

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 19:36:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472641.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_SRR3472641 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472641_1.fastq.gz SRR3472641_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 19:36:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472641.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,043,086
Mapped reads	15,947,778 / 99.41%
Unmapped reads	95,308 / 0.59%
Mapped paired reads	15,947,778 / 99.41%
Mapped reads, first in pair	7,992,831 / 49.82%
Mapped reads, second in pair	7,954,947 / 49.58%
Mapped reads, both in pair	15,883,826 / 99.01%
Mapped reads, singletons	63,952 / 0.4%
Secondary alignments	0
Supplementary alignments	79,331 / 0.49%
Read min/max/mean length	30 / 101 / 99.57
Duplicated reads (estimated)	11,267,787 / 70.23%
Duplication rate	49.48%
Clipped reads	1,152,616 / 7.18%

2.2. ACGT Content

Number/percentage of A's	423,376,414 / 27.04%
Number/percentage of C's	361,449,139 / 23.08%
Number/percentage of T's	424,028,820 / 27.08%
Number/percentage of G's	356,651,843 / 22.78%
Number/percentage of N's	292,142 / 0.02%

GC Percentage	45.86%
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2.3. Coverage

Mean	0.5059
Standard Deviation	23.5799

2.4. Mapping Quality

Mean Mapping Quality	54.94
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2.5. Insert size

Mean	18,805.66
Standard Deviation	1,389,765.06
P25/Median/P75	143 / 196 / 264

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	8,538,708
Insertions	90,577
Mapped reads with at least one insertion	0.56%
Deletions	74,443
Mapped reads with at least one deletion	0.46%
Homopolymer indels	46.96%

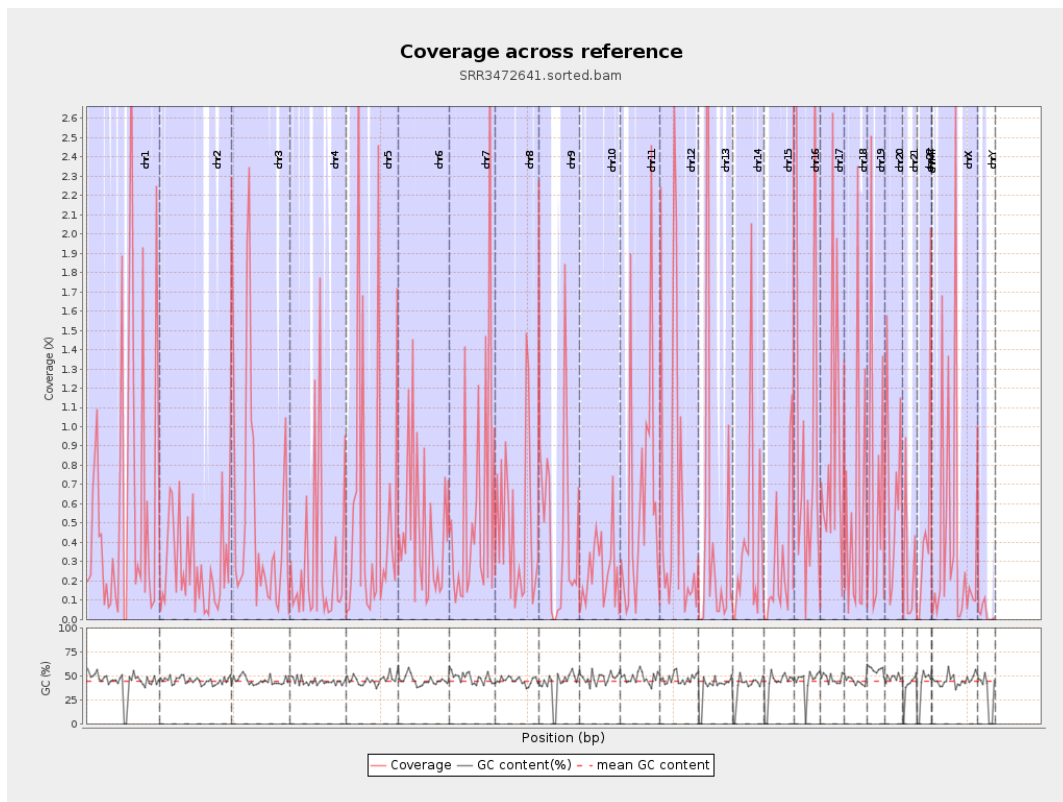
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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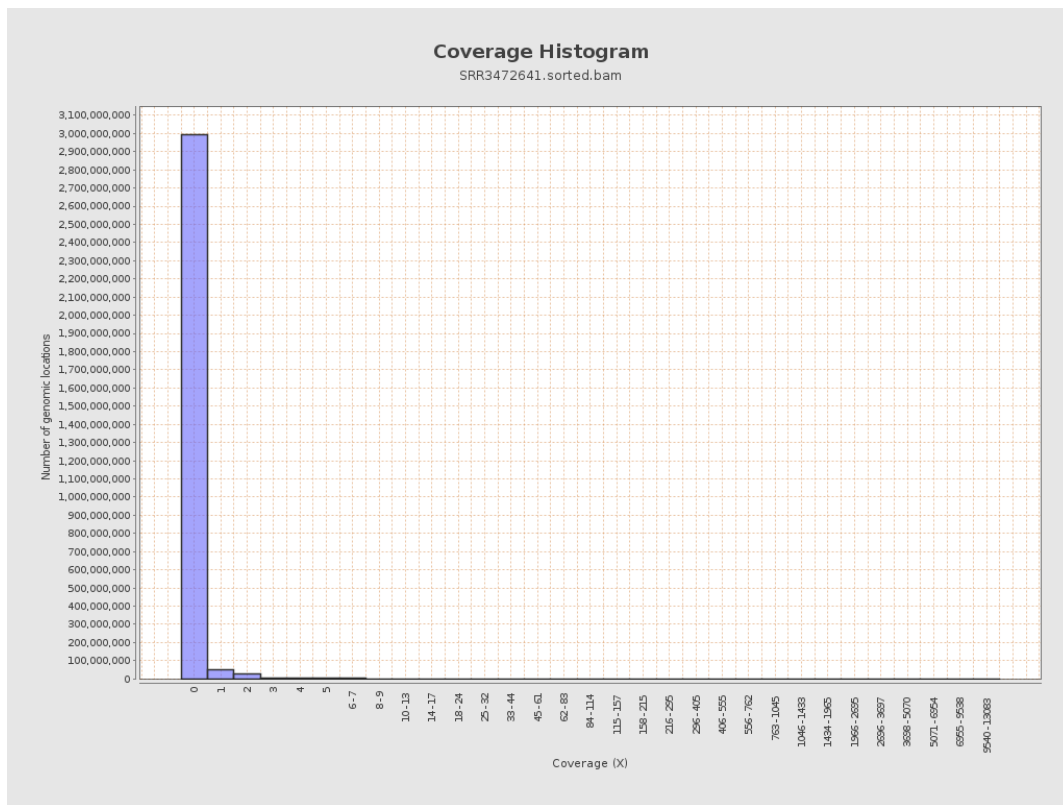
		bases	coverage	deviation
chr1	249250621	158596258	0.6363	27.5476
chr2	243199373	68650804	0.2823	12.0039
chr3	198022430	110070159	0.5558	19.2218
chr4	191154276	55052453	0.288	14.3938
chr5	180915260	107691526	0.5953	28.8167
chr6	171115067	77505954	0.4529	15.4778
chr7	159138663	95612070	0.6008	29.8529
chr8	146364022	71033074	0.4853	22.0188
chr9	141213431	68160379	0.4827	16.7693
chr10	135534747	34877098	0.2573	11.4068
chr11	135006516	84060187	0.6226	25.7418
chr12	133851895	81739757	0.6107	21.5598
chr13	115169878	54924816	0.4769	24.2795
chr14	107349540	40263377	0.3751	15.3387
chr15	102531392	31310481	0.3054	12.469
chr16	90354753	115087315	1.2737	46.8019
chr17	81195210	73347955	0.9034	29.0865
chr18	78077248	45353169	0.5809	36.6969
chr19	59128983	44448860	0.7517	26.5725
chr20	63025520	42114179	0.6682	35.2787
chr21	48129895	11857646	0.2464	17.6695
chr22	51304566	26549502	0.5175	23.2298
chrMT	16571	395	0.0238	0.1525
chrX	155270560	65667236	0.4229	28.613

chrY	59373566	1998842	0.0337	2.0414
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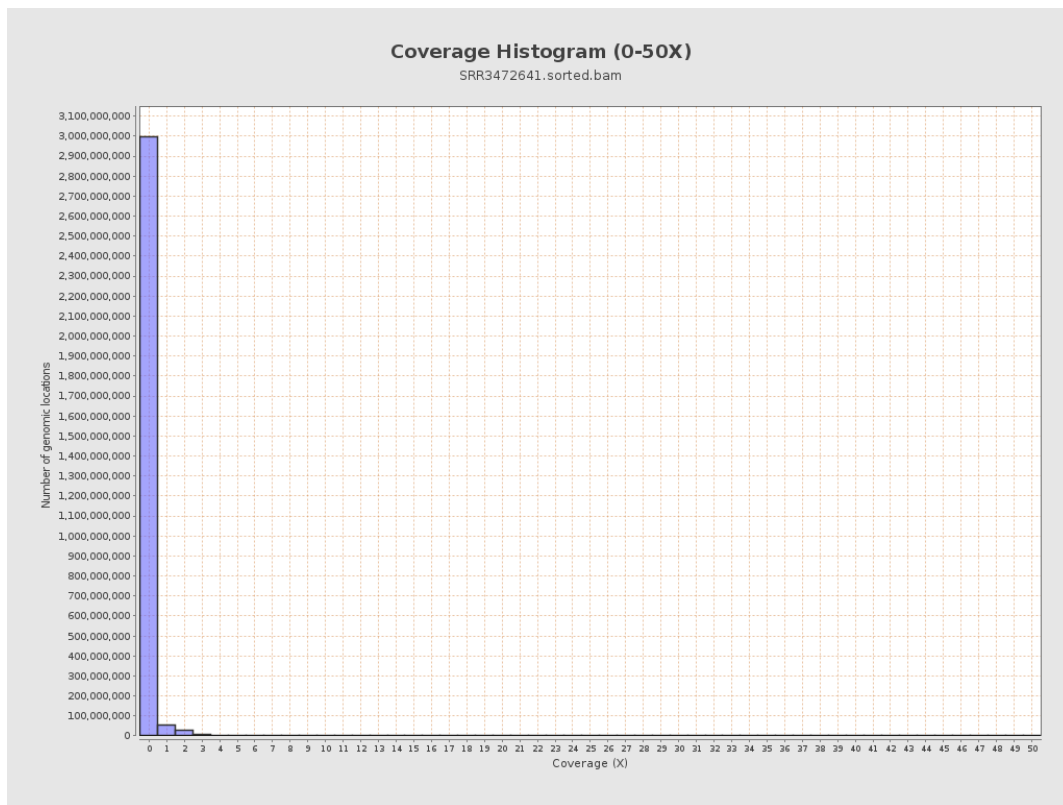
3. Results : Coverage across reference



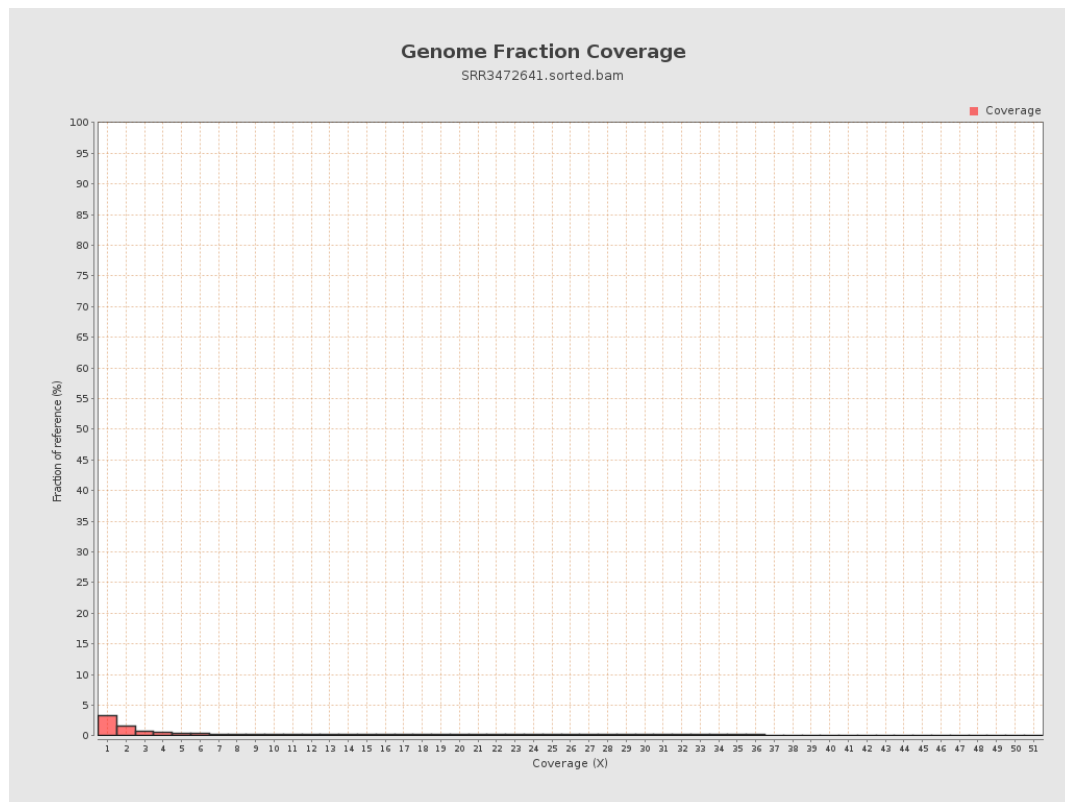
4. Results : Coverage Histogram



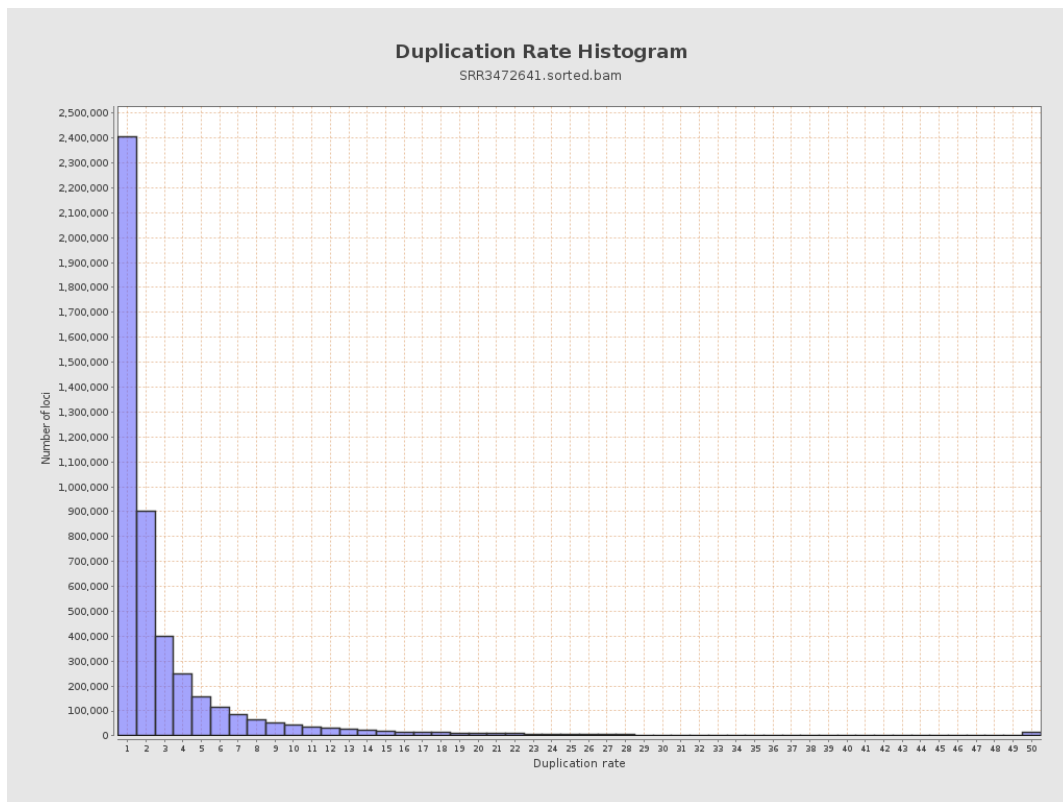
5. Results : Coverage Histogram (0-50X)



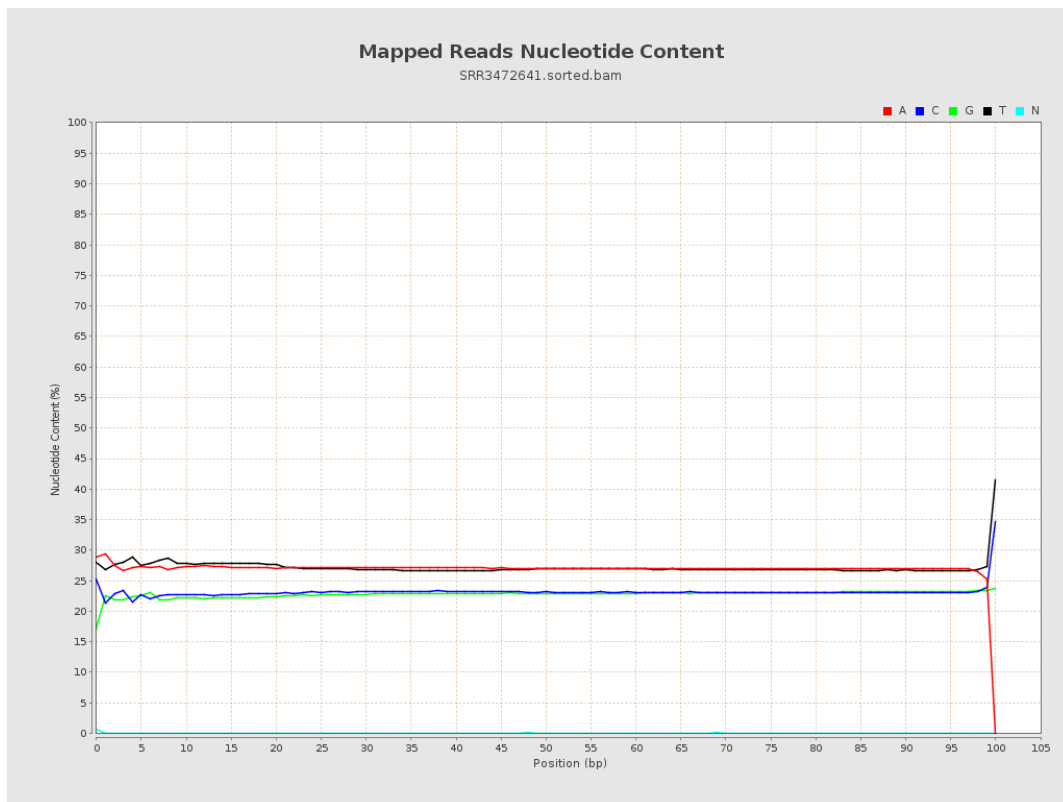
6. Results : Genome Fraction Coverage



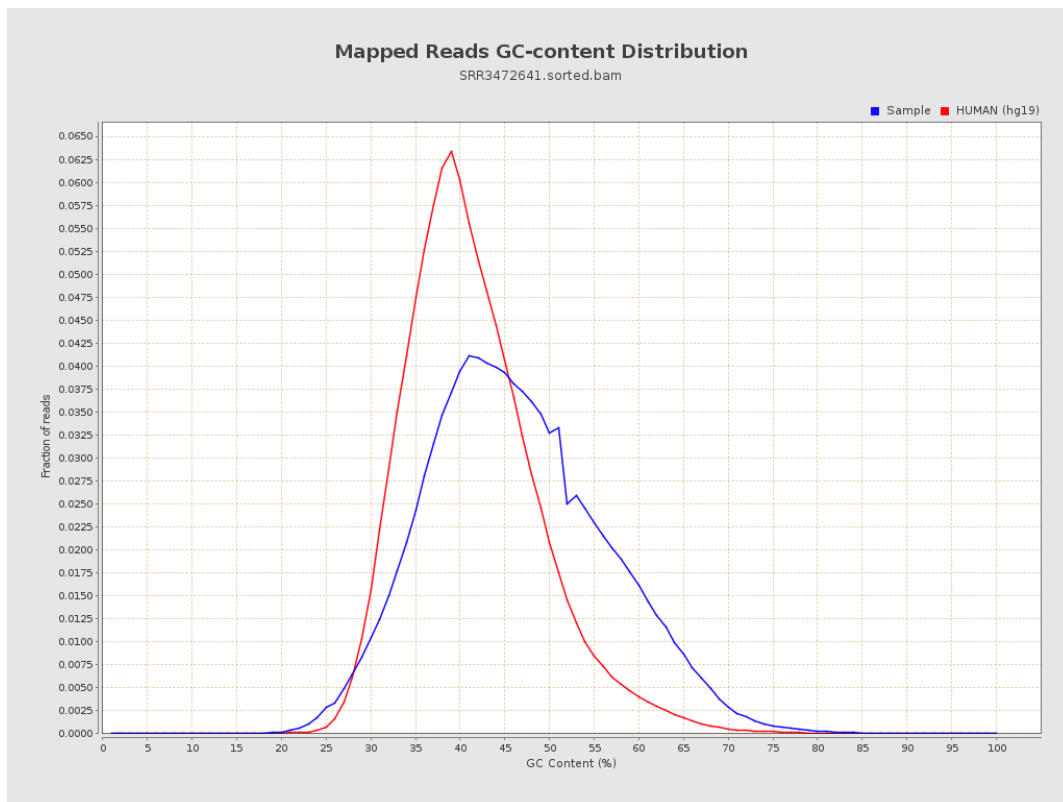
7. Results : Duplication Rate Histogram



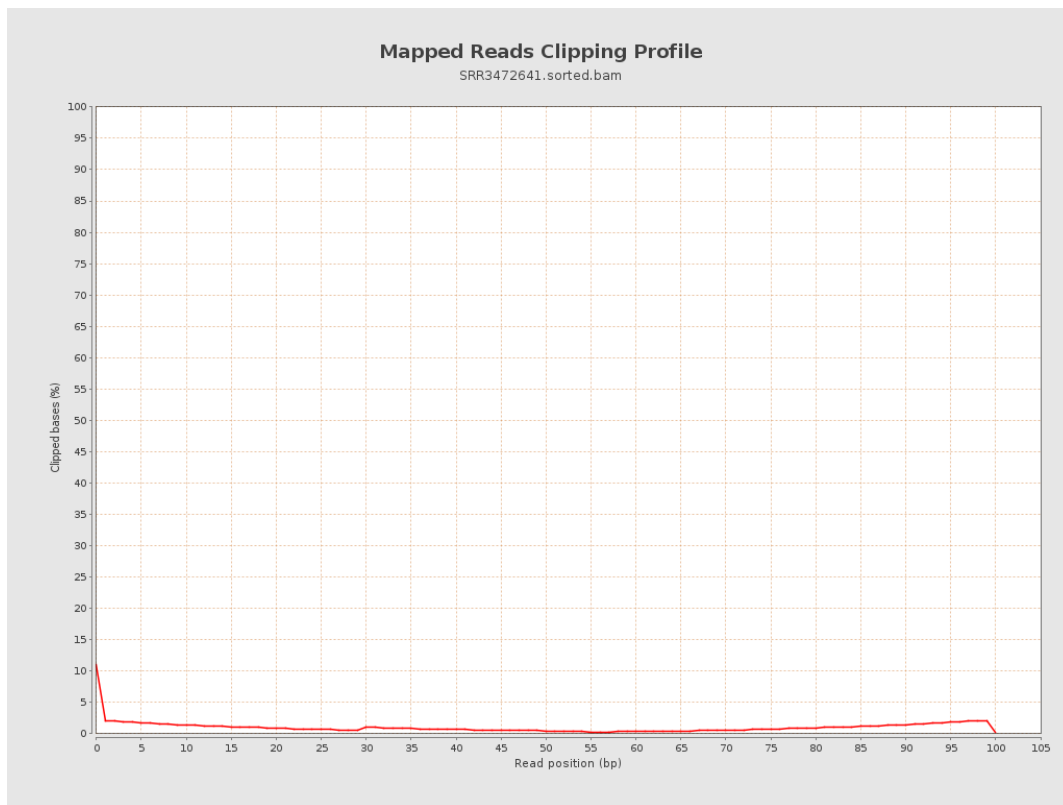
8. Results : Mapped Reads Nucleotide Content



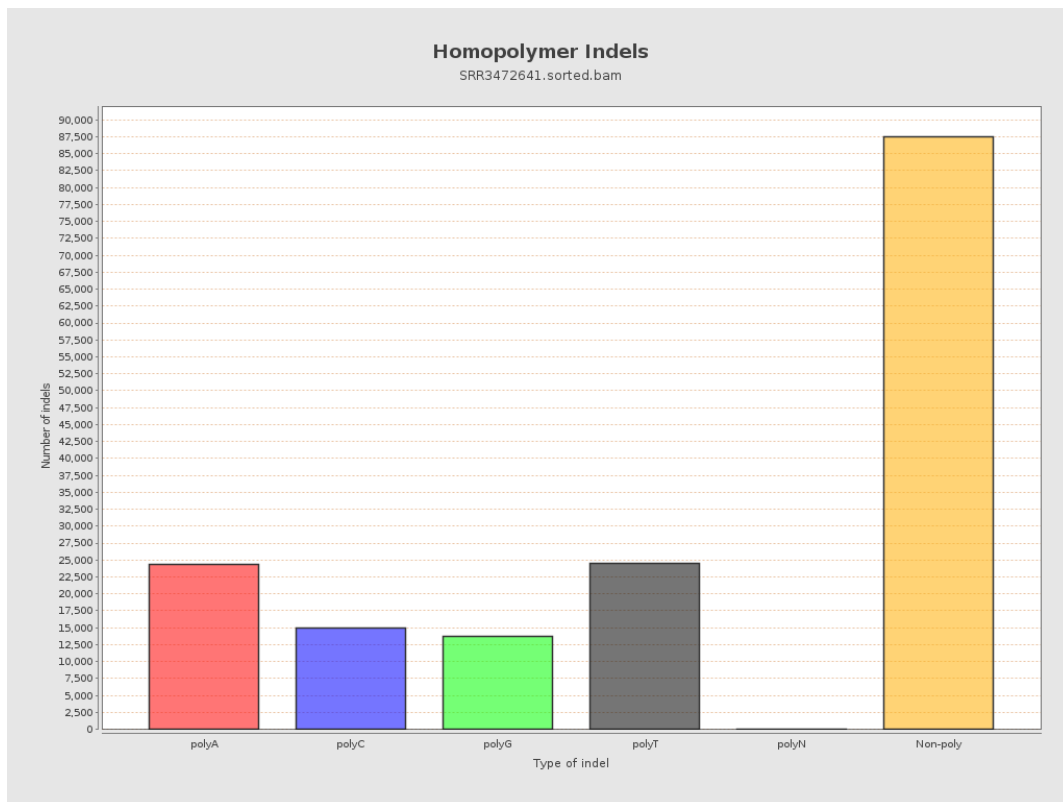
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



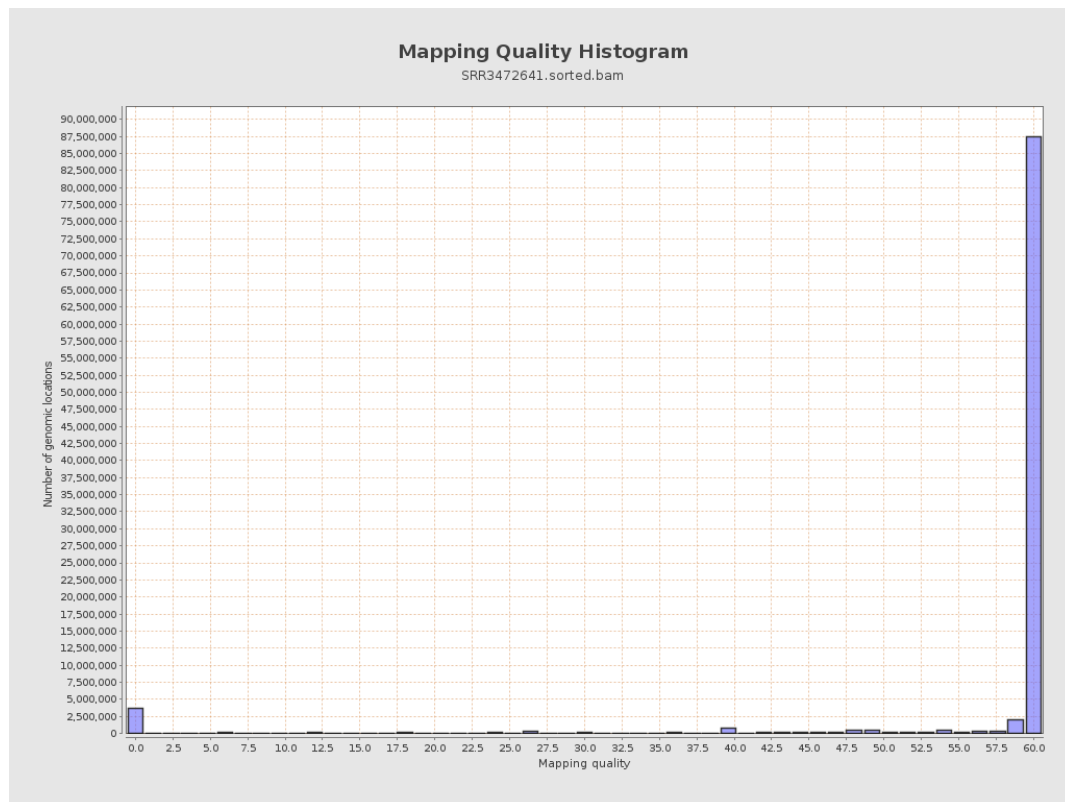
11. Results : Homopolymer Indels



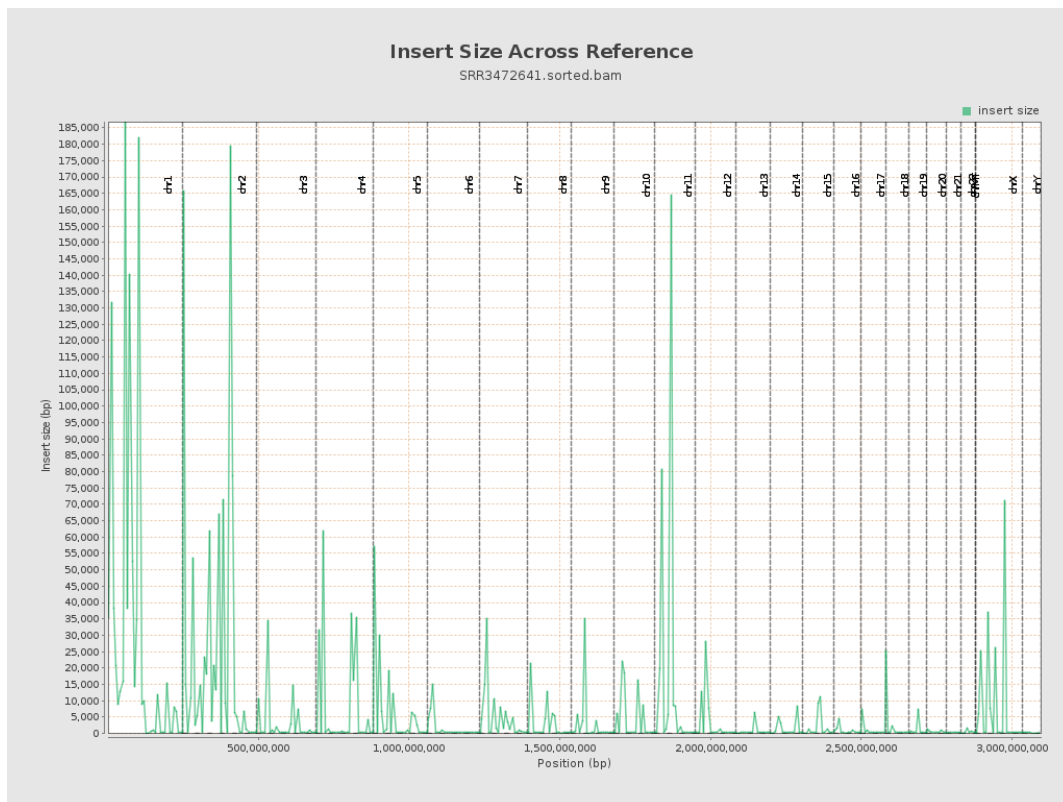
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

