Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:16:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524526.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_SRR10524526 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524526.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:16:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524526.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	838,625
Mapped reads	769,361 / 91.74%
Unmapped reads	69,264 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,193 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	29,220 / 3.48%
Duplication rate	3.02%
Clipped reads	770,162 / 91.84%

2.2. ACGT Content

Number/percentage of A's	11,530,896 / 25.64%
Number/percentage of C's	8,460,181 / 18.81%
Number/percentage of T's	14,446,717 / 32.13%
Number/percentage of G's	10,528,664 / 23.41%
Number/percentage of N's	727 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1667

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

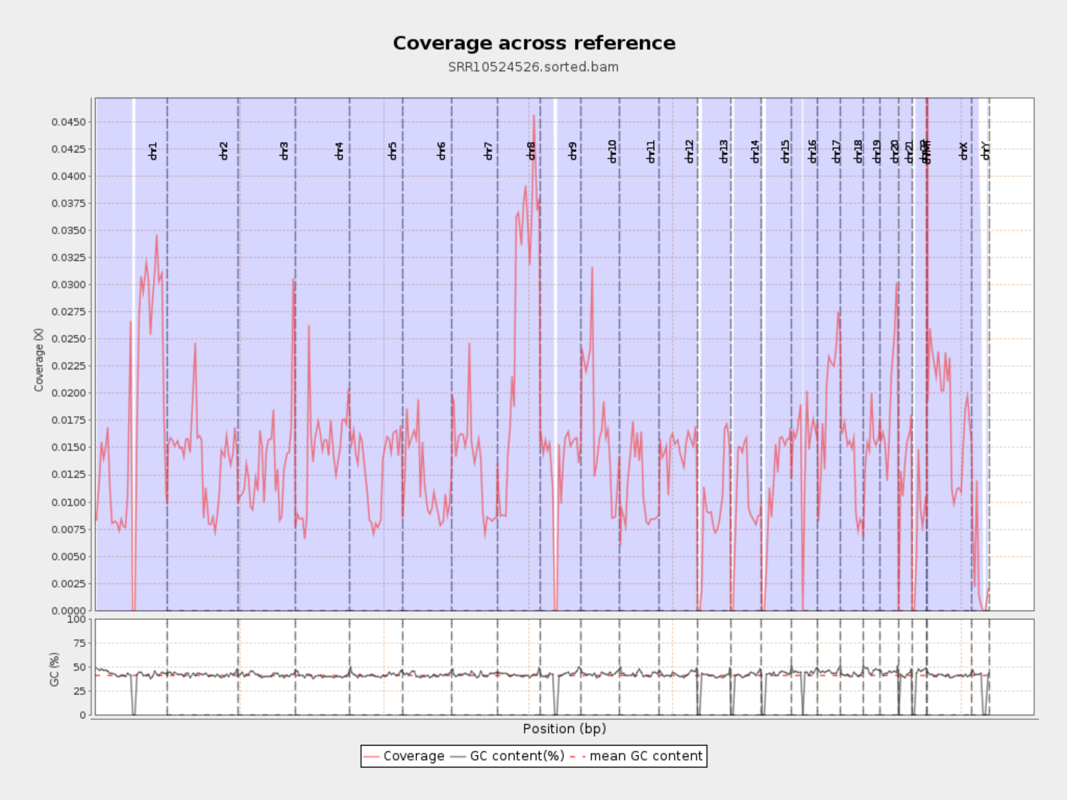
General error rate	0.53%
Mismatches	230,658
Insertions	3,515
Mapped reads with at least one insertion	0.45%
Deletions	8,505
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.36%

2.6. Chromosome stats

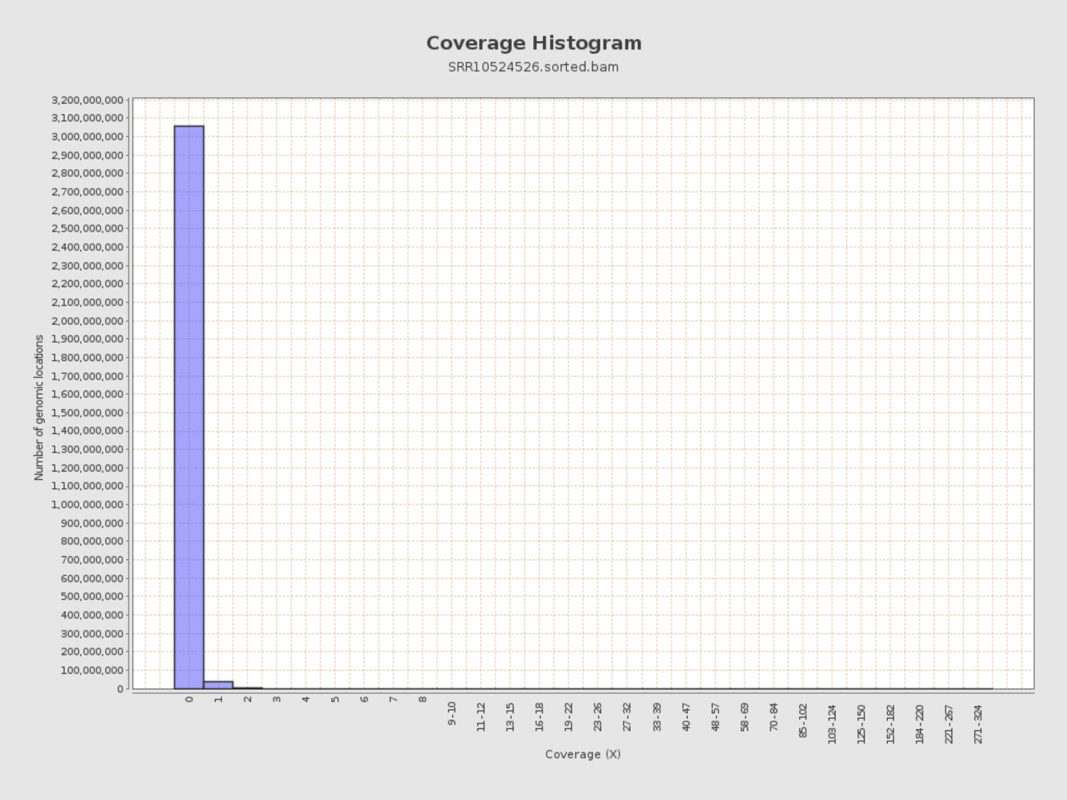
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4363617	0.0175	0.2794
chr2	243199373	3424020	0.0141	0.1909
chr3	198022430	2686648	0.0136	0.1253
chr4	191154276	2761633	0.0144	0.1481
chr5	180915260	2388224	0.0132	0.1233
chr6	171115067	2049605	0.012	0.1308
chr7	159138663	2179891	0.0137	0.1896

chr8	146364022	3968988	0.0271	0.2005
chr9	141213431	1848161	0.0131	0.1382
chr10	135534747	2370897	0.0175	0.1845
chr11	135006516	1502860	0.0111	0.1452
chr12	133851895	2004884	0.015	0.1324
chr13	115169878	1047961	0.0091	0.1024
chr14	107349540	1049756	0.0098	0.1077
chr15	102531392	1149289	0.0112	0.1133
chr16	90354753	1348351	0.0149	0.1352
chr17	81195210	1585987	0.0195	0.1537
chr18	78077248	1028355	0.0132	0.2208
chr19	59128983	912691	0.0154	0.1972
chr20	63025520	1236448	0.0196	0.1522
chr21	48129895	622021	0.0129	0.1332
chr22	51304566	382166	0.0074	0.0934
chrMT	16571	10631	0.6415	0.8726
chrX	155270560	2878171	0.0185	0.1524
chrY	59373566	180197	0.003	0.1125

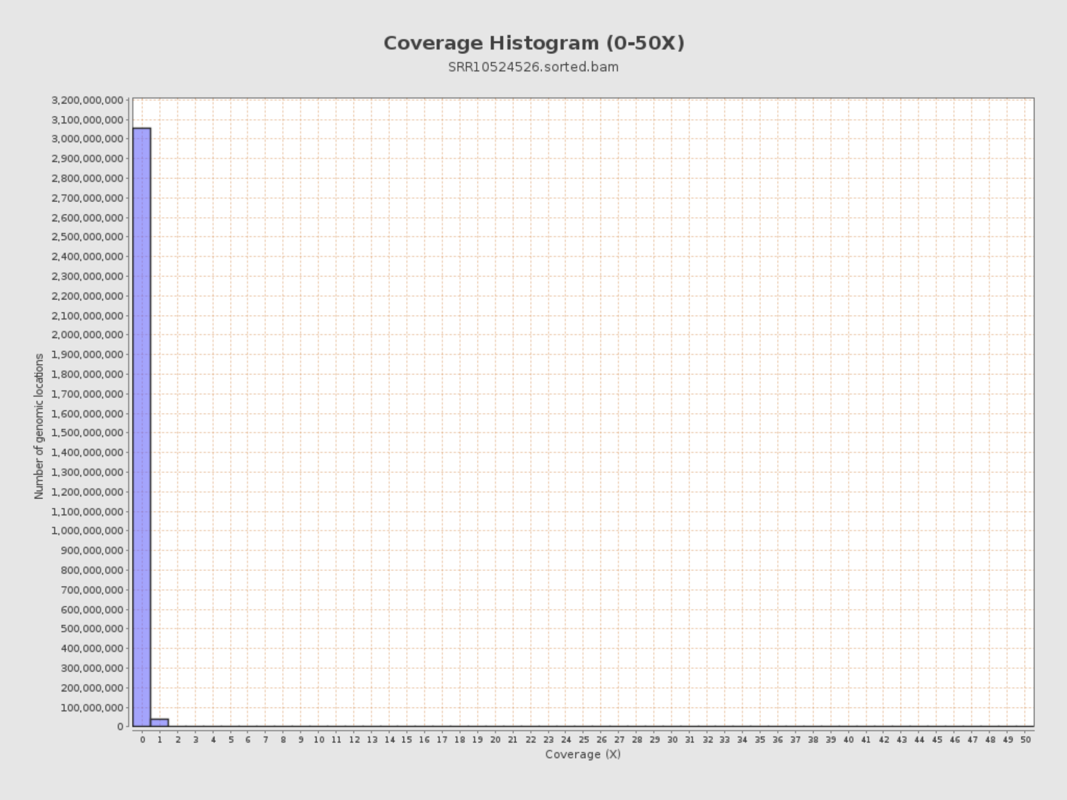
3. Results : Coverage across reference



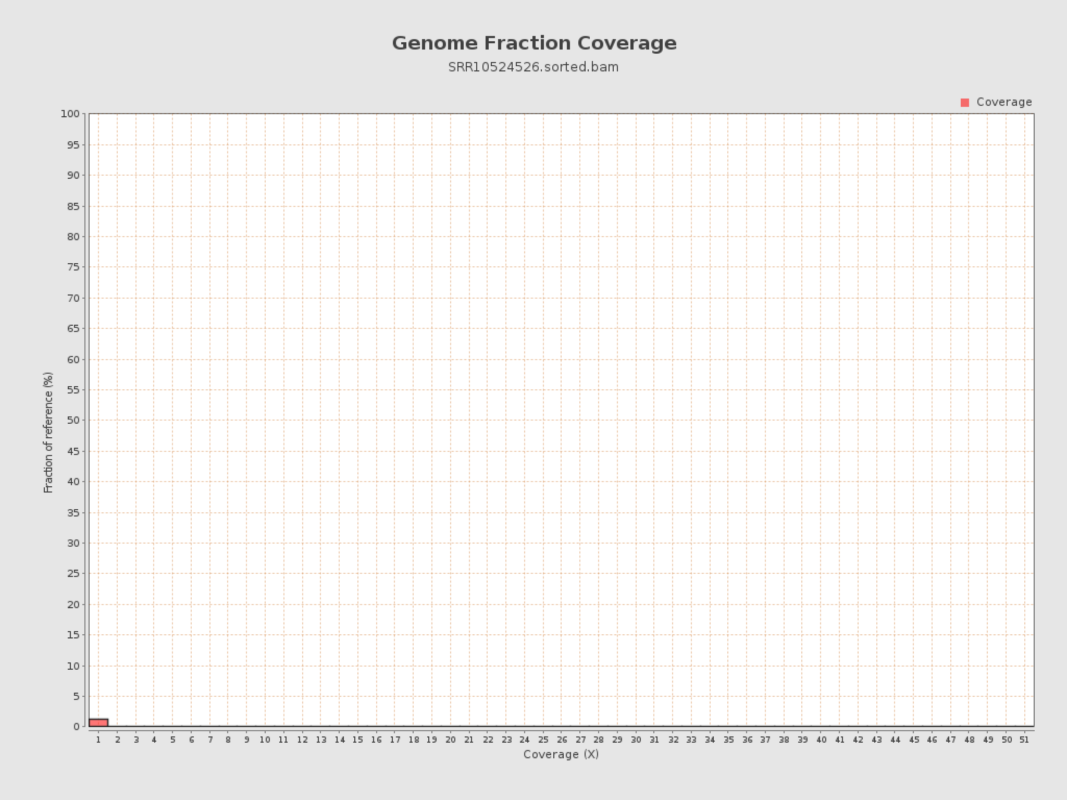
4. Results : Coverage Histogram



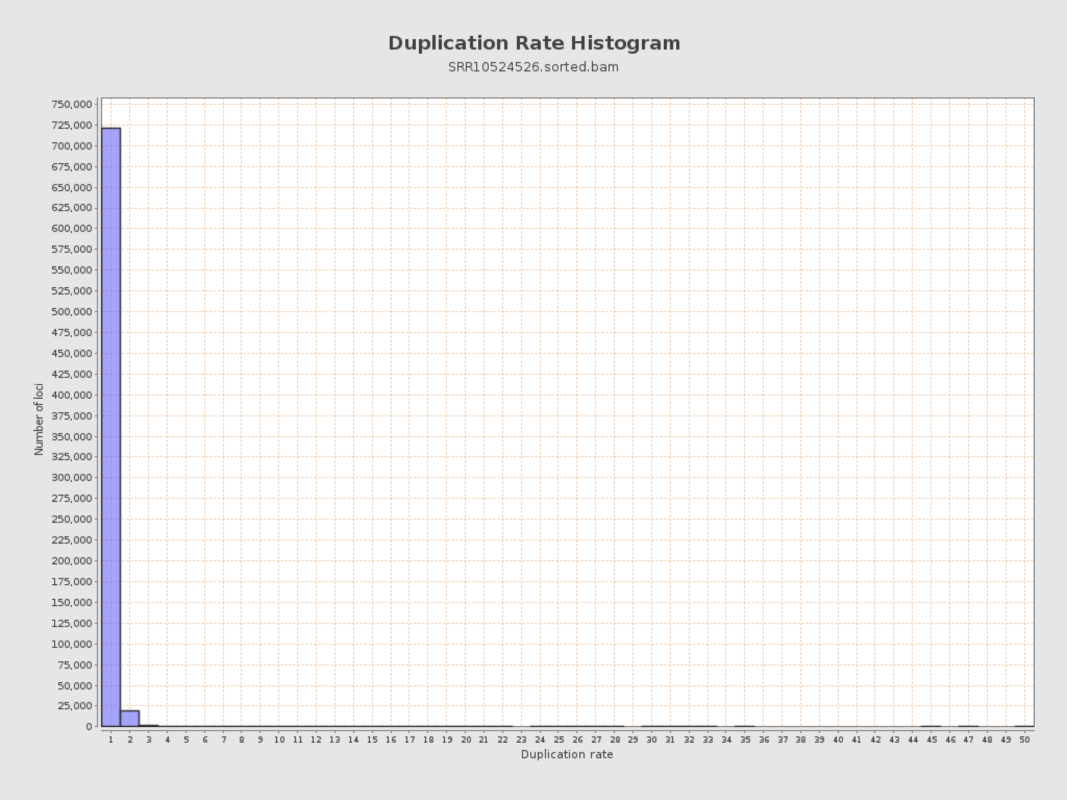
5. Results : Coverage Histogram (0-50X)



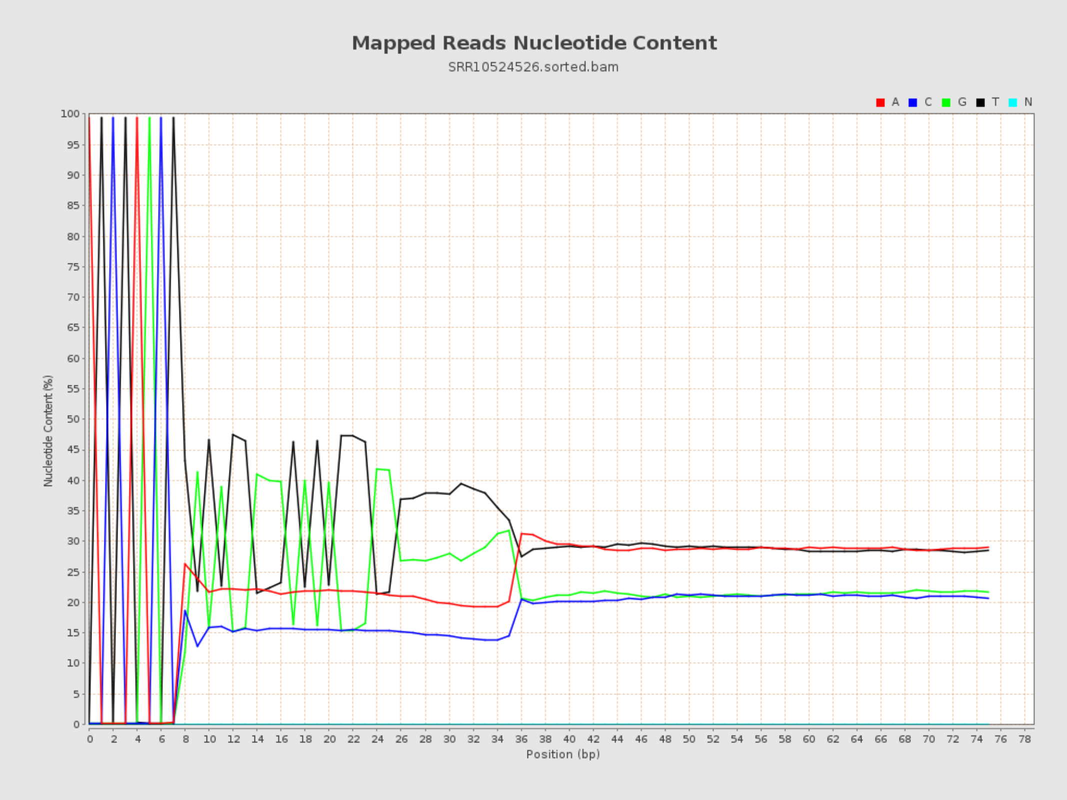
6. Results : Genome Fraction Coverage



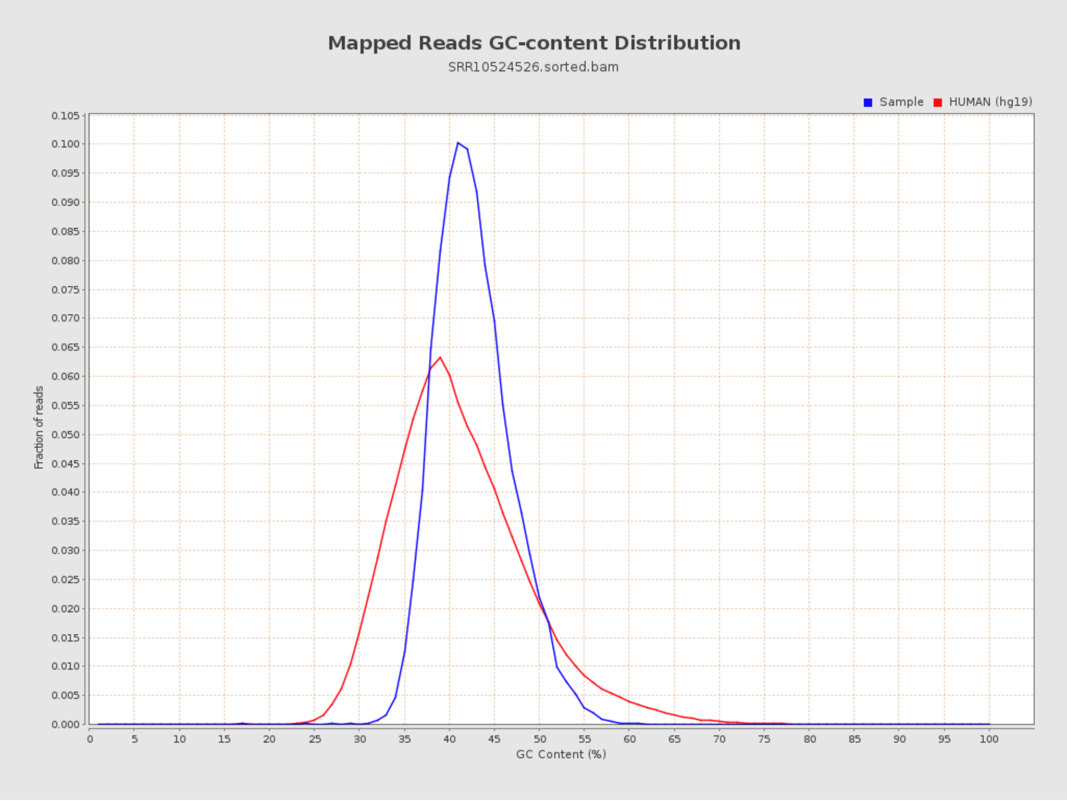
7. Results : Duplication Rate Histogram



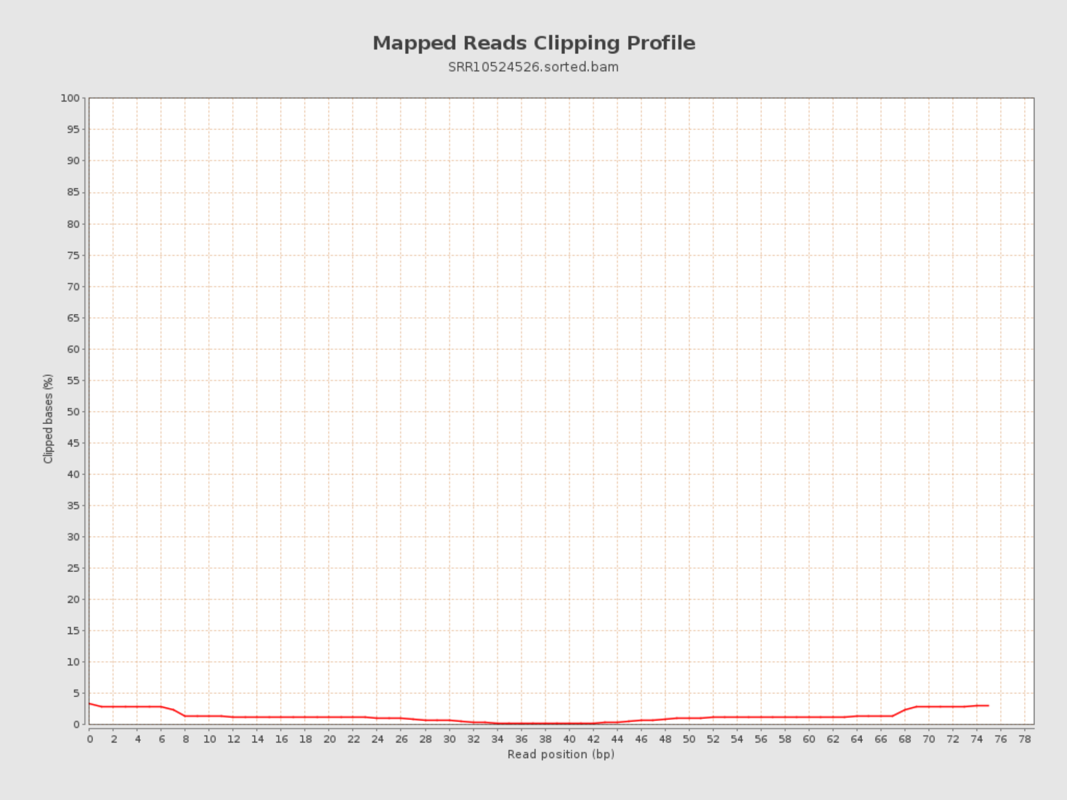
8. Results : Mapped Reads Nucleotide Content



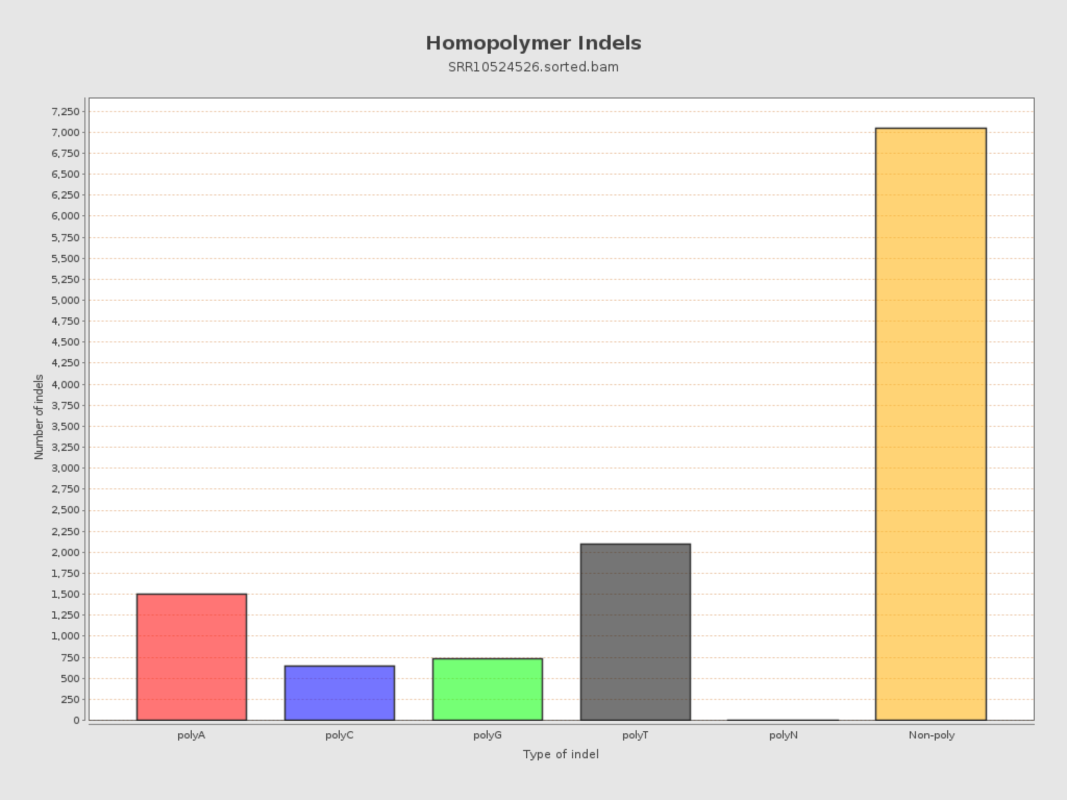
9. Results : Mapped Reads GC-content Distribution



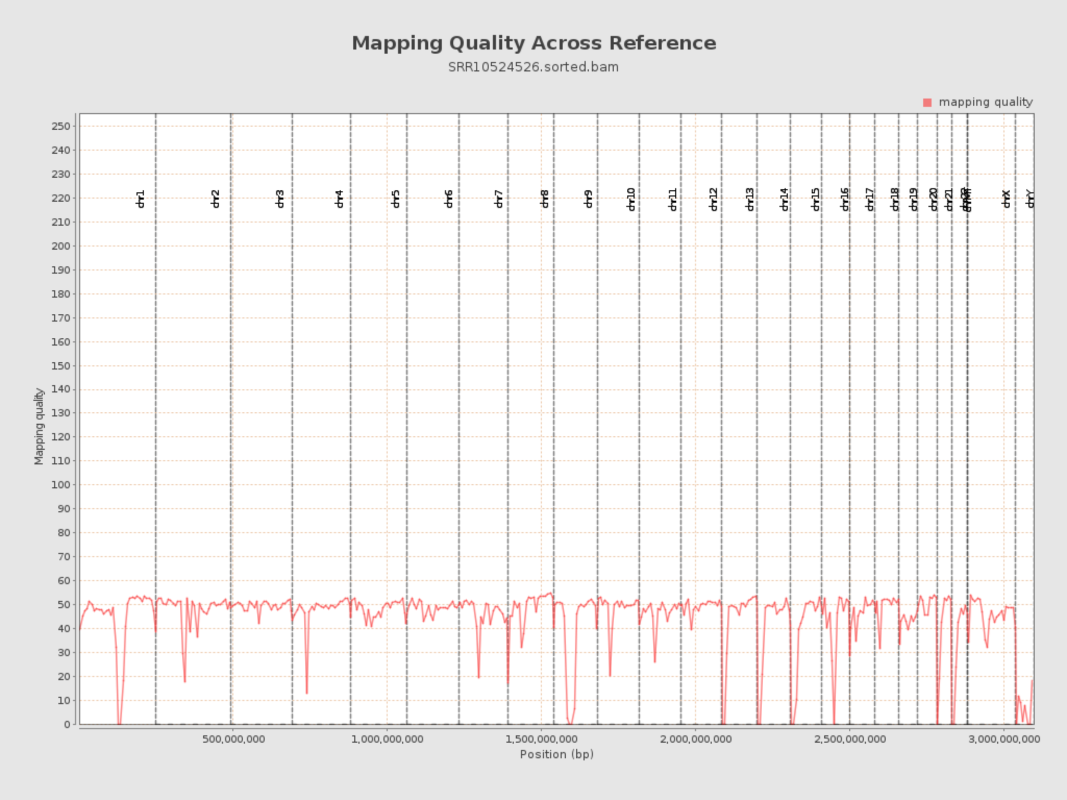
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram