

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 20:20:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046491.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_SRR2046491 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046491_1.fastq.gz SRR2046491_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 20:20:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046491.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,214,848
Mapped reads	13,165,972 / 99.63%
Unmapped reads	48,876 / 0.37%
Mapped paired reads	13,165,972 / 99.63%
Mapped reads, first in pair	6,596,484 / 49.92%
Mapped reads, second in pair	6,569,488 / 49.71%
Mapped reads, both in pair	13,129,780 / 99.36%
Mapped reads, singletons	36,192 / 0.27%
Secondary alignments	0
Supplementary alignments	50,358 / 0.38%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	9,520,709 / 72.05%
Duplication rate	35.01%
Clipped reads	1,175,017 / 8.89%

2.2. ACGT Content

Number/percentage of A's	372,186,121 / 28.67%
Number/percentage of C's	275,837,845 / 21.24%
Number/percentage of T's	374,530,700 / 28.85%
Number/percentage of G's	275,712,210 / 21.23%
Number/percentage of N's	122,855 / 0.01%

GC Percentage	42.48%
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2.3. Coverage

Mean	0.4195
Standard Deviation	26.5857

2.4. Mapping Quality

Mean Mapping Quality	53.91
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2.5. Insert size

Mean	15,192.88
Standard Deviation	1,223,915.59
P25/Median/P75	131 / 163 / 199

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	4,569,478
Insertions	94,311
Mapped reads with at least one insertion	0.7%
Deletions	118,902
Mapped reads with at least one deletion	0.88%
Homopolymer indels	48.7%

