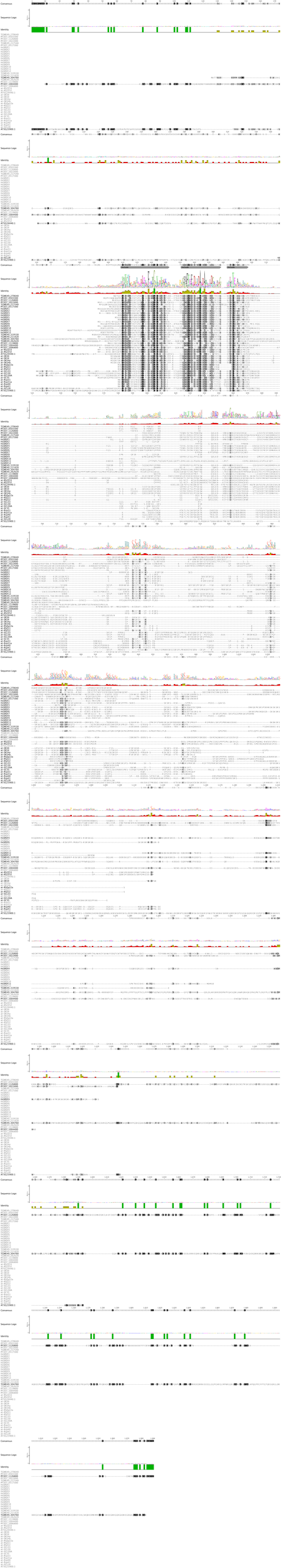
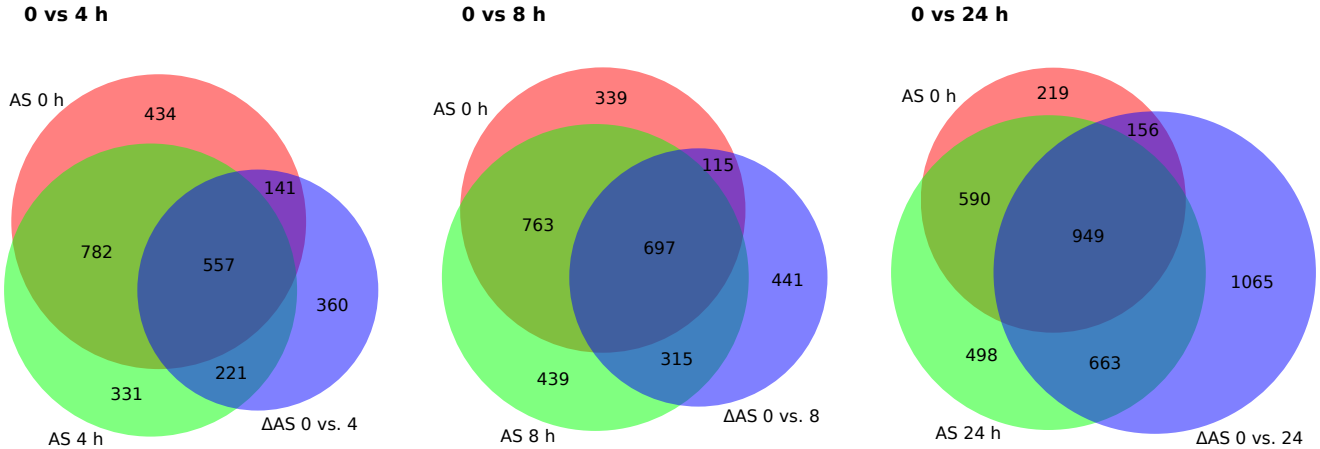

Consensus
Sequence Logo
Identity
TCAB45.270640
BCI1.1126800
TCAB45.270750
HUSRF1.1012500
HUSRF1
HUSRF2
HUSRF3
HUSRF4
HUSRF5
HUSRF6
HUSRF7
HUSRF8
HUSRF9
HUSRF10
HUSRF11
HUSRF12
HUSRF13
TCAB45.119530
TCAB45.304750
BCI1.1126800
BCI1.1004600

Supplementary Figure S1: Alignment used to generate phylogeny of SR proteins. Shading indicates (in order from darkest to lightest), similarity of 100%, 80–100%, 60–80%, and less than 60%, scored using the Blosum62 matrix. Regions marked "Include" were used to create the phylogenetic tree.



Supplementary Figure S2: Proportional Venn diagrams comparing genes identified as alternatively spliced in a single condition (not including intron retention), versus genes identified as having their alternative splicing changed after overexpression of TgSR3. Red regions represent alternatively-spliced genes in a single, uninduced condition; green regions represent alternatively-spliced genes in a single, induced condition, after 4, 8 or 24 hours overexpression of TgSR3; blue regions represent genes that had their alternative splicing altered between two conditions, after overexpression.