Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:08:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971302.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_SRR2971302 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971302.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:08:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971302.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,368,745
Mapped reads	7,065,619 / 84.43%
Unmapped reads	1,303,126 / 15.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	370,914 / 4.43%
Duplication rate	4%
Clipped reads	648,209 / 7.75%

2.2. ACGT Content

Number/percentage of A's	81,507,678 / 29.24%
Number/percentage of C's	56,419,348 / 20.24%
Number/percentage of T's	83,216,727 / 29.85%
Number/percentage of G's	57,616,726 / 20.67%
Number/percentage of N's	15,608 / 0.01%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0901
Standard Deviation	0.7582

2.4. Mapping Quality

Mean Mapping Quality	40.63

2.5. Mismatches and indels

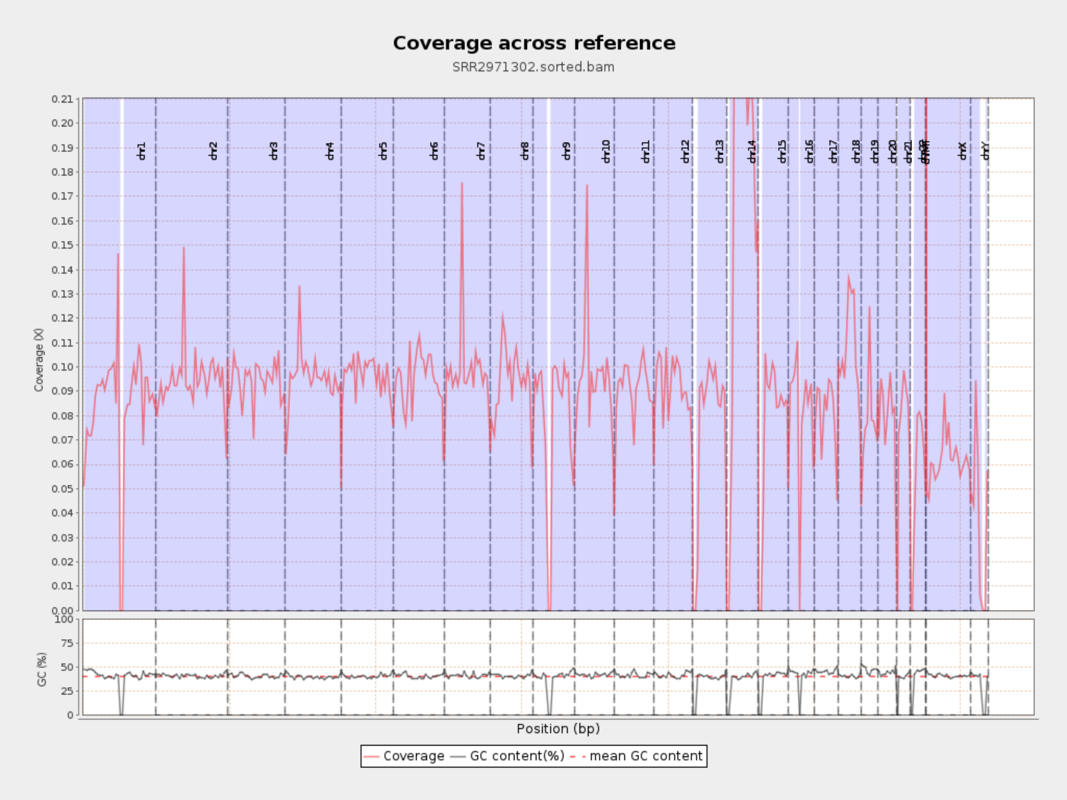
General error rate	0.3%
Mismatches	819,625
Insertions	9,528
Mapped reads with at least one insertion	0.13%
Deletions	22,691
Mapped reads with at least one deletion	0.32%
Homopolymer indels	40.98%

