Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:59:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971293.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_SRR2971293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971293.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:59:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971293.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,110,562
Mapped reads	10,433,982 / 86.16%
Unmapped reads	1,676,580 / 13.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	743,005 / 6.14%
Duplication rate	5.85%
Clipped reads	780,259 / 6.44%

2.2. ACGT Content

Number/percentage of A's	118,940,518 / 28.82%
Number/percentage of C's	85,028,850 / 20.61%
Number/percentage of T's	121,085,918 / 29.34%
Number/percentage of G's	87,571,802 / 21.22%
Number/percentage of N's	7,207 / 0%
GC Percentage	41.83%

2.3. Coverage

Mean	0.1333
Standard Deviation	0.9696

2.4. Mapping Quality

Mean Mapping Quality	41.91

2.5. Mismatches and indels

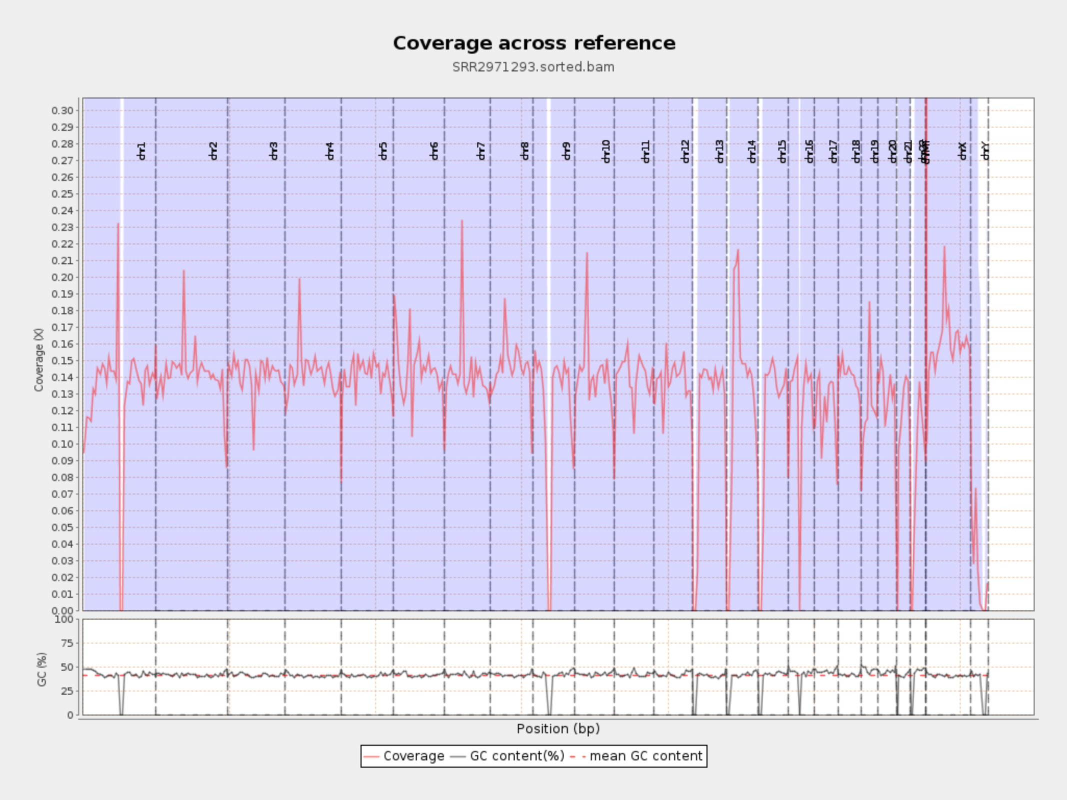
General error rate	0.26%
Mismatches	1,048,865
Insertions	11,066
Mapped reads with at least one insertion	0.11%
Deletions	26,594
Mapped reads with at least one deletion	0.25%
Homopolymer indels	41.07%

