

Supporting Table 1. Total list of the 103 probes.

Gene Symbol	Fold value more than 2 compare with control		Functional category
	MB247; tub-Gal80 ^{IS} >UAS-PKA ^{DN}	MB247; tub-Gal80 ^{IS} >UAS-PKA ^{CA}	
CG4650	0.05462545	0.18353308	Proteolysis
CG13646	0.38492279	0.33395972	Amino acid transport
CG7763	0.37176426	0.33785872	N/A
CG8713	0.17261539	0.34251213	Potassium ion transport
CG8193	0.38644473	0.37035790	Oxygen transporter
Bc	0.32859148	0.39365999	Melanization defense response
CG7738	0.45168221	0.42349006	N/A
Eip74EF	0.35456597	0.47670544	Transcription factor
CG11852	2.06968183	2.04899718	N/A
Acp1 (CG31904)	3.12055794	2.08231164	Structural constituent of adult cuticle
p38c	2.09828406	2.43528395	MAP kinase
CG32850	2.07906087	2.44630621	Zinc ion binding
CG7214	3.52039424	2.69286704	Regulation of NFAT
Cyp6a17	0.20840532	3.03124613	Monoxygenase
CG31685	3.03643187	3.11841298	N/A
CG10924	4.58314522	4.86540533	Gluconeogenesis
CG11893	9.92378858	7.62364531	N/A
CG2177	10.06949900	10.55403670	Metal ion transport
Transposon.32	6.56581454	14.01341819	Transposon
Transposon.17	8.91080024	14.91172237	Transposon
path	0.23115653	1.16722040	Regulation of growth
CG31038	0.26355738	1.70542700	N/A
CR31614	0.28676304	0.54815432	N/A
CG33296	0.29712584	0.65189703	Neurotransmitter transport
CG9512	0.35926966	0.65928310	Alcohol metabolic process
CG31809	0.40768337	0.75573639	Steroid metabolic process
pgant4	0.43227970	0.52068365	Polypeptide N-acetylgalactosaminyl transferase
regucalcin	0.43480216	0.79394667	Lipid particle
TotA	0.44192701	0.88571840	Response to stress
CG2781	0.44634557	0.99414693	Fatty acid elongation
HDC07874	0.46297494	0.69483484	RNAi reagent
Amph	0.46755857	1.04774018	Neurotransmitter secretion
Os-C	0.47353468	0.53434707	Pheromone binding
CG32364	0.47360723	0.56594745	Nucleic acid binding
CG3513	2.07621234	1.23572096	Endopeptidase inhibitor
Cyp9c1	2.08830871	0.85557071	Monoxygenase
Ssl2	2.09409806	0.87558309	Strictosidine synthase
Rab2	2.13104639	1.04633440	GTPase
Edg91	2.19929632	1.07025902	Structural constituent of pupal cuticle
Def	2.20113861	0.96875382	Defense response to bacterium
CG8012	2.22890789	1.61419067	N/A
CecC	2.23797667	0.87502128	Defense response to bacterium
CG33868	2.28082854	1.57578969	Chromatin remodeling
α -Est2	2.35839603	1.60646105	Carboxylesterase
neb	2.40444012	0.93318434	Chromosome segregation
Su(var)3-3	2.45636849	1.68926071	Histone demethylation
CG5172	2.52585006	1.00000000	N/A
Cyp6a8	2.56855862	0.78826521	Insecticide metabolic process
CG8539	2.59846387	1.37374097	Proteolysis
CG14221	2.68433923	1.79533616	Cell redox homeostasis
AttC	2.75668419	1.68841787	Antibacterial humoral response
dro4	2.76519649	0.84640145	Defense response to fungus
Glut1	3.20877360	0.91934483	Regulation of cell cycle
CG1942	3.39646738	1.31813305	Mesoderm development
CG17567	3.46586870	1.00952735	N/A
DptB	3.75399050	1.66270243	Antibacterial humoral response
CG32594	4.14788817	1.57232342	N/A

Supporting Table 1. Total list of the 103 probes. (continued)

Gene Symbol	Fold value more than 2 compare with control		Functional category
	MB247; tub-Gal80 ^{ts} >UAS-PKA ^{DN}	MB247; tub-Gal80 ^{ts} >UAS-PKA ^{CA}	
Snoo	4.18018560	0.97805873	Neuron development
dro5	4.25088138	0.88446012	Defense response to fungus
CG10148	4.44437022	0.91550204	Protein binding
AttA	11.38347400	1.20780370	Antibacterial humoral response
AttB	12.10004913	1.56159896	Antibacterial humoral response
CG5246	14.87449723	1.45160507	Proteolysis
mthl6	27.13174625	1.30304237	G-protein coupled receptor
Cyp4g1	0.68625373	0.14760311	Lipid metabolic process
CG4757	0.79106053	0.31502146	Carboxylesterase
Cyp12d1-d (Cyp12d1-p)	1.14747363	0.32020528	Monooxygenase
CG18343	1.62984639	0.33558822	N/A
Cyp6a2	1.07802677	0.35180186	Response to caffeine and insecticide
CG6234	0.56344160	0.37776816	N/A
CG13022	1.20618316	0.38462595	N/A
CG18673	1.65334638	0.39260569	Carbonate dehydratase
CG13091	0.63889422	0.39279651	Metabolic process
CG13428	0.56814024	0.40542698	N/A
CG4446	0.77331227	0.40591709	N/A
CG3790	0.59197945	0.42939938	Carnitine transporter
e	0.57661809	0.44989742	β -alanyl-dopamine synthase
CG40485	1.40489859	0.45862058	Oxidoreductase
CG6639	1.04399587	0.46297558	Proteolysis
CG31809	0.50393061	0.46758936	Steroid metabolic process
CG7194	1.20777189	2.01424476	Gonad development
Obp83cd	1.12733946	2.02309771	Sensory perception of chemical stimulus
CG33640	1.01327376	2.02588180	N/A
CG9837	1.15903168	2.04624515	N/A
Ugt37c1	1.38855180	2.04678703	Glucuronosyltransferase
llp5	1.24536617	2.11140304	Insulin receptor signaling pathway
copiaGIP	1.30491877	2.13132411	DNA integration
Lsp1 β	1.25239530	2.13392578	Nutrient reservoir
Transposon.35	1.46128340	2.16903450	Transposon
CG31157	0.98758033	2.31018278	N/A
CG8757	0.97552517	2.32367290	Oxidation reduction
CG17189	1.16356112	2.32393546	N/A
CG11425	1.32017392	2.41124626	Phosphatidate phosphatase
MtnD	1.09222342	2.41458793	Metal ion binding
CG13641	1.22003286	2.47338530	N/A
Obp99a	1.76759653	2.47462342	Response to pheromone
CG10962	1.54358080	2.53717143	Oxidation reduction
Transposon.39	0.97334692	2.58391390	Transposon
ninaD	0.70583310	2.71650744	Phototransduction
CG10962	1.58207281	2.77948000	Oxidation reduction
Prx2540-2	1.81008695	2.98099096	Hydrogen peroxide catabolic process
Transposon.75	1.73781198	4.24100740	Transposon
Hsc70-2	1.03142291	4.93773017	Response to heat

Red indicates up-regulation in the experimental sample, and blue represents down-regulation compare to control transgenic flies (*MB247-Gal4; tub-Gal80^{ts}/+*). N/A means not available.