Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:08:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525031.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_SRR10525031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525031.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:08:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	918,281
Mapped reads	843,620 / 91.87%
Unmapped reads	74,661 / 8.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,257 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	23,167 / 2.52%
Duplication rate	2.06%
Clipped reads	844,522 / 91.97%

2.2. ACGT Content

Number/percentage of A's	12,511,300 / 25.6%
Number/percentage of C's	9,025,054 / 18.47%
Number/percentage of T's	15,825,801 / 32.38%
Number/percentage of G's	11,510,495 / 23.55%
Number/percentage of N's	521 / 0%
GC Percentage	42.02%

2.3. Coverage

Mean	0.0158

Standard Deviation	0.1687

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

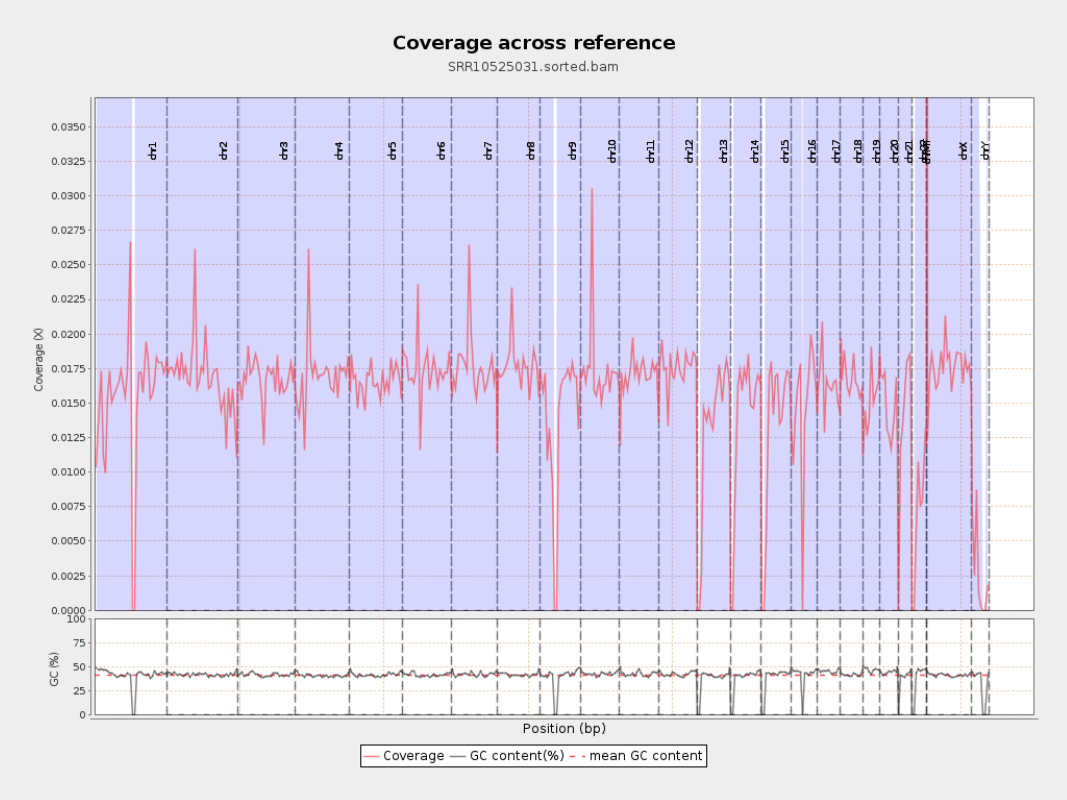
General error rate	0.51%
Mismatches	240,797
Insertions	3,171
Mapped reads with at least one insertion	0.37%
Deletions	9,311
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.85%

2.6. Chromosome stats

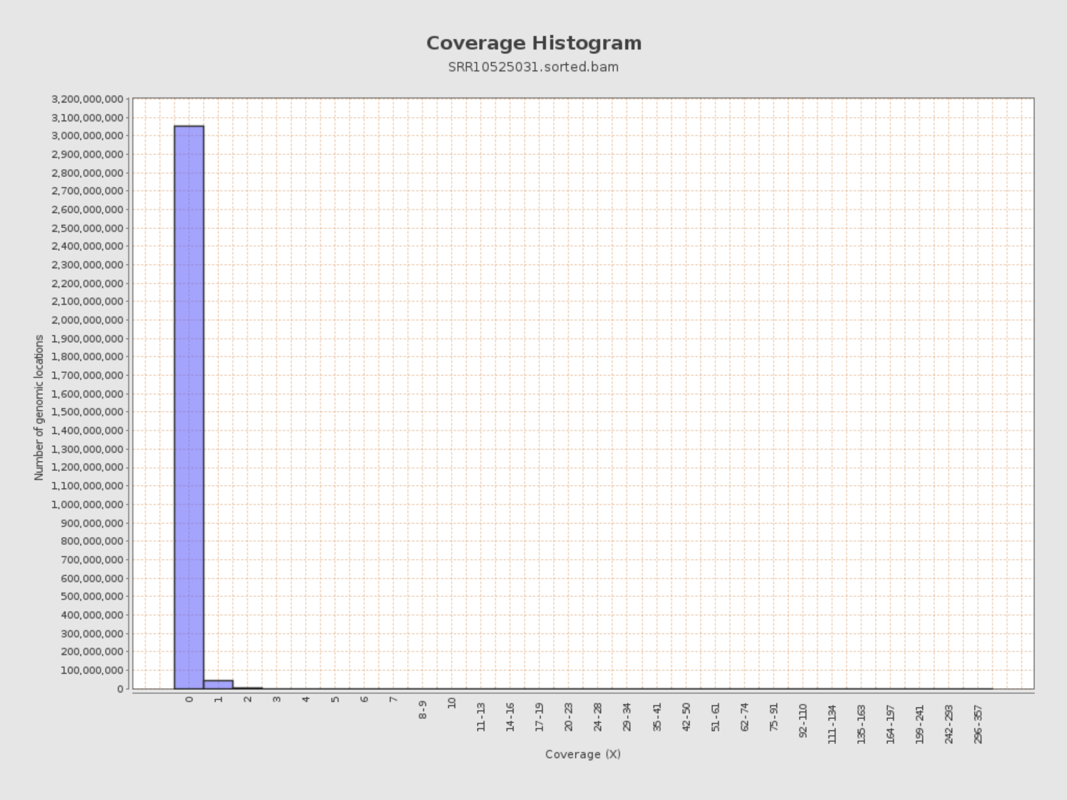
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3831224	0.0154	0.2804
chr2	243199373	4095409	0.0168	0.1906
chr3	198022430	3316102	0.0167	0.1365
chr4	191154276	3252776	0.017	0.1491
chr5	180915260	3011681	0.0166	0.1365
chr6	171115067	2977221	0.0174	0.1564
chr7	159138663	2818894	0.0177	0.1969

chr8	146364022	2593005	0.0177	0.1772
chr9	141213431	1941775	0.0138	0.1416
chr10	135534747	2369811	0.0175	0.1791
chr11	135006516	2316210	0.0172	0.1639
chr12	133851895	2355331	0.0176	0.1411
chr13	115169878	1494015	0.013	0.1203
chr14	107349540	1480326	0.0138	0.1278
chr15	102531392	1333511	0.013	0.1233
chr16	90354753	1300099	0.0144	0.1324
chr17	81195210	1327980	0.0164	0.143
chr18	78077248	1312212	0.0168	0.2118
chr19	59128983	901726	0.0153	0.1898
chr20	63025520	926316	0.0147	0.1307
chr21	48129895	672634	0.014	0.1329
chr22	51304566	372449	0.0073	0.0897
chrMT	16571	9664	0.5832	0.8831
chrX	155270560	2729099	0.0176	0.1467
chrY	59373566	149149	0.0025	0.082

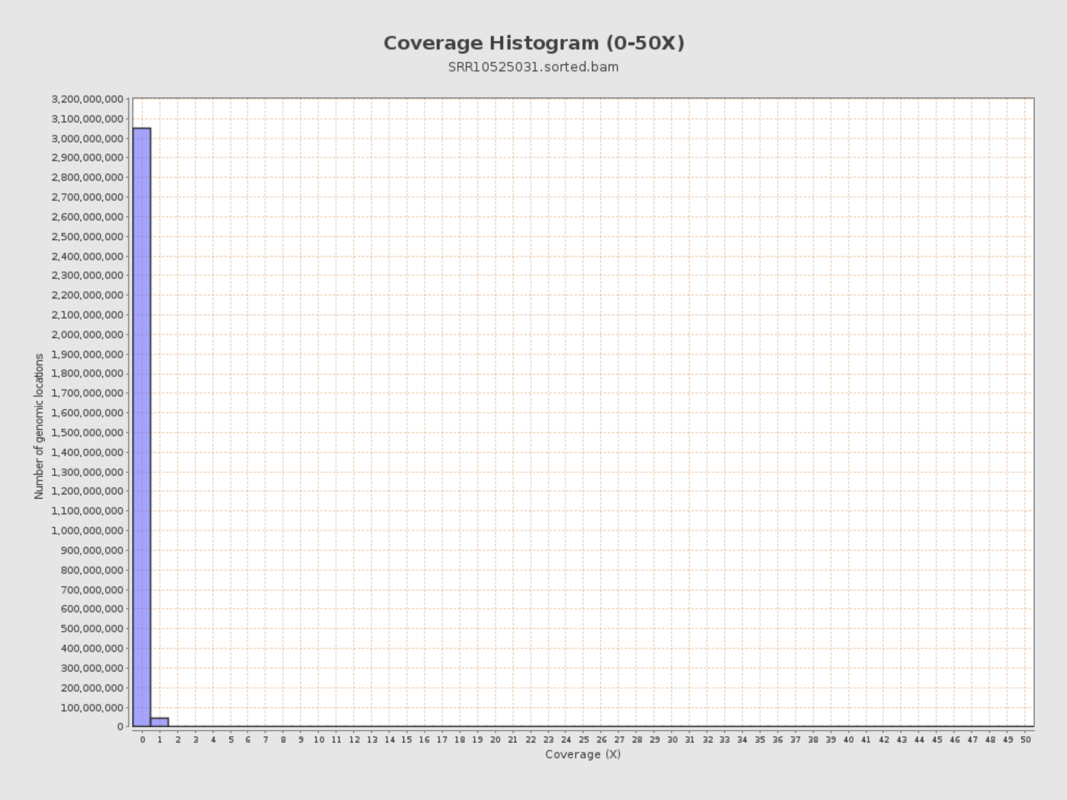
3. Results : Coverage across reference



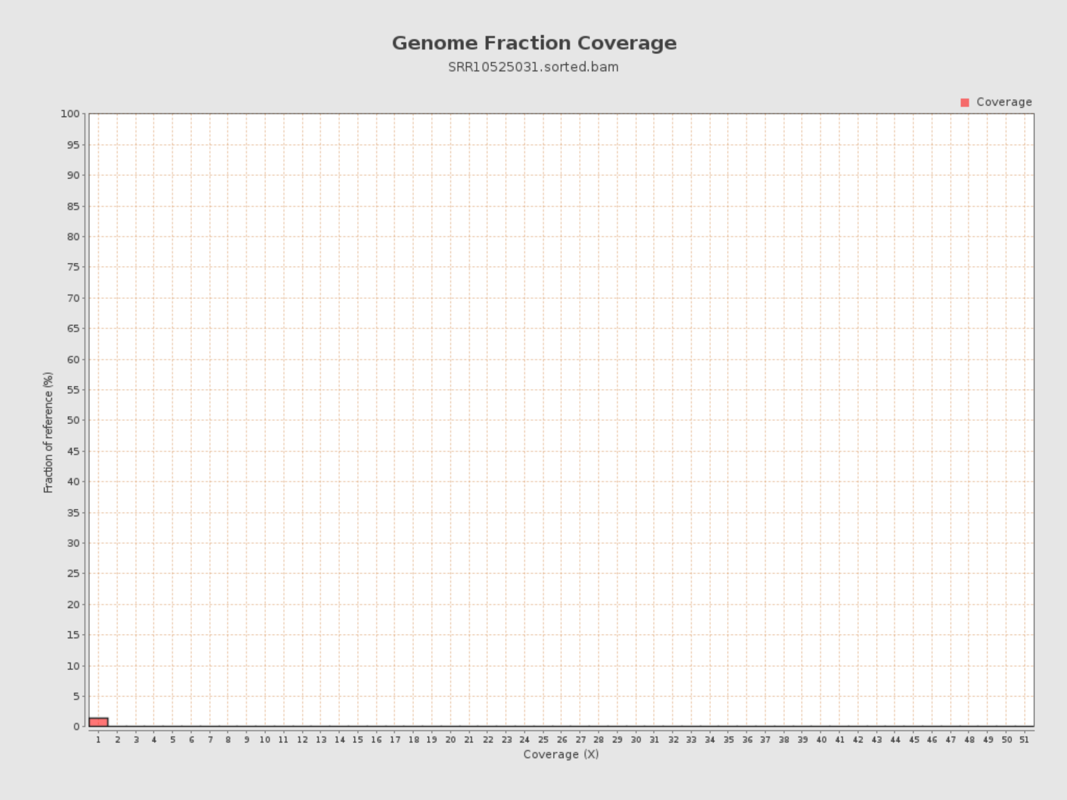
