Table S4: Summary genome-wide SPE2 prediction

1	2	3	4	5		6		7		8		9	
SPE2 classification	**SPE2 type**	**total #**	**# of genes**	**chr. location**		**orientation**		**clustered SPE2 elements**		**spacing between half sites**		**rel. position to ATG**	
				subtel.	**cen.**	**sense**	**antisense**	**avg. distance**	**avg. # of SPE2**	**4 bp**	**5 bp**	**first**	**last**
var genes	**upsB**	**330**	**24**	**328**	**2**	**297**	**33**			**268**	**62**		
	cluster 1	264	24	262	2	264	0	12.3 (+/- 5.9)	11.0 (+/- 5.7)	264	0	2132.4 (+/- 70.2)	2403.1 (+/- 172.2)
	cluster 2	66	22	66	0	33	33	62.1 (+/- 43.2)	3.0 (+/- 1.3)	4	62	2698.7 (+/- 162.3)	2774.3 (+/- 162.8)
other genes	**single SPE2**	**42**	**37**	**6**	**36**	**33**	**4**			**27**	**15**		
	upstream	27	27	3	24	27	0			18	9	1096.0 (+/- 646.8)	
	cds	10	10	2	8	6	4			6	4		
	intergenic	5		1	4					3	2		
	multiple SPE2	**3**	1	1	0	1	2			3	0	574	2182
TARE	**all**	**402**		**402**	**0**	**181**	**221**	**379.6 (+/- 525.2)**	**18.3 (+/- 2.5)**	**379**	**23**		
	left	232		232	0	47	185	365.1 (+/- 487.7)	19.3 (+/- 3.0)	219	13		
	right	170		170	0	134	36	399.5 (+/- 573.7)	17.0 (+/- 0.9)	160	10		
	TOTAL	**777**								**677**	**100**		