2.6. Chromosome stats

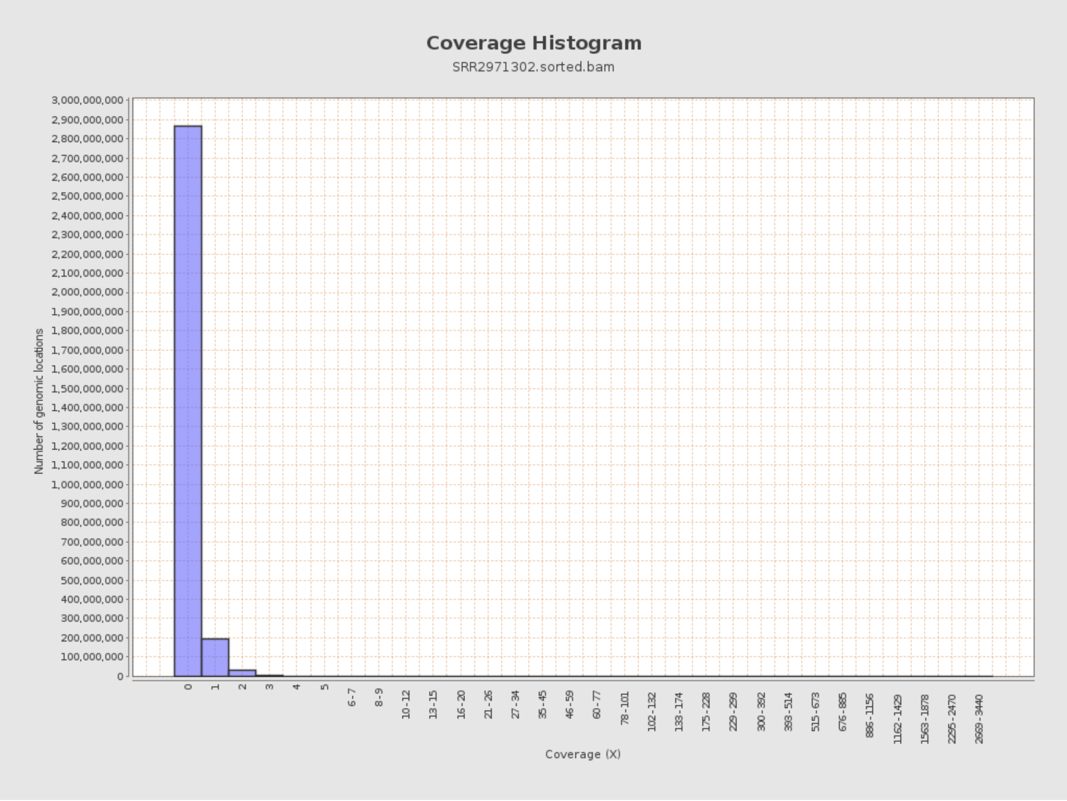
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20995020	0.0842	1.3166
chr2	243199373	23088566	0.0949	0.6136
chr3	198022430	18699705	0.0944	0.3719
chr4	191154276	18308932	0.0958	0.4161
chr5	180915260	17403179	0.0962	0.375
chr6	171115067	16331854	0.0954	0.3985
chr7	159138663	15772533	0.0991	1.0656
chr8	146364022	13784031	0.0942	1.7127

chr9	141213431	11167378	0.0791	0.6218
chr10	135534747	13051134	0.0963	0.703
chr11	135006516	12310635	0.0912	0.6061
chr12	133851895	12362838	0.0924	0.3736
chr13	115169878	8836011	0.0767	0.3173
chr14	107349540	18736941	0.1745	0.5467
chr15	102531392	7646311	0.0746	0.3162
chr16	90354753	7147006	0.0791	0.4259
chr17	81195210	6662757	0.0821	0.3823
chr18	78077248	8445683	0.1082	1.2527
chr19	59128983	4717353	0.0798	1.2037
chr20	63025520	5132577	0.0814	0.3597
chr21	48129895	3604675	0.0749	0.4085
chr22	51304566	2744647	0.0535	0.2952
chrMT	16571	17689	1.0675	1.3469
chrX	155270560	9544111	0.0615	0.3727
chrY	59373566	2293003	0.0386	0.3879

