Supplementary Table 2. *ND5* deletion heteroplasmy data.

	Natural Isolate (in order of increasing ND5%)								
Banding Pattern	ED3092	ED3101	EG4181	JU726	PB800	AF16	VT847	HK104	HK105
Intact only	8	8	0	0	0	0	0	0	0
Large only	0	0	6	4	2	0	0	0	0
Large+small	0	0	2	4	6	5	1	0	0
Small only	0	0	0	0	0	3	7	8	8
***ND5*%**	0	0	11	18	24	40	56	60	60

Howe and Denver [10] quantified *ND5* deletion heteroplasmy levels using qPCR and conventional PCR-based analyses of L1-stage nematodes (Fig. 1). To verify that average *ND5* deletion heteroplasmy levels were the same in young adult-stage animals, we applied the latter of these approaches to DNA extractions from single young adult nematodes from each natural isolate. This qualitative assay used primers flanking the *ND5* deletion area and produced banding patterns: Intact only = intact genomes lacking the pseudogenetic element, *ΨND5-2*, only observed; Large only = intact genomes containing *ΨND5-2* only observed; Large+small = intact and deletion-bearing genomes containing *ΨND5-2* observed; Small only = deletion-bearing genomes only observed. The assay produced only single large amplicons in nematodes where ND5 deletion-bearing genomes are ~5% of the total, both a large and a small amplicon in nematodes where deletion levels are ~30%, and only the small amplicon in cases where deletion levels are ~60% [see 10]. Using these rough guidelines, we estimated *ND5* deletion heteroplasmy levels (***ND5*%**) among young adult animals to be slightly higher than previous estimates from L1-stage animals, but of an identical pattern in terms of the rank order of isolate-specific heteroplasmy levels (Fig. 1). We used the more quantitative estimates of *ND5*% in Fig. 1 for all analyses.