2.6. Chromosome stats

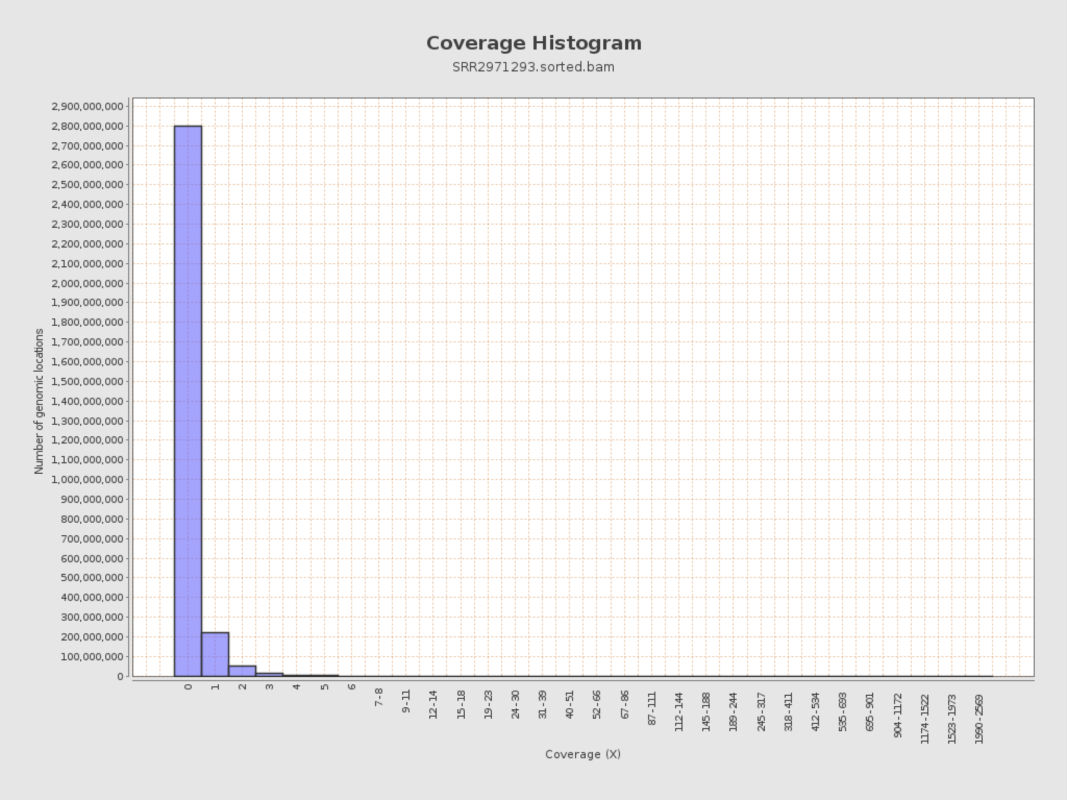
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32585913	0.1307	2.0809
chr2	243199373	34497649	0.1418	0.8193
chr3	198022430	27997575	0.1414	0.4978
chr4	191154276	27439431	0.1435	0.5773
chr5	180915260	25531185	0.1411	0.5134
chr6	171115067	24894071	0.1455	0.6297
chr7	159138663	22581789	0.1419	1.2877
chr8	146364022	21267937	0.1453	1.088

chr9	141213431	17065201	0.1208	0.7747
chr10	135534747	19269409	0.1422	0.8532
chr11	135006516	18888968	0.1399	0.7837
chr12	133851895	18453605	0.1379	0.521
chr13	115169878	13303196	0.1155	0.4396
chr14	107349540	14196431	0.1322	0.627
chr15	102531392	11578610	0.1129	0.4467
chr16	90354753	10916295	0.1208	0.5586
chr17	81195210	9918050	0.1222	0.5571
chr18	78077248	11021126	0.1412	1.8336
chr19	59128983	7288022	0.1233	1.7587
chr20	63025520	8229751	0.1306	0.5127
chr21	48129895	5276559	0.1096	0.5679
chr22	51304566	4211098	0.0821	0.3703
chrMT	16571	46529	2.8079	3.3403
chrX	155270560	24766458	0.1595	0.658
chrY	59373566	1444571	0.0243	0.3751

