

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 15:36:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046454.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_SRR2046454 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046454_1.fastq.gz SRR2046454_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 15:36:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046454.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,776,796
Mapped reads	5,698,302 / 98.64%
Unmapped reads	78,494 / 1.36%
Mapped paired reads	5,698,302 / 98.64%
Mapped reads, first in pair	2,865,848 / 49.61%
Mapped reads, second in pair	2,832,454 / 49.03%
Mapped reads, both in pair	5,639,864 / 97.63%
Mapped reads, singletons	58,438 / 1.01%
Secondary alignments	0
Supplementary alignments	59,448 / 1.03%
Read min/max/mean length	30 / 100 / 100.42
Duplicated reads (estimated)	3,866,633 / 66.93%
Duplication rate	47.26%
Clipped reads	2,803,787 / 48.54%

2.2. ACGT Content

Number/percentage of A's	148,135,358 / 29.15%
Number/percentage of C's	106,788,921 / 21.02%
Number/percentage of T's	142,150,389 / 27.98%
Number/percentage of G's	110,992,408 / 21.84%
Number/percentage of N's	39,520 / 0.01%

GC Percentage	42.86%
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2.3. Coverage

Mean	0.1642
Standard Deviation	10.2042

2.4. Mapping Quality

Mean Mapping Quality	52.66
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2.5. Insert size

Mean	109,922.33
Standard Deviation	3,272,335.18
P25/Median/P75	80 / 102 / 143

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	2,132,690
Insertions	37,877
Mapped reads with at least one insertion	0.65%
Deletions	48,284
Mapped reads with at least one deletion	0.83%
Homopolymer indels	46.56%

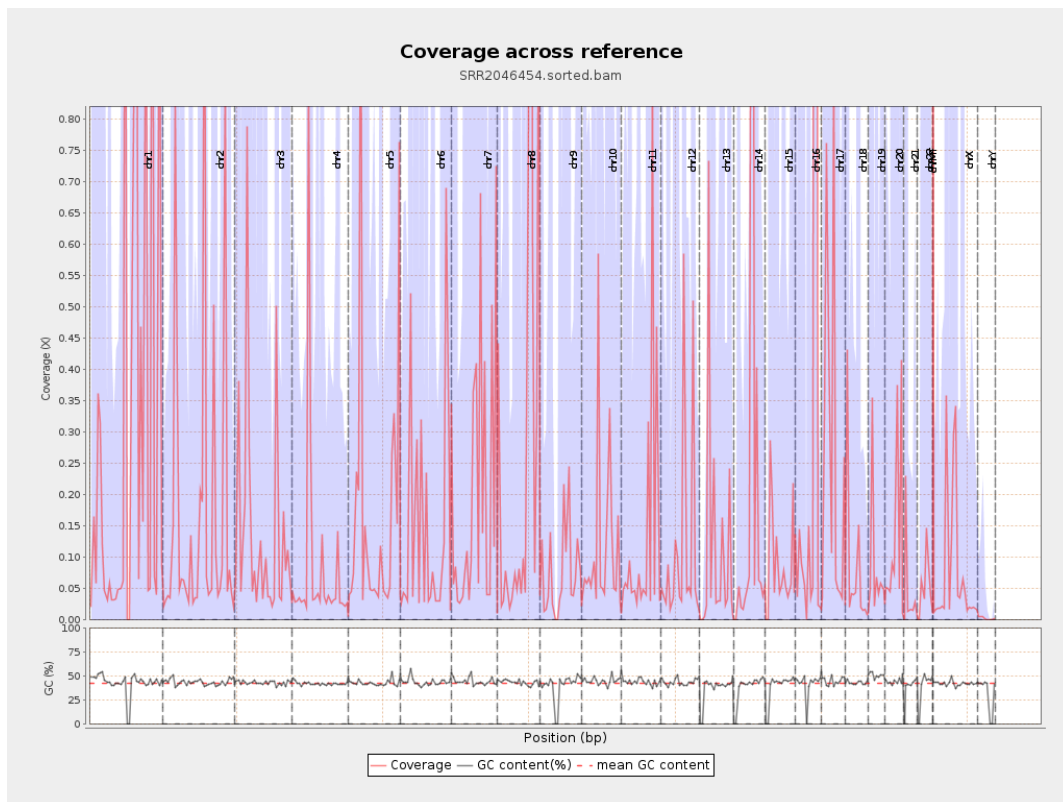
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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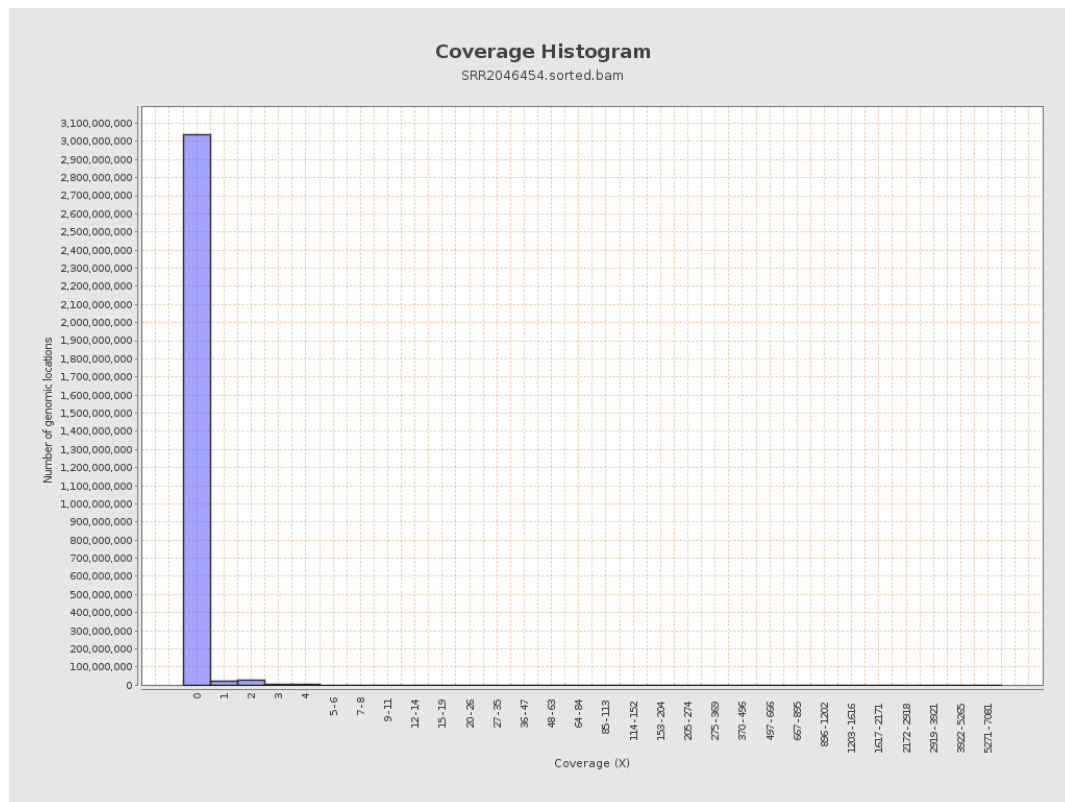
		bases	coverage	deviation
chr1	249250621	78671391	0.3156	16.3033
chr2	243199373	43247340	0.1778	9.1204
chr3	198022430	26822849	0.1355	7.2633
chr4	191154276	15884301	0.0831	5.0406
chr5	180915260	31619661	0.1748	9.4992
chr6	171115067	24058683	0.1406	5.9919
chr7	159138663	32532243	0.2044	9.7687
chr8	146364022	52861259	0.3612	18.5041
chr9	141213431	10498952	0.0743	5.0625
chr10	135534747	16184841	0.1194	6.7326
chr11	135006516	17977902	0.1332	8.2243
chr12	133851895	14281297	0.1067	7.2846
chr13	115169878	12599279	0.1094	6.2357
chr14	107349540	24453968	0.2278	12.7339
chr15	102531392	9314438	0.0908	4.4336
chr16	90354753	37963204	0.4202	25.7082
chr17	81195210	22357616	0.2754	11.0139
chr18	78077248	6104230	0.0782	4.3531
chr19	59128983	5016067	0.0848	3.9505
chr20	63025520	8783015	0.1394	9.0874
chr21	48129895	2338707	0.0486	4.4945
chr22	51304566	2861669	0.0558	2.5692
chrMT	16571	33669	2.0318	2.001
chrX	155270560	11670370	0.0752	5.3077

chrY	59373566	104226	0.0018	0.1001
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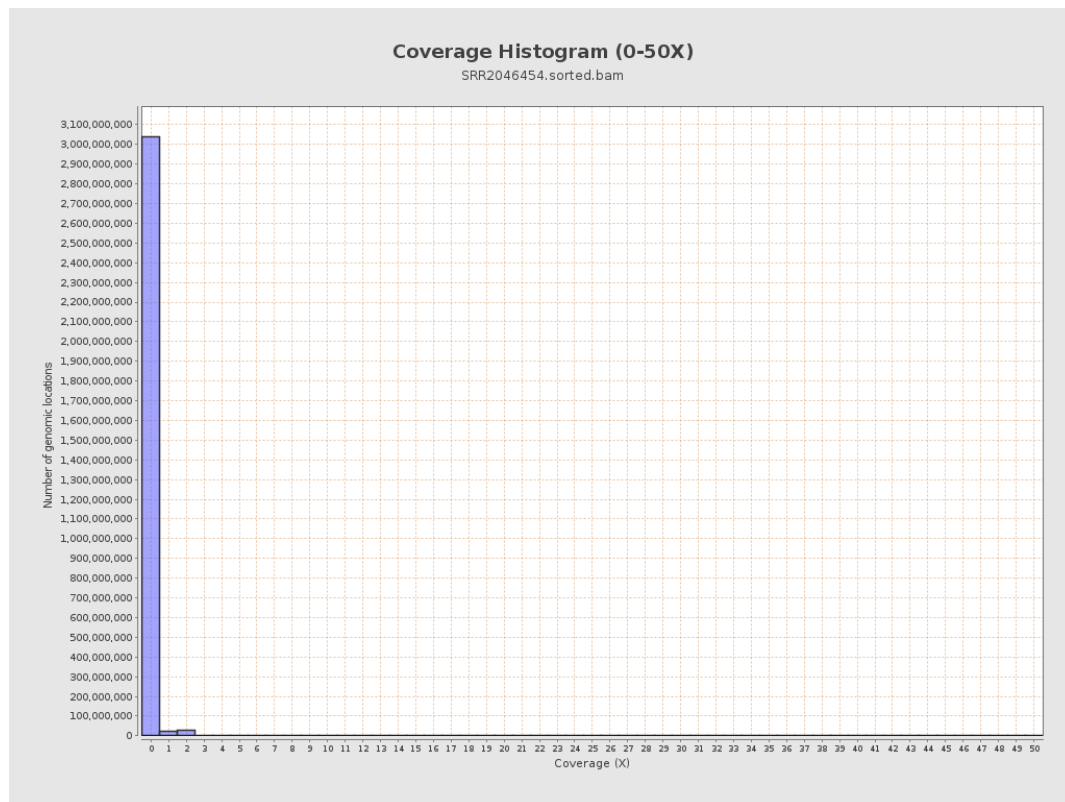
3. Results : Coverage across reference



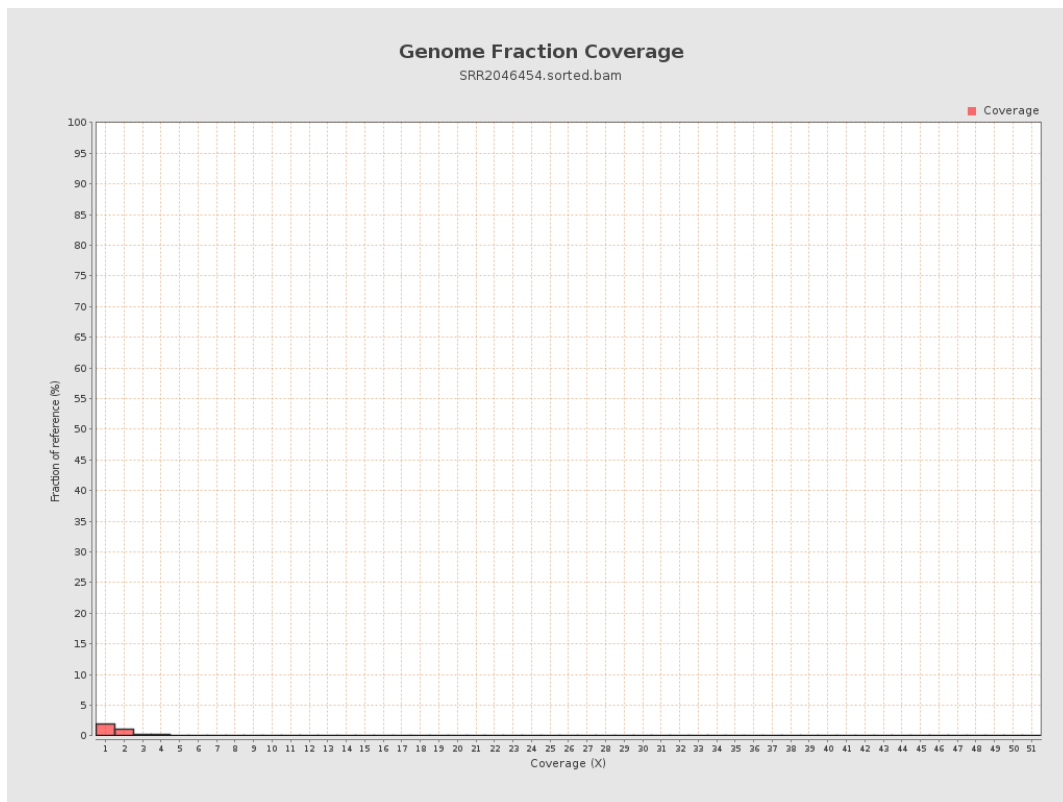
4. Results : Coverage Histogram



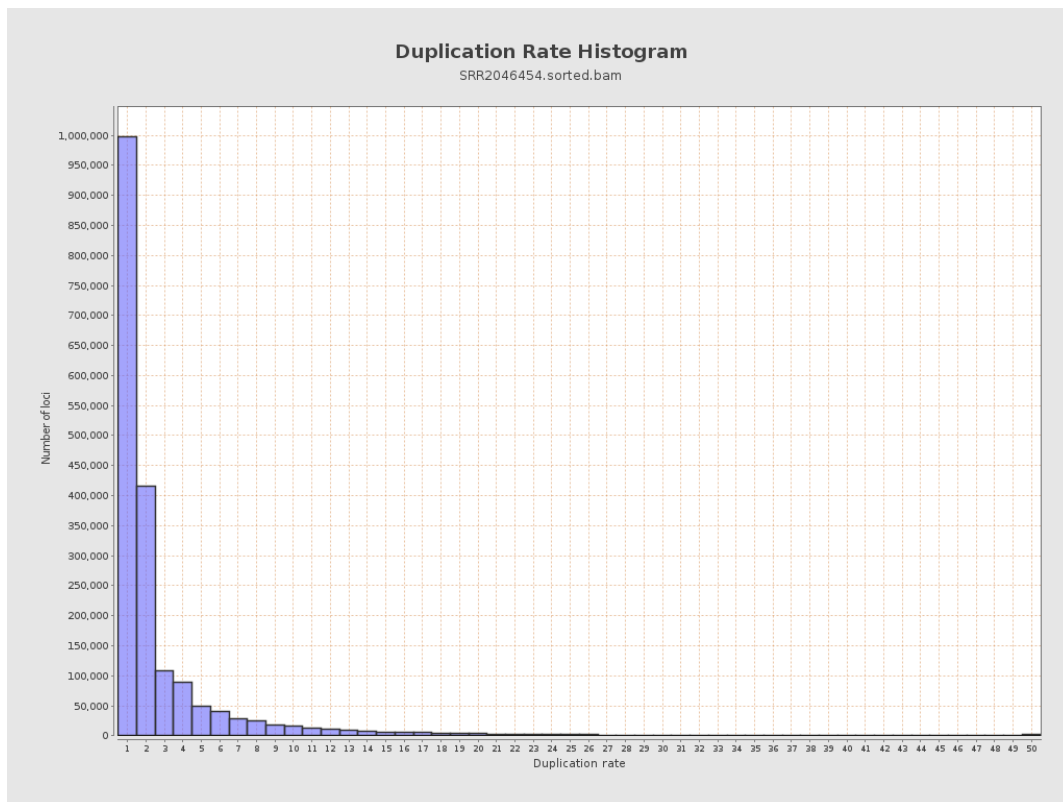
5. Results : Coverage Histogram (0-50X)



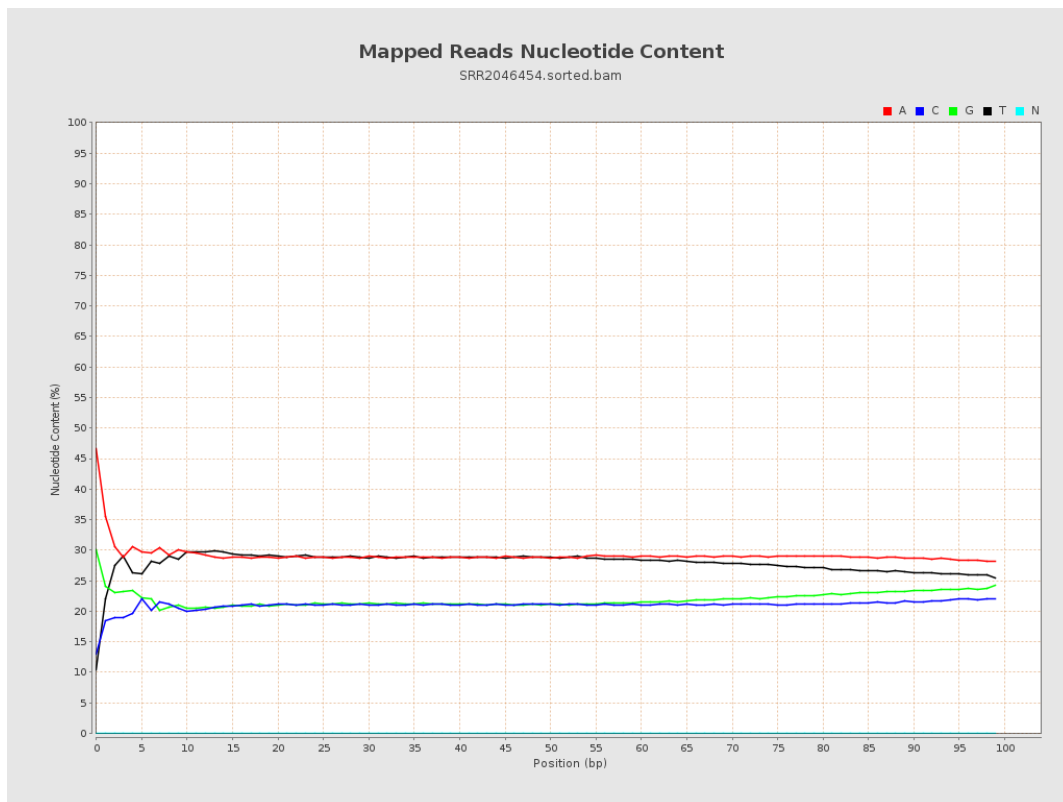
6. Results : Genome Fraction Coverage



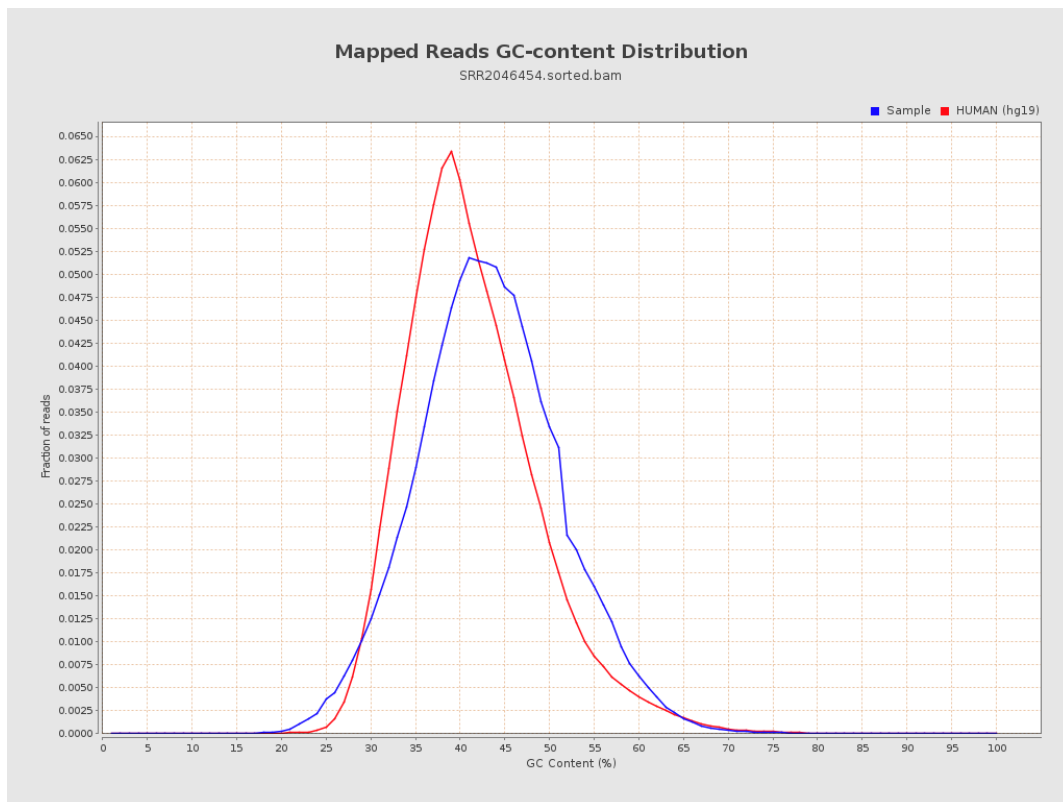
7. Results : Duplication Rate Histogram



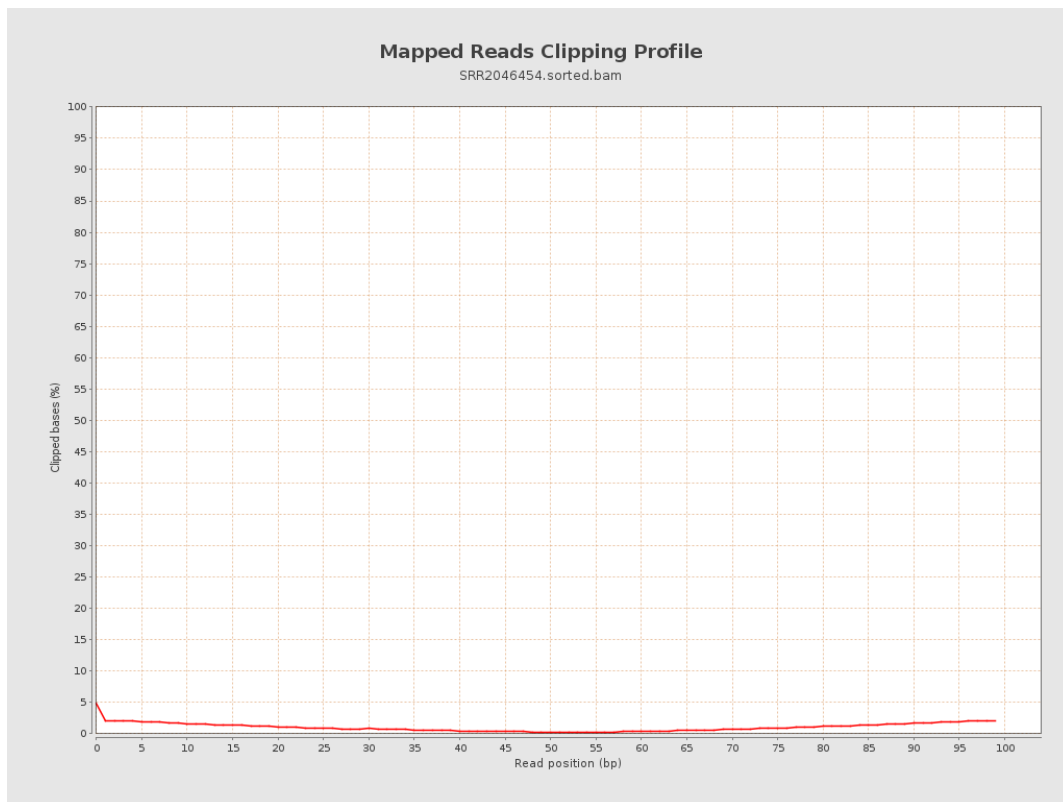
8. Results : Mapped Reads Nucleotide Content



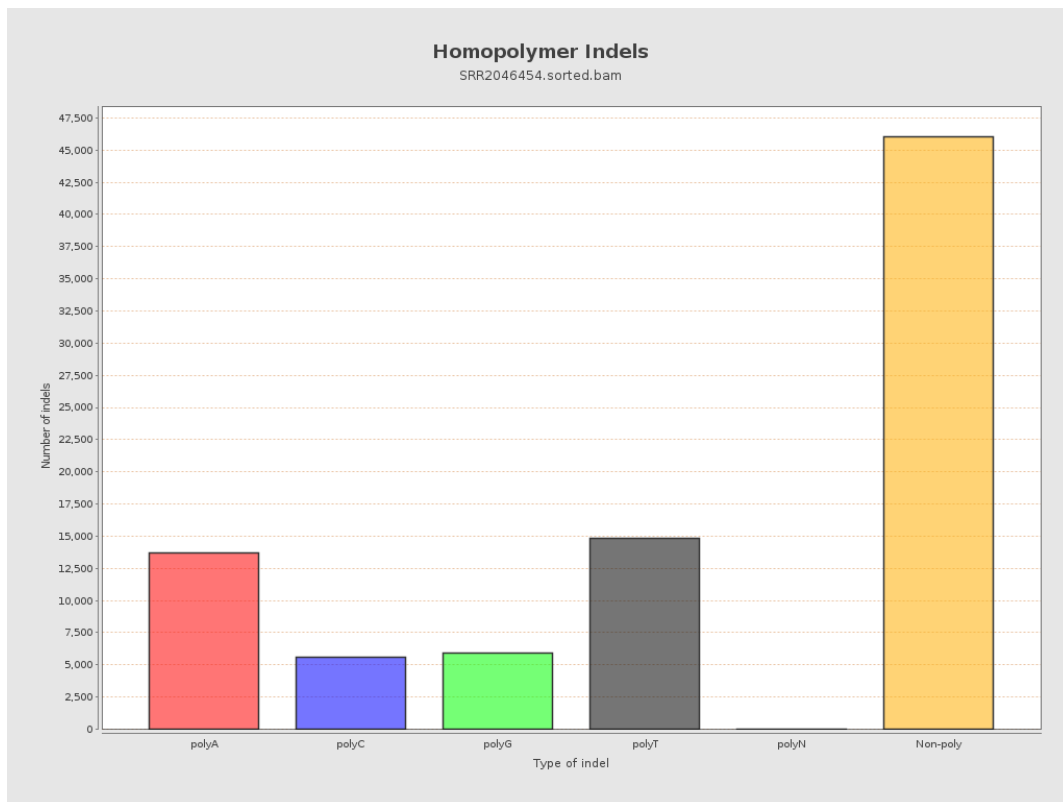
9. Results : Mapped Reads GC-content Distribution



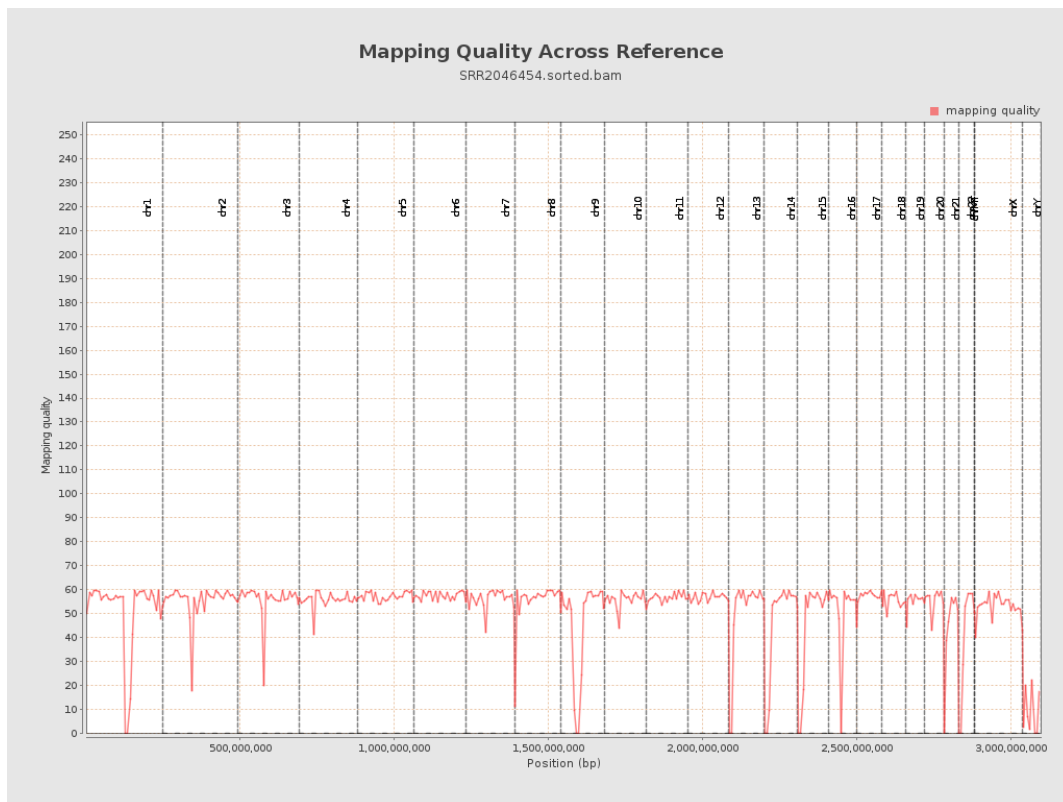
10. Results : Mapped Reads Clipping Profile



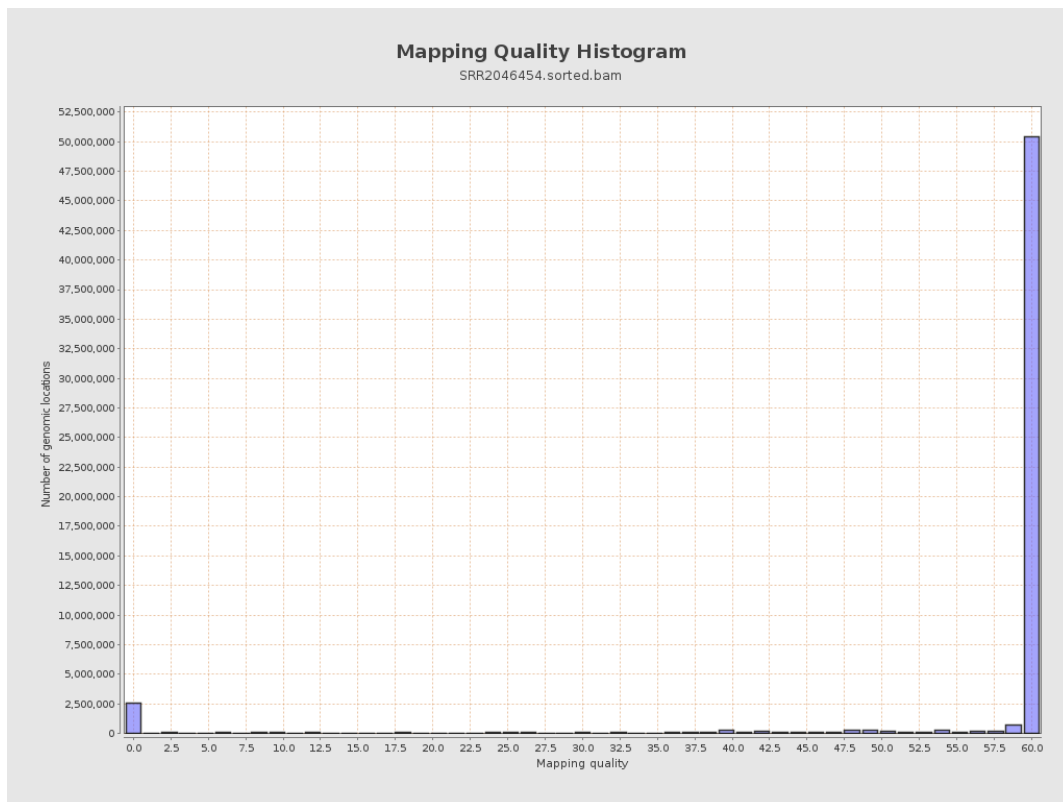
11. Results : Homopolymer Indels



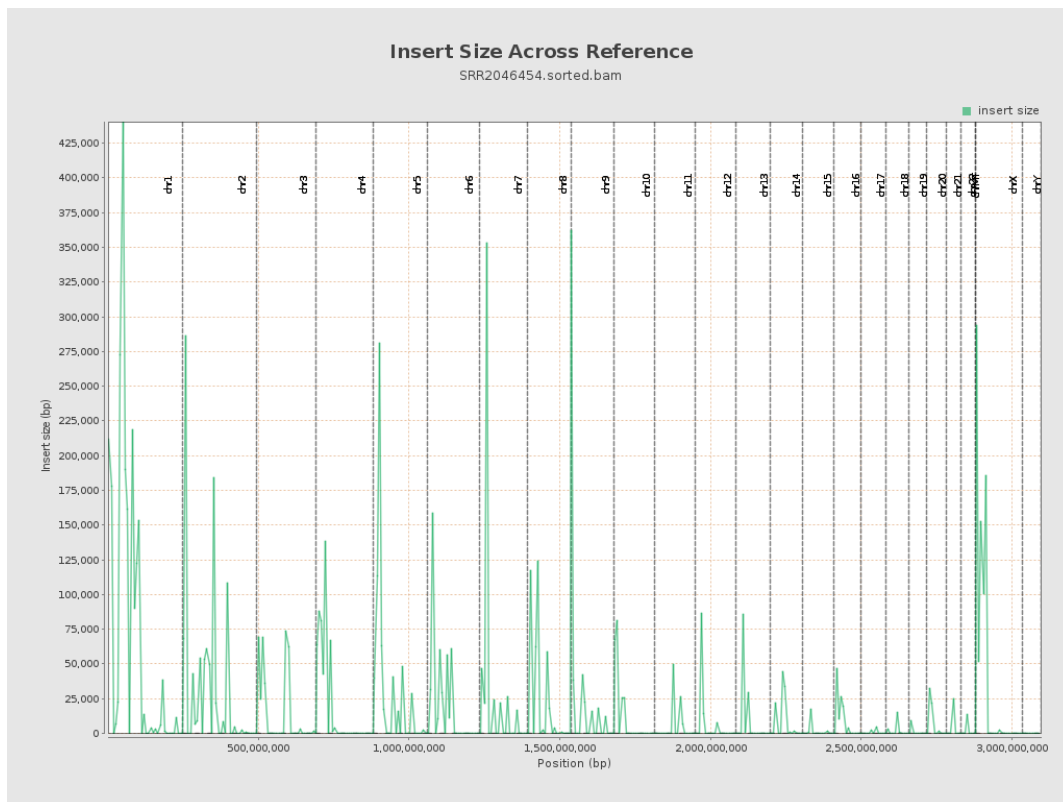
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

