Table S1. Statistical analysis of *C. elegans* survival time under heat stress after curcumin treatment.

Group	Number (*n*)	Mean time (h)	% extension	*P*	
				Ctl	RAP
Ctl	77	10.130±0.349			<0.001
RAP	78	12.647±0.385	24.847	<0.001	
25 μM	77	11.333±0.386	11.876	0.020	0.004
50 μM	90	11.622±0.340	14.729	<0.001	0.066
100 μM	86	11.814±0.295	16.624	<0.001	0.006
200 μM	86	12.140±0.317	19.842	<0.001	0.245

Table S2. Statistical analysis of *C. elegans* survival time under heat stress after BDMC treatment.

Group	Number (*n*)	Mean time (h)	% extension	*P*	
				Ctl	RAP
Ctl	77	10.13±0.349			<0.001
RAP	78	12.647±0.385	24.847	<0.001	
25 μM	75	11.307±0.377	11.619	0.006	0.009
50 μM	90	12.28±0.273	21.224	<0.001	0.106
100 μM	66	12.697±0.339	25.341	<0.001	0.798
200 μM	88	12.168±0.286	20.118	<0.001	0.495

Table S3. Statistical analysis of *C. elegans* survival time under heat stress after demethoxycurcumin treatment.

Group	Number (*n*)	Mean time (h)	% extension	*P*	
				Ctl	RAP
Ctl	73	8.849±0.276			<0.001
RAP	74	11.364±0.566	28.421	<0.001	
25 μM	78	9.462±0.205	6.927	0.206	<0.001
50 μM	88	10.045±0.194	13.516	0.001	<0.001
100 μM	90	9.289±0.193	4.972	0.428	<0.001
200 μM	82	9.683±0.201	9.425	0.048	<0.001

Table S4. Statistical analysis of *C. elegans* survival time under heat stress after tetrahydrocurcumin treatment.

Group	Number (*n*)	Mean time (h)	% extension	*P*	
				Ctl	RAP
Ctl	73	8.849±0.276			<0.001
RAP	74	11.364±0.566	28.421	<0.001	
25 μM	85	10.071±0.172	13.809	0.001	<0.001
50 μM	82	9.829±0.174	11.075	0.022	<0.001
100 μM	86	9.233±0.239	4.339	0.298	<0.001
200 μM	70	9.343±0.229	5.583	0.383	<0.001

Table S5. Statistical analysis of *C. elegans* survival time in lifespan assays after curcumin treatment.

Group	Number (*n*)	Mean time (h)	% extension	*P*	
				Ctl	RAP
Ctl	75	20.133±0.662			<0.001
RAP	71	24.341±0.957	20.901	<0.001	
25 μM	73	20.302±0.878	0.839	0.598	0.002
50 μM	71	21.020±0.897	4.406	0.165	0.015
100 μM	72	22.419±0.854	11.354	0.006	0.193
200 μM	73	22.868±0.957	13.585	0.002	0.501

Table S6. Statistical analysis of *C. elegans* survival time in lifespan assays after BDMC treatment.

Group	Number (*n*)	Mean time (d)	% extension	*P*	
				Ctl	RAP
Ctl	98	20.388±0.478			<0.001
RAP	75	24.215±0.667	18.771	<0.001	
25 μM	86	22.981±0.535	12.718	<0.001	0.162
50 μM	88	23.188±0.552	13.734	<0.001	0.308
100 μM	87	24.000±0.469	17.716	<0.001	0.506
200 μM	85	23.398±0.467	14.764	<0.001	0.146

Table S7. Statistical analysis of *C. elegans* survival time in lifespan assays after demethoxycurcumin treatment.

Group	Number (*n*)	Mean time (d)	% extension	*P*	
				Ctl	RAP
Ctl	75	20.133±0.662			<0.001
RAP	81	24.341±0.957	20.901	<0.001	
25 μM	78	22.923±0.720	13.858	0.001	0.271
50 μM	71	22.000±0.896	9.273	0.012	0.153
100 μM	81	21.827±0.734	8.414	0.016	0.051
200 μM	89	21.056±0.715	4.585	0.094	0.026

Table S8. Statistical analysis of *C. elegans* survival time in lifespan assays after tetrahydrocurcumin treatment.

Group	Number (*n*)	Mean time (d)	% extension	*P*	
				Ctl	RAP
Ctl	75	20.133±0.662			<0.001
RAP	81	24.341±0.957	20.901	<0.001	
25 μM	90	22.022±0.698	9.383	0.010	0.078
50 μM	83	22.072±0.744	9.631	0.007	0.094
100 μM	87	21.047±0.674	4.540	0.057	0.020
200 μM	76	20.053±0.727	-0.397	0.657	0.001

Table S9. Statistical analysis of *C. elegans* survival time in lifespan assays after early-life BDMC treatment.

Group	Number (*n*)	Mean time (d)	% extension	*P*	
				Ctl	RAP
Ctl	80	22.850±0.886			0.212
RAP	81	24.049±0.883	5.247	0.212	
100 μM	79	24.696±0.901	8.079	0.156	0.848

Table S10. Statistical analysis of *C. elegans* survival time in lifespan assays after mid-life BDMC treatment.

Group	Number (*n*)	Mean time (d)	% extension	*P*	
				Ctl	RAP
Ctl	75	20.613±0.678			<0.001
RAP	77	25.584±0.646	24.116	<0.001	
100 μM	70	25.600±0.721	24.193	<0.001	0.619

Table S11. Statistical analysis of *C. elegans* survival time in lifespan assays after late-life BDMC treatment.

Group	Number (*n*)	Mean time (d)	% extension	*P*	
				Ctl	RAP
Ctl	72	19.577±0.835			<0.001
RAP	85	23.741±0.837	21.270	<0.001	
100 μM	92	23.565±0.766	20.371	0.000	0.666

Table S12. Statistical analysis of heat stress survival in *C. elegans* after BDMC treatment under let-23 RNAi conditions.

Group	Number (*n*)	Mean time (d)	% extension	*P*
L4440	90	10.133±0.186		
L4440+100 μM BDMC	90	11.771±0.229	16.165	<0.001[a]
let-23-RNAi	79	8.949±0.303		0.002[a]
let-23-RNAi+100 μM BDMC	87	9.883±0.201	10.437	0.015[b]

Note: [a] compared with the L4440 group; [b] compared with the let-23 RNAi group.

Table S13. Statistical analysis of lifespan in *C. elegans* after BDMC treatment under let-23 RNAi conditions.

Group	Number (*n*)	Mean time(d)	% extension	*P*
L4440	88	18.341±0.443		
L4440+100 μM BDMC	90	21.824±0.440	18.990	<0.001[a]
let-23-RNAi	90	16.879±0.474		0.068[a]
let-23-RNAi+100 μM BDMC	86	18.326±0.429	8.573	0.094[b]

Note: [a] compared with the L4440 group; [b] compared with the let-23 RNAi group.

Table S14. Statistical analysis of *daf-2* (*e1370*) and *daf-16* (*mu86*) mutant survival time in lifespan assays after BDMC treatment.

Group	Number (*n*)	Mean time (d)	% extension	*P*
daf-2	89	37.528±1.462		
daf-2+100 μM BDMC	89	39.528±1.524	5.329	0.214
daf-16	77	15.193±0.842		
daf-16+100 μM BDMC	78	17.103±0.797	12.572	0.106

Note: Data are presented as mean ± SD. Percentage extension was calculated as (T − C)/C × 100, where T represents the mean survival time of treated worms and C represents the mean survival time of the corresponding control group.

Table S15. mRNA qRT-PCR primer sequences.

NO.	Gene	Primer sequence
1	*Act-1*	Forward: CCAGGAATTGCTGATCGTATGCAGAA Reverse: TGGAGAGGGAAGCGAGGATAGA
2	*let-23 (EGFR)*	Forward: GCATCACCAACGTCAACACA Reverse: CGACACCCTCGGTACATAGTT
3	*let-60 (HRAS)*	Forward: AGCTTGTGGTAGTTGGAGATGG Reverse: TCCAATATGTCGAGGAGGCATG
4	*lin-45 (BRAF)*	Forward: AGTGACAAGGAACCGCCAAA Reverse: TCACCGGGACGAACTTCAAC
5	*mpk-1 (MAPK1)*	Forward: TGAAATGACTGGATACGTGGCA Reverse: ACCATACATCAACAGTCTGCGT
6	*aap-1 (PIK3R1)*	Forward: TGAGCACAACACCTGGAACT Reverse: GGGCGGCAAATTTCACAGA
7	*akt-1 (AKT1)*	Forward: AGTCGGCAGAAGTTCGTCAG Reverse: TGGCTGCTGATTGGTTTCCA

Table S16. Core genes identified by network topology analysis using the CytoNCA plugin in Cytoscape.

No.	Gene symbol	Degree	Eigenvector centrality	Betweenness centrality	Closeness
1	*PIK3R1*	24	0.2922055	2399.6387	0.06591422
2	*SRC*	24	0.3494424	5099.901	0.066911094
3	*AKT1*	20	0.25420272	1752.497	0.06600361
4	*EGFR*	18	0.2564951	789.8292	0.065412186
5	*ESR1*	17	0.27177474	1048.0261	0.06657547
6	*HSP90AA1*	17	0.2030865	3807.3066	0.06597379
7	*MAPK1*	15	0.20987594	1964.7164	0.066454254
8	*PRKACA*	14	0.15096831	3461.9731	0.06520768
9	*HRAS*	13	0.18804647	448.02173	0.06532439
10	*MAPK8*	13	0.16735795	2960.0068	0.06561798
11	*AKT2*	11	0.14421752	478.2186	0.06500445
12	*MAPK14*	11	0.16373509	167.13095	0.06460177
13	*PTK2*	11	0.19004983	427.13943	0.06520768
14	*IGF1R*	10	0.18479088	327.05997	0.06512043
15	*JAK2*	10	0.1672048	64.60976	0.06460177
16	*BCL2L1*	9	0.06398686	987.3199	0.06367204
17	*KDR*	9	0.13839178	696.581	0.06512043
18	*CASP3*	8	0.068253376	878.7246	0.06434552
19	*CDC42*	8	0.16004004	139.36507	0.065353625
20	*ESR2*	7	0.12259636	230.47177	0.06538289
21	*IGF1*	7	0.11601191	73.0759	0.063894965
22	*MAP2K1*	7	0.09541642	120.6365	0.06465899
23	*PGR*	7	0.14508206	429.25125	0.06612319
24	*RHOA*	7	0.1389702	285.4469	0.065559044
25	*STAT1*	7	0.1444596	64.731926	0.064831264
26	*BRAF*	6	0.08467931	146.4672	0.06468764
27	*GSK3B*	6	0.08485257	217.07234	0.064831264
28	*NOS3*	6	0.060627107	369.35156	0.06312149
29	*JAK3*	5	0.07948137	101.40497	0.063094206
30	*NOS2*	5	0.043784257	168.31776	0.06241984
31	*AR*	4	0.088524945	190.20164	0.06512043
32	*HSPA1B*	4	0.0591828	286.94727	0.06431718
33	*THRB*	4	0.049310494	1359.6282	0.06445916

Table S17. KEGG pathway IDs and corresponding pathway names involved in the “drug-disease-target-pathway” network.

NO.	KEGG ID	Pathway name
1	hsa01522	Endocrine resistance
2	hsa05205	Proteoglycans in cancer
3	hsa01521	EGFR tyrosine kinase inhibitor resistance
4	hsa04917	Prolactin signaling pathway
5	hsa05417	Lipid and atherosclerosis
6	hsa04510	Focal adhesion
7	hsa04915	Estrogen signaling pathway
8	hsa04370	VEGF signaling pathway
9	hsa04062	Chemokine signaling pathway
10	hsa04935	Growth hormone synthesis, secretion and action
11	hsa05215	Prostate cancer
12	hsa05224	Breast cancer
13	hsa04914	Progesterone-mediated oocyte maturation
14	hsa04012	ErbB signaling pathway
15	hsa05210	Colorectal cancer
16	hsa05161	Hepatitis B
17	hsa04015	Rap1 signaling pathway
18	hsa05207	Chemical carcinogenesis - receptor activation
19	hsa04926	Relaxin signaling pathway
20	hsa04933	AGE-RAGE signaling pathway in diabetic complications