

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 15:31:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046453.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_SRR2046453 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046453_1.fastq.gz SRR2046453_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 15:31:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046453.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,366,800
Mapped reads	5,240,517 / 97.65%
Unmapped reads	126,283 / 2.35%
Mapped paired reads	5,240,517 / 97.65%
Mapped reads, first in pair	2,673,154 / 49.81%
Mapped reads, second in pair	2,567,363 / 47.84%
Mapped reads, both in pair	5,124,696 / 95.49%
Mapped reads, singletons	115,821 / 2.16%
Secondary alignments	0
Supplementary alignments	35,627 / 0.66%
Read min/max/mean length	30 / 100 / 100.27
Duplicated reads (estimated)	3,406,638 / 63.48%
Duplication rate	31%
Clipped reads	1,124,635 / 20.96%

2.2. ACGT Content

Number/percentage of A's	149,620,316 / 29.66%
Number/percentage of C's	103,003,351 / 20.42%
Number/percentage of T's	149,338,602 / 29.6%
Number/percentage of G's	102,505,627 / 20.32%
Number/percentage of N's	39,487 / 0.01%

GC Percentage	40.73%
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2.3. Coverage

Mean	0.163
Standard Deviation	16.5506

2.4. Mapping Quality

Mean Mapping Quality	51.28
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2.5. Insert size

Mean	58,759.17
Standard Deviation	2,275,691.9
P25/Median/P75	107 / 135 / 170

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	2,065,042
Insertions	44,736
Mapped reads with at least one insertion	0.83%
Deletions	54,282
Mapped reads with at least one deletion	1.01%
Homopolymer indels	47.52%

