

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 15:44:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046455.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_SRR2046455 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046455_1.fastq.gz SRR2046455_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 15:44:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046455.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,567,356
Mapped reads	9,528,680 / 99.6%
Unmapped reads	38,676 / 0.4%
Mapped paired reads	9,528,680 / 99.6%
Mapped reads, first in pair	4,768,689 / 49.84%
Mapped reads, second in pair	4,759,991 / 49.75%
Mapped reads, both in pair	9,500,886 / 99.31%
Mapped reads, singletons	27,794 / 0.29%
Secondary alignments	0
Supplementary alignments	54,350 / 0.57%
Read min/max/mean length	30 / 100 / 100.23
Duplicated reads (estimated)	7,449,799 / 77.87%
Duplication rate	36.96%
Clipped reads	1,323,738 / 13.84%

2.2. ACGT Content

Number/percentage of A's	272,582,188 / 29.3%
Number/percentage of C's	193,454,650 / 20.79%
Number/percentage of T's	273,256,267 / 29.37%
Number/percentage of G's	190,951,136 / 20.53%
Number/percentage of N's	81,597 / 0.01%

GC Percentage	41.32%
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2.3. Coverage

Mean	0.3006
Standard Deviation	31.9922

2.4. Mapping Quality

Mean Mapping Quality	52.62
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2.5. Insert size

Mean	19,036.46
Standard Deviation	1,359,043.01
P25/Median/P75	126 / 165 / 207

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	3,004,446
Insertions	77,191
Mapped reads with at least one insertion	0.8%
Deletions	86,230
Mapped reads with at least one deletion	0.88%
Homopolymer indels	47.48%