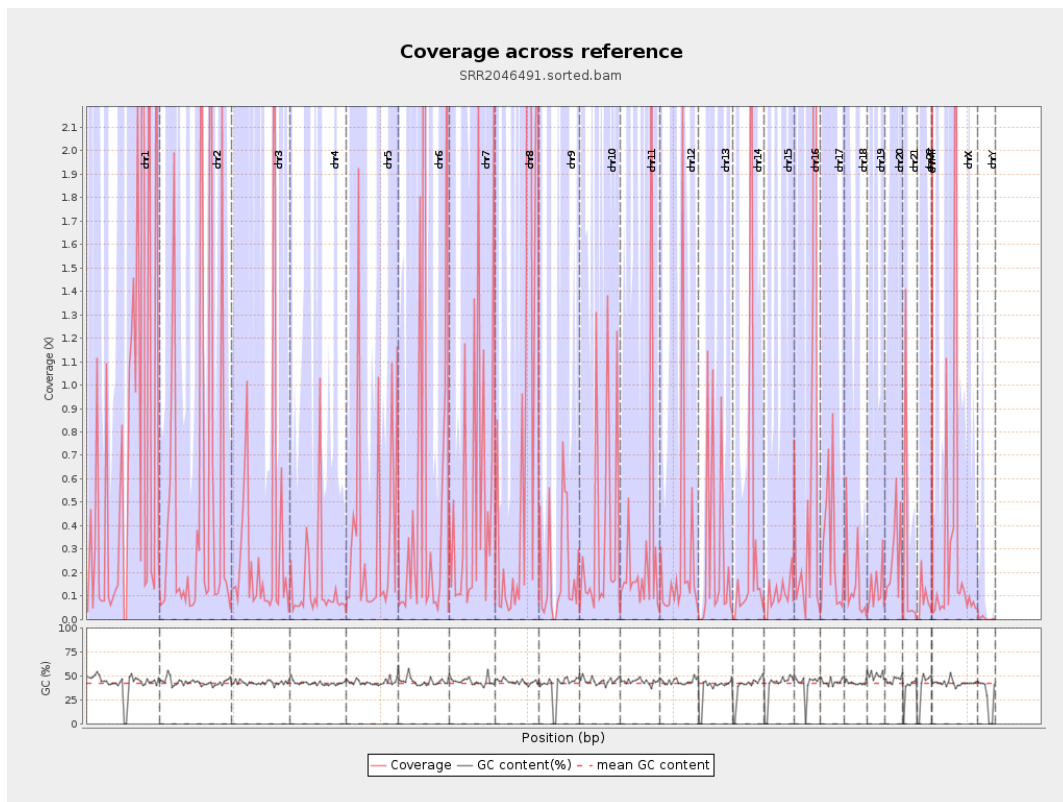
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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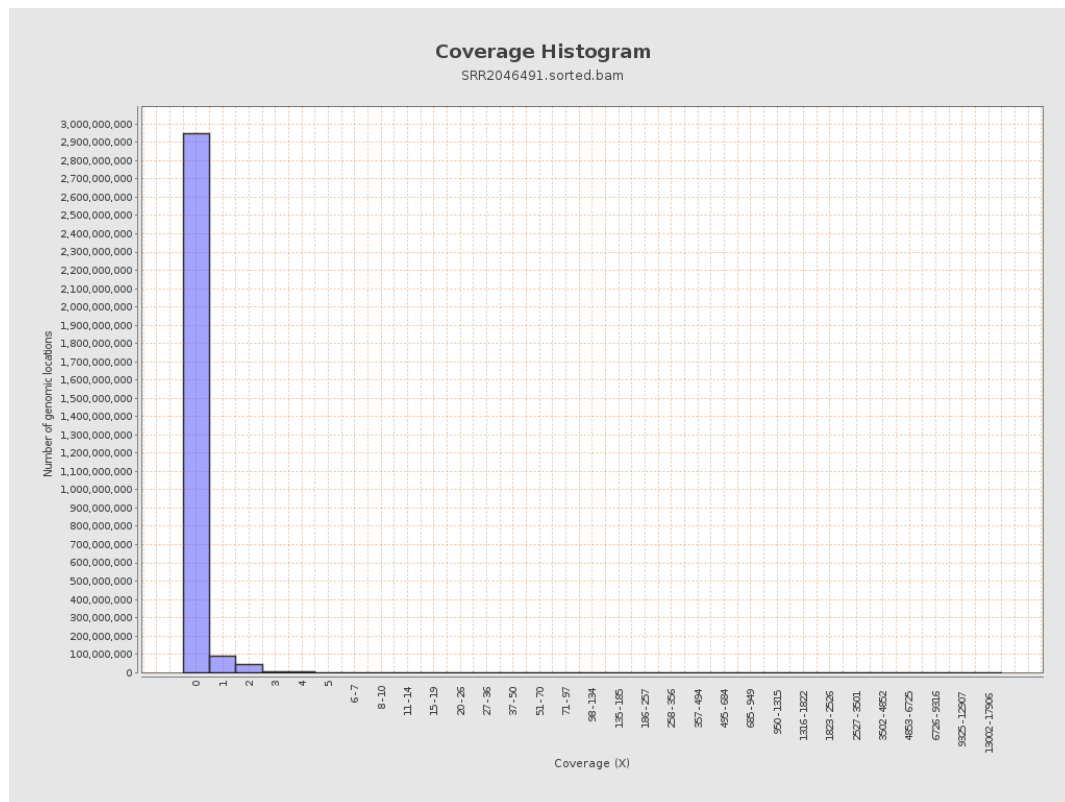
		bases	coverage	deviation
chr1	249250621	192216433	0.7712	36.9669
chr2	243199373	132673782	0.5455	27.7883
chr3	198022430	69361700	0.3503	24.0363
chr4	191154276	26301752	0.1376	9.8648
chr5	180915260	65918885	0.3644	21.2888
chr6	171115067	104962171	0.6134	39.3684
chr7	159138663	92942388	0.584	27.3327
chr8	146364022	177525081	1.2129	54.8637
chr9	141213431	31182225	0.2208	17.6579
chr10	135534747	47340804	0.3493	22.9017
chr11	135006516	43979735	0.3258	22.2034
chr12	133851895	35736788	0.267	16.2057
chr13	115169878	31150089	0.2705	19.0155
chr14	107349540	34978427	0.3258	21.3123
chr15	102531392	11141229	0.1087	4.223
chr16	90354753	70562535	0.7809	41.012
chr17	81195210	24796504	0.3054	13.0939
chr18	78077248	12419605	0.1591	6.9006
chr19	59128983	8256665	0.1396	6.0915
chr20	63025520	16904762	0.2682	12.261
chr21	48129895	12050721	0.2504	24.9173
chr22	51304566	4328237	0.0844	4.2115
chrMT	16571	97051	5.8567	3.3035
chrX	155270560	51644619	0.3326	25.2002

