Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:53:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971286.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_SRR2971286 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971286.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:53:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971286.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,647,048
Mapped reads	9,254,510 / 86.92%
Unmapped reads	1,392,538 / 13.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	1,040,300 / 9.77%
Duplication rate	8.37%
Clipped reads	1,087,829 / 10.22%

2.2. ACGT Content

Number/percentage of A's	101,156,003 / 27.8%
Number/percentage of C's	78,568,712 / 21.59%
Number/percentage of T's	104,183,762 / 28.63%
Number/percentage of G's	79,984,574 / 21.98%
Number/percentage of N's	2,659 / 0%
GC Percentage	43.57%

2.3. Coverage

Mean	0.1176
Standard Deviation	1.7172

2.4. Mapping Quality

Mean Mapping Quality	30.57

2.5. Mismatches and indels

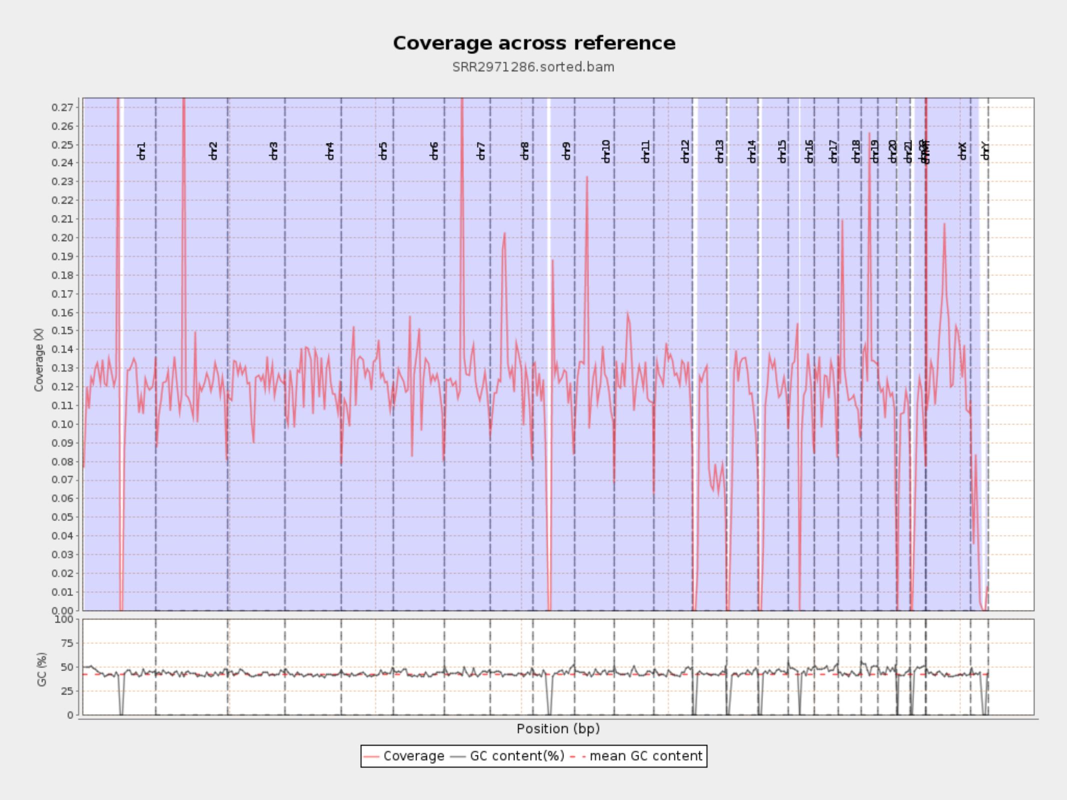
General error rate	0.39%
Mismatches	1,418,115
Insertions	15,788
Mapped reads with at least one insertion	0.17%
Deletions	29,396
Mapped reads with at least one deletion	0.32%
Homopolymer indels	36.07%

2.6. Chromosome stats

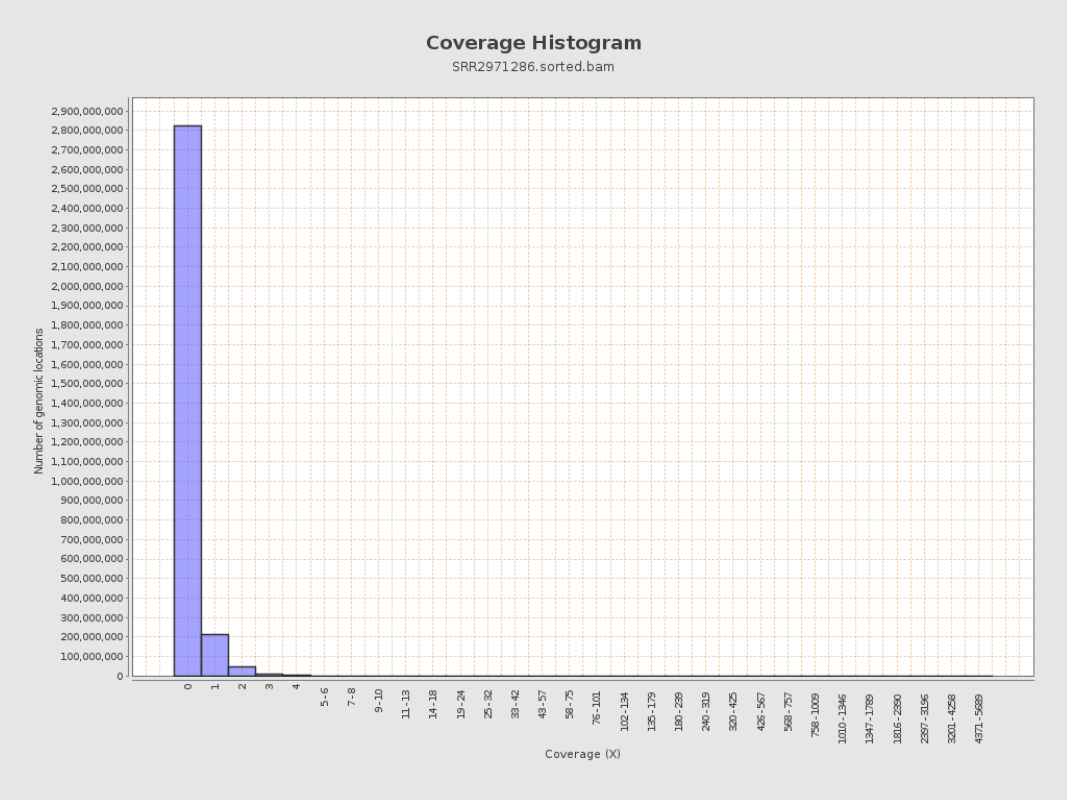
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29731556	0.1193	3.813
chr2	243199373	30421722	0.1251	1.575
chr3	198022430	24259582	0.1225	0.4704
chr4	191154276	23458465	0.1227	0.4929
chr5	180915260	22409212	0.1239	0.5695
chr6	171115067	21027553	0.1229	0.5831
chr7	159138663	20833645	0.1309	1.996
chr8	146364022	18793162	0.1284	2.5976

chr9	141213431	15466285	0.1095	1.557
chr10	135534747	17298253	0.1276	1.2648
chr11	135006516	16859293	0.1249	1.2031
chr12	133851895	17016424	0.1271	0.6118
chr13	115169878	8553551	0.0743	0.3348
chr14	107349540	11075616	0.1032	0.9435
chr15	102531392	10067411	0.0982	0.4065
chr16	90354753	9900224	0.1096	0.7042
chr17	81195210	9810373	0.1208	0.5718
chr18	78077248	9771340	0.1251	3.6044
chr19	59128983	8774208	0.1484	3.7513
chr20	63025520	7101174	0.1127	0.6246
chr21	48129895	4277420	0.0889	0.6271
chr22	51304566	3965543	0.0773	0.3564
chrMT	16571	27046	1.6321	2.1059
chrX	155270560	21246899	0.1368	1.0397
chrY	59373566	1785257	0.0301	0.3106

