

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 16:01:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006043.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_SRR1006043 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006043_1.fastq.gz SRR1006043_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 16:01:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006043.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,156,214
Mapped reads	7,109,087 / 87.16%
Unmapped reads	1,047,127 / 12.84%
Mapped paired reads	7,109,087 / 87.16%
Mapped reads, first in pair	3,610,327 / 44.26%
Mapped reads, second in pair	3,498,760 / 42.9%
Mapped reads, both in pair	6,603,852 / 80.97%
Mapped reads, singletons	505,235 / 6.19%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	225,523 / 2.77%
Duplication rate	2.7%
Clipped reads	478,327 / 5.86%

2.2. ACGT Content

Number/percentage of A's	76,025,870 / 27.64%
Number/percentage of C's	60,141,951 / 21.86%
Number/percentage of T's	77,381,558 / 28.13%
Number/percentage of G's	61,434,243 / 22.33%
Number/percentage of N's	109,891 / 0.04%
GC Percentage	44.19%

2.3. Coverage

Mean	0.0889
Standard Deviation	0.4426

2.4. Mapping Quality

Mean Mapping Quality	47.72
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2.5. Insert size

Mean	48,566.99
Standard Deviation	2,158,402.22
P25/Median/P75	64 / 93 / 137

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	1,540,402
Insertions	8,496
Mapped reads with at least one insertion	0.12%
Deletions	23,306
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45.76%

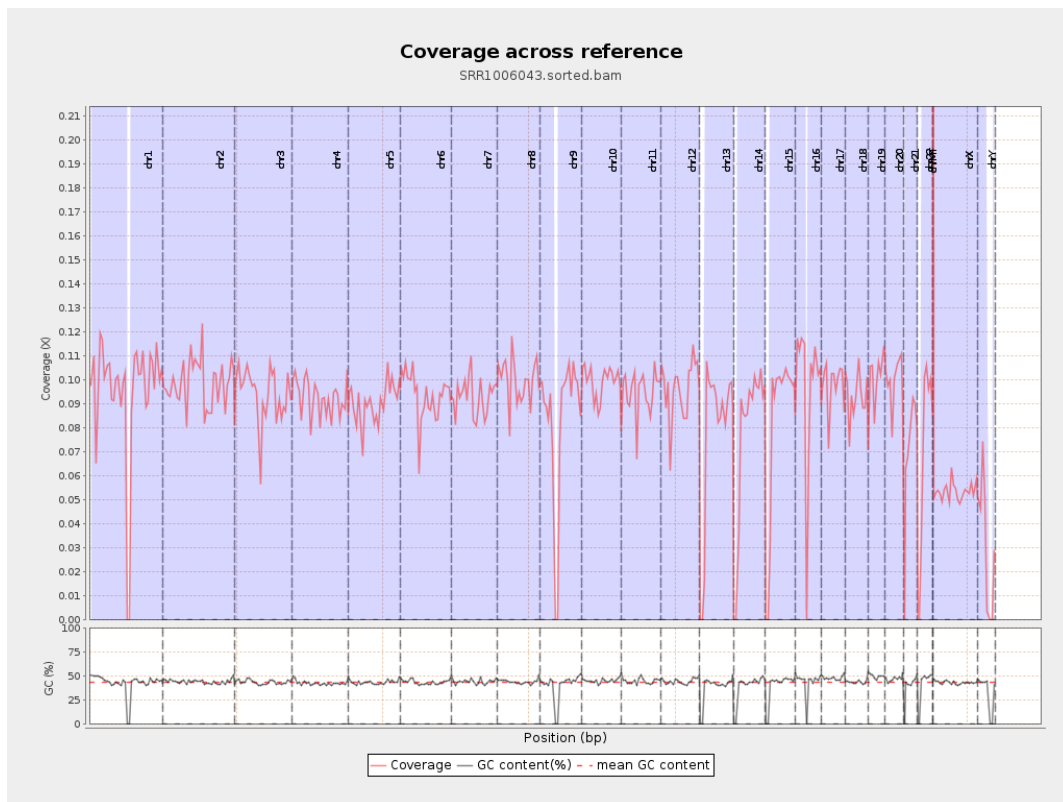
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

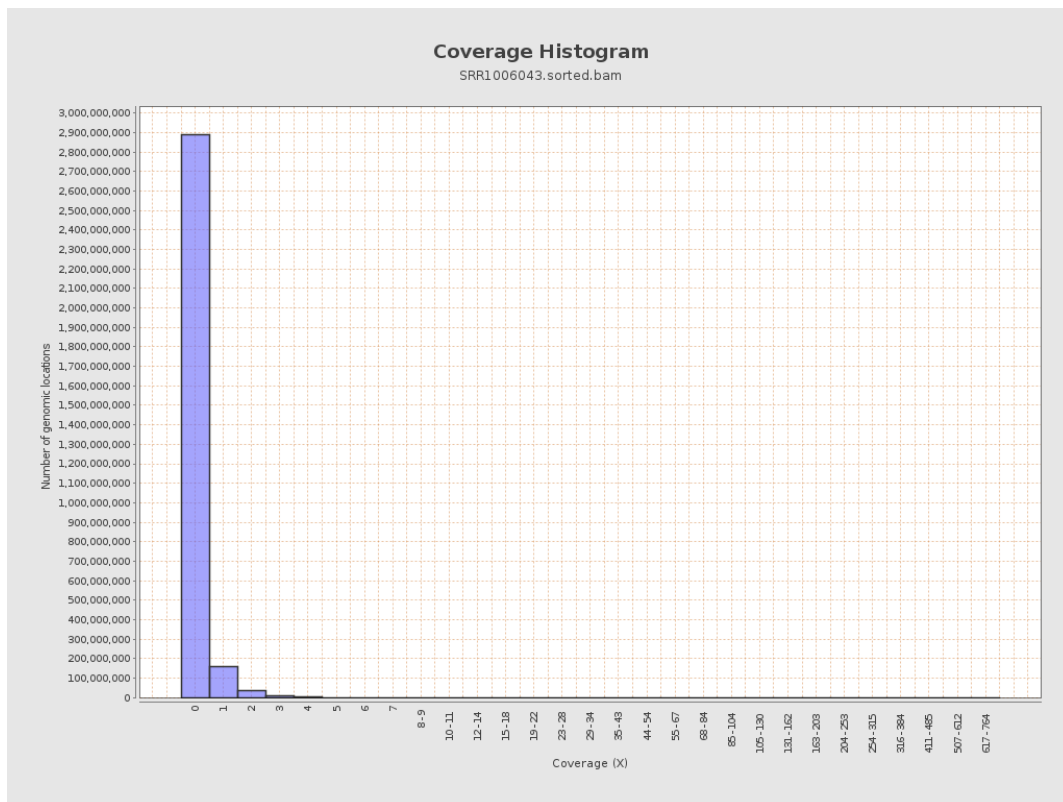
chr1	249250621	23602622	0.0947	0.5123
chr2	243199373	23988894	0.0986	0.5015
chr3	198022430	18541054	0.0936	0.379
chr4	191154276	17662119	0.0924	0.3986
chr5	180915260	16357785	0.0904	0.3733
chr6	171115067	15967225	0.0933	0.4118
chr7	159138663	14819390	0.0931	0.6042
chr8	146364022	14535086	0.0993	0.4642
chr9	141213431	11697622	0.0828	0.4276
chr10	135534747	13462622	0.0993	0.4288
chr11	135006516	12758448	0.0945	0.5725
chr12	133851895	12919912	0.0965	0.3894
chr13	115169878	8983339	0.078	0.3486
chr14	107349540	8336481	0.0777	0.3626
chr15	102531392	8261620	0.0806	0.353
chr16	90354753	8640967	0.0956	0.4281
chr17	81195210	7968983	0.0981	0.442
chr18	78077248	7229803	0.0926	0.6027
chr19	59128983	5962150	0.1008	0.5124
chr20	63025520	6282368	0.0997	0.4011
chr21	48129895	3451693	0.0717	0.3949
chr22	51304566	3546077	0.0691	0.3644
chrMT	16571	15285	0.9224	1.5435
chrX	155270560	8303251	0.0535	0.3112