chrY	59373566	235748	0.004	0.5158
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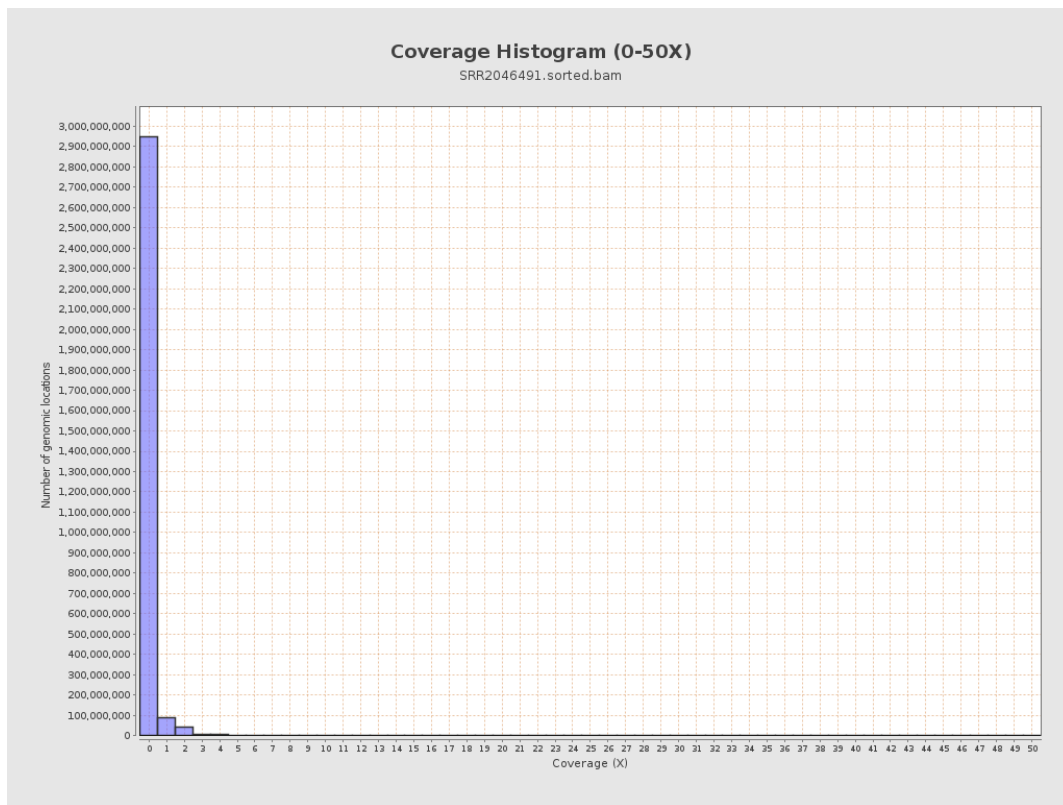
3. Results : Coverage across reference



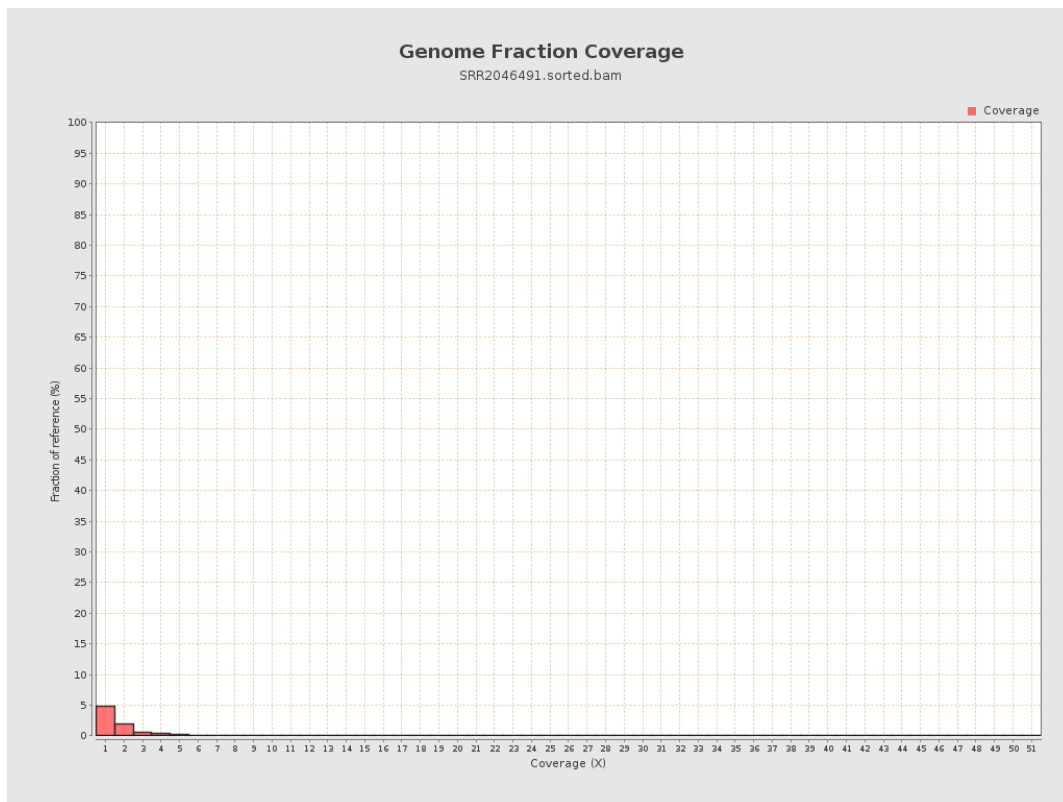
4. Results : Coverage Histogram



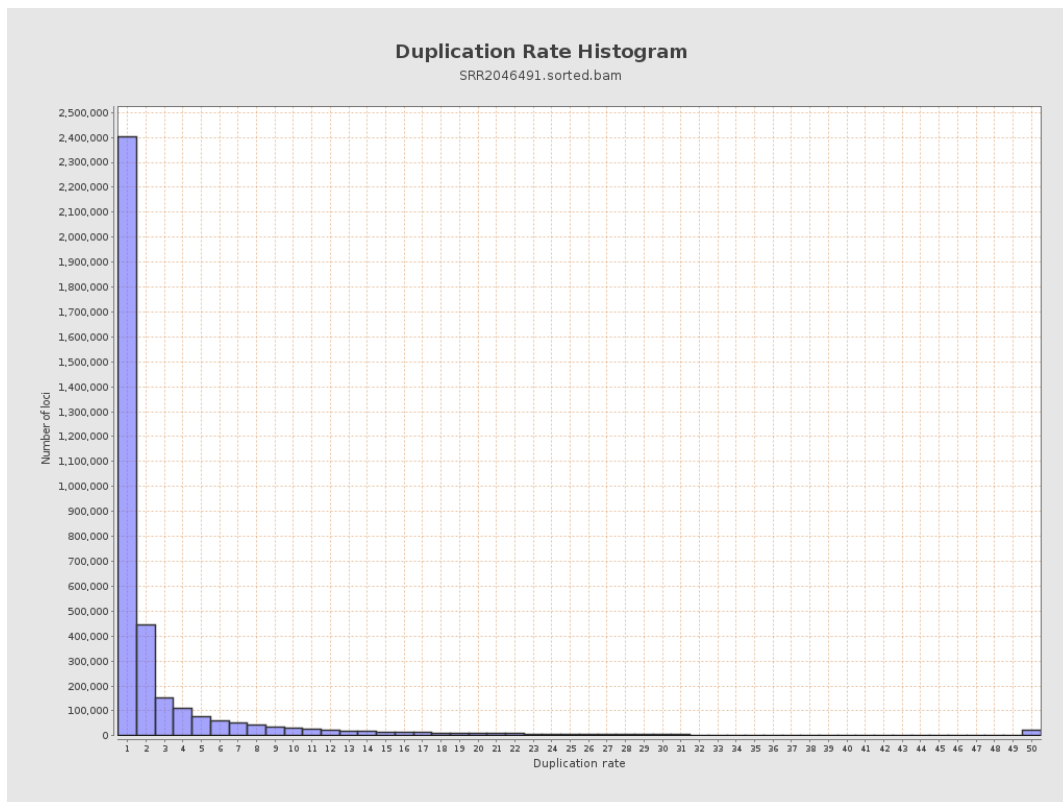
5. Results : Coverage Histogram (0-50X)



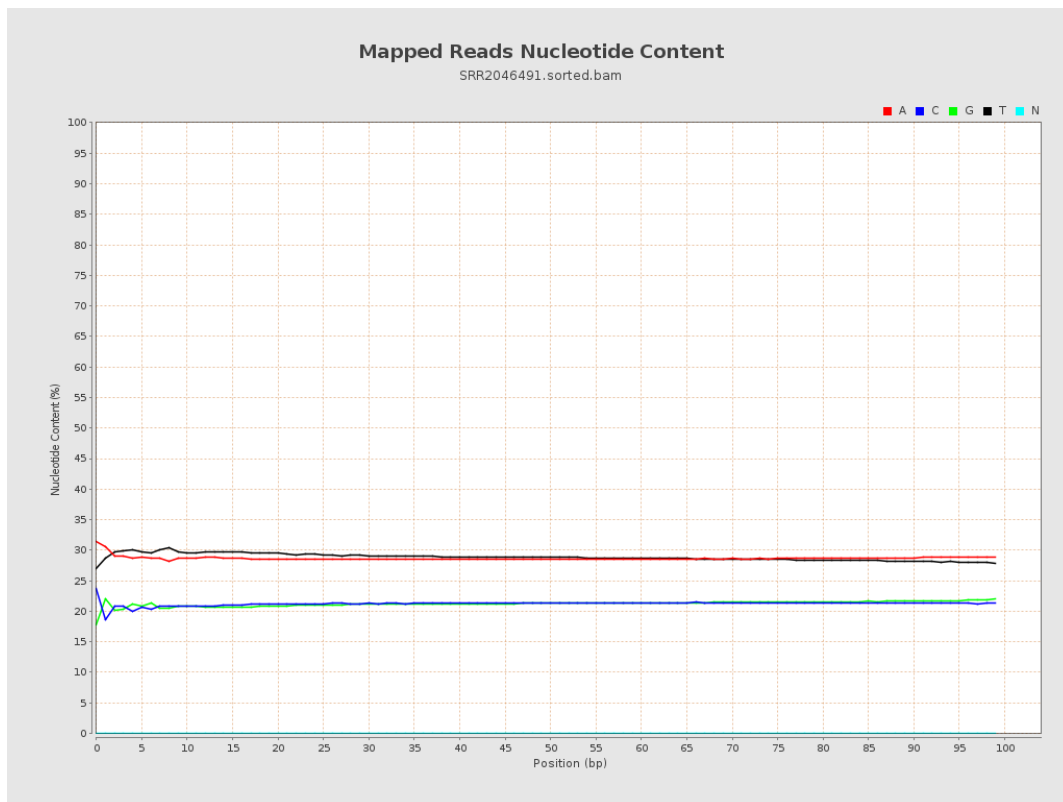
6. Results : Genome Fraction Coverage



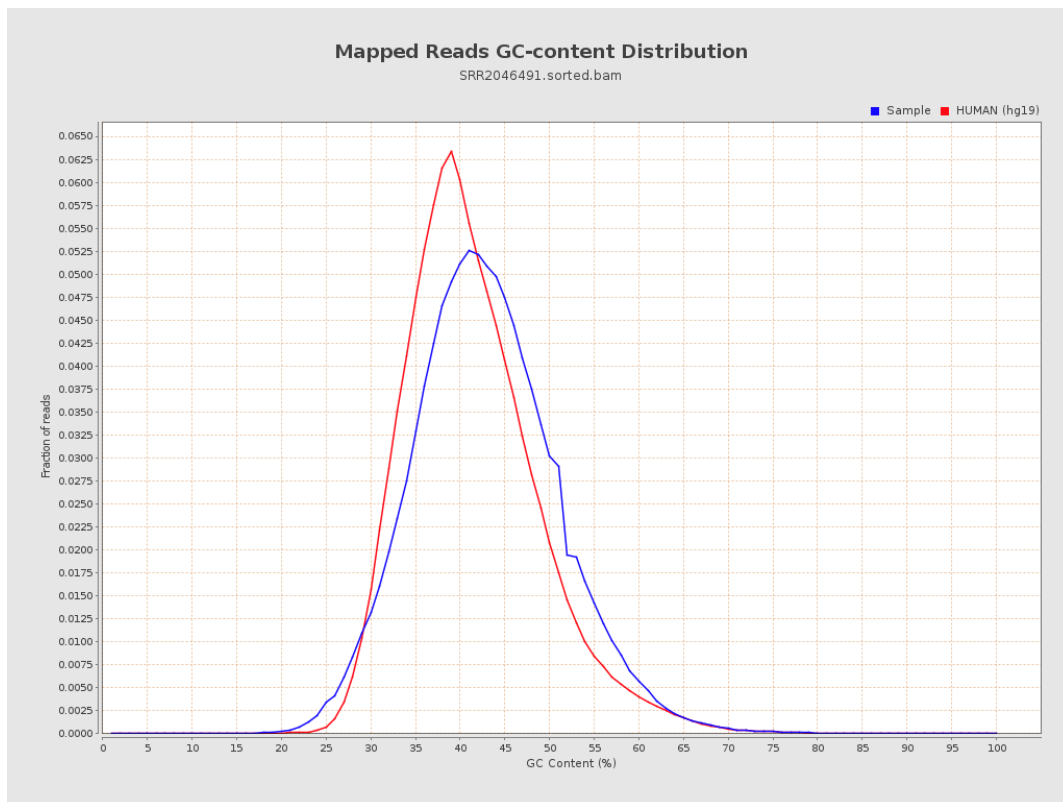
7. Results : Duplication Rate Histogram



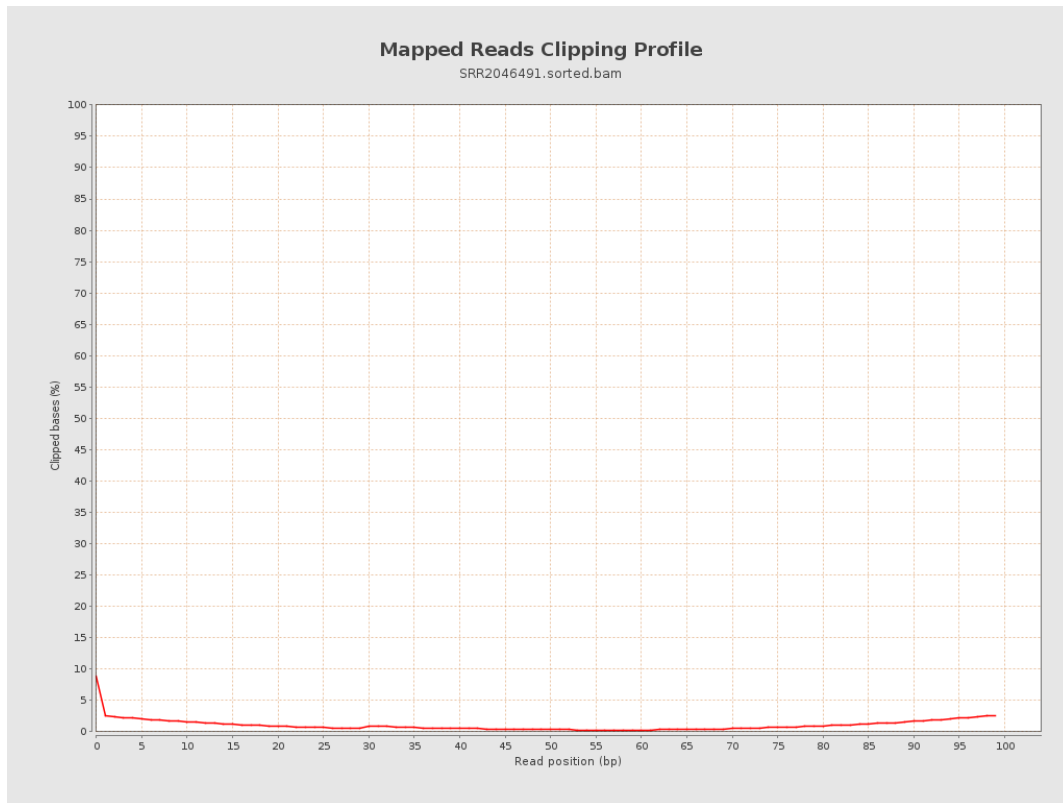
8. Results : Mapped Reads Nucleotide Content



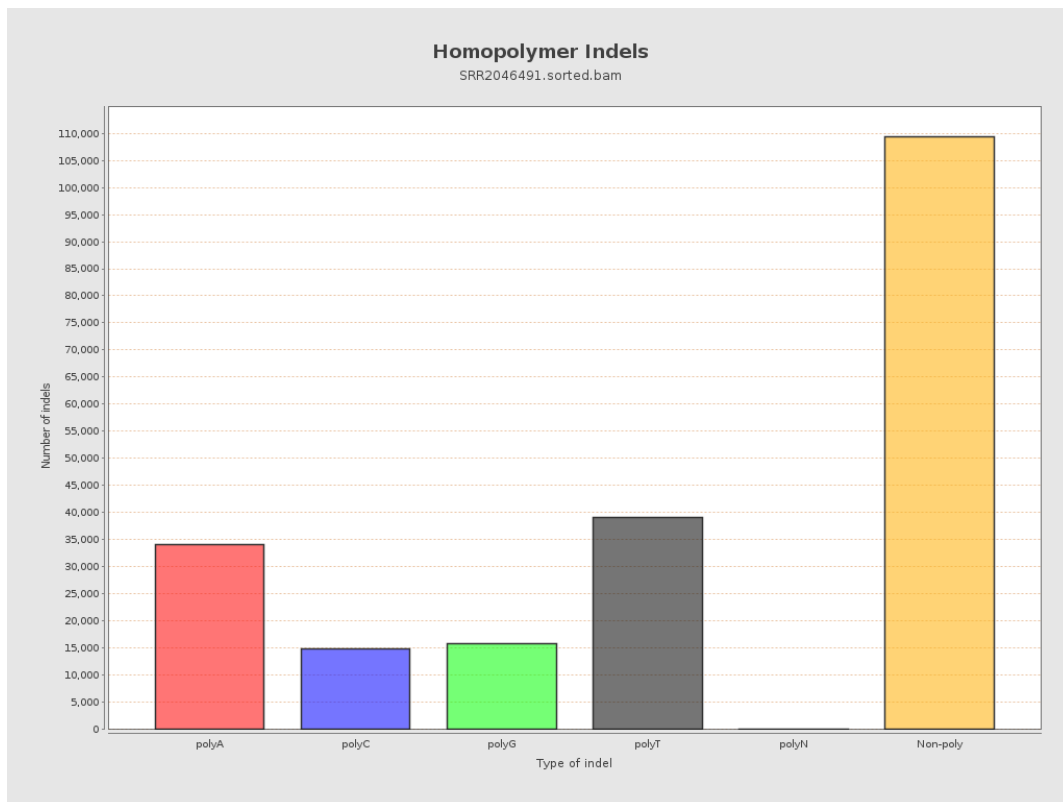
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



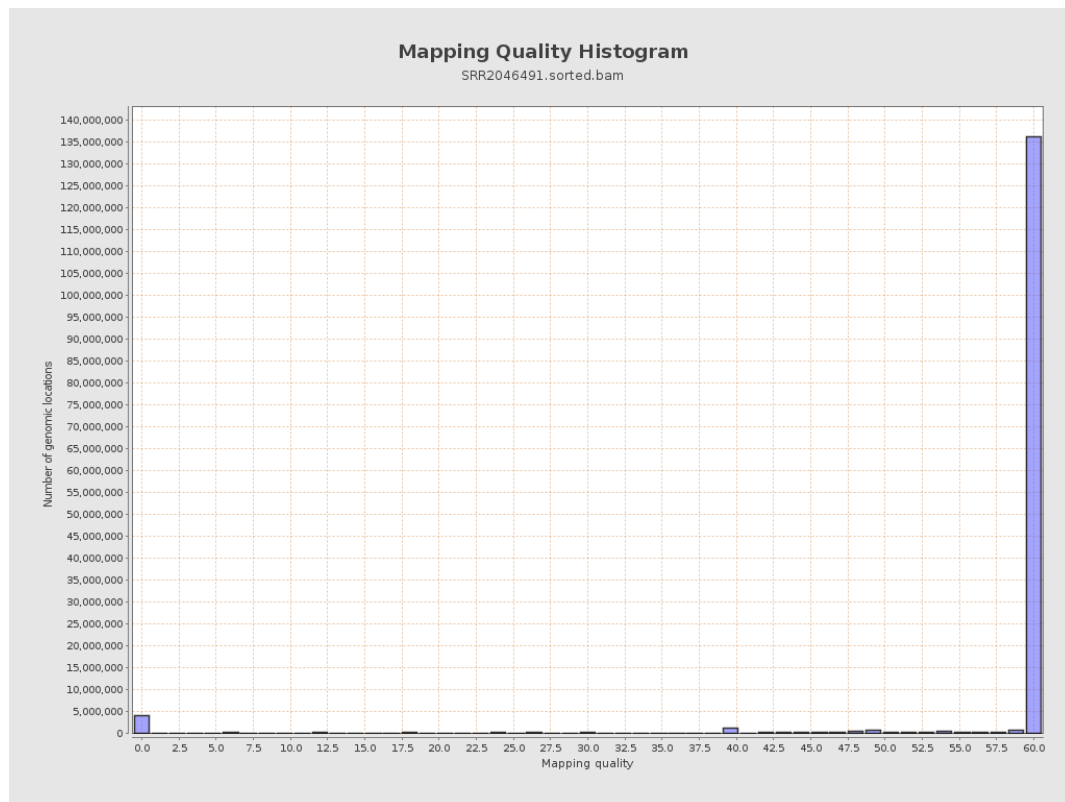
11. Results : Homopolymer Indels



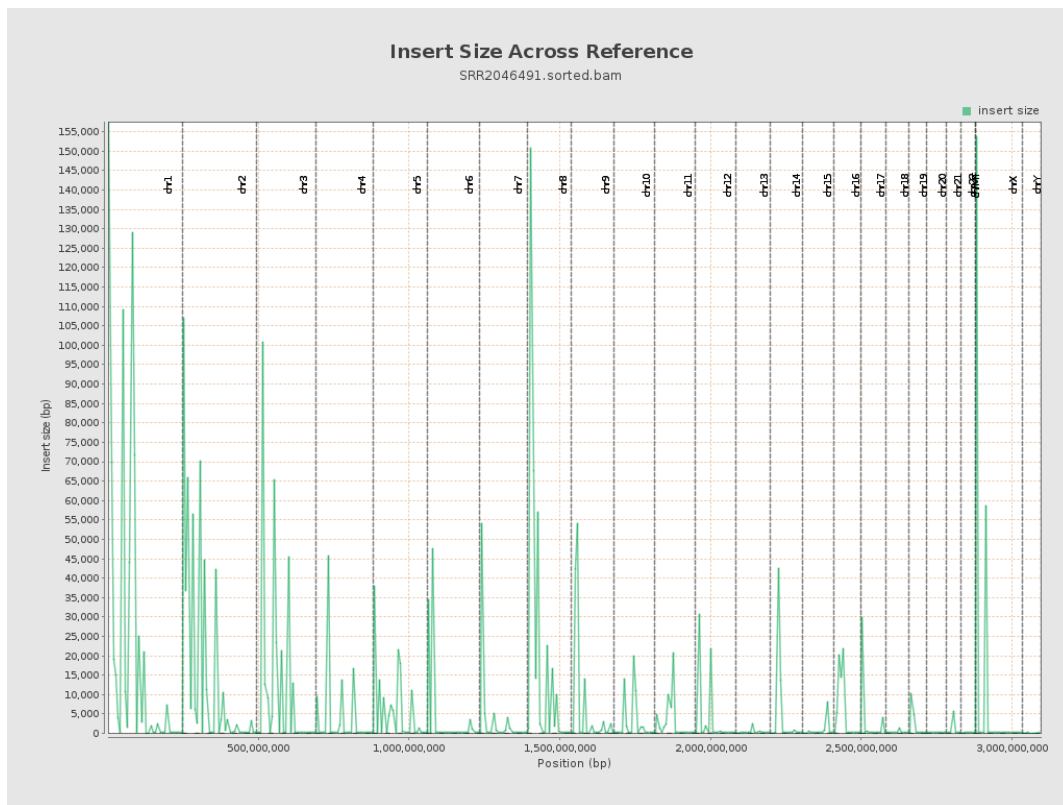
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

