	FN M_3 Line							
	E71	**E99**	**E125**	**E128**	**E138**	**E216**	**Total**	**Total (minus spontaneous rate)**
Single base substitutions								
M_3 homozygous variants	18	10	18	6	7	5	64	52.2
M_2 homozygous variants	12.0	6.7	12.0	4.0	4.7	3.3	42.7	34.8
M_1 heterozygous variants	48.0	26.7	48.0	16.0	18.7	13.3	170.7	139.3
M_1 FN mutation rate	**446.5**	**248.1**	**446.5**	**148.8**	**173.6**	**124.0**	**264.6**	**216.0**
Standard error	64.4	48.0	64.4	37.2	40.2	34.0	20.3	18.3
Single base deletions								
M_3 homozygous variants	3	3	4	2	3	3	18	17.0
M_2 homozygous variants	2.0	2.0	2.7	1.3	2.0	2.0	12.0	11.4
M_1 heterozygous variants	8.0	8.0	10.7	5.3	8.0	8.0	48.0	45.4
M_1 FN mutation rate	**74.4**	**74.4**	**99.2**	**49.6**	**74.4**	**74.4**	**74.4**	**70.4**
Standard error	26.3	26.3	30.4	21.5	26.3	26.3	10.7	10.5
Single base insertions								
M_3 homozygous variants	2	0	2	0	1	0	5	4.5
M_2 homozygous variants	1.3	0.0	1.3	0.0	0.7	0	3.3	3.0
M_1 heterozygous variants	5.3	0.0	5.3	0.0	2.7	0	13.3	12.1
M_1 FN mutation rate	**49.6**	**0.0**	**49.6**	**0.0**	**24.8**	**0**	**20.7**	**18.7**
Standard error	21.5	0.0	21.5	0.0	15.2	0.0	5.7	5.4
All single base variants								
M_3 homozygous variants	23	13	24	8	11	8	87	73.2
M_2 homozygous variants	15.3	9	16.0	5	7.3	5	58.0	48.8
M_1 heterozygous variants	61.3	35	64.0	21	29.3	21	232.0	195.2
M_1 FN mutation rate	**570.5**	**322**	**595.3**	**198**	**272.9**	**198**	**359.7**	**302.6**
Standard error	72.9	54.8	74.4	43.0	50.4	43.0	23.6	21.7

Supplemental Table 5. Calculated single base nucleotide mutation rates of six FN M_3 mutagenized *Arabidopsis* lines and correction for spontaneous mutations in each generation using Col-0 MA line mutation rates (Ossowski et al. 2010). Mutation rates were determined from homozygous variants detected in six FN irradiated M_3 plant lines (see Supplemental Table 1). Mutations identified in E99 and E125 lines were validated by Sanger sequencing.