(a) Pie charts showing the percentage of reads relative to total reads with perfect match to the BTx623 genome for different libraries:
- Mix: 76%
- BTx623: 77%
- Rio: 76%
- LB/EF F2s: 74%
- HB/LF F2s: 75%

(b) Bar graph showing the number of reads mapped to different regions:
- Mix: 0 to 100 reads
- BTx623: 0 to 100 reads
- Rio: 0 to 100 reads
- LB/EF F2s: 0 to 100 reads
- HB/LF F2s: 0 to 100 reads

(c) Table showing the percentage of reads relative to total number of 22 nt reads in the library:
- Mix: 22%
- BTx623: 23%
- Rio: 22%
- LB/EF F2s: 22%
- HB/LF F2s: 22%

miR172c (22 nt) in our sequencing data in BTx623

miR172c (20 nt) in miRBase prediction

sbi-MIR172c (prenucleotide)

AGAAUCUUGAUGAUGCUGCAUC,

31869

GUGCAGCACCAUCAAGAUUCACAUGGUCCAACUCAUGCAUCUUCAGUGAUGCUCAUGUGAUGGCUCGCAGUUGCUAUAUAUGCAUAUGUGAUGAGAUG

miR172c (20 nt) in miRBase prediction

sbi-MIR172c (prenucleotide)