Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:21:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082976.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_SRR3082976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082976.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:21:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,255,716
Mapped reads	2,635,694 / 80.96%
Unmapped reads	620,022 / 19.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,668 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	106,485 / 3.27%
Duplication rate	3.23%
Clipped reads	1,291,098 / 39.66%

2.2. ACGT Content

Number/percentage of A's	49,672,676 / 28.57%
Number/percentage of C's	31,708,309 / 18.24%
Number/percentage of T's	54,809,142 / 31.53%
Number/percentage of G's	37,626,007 / 21.64%
Number/percentage of N's	16,661 / 0.01%
GC Percentage	39.89%

2.3. Coverage

Mean	0.0562

Standard Deviation	0.405

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

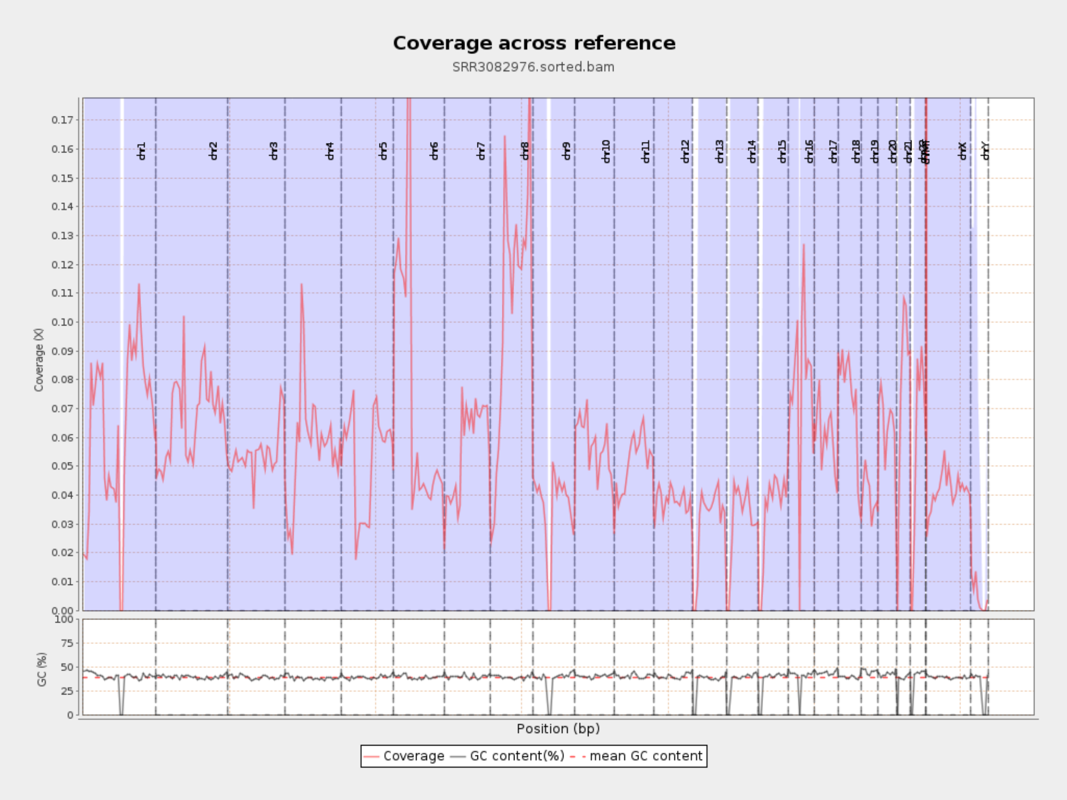
General error rate	0.95%
Mismatches	1,623,998
Insertions	14,904
Mapped reads with at least one insertion	0.56%
Deletions	40,110
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.48%

2.6. Chromosome stats

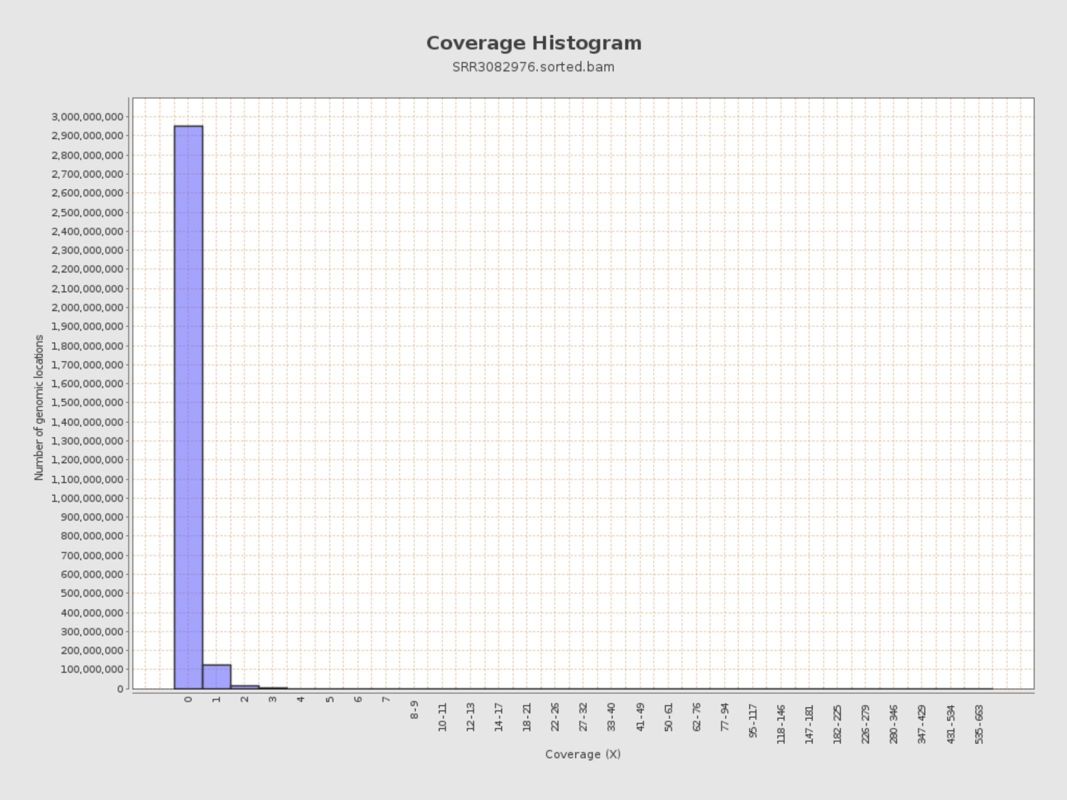
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15911828	0.0638	0.5577
chr2	243199373	16209372	0.0667	0.5501
chr3	198022430	10784323	0.0545	0.2671
chr4	191154276	11042648	0.0578	0.2804
chr5	180915260	9457670	0.0523	0.2631
chr6	171115067	12938776	0.0756	0.4363
chr7	159138663	8968661	0.0564	0.4719

chr8	146364022	15588558	0.1065	0.584
chr9	141213431	5066126	0.0359	0.3769
chr10	135534747	7816981	0.0577	0.3482
chr11	135006516	6942153	0.0514	0.3544
chr12	133851895	5093640	0.0381	0.2269
chr13	115169878	3522358	0.0306	0.2
chr14	107349540	3401779	0.0317	0.23
chr15	102531392	3424299	0.0334	0.2092
chr16	90354753	6997599	0.0774	0.3654
chr17	81195210	4946318	0.0609	0.3566
chr18	78077248	5805052	0.0744	0.8527
chr19	59128983	2387366	0.0404	0.4194
chr20	63025520	4099672	0.065	0.305
chr21	48129895	3625529	0.0753	0.3257
chr22	51304566	2916362	0.0568	0.2754
chrMT	16571	211177	12.7438	8.4488
chrX	155270560	6457546	0.0416	0.2774
chrY	59373566	286519	0.0048	0.0976

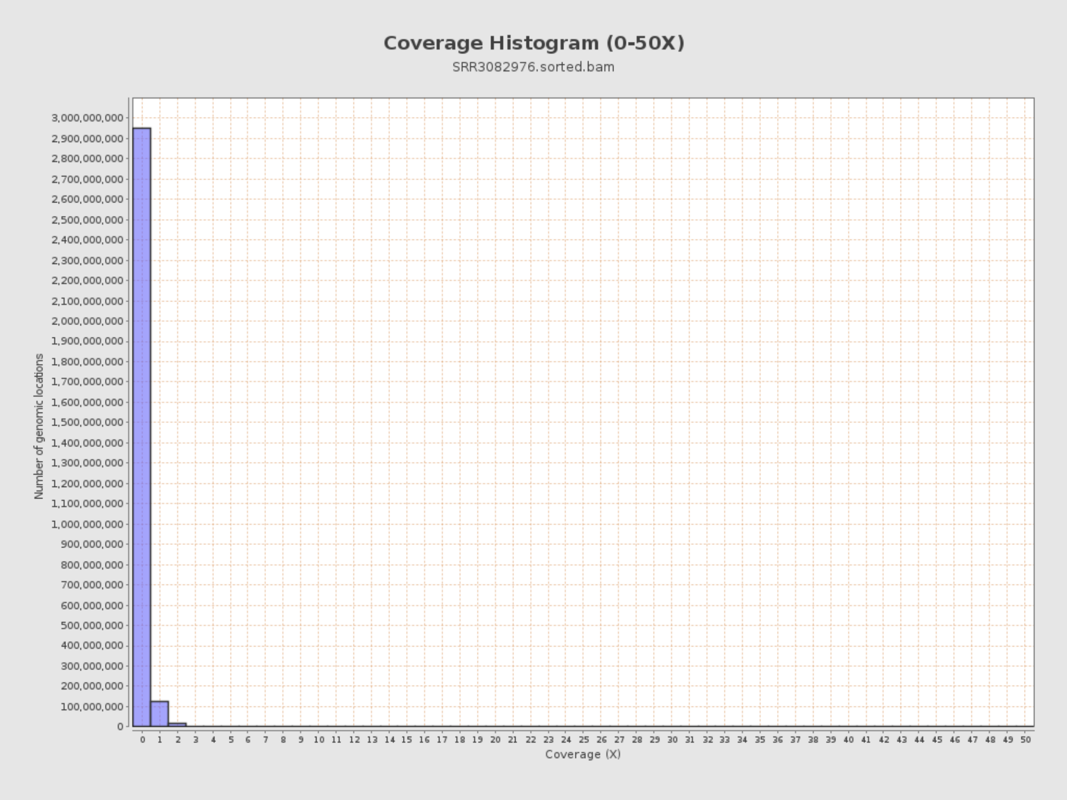
3. Results : Coverage across reference



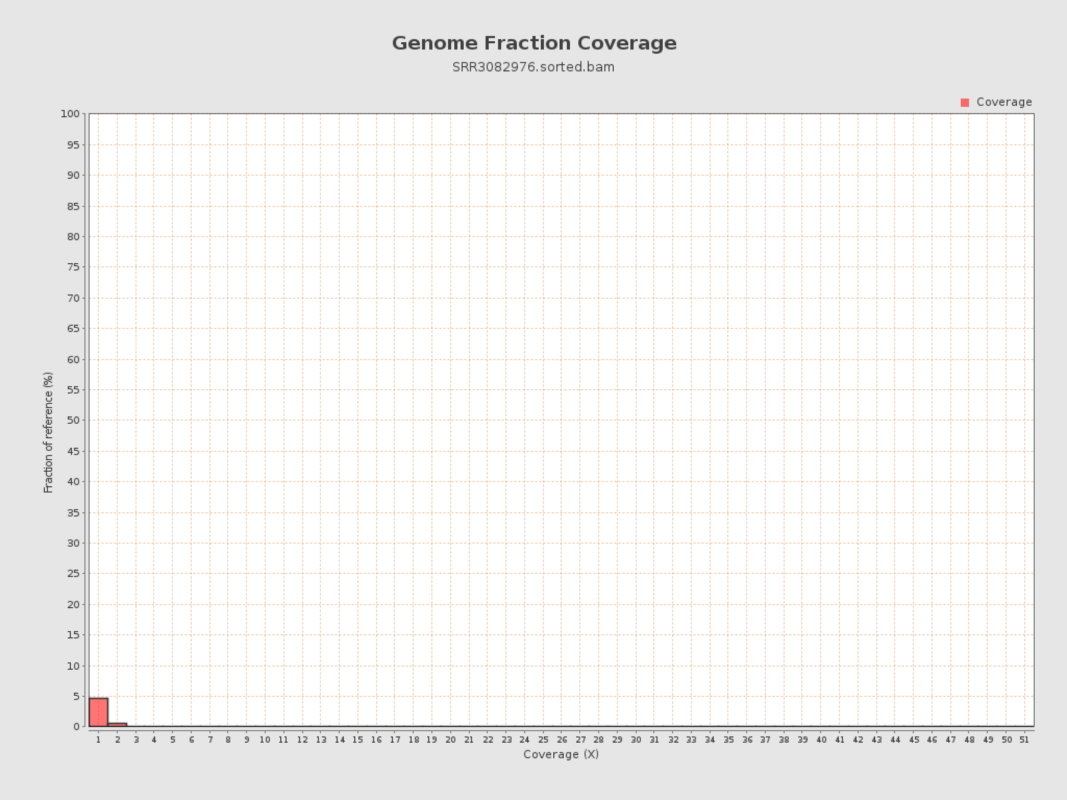
4. Results : Coverage Histogram



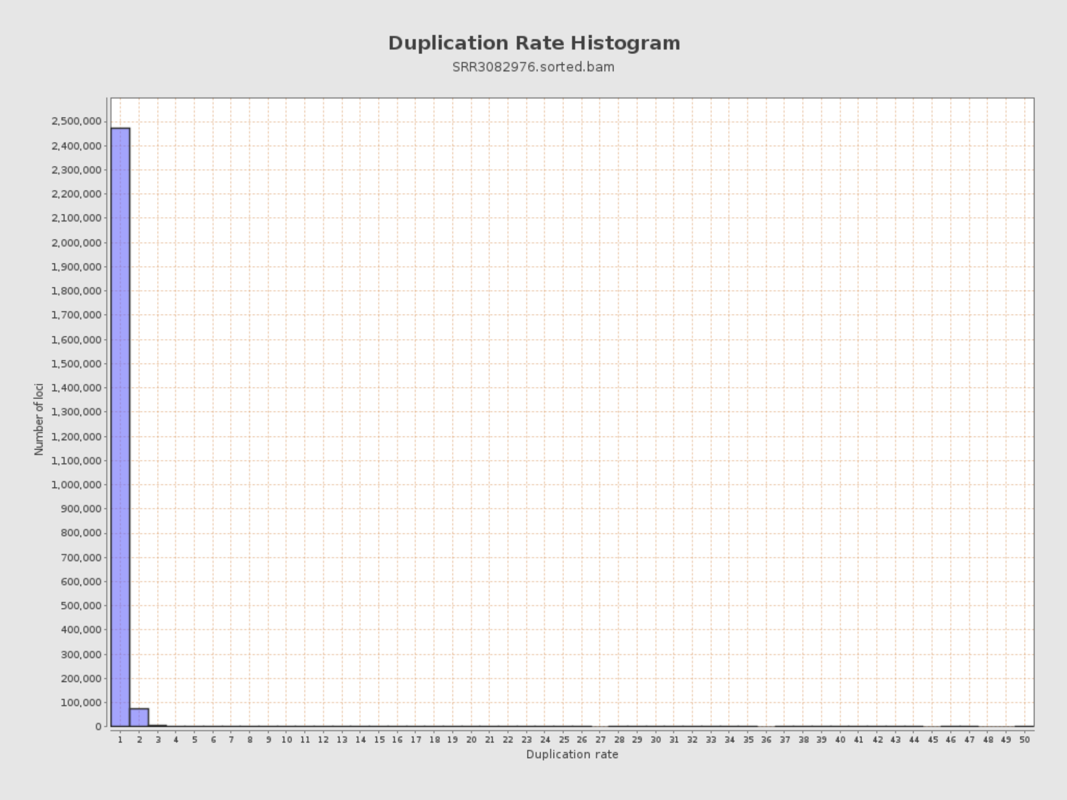
5. Results : Coverage Histogram (0-50X)



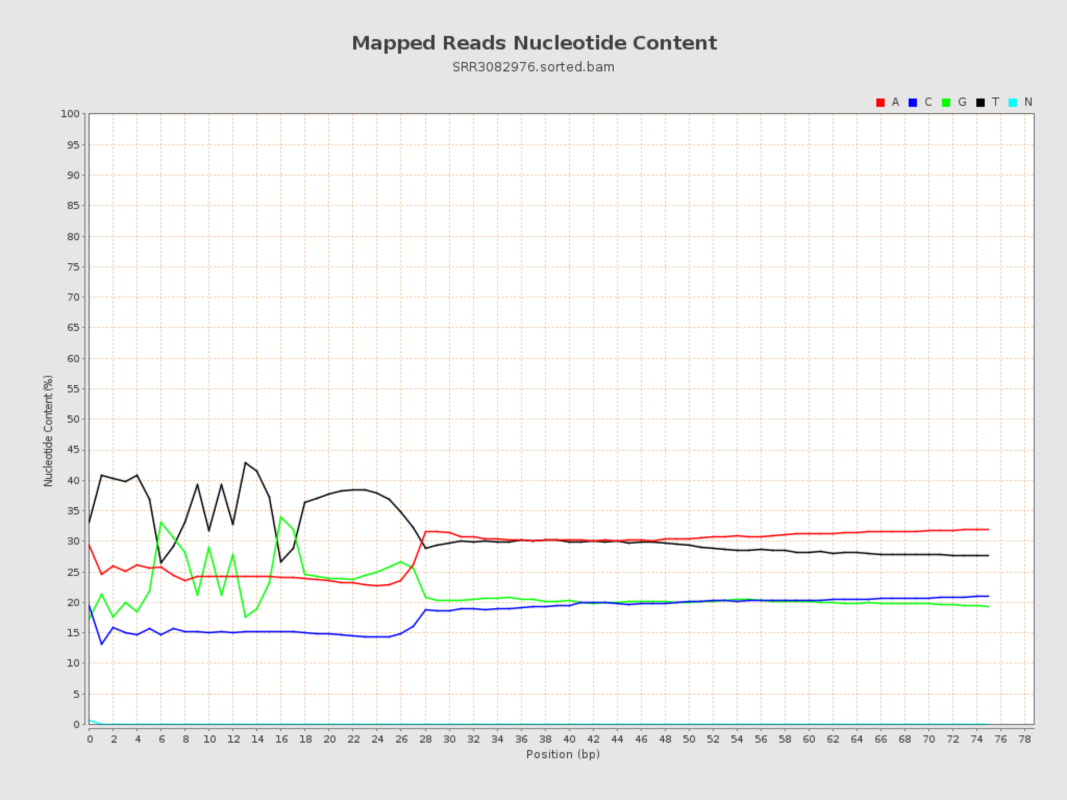
6. Results : Genome Fraction Coverage



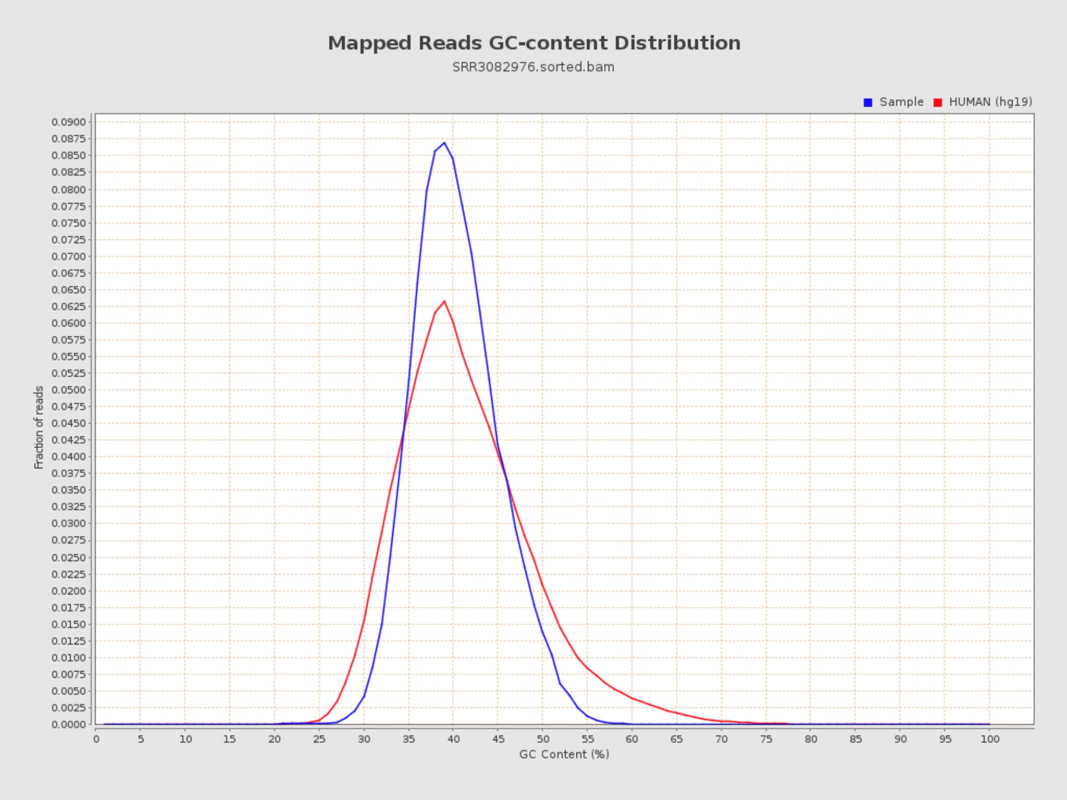
7. Results : Duplication Rate Histogram



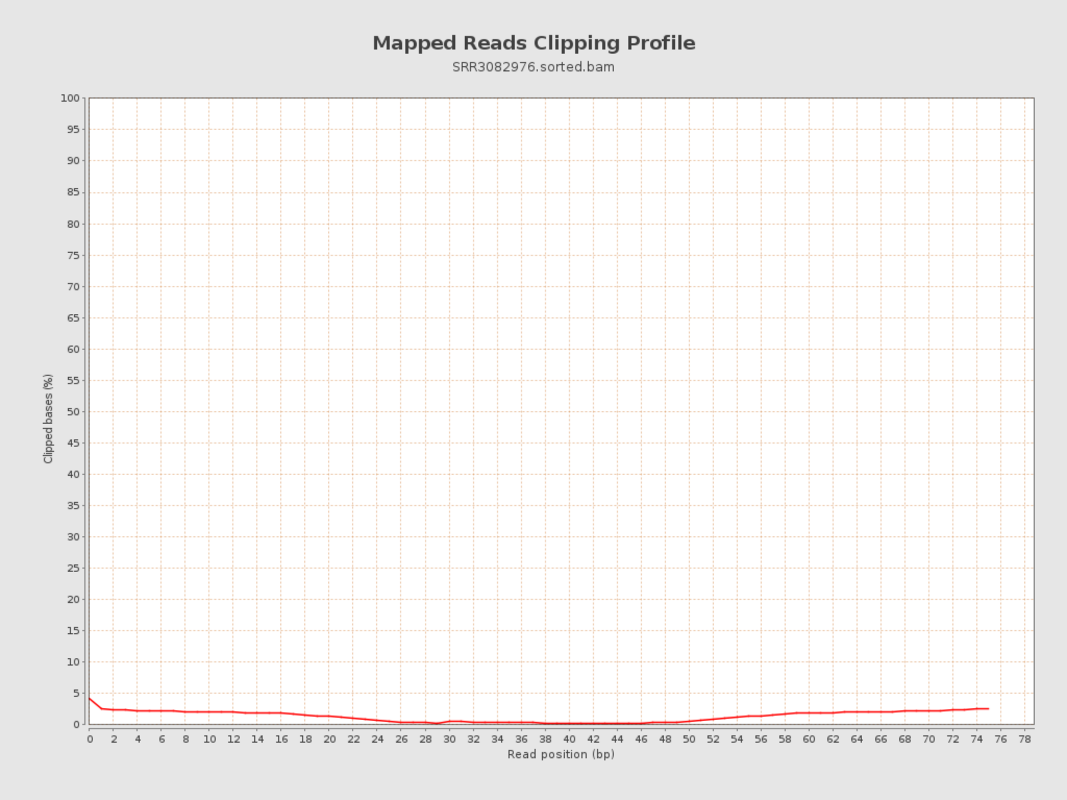
8. Results : Mapped Reads Nucleotide Content



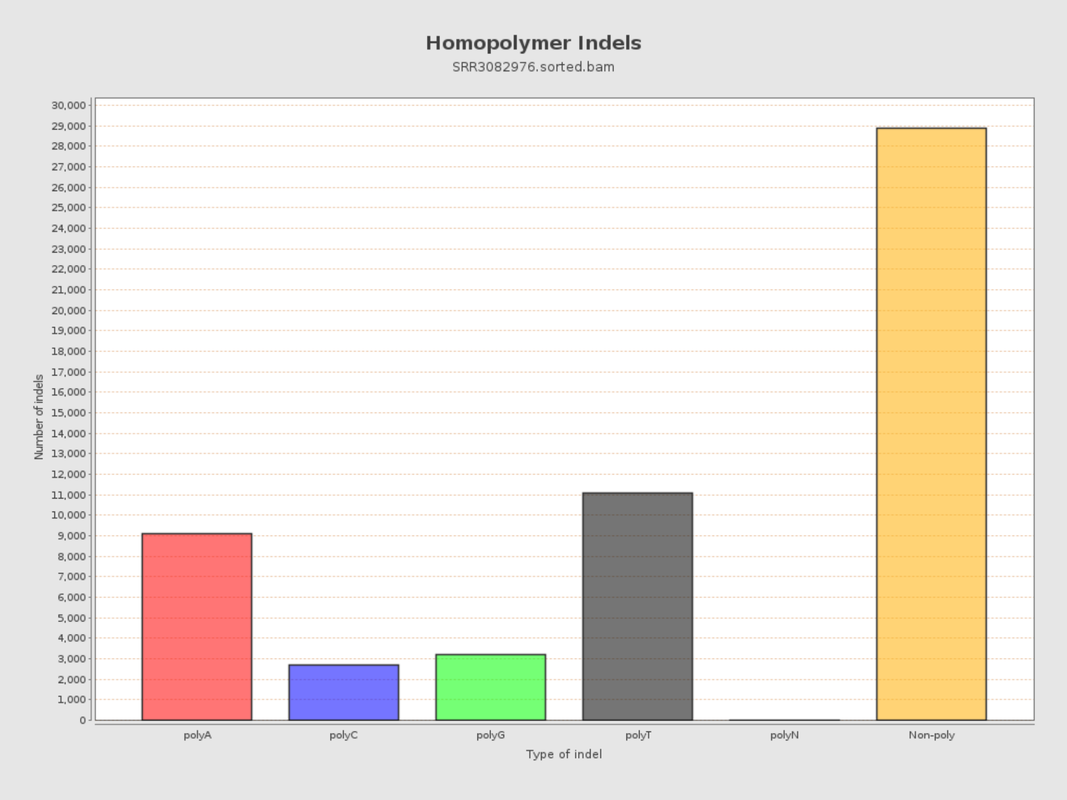
9. Results : Mapped Reads GC-content Distribution



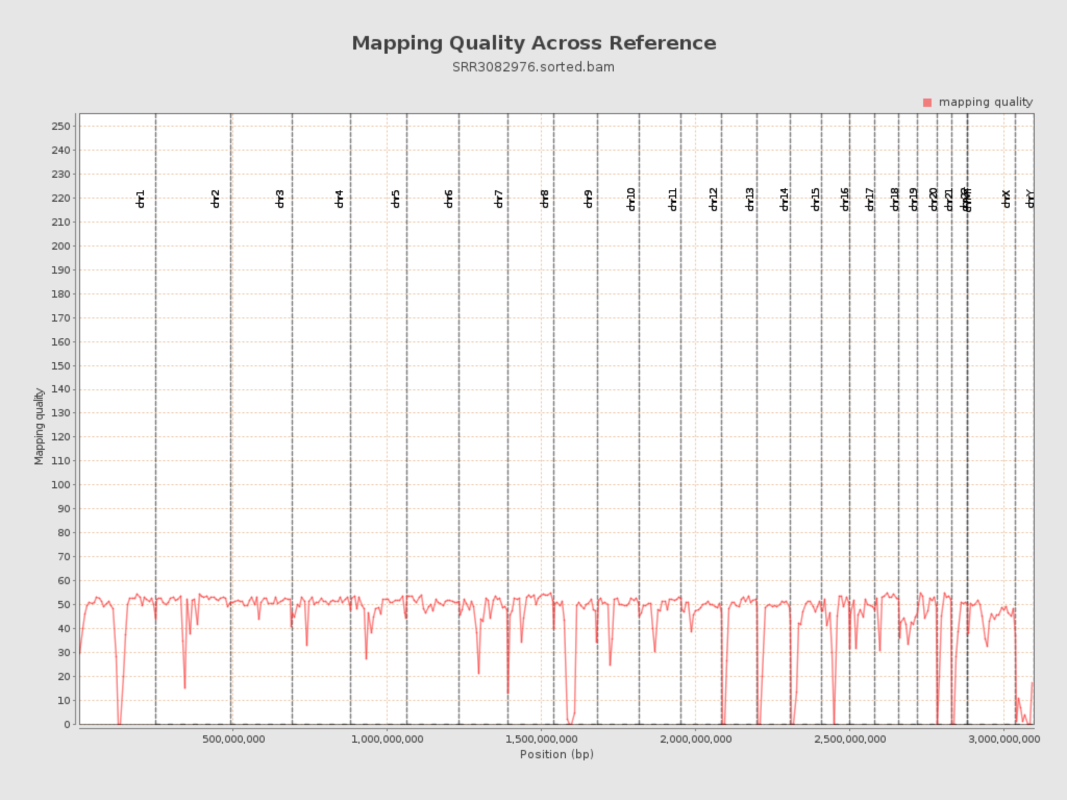
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram