SUPPLEMENTARY DATA

Figure S1

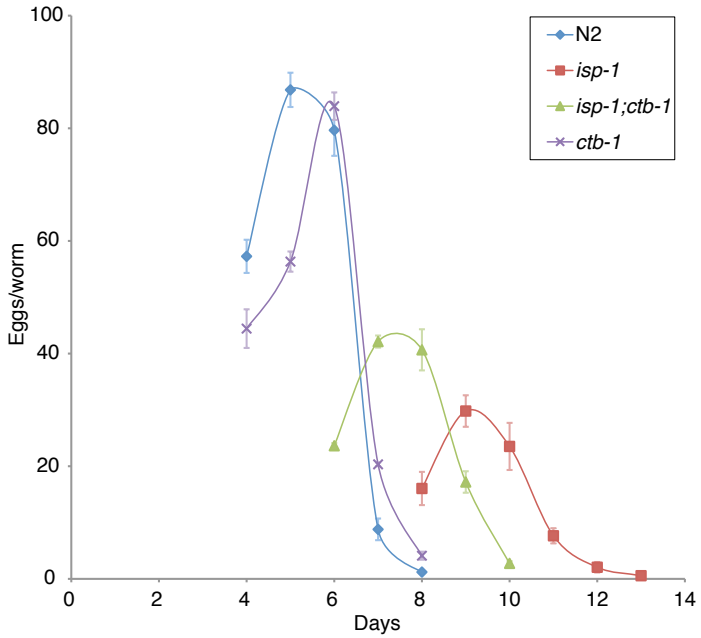

Fig. S1. Number of eggs per worm per day in complex III mutants and wild type. Plates were examined every 24 hours. Day 0 is the day that parental animals were hatched. Data are represented as mean +/- SEM from three independent worm cultures (totaling 30 adult animals for each strain).

Figure S2

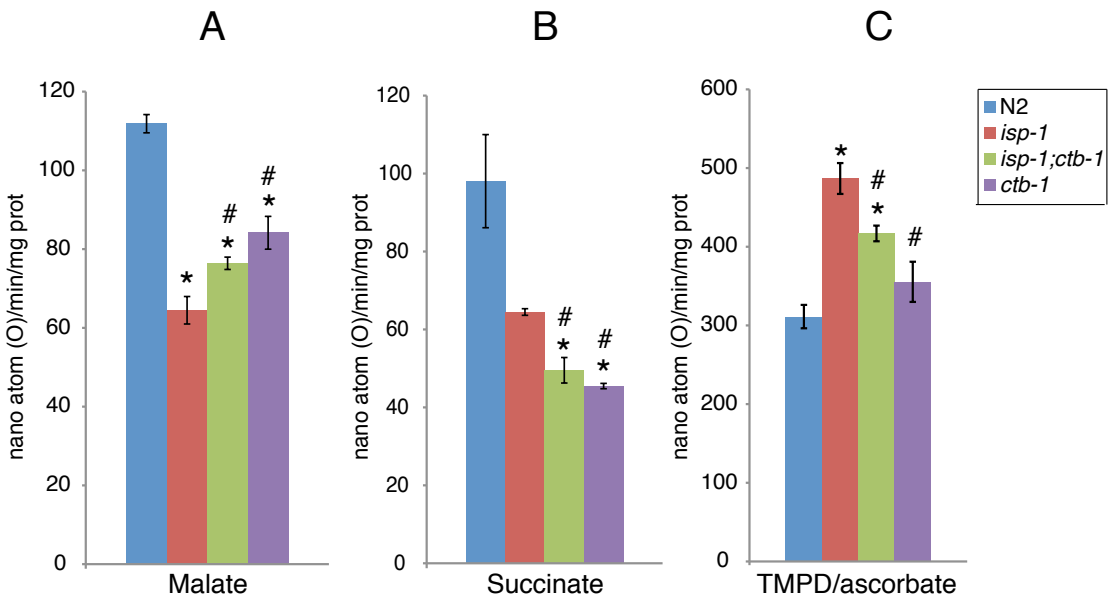

Fig. S2. Integrated Mitochondrial Function. Intact mitochondria were isolated from complex III mutants and wild type, then assayed for oxygen consumption rates. Malate, succinate and TMPD/ascorbate were the substrates to stimulate complex I-, complex II- and complex IV-dependent respiration, respectively. Data are represented as mean +/- SEM from four independent experiments. * and # indicate statistical significances as $p < 0.05$ in comparison to wild type and *isp-1*, respectively.

Figure S3

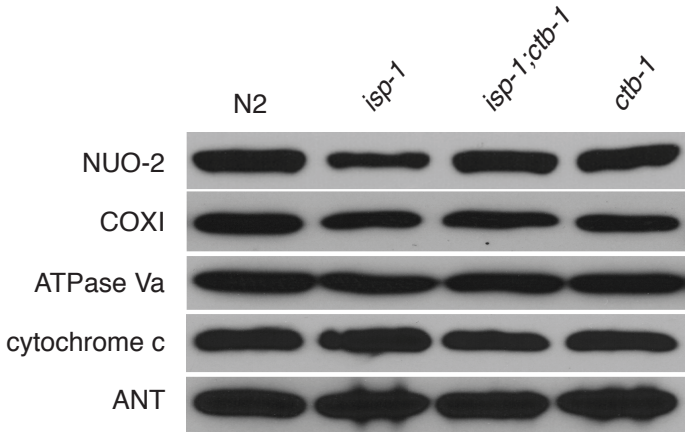

Fig. S3. The stead-state level of respiratory chain subunits. SDS-PAGE/Western blot analysis of NUO-2 subunit of complex I, COX I subunit of complex IV, ATPase subunit Va and cytochrome c; ANT was a loading control. (Quantification of the bands is shown in Table S3).

Table S1

Strain	L3	L4	Adult	Total eggs/worm
N2	D2.5	D3	D3.5	223.8±3.9
isp-1	D5.5	D6.5	D7.5	79.6±10.7
isp-1;ctb-1	D3.5	D4.5	D5	126.4±9.3
ctb-1	D2.5	D3	D3.5	209±9.2

Table S1. Development of complex III mutants and N2 at 20° C. Synchronized cultures of worms were studied for the rate of development to adulthood and subsequent fecundity. Three independent cultures totaling 30 animals for each strain were studied. Error is ± S.D.

Table S2

C. elegans	Human	*isp-1*'s unique bands	
		ISP-A	ISP-B
Y56A3A.19	NDUFB1		+
C18E9.4	NDUFB3		+
W01A8.4	NDUFB4	+	+
ZK809.3	NDUFB6	+	+
D2030.4	NDUFB7	+	+
Y51H1A.3a	NDUFB8	+	+
C16A3.5	NDUFB9	+	+
F59C6.5	NDUFB10	+	+
Y71H2AM.4	NDUFC2	+	+
Y54F10AM.5	NDUFA8	+	
Y54E10BL.5	NDUFS5	+	
MTCE.25	ND4	+	
MTCE.35	ND5	+	
F42G8.12	UQCRFS1	+	+
MTCE.21	MT-CYB	+	
C54G4.8	CYC1	+	+
F56D2.1	UQCRC1	+	+
T10B10.2	UQCRC2	+	+
VW06B3R.1a	UQCRC2	+	
T02H6.11	UQCRB	+	+
F45H10.2	UQCRQ	+	+
MTCE.31	MT-CO2	+	+
W09C5.8	COX4l1	+	+
F26E4.6	COX7C	+	+
cco-2	COX5A		+
Y71H2AM.5	COX6B	+	+

Table S2. Proteomic analysis of ISP-A and ISP-B. Only MRC encoding genes are listed. *C. elegans* and human gene names encoding the identified proteins are obtained from the *C. elegans* Genetics Center and HUGO Gene Nomenclature Committee respectively. Absence of a subunit does not preclude its presence in the protein band as mass spectrometry may miss individual proteins. Turquoise shading indicates complex I subunits, yellow complex III, and peach complex IV.

Table S3

	N2	*isp-1*	*isp-1;ctb-1*	*ctb-1*
NUO-2	100%	68.77±5.44% (0.01)	100.78±1.94% (0.56)	92.21±3.91% (0.08)
Cytochrome c	100%	107.59±7% (0.2)	116.38±23.84% (0.35)	103.13±9.58% (0.63)
COX I	100%	83.32±27.1% (0.4)	96.44±28.12% (0.85)	109.94±34.49% (0.73)

Table S3. Relative expression of NUO-2, cytochrome c and COX I in complex III mutants when ANT is used as a loading control. N2 = 100% expression (n= 3, *p*-values in the parentheses).