

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 16:24:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006048.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_SRR1006048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006048_1.fastq.gz SRR1006048_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 16:24:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,352,700
Mapped reads	4,602,002 / 85.98%
Unmapped reads	750,698 / 14.02%
Mapped paired reads	4,602,002 / 85.98%
Mapped reads, first in pair	2,347,187 / 43.85%
Mapped reads, second in pair	2,254,815 / 42.12%
Mapped reads, both in pair	4,173,682 / 77.97%
Mapped reads, singletons	428,320 / 8%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	224,830 / 4.2%
Duplication rate	4.47%
Clipped reads	416,557 / 7.78%

2.2. ACGT Content

Number/percentage of A's	47,381,686 / 26.69%
Number/percentage of C's	39,775,836 / 22.41%
Number/percentage of T's	48,840,051 / 27.51%
Number/percentage of G's	41,442,484 / 23.35%
Number/percentage of N's	70,942 / 0.04%
GC Percentage	45.75%

2.3. Coverage

Mean	0.0573
Standard Deviation	0.3738

2.4. Mapping Quality

Mean Mapping Quality	46.12
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2.5. Insert size

Mean	68,526.44
Standard Deviation	2,579,360.87
P25/Median/P75	62 / 87 / 124

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	1,080,404
Insertions	5,644
Mapped reads with at least one insertion	0.12%
Deletions	14,549
Mapped reads with at least one deletion	0.32%
Homopolymer indels	44.28%

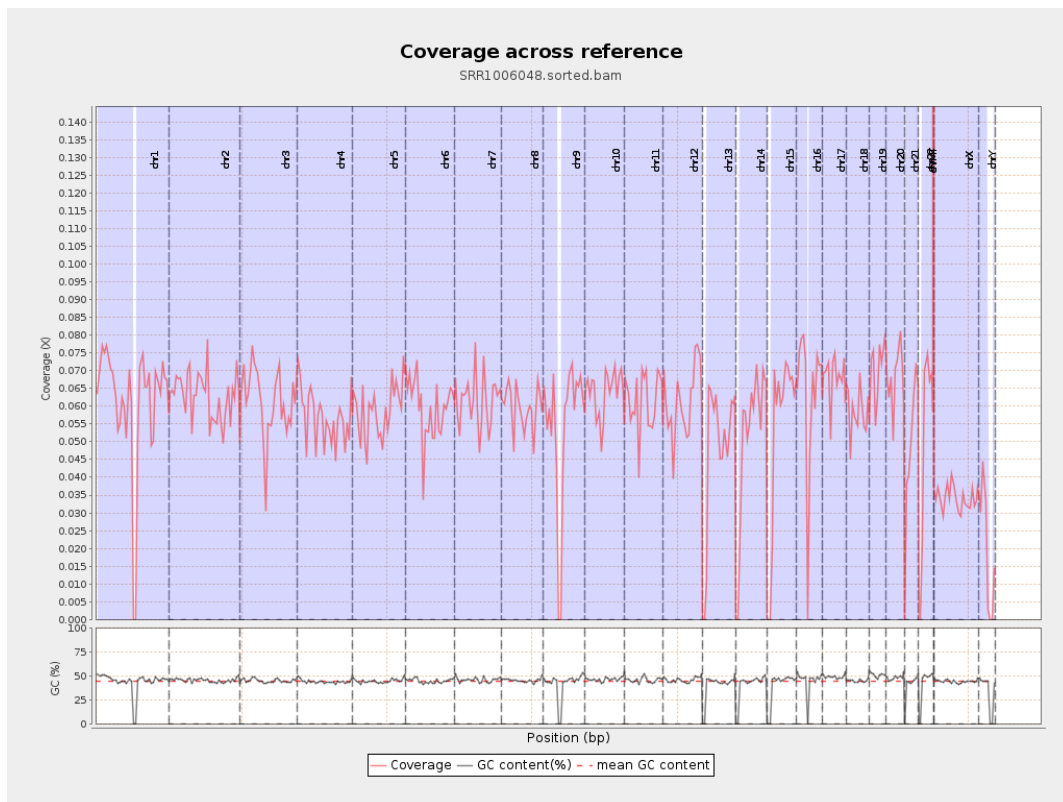
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

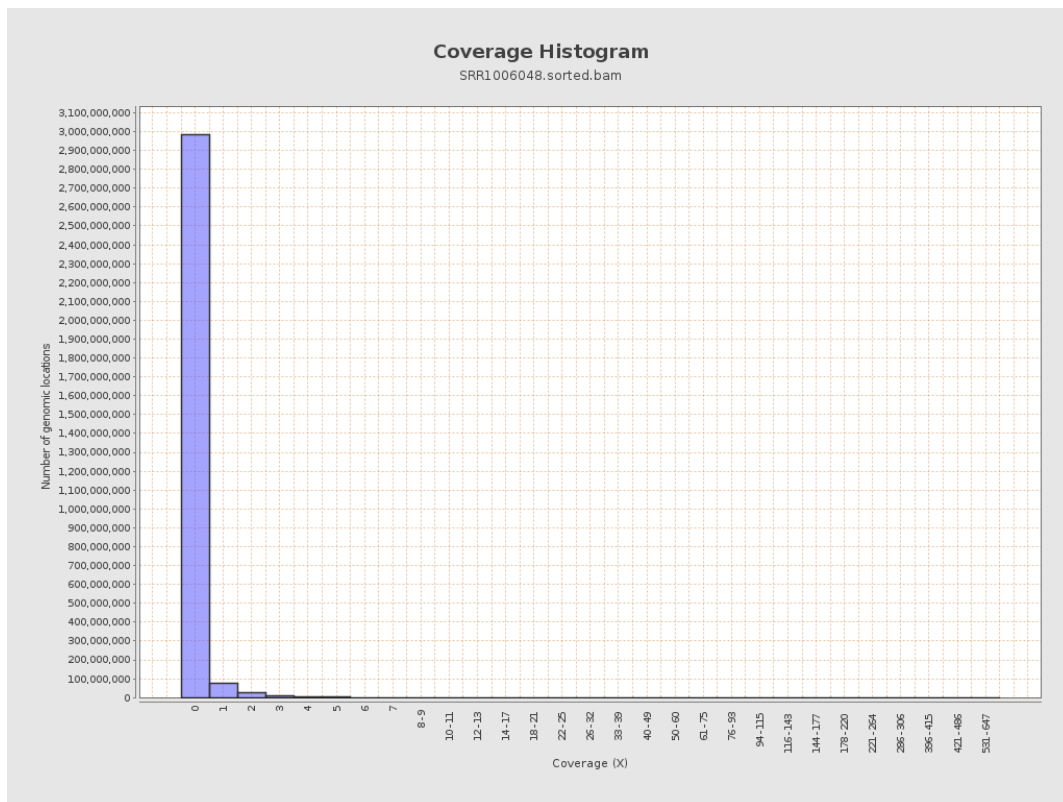
chr1	249250621	15256998	0.0612	0.4005
chr2	243199373	15302175	0.0629	0.4096
chr3	198022430	12128057	0.0612	0.3531
chr4	191154276	10808869	0.0565	0.3504
chr5	180915260	10612255	0.0587	0.3454
chr6	171115067	10222197	0.0597	0.3937
chr7	159138663	9753514	0.0613	0.4279
chr8	146364022	8737153	0.0597	0.3899
chr9	141213431	7591029	0.0538	0.3476
chr10	135534747	8679180	0.064	0.3756
chr11	135006516	8295475	0.0614	0.4942
chr12	133851895	8205091	0.0613	0.3553
chr13	115169878	5408723	0.047	0.3108
chr14	107349540	5441177	0.0507	0.3253
chr15	102531392	5485732	0.0535	0.3346
chr16	90354753	5766729	0.0638	0.3808
chr17	81195210	5530874	0.0681	0.3996
chr18	78077248	4563066	0.0584	0.3936
chr19	59128983	4155099	0.0703	0.437
chr20	63025520	4274523	0.0678	0.3797
chr21	48129895	2373110	0.0493	0.3422
chr22	51304566	2464383	0.048	0.3367
chrMT	16571	12387	0.7475	1.2251
chrX	155270560	5314733	0.0342	0.27

chrY	59373566	1146803	0.0193	0.2072
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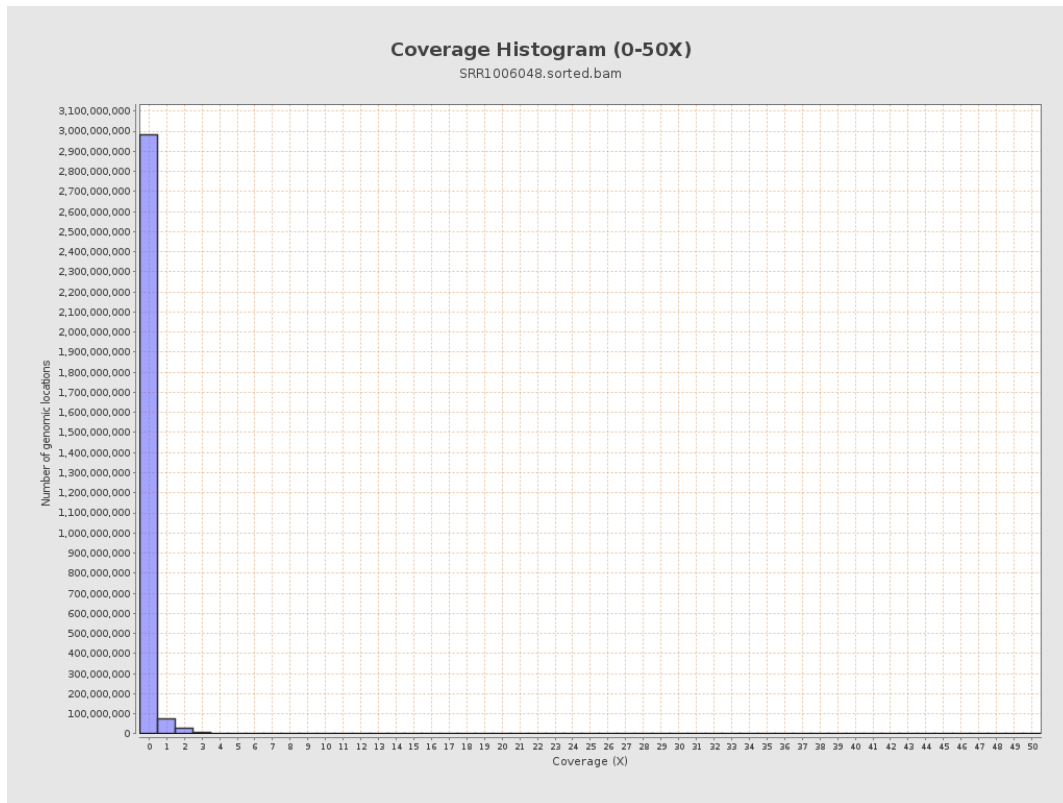
3. Results : Coverage across reference



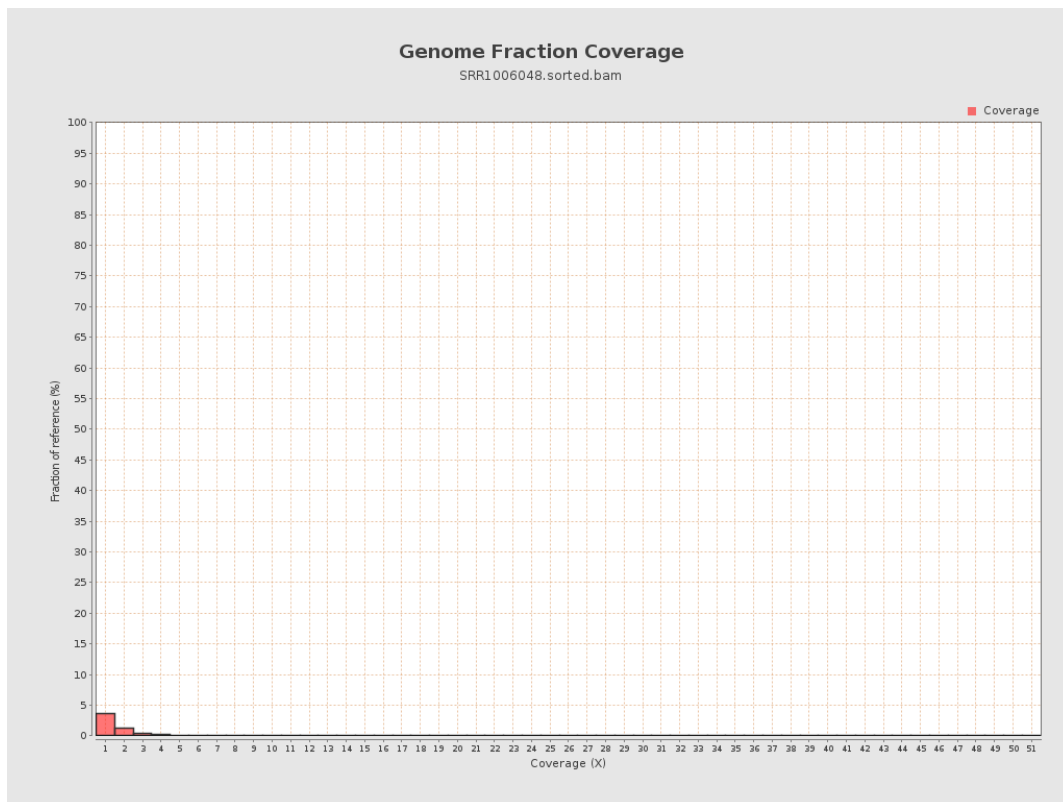
4. Results : Coverage Histogram



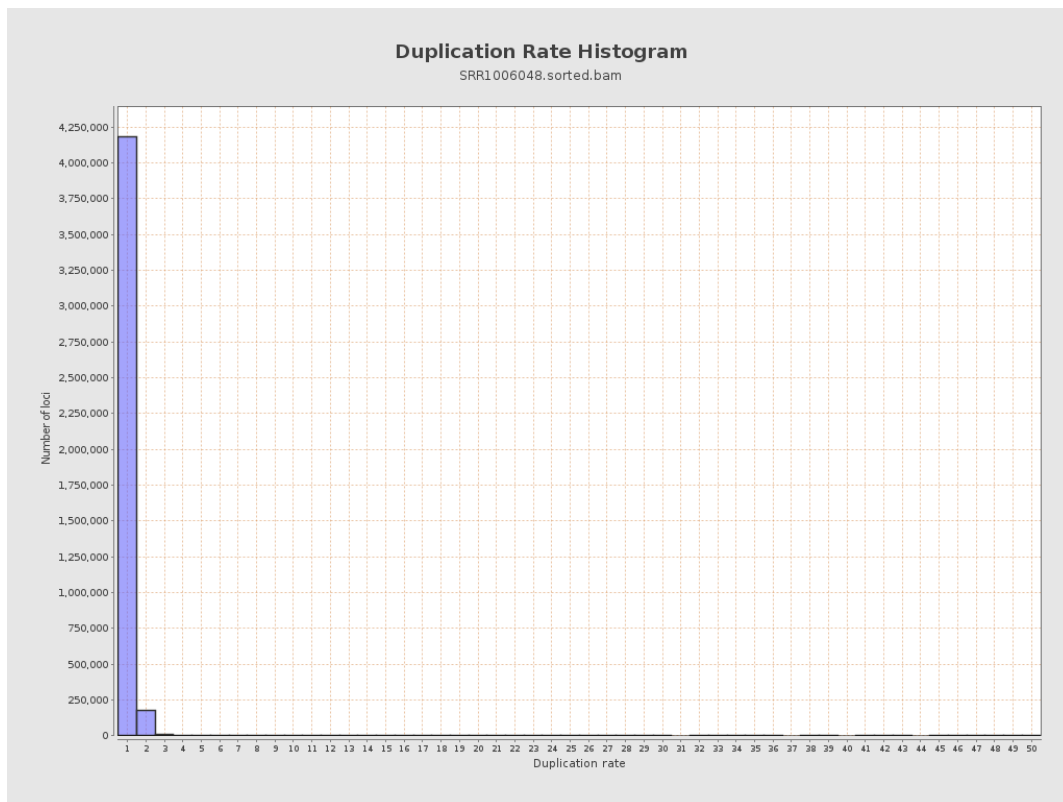
5. Results : Coverage Histogram (0-50X)



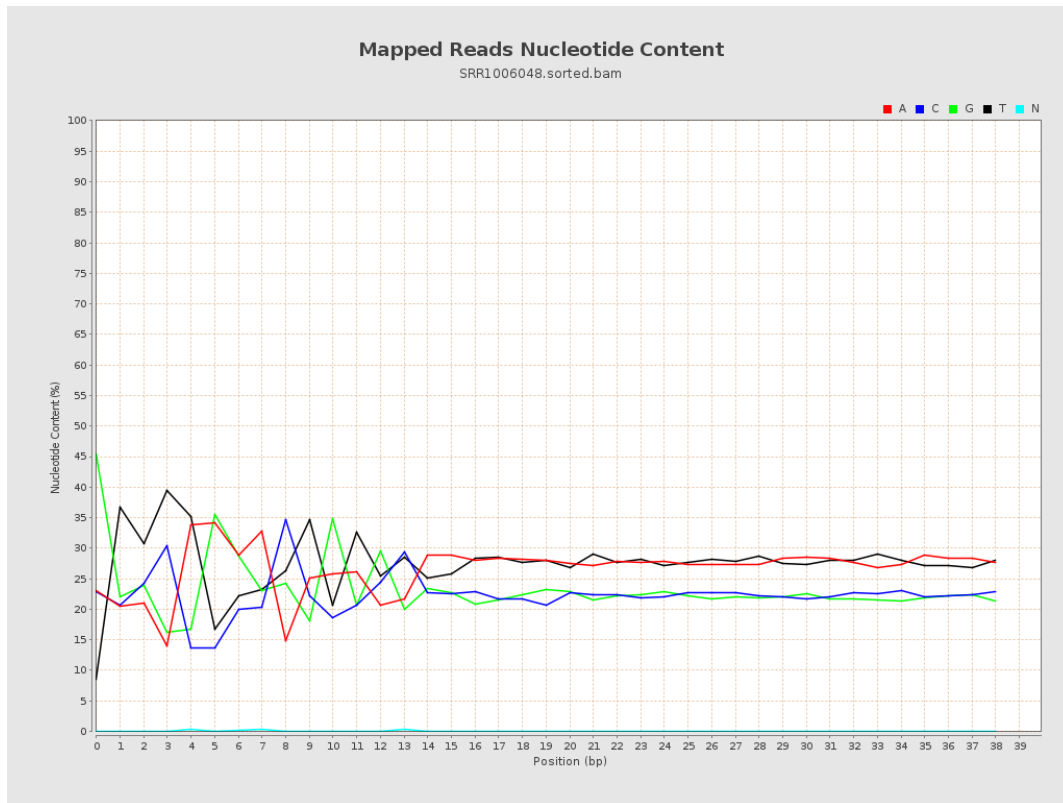
6. Results : Genome Fraction Coverage



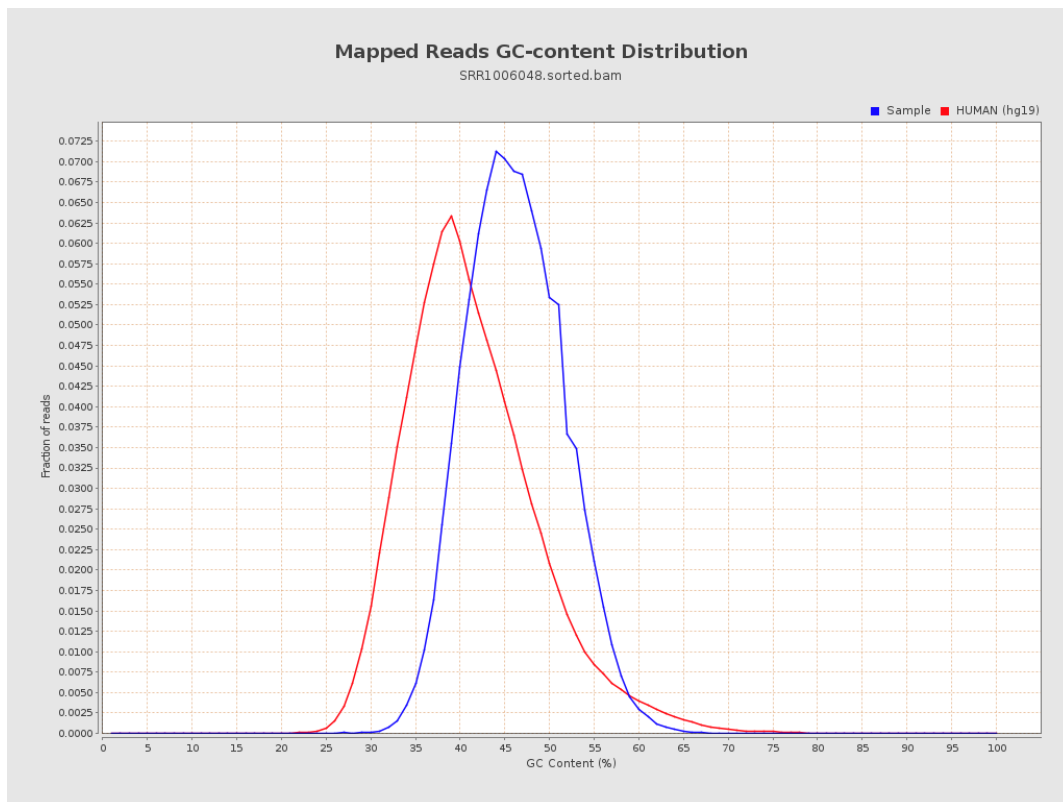
7. Results : Duplication Rate Histogram



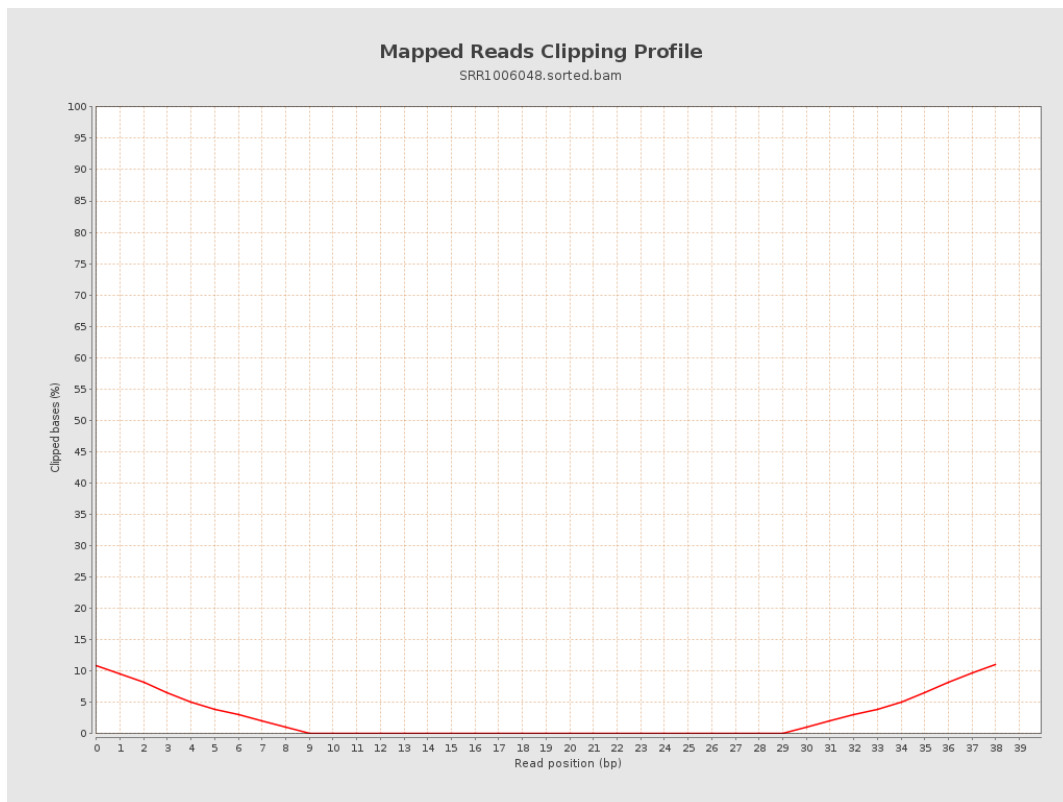
8. Results : Mapped Reads Nucleotide Content



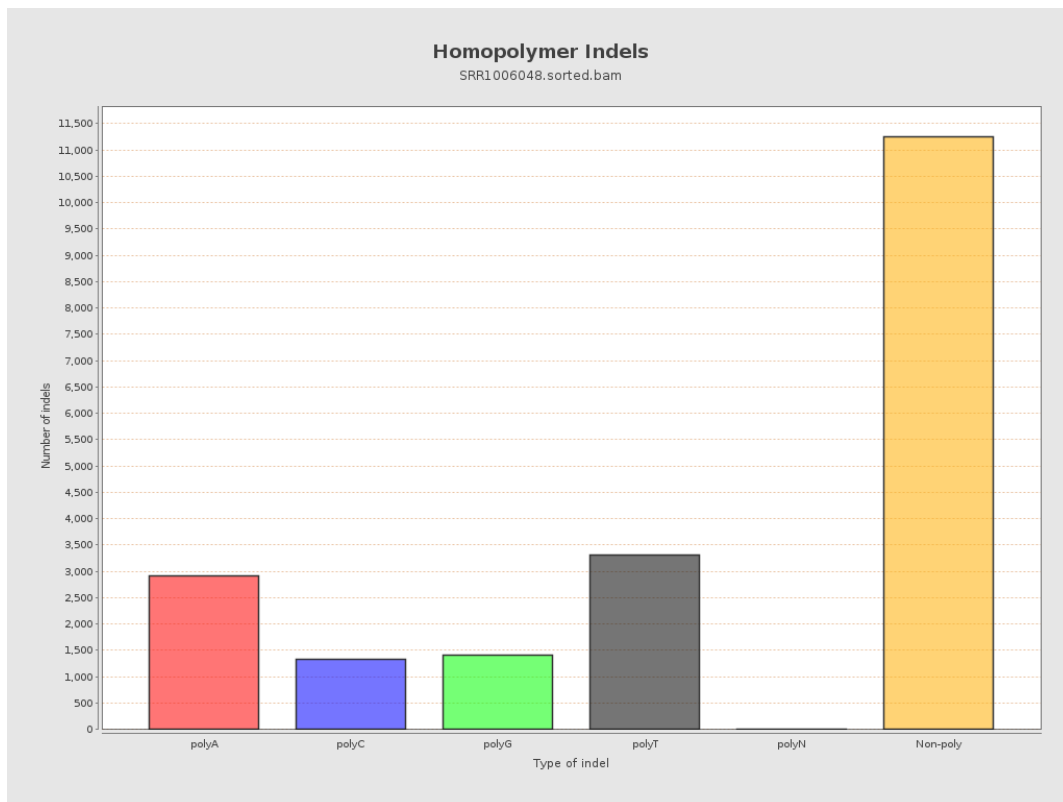
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



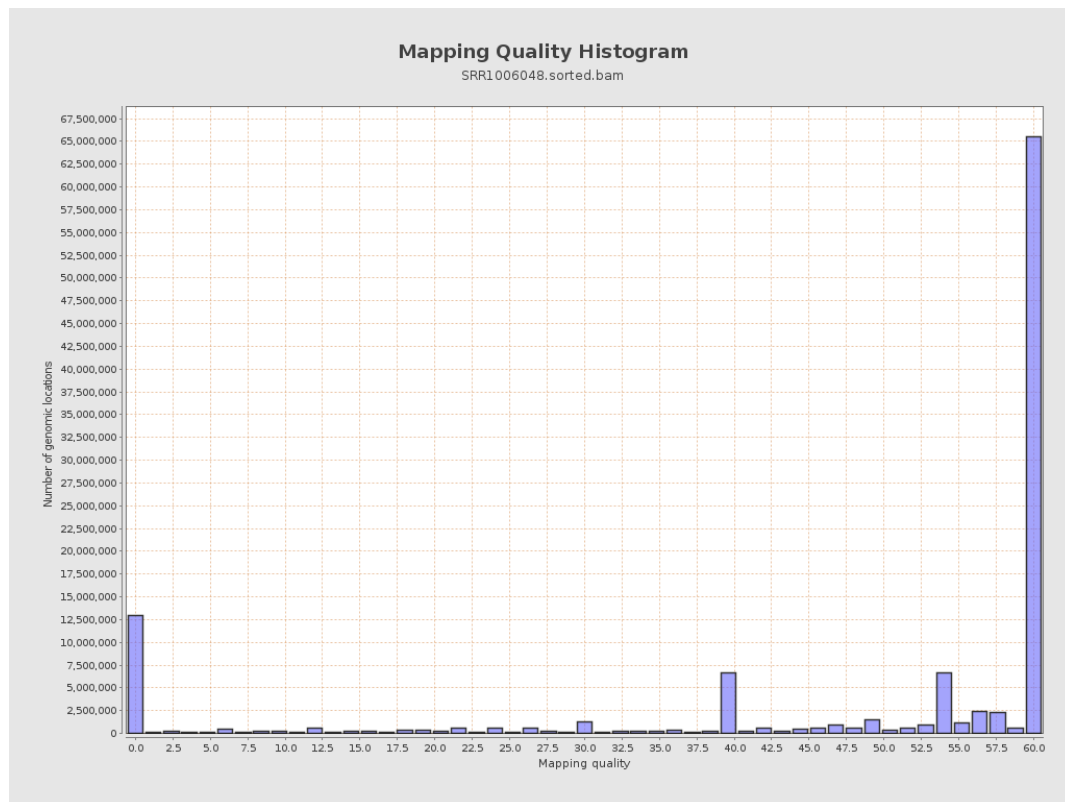
11. Results : Homopolymer Indels



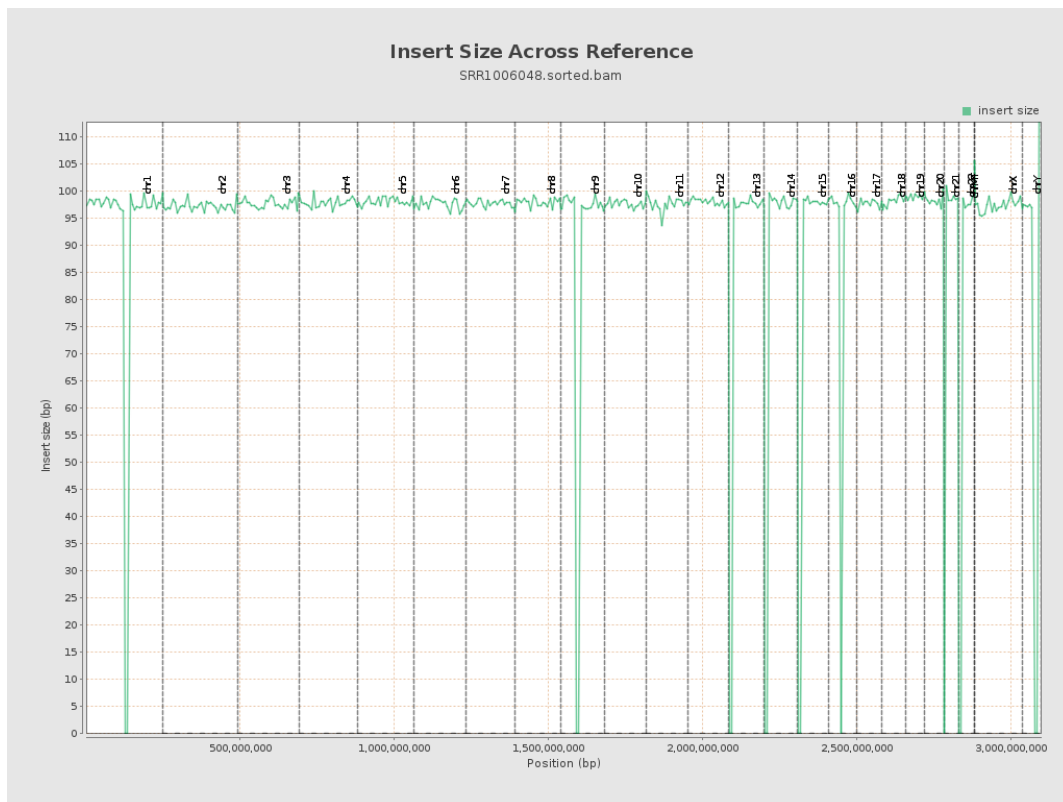
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