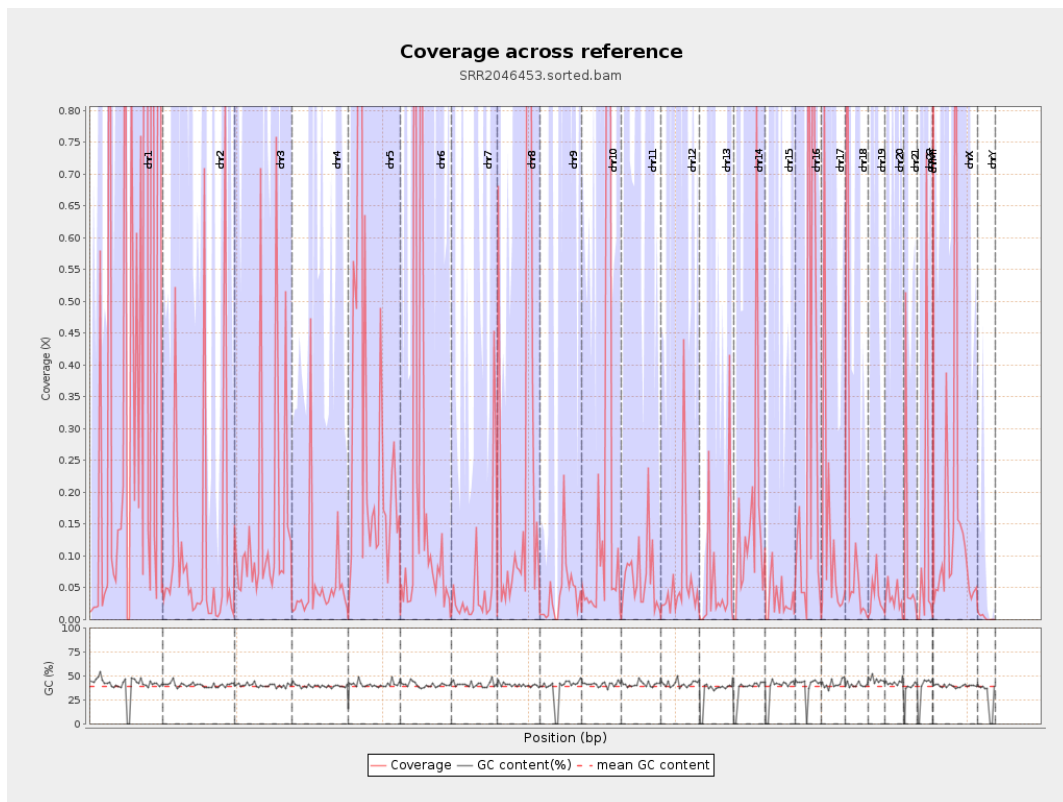
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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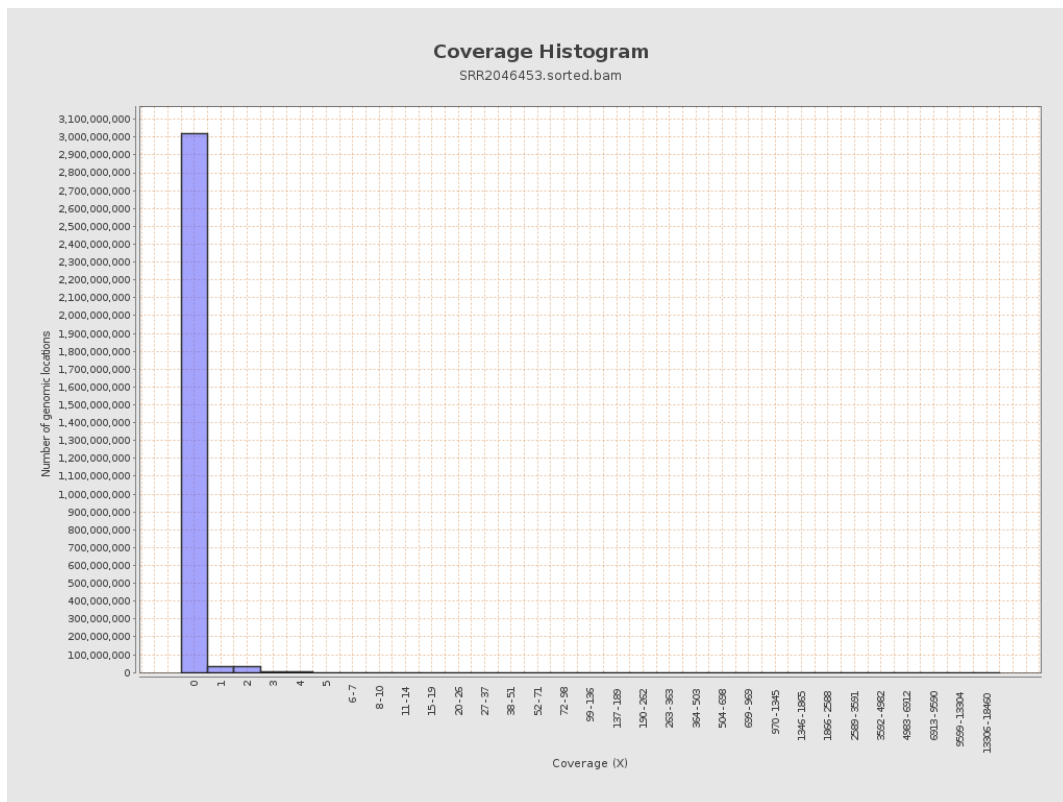
		bases	coverage	deviation
chr1	249250621	117238323	0.4704	31.7012
chr2	243199373	25300737	0.104	10.3454
chr3	198022430	30073251	0.1519	10.2878
chr4	191154276	10733262	0.0561	4.9783
chr5	180915260	61472351	0.3398	21.543
chr6	171115067	35928472	0.21	16.3122
chr7	159138663	9388809	0.059	6.1805
chr8	146364022	40970048	0.2799	28.1364
chr9	141213431	6204663	0.0439	3.1376
chr10	135534747	29171991	0.2152	29.2927
chr11	135006516	9289134	0.0688	2.3065
chr12	133851895	7935531	0.0593	6.0353
chr13	115169878	7463224	0.0648	7.3759
chr14	107349540	16493677	0.1536	9.205
chr15	102531392	3303894	0.0322	2.6157
chr16	90354753	29412642	0.3255	27.2734
chr17	81195210	11353193	0.1398	16.347
chr18	78077248	12418698	0.1591	11.2038
chr19	59128983	2258577	0.0382	0.9464
chr20	63025520	2217984	0.0352	1.263
chr21	48129895	5031783	0.1045	13.5165
chr22	51304566	6761802	0.1318	17.4458
chrMT	16571	65363	3.9444	2.906
chrX	155270560	24011093	0.1546	14.2789

chrY	59373566	160161	0.0027	0.1805
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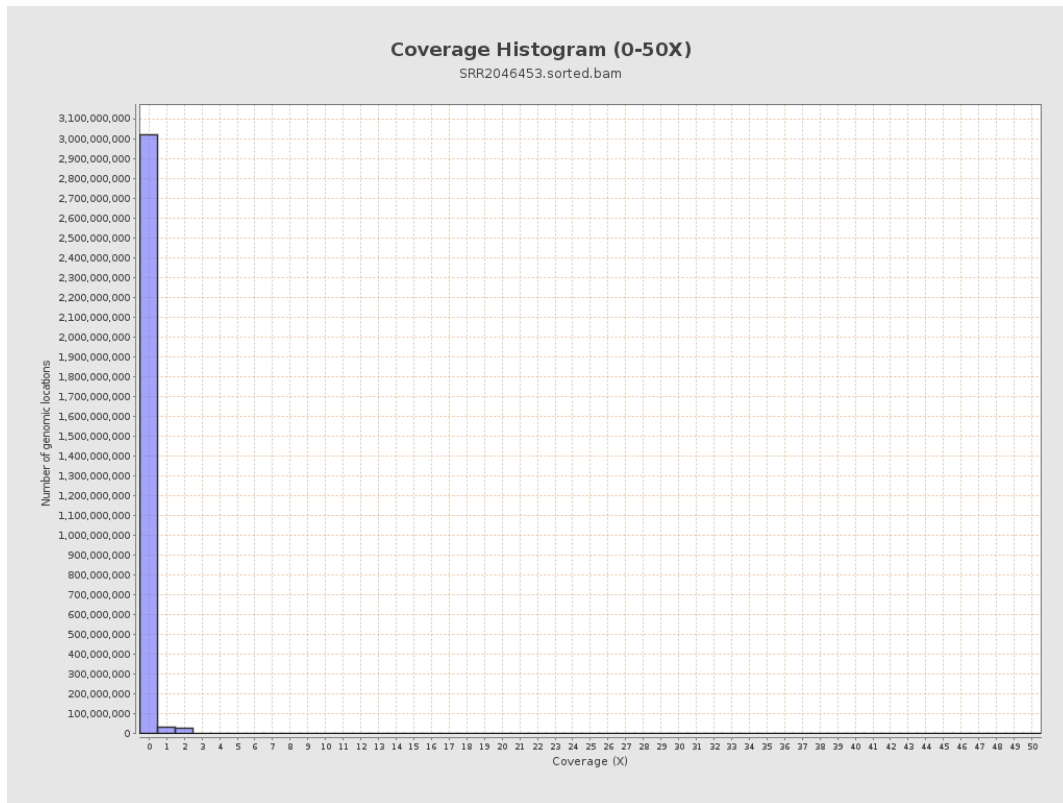
3. Results : Coverage across reference



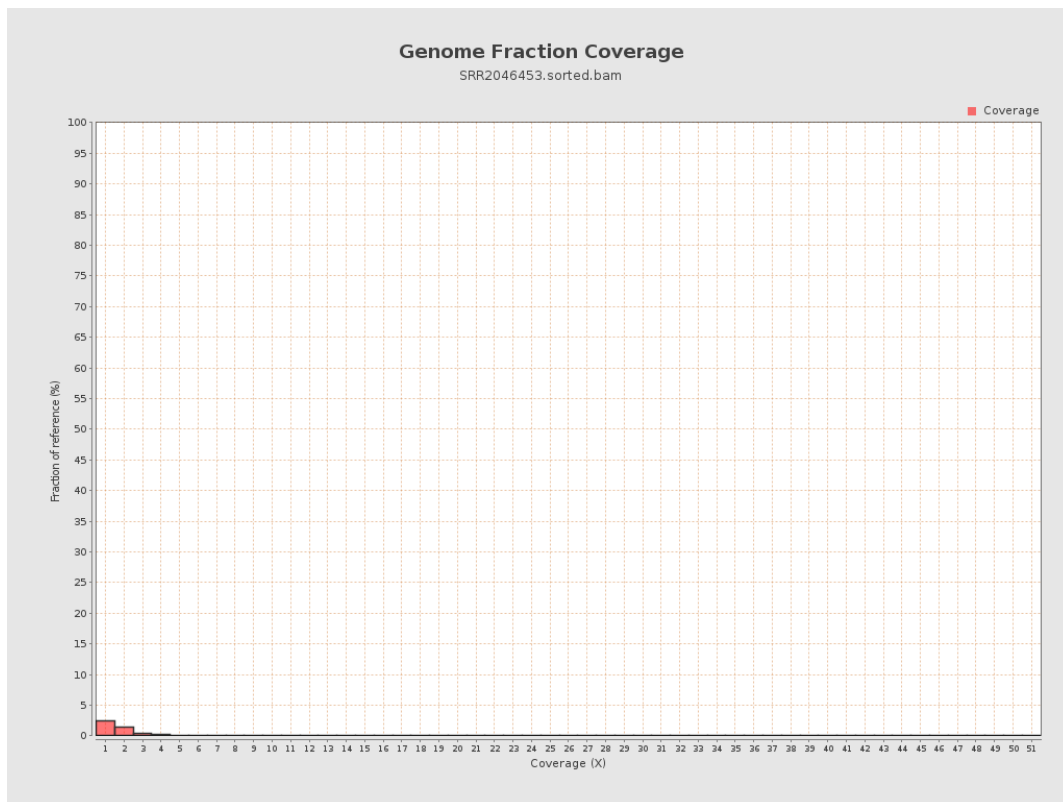
4. Results : Coverage Histogram



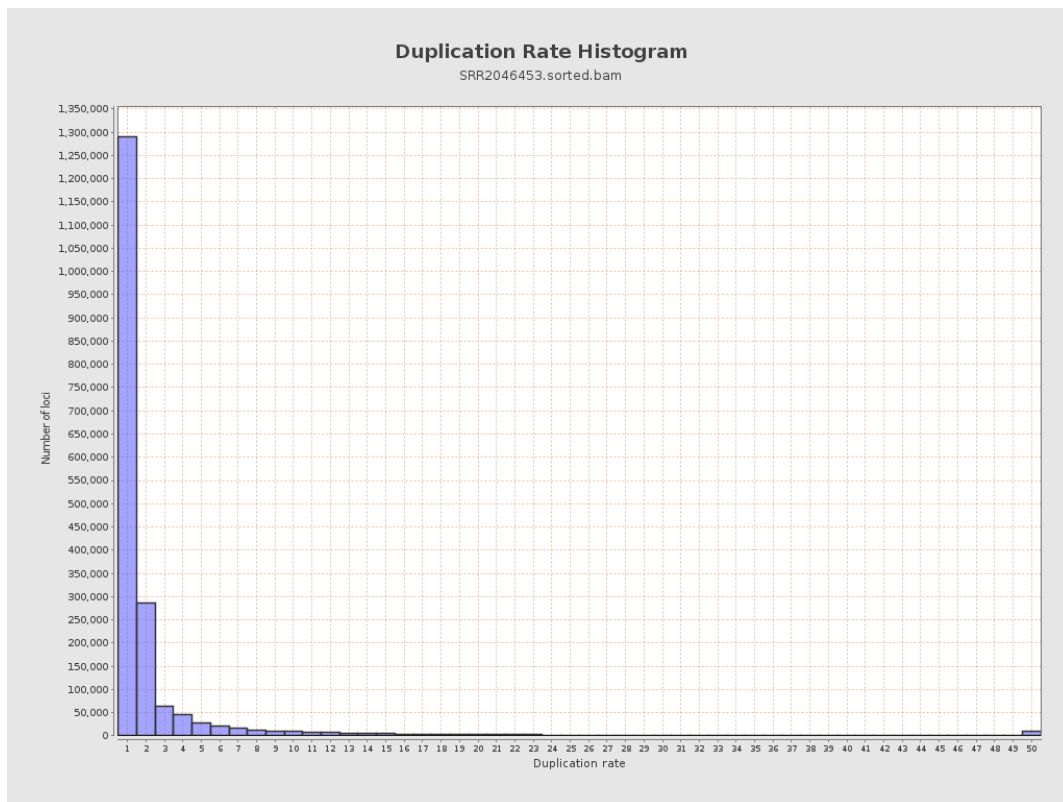
5. Results : Coverage Histogram (0-50X)



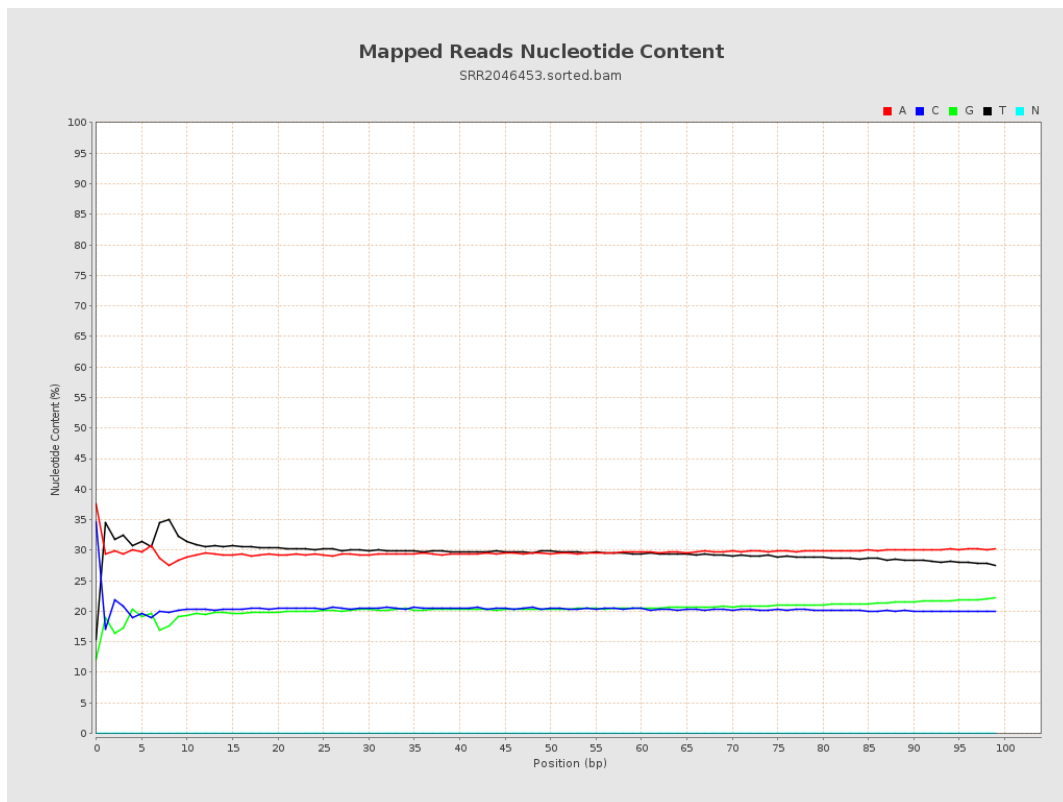
6. Results : Genome Fraction Coverage



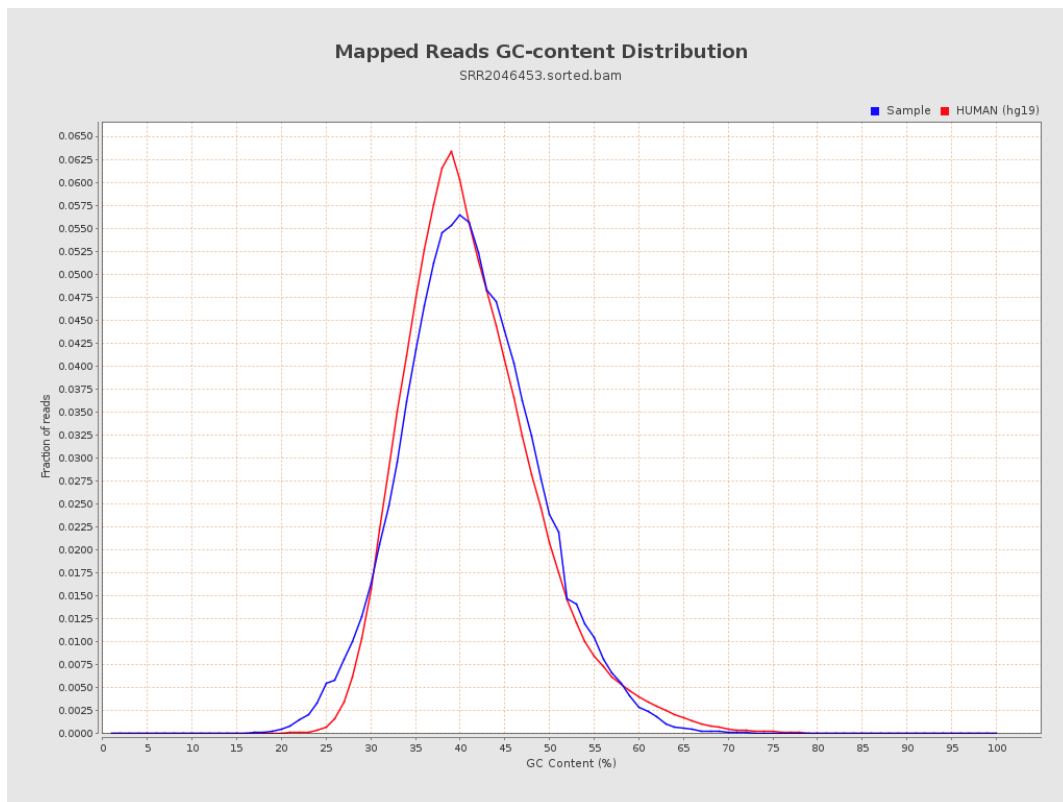
7. Results : Duplication Rate Histogram



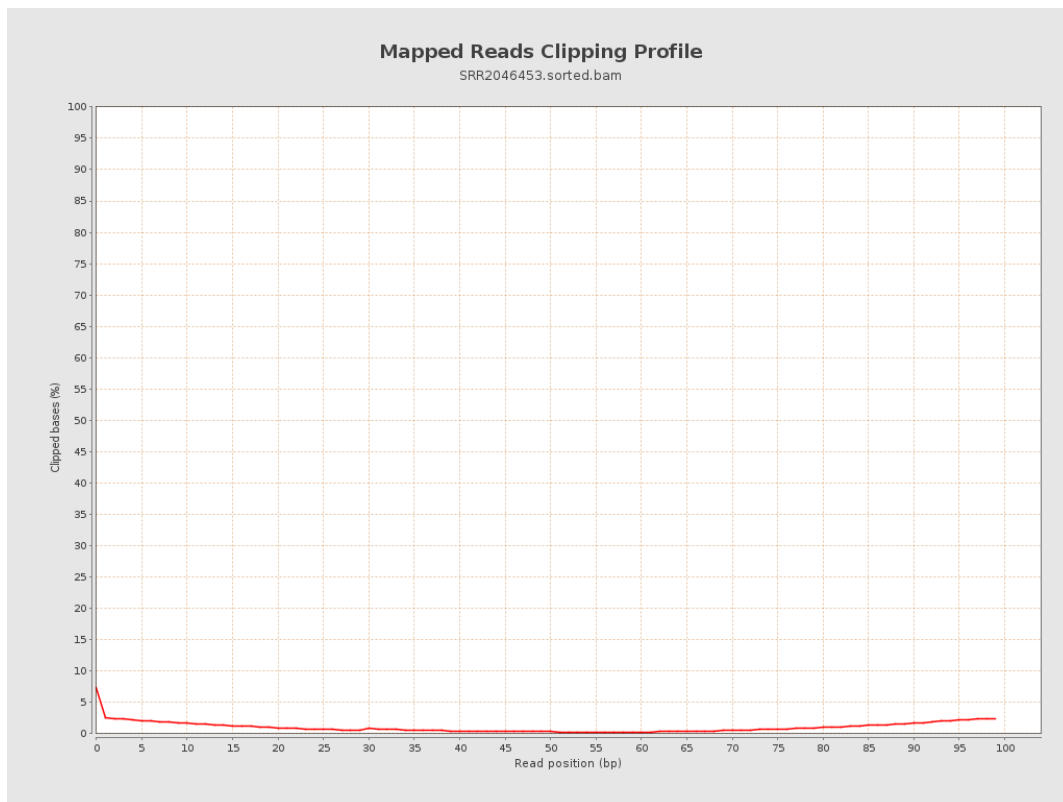
8. Results : Mapped Reads Nucleotide Content



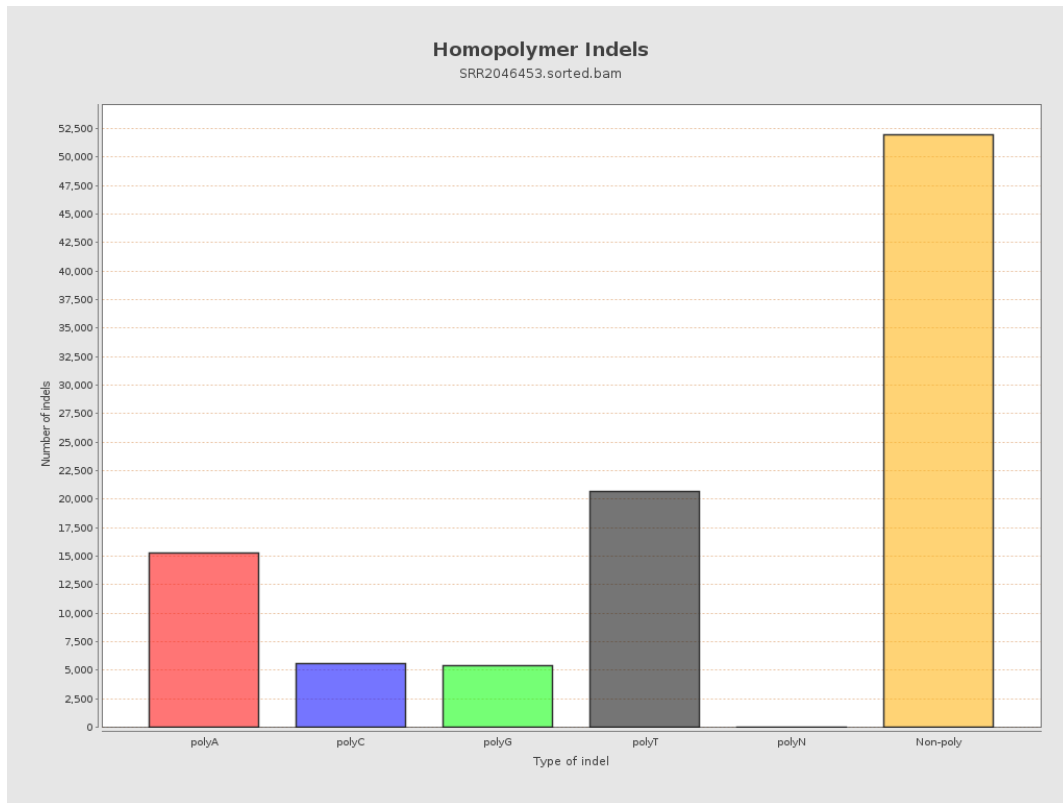
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



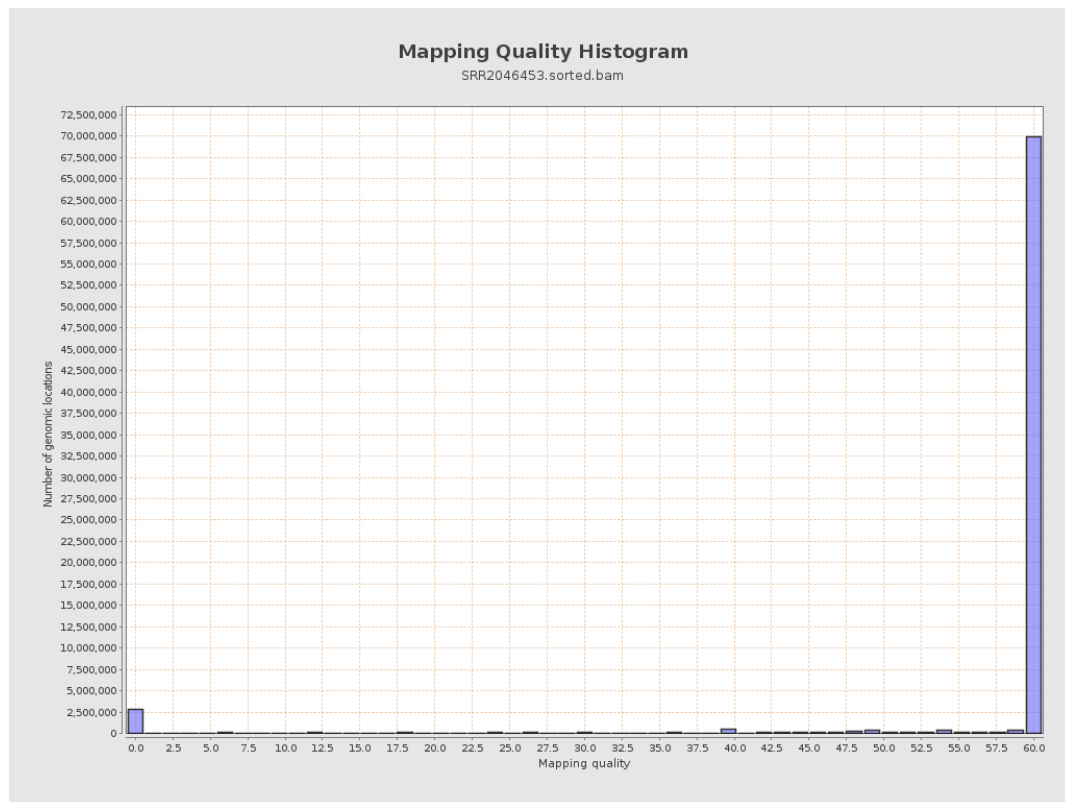
11. Results : Homopolymer Indels



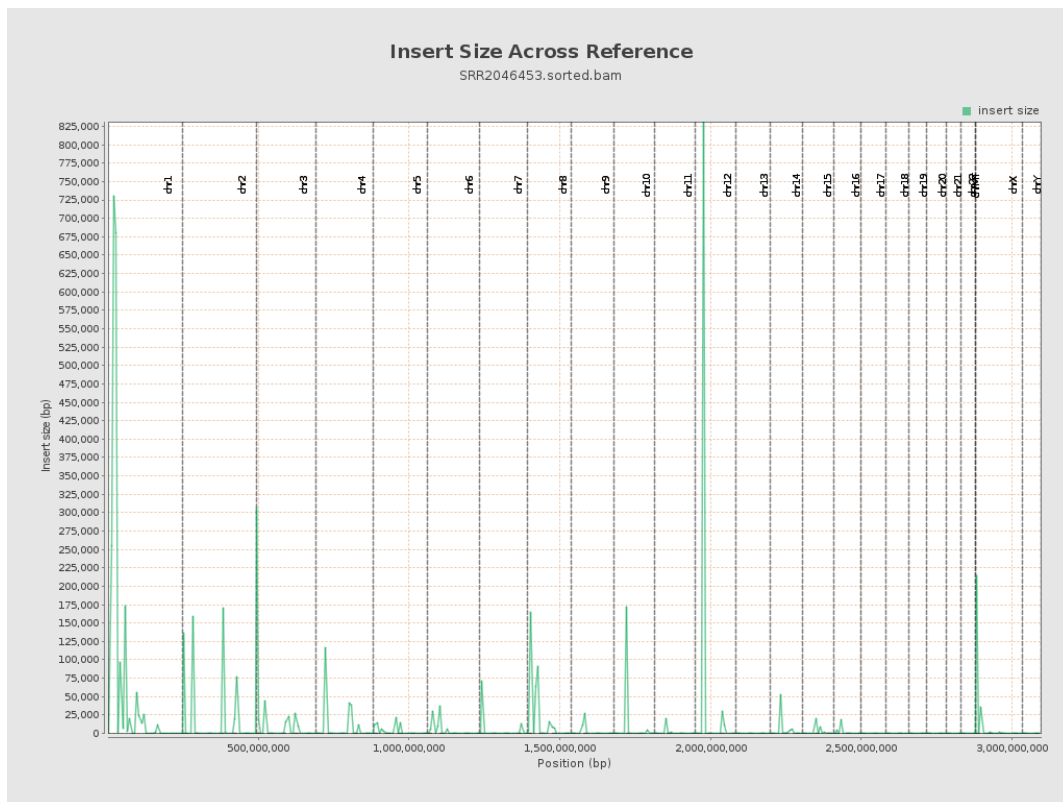
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

