



Supplementary Figure 3. Multiple sequence alignment of the six predicted bovine miRNAs and corresponding genes in 15 other species using MultiAlin; bta-miR-24-3p, bta-miR-149-5p, bta-miR-185, bta-miR-223, bta-miR-328, and bta-miR-874. The highlighted yellow region within the gene sequences represent the miRNA sequence. Red indicates regions of high consensus and blue low consensus.