Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:17:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971303.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_SRR2971303 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971303.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:17:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971303.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,819,028
Mapped reads	7,400,721 / 83.92%
Unmapped reads	1,418,307 / 16.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	395,947 / 4.49%
Duplication rate	4.35%
Clipped reads	652,895 / 7.4%

2.2. ACGT Content

Number/percentage of A's	85,877,674 / 29.4%
Number/percentage of C's	58,539,098 / 20.04%
Number/percentage of T's	87,770,217 / 30.05%
Number/percentage of G's	59,900,185 / 20.51%
Number/percentage of N's	17,406 / 0.01%
GC Percentage	40.55%

2.3. Coverage

Mean	0.0944
Standard Deviation	0.7192

2.4. Mapping Quality

Mean Mapping Quality	42.46

2.5. Mismatches and indels

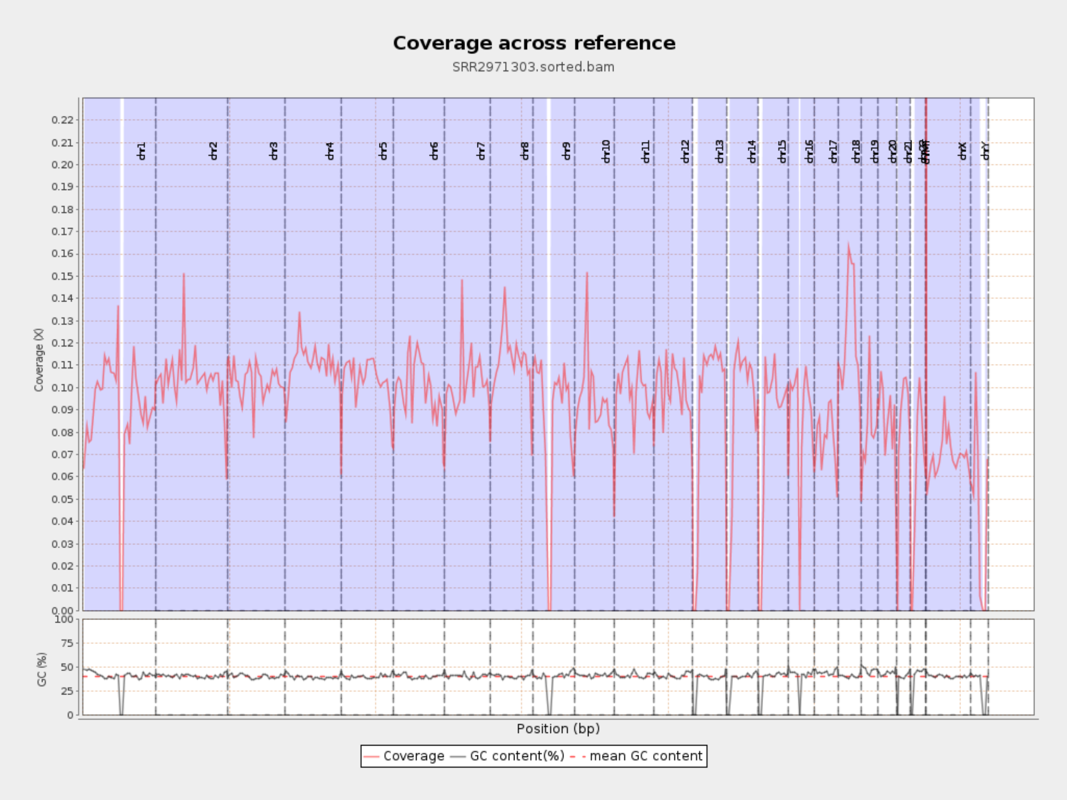
General error rate	0.28%
Mismatches	802,644
Insertions	9,677
Mapped reads with at least one insertion	0.13%
Deletions	23,817
Mapped reads with at least one deletion	0.32%
Homopolymer indels	41.34%

