S9 Table. *Strongyloides* CRISPR target sequences. The PAM for each target sequence is underlined. Note that each target sequence contains guanine residues in the 1st, 19th, and 20th positions (GN(17)GG), as recommended in Farboud *et al.* 2015 [49].

target	sequence
Ss-unc-22 site #1	GTCCAGACCAATTCTGGTGG<u>TGG</u>
Ss-unc-22 site #2	GGATCAGTTGACAATAATGG<u>TGG</u>
Ss-unc-22 site #3	GTACAATCAGGTGTTCCAGG<u>TGG</u>
Sr-unc-22 site #1	GTCCAAACCAATTCTGGAGG<u>TGG</u>
Sr-unc-22 site #2	GGATCAACAGATAATAATGG<u>TGG</u>
Ss-tax-4 site #1	GTAACATTTGACTTGATGGG<u>TGG</u>
	PAM