

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 05:24:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779306.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_SRR1779306 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779306_1.fastq.gz SRR1779306_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 05:24:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779306.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,691,128
Mapped reads	16,933,997 / 90.6%
Unmapped reads	1,757,131 / 9.4%
Mapped paired reads	16,933,997 / 90.6%
Mapped reads, first in pair	8,525,219 / 45.61%
Mapped reads, second in pair	8,408,778 / 44.99%
Mapped reads, both in pair	16,773,474 / 89.74%
Mapped reads, singletons	160,523 / 0.86%
Secondary alignments	0
Supplementary alignments	53,131 / 0.28%
Read min/max/mean length	30 / 80 / 80.1
Duplicated reads (estimated)	852,815 / 4.56%
Duplication rate	4.58%
Clipped reads	601,797 / 3.22%

2.2. ACGT Content

Number/percentage of A's	417,165,474 / 30.97%
Number/percentage of C's	255,142,826 / 18.94%
Number/percentage of T's	413,257,015 / 30.68%
Number/percentage of G's	260,988,454 / 19.38%
Number/percentage of N's	356,824 / 0.03%

GC Percentage	38.32%
---------------	--------

2.3. Coverage

Mean	0.4352
Standard Deviation	1.9981

2.4. Mapping Quality

Mean Mapping Quality	52.81
----------------------	-------

2.5. Insert size

Mean	48,721.87
Standard Deviation	2,035,560.44
P25/Median/P75	156 / 209 / 287

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	4,833,172
Insertions	100,739
Mapped reads with at least one insertion	0.59%
Deletions	130,892
Mapped reads with at least one deletion	0.76%
Homopolymer indels	46.46%

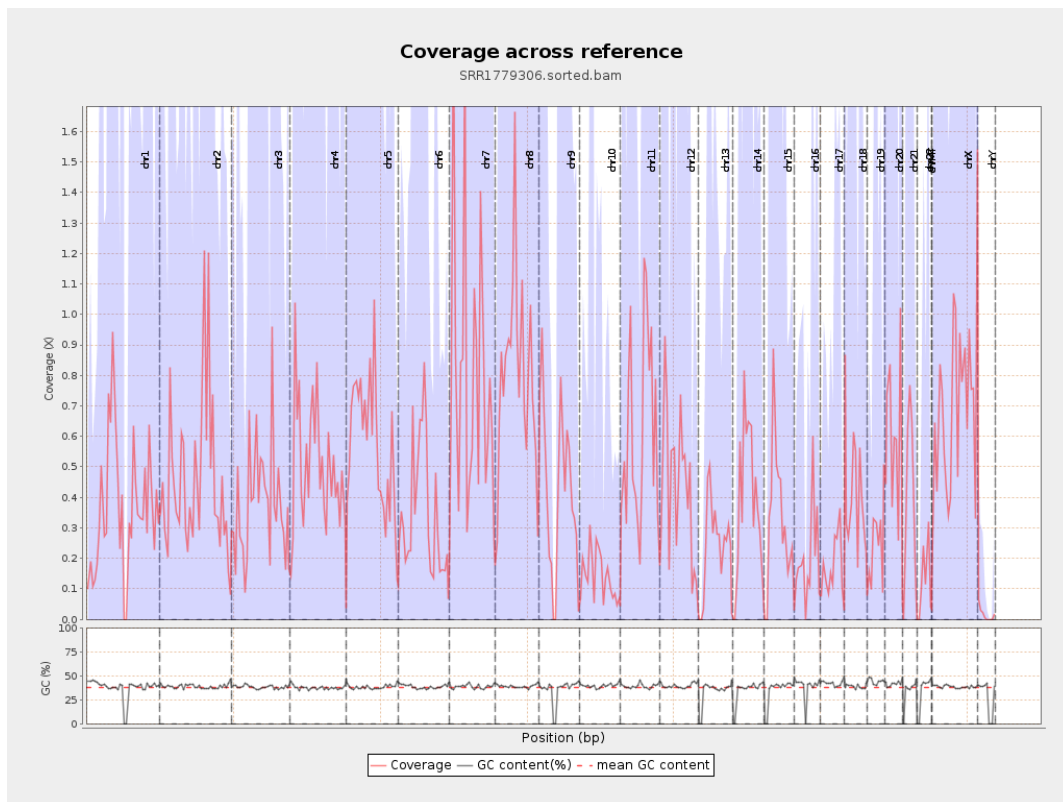
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

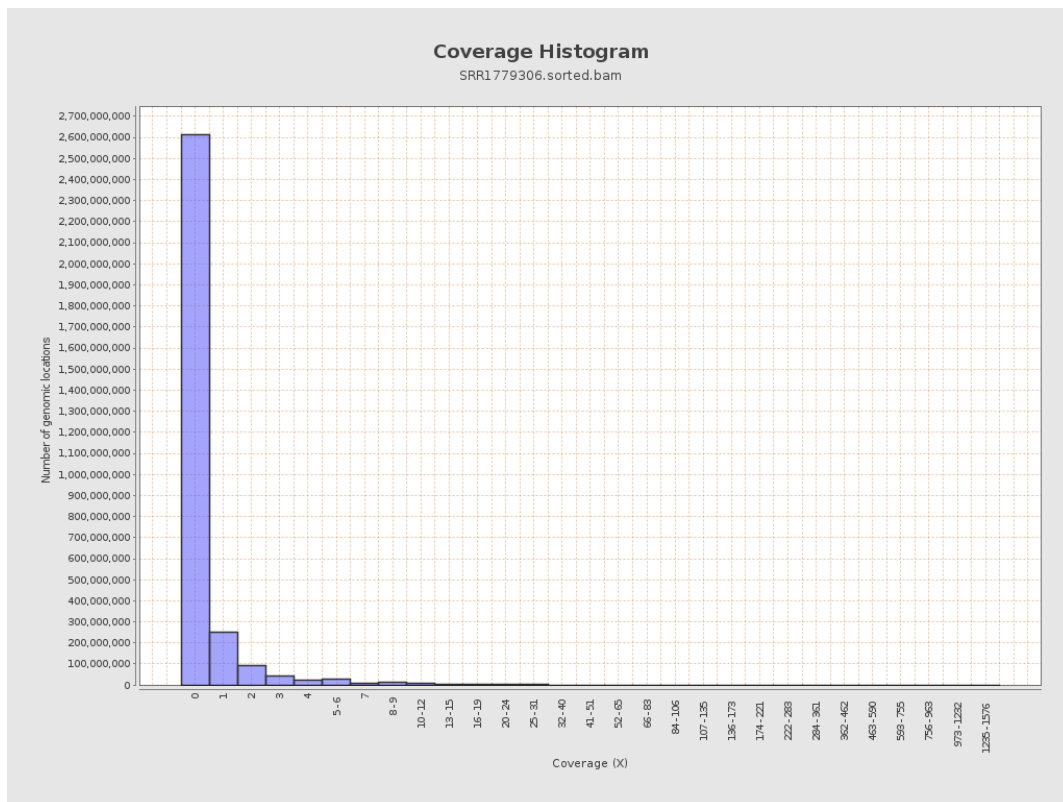
		bases	coverage	deviation
chr1	249250621	90598688	0.3635	2.2857
chr2	243199373	111416744	0.4581	1.8216
chr3	198022430	75535449	0.3814	1.7873
chr4	191154276	96603681	0.5054	2.0586
chr5	180915260	101917591	0.5633	2.1428
chr6	171115067	60515019	0.3537	1.4729
chr7	159138663	127081115	0.7986	3.0388
chr8	146364022	118805904	0.8117	2.6281
chr9	141213431	58553286	0.4146	1.8202
chr10	135534747	19295960	0.1424	1.5589
chr11	135006516	81695148	0.6051	2.2658
chr12	133851895	57581301	0.4302	1.6977
chr13	115169878	28349761	0.2462	1.057
chr14	107349540	41277770	0.3845	1.6256
chr15	102531392	32899535	0.3209	1.7568
chr16	90354753	17183481	0.1902	0.8996
chr17	81195210	13604477	0.1676	0.8792
chr18	78077248	31324048	0.4012	1.5569
chr19	59128983	13336181	0.2255	1.3259
chr20	63025520	36778929	0.5836	2.1207
chr21	48129895	19834578	0.4121	2.1265
chr22	51304566	6390044	0.1246	0.9328
chrMT	16571	1515	0.0914	0.3107
chrX	155270560	105669873	0.6806	3.0375

chrY	59373566	928888	0.0156	0.2138
------	----------	--------	--------	--------

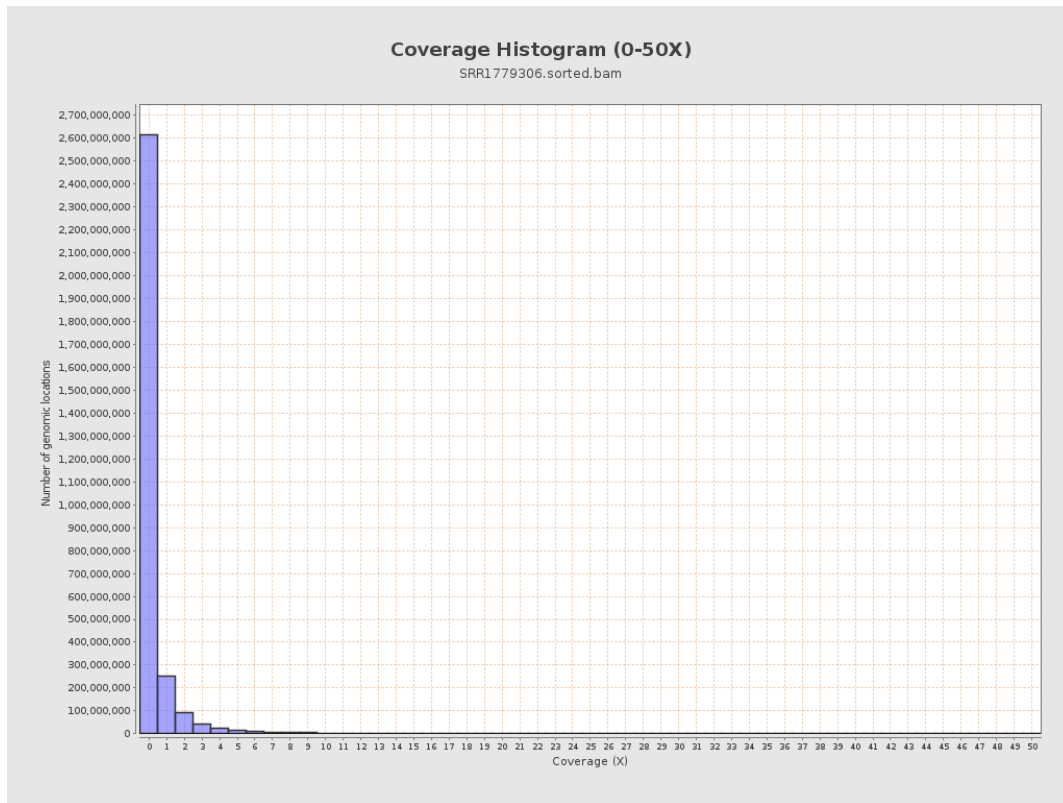
3. Results : Coverage across reference



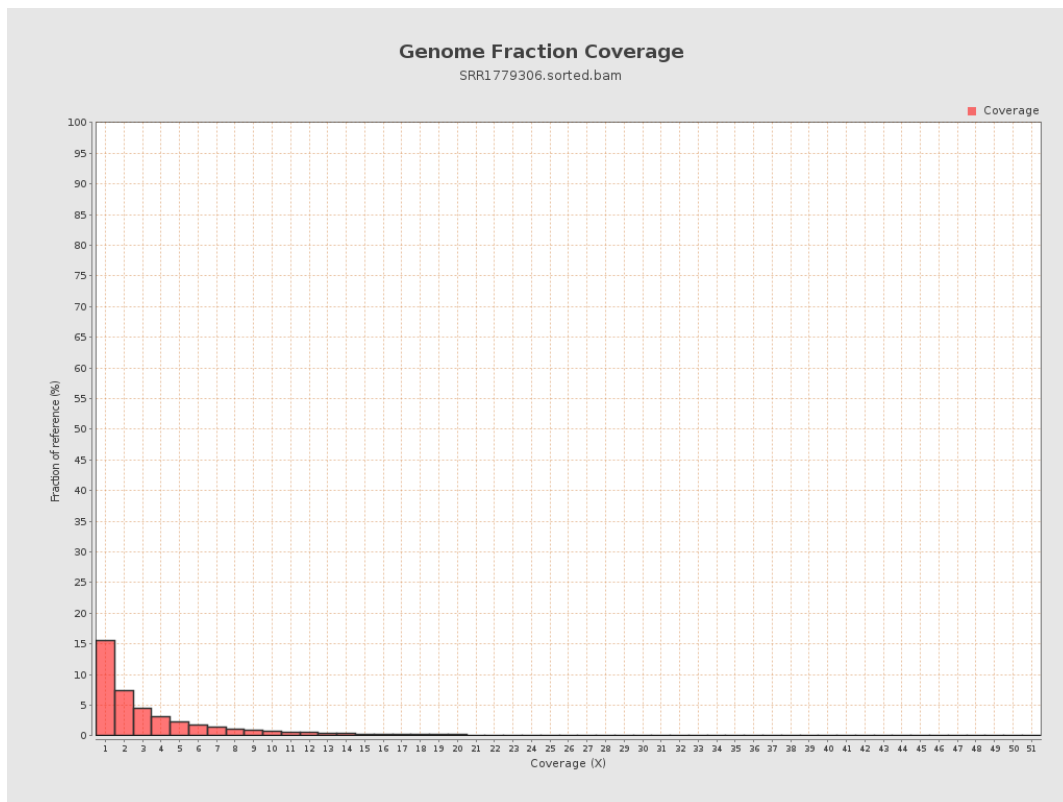
4. Results : Coverage Histogram



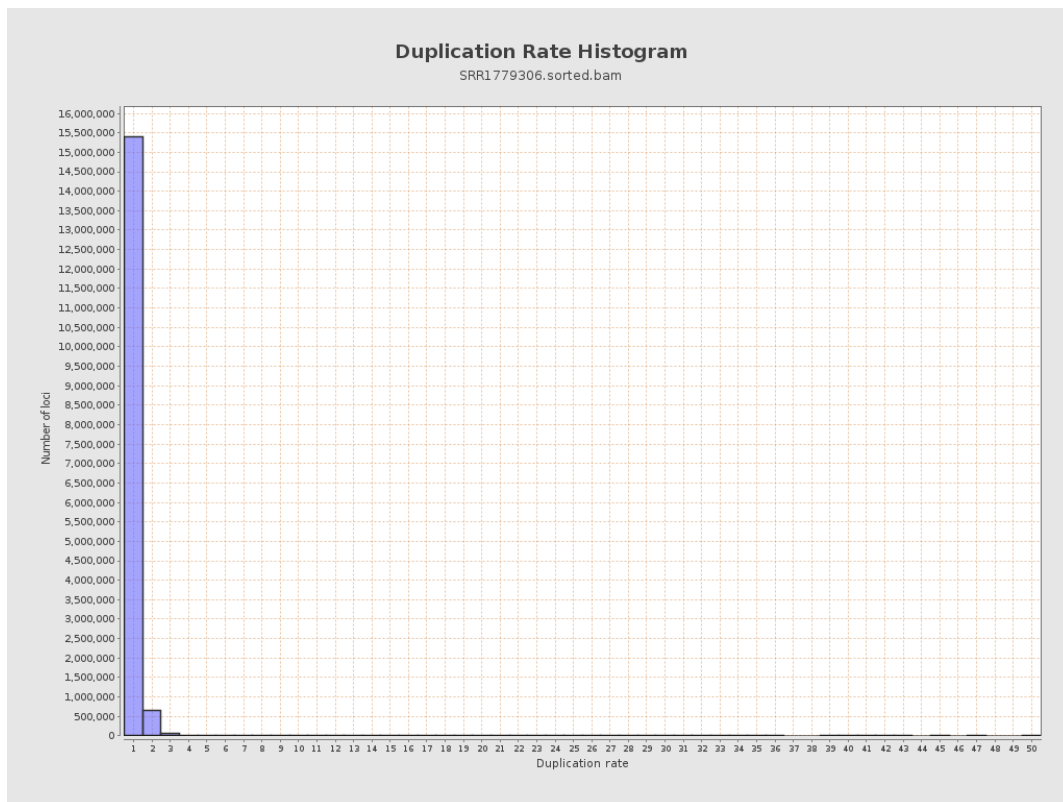
5. Results : Coverage Histogram (0-50X)



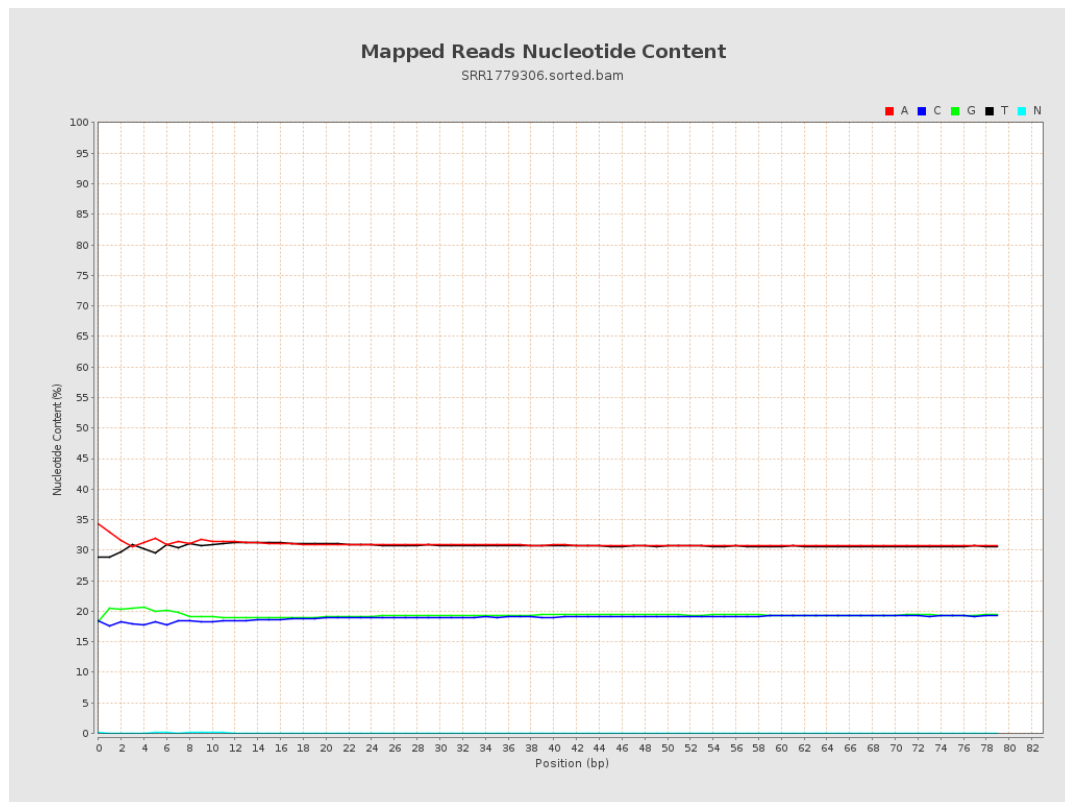
6. Results : Genome Fraction Coverage



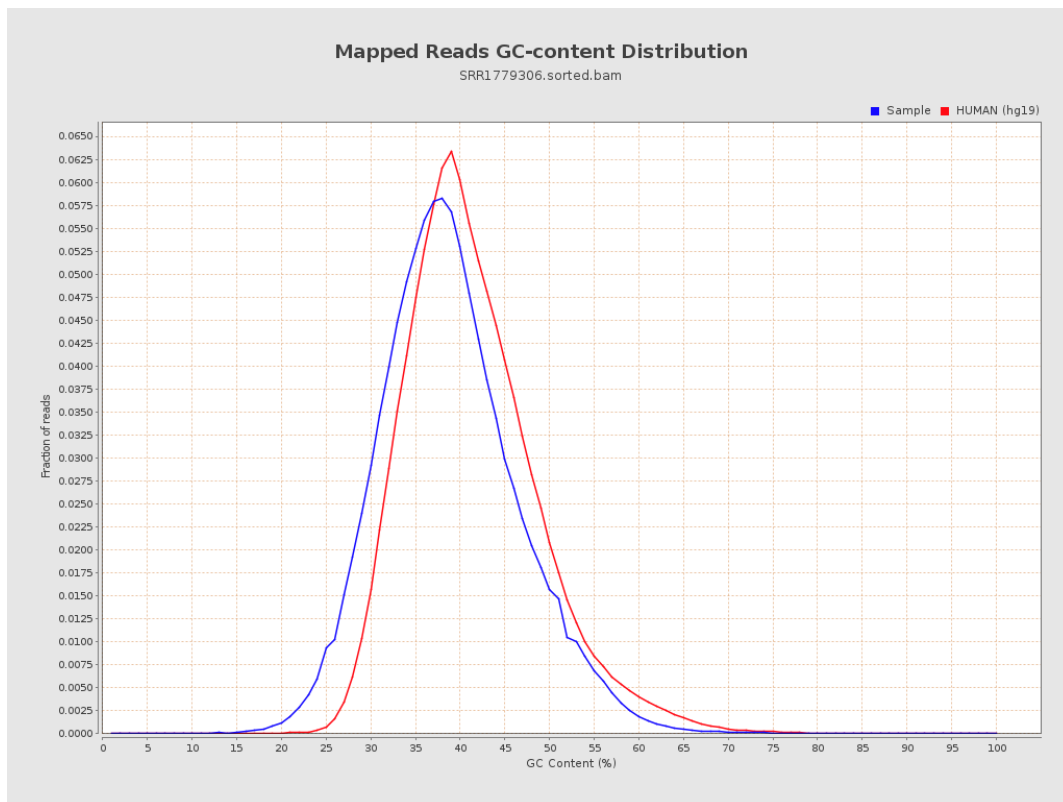
7. Results : Duplication Rate Histogram



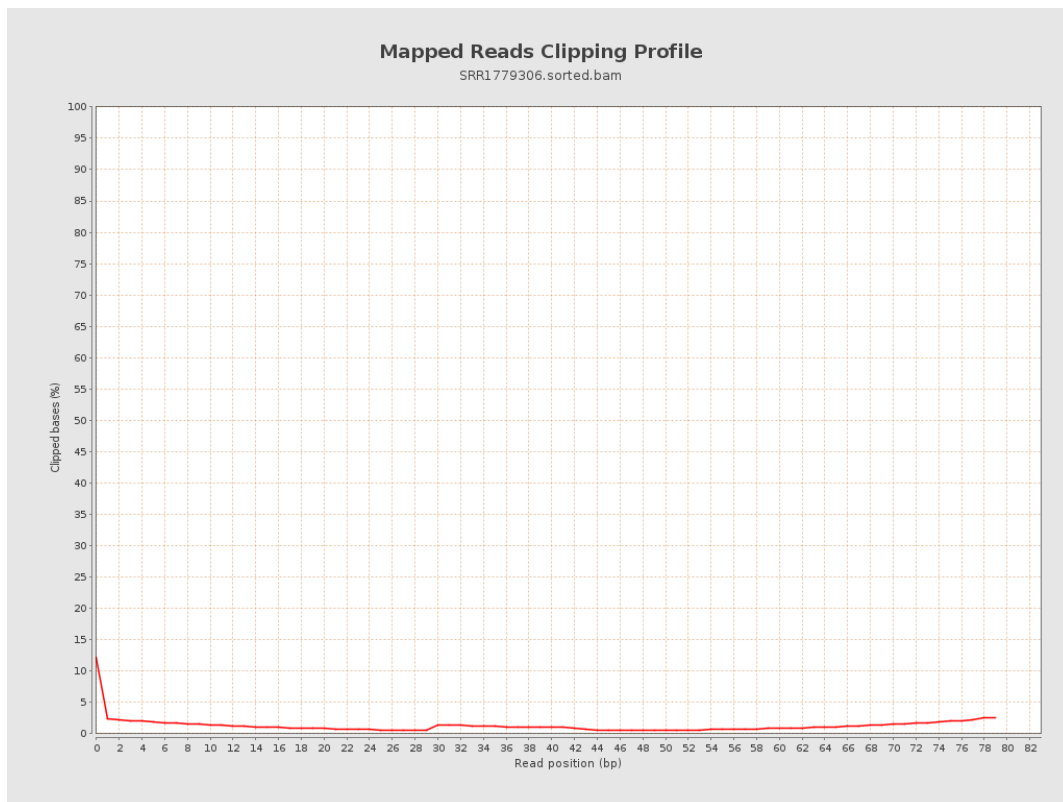
8. Results : Mapped Reads Nucleotide Content



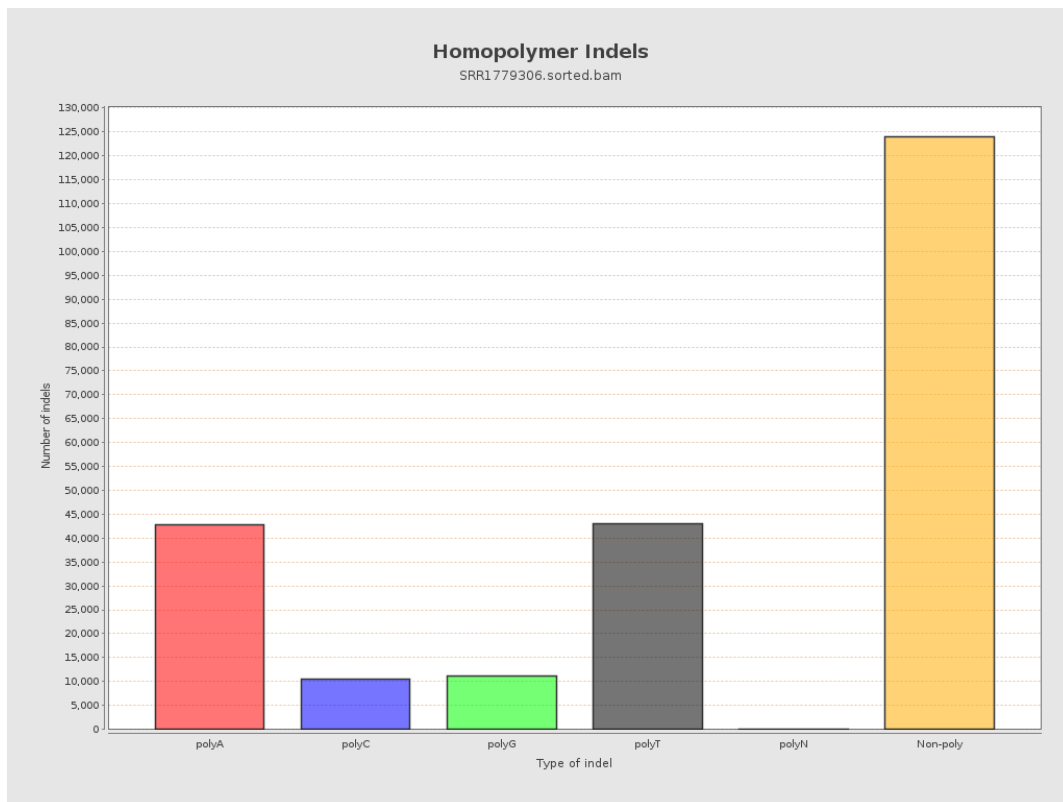
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



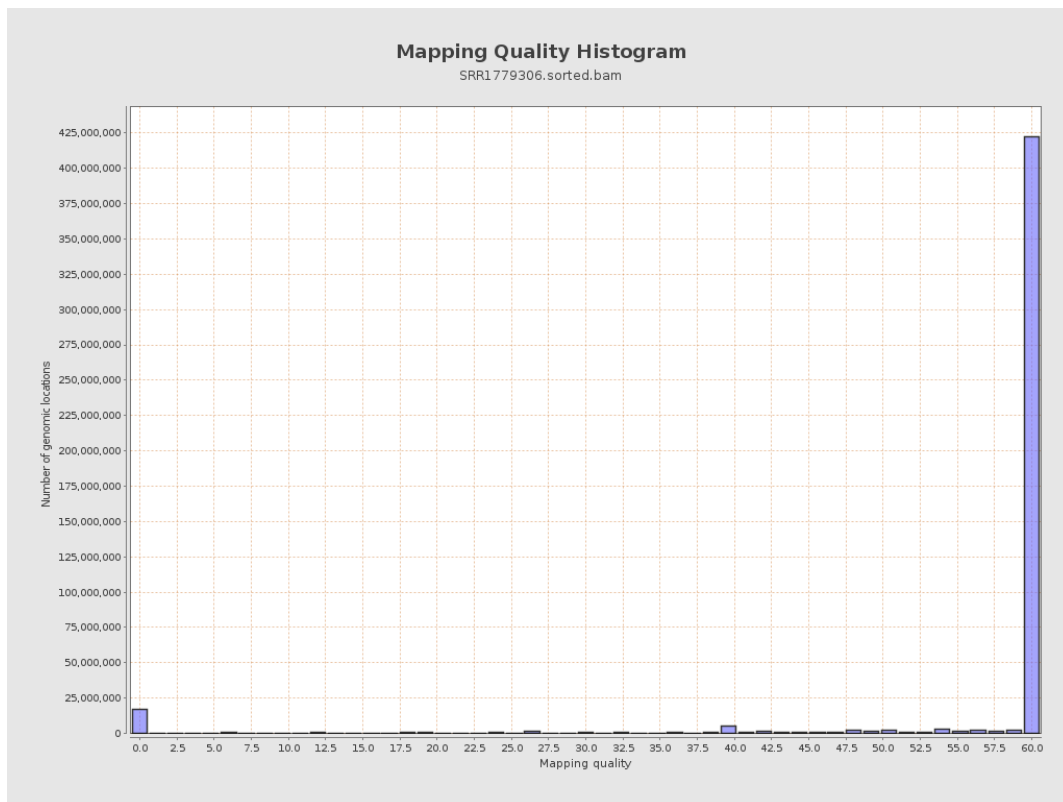
11. Results : Homopolymer Indels



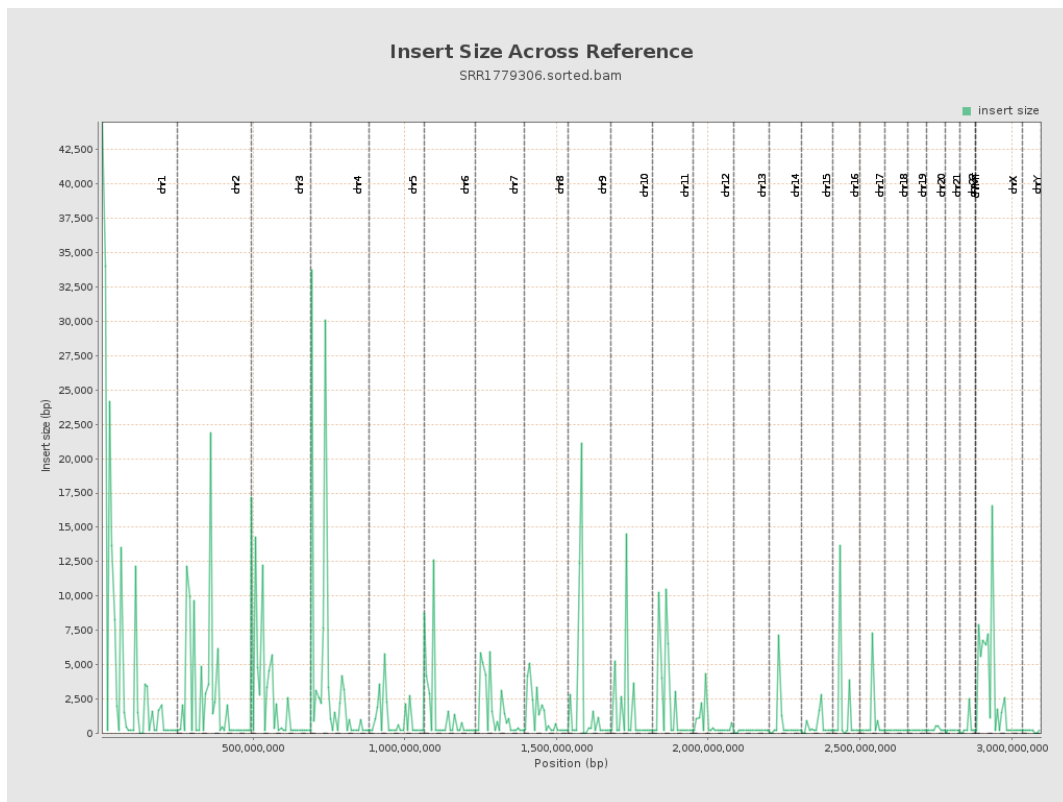
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

