Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:40:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971285.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_SRR2971285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971285.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:40:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971285.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,545,241
Mapped reads	9,708,448 / 84.09%
Unmapped reads	1,836,793 / 15.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	735,551 / 6.37%
Duplication rate	6.03%
Clipped reads	942,791 / 8.17%

2.2. ACGT Content

Number/percentage of A's	110,781,466 / 28.95%
Number/percentage of C's	77,714,669 / 20.31%
Number/percentage of T's	114,220,826 / 29.85%
Number/percentage of G's	79,905,083 / 20.88%
Number/percentage of N's	2,802 / 0%
GC Percentage	41.19%

2.3. Coverage

Mean	0.1236
Standard Deviation	1.2352

2.4. Mapping Quality

Mean Mapping Quality	39.28

2.5. Mismatches and indels

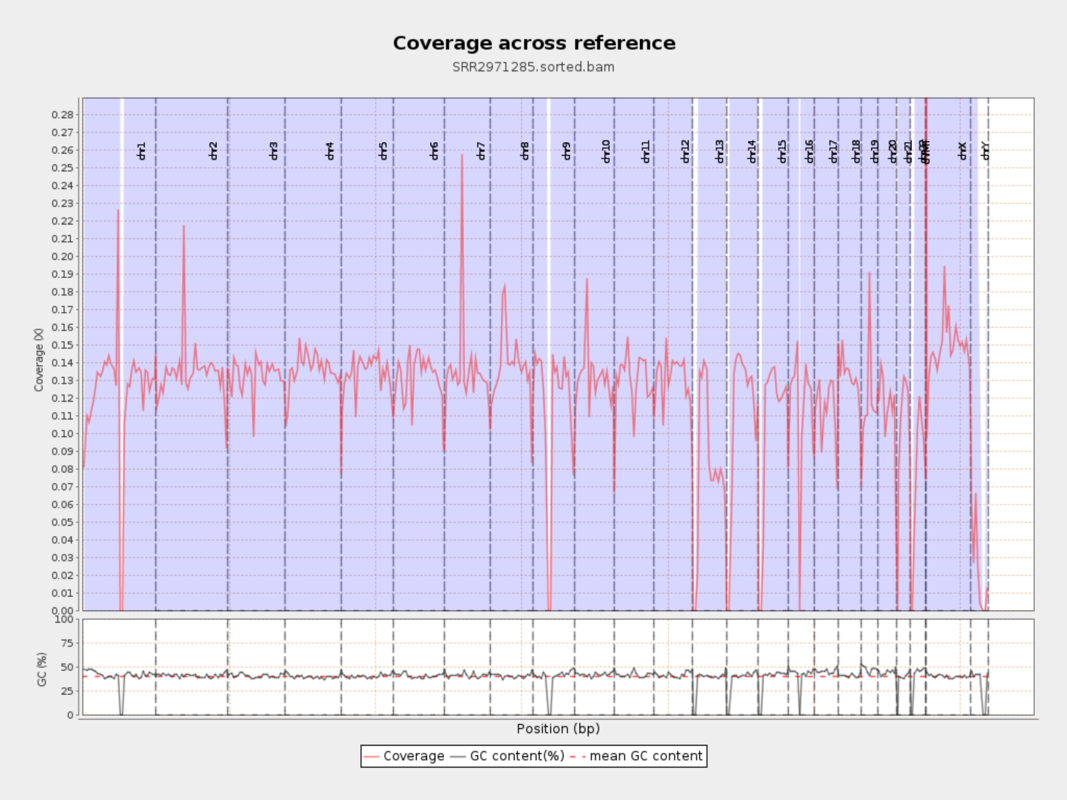
General error rate	0.31%
Mismatches	1,163,845
Insertions	13,885
Mapped reads with at least one insertion	0.14%
Deletions	31,044
Mapped reads with at least one deletion	0.32%
Homopolymer indels	40.32%

