



ALLEN
BRAIN ATLAS
MOUSE BRAIN

FACIAL MOTOR NUCLEUS (VII)

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Introduction

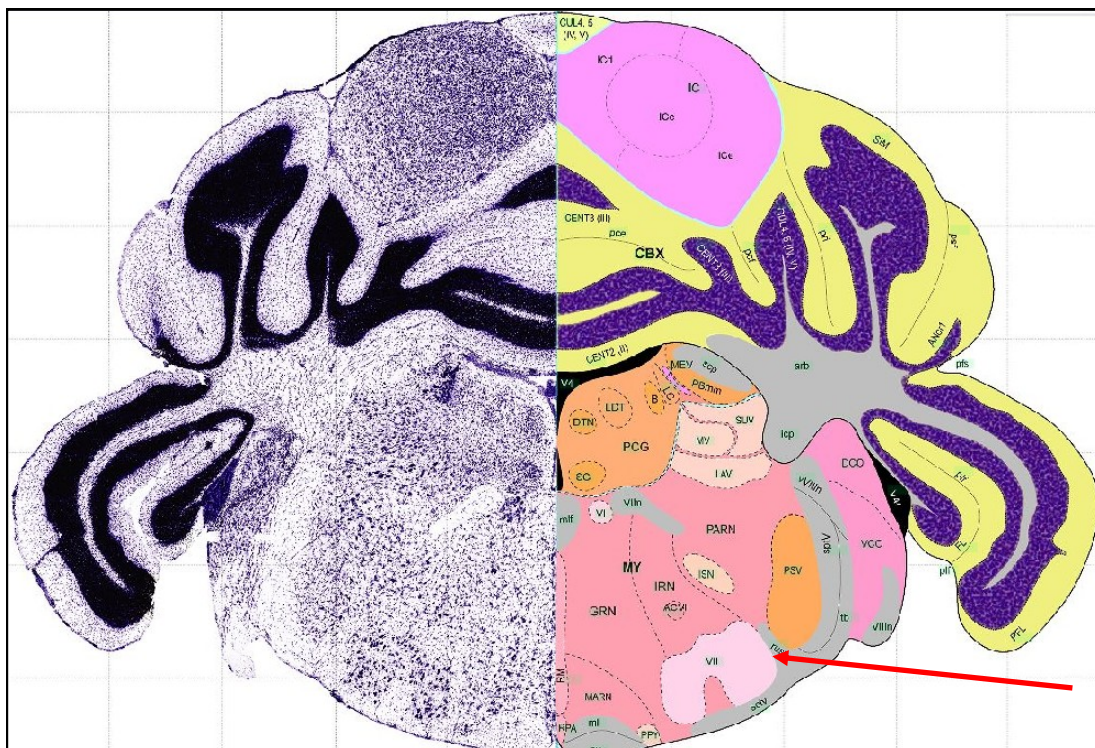
This report contains a summary of expression patterns for genes that are enriched in the facial motor nucleus (VII) of the medulla. All data is derived from the [Allen Brain Atlas \(ABA\)](#) *in situ* hybridization mouse project. The structure's location and morphological characteristics in the mouse brain are described using the Nissl data found in the [Allen Reference Atlas](#). Using an established algorithm, the expression values of the facial motor nucleus were compared to the values of its larger parent structure, in this case the medulla, for the purpose of extracting regionally selective gene expression data. The highest ranking genes were manually curated and verified. 50 genes were then selected and compiled for expression analysis. The experimental data for each gene may be accessed via the links provided; additional data in the sagittal plane may also be accessed using the [ABA](#). Correlations between gene expression in the facial motor nucleus and the rest of the brain, across all genes in the coronal dataset (~4300 genes), were derived computationally. A gene ontology table (derived from DAVID Bioinformatics Resources 2007) is also included, highlighting possible functions of the 50 genes selected for this report.

To read more about how our 50 Select Genes list is derived, please refer to the [Fine Structure Annotation white paper](#).

Allen Reference Atlas Coronal Levels: 107-115

Allen Reference Atlas Sagittal Levels: 11-15

Shown below is a plate from the Allen Reference Atlas, depicting the facial motor nucleus (level [110](#)):



Description of Structure:

LOCATION and STRUCTURAL ANATOMY:

The hierarchical relationship within the brain is depicted below in the structure [legend](#). The Allen Reference Atlas (based on Nissl-stained sections scanned at 10X) was the primary resource for the following descriptions.

For additional information please refer to the [Allen Reference Atlas white paper](#).
[BrainInfo](#) houses a search engine that allows searches for structure name aliases.

The facial motor nucleus is located in the ventral aspect of the caudal pons and rostral medulla and is composed of neurons that innervate facial muscles. In the coronal plane, the nucleus is bordered dorsally and medially by the gigantocellular, intermediate, and parvicellular reticular nuclei. On the lateral and ventral side the facial motor nucleus is bordered by the rubrospinal and spinocerebellar tracts, respectively. At its most rostral aspect, the accessory facial motor nucleus can be seen just dorsal to the main facial motor nucleus. The superior olivary complex borders the nucleus rostrally, while the lateral portion of the paragigantocellular reticular nucleus envelops it caudally, as can be seen in sagittal images. In the coronal plane, the nucleus often appears to be shaped like a horseshoe, making it easily recognizable.

