

Table S2: Mutation frequencies in Triticale protoplasts acquired by deep-sequencing of short reads. Type and size of mutation generated by individual constructs was quantified as a percentage of the total construct efficiency.

		gRNA-ABA/1/364			gRNA-ABA/1/364+ TREX2			gRNA-ABA/2/323			gRNA-ABA/2/323+ TREX2		
		genome			genome			genome			genome		
		A	B	R	A	B	R	A	B	R	A	B	R
Mutation type frequency [%]	del	0.37	0.25	0.59	0.09	0.04	0.00	36.23	39.06	41.78	0.89	0.15	0.04
	1 bp ins	0.03	0.04	0.07	0.00	0.02	0.00	19.29	26.31	21.60	0.00	0.00	0.00
	sub	3.01	0.17	1.23	0.01	0.15	0.00	2.67	1.23	0.38	0.09	0.30	0.00
	del	28.92	30.46	28.07	14.04	12.00	11.24	32.65	28.70	35.48	14.42	15.19	12.31
	2-10 bp ins	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.23	0.00	0.00	0.00	0.00
	sub	0.08	0.17	0.62	0.01	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00
	del	66.08	66.30	68.06	83.88	85.01	86.37	2.82	2.46	0.66	82.60	83.64	84.09
	11-99 bp ins	0.55	0.66	0.13	0.02	0.06	0.00	6.34	2.01	0.09	0.00	0.00	0.00
	sub	0.06	0.92	0.00	0.01	1.80	0.15	0.00	0.00	0.00	0.00	0.00	0.00
	del	0.28	0.04	0.57	1.39	0.89	2.03	0.00	0.00	0.00	1.60	0.41	3.49
	>100 bp ins	0.07	0.00	0.04	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
	sub	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Complex modifications	0.54	0.99	0.62	0.43	0.04	0.19	0.00	0.00	0.00	0.34	0.32	0.07