2.6. Chromosome stats

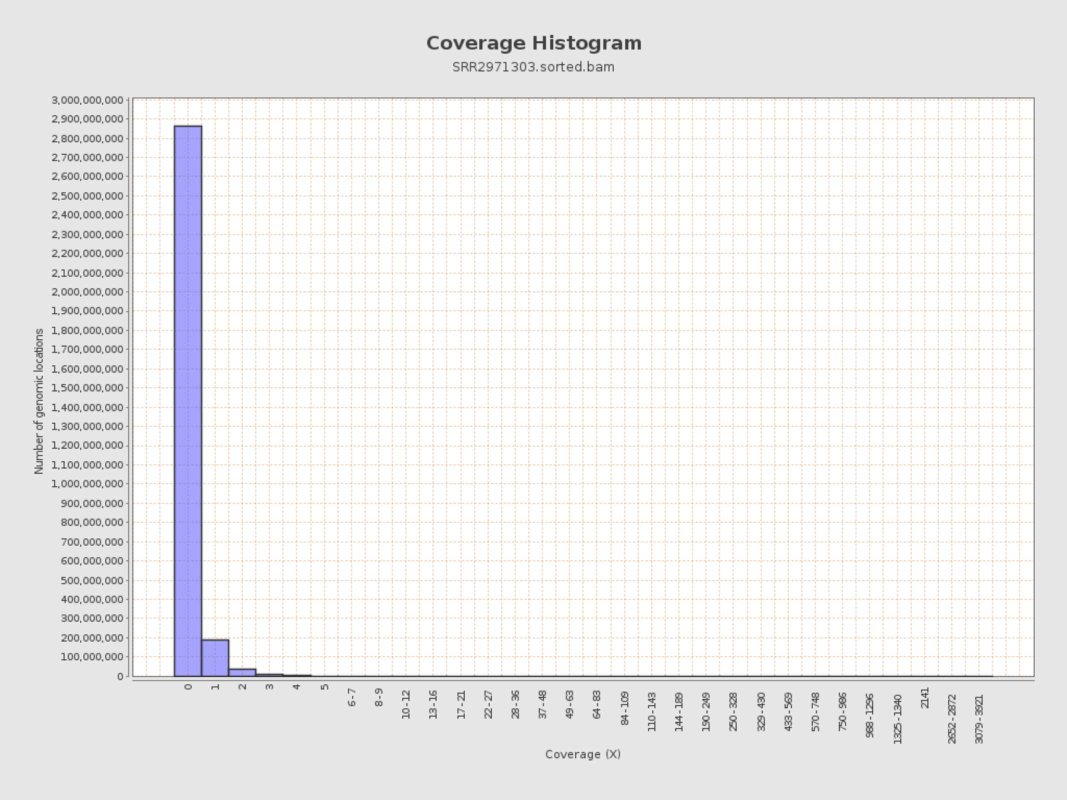
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22224332	0.0892	1.0864
chr2	243199373	25385280	0.1044	0.5731
chr3	198022430	20363328	0.1028	0.3879
chr4	191154276	21167088	0.1107	0.4373
chr5	180915260	18661264	0.1031	0.3941
chr6	171115067	17171248	0.1003	0.4168
chr7	159138663	16274824	0.1023	0.8789
chr8	146364022	16352510	0.1117	1.9406

chr9	141213431	12128860	0.0859	0.5324
chr10	135534747	12828663	0.0947	0.6227
chr11	135006516	13203133	0.0978	0.5497
chr12	133851895	13341095	0.0997	0.3928
chr13	115169878	10579639	0.0919	0.3615
chr14	107349540	9532533	0.0888	0.4409
chr15	102531392	8384044	0.0818	0.3405
chr16	90354753	7704955	0.0853	0.4071
chr17	81195210	6325660	0.0779	0.3674
chr18	78077248	9710683	0.1244	1.0456
chr19	59128983	4867504	0.0823	0.9973
chr20	63025520	5476779	0.0869	0.3761
chr21	48129895	3976853	0.0826	0.4169
chr22	51304566	3097708	0.0604	0.3244
chrMT	16571	11656	0.7034	1.0453
chrX	155270560	10706016	0.069	0.3855
chrY	59373566	2658872	0.0448	0.4211

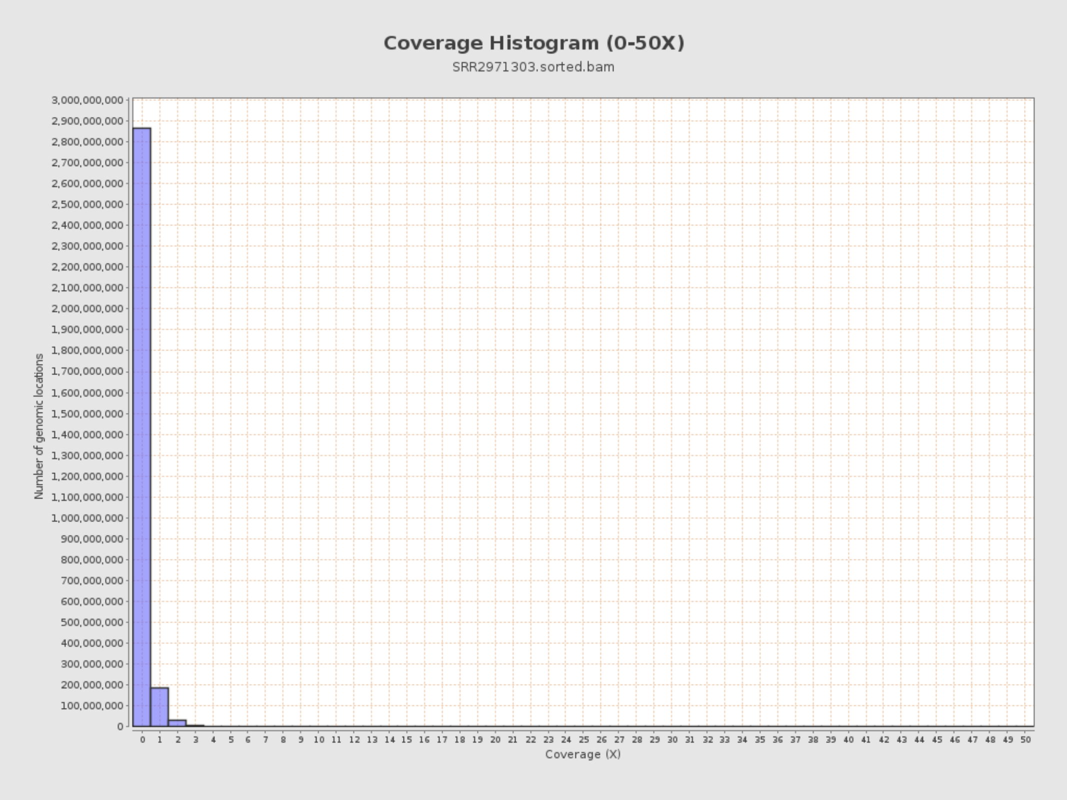
3. Results : Coverage across reference



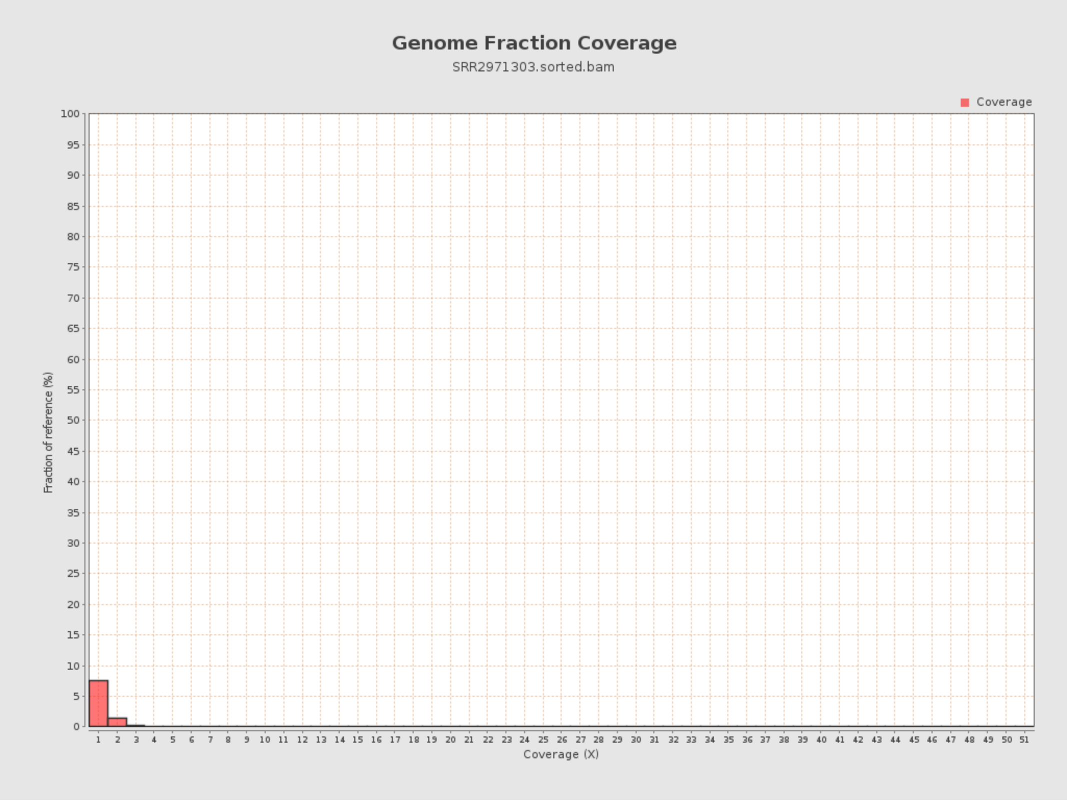
4. Results : Coverage Histogram



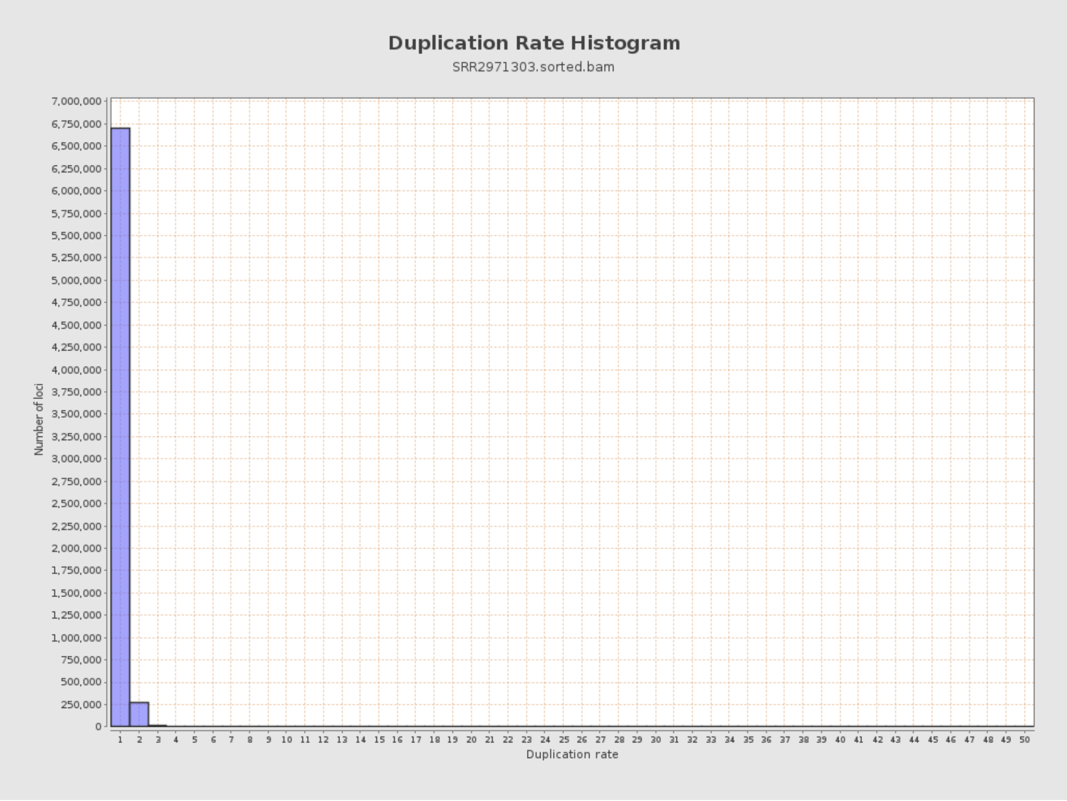
5. Results : Coverage Histogram (0-50X)



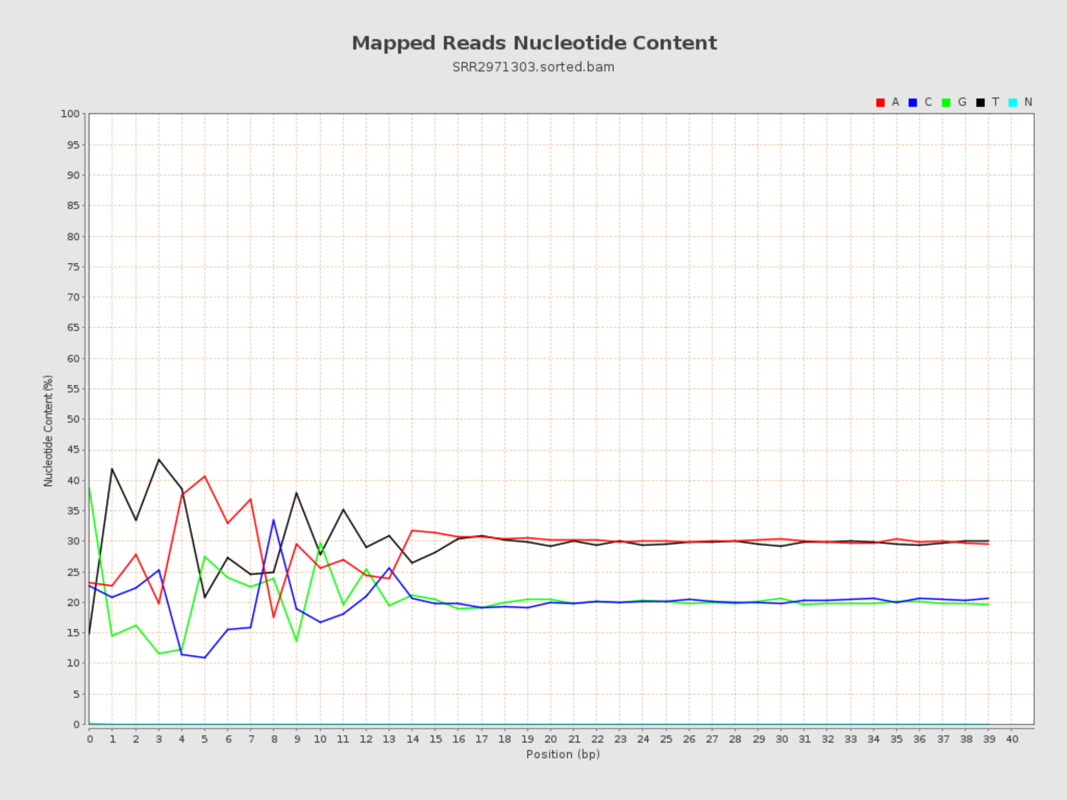
6. Results : Genome Fraction Coverage



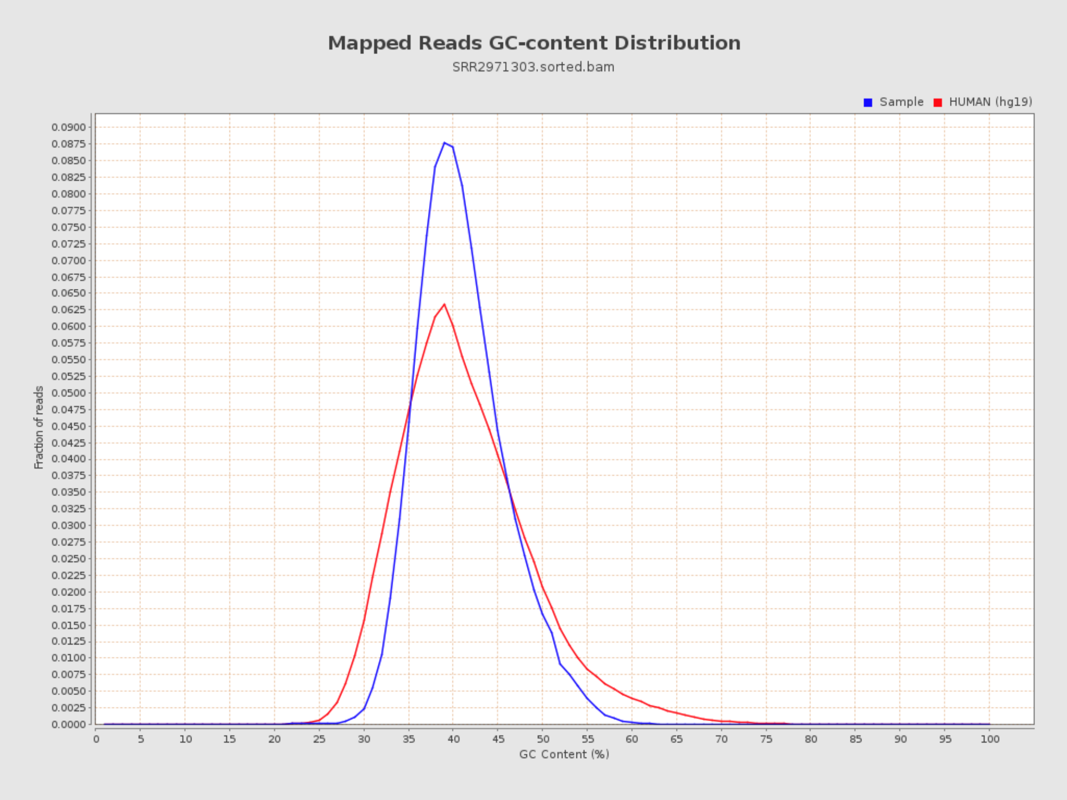
