

Supplementary material

Comparative transcriptome analyses of adzuki bean weevil (*Callosobruchus chinensis*) response to hypoxia and hypoxia/hypercapnia

S.F.Cui¹, L. Wang¹, L. Ma², J.P. Qiu¹, Y.L.W¹, Zh.Ch.Liu^{1*}, and X.Q.Geng^{1*}

¹Department of Resources and Environment, School of Agriculture and Biology, Shanghai Jiao Tong University, Shanghai 200240, China

²Behavioral & Physiological Ecology (BPE) Group, Groningen Institute for Evolutionary Life Sciences, University of Groningen, Nijenborgh 7, 9747 AG Groningen, Netherlands

Table S1. DEGs in (A) HHA vs. NOR, (B) HA vs. NOR, and (C) HHA vs. HA.

Table S2. Summary of DEGs in the GO enrichment (HHA-HA-NOR).

Table S3. Summary of DEGs in the KEGG enrichment (HHA-HA-NOR).

Table S4. List of DEGs in biological processes based on the KEGG database.

Table S5. List of DEGs related to the function of immune, signal transduction, and stress responses based on the GO database.

Table S6. Primers used for q-PCR certification.

Table S1 DEGs in (A)HHA vs. NOR,(B)HA vs.NOR and (C) HHA vs. HA.

(A)DEGs in HHA vs. NOR.

ID	Name	Putative function	HHA vs. NOR	
			^a Fold change	p-value
c594_g1_i1	<i>XP002581749.1</i>	XP002581749.1	14.18	2.59E-02
c7162_g1_i1	<i>ART2</i>	Putative uncharacterized protein ART2	16.04	7.03E-03
c10028_g1_i1	<i>CCCP</i>	Circadian clock-controlled protein	7.92	3.24E-03
c10085_g1_i1	<i>ENN78907.1</i>	ENN78907.1	4.56	3.72E-03
c17791_g1_i1	<i>COX6C</i>	Cytochrome c oxidase subunit 6C	3.95	4.36E-02
c24002_g1_i1	<i>MYROI</i>	Myrosinase 1	440.98	5.94E-09
c24102_g1_i1	<i>TAR1</i>	Protein TAR1	10.97	2.15E-02
c28303_g1_i1	<i>PAPSS</i>	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase	9.56	5.43E-03
c32697_g1_i2	<i>YC9I</i>	Uncharacterized MFS-type transporter C09D4.1	37.35	1.10E-03
c36719_g1_i1	<i>EFX67914.1</i>	EFX67914.1	6.06	3.00E-02
c39455_g1_i1	<i>AEE63548.1</i>	AEE63548.1	15.66	5.27E-03
c40459_g1_i1	<i>TRY7</i>	Trypsin-7	153.20	4.91E-03
c40830_g1_i1	<i>MLC1</i>	Myosin light chain alkali	4.71	1.35E-03
c44529_g1_i1	<i>ENN75976.1</i>	ENN75976.1	4.12	3.39E-03
c46621_g1_i1	<i>ENN81187.1</i>	ENN81187.1	2.73	4.17E-02
c49368_g1_i1	<i>VCP</i>	Venom serine carboxypeptidase	36.51	3.01E-03
c49539_g1_i1	<i>YRBE</i>	Uncharacterized oxidoreductase	6.60	2.81E-02
c51118_g1_i2	<i>FAAH2</i>	Fatty-acid amide hydrolase 2	3.15	3.19E-02
c51780_g1_i1	<i>MOT7</i>	Monocarboxylate transporter 7	14.71	1.59E-04
c51837_g1_i2	<i>ENN74354.1</i>	ENN74354.1	3.76	9.75E-03
c52661_g1_i1	<i>ENO</i>	Enolase	2.97	2.18E-02
c56482_g1_i1	<i>CISY2</i>	Probable citrate synthase 2, mitochondrial	3.25	1.45E-02
c56483_g1_i1	<i>AEE61942.1</i>	AEE61942.1	6.40	4.56E-04
c57700_g2_i1	<i>IDHP</i>	Isocitrate dehydrogenase [NADP], mitochondrial	4.94	3.66E-03

c57735_g1_i1	<i>MYROI</i>	Myrosinase 1	1280.78	1.39E-09
c57898_g1_i1	<i>TRET1</i>	Facilitated trehalose transporter Tret1	23.76	4.21E-03
c58957_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	11.60	1.95E-02
c59848_g1_i1	<i>GLBL2</i>	Beta-galactosidase-1-like protein 2	#DIV/0!	2.46E-02
c60313_g1_i1	<i>ENN77113.1</i>	ENN77113.1	28.96	9.72E-03
c60540_g1_i1	<i>ABC40570.1</i>	ABC40570.1	367.65	8.43E-04
c60824_g1_i1	<i>ADT</i>	ADP,ATP carrier protein	4.28	3.05E-02
c62364_g1_i1	<i>PUR6</i>	Multifunctional protein ADE2	5.39	1.79E-02
c62738_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	144.47	4.37E-14
c62948_g1_i2	<i>ENN74273.1</i>	ENN74273.1	365.91	1.57E-04
c63178_g2_i1	<i>PGLR</i>	Probable polygalacturonase	1954.21	1.62E-08
c64120_g1_i1	<i>VPP1</i>	V-type proton ATPase 116 kDa subunit a isoform 1	3.97	5.44E-03
c64703_g1_i1	<i>ELU18102.1</i>	ELU18102.1	10.71	5.43E-03
c64875_g1_i1	<i>XP976338.1</i>	XP976338.1	4.80	4.79E-02
c65123_g1_i1	<i>ENN79163.1</i>	ENN79163.1	10.05	2.41E-04
c66392_g1_i1	<i>PR5</i>	Pathogenesis-related protein 5	42.64	7.17E-04
c66444_g1_i1	<i>DCXR</i>	L-xylulose reductase	61.23	2.25E-05
c66790_g1_i2	<i>SV2B</i>	Synaptic vesicle glycoprotein 2B	7.97	5.36E-04
c67074_g1_i1	<i>TNNI</i>	Troponin I	3.76	5.18E-03
c67276_g1_i1	<i>ACADV</i>	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	3.03	1.73E-02
c67339_g1_i1	<i>C6A14</i>	Probable cytochrome P450 6a14	11.94	3.29E-04
c67610_g1_i1	<i>TAKT</i>	Protein takeout	4.71	3.47E-02
c67642_g1_i1	<i>SERA</i>	D-3-phosphoglycerate dehydrogenase	4.56	2.42E-03
c67922_g1_i1	<i>CUD2</i>	Endocuticle structural glycoprotein	98.46	9.21E-07
c68525_g1_i1	<i>CTRB1</i>	Chymotrypsin BI	9.38	3.59E-03
c68798_g1_i2	<i>ATPK</i>	Putative ATP synthase subunit f, mitochondrial	2.52	4.78E-02
c68968_g1_i2	<i>ASM</i>	Sphingomyelin phosphodiesterase	7.84	3.76E-02
c70242_g1_i2	<i>MANA</i>	Mannan endo-1,4-beta-mannosidase	18.95	1.92E-02
c70347_g1_i2	<i>ENN80002.1</i>	ENN80002.1	23.38	1.18E-02
c70382_g1_i1	<i>HTXA</i>	Probable alpha-ketoglutarate-dependent hypophosphite dioxygenase	81.69	1.17E-03

c71187_g1_i2	<i>5NTC</i>	Cytosolic purine 5'-nucleotidase	3.14	1.94E-02
c71350_g1_i1	<i>CD63</i>	CD63 antigen	3.89	4.95E-03
c71513_g1_i1	<i>CAH3</i>	Putative carbonic anhydrase 3	3.33	1.65E-02
c71701_g1_i1	<i>SODMI</i>	Superoxide dismutase [Mn] 1, mitochondrial	3.39	4.99E-02
c71950_g1_i1	<i>TAKT</i>	Protein takeout	5.89	2.30E-03
c72119_g1_i1	<i>EFA06914.1</i>	EFA06914.1	7.48	2.30E-02
c72231_g1_i1	<i>GLCM</i>	Glucosylceramidase	#DIV/0!	7.18E-03
c72554_g1_i1	<i>EFA08774.1</i>	EFA08774.1	76.85	5.51E-05
c72595_g1_i1	<i>HUTH</i>	Histidine ammonia-lyase	321.21	1.14E-04
c72674_g1_i3	<i>ABV44725.1</i>	ABV44725.1	6.46	4.12E-02
c72801_g1_i1	<i>EFA07059.1</i>	EFA07059.1	17.42	1.86E-02
c73204_g1_i1	<i>MGST1</i>	Microsomal glutathione S-transferase 1	2.60	4.20E-02
c74226_g1_i1	<i>ABQ65714.1</i>	ABQ65714.1	2.76	2.42E-02
c74383_g1_i1	<i>DJC28</i>	DnaJ homolog subfamily C member 28	12.09	4.24E-05
c74631_g1_i1	<i>UK114</i>	Ribonuclease UK114	5.90	1.17E-02
c74930_g1_i1	<i>CO2A1</i>	Collagen alpha-1(II) chain	70.23	5.81E-06
c75126_g1_i1	<i>L2EFL</i>	Protein lethal(2)essential for life	5.55	2.44E-02
c75166_g1_i1	<i>CBPA1</i>	Zinc carboxypeptidase A	66.75	1.58E-08
c75258_g1_i2	<i>CYB5R</i>	Cytochrome b5-related protein	19.71	1.29E-02
c75496_g1_i1	<i>XP1812398.1</i>	XP1812398.1	28.96	5.53E-04
c75563_g1_i1	<i>TP1B</i>	Thaumatococcus-like protein 1b (Fragment)	3.18	2.71E-02
c75667_g1_i1	<i>PEB3</i>	Ejaculatory bulb-specific protein 3	82.81	1.04E-05
c75709_g1_i1	<i>SERP1</i>	Stress-associated endoplasmic reticulum protein 1	2.92	1.85E-02
c75875_g1_i1	<i>B1</i>	protein (Fragment)	3.65	8.45E-03
c75951_g1_i1	<i>FOXJ2</i>	Forkhead box protein L2	3.55	2.49E-02
c76366_g1_i1	<i>PEB3</i>	Ejaculatory bulb-specific protein 3	4.47	3.04E-03
c76439_g1_i1	<i>KARG</i>	Arginine kinase	2.82	2.62E-02
c76453_g1_i1	<i>SERC</i>	Probable phosphoserine aminotransferase	8.52	1.56E-05
c76501_g1_i1	<i>NP1127918.1</i>	NP1127918.1	4.97	1.87E-03
c76624_g1_i1	<i>NEPL2</i>	Nephrilysin-2	20.77	4.08E-02

c76725_g1_i1	<i>SAP</i>	Proactivator polypeptide	19.89	7.65E-09
c76726_g1_i2	<i>VCP</i>	Venom serine carboxypeptidase	240.85	2.73E-03
c76996_g2_i1	<i>PICO</i>	Putative inorganic phosphate cotransporter	8.75	7.51E-04
c77161_g1_i1	<i>ADT2</i>	ADP/ATP translocase 2	4.14	2.71E-02
c77238_g1_i1	<i>LYS</i>	Lysozyme	8.42	9.01E-05
c77266_g1_i1	<i>ENN78370.1</i>	ENN78370.1	71.47	1.68E-14
c78105_g1_i1	<i>AATM</i>	Aspartate aminotransferase, mitochondrial	2.74	3.18E-02
c78243_g1_i1	<i>CFB</i>	Clotting factor B	5.24	2.09E-02
c78252_g1_i1	<i>EFA02620.1</i>	EFA02620.1	18.19	2.60E-02
c78278_g1_i1	<i>ENN78713.1</i>	ENN78713.1	9.80	1.22E-04
c78366_g1_i2	<i>XP971465.2</i>	XP971465.2	137.53	6.08E-08
c78375_g1_i1	<i>DCXR</i>	L-xylulose reductase	33.46	3.03E-02
c78523_g1_i1	<i>RNOY</i>	Ribonuclease Oy	4.29	5.24E-03
c78599_g1_i1	<i>CYB5</i>	Cytochrome b5	39.11	6.81E-05
c78735_g1_i1	<i>FPPS</i>	Farnesyl pyrophosphate synthase	3.55	1.27E-02
c78793_g2_i1	<i>EFX82265.1</i>	EFX82265.1	30.18	1.23E-02
c78811_g1_i1	<i>SARDH</i>	Sarcosine dehydrogenase, mitochondrial	137.65	8.63E-17
c79123_g1_i1	<i>SCOT1</i>	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	6.34	2.27E-04
c79336_g1_i2	<i>GABT</i>	4-aminobutyrate aminotransferase, mitochondrial	3.25	1.67E-02
c79374_g1_i3	<i>S36A4</i>	Proton-coupled amino acid transporter 4	5.13	9.24E-04
c79677_g1_i1	<i>VCP</i>	Venom serine carboxypeptidase	64.64	6.58E-10
c79695_g1_i1	<i>LARP6</i>	La-related protein 6	4.45	3.55E-02
c79773_g1_i1	<i>EFA06160.1</i>	EFA06160.1	3.21	2.49E-02
c79812_g1_i1	<i>PGLR</i>	Probable polygalacturonase	#DIV/0!	1.27E-02
c79888_g1_i1	<i>CU12</i>	Flexible cuticle protein 12	4.24	3.29E-03
c79907_g1_i1	<i>HYEP1</i>	Juvenile hormone epoxide hydrolase 1	6.98	3.05E-03
c79951_g1_i2	<i>S26A4</i>	Pendrin	16.49	2.21E-04
c79960_g1_i1	<i>ENN79866.1</i>	ENN79866.1	#DIV/0!	5.84E-04
c80062_g1_i1	<i>NB5R3</i>	NADH-cytochrome b5 reductase 3 (Fragment)	4.52	2.89E-03
c80090_g1_i1	<i>XP1850961.1</i>	XP1850961.1	#DIV/0!	3.25E-05

c80135_g1_i1	<i>TRY1</i>	Trypsin-1	33.75	1.42E-05
c80171_g1_i1	<i>AEX93420.1</i>	juvenile hormone binding protein 5p2, partial	3155.52	1.83E-26
c80276_g1_i1	<i>PERO</i>	Peroxidase	37.71	4.25E-06
c80333_g1_i1	<i>XP968599.1</i>	similar to GA15997-PA	40.35	5.81E-04
c80440_g1_i3	<i>RXRA</i>	Retinoic acid receptor RXR-alpha	3.20	3.65E-02
c80480_g2_i1	<i>AEE63278.1</i>	SV2-like protein 2	4.55	2.59E-02
c80480_g1_i1	<i>SV2B</i>	Synaptic vesicle glycoprotein 2B	5.72	2.70E-04
c80629_g1_i1	<i>ENN73077.1</i>	hypothetical protein YQE10281, partial	6.28	2.52E-02
c80699_g1_i1	<i>EHJ74970.1</i>	hypothetical protein KGM	98.07	7.84E-06
c80976_g1_i1	<i>XP1956621.1</i>	GF25305	20.44	2.13E-02
c81004_g1_i1	<i>UD11</i>	UDP-glucuronosyltransferase 1-1	7.34	1.72E-04
c81155_g1_i1	<i>S17A5</i>	Sialin	26.79	1.76E-02
c81269_g1_i1	<i>NCASE</i>	Neutral ceramidase	5.83	6.89E-04
c81307_g1_i1	<i>PRS48</i>	Serine protease 48	10.31	3.39E-05
c81351_g1_i2	<i>S39AB</i>	Zinc transporter ZIP11	5.48	1.93E-03
c81375_g1_i1	<i>LECM</i>	C-type lectin mannose-binding isoform	5.02	1.48E-03
c81419_g2_i1	<i>AMPN</i>	Aminopeptidase N	7.71	3.21E-03
c81525_g1_i2	<i>ENN80187.1</i>	hypothetical protein YQE_03382, partial	8.45	1.63E-02
c81567_g1_i1	<i>MP20</i>	Muscle-specific protein 20	2.59	3.65E-02
c81726_g1_i1	<i>B1</i>	B1 protein (Fragment)	3.57	2.11E-02
c81853_g1_i1	<i>ASM</i>	Sphingomyelin phosphodiesterase	3.06	3.61E-02
c81881_g3_i2	<i>DEOC</i>	Putative deoxyribose-phosphate aldolase	4.23	3.13E-02
c81898_g1_i1	<i>ACPI8827.1</i>	chitin deacetylase 1	12.88	1.19E-03
c81901_g1_i1	<i>QCR2</i>	Cytochrome b-c1 complex subunit 2, mitochondrial	2.71	3.96E-02
c82125_g1_i1	<i>DHC24</i>	Delta(24)-sterol reductase	6.27	2.88E-03
c82227_g1_i1	<i>CRYL1</i>	Lambda-crystallin homolog	4.33	3.47E-03
c82346_g1_i2	<i>EST6</i>	carboxylesterase-6	#DIV/0!	7.53E-05
c82355_g1_i1	<i>EFA09024.1</i>	hypothetical protein TcasGA2-TC013968	120.34	4.07E-03
c82474_g1_i1	<i>ATPA</i>	ATP synthase subunit alpha, mitochondrial	2.65	3.91E-02
c82491_g1_i2	<i>ALO3</i>	Antimicrobial peptide Alo-3	17.87	5.53E-08

c82738_g1_i1	<i>CAP1</i>	Adenylyl cyclase-associated protein 1	4.66	1.20E-02
c82824_g1_i1	<i>IDGF4</i>	Chitinase-like protein Idgf4	3.07	1.82E-02
c82842_g1_i1	<i>ERG31</i>	C-5 sterol desaturase erg31	37.12	9.77E-08
c82925_g1_i2	<i>MLR</i>	Myosin regulatory light chain 2	5.47	4.42E-04
c83111_g1_i1	<i>XP1814267.1</i>	similar to GM14937p	15.73	2.82E-02
c83159_g1_i1	<i>SNMP2</i>	Sensory neuron membrane protein 2	#DIV/0!	8.26E-04
c83391_g1_i1	<i>HPPD</i>	4-hydroxyphenylpyruvate dioxygenase	6.95	6.70E-03
c83396_g1_i1	<i>GPDM</i>	Glycerol-3-phosphate dehydrogenase, mitochondrial	5.12	1.21E-03
c83408_g1_i2	<i>SFXN1</i>	Sideroflexin-1	8.30	3.19E-02
c83414_g1_i1	<i>MTND</i>	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	5.05	9.36E-03
c83439_g1_i1	<i>XP1809216.1</i>	hypothetical protein YQE01796, partial	4.97	1.47E-02
c83441_g1_i2	<i>AMP1</i>	Antimicrobial peptide 1	113.20	3.16E-16
c83496_g1_i1	<i>CUO6</i>	Cuticle protein 6	23.53	2.21E-08
c83529_g1_i1	<i>PNPH</i>	Purine nucleoside phosphorylase	3.92	3.35E-02
c83630_g1_i1	<i>TRE12</i>	Facilitated trehalose transporter Tret1-2 homolog	12.08	1.51E-04
c83660_g1_i1	<i>PTGR1</i>	Prostaglandin reductase 1	2.94	4.32E-02
c83678_g1_i1	<i>PDII</i>	Putative protein disulfide-isomerase C1F5.02	5.65	2.86E-02
c83688_g1_i2	<i>CATB</i>	Cathepsin B	539.47	6.93E-04
c83711_g1_i3	<i>GRHPR</i>	Glyoxylate reductase/hydroxypyruvate reductase	5.09	2.87E-02
c83731_g1_i2	<i>HEXA</i>	Hexamerin	27.45	2.85E-02
c83746_g1_i1	<i>GPAT4</i>	Glycerol-3-phosphate acyltransferase 4	2.65	4.86E-02
c83767_g1_i1	<i>GLBL3</i>	Beta-galactosidase-1-like protein 3	96.65	4.50E-02
c83822_g1_i1	<i>ATPG</i>	ATP synthase subunit gamma, mitochondrial	3.21	1.30E-02
c83947_g1_i1	<i>TNNC2</i>	Troponin C, isoform 2	7.23	2.90E-02
c84027_g1_i1	<i>CHIT</i>	Endochitinase	66.40	7.53E-10
c84089_g1_i1	<i>ENN70817.1</i>	hypothetical protein YQE12482, partial	3.71	4.27E-02
c84148_g1_i1	<i>SIDT1</i>	SID1 transmembrane family member 1	3.78	1.39E-02
c84162_g1_i1	<i>TRE12</i>	Facilitated trehalose transporter Tret1-2 homolog	14.60	1.64E-03
c84173_g1_i1	<i>CP303</i>	Probable cytochrome P450 303a1	113.40	4.77E-04
c84197_g1_i1	<i>CP4C1</i>	Cytochrome P450 4C1	5.41	1.80E-02

c84248_g1_i1	<i>EAST</i>	Serine protease easter	2.83	4.27E-02
c84331_g1_i1	<i>ENN73465.1</i>	hypothetical protein YQE_09920, partial	5.89	4.71E-04
c84333_g1_i1	<i>MCCB</i>	Probable methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	2.95	3.06E-02
c84338_g1_i1	<i>TKTL2</i>	Transketolase-like protein 2	3.97	6.61E-03
c84359_g1_i1	<i>LIPH</i>	Lipase member H	62.56	5.74E-07
c84396_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	347.34	7.16E-03
c84410_g2_i1	<i>ENN78369.1</i>	hypothetical protein YQE05171, partial	108.41	9.90E-05
c84547_g1_i2	<i>OAT</i>	Ornithine aminotransferase, mitochondrial	4.41	2.46E-03
c84584_g1_i1	<i>MFD6A</i>	Major facilitator superfamily domain-containing protein 6-A	4.57	1.84E-02
c84612_g11_i2	<i>IMPI</i>	Inducible metalloproteinase inhibitor protein	12.14	4.98E-05
c84622_g1_i1	<i>BAM17691.1</i>	cuticular protein PxutCPT1	10.62	6.99E-03
c84642_g1_i1	<i>ENN82847.1</i>	hypothetical protein YQE_00784, partial	3.69	5.93E-03
c84667_g1_i1	<i>CYB</i>	Cytochrome b	2.53	4.76E-02
c84683_g1_i1	<i>CATL</i>	Cathepsin L	595.30	1.51E-09
c84762_g1_i2	<i>DCOR</i>	Ornithine decarboxylase	164.51	9.81E-11
c84766_g1_i1	<i>DUS23</i>	Dual specificity protein phosphatase 23	5.41	1.48E-02
c84874_g1_i1	<i>XP_972702.1</i>	similar to CG33205 CG33205-PH	4.22	2.98E-03
c84928_g2_i9	<i>ACBG2</i>	Long-chain-fatty-acid--CoA ligase	3.79	2.32E-02
c84940_g1_i2	<i>PAXI</i>	Paxillin	2.60	3.51E-02
c84975_g2_i2	<i>SCRB1</i>	Scavenger receptor class B member 1	17.03	8.90E-06
c84977_g1_i1	<i>NCPR</i>	NADPH--cytochrome P450 reductase	4.74	1.73E-03
c85005_g1_i1	<i>TALDO</i>	Transaldolase	3.05	1.97E-02
c85042_g1_i2	<i>PE1</i>	Peritrophin-1	574.19	4.06E-09
c85061_g1_i1	<i>L2EFL</i>	Protein lethal(2)essential for life	2.65	3.27E-02
c85244_g1_i2	<i>235L</i>	Putative methyltransferase 235L	19.88	3.62E-06
c85248_g1_i1	<i>FXRDI</i>	FAD-dependent oxidoreductase domain-containing protein 1	3.59	3.25E-02
c85369_g1_i1	<i>PUR6</i>	Multifunctional protein ADE2	3.01	3.17E-02
c85373_g1_i1	<i>APMAP</i>	Adipocyte plasma membrane-associated protein	3.58	1.88E-02
c85398_g1_i1	<i>XP_975933.1</i>	hypothetical protein TcasGA2_TC000139	5.21	6.74E-03
c85422_g1_i1	<i>ACE</i>	Angiotensin-converting enzyme	5.29	1.18E-03

c85439_g1_i1	<i>S2611</i>	Sodium-independent sulfate anion transporter	50.73	3.32E-04
c85439_g2_i1	<i>S2611</i>	Sodium-independent sulfate anion transporter	12.35	2.80E-02
c85474_g1_i1	<i>NIPSN</i>	Protein NipSnap	3.75	1.29E-02
c85515_g1_i1	<i>HGD</i>	Homogentisate 1,2-dioxygenase	2.78	4.33E-02
c85545_g1_i2	<i>CU22</i>	Larval cuticle protein LCP-22	19.01	1.86E-02
c85557_g2_i1	<i>PYC</i>	Pyruvate carboxylase, mitochondrial	3.33	1.32E-02
c85557_g1_i1	<i>PYC1</i>	Pyruvate carboxylase 1	3.23	2.97E-02
c85590_g1_i2	<i>TRET1</i>	Facilitated trehalose transporter Tret1	3.05	2.22E-02
c85611_g1_i1	<i>DHSO</i>	Sorbitol dehydrogenase	16.13	6.44E-03
c85706_g1_i1	<i>BPHL</i>	Valacyclovir hydrolase	7.87	2.95E-02
c85736_g1_i1	<i>MAOX</i>	NADP-dependent malic enzyme	4.71	1.16E-02
c85764_g1_i1	<i>LIP1</i>	Lipase 1	26.18	2.63E-04
c85790_g1_i2	<i>ISLR2</i>	Immunoglobulin superfamily containing leucine-rich repeat protein 2	6.92	1.37E-02
c85798_g1_i1	<i>LIP3</i>	Lipase 3	76.47	1.25E-02
c85829_g1_i2	<i>TRET1</i>	Facilitated trehalose transporter Tret1	65.95	1.77E-04
c85852_g1_i2	<i>SAHH</i>	Adenosylhomocysteinase	2.93	2.24E-02
c85861_g1_i1	<i>ARSB</i>	Arylsulfatase B	17.25	2.08E-04
c85862_g1_i1	<i>ARD1</i>	D-arabinitol dehydrogenase 1	4.37	1.02E-02
c85874_g1_i1	<i>CATL</i>	Cathepsin L	15.26	3.65E-04
c85899_g1_i1	<i>EFA01822.1</i>	hypothetical protein TcasGA2_TC007424	7.24	2.30E-02
c85928_g1_i1	<i>S2535</i>	Solute carrier family 25 member 35	3.91	4.00E-03
c85930_g1_i1	<i>CTRB2</i>	Chymotrypsin BII	15.09	7.80E-06
c85935_g3_i1	<i>MLP2</i>	Muscle LIM protein Mlp84B	2.97	1.66E-02
c86029_g1_i1	<i>PE1</i>	Peritrophin-1	436.88	1.88E-14
c86033_g2_i1	<i>GBA3</i>	Cytosolic beta-glucosidase	#DIV/0!	8.18E-06
c86036_g1_i1	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	2.81	3.14E-02
c86048_g1_i1	<i>6PGD</i>	6-phosphogluconate dehydrogenase, decarboxylating	3.11	1.49E-02
c86067_g1_i1	<i>VNNL3</i>	Vanin-like protein 3	6.32	2.42E-04
c86079_g1_i1	<i>FAS</i>	Fatty acid synthase	5.34	7.80E-04
c86129_g1_i1	<i>C6A23</i>	Probable cytochrome P450 6a23	13.16	3.98E-04

c86139_g1_i1	<i>TNNT</i>	Troponin T	4.32	2.08E-03
c86424_g1_i1	<i>XP_972388.2</i>	similar to quick-to-court	4.76	3.83E-03
c86459_g1_i1	<i>CAD</i>	Homeotic protein caudal	3.08	3.66E-02
c86541_g2_i2	<i>PGLR</i>	Polygalacturonase	3.29	1.26E-02
c86573_g1_i1	<i>XP_967001.1</i>	similar to 10G08	3.83	2.19E-02
c86594_g1_i1	<i>UD2B7</i>	UDP-glucuronosyltransferase 2B7	14.16	2.03E-02
c86608_g1_i1	<i>ASPG</i>	L-asparaginase	17.48	2.17E-02
c86613_g2_i1	<i>ATTY</i>	Tyrosine aminotransferase	8.20	1.97E-03
c86613_g1_i1	<i>ATTY</i>	Tyrosine aminotransferase	17.77	3.54E-02
c86626_g1_i1	<i>PEI</i>	Peritrophin-1	89.97	5.29E-14
c86650_g1_i1	<i>COXI</i>	Cytochrome c oxidase subunit 1	2.56	4.03E-02
c86652_g1_i1	<i>AASS</i>	Alpha-aminoadipic semialdehyde synthase, mitochondrial	62.31	7.43E-06
c86682_g1_i1	<i>PRPS1</i>	Ribose-phosphate pyrophosphokinase 1	2.84	3.06E-02
c86725_g1_i1	<i>TRET1</i>	Facilitated trehalose transporter Tret1	37.59	3.32E-04
c86782_g1_i1	<i>ALDR</i>	Aldose reductase	5.58	6.70E-04
c86859_g1_i1	<i>XP975880.1</i>	similar to CG9572 CG9572-PA isoform 2	6.68	2.09E-04
c86860_g1_i1	<i>IVD</i>	Isovaleryl-CoA dehydrogenase, mitochondrial	4.14	1.37E-02
c86907_g1_i1	<i>CGT</i>	2-hydroxyacylsphingosine 1-beta-galactosyltransferase	23.04	1.27E-05
c87020_g1_i1	<i>ODP2</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	3.71	2.49E-02
c87025_g1_i1	<i>CUDI</i>	Endocuticle structural glycoprotein SgAbd-1	64.35	2.04E-03
c87094_g1_i2	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	3.57	7.82E-03
c87130_g1_i1	<i>FGFRI</i>	Fibroblast growth factor receptor 1	12.00	6.99E-03
c87156_g1_i1	<i>AEV76946.</i>	putative juvenile hormone-inducible protein	65.18	9.31E-04
c87169_g1_i2	<i>K1161</i>	Uncharacterized family 31 glucosidase KIAA1161	189.66	3.91E-02
c87237_g1_i1	<i>TRET1</i>	Facilitated trehalose transporter Tret1	40.95	9.01E-07
c87239_g1_i2	<i>PNR</i>	GATA-binding factor A	4.74	2.21E-02
c87295_g1_i1	<i>ENN73638.1</i>	hypothetical protein YQE_09884, partial	20.92	4.32E-08
c87448_g2_i1	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	83.17	1.91E-09
c87610_g1_i2	<i>XP976439.1</i>	hypothetical protein TcasGA2_TC015508	3.12	4.80E-02

c87633_g1_i1	<i>APY</i>	Apyrase	183.50	3.72E-06
c87672_g1_i1	<i>XP970545.1</i>	similar to AGAP006068-PA	4.59	6.50E-03
c87677_g1_i1	<i>AL3A2</i>	Fatty aldehyde dehydrogenase	7.20	1.95E-02
c87735_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	316.18	1.08E-09
c87749_g1_i1	<i>EDL11</i>	Sugar transporter ERD6-like 11	111.03	6.11E-03
c87787_g1_i1	<i>XP_001809722.1</i>	similar to Muscle-specific protein 300 CG33715-PD	4.25	3.57E-02
c87825_g2_i1	<i>LUCI</i>	Luciferin 4-monooxygenase	3.04	2.19E-02
c87944_g1_i1	<i>ARH</i>	Low density lipoprotein receptor adapter protein 1	3.65	7.77E-03
c88030_g1_i2	<i>CP6K1</i>	Cytochrome P450 6k1	19.67	3.52E-04
c88044_g1_i1	<i>SBPIA</i>	Selenium-binding protein 1-A	6.41	2.44E-04
c88046_g1_i3	<i>XP_970759.2</i>	similar to conserved hypothetical protein	3.33	1.33E-02
c88083_g3_i1	<i>CAM36311.1</i>	hypothetical protein	2.85	2.10E-02
c88119_g1_i1	<i>GPDA</i>	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	3.49	9.99E-03
c88155_g1_i1	<i>PLPL2</i>	Patatin-like phospholipase domain-containing protein 2	2.98	3.03E-02
c88165_g1_i1	<i>FACRI</i>	Putative fatty acyl-CoA reductase	3.82	4.75E-02
c88264_g1_i1	<i>PUR8</i>	Adenylosuccinate lyase	4.59	5.63E-03
c88310_g1_i1	<i>GANAB</i>	Neutral alpha-glucosidase AB	57.96	7.87E-06
c88361_g1_i1	<i>GCDH</i>	Glutaryl-CoA dehydrogenase, mitochondrial	2.66	4.38E-02
c88366_g2_i1	<i>AGT2L</i>	Alanine--glyoxylate aminotransferase 2-like	3.12	1.64E-02
c88376_g1_i1	<i>ODPB</i>	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	3.22	1.87E-02
c88397_g1_i1	<i>ENOF1</i>	Mitochondrial enolase superfamily member 1	3.80	6.17E-03
c88568_g2_i1	<i>STIE1</i>	Estrogen sulfotransferase	68.74	1.80E-07
c88715_g4_i1	<i>PUR1</i>	Amidophosphoribosyltransferase	3.87	7.42E-03
c88759_g1_i1	<i>SRCA</i>	Sarcalumenin	4.26	3.95E-03
c88770_g1_i1	<i>ZN263</i>	Zinc finger protein 26	11.50	5.51E-04
c88844_g1_i1	<i>LIPP</i>	Pancreatic triacylglycerol lipase	4.37	5.36E-03
c88850_g1_i1	<i>CUE</i>	Protein cueball	4.44	1.25E-02
c88874_g2_i1	<i>CO9A1</i>	Collagen alpha-1(IX) chain	26.91	4.88E-06
c88874_g1_i1	<i>XP_392960.4</i>	collagen alpha-2(IV) chain-like	3.39	4.56E-02
c88878_g1_i1	<i>TITIN</i>	Titin	6.48	3.42E-02

c88995_g1_i1	<i>MDHM</i>	Malate dehydrogenase, mitochondrial	3.07	1.69E-02
c89056_g1_i1	<i>XP_001866279.</i>	conserved hypothetical protein	78.11	1.35E-08
c89106_g1_i2	<i>PR3CB</i>	Protein phosphatase 1 regulatory subunit 3C-B	6.27	3.45E-04
c89198_g5_i1	<i>GILT</i>	Gamma-interferon-inducible lysosomal thiol reductase	6.28	4.61E-02
c89205_g1_i2	<i>EFA13543.1</i>	hypothetical protein TcasGA2_TC001783	4.83	1.17E-03
c89234_g1_i1	<i>AADAT</i>	Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial	17.95	7.67E-08
c89266_g2_i4	<i>AMPN</i>	Aminopeptidase N	2.78	2.23E-02
c89282_g1_i1	<i>FAT4</i>	Protocadherin Fat 4	18.66	2.14E-02
c89357_g1_i1	<i>P5CS</i>	Delta-1-pyrroline-5-carboxylate synthase	3.66	5.62E-03
c89371_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	573.30	1.03E-09
c89444_g1_i1	<i>ARGI2</i>	Arginase-2, mitochondrial	3.43	1.36E-02
c89540_g2_i2	<i>ACO11</i>	Acyl-CoA Delta(11) desaturase	34.60	1.28E-03
c89550_g1_i4	<i>TSP1</i>	Thrombospondin-1	8.62	1.40E-03
c89639_g3_i2	<i>IMPA1</i>	Inositol monophosphatase 1	5.12	4.68E-02
c89653_g1_i2	<i>UNI3D</i>	Protein unc-13 homolog D	3.21	2.38E-02
c89693_g2_i2	<i>EEZ98245.1</i>	hypothetical protein TcasGA2_TC000684	5.35	7.18E-03
c89796_g1_i2	<i>PO11</i>	Retrovirus-related For polyprotein from type-1 retrotransposable element R1 (Fragment)	4.12	3.62E-02
c89808_g1_i1	<i>EST6</i>	carboxylesterase-6	50.25	2.63E-03
c89857_g1_i1	<i>POL</i>	Gag-Pol polyprotein	7.62	7.68E-03
c89860_g1_i3	<i>MANA</i>	Mannan endo-1,4-beta-mannosidase	185.88	1.74E-02
c90106_g1_i4	<i>CREBA</i>	Cyclic AMP response element-binding protein A	3.10	2.81E-02
c90136_g1_i1	<i>LUCI</i>	Luciferin 4-monooxygenase	11.68	4.06E-02
c90197_g2_i1	<i>ADI61825.1</i>	endonuclease-reverse transcriptase	2.62	3.88E-02
c90293_g1_i3	<i>ERDL2</i>	Sugar transporter ERD6-like 2	4.87	3.98E-02
c90323_g1_i2	<i>PCKG</i>	Phosphoenolpyruvate carboxykinase [GTP]	7.05	2.51E-02
c90342_g2_i1	<i>ENN81685.1</i>	hypothetical protein YQE_01891, partial	4.54	2.43E-02
c90412_g1_i1	<i>L259</i>	Probable multidrug resistance-associated protein lethal(2)03659	99.34	4.46E-11
c90457_g1_i2	<i>5NTD</i>	Protein 5NUC	6.16	3.42E-04
c90669_g3_i1	<i>Y2R2</i>	Putative 115 kDa protein in type-1 retrotransposable element R1DM	4.43	2.87E-02
c90734_g3_i1	<i>PO11</i>	Retrovirus-related For polyprotein from type-1 retrotransposable element R1 (Fragment)	3.74	3.66E-02

c90791_g1_i1	<i>L259</i>	Probable multidrug resistance-associated protein lethal(2)03659	3.19	2.90E-02
c90870_g1_i1	<i>YF64</i>	Uncharacterized protein R102.4	6.26	3.73E-02
c91119_g1_i1	<i>MYROI</i>	Myrosinase 1	17.20	3.17E-02
c91145_g2_i4	<i>RTJK</i>	RNA-directed DNA polymerase from mobile element jockey	3.13	2.53E-02
c91248_g1_i1	<i>MYSA</i>	Myosin heavy chain	2.62	3.40E-02
c91407_g2_i1	<i>TITIN</i>	Titin	3.03	1.55E-02
c91444_g1_i1	<i>ACAC</i>	Acetyl-CoA carboxylase	3.64	3.08E-02
c91460_g2_i1	<i>GDE</i>	Glycogen debranching enzyme	2.96	4.08E-02
c91486_g1_i2	<i>ENN78530.1</i>	hypothetical protein YQE_05004, partial	2.69	4.65E-02
c91494_g1_i1	<i>SYNE1</i>	Nesprin-1	3.71	1.16E-02
c91617_g1_i3	<i>Y2R2</i>	Putative 115 kDa protein in type-1 retrotransposable element R1DM	3.96	4.66E-02
c91624_g1_i1	<i>RTBS</i>	Probable RNA-directed DNA polymerase from transposon BS	2.91	4.07E-02
c91627_g3_i1	<i>UNC22</i>	Twitchin	5.21	2.37E-03
c91627_g5_i1	<i>UNC22</i>	Twitchin	4.21	2.46E-03
c91627_g4_i1	<i>UNC22</i>	Twitchin	6.09	2.00E-03
c112579_g1_i1	<i>PGSC2</i>	Peptidoglycan-recognition protein SC2	4.27	5.71E-03
c132611_g1_i1	<i>YD62</i>	Uncharacterized protein C17G8.02	17.70	9.32E-07
c133618_g1_i1	<i>PGRP2</i>	Peptidoglycan-recognition protein 2	7.46	1.30E-02
c156306_g1_i1	<i>URAD</i>	2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase	3.33	2.53E-02
c159762_g1_i1	<i>ATPO</i>	ATP synthase subunit O, mitochondrial	3.56	3.17E-02
c175681_g1_i1	<i>MAL1</i>	Maltase 1	4.84	3.23E-02
c205180_g1_i1	<i>KLOT</i>	Klotho	71.24	9.76E-06
c555_g1_i2	<i>ROA2</i>	Heterogeneous nuclear ribonucleoproteins A2/B1	0.00	4.87E-02
c852_g1_i1	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	0.00	3.44E-02
c871_g1_i1	<i>RL6</i>	60S ribosomal protein L6	0.00	3.95E-02
c901_g1_i1	<i>RL17</i>	60S ribosomal protein L17	0.00	4.81E-02
c2627_g1_i1	<i>RL10A</i>	60S ribosomal protein L10a	0.00	4.06E-02
c3004_g1_i2	<i>SHAKB</i>	Innexin shaking-B	0.25	2.71E-02
c7163_g1_i1	<i>ENN76126.1</i>	hypothetical protein YQE	0.00	3.31E-02
c7566_g1_i1	<i>K2C8</i>	Keratin, type II cytoskeletal 8	0.00	3.03E-02

c8048_g1_i1	<i>RS16</i>	40S ribosomal protein S16	0.00	4.83E-02
c10038_g1_i1	<i>EF1B</i>	Elongation factor 1-beta	0.00	4.42E-02
c10043_g1_i1	<i>NP1950.1</i>	elongation factor 1-beta	0.00	4.33E-02
c10089_g1_i1	<i>RL13A</i>	60S ribosomal protein L13a	0.00	2.37E-02
c10091_g1_i1	<i>ERRFI</i>	ERBB receptor feedback inhibitor 1	0.00	4.31E-02
c10151_g1_i1	<i>YS049</i>	Zinc finger protein	0.00	4.44E-02
c10286_g1_i2	<i>XP3832743.1</i>	putative uncharacterized protein encoded by LINC00596-like	0.00	1.69E-02
c10389_g1_i1	<i>RL9</i>	60S ribosomal protein L9	0.00	4.00E-02
c10392_g1_i1	<i>XP3953487.1</i>	60S ribosomal protein L9-like isoform 1	0.02	1.79E-03
c10405_g1_i1	<i>IF4AI</i>	Eukaryotic initiation factor 4A-I	0.00	4.19E-02
c12875_g1_i1	<i>EF1G</i>	Elongation factor 1-gamma	0.00	4.31E-02
c13517_g1_i1	<i>RL36</i>	60S ribosomal protein L36	0.00	4.58E-02
c15385_g1_i1	<i>COX1</i>	Cytochrome c oxidase subunit 1	0.00	2.97E-02
c15812_g1_i1	<i>CDC20</i>	Cell division cycle protein 20 homolog	0.35	3.09E-02
c17533_g1_i1	<i>XP969612</i>	similar to WD repeat-containing protein slp1	0.03	1.51E-02
c17599_g1_i1	<i>S22A3</i>	Solute carrier family 22 member 3	0.16	4.49E-04
c18144_g1_i1	<i>KPYM</i>	Pyruvate kinase PKM	0.00	2.90E-02
c22513_g1_i1	<i>HUNIN</i>	Putative humanin peptide	0.00	1.61E-02
c24111_g1_i1	<i>JC1348</i>	hypothetical 18K protein - goldfish mitochondrion	0.00	4.35E-02
c24280_g1_i1	<i>RLA1</i>	60S acidic ribosomal protein P1	0.00	3.24E-02
c26234_g1_i1	<i>TYB10</i>	Thymosin beta-10	0.00	3.38E-02
c26429_g1_i1	<i>RL3</i>	60S ribosomal protein L3	0.00	3.64E-02
c29016_g1_i1	<i>LIPH</i>	Lipase member H	0.05	6.94E-03
c32642_g1_i1	<i>EFA09985.1</i>	hypothetical protein TcasGA2	0.01	2.78E-03
c33481_g1_i1	<i>CALR</i>	Calreticulin	0.00	2.85E-02
c33573_g1_i2	<i>AKA12</i>	A-kinase anchor protein 12	0.00	2.37E-02
c33746_g1_i1	<i>BAE06085.1</i>	AKAP12 variant protein	0.00	2.37E-02
c34613_g1_i1	<i>ROA1</i>	Heterogeneous nuclear ribonucleoprotein A1	0.00	3.10E-02
c34884_g1_i1	<i>RLA0</i>	acidic ribosomal protein P0	0.00	1.86E-02
c34967_g1_i1	<i>K1C19</i>	Keratin, type I cytoskeletal 19	0.00	4.96E-02

c35619_g1_i3	<i>ANXA2</i>	Annexin A2	0.00	3.78E-02
c41764_g1_i1	<i>PABP1</i>	Polyadenylate-binding protein 1	0.00	3.95E-02
c43808_g1_i1	<i>BASI</i>	Basigin	0.00	4.96E-02
c44563_g1_i1	<i>APOD</i>	Apolipoprotein D	0.06	5.49E-04
c46706_g1_i1	<i>EFA11278.1</i>	hypothetical protein TcasGA2	0.00	1.69E-02
c48948_g1_i1	<i>ALDOA</i>	Fructose-bisphosphate aldolase A	0.00	4.38E-02
c50949_g1_i1	<i>RL8</i>	60S ribosomal protein L8	0.00	2.79E-02
c51199_g1_i1	<i>NP964.1</i>	60S ribosomal protein L8	0.01	1.97E-02
c52074_g1_i1	<i>XP1812500.1</i>	similar to CG34115 CG34115-PA	0.00	3.13E-02
c54231_g1_i1	<i>GFII</i>	Zinc finger protein sens	0.09	7.30E-04
c54262_g1_i1	<i>XRCC6</i>	X-ray repair cross-complementing protein 6	0.00	4.63E-02
c55505_g1_i1	<i>PDIA1</i>	Protein disulfide-isomerase	0.00	3.08E-02
c56166_g2_i1	<i>XP4040818.1</i>	protein disulfide-isomerase	0.00	4.70E-02
c56546_g1_i1	<i>PDIA4</i>	Protein disulfide-isomerase A4	0.00	4.96E-02
c57175_g1_i2	<i>CALX</i>	Calnexin	0.00	4.67E-02
c57389_g1_i2	<i>BAG57859.1</i>	unnamed protein product	0.03	2.02E-02
c57411_g1_i1	<i>ELOV7</i>	Elongation of very long chain fatty acids protein 7	0.00	2.85E-02
c59041_g1_i1	<i>Y2R2</i>	Putative 115 kDa protein in type-1 retrotransposable element R1DM	0.01	4.03E-02
c60921_g1_i1	<i>SAP</i>	Proactivator polypeptide	0.00	4.50E-02
c63809_g1_i1	<i>NP2769.1</i>	proactivator polypeptide isoform a preproprotein	0.00	9.20E-03
c64025_g1_i1	<i>EF2</i>	Elongation factor 2	0.00	1.60E-02
c65249_g1_i1	<i>NP1952.1</i>	elongation factor 2	0.10	4.24E-02
c65861_g1_i1	<i>ENN70557.1</i>	hypothetical protein YQE12732, partial	0.01	1.72E-06
c66236_g1_i1	<i>ENN70941.1</i>	hypothetical protein YQE12343, partial	0.35	3.54E-02
c66535_g1_i1	<i>ENN79650.1</i>	hypothetical protein YQE03909, partial	0.18	1.82E-03
c66811_g1_i3	<i>AAF74117.1</i>	unknown	0.00	4.94E-02
c68544_g1_i1	<i>EAX03762.1</i>	high mobility group AT-hook 1, isoform CRA_a	0.00	3.12E-02
c69172_g1_i1	<i>METL6</i>	Methyltransferase-like protein 6	0.24	2.90E-02
c69451_g1_i1	<i>RHPN2</i>	Rhopilin-2	0.15	9.28E-04
c69600_g1_i1	<i>CC85C</i>	Coiled-coil domain-containing protein 85C	0.35	3.49E-02

c70065_g1_i1	<i>SCD5</i>	Stearoyl-CoA desaturase 5	0.01	1.75E-02
c71181_g1_i1	<i>MUG1</i>	Murinoglobulin-1	0.17	8.67E-03
c71276_g2_i1	<i>RL40</i>	Ubiquitin-60S ribosomal protein L40	0.00	4.67E-02
c71708_g1_i2	<i>SYAC</i>	Alanine--tRNA ligase, cytoplasmic	0.00	4.50E-02
c72030_g1_i1	<i>NPC2</i>	Protein NPC2 homolog	0.14	2.10E-04
c72047_g1_i1	<i>PEB3</i>	Ejaculatory bulb-specific protein 3	0.00	3.34E-02
c72375_g1_i1	<i>ACE</i>	Angiotensin-converting enzyme	0.14	1.42E-03
c72440_g1_i1	<i>ESCA</i>	Protein escargot	0.16	1.86E-03
c72511_g1_i1	<i>EZRI</i>	Ezrin	0.00	3.49E-02
c72677_g1_i1	<i>HNRPC</i>	Heterogeneous nuclear ribonucleoprotein C	0.00	4.23E-02
c72914_g1_i1	<i>CU08</i>	Cuticle protein 8	0.12	1.66E-02
c72930_g1_i1	<i>RS18</i>	40S ribosomal protein S18	0.00	2.12E-02
c72990_g1_i1	<i>MPIP</i>	M-phase inducer phosphatase	0.21	5.74E-03
c73102_g1_i2	<i>BXA1</i>	Bombyxin A-1	0.05	1.20E-02
c73222_g2_i3	<i>STUB</i>	Serine proteinase stubble	0.00	3.82E-02
c73598_g1_i1	<i>XP_001813945.1</i>	similar to trypsin-like serine protease	0.22	3.60E-03
c73608_g1_i1	<i>HYOU1</i>	Hypoxia up-regulated protein 1	0.00	3.84E-02
c73645_g1_i1	<i>HEXIM</i>	Protein HEXIM	0.28	4.66E-02
c74915_g1_i1	<i>LIPR2</i>	Pancreatic lipase-related protein 2	0.01	1.69E-07
c75007_g1_i1	<i>CU19</i>	Cuticle protein 19	0.00	4.57E-02
c75642_g1_i4	<i>CUC1B</i>	Pupal cuticle protein C1B	0.00	2.83E-09
c76176_g2_i1	<i>PRAX</i>	Periaxin	0.00	4.16E-02
c76379_g1_i1	<i>APOD</i>	Apolipoprotein D	0.29	1.38E-02
c76730_g1_i2	<i>SQSTM</i>	Sequestosome-1	0.00	4.94E-02
c77271_g1_i3	<i>ADH2</i>	Alcohol dehydrogenase 2	0.05	2.22E-07
c77350_g1_i1	<i>XP_966954.2</i>	similar to putative alcohol dehydrogenase	0.17	8.88E-03
c77388_g1_i1	<i>DHR13</i>	Dehydrogenase/reductase SDR family member 13	0.00	4.90E-02
c77620_g1_i1	<i>EFA12116.1</i>	hypothetical protein TcasGA2_TC002262	0.03	4.46E-05
c78227_g1_i1	<i>TNNC</i>	Troponin C	0.27	1.20E-02
c78273_g1_i1	<i>SODC</i>	Superoxide dismutase [Cu-Zn]	0.23	1.37E-02

c78450_g1_i1	<i>AEY77316.1</i>	extracellular Cu/Zn-superoxide dismutase	0.16	8.39E-03
c78525_g1_i1	<i>EFA04340.1</i>	hypothetical protein TcasGA2_TC014634	0.00	1.54E-02
c78728_g2_i2	<i>INO1A</i>	Inositol-3-phosphate synthase 1-A	0.28	1.14E-02
c78930_g1_i1	<i>XP_967186.1</i>	similar to myo-inositol-1 phosphate synthase	0.00	4.91E-02
c79208_g1_i2	<i>HR3</i>	Probable nuclear hormone receptor HR3	0.29	1.77E-02
c79446_g1_i1	<i>MLP2</i>	Muscle LIM protein Mlp84B	0.00	3.78E-02
c79470_g2_i1	<i>NP_001103762.1</i>	muscle LIM protein isoform 1	0.32	2.50E-02
c79621_g1_i1	<i>CNTRB</i>	Centrobilin	0.26	6.51E-03
c79649_g1_i1	<i>A1A1A</i>	Alcohol dehydrogenase [NADP(+)] A	0.12	2.61E-02
c79842_g1_i1	<i>PROC</i>	Vitamin K-dependent protein C	0.19	2.48E-02
c79869_g1_i5	<i>VIGLN</i>	Vigilin	0.00	4.58E-02
c79983_g1_i1	<i>TBB</i>	Tubulin beta chain (Fragment)	0.35	4.54E-02
c80776_g1_i1	<i>AAI27875.1</i>	Unknown (protein for IMAGE:40134249)	0.26	1.80E-02
c80861_g1_i1	<i>HCE1</i>	High choriolytic enzyme 1	0.01	1.05E-02
c81104_g1_i1	<i>CUO6</i>	Cuticle protein 6	0.04	1.63E-02
c81291_g1_i1	<i>HEXA</i>	Hexamerin	0.07	4.95E-07
c81347_g1_i1	<i>ESMC</i>	Enhancer of split mgamma protein	0.27	1.91E-02
c81386_g1_i1	<i>XP_972685.1</i>	similar to AGAP012342-PA	0.20	4.50E-02
c81430_g1_i1	<i>CUT1</i>	Cuticlin-1	0.18	1.36E-03
c81593_g1_i1	<i>XP_968958.1</i>	similar to miniature CG9369-PA	0.00	1.04E-03
c81654_g1_i1	<i>XP_975369.1</i>	similar to AGAP010294-PA	0.20	3.90E-02
c81663_g1_i1	<i>TBB4B</i>	Tubulin beta-4B chain (Fragments)	0.33	2.03E-02
c81667_g1_i1	<i>XP_967348.1</i>	similar to AGAP010510-PA	0.17	6.63E-04
c82022_g1_i1	<i>XP_972121.1</i>	similar to AGAP001449-PA	0.05	2.72E-02
c82080_g1_i1	<i>XP_975669.1</i>	similar to cuticular protein 1, RR-2 family (AGAP001664-PA)	0.14	3.26E-02
c82081_g1_i1	<i>ENN74650.1</i>	hypothetical protein YQE_08767, partial	0.15	2.33E-04
c82085_g1_i2	<i>CUC1B</i>	Pupal cuticle protein C1B	0.03	7.26E-05
c82215_g1_i1	<i>AST3</i>	Achaete-scute complex protein T3	0.07	4.79E-02
c82492_g1_i1	<i>NLGNX</i>	Neuroigin-4, X-linked	0.18	1.78E-03
c82561_g1_i1	<i>DL</i>	Neurogenic locus protein delta	0.01	1.16E-09

c82604_g2_i1	<i>EFA01689.1</i>	hypothetical protein TcasGA2_TC007264	0.28	3.75E-02
c82698_g1_i1	<i>XP_969862.1</i>	similar to conserved hypothetical protein	0.24	1.55E-02
c82702_g1_i3	<i>XP_971367.2</i>	similar to CG15786 CG15786-PA	0.07	5.62E-07
c82727_g3_i2	<i>FBLN1</i>	Fibulin-1	0.01	4.39E-03
c82837_g2_i1	<i>STUB</i>	Serine proteinase stubble	0.00	1.21E-02
c82918_g1_i1	<i>THIC</i>	Acetyl-CoA acetyltransferase, cytosolic	0.24	1.99E-02
c83007_g1_i2	<i>CED6</i>	PTB domain-containing adapter protein ced-6	0.35	4.28E-02
c83023_g1_i1	<i>SCA</i>	Protein scabrous	0.09	3.27E-06
c83030_g1_i1	<i>XP_972571.1</i>	similar to scabrous protein	0.30	4.32E-02
c83323_g2_i1	<i>SH24A</i>	SH2 domain-containing protein 4A	0.34	3.31E-02
c83326_g1_i1	<i>CP18A</i>	Cytochrome P450 18a1	0.20	3.44E-03
c83657_g1_i4	<i>XP_968477.1</i>	similar to cytochrome P450, partial	0.08	4.56E-05
c83722_g2_i2	<i>FAA00648.1</i>	putative cuticle protein	0.02	4.72E-02
c84109_g1_i1	<i>EFA06938.1</i>	hypothetical protein TcasGA2_TC009889	0.38	4.63E-02
c84257_g1_i1	<i>ENN81522.1</i>	hypothetical protein YQE_02051, partial	0.04	4.51E-07
c84349_g1_i1	<i>SNMP2</i>	Sensory neuron membrane protein 2	0.06	1.81E-06
c84409_g1_i1	<i>CBPB</i>	Carboxypeptidase B	0.02	7.29E-03
c84472_g1_i2	<i>CU07</i>	Cuticle protein 7	0.04	5.08E-03
c84528_g1_i1	<i>GEM</i>	GTP-binding protein GEM	0.09	2.76E-03
c84634_g1_i2	<i>XP_968810.1</i>	similar to AGAP005243-PA	0.00	1.36E-02
c84653_g1_i1	<i>PIPE</i>	Heparan sulfate 2-O-sulfotransferase pipe	0.05	2.25E-02
c84739_g1_i1	<i>EFA12172.</i>	pipe	0.35	3.64E-02
c84772_g1_i2	<i>MTP</i>	Microsomal triglyceride transfer protein large subunit	0.35	4.69E-02
c84780_g1_i2	<i>CADE</i>	CADE_DROME DE-cadherin	0.21	3.74E-03
c85083_g2_i2	<i>KLH17</i>	Kelch-like protein 17 OS=Rattus norvegicus	0.02	1.23E-02
c85157_g1_i3	<i>LIPR2</i>	Pancreatic lipase-related protein 2	0.00	2.32E-02
c85195_g1_i1	<i>AMERL</i>	AMMECR1-like protein	0.28	2.76E-02
c85433_g1_i1	<i>S16C6</i>	Short-chain dehydrogenase/reductase family 16C member 6	0.00	6.88E-04
c85636_g1_i2	<i>CU03</i>	Cuticle protein 3	0.03	1.90E-09
c85642_g1_i2	<i>DDX6</i>	Putative ATP-dependent RNA helicase me31b	0.34	2.91E-02

c85675_g1_i1	<i>RGN</i>	Regucalcin	0.25	3.88E-03
c85776_g3_i1	<i>XP_967668.1</i>	similar to luciferin-regenerating enzyme	0.31	1.39E-02
c86202_g1_i1	<i>ENN75917.1</i>	hypothetical protein YQE_07558, partial	0.01	2.67E-02
c86272_g1_i1	<i>ENN79214.1</i>	hypothetical protein YQE_04398, partial	0.02	4.37E-02
c86333_g9_i1	<i>CU08</i>	Cuticle protein 8	0.00	4.79E-02
c86521_g2_i1	<i>KLKB1</i>	Plasma kallikrein	0.08	2.02E-06
c86538_g1_i1	<i>PRS27</i>	Serine protease 27	0.16	8.60E-04
c86583_g1_i1	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	0.25	1.27E-02
c86784_g1_i1	<i>DL</i>	Neurogenic locus protein delta	0.27	4.83E-02
c87037_g1_i1	<i>ANR29</i>	Ankyrin repeat domain-containing protein 29	0.29	3.02E-02
c87402_g2_i1	<i>EFHD</i>	EF-hand domain-containing protein CG10641	0.26	2.53E-02
c87417_g1_i1	<i>AEE62128.1</i>	unknown	0.02	3.82E-11
c87445_g1_i2	<i>EFA10390.1</i>	hypothetical protein TcasGA2_TC012621	0.32	2.21E-02
c87532_g1_i2	<i>SES1B</i>	SEC14 domain and spectrin repeat-containing protein 1-B	0.08	2.29E-02
c87573_g1_i1	<i>CATA</i>	Catalase	0.33	1.90E-02
c87630_g1_i1	<i>TBA1C</i>	Tubulin alpha-1C chain	0.26	4.59E-02
c87651_g2_i2	<i>CUA2B</i>	Larval cuticle protein	0.03	2.38E-02
c87651_g3_i1	<i>CUA2B</i>	Larval cuticle protein A2B	0.06	3.19E-06
c87904_g3_i2	<i>BAM19289.1</i>	cuticular protein PpolCPR67A	0.16	4.56E-03
c88121_g1_i1	<i>SPON2</i>	Spondin-2	0.31	3.38E-02
c88326_g1_i1	<i>XP_972867.1</i>	similar to GA10108-PA	0.21	1.83E-02
c88332_g1_i2	<i>XP_001808976.1</i>	hypothetical protein TcasGA2_TC015091	0.22	2.54E-02
c88443_g1_i1	<i>EFA13346.1</i>	hypothetical protein TcasGA2_TC002325	0.10	7.46E-03
c88484_g1_i1	<i>ENN83446.1</i>	hypothetical protein YQE_00194, partial	0.20	5.59E-03
c88588_g1_i1	<i>ELVL1</i>	Elongation of very long chain fatty acids protein AAEL008004	0.27	1.94E-02
c88821_g1_i1	<i>TRETI</i>	Facilitated trehalose transporter Tret1	0.31	3.70E-02
c88915_g1_i4	<i>MOT10</i>	Monocarboxylate transporter 10	0.34	3.21E-02
c88925_g1_i3	<i>NBL1</i>	Neuroblastoma suppressor of tumorigenicity 1	0.33	2.80E-02
c89047_g1_i4	<i>STUB</i>	Serine proteinase stubble	0.04	7.42E-08
c89131_g5_i2	<i>XP_973911.2</i>	similar to serine proteinase stubble	0.15	3.30E-02

c89184_g1_i1	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	0.07	6.20E-03
c89360_g1_i1	<i>SVEP1</i>	von Willebrand factor type A, EGF and pentraxin domain-containing protein 1	0.04	1.10E-02
c89489_g6_i1	<i>CBPM</i>	Carboxypeptidase M	0.10	2.15E-02
c89523_g6_i2	<i>DPS1</i>	Decaprenyl-diphosphate synthase subunit 1	0.37	4.81E-02
c89639_g2_i1	<i>CAD96</i>	Tyrosine kinase receptor Cad96Ca	0.28	4.79E-02
c89751_g1_i5	<i>ZBT48</i>	Zinc finger and BTB domain-containing protein 48	0.22	3.97E-02
c89779_g1_i5	<i>LIPP</i>	Pancreatic triacylglycerol lipase (Fragment)	0.26	3.88E-02
c89802_g3_i1	<i>XP_969219.2</i>	similar to pancreatic lipase	0.16	4.16E-04
c89939_g1_i1	<i>MMEL1</i>	Membrane metallo-endopeptidase-like 1	0.20	9.57E-04
c89983_g2_i2	<i>CPN2</i>	Carboxypeptidase N subunit 2	0.18	1.51E-03
c90320_g1_i2	<i>EFA04067.1</i>	hypothetical protein TcasGA2_TC014301	0.08	5.89E-03
c90488_g3_i1	<i>ELOV4</i>	Elongation of very long chain fatty acids protein 4	0.00	3.57E-02
c90498_g1_i1	<i>DDR1</i>	Epithelial discoidin domain-containing receptor 1	0.29	3.64E-02
c90515_g1_i1	<i>MMP14</i>	Matrix metalloproteinase-14	0.35	3.20E-02
c90553_g2_i1	<i>PCD15</i>	Protocadherin-15	0.21	3.49E-03
c90572_g1_i3	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	0.20	4.82E-02
c90792_g1_i1	<i>CSMD2</i>	CUB and sushi domain-containing protein 2	0.22	1.13E-02
c90797_g1_i1	<i>CORIN</i>	Atrial natriuretic peptide-converting enzyme	0.09	2.63E-02
c91160_g1_i1	<i>PLXB</i>	Plexin-B	0.31	4.01E-02
c91176_g1_i3	<i>ZN197</i>	Zinc finger protein 197	0.01	3.18E-08
c91201_g1_i1	<i>SP63</i>	sperm flagellar membrane protein	0.18	5.65E-04
c91281_g1_i1	<i>AGO2</i>	Protein argonaute-2	0.31	2.66E-02
c91369_g1_i1	<i>MBLK1</i>	Mushroom body large-type Kenyon cell-specific protein 1	0.21	2.39E-03
c91467_g1_i1	<i>CHS8</i>	Chitin synthase 8	0.15	5.77E-04
c91810_g1_i1	<i>RLA2</i>	60S acidic ribosomal protein P2	0.00	3.87E-02
c91850_g1_i1	<i>EF1A1</i>	Elongation factor 1-alpha 1	0.00	2.19E-02
c91870_g1_i1	<i>EDL77725.1</i>	rCG25445, isoform CRA	0.00	3.53E-02
c92912_g1_i1	<i>AEE63393.1</i>	hypothetical protein YQE_04422, partial	0.00	2.78E-02
c93759_g1_i1	<i>FRIL</i>	Ferritin light chain	0.00	3.57E-02

c96387_g1_i1	<i>CAE11873.1</i>	hypothetical protein	0.00	1.74E-02
c97179_g1_i1	<i>ENN79217.1</i>	hypothetical protein YQE04401, partial	0.00	3.37E-02
c98088_g1_i1	<i>RL32</i>	60S ribosomal protein L32	0.00	4.11E-02
c99730_g1_i1	<i>RS23</i>	40S ribosomal protein S23	0.00	3.52E-02
c100361_g1_i1	<i>RS25</i>	40S ribosomal protein S25	0.00	4.42E-02
c112250_g1_i1	<i>NU5M</i>	NADH-ubiquinone oxidoreductase chain 5	0.00	3.36E-02
c112302_g1_i1	<i>AFA30142.1</i>	NADH dehydrogenase subunit 5	0.00	4.33E-02
c112562_g1_i1	<i>RS15A</i>	40S ribosomal protein S15a	0.00	3.87E-02
c112686_g1_i1	<i>EF1A2</i>	Elongation factor 1-alpha 2	0.00	4.61E-02
c113028_g1_i1	<i>COX2</i>	Cytochrome c oxidase subunit 2	0.00	2.46E-02
c113237_g1_i1	<i>RL12</i>	60S ribosomal protein L12	0.00	2.86E-02
c113282_g1_i1	<i>ACT</i>	Actin (Fragment)	0.00	3.63E-02
c113921_g1_i1	<i>YBOX1</i>	Nuclease-sensitive element-binding protein 1	0.00	4.34E-02
c114678_g1_i1	<i>RS12</i>	40S ribosomal protein S12	0.00	3.74E-02
c115380_g1_i1	<i>TCTP</i>	Translationally-controlled tumor protein	0.00	3.19E-02
c115414_g1_i1	<i>RL18</i>	60S ribosomal protein L18	0.00	4.41E-02
c117441_g1_i1	<i>RL30</i>	60S ribosomal protein L30	0.00	4.56E-02
c121636_g1_i1	<i>NPM</i>	Nucleophosmin	0.00	3.98E-02
c132573_g1_i1	<i>XP4043035.1</i>	uncharacterized protein LOC101141636, partial	0.00	8.86E-03
c132604_g1_i1	<i>ENN79216.1</i>	hypothetical protein YQE_04400, partial	0.00	1.91E-02
c132624_g1_i1	<i>RS2</i>	40S ribosomal protein S2	0.00	3.63E-02
c132634_g1_i1	<i>COX3</i>	Cytochrome c oxidase subunit 3	0.00	2.30E-02
c132698_g1_i1	<i>ABJ89544.1</i>	cytochrome c oxidase subunit III	0.00	1.80E-02
c133702_g1_i1	<i>ATPB</i>	ATP synthase subunit beta, mitochondrial	0.00	4.51E-02
c133726_g1_i1	<i>RL26</i>	60S ribosomal protein L26	0.00	4.44E-02
c133933_g1_i1	<i>RL35A</i>	60S ribosomal protein L35a	0.00	4.29E-02
c134133_g1_i1	<i>RL7A</i>	60S ribosomal protein L7a	0.00	4.31E-02
c134303_g1_i1	<i>RL29</i>	60S ribosomal protein L29	0.00	3.81E-02
c134358_g1_i1	<i>RS9</i>	40S ribosomal protein S9	0.00	3.62E-02
c135118_g1_i1	<i>RL19</i>	60S ribosomal protein L19	0.00	3.50E-02

c154290_g1_i1	<i>RL4</i>	60S ribosomal protein L4	0.00	2.59E-02
c154332_g1_i1	<i>RS11</i>	40S ribosomal protein S11	0.00	3.41E-02
c154438_g1_i1	<i>NP_001006.1</i>	40S ribosomal protein S11	0.00	7.61E-03
c154564_g1_i1	<i>ENOA</i>	Alpha-enolase	0.00	2.90E-02
c154635_g1_i1	<i>NU1M</i>	NADH-ubiquinone oxidoreductase chain 1	0.00	4.14E-02
c154798_g1_i1	<i>ABO39864.1</i>	NADH dehydrogenase subunit 1	0.00	1.37E-02
c155410_g1_i1	<i>HS90B</i>	Heat shock protein HSP 90-beta	0.00	3.00E-02
c155448_g1_i1	<i>ENPL</i>	Endoplasmin	0.00	4.93E-02
c155854_g1_i1	<i>BAD92771.1</i>	tumor rejection antigen (gp96) 1 variant	0.00	5.09E-03
c155905_g1_i1	<i>IMDH2</i>	Inosine-5'-monophosphate dehydrogenase 2	0.00	3.92E-02
c156264_g1_i1	<i>RL24</i>	60S ribosomal protein L24	0.00	4.55E-02
c158754_g1_i1	<i>XP4479299.1</i>	60S ribosomal protein L24	0.15	2.52E-02
c175672_g1_i1	<i>RS6</i>	40S ribosomal protein S6	0.00	2.53E-02
c175883_g1_i1	<i>IEX1</i>	Radiation-inducible immediate-early gene IEX-1	0.00	4.86E-02
c176015_g1_i1	<i>CAA65304.1</i>	radiation-inducible immediate early response gene IEX1	0.01	2.47E-02
c176384_g1_i1	<i>RL15</i>	60S ribosomal protein L15	0.00	3.56E-02
c176496_g1_i1	<i>RS10</i>	40S ribosomal protein S10	0.00	3.95E-02
c176866_g1_i1	<i>XP3770768.1</i>	40S ribosomal protein S10-like, partial	0.00	2.54E-02
c177317_g1_i1	<i>RSSA</i>	40S ribosomal protein SA	0.00	2.12E-02
c177617_g1_i1	<i>RL27</i>	60S ribosomal protein L27	0.00	4.62E-02
c178017_g1_i1	<i>GBLP</i>	Guanine nucleotide-binding protein subunit beta-2-like 1	0.00	3.08E-02
c178031_g1_i1	<i>K1C18</i>	Keratin, type I cytoskeletal 18	0.00	4.39E-02
c178714_g1_i1	<i>RS3</i>	40S ribosomal protein S3	0.00	2.68E-02
c179878_g1_i1	<i>RL35</i>	60S ribosomal protein L35	0.00	4.23E-02
c180255_g1_i1	<i>RL7</i>	60S ribosomal protein L7	0.00	4.08E-02
c180936_g1_i1	<i>RS20</i>	40S ribosomal protein S20	0.00	4.39E-02
c181784_g1_i1	<i>RL37</i>	60S ribosomal protein L37	0.00	4.13E-02
c196905_g1_i1	<i>CUT1</i>	Cuticlin-1	0.01	8.68E-16
c196918_g1_i1	<i>XP969031.2</i>	similar to dusky CG9355-PA	0.00	2.61E-02
c197549_g1_i1	<i>EF1A1</i>	Elongation factor 1-alpha 1	0.00	2.23E-02

c197669_g1_i1	<i>S10A6</i>	Protein S100-A6	0.00	3.37E-02
c197870_g1_i1	<i>GRP78</i>	78 kDa glucose-regulated protein	0.00	2.10E-02
c197951_g1_i1	<i>PPIA</i>	Peptidyl-prolyl cis-trans isomerase A	0.00	3.02E-02
c198512_g1_i1	<i>RS19</i>	40S ribosomal protein S19	0.00	4.50E-02
c199675_g1_i1	<i>RL23A</i>	60S ribosomal protein L23a	0.00	4.34E-02
c200324_g1_i1	<i>RS8</i>	40S ribosomal protein S8	0.00	3.17E-02
c200605_g1_i1	<i>RL37P</i>	Putative 60S ribosomal protein L37a	0.00	4.00E-02
c203632_g1_i1	<i>RL31</i>	60S ribosomal protein L31	0.00	4.96E-02

^{a#}DIV/0 in Fold change meant a gene undetected or unexpressed in NOR, but highly expressed in HHA.

(B)DEGs in HA vs.NOR.

ID	Name	Putative function	HA vs NOR	
			Fold change	pvalue
c2900_g1_i1	<i>ENN71770.1</i>	hypothetical protein YQE_11505, partial	2.27	3.10E-02
c10174_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	13.35	4.82E-02
c55723_g1_i2	<i>CHIT3</i>	Probable chitinase 3	2.94	3.75E-02
c58497_g1_i1	<i>TM205</i>	Transmembrane protein 205	4.82	5.01E-04
c67642_g1_i1	<i>SERA</i>	D-3-phosphoglycerate dehydrogenase	2.31	4.37E-02
c67922_g1_i1	<i>CUD2</i>	Endocuticle structural glycoprotein SgAbd-2	17.52	1.75E-03
c68182_g1_i1	<i>CP314</i>	Ecdysone 20-monooxygenase	5.14	1.56E-02
c69225_g1_i1	<i>ARH40</i>	Rho guanine nucleotide exchange factor 40	4.47	2.43E-02
c69795_g1_i1	<i>CP307</i>	Cytochrome P450 307a1	8.83	2.91E-02
c71312_g1_i1	<i>CP315</i>	Cytochrome P450 315a1, mitochondrial	5.07	1.18E-03
c71877_g1_i2	<i>EFA04107.1</i>	hypothetical protein TcasGA2	3.83	3.17E-02
c75875_g1_i1	<i>B1</i>	B1 protein (Fragment)	3.03	8.51E-03
c76501_g1_i1	<i>NP1127918.1</i>	uncharacterized protein LOC100187736	6.65	2.05E-05
c76865_g1_i1	<i>ENN79333.1</i>	hypothetical protein YQE	2.95	2.74E-02
c79695_g1_i1	<i>LARP6</i>	La-related protein 6	3.12	3.76E-03
c79773_g1_i1	<i>EFA06160.1</i>	hypothetical protein TcasGA2	4.38	4.82E-02
c80171_g1_i1	<i>AEX93420.1</i>	juvenile hormone binding protein 5p2, partial	28.03	4.76E-03
c81525_g1_i2	<i>ENN80187.1</i>	hypothetical protein YQE	25.68	2.55E-02

c81819_g1_i2	<i>EFA05035.1</i>	hypothetical protein TcasGA2	74.81	2.69E-02
c82605_g1_i2	<i>ENN79626.1</i>	hypothetical protein YQE	2.50	1.63E-02
c82775_g1_i1	<i>CATL</i>	Cathepsin L	4.48	7.39E-03
c82873_g1_i1	<i>LSD1</i>	Lipid storage droplets surface-binding protein 1	3.29	2.34E-03
c82907_g1_i1	<i>UBIQP</i>	Polyubiquitin (Fragment)	2.74	4.47E-02
c83153_g1_i1	<i>COX6C</i>	Cytochrome c oxidase subunit 6C	17.63	4.99E-02
c83372_g2_i1	<i>BAT1</i>	B(0,+)-type amino acid transporter 1	3.38	3.53E-02
c83414_g1_i1	<i>MTND</i>	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	4.88	7.29E-03
c83592_g1_i1	<i>UCK</i>	Probable uridine-cytidine kinase	2.37	4.02E-02
c84162_g1_i1	<i>TRE12</i>	Facilitated trehalose transporter Tret1-2	20.48	4.96E-07
c84197_g1_i1	<i>CP4C1</i>	Cytochrome P450 4C1	5.48	1.52E-02
c84350_g1_i1	<i>GLB</i>	Globin	3.05	4.68E-02
c84587_g1_i1	<i>XP968587.1</i>	similar to 10G08	2.22	4.67E-02
c84667_g1_i1	<i>CYB</i>	Cytochrome b	2.78	9.78E-03
c85250_g1_i6	<i>GD</i>	Serine protease	4.71	4.03E-02
c85373_g1_i1	<i>APMAP</i>	Adipocyte plasma membrane-associated protein	3.02	3.28E-02
c85422_g1_i1	<i>ACE</i>	Angiotensin-converting enzyme	6.07	4.87E-02
c85423_g1_i1	<i>TRET1</i>	Facilitated trehalose transporter Tret1	3.84	2.34E-03
c85790_g1_i2	<i>ISLR2</i>	Immunoglobulin superfamily containing leucine-rich repeat protein 2	7.98	3.69E-02
c85820_g1_i1	<i>XP_967178.1</i>	XP967178.1	3.06	1.26E-02
c85935_g3_i1	<i>MLP2</i>	Muscle LIM protein Mlp84B	2.46	3.05E-02
c86023_g1_i1	<i>TRET1</i>	Facilitated trehalose transporter Tret1	2.44	2.97E-02
c86079_g1_i1	<i>FAS</i>	Fatty acid synthase	2.99	7.61E-03
c86416_g1_i1	<i>CU30</i>	Larval cuticle protein LCP-30	2.33	2.46E-02
c86650_g1_i1	<i>COX1</i>	Cytochrome c oxidase subunit 1	2.39	2.05E-02
c87130_g1_i1	<i>FGFR1</i>	Fibroblast growth factor receptor 1	10.09	2.61E-02
c87377_g4_i1	<i>XP971678.1</i>	similar to Cuticular protein 62Bc CG1919-PA	8.51	9.32E-03
c87418_g1_i1	<i>LRC20</i>	Leucine-rich repeat-containing protein 20	2.71	1.08E-02
c87460_g5_i1	<i>LDH</i>	L-lactate dehydrogenase	20.30	4.10E-02
c87559_g1_i3	<i>U483</i>	UPF0483 protein AGAP003155	2.57	4.65E-02

c87591_g2_i1	<i>HARB1</i>	Putative nuclease HARB1	4.49	3.44E-02
c87749_g1_i1	<i>EDL11</i>	Sugar transporter ERD6-like 11	221.16	3.31E-02
c87825_g2_i1	<i>LUCI</i>	Luciferin 4-monooxygenase	2.33	3.46E-02
c87890_g1_i1	<i>CP6J1</i>	Cytochrome P450 6j1	4.09	2.37E-02
c88018_g1_i3	<i>TRET1</i>	Facilitated trehalose transporter Tret1	5.92	3.66E-02
c88083_g3_i1	<i>CAM36311.1</i>	hypothetical protein	2.56	1.91E-02
c88165_g1_i1	<i>FACR1</i>	Putative fatty acyl-CoA reductase CG5065	3.76	3.89E-02
c88407_g3_i1	<i>LUCI</i>	Luciferin 4-monooxygenase	3.37	7.45E-03
c88522_g1_i2	<i>EFN65995.1</i>	hypothetical protein EAG	37.98	1.83E-02
c88775_g3_i1	<i>DIHR</i>	Diuretic hormone receptor	3.81	4.61E-02
c88844_g1_i1	<i>LIPP</i>	Pancreatic triacylglycerol lipase	6.95	4.56E-02
c88850_g1_i1	<i>CUE</i>	Protein cueball	3.58	3.91E-02
c88988_g1_i1	<i>RECA</i>	Protein RecA	7726.97	2.25E-02
c89511_g1_i1	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	6.54	5.48E-04
c89528_g1_i1	<i>SPT20</i>	Spermatogenesis-associated protein 20	2.42	4.07E-02
c89954_g1_i1	<i>EFA09055.1</i>	hypothetical protein TcasGA2	3.07	8.32E-03
c89969_g1_i1	<i>OVO</i>	Protein ovo	4.16	3.87E-02
c90215_g1_i1	<i>CRGM2</i>	CRGM2_CYPCA	18.39	3.22E-02
c90270_g4_i1	<i>HIF1N</i>	Hypoxia-inducible factor 1-alpha inhibitor	9.68	2.75E-03
c90322_g3_i1	<i>ADZ95996.1</i>	reverse transcriptase, partial	55.56	1.72E-02
c91317_g1_i4	<i>EFA06632.1</i>	hypothetical protein TcasGA2	7.27	3.67E-05
c91530_g1_i1	<i>CHIT3</i>	Probable chitinase 3	3.36	2.46E-02
c91530_g2_i1	<i>CHIT3</i>	Probable chitinase 3	3.52	5.67E-03
c133618_g1_i1	<i>PGRP2</i>	Peptidoglycan-recognition protein 2	5.35	4.64E-02
c154518_g1_i1	<i>SEPT5</i>	Septin-5	10.35	7.22E-03
c178137_g1_i1	<i>XP1916399.1</i>	hypothetical protein LOC100147469	143.05	2.96E-02
c510_g1_i1	<i>RL13</i>	60S ribosomal protein L13	0.00	3.17E-02
c555_g1_i2	<i>ROA2</i>	Heterogeneous nuclear ribonucleoproteins A2/B1	0.00	4.99E-02
c852_g1_i1	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	0.00	1.96E-02
c901_g1_i1	<i>RL17</i>	60S ribosomal protein L17	0.00	4.93E-02

c2627_g1_i1	<i>RL10A</i>	60S ribosomal protein L10a	0.00	4.18E-02
c5887_g1_i1	<i>RS7</i>	40S ribosomal protein S7	0.00	4.52E-02
c7566_g1_i1	<i>K2C8</i>	Keratin, type II cytoskeletal 8	0.00	3.16E-02
c8048_g1_i1	<i>RS16</i>	40S ribosomal protein S16	0.00	4.95E-02
c10038_g1_i1	<i>EF1B</i>	Elongation factor 1-beta	0.00	4.55E-02
c10091_g1_i1	<i>ERRFI</i>	ERBB receptor feedback inhibitor 1	0.00	4.44E-02
c10151_g1_i1	<i>YS049</i>	Zinc finger protein ENSP00000375192	0.00	4.57E-02
c10286_g1_i2	<i>XP_972042.1</i>	similar to Osiris, putative	0.00	2.26E-02
c10389_g1_i1	<i>RL9</i>	ribosomal protein L9	0.00	4.12E-02
c12875_g1_i1	<i>EF1G</i>	Elongation factor 1-gamma	0.00	3.59E-02
c13517_g1_i1	<i>RL36</i>	60S ribosomal protein L36	0.00	4.70E-02
c15385_g1_i1	<i>COX1</i>	Cytochrome c oxidase subunit 1	0.00	3.11E-02
c15812_g1_i1	<i>CDC20</i>	Cell division cycle protein 20	0.10	3.01E-07
c16432_g1_i1	<i>RS14</i>	40S ribosomal protein S14	0.00	3.85E-02
c17533_g1_i1	<i>gb/ABW74141.1</i>	cuticular protein Ld-CP1v2	0.06	3.21E-02
c18144_g1_i1	<i>KPYM</i>	Pyruvate kinase PKM	0.00	3.03E-02
c22513_g1_i1	<i>HUNIN</i>	Putative humanin peptide	0.00	1.71E-02
c24111_g1_i1	<i>XP_004450492.1</i>	translation initiation factor IF-2-like	0.00	4.47E-02
c24280_g1_i1	<i>RLA1</i>	60S acidic ribosomal protein P1	0.00	3.37E-02
c24290_g1_i2	<i>XP_004520776.1</i>	uncharacterized protein LOC101449037	0.00	3.01E-02
c25902_g1_i1	<i>RL27A</i>	60S ribosomal protein L27a	0.00	3.57E-02
c26234_g1_i1	<i>TYB10</i>	Thymosin beta-10	0.00	3.51E-02
c26429_g1_i1	<i>RL3</i>	60S ribosomal protein L3	0.00	2.06E-02
c32642_g1_i1	<i>ENN81692.1</i>	hypothetical protein YQE_01898, partial	0.02	6.61E-03
c32676_g1_i1	<i>4F2</i>	4F2 cell-surface antigen heavy chain	0.00	4.58E-02
c33481_g1_i1	<i>CALR</i>	Calreticulin	0.00	2.98E-02
c33573_g1_i2	<i>AKA12</i>	A-kinase anchor protein 12	0.00	2.49E-02
c34613_g1_i1	<i>ROA1</i>	Heterogeneous nuclear ribonucleoprotein A1	0.00	3.23E-02
c34884_g1_i1	<i>RLA0</i>	60S acidic ribosomal protein P0	0.00	3.62E-02
c41764_g1_i1	<i>PABP1</i>	Polyadenylate-binding protein 1	0.00	4.08E-02

c44142_g1_i1	<i>CU20</i>	Adult-specific cuticular protein ACP-20	0.00	4.30E-02
c46706_g1_i1	<i>c46706_g1_i1</i>	unknown	0.00	3.41E-02
c48948_g1_i1	<i>ALDOA</i>	Fructose-bisphosphate aldolase A	0.00	4.50E-02
c50261_g1_i1	<i>RS19A</i>	40S ribosomal protein S19a	0.35	2.04E-02
c50949_g1_i1	<i>RL8</i>	60S ribosomal protein L8	0.00	2.92E-02
c51924_g1_i2	<i>CB5D1</i>	Cytochrome b5 domain-containing protein 1	0.00	2.49E-02
c52074_g1_i1	<i>EFA02501.1</i>	hypothetical protein TcasGA2_TC008197	0.00	3.22E-02
c54009_g1_i1	<i>PSB1</i>	Proteasome subunit beta type-1	0.36	3.85E-02
c54231_g1_i1	<i>GFII</i>	Zinc finger protein sens	0.18	8.45E-03
c54262_g1_i1	<i>XRCC6</i>	X-ray repair cross-complementing protein 6	0.00	4.76E-02
c55004_g1_i1	<i>ST1B1</i>	Sulfotransferase family cytosolic 1B member 1	0.00	4.72E-02
c55505_g1_i1	<i>PDIA1</i>	Protein disulfide-isomerase	0.00	3.21E-02
c55570_g1_i1	<i>RL37</i>	60S ribosomal protein L37	0.09	1.67E-03
c57175_g1_i2	<i>CALX</i>	Calnexin	0.00	4.79E-02
c58720_g1_i1	<i>RL9</i>	60S ribosomal protein L9	0.31	9.63E-03
c59759_g1_i2	<i>CHD4</i>	Chromodomain-helicase-DNA-binding protein 4	0.00	7.62E-03
c60921_g1_i1	<i>SAP</i>	Proactivator polypeptide	0.00	4.62E-02
c64025_g1_i1	<i>EF2</i>	Elongation factor 2	0.00	4.80E-02
c65861_g1_i1	<i>ENN70941.1</i>	hypothetical protein YQE_12343, partial	0.16	2.12E-02
c66811_g1_i3	<i>EAX03762.1</i>	high mobility group AT-hook 1, isoform CRA_a	0.00	4.11E-02
c68311_g1_i1	<i>ENN82170.1</i>	hypothetical protein YQE_01454, partial	0.00	4.91E-02
c68544_g1_i1	<i>XP_001810980.1</i>	similar to CG12164 CG12164-PA	0.00	4.77E-02
c71708_g1_i2	<i>SYAC</i>	Alanine--tRNA ligase, cytoplasmic	0.00	4.61E-02
c72030_g1_i1	<i>NPC2</i>	Protein NPC2 homolog	0.12	5.11E-06
c72511_g1_i1	<i>EZRI</i>	Ezrin	0.00	3.62E-02
c72677_g1_i1	<i>HNRPC</i>	Heterogeneous nuclear ribonucleoprotein C	0.00	4.36E-02
c72914_g1_i1	<i>CU08</i>	uticle protein 8	0.11	9.23E-03
c73222_g2_i3	<i>STUB</i>	Serine proteinase stubble	0.00	4.91E-02
c73608_g1_i1	<i>HYOU1</i>	Hypoxia up-regulated protein 1	0.00	3.97E-02
c73752_g1_i1	<i>XP_001809747.1</i>	similar to AGAP009011-PA	0.39	3.72E-02

c74915_g1_i1	<i>LIPR2</i>	Pancreatic lipase-related protein 2	0.08	1.02E-03
c75007_g1_i1	<i>CU19</i>	Cuticle protein 19	0.00	4.71E-02
c75642_g1_i4	<i>CUC1B</i>	Pupal cuticle protein C1B	0.03	8.20E-06
c77271_g1_i3	<i>ADH2</i>	Alcohol dehydrogenase 2	0.20	1.13E-03
c78273_g1_i1	<i>SODC</i>	Superoxide dismutase [Cu-Zn]	0.18	1.09E-02
c78450_g1_i1	<i>EFA04340.1</i>	hypothetical protein TcasGA2_TC014634	0.23	2.71E-02
c79334_g1_i1	<i>RS13</i>	40S ribosomal protein S13	0.30	3.61E-02
c79869_g1_i5	<i>VIGLN</i>	Vigilin	0.00	4.70E-02
c80534_g1_i3	<i>YLAT2</i>	Y+L amino acid transporter 2	0.36	4.52E-02
c80861_g1_i1	<i>HCE1</i>	High choriolytic enzyme 1	0.03	2.51E-02
c80896_g1_i1	<i>CUD2</i>	Endocuticle structural glycoprotein	0.22	2.93E-03
c80989_g1_i3	<i>LSD1</i>	Lipid storage droplets surface-binding protein 1	0.31	1.93E-03
c81104_g1_i1	<i>CUO6</i>	Cuticle protein 6 OS=Blaberus craniifer	0.07	4.82E-02
c82022_g1_i1	<i>XP_975669.</i>	similar to cuticular protein 1, RR-2 family (AGAP001664-PA)	0.04	1.45E-02
c82085_g1_i2	<i>CUC1B</i>	Pupal cuticle protein C1B	0.02	1.84E-06
c82090_g1_i1	<i>ANO6</i>	Anoctamin-6 OS=Homo sapiens	0.07	1.41E-02
c82777_g1_i1	<i>FGGY</i>	carbohydrate kinase domain-containing protein	0.32	7.48E-03
c83023_g1_i1	<i>SCA</i>	Protein scabrous	0.22	5.37E-04
c83657_g1_i4	<i>FAA00648.</i>	putative cuticle protein	0.08	2.40E-06
c84117_g1_i1	<i>CFDP2</i>	Craniofacial development protein 2	0.38	2.16E-02
c84257_g1_i1	<i>ENN70641.1</i>	hypothetical protein YQE_12586, partial	0.18	2.75E-03
c84349_g1_i1	<i>SNMP2</i>	Sensory neuron membrane protein 2	0.31	3.24E-02
c84472_g1_i2	<i>CU07</i>	Cuticle protein 7	0.02	2.32E-03
c84634_g1_i2	<i>ENN70572.1</i>	hypothetical protein YQE_12747, partial	0.00	4.23E-02
c84653_g1_i1	<i>PIPE</i>	Heparan sulfate 2-O-sulfotransferase pipe	0.08	3.36E-02
c85636_g1_i2	<i>CU03</i>	Cuticle protein 3	0.06	1.20E-08
c85675_g1_i1	<i>RGN</i>	Regucalcin	0.38	1.18E-02
c85776_g3_i1	<i>ENN75917.1</i>	hypothetical protein YQE_07558, partial	0.41	2.29E-02
c86759_g2_i1	<i>DYXC1</i>	Dyslexia susceptibility 1 candidate gene 1 protein homolog	0.22	3.05E-02
c86802_g1_i1	<i>MYOM</i>	Myosin-M heavy chain	0.27	3.28E-02

c87159_g1_i1	<i>BAD99297.1</i>	ecdysone receptor B1 isoform	0.23	9.70E-03
c87651_g2_i2	<i>CUA2B</i>	Larval cuticle protein A2B	0.01	6.96E-03
c87651_g3_i1	<i>CUA2B</i>	Larval cuticle protein A2B	0.08	1.13E-06
c87726_g1_i1	<i>CH60</i>	60 kDa heat shock protein, mitochondrial	0.41	2.84E-02
c87995_g2_i1	<i>CYB5R</i>	Cytochrome b5-related protein	0.09	4.63E-02
c88210_g1_i1	<i>DPYD</i>	Dihydropyrimidine dehydrogenase [NADP(+)]	0.39	4.37E-02
c88443_g1_i1	<i>ENN83446.1</i>	hypothetical protein YQE_00194, partial	0.18	1.76E-02
c88546_g2_i1	<i>UPP2</i>	Uridine phosphorylase 2	0.13	7.80E-04
c88588_g1_i1	<i>ELVLI</i>	Elongation of very long chain fatty acids protein AAEL008004	0.35	3.24E-02
c88653_g1_i2	<i>ENN79208.1</i>	hypothetical protein YQE_04392, partial	0.00	3.24E-04
c89047_g1_i4	<i>STUB</i>	Serine proteinase stubble	0.19	1.05E-03
c89108_g1_i1	<i>PICAL</i>	Phosphatidylinositol-binding clathrin assembly protein LAP	0.23	2.62E-02
c89523_g6_i2	<i>DPS1</i>	Decaprenyl-diphosphate synthase subunit 1	0.29	4.47E-03
c89639_g2_i1	<i>CAD96</i>	Tyrosine kinase receptor Cad96Ca	0.30	4.14E-02
c90034_g1_i4	<i>GUS</i>	Protein gustavus	0.30	1.43E-02
c90252_g1_i1	<i>AMFR</i>	E3 ubiquitin-protein ligase AMFR	0.24	1.30E-02
c90353_g1_i1	<i>ABR</i>	Active breakpoint cluster region-related protein	0.29	2.99E-02
c90401_g2_i1	<i>EFA13323.1</i>	hypothetical protein TcasGA2_TC006846	0.21	3.27E-02
c90401_g1_i2	<i>NP_001103739.1</i>	chitin deacetylase 5 isoform A precursor	0.27	1.56E-02
c90716_g1_i3	<i>ZSWM8</i>	Zinc finger SWIM domain-containing protein 8	0.36	2.87E-02
c91138_g1_i1	<i>ECR</i>	Ecdysone receptor	0.43	4.05E-02
c91176_g1_i3	<i>ZN197</i>	Zinc finger protein 197	0.20	2.53E-02
c91234_g1_i1	<i>CSTN1</i>	Calsyntenin-1	0.19	5.41E-04
c91269_g2_i1	<i>HMCN1</i>	Hemicentin-1	0.27	6.92E-03
c91467_g1_i1	<i>CHS8</i>	Chitin synthase 8	0.25	5.14E-03
c91550_g1_i1	<i>MBD6</i>	Methyl-CpG-binding domain protein 6	0.35	1.81E-02
c91570_g2_i2	<i>XP_967813.1</i>	similar to brain chitinase and chia	0.30	4.74E-02
c91850_g1_i1	<i>EF1A1</i>	Elongation factor 1-alpha 1	0.00	3.01E-02
c91870_g1_i1	<i>AEE63393.1</i>	hypothetical protein YQE_04422, partial [D	0.00	2.73E-02
c92107_g1_i1	<i>FRIH</i>	Ferritin heavy chain	0.00	2.88E-02

c97179_g1_i1	<i>AAH89817.1</i>	hypothetical protein YQE_04412, partial	0.00	3.47E-02
c97350_g1_i1	<i>RS27</i>	40S ribosomal protein S27	0.00	4.24E-02
c98088_g1_i1	<i>RL32</i>	60S ribosomal protein L32	0.00	4.24E-02
c100361_g1_i1	<i>RS25</i>	40S ribosomal protein S25	0.00	4.55E-02
c112250_g1_i1	<i>NU5M</i>	NADH-ubiquinone oxidoreductase chain 5	0.00	3.50E-02
c112562_g1_i1	<i>RS15A</i>	40S ribosomal protein S15a	0.00	4.00E-02
c113014_g1_i1	<i>TPIS</i>	Triosephosphate isomerase	0.00	4.60E-02
c113028_g1_i1	<i>COX2</i>	Cytochrome c oxidase subunit 2	0.00	2.58E-02
c113282_g1_i1	<i>ACT</i>	Actin (Fragment)	0.00	3.76E-02
c113921_g1_i1	<i>YBOX1</i>	Nuclease-sensitive element-binding protein 1	0.00	4.46E-02
c114678_g1_i1	<i>RS12</i>	40S ribosomal protein S12	0.00	3.86E-02
c115380_g1_i1	<i>TCTP</i>	Translationally-controlled tumor protein	0.00	3.33E-02
c115414_g1_i1	<i>RL18</i>	60S ribosomal protein L18	0.00	4.53E-02
c116965_g1_i1	<i>RS17</i>	40S ribosomal protein S17	0.00	3.50E-02
c117441_g1_i1	<i>RL30</i>	60S ribosomal protein L30	0.00	4.68E-02
c121636_g1_i1	<i>NPM</i>	Nucleophosmin	0.00	4.11E-02
c132573_g1_i1	<i>ENN79216.1</i>	hypothetical protein YQE_04400, partial	0.00	4.02E-02
c132624_g1_i1	<i>RS2</i>	40S ribosomal protein S2	0.00	2.06E-02
c132634_g1_i1	<i>COX3</i>	Cytochrome c oxidase subunit 3	0.00	1.64E-02
c132897_g1_i1	<i>XP_001809624.1</i>	similar to AGAP001118-PA	0.00	4.66E-02
c132920_g1_i1	<i>RL10</i>	60S ribosomal protein L10	0.00	2.93E-02
c133702_g1_i1	<i>ATPB</i>	ATP synthase subunit beta, mitochondrial	0.00	4.62E-02
c133726_g1_i1	<i>RL26</i>	60S ribosomal protein L26	0.00	4.57E-02
c133933_g1_i1	<i>RL35A</i>	60S ribosomal protein L35a	0.00	4.42E-02
c134133_g1_i1	<i>RL7A</i>	60S ribosomal protein L7a	0.00	3.01E-02
c134303_g1_i1	<i>RL29</i>	60S ribosomal protein L29	0.00	3.94E-02
c134358_g1_i1	<i>RS9</i>	40S ribosomal protein S9	0.00	3.74E-02
c135118_g1_i1	<i>RL19</i>	60S ribosomal protein L19	0.00	3.63E-02
c154290_g1_i1	<i>RL4</i>	60S ribosomal protein L4	0.00	2.71E-02
c154564_g1_i1	<i>ENOA</i>	Alpha-enolase	0.00	3.02E-02

c154635_g1_i1	<i>NUIM</i>	NADH-ubiquinone oxidoreductase chain 1	0.00	4.27E-02
c155410_g1_i1	<i>HS90B</i>	Heat shock protein HSP 90-beta	0.00	3.13E-02
c155905_g1_i1	<i>IMDH2</i>	Inosine-5'-monophosphate dehydrogenase 2	0.00	4.05E-02
c156264_g1_i1	<i>RL24</i>	ribosomal protein L24	0.00	4.67E-02
c175672_g1_i1	<i>RS6</i>	40S ribosomal protein S6	0.00	2.66E-02
c175883_g1_i1	<i>IEX1</i>	Radiation-inducible immediate-early gene IEX-1	0.00	4.98E-02
c176384_g1_i1	<i>RL15</i>	60S ribosomal protein L15	0.00	3.69E-02
c177317_g1_i1	<i>RSSA</i>	40S ribosomal protein SA	0.00	4.74E-02
c177617_g1_i1	<i>RL27</i>	60S ribosomal protein L27	0.00	4.74E-02
c178031_g1_i1	<i>K1C18</i>	Keratin, type I cytoskeletal 18	0.00	4.51E-02
c178714_g1_i1	<i>RS3</i>	40S ribosomal protein S3	0.00	2.81E-02
c179028_g1_i1	<i>XP_003756572.1</i>	uncharacterized protein LOC100925129	0.00	2.43E-02
c179589_g1_i1	<i>RL23</i>	60S ribosomal protein L23	0.00	4.68E-02
c180255_g1_i1	<i>RL7</i>	60S ribosomal protein L7	0.00	4.21E-02
c180936_g1_i1	<i>RS20</i>	40S ribosomal protein S20	0.00	4.51E-02
c181784_g1_i1	<i>RL37</i>	60S ribosomal protein L37	0.00	4.26E-02
c196905_g1_i1	<i>CUT1</i>	Cuticlin-1	0.09	1.27E-06
c196918_g1_i1	<i>XP_003941011.1</i>	prothymosin alpha-like	0.00	2.74E-02
c197549_g1_i1	<i>EF1A1</i>	Elongation factor 1-alpha 1	0.00	1.59E-02
c197669_g1_i1	<i>S10A6</i>	Protein S100-A6	0.00	3.50E-02
c197870_g1_i1	<i>GRP78</i>	78 kDa glucose-regulated protein	0.00	4.07E-02
c197951_g1_i1	<i>PPIA</i>	Peptidyl-prolyl cis-trans isomerase A	0.00	3.14E-02
c198512_g1_i1	<i>RS19</i>	40S ribosomal protein S19	0.00	4.62E-02
c199675_g1_i1	<i>RL23A</i>	60S ribosomal protein L23a	0.00	4.46E-02
c200605_g1_i1	<i>RL37P</i>	Putative 60S ribosomal protein L37a	0.00	4.12E-02

(C)DEGs in HA vs.HHA.

ID	Name	Putative function	HHA vs. HA	
			^a Fold change	pvalue
c637_g1_i1	<i>CALMB</i>	Calmodulin-B	96.27	8.83E-08

c1239_g1_i1	<i>WDR78</i>	repeat-containing protein 78	50.70	3.65E-09
c2440_g1_i1	<i>CDD</i>	Cytidine deaminase	4.33	2.24E-03
c2528_g1_i1	<i>ZMY10</i>	Zinc finger MYND domain-containing protein 10	11.24	9.30E-03
c3142_g1_i1	<i>NDUS2</i>	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	#DIV/0!	1.08E-02
c3337_g2_i1	<i>EFA05480.1</i>	hypothetical protein TcasGA2TC015664	#DIV/0!	2.78E-02
c3479_g1_i1	<i>THIO</i>	Thioredoxin	#DIV/0!	1.97E-02
c5822_g1_i1	<i>AFE88625.1</i>	similar to Jupiter CG31363-PB	26.87	6.86E-09
c7716_g1_i1	<i>DYH3</i>	Dynein heavy chain 3, axonemal	28.78	6.27E-03
c8207_g1_i1	<i>EFA04409.1</i>	Phosphoglycerate mutase 1	69.09	1.34E-16
c9407_g1_i1	<i>PGAM1</i>	Phosphoglycerate mutase 1	10.60	7.16E-08
c9650_g1_i1	<i>SUCA</i>	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	22.23	9.81E-07
c10028_g1_i1	<i>CCCP</i>	Circadian clock-controlled protein	12.35	6.90E-06
c10291_g1_i1	<i>TBB1</i>	Tubulin beta-1 chain	48.98	1.19E-08
c10490_g1_i1	<i>EFA06876.1</i>	hypothetical protein TcasGA2	#DIV/0!	9.09E-03
c11071_g1_i1	<i>MARH3</i>	ubiquitin-protein ligase	69.25	2.44E-12
c11177_g1_i1	<i>EFA03059.1</i>	hypothetical protein TcasGA2_TC010915	102.90	1.24E-07
c13824_g1_i1	<i>CX6B1</i>	Cytochrome c oxidase subunit 6B1	2.28	3.90E-02
c14627_g1_i1	<i>ENN71108.1</i>	hypothetical protein YQE_12041, partial	25.91	1.82E-13
c15812_g1_i1	<i>CDC20</i>	Cell division cycle protein 20 homolog	3.40	5.42E-04
c16555_g1_i1	<i>MAAT1</i>	Protein MAATS1	47.26	1.58E-05
c17024_g1_i1	<i>EFA05939.1</i>	hypothetical protein TcasGA2_TC008755	4.02	1.78E-02
c17314_g1_i1	<i>ENN81322.1</i>	hypothetical protein YQE_02289, partial	39.98	2.11E-17
c17427_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	7.08	5.96E-03
c17473_g1_i2	<i>NEDD1</i>	Protein NEDD1	56.13	1.01E-18
c17995_g1_i1	<i>CD63</i>	CD63 antigen	#DIV/0!	2.06E-06
c18249_g1_i1	<i>ABCBB</i>	Bile salt export pump	#DIV/0!	2.66E-02
c18323_g1_i1	<i>S15A1</i>	Solute carrier family 15 member 1	#DIV/0!	1.10E-02
c18685_g1_i1	<i>TTPA</i>	Alpha-tocopherol transfer protein	3.22	6.40E-03
c21840_g1_i1	<i>CP080</i>	UPF0468 protein C16orf80 homolog	29.21	2.50E-11
c23617_g1_i1	<i>CX6B1</i>	Cytochrome c oxidase subunit 6b-1	#DIV/0!	4.46E-02

c23890_g1_i1	<i>FAKD5</i>	FAST kinase domain-containing protein 5	7.51	1.20E-07
c24002_g1_i1	<i>MYRO1</i>	Myrosinase 1	153.91	1.84E-07
c24016_g1_i1	<i>SV2B</i>	Synaptic vesicle glycoprotein 2B	#DIV/0!	4.95E-02
c25376_g1_i1	<i>CA177</i>	Uncharacterized protein Clorf177 homolog	#DIV/0!	7.99E-03
c26955_g1_i1	<i>ROST</i>	Protein rolling stone	#DIV/0!	1.80E-02
c27681_g1_i1	<i>DHE3</i>	Glutamate dehydrogenase, mitochondrial	2.00	4.40E-02
c28303_g1_i1	<i>PAPSS</i>	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase=1	19.17	3.98E-04
c29448_g1_i1	<i>EFEB2</i>	EF-hand calcium-binding domain-containing protein 2	44.79	5.18E-07
c30387_g1_i1	<i>EFA02780.1</i>	hypothetical protein TcasGA2_TC008517	28.20	9.51E-07
c31742_g1_i1	<i>SPAG6</i>	Sperm-associated antigen 6	#DIV/0!	2.52E-05
c32232_g1_i1	<i>IPP2</i>	Protein phosphatase inhibitor 2	#DIV/0!	6.02E-08
c32697_g1_i2	<i>YC91</i>	Uncharacterized MFS-type transporter C09D4.1	5.16	2.27E-03
c32951_g1_i1	<i>ENN71635.1</i>	hypothetical protein YQE_11733, partial	126.30	2.43E-07
c33011_g1_i1	<i>TPH</i>	Tryptophan 5-hydroxylase	6.69	3.57E-02
c33213_g1_i1	<i>TREA</i>	Trehalase	40.12	2.76E-09
c34739_g2_i1	<i>EFA08011.1</i>	hypothetical protein TcasGA2_TC005600	2.03	3.78E-02
c35472_g1_i2	<i>RHGBA</i>	Rho GTPase-activating protein 11A	#DIV/0!	6.03E-06
c35538_g1_i1	<i>ZN706</i>	Zinc finger protein 706	31.45	1.26E-07
c35582_g1_i1	<i>TRY3</i>	Trypsin-3 OS=Anopheles gambiae	14.43	3.32E-02
c36323_g1_i2	<i>DYH12</i>	Dynein heavy chain 12, axonemal	#DIV/0!	3.69E-02
c36719_g1_i1	<i>EFX67914.1</i>	hypothetical protein DAPPUDRAFT_330595	2.55	3.12E-02
c38213_g1_i1	<i>XP_970201.2</i>	similar to GA12375-PA	25.09	1.86E-06
c38859_g1_i1	<i>PPK28</i>	Pickpocket protein 28	#DIV/0!	3.42E-04
c40892_g1_i1	<i>XP_966429.2</i>	similar to lethal with a checkpoint kinase CG4943-PA isoform 1	10.19	4.44E-02
c41203_g1_i1	<i>ABCA3</i>	ATP-binding cassette sub-family A member 3	21.48	4.35E-02
c41378_g1_i1	<i>ENN77898.</i>	hypothetical protein YQE_05575, partial	37.01	4.04E-13
c43253_g2_i2	<i>ANO2</i>	Anoctamin-2	#DIV/0!	2.37E-02
c43701_g1_i2	<i>DERP3</i>	Mite allergen Der p 3	26.58	2.15E-09
c43787_g1_i2	<i>MOT14</i>	Monocarboxylate transporter 14	12.35	1.73E-04
c43897_g1_i1	<i>PKIL2</i>	Polycystic kidney disease protein 1-like 2	12.49	3.62E-02

c44147_g1_i2	<i>EFA13049.1</i>	hypothetical protein TcasGA2_TC010751	#DIV/0!	3.69E-02
c46177_g1_i1	<i>EFA04228.1</i>	hypothetical protein TcasGA2_TC014479	49.24	1.05E-05
c46621_g1_i1	<i>ENN81187.1</i>	hypothetical protein YQE_02404, partial	3.01	3.00E-02
c46842_g1_i1	<i>KGUA</i>	Guanylate kinase	#DIV/0!	1.37E-03
c47067_g1_i1	<i>ENN79674.</i>	hypothetical protein YQE_03879, partial	13.79	4.51E-05
c48002_g1_i1	<i>DYH6</i>	Dynein heavy chain 6, axonemal	#DIV/0!	2.69E-02
c48447_g1_i1	<i>RL37A</i>	60S ribosomal protein L37a	40.18	1.68E-05
c49368_g1_i1	<i>VCP</i>	Venom serine carboxypeptidase	125.75	5.78E-08
c49539_g1_i1	<i>YRBE</i>	Uncharacterized oxidoreductase YrbE	4.91	4.72E-02
c49920_g1_i1	<i>ENN76287.1</i>	hypothetical protein YQE_07250, partial	26.11	5.13E-12
c50257_g1_i1	<i>OTC</i>	Ornithine carbamoyltransferase, mitochondrial	2.84	4.41E-02
c51924_g1_i2	<i>CB5D1</i>	Cytochrome b5 domain-containing protein 1	#DIV/0!	1.87E-03
c53115_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	6.27	3.55E-03
c53300_g1_i1	<i>CNDP1</i>	Beta-Ala-His dipeptidase	65.96	5.58E-09
c53497_g1_i2	<i>EFA08305.1</i>	hypothetical protein TcasGA2_TC005941	57.44	1.97E-20
c53666_g1_i1	<i>MARH3</i>	E3 ubiquitin-protein ligase MARCH3	18.89	5.76E-07
c54151_g2_i1	<i>MDHG2</i>	Probable malate dehydrogenase, glyoxysomal	19.74	1.49E-05
c54618_g1_i1	<i>ENN70724.1</i>	hypothetical protein YQE_12554, partial	#DIV/0!	8.71E-03
c54775_g1_i1	<i>ENN75695.1</i>	hypothetical protein YQE_07656, partial	107.38	1.37E-03
c54893_g1_i2	<i>DHE3</i>	Glutamate dehydrogenase, mitochondrial	3.90	1.83E-03
c54901_g1_i1	<i>XP_971008.1</i>	similar to conserved hypothetical protein	#DIV/0!	1.10E-02
c55016_g1_i2	<i>VA3</i>	Venom allergen 3	#DIV/0!	5.08E-04
c55232_g1_i1	<i>EEZ97552.1</i>	hypothetical protein TcasGA2_TC011402	24.27	3.03E-04
c55589_g1_i2	<i>CD022</i>	Uncharacterized protein C4orf22	25.61	2.48E-03
c55851_g1_i1	<i>IPYR</i>	Inorganic pyrophosphatase	2.16	3.27E-02
c56151_g1_i1	<i>LRGUK</i>	Leucine-rich repeat and guanylate kinase domain-containing protein	#DIV/0!	1.35E-06
c56425_g1_i1	<i>GEFE</i>	Ras guanine nucleotide exchange factor E	24.78	3.87E-12
c56482_g1_i1	<i>CISY2</i>	Probable citrate synthase 2, mitochondrial	2.42	8.90E-03
c56483_g1_i1	<i>AEE61942.1</i>	unknown	4.12	3.88E-03
c57028_g1_i1	<i>GBA3</i>	Cytosolic beta-glucosidase	#DIV/0!	2.30E-02

c57228_g1_i1	<i>YPC2</i>	Putative serine/threonine-protein kinase C05D10.2	18.16	1.10E-08
c57310_g1_i1	<i>ENN74879.1</i>	hypothetical protein YQE_08544, partial	67.96	1.16E-11
c57694_g1_i2	<i>CH10</i>	10 kDa heat shock protein, mitochondrial	140.04	3.62E-09
c57727_g1_i1	<i>LUCI</i>	Luciferin 4-monooxygenase	#DIV/0!	2.17E-03
c57735_g1_i1	<i>MYRO1</i>	Myrosinase 1	373.06	4.33E-08
c58187_g1_i2	<i>EFHB</i>	EF-hand domain-containing family member B	150.04	9.40E-10
c58299_g1_i1	<i>L2CC</i>	Protein l(2)37Cc	2.05	4.38E-02
c58403_g1_i1	<i>ENN71950.1</i>	hypothetical protein YQE_11384, partial	#DIV/0!	1.30E-02
c58720_g1_i1	<i>RL9</i>	60S ribosomal protein L9	4.95	3.58E-02
c58846_g1_i1	<i>NXNL2</i>	Nucleoredoxin-like protein 2	#DIV/0!	1.97E-02
c59514_g1_i1	<i>NDUS8</i>	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	5.56	4.60E-02
c59759_g1_i2	<i>CHD4</i>	Chromodomain-helicase-DNA-binding protein 4	#DIV/0!	1.69E-03
c59848_g1_i1	<i>GLBL2</i>	Beta-galactosidase-1-like protein 2	84.80	3.73E-03
c60088_g1_i1	<i>TRPL</i>	Transient-receptor-potential-like protein	15.01	3.63E-02
c60435_g1_i1	<i>EHD1</i>	EH domain-containing protein 1	43.27	1.64E-13
c60540_g1_i1	<i>ABC40570.1</i>	putative antimicrobial knottin protein Btk-2	29.38	1.65E-02
c60599_g1_i1	<i>MAL1</i>	Maltase 1	9.91	3.62E-02
c60824_g1_i1	<i>ADT</i>	ADP,ATP carrier protein 4	7.43	1.47E-06
c61000_g2_i2	<i>LRC27</i>	Leucine-rich repeat-containing protein 27	#DIV/0!	9.31E-03
c61014_g1_i1	<i>COX4I</i>	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	2.21	2.21E-02
c61175_g1_i2	<i>EFA09367.1</i>	hypothetical protein TcasGA2_TC001928	15.53	3.39E-04
c61365_g1_i1	<i>TRET1</i>	Facilitated trehalose transporter Tret1	29.75	2.49E-02
c61764_g1_i1	<i>EFA04084.1</i>	hypothetical protein TcasGA2_TC014318	62.43	1.49E-12
c62364_g1_i1	<i>PUR6</i>	Multifunctional protein ADE2	2.97	1.16E-02
c62660_g1_i1	<i>THIOT</i>	Thioredoxin-T OS=Drosophila melanogaster	#DIV/0!	5.44E-06
c62664_g1_i1	<i>XP_002075325.1</i>	GK15823	25.55	3.96E-02
c62738_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	60.82	2.32E-12
c62948_g1_i2	<i>ENN74273.1</i>	hypothetical protein YQE_09245, partial	9.27	2.24E-02
c63031_g1_i1	<i>AMPL</i>	Cytosol aminopeptidase	58.27	1.10E-05
c63178_g2_i1	<i>PGLR</i>	Probable polygalacturonase	152.65	1.55E-05

c63307_g1_i1	<i>SPT17</i>	Spermatogenesis-associated protein 17	#DIV/0!	2.02E-02
c63547_g1_i1	<i>CSRI</i>	Phosphatidylinositol transfer protein CSR1	#DIV/0!	3.61E-03
c64133_g1_i2	<i>ENN75126.1</i>	hypothetical protein YQE_08306, partial	4.74	1.77E-02
c64345_g1_i1	<i>NEDD8</i>	NEDD8	#DIV/0!	2.81E-02
c64457_g1_i1	<i>KAD8</i>	Adenylate kinase 8	32.84	9.18E-04
c64617_g1_i1	<i>HSP7A</i>	Heat shock 70 kDa protein cognate 1	20.26	3.37E-05
c64719_g1_i1	<i>CAX70371.1</i>	25 kDa integral membrane protein	#DIV/0!	9.83E-04
c64875_g1_i1	<i>XP_976338.</i>	hypothetical protein TcasGA2_TC013967	24.38	6.02E-06
c64890_g1_i1	<i>DYHI</i>	Dynein heavy chain 1, axonemal	#DIV/0!	1.20E-04
c64994_g1_i1	<i>OAT</i>	Ornithine aminotransferase, mitochondrial	4.42	4.73E-02
c65031_g1_i1	<i>GAS8</i>	Growth arrest-specific protein 8	20.44	1.68E-04
c65087_g1_i1	<i>ENN80601.1</i>	hypothetical protein YQE_02980, partial	26.33	3.39E-03
c65109_g1_i1	<i>PRT</i>	Protamine	35.49	4.85E-16
c65123_g1_i1	<i>ENN79163.</i>	hypothetical protein YQE_04348, partial	3.97	6.36E-04
c65230_g2_i1	<i>XYLB</i>	Xylulose kinase	2.12	4.27E-02
c65317_g1_i2	<i>EFA10579.1</i>	hypothetical protein TcasGA2_TC012835	3.02	4.49E-02
c65730_g1_i1	<i>ENN70474.1</i>	hypothetical protein YQE_12977, partial	5.93	2.31E-02
c65931_g1_i1	<i>ENN82723.1</i>	hypothetical protein YQE_00909, partial	93.90	7.85E-19
c66126_g1_i1	<i>XP_003399497.1</i>	CD63 antigen-like	8.47	4.98E-02
c66159_g1_i1	<i>PACRG</i>	Parkin coregulated gene protein homolog	3.13	1.76E-03
c66184_g1_i1	<i>EMAL</i>	Echinoderm microtubule-associated protein-like CG42247 SV=3	6.00	2.15E-02
c66234_g1_i1	<i>BOULE</i>	Protein boule	4.50	9.68E-05
c66392_g1_i1	<i>PR5</i>	Pathogenesis-related protein 5	32.30	1.74E-03
c66444_g1_i1	<i>DCXR</i>	L-xylulose reductase	11.57	2.38E-03
c66772_g1_i1	<i>UFM1</i>	Ubiquitin-fold modifier 1	3.16	1.19E-03
c66780_g1_i1	<i>XP_976261.1</i>	hypothetical protein	#DIV/0!	3.32E-03
c66834_g1_i1	<i>EFA02036.1</i>	hypothetical protein TcasGA2_TC007663	#DIV/0!	1.16E-06
c67009_g1_i1	<i>AT8A1</i>	Probable phospholipid-transporting ATPase IA	28.69	1.23E-02
c67075_g1_i1	<i>S36A4</i>	Proton-coupled amino acid transporter 4	24.61	2.24E-06
c67176_g1_i1	<i>CH10</i>	10 kDa heat shock protein, mitochondrial	2.49	9.04E-03

c67252_g1_i1	<i>CUD2</i>	Endocuticle structural glycoprotein SgAbd-2	4.00	4.05E-02
c67339_g1_i1	<i>C6A14</i>	Probable cytochrome P450 6a14	3.61	1.96E-02
c67470_g1_i1	<i>GLTP</i>	Glycolipid transfer protein	7.88	1.65E-05
c67610_g1_i1	<i>TAKT</i>	Protein takeout	2.67	2.59E-02
c67660_g1_i1	<i>ENN77176.1</i>	hypothetical protein YQE_06314, partial	14.84	9.68E-05
c67848_g1_i1	<i>ENN71713.1</i>	hypothetical protein YQE_11636, partial	75.68	4.15E-10
c67892_g1_i2	<i>XP_003388159.1</i>	hypothetical protein LOC100641088	23.72	1.43E-04
c67922_g1_i1	<i>CUD2</i>	Endocuticle structural glycoprotein SgAbd-2	5.56	9.58E-03
c68183_g1_i3	<i>POL</i>	Gag-Pro-Pol polyprotein	11.48	2.43E-02
c68233_g1_i1	<i>DYHI</i>	Dynein heavy chain 1, axonemal	#DIV/0!	7.49E-06
c68311_g1_i1	<i>ENN82170.1</i>	hypothetical protein YQE_01454, partial	#DIV/0!	1.29E-15
c68378_g1_i1	<i>PPIL6</i>	Peptidyl-prolyl cis-trans isomerase-like 6	#DIV/0!	2.88E-06
c68503_g1_i1	<i>XP_976355.1</i>	hypothetical protein	30.23	8.91E-10
c68525_g1_i1	<i>CTRBI</i>	Chymotrypsin BI	36.31	3.66E-09
c68612_g1_i1	<i>ENN71634.1</i>	hypothetical protein YQE_11732, partial	76.39	9.25E-10
c68798_g1_i2	<i>ATPK</i>	Putative ATP synthase subunit f, mitochondrial	2.03	3.77E-02
c68878_g1_i1	<i>PK2L1</i>	Polycystic kidney disease 2-like 1 protein	24.54	4.49E-02
c68968_g1_i2	<i>ASM</i>	Sphingomyelin phosphodiesterase	8.42	2.75E-02
c69874_g1_i1	<i>ENN77573.1</i>	hypothetical protein YQE_05869, partial	58.19	1.21E-04
c69895_g1_i1	<i>XP_002402857.1</i>	antigenic peptide RU2S, putative	28.15	1.36E-05
c70128_g1_i1	<i>ENN81696.1</i>	hypothetical protein YQE_01902, partial	28.05	3.89E-06
c70154_g1_i1	<i>ENN76365.1</i>	hypothetical protein YQE_07114, partial	94.50	2.25E-09
c70242_g1_i2	<i>MANA</i>	Mannan endo-1,4-beta-mannosidase	80.77	1.87E-03
c70270_g1_i1	<i>EFA07861.1</i>	hypothetical protein TcasGA2_TC005435	#DIV/0!	9.83E-05
c70283_g1_i1	<i>NNRD</i>	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	3.75	6.59E-03
c70298_g1_i1	<i>ENN75838.1</i>	hypothetical protein YQE_07568, partial	20.88	5.04E-06
c70382_g1_i1	<i>HTXA</i>	Probable alpha-ketoglutarate-dependent hypophosphite dioxygenase	21.67	9.97E-03
c70617_g1_i1	<i>AAA64736.1</i>	apolipoporphin-III, partial	2.49	1.63E-02
c71183_g1_i1	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	2.56	1.71E-02
c71187_g1_i2	<i>5NTC</i>	Cytosolic purine 5'-nucleotidase	2.02	2.77E-02

c71251_g1_i1	<i>DYHC</i>	Dynein beta chain, ciliary	26.71	1.85E-02
c71296_g1_i1	<i>ENN74542.1</i>	hypothetical protein YQE_08865, partial	37.44	8.68E-19
c71403_g1_i1	<i>ENN80979.1</i>	hypothetical protein YQE_02610, partial	22.39	2.27E-12
c71513_g1_i1	<i>CAH3</i>	Putative carbonic anhydrase 3	2.49	7.95E-03
c71576_g1_i2	<i>PIEZ2</i>	Piezo-type mechanosensitive ion channel component 2	43.49	2.22E-02
c71599_g1_i2	<i>TRYT</i>	Trypsin theta	18.65	1.42E-02
c71668_g1_i1	<i>EEZ99533.1</i>	hypothetical protein TcasGA2_TC000115	3.38	4.30E-03
c71685_g1_i1	<i>DYHI</i>	Dynein heavy chain 1, axonemal	11.50	4.13E-04
c71707_g1_i1	<i>CYC</i>	Cytochrome c	152.11	2.52E-19
c71785_g1_i1	<i>KAD5</i>	Adenylate kinase isoenzyme 5	9.14	1.58E-07
c71876_g1_i1	<i>COX5A</i>	Cytochrome c oxidase subunit 5A, mitochondrial	2.50	3.28E-02
c71947_g1_i1	<i>UK114</i>	Ribonuclease UK114	3.04	2.26E-02
c71965_g1_i2	<i>ENN76461.1</i>	hypothetical protein YQE_06915, partial	10.36	4.40E-02
c72088_g1_i1	<i>PH4H</i>	Protein henna	10.82	2.12E-04
c72110_g1_i1	<i>EHJ68545.1</i>	hypothetical protein KGM_03871	8.95	4.18E-02
c72119_g1_i1	<i>EFA06914.1</i>	hypothetical protein TcasGA2_TC009863	9.25	8.34E-03
c72212_g1_i1	<i>FOPNL</i>	LisH domain-containing protein	32.56	4.18E-02
c72231_g1_i1	<i>GLCM</i>	Glucosylceramidase	16.92	1.25E-04
c72316_g1_i1	<i>XP_308877.3</i>	AGAP006879-PA	19.02	3.13E-03
c72319_g1_i3	<i>NDUB8</i>	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	3.18	8.86E-04
c72390_g1_i1	<i>TTC19</i>	Tetratricopeptide repeat protein 19, mitochondrial	41.82	1.55E-05
c72554_g1_i1	<i>EFA08774.1</i>	hypothetical protein TcasGA2_TC006464	36.45	3.39E-04
c72601_g2_i1	<i>SV2B</i>	Synaptic vesicle glycoprotein 2B	6.36	2.58E-02
c72637_g1_i1	<i>HAOX1</i>	Hydroxyacid oxidase 1	2.86	1.14E-02
c72674_g1_i3	<i>ABV44725.1</i>	9.2 kDa midgut protein	2.98	1.19E-02
c72711_g1_i1	<i>PDIA1</i>	Protein disulfide-isomerase	55.17	1.09E-09
c72874_g1_i1	<i>STNB</i>	Protein stoned-B	6.29	3.26E-04
c72894_g1_i1	<i>S2551</i>	Solute carrier family 25 member 51	14.48	3.75E-02
c73093_g1_i1	<i>ENN76374.1</i>	hypothetical protein YQE_07096, partial	27.32	1.90E-05
c73118_g1_i1	<i>EFN87139.1</i>	Endochitinase	86.33	4.79E-04

c73138_g1_i1	<i>PRX2B</i>	Peroxiredoxin-2B OS=Arabidopsis thaliana	53.93	3.40E-15
c73204_g1_i1	<i>MGST1</i>	Microsomal glutathione S-transferase 1	2.35	1.12E-02
c73339_g1_i2	<i>ENN80991.1</i>	hypothetical protein YQE_01210, partial	12.11	4.05E-03
c73443_g1_i1	<i>PIF1</i>	ATP-dependent DNA helicase PIF1	7.56	2.77E-02
c73551_g1_i1	<i>HYDIN</i>	Hydrocephalus-inducing protein	#DIV/0!	5.90E-03
c73706_g1_i1	<i>XP_001635890.1</i>	predicted protein	#DIV/0!	1.63E-03
c73927_g1_i2	<i>CDO1</i>	Cysteine dioxygenase type 1	2.04	3.55E-02
c74000_g1_i1	<i>ATAD2</i>	ATPase family AAA domain-containing protein 2	62.73	9.25E-20
c74031_g1_i1	<i>PSMD6</i>	26S proteasome non-ATPase regulatory subunit 6	25.18	2.37E-02
c74226_g1_i1	<i>ABQ65714.1</i>	encapsulation-relating protein variant b	2.47	1.62E-02
c74370_g1_i1	<i>CU19</i>	Cuticle protein 19	#DIV/0!	3.02E-04
c74568_g1_i1	<i>MORN3</i>	MORN repeat-containing protein 3	30.39	6.29E-03
c74573_g2_i1	<i>TSP1</i>	Thrombospondin-1	#DIV/0!	1.60E-06
c74606_g1_i1	<i>XP_004070198.1</i>	uncharacterized protein LOC101171909	69.06	1.73E-03
c74882_g1_i1	<i>HSP23</i>	Heat shock protein 23	2.66	1.01E-02
c74930_g1_i1	<i>CO2A1</i>	Collagen alpha-1(II) chain	18.38	4.23E-04
c74938_g1_i3	<i>VA5</i>	Venom allergen 5	52.28	6.54E-17
c75053_g1_i1	<i>ENN78515.1</i>	hypothetical protein YQE_05016, partial	33.60	5.75E-03
c75119_g1_i1	<i>AEE62598.1</i>	unknown	62.44	4.72E-09
c75120_g1_i1	<i>SUN2</i>	SUN domain-containing protein 2	19.44	1.61E-03
c75126_g1_i1	<i>L2EFL</i>	Protein lethal(2)essential for life	3.49	9.39E-03
c75156_g1_i1	<i>TENA</i>	Teneurin-a	2.15	3.34E-02
c75160_g1_i1	<i>XP_967661.1</i>	similar to CG8813 CG8813-PA	27.53	8.67E-10
c75166_g1_i1	<i>CBPA1</i>	Zinc carboxypeptidase A	23.52	3.65E-12
c75202_g1_i1	<i>TBC30</i>	TBC1 domain family member 30	10.62	3.72E-02
c75252_g1_i1	<i>CHIT1</i>	Chitotriosidase-1	3.05	4.30E-02
c75263_g1_i1	<i>PIHD3</i>	Protein PIH1D3	22.29	5.62E-03
c75280_g1_i1	<i>HTRA2</i>	Serine protease HTRA2, mitochondrial	49.03	2.98E-07
c75304_g1_i1	<i>YV012</i>	Leucine-rich repeat-containing protein LOC400891	55.27	4.30E-06
c75307_g1_i1	<i>PEB3</i>	Ejaculatory bulb-specific protein 3	2.24	4.75E-02

c75393_g1_i1	<i>PGDH</i>	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	#DIV/0!	1.07E-03
c75412_g1_i1	<i>TRYP</i>	Trypsin	#DIV/0!	2.63E-09
c75459_g1_i1	<i>FEZF2</i>	Fez family zinc finger protein 2	25.84	2.11E-02
c75518_g1_i1	<i>STPG2</i>	Sperm-tail PG-rich repeat-containing protein 2	13.93	4.91E-03
c75536_g1_i1	<i>GLNA2</i>	Glutamine synthetase 2 cytoplasmic	63.45	2.41E-16
c75623_g1_i1	<i>ENN70815.1</i>	hypothetical protein YQE_12480, partial	35.70	7.96E-12
c75631_g1_i1	<i>ENO</i>	Enolase	5.57	5.69E-06
c75714_g1_i1	<i>H2B3</i>	Histone H2B.3	#DIV/0!	8.93E-10
c75736_g1_i1	<i>ENN77991.1</i>	hypothetical protein YQE_05666, partial	63.99	9.61E-18
c75743_g1_i1	<i>EFA00614.1</i>	hypothetical protein TcasGA2_TC003489	15.01	3.63E-02
c75772_g1_i2	<i>TSSK1</i>	Testis-specific serine/threonine-protein kinase 1	52.07	6.48E-10
c75838_g1_i1	<i>XP_976251.1</i>	hypothetical protein	19.86	1.43E-02
c75853_g1_i2	<i>TC1D1</i>	Tctex1 domain-containing protein 1	72.61	2.14E-05
c75866_g1_i1	<i>MORN5</i>	MORN repeat-containing protein 5	28.55	1.52E-13
c75951_g1_i1	<i>FOXL2</i>	Forkhead box protein L2	2.99	3.96E-03
c75959_g1_i1	<i>CDKL4</i>	Cyclin-dependent kinase-like 4	11.96	4.42E-03
c76058_g2_i1	<i>CCD63</i>	Coiled-coil domain-containing protein 63	#DIV/0!	8.60E-07
c76133_g1_i1	<i>CLUA1</i>	Clusterin-associated protein 1	7.48	5.72E-03
c76134_g1_i1	<i>LYPA1</i>	Acyl-protein thioesterase 1	2.58	3.76E-02
c76224_g1_i1	<i>CAH7</i>	Carbonic anhydrase 7	#DIV/0!	5.01E-05
c76271_g1_i1	<i>EFA03536.1</i>	hypothetical protein TcasGA2_TC013539	44.94	4.54E-10
c76287_g1_i3	<i>ENN74639.1</i>	hypothetical protein YQE_08758, partial	36.59	1.74E-04
c76446_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	5.98	2.00E-02
c76453_g1_i1	<i>SERC</i>	Probable phosphoserine aminotransferase	2.28	1.66E-02
c76539_g2_i1	<i>UB2L3</i>	Ubiquitin-conjugating enzyme E2 L3	63.64	5.46E-07
c76552_g1_i1	<i>DHSB</i>	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	30.07	2.64E-11
c76691_g1_i1	<i>STNA</i>	Protein stoned-A	19.98	6.27E-03
c76725_g1_i1	<i>SAP</i>	Proactivator polypeptide	3.11	4.28E-03
c76726_g1_i2	<i>VCP</i>	Venom serine carboxypeptidase	47.52	1.40E-04
c76845_g1_i2	<i>TT30A</i>	Tetratricopeptide repeat protein 30A	4.87	1.46E-02

c76971_g1_i1	<i>TACC3</i>	Transforming acidic coiled-coil-containing protein 3	76.70	9.77E-06
c76996_g2_i1	<i>PICO</i>	Putative inorganic phosphate cotransporter	2.59	7.92E-03
c77004_g1_i1	<i>TTC25</i>	Tetratricopeptide repeat protein 25	18.63	1.20E-06
c77161_g1_i1	<i>ADT2</i>	ADP/ATP translocase 2	8.98	2.09E-07
c77215_g1_i1	<i>ESTE</i>	Esterase E4	3.81	7.18E-03
c77266_g1_i1	<i>ENN78370.1</i>	hypothetical protein YQE_05172, partial	96.28	7.37E-26
c77294_g1_i1	<i>EFA08669.1</i>	hypothetical protein TcasGA2_TC006335	#DIV/0!	4.91E-08
c77303_g1_i1	<i>MDHM</i>	Malate dehydrogenase, mitochondrial	3.69	4.93E-03
c77307_g1_i1	<i>AZII</i>	5-azacytidine-induced protein 1	17.83	5.20E-06
c77468_g1_i1	<i>XP_002406442.1</i>	protein disulfide isomerase, putative	#DIV/0!	2.32E-02
c77468_g2_i1	<i>PDIA3</i>	Protein disulfide-isomerase A3	59.17	9.99E-04
c77587_g1_i2	<i>ORNT1</i>	Mitochondrial ornithine transporter 1	33.39	2.02E-06
c77596_g1_i1	<i>EFZ11798.1</i>	hypothetical protein SINV_03639	43.57	1.17E-06
c77726_g1_i1	<i>NP_001082528.1</i>	otogelin precursor	16.47	2.89E-04
c77727_g1_i1	<i>TBA1C</i>	Tubulin alpha-1C chain	54.72	4.33E-07
c77753_g1_i2	<i>PI5K1</i>	Phosphatidylinositol 4-phosphate 5-kinase 1	#DIV/0!	3.33E-06
c77754_g1_i1	<i>TXND6</i>	Thioredoxin domain-containing protein 6	23.26	3.33E-08
c77761_g1_i1	<i>EFHC2</i>	EF-hand domain-containing family member C2	3.52	3.78E-02
c77762_g1_i1	<i>TEKT2</i>	Tektin-2	20.47	1.69E-11
c77779_g1_i1	<i>MDHM</i>	Malate dehydrogenase, mitochondrial	44.65	2.84E-08
c77800_g1_i1	<i>VATF</i>	V-type proton ATPase subunit F (Fragment)	32.17	2.24E-05
c77803_g1_i2	<i>EEZ98718.1</i>	hypothetical protein TcasGA2_TC001264	5.75	1.32E-04
c77956_g1_i1	<i>NDUAC</i>	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	48.94	1.29E-11
c77978_g1_i1	<i>SYNE1</i>	Nesprin-1	2.96	1.63E-02
c78031_g1_i2	<i>GGT1</i>	Gamma-glutamyltranspeptidase 1	13.72	1.21E-04
c78111_g1_i3	<i>VSPPA</i>	Venom plasminogen activator Haly-PA	47.71	1.56E-02
c78116_g1_i1	<i>WDR52</i>	WD repeat-containing protein 52	10.49	1.21E-03
c78152_g2_i1	<i>FABP4</i>	Fatty acid-binding protein, adipocyte	26.98	2.08E-02
c78243_g1_i1	<i>CFB</i>	Clotting factor B	2.21	4.41E-02
c78252_g1_i1	<i>EFA02620.1</i>	hypothetical protein TcasGA2_TC008340	2.66	4.31E-02

c78282_g2_i1	<i>EFA11121.1</i>	hypothetical protein YQE_00236, partial	13.55	2.39E-02
c78306_g1_i1	<i>UNC22</i>	Twitchin	5.08	5.78E-03
c78320_g1_i1	<i>NEDD1</i>	Protein NEDD1	13.76	4.02E-10
c78356_g1_i1	<i>GSTT1</i>	Glutathione S-transferase 1	3.87	6.46E-03
c78366_g1_i2	<i>XP_971465.2</i>	similar to AGAP011620-PA	21.56	7.47E-05
c78429_g1_i2	<i>TTLL5</i>	Tubulin polyglutamylase TTLL5	31.39	2.00E-06
c78441_g1_i1	<i>ENN71248.1</i>	hypothetical protein YQE_12175, partial	22.78	5.86E-07
c78599_g1_i1	<i>CYB5</i>	Cytochrome b5	4.01	3.87E-04
c78609_g1_i1	<i>DPOA2</i>	DNA polymerase alpha subunit B	2.29	2.72E-02
c78678_g1_i1	<i>CCD42</i>	Coiled-coil domain-containing protein 42 homolog	#DIV/0!	3.34E-11
c78702_g1_i1	<i>EFN81464.1</i>	Trypsin-1	13.99	1.33E-02
c78718_g1_i1	<i>CLVS2</i>	Clavesin-2	3.48	5.78E-03
c78793_g2_i1	<i>EFX82265.1</i>	hypothetical protein DAPPUDRAFT_223905	13.43	2.69E-04
c78797_g1_i2	<i>ENN74924.1</i>	hypothetical protein YQE_08502, partial	#DIV/0!	1.57E-04
c78811_g1_i1	<i>SARDH</i>	Sarcosine dehydrogenase, mitochondrial	9.74	1.39E-09
c78902_g1_i2	<i>THIO2</i>	Thioredoxin-2	61.89	7.80E-07
c78939_g1_i1	<i>LFG2</i>	Protein lifeguard 2	#DIV/0!	2.19E-04
c79008_g1_i1	<i>ADCYA</i>	Adenylate cyclase type 10	22.48	1.16E-04
c79017_g1_i1	<i>XP_970792.1</i>	similar to CG13296 CG13296-PA	23.70	1.04E-04
c79064_g1_i1	<i>HYDIN</i>	Hydrocephalus-inducing protein homolog	#DIV/0!	8.86E-08
c79068_g2_i1	<i>ENN81527.1</i>	hypothetical protein YQE_02056, partial	52.18	2.77E-10
c79092_g1_i1	<i>CTRB2</i>	Chymotrypsin BII	6.09	3.32E-02
c79108_g1_i1	<i>PIEZ2</i>	Piezo-type mechanosensitive ion channel component 2	38.76	2.48E-02
c79123_g1_i1	<i>SCOT1</i>	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	4.86	9.66E-05
c79132_g1_i2	<i>ENN74390.1</i>	hypothetical protein YQE_09023, partial	36.00	1.53E-13
c79177_g1_i2	<i>COX42</i>	Cytochrome c oxidase subunit 4 isoform 2, mitochondrial	#DIV/0!	2.08E-06
c79199_g1_i1	<i>STT3B</i>	Donchryi-tripnospingosaccharide--protein glycosyltransferase subunit STT3B	2.47	1.49E-02
c79281_g1_i1	<i>CC170</i>	Coiled-coil domain-containing protein 170	2.84	3.80E-02
c79322_g1_i1	<i>LIN54</i>	Protein lin-54 homolog	2.12	3.87E-02
c79336_g1_i2	<i>GABT</i>	4-aminobutyrate aminotransferase, mitochondrial	5.00	2.87E-03

c79345_g1_i1	<i>ANK3</i>	Ankyrin-3	4.58	3.57E-02
c79408_g1_i1	<i>DYHC</i>	Dynein beta chain, ciliary	#DIV/0!	1.79E-02
c79415_g1_i4	<i>IQCAL</i>	IQ and AAA domain-containing protein 1-like	3.95	1.02E-02
c79538_g1_i1	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	23.93	7.36E-04
c79549_g1_i1	<i>CCD96</i>	Coiled-coil domain-containing protein 96	120.52	4.13E-18
c79577_g1_i1	<i>KRP85</i>	Kinesin-II 85 kDa subunit	#DIV/0!	2.66E-06
c79590_g1_i2	<i>EFA00248.1</i>	hypothetical protein TcasGA2_TC003077	#DIV/0!	1.27E-02
c79677_g1_i1	<i>VCP</i>	Venom serine carboxypeptidase	113.11	1.12E-23
c79697_g2_i1	<i>PGDH</i>	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	37.10	4.82E-16
c79724_g1_i1	<i>ENN83007.1</i>	hypothetical protein YQE_00629, partial	173.39	1.44E-13
c79749_g1_i1	<i>IF23A</i>	Insulin-like growth factor 2 mRNA-binding protein 3-A	69.20	1.12E-08
c79756_g1_i1	<i>ENN70464.1</i>	hypothetical protein YQE_12967, partial	36.56	5.83E-06
c79777_g1_i1	<i>ENN73269.1</i>	hypothetical protein YQE_10112, partial	36.18	3.68E-03
c79783_g1_i1	<i>EFA00110.1</i>	hypothetical protein TcasGA2_TC002926	43.90	1.46E-06
c79787_g1_i1	<i>K1841</i>	Uncharacterized protein KIAA1841 homolog	3.18	8.04E-03
c79811_g1_i2	<i>ENO</i>	Enolase	51.21	6.21E-06
c79812_g1_i1	<i>PGLR</i>	Probable polygalacturonase	#DIV/0!	1.71E-02
c79831_g1_i1	<i>CX6A1</i>	Cytochrome c oxidase subunit 6A1, mitochondrial	21.13	3.68E-02
c79907_g1_i1	<i>HYEP1</i>	Juvenile hormone epoxide hydrolase 1	3.47	7.08E-04
c79944_g1_i1	<i>CD047</i>	UPF0602 protein C4orf47 homolog	28.95	1.84E-10
c79974_g1_i1	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	17.57	2.71E-06
c80002_g1_i2	<i>AEE61805.1</i>	unknown	6.32	3.42E-02
c80062_g1_i1	<i>NB5R3</i>	NADH-cytochrome b5 reductase 3 (Fragment)	2.75	1.35E-02
c80072_g1_i1	<i>PGDH</i>	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	60.45	2.50E-11
c80118_g1_i1	<i>ENN71128.1</i>	hypothetical protein YQE_12060, partial	14.60	7.49E-07
c80134_g1_i1	<i>FAHD2</i>	Fumarylacetoacetate hydrolase domain-containing protein 2	2.91	6.38E-03
c80162_g1_i5	<i>KADI</i>	Adenylate kinase isoenzyme 1	3.29	2.77E-02
c80171_g1_i1	<i>AEX93420.1</i>	juvenile hormone binding protein 5p2, partial	111.21	4.57E-14
c80180_g1_i2	<i>AQP4</i>	Aquaporin-4	13.19	6.06E-03
c80259_g1_i1	<i>TEKT3</i>	Tektin-3	7.48	1.11E-03

c80268_g1_i1	<i>ENN82475.1</i>	hypothetical protein YQE_01150, partial	39.53	1.62E-17
c80276_g1_i1	<i>PERO</i>	Peroxidase	38.84	2.86E-06
c80289_g1_i1	<i>FA60A</i>	Protein FAM60A	54.46	1.97E-04
c80298_g1_i1	<i>IQCA1</i>	IQ and AAA domain-containing protein 1	80.94	2.95E-12
c80318_g1_i1	<i>KCY</i>	UMP-CMP kinase	2.31	1.66E-02
c80333_g1_i1	<i>XP_968599.1</i>	similar to GA15997-PA	4.03	1.65E-03
c80377_g1_i1	<i>DCST1</i>	DC-STAMP domain-containing protein 1	16.97	4.34E-02
c80440_g1_i3	<i>RXRA</i>	Retinoic acid receptor RXR-alpha	2.50	5.37E-03
c80461_g1_i1	<i>ENN72747.1</i>	hypothetical protein YQE_10552, partial	8.08	1.71E-04
c80480_g1_i1	<i>SV2B</i>	Synaptic vesicle glycoprotein 2B	2.13	1.56E-02
c80510_g1_i2	<i>RTDR1</i>	Rhabdoid tumor deletion region protein 1	14.07	4.84E-03
c80537_g1_i1	<i>TBB</i>	Tubulin beta chain	17.84	1.15E-10
c80563_g1_i1	<i>EVG1</i>	UPF0193 protein EVG1	3.74	1.66E-02
c80604_g1_i2	<i>XP_966751.1</i>	similar to AGAP006524-PA	#DIV/0!	9.21E-04
c80626_g1_i1	<i>CO5A1</i>	Collagen alpha-1(V) chainE=2 SV=1	5.27	3.66E-02
c80629_g1_i1	<i>ENN73077.1</i>	hypothetical protein YQE_10281, partial	2.86	4.14E-02
c80702_g1_i1	<i>CU059</i>	Uncharacterized protein C21orf59	52.61	1.43E-11
c80723_g1_i1	<i>LIAS</i>	Lipoyl synthase, mitochondrial 1	2.75	3.89E-02
c80725_g1_i1	<i>SPEF2</i>	Sperm flagellar protein 2	#DIV/0!	2.62E-02
c80783_g1_i1	<i>ENN81501.1</i>	hypothetical protein YQE_02030, partial	17.59	8.92E-05
c80813_g1_i1	<i>VDPP4</i>	Venom dipeptidyl peptidase 4	52.66	2.67E-04
c80834_g1_i1	<i>EFA09435.1</i>	hypothetical protein TcasGA2_TC010647	#DIV/0!	1.27E-02
c80871_g1_i1	<i>PRT</i>	Protamine	66.13	2.15E-20
c80896_g1_i1	<i>CUD2</i>	Endocuticle structural glycoprotein SgAbd-2	2.64	3.04E-02
c80965_g1_i1	<i>POXN</i>	Paired box pox-neuro protein	4.36	1.91E-02
c80989_g1_i3	<i>LSD1</i>	Lipid storage droplets surface-binding protein 1	3.84	5.21E-04
c81003_g2_i1	<i>APT</i>	Adenine phosphoribosyltransferase	2.07	4.49E-02
c81004_g1_i1	<i>UD11</i>	UDP-glucuronosyltransferase 1-1	3.18	6.88E-04
c81007_g1_i2	<i>ENN71068.1</i>	hypothetical protein YQE_12002, partial	43.49	1.50E-07
c81088_g1_i1	<i>DNAJ1</i>	DnaJ protein homolog 1	68.10	1.32E-04

c81094_g1_i1	<i>TSSK2</i>	Testis-specific serine/threonine-protein kinase 2	57.10	6.06E-20
c81105_g1_i1	<i>ENN79287.1</i>	hypothetical protein YQE_04263, partial	17.14	1.43E-09
c81148_g1_i1	<i>VA5</i>	Venom allergen 5	#DIV/0!	9.88E-04
c81155_g1_i1	<i>SI7A5</i>	Sialin	2.81	3.07E-02
c81182_g1_i1	<i>DYLT1</i>	Dynein light chain Tctex-type 1	3.25	2.80E-03
c81195_g1_i2	<i>ENN75854.1</i>	hypothetical protein YQE_07583, partial	44.04	7.22E-08
c81222_g1_i1	<i>L259</i>	Probable multidrug resistance-associated protein lethal(2)03659	3.44	4.23E-02
c81224_g1_i1	<i>ENN74569.1</i>	hypothetical protein YQE_08891, partial	13.96	1.18E-04
c81229_g1_i1	<i>4CL</i>	4-coumarate--CoA ligase	52.02	5.79E-06
c81248_g1_i1	<i>LIPP</i>	Pancreatic triacylglycerol lipase	24.23	6.61E-03
c81260_g1_i1	<i>ENN78253.1</i>	hypothetical protein YQE_05404, partial	139.86	9.29E-05
c81269_g1_i1	<i>NCASE</i>	Neutral ceramidase	11.74	2.09E-10
c81283_g1_i1	<i>KAD7</i>	Adenylate kinase 7 (Fragment)	22.55	8.60E-11
c81288_g1_i1	<i>OXDD</i>	D-aspartate oxidase	2.15	3.28E-02
c81307_g1_i1	<i>PRS48</i>	Serine protease 48	37.44	3.41E-16
c81351_g1_i2	<i>S39AB</i>	Zinc transporter ZIP11	2.04	2.96E-02
c81375_g1_i1	<i>LECM</i>	C-type lectin mannose-binding isoform	16.70	1.43E-11
c81419_g2_i1	<i>AMPN</i>	Aminopeptidase N	7.52	7.74E-04
c81431_g1_i1	<i>gb/EEZ97958.1</i>	hypothetical protein TcasGA2_TC000349	152.86	8.25E-06
c81451_g1_i4	<i>BAI83418.1</i>	sugar transporter 4	21.05	7.83E-03
c81452_g1_i1	<i>ENKDI</i>	Enkurin domain-containing protein 1	4.75	5.68E-05
c81560_g1_i2	<i>GSI</i>	Probable pseudouridine-5'-monophosphatase	#DIV/0!	3.73E-02
c81575_g1_i1	<i>CAH5</i>	OS=Caenorhabditis elegans	47.70	1.01E-05
c81584_g1_i1	<i>TTC18</i>	Tetratricopeptide repeat protein 18	5.92	3.70E-02
c81602_g1_i1	<i>WDR52</i>	WD repeat-containing protein 52	16.64	2.37E-05
c81657_g1_i1	<i>EFA09110.1</i>	hypothetical protein TcasGA2_TC015485	#DIV/0!	1.44E-02
c81689_g1_i2	<i>SUN2</i>	SUN domain-containing protein 2	118.59	1.57E-13
c81693_g1_i3	<i>EFZ21444.1</i>	hypothetical protein SINV_09875	9.75	1.77E-05
c81726_g1_i1	<i>B1</i>	B1 protein (Fragment)	5.53	8.19E-03
c81751_g1_i1	<i>AT5F1</i>	ATP synthase subunit b, mitochondrial	6.98	7.82E-03

c81851_g1_i1	<i>SPEF1</i>	Sperm flagellar protein 1	#DIV/0!	2.99E-06
c81852_g1_i1	<i>PEF1</i>	Peflin	39.65	1.73E-12
c81855_g1_i1	<i>UCRI</i>	Cytochrome b-c1 complex subunit Rieske, mitochondrial	5.11	2.15E-02
c81857_g1_i1	<i>DYH8</i>	Dynein heavy chain 8, axonemal	31.70	3.67E-06
c81873_g1_i1	<i>ALAT2</i>	Alanine aminotransferase 2	2.03	3.29E-02
c81875_g1_i2	<i>EFA10093.1</i>	hypothetical protein TcasGA2_TC012271	10.52	1.54E-05
c81887_g1_i2	<i>ENN79193.1</i>	hypothetical protein YQE_04377, partial	#DIV/0!	2.50E-07
c81898_g1_i1	<i>ACP18827.1</i>	chitin deacetylase 1	6.29	4.73E-03
c81914_g1_i1	<i>ENN76450.1</i>	hypothetical protein YQE_06904, partial	19.16	1.26E-02
c81918_g1_i1	<i>EFA04080.1</i>	hypothetical protein TcasGA2_TC014314	5.00	3.28E-02
c82028_g1_i1	<i>EFN79454.1</i>	hypothetical protein EAI_03520	7.59	2.02E-03
c82036_g1_i1	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	18.50	2.07E-03
c82037_g1_i1	<i>CATA</i>	Catalase	11.96	1.44E-03
c82069_g1_i3	<i>5NTD</i>	5'-nucleotidase	3.88	1.84E-02
c82090_g1_i1	<i>ANO6</i>	Anoctamin-6	5.31	1.20E-02
c82096_g1_i11	<i>EFCB1</i>	EF-hand calcium-binding domain-containing protein 1	10.42	3.90E-03
c82125_g1_i1	<i>DHC24</i>	Delta(24)-sterol reductase	5.31	9.91E-06
c82190_g1_i1	<i>SPA6L</i>	Spermatogenesis associated 6-like protein	138.58	1.34E-03
c82206_g1_i7	<i>TTL3A</i>	Tubulin glycolase 3A	7.52	5.60E-05
c82227_g1_i1	<i>CRYL1</i>	Lambda-crystallin homolog	2.80	7.88E-03
c82236_g1_i1	<i>GLNA2</i>	Glutamine synthetase 2 cytoplasmic	3.06	1.16E-03
c82273_g1_i1	<i>RDH13</i>	Retinol dehydrogenase 13	10.27	1.86E-06
c82299_g1_i1	<i>XP_975076.1</i>	similar to bc8 orange interacting protein	10.61	4.68E-04
c82346_g1_i2	<i>EST6</i>	Venom carboxylesterase-6	2.95	1.43E-02
c82347_g1_i4	<i>INE</i>	Sodium- and chloride-dependent GABA transporterine	2.58	8.31E-03
c82355_g1_i1	<i>EFA03852.1</i>	hypothetical protein TcasGA2_TC013968	175.62	2.27E-03
c82368_g1_i2	<i>MFS6</i>	Major facilitator superfamily domain-containing protein 6	7.49	3.14E-02
c82451_g1_i1	<i>DLDH</i>	Dihydrolipoyl dehydrogenase, mitochondrial	2.10	3.84E-02
c82452_g1_i1	<i>MATN2</i>	Matrilin-2	2.46	2.82E-02
c82480_g1_i1	<i>TGIF2</i>	Homeobox protein TGIF2	3.40	4.92E-02

c82491_g1_i2	<i>ALO3</i>	Antimicrobial peptide Alo-3	3.95	3.42E-05
c82585_g1_i1	<i>ENN80353.1</i>	hypothetical protein YQE_03212, partial	#DIV/0!	9.49E-06
c82592_g1_i2	<i>PIEZ1</i>	Piezo-type mechanosensitive ion channel component 1	#DIV/0!	2.78E-02
c82600_g1_i1	<i>TRY3</i>	Trypsin-3 (Fragment)	23.67	4.79E-08
c82600_g2_i1	<i>TRY3</i>	Trypsin-3 (Fragment)	17.77	1.16E-05
c82628_g1_i1	<i>KARG</i>	Arginine kinase	65.49	2.28E-06
c82659_g1_i1	<i>AMPL</i>	Cytosol aminopeptidase	73.24	1.16E-23
c82725_g1_i1	<i>DYH7</i>	Dynein heavy chain 7, axonemal	#DIV/0!	1.57E-02
c82738_g1_i1	<i>CAP1</i>	Adenylyl cyclase-associated protein 1	2.80	3.44E-02
c82760_g1_i1	<i>DHB12</i>	Estradiol 17-beta-dehydrogenase 12	3.97	4.00E-03
c82768_g1_i1	<i>KATL2</i>	Katanin p60 ATPase-containing subunit A-like 2	#DIV/0!	1.05E-03
c82777_g1_i1	<i>FGGY</i>	FGGY carbohydrate kinase domain-containing protein	5.50	2.91E-02
c82836_g1_i1	<i>XP_970733.2</i>	similar to CG7368 CG7368-PB	17.07	1.35E-02
c82842_g1_i1	<i>ERG31</i>	C-5 sterol desaturase erg31	16.04	7.90E-06
c82856_g1_i1	<i>TI50C</i>	Mitochondrial import inner membrane translocase subunit TIM50-C	38.97	1.06E-12
c82890_g1_i1	<i>RT26</i>	Probable 28S ribosomal protein S26, mitochondrial	2.23	3.37E-02
c82925_g1_i2	<i>MLR</i>	Myosin regulatory light chain 2	2.28	2.05E-02
c82945_g1_i1	<i>CU198</i>	Cuticle protein 19.8	14.28	1.62E-02
c82978_g1_i2	<i>ENN76642.</i>	hypothetical protein YQE_06821, partia	10.63	4.23E-02
c83029_g1_i1	<i>EFC10</i>	EF-hand calcium-binding domain-containing protein 10	22.88	2.04E-05
c83133_g1_i1	<i>ENN75517.1</i>	hypothetical protein YQE_07861, partial	9.06	5.03E-03
c83159_g1_i1	<i>SNMP2</i>	Sensory neuron membrane protein 2	41.40	1.26E-07
c83169_g1_i1	<i>KIF2A</i>	Kinesin-like protein KIF2A	11.90	1.02E-02
c83191_g1_i1	<i>C49A1</i>	Probable cytochrome P450 49a1	102.17	6.78E-10
c83213_g1_i1	<i>MAATI</i>	Protein MAATS1	8.34	2.36E-04
c83260_g1_i1	<i>EFA02430.1</i>	hypothetical protein TcasGA2_TC008117	26.65	1.46E-04
c83312_g1_i1	<i>VSPSN</i>	Snake venom serine protease salmobin	61.67	4.13E-16
c83391_g1_i1	<i>HPPD</i>	4-hydroxyphenylpyruvate dioxygenase	6.09	8.73E-03
c83396_g1_i1	<i>GPDM</i>	Glycerol-3-phosphate dehydrogenase, mitochondrial	2.49	8.91E-03
c83416_g1_i1	<i>XP_973703.1</i>	similar to conserved hypothetical protein	5.86	1.20E-04

c83448_g1_i1	<i>ENN76414.1</i>	hypothetical protein YQE_07075, partial	#DIV/0!	1.33E-10
c83472_g2_i1	<i>XP_001811836.1</i>	similar to Cuticular protein 97Ea CG6131-PA	13.15	1.01E-03
c83490_g1_i2	<i>FAHD1</i>	Acylpyruvase FAHD1, mitochondrial	2.82	2.56E-02
c83493_g1_i1	<i>C1116</i>	UPF0691 protein C9orf116	52.42	5.07E-12
c83496_g1_i1	<i>CUO6</i>	Cuticle protein 6	3.77	1.39E-03
c83511_g1_i2	<i>TUSC3</i>	Tumor suppressor candidate 3	2.38	4.23E-02
c83518_g1_i2	<i>CTR</i>	Chymotrypsin	23.60	3.40E-05
c83520_g1_i1	<i>RMD1</i>	Regulator of microtubule dynamics protein 1	9.41	1.69E-03
c83526_g1_i2	<i>ERDL6</i>	Sugar transporter ERD6-like 6	29.51	3.81E-07
c83529_g1_i1	<i>PNPH</i>	Purine nucleoside phosphorylase	3.53	4.82E-02
c83589_g1_i1	<i>ENN72895.1</i>	hypothetical protein YQE_10465, partial	39.92	3.78E-11
c83595_g1_i1	<i>ENN71505.1</i>	hypothetical protein YQE_11798, partial	22.38	1.29E-03
c83609_g1_i1	<i>PABP1</i>	Polyadenylate-binding protein 1	38.78	3.91E-08
c83613_g1_i1	<i>ENN77148.1</i>	hypothetical protein YQE_06287, partial	115.29	1.63E-02
c83626_g1_i1	<i>CUL4A</i>	Cullin-4A	10.21	5.95E-04
c83642_g1_i1	<i>REG2</i>	Rhythmically expressed gene 2 protein	4.53	3.54E-05
c83678_g1_i1	<i>PDII</i>	Putative protein disulfide-isomerase C1F5.02	3.59	8.70E-03
c83688_g1_i2	<i>CATB</i>	Cathepsin B	240.11	1.61E-03
c83706_g1_i3	<i>PNPH</i>	Purine nucleoside phosphorylase	4.99	1.40E-02
c83723_g1_i1	<i>ENN80557.1</i>	hypothetical protein YQE_03022, partial	#DIV/0!	9.30E-05
c83728_g1_i1	<i>EFZ15369.1</i>	hypothetical protein SINV_14639	27.87	2.44E-13
c83755_g1_i2	<i>TPSA</i>	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] A2 SV=1	2.04	4.92E-02
c83767_g1_i1	<i>GLBL3</i>	Beta-galactosidase-1-like protein 3	6.55	2.48E-02
c83786_g1_i3	<i>XP_970541.1</i>	similar to CG3706 CG3706-P	3.88	1.69E-02
c83800_g2_i1	<i>NN77876.1</i>	hypothetical protein YQE_05554, partial	#DIV/0!	5.90E-03
c83803_g1_i1	<i>MED6</i>	Mediator of RNA polymerase II transcription subunit 6	2.32	4.47E-02
c83822_g1_i1	<i>ATPG</i>	ATP synthase subunit gamma, mitochondrial	2.22	1.93E-02
c83824_g1_i2	<i>MORN5</i>	MORN repeat-containing protein 5	42.51	4.15E-07
c83862_g1_i1	<i>HCN2</i>	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2	53.14	2.45E-08
c83889_g1_i1	<i>Y1674</i>	Uncharacterized protein Saci1674	6.93	3.94E-02

c83893_g2_i1	<i>XP_971263.</i>	similar to armadillo repeat containing 3	#DIV/0!	2.03E-02
c83942_g1_i1	<i>EFA01544.1</i>	hypothetical protein TcasGA2_TC00710	#DIV/0!	1.21E-04
c83959_g1_i1	<i>NRF6</i>	Nose resistant to fluoxetine protein 6	4.47	3.91E-02
c83962_g1_i4	<i>PHKG2</i>	Phosphorylase b kinase gamma catalytic chain, liver/testis isoform	2.38	1.85E-02
c83966_g2_i1	<i>ODF3A</i>	Outer dense fiber protein 3	29.32	3.45E-15
c84027_g1_i1	<i>CHIT</i>	Endochitinase	10.81	2.91E-05
c84063_g1_i1	<i>GST1</i>	Glutathione S-transferase	2.50	7.63E-03
c84115_g1_i1	<i>LCA5L</i>	Lebercilin-like protein	#DIV/0!	5.14E-06
c84146_g1_i1	<i>TTPAL</i>	Alpha-tocopherol transfer protein-like	4.95	3.56E-02
c84328_g1_i1	<i>PGDH</i>	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	4.74	3.92E-04
c84331_g1_i1	<i>ENN73465.1</i>	hypothetical protein YQE_09920, partial	5.64	7.81E-05
c84338_g1_i1	<i>TKTL2</i>	Transketolase-like protein 2	2.55	3.85E-02
c84359_g1_i1	<i>LIPH</i>	Lipase member H	4.04	2.03E-02
c84387_g1_i1	<i>ENN83608.1</i>	hypothetical protein YQE_00037, partial	36.87	4.79E-17
c84402_g1_i1	<i>TBC19</i>	TBC1 domain family member 19	52.79	2.90E-11
c84405_g1_i1	<i>WDR34</i>	WD repeat-containing protein 34	2.85	8.62E-03
c84410_g2_i1	<i>ENN78369.1</i>	hypothetical protein YQE_05171, partia	7.59	2.05E-02
c84443_g1_i1	<i>XP_966410.1</i>	hypothetical protein YQE_08018, partial	47.02	1.61E-12
c84518_g1_i1	<i>HXK2</i>	Hexokinase type 2	51.37	2.20E-19
c84523_g1_i1	<i>TRY1</i>	Trypsin-1	95.90	1.80E-09
c84547_g1_i2	<i>OAT</i>	Ornithine aminotransferase, mitochondrial	3.36	2.51E-03
c84560_g2_i1	<i>ZN596</i>	Zinc finger protein 596	19.49	1.64E-06
c84563_g1_i1	<i>ECHD3</i>	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial	3.71	3.67E-02
c84584_g1_i1	<i>MFD6A</i>	Major facilitator superfamily domain-containing protein 6-A	3.16	5.53E-03
c84622_g1_i1	<i>BAM17691.1</i>	cuticular protein PxutCPT	6.02	1.31E-02
c84626_g1_i1	<i>DJB13</i>	DnaJ homolog subfamily B member 13	124.14	1.64E-08
c84649_g1_i1	<i>ENN72830.1</i>	hypothetical protein YQE_10633, partia	14.70	1.88E-02
c84659_g1_i1	<i>CC113</i>	Coiled-coil domain-containing protein 113	#DIV/0!	7.72E-03
c84665_g1_i1	<i>HEAT2</i>	HEAT repeat-containing protein 2	3.12	6.18E-03
c84674_g1_i1	<i>GSB</i>	Protein gooseberry	2.41	4.99E-02

c84681_g1_i1	<i>NRF6</i>	Nose resistant to fluoxetine protein 6	3.42	3.84E-02
c84683_g1_i1	<i>CATL</i>	Cathepsin L	184.91	1.37E-07
c84764_g1_i3	<i>FBXL7</i>	F-box/LRR-repeat protein 7	2.36	4.52E-02
c84804_g1_i1	<i>DRD2L</i>	Dopamine D2-like receptor	3.50	1.04E-02
c84808_g1_i2	<i>ESTF</i>	Esterase FE4	6.53	1.45E-04
c84820_g1_i1	<i>XP_003708211.1</i>	sperm flagellar protein 2-like	14.61	2.84E-04
c84856_g2_i1	<i>ELVL1</i>	Elongation of very long chain fatty acids protein AAEL008004	3.15	1.58E-02
c84868_g1_i1	<i>TRY4</i>	Trypsin-4 OS=Anopheles gambiae	2.09	4.42E-02
c84917_g1_i1	<i>ENN75467.1</i>	hypothetical protein YQE_08016, partial	15.79	1.99E-03
c84927_g1_i1	<i>TTPA</i>	Alpha-tocopherol transfer protein	4.87	1.36E-02
c84957_g1_i1	<i>TILB</i>	Protein tilB homolog	87.40	1.67E-06
c84970_g1_i1	<i>EFA01945.1</i>	hypothetical protein TcasGA2_TC007559	29.38	8.66E-06
c84972_g1_i1	<i>DYH7</i>	Dynein heavy chain 7, axonemal	19.92	6.18E-03
c84988_g1_i1	<i>ENN71116.1</i>	hypothetical protein YQE_12049, partial	45.75	1.37E-08
c85005_g1_i1	<i>TALDO</i>	Transaldolase	2.30	3.17E-02
c85007_g1_i1	<i>IQCA1</i>	IQ and AAA domain-containing protein 1	36.80	5.71E-06
c85026_g1_i1	<i>XP_002425066.1</i>	hypothetical protein Phum_PHUM171650	5.13	1.81E-04
c85042_g1_i2	<i>PE1</i>	Peritrophin-1	66.12	4.98E-06
c85044_g2_i1	<i>ENN72569.1</i>	hypothetical protein YQE_10794, partial	24.02	1.49E-11
c85051_g1_i1	<i>ENN76522.1</i>	hypothetical protein YQE_06973, partial	45.74	2.68E-19
c85058_g1_i1	<i>EFA09111.1</i>	hypothetical protein TcasGA2_TC01548	24.15	7.92E-09
c85060_g1_i1	<i>LRP1B</i>	Low-density lipoprotein receptor-related protein 1B	2.76	1.86E-02
c85073_g1_i1	<i>BTBD1</i>	BTB/POZ domain-containing protein 18	11.26	8.15E-05
c85079_g2_i2	<i>PAR1</i>	Serine/threonine-protein kinase par-1	6.97	1.09E-05
c85109_g1_i1	<i>FBX39</i>	F-box only protein 39	4.08	2.04E-03
c85186_g1_i1	<i>ENN71240.1</i>	hypothetical protein YQE_12167, partial	11.05	1.20E-06
c85194_g1_i1	<i>ENN71636.1</i>	hypothetical protein YQE_11734, partial	66.58	1.79E-05
c85196_g1_i1	<i>ENN75524.1</i>	hypothetical protein YQE_07867, partial	24.78	3.14E-15
c85200_g1_i1	<i>KBP</i>	Protein KBP homolog	43.59	6.21E-17
c85208_g1_i1	<i>ARMC2</i>	Armadillo repeat-containing protein 2	20.46	3.75E-07

c85213_g6_i1	<i>FTN</i>	Flightin	3.76	3.52E-02
c85229_g1_i2	<i>SC6A4</i>	Sodium-dependent serotonin transporter	71.59	1.13E-03
c85248_g1_i1	<i>FXRDI</i>	FAD-dependent oxidoreductase domain-containing protein 1	2.69	6.88E-03
c85269_g1_i2	<i>PGDH</i>	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	#DIV/0!	4.10E-12
c85271_g1_i1	<i>ODPA</i>	Probable pyruvate dehydrogenase E1 component subunit alpha, mitochondrial	48.16	9.03E-09
c85289_g1_i1	<i>PRDX4</i>	Peroxiredoxin-4	9.14	1.30E-03
c85304_g1_i1	<i>ENN81933.1</i>	hypothetical protein YQE_01644, partial	47.31	4.50E-18
c85322_g1_i1	<i>NDUS7</i>	Probable NADH dehydrogenase [ubiquinone] non-sulfur protein 7, mitochondrial	17.33	8.40E-07
c85325_g1_i2	<i>TAF4</i>	Transcription initiation factor TFIID subunit 4	#DIV/0!	9.24E-05
c85364_g1_i1	<i>CEP78</i>	Protein Cep78 homolog	#DIV/0!	6.05E-08
c85366_g1_i1	<i>XP_003704058.1</i>	uncharacterized protein LOC100883287	40.86	1.25E-03
c85369_g1_i1	<i>PUR6</i>	Multifunctional protein ADE2	2.33	1.29E-02
c85370_g1_i1	<i>ENN74906.1</i>	hypothetical protein YQE_08484, partial	2.06	3.81E-02
c85385_g1_i1	<i>DYH10</i>	Dynein heavy chain 10, axonemal	4.04	1.59E-02
c85398_g1_i1	<i>XP_975933.1</i>	hypothetical protein	4.51	1.07E-02
c85401_g1_i1	<i>RAD51</i>	DNA repair protein RAD51 homolog 1	2.45	3.15E-02
c85439_g1_i1	<i>S2611</i>	Sodium-independent sulfate anion transporter	6.78	2.16E-02
c85444_g1_i1	<i>NN81733.1</i>	hypothetical protein YQE_01872, partial	2.91	1.53E-02
c85448_g1_i2	<i>TRY7</i>	Trypsin-7	4.45	2.23E-02
c85488_g1_i1	<i>XP_974758.1</i>	similar to centrosomal protein 290	15.56	2.41E-06
c85506_g2_i1	<i>EEZ98110.1</i>	hypothetical protein TcasGA2_TC000526	34.43	1.15E-12
c85508_g2_i1	<i>PAQR4</i>	Progesterin and adipoQ receptor family member 4	16.37	3.43E-06
c85515_g1_i1	<i>HGD</i>	Homogentisate 1,2-dioxygenase	2.60	3.28E-02
c85545_g1_i2	<i>CU22</i>	Larval cuticle protein LCP-22	14.32	1.64E-02
c85553_g1_i1	<i>CCD94</i>	Coiled-coil domain-containing protein 94	21.89	8.58E-15
c85557_g1_i1	<i>PYC1</i>	Pyruvate carboxylase 1	2.34	1.57E-02
c85557_g2_i1	<i>PYC</i>	Pyruvate carboxylase, mitochondrial	2.08	2.83E-02
c85559_g1_i1	<i>PCY1B</i>	Choline-phosphate cytidyltransferase B	5.57	6.21E-05
c85565_g1_i1	<i>NDUS4</i>	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	2.55	1.16E-02
c85590_g1_i2	<i>TRET1</i>	Facilitated trehalose transporter Tret1	2.96	2.91E-03

c85601_g1_i2	<i>RFX3</i>	Transcription factor RFX3	3.58	4.42E-03
c85611_g1_i1	<i>DHSO</i>	Sorbitol dehydrogenase	11.81	9.99E-03
c85638_g1_i1	<i>EFA00638.1</i>	hypothetical protein TcasGA2_TC003514	3.40	4.52E-03
c85644_g1_i2	<i>4CL3</i>	Probable 4-coumarate--CoA ligase 3	4.04	1.85E-02
c85659_g1_i2	<i>PO11</i>	Retrovirus-related P10 polyprotein from type-1 retrotransposable element RT1 (Eragrostis)	3.36	3.97E-02
c85671_g2_i2	<i>XP_966903.1</i>	similar to 10G08	3.73	1.30E-02
c85706_g1_i1	<i>BPHL</i>	Valacyclovir hydrolase	3.48	9.35E-03
c85727_g1_i2	<i>CF165</i>	UPF0704 protein C6orf165	75.01	4.58E-07
c85764_g1_i1	<i>LIP1</i>	Lipase 1	50.62	8.06E-05
c85811_g2_i1	<i>CT026</i>	Uncharacterized protein C20orf26	20.47	2.82E-04
c85826_g1_i1	<i>CUL4A</i>	Cullin-4A	17.06	1.43E-02
c85829_g1_i2	<i>TRET1</i>	Facilitated trehalose transporter Tret1	4.32	5.64E-03
c85840_g1_i1	<i>ENN78538.1</i>	hypothetical protein YQE_05003, partial	6.13	9.71E-05
c85852_g1_i2	<i>SAHH</i>	Adenosylhomocysteinase	3.20	7.19E-04
c85861_g1_i1	<i>ARSB</i>	Arylsulfatase B	5.04	4.19E-03
c85862_g1_i1	<i>ARD1</i>	D-arabinitol dehydrogenase 1	3.36	2.79E-02
c85866_g1_i2	<i>ENN70834.1</i>	hypothetical protein YQE_12498, partial	14.84	9.76E-03
c85874_g1_i1	<i>CATL</i>	Cathepsin L	3.56	2.81E-02
c85902_g1_i1	<i>NN81589.1</i>	hypothetical protein YQE_01999, partial	#DIV/0!	9.81E-12
c85911_g1_i1	<i>SMOX</i>	Spermine oxidase	63.35	5.03E-20
c85926_g2_i1	<i>TEKT1</i>	Tektin-1	52.55	1.15E-07
c85930_g1_i1	<i>CTRB2</i>	Chymotrypsin BII	2.84	4.94E-03
c85948_g1_i1	<i>EFA04347.1</i>	hypothetical protein TcasGA2_TC014643	#DIV/0!	9.49E-06
c85991_g1_i1	<i>CCD39</i>	Coiled-coil domain-containing protein 39	4.38	9.29E-04
c86028_g1_i4	<i>E74EA</i>	Ecdysone-induced protein 74EF isoform A	2.60	3.41E-03
c86029_g1_i1	<i>PE1</i>	Peritrophin-1	5.37	2.39E-03
c86033_g2_i1	<i>GBA3</i>	Cytosolic beta-glucosidase	144.02	2.93E-04
c86036_g1_i1	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	3.21	5.60E-03
c86048_g1_i1	<i>6PGD</i>	6-phosphogluconate dehydrogenase, decarboxylating	2.42	3.30E-02
c86067_g1_i1	<i>VNNL3</i>	Vanin-like protein 3	6.23	4.53E-07

c86129_g1_i1	<i>C6A23</i>	Probable cytochrome P450 6a23	2.39	1.85E-02
c86134_g1_i2	<i>APTX</i>	Aprataxin	7.81	3.21E-02
c86139_g1_i1	<i>TNNT</i>	Troponin T	2.41	7.35E-03
c86179_g1_i1	<i>EFA06870.1</i>	hypothetical protein TcasGA2_TC00981	19.05	2.93E-07
c86191_g1_i1	<i>RSPH3</i>	Radial spoke head protein 3 homolog	6.01	1.38E-05
c86260_g1_i1	<i>EFTU</i>	Elongation factor Tu, mitochondrial	2.10	4.18E-02
c86266_g1_i2	<i>NSUN7</i>	Putative methyltransferase NSUN7	75.89	3.98E-10
c86317_g1_i1	<i>PO11</i>	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R1 (Fragment)	3.79	2.78E-02
c86329_g1_i1	<i>ATAT</i>	Alpha-tubulin N-acetyltransferase	2.63	8.32E-03
c86340_g1_i1	<i>BAA78480.</i>	56 kDa early-staged encapsulation-inducing protein	2.26	3.10E-02
c86343_g1_i1	<i>EFA08508.1</i>	hypothetical protein TcasGA2_TC006160	4.87	2.68E-03
c86358_g2_i1	<i>RIBC2</i>	RIB43A-like with coiled-coils protein 2	20.79	4.77E-11
c86362_g1_i1	<i>HCNI</i>	potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1	38.60	1.90E-02
c86379_g1_i1	<i>PDE10</i>	cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A	22.14	4.56E-11
c86419_g1_i3	<i>MFD6A</i>	Major facilitator superfamily domain-containing protein 6-A	3.42	1.76E-03
c86421_g1_i4	<i>MYCB2</i>	Probable E3 ubiquitin-protein ligase MYCBP2	5.21	5.53E-03
c86424_g1_i1	<i>XP_972388.2</i>	similar to quick-to-court	2.57	1.64E-02
c86458_g1_i1	<i>MPPB</i>	Mitochondrial-processing peptidase subunit beta	2.06	4.66E-02
c86460_g1_i1	<i>EEZ97824.1</i>	hypothetical protein TcasGA2_TC000191	61.61	6.63E-09
c86471_g1_i5	<i>FBX36</i>	F-box only protein 36	6.67	2.88E-03
c86499_g1_i1	<i>RAD54</i>	DNA repair and recombination protein RAD54-like	2.21	2.76E-02
c86516_g1_i1	<i>DRC1</i>	Dynein regulatory complex protein 1	39.04	1.90E-14
c86519_g1_i1	<i>NUD14</i>	Uridine diphosphate glucose pyrophosphatase	3.13	4.85E-02
c86541_g2_i2	<i>PGLR</i>	Polygalacturonase	2.31	1.03E-02
c86549_g1_i2	<i>ENN79794.1</i>	hypothetical protein YQE_03850, partial	5.28	2.02E-05
c86571_g1_i4	<i>GAGT3</i>	Gamma-glutamyltranspeptidase 3	28.84	7.69E-08
c86586_g2_i2	<i>GBA3</i>	Cytosolic beta-glucosidase	5.94	9.48E-03
c86605_g1_i1	<i>FBLN5</i>	Fibulin-5	3.91	8.21E-03
c86613_g1_i1	<i>ATTY</i>	Tyrosine aminotransferase	5.14	3.52E-02

c86613_g2_i1	<i>ATTY</i>	Tyrosine aminotransferase	4.32	7.13E-04
c86615_g1_i2	<i>RDHE2</i>	Epidermal retinol dehydrogenase 2	2.42	1.33E-02
c86624_g1_i3	<i>RSH4A</i>	Radial spoke head protein 4 homolog A	16.53	3.74E-04
c86626_g1_i1	<i>PEI</i>	Peritrophin-1	43.11	6.05E-13
c86628_g2_i1	<i>EFA12741.1</i>	EFA12741.1 Rm62	49.97	5.12E-03
c86638_g1_i2	<i>CCD11</i>	Coiled-coil domain-containing protein 11	11.14	5.90E-05
c86652_g1_i1	<i>AASS</i>	Alpha-aminoadipic semialdehyde synthase, mitochondrial	5.78	1.02E-02
c86658_g1_i1	<i>IQUB</i>	IQ and ubiquitin-like domain-containing protein	41.32	1.24E-11
c86737_g1_i1	<i>CCD19</i>	Coiled-coil domain-containing protein 19, mitochondrial	31.69	4.27E-11
c86752_g2_i1	<i>ROP1L</i>	Ropporin-1-like protein	17.40	3.57E-08
c86759_g2_i1	<i>DYXC1</i>	Dyslexia susceptibility 1 candidate gene 1 protein homolog	4.64	6.68E-05
c86768_g2_i1	<i>HPSE</i>	Heparanase	8.83	6.97E-04
c86782_g1_i1	<i>ALDR</i>	Aldose reductase	2.38	2.40E-02
c86790_g1_i1	<i>ATPB</i>	ATP synthase subunit beta, mitochondrial	2.12	2.77E-02
c86832_g7_i1	<i>MMP24</i>	Matrix metalloproteinase-24	3.07	1.63E-03
c86839_g1_i2	<i>XP_003701630.</i>	major antigen-like	43.37	2.89E-05
c86857_g1_i1	<i>SCRA</i>	Alpha-scruin	21.90	1.91E-06
c86866_g1_i1	<i>IFT80</i>	Intraflagellar transport protein 80 homolog	37.71	1.96E-06
c86876_g1_i1	<i>CAH2</i>	Carbonic anhydrase 2	65.62	5.61E-11
c86882_g1_i1	<i>CALCR</i>	Calcitonin receptor	3.01	2.67E-02
c86907_g1_i1	<i>CGT</i>	2-hydroxyacylsphingosine 1-beta-galactosyltransferase	6.76	8.42E-07
c86980_g1_i1	<i>NDK5</i>	Nucleoside diphosphate kinase homolog 5	22.37	1.76E-09
c87020_g1_i1	<i>ODP2</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	3.57	1.95E-02
c87025_g1_i1	<i>CUD1</i>	Endocuticle structural glycoprotein SgAbd-1	23.70	7.69E-03
c87059_g1_i4	<i>ERIC2</i>	Glutamate-rich protein 2	3.55	8.80E-03
c87077_g2_i1	<i>Y4893</i>	TPPP family protein CG4893	10.56	3.61E-05
c87095_g1_i1	<i>PICO</i>	Putative inorganic phosphate cotransporter	67.55	8.95E-15
c87116_g1_i4	<i>TM189</i>	Transmembrane protein 189	3.27	3.39E-03
c87140_g1_i1	<i>CNBD2</i>	Cyclic nucleotide-binding domain-containing protein 2	21.91	6.35E-05

c87168_g1_i1	<i>ARMC4</i>	Armadillo repeat-containing protein 4	7.53	9.91E-04
c87182_g1_i1	<i>KLH10</i>	Kelch-like protein 10	26.63	1.80E-14
c87232_g1_i2	<i>POLR</i>	Retrovirus-related P10 polyprotein from type-2 retrotransposable element P10DM	3.13	4.86E-02
c87237_g1_i1	<i>TRET1</i>	Facilitated trehalose transporter Tret1	3.34	3.52E-02
c87273_g1_i1	<i>CBPB</i>	Carboxypeptidase B	28.55	2.18E-12
c87283_g1_i1	<i>EFA07368.1</i>	hypothetical protein TcasGA2_TC016343	123.52	1.19E-11
c87294_g1_i2	<i>KC1G1</i>	Casein kinase I isoform gamma-1	33.21	6.11E-06
c87341_g1_i1	<i>IQCG</i>	IQ domain-containing protein G	29.68	3.70E-05
c87373_g1_i2	<i>LIN41</i>	E3 ubiquitin-protein ligase TRIM71	22.31	1.88E-12
c87381_g2_i2	<i>ELU07542.1</i>	hypothetical protein CAPTEDRAFT_48911, partial	3.29	2.39E-02
c87411_g1_i2	<i>GATA3</i>	Transcription factor GATA-3	2.91	1.75E-03
c87448_g2_i1	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	3.11	1.94E-03
c87527_g3_i1	<i>GAGXE</i>	Nucleic-acid-binding protein from transposon X-element	3.02	3.33E-02
c87561_g1_i6	<i>TRET1</i>	Facilitated trehalose transporter Tret1	88.34	2.02E-08
c87595_g7_i2	<i>WDR92</i>	WD repeat-containing protein 92	11.35	1.95E-04
c87607_g1_i1	<i>ALG2</i>	Alpha-1,3/1,6-mannosyltransferase ALG2	38.28	1.06E-09
c87621_g1_i1	<i>KII0A</i>	Kinesin-like protein Klp10A	5.23	1.97E-05
c87623_g1_i2	<i>EFA10064.1</i>	hypothetical protein TcasGA2_TC012238	24.12	1.12E-11
c87633_g1_i1	<i>APY</i>	Apyrase	6.64	1.40E-02
c87642_g1_i4	<i>DYH10</i>	Dynein heavy chain 10, axonemal	4.63	3.06E-02
c87651_g2_i2	<i>CUA2B</i>	Larval cuticle protein A2B	3.54	9.78E-03
c87672_g1_i1	<i>P_970545.1</i>	similar to AGAP006068-PA	2.35	1.82E-02
c87691_g1_i1	<i>EFA04034.1</i>	hypothetical protein TcasGA2_TC014263	24.94	1.35E-13
c87725_g1_i1	<i>DYH12</i>	Dynein heavy chain 12, axonemal	29.53	5.42E-05
c87726_g1_i1	<i>CH60</i>	60 kDa heat shock protein, mitochondrial	2.04	4.29E-02
c87731_g1_i1	<i>DYH5</i>	Dynein heavy chain 5, axonemal	43.44	2.33E-07
c87735_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	17.21	3.96E-11
c87746_g1_i1	<i>KAPCA</i>	cAMP-dependent protein kinase catalytic subunit alpha	8.50	2.01E-07
c87787_g1_i1	<i>P_001809722.1</i>	similar to Muscle-specific protein 300 CG33715-PD	5.29	6.28E-03
c87860_g1_i2	<i>MAL1</i>	Maltase 1	3.32	2.86E-02

c87879_g1_i1	<i>CBPA1</i>	Zinc carboxypeptidase A 1	94.55	2.60E-06
c87899_g1_i1	<i>ODFP2</i>	Outer dense fiber protein 2	61.85	1.44E-16
c87938_g1_i1	<i>EFA06601.1</i>	hypothetical protein TcasGA2_TC009516	94.14	2.90E-18
c87944_g1_i1	<i>ARH</i>	Low density lipoprotein receptor adapter protein 1	2.51	8.41E-03
c87989_g1_i4	<i>ENN78543.1</i>	hypothetical protein YQE_04993, partial	4.55	3.10E-02
c88036_g1_i2	<i>CUBN</i>	Cubilin	7.54	1.42E-02
c88044_g1_i1	<i>SBPIA</i>	Selenium-binding protein 1-A	7.49	1.47E-04
c88053_g2_i1	<i>LRP3</i>	Low-density lipoprotein receptor-related protein 3	12.61	8.26E-03
c88068_g1_i1	<i>CCNA</i>	G2/mitotic-specific cyclin-A	6.59	1.05E-04
c88119_g1_i1	<i>GPDA</i>	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	2.22	1.81E-02
c88122_g1_i1	<i>PPR36</i>	Protein phosphatase 1 regulatory subunit 36	2.35	4.75E-02
c88205_g1_i3	<i>NOVA1</i>	RNA-binding protein Nova-1	5.15	7.24E-06
c88210_g1_i1	<i>DPYD</i>	Dihydropyrimidine dehydrogenase [NADP(+)]	2.18	3.59E-02
c88212_g1_i2	<i>XP_976368.1</i>	hypothetical protein TcasGA2_TC011931	53.73	2.59E-21
c88264_g1_i1	<i>PUR8</i>	Adenylosuccinate lyase	4.62	5.42E-03
c88287_g1_i2	<i>DAAF1</i>	Dynein assembly factor 1, axonemal	25.50	1.16E-12
c88309_g1_i1	<i>SRY</i>	Sex-determining region Y protein	53.01	4.02E-09
c88310_g1_i1	<i>GANAB</i>	Neutral alpha-glucosidase AB	10.92	8.13E-04
c88328_g1_i1	<i>ODPA</i>	Pyruvate dehydrogenase E1 component subunit alpha type I, mitochondrial	77.30	2.83E-14
c88334_g1_i1	<i>ENN80109.1</i>	hypothetical protein YQE_03468, partial	10.16	1.06E-07
c88343_g1_i1	<i>Y2R2</i>	Putative 115 kDa protein in type-1 retrotransposable element R1DM	2.85	4.46E-02
c88347_g1_i1	<i>ENN75023.1</i>	hypothetical protein YQE_08338, partial	99.38	4.32E-18
c88351_g1_i1	<i>MOT12</i>	Monocarboxylate transporter 12	3.44	1.94E-02
c88361_g1_i1	<i>GCDH</i>	Glutaryl-CoA dehydrogenase, mitochondrial	2.47	7.77E-03
c88376_g1_i1	<i>ODPB</i>	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	2.24	4.77E-02
c88387_g1_i3	<i>CSRP3</i>	Cysteine and glycine-rich protein 3	56.50	6.52E-16
c88397_g1_i1	<i>ENOF1</i>	Mitochondrial enolase superfamily member 1	2.55	1.56E-02
c88429_g1_i1	<i>XP_002054537.1</i>	GJ22753	110.48	7.25E-11
c88448_g1_i1	<i>DHE3</i>	Glutamate dehydrogenase, mitochondrial	#DIV/0!	1.28E-09
c88527_g3_i3	<i>NAKD2</i>	NAD kinase 2, mitochondrial	2.24	2.45E-02

c88546_g2_i1	<i>UPP2</i>	Uridine phosphorylase 2	4.83	1.20E-02
c88568_g2_i1	<i>STIE1</i>	Estrogen sulfotransferase	22.37	1.85E-05
c88581_g1_i1	<i>TEKT4</i>	Tektin-4	43.39	8.83E-17
c88589_g1_i1	<i>KPYM</i>	Pyruvate kinase PKM	54.30	1.84E-17
c88605_g1_i1	<i>EEZ97553.1</i>	hypothetical protein TcasGA2_TC011403	5.40	2.69E-02
c88640_g2_i2	<i>DYI2</i>	Dynein intermediate chain 2, ciliary	10.27	1.26E-06
c88653_g1_i2	<i>NN79208.1</i>	hypothetical protein YQE_04392, partial	164.30	1.09E-07
c88655_g2_i5	<i>OTOF</i>	Otoferlin	8.97	3.68E-05
c88670_g1_i1	<i>EFHC1</i>	EF-hand domain-containing protein 1	15.28	1.47E-03
c88732_g1_i1	<i>FA11679.1</i>	hypothetical protein TcasGA2_TC008543	9.37	9.51E-03
c88759_g1_i1	<i>SRCA</i>	Sarcalumenin	2.01	4.99E-02
c88760_g1_i6	<i>CD22</i>	B-cell receptor CD22	2.38	3.38E-02
c88816_g3_i1	<i>ENN77568.1</i>	hypothetical protein YQE_05864, partial	4.84	5.06E-03
c88869_g2_i1	<i>AMPL</i>	Cytosol aminopeptidase	29.98	5.26E-17
c88874_g2_i1	<i>CO9A1</i>	Collagen alpha-1(IX) chain	20.27	2.23E-12
c88874_g1_i1	<i>XP_392960.4</i>	collagen alpha-2(IV) chain-like	2.54	1.29E-02
c88878_g1_i1	<i>TITIN</i>	Titin	5.55	2.58E-04
c88881_g1_i1	<i>PUR2</i>	Trifunctional purine biosynthetic protein adenosine-3	4.45	1.75E-02
c88901_g3_i2	<i>FKBP2</i>	FK506-binding protein 2	2.06	3.35E-02
c88919_g1_i1	<i>GABT</i>	4-aminobutyrate aminotransferase, mitochondrial	73.65	6.62E-13
c88940_g5_i1	<i>WDR63</i>	WD repeat-containing protein 63	24.41	9.73E-06
c88993_g3_i1	<i>EFA04937.1</i>	hypothetical protein TcasGA2_TC015004	7.33	3.17E-05
c88995_g1_i1	<i>MDHM</i>	Malate dehydrogenase, mitochondrial	2.61	2.16E-02
c89005_g1_i3	<i>NN81852.</i>	hypothetical protein YQE_01790, partial	68.28	2.18E-23
c89022_g1_i2	<i>KEN</i>	Probable transcription factor Ken (Fragment)	8.50	1.05E-02
c89056_g1_i1	<i>XP_001866279.1</i>	conserved hypothetical protein	9.81	1.51E-04
c89059_g2_i1	<i>NKCL</i>	Bumetanide-sensitive sodium-(potassium)-chloride cotransporter	2.21	3.05E-02
c89063_g2_i1	<i>TESK2</i>	Dual specificity testis-specific protein kinase 2	9.48	1.25E-03
c89075_g1_i1	<i>FD4</i>	Fork head domain-containing protein FD4	2.06	4.18E-02
c89106_g1_i2	<i>PR3CB</i>	Protein phosphatase 1 regulatory subunit 3C-B	4.85	1.03E-05

c89111_g2_i2	<i>TAF5</i>	Transcription initiation factor TFIID subunit 5	4.39	6.57E-04
c89161_g1_i6	<i>PCTL</i>	PCTP-like protein	5.41	1.03E-04
c89176_g1_i1	<i>CGL</i>	Cystathionine gamma-lyase	2.59	4.74E-02
c89178_g1_i5	<i>PICO</i>	Putative inorganic phosphate cotransporter	5.24	1.04E-03
c89180_g1_i3	<i>NOTCH</i>	Neurogenic locus notch protein homolog	4.79	9.18E-03
c89198_g5_i1	<i>GILT</i>	Gamma-interferon-inducible lysosomal thiol reductase	10.25	2.72E-05
c89246_g1_i1	<i>KLHL6</i>	Kelch-like protein 6	53.21	1.96E-09
c89266_g2_i4	<i>AMPN</i>	Aminopeptidase N	3.03	1.58E-03
c89281_g1_i1	<i>ALS</i>	Insulin-like growth factor-binding protein complex acid labile subunit	2.15	4.06E-02
c89286_g1_i2	<i>EFA04464.1</i>	hypothetical protein TcasGA2_TC014768	35.42	1.38E-14
c89287_g1_i1	<i>TBA</i>	Tubulin alpha chain	13.57	1.59E-09
c89350_g1_i1	<i>ENN77178.1</i>	hypothetical protein YQE_06316, partial	3.94	1.01E-02
c89357_g1_i1	<i>P5CS</i>	Delta-1-pyrroline-5-carboxylate synthase	3.16	4.37E-04
c89371_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	226.03	3.85E-11
c89413_g1_i2	<i>C6A18</i>	Probable cytochrome P450 6a18	2.42	4.71E-02
c89444_g1_i1	<i>ARGI2</i>	Arginase-2, mitochondrial	4.29	1.81E-04
c89458_g2_i1	<i>NAA60</i>	N-alpha-acetyltransferase 60	4.38	3.71E-04
c89465_g1_i1	<i>Y2R2</i>	Putative 115 kDa protein in type-1 retrotransposable element R1DM	2.22	3.38E-02
c89540_g2_i2	<i>ACO11</i>	Acyl-CoA Delta(11) desaturase	9.45	1.61E-02
c89558_g1_i1	<i>WDY</i>	WD repeat-containing protein on Y chromosome	142.57	2.32E-12
c89572_g2_i1	<i>FOXO</i>	Forkhead box protein O	3.06	4.25E-03
c89608_g1_i1	<i>EFA12914.1</i>	hypothetical protein TcasGA2_TC006984	46.71	1.77E-05
c89611_g2_i3	<i>DPP6</i>	Dipeptidyl aminopeptidase-like protein 6	4.01	9.35E-03
c89615_g1_i1	<i>ENN74040.1</i>	hypothetical protein YQE_09365, partial	33.89	3.29E-02
c89622_g2_i1	<i>TITIN</i>	Titin	2.39	1.08E-02
c89639_g3_i2	<i>IMPA1</i>	Inositol monophosphatase 1	3.39	5.05E-03
c89650_g1_i4	<i>NAC3</i>	Sodium/calcium exchanger 3	3.15	1.54E-03
c89653_g1_i2	<i>UN13D</i>	Protein unc-13 homolog D	2.46	6.51E-03
c89693_g2_i2	<i>EEZ98245.1</i>	hypothetical protein TcasGA2_TC000684	4.99	1.39E-03
c89710_g1_i1	<i>EGR4</i>	Early growth response protein 4	2.43	3.18E-02

c89731_g1_i1	<i>ENN78198.1</i>	hypothetical protein YQE_05350, partial	94.06	3.85E-05
c89767_g1_i1	<i>A1A1A</i>	Alcohol dehydrogenase [NADP(+)] A	4.67	2.06E-02
c89778_g2_i1	<i>EFA03938.1</i>	hypothetical protein TcasGA2_TC014079	44.15	1.11E-03
c89800_g1_i1	<i>C1117</i>	Uncharacterized protein C9orf117 homolog	135.45	5.98E-06
c89808_g1_i1	<i>EST6</i>	Venom carboxylesterase-6	7.81	3.77E-02
c89812_g1_i1	<i>CCD65</i>	Coiled-coil domain-containing protein 65	23.52	2.34E-08
c89824_g1_i1	<i>TLL6</i>	Tubulin polyglutamylase TLL6	103.45	6.16E-06
c89826_g1_i1	<i>KLH10</i>	Kelch-like protein 10	121.92	2.53E-23
c89852_g1_i2	<i>ENN79934.1</i>	hypothetical protein YQE_03630, partial	61.45	4.75E-19
c89888_g1_i1	<i>DET1</i>	DET1 homolog	2.29	3.53E-02
c89899_g1_i1	<i>EFCB1</i>	EF-hand calcium-binding domain-containing protein 1	#DIV/0!	6.91E-03
c89929_g1_i1	<i>DHSA</i>	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	59.30	1.42E-18
c89967_g2_i6	<i>RTBS</i>	Probable RNA-directed DNA polymerase from transposon BS	2.58	4.58E-02
c89971_g2_i1	<i>EEZ99627.1</i>	hypothetical protein TcasGA2_TC002146	37.93	2.77E-16
c89994_g1_i1	<i>OMB</i>	Optomotor-blind protein	2.12	2.58E-02
c90004_g1_i1	<i>ENN75344.1</i>	hypothetical protein YQE_08120, partial	22.57	5.09E-14
c90017_g1_i1	<i>HCN4</i>	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4	15.69	1.59E-04
c90025_g2_i4	<i>EFA10004.1</i>	hypothetical protein TcasGA2_TC012174	34.73	1.88E-14
c90106_g1_i4	<i>CREBA</i>	Cyclic AMP response element-binding protein A	2.29	2.24E-02
c90113_g1_i1	<i>KIF9</i>	Kinesin-like protein KIF9	32.12	4.83E-06
c90176_g1_i1	<i>GALT</i>	Probable galactose-1-phosphate uridylyltransferase	2.63	1.02E-02
c90183_g2_i1	<i>PR15A</i>	Protein phosphatase 1 regulatory subunit 15A	2.55	2.24E-02
c90186_g1_i1	<i>PHP</i>	Polyhomeotic-proximal chromatin protein	2.04	4.26E-02
c90198_g1_i1	<i>NOS</i>	Nitric oxide synthase	3.34	5.19E-03
c90226_g1_i3	<i>AXP83</i>	Axonemal 84 kDa protein	10.25	3.87E-04
c90232_g1_i3	<i>CSN2</i>	COP9 signalosome complex subunit 2	13.18	6.66E-05
c90248_g1_i1	<i>CC135</i>	Coiled-coil domain-containing protein lobo homolog	3.52	3.72E-02
c90268_g1_i6	<i>ENN76003.1</i>	hypothetical protein YQE_07383, partial	82.87	8.76E-25
c90290_g1_i1	<i>ENN79754.1</i>	hypothetical protein YQE_03810, partial	3.25	5.65E-03
c90300_g1_i1	<i>ENN77454.1</i>	hypothetical protein YQE_06278, partial	60.50	1.04E-11

c90316_g1_i2	<i>EEZ98963.1</i>	hypothetical protein TcasGA2_TC004817	6.27	3.06E-06
c90327_g1_i1	<i>SPEF2</i>	Sperm flagellar protein 2	13.92	2.40E-04
c90339_g2_i1	<i>Y2R2</i>	Putative 115 kDa protein in type-1 retrotransposable element R1DM	2.45	2.04E-02
c90343_g1_i3	<i>YK006</i>	Putative uncharacterized protein FLJ37770	2.76	3.17E-02
c90393_g1_i1	<i>DACH1</i>	Dachshund homolog 1	3.24	1.73E-03
c90415_g3_i3	<i>TSSK4</i>	Testis-specific serine/threonine-protein kinase 4	3.17	6.46E-03
c90440_g1_i5	<i>XP_001984547.1</i>	GH14966	4.55	1.98E-02
c90457_g1_i2	<i>5NTD</i>	Protein 5NUC	3.74	1.08E-04
c90486_g2_i9	<i>CAH1</i>	Carbonic anhydrase 1	5.08	4.53E-03
c90492_g3_i1	<i>MRP4</i>	Multidrug resistance-associated protein 4	3.29	7.08E-03
c90511_g1_i1	<i>CLPX</i>	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	5.53	4.22E-05
c90539_g2_i2	<i>ENN78015.1</i>	hypothetical protein YQE_05500, partial	37.85	9.28E-18
c90588_g1_i1	<i>NNAD</i>	Cytosolic carboxypeptidase NnaD	5.08	3.13E-05
c90590_g1_i1	<i>AKD1</i>	Adenylate kinase domain-containing protein 1	7.24	4.27E-05
c90593_g2_i1	<i>GAWKY</i>	Protein Gawky	3.09	3.79E-02
c90642_g1_i1	<i>WDR16</i>	WD repeat-containing protein 16	25.65	1.13E-13
c90652_g1_i1	<i>ENN77788.1</i>	hypothetical protein YQE_05759, partial	52.94	1.21E-20
c90669_g3_i1	<i>Y2R2</i>	Putative 115 kDa protein in type-1 retrotransposable element R1DM	3.43	2.00E-03
c90682_g1_i4	<i>Y1R1</i>	Uncharacterized 50 kDa protein in type I retrotransposable element R1DM	3.20	6.87E-03
c90733_g1_i2	<i>ENN78574.1</i>	hypothetical protein YQE_04942, partial	33.34	2.48E-06
c90737_g1_i1	<i>XP_003490437.1</i>	sporulation-specific protein 15-like	30.12	1.49E-11
c90741_g1_i1	<i>ENN75984.1</i>	hypothetical protein YQE_07516, partial [<i>Dendroctonus ponderosae</i>]	71.33	4.49E-08
c90742_g2_i2	<i>PREP</i>	Presequence protease, mitochondrial	2.56	1.03E-02
c90743_g1_i1	<i>MYCB2</i>	Probable E3 ubiquitin-protein ligase MYCBP2	4.25	1.27E-03
c90786_g2_i4	<i>DYH2</i>	Dynein heavy chain 2, axonemal	2.87	1.17E-02
c90791_g1_i1	<i>L259</i>	Probable multidrug resistance-associated protein lethal(2)03659	3.07	4.12E-03
c90827_g1_i2	<i>PITX</i>	Pituitary homeobox homolog Ptx1	2.17	4.88E-02
c90832_g1_i2	<i>DNAI2</i>	Dynein intermediate chain 2, axonemal	18.06	2.42E-07
c90841_g2_i4	<i>ENN71842.1</i>	hypothetical protein YQE_11460, partial	9.92	2.98E-07
c90881_g1_i2	<i>EST1A</i>	Telomerase-binding protein EST1A	2.33	4.33E-02

c90899_g1_i1	<i>DYHC</i>	Dynein beta chain, ciliary	26.19	2.94E-03
c90910_g1_i1	<i>CCD40</i>	Coiled-coil domain-containing protein 40	52.84	1.36E-19
c90913_g1_i3	<i>PO21</i>	Retrovirus-related P10 protein from type-1 retrotransposable element RZ (Fragment)	2.00	4.86E-02
c90934_g1_i1	<i>ENN70820.1</i>	hypothetical protein YQE_12485, partial	5.63	8.08E-05
c90941_g1_i3	<i>ZFP90</i>	Zinc finger protein 90	2.93	1.78E-02
c91007_g1_i1	<i>PIEZ2</i>	Piezo-type mechanosensitive ion channel component 2	20.97	2.51E-04
c91054_g1_i1	<i>ATS7</i>	A disintegrin and metalloproteinase with thrombospondin motifs 7	32.23	1.28E-15
c91076_g1_i1	<i>XP_976162.1</i>	hypothetical protein TcasGA2_TC006316	53.49	1.07E-20
c91119_g1_i1	<i>MYRO1</i>	Myrosinase 1	17.86	2.44E-02
c91133_g2_i1	<i>UN93L</i>	UNC93-like protein	2.01	4.42E-02
c91138_g1_i1	<i>ECR</i>	Ecdysone receptor	2.52	8.02E-03
c91145_g2_i4	<i>RTJK</i>	RNA-directed DNA polymerase from mobile element jockey	6.09	8.34E-07
c91149_g1_i2	<i>KPC4</i>	Putative protein kinase C delta type homolog	3.04	3.10E-03
c91158_g1_i4	<i>QRIC2</i>	Glutamine-rich protein 2	4.87	1.68E-05
c91244_g1_i1	<i>XP_001809336.1</i>	similar to Ank2 CG34416-PI	2.73	3.32E-02
c91248_g1_i1	<i>MYSA</i>	Myosin heavy chain, muscle	2.28	1.67E-02
c91321_g2_i4	<i>TTBK1</i>	Tau-tubulin kinase 1	2.09	4.01E-02
c91353_g1_i3	<i>ANK3</i>	Ankyrin-3	2.59	1.29E-02
c91354_g1_i1	<i>DYH7</i>	Dynein heavy chain 7, axonemal	100.12	9.54E-19
c91432_g1_i1	<i>FA10026.1</i>	hypothetical protein TcasGA2_TC012198	2.42	4.13E-02
c91444_g1_i1	<i>ACAC</i>	Acetyl-CoA carboxylase	3.67	3.00E-02
c91464_g1_i2	<i>DS</i>	Protein dachsous	2.08	2.79E-02
c91470_g1_i2	<i>MDN1</i>	Midasin	3.80	3.44E-02
c91494_g1_i1	<i>SYNE1</i>	Nesprin-1	5.30	1.68E-03
c91528_g1_i2	<i>PKCB1</i>	Protein kinase C-binding protein 1	2.16	4.16E-02
c91555_g2_i1	<i>YIR1</i>	Uncharacterized 50 kDa protein in type I retrotransposable element R1DM	2.65	1.52E-02
c91617_g1_i3	<i>Y2R2</i>	Putative 115 kDa protein in type-1 retrotransposable element R1DM	2.86	4.87E-03
c91627_g3_i1	<i>UNC22</i>	Twitchin	6.83	4.62E-07
c91627_g4_i1	<i>UNC22</i>	Twitchin	8.54	6.68E-08
c91627_g5_i1	<i>UNC22</i>	Twitchin	3.90	6.24E-05

c92510_g1_i1	<i>RSPH1</i>	Radial spoke head 1 homolog	73.89	5.57E-11
c95932_g1_i1	<i>DYH3</i>	Dynein heavy chain 3, axonemal	12.58	7.22E-04
c99695_g1_i1	<i>COX6C</i>	Cytochrome c oxidase subunit 6C	35.74	1.51E-03
c112459_g1_i1	<i>L259</i>	Probable multidrug resistance-associated protein lethal(2)03659	10.35	3.53E-02
c112528_g1_i1	<i>THAP4</i>	THAP domain-containing protein 4	143.00	6.70E-17
c112610_g1_i1	<i>QCR10</i>	Cytochrome b-c1 complex subunit 10	#DIV/0!	9.87E-04
c115210_g1_i1	<i>NDUBB</i>	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	2.13	3.93E-02
c116401_g1_i1	<i>ENN81684.1</i>	hypothetical protein YQE_01936, partial	29.34	1.29E-05
c121467_g1_i1	<i>XP_004519945.1</i>	carboxypeptidase B-like	#DIV/0!	4.68E-06
c122416_g1_i1	<i>RL17</i>	60S ribosomal protein L17	25.62	3.77E-04
c132588_g1_i1	<i>THIL</i>	Acetyl-CoA acetyltransferase, mitochondrial	2.09	3.01E-02
c132635_g1_i1	<i>TRI37</i>	E3 ubiquitin-protein ligase TRIM37	100.39	2.31E-14
c135743_g1_i1	<i>THIOT</i>	Thioredoxin-T	#DIV/0!	2.18E-02
c135816_g1_i1	<i>EFA09045.1</i>	hypothetical protein TcasGA2_TC006758	23.59	1.86E-12
c137657_g1_i1	<i>TRX1</i>	Thioredoxin-T OS=Schizosaccharomyces pombe (strain 9727 ATCC 24842)	47.94	5.25E-12
c138879_g1_i1	<i>CO026</i>	Uncharacterized protein C15orf26 homolog	14.64	4.25E-02
c139273_g1_i1	<i>EEZ98289.1</i>	hypothetical protein TcasGA2_TC000738	43.19	5.78E-04
c142944_g1_i1	<i>HES1</i>	Transcription factor HES-1	#DIV/0!	4.95E-02
c145407_g1_i1	<i>GAA55584.1</i>	23 kDa integral membrane protein, partial	#DIV/0!	1.08E-02
c154560_g1_i1	<i>ABCA3</i>	ATP-binding cassette sub-family A member 3	#DIV/0!	1.81E-03
c154591_g1_i1	<i>HSP68</i>	Heat shock protein 68	2.87	5.14E-03
c154775_g1_i1	<i>PP1B</i>	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	75.22	1.58E-18
c155579_g1_i1	<i>EFN64022.1</i>	Adenylyl cyclase-associated protein 1	23.02	1.43E-06
c156306_g1_i1	<i>URAD</i>	2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazole decarboxylase	3.17	2.00E-03
c160158_g1_i1	<i>DYH5</i>	Dynein heavy chain 5, axonemal	#DIV/0!	4.95E-02
c164613_g1_i1	<i>Adenylyl cyclase-associated protein 1</i>		43.42	4.72E-06
c176768_g1_i1	<i>DNJB2</i>	DnaJ homolog subfamily B member 2	#DIV/0!	1.97E-02
c177332_g1_i1	<i>DYH3</i>	Dynein heavy chain 3, axonemal	12.77	1.35E-03
c177848_g1_i1	<i>PSMD2</i>	26S proteasome non-ATPase regulatory subunit 2	87.56	5.67E-06
c177866_g1_i1	<i>PSMD2</i>	26S proteasome non-ATPase regulatory subunit 2	14.50	4.11E-02

c177948_g1_i1	<i>ENKUR</i>	Enkurin	19.51	1.54E-09
c181946_g1_i1	<i>GAGXE</i>	Nucleic-acid-binding protein from transposon X-element	#DIV/0!	1.46E-02
c183659_g1_i1	<i>MALI</i>	Maltase 1	14.23	8.92E-03
c185003_g1_i1	<i>GAS8</i>	Growth arrest-specific protein 8 homolog	45.39	7.99E-06
c185906_g1_i1	<i>U728</i>	UPF0728 protein	62.19	2.09E-06
c197810_g1_i1	<i>DYH8</i>	Dynein heavy chain 8, axonemal	22.82	3.45E-02
c204819_g1_i1	<i>VSP2</i>	Snake venom serine protease 2	#DIV/0!	3.88E-05
c205180_g1_i1	<i>KLOT</i>	Klotho	72.22	1.29E-07
c207700_g1_i1	<i>ENN71177.1</i>	hypothetical protein YQE_12107, partial	#DIV/0!	2.79E-02
c208140_g1_i1	<i>NN73950.1</i>	hypothetical protein YQE_09452, partial	28.87	1.12E-03
c208577_g1_i1	<i>EZ97403.1</i>	hypothetical protein TcasGA2_TC011232	#DIV/0!	1.26E-02
c1837_g1_i1	<i>RTBS</i>	Probable RNA-directed DNA polymerase from transposon BS	0.15	4.76E-02
c2900_g1_i1	<i>NN71770.1</i>	hypothetical protein YQE_11505, partial	0.36	2.05E-02
c8045_g1_i1	<i>P_003730187.1</i>	uncharacterized protein LOC100888907	0.22	4.82E-02
c8668_g1_i1	<i>FN72308.1</i>	Putative odorant receptor 22c	0.15	3.88E-02
c20633_g1_i1	<i>P_002740108.1</i>	tigger transposable element derived 6-like	0.06	4.15E-02
c21828_g1_i1	<i>NHP10</i>	Non-histone protein 10 OS= <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c)	0.42	3.31E-02
c32533_g1_i1	<i>CEGT</i>	Ceramide glucosyltransferase	0.46	4.01E-02
c32982_g1_i1	<i>DJC21</i>	DnaJ homolog subfamily C member 21	0.41	4.17E-02
c34576_g1_i1	<i>ELA1</i>	Elastase-1	0.04	2.95E-02
c37767_g1_i1	<i>TRY3</i>	Trypsin-3 (Fragment)	0.06	2.18E-02
c38507_g1_i1	<i>GDC</i>	Graves disease carrier protein homolog	0.45	2.97E-02
c47809_g1_i1	<i>TNNC1</i>	Troponin C, isoform 1	0.09	1.25E-03
c48933_g1_i2	<i>XP_001807061.1</i>	similar to CG16886 CG16886-PA, partial	0.27	4.05E-02
c50265_g1_i2	<i>SV2B</i>	Synaptic vesicle glycoprotein 2B	0.29	8.18E-03
c54716_g1_i1	<i>AAU06491.1</i>	putative salivary protein	0.00	4.34E-02
c57605_g1_i2	<i>AAC46946.1</i>	mariner transposase	0.43	4.56E-02
c58497_g1_i1	<i>TM205</i>	Transmembrane protein 205	0.49	4.17E-02
c62878_g1_i1	<i>CUD8</i>	Endocuticle structural glycoprotein SgAbd-8	0.30	2.74E-02
c63934_g1_i1	<i>LDH6B</i>	L-lactate dehydrogenase A-like 6B	0.21	2.15E-04

c65249_g1_i1	<i>ENN70557.1</i>	hypothetical protein YQE_12732, partial	0.24	2.70E-02
c66417_g1_i1	<i>CP307</i>	Cytochrome P450 307a1	0.13	2.35E-02
c66535_g1_i1	<i>AAF74117.1</i>	unknown	0.33	3.13E-03
c66860_g1_i1	<i>POMP</i>	Proteasome maturation protein	0.43	4.68E-02
c67185_g1_i1	<i>LDH</i>	L-lactate dehydrogenase	0.30	5.92E-04
c67603_g1_i1	<i>CB043</i>	UPF0554 protein C2orf43 homolog	0.43	4.24E-02
c68200_g1_i1	<i>NN73712.1</i>	hypothetical protein YQE_09682, partial	0.19	1.56E-03
c68719_g2_i1	<i>NP_001232998.1</i>	uncharacterized protein LOC100575320	0.31	4.53E-02
c69172_g1_i1	<i>METL6</i>	Methyltransferase-like protein 6	0.26	5.21E-04
c69225_g1_i1	<i>ARH40</i>	Rho guanine nucleotide exchange factor 40	0.27	1.34E-03
c69451_g1_i1	<i>RHPN2</i>	Rhopilin-2	0.26	3.20E-04
c70672_g1_i1	<i>TIOB</i>	Mitochondrial import inner membrane translocase subunit Tim10 B	0.25	4.80E-02
c71312_g1_i1	<i>CP315</i>	Cytochrome P450 315a1, mitochondrial	0.38	6.05E-03
c71349_g1_i1	<i>AEE63003.1</i>	unknown	0.27	3.28E-02
c72375_g1_i1	<i>ACE</i>	Angiotensin-converting enzyme	0.27	8.67E-03
c72440_g1_i1	<i>ESCA</i>	Protein escargot	0.31	3.99E-02
c72715_g2_i1	<i>BMAL1</i>	Aryl hydrocarbon receptor nuclear translocator-like protein 1	0.34	4.75E-03
c72990_g1_i1	<i>MPIP</i>	M-phase inducer phosphatase	0.27	2.07E-02
c73469_g1_i2	<i>SVOP</i>	Synaptic vesicle 2-related protein	0.22	2.93E-02
c73598_g1_i1	<i>XP_976380.1</i>	hypothetical protein	0.32	1.23E-03
c73645_g1_i1	<i>HEXIM</i>	Protein HEXIM	0.35	7.40E-03
c74049_g1_i1	<i>ENN81062.1</i>	hypothetical protein YQE_02431, partial	0.40	2.21E-02
c74578_g1_i1	<i>XP_976170.1</i>	hypothetical protein	0.33	2.32E-02
c75235_g1_i2	<i>XP_001814929.1</i>	similar to protease inhibitor-like protein	0.30	2.79E-02
c75544_g1_i2	<i>TTPAL</i>	Alpha-tocopherol transfer protein-like	0.38	2.09E-02
c76176_g2_i1	<i>PRAX</i>	Periaxin	0.22	2.05E-03
c76275_g1_i1	<i>DHR11</i>	Dehydrogenase/reductase SDR family member 11	0.31	1.60E-02
c76382_g1_i2	<i>CTRA</i>	Chymotrypsin A	0.04	5.67E-03
c76865_g1_i1	<i>ENN79333.1</i>	hypothetical protein YQE_04242, partial	0.43	2.14E-02
c77454_g1_i2	<i>BGH3</i>	Transforming growth factor-beta-induced protein ig-h3	0.15	1.03E-02

c77774_g1_i5	<i>GTR1</i>	Solute carrier family 2, facilitated glucose transporter member 1	0.41	1.62E-02
c77983_g2_i2	<i>ACT2</i>	Actin-2	0.31	3.15E-03
c77994_g1_i1	<i>XP_004206551.1</i>	histone-lysine N-methyltransferase SETMAR-like	0.08	5.18E-04
c78140_g1_i2	<i>LACH</i>	Lachesin	0.23	4.48E-02
c78303_g1_i4	<i>TYB12</i>	Thymosin beta-12	0.44	2.03E-02
c78558_g1_i1	<i>ENN74570.1</i>	hypothetical protein YQE_08892, partial	0.41	1.98E-02
c78612_g1_i1	<i>EXOS8</i>	Exosome complex component RRP43	0.49	4.54E-02
c78816_g1_i1	<i>CP305</i>	Probable cytochrome P450 305a1	0.26	9.28E-03
c79133_g1_i1	<i>CBR3</i>	Carbonyl reductase [NADPH] 3	0.19	3.38E-05
c79179_g1_i2	<i>PCE</i>	Proclotting enzyme	0.36	3.45E-02
c79470_g2_i1	<i>NP_001161909.1</i>	cuticular protein analogous to peritrophins 3-A2 precursor	0.48	3.92E-02
c79506_g1_i2	<i>SEC20</i>	Vesicle transport protein SEC20	0.38	1.35E-02
c79621_g1_i1	<i>CNTRB</i>	Centrobin OS=Homo sapiens	0.47	3.19E-02
c79649_g1_i1	<i>A1A1A</i>	Alcohol dehydrogenase [NADP(+)] A	0.19	2.64E-02
c80109_g1_i2	<i>4CLL7</i>	4-coumarate--CoA ligase-like 7	0.05	2.09E-03
c80513_g1_i1	<i>BAM18756.1</i>	unknown secreted protein	0.43	2.72E-02
c80598_g1_i5	<i>ENN72109.1</i>	hypothetical protein YQE_11248, partial	0.21	2.74E-02
c80776_g1_i1	<i>EFA08263.1</i>	hypothetical protein TcasGA2_TC005893	0.35	5.48E-03
c81263_g1_i1	<i>ATOH8</i>	Protein atonal homolog 8	0.41	1.80E-02
c81291_g1_i1	<i>HEXA</i>	Hexamerin	0.14	9.78E-03
c81312_g1_i1	<i>SNX17</i>	Sorting nexin-17	0.49	4.55E-02
c81347_g1_i1	<i>ESMC</i>	Enhancer of split mgamma protein	0.42	1.58E-02
c81530_g1_i3	<i>ENN73538.1</i>	hypothetical protein YQE_09789, partial	0.25	2.32E-02
c81647_g2_i4	<i>RBM38</i>	RNA-binding protein 38	0.49	4.69E-02
c81654_g1_i1	<i>XP_003399674.1</i>	uncharacterized protein C9E9.15-like	0.19	8.55E-04
c81663_g1_i1	<i>TBB4B</i>	Tubulin beta-4B chain (Fragments)	0.44	1.95E-02
c81667_g1_i1	<i>XP_972121.1</i>	similar to AGAP001449-PA	0.36	2.95E-02
c81831_g1_i1	<i>POGK</i>	Pogo transposable element with KRAB domain	0.31	4.30E-03
c82428_g2_i1	<i>TRY1</i>	Trypsin-1	0.00	3.49E-02
c82492_g1_i1	<i>NLGX</i>	Neurologin-4, X-linked	0.35	3.04E-02

c82604_g2_i1	<i>XP_969862.1</i>	similar to conserved hypothetical protein	0.43	3.07E-02
c82606_g1_i1	<i>/EFN73455.1</i>	hypothetical protein EAG_10764	0.21	1.56E-02
c82727_g3_i2	<i>FBLN1</i>	Fibulin-1	0.01	2.03E-02
c82826_g1_i1	<i>SMYD4</i>	SET and MYND domain-containing protein 4	0.37	3.86E-02
c82866_g1_i1	<i>SL9B2</i>	Mitochondrial sodium/hydrogen exchanger 9B2	0.43	1.42E-02
c82873_g1_i1	<i>LSD1</i>	Lipid storage droplets surface-binding protein 1	0.40	7.86E-03
c82976_g1_i1	<i>ENN70264.1</i>	hypothetical protein YQE_13047, partial	0.20	7.41E-03
c83131_g1_i1	<i>EEZ98147.1</i>	hypothetical protein TcasGA2_TC000572	0.46	3.76E-02
c83175_g1_i2	<i>LACH</i>	Lachesin	0.16	1.95E-02
c83286_g1_i1	<i>PARVB</i>	Beta-parvin	0.49	4.54E-02
c83326_g1_i1	<i>CP18A</i>	Cytochrome P450 18a1	0.37	7.03E-03
c83405_g1_i3	<i>FA04956.1</i>	hypothetical protein TcasGA2_TC015025	0.28	7.02E-03
c83592_g1_i1	<i>UCK</i>	Probable uridine-cytidine kinase	0.37	5.44E-03
c83686_g1_i1	<i>RYK2</i>	Tyrosine-protein kinase Dnt	0.31	3.74E-02
c83765_g1_i1	<i>PTN7</i>	Tyrosine-protein phosphatase non-receptor type 7	0.44	1.64E-02
c83857_g1_i1	<i>SKEL1</i>	Protein Skeletor, isoforms B/C	0.49	4.69E-02
c84071_g2_i2	<i>FA06434.1</i>	hypothetical protein TcasGA2_TC009315	0.26	9.63E-03
c84181_g1_i2	<i>UAPI</i>	UDP-N-acetylhexosamine pyrophosphorylase	0.33	4.85E-03
c84254_g1_i1	<i>EFA09394.1</i>	hypothetical protein TcasGA2_TC004312	0.43	3.14E-02
c84452_g1_i1	<i>ENN71146.1</i>	hypothetical protein YQE_12077, partial	0.38	1.21E-02
c84545_g1_i1	<i>GAGT2</i>	Gamma-glutamyltranspeptidase 2	0.22	2.44E-02
c84623_g1_i2	<i>TG325</i>	WW domain-containing protein tag-325	0.47	3.61E-02
c84746_g1_i1	<i>PXDC2</i>	Plexin domain-containing protein 2	0.47	3.38E-02
c84772_g1_i2	<i>MTP</i>	Microsomal triglyceride transfer protein large subunit	0.38	1.60E-02
c84783_g1_i5	<i>ABP1</i>	Probable antibacterial peptide polyprotein	0.18	1.99E-02
c84938_g1_i1	<i>XP_003425006.1</i>	hypothetical protein LOC100679608	0.39	3.80E-02
c84960_g1_i1	<i>RASA1</i>	Ras GTPase-activating protein 1	0.38	2.54E-02
c85372_g11_i3	<i>GA45A</i>	Growth arrest and DNA damage-inducible protein GADD45 alpha	0.27	4.49E-02
c85423_g1_i1	<i>TRET1</i>	Facilitated trehalose transporter Tret1	0.30	1.31E-02
c85437_g1_i1	<i>SAS</i>	Putative epidermal cell surface receptor	0.28	2.29E-03

c85470_g1_i1	<i>XP_001815629.1</i>	similar to conserved hypothetical protein	0.39	1.14E-02
c85537_g3_i2	<i>OSTM1</i>	Osteopetrosis-associated transmembrane protein 1	0.42	3.28E-02
c85642_g1_i2	<i>DDX6</i>	Putative ATP-dependent RNA helicase me31b	0.49	4.10E-02
c85830_g1_i1	<i>ALS</i>	Insulin-like growth factor-binding protein complex acid labile subunit	0.26	1.68E-02
c85833_g1_i1	<i>AEE63111.1</i>	unknown	0.44	4.59E-02
c85936_g1_i1	<i>ARHG7</i>	Rho guanine nucleotide exchange factor 7	0.37	4.84E-02
c86141_g2_i1	<i>LRC15</i>	Leucine-rich repeat-containing protein 15	0.22	9.05E-03
c86153_g1_i1	<i>XP_003699527.1</i>	uncharacterized protein LOC100876895	0.21	3.90E-02
c86202_g1_i1	<i>ENN79214.1</i>	hypothetical protein YQE_04398, partial	0.11	2.48E-02
c86217_g1_i1	<i>TES</i>	Testin	0.18	3.38E-02
c86410_g1_i1	<i>PDZD2</i>	PDZ domain-containing protein 2	0.24	9.80E-03
c86416_g1_i1	<i>CU30</i>	Larval cuticle protein LCP-30	0.29	7.76E-03
c86583_g1_i1	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	0.13	4.41E-03
c86611_g1_i1	<i>CHD1</i>	Chromodomain-helicase-DNA-binding protein 1	0.46	3.12E-02
c86678_g1_i4	<i>LU05045.1</i>	hypothetical protein CAPTEDRAFT_186396	0.34	2.05E-02
c86810_g1_i3	<i>PUR1</i>	Amidophosphoribosyltransferase	0.27	1.08E-02
c86837_g1_i1	<i>GLIS3</i>	Zinc finger protein GLIS3	0.45	4.29E-02
c86950_g1_i2	<i>ITA3</i>	Integrin alpha-PS3	0.20	1.86E-02
c87230_g1_i1	<i>P_001807200.1</i>	similar to tyrosine recombinase, partial	0.36	5.20E-03
c87377_g4_i1	<i>XP_971678.1</i>	similar to Cuticular protein 62Bc CG1919-PA	0.19	2.75E-02
c87402_g2_i1	<i>EFHD</i>	EF-hand domain-containing protein CG10641	0.28	2.58E-03
c87454_g2_i1	<i>PROML</i>	Prominin-like protein	0.49	3.51E-02
c87460_g5_i1	<i>LDH</i>	L-lactate dehydrogenase	0.02	3.44E-07
c87541_g1_i1	<i>XP_003425202.1</i>	hypothetical protein LOC100121748	0.39	1.86E-02
c87566_g1_i1	<i>IMPL2</i>	Neural/ectodermal development factor IMP-L2	0.32	1.47E-03
c87567_g1_i1	<i>MKX</i>	Homeobox protein Mohawk	0.15	1.49E-02
c87673_g1_i2	<i>FX63797.</i>	hypothetical protein DAPPUDRAFT_118838	0.18	2.59E-03
c87688_g1_i2	<i>MTR1</i>	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1	0.42	3.60E-02
c87713_g1_i1	<i>YQI7</i>	Uncharacterized protein C45G9.7	0.28	3.13E-02
c87776_g1_i1	<i>CP6A1</i>	Cytochrome P450 6A1	0.41	4.61E-02

c87847_g2_i1	<i>2-Sep</i>	Septin-2	0.48	4.08E-02
c87848_g1_i2	<i>MTF1</i>	Metal regulatory transcription factor 1	0.41	4.97E-02
c87874_g2_i1	<i>XP_004568599.1</i>	uncharacterized protein LOC101485038 isoform X2	0.13	3.17E-03
c87904_g3_i2	<i>XP_971483.1</i>	similar to AGAP002361-PA	0.37	1.28E-02
c87922_g1_i3	<i>CTLI</i>	Choline transporter-like protein 1	0.33	4.21E-03
c88002_g1_i2	<i>EZ98475.1</i>	hypothetical protein TcasGA2_TC000967	0.48	3.43E-02
c88018_g1_i3	<i>TRET1</i>	Facilitated trehalose transporter Tret1	0.22	1.06E-03
c88072_g1_i4	<i>CHSTB</i>	Carbohydrate sulfotransferase 11	0.18	5.60E-04
c88086_g1_i1	<i>DAN</i>	Protein distal antenna	0.41	1.93E-02
c88244_g1_i1	<i>FURIC</i>	Furin-like protease 1, isoform 1-CRR	0.49	4.93E-02
c88293_g1_i1	<i>ACOD2</i>	Acyl-CoA desaturase 2	0.36	2.34E-02
c88332_g1_i2	<i>FA13346.1</i>	hypothetical protein TcasGA2_TC002325	0.44	4.18E-02
c88371_g3_i2	<i>XP_004212605.1</i>	RNA-directed DNA polymerase from mobile element jockey-like	0.35	3.56E-02
c88560_g1_i2	<i>PP1RA</i>	Serine/threonine-protein phosphatase 1 regulatory subunit 10	0.44	1.63E-02
c88612_g1_i1	<i>LIPK</i>	Lipase member K OS=Mus musculus	0.50	4.21E-02
c88719_g1_i3	<i>FGFR1</i>	Fibroblast growth factor receptor homolog 1	0.37	3.24E-02
c88771_g1_i2	<i>ITBX</i>	Integrin beta-PS	0.37	8.92E-03
c88803_g1_i1	<i>SCRBI</i>	Scavenger receptor class B member 1	0.41	1.24E-02
c88876_g3_i1	<i>RTJK</i>	RNA-directed DNA polymerase from mobile element jockey	0.24	8.42E-03
c88917_g5_i1	<i>S22A3</i>	Solute carrier family 22 member 3	0.20	2.98E-03
c88988_g1_i1	<i>RECA</i>	Protein RecA	0.00	2.53E-02
c89038_g1_i1	<i>CYB5</i>	Cytochrome b5	0.20	3.98E-02
c89131_g5_i2	<i>EFA10695.1</i>	hypothetical protein TcasGA2_TC011770	0.40	4.17E-02
c89132_g3_i1	<i>PISD</i>	Phosphatidylserine decarboxylase proenzyme	0.42	2.06E-02
c89284_g1_i1	<i>NP_001161918.1</i>	cuticular protein analogous to peritrophins 1-H precursor	0.39	3.88E-02
c89464_g1_i1	<i>EFA09543.1</i>	hypothetical protein TcasGA2_TC011651	0.31	3.33E-02
c89617_g1_i2	<i>MINP1</i>	Multiple inositol polyphosphate phosphatase 1	0.44	3.02E-02
c89672_g1_i1	<i>SRAC1</i>	Protein SERAC1	0.32	4.50E-02
c89779_g1_i5	<i>LIPP</i>	Pancreatic triacylglycerol lipase (Fragment)	0.36	1.07E-02
c89823_g1_i2	<i>ACE</i>	Angiotensin-converting enzyme	0.20	8.10E-03

c89833_g1_i1	<i>YI760</i>	Probable G-protein coupled receptor CG31760	0.38	1.18E-02
c89837_g4_i1	<i>VAMP7</i>	Vesicle-associated membrane protein 7	0.48	4.71E-02
c89919_g1_i4	<i>PNR</i>	GATA-binding factor A	0.43	2.82E-02
c89968_g1_i6	<i>EFA08559.1</i>	hypothetical protein TcasGA2_TC006214	0.34	6.40E-03
c90019_g2_i2	<i>MTH5</i>	Probable G-protein coupled receptor Mth-like 5	0.39	4.80E-02
c90182_g1_i1	<i>P3</i>	P3 protein	0.35	8.70E-03
c90270_g4_i1	<i>HIF1N</i>	Hypoxia-inducible factor 1-alpha inhibitor	0.21	1.87E-02
c90304_g1_i2	<i>ZNHI3</i>	Zinc finger HIT domain-containing protein 3	0.38	3.49E-02
c90553_g2_i1	<i>PCD15</i>	Protocadherin-15	0.47	4.25E-02
c90594_g1_i3	<i>CHSTB</i>	Carbohydrate sulfotransferase 11	0.36	1.93E-02
c90619_g1_i1	<i>CNTP2</i>	Contactin-associated protein-like 2	0.39	2.43E-02
c90665_g1_i1	<i>ARL5B</i>	ADP-ribosylation factor-like protein 5B	0.38	1.42E-02
c90723_g1_i1	<i>ITA3</i>	Integrin alpha-PS3	0.22	8.65E-04
c90738_g6_i3	<i>EFA12801.1</i>	hypothetical protein TcasGA2_TC001864	0.18	3.62E-02
c90934_g2_i3	<i>NRX4</i>	Neurexin-4	0.39	1.24E-02
c91089_g2_i4	<i>YG31B</i>	Transposon Ty3-G Gag-Pol polyprotein	0.39	1.56E-02
c91175_g1_i1	<i>BN3D2</i>	Probable RNA methyltransferase CG1239	0.44	2.36E-02
c91266_g1_i1	<i>PO22</i>	Retrovirus-related P10 polyprotein from type-1 retrotransposable element KZ (Fragment)	0.50	3.68E-02
c91317_g1_i4	<i>FA06632.1</i>	hypothetical protein TcasGA2_TC009552	0.33	2.60E-03
c91451_g1_i1	<i>YI31B</i>	Transposon Ty3-I Gag-Pol polyprotein	0.49	4.92E-02
c91598_g3_i1	<i>AAC28141.1</i>	XP_002736114.1	0.19	3.44E-04
c112302_g1_i1	<i>XP_002736114.1</i>	hypothetical protein, partial	0.00	2.05E-02
c154518_g1_i1	<i>SEPT5</i>	Septin-5	0.18	4.05E-02
c177676_g1_i1	<i>DHR11</i>	Dehydrogenase/reductase SDR family member 11	0.10	1.18E-02
c178137_g1_i1	<i>XP_001916399.1</i>	hypothetical protein LOC100147469	0.00	9.97E-03
c199391_g1_i1	<i>JERKL</i>	Jerky protein homolog-like	0.03	1.52E-13

^{a#}DIV/0 in Fold change meant a gene undetected or unexpressed in HA, while highly expressed in HHA.

Table S2.Summary of DEGs in the GO enrichment (HHA-HA-NOR).

Categories	GOslim	HHA vs NOR					
		Up	Down	DEG	Unigene	pvalue	-LOG ₁₀ (P-value)
	biological_process	83	71	154	10259	6.41E-01	0.19
	aging	0	3	3	285	8.15E-01	0.09
	anatomical structure development	2	28	30	4941	1.00E+00	0.00
	anatomical structure formation involved in morphoge	1	4	5	1062	1.00E+00	0.00
	biosynthetic process	28	82	110	8419	9.77E-01	0.01
	carbohydrate metabolic process	17	10	27	1343	9.56E-02	1.02
	catabolic process	19	58	77	4674	2.70E-01	0.57
	cell adhesion	1	5	6	947	9.97E-01	0.00
	cell cycle	0	8	8	2418	1.00E+00	0.00
	cell death	1	20	21	2112	9.89E-01	0.00
	cell differentiation	2	22	24	3421	1.00E+00	0.00
	cell division	0	5	5	1069	1.00E+00	0.00
	cell junction organization	0	0	0	344	1.00E+00	0.00
	cell morphogenesis	1	5	6	1394	1.00E+00	0.00
	cell motility	0	7	7	1136	9.99E-01	0.00
	cell proliferation	1	8	9	1761	1.00E+00	0.00
	cell wall organization or biogenesis	2	0	2	8	6.19E-03	2.21
	cell-cell signaling	1	2	3	819	1.00E+00	0.00
	cellular component assembly	1	19	20	2727	1.00E+00	0.00
	cellular nitrogen compound metabolic process	24	75	99	9618	1.00E+00	0.00
	cellular protein modification process	3	18	21	4497	1.00E+00	0.00
	chromosome organization	1	3	4	1579	1.00E+00	0.00
	chromosome segregation	0	0	0	306	1.00E+00	0.00
	circulatory system process	0	1	1	287	9.88E-01	0.01
	cofactor metabolic process	3	0	3	487	9.81E-01	0.01
	cytoskeleton organization	3	9	12	1490	9.96E-01	0.00
	developmental maturation	0	1	1	187	9.45E-01	0.02
	embryo development	0	5	5	1249	1.00E+00	0.00

biological process

extracellular matrix organization	0	3	3	331	8.85E-01	0.05
generation of precursor metabolites and energy	9	10	19	775	3.23E-02	1.49
growth	0	3	3	998	1.00E+00	0.00
helicase activity	0	3	3	501	9.84E-01	0.01
homeostatic process	2	13	15	1392	9.43E-01	0.03
hydrolase activity, acting on carbon-nitrogen	1	0	1	215	9.64E-01	0.02
hydrolase activity, acting on glycosyl bonds	10	1	11	294	6.16E-03	2.21
immune system process	2	15	17	2109	9.99E-01	0.00
isomerase activity	2	8	10	533	3.05E-01	0.52
kinase activity	11	19	30	2418	9.06E-01	0.04
ligase activity	5	2	7	1167	9.99E-01	0.00
lipid metabolic process	9	13	22	1404	4.91E-01	0.31
locomotion	0	9	9	1582	1.00E+00	0.00
lyase activity	10	10	20	644	2.59E-03	2.59
membrane organization	1	48	49	1749	4.49E-05	4.35
methyltransferase activity	0	0	0	422	1.00E+00	0.00
mitochondrion organization	1	1	2	562	9.98E-01	0.00
mitosis	0	2	2	635	9.99E-01	0.00
mRNA processing	0	6	6	858	9.91E-01	0.00
neurological system process	0	1	1	606	1.00E+00	0.00
nitrogen cycle metabolic process	1	0	1	27	3.41E-01	0.47
nucleic acid binding transcription factor activity	3	6	9	1471	1.00E+00	0.00
nucleotidyltransferase activity	0	0	0	389	1.00E+00	0.00
oxidoreductase activity	45	23	68	1988	7.42E-10	9.13
phosphatase activity	2	1	3	598	9.95E-01	0.00
photosynthesis	0	0	0	0	1.00E+00	0.00
pigmentation	0	0	0	95	1.00E+00	0.00
plasma membrane organization	0	4	4	272	6.02E-01	0.22
protein binding transcription factor activity	0	2	2	809	1.00E+00	0.00
protein folding	1	9	10	442	1.46E-01	0.84
protein maturation	14	21	35	2082	3.13E-01	0.50
reproduction	0	4	4	1074	1.00E+00	0.00

	response to stress	1	27	28	3894	1.00E+00	0.00
	ribosome biogenesis	0	12	12	419	2.98E-02	1.53
	secondary metabolic process	0	0	0	30	1.00E+00	0.00
	signal transduction	3	29	32	5173	1.00E+00	0.00
	small molecule metabolic process	42	31	73	5046	7.24E-01	0.14
	sulfur compound metabolic process	2	0	2	321	9.59E-01	0.02
	symbiosis, encompassing mutualism through parasitism	0	43	43	1055	9.50E-09	8.02
	transferase activity, transferring acyl groups	4	2	6	477	7.42E-01	0.13
	transferase activity, transferring alkyl or aryl	1	0	1	84	7.28E-01	0.14
	transferase activity, transferring glycosyl groups	3	3	6	370	5.03E-01	0.30
	translation	1	57	58	1827	1.81E-07	6.74
	transport	28	68	96	5804	2.28E-01	0.64
	transposition	0	0	0	10	1.00E+00	0.00
cellular component	cellular_component	22	86	108	6752	3.34E-01	0.48
	cell	32	109	141	18025	1.00E+00	0.00
	cytoplasm	25	105	130	13065	1.00E+00	0.00
	cytosol	1	65	66	3795	1.57E-01	0.80
	external encapsulating structure	0	0	0	7	1.00E+00	0.00
	extracellular region	7	70	77	3970	1.97E-02	1.71
	extracellular space	1	10	11	753	6.08E-01	0.22
	intracellular	32	107	139	17261	1.00E+00	0.00
	microtubule organizing center	0	3	3	831	1.00E+00	0.00
	nuclear envelope	1	4	5	600	9.54E-01	0.02
	nucleoplasm	0	13	13	4238	1.00E+00	0.00
	organelle	23	104	127	15633	1.00E+00	0.00
	plasma membrane	3	38	41	6162	1.00E+00	0.00
	protein complex	16	33	49	6318	1.00E+00	0.00
	proteinaceous extracellular matrix	1	3	4	243	5.14E-01	0.29
thylakoid	0	0	0	0	1.00E+00	0.00	
molecular function	molecular_function	64	91	155	12770	1.00E+00	0.00
	cytoskeletal protein binding	3	7	10	1222	9.91E-01	0.00
	DNA binding	5	18	23	3614	1.00E+00	0.00

molecular function	enzyme binding	2	21	23	2763	1.00E+00	0.00
	enzyme regulator activity	2	5	7	924	9.88E-01	0.01
	histone binding	0	0	0	276	1.00E+00	0.00
	ion binding	55	53	108	9502	1.00E+00	0.00
	lipid binding	0	4	4	687	9.94E-01	0.00
	protein binding, bridging	0	0	0	183	1.00E+00	0.00
	RNA binding	2	74	76	3316	3.08E-04	3.51
	small conjugating protein binding	0	1	1	174	9.33E-01	0.03
	structural molecule activity	4	59	63	1565	4.77E-12	11.32
	transcription factor binding	0	5	5	1241	1.00E+00	0.00
	unfolded protein binding	0	5	5	247	3.30E-01	0.48

Categories	GOslim	HA vs NOR					
		Up	Down	DEG	Unigene	pvalue	-LOG ₁₀ (P-value)
	biological_process	13	44	57	10259	8.33E-01	0.08
	aging	0	3	3	285	2.57E-01	0.59
	anatomical structure development	1	22	23	4941	9.42E-01	0.03
	anatomical structure formation involved in morphoge	0	2	2	1062	9.90E-01	0.00
	biosynthetic process	4	73	77	8419	1.13E-04	3.95
	carbohydrate metabolic process	1	12	13	1343	7.34E-02	1.13
	catabolic process	0	49	49	4674	1.36E-04	3.87
	cell adhesion	0	5	5	947	6.95E-01	0.16
	cell cycle	1	6	7	2418	9.93E-01	0.00
	cell death	0	16	16	2112	2.31E-01	0.64
	cell differentiation	1	16	17	3421	8.52E-01	0.07
	cell division	0	4	4	1069	8.97E-01	0.05
	cell junction organization	0	0	0	344	1.00E+00	0.00
	cell morphogenesis	0	5	5	1394	9.33E-01	0.03
	cell motility	0	5	5	1136	8.31E-01	0.08
	cell proliferation	0	8	8	1761	8.53E-01	0.07
	cell wall organization or biogenesis	0	0	0	8	1.00E+00	0.00
	cell-cell signaling	0	1	1	819	9.94E-01	0.00

biological process	cellular component assembly	0	12	12	2727	9.15E-01	0.04
	cellular nitrogen compound metabolic process	4	66	70	9618	6.43E-02	1.19
	cellular protein modification process	1	10	11	4497	1.00E+00	0.00
	chromosome organization	0	4	4	1579	9.89E-01	0.00
	chromosome segregation	0	0	0	306	1.00E+00	0.00
	circulatory system process	0	1	1	287	8.31E-01	0.08
	cofactor metabolic process	0	1	1	487	9.51E-01	0.02
	cytoskeleton organization	1	8	9	1490	5.70E-01	0.24
	developmental maturation	0	1	1	187	6.86E-01	0.16
	embryo development	0	3	3	1249	9.84E-01	0.01
	extracellular matrix organization	0	1	1	331	8.71E-01	0.06
	generation of precursor metabolites and energy	2	10	12	775	3.34E-03	2.48
	growth	0	3	3	998	9.47E-01	0.02
	helicase activity	0	2	2	501	8.16E-01	0.09
	homeostatic process	0	12	12	1392	1.53E-01	0.82
	hydrolase activity, acting on carbon-nitrogen	0	2	2	215	3.82E-01	0.42
	hydrolase activity, acting on glycosyl bonds	2	1	3	294	2.72E-01	0.57
	immune system process	1	13	14	2109	4.25E-01	0.37
	isomerase activity	0	7	7	533	4.80E-02	1.32
	kinase activity	2	12	14	2418	6.31E-01	0.20
	ligase activity	0	1	1	1167	9.99E-01	0.00
	lipid metabolic process	0	6	6	1404	8.66E-01	0.06
	locomotion	0	7	7	1582	8.58E-01	0.07
	lyase activity	2	10	12	644	7.16E-04	3.15
	membrane organization	0	39	39	1749	3.70E-12	11.43
	methyltransferase activity	0	0	0	422	1.00E+00	0.00
	mitochondrion organization	0	1	1	562	9.70E-01	0.01
	mitosis	0	2	2	635	9.04E-01	0.04
	mRNA processing	0	5	5	858	6.10E-01	0.21
	neurological system process	0	1	1	606	9.77E-01	0.01
	nitrogen cycle metabolic process	0	0	0	27	1.00E+00	0.00
	nucleic acid binding transcription factor activity	1	5	6	1471	8.93E-01	0.05

	nucleotidyltransferase activity	0	0	0	389	1.00E+00	0.00
	oxidoreductase activity	13	17	30	1988	6.07E-06	5.22
	phosphatase activity	1	0	1	598	9.76E-01	0.01
	photosynthesis	0	0	0	0	1.00E+00	0.00
	pigmentation	0	0	0	95	1.00E+00	0.00
	plasma membrane organization	0	1	1	272	8.14E-01	0.09
	protein binding transcription factor activity	0	2	2	809	9.61E-01	0.02
	protein folding	0	7	7	442	2.03E-02	1.69
	protein maturation	2	10	12	2082	6.33E-01	0.20
	reproduction	0	3	3	1074	9.62E-01	0.02
	response to stress	0	19	19	3894	8.83E-01	0.05
	ribosome biogenesis	0	12	12	419	1.31E-05	4.88
	secondary metabolic process	0	0	0	30	1.00E+00	0.00
	signal transduction	2	21	23	5173	9.67E-01	0.01
	small molecule metabolic process	3	22	25	5046	8.99E-01	0.05
	sulfur compound metabolic process	0	0	0	321	1.00E+00	0.00
	symbiosis, encompassing mutualism through parasitism	0	35	35	1055	6.21E-16	15.21
	transferase activity, transferring acyl groups	1	1	2	477	7.94E-01	0.10
	transferase activity, transferring alkyl or aryl	0	0	0	84	1.00E+00	0.00
	transferase activity, transferring glycosyl groups	0	4	4	370	1.95E-01	0.71
	translation	0	52	52	1827	1.59E-20	19.80
	transport	8	54	62	5804	7.44E-06	5.13
	transposition	0	0	0	10	1.00E+00	0.00
cellular component	cellular_component	9	66	75	6752	1.08E-07	6.97
	cell	5	99	104	18025	8.27E-01	0.08
	cytoplasm	3	96	99	13065	7.84E-03	2.11
	cytosol	0	57	57	3795	1.93E-10	9.72
	external encapsulating structure	0	0	0	7	1.00E+00	0.00
	extracellular region	0	58	58	3970	3.69E-10	9.43
	extracellular space	0	10	10	753	1.90E-02	1.72
	intracellular	5	99	104	17261	6.35E-01	0.20
	microtubule organizing center	0	5	5	831	5.82E-01	0.24

	nuclear envelope	0	4	4	600	5.06E-01	0.30
	nucleoplasm	0	13	13	4238	9.99E-01	0.00
	organelle	4	94	98	15633	4.31E-01	0.37
	plasma membrane	0	30	30	6162	9.35E-01	0.03
	protein complex	0	27	27	6318	9.88E-01	0.01
	proteinaceous extracellular matrix	0	2	2	243	4.42E-01	0.35
	thylakoid	0	0	0	0	1.00E+00	0.00
molecular function	molecular_function	13	67	80	12770	4.47E-01	0.35
	cytoskeletal protein binding	0	6	6	1222	7.66E-01	0.12
	DNA binding	1	16	17	3614	9.04E-01	0.04
	enzyme binding	0	15	15	2763	7.29E-01	0.14
	enzyme regulator activity	0	2	2	924	9.79E-01	0.01
	histone binding	0	0	0	276	1.00E+00	0.00
	ion binding	13	35	48	9502	9.52E-01	0.02
	lipid binding	0	5	5	687	4.16E-01	0.38
	protein binding, bridging	0	0	0	183	1.00E+00	0.00
	RNA binding	1	65	66	3316	6.37E-18	17.20
	small conjugating protein binding	0	0	0	174	1.00E+00	0.00
	structural molecule activity	0	55	55	1565	4.74E-26	25.32
	transcription factor binding	0	6	6	1241	7.78E-01	0.11
unfolded protein binding	0	4	4	247	6.70E-02	1.17	

Categories	GOslim	HHA vs HA					
		Up	Down	DEG	Unigene	pvalue	log ₁₀ (pvalue)
	biological_process	187	34	221	10259	1.00E+00	0.00
	aging	1	0	1	285	1.00E+00	0.00
	anatomical structure development	13	3	16	4941	1.00E+00	0.00
	anatomical structure formation involved in morphoge	4	0	4	1062	1.00E+00	0.00
	biosynthetic process	52	11	63	8419	1.00E+00	0.00
	carbohydrate metabolic process	27	5	32	1343	8.27E-01	0.08
	catabolic process	52	6	58	4674	1.00E+00	0.00
	cell adhesion	1	2	3	947	1.00E+00	0.00

biological process	cell cycle	5	3	8	2418	1.00E+00	0.00
	cell death	2	0	2	2112	1.00E+00	0.00
	cell differentiation	10	1	11	3421	1.00E+00	0.00
	cell division	1	0	1	1069	1.00E+00	0.00
	cell junction organization	0	0	0	344	1.00E+00	0.00
	cell morphogenesis	5	1	6	1394	1.00E+00	0.00
	cell motility	6	0	6	1136	1.00E+00	0.00
	cell proliferation	2	0	2	1761	1.00E+00	0.00
	cell wall organization or biogenesis	2	0	2	8	1.91E-02	1.72
	cell-cell signaling	3	0	3	819	1.00E+00	0.00
	cellular component assembly	10	1	11	2727	1.00E+00	0.00
	cellular nitrogen compound metabolic process	77	15	92	9618	1.00E+00	0.00
	cellular protein modification process	24	5	29	4497	1.00E+00	0.00
	chromosome organization	5	0	5	1579	1.00E+00	0.00
	chromosome segregation	0	0	0	306	1.00E+00	0.00
	circulatory system process	0	0	0	287	1.00E+00	0.00
	cofactor metabolic process	5	0	5	487	9.98E-01	0.00
	cytoskeleton organization	9	2	11	1490	1.00E+00	0.00
	developmental maturation	1	0	1	187	9.95E-01	0.00
	embryo development	0	0	0	1249	1.00E+00	0.00
	extracellular matrix organization	0	0	0	331	1.00E+00	0.00
	generation of precursor metabolites and energy	14	1	15	775	9.43E-01	0.03
	growth	1	0	1	998	1.00E+00	0.00
	helicase activity	1	2	3	501	1.00E+00	0.00
	homeostatic process	5	0	5	1392	1.00E+00	0.00
	hydrolase activity, acting on carbon-nitrogen	2	0	2	215	9.83E-01	0.01
	hydrolase activity, acting on glycosyl bonds	10	0	10	294	2.96E-01	0.53
	immune system process	2	0	2	2109	1.00E+00	0.00
	isomerase activity	7	1	8	533	9.81E-01	0.01
	kinase activity	30	5	35	2418	1.00E+00	0.00
	ligase activity	10	0	10	1167	1.00E+00	0.00
	lipid metabolic process	10	4	14	1404	1.00E+00	0.00

locomotion	6	1	7	1582	1.00E+00	0.00
lyase activity	10	2	12	644	9.43E-01	0.03
membrane organization	3	0	3	1749	1.00E+00	0.00
methyltransferase activity	1	2	3	422	9.99E-01	0.00
mitochondrion organization	1	0	1	562	1.00E+00	0.00
mitosis	0	0	0	635	1.00E+00	0.00
mRNA processing	0	0	0	858	1.00E+00	0.00
neurological system process	1	0	1	606	1.00E+00	0.00
nitrogen cycle metabolic process	1	0	1	27	5.31E-01	0.28
nucleic acid binding transcription factor activity	10	2	12	1471	1.00E+00	0.00
nucleotidyltransferase activity	2	1	3	389	9.99E-01	0.00
oxidoreductase activity	72	12	84	1988	8.25E-05	4.08
phosphatase activity	1	1	2	598	1.00E+00	0.00
photosynthesis	0	0	0	0	1.00E+00	0.00
pigmentation	1	0	1	95	9.30E-01	0.03
plasma membrane organization	0	0	0	272	1.00E+00	0.00
protein binding transcription factor activity	1	0	1	809	1.00E+00	0.00
protein folding	6	0	6	442	9.84E-01	0.01
protein maturation	27	10	37	2082	9.99E-01	0.00
reproduction	6	0	6	1074	1.00E+00	0.00
response to stress	4	1	5	3894	1.00E+00	0.00
ribosome biogenesis	0	0	0	419	1.00E+00	0.00
secondary metabolic process	0	0	0	30	1.00E+00	0.00
signal transduction	14	8	22	5173	1.00E+00	0.00
small molecule metabolic process	78	9	87	5046	1.00E+00	0.00
sulfur compound metabolic process	3	1	4	321	9.78E-01	0.01
symbiosis, encompassing mutualism through parasitism	0	0	0	1055	1.00E+00	0.00
transferase activity, transferring acyl groups	8	1	9	477	9.12E-01	0.04
transferase activity, transferring alkyl or aryl	0	1	1	84	9.05E-01	0.04
transferase activity, transferring glycosyl groups	6	1	7	370	8.87E-01	0.05
translation	3	0	3	1827	1.00E+00	0.00
transport	42	10	52	5804	1.00E+00	0.00

	transposition	0	0	0	10	1.00E+00	0.00
cellular component	cellular_component	38	18	56	6752	1.00E+00	0.00
	cell	114	17	131	18025	1.00E+00	0.00
	cytoplasm	60	8	68	13065	1.00E+00	0.00
	cytosol	5	0	5	3795	1.00E+00	0.00
	external encapsulating structure	0	0	0	7	1.00E+00	0.00
	extracellular region	9	5	14	3970	1.00E+00	0.00
	extracellular space	1	0	1	753	1.00E+00	0.00
	intracellular	111	15	126	17261	1.00E+00	0.00
	microtubule organizing center	4	0	4	831	1.00E+00	0.00
	nuclear envelope	3	0	3	600	1.00E+00	0.00
	nucleoplasm	5	1	6	4238	1.00E+00	0.00
	organelle	84	8	92	15633	1.00E+00	0.00
	plasma membrane	5	3	8	6162	1.00E+00	0.00
	protein complex	58	1	59	6318	1.00E+00	0.00
	proteinaceous extracellular matrix	1	0	1	243	9.99E-01	0.00
thylakoid	0	0	0	0	1.00E+00	0.00	
molecular function	molecular_function	142	27	169	12770	1.00E+00	0.00
	cytoskeletal protein binding	6	2	8	1222	1.00E+00	0.00
	DNA binding	22	5	27	3614	1.00E+00	0.00
	enzyme binding	6	4	10	2763	1.00E+00	0.00
	enzyme regulator activity	4	4	8	924	1.00E+00	0.00
	histone binding	0	0	0	276	1.00E+00	0.00
	ion binding	127	23	150	9502	1.00E+00	0.00
	lipid binding	2	1	3	687	1.00E+00	0.00
	protein binding, bridging	0	0	0	183	1.00E+00	0.00
	RNA binding	8	1	9	3316	1.00E+00	0.00
	small conjugating protein binding	0	0	0	174	1.00E+00	0.00
	structural molecule activity	12	2	14	1565	1.00E+00	0.00
	transcription factor binding	2	0	2	1241	1.00E+00	0.00
	unfolded protein binding	3	0	3	247	9.68E-01	0.01

Table S3.Summary of DEGs in the KEGG enrichment (HHA-HA-NOR).

Category	Pathway	HHA vs. NOR			
		Unigene	DEG	Pvalue	-LOG ₁₀ (P-value)
Metabolism	Overview	213	47	4.15E-40	39.38
Metabolism	Carbohydrate metabolism	395	69	2.79E-51	50.55
Metabolism	Energy metabolism	235	26	5.45E-15	14.26
Metabolism	Lipid metabolism	252	28	4.36E-16	15.36
Metabolism	Nucleotide metabolism	220	13	4.07E-05	4.39
Metabolism	Amino acid metabolism	294	51	6.59E-38	37.18
Metabolism	Metabolism of other amino acids	85	5	1.01E-02	2.00
Metabolism	Glycan biosynthesis and metabolism	171	2	7.40E-01	0.13
Metabolism	Metabolism of cofactors and vitamins	120	15	5.63E-10	9.25
Metabolism	Metabolism of terpenoids and polyketides	50	8	8.97E-07	6.05
Metabolism	Biosynthesis of other secondary metabolites	38	9	4.90E-09	8.31
Metabolism	Xenobiotics biodegradation and metabolism	85	15	3.50E-12	11.46
Metabolism	Enzyme families	0	0	1.00E+00	0.00
Genetic Information Processing	Transcription	197	0	1.00E+00	0.00
Genetic Information Processing	Translation	558	15	2.71E-02	1.57
Genetic Information Processing	Folding, sorting and degradation	417	8	3.12E-01	0.51
Genetic Information Processing	Replication and repair	205	1	9.58E-01	0.02
Genetic Information Processing	RNA family	0	0	1.00E+00	0.00
Environmental Information Processing	Membrane transport	18	2	3.06E-02	1.51
Environmental Information Processing	Signal transduction	1027	20	1.67E-01	0.78
Environmental Information Processing	Signaling molecules and interaction	95	4	5.88E-02	1.23
Cellular Processes	Transport and catabolism	332	15	2.22E-04	3.65
Cellular Processes	Cell motility	72	0	1.00E+00	0.00
Cellular Processes	Cell growth and death	351	4	7.89E-01	0.10
Cellular Processes	Cell communication	196	2	8.05E-01	0.09
Organismal Systems	Immune system	378	5	6.91E-01	0.16
Organismal Systems	Endocrine system	546	20	3.58E-04	3.45
Organismal Systems	Circulatory system	159	8	3.31E-03	2.48

Organismal Systems	Digestive system	197	13	1.28E-05	4.89
Organismal Systems	Excretory system	86	3	1.46E-01	0.84
Organismal Systems	Nervous system	390	4	8.51E-01	0.07
Organismal Systems	Sensory system	81	0	1.00E+00	0.00
Organismal Systems	Development	91	2	4.08E-01	0.39
Organismal Systems	Environmental adaptation	83	1	7.23E-01	0.14
Human Diseases	Cancers	826	11	7.24E-01	0.14
Human Diseases	Immune diseases	65	2	2.63E-01	0.58
Human Diseases	Neurodegenerative diseases	548	32	1.71E-10	9.77
Human Diseases	Substance dependence	171	3	4.89E-01	0.31
Human Diseases	Cardiovascular diseases	78	3	1.18E-01	0.93
Human Diseases	Endocrine and metabolic diseases	169	5	1.20E-01	0.92
Human Diseases	Infectious diseases	957	16	3.99E-01	0.40
Human Diseases	Drug resistance	0	0	1.00E+00	0.00

Category	Pathway	HA vs. NOR			
		Unigene	DEG	Pvalue	-LOG ₁₀ (P-value)
Metabolism	Overview	213	6	2.15E-03	2.67
Metabolism	Carbohydrate metabolism	395	6	3.63E-02	1.44
Metabolism	Energy metabolism	235	8	1.13E-04	3.95
Metabolism	Lipid metabolism	252	0	1.00E+00	0.00
Metabolism	Nucleotide metabolism	220	3	1.55E-01	0.81
Metabolism	Amino acid metabolism	294	1	8.38E-01	0.08
Metabolism	Metabolism of other amino acids	85	1	4.09E-01	0.39
Metabolism	Glycan biosynthesis and metabolism	171	0	1.00E+00	0.00
Metabolism	Metabolism of cofactors and vitamins	120	2	1.69E-01	0.77
Metabolism	Metabolism of terpenoids and polyketides	50	4	2.58E-04	3.59
Metabolism	Biosynthesis of other secondary metabolites	38	0	1.00E+00	0.00
Metabolism	Xenobiotics biodegradation and metabolism	85	3	1.57E-02	1.80
Metabolism	Enzyme families	0	0	1.00E+00	0.00
Genetic Information Processing	Transcription	197	0	1.00E+00	0.00
Genetic Information Processing	Translation	558	16	4.65E-07	6.33

Genetic Information Processing	Folding, sorting and degradation	417	7	1.53E-02	1.82
Genetic Information Processing	Replication and repair	205	1	7.19E-01	0.14
Genetic Information Processing	RNA family	0	0	1.00E+00	0.00
Environmental Information Processing	Membrane transport	18	0	1.00E+00	0.00
Environmental Information Processing	Signal transduction	1027	8	3.00E-01	0.52
Environmental Information Processing	Signaling molecules and interaction	95	1	4.44E-01	0.35
Cellular Processes	Transport and catabolism	332	3	3.35E-01	0.47
Cellular Processes	Cell motility	72	0	1.00E+00	0.00
Cellular Processes	Cell growth and death	351	4	1.72E-01	0.77
Cellular Processes	Cell communication	196	0	1.00E+00	0.00
Organismal Systems	Immune system	378	3	4.12E-01	0.39
Organismal Systems	Endocrine system	546	4	4.34E-01	0.36
Organismal Systems	Circulatory system	159	4	1.71E-02	1.77
Organismal Systems	Digestive system	197	3	1.22E-01	0.91
Organismal Systems	Excretory system	86	0	1.00E+00	0.00
Organismal Systems	Nervous system	390	1	9.11E-01	0.04
Organismal Systems	Sensory system	81	0	1.00E+00	0.00
Organismal Systems	Development	91	0	1.00E+00	0.00
Organismal Systems	Environmental adaptation	83	1	4.01E-01	0.40
Human Diseases	Cancers	826	4	7.50E-01	0.12
Human Diseases	Immune diseases	65	0	1.00E+00	0.00
Human Diseases	Neurodegenerative diseases	548	16	3.66E-07	6.44
Human Diseases	Substance dependence	171	0	1.00E+00	0.00
Human Diseases	Cardiovascular diseases	78	1	3.82E-01	0.42
Human Diseases	Endocrine and metabolic diseases	169	5	4.05E-03	2.39
Human Diseases	Infectious diseases	957	7	3.76E-01	0.43
Human Diseases	Drug resistance	0	0	1.00E+00	0.00

Category	Pathway	HHA vs. HA			
		Unigene	DEG	Pvalue	-LOG ₁₀ (P-value)
Metabolism	Overview	213	41	9.00E-23	22.05
Metabolism	Carbohydrate metabolism	395	78	4.34E-43	42.36

Metabolism	Energy metabolism	235	33	2.11E-14	13.68
Metabolism	Lipid metabolism	252	32	8.69E-13	12.06
Metabolism	Nucleotide metabolism	220	28	2.17E-11	10.66
Metabolism	Amino acid metabolism	294	58	2.79E-32	31.55
Metabolism	Metabolism of other amino acids	85	18	1.60E-11	10.80
Metabolism	Glycan biosynthesis and metabolism	171	7	1.95E-01	0.71
Metabolism	Metabolism of cofactors and vitamins	120	17	3.67E-08	7.44
Metabolism	Metabolism of terpenoids and polyketides	50	8	6.32E-05	4.20
Metabolism	Biosynthesis of other secondary metabolites	38	6	5.66E-04	3.25
Metabolism	Xenobiotics biodegradation and metabolism	85	18	1.60E-11	10.80
Metabolism	Enzyme families	0	0	1.00E+00	0.00
Genetic Information Processing	Transcription	197	0	1.00E+00	0.00
Genetic Information Processing	Translation	558	6	9.98E-01	0.00
Genetic Information Processing	Folding, sorting and degradation	417	13	3.67E-01	0.43
Genetic Information Processing	Replication and repair	205	4	8.20E-01	0.09
Genetic Information Processing	RNA family	0	0	1.00E+00	0.00
Environmental Information Processing	Membrane transport	18	1	3.96E-01	0.40
Environmental Information Processing	Signal transduction	1027	25	7.67E-01	0.11
Environmental Information Processing	Signaling molecules and interaction	95	11	6.37E-05	4.20
Cellular Processes	Transport and catabolism	332	15	4.40E-02	1.36
Cellular Processes	Cell motility	72	4	1.38E-01	0.86
Cellular Processes	Cell growth and death	351	12	2.66E-01	0.58
Cellular Processes	Cell communication	196	8	1.77E-01	0.75
Organismal Systems	Immune system	378	7	8.99E-01	0.05
Organismal Systems	Endocrine system	546	18	2.54E-01	0.60
Organismal Systems	Circulatory system	159	11	4.82E-03	2.32
Organismal Systems	Digestive system	197	15	4.10E-04	3.39
Organismal Systems	Excretory system	86	3	4.25E-01	0.37
Organismal Systems	Nervous system	390	10	6.37E-01	0.20
Organismal Systems	Sensory system	81	2	6.59E-01	0.18
Organismal Systems	Development	91	2	7.20E-01	0.14
Organismal Systems	Environmental adaptation	83	4	1.97E-01	0.71

Human Diseases	Cancers	826	27	2.10E-01	0.68
Human Diseases	Immune diseases	65	1	8.38E-01	0.08
Human Diseases	Neurodegenerative diseases	548	53	3.96E-15	14.40
Human Diseases	Substance dependence	171	5	5.11E-01	0.29
Human Diseases	Cardiovascular diseases	78	7	5.79E-03	2.24
Human Diseases	Endocrine and metabolic diseases	169	15	7.62E-05	4.12
Human Diseases	Infectious diseases	957	32	1.55E-01	0.81
Human Diseases	Drug resistance	0	0	1.00E+00	0.00

Table S4. List of DEGs in biological process based on the KEGG database.

Biological processes	Pathway	ID	name	putative function	HH vs NOR		HA vs NOR		HHA vs HA	
					^a Fold change	P-value	^b Fold change	^b P-value	^c Fold change	^d P-value
Glycolysis /Gluconeogenesis		c852_g1_i1	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	0.00	3.44E-02	0.00	1.96E-02	#DIV/0!	8.93E-01
		c48948_g1_i1	<i>ALDOA</i>	A	0.00	4.38E-02	0.00	4.50E-02	NA	NA
		c52661_g1_i1	<i>ENO</i>	Enolase	2.97	2.18E-02	2.21	5.12E-02	1.33	3.82E-01
		c86036_g1_i1	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	2.81	3.14E-02	0.86	6.15E-01	3.21	5.60E-03
		c87020_g1_i1	<i>ODP2</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	3.71	2.49E-02	1.02	9.25E-01	3.57	1.95E-02
		c87094_g1_i2	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	3.57	7.82E-03	1.69	2.00E-01	2.09	6.52E-02
		c88376_g1_i1	<i>ODPB</i>	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	3.22	1.87E-02	1.41	4.56E-01	2.24	4.77E-02
		c90323_g1_i2	<i>PCKG</i>	Phosphoenolpyruvate carboxykinase [GTP]	7.05	2.51E-02	2.05	5.19E-02	3.41	1.05E-01
		c56482_g1_i1	<i>CISY2</i>	Probable citrate synthase 2, mitochondrial	3.25	1.45E-02	1.32	5.69E-01	2.42	8.90E-03
		c57700_g2_i1	<i>IDHP</i>	Isocitrate dehydrogenase [NADP], mitochondrial	4.94	3.66E-03	2.46	1.48E-01	1.98	3.67E-02
		c85557_g2_i1	<i>PYC</i>	Pyruvate carboxylase, mitochondrial	3.33	1.32E-02	1.58	3.14E-01	2.08	2.83E-02
		c87020_g1_i1	<i>ODP2</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	3.71	2.49E-02	1.02	9.25E-01	3.57	1.95E-02

Citrate cycle (TCA cycle)	c88376_g1_i1	<i>ODPB</i>	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	3.22	1.87E-02	1.41	4.56E-01	2.24	4.77E-02
	c88995_g1_i1	<i>MDHM</i>	Malate dehydrogenase, mitochondrial	3.07	1.69E-02	1.17	7.49E-01	2.61	2.16E-02
	c90323_g1_i2	<i>PCKG</i>	Phosphoenolpyruvate carboxykinase [GTP]	7.05	2.51E-02	2.05	5.19E-02	3.41	1.05E-01
Pentose phosphate pathway	c48948_g1_i1	<i>ALDOA</i>	Fructose-bisphosphate aldolase A	0.00	4.38E-02	0.00	4.50E-02	NA	NA
	c81881_g3_i2	<i>DEOC</i>	Putative deoxyribose-phosphate aldolase	4.23	3.13E-02	2.52	4.39E-01	1.66	2.10E-01
	c84338_g1_i1	<i>TKTL2</i>	Transketolase-like protein 2	3.97	6.61E-03	1.54	3.17E-01	2.55	3.85E-02
	c85005_g1_i1	<i>TALDO</i>	Transaldolase	3.05	1.97E-02	1.31	4.54E-01	2.30	3.17E-02
	c86048_g1_i1	<i>6PGD</i>	6-phosphogluconate dehydrogenase, decarboxylating	3.11	1.49E-02	1.27	4.74E-01	2.42	3.30E-02
	c86682_g1_i1	<i>PRPS1</i>	Ribose-phosphate pyrophosphokinase 1	2.84	3.06E-02	1.43	4.72E-01	1.95	4.01E-02
Pentose and glucuronate interconversions	c66444_g1_i1	<i>DCXR</i>	L-xylulose reductase	61.23	2.25E-05	5.28	2.19E-01	11.57	2.38E-03
	c78375_g1_i1	<i>DCXR</i>	L-xylulose reductase	33.46	3.03E-02	1.49	9.21E-01	22.12	5.07E-02
	c81004_g1_i1	<i>UD11</i>	UDP-glucuronosyltransferase 1-1	7.34	1.72E-04	2.28	1.80E-01	3.18	6.88E-04
	c82227_g1_i1	<i>CRYL1</i>	Lambda-crystallin homolog	4.33	3.47E-03	1.54	3.75E-01	2.80	7.88E-03
	c86036_g1_i1	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	2.81	3.14E-02	0.86	6.15E-01	3.21	5.60E-03
	c86594_g1_i1	<i>UD2B7</i>	UDP-glucuronosyltransferase 2B7	14.16	2.03E-02	10.58	3.41E-01	1.33	5.95E-01
	c86782_g1_i1	<i>ALDR</i>	Aldose reductase	5.58	6.70E-04	2.30	3.04E-01	2.38	2.40E-02
	c86907_g1_i1	<i>CGT</i>	2-hydroxyacylsphingosine 1-beta-galactosyltransferase	23.04	1.27E-05	3.35	3.48E-01	6.76	8.42E-07
	c82918_g1_i1	<i>THIC</i>	Acetyl-CoA acetyltransferase, cytosolic	0.24	1.99E-02	0.39	1.04E-01	0.60	1.38E-01
	c85557_g2_i1	<i>PYC</i>	Pyruvate carboxylase, mitochondrial	3.33	1.32E-02	1.58	3.14E-01	2.08	2.83E-02
	c85736_g1_i1	<i>MAOX</i>	NADP-dependent malic enzyme	4.71	1.16E-02	1.71	3.76E-01	2.70	5.35E-02

Carbohydrate metabolism	Pyruvate metabolism	c86036_g1_i1	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	2.81	3.14E-02	0.86	6.15E-01	3.21	5.60E-03
		c86782_g1_i1	<i>ALDR</i>	Aldose reductase	5.58	6.70E-04	2.30	3.04E-01	2.38	2.40E-02
		c87020_g1_i1	<i>ODP2</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	3.71	2.49E-02	1.02	9.25E-01	3.57	1.95E-02
		c88376_g1_i1	<i>ODPB</i>	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	3.22	1.87E-02	1.41	4.56E-01	2.24	4.77E-02
		c88995_g1_i1	<i>MDHM</i>	Malate dehydrogenase, mitochondrial	3.07	1.69E-02	1.17	7.49E-01	2.61	2.16E-02
		c90323_g1_i2	<i>PCKG</i>	Phosphoenolpyruvate carboxykinase [GTP]	7.05	2.51E-02	2.05	5.19E-02	3.41	1.05E-01
		c91444_g1_i1	<i>ACAC</i>	Acetyl-CoA carboxylase	3.64	3.08E-02	0.98	9.60E-01	3.67	3.00E-02
		Energy metabolism	Oxidative phosphorylation	c17791_g1_i1	<i>COX6C</i>	Cytochrome c oxidase subunit 6C	3.95	4.36E-02	1.19	8.12E-01
c46621_g1_i1	<i>ENN8118</i>			ENN81187.1	2.73	4.17E-02	0.90	7.18E-01	3.01	3.00E-02
c64120_g1_i1	<i>VPP1</i>			V-type proton ATPase 116 kDa subunit a isoform 1	3.97	5.44E-03	2.23	3.03E-01	1.76	1.35E-01
c68798_g1_i2	<i>ATPK</i>			Putative ATP synthase subunit f, mitochondrial	2.52	4.78E-02	1.23	6.23E-01	2.03	3.77E-02
c81901_g1_i1	<i>QCR2</i>			Cytochrome b-c1 complex subunit 2, mitochondrial	2.71	3.96E-02	1.12	8.18E-01	2.40	5.97E-02
c82474_g1_i1	<i>ATPA</i>			ATP synthase subunit alpha, mitochondrial	2.65	3.91E-02	1.43	4.26E-01	1.83	6.63E-02
c83822_g1_i1	<i>ATPG</i>			ATP synthase subunit gamma, mitochondrial	3.21	1.30E-02	1.43	4.11E-01	2.22	1.93E-02
c84667_g1_i1	<i>CYB</i>			Cytochrome b	2.53	4.76E-02	2.78	9.78E-03	0.90	7.57E-01
c86650_g1_i1	<i>COX1</i>			Cytochrome c oxidase subunit 1	2.56	4.03E-02	2.39	2.05E-02	1.06	8.94E-01
c132634_g1_i1	<i>COX3</i>			Cytochrome c oxidase subunit 3	0.00	2.30E-02	0.00	1.64E-02	#DIV/0!	1.00E+00
c159762_g1_i1	<i>ATPO</i>			ATP synthase subunit 0, mitochondrial	3.56	3.17E-02	1.80	3.16E-01	1.96	9.67E-02

		c67276_g1_i1	<i>ACADV</i>	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	3.03	1.73E-02	1.50	6.43E-01	2.00	2.37E-02
		c82918_g1_i1	<i>ACBG2</i>	Long-chain-fatty-acid--CoA ligase	3.79	2.32E-02	0.39	1.04E-01	0.60	1.38E-01
		c84928_g2_i9	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	2.81	3.14E-02	1.82	3.00E-01	2.07	5.34E-02
		c86036_g1_i1	<i>GCDH</i>	Glutaryl-CoA dehydrogenase, mitochondrial	2.66	4.38E-02	0.86	6.15E-01	3.21	5.60E-03
	Fatty acid degradation	c88361_g1_i1	<i>THIC</i>	Acetyl-CoA acetyltransferase, cytosolic	0.24	1.99E-02	1.07	9.46E-01	2.47	7.77E-03
	Steroid biosynthesis	c82125_g1_i1	<i>DHC24</i>	Delta(24)-sterol reductase	6.27	2.88E-03	1.16	9.35E-01	5.31	9.91E-06
		c82842_g1_i1	<i>ERG31</i>	C-5 sterol desaturase erg31	37.12	9.77E-08	2.30	4.59E-01	16.04	7.90E-06
	Steroid hormone biosynthesis	c81004_g1_i1	<i>UD11</i>	UDP-glucuronosyltransferase 1-1	7.34	1.72E-04	2.28	1.80E-01	3.18	6.88E-04
		c86594_g1_i1	<i>UD2B7</i>	UDP-glucuronosyltransferase 2B7	14.16	2.03E-02	10.58	3.41E-01	1.33	5.95E-01
		c86907_g1_i1	<i>CGT</i>	2-hydroxyacylsphingosine 1-beta-galactosyltransferase	23.04	1.27E-05	3.35	3.48E-01	6.76	8.42E-07
	Glycerolipid metabolism	c83746_g1_i1	<i>GPAT4</i>	Glycerol-3-phosphate acyltransferase 4	2.65	4.86E-02	1.26	7.02E-01	2.08	5.05E-02
		c86036_g1_i1	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	2.81	3.14E-02	0.86	6.15E-01	3.21	5.60E-03
		c86782_g1_i1	<i>ALDR</i>	Aldose reductase	5.58	6.70E-04	2.30	3.04E-01	2.38	2.40E-02
		c89779_g1_i5	<i>LIPP</i>	Pancreatic triacylglycerol lipase (Fragment)	0.26	3.88E-02	0.70	5.55E-01	0.36	1.07E-02
	Glycerophospholipid metabolism	c83396_g1_i1	<i>GPDM</i>	Glycerol-3-phosphate dehydrogenase, mitochondrial	5.12	1.21E-03	2.03	1.14E-01	2.49	8.91E-03
		c83746_g1_i1	<i>GPAT4</i>	Glycerol-3-phosphate acyltransferase 4	2.65	4.86E-02	1.26	7.02E-01	2.08	5.05E-02
		c88119_g1_i1	<i>GPDA</i>	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	3.49	9.99E-03	1.55	3.32E-01	2.22	1.81E-02
		c88366_g2_i1	<i>AGT2L</i>	Alanine--glyoxylate aminotransferase 2-like	3.12	1.64E-02	3.14	1.39E-01	0.98	8.88E-01

Lipid metabolism	Sphingolipid metabolism	c68968_g1_i2	<i>ASM</i>	Sphingomyelin phosphodiesterase	7.84	3.76E-02	0.93	9.76E-01	8.42	2.75E-02
		c72231_g1_i1	<i>GLCM</i>	Glucosylceramidase	#DIV/0!	7.18E-03	#DIV/0!	8.23E-01	16.92	1.25E-04
		c81269_g1_i1	<i>NCASE</i>	Neutral ceramidase	5.83	6.89E-04	0.49	2.14E-01	11.74	2.09E-10
		c81853_g1_i1	<i>ASM</i>	Sphingomyelin phosphodiesterase	3.06	3.61E-02	1.88	2.16E-01	1.62	2.09E-01
Alanine, aspartate and glutamate metabolism		c78105_g1_i1	<i>AATM</i>	Aspartate aminotransferase, mitochondrial	2.74	3.18E-02	1.86	3.83E-01	1.46	2.03E-01
		c79336_g1_i2	<i>GABT</i>	4-aminobutyrate aminotransferase, mitochondrial	3.25	1.67E-02	0.65	3.76E-01	5.00	2.87E-03
		c88264_g1_i1	<i>PUR8</i>	Adenylosuccinate lyase	4.59	5.63E-03	0.98	9.22E-01	4.62	5.42E-03
		c88715_g4_i1	<i>PUR1</i>	Amidophosphoribosyltransferase	3.87	7.42E-03	2.40	4.68E-01	1.59	2.92E-01
Glycine, serine and threonine metabolism		c67642_g1_i1	<i>SERA</i>	D-3-phosphoglycerate dehydrogenase	4.56	2.42E-03	2.31	4.37E-02	1.94	7.17E-02
		c76453_g1_i1	<i>SERC</i>	Probable phosphoserine aminotransferase	8.52	1.56E-05	3.70	2.82E-01	2.28	1.66E-02
		c78811_g1_i1	<i>SARDH</i>	Sarcosine dehydrogenase, mitochondrial	137.65	8.63E-17	13.90	3.08E-01	9.74	1.39E-09
		c86583_g1_i1	<i>YF64</i>	Uncharacterized protein R102.4	6.26	3.73E-02	1.91	1.61E-01	0.13	4.41E-03
		c89184_g1_i1	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	0.25	1.27E-02	0.27	1.36E-01	0.28	8.69E-02
		c90572_g1_i3	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	0.07	6.20E-03	0.70	6.89E-01	0.28	5.54E-02
		c90870_g1_i1	<i>DHGL</i>	Glucose dehydrogenase [acceptor]	0.20	4.82E-02	1.52	3.77E-01	4.08	7.62E-02
Cysteine and methionine metabolism		c78105_g1_i1	<i>AATM</i>	Aspartate aminotransferase, mitochondrial	2.74	3.18E-02	1.86	3.83E-01	1.46	2.03E-01
		c85852_g1_i2	<i>SAHH</i>	Adenosylhomocysteinase	2.93	2.24E-02	0.91	7.51E-01	3.20	7.19E-04
		c86613_g1_i1	<i>ATTY</i>	Tyrosine aminotransferase	17.77	3.54E-02	3.38	7.35E-01	5.14	3.52E-02
		c88995_g1_i1	<i>MDHM</i>	Malate dehydrogenase, mitochondrial	3.07	1.69E-02	1.17	7.49E-01	2.61	2.16E-02

Valine, leucine and isoleucine degradation	c79123_g1_i1	<i>SCOT1</i>	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	6.34	2.27E-04	1.29	6.86E-01	4.86	9.66E-05
	c79336_g1_i2	<i>GABT</i>	4-aminobutyrate aminotransferase, mitochondrial	3.25	1.67E-02	0.65	3.76E-01	5.00	2.87E-03
	c82918_g1_i1	<i>MCCB</i>	Probable methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	2.95	3.06E-02	0.39	1.04E-01	0.60	1.38E-01
	c84333_g1_i1	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	2.81	3.14E-02	1.59	3.15E-01	1.84	7.58E-02
	c86036_g1_i1	<i>IVD</i>	Isovaleryl-CoA dehydrogenase, mitochondrial	4.14	1.37E-02	0.86	6.15E-01	3.21	5.60E-03
	c86860_g1_i1	<i>THIC</i>	Acetyl-CoA acetyltransferase, cytosolic	0.24	1.99E-02	1.90	3.18E-01	2.16	7.67E-02
Lysine degradation	c82918_g1_i1	<i>THIC</i>	Acetyl-CoA acetyltransferase, cytosolic	0.24	1.99E-02	0.39	1.04E-01	0.60	1.38E-01
	c86036_g1_i1	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	2.81	3.14E-02	0.86	6.15E-01	3.21	5.60E-03
	c86652_g1_i1	<i>AASS</i>	Alpha-aminoadipic semialdehyde synthase, mitochondrial	62.31	7.43E-06	10.67	2.02E-01	5.78	1.02E-02
	c88361_g1_i1	<i>GCDH</i>	Glutaryl-CoA dehydrogenase, mitochondrial	2.66	4.38E-02	1.07	9.46E-01	2.47	7.77E-03
	c89234_g1_i1	<i>AADAT</i>	Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial	17.95	7.67E-08	10.20	2.90E-01	1.73	2.96E-01
	c76439_g1_i1	<i>KARG</i>	Arginine kinase	2.82	2.62E-02	1.50	5.37E-01	1.87	5.70E-02
	c78105_g1_i1	<i>AATM</i>	Aspartate aminotransferase, mitochondrial	2.74	3.18E-02	1.86	3.83E-01	1.46	2.03E-01
	c84547_g1_i2	<i>OAT</i>	Ornithine aminotransferase, mitochondrial	4.41	2.46E-03	1.30	5.94E-01	3.36	2.51E-03
	c86036_g1_i1	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	2.81	3.14E-02	0.86	6.15E-01	3.21	5.60E-03

Amino acid metabolism	Arginine and proline metabolism	c89357_g1_i1	<i>P5CS</i>	Delta-1-pyrroline-5-carboxylate synthase	3.66	5.62E-03	1.15	9.43E-01	3.16	4.37E-04	
		c89444_g1_i1	<i>ARGI2</i>	Arginase-2, mitochondrial	3.43	1.36E-02	0.79	7.12E-01	4.29	1.81E-04	
		Tyrosine metabolism	c69172_g1_i1	<i>METL6</i>	Methyltransferase-like protein 6	0.24	2.90E-02	0.92	9.72E-01	0.26	5.21E-04
			c78105_g1_i1	<i>AATM</i>	Aspartate aminotransferase, mitochondrial	2.74	3.18E-02	1.86	3.83E-01	1.46	2.03E-01
			c83391_g1_i1	<i>HPPD</i>	4-hydroxyphenylpyruvate dioxygenase	6.95	6.70E-03	1.13	9.22E-01	6.09	8.73E-03
			c85515_g1_i1	<i>HGD</i>	Homogentisate 1,2-dioxygenase	2.78	4.33E-02	1.06	8.72E-01	2.60	3.28E-02
			c86613_g1_i1	<i>ATTY</i>	Tyrosine aminotransferase	17.77	3.54E-02	3.38	7.35E-01	5.14	3.52E-02
			c82918_g1_i1	<i>THIC</i>	Acetyl-CoA acetyltransferase, cytosolic	0.24	1.99E-02	0.39	1.04E-01	0.60	1.38E-01
			c86036_g1_i1	<i>ALDH2</i>	Aldehyde dehydrogenase, mitochondrial	2.81	3.14E-02	0.86	6.15E-01	3.21	5.60E-03
			c87573_g1_i1	<i>CATA</i>	Catalase	0.33	1.90E-02	0.99	8.68E-01	0.32	5.54E-02
			c88361_g1_i1	<i>GCDH</i>	Glutaryl-CoA dehydrogenase, mitochondrial	2.66	4.38E-02	1.07	9.46E-01	2.47	7.77E-03
		Tryptophan metabolism	c89234_g1_i1	<i>AADAT</i>	Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial	17.95	7.67E-08	10.20	2.90E-01	1.73	2.96E-01
			c852_g1_i1	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	0.00	3.44E-02	0.00	1.96E-02	#DIV/0!	8.93E-01
			c52661_g1_i1	<i>ENO</i>	Enolase	2.97	2.18E-02	2.21	5.12E-02	1.33	3.82E-01
			c87094_g1_i2	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	3.57	7.82E-03	1.69	2.00E-01	2.09	6.52E-02
		HIF-1 signaling pathway	c88376_g1_i1	<i>ODPB</i>	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	3.22	1.87E-02	1.41	4.56E-01	2.24	4.77E-02
			c175672_g1_i1	<i>RS6</i>	40S ribosomal protein S6	0.00	2.53E-02	0.00	2.66E-02	NA	NA
			c90106_g1_i4	<i>CREBA</i>	Cyclic AMP response element-binding protein A	3.10	2.81E-02	1.34	5.17E-01	2.29	2.24E-02

Signal transduction	PI3K-Akt signaling pathway	c90323_g1_i2	<i>PCKG</i>	Phosphoenolpyruvate carboxykinase [GTP]	7.05	2.51E-02	2.05	5.19E-02	3.41	1.05E-01
		c155410_g1_i1	<i>HS90B</i>	Heat shock protein HSP 90-beta	0.00	3.00E-02	0.00	3.13E-02	NA	NA
		c175672_g1_i1	<i>RS6</i>	40S ribosomal protein S6	0.00	2.53E-02	0.00	2.66E-02	NA	NA
	Two-component system	c84667_g1_i1	<i>CYB</i>	Cytochrome b	2.53	4.76E-02	2.78	9.78E-03	0.90	7.57E-01
		c82918_g1_i1	<i>THIC</i>	Acetyl-CoA acetyltransferase, cytosolic	0.24	1.99E-02	2.78	9.78E-03	0.90	7.57E-01
	MAPK signaling pathway - fly	c87130_g1_i1	<i>FGFR1</i>	Fibroblast growth factor receptor 1	12.00	6.99E-03	0.39	1.04E-01	0.60	1.38E-01
	Notch signaling pathway	c86784_g1_i1	<i>DL</i>	Neurogenic locus protein delta	0.27	4.83E-02	0.39	1.40E-01	0.68	3.04E-01
	TNF signaling pathway	c90515_g1_i1	<i>MMP14</i>	Matrix metalloproteinase-14	0.35	0.031991	1.04	8.15E-01	0.33	1.46E-01
	Fox0 signaling pathway	c87573_g1_i1	<i>CATA</i>	Catalase	0.33	1.90E-02	0.99	8.68E-01	0.32	5.54E-02
		c90323_g1_i2	<i>PCKG</i>	Phosphoenolpyruvate carboxykinase [GTP]	7.05	2.51E-02	2.05	5.19E-02	3.41	1.05E-01
c71701_g1_i1		<i>SODM1</i>	Superoxide dismutase [Mn] 1, mitochondrial	3.39	4.99E-02	1.58	5.21E-01	2.12	5.98E-02	
mTOR signaling pathway	c175672_g1_i1	<i>RS6</i>	40S ribosomal protein S6	0.00	2.53E-02	0.00	2.66E-02	NA	NA	
Immune system	Antigen processing and presentation	c33481_g1_i1	<i>CALR</i>	Calreticulin	0.00	2.85E-02	0.00	2.98E-02	NA	NA
		c85874_g1_i1	<i>CATL</i>	Cathepsin L	15.26	3.65E-04	4.18	2.38E-01	3.56	2.81E-02
		c89198_g5_i1	<i>GILT</i>	Gamma-interferon-inducible lysosomal thiol reductase	6.28	4.61E-02	0.61	8.62E-01	10.25	2.72E-05
		c155410_g1_i1	<i>HS90B</i>	Heat shock protein HSP 90-beta	0.00	3.00E-02	0.00	3.13E-02	NA	NA

^a#DIV/0 in Fold change meant a gene undetected or unexpressed in NOR, while highly expressed in HHA; ^b#DIV in Fold change meant a gene undetected or unexpressed in NOR, while highly expressed in HA; ^c#DIV in Fold change meant a gene undetected or unexpressed in HA, while highly expressed in HHA; NA in fold change meant a gene undetected or unexpressed both in HHA and HA. ^dNA in p-value meant no difference between HHA and HA.

Table S5. List of DEGs related to the function of immune, signal transduction and stress response based on the GO database.

Biological process	number	name	putative function	HA vs NOR		HHA vs NOR		HHA vs HA	
				Fold change	P-value	Fold change	P-value	^a Fold change	^b P-value
18 common elements in "HHA vs NOR" and "HA vs NOR"	c852_g1_i1	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	0.00	1.96E-02	0.00	3.44E-02	NA	NA
	c7566_g1_i1	<i>K2C8</i>	Keratin, type II cytoskeletal 8	0.00	3.16E-02	0.00	3.03E-02	NA	NA
	c10091_g1_i1	<i>ERRFI</i>	ERBB receptor feedback inhibitor 1	0.00	4.44E-02	0.00	4.31E-02	NA	NA
	c33481_g1_i1	<i>CALR</i>	Calreticulin	0.00	2.98E-02	0.00	2.85E-02	NA	NA
	c48948_g1_i1	<i>ALDOA</i>	Fructose-bisphosphate aldolase	0.00	4.50E-02	0.00	4.38E-02	NA	NA
	c54262_g1_i1	<i>XRCC6</i>	X-ray repair cross-complementing protein 6	0.00	4.76E-02	0.00	4.63E-02	NA	NA
	c55505_g1_i1	<i>PDIA1</i>	disulfide-isomerase	0.00	3.21E-02	0.00	3.08E-02	NA	NA
	c60921_g1_i1	<i>SAP</i>	Proactivator polypeptide	0.00	4.62E-02	0.00	4.50E-02	NA	NA
	c66811_g1_i3	<i>EAX03762.1</i>	high mobility group AT-hook 1, isoform	0.00	9.87E-01	0.00	4.94E-02	2.88	9.92E-01
	c71708_g1_i2	<i>SYAC</i>	Alanine--tRNA ligase	0.00	4.61E-02	0.00	4.50E-02	1.25	NA
	c73608_g1_i1	<i>HYOU1</i>	Hypoxia up-regulated protein 1	0.00	3.97E-02	0.00	3.84E-02	NA	NA
	c78273_g1_i1	<i>SODC</i>	Superoxide dismutase	0.18	1.09E-02	0.23	1.37E-02	NA	6.37E-01
	c115380_g1_i1	<i>TCTP</i>	Translationally-controlled tumor protein	0.00	3.33E-02	0.00	3.19E-02	2.88	NA
	c155410_g1_i1	<i>HS90B</i>	Heat shock protein HSP 90-beta	0.00	3.13E-02	0.00	3.00E-02	NA	NA
	c175883_g1_i1	<i>IEX1</i>	Radiation-inducible immediate-early gene IEX-1	0.00	4.98E-02	0.00	4.86E-02	NA	NA
	c178714_g1_i1	<i>RS3</i>	40S ribosomal protein	0.00	2.81E-02	0.00	2.68E-02	NA	NA
	c197870_g1_i1	<i>GRP78</i>	78 kDa glucose-regulated protein	0.00	4.07E-02	0.00	2.10E-02	0.00	9.16E-01
	c198512_g1_i1	<i>RS19</i>	40S ribosomal protein S19	0.00	4.62E-02	0.00	4.50E-02	NA	NA
10 elements included exclusively in "response to stress"	c10089_g1_i1	<i>RL13A</i>	60S ribosomal protein L13a	0.00	5.29E-02	0.00	2.37E-02	0.00	7.71E-01
	c35619_g1_i3	<i>ANXA2</i>	Annexin A2	0.00	7.14E-02	0.00	3.78E-02	0.00	9.16E-01
	c43808_g1_i1	<i>BAXI</i>	Basigin	0.00	9.23E-02	0.00	4.96E-02	0.00	9.16E-01
	c56546_g1_i1	<i>PDIA4</i>	Protein disulfide	0.00	5.08E-02	0.00	4.96E-02	NA	NA

ely in "HHA vs NOR"	c71276_g2_i1	<i>RL40</i>	Ubiquitin-60S ribosomal protein L40	0.00	8.75E-02	0.00	4.67E-02	0.00	9.16E-01
	c71701_g1_i1	<i>SODM1</i>	Superoxide dismutase [Mn] 1, mitochondrial	1.58	5.21E-01	3.39	4.99E-02	2.12	5.98E-02
	c76730_g1_i2	<i>SQSTM</i>	Sequestosome-1	0.00	5.05E-02	0.00	4.94E-02	NA	NA
	c87573_g1_i1	<i>CATA</i>	Catalase	0.99	8.68E-01	0.33	1.90E-02	0.32	5.54E-02
	c155448_g1_i1	<i>ENPL</i>	Endoplasmin	0.00	5.05E-02	0.00	4.93E-02	NA	NA
	c178017_g1_i1	<i>GBLP</i>	Guanine nucleotide	0.00	7.61E-02	0.00	3.08E-02	0.00	7.50E-01
1 elements included exclusiv ely in "HA vs NOR"	c32676_g1_i1	<i>4F2</i>	cell-surface antigen heavy chain	0.00	4.58E-02	0.00	8.25E-02	NA	8.87E-01
4 elements included exclusiv ely in "HHA vs HA "	c73138_g1_i1	<i>PRX2B</i>	Peroxiredoxin-2B	0.02	1.54E-01	0.99	9.19E-01	53.93	3.40E-15
	c82037_g1_i1	<i>CATA</i>	Catalase	0.73	8.49E-01	8.96	5.66E-02	0.08	1.44E-03
	c85401_g1_i1	<i>RAD51</i>	repair protein RAD51 homolog 1	0.41	2.52E-01	1.04	1.00E+00	0.41	3.15E-02
	c85826_g1_i1	<i>CUL4A</i>	Cullin-4A	0.06	3.96E-01	1.08	9.96E-01	0.06	1.43E-02
	c89464_g1_i1	<i>TC011651</i>	hypothetical protein TcasGA2 TC011651	0.03	1.20E-01	0.01	5.37E-02	3.20	3.33E-02
10 common elements in "HHA " and "HA":	c852_g1_i1	<i>G3P</i>	Glyceraldehyde-3-phosphate dehydrogenase	0.00	1.96E-02	0.00	3.44E-02	NA	8.93E-01
	c33481_g1_i1	<i>CALR</i>	Calreticulin	0.00	2.98E-02	0.00	2.85E-02	NA	NA
	c54262_g1_i1	<i>XRCC6</i>	X-ray repair cross-complementing protein 6	0.00	4.76E-02	0.00	4.63E-02	NA	NA
	c57175_g1_i2	<i>CALX</i>	Calnexin	0.00	4.79E-02	0.00	4.67E-02	NA	NA
	c64025_g1_i1	<i>EF2</i>	Elongation factor 2	0.00	4.80E-02	0.00	1.60E-02	0.00	6.01E-01
	c133618_g1_i1	<i>PGRP2</i>	Peptidoglycan-recognition protein 2	5.35	4.64E-02	7.46	1.30E-02	1.38	4.33E-01
	c155410_g1_i1	<i>HS90B</i>	Heat shock protein HSP 90-beta	0.00	3.13E-02	0.00	3.00E-02	NA	NA
	c155905_g1_i1	<i>IMDH2</i>	Inosine-5'-monophosphate dehydrogenase 2	0.00	4.05E-02	0.00	3.92E-02	NA	NA
	c175672_g1_i1	<i>RS6</i>	40S ribosomal protein S6	0.00	2.66E-02	0.00	2.53E-02	NA	NA

immune systems		c198512_g1_i1	<i>RS19</i>	40S ribosomal protein S19	0.00	4.62E-02	0.00	4.50E-02	NA	NA
	7 elements included	c10089_g1_i1	<i>RL13A</i>	60S ribosomal protein L13a	0.00	5.29E-02	0.00	2.37E-02	0.00	7.71E-01
		c35619_g1_i3	<i>ANXA2</i>	Annexin A2	0.00	7.14E-02	0.00	3.78E-02	0.00	9.16E-01
		c43808_g1_i1	<i>BASI</i>	Basigin	0.00	9.23E-02	0.00	4.96E-02	0.00	9.16E-01
	exclusively in "HHA vs NOR"	c71276_g2_i1	<i>RL40</i>	Ubiquitin-60S ribosomal protein L40	0.00	8.75E-02	0.00	4.67E-02	0.00	9.16E-01
		c76730_g1_i2	<i>SQSTM</i>	Sequestosome-1	0.00	5.05E-02	0.00	4.94E-02	NA	NA
		c112579_g1_i1	<i>PGRP-SC2</i>	Peptidoglycan-recognition protein SC2	2.98	1.12E-01	4.27	5.71E-03	1.42	2.32E-01
					0.00	5.05E-02	0.00	4.93E-02	NA	NA
		c155448_g1_i1	<i>ENPL</i>	Endoplasmin						
	4 elements included	c16432_g1_i1	<i>RS14</i>	40S ribosomal protein S14	0.00	3.85E-02	0.00	6.92E-02	NA	8.93E-01
		c32676_g1_i1	<i>4F2</i>	4F2 cell-surface antigen heavy chain	0.00	4.58E-02	0.00	8.25E-02	NA	8.87E-01
	exclusively in "HA vs NOR"	c92107_g1_i1	<i>FRIH</i>	Ferritin heavy chain	0.00	2.88E-02	0.00	5.13E-02	NA	8.93E-01
					0.00	3.50E-02	0.00	6.29E-02	NA	8.93E-01
		c116965_g1_i1	<i>RS17</i>	40S ribosomal protein S17						
	2 elements included				0.02	1.54E-01	0.99	9.19E-01	53.93	3.40E-15
exclusively in "HHA vs HA":	c73138_g1_i1	<i>PRX2B</i>	Peroxiredoxin-2B							
				0.06	3.96E-01	1.08	9.96E-01	0.06	1.43E-02	
	c85826_g1_i1	<i>CUL4A</i>	Cullin-4A							

17 common elements in "HHA " and "HA":	c7566_g1_i1	<i>K2C8</i>	Keratin, type II cytoskeletal 8	0.00	3.16E-02	0.00	3.03E-02	NA	NA
	c10091_g1_i1	<i>ERRFI</i>	receptor feedback inhibitor 1	0.00	4.44E-02	0.00	4.31E-02	NA	NA
	c33481_g1_i1	<i>CALR</i>	Calreticulin	0.00	2.98E-02	0.00	2.85E-02	NA	NA
	c33573_g1_i2	<i>AKA12</i>	A-kinase anchor protein 12	0.00	2.49E-02	0.00	2.37E-02	NA	NA
	c55505_g1_i1	<i>PDIA1</i>	Protein disulfide-isomerase	0.00	3.21E-02	0.00	3.08E-02	NA	NA
	c60921_g1_i1	<i>SAP</i>	Proactivator polypeptide	0.00	4.62E-02	0.00	4.50E-02	NA	NA
	c71708_g1_i2	<i>SYAC</i>	Alanine--tRNA ligase, cytoplasmic	0.00	4.61E-02	0.00	4.50E-02	NA	NA
	c73608_g1_i1	<i>HYOU1</i>	Hypoxia up-regulated protein 1	0.00	3.97E-02	0.00	3.84E-02	NA	NA
	c113921_g1_i1	<i>YBOX1_</i>	Nuclease-sensitive element- binding protein 1	0.00	4.46E-02	0.00	4.34E-02	NA	NA
	c115380_g1_i1	<i>TCTP</i>	Translationally-controlled tumor protein	0.00	3.33E-02	0.00	3.19E-02	NA	NA
	c155410_g1_i1	<i>HS90B</i>	Heat shock protein HSP 90-beta	0.00	3.13E-02	0.00	3.00E-02	NA	NA
	c175672_g1_i1	<i>RS6</i>	40S ribosomal protein S6	0.00	2.66E-02	0.00	2.53E-02	NA	NA
	c175883_g1_i1	<i>IEX1</i>	Radiation-inducible immediate- early gene IEX-1	0.00	4.98E-02	0.00	4.86E-02	NA	NA
	c178031_g1_i1	<i>K1C18_</i>	Keratin, type I cytoskeletal 18	0.00	4.51E-02	0.00	4.39E-02	NA	NA
	c178714_g1_i1	<i>RS3</i>	40S ribosomal protein S3	0.00	2.81E-02	0.00	2.68E-02	NA	NA
c197669_g1_i1	<i>S10A6</i>	Protein S100-A6	0.00	3.50E-02	0.00	3.37E-02	NA	NA	
c197870_g1_i1	<i>GRP78</i>	78 kDa glucose-regulated protein	0.00	4.07E-02	0.00	2.10E-02	NA	NA	
10 elements included exclusiv ely in "HHA vs NOR"	c91160_g1_i1	<i>PLXB</i>	Plexin-B	0.00	7.84E-02	0.00	4.19E-02	0.00	8.83E-01
	c86784_g1_i1	<i>DL</i>	Neurogenic locus protein delta	0.00	9.23E-02	0.00	4.96E-02	0.00	9.16E-01
	c43808_g1_i1	<i>BASI</i>	Basigin	0.00	8.75E-02	0.00	4.67E-02	0.00	9.16E-01
	c178017_g1_i1	<i>GBLP</i>	Guanine nucleotide-binding protein subunit beta-2-like 1	0.00	5.05E-02	0.00	4.94E-02	NA	NA
	c71276_g2_i1	<i>RL40</i>	Ubiquitin-60S ribosomal protein L40	1.94	5.25E-01	0.29	1.77E-02	0.15	3.08E-01
	c84528_g1_i1	<i>GEM</i>	GTP-binding protein GEM	0.58	5.26E-01	0.09	2.76E-03	0.15	1.52E-01
	c10405_g1_i1	<i>IF4A1</i>	Eukaryotic initiation factor 4A-I	0.39	1.40E-01	0.27	4.83E-02	0.68	3.04E-01

signal
transduction

	c76730_g1_i2	<i>SQSTM</i>	Sequestosome-1	0.60	3.54E-01	0.31	4.01E-02	0.51	6.94E-02
	c79208_g1_i2	<i>HR3</i>	Probable nuclear hormone receptor HR3	1.94	5.25E-01	0.29	1.77E-02	NA	NA
	c155448_g1_i1	<i>ENPL</i>	Endoplasmin	0.00	5.05E-02	0.00	4.93E-02	0.00	7.50E-01
4 elements included exclusively in "HA vs NOR"	c87159_g1_i1	<i>ERB1</i>	ecdysone receptor B1 isoform	0.23	9.70E-03	0.46	1.90E-01	1.94	7.85E-02
	c88775_g3_i1	<i>DIHR</i>	Diuretic hormone receptor	3.81	4.61E-02	2.71	1.81E-01	0.71	3.78E-01
	c90034_g1_i4	<i>GUS</i>	Protein gustavus	0.30	1.43E-02	0.49	1.55E-01	1.63	3.21E-01
	c90353_g1_i1	<i>ABR</i>	Active breakpoint cluster region-related protein	0.29	2.99E-02	0.34	6.43E-02	1.17	8.91E-01
15 elements included exclusively in "HHA VS HA "	c57228_g1_i1	<i>YPC2</i>	Putative serine/threonine-protein kinase C05D10.2	0.04	2.03E-01	0.70	7.36E-01	18.16	1.10E-08
	c64345_g1_i1	<i>NEDD8</i>	NEDD8	0.00	2.07E-01	1.07	9.82E-01	Inf	2.81E-02
	c66184_g1_i1	<i>EMA</i>	Echinoderm microtubule-associated protein-like	0.24	5.60E-01	1.46	8.23E-01	6.00	2.15E-02
	c83595_g1_i1	<i>YQE_11798</i>	hypothetical protein YQE 11798, partial	0.03	1.92E-01	0.74	7.65E-01	22.38	1.29E-03
	c84804_g1_i1	<i>DRD2L</i>	Dopamine D2-like receptor	1.62	8.97E-01	5.78	1.73E-01	3.50	1.04E-02
	c85936_g1_i1	<i>ARHG7</i>	Rho guanine nucleotide exchange factor 7	1.80	4.16E-01	0.67	7.76E-01	0.37	4.84E-02
	c86866_g1_i1	<i>IFT80</i>	Intraflagellar transport protein 80 homolog	0.03	2.09E-01	1.04	9.59E-01	37.71	1.96E-06
	c86882_g1_i1	<i>CALCR</i>	Calcitonin receptor	1.17	9.74E-01	3.59	2.74E-01	3.01	2.67E-02
	c87294_g1_i2	<i>KC1G1</i>	Casein kinase I isoform gamma-1	0.02	1.62E-01	0.67	7.24E-01	33.21	6.11E-06
	c87713_g1_i1	<i>YQI7</i>	Uncharacterized protein C45G9.7	1.81	6.48E-01	0.51	6.84E-01	0.28	3.13E-02
	c89833_g1_i1	<i>Y1760</i>	Probable G-protein coupled receptor CG31760	1.19	6.70E-01	0.46	2.23E-01	0.38	1.18E-02
	c90019_g2_i2	<i>MTH5</i>	Probable G-protein coupled receptor Mth-like 5	1.17	8.25E-01	0.46	4.64E-01	0.39	4.80E-02

	c90665_g1_i1	<i>ARL5B</i>	ADP-ribosylation factor-like protein 5B	1.77	2.96E-01	0.69	6.59E-01	0.38	1.42E-02
	c91149_g1_i2	<i>KPCA</i>	Putative protein kinase C delta type homolog	0.23	2.46E-01	0.71	6.56E-01	3.04	3.10E-03
	c91353_g1_i3	<i>ANK3</i>	Ankyrin-3	0.97	9.38E-01	2.53	7.05E-02	2.59	1.29E-02
5 common elements in "HHA" and "HHA VS HA "	c65249_g1_i1	<i>YQE_1273_2</i>	hypothetical protein YQE 12732, partial	0.41	3.44E-01	0.10	4.24E-02	0.24	2.70E-02
	c69451_g1_i1	<i>RHPN2</i>	Rhopilin-2	0.56	2.64E-01	0.15	9.28E-04	0.26	3.20E-04
	c77161_g1_i1	<i>AAT2</i>	ADP/ATP translocase 2	0.46	4.26E-01	4.14	2.71E-02	8.98	2.09E-07
	c80440_g1_i3	<i>RXRA</i>	Retinoic acid receptor RXR-alpha	1.26	9.01E-01	3.20	3.65E-02	2.50	5.37E-03
	c91627_g3_i1	<i>UNC22</i>	Twitchin	0.75	6.46E-01	5.21	2.37E-03	6.83	4.62E-07
	c91138_g1_i1	<i>ECR</i>	Ecdysone receptor	0.43	4.05E-02	1.11	8.31E-01	2.52	8.02E-03
2 common elements in "HA" and "HHA VS HA "	c154518_g1_i1	<i>SEPT5</i>	Septin-5	10.35	7.22E-03	1.85	5.97E-01	0.18	4.05E-02

^aNA in Fold change meant a gene undetected or unexpressed both in HHA and HA; ^bNA in p-value meant no difference between HHA and HA.

Table S6. Primers used for q-PCR certification.

Number	Name	Primers(5'-3')		Product length (bp)
		F	R	
c86036_g1_i1	<i>ALD</i>	GGCTCTTTCAACGGACCTCTCG	GGTCAAGTGTGCTGTGCTGGAT	84
c85557_g2_i1	<i>PYC</i>	CGTGGGTGTGGATGTGAATGGG	GACGAGCTGGTGAAGGCTGGTA	139
c84338_g1_i1	<i>tktA /B</i>	TTAGGCGACCAAGCGGACAGA	TCTACTGGAGGTGCGTCGTCTT	113
c91444_g1_i1	<i>ACAC</i>	TGCTGTTGCTCTTGCTGCTGTT	GTGGCGTTCTGGAACCTGAAGG	142
c89767_g1_i1	<i>AKR</i>	GCCTGTGGCGTACAAGGAAGAA	CACACTCCTCCAACGCTTTCCA	110
c77779_g1_i1	<i>MDH</i>	CAAGCTGAATCCTCGCCGCATA	ACGCCGCACATTTACCTACG	84
c82236_g1_i1	<i>GLNA</i>	TCCCAGCGACATCCATCCTTGT	GGTAGACGGAGCGACTGAGTGA	93
c81873_g1_i1	<i>ALT</i>	CGGATGAACGTGATCGGCTGTT	GCTGGTTATTCGGGCTGGTGAA	129
c76453_g1_i1	<i>PSAT</i>	ACGACGCCATCAACAACCTCAA	TCAGCAGCTTCTCGGCCTCTT	150
c73927_g1_i2	<i>CDO</i>	GTTCGCAATCCACGACCACAA	CACCATCCTTCTCAGGCCAAGC	99
c83391_g1_i1	<i>HPD</i>	TTCCAGCCCTTTGTACGCCAAG	AGGACCAAAGCCTACCAACGGA	133
c81288_g1_i1	<i>DDO</i>	GGCTGTCGCCAATACGAGTCAT	GGCTTCTGTGCGGTCTCAATCC	139
c78811_g1_i1	<i>SARDH</i>	TTGGTGGAGGTGCCTCAGGAT	GTGCCATGTCGTACTIONGCTTGCT	107
c88361_g1_i1	<i>GCDH</i>	GCGTACACCCTCGACAGGAAAC	TCCGTCATCATGTCCGCCATCT	86
c72231_g1_i1	<i>GBA</i>	GGTTGGGTGGACTGGAACATGG	CGGCTGTGGCGTTGACTACTAT	97
c86907_g1_i1	<i>UGT</i>	ACGGAGGGCATGGATGGGTTAC	GCTCACTTCGACGCTCACTTGG	92
c88719_g1_i3	<i>FGFR2</i>	GGCAAGGGCTGCAATTGTCACT	TCTCCTGAAGCGTAGGCGTTCG	144
c84960_g1_i1	<i>RASGAP</i>	ACGCCACAGACTGCCTTACA	TTGGCTCTCGTCCTGGCTACTC	91
c89572_g2_i1	<i>FOXO3</i>	CGCCGCTGAAGTTGAAGTCCA	CGCTGAACAACCACGCCATCA	138
c82037_g1_i1	<i>katE</i>	TGTCAGAGGGTTCGCCGTCAA	CTGCGTGTGGATGAAGTGTGGA	121
c90106_g1_i4	<i>CREB</i>	GGTGTTGGTGACGGAGACGATG	AAGACGAGCCGAACAGCGAGA	127