Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:48:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524961.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_SRR10524961 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524961.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:48:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,366,105
Mapped reads	1,269,723 / 92.94%
Unmapped reads	96,382 / 7.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,072 / 0.22%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	36,058 / 2.64%
Duplication rate	2.01%
Clipped reads	1,270,277 / 92.99%

2.2. ACGT Content

Number/percentage of A's	18,567,833 / 25.04%
Number/percentage of C's	13,098,650 / 17.67%
Number/percentage of T's	23,086,496 / 31.14%
Number/percentage of G's	19,391,019 / 26.15%
Number/percentage of N's	764 / 0%
GC Percentage	43.82%

2.3. Coverage

Mean	0.024

Standard Deviation	0.2326

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

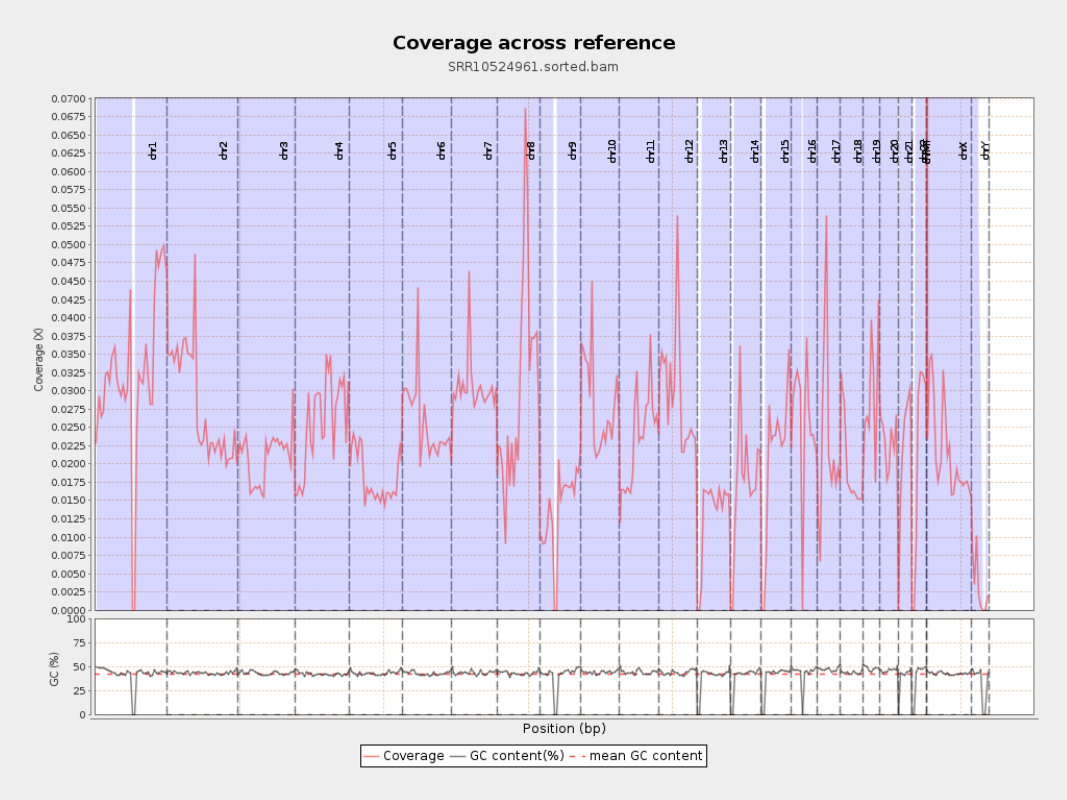
General error rate	0.49%
Mismatches	353,066
Insertions	4,639
Mapped reads with at least one insertion	0.36%
Deletions	14,167
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.96%

2.6. Chromosome stats

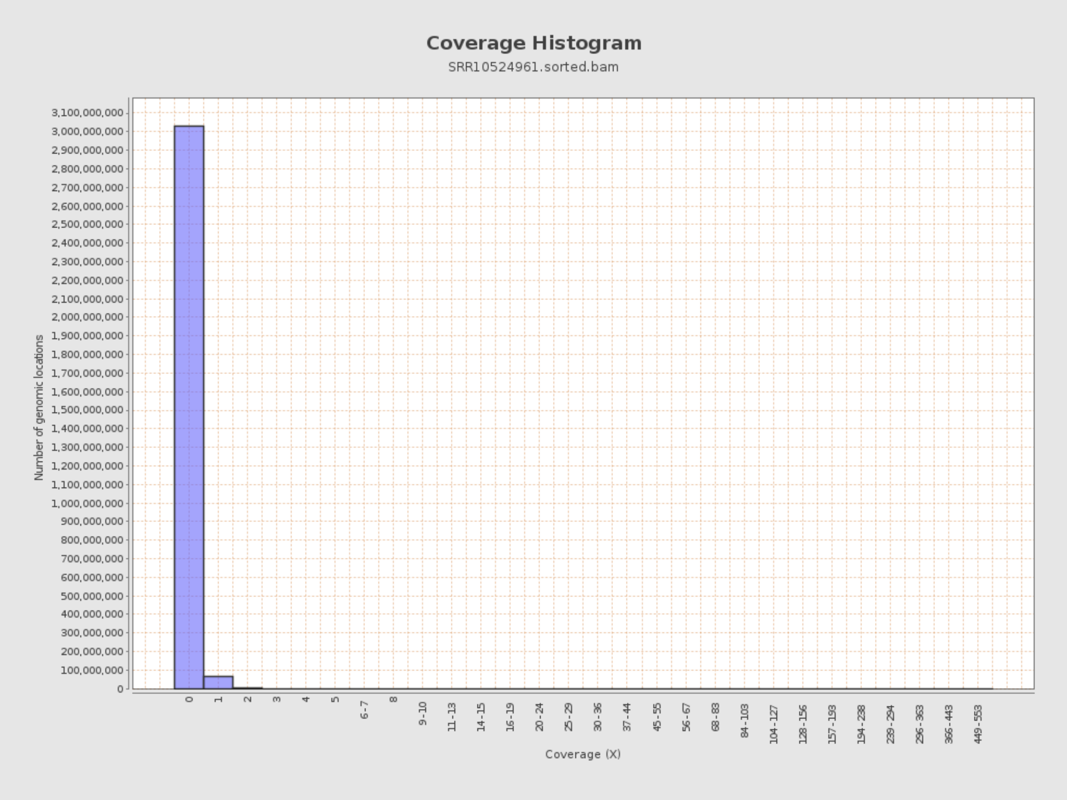
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8014951	0.0322	0.4386
chr2	243199373	6819007	0.028	0.2571
chr3	198022430	4168775	0.0211	0.1548
chr4	191154276	4947655	0.0259	0.1822
chr5	180915260	3275862	0.0181	0.146
chr6	171115067	4407031	0.0258	0.2378
chr7	159138663	4857605	0.0305	0.3149

chr8	146364022	4496859	0.0307	0.2333
chr9	141213431	1904122	0.0135	0.1708
chr10	135534747	3856945	0.0285	0.2293
chr11	135006516	3189902	0.0236	0.2101
chr12	133851895	3961781	0.0296	0.185
chr13	115169878	1498021	0.013	0.125
chr14	107349540	1877225	0.0175	0.144
chr15	102531392	2164787	0.0211	0.1634
chr16	90354753	2322694	0.0257	0.1776
chr17	81195210	1897298	0.0234	0.2018
chr18	78077248	1522997	0.0195	0.2735
chr19	59128983	1741315	0.0294	0.2796
chr20	63025520	1433067	0.0227	0.1617
chr21	48129895	1066652	0.0222	0.165
chr22	51304566	1090408	0.0213	0.155
chrMT	16571	65997	3.9827	3.0764
chrX	155270560	3401589	0.0219	0.1769
chrY	59373566	186084	0.0031	0.0797