7. Results : Duplication Rate Histogram



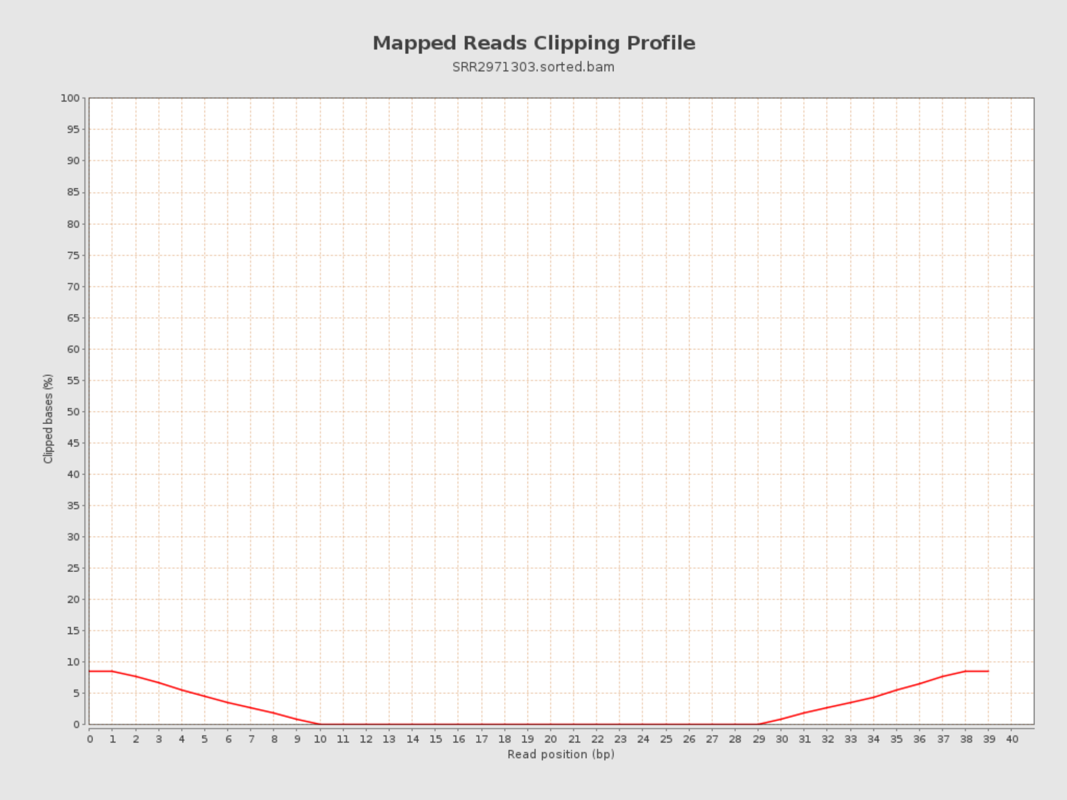
8. Results : Mapped Reads