

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 04:07:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779429.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_SRR1779429 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779429_1.fastq.gz SRR1779429_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 04:07:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779429.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,714,996
Mapped reads	11,321,554 / 89.04%
Unmapped reads	1,393,442 / 10.96%
Mapped paired reads	11,321,554 / 89.04%
Mapped reads, first in pair	5,687,398 / 44.73%
Mapped reads, second in pair	5,634,156 / 44.31%
Mapped reads, both in pair	11,216,244 / 88.21%
Mapped reads, singletons	105,310 / 0.83%
Secondary alignments	0
Supplementary alignments	189,481 / 1.49%
Read min/max/mean length	30 / 80 / 80.53
Duplicated reads (estimated)	10,452,995 / 82.21%
Duplication rate	38%
Clipped reads	1,335,131 / 10.5%

2.2. ACGT Content

Number/percentage of A's	269,761,828 / 30.26%
Number/percentage of C's	175,766,553 / 19.71%
Number/percentage of T's	266,945,113 / 29.94%
Number/percentage of G's	178,946,701 / 20.07%
Number/percentage of N's	188,983 / 0.02%

GC Percentage	39.78%
---------------	--------

2.3. Coverage

Mean	0.2881
Standard Deviation	45.1661

2.4. Mapping Quality

Mean Mapping Quality	50.15
----------------------	-------

2.5. Insert size

Mean	99,278.26
Standard Deviation	3,019,524.34
P25/Median/P75	137 / 182 / 235

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	4,403,693
Insertions	90,905
Mapped reads with at least one insertion	0.8%
Deletions	111,774
Mapped reads with at least one deletion	0.98%
Homopolymer indels	50.68%

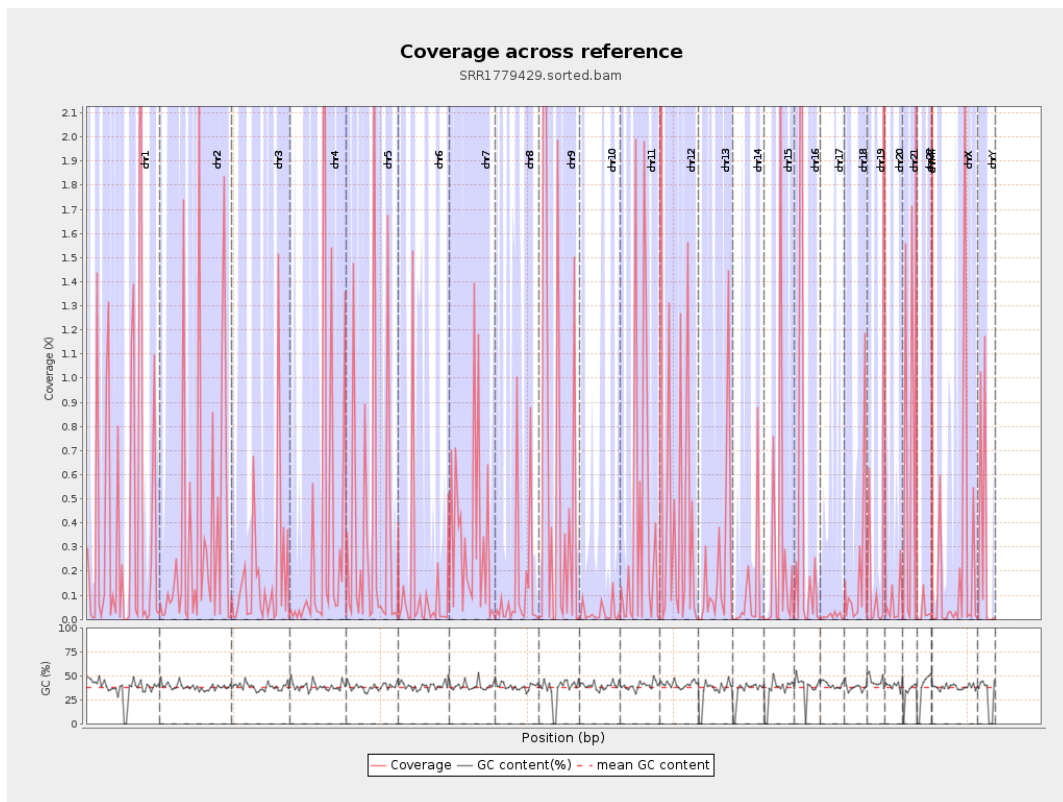
2.7. Chromosome stats

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

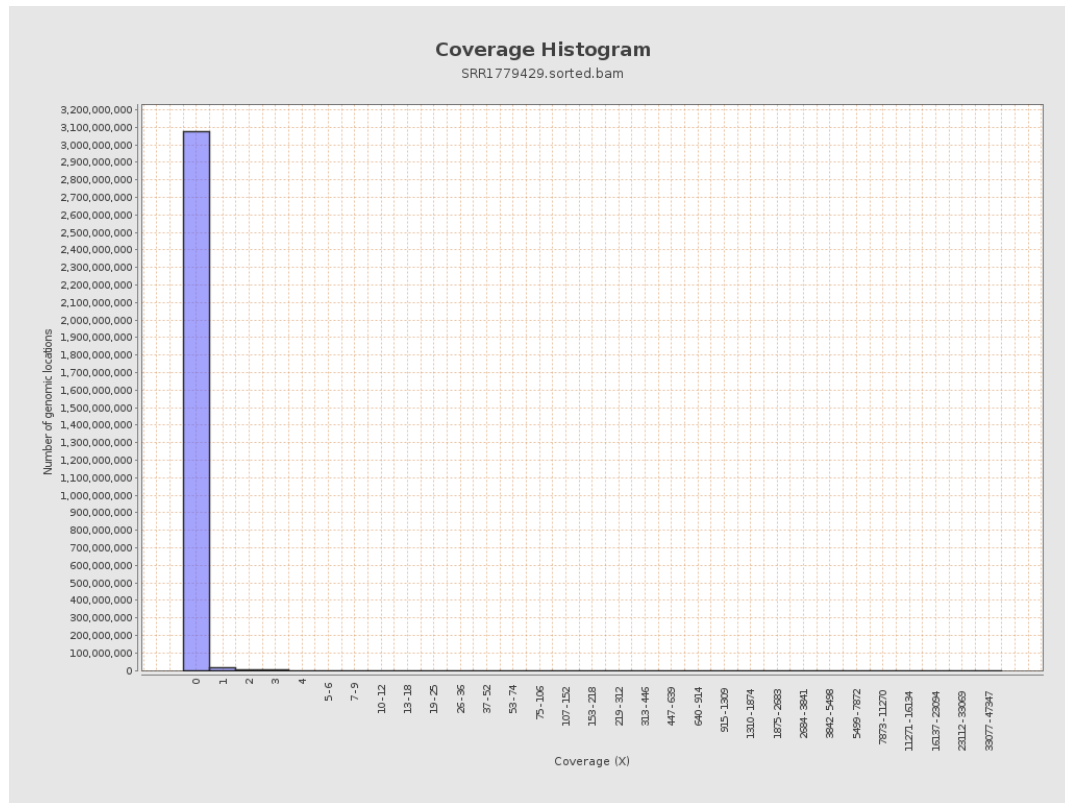
		bases	coverage	deviation
chr1	249250621	98922001	0.3969	53.1402
chr2	243199373	89719117	0.3689	41.7845
chr3	198022430	34957125	0.1765	21.5024
chr4	191154276	64564483	0.3378	75.9785
chr5	180915260	67985496	0.3758	55.76
chr6	171115067	20361796	0.119	27.3911
chr7	159138663	54686371	0.3436	29.4972
chr8	146364022	20554613	0.1404	20.0628
chr9	141213431	79737682	0.5647	63.617
chr10	135534747	3764962	0.0278	3.8772
chr11	135006516	54364655	0.4027	49.7671
chr12	133851895	75797030	0.5663	58.9518
chr13	115169878	27714546	0.2406	33.5455
chr14	107349540	10509577	0.0979	15.354
chr15	102531392	28472230	0.2777	34.8263
chr16	90354753	36211896	0.4008	53.9619
chr17	81195210	1169577	0.0144	1.1575
chr18	78077248	14503745	0.1858	24.9704
chr19	59128983	14113054	0.2387	48.609
chr20	63025520	4171352	0.0662	8.7509
chr21	48129895	39529162	0.8213	71.6155
chr22	51304566	1603761	0.0313	5.3926
chrMT	16571	239722	14.4664	7.5501
chrX	155270560	30391025	0.1957	62.3398

chrY	59373566	17781594	0.2995	49.0318
------	----------	----------	--------	---------

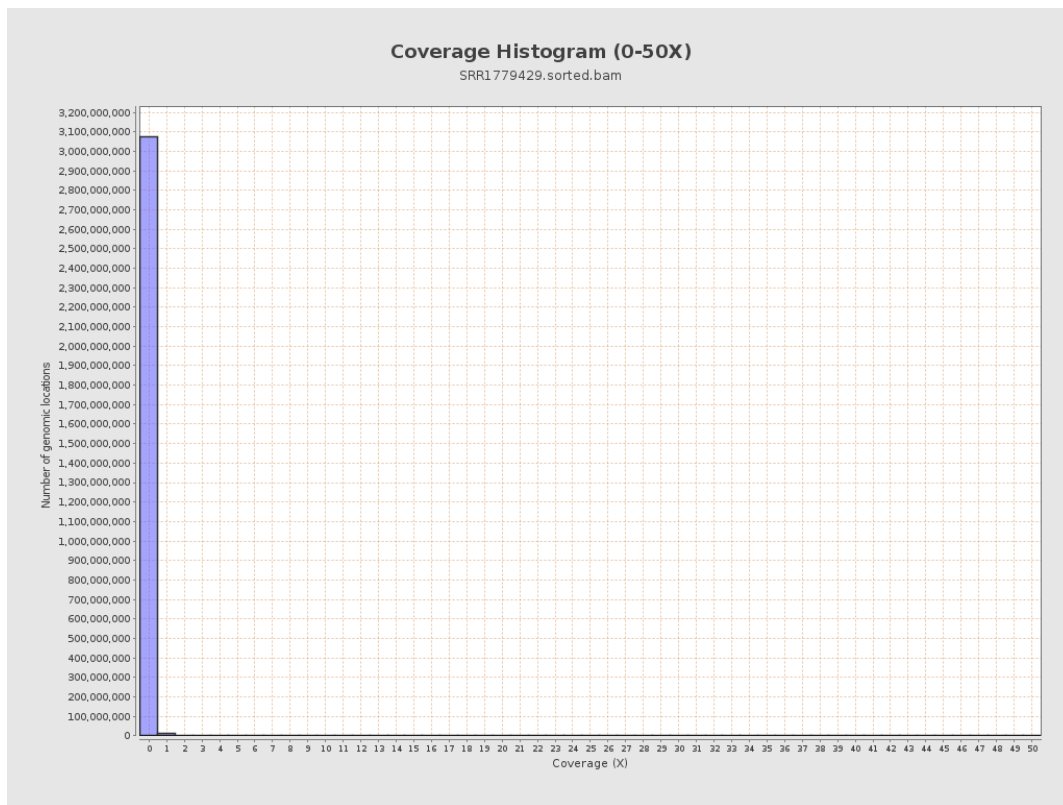
3. Results : Coverage across reference



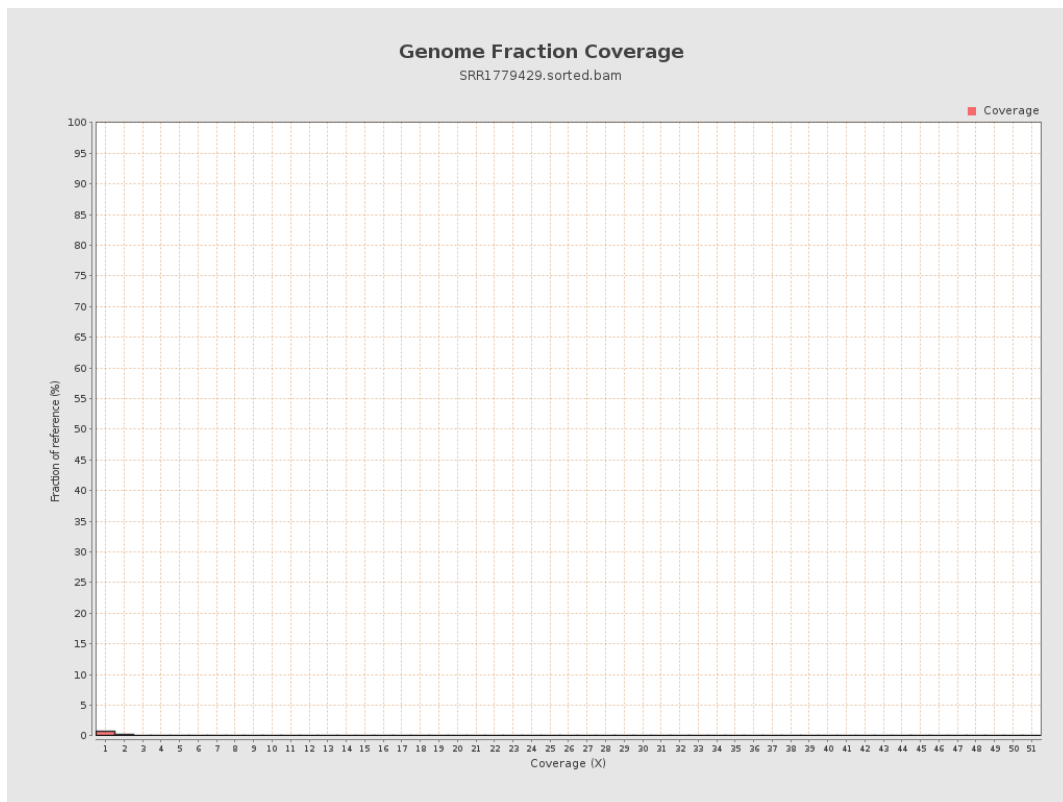
4. Results : Coverage Histogram



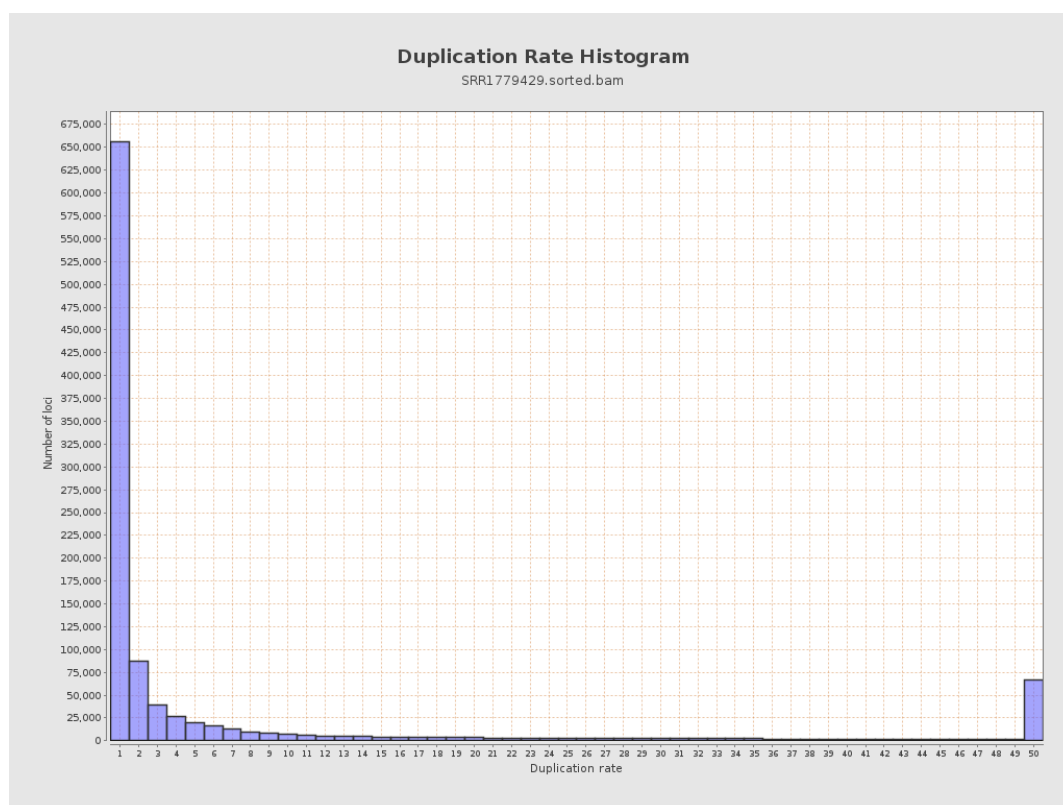
5. Results : Coverage Histogram (0-50X)



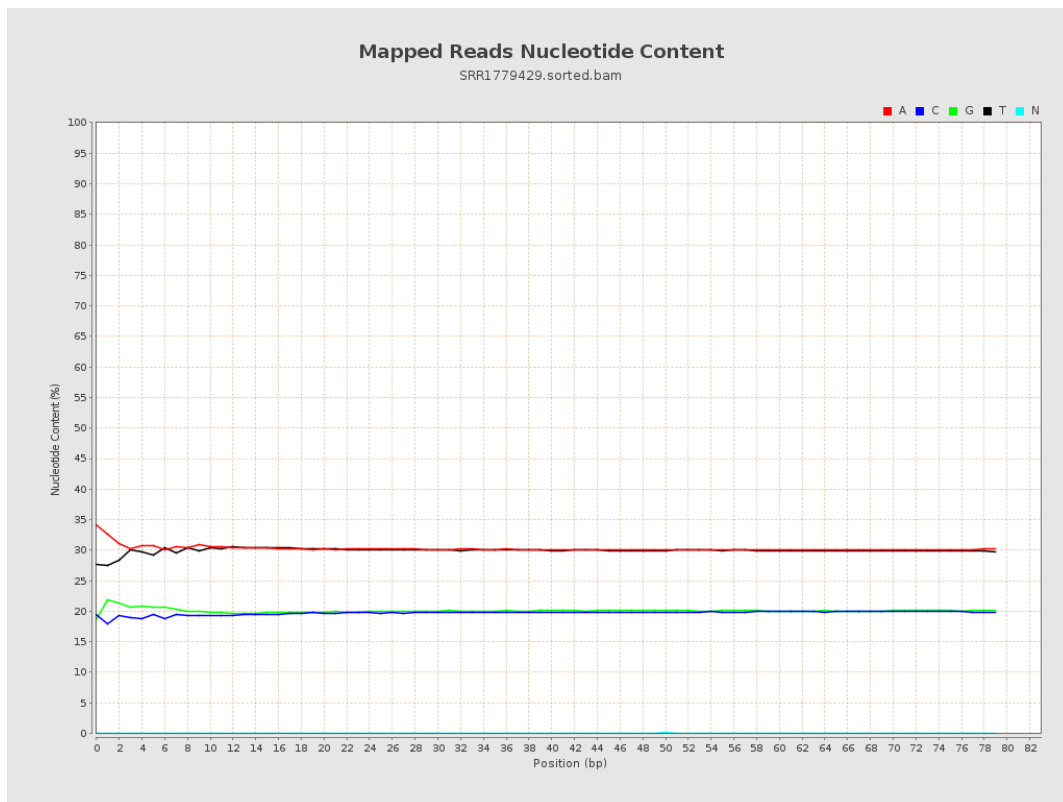
6. Results : Genome Fraction Coverage



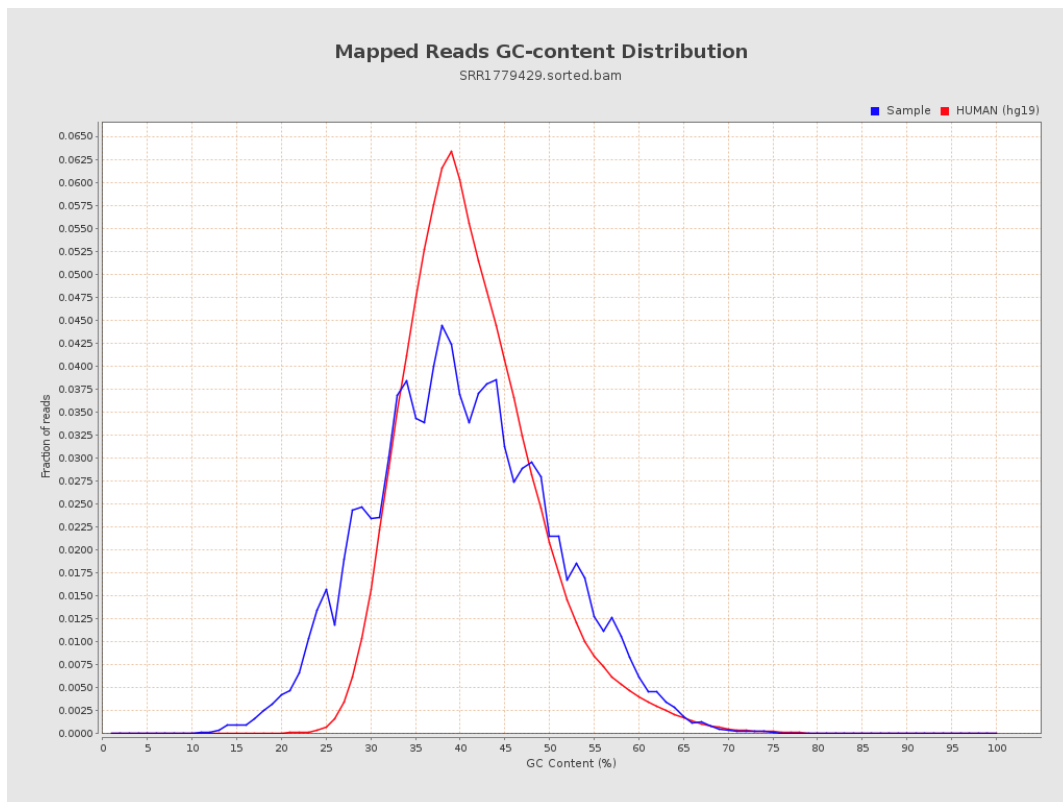
7. Results : Duplication Rate Histogram



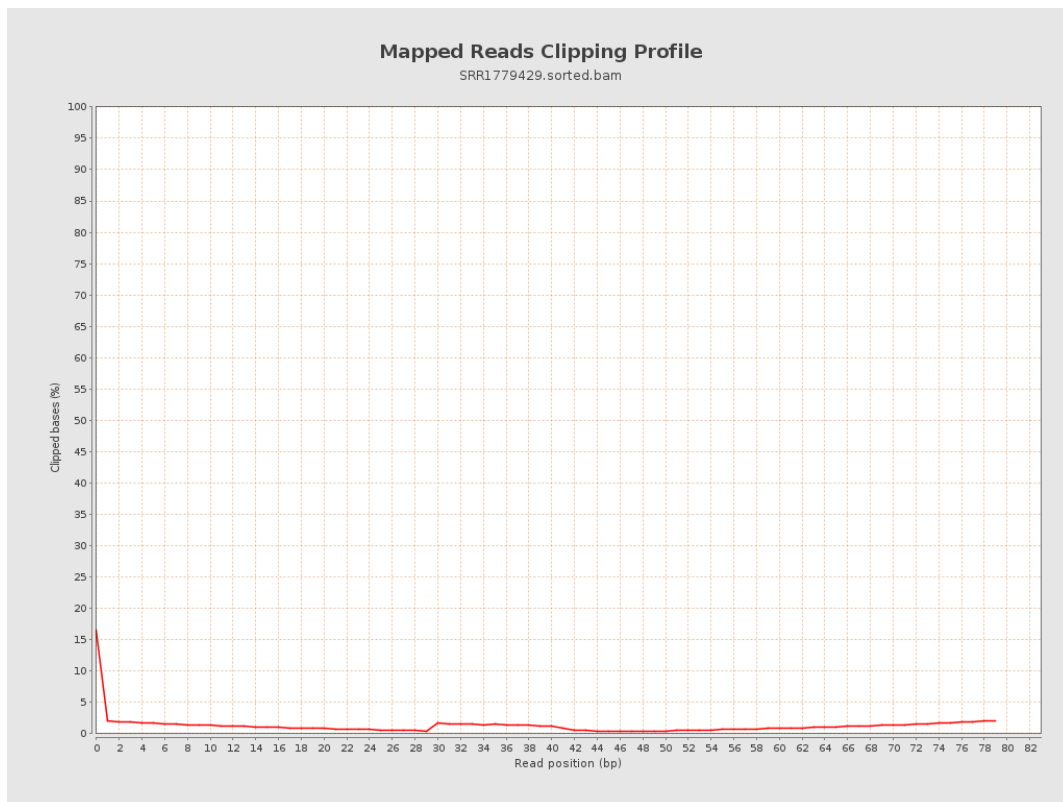
8. Results : Mapped Reads Nucleotide Content



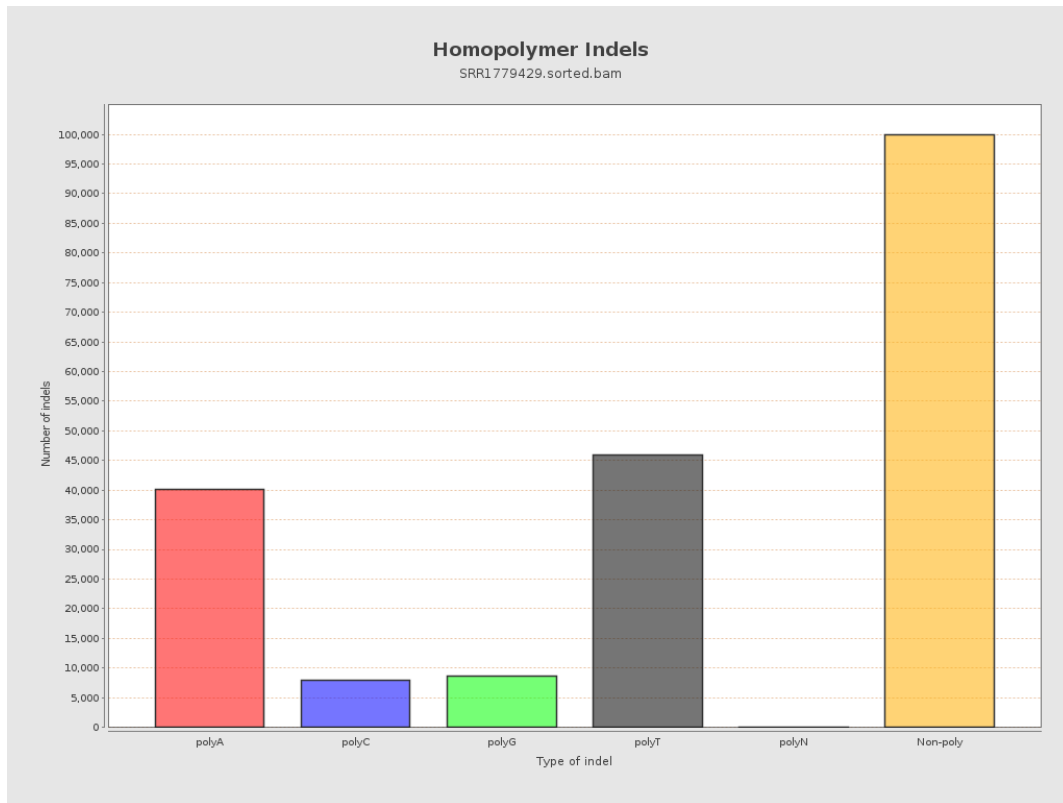
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



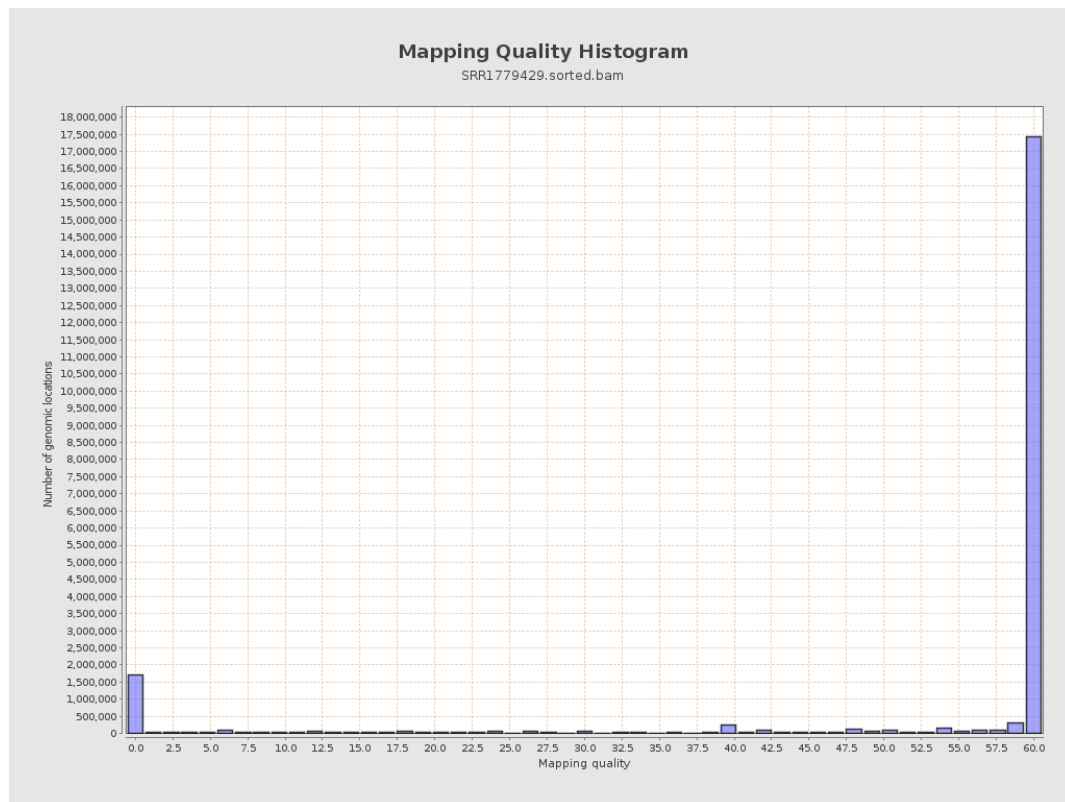
11. Results : Homopolymer Indels



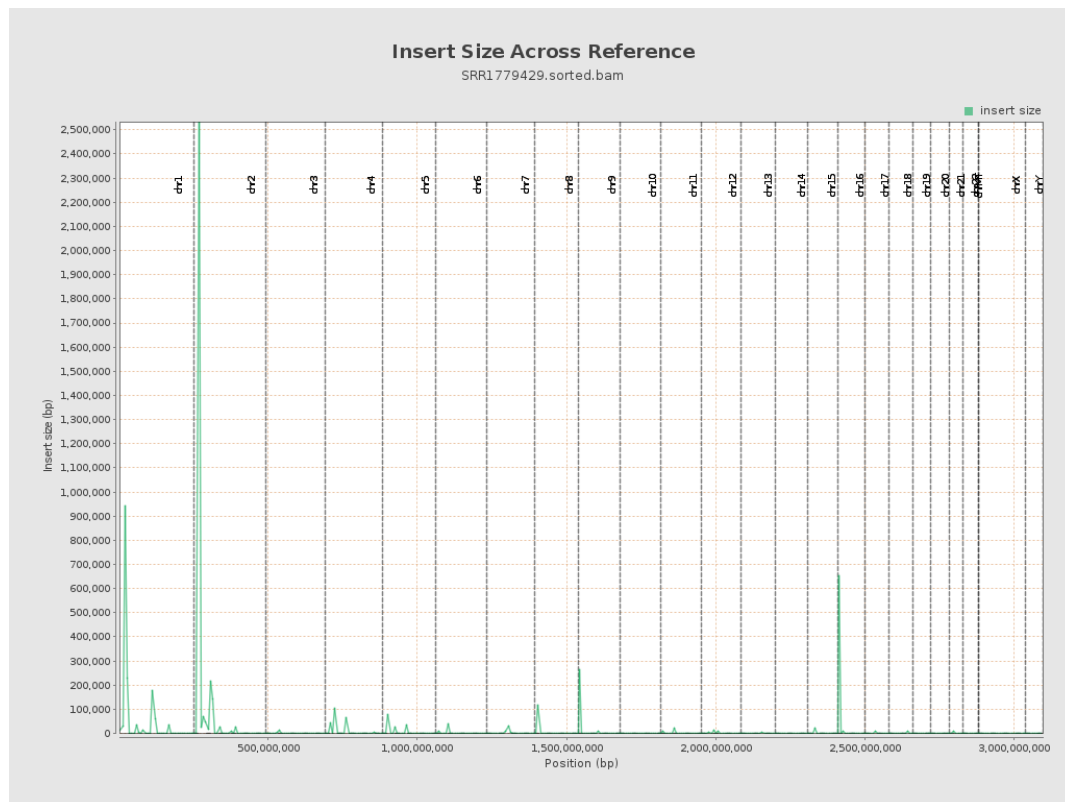
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

