

Supporting Information:

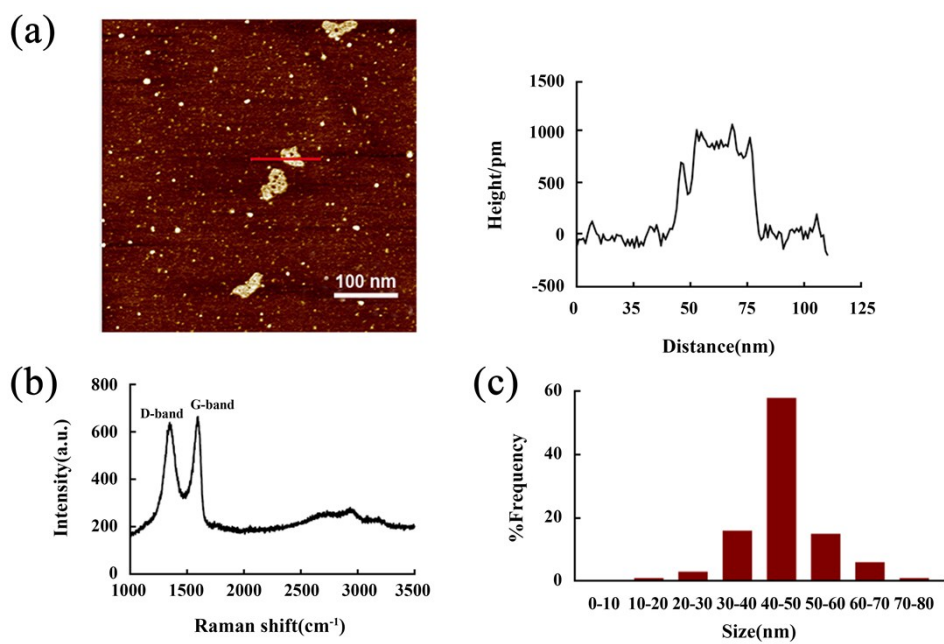


Fig. S1. Physicochemical characterization of GO. (a) AFM analysis of GO after sonification. (b) Raman spectrum of GO. (c) Size distribution of GO after sonication.

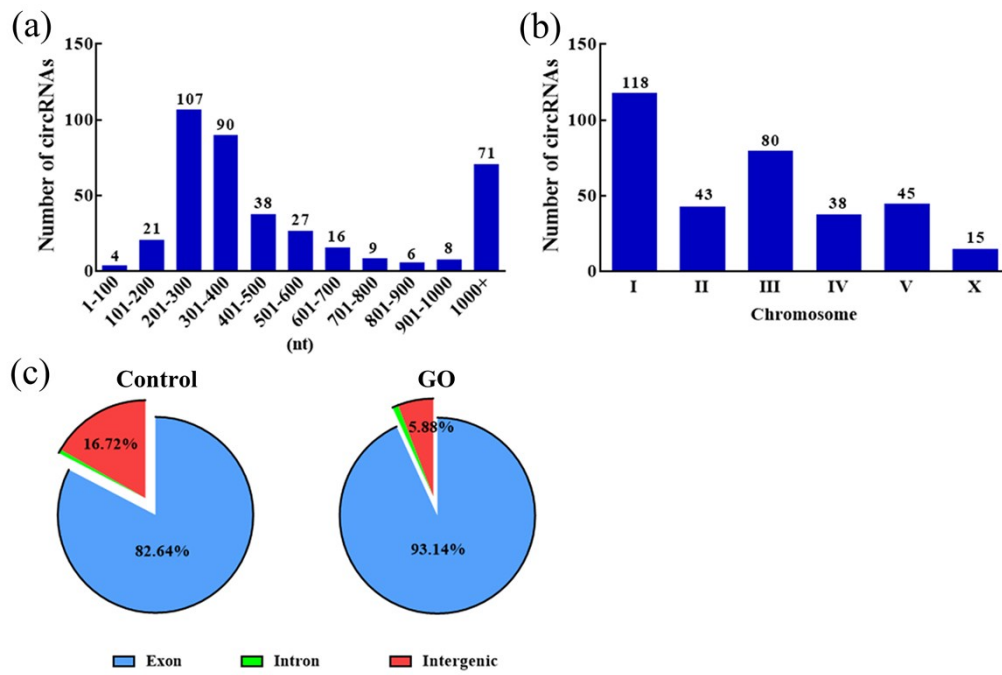


Fig. S2. Transcriptome-wide sequencing of circRNAs. (a) Length distribution for circRNAs. (b) Chromosome distribution of circRNAs. (c) Genome region distribution of circRNAs.

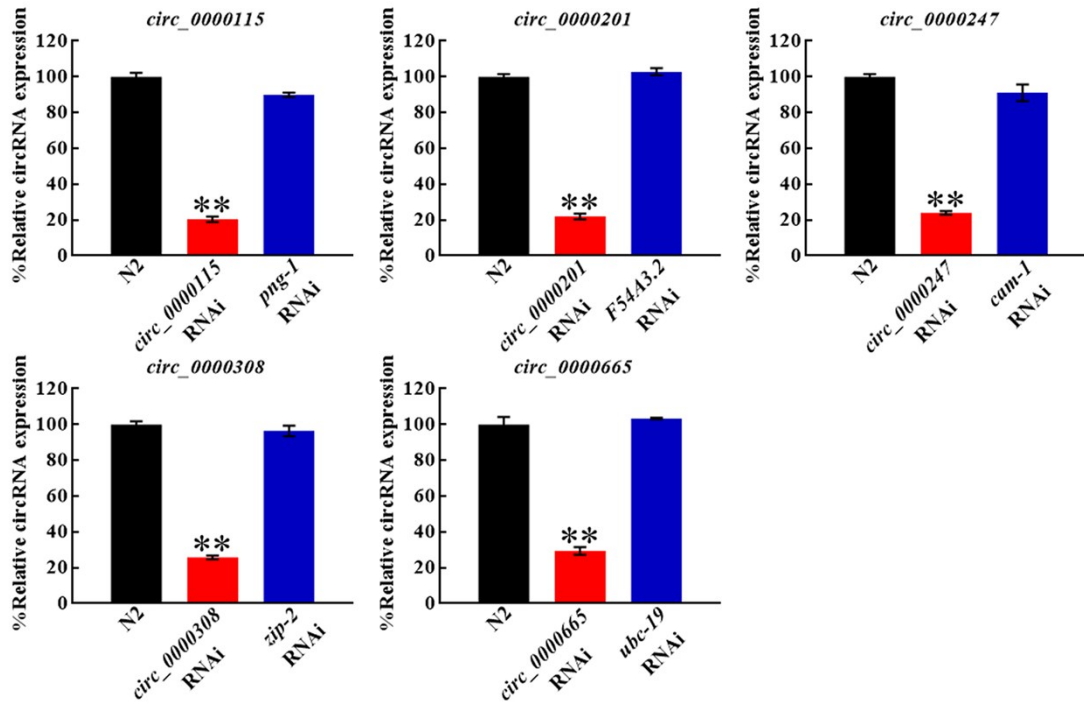


Fig. S3. RNAi efficiency confirmation of five circRNAs (*circ_0000115*, *circ_0000201*, *circ_0000247*, *circ_0000308* and *circ_0000665*). Bars represent means \pm SD. ** $p < 0.01$ vs wild-type N2.

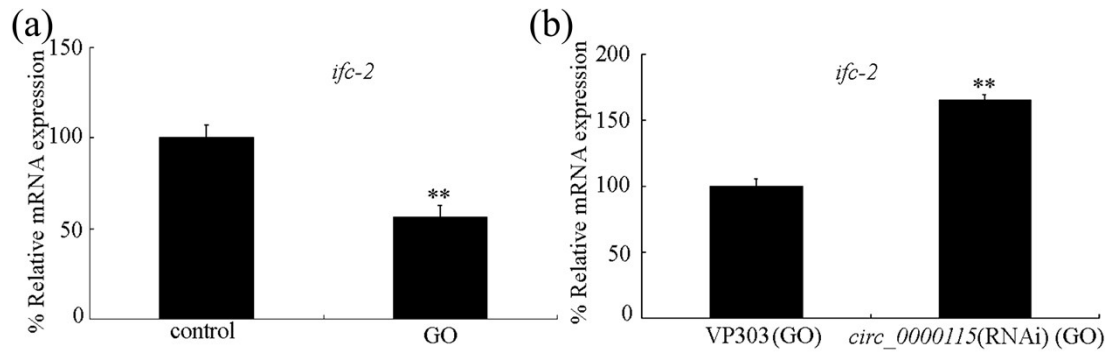


Fig. S4. IFC-2 expression in GO exposed nematodes. (a) Effect of GO exposure on *ifc-2* expression. (b) Effect of *circ_0000115* RNAi knockdown on *ifc-2* expression in GO exposed wild-type nematodes. GO concentration is 100 $\mu\text{g L}^{-1}$. Prolonged exposure to GO was performed from L1-larvae to adult day-1. Bars represent means \pm SD. ** $p < 0.01$ vs control or VP303(GO).

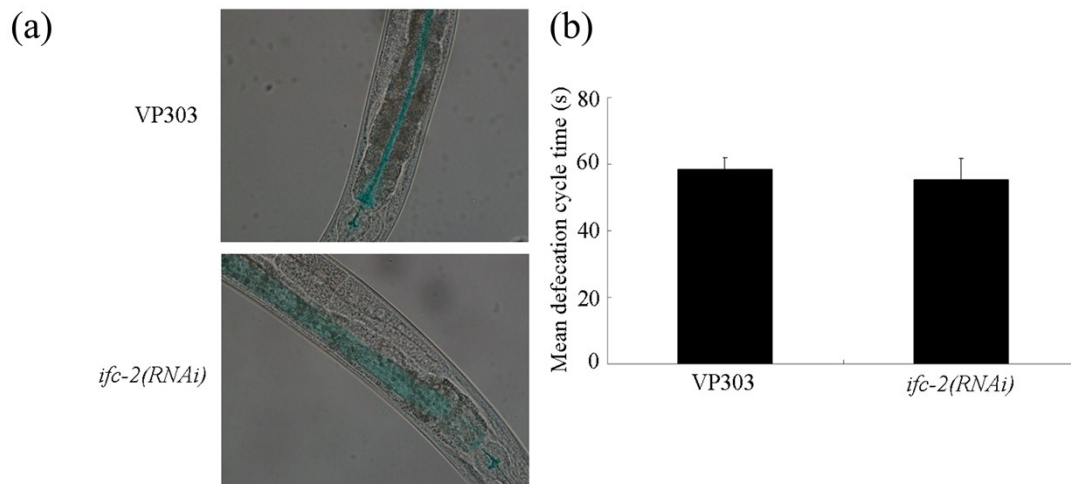


Fig. S5. Effect of intestine-specific RNAi knockdown of *ifc-2* on intestinal permeability and defecation behavior. (a) Effect of intestine-specific RNAi knockdown of *ifc-2* on intestinal permeability and defecation behavior. The nematodes were suspended in blue food dye (eriolgaucine disodium, 5.0% wt/vol) for 3 h, and then analyzed the distribution of blue food dye in the body using a microscope. Twenty nematodes were examined per treatment. The blue dye was distributed in the intestinal lumen of both VP303 and *ifc-2(RNAi)* nematodes. (b) Effect of intestine-specific RNAi knockdown of *ifc-2* on mean defecation cycle length. Individual animal was examined for a fixed number of cycles, and a cycle period was defined as the interval between the initiations of two successive posterior body-wall muscle contraction steps. Thirty replicates were performed. Bars represent means \pm SD.

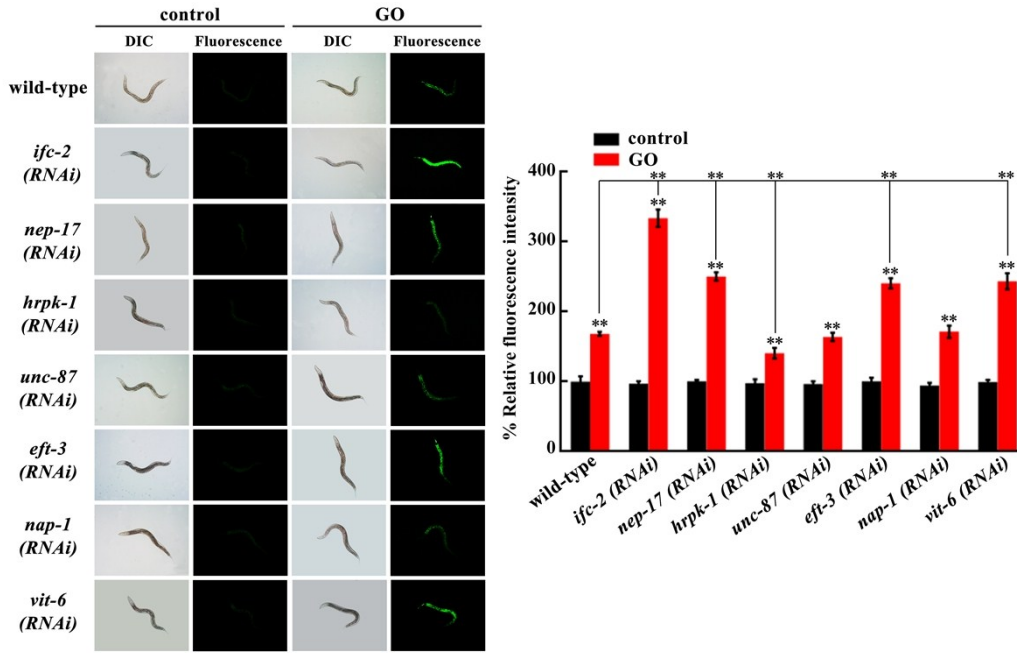


Fig. S6. Effect of RNAi knockdown of seven genes on GO toxicity in inducing ROS production. GO concentration is 100 $\mu\text{g L}^{-1}$. Prolonged exposure to GO was performed from L1-larvae to adult day-1. Bars represent means \pm SD. ** $p < 0.01$ vs control (if not specially indicated).

Table S1. Primer information for qRT-PCR of circRNAs

Gene	Forward primer (5'-3')	Reverse primer (5'-3')	Primer type
<i>circ_0000032</i>	TTAAGCTGGCTGCTCCAAG	ATCCATTGAGGAGAGGGGG	Divergent Primer
<i>circ_0000035</i>	TGGAAAGAGTGTGGCTGAC	CGGCATTGCAGTTGAACTTG	Divergent Primer
<i>circ_0000097</i>	AACGAAACCAGCTACTTCAACA	AGAATCGCTTTGAGAACGTTTC	Divergent Primer
<i>circ_0000107</i>	TGATCTACAAACTGGAAAACCC	GCCGATTTTCAGATTTTCCAGT	Divergent Primer
<i>circ_0000115</i>	GTGGATGGGGAAAGACACTG	ATTAAGAGCGGCAAGCAGAA	Divergent Primer
<i>circ_0000119</i>	ACAAAGGCTGCGCATTCTC	CCAAATTGCTCAAATAGGTG	Divergent Primer
<i>circ_0000132</i>	GCTAAATTCTGTGCGATACCAA	TTTCGAATGTTTTCAACGCC	Divergent Primer
<i>circ_0000155</i>	CACCGTGTACCTACAGCCTTCA	GTTTTACTTGGCGCATTC	Divergent Primer
<i>circ_0000160</i>	GCGTATTGTGGATCCTTATGGC	CAAACGACGCGTAGAAATGGAC	Divergent Primer
<i>circ_0000201</i>	TTTACGCATATTTCTGCCGC	GGAAGTTGTCGTATCAGCCA	Divergent Primer
<i>circ_0000247</i>	TTGTCTCAAATCCAGCAGCC	TCGCACTTAAACCGAACCTC	Divergent Primer
<i>circ_0000281</i>	ATTACACGACGACGACCTTG	AATCGATGCTCCGAACGAAA	Divergent Primer
<i>circ_0000304</i>	GAACTTCTCGACCGTGGATT	TACTTGGACCATCCGTCTCG	Divergent Primer
<i>circ_0000308</i>	CATCTCTGACGCCTACATTCA	TCTTTGCGTGATACATTGTGG	Divergent Primer
<i>circ_0000311</i>	GGGACGCCGTCACAGATTAA	GCAGCACATAAACCACTCGAT	Divergent Primer
<i>circ_0000313</i>	GCCGACTGGATTCGAGACAA	GCTGAATCGCTTCGAGACCT	Divergent Primer
<i>circ_0000315</i>	GCTGTTCGAGTGGTGTGAC	TGAGTCGGCTCCAATCTCAT	Divergent Primer
<i>circ_0000329</i>	GAATTGCCGACACCATCAGT	GATTTCCCGCTCCTCACAAG	Divergent Primer
<i>circ_0000333</i>	ACGCAGAGATTACAGTCGGA	TGATTTTCACGTTTCGGGGT	Divergent Primer
<i>circ_0000342</i>	ATTCCACGTCGAATTTCTCTC	GACCACCTTGAACCCAACAA	Divergent Primer
<i>circ_0000352</i>	CGTCGCTAAGCAAGTCTGAA	CTGGTTTCTGTGATCGGGTG	Divergent Primer
<i>circ_0000356</i>	TTCGCTTTTTCGTTGGGAAT	GGTCGAGAATTTGGGATTGT	Divergent Primer
<i>circ_0000363</i>	CCACATTCGTCATTCTTGCC	ATAGGTGAGCCAGTTGGTGA	Divergent Primer
<i>circ_0000364</i>	GGAATGTTTGACGGGGTTGA	CGTGGATTTCGACAGGGTTAC	Divergent Primer
<i>circ_0000451</i>	CGACATCATAAATACTTTGCCG	TTTCCAATCGGCTGCATTTT	Divergent Primer
<i>circ_0000488</i>	GTGTGGTAACATGCGTTCCGG	AACACTTGCAACCCATGACA	Divergent Primer
<i>circ_0000558</i>	CCACAACACTGGAACAACAAC	AGTCCTTCCGATCCCATCAG	Divergent Primer

<i>circ_0000603</i>	GCCGAGACTAGACTTTGAGC	CCGGCTGAAATCCGTGATAC	Divergent Primer
<i>circ_0000653</i>	AGCAATTAATGGTTATGCGGAG	ATTCGGCGGCTTTCAGTAGA	Divergent Primer
<i>circ_0000665</i>	AAAAGCATAGCCTGAGACGG	TCCAGCGGAATGTGAATGTT	Divergent Primer
<i>circ_0000672</i>	TTGAAAAGTGGCACGGATACA	GTGCATCCATTCTAGCCAA	Divergent Primer
<i>circ_0000699</i>	CTGCTGGCAGAGTTGAAAGA	GCTCATTTTCGGAGACTTCTGC	Divergent Primer
<i>circ_0000713</i>	TCGATGAAGTGTGCGTGAG	TCCCTACGTGGATTCATGGTT	Divergent Primer
<i>circ_0000115</i>	AATTGTTTCGGGCTTCTGC	CGGTCGATCCATAGTATTTTCA	Convergent Primer
<i>tba-1</i>	TCAACACTGCCATCGCCGCC	TCCAAGCGAGACCAGGCTTCAG	Convergent Primer

Table S2. Primer information for RNAi of certain circRNA or gene

Gene	Forward primer (5'-3')	Reverse primer (5'-3')	Restriction enzyme site
<i>circ_0000115</i> RNAi	CAGTCTAGAGATCATGTGGTTG ACG	GTCAAGCTTGAAACAATTGGCC CA	XbaI/HindIII
<i>circ_0000201</i> RNAi	GCACTGCAGATCCAATTTATTA AGAC	ATCAAGCTTCGTTCTTCTTCTTA TCC	PstI/HindIII
<i>circ_0000247</i> RNAi	TATCCATGGTTGTCTCAAATCC AGCA	ATAAAGCTTCGGTCGTTGACCA GTT	NcoI/HindIII
<i>circ_0000308</i> RNAi	CTGCCATGGAGTTCTTTCCACA GCT	CGCCTGCAGCGAAATCTAGTGA CAA	NcoI/PstI
<i>circ_0000665</i> RNAi	ACGCCATGGAAAGGAAAAGCA TAGCC	ACTCTGCAGCGCCAAAAATCCC TTT	NcoI/PstI
<i>png-1 RNAi</i>	ATATCTAGAACATTGTCCAGCG GT	TATAAGCTTGAGCCTTGAACAC CT	XbaI/HindIII
<i>F54A3.2 RNAi</i>	ATACCATGGGCTCTAAACACTC AA	TAGCTGCAGTTCCAATAAATCC AG	NcoI/PstI
<i>cam-1 RNAi</i>	GCGTCTAGAATGATGGATCGTG GA	ATACCATGGGTTGCCGACACTT TT	XbaI/NcoI
<i>zip-2 RNAi</i>	ATACCATGGGGAAAATCCACGT CATCG	ATGCTGCAGTGTAGTCCTCGAC TTG	NcoI/PstI
<i>ubc-19 RNAi</i>	TACTCTAGATGGACACCGACAA GTGCA	AGTCCATGGGGTGATCACAGTC ATC	XbaI/NcoI
<i>ifc-2 RNAi</i>	CGATCTAGAAGCAAACAACCG CTCACCG	ATACCATGGACGGAGGGTCGCA ATCT	XbaI/NcoI
<i>nep-17 RNAi</i>	ATACTGCAGCCAAAACCTCCAT CCG	ATAGGTACCTTGCATAGGCCTT CTG	PstI/KpnI
<i>hrpk-1 RNAi</i>	GAGTCTAGATTCCCTTCAGTTC CGTG	ATACCATGGGATCCACCGAATC GTTC	XbaI/NcoI
<i>unc-87 RNAi</i>	AGATCTAGAATCATCAATTGGA CCACCAC	ATACTGCAGTTGGTTGCTCCTG ATT	XbaI/PstI
<i>eft-3 RNAi</i>	CGATCTAGATGGAGTCAAGCA ACTC	ATACTGCAGTTCTTCTTTGGTGC AGC	XbaI/PstI
<i>nap-1 RNAi</i>	TGATCTAGATCAGGCTTTGCCT CTC	ATAGGTACCCTGACACATCATC ACC	XbaI/KpnI
<i>vit-6 RNAi</i>	CGACCATGGCAATCAATGTTGA ACC	ATAGGTACCCTCCTCCATTTGT GGT	NcoI/KpnI

Table S3. Primer information for vector construction

	Forward primer (5'-3')	Reverse primer (5'-3')	Restriction enzyme site
<i>Pges-1</i>	ATATCTAGAAGCCACTCAGCCA CTTCA	ATAGGATCCCATCTGAATTCAA AGATA	XbaI/BamHI
<i>ifc-2/M6.1d</i>	ATAGGATCCATGTTCGACTTACG CGGCCT	TAACCCGGGGTCAAGGTAGACA AACCA	BamHI/SmaI

Table S4. Information for dysregulated known circRNAs

CircRNA ID	CircRN		Chromosome location	Gene ID	Gene	logFC
		A type				
<i>circ_0000032</i>	exon		I :1817301:1817613	WBGene00022142	<i>Y71G12B.2</i>	-7.451958
<i>circ_0000304</i>	exon		III:730585:731798	WBGene00003936	<i>gei-16</i>	-7.039664
<i>circ_0000035</i>	exon		I :1999954:2001195	WBGene00021238	<i>Y51F10.9</i>	-6.558617
<i>circ_0000247</i>	exon		II :9304008:9304745	WBGene00000289	<i>cam-1</i>	-6.354519
<i>circ_0000097</i>	exon		I :9548218:9548654	WBGene00007985	<i>C36F7.2</i>	-6.116712
<i>circ_0000558</i>	exon		IV:11722489:1172305 5	WBGene00010444	<i>magi-1</i>	-6.110452
<i>circ_0000315</i>	exon		III:1187295:1187741	WBGene00022491	<i>Y119D3B.14</i>	-5.981286
<i>circ_0000313</i>	exon		III:1074167:1076543	WBGene00006697	<i>Y92C3B.2a.1</i>	-5.834821
<i>circ_0000311</i>	exon		III:987238:987508	WBGene00019915	<i>tbc-10</i>	-5.831819
<i>circ_0000160</i>	exon		I:14427055:14428997	WBGene00013670	<i>Y105E8A.10</i>	-5.831819
<i>circ_0000653</i>	exon		V:18065061:1806546 3	WBGene00013345	<i>Y59A8B.8</i>	-5.831801
<i>circ_0000713</i>	exon		X:9510459:9511097	WBGene00001516	<i>gap-2</i>	-5.733819
<i>circ_0000132</i>	exon		I :12878627:1287958 2	WBGene00003905	<i>pad-1</i>	-5.476467
<i>circ_0000342</i>	exon		III:2140079:2140320	WBGene00021698	<i>fri-1</i>	-5.466567
<i>circ_0000356</i>	exon		III:3088300:3088575	WBGene00004787	<i>sft-1</i>	-5.446967
<i>circ_0000488</i>	exon		IV:2229794:2230105	WBGene00020208	<i>T04C4.1</i>	-5.476467
<i>circ_0000107</i>	exon		I :10977642:1097804 9	WBGene00013123	<i>Y52B11A.3</i>	-5.259465
<i>circ_0000119</i>	exon		I :11593916:1159429 4	WBGene00006807	<i>unc-75</i>	-5.239265
<i>circ_0000155</i>	exon		I :13944636:1394639 1	WBGene00013506	<i>usp-3</i>	-5.229495
<i>circ_0000451</i>	exon		III:12631806:1263480	WBGene00004161	<i>Y111B2A.14.</i>	-5.219665

		9		2	
<i>circ_0000352</i>	exon	III:2482724:2483108	WBGene00004884	<i>smg-6</i>	-2.795358
<i>circ_0000364</i>	exon	III:3299365:3299857	WBGene00021812	<i>Y53G8AR.5</i>	-2.775752
<i>circ_0000281</i>	exon	II:14870599:1487100	WBGene00011044	<i>R05H10.3</i>	-2.739129
		6			
<i>circ_0000672</i>	exon	V:18956093:1895642	WBGene00013587	<i>Y80D3A.9</i>	-2.253039
		3			
<i>circ_0000665</i>	exon	V:18688227:1868846	WBGene00006714	<i>ubc-19</i>	-2.174839
		9			
<i>circ_0000329</i>	exon	III:1675421:1675681	WBGene00021260	<i>Y22D7AR.6</i>	-2.124374
<i>circ_0000201</i>	exon	II:2246478:2246959	WBGene00018781	<i>F54A3.2</i>	-2.031746
<i>circ_0000603</i>	exon	V:4571714:4572374	WBGene00022015	<i>Y61A9LA.3</i>	-1.837405
<i>circ_0000115</i>	exon	I:11384076:1138435	WBGene00010160	<i>png-1</i>	-1.796724
		6			
<i>circ_0000333</i>	exon	III:1927665:1927938	WBGene00004128	<i>F53A3.6</i>	-1.196125
<i>circ_0000363</i>	exon	III:3113760:3114033	WBGene00021820	<i>nipa-1</i>	-1.14193
<i>circ_0000699</i>	exon	X:344165:345275	WBGene00015430	<i>C04E7.3</i>	5.8348208
<i>circ_0000308</i>	exon	III:834296:835205	WBGene00019327	<i>zip-2</i>	6.0936363

Table S5. Information for dysregulated novel circRNAs

CircRNA ID	CircRNA type	Gene ID	logFC	New ID (Ivanov 2015)
IV:17278959:17279168	exon	WBGene00002005	-7.568977	
X:8718612:8718907	exon	WBGene00018731	-7.379973	
II:10013295:10013341	exon	WBGene00002265	-6.650769	
I:1670969:1671255	exon	WBGene00022158	-5.981286	<i>cel_circ_000086</i>
II:11133703:11133837	exon	WBGene00009578	-5.971216	
III:2745138:2745409	exon	WBGene00022179	-5.811319	<i>cel_circ_000101</i>
V:18857769:18858076	exon	WBGene00006945	-5.476467	<i>cel_circ_000077</i>
I:1674941:1675386	exon	WBGene00185098	5.519198	<i>cel_circ_000121</i>
I:3142042:3142265	exon	WBGene00019597	5.509298	<i>cel_circ_000142</i>
IV:11275681:11276616	exon	WBGene00001796	5.501128	<i>cel_circ_000078</i>

Table S6. Information for mass spectrometry result (top 15 proteins)

No	Score	Name	Gene	Peptides (95%)
1	49.15	tr Q6LD30 Q6LD30_CAEEL	<i>unc-87</i>	47
2	45.08	tr G8JY94 G8JY94_CAEEL	<i>ifc-2</i>	23
3	38.61	sp P98080 UCR1_CAEEL	<i>ucr-1</i>	21
4	30.46	sp P53013 EF1A_CAEEL	<i>eft-3</i>	16
5	26.34	tr Q23050 Q23050_CAEEL	<i>clik-1</i>	17
6	25.79	tr M1Z854 M1Z854_CAEEL	<i>ifb-2</i>	14
7	22.56	tr H2KYS1 H2KYS1_CAEEL	<i>hsp-43</i>	16
8	22.12	tr Q19007 Q19007_CAEEL	<i>nap-1</i>	11
9	19.89	tr Q9XW17 Q9XW17_CAEEL	<i>car-1</i>	10
10	19.04	sp Q19289 IFB1_CAEEL	<i>ifb-1</i>	13
11	18.36	tr P91277 P91277_CAEEL	<i>hrpk-1</i>	11
12	18.17	tr G4SI07 G4SI07_CAEEL	<i>gei-15</i>	10
13	18.11	sp P10567 MYSP_CAEEL	<i>unc-15</i>	10
14	17.51	sp P18948 VIT6_CAEEL	<i>vit-6</i>	11
15	16.71	tr O45569 O45569_CAEEL	<i>nep-17</i>	10

Table S7. RPIseq prediction result of *circ_0000115*-protein binding capacity

No	Gene name	<i>circ_0000115</i>-protein RPIseq
1	<i>ifc-2</i>	0.8
2	<i>nep-17</i>	0.7
3	<i>hsp-43</i>	0.65
4	<i>hrpk-1</i>	0.65
5	<i>unc-87</i>	0.6
6	<i>eft-3</i>	0.6
7	<i>clik-1</i>	0.55
8	<i>nap-1</i>	0.55
9	<i>vit-6</i>	0.55
10	<i>car-1</i>	0.5