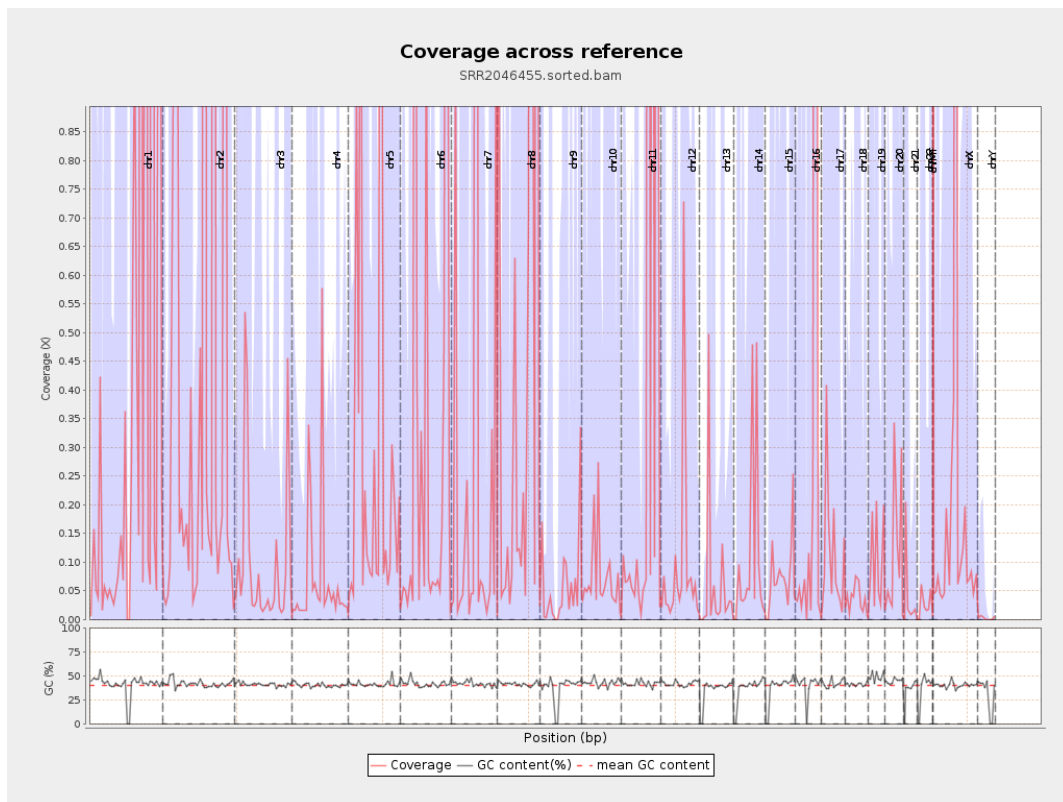
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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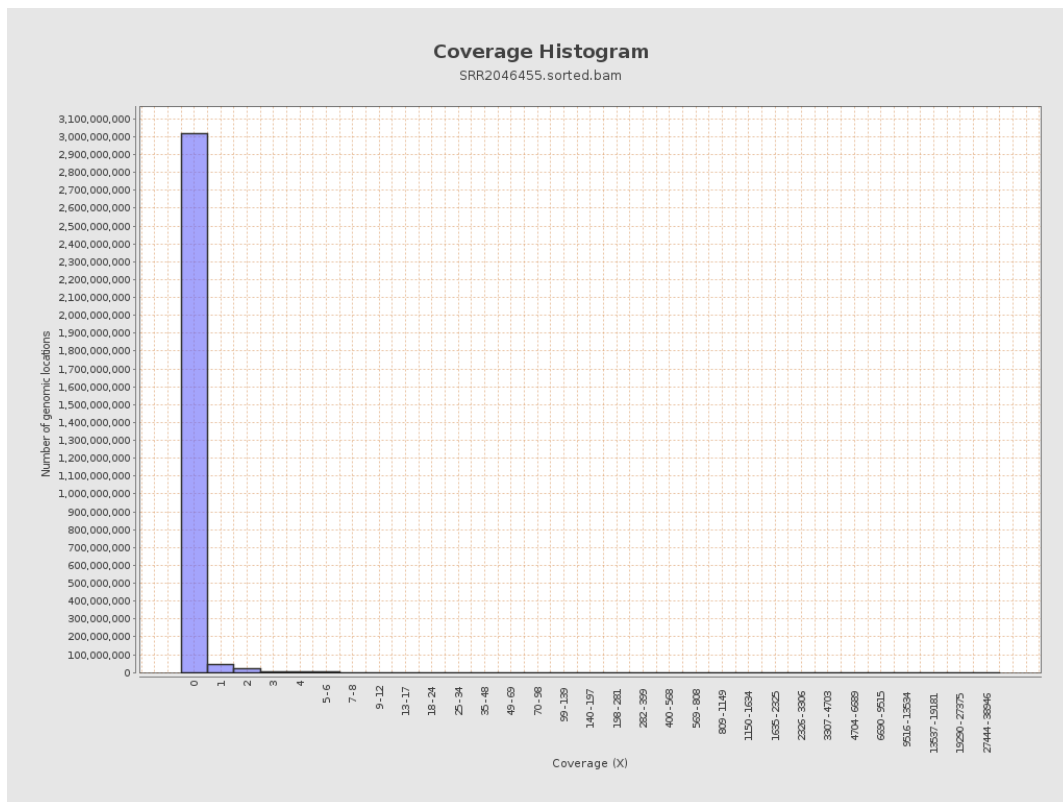
		bases	coverage	deviation
chr1	249250621	156642180	0.6285	59.3056
chr2	243199373	234816034	0.9655	56.2819
chr3	198022430	19164065	0.0968	9.4582
chr4	191154276	14147973	0.074	6.2679
chr5	180915260	57627179	0.3185	20.7005
chr6	171115067	64338226	0.376	31.4982
chr7	159138663	47778181	0.3002	27.6386
chr8	146364022	98573502	0.6735	55.1056
chr9	141213431	8075665	0.0572	3.9613
chr10	135534747	9895922	0.073	4.5469
chr11	135006516	78365229	0.5805	60.0544
chr12	133851895	11557361	0.0863	6.4341
chr13	115169878	6511934	0.0565	3.8619
chr14	107349540	11292643	0.1052	9.0714
chr15	102531392	7826487	0.0763	5.5076
chr16	90354753	37912490	0.4196	27.2886
chr17	81195210	8909825	0.1097	11.6625
chr18	78077248	2862531	0.0367	1.4526
chr19	59128983	5936538	0.1004	5.5235
chr20	63025520	7520982	0.1193	6.1817
chr21	48129895	2028876	0.0422	4.4692
chr22	51304566	1315406	0.0256	1.6197
chrMT	16571	56595	3.4153	2.4982
chrX	155270560	37253232	0.2399	23.7674

