

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:11:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006412.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_SRR1006412 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006412_1.fastq.gz SRR1006412_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:11:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006412.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,657,332
Mapped reads	8,526,090 / 88.29%
Unmapped reads	1,131,242 / 11.71%
Mapped paired reads	8,526,090 / 88.29%
Mapped reads, first in pair	4,299,684 / 44.52%
Mapped reads, second in pair	4,226,406 / 43.76%
Mapped reads, both in pair	7,800,062 / 80.77%
Mapped reads, singletons	726,028 / 7.52%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	369,847 / 3.83%
Duplication rate	3.68%
Clipped reads	454,640 / 4.71%

2.2. ACGT Content

Number/percentage of A's	92,421,962 / 28%
Number/percentage of C's	70,587,404 / 21.38%
Number/percentage of T's	94,072,692 / 28.5%
Number/percentage of G's	73,020,496 / 22.12%
Number/percentage of N's	13,848 / 0%
GC Percentage	43.5%

2.3. Coverage

Mean	0.1067
Standard Deviation	0.6013

2.4. Mapping Quality

Mean Mapping Quality	48.28
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2.5. Insert size

Mean	76,412.3
Standard Deviation	2,596,967.38
P25/Median/P75	121 / 156 / 210

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	1,112,911
Insertions	8,979
Mapped reads with at least one insertion	0.11%
Deletions	30,133
Mapped reads with at least one deletion	0.35%
Homopolymer indels	43.99%

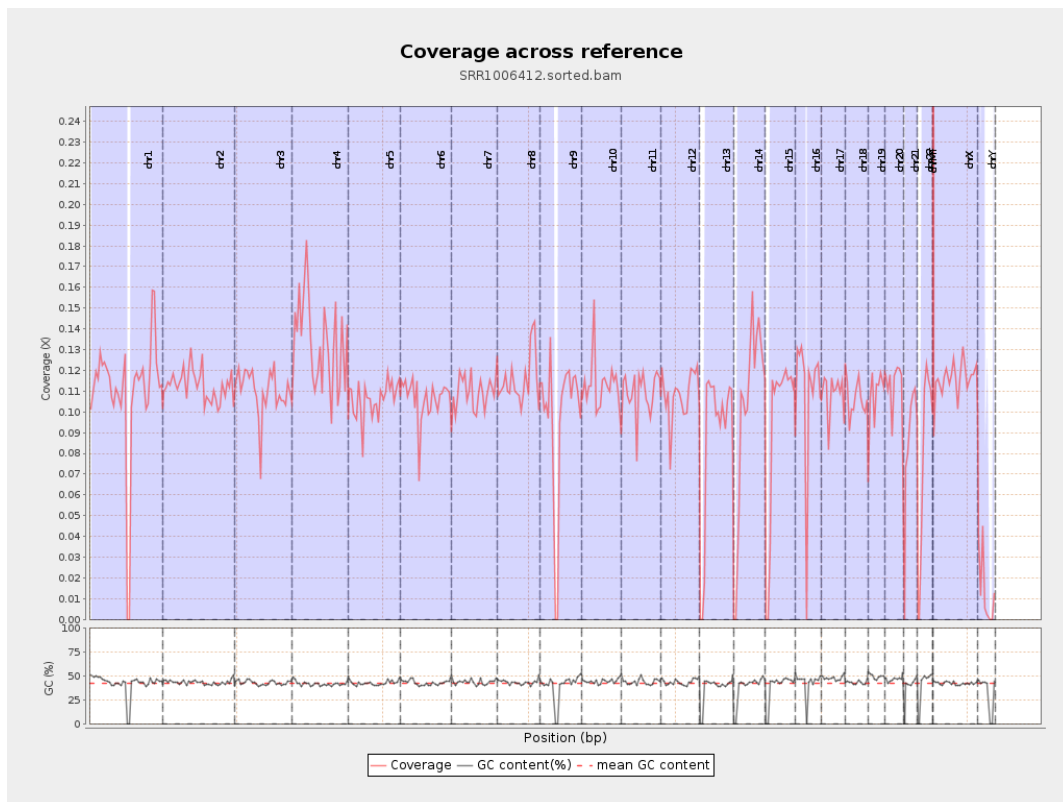
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

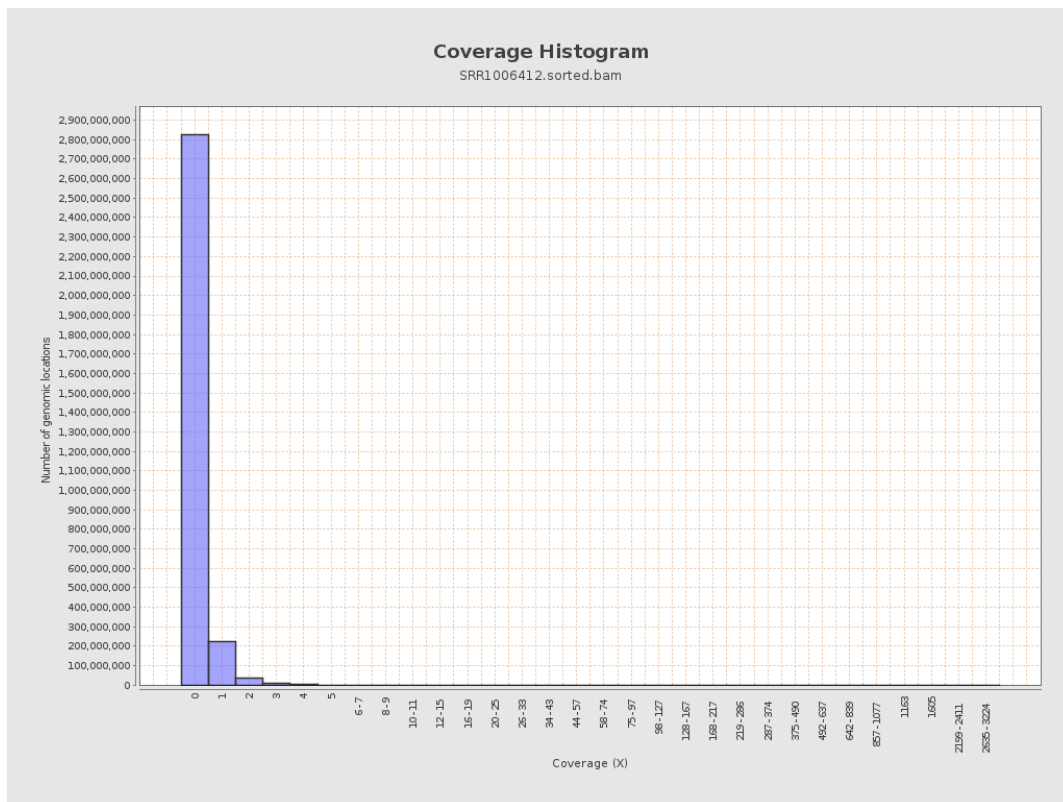
chr1	249250621	27435116	0.1101	0.7894
chr2	243199373	27428733	0.1128	0.5159
chr3	198022430	21787238	0.11	0.3855
chr4	191154276	25565538	0.1337	0.4918
chr5	180915260	19221750	0.1062	0.3776
chr6	171115067	18184416	0.1063	0.4191
chr7	159138663	17363232	0.1091	0.6
chr8	146364022	16909011	0.1155	1.6141
chr9	141213431	13716328	0.0971	0.4336
chr10	135534747	15274523	0.1127	0.5986
chr11	135006516	14706195	0.1089	0.4725
chr12	133851895	14568452	0.1088	0.3868
chr13	115169878	10117496	0.0878	0.3454
chr14	107349540	11005613	0.1025	0.4086
chr15	102531392	9483403	0.0925	0.354
chr16	90354753	9770685	0.1081	0.4718
chr17	81195210	8866826	0.1092	0.4099
chr18	78077248	8259886	0.1058	0.7493
chr19	59128983	6441749	0.1089	0.587
chr20	63025520	7080808	0.1123	0.4125
chr21	48129895	4156548	0.0864	0.4033
chr22	51304566	4059338	0.0791	0.3401
chrMT	16571	21073	1.2717	1.3746
chrX	155270560	17936048	0.1155	0.436

chrY	59373566	796529	0.0134	0.3249
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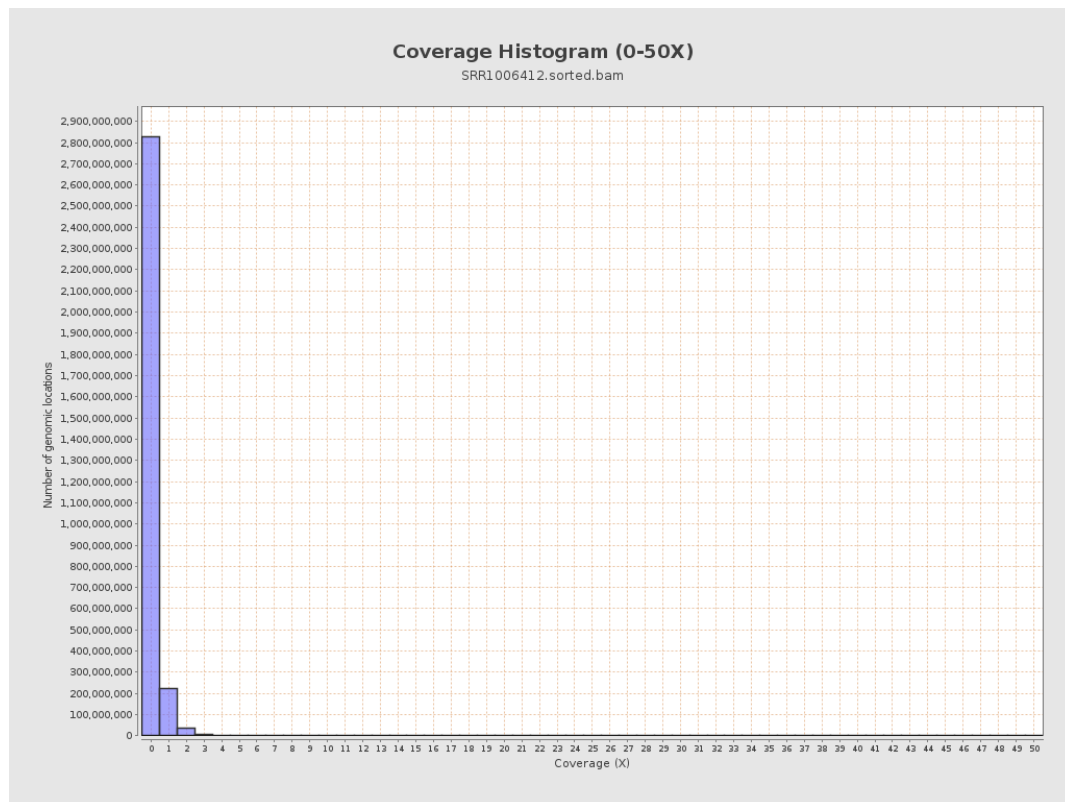
3. Results : Coverage across reference



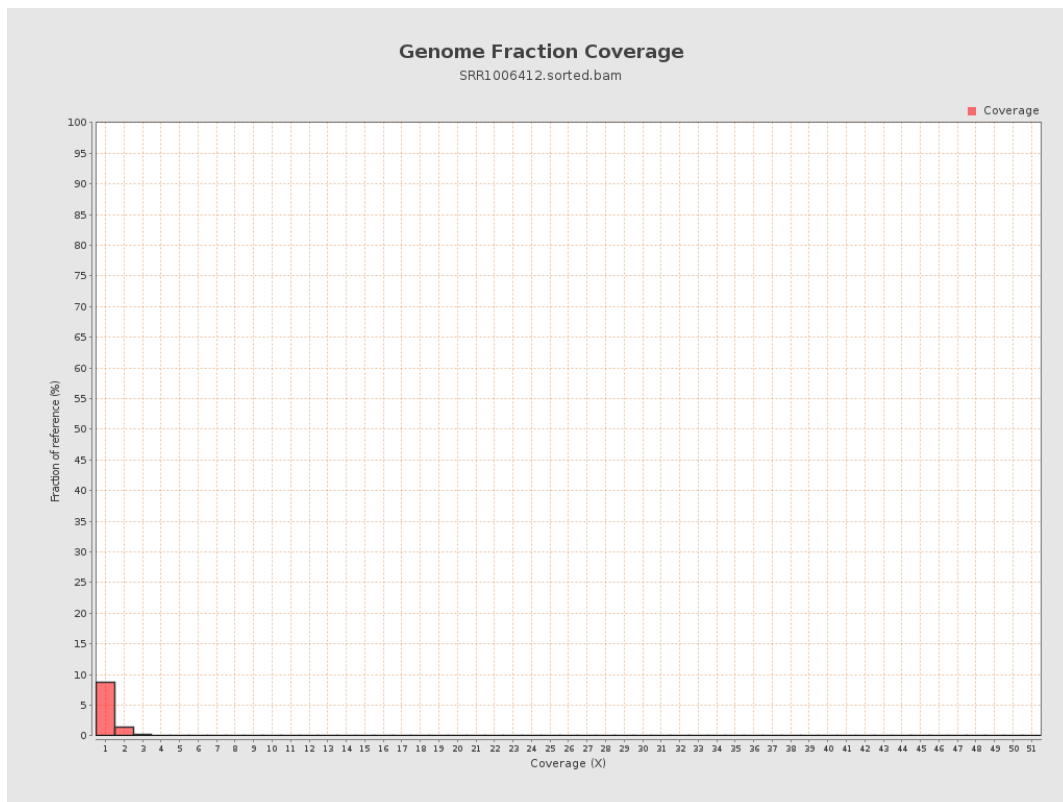
4. Results : Coverage Histogram



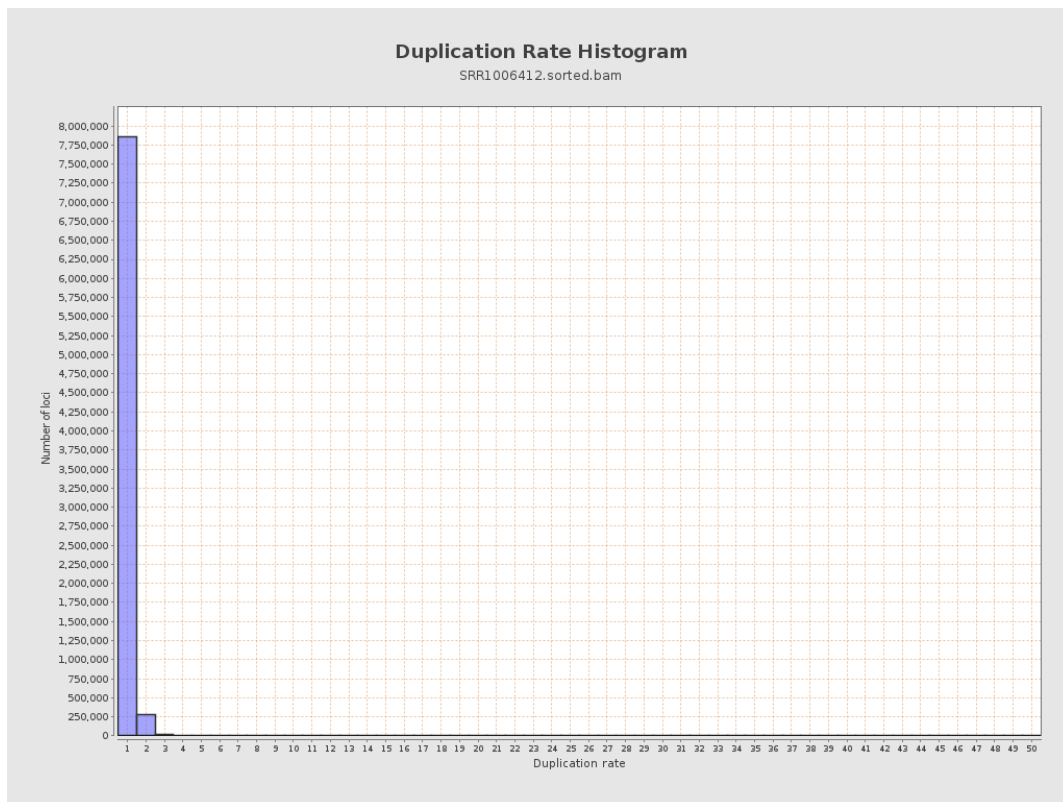
5. Results : Coverage Histogram (0-50X)



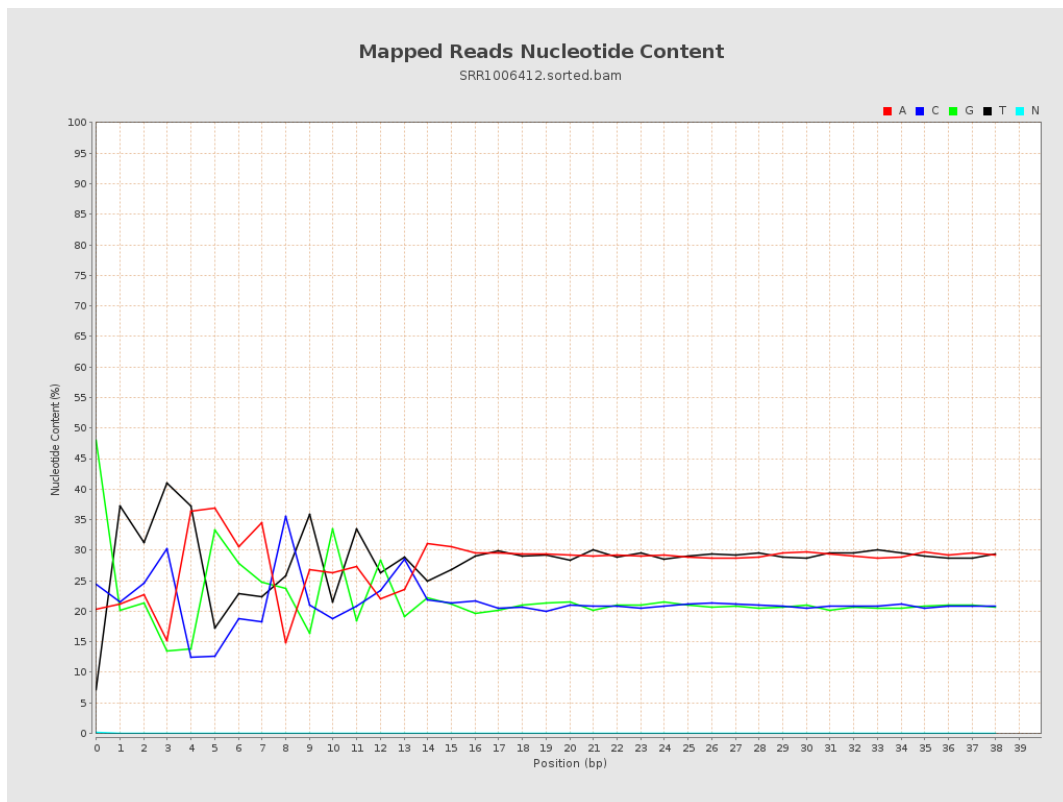
6. Results : Genome Fraction Coverage



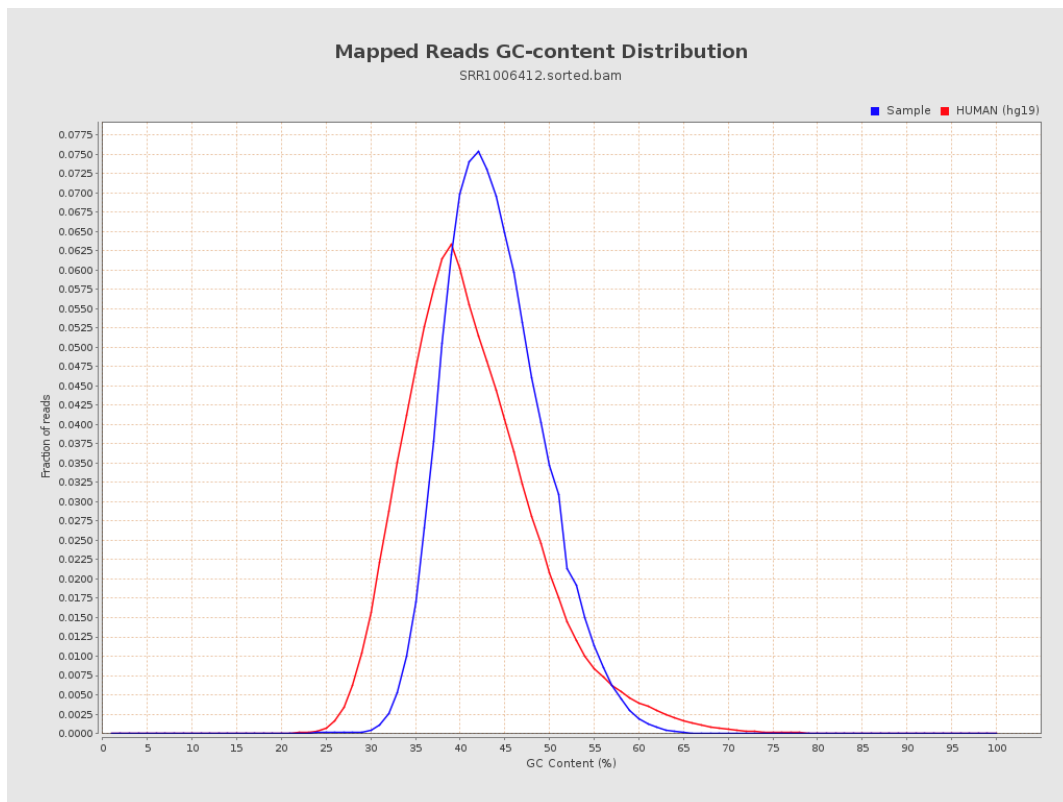
7. Results : Duplication Rate Histogram



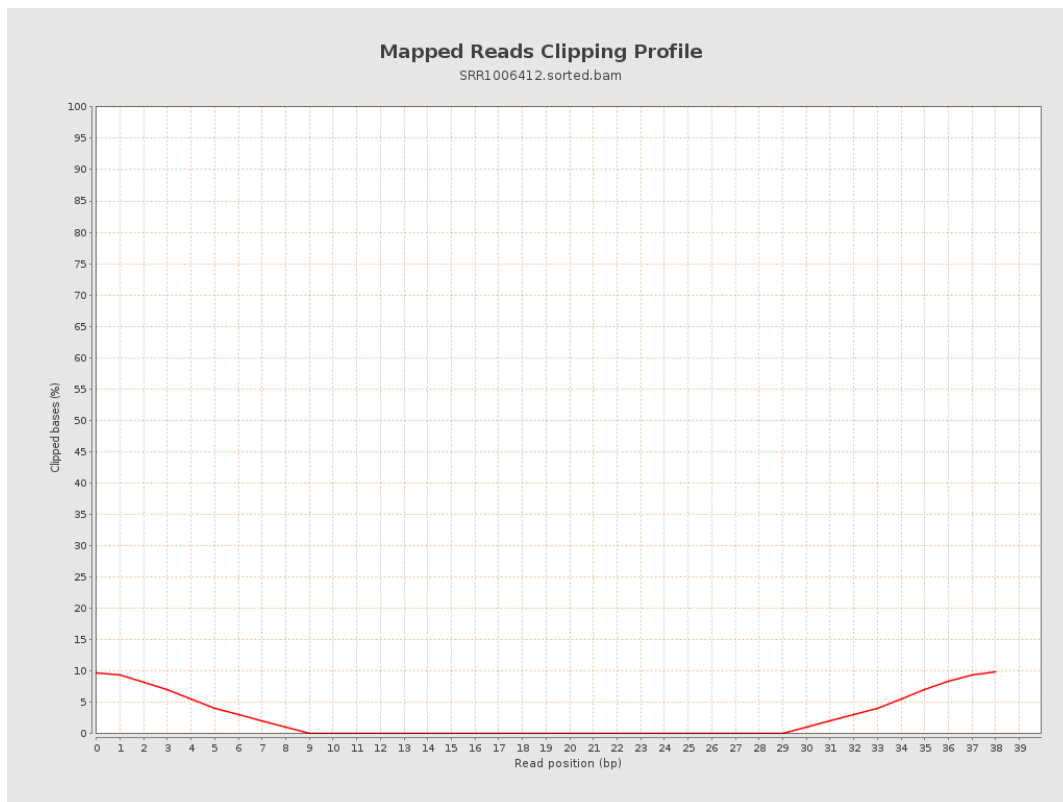
8. Results : Mapped Reads Nucleotide Content



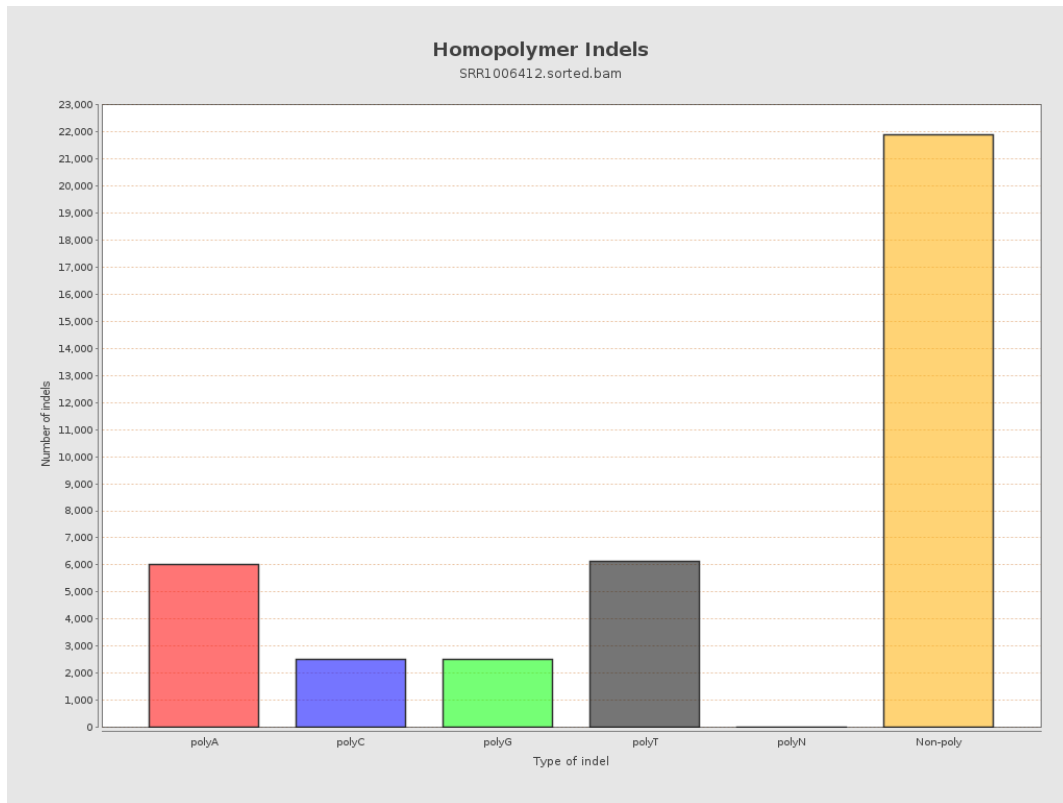
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



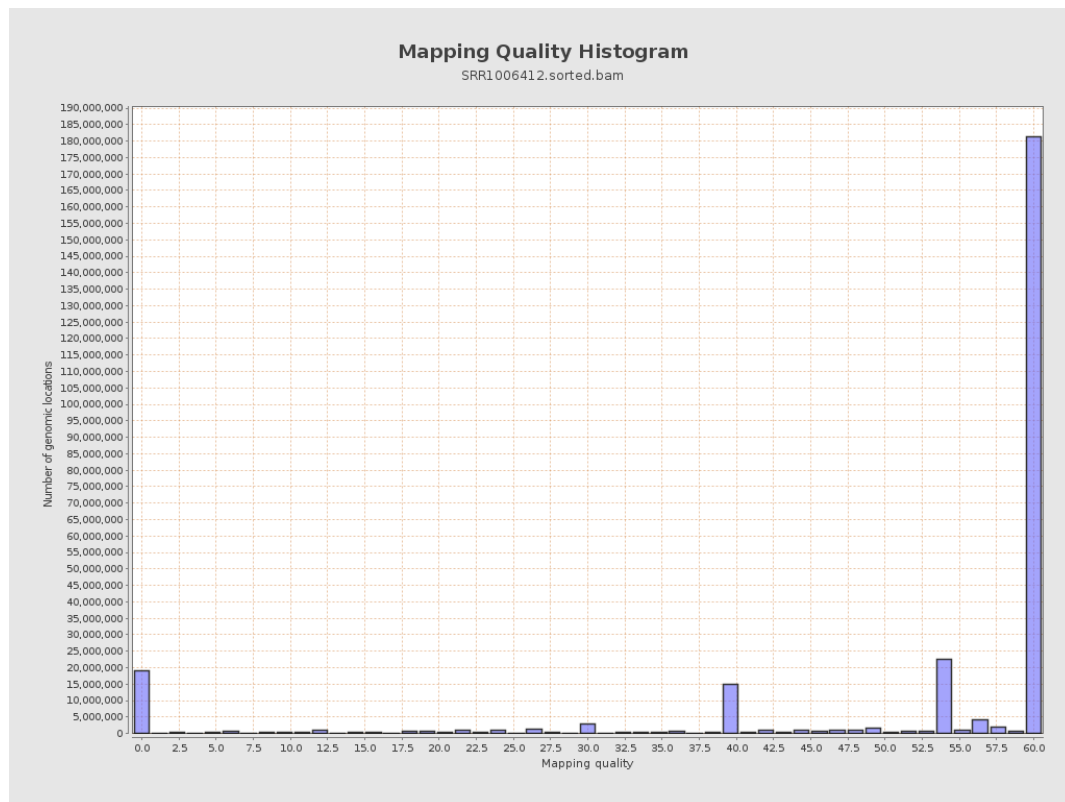
11. Results : Homopolymer Indels



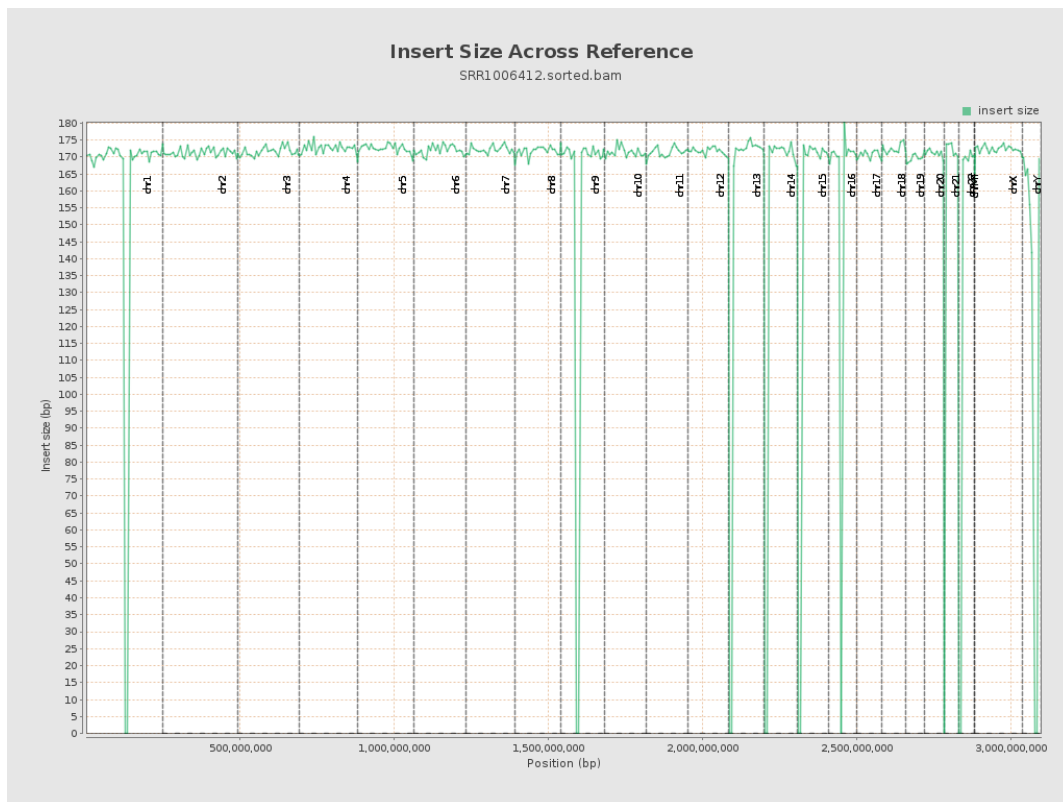
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

