

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 21:17:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046538.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_SRR2046538 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046538_1.fastq.gz SRR2046538_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 21:17:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046538.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,924,328
Mapped reads	5,792,441 / 97.77%
Unmapped reads	131,887 / 2.23%
Mapped paired reads	5,792,441 / 97.77%
Mapped reads, first in pair	2,945,985 / 49.73%
Mapped reads, second in pair	2,846,456 / 48.05%
Mapped reads, both in pair	5,678,388 / 95.85%
Mapped reads, singletons	114,053 / 1.93%
Secondary alignments	0
Supplementary alignments	37,259 / 0.63%
Read min/max/mean length	30 / 100 / 100.25
Duplicated reads (estimated)	3,924,955 / 66.25%
Duplication rate	29.2%
Clipped reads	1,574,260 / 26.57%

2.2. ACGT Content

Number/percentage of A's	156,983,422 / 28.57%
Number/percentage of C's	118,368,626 / 21.54%
Number/percentage of T's	155,809,689 / 28.35%
Number/percentage of G's	118,309,985 / 21.53%
Number/percentage of N's	51,139 / 0.01%

GC Percentage	43.07%
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2.3. Coverage

Mean	0.1776
Standard Deviation	26.9436

2.4. Mapping Quality

Mean Mapping Quality	52.01
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2.5. Insert size

Mean	37,018.13
Standard Deviation	1,959,207.68
P25/Median/P75	100 / 127 / 158

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	2,285,632
Insertions	57,729
Mapped reads with at least one insertion	0.98%
Deletions	69,993
Mapped reads with at least one deletion	1.17%
Homopolymer indels	47.87%

