Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:15:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971276.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_SRR2971276 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971276.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:15:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971276.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,262,167
Mapped reads	8,274,120 / 73.47%
Unmapped reads	2,988,047 / 26.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	411,491 / 3.65%
Duplication rate	4.2%
Clipped reads	719,147 / 6.39%

2.2. ACGT Content

Number/percentage of A's	93,729,616 / 28.7%
Number/percentage of C's	67,383,519 / 20.64%
Number/percentage of T's	95,785,063 / 29.33%
Number/percentage of G's	69,631,507 / 21.32%
Number/percentage of N's	2,753 / 0%
GC Percentage	41.96%

2.3. Coverage

Mean	0.1055
Standard Deviation	0.714

2.4. Mapping Quality

Mean Mapping Quality	42.23

2.5. Mismatches and indels

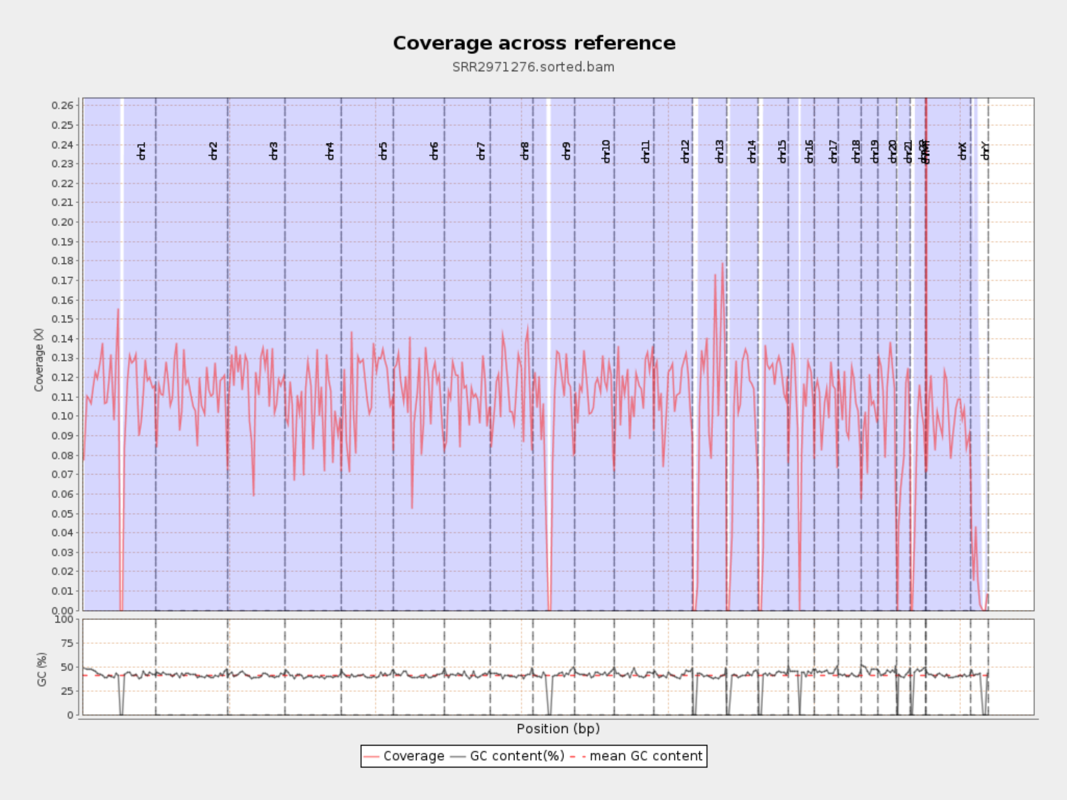
General error rate	0.27%
Mismatches	872,444
Insertions	10,568
Mapped reads with at least one insertion	0.13%
Deletions	25,623
Mapped reads with at least one deletion	0.31%
Homopolymer indels	40.76%

2.6. Chromosome stats

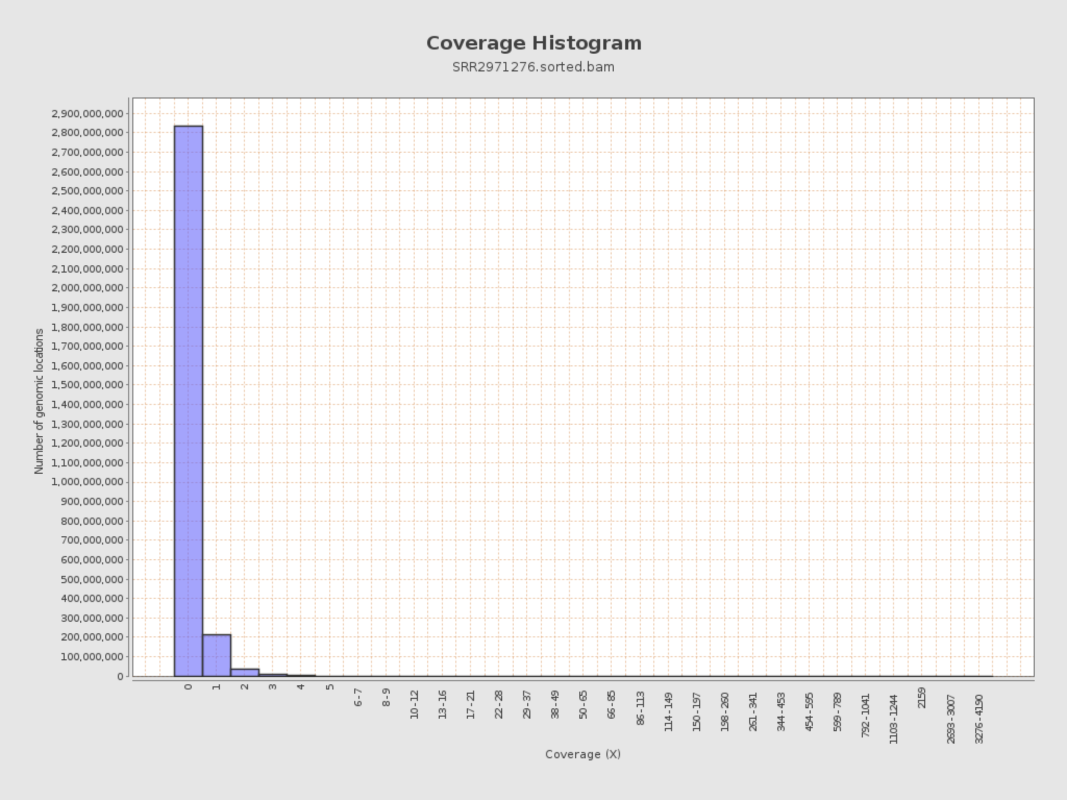
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27192819	0.1091	0.9988
chr2	243199373	27369118	0.1125	0.547
chr3	198022430	23051516	0.1164	0.411
chr4	191154276	19797583	0.1036	0.4004
chr5	180915260	20682038	0.1143	0.4123
chr6	171115067	19135803	0.1118	0.4865
chr7	159138663	17453792	0.1097	0.7329
chr8	146364022	16647495	0.1137	2.0648

chr9	141213431	13599972	0.0963	0.5407
chr10	135534747	15424432	0.1138	0.509
chr11	135006516	15569538	0.1153	0.6985
chr12	133851895	15287806	0.1142	0.4173
chr13	115169878	12110807	0.1052	0.3882
chr14	107349540	10213374	0.0951	0.4092
chr15	102531392	10139814	0.0989	0.3735
chr16	90354753	9146403	0.1012	0.4042
chr17	81195210	8823043	0.1087	0.4438
chr18	78077248	8354905	0.107	0.9115
chr19	59128983	5780295	0.0978	0.8778
chr20	63025520	7207207	0.1144	0.4138
chr21	48129895	3718596	0.0773	0.3694
chr22	51304566	3595857	0.0701	0.3153
chrMT	16571	26257	1.5845	2.0402
chrX	155270560	15367808	0.099	0.4346
chrY	59373566	868714	0.0146	0.2273

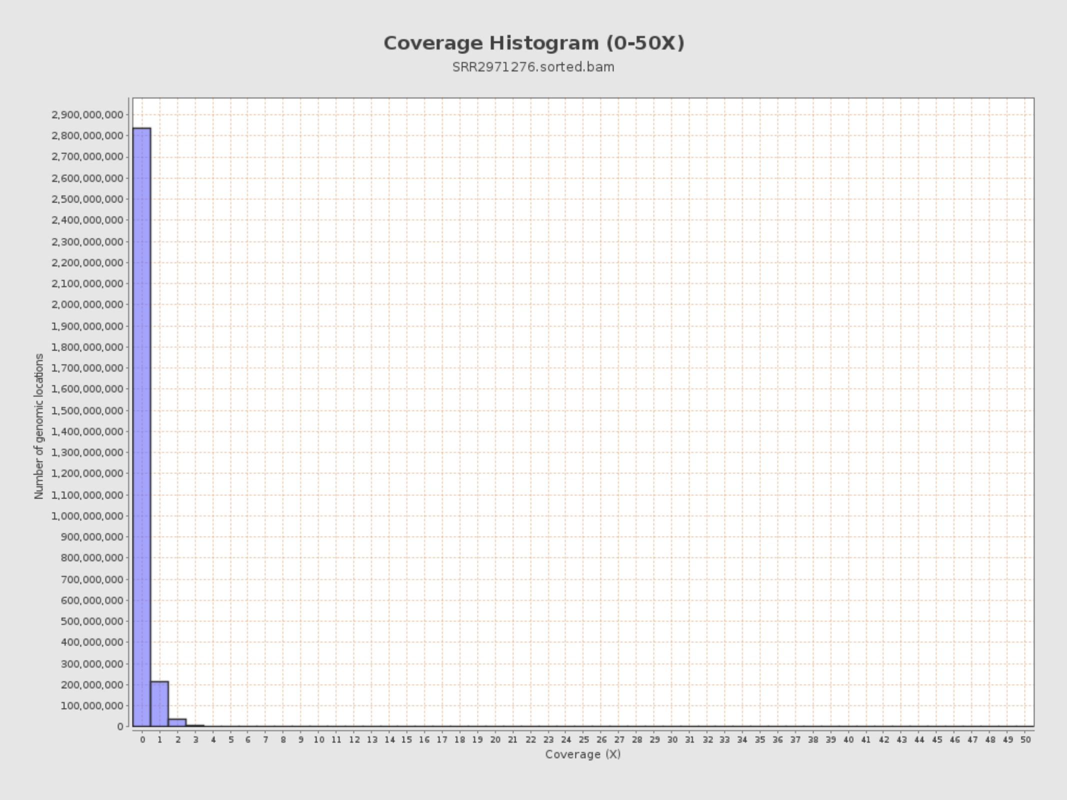
3. Results : Coverage across reference



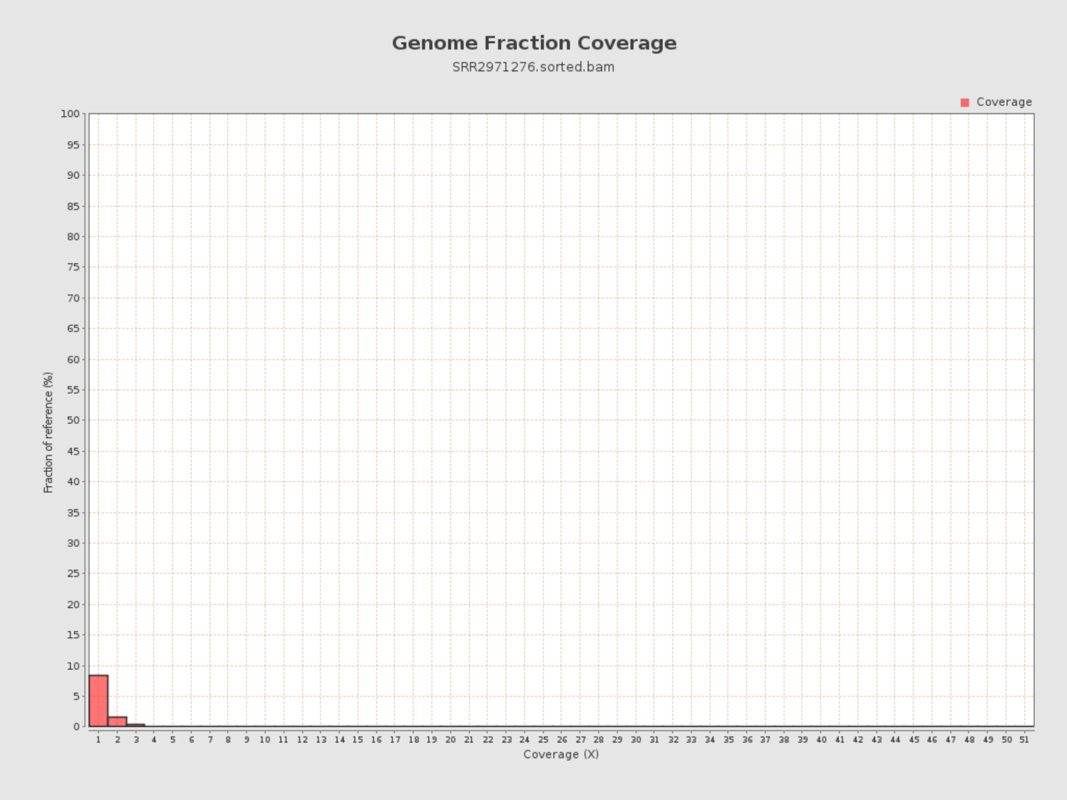
4. Results : Coverage Histogram



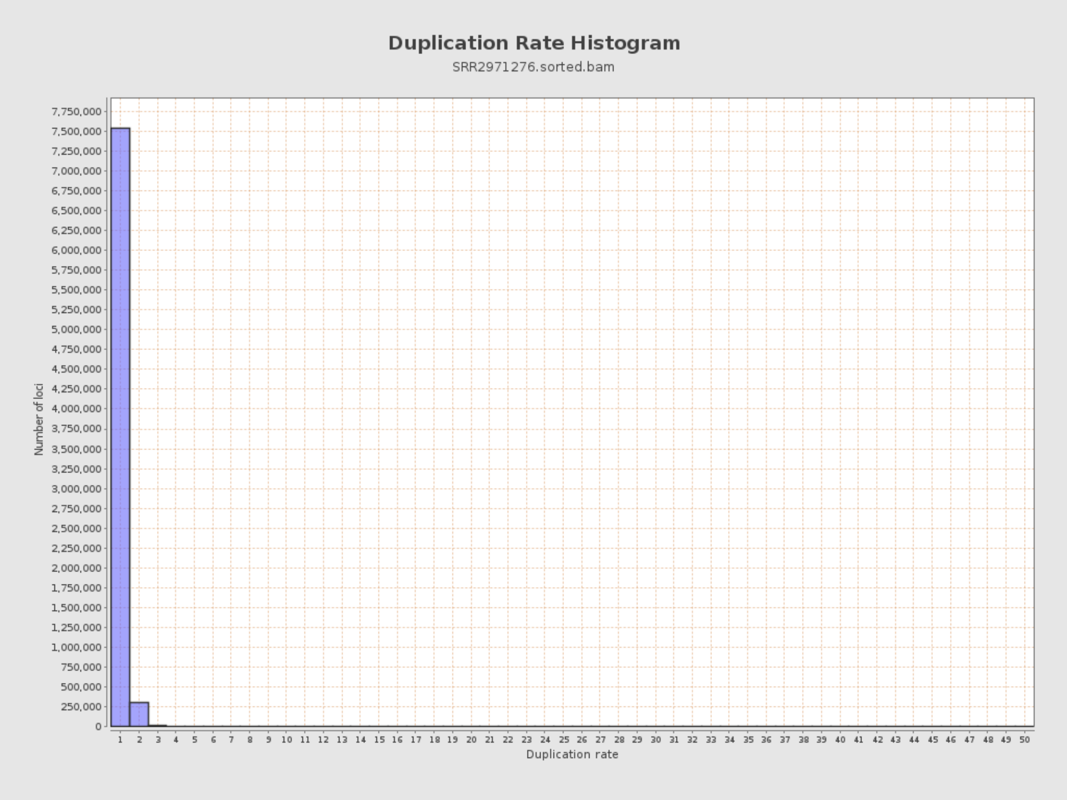
5. Results : Coverage Histogram (0-50X)



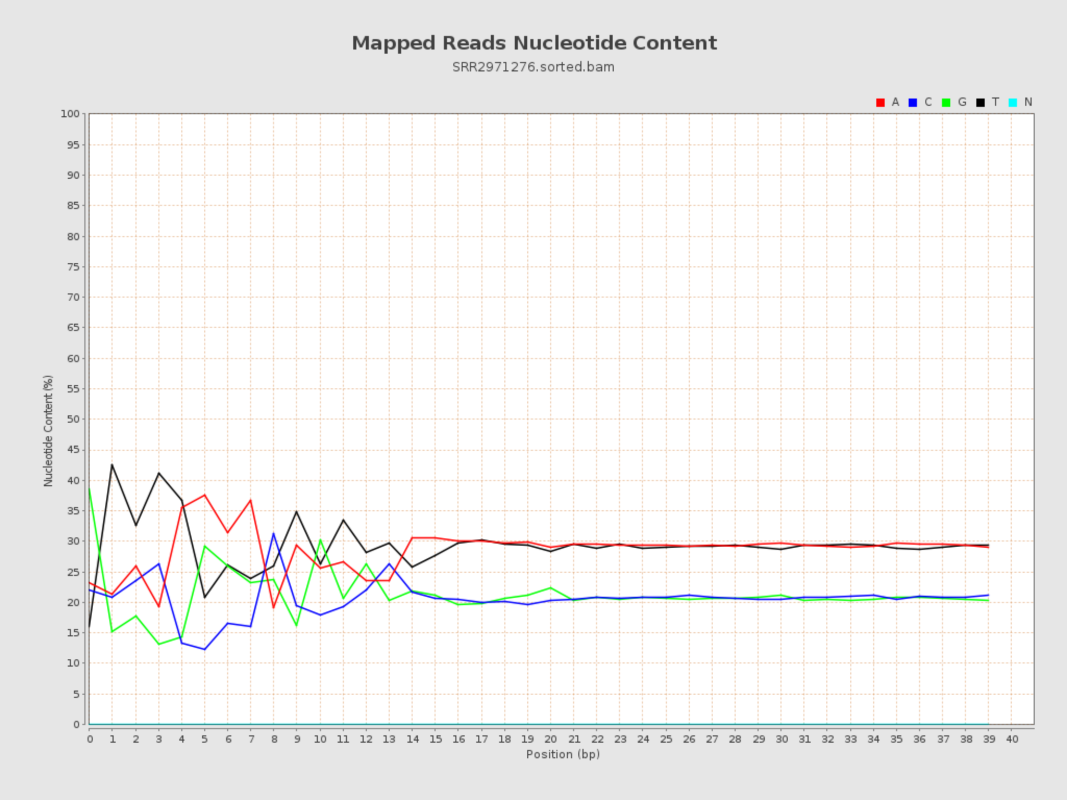
6. Results : Genome Fraction Coverage



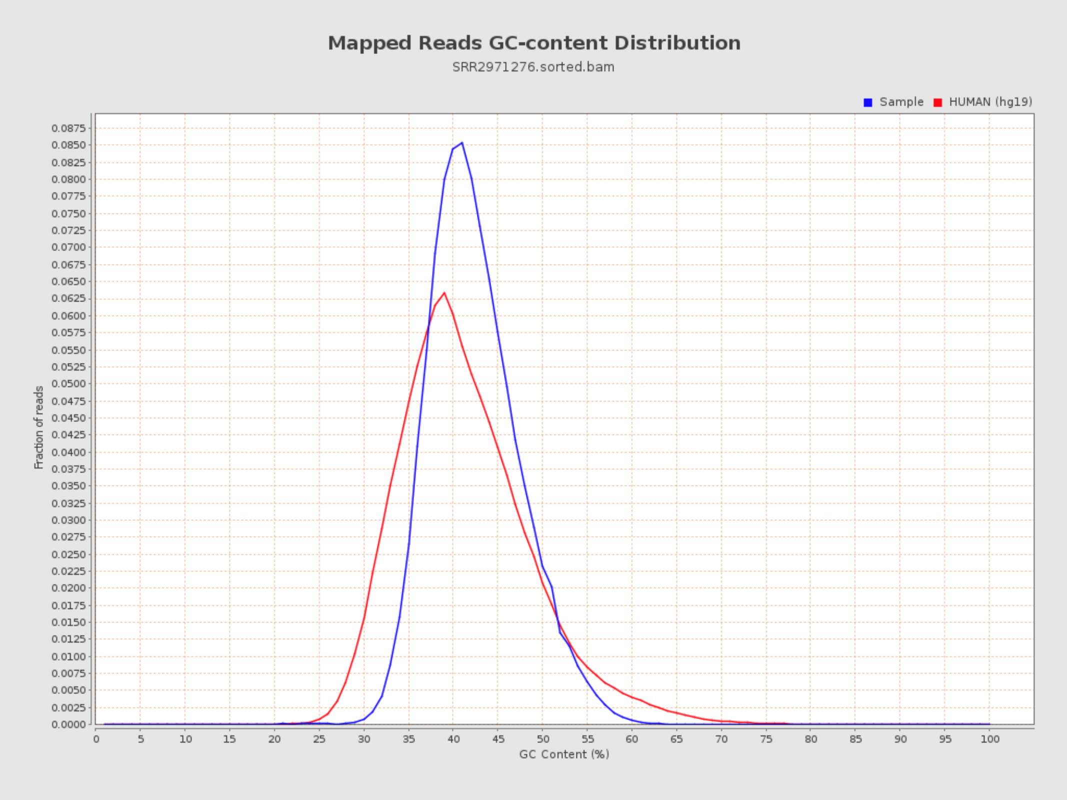
7. Results : Duplication Rate Histogram



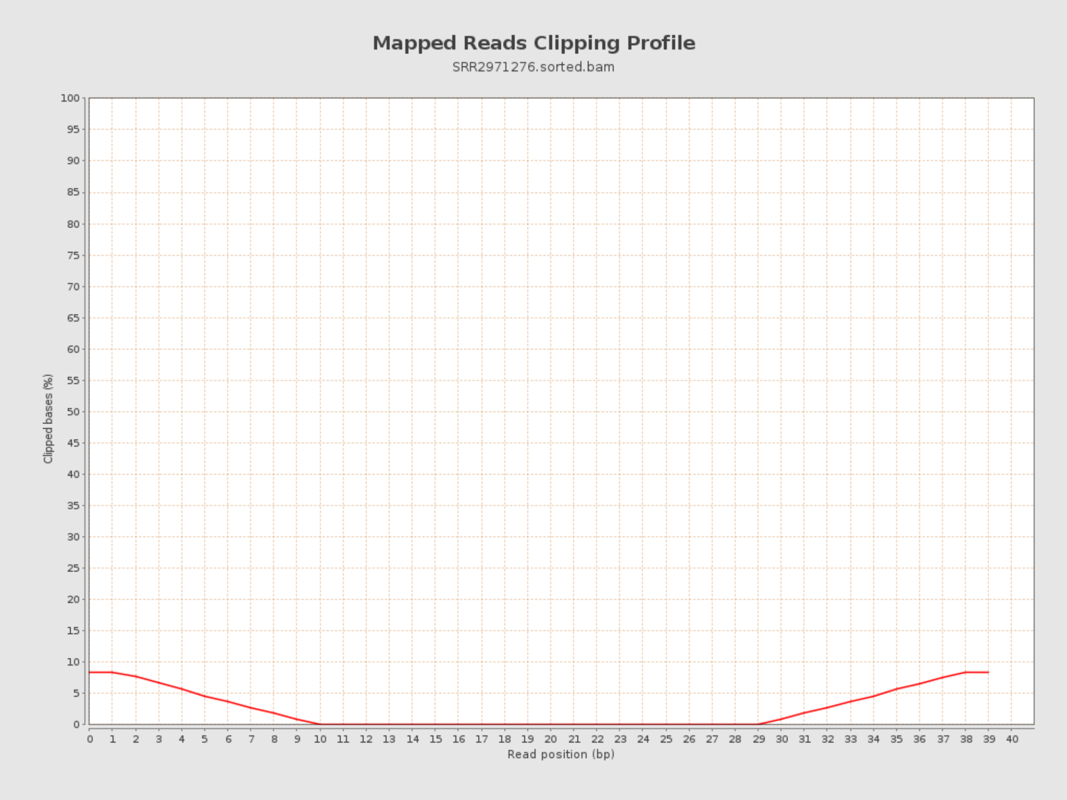
8. Results : Mapped Reads Nucleotide Content



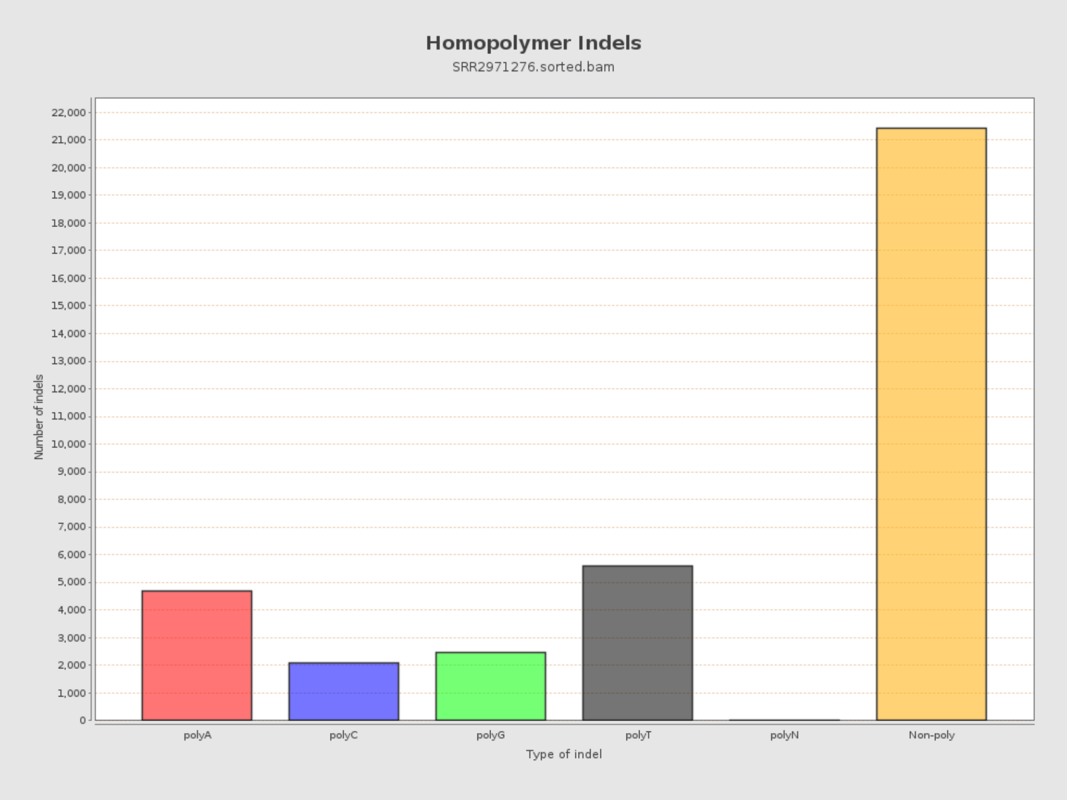
9. Results : Mapped Reads GC-content Distribution



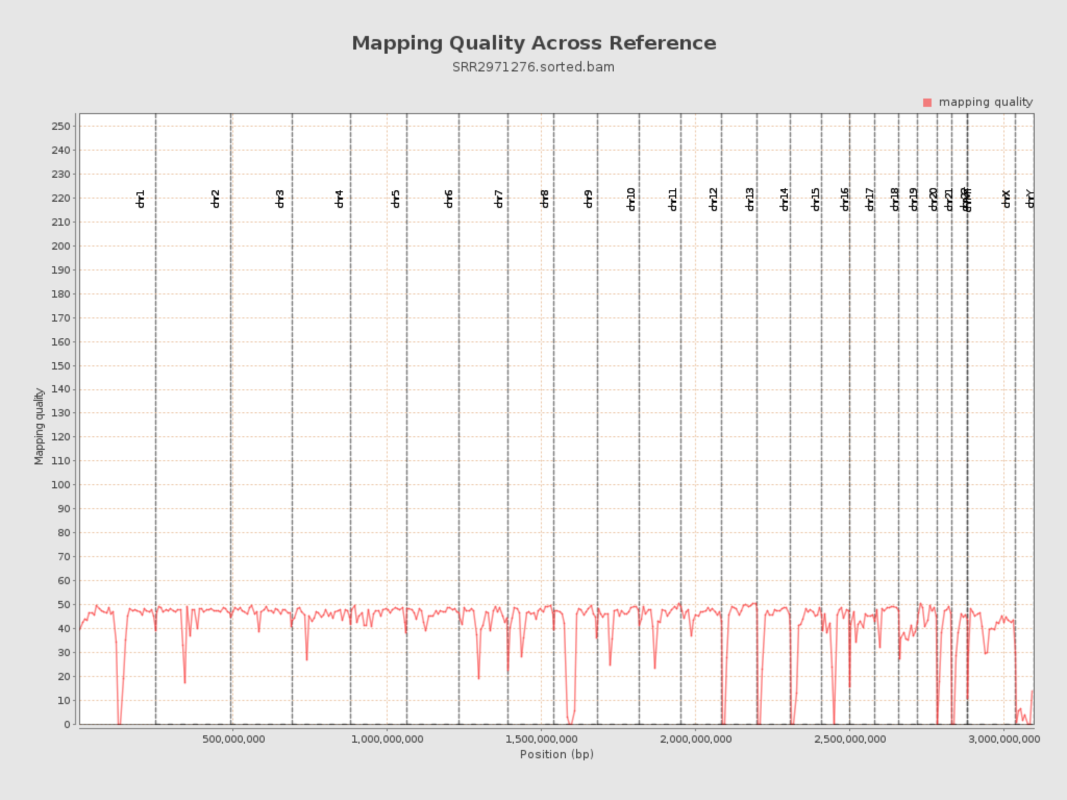
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram