Cumulative distribution function (CDF) plots of log2-transformed gene expression (cpm) ratios. Each ratio is calculated as the expression of a bovine mRNA divided by the expression of its human orthologue. (A) The CDF for targets of highly expressed cattle-specific miRNAs (n= 1829) and all orthologous genes (n= 9442) is significantly different (p < 2.2e-16) by the Kolmogorov-Smirnov test. Genes that are targeted by both conserved and cattle-specific miRNAs were excluded from this analysis. (B) The CDFs for targets of highly expressed cattle-specific miRNAs with conserved target sites (n= 830) and all orthologous genes (n=9442) are significantly different (p = 8.554e-16) by the Kolmogorov-Smirnov test, as are the CDFs for targets of highly expressed cattle-specific miRNAs with cattle-specific target sites (n= 1161) and all orthologous genes (p = 2.821e-13). However, the CDF for targets of highly expressed cattle-specific miRNAs with conserved target sites is not significantly different from the CDF for targets of highly expressed cattle-specific miRNAs with cattle-specific target sites (p=0.25).