chrY	59373566	155522	0.0026	0.1136
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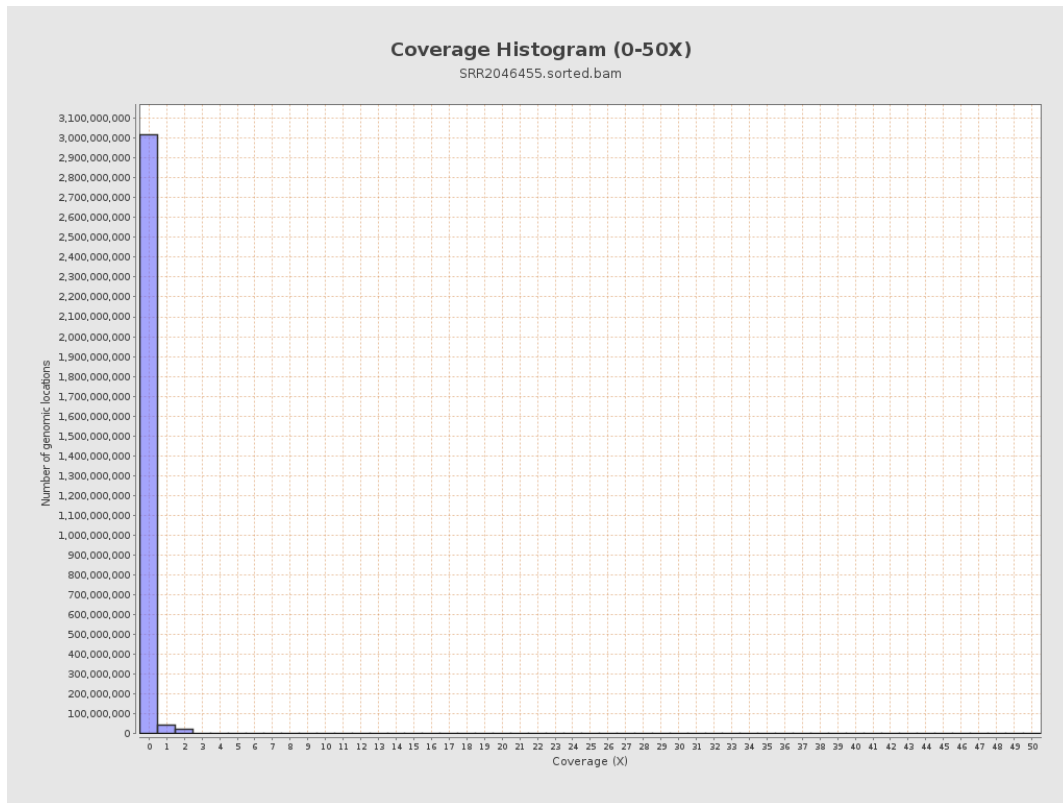
3. Results : Coverage across reference



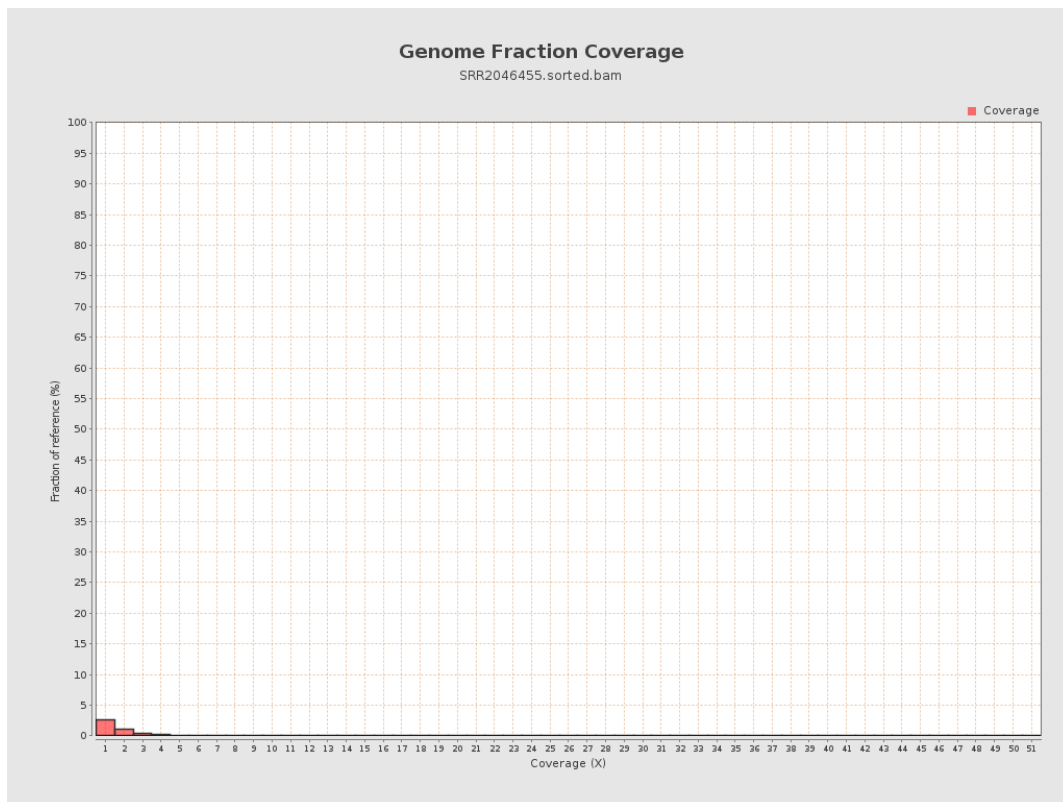
4. Results : Coverage Histogram



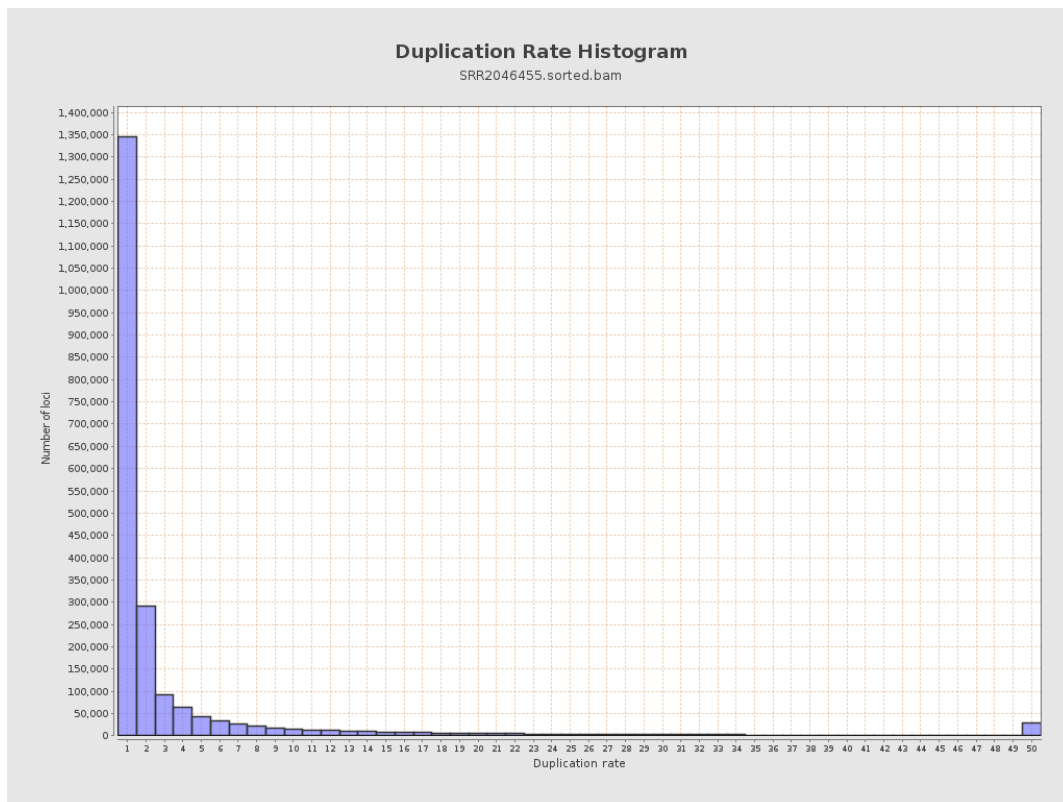
5. Results : Coverage Histogram (0-50X)



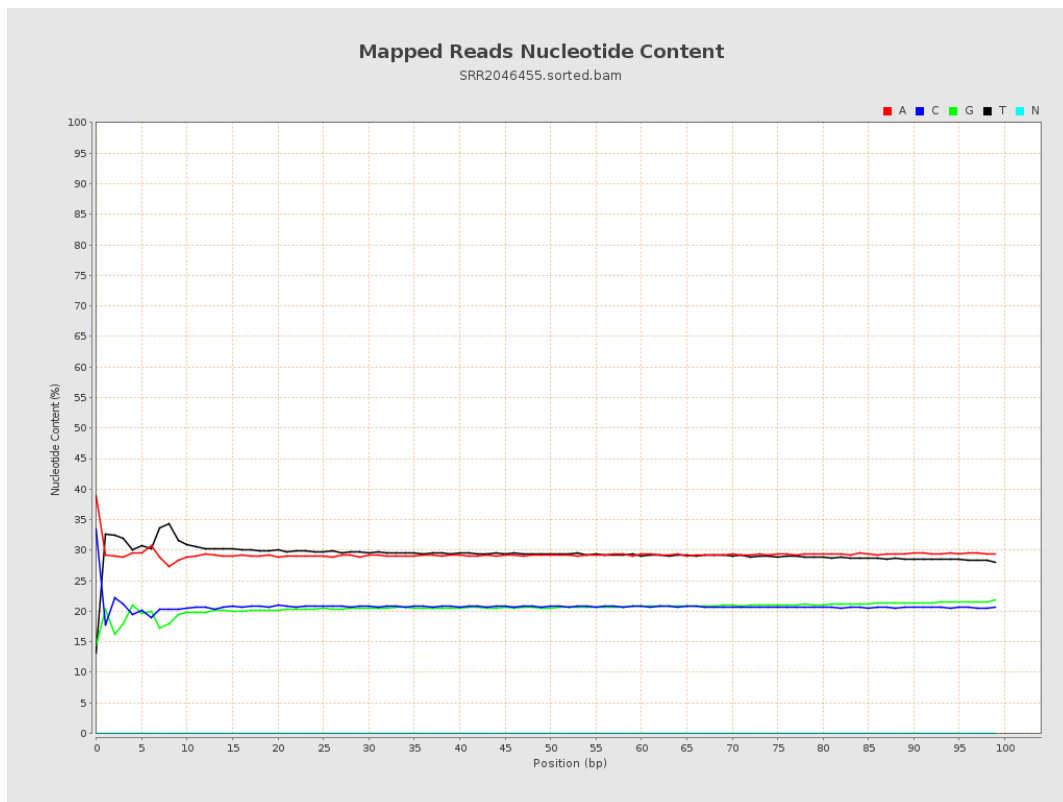
6. Results : Genome Fraction Coverage



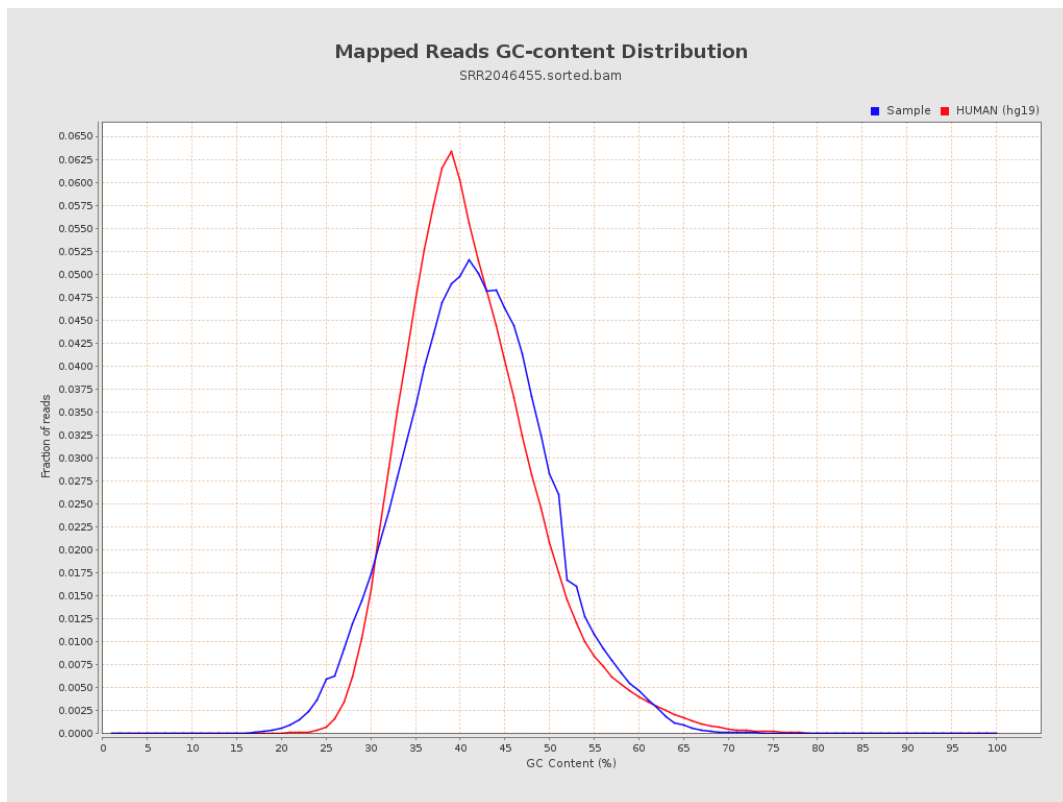
7. Results : Duplication Rate Histogram



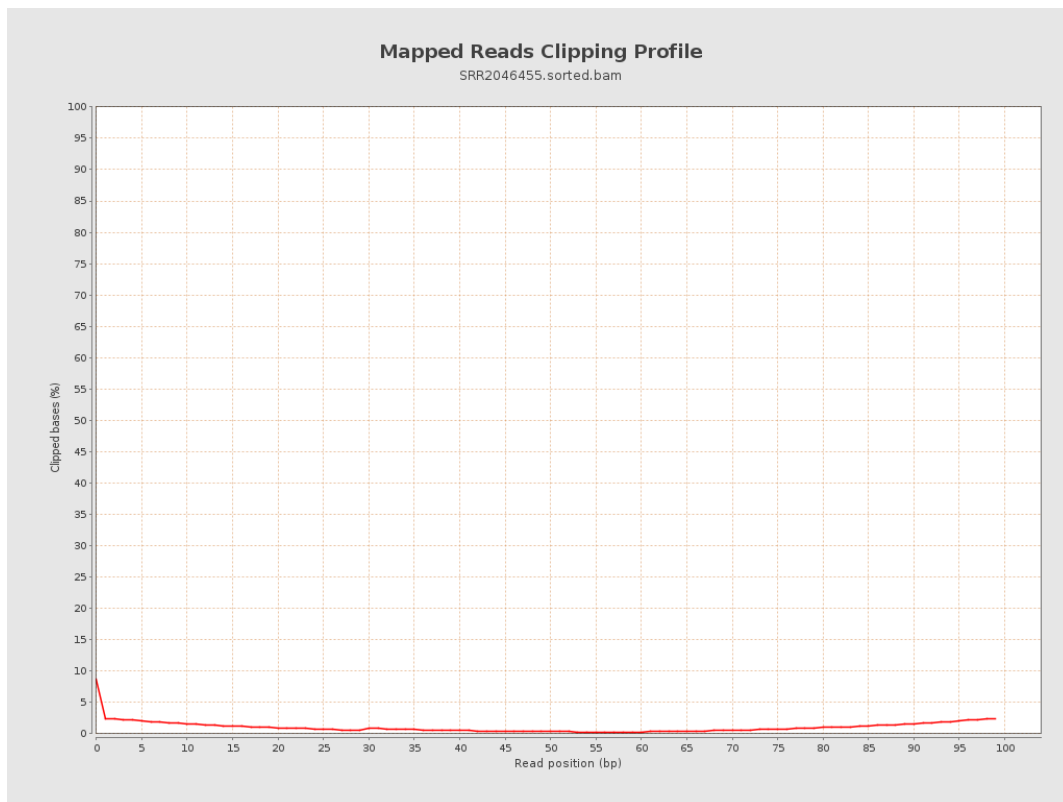
8. Results : Mapped Reads Nucleotide Content



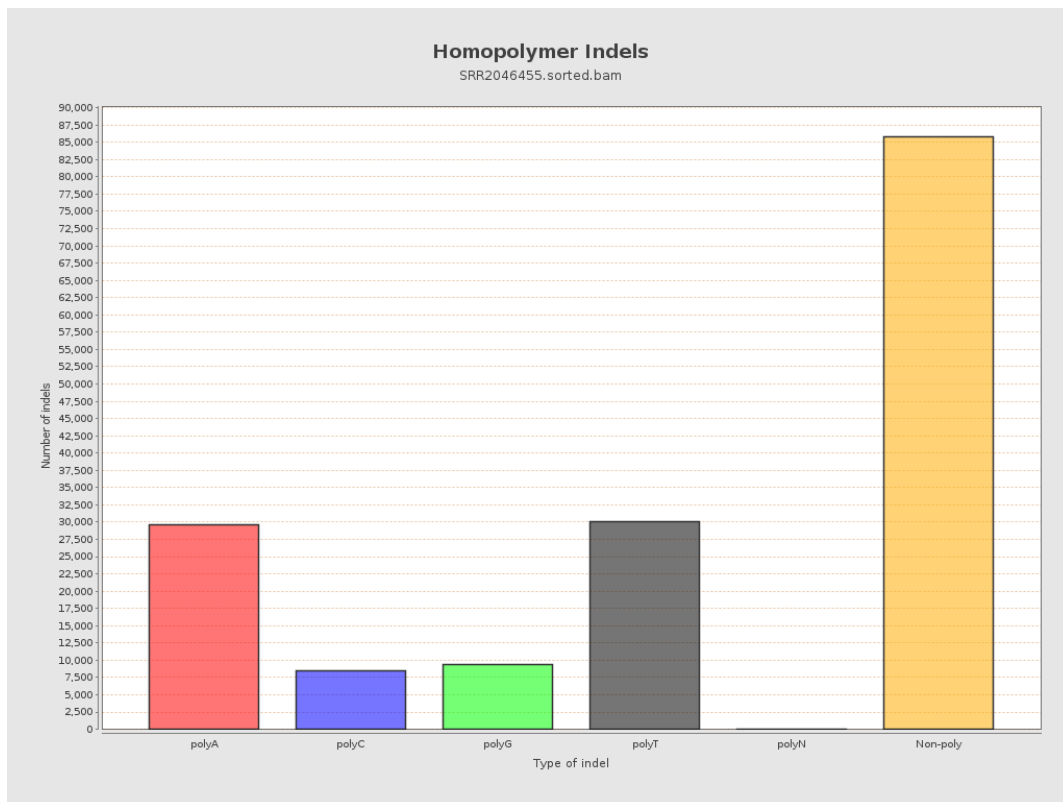
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



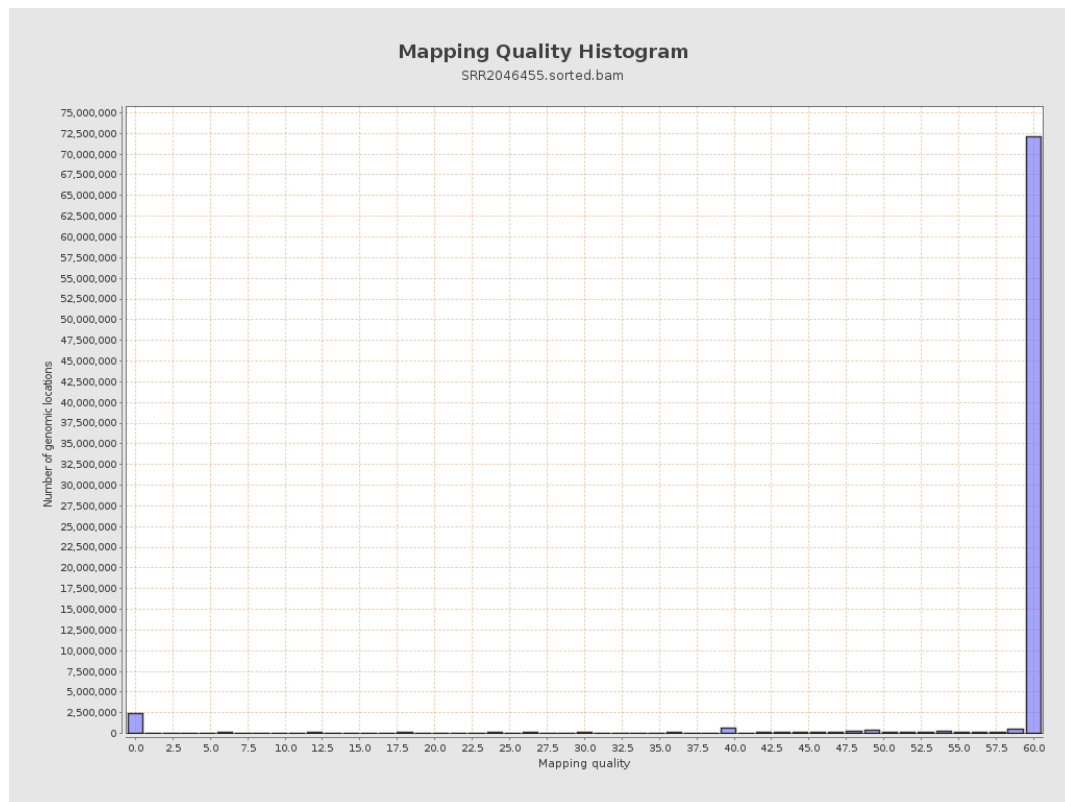
11. Results : Homopolymer Indels



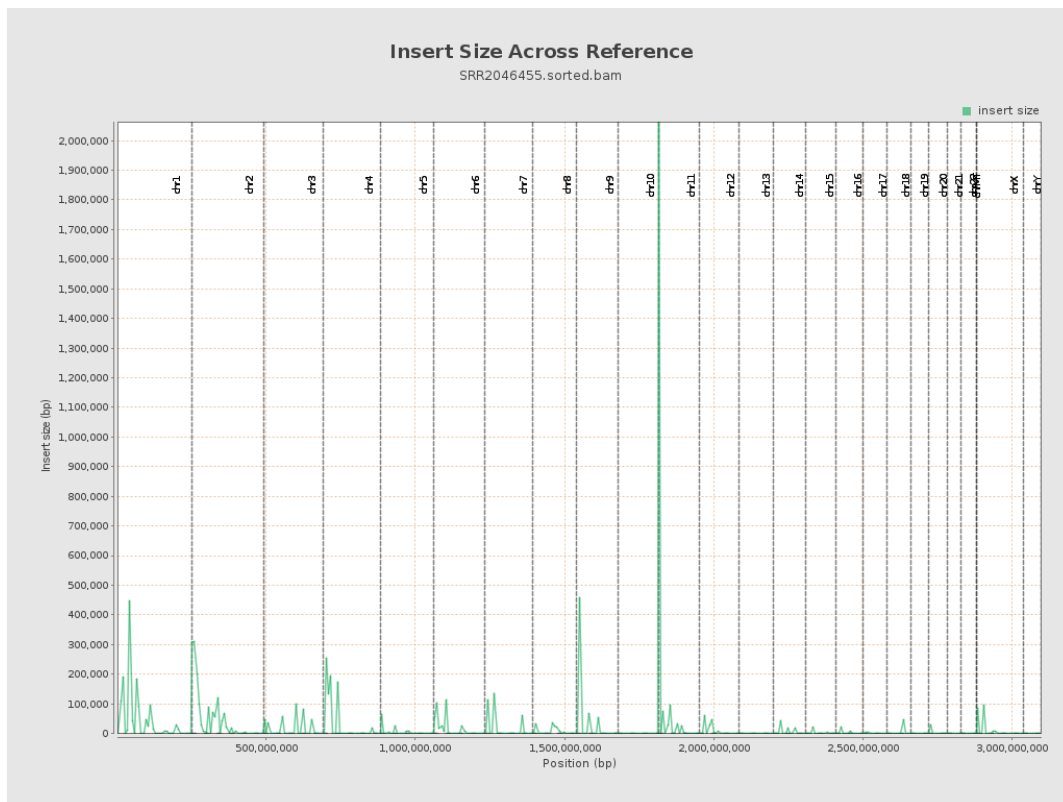
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

