

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 14:43:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046438.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_SRR2046438 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046438_1.fastq.gz SRR2046438_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 14:43:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046438.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,821,352
Mapped reads	4,783,124 / 99.21%
Unmapped reads	38,228 / 0.79%
Mapped paired reads	4,783,124 / 99.21%
Mapped reads, first in pair	2,392,891 / 49.63%
Mapped reads, second in pair	2,390,233 / 49.58%
Mapped reads, both in pair	4,761,930 / 98.77%
Mapped reads, singletons	21,194 / 0.44%
Secondary alignments	0
Supplementary alignments	38,589 / 0.8%
Read min/max/mean length	30 / 100 / 100.32
Duplicated reads (estimated)	3,533,538 / 73.29%
Duplication rate	32.65%
Clipped reads	1,761,800 / 36.54%

2.2. ACGT Content

Number/percentage of A's	127,080,222 / 28.63%
Number/percentage of C's	95,365,384 / 21.48%
Number/percentage of T's	125,036,846 / 28.17%
Number/percentage of G's	96,378,151 / 21.71%
Number/percentage of N's	38,285 / 0.01%

GC Percentage	43.2%
---------------	-------

2.3. Coverage

Mean	0.1435
Standard Deviation	24.3573

2.4. Mapping Quality

Mean Mapping Quality	51.34
----------------------	-------

2.5. Insert size

Mean	20,533.35
Standard Deviation	1,416,052.64
P25/Median/P75	91 / 115 / 145

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	1,693,314
Insertions	48,220
Mapped reads with at least one insertion	0.99%
Deletions	58,315
Mapped reads with at least one deletion	1.17%
Homopolymer indels	48.01%

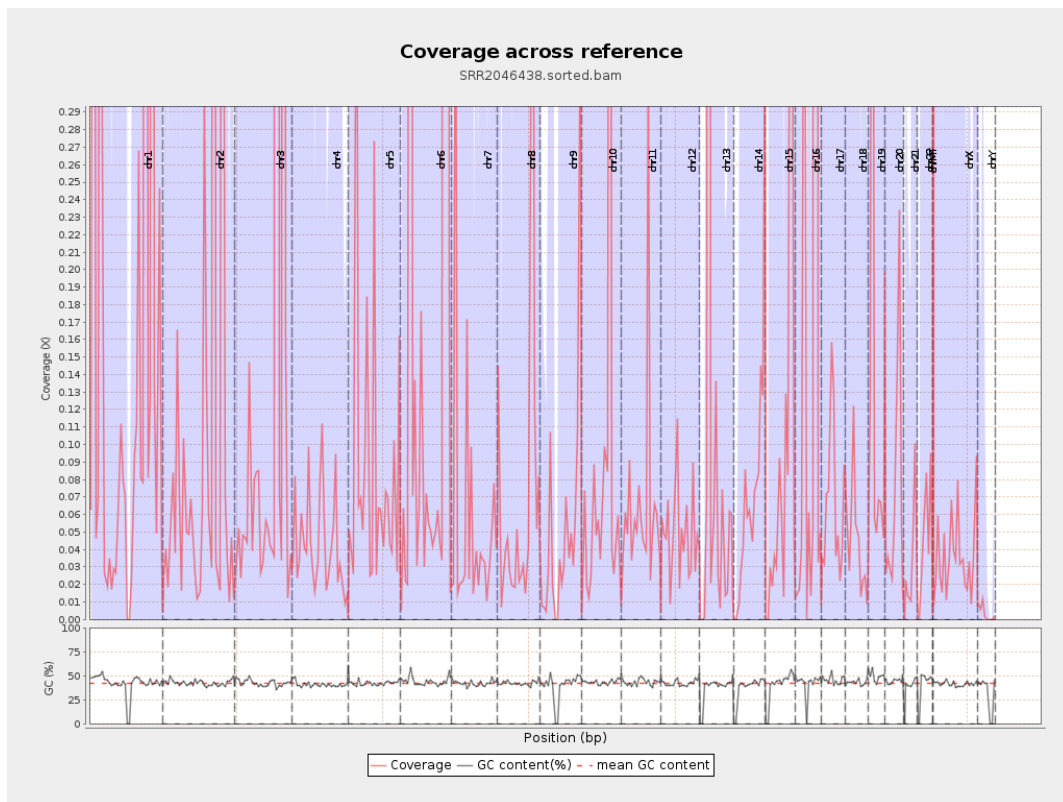
2.7. Chromosome stats

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

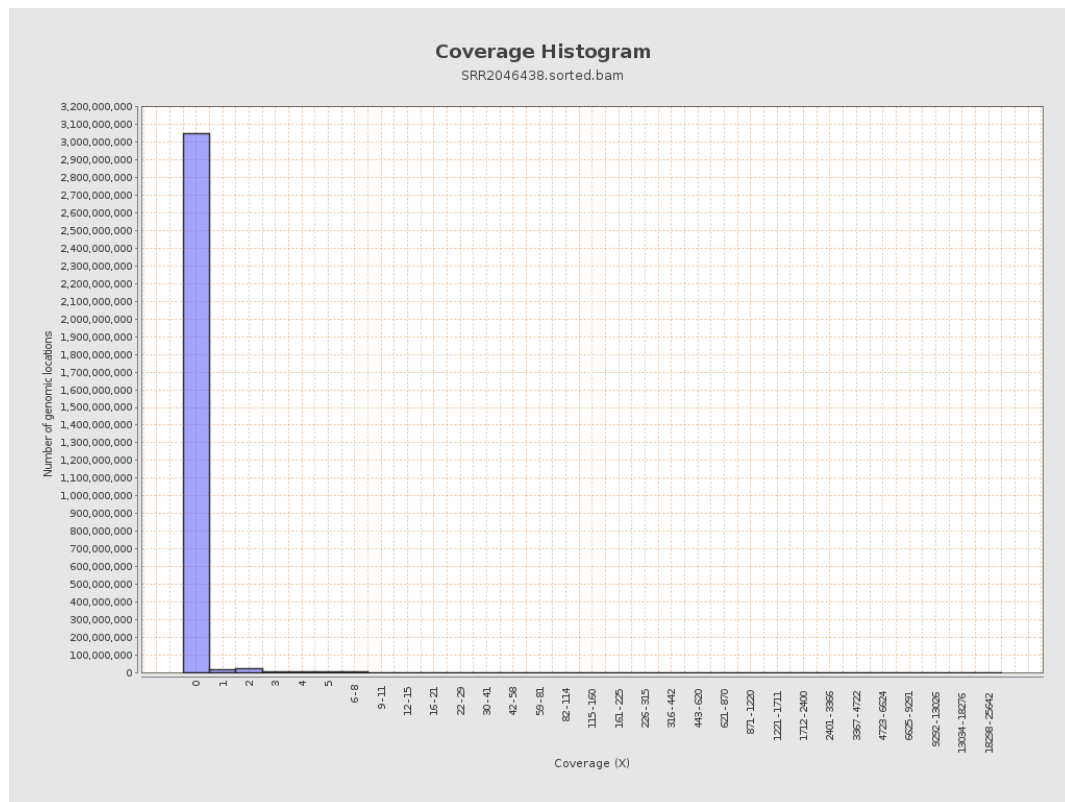
		bases	coverage	deviation
chr1	249250621	57363037	0.2301	27.009
chr2	243199373	35179904	0.1447	21.416
chr3	198022430	82848110	0.4184	53.6157
chr4	191154276	8544443	0.0447	1.8903
chr5	180915260	15972801	0.0883	11.1931
chr6	171115067	68260218	0.3989	45.1693
chr7	159138663	9460325	0.0594	7.8221
chr8	146364022	12155830	0.0831	8.5075
chr9	141213431	7572808	0.0536	6.3699
chr10	135534747	13531614	0.0998	15.1984
chr11	135006516	9023091	0.0668	3.6149
chr12	133851895	6788520	0.0507	1.5928
chr13	115169878	20576490	0.1787	23.3975
chr14	107349540	6832665	0.0636	2.6539
chr15	102531392	10577831	0.1032	12.2595
chr16	90354753	45683953	0.5056	70.7043
chr17	81195210	5355658	0.066	2.5029
chr18	78077248	3658574	0.0469	2.0719
chr19	59128983	9504581	0.1607	11.5593
chr20	63025520	4684144	0.0743	4.5991
chr21	48129895	1593813	0.0331	3.3017
chr22	51304566	2329671	0.0454	2.1082
chrMT	16571	790750	47.7189	17.3398
chrX	155270560	5580532	0.0359	1.1985

chrY	59373566	211840	0.0036	0.1694
------	----------	--------	--------	--------

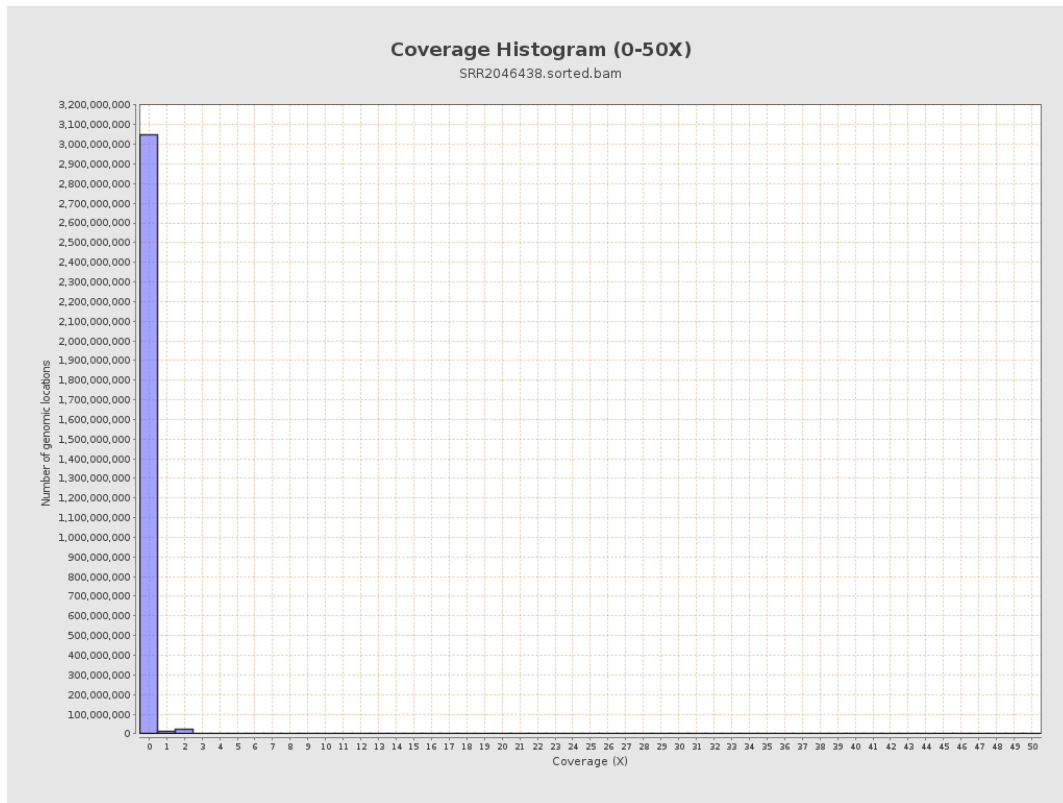
3. Results : Coverage across reference



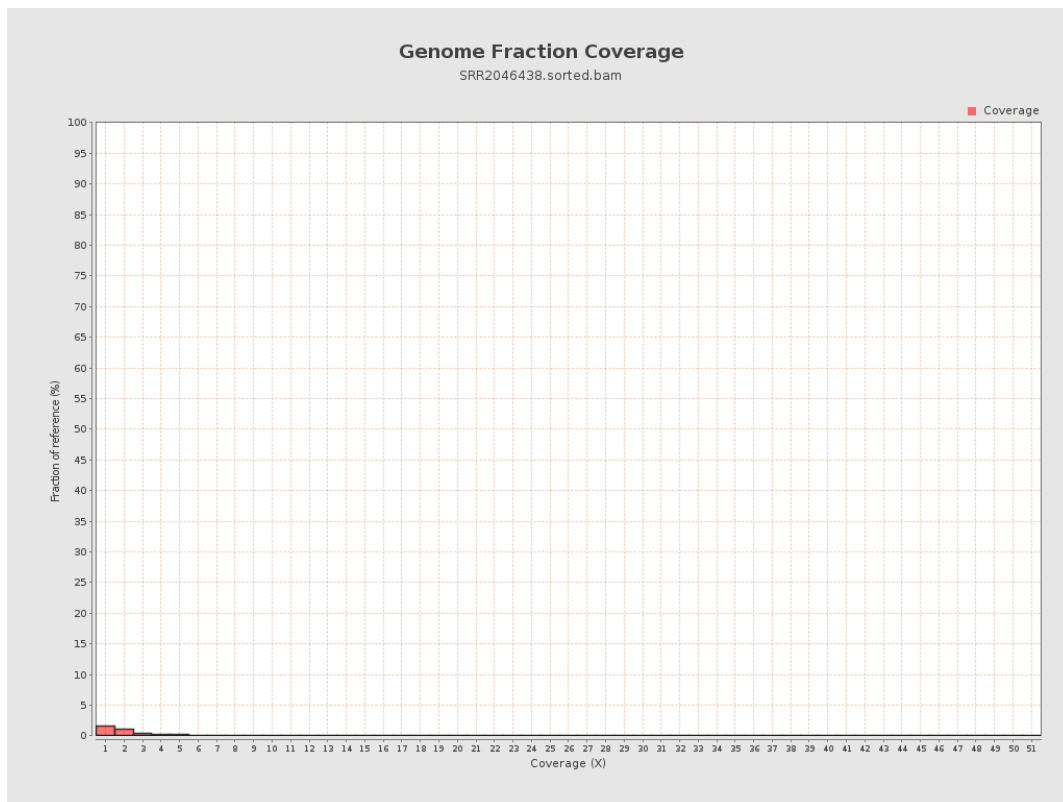
4. Results : Coverage Histogram



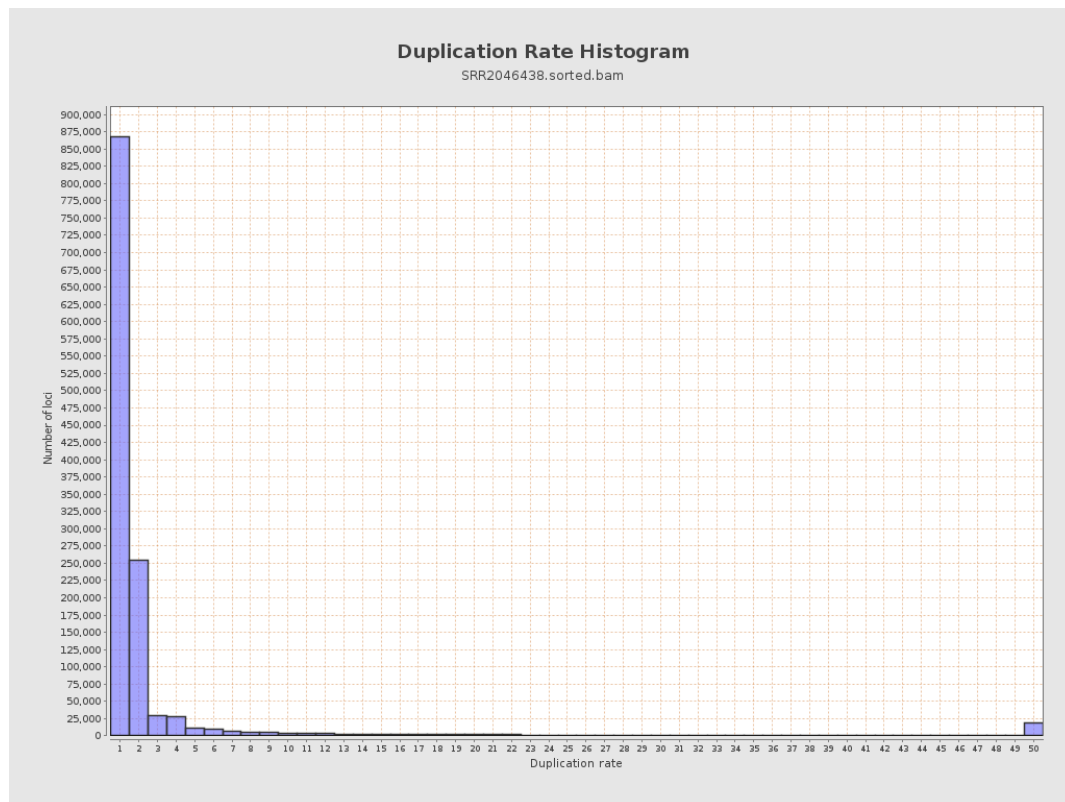
5. Results : Coverage Histogram (0-50X)



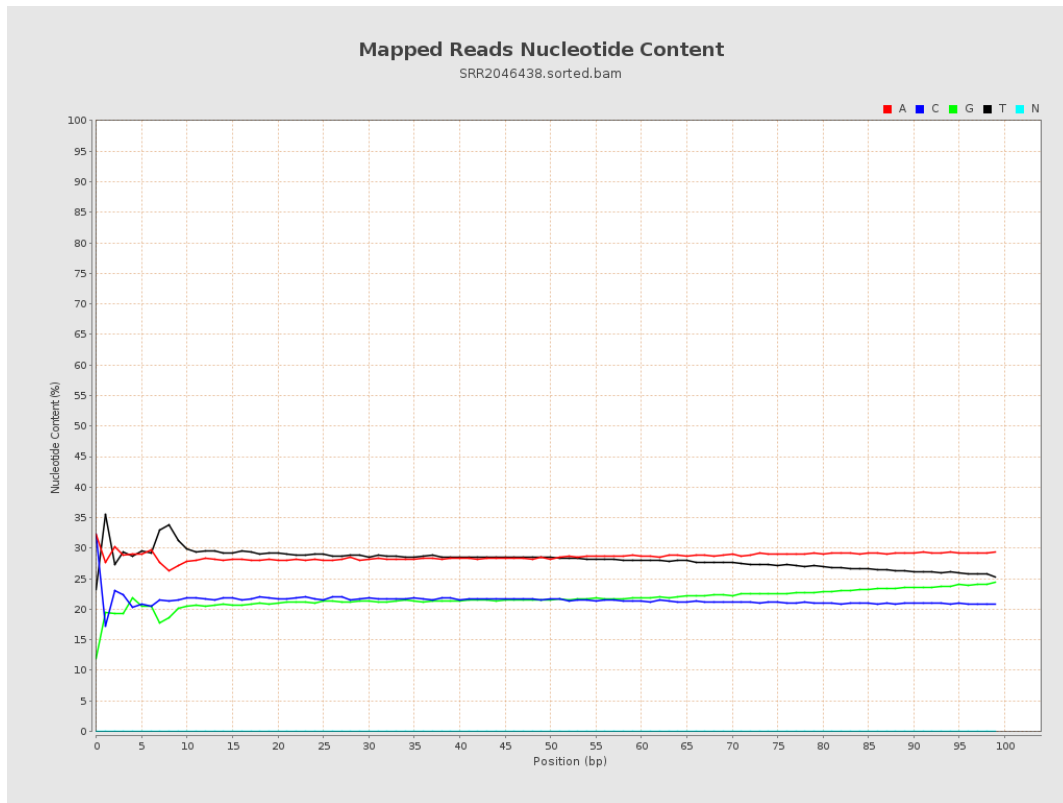
6. Results : Genome Fraction Coverage



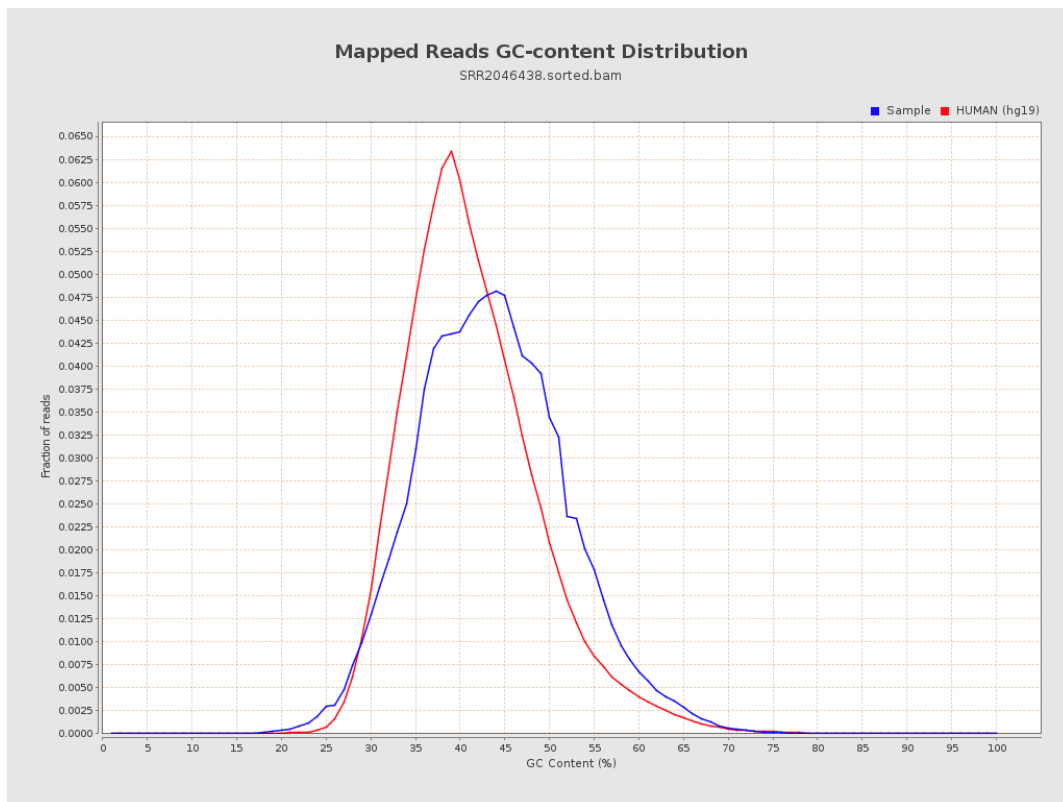
7. Results : Duplication Rate Histogram



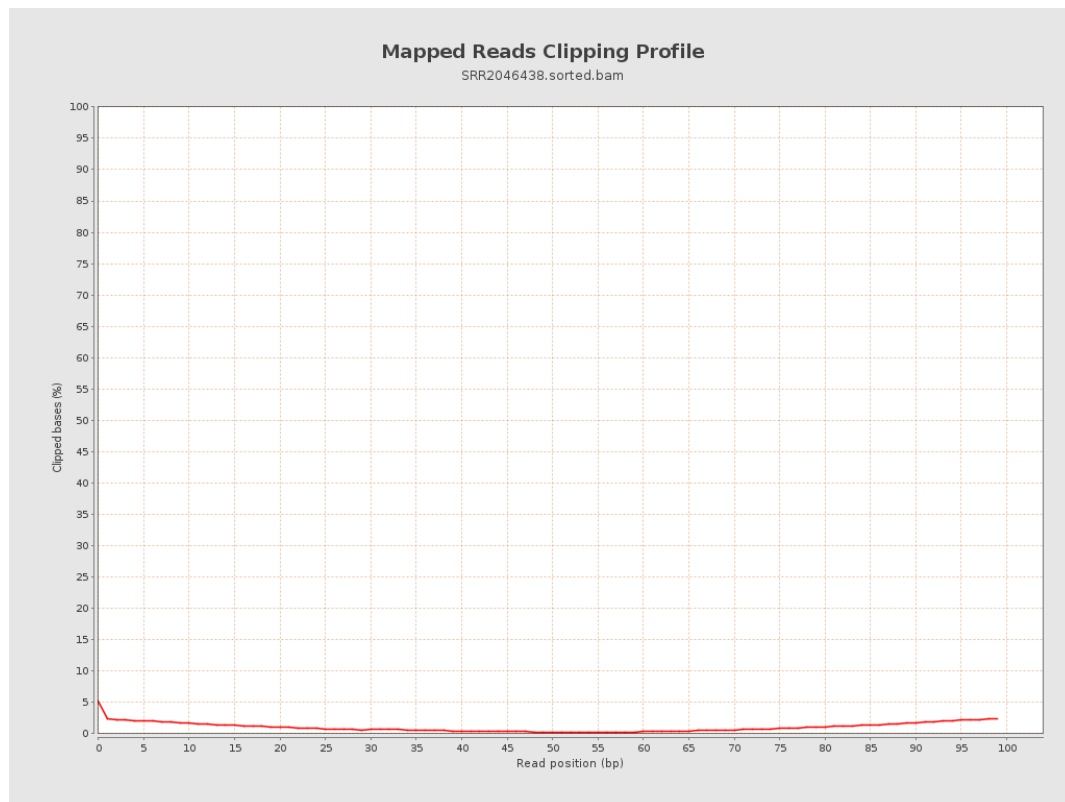
8. Results : Mapped Reads Nucleotide Content



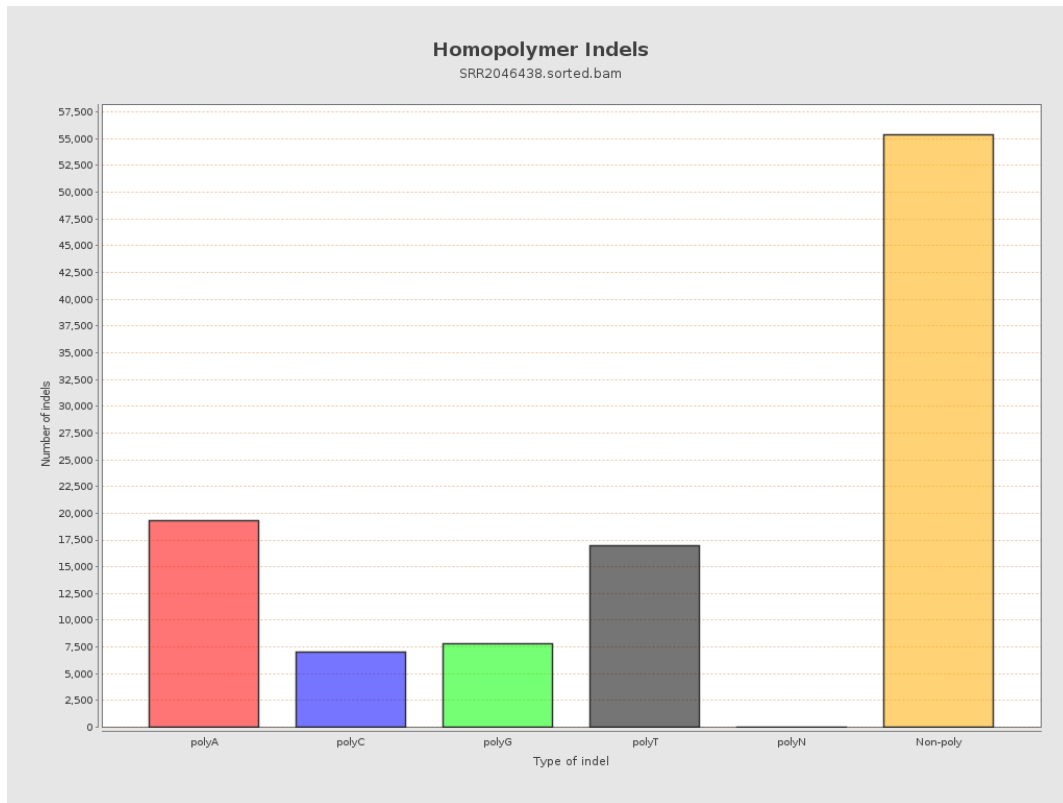
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



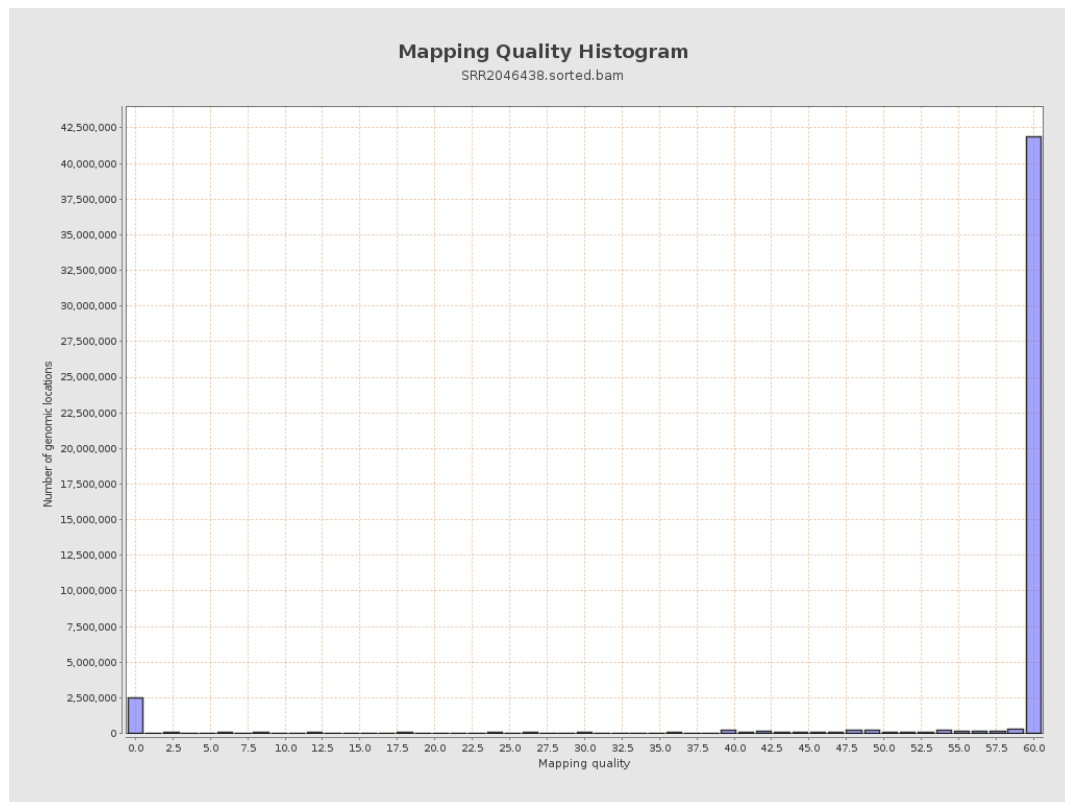
11. Results : Homopolymer Indels



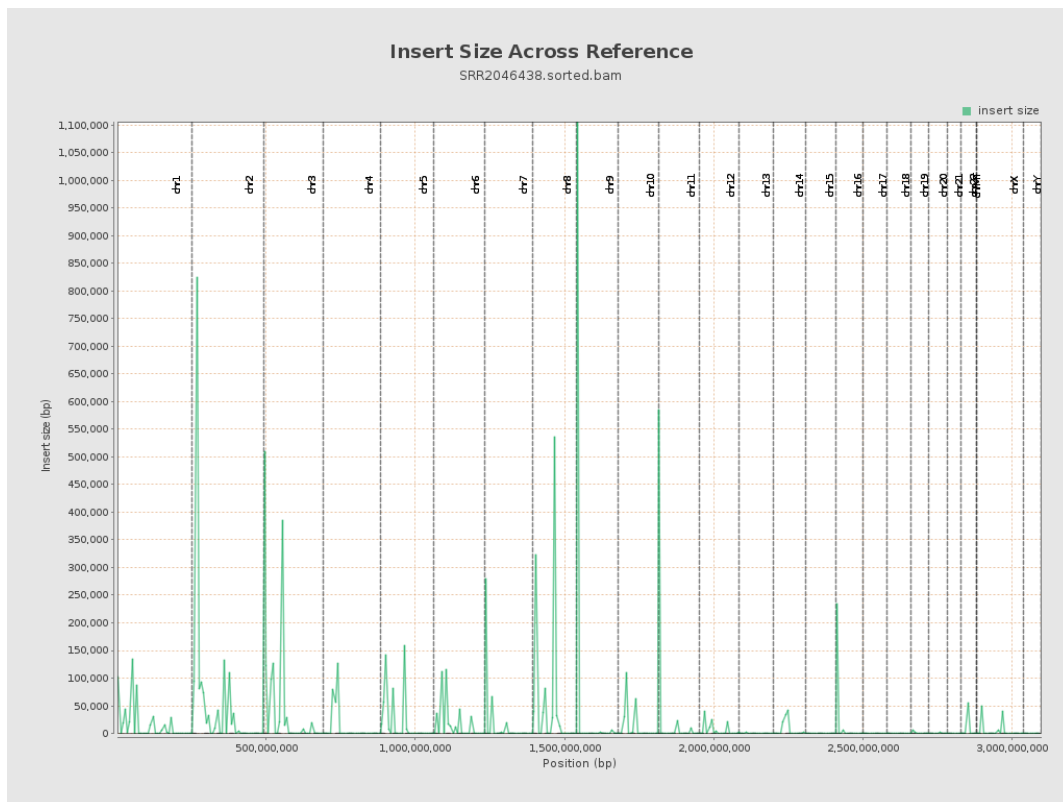
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

