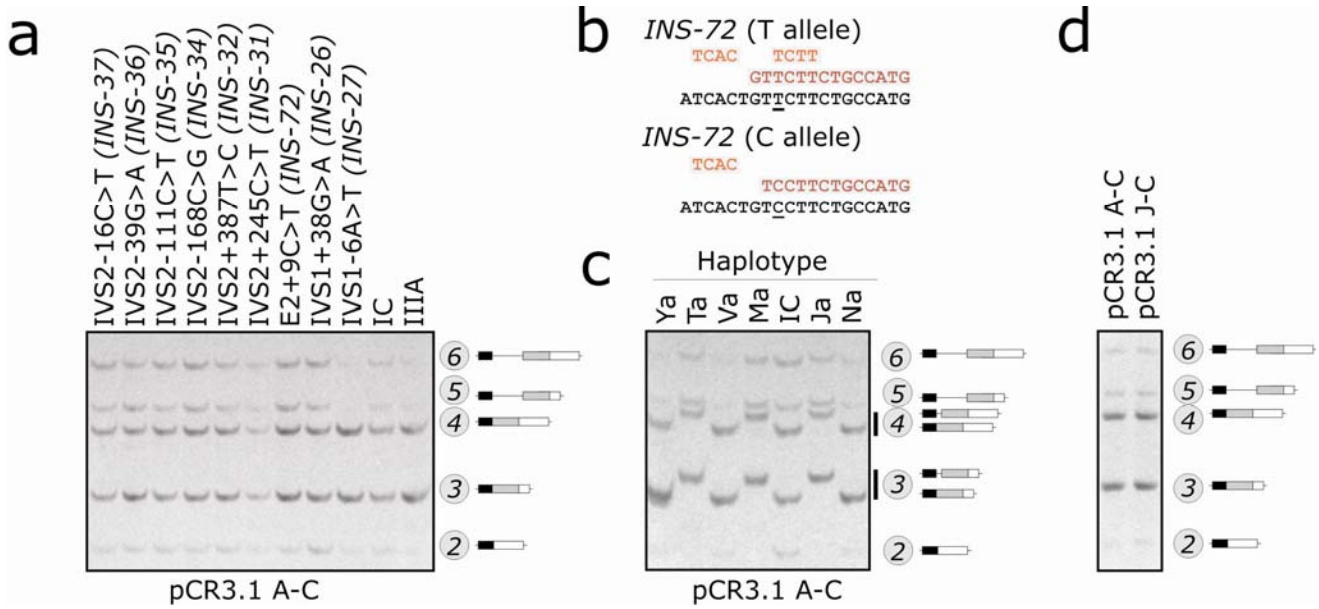
SUPPLEMENTAL DATA

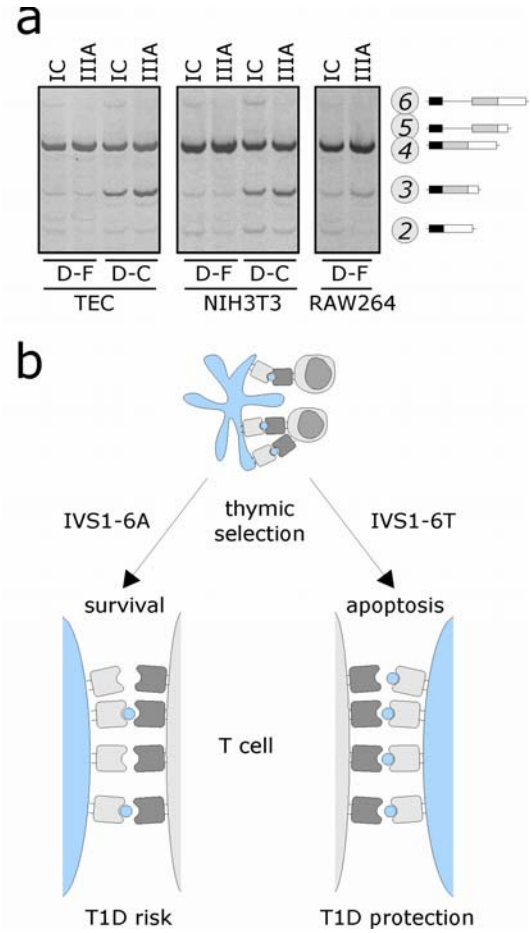
SUPPLEMENTAL FIGURES

SUPPLEMENTAL FIGURE 1 Dissection of haplotype-dependent *INS* pre-mRNA splicing



Legend: *(A)* Splicing pattern of reporter constructs mutated at naturally occurring *INS* variants. Mutations are denoted by the traditional nomenclature (http://www.hgvs.org/mutnomen/). The original designation (Stead et al. 2003) of the variant is followed in parentheses. RNA products are shown schematically to the right; template reporters for overlap-extension PCR are at the bottom. *(B)* Predicted auxiliary splicing elements at *INS-72*. Putative splicing regulatory motifs are shown above the sequence; variant residues at *INS-72* are underlined. *(C)* Splicing pattern of African-specific haplotypes with (Ta, Ma, Ja) or without (Ya, Va, Na) the 4-nt insertion allele at *INS-69*. The IC haplotype is shown as a control. Haplotype designation was as previously described (Stead et al. 2003). *(D)* Splicing of reporter constructs with (primers J-C) and without (primers A-C) upstream minisatellite (VNTR) sequences is identical. Amplifications shown for panels *B* and *C* was with primers PL3 (Kralovicova et al. 2006a) and E. In experiment shown in panel *D* we employed PCR primers D and PL4 (Kralovicova et al. 2006a) (Figure 1).

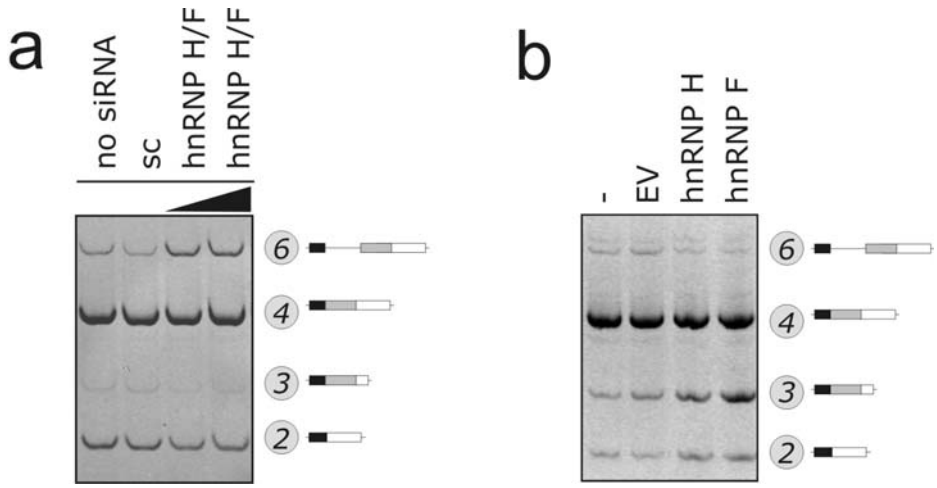
SUPPLEMENTAL FIGURE 2 Allele-specific *INS* splicing in mouse cell lines



Legend: *(A)* Increased IR of the *INS* class IC haplotype as compared to the class IIIA haplotype in the *Aire*-expressing TEC cell line derived from thymic epithelial cells and in the macrophage cell line RAW264; NIH3T3 cells are shown as controls. The *INS* splicing pattern was not significantly different in a TEC cell line lacking *Aire* (data not shown). Haplotypes are at the top of each panel and mRNA isoforms to the right. Cloning primers are shown at the bottom; their location is depicted in Figure 1A. The extended 3' segment of D-F reporters inhibits the cryptic 3' splice site in *INS* exon 3 (cr3'ss+126), which is most likely mediated by the 3'end processing machinery that can influence selection of 3'ss of the last intron (Rigo and Martinson 2008). *(B)* A proposed model for genetic susceptibility to T1D at *IDDM2*. Unlike *INS-69*, which is confined to Africans, the *INS-27*A allele (IVS1-6A) has a high frequency in whites (Stead et al. 2003), indicating that this variant is critical for the haplotype-dependent proinsulin expression in this population. Antigen presenting cells will have a lower number of the MHC/proinsulin peptide complexes in carriers of the low-expressing and T1D-predisposing A alleles than in carriers of the T alleles. Their lower number would be associated with the lower probability of inducing apoptosis of autoreactive T cells in the thymus during negative selection. Antigen-presenting cells/antigenic peptides are in blue. MHC molecules and T-cell receptors are highlighted in light and dark gray, respectively.

SUPPLEMENTAL FIGURE 3 Heterogenous nuclear RIBONUCLEOPROTEINS F/H in *INS* intron 1 splicing

Legend: *(A)* Increased intron 1 retention and decreased utilization of cr3'ss+126 in hnRNP F/H-depleted cells. siRNAs are at the top, RNA products to the right; sc, scrambled control. The final concentration of siRNAs in culture media was 80 (sc), 60 and 100 nM (hnRNP H/F). The D-F constructs used for this experiment contained the class IC haplotype. *(B)* Improved efficiency of intron 1 removal and cr3'ss+126 activation in cells overexpressing hnRNP H (1 μg of pcDNA-hnRNP-H) and hnRNP F (1 μg of pCI-hnRNP-F). EV, empty vector.



SUPPLEMENTAL FIGURE 4 Sequence alignment of the 5' untranslated region of the proinsulin gene in primates

Legend: Intronic sequences are in lower case, exonic sequences are in upper case. Lineage-specific changes observed in at least two species/animals are highlighted in gray. Naturally occurring human polymorphisms are in red. Alignment was carried out using the Clustal-Wallis algorithm (v. 2.0). Hs, *Homo sapiens* (Stead et al. 2003)(Genbank accession numbers AY138590 and L15440); Pt1-2, *Pan troglodytes* (Stead et al. 2003) (this study); Gg, *Gorilla gorilla* (Stead et al. 2003)(AY137500); Pp1-2, *Pongo pygmeus* and *abelii* (AY137503 and AC199962); Hg1, Hg2, *Hylobates gabriellae* (this study); Eryp, *Erythrocebus patas* (this study); Cae, *Chlorocebus aethiops* (X61092); Cc116, *Cercopithecus campbelli* (this study); Cd2A, *Cercopithecus diana* (this study); Ca303, *Cercopithecus ascanius* (this study); Mt114, *Macaca tonkeana* (this study); Mf, *Macaca fuscata* (this study); Mm1,Mm2, *Macaca mulatta* (Indian and Chinese, respectively; this study); Ms, *Macaca sylvanus* (this study); Ph100, *Papio hamydras* (this study); Msp119, Msp102, *Mandrillus sphinx* (this study); Cang, *Colobus angolensis* (this study); Ac1af, *Colobus guereza* (this study); Se117, Se2, *Semnopithecus entellus* (this study); Pn, *Pygathrix nemaeus* (this study); To, *Trachypithecus obscurus* (this study); Ta, *Trachypithecus auratus* (this study); Sv, *Semnopithecus vetulus* (this study); Pm, *Presbytis melalophos* (this study); Nl, *Nasalis larvatus* (this study); Cj, *Callithrix jacchus* (this study); So1, *Saguinus oedipus* (this study); Smid92; *Saguinus midas* (this study); Sfl15, *Saguinus fuscicollis* (this study); Calgo6, *Callimico goeldii* (this study); Aab203, *Aotus azarae* (this study); At, *Aotus trivirgatus* (J02989); Mur, *Microcebus murinus* (Ensembl scaffold sequence, www.ensembl.org). Y, C or T; W, A or T; N, C or G or T or A. Genbank accession numbers of new sequences: GU901169-GU901198.

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Pp2             CAGCCCTCCGGGACAGGCTGCATCAGAAGAGGCCATCAAGCAGgtct----gttccaagg 56
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Mur           cccagctctgcatggtggtggtggggagggacgtgggctcctctcgtggggcatttgggg 145
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Pt2         gtgagcccaggggccccaaggcagggcanctg-ccttcagccggcctcagccctgcctgt 214
Gg          gtgagcccaggggccccaaggcagggcaactggccttcagccggcctcagccctgcctgt 231
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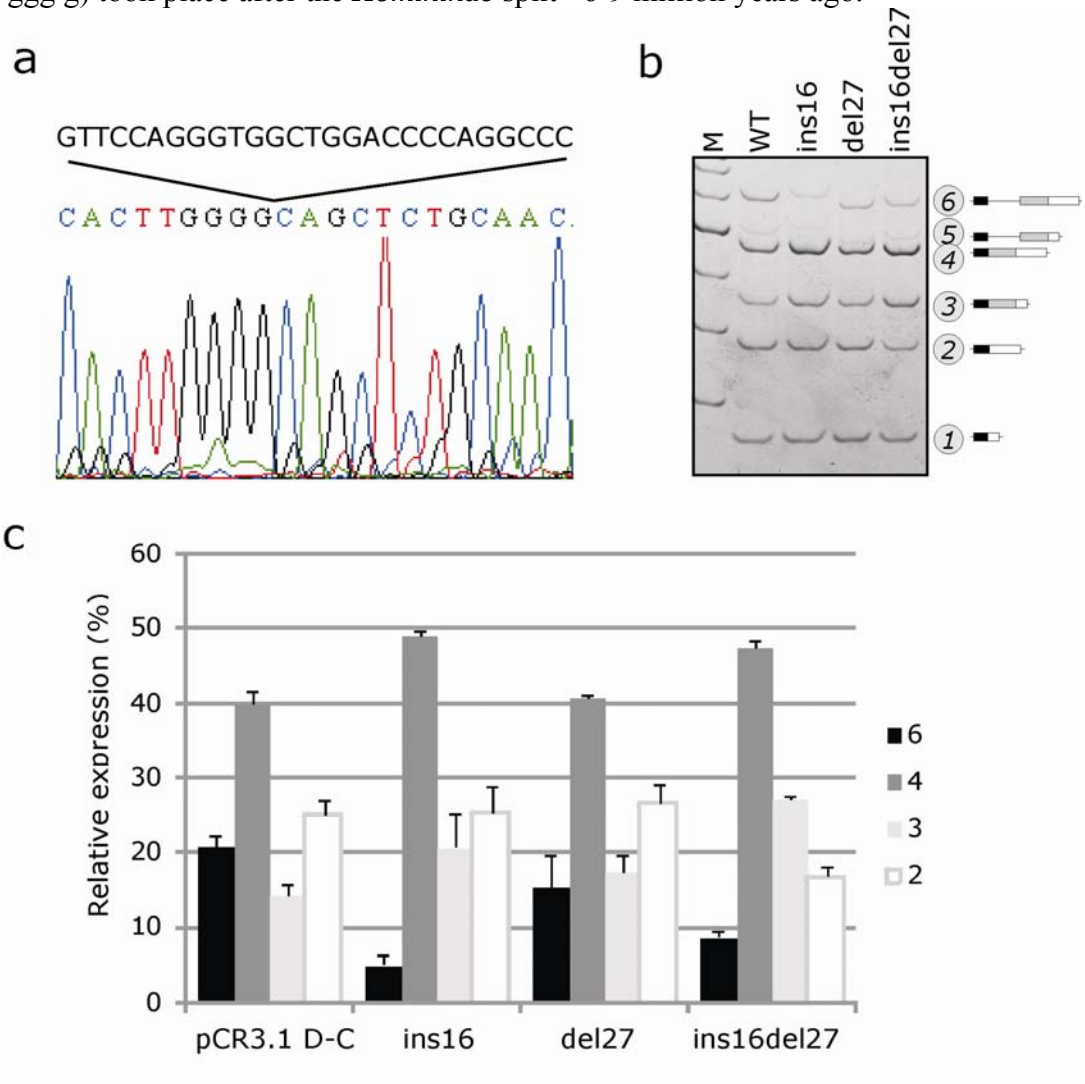
Ac1af       ctcccagGTCACTGTCCTT---CCGCCATG 258
Se117       ctcccagGTCACTGTCCTT---CCGCCATG 231
Se2         ctcccagGTCACTGTCCTT---CCGCCATG 231
Pn          ctcccagGTCACTGTCCTT---CCGCCATG 231
To          ctcccagGTCACTGTCCTT---CCGCCATG 231
Ta          ctcccagGTCACTGTCCTT---CTGCCATG 231
Sv          ctcccagGTCACTGTCCTT---CCGCCATG 231
Pm          ctcccagGTCACTGTCCTT---CTGCCATG 231
Nl          ctcccagGTCACTGTCCTT---CCGCCATG 231
Cj          ctcccagGCCGCTGTGCTT---CCACCATG 255
So1         ctcccagGTCGCTGTCCTT---CCACCATG 255
Smid92      ctcccagGTCGCTGTCCTT---CCACCATG 255
Sfl15       ctcccagGTCGCTGTCCTT---CCACCATG 255
Calgo6      ctcccagGTCGCTGTCCTT---CCACCATG 252
Aab203      ctcccagGTCGCTGTCCTT---CCACCATG 248
At          ctcccagGTCTCTGTCCTT---CCACCATG 243
Mur         ctcccagGTCTTTGCCCCCGCCCCGCCATG 233
```

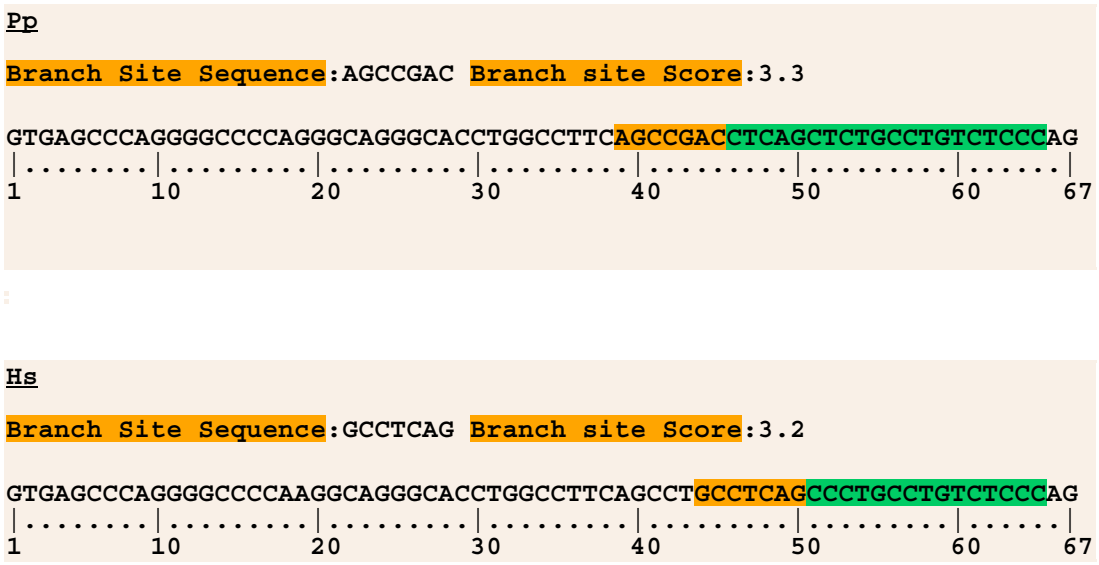
SUPPLEMENTAL FIGURE 5 Ancestral deletions of *INS* intron 1 in primates and their effect on splicing

Legend: *(A)* A colobine-specific, 27-nucleotide deletion in *INS* intron 1. The deleted sequence is shown at the top. *(B)* Splicing pattern of human reporter constructs with two large deletions that took place during primate evolution. 293T cells were transfected with pCR3.1 containing *INS* segments defined by primers D and C, as shown in Figure 1A. Deletions are at the top and RNA products to the right; M, 100-nt size marker. Total RNA was isolated 48 hours post-transfection, reverse transcribed using oligo-d$(T)_{15}$ and complementary DNA products were visualized using PCR with vector-specific primers PL3 and PL4 and/or PL3 and E (Kralovicova et al. 2004) (Figure 1A). *(C)* Relative expression of *INS* isoforms in the wild-type reporter and plasmids containing *Hominini*- and *Colobinae*-specific deletions and their combination. The alignment of intron 1 sequences in primates is shown in Supplemental Figure 4. The 16-nt deletion (ctg ccc cac ttg ggg g) took place after the *Homininae* split ~6-9 million years ago.



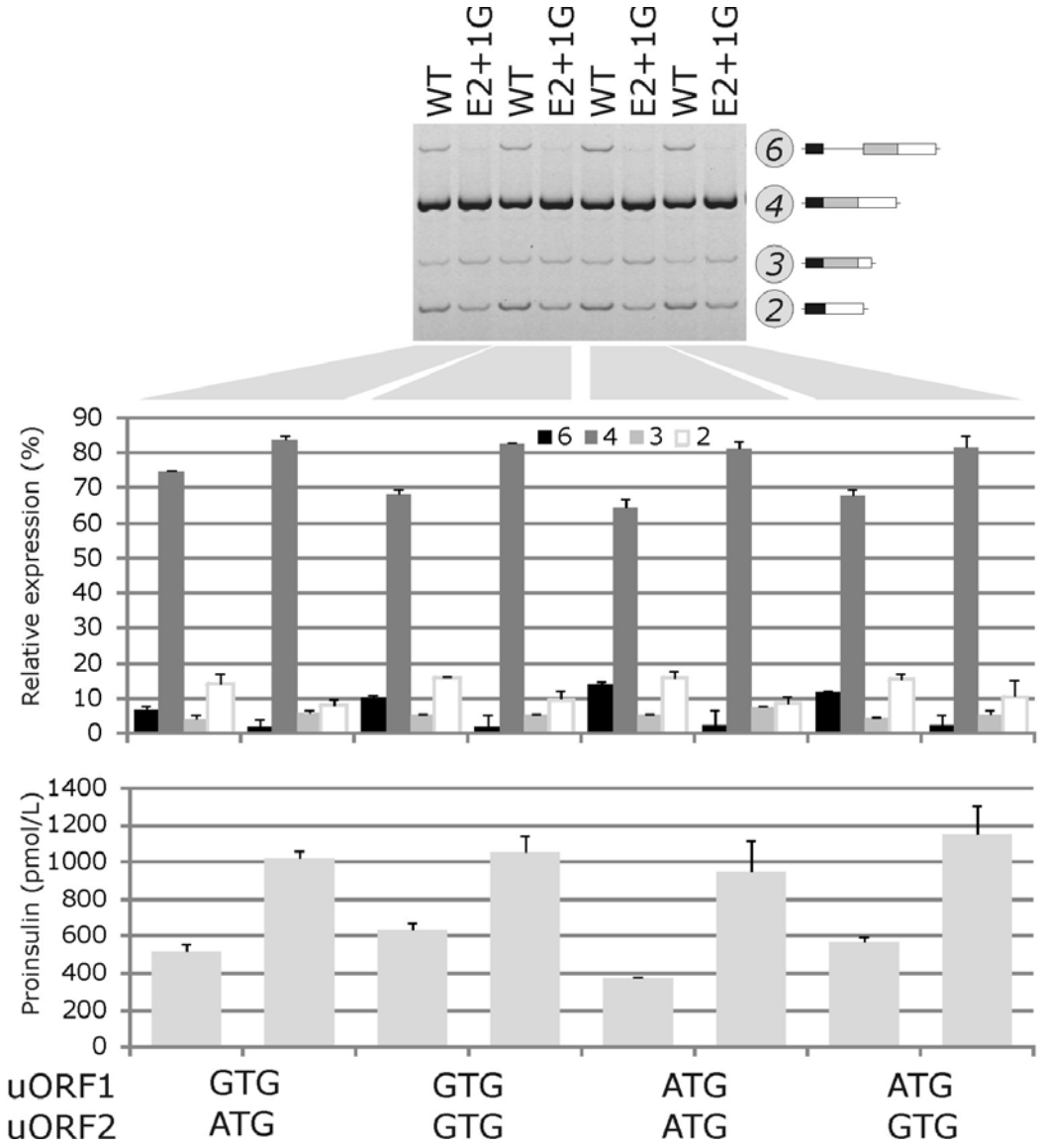
SUPPLEMENTAL FIGURE 6 Predicted branch point sequence and polypyrimidine tract in *INS* intron 1 in primates

Legend: Pp, orangutan; Hs, human. Predicted branch point sequence (orange) and polypyrimidine tracts (green) were determined using an algorithm derived from a comparative analysis of these signals that were conserved between human and mouse (Kol et al. 2005). Predicted branch point sequences in the remaining primates (Supplemental Figure 4) were identical to the human sequence.



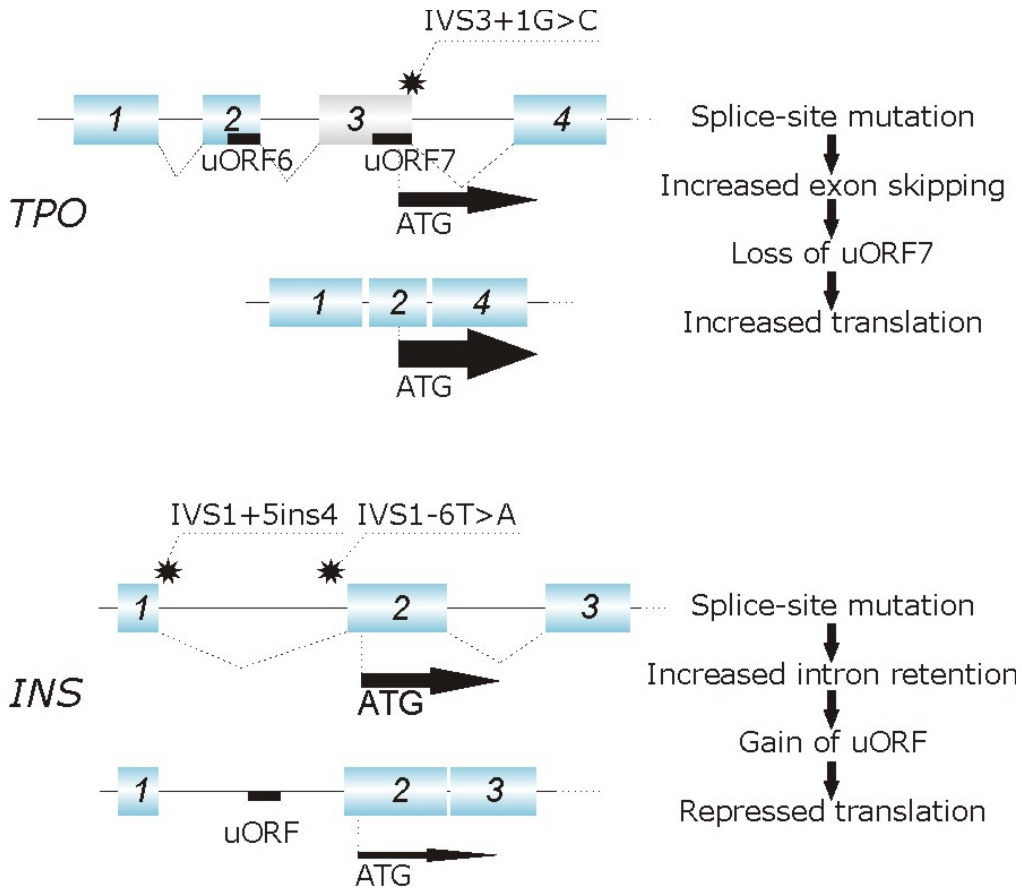
SUPPLEMENTAL FIGURE 7 Coupled translation and splicing regulation of *INS* expression by upstream open reading frames

Legend: *Upper panel*, the splicing pattern of wild-type (WT; E2+1A) and mutated (E2+1G) reporter constructs 48 hours post-trasfection into 293T cells. RNA products are schematically shown to the right; *middle panel,* quantification of mRNA isoforms. *Lower panel,* proinsulin concentration in cultures. Mutations introduced in two upstream open reading frames are shown at the bottom and their location and natural variability in primates is shown in Figure 3. E2+1A (WT) is specific for Great Apes, whereas E2+1G was found in all lower primates.



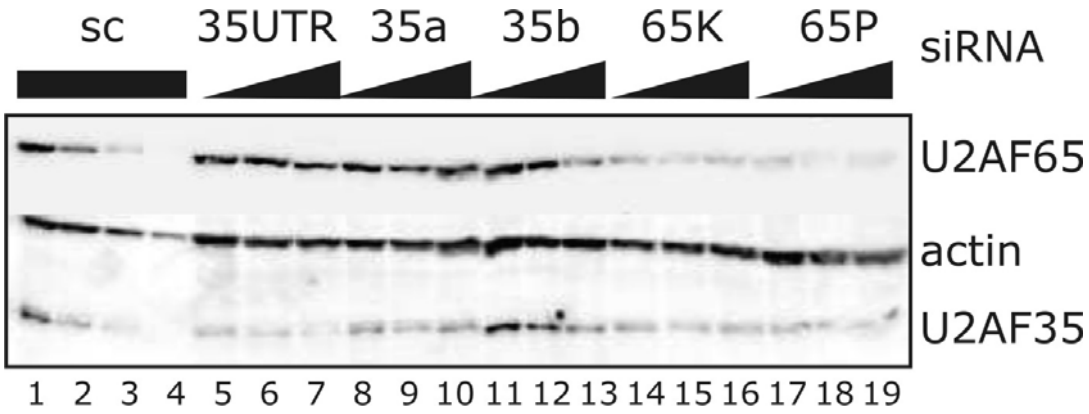
SUPPLEMENTAL FIGURE 8 Extending translational pathophysiology: gain and loss of upstream open reading frames (uORFs) in disease predisposition

Legend: Splicing mutations in the gene for thrombopoetin (*TPO*) induce exon skipping and a loss of the seventh uORF, leading to derepression of translation, excess of TPO and thrombocytosis (Wiestner et al. 1998) *(upper panel)*. In contrast, variants that influence splicing of *INS* intron 1 result in a gain of uORF that curtails translation of intron 1-containing transcripts *(lower panel)*. These transcripts are exported from the nucleus to the cytoplasm (Kralovicova et al. 2006a; Wang et al. 1997). Exons are denoted by numbered boxes, introns as lines, uORFs by black rectangles, disease-causing or -predisposing mutations by stars, and the increase *(upper panel)* or decrease *(lower panel)* of translated products by arrows. The degree of translation efficiency corresponds to the vertical size of the indicated arrows.



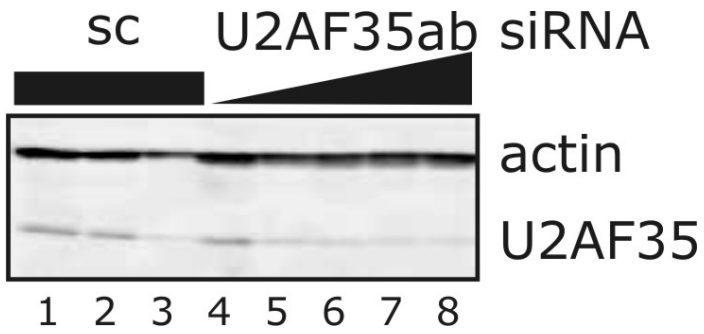
SUPPLEMENTAL FIGURE 9 RNAi-mediated depletion of U2AF subunits

Legend: Western blot analysis of HeLa cells transfected with siRNAs individually targeting U2AF subunits and their isoforms. Final concentrations of each siRNA in culture media were 10, 33 and 100 nM; a scrambled control (GC content 68%) was added at a final concentration of 48 nM. Antibodies are shown to the right. Lanes 2-4 contain two-, four- and eight-fold dilutions, respectively, of the total cell lysate shown in lane 1.



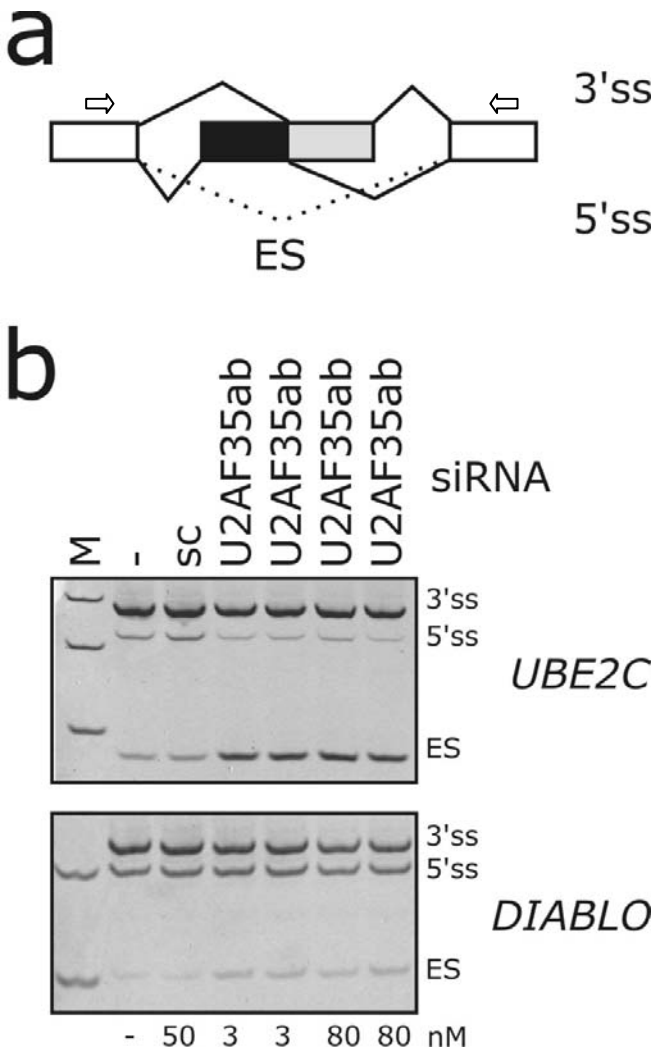
SUPPLEMENTAL FIGURE 10 U2AF35 is effectively downregulated at low concentrations of the U2AF35ab duplex

Legend: Western blot analysis was performed with antibodies shown to the right. Final concentration of the U2AF35ab siRNA in HeLa cell cultures was 0.1, 0.33, 1.0, 3.3 and 10 nM. sc, scrambled siRNA control (47% GC).



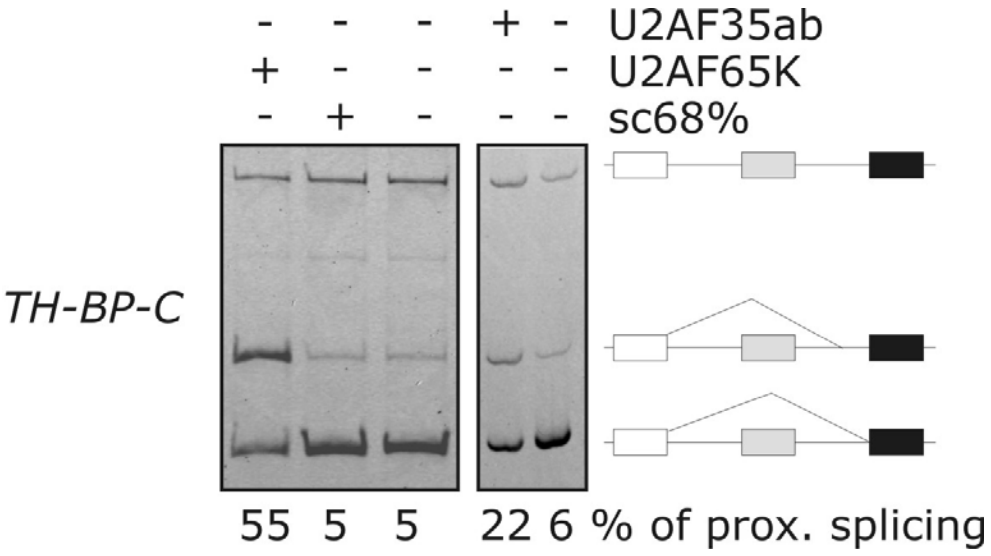
SUPPLEMENTAL FIGURE 11 Selection of dual-specificity splice sites by U2AF35

Legend: *(A)* Schematics of the splicing pattern and location of primers (arrows) used to detect isoforms that result from the use of the 5'ss or 3'ss in *UBE2C/DIABLO* transcripts. ES, exon skipping. *(B)* RT-PCR analysis of total RNA extracted from HeLa cells transfected with U2AF35ab siRNA and a scrambled control (sc). Final concentrations of siRNAs are shown at the bottom. M, 100-nt size marker.

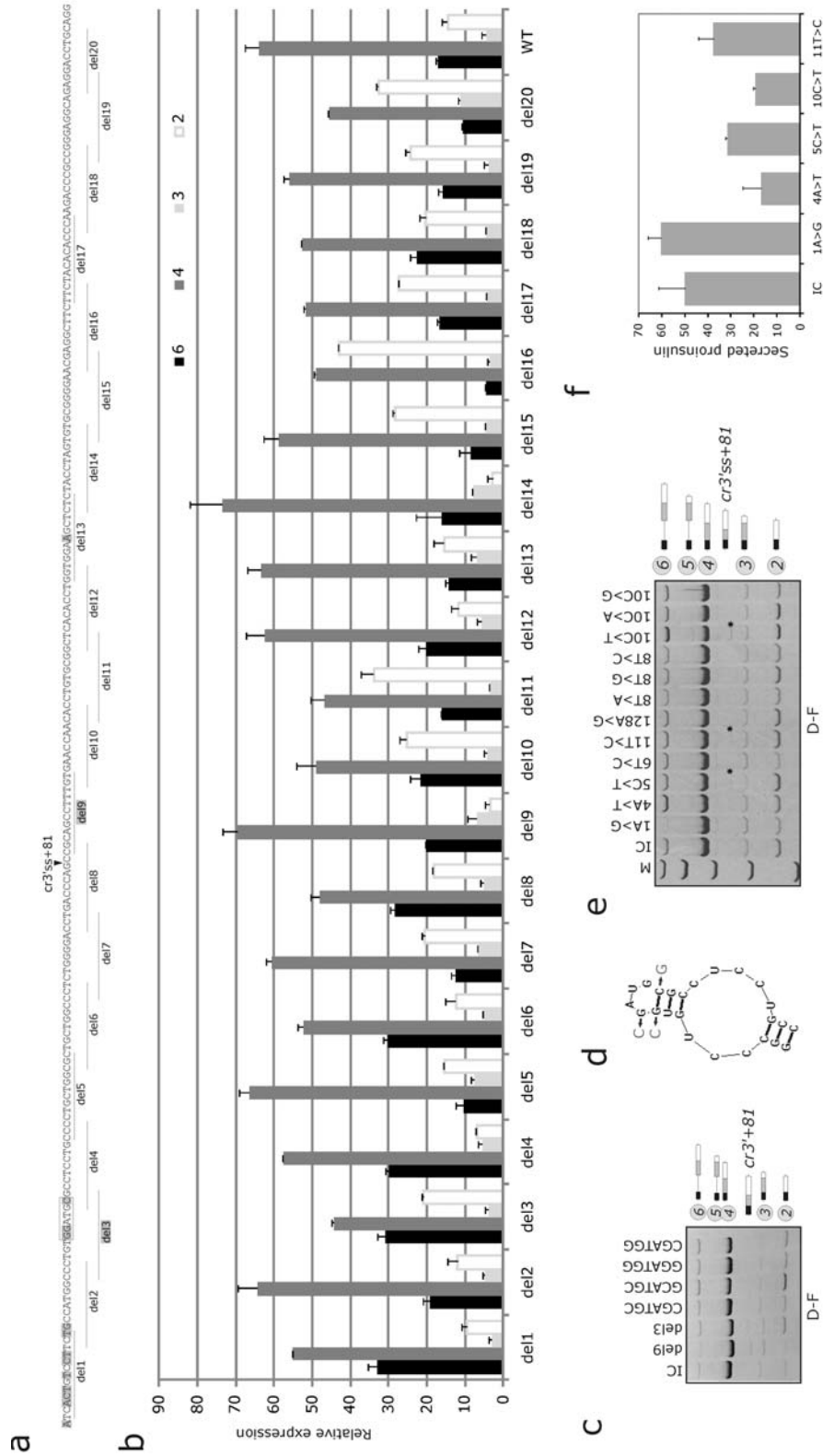


SUPPLEMENTAL FIGURE 12 Skipping of short exons in U2AF-depleted cells

Legend: An example of a reporter construct with a short central exon (96 nt). The reporter construct was described previously (Kralovicova et al. 2006b). siRNAs are shown at the top, RNA products to the right, the name of the reporter to the left and utilization of the intron-proximal 3'ss at the bottom.



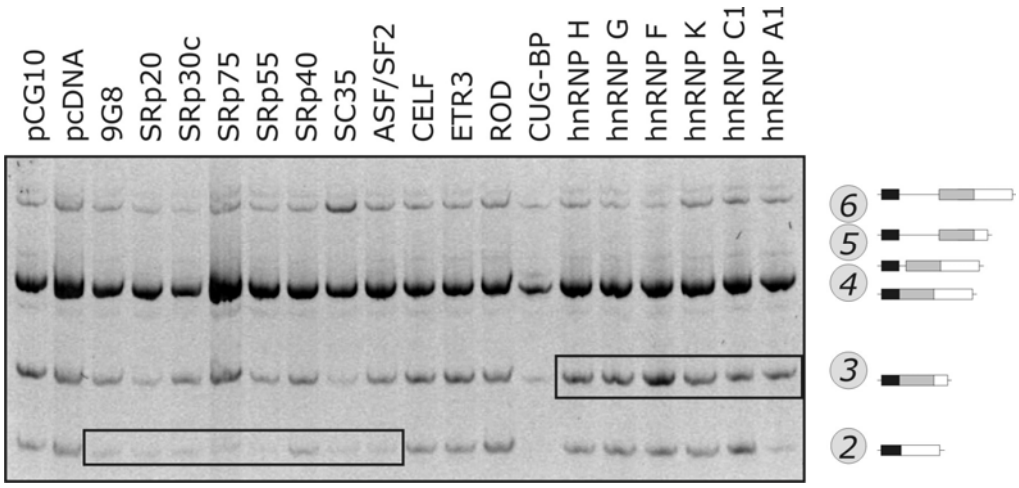
SUPPLEMENTAL FIGURE 13 Identification of auxiliary splicing sequences in exon 2



Legend: *(A) INS* exon 2 deletion constructs (D-F) on the class IC haplotype background. Deletions are shown as horizontal lines (denoted del1-del20). Mutated residues and two deletions that activated cr3'ss+81 are highlighted in gray. *(B)* Relative expression (%) of four *INS* mRNA isoforms in each deletion reporter. Error bars indicate s.d. determined from duplicate wells. The utilization of the remaining isoforms was negligible, except for activation of cr3'ss+81 in del3 and del9. *(C)* Identification of a splicing enhancer in exon 2. Mutations in a putative RESCUE-ESE (Fairbrother et al. 2004) (boxed in panel *(A)* Are shown at the top. RNA products are shown to the right and the *INS* reporter at the bottom. *(D)* A putative structure of the newly identified splicing enhancer in exon 2. Mutations are shown by arrows. *(E)* Activation of cr3'ss+81 by point mutations at exon positions 5, 10 and 11. Mutated positions are highlighted in gray in panel *(A)*. M, 100-nt size marker. *(F)* Secreted proinsulin is shown on the pmol/L scale. Error barrs denote standard deviations of a single transfection experiment in duplicate.

SUPPLEMENTAL FIGURE 14 Coexpression of SR proteins/hnRNPs and *INS* in 293T cells

Legend: Individual SR proteins/hnRNPs are shown at the top, RNA products to the right. Reduction of exon skipping upon individual overexpression of SR proteins is highlighted. An increase of cr3'ss+126 utilization observed for a subset of hnRNPs is also boxed.



SUPPLEMENTAL TABLES

SUPPLEMENTAL TABLE 1 Phylogeneny of G runs in *INS* intron 1 in primates

G run	Great Apes	Old World Monkeys	New World Monkeys	*Strepsirrhini*
G0	x	x	x	x
G1	x	x	x[1]	
G2	x	x[2]		
G3	x	x	x[1,3]	x
G4	x	x	x	
G5	x[4]	x[5]	x[6]	x[4]
G6	x[7]	x[8]	x[7]	x[7]
G7	x	x	x	x

Legend: G runs are numbered as in Supplemental Figure 4. 'x' denotes a conserved G run. [1], G run was shifted by 1 nucleotide in a subset of New World Monkeys; [2], G run was deleted in all examined genera of Asian colobines; [3], extra G_3 in the vicinity; [4], G_5; [5], G_5, except for *Cercopithecini;* [6] G_4; [7], G_4; [8] G_4, except for *Colobinae.*

SUPPLEMENTAL TABLE 2 Predicted strength of *INS* splice sites

Intron	Splice site[1]	Consensus sequence[2]	Maximum entropy score (allele)[3]
1	5'ss	CAG/GTCTKT	6.84 (*INS-69*del), 2.36 (*INS-69*ins)
1	Cr5'ss+30	CAG/GTGGRC	8.07 (*INS-26*G), 3.09 (*INS-26*A)
1	3'ss	CAGCCCTGCCTGTCWCCCAG/ATC	7.57 (*INS-27*T), 4.75 (*INS-27*A)
1	Cr3'ss+81	CCTCTGGGGACCTGACCCAG/CCG	-1.12
2	5'ss	AGG/GTGAGC	7.75
2	3'ss	TGCGCGGCACGTCCTGGCAG/TGG	4.36
2	Cr3'ss+35	GGGCGGGGGCCCTGGTGCAG/GCA	1.54
2	Cr3'ss+126	GCATCTGCTCCCTCTACCAG/CTG	8.24

Legend: [1]Cryptic (Cr) splice sites are denoted by their exon/intron position (in nucleotides) relative to their authentic counterparts; [2], IUB codes: K is G or T, R is A or G, W is A or T. GT and AG dinucleotides are underlined. Exon/intron boundaries are denoted by a slash. [3], Maximum entropy scores were computed as described (Buratti et al. 2007; Vorechovsky 2006; Yeo and Burge 2004). Location of the three variants is shown in Figure 1A. Their designation is according to the previously published nomenclature (Stead et al. 2003); del/ins, 4-nucleotide deletion/insertion allele at *INS-69*. The composite score of intron 1 splice sites is 11.59/14.41 (haplotype I/III, respectively), which is comparable to the composite score of intron 2 splice sites (12.01).

SUPPLEMENTAL TABLE 3 Oligonucleotide primers amplifying competing 3'ss in endogenous transcripts

Gene	Exon	ID#[1]	Primers (5'-3')	Size of PCR products	Distance between competing 3'ss
SERBP1	5	Far2	CTCACAACTGGGGAACTGTC TGTCTGCCACTGGATGATGT	102/147	45
SRRM1	6	Far3	AAAAAAGGGAGCGGTCTCGTA AAGTAGCCTCTTGTACTGAA	138/228	90
SLC15A4	3	Far12	CTGTTCCCAGAAGCGAAGTG GAAAACAGGGACAATCTTGA	114/172	58
CIT	30	Far13	TGAAAATGGAAGGCACTATT GAAGGGCTTCCTCTAGCTCT	165/210	45
LRRC28	6	Far15	GGATCTTAGTGACAATGCCT AAGTGGCAAAAATGCAAGAC	226/321	95
SEPT4	11	Far19	GGACCTGAAGGATGTGACAC CCTCATCTTTCTCTCGGATA	144/197	53
STAT3	23	Far20	CGCTGCCCCATACCTGAAGA TGAGGGTTCAGCACCTTCAC	89/139	50
ATP13A1	14	Far24	GGAGGTGACCCCAGTGTCCA TACGAGGCAAGCACGGACAT	182/252	70
FAM134A	4	Far25	CCTTCTTCCTACTCAGCGTC GCTGGATTCTGCCTCTTGTA	156/244	88
MAP4K4	11	Far27	GAAGAGGAGCAGCGGCACTT CTCGGTCAGCAGGCTCGTAG	187/280	93
C20orf30	3	Far28	TTATGATGCCGTCCCGTACC CCTTTGCTGATGTAGCCTGA	135/223	88
SLC35C2	3	Far29	TTTGTGGAAGGCGGTGTTGA CCCAGCTCAGCACCACACGG	141/212	71
SFRS15	19	Far30	CCTCACACTCCACCAATAAG GTGAAACAGGCTGGGTTACA	151/217	66
FMR1-201	15	E15	GACGCGGTCCTGGATATACTT CCTCCACGCCGCCGTCCGT	85/124/160	39/36
FMR1-201	16	E16	GTAATCCAAGAGAGGCTAAAG TTGCTGACCATCCACGCTGTC	134/185	51
ECM1[2]	4	Far1	CCCCACCCCTATCCCGAAGC GGGAGTTGGGCAGGTAGCAG	148/235	87
SPOPL[2]	4	Far26	AGGAAATGGGTGAAGTGTTA TTGTTTCTTCCCTTTTAGCA	136/207	71
PRP3[2]	12	Far4	TTTGATGCGAGTATTAGGAA TTTTAATTTTCTTGACCTTT	155/213	58
EIF3S7[2]	15	-	CTGATGGCACCTTCAGCTCT CCTCGTAGTCTCGGTGGAAG	127/295	168
PTK9[2]	12	-	GAGGAGCAGCCACTTCCTG CTCCACTGTCCCAGCTCTTC	128/247	119
CUEDC1	17	-	GCCTGCGAGAAGGACAGTAA TCGGTTCTCAAGCACCATCT	141/213	72

Legend: [1], Identity number corresponding to a previously described set of tandem 3'ss separated by >39 nt (Akerman and Mandel-Gutfreund 2007). [2], PCR products did not show the predicted size or failed to amplify.

SUPPLEMENTAL TABLE 4 Selection of competing 3'ss upon depletion of U2AF subunits

Gene	ID 3'ss[4]	ID 3'ss in U2AF35(-)[5]	3'ss promoted in U2AF35(-) cells	ID 3'ss in U2AF65(-)	3'ss promoted in U2AF65(-) cells	Intron- proximal 3'ss (ME score)	Intron-distal 3'ss (ME score)	Splice site more dependent on U2AF
MAP4K4[1]	50	39	Intron-proximal	38	Intron-proximal	AAG/G (7.8)	CAG/C (9.6)	Intron-distal (stronger)
SLC35C2[1]	12	51	Intron-distal	63	Intron-distal	CAG/A (5.7)	CAG/G (8.9)	Intron-proximal (weaker)
SRRM1[1]	10	1	Intron-proximal	1	Intron-proximal	TAG/A (4.5)	CAG/A (7.4)	Intron-distal (stronger)
FMR1-201[1]	17	8	Intron-proximal	9	Intron-proximal	TAG/G (7.4)	TAG/C (-0.7)	Intron-distal (weaker)
						CAG/A (4.0)		
CUEDC1[1]	82	90	Intron-distal	88	Intron-distal	CAG/G (8.3)	CAG/A (0.8)	Intron-proximal (weaker)
UBE2C[1,2]	78	90	Intron-distal	N.D.	N.D.	AAG/G (3.0)	CAG/G (6.7)	Intron-proximal (weaker)
DIABLO[1,2]	65	60	Intron-proximal	N.D.	N.D.	TAG/G (10.4)	CAG/G (8.8)	Intron-distal (weaker)
INS intron 1(cr3'ss+81)[3]	0	19	Intron-distal	0	N.I.	CAG/A (4.8)	CAG/C (-1.1)	Intron-proximal (stronger)
INS intron 2(cr3'ss+126)[3]	15 (IC D-F)[6]	0 (IC D-F)[6]	Intron-proximal	2 (IC D-F)[6]	Intron-proximal	CAG/T (4.4)	CAG/C (8.2)	Intron-distal (stronger)
	55 (IC D-C)[6]	3 (IC D-C)[6]		9 (IC D-C)[6]				
LIPC (ESS13, SS63)[3]	54	40	Intron-proximal	38	Intron-proximal	TAG/A (6.2)	CAG/T (-2.3)	Intron-distal (weaker)
TH-BP-C[3]	95	78	Intron-proximal	45	Intron-proximal	CAG/G (5.2)	CAG/C (5.1)	Intron-distal (weaker)

Legend: [1], endogenous transcripts; [2], dual-specificity splice sites (Zhang et al. 2007); [3], exogenous transcripts; *LIPC* and *TH* minigenes were described previously (Kralovicova et al. 2006b; Kralovicova and Vorechovsky 2007); [4], % of splicing to intron-distal 3'ss in untreated cells; [5], % of splicing to intron-distal 3'ss in U2AF35-deficient (-) cells; [6], haplotype and primers used for minigene cloning are in parentheses. N.I., not informative; N.D., not determined; ME (maximum entropy) scores were computed as described previously (Buratti et al. 2007; Vorechovsky 2006; Yeo and Burge 2004).

SUPPLEMENTAL TABLE 5 A list of synthetic small interfering RNAs

Target	siRNA	Source
U2AF35a	CCAUUGCCCUCUUGAACAU	(Pacheco et al. 2006)
U2AF35b	CCAUCUUGAUUCAAAACAU	(Pacheco et al. 2006)
hU2AF35ab	GGCUGUGAUUGACUUGAAU	(Pacheco et al. 2006)
U2AF35-UTR	AGUGUUGUAGUUGAUUGAC	This study
U2AF26-UTR	AGCCCCCUUCACUCUCCUG	This study
U2AF26-83	GGACAAGGUUAACUGCUCU	This study
U2AF65K	GCAAGUACGGGCUUGUCAA	(Hastings et al. 2007)
U2AF65P	GCACGGUGGACUGAUUCGU	(Pacheco et al. 2006)
PUF60	GCAGAUGAACUCGGUGAUG	(Hastings et al. 2007)
nPTB-N1	GAGAGGAUCUGACGAACUA	(Spellman et al. 2007)
nPTB-N3	UAAGAAACCUGGAUCCAAA	(Spellman et al. 2007)
PTB	CUUCCAUCAUUCCAGAGAA	(Wollerton et al. 2004)
9G8-Gao	AGAUCAAGAUCCAGGUCUA	(Gao et al. 2007)
9G8-UTR	GGGAUUUGUGAUGUCUGUA	This study
9G8-UTR2	GUGUAACCUAGGAAAGAUA	This study
SRp75-1	AGACCAAGCUGAAGAGAAG	This study
SRp75-2	AGCAGUCAUUCUAAGAGUA	This study
SRp55-1	GCAGAUCUAAGGAUGAGUA	This study
SRp55-2	AAGAUGAGGCUCUAAGGAA	This study
SRp40-1	UGCUCCACCUGUAAGAACA	This study
SRp40-2	ACGUGGUUCUUCAAGUAGA	This study
SRp30c	AGAGGAUGCUAUUUAUGGA	(Paradis et al. 2007)
SRp30b/SC35	AAUCCAGGUCGCGAUCGAA	(Gabut et al. 2005),
SRp30b/SC35	CAAGCAACUGGCUAUUGAA	This study
SRp30a/ASF	ACGAUUGCCGCAUCUACGU	(Karni et al. 2007)
SRp20-1	GGAAAUAGAAGACAGUUUG	(Bedard et al. 2007)
SRp20-2	GGUCCCUUUCUAGAGAUAG	(Bedard et al. 2007)
RSRC1-ORF1	GAACGCGUAGUCGGUCUCG	This study
RSRC1-ORF2	UGGGCAGUCCUGUGGCCUA	This study
Scrambled control (47% CG)	AGGUAGUGUAAUCGCCUUG	This study
Scrambled control (68% CG)	UGCGCUAGGCCUCGGUUGC	This study
hnRNP H	UCAGAAGAUGAAGUCAAAU	(Paul et al. 2006)
hnRNP-F	GCGACCGAGAACGACAUUU	(Garneau et al. 2005)
Tra2α-UTR	CGGAAUGGUUGCAAUUAAG	This study
Tra2β-UTR	GCAUGAAGACUUUCUGAAA	This study
ZRSR1/2	CAACAACUAGAAGAAGAGA	This study
ZRSR2-UTR	GGCUAUGAACGCAGAUGGG	This study
CAPERα-UTR	GGAUCUACUGUCAUUUGUA	This study
CAPERβ-UTR	UCAGUGGCACAGUAUACUG	This study
hSlu7-ORF	GUGAGUUAUGCUGGAGAUA	This study
hSlu7-UTR	GACCAUCCAAGAUAGAUGC	This study

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