

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 17:07:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046484.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_SRR2046484 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046484_1.fastq.gz SRR2046484_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 17:07:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046484.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,437,376
Mapped reads	13,380,799 / 99.58%
Unmapped reads	56,577 / 0.42%
Mapped paired reads	13,380,799 / 99.58%
Mapped reads, first in pair	6,703,201 / 49.88%
Mapped reads, second in pair	6,677,598 / 49.69%
Mapped reads, both in pair	13,342,146 / 99.29%
Mapped reads, singletons	38,653 / 0.29%
Secondary alignments	0
Supplementary alignments	49,787 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	9,950,199 / 74.05%
Duplication rate	22.32%
Clipped reads	1,275,295 / 9.49%

2.2. ACGT Content

Number/percentage of A's	333,739,383 / 25.33%
Number/percentage of C's	325,000,045 / 24.66%
Number/percentage of T's	332,147,772 / 25.21%
Number/percentage of G's	326,773,653 / 24.8%
Number/percentage of N's	118,858 / 0.01%

GC Percentage	49.46%
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2.3. Coverage

Mean	0.4258
Standard Deviation	59.6592

2.4. Mapping Quality

Mean Mapping Quality	53.18
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2.5. Insert size

Mean	18,259.22
Standard Deviation	1,275,439.89
P25/Median/P75	132 / 164 / 202

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	6,002,500
Insertions	130,443
Mapped reads with at least one insertion	0.95%
Deletions	120,807
Mapped reads with at least one deletion	0.88%
Homopolymer indels	49.65%

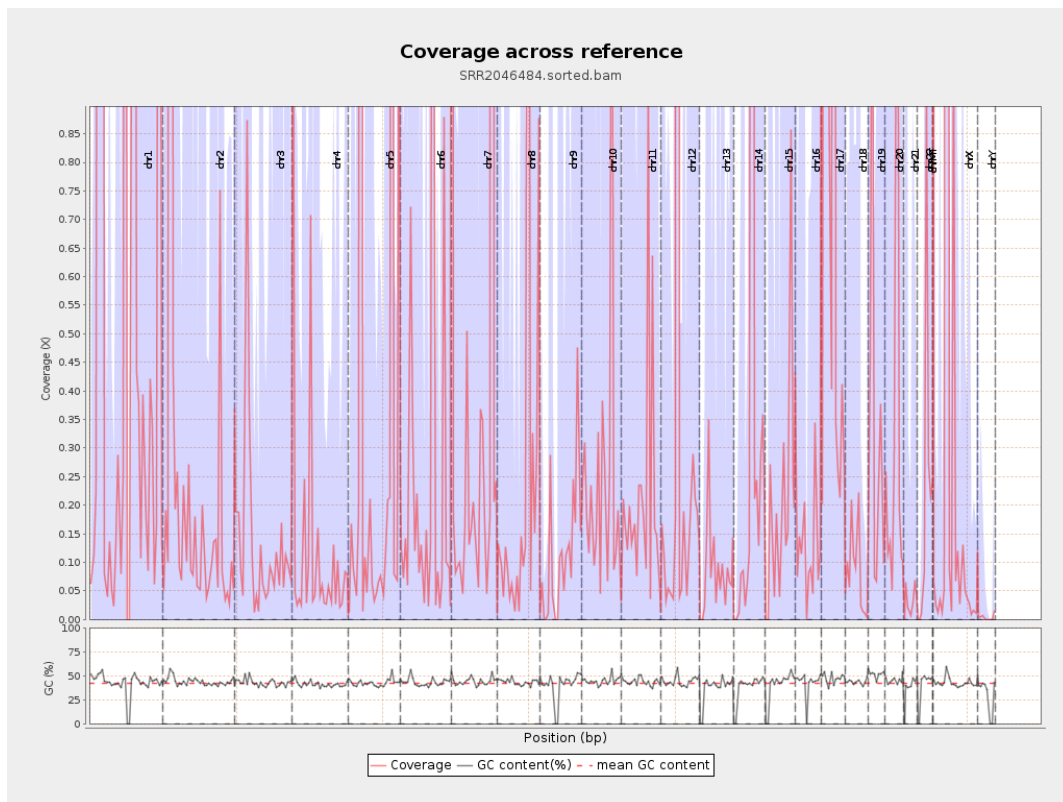
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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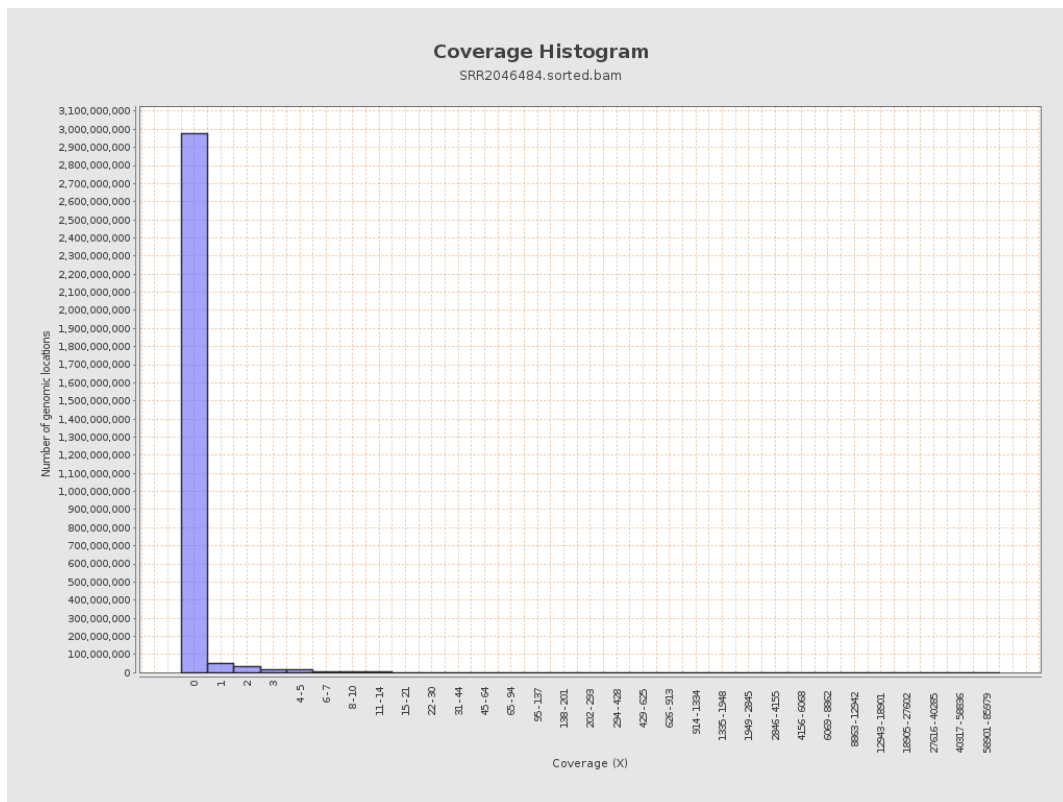
		bases	coverage	deviation
chr1	249250621	214074950	0.8589	68.8706
chr2	243199373	105908496	0.4355	64.278
chr3	198022430	28807294	0.1455	6.8481
chr4	191154276	24337596	0.1273	17.3759
chr5	180915260	109974293	0.6079	65.6285
chr6	171115067	43223403	0.2526	24.3118
chr7	159138663	153629325	0.9654	143.1182
chr8	146364022	38303003	0.2617	38.6759
chr9	141213431	16066549	0.1138	5.4251
chr10	135534747	36223588	0.2673	14.3254
chr11	135006516	29647645	0.2196	21.3573
chr12	133851895	162750211	1.2159	90.0873
chr13	115169878	9986112	0.0867	3.2109
chr14	107349540	46342326	0.4317	51.9007
chr15	102531392	20187996	0.1969	11.9692
chr16	90354753	12611874	0.1396	4.596
chr17	81195210	126509232	1.5581	85.3036
chr18	78077248	6653851	0.0852	2.3675
chr19	59128983	21350369	0.3611	18.253
chr20	63025520	20610050	0.327	26.9081
chr21	48129895	1611765	0.0335	1.1051
chr22	51304566	12265952	0.2391	21.297
chrMT	16571	282492	17.0474	6.515
chrX	155270560	76565081	0.4931	120.0603

chrY	59373566	234714	0.004	0.1751
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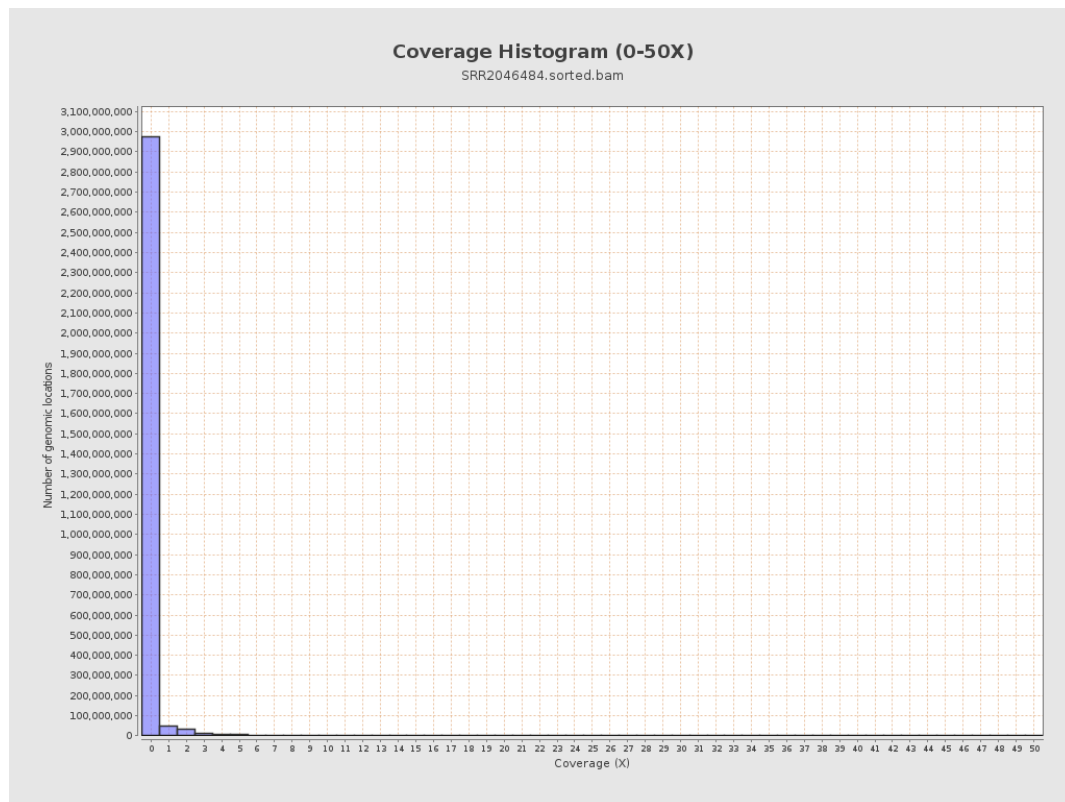
3. Results : Coverage across reference



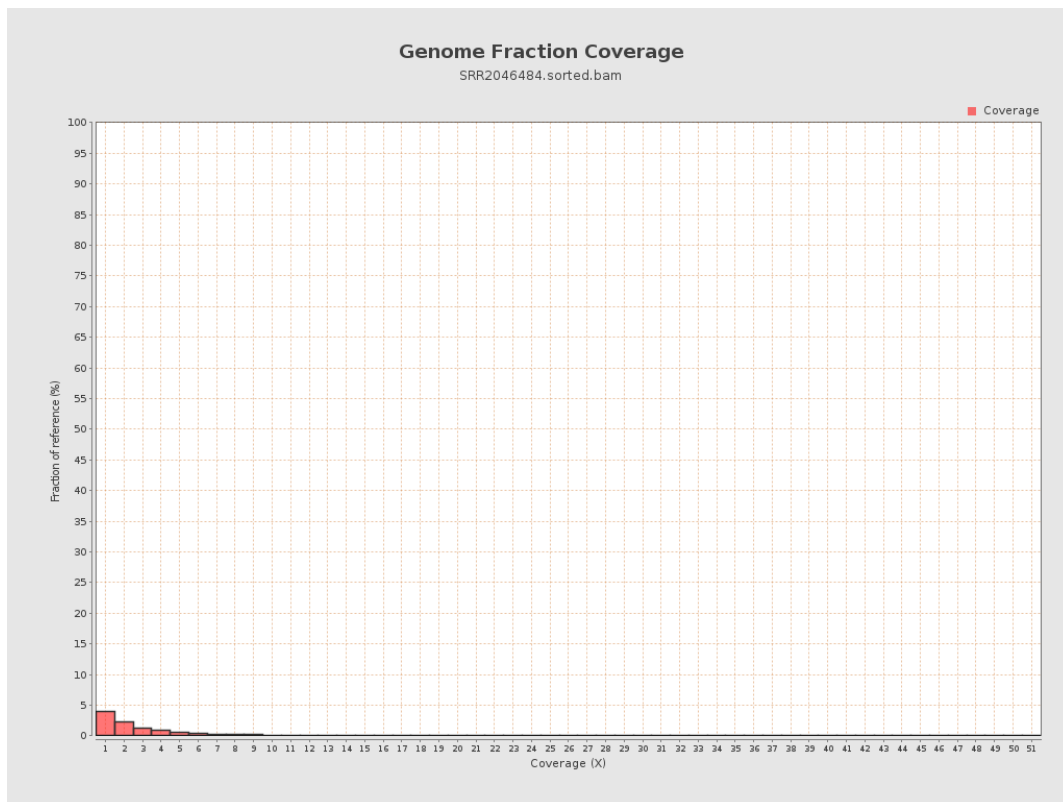
4. Results : Coverage Histogram



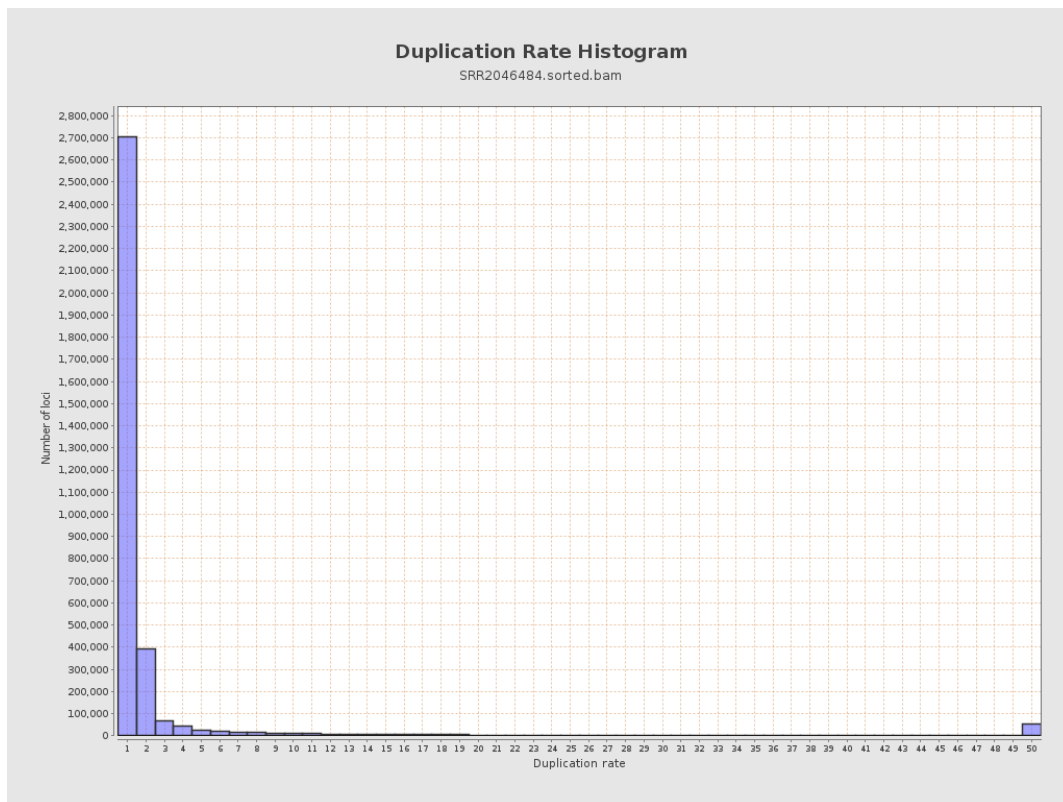
5. Results : Coverage Histogram (0-50X)



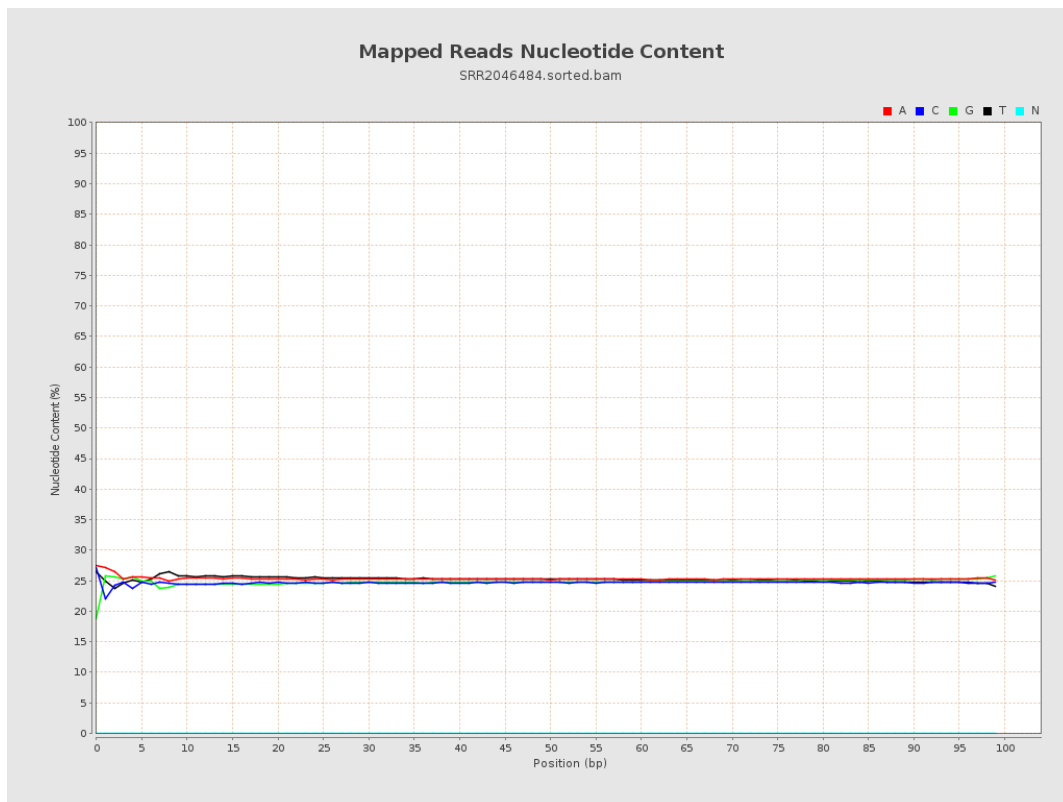
6. Results : Genome Fraction Coverage



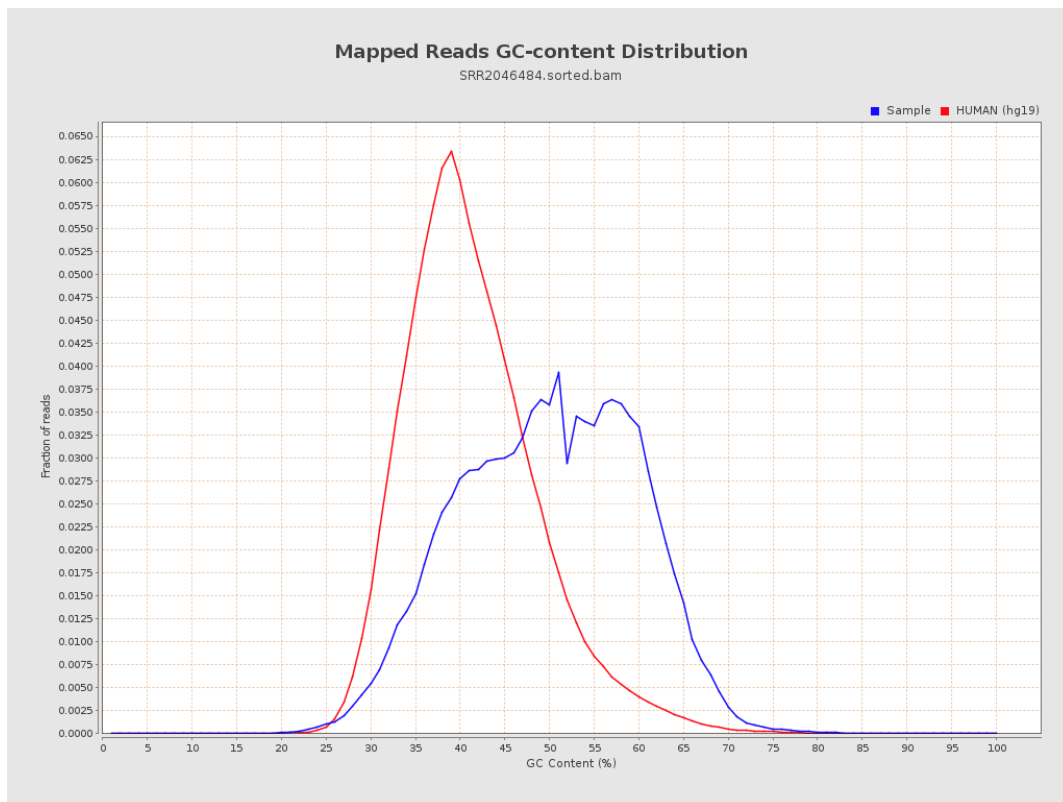
7. Results : Duplication Rate Histogram



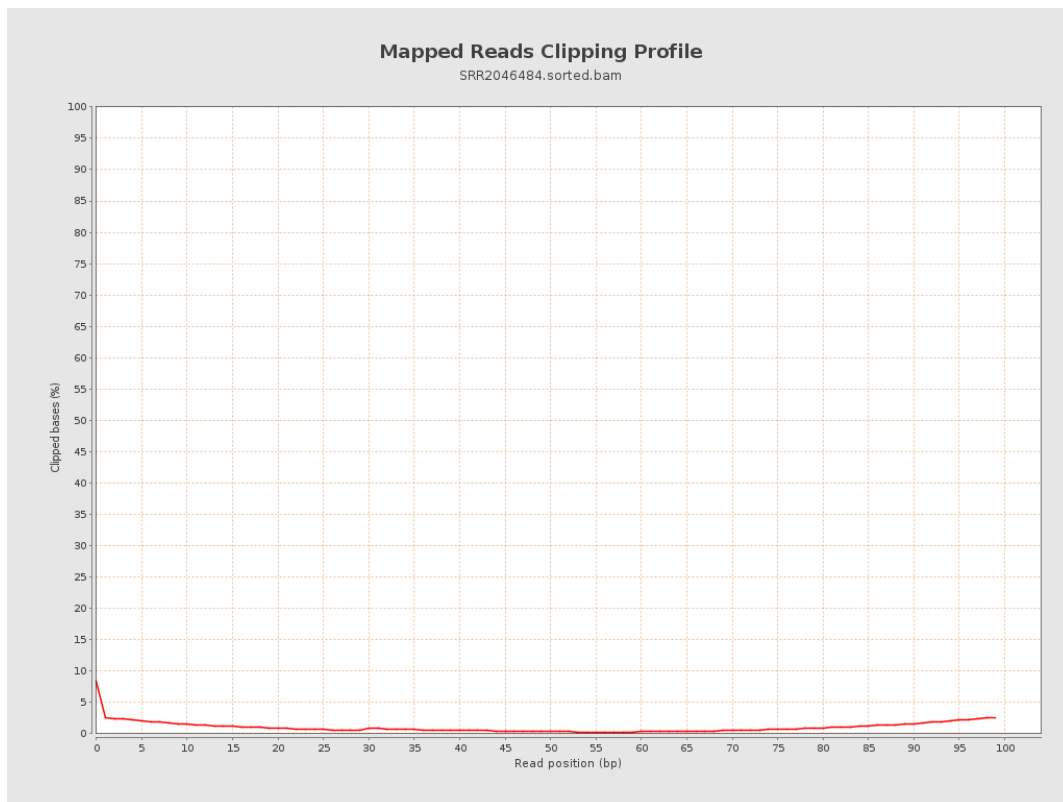
8. Results : Mapped Reads Nucleotide Content



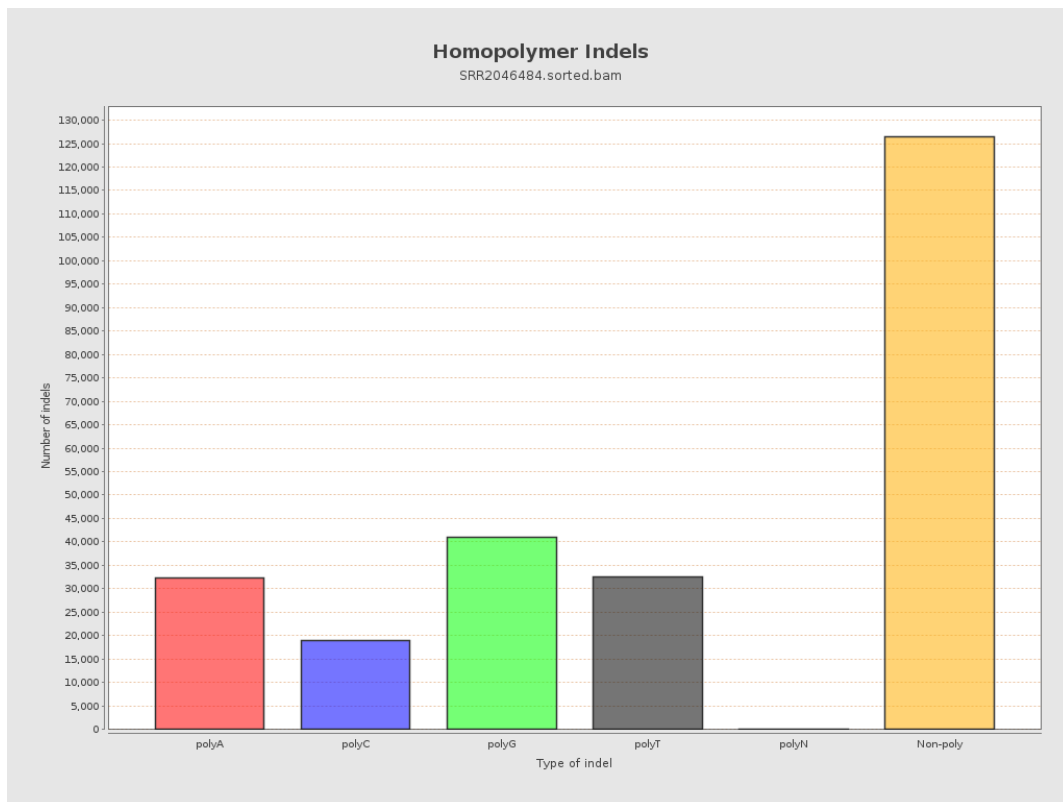
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



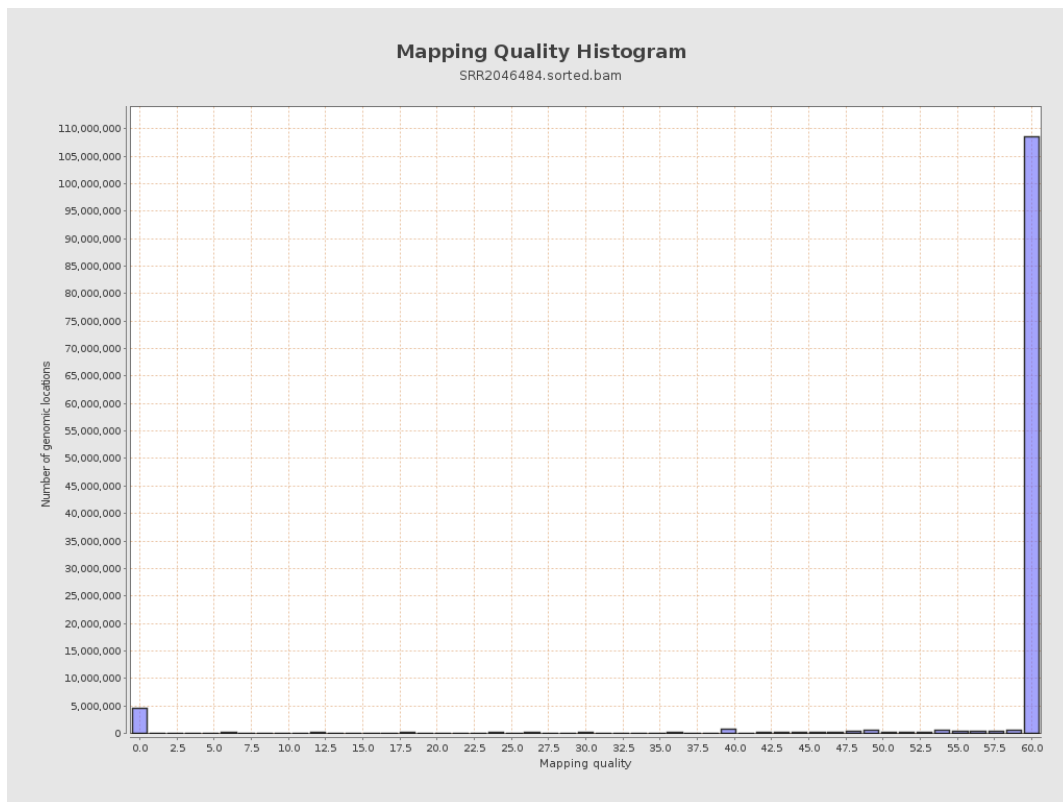
11. Results : Homopolymer Indels



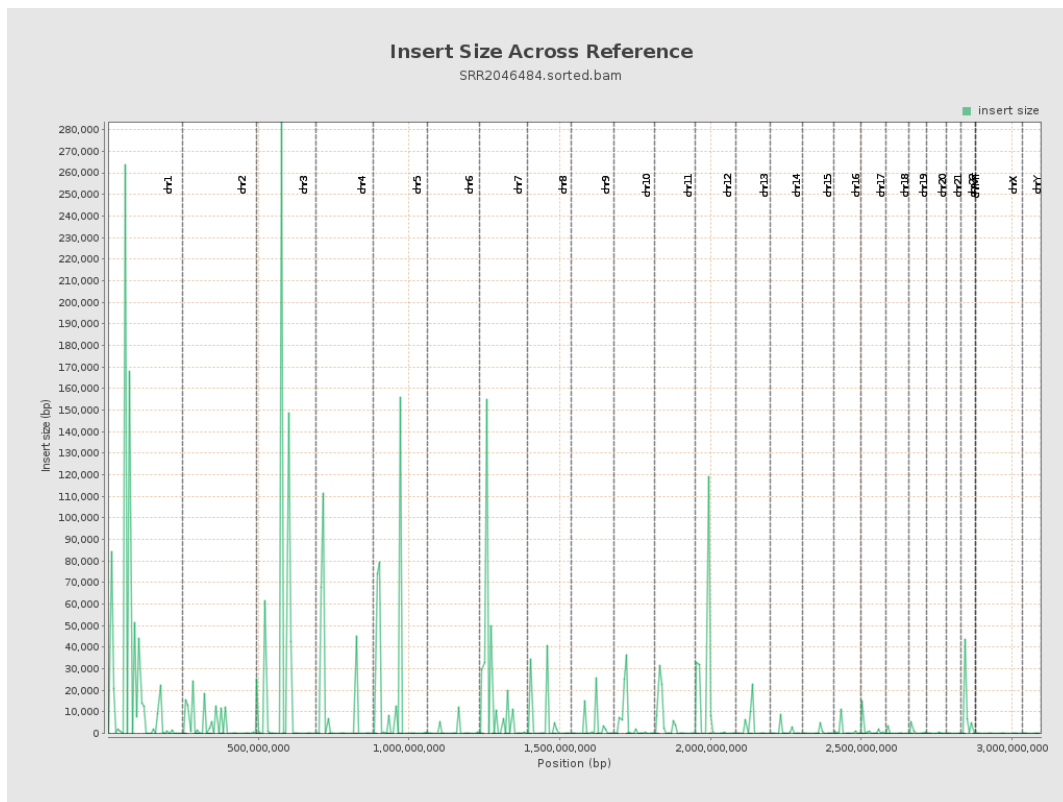
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

