

S2 Table. Estimated copy number of transgenic insertions. Number of insertions in each transgenic event based on T₁ plants and a TaqMan copy number assay of the transgenic plants relative to *CSSr2I* (1 copy).

		Transgenic family				
		T ₁ Sr21-02	T ₁ Sr21-03	T ₁ Sr21-04	T ₁ Sr21-09	T ₁ Sr21-14
<i>CNLI</i> DNA marker ¹	present	49	57	56	47	44
	absent	0	0	0	1	1
χ^2 <i>P</i> value	1 copy	<0.0001	<0.0001	<0.0001	0.0002	0.0004
	2 copies	0.0707	0.0513	0.0533	0.233	0.2643
	3 copies	0.3778	0.3415	0.3458	0.7711	0.7212
	4 copies	0.6611	0.6364	0.6393	0.0601	0.0489
	5 copies	0.8268	0.8134	0.815	<0.0001	<0.0001
	6 copies	0.9129	0.9061	0.9069	<0.0001	<0.0001
TaqMan	Transgene ² / <i>CSSr2I</i>	4.57	4.98	6.02	3.03	3.71
Copy No.	from genotype	4 to 5	5	6	3	3
	from phenotype	2	2	2	2	1
Expression ³	T ₁ / <i>CSSr2I</i>	2.55	4.77	5.72	4.33	2.97

¹ Genotyped with markers S21CNLI1F5R5 (digested with *SphI*) and Sr21TRYF6-1R5 (Table S1). The estimated number integrates information from TaqMan and segregation data.

² Since T₁s were segregating for copy number, we divided the average of the two highest copy number values in the progeny by *CSSr2I* average copy number.

³ We divided the average of the two highest expression values in the progeny by *CSSr2I* expression value.