

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/29 00:44:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779331.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_SRR1779331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779331_1.fastq.gz SRR1779331_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 29 00:44:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779331.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	271,951,602
Mapped reads	267,184,282 / 98.25%
Unmapped reads	4,767,320 / 1.75%
Mapped paired reads	267,184,282 / 98.25%
Mapped reads, first in pair	134,424,999 / 49.43%
Mapped reads, second in pair	132,759,283 / 48.82%
Mapped reads, both in pair	265,264,358 / 97.54%
Mapped reads, singletons	1,919,924 / 0.71%
Secondary alignments	0
Supplementary alignments	1,119,095 / 0.41%
Read min/max/mean length	30 / 101 / 101.17
Duplicated reads (estimated)	44,633,862 / 16.41%
Duplication rate	15.38%
Clipped reads	22,213,048 / 8.17%

2.2. ACGT Content

Number/percentage of A's	8,197,524,405 / 30.74%
Number/percentage of C's	5,168,918,596 / 19.38%
Number/percentage of T's	7,965,704,687 / 29.87%
Number/percentage of G's	5,330,396,008 / 19.99%
Number/percentage of N's	7,234,981 / 0.03%

GC Percentage	39.37%
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2.3. Coverage

Mean	8.6172
Standard Deviation	16.552

2.4. Mapping Quality

Mean Mapping Quality	53.85
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2.5. Insert size

Mean	215,091.83
Standard Deviation	4,465,291.7
P25/Median/P75	154 / 220 / 310

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	76,367,343
Insertions	2,270,484
Mapped reads with at least one insertion	0.84%
Deletions	2,833,511
Mapped reads with at least one deletion	1.04%
Homopolymer indels	47.62%

