Table 1. Estimated numbers of mutagenized lines required to identify a truncation mutation in mutagenized populations of different plant species

The table shows the number of lines screened to be 95% confident of identifying a non-sense (truncation) mutation in a typical 1.0 kbp of coding region, assuming that such mutations represent 5% of the total.

Species	Ploidy	Mutagen	Mutation frequency (per 10^6 bp)	Number of lines required	Reference
Arabidopsis	Diploid	EMS	3.3	~18 000	Greene *et al.* 2003
Rice	Diploid	MNU	7.4	~8 000	Suzuki *et al.*, 2008
Barley	Diploid	EMS	1.0	~60 000	Caldwell *et al.*, 2004
		NaN$_3$	2.6	~23 000	Talamè *et al.*, 2008
Durum wheat	Tetraploid	EMS	25	~2 400	Slade *et al.*, 2005
Bread wheat	Hexaploid	EMS	42	~1 400	Slade *et al.*, 2005