

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 06:43:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472681.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_SRR3472681 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472681_1.fastq.gz SRR3472681_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 06:43:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472681.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,102,782
Mapped reads	19,936,254 / 99.17%
Unmapped reads	166,528 / 0.83%
Mapped paired reads	19,936,254 / 99.17%
Mapped reads, first in pair	9,994,043 / 49.71%
Mapped reads, second in pair	9,942,211 / 49.46%
Mapped reads, both in pair	19,819,878 / 98.59%
Mapped reads, singletons	116,376 / 0.58%
Secondary alignments	0
Supplementary alignments	119,384 / 0.59%
Read min/max/mean length	30 / 101 / 99.86
Duplicated reads (estimated)	14,088,922 / 70.08%
Duplication rate	50.75%
Clipped reads	1,460,575 / 7.27%

2.2. ACGT Content

Number/percentage of A's	535,443,688 / 27.29%
Number/percentage of C's	449,759,757 / 22.92%
Number/percentage of T's	534,141,548 / 27.22%
Number/percentage of G's	442,583,105 / 22.55%
Number/percentage of N's	375,317 / 0.02%

GC Percentage	45.47%
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2.3. Coverage

Mean	0.634
Standard Deviation	33.7507

2.4. Mapping Quality

Mean Mapping Quality	54.96
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2.5. Insert size

Mean	24,469.94
Standard Deviation	1,533,511.52
P25/Median/P75	166 / 228 / 301

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	12,591,651
Insertions	131,182
Mapped reads with at least one insertion	0.65%
Deletions	92,239
Mapped reads with at least one deletion	0.46%
Homopolymer indels	46.43%

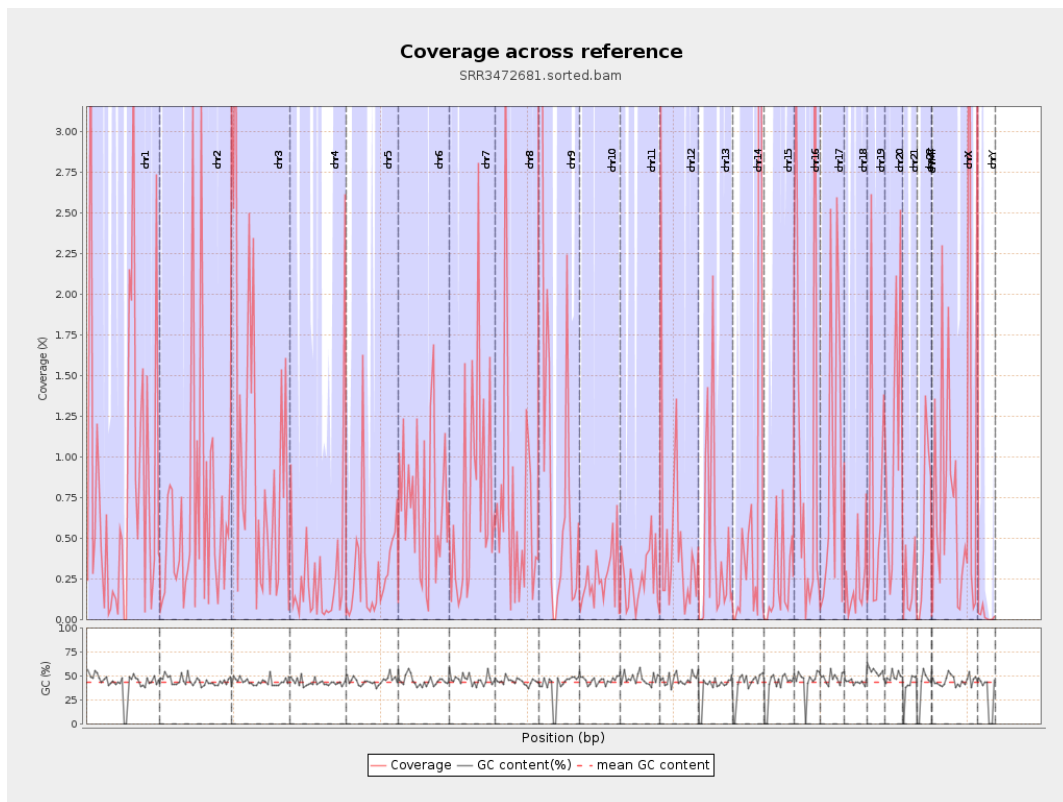
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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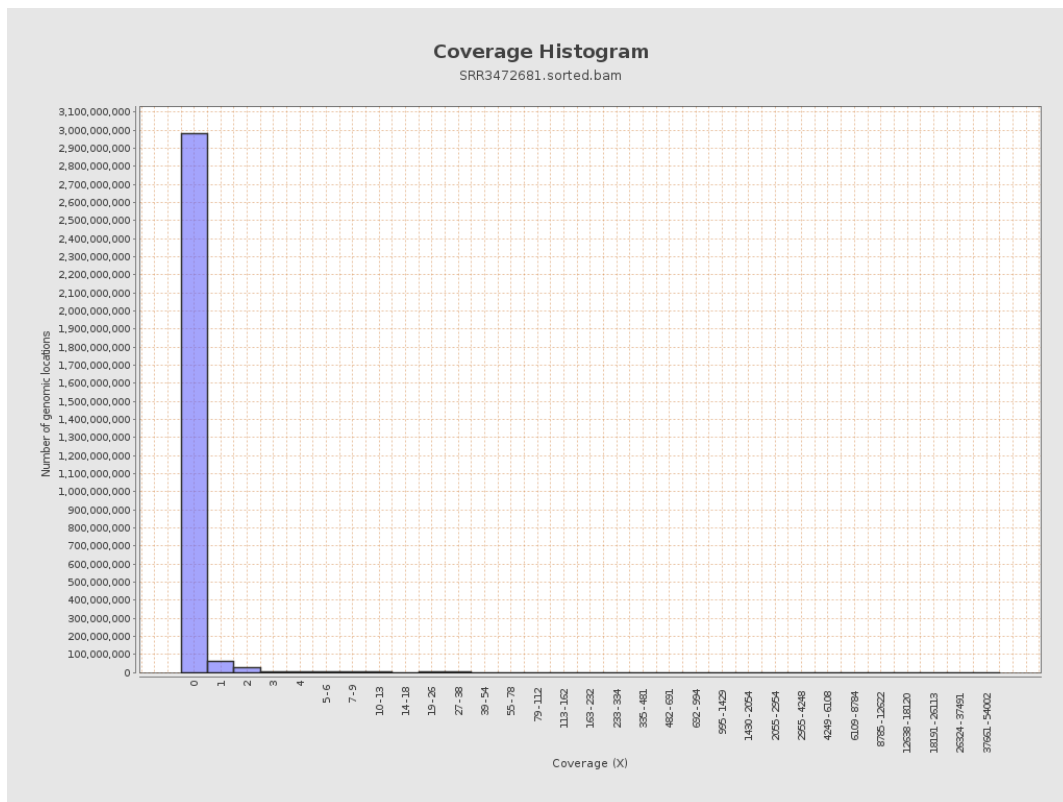
		bases	coverage	deviation
chr1	249250621	211198401	0.8473	28.6447
chr2	243199373	156849886	0.6449	27.0601
chr3	198022430	210601250	1.0635	37.4752
chr4	191154276	53133807	0.278	16.4351
chr5	180915260	55385252	0.3061	12.7341
chr6	171115067	121541036	0.7103	22.467
chr7	159138663	119719738	0.7523	25.0699
chr8	146364022	102282051	0.6988	28.0246
chr9	141213431	147128398	1.0419	27.9529
chr10	135534747	34649304	0.2556	13.2354
chr11	135006516	34497690	0.2555	9.8792
chr12	133851895	69810124	0.5215	15.7058
chr13	115169878	51941969	0.451	24.3545
chr14	107349540	78577295	0.732	124.157
chr15	102531392	24446961	0.2384	13.093
chr16	90354753	100095550	1.1078	36.1131
chr17	81195210	74889477	0.9223	30.4472
chr18	78077248	18088186	0.2317	12.7474
chr19	59128983	43877011	0.7421	20.9461
chr20	63025520	69911554	1.1093	28.0948
chr21	48129895	10010595	0.208	9.4162
chr22	51304566	29630197	0.5775	28.2539
chrMT	16571	9158	0.5527	0.9196
chrX	155270560	142885783	0.9202	38.9207

chrY	59373566	1369021	0.0231	1.6914
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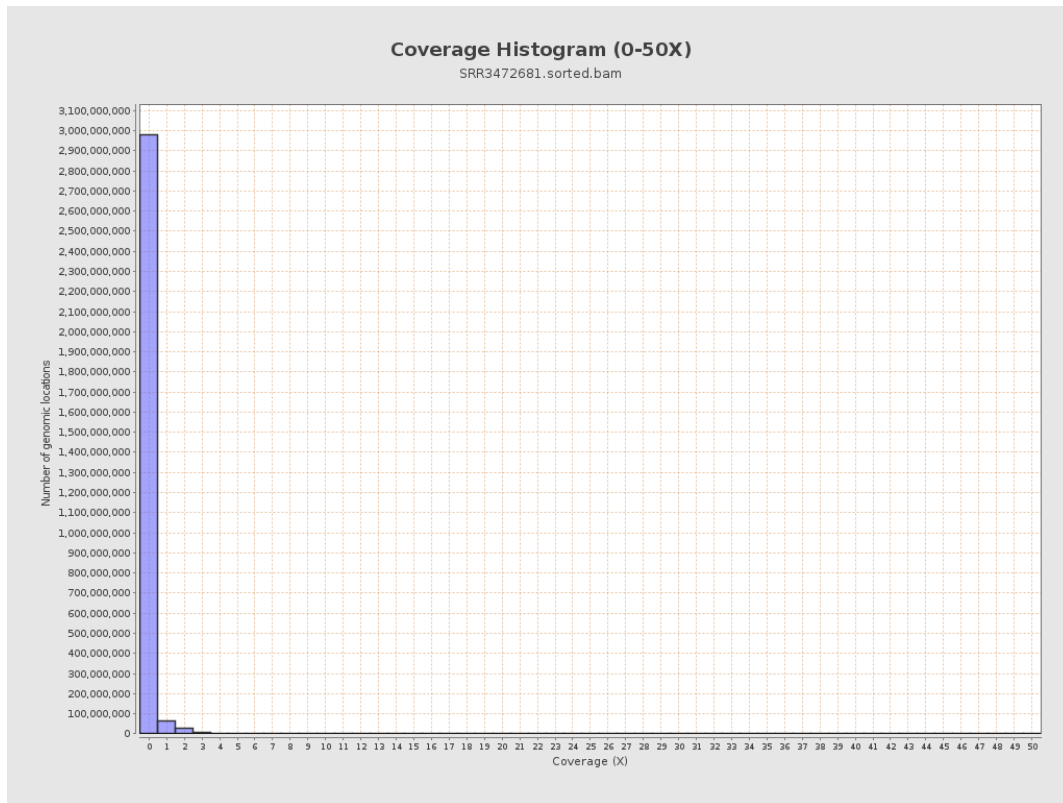
3. Results : Coverage across reference



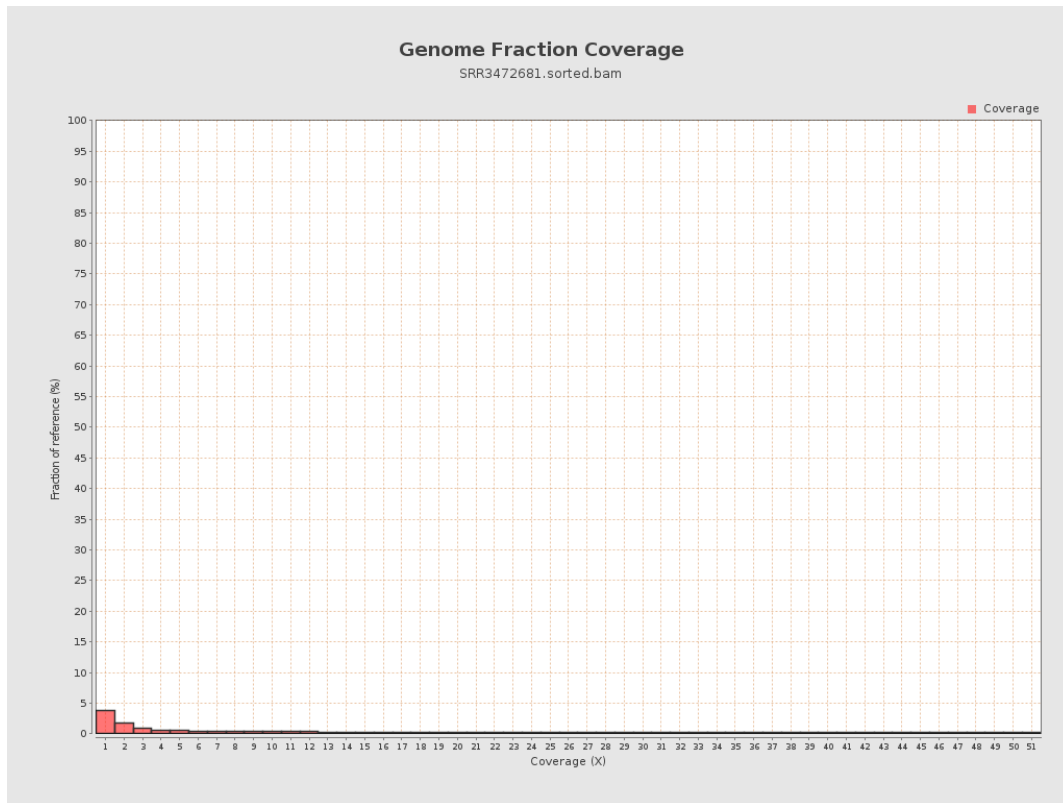
4. Results : Coverage Histogram



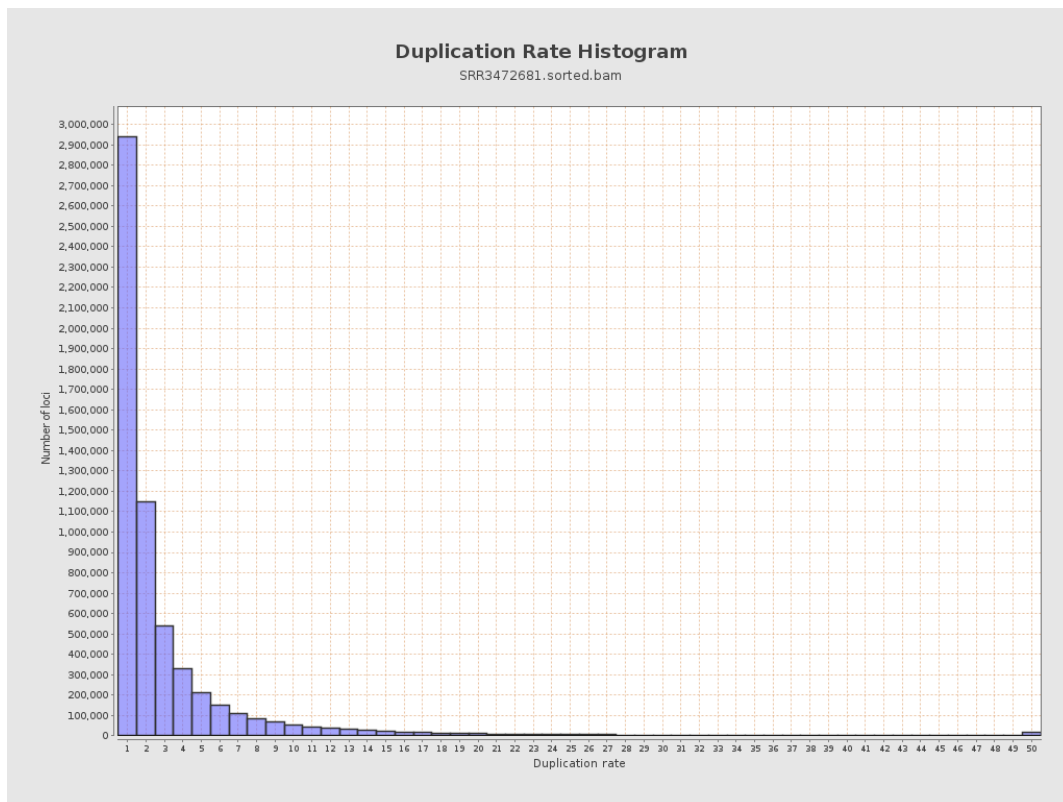
5. Results : Coverage Histogram (0-50X)



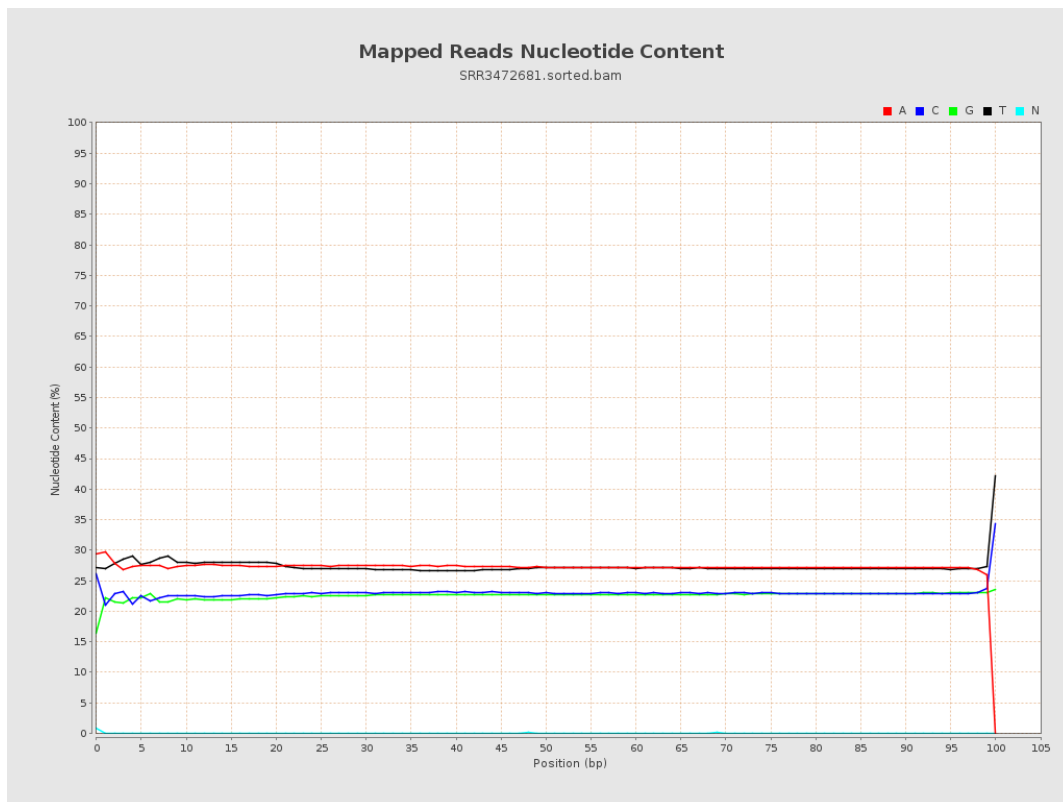
6. Results : Genome Fraction Coverage



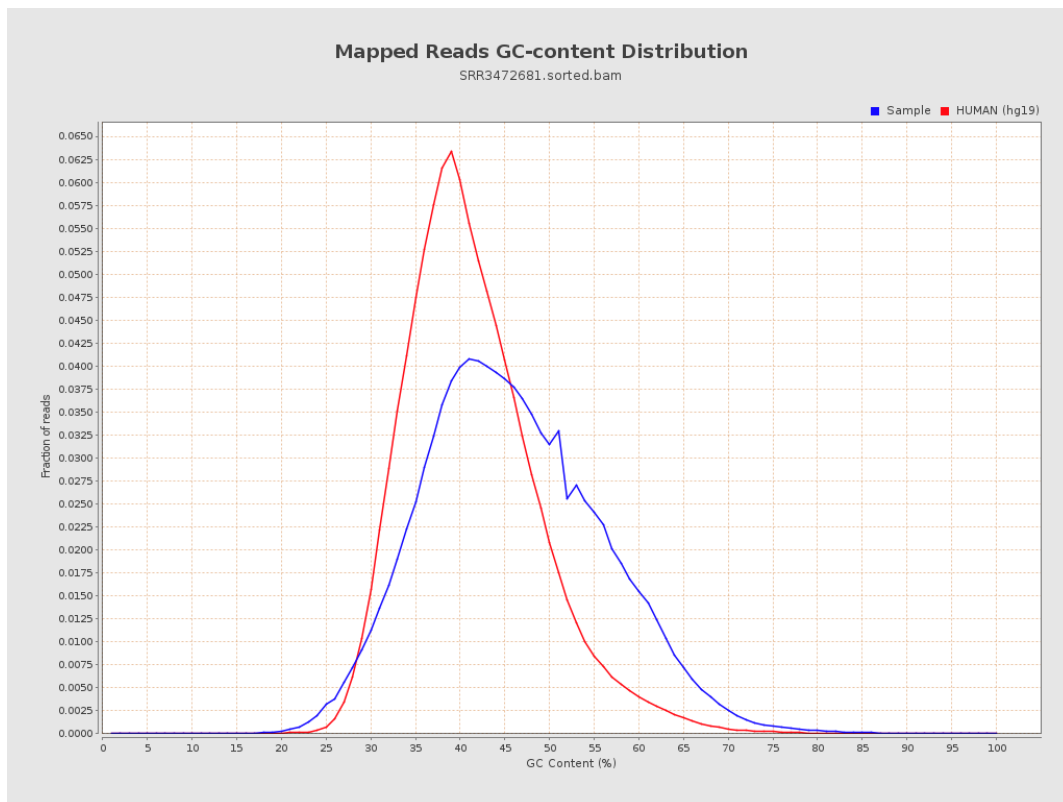
7. Results : Duplication Rate Histogram



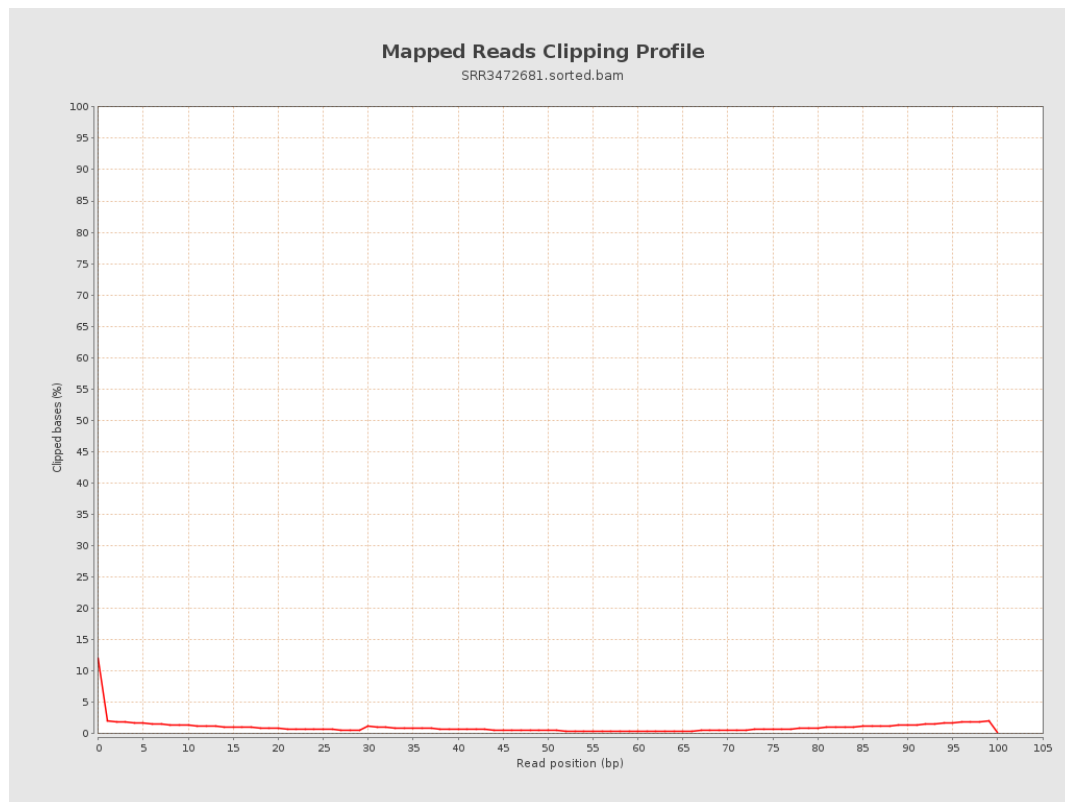
8. Results : Mapped Reads Nucleotide Content



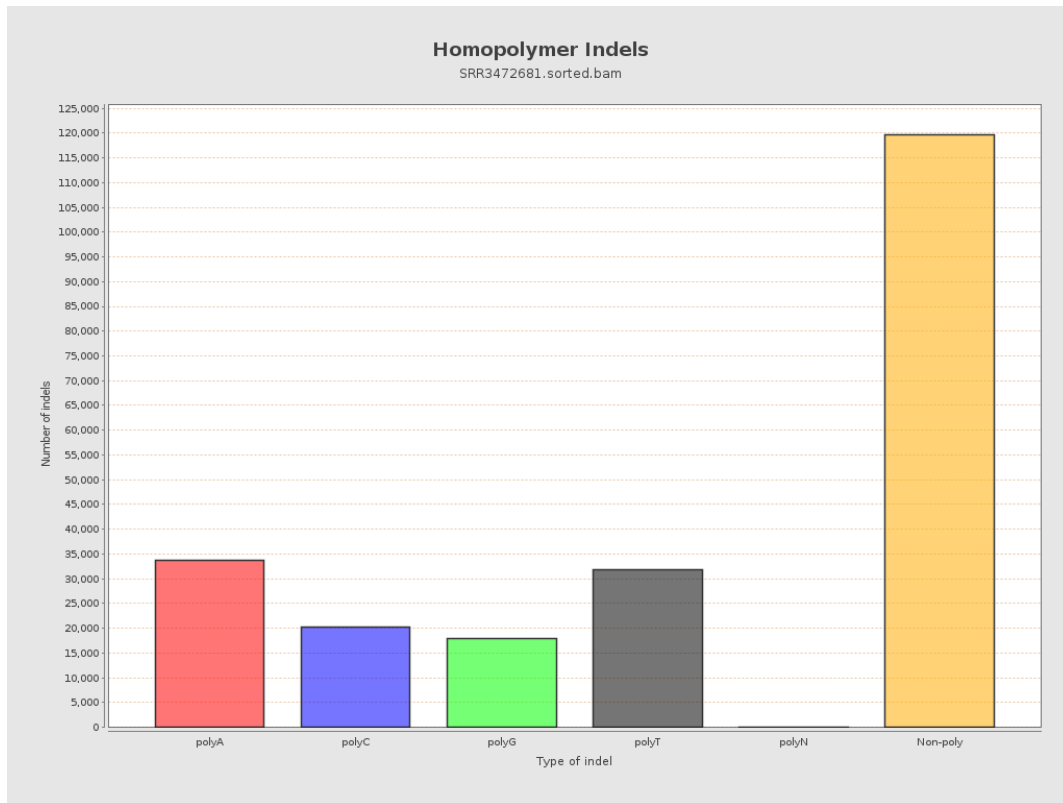
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



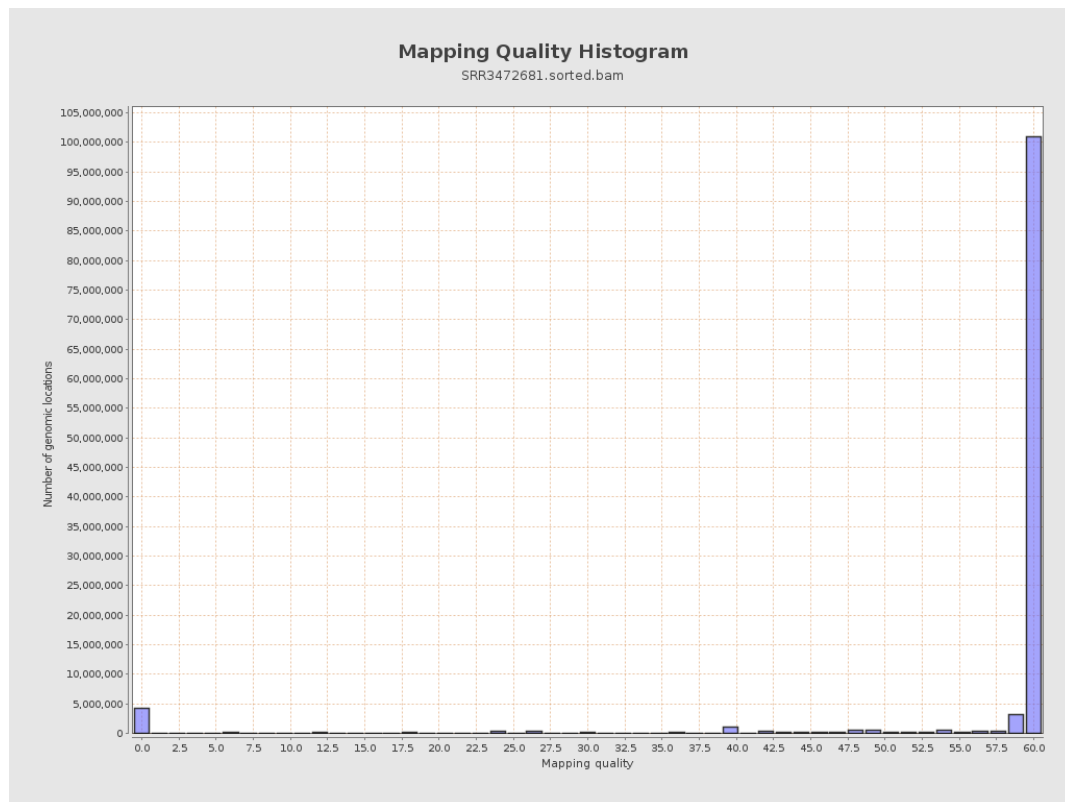
11. Results : Homopolymer Indels



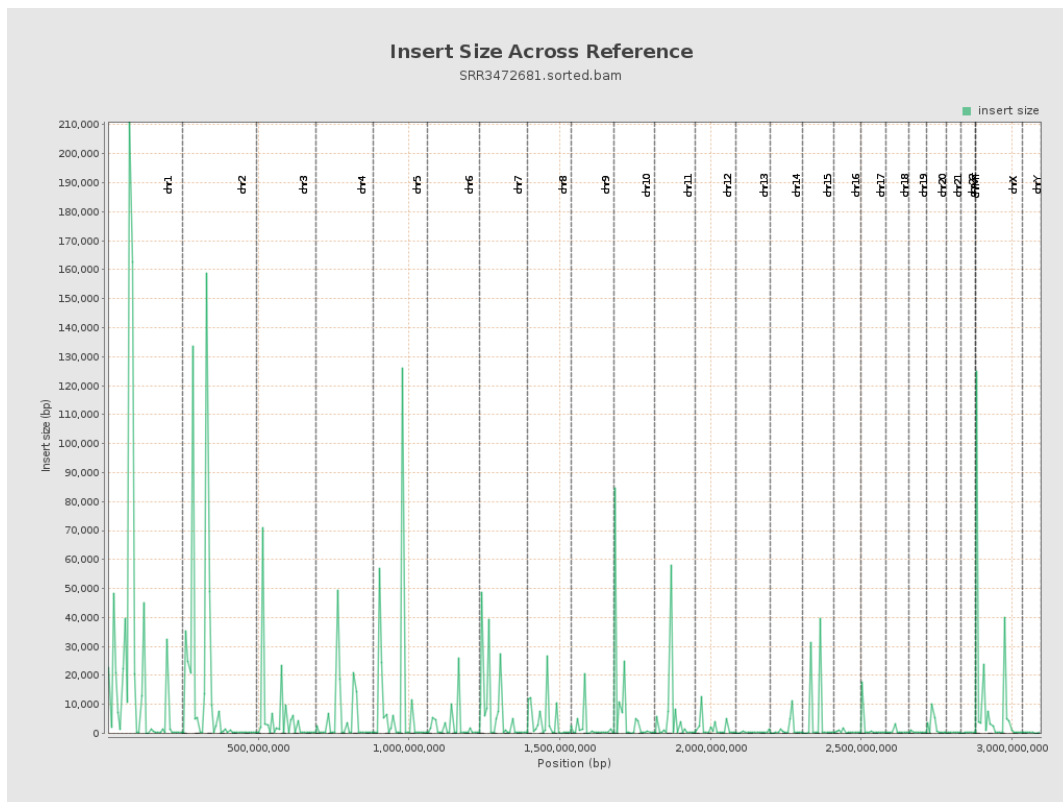
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

