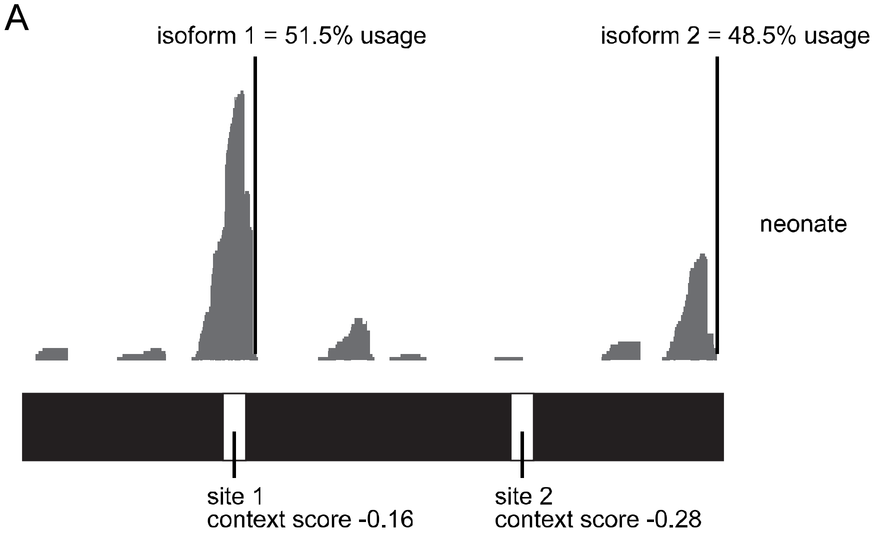

Actual score=(isoform 1 usage x site 1 score) + (isoform 2 usage x site 1 score) + (isoform 2 usage x site 2 score)
Acutal score=(0.515 x -0.16) + (0.485 x -0.16) + (0.485 x -0.28) = -0.29429
Expected score=-0.16-0.28=-0.44

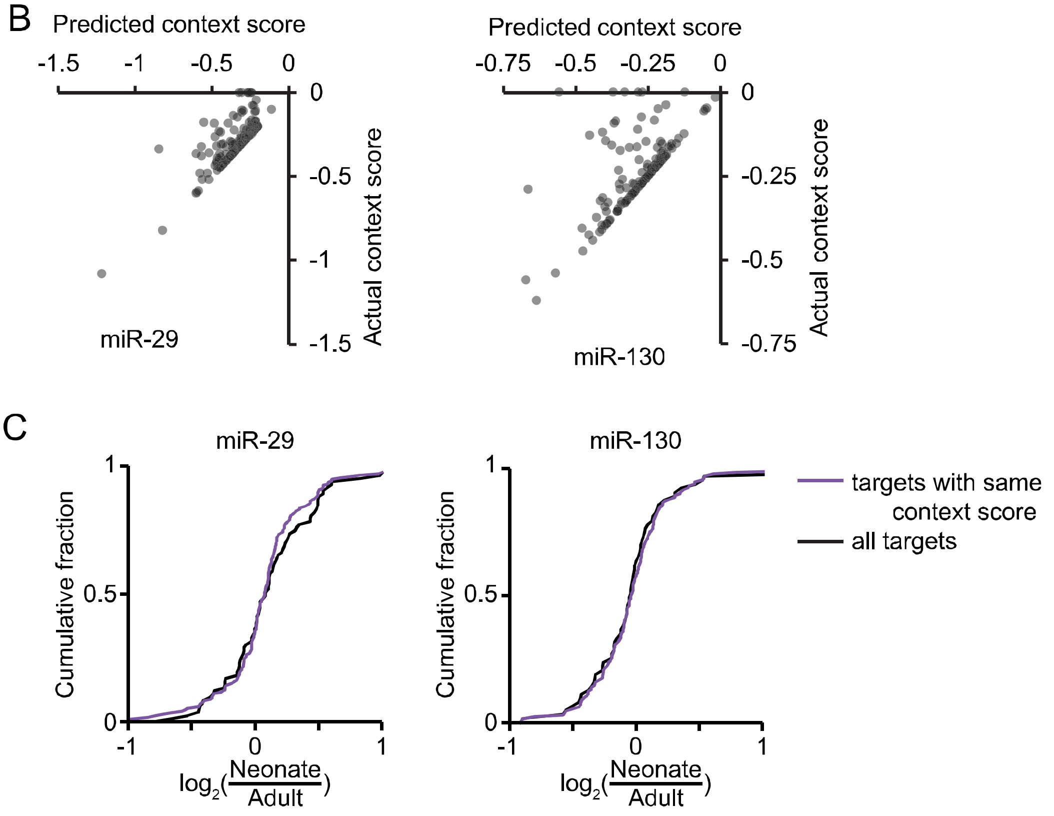

Figure S7 Context scores for isoforms of miRNA targets expressed in CD8+ T cells. (A) Example of calculation of actual context scores using experimentally verified 3’UTR isoforms. For each target, we found expressed isoforms (each isoform consisting of ≥20% of the reads for that gene), then found the context scores for the individual miRNA target sites in all expressed isoforms. We calculated an average context scores of the target sites, weighting them by the usage of that site, as determined by 3’-Seq. *Eomes* has two isoforms and two target sites. One target site is found in both isoforms, whereas the second is found only in the longer isoform. Their scores are weighted based on site usage (51.5% usage for site 1 and 48.5% usage for site 2 in neonates). (B) For each strong predicted target of miR-29a-3p (left) or miR-130b-3p (right), we calculated an actual context score, taking into account the miRNA target sites present. We then compared the average context score for adults and neonates to the expected score (Pearson r=0.789 for miR-29a-3p targets; Pearson r=0.628 for miR-130b-3p targets); high correlations indicate most, but not all, targets have very similar context scores to predicted. (C) We compared the fold-change difference in expression for all predicted targets of miR-29a-3p (left) and miR-130b-3p (right) to fold-change differences for only targets whose experimentally determined isoforms have the predicted context scores. The two groups are not significantly different according to two-sided Kolmogorov–Smirnov tests (miR-29a-3p: p=0.825; miR-130b-3p: p=0.991).