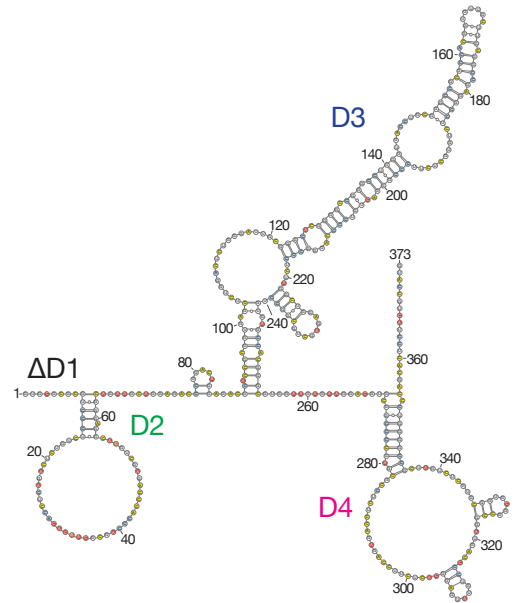
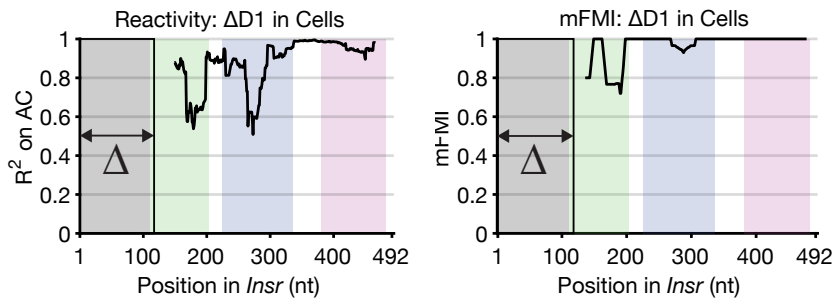


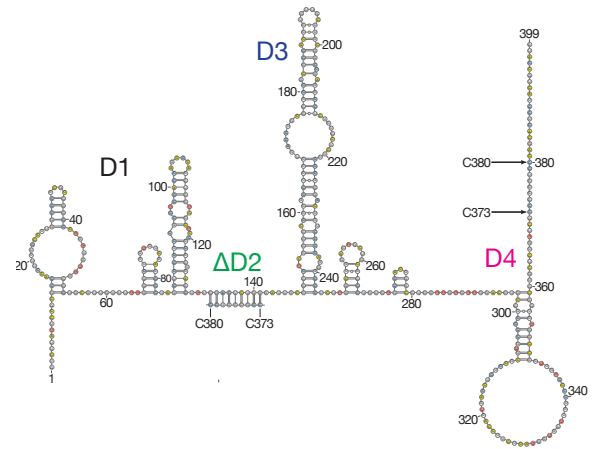
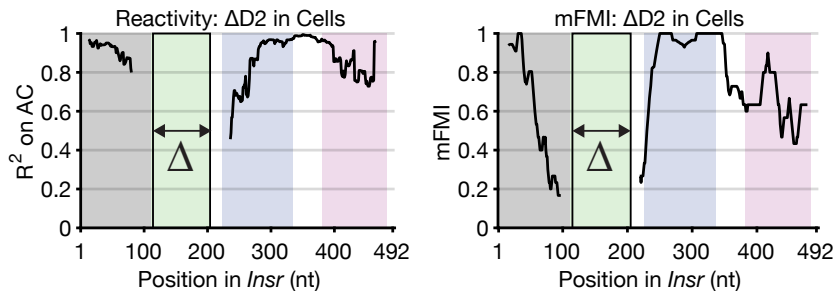
Supplemental Figure S5. Secondary structure is disrupted in all broad domain deletion mutants

Related to Figure 5B. For each subfigure: at left, coefficient of determination between DMS signal of this mutant compared to full-length *Insr* 5'UTR across their shared sequence range, considering only signal on As and Cs, calculated in windows (see Methods). Center, mFMI comparison between the predicted structure and full-length. Right, the secondary structure model of the mutant. Indexes in the structures correspond to the mutant UTR, not full-length. The mutations and AUROC values are indicated with domains labeled. **(A)** DMS-MaPseq constrained model of $\Delta D1$ in live cells. **(B)** DMS-MaPseq constrained model of $\Delta D2$ in live cells. Modeled base-pairs removed for clarity are depicted (C373-C380 with (G133-G141)). **(C)** DMS-MaPseq constrained model of $\Delta D3$ in live cells.

A $\Delta D1$ in Cells, AUROC = 0.85, Mutation: G1-C118 removed



B $\Delta D2$ in Cells, AUROC = 0.87, Mutation: C115-A205 removed



C $\Delta D3$ in Cells, AUROC = 0.87, Mutation: U225-C327 removed