Nucleotide Content



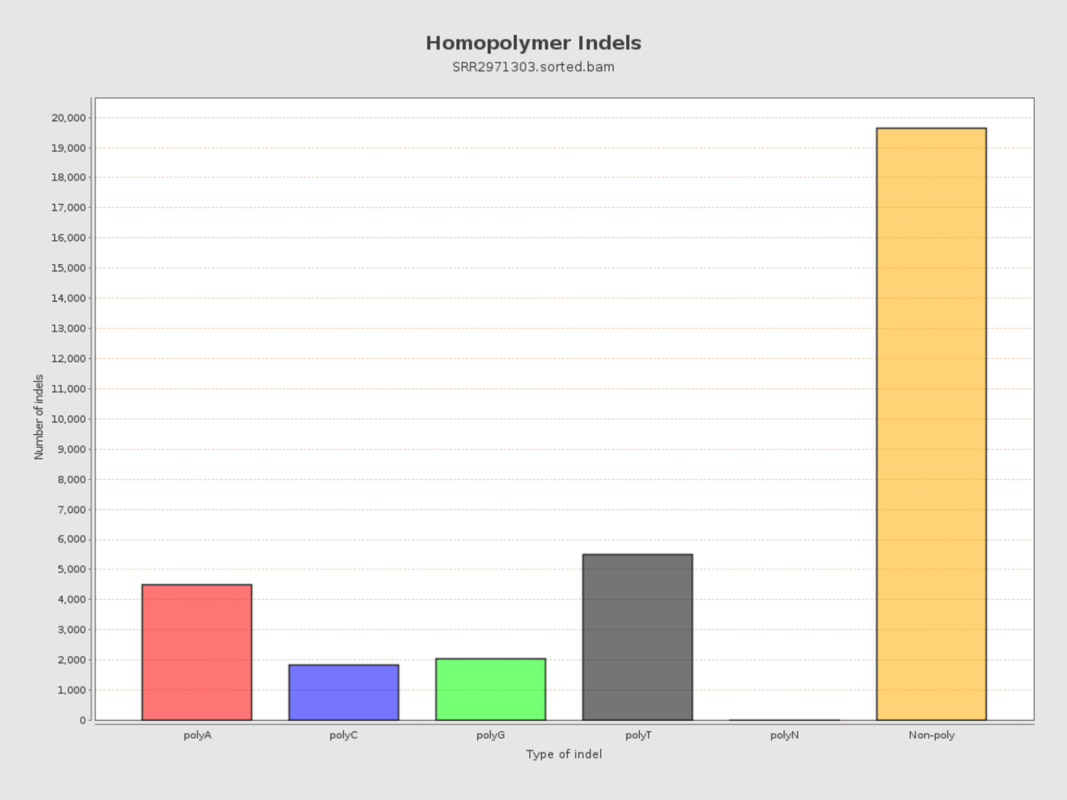
9. Results : Mapped Reads GC-content Distribution



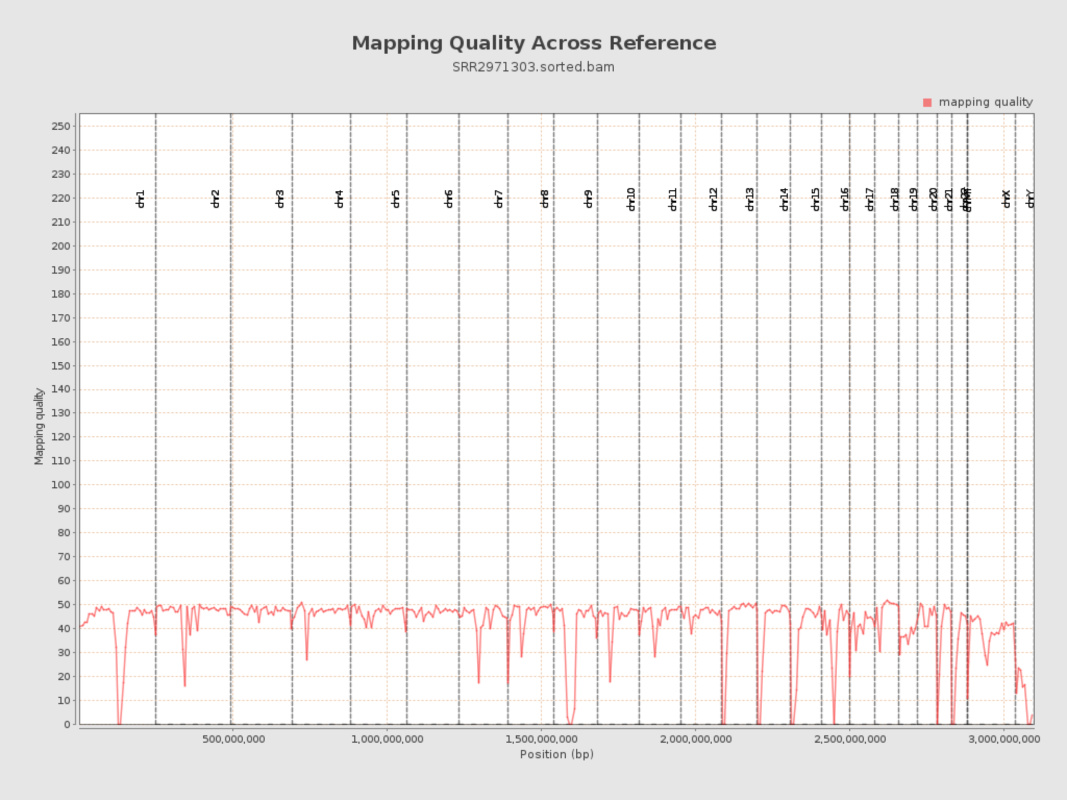
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram