

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 13:06:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006013.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_SRR1006013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006013_1.fastq.gz SRR1006013_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 13:06:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,548,910
Mapped reads	8,045,349 / 64.11%
Unmapped reads	4,503,561 / 35.89%
Mapped paired reads	8,045,349 / 64.11%
Mapped reads, first in pair	4,040,935 / 32.2%
Mapped reads, second in pair	4,004,414 / 31.91%
Mapped reads, both in pair	7,233,006 / 57.64%
Mapped reads, singletons	812,343 / 6.47%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	378,595 / 3.02%
Duplication rate	4.04%
Clipped reads	825,543 / 6.58%

2.2. ACGT Content

Number/percentage of A's	84,534,763 / 27.29%
Number/percentage of C's	68,612,080 / 22.15%
Number/percentage of T's	86,545,490 / 27.94%
Number/percentage of G's	69,991,273 / 22.6%
Number/percentage of N's	69,183 / 0.02%
GC Percentage	44.75%

2.3. Coverage

Mean	0.1001
Standard Deviation	0.7309

2.4. Mapping Quality

Mean Mapping Quality	44.76
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2.5. Insert size

Mean	73,675.81
Standard Deviation	2,634,928.44
P25/Median/P75	52 / 69 / 93

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	1,643,439
Insertions	11,014
Mapped reads with at least one insertion	0.14%
Deletions	33,219
Mapped reads with at least one deletion	0.41%
Homopolymer indels	41.33%

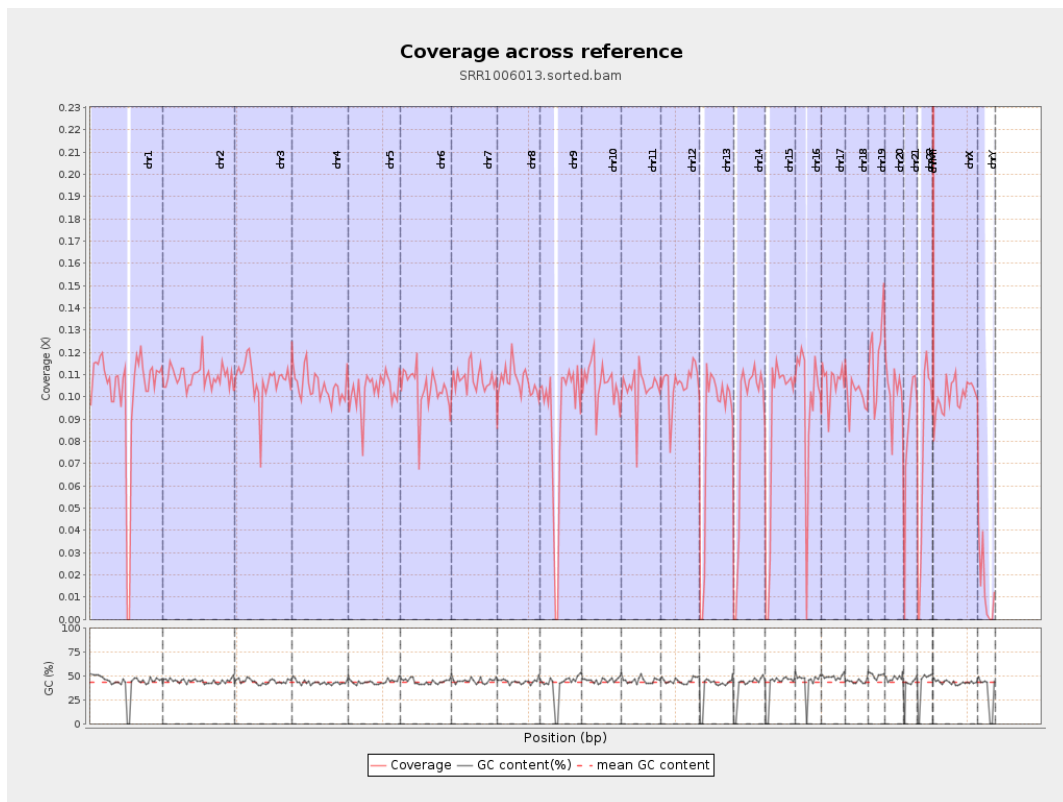
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

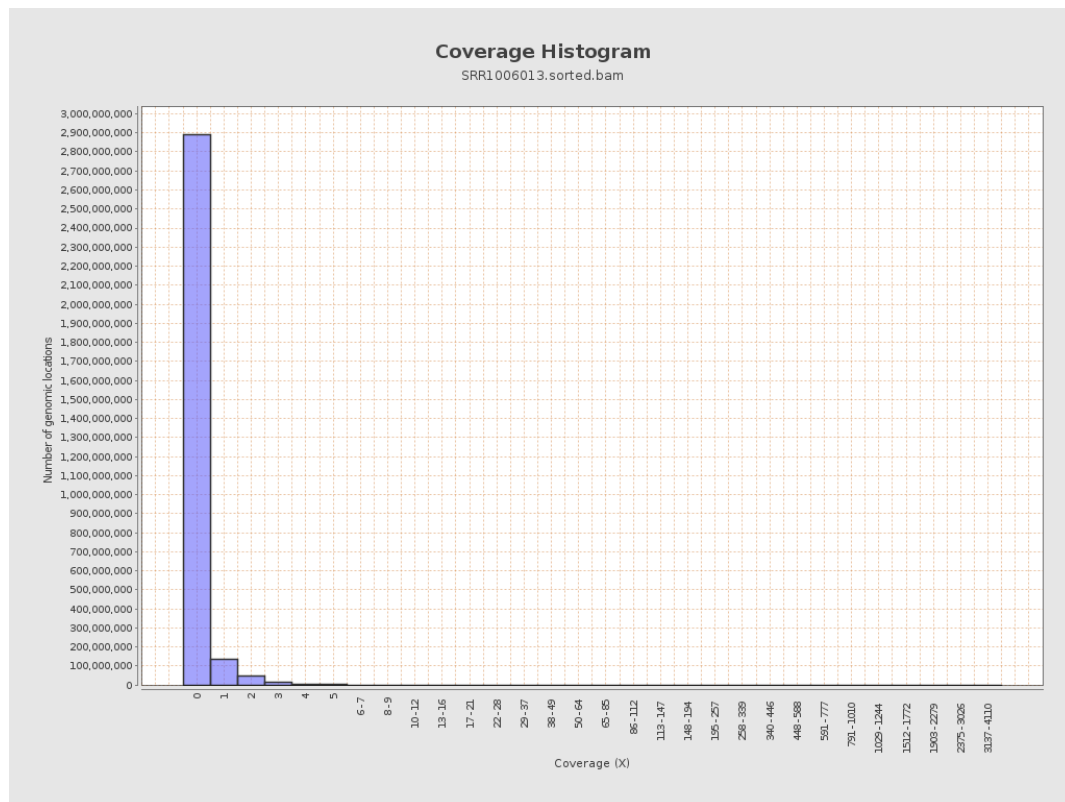
chr1	249250621	25518754	0.1024	0.771
chr2	243199373	26559027	0.1092	0.6153
chr3	198022430	21290033	0.1075	0.456
chr4	191154276	20048447	0.1049	0.4701
chr5	180915260	18594344	0.1028	0.4422
chr6	171115067	17719610	0.1036	0.5152
chr7	159138663	17186239	0.108	0.6237
chr8	146364022	15635801	0.1068	1.2789
chr9	141213431	12663819	0.0897	0.4555
chr10	135534747	14383305	0.1061	0.545
chr11	135006516	14053873	0.1041	0.4881
chr12	133851895	14232396	0.1063	0.4691
chr13	115169878	9918134	0.0861	0.4142
chr14	107349540	9529412	0.0888	0.438
chr15	102531392	8938469	0.0872	0.419
chr16	90354753	8875514	0.0982	0.5012
chr17	81195210	8707345	0.1072	0.4697
chr18	78077248	7877285	0.1009	0.5856
chr19	59128983	7044172	0.1191	3.2344
chr20	63025520	6435375	0.1021	0.4593
chr21	48129895	4120415	0.0856	0.4345
chr22	51304566	3908623	0.0762	0.4876
chrMT	16571	136548	8.2402	5.8329
chrX	155270560	15586794	0.1004	0.4539

chrY	59373566	833991	0.014	0.2538
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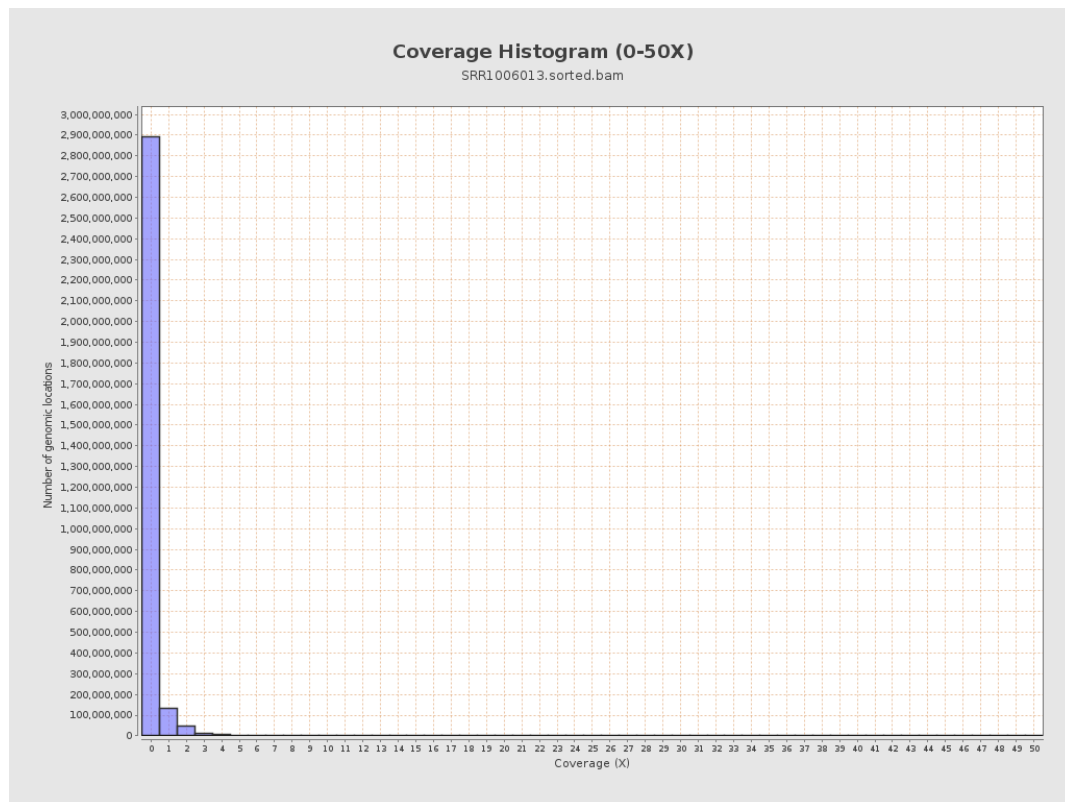
3. Results : Coverage across reference



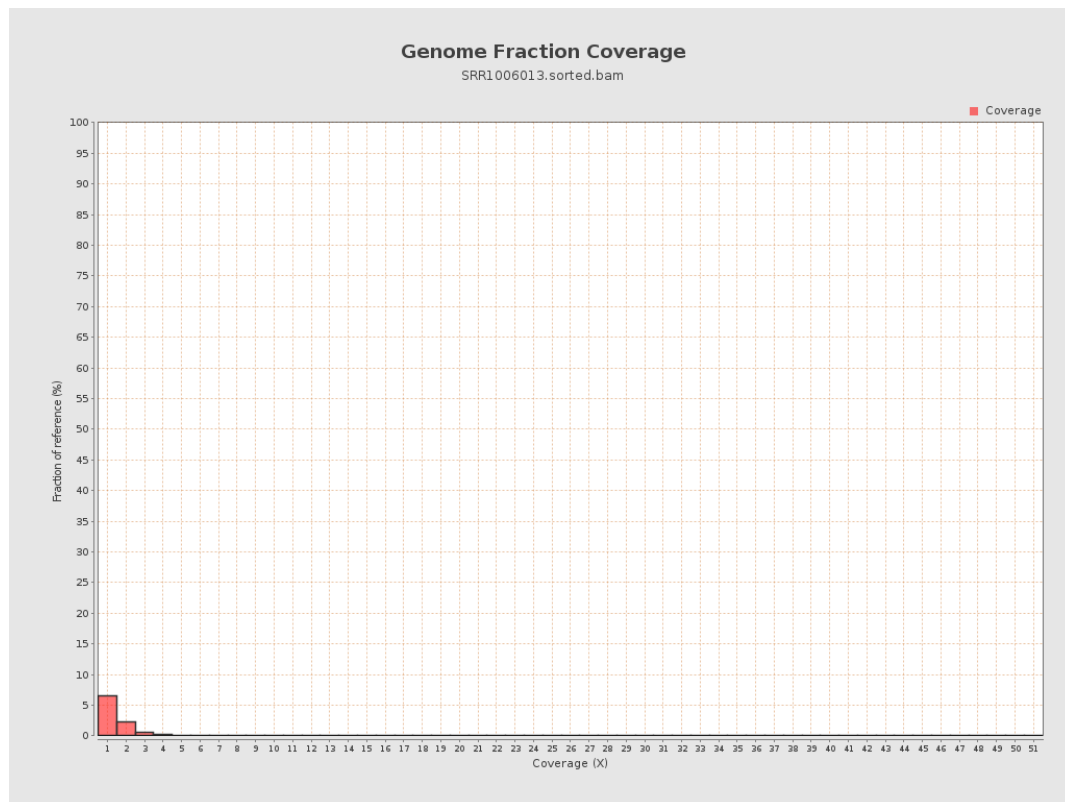
4. Results : Coverage Histogram



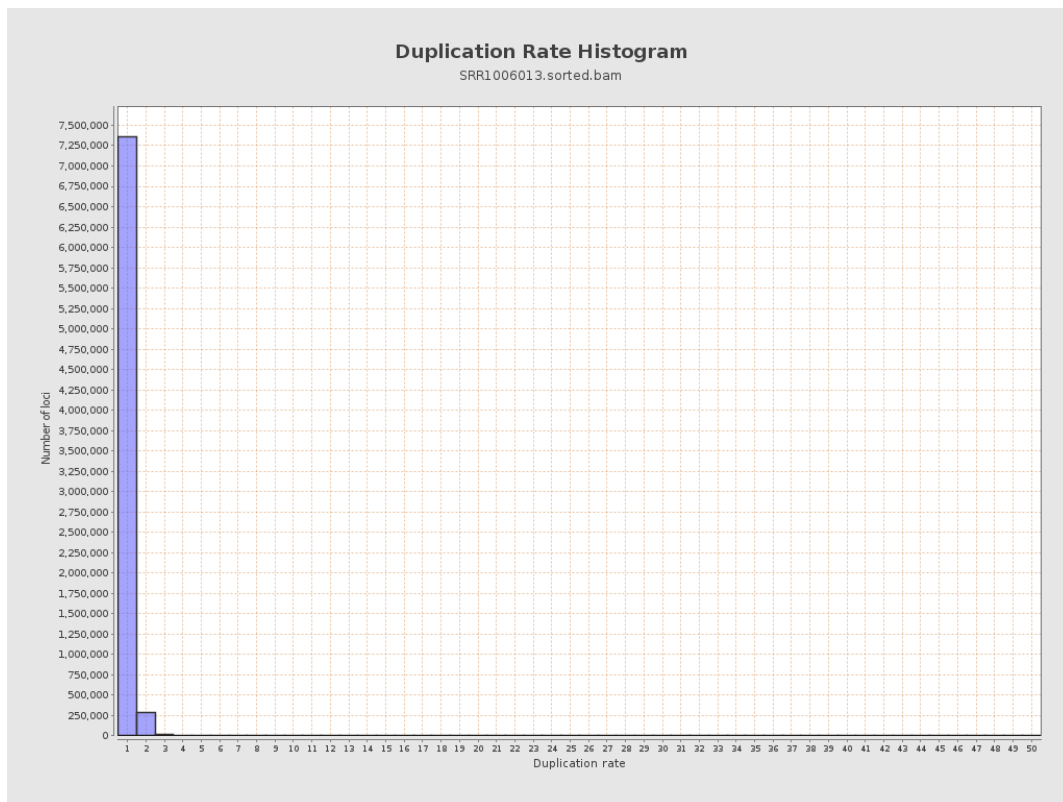
5. Results : Coverage Histogram (0-50X)



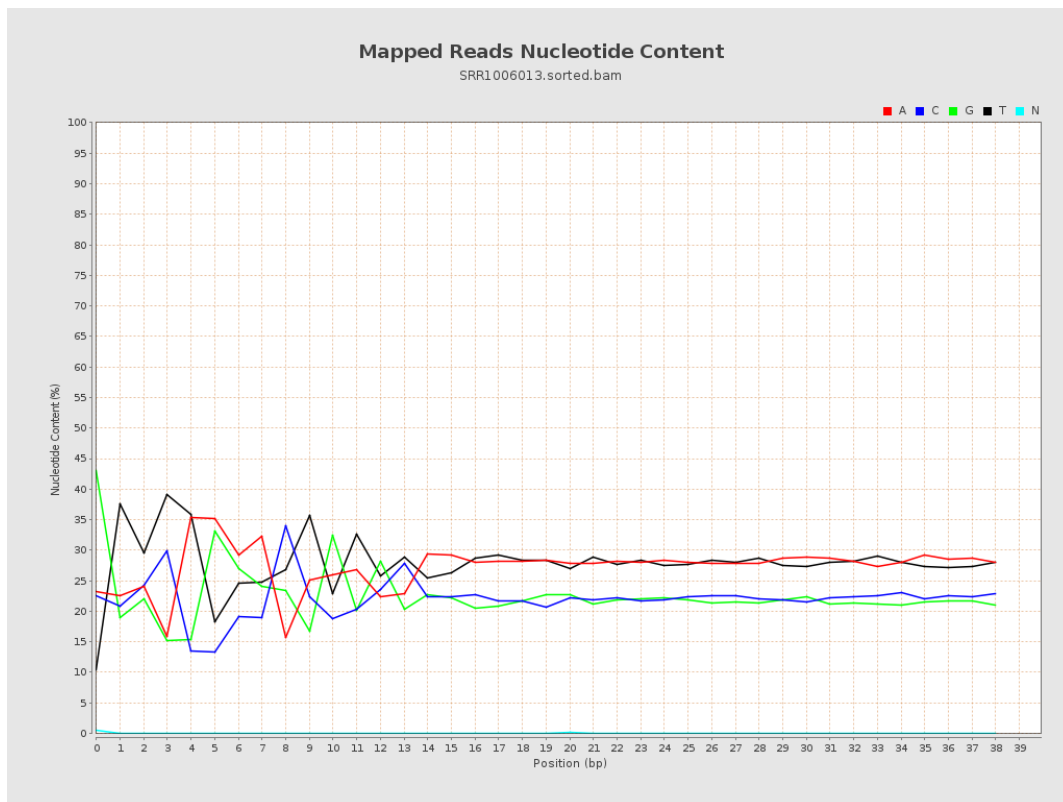
6. Results : Genome Fraction Coverage



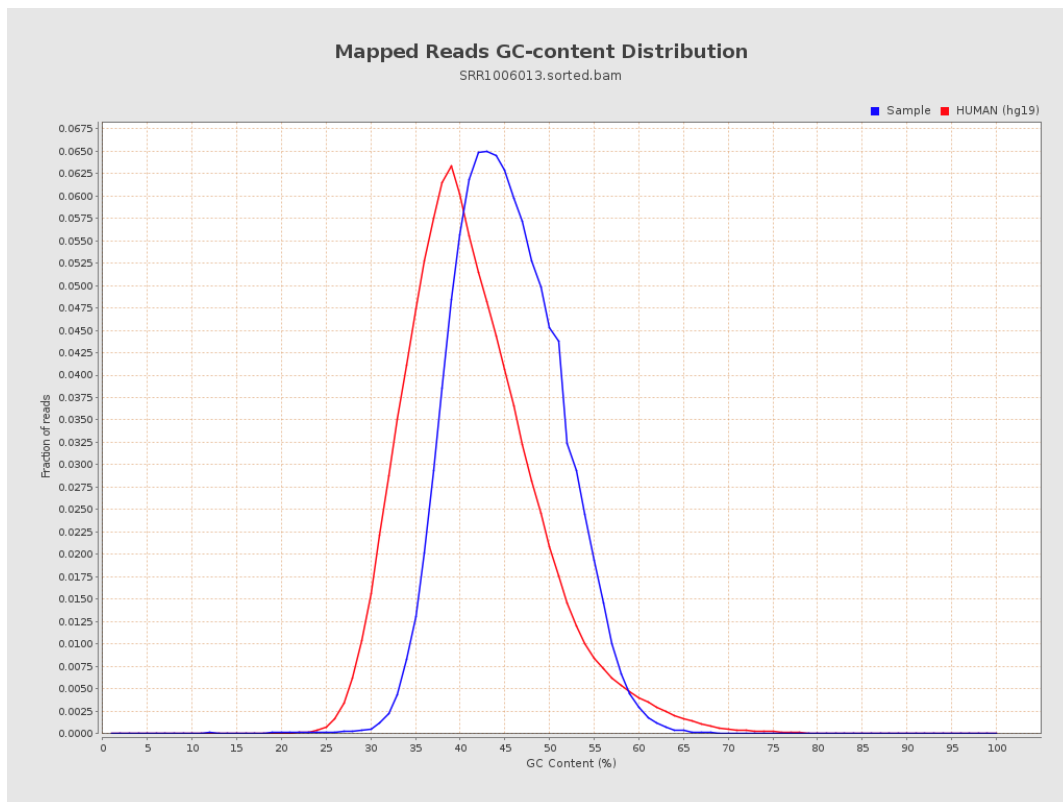
7. Results : Duplication Rate Histogram



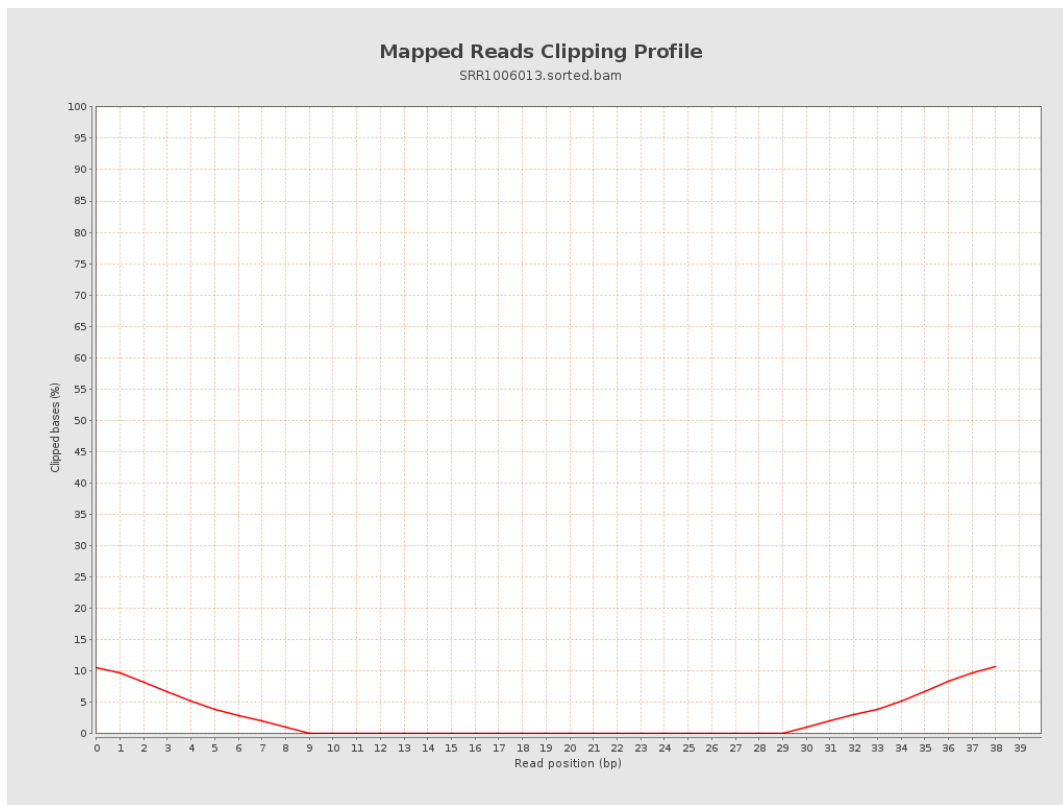
8. Results : Mapped Reads Nucleotide Content



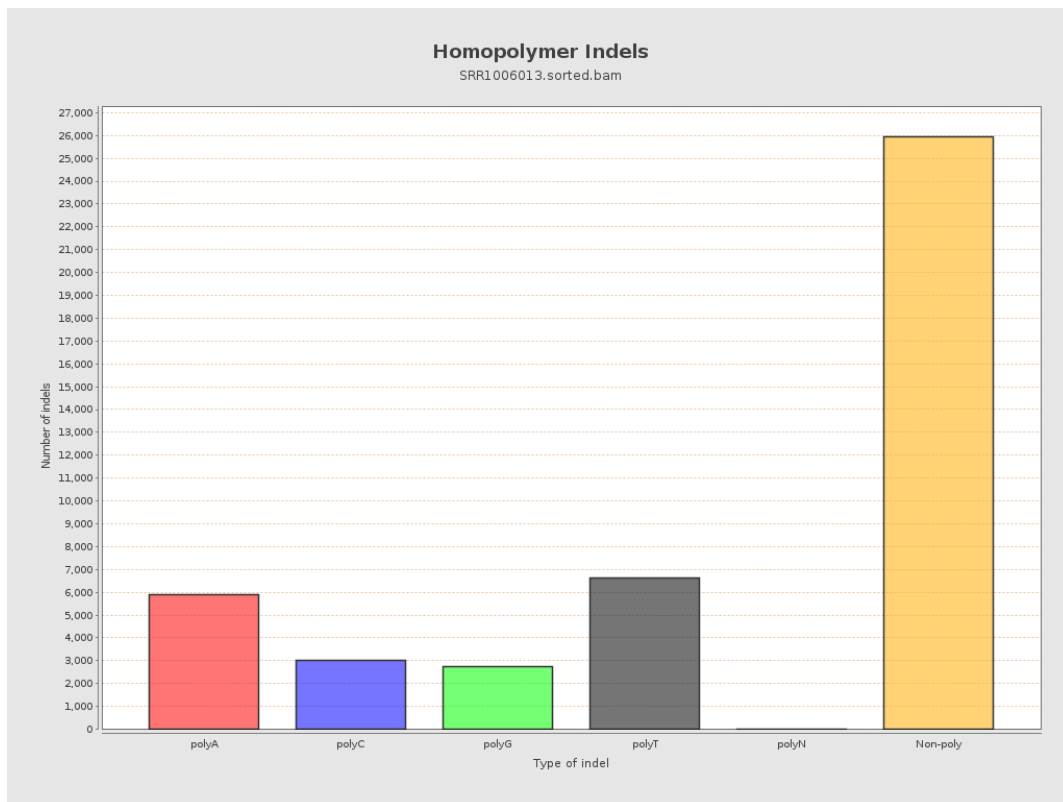
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



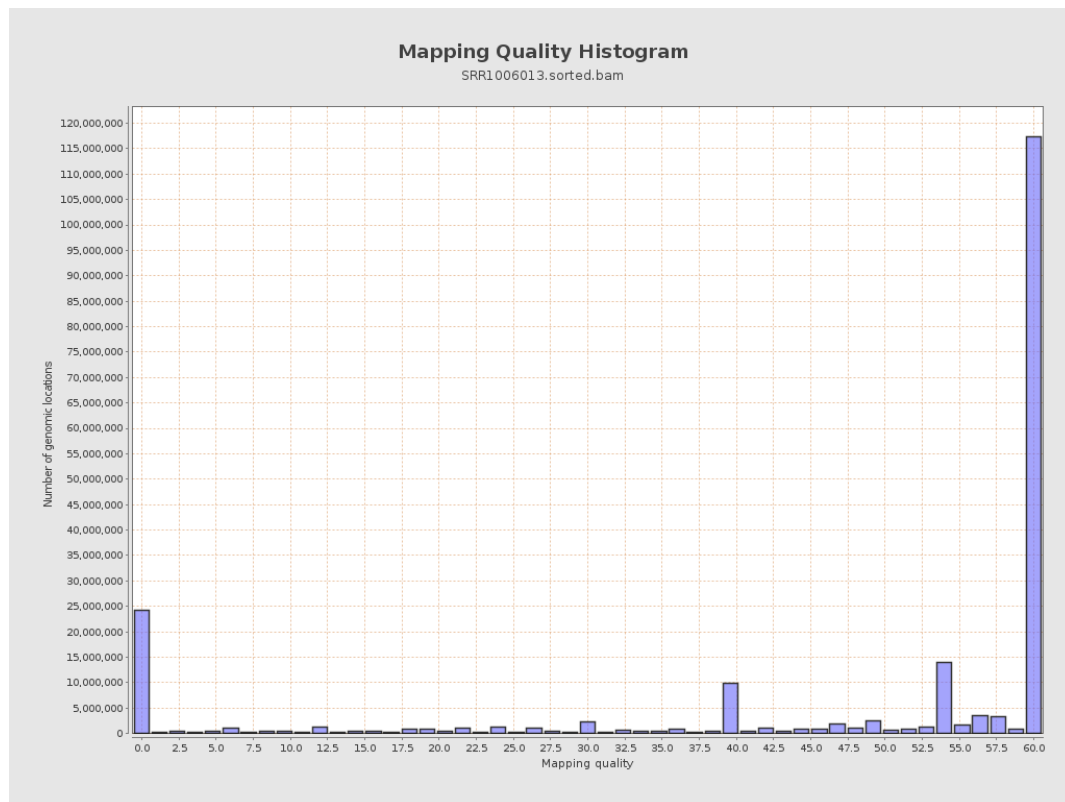
11. Results : Homopolymer Indels



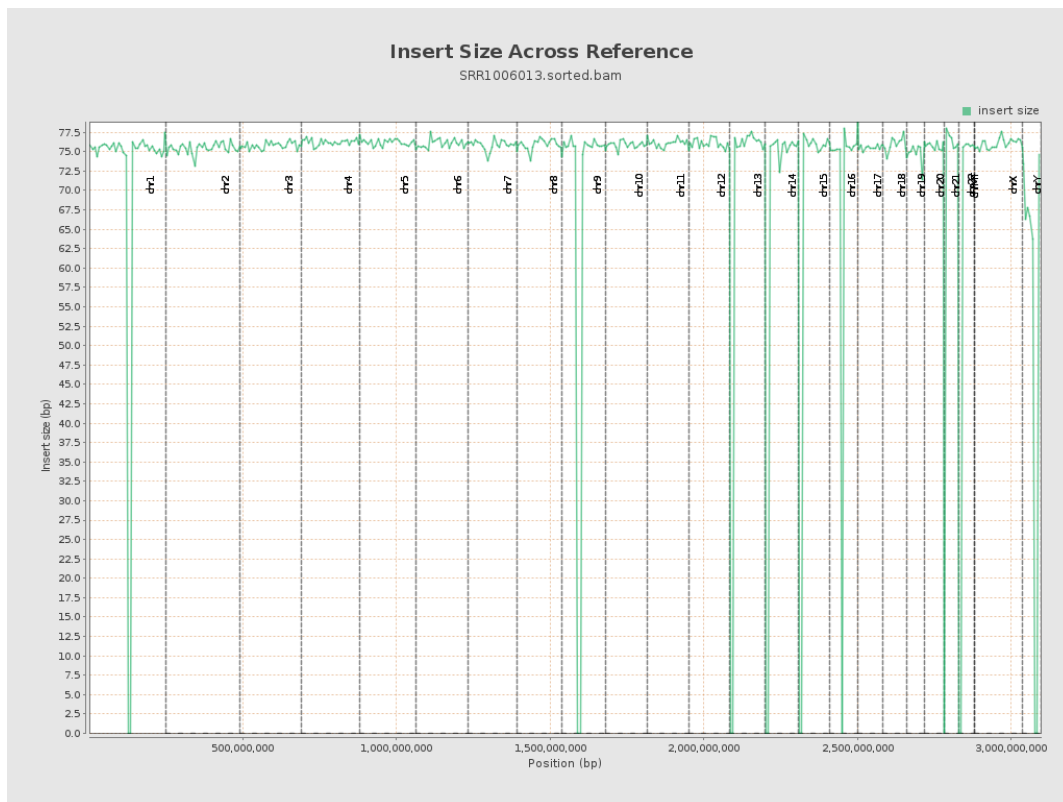
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

