

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:41:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971291.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_SRR2971291 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971291.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:41:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971291.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,796,278
Mapped reads	5,743,273 / 84.51%
Unmapped reads	1,053,005 / 15.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	274,902 / 4.04%
Duplication rate	3.56%
Clipped reads	516,207 / 7.6%

2.2. ACGT Content

Number/percentage of A's	66,916,501 / 29.52%
Number/percentage of C's	45,461,858 / 20.06%
Number/percentage of T's	67,976,343 / 29.99%
Number/percentage of G's	46,299,040 / 20.43%
Number/percentage of N's	11,793 / 0.01%
GC Percentage	40.48%

2.3. Coverage

Mean	0.0732
Standard Deviation	0.6826

2.4. Mapping Quality

Mean Mapping Quality	41.09
----------------------	-------

2.5. Mismatches and indels

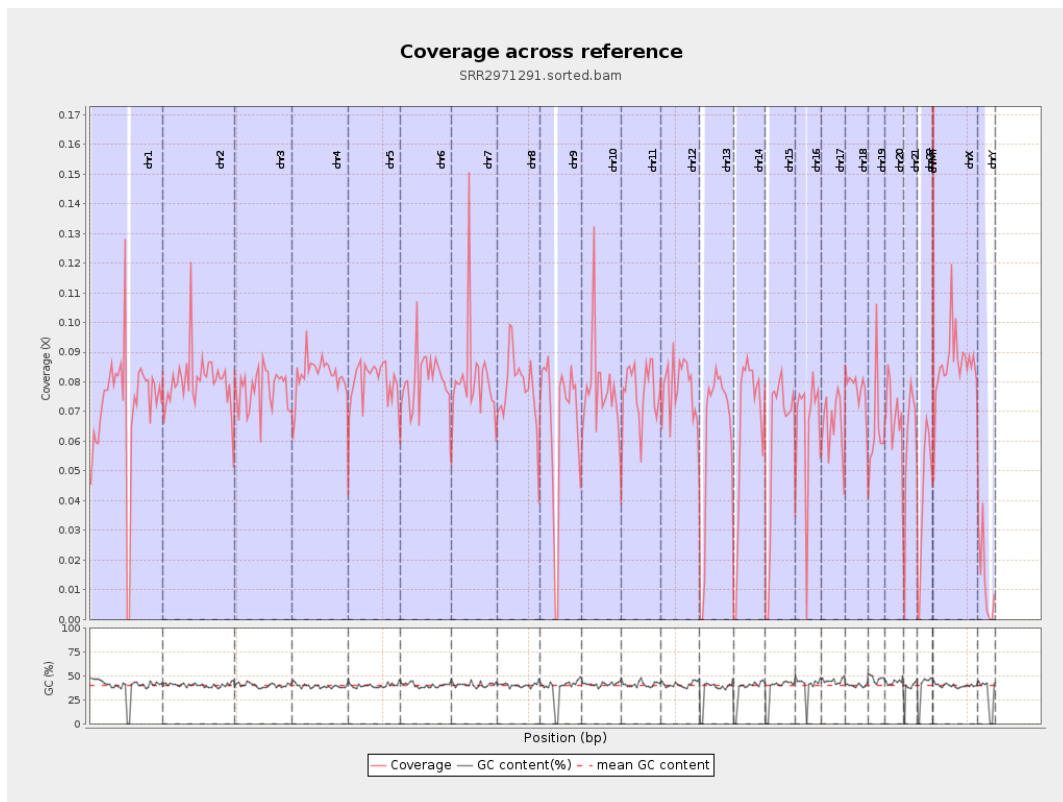
General error rate	0.3%
Mismatches	660,524
Insertions	7,617
Mapped reads with at least one insertion	0.13%
Deletions	18,799
Mapped reads with at least one deletion	0.33%
Homopolymer indels	40.79%

2.6. Chromosome stats

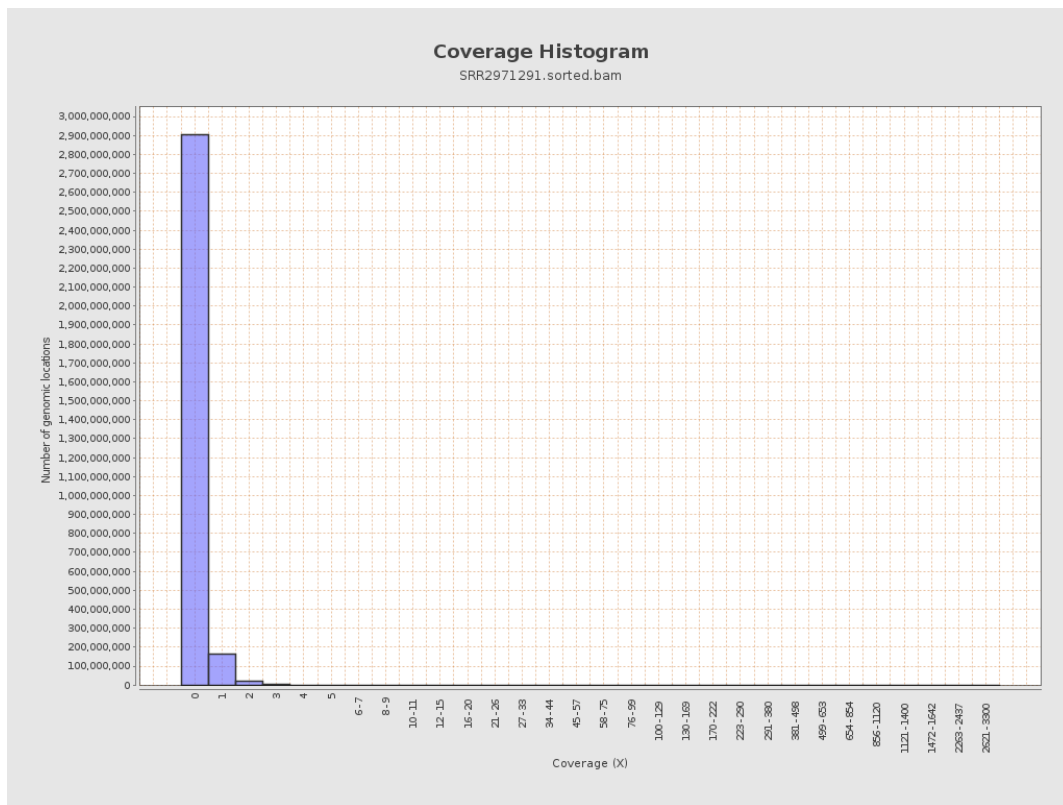
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17898558	0.0718	1.2352
chr2	243199373	19506917	0.0802	0.5181
chr3	198022430	15348777	0.0775	0.3198
chr4	191154276	15754723	0.0824	0.3496
chr5	180915260	14437984	0.0798	0.3304
chr6	171115067	13817273	0.0807	0.4251
chr7	159138663	12829020	0.0806	0.9562
chr8	146364022	11384161	0.0778	1.6352

chr9	141213431	9439216	0.0668	0.5023
chr10	135534747	10463878	0.0772	0.5642
chr11	135006516	10373966	0.0768	0.4349
chr12	133851895	10385822	0.0776	0.3316
chr13	115169878	7185485	0.0624	0.2813
chr14	107349540	7062179	0.0658	0.3726
chr15	102531392	6195391	0.0604	0.2794
chr16	90354753	5811728	0.0643	0.3502
chr17	81195210	5386399	0.0663	0.3145
chr18	78077248	6094693	0.0781	0.9463
chr19	59128983	3822567	0.0646	1.1662
chr20	63025520	4353020	0.0691	0.3231
chr21	48129895	2875275	0.0597	0.3298
chr22	51304566	2171733	0.0423	0.2346
chrMT	16571	11562	0.6977	0.9816
chrX	155270560	13313869	0.0857	0.4218
chrY	59373566	764781	0.0129	0.1974

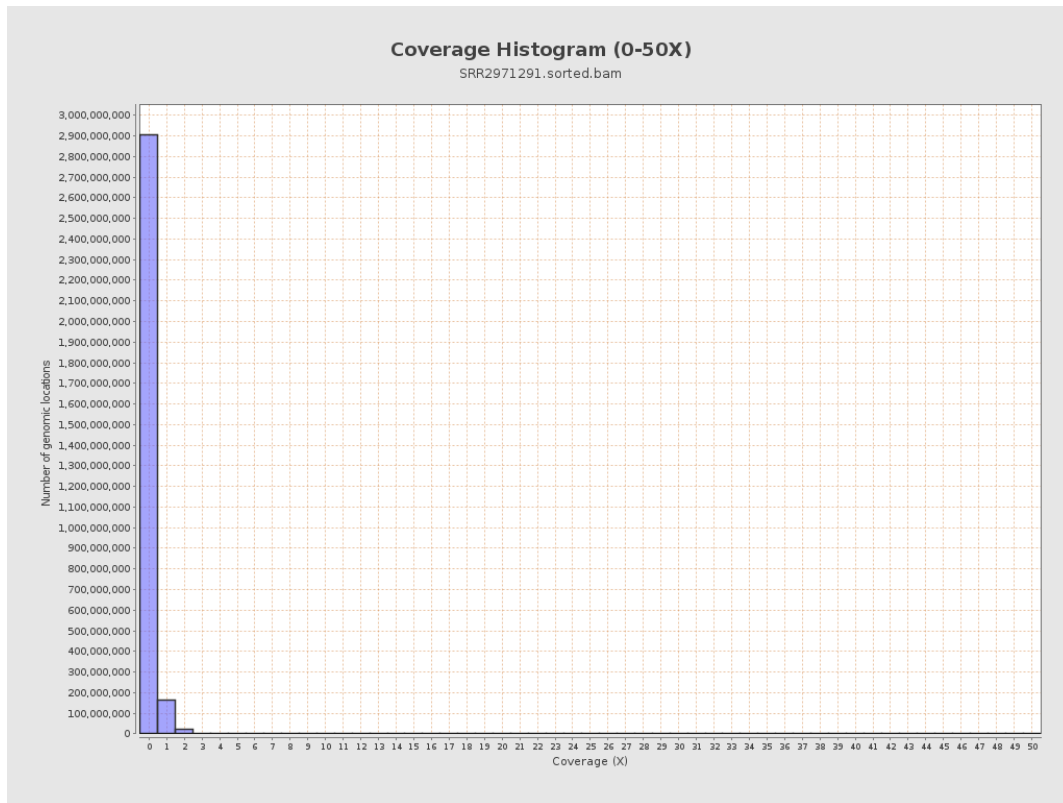
3. Results : Coverage across reference



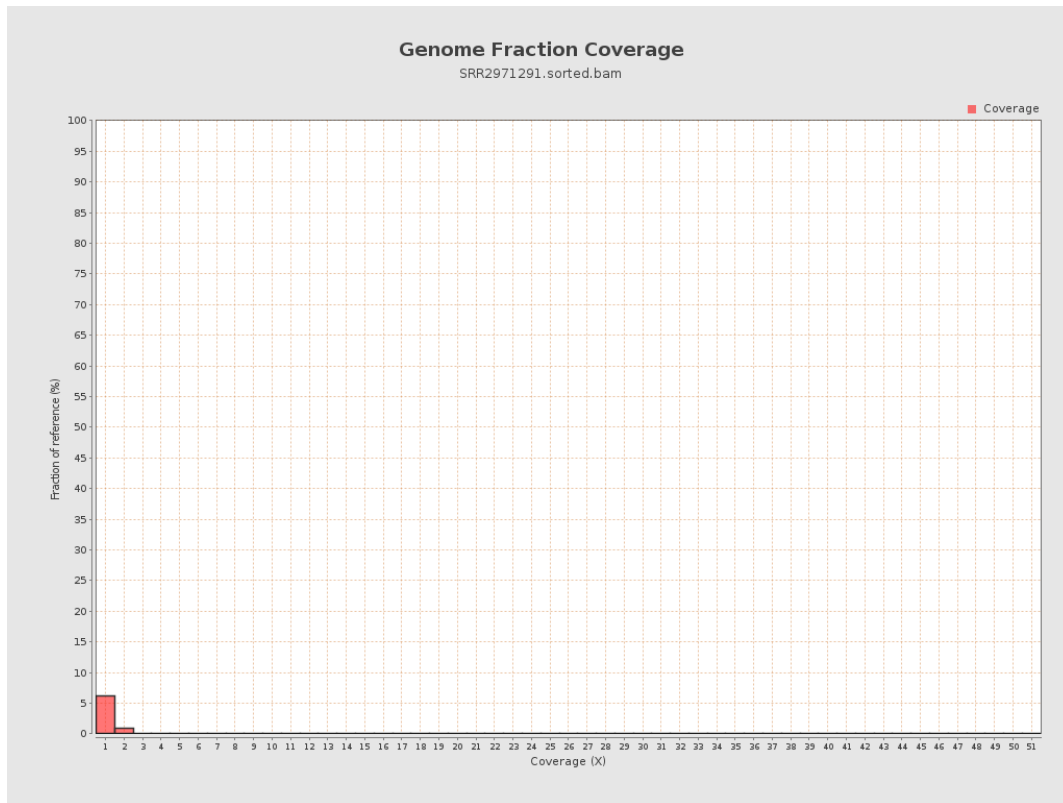
4. Results : Coverage Histogram



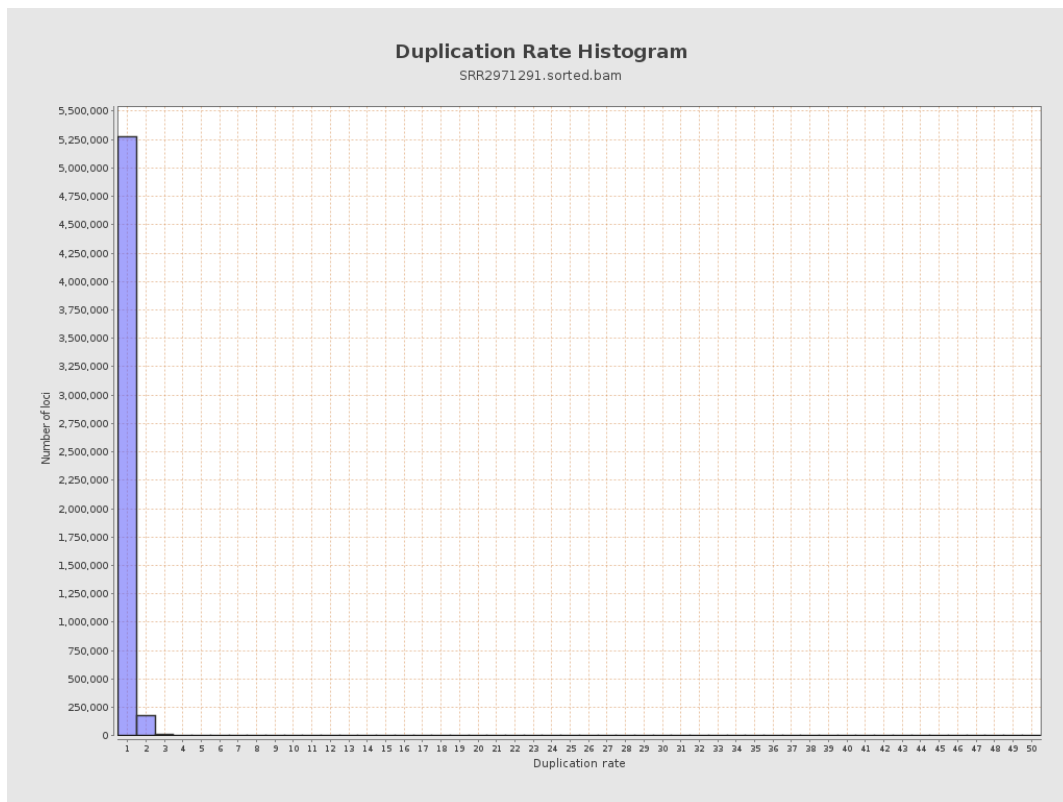
5. Results : Coverage Histogram (0-50X)



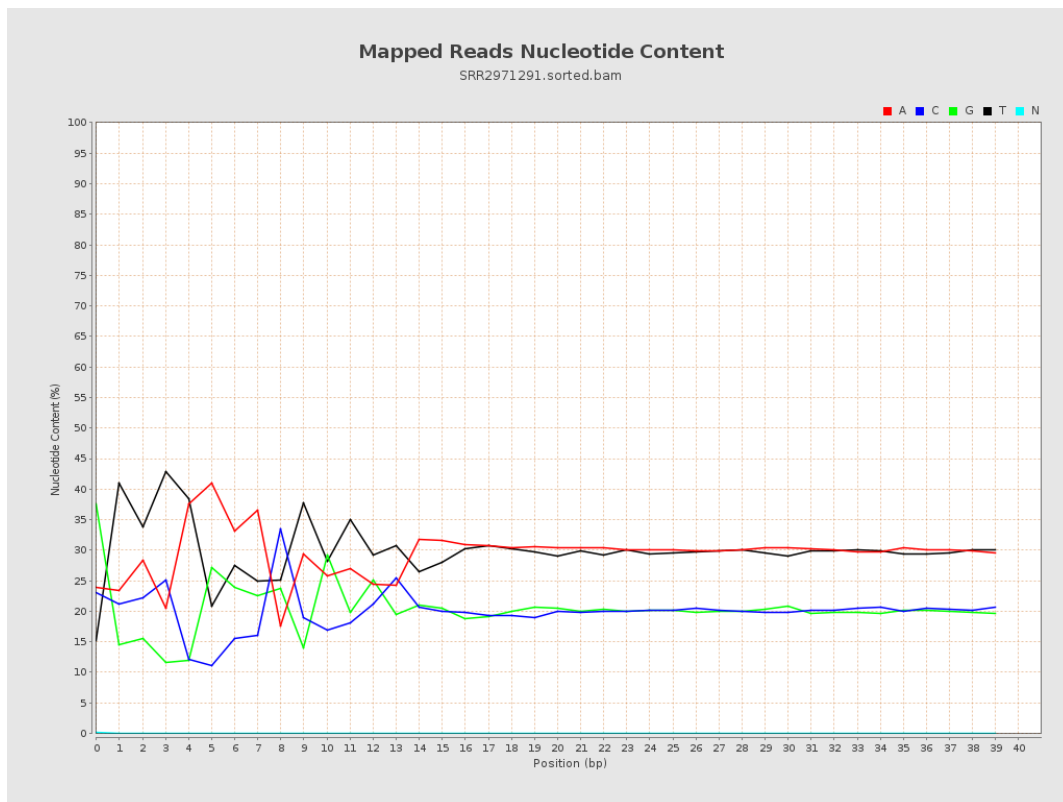
6. Results : Genome Fraction Coverage



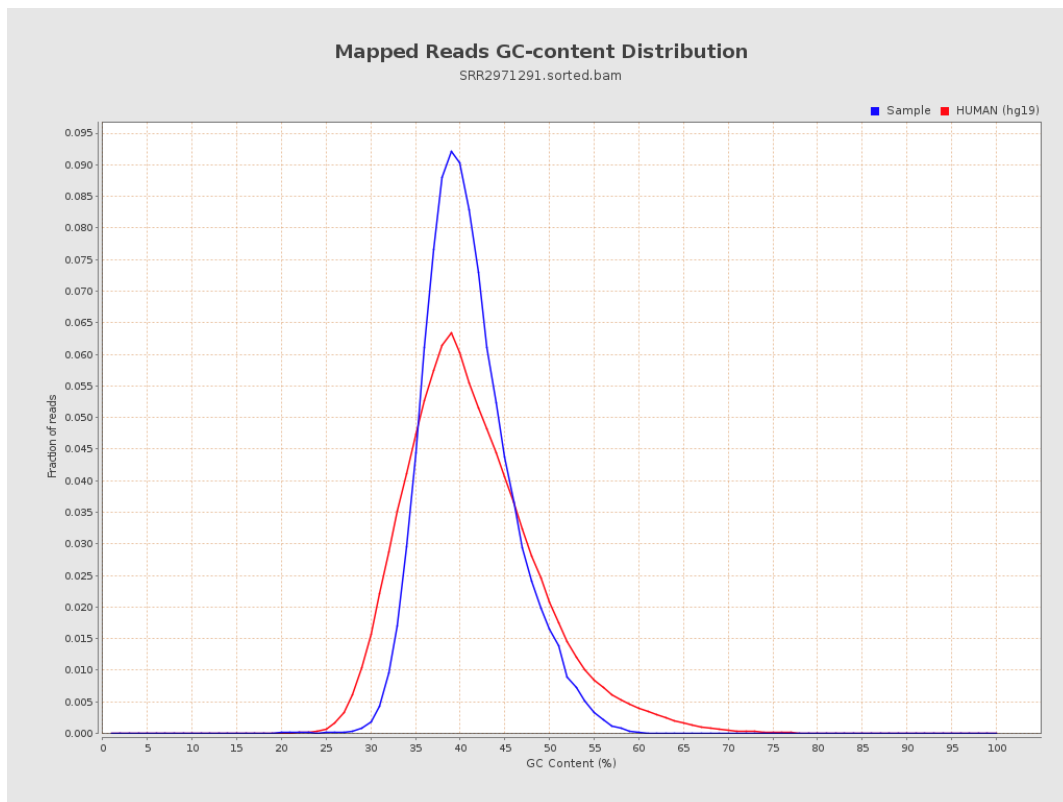
7. Results : Duplication Rate Histogram



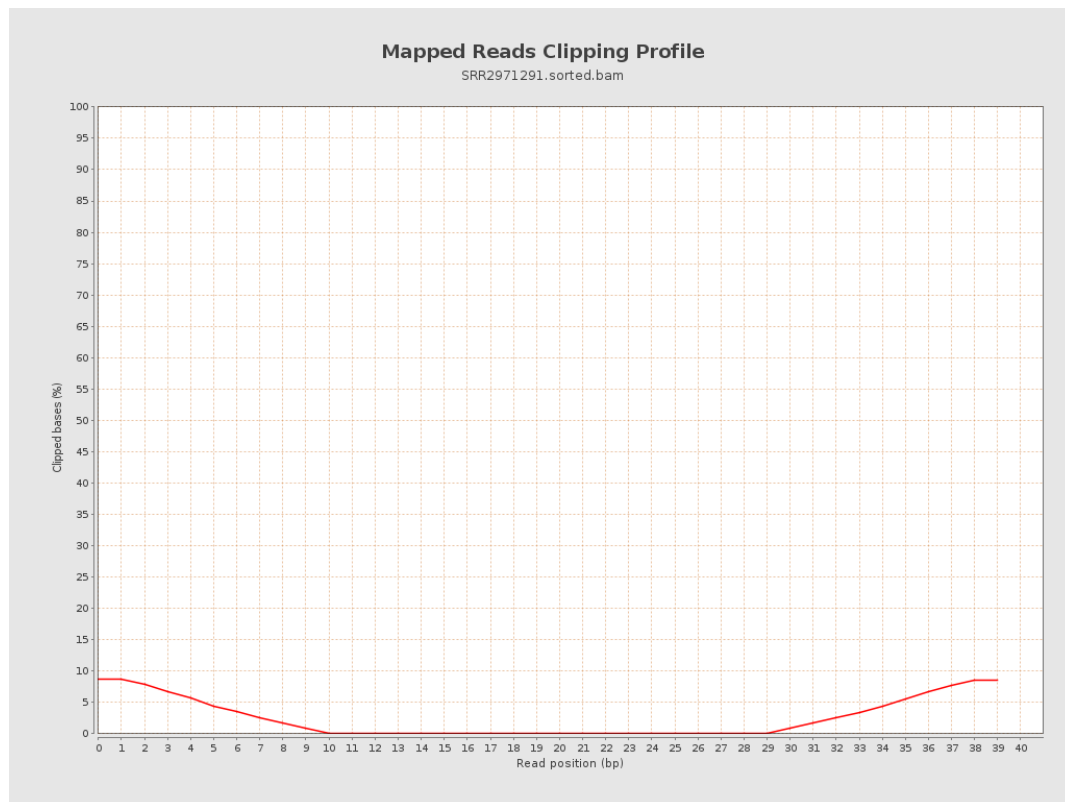
8. Results : Mapped Reads Nucleotide Content



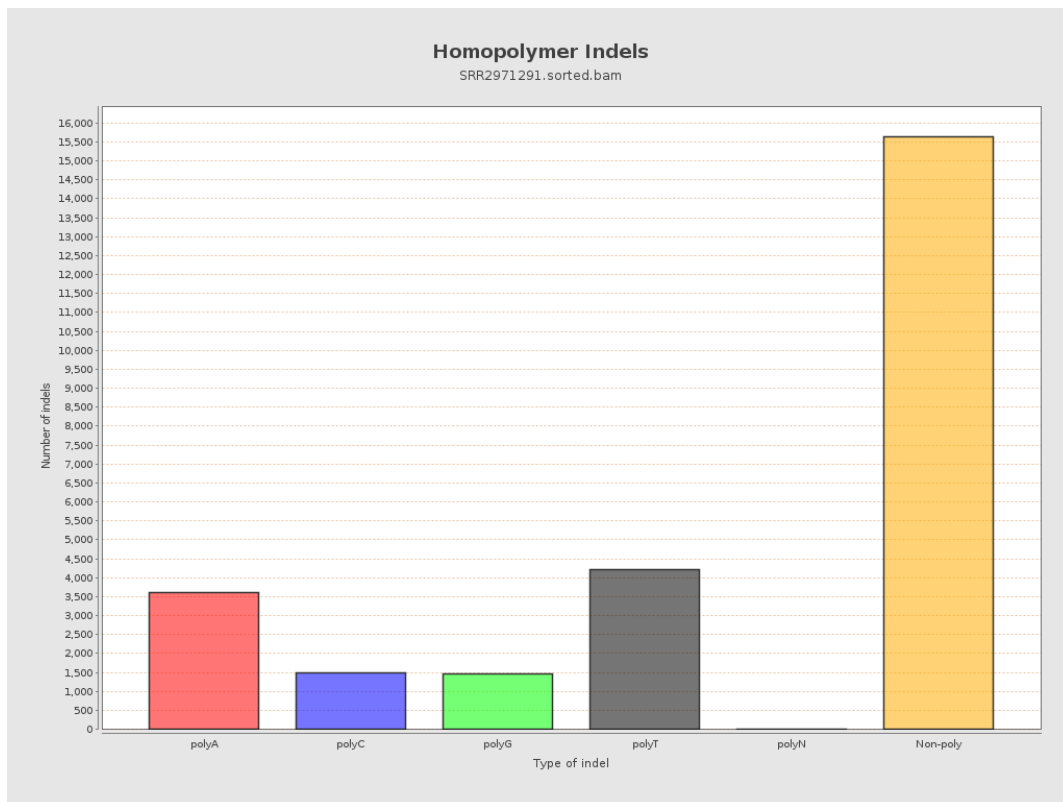
9. Results : Mapped Reads GC-content Distribution



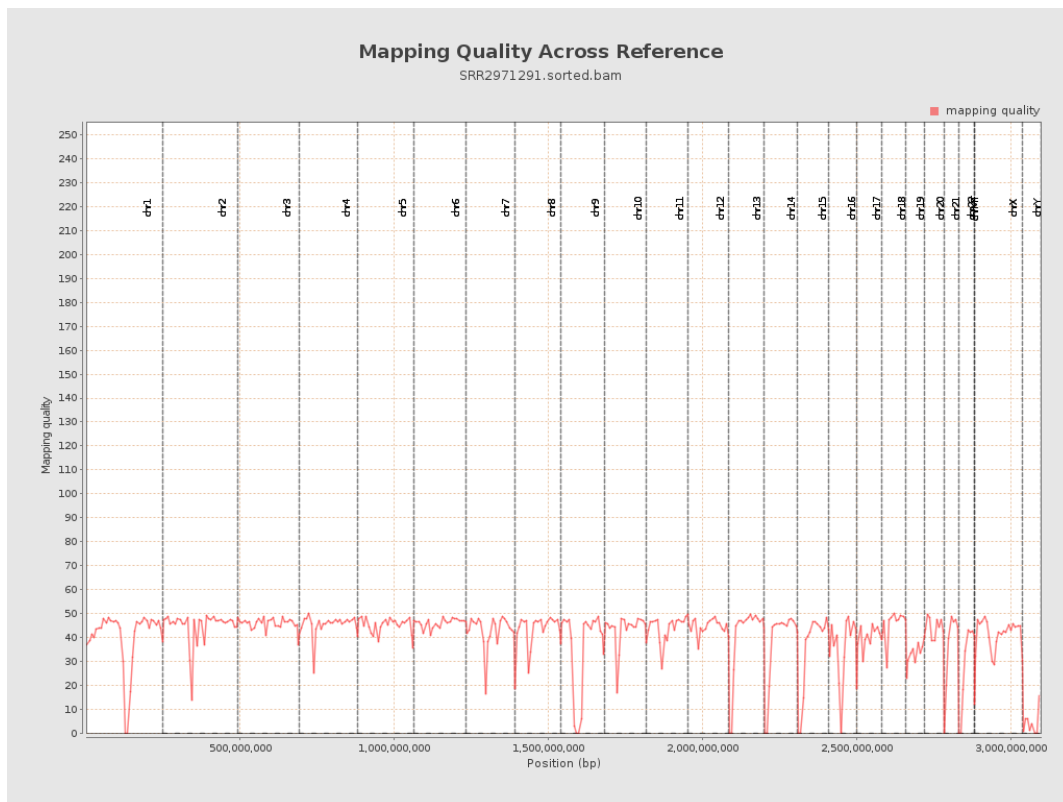
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

