Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:45:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472826.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_SRR3472826 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472826.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:45:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472826.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,792,904
Mapped reads	1,936,085 / 69.32%
Unmapped reads	856,819 / 30.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,138 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	59,036 / 2.11%
Duplication rate	2.29%
Clipped reads	1,035,330 / 37.07%

2.2. ACGT Content

Number/percentage of A's	33,988,731 / 27.31%
Number/percentage of C's	24,032,557 / 19.31%
Number/percentage of T's	37,660,785 / 30.26%
Number/percentage of G's	28,759,788 / 23.11%
Number/percentage of N's	2,950 / 0%
GC Percentage	42.42%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.3084

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Mismatches and indels

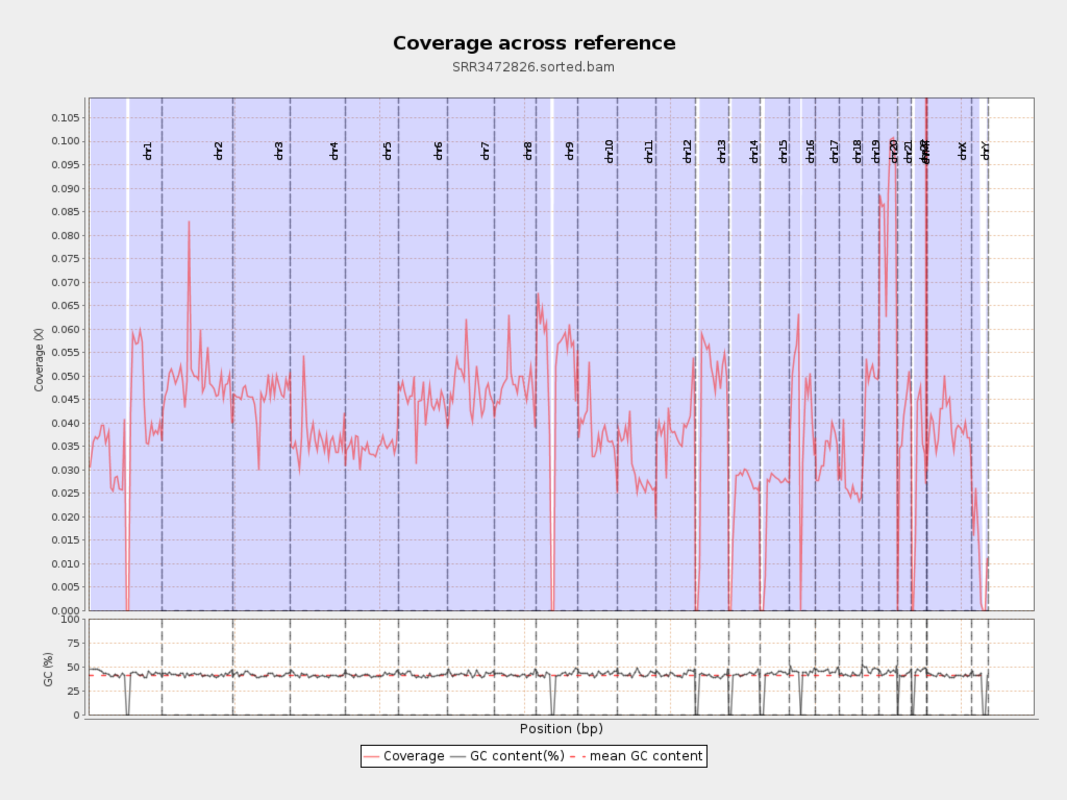
General error rate	0.88%
Mismatches	1,072,766
Insertions	10,027
Mapped reads with at least one insertion	0.51%
Deletions	29,172
Mapped reads with at least one deletion	1.49%
Homopolymer indels	45.63%

2.6. Chromosome stats

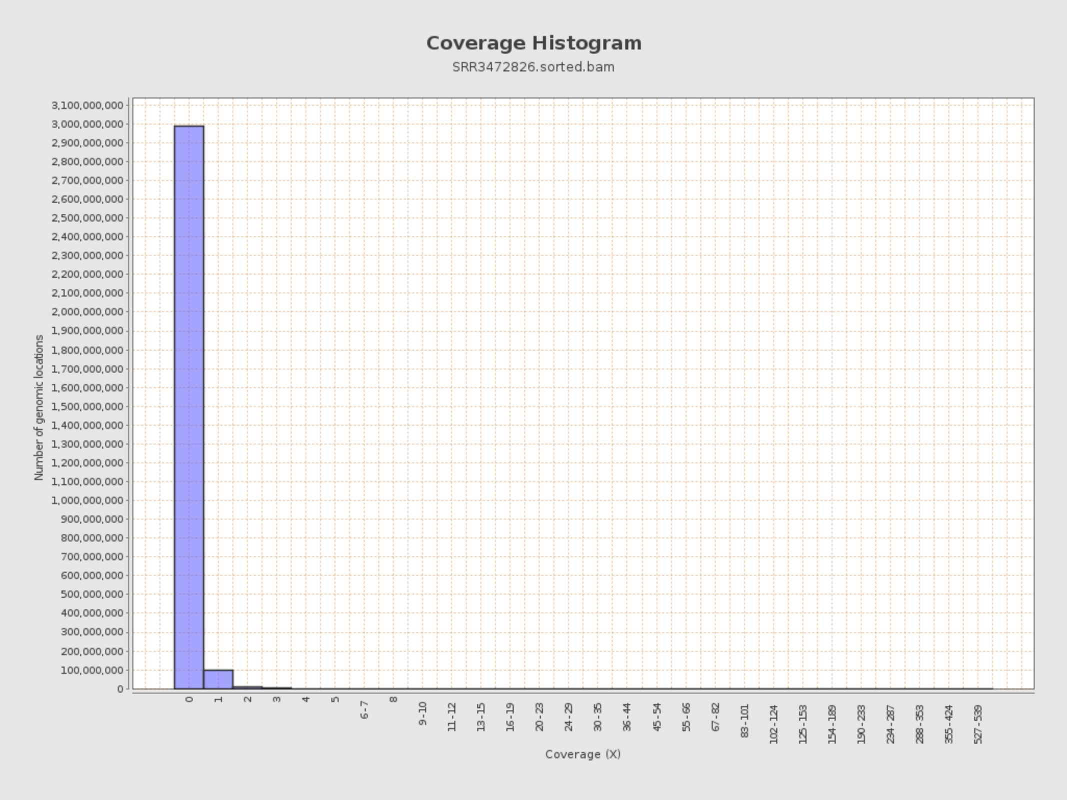
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9126918	0.0366	0.3966
chr2	243199373	12127958	0.0499	0.4548
chr3	198022430	9032580	0.0456	0.2341
chr4	191154276	6988634	0.0366	0.229
chr5	180915260	6290427	0.0348	0.2064
chr6	171115067	7640611	0.0447	0.2545
chr7	159138663	7589313	0.0477	0.3995

chr8	146364022	7027216	0.048	0.3492
chr9	141213431	7153314	0.0507	0.3604
chr10	135534747	5112483	0.0377	0.274
chr11	135006516	4167158	0.0309	0.2734
chr12	133851895	5227972	0.0391	0.2239
chr13	115169878	5062832	0.044	0.2394
chr14	107349540	2540498	0.0237	0.1945
chr15	102531392	2304354	0.0225	0.1782
chr16	90354753	3886155	0.043	0.2471
chr17	81195210	2713652	0.0334	0.2169
chr18	78077248	2113842	0.0271	0.5435
chr19	59128983	2835299	0.048	0.3384
chr20	63025520	5504800	0.0873	0.3413
chr21	48129895	1834536	0.0381	0.2434
chr22	51304566	1413431	0.0275	0.1904
chrMT	16571	66292	4.0005	3.5576
chrX	155270560	6095699	0.0393	0.2453
chrY	59373566	640646	0.0108	0.1527

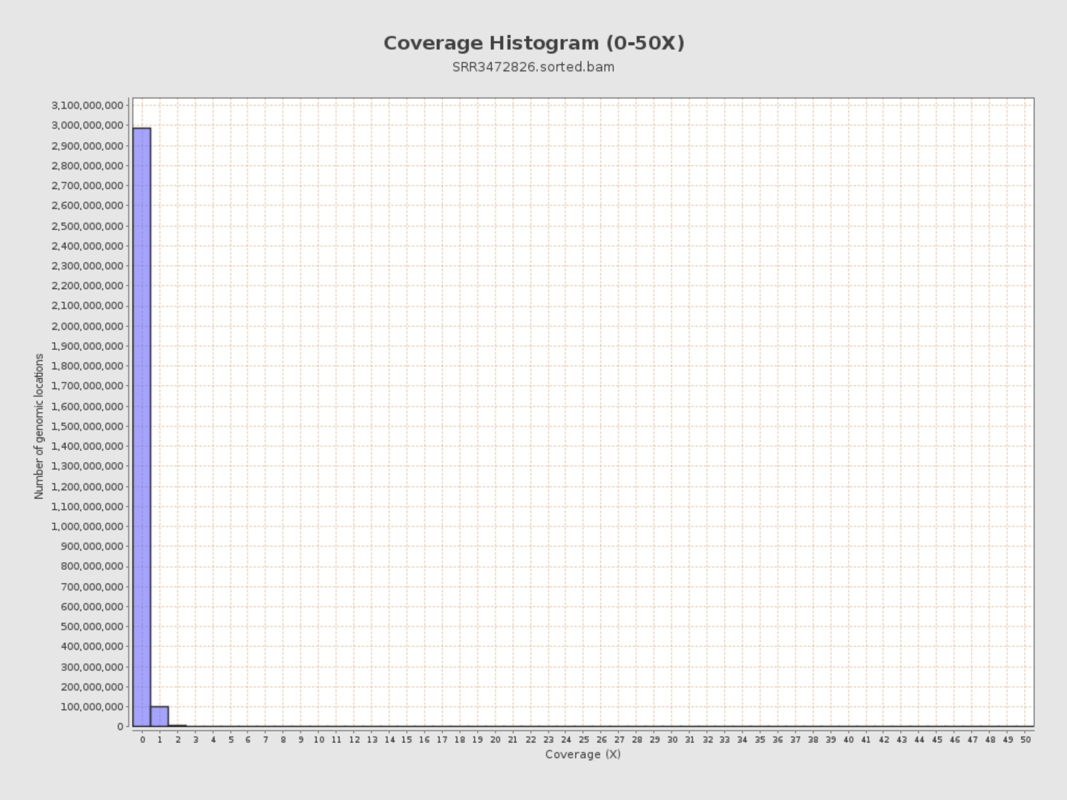
3. Results : Coverage across reference



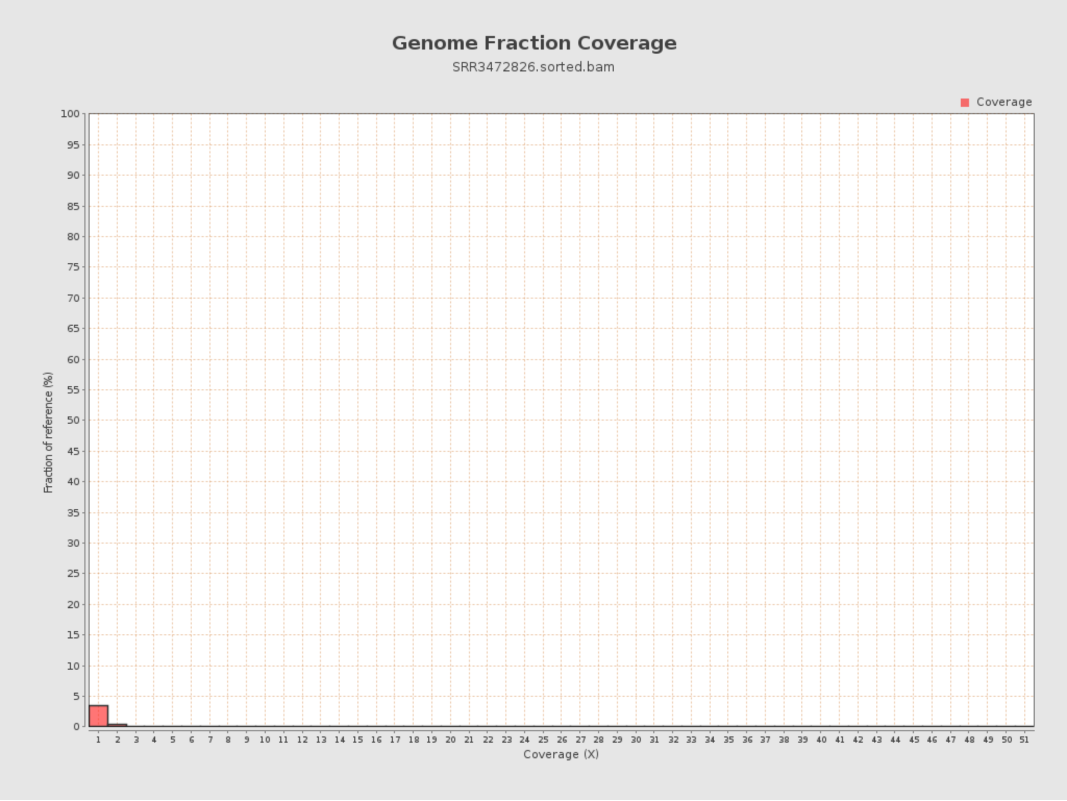
4. Results : Coverage Histogram



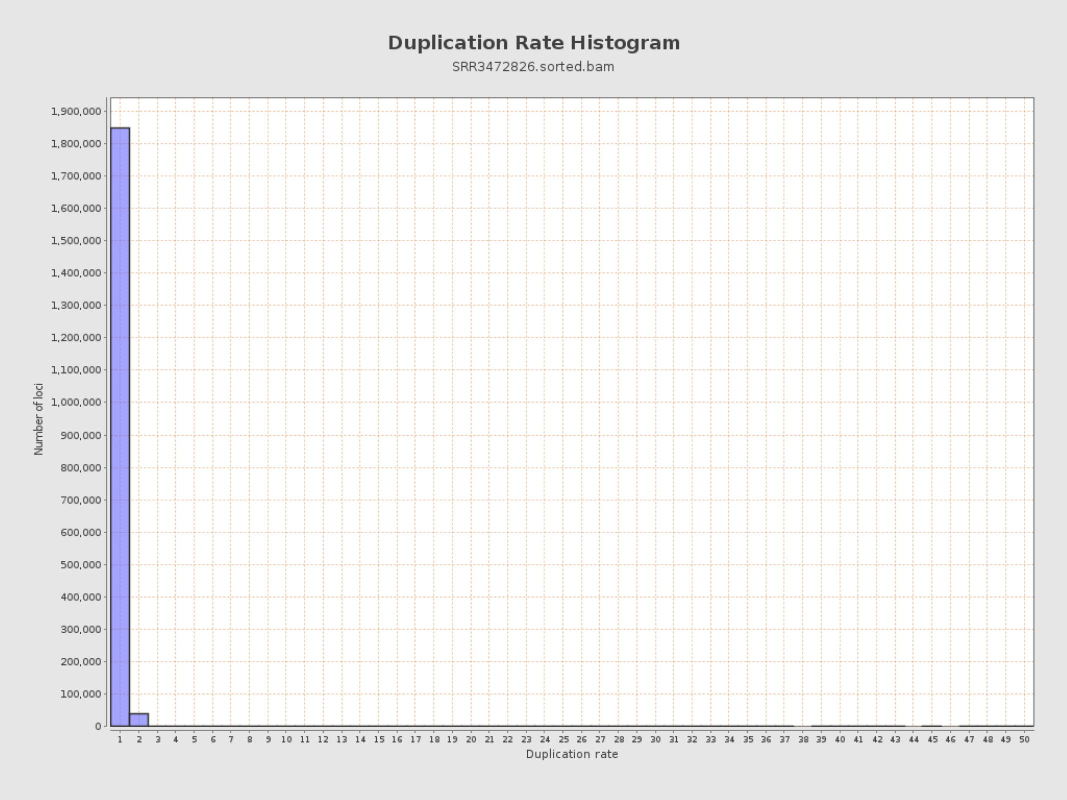
5. Results : Coverage Histogram (0-50X)