4. Results : Coverage Histogram



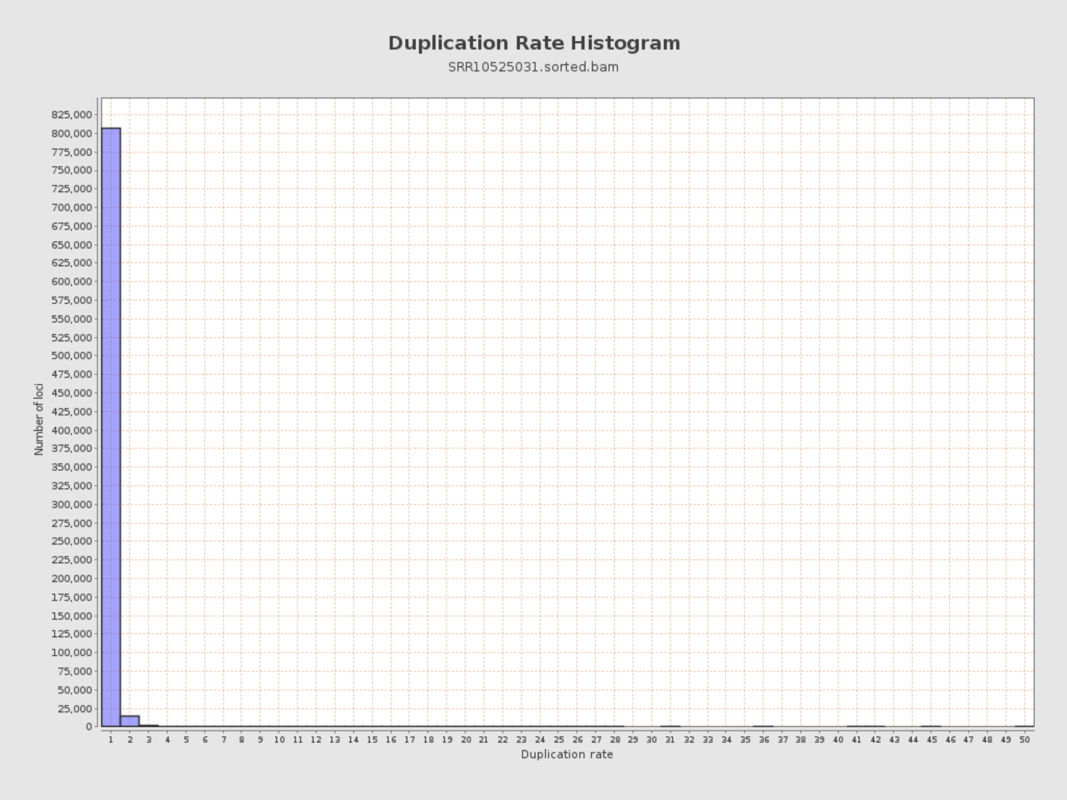
5. Results : Coverage Histogram (0-50X)