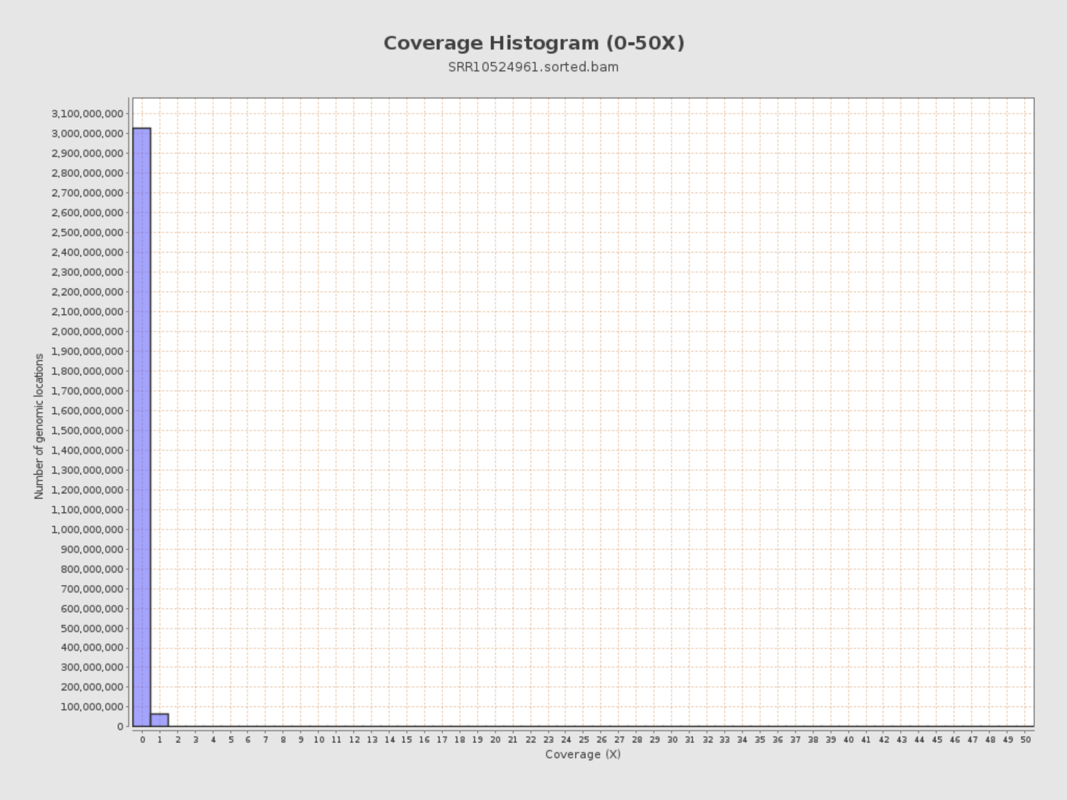
3. Results : Coverage across reference



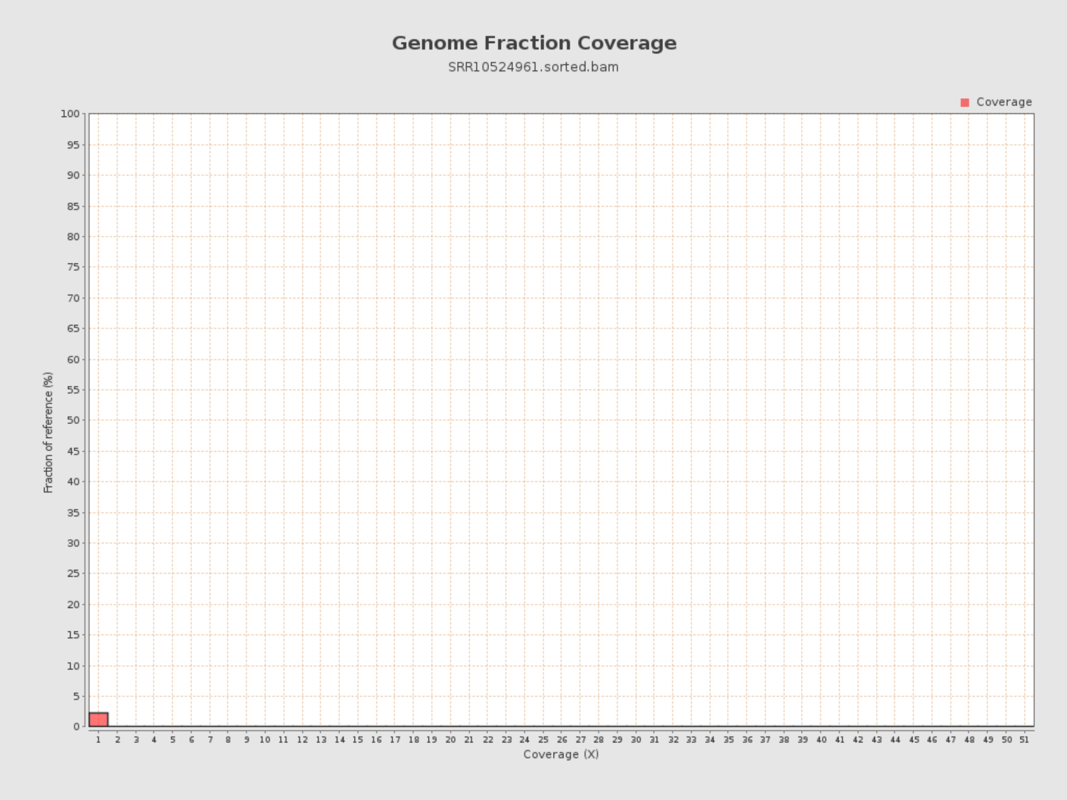