The large motor neurons of VII are not tightly packed but because of their relative size the nucleus is easily distinguishable from surrounding structures in Nissl stained sections. Except at the rostral and caudal poles, obvious subdivisions within the nucleus can be seen; the cells that make up these subdivision do not differ in size or shape but the subdivisions are separated from each other by thin bands of white matter.

The appearance and location of the facial motor nucleus can be appreciated on the following two pages. Nissl-stained sections and Allen Reference Atlas plates reveal the cytoarchitecture and extent of the facial motor nucleus, and its location in relation to surrounding structures.

Alphabetically | By Structure

Allen Brain Atlas: Structural Relationships

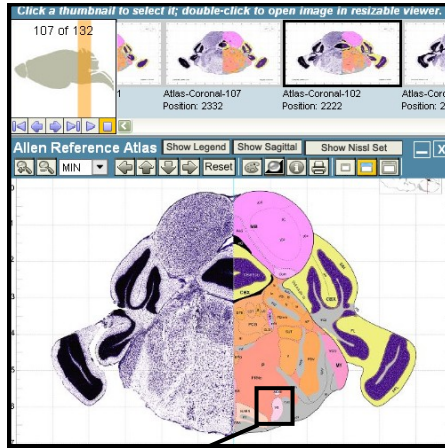
Click on a row to see what structures it contains.

show all | hide all

- Basic Cell Groups and Regions
 - Cerebrum [CH]
 - Cerebellum [CB]
- Brain stem [BS]
 - Interbrain [IB]
 - Midbrain [MB]
 - Hindbrain [HB]
 - Pons [P]
 - Pons, sensory related [P-sen]
 - Pons, motor related [P-mot]
 - Accessory abducens nucleus [ACVI]
 - Accessory facial motor nucleus [ACVII]
 - Barrington's nucleus [B]
 - Dorsal tegmental nucleus [DTN]
 - Lateral tegmental nucleus [LTN]
 - Pontine central gray [PCG]
 - Pontine gray [PG]
 - Pontine reticular nucleus, caudal part [PRNc]
 - Pontine reticular nucleus, ventral part [PRNv]
 - Supragenual nucleus [SG]
 - Superior salivatory nucleus [SSN]
 - Supratrigeminal nucleus [SUT]
 - Tegmental reticular nucleus [TRN]
 - Motor nucleus of trigeminal [V]
 - Abducens nucleus [VI]
 - Facial motor nucleus [VII]**
 - Pons, behavioral state related [P-sat]
 - Medulla [MY]
- fiber tracts
- Grooves
- ventricular systems

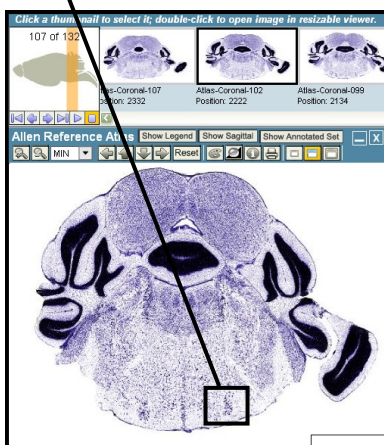
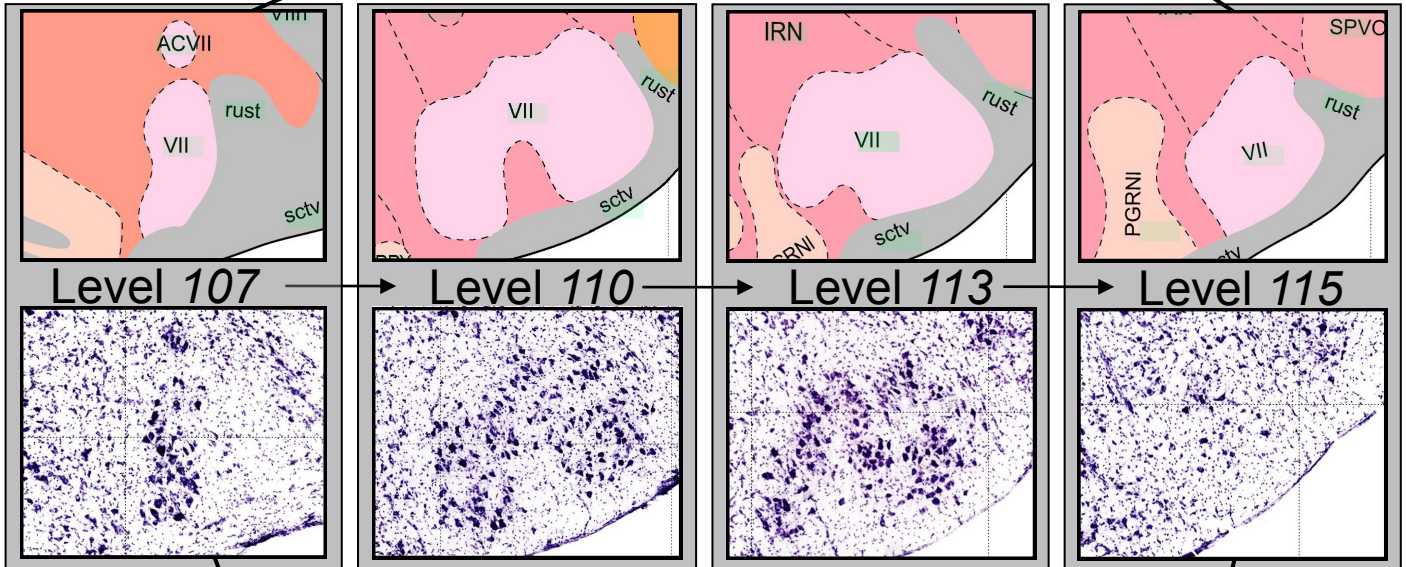
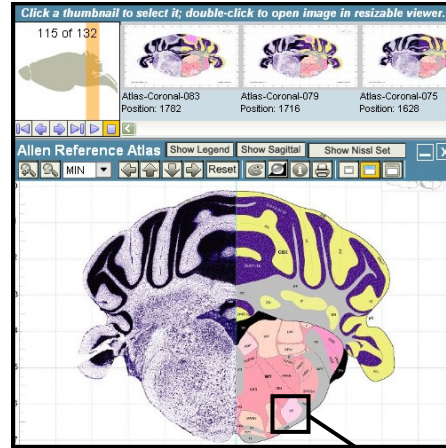
Atlas and Nissl: Coronal:

Rostral

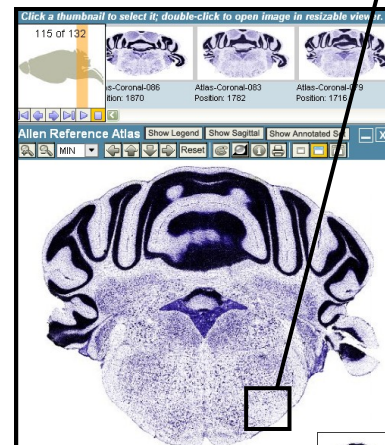


Reference
Atlas

Caudal



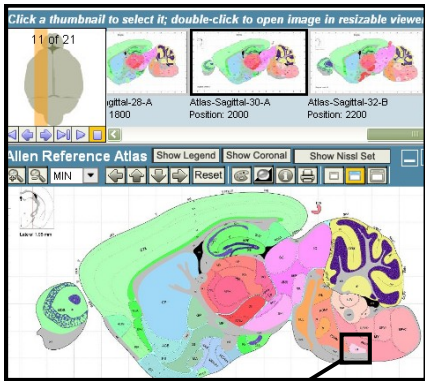
Nissl



Atlas and Nissl:

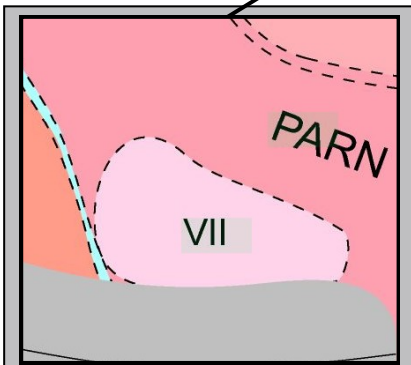
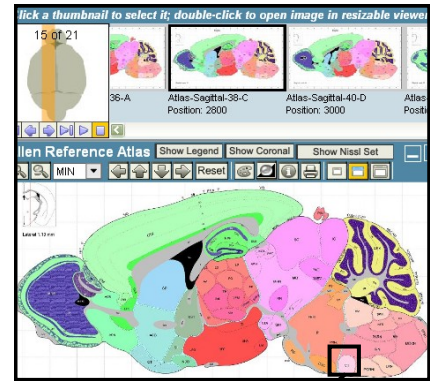
Sagittal:

Lateral

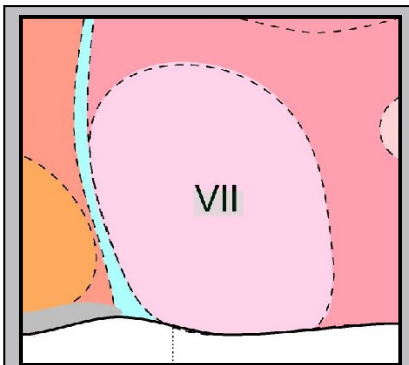


Reference
Atlas

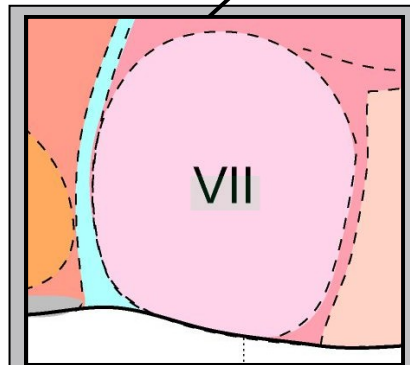
Medial



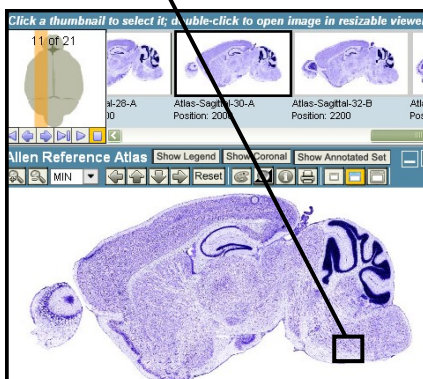
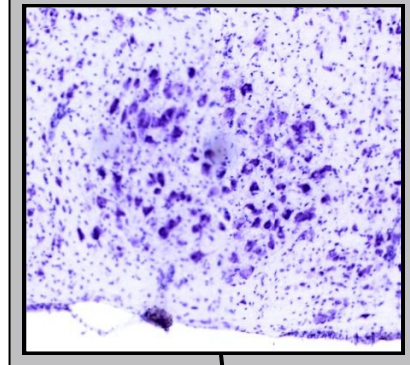
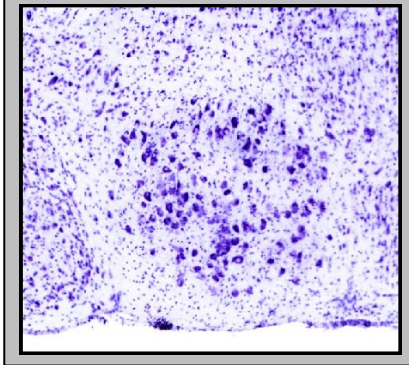
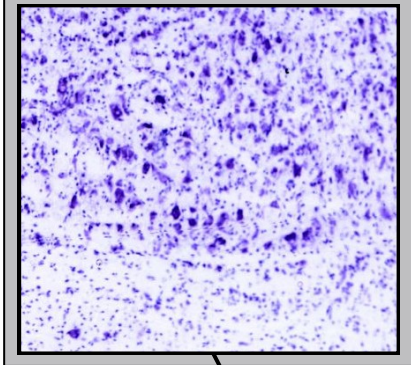
Level 11



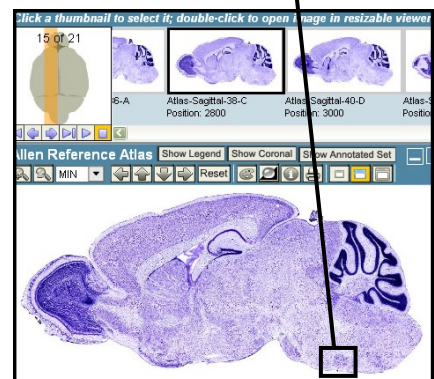
Level 13



Level 15



Nissl



In Situ Hybridization Expression Patterns of 50 Select Genes:

The in situ hybridization (ISH) data below presents the facial motor nucleus' anatomical and cytoarchitectural characteristics in the context of actual gene expression. In addition to presenting molecularly defined borders, ISH gene expression patterns also aid in phenotyping cell populations that otherwise can not be differentiated on purely morphological grounds. The 50 genes in this section were selected based on a mathematical algorithm to identify gene expression patterns that allow selective identification of the facial motor nucleus. The gene expression patterns were then verified manually. As such, these genes do not represent the only genes found in this structure, genes specific to this structure, or genes expressing at the highest level within this structure.

Please refer to our protocol in the [Data Production Processes white paper](#).

To read about heat map conversion, refer to the [Informatics Data Processing white paper](#).

The expression data presented can be further explored, in coronal and sagittal planes, at brain-map.org.

The 50 Select Genes examined here are universally expressed throughout the facial motor nucleus. Although the subdivisions within this nucleus are visible in the ISH labeled tissue, all of the genes examined are expressed in all subdivisions. Within these select genes, expression intensity ranges from medium (*Hspb1*, *Trim16*) to very high (*Kcnbm4*, *Slc5a7*), and expression density ranged from medium (*Pde8b*, *Calca*), to high (*Anxa2*, *Trim16*).

Cellular density expression key		Cellular intensity expression key	
None	No expression	No color	Very low intensity
Sparse	Very few cells expressing	Blue	Low intensity
Scattered	Less than 10% of cells expressing in scattered pattern	Green	Medium intensity
Medium	10-80% of cells expressing	Yellow	High intensity
High	Greater than 80% of cells expressing	Red	Very high intensity

To view heat map at brain-map.org, right click on the ISH image and select "Show Expression Analysis."

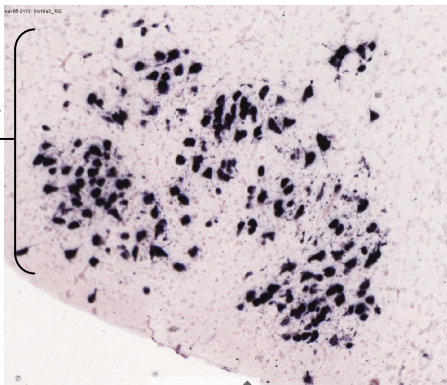
ISH DATA The images below were selected to highlight the expression pattern of the facial motor nucleus.

ISH

[Slc18a3](#)

Coronal: *Slc18a3* expresses with high density and very high intensity across the entire nucleus.

Facial motor nucleus

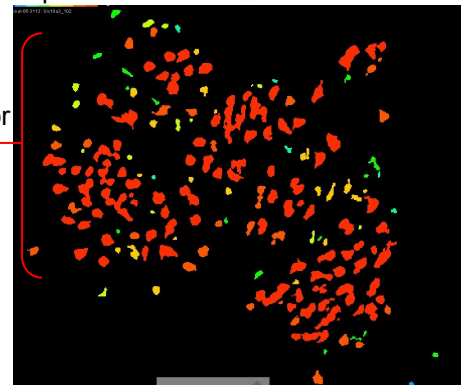


Heat map

[Slc18a3](#)

Coronal: The heat map makes apparent the very high intensity of *Slc18a3* expression.

Facial motor nucleus

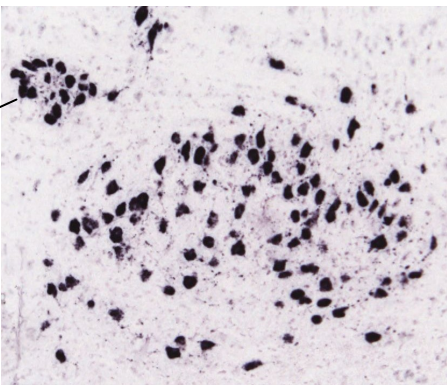


ISH

[Slc18a3](#)

Sagittal:

Accessory facial motor nucleus

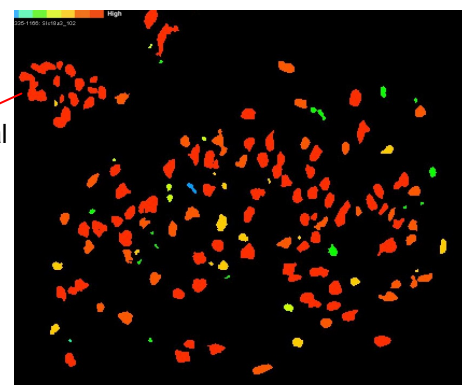


Heat map

[Slc18a3](#)

Sagittal:

Accessory facial motor nucleus



50 SELECT GENES:

This gene list was generated by manual curation of an [algorithmically](#) derived list that compared gene expression values of the facial motor nucleus to those of the medulla. Categories of expression are subjectively grouped by relative expression characteristics.

Curation of 50 Select Genes List: May 2008

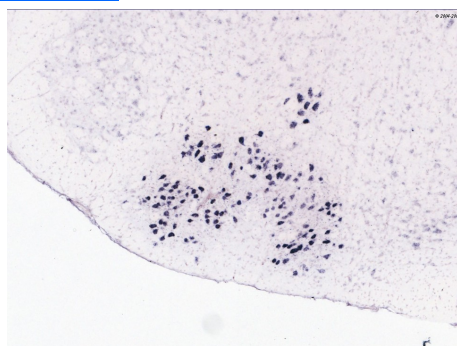
General Expression Pattern

Number	Gene Symbol	Gene Name	Expression Pattern
1	Kcnmb4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	High density and very high intensity
2	Ngef	neuronal guanine nucleotide exchange factor	High density and very high intensity
3	Kcnj14	potassium inwardly-rectifying channel, subfamily J, member 14	High density and very high intensity
4	Slc10a4	solute carrier family 10 (sodium/bile acid cotransporter family), member 4	High density and very high intensity
5	Lxn	latexin	High density and very high intensity
6	Anxa2	annexin A2	High density and very high intensity
7	Itpr3	inositol 1,4,5-triphosphate receptor 3	High density and intensity
8	Slc41a3	solute carrier family 41, member 3	High density and intensity
9	Daf2	decay accelerating factor 2	Medium density and high intensity
10	Slc18a3	solute carrier family 18 (vesicular monoamine), member 3	High density and very high intensity
11	Wfs1	Wolfram syndrome 1 homolog (human)	Medium density and very high intensity
12	Hspb1	heat shock protein 1	Medium density and intensity
13	Cyb5r1	cytochrome b5 reductase 1	High density and medium intensity
14	Slc5a7	solute carrier family 5 (choline transporter), member 7	High density and very high intensity
15	Prss12	protease, serine, 12 neurotrypsin (motopsin)	High density and very high intensity
16	Stk32a	serine/threonine kinase 32A	High density and very high intensity
17	A830018L16Rik	RIKEN cDNA A830018L16 gene	High density and intensity
18	Serpina3c	serine (or cysteine) peptidase inhibitor, clade A, member 3C	Medium density and high intensity
19	Dpysl3	dihydropyrimidinase-like 3	High density and intensity
20	Rps6ka3	ribosomal protein S6 kinase polypeptide 3	Medium density and intensity
21	1700010C24Rik	RIKEN cDNA 1700010C24 gene	High density and very high intensity
22	Plcb1	phospholipase C, beta 1	High density and intensity
23	Pde8b	phosphodiesterase 8B	Medium density and high intensity
24	Pacrg	Park2 co-regulated	High density and intensity
25	Serpina3k	serine (or cysteine) peptidase inhibitor, clade A, member 3K	Medium density and high intensity
26	2610019F03Rik	RIKEN cDNA 2610019F03 gene	High density and intensity
27	Trim16	tripartite motif protein 16	High density and medium intensity
28	Anxa4	annexin A4	Medium density and high intensity
29	Ankrd6	ankyrin repeat domain 6	High density and intensity
30	Sec14l1	SEC14-like 1 (<i>S. cerevisiae</i>)	High density and medium intensity
31	Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	Medium density and high intensity
32	Utn	utrophin	Medium density and high intensity
33	Isoc1	isochorismatase domain containing 1	High density and very high intensity
34	Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	High density and very high intensity
35	Cd59a	CD59a antigen	High density and intensity
36	Lgals1	lectin, galactose binding, soluble 1	High density and very high intensity
37	Cast	calpastatin	High density and intensity
38	S100a10	S100 calcium binding protein A10 (calpactin)	High density and very high intensity
39	Slitrk4	SLIT and NTRK-like family, member 4	High density and medium intensity

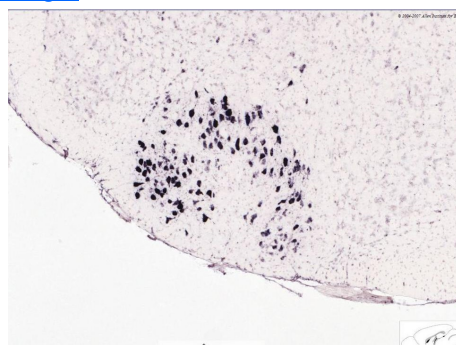
General Expression Pattern

Number	Gene Symbol	Gene Name	Expression Pattern
40	Calca	calcitonin/calcitonin-related polypeptide, alpha	Medium density and very high intensity
41	Slc35f3	solute carrier family 35, member F3	High density and medium intensity
42	Man2b1	mannosidase 2, alpha B1	Medium density and high intensity
43	A330043P19Rik*	RIKEN cDNA A330043P19 gene (non-RefSeq)	High density and very high intensity
44	Gem	GTP binding protein (gene overexpressed in skeletal muscle)	High density and intensity
45	A230083H22Rik	RIKEN cDNA A230083H22 gene	High density and very high intensity
46	Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	Medium density and high intensity
47	Ecel1	endothelin converting enzyme-like 1	High density and very high intensity
48	Tmem63c	transmembrane protein 63c	Medium density and high intensity
49	Susd2	sushi domain containing 2	High density and very high intensity
50	Sncg	synuclein, gamma	High density and very high intensity

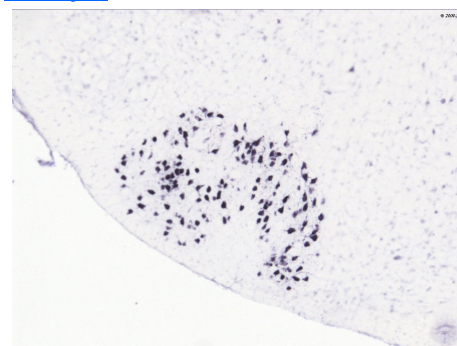
1. [Kcnmb4](#)



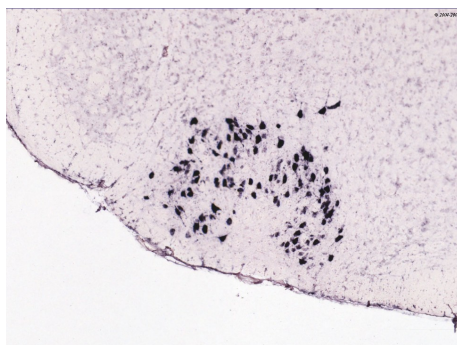
2. [Ngef](#)



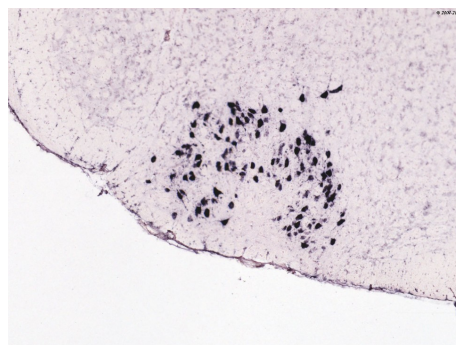
3. [Kcnj14](#)



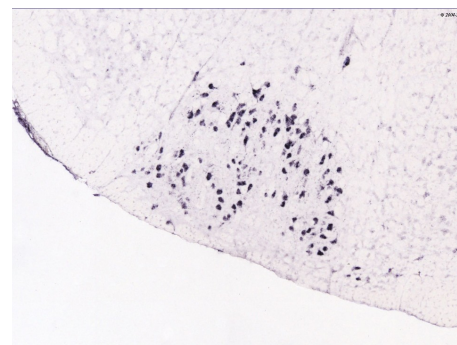
4. [Slc10a4](#)



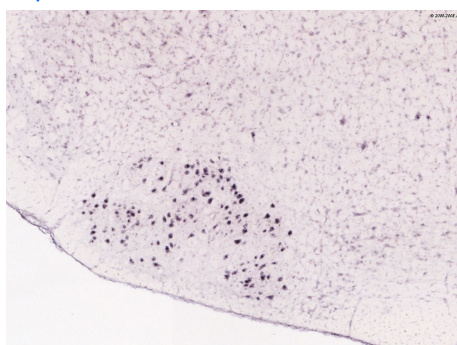
5. [Lxn](#)



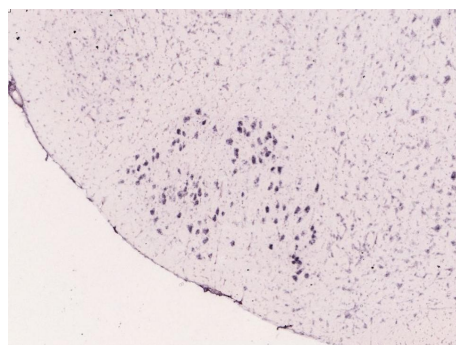
6. [Anxa2](#)



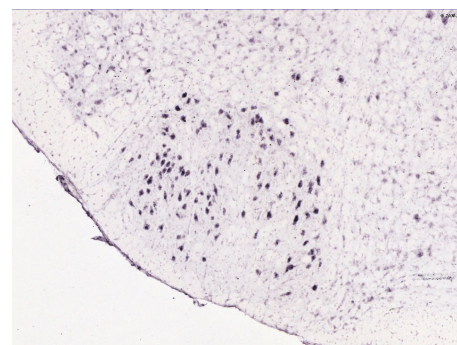
7. [Itpr3](#)



8. [Slc41a3](#)

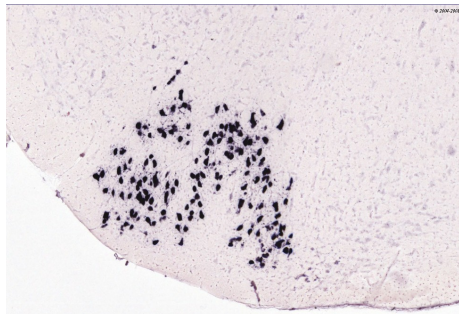


9. [Daf2](#)

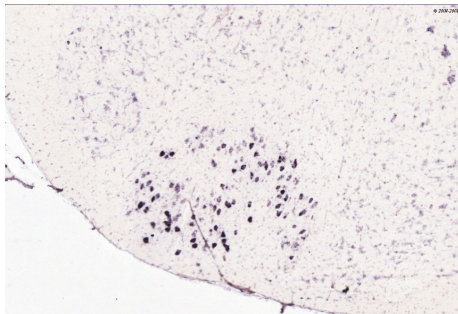


General Expression Pattern

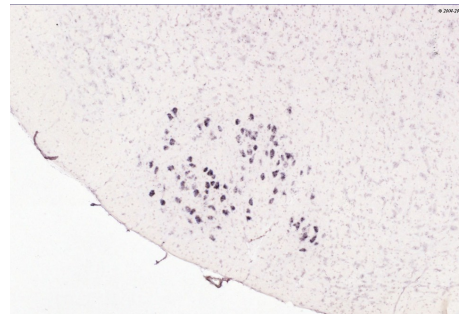
[10.Slc18a3](#)



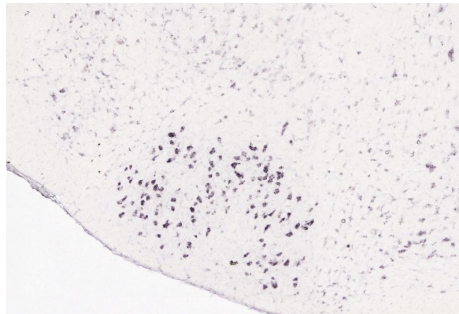
[11.Wfs1](#)



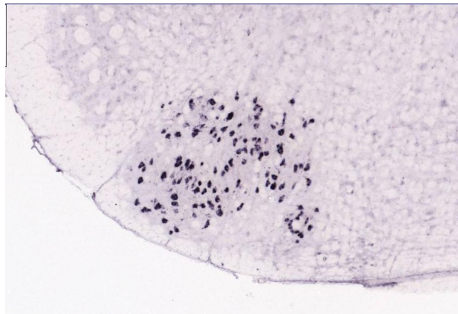
[12.Hspb1](#)



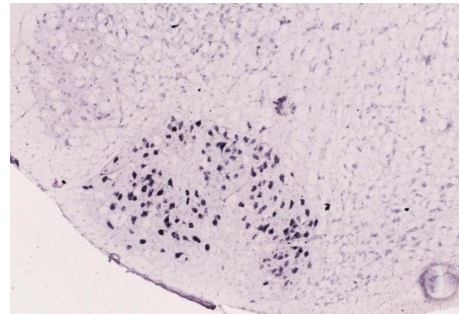
[13.Cyb5r1](#)



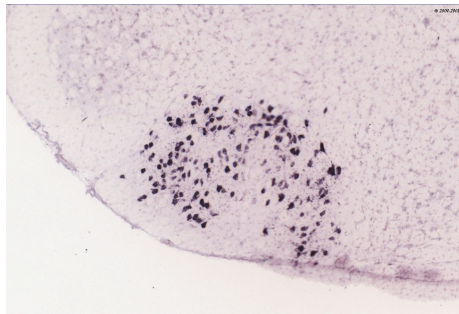
[14.Slc5a7](#)



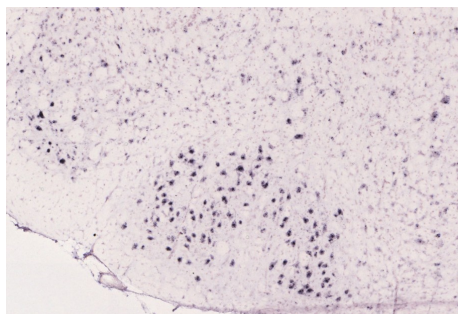
[15.Prss12](#)



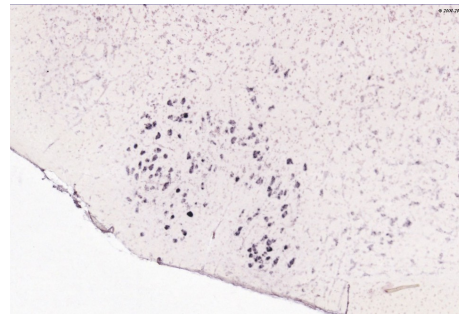
[16.Stk32a](#)



