Supplementary data

Transcriptome Analysis of Alternative Splicing Events Regulated by SRSF10 Reveals Position-Dependent Splicing Modulation

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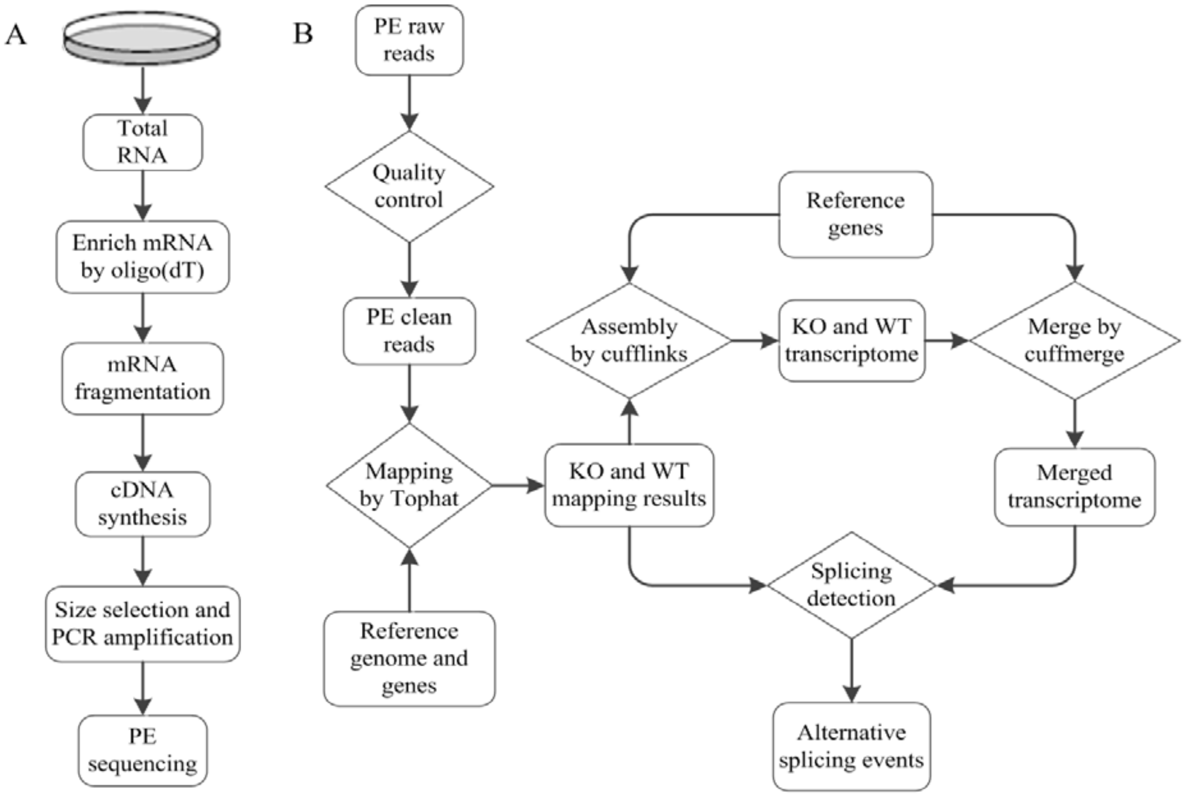
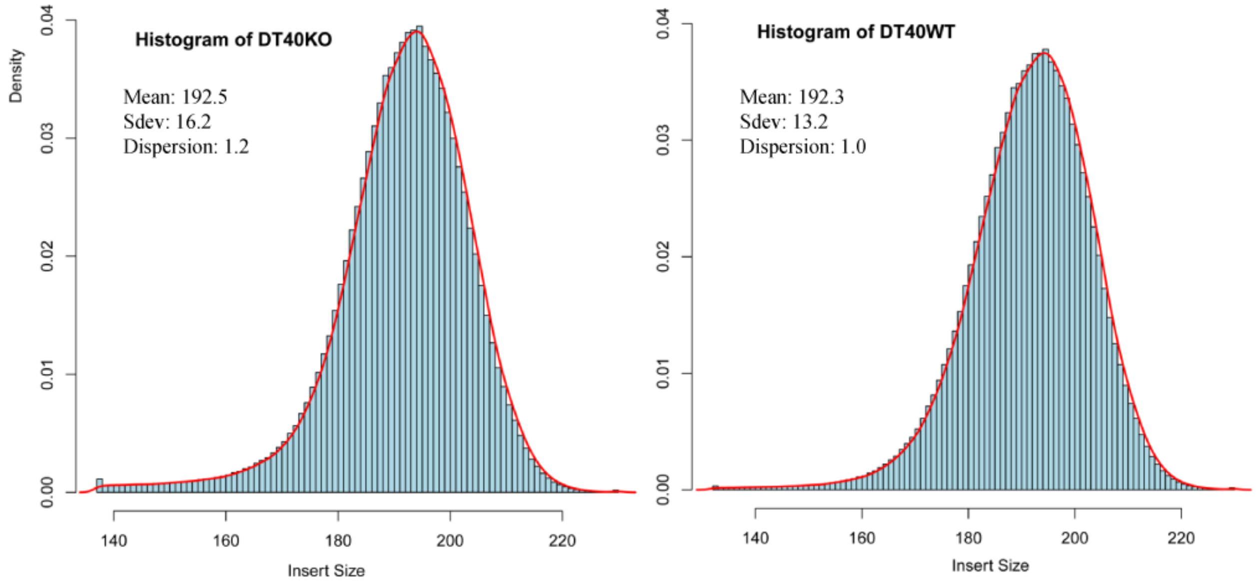
The authors declare no conflict of interest.

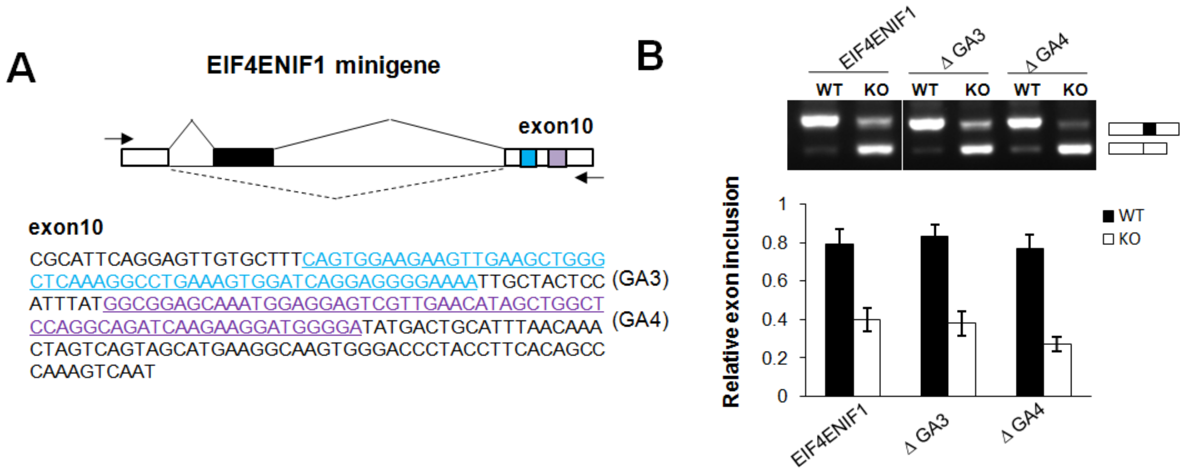
This PDF file includes: Supplementary Figures S1-S4, Supplementary Tables S1-S3 and one Supplementary Method.



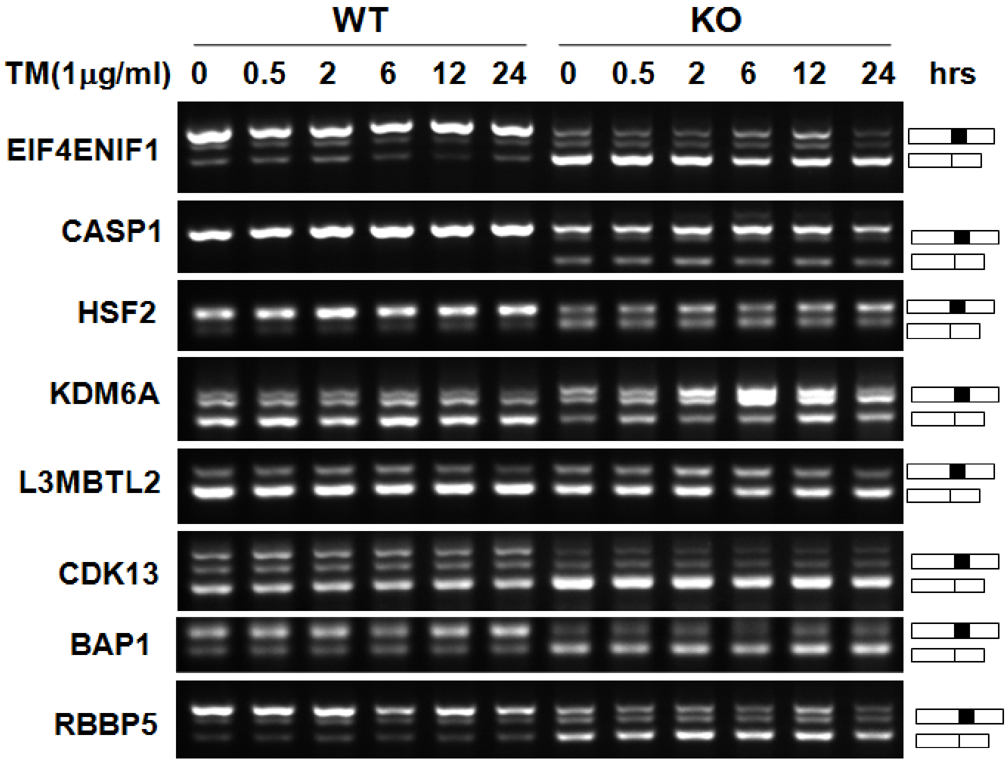
Supplementary Figure S1. Experimental design and bioinformatics pipelines. (A) General strategy for RNA sequencing. Total RNA was isolated from KO and WT cells and prepared for paired-end sequencing. (B) Bioinformatics analysis.



Supplementary Figure S2. Distribution of insert size for mapping paired-end reads. Distribution of the insert size of the libraries as determined by alignment to gal4 genome and transcriptome.



Supplementary Figure S3. Characteristics of SRSF10-regulated exon inclusion. (A)Schematic representation of the EIF4ENIF1 minigene construct (top). The exon 10 sequences are shown at the bottom, with two GA-rich motifs (GA3 and GA4), each marked with a different color. (B) RT-PCR analysis of the KDM6A minigene or each of indicated mutants transfected in WT or KO cells, respectively. The histogram below shows mean the percentage of exon inclusion ± SD, n=3.



Supplementary Figure S4. RT-PCR analysis was performed on the SRSF10-dependent exon inclusion or skipping events under ER stress conditions. WT and KO cells were subjected to TM-induced ER stress for the indicated times followed by RT-PCR analysis.

Supplementary Method

The equation used in the current study is:

$$Pvalue_{adjusted} = w \times Pvalue_{first} + (1 - w) \times Pvalue_{\sec ond} \qquad (1)$$

Where w indicates the weight of the $Pvalue_{first}$ on detection of differential alternative splicing events and its value depends on the size of an alternative exon and RNA-seq read length. To determine the value for w, another variable was introduced and calculated by:

$$R = \frac{E_l}{3R_l} \qquad (2)$$

Where E_i and R_i indicates the size for an alternative exon and the length of RNA-seq reads, respectively. If R is bigger than one, the weight w is determined by $0.5^{\frac{1}{R}}$. In the case of R less than one, w is determined by $1 - 0.5^{R}$.

Supplementary Table S1. List of significant alternative splicing events affected by SRSF10

Gene Symbol	Exon coordinates	Reads coverage (Ex::In)		adjusted P-Value	AS type
		WT	KO		
MKS1	chr19_JH375211_random:12727-13238	254::0	0::249	6.14E-76	alt5
PHF20L1	chr2:141308382-141308600	40::241	134::88	1.84E-13	cassette
EPRS	chr3:18200072-18200150	122::168	0::214	8.31E-12	cassette
KIFC1	chr16:289927-289966	72::0	60::314	8.89E-08	alt5
CLASP2	chr2:45303179-45303202	44::74	35::4	1.39E-06	cassette
SLTM	chr10:6388345-6388505	344::214	305::367	5.89E-05	cassette
TRIP12	chr9:9598618-9598656	121::49	172::13	1.84E-04	cassette
BAP1	chr12:3106991-3107151	73::112	109::27	1.97E-04	alt5
BAG4	chr22:2270319-2270423	149::33	116::115	2.09E-04	cassette
ARNT	chr25:1718589-1718654	32::29	30::97	2.31E-04	cassette
SLMAP	chr12:8799021-8799077	43::343	69::120	2.51E-04	cassette
EWSR1	chr15:11167082-11167159	336::32	175::60	2.62E-04	cassette
PIP5K1B	chrz:34371671-34371754	34::2	9::11	3.73E-04	cassette
INTS4	chr1:192088711-192089002	35::0	25::15	4.44E-04	alt5
GPR107	chr17:5827330-5827529	21::0	20::33	5.58E-04	cassette
RBBP5	chr26:1959308-1959502	73::19	52::38	5.92E-04	alt5
EIF4ENIF1	chr15:8990976-8991155	0::47	17::26	6.54E-04	cassette
CDK13	chr2:50540721-50540901	82::119	116::50	6.97E-04	alt3
R3HDM1	chr7:30093934-30094023	241::164	136::33	7.77E-04	Undefined
KDM6A	chr1:110202915-110203049	37::37	20::103	8.71E-04	cassette
HSF2	chr3:60784335-60784388	79::587	97::309	8.96E-04	cassette

CASP1	chr19:706695-706847	0::34	7::30	9.28E-04	cassette
CAST	chrZ:56851658-56851741	4::37	20::34	9.64E-04	cassette
MDM4	chr26:1767300-1767361	28::39	25::69	9.93E-04	cassette
KIFC1	chr16:228615-228653	72::68	60::461	0.001357388	cassette
NCAPG2	chr2:9476774-9476836	180::72	113::109	0.00156482	cassette
GART	chr1:104769317-104769435	204::30	243::10	0.001672557	cassette
PHF20	chr20:930580-930708	65::55	68::134	0.002039575	cassette
DNAJC13	chr2:42857095-42857109	49::7	82::55	0.002059832	cassette
R3HDM1	chr7:30105687-30105737	215::507	134::137	0.002572598	cassette
GALNT2	chr3:39602674-39602742	37::32	90::16	0.002758002	cassette
ADD1	chr4:81866456-81866489	112::29	122::0	0.003207223	cassette
UBN1	chr14:13240523-13240666	17::22	4::78	0.003341427	cassette
ARHGAP17	chr14:6571318-6571560	49::57	57::19	0.003487858	cassette
SPTAN1	chr17:5162818-5162877	55::44	80::12	0.00433839	cassette
BCOR	chr1:111738445-111738498	50::23	60::68	0.004569101	cassette
BANP	chr11:17497677-17497748	27::0	16::11	0.004578728	cassette
ATP2C1	chr2:42272625-42272707	133::8	98::20	0.004714597	cassette
CCDC6	chr6:8567839-8567933	278::104	282::52	0.004903683	cassette
L3MBTL2	chr1:49618440-49618505	183::80	98::120	0.005649912	cassette
EIF4G3	chr21:6653638-6653670	98::223	85::82	0.005741709	cassette
ARID1B	chr3:50721969-50722127	21::109	44::63	0.006034	cassette
DIAPH1	chr4:5922036-5922068	50::41	61::17	0.006475045	cassette
PRPF40A	chr7:35050583-35050717	165::607	250::356	0.006943288	cassette
LRRFIP2	chr2:49641926-49641997	212::58	174::8	0.007063389	cassette
SREK1	chrz:20743173-20743270	5::96	43::56	0.007074823	Undefined

IMPDH2	chr12:11622485-11622556	322::467	486::103	0.007237341	cassette
ENSGALG00000004133	23:5573373-5573396	0::46	18::1	0.007337328	alt3
RCBTB1	chr1:168557474-168557533	41::23	32::3	0.007351101	cassette
MTM1	chr4:17706055-17706108	31::0	30::10	0.007422496	cassette
RAB24	13:9529264-9529552	38::0	118::133	0.007796516	alt3
FKBP14	chr2:34430018-34430096	69::22	32::41	0.008083602	cassette
PNRC2	23:5576823-5576890	43::107	5::62	0.008189894	alt3
TUBGCP5	chr1:129712351-129712461	41::2	32::20	0.008236659	cassette
NF2	chr15:11066823-11066867	169::124	254::74	0.008305831	cassette
GPLD1	chr2:57940708-57940825	26::16	21::1	0.00890215	cassette
EHMT1	chr17:2054308-2054451	121::20	123::60	0.009900268	cassette
LRCH3	chr9:14555834-14555926	143::25	184::65	0.01131466	cassette
ARHGAP17	chr14:6567229-6567276	109::166	97::20	0.011341526	cassette
VPS33B	chr10:19554214-19554622	92::109::17	175::287::112	0.011811838	Undefined
SBF2	chr5:8437715-8437789	15::0	13::12	0.012335786	cassette
CEP44	chr4:43149697-43149749	11::3	6::17	0.012462488	cassette
C1H11orf30	chr1:192888714-192888868	25::44	12::65	0.012512811	cassette
ELMO1	chr2:46933639-46933776	57::53	40::91	0.012952994	cassette
MAP4	chr2:696865-696993	101::170	91::76	0.013044062	cassette
HMGXB4	chr1:51990924-51990930	0::87	17::24	0.013103816	cassette
BIVM	chr1:142029884-142029955	178::92	190::158	0.013661148	cassette
PAPD4	chrz:22073017-22073103	39::76	24::107	0.013962925	cassette
PCM1	chr4:62447489-62447659	8::102	21::42	0.014079953	cassette
EHMT1	chr17:2044766-2044954	20::65	17::143	0.014267655	cassette
TCOF1	chr13:12476124-12476297	477::549	391::279	0.014721754	cassette

AGL	chr8:11021058-11021183	56::2	45::14	0.015169638	cassette
VPS13B	chr2:127973250-127973268	2::10	6::0	0.015299826	alt5
MAP7D3	chr4:4225622-4225720	98::125	119::74	0.015320293	cassette
RBFOX2	chr1:51818455-51818508	7::22	2::46	0.015348726	cassette
ZNF706	chr2:128506092-128506129	37::659	166::560	0.016001794	alt5
RALGAPA1	chr5:35520990-35521020	14::28	20::11	0.01665272	cassette
MBNL1	chr9:22851960-22852054	107::407	148::325	0.016833581	cassette
NISCH	chr12:565290-565406	8::0	4::18	0.016949263	mutually_exclusive
BBX	chr1:86694602-86694682	7::55	35::56	0.017074685	cassette
ZYX	chr1:77018753-77018845	90::46	45::57	0.017262556	cassette
PPP3CB	chr6:15746118-15746147	96::227	57::382	0.017534165	cassette
TMEM156	chr4:69076352-69076402	188::164	205::94	0.017608468	cassette
RIF1	chr7:34670710-34670787	40::173	76::123	0.017640415	cassette
PHF20	chr20:906237-906515	16::158	53::139	0.017665313	Undefined
PSEN1	chr5:25694773-25694826	382::254	319::460	0.017758277	cassette
VDAC2	chr6:14420491-14420545	79::11	71::48	0.0177604	cassette
ATAD2B	chr3:103687022-103687083	46::4	52::32	0.018369649	cassette
TRIM33	chr26:3788530-3788580	80::134	131::159	0.020037418	cassette
BLVRA	chr2:52209915-52210086	12::21	11::84	0.020118679	cassette
MAP4K5	chr5:57706279-57706323	14::11	42::2	0.020122496	cassette
TMEM16E	chr5:2751365-2751409	6::10	5::42	0.021040507	cassette
LOC100858086	chr3:54492761-54493286	112::21	11::88	0.021329717	alt3
CERS5	lge22c19w28_e50c23:287258-287492	8::0	6::10	0.021381442	alt3
UBXN2A	chr3:103726849-103727041	19::1	10::8	0.021693631	cassette
ASB9	chr1:121515530-121515680	6::19	1::34	0.021819143	cassette

DBT	chr8:10861196-10861362	0::27	8::9	0.022298728	cassette
ANXA10	chr4:24382201-24382333	8::8	24::4	0.022337132	cassette
KLHDC10	chr1:866016-866063	17::36	11::72	0.022548736	cassette
ANKHD1	chr13:1057559-1058302	22::38	39::23	0.024094827	cassette
ANGPT1	chr2:130970200-130970288	4::13	8::0	0.024795255	cassette
SNX14	chr3:76351237-76351263	107::60	133::27	0.024977105	cassette
KTN1	chr5:55992839-55992922	12::144	20::100	0.025047576	cassette
GIT2	chr15_jh375192_random:60606-60695	166::136	174::76	0.02551801	cassette
BCLAF1	3:54492761-54493286	111::27	7::91	0.025640059	alt3
TUBGCP2	chr6:8903470-8903638	15::40	1::74	0.025832341	cassette
PTPRC	chr8:2045308-2045445	244::712	28::1383	0.025837247	cassette
ZZEF1	chr19:3244567-3244585	59::0	35::16	0.02589455	alt3
PCYT2	chr18:10234270-10234345	78::4	86::29	0.02623215	cassette
ATG13	chr5:22793477-22793575	28::100	21::181	0.026293096	cassette
PROSER1	chr1:170544310-170544375	11::51	3::80	0.026812788	cassette
C28H19orf6	chr28:2819021-2819075	44::0	27::6	0.026830556	alt5
PTRHD1	chr3:105096408-105096491	73::20	116::12	0.027158141	cassette
DCX	chr4:13249337-13249352	21::22	8::0	0.027418007	alt5
ATG16L1	chr9:696583-696639	37::48	22::64	0.027599695	cassette
MEF2A	chr10:16547260-16547397	210::190	142::294	0.028243093	cassette
CRKL	15:8265460-8265478	27::170	0::80	0.028294434	alt3
IDI1	chr2:10372960-10373419	543::308	543::745	0.028400116	retain_intron
INCENP	chr5:16401957-16402070	323::453	261::801	0.028558215	cassette
KIAA1530	chr4:84025954-84026014	35::3	21::11	0.028618104	cassette
ZNF341	chr20:2457039-2457143	16::11	8::25	0.029116067	cassette

OPA1	chr9:12544358-12544468	21::59	16::119	0.029317093	cassette
MDM2	chr1:35261089-35261344	23::0	18::7	0.029410293	cassette
DTX2	chr19:4190634-4190765	50::26	50::8	0.029822452	cassette
EPB41	23:2578012-2578029	19::12	99::0	0.030135461	alt3
MAT1A	chr6:3916128-3916290	17::12	5::27	0.030155396	cassette
CASC4	chr10:19316145-19316312	263::124	162::134	0.030186621	cassette
CPSF6	chr1:35357856-35357948	275::146	272::251	0.030354887	cassette
UNK	chr18:4654011-4654058	28::47	11::66	0.030540041	cassette
PNPLA6	chrun_aadn03027100:4216-4380	26::0	10::5	0.030658042	alt3
ARHGAP17	chr14:6565266-6565310	160::41	109::6	0.030834567	cassette
BPTF	chr18:6987883-6988044	163::60	144::106	0.030835951	cassette
ADARB1	chr7:7271419-7271483	11::8	11::36	0.030936469	cassette
LIN9	chr3:16410115-16410125	19::13	35::3	0.030990087	alt5
SFPQ	chr23:4353931-4354048	99::193	79::99	0.031563062	Undefined
SNX13	chr2:29122018-29122098	77::6	42::15	0.031573186	cassette
LIN54	chr4:45724039-45724194	83::9	62::25	0.032213175	cassette
DEPDC5	chr15:8859611-8859727	21::7	42::2	0.034078523	cassette
ZNF407	chr2:91799459-91799512	9::10	13::1	0.034845501	cassette
DDX26B	chr4:4132849-4132929	51::1	43::20	0.034913219	cassette
FAM76B	chr1:184508642-184508722	72::80	90::155	0.035399748	cassette
ZDHHC14	chr3:50907794-50907806	122::8	48::11	0.036064719	alt5
MKI67	chr6:32893586-32893601	0::77	37::88	0.036117136	alt3
SLC1A4	3:9807250-9807329	13::21	40::37	0.036125254	alt3
ATF1	chrlge22c19w28_e50c23:146287-146363	20::113	19::239	0.036389919	cassette
INTU	chr4:33736068-33736154	44::0	27::6	0.036450216	cassette

ZNF217	chr20:12874597-12874722	2::113	13::108	0.036934939	cassette
OGT	chr4:2193402-2193432	88::62	123::30	0.03698717	alt3
MTMR14	chr12:11441665-11441820	77::171	74::81	0.037043324	cassette
PPP2R2D	chr6:34313353-34313450	10::103	25::94	0.037325535	Undefined
LRP8	chr8:23579431-23579553	1::28	3::1	0.037845518	cassette
CHD1	chrz:51138417-51138680	19::59	21::34	0.038259004	cassette
GBE1	chr1:94624127-94624189	14::0	2::11	0.038534116	cassette
CDKN2AIP	chr4:39281330-39281361	43::45	34::85	0.039534738	alt5
CRTC1	chr28:3586998-3587099	33::17	45::20	0.040126567	cassette
DCUN1D2	chr1:136737893-136737989	10::2	3::8	0.040129344	cassette
U2SURP	chr9:10110769-10110810	88::150	115::90	0.041468846	cassette
SAAL1	chr5:11868618-11868642	34::6	41::0	0.041671631	alt5
CIRH1A	11:18360385-18360426	158::72	40::40	0.041783217	alt3
TIAL1	chr6:29789920-29789971	53::157	78::106	0.041922553	alt3
PPP2R5C	chr5:49284040-49284163	79::18	126::31	0.042679818	cassette
FAM107B	chr1:7218739-7218852	69::11	66::1	0.042809815	cassette
RNF149	chr1:132823237-132823266	49::84	78::52	0.042896094	cassette
UBR2	chr3:22338664-22338762	47::49	60::40	0.043248631	mutually_exclusive
DOCK10	chr9:8015337-8015352	10::14	5::48	0.043754113	alt3
TRERF1	chr3:22206820-22207008	30::155	21::173	0.044076746	cassette
MEF2A	chr10:16547063-16547194	211::64	143::82	0.044867946	mutually_exclusive
ATG4C	chr8:26499100-26499169	13::0	12::9	0.045712468	alt5
SEC16A	chr17:7871154-7871213	33::45	58::29	0.046019996	cassette
CCNL1	chr9:22238440-22238512	84::66	91::54	0.047654712	cassette
HPRT1	chr4:4014253-4014270	19::662	40::675	0.048052692	cassette

LOC421259	chr3:5333911-5333920	2::0	0::7	0.049115572	alt5
XLOC_018851	chr8_jh375182_random:45431-45585	40::27	76::18	0.049920647	alt5

Abbreviations: Ex: exclusion, In: inclusion

Supplementary Table S2. List of validated and significantly changed splicing events regulated by SRSF10

Gene	Description	AS type	annotation&
EIF4ENIF1	eukaryotic translation initiation factor 4E nuclear import factor 1	exon inclusion	A+U
CAST	calpastatin	exon inclusion	A+U
CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	exon inclusion	A+U
MBNL2	muscleblind-like 2 (Drosophila)	exon inclusion	A+A
HSF2	heat shock transcription factor 2	exon inclusion	A+A
CRTC1	CREB regulated transcription coactivator 1	exon inclusion	A+U
PHF20L1	PHD finger protein 20-like 1	exon inclusion	A+U
LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	exon inclusion	A+A
CHD1	chromodomain helicase DNA binding protein 1	exon inclusion	A+A
TRERF1	transcriptional regulating factor 1	exon inclusion	A+U
CCNL1	cyclin L1	exon inclusion	A+U
TRIM33	tripartite motif containing 33	exon inclusion	A+U
PCM1	pericentriolar material 1	exon inclusion	A+A

DBT	dihydrolipoamide branched chain transacylase E2	exon inclusion	A+A
LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	exon inclusion	A+A
EPRS	glutamyl-prolyl-tRNA synthetase	exon exclusion	A+A
KDM6A	lysine (K)-specific demethylase 6A	exon exclusion	A+U
CEP44	centrosomal protein 44kDa	exon exclusion	A+U
L3MBTL2	l(3)mbt-like 2 (Drosophila)	exon exclusion	A+U
MDM4	Mdm4 p53 binding protein homolog (mouse)	exon exclusion	A+U
PCYT2	phosphate cytidylyltransferase 2, ethanolamine	exon exclusion	A+U
SEC16A	SEC16 homolog A (S. cerevisiae)	exon exclusion	A+U
PTPRC	protein tyrosine phosphatase, receptor type, C	exon exclusion	A+U
FKBP14	FK506 binding protein 14, 22 kDa	exon exclusion	A+U
TUBGCP5	tubulin, gamma complex associated protein 5	exon exclusion	A+U
NCAPG2	non-SMC condensin II complex, subunit G2	exon exclusion	A+U
ZNF341	zinc finger protein 341	exon exclusion	A+A
PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	exon exclusion	A+U
CDK13	cyclin-dependent kinase 13	alternative 3'	A+U
SLTM	SAFB-like, transcription modulator	alternative 5'	A+U
BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	alternative 5'	A+U

RBBP5	retinoblastoma binding protein 5	alternative 5'	A+U

#: Note that these exons map to Gallus4.0.

Supplementary Table S3: list of primer pairs used for identification of SRSF10-regulated splicing events

Gene Symbol	primer-F	primer-R
EIF4ENIF1	GTCGTTCTGGAAGTCGGTCAA	TGGGCTGTGAAGGTAGGGTC
CAST	AAGAAAAGAAACCTGCTGTGGA	AAAATCCCTTTGTCAAACCTTC
CASP1	GGCAAACCCAAAGTGGTCATT	CGGAACATCTCCTGCAAGTCA
MBNL2	AAAAGGTCGTTGCATGAGGG	AGGGAGGCTTCGTGGCACTC
HSF2	TCAGGACGACAGTTCAGCATAG	GACCAGCATTACTCTTGGTAGTTT
CRTC1	GTGGCGATGGATGCGTTGT	TGATGGGATAGGGCATTAGC
PHF20L1	ACCCTGTCTCCCTCTTGATTT	CTTTTCCTTTTCTTTCCACTC
LRRFIP2	GATGCCTCGCTCAGTGAATTA	TTCCCTGTGGTACTCTGCTATT
CHD1	ATTCTTCACCACAACCCTCAG	TTTCAGTGCTGCTTTGACAGG
TRERF1	AGTTTGCCTGCTCTGAATGGT	CTGTGCCGATACTTCTTCTTGT
CCNL1	CAACGTGTTTCACCACCTGAG	ACCCTCCTTTCTGCTTTGATTAC
TRIM33	TGTGGCTGATGTCCGGTTGAT	GCTGGAAGGTCCTGTCTGGGT
PCM1	GGGAGCCACTGCAATGTAAAG	CGGAATCATCCACAACAGCAA
DBT	AACAAACAGGAGCTATCCTACC	TTGACAGCCTTCATCCAAAGA
LRP8	CTGACAACAGTGACGAGGCA	GGCATTCACATTCGTAGCCT
EPRS	GAGACATGAAGAGCCAACA	GATCCAATCCTCGCACTCA
KDM6A	GTTGTCGTTTTAGTCGGATACC	GTCCTGACCAGTCCAGTAGATG
CEP44	AGATTCGGGCGCCTGAG	TGCGAAGTCCTTGTTCTATTTT
L3MBTL2	GCAGAGGAATCGTAGGTAAAACT	CCAAAACCGTCCATTGAAAAAAG
MDM4	ATCCAAGCCCAGTCTATGAG	TGAAACAATGGCAGTGTCTAT

PCYT2	GTCCACTTTGGGGAGAAGG	CTCGGCCAGCGCGAAGATG
SEC16A	AAGATTTCTACAGCAGAATGGCTAG	TGGAACAGGTGGAGAAGGAGG
PTPRC	TCTGACTTCTGGCAAATGGTA	CGACTAAATCTTTGGGGTCTT
FKBP14	GGAATGGACCCAGGTCTCAT	AACCCATCACTGTCTTCATCTTCT
TUBGCP5	TGATTCTCCATCTAACACCACC	CTTCCAACAAATACTTTCCCCA
NCAPG2	TACCCGACAGAAGACGTAACGAA	CCAACCCTAACGACAAATCAAAG
ZNF341	GGGGAAGTTGTGCGTTGCT	GAAGTTCTTTCGCCGGGAG
PIP5K1B	GCTCCAGATGACTTGCCTTGT	TTGGCTTTCCAGCAGTAACAT
CDK13	GCATGCAAACTTCTTCCCAACT	TTTTCCTTCTCCTCCAACACCA
SLTM	GTAAAGAAGGCAAGAAAACAGAAG	GTTTGGTCAAGAACTACAACGTGA
BAP1	GTTTGATGGAAGGGGGGGAG	CTGAAGTGTGTGGAGGCGGA
RBBP5	TTAGGTTCTTCTTCGTTCGTCC	TCTCCGTTAATTCCTTCTTGCT
HPRT1	TATAAAAGTCATTGGTGGGGATG	CGTTTTCATTGTTTTCCCAGTAT
MAT1A	GTCCTGCTCAGAAAGAACCCT	CAGTACAGCATCGCTGATTTG
MAP4K5	TTCGCATTGGAATCCTTTTGTT	CAGGGAAGTGTTTTATCGTCTCAG
MDM2	GCAACTTCCCAGCCAACAA	CCCGCTCACCACACACCAT
ZZEF1	TGGAAGATAACATTACCCCAACA	TCTGAGAGCACTCAGCAAAAACT
ZYX	CCCTGTGGAACATCAAGACGA	CTCCCTTGGAATACGAATACTGCTA
PPP2R5C	CGCCAGAGTTCATCAAGGTTTA	TGCTCGTTTTACTTCCTTCCAC
IDI1	TCCTTCAGGGGCGGTGCT	GTGGCAGTTTTTCTTCGTGTCC
INTS4	GCGGGTGTATGAGGAGTTCAC	CTCTCCACTTCCACAGGCTTC
MKS1	AGGAGCCTACTGGATTGAGC	TCGTCCTCTTGGGTGATAAA
UBR2	ATGGCCTTCGTCGAGTATTGT	AAACTGAAACCTGCCTTGGAT
MEF2A	ATACAACGAGCCCCATGAAA	GACACTGGAACCGTAACCGA