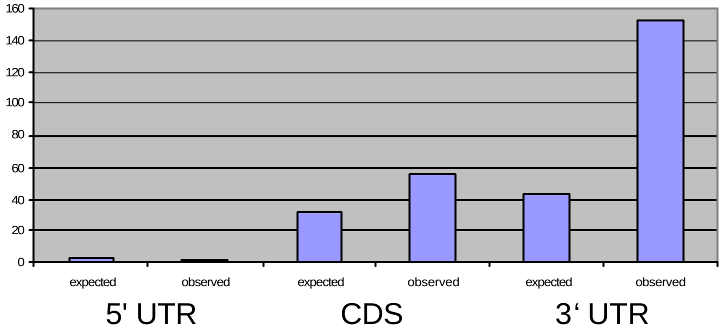
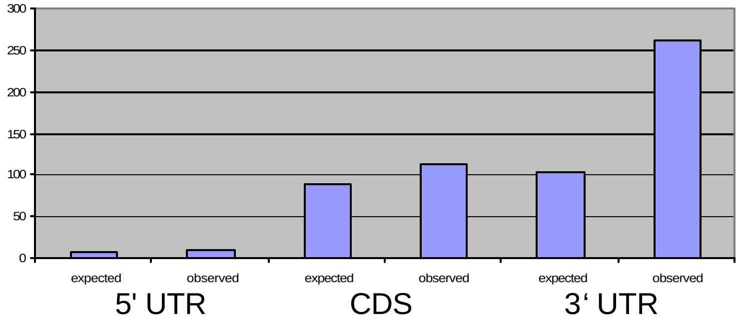
Supplementary Figure 3. Expected and observed CAUUCC and UGCCUU word counts in different regions of miR-1 or miR-124 downregulated transcripts. Expected frequencies were calculated using the sequences of all LocusLink genes represented on the microarray.



CAUUCC counts in miR-1 downregulated transcripts



UGCCUU counts in miR-124 downregulated transcripts