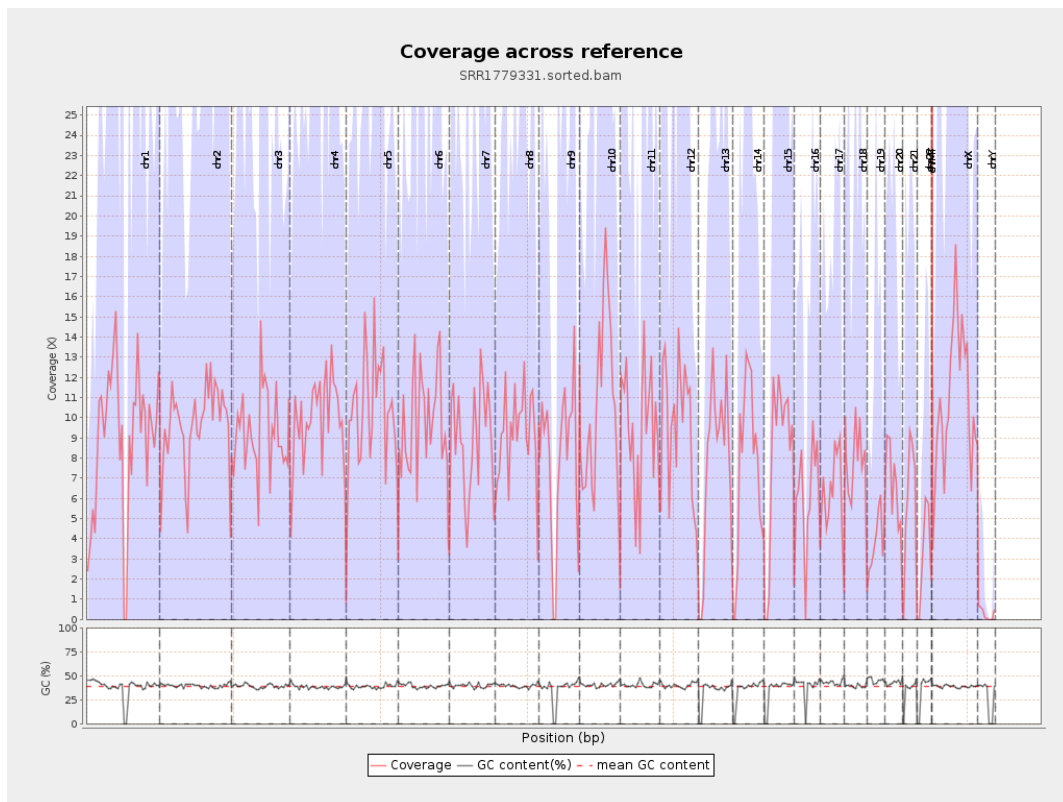
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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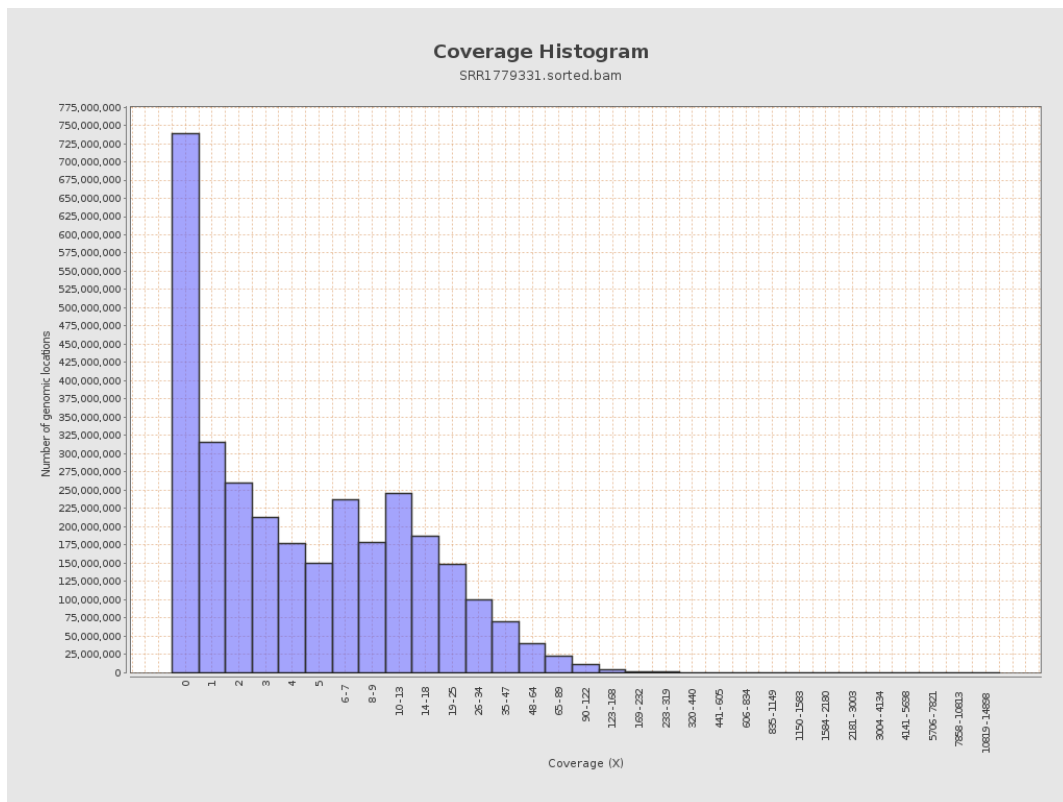
		bases	coverage	deviation
chr1	249250621	2238531699	8.981	18.5317
chr2	243199373	2337152428	9.61	15.8979
chr3	198022430	1821904245	9.2005	15.6666
chr4	191154276	1907290744	9.9778	15.8411
chr5	180915260	1852679550	10.2406	16.8965
chr6	171115067	1693889085	9.8991	15.9854
chr7	159138663	1401349487	8.8058	17.1215
chr8	146364022	1347248708	9.2048	15.0237
chr9	141213431	1101052703	7.7971	15.0657
chr10	135534747	1442241872	10.6411	30.7389
chr11	135006516	1284813498	9.5167	15.8079
chr12	133851895	1262286327	9.4305	16.2592
chr13	115169878	900011113	7.8146	14.4838
chr14	107349540	818726528	7.6267	13.4829
chr15	102531392	818646356	7.9843	15.8726
chr16	90354753	536812789	5.9412	11.2556
chr17	81195210	507374768	6.2488	11.9479
chr18	78077248	614672307	7.8726	14.5962
chr19	59128983	225393738	3.8119	11.0986
chr20	63025520	409958250	6.5046	12.4337
chr21	48129895	296243770	6.1551	12.5181
chr22	51304566	159208781	3.1032	7.4327
chrMT	16571	1005394	60.6719	23.4052
chrX	155270560	1681023873	10.8264	18.1042

chrY	59373566	16545380	0.2787	3.0455
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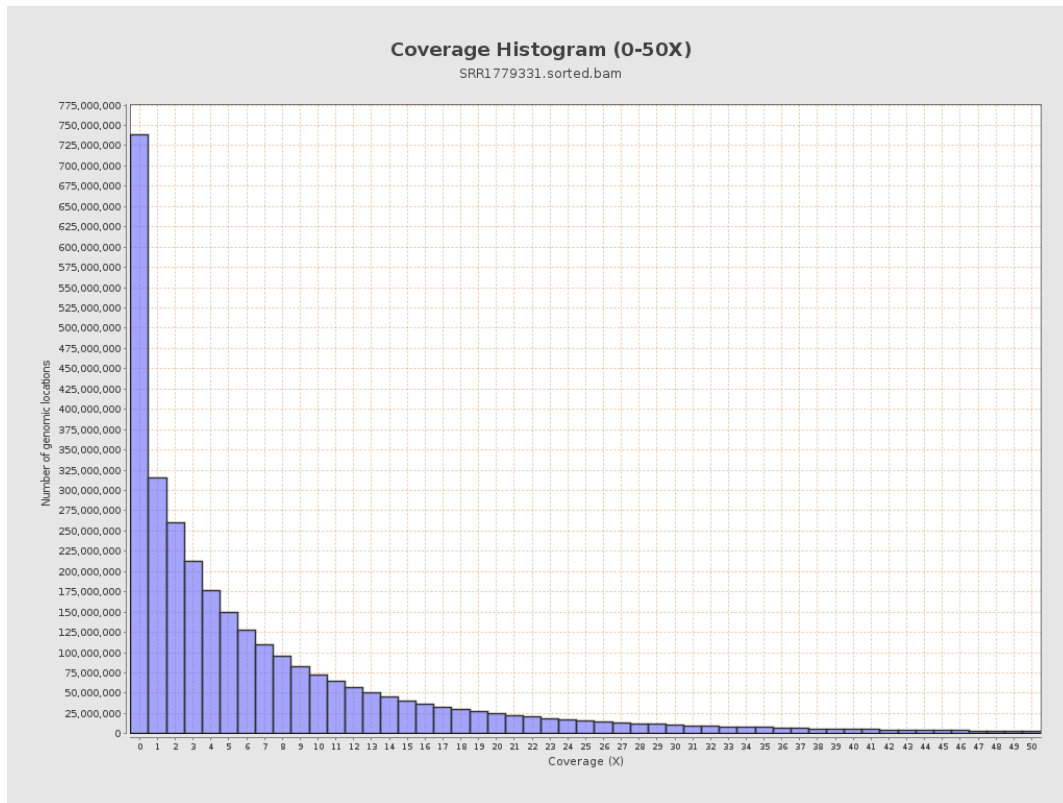
3. Results : Coverage across reference



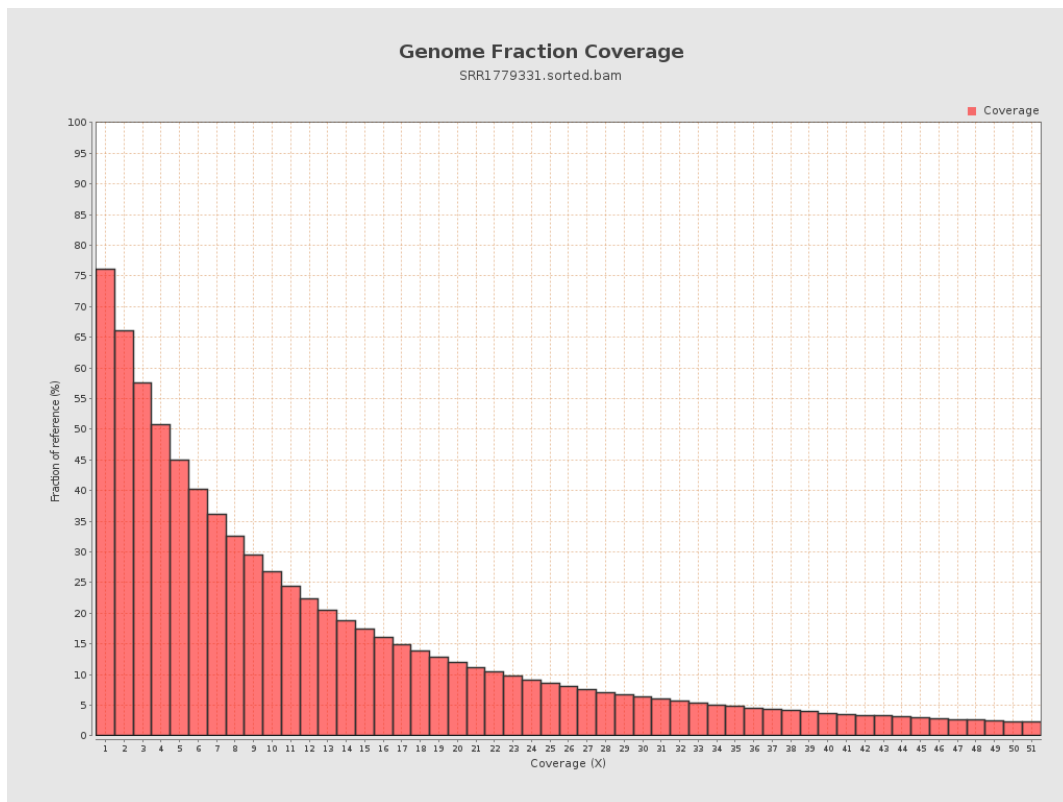
4. Results : Coverage Histogram



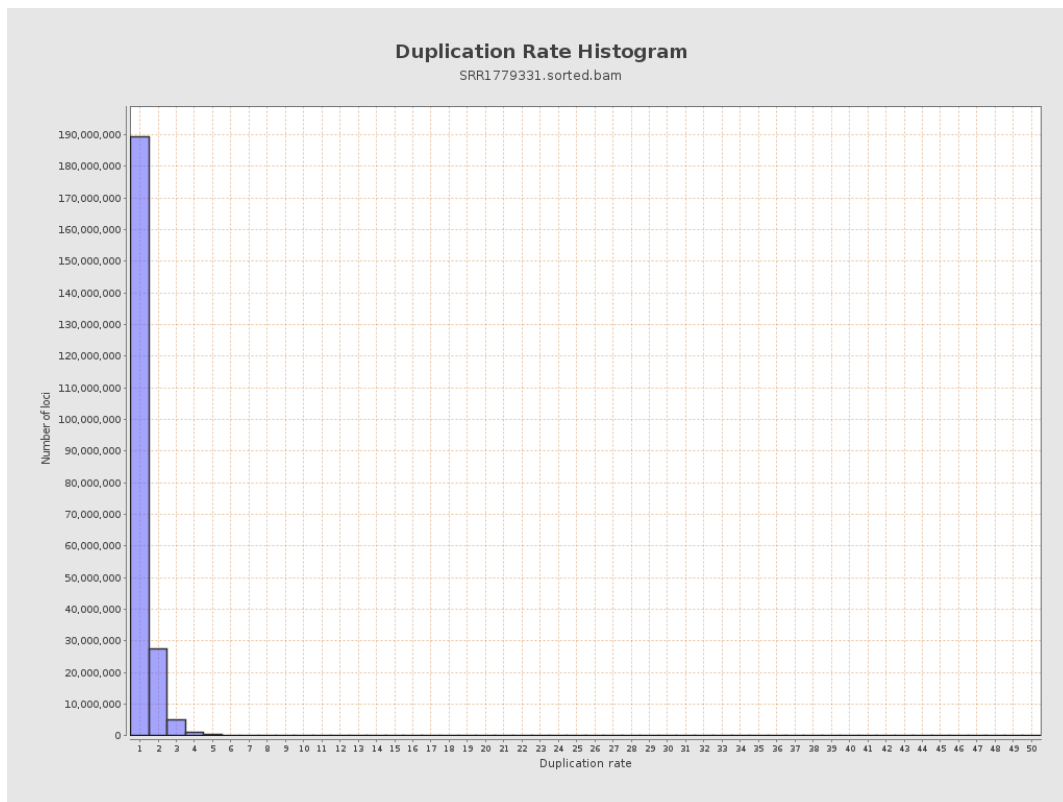
5. Results : Coverage Histogram (0-50X)



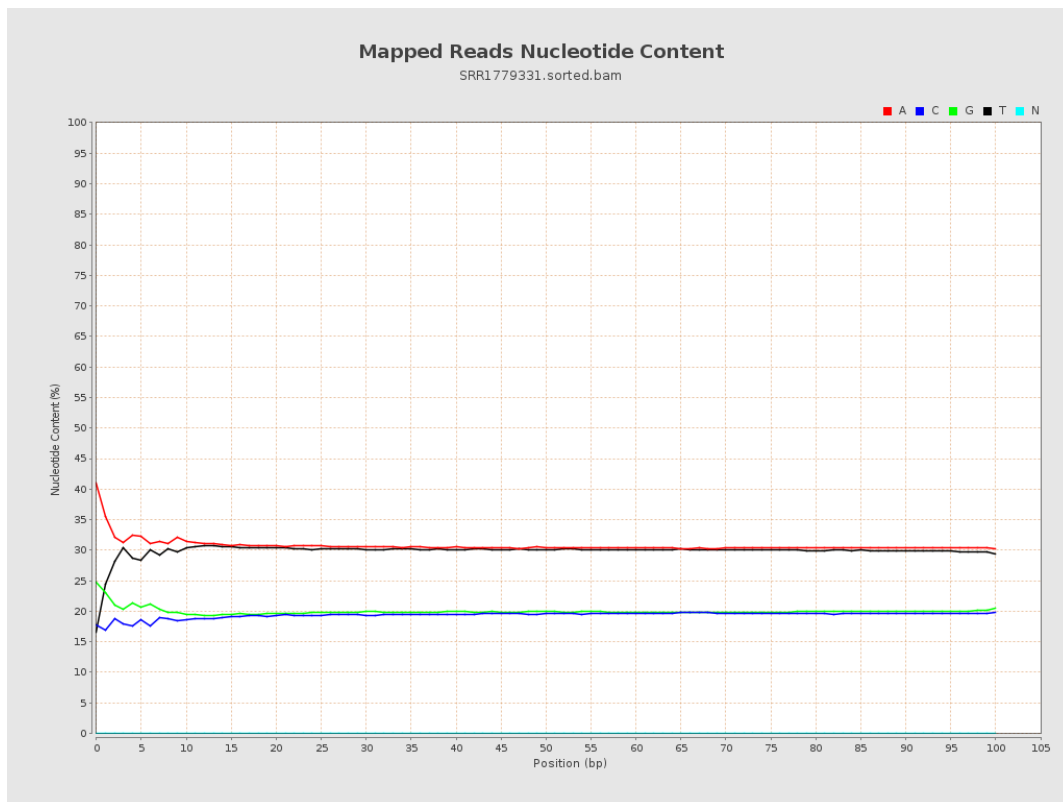
6. Results : Genome Fraction Coverage



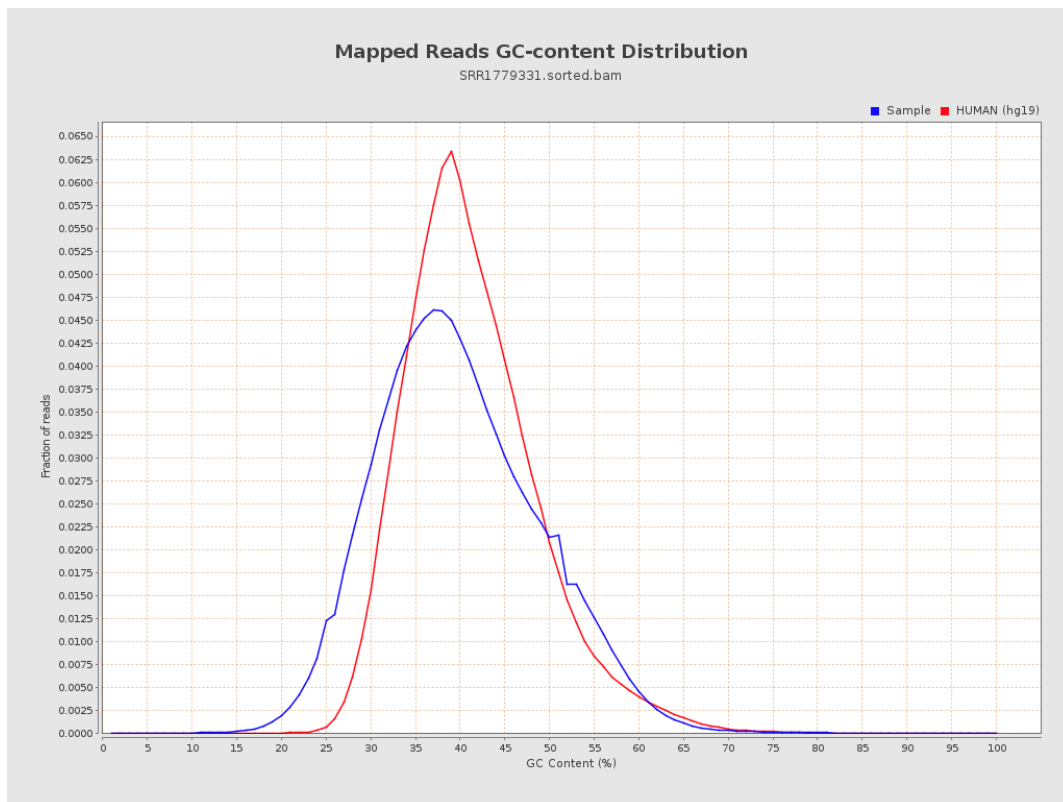
7. Results : Duplication Rate Histogram



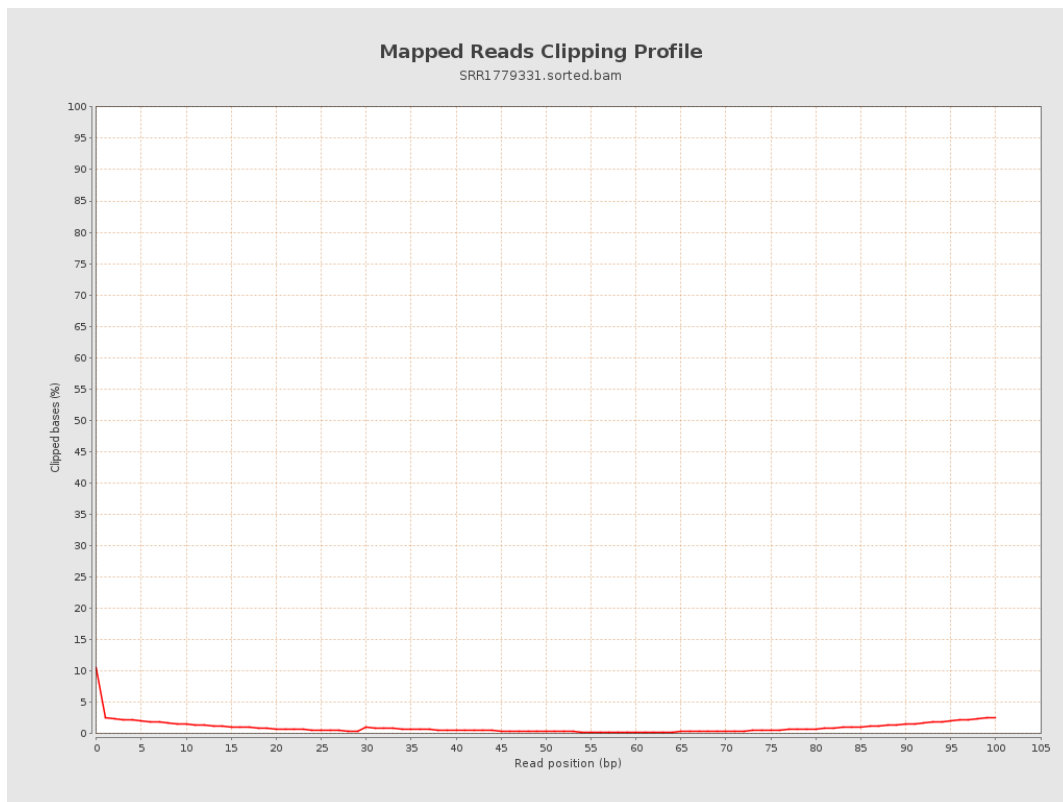
8. Results : Mapped Reads Nucleotide Content



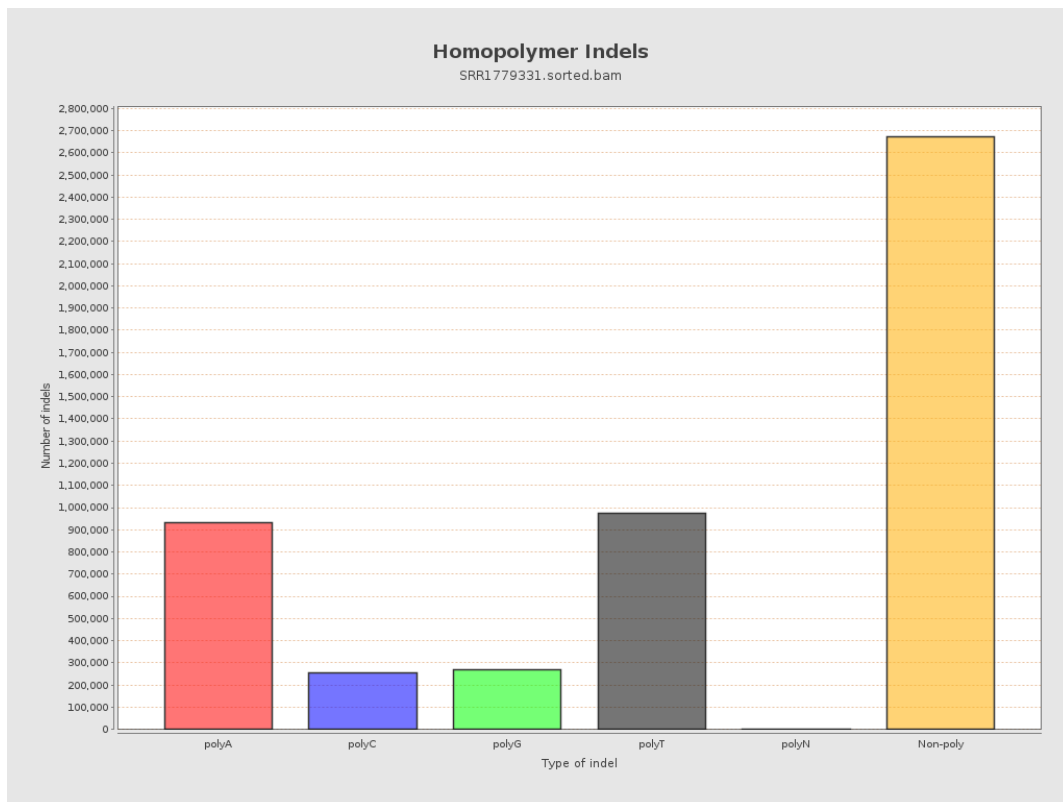
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



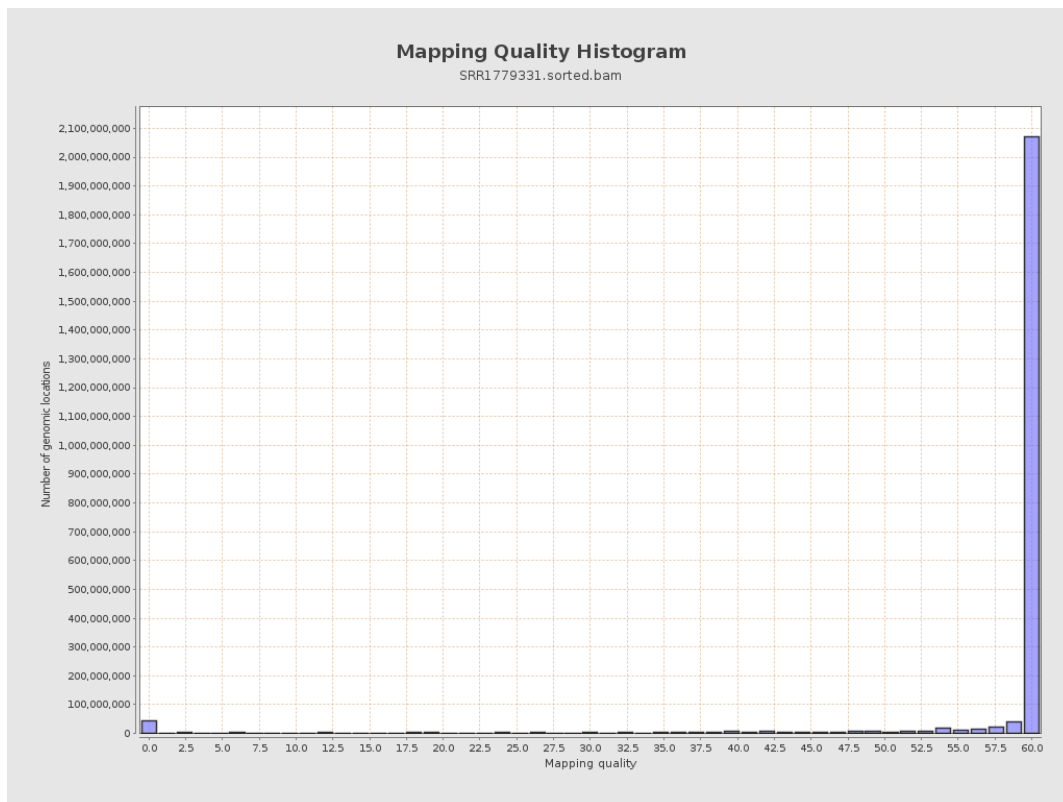
11. Results : Homopolymer Indels



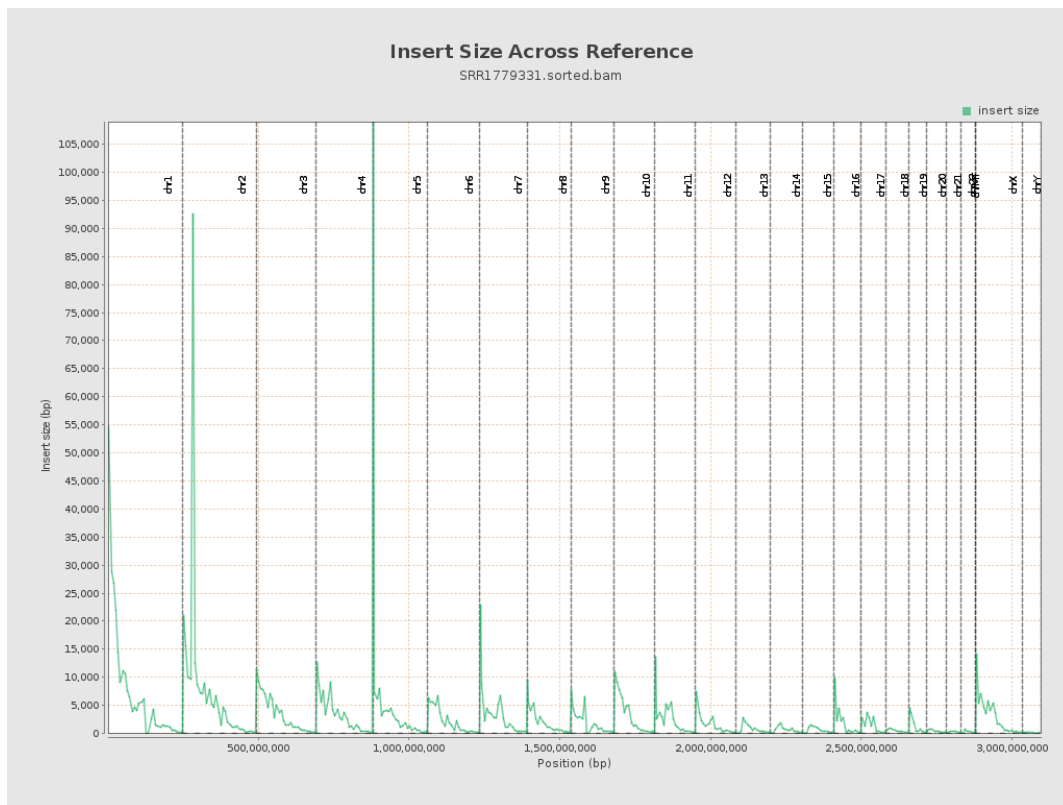
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