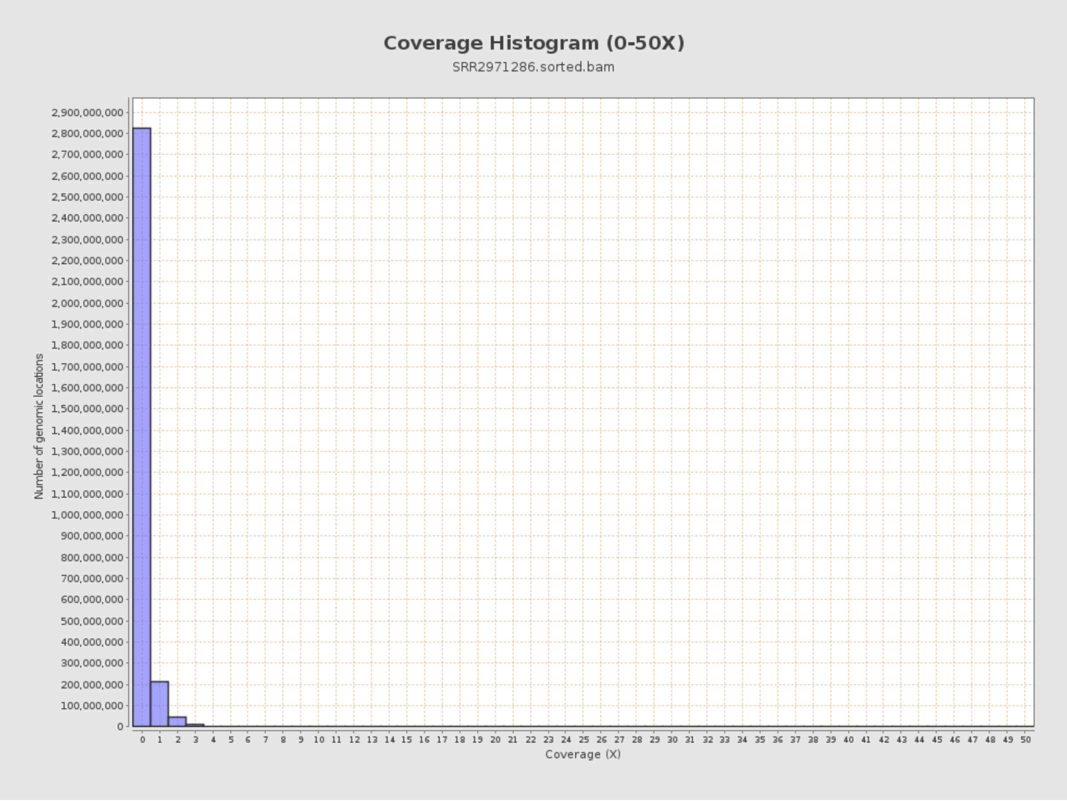
3. Results : Coverage across reference



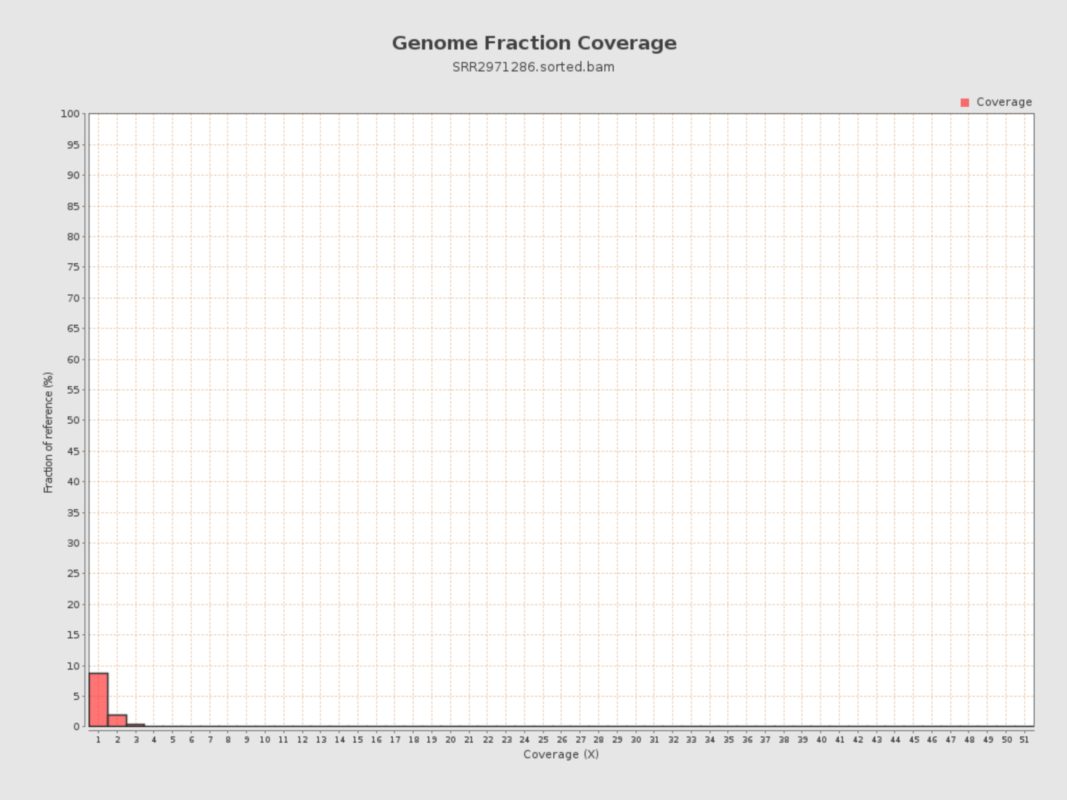
4. Results : Coverage Histogram



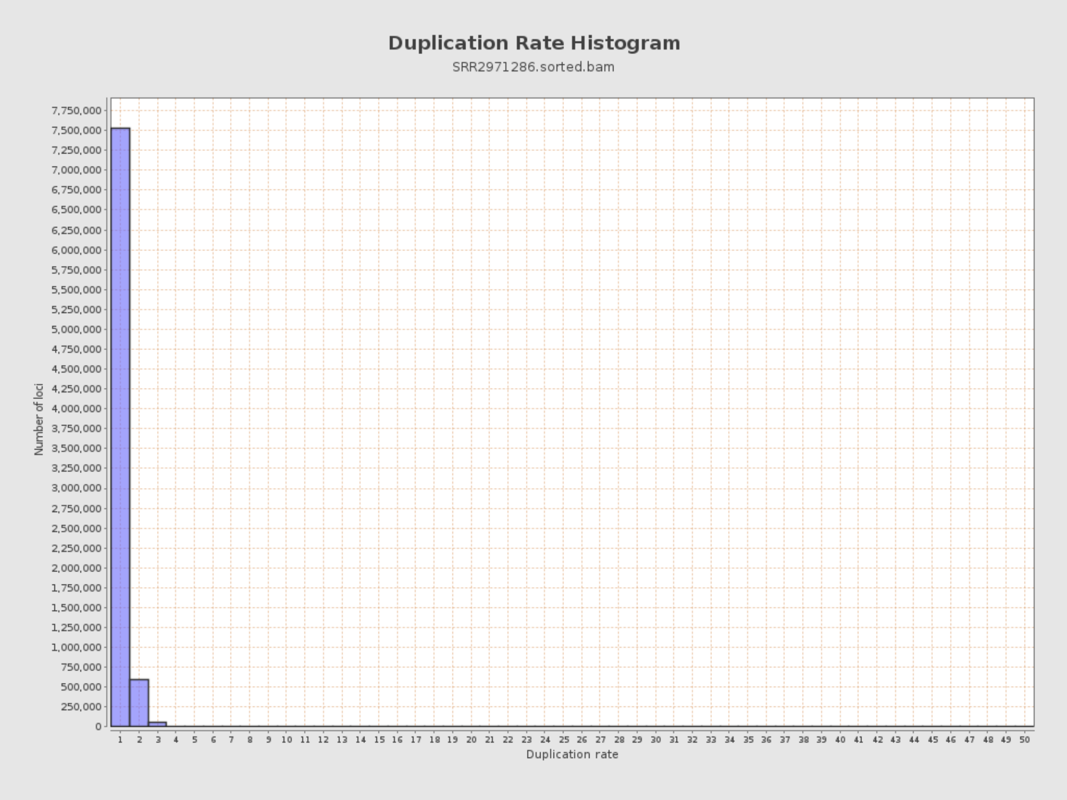
5. Results : Coverage Histogram (0-50X)



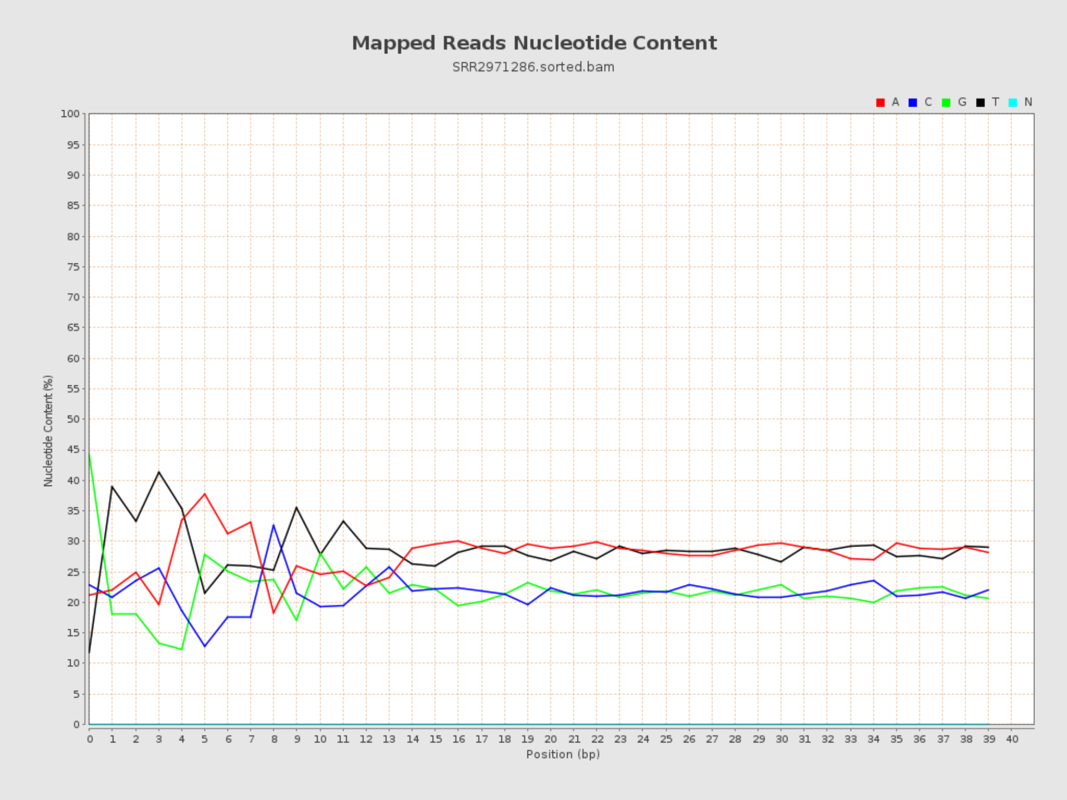
6. Results : Genome Fraction Coverage



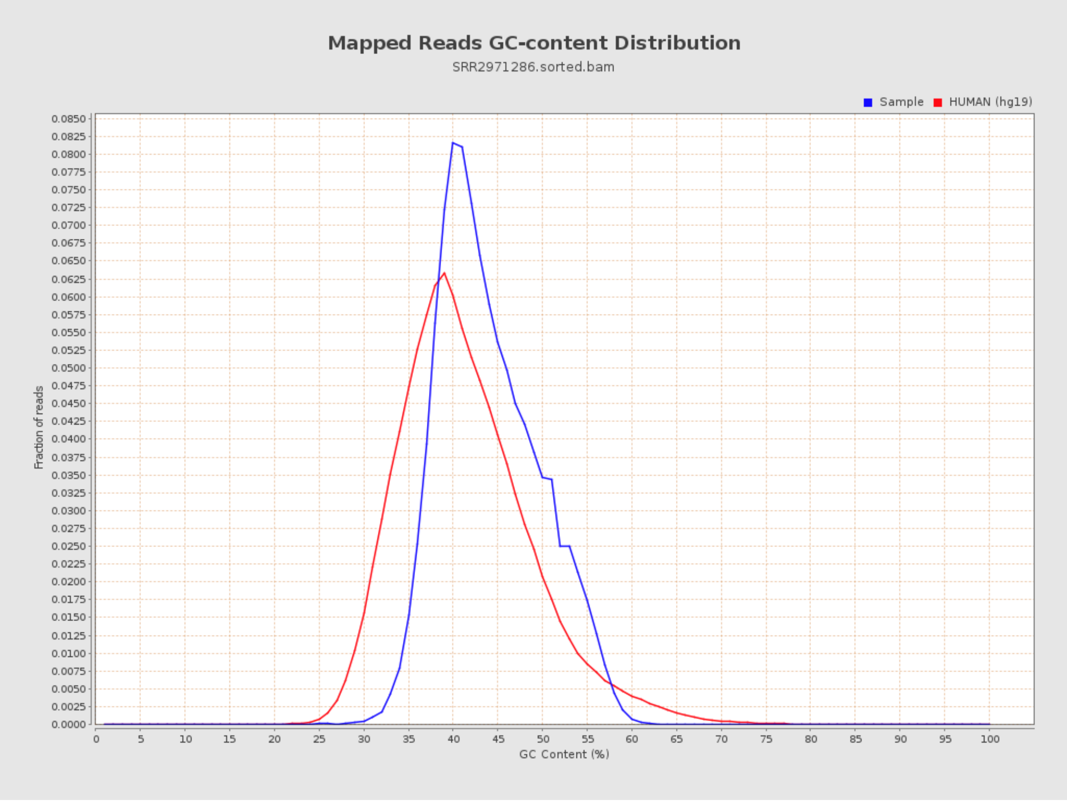
