

**Table S3. Genes identified in screen by automated analysis**

CG#	Note	Symbol	Function	Repeat screen left primer	Repeat screen right primer
CG17608	T	fu12	1-acylglycerol-3-phosphate O-acyltransferase activity	TAATACGACTCACTATAGGGGGAAACAGTATTTCCCTCTATGGG	TAATACGACTCACTATAGGGGGACTCTTGTAG
CG9390	T	AcCoAS	acetate-CoA ligase activity	TAATACGACTCACTATAGGGGTTCTAACGTTGCCACTAGG	TAATACGACTCACTATAGGGTCAAAAAGAAC
CG7379	C		acetyltransferase activity; protein binding	TAATACGACTCACTATAGGGGACCTAAACCATAGAAGCGAGG	TAATACGACTCACTATAGGGTCCCTGGTACT/
CG10996	M		aldose 1-epimerase activity	TAATACGACTCACTATAGGGCACAAAGCCACCATTAGTTTGG	TAATACGACTCACTATAGGGTGGAGGACATC
CG9143	C		ATP-dependent RNA helicase activity	TAATACGACTCACTATAGGGACTGGACTCCTCACTGTTGTCG	TAATACGACTCACTATAGGGTGGCAGAAGGT
CG32465	T	CG34127	carboxylesterase activity	TAATACGACTCACTATAGGGTCATATATAGAGACAGCTGAAACGC	TAATACGACTCACTATAGGGTGCAGAATCAT/
CG7094	T		casein kinase I activity	TAATACGACTCACTATAGGGATTTCGAAATAAAACCACTCC	TAATACGACTCACTATAGGGACTATATATATC
CG5452	M	dnk	deoxynucleoside kinase activity; ATP binding	TAATACGACTCACTATAGGGATCTGAACTGGAAAACATTGG	TAATACGACTCACTATAGGGCACAAAAATAG
CG16713	T		erine-type endopeptidase inhibitor activity	TAATACGACTCACTATAGGGACACTTGTCTTCACAGATTCC	TAATACGACTCACTATAGGGGCTTTGTGGC/
CG7440	T,M,C	tgy	galactosyltransferase activity	TAATACGACTCACTATAGGGGAGCAGCATCTGGCAGC	TAATACGACTCACTATAGGGGGTGGCCTTTC
CG9042	T	Gpdh	glycerol-3-phosphate dehydrogenase (NAD+) activity	TAATACGACTCACTATAGGGAAACAATACCAGGATGTACTGCG	TAATACGACTCACTATAGGGGCACACATTTAC
CG12530	T	Cdc42	GTPase activity	TAATACGACTCACTATAGGGTTACGTTATTCGATTAAGCCC	TAATACGACTCACTATAGGGTACTTAATTCG/
CG8287	M	Rab8	GTPase activity	TAATACGACTCACTATAGGGGTCCTCAGAGAATCGGAAGAGG	TAATACGACTCACTATAGGGACACACCCAGC
CG3949	M	hoip	mRNA binding; structural constituent of ribosome	TAATACGACTCACTATAGGGACTGAGGAAGTTAATCCCAAGG	TAATACGACTCACTATAGGGAAGGGTTACTA/
CG11027	T	Arf102F	NAD(P)+-protein-arginine ADP-ribosyltransferase activity	TAATACGACTCACTATAGGGCCAATCCATGTTATTTTCC	TAATACGACTCACTATAGGGAATCAAGTCTT/
CG7368	T		nucleic acid binding; zinc ion binding	TAATACGACTCACTATAGGGGCAACAGGTAACCGATTGG	TAATACGACTCACTATAGGGAGACTCTGGGT/
CG7054	T		phosphatidylethanolamine binding; kinase inhibitor activity	TAATACGACTCACTATAGGGCATAAAAGCTTGCTTACGTGG	TAATACGACTCACTATAGGGATGTTACGTGT/
CG9060	T	Zpr1	protein binding; zinc ion binding	TAATACGACTCACTATAGGGAGTACGAAGCTTTAGCTGCGG	TAATACGACTCACTATAGGGCAGGAACCTTC/
CG1210	M	Pk61C	protein serine/threonine kinase activity	TAATACGACTCACTATAGGGCCAATCGAACCTTATACCTGG	TAATACGACTCACTATAGGGGAGACACCTGC
CG9635	M	RhoGEF2	Rho guanyl-nucleotide exchange factor activity	TAATACGACTCACTATAGGGAAAGACCTAACGACTTCATCTCC	TAATACGACTCACTATAGGGACATCTTAGGA
CG7269	T	Hel25E	RNA helicase activity	TAATACGACTCACTATAGGGATGTTACATCGAAACGATCC	TAATACGACTCACTATAGGGTCTTTGTGAAG
CG7577	C	ppk20	serine-type peptidase activity	TAATACGACTCACTATAGGGATTAGATCAAAAATCAAGCCCG	TAATACGACTCACTATAGGGGGCTGTCCCTT
CG7352	T		structural constituent of cytoskeleton	TAATACGACTCACTATAGGGAAAGCAACTGGATGAATATCGC	TAATACGACTCACTATAGGGCTATGCCACTG/
CG7627	T,C		ATPase activity; transporter activity	TAATACGACTCACTATAGGGTTCAGCAGACTCTCATAGTGG	TAATACGACTCACTATAGGGTCTGTGCTCAT/
CG15319	M	nej	transcription coactivator activity; acetyltransferase activity	TAATACGACTCACTATAGGGTAACCATATTGTTGGTCACTCCC	TAATACGACTCACTATAGGGTGCATAATCTCC
CG6964	M	Gug	transcription corepressor activity	TAATACGACTCACTATAGGGAGAAGGAGGACCTCCAGAACC	TAATACGACTCACTATAGGGATCCTTAGACG/
CG17888	T	Pdp1	transcription factor activity	TAATACGACTCACTATAGGGGAATCATTGCTGCTAACACTGC	TAATACGACTCACTATAGGGCGTAACCACTG/
CG7734	C	shn	transcription factor activity	TAATACGACTCACTATAGGGACCGCTACATGTTGATACTCCC	TAATACGACTCACTATAGGGAATCCTCATGA/
CG9954	C	maf-S	transcription factor activity	TAATACGACTCACTATAGGGTTTCGGTAAGGGATCTTAATCG	TAATACGACTCACTATAGGGACAGAAACAGG
CG10543	T		transcription regulator activity	TAATACGACTCACTATAGGGCGAATCTCATTGACACAAATCC	TAATACGACTCACTATAGGGTGGGTAGTAGA
CG7036	C	rno	transcription regulator activity	TAATACGACTCACTATAGGGTCCGAGTAGATATGCTGTCCC	TAATACGACTCACTATAGGGTACATCCAAG/
CG7372	C		transcription regulator activity	TAATACGACTCACTATAGGGAGGTCAAACCTTGATGGATCTGG	TAATACGACTCACTATAGGGATAAGATTGAA
CG8950	T		transcription regulator activity	TAATACGACTCACTATAGGGTTATATCCTCCAGGGTGAATCG	TAATACGACTCACTATAGGGGATTTATGAGA/
CG2238	M	Ef2b	translation elongation factor activity	TAATACGACTCACTATAGGGTCCGTCATCGTTATAGGTGG	TAATACGACTCACTATAGGGTCCATGTACTTT
CG9596	T		translation initiation factor activity	TAATACGACTCACTATAGGGAAAAGGTAGCCACTATTTCCGC	TAATACGACTCACTATAGGGTTAAGGGAGTT
CG7375	T,C		ubiquitin-protein ligase activity	TAATACGACTCACTATAGGGGAGAAATGGTGACTTGACTCGG	TAATACGACTCACTATAGGGTCCGAAACAA
CG11132	M	DMAP1	unknown	TAATACGACTCACTATAGGGATGCATAGGGAGGTTGTTGC	TAATACGACTCACTATAGGGAATAGGTGATC/
CG16783	T	fzr2	unknown	TAATACGACTCACTATAGGGCGATTTCGGTTAGGTAGAATGC	TAATACGACTCACTATAGGGTTTCGACGACC/
CG30118	C		unknown	TAATACGACTCACTATAGGGCTTATAAATATCAAGCTGAAAATATTGG	TAATACGACTCACTATAGGGCCGGACAGCG/
CG3885	M	sec3	unknown	TAATACGACTCACTATAGGGTTCCTTTAAGGCCTAGTCTCG	TAATACGACTCACTATAGGGGTGAAGAAAGG
CG5114	M		unknown	TAATACGACTCACTATAGGGTACGTGACCGTGAGAGAATAGC	TAATACGACTCACTATAGGGTCCCAAGATTT/
CG5308	C	dpr5	unknown	TAATACGACTCACTATAGGGGTCCAACCTTGATACCAGATAATTACG	TAATACGACTCACTATAGGGTGTAGGCCAG
CG7085	T	l(2)s5379	unknown	TAATACGACTCACTATAGGGCAATAATACCAATCAAAACGCTCC	TAATACGACTCACTATAGGGCATTGCCTAGA
CG7946	T		unknown	TAATACGACTCACTATAGGGCAAACTGAACTAGAGAGCCGGC	TAATACGACTCACTATAGGGGTCTCCGATC/
CG8309	T	Tango7	unknown	TAATACGACTCACTATAGGGCAGGTCTATGAAACCGGATGC	TAATACGACTCACTATAGGGCCACATTTATTC
CG9047	T		unknown	TAATACGACTCACTATAGGGACAAGTATGCCAACACATCCG	TAATACGACTCACTATAGGGGCTCTGGAATA
CG9422	T		unknown	TAATACGACTCACTATAGGGACACAGCCACTCCCACTTTCC	TAATACGACTCACTATAGGGGGCAAAATAG

Note: T: altered total signal  
M: altered mean signal  
C: altered cluster number