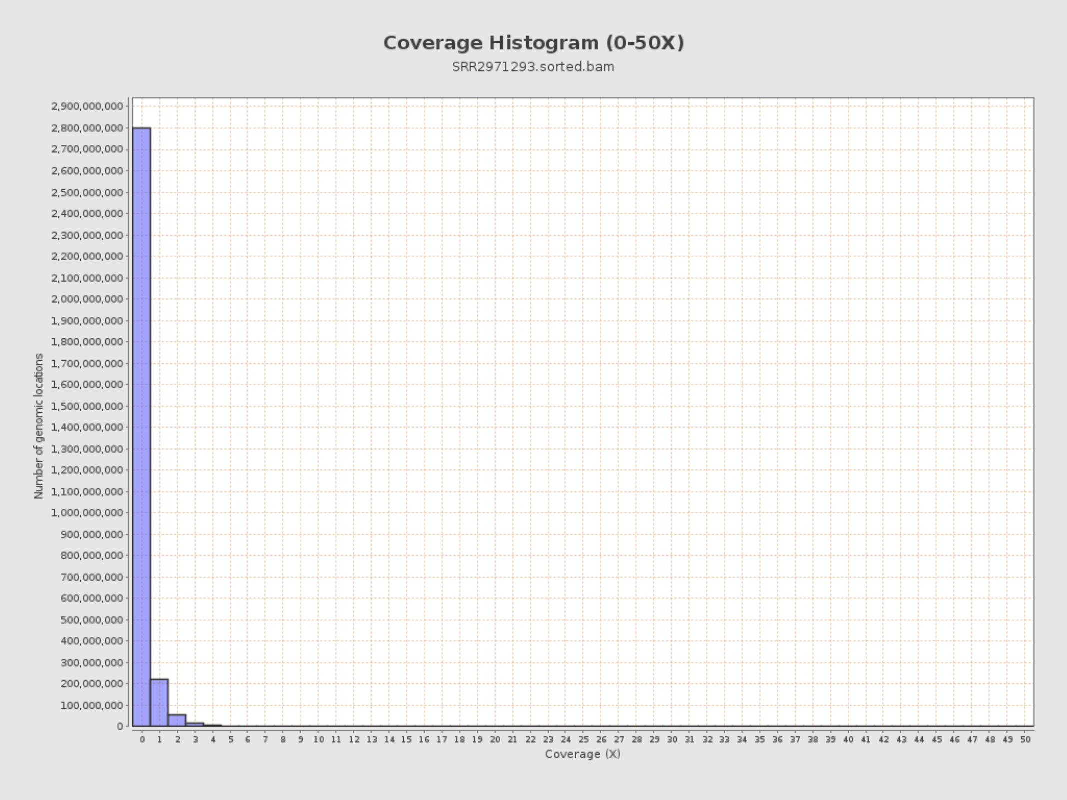
3. Results : Coverage across reference



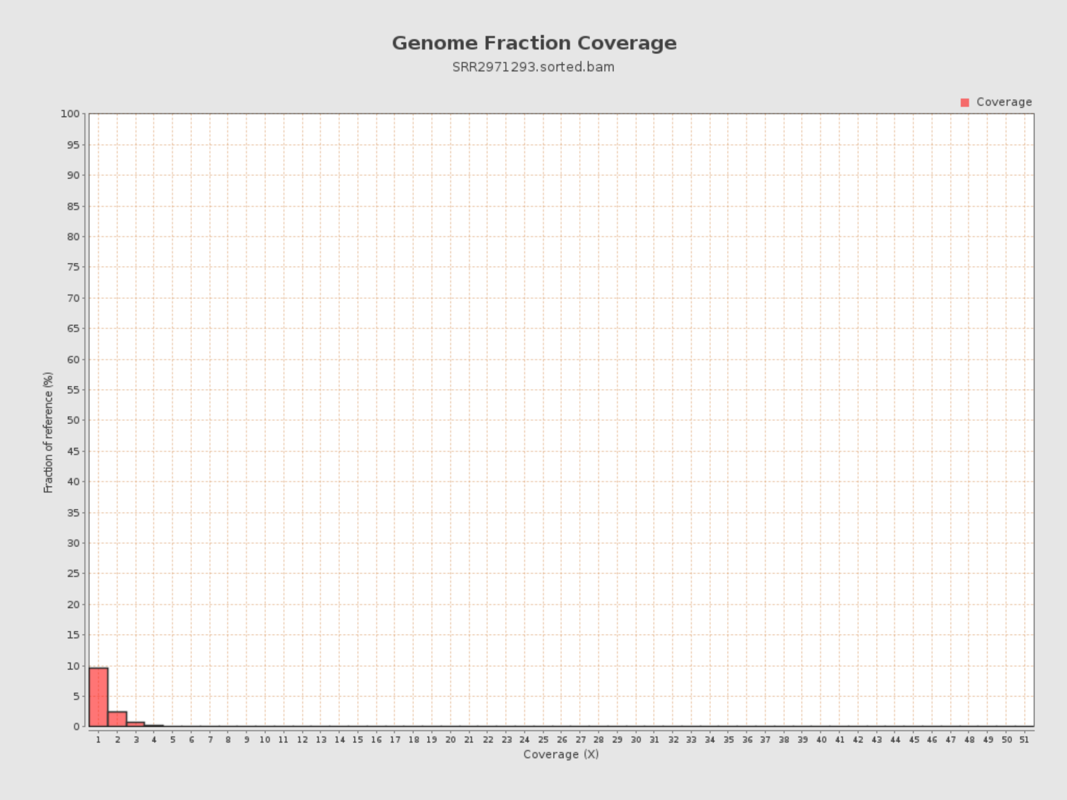
