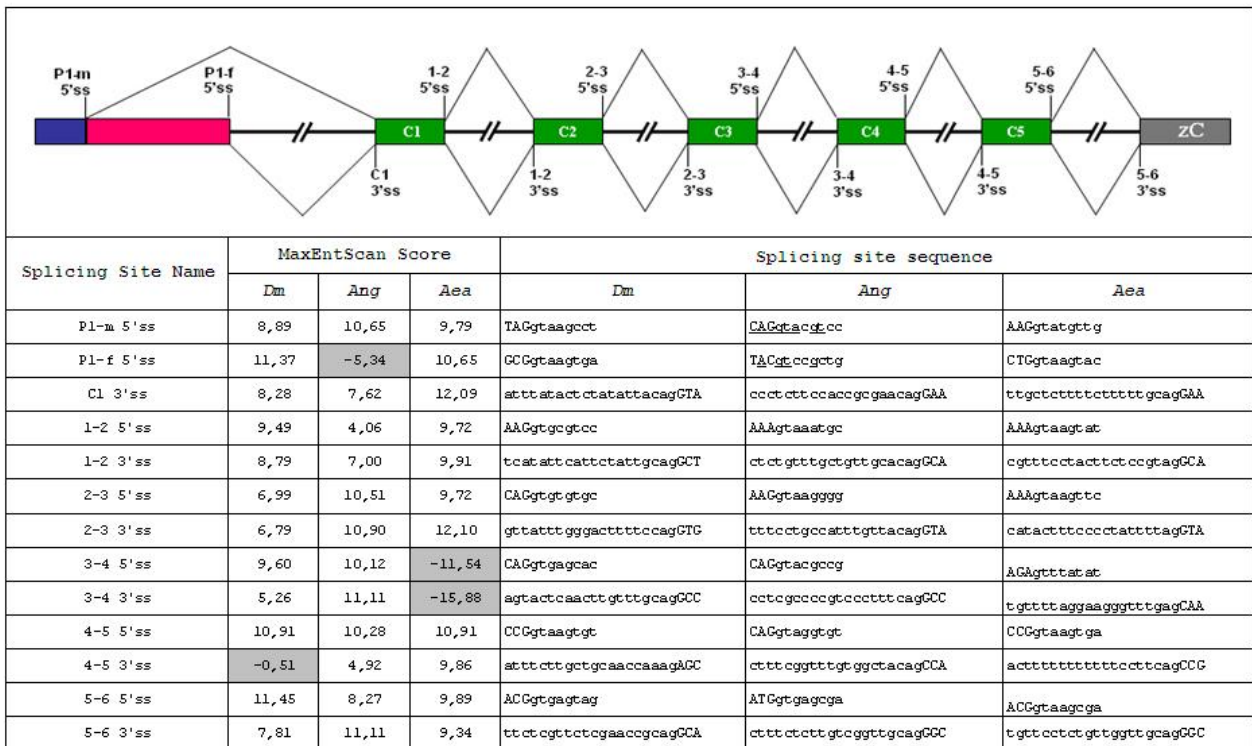


Figure S3 – Exon/Intron junctions and MaxEntScan scores of *fru* genes

A

<i>Aeaf_{ru}</i> gene					
Exon No.	Exon size (bp)	5'ss	Intron size (bp)	3'ss	N° of Y
P1-m	149	R R CCG AAG /gtatggtgagcggggt	425673	N S tcttttcttttttcag/GAACAG	12
P1-f	1299	n.c. CGG CTG /gtaagtacttttggtgg	424374	N S tcttttcttttttcag/GAACAG	12
C1	148	V K GTC AAA /gtaagtattctatggg	9859	A H tcttacttctccgtag/GCACAT	11
C2	201	L K TTG AAA /gtaagttcccgatggc	75	V R ctttcccttatttttag/GTACGA	11
C3	516	S R TCT AGA /gttta g atgcaaatct	8321	Q H tttaggaagggttttcag/CAACAC	4
C4	279	L P ITG CCG /gtaagtgatgagtttc	46633	P I tcttttttctcttcag/CCGATC	12
C5	130	D G TCG ACG /gtaagcgaacacgatac	39889	F G cctctgtttggttcag/GCCCG	9
zC	693	Q M * CAGATGTAAacottcagatcat			
Consensus		MAG/gtRagt		YYYYYYYYYYYYNYag/G	8,02 +/- 2,15

B



A) Coding sequences are shown in upper case letters and non-coding regions in lower case letters. The 5'ss consensus sequence is MAG/GTRAGT and the 3'ss consensus is Y_nNYAG (Mount et al. 1992). The number of pyrimidines (N° of Y) in the 12 bp preceding the 3' ss (NYAG) is indicated for each 3'ss. The consensus number of pyrimidines for *Ae. aegypti* (8,02±2,15) is derived from the tabulation of 4688 *Ae. aegypti* splice-acceptor sites (Salvemini et al., 2011). M= A or C. R=A or G nucleotide. Y=T or C or nucleotide. N=any nucleotide. B) Schematic representation of *fru*-P1 gene. Shaded in grey negative MaxEntScan scores.