

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 03:10:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053676.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_SRR053676 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053676.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 03:10:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053676.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,738,193
Mapped reads	2,794,940 / 74.77%
Unmapped reads	943,253 / 25.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	127 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	653,426 / 17.48%
Duplication rate	17.02%
Clipped reads	425,703 / 11.39%

2.2. ACGT Content

Number/percentage of A's	40,032,194 / 30.74%
Number/percentage of C's	27,175,318 / 20.87%
Number/percentage of T's	34,889,892 / 26.79%
Number/percentage of G's	28,100,295 / 21.58%
Number/percentage of N's	41,009 / 0.03%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0421

Standard Deviation	0.4919
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2.4. Mapping Quality

Mean Mapping Quality	42.72
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2.5. Mismatches and indels

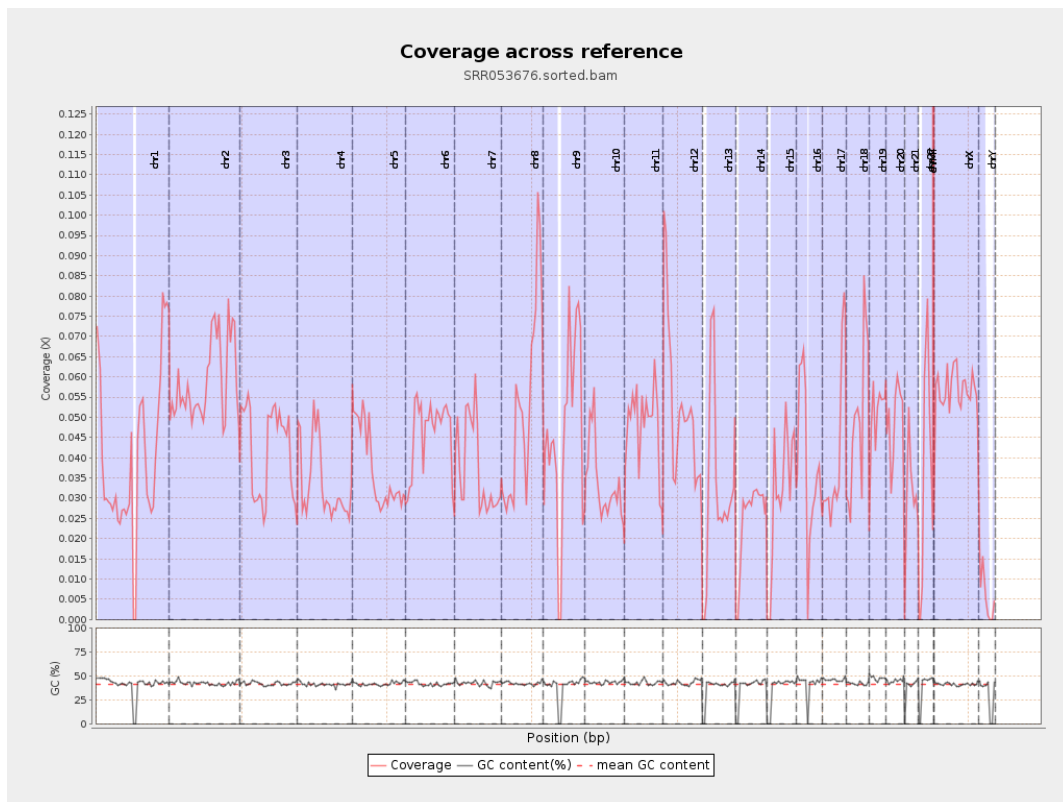
General error rate	0.67%
Mismatches	865,959
Insertions	6,078
Mapped reads with at least one insertion	0.22%
Deletions	16,517
Mapped reads with at least one deletion	0.59%
Homopolymer indels	41.13%

2.6. Chromosome stats

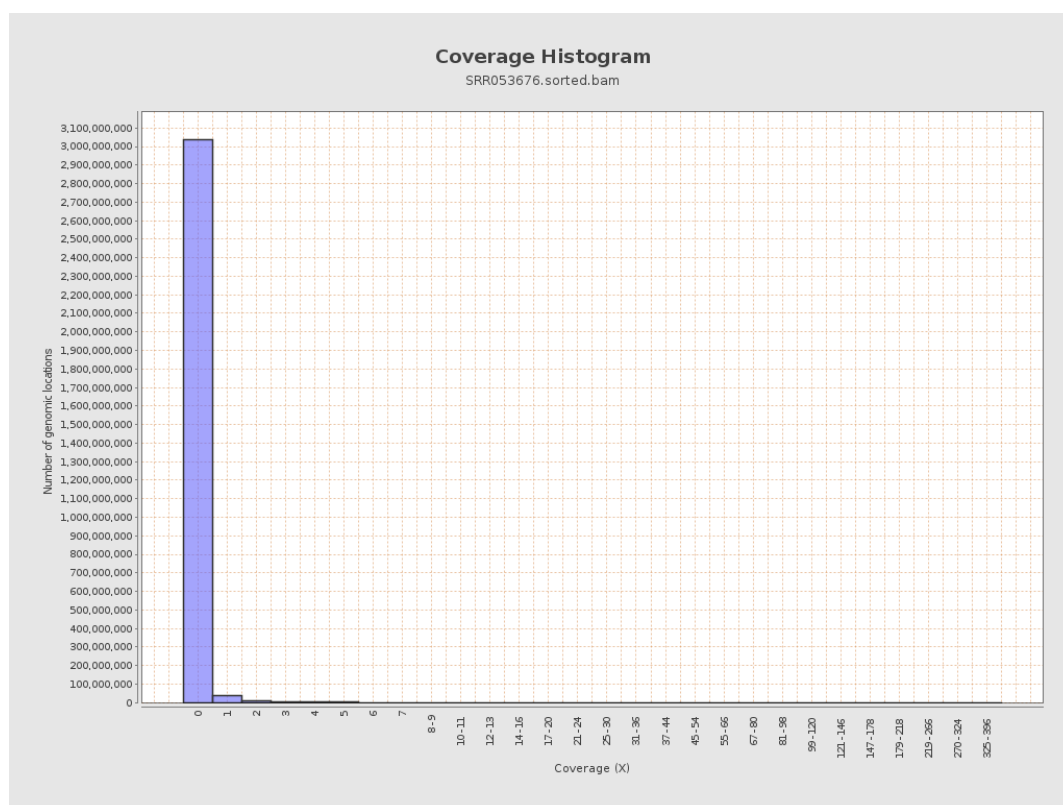
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9789493	0.0393	0.4791
chr2	243199373	14321240	0.0589	0.6427
chr3	198022430	8333870	0.0421	0.4627
chr4	191154276	6387948	0.0334	0.4626
chr5	180915260	6688682	0.037	0.4222
chr6	171115067	7828314	0.0457	0.5212
chr7	159138663	5944408	0.0374	0.5288

chr8	146364022	7777359	0.0531	0.5533
chr9	141213431	6595310	0.0467	0.5006
chr10	135534747	4628709	0.0342	0.4238
chr11	135006516	6413446	0.0475	0.5145
chr12	133851895	7017034	0.0524	0.5328
chr13	115169878	3537227	0.0307	0.3913
chr14	107349540	2630545	0.0245	0.3618
chr15	102531392	3192811	0.0311	0.392
chr16	90354753	3519175	0.0389	0.4502
chr17	81195210	3334708	0.0411	0.4512
chr18	78077248	3830122	0.0491	0.52
chr19	59128983	3018717	0.0511	0.5354
chr20	63025520	3058678	0.0485	0.5245
chr21	48129895	1485383	0.0309	0.4185
chr22	51304566	1837647	0.0358	0.4396
chrMT	16571	21547	1.3003	5.3176
chrX	155270560	8716943	0.0561	0.5531
chrY	59373566	354293	0.006	0.187

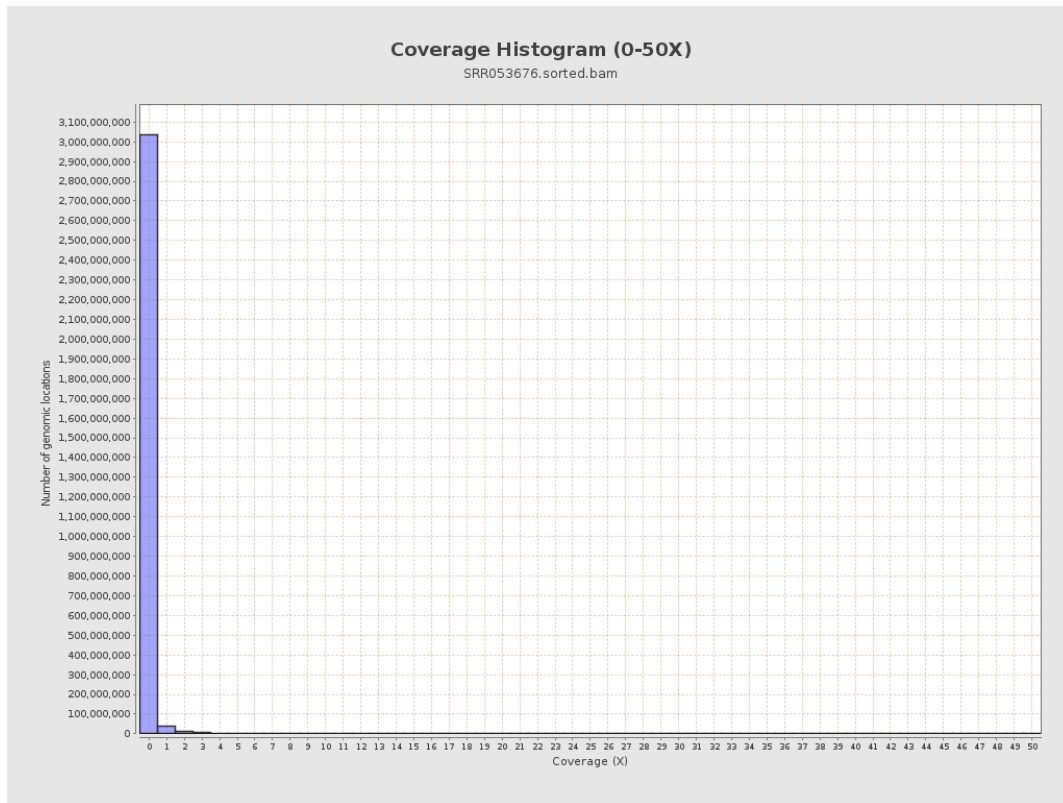
3. Results : Coverage across reference



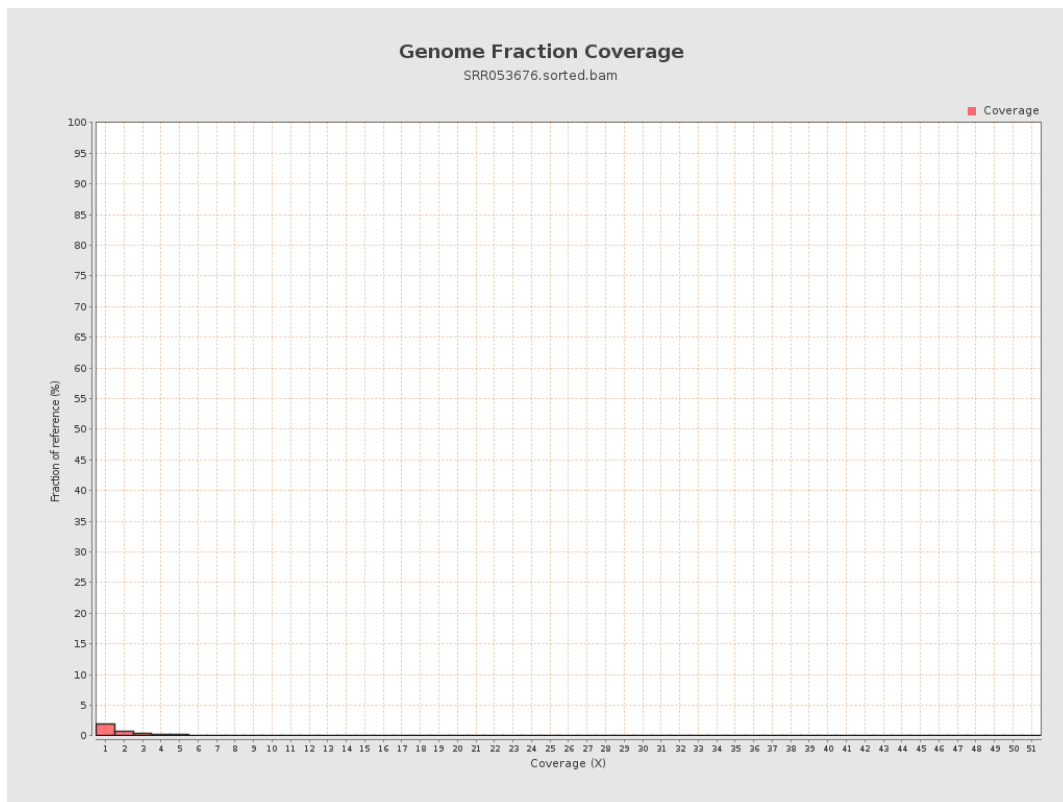
4. Results : Coverage Histogram



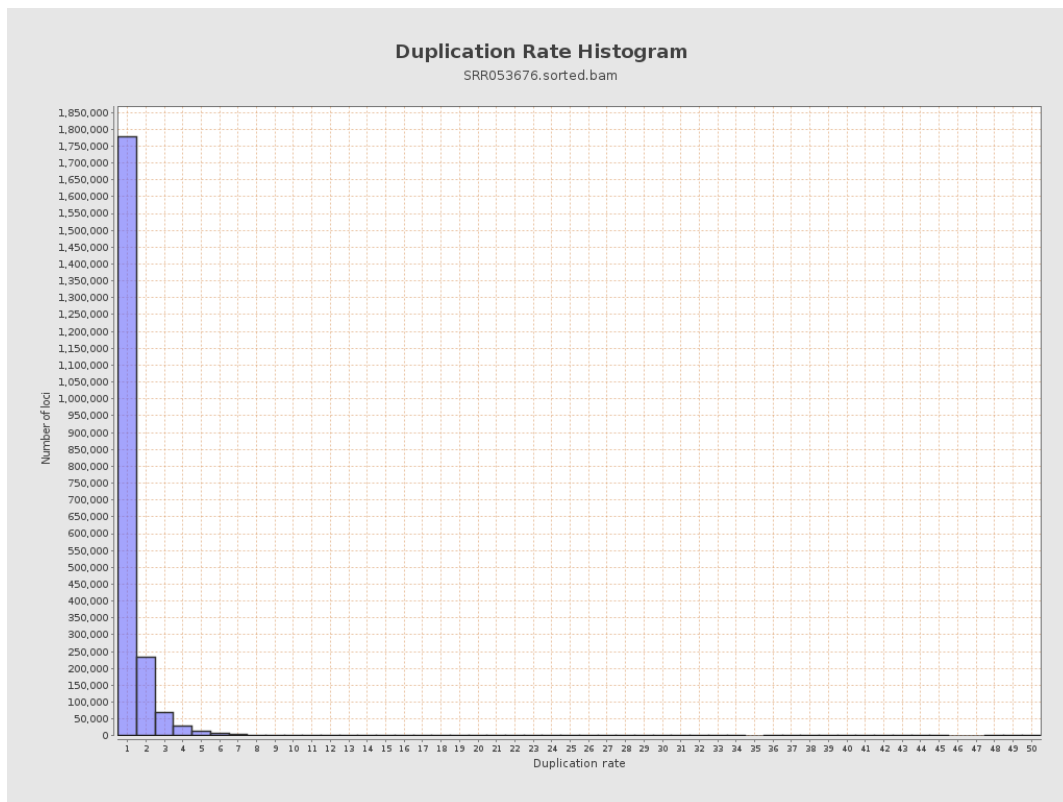
5. Results : Coverage Histogram (0-50X)



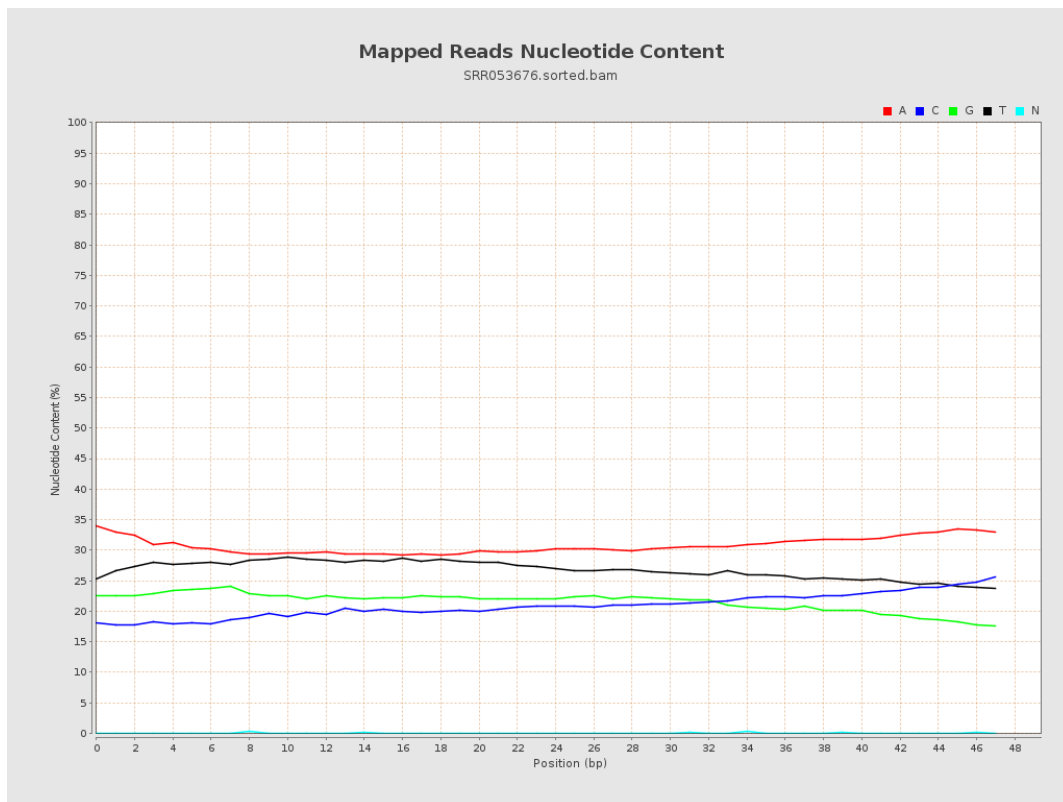
6. Results : Genome Fraction Coverage



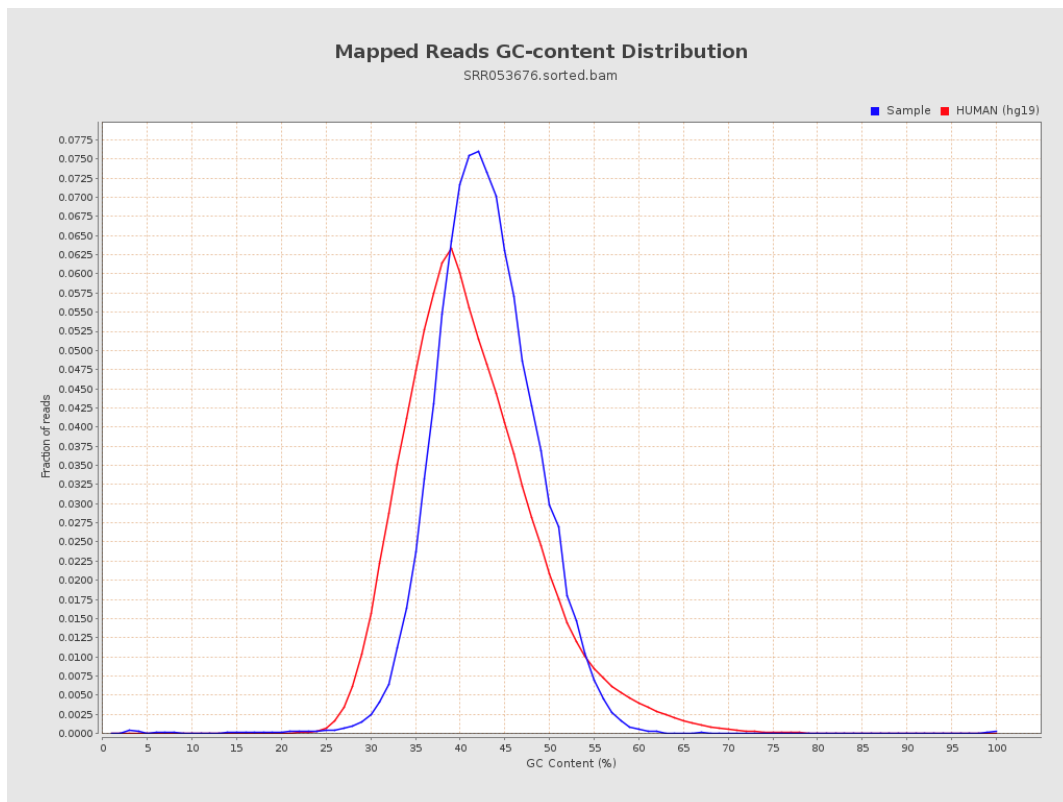
7. Results : Duplication Rate Histogram



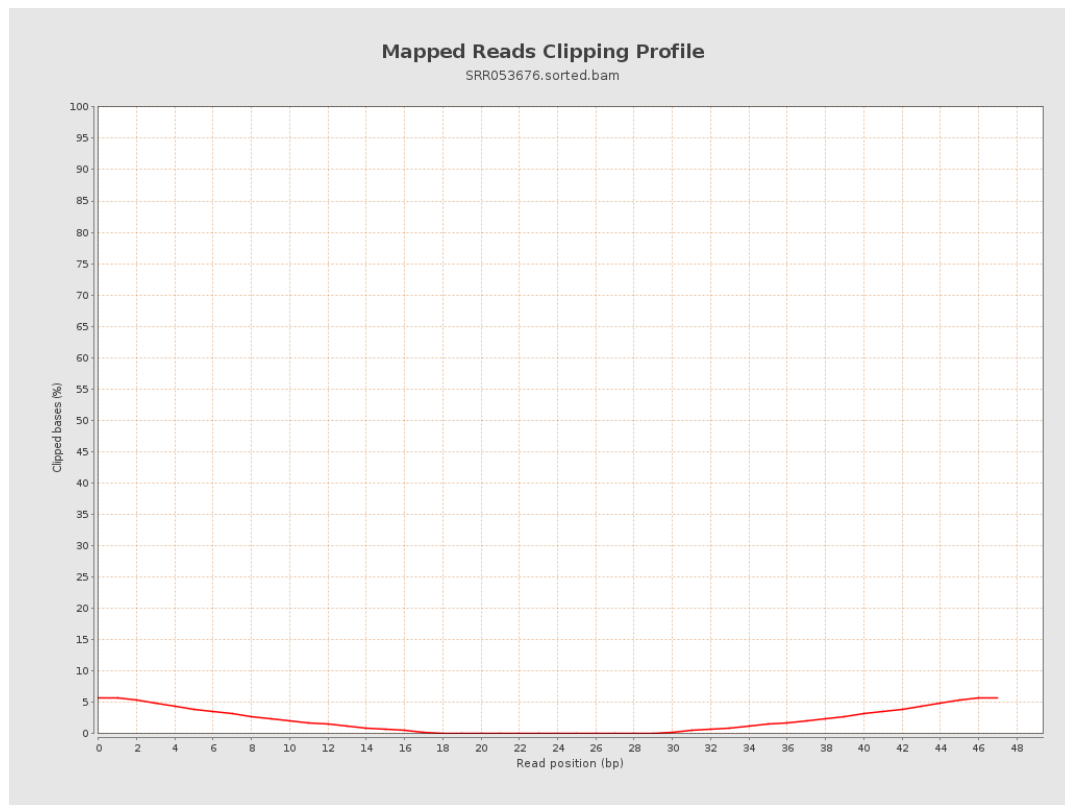
8. Results : Mapped Reads Nucleotide Content



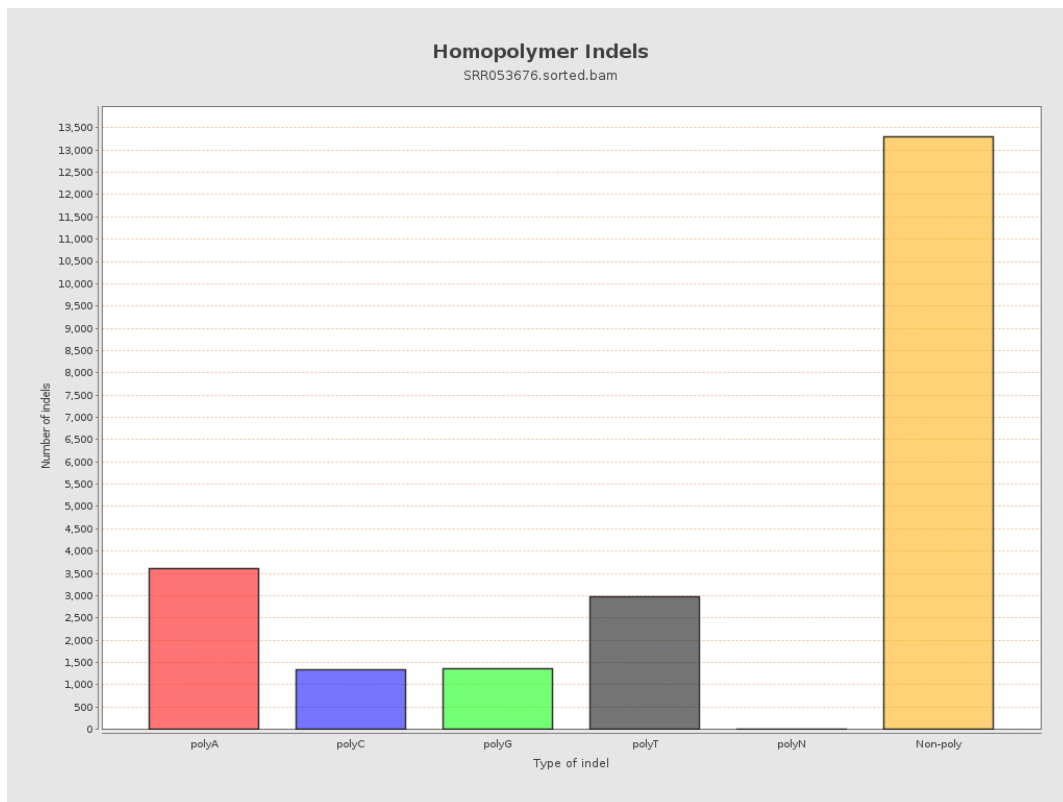
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