4. Results : Coverage Histogram



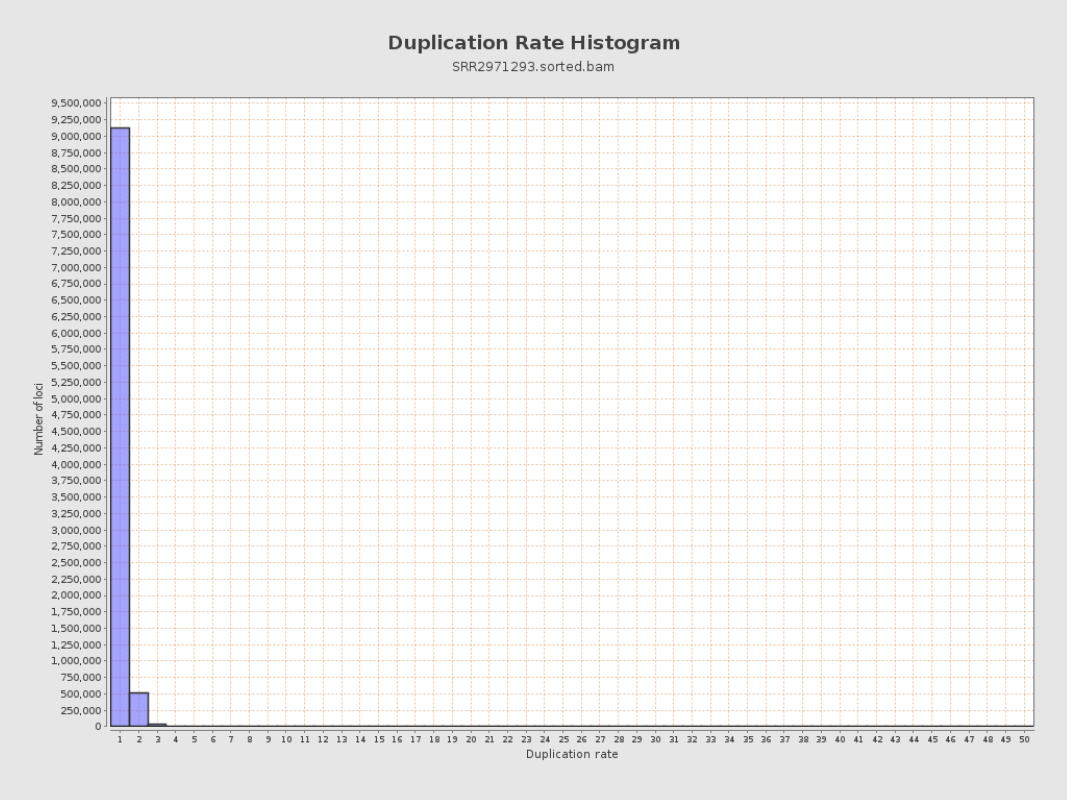
5. Results : Coverage Histogram (0-50X)