7. Results : Duplication Rate Histogram



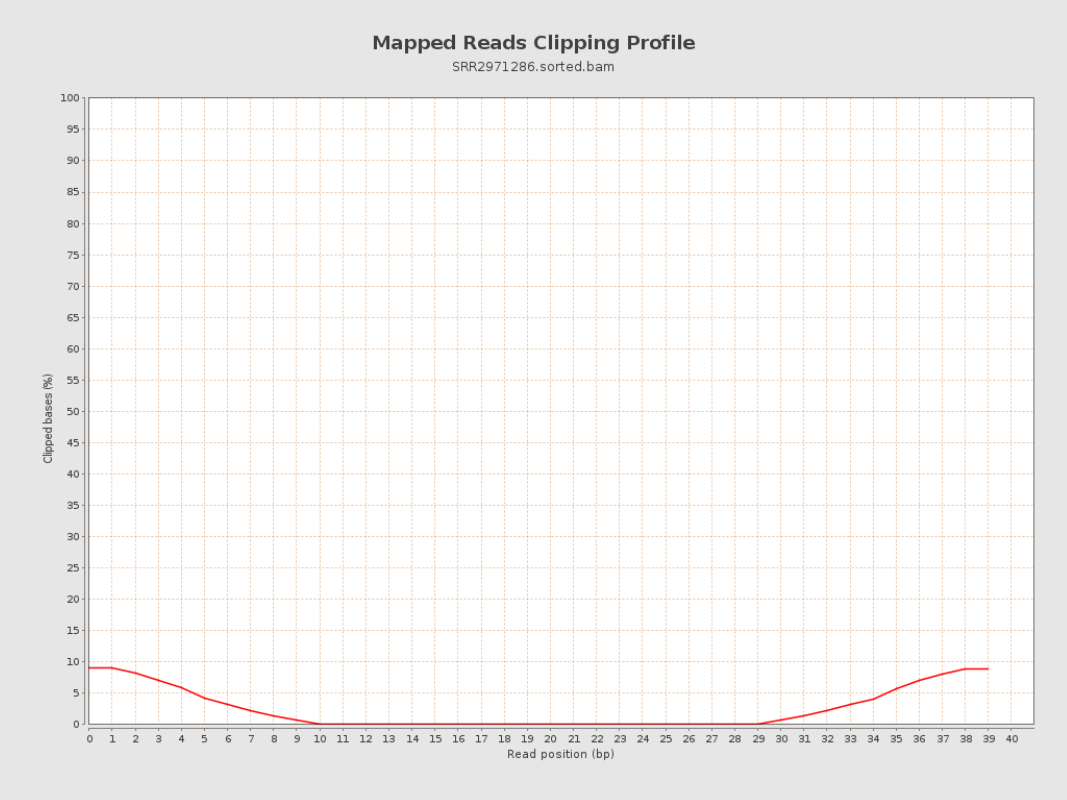
8. Results : Mapped Reads Nucleotide Content



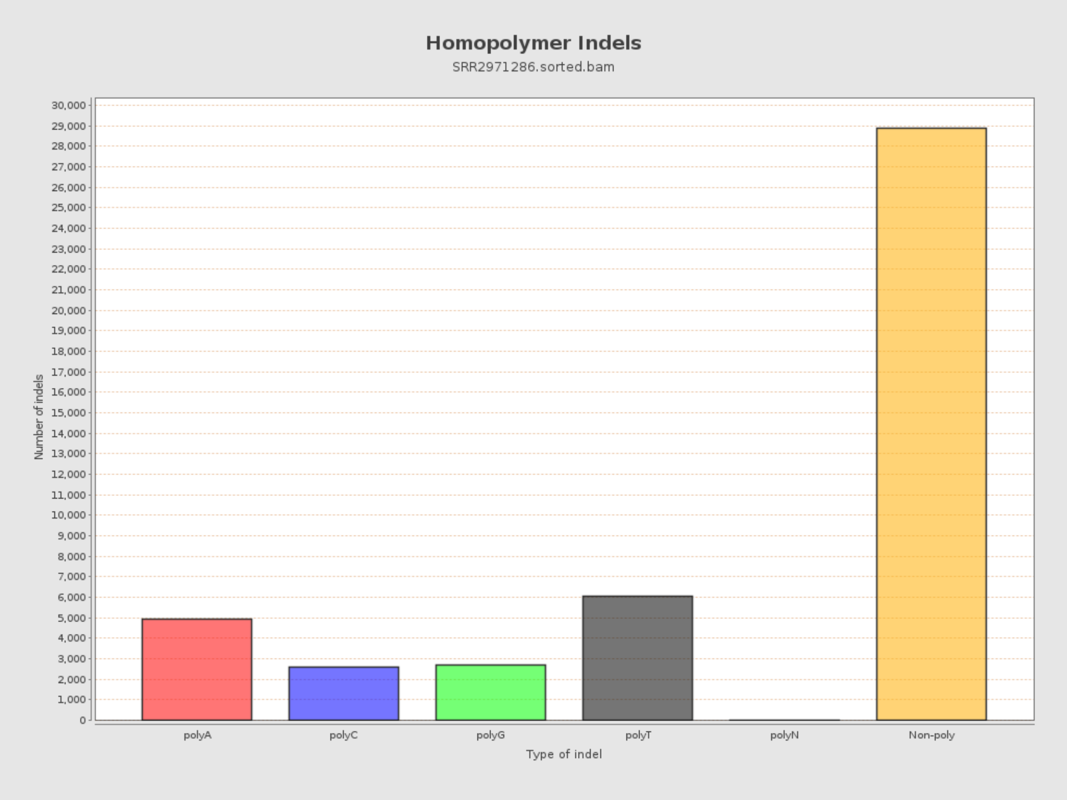
9. Results : Mapped Reads GC-content Distribution



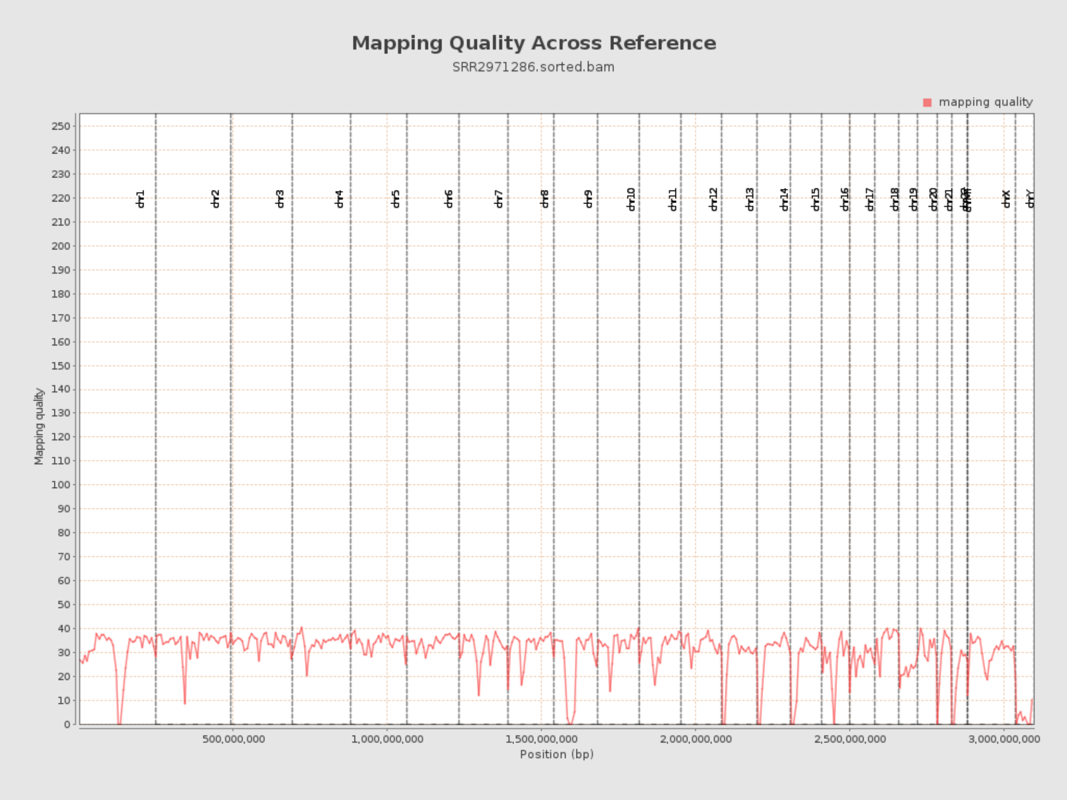
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram