



Supplemental Figure S18 – Chicken co-regulated splicing network analysis

A,B) Left: Graphical representation of the chicken splicing networks, highlighting the different exon communities for the 1st (A) and 2nd (B) layer networks. Right: Plot of the mean absolute Z-score across tissues for each community of the 1st (A) and 2nd (B) layer chicken networks. Dominant tissues are highlighted. Communities were named based on dominant tissues, when possible. For simplicity, only communities with 10 or more AS events are displayed. C) Heatmap showing the percent of node (exon) overlap between chicken (Y-axes) and human (X-axes) communities for the 1st (left) and 2nd (right) layer networks. P-values correspond to Bonferroni corrected one-sided Fisher's exact tests. E) Percent of edge conservation for each main chicken community in the human network, for the 1st (left) and 2nd (right) layer networks, and expected percent of conservation based on randomized networks of the same size of the tested community. Error bars in controls represent first and third quartiles of the distribution. P-values correspond to permutation tests with 1,000 random networks: *** P-value $\leq 10^{-3}$, ** $10^{-3} < \text{P-value} < 0.01$, * $0.01 \leq \text{P-value} < 0.05$.