

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 17:55:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779396.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_SRR1779396 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779396_1.fastq.gz SRR1779396_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 17:55:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779396.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,123,846
Mapped reads	12,271,614 / 81.14%
Unmapped reads	2,852,232 / 18.86%
Mapped paired reads	12,271,614 / 81.14%
Mapped reads, first in pair	6,178,241 / 40.85%
Mapped reads, second in pair	6,093,373 / 40.29%
Mapped reads, both in pair	12,112,002 / 80.09%
Mapped reads, singletons	159,612 / 1.06%
Secondary alignments	0
Supplementary alignments	48,012 / 0.32%
Read min/max/mean length	30 / 80 / 80.12
Duplicated reads (estimated)	978,366 / 6.47%
Duplication rate	6.87%
Clipped reads	782,459 / 5.17%

2.2. ACGT Content

Number/percentage of A's	284,525,475 / 29.29%
Number/percentage of C's	199,588,578 / 20.54%
Number/percentage of T's	283,413,325 / 29.17%
Number/percentage of G's	203,815,725 / 20.98%
Number/percentage of N's	215,261 / 0.02%

GC Percentage	41.52%
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2.3. Coverage

Mean	0.3139
Standard Deviation	2.5215

2.4. Mapping Quality

Mean Mapping Quality	49.28
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2.5. Insert size

Mean	62,477.06
Standard Deviation	2,603,589.1
P25/Median/P75	121 / 158 / 204

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	3,539,006
Insertions	97,436
Mapped reads with at least one insertion	0.79%
Deletions	115,698
Mapped reads with at least one deletion	0.93%
Homopolymer indels	46.49%

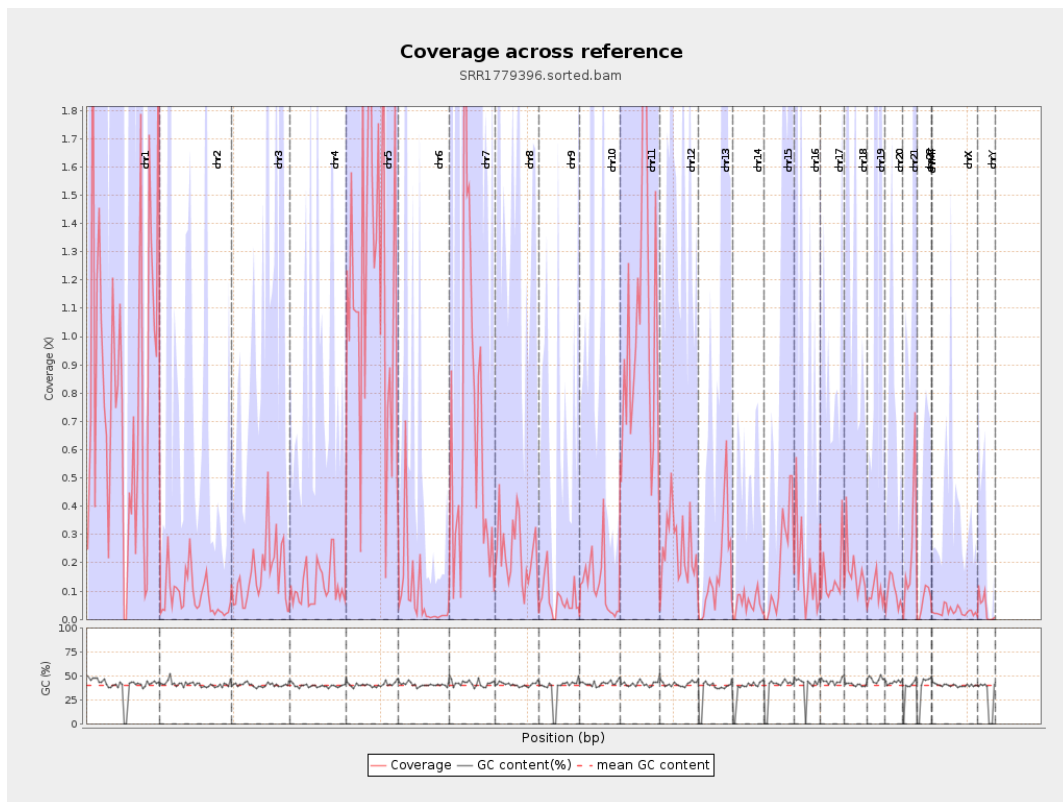
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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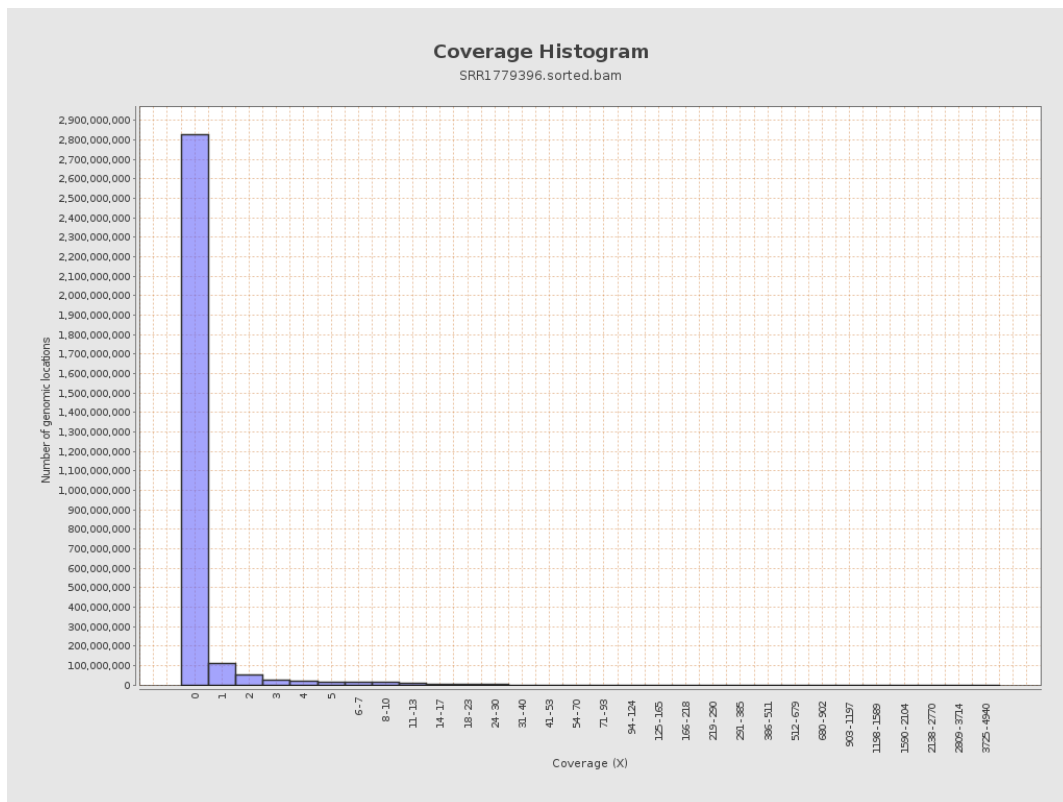
		bases	coverage	deviation
chr1	249250621	204792557	0.8216	5.7581
chr2	243199373	19741250	0.0812	1.0603
chr3	198022430	31429188	0.1587	2.235
chr4	191154276	22296667	0.1166	0.9016
chr5	180915260	214255252	1.1843	3.6093
chr6	171115067	13682291	0.08	0.7622
chr7	159138663	105780625	0.6647	3.8602
chr8	146364022	34880498	0.2383	1.1778
chr9	141213431	9977335	0.0707	0.8238
chr10	135534747	16481719	0.1216	3.0216
chr11	135006516	143755856	1.0648	3.6125
chr12	133851895	33895105	0.2532	1.186
chr13	115169878	20216930	0.1755	1.1072
chr14	107349540	6127806	0.0571	0.4432
chr15	102531392	20462294	0.1996	1.1392
chr16	90354753	14956488	0.1655	1.1828
chr17	81195210	11776540	0.145	0.8202
chr18	78077248	13538057	0.1734	1.1201
chr19	59128983	5525394	0.0934	3.0164
chr20	63025520	5724773	0.0908	0.7594
chr21	48129895	12207266	0.2536	1.3976
chr22	51304566	3375143	0.0658	0.5028
chrMT	16571	400	0.0241	0.1703
chrX	155270560	4493780	0.0289	0.4606

chrY	59373566	2432708	0.041	0.3684
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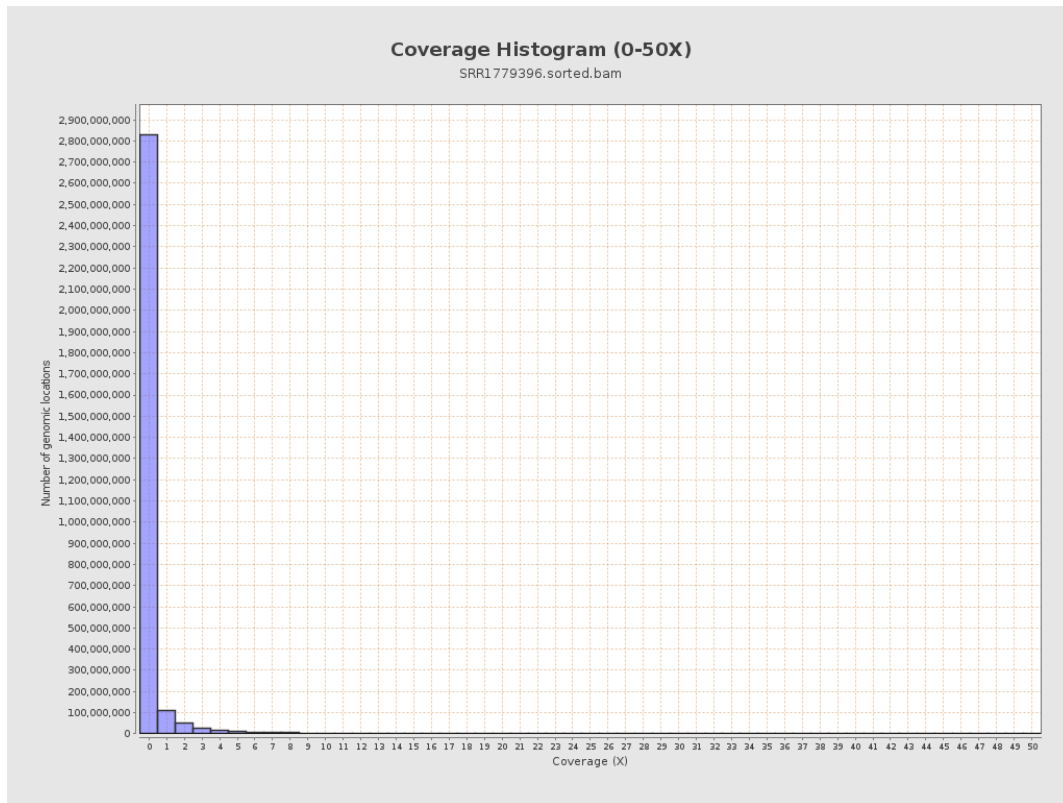
3. Results : Coverage across reference



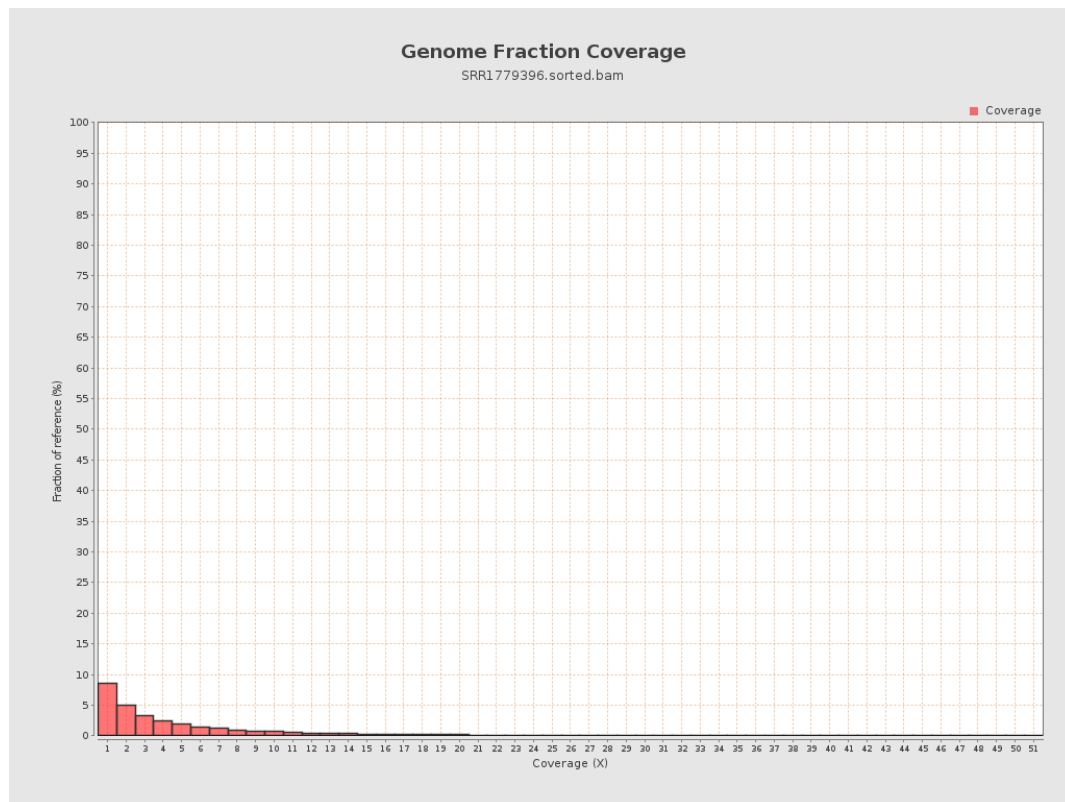
4. Results : Coverage Histogram



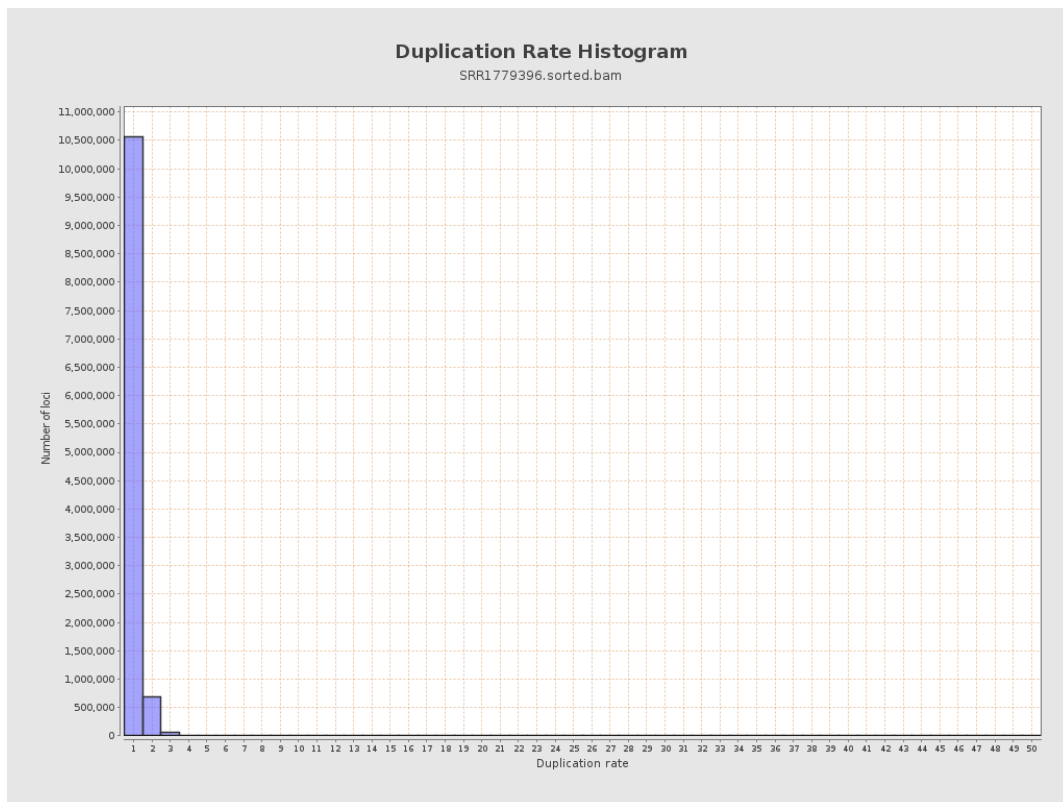
5. Results : Coverage Histogram (0-50X)



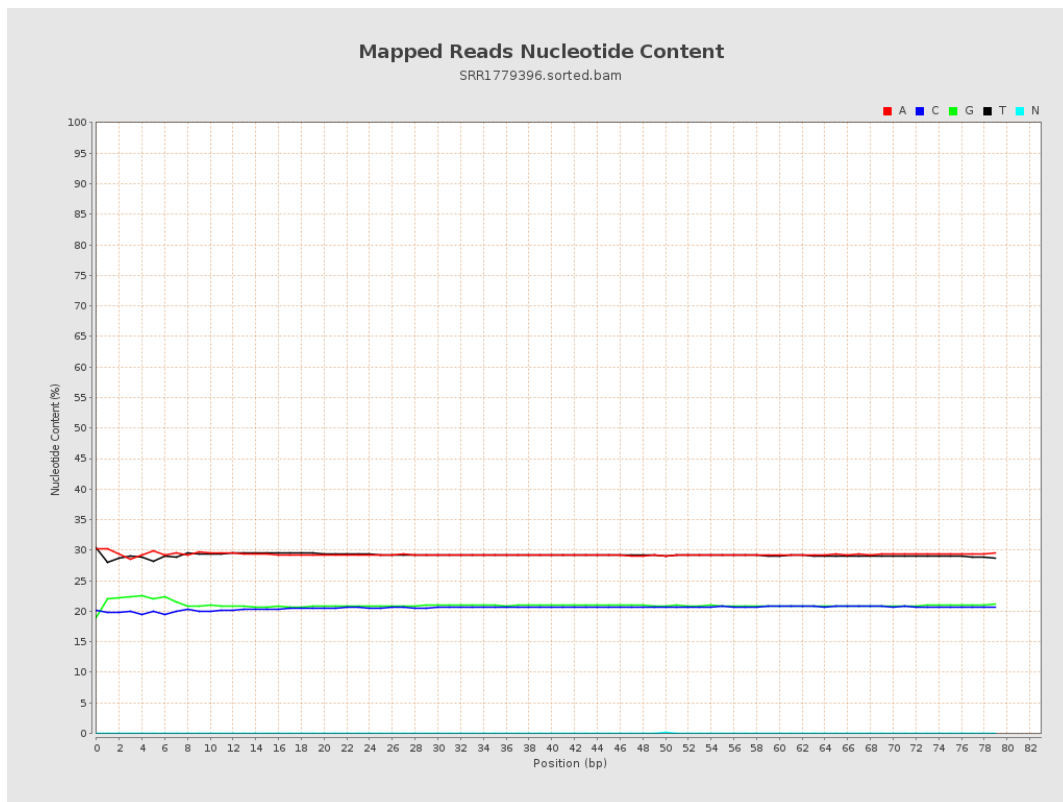
6. Results : Genome Fraction Coverage



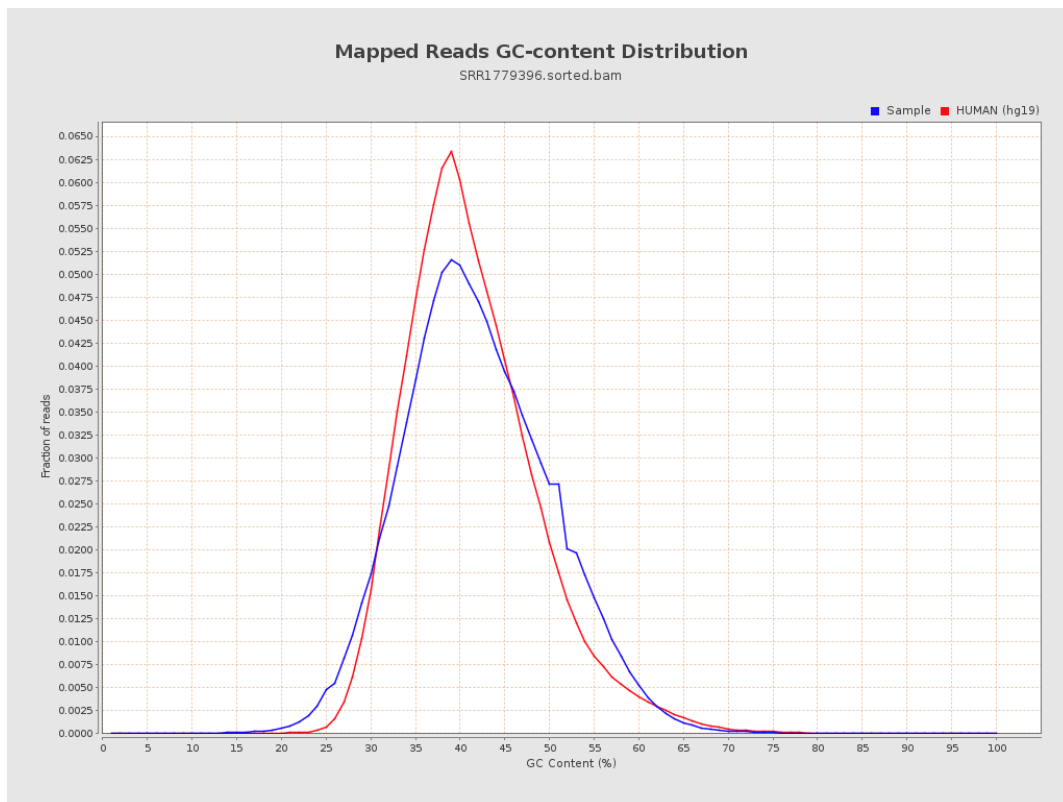
7. Results : Duplication Rate Histogram



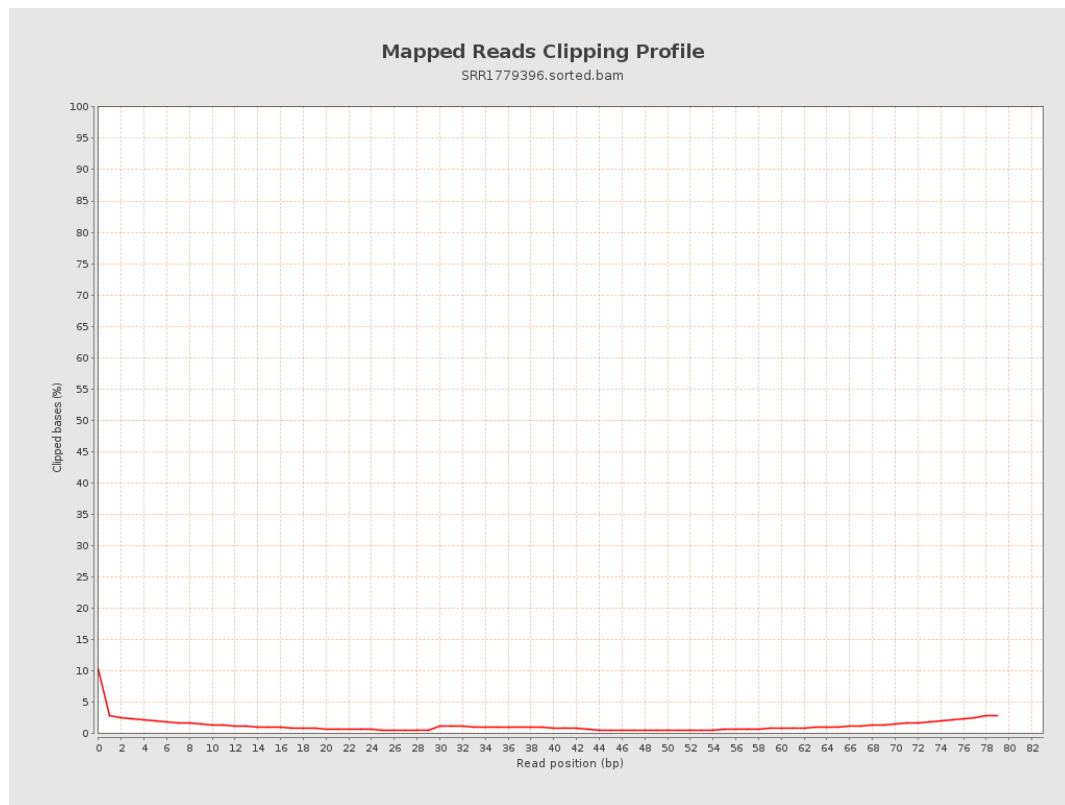
8. Results : Mapped Reads Nucleotide Content



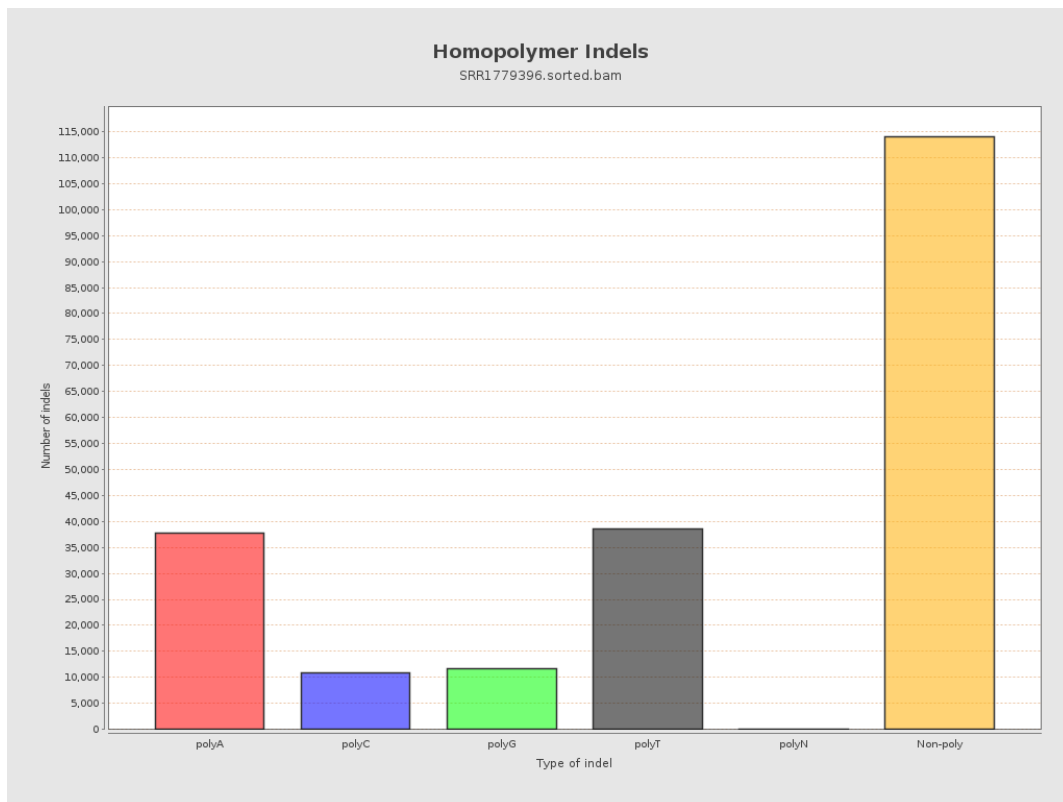
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



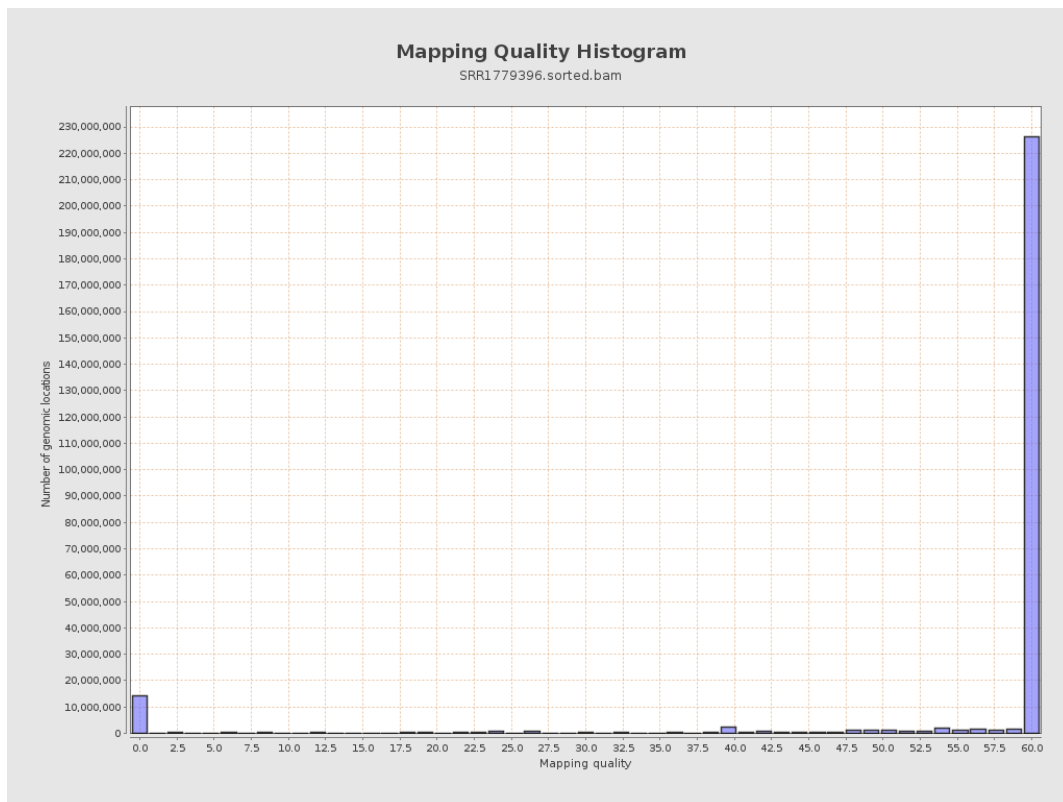
11. Results : Homopolymer Indels



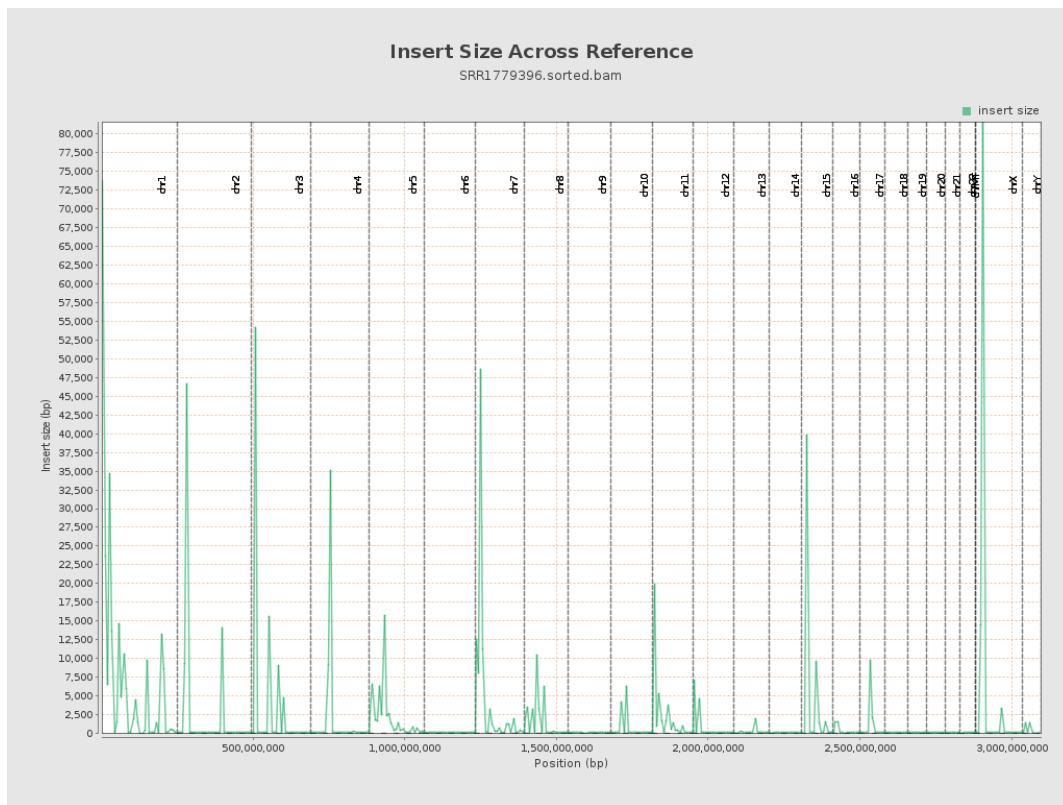
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

