

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 13:39:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046414.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_SRR2046414 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046414_1.fastq.gz SRR2046414_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 13:39:15 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046414.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,791,526
Mapped reads	6,759,371 / 99.53%
Unmapped reads	32,155 / 0.47%
Mapped paired reads	6,759,371 / 99.53%
Mapped reads, first in pair	3,381,975 / 49.8%
Mapped reads, second in pair	3,377,396 / 49.73%
Mapped reads, both in pair	6,737,016 / 99.2%
Mapped reads, singletons	22,355 / 0.33%
Secondary alignments	0
Supplementary alignments	40,951 / 0.6%
Read min/max/mean length	30 / 100 / 100.25
Duplicated reads (estimated)	4,777,652 / 70.35%
Duplication rate	39.26%
Clipped reads	964,588 / 14.2%

2.2. ACGT Content

Number/percentage of A's	196,447,119 / 29.71%
Number/percentage of C's	134,575,045 / 20.35%
Number/percentage of T's	198,485,118 / 30.01%
Number/percentage of G's	131,751,291 / 19.92%
Number/percentage of N's	58,205 / 0.01%

GC Percentage	40.27%
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2.3. Coverage

Mean	0.2137
Standard Deviation	14.8169

2.4. Mapping Quality

Mean Mapping Quality	53.37
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2.5. Insert size

Mean	18,016.89
Standard Deviation	1,335,864.53
P25/Median/P75	118 / 147 / 179

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	2,585,549
Insertions	61,680
Mapped reads with at least one insertion	0.89%
Deletions	72,356
Mapped reads with at least one deletion	1.04%
Homopolymer indels	48.75%

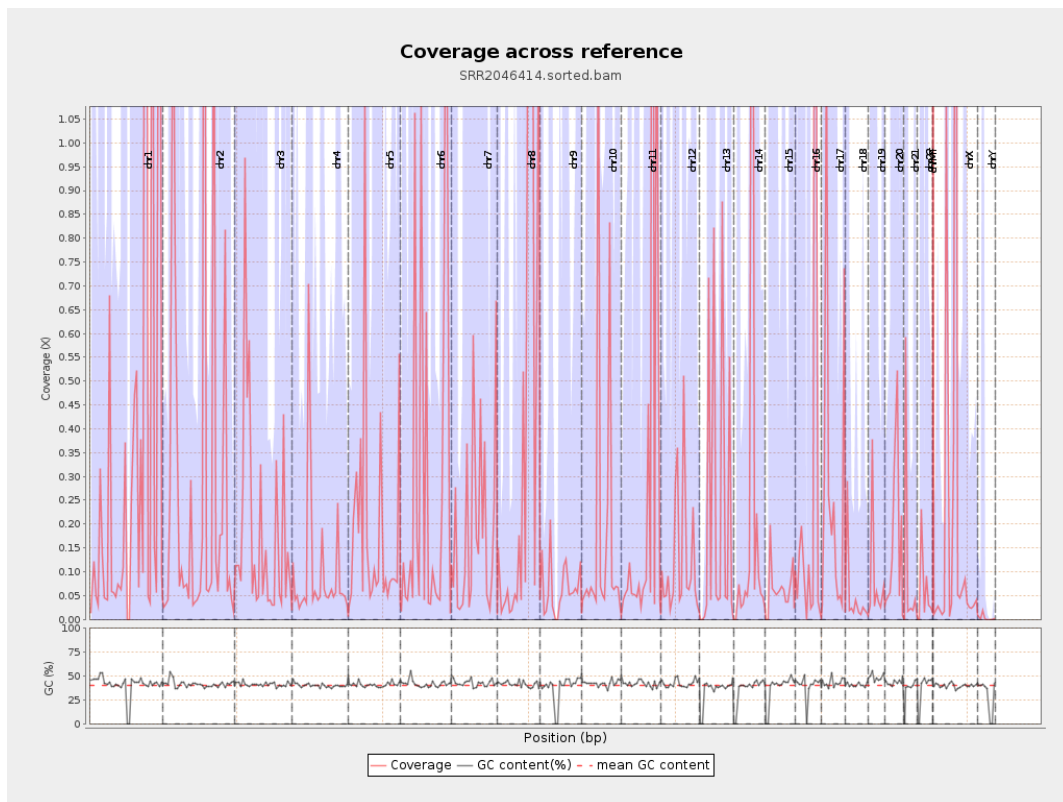
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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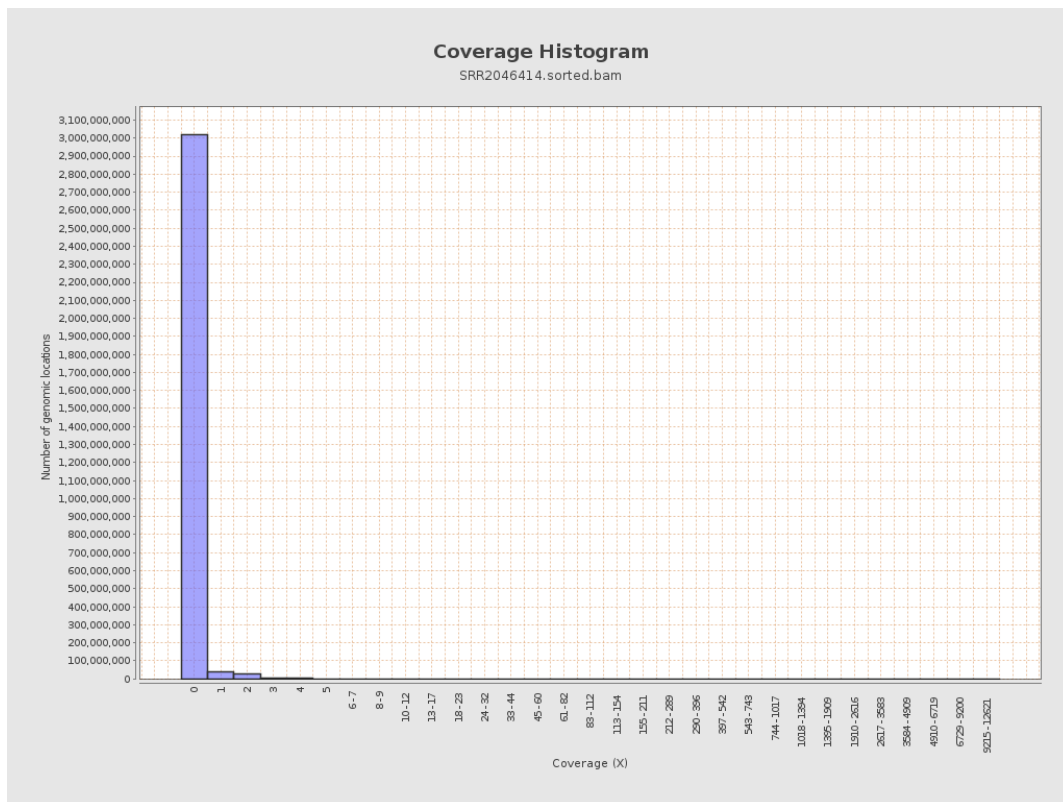
		bases	coverage	deviation
chr1	249250621	93995624	0.3771	19.4221
chr2	243199373	72787442	0.2993	20.8492
chr3	198022430	36074948	0.1822	9.8613
chr4	191154276	19607523	0.1026	5.606
chr5	180915260	33870927	0.1872	11.5984
chr6	171115067	50493797	0.2951	14.5953
chr7	159138663	31014137	0.1949	11.7616
chr8	146364022	70466615	0.4814	25.5784
chr9	141213431	9290523	0.0658	3.2488
chr10	135534747	25196021	0.1859	14.9278
chr11	135006516	41415486	0.3068	22.572
chr12	133851895	16714111	0.1249	6.8752
chr13	115169878	25628117	0.2225	16.0813
chr14	107349540	23920938	0.2228	11.6173
chr15	102531392	6702808	0.0654	2.6983
chr16	90354753	22064046	0.2442	15.3659
chr17	81195210	22225862	0.2737	13.3134
chr18	78077248	3671081	0.047	2.7193
chr19	59128983	4929395	0.0834	3.6905
chr20	63025520	10653677	0.169	9.2217
chr21	48129895	5388390	0.112	12.9965
chr22	51304566	3048947	0.0594	7.7142
chrMT	16571	39794	2.4014	2.2838
chrX	155270560	32118711	0.2069	21.3111

chrY	59373566	205982	0.0035	0.749
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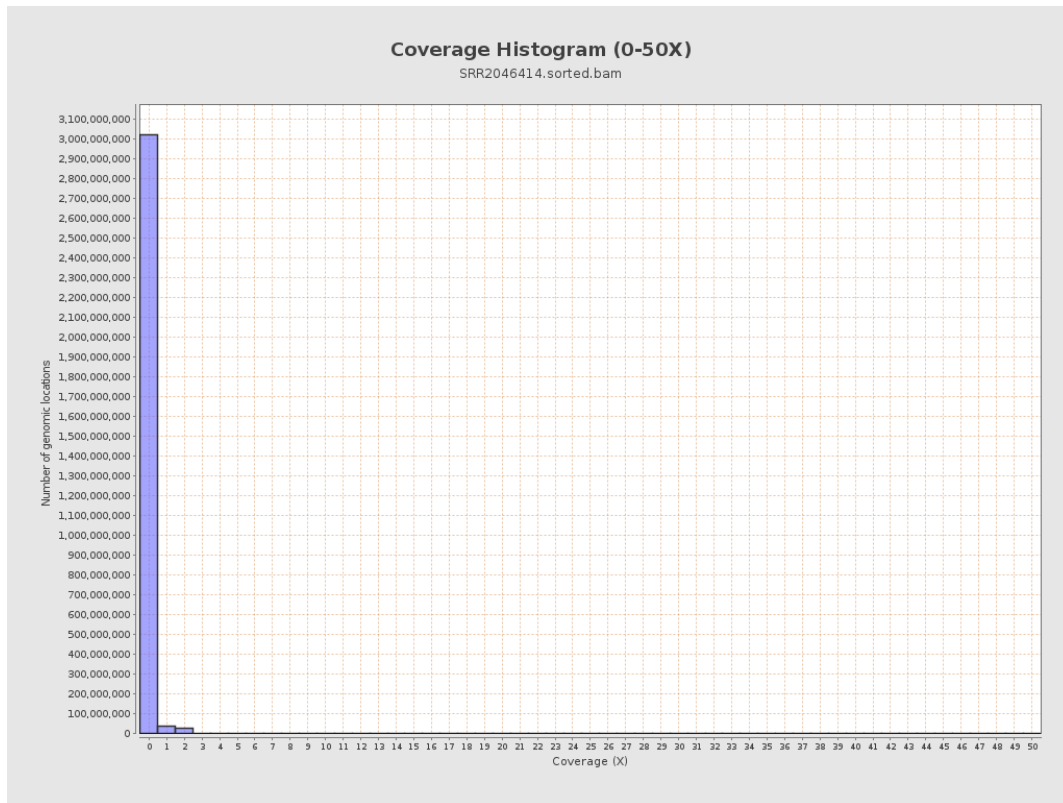
3. Results : Coverage across reference



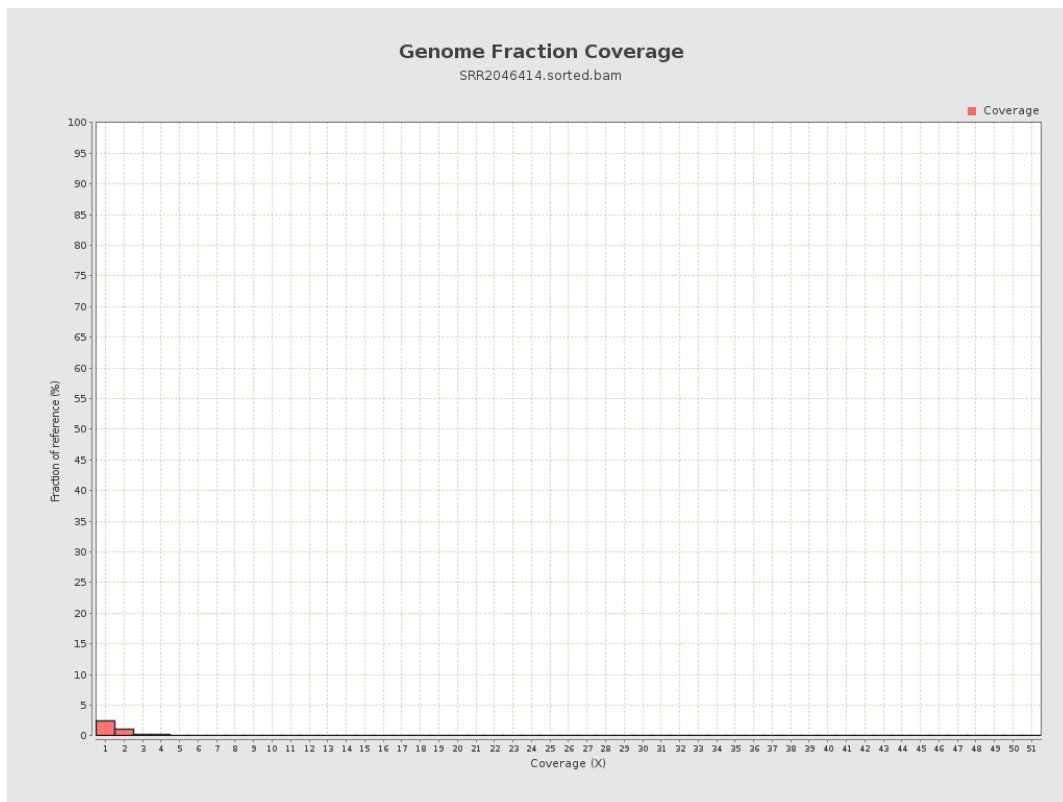
4. Results : Coverage Histogram



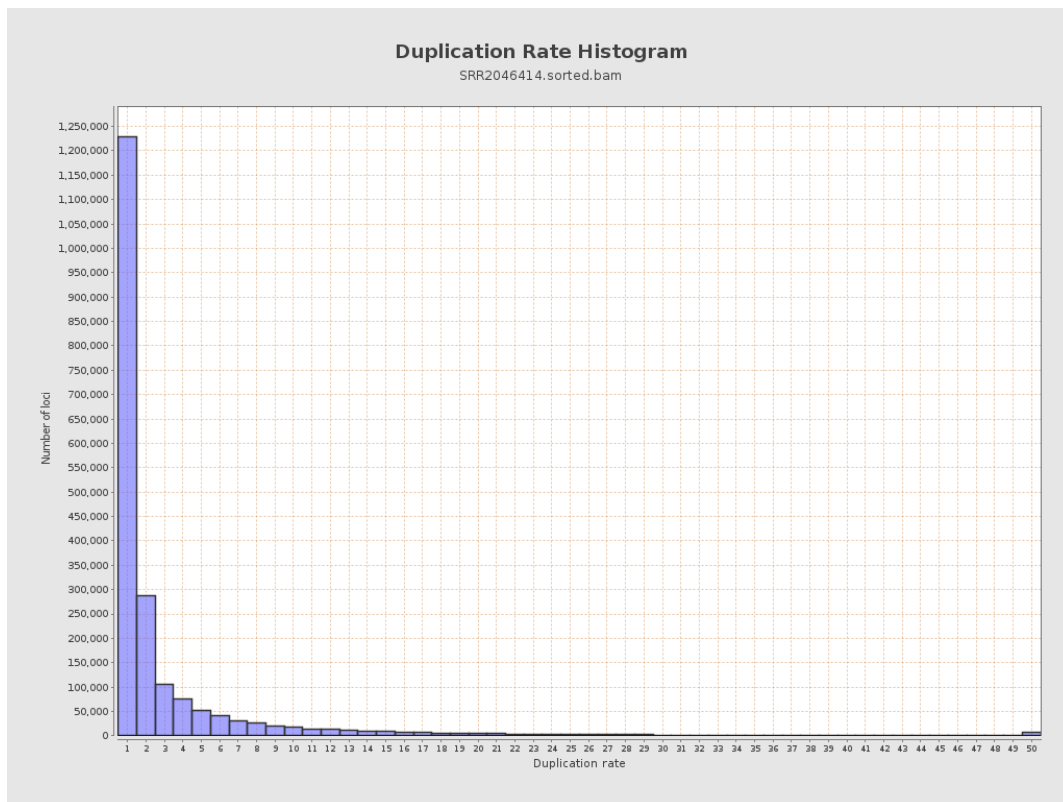
5. Results : Coverage Histogram (0-50X)



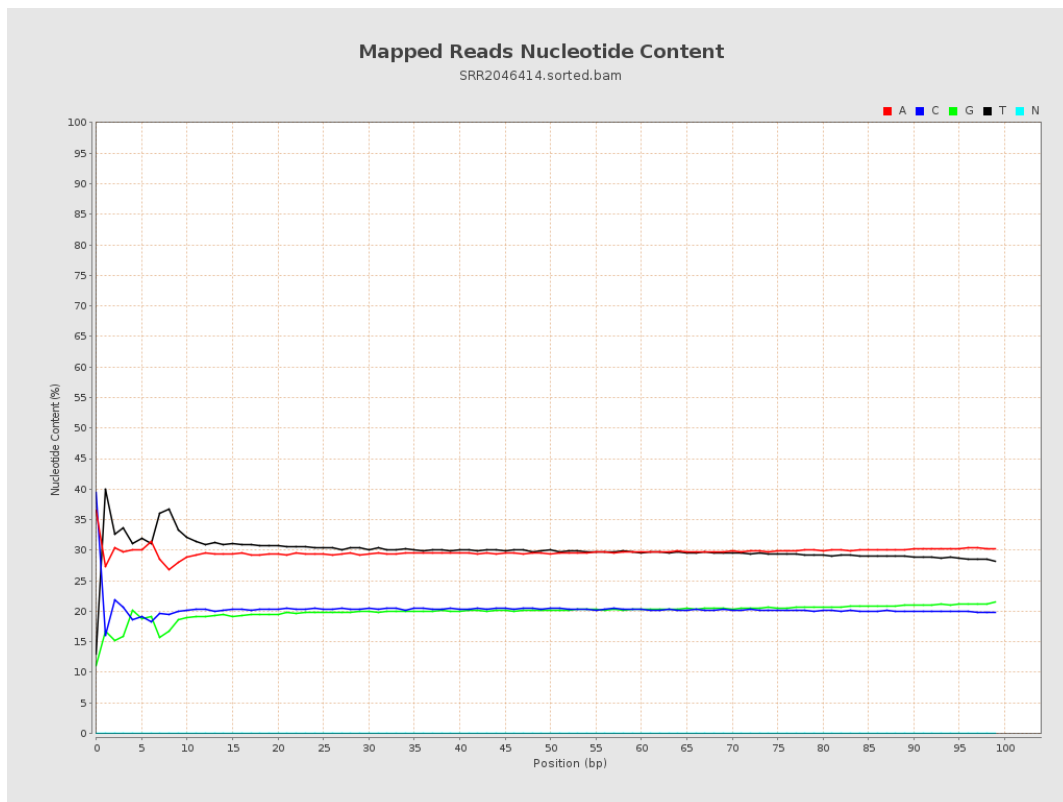
6. Results : Genome Fraction Coverage



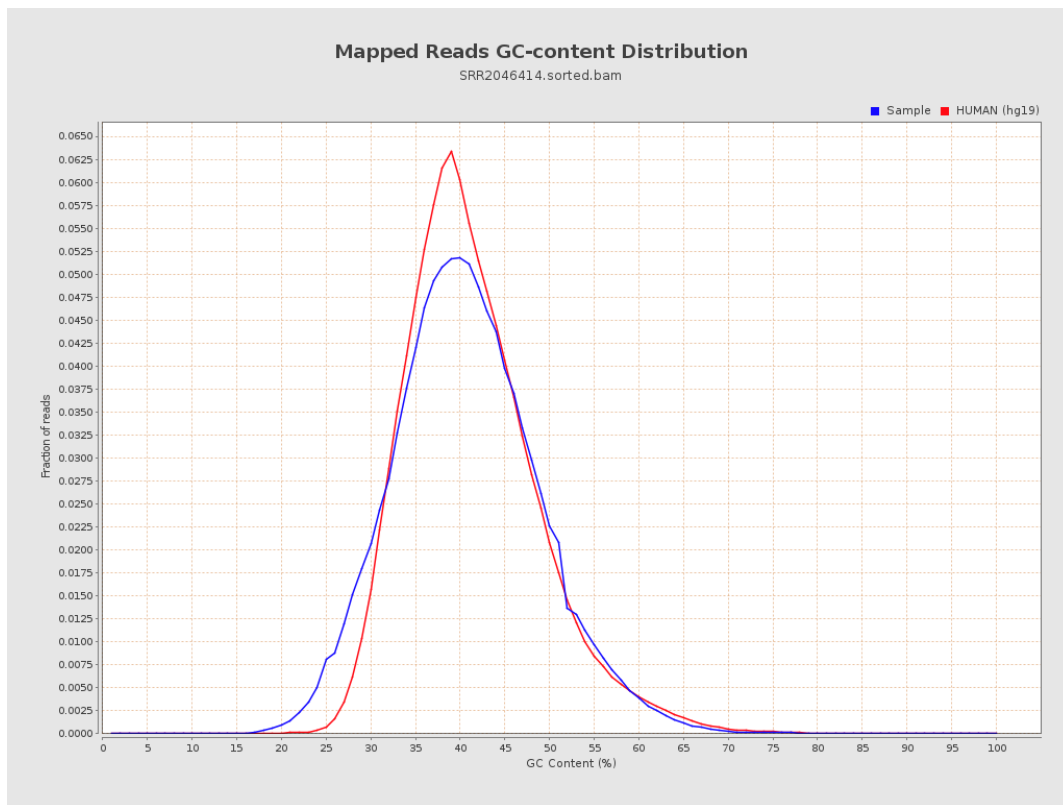
7. Results : Duplication Rate Histogram



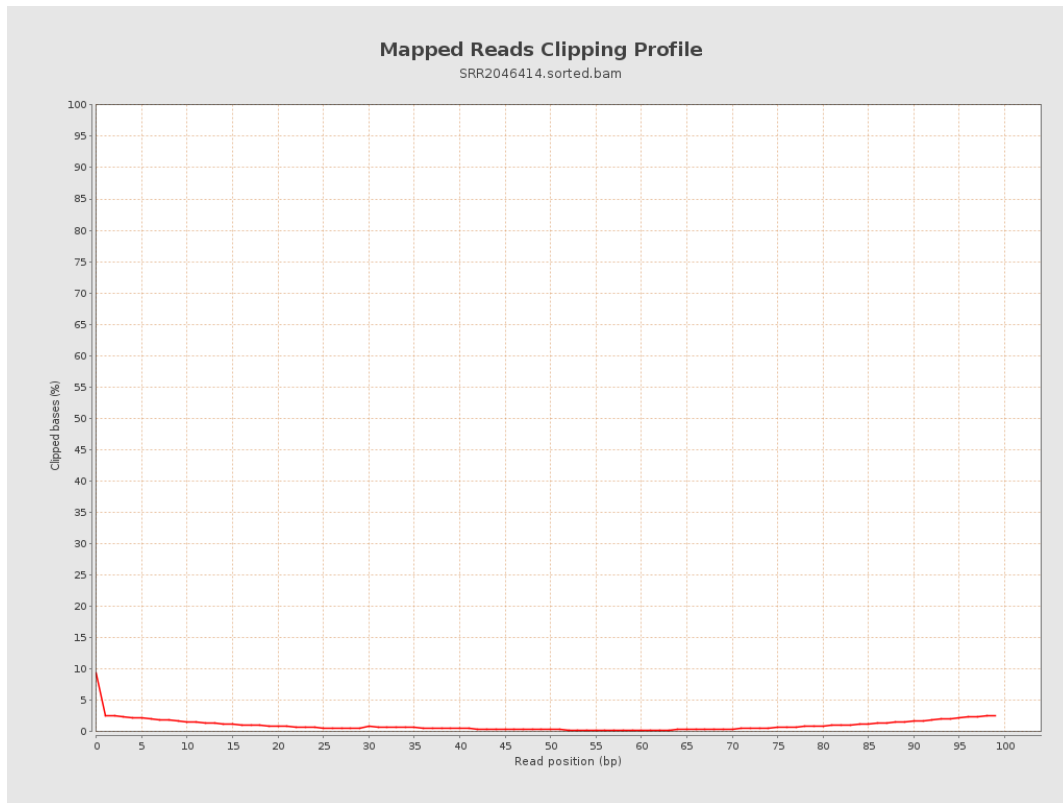
8. Results : Mapped Reads Nucleotide Content



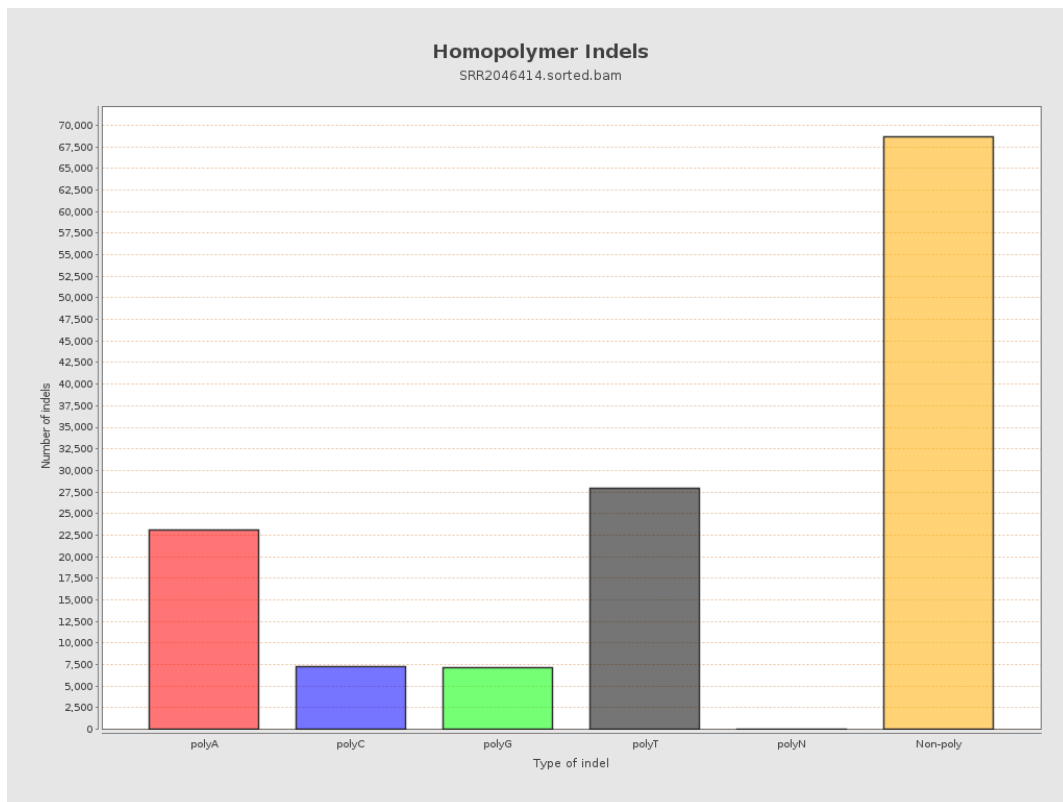
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



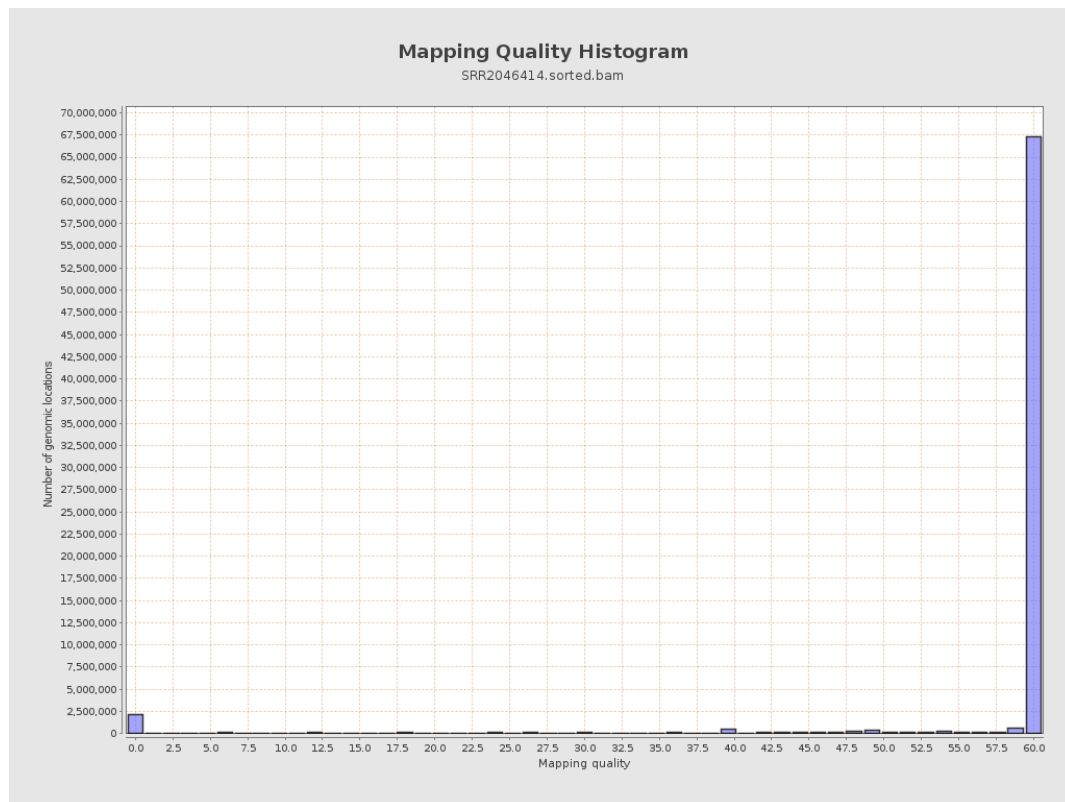
11. Results : Homopolymer Indels



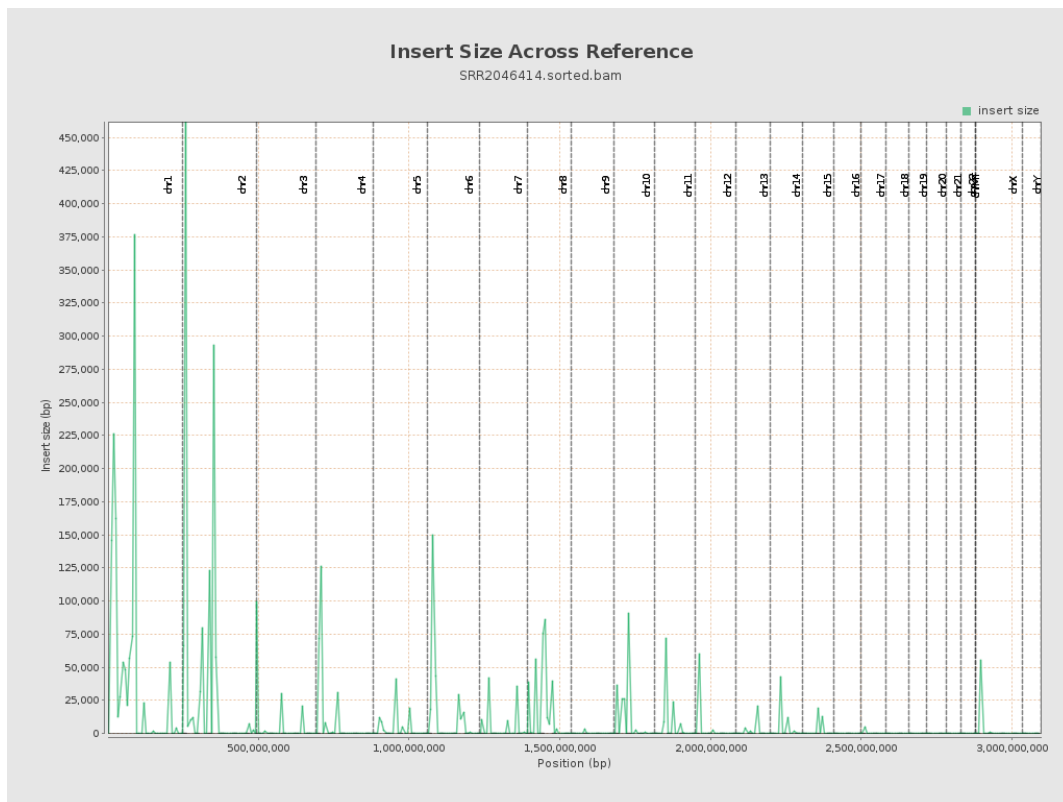
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