chrY	59373566	1828418	0.0308	0.279
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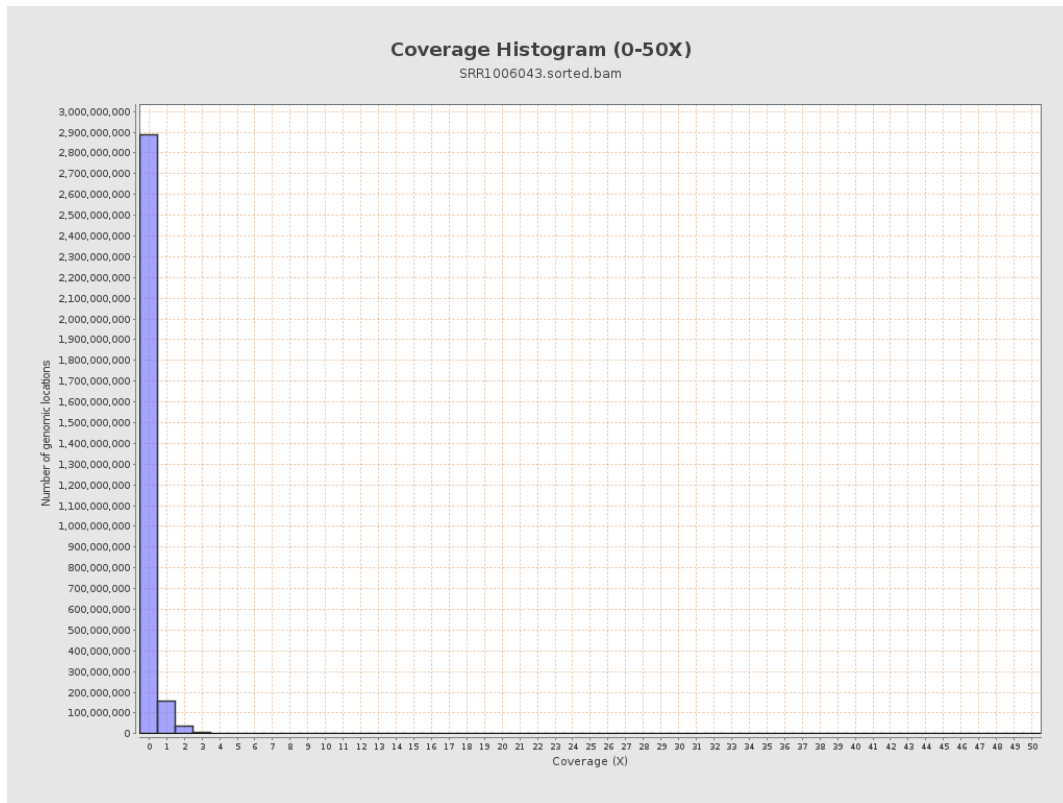
3. Results : Coverage across reference



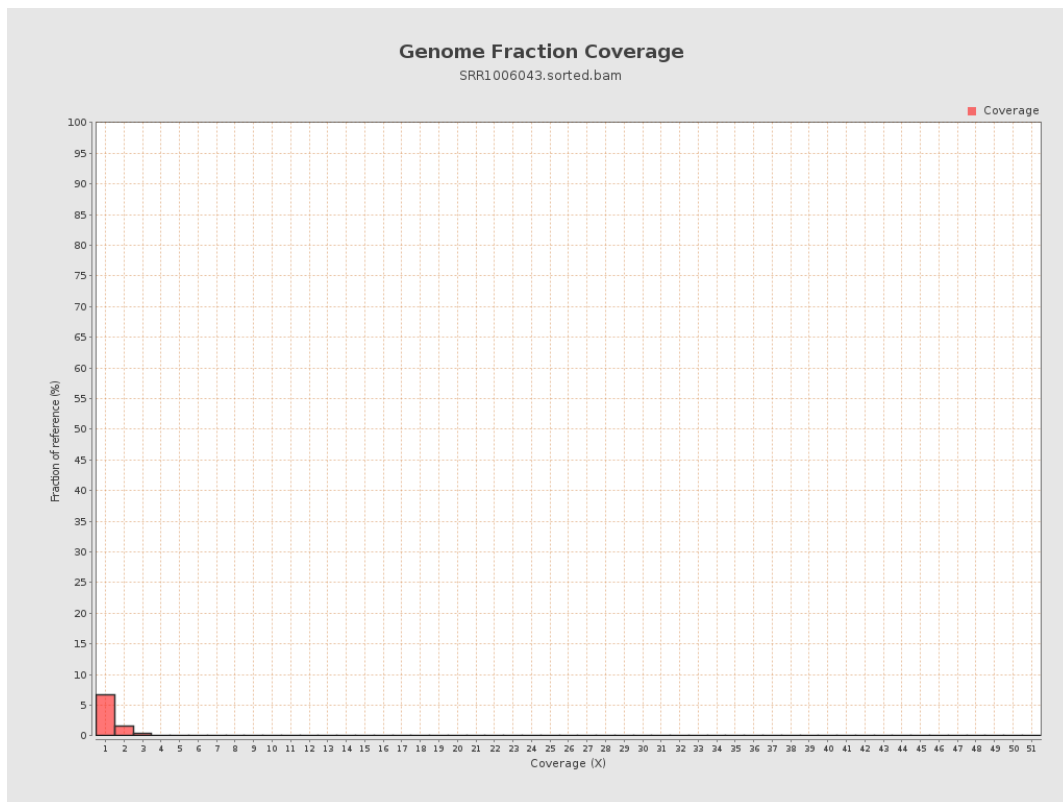
4. Results : Coverage Histogram



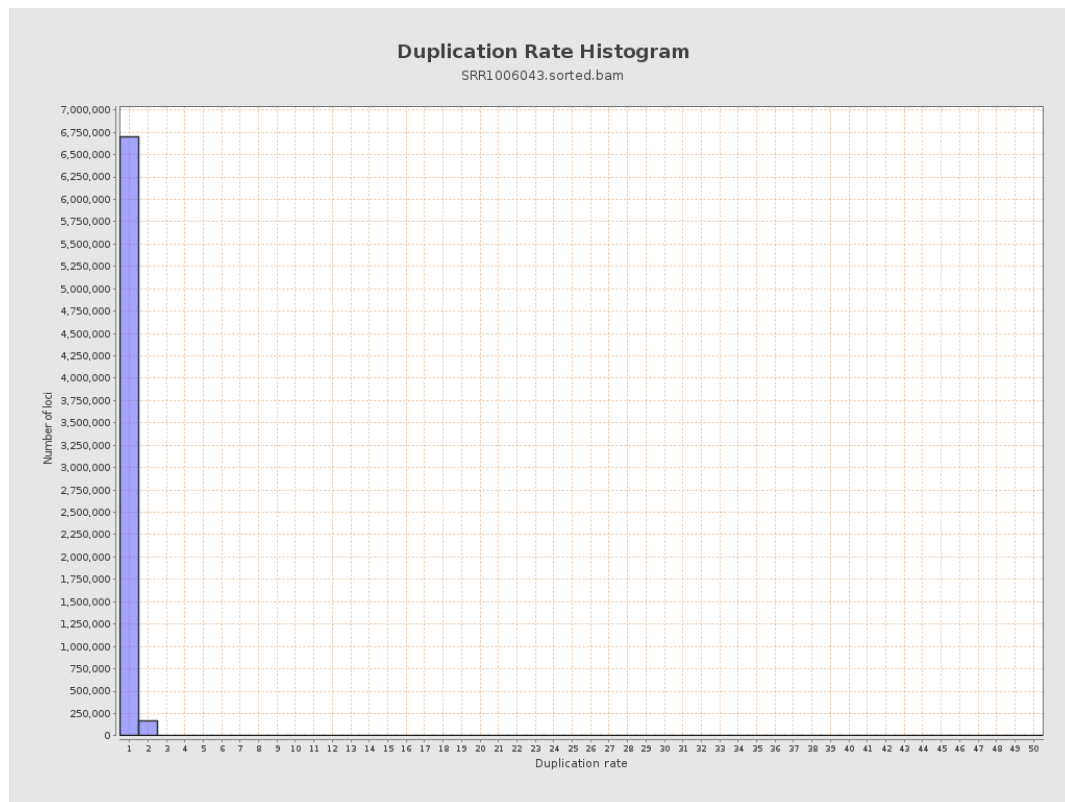
5. Results : Coverage Histogram (0-50X)



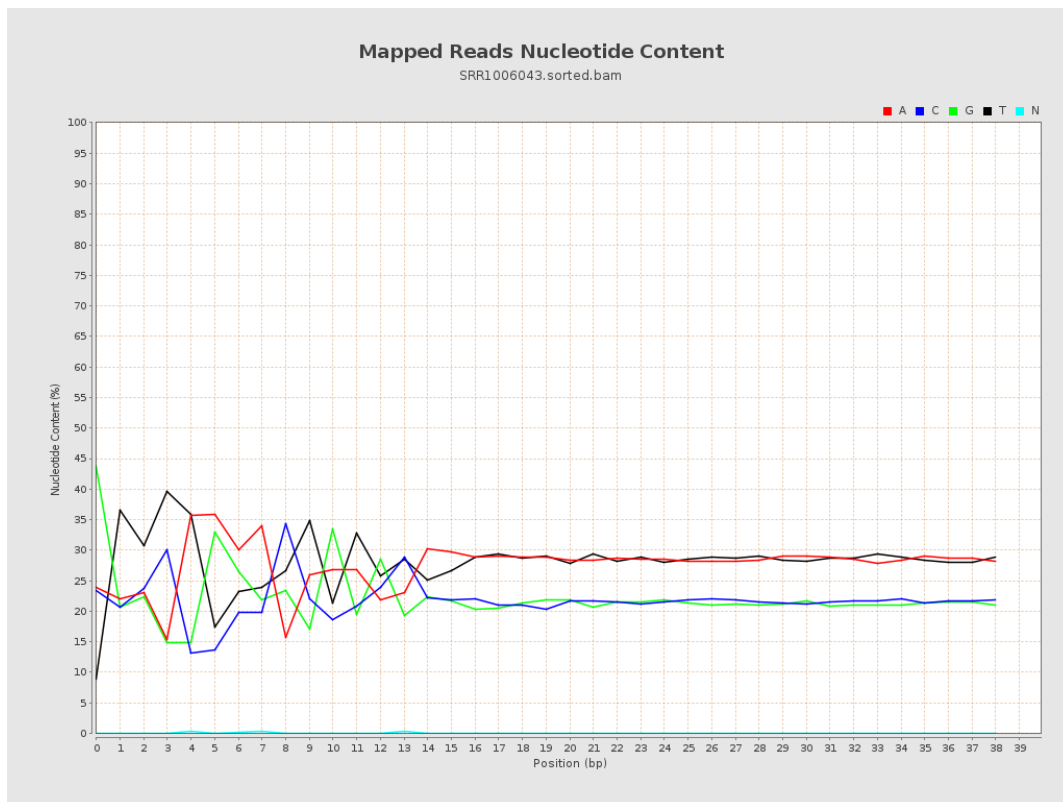
6. Results : Genome Fraction Coverage



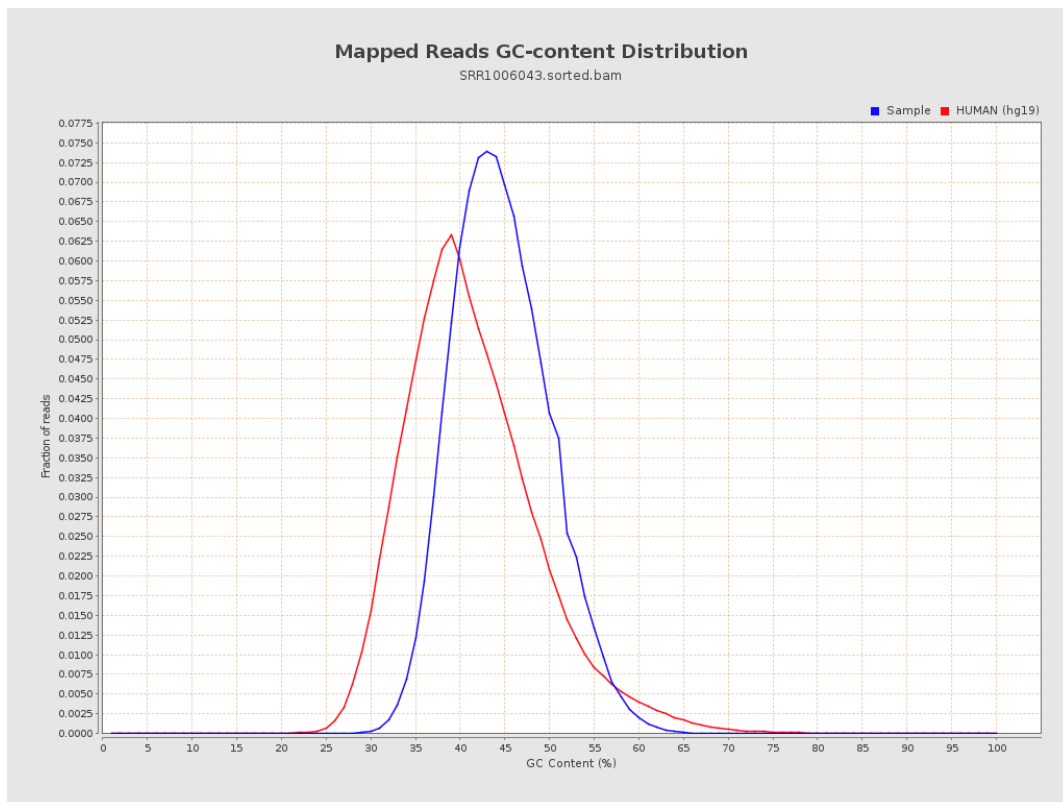
7. Results : Duplication Rate Histogram



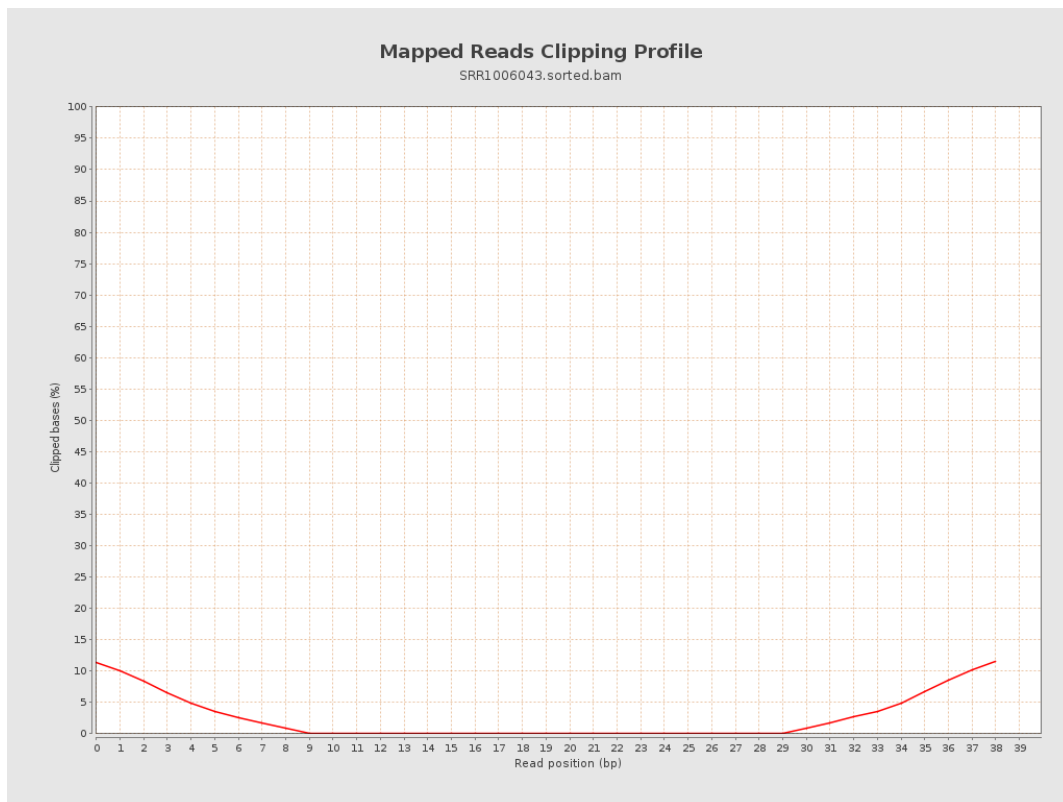
8. Results : Mapped Reads Nucleotide Content



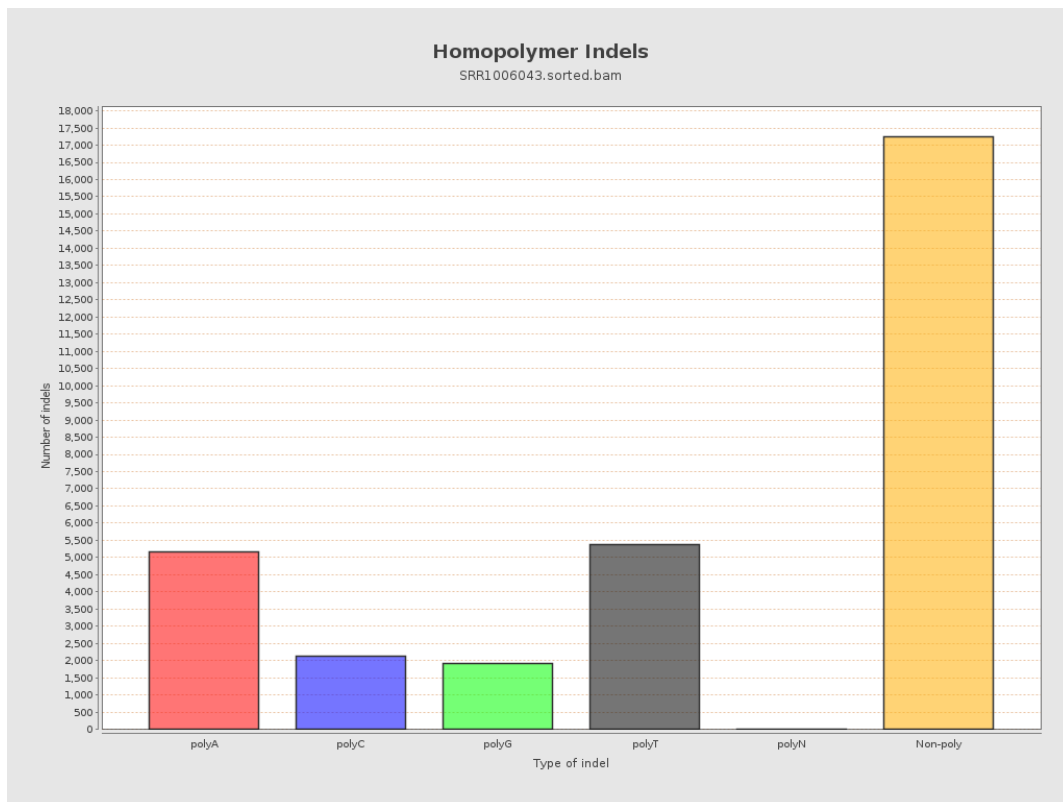
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



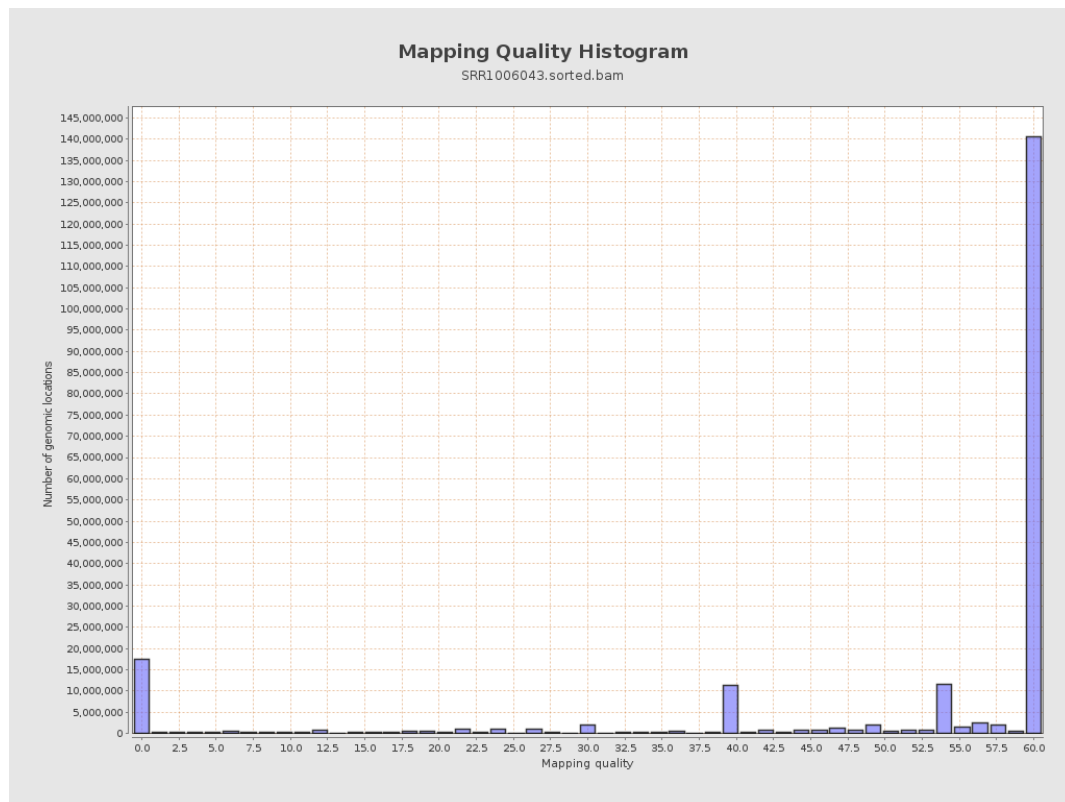
11. Results : Homopolymer Indels



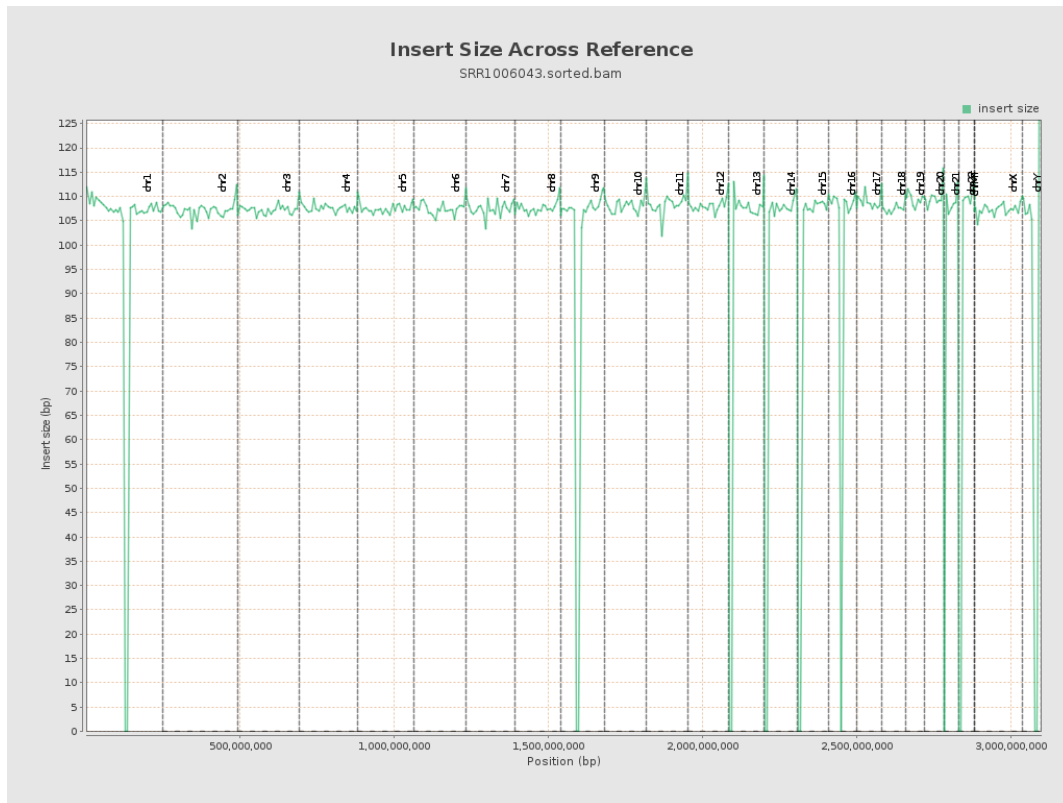
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

