Supporting Information

Rincón-Cortés et al. 10.1073/pnas.1416065112

SI Materials and Methods

Subjects. Long-Evans rats were born and bred in our colony, housed in polypropylene cages (34 × 29 × 17 cm) with an abundant amount of wood shavings for nest building, and kept in a 20 ± 1 °C environment with a 12:12 light-dark cycle. Food and water were available ad libitum. The day of birth was considered postnatal day (PN) 0, and litters were culled to 12 pups on PN1. Both males and females were used during infancy, but only males were used in adulthood. All animal care and experimental procedures were approved by the Institutional Animal Care and Use Committees, which follow the guidelines from the National Institutes of Health.

Infant Procedures.

Infant odor-shock conditioning. Odor-shock conditioning began during the sensitive period (PN8) and continued past the end of the sensitive period (PN10) into the transitional sensitive period, which is characterized by maternal presence reinstating sensitive-period learning (1). Our laboratory has previously shown that, provided odor-shock conditioning is initiated during the sensitive period (before PN10) and ends before the termination of the transitional sensitive period (PN15), odor-shock conditioning continues to support the unique sensitive-period odor-preference learning (2, 3).

At PN8, pups were placed in individual 600-mL beakers and given a 10-min acclimation period before conditioning to allow for recovery from experimental handling. During a conditioning session, pups received 9–11 pairings of a 30-s peppermint odor with 0.5 mA hindlimb shock during the last 1 s of odor, with an intertrial interval (ITI) of 4 min. The odor (peppermint; McCormick & Co. Inc.) was delivered by a flow dilution olfactometer (2 L/min flow rate) at a concentration of 1:10 peppermint vapor. The control group did not receive shock. Pups were returned to the home cage immediately after conditioning.

Maternal behavior assessment. Maternal behaviors were recorded daily (30-min session divided into 6 × 5-min segments) from PN8 to PN12 to ensure that the adult effects observed in paired odor-shock animals were not due to atypical maternal care. Behavioral values are expressed as percentage of observation periods in which behaviors occur for each of the observation periods. Percentages of behavioral measures do not add to 100% because behaviors can cooccur or not.

Verification of Infant Maternal Odor (i.e., Preference) Learning.

Behavioral activation. To verify associative learning during the training session, pups' behavioral responses to conditioned stimulus (CS) odor presentation during the 20 s before the shock were recorded and used to construct acquisition curves in which each data point represents the summation of behavior from two consecutive trials (4, 5). Due to motor immaturity, an age-appropriate behavioral rating scale (0–5) in which 0 indicates no movement and 5 indicates movement of all limbs and head was used to evaluate learning.

Y-maze. To ensure that odor-shock conditioning resulted in an odor preference, pups were given a 5-trial Y-maze test after odor-shock conditioning (2, 6). The Plexiglas Y-maze consisted of a start box (8.5 × 10 × 8 cm) and two choice arms (8.5 × 24 × 8 cm): one containing 20 μL of peppermint (on a Kim Wipe in a Petri dish) and the other one containing a neutral but familiar odor (i.e., 20 mL of clean bedding in a Petri dish). Pups were placed in the start box in a counterbalanced direction for each trial, and the doors to each arm were opened after 5 s. Approach responses to the peppermint odor paired with shock or the neutral odor (i.e., clean bedding) were measured in 5 × 60-s trials. A response was considered a choice when a pup's head and two front paws moved beyond the entrance to the alley. Trials were separated by a 5-s interval, and the floor was wiped clean in between each trial.

Nipple attachment. To verify that the odor paired with shock acquired properties of the maternal odor, pups were tested using a nipple attachment test with an anesthetized mother (urethane, 1.5 g/kg, i.p., prevents milk letdown) after conditioning (2). Because the maternal odor is required for pups' nipple attachment (7), the natural maternal odor was removed through chemical wash of the mother's ventrum—5-min wash of acetone, 5-min wash of alcohol, 5-min wash with water, and drying (8, 9). The washed mother was then placed in the testing chamber (25 × 40 × 20 cm) on her side to provide pup access to nipples. An individual pup was placed in the testing apparatus, perpendicular to the mother's ventrum, and the learned (peppermint) odor was presented in an air stream 2 cm above the center of the mother's ventrum (2 L/min, 1:10 maternal odor:air). The time pups spent attached to the nipple was recorded during a 3-min test.

Infant Microdialysis/HPLC. Two days before the PN12 conditioning session, pups were anesthetized by isoflurane inhalation and placed in a stereotaxic apparatus, and a microdialysis guide cannula (EICOM Corp.; 8 mm long, 500 μm diameter acrylic resin) was implanted unilaterally in the BLA through holes drilled in the overlying skull. Stereotaxic coordinates derived from the Paxinos atlas (10) were adapted through pilot work for implanting cannulae into the infant amygdala (BLA: caudal −0.90 mm from bregma; lateral ±4.50 mm from lambda; lowered 0.6 mm from the surface of the skull) (5). After recovery from surgery (generally within 30 min), pups were returned to the litter and dam. On the day of the experiment (PN12), pups were placed in a 27-cm-diameter acrylic circular cage (EICOM Corp.) that allowed them to move freely, the microdialysis probes (EICOM Corp.; A-I-8-02, 8 mm length, 2 mm membrane, 220 μm diameter) were inserted into the guide cannula, and the probes were perfused with artificial cerebrospinal fluid (ACSF; 147 mM NaCl, 2.7 mM KCl, 1.2 mM $CaCl_2$, 0.85 mM $MgCl_2$) at a flow rate of 1.5 μL/min. Dialysate was collected automatically every 10 min in a refrigerated (4 °C) microfraction collector (EFC-82; EICOM Corp.) in vials containing 2 μL of 12.5 mM perchloric acid/250 μM EDTA during a 2-h baseline period, a 45-min conditioning session, and a recovery period of at least 1 h. After completion of the experiment, dialysate samples were immediately stored at −80 °C until analyzed for 5-HT using an EICOM ECD-300 HPLCy with electrochemical detection (5, 11). Sample aliquots (10 μL) were injected, and separation was achieved using a reverse-phase octadecylsilane (ODS) column (Eicompak SC-5ODS, 2.1 mm i.d. × 150 mm, 5 μm particle; EICOM) with the potential of the graphite electrode set to +750 mV against the Ag/AgCl reference electrode. The column temperature was maintained at 25 °C. The mobile phase consisted of 100 mM citric acid, 0.25 mM octyl sulfate sodium salt, 0.5 mM EDTA, 0.085 mM tryethylamin, and 6% (vol/vol) acetonitrile, adjusted to pH 2.4, and the flow rate was set at 0.23 mL/min.

Infant FLX Administration. No pups were away from the nest beyond that required for cage cleaning and administering injections, which were conducted typically within 5 min, and pups were returned to the mother. Injections occurred from PN12 to -22, and maternal behaviors were recorded daily (30-min sessions, 6 × 5-min sessions). Behavioral values are expressed as percentage of observation periods in which behaviors occur for each of the observation periods. Percentages of behavioral measures do not add to 100% because behaviors can cooccur or not.

Adult Behavioral Assays.

Social behavior test. Social behavior was tested in a two-chamber apparatus (60 w × 60 l × 70 h cm) built out of black Plexiglas sheets for the sides and white bottom to form an open-top box. A black Plexiglas division (60 × 60 cm) separated the two chambers and a (15 × 13 cm) square opening allowed animals to move between chambers. Two metal chambers (6 × 6 × 6 cm) with circular holes (1 cm) placed 1 cm apart in each of the four sides and a metal grid with 0.5-cm openings 0.5 cm apart on the top were placed in each chamber during an acclimation period of 5 min. After acclimation, a younger (PN30 to 50) same-sex animal was placed inside one of the metal cubes, and time spent in each chamber, as well as number of chamber crossings, was recorded for 10 min. For odor presentation, two olfactometer output tubes per chamber were placed on the interior of the chamber walls during testing.

Forced swim test (FST). Depressive-like behavior was tested in a cylinder that was filled with water (25 ± 1 °C and changed for each test) to achieve a depth that prevented both escape and the tail from touching the bottom (2, 12, 13). Animals were habituated for 15 min one day before testing (day 1), and tested for a duration of 5 min on the next day (day 2). The time the animal spent immobile, defined as passive floating without struggling, in a slightly hunched but upright position with the head slightly immersed and minor movements necessary to maintain the head above water, was recorded (14, 15). For odor presentation during the FST, a Plexiglas lid containing an odor tube covered the FST apparatus to ensure the odor did not dissipate similar to ref. 3. No animal was tested more than once in the FST, and these animals were used for gene-expression assessment. Additional animals were generated to assess social behavior, in which case this testing was conducted 1 wk before the FST. No animals received odor presentations more than once (either social behavior or FST—not both).

RIA. Thirty minutes after the end of the adult FST, trunk-blood samples were collected in 1.5-mL Eppendorf tubes and centrifuged at 3,000 rpm (Fisher Scientific accuSpin model Micro17R Microcentrifuge) at 4 °C for 15 min to separate the red blood cells from the plasma. Aliquotted plasma samples were stored at −80 °C until RIA analysis. The samples were analyzed using the Rat Corticosterone Coat-A-Count Kit (Siemens) and a gamma counter.

Gene-Expression Analysis.

Amygdala dissection. The brain was cut in two hemispheres. Dissection included bilateral localization of the amygdala using the ventral hippocampus and putamen landmarks for the rostral and caudal cuts. The brain was turned to obtain a coronal view, where the rhinal fissure could be easily seen and used as a landmark to make the dorsal cut. The medial cut included a 45° cut from the optic chiasm and the removal of the lateral overlying cortical tissue. Enriched amygdala tissue was removed, frozen, and stored at −80 °C until further use.

Microarray. Frozen harvested amygdala sections ($n = 8$ per group) were processed for total RNA (Qiagen RNeasy Micro Kit). RNA was extracted using elution columns; residual buffers and enzymes were removed. mRNA was amplified linearly, and hybridized to Affymetrix rat 2.0 chips, as specified by Affymetrix and NuGEN (Pico system). To reduce the influence of technical variability, samples for each condition were always prepared and hybridized at the same time. Two separate comparisons were conducted. To assess gene changes in the depressive phenotype, infant odor-shock paired animals and infant nonshocked animals that were tested in the adult FST without the odor were compared. To assess the effects of the odor, which rescued the depressive phenotype, we compared infant odor-shock paired groups, tested in the FST with and without the infant odor. We refer to this condition as the rescue phenotype.

Adult Surgery and Intraamygdala Drug Infusion. Adult male rats were anesthetized by isoflurane inhalation and placed in a stereotaxic apparatus. Stereotaxic coordinates, derived from the Paxinos atlas (16) and adapted through pilot work, were used for implanting bilateral cannulae (23-gauge tubing) into the amygdala (caudal, 2.3 mm; lateral, 5.4 mm from bregma; lowered 8.5), which were fixed to the skull with screws and dental cement. After recovery from surgery (generally within 30 min), rats were returned to the home cage for a 7-d recovery period until testing.

On the test day, the rats' bilateral cannulae were attached via PE50 tubing to a Harvard PHD 2000 syringe pump driving two Hamilton microliter (μL) syringes. The cannulae were filled with serotonin hydrochloride (1 mg/62.5 μL; Sigma), serotonin receptor antagonist methysergide maleate salt (2.5 μg/0.5 μL; Sigma), or physiological saline (0.9%). Rats were infused at 0.1 μL/min for 5 min for an infusion volume of 0.5 μL per hemisphere and a total infusion volume of 1 μL. After infusion, 1 min was allowed for diffusion before removing the PE50 tubing. The FST started 15 min after the infusion. To determine whether a 5-HT/CORT interaction (i.e., low 5-HT, high CORT) contributes to the expression of depressive-like behavior in the FST after infant paired odor shock, some animals received systemic metyrapone (i.p.; 50 mg/kg), a corticosterone synthesis inhibitor (Tocris), ∼30 min before the FST (Fig. 4). After testing, brains were removed, frozen, sectioned (20 μm) in a −20 °C cryostat, and stained with cresyl violet for identification of the cannula placement in relation to the amygdala using an atlas (16). The identification was done blind to the experimental groups.

Adult in Vivo Amygdala Electrophysiology. Animals were anesthetized with Equithesin (mixture of chloral hydrate and sodium pentobarbital; 3 mL/kg, i.p.) and placed in a stereotaxic apparatus. A bipolar stimulating electrode was lowered in the left olfactory bulb. Three monopolar recording electrodes were implanted ipsilaterally in the olfactory cortex [anteroposterior (A/P) −1.8 mm, lateromedial (L/M) 5.5 mm to Bregma], basolateral amygdala (A/P −2.8 mm, L/M 5.1 mm relative to Bregma) and cortical nucleus of the amygdala (A/P −2.3 mm, L/M 3.3 mm relative to Bregma). Accurate positioning of recording electrodes tips was achieved using the field potential profile evoked in response to electrical stimulation of the olfactory bulb (17). Electrical stimulation was delivered through a Master-8 stimulator (AMPI). The electrical stimulus was a single monophasic square pulse, 0.1 ms duration, 0.2 Hz frequency, 300–500 μA intensity.

The amplitude of the signal collected in the three recording sites in response to single-pulse stimulation of the olfactory bulb was measured. Paired-pulse (using 30 ms interpulse interval) stimulation of the olfactory bulb was used to assess the level of amygdala inhibitory interneuron activity (18, 19). The effect of the conditioning (first) pulse was assessed by measuring changes in the response to the test (second) pulse. A percentage below 100 is observed when the response to the test pulse is smaller than the response to the conditioning pulse and characterizes paired-pulse inhibition whereas a percentage above 100 characterizes paired-pulse facilitation. Evoked field potentials were recorded in the presence and absence of the infant odor previously paired with shock (20 μL of peppermint odor placed on a KimWipe in a syringe and delivered in front of the animal's nose during the recording sessions).

Statistical Analysis.

Behavior. Infant behavioral data and adolescent FST data after infant FLX treatment were analyzed by *t* tests, and differences were considered significant when $P < 0.05$. Infant microdialysis data were analyzed by one-way ANOVA. Adult social behavior and FST data were analyzed by two-way ANOVA (infant condition, infant trauma odor as factors) (Fig. 3 *A–D*). Intraamygdala manipulations in the presence of odor data were analyzed by two-way ANOVA (infant-trauma odor, drug as factors) (Fig. 5*A*). Intraamygdala manipulations in paired animals (no odor) were analyzed by one-way ANOVA (Fig. 5*B*). All ANOVA analyses were followed by post hoc Fisher tests.

Microarray. We used BrainArray custom chip definition files (CDFs) (University of Michigan; brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/CDF_download.asp) to preprocess and define genes from the Affymetrix perfect match probes (20). We determined differential expression between the two "depressive" phenotype groups (odor-shock paired vs. nonshocked) and the "rescue" phenotype (FST with and without odor) by Ranked Products (21). Correction for multiple testing was with the minimum pfp statistic [percentage of false predictions (pfp)]. From these Ranked Product results, we determined the percentage of differentially regulated genes that fit into different biological processes, molecular function, and cellular component GO categories [protein analysis through evolutionary relationships (PANTHER)] (22). We input all probes with a pfp <0.10. We initially input up- and down-regulated probes separately because, in other studies, the gene ontology (GO) categories differed by direction of regulation (23). However, here they did not, and we discuss them together.

Consistent changes in gene expression associated with specific pathways, even if small, are likely more important than changes in individual genes. Thus, we used methods to determine functional classifications. We were interested in functional pathways that were altered by the early learning, and we selected all probes with a pfp <0.10 and entered them in DAVID for Gene Ontology using the functional classification algorithm to cluster probes based on gene-to-gene similarities (24, 25). Up- and down-regulated genes were analyzed together given that there were no differences in GO categories in the Panther analysis. We visualized those gene ontology results by directed acyclic graph (DAG) diagrams using the "Gene Ontology enrichment analysis and visualization" tool (GOrilla) (26, 27).

To determine pathways involved in the depressive and rescue phenotypes, we used Ingenuity Pathways Analysis (IPA; Ingenuity Systems, www.ingenuity.com) to define networks from the top 100 up-regulated and top 100 down-regulated probes ordered by fold change. We included up- and down-regulated genes together because the analytic methods in IPA generate pathways from both. We used the "direct connection" to mapped probes to their corresponding objects in Ingenuity's Knowledge Base. The IPA Functional Analysis identifies the biological functions most significant to the dataset. Predefined canonical pathways were identified from the Ingenuity Pathways Analysis library. The significance of the association between the dataset and the canonical pathway was measured by Fisher's exact test for the probability that the association between the genes in the dataset and the canonical pathway was not by chance (Ingenuity Systems, 2009, www.ingenuity.com). For descriptive purposes and for clarity of presentation, we show canonical paths typical of those paths.

Electrophysiology. Electrophysiological data (signal amplitude and paired-pulse ratios) were analyzed using repeated measures two-way ANOVA (infant condition and infant-trauma odor as factors) followed by post hoc Fisher tests (Fig. 3 *E* and *F* and Fig. S2).

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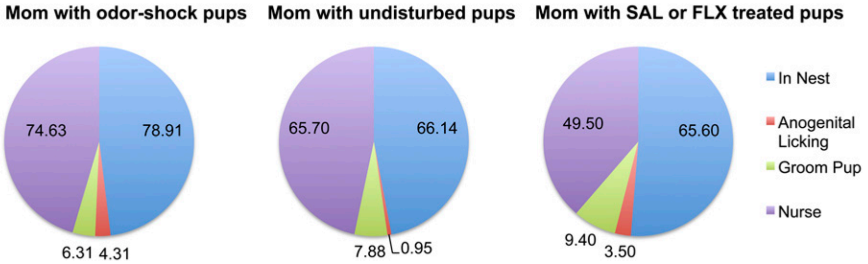

Fig. S1. Maternal behaviors of dams whose pups underwent conditioning during infancy, dams with control pups, or dams whose pups were treated with SAL/FLX (half litter SAL; half litter FLX).

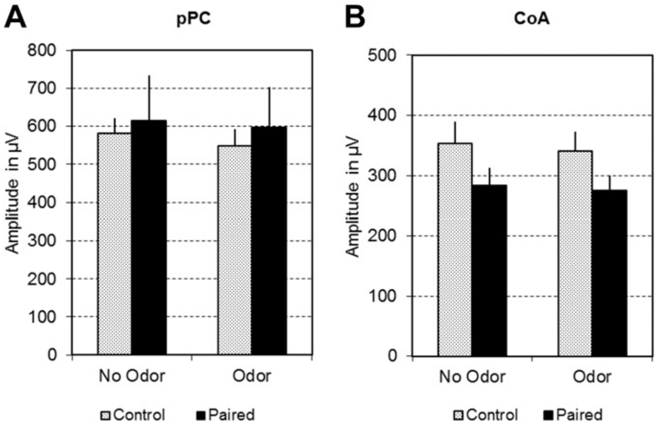

Fig. S2. Infant trauma animals did not differ from control animals in the amplitude of the signal induced in the olfactory posterior piriform cortex ($n = 6–7$, $P = 0.753$) (*A*) or the cortical nucleus of the amygdala ($n = 6–7$, $P = 0.147$) (*B*) in response to electrical stimulation of the olfactory bulb. No odor effect was found.

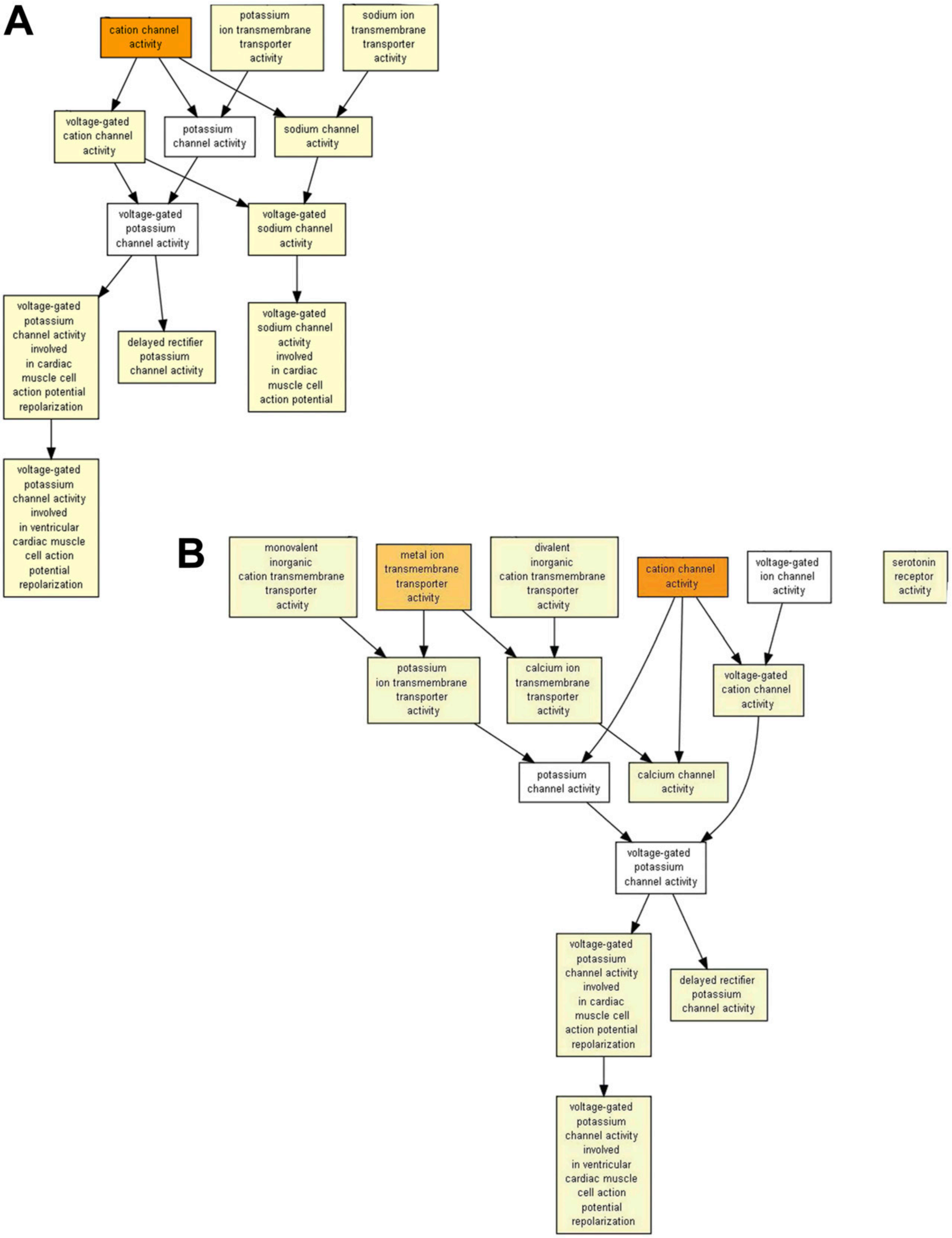

Fig. S3. Directed acyclic graph (DAG) diagrams of the molecular function gene ontology and IPA Networks. The input to DAVID were all probes with the pfp <0.10 (from Tables S1 and S2) using the medium stringency option. Note that only probe names are given, not the magnitude or direction of change. For the depressive phenotype (*A*), there were three gene groups that were largely solute carriers for cations, and sodium and potassium channels. The rescue phenotype (*B*) also shows changes in potassium channel activity, but altered 5-HT binding as well. Note that the full DAG was cropped for clarity and "parent" GO terms are not shown (e.g., 5-HT receptor activity; *B*).

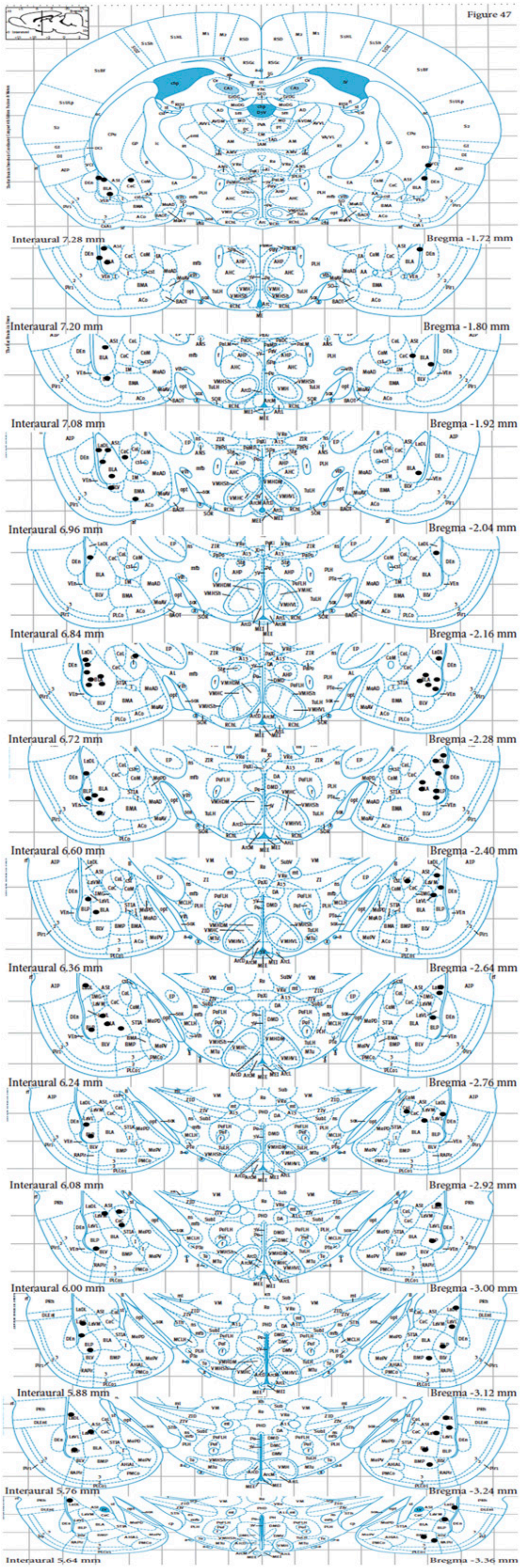

Fig. S4. Related to Fig. 5, shown are amygdala cannula placements in which schematics of brain sections are displayed from rostral to caudal.

Table S1. Significant probes, depressive phenotype, and infant odor-shock conditioning vs. no shock

Gene_ID	Symbol	Title	Min PFP	Fold
266803	Sostdc1	Sclerostin domain containing 1	0.000	−7.61
57395	Tmem27	Transmembrane protein 27	0.000	−7.15
24856	Ttr	Transthyretin	0.000	−7.10
315597	Mfrp	Membrane frizzled-related protein	0.000	−6.56
300920	Cldn2	Claudin 2	0.000	−6.21
304929	F5	Coagulation factor V (proaccelerin, labile factor)	0.000	−6.16
80900	Slco1a5	Solute carrier organic anion transporter family, member 1a5	0.000	−6.06
305858	Otx2	Orthodenticle homeobox 2	0.000	−4.53
25258	Glycam1	Glycosylation dependent cell adhesion molecule 1	0.000	−4.02
171049	Folr1	Folate receptor 1 (adult)	0.000	−3.79
297738	Steap1	Six transmembrane epithelial antigen of the prostate 1	0.000	−3.14
84024	Pon1	Paraoxonase 1	0.000	−2.92
309100	Scgb1c1	Secretoglobin, family 1C, member 1	0.000	−2.88
25250	Cox8b	Cytochrome *c* oxidase, subunit VIIIb	0.000	−2.68
500945	RGD1561795	Similar to RIKEN cDNA 1700012B09	0.000	−2.63
25240	Aqp1	Aquaporin 1	0.000	−2.61
311061	Itgb6	Integrin, beta 6	0.000	−2.60
29354	Pla2g5	Phospholipase A2, group V	0.000	−2.59
81512	Lect1	Leukocyte cell derived chemotaxin 1	0.000	−2.48
310836	Abca4	ATP-binding cassette, subfamily A (ABC1), member 4	0.000	−2.34
24684	Prlr	Prolactin receptor	0.000	−2.30
498278	RGD1562658	Similar to RIKEN cDNA 1700009P17	0.000	−2.28
294806	C1qtnf3	C1q and tumor necrosis factor related protein 3	0.000	−2.21
305340	Rbm47	RNA binding motif protein 47	0.000	−2.21
312086	Pon3	Paraoxonase 3	0.000	−2.17
24310	Ace	Angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	0.000	−2.10
308565	Klk8	Kallikrein related-peptidase 8	0.000	2.02
315820	Myo5c	Myosin VC	0.000	−1.98
366035	Wdr38	WD repeat domain 38	0.000	−1.97
171138	Kcne2	Potassium voltage-gated channel, Isk-related subfamily, gene 2	0.000	−1.94
294255	Slc44a4	Solute carrier family 44, member 4	0.000	−1.89
79247	Htr5b	5-Hydroxytryptamine (serotonin) receptor 5B	0.000	1.84
84050	Enpp2	Ectonucleotide pyrophosphatase/phosphodiesterase 2	0.000	−1.83
289230	Nhlh1	Nescient helix loop helix 1	0.000	1.83
81710	Msx1	Msh homeobox 1	0.000	−1.81
25626	Krt8	Keratin 8	0.000	−1.79
83504	Kl	Klotho	0.000	−1.77
312677	Ccdc77	Coiled-coil domain containing 77	0.000	1.75
81517	Mdk	Midkine	0.000	−1.70
361415	Dynlrb2	Dynein light chain roadblock-type 2	0.000	−1.68
116777	Cdh3	Cadherin 3	0.000	−1.68
266775	Serpinb10	Serpin peptidase inhibitor, clade B (ovalbumin), member 10	0.000	1.59
680802	LOC680802	Similar to Zinc finger protein 45 (BRC1744)	0.000	1.59
192110	Pou3f1	POU class 3 homeobox 1	0.000	1.55
360613	Ccdc49	Coiled-coil domain containing 49	0.000	1.49
313373	Cyp2j10	Cytochrome P450, family 2, subfamily j, polypeptide 10	0.000	1.46
192203	Fap	Fibroblast activation protein, alpha	0.000	1.46
25400	Camk2a	Calcium/calmodulin-dependent protein kinase II alpha	0.000	1.44
65153	Freq	Frequenin homolog (*Drosophila*)	0.000	1.41
314416	Ak7	Adenylate kinase 7	0.000	−1.58
301525	Glb1l	Galactosidase, beta 1-like	0.001	−1.64
363144	Cdh29	Cadherin-like 29	0.001	−1.59
362424	Tmem72	Transmembrane protein 72	0.001	−1.64
300663	Ccdc153	Coiled-coil domain containing 153	0.001	−1.55
171045	Mmp3	Matrix metallopeptidase 3	0.001	−1.59
304021	Col8a1	Collagen, type VIII, alpha 1	0.001	−1.62
297444	Ccdc37	Coiled-coil domain containing 37	0.001	−1.59
654482	LOC654482	Hypothetical protein LOC654482	0.001	−1.54
24780	Slc4a2	Solute carrier family 4 (anion exchanger), member 2	0.001	−1.60
366366	Igfbpl1	Insulin-like growth factor binding protein-like 1	0.001	−1.59
170496	Lcn2	Lipocalin 2	0.001	−1.39
691455	Calml4	Calmodulin-like 4	0.001	−1.56
171339	Dnah1	Dynein, axonemal, heavy chain 1	0.002	−1.48

Table S1. Cont.

Gene_ID	Symbol	Title	Min PFP	Fold
171409	Tnnt1	Troponin T type 1 (skeletal, slow)	0.002	−1.49
315564	Robo3	Roundabout homolog 3 (*Drosophila*)	0.002	1.62
286918	Mx2	Myxovirus (influenza virus) resistance 2	0.003	1.25
680210	Psca	Prostate stem cell antigen	0.003	−1.53
290354	Pdlim2	PDZ and LIM domain 2	0.003	−1.46
25662	Igfbp2	Insulin-like growth factor binding protein 2	0.004	−1.49
313495	Car9	Carbonic anhydrase 9	0.004	−1.45
64030	Kit	V-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	0.004	1.44
114592	Aurkb	Aurora kinase B	0.004	−1.43
690286	LOC690286	Similar to hepatic leukemia factor	0.004	1.33
83502	Cdh1	Cadherin 1	0.005	1.35
65129	Cldn1	Claudin 1	0.005	−1.44
306454	Cldn22	Claudin 22	0.005	−1.46
25049	Atxn1	Ataxin 1	0.005	1.34
25102	Chrna5	Cholinergic receptor, nicotinic, alpha 5	0.005	1.31
414788	RT1-T24-3	RT1 class I, locus T24, gene 3	0.005	−1.57
290803	Tex15	Testis expressed 15	0.005	−1.49
293154	Folr2	Folate receptor 2 (fetal)	0.006	1.19
308958	Cdr2	Cerebellar degeneration-related 2	0.006	−1.48
499017	Sytl3	Synaptotagmin-like 3	0.006	−1.46
301295	Efhc1	EF-hand domain (C-terminal) containing 1	0.007	−1.44
252959	Dnah12	Dynein, axonemal, heavy chain 12	0.007	−1.46
499660	Sprr1al	Small proline-rich protein 1A-like	0.007	−1.40
84550	Slc24a2	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	0.008	1.39
25349	Scn2b	Sodium channel, voltage-gated, type II, beta	0.008	1.40
288478	Rsph10b	Radial spoke head 10 homolog B (Chlamydomonas)	0.008	−1.42
361195	Cdc14b	CDC14 cell division cycle 14 homolog B (*S. cerevisiae*)	0.009	−1.42
298524	Dnali1	Dynein, axonemal, light intermediate chain 1	0.009	−1.44
24443	Hdc	Histidine decarboxylase	0.009	−1.55
290558	Nt5dc2	5′-Nucleotidase domain containing 2	0.009	−1.43
83687	Defb1	Defensin beta 1	0.010	1.37
50555	Ugt8	UDP glycosyltransferase 8	0.010	1.33
315691	Lingo1	Leucine rich repeat and Ig domain containing 1	0.011	1.25
290372	RGD1560137	Similar to expressed sequence AU021034	0.011	−1.45
29279	Meox2	Mesenchyme homeobox 2	0.012	1.37
498356	Shisa3	Shisa homolog 3 (*Xenopus laevis*)	0.012	1.25
299757	Nts	Neurotensin	0.012	1.32
315731	Larp6	La ribonucleoprotein domain family, member 6	0.012	1.44
361170	Adam32	ADAM metallopeptidase domain 32	0.012	1.29
294254	Hspa1b	Heat shock 70kD protein 1B (mapped)	0.012	−1.24
58982	Ncan	Neurocan	0.013	1.32
315609	Cd3e	CD3 molecule, epsilon	0.013	1.78
56824	Ifit1	IFN-induced protein with tetratricopeptide repeats 1	0.013	1.09
362867	Mybpc1	Myosin binding protein C, slow type	0.013	1.33
361993	C2cd4d	C2 calcium-dependent domain containing 4D	0.013	1.37
310694	Fcrls	Fc receptor-like S, scavenger receptor	0.015	−1.58
310483	Mlf1	Myeloid leukemia factor 1	0.015	−1.39
85270	Tekt1	Tektin 1	0.015	−1.40
25041	P2rx6	Purinergic receptor P2X, ligand-gated ion channel, 6	0.015	−1.40
287346	Fam183b	Family with sequence similarity 183, member B	0.015	−1.42
360478	RGD1563547	RGD1563547	0.015	−1.40
313592	Col8a2	Collagen, type VIII, alpha 2	0.015	−1.36
499586	Tmem212	Transmembrane protein 212	0.015	−1.37
84386	Slpi	Secretory leukocyte peptidase inhibitor	0.015	−1.41
315611	Scn4b	Sodium channel, voltage-gated, type IV, beta	0.015	1.32
691223	LOC691223	Hypothetical protein LOC691223	0.015	−1.41
116506	Calcr	Calcitonin receptor	0.016	−1.25
289178	Dpt	Dermatopontin	0.016	−1.41
83567	Mchr1	Melanin-concentrating hormone receptor 1	0.016	1.31
315863	Ube2cbp	Ubiquitin-conjugating enzyme E2C binding protein	0.016	−1.33

Table S1. Cont.

Gene_ID	Symbol	Title	Min PFP	Fold
305066	Prox1	Prospero homeobox 1	0.016	1.38
362325	Mdfic	MyoD family inhibitor domain containing	0.017	−1.36
24471	Hspb1	Heat shock protein 1	0.017	−1.41
25628	Nkx2-1	NK2 homeobox 1	0.017	−1.45
499991	Steap4	STEAP family member 4	0.017	−1.30
690188	Fam168b	Family with sequence similarity 168, member B	0.019	1.25
50577	Galr1	Galanin receptor 1	0.020	−1.18
291847	Ccdc113	Coiled-coil domain containing 113	0.022	−1.38
378947	Bst2	Bone marrow stromal cell antigen 2	0.023	−1.35
363139	Zmynd10	Zinc finger, MYND-type containing 10	0.024	−1.38
296608	RGD1306233	Similar to hypothetical protein MGC29761	0.024	−1.33
305974	Scara5	Scavenger receptor class A, member 5 (putative)	0.024	−1.38
501185	RGD1563692	Similar to hypothetical protein FLJ22671	0.024	−1.39
302991	Tekt4	Tektin 4	0.024	−1.36
246245	Fmo2	Flavin containing monooxygenase 2	0.024	−1.31
497957	RGD1565611	RGD1565611	0.024	−1.34
365972	Bhmt2	Betaine-homocysteine methyltransferase 2	0.025	−1.32
304282	Baiap2l1	BAI1-associated protein 2-like 1	0.025	−1.39
54237	Cdk1	Cyclin-dependent kinase 1	0.026	−1.22
66026	Trpv4	Transient receptor potential cation channel, subfamily V, member 4	0.026	−1.37
315741	Paqr5	Progestin and adipoQ receptor family member V	0.026	−1.36
81686	Mmp2	Matrix metallopeptidase 2	0.028	−1.38
293012	Olig3	Oligodendrocyte transcription factor 3	0.028	−1.29
296610	Rsb66	Rsb-66 protein	0.029	−1.30
54410	Enpp3	Ectonucleotide pyrophosphatase/phosphodiesterase 3	0.030	−1.32
313057	Serinc2	Serine incorporator 2	0.030	−1.30
681288	T2	Brachyury 2	0.033	−1.32
406161	C4-2	Complement component 4, gene 2	0.033	−1.26
100362950	LOC100362950	CG11699-like	0.033	−1.33
683514	LOC683514	Hypothetical protein LOC683514	0.035	−1.34
500137	Neurod6	Neurogenic differentiation 6	0.036	1.29
50658	Mapk9	Mitogen-activated protein kinase 9	0.036	1.22
300870	Fam46a	Family with sequence similarity 46, member A	0.037	−1.34
252854	Slc5a11	Solute carrier family 5 (sodium/glucose cotransporter), member 11	0.038	1.20
360919	LOC360919	Similar to alpha-fetoprotein	0.039	1.13
29699	Prkar2a	Protein kinase, cAMP dependent regulatory, type II alpha	0.039	1.38
362511	Fbxo10	F-box protein 10	0.040	1.31
305441	Sh3tc1	SH3 domain and tetratricopeptide repeats 1	0.040	−1.28
293624	Irf7	IFN regulatory factor 7	0.041	−1.36
117548	Kif1b	Kinesin family member 1B	0.041	1.21
295704	Ube2l6	Ubiquitin-conjugating enzyme E2L 6	0.043	−1.34
307562	Dsg2	Desmoglein 2	0.043	−1.35
29413	Adra1d	Adrenergic, alpha-1D-, receptor	0.043	1.23
24785	Slc9a4	Solute carrier family 9 (sodium/hydrogen exchanger), member 4	0.044	1.28
299153	RGD1309051	Similar to chromosome 14 ORF 50	0.044	−1.35
25611	Otc	Ornithine carbamoyltransferase	0.045	−1.35
313479	Orc1l	Origin recognition complex, subunit 1-like (yeast)	0.045	1.32
291541	Cidea	Cell death-inducing DFFA-like effector a	0.048	−1.27
25456	Glrb	Glycine receptor, beta	0.051	1.26
312912	Prex2	Phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	0.053	1.25
314964	Phf20l1	PHD finger protein 20-like 1	0.053	1.34
29503	Slc22a2	Solute carrier family 22 (organic cation transporter), member 2	0.057	1.23
60324	Synpo	Synaptopodin	0.057	1.22
24477	Ibsp	Integrin-binding sialoprotein	0.057	1.36
78973	Senp2	Sumo1/sentrin/SMT3 specific peptidase 2	0.057	1.28
25292	Apoc1	Apolipoprotein C-I	0.058	1.30
252958	Iiig9	IIIG9 protein	0.058	−1.31
292843	Siglec5	Sialic acid binding Ig-like lectin 5	0.059	−1.11
24616	Pah	Phenylalanine hydroxylase	0.059	1.25

Table S1. Cont.

Gene_ID	Symbol	Title	Min PFP	Fold
114505	Klf4	Kruppel-like factor 4 (gut)	0.060	1.19
308794	RGD1310371	Similar to RIKEN cDNA 1700026D08	0.061	−1.26
24769	Sct	Secretin	0.061	−1.25
302507	Efhc2	EF-hand domain (C-terminal) containing 2	0.062	−1.31
117130	Grifin	Galectin-related interfiber protein	0.068	−1.26
24483	Igf2	Insulin-like growth factor 2	0.069	−1.23
25599	Cd74	Cd74 molecule, major histocompatibility complex, class II invariant chain	0.070	−1.28
252916	Rab38	RAB38, member RAS oncogene family	0.070	1.21
690020	LOC690020	Similar to killer cell lectin-like receptor, subfamily A, member 17	0.070	−1.17
309888	Sim1	Single-minded homolog 1 (*Drosophila*)	0.070	−1.41
100359753	LOC100359753	Hypothetical protein LOC100359753	0.071	−1.25
312647	Atg7	ATG7 autophagy related 7 homolog (*S. cerevisiae*)	0.071	1.25
303924	Upk1b	Uroplakin 1B	0.073	1.24
25513	Pik3r1	Phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	0.073	1.22
361818	Rsph1	Radial spoke head 1 homolog (Chlamydomonas)	0.075	−1.31
360605	Epn3	Epsin 3	0.076	−1.30
309526	Ifit3	IFN-induced protein with tetratricopeptide repeats 3	0.076	1.14
361300	Mocos	Molybdenum cofactor sulfurase	0.077	−1.27
171519	Calcb	Calcitonin-related polypeptide, beta	0.077	1.28
84020	Kcnq1	Potassium voltage-gated channel, KQT-like subfamily, member 1	0.077	−1.30
29248	Tnni3	Troponin I type 3 (cardiac)	0.078	−1.28
366140	Fjx1	Four jointed box 1 (*Drosophila*)	0.079	−1.67
315427	Sesn3	Sestrin 3	0.079	−1.17
368066	Inmt	Indolethylamine *N*-methyltransferase	0.081	−1.19
25369	Adora2a	Adenosine A2a receptor	0.081	−1.22
309368	Lama2	Laminin, alpha 2	0.081	−1.29
171163	Slc6a13	Solute carrier family 6 (neurotransmitter transporter, GABA), member 13	0.082	1.23
24974	RT1-A2	RT1 class Ia, locus A2	0.082	−1.28
302996	RGD1560244	Similar to hypothetical protein FLJ34512	0.082	−1.28
303772	Slc16a6	Solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	0.083	−1.29
362708	Trim54	Tripartite motif-containing 54	0.084	−1.16
64536	Esm1	Endothelial cell-specific molecule 1	0.085	−1.24
688394	Mab21l1	Mab-21-like 1 (C. elegans)	0.085	−1.20
690825	Gngt2	Guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	0.085	−1.26
502684	LOC502684	Hypothetical protein LOC502684	0.085	−1.27
302554	Glod5	Glyoxalase domain containing 5	0.086	−1.28
114587	Dlk1	Delta-like 1 homolog (*Drosophila*)	0.086	−1.32
305135	Lrrc8b	Leucine rich repeat containing 8 family, member B	0.087	1.25
81780	Ccl5	Chemokine (C-C motif) ligand 5	0.088	−1.32
309242	Gna14	Guanine nucleotide binding protein, alpha 14	0.089	1.24
307767	Frem3	FRAS1 related extracellular matrix 3	0.089	−1.28
266774	Znf597	Zinc finger protein 597	0.090	−1.10
311151	Dusp19	Dual specificity phosphatase 19	0.090	1.21
24688	Prph	Peripherin	0.092	−1.20
29755	Colq	Collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase	0.093	−1.23
292697	Apoc2	Apolipoprotein C-II	0.093	−1.27
310707	Chd1l	Chromodomain helicase DNA binding protein 1-like	0.094	−1.21
24954	Insr	Insulin receptor	0.096	1.14
294071	Hells	Helicase, lymphoid specific	0.098	1.28
307486	Pcdhb22	Protocadherin beta 22	0.098	1.21
83781	Lgals3	Lectin, galactoside-binding, soluble, 3	0.099	−1.32
24659	Pmch	Promelanin-concentrating hormone	0.099	−1.67

Entries are ordered by the minimum pfp value. Probes were up-regulated if the gene expression of the infant paired was greater than no shock. This classification captured the majority of probes with high fold changes. Only tyrosine hydroxylase (Th; fold = 1.54) and paired-like homeodomain 2 (Pitx2; fold = 1.62) exceeded fold >1.5 but were not significant by the minimum pfp score.

Table S2. Significant probes, rescue phenotype, and FST with and without infant conditioned odor

Gene_ID	Symbol	Title	Min PFP	Fold
57395	Tmem27	Transmembrane protein 27	0.000	3.45
4266803	Sostdc1	Sclerostin domain containing 1	0.000	3.44
80900	Slco1a5	Solute carrier organic anion transporter family, member 1a5	0.000	3.36
300920	Cldn2	Claudin 2	0.000	3.28
304929	F5	Coagulation factor V (proaccelerin, labile factor)	0.000	3.06
315597	Mfrp	Membrane frizzled-related protein	0.000	3.02
24856	Ttr	Transthyretin	0.000	3.00
171049	Folr1	Folate receptor 1 (adult)	0.000	2.81
81512	Lect1	Leukocyte cell derived chemotaxin 1	0.000	2.73
305858	Otx2	Orthodenticle homeobox 2	0.000	2.72
84024	Pon1	Paraoxonase 1	0.000	2.40
25258	Glycam1	Glycosylation dependent cell adhesion molecule 1	0.000	2.37
297738	Steap1	Six transmembrane epithelial antigen of the prostate 1	0.000	2.28
500945	RGD1561795	Similar to RIKEN cDNA 1700012B09	0.000	2.15
308565	Klk8	Kallikrein related-peptidase 8	0.000	−2.14
29354	Pla2g5	Phospholipase A2, group V	0.000	2.08
289230	Nhlh1	Nescient helix loop helix 1	0.000	−2.07
25240	Aqp1	Aquaporin 1	0.000	2.06
498278	RGD1562658	Similar to RIKEN cDNA 1700009P17	0.000	2.01
294806	C1qtnf3	C1q and tumor necrosis factor related protein 3	0.000	1.98
25250	Pon3	Paraoxonase 3	0.000	1.95
311061	Abca4	ATP-binding cassette, subfamily A (ABC1), member 4	0.000	1.93
312086	Slc44a4	Solute carrier family 44, member 4	0.000	1.90
310836	Prlr	Prolactin receptor	0.000	1.87
309100	Wdr38	WD repeat domain 38	0.000	1.86
294255	Myo5c	Myosin VC	0.000	1.81
305340	Robo3	Roundabout homolog 3 (*Drosophila*)	0.000	−1.75
24684	Krt8	Keratin 8	0.000	1.75
366035	Cdh29	Cadherin-like 29	0.000	1.70
286918	Htr5b	5-Hydroxytryptamine (serotonin) receptor 5B	0.000	−1.64
366140	Fap	Fibroblast activation protein, alpha	0.000	−1.63
315820	Pou3f1	POU class 3 homeobox 1	0.000	−1.58
362424	Slc35d3	Solute carrier family 35, member D3	0.000	−1.49
315564	Adam32	ADAM metallopeptidase domain 32	0.000	−1.49
25626	Dnah1	Dynein, axonemal, heavy chain 1	0.000	1.58
315609	Scgb1c1	Secretoglobin, family 1C, member 1	0.000	1.92
363144	LOC654482	Hypothetical protein LOC654482	0.000	1.62
24310	Aurkb	Aurora kinase B	0.000	1.57
81710	Scara5	Scavenger receptor class A, member 5 (putative)	0.000	1.65
84386	Dynlrb2	Dynein light chain roadblock-type 2	0.000	1.63
305974	Tmem72	Transmembrane protein 72	0.000	1.78
79247	Ak7	Adenylate kinase 7	0.000	1.61
361415	Itgb6	Integrin, beta 6	0.000	1.96
192203	Cox8b	Cytochrome *c* oxidase, subunit VIIIb	0.000	1.97
654482	Rbm47	RNA binding motif protein 47	0.000	1.89
314416	Serpinb2	Serpin peptidase inhibitor, clade B (ovalbumin), member 2	0.001	1.49
171339	Mx2	Myxovirus (influenza virus) resistance 2	0.001	1.83
192110	Slpi	Secretory leukocyte peptidase inhibitor	0.001	1.66
315611	Ace	Angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	0.001	1.70
171138	Msx1	Msh homeobox 1	0.001	1.68
114592	Steap4	STEAP family member 4	0.001	1.55
499991	Ccdc49	Coiled-coil domain containing 49	0.001	−1.31
680210	Ccdc153	Coiled-coil domain containing 153	0.001	1.46
83504	Prox1	Prospero homeobox 1	0.002	−1.50
252959	Meox2	Mesenchyme homeobox 2	0.002	−1.43
306454	Chrna5	Cholinergic receptor, nicotinic, alpha 5	0.002	−1.45
301525	LOC680802	Similar to Zinc finger protein 45 (BRC1744)	0.002	−1.44
84050	Freq	Frequenin homolog (*Drosophila*)	0.002	−1.21
297444	Larp6	La ribonucleoprotein domain family, member 6	0.002	−1.47
305066	Cyp2j10	Cytochrome P450, family 2, subfamily j, polypeptide 10	0.002	−1.45
308717	Fjx1	Four jointed box 1 (*Drosophila*)	0.002	−1.82
361170	Kl	Klotho	0.002	1.52
60325	Cldn22	Claudin 22	0.003	1.51

Table S2. Cont.

Gene_ID	Symbol	Title	Min PFP	Fold
691455	Inmt	Indolethylamine *N*-methyltransferase	0.003	1.42
64536	Folr2	Folate receptor 2 (fetal)	0.003	−1.29
24780	Calml4	Calmodulin-like 4	0.003	1.49
290803	Psca	Prostate stem cell antigen	0.003	1.55
81517	Kcne2	Potassium voltage-gated channel, Isk-related subfamily, gene 2	0.003	1.57
315731	Dnah12	Dynein, axonemal, heavy chain 12	0.003	1.52
300663	Ccdc37	Coiled-coil domain containing 37	0.003	1.50
691223	Scn4b	Sodium channel, voltage-gated, type IV, beta	0.003	−1.58
313495	Tex15	Testis expressed 15	0.003	1.48
25102	Car9	Carbonic anhydrase 9	0.003	1.45
310483	RGD1563692	Similar to hypothetical protein FLJ22671	0.003	1.43
66026	LOC690286	Similar to hepatic leukemia factor	0.003	−1.37
313373	RGD1310371	Similar to RIKEN cDNA 1700026D08	0.003	1.44
84020	Col8a1	Collagen, type VIII, alpha 1	0.003	1.42
301295	Cdh3	Cadherin 3	0.003	1.44
680802	Glb1l	Galactosidase, beta 1-like	0.003	1.51
308794	Slc4a2	Solute carrier family 4 (anion exchanger), member 2	0.003	1.48
116777	LOC360919	Similar to alpha-fetoprotein	0.003	−1.26
65129	Enpp2	Ectonucleotide pyrophosphatase/phosphodiesterase 2	0.003	1.51
29279	Mlf1	Myeloid leukemia factor 1	0.004	1.45
501185	Cldn1	Claudin 1	0.004	1.43
366366	LOC679818	Similar to Maltase-glucoamylase, intestinal	0.004	−1.42
365972	Mdk	Midkine	0.004	1.47
287346	Fam159b	Family with sequence similarity 159, member B	0.004	−1.34
368066	Camk2a	Calcium/calmodulin-dependent protein kinase II alpha	0.004	−1.22
679818	Kcnq1	Potassium voltage-gated channel, KQT-like subfamily, member 1	0.005	1.44
304021	Trpv4	Transient receptor potential cation channel, subfamily V, member 4	0.005	1.45
81686	Igfbpl1	Insulin-like growth factor binding protein-like 1	0.005	1.43
288478	Amy1a	Amylase, alpha 1A (salivary)	0.005	1.16
298524	Mmp2	Matrix metallopeptidase 2	0.005	1.42
300870	Efhc1	EF-hand domain (C-terminal) containing 1	0.005	1.44
499017	LOC691223	Hypothetical protein LOC691223	0.005	1.46
290372	Dsg2	Desmoglein 2	0.005	1.36
363139	Rsb66	Rsb-66 protein	0.005	1.36
360478	RGD1306233	Similar to hypothetical protein MGC29761	0.005	1.37
295337	Fmo2	Flavin containing monooxygenase 2	0.006	1.32
24477	Dnali1	Dynein, axonemal, light intermediate chain 1	0.006	1.41
24805	Rsph10b	Radial spoke head 10 homolog B (Chlamydomonas)	0.006	1.41
690286	Sytl3	Synaptotagmin-like 3	0.006	1.40
681288	Esm1	Endothelial cell-specific molecule 1	0.006	1.48
171519	Olig3	Oligodendrocyte transcription factor 3	0.006	1.36
296608	Ifit1	IFN-induced protein with tetratricopeptide repeats 1	0.006	−1.26
290354	Fam183b	Family with sequence similarity 183, member B	0.006	1.43
309526	Cdr2	Cerebellar degeneration-related 2	0.006	1.36
499660	Mybpc1	Myosin binding protein C, slow type	0.006	−1.36
25662	RGD1562344	Similar to Gm566 protein	0.007	1.39
291847	Calcb	Calcitonin-related polypeptide, beta	0.007	−1.37
85270	Pdlim2	PDZ and LIM domain 2	0.007	1.37
290558	Ifit3	IFN-induced protein with tetratricopeptide repeats 3	0.007	−1.36
362867	Tc2n	Tandem C2 domains, nuclear	0.007	1.36
296610	Fam46a	Family with sequence similarity 46, member A	0.007	1.40
302934	Tnni3	Troponin I type 3 (cardiac)	0.008	1.35
307562	Nts	Neurotensin	0.008	−1.29
500707	Ccdc77	Coiled-coil domain containing 77	0.009	−1.20
293012	RGD1560137	Similar to expressed sequence AU021034	0.009	1.39
308958	Calcr	Calcitonin receptor	0.009	1.31
29248	Tekt1	Tektin 1	0.010	1.36
291962	Igfbp2	Insulin-like growth factor binding protein 2	0.011	1.36
499586	Nt5dc2	5′-Nucleotidase domain containing 2	0.011	1.36
499765	Lingo1	Leucine rich repeat and Ig domain containing 1	0.012	−1.18
25041	Tnnt1	Troponin T type 1 (skeletal, slow)	0.013	1.32
304282	Zmynd10	Zinc finger, MYND-type containing 10	0.013	1.39

Table S2. Cont.

Gene_ID	Symbol	Title	Min PFP	Fold
29699	T2	Brachyury 2	0.013	1.37
59109	Tmem212	Transmembrane protein 212	0.014	1.35
499520	Grifin	Galectin-related interfiber protein	0.015	−1.27
100359739	RGD1563547	RGD1563547	0.016	1.39
302507	Ccdc113	Coiled-coil domain containing 113	0.018	1.36
64555	Dmkn	Dermokine	0.018	−1.26
683514	Dpt	Dermatopontin	0.018	1.24
24710	Rbp2	Retinol binding protein 2, cellular	0.018	1.32
474143	Clecsf6	C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 6	0.020	−1.32
246245	Shisa3	Shisa homolog 3 (*Xenopus laevis*)	0.021	−1.20
361818	Serpinb10	Serpin peptidase inhibitor, clade B (ovalbumin), member 10	0.021	−1.24
171409	Baiap2l1	BAI1-associated protein 2-like 1	0.021	1.34
245955	RGD1564114	Similar to FLJ46082 protein	0.021	1.34
116506	Gpx2	Glutathione peroxidase 2	0.024	−1.28
360613	Cidea	Cell death-inducing DFFA-like effector a	0.024	1.24
54289	Rgs1	Regulator of G protein signaling 1	0.025	−1.31
362285	Cdh1	Cadherin 1	0.025	−1.27
502684	Sprr1al	Small proline-rich protein 1A-like	0.025	−1.36
298534	Epb4.1l5	Erythrocyte protein band 4.1-like 5	0.025	1.25
363654	Bmper	BMP-binding endothelial regulator	0.025	−1.26
305078	Efhc2	EF-hand domain (C-terminal) containing 2	0.027	1.33
293154	Znf597	Zinc finger protein 597	0.027	1.19
681210	Galr1	Galanin receptor 1	0.027	1.20
299757	Lgals3bp	Lectin, galactoside-binding, soluble, 3 binding protein	0.027	1.31
315665	LOC100359739	F-box and leucine-rich repeat protein 13-like	0.028	1.33
29190	Pik3r1	Phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	0.029	−1.18
24471	Cdc14b	CDC14 cell division cycle 14 homolog B (*S. cerevisiae*)	0.031	1.28
315741	Myh3	Myosin, heavy chain 3, skeletal muscle, embryonic	0.031	−1.17
361195	Siglec5	Sialic acid binding Ig-like lectin 5	0.031	1.08
311821	LOC502684	Hypothetical protein LOC502684	0.031	1.30
363674	P2rx6	Purinergic receptor P2X, ligand-gated ion channel, 6	0.031	1.34
114246	Spef2	Sperm flagellar 2	0.032	1.32
29326	LOC100362102	LSM14 homolog B	0.033	−1.19
685158	Col9a3	Procollagen, type IX, alpha 3	0.034	1.30
25628	Paqr5	Progestin and adipoQ receptor family member V	0.034	1.29
83502	Col8a2	Collagen, type VIII, alpha 2	0.035	1.24
59296	Lrrc36	Leucine rich repeat containing 36	0.035	1.27
302554	LOC100359753	Hypothetical protein LOC100359753	0.036	1.26
25611	Hspa1b	Heat shock 70kD protein 1B (mapped)	0.036	1.23
252859	Tmem2	Transmembrane protein 2	0.036	1.04
315645	Trim54	Tripartite motif-containing 54	0.038	1.25
291388	Elmo3	Engulfment and cell motility 3	0.038	1.35
117130	Igf2	Insulin-like growth factor 2	0.038	1.25
24840	LOC290595	Hypothetical gene supported by AF152002	0.040	−1.22
296369	Abcc6	ATP-binding cassette, subfamily C (CFTR/MRP), member 6	0.040	1.26
497957	Clspn	Claspin homolog (*Xenopus laevis*)	0.040	−1.30
298282	LOC683514	Hypothetical protein LOC683514	0.041	1.32
361394	Agpat2	1-Acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	0.041	1.28
306761	Tmigd1	Transmembrane and Ig domain containing 1	0.043	1.30
314386	Rsph1	Radial spoke head 1 homolog (Chlamydomonas)	0.043	1.32
24278	Mmp9	Matrix metallopeptidase 9	0.044	−1.25
171287	Cd3e	CD3 molecule, epsilon	0.044	−1.72
294449	Ppl	Periplakin	0.047	−1.36
300455	MGC116202	Hypothetical protein LOC688736	0.048	1.25
363632	Tmem100	Transmembrane protein 100	0.049	1.26
79110	Ptk2b	PTK2B protein tyrosine kinase 2 beta	0.049	1.25
297804	Htr2b	5-Hydroxytryptamine (serotonin) receptor 2B	0.049	1.25
56824	Nkx2-1	NK2 homeobox 1	0.049	1.28
308015	Mx1	Myxovirus (influenza virus) resistance 1	0.050	1.14
81642	Ccdc117	Coiled-coil domain containing 117	0.050	1.25

Table S2. Cont.

Gene_ID	Symbol	Title	Min PFP	Fold
308212	Mocos	Molybdenum cofactor sulfurase	0.050	1.24
498060	Lamb3	Laminin, beta 3	0.051	−1.30
298532	Lcn2	Lipocalin 2	0.052	1.18
360919	Hspb1	Heat shock protein 1	0.052	1.29
100359753	Mdfic	MyoD family inhibitor domain containing	0.055	1.25
361548	Glod5	Glyoxalase domain containing 5	0.055	1.27
497979	Otc	Ornithine carbamoyltransferase	0.056	1.27
100361383	Lama2	Laminin, alpha 2	0.056	1.24
24483	Stra6	Stimulated by retinoic acid gene 6	0.056	1.19
316273	Dnase2b	DNase II beta	0.059	−1.27
498404	Ibsp	Integrin-binding sialoprotein	0.059	−1.38
81687	Mfap5	Microfibrillar associated protein 5	0.059	−1.25
29581	MGC94891	Hypothetical protein LOC681210	0.061	1.29
25341	Bhmt2	Betaine-homocysteine methyltransferase 2	0.062	1.43
500590	Nostrin	Nitric oxide synthase trafficker	0.062	1.25
362708	Ctsc	Cathepsin C	0.062	1.21
304733	Epn3	Epsin 3	0.062	1.21
688736	Mcm3	Minichromosome maintenance complex component 3	0.063	1.25
362429	Crygd	Crystallin, gamma D	0.064	−1.26
362325	Prkar2a	Protein kinase, cAMP dependent regulatory, type II alpha	0.066	−1.34
50646	Pdyn	Prodynorphin	0.067	−1.29
252958	Nudt7	Nudix (nucleoside diphosphate linked moiety X)-type motif 7	0.067	1.25
311111	Atxn1	Ataxin 1	0.067	−1.07
64626	RGD1561916	Similar to testes development-related NYD-SP22 isoform 1	0.067	1.25
289733	RGD1565611	RGD1565611	0.067	1.27
500441	Tnfrsf9	Tumor necrosis factor receptor superfamily, member 9	0.070	−1.25
361413	Trpv6	Transient receptor potential cation channel, subfamily V, member 6	0.070	−1.28
64507	Odf3b	Outer dense fiber of sperm tails 3B	0.070	1.24
56781	Mepe	Matrix extracellular phosphoglycoprotein	0.070	1.26
53949	LOC100361383	Extracellular matrix protein 2-like	0.070	1.25
25085	Ncan	Neurocan	0.071	−1.17
25148	Egflam	EGF-like, fibronectin type III and laminin G domains	0.071	1.05
316238	RGD1311251	Similar to RIKEN cDNA 4930550C14	0.071	1.29
291541	Cxcl13	Chemokine (C-X-C motif) ligand 13	0.075	−1.19
309368	Iiig9	IIIG9 protein	0.079	1.25
287424	Tekt2	Tektin 2 (testicular)	0.080	1.26
361129	Slc16a6	Solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	0.081	1.24
289178	Gpr88	G protein coupled receptor 88	0.082	−1.22
313592	Tnnc2	Troponin C type 2 (fast)	0.085	−1.27
312707	Sirt4	Sirtuin (silent mating type information regulation 2 homolog) 4 (*S. cerevisiae*)	0.086	1.23
59320	Gal	Galanin prepropeptide	0.089	1.09
266775	Pah	Phenylalanine hydroxylase	0.089	−1.23
361300	Syt2	Synaptotagmin II	0.091	−1.37
100363441	Antxr1	Anthrax toxin receptor 1	0.092	1.20
500566	LOC685158	Similar to CG8138-PA	0.092	1.28
303772	Fscn2	Fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus)	0.092	1.22
500917	Upk1b	Uroplakin 1B	0.094	−1.20
362712	Slc22a2	Solute carrier family 22 (organic cation transporter), member 2	0.094	−1.21
60563	Slc24a2	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	0.096	−1.23
294254	Pih1d2	PIH1 domain containing 2	0.100	1.27

Details are as for Table S1. Up-regulated genes had higher expression levels in the “Odor” condition compared with the “No odor” condition in the FST. No probes with a pfp >0.10 criteria exceeded a fold >1.50.

Table S3. Genes/gene groups for canonical paths for Fig. 4*A*

Entrez gene name	Symbol	Entrez gene ID
AMPK signaling		
Adrenergic receptor, alpha 1d	ADRA1D	29413
Adrenergic receptor, beta 3	ADRB3	25645
Alpha serine-threonine protein kinase	Akt	Group
G protein-coupled receptor	Gpcr	Group
p85 Pi3kinase	p85 (pik3r)	Group
p85-α regulatory subunit of phosphatidylinositol 3-kinase	PIK3R1	25513
Protein phosphatase type 2a	PP2A	Complex
CREB signaling in neurons		
14–3-3	CBB	Group
AKT1/2/3	Akt	Group
Calmodulin	CALM	Group
Calcium/calmodulin-dependent protein kinase II alpha	CAMK2A	25400
G protein-coupled receptor	Gpcr	Group
p85 Pi3kinase	p85 (pik3r)	Group
p85-α regulatory subunit of phosphatidylinositol 3-kinase	PIK3R1	25513
GPCR Signaling		
Adrenergic receptor, alpha 1d	ADRA1D	29413
Adrenergic receptor, beta 3	ADRB3	25645
AKT1/2/3	Akt	Group
Calmodulin	CALM	Group
Calcium/calmodulin-dependent protein kinase II alpha	CAMK2A	25400
G protein-coupled receptor	Gpcr	Group
5-Hydroxytryptamine (serotonin) receptor 1A, G protein-coupled	HTR1A	24473
Nociceptin/orphanin FQ receptor	OPRL1	29256
p85 Pi3kinase	p85 (pik3r)	Group
p85-α regulatory subunit of phosphatidylinositol 3-kinase	PIK3R1	25513

Table S4. Genes/gene groups for canonical paths for Fig. 4*B*

Entrez gene name	Symbol	Entrez gene ID
Glucocorticoid receptor signaling		
cAMP response element binding	Creb	Group
G protein-coupled receptor	Gpcr	Group
H3, H3.3, Histone H3B	Histone h3	Group
Nuclear factor κ b transcription factor	NFkB (complex)	Group
Ikb kinase alpha	NFKBIA	25493
p85 Pi3kinase	p85 (pik3r)	Group
RNA polymerase II	RNA polymerase II	Group
GPCR signaling		
Calmodulin	CALM	Group
Cholinergic receptor, muscarinic 5	CHRM5	53949
cAMP response element binding	Creb	Group
G protein-coupled receptor	Gpcr	Group
5-Hydroxytryptamine (serotonin) receptor 1A, G protein-coupled	HTR1A	24473
5-Hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	HTR2B	29581
5-Hydroxytryptamine (serotonin) receptor 5B	Htr5b	79247
Nuclear factor κ b transcription factor	NFkB (complex)	Group
Nuclear factor κ b transcription factor	NFKBIA	25493
p85 Pi3kinase	p85 (pik3r)	Group
Protein kinase, cAMP-dependent, regulatory, type II, alpha	PRKAR2A	29699
Serotonin receptor	Serotonin receptor	Group
Protein kinase A signaling		
A kinase (PRKA) anchor protein 4	AKAP4	78254
Calmodulin	CALM	Group
cAMP response element binding	Creb	Group
G protein-coupled receptor	Gpcr	Group
H3, H3.3, Histone H3B	Histone h3	Group
Nuclear factor κ b transcription factor	NFkB (complex)	Group
Nuclear factor κ b transcription factor	NFKBIA	25493
Protein kinase, cAMP-dependent, regulatory, type II, alpha	PRKAR2A	29699
Serotonin receptor signaling		
G protein-coupled receptor	Gpcr	Group
5-Hydroxytryptamine (serotonin) receptor 1A, G protein-coupled	HTR1A	24473
5-Hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	HTR2B	29581
5-Hydroxytryptamine (serotonin) receptor 5B	Htr5b	79247
Serotonin receptor	Serotonin receptor	Group