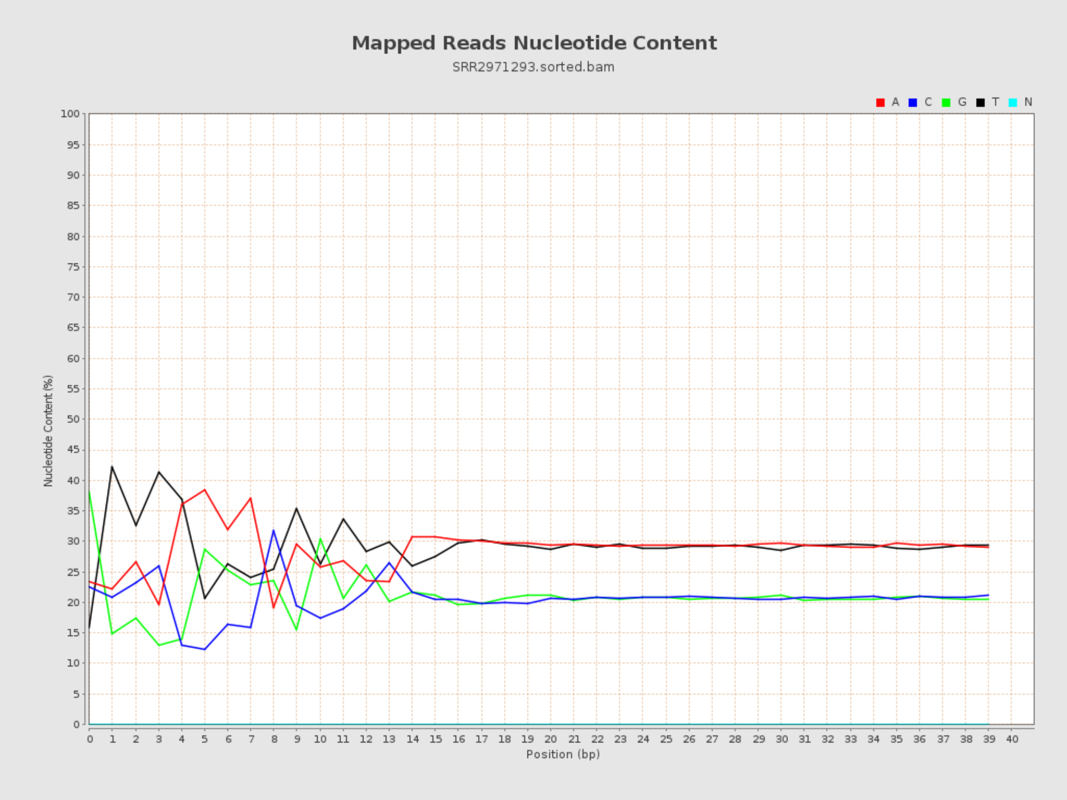
6. Results : Genome Fraction Coverage



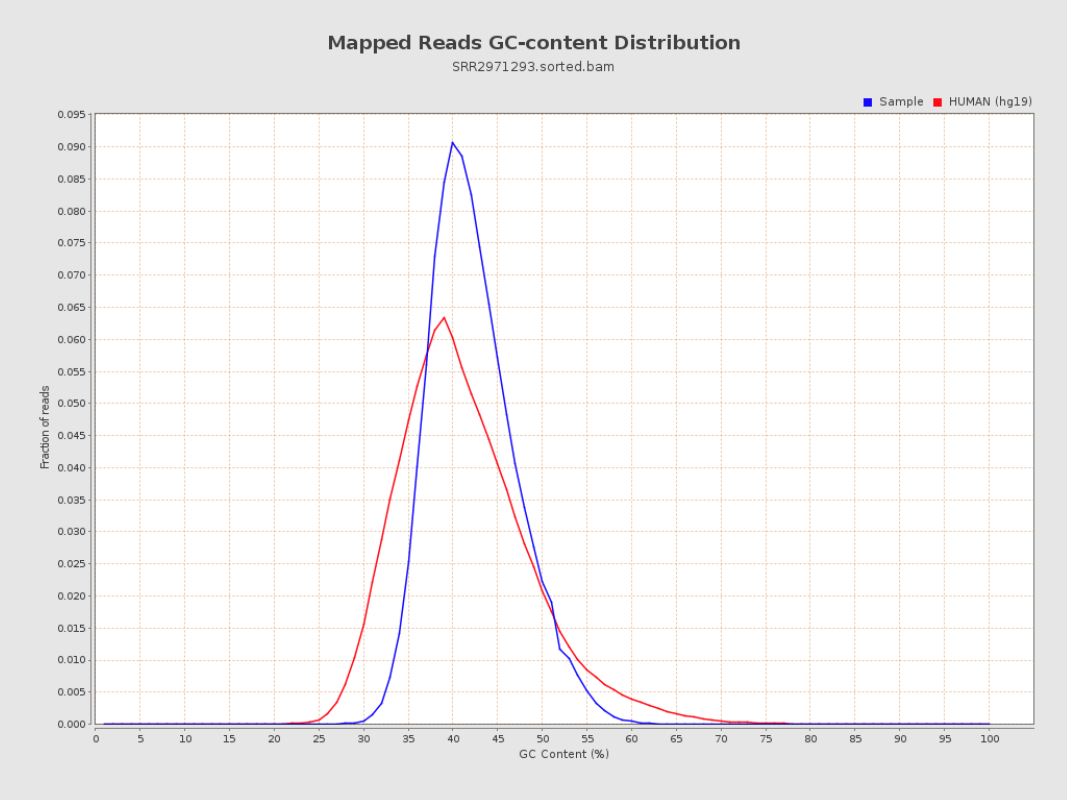
7. Results : Duplication Rate Histogram



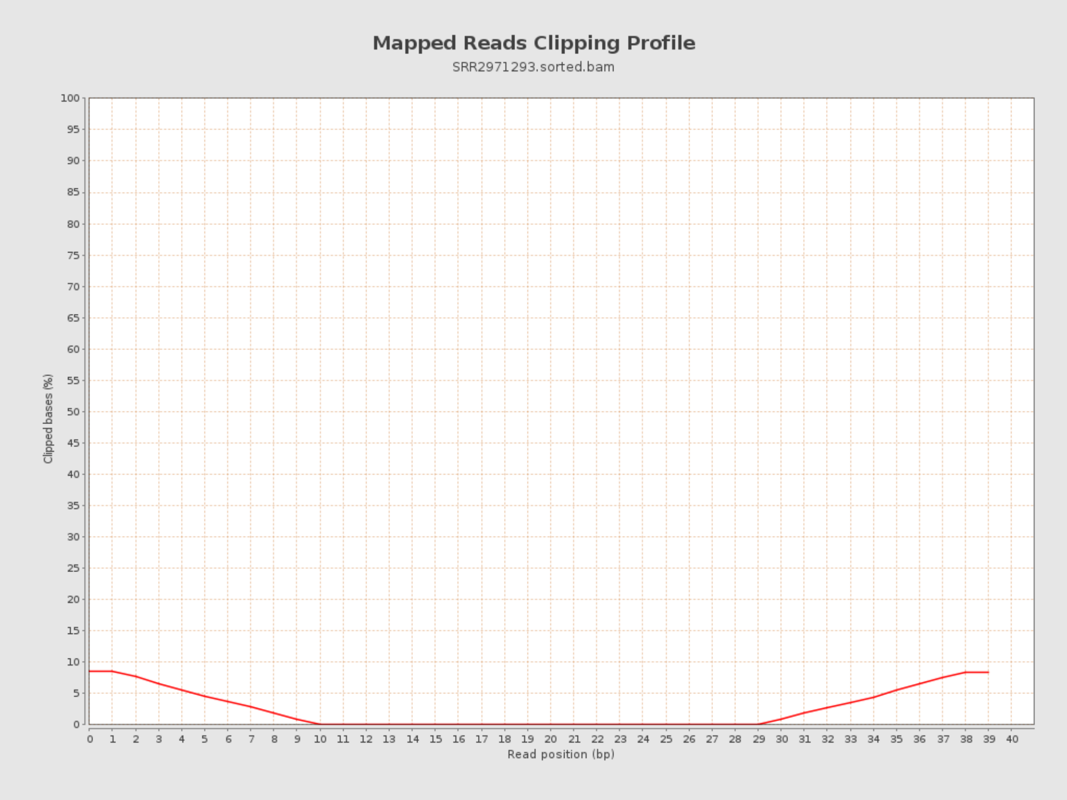
8. Results : Mapped Reads