

Electronic supplementary material

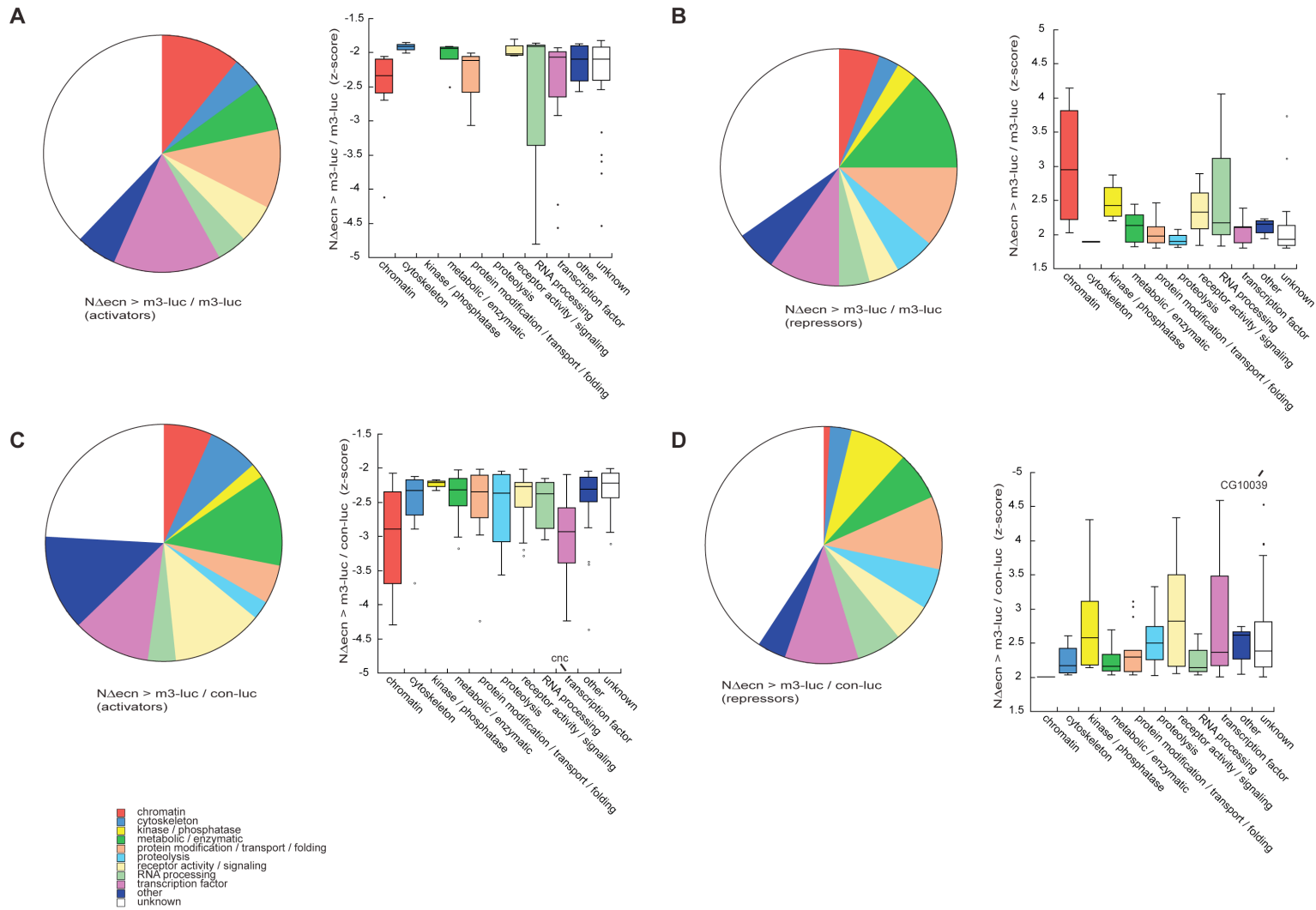


Figure S1: Figure representing the distribution of Notch modifiers by gene ontology classes. Pie chart distributions for percentage of genes represented in major gene ontology classes and corresponding box plots of median z-scores for the various classes. Box plots are graphed as in Figure 1a. **A.** Distribution of genes that enhance the Notch induced signal as normalized by the uninduced *E(spl)m3* promoter. **B.** Distribution of genes that suppress the Notch induced signal as normalized by the uninduced *E(spl)m3* promoter. **C.** Distribution of genes that enhance the Notch induced signal as normalized by the unrelated control promoter (*con-luc*). **D.** Distribution of genes that suppress the Notch induced signal as normalized by *con-luc*. (PDF 365 KB)

Table S1: Excel table of screening data for Notch induced transcription normalized by the unrelated control promoter (N Δ ecn > m3-luc/con-luc). Hits listed from initial screen with potential agonists of Notch induced transcription listed in **A.** and potential antagonists listed in **B.** (XLS 248 KB)

Table S2: Excel table of screening data for Notch induced transcription normalized by the uninduced *E(spl)m3* promoter (N Δ ecn > m3-luc/m3-luc). Hits listed from initial screen with potential agonists of Notch induced transcription or antagonists of uninduced *E(spl)m3* transcription listed in **A.** and vice versa in **B.** (XLS 143 KB)

Table S3: Excel table of orthology predictions. Human orthologs of the *Drosophila* genes identified in the screen were predicted using InParanoid [52]. Human diseases associated with the predicted genetic counterparts are also listed. (XLS 30 KB)

Table S4: Excel table of re-test data for the redesigned dsRNA. Genes were chosen for retesting that were selected as positive by both normalization methods (Figure 2c, area a.). This second set of 28 dsRNAs were independently redesigned by the method of Arziman et al. with no predicted off targets and are listed in Additional file 5[50]. Retests were done in quadruplicate for each dsRNA, and the results are given for the 22 positive retests that have p-values < 0.05 (compared with control dsRNA treated cells). (XLS 60 KB)

Notch interaction network file. A network file that can be viewed in detail using the open source Cytoscape viewer <http://www.cytoscape.org>[51]. The Notch interaction network was generated by using Notch transcription modifiers identified in the genome-wide study as nodes and physical interactions (e.g. two-hybrid data) for edges. Genetic interactions were not used for the network map. (CYS 2 MB)