

Table S1. Number of AUG (start) codons in 5' UTR

(a) Stringent set			(b) Less stringent set			(c) Stringent set							
value	NMD target	NMD nontarget	value	NMD target	NMD nontarget	NMD nontarget							
0	29	30	0	119	122	0	1	2	3	5	6		
1	8	7	1	42	37	0	25	1	0	1	1	1	
2	2	2	2	10	8	1	1	6	0	1	0	0	
3	1	2	3	13	10	2	0	0	2	0	0	0	
5	1	2	4	1	5	3	1	0	0	0	0	0	
6	0	1	5	7	6	5	0	0	0	0	1	0	
			6	1	1								
			7	2	4								
			8	1	1								
			9	0	2								
			11	1	0								
			12	1	1								
			15	0	1								

(d) Less stringent set													
	NMD nontarget												
	0	1	1.5	2	3	4	4.5	5	6	7	9	12	15
0	93	7	0	0	0	2	1	1	1	2	1	0	1
0.5	0	1	0	0	0	0	0	0	0	0	0	0	0
0.67	1	0	0	0	0	0	0	0	0	0	0	0	0
1	7	25	0	1	2	1	0	0	0	0	0	0	0
2	0	2	0	5	2	0	0	0	0	0	0	0	0
3	3	1	1	3	3	0	0	1	0	0	0	0	0
4	0	0	0	0	0	1	0	0	0	0	0	0	0
5	1	1	0	0	0	1	0	4	0	0	0	0	0
6	1	0	0	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0	0	2	0	0	0
8	0	0	0	0	0	1	0	0	0	0	0	0	0
11.5	0	0	0	0	0	0	0	0	0	0	0	1	0

Tables (a) and (b) show an unpaired comparison between the NMD-target mRNAs and the NMD nontarget mRNAs for the stringent and the less stringent set of *upf1*-affected genes, for the feature “number of AUG (start) codons in 5' UTR.” Tables (c) and (d) show a paired comparison between the two sets of mRNAs, for the stringent and the less stringent set of genes.