

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 19:50:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779231.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_SRR1779231 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779231_1.fastq.gz SRR1779231_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 19:50:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779231.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,470,910
Mapped reads	8,015,465 / 94.62%
Unmapped reads	455,445 / 5.38%
Mapped paired reads	8,015,465 / 94.62%
Mapped reads, first in pair	4,077,657 / 48.14%
Mapped reads, second in pair	3,937,808 / 46.49%
Mapped reads, both in pair	7,863,234 / 92.83%
Mapped reads, singletons	152,231 / 1.8%
Secondary alignments	0
Supplementary alignments	18,749 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	139,461 / 1.65%
Duplication rate	1.61%
Clipped reads	267,445 / 3.16%

2.2. ACGT Content

Number/percentage of A's	195,812,706 / 30.71%
Number/percentage of C's	122,012,298 / 19.14%
Number/percentage of T's	195,420,511 / 30.65%
Number/percentage of G's	124,254,188 / 19.49%
Number/percentage of N's	117,909 / 0.02%

GC Percentage	38.62%
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2.3. Coverage

Mean	0.206
Standard Deviation	0.8442

2.4. Mapping Quality

Mean Mapping Quality	52.78
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2.5. Insert size

Mean	53,821.02
Standard Deviation	2,216,733.24
P25/Median/P75	162 / 216 / 293

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	2,544,504
Insertions	46,664
Mapped reads with at least one insertion	0.58%
Deletions	58,952
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.98%

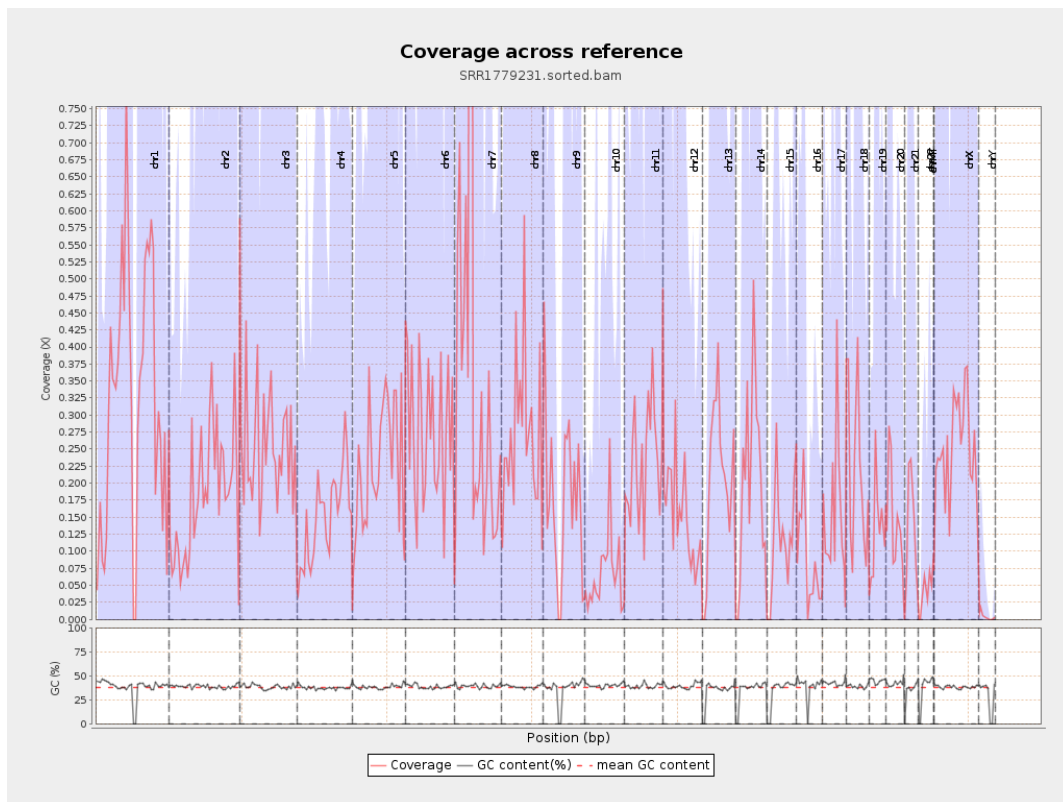
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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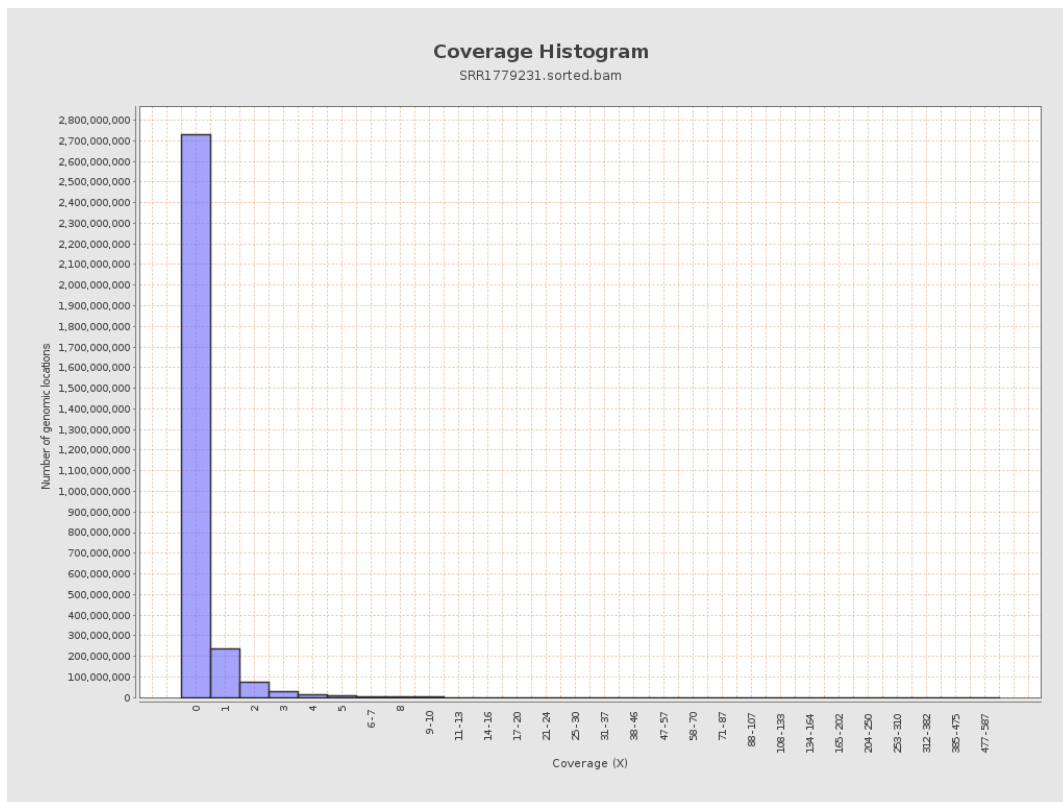
		bases	coverage	deviation
chr1	249250621	80463942	0.3228	1.1026
chr2	243199373	44088820	0.1813	0.6524
chr3	198022430	50002557	0.2525	0.7967
chr4	191154276	29206309	0.1528	0.5611
chr5	180915260	41046977	0.2269	0.7365
chr6	171115067	47325713	0.2766	0.8541
chr7	159138663	62979379	0.3958	2.0265
chr8	146364022	39420268	0.2693	0.8218
chr9	141213431	24385923	0.1727	0.6715
chr10	135534747	9511529	0.0702	0.4636
chr11	135006516	30976218	0.2294	0.7842
chr12	133851895	19951294	0.1491	0.6277
chr13	115169878	23444785	0.2036	0.6739
chr14	107349540	21582272	0.201	0.7295
chr15	102531392	12298932	0.12	0.5056
chr16	90354753	8005890	0.0886	0.3956
chr17	81195210	12604589	0.1552	0.635
chr18	78077248	16527093	0.2117	0.7207
chr19	59128983	7965484	0.1347	0.6053
chr20	63025520	9136753	0.145	0.5962
chr21	48129895	5983473	0.1243	0.5571
chr22	51304566	2071223	0.0404	0.2803
chrMT	16571	1619	0.0977	0.3254
chrX	155270560	38482711	0.2478	0.8068

chrY	59373566	276454	0.0047	0.0905
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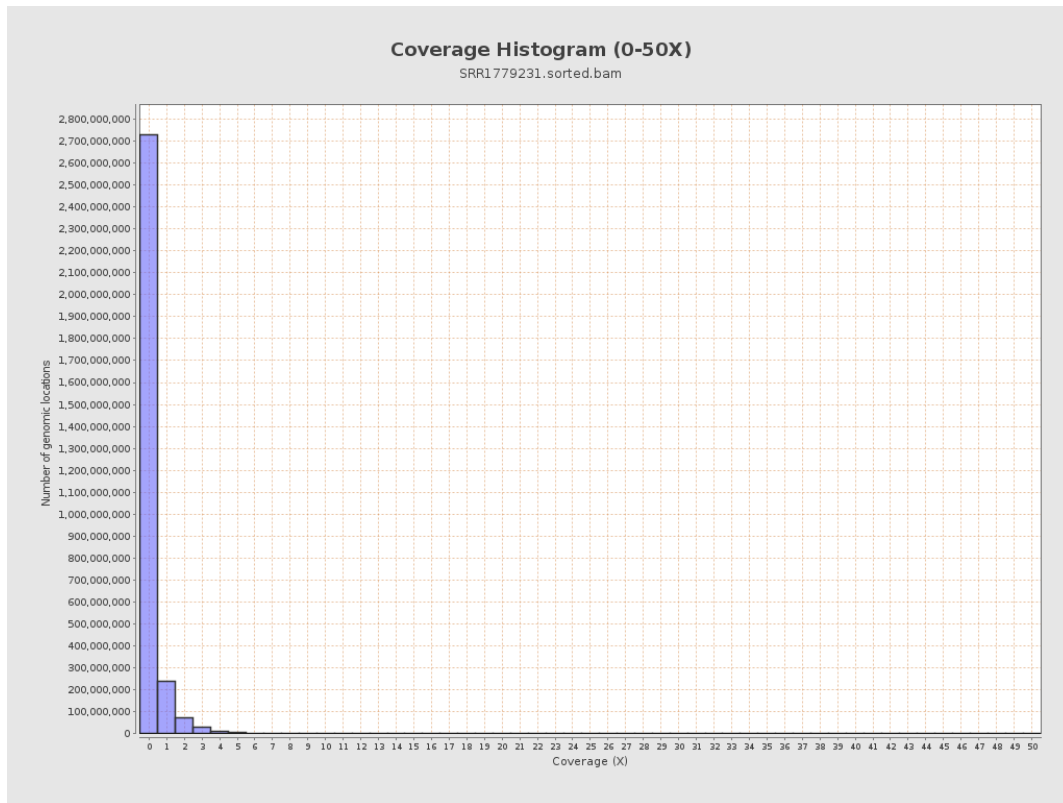
3. Results : Coverage across reference



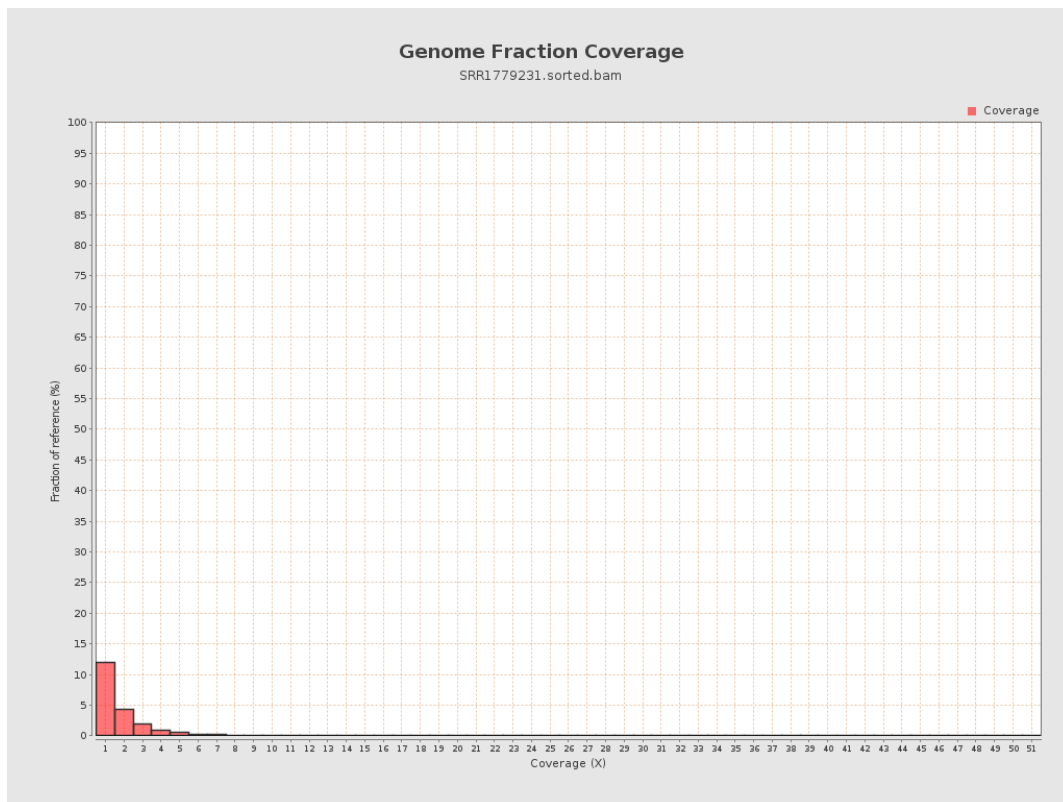
4. Results : Coverage Histogram



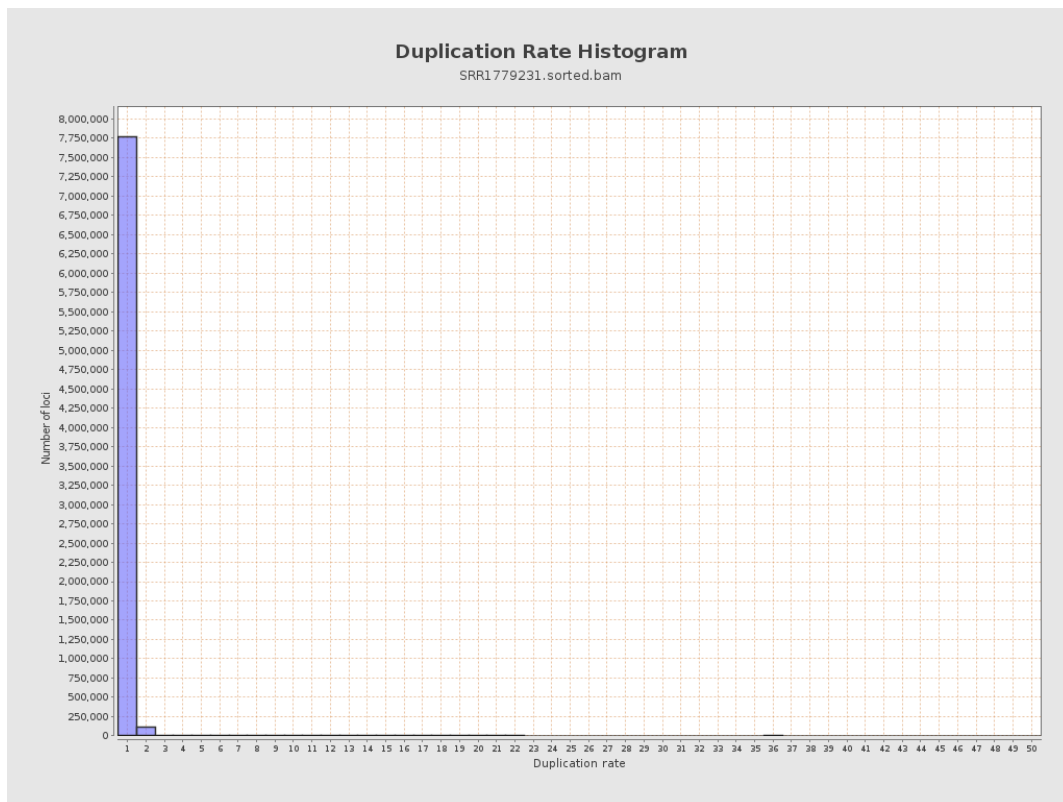
5. Results : Coverage Histogram (0-50X)



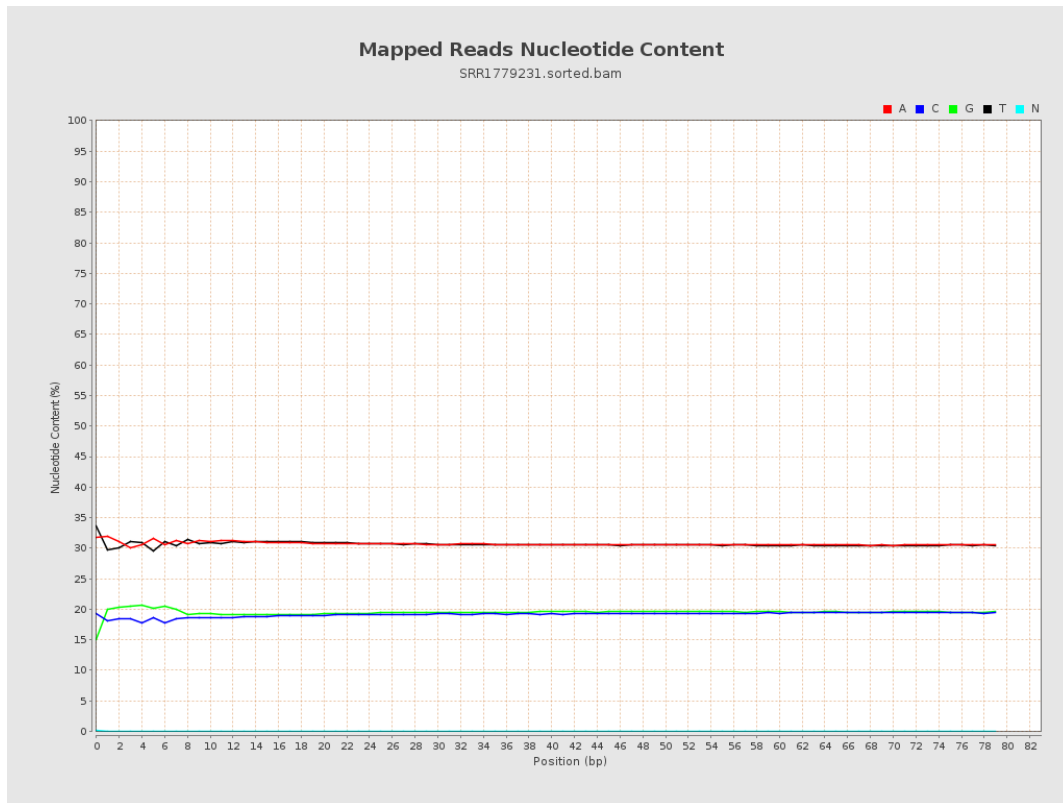
6. Results : Genome Fraction Coverage



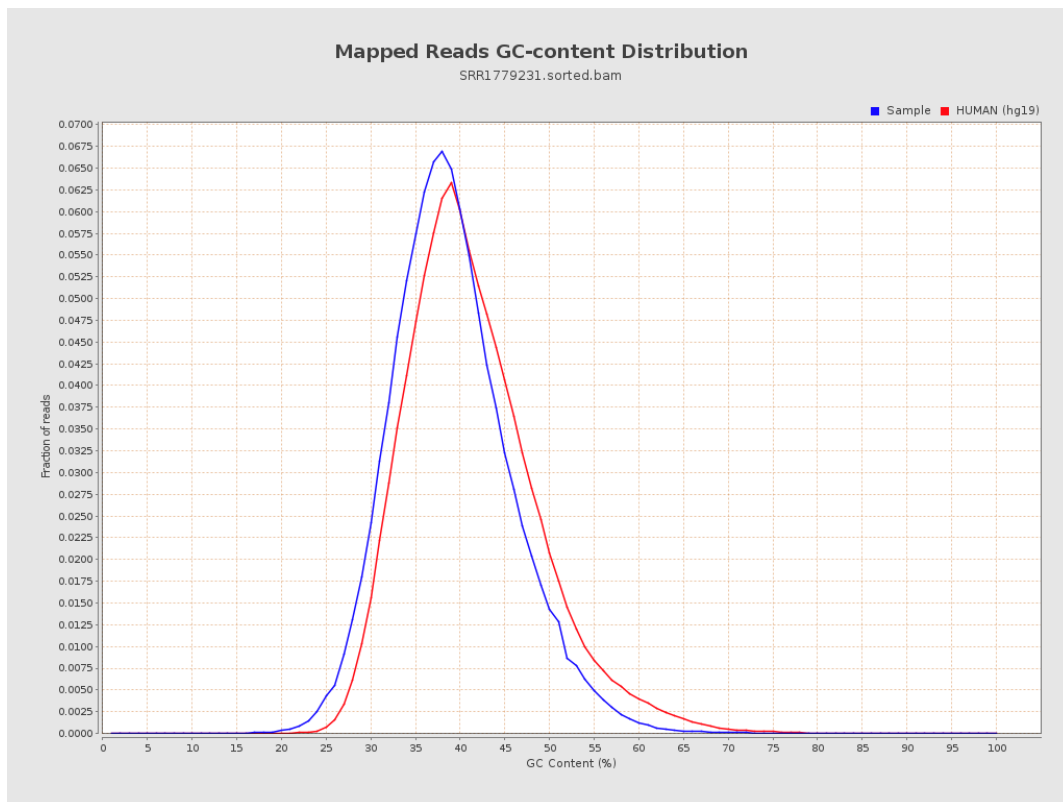
7. Results : Duplication Rate Histogram



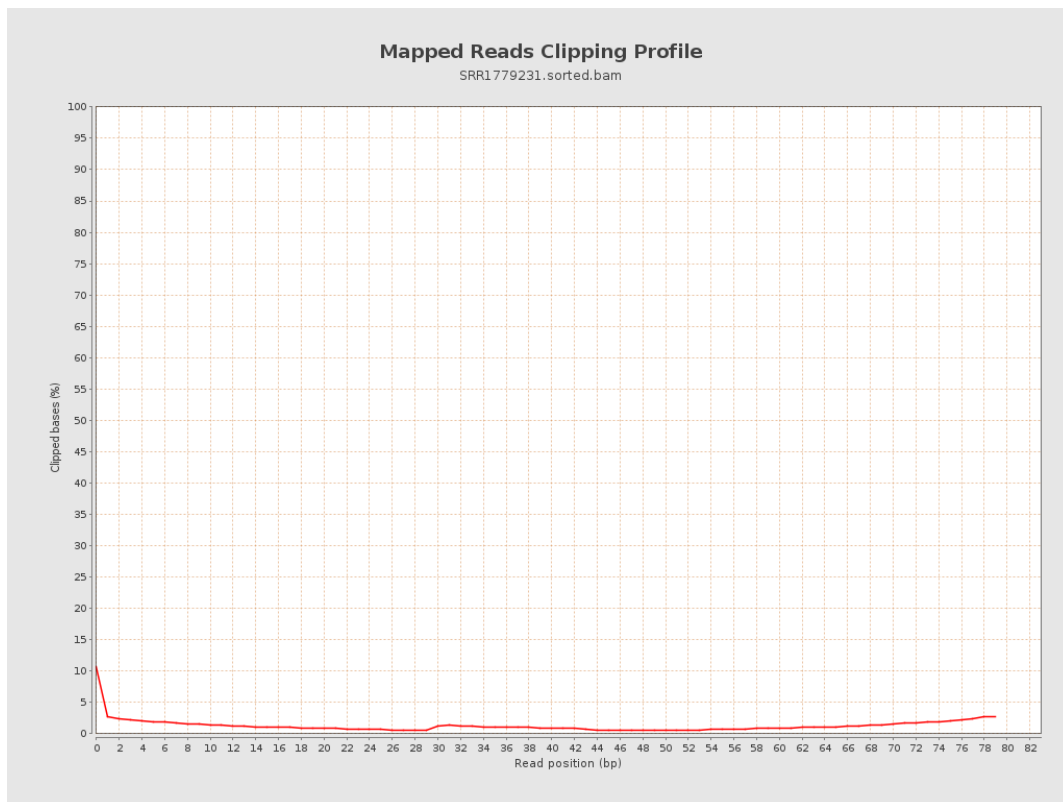
8. Results : Mapped Reads Nucleotide Content



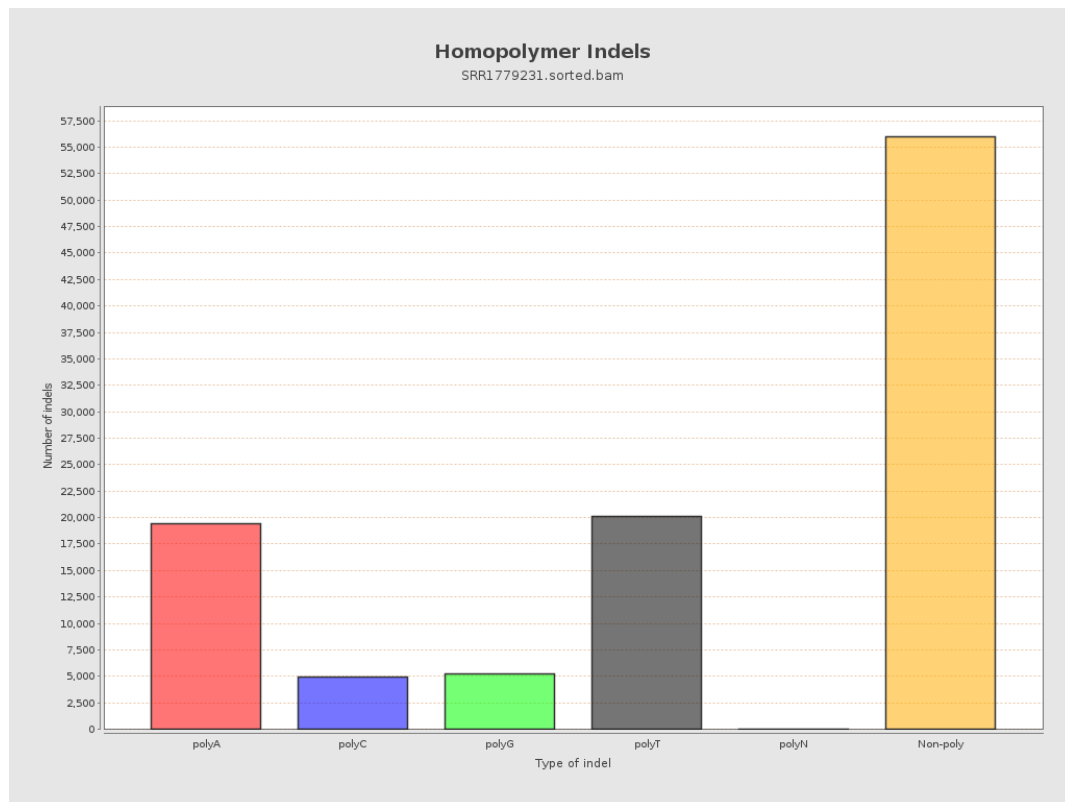
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



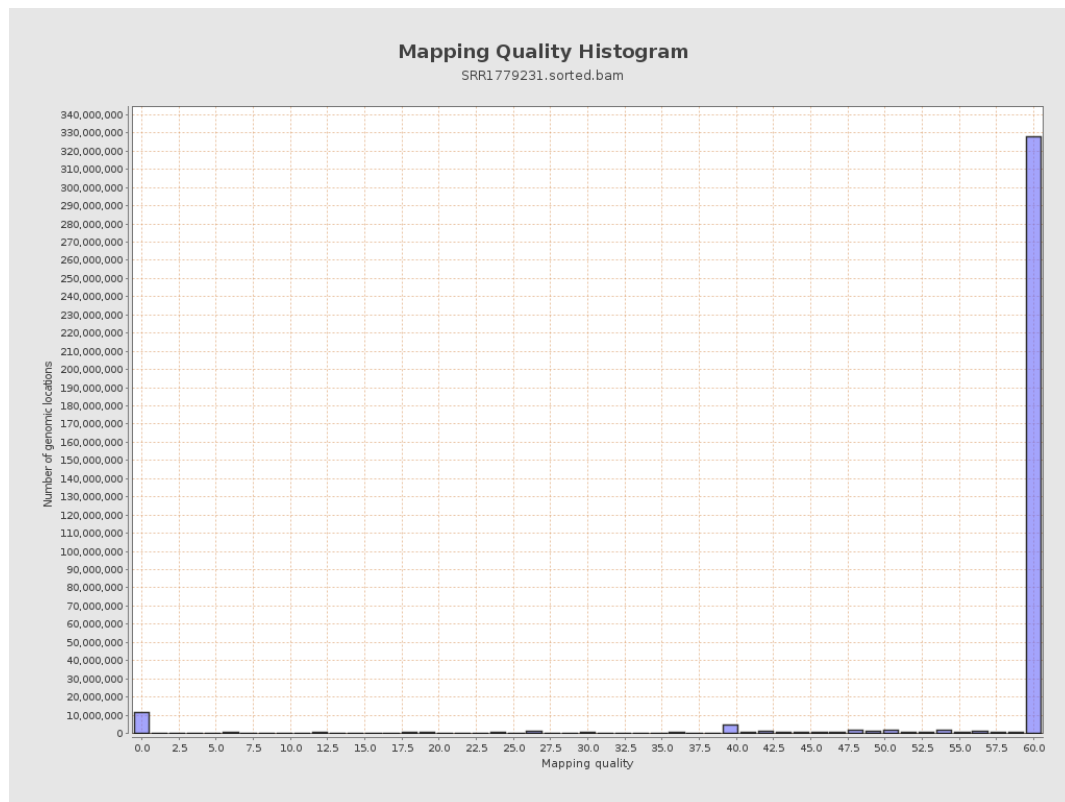
11. Results : Homopolymer Indels



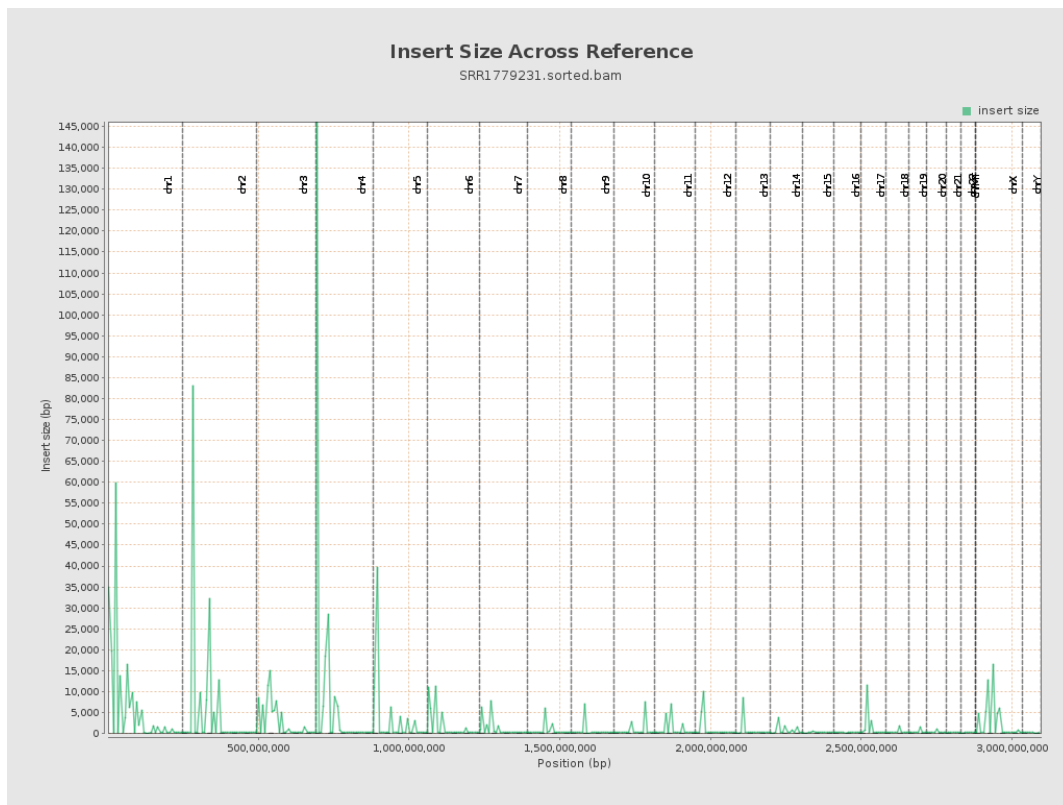
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

