SI Appendix

SUPPLEMENTAL METHODS

Cell collection.

A Vaseline well was constructed around the ganglion, in which ~2.5 mg/ml protease (Sigma – P6911, St. Louis, MO) in chilled physiological saline was added to disrupt connective tissue and loosen adherent support cells during a 10-15 minute incubation. The well was then thoroughly washed with fresh physiological saline to halt further enzymatic activity and remove any loose support or connective cells. Chilled ethylene glycol was gradually added in increasing concentration until a 70% solution of chilled ethylene glycol in saline was present to the well. During the process of protease digestion, normal activity continues in the STG (1), and this activity maintains patterns of gene expression in STG neurons for at least some classes of gene products (2, 3). Furthermore, the time from the initiation of protease digestion to suspension in cold ethylene glycol (which represents a stable end point) is < 45 minutes. Normal STG output can be maintained for many days (4, 5), and steady state mRNA levels remain relatively stable for at least 72 hours as long as activity is maintained (3). When activity is disrupted, significant changes in channel mRNAs can be detected only on the order of 8 hours (2), and our preliminary data show no changes within 2 hours in cardiac motor neurons (LCs; unpublished observation). While we cannot determine whether the collection process does not alter steady state mRNA levels for all gene products, present evidence suggests that the time frame over which the the neurons are harvested is not likely to substantially change the state of these neurons relative to those in intact ganglia. Once the ganglia were suspended in cold 70% ethylene glycol solution, the saline outside the well was replaced with distilled water, and the entire dish was frozen at -20°C for 30 minutes. This constitutes a freeze substitution that allows the easy hand-dissection and removal of single, intact neurons for biochemical and molecular analyses (6). Due to the large size of *C. borealis* STG neuronal somata (50-150 μM in diameter) (7), fine forceps were used to manually remove each neuron.

Statistical Analysis.

All statistical analyses were performed using R version 3.5.3 (2019-03-11) -- "Great Truth" (8). We used single cell RNA-seq data to evaluate our methods under expected and near best case scenarios. To this end, we reduced the dimensionality of the data (28,695 contigs) by selecting the 2000 most variable contig and by selecting 922 highly variable contigs selected using the M3Drop implementation of the Brennecke method (9) (i.e. M3Drop:: BrenneckeGetVariableGenes() function (10)) assuming a 0.2 false discovery rate. To test performance under ideal conditions we selected those contigs differentially expressed at an alpha of 0.2 or 0.05. We centered and scaled the aforementioned datasets and their progenitors via the caret::predict() and caret::preprocess() functions (11). We also tested dimensionality reduction via PCA. We further used PCA in exploratory data analysis to determine if any of the cell types were visually separable across four subsets of the data (Seq H2K, Seq HVG, Seq DE0.2, and Seq DE0.05).

Next, we performed cluster estimation using the optClust() function of the optCluster package (12). The algorithms used on each dataset varied by whether the data were counts or continuous. Allowed k values ranged from 2-10 (i.e. cells in dataset / 4, rounding up). We selected the top three predicted k values from each algorithm for visualization of the spread of predicted ks.

To assess the performance of unsupervised machine learning methods we tested several clustering algorithms – k-means clustering, hierarchical clustering (using a variety of distance metrics, (euclidean, maximum, manhattan, canberra, binary, minkowski, correlation, uncentered) and clustering methods (ward.D, ward.D2, single, complete, average, mcquitty, median, centroid, ward.D2)), and SNN-Cliq clustering (13). We then selected high performing clustering methods based on the Jaccard index calculated against cell identity. We selected one of the best performing combinations (Ward's method with correlation as the distance metric) for visualization.

We applied several supervised machine learning methods to evaluate predictive power of expression data in ideal circumstances (i.e. prior knowledge of a given cell type's molecular identity). Specifically, we tested elastic regression, k-nearest neighbors, linear discriminant analysis, neural network, multinomial neural network, random forest, support vector machine with a radial kernel, and support vector machine with a linear kernel. For each of these models we tested a variety of tuning parameters and selected the most effective parameter set before comparison with other methods. Methods were evaluated by using cross validation (with five folds) to produce the expected accuracy on new data. The same approaches were applied to the single cell RT-qPCR data set, with a few caveats. Given its relatively smaller size, dimensionality reduction was not necessary to overcome technical or practical hurdles. Thus, we tested both the raw and centered and scaled dataset in addition to PCA transformations of the same. We also increased the maximum k allowed in cluster estimation to 32.

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SUPPLEMENTAL FIGURES

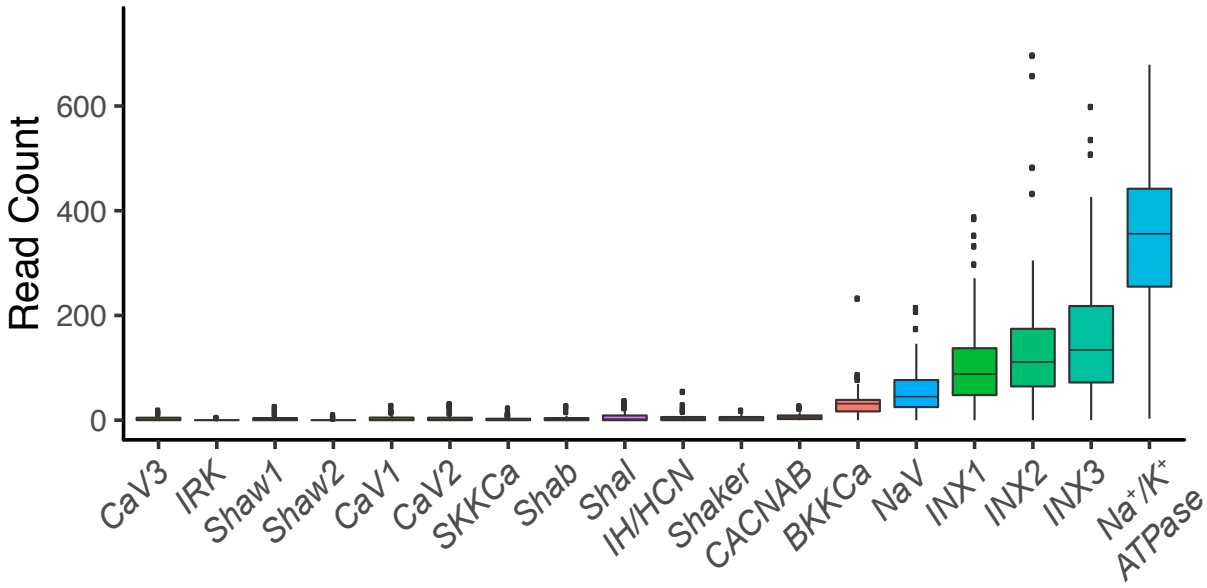

Figure S1. Count numbers for selected voltage-gated ion channels from the RNA-seq data. The median counts for each of the voltage-gated channels used in the RT-PCR analysis was generated by pooling cell type. Innexins and the Na+/K+ ATPase are used as a reference of more highly abundant gene products.

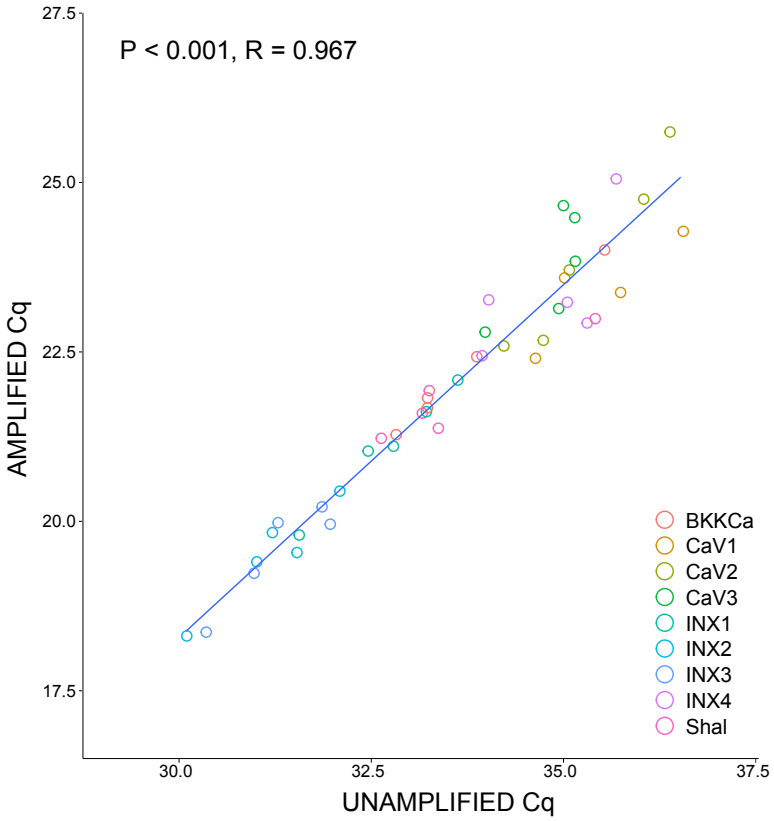

Figure S2. Comparison of expression levels of the same single cell samples (N = 5) before (Unamplified) and after (Amplified) 14 cycles of preamplification of cDNA. Each sample represents a cDNA pool from a single identified neuron, half of which was preamplified and half remained unamplified. Data are shown as quantitation cycle (Cq) values. Statistics shown report values for Pearson's Correlation test.

SUPPLEMENTAL TABLES

Table S1. Top ten contributing genes or contigs to PCs1-3 for each dataset.

Dataset	Rank	PC1	PC1 value	PC2	PC2 value	PC3	PC3 value
qRTPCR	1	LCCH3r	3.54	NaV	6.30	GluCl	9.12
qRTPCR	2	mGABA3	3.10	Shal	5.65	GABAB_R1	8.04
qRTPCR	3	mGluR5	3.06	NMDA_1A	5.16	vAChT	7.56
qRTPCR	4	CaV2	3.05	KCNK1	4.95	HisCL	6.74
qRTPCR	5	Shab	3.02	Shaker	4.54	ChAT	6.57
qRTPCR	6	KCNH3	2.97	IH	3.47	IH	6.16
qRTPCR	7	DAR1A	2.91	KCNK2	3.45	INX4	6.13
qRTPCR	8	SKKCa	2.87	BKKCa	3.10	vGluT	5.29
qRTPCR	9	His_3r	2.86	Dopa_1Br	3.06	RDLr	4.16
qRTPCR	10	TRP_A_like	2.82	RDLr	2.93	CCAPr	3.11
seq_h2k	1	c1318	0.10	c4636	0.50	c4191	0.59
seq_h2k	2	c724	0.10	c8463	0.50	c751	0.58
seq_h2k	3	c2022	0.10	c28755	0.50	c8533	0.49
seq_h2k	4	c1834	0.10	c17319	0.50	c953	0.46
seq_h2k	5	c718	0.10	c10220	0.50	c2665	0.46
seq_h2k	6	c2357	0.10	c27163	0.49	c2126	0.45
seq_h2k	7	c196	0.10	c5528	0.49	c2981	0.45
seq_h2k	8	c739	0.10	c10716	0.49	c3881	0.42
seq_h2k	9	c2301	0.10	c9333	0.49	c23433	0.41
seq_h2k	10	c1048	0.10	c13463	0.49	c1647	0.40
seq_hvg	1	c38450	0.50	c18443	0.63	c29394	0.80
seq_hvg	2	c5595	0.50	c17911	0.63	c23916	0.80
seq_hvg	3	c28755	0.50	c13615	0.63	c39794	0.80
seq_hvg	4	c11256	0.49	c16416	0.63	c24360	0.80
seq_hvg	5	c20433	0.49	c17569	0.63	c18403	0.79
seq_hvg	6	c39762	0.49	c17622	0.63	c7694	0.79
seq_hvg	7	c13489	0.49	c18306	0.63	c11984	0.79
seq_hvg	8	c19224	0.49	c19165	0.63	c16991	0.79
seq_hvg	9	c30088	0.49	c19999	0.63	c18899	0.79
seq_hvg	10	c4923	0.49	c22142	0.63	c25542	0.79
seq_DE0.2	1	c5749	1.62	c4517	3.20	c13441	5.94
seq_DE0.2	2	c1898	1.44	c398	2.92	c1058	4.27
seq_DE0.2	3	c23967	1.43	c878	2.92	c31757	3.14
seq_DE0.2	4	c5120	1.41	c4945	2.87	c9248	3.05
seq_DE0.2	5	c1219	1.39	c3559	2.69	c2212	3.02
seq_DE0.2	6	c8871	1.37	c15559	2.64	c4534	2.63
seq_DE0.2	7	c972	1.35	c8507	2.50	c8114	2.61
seq_DE0.2	8	c973	1.33	c1151	2.15	c10145	2.57
seq_DE0.2	9	c12663	1.32	c8323	2.06	c2981	2.47
seq_DE0.2	10	c910	1.30	c1800	2.00	c14660	2.35
seq_DE0.05	1	c21272	4.69	c4517	8.85	c1058	13.16
seq_DE0.05	2	c5716	4.21	c16963	7.16	c13441	11.60
seq_DE0.05	3	c5120	4.14	c3348	6.68	c2212	10.64
seq_DE0.05	4	c3737	3.77	c1151	6.05	c2586	7.17
seq_DE0.05	5	c8114	3.72	c14320	5.14	c5845	5.83
seq_DE0.05	6	c16240	3.59	c5222	4.93	c14320	4.87
seq_DE0.05	7	c2796	3.56	c8323	4.57	c4997	4.10
seq_DE0.05	8	c1713	3.43	c5067	4.35	c14660	4.06
seq_DE0.05	9	c49	3.38	c1324	4.12	c3348	4.00
seq_DE0.05	10	c3716	3.23	c24846	4.08	c4534	3.86

Table S2. Gene Ontology Enrichment analysis of Molecular Function for H2K RNAseq data.

GO term: molecular function	Fold Enrichment	FDR p-value
proton-transporting ATP synthase activity, rotational mechanism (GO:0046933)	8.08+	2.88E-04
clathrin binding (GO:0030276)	6.82+	4.51E-03
ubiquitin conjugating enzyme activity (GO:0061631)	4.6+	1.59E-02
intramolecular oxidoreductase activity (GO:0016860)	4.32+	2.22E-02
structural constituent of ribosome (GO:0003735)	4.02+	4.61E-11
proton-transporting ATPase activity, rotational mechanism (GO:0046961)	3.84+	4.35E-02
structural constituent of cytoskeleton (GO:0005200)	3.84+	4.30E-02
unfolded protein binding (GO:0051082)	3.8+	4.00E-05
heat shock protein binding (GO:0031072)	3.73+	5.01E-02
mRNA 3'-UTR binding (GO:0003730)	3.73+	4.96E-02
cell adhesion molecule binding (GO:0050839)	3.57+	3.89E-02
translation factor activity, RNA binding (GO:0008135)	3.27+	4.57E-03
electron transfer activity (GO:0009055)	3.07+	1.79E-02
GTPase activity (GO:0003924)	3.07+	6.09E-05
GTP binding (GO:0005525)	2.97+	6.78E-05
actin binding (GO:0003779)	2.95+	4.42E-04
kinase binding (GO:0019900)	2.85+	7.78E-03
microtubule binding (GO:0008017)	2.75+	3.98E-03
phospholipid binding (GO:0005543)	2.56+	3.16E-02
calcium ion binding (GO:0005509)	2.4+	1.60E-03
protein-containing complex binding (GO:0044877)	2.39+	7.29E-04
ATP binding (GO:0005524)	2.31+	1.36E-10
protein serine/threonine kinase activity (GO:0004674)	2.17+	1.31E-02
enzyme regulator activity (GO:0030234)	1.83+	1.40E-02
DNA-binding transcription factor activity (GO:0003700)	0.41-	1.79E-02
serine-type endopeptidase activity (GO:0004252)	0.1-	1.90E-03

Table S3. Gene Ontology Enrichment analysis of Biological Process for H2K RNAseq data.

GO term: biological process	Fold Enrichment	FDR p-value
regulation of short-term neuronal synaptic plasticity (GO:0048172)	10.96+	6.64E-03
positive regulation of neuron remodeling (GO:1904801)	10.63+	7.39E-05
substrate adhesion-dependent cell spreading (GO:0034446)	10.23+	2.68E-03
actin filament polymerization (GO:0030041)	9.59+	9.52E-03
clathrin-dependent synaptic vesicle endocytosis (GO:0150007)	8.77+	3.43E-02
protein N-linked glycosylation via asparagine (GO:0018279)	8.77+	3.42E-02
gluconeogenesis (GO:0006094)	8.53+	1.31E-02
dorsal closure, spreading of leading edge cells (GO:0007395)	8.53+	1.31E-02
morphogenesis of larval imaginal disc epithelium (GO:0016335)	7.67+	4.63E-02
retrograde axonal transport (GO:0008090)	7.67+	1.79E-02
ATP synthesis coupled proton transport (GO:0015986)	7.03+	1.14E-04
vesicle transport along microtubule (GO:0047496)	6.98+	2.40E-02
axonal transport of mitochondrion (GO:0019896)	6.98+	2.39E-02
anterograde axonal transport (GO:0008089)	6.98+	2.39E-02
cellular response to metal ion (GO:0071248)	6.39+	3.07E-02
axonal fasciculation (GO:0007413)	6.14+	3.23E-03
female germ-line stem cell asymmetric division (GO:0048132)	5.97+	7.80E-03
regulation of reactive oxygen species metabolic process (GO:2000377)	5.9+	3.80E-02
actin nucleation (GO:0045010)	5.48+	4.75E-02
positive regulation of photoreceptor cell differentiation (GO:0046534)	5.48+	4.74E-02
sevenless signaling pathway (GO:0045500)	5.42+	2.40E-02
ovarian follicle cell stalk formation (GO:0030713)	5.42+	2.39E-02
synaptic vesicle priming (GO:0016082)	5.42+	2.39E-02
flight behavior (GO:0007629)	5.42+	2.39E-02
positive regulation of endocytosis (GO:0045807)	5.42+	3.15E-04
positive regulation of lipid localization (GO:1905954)	5.42+	2.38E-02
positive regulation of canonical Wnt signaling pathway (GO:0090263)	5.39+	1.58E-04
ribosomal large subunit assembly (GO:0000027)	5.37+	1.19E-02
positive regulation of smoothened signaling pathway (GO:0045880)	5.31+	3.15E-03
positive regulation of protein modification by small protein conjugation or removal (GO:1903322)	5.12+	2.94E-02
glucose homeostasis (GO:0042593)	5.12+	2.40E-04
lumen formation, open tracheal system (GO:0035149)	5.12+	3.83E-03
cellular protein complex disassembly (GO:0043624)	5.12+	7.47E-03
glycolytic process (GO:0006096)	4.91+	8.93E-03
oocyte microtubule cytoskeleton polarization (GO:0008103)	4.85+	3.49E-02
hemocyte migration (GO:0035099)	4.6+	4.17E-02
negative regulation of supramolecular fiber organization (GO:1902904)	4.55+	1.26E-02
maintenance of protein location in cell (GO:0032507)	4.51+	4.05E-03
regulation of R7 cell differentiation (GO:0045676)	4.39+	4.95E-02
cell adhesion mediated by integrin (GO:0033627)	4.39+	4.94E-02
positive regulation of neuromuscular junction development (GO:1904398)	4.39+	4.76E-03
terminal branching, open tracheal system (GO:0007430)	4.39+	1.49E-02
pole plasm oskar mRNA localization (GO:0045451)	4.32+	9.07E-03
positive regulation of organ growth (GO:0046622)	4.3+	3.01E-02
antibiotic metabolic process (GO:0016999)	4.3+	3.00E-02
adherens junction organization (GO:0034332)	4.26+	5.62E-03
epithelial cell migration, open tracheal system (GO:0007427)	4.26+	5.61E-03
regulation of cell-cell adhesion (GO:0022407)	4.23+	1.77E-02
intestinal stem cell homeostasis (GO:0036335)	4.23+	1.77E-02
regulation of filopodium assembly (GO:0051489)	4.19+	1.06E-02
heart morphogenesis (GO:0003007)	4.15+	6.50E-03
negative regulation of autophagy (GO:0010507)	4.13+	3.47E-02
reactive oxygen species metabolic process (GO:0072593)	4.13+	3.45E-02
plasma membrane invagination (GO:0099024)	4.13+	3.45E-02
ATP hydrolysis coupled proton transport (GO:0015991)	4.04+	7.57E-03
olfactory learning (GO:0008355)	4.04+	7.54E-03
positive regulation of translation (GO:0045727)	4.04+	7.50E-03
rhabdomere development (GO:0042052)	4.02+	4.61E-03
synaptic growth at neuromuscular junction (GO:0051124)	3.95+	1.43E-02
protein folding (GO:0006457)	3.93+	6.74E-08
establishment of mitotic spindle localization (GO:0040001)	3.84+	4.66E-02
salivary gland cell autophagic cell death (GO:0035071)	3.84+	4.65E-02
insulin receptor signaling pathway (GO:0008286)	3.84+	4.64E-02

regulation of lipid storage (GO:0010883)	3.74+	1.15E-02
negative regulation of cytoskeleton organization (GO:0051494)	3.72+	3.20E-02
negative regulation of smoothened signaling pathway (GO:0045879)	3.72+	3.20E-02
mitochondrial ATP synthesis coupled electron transport (GO:0042775)	3.65+	1.75E-04
regulation of peptide secretion (GO:0002791)	3.64+	2.21E-02
behavioral response to ethanol (GO:0048149)	3.63+	3.40E-03
regulation of chemotaxis (GO:0050920)	3.61+	3.63E-02
response to unfolded protein (GO:0006986)	3.61+	3.62E-02
positive regulation of cell size (GO:0045793)	3.57+	1.48E-02
tight junction organization (GO:0120193)	3.54+	2.50E-02
apical junction assembly (GO:0043297)	3.52+	1.02E-02
cytosolic transport (GO:0016482)	3.5+	4.39E-03
cytokinetic process (GO:0032506)	3.49+	1.69E-02
regulation of axonogenesis (GO:0050770)	3.47+	3.00E-03
negative regulation of protein phosphorylation (GO:0001933)	3.44+	2.05E-03
positive regulation of cell morphogenesis involved in differentiation (GO:0010770)	3.41+	4.69E-02
establishment or maintenance of apical/basal cell polarity (GO:0035088)	3.37+	3.20E-02
regulation of multicellular organism growth (GO:0040014)	3.34+	2.20E-02
morphogenesis of follicular epithelium (GO:0016333)	3.31+	1.47E-02
translational initiation (GO:0006413)	3.25+	1.65E-02
regulation of protein stability (GO:0031647)	3.25+	1.65E-02
neuromuscular synaptic transmission (GO:0007274)	3.23+	1.13E-02
autophagy (GO:0006914)	3.23+	4.15E-04
imaginal disc-derived wing margin morphogenesis (GO:0008587)	3.19+	1.86E-02
mitotic cytokinesis (GO:0000281)	3.16+	6.07E-03
long-term memory (GO:0007616)	3.15+	4.15E-03
germ-line stem cell population maintenance (GO:0030718)	3.15+	2.84E-03
asymmetric neuroblast division (GO:0055059)	3.14+	4.50E-02
cell redox homeostasis (GO:0045454)	3.13+	3.09E-02
response to growth factor (GO:0070848)	3.13+	3.08E-02
synaptic target recognition (GO:0008039)	3.13+	3.07E-02
amino acid transport (GO:0006865)	3.01+	3.76E-02
axon guidance (GO:0007411)	2.94+	1.77E-08
positive regulation of locomotion (GO:0040017)	2.63+	4.08E-02
negative regulation of neurogenesis (GO:0050768)	2.63+	3.09E-02

Table S4. Gene Ontology Enrichment analysis of Molecular Function for HVG RNAseq data.

GO term: molecular function	Fold Enrichment	FDR p-value
ATP binding (GO:0005524)	3.1+	1.72E-03
transferase activity (GO:0016740)	2+	2.38E-02

Table S5. Gene Ontology Enrichment analysis of Biological Process for HVG RNAseq data.

GO term: molecular function	Fold Enrichment	FDR p-value
regulation of protein localization to plasma membrane (GO:1903076)	35.33+	4.79E-02
chromatin silencing (GO:0006342)	7.69+	3.12E-02
nucleic acid metabolic process (GO:0090304)	2.17+	3.74E-02
macromolecule modification (GO:0043412)	2.08+	3.91E-02
cellular macromolecule metabolic process (GO:0044260)	1.84+	2.22E-02

Table S6. Gene Ontology Enrichment analysis of Molecular Function for DE0.2 RNAseq data.

GO term: molecular function	Fold Enrichment	raw p-value
choline:sodium symporter activity (GO:0005307)	> 100+	7.51E-03
acetylcholine transmembrane transporter activity (GO:0005277)	> 100+	7.51E-03
dihydroorotase activity (GO:0004151)	> 100+	7.51E-03
choline O-acetyltransferase activity (GO:0004102)	> 100+	7.51E-03
carboxyl- or carbamoyltransferase activity (GO:0016743)	> 100+	7.51E-03
carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity (GO:0004088)	> 100+	7.51E-03
aspartate carbamoyltransferase activity (GO:0004070)	> 100+	7.51E-03
very-long-chain-acyl-CoA dehydrogenase activity (GO:0017099)	> 100+	7.51E-03
latrotoxin receptor activity (GO:0016524)	> 100+	7.51E-03
glutamine binding (GO:0070406)	> 100+	7.51E-03
L-iduronidase activity (GO:0003940)	> 100+	7.51E-03
choline binding (GO:0033265)	> 100+	7.51E-03
myosin II light chain binding (GO:0032033)	> 100+	1.12E-02
kinetochore binding (GO:0043515)	> 100+	1.12E-02
GABA-gated chloride ion channel activity (GO:0022851)	88.25+	1.50E-02
receptor antagonist activity (GO:0048019)	88.25+	1.50E-02
GABA-A receptor activity (GO:0004890)	66.19+	1.87E-02
smoothened binding (GO:0005119)	66.19+	1.87E-02
patched binding (GO:0005113)	66.19+	1.87E-02
histone demethylase activity (H3-K4 specific) (GO:0032453)	66.19+	1.87E-02
kinesin binding (GO:0019894)	58.83+	7.47E-04
histone demethylase activity (H3-K36 specific) (GO:0051864)	52.95+	2.24E-02
morphogen activity (GO:0016015)	52.95+	2.24E-02
MAP-kinase scaffold activity (GO:0005078)	52.95+	2.24E-02
extracellular matrix binding (GO:0050840)	52.95+	2.24E-02
axon guidance receptor activity (GO:0008046)	44.12+	2.61E-02
protein kinase C binding (GO:0005080)	44.12+	2.61E-02
RNA polymerase II activity (GO:0001055)	29.42+	3.70E-02
epidermal growth factor receptor binding (GO:0005154)	29.42+	3.70E-02
phosphatidylserine binding (GO:0001786)	29.42+	3.70E-02
cell-cell adhesion mediator activity (GO:0098632)	24.07+	4.42E-02
fatty-acyl-CoA binding (GO:0000062)	24.07+	4.42E-02
microtubule plus-end binding (GO:0051010)	22.06+	4.78E-02
calcium-dependent phospholipid binding (GO:0005544)	22.06+	4.78E-02
amino acid transmembrane transporter activity (GO:0015171)	9.46+	2.01E-02
flavin adenine dinucleotide binding (GO:0050660)	7.79+	2.85E-02
GTP binding (GO:0005525)	5.12+	2.15E-02

Table S7. Target primer and probe sequences for qRT-PCR Multiplex assays. Each box represents a group of four to five genes that were combined into a single multiplex reaction.

Gene	*Accession #*	*Forward / Reverse Primer 5'-3' sequence*	*Probe 5'-3' sequence*
HTR1A	KU710381.1	AACCGCTGTGGTAGTTTCCA / TGCTCGTTAACCCGGACTAAG	AGCGCCTTTATTTGGCTGGAAGGA
HTR2	KU710380.1	TCCGCCTCCATCAAGTTTGT / GCACGTTGGCGATGAAGAAC	TCATCGAAGAGACACGGGAGGACC
HTR7	KU710379.1	ACGGCGATGGCTCCATCTG / CGGTGAGCGGGATGTAGAAG	TGAGGTGTGCAACAACTTCTGGTACC
DAR2	KU710378.1	GAAGCCGAAAGTGAGTGAGATCA / TCCGAACTAAGCGCTGTTTC	TGTGATCGAGAATGTGACACAGACGA
DAR1A	KU710377.1	GGCGCCTGTCCATTCACT / CGCGGTAGATGCGGAAGTAAG	ACCTTGTGTTCTCCTCTACTATCAGCTTCT
GABAB-R1	KU986868.1	TCGTCTCGTTTGCCATCATC / GGTGCCGAACCTCAATGATC	TCTGCTGCTTCCTCTCCATGGCT
LCCH3r	KU986871.1	TGACGGCTCCATCACCTATGG / TTGGGTGTCGAGTGGATAGTAG	TTCACCACTACGTTGGCCTGCAT
RDLr	KU986872.1	TGGTGTTTGCCTCGCTTCTAG / TCCGCTGTTCTGCTAACTTC	AATACGCCGCGGTGGGCTACAT
GluCl	KX059698.1	ACGGAGGATCTGGTGTTTCTG / ACCCGTGTTGGTCTTGCTGTT	TACAGGTGACCAAGAACCTTCACC
NALCN	KU681457.1	TCGCTTCCACGGTGTACATTC / GCGGTGCCTTTGTTCTCAG	TCTTCGTCTTCCTTGGCTGCATGA
CACNAB	GEFB01006512	GCAGCTGGCCAAGACTTCTTT / AGACGCTGCAATACCTTAGGA	AGCGCCCATCCTCGTGTACCTTAAG
IRK	KU681451.1	TACAGTGGCGTTGGACTCTAC / TCCACCACACCAAGGCAAATAG	TCGTGTTCGCTATGTCATTCATCAGC
IH	DQ103257.3	TCGGTGCCACTAGACTACATC / GACCCGCGTGGAGAATCTG	TCCTCATCTTCAACCAGGACTTCAGC
SKKCa	KU710383.1	GCATCGGAGCATTGAACAGAA / GCCCGGACAGATAGTCATCAG	CAACTTCAACACTCGGTTTGTCCTCAA
INX1	JQ994479.1	TGGAGCGTCATGATGCATTC / GAGCAGGATGGCAAGGATCAC	TGCTGCCTCTCAACATTCTTAACGAA
INX2	JQ994480.1	GGCTGTGGTGTCTGGTGTAG / GCGAGAGCGTGTCCTTAACAG	CTGCTGTACCGCCTCGCCACTTT
INX3	JQ994481.1	TGTCGGCCCTAGTGAAAGAG / GGTACCGTGGGATGTAGAACA	TGACGAGATTGTGTACCACGCTTAC
INX4	KJ642222.1	CTGGCGTTCAGCCTCATTGTC / CACGTCCTCTGGGATCTCCTTAG	CACGCGTCAGTATGTCGGGAACC
INX5	KJ817410.1	TGCCTTCCCTGCTGGATAA / GCGTCACCCATTGGTAGTAAC	AGGTGGCTCATCCAGGCATCGGT
Shaw1	KU681456.1	CGCGTCACTCCTCAGGACTT / CCCAGCACCAGGAAGAACAC	TGATACAGACTTTCCGTGCATCCGC
Shaw2	KU681455.1	GAACGCCATCAAGCACTATCATC / ATGGCGCCCGACAGCTTAG	TGGCTTGAAGGACGGTCTCACA
NaV	EF089568.2	TCAACGGGAGGTACCATAAGTG / TCGCTGTTCACCCAAGAGTAG	CGGAGGGATTGAAGCTCAACGCA
Shaker	FJ263946.1	GAGGCTCAGAAGACCAGTCAAC / TGGCGATATCACCGAGCTCAT	CACTCGATGTCTTCGCGGAGGAGAT
Shab	DQ103255.1	GAGCCGGACAGACAGGAAC / TGCGCCTCCTTCTGTAGTC	AAGAACCACGAACACCACATGGGTC
CaV1	JN809809.1	CCAGGCCTTCTACTGGCTCATT / GCTGGCGATAGTGCTCACTG	TGTGCTCGTCTTCCTCAACACGG
CaV2	JN809808.1	ATCCGGCGGACAGTAAAGC / GTTCGGCAGCAACACAAAC	TGGTTCTACTGGTTCGTCATCATACTTGT
CaV3	JN809810.1	TGGCTGCCACCGATACTTC / CAGCACAATGCCCACAACTG	CAGGACAGAGATGGAACCAGTTGGA
Shal	DQ103254.1	GACACCACCTTCACCTCCATTC / GAACCATGTCGCCGTATCCTA	CGGCGTTTTGGTACACCATTGTCAC
BKKCa	DQ103256.4	GCTCAAACTCGGCTTCATTG / CTGCGTGTCTGGAGAAGTTT	AGAATCCCGGCGCTAAACATGACT
mGluR1	KU986879.1	GCATCGTGTGGCTCATCTTTG / GGCCAACGTGACCACTCTAAT	ACCTGTCAGCGGGAGTCACTGATG
mGluR2	KU986880.1	TCCGCAGGTGAGTTTCTTC / CCATGGCTTTCACTTGGTAATGG	CCACGTCGCCTGAACTGAGTAACA
mGluR4	KU986882.1	GCGCGTTGATTCCGGTACT / CCACTCATCGTCCTCAACTTC	AAGTCTTCCCGCTGGACTACGAAC
mGluR5	KU986883.1	GCCTGTCCTTTGCCATGATC / TGCGCATCGTGATCTTCTTG	CGCTTGTCACCAAGACCAACCGC
mGluR7	KU986884.1	ACCGCGCTCGCAGATTGTC / TGGCTGGCGTTTCCACTATC	TTCTGGACTGGTGAGTGTTCAGCT
mAChrA	KX021822.1	GGTGTCGATGCCTTTGTTCAC / GCCAGCCAGGTGTCACATAT	TGTACACGCTGATGGGATACTGGC
mAChrB	KX021821.1	GCGGACCATCTCCATCATTC / TGGTGCACTGACAGAAGCT	CCTTTGTGGCCTGTTGGACGCC
mGABA2	KU986869.1	TGCCTACAAAGGTCTGCTAATGG / TCGTTCAAGGCGGGTATGTT	TGGTTGTTTCCTGGCCTGGGAAA
mGABA3	KU986870.1	CGATCCCATGACGAGACACAT / TCCACCTGTGGCTGATAGAC	CCTCACCTTAGAAGTGTCAGCCGA
mGluR3	KU986881.1	CACCGTGTATGCCGTCAAGAC / CCCGGTGCCGAAGTAGATG	CCCCGAGAATTTCAACGAGAGCAAGT
TRP-M3	KX037433.1	CCGCACCATCTACGAGAAC / TGCTGGCCTGGAAGATGT	TGCTCAAGTCTCCTCGTCTTCACC
TRP-A-like	KX037434.1	TCGCGACCTTCCTCAAATTC / CGGTACCTGAGTCCTCAACAC	CACGGTCTTCTTACTCTTCCTCATCGC
TRP-A1	KX037435.1	CTGCCAAGTACGGTCGTTACAAC / CCCTCGTCATTGCACTCGTTA	ACGTCAGCTTGTGGAGTCTCTGAA
TRP-M1	KX037436.1	GAGGGCGGACCTCAAACTATC / TGTCGGCTGCTCTTCCTGTT	CGTCAGGTGCTGGAGTATGTCACTG
TRP-M-like	KX037437.1	GACGGGACGCAGATCCTCTT / GAGTGCTTGGGCTGTTAGGT	ACGGTATACGGTTGGCTATTTCCCA
Dopa-1Br	KU710376.1	CGCAAGATTGGCAACCTCTTC / ACGAGGGCAAAGCTCATCAC	TGTCCTTGGCTATCGCTGACCTCTT
5HTR-1Br	KU710382.1	TGACGCAGGTGGACTACATTC / GGAACGACACCACCCAGATC	ACCGATCGCCGCGTCGCATC
His-1r	KU716100.1	TGCCTGCCAGAGTAACCTTAG / GACAGGTGGGAGGGATTTCTG	CATCACTTCTCACTCTGTCAACCCAACA
His-2r	KU716101.1	CCGCCACAGTCTCAAGGTAATC / GCGTAGGTCATGGAACTCTCATC	ACGGTAGTCTACTTCCACGTCACA
His-3r	KU716102.1	ATCCGCCGCAACAAAGCAT / GAGAGCGAAGGAGGTTGGAA	TGATGGTGGATCGAGTCTCAAGATATGTAT
kainate-1A	KX016772.1	CAGGTCGGAGTGCAGTAAAGAC / GCCACCAGTCAGGATGTAGAAG	CGATGACCACCCAGACGAGTGC
kainate-1B	KX016773.1	TGAGCAGAACGAGATCGAGTATG / CGCCACATGTTCTGATACGTC	AGGGCGGGTCTACCATGGCCTT
kainate-2A	KX016774.1	CGCATGGAGTCACCTATTGAGA / AGGCGAAAGTGGTGCCAGTTG	TGAGGACCTTGCTAACCAGGACAA
kainate-2B	KX016775.1	GCACGGCAAGTTTGACAAGAAG / TGCTCCCTCTCGTAAGTGATG	AACGGCATGATTGGGCAGCTGTT
kainate-2C	KX016776.1	GGCTTGGTCAGGGAACTCAAG / GCTCTCCCTCGCGTAGTTG	TGATCTAGCGGTGGGTTCTATGACTA
NMDA-1A	KX016782.1	GCCGTCAAATCAGGGAGGTT / ACCGGCGGTTACCAGTTCAC	AGGCGTTCATCTGGGACAGTTCACGT
NMDA-1B	KX016783.1	ACAGCCAAGACGAAGAAGAC / CCGCTGTTCAGGATGACAGA	TGAGTTCATGGCCATCTCGGAGTC
NMDA-2A	KX016785.1	TCGGGTTCGTTCCCTTCAC / TGATGCCGTCCGTGATAGAAG	TGAGACCATCCTTGCCAAGCACC
NMDA-2B	KX016786.1	GCAAGGGTCACCATCAGACA / CGCTGTGAGCATGATGTAGGTA	TGGAGAAACAACTTGAGGCCAATGGA
NMDA-2-like	KX016784.1	GCGTTGGAGCAGTTCATGTC / GCCACATACTGACGGAAGTAC	CACGTTCCTGCTGTTGGGTTGTG
KCNK2	KU681437.1	GACGCCTTCTACTACTGCTTCATC / GAGGGCGTTCTCCTTCTGTAG	CCCTCACTACCATTGGCTTCGGG
KCNK1	KU681438.1	TGGCGAACGACTCAACAAAG / GTCCTGGCACTTAAGGATCTTC	CTCCTCCATCGGCATCAGGCAA
KCNQ1	KU681453.1	GAGCCTCCTTGGGAAACCTATC / CCGCTCCAGGAAGTTGTAGAC	CTCTCGCAGGGACGTCCGCTAC
KCNQ2	KU681452.1	GCTGCCATGTTGATCCAGTG / CCACGTTGCTGTAGAGTTGAAG	TGTGGCGTTGTTATGCTGCAGATAA
KCNH2	KU681459.1	CACCGCGAGATCCTTTCAC / CCTGATGTGGAGGCTGAGTAG	CATCTTCGAGACAGCGTCGCAGG
KCNH3	KU681460.1	GAGGCGACGTACTTACCTCTATG / AGTGGCGTACATGCAAGGATTC	ACTTCATCTCAAGAGGCTCGCTAGA
KCNH1	KU681458.1	GGTCACGTCACCACCATCATC / CCGCACGTTGTTGAGCATTTC	ATGACCTCCGCCACCGCCAAGT
KCNT1	KU681454.1	CGTCCAGACCATGTTCAAGTTC / AAGCGCATGTTGGACGACTG	TCCCCAACATCAAAATCATCACGGA
CCAPr	KM349850.1	GCCCTTCTCCTCTCCAAATCAC / GTCGGTGAGAACGCTGATGAG	CCAGGACCAACTTCTTCATCATGCATCT
vGluT	MK958905	GCGTTCGTGGACCTTCTAC / TCAGCCACCCTGTAATGGAA	ATCACAGCCAACCTACTTCAGCGAG
ChAT	MK958903	GGACCGCCTGGCTAAGTAC / TCGCGGAGTCCCATAAGG	AGGCGGCGCTCAAGCTTCAGAC
vAChT	MK958904	GCGTCAGCTGCTTCTTCCT / CAGCAGTGCCGTGTCTATGAG	TTCGCCAGCAACTACTGGGTGTT
ACHE	MK958902	GGGCAACATGGGCATGTAC / GGTCACCACCGAAGAATTCAATG	AGGCGCTGGCCATCAAGTGGATAC