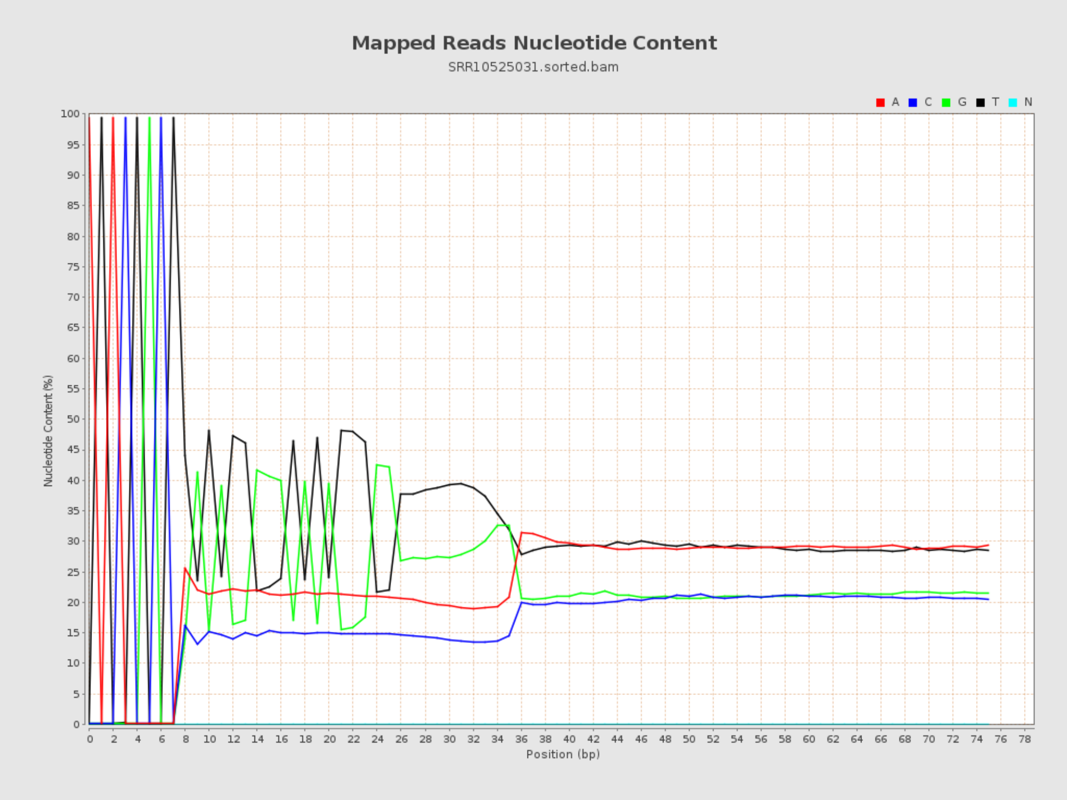
6. Results : Genome Fraction Coverage



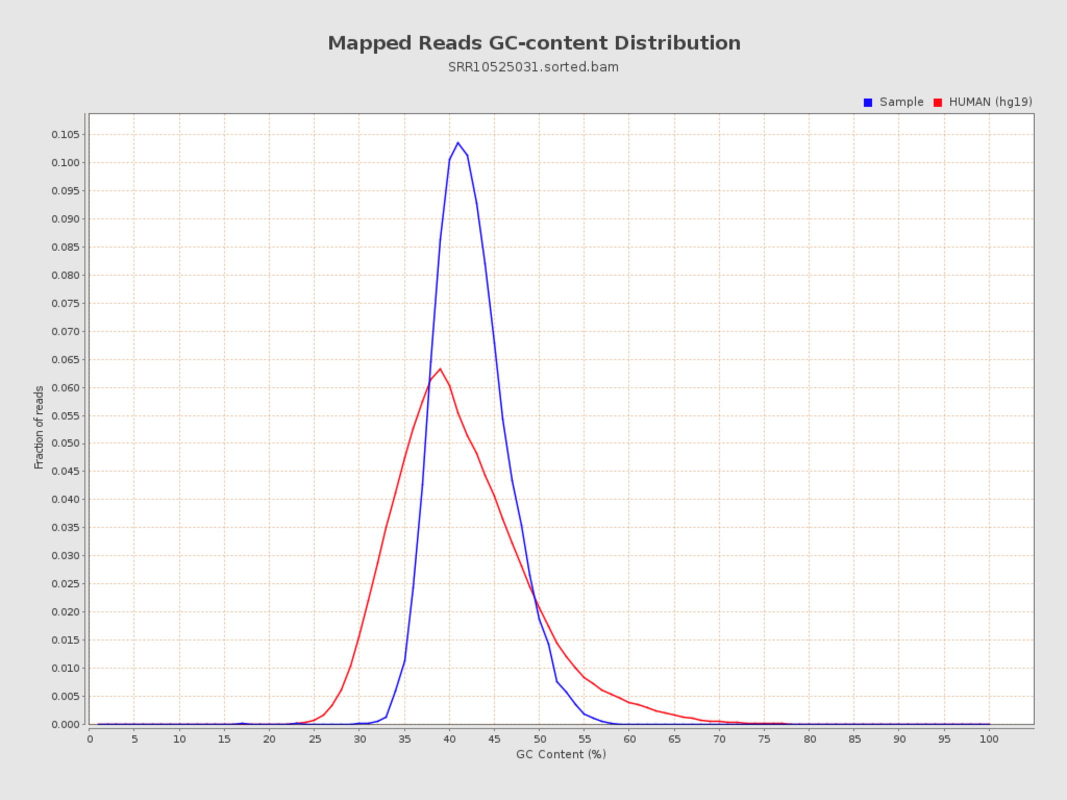
7. Results : Duplication Rate Histogram



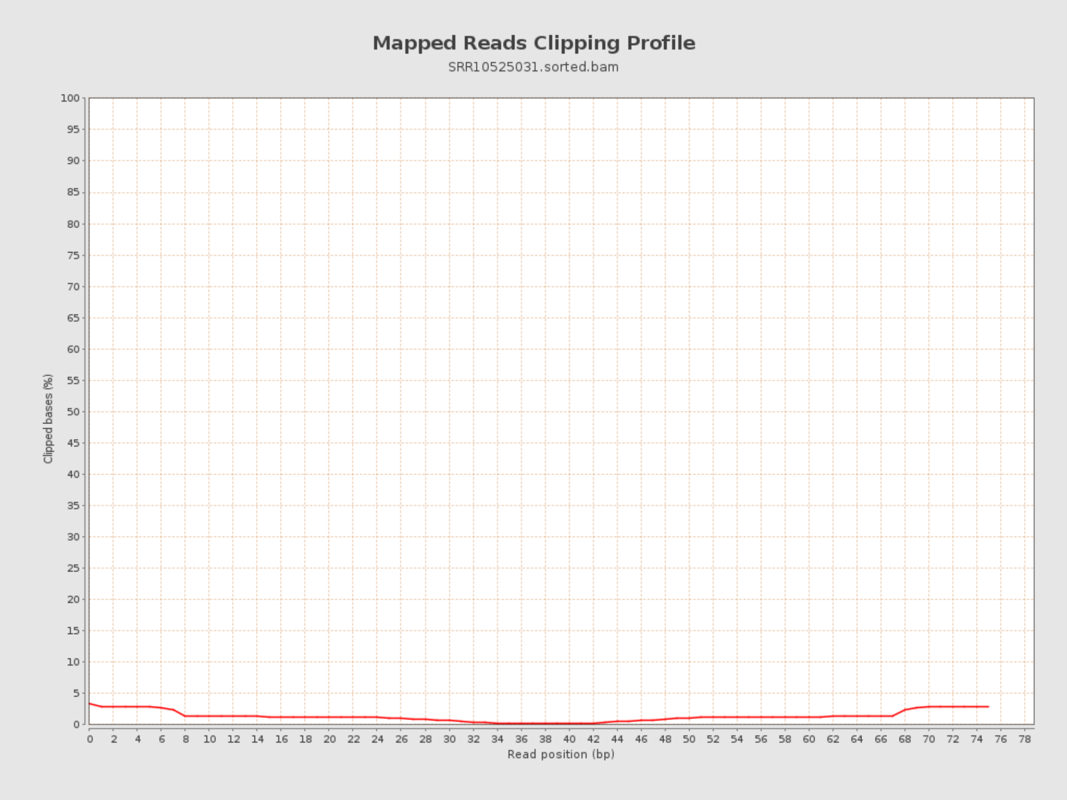
8. Results : Mapped Reads Nucleotide Content



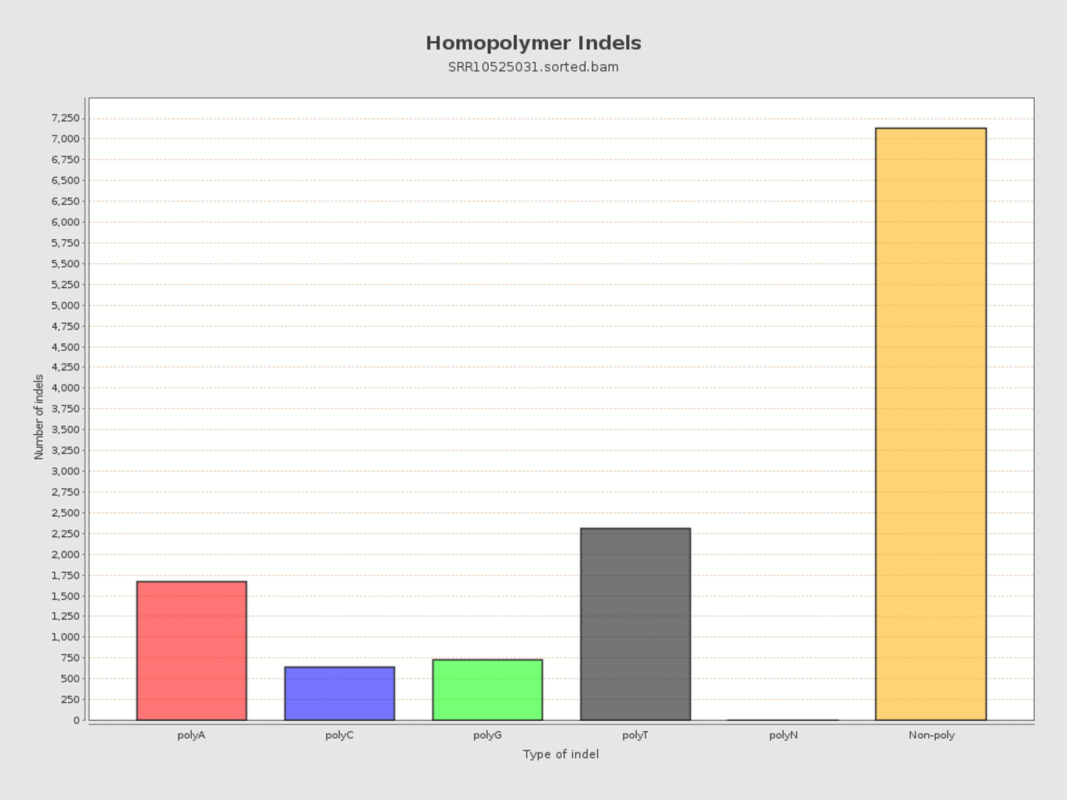
9. Results : Mapped Reads GC-content Distribution



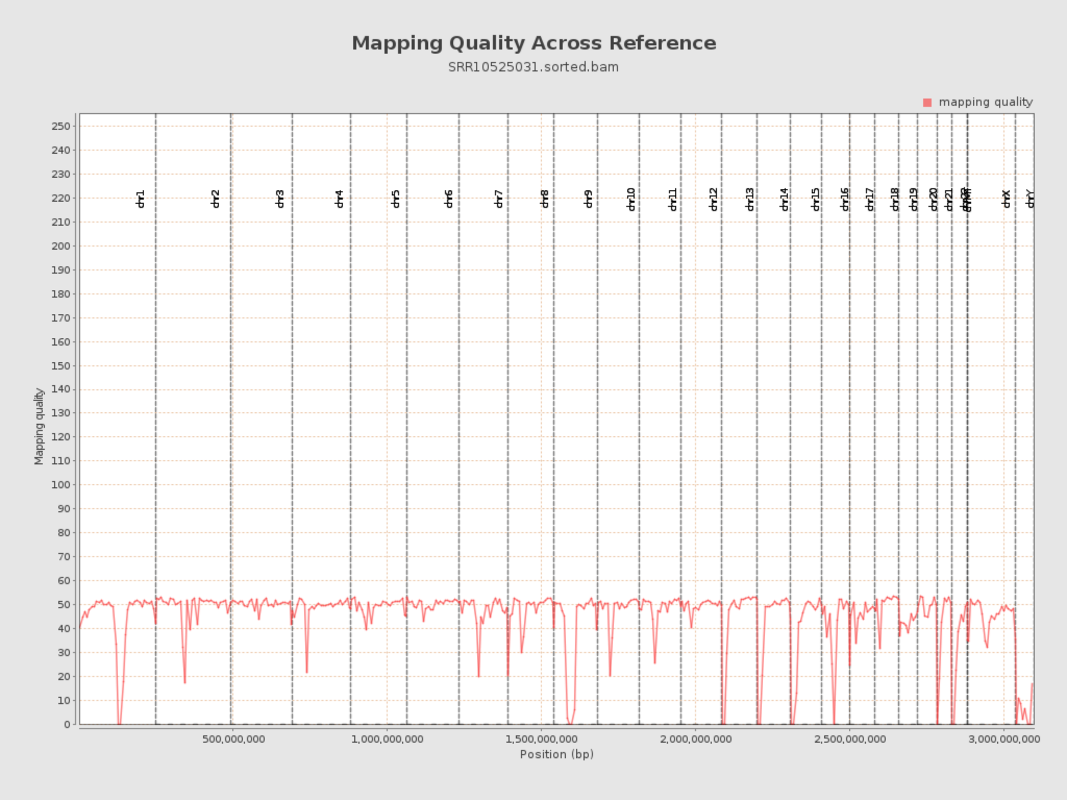
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram