

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 16:10:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038451.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_SRR5038451 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038451_1.fastq.gz SRR5038451_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 16:10:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038451.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,114,194
Mapped reads	14,398,463 / 95.26%
Unmapped reads	715,731 / 4.74%
Mapped paired reads	14,398,463 / 95.26%
Mapped reads, first in pair	7,262,172 / 48.05%
Mapped reads, second in pair	7,136,291 / 47.22%
Mapped reads, both in pair	14,242,234 / 94.23%
Mapped reads, singletons	156,229 / 1.03%
Secondary alignments	0
Supplementary alignments	316,699 / 2.1%
Read min/max/mean length	30 / 150 / 151.09
Duplicated reads (estimated)	2,929,399 / 19.38%
Duplication rate	10.6%
Clipped reads	3,350,386 / 22.17%

2.2. ACGT Content

Number/percentage of A's	613,881,952 / 29.79%
Number/percentage of C's	412,730,301 / 20.03%
Number/percentage of T's	612,311,264 / 29.71%
Number/percentage of G's	421,688,954 / 20.46%
Number/percentage of N's	44,682 / 0%

GC Percentage	40.49%
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2.3. Coverage

Mean	0.6662
Standard Deviation	15.2855

2.4. Mapping Quality

Mean Mapping Quality	53.56
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2.5. Insert size

Mean	72,020.49
Standard Deviation	2,456,077.25
P25/Median/P75	201 / 246 / 303

2.6. Mismatches and indels

General error rate	1.59%
Mismatches	31,320,534
Insertions	450,253
Mapped reads with at least one insertion	2.9%
Deletions	775,206
Mapped reads with at least one deletion	5.15%
Homopolymer indels	45.68%

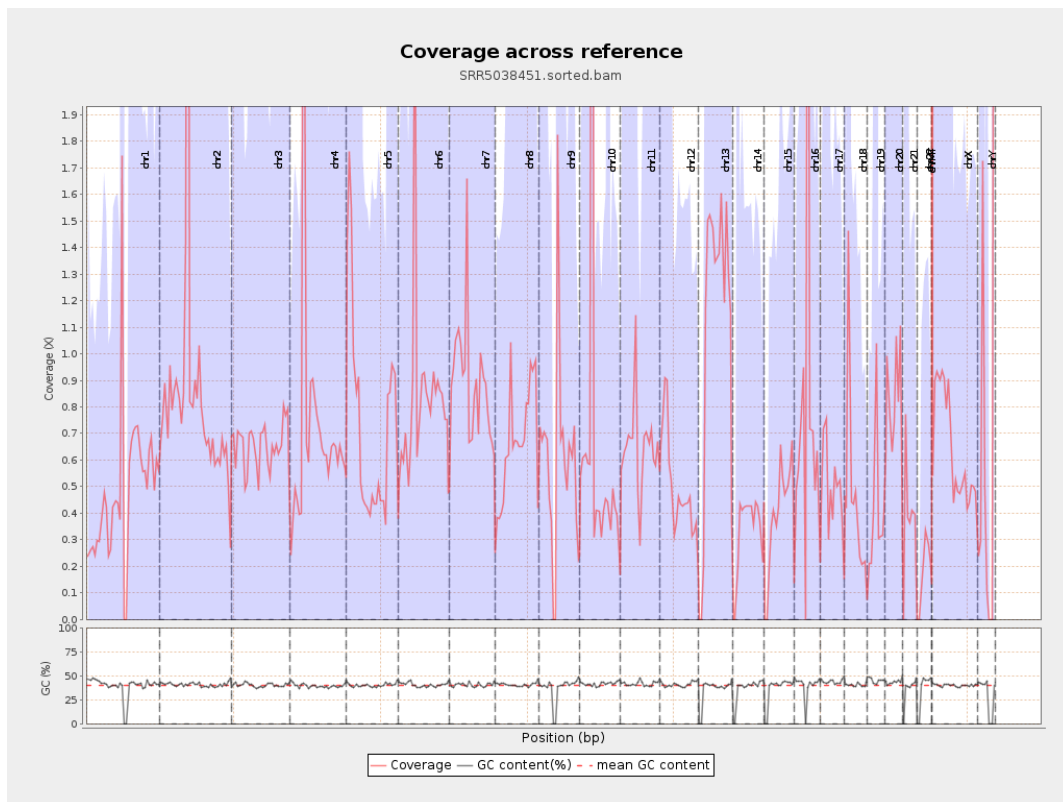
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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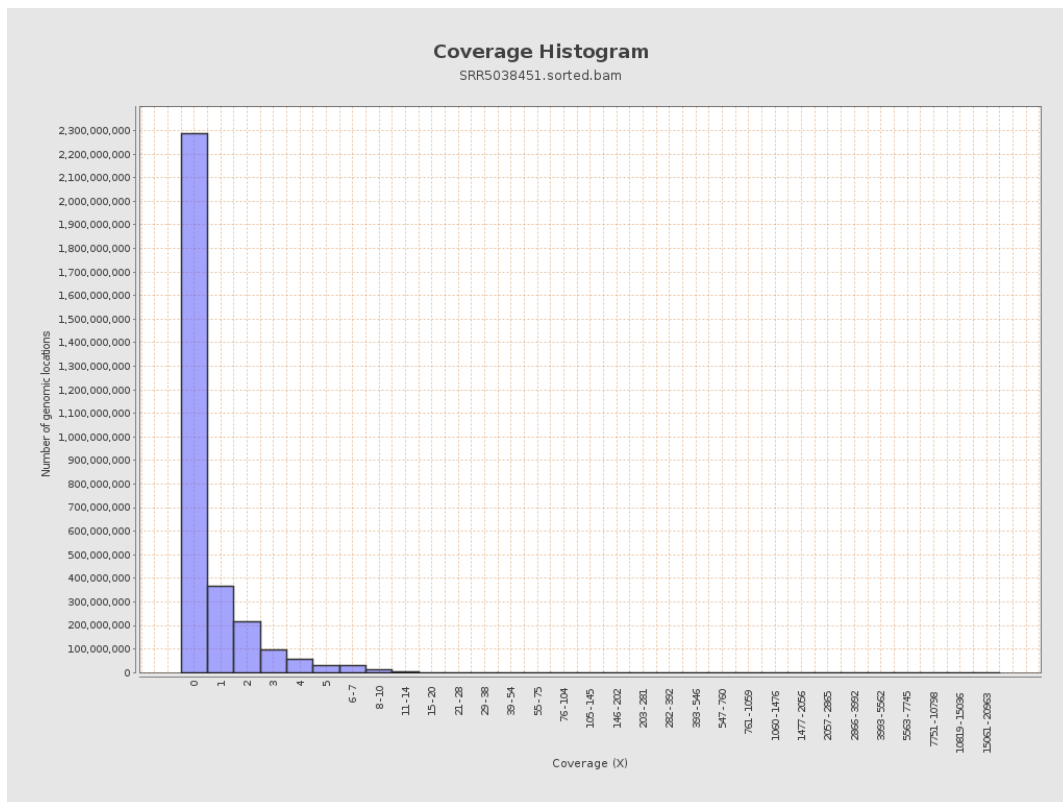
		bases	coverage	deviation
chr1	249250621	120360449	0.4829	21.8251
chr2	243199373	212416016	0.8734	19.562
chr3	198022430	129649671	0.6547	1.5729
chr4	191154276	136540643	0.7143	17.618
chr5	180915260	132654651	0.7332	1.8133
chr6	171115067	145508874	0.8504	19.0707
chr7	159138663	140535780	0.8831	13.5541
chr8	146364022	98605601	0.6737	3.8725
chr9	141213431	81860969	0.5797	23.0486
chr10	135534747	95505087	0.7047	31.7795
chr11	135006516	85716777	0.6349	7.2688
chr12	133851895	67331921	0.503	1.3477
chr13	115169878	130611144	1.1341	2.0633
chr14	107349540	35759550	0.3331	1.3983
chr15	102531392	41171876	0.4016	1.084
chr16	90354753	76117523	0.8424	20.5006
chr17	81195210	39643365	0.4882	6.6737
chr18	78077248	35270865	0.4517	19.2664
chr19	59128983	22650328	0.3831	12.233
chr20	63025520	51642063	0.8194	5.2787
chr21	48129895	18845482	0.3916	8.0432
chr22	51304566	9191596	0.1792	0.8436
chrMT	16571	4308035	259.9744	153.0884
chrX	155270560	99272527	0.6394	2.3726

chrY	59373566	51203558	0.8624	29.1676
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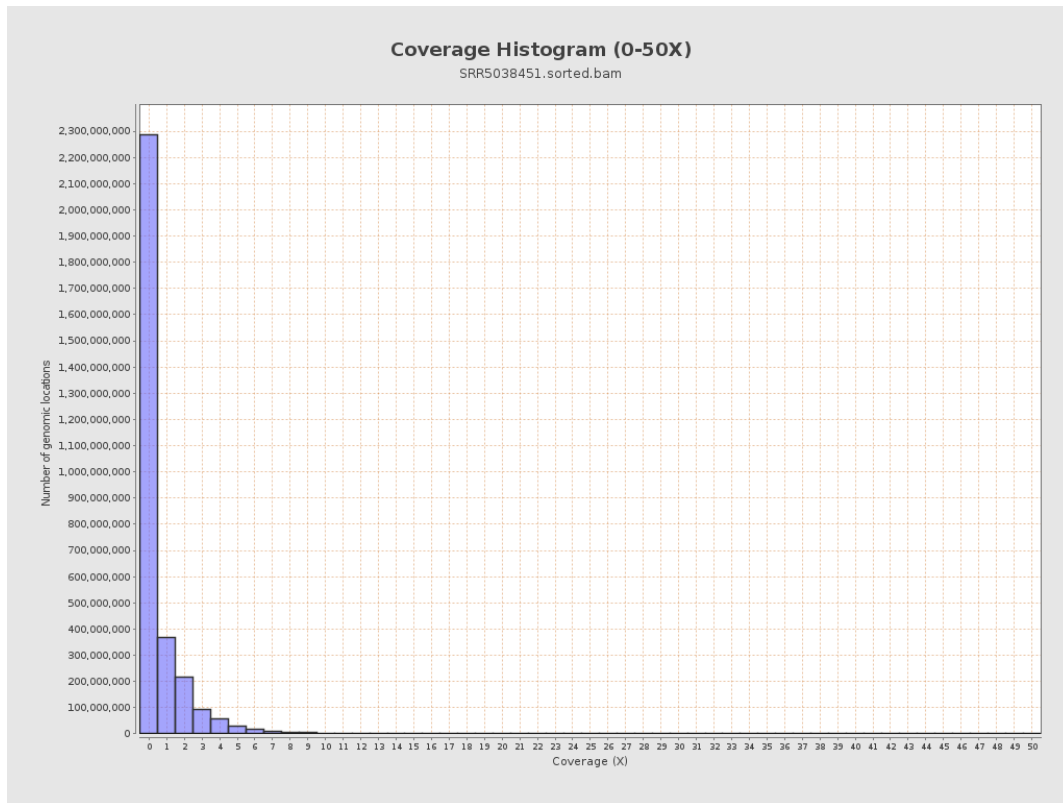
3. Results : Coverage across reference



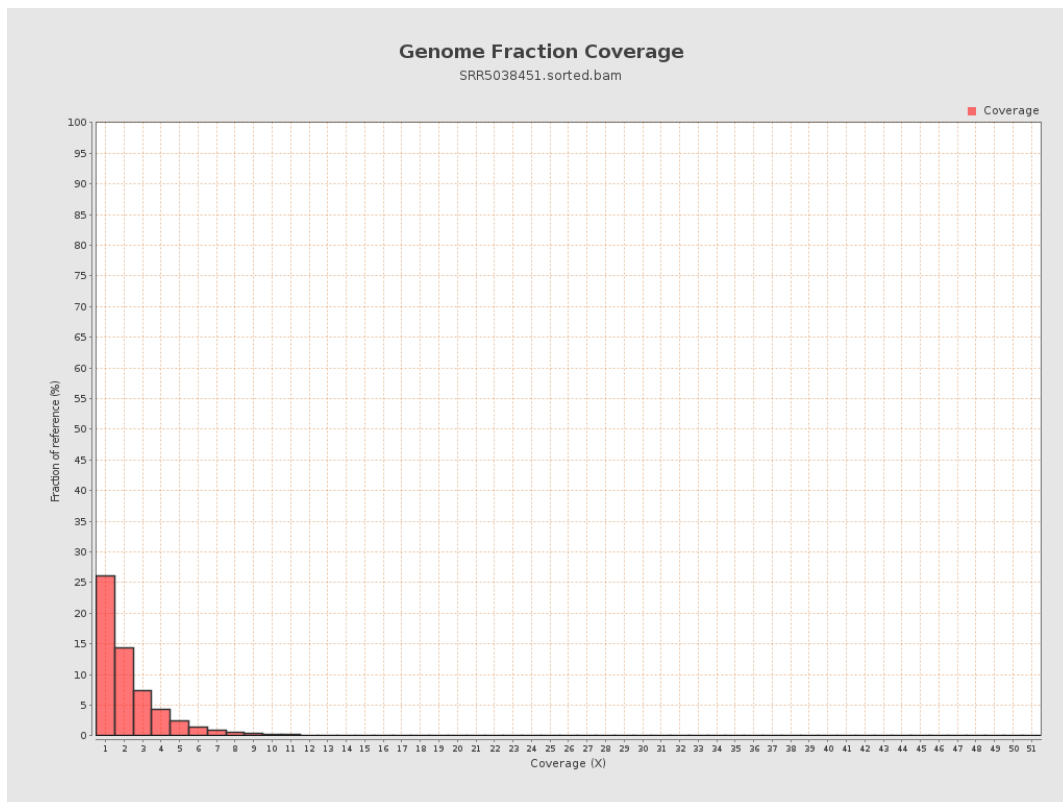
4. Results : Coverage Histogram



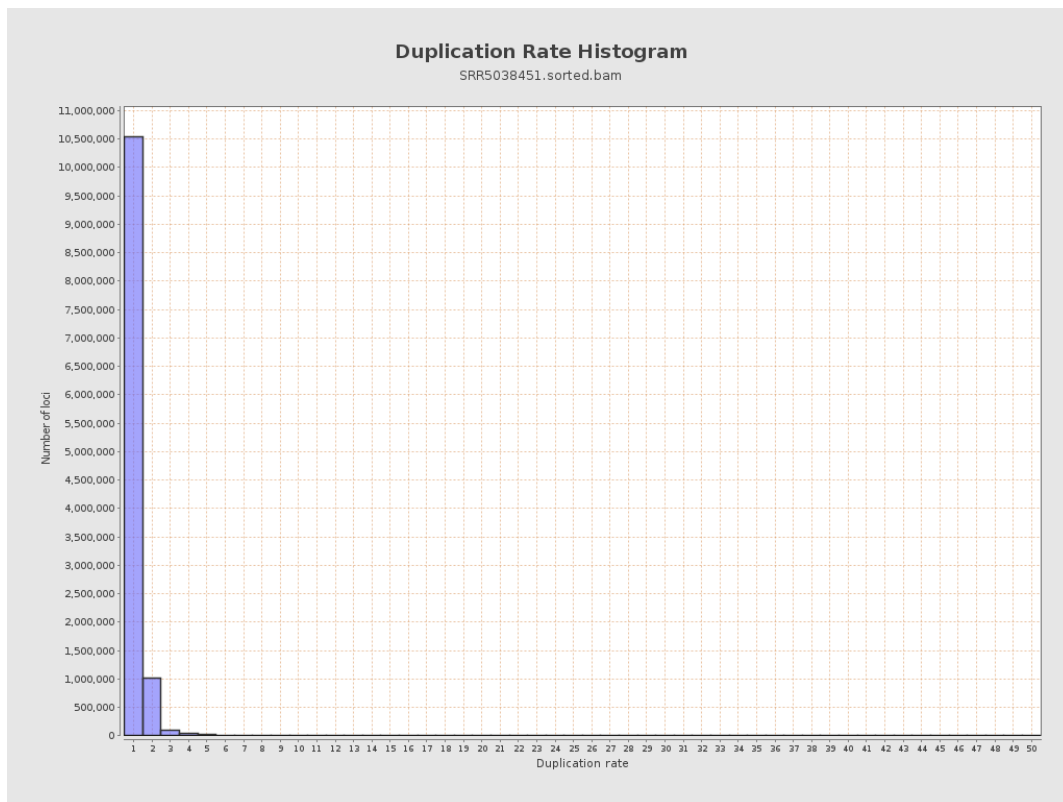
5. Results : Coverage Histogram (0-50X)



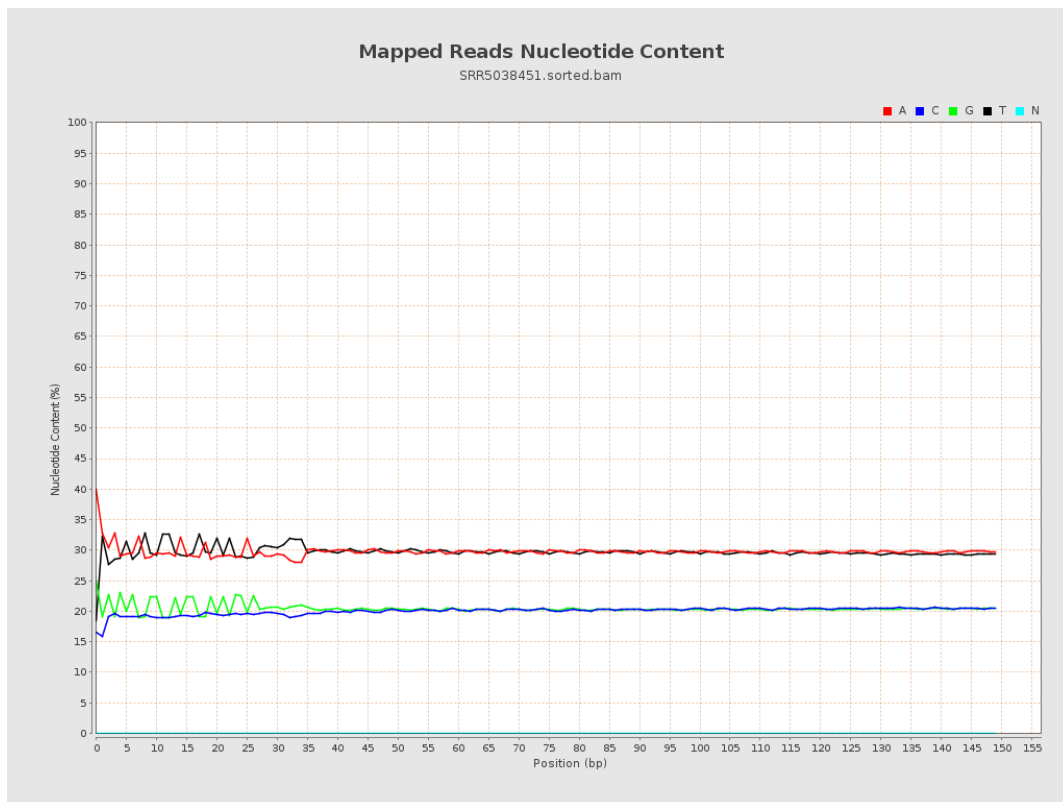
6. Results : Genome Fraction Coverage



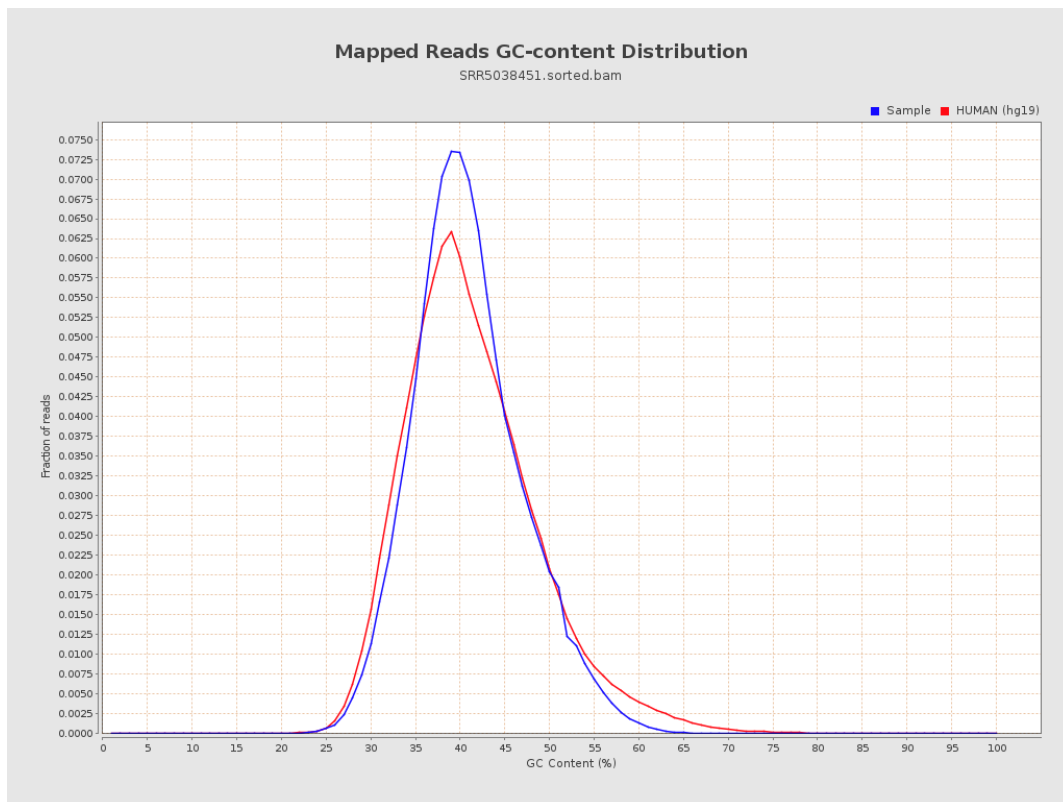
7. Results : Duplication Rate Histogram



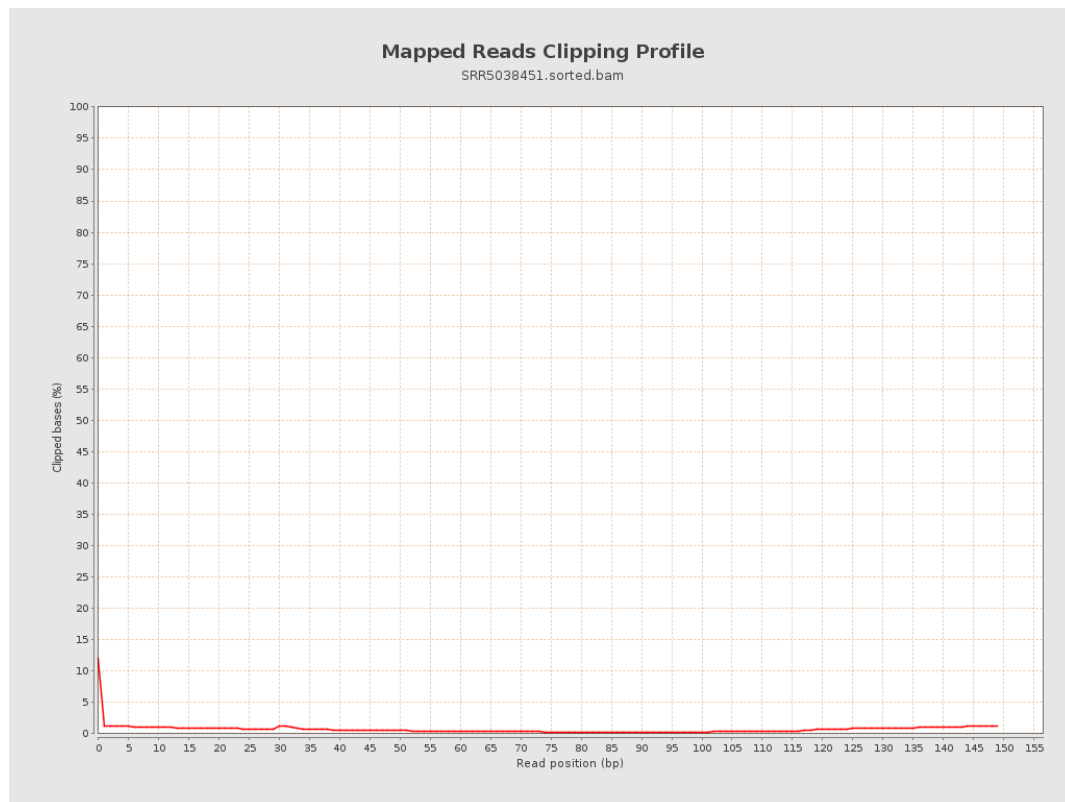
8. Results : Mapped Reads Nucleotide Content



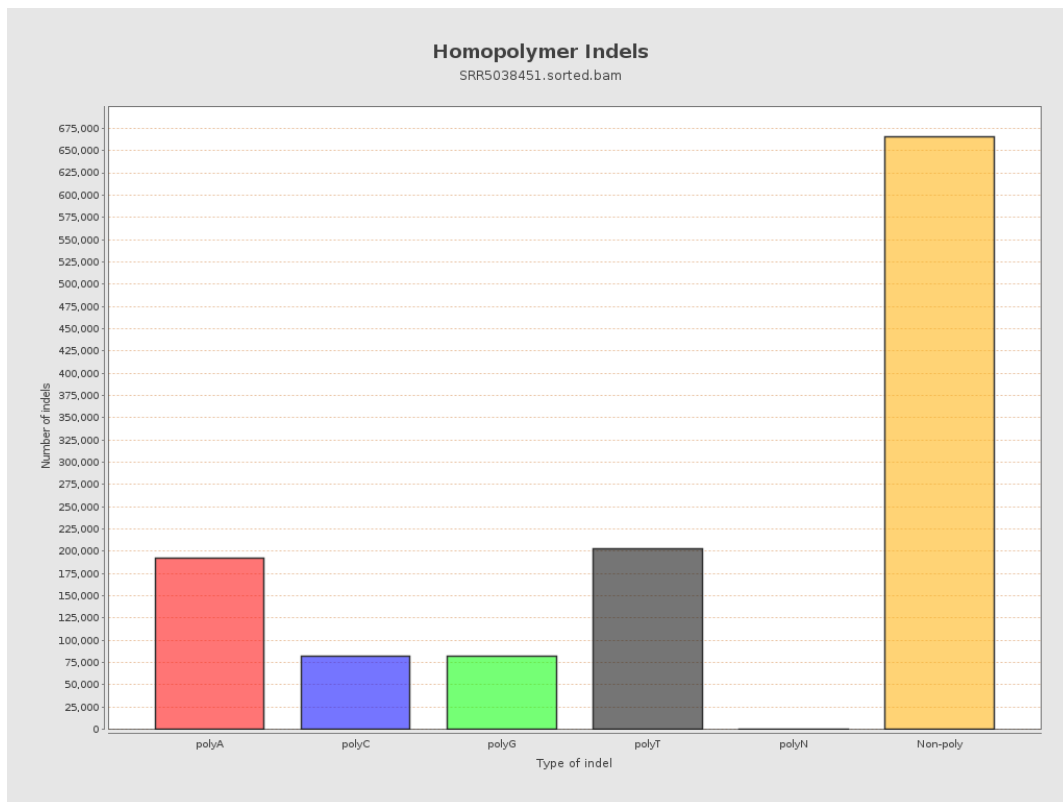
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



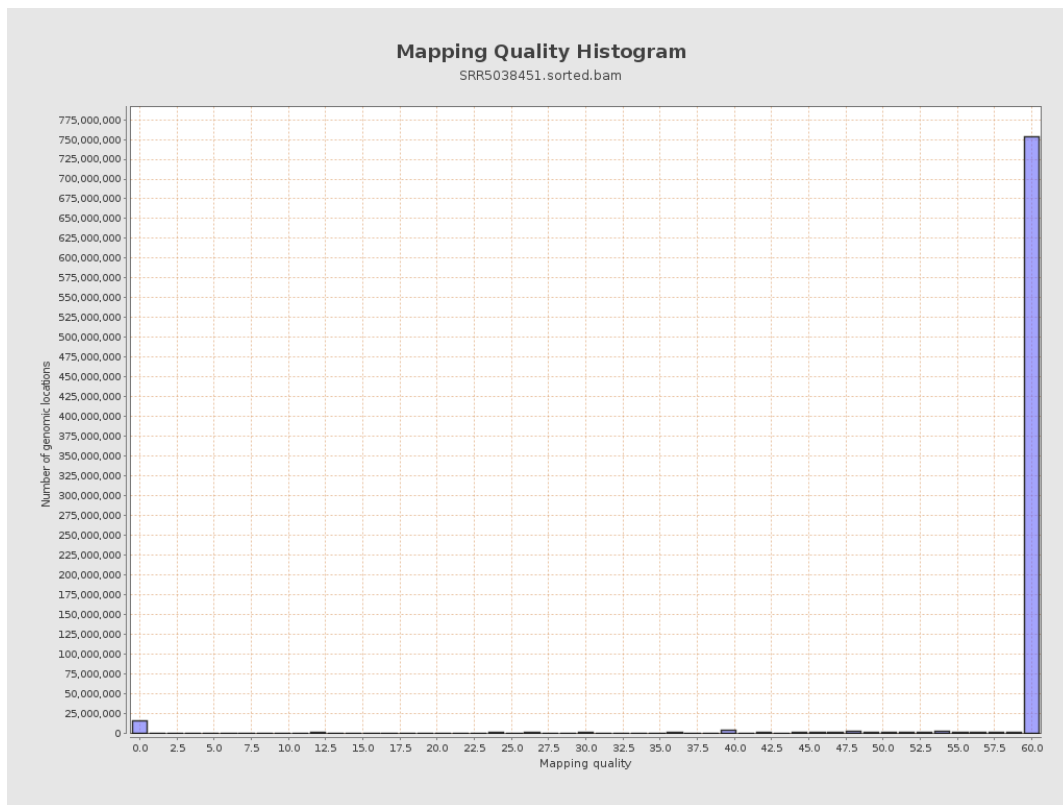
11. Results : Homopolymer Indels



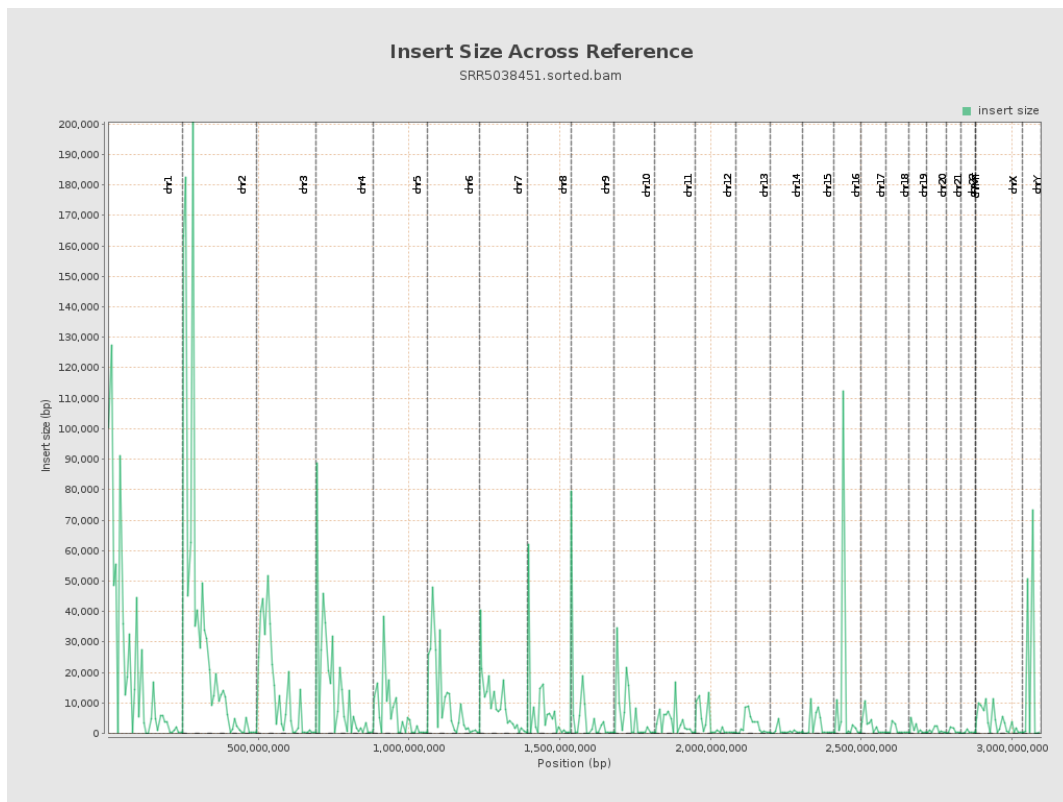
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