2.6. Chromosome stats

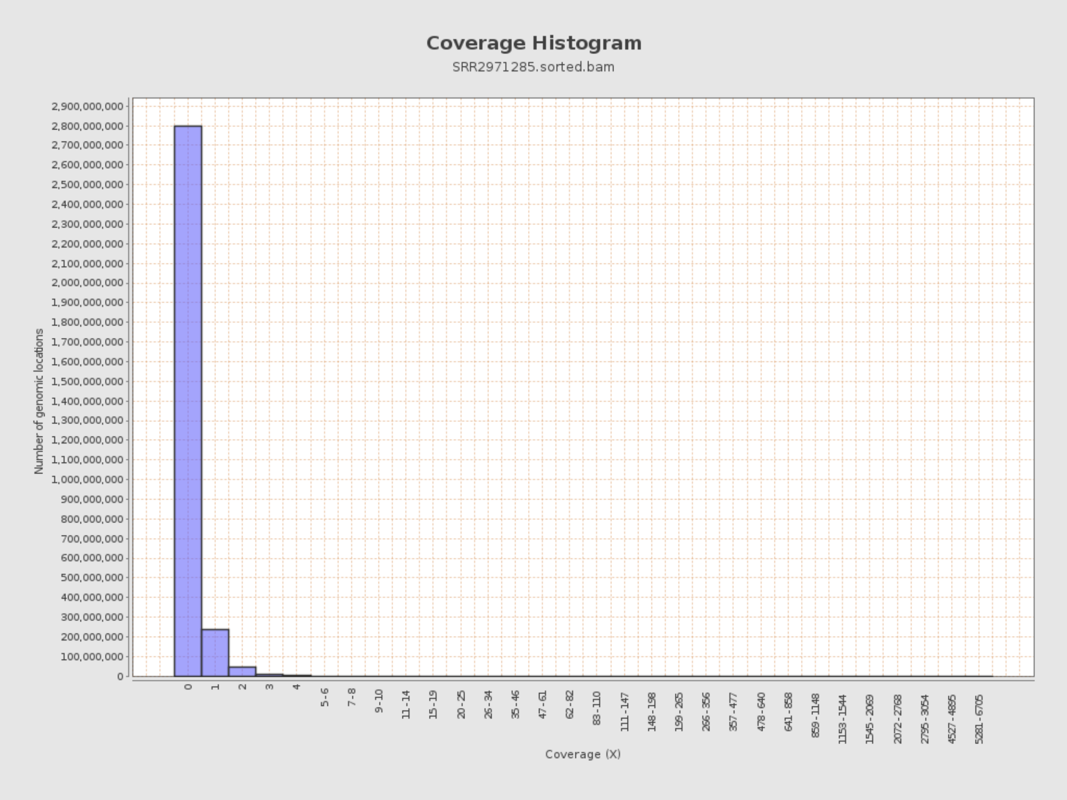
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30580913	0.1227	2.235
chr2	243199373	32765273	0.1347	0.8927
chr3	198022430	26359044	0.1331	0.4546
chr4	191154276	26093450	0.1365	0.4841
chr5	180915260	24134211	0.1334	0.485
chr6	171115067	22704273	0.1327	0.5145
chr7	159138663	21722495	0.1365	1.6388
chr8	146364022	20186782	0.1379	3.2793

chr9	141213431	16159899	0.1144	0.9071
chr10	135534747	17954096	0.1325	0.825
chr11	135006516	17620036	0.1305	0.7868
chr12	133851895	17605657	0.1315	0.4991
chr13	115169878	9155517	0.0795	0.3365
chr14	107349540	11818471	0.1101	0.6545
chr15	102531392	10486088	0.1023	0.3884
chr16	90354753	10040742	0.1111	0.5004
chr17	81195210	9346452	0.1151	0.5177
chr18	78077248	10409557	0.1333	1.9476
chr19	59128983	7088624	0.1199	2.0758
chr20	63025520	7361364	0.1168	0.478
chr21	48129895	4858792	0.101	0.5117
chr22	51304566	3820016	0.0745	0.3318
chrMT	16571	40207	2.4263	2.896
chrX	155270560	22995252	0.1481	0.6975
chrY	59373566	1356649	0.0228	0.2806

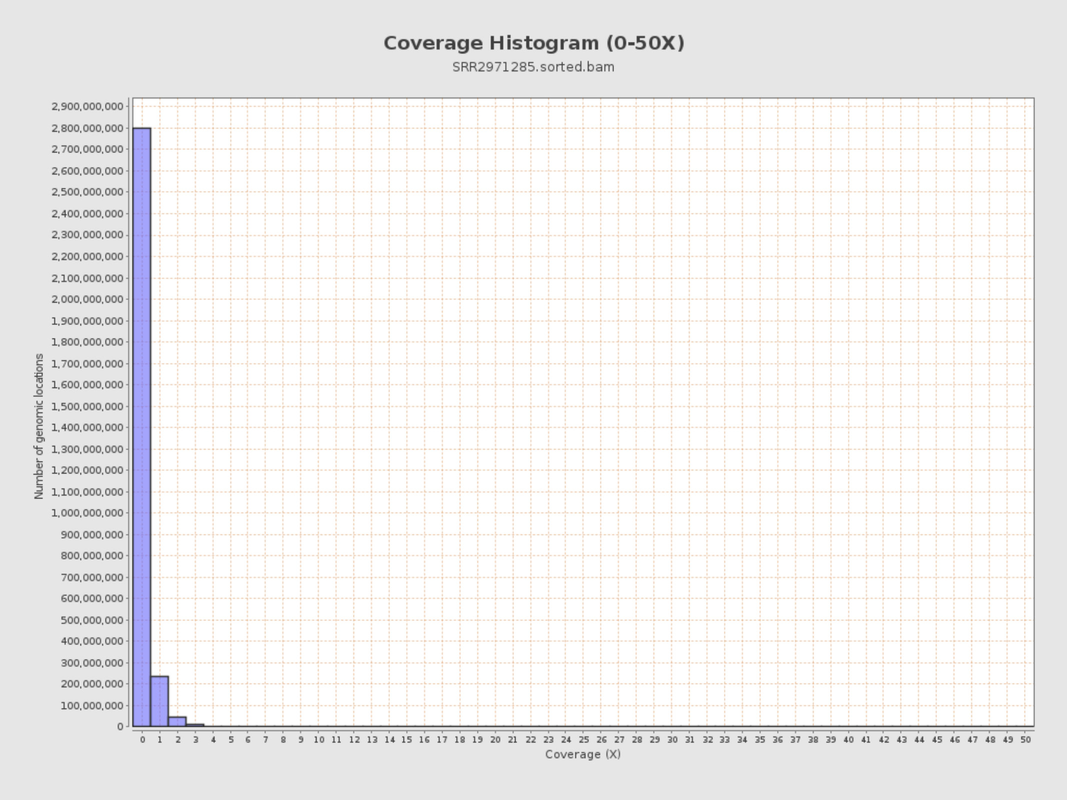
3. Results : Coverage across reference



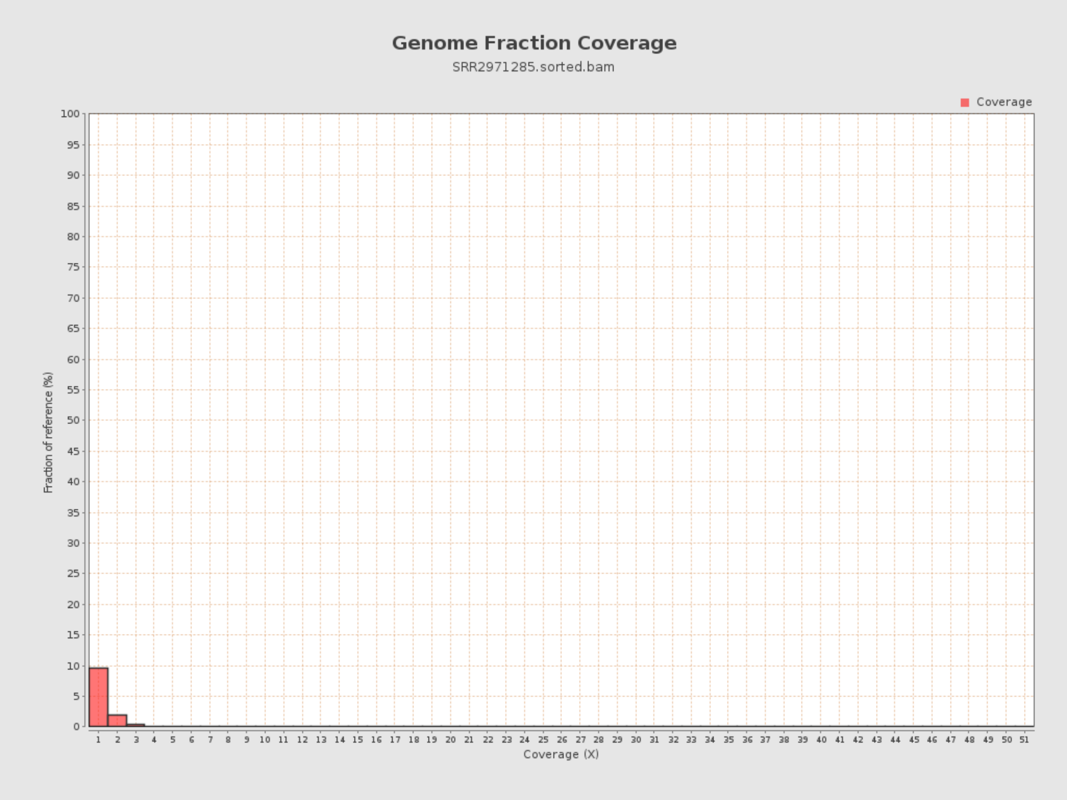
4. Results : Coverage Histogram



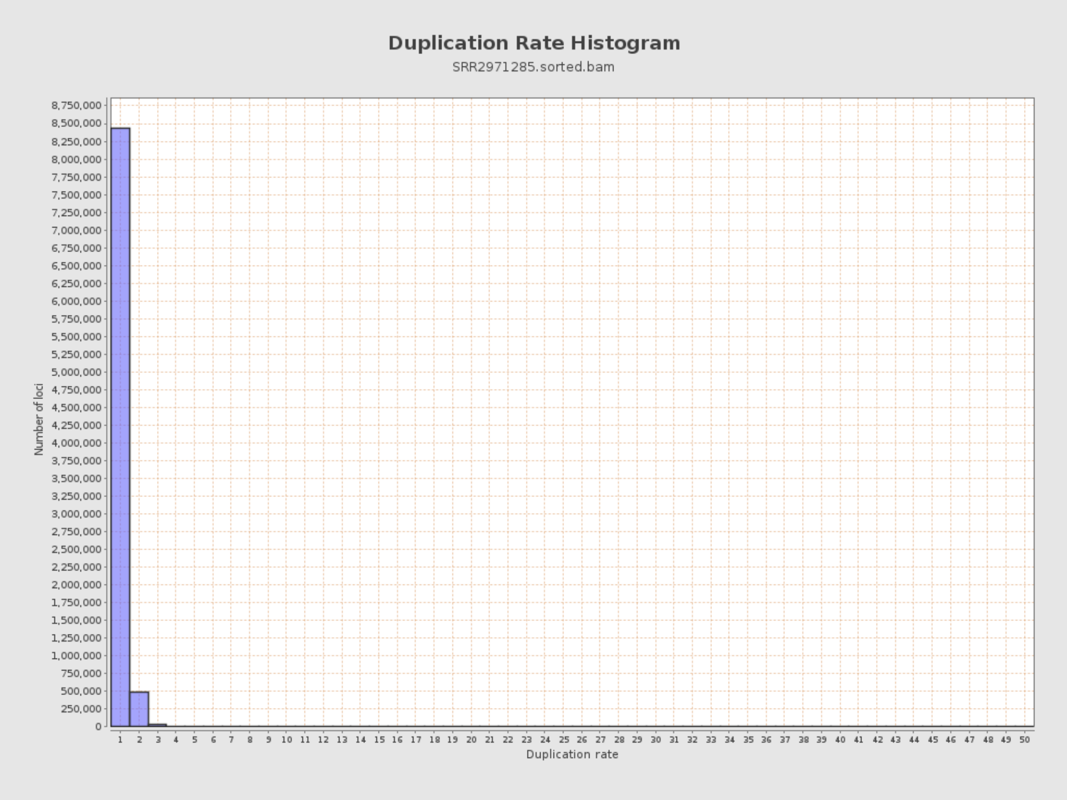
5. Results : Coverage Histogram (0-50X)



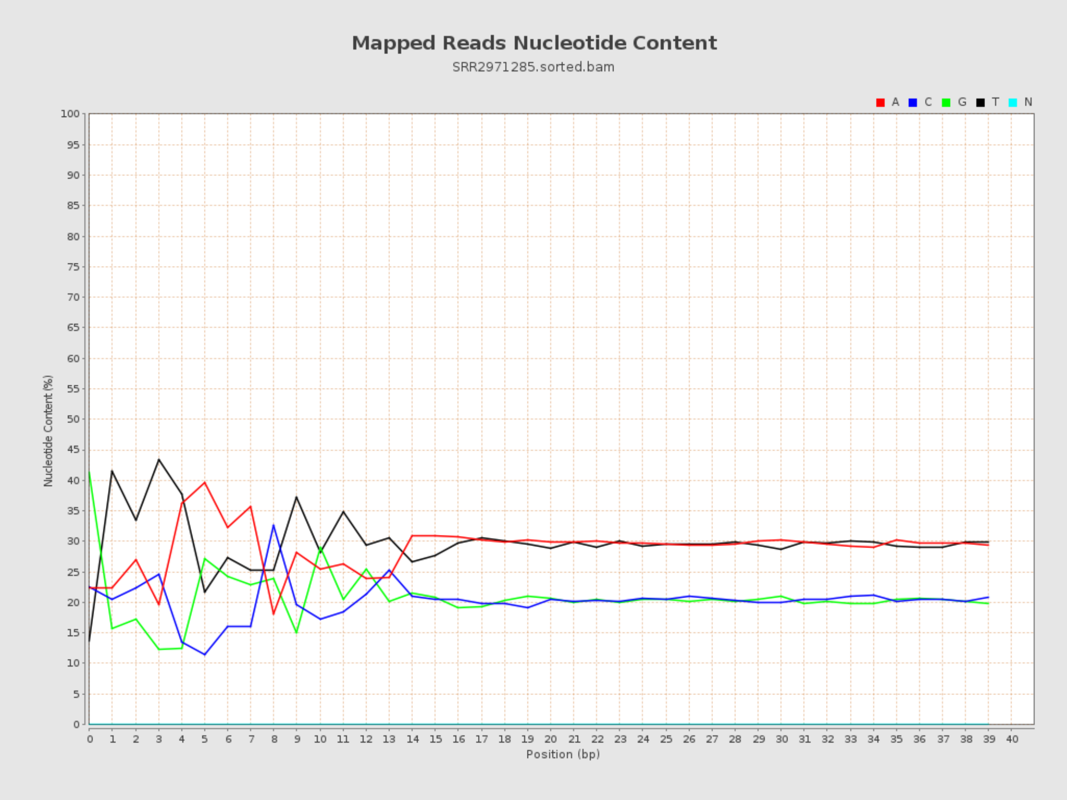
6. Results : Genome Fraction Coverage



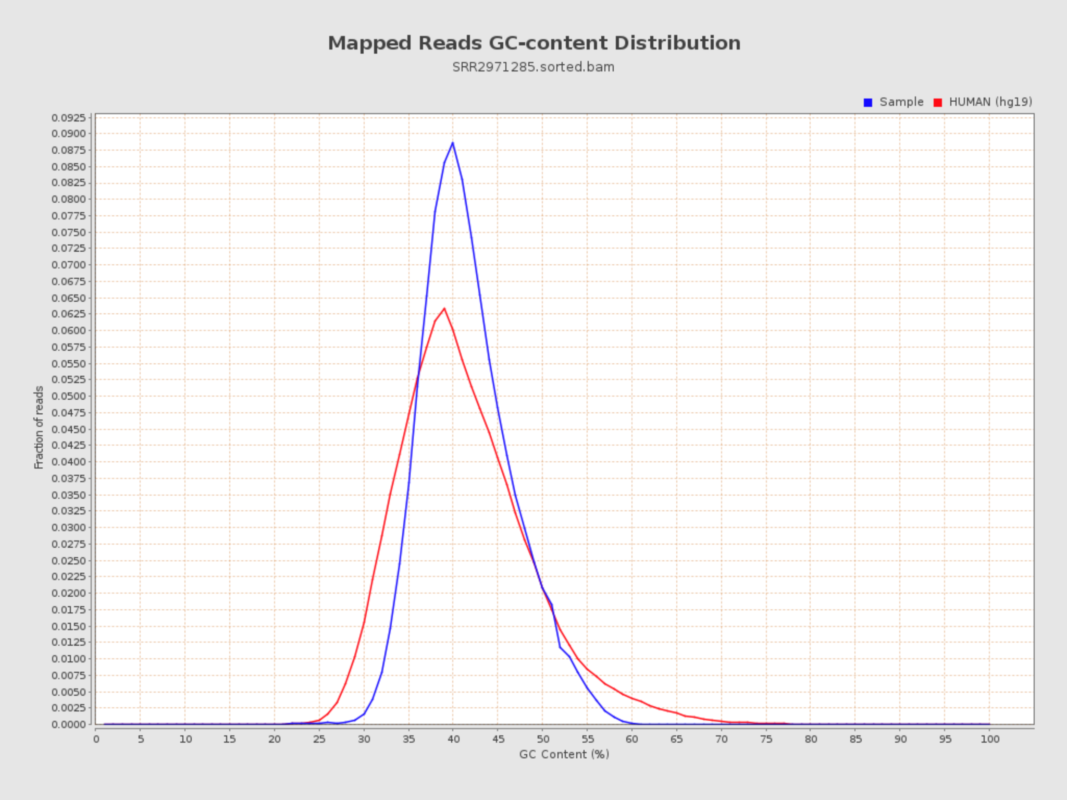
7. Results : Duplication Rate Histogram



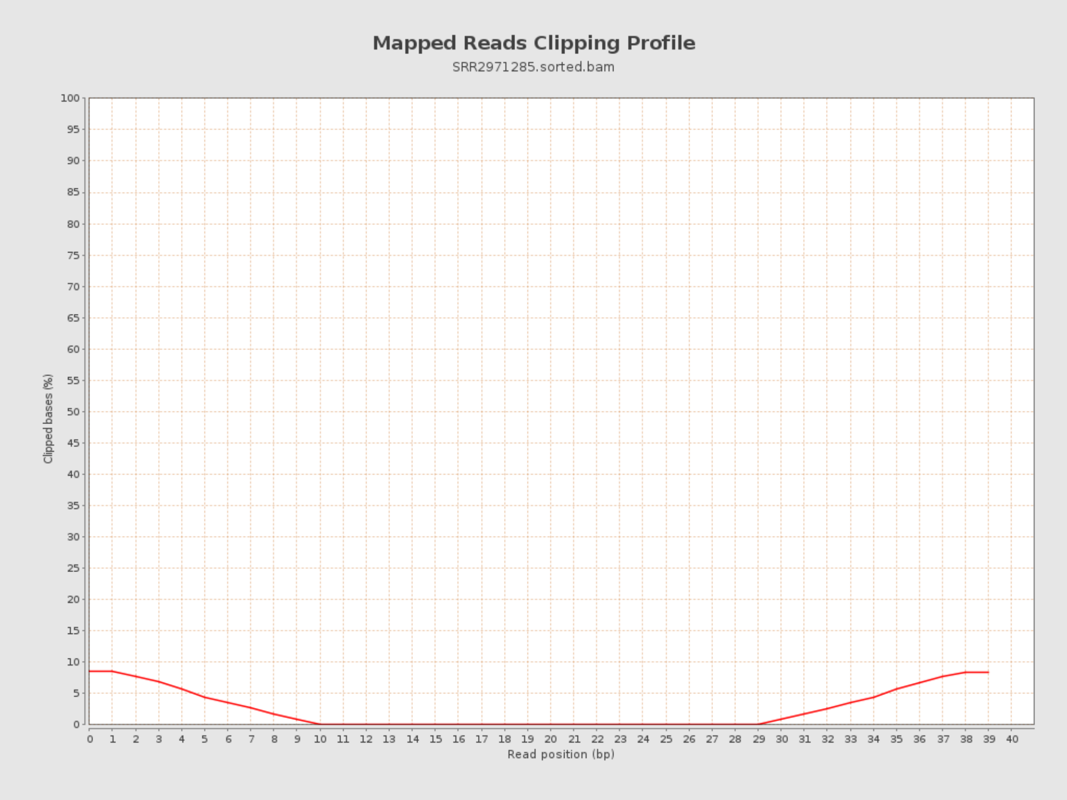
8. Results : Mapped Reads Nucleotide Content



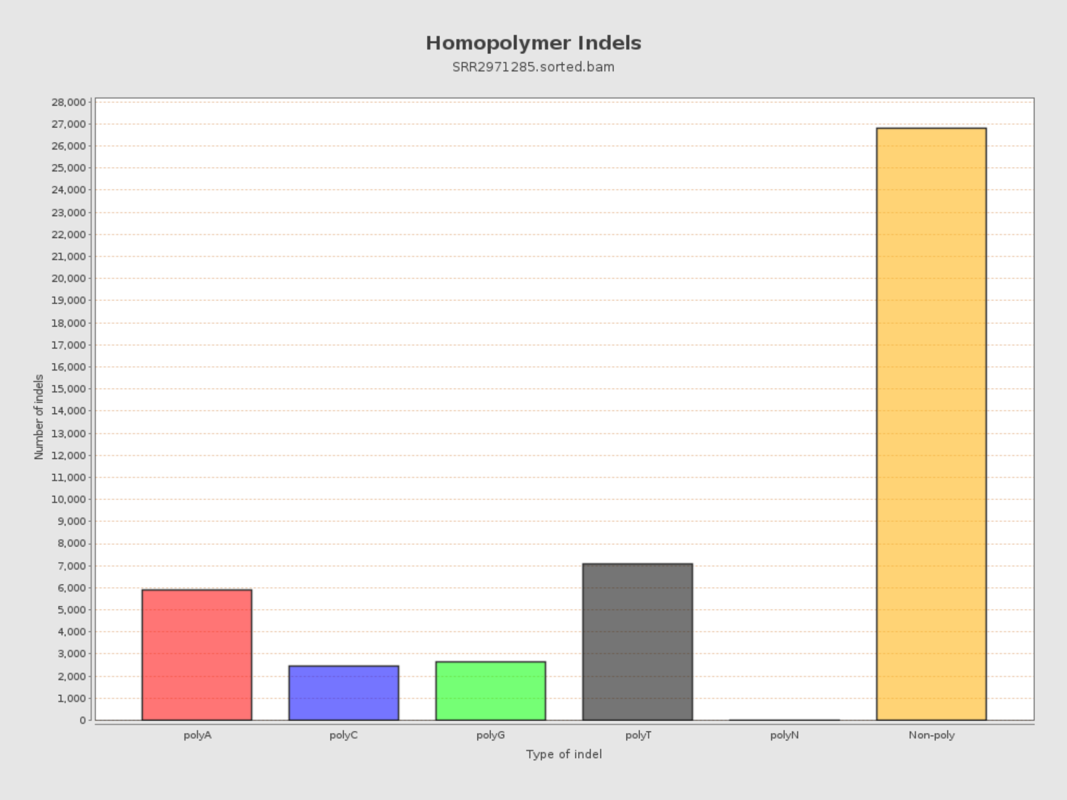
9. Results : Mapped Reads GC-content Distribution



