

S3 Table. Summary of *Ss-unc-22* deletions. Individual wild-type iL3s, and *unc* F₁ iL3s that displayed a nicotine-twitching phenotype, were collected and genomic DNA was prepared. For each iL3, the region around the *Ss-unc-22* target was PCR-amplified along with a control reaction from a different contig than *Ss-unc-22*, as shown in Fig 4A. Instances where the *Ss-unc-22* target failed to amplify but the control reaction was present were considered putative homozygous deletions of *Ss-unc-22*.

target	delivery	repair	# iL3s genotyped	# putative <i>Ss-unc-22</i> -/- deletions (%)
1 (wild type)	—	—	38	0 (0%)
1	RNP	—	36	0 (0%)
2 (wild type)	—	—	76	0 (0%)
2	RNP	—	54	1 (1.9%)
3 (wild type)	—	—	46	0 (0%)
3	RNP	—	18	1 (5.6%)
3	RNP	ssODN	119	6 (5%)