Nucleotide Content



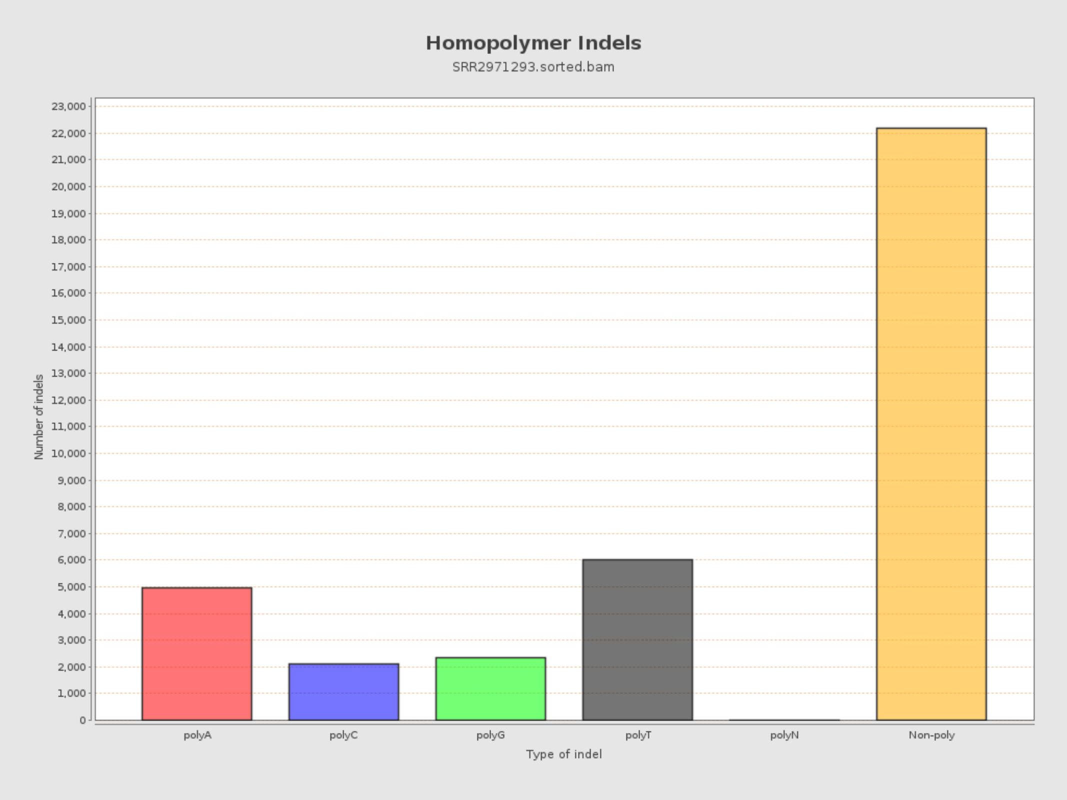
9. Results : Mapped Reads GC-content Distribution



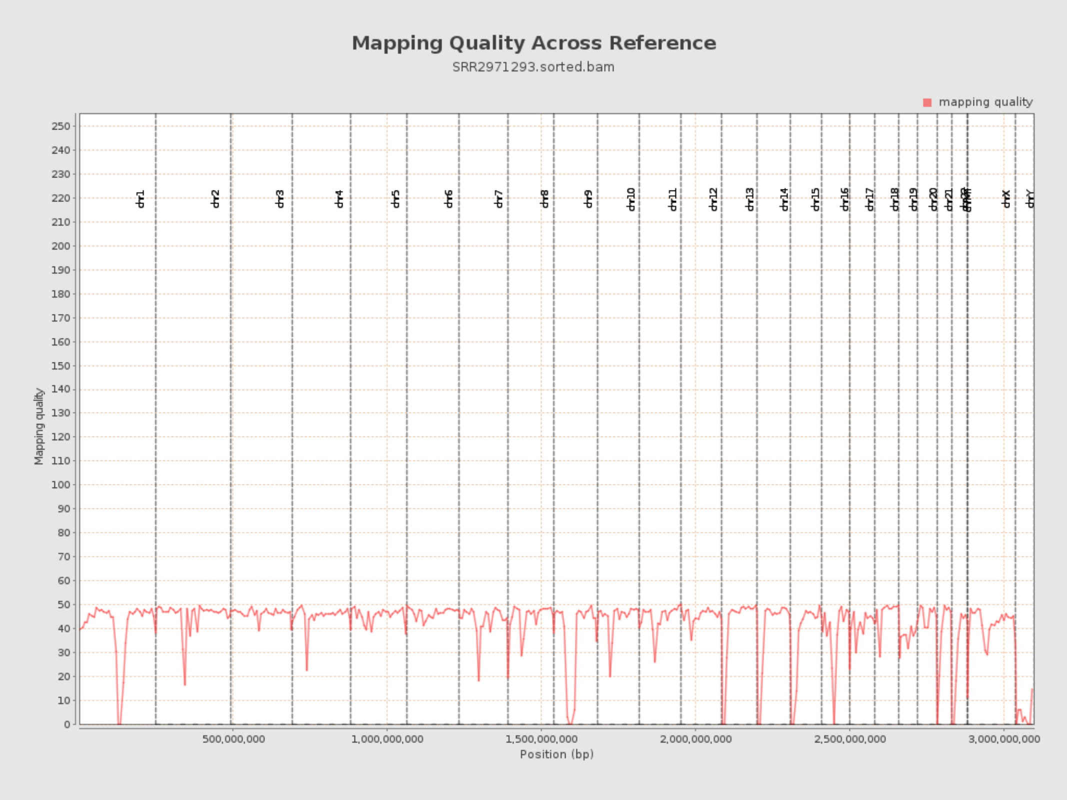
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram