Fig. S1. Effects of exposure to coal combustion related $PM_{2.5}$ on transcriptional expressions of *sod-3*, *sod-4*, and *ctl-3*.   Bars represent means ± SD.   [**]$P < 0.01$ *vs* N2 (if not specially indicated).

Table S1. Primers for reverse transcription of miRNAs

miRNA	Primer
mir-230	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTGGATACG ACTCTCCTG
mir-231	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTGGATACG ACTTCTGCC
mir-232	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTGGATACG ACTCACCGC
mir-83	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTGGATACG ACTTACTGA
mir-62	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTGGATACG ACCTGTAAG
mir-251	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTGGATACG ACTAAGAGC
mir-234	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTGGATACG ACAAGGGTA
mir-35	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTGGATACG ACACTGCTA

Table S2. Primers for quantitative real-time PCR of miRNAs

miRNA	primer
mir-230	CTACATGTATTAGTTGTGCGACCAGGAGA
mir-231	TTATACTAAGCTCGTGATCAACAGGCAGAA
mir-232	ATACGTTAAATGCATCTTAACTGCGGTGA
mir-83	CCGCGCTAGCACCATATAAATTCAGTAA
mir-62	TGCATATGATATGTAATCTAGCTTACAG
mir-251	TATCTATTAAGTAGTGGTGCCGCTCTTA
mir-234	TATCCGTTATTGCTCGAGAATACCCTT
mir-35	TACGTATCACCGGGTGGAAACTAGCAGT
Common reward primer	GTGCAGGGTCCGAGGT

Table S3. Primers used for quantitative real-time PCR of genes

Gene	Forward Primer	Reverse Primer
tba-1	TCAACACTGCCATCGCCGCC	TCCAAGCGAGACCAGGCTTCAG
clk-1	GCTTATGCTCTCGGTGTCGGTTCA	ATCGTCGGCAAGGAGTTCTTTCAA
gas-1	ACCCAAACCCGAAACTCCCACACA	TTCTCGTCGAAATCCGAAACCCGC
isp-1	CATTCCCCGATATGTCAAACTATC	TGTACAACTTCCTTTCCGGCCCAC
sod-1	GAATCTTCTCACTCAGGTCTCCAA	TTCTGTGTGATCCAGATAGTACCG
sod-2	ACTATGCTGATTTGGAGCCTGTAA	GTGAAGCTTTTCCTCAATTTGGTT
sod-3	ATCACTATTGCGGTTCAAGGCTCT	AATTCCAAAAAGTGGGACCATTCC
sod-4	GTTTCCGACTCTCTTGCCTCATTA	GCTTCCAGCATTTCCAGTTGTTTT
ctl-1	CTCCTACACGGACACGCAT	GCATCTCCCTGGCTTTCAT
ctl-2	CGAACAGCTTCAACTATGG	GTGGCTGGGAATGTGGTAT
ctl-3	TTCTCCTACACGGACACGC	GCATCTCCCTGGCTTTCAT
mev-1	GGAATTCGCTTCTTAGGAT	GCAGTCTTGTTGCTCTTGT
smk-1	AACGAGACGCAACCAACC	CTCACCCAGCCTCCCAAT

Table S4. Primers used for RNAi construction

Gene	Forward Primer	Reverse Primer
sod-3	CTATCTAGATACTGCTCGCACTGC	CTGCCATGGTTATTGTCGAGCATT
sod-4	AGCTCTAGAGCACGTGCCTACATTT	TATCCATGGCGATAGTTCCACATGCA
ctl-3	GCGTCTAGACGGTCAACGACACAAA	TATCCATGGCTTGCCGACCTCGATC

Table S5. The dysregulated miRNAs in coal combustion related PM$_{2.5}$ exposed nematodes

miRNA	chromosome	start	end	strand	FC	Regulation
mir-1020-5p	III	10047794	10047815	-	5.74628	up
mir-124-3p	IV	11871798	11871818	+	3.16375	up
mir-229-5p	III	2172459	2172484	+	3.10218	up
mir-230-5p	X	5803908	5803930	+	-2.84277	down
mir-231-3p	III	7545072	7545095	-	3.28045	up
mir-232-3p	IV	10994184	10994206	-	3.00402	up
mir-234-3p	II	14466278	14466298	-	-2.57702	down
mir-251	X	11004746	11004767	+	3.32446	up
mir-35-3p	II	11537668	11537689	+	-3.71203	down
mir-37-3p	II	11537893	11537914	+	-3.32492	down
mir-38-3p	II	11537990	11538011	+	-3.14307	down
mir-392-3p	X	13597298	13597319	+	5.44682	up
mir-40-3p	II	11538239	11538260	+	-4.21407	down
mir-43-3p	II	11889970	11889992	+	4.15692	up
mir-4816-3p	I	6185122	6185144	+	4.87381	up
mir-49-3p	X	9989342	9989363	+	-2.56882	down
mir-61-5p	V	11770111	11770132	-	-3.10609	down
mir-62	X	12692644	12692665	+	2.98290	up
mir-67-3p	III	5931364	5931387	-	4.97758	up
mir-784-5p	X	8074975	8074996	-	-3.58725	down
mir-792-3p	V	3042105	3042127	-	2.99367	up
mir-79-3p	I	9333006	9333027	+	2.93680	up
mir-797-5p	X	4757123	4757147	+	4.84776	up
mir-799	X	8600657	8600678	-	4.87381	up
mir-83-3p	IV	7841691	7841712	+	-2.71474	down

Table S6. Gene ontology (GO) terms with gene counts more than 20 based on predicted targets of down-regulated miRNA induced by coal combustion related PM$_{2.5}$

NO	GO ID	GO Term	Count
1	GO:0040011	locomotion	478
2	GO:0009792	embryonic development	381
3	GO:0002119	larval development	361
4	GO:0040010	positive regulation of growth rate	355
5	GO:0000003	reproduction	276
6	GO:0040007	growth	235
7	GO:0010171	body morphogenesis	183
8	GO:0018991	oviposition	129
9	GO:0040017	positive regulation of locomotion	126
10	GO:0040035	hermaphrodite genitalia development	118
11	GO:0040018	positive regulation of body size	109
12	GO:0018996	molting cycle	107
13	GO:0006468	protein amino acid phosphorylation	96
14	GO:0007165	signal transduction	93
15	GO:0002009	morphogenesis of an epithelium	83
16	GO:0008152	metabolism	80
17	GO:0008340	determination of adult life span	75
18	GO:0006810	transport	71
19	GO:0006508	proteolysis	57
20	GO:0007242	intracellular signaling cascade	55
21	GO:0006811	ion transport	55
22	GO:0043051	regulation of pharyngeal pumping	54
23	GO:0009790	embryonic development	53
24	GO:0006952	defense response	52
25	GO:0006886	intracellular protein transport	48
26	GO:0040002	cuticle biosynthesis	47

27	GO:0045449	regulation of transcription	46
28	GO:0007264	small GTPase mediated signal transduction	45
29	GO:0016477	cell migration	39
30	GO:0007155	cell adhesion	37
31	GO:0006412	protein biosynthesis	34
32	GO:0046662	regulation of oviposition	30
33	GO:0015031	protein transport	30
34	GO:0048489	synaptic vesicle transport	26
35	GO:0016311	dephosphorylation	26
36	GO:0005975	carbohydrate metabolism	26
37	GO:0006470	protein amino acid dephosphorylation	24
38	GO:0044262	cellular carbohydrate metabolism	24
39	GO:0007186	G-protein coupled receptor protein signaling pathway	24
40	GO:0048488	synaptic vesicle endocytosis	23
41	GO:0007517	muscle development	23
42	GO:0040012	regulation of locomotion	23
43	GO:0007617	mating behavior	22
44	GO:0006937	regulation of muscle contraction	22
45	GO:0040015	negative regulation of body size	22
46	GO:0040024	dauer larval development	20
47	GO:0006813	potassium ion transport	20

Table S7. Gene ontology (GO) terms with gene counts more than 20 based on predicted targets of up-regulated miRNA induced by coal combustion related PM$_{2.5}$

NO	GO ID	GO Term	Count
1	GO:0009792	embryonic development	691
2	GO:0002119	larval development	585
3	GO:0040010	positive regulation of growth rate	561
4	GO:0040011	locomotion	540
5	GO:0000003	reproduction	432
6	GO:0040007	growth	406
7	GO:0040035	hermaphrodite genitalia development	247
8	GO:0010171	body morphogenesis	226
9	GO:0006468	protein amino acid phosphorylation	188
10	GO:0018991	oviposition	171
11	GO:0002009	morphogenesis of an epithelium	166
12	GO:0040018	positive regulation of body size	153
13	GO:0006810	transport	133
14	GO:0007165	signal transduction	117
15	GO:0018996	molting cycle	109
16	GO:0008152	metabolism	103
17	GO:0040017	positive regulation of locomotion	90
18	GO:0009790	embryonic development	85
19	GO:0006952	defense response	70
20	GO:0008340	determination of adult life span	66
21	GO:0016477	cell migration	65
22	GO:0006508	proteolysis	65
23	GO:0007242	intracellular signaling cascade	63
24	GO:0045449	regulation of transcription	49
25	GO:0007186	G-protein coupled receptor protein signaling pathway	43
26	GO:0008406	gonad development	42

27	GO:0005975	carbohydrate metabolism	42
28	GO:0040025	vulval development	39
29	GO:0006811	ion transport	38
30	GO:0040024	dauer larval development	37
31	GO:0007264	small GTPase mediated signal transduction	35
32	GO:0006412	protein biosynthesis	35
33	GO:0007638	mechanosensory behavior	34
34	GO:0006470	protein amino acid dephosphorylation	34
35	GO:0006813	potassium ion transport	32
36	GO:0051056	regulation of small GTPase mediated signal transduction	32
37	GO:0040027	negative regulation of vulval development	31
38	GO:0016311	dephosphorylation	31
39	GO:0007052	mitotic spindle organization and biogenesis	29
40	GO:0015031	protein transport	29
41	GO:0009612	response to mechanical stimulus	28
42	GO:0045132	meiotic chromosome segregation	28
43	GO:0000910	cytokinesis	28
44	GO:0030421	defecation	26
45	GO:0040026	positive regulation of vulval development	26
46	GO:0048477	oogenesis	26
47	GO:0006886	intracellular protein transport	26
48	GO:0040015	negative regulation of body size	25
49	GO:0044262	cellular carbohydrate metabolism	24
50	GO:0006812	cation transport	24
51	GO:0045138	tail tip morphogenesis	21
52	GO:0009952	anterior/posterior pattern formation	20
53	GO:0006816	calcium ion transport	20
54	GO:0043062	extracellular structure organization and biogenesis	20
55	GO:0035046	pronuclear migration	20

| 56 | GO:0006418 | tRNAaminoacylation for protein translation | 20 |

Table S8. Signaling pathways with gene counts more than 4 based on predicted targets of up-regulated miRNAs in coal combustion related $PM_{2.5}$ exposed nematodes (Gene counts > 4)

No.	pathway	gene count
1	Oxidative stress response	4
2	Oxytocin receptor mediated signaling pathway	7
3	Hedgehog signaling pathway	4
4	Beta2 adrenergic receptor signaling pathway	4
5	EGF receptor signaling pathway	12
6	TGF-beta signaling pathway	4
7	Muscarinic acetylcholine receptor 2 and 4 signaling pathway	7
8	Endothelin signaling pathway	12
9	Adrenaline and noradrenaline biosynthesis	5
10	Wnt signaling pathway	16
11	Metabotropic glutamate receptor group II pathway	5
12	Notch signaling pathway	6
13	FGF signaling pathway	13
14	Beta1 adrenergic receptor signaling pathway	4
15	Parkinson disease	5
16	Muscarinic acetylcholine receptor 1 and 3 SP	7
17	Apoptosis signaling pathway	7
18	Alzheimer disease-presenilin pathway	6
19	Metabotropic glutamate receptor group III pathway	7
20	Integrin signaling pathway	11
21	Histamine H1 receptor mediated signaling pathway	5
22	Inflammation mediated by chemokine and cytokine signaling pathway	13
23	VEGF signaling pathway	6
24	Cadherin signaling pathway	6
25	Nicotinic acetylcholine receptor signaling pathway	14
26	PI3 kinase pathway	4

27	Ubiquitin proteasome pathway	6
28	PDGF signaling pathway	10
29	Ionotropic glutamate receptor pathway	6
30	Thyrotropin-releasing hormone receptor signaling pathway	6
31	Alzheimer disease-amyloid secretase pathway	9

Table S9. Signaling pathways with gene counts more than 4 based on predicted targets of based on down-regulated miRNAs in coal combustion related $PM_{2.5}$ exposed nematodes

No.	pathway	gene count
1	Oxytocin receptor mediated signaling pathway	6
2	Beta2 adrenergic receptor signaling pathway	4
3	EGF receptor signaling pathway	4
4	Muscarinic acetylcholine receptor 2 and 4 signaling pathway	9
5	Endothelin signaling pathway	6
6	Wnt signaling pathway	6
7	Metabotropic glutamate receptor group II pathway	7
8	FGF signaling pathway	9
9	Parkinson disease	4
10	Muscarinic acetylcholine receptor 1 and 3 signaling pathway	6
11	Alzheimer disease-presenilin pathway	5
12	Metabotropic glutamate receptor group III pathway	6
13	Integrin signaling pathway	6
14	Inflammation mediated by chemokine and cytokine signaling pathway	5
15	Cadherin signaling pathway	4
16	Nicotinic acetylcholine receptor signaling pathway	12
17	PI3 kinase pathway	4
18	PDGF signaling pathway	5
19	Thyrotropin-releasing hormone receptor signaling pathway	6
20	Alzheimer disease-amyloid secretase pathway	5