

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 13:33:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046413.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_SRR2046413 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046413_1.fastq.gz SRR2046413_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 13:33:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046413.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,853,148
Mapped reads	5,813,818 / 99.33%
Unmapped reads	39,330 / 0.67%
Mapped paired reads	5,813,818 / 99.33%
Mapped reads, first in pair	2,905,949 / 49.65%
Mapped reads, second in pair	2,907,869 / 49.68%
Mapped reads, both in pair	5,786,296 / 98.86%
Mapped reads, singletons	27,522 / 0.47%
Secondary alignments	0
Supplementary alignments	47,957 / 0.82%
Read min/max/mean length	30 / 100 / 100.33
Duplicated reads (estimated)	4,525,972 / 77.33%
Duplication rate	40.98%
Clipped reads	1,771,018 / 30.26%

2.2. ACGT Content

Number/percentage of A's	164,658,471 / 29.94%
Number/percentage of C's	110,939,330 / 20.17%
Number/percentage of T's	163,873,419 / 29.8%
Number/percentage of G's	110,482,025 / 20.09%
Number/percentage of N's	45,862 / 0.01%

GC Percentage	40.26%
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2.3. Coverage

Mean	0.1777
Standard Deviation	22.7204

2.4. Mapping Quality

Mean Mapping Quality	52.12
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2.5. Insert size

Mean	15,058.28
Standard Deviation	1,211,555.78
P25/Median/P75	97 / 122 / 154

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	1,846,836
Insertions	43,650
Mapped reads with at least one insertion	0.74%
Deletions	49,984
Mapped reads with at least one deletion	0.84%
Homopolymer indels	47.64%

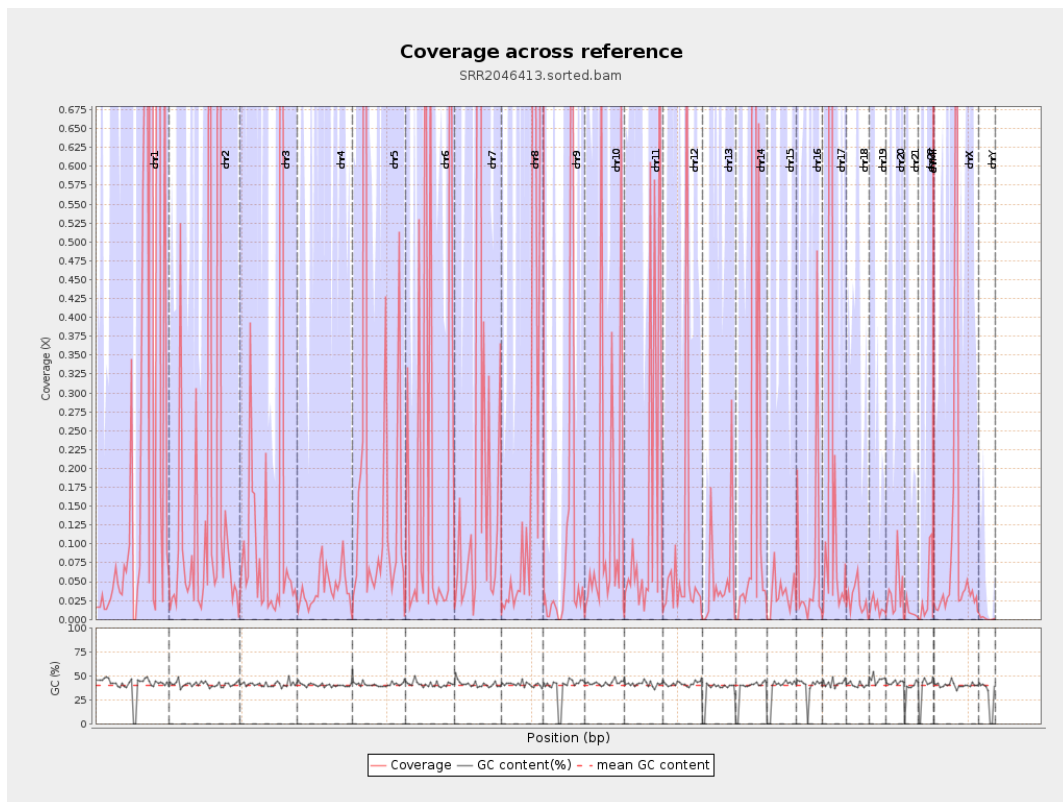
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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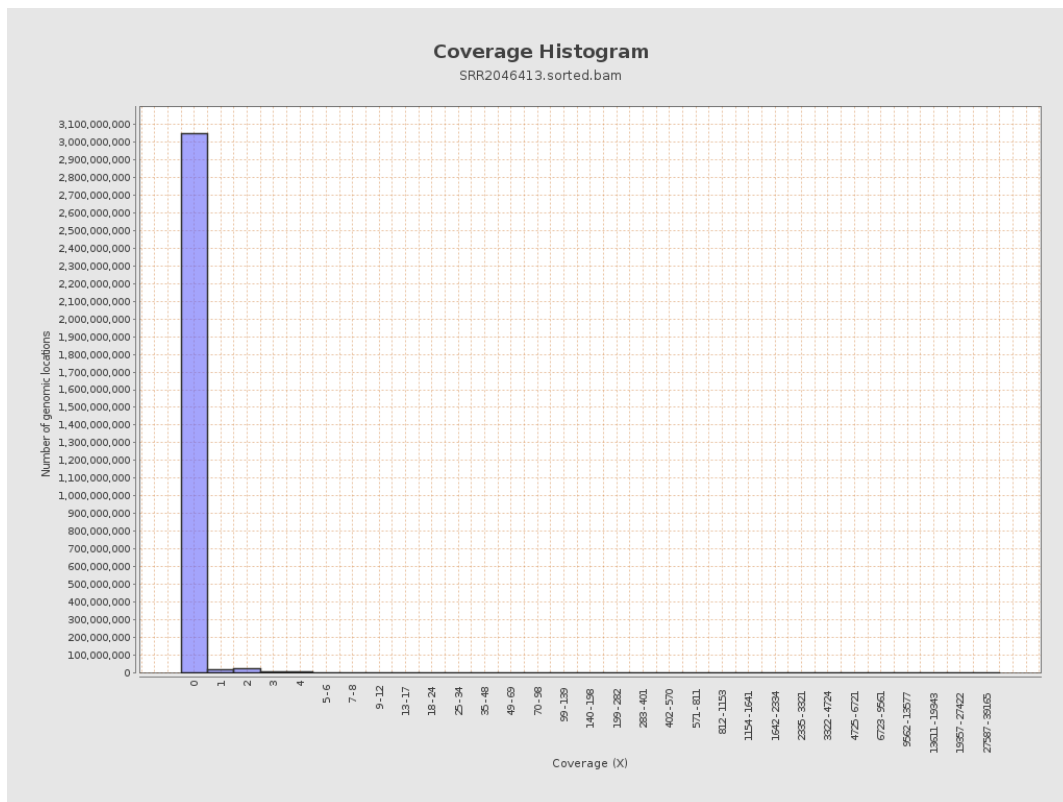
		bases	coverage	deviation
chr1	249250621	89323244	0.3584	25.0099
chr2	243199373	55471209	0.2281	19.332
chr3	198022430	40021977	0.2021	26.4608
chr4	191154276	7933937	0.0415	2.0056
chr5	180915260	38543157	0.213	19.9115
chr6	171115067	37682586	0.2202	17.1147
chr7	159138663	48583853	0.3053	28.4908
chr8	146364022	60605317	0.4141	65.9175
chr9	141213431	14281775	0.1011	16.9884
chr10	135534747	19628888	0.1448	14.9323
chr11	135006516	21238174	0.1573	13.678
chr12	133851895	11483577	0.0858	8.9172
chr13	115169878	6229329	0.0541	4.2451
chr14	107349540	34245029	0.319	23.5044
chr15	102531392	3435925	0.0335	1.4749
chr16	90354753	6414896	0.071	8.7795
chr17	81195210	33053836	0.4071	39.5441
chr18	78077248	2041475	0.0261	0.4179
chr19	59128983	988771	0.0167	0.8915
chr20	63025520	2322749	0.0369	1.5265
chr21	48129895	477000	0.0099	0.5894
chr22	51304566	2019018	0.0394	4.0308
chrMT	16571	27809	1.6782	1.8184
chrX	155270560	13979979	0.09	11.7176

chrY	59373566	98467	0.0017	0.1156
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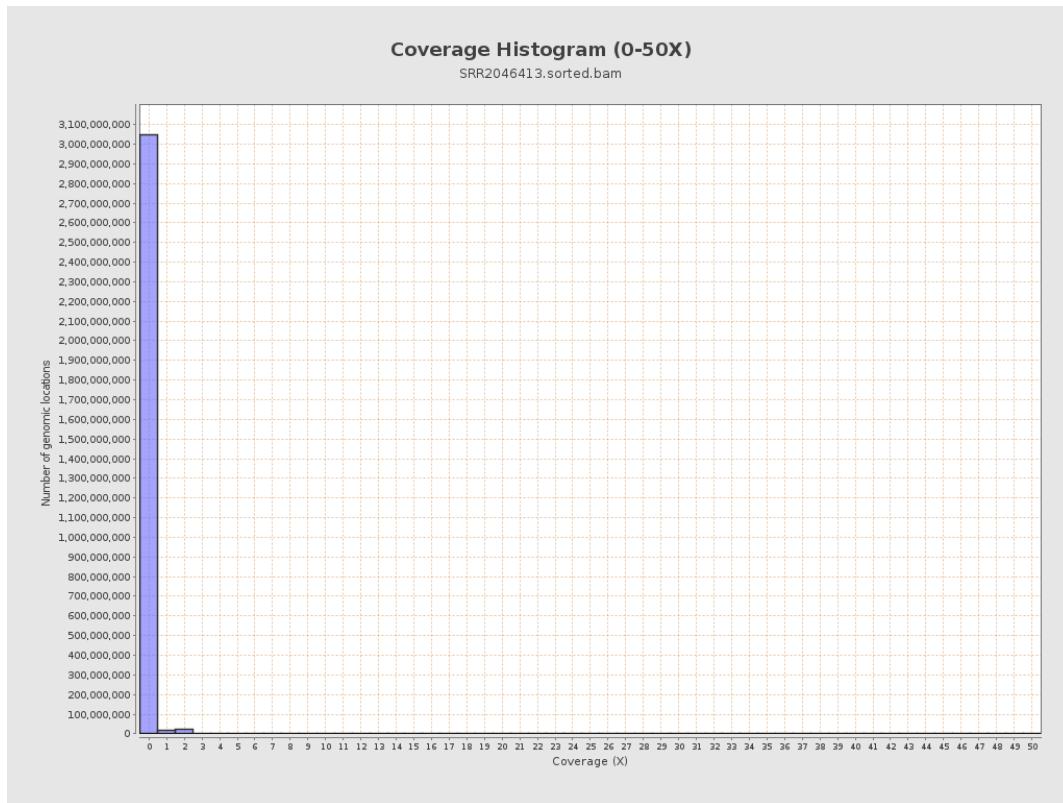
3. Results : Coverage across reference



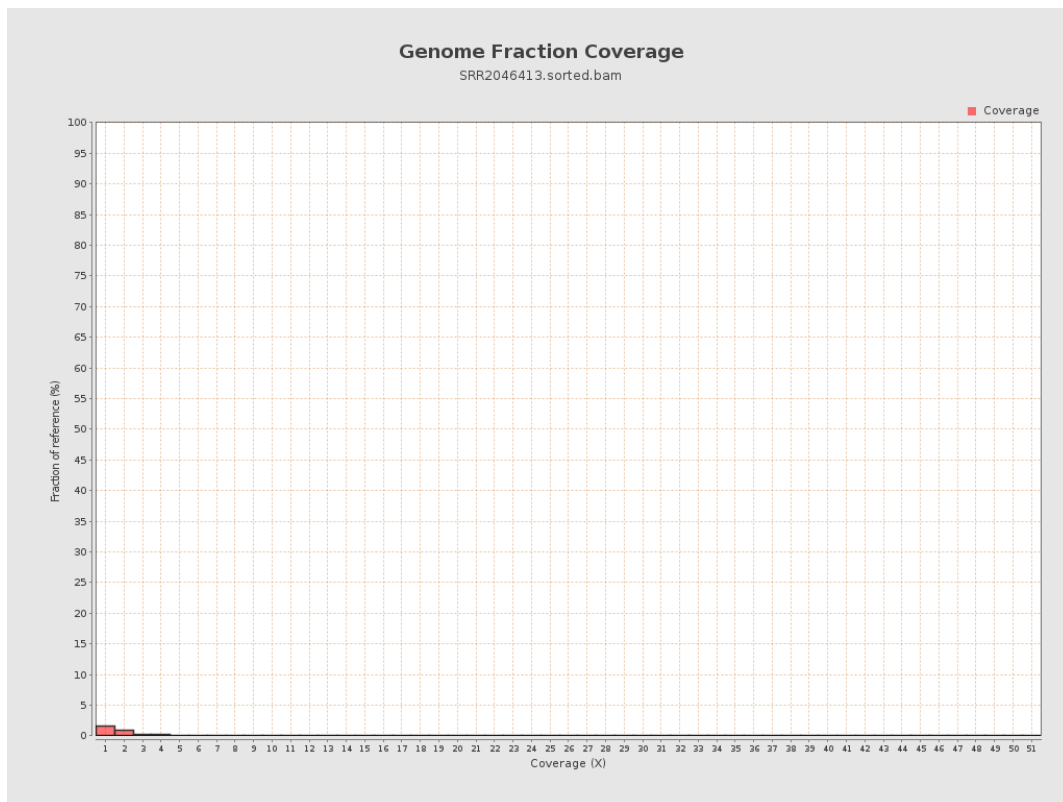
4. Results : Coverage Histogram



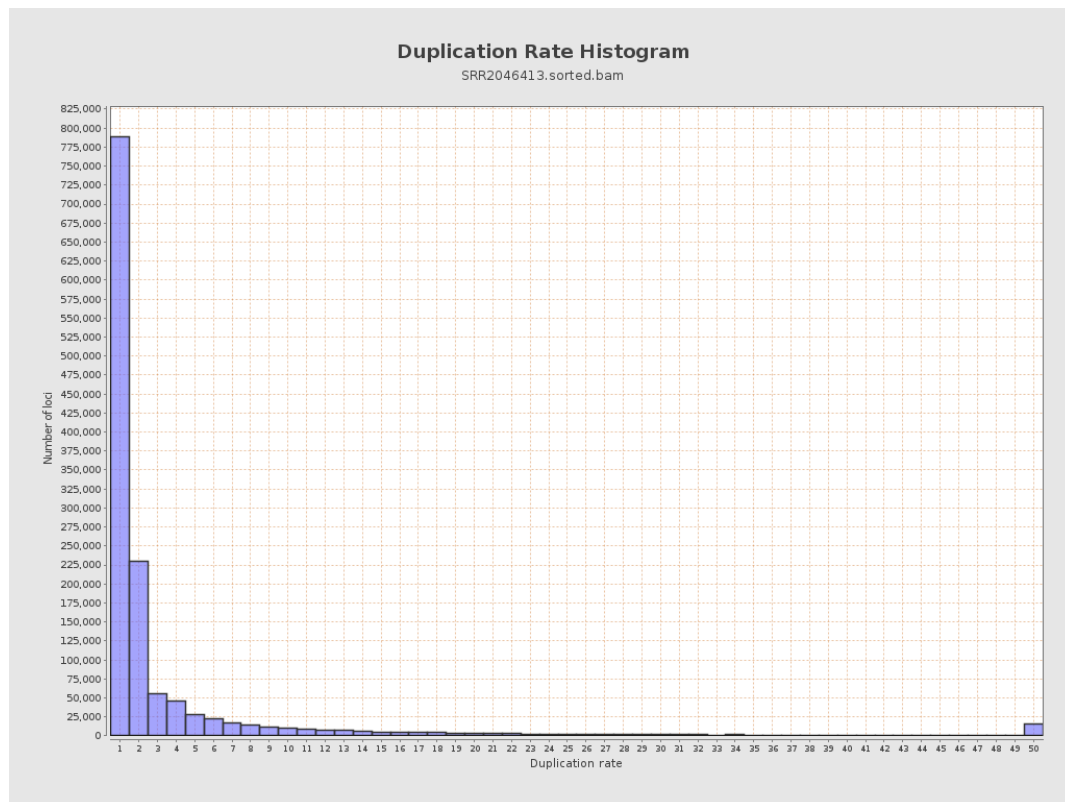
5. Results : Coverage Histogram (0-50X)



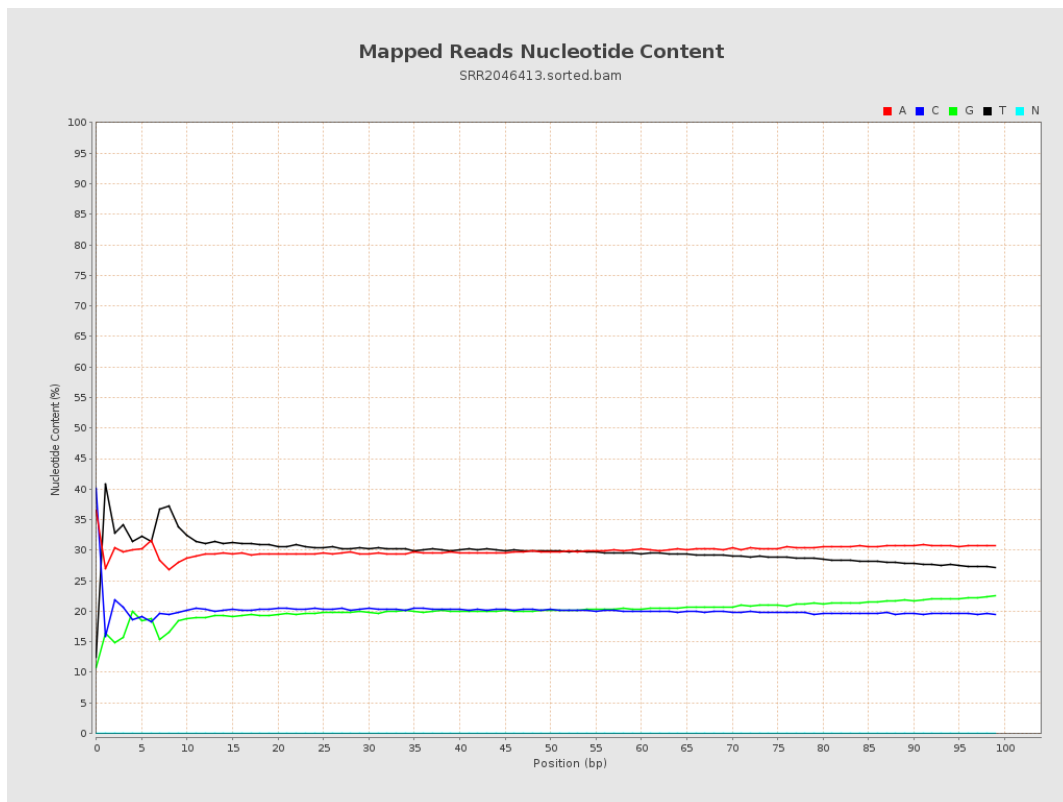
6. Results : Genome Fraction Coverage



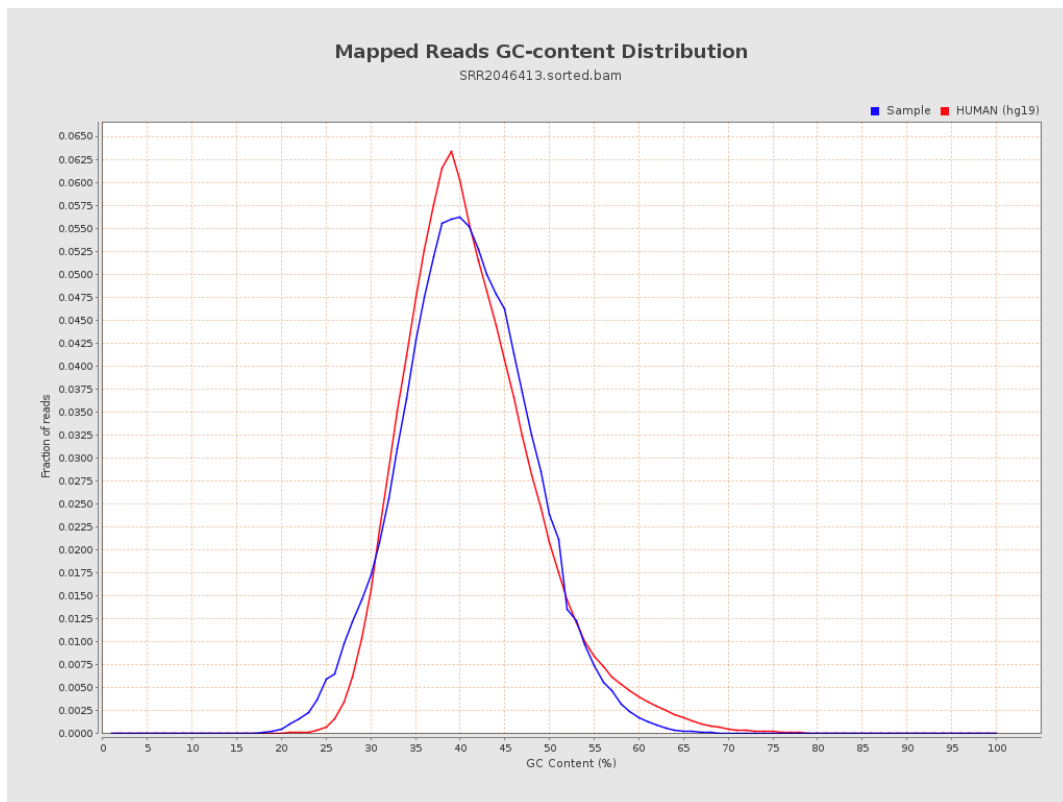
7. Results : Duplication Rate Histogram



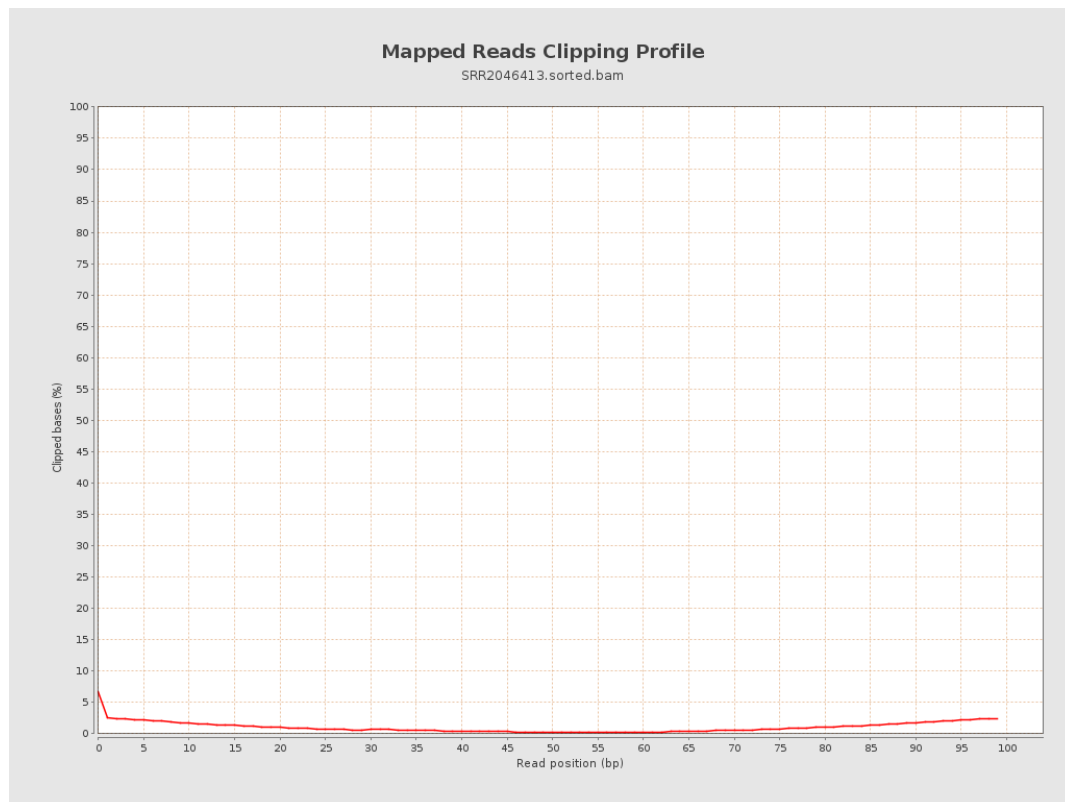
8. Results : Mapped Reads Nucleotide Content



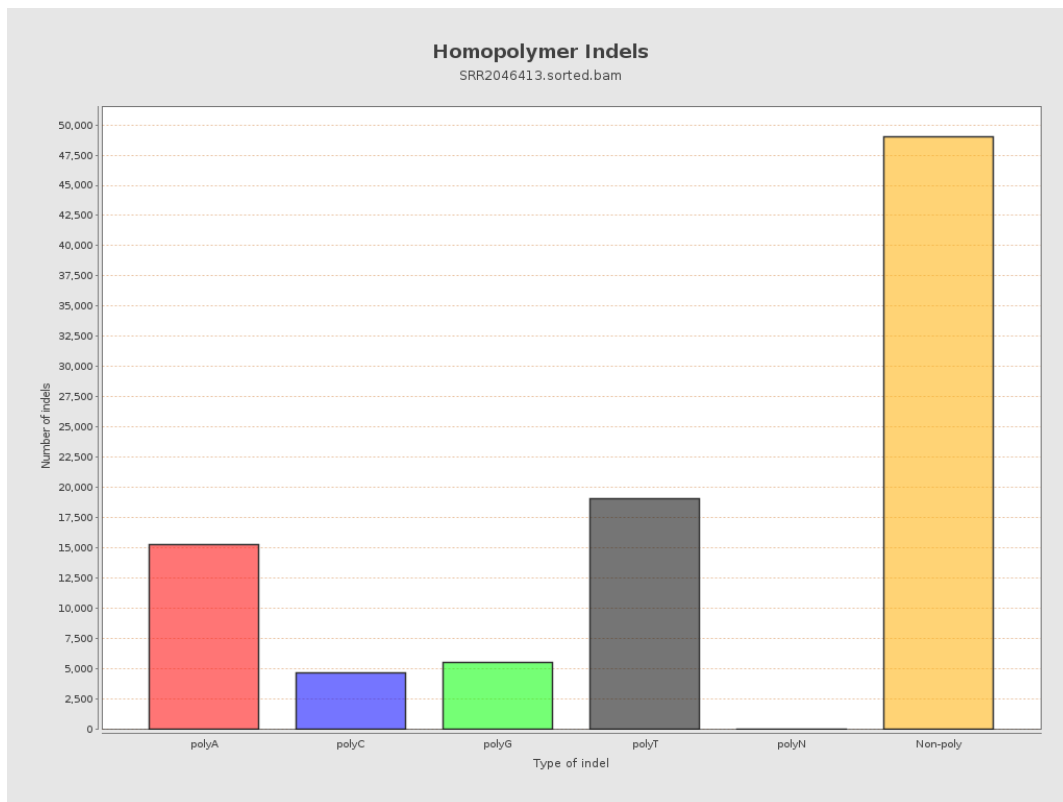
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



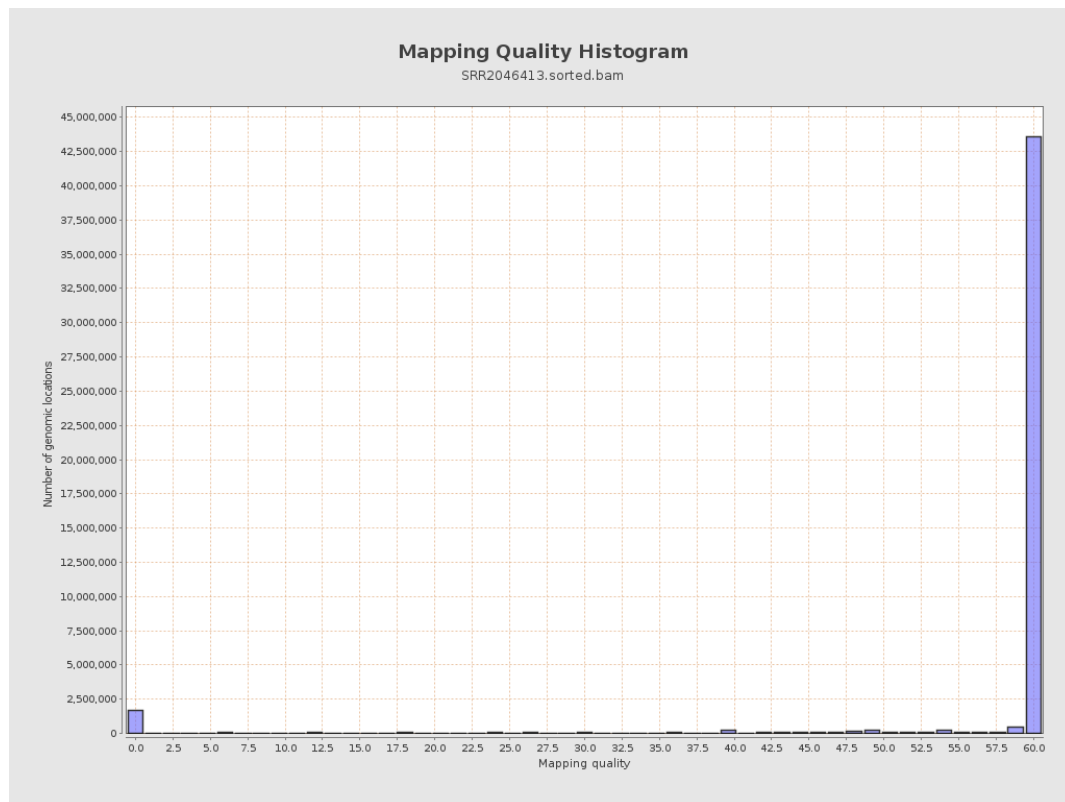
11. Results : Homopolymer Indels



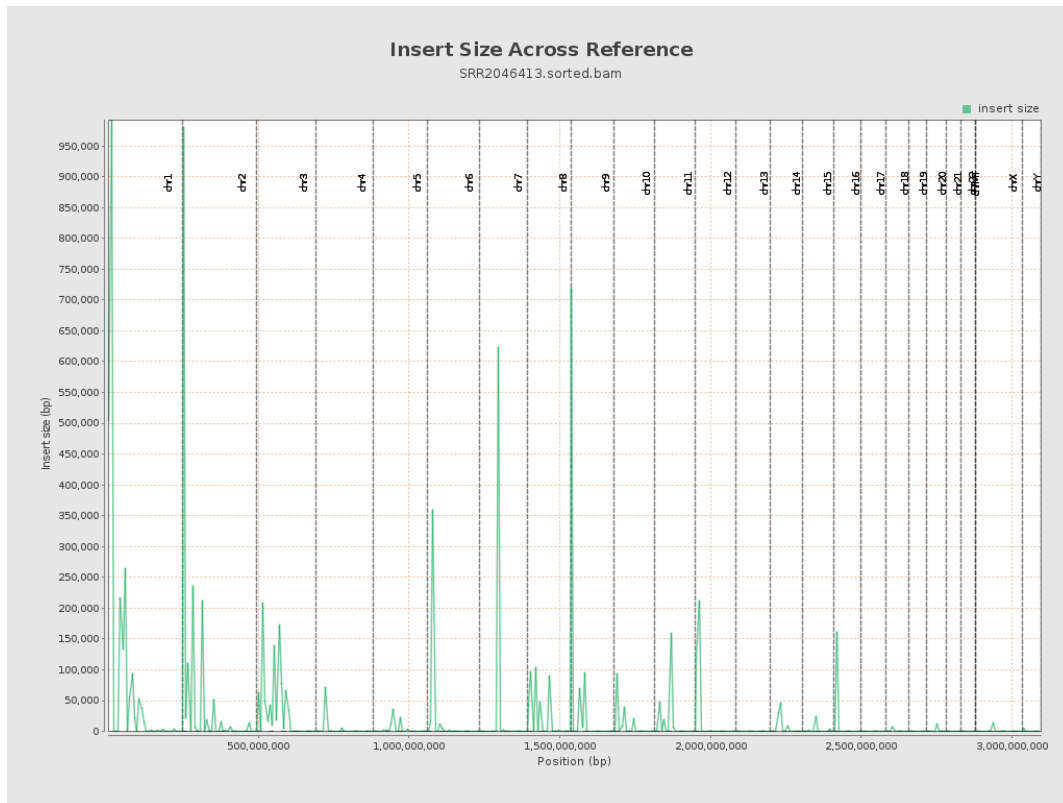
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

