

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 16:04:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046481.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_SRR2046481 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046481_1.fastq.gz SRR2046481_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 16:04:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046481.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,977,180
Mapped reads	4,947,865 / 99.41%
Unmapped reads	29,315 / 0.59%
Mapped paired reads	4,947,865 / 99.41%
Mapped reads, first in pair	2,476,451 / 49.76%
Mapped reads, second in pair	2,471,414 / 49.65%
Mapped reads, both in pair	4,928,596 / 99.02%
Mapped reads, singletons	19,269 / 0.39%
Secondary alignments	0
Supplementary alignments	26,862 / 0.54%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	3,552,383 / 71.37%
Duplication rate	38.41%
Clipped reads	1,893,843 / 38.05%

2.2. ACGT Content

Number/percentage of A's	128,282,416 / 27.86%
Number/percentage of C's	102,597,556 / 22.28%
Number/percentage of T's	125,513,125 / 27.26%
Number/percentage of G's	103,992,055 / 22.59%
Number/percentage of N's	35,509 / 0.01%

GC Percentage	44.87%
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2.3. Coverage

Mean	0.1488
Standard Deviation	18.1685

2.4. Mapping Quality

Mean Mapping Quality	51.11
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2.5. Insert size

Mean	20,351.09
Standard Deviation	1,409,819.8
P25/Median/P75	90 / 110 / 137

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	1,692,538
Insertions	45,845
Mapped reads with at least one insertion	0.9%
Deletions	59,874
Mapped reads with at least one deletion	1.17%
Homopolymer indels	47.69%

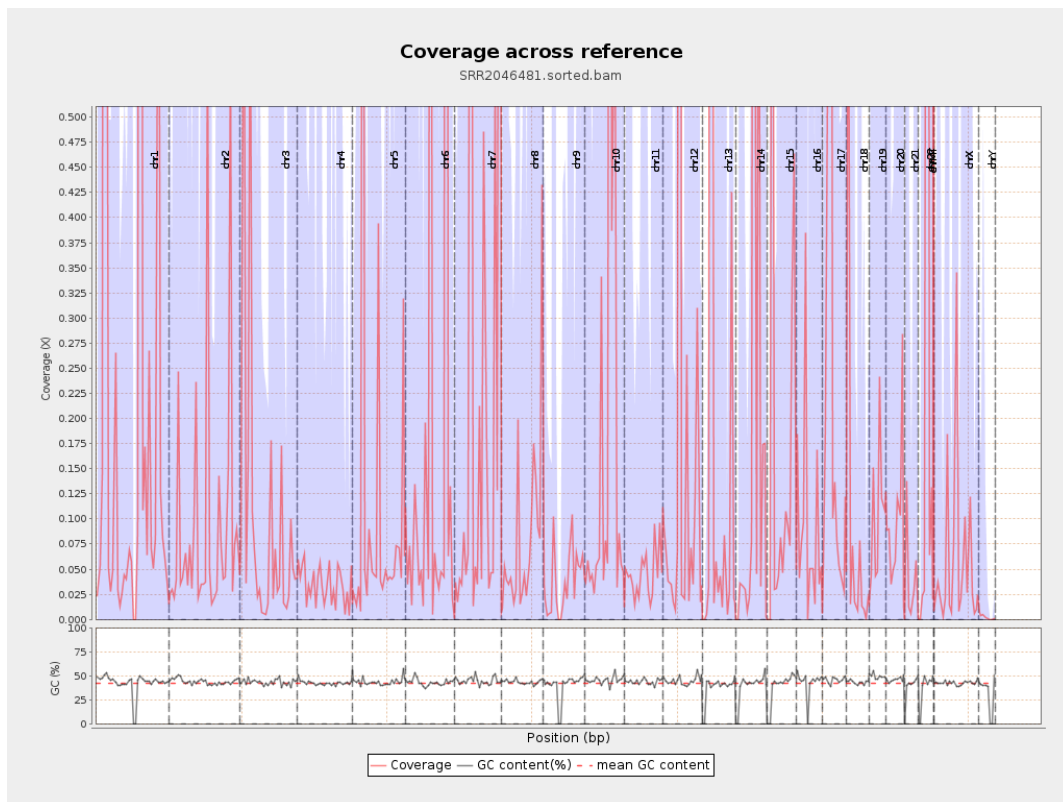
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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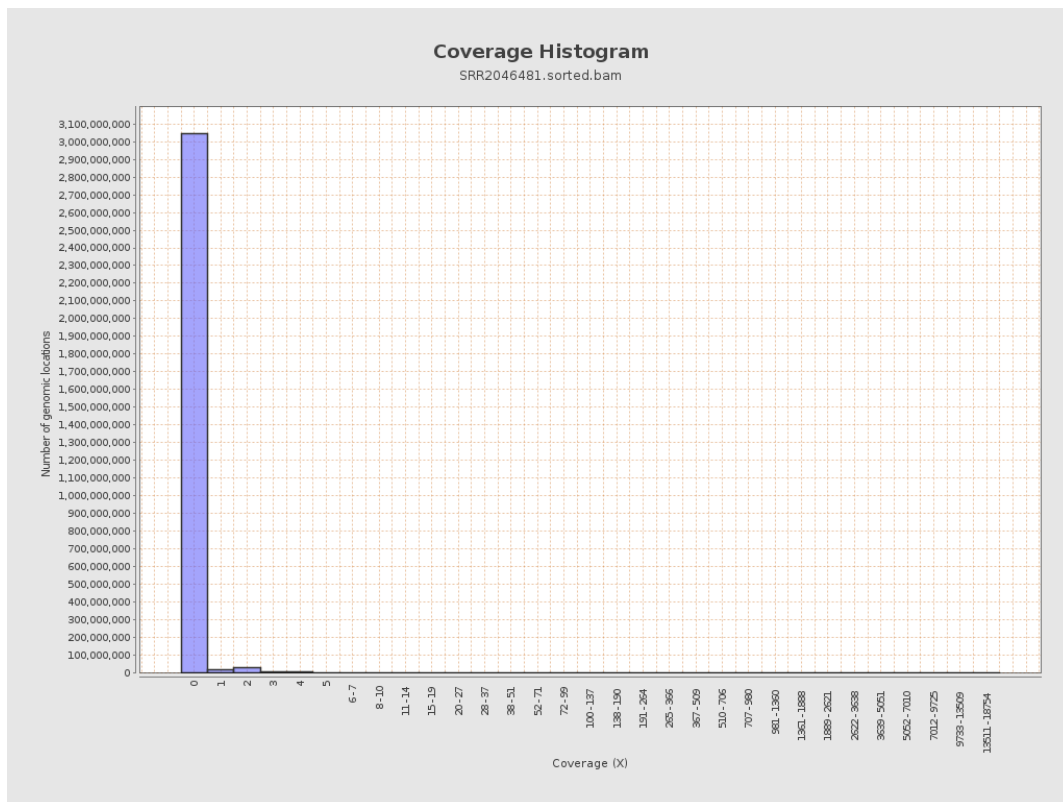
		bases	coverage	deviation
chr1	249250621	72082644	0.2892	24.3581
chr2	243199373	23826778	0.098	9.1214
chr3	198022430	20950458	0.1058	10.2443
chr4	191154276	6524963	0.0341	1.0407
chr5	180915260	21867994	0.1209	18.4456
chr6	171115067	44278375	0.2588	37.4336
chr7	159138663	41359691	0.2599	26.9697
chr8	146364022	12119630	0.0828	6.6506
chr9	141213431	5120535	0.0363	2.03
chr10	135534747	28432034	0.2098	27.557
chr11	135006516	6026791	0.0446	1.5544
chr12	133851895	31764332	0.2373	22.0622
chr13	115169878	26531249	0.2304	24.6165
chr14	107349540	21442905	0.1997	13.9325
chr15	102531392	19583742	0.191	15.6007
chr16	90354753	8429430	0.0933	6.8097
chr17	81195210	23374230	0.2879	22.741
chr18	78077248	8034961	0.1029	9.1438
chr19	59128983	6180298	0.1045	5.0077
chr20	63025520	6286886	0.0998	3.8263
chr21	48129895	1891583	0.0393	4.7102
chr22	51304566	15703673	0.3061	34.7049
chrMT	16571	33023	1.9928	2.1216
chrX	155270560	8638758	0.0556	6.5344

chrY	59373566	121785	0.0021	0.2002
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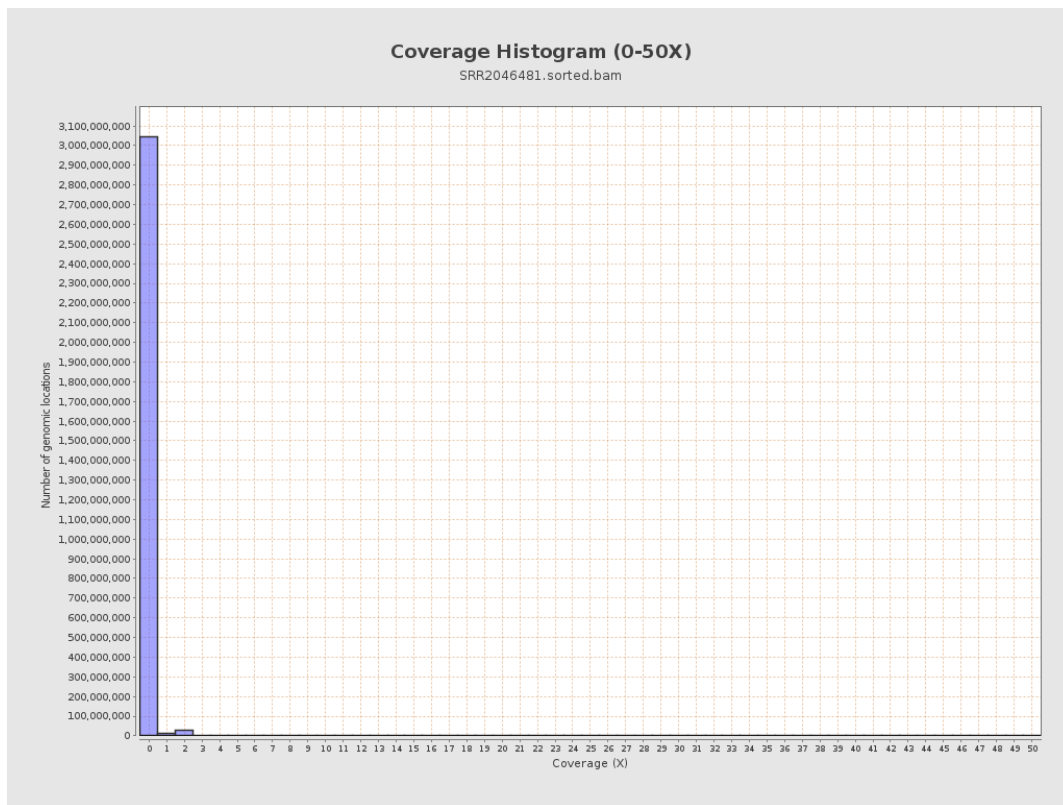
3. Results : Coverage across reference



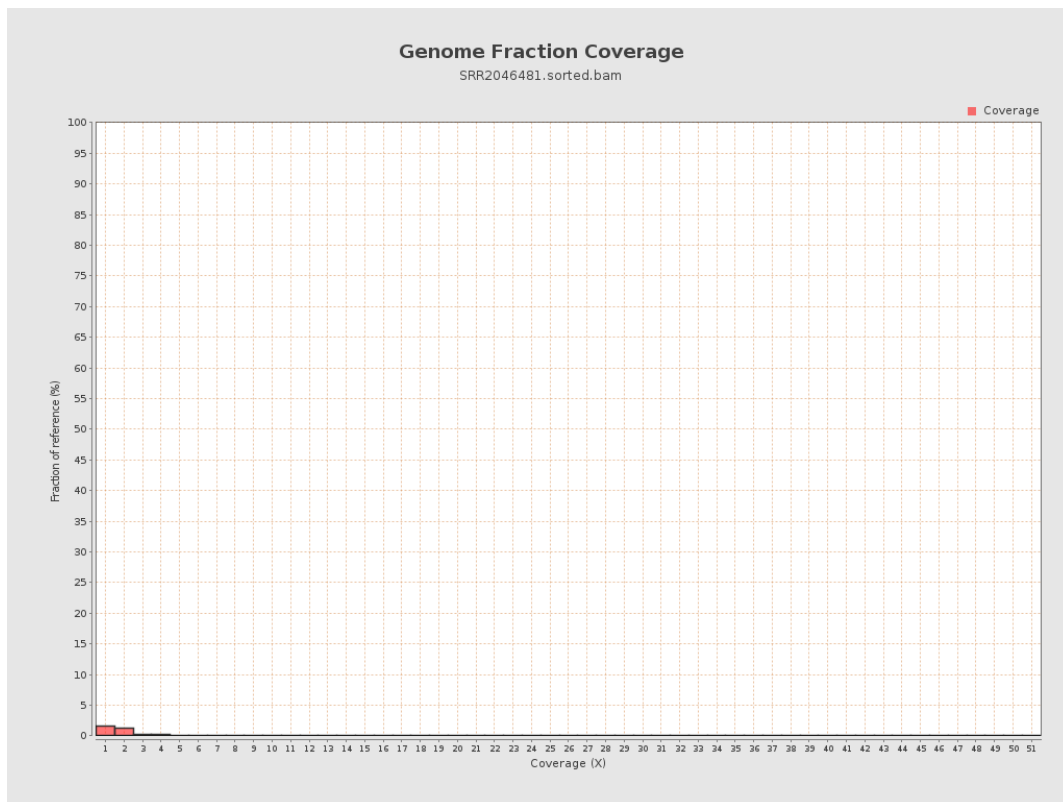
4. Results : Coverage Histogram



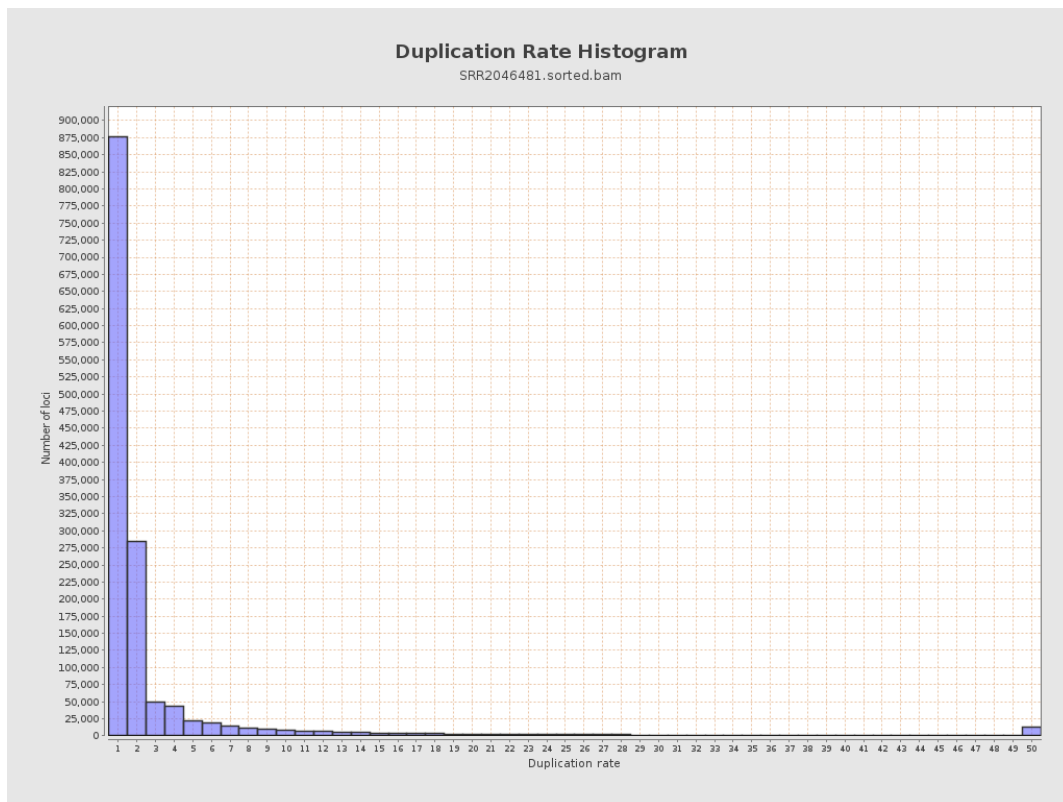
5. Results : Coverage Histogram (0-50X)



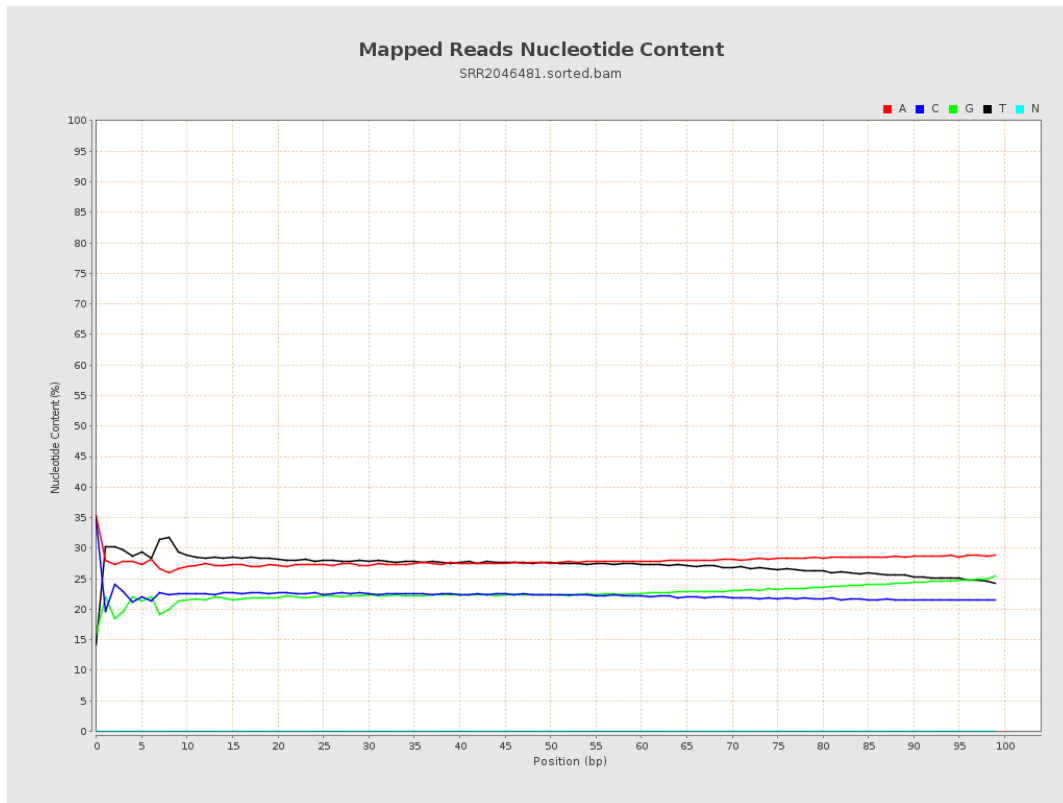
6. Results : Genome Fraction Coverage



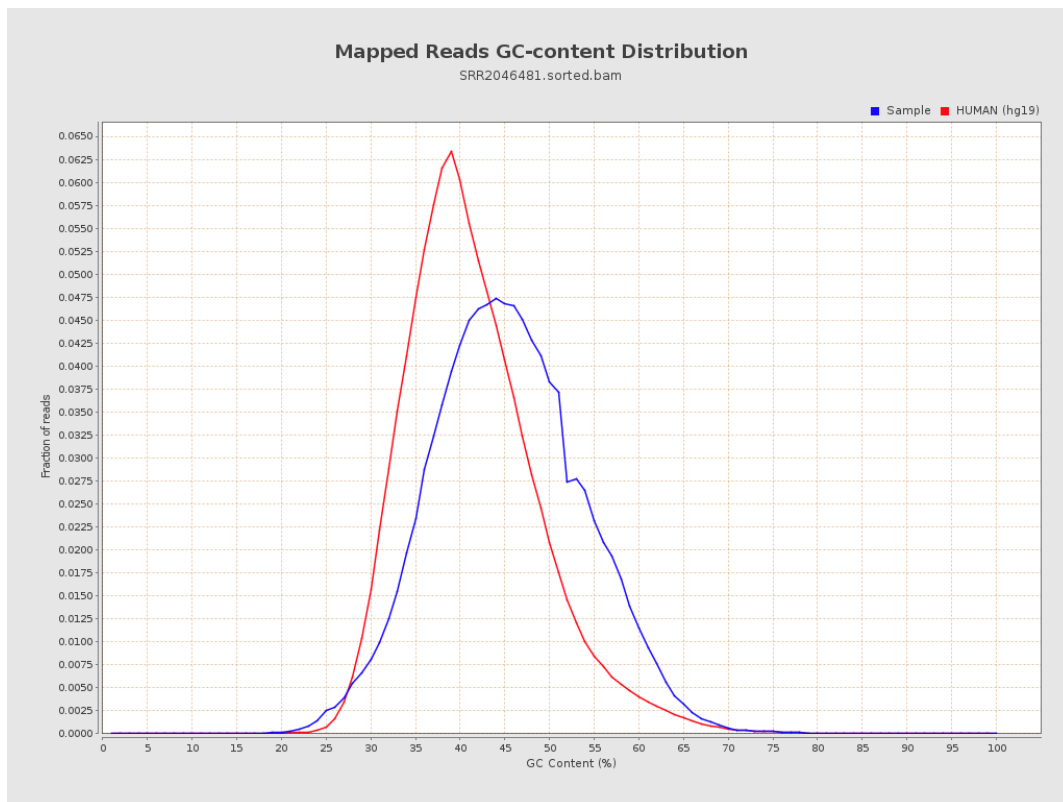
7. Results : Duplication Rate Histogram



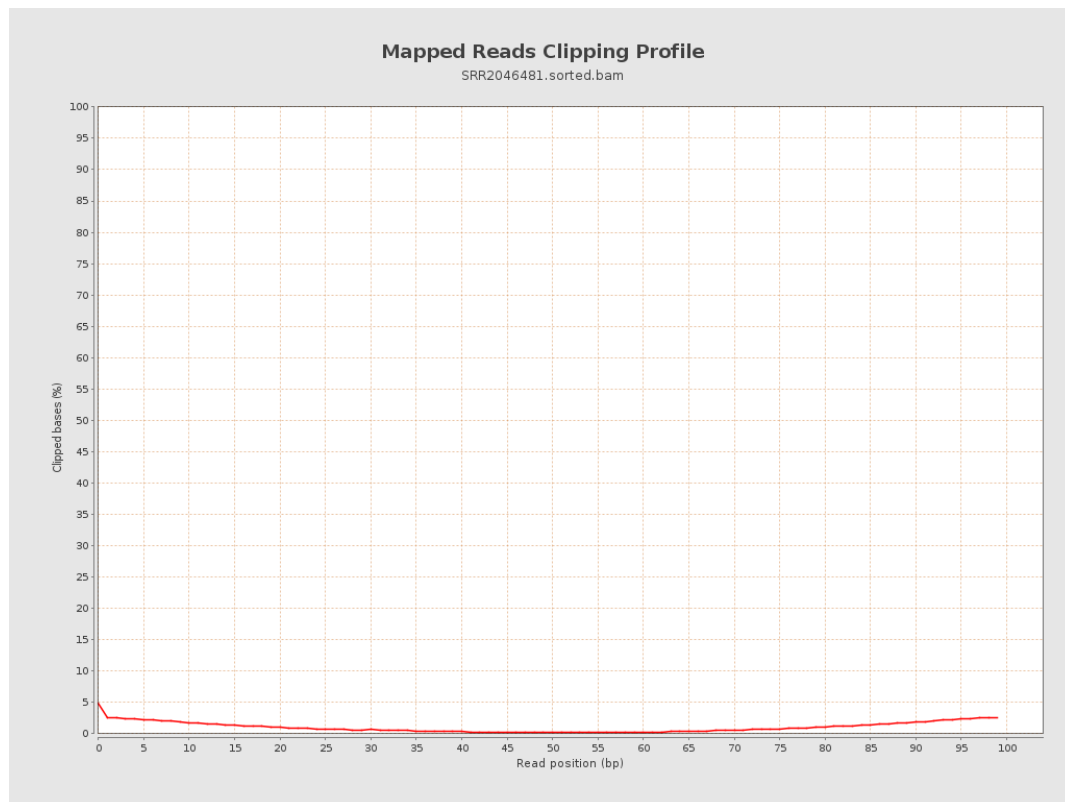
8. Results : Mapped Reads Nucleotide Content



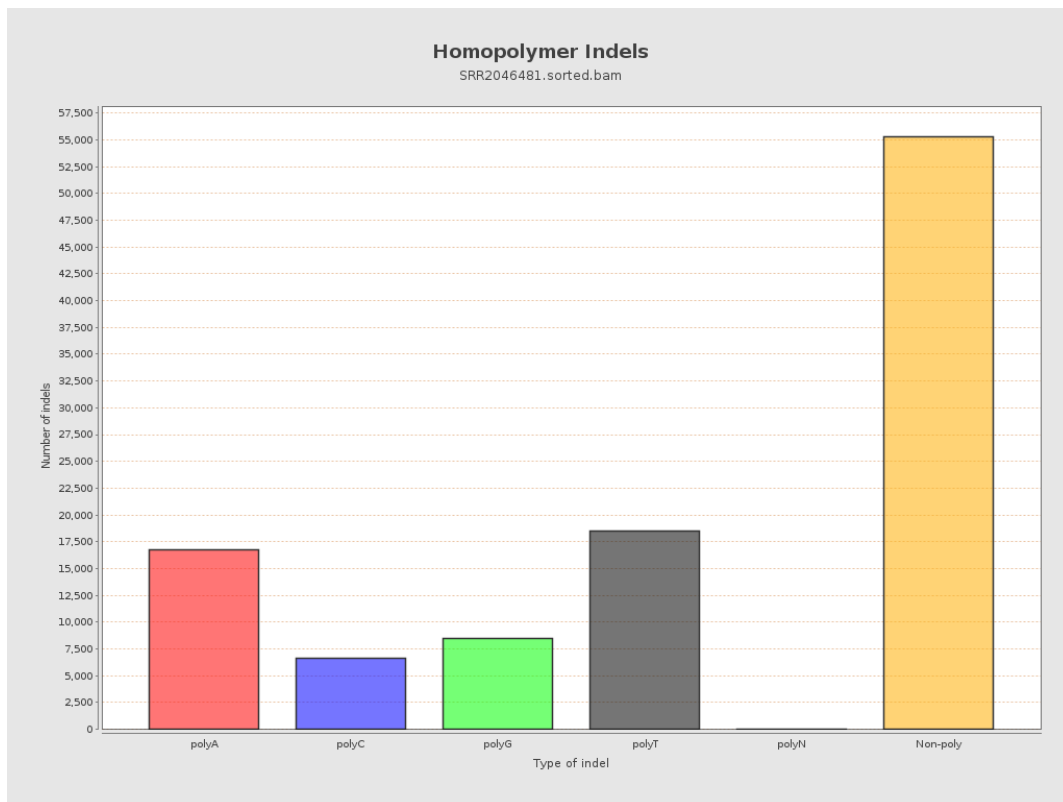
9. Results : Mapped Reads GC-content Distribution



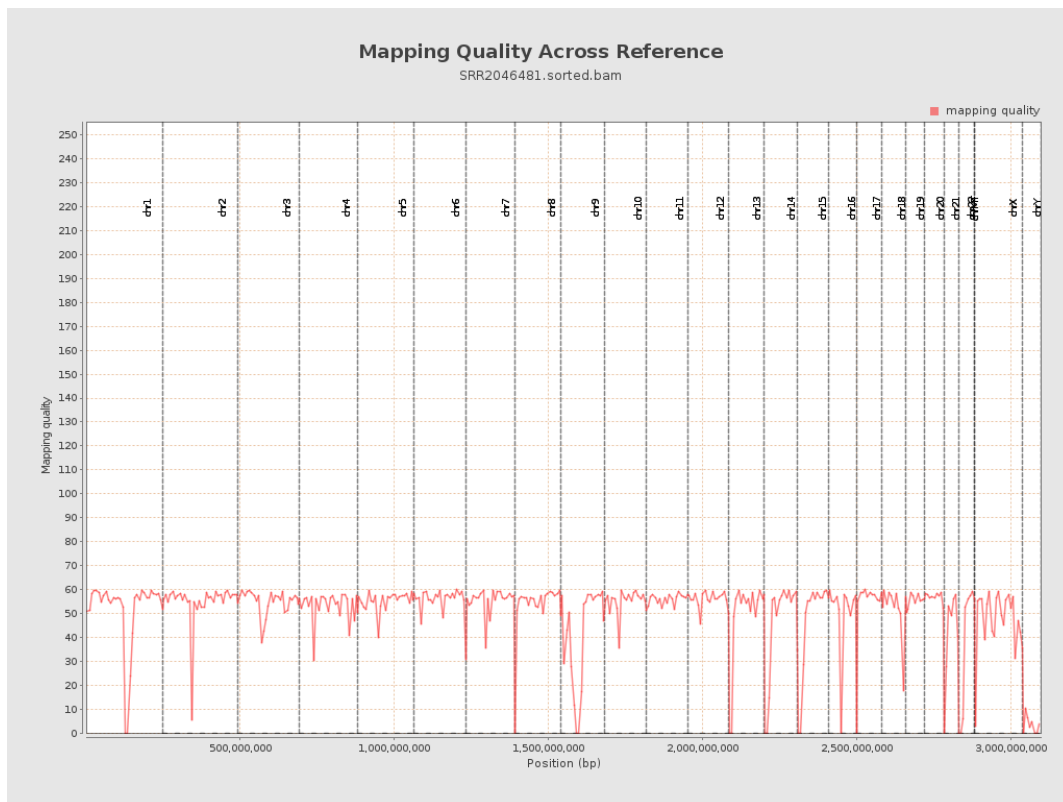
10. Results : Mapped Reads Clipping Profile



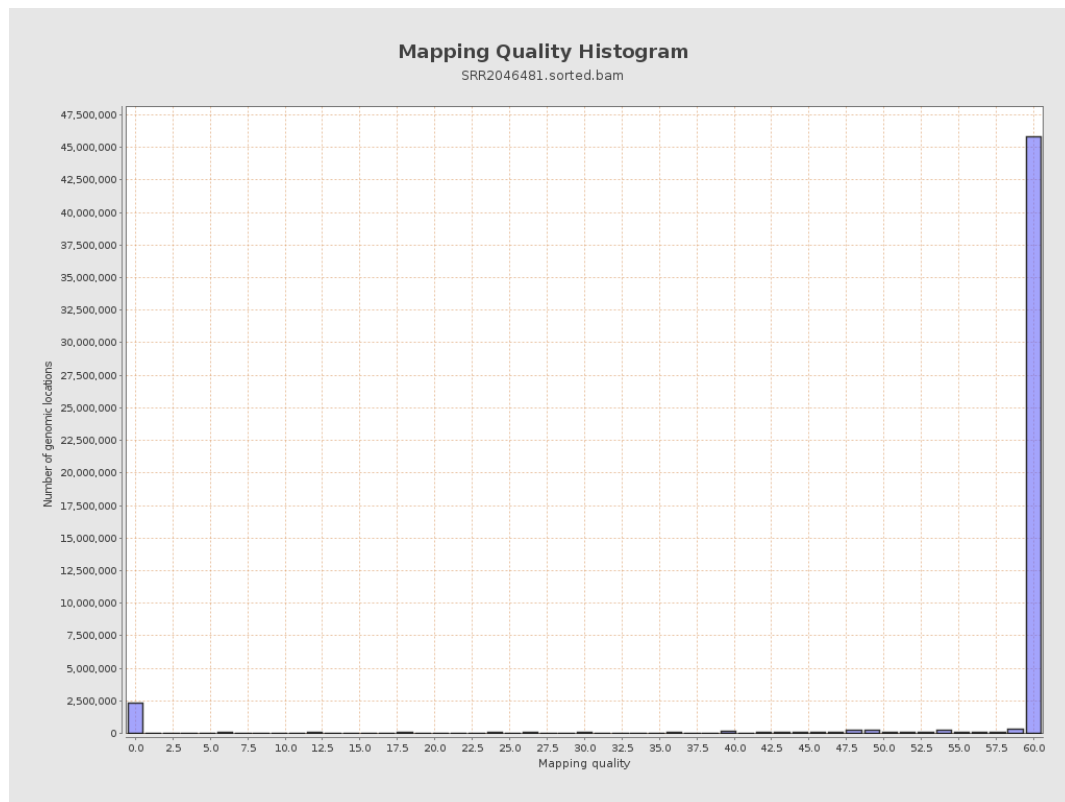
11. Results : Homopolymer Indels



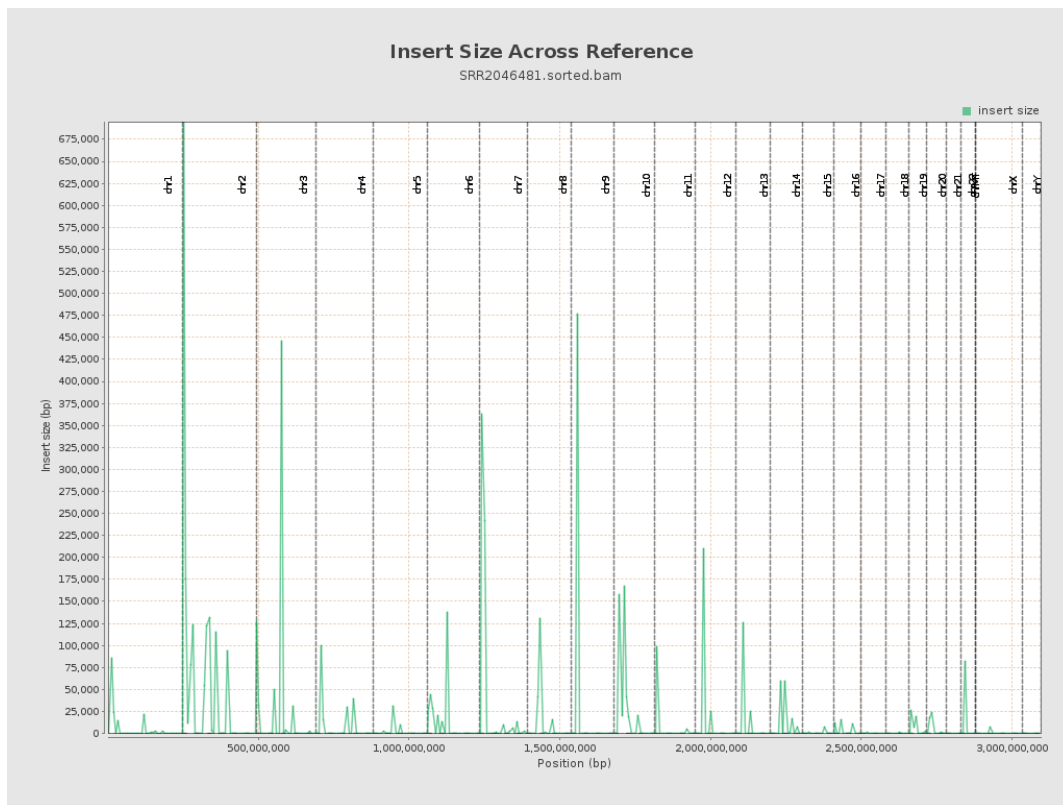
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

