Supplemental table S6. GO terms significantly enriched in significantly downregulated genes of the microarray. K: number of genes from the input cluster in the given category. F: number of total genes in the given category.

Biological Process GO Terms: Over Representation		Sorting Results by: the p-Value in an ascending order.		
Category	GO Level	p-value	k	f
[GO:0008150] biological_process	0	3.41E-12	140	16056
[GO:0051179] localization	2	1.69E-07	46	2975
[GO:0019752] carboxylic acid metabolism	7	2.22E-07	17	521
[GO:0006082] organic acid metabolism	6	2.28E-07	17	522
[GO:0006066] alcohol metabolism	6	2.74E-07	13	300
[GO:0051234] establishment of localization	3	8.48E-07	44	2935
[GO:0006810] transport	6	3.03E-06	39	2558
[GO:0007582] physiological process	1	7.27E-06	119	13342
[GO:0050875] cellular physiological process	3	1.33E-05	103	10888
[GO:0006812] cation transport	8	1.80E-05	14	506
[GO:0008542] visual learning	9	2.00E-05	3	8
[GO:0009987] cellular process	1	2.08E-05	121	13877
[GO:0006629] lipid metabolism	4	2.35E-05	16	662
[GO:0006631] fatty acid metabolism	11	3.28E-05	8	170
[GO:0030001] metal ion transport	9	3.37E-05	12	400
[GO:0007275] development	1	3.56E-05	36	2523
[GO:0001505] regulation of neurotransmitter levels	9	4.78E-05	6	90
[GO:0044255] cellular lipid metabolism	8	4.86E-05	14	554
[GO:0000303] response to superoxide	13	5.16E-05	2	2
[GO:0007632] visual behavior	6	5.80E-05	3	11
[GO:0006000] fructose metabolism	13	9.95E-05	3	13
[GO:0015672] monovalent inorganic cation transport	9	0.000117	10	322
[GO:0007267] cell-cell signaling	3	0.000118	13	528
[GO:0042752] regulation of circadian rhythm	6	0.000154	2	3
[GO:0000305] response to oxygen radical	12	0.000154	2	3

[GO:0001975] response to amphetamine	4	0.000154	2	3
[GO:0005975] carbohydrate metabolism	5	0.000186	12	479
[GO:0044262] cellular carbohydrate metabolism	6	0.00027	10	357
[GO:0006003] fructose 2,6-bisphosphate metabolism	14	0.000307	2	4
[GO:0009314] response to radiation	3	0.000317	5	82
[GO:0010033] response to organic substance	3	0.000327	3	19
[GO:0006811] ion transport	7	0.000347	15	751
[GO:0048856] anatomical structure development	2	0.000434	28	1998
[GO:0043279] response to alkaloid	4	0.000509	2	5
[GO:0048468] cell development	4	0.00074	11	481
[GO:0019751] polyol metabolism	7	0.000751	3	25
[GO:0001974] blood vessel remodeling	12	0.00076	2	6
[GO:0030154] cell differentiation	3	0.00078	18	1081
[GO:0007610] behavior	2	0.000871	9	343
[GO:0048514] blood vessel morphogenesis	8	0.001044	6	159
[GO:0045176] apical protein localization	5	0.001059	2	7
[GO:0009416] response to light stimulus	4	0.001109	4	63
[GO:0007512] adult heart development	7	0.001405	2	8
[GO:0007612] learning	4	0.001423	3	31
[GO:0019318] hexose metabolism	12	0.001428	6	169
[GO:0019226] transmission of nerve impulse	7	0.001552	8	301
[GO:0046942] carboxylic acid transport	8	0.001557	4	69
[GO:0015849] organic acid transport	7	0.001642	4	70
[GO:0005996] monosaccharide metabolism	11	0.001657	6	174
[GO:0015980] energy derivation by oxidation of organic compounds	7	0.001706	6	175
[GO:0046928] regulation of neurotransmitter secretion	21	0.001798	2	9
[GO:0030534] adult behavior	3	0.001864	3	34
[GO:0007286] spermatid development	11	0.002201	3	36
[GO:0042135] neurotransmitter catabolism	16	0.002237	2	10
[GO:0008105] asymmetric protein localization	4	0.002237	2	10
[GO:0001568] blood vessel development	5	0.002256	6	185
[GO:0001944] vasculature development	4	0.002445	6	188

[GO:0048515] spermatid differentiation	9	0.002573	3	38
[GO:0016049] cell growth	11	0.002612	5	131
[GO:0042592] homeostasis	2	0.002697	8	329
[GO:0006936] muscle contraction	3	0.002788	5	133
[GO:0007411] axon guidance	30	0.002804	4	81
[GO:0007268] synaptic transmission	8	0.002888	7	261
[GO:0008361] regulation of cell size	9	0.002974	5	135
[GO:0042493] response to drug	3	0.003201	3	41
[GO:0042596] fear response	3	0.003249	2	12
[GO:0001676] long-chain fatty acid metabolism	12	0.003249	2	12
[GO:0007009] plasma membrane organization and biogenesis	6	0.003249	2	12
[GO:0042632] cholesterol homeostasis	3	0.003249	2	12
[GO:0008016] regulation of heart contraction	7	0.003429	3	42
[GO:0007626] locomotory behavior	3	0.004023	6	208
[GO:0009653] morphogenesis	3	0.004391	17	1166
[GO:0019439] aromatic compound catabolism	9	0.004438	2	14
[GO:0008152] metabolism	2	0.004615	75	8216
[GO:0042417] dopamine metabolism	24	0.005097	2	15
[GO:0006637] acyl-CoA metabolism	14	0.005798	2	16
[GO:0030048] actin filament-based movement	15	0.005798	2	16
[GO:0007269] neurotransmitter secretion	17	0.005935	3	51
[GO:0000302] response to reactive oxygen species	11	0.00654	2	17
[GO:0009628] response to abiotic stimulus	2	0.00676	5	164
[GO:0006865] amino acid transport	10	0.006959	3	54
[GO:0045062] extrathymic T cell selection	20	0.007211	1	1
[GO:0048149] behavioral response to ethanol	7	0.007211	1	1
[GO:0009399] nitrogen fixation	4	0.007211	1	1
[GO:0051125] regulation of actin nucleation	15	0.007211	1	1
[GO:0006463] steroid hormone receptor complex assembly	7	0.007211	1	1
[GO:0045819] positive regulation of glycogen catabolism	49	0.007211	1	1
[GO:0031331] positive regulation of cellular catabolism	23	0.007211	1	1
[GO:0001315] age-dependent response to reactive oxygen species	12	0.007211	1	1

[GO:0031329] regulation of cellular catabolism	15	0.007211	1	1
[GO:0000147] actin cortical patch assembly	11	0.007211	1	1
[GO:0031330] negative regulation of cellular catabolism	23	0.007211	1	1
[GO:0031000] response to caffeine	6	0.007211	1	1
[GO:0050758] regulation of thymidylate synthase biosynthesis	26	0.007211	1	1
[GO:0005981] regulation of glycogen catabolism	34	0.007211	1	1
[GO:0050757] thymidylate synthase biosynthesis	15	0.007211	1	1
[GO:0042309] homoiothermy	5	0.007211	1	1
[GO:0043278] response to morphine	6	0.007211	1	1
[GO:0051127] positive regulation of actin nucleation	21	0.007211	1	1
[GO:0006198] cAMP catabolism	15	0.007211	1	1
[GO:0050802] circadian sleep/wake cycle, sleep	11	0.007211	1	1
[GO:0001982] baroreceptor response to lowering of blood pressure	8	0.007211	1	1
[GO:0001987] vasoconstriction of artery during baroreceptor response to lowering of blood pressure	11	0.007211	1	1
[GO:0045187] regulation of circadian sleep/wake cycle, sleep	17	0.007211	1	1
[GO:0006060] sorbitol metabolism	14	0.007211	1	1
[GO:0007522] visceral muscle development	5	0.007211	1	1
[GO:0006848] pyruvate transport	10	0.007211	1	1
[GO:0045818] negative regulation of glycogen catabolism	49	0.007211	1	1
[GO:0050760] negative regulation of thymidylate synthase biosynthesis	37	0.007211	1	1
[GO:0043462] regulation of ATPase activity	4	0.007211	1	1
[GO:0042749] regulation of circadian sleep/wake cycle	15	0.007211	1	1
[GO:0009386] translational attenuation	27	0.007211	1	1
[GO:0006813] potassium ion transport	11	0.007284	5	167
[GO:0042310] vasoconstriction	5	0.007323	2	18
[GO:0042219] amino acid derivative catabolism	11	0.007323	2	18
[GO:0001558] regulation of cell growth	17	0.008292	4	110
[GO:0044275] cellular carbohydrate catabolism	15	0.008292	4	110
[GO:0016052] carbohydrate catabolism	8	0.008292	4	110
[GO:0045055] regulated secretory pathway	9	0.008478	3	58
[GO:0006094] gluconeogenesis	27	0.009008	2	20

[GO:0051239] regulation of organismal physiological process	5	0.009446	6	249
[GO:0006732] coenzyme metabolism	7	0.009667	5	179