

Table S1. List of genes from the screen that when knocked down using elav-Gal4 show hypo or hyper-arousable phenotypes. Related to Figure 1.

Screen hits hyper-arousable	Screen hits hypo-arousable
CG10001	CG10006
CG10002	CG1004
CG1004	CG10143
CG10268	CG10295
CG10377	CG10334
CG10449	CG10388
CG10899	CG10537
CG1098	CG10572
CG10990	CG10579
CG11177	CG10701
CG12069	CG10823
CG12367	CG10850
CG12819	CG10877
CG13575	CG10901
CG14026	CG10907
CG14230	CG10967
CG14358	CG10990
CG14472	CG11331
CG14686	CG11420
CG15497	CG11556
CG15522	CG11937
CG16725	CG12170
CG16901	CG12348
CG17161	CG12386
CG17471	CG12505
CG17686	CG12559
CG18402	CG13204
CG18572	CG13575
CG18660	CG13779
CG1887	CG13784
CG2087	CG14562
CG2615	CG1464
CG2845	CG15793

CG2846	CG1641
CG30106	CG16725
CG3143	CG16901
CG3171	CG17077
CG3178	CG17239
CG32110	CG17269
CG32139	CG1773
CG32281	CG18455
CG32445	CG1848
CG32498	CG2124
CG33276	CG2210
CG34381	CG2331
CG3593	CG2647
CG3705	CG31000
CG42250	CG31522
CG42341	CG3225
CG4313	CG32425
CG4322	CG33119
CG4385	CG3326
CG4637	CG33467
CG4927	CG33956
CG5216	CG3466
CG5517	CG3613
CG5671	CG3871
CG6054	CG3884
CG6315	CG4016
CG6355	CG40351
CG6438	CG42341
CG6496	CG4320
CG6951	CG4444
CG7437	CG4475
CG8167	CG4703
CG8173	CG4706
CG8318	CG5025
CG8726	CG5308
CG8950	CG5432
CG9696	CG5436
	CG5610
	CG5813

	CG5920
	CG5941
	CG5992
	CG6196
	CG6496
	CG6498
	CG6703
	CG6736
	CG6854
	CG6963
	CG7204
	CG7281
	CG7391
	CG7429
	CG7599
	CG7643
	CG7971
	CG8172
	CG8318
	CG8525
	CG8795
	CG8952
	CG8964
	CG9310
	CG9554
	CG9746

Table S2. Gene ontology analysis of genes from the screen that when knocked down using elav-Gal4 show hypo or hyper-arousable phenotypes (shown in Table S1) for biological process and molecular function. Related to Figure 1.

GO Term	GO for hits from the screen normalized to GO representation in the genome (\log_{10})
BIOLOGICAL PROCESS	
homeostatic process	1.065574865
aging	0.987099215
protein maturation	0.956430396
cell proliferation	0.912651471
autophagy	0.841718299
growth	0.830187807
nucleocytoplasmic transport	0.732199922
cell motility	0.716456307
cell junction organization	0.712243195
embryo development	0.666625448
anatomical structure formation involved in morphogenesis	0.665384621
developmental maturation	0.660551223
signal transduction	0.657551721
mRNA processing	0.637099248
cell morphogenesis	0.59315913
cell death	0.584547386
vacuolar transport	0.582121661
cell division	0.576073637
immune system process	0.574577207
extracellular matrix organization	0.529733592
cell-cell signaling	0.529229621
locomotion	0.525177073
carbohydrate metabolic process	0.518295756
tRNA metabolic process	0.497947583
cell adhesion	0.481016299
cell differentiation	0.447255037
reproduction	0.441586708
cellular protein modification process	0.441004956
catabolic process	0.392757579
vesicle-mediated transport	0.387641945
response to stress	0.37764218

secondary metabolic process	0.367006294
cytoskeleton organization	0.361104894
cellular amino acid metabolic process	0.358399893
nucleobase-containing compound catabolic process	0.351819547
anatomical structure development	0.343807062
pigmentation	0.340677356
lipid metabolic process	0.332409353
small molecule metabolic process	0.328735463
mitotic cell cycle	0.316436327
cell cycle	0.306889032
nervous system process	0.266357462
cellular component assembly	0.253477679
transport	0.2194312
cellular nitrogen compound metabolic process	0.218271345
cofactor metabolic process	0.2155998
ribonucleoprotein complex assembly	0.173186268
sulfur compound metabolic process	0.12786329
DNA metabolic process	0.072550667
biosynthetic process	0.064588952
chromosome organization	0.046000045
generation of precursor metabolites and energy	0
membrane organization	-0.052123013
transmembrane transport	-0.17366367
translation	-0.277145243
protein-containing complex assembly	-0.451095827
MOLECULAR FUNCTION	
kinase activity	0.858508
hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	0.724804
transcription factor binding	0.65505
lyase activity	0.446828
ubiquitin-like protein binding	0.439333
mRNA binding	0.42928
protein binding, bridging	0.38818
DNA-binding transcription factor activity	0.385194
ion binding	0.331274
methyltransferase activity	0.321338
peptidase activity	0.272028
isomerase activity	0.269316
phosphatase activity	0.197556

enzyme binding	0.184427
enzyme regulator activity	0.176641
lipid binding	0.173892
DNA binding	0.168122
RNA binding	0.138185
cytoskeletal protein binding	0.089542
histone binding	0.034214
unfolded protein binding	0.027152
ATPase activity	0.006664
helicase activity	0.006631
hydrolase activity, acting on glycosyl bonds	-0.043779
transferase activity, transferring acyl groups	-0.058403
ligase activity	-0.109875
transmembrane transporter activity	-0.11521
nuclease activity	-0.119975
transferase activity, transferring glycosyl groups	-0.294399
structural constituent of ribosome	-0.45921
oxidoreductase activity	-0.545007
structural molecule activity	-0.782516