



Figure S4. Overrepresentation of epigenetically controlled IESs in the somatic set before (left) and after (right) normalization of potentially confounding variables. (A) IES size, (B) TPM (of somatic-IES bearing genes), and (C) C_{in} score (proxy for splicing signal strength) distributions for the 32°C-experimental sample (red) and a random sample of the same size extracted from the PGM-set (blue), before (left) and after (right) normalization. (D) Back to back stacked bar chart showing the number of intra-exonic somatic IESs before and after normalization. For each temperature, IES counts are broken down into Dcl2/3-controlled IESs ($Dcl2/3^+ | Dcl5^-$, Purple), Dcl5-controlled IESs ($Dcl2/3^- | Dcl5^+$, Orange), Dcl2/3-Dcl5-co-controlled IESs ($Dcl2/3^+ | Dcl5^+$, Fuchsia) and Dcl-independent IESs ($Dcl2/3^- | Dcl5^-$, green). Expected proportion of Dcl-dependent IESs for random samples of the same size (expected) extracted from the PGM-set are shown back to back with the observed data (observed). Two proportions z-test returns a p -value < 0.01 for all expected/observed contrasts before and after normalization. For all temperatures, IES

size, TPM and C_{in} score distributions of the random sample were matched to the observed distributions using a value-matching procedure during drawing ([FigS4_script.R](#)).