

<i>C. briggsae</i> ortholog of the following <i>C.elegans</i> genes:	3'UTR Complementarity with <i>C. briggsae</i> <i>Isy-6</i> (red)	distance from stop codon in <i>C.briggsae</i> (<i>C.elegans</i>)
<i>cog-1</i>	<pre> 5' AC 5'-AAU-CGUC UUAUACAAAA : UUA GCAG--AGUAUGUUUU-5' GCC C </pre>	294 bp (283 bp)
C27H6.3	<pre> UUU UAAAAUUUUUAU 5'- CGGA --UCUU UACAAAA : GCCU AGAG -----AUGUUUU-5' UACGC U </pre>	48 bp (159 bp)
F40H3.4	<pre> AA A 5'-UGU CU GUACAAAA : : : ACG GA UAUGUUUU-5' GCCUU CA G </pre>	122 bp (68 bp)
F55G1.12	<pre> GCUUGUAAAGUU 5'-UGCGUUUU AUACAAAA : : : ACGCAGAG-----UAUGUUUU-5' GCCUU </pre>	79 bp (84 bp)
C02B8.4	<pre> A AAAAA A 5'- AAUG GUCU CAUAUAA : UUAC ---CAGA-GUAUGUU -5' GCC G U </pre>	165 bp (275 bp)
T05C12.8	<pre> A AA A C 5'- G UC AUACAAA C AG-UAUGUUU -5' GCCUUACG AG U </pre>	66 bp (57 bp)
C48D5.2a	<pre> CGAA AA A 5'- GGA G UC AUACAAAA CCU C AG-UAUGUUUU-5' G UACG AG </pre>	406 bp (423 bp)
F59A6.1	<pre> AUUCC UUUCUGA 5'-UGUG UCUU AUACAAA : : ACGC AGAG-----UAUGUUU -5' GCCUU U </pre>	115 bp (323 bp)
ZK637.13	<pre> 5'-UUUUGUACAAAA : : AGAGUAUGUUUU-5' GCCUUACGC </pre>	124 bp (91 bp)
T14G12.2	<pre> AA UCACAGUA 5'-GAAU UGUUUCA UACAAAA : : CUUA -GCAGAGU-----AUGUUUU-5' GC C </pre>	166 bp (155 bp)
T20G5.9	<pre> A 5'-GAUGC GU---GUACAAAA : : UUACG-CA UAUGUUUU-5' GCC GAG </pre>	192 bp (140 bp)
R07E3.5	<pre> 5'-UUUUGUACAAAA : : AGAGUAUGUUUU-5' GCCUUACGC </pre>	65 bp (36 bp)
T04C9.2	<pre> C 5'-GC-UC UAUACAAA CG AG GUAUGUUU -5' GCCUUA C A U </pre>	30 bp (30 bp)

Supplementary Figure 2: Conservation of seed matches to *Isy-6* from *C. elegans* to *C. briggsae*. The pairing of the 3'UTRs of the *C.briggsae* orthologs of the genes shown in Fig.2B to *C.briggsae* *Isy-6* is shown. The conservation of the seed matches may indicate that the seed matches are important in some context, but as we show in this report, they are clearly not a sufficient predictor of a functional *Isy-6* interaction.