

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 14:59:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046442.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_SRR2046442 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046442_1.fastq.gz SRR2046442_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 14:59:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046442.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,593,304
Mapped reads	8,550,915 / 99.51%
Unmapped reads	42,389 / 0.49%
Mapped paired reads	8,550,915 / 99.51%
Mapped reads, first in pair	4,279,792 / 49.8%
Mapped reads, second in pair	4,271,123 / 49.7%
Mapped reads, both in pair	8,521,270 / 99.16%
Mapped reads, singletons	29,645 / 0.34%
Secondary alignments	0
Supplementary alignments	45,827 / 0.53%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	6,598,699 / 76.79%
Duplication rate	39.79%
Clipped reads	1,767,330 / 20.57%

2.2. ACGT Content

Number/percentage of A's	241,171,385 / 29.23%
Number/percentage of C's	172,000,363 / 20.84%
Number/percentage of T's	241,002,867 / 29.21%
Number/percentage of G's	170,959,697 / 20.72%
Number/percentage of N's	71,521 / 0.01%

GC Percentage	41.56%
---------------	--------

2.3. Coverage

Mean	0.2666
Standard Deviation	27.529

2.4. Mapping Quality

Mean Mapping Quality	52.6
----------------------	------

2.5. Insert size

Mean	22,073.79
Standard Deviation	1,466,210.52
P25/Median/P75	107 / 134 / 170

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	2,806,625
Insertions	72,120
Mapped reads with at least one insertion	0.83%
Deletions	96,898
Mapped reads with at least one deletion	1.11%
Homopolymer indels	47.88%

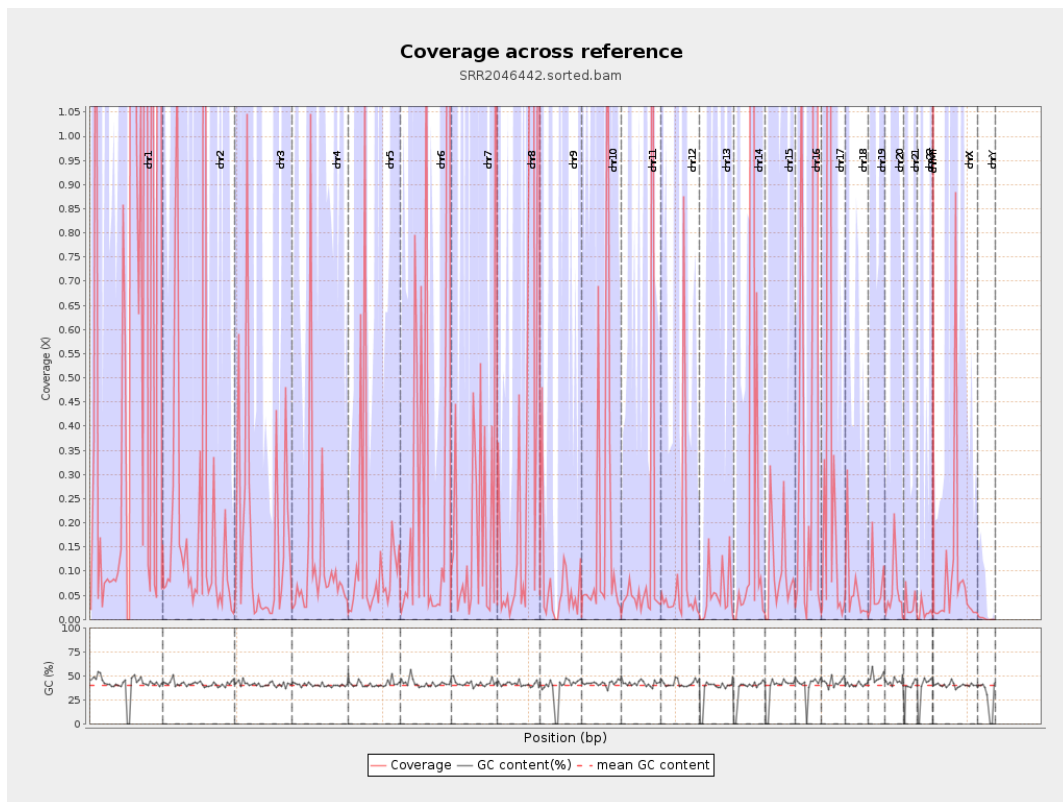
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

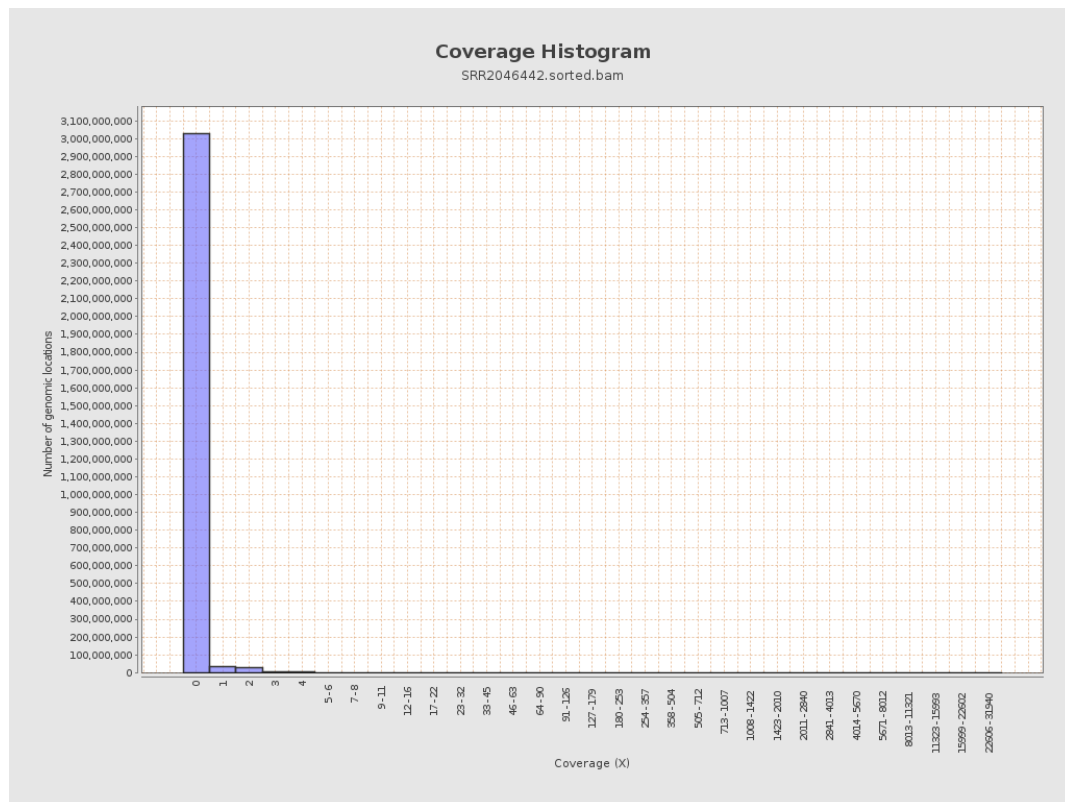
		bases	coverage	deviation
chr1	249250621	198296301	0.7956	54.3195
chr2	243199373	62922602	0.2587	18.4823
chr3	198022430	32597039	0.1646	11.3064
chr4	191154276	23128693	0.121	10.0502
chr5	180915260	25498807	0.1409	9.7995
chr6	171115067	63231724	0.3695	31.85
chr7	159138663	39962124	0.2511	18.2695
chr8	146364022	74010783	0.5057	36.5436
chr9	141213431	10095092	0.0715	6.4884
chr10	135534747	25146895	0.1855	22.3746
chr11	135006516	20060878	0.1486	13.4954
chr12	133851895	11267933	0.0842	6.9433
chr13	115169878	6335069	0.055	3.1558
chr14	107349540	49013502	0.4566	34.2763
chr15	102531392	10934511	0.1066	5.6325
chr16	90354753	108916951	1.2054	85.7512
chr17	81195210	35899359	0.4421	40.3836
chr18	78077248	4932930	0.0632	3.0287
chr19	59128983	3751612	0.0634	3.8763
chr20	63025520	3708771	0.0588	3.3899
chr21	48129895	1488606	0.0309	1.7643
chr22	51304566	765643	0.0149	1.1888
chrMT	16571	38151	2.3023	2.3162
chrX	155270560	13349980	0.086	7.3728

chrY	59373566	102148	0.0017	0.0947
------	----------	--------	--------	--------

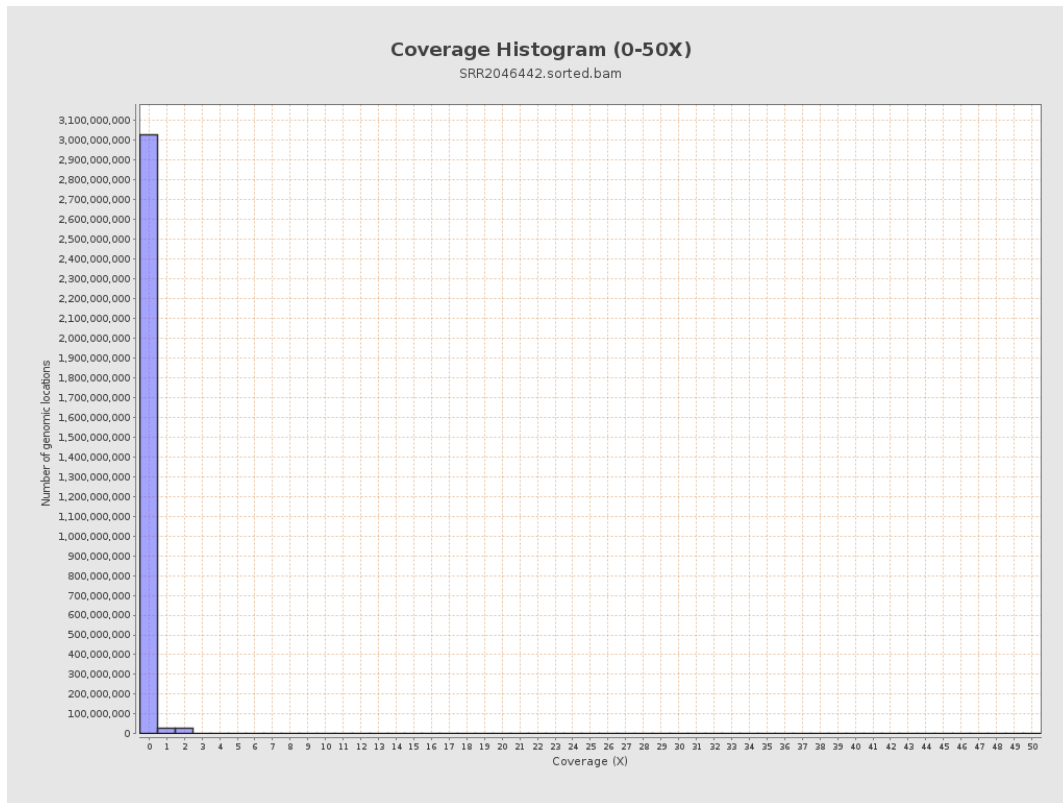
3. Results : Coverage across reference



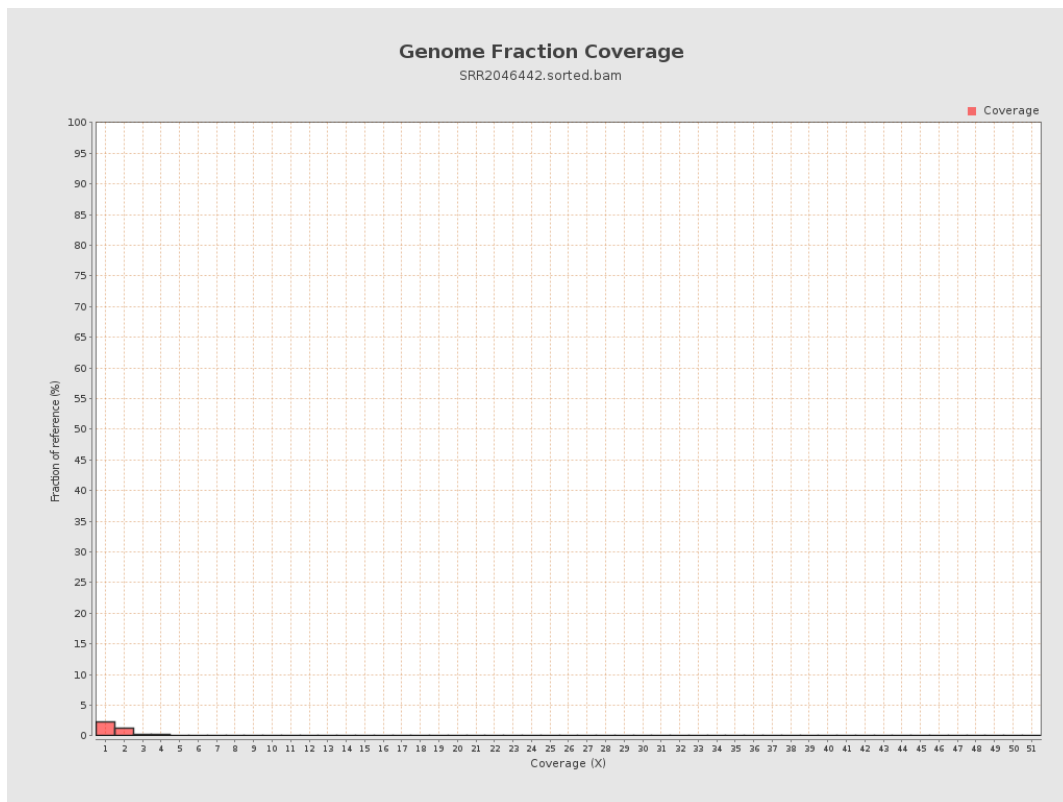
4. Results : Coverage Histogram



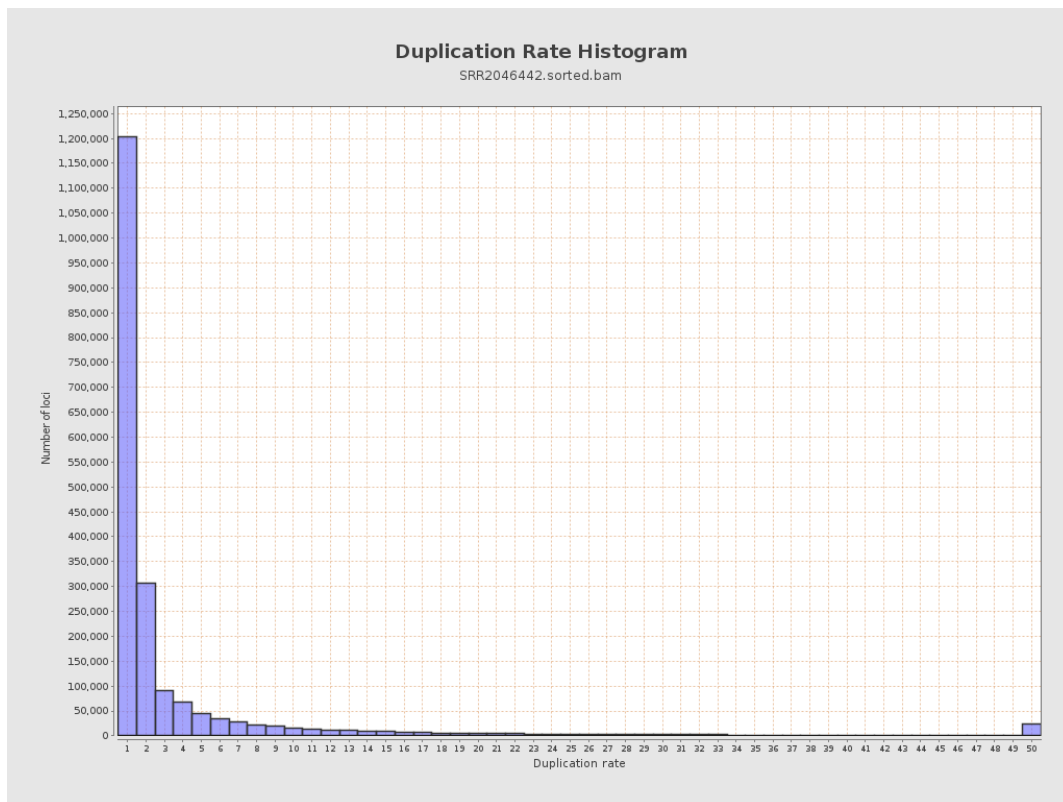
5. Results : Coverage Histogram (0-50X)



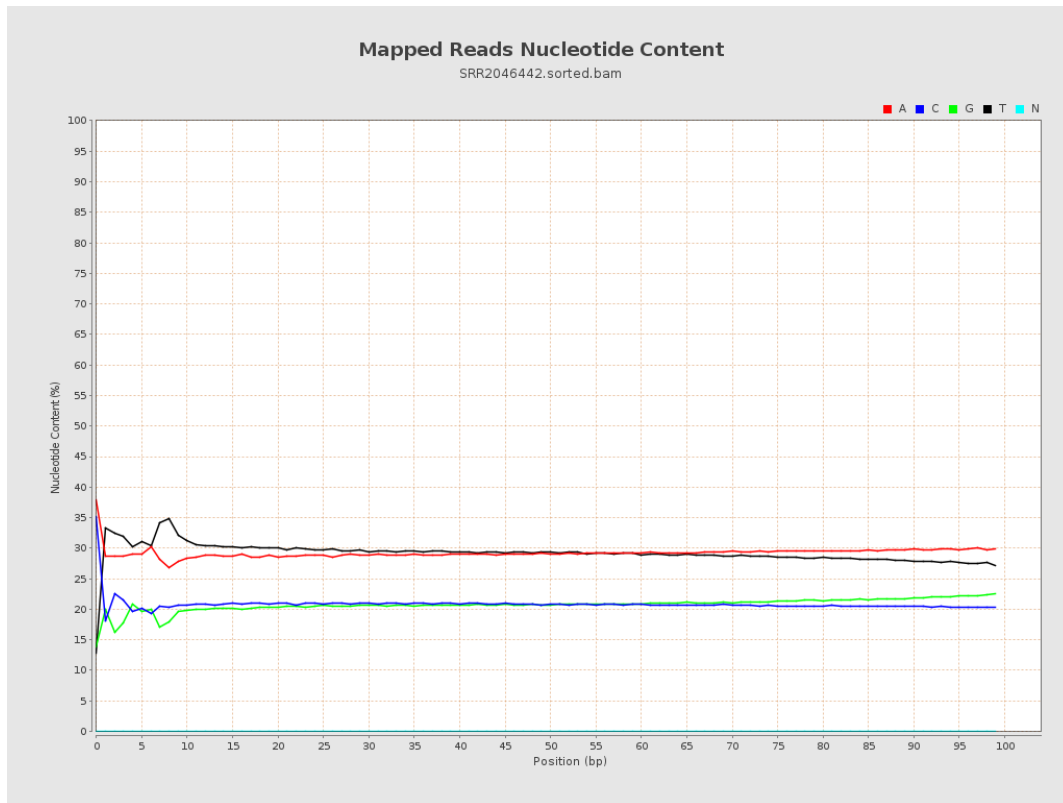
6. Results : Genome Fraction Coverage



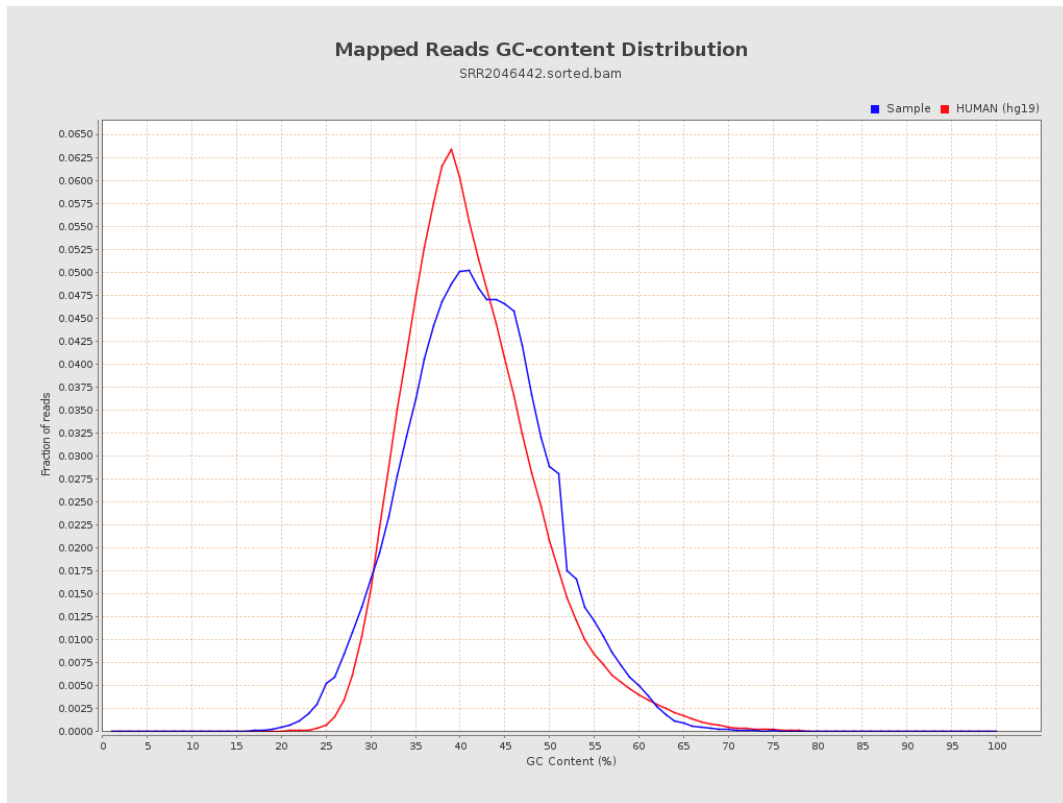
7. Results : Duplication Rate Histogram



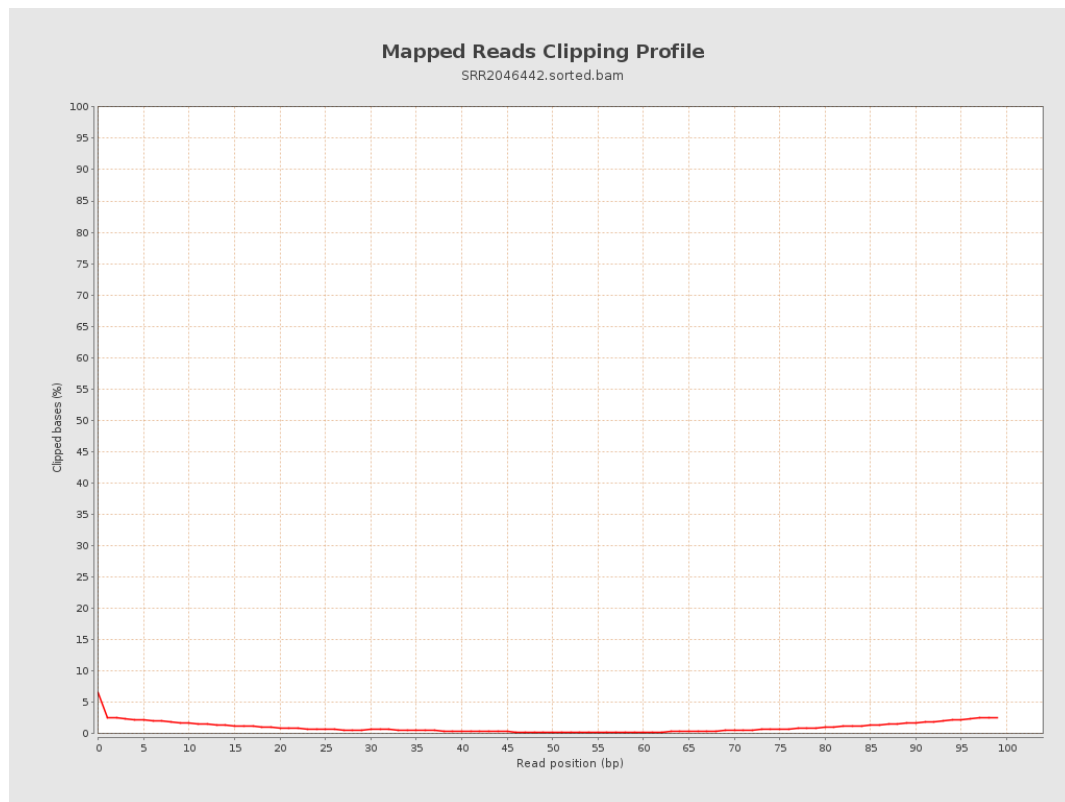
8. Results : Mapped Reads Nucleotide Content



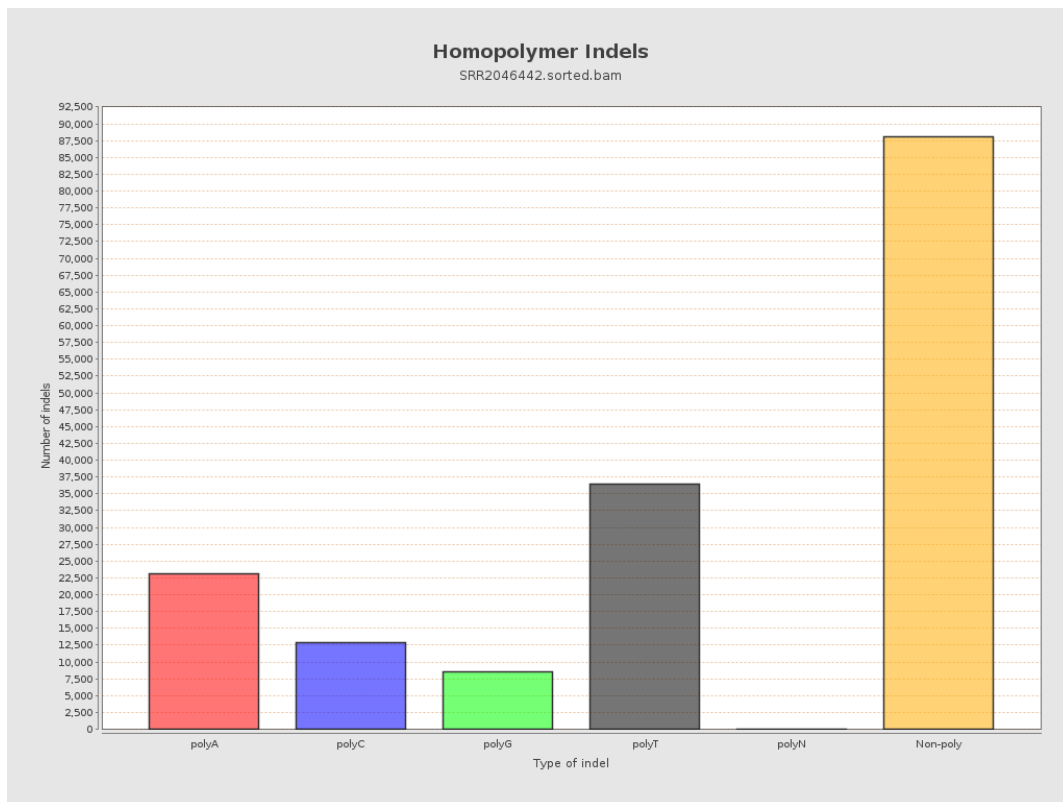
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



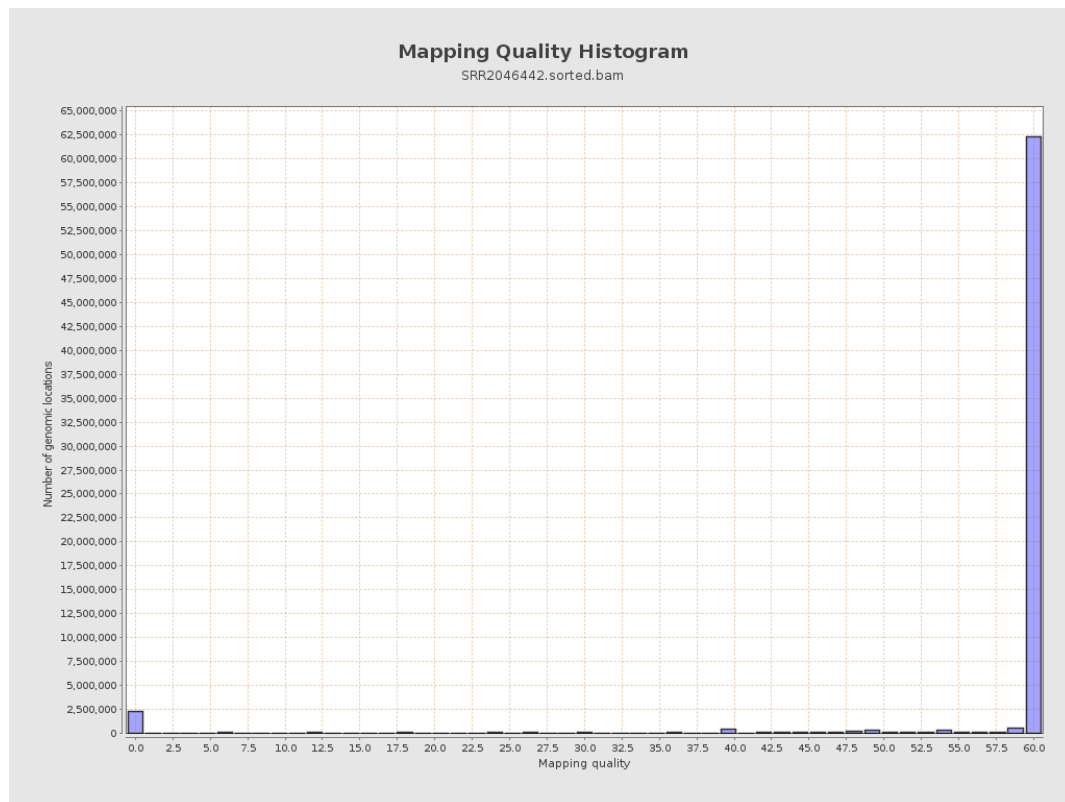
11. Results : Homopolymer Indels



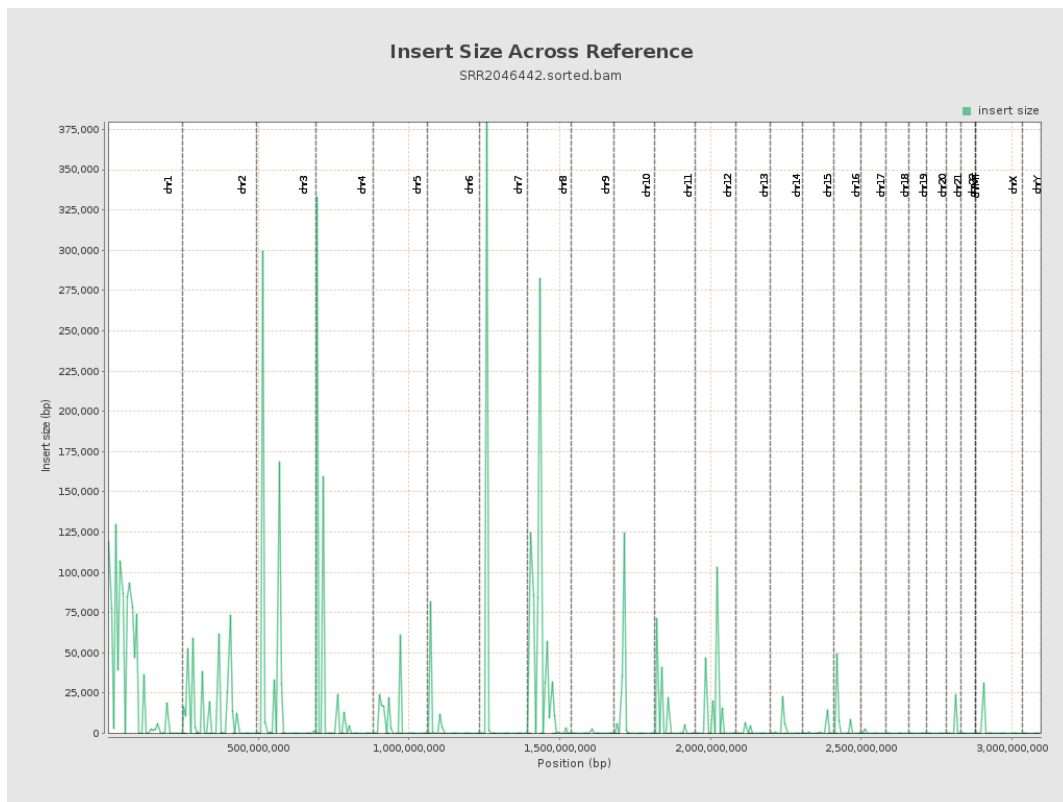
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