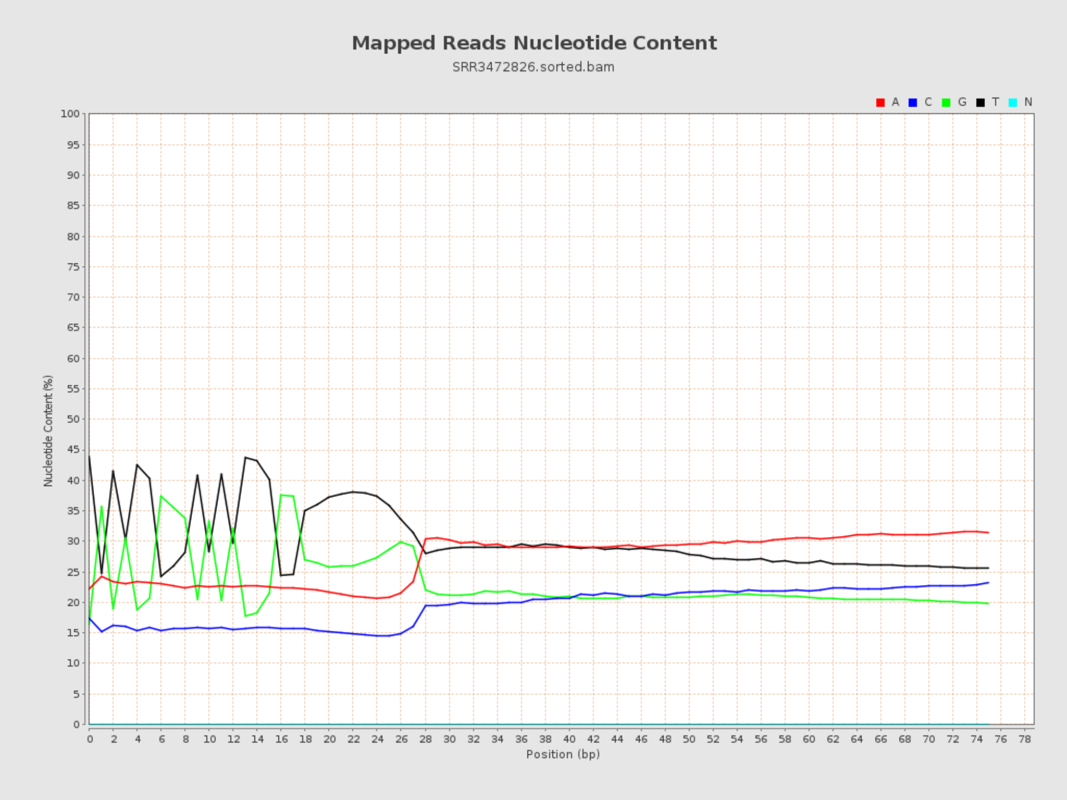
6. Results : Genome Fraction Coverage



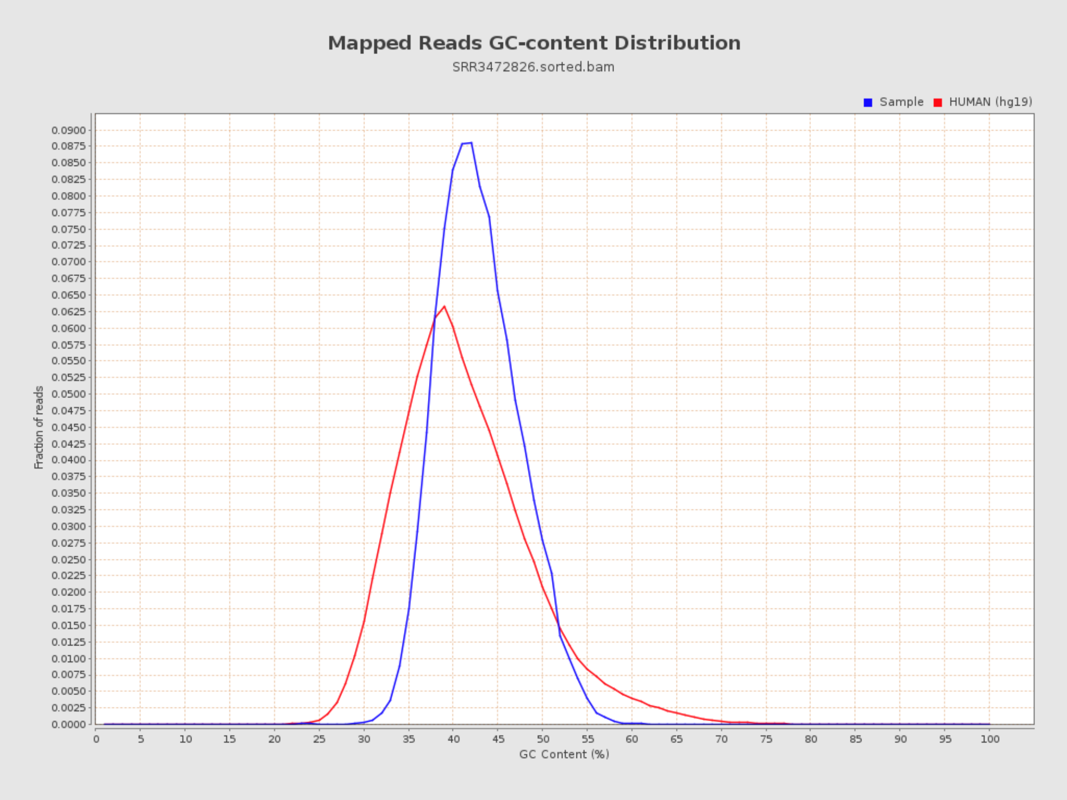
7. Results : Duplication Rate Histogram



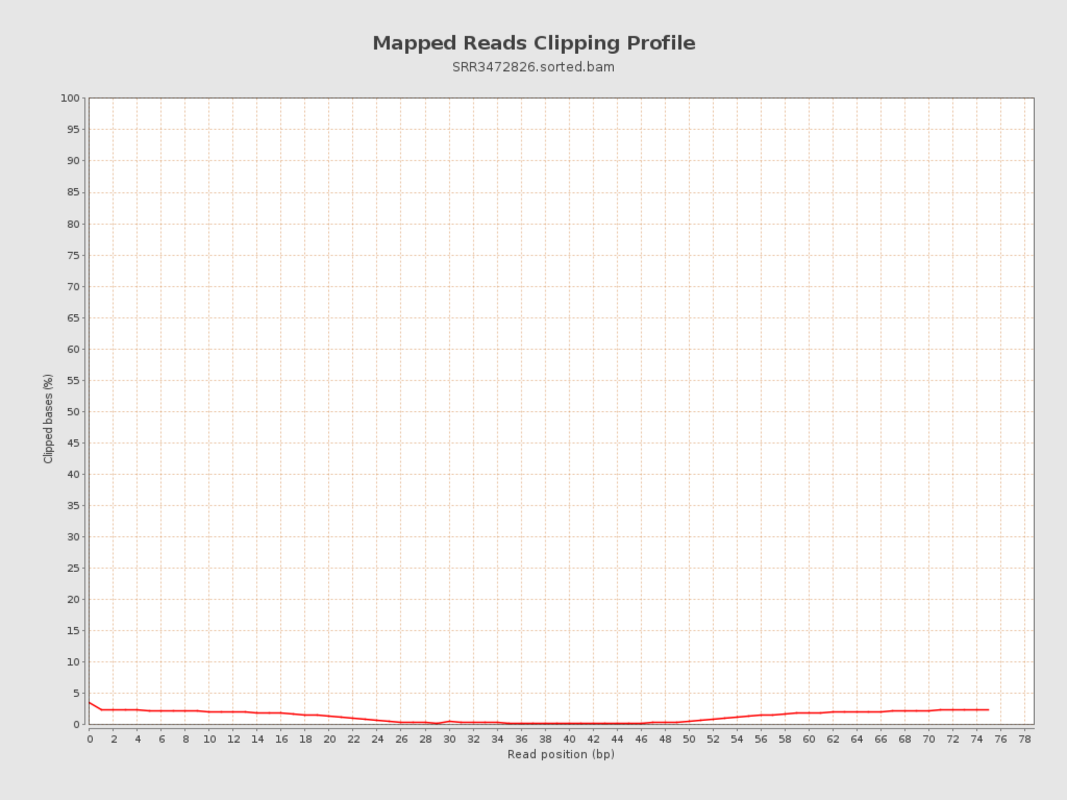
8. Results : Mapped Reads Nucleotide Content



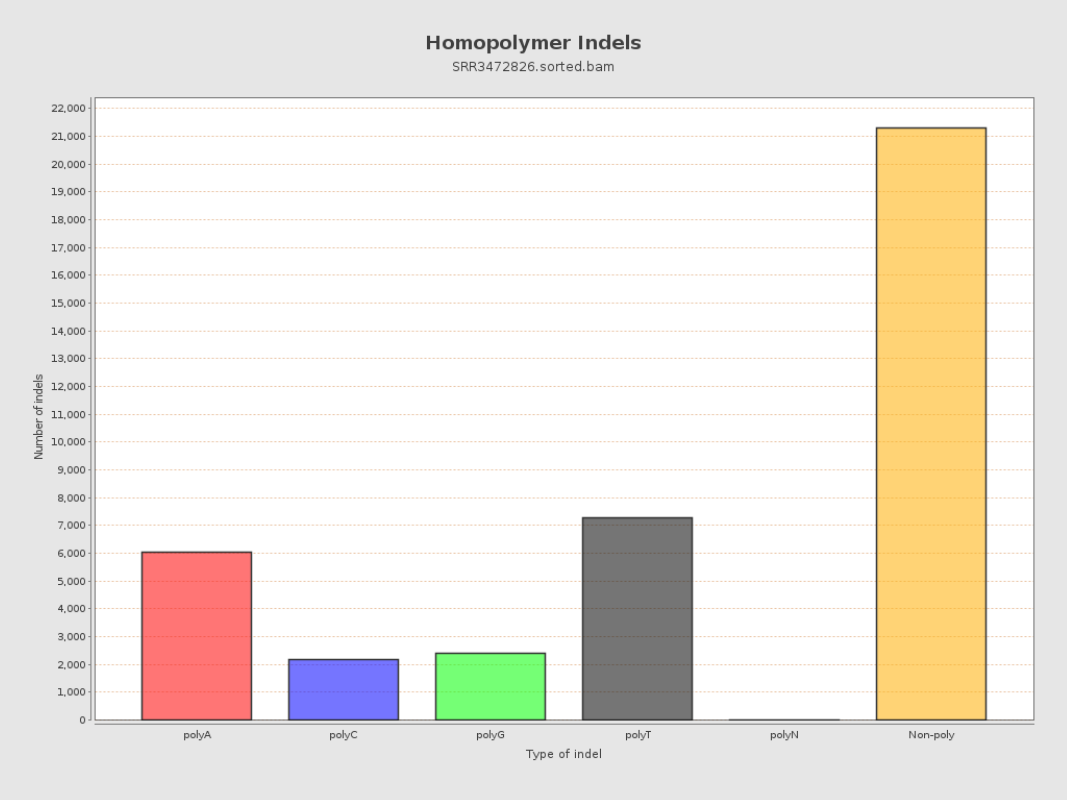
9. Results : Mapped Reads GC-content Distribution



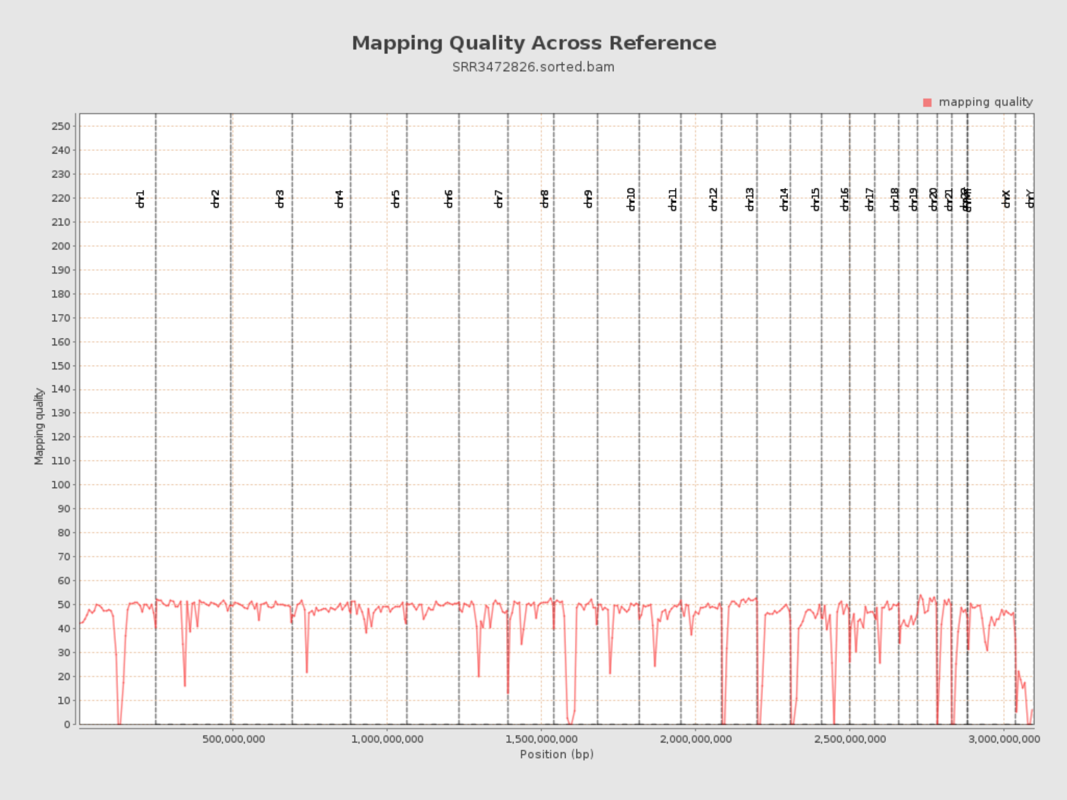
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram