Supplemental Table 1 – Primer pair number and primer sequences used to amplify alternative splicing events on RT-PCR panel with gene ID and localisation of AS event

Primer pair	Gene ID	Localization	Primer Forward (labelled)	Primer Reverse
1	**At1g02840**	CDS/3'UTR	GGCCCCCGCTCGAAGTCAAGG	GGTAGAGGAGATCTTGATCTTG
2	**At1g04400**	5'UTR	GGAAGAAAGAAGAGTCAAG	GGATTATCCTCAATCCTTAGG
3	**At1g09140**	CDS/3'UTR	CCTGCTAGATCCATTTCCCC	GATCTTGATCTTGATTTTG
7	**At1g55310**	CDS	GGAAGTCGTTTGAGCAGTTTGG	GGTTTCTTTCTGTTCTCTTCTG
12	**At1g72320**	5'UTR/CDS	CGTCAACTGTGTTTTTGCATCC	CATCAAATCCACGGTTACCC
13	**At1g79650**	CDS	GGAGAACAAAGTTACGGAGG	GGAACAGGTGAAGACTGGG
19	**At2g32330**	CDS	CTTTTGGAATGAGCACTCC	CCGTAGGCAAAGGCAATATCC
21	**At2g37340**	5'UTR/CDS	GGACCCGAGACCTTGAACG	GGTAATGTCTTGCATCATCAG
23	**At2g39730**	CDS	CCTCCCGTGTTCGAGCAACCC	CCGTTGGATCAAAGTTTTCAGCC
30	**At3g53270**	5'UTR	CCAACATCATCATCTTCTC	CCACAAACTCGTCTATCAGC
36	**At4g12790**	5'UTR	GGTTTTGAGAGCAAAGAAAAACG	GGTTAACAACATGCATTGTTCG
42	**At5g04430**	CDS	CCTTCGAGGAGCAGATGCGGGC	CCTCCAGAACCGTTGGGTGC
43	**At5g09230**	5'UTR	CATCCGCCATTAACGACCTC	CTCACAAACCGTCTGCATCC
44	**At5g13730**	CDS	GGGTACCAAGGCAAAGGTTTG	GCAATCTCTTCACAGCTTGG
47	**At5g20250**	5'UTR	CCATTCAAATCTCACATTCCC	CCCGTCGGAAATACGAACCGCC
48	**At5g35680**	5'UTR	CCTAATCACTTTCAACAACTC	CCGTCAATGCACATAACGTC
49	**At5g41150**	CDS	CCATCCTGACATGGGTTTTGTC	CCAGTTCCTTTCTTCCGCCTGC
50	**At5g43910**	CDS	GGTTGTGTGATGCTTGAGAG	GGTTGTGTCTATGAGTTCCG
51	**At5g45510**	CDS	GGAGAAAGTTGTTGTAGGAG	GGTGGAGGTACATCACTGTGG
57	**At5g63870**	5'UTR	GGTCCAAGATCCAAGCTTTGG	GGGAAGGAGGTAGATTCCATG
58	**At5g65050**	CDS	CAAAGATCATTGATCGTTAC	CTTCACTTCCCCCATCATTAGTTC
59	**At5g66010**	CDS	GGCGGCAGGTCATGTACGG	GGGAAGACCCCTGAGGCGAACG
63	**At3g12110**	CDS	GGCTCCTCTCAACCCCAAGG	GGTAATCAGTAAGGTCACGG
64	**At5g60670**	CDS	GTCACCGGAGGTGAGGTCGG	GATGACTAGAGCCGCTGCGG
66	**At4g02560**	CDS	CGCAAATTGATTCGCAGAGTC	CCACCATCTGTACTTTCCTGC
68	**At1g23970**	CDS	CTTGCACATGATCCCGATCC	CCATCGCCCAATGCGCCACC
70	**At1g54360**	CDS	CCTTCCATTCCACAGAATTC	CCAGATTGAGTCAAAGCCCAC
72	**At2g04790**	CDS	CCCTGAAAGCATAGAAGCAGC	CCCATGACTTATTAAACTCC
73	**At2g21620**	CDS	CCGGAACTTGAGAGAGAGAGC	CCATGAGGGCTTGGCTCGTC
75	**At2g36000**	CDS/3'UTR	CTCGTTTAGTTTGGAGAATC	CTTCATCAGCATTCATTAC
82	**At3g14230**	CDS	CCTTTCGTCTTCACCGCAAC	CCAAGCCATTCTCGGGAGCC
86	**At4g16845**	CDS	GGATTGTTCTTGTCCATTTTG	GCAAGCTCTGTTGCCTCGGG
87	**At4g35450**	5'UTR	CCACCACAACATTGTCTTTTC	CCAGCGTTAGGAATAGATCTC
89	**At4g38510**	5'UTR	CCTCTACACAGATCTTTGGATTC	CTTGACCACGTCGGGTAGTTCC
90	**At4g39260**	CDS	GGTGCTTTGTCGGCGGCCTTG	GGCTTTCTCGTCCTTGAAGG
97	**At3g61860**	CDS	GCGAATTAAGATAAAGATGAGG	GGAAAATTGTCGAGTTTGCG
102	**At1g27370**	5'UTR	CCTCCTTCTCACTCTCGCTC	CCCACGGGAACGAAGATACC
103	**At1g30500**	CDS	CCAACCACCAATCCCTTCTGC	CTTGCTCTTGATTGTCTGCGCC
105	**At1g33060**	CDS	GGCTAATTTAAGTGCTCAGGGG	GCTACATTTCGCATCACTTG
106	**At1g49950**	5'UTR	CCTTGTATTCGCATTAACCC	CCAGGTCCATGCTTTATAACTCC
107	**At1g59750**	CDS	CCGTCTTCACAACCTCAGCC	CCCACCATGACCAAACGTAGC
108	**At1g30200**	3'UTR	GGAACCGTTTGGGACTGTG	GCAGATTCATTCGACGCAGG
109	**At1g77080**	CDS	GATCTTGAAGAAAAAATTCAG	CCTAGCTCTACTTACGGACAG
110	**At1g72050**	CDS/ 5'UTR	GGTTGATGAGGAGTCTTCAAG	GGACACTTAAAGAGCTTCCC
111	**At1g61660**	CDS	GGACATGGTCTATGTCTCGTCC	GCTTTAGAGTCTCCAAGCTG
112	**At1g09530**	5'UTR	CCGTCTTGTGCGTCGATTTG	CCTGTCTTGAGCAGATTCAAGC

113	**At1g72650**	CDS	GGTTTATTGCATTCTGATAATG	GGTGGACTTGATCCTCCTC
116	**At1g18660**	5'UTR	GGATTCACCTTTAGTGACTG	GAGACTCTTTGAATGATTGG
117	**At2g22670**	CDS	GAAACTGAAGATCATGAAGGG	GAGACGAAATATCTTGAAGG
118	**At2g02960**	5'UTR	GGGGAGCTTTCACCAATTAG	GCCTTATCATTAACCACCGG
120	**At2g41710**	CDS	GGCTGCTGCTAGAGCTTACG	GGTCCAGGCATACGACTGG
121	**At2g18300**	CDS	GGATGCAATAAGGTCACAGG	GGTCTAACGGAAACAATGG
122	**At2g36010**	CDS	CCAAAGATGGAATGCTGGACC	CTCAGGTCTCTTAATCTTTCC
124	**At2g37060**	5'UTR	CCCTCTCTGCCTCCTCTCTTCC	CCCATTAGCAGGAAGACCTC
125	**At2g46790**	CDS/5'UTR	GGATTTGCCATCTATATCTGG	GCTTTGAGCATGAGCAGTAGG
126	**At2g34830**	CDS	CCGCTATGAACAGCCGGTCC	CCATGGGTGGTTATGCTCAG
127	**At2g43010**	CDS	CCGGTTATGGATCAGTCTGC	CCGTCGGTGGTCTTCGTCGGC
128	**At2g15530**	5'UTR	CCCAGAAATTGAAACTACC	CCCTTGCATTGGATTCATACC
129	**At2g40830**	5'UTR	CTAGGGTTTCTCATTCCGATCC	CCGTGAAGGCGGACAGCACGC
130	**At2g38185**	CDS	GCTTGATTACTCAGAACCAGGG	GAACCGCAGAACCTTGTGG
131	**At2g38880**	3'UTR	GGCAACATTAGGATTTGAGG	GGAAACAATAAACCAAACG
132	**At2g31370**	3'UTR	CCAACAGCAGCAGCAGCAAC	CCAAAAGGTTTCTTCTACGTACC
133	**At2g32250**	CDS	CCCATCGATTTCTTCCATCC	CTTCGATGTCATAGCAGCC
134	**At3g08505**	3'UTR	CTATCAGAGTTCCTTGGTGGCC	CATTGAGTTTCTCCTGTGTCC
135	**At3g54480**	CDS	GGAGTTACATGAGATCTCAAAG	GATAAATCCTTGACAAAACGG
136	**At3g07740**	CDS/5'UTR	GGGAAGAAGTGCGAGCTTGG	GGTGGAAATTGATGCCGCAG
137	**At3g14740**	CDS	CCGGAAGTTTACTTTGAGGATCC	CAACAATCTTGTACTTTCC
138	**At3g10490**	CDS/3'UTR	GGAATGGGCTGATGATGAAGG	GGTCCGATTCGATATCCAGTGG
139	**At3g04030**	CDS	GCACTGCAAATGCAAATAGAGG	GGCAGCTTCGATCCCAGCTG
140	**At3g15030**	3'UTR	GAAGAGGAGCAGCACGACGG	GGCCATTGACTACACAAACCG
141	**At3g51880**	CDS	GGGAGTGATGAATCTGAAAAG	GGATCTGCAGTTAAGCTTGAG
142	**At3g12250**	5'UTR	GGACAACCTTTTACTCAGACAGG	GGTATCAGCCATACTAGTTTCTG
143	**At3g12250**	CDS/5'UTR	CCCTCTAGTGTGAAACTCTGC	CCTTTGATCGATCACTGGAATC
144	**At3g23280**	CDS	GCACAGTGATGCCTTTGTGG	GGCTGTCACCTTCAGTCGAAGG
145	**At3g17609**	CDS	CCAACGACCCAATGGGAACTC	CGTTTAGCTGTAGAGACTCC
146	**At3g24120**	CDS	CCAAGTCACCGAAGCTCTAC	CCAGCAAAAGTAGCAGCTTGC
148	**At1g76510**	5'UTR	CCGTTTCTCGCTTCTTTTTCTC	CCTCTACAACACCTTTGGTACC
149	**At2g27230**	5'UTR	GGCATGTCGGAGTATGATCG	GACCTTAAAGCTTCTCTTAG
151	**At3g47550**	CDS	CCTTCTTCGTGCTGCTGGTTTTC	CCTTAACGGAGAATCATTGCC
152	**At3g58030**	5'UTR	CCATCTCTATTCGTAATTAGC	CCCAAGATTCAAATCCAGGTTC
153	**At3g59060**	CDS	CCATCCCGGTTTAGTATGTC	CCTATTTTACCCATATGAAGACTGTC
154	**At4g01060**	CDS	GGTGCCGTTTGACATGGATAACC	GTCACCGACAAGCTTATGCATTC
155	**At4g27050**	5'UTR	GGTTCTTTCTTTGTGAACAAC	GGGAAACTCCTTAGACAGCAG
156	**At4g34430**	CDS	GGGCTTCCATTAAATCTCTTCACAG	GGAGACCTCTTCTGCTTTTTTG
157	**At4g38900**	CDS	GGGAACTCGGGTGCTGCTTTTAG	GGTAGCCTCGGTCTGAAGAGTCTG
158	**At4g32730**	5'UTR	CTCAGCGTCTTAATTACTTCAG	CCTTGGAGACTCTCTAGTGGAG
159	**At4g37180**	CDS	CGAGGATCAAAGACAATCATTCC	GGTTTTGCCCTTTCAACATC
160	**At4g14410**	CDS/5'UTR	CCTTCTCTCGACGATGATTTCG	CCAATACTAAAGACTTCATCTGG
161	**At4g28790**	CDS	CCATGCTGGATGATGTTATAG	CCTAGGGAAAGGTATGAATGC
163	**At4g13100**	CDS	CCTCCTCACTAACTCGGAGAC	CCTCTCCTCCCCCTCGCAGC
165	**At4g16420**	CDS	GCAGAACATGAAAGAAGAGTAC	GCTCAGCATCATTGTCATATTC
166	**At4g25990**	CDS	GTTCGGAGAAAGTGGTATGAGAG	CGTAGACCACTTAAATTCCTTG
167	**At4g18020**	CDS	CCGATCATTGCATCACTACTAC	CCTTATGAACAACATGCTGC
168	**At5g18240**	CDS	CCCATAAGTGATGCCCTTCAAATG	CCCAGCTGCACCTAGGTTCTG
169	**At5g24520**	CDS/3'UTR	GGTCTTCTTCGCAGCCTGATTG	GGAGCGCAAACCAAACCTAC
170	**At5g28770**	CDS	GGTGTTTCCGTCTCCTCTCC	GGAAGAAGCAAGAGAGGCTTG
171	**At5g18620**	CDS	CCATCAAAACGACCTTCGGG	CCTTGTCTCTAAGGAGCTTC
172	**At5g60580**	CDS	GGTACAGGTGCCATCGCTATATC	GGGCGAAGAGAACGACCAACGC

174	**At5g13220**	CDS/3'UTR	CCCATCGCAAGGAGAAAGTC	CCAAATCCAAAAACGAACATGG
176	**At5g06960**	5'UTR/CDS	CCACGTCTTTGCAGTTGTAG	CCATCTGTTGAGACTGATGTTC
177	**At5g59780**	CDS	GGACCGTGGACAGAACAGGAGG	GGCGTGAAGCTCAAGGACTAAAC
178	**At5g67580**	5'UTR	GCGAATCACATTTGATCTATG	GCTTAAGAACTCCAGCTTTAAG
179	**At5g48150**	5'UTR	CCTTGTCTCCGACAACTTTC	CCTAAGCTTCTCAACAGAGTTAG
181	**At5g05550**	CDS/3'UTR	GGAGAAGCAGAGAATGGAAG	GGATCCTCCAATTTCAATGAG
182	**At5g16820**	3'UTR	GGAGAATAATGACTTGGTATTGG	GGTAAATCTTTTATGTTTCTTC
183	**At5g22000**	3'UTR	CCTGAAACAAACAATGAGCAC	CCTTCTTCCTATGCTCCACAC
184	**At5g23090**	5'UTR	GGAGAGAGAAAATCCCTCCG	GGAAGAGAAGCGTCTTCCTTGG
185	**At5g23090**	CDS	GGATCCAATGGATATAGTCG	GGAGCAATCGTCCGTTTATCC
186	**At5g12840**	CDS	GGATTGATGGGAGCATATGG	GGCACGTGCTTTTCTTCGCC
187	**At5g02470**	5'UTR	CAGTTTGTTTGTTTGTTTATAG	CCAATTTCAGAATCATCATC
188	**At5g02840**	CDS	GCTGTTGATGAGAAACCTCAC	GCTGGTAGAGAGTTGTTGCG
189	**At5g43270**	5'UTR	CCTCTGGGATCCATAAGTTTTG	CCATCAATTTCCCACTCCATTG
190	**At5g56370**	5'UTR	GGGCAAAATGTCAAATTAGG	GGAAGCAATGACAGTATGCGC
191	**At5g18830**	CDS	GGAGCCAGACAGTCTTGTTCAC	GGATCAGTCTCTTTTCCGCC
192	**At2g46370**	5'UTR	CCTTTTTTCTCTCTCTCTCTCTATCC	CCACAGTTTTGTAAGTAAATGGC
193	**At1g07350**	CDS/3'UTR	CCTTGTCCTGGACCCATGGAC	CTCGAGCAGTTCTCAGCCCC
194	**At3g49430**	5'UTR	CCTCCGAGTATTGTTGGCTTCAGACC	CCTAATGTCACCGGGCAAGTTACC
195	**At3g01150**	CDS	GGCCAAAGAAGCACTGGAAGG	GGGTTCTGCCAACCTGCTGGTGG
196	**At3g01150**	CDS	CCATGAGATTGTTAACAATCAGAGTCC	CCAGCAGCTTTCTCAAATGTGGC
198	**At4g36690**	CDS	GGATGAGCTTAGAGATGATGAGG	GGCCTGCCACTGGCTGACCATTGG
199	**At1g79880**	CDS	GGGAGATGGAGAGAGAGTTGTGG	GGCTCCTTTCGGGCCTTCTTGG
200	**At1g79880**	CDS,/5'UTR	GGCCTCCTCCTTCAACGAAG	GGCCATCTTTGCTCTTGGTG
202	**At3g13570**	CDS	GGAGGCCATTTGAGCAGTTTGG	GGTTTTCTTCAGCAAATACGACAG
203	**At1g11650**	CDS/3'UTR	CCAGAGCTCTGCTGCAGGGGTAAC	CGCAAACAACAAGCAGAGTGAC
204	**At3g53500**	CDS/5'UTR	GGAAACACTCGCCTCTATGTTGG	GCGTCATCAGCATCACGAGG
205	**At3g61860**	CDS	GGCAATTTCGAGTATGAAACTCGCCAGTCGG	GGAAAATTGTCGAGTTTGCGAATAG
206	**At2g21660**	CDS	GGCGTCCGGTGATGTTGAGTATCGG	GGCTTTCTCATCCTTGAAGG
207	**At2g47580**	CDS	GGCGTTTAAGACCTTTAAGCACAAAGG	GGTTTTGGACAAAGAGAATATTATTTGG
208	**At1g09230**	CDS	CCGTCGGTTGTACTGTATATCAAAAACC	CTGCATTAGCCTCACACCAAGAC
209	**At2g16940**	CDS	GGAGTCAGGAAAGAGAAAAGCTTGG	GTTCTCTGATCTCTTTCAGG
210	**At4g02430**	CDS	CACATGCGTAAAGGAGGAGAAG	CCGAACATATTCATGAGAAAAC
212	**At4g02430**	CDS/3'UTR	CCTGCAAAATCTACATCGAGATCTCC	CTGTCCTAGCTCGATGGGTCC
213	**At5g53180**	CDS	GGATGTTGTGGGGAATGTTCTTCTGG	GGTATCCGGCTGTCTTCTCGAAAG
214	**At1g31600**	CDS	CTCGCTTCGACCTCTCTTTC	CTAACCACAGAGACTTTGTTCC
215	**At1g31600**	5'UTR	GACCATGTCCTGACCTTAAAGG	GGTAACAAGAAAAGCCCTGG
216	**At2g42890**	CDS	GTACACTTACAAGATGCTGGTGG	GGAAGGGAACGATGTGCAATGG
217	**At1g16610**	CDS	CCTAAACCTGTCTCAGCTGCACC	CCTTCTAGGTGATAAGCCTCTCC
218	**At2g30260**	CDS	CCACCGAATCAATCAATCTACATCC	CAGTGACTTCACTAAAAGTAACCC
219	**At4g25500**	CDS/5'UTR	GGTGACCTGGAACGACTATTCAGG	GCGGTCAAGTGCTCGGATGG
220	**At3g55460**	CDS	CCCTTTGAGAGGTTTGGACC	CCTGTTCATGCTTCTTTGAGCC
222	**At5g06160**	CDS	GGAGCCACCGTCCAGCAAGG	GTCGCAGTCTGGCCACCAAGCGCTG
223	**At2g29210**	CDS	GCAAATGAAATAATGAAGAAGAGGG	GTCAGCCCTTCTCCCATCCTCTGG
224	**At1g15200**	CDS	CAAAAGAAATTGGAATTGCTTTTCC	CCTCACTTGTATCTTCTTCC
225	**At3g53570**	5'UTR	CCGGCGATCAAATTACGACAGCGAC	CCGATGAGGGAATTCAACATTCC
226	**At4g24740**	CDS	GGTGTGAAGAAATACCGTGAGG	GGAGACTAACAGAATATTTTCTGG
227	**At4g24740**	CDS, 5'UTR	CCTCATACTCACATGGATCGTCGTCC	CCATTTCCTTCCTCTCCCTATCCC
228	**At4g32660**	CDS, 3'UTR	GGGGTGCTGAGAAATATTTCAGG	GCTGTGAGACGCTCAGATGG
229	**At4g35785**	3'UTR	GGTGCATTAAATATCTCAACCAG	GGAGCTTTTCAAGCCAAGATAGTGG
232	**At1g48960**	CDS	CCACGGCGGCGCGTCTCCTCCGCC	CCAACGAGAAGCATCGAAGCACC

233	**At5g54430**	CDS	GGTGGAGATGATGATGGAGATG	GGTGATATATTACTTAGATCCCACG
234	**At1g55870**	CDS	CTACATCAATGGATTTTCTTGCC	CCAACTTTAACTCTTCAGTTTCACC
235	**At1g69080**	CDS	GGAGAAGACGAATCTTGTG	GGCATGTTGTTTCTTCTGG
236	**At1g04950**	5'UTR	GGATCTTCGTCGCTCAACG	GGAGCAAGCATAAGAGCAGCTTCAGG
237	**At1g07830**	5'UTR	CCATTCTCTGTGGCCGTCACCGTCGCC	CCGAATCGTCGAGGCAGCTGCTGC
239	**At1g31500**	CDS/5'UTR	CTACAACTCTGCATCATCTTCC	CCTTCAACAGATTCAAATTTGC
241	**At1g02090**	CDS	CAAAAAACATCGTAAGGAAGC	CCCATCTTCTTCGTAGTCC
242	**At1g60850**	5'UTR	CTAAATTGCTCAATTCTCTCGGCC	CCGGCAGGGACGTCAGGGAGATC
243	**At2g33830**	CDS	CCGGACCTAAACCGGAGCATGGCC	CCGATCCTGGCGTCGTCGGAGTTCC
244	**At5g09230**	CDS	CATACAGTTCTGGTTTCAAACC	CCTGGTTGTGCTGCAGTGAACC
245	**At5g46110**	CDS/5'UTR	GGCGATCAACGGAGGAGAGAAAAG	GAAGAATCCAGTGACTAGCCATGG
246	**At5g59440**	CDS/5'UTR	GAAACGGATCTGCTCGGTTTCAAG	GGTTCTGACACCAGAAGAAAAG
249	**At1g72560**	3'UTR	GGCTTCAACAAAACGGGAGTCACG	GGATGGTGAAAGCGAACCTTG
251	**At1g37150**	CDS	GGACAAAGAGTGATTGCTGAAG	CCATCAGGATGAAGCTCATAC
254	**At5g50240**	CDS	CCGCTACAATTCATCATCATC	CCTCTATCTAAAGCCTCCATAAC
256	**At1g54080**	CDS	CCAGAGGTTACTGATGCAGC	CCATCAGAGCTATGTTTGTCC
259	**At3g17090**	CDS	GGGACTTTTGTTGGTGTTTACG	GGTATTTCTTGCCACAGCTCTG
260	**At3g26740**	CDS	CCAACTATTCTTCTTCCTCTTCC	CCACTGATTACTTCGCATGC
261	**At4g10100**	5'UTR	CTCATGTGTGTGGTATTCACC	CAGTGTTAGATCAGGCACACC
262	**At5g20040**	CDS	CCGGAGTCTCTAAGAATGAGC	CCACGCATGAAGCTTCACTC
264	**At5g65430**	CDS	CCGATCAGGCTTGGTTTGGC	CCGTCTTTTCTTCCATTAGACC
267	**At2g42245**	CDS	CAGGGTACATATGGGACTCC	CCCTAATTAATCTTCTTACGC
268	**At1g03457**	CDS	CCGTTGCAAGTTAAGTATGC	CCCTCTTAGAATCTGTAGATCC
270	**At1g53650**	CDS	CCATGTTCAAGAAACTCAATCC	CCTTAGAAGCTCTTCCAGGTAACC
272	**At3g23900**	3'UTR	GGATTATTCTTAAGTCATAGG	GGAGTGAAGGTGGTTCTTGG
273	**At3g07810**	CDS	GCTAGAAGTTCATCTCCAGG	GGAAAAGAAGATAATCTAAAAG
274	**At5g19030**	CDS	GGTTTTCGGATTCAGTGAGTGAAGG	GGCTTCGACAGCCGACTGTG
275	**At5g19030**	CDS	GGACTCGGCAGTCACTAGGATACGG	GGAAATCGGAATGTGGTCTCCGG
277	**At3g23830**	5'UTR	CCTCTTTTCTCACTCACTGTTAC	CCATTTGAGCTCTGAGAAACCCC
278	**At2g02570**	CDS	GGCAGCTTTTGTCAGAGGATCCTAGG	GGAGTTGCTTCAGCACTAACTCCGG
279	**At3g25840**	5'UTR/CDS	GGAGAGATTTTAGAAGAAGATGGG	GTTAGACTGCCTGCTGTTTGACGG
280	**At5g11200**	CDS	GGTACGTGGGAATACACAGTTCTGG	GGAGATGGTTCAATCTGTTGTAG
281	**At5g47210**	CDS	CCAAAGTGTTTGAGTCCATGCAAC	CCACCTCTCCCGTTGTACCTC
282	**At5g63120**	CDS/3'UTR	GGTGACAAGACCCAATCGG	GGTTCGACCAATCCTATGG
283	**At3g01540**	CDS	CCAAGTACCACCACCTCTAATGTCC	CCTACCTTGCATAGCAATGGGCC
284	**At4g33060**	CDS	GGAGAAGAAGCTGAAGAAGAGG	GAAAAGCTTTTATCTTTTTGAG
285	**At3g19840**	CDS	CCATATTCTGGTTCTCATCC	CCAGGCATCTAACCGATTTCC
286	**At1g67210**	CDS	GAACTCGATCCTCCTCCATGG	GAGGGCTAGCTTTTTCCAAG
288	**At3g12570**	5'UTR	CCATGTGTTGTACTAGTGCC	CCATGGATAGCAGTGTTGAC
289	**At3g12570**	5'UTR	GGGATCATTTTGATAGGAGCG	GGTGATAGTTCTCCATAGACAGG
291	**At2g46270**	CDS	CTCATTTCATTCTGTTTCTCC	CCTTAATCTTGACCTTCTAGC
292	**At4g36730**	CDS	GATGAAAGTGTCACAGCGGG	GGCTTCATGGGCACCGAACCTTGG
293	**At2g20180**	CDS/5'UTR	CCGATGATGATTATGTCAACAACC	CCATAGAAGGAAGAAGCTTC
295	**At2g02390**	CDS	GGCTTGATTATGAGTATATACCAG	GGTAACAAAGGTGGCTCAGGG
296	**At1g67980**	CDS	CACAAGATTAATTTTATCCATTCC	CCTTCACCAATTTTAGAAGCC
297	**At3g44300**	CDS	GGTGGATGTTTCGTATTGTCGG	GGTCAAGTGTAAAACATCTGG
298	**At5g09880**	CDS	GGGATGTGCGATTGATCATGG	GGGCTTAACCATCACAGG
299	**At5g11330**	CDS	CCTCAGGCTCGGCAGATCATC	CCGAATCGAAGACAAACACCC
300	**At5g59300**	CDS	CCGAAAATTCACAAAATCAGAACC	CAGGAGGTCCGATAATGGTAAC
301	**At5g09790**	CDS	CCCATTGTTGTTCGTGTCCCC	CCGTTAATGCAGAAGCAAGTGTTCC
302	**At5g09790**	CDS	CATCCTCCTGGTGATGATCC	CCTCAACGTTTGCTGGAGATTC
303	**At3g46460**	CDS	GGACTCAGTGGAGAAGAAGAAG	GAGGAACGCAACATTCTCCGG

304	**At5g18800**	5'UTR	CCGATCATCAATGGCCGCCGTGCC	CCACTGAGAATGATTTCCAAC
305	**At1g01060**	5'UTR	CCCGGTGAGATGATAAGTC	CCATCTTTGATCTCCCCAAAC
306	**At2g46830**	CDS/5'UTR	GGACTGAGGAAGAACATAATAG	GGTTTACGCTTAGGCCGTGG
307	**At3g11540**	CDS	GAGAAGGCTGCACTTGAGAGG	GAATCTGGATCTATCTTAAGG
308	**At5g10140**	CDS/3'UTR	GGAGGAACACCTTGAGACTG	GAGTCACCGGAAGATTGTCGG
309	**At5g65060**	CDS	CAAGGAGTTACTAGAAATAGTCC	CCCGTGACATTCCTCTGTCACC
310	**At5g65070**	CDS	CCGTCGCTCTTATCATCATCTC	CCGGTGACATTGCTCTTGCATCC
311	**At5g65080**	CDS	GTCAACTCTCAATTCTCTGTGG	GTGGCCAGAGCTATTTTCCGG
312	**At5g13790**	CDS	GGGTTACTTAAGAAAGCTCG	GTAGGATGGAACATAGTGGG
313	**At5g37055**	CDS	GGAAGAGATGTCGAACCGTCG	GCTGCTTTCAAGTAAGTCGG
314	**At2g43410**	CDS	GGGCTGGCTCTTACGATAACAG	GATGGCCTCCTCCAGTTTGG
315	**At4g31120**	CDS	CTCAACGAAAGTCAACAACC	CCAACCCAGTACGAACGGCC
316	**At2g28550**	CDS	CGAAATTGGTAACTCCGGTTCC	CCAAGAGTAAAGTTGATATC
317	**At2g28550**	CDS	CTTGGGAATCTCTTTATCGACC	CCCCAGTTACTCATCATCCC
318	**At5g48560**	CDS	GGACGCTCTTGTGTCAAAGG	GTTGAGATTCATTGTTGGGG
319	**At5g65640**	CDS	CCTCTGGTCAGAAACTCACC	CATTGTTCAATCTCCAAGCC
320	**At5g24590**	CDS	CCCTGAGGTTACAACCACC	CCACATCCTTTCGTCATAGTTTCC
321	**At4g27410**	CDS	CGATCTCTACAAGTTCGATCC	CTTGTAAATTCGACACAACACCC
322	**At2g33480**	CDS	CCGATGTTTGTAAATCCGATCC	CTGTCTCTTTCTCATTCTCC
323	**At1g76580**	CDS	GGGTAACTACGCGTCAATGG	GATTCAACTCTTTGCAAATCGTGG
324	**At5g43270**	5'UTR	GGGATCCATAAGTTTTGAG	GCTTGAAGAATACAGAGAGG
325	**At2g47890**	CDS	CCACGGATGTTCCTCCTCTGCC	CGAACCTTGCGTGATTCATACC
326	**At1g69250**	CDS	GGTCCTATCAAAGAAAACGGG	GGTCTGCAAGCATGAAGGGCG
327	**At5g59950**	CDS	CTGCTCCATACCAATCAGCC	CCACTTCTATCAAAATGAAC
328	**At5g52310**	CDS	GGTCAATGAGAAGGATCAAG	GATTGTGGTGACTCTTCAACGG
329	**At4g17615**	CDS	GCAGTTCGGTTGTTGATGATGG	GGGGTGGAAAACATTGAGTG
330	**At3g10300**	CDS	CTCCTTATGTATCTATTCACC	CCGCTTCTGTCCTTATCAAACC
331	**At3g10300**	CDS/5'UTR	CTTCACTTTTCTTTAGTCTTC	GGTAAAACAGTGAGCATGAAG
332	**At3g16800**	5'UTR	GAATATTCATATCAGAGAAG	GGCTATCACATGTCCCCATGG
333	**At3g16800**	CDS	CCCGGTTCAGCTCTCGGTAGAC	CCTCTTACTATCTCCACTGCC
334	**At1g01140**	CDS	CCATCATTGCATGTGGTAGAGC	CAGTATTCCAGACTACATCC
335	**At5g66210**	CDS/3'UTR	CAAAGACGGGTACATAACGCC	CCTCTTGCATCTAGTGCACC
336	**At5g28080**	5'UTR/CDS	GTTGAAGTTGATCCTACTGG	GAGCCTCTCTAGCTCTTGAGG
337	**At5g28080**	CDS	GTCAAGATTGGAGATCTTGG	GAGTCTAAGGGACACTGTGG
338	**At5g57630**	CDS	CAGATGCTAGAAAACTTTTCC	CCATACATCTACTGCTGCTCC
339	**At4g13020**	CDS	GTAGATACTTGTTCTTCAAGG	GGATGATTTAGCTTACGAAG
340	**At5g63990**	CDS	CGAGTTTCTTCGAGTCATACC	CTGCGTCGTAACGACGATTCC
341	**At2g15970**	CDS	CACTATCGCTGCTAAGAACC	CTACGAAAGCAATCCATTTACC
342	**At3g01090**	5'UTR/CDS	CCGAATTTTCTCCTCCGCC	CCAATACCAAGAGTTCTCCC
343	**At3g29160**	5'UTR	CCTGACTCAGCTCTGCGTCACC	CCCAATTCCAAGAGTTTTACC
344	**At3g29160**	CDS	CCTGTTATTGGATAACCGGTTCC	CCAAGAGCCCATTTTCGATCAAC
345	**At1g49730**	CDS	CTAAGCTGCATCACCGTAACC	CTTGATTTAATATCTCTATGAC
346	**At4g23260**	CDS	GGGAAGTGTATCCCTTCTCTGG	GGAAAAGTTGCTTGTCGCCG
347	**At4g34460**	CDS	CCAACTCCAGGTCTATCAGCC	CCTGTACACAAGGCACTTCC
348	**At4g34460**	CDS	CGCCTCCAGCTCCTCGATACC	CTTGAGATGCACTGACAATCC
349	**At5g40280**	CDS	CTTTAGGAGGTGACAAAGCCC	CCCTGGGTGAGTTCATCATCC
350	**At1g77740**	CDS	CAGCGGTGAGGCTAAGAAACC	CAGGATCCACCGTGAATAGCTCCC
351	**At2g18960**	CDS	CACTAGCAGAGCTATCTTCC	CGCTGAGAAGTCAAATTCCC
352	**At5g57110**	5'UTR	CTTACCGGAATTTTCTCTCC	CCCAGACTCCACATCGCCTCC
353	**At1g27770**	CDS	CGAAGCACTTCGAACTCTTTGCC	CTCACCAAAGTATGCTTATCC
354	**At5g23450**	5'UTR	CTTTTGCTGATACACTTCTCTCC	CGTCTAAGCGACTGTTGTGCC
355	**At3g16785**	CDS	CTCTCTTTGTGGTCCGAACACC	CCCAAATCGATCGTTGTGTGTCCC

356	**At3g56860**	3'UTR	CACTAAATGTATCATGTATCC	CGTTGAGAAGCTTGCACCAC
357	**At1g54100**	5'UTR	CATTTCTTCGATACGATCAACC	CCATATTTTAGCTGCTTCCTC
358	**At1g09000**	CDS	CCGTTACAGATAAATAACACC	CCATTACCAGGACTTTCGTC
359	**At2g38170**	CDS	GGAAATGCAGCTGAACATGCTGG	GGACCAGTCCCTTCATGTAG
360	**At3g06510**	CDS	CTCTACCAATGGGTGTATTCC	CCCGATTCACTGTATTCATC
361	**At4g13850**	CDS	CCTTAAGGGATGCTTTTGCTC	CCTCCTCTGTTTAGAAACCACC
362	**At4g26070**	CDS	CCTTCAAACTTGCTAATCAATC	CCTGCGTCGGTGAAGTAAGCC
363	**At5g24270**	CDS	GAGTTTGGTGAATTTGTCCGG	GGCAAAGTCATGTTCTTGATG
364	**At5g67030**	CDS	CCATCGATGCTTGACTGGGTCC	CCGAAACGCAACAATCGTCGCC
365	**At4g34000**	CDS	GGTGCAGTTCTGGAGAAAGTG	GCATCCCATTCCCCATGGCTGG
366	**At5g25610**	CDS	CCTCTGATCTGTCTTCTTGGTTC	CCAACGTTCACGGCGGTTCC
367	**At1g71860**	CDS / 3'UTR	CCACCTAGTCTCGGCCCAATC	CCCTCTCTAAGCAGACGAACC
368	**At1g78290**	5'UTR	CTTCCCAAGAAGATCAAATCC	CCTATGGTTCATGATTTCTC
369	**At4g31720**	5'UTR	CGTCTCAGCTCAATTCTCTTCC	CTCTTAGCCAAGTAGTGCTCC
370	**At5g35410**	CDS	CAGCAGAGTTTTCTTGTCCACC	CCAAGGATCTTTCTTGATTCC
371	**At5g37370**	CDS	GGACGGATGACGACAATGGG	GGGCAGTGTCTTCTGAGCCACGGG
372	**At1g76460**	CDS	GGTCGATCCAAAGGATATGG	GGAAGTGGTTGCTGATACGG
373	**At3g13224**	CDS	GTTGGTGGTATACCCTCAACGG	GGGTGACTACCGTAAGAAGG
374	**At4g36960**	5'UTR	GTTTAGGGCATCCTTGTGGG	GTAATCCTTAAGCCCATCGG
375	**At3g20270**	5'UTR	CTCAGGGATTACTTACTACC	CTCCGCGGAATAAATTAGCCC
376	**At1g64625**	CDS	GGGAGAAGTAGCTTCATCCGG	GAGTAGATCCTAGCTGAACAACG
377	**At3g51530**	CDS	CCGTCGTCGTATGTCTCTCTC	CCCATACTCCAACATAAACACC
378	**At3g62190**	CDS	CCTGATGATCAGAAGCTTGTTGCC	CCGAGGAACCCCAGTCTTGAC
379	**At5g04275**	pri- miRNA	GTTTGTTGTGTGTGAGACTTTGG	AGATGAGCTTTCTTCCATGG
380	**At5g08185**	pri -miRNA	GTCCATTTGGTTTCATAAGG	GCTTTCCCAGAAAAGTAATCGG
381	**At5g53450**	5'UTR/CDS	GGGAAAGAATCAAACTTTTG	GGTTTCGTTTATAACCAATG
382	**At1g44910**	CDS	GCAAAATTCAAGATAGACTGG	GGCTGTAAGGATGCCTGCAG
383	**At2g43640**	5'UTR	CCTTTTTACCGAAGAGACTCC	CCCTTCTCTTTGCTTTTCTC
384	**At4g02200**	CDS	GTGTCACCATATCGATGAGG	GACATCTCTATGCTGAGTGG
385	**At2g43810**	5'UTR	GGCTGCTTCATCGAGCGGAAG	GTTGAGCTTGACAACAACTGG
386	**At4g01250**	CDS	CCGGTAGCGTCACTAGCAAACCC	CTTGTTTACGGGCTAAACAACC
393	**At2g26150**	CDS	GGAAATGGAGGAAGAAACGG	GCCTCAACCTAACTACCTCAG
411	**At3g26744**	5'UTR	GGAGAAATAGTGACGGTGAG	GATCTTGTGGATGTGGTTGG
412	**At4g29810**	CDS	GGATTCAGCAATAATCTCAAG	GCTCAGCTGATCATCAGCTGG
413	**At2g33120**	CDS	CCTTCTTCTAACAACAAGTTTACC	CCATATCTCTTGTTGAAATCC

Supplemental Table 2

Gene transcripts significantly up-regulated in either *upf1-5, upf3-1* mutants and/or CHX treatment

Peaks that change significantly in both *upf* mutants and CHX treatment

Primer pair	Band Size (bp)	Gene Identifier	Gene name/function	Wt mean	SE	*upf1-5* mean	SE	p =<0.1	*upf3-1* mean	SE	p =<0.1	CHX mean	SE	p =<0.1	Exon No.	Transcript features	AS event	PTC to pA	Auth stop to pA
21	341	**At2g37340**	RS2Z33, RSZ33 (ARGININE/SERINE-RICH ZINC KNUCKLE-CONTAINING PROTEIN 33) - pre-mRNA splicing factor/ SR protein/ nucleic acid binding / nucleotide binding / zinc ion binding	**0.04**	0.00	**0.07**	0.01	0.064	**0.13**	0.04	0.000	**0.20**	0.03	0.000	7	PTC+; ds splice junctions	Alt 3' in IVS2 adds 218 nt.	**1070**	**225**
30	277	**At3g53270**	Unknown protein - similar to unnamed protein product [Vitis vinifera] (GB:CAO65717.1); contains domain PTHR15131 (PTHR15131)	**0.10**	0.01	**0.14**	0.01	0.012	**0.16**	0.01	0.001	**0.15**	0.01	0.004	9	No reason for NMD from AS event - uORFs	Alt 3'ss and alt 5'ss in IVS1 (5'UTR) - uORFs of 43 aas but in non-NMD isoforms also		
44	288	**At5g13730**	SIG4 (SIGMA FACTOR 4); DNA binding/ DNA-directed RNA polymerase/ transcription factor/ regulation of plastid-encoded RNA polymerase PEP	**0.22**	0.02	**0.53**	0.01	0.000	**0.56**	0.06	0.000	**0.46**	0.02	0.000	4	PTC+; ds splice junctions	Alt 3'ss in IVS2 adds 14 nt to transcript	**492**	**22**
50	190	**At5g43910**	pfkB-type carbohydrate kinase family protein	**0.35**	0.02	**0.48**	0.04	0.005	**0.56**	0.02	0.000	**0.44**	0.03	0.033	12	PTC+; ds splice junctions	Alt 3'ss in exon 10 removes 31 nt	**351**	**130**
72	190	**At2g04790**	Unknown protein - similar to unnamed protein product [Vitis vinifera] (GB:CAO23994.1)	**0.29**	0.02	**0.46**	0.04	0.000	**0.53**	0.04	0.000	**0.38**	0.01	0.007	4	PTC+; ds splice junctions	Alt 5'ss in IVS2 adds 23 nt	**348**	**133**
110	380	**At1g72050**	TFIIIA (TRANSCRIPTION FACTOR IIIA) - zinc finger (C2H2 type) family protein/ required for transcription of 5S rRNA genes	**0.61**	0.06	**0.72**	0.06	0.064	**0.86**	0.05	0.000	**0.91**	0.01	0.000	6 or 7	PTC+; ds splice junctions	Alt 3'ss and Alt 5'ss leave 175 nt of IVS2	**1329**	**242**
121	228	**At2g18300**	Basic helix-loop-helix (bHLH) family protein; transcription factor involved in response to cytokinin stimulus	**0.80**	0.07	**0.88**	0.02	0.076	**0.89**	0.01	0.050	**0.89**	0.01	0.060	6	No reason for NMD from AS event	Alt 3'ss in IVS 4 adds 6 nt in frame		
125	251	**At2g46790**	APRR9 (PSEUDO-RESPONSE REGULATOR 9) - transcription regulator/clock function - essential to temperature-sensitive circadian system	**0.22**	0.02	**0.32**	0.01	0.007	**0.47**	0.02	0.000	**0.37**	0.01	0.000	7	PTC+; ds splice junctions	Alt 5'ss in IVS2 adds 8 nt of IVS2	**1218**	**184**
143	329	**At3g12250**	TGA6 (TGA1a-related gene 6); DNA binding /basic leucine zipper transcription factor/ activation of SA-responsive genes factor	**0.03**	0.01	**0.08**	0.01	0.003	**0.11**	0.02	0.000	**0.07**	0.01	0.016	9	PTC+; ds splice junctions	Alt 5'ss in IVS2 adds 109 nt of IVS2	**1421**	**364**
193	294	**At1g07350**	Pre-mRNA splicing factor - Transformer serine/arginine-rich ribonucleoprotein, putative	**0.27**	0.02	**0.34**	0.02	0.067	**0.48**	0.07	0.000	**0.56**	0.02	0.000	7 or 8	PTC+; ds splice junctions	Alt 3'ss and alt 5'ss adds exon of 96nt from IVS4	**1072**	**307**
194	366	**At3g49430**	SR34A (SER/ARG-RICH PROTEIN 34A) - pre-mRNA splicing factor - SR protein	**0.07**	0.01	**0.21**	0.03	0.002	**0.35**	0.08	0.000	**0.30**	0.03	0.000	30	uORFs of 10, 30 and 61 aas - 61 aa uORF overlaps AUG of main ORFstops at AUG	Alt 3'ss and 5'ss includes 224 nt of IVS1		
206	349	**At2g21660**	ATGRP7 (GLYCINE-RICH RNA-BINDING PROTEIN 7), CCR2 (COLD-CIRCADIAN RHYTHM AND RNA BINDING 2) - RNA binding/ double-stranded DNA binding/ single-stranded DNA binding/ regulates circadian oscillations of GRP7/GRP8 transcript/ cold-induced/ response to salt and dehydration stress conditions/ mediates innate immune response.	**0.02**	0.00	**0.07**	0.03	0.031	**0.16**	0.08	0.000	**0.13**	0.00	0.004	2	PTC+; no ds splice junctions; long 3'UTR	Alt 5'ss in IVS1 (only intron) adds 166 nt	**778**	**228**
219	382	**At4g25500**	RS40 - pre-mRNA splicing factor/ SR protein/ RNA binding (previously ATRSP35 [Arabidopsis thaliana arginine/serine-rich splicing factor 35])	**0.14**	0.05	**0.33**	0.07	0.002	**0.54**	0.07	0.000	**0.34**	0.03	0.001	6	PTC+; ds splice junctions	Alt 3' and 5' ss in IVS2 includes new exon of 257 nt	**1390**	**197**
220	590	**At3g55460**	SCL30 (SC35-LIKE SPLICING FACTOR 30) - pre-mRNA splicing factor/ SR protein/ RNA binding	**0.01**	0.00	**0.05**	0.01	0.057	**0.11**	0.04	0.000	**0.08**	0.01	0.003	8	PTC+; ds splice junctions	Alt 3'ss and alt 5'ss leaves 449nt of IVS3	**1184**	**261**
224	236	**At1g15200**	Pinin - exon junction complex protein; protein-protein interaction regulator family protein	**0.11**	0.02	**0.19**	0.03	0.051	**0.27**	0.04	0.002	**0.39**	0.04	0.000	10	PTC+; ds splice junctions	Alt 3'ss and alt 5'ss leaves 104 nt of IVS8	**686**	**141**
237	273	**At1g07830**	RPL29 - ribosomal protein L29 family protein	**0.02**	0.00	**0.05**	0.01	0.016	**0.09**	0.01	0.000	**0.07**	0.02	0.001	4	uORF of 20 aas - predicted	Alt 5'ss in IVS1		
241	119	**At1g02090**	FUS5 (FUSCA 5), CSN7 (COP9 SIGNALOSOME SUBUNIT 7), COP15 (CONSTITUTIVE PHOTOMORPHOGENIC 15) - MAP kinase kinase/ phosphoprotein	**0.15**	0.08	**0.27**	0.01	0.060	**0.29**	0.02	0.006	**0.30**	0.01	0.001	9	PTC+; ds splice junctions	Alt 3'ss in exon 8 removes 17 nt.	**290**	**202**
244	131	**At5g09230**	SRT2 - member of SIR2 (sirtuin) family histone deacetylases (HDAC) - chromatin silencing/ DNA binding	**0.26**	0.02	**0.33**	0.01	0.066	**0.49**	0.06	0.000	**0.48**	0.02	0.000	11	PTC+; ds splice junctions	Alt 5'ss in IVS5 adds 11 nt from IVS	**913**	**176**
245	138	**At5g46110**	APE2 - ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT 2 - antiporter/ triose-phosphate transmembrane transporter/ involved in acclimation responses	**0.01**	0.01	**0.05**	0.00	0.013	**0.12**	0.03	0.000	**0.11**	0.01	0.000	12	PTC+; ds splice junctions	Alt 5'ss in IVS1 adds 7nt	**1402**	**444**
282	471	**At5g63120**	RH30 - ethylene-responsive putative DEAD box RNA helicase	**0.05**	0.01	**0.10**	0.02	0.037	**0.17**	0.04	0.000	**0.21**	0.02	0.000	10	PTC+; ds splice junctions	Alt 5' ss adds 294 nt from IVS8	**836**	**215**
285	207	**At3g19840**	PRP40C - Pre-mRNA-processing protein 40C/ binds CTD of RNA polymerase II/ scaffold for RNA processing machineries/ FF domain-containing protein / WW domain-containing protein	**0.66**	0.01	**0.72**	0.03	0.016	**0.81**	0.03	0.000	**0.87**	0.01	0.000	13	PTC+; ds splice junctions	Alt 5'ss in IVS2 adds 36 nt - No 3'UTR in TAIR	**1800**	
298	219	**At5g09880**	RNA recognition motif (RRM)-containing protein	**0.14**	0.00	**0.19**	0.01	0.081	**0.23**	0.03	0.002	**0.22**	0.02	0.007	13	PTC+; ds splice junctions	Alt 3'ss and alt 5'ss in IVS4 leaves 76nt of IVS4 in transcript	**1171**	**204**
301	275	**At5g09790**	ATXR5/SDG15 (SETDOMAIN GROUP 15) - contains SET-domain and PCNA-binding domain/ DNA binding/ possible role in cell-cycle regulation or progression.	**0.03**	0.00	**0.07**	0.01	0.001	**0.09**	0.00	0.000	**0.06**	0.01	0.002	5	PTC+; ds splice junctions	Predicted - Alt 5'ss in exon 1 removes 7 nt and alt 3'' ss in exon 2 removes 3nt	**930**	**233**
309	223	**At5g65060**	MAF3 - MADS AFFECTING FLOWERING 3 - MADS domain protein/flowering regulator/ transcription factor/ closely related to FLC	**0.19**	0.01	**0.35**	0.01	0.000	**0.42**	0.00	0.000	**0.38**	0.02	0.000	7	PTC+; ds splice junctions	Alt 3'ss in exon 4 removes 38 nt	**446**	**250**
310	368	**At5g65070**	MAF4 - MADS AFFECTING FLOWERING 4 - MADS domain protein/flowering regulator/ transcription factor/ closely related to FLC	**0.02**	0.01	**0.06**	0.01	0.007	**0.07**	0.01	0.003	**0.10**	0.02	0.000	7 or 8	PTC+; ds splice junctions	Exon 2 and 3 skip	**518**	**165**
327	421	**At5g59950**	Aly/REF - RNA and export factor-binding protein, putative	**0.16**	0.04	**0.30**	0.04	0.021	**0.47**	0.05	0.000	**0.41**	0.08	0.001	5	PTC+; ds splice junctions	IVS1 retained (196nt)	**1063**	**354**
344	195	**At3g29160**	AKIN11 (ARABIDOPSIS SNF1 KINASE HOMOLOG 11) - SNF1-related protein kinase - interacts with SCF subunit SKP1/ASK1 and 20S proteosome subunit PAD1	**0.08**	0.01	**0.12**	0.01	0.057	**0.17**	0.02	0.000	**0.15**	0.02	0.002	11	PTC+; ds splice junctions	Alt 3'ss in exon 9 removes 5 nt	**722**	**268**
345	274	**At1g49730**	Protein kinase family protein	**0.08**	0.01	**0.16**	0.02	0.012	**0.21**	0.06	0.001	**0.20**	0.02	0.001	9 or 10	PTC+; ds splice junctions	Alt 3'ss in IVS6 adds 37 nt	**773**	**112**
370	120	**At5g35410**	SOS2 (SALT OVERLY SENSITIVE 2), CIPK24 (CBL-INTERACTING PROTEIN KINASE 24) - kinase/ regulatory component controlling plant potassium nutrition	**0.42**	0.01	**0.49**	0.01	0.020	**0.59**	0.03	0.000	**0.63**	0.01	0.000	14	PTC+; ds splice junctions	Alt 3'ss in IVS8 adds 5 nt	**775**	**233**
375	195	**At3g20270**	Lipid-binding serum glycoprotein family protein	**0.54**	0.01	**0.62**	0.03	0.004	**0.64**	0.01	0.000	**0.59**	0.01	0.053	11	uORF of 22 aas overlaps start of main ORF	Fully spliced		**80**
378	218	**At3g62190**	DNAJ heat shock N-terminal domain-containing protein	**0.09**	0.00	**0.13**	0.01	0.095	**0.16**	0.01	0.004	**0.17**	0.01	0.002	6	PTC+; ds splice junctions	IVS4 (75 nt) retained	**1091**	**718**
384	149	**At4g02200**	Drought-induced-19-like 1 - drought-responsive family protein	**0.06**	0.01	**0.13**	0.02	0.032	**0.21**	0.03	0.000	**0.22**	0.03	0.000	5 or 6	PTC+; ds splice junctions	Alt 5'ss in IVS2 adds 32 nt	**496**	**114**
393	565	**At2g26150**	ATHSFA2 (Arabidopsis thaliana HEAT SHOCK TRANSCRIPTION FACTOR A2) - DNA binding/ Involved in response to misfolded protein accumulation in the cytosol	**0.66**	0.05	**0.79**	0.02	0.008	**0.84**	0.01	0.001	**0.85**	0.01	0.001	2 or 3	PTC+; ds splice junctions	Alt 3' and alt 5' splice sites add 31 nt of IVS1 as a mini-exon.	**1217**	**179**

Peaks that change significantly in both *upf* mutants

Primer pair	Band Size (bp)	Gene Identifier	Gene name/function	Wt mean	SE	*upf1-5* mean	SE	p =<0.1	*upf3-1* mean	SE	p =<0.1	CHX mean	SE	p =<0.1		Transcript features	AS event	PTC to pA	Auth stop to pA
106	236	**At1g49950**	TRB1 - TELOMERE REPEAT BINDING FACTOR 1 - telomeric DNA binding protein/ DNA binding / transcription factor	**0.08**	0.01	**0.13**	0.00	0.001	**0.12**	0.01	0.006	**0.10**	0.01	>0.1	7	No reason for NMD from AS event - uORFs	Alt 5'ss in IVS1 leaves 45 nt of IVS1 in transcript		
109	118	**At1g77080**	FLM (FLOWERING LOCUS M), MAF1 (MADS AFFECTING FLOWERING 1) - MADS domain protein/flowering regulator/ transcription factor/ closely related to FLC	**0.14**	0.03	**0.22**	0.05	0.070	**0.29**	0.05	0.003	**0.19**	0.02	>0.1	7	PTC+; ds splice junctions	Alt 3' ss removes 38 nt from exon 4.	**468**	**251**
141	202	**At3g51880**	HMGB1 (HIGH MOBILITY GROUP B 1), NFD1 (NUCLEOSOME/CHROMATIN ASSEMBLY FACTOR D1) - transcription factor	**0.88**	0.06	**0.94**	0.01	0.012	**0.94**	0.01	0.011	**0.90**	0.01	>0.1	8	No reason for NMD from AS event	Alt 5'ss in exon 7 in frame		
200	104	**At1g79880**	La domain-containing protein	**0.08**	0.02	**0.13**	0.02	0.041	**0.13**	0.02	0.044	**0.06**	0.01	>0.1	11	PTC+; ds splice junctions	Alt 3' ss in in exon 2 removes 17 nt	**1401**	**194**
229	153	**At4g35785**	Transformer serine/arginine-rich ribonucleoprotein; Nucleic acid binding / nucleotide binding	**0.07**	0.01	**0.11**	0.01	0.020	**0.12**	0.01	0.001	**0.07**	0.01	>0.1	8	PTC+; no ds splice junctions; long 3'UTR	Alt 3'ss and alt 5'ss adds alternative exon of 37 nt	**441**	**248**

Supplemental Table 2

229	281	**At4g35785**	Transformer serine/arginine-rich ribonucleoprotein; Nucleic acid binding / nucleotide binding	**0.10**	0.00	**0.13**	0.02	0.019	**0.14**	0.01	0.003	**0.12**	0.01	>0.1	8	PTC+; no ds splice junctions; long 3'UTR	Alt 3'ss and alt 5'ss adds alternative exon of 166 nt	**441**	**248**
251	106	**At1g37150**	HCS2 (HOLOCARBOXYLASE SYNTHETASE 2) - catalytic/ involved in protein modification - biotin-[acetyl-CoA-carboxylase] ligase activity	**0.20**	0.06	**0.33**	0.07	0.093	**0.43**	0.07	0.007	**0.24**	0.03	>0.1	10	PTC+; ds splice junctions	Alt 3'ss in exon 9 which removes 28 nt from the transcript.	**116**	**48**
324	270	**At5g43270**	correct development of lateral organs in association with shoot maturation in the reproductive phase (with SPL10 and SPL11)	**0.07**	0.01	**0.11**	0.01	0.086	**0.11**	0.02	0.062	**0.07**	0.01	>0.1	5	uORFs of 9, 12 and 5 aas	Alt 5'ss in IVS1 (5'UTR intron) leaves 84 nt of IVS in transcript		
372	314	**At1g76460**	RNA recognition motif (RRM)-containing protein	**0.05**	0.01	**0.08**	0.01	0.081	**0.12**	0.00	0.001	**0.08**	0.02	>0.1	8	PTC+; ds splice junctions	Alt 3'ss in IVS1 adds 54 nt to transcript	**1340**	**650**
374	399	**At4g36960**	RNA recognition motif (RRM)-containing protein	**0.05**	0.01	**0.15**	0.02	0.005	**0.32**	0.05	0.000	**0.09**	0.01	>0.1	13	uORFs of 38 and 73 aas - 73 aa uORF overlaps AUG of main ORF	IVS1 (5' UTR) retained		

Peaks that change significantly in *upf3-1* and CHX treatment

Primer pair	Band Size (bp)	Gene Identifier	Gene name/function	Wt mean	SE	*upf1-5* mean	SE	p =<0.1	*upf3-1* mean	SE	p =<0.1	CHX mean	SE	p =<0.1		Transcript features	AS event	PTC to pA	Auth stop to pA
7	361	**At1g55310**	SCL33, SR33 (SC35-like splicing factor 33) - pre-mRNA splicing factor/ SR protein/ RNA binding	**0.15**	0.01	**0.19**	0.01	>0.1	**0.32**	0.09	0.001	**0.47**	0.04	0.027	11 or 12	PTC+; ds splice junctions	Alt 3'ss in IVS3 adds 162 nt to transcript from IVS3	**875**	**203**
7	364	**At1g55310**	SCL33, SR33 (SC35-like splicing factor 33) - pre-mRNA splicing factor/ SR protein/ RNA binding	**0.02**	0.00	**0.03**	0.00	>0.1	**0.05**	0.02	0.001	**0.08**	0.00	0.058	11 or 12	PTC+; ds splice junctions	Alt 3'ss and alt 5'ss adds 165nt of IVS3 - also alt 3'ss (NAGNAG) in IVS3 adds 165 nt	**974**	**203**
47	203	**At5g20250**	DIN10 (DARK INDUCIBLE 10) - member of glycosyl hydrolase family 36/ hydrolyzing O-glycosyl compounds	**0.24**	0.02	**0.28**	0.01	>0.1	**0.33**	0.01	0.001	**0.33**	0.00	0.001	5	uORF of 90 aas - overlaps AUG of main ORF	Fully spliced		
58	237	**At5g65050**	MAF2 (MADS AFFECTING FLOWERING 2), AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31) - transcription factor/ MADS box genes involved in control of flowering time	**0.02**	0.00	**0.04**	0.00	0.000	**0.05**	0.01	0.000	**0.06**	0.00	0.000	7	PTC+; ds splice junctions	Alt 3'ss in exon 5 removes 4nt	**388**	**212**
82	213	**At3g14230**	RAP2.2 - member of the ERF (ethylene response factor) subfamily B-2 of ERF/AP2 transcription factor family/ DNA binding	**0.14**	0.00	**0.13**	0.01	>0.1	**0.18**	0.01	0.009	**0.17**	0.01	0.018	3	SJ 45 nt downstream (<50-55nt); Long 3' UTR	Alt 5'ss in exon 1 removes 12 nt and alt 3'ss in exon 2 removes 3nt in frame		**372**
86	396	**At4g16845**	VRN2 (REDUCED VERNALIZATION RESPONSE 2) - transcription factor/ mediates vernalization/ encodes zinc finger protein similar to Polycomb group (PcG) proteins/ maintains FLC repression cold treatment	**0.07**	0.00	**0.09**	0.00	>0.1	**0.12**	0.02	0.008	**0.13**	0.01	0.002	15	PTC+; ds splice junctions	Alt 5'ss in IVS5 adds 22nt of IVS5 to transcript and alt 3' ss in exon 5 removes 4 nt and IVS2 unspliced	**1522**	**153**
90	316	**At4g39260**	ATGRP8 (GLYCINE-RICH RNA-BINDING PROTEIN 8), CCR1 (COLD-CIRCADIAN RHYTHM AND RNA BINDING 1) - regulates circadian oscillations of GRP7/GRP8 transcripts/ cold-induced/ RNA binding	**0.03**	0.00	**0.05**	0.01	>0.1	**0.12**	0.04	0.003	**0.14**	0.02	0.001	2 or 3	PTC+; ds splice junctions	Alt 5'ss in IVS1 leaves 158 nt of intron	**779**	**267**
118	233	**At2g02960**	Zinc finger (C3HC4-type RING finger) family protein	**0.03**	0.00	**0.05**	0.00	>0.1	**0.07**	0.01	0.002	**0.07**	0.01	0.001	6	uORFs of 8 and 26 aas; 26 aa uORF overlaps AUG of main ORF	Predicted alt 3'ss in IVS1 adds 37 nt		
118	237	**At2g02960**	Zinc finger (C3HC4-type RING finger) family protein	**0.04**	0.00	**0.05**	0.00	>0.1	**0.07**	0.01	0.010	**0.07**	0.01	0.007	6	uORFs of 8 and 26 aas; 26 uORF overlaps AUG of main ORF.	Predicted alt 3'ss in IVS1 adds 41 nt		
131	373	**At2g38880**	NF-YB1 (NUCLEAR FACTOR Y SUBUNIT B1), HAP3A (HEME ACTIVATOR PROTEIN (YEAST) HOMOLOG 3A) - transcription factor/ confers drought tolerance	**0.21**	0.02	**0.26**	0.02	>0.1	**0.30**	0.03	0.069	**0.41**	0.06	0.001	7	Intron in 3'UTR	Alt 5'ss in IVS6 which adds 62 nt to transcript		
195	156	**At3g01150**	PTB1 - POLYPYRIMIDINE TRACT-BINDING PROTEIN 1 - pre-mRNA splicing - role in pollen germination	**0.10**	0.03	**0.12**	0.02	>0.1	**0.16**	0.02	0.021	**0.19**	0.02	0.001	9	PTC+; no ds splice junction - possible long 3'UTR	Alt 5'ss in exon 8 removes 47 nt of exon 8	**370**	**162**
196	268	**At3g01150**	PTB1 - POLYPYRIMIDINE TRACT-BINDING PROTEIN 1 - pre-mRNA splicing - role in pollen germination	**0.11**	0.02	**0.17**	0.03	>0.1	**0.25**	0.07	0.016	**0.37**	0.05	0.000	9	PTC+; ds splice junctions	Alt 3'ss and alt 5'ss includes 102 nt from IVS2	**1050**	**162**
202	351	**At3g13570**	SCL30A (SC35-LIKE SPLICING FACTOR 30A) - pre-mRNA splicing factor/ SR protein/ RNA binding	**0.18**	0.01	**0.30**	0.01	>0.1	**0.48**	0.12	0.002	**0.52**	0.05	0.001	6	PTC+; ds splice junctions	IVS3	**958**	**266**
204	376	**At3g53500**	RS2Z32 - pre-mRNA splicing factor / SR protein/ nucleic acid binding	**0.09**	0.01	**0.11**	0.03	>0.1	**0.25**	0.06	0.000	**0.40**	0.02	0.000	7	PTC+; ds splice junctions	Alt 3'ss in in IVS2 leaves 218 of IVS2 in transcript	**1122**	**214**
205	556	**At3g61860**	RS31 (ARGININE/SERINE-RICH SPLICING FACTOR 31) - pre-mRNA splicing factor/ SR protein/ RNA binding	**0.01**	0.00	**0.04**	0.00	>0.1	**0.10**	0.04	0.012	**0.27**	0.07	0.000	6	PTC+; ds splice junctions	Alt 3'ss adding 513 nt from IVS2 plus alt 5'ss in IVS2 removes another 120 nt at 3' end of IVS2	**1215**	**243**
209	227	**At2g16940**	RNA recognition motif (RRM)-containing protein	**0.06**	0.01	**0.07**	0.01	>0.1	**0.13**	0.04	0.001	**0.19**	0.01	0.000	14	Unknown			
213	198	**At5g53180**	PTB2, POLYPYRIMIDINE TRACT-BINDING PROTEIN 2 - pre-mRNA splicing - role in pollen germination	**0.08**	0.01	**0.12**	0.02	>0.1	**0.19**	0.07	0.008	**0.31**	0.02	0.000	9	PTC+; ds splice junctions	Alt 5' and 3' adds 58nt from IVS3	**1109**	**213**
213	201	**At5g53180**	PTB2, POLYPYRIMIDINE TRACT-BINDING PROTEIN 2 - pre-mRNA splicing - role in pollen germination	**0.06**	0.00	**0.09**	0.01	>0.1	**0.14**	0.05	0.006	**0.22**	0.01	0.000	9	PTC+; ds splice junctions	Alt 5' and 3' adds 61nt from IVS3	**1112**	**213**
217	175	**At1g16610**	SR45 (ARGININE/SERINE-RICH 45), RNPS1 - pre-mRNA splicing factor/ exon junction complex protein/ heterochromatic siRNA pathway/ involved in plant sugar response	**0.68**	0.02	**0.71**	0.03	>0.1	**0.72**	0.01	0.062	**0.77**	0.02	0.001	12	No reason for NMD from AS event			
218	134	**At2g30260**	U2B''(U2 SMALL NUCLEAR RIBONUCLEOPROTEIN B'') - component of the U2 snRNP complex/ RNA binding	**0.05**	0.00	**0.09**	0.01	>0.1	**0.19**	0.03	0.000	**0.17**	0.02	0.000	5	PTC+; ds splice junctions	Alt 5'ss removes 35 nt from exon 2.	**729**	**195**
220	673	**At3g55460**	SCL30 (SC35-LIKE SPLICING FACTOR 30) - pre-mRNA splicing factor / SR protein/ RNA binding	**0.01**	0.00	**0.02**	0.00	>0.1	**0.05**	0.03	0.008	**0.13**	0.02	0.000	8	Unknown			
223	202	**At2g29210**	Splicing factor PWI domain-containing protein	**0.36**	0.04	**0.36**	0.08	>0.1	**0.59**	0.02	0.009	**0.63**	0.04	0.004	11	PTC+; ds splice junctions	Alt 3'ss in IVS5 which adds 50 nt from IVS5	**2327**	**180**
226	143	**At4g24740**	AFC2 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 2) - LAMMER kinase/ putative role in phosphorylation of SR protein splicing factors	**0.11**	0.01	**0.17**	0.04	>0.1	**0.27**	0.02	0.002	**0.19**	0.02	0.075	12	PTC+; ds splice junctions	Exons 5 and 6 skipped - removes 164 nt	**810**	**200**
229	302	**At4g35785**	Transformer serine/arginine-rich ribonucleoprotein; Nucleic acid binding / nucleotide binding	**0.02**	0.00	**0.03**	0.00	0.058	**0.05**	0.01	0.001	**0.07**	0.00	0.000	8	PTC+; ds splice junctions	Alt 3'ss and alt 5'ss adds alternative exon of 187 nt	**531**	**248**
268	109	**At1g03457**	RNA-binding protein, putative	**0.22**	0.05	**0.27**	0.02	>0.1	**0.44**	0.12	0.045	**0.68**	0.08	0.001	9	Unknown			
278	221	**At2g02570**	SPF30 - Nucleic acid binding	**0.00**	0.00	**0.01**	0.00	>0.1	**0.03**	0.01	0.004	**0.06**	0.01	0.000	9	Unknown			
279	341	**At3g25840**	Protein kinase family protein	**0.10**	0.01	**0.09**	0.01	>0.1	**0.14**	0.01	0.061	**0.22**	0.03	0.000	14	PTC+; ds splice junctions	Alt 3' and 5' SS adds 56 nt from IVS1.	**2828**	**330**
280	357	**At5g11200**	UAP56a - DEAD/DEAH box helicase - exon junction protein	**0.07**	0.02	**0.11**	0.02	>0.1	**0.18**	0.04	0.001	**0.25**	0.01	0.000	15	PTC+; ds splice junctions	Alt 3'ss in IVS3 adds 136 nt to transcript.	**1521**	**329**
283	480	**At3g01540**	DRH1 (DEAD BOX RNA HELICASE 1)	**0.01**	0.00	**0.02**	0.00	>0.1	**0.05**	0.02	0.009	**0.06**	0.01	0.001	9	PTC+; ds splice junctions	Alt 3'ss in IVS4 leaves 345 nt of IVS4	**1772**	**326**
284	290	**At4g33060**	CYP57 (Cyclophilin 57; Peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein)	**0.26**	0.05	**0.34**	0.03	>0.1	**0.49**	0.06	0.002	**0.71**	0.04	0.000	10	PTC+; ds splice junctions	Alt 3' and alt 5' ss in IVS5 which adds 87 nt to transcript	**1112**	**269**
284	295	**At4g33060**	CYP57 (Cyclophilin 57; Peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein)	**0.05**	0.01	**0.06**	0.00	>0.1	**0.08**	0.01	0.017	**0.11**	0.01	0.000	10	PTC+; ds splice junctions	Alt 3' and alt 5' ss in IVS5 which adds 92 nt to transcript	**1066**	**269**
298	299	**At5g09880**	RNA recognition motif (RRM)-containing protein	**0.10**	0.01	**0.11**	0.01	>0.1	**0.18**	0.06	0.018	**0.33**	0.01	0.000	13	PTC+; ds splice junctions	Two alt 3'ss and alt 5'ss includes two new exons of 76 and 81 nt in IVS4	**1252**	**204**
303	171	**At3g46460**	UBC13 (UBIQUITIN-CONJUGATING ENZYME 13) - ubiquitin potein ligase	**0.08**	0.01	**0.10**	0.01	>0.1	**0.14**	0.02	0.078	**0.20**	0.02	0.017	6	PTC+; ds splice junction	Alt 5'ss in IVS4 which adds 31 nt to transcript	**391**	**240**
306	218	**At2g46830**	CCA1, CIRCADIAN CLOCK ASSOCIATED 1 - transcription factor/ Myb-like transcriptional repressor in regulating circadian rhythms/ binds evening element in TOC1 to repress TOC1	**0.79**	0.03	**0.85**	0.04	>0.1	**0.87**	0.05	0.047	**0.89**	0.01	0.019	8	No reason for NMD from AS event - other AS/NMD events known	Fully spliced		

Supplemental Table 2

309	219	**At5g65060**	MAF3 - MADS AFFECTING FLOWERING 3 - MADS domain protein/flowering regulator/ transcription factor/ closely related to FLC	**0.04**	0.00	**0.06**	0.00	0.006	**0.08**	0.00	0.000	**0.07**	0.01	0.000	7	PTC+; ds splice junctions	Alt 3'ss in exon 4 removes 38 nt from exon 4 plus alt 3'ss in exon 5 removes 4 nt from exon 5	**442**	**250**
313	346	**At5g37055**	SEF (SERRATED LEAVES AND EARLY FLOWERING), SWC6 (homologue of yeast SWC6 protein) - conserved subunit of SWR1/SRCAP complex.	**0.02**	0.00	**0.04**	0.00	0.001	**0.05**	0.00	0.000	**0.05**	0.00	0.000	4	PTC+; ds splice junctions	Alt 3'ss in exon 2 removes 10 nt	**354**	**83**
316	262	**At2g28550**	TOE1 (TARGET OF EAT1 1), RAP2.7 (RELATED TO AP2.7) - DNA binding/ transcription factor	**0.93**	0.01	**0.94**	0.01	>0.1	**0.96**	0.02	0.071	**0.97**	0.00	0.013	8	No reason for NMD	Fully spliced		**217**
332	568	**At3g16800**	PP2C (Protein phosphatase 2C), putative	**0.05**	0.00	**0.07**	0.01	0.037	**0.10**	0.01	0.000	**0.10**	0.01	0.000	6	PTC+; ds splice junctions	IVS 2 retained	**1253**	**262**
343	159	**At3g29160**	AKIN11 (ARABIDOPSIS SNF1 KINASE HOMOLOG 11) - SNF1-related protein kinase - interacts with SCF subunit SKP1/ASK1 and 20S proteosome subunit PAD1	**0.27**	0.03	**0.27**	0.02	>0.1	**0.34**	0.06	0.088	**0.40**	0.01	0.005	11	No reason for NMD from AS event - other AS/NMD events known	Fully spliced		
347	221	**At4g34460**	AGB1 (GTP BINDING PROTEIN BETA 1), ELK4 (ERECTA-LIKE 4) - heterotrimeric G-protein beta subunit involved in organ shape/ nucleotide binding	**0.01**	0.00	**0.02**	0.01	>0.1	**0.04**	0.02	0.041	**0.05**	0.01	0.004	6	PTC+ - predicted transcript	Predicted alt 5'ss and alt 3'ss in IVS4	**388**	**287**
360	343	**At3g06510**	SFR2 (SENSITIVE TO FREEZING 2) - encodes protein with beta-glucosidase activity/ hydrolase - hydrolyzing O-glycosyl compounds/ freezing response	**0.01**	0.00	**0.02**	0.00	0.004	**0.04**	0.01	0.000	**0.04**	0.00	0.000	9 or 10	PTC+; ds splice junctions	Alt 3'ss IVS6 adds 28 nt	**886**	**141**
360	307	**At3g06510**	SFR2 (SENSITIVE TO FREEZING 2) - encodes protein with beta-glucosidase activity/ hydrolase - hydrolyzing O-glycosyl compounds/ freezing response	**0.02**	0.01	**0.04**	0.03	0.048	**0.06**	0.02	0.000	**0.10**	0.07	0.000	9 or 10	PTC+; ds splice junctions	Alt 3'ss in exon 7 removes 7 nt from exon 7	**848**	**141**
363	337	**At5g24270**	SOS3 (SALT OVERLY SENSITIVE 3), CBL4 (CALCINEURIN B-LIKE PROTEIN 4) - encodes a calcium sensor essential for K+ nutrition, K+/Na+ selectivity, and salt tolerance	**0.06**	0.01	**0.08**	0.01	>0.1	**0.13**	0.05	0.008	**0.25**	0.02	0.000	9	PTC+; ds splice junctions	Alt 5'SS in IVS5 adds 29 nt - No 3'UTR in TAIR		
383	143	**At2g43640**	SRP14, signal recognition particle 14 kDa family protein	**0.07**	0.01	**0.09**	0.01	0.091	**0.12**	0.03	0.006	**0.11**	0.01	0.013	5	uORF of 19 aas overlaps with AUG of main ORF	Alt 5'ss in IVS1 and exon 2 skip		

Peaks that change significantly in *upf 1-5* only

Primer pair	Band Size (bp)	Gene Identifier	Gene name/function	Wt mean	SE	*upf1-5* mean	SE	p =<0.1	*upf3-1* mean	SE	p =<0.1	CHX mean	SE	p =<0.1		Transcript features	AS event	PTC to pA	Auth stop to pA
124	140	**At2g37060**	NF-YB8, NUCLEAR FACTOR Y, SUBUNIT B8	**0.07**	0.04	**0.21**	0.07	0.059	**0.15**	0.05	>0.1	**0.13**	0.03	>0.1	7	Unknown			
249	174	**At1g72560**	PSD, PAUSED - encodes a karyopherin/ ortholog of LOS1/XPOT/ tRNA binding/ mediates nuclear export of tRNAs	**0.04**	0.00	**0.15**	0.10	0.028	**0.04**	0.01	>0.1	**0.05**	0.00	>0.1	14	Intron in 3' UTR	Alt 5'ss in 3'UTR intron adds 25 nt - distance from authentic stop to splice junction is 68nt		
254	198	**At5g50240**	PIMT2 (PROTEIN-L-ISOASPARTATE METHYLTRANSFERASE 2)	**0.19**	0.04	**0.41**	0.16	0.081	**0.15**	0.07	>0.1	**0.10**	0.02	>0.1	4	Unknown			
311	462	**At5g65080**	MAF5 (MADS AFFECTING FLOWERING 5)	**0.76**	0.04	**0.82**	0.02	0.089	**0.80**	0.01	>0.1	**0.75**	0.02	>0.1	7	PTC+; ds splice junctions	Alt 3' SS in exon 5 removes 4 nt	**433**	**254**

Peaks that change significantly in *upf 3-1* only

Primer pair	Band Size (bp)	Gene Identifier	Gene name/function	Wt mean	SE	*upf1-5* mean	SE	p =<0.1	*upf3-1* mean	SE	p =<0.1	CHX mean	SE	p =<0.1		Transcript features	AS event	PTC to pA	Auth stop to pA
7	293	**At1g55310**	SCL33, SR33 (SC35-like splicing factor 33) - pre-mRNA splicing factor/ SR protein/ RNA binding	**0.05**	0.00	**0.08**	0.01	>0.1	**0.09**	0.01	0.035	**0.07**	0.01	0.074	6	Unknown			
12	215	**At1g72320**	APUM23 (ARABIDOPSIS PUMILIO 23) - member of Pumilio RNA-binding protein family/ regulates mRNA stability and translation by sequence-specific binding to 3' UTR of target mRNAs	**0.53**	0.11	**0.66**	0.05	>0.1	**0.68**	0.02	0.097	**0.61**	0.08	>0.1	6	No reason for NMD from AS event			
19	202	**At2g32330**	Unknown protein	**0.34**	0.02	**0.39**	0.02	>0.1	**0.42**	0.01	0.019	**0.35**	0.02	>0.1	15	PTC+; ds splice junctions	Alt 3'ss in exon 10 that removes 71 nt	**931**	**339**
43	112	**At5g09230**	SRT2 - member of SIR2 (sirtuin) family histone deacetylases (HDAC) - chromatin silencing/ DNA binding	**0.13**	0.00	**0.08**	0.03	>0.1	**0.23**	0.03	0.045	**0.18**	0.01	>0.1	11	No reason for NMD from AS event - other AS/NMD events known	Exon 2 skip - incl. AUG		
108	259	**At1g30200**	F-box family protein	**0.37**	0.01	**0.39**	0.01	>0.1	**0.41**	0.01	0.034	**0.39**	0.01	>0.1	2	No reason for NMD from AS event	Transcripts have long 3'UTRs - do not correlate with NMD		**473**
128	381	**At2g15530**	zinc finger (C3HC4-type RING finger) family protein	**0.17**	0.00	**0.19**	0.02	>0.1	**0.22**	0.03	0.046	**0.20**	0.01	>0.1	7	No reason for NMD from AS event - uORFs	Multiple small uORFs in 5' UTR of fully spliced and AS		
160	341	**At4g14410**	basic helix-loop-helix (bHLH) family protein	**0.06**	0.02	**0.10**	0.02	>0.1	**0.36**	0.21	0.014	**0.08**	0.02	>0.1	5	PTC+; ds splice junctions	Alt 3'ss in IVS1 adds 157 nt	**1095**	**164**
168	145	**At5g18240**	MYR1 (MYB-RELATED PROTEIN 1) - transcription factor	**0.20**	0.01	**0.28**	0.04	>0.1	**0.34**	0.08	0.032	**0.14**	0.02	>0.1	7	Long 3'UTR - predicted AS event	Alt 3'ss removes 23 nt from exon 7	**930**	**332**
236	267	**At1g04950**	TAF6 (TBP-ASSOCIATED FACTOR 6), TAFII59 (TATA BOX ASSOCIATED FACTOR II 59) - transcription initiation factor/ mutant is embryo lethal/ reduced pollen growth	**0.03**	0.01	**0.04**	0.00	>0.1	**0.08**	0.02	0.019	**0.05**	0.01	>0.1	13	uORF of 17aa - correlates with NMD			
256	259	**At1g54080**	UBP1A, OLIGOURIDYLATE-BINDING PROTEIN 1A - mRNA 3'-UTR binding	**0.22**	0.06	**0.25**	0.05	>0.1	**0.48**	0.20	0.096	**0.20**	0.09	>0.1	12	No reason for NMD from AS event	Alt 3'ss in exon 7 removes 12 nt (in frame).		
259	214	**At3g17090**	PP2C (Protein phosphatase 2C) family protein	**0.07**	0.00	**0.11**	0.06	>0.1	**0.23**	0.03	0.040	**0.14**	0.05	>0.1	4	PTC+; ds splice junctions	Alt 3'ss in IVS1 adds 17 nt	**1103**	**306**
281	170	**At5g47210**	Nuclear RNA-binding protein, putative	**0.08**	0.02	**0.07**	0.03	>0.1	**0.17**	0.08	0.062	**0.04**	0.01	>0.1	7	PTC+; no ds splice junction - possible long 3' UTR	Alt 3'ss in exon 7 removes 8 nt	**366**	**200**
299	189	**At5g11330**	Monooxygenase family protein	**0.01**	0.00	**0.02**	0.01	0.028	**0.04**	0.01	0.000	**0.02**	0.00	0.010	4	PTC+; ds splice junctions	Alt 3'ss removes 170 nt from exon 2	**857**	**127**
332	399	**At3g16800**	Protein phosphatase 2C	**0.05**	0.01	**0.06**	0.01	>0.1	**0.09**	0.01	0.006	**0.06**	0.01	>0.1	6	Unknown			
372	268	**At1g76460**	RNA recognition motif (RRM)-containing protein	**0.04**	0.00	**0.05**	0.00	0.001	**0.07**	0.00	0.000	**0.04**	0.00	0.076	8	PTC+; ds splice junctions	Alt 3'ss in IVS1 adds 9 nt to transcript	**1301**	**650**

Peaks that change significantly in CHX treatment only

Primer pair	Band Size (bp)	Gene Identifier	Gene name/function	Wt mean	SE	*upf1-5* mean	SE	p =<0.1	*upf3-1* mean	SE	p =<0.1	CHX mean	SE	p =<0.1		Transcript features	AS event	PTC to pA	Auth stop to pA
30	264	**At3g53270**	Unknown protein - similar to unnamed protein product [Vitis vinifera] (GB:CAO65717.1); contains domain PTHR15131 (PTHR15131)	**0.25**	0.02	**0.19**	0.01	0.098	**0.22**	0.05	>0.1	**0.37**	0.01	0.006	9	No reason for NMD from AS event	Alt 3'ss in IVS1 (5'UTR intron) - no uORFs		
49	346	**At5g41150**	RAD1, UVH1(ULTRAVIOLET HYPERSENSITIVE 1) - DNA repair/ confers resistance to UV radiation	**0.20**	0.03	**0.24**	0.06	>0.1	**0.28**	0.03	>0.1	**0.34**	0.06	0.096	11	PTC+; ds splice junctions	Alt 3'ss in IVS5 adds 53 nt	**1020**	**280**
58	241	**At5g65050**	MAF2 (MADS AFFECTING FLOWERING 2), AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31) - transcription factor/ MADS box genes involved in control of flowering time	**0.30**	0.03	**0.26**	0.02	>0.1	**0.28**	0.04	>0.1	**0.39**	0.01	0.011	7	No reason for NMD - AS events elsewhere in transcript	Fully spliced		
58	351	**At5g65050**	MAF2 (MADS AFFECTING FLOWERING 2), AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31) - transcription factor/ MADS box genes involved in control of flowering time	**0.00**	0.00	**0.01**	0.00	>0.1	**0.02**	0.01	0.015	**0.04**	0.01	0.000	7	PTC+; ds splice junctions	Predicted - Alt 5'ss in IVS2 adds 109nt	**660**	**212**
59	182	**At5g66010**	RNA binding protein	**0.37**	0.08	**0.27**	0.03	>0.1	**0.27**	0.04	>0.1	**0.52**	0.06	0.049					
68	190	**At1g23970**	Unknown protein	**0.74**	0.01	**0.72**	0.00	>0.1	**0.73**	0.00	>0.1	**0.79**	0.01	0.001					
70	152	**At1g54360**	TAF6B1/TAF6B2/TAF6B3/TAF6B4 (TBP-ASSOCIATED FACTOR 6B1) - similar to histone fold TBP-associated factor TAF6/ RNA polymerase II transcription factor/ transcription initiation factor	**0.89**	0.01	**0.88**	0.00	>0.1	**0.88**	0.01	>0.1	**0.92**	0.01	0.053					
111	186	**At1g61660**	Basic helix-loop-helix (bHLH) family protein	**0.06**	0.01	**0.06**	0.01	>0.1	**0.08**	0.02	>0.1	**0.12**	0.03	0.030					

Supplemental Table 2

116	338	**At1g18660**	Zinc finger (C3HC4-type RING finger) family protein	**0.06**	0.04	**0.11**	0.00	>0.1	**0.11**	0.01	>0.1	**0.12**	0.00	0.071					
118	289	**At2g02960**	Zinc finger (C3HC4-type RING finger) family protein	**0.25**	0.01	**0.30**	0.03	>0.1	**0.33**	0.02	>0.1	**0.51**	0.06	0.000	6	uORFs of 8 and 26 aas; 26 uORF overlaps auth AUG of main ORF.	Predicted alt 3'ss in IVS1 adds 92 nt		
122	275	**At2g36010**	E2F3 (E2F TRANSCRIPTION FACTOR 3) - transcription factor/ cell cycle genes, key components of the cyclin D/retinoblastoma/E2F pathway.	**0.55**	0.01	**0.55**	0.01	>0.1	**0.54**	0.01	>0.1	**0.62**	0.00	0.000					
128	363	**At2g15530**	Zinc finger (C3HC4-type RING finger) family protein	**0.15**	0.01	**0.15**	0.01	>0.1	**0.15**	0.01	>0.1	**0.22**	0.03	0.002					
129	230	**At2g40830**	RHC1A (RING-H2 finger protein C1A), putative - cell wall/ protein binding / zinc ion binding	**0.12**	0.01	**0.13**	0.01	>0.1	**0.13**	0.01	>0.1	**0.24**	0.02	0.000					
136	240	**At3g07740**	ADA2A (HOMOLOG OF YEAST ADA2 2A) - DNA binding/ transcription factor/ transcriptional adaptor ADA2a that interacts with histone acetyltransferase GCN5 homolog and CBF1/ response to cold	**0.01**	0.00	**0.03**	0.01	>0.1	**0.04**	0.02	>0.1	**0.05**	0.02	0.097					
155	178	**At4g27050**	F-box family protein	**0.33**	0.05	**0.36**	0.07	>0.1	**0.33**	0.05	>0.1	**0.47**	0.01	0.090					
155	233	**At4g27050**	F-box family protein	**0.11**	0.00	**0.11**	0.01	>0.1	**0.13**	0.03	>0.1	**0.19**	0.01	0.003					
171	221	**At5g18620**	CHR17 (CHROMATIN REMODELING FACTOR 17) - DNA-dependent ATPase	**0.26**	0.01	**0.26**	0.01	>0.1	**0.28**	0.01	>0.1	**0.29**	0.00	0.013					
174	224	**At5g13220**	JAS1 (JASMONATE-ASSOCIATED 1), JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10) - regulation of systemic acquired resistance/ response to jasmonic acid stimulus and wounding	**0.34**	0.02	**0.35**	0.00	>0.1	**0.36**	0.04	>0.1	**0.47**	0.01	0.000					
182	241	**At5g16820**	HSF3 (HEAT SHOCK FACTOR 3) - DNA binding / transcription factor/ not induced by heat/ required early in heat stress response	**0.66**	0.01	**0.66**	0.00	>0.1	**0.66**	0.01	>0.1	**0.69**	0.00	0.003					
193	297	**At1g07350**	Pre-mRNA splicing factor - Transformer serine/arginine-rich ribonucleoprotein	**0.03**	0.00	**0.03**	0.00	>0.1	**0.05**	0.01	0.001	**0.06**	0.00	0.000					
198	129	**At4g36690**	ATU2AF65A - spliceosomal protein/ RNA binding	**0.43**	0.08	**0.44**	0.06	>0.1	**0.51**	0.09	>0.1	**0.61**	0.07	0.043					
209	209	**At2g16940**	RNA recognition motif (RRM)-containing protein	**0.02**	0.00	**0.02**	0.00	>0.1	**0.03**	0.01	0.003	**0.05**	0.00	0.000	14	PTC+; ds splice junctions	Alt 3’ and alt 5’ ss adds 70 nt from IVS-2	**1505**	**262**
212	332	**At4g02430**	SR34b - pre-mRNA splicing factor/ SR protein	**0.00**	0.00	**0.00**	0.00	>0.1	**0.01**	0.01	>0.1	**0.08**	0.02	0.000					
212	389	**At4g02430**	SR34b - pre-mRNA splicing factor/ SR protein	**0.04**	0.02	**0.02**	0.01	>0.1	**0.05**	0.03	>0.1	**0.16**	0.02	0.001					
225	300	**At3g53570**	AFC1 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 1) - member of LAMMER kinase (CDC2-related) subfamily/ activates STE12-dependent functions in yeast	**0.01**	0.00	**0.01**	0.00	>0.1	**0.01**	0.01	>0.1	**0.05**	0.01	0.001					
229	414	**At4g35785**	Transformer serine/arginine-rich ribonucleoprotein; Nucleic acid binding / nucleotide binding	**0.36**	0.04	**0.41**	0.05	>0.1	**0.43**	0.04	>0.1	**0.53**	0.04	0.004	8	PTC+; ds splice junctions	Alt 3’ss in IVS6 adds 298nt to transcript	**642**	**248**
236	295	**At1g04950**	TAF6 (TBP-ASSOCIATED FACTOR 6), TAFII59 (TATA BOX ASSOCIATED FACTOR II 59) - transcription initiation factor/ mutant is embryo lethal/ reduced pollen growth	**0.02**	0.02	**0.04**	0.03	>0.1	**0.03**	0.01	>0.1	**0.12**	0.08	0.016					
282	366	**At5g63120**	RH30 - ethylene-responsive putative DEAD box RNA helicase	**0.00**	0.00	**0.00**	0.00	>0.1	**0.01**	0.00	0.013	**0.04**	0.01	0.000	10 or 11	PTC+; ds splice junctions	Alt 3'ss and alt 5'ss include an additional exon of 187nt in IVS8	**723**	**215**
283	387	**At3g01540**	DRH1 (DEAD BOX RNA HELICASE 1)	**0.00**	0.00	**0.01**	0.00	>0.1	**0.02**	0.01	0.003	**0.03**	0.00	0.000		PTC+; ds splice junctions	Alt 3'ss and alt 5'ss in IVS4 leaves alt exon of 252 nt of IVS4 in transcript	**1772**	**326**
283	349	**At3g01540**	DRH1 (DEAD BOX RNA HELICASE 1)	**0.01**	0.00	**0.01**	0.00	>0.1	**0.03**	0.02	0.011	**0.04**	0.00	0.000					
288	189	**At3g12570**	FYD - in chloroplast envelope	**0.57**	0.03	**0.56**	0.02	>0.1	**0.63**	0.03	>0.1	**0.66**	0.03	0.026					
289	141	**At3g12570**	FYD - in chloroplast envelope	**0.11**	0.00	**0.08**	0.01	0.052	**0.09**	0.03	0.076	**0.20**	0.01	0.001					
289	259	**At3g12570**	FYD - in chloroplast envelope	**0.08**	0.01	**0.07**	0.01	>0.1	**0.08**	0.01	>0.1	**0.11**	0.01	0.061					
298	341	**At5g09880**	RNA recognition motif (RRM)-containing protein	**0.00**	0.00	**0.00**	0.00	>0.1	**0.01**	0.00	>0.1	**0.04**	0.02	0.002	13	PTC+; ds splice junctions	Three alt 3'ss and alt 5'ss includes three new exons of 76, 40 and 81 nt in IVS4	**1263**	**204**
298	464	**At5g09880**	RNA recognition motif (RRM)-containing protein	**0.00**	0.00	**0.00**	0.00	>0.1	**0.01**	0.00	>0.1	**0.03**	0.01	0.000	13	PTC+; ds splice junctions	Two alt 3'ss and alt 5'ss includes two new exons of 240 and 81 nt in IVS4	**1387**	**204**
310	509	**At5g65070**	MAF4 - MADS AFFECTING FLOWERING 4 - MADS domain protein/flowering regulator/ transcription factor/ closely related to FLC	**0.02**	0.01	**0.01**	0.00	>0.1	**0.01**	0.01	>0.1	**0.05**	0.01	0.009					
312	469	**At5g13790**	AGL15 (AGAMOUS-LIKE 15) - DNA binding/ transcription factor/ member of the MADS domain family of regulatory factors	**0.29**	0.01	**0.30**	0.02	>0.1	**0.30**	0.02	>0.1	**0.34**	0.01	0.031					
313	355	**At5g37055**	SEF (SERRATED LEAVES AND EARLY FLOWERING), SWC6 (homologue of yeast SWC6 protein) - conserved subunit of SWR1/SRCAP complex.	**0.79**	0.01	**0.78**	0.01	>0.1	**0.77**	0.01	>0.1	**0.84**	0.01	0.049					
321	348	**At4g27410**	RD26 (RESPONSIVE TO DESICCATION 26) - NAC transcription factor/ transcriptional activator in ABA-mediated dehydration response	**0.01**	0.01	**0.01**	0.00	>0.1	**0.03**	0.02	>0.1	**0.05**	0.03	0.063					
322	399	**At2g33480**	ANAC041 (NAC DOMAIN CONTAINING PROTEIN 41) - transcription factor	**0.60**	0.02	**0.57**	0.02	>0.1	**0.61**	0.05	>0.1	**0.73**	0.00	0.004					
324	503	**At5g43270**	SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2) - DNA binding / transcription factor/ controls correct development of lateral organs in association with shoot maturation in the reproductive phase (with SPL10 and SPL11)	**0.24**	0.14	**0.10**	0.03	>0.1	**0.11**	0.05	>0.1	**0.45**	0.10	0.066					
326	147	**At1g69250**	NTF2 (nuclear transport factor 2) family protein - RNA recognition motif (RRM)-containing protein	**0.92**	0.01	**0.92**	0.00	>0.1	**0.94**	0.00	0.047	**0.96**	0.00	0.000					
330	118	**At3g10300**	Calcium-binding EF hand family protein	**0.18**	0.03	**0.21**	0.06	>0.1	**0.23**	0.08	>0.1	**0.34**	0.04	0.035					
335	327	**At5g66210**	CPK28 (calcium-dependent protein kinase 28) - calmodulin-dependent protein kinase/ member of Calcium Dependent Protein Kinase family	**0.01**	0.00	**0.01**	0.00	>0.1	**0.01**	0.01	>0.1	**0.07**	0.02	0.001					
335	295	**At5g66210**	CPK28 (calcium-dependent protein kinase 28) - calmodulin-dependent protein kinase/ member of Calcium Dependent Protein Kinase family	**0.05**	0.00	**0.05**	0.01	>0.1	**0.06**	0.01	>0.1	**0.09**	0.01	0.025					
338	253	**At5g57630**	CIPK21 (CBL-INTERACTING PROTEIN KINASE 21), SNRK3.4 (SNF1-RELATED PROTEIN KINASE 3.4) - CBL-interacting protein kinase	**0.62**	0.03	**0.62**	0.01	>0.1	**0.64**	0.04	>0.1	**0.81**	0.01	0.000					
346	285	**At4g23260**	CRK18 (CYSTEINE-RICH RLK [RECEPTOR-LIKE PROTEIN KINASE] 18 - cysteine-rich receptor-like protein kinase/ response to ABA	**0.09**	0.02	**0.09**	0.01	>0.1	**0.17**	0.05	0.097	**0.34**	0.03	0.000					
348	416	**At4g34460**	AGB1 (GTP BINDING PROTEIN BETA 1), ELK4 (ERECTA-LIKE 4) - heterotrimeric G-protein beta subunit involved in organ shape/ nucleotide binding	**0.01**	0.00	**0.01**	0.00	>0.1	**0.02**	0.01	>0.1	**0.05**	0.01	0.000					
360	314	**At3g06510**	SFR2 (SENSITIVE TO FREEZING 2) - encodes protein with beta-glucosidase activity/ hydrolase - hydrolyzing O-glycosyl compounds/ freezing response	**0.83**	0.02	**0.83**	0.01	>0.1	**0.82**	0.01	>0.1	**0.90**	0.01	0.002					
362	459	**At4g26070**	MEK1 (MAP KINASE/ ERK KINASE 1), MKK1 (MITOGEN ACTIVATED PROTEIN KINASE KINASE 1) - MAP Kinase Kinase/ stress-activated MAPK pathway/ phosphorylates the MAPK AtMPK4 in response to stress/ phosphorylated by MEKK1 in response to wounding.	**0.48**	0.09	**0.44**	0.13	>0.1	**0.63**	0.08	>0.1	**0.74**	0.05	0.066					
362	548	**At4g26070**	MEK1 (MAP KINASE/ ERK KINASE 1), MKK1 (MITOGEN ACTIVATED PROTEIN KINASE KINASE 1) - MAP Kinase Kinase/ stress-activated MAPK pathway/ phosphorylates the MAPK AtMPK4 in response to stress/ phosphorylated by MEKK1 in response to wounding.	**0.03**	0.01	**0.03**	0.01	>0.1	**0.04**	0.01	>0.1	**0.06**	0.01	0.005					
373	267	**At3g13224**	RNA recognition motif (RRM)-containing protein	**0.90**	0.02	**0.89**	0.01	>0.1	**0.90**	0.01	>0.1	**0.96**	0.01	0.001					
376	135	**At1g64625**	Transcription factor	**0.26**	0.02	**0.23**	0.03	>0.1	**0.27**	0.05	>0.1	**0.37**	0.01	0.009					
380	167	**At5g08185**	MIR162A, MICRORNA 162A - targets DCL1	**0.14**	0.02	**0.13**	0.01	>0.1	**0.15**	0.02	>0.1	**0.18**	0.01	0.075					
380	170	**At5g08185**	MIR162A, MICRORNA 162A - targets DCL1	**0.16**	0.02	**0.16**	0.03	>0.1	**0.17**	0.03	>0.1	**0.22**	0.03	0.073					
384	110	**At4g02200**	Drought-induced-19-like 1 - drought-responsive family protein	**0.01**	0.00	**0.01**	0.00	>0.1	**0.02**	0.01	>0.1	**0.04**	0.01	0.009					
385	256	**At2g43810**	SmF (Small nuclear ribonucleoprotein F) - spliceosomal snRNP protein	**0.07**	0.02	**0.09**	0.02	>0.1	**0.10**	0.02	>0.1	**0.13**	0.03	0.027					
385	264	**At2g43810**	SmF (Small nuclear ribonucleoprotein F) - spliceosomal snRNP protein	**0.04**	0.01	**0.05**	0.01	>0.1	**0.06**	0.01	>0.1	**0.08**	0.03	0.058					
412	212	**At4g29810**	MKK2 (MAP KINASE KINASE 2) - MKK2 regulates MPK6 and MPK4 in response to cold and salt stresses.	**0.04**	0.00	**0.04**	0.00	>0.1	**0.05**	0.01	>0.1	**0.08**	0.01	0.002					
																	Total	**75961**	**19870**

Supplemental Table 2

n **79** **82**
Mean **962** **242**

Selected peaks that change significantly in upf mutants and/or cycloheximide treatment where the change is <3%

Primer pair	**Band Size (bp)**	**Gene Identifier**	**Gene name/function**	**Wt mean**	**SE**	***upf1-5* mean**	**SE**	**p =<0.1**	***upf3-1* mean**	**SE**	**p =<0.1**	**CHX mean**	**SE**	**p =<0.1**		**Transcript features**	**AS event**	**PTC to pA**	**Auth stop to pA**
58	174	**At5g65050**	MAF2 (MADS AFFECTING FLOWERING 2), AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31) - transcription factor/ MADS box genes involved in control of flowering time	**0.00**	0.00	**0.00**	0.00	>0.1	**0.01**	0.00	0.003	**0.00**	0.00	>0.1	7	PTC+; ds splice junctions	Predicted - Exon 3 skip; alt 3'ss in exon 5 removes 4 nt		
58	178	**At5g65050**	transcription factor/ MADS box genes involved in control of flowering time	**0.01**	0.00	**0.02**	0.00	0.000	**0.02**	0.00	0.000	**0.01**	0.00	0.058	7	PTC+; ds splice junctions	Exon 3 skip		
58	205	**At5g65050**	MAF2 (MADS AFFECTING FLOWERING 2), AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31) - transcription factor/ MADS box genes involved in control of flowering time	**0.01**	0.00	**0.01**	0.00	0.056	**0.01**	0.00	0.006	**0.01**	0.00	>0.1	7	PTC+; ds splice junctions	Predicted - alt 3'ss in exon 4 removes 33 nt; alt 3'ss in exon 5 removes 4 nt		
58	351	**At5g65050**	MAF2 (MADS AFFECTING FLOWERING 2), AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31) - transcription factor/ MADS box genes involved in control of flowering time	**0.02**	0.00	**0.02**	0.00	>0.1	**0.02**	0.01	>0.1	**0.04**	0.00	0.000	7	PTC+; ds splice junctions	Predicted - alt 5'ss in intron 2 adds 109 nt		
58	347	**At5g65050**	MAF2 (MADS AFFECTING FLOWERING 2), AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31) - transcription factor/ MADS box genes involved in control of flowering time	**0.00**	0.00	**0.00**	0.00	>0.1	**0.00**	0.00	>0.1	**0.01**	0.00	0.000	7	PTC+; ds splice junctions	Predicted - alt 5'ss in intron 2 adds 109 nt; alt 3'ss in exon 5 removes 4 nt		
58	433	**At5g65050**	MAF2 (MADS AFFECTING FLOWERING 2), AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31) - transcription factor/ MADS box genes involved in control of flowering time	**0.00**	0.00	**0.01**	0.00	>0.1	**0.01**	0.00	0.044	**0.01**	0.00	0.011	7	PTC+; ds splice junctions	Predicted - alt 5'ss in intron 2 adds 109 nt; intron 3 retained; alt 3' ss in exon 5 removes 4 nt		
58	437	**At5g65050**	MAF2 (MADS AFFECTING FLOWERING 2), AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31) - transcription factor/ MADS box genes involved in control of flowering time	**0.03**	0.01	**0.04**	0.00	>0.1	**0.04**	0.01	>0.1	**0.06**	0.01	0.007	7	PTC+; ds splice junctions	Predicted - alt 5'ss in intron 2 adds 109 nt; intron 3 retained		
118	240	**At2g02960**	Zinc finger (C3HC4-type RING finger) family protein	**0.02**	0.00	**0.02**	0.00	>0.1	**0.03**	0.00	0.094	**0.02**	0.00	>0.1	6	uORFs of 8 and 26 aas; 26 uORF overlaps auth AUG.	Predicted alt 3'ss in IVS1 adds 44 nt		
193	279	**At1g07350**	Pre-mRNA splicing factor - Transformer serine/arginine-rich ribonucleoprotein	**0.01**	0.00	**0.02**	0.00	>0.1	**0.03**	0.00	0.005	**0.03**	0.00	0.002	7 or 8	PTC+; ds splice junctions	Predicted - Alt 3'ss and alt 5'ss in IVS4 adds 81nt of IVS4 to transcript		
193	282	**At1g07350**	Pre-mRNA splicing factor - Transformer serine/arginine-rich ribonucleoprotein	**0.01**	0.00	**0.01**	0.00	0.023	**0.01**	0.00	0.000	**0.01**	0.00	0.000	7 or 8	PTC+; ds splice junctions	Predicted - alt 3'ss and alt 5'ss in IVS4 adds 84nt of IVS4 to transcript		
237	123	**At1g07830**	RPL29 - ribosomal protein L29 family protein	**0.01**	0.00	**0.02**	0.01	0.006	**0.03**	0.00	0.000	**0.02**	0.00	>0.1	4	uORF of 31 aas overlaps with AUG of main ORF	Alt 3'ss removes 70 nt of exon 2 (including authentic AUG		
298	270	**At5g09880**	RNA recognition motif (RRM)-containing protein	**0.02**	0.00	**0.02**	0.00	>0.1	**0.02**	0.01	0.077	**0.03**	0.00	0.001	13	PTC+; ds splice junctions	Two alternative exons from IVS 4; alt 3'ss in exon 5 removes 29 nt		
299	253	**At5g11330**	Monooxygenase family protein	**0.00**	0.00	**0.00**	0.00	>0.1	**0.01**	0.00	>0.1	**0.01**	0.00	0.002	4	PTC+; ds splice junctions	Alt 5'ss and alt 3'ss removes cryptic intron from exon 2 of 106 nt		
299	289	**At5g11330**	Monooxygenase family protein	**0.00**	0.00	**0.01**	0.00	0.088	**0.02**	0.01	0.000	**0.02**	0.00	0.000	4	PTC+; ds splice junctions	Alt 5'ss and alt 3'ss removes cryptic intron from exon 2 of 70 nt		

Means and standard errors of ratios of up-regulated transcripts are given for wild-type, upf1-5, upf3-1 plants and plants treated with cycloheximide (CHX)

Green shading - significantly up-regulated with >3% change from wild-type; Blue shading - significantly up-regulated with <3% changefrom wild-type; pink - significantly down-regulated with >3% change form wild-type.

Abbreviatios: PTC+ - PTC-containg transcripts; ds - downstream; uORF - upstream open reading frame; aas - amino acids; ss - splice site; alt - alternative; IVSn - intervening sequence = intron where n is the intron number;
Exon number: where two numbers are given, alternatively spliced transcripts include or exclude an alternative exon giving two possibilities.

Table S3. List of alternatively spliced genes showing splice isoform upregulation upon inhibition of nonsense-mediated decay

Gene ID	Gene Name
At1g02090	FUS5 (FUSCA 5), CSN7 (COP9 SIGNALOSOME SUBUNIT 7), COP15 (CONSTITUTIVE PHOTOMORPHOGENIC 15) - MAP kinase kinase/ phosphoprotein
At1g03457	RNA-binding protein, putative
At1g04950	TAF6 (TBP-ASSOCIATED FACTOR 6), TAFII59 (TATA BOX ASSOCIATED FACTOR II 59) - transcription initiation factor/ mutant is embryo lethal/ reduced pollen growth
At1g07350	Pre-mRNA splicing factor - Transformer serine/arginine-rich ribonucleoprotein, putative
At1g07830	RPL29 - ribosomal protein L29 family protein
At1g15200	Pinin - exon junction complex protein; protein-protein interaction regulator family protein
At1g16610	SR45 (ARGININE/SERINE-RICH 45), RNPS1 - pre-mRNA splicing factor/ exon junction complex protein/ heterochromatic siRNA pathway/ involved in plant sugar response
At1g18660	Zinc finger (C3HC4-type RING finger) family protein
At1g23970	Unknown protein
At1g30200	F-box family protein
At1g37150	HCS2 (HOLOCARBOXYLASE SYNTHETASE 2) - catalytic/ involved in protein modification - biotin-[acetyl-CoA-carboxylase] ligase activity
At1g49730	Protein kinase family protein
At1g49950	TRB1 - TELOMERE REPEAT BINDING FACTOR 1 - telomeric DNA binding protein/ DNA binding / transcription factor
At1g54080	UBP1A, OLIGOURIDYLATE-BINDING PROTEIN 1A - mRNA 3'-UTR binding
At1g54360	TAF6B1/TAF6B2/TAF6B3/TAF6B4 (TBP-ASSOCIATED FACTOR 6B1) - similar to histone fold TBP-associated factor TAF6/ RNA polymerase II transcription factor/ transcription initiation factor
At1g55310	SCL33, SR33 (SC35-like splicing factor 33) - pre-mRNA splicing factor/ SR protein/ RNA binding
At1g61660	Basic helix-loop-helix (bHLH) family protein
At1g64625	Transcription factor
At1g69250	NTF2 (nuclear transport factor 2) family protein - RNA recognition motif (RRM)-containing protein
At1g72050	TFIIIA (TRANSCRIPTION FACTOR IIIA) - zinc finger (C2H2 type) family protein/ required for transcription of 5S rRNA genes
At1g72320	APUM23 (ARABIDOPSIS PUMILIO 23) - member of Pumilio RNA-binding protein family/ regulates mRNA stability and translation by sequence-specific binding to 3' UTR of target mRNAs
At1g72560	PSD, PAUSED - encodes a karyopherin/ ortholog of LOS1/XPOT/ tRNA binding/ mediates nuclear export of tRNAs
At1g76460	RNA recognition motif (RRM)-containing protein
At1g77080	FLM (FLOWERING LOCUS M), MAF1 (MADS AFFECTING FLOWERING 1) - MADS domain protein/flowering regulator/ transcription factor/ closely related to FLC
At1g79880	La domain-containing protein
At2g02570	SPF30 - Nucleic acid binding
At2g02960	Zinc finger (C3HC4-type RING finger) family protein
At2g04790	Unknown protein - similar to unnamed protein product [Vitis vinifera] (GB:CAO23994.1)
At2g15530	zinc finger (C3HC4-type RING finger) family protein
At2g16940	RNA recognition motif (RRM)-containing protein
At2g18300	Basic helix-loop-helix (bHLH) family protein; transcription factor involved in response to cytokinin stimulus

At2g21660	ATGRP7 (GLYCINE-RICH RNA-BINDING PROTEIN 7), CCR2 (COLD-CIRCADIAN RHYTHM AND RNA BINDING 2) - RNA binding/ double-stranded DNA binding/ single-stranded DNA binding/ regulates circadian oscillations of GRP7/GRP8 transcript/ cold-induced/ response to salt and dehydration stress conditions/ mediates innate immune response.
At2g26150	ATHSFA2 (Arabidopsis thaliana HEAT SHOCK TRANSCRIPTION FACTOR A2) - DNA binding/ Involved in response to misfolded protein accumulation in the cytosol
At2g28550	TOE1 (TARGET OF EAT1 1), RAP2.7 (RELATED TO AP2.7) - DNA binding/ transcription factor
At2g29210	Splicing factor PWI domain-containing protein
At2g30260	U2B"(U2 SMALL NUCLEAR RIBONUCLEOPROTEIN B") - component of the U2 snRNP complex/ RNA binding
At2g32330	Unknown protein
At2g33480	ANAC041 (NAC DOMAIN CONTAINING PROTEIN 41) - transcription factor
At2g36010	E2F3 (E2F TRANSCRIPTION FACTOR 3) - transcription factor/ cell cycle genes, key components of the cyclin D/retinoblastoma/E2F pathway.
At2g37060	NF-YB8, NUCLEAR FACTOR Y, SUBUNIT B8
At2g37340	RS2Z33, RSZ33 (ARGININE/SERINE-RICH ZINC KNUCKLE-CONTAINING PROTEIN 33) - pre-mRNA splicing factor/ SR protein/ nucleic acid binding / nucleotide binding / zinc ion binding
At2g38880	NF-YB1 (NUCLEAR FACTOR Y SUBUNIT B1), HAP3A (HEME ACTIVATOR PROTEIN (YEAST) HOMOLOG 3A) - transcription factor/ confers drought tolerance
At2g40830	RHC1A (RING-H2 finger protein C1A), putative - cell wall/ protein binding / zinc ion binding
At2g43640	SRP14, signal recognition particle 14 kDa family protein
At2g43810	SmF (Small nuclear ribonucleoprotein F) - spliceosomal snRNP protein
At2g46790	APRR9 (PSEUDO-RESPONSE REGULATOR 9) - transcription regulator/clock function - essential to temperature-sensitive circadian system
At2g46830	CCA1, CIRCADIAN CLOCK ASSOCIATED 1 - transcription factor/ Myb-like transcriptional repressor in regulating circadian rhythms/ binds evening element in TOC1 to repress TOC1
At3g01150	PTB1 - POLYPYRIMIDINE TRACT-BINDING PROTEIN 1 - pre-mRNA splicing - role in pollen germination
At3g01540	DRH1 (DEAD BOX RNA HELICASE 1)
At3g06510	SFR2 (SENSITIVE TO FREEZING 2) - encodes protein with beta-glucosidase activity/ hydrolase - hydrolyzing O-glycosyl compounds/ freezing response
At3g07740	ADA2A (HOMOLOG OF YEAST ADA2 2A) - DNA binding/ transcription factor/ transcriptional adaptor ADA2a that interacts with histone acetyltransferase GCN5 homolog and CBF1/ response to cold
At3g10300	Calcium-binding EF hand family protein
At3g12250	TGA6 (TGA1a-related gene 6); DNA binding /basic leucine zipper transcription factor/ activation of SA-responsive genes factor
At3g12570	FYD - in chloroplast envelope
At3g13224	RNA recognition motif (RRM)-containing protein
At3g13570	SCL30A (SC35-LIKE SPLICING FACTOR 30A) - pre-mRNA splicing factor/ SR protein/ RNA binding
At3g14230	RAP2.2 - member of the ERF (ethylene response factor) subfamily B-2 of ERF/AP2 transcription factor family/ DNA binding
At3g16800	PP2C (Protein phosphatase 2C), putative
At3g17090	PP2C (Protein phosphatase 2C) family protein
At3g19840	PRP40C - Pre-mRNA-processing protein 40C/ binds CTD of RNA polymerase II/ scaffold for RNA processing machineries/ FF domain-containing protein / WW domain-containing protein
At3g20270	Lipid-binding serum glycoprotein family protein
At3g25840	Protein kinase family protein

At3g29160	AKIN11 (ARABIDOPSIS SNF1 KINASE HOMOLOG 11) - SNF1-related protein kinase - interacts with SCF subunit SKP1/ASK1 and 20S proteosome subunit PAD1
At3g46460	UBC13 (UBIQUITIN-CONJUGATING ENZYME 13) - ubiquitin potein ligase
At3g49430	SR34A (SER/ARG-RICH PROTEIN 34A) - pre-mRNA splicing factor - SR protein
At3g51880	HMGB1 (HIGH MOBILITY GROUP B 1), NFD1 (NUCLEOSOME/CHROMATIN ASSEMBLY FACTOR D1) - transcription factor
At3g53270	Unknown protein - similar to unnamed protein product [Vitis vinifera] (GB:CAO65717.1); contains domain PTHR15131 (PTHR15131)
At3g53500	RS2Z32 - pre-mRNA splicing factor / SR protein/ nucleic acid binding
At3g53570	AFC1 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 1) - member of LAMMER kinase (CDC2-related) subfamily/ activates STE12-dependent functions in yeast
At3g55460	SCL30 (SC35-LIKE SPLICING FACTOR 30) - pre-mRNA splicing factor/ SR protein/ RNA binding
At3g61860	RS31 (ARGININE/SERINE-RICH SPLICING FACTOR 31) - pre-mRNA splicing factor/ SR protein/ RNA binding
At3g62190	DNAJ heat shock N-terminal domain-containing protein
At4g02200	Drought-induced-19-like 1 - drought-responsive family protein
At4g02430	SR34b - pre-mRNA splicing factor/ SR protein
At4g14410	basic helix-loop-helix (bHLH) family protein
At4g16845	VRN2 (REDUCED VERNALIZATION RESPONSE 2) - transcription factor/ mediates vernalization/ encodes zinc finger protein similar to Polycomb group (PcG) proteins/ maintains FLC repression cold treatment
At4g23260	CRK18 (CYSTEINE-RICH RLK [RECEPTOR-LIKE PROTEIN KINASE] 18 - cysteine-rich receptor-like protein kinase/ response to ABA
At4g24740	AFC2 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 2) - LAMMER kinase/ putative role in phosphorylation of SR protein splicing factors
At4g25500	RS40 - pre-mRNA splicing factor/ SR protein/ RNA binding (previously ATRSP35 [Arabidopsis thaliana arginine/serine-rich splicing factor 35])
At4g26070	MEK1 (MAP KINASE/ ERK KINASE 1), MKK1 (MITOGEN ACTIVATED PROTEIN KINASE KINASE 1) - MAP Kinase Kinase/ stress-activated MAPK pathway/ phosphorylates the MAPK AtMPK4 in response to stress/ phosphorylated by MEKK1 in response to wounding.
At4g27050	F-box family protein
At4g27410	RD26 (RESPONSIVE TO DESICCATION 26) - NAC transcription factor/ transcriptional activator in ABA-mediated dehydration response
At4g29810	MKK2 (MAP KINASE KINASE 2) - MKK2 regulates MPK6 and MPK4 in response to cold and salt stresses.
At4g33060	CYP57, Peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein
At4g34460	AGB1 (GTP BINDING PROTEIN BETA 1), ELK4 (ERECTA-LIKE 4) - heterotrimeric G-protein beta subunit involved in organ shape/ nucleotide binding
At4g35785	Transformer serine/arginine-rich ribonucleoprotein; Nucleic acid binding / nucleotide binding
At4g36690	ATU2AF65A - spliceosomal protein/ RNA binding
At4g36960	RNA recognition motif (RRM)-containing protein
At4g39260	ATGRP8 (GLYCINE-RICH RNA-BINDING PROTEIN 8), CCR1 (COLD-CIRCADIAN RHYTHM AND RNA BINDING 1) - regulates circadian oscillations of GRP7/GRP8 transcripts/ cold-induced/ RNA binding
At5g08185	MIR162A, MICRORNA 162A - targets DCL1
At5g09230	SRT2 - member of SIR2 (sirtuin) family histone deacetylases (HDAC) - chromatin silencing/ DNA binding
At5g09790	ATXR5/SDG15 (SETDOMAIN GROUP 15) - contains SET-domain and PCNA-binding domain/ DNA binding/ possible role in cell-cycle regulation or progression.

At5g09880	RNA recognition motif (RRM)-containing protein
At5g11200	UAP56a - DEAD/DEAH box helicase - exon junction protein
At5g11330	Monooxygenase family protein
At5g13220	JAS1 (JASMONATE-ASSOCIATED 1), JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10) - regulation of systemic acquired resistance/ response to jasmonic acid stimulus and wounding
At5g13730	SIG4 (SIGMA FACTOR 4); DNA binding/ DNA-directed RNA polymerase/ transcription factor/ regulation of plastid-encoded RNA polymerase PEP
At5g13790	AGL15 (AGAMOUS-LIKE 15) - DNA binding/ transcription factor/ member of the MADS domain family of regulatory factors
At5g16820	HSF3 (HEAT SHOCK FACTOR 3) - DNA binding / transcription factor/ not induced by heat/ required early in heat stress response
At5g18240	MYR1 (MYB-RELATED PROTEIN 1) - transcription factor
At5g18620	CHR17 (CHROMATIN REMODELING FACTOR 17) - DNA-dependent ATPase
At5g20250	DIN10 (DARK INDUCIBLE 10) - member of glycosyl hydrolase family 36/ hydrolyzing O-glycosyl compounds
At5g24270	SOS3 (SALT OVERLY SENSITIVE 3), CBL4 (CALCINEURIN B-LIKE PROTEIN 4) - encodes a calcium sensor essential for K+ nutrition, K+/Na+ selectivity, and salt tolerance
At5g35410	SOS2 (SALT OVERLY SENSITIVE 2), CIPK24 (CBL-INTERACTING PROTEIN KINASE 24) - kinase/ regulatory component controlling plant potassium nutrition
At5g37055	SEF (SERRATED LEAVES AND EARLY FLOWERING), SWC6 (homologue of yeast SWC6 protein) - conserved subunit of SWR1/SRCAP complex.
At5g41150	RAD1, UVH1(ULTRAVIOLET HYPERSENSITIVE 1) - DNA repair/ confers resistance to UV radiation
At5g43270	SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2) - DNA binding / transcription factor/ controls correct development of lateral organs in association with shoot maturation in the reproductive phase (with SPL10 and SPL11)
At5g43910	pfkB-type carbohydrate kinase family protein
At5g46110	APE2 - ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT 2 - antiporter/ triose-phosphate transmembrane transporter/ involved in acclimation responses
At5g47210	Nuclear RNA-binding protein, putative
At5g50240	PIMT2 (PROTEIN-L-ISOASPARTATE METHYLTRANSFERASE 2)
At5g53180	PTB2, POLYPYRIMIDINE TRACT-BINDING PROTEIN 2 - pre-mRNA splicing - role in pollen germination
At5g57630	CIPK21 (CBL-INTERACTING PROTEIN KINASE 21), SNRK3.4 (SNF1-RELATED PROTEIN KINASE 3.4) - CBL-interacting protein kinase
At5g59950	Aly/REF - RNA and export factor-binding protein, putative
At5g63120	RH30 - ethylene-responsive putative DEAD box RNA helicase
At5g65050	MAF2 (MADS AFFECTING FLOWERING 2), AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31) - transcription factor/ MADS box genes involved in control of flowering time
At5g65060	MAF3 - MADS AFFECTING FLOWERING 3 - MADS domain protein/flowering regulator/ transcription factor/ closely related to FLC
At5g65070	MAF4 - MADS AFFECTING FLOWERING 4 - MADS domain protein/flowering regulator/ transcription factor/ closely related to FLC
At5g65080	MAF5 (MADS AFFECTING FLOWERING 5)
At5g66010	RNA binding protein
At5g66210	CPK28 (calcium-dependent protein kinase 28) - calmodulin-dependent protein kinase/ member of Calcium Dependent Protein Kinase family

Table S4. Comparison of the degree of change in NMD-sensitive AS transcripts between *upf3-1* and *upf1-5*

Groups of transcripts	**Number of up-regulated transcripts**		
	upf3-1>upf1-5	***upf3-1=upf1-5***	***upf1-5>upf3-1***
upf1-5/*upf3-1*/cycloheximide	32	0	0
upf1-5/*upf3-1*	7	2	1
cycloheximide	52	3	6
Total	**91**	**5**	**7**

Supplementary Table 5. Comparison of the degree of change in NMD-sensitive AS transcripts between CHX and *upf* mutants

Groups of transcripts	**Number of up-regulated transcripts**	
	***upf*>CHX**	**CHX>*upf***
upf1-5/*upf3-1*/cycloheximide	20	12
upf3-1/cycloheximide	7	34
Total	**27**	**46**

Supplemental Table 6. Intron retention transcripts which are NMD sensitive, not expected to be turned over by NMD or cryptic introns

Primer pair	**Gene ID**	**Name**	**Exon No.**	**Primer sites**	**AS event**	**Transcript**	**wt**	***upf 1-5***	***upf 3-1***	**NMD**
Intron retention events not expected to be NMD - in frame introns										
314	At2g43410	FPA	7	Ex3-5	FS		0.34	0.31	0.31	
					IR4	In frame	0.66	0.69	0.69	No NMD
360	At3g06510	SFR2	10	Ex5-7	FS		0.83	0.83	0.82	
					IR6	In frame	0.12	0.09	0.07	No NMD
					E7 Alt 3'ss(+28)	PTC+; ds SJ	0.01	***0.02***	**0.04**	NMD
					E7 Alt 3'ss(-7)	PTC+; ds SJ	0.02	***0.04***	**0.06**	NMD
Intron retention events not expected to be NMD – 5'UTR intron with uORFs in all transcripts										
305	At1g01060	LHY	10	Ex1-3	FS		0.89	0.85	0.89	
					IR1 (5' UTR)	uORFs	0.06	0.07	0.06	No NMD
Intron retention events not expected to be NMD – C-terminal change										
325	At2g47890	Zn finger (B-box type) protein	4	Ex1-4	FS		0.92	0.93	0.88	
					IR3	C-terminal change	0.06	0.06	0.10	No NMD
Cryptic intron – splicing event not observed										
353	At1g27770	ACA1/PEA1	8	Ex3-5	FS	Not observed	0.00	0.00	0.00	
					IR 3	In frame	0.91	0.86	0.94	No NMD
361	At4g13850	AtGRP2	6	Ex3-6	FS	Not observed	0.00	0.00	0.00	
					IR5	In frame	1.00	1.00	1.00	No NMD
Intron retention transcripts which are NMD sensitive										
327	At5g59950	Aly/REF protein	5	Ex1-3	FS		0.84	0.70	0.53	
					IR1	PTC+; ds SJ	0.16	**0.30**	**0.47**	NMD
332	At3g16800	PP2C	6	Ex1-3	FS		0.84	0.81	0.75	
					IR2 (IVS1 spliced to distal site)	PTC+; ds SJ	0.05	***0.07***	**0.10**	NMD
					E2 Alt 3'ss(+18) (5' UTR)		0.06	0.06	0.06	No NMD
					Unknown (399 bp)		0.05	0.06	**0.09**	NMD
374	At4g36960	RRM-containing protein	13	Ex1-3	FS		0.84	0.74	0.61	
					I1R (5' UTR)	PTC+; uORF in 5' UTR	0.05	**0.15**	**0.32**	NMD
378	At3g62190	DNAJ – N-terminal domain-containing protein	6		FS					
					IR4	PTC+; ds SJ	0.09	**0.13**	**0.16**	NMD