

Supplementary Table S1 |

Statistical data for *C. elegans* lifespan experiments

strain name	treatment	mean	p (Log-rank test)	%change	75%	n
<i>N2</i>	0	20.1 ± 0.51			23	60/72
<i>N2</i>	2	22.4 ± 0.78	0.0159	11.4	25	54/72
<i>N2</i>	20	23.3 ± 1.21	0.0038	15.9	27	30/72
<i>N2</i>	0	24.3 ± 0.59			29	57/72
<i>N2</i>	2	26.2 ± 0.33	0.0384	7.8	29	57/72
<i>N2</i>	20	26.5 ± 0.46	0.0028	9.1	29	60/96
<i>N2</i>	0	25.7 ± 0.84			29	45/72
<i>N2</i>	20	29.4 ± 0.77	0.0001	14.4	31	42/72
<i>N2</i>	0	22.1 ± 1.49			27	57/72
<i>N2</i>	20	25.6 ± 2.01	0.0009	15.8	31	48/72
<i>daf-16(mu86)</i>	0	19.5 ± 0.50			23	46/72
<i>daf-16(mu86)</i>	20	21.7 ± 1.06	0.0081	11.3	25	50/72

Supplementary Figure S1

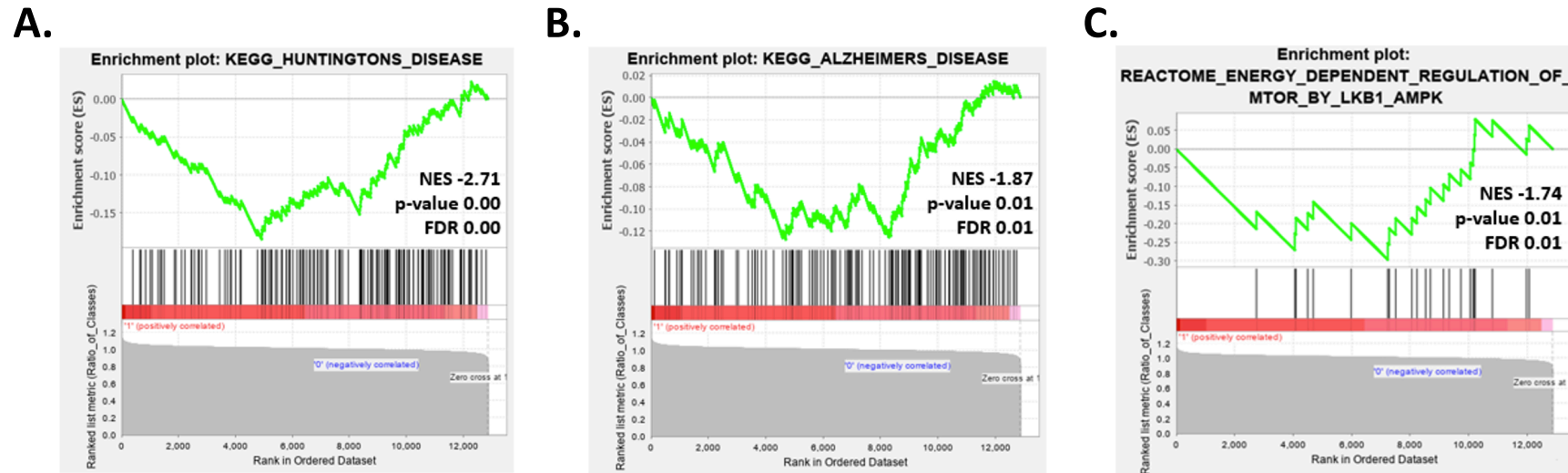


Figure S1. Gene set enrichment analysis (GSEA) of the microarray data from HT29 cells treated with HH-F3. GSEA enrichment plots of disease-related gene sets include **(A)** Huntington's disease (KEGG: 05016), **(B)** Alzheimer's disease (KEGG: 05010), and **(C)** energy dependent regulation of mTOR by LKB1-AMPK. ES: Enrichment scores; NES: Normalized enrichment scores; FDR: False discovery rate.