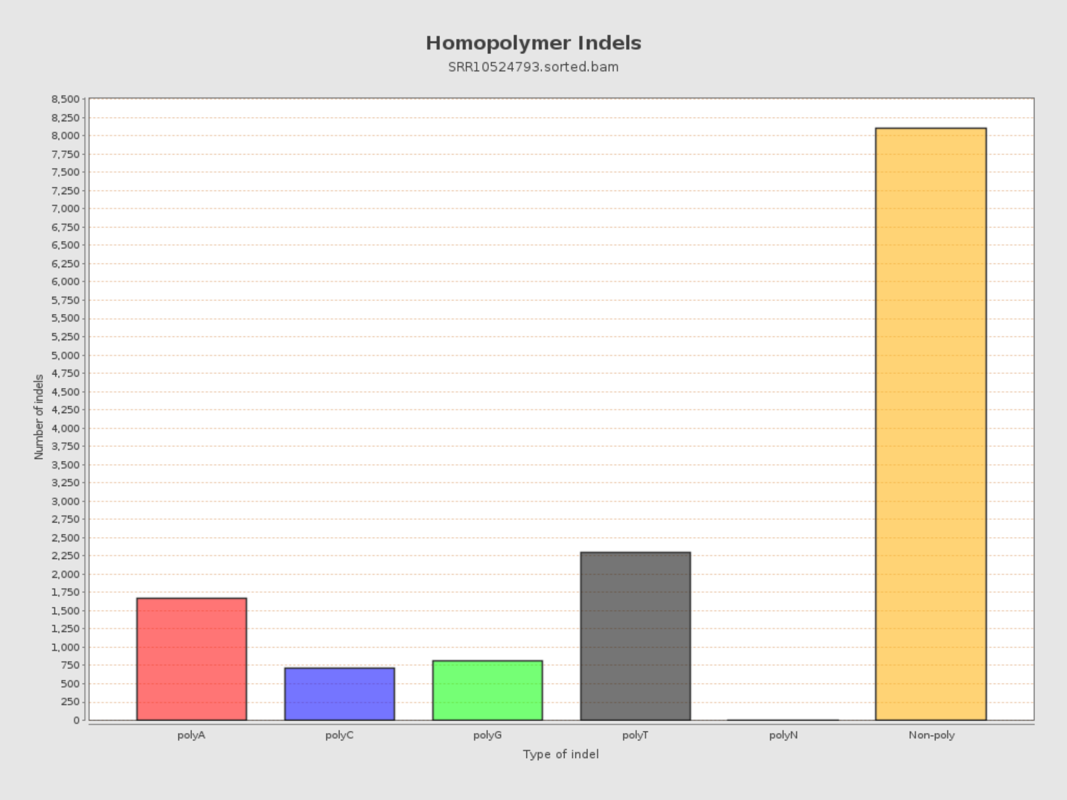
9. Results : Mapped Reads GC-content Distribution



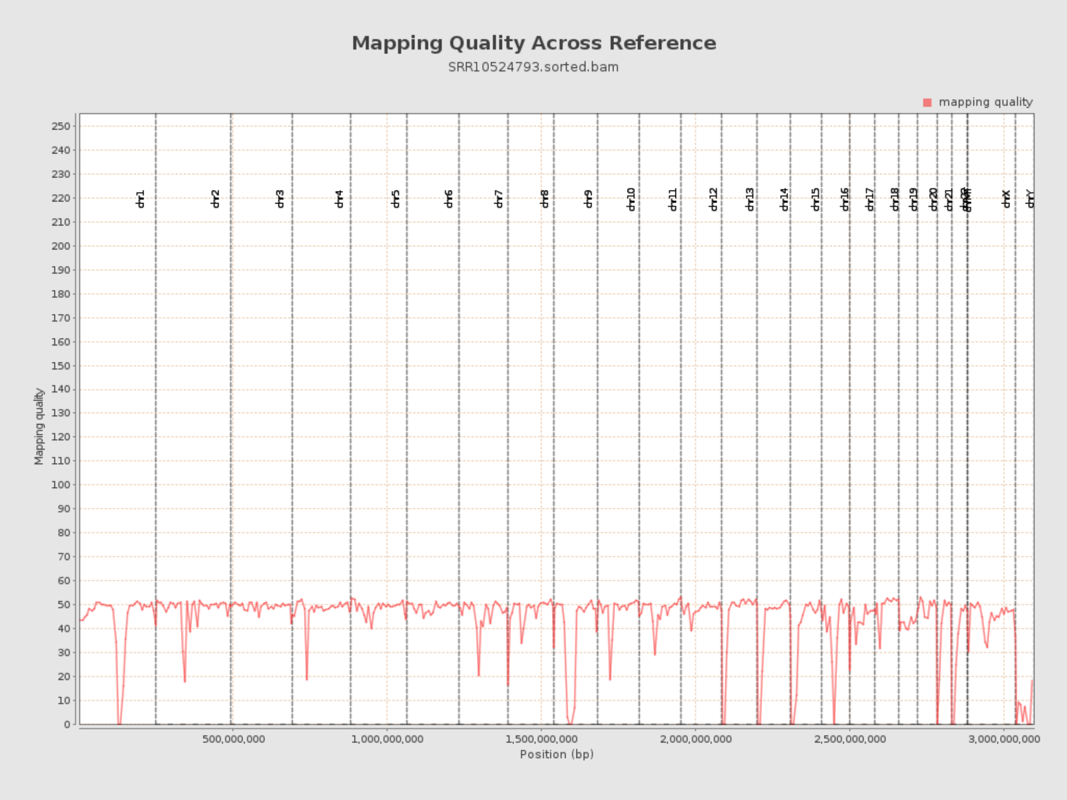
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram