

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:48:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971280.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_SRR2971280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971280.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:48:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971280.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,683,360
Mapped reads	8,538,630 / 73.08%
Unmapped reads	3,144,730 / 26.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	672,090 / 5.75%
Duplication rate	6.85%
Clipped reads	745,564 / 6.38%

2.2. ACGT Content

Number/percentage of A's	95,895,476 / 28.46%
Number/percentage of C's	70,555,488 / 20.94%
Number/percentage of T's	97,841,045 / 29.04%
Number/percentage of G's	72,653,820 / 21.56%
Number/percentage of N's	2,885 / 0%
GC Percentage	42.5%

2.3. Coverage

Mean	0.1089
Standard Deviation	1.2338

2.4. Mapping Quality

Mean Mapping Quality	43.16
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2.5. Mismatches and indels

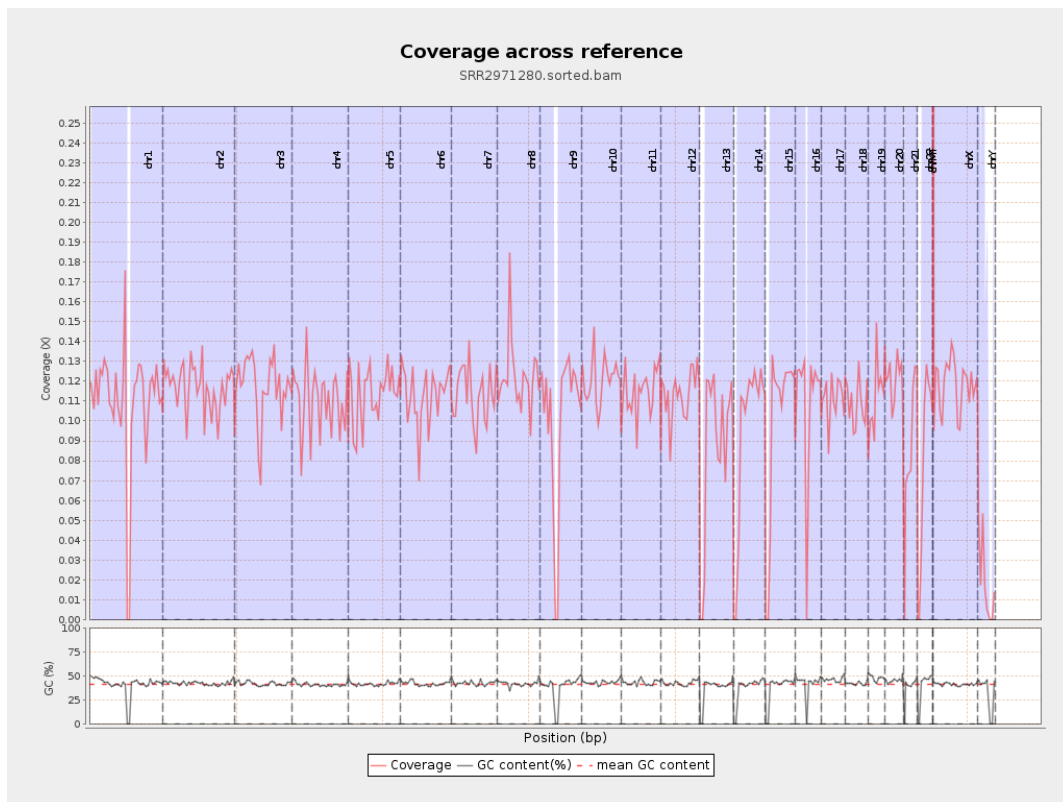
General error rate	0.27%
Mismatches	885,299
Insertions	10,973
Mapped reads with at least one insertion	0.13%
Deletions	26,263
Mapped reads with at least one deletion	0.31%
Homopolymer indels	39.47%

2.6. Chromosome stats

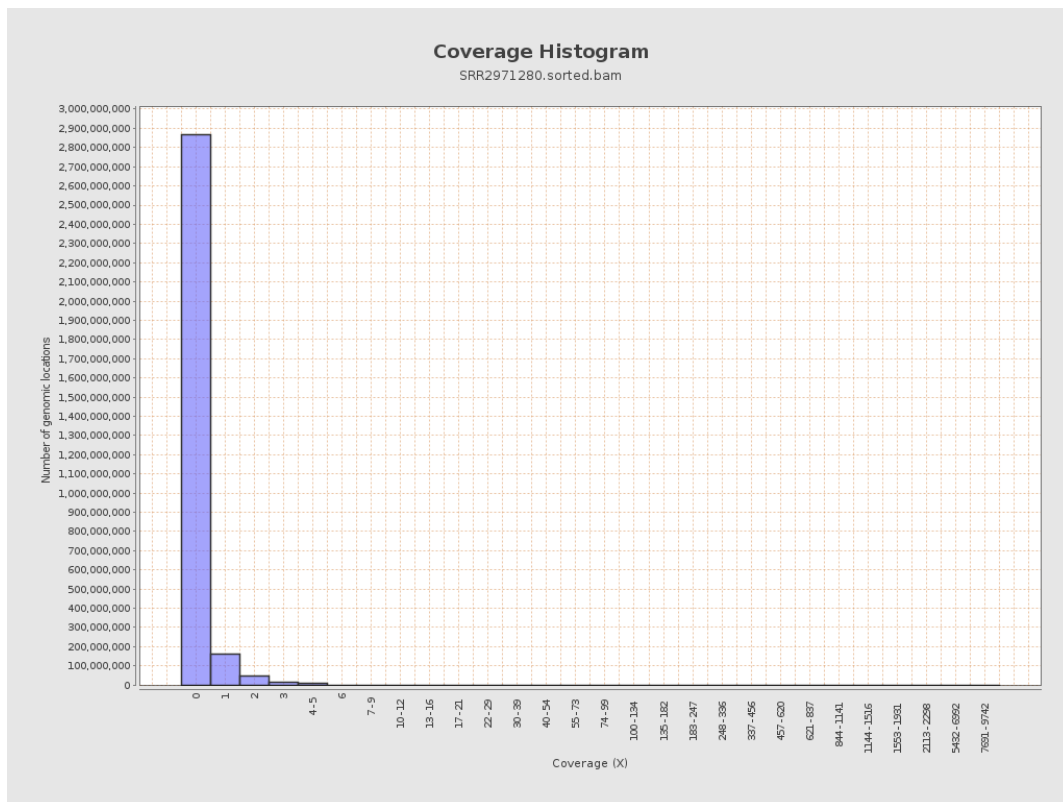
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27302503	0.1095	1.5207
chr2	243199373	28501398	0.1172	0.5837
chr3	198022430	23137445	0.1168	0.4719
chr4	191154276	21113031	0.1105	0.5026
chr5	180915260	20640153	0.1141	0.4714
chr6	171115067	19304581	0.1128	0.4791
chr7	159138663	18070751	0.1136	0.8102
chr8	146364022	17845474	0.1219	4.7036

chr9	141213431	14295945	0.1012	0.5555
chr10	135534747	16286930	0.1202	0.6628
chr11	135006516	15483178	0.1147	0.5545
chr12	133851895	15268622	0.1141	0.4826
chr13	115169878	10012988	0.0869	0.4069
chr14	107349540	10336578	0.0963	0.4853
chr15	102531392	10047391	0.098	0.4278
chr16	90354753	9722580	0.1076	0.4827
chr17	81195210	9061314	0.1116	0.5006
chr18	78077248	8486120	0.1087	0.8836
chr19	59128983	6664790	0.1127	1.3638
chr20	63025520	7639192	0.1212	0.5134
chr21	48129895	4193715	0.0871	0.474
chr22	51304566	4112840	0.0802	0.4155
chrMT	16571	35925	2.1679	2.8256
chrX	155270560	18339567	0.1181	0.5403
chrY	59373566	1079379	0.0182	0.2881

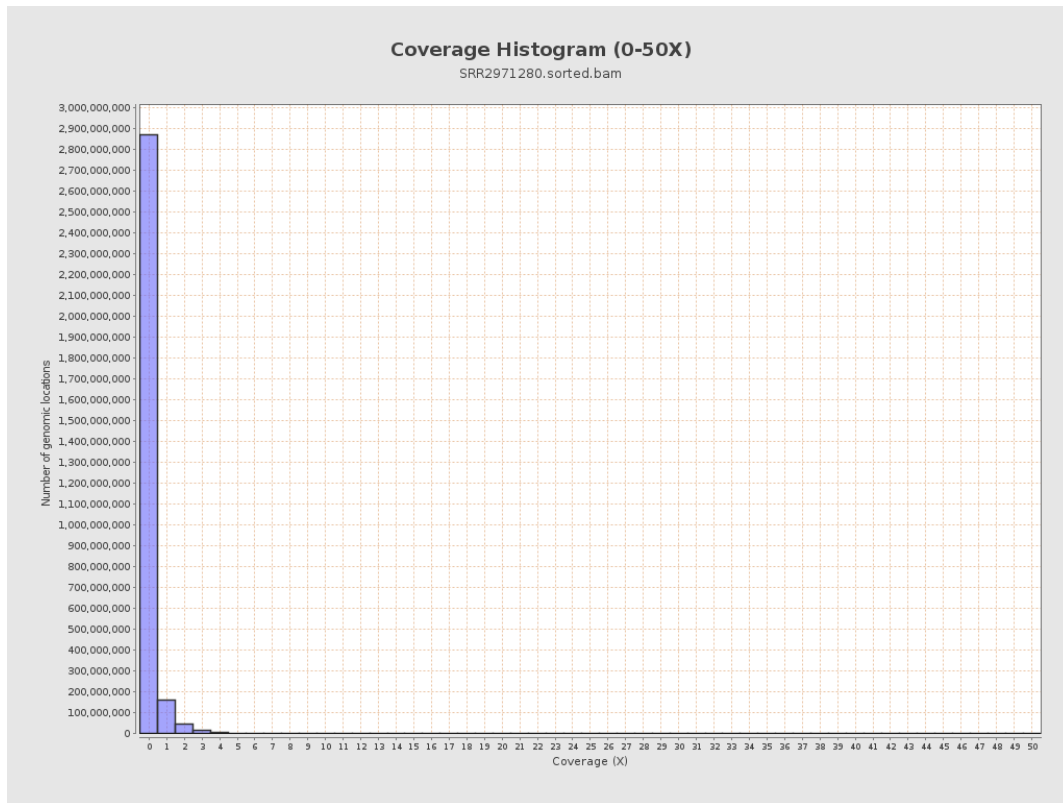
3. Results : Coverage across reference



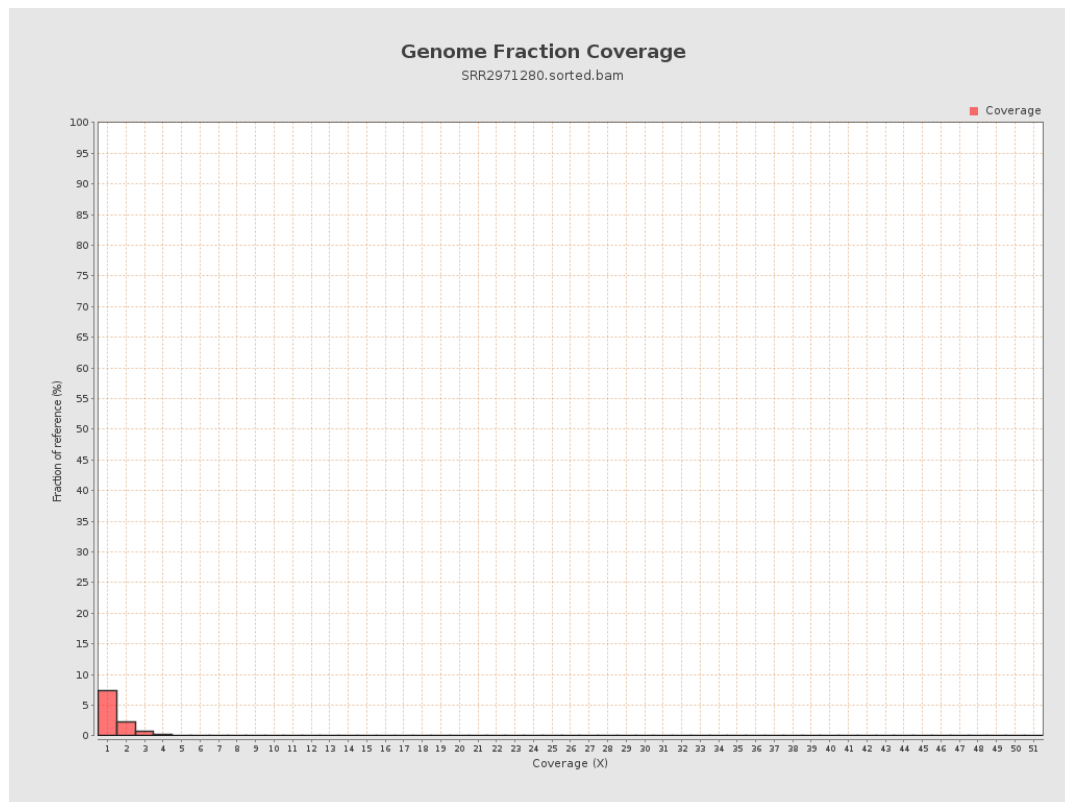
4. Results : Coverage Histogram



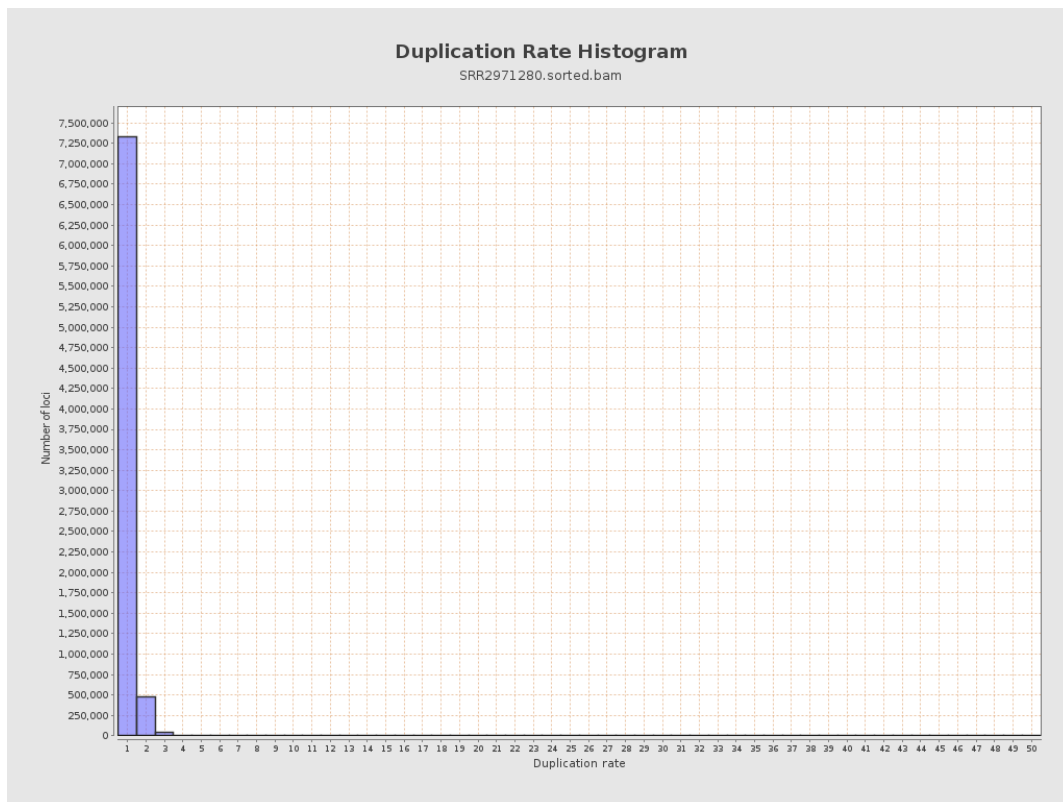
5. Results : Coverage Histogram (0-50X)



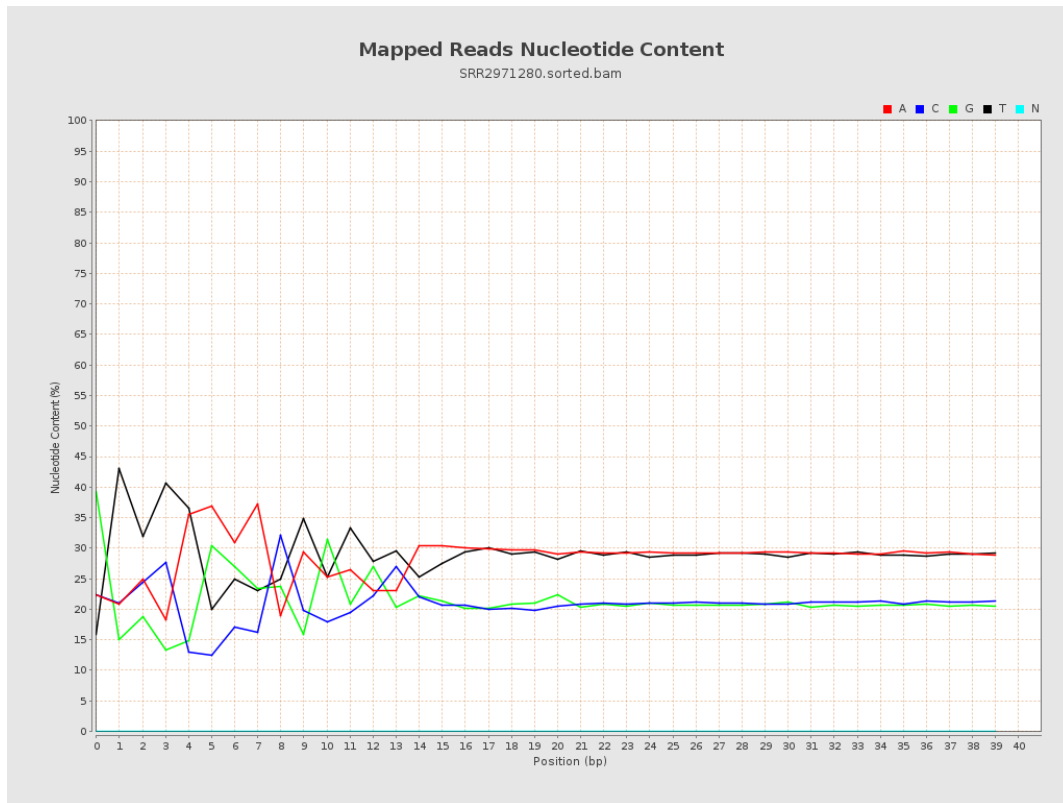
6. Results : Genome Fraction Coverage



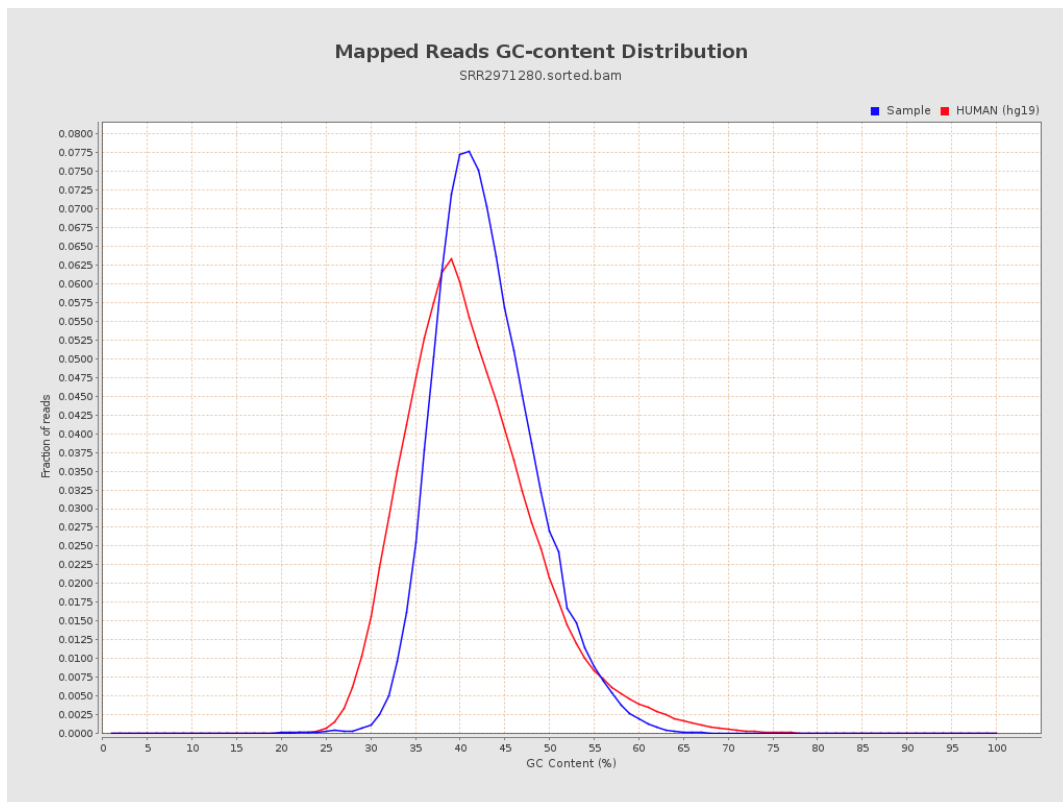
7. Results : Duplication Rate Histogram



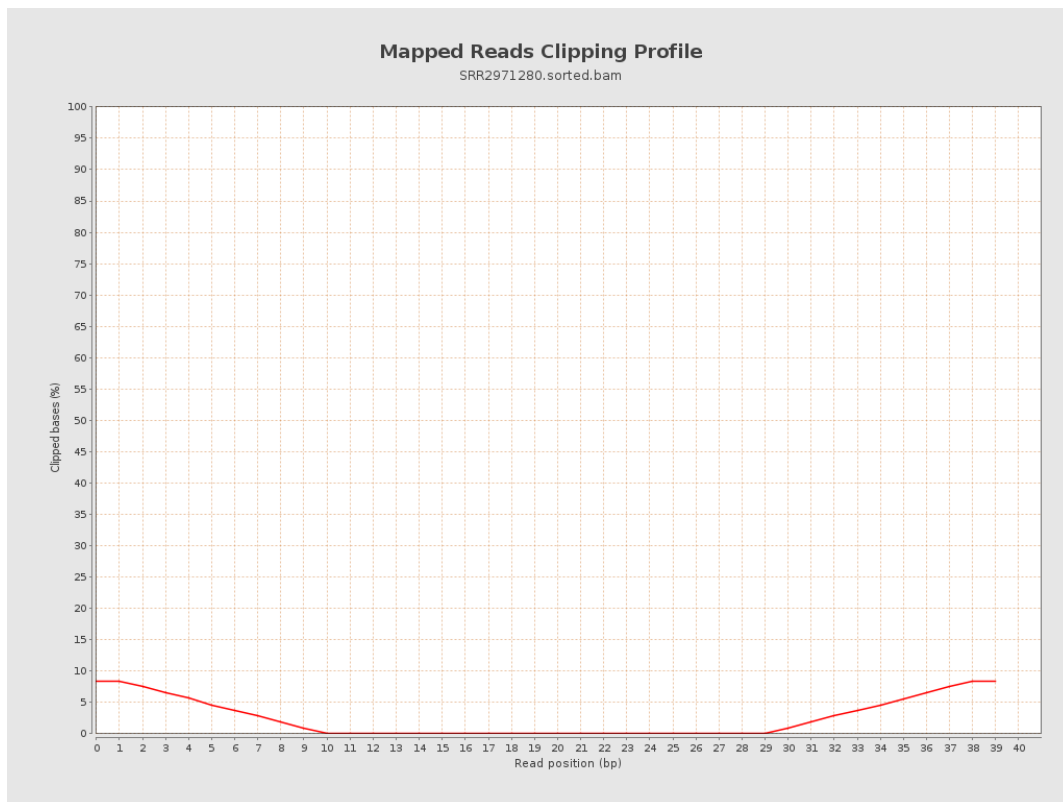
8. Results : Mapped Reads Nucleotide Content



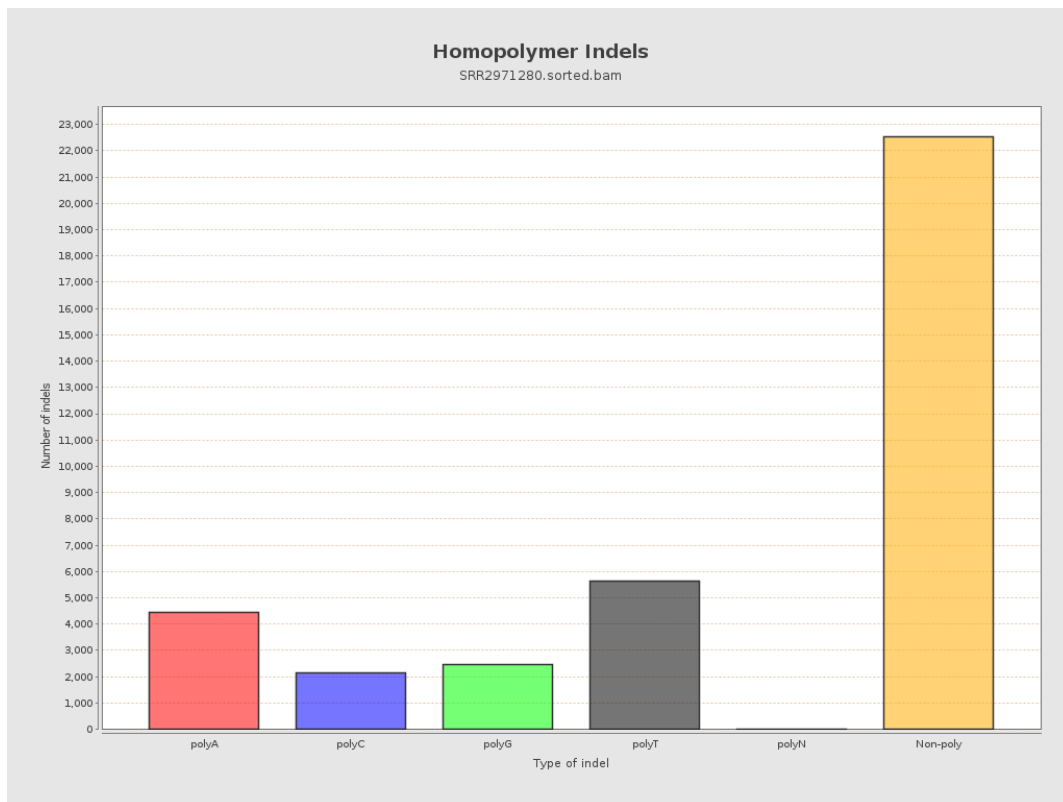
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

