File S1

Supporting Methods

Strains: C. elegans strains are listed in the order in which they appear in the figures. The following strains were used: EAH14 bruEx12[ets-5::mCherry, pax-2::GFP]; N2; FX1734 ets-5(tm1734); FX0866 ets-5(tm866); FX1755 ets-5(tm1755); EAH41 ets-5(tm866); bruEx12[ets-5::mCherry, pax-2::GFP]; DA1290 lin-15B[n765] X; adEx1290[gcy-33::GFP, lin-15(+)]; EAH43 ets-5(tm866); adEx1290[gcy-33::GFP, lin-15(+)]; OH4841 otis92[flip-10::GFP]; EAH18 otis92[flip-10::GFP]; ets-5(tm866); NY2064 ynl64[flip-17::GFP]; him-5(e1490); EAH20 ynl64[flip-17::GFP]; ets-5(tm866); EAH65 bruEx47[gcy-9::GFP, pax-2::GFP]; EAH77 ets-5(tm866); bruEx59[gcy-9::GFP, pax-2::GFP]; EAH26 kyEx2116[gcy-31::SL2::GFP, odr-1::DsRed2]; EAH27 ets-5(tm866); kyEx2116[gcy-31::SL2::GFP, odr-1::DsRed2]; CX3584 kyls111[tax-2::GFP]; lin-15[n765ts]; EAH22 kyls111[tax-2::GFP]; ets-5(tm866); BC13862 dpy-5[e907]; sEx13862 [tax-4::GFP, pCeh361]; EAH24 ets-5(tm866); sEx13862[tax-4::GFP, pCeh361]; EAH19 otis92[flip-10::GFP]; ets-5(tm1734); EAH21 ynl64[flip-17::GFP]; ets-5(tm1734); EAH78 ets-5(tm1734); bruEx60[gcy-9::GFP, pax-2::GFP]; EAH28 ets-5(tm1734); kyEx2116[gcy-31::SL2::GFP, odr-1::DsRed2]; EAH48 ets-5(tm1734); adEx1290[gcy-33::GFP, lin-15(+)]; EAH23 kyls111[tax-2::GFP]; ets-5(tm1734); EAH25 ets-5(tm1734); sEx13862[tax-4::GFP, pCeh361]; EAH68 bruEx50[gcy-31::GFP, pax-2::GFP]; EAH69 bruEx51[gcy-31::GFP, pax-2::GFP]; EAH70 bruEx52[gcy-31::GFP, pax-2::GFP]; EAH71 bruEx53[gcy-31::GFP, pax-2::GFP]; EAH72 bruEx54[gcy-31Mut::GFP, pax-2::GFP]; EAH73 bruEx55[gcy-31Mut::GFP, pax-2::GFP]; EAH74 bruEx56[gcy-31Mut::GFP, pax-2::GFP]; EAH75 bruEx57[gcy-31Mut::GFP, pax-2::GFP]; EAH76 bruEx58[gcy-31Mut::GFP, pax-2::GFP].

Phylogenetic analysis: Phylogenetic trees of the ETS proteins were generated from an alignment of the ETS domains. C. elegans sequences were obtained from WormBase (www.WormBase.org) and H. sapiens sequences were obtained from the NCBI protein database. Protein sequences of the ETS domains were aligned with ClustalW using the default settings in Lasergene (DNASTAR, Madison, WI). An unrooted phylogenetic tree was then constructed from the aligned ETS domains with PHYLIP 3.65 (Joseph Felsenstein, University of Washington, Seattle, WA). Bootstrapping was performed using 100 replicates.

Lifespan assays: For lifespan assays, 10 L4 hermaphrodites were placed onto each NGM agar plate seeded with OP50. Animals were transferred to fresh plates every day for the first 8 days. The number of live, dead, or censored (missing or bagged) animals was recorded every day for the first 8 days. After 8 days, animals were transferred to fresh plates every 2 days for the remainder of the assay. The number of live, dead, or censored animals was recorded every 2 days until all animals were dead or censored. The percentage of surviving worms was then calculated for each of the recorded days.

Brood size assays: To assay brood sizes, individual L4 hermaphrodites were placed onto NGM agar plates seeded with OP50. Animals were transferred to a fresh plate every 24 hours for 4 days. The total number of progeny on all of the plates was then scored.

SUPPORTING REFERENCES
