Supporting Table 1. Functional over-representation of genes in three clusters discovered by SSC in *C. elegans* (worm) time course micoarray data[*].

Cluster	GO Description	Fraction	*P*-value	Corrected *P*
6A	growth	165/565	5.23E-53	1.64E-50
	development	216/565	1.47E-48	4.60E-46
	larval development (sensu Nematoda)	112/565	7.19E-40	2.25E-37
	positive regulation of growth rate	111/565	3.81E-34	1.19E-31
	metabolism	213/565	1.03E-29	3.21E-27
	reproduction	98/565	1.83E-29	5.74E-27
6B	locomotory behavior	17/67	2.02E-09	2.34E-07
	regulation of growth	16/67	2.82E-06	0.000327
	cuticle biosynthesis (sensu Nematoda)	3/67	5.50E-05	0.006384
	amine biosynthesis	3/67	0.00011	0.012709
	visual perception	2/67	1.38E-04	0.015981
	aging	4/67	0.00019	0.022013
6C	embryonic development (sensu Animalia)	86/420	4.41E-16	1.04E-13
	cell cycle	16/420	5.51E-05	0.012948
	cell proliferation	17/420	6.99E-05	0.016436
	DNA replication and chromosome cycle	12/420	0.000291	0.068376
	female gamete generation	2/420	0.005269	1.000000
	gametogenesis	20/420	0.007783	1.000000

Supporting Table 1. Gene function over-representation in 4 clusters discovered by SSC of worm microarray data[*] corresponding to Fig. 6A-C in the main text. See Supporting Table 3 for over-representation results for all 16 clusters.

[*] Jiang, M., Ryu, J., Kiraly, M., Duke, K., Reinke, V., & Kim, S. K. (2001) *Proc. Natl. Acad. Sci.* USA **98**, 218-23.