

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 17:54:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006076.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_SRR1006076 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006076_1.fastq.gz SRR1006076_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 17:54:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,246,460
Mapped reads	7,859,417 / 85%
Unmapped reads	1,387,043 / 15%
Mapped paired reads	7,859,417 / 85%
Mapped reads, first in pair	3,999,363 / 43.25%
Mapped reads, second in pair	3,860,054 / 41.75%
Mapped reads, both in pair	7,039,918 / 76.14%
Mapped reads, singletons	819,499 / 8.86%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	579,661 / 6.27%
Duplication rate	6.73%
Clipped reads	725,503 / 7.85%

2.2. ACGT Content

Number/percentage of A's	80,675,954 / 26.63%
Number/percentage of C's	66,901,470 / 22.09%
Number/percentage of T's	83,784,219 / 27.66%
Number/percentage of G's	71,527,820 / 23.61%
Number/percentage of N's	12,169 / 0%
GC Percentage	45.7%

2.3. Coverage

Mean	0.0979
Standard Deviation	0.571

2.4. Mapping Quality

Mean Mapping Quality	46.47
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2.5. Insert size

Mean	76,066.91
Standard Deviation	2,745,426.92
P25/Median/P75	71 / 103 / 140

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	1,525,849
Insertions	10,354
Mapped reads with at least one insertion	0.13%
Deletions	26,528
Mapped reads with at least one deletion	0.34%
Homopolymer indels	45.18%

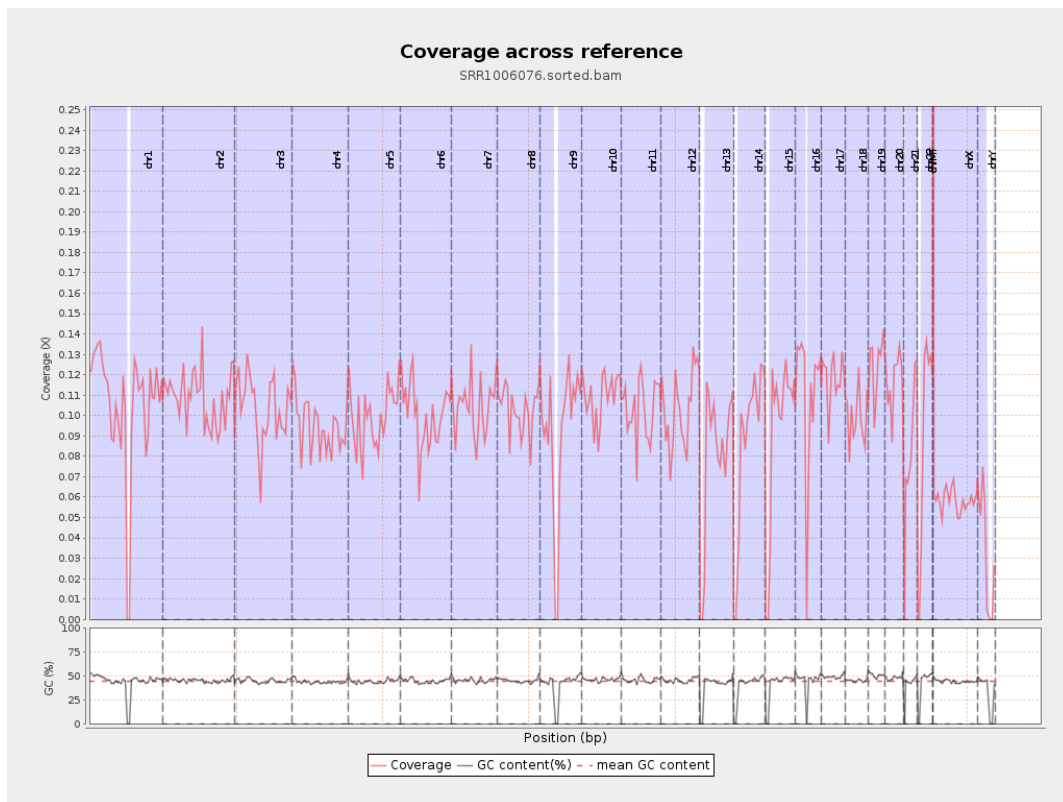
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

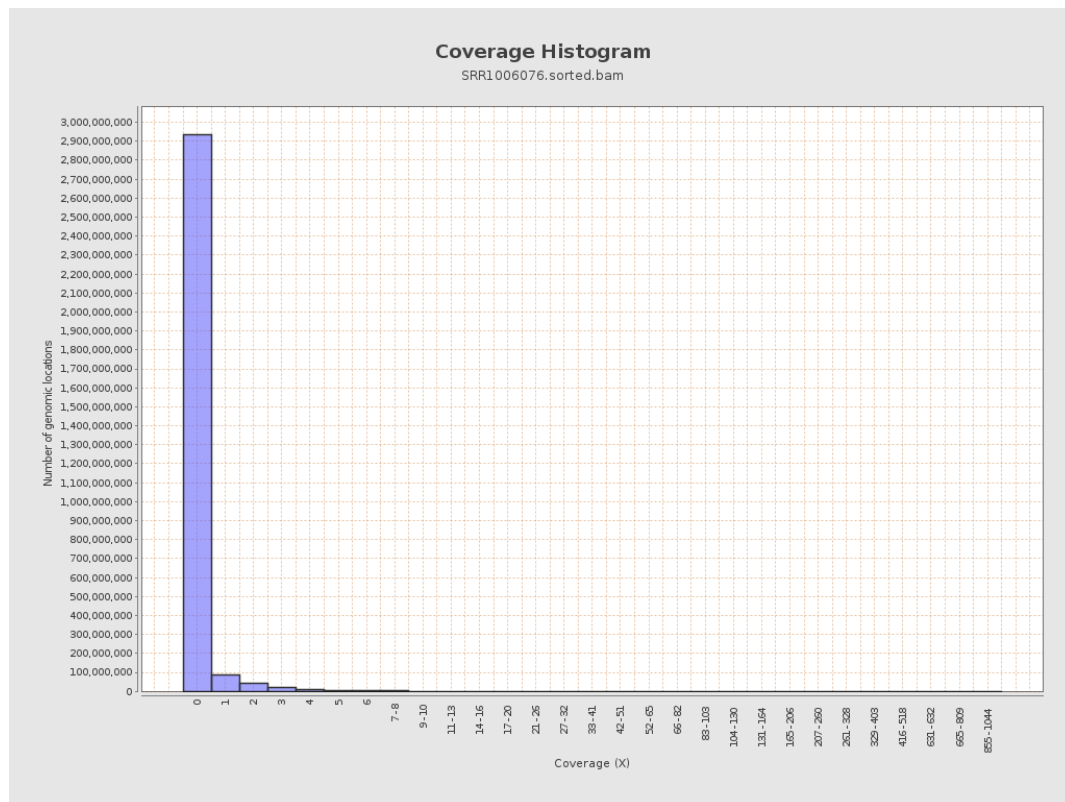
chr1	249250621	26156934	0.1049	0.6407
chr2	243199373	26446626	0.1087	0.6293
chr3	198022430	20502622	0.1035	0.5267
chr4	191154276	18100574	0.0947	0.5222
chr5	180915260	18092085	0.1	0.5185
chr6	171115067	17125914	0.1001	0.5988
chr7	159138663	16652468	0.1046	0.6602
chr8	146364022	15010851	0.1026	0.6023
chr9	141213431	12845329	0.091	0.5218
chr10	135534747	14781180	0.1091	0.5625
chr11	135006516	13920701	0.1031	0.7696
chr12	133851895	13929169	0.1041	0.5329
chr13	115169878	9128455	0.0793	0.4646
chr14	107349540	9458511	0.0881	0.4969
chr15	102531392	9279977	0.0905	0.5007
chr16	90354753	9817264	0.1087	0.5718
chr17	81195210	9645781	0.1188	0.6103
chr18	78077248	7654344	0.098	0.5946
chr19	59128983	7358687	0.1245	0.6871
chr20	63025520	7353465	0.1167	0.5736
chr21	48129895	4029119	0.0837	0.5156
chr22	51304566	4556078	0.0888	0.511
chrMT	16571	26696	1.611	2.5024
chrX	155270560	9101236	0.0586	0.4062

chrY	59373566	1960996	0.033	0.3178
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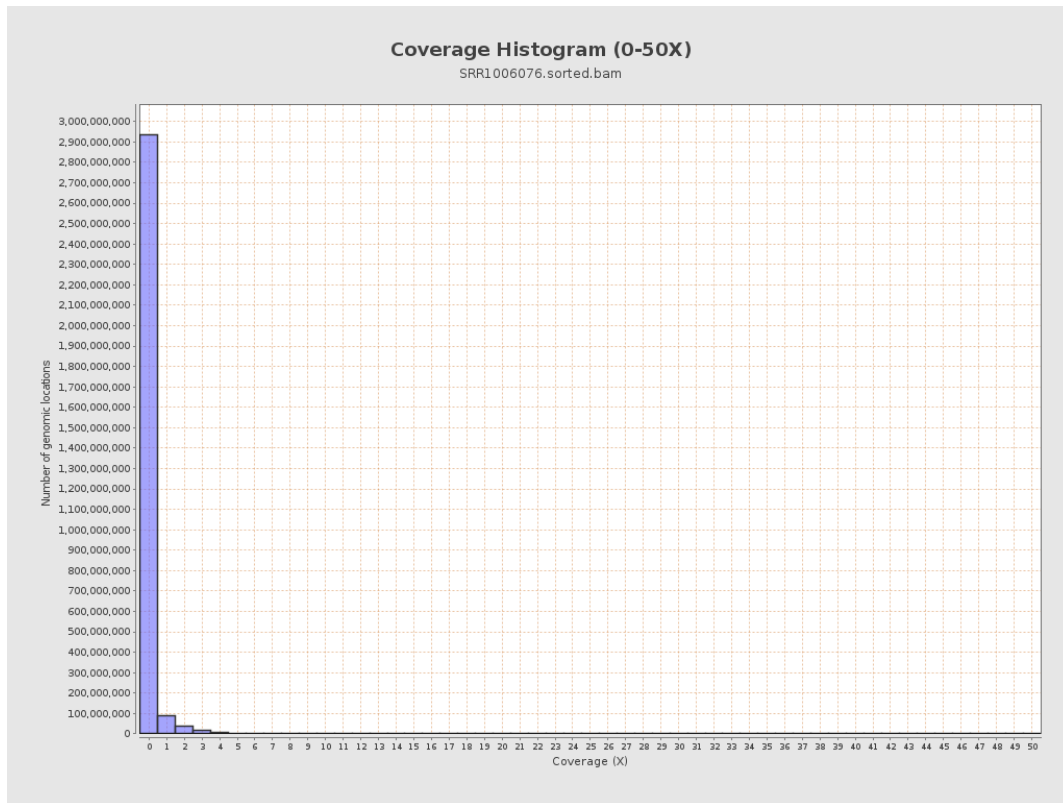
3. Results : Coverage across reference



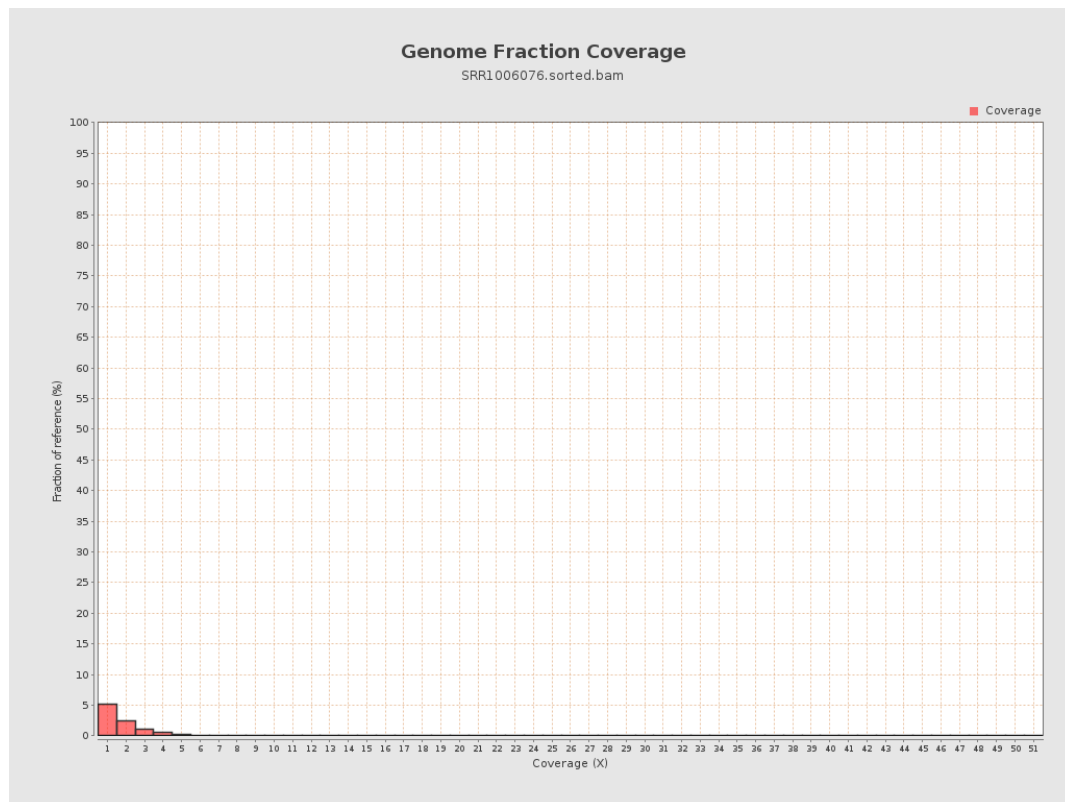
4. Results : Coverage Histogram



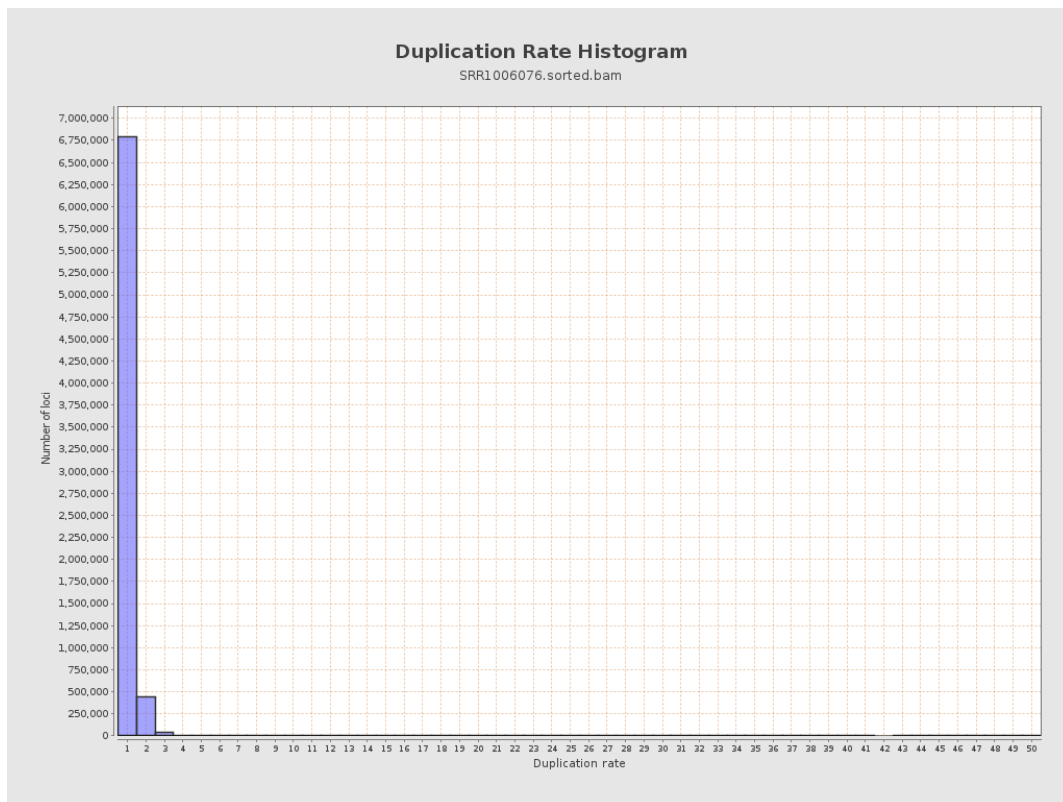
5. Results : Coverage Histogram (0-50X)



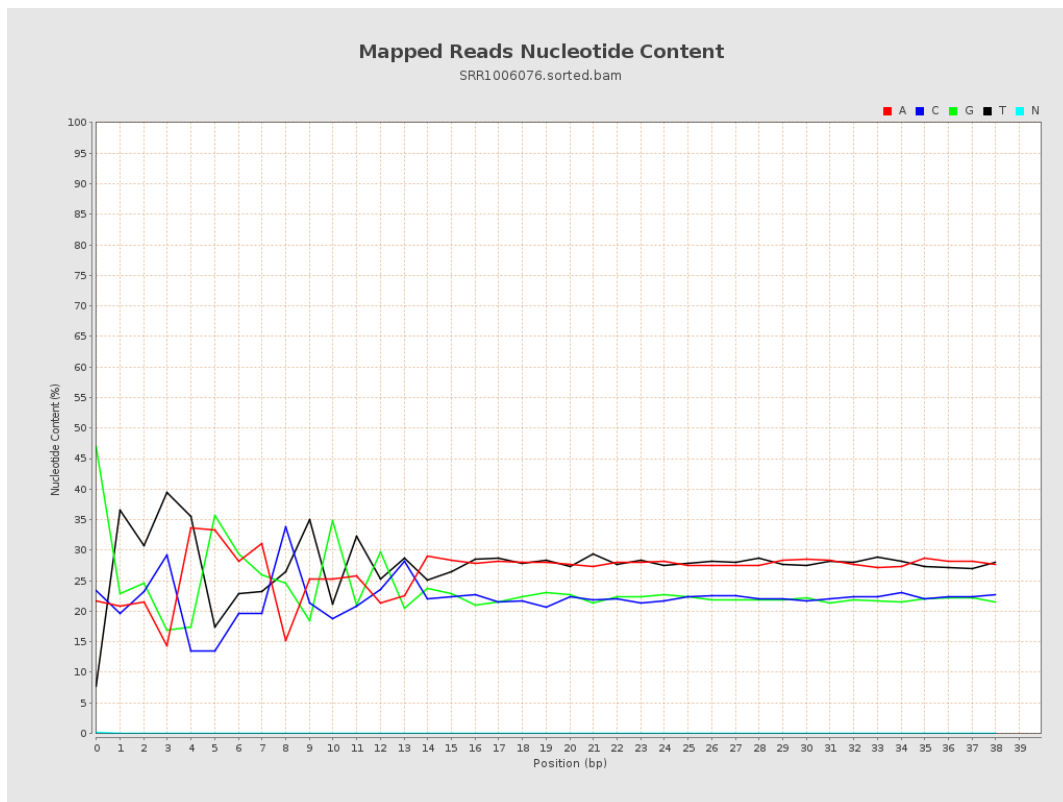
6. Results : Genome Fraction Coverage



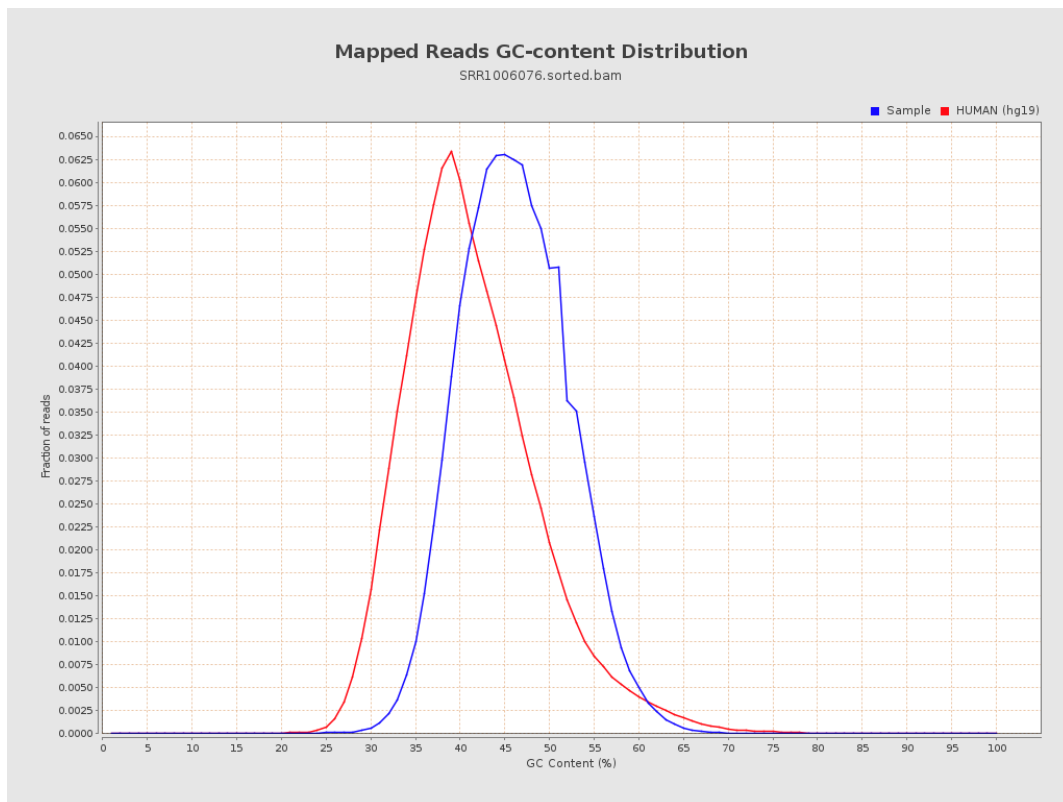
7. Results : Duplication Rate Histogram



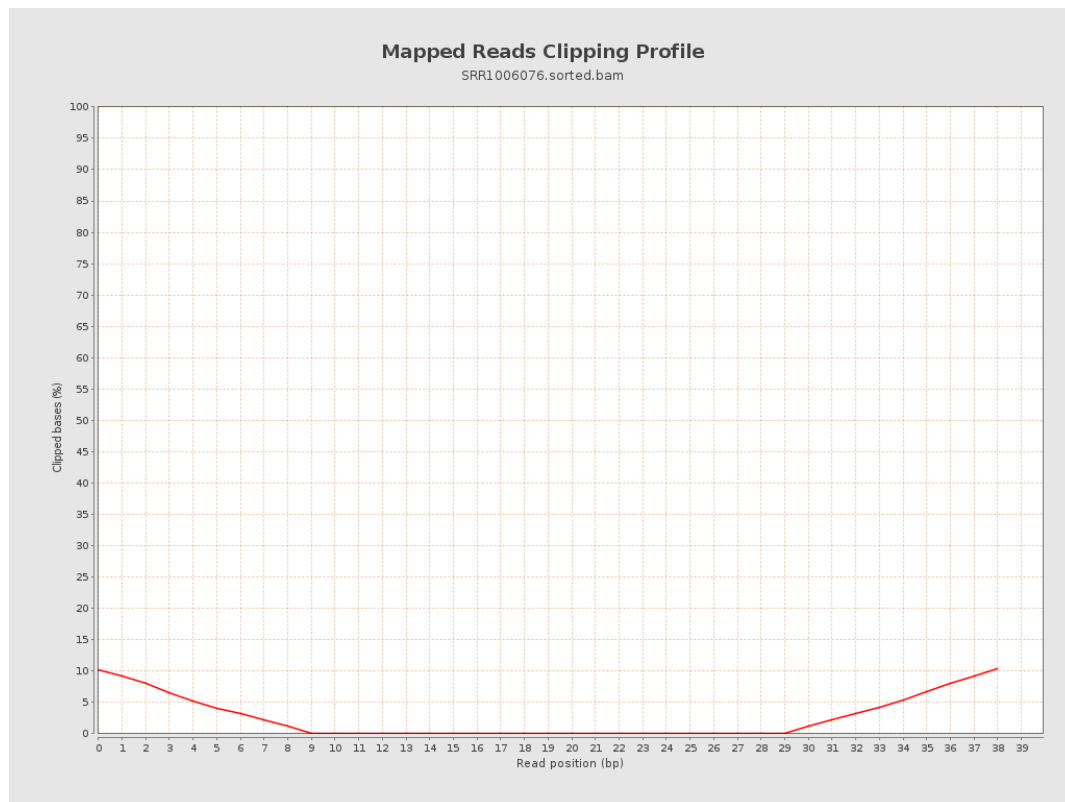
8. Results : Mapped Reads Nucleotide Content



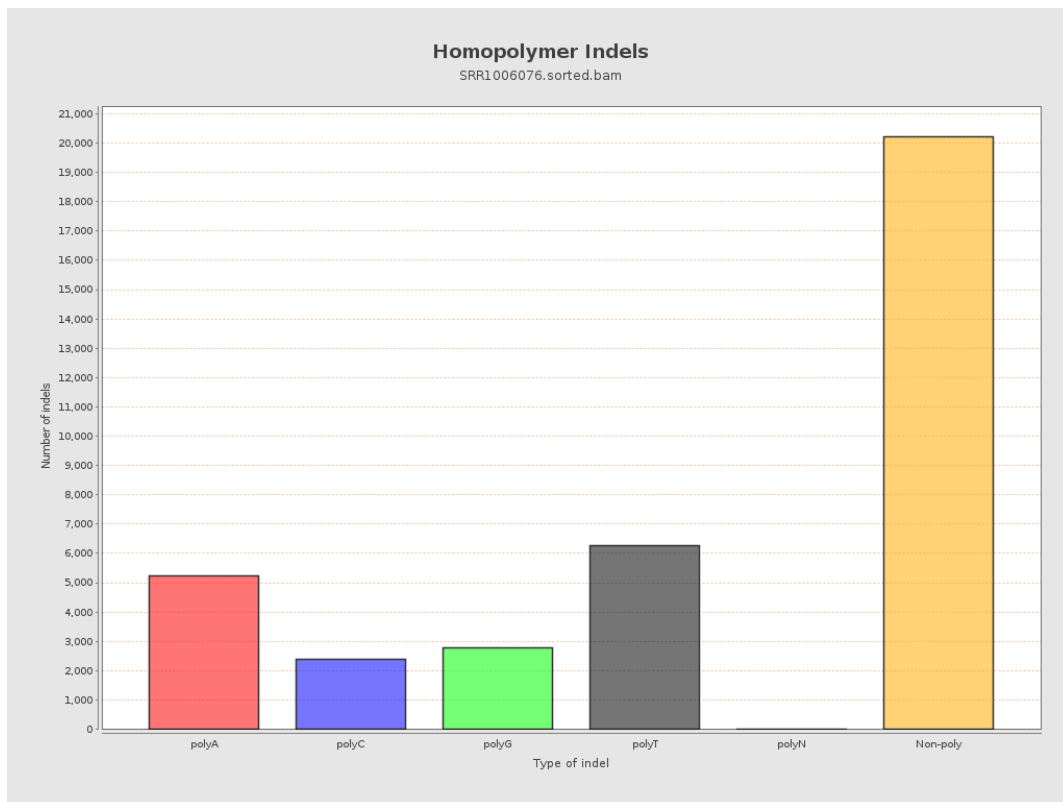
9. Results : Mapped Reads GC-content Distribution



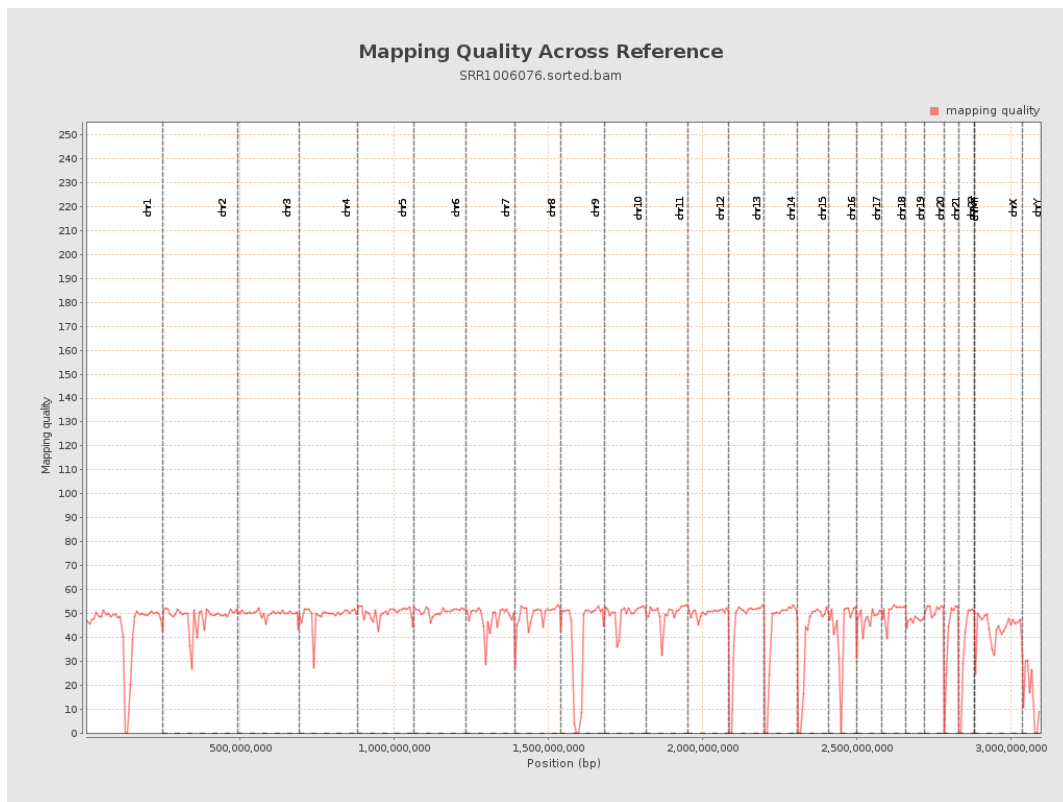
10. Results : Mapped Reads Clipping Profile



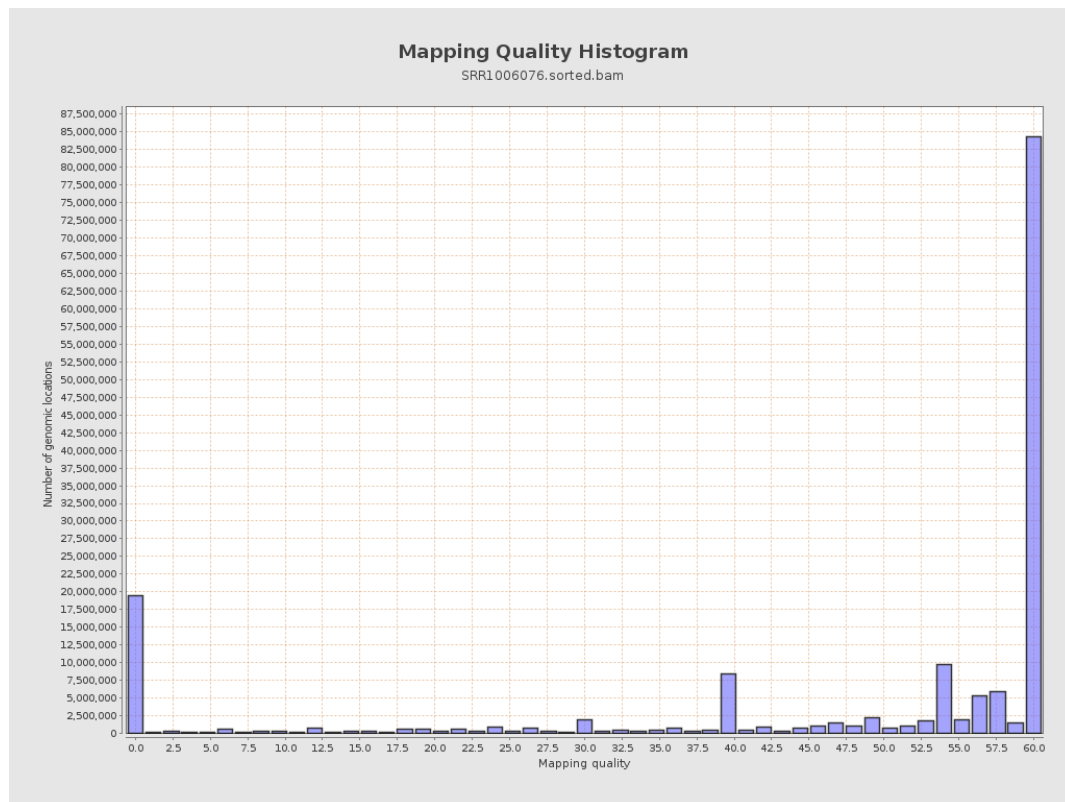
11. Results : Homopolymer Indels



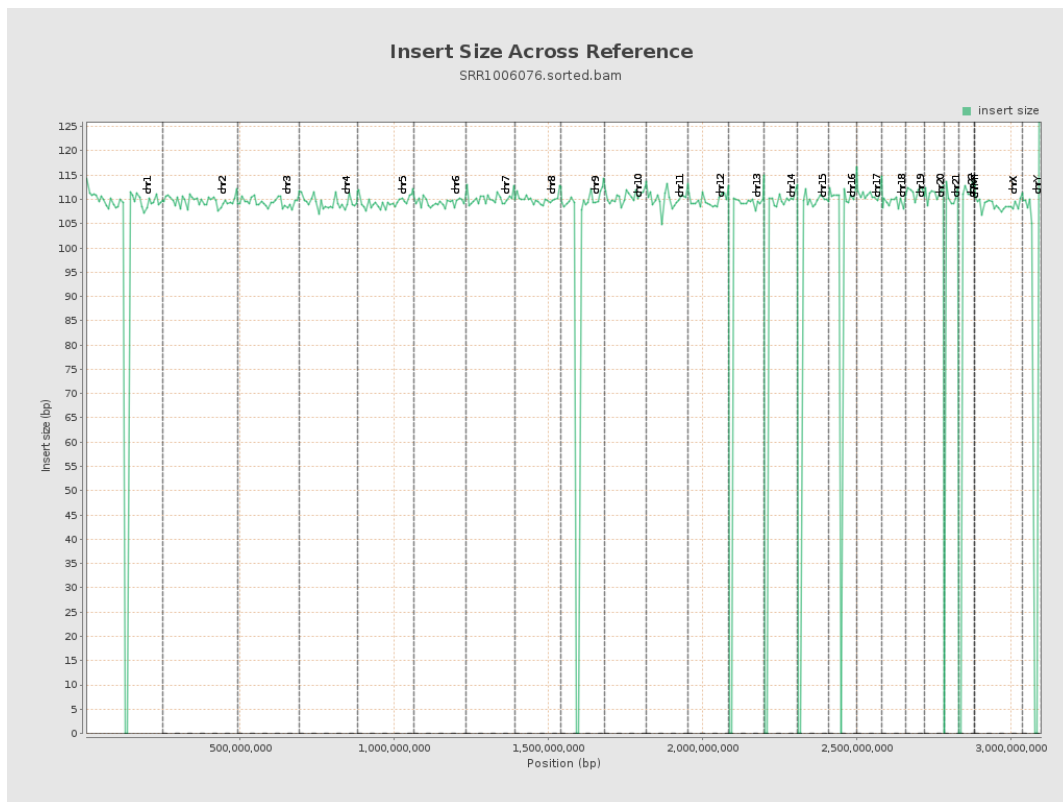
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