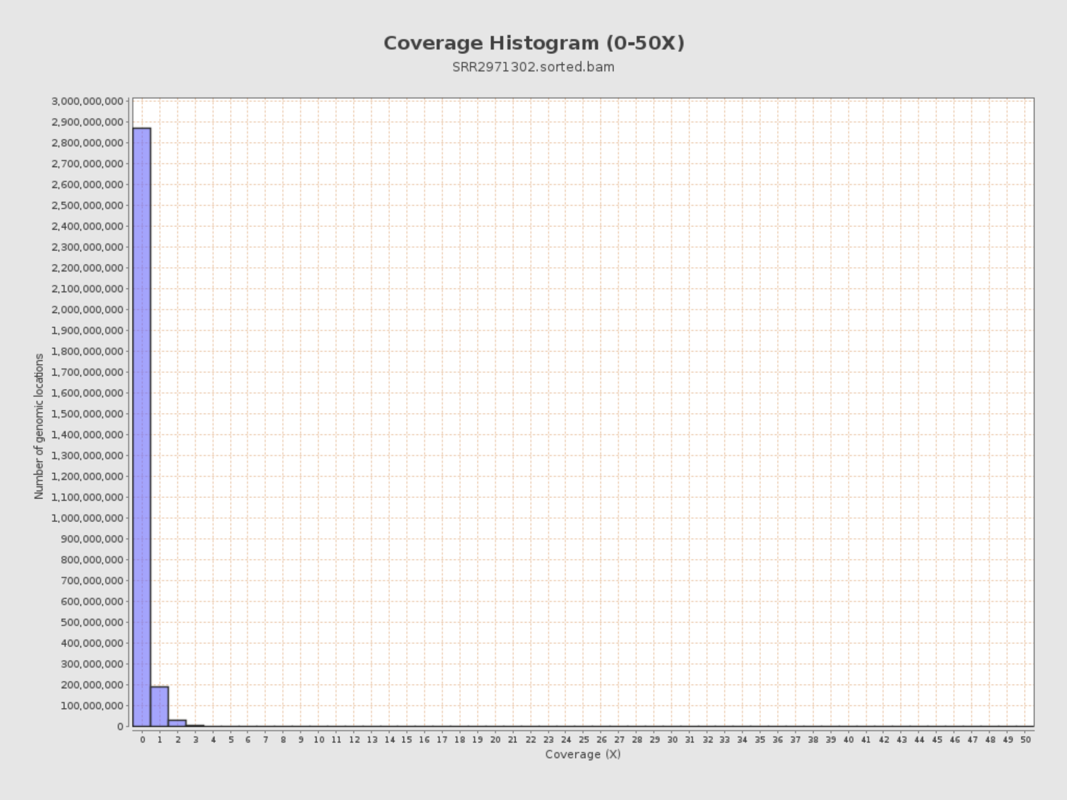
3. Results : Coverage across reference



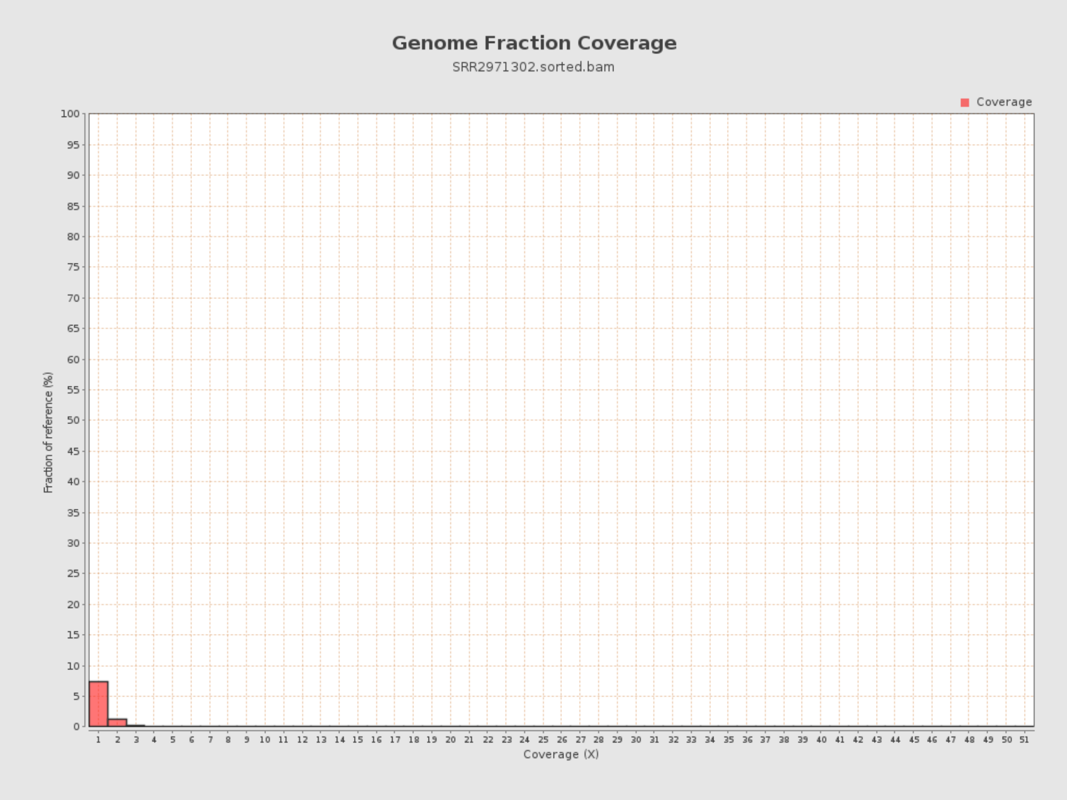
4. Results : Coverage Histogram



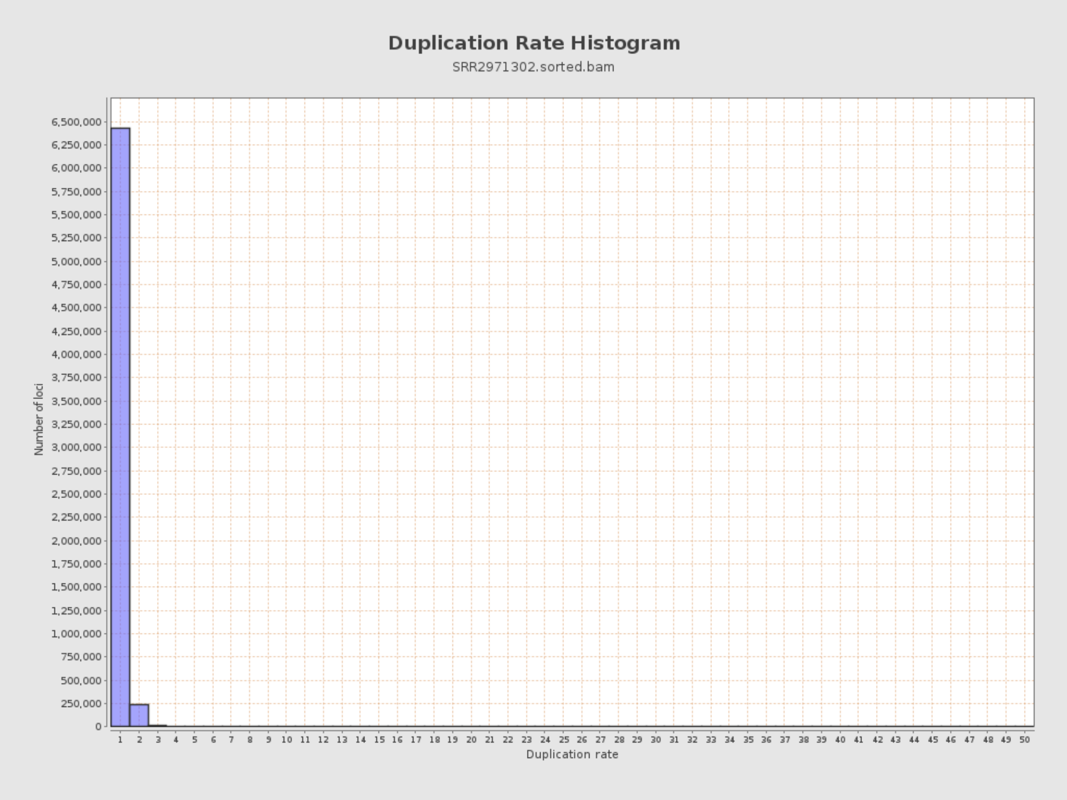
5. Results : Coverage Histogram (0-50X)



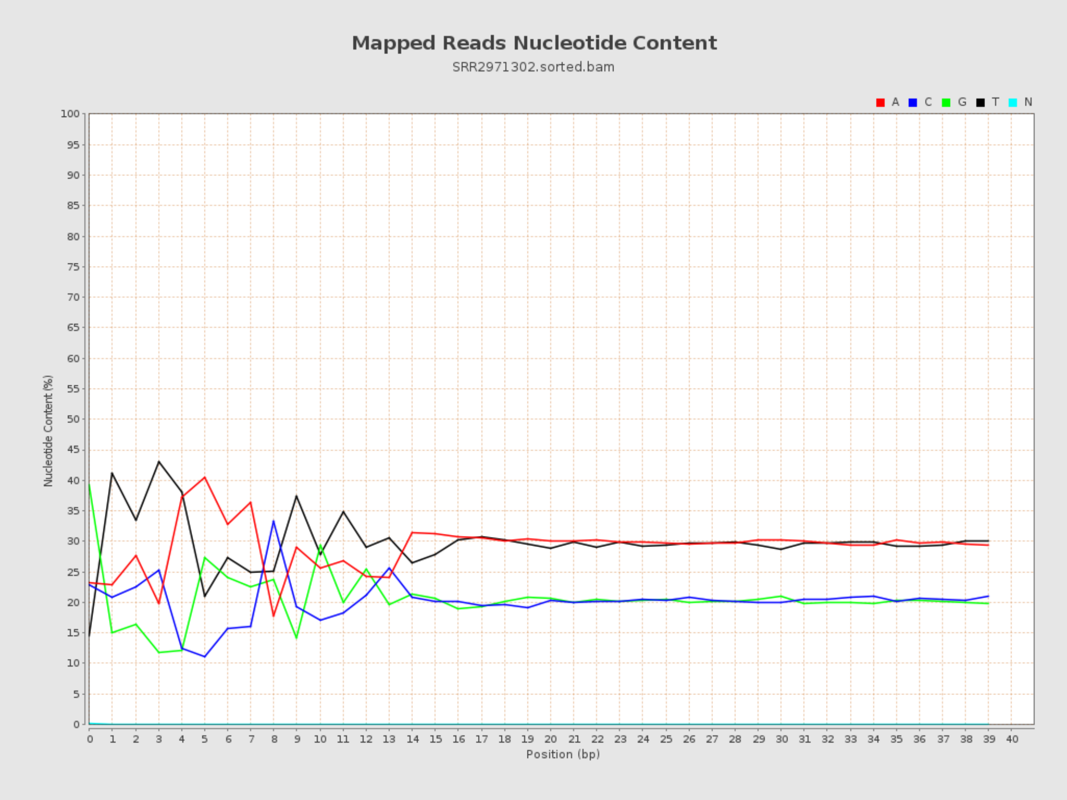
6. Results : Genome Fraction Coverage



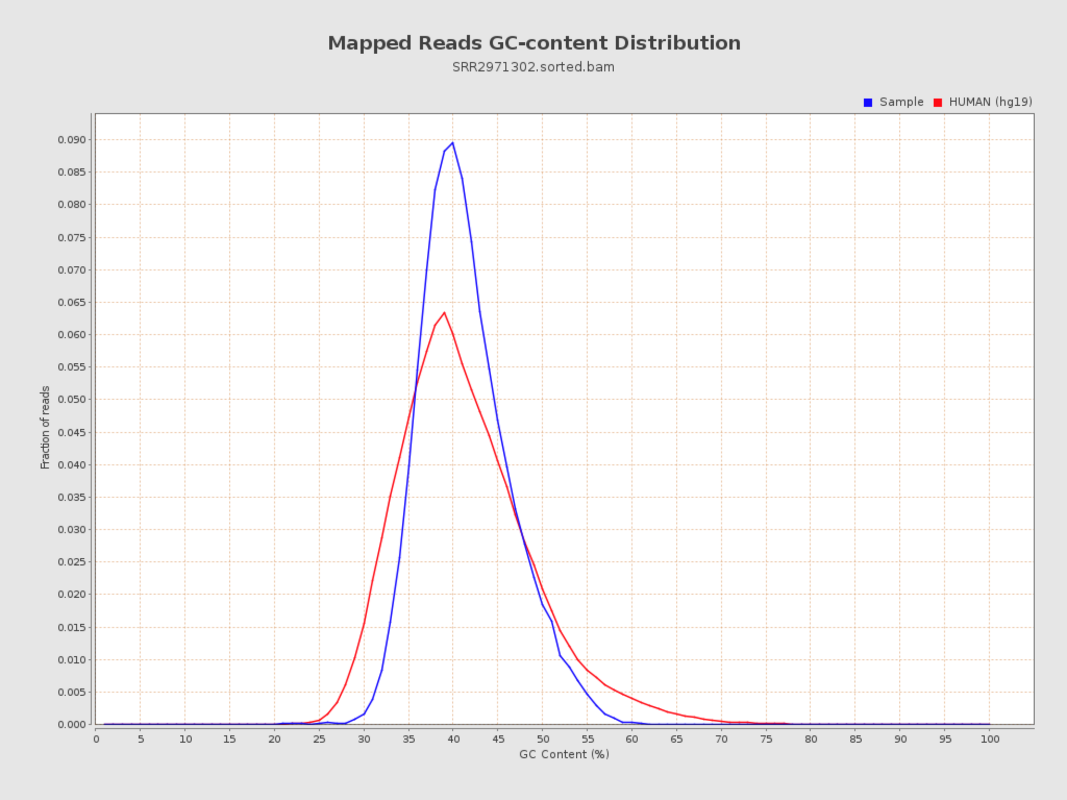
7. Results : Duplication Rate Histogram



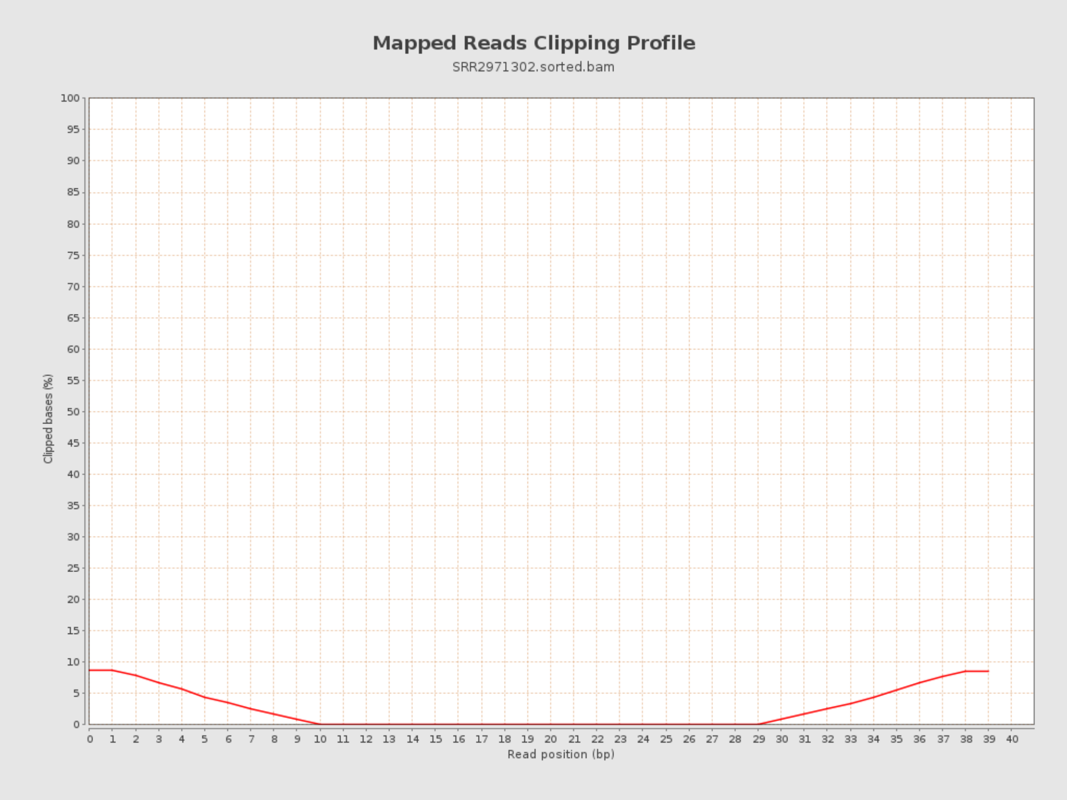
8. Results : Mapped Reads Nucleotide Content



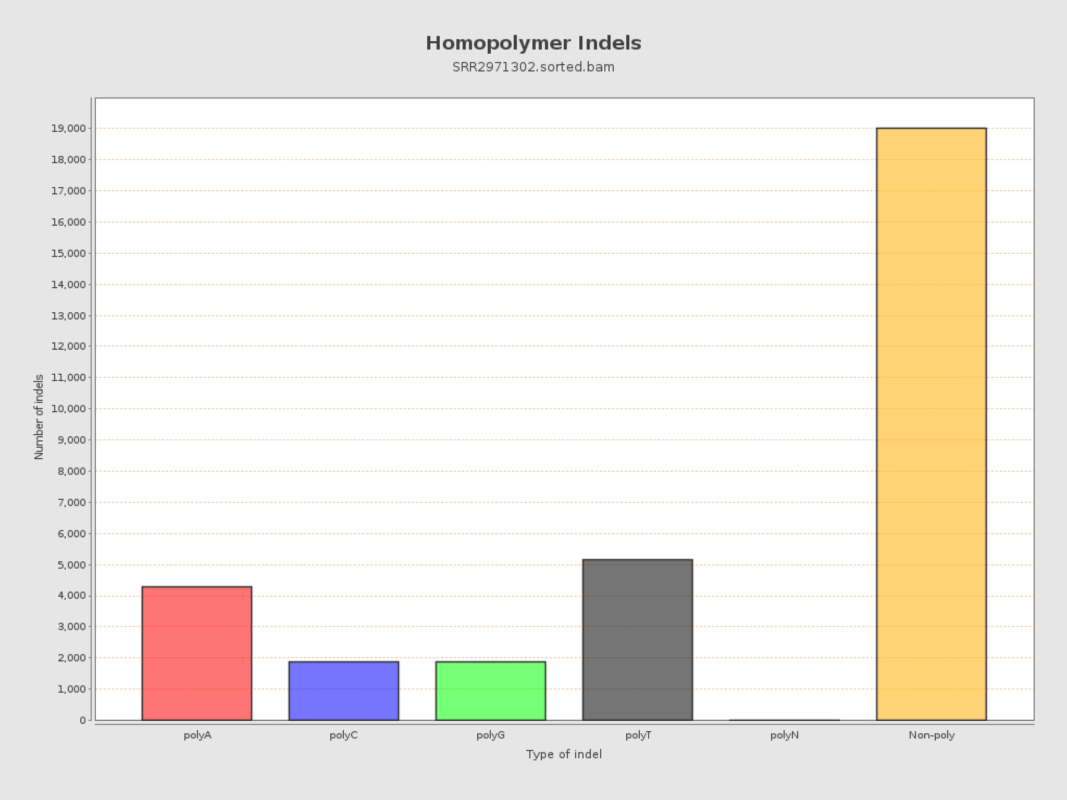
9. Results : Mapped Reads GC-content Distribution



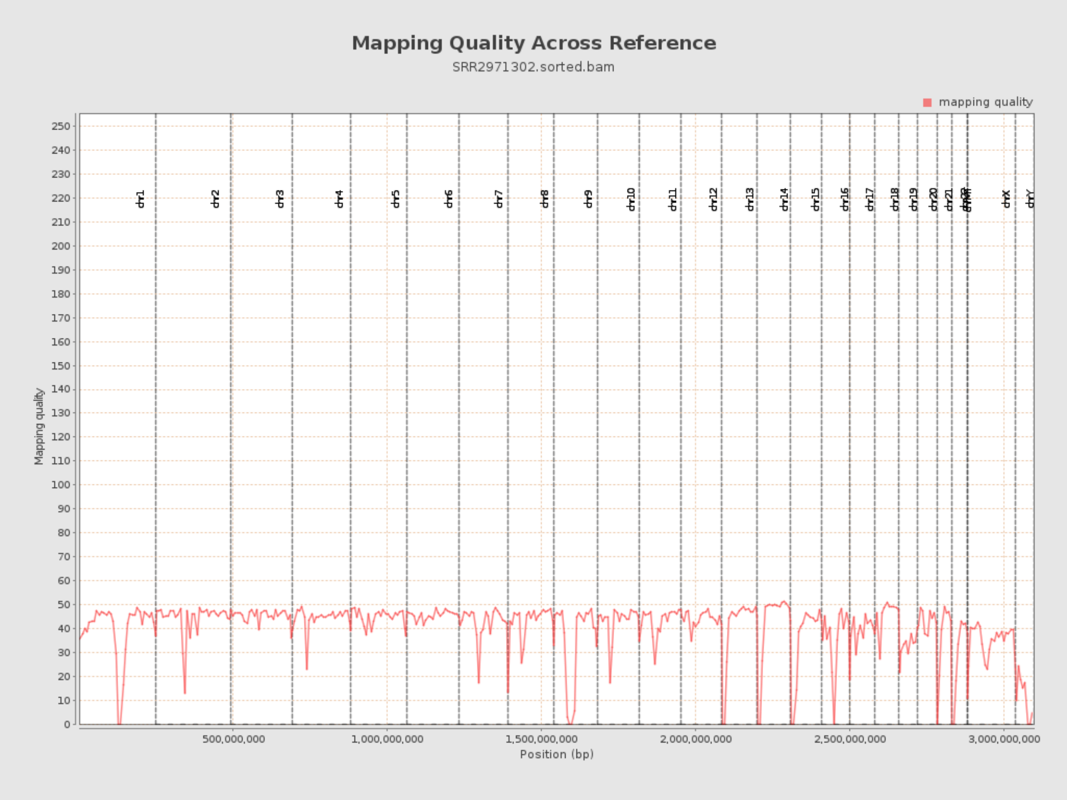
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram