



RNA extracted from: brain



miR-132 RNA extracted from: brain







RNA extracted from: 15 day embryo



miR-143

RNA extracted from: stomach







RNA extracted from: spleen



miR-151

RNA extracted from: liver



miR-133

RNA extracted from: muscle





RNA extracted from: brain



miR-23b

RNA extracted from: heart



miR-183 RNA extracted from: 9.5 day placenta





RNA extracted from: lung





miR-99a

RNA extracted from: heart





RNA extracted from: lung



miR-194

RNA extracted from: intestine







RNA extracted from: ES cells



miR-206

RNA extracted from: muscle







## RNA extracted from: muscle



Page 8



## Figure S3.

Pages 1-7: Tiling results showing detection of only the mature form miRNA by microarray. Signal spikes in unexpected regions are likely due to non-specific hybridization arising from simple repeat sequences in the flanks of the precursor. This is exemplified in the probe sequences shown for miR-145 at position 229 (p. 2), miR-187 at position 37 (p. 5), and miR-182 at position 223 (p. 7).

Page 8: A) Tiling across miR-207 precursor RNA suggests presence of precursor RNA. However, the signal likely arises from GC repeats (B). Northern analysis of miR-207 suggests possible hybridization to large transcripts. C) northern analysis using probe complementary to miR-207 (GAGGGAGGAGGAGAGCCAGGAGAAGC), D) northern analysis using probe complementary to miR-207 pre-cursor position 113 (tiling position with greatest signal; CGGCTCCTCCGGCAGCCC). M is a 25 nt DNA oligo. Repeat-masking was done using Scylla Paracel Package v2.6.2 (www.paracel.com), set for detecting low-complexity regions.

This page: northern analysis probing with sequence that resulted in an ES-specific signal in the pre-miRNA flanking region. M = 10 bp DNA ladder. The probe sequence was CATGTCAGATATCCAAACATAATACAACTG.