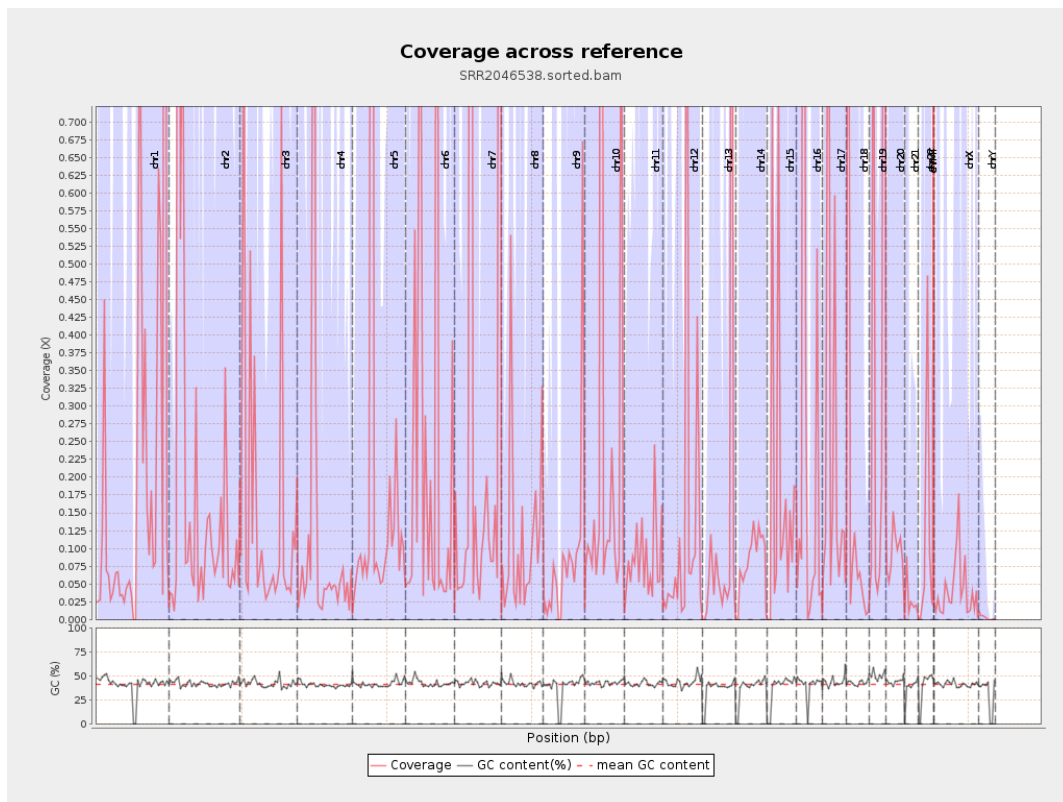
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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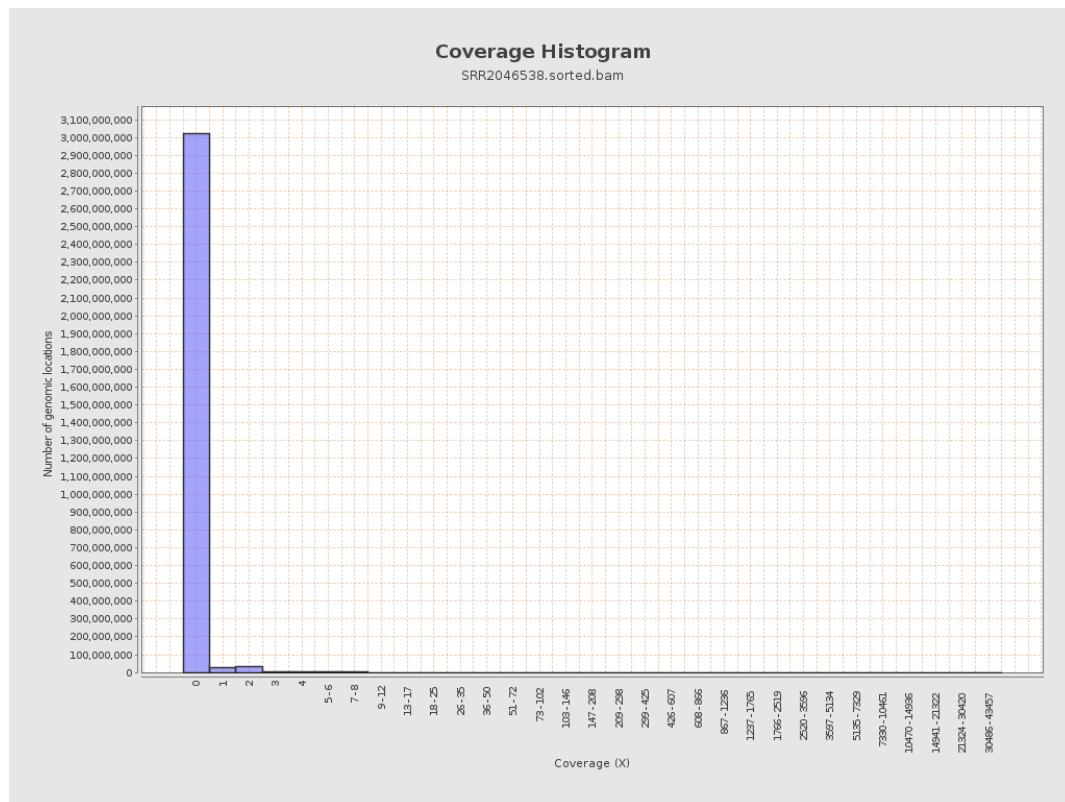
		bases	coverage	deviation
chr1	249250621	56033190	0.2248	22.8854
chr2	243199373	54559428	0.2243	36.1278
chr3	198022430	30177115	0.1524	14.5106
chr4	191154276	20768799	0.1086	10.719
chr5	180915260	35194788	0.1945	25.5218
chr6	171115067	43413962	0.2537	25.2789
chr7	159138663	52534258	0.3301	57.6481
chr8	146364022	16229064	0.1109	7.6183
chr9	141213431	12722836	0.0901	8.2633
chr10	135534747	46263239	0.3413	58.85
chr11	135006516	11306467	0.0837	2.6196
chr12	133851895	18954152	0.1416	36.4698
chr13	115169878	15670853	0.1361	20.7107
chr14	107349540	8997235	0.0838	2.0933
chr15	102531392	19041739	0.1857	16.4921
chr16	90354753	26355293	0.2917	28.7907
chr17	81195210	20054771	0.247	20.8147
chr18	78077248	15011768	0.1923	18.903
chr19	59128983	27152720	0.4592	38.4516
chr20	63025520	5908567	0.0937	5.3756
chr21	48129895	1272222	0.0264	2.6199
chr22	51304566	5262427	0.1026	12.2289
chrMT	16571	78825	4.7568	3.1461
chrX	155270560	6608417	0.0426	0.9913

chrY	59373566	163373	0.0028	0.1507
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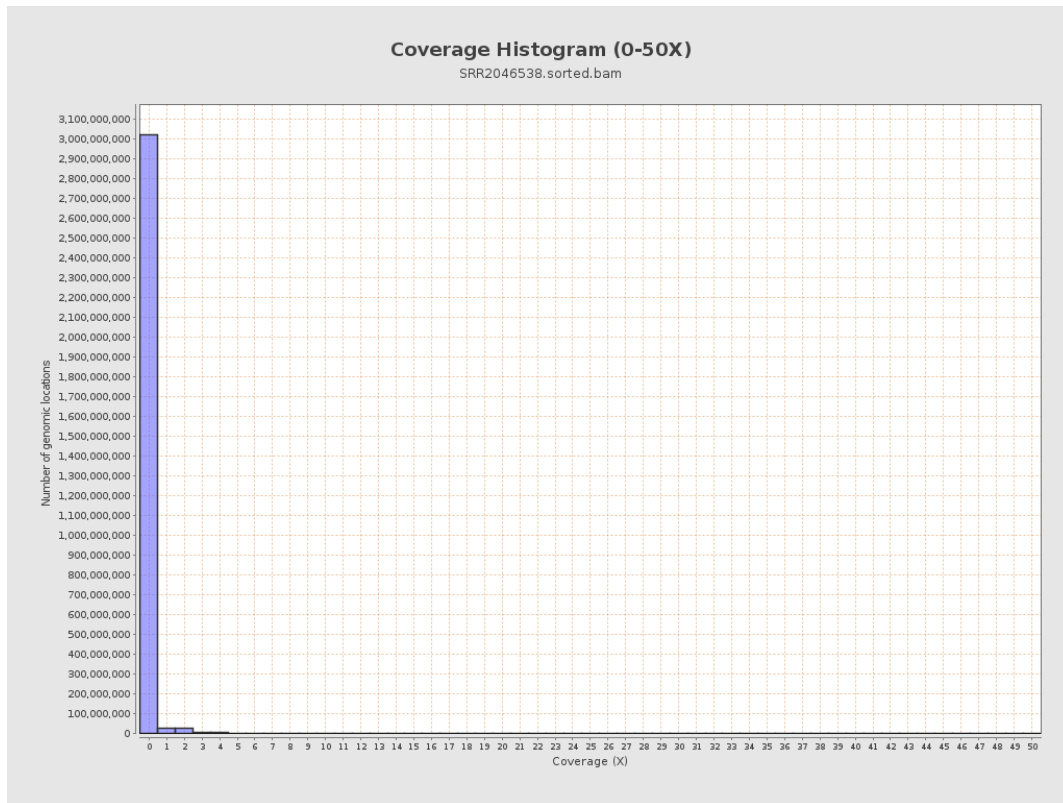
3. Results : Coverage across reference



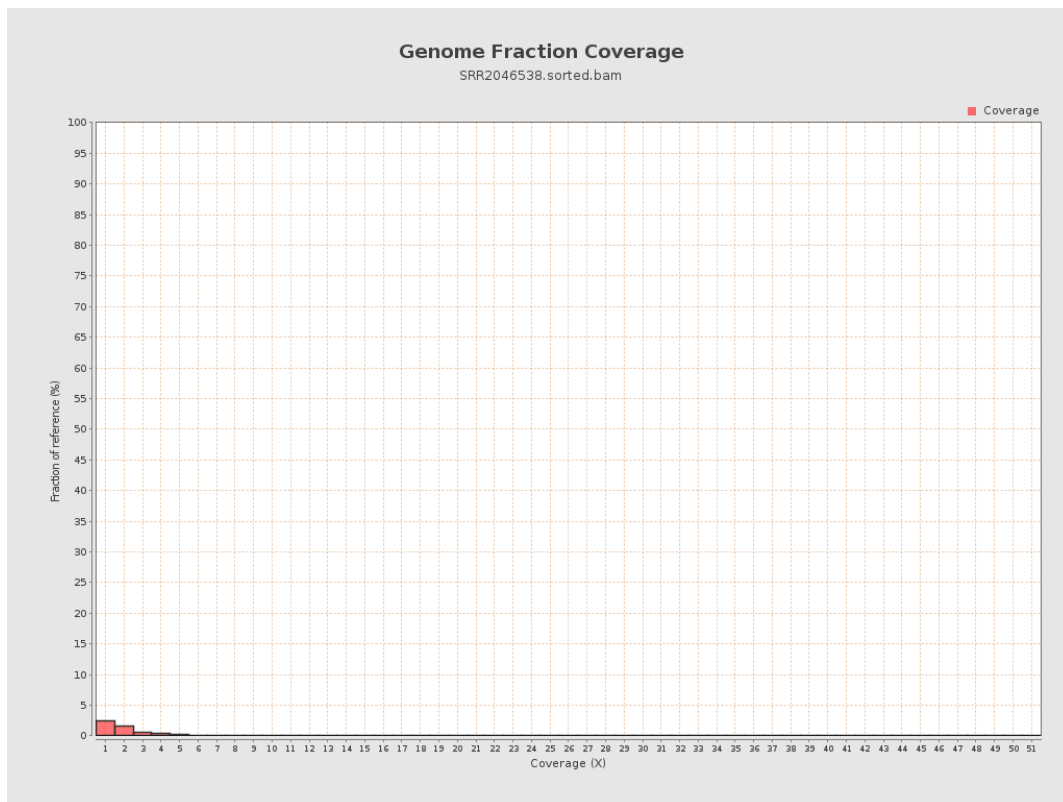
4. Results : Coverage Histogram



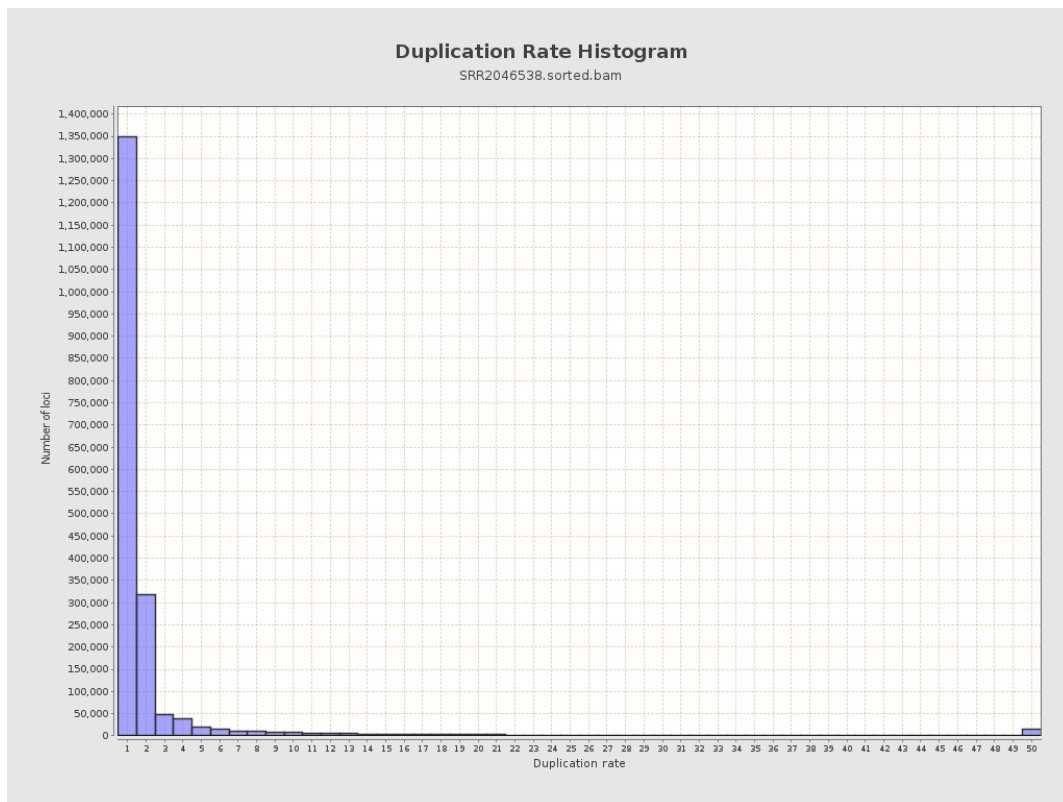
5. Results : Coverage Histogram (0-50X)



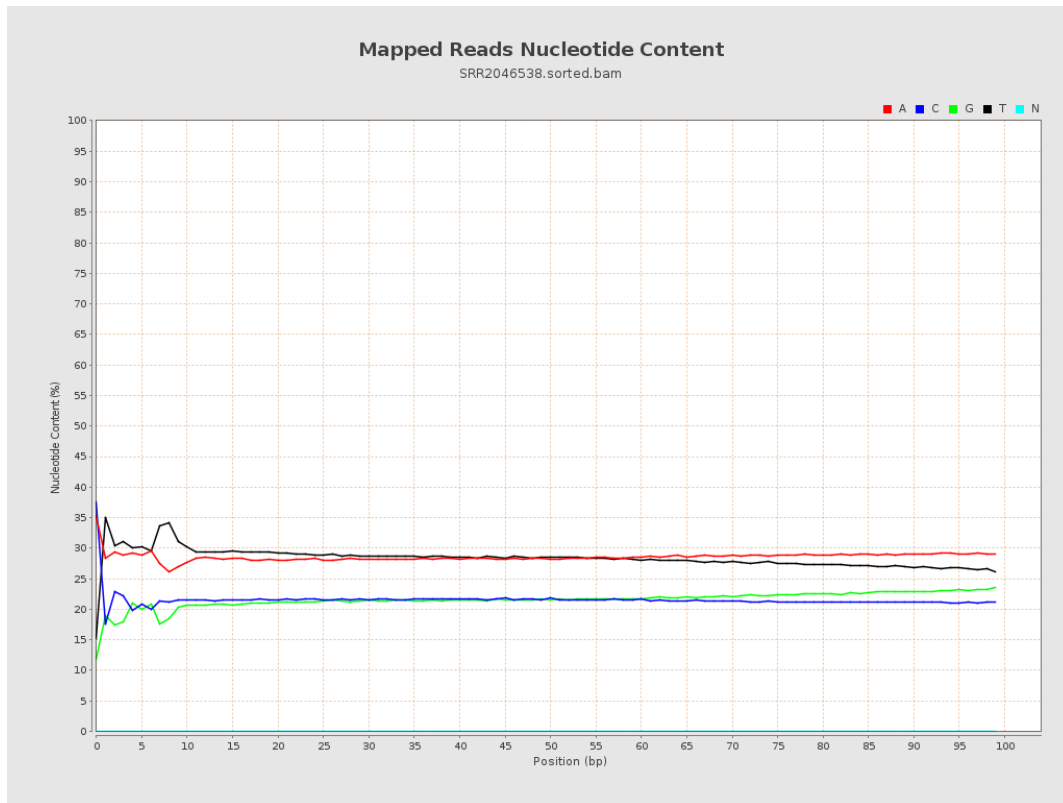
6. Results : Genome Fraction Coverage



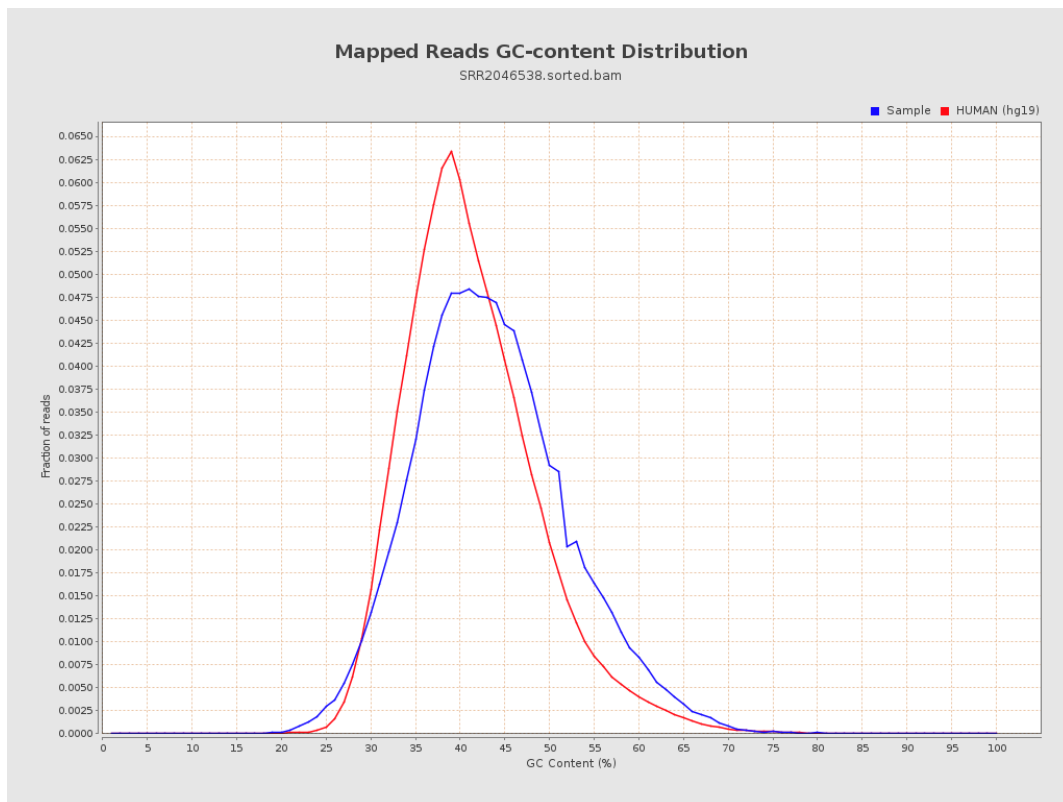
7. Results : Duplication Rate Histogram



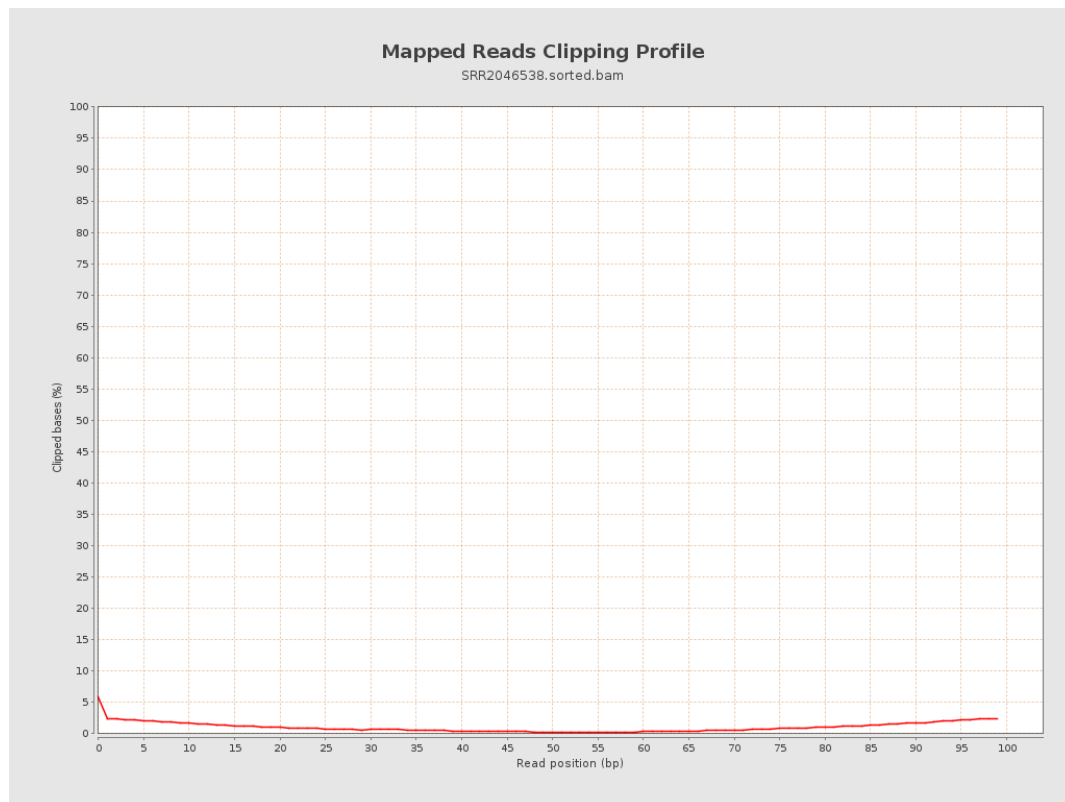
8. Results : Mapped Reads Nucleotide Content



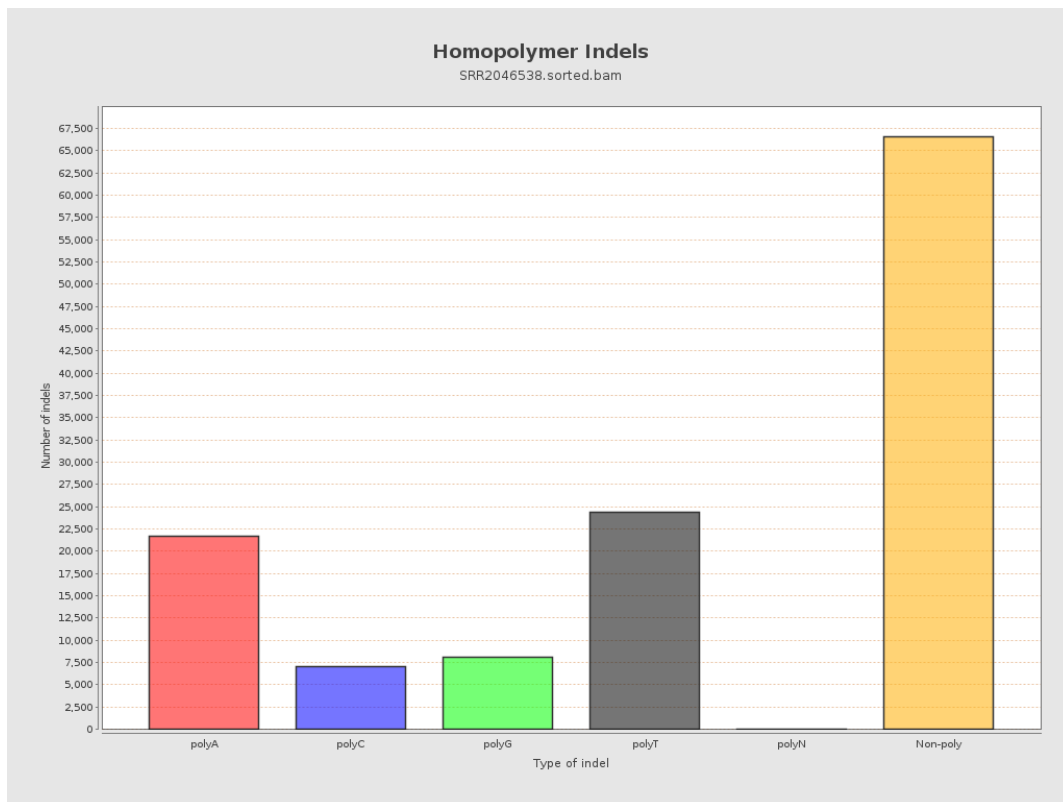
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



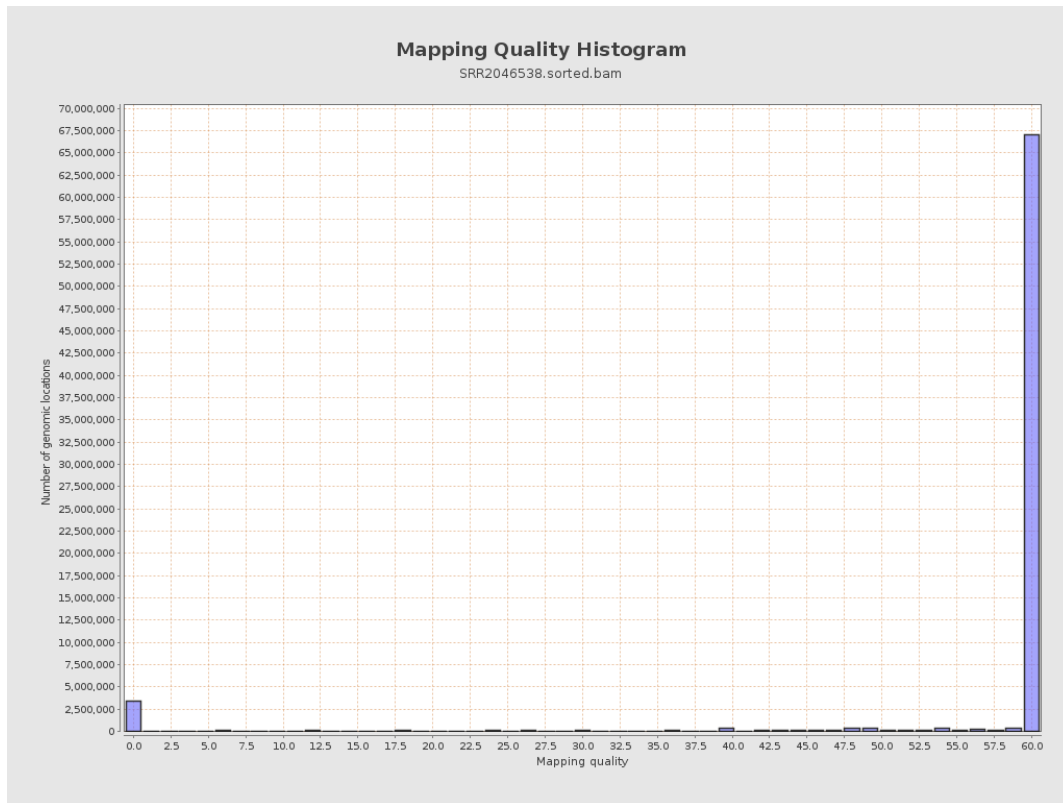
11. Results : Homopolymer Indels



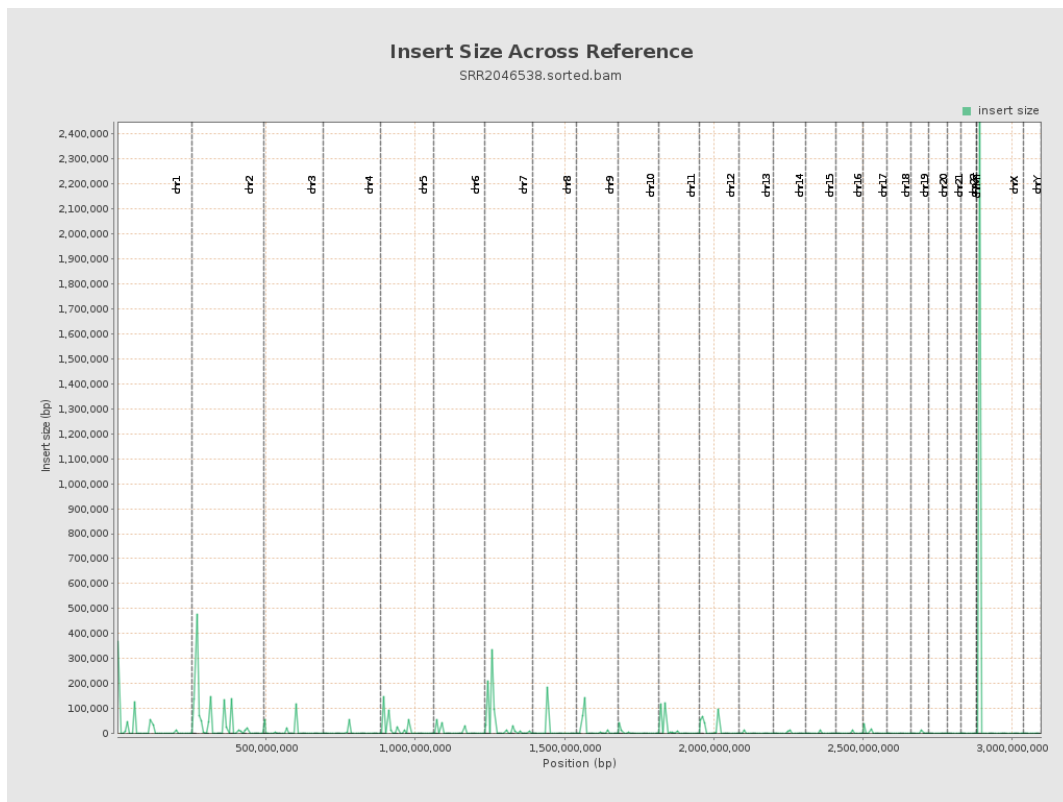
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