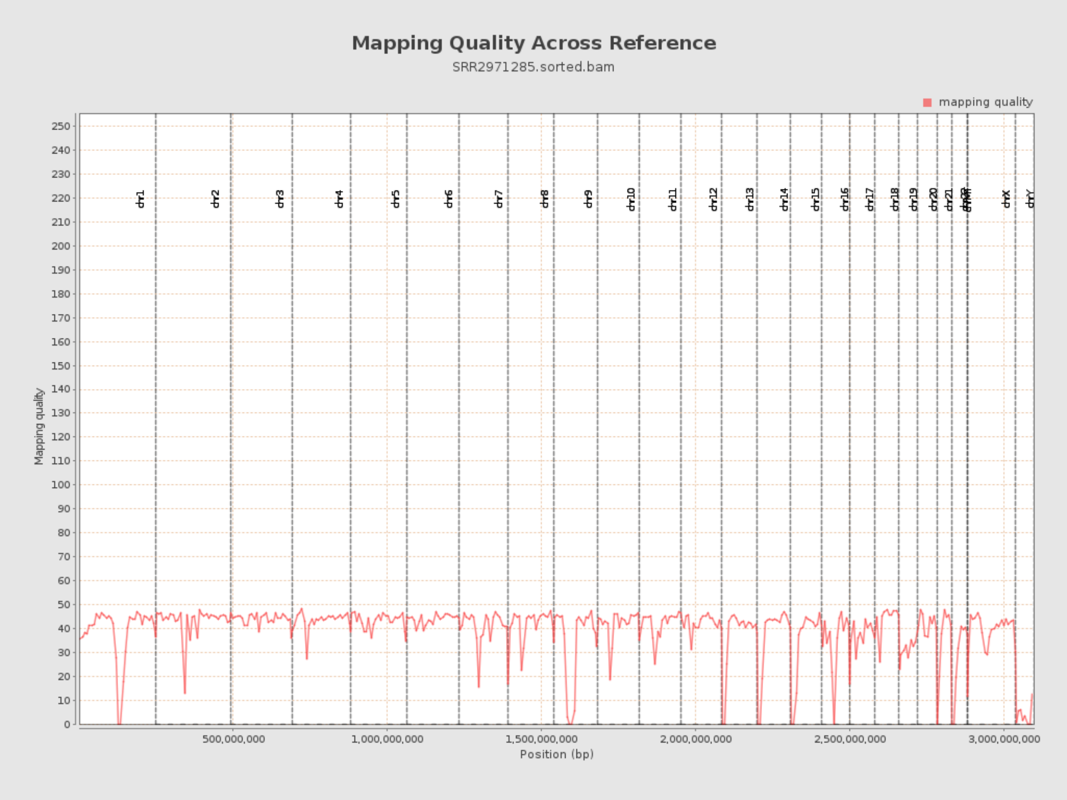
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram