Stable modules	Process	Gene Ontology annotation	Genes count / total	P-value
epi-1 (fbl-1 (nid-1)	Proteins of basement membrane	Proteinaceous extracellular matrix	2/23	0.00050
C54E42 C31B8 8	Protease inhibitors	Serine-type endopeptidase inhibitor activity Proteinaceous extracellular matrix	2/20 2/23	0.00066 0.00028
\$sm-} \$3	Sphingomyelinases	Sphingolipid catabolic process	2/2	2.6e-07
unc-95 hsp-16 2 tim-1 lec-2 sup-10 unc-93 C 4C12.5 M05D6-2 unc-15 - 606E2 1	Channel complex subunits, lectins, innexins	N/A	N/A	N/A
(ev-1) tinc-29 tinc-122 5	Acetylcholine receptor and extracellular matrix	Nicotinic acetylcholine- activated cation- selective channel activity	2/11	0.0004
wht-2 wht-7	Transporters, ABC superfamily	N/A	N/A	N/A
(Ip-1) 6mk-) 7	Kinesin-like proteins	Cytoskeleton- dependent intracellular transport	2/34	0.00031
F\$5A1].4 cal-1 myo-3 tinc-15 M05D6.2 8	Cytoskeleton and Calcium binding proteins	N/A	N/A	N/A
mh-2 map- cor-	Enzymes of mitochondrial translation	N/A	N/A	N/A
/ et-72 1 F63A3 7 10	Electron transfer flavoprotein ubiquinone oxidoreductase	N/A	N/A	N/A
T(14B4)2 B(1205)11 Z(262)8 11	Mitochondrial/chloropl ast ribosomal proteins S18	Ribonucleoprotein complex structural Constituent of ribosome	3/153 3/116	0.00021 1.5e-05
(in-9) (in-1) (dp-)	Mitochondrial import inner membrane translocases	N/A	N/A	N/A
drs-3 - Y5007A.9 13	Enzymes, mitochondrial	N/A	N/A	N/A

	Golgi proteins	N/A	N/A	N/A
dogc-4	Goigi proteiris	N/A	IN/A	IN/A
T(2D8)9 C43E11)11				
T(2D8)9 / C43E11)11				
cogc-)s cogc-2				
	Centromere protein,	N/A	N/A	N/A
(sc-1) (sc-1)	chromosome			
	segregation Predicted RNA-	N/A	N/A	N/A
C30B3 4 R68D7 1 16	binding protein			
tbx-2 mls-1	T-box transcription	N/A	N/A	N/A
17	factors			
	Proteins of cell cycle	N/A	N/A	N/A
mdf-1				
(ify-1) emb-30				
s ept-0 1 18				
F\$5C\$2	DNA polymerases	DNA repair	3/75	0.00020
polk-		response to DNA		
rev-1		Damage stimulus Response to stress	3/84 3/140	0.00020 0.00069
19	Y18D10A.9, WD40	N/A	3/140 N/A	0.00069 N/A
F45G2)10 Y18D10A.9	repeat protein			
200	Enzymes of carbohydrate	Energy derivation by oxidation of	5/24	5.3e-09
C08B1)1.8 ZC410.3 CC4B9.8	metabolism	organic compounds		
T04A8.7 T22F3.3 C46F11.2				
gsy-1				
9(1x-10) 21				
R07H5.8				
T09A5.9 WILL R08B4.3				
fre-1 dcs-1				
C16C10.11 K08E3.3 (ps.) 4CS. 17				
F57B10.3 Godh 2 F54D5)12				
(pi-) F46E10.10 Y65 <mark>B4</mark> ÈL.7				
	Enzymes of glucose	Monocarboxylic		
alh-9	metabolism and	acid metabolic	E/40	0.0- 05
100-3 TETAS 6	energy metabolism	process	5/48	2.3e-05
alh-8		Ligase activity, forming carbon-		
ZK822 5		carbon bonds	2/2	0.00068
E04F6 5 gccb-1				
ech-1 Tb2G5/4 F02B6/2 ZIK1320.9				
B(0303)3 C(05C10.3 22				
	Enzymes of galactose	Galactose	0.10	0.00000
C01B4.7 (rh-1)	metabolism	metabolic process	2/3	0.00036
Y19D10A.4 C(15H9).7 Y45F10D.4				
ZIK1058.3				
K06A4)5 T(4D7)1				
23				

		Dontalina of	NI/A	NI/A	NI/A
(qv-) (qv-3)	24	Proteins of carbohydrate	N/A	N/A	N/A
<u> </u>	24	metabolism			
16g-173 Y36A10A.5		Enzymes of lipid metabolism	N/A	N/A	N/A
Z(668)4 Y39E4A 3 Unc.68					
LC1.5 PAD-2 F(3F13.9	25				
ZK1236.1 Y49E10.4		Enzymes of lipid metabolism	N/A	N/A	N/A
gbh-2 E02H1) 2 W06D4.4 tug-170 Y48G1¢.4					
Y36A10A.6	26	Father and the baddens	Limit de la la matter de	0/44	7.0 - 07
(bp-1 bp-2		Fatty acid-binding proteins	Lipid binding	3/44	7.9e-07
	27				
ZK <mark>1127:2 T09B4</mark> 8 T2 <mark>6C1</mark> 2.1	28	Enzymes of metabolism	N/A	N/A	N/A
mut-16 pw-3	29	Translation initiation factors and related proteins	N/A	N/A	N/A
(thp-2 F(13H8)7	30	Hydrolases	N/A	N/A	N/A
hkat-3 - C 4F1).1 C 2C1.13	31	Transaminases	Transaminase activity	2/21	0.00044
gln-3 Z(829)4	32	Glutamine synthetase, glutamate dehydsrogenase	N/A	N/A	N/A
Z(328)4 Z(973)1	33	Metalloprotease and Transcription accessory protein	N/A	N/A	N/A
F(3D1), 6 T(9B1), 3 H22K11, 2		Beta-galactosidases and serine carboxy peptidases	Beta-galactosidase activity	2/2	3.6e-06
F41C3 5	34		Serine carboxy- peptidase activity	2/6	3.6e-05
<mark>(1a-2) €24G</mark> 6.8	35	rla-2, acidic ribosomal subunit protein P2	N/A	N/A	N/A
glh-2 glh-3 glh-1 2yx-1	36	ATP-dependent RNA helicases and focal adhesion adaptator	JUN kinase binding ATP-dependent Helicase activity	3/4 3/62	9.6e-09 3.3e-05
		protein	Pole plasm	3/21	3.6e-06
F(5D3)7		Chaperones, cytoskeletal and mitochondrial proteins	Ubiquitin protein ligase binding	2/3	9.2e-05
u <mark>nc-45 (hn-) \$cpl-4 E04A4.5 F45G2</mark> 8	37				
hsp-12.2 F39B2 3 hsp-25		Heat shock proteins	N/A	N/A	N/A
hsp-12.3 hsp-12.6	38				
6ag-) unc-23	39	Chaperones	N/A	N/A	N/A
	39				

M01A10.1 4mg-1 unc-190 unc-129	Wnt signaling pathway, transcription factors and axonal guidance	Microtubule cytoskeleton organization and biogenesis	4/80	0.00047
zl(973.3 tog-) res-1 (wn-)2 egl-20		Microtubule-based process	4/106	0.00096
mes 3 40				