4. Results : Coverage Histogram



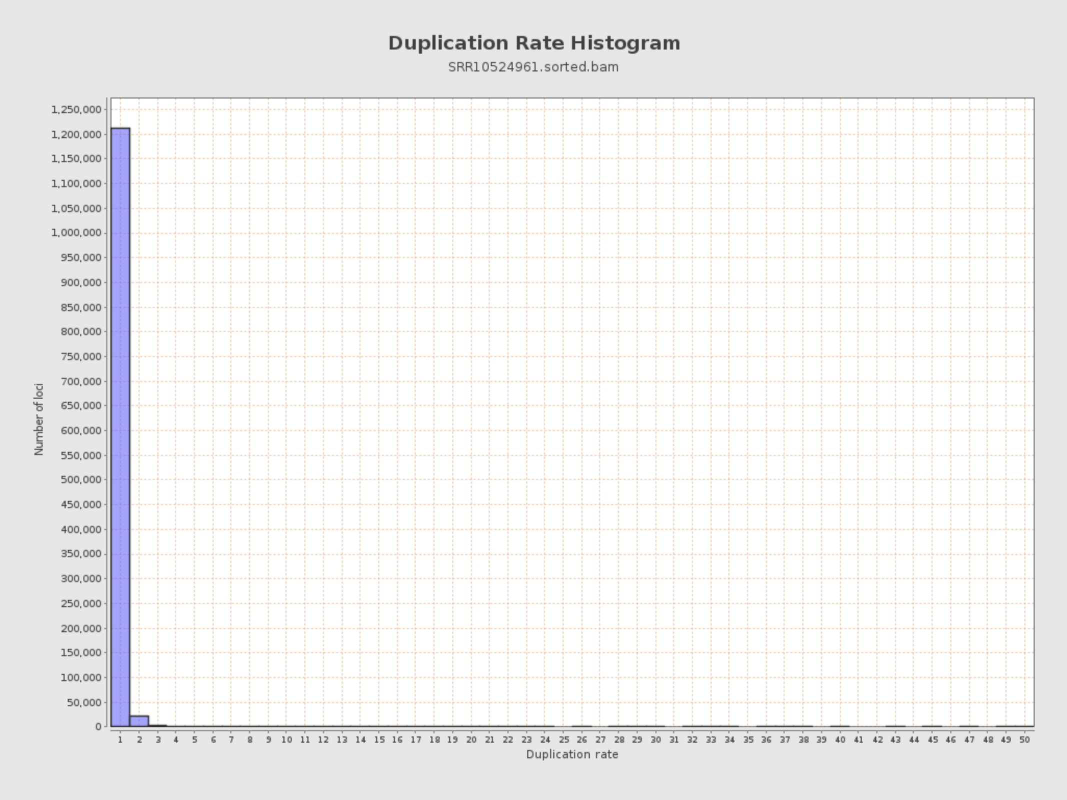
5. Results : Coverage Histogram (0-50X)



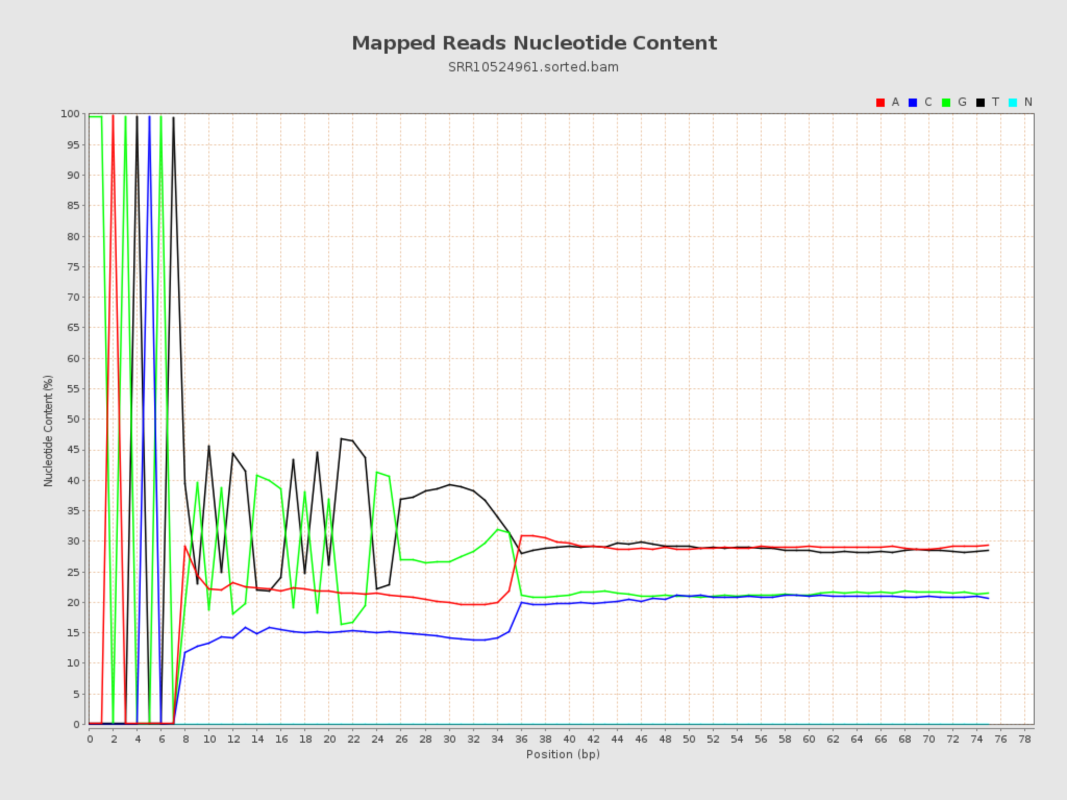
6. Results : Genome Fraction Coverage



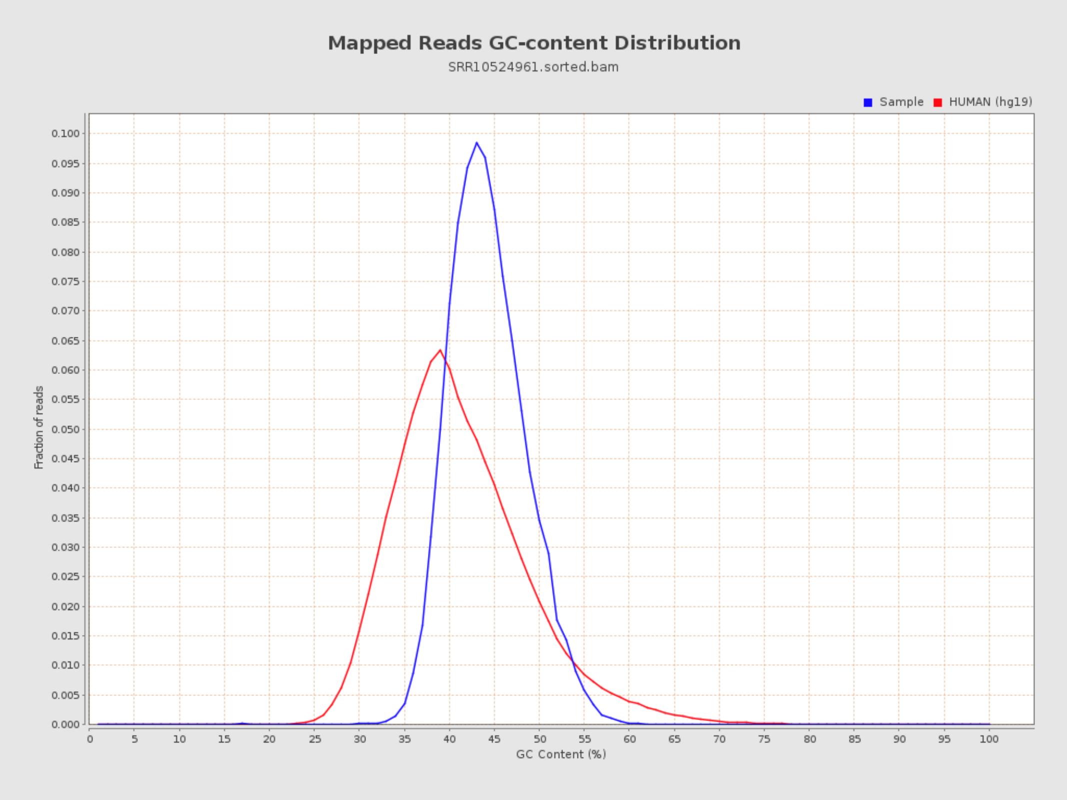
7. Results : Duplication Rate Histogram



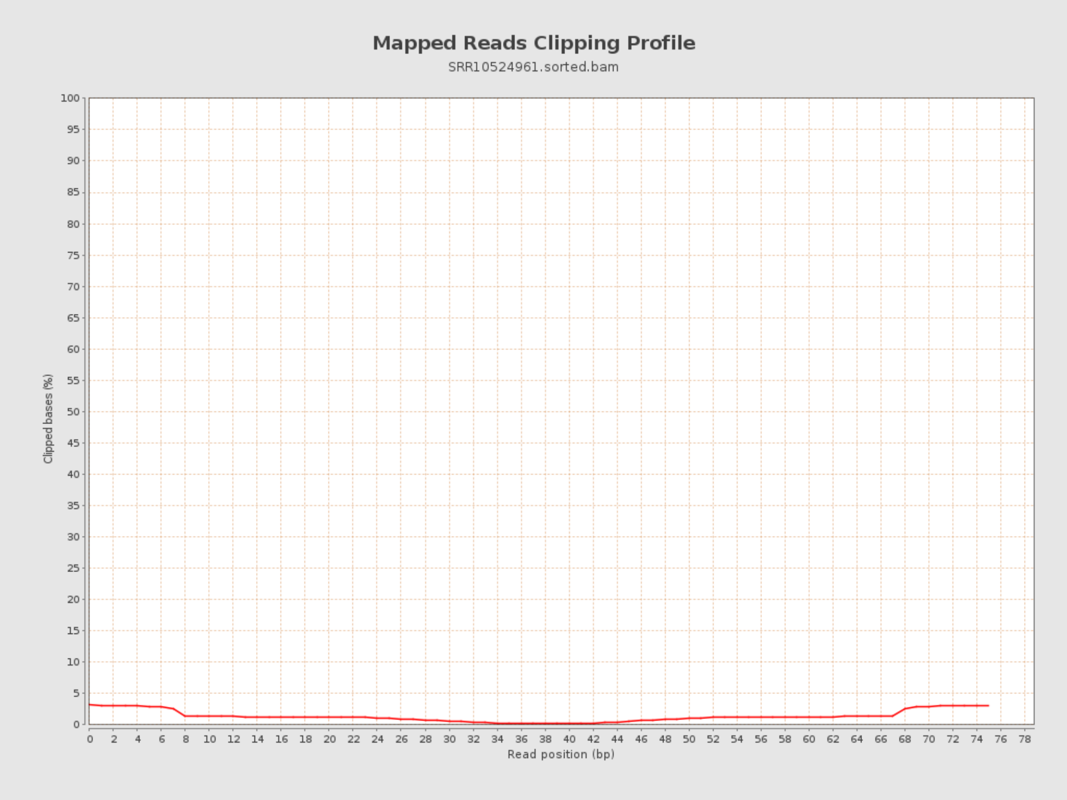
8. Results : Mapped Reads Nucleotide Content



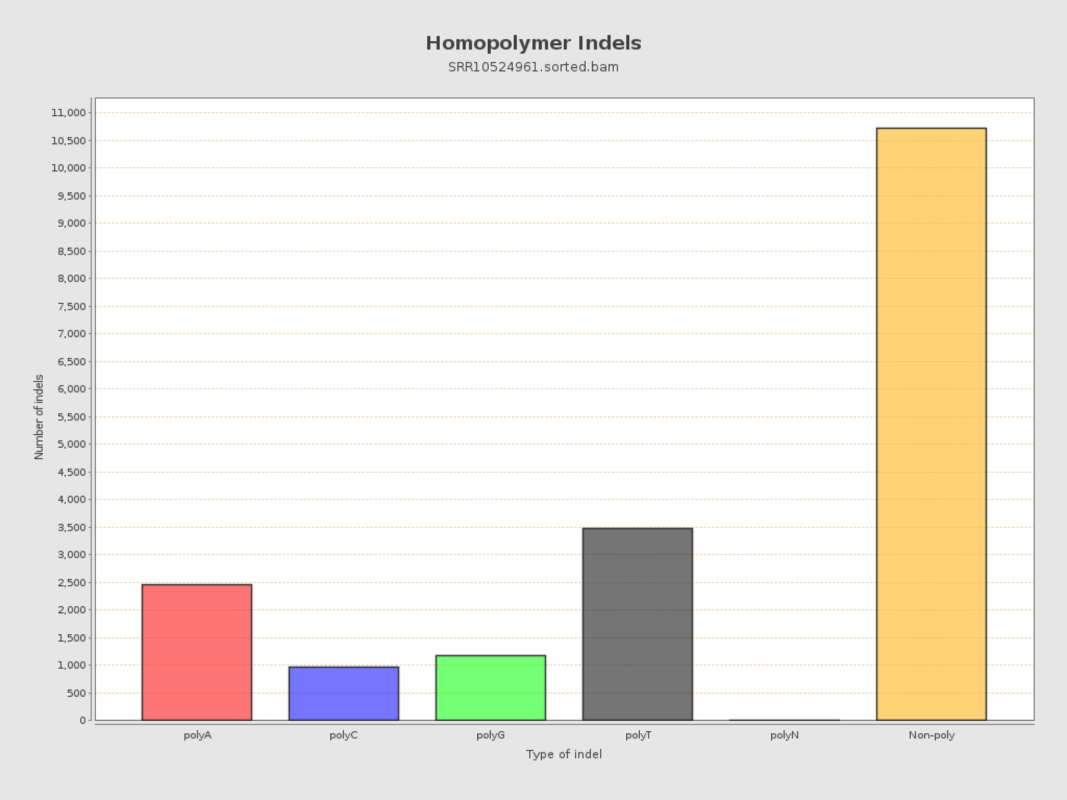
9. Results : Mapped Reads GC-content Distribution



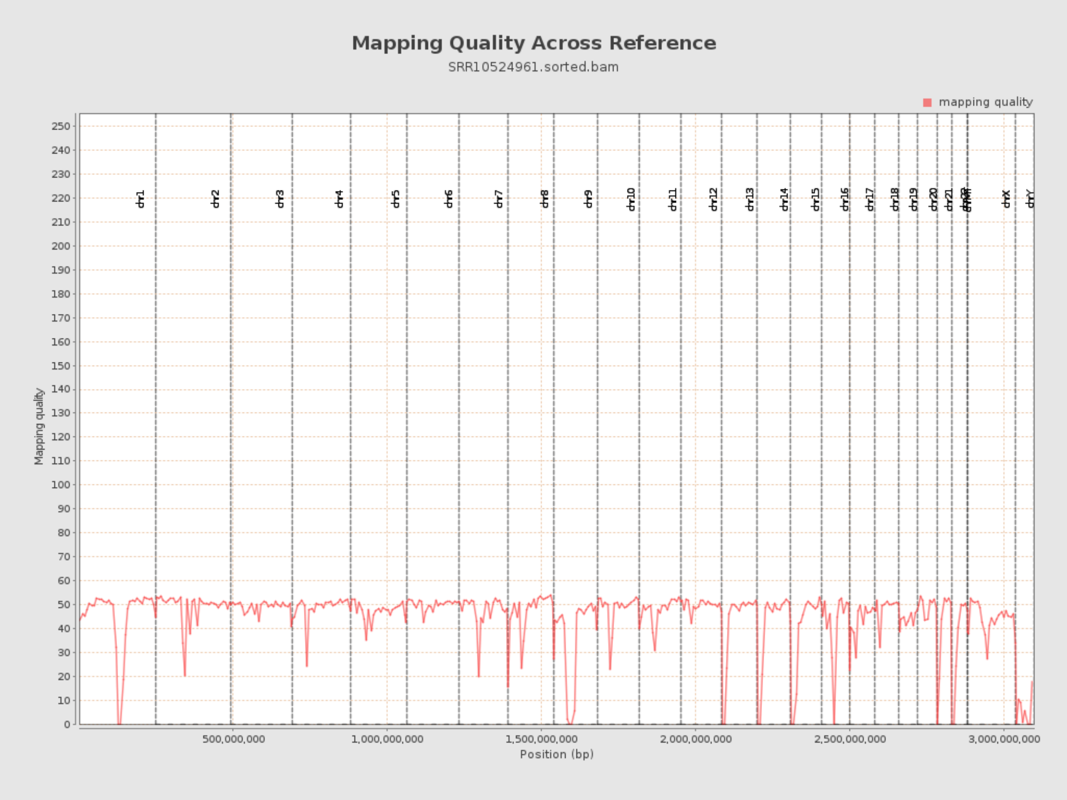
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram