

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 14:09:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046428.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_SRR2046428 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046428_1.fastq.gz SRR2046428_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 14:09:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046428.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,389,388
Mapped reads	8,350,386 / 99.54%
Unmapped reads	39,002 / 0.46%
Mapped paired reads	8,350,386 / 99.54%
Mapped reads, first in pair	4,178,802 / 49.81%
Mapped reads, second in pair	4,171,584 / 49.72%
Mapped reads, both in pair	8,323,334 / 99.21%
Mapped reads, singletons	27,052 / 0.32%
Secondary alignments	0
Supplementary alignments	49,977 / 0.6%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	6,405,848 / 76.36%
Duplication rate	39.73%
Clipped reads	1,517,177 / 18.08%

2.2. ACGT Content

Number/percentage of A's	241,120,298 / 29.74%
Number/percentage of C's	164,068,833 / 20.24%
Number/percentage of T's	242,255,832 / 29.88%
Number/percentage of G's	163,126,586 / 20.12%
Number/percentage of N's	73,001 / 0.01%

GC Percentage	40.36%
---------------	--------

2.3. Coverage

Mean	0.2619
Standard Deviation	25.5671

2.4. Mapping Quality

Mean Mapping Quality	51.6
----------------------	------

2.5. Insert size

Mean	17,712.16
Standard Deviation	1,320,658.04
P25/Median/P75	111 / 140 / 173

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	3,180,788
Insertions	70,897
Mapped reads with at least one insertion	0.83%
Deletions	94,576
Mapped reads with at least one deletion	1.1%
Homopolymer indels	49.31%

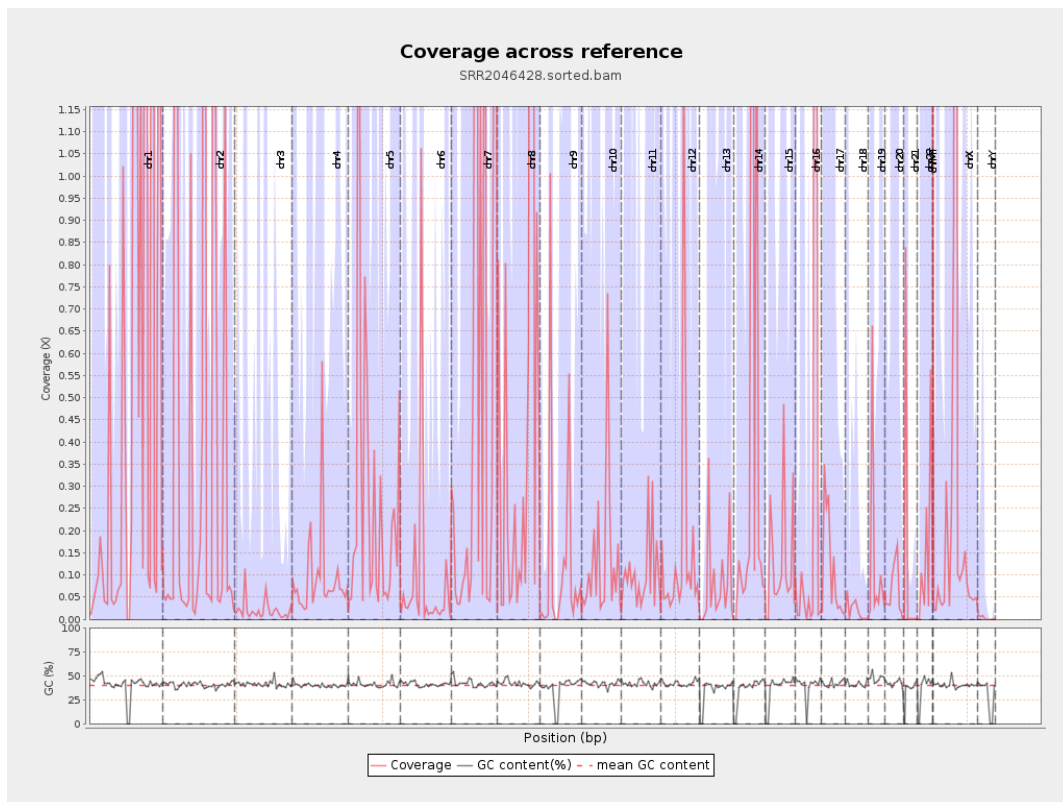
2.7. Chromosome stats

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

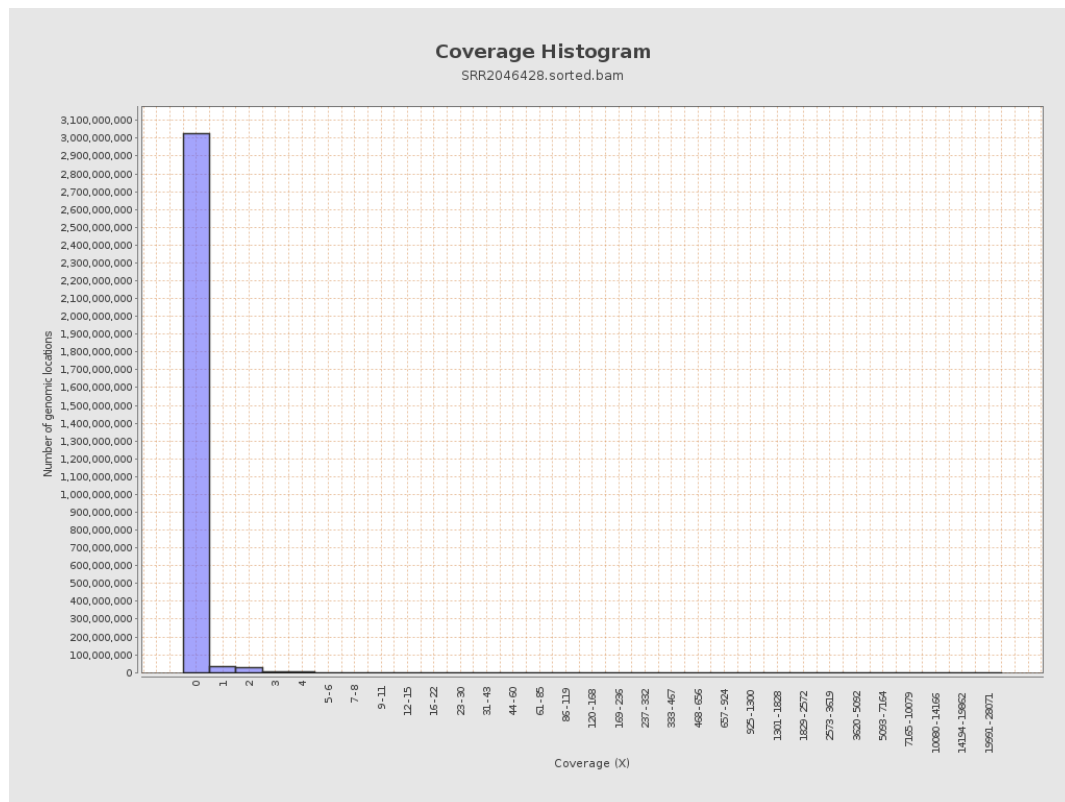
		bases	coverage	deviation
chr1	249250621	163861866	0.6574	43.6804
chr2	243199373	126170219	0.5188	37.207
chr3	198022430	4004890	0.0202	1.5435
chr4	191154276	18164899	0.095	5.1582
chr5	180915260	51598955	0.2852	24.0006
chr6	171115067	14494710	0.0847	9.5371
chr7	159138663	92198368	0.5794	39.1541
chr8	146364022	86715673	0.5925	41.8016
chr9	141213431	17155323	0.1215	19.147
chr10	135534747	17975234	0.1326	13.5608
chr11	135006516	14201478	0.1052	3.7459
chr12	133851895	20177982	0.1507	9.7218
chr13	115169878	9210998	0.08	5.6241
chr14	107349540	39983607	0.3725	25.6803
chr15	102531392	14013341	0.1367	9.0364
chr16	90354753	32250221	0.3569	34.6237
chr17	81195210	9298044	0.1145	7.7883
chr18	78077248	1625482	0.0208	0.8812
chr19	59128983	7440165	0.1258	6.0081
chr20	63025520	4065459	0.0645	7.1759
chr21	48129895	6544851	0.136	17.8798
chr22	51304566	7677973	0.1497	9.0672
chrMT	16571	27178	1.6401	1.7162
chrX	155270560	51854806	0.334	41.9931

chrY	59373566	182084	0.0031	0.2894
------	----------	--------	--------	--------

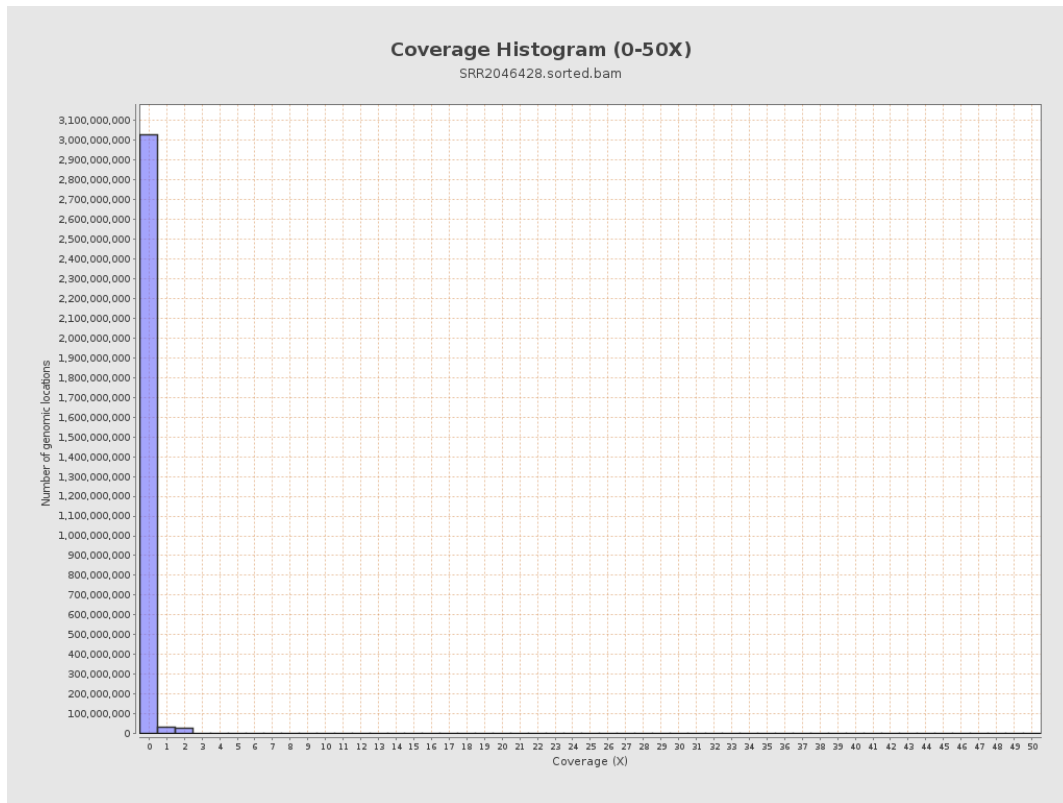
3. Results : Coverage across reference



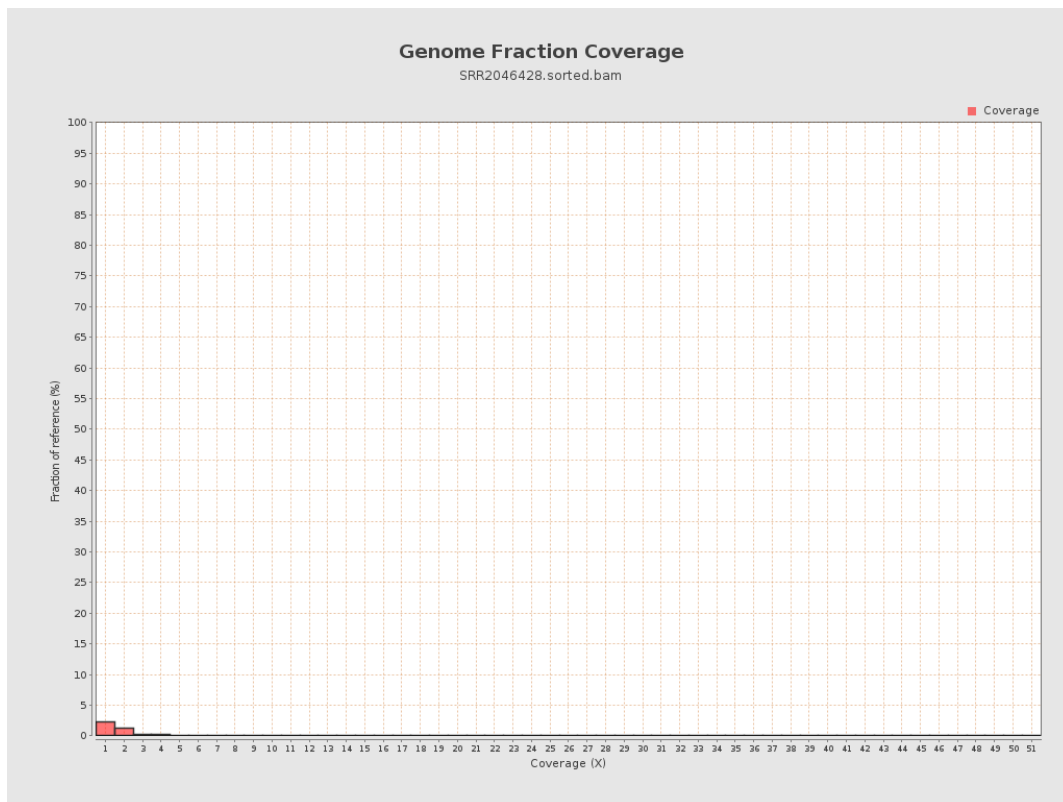
4. Results : Coverage Histogram



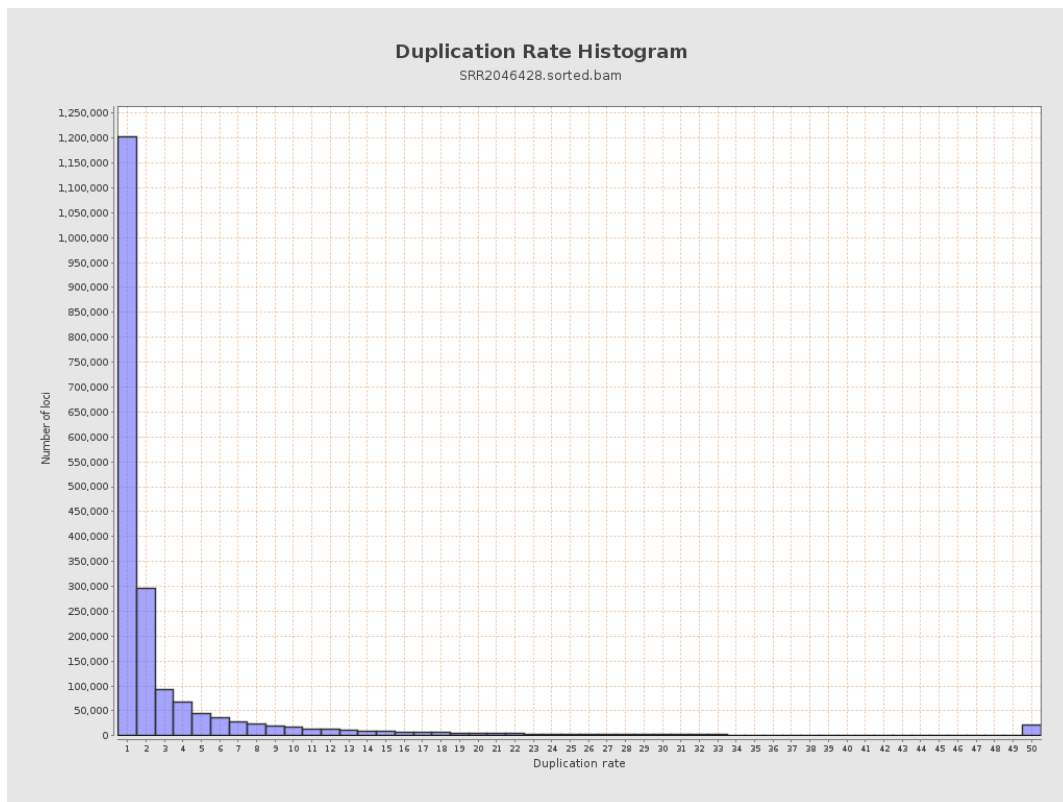
5. Results : Coverage Histogram (0-50X)



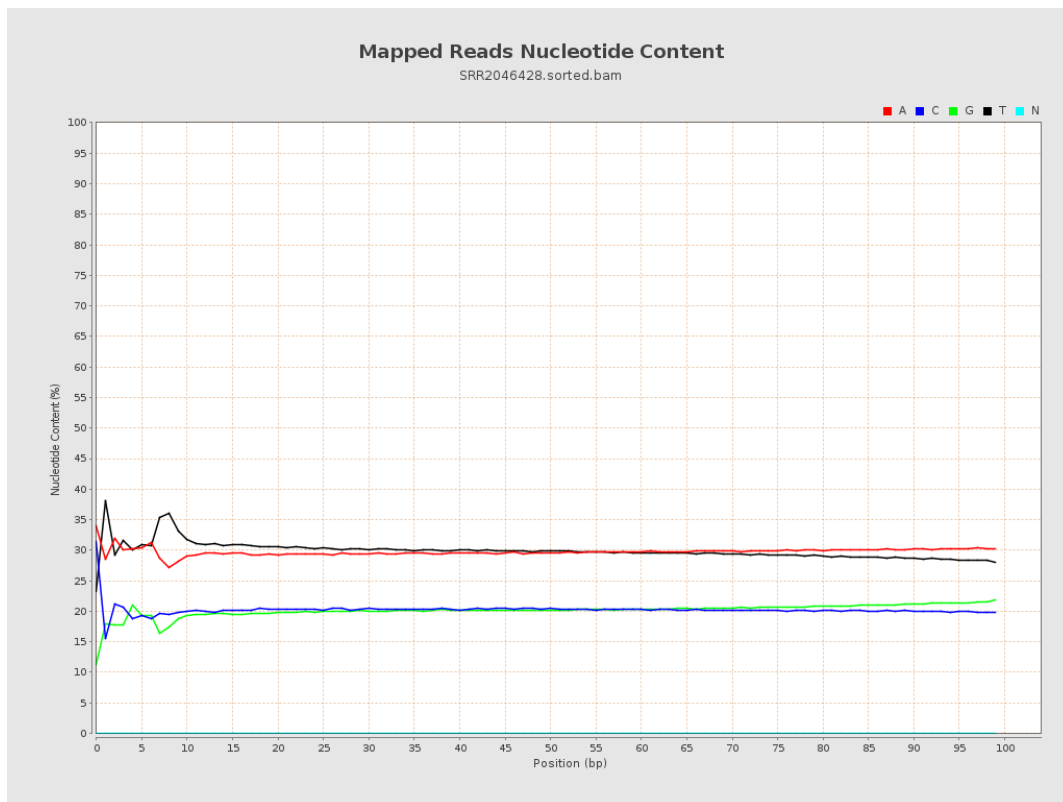
6. Results : Genome Fraction Coverage



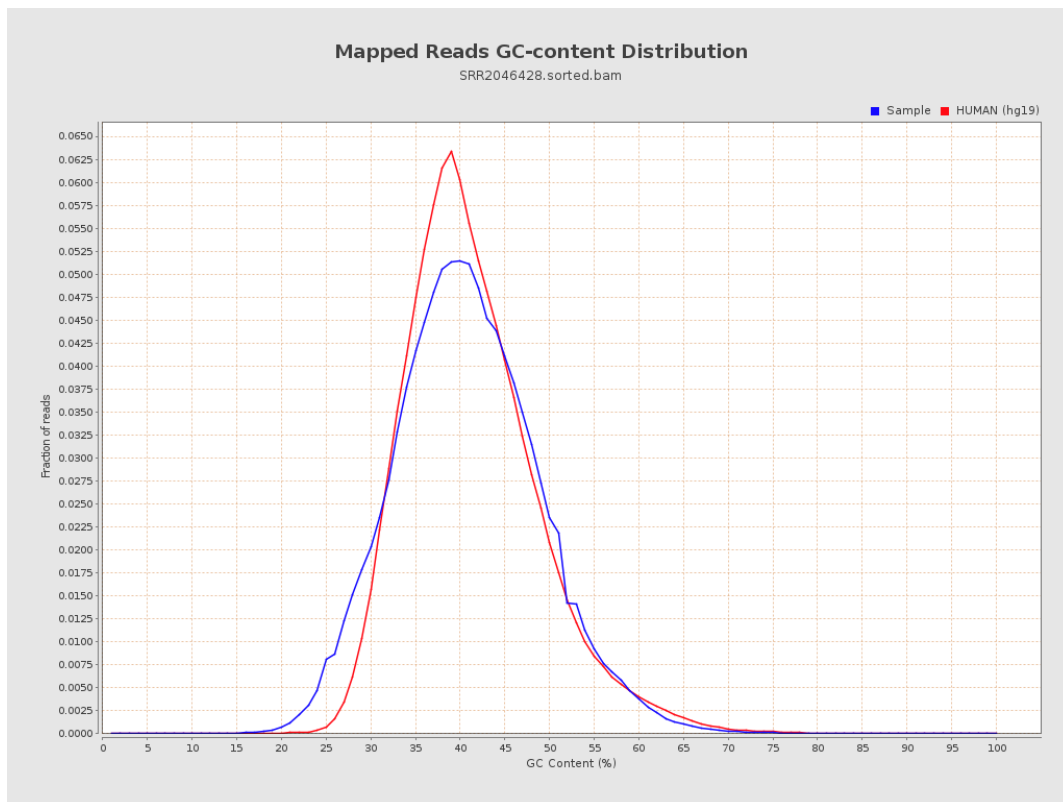
7. Results : Duplication Rate Histogram



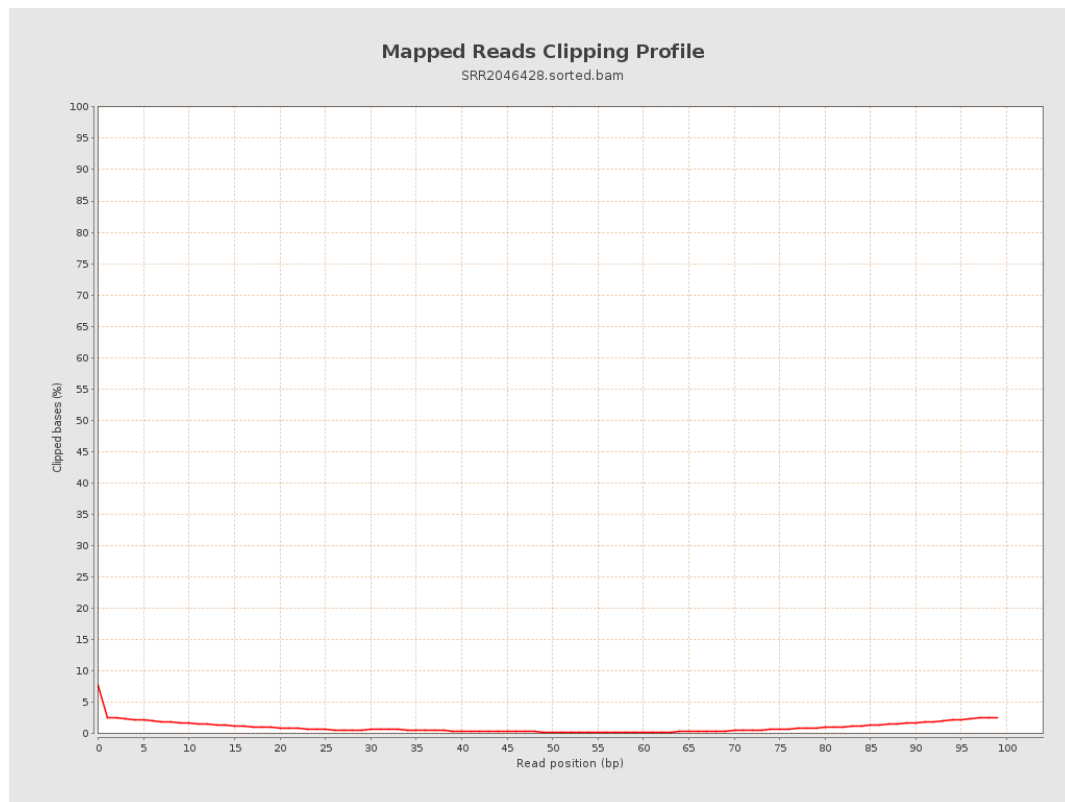
8. Results : Mapped Reads Nucleotide Content



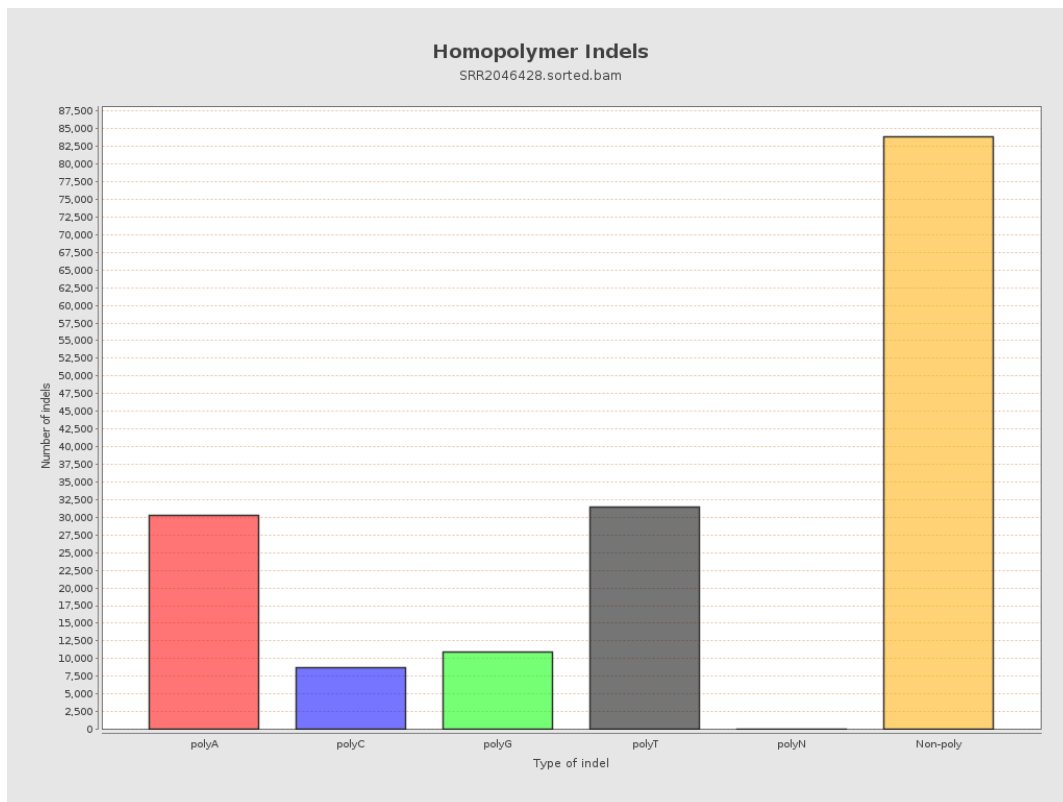
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



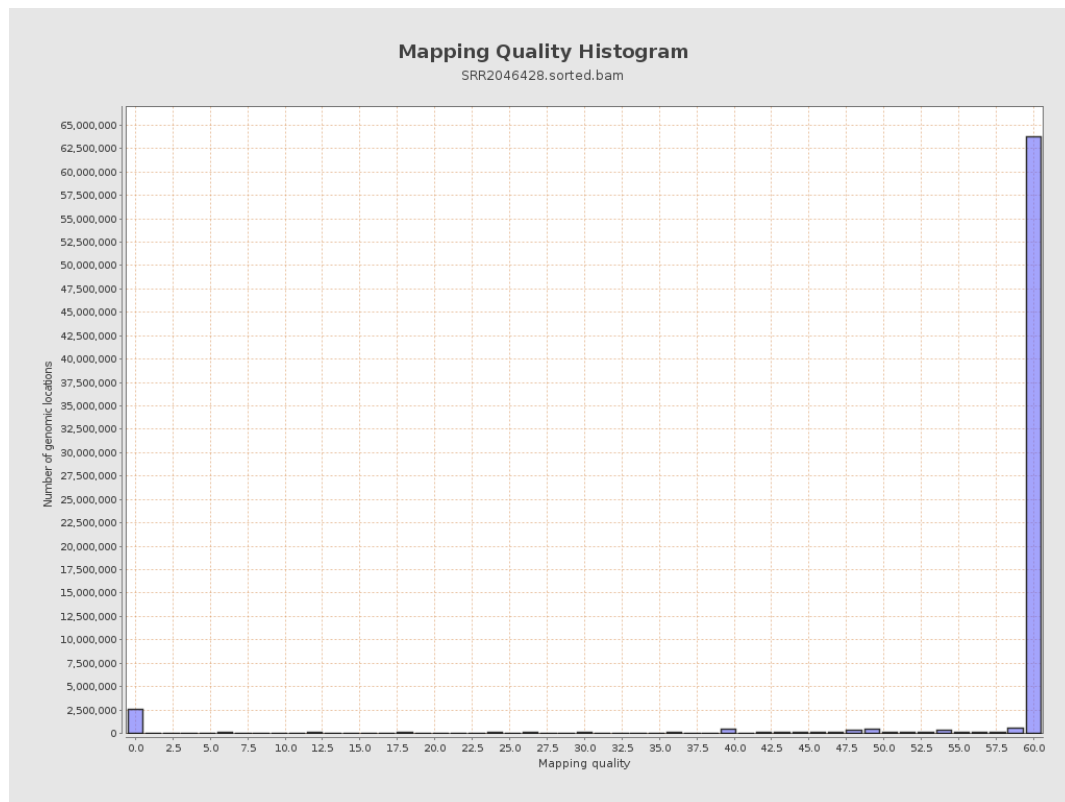
11. Results : Homopolymer Indels



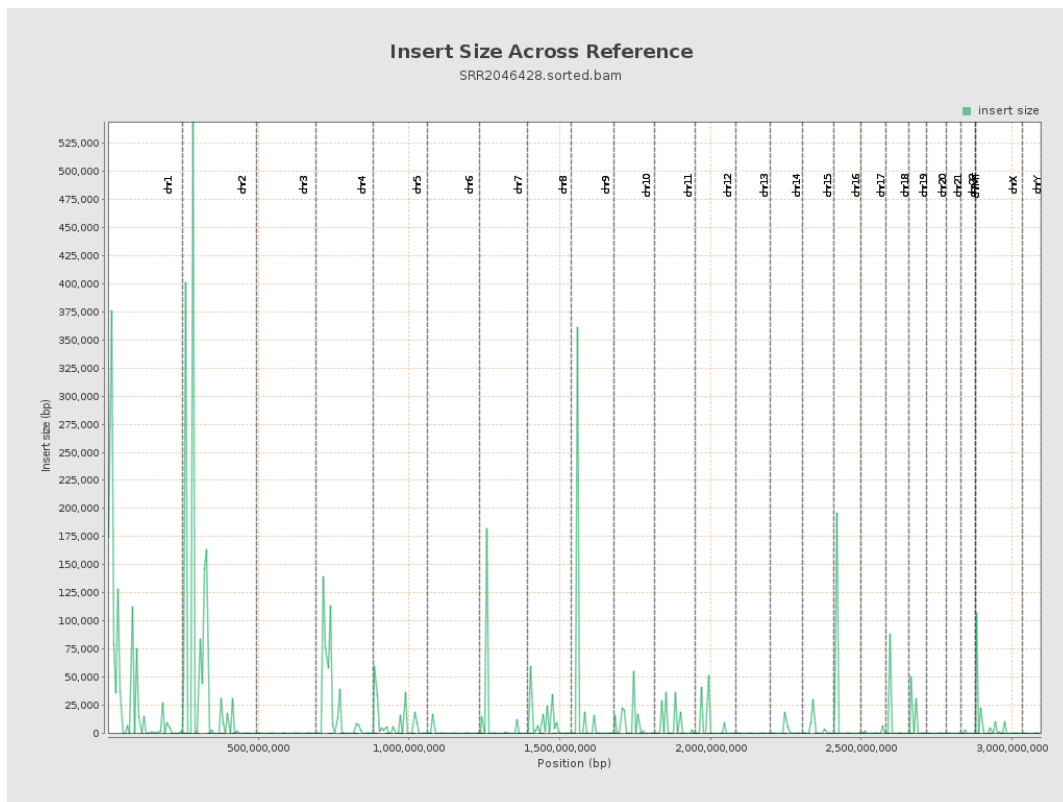
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