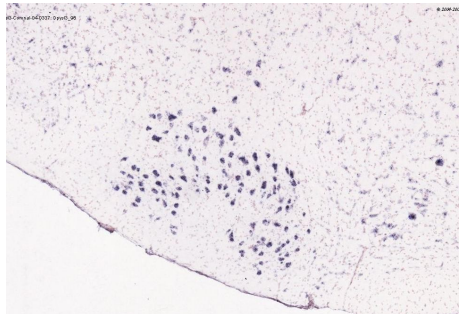
[17.A830018L16Rik](#)



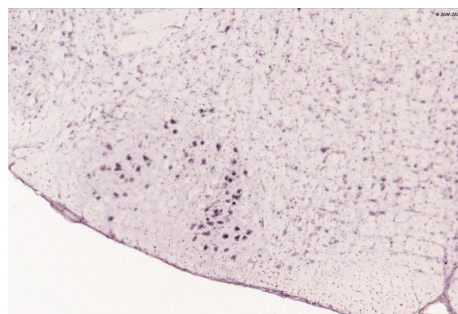
[18.Serpina3c](#)



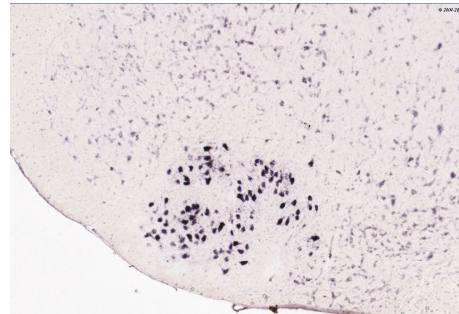
[19.Dpysl3](#)



[20.Rps6ka3](#)

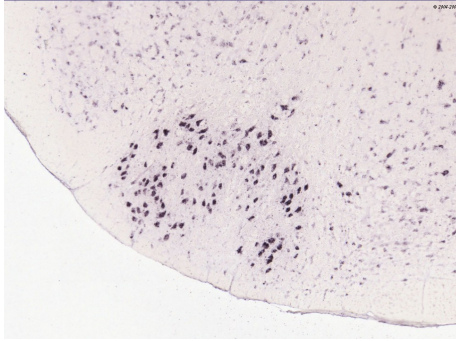


[21.1700010C24Rik](#)

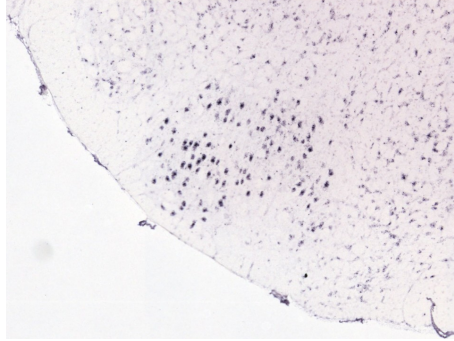


General Expression Pattern

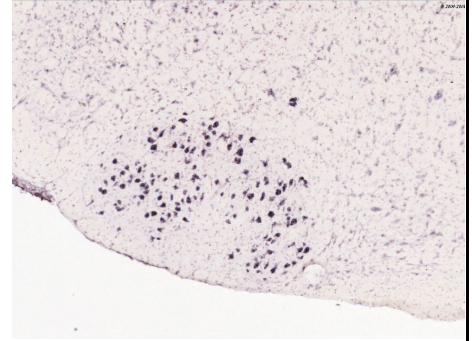
[22.Plcb1](#)



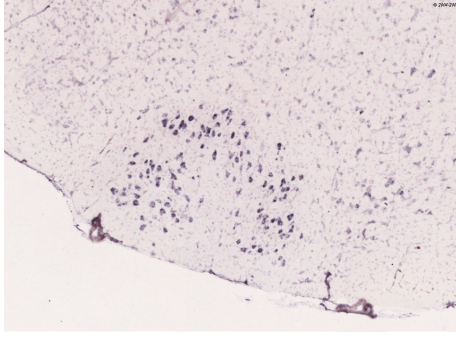
[23.Pde8b](#)



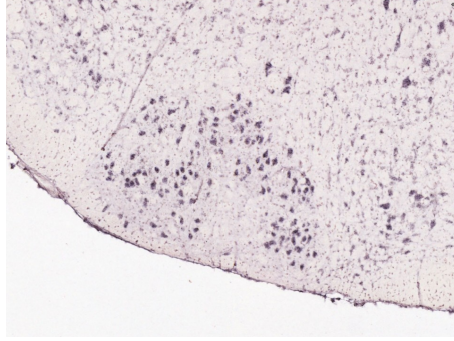
[24.Pacrg](#)



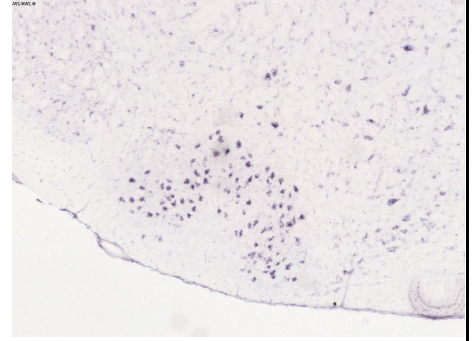
[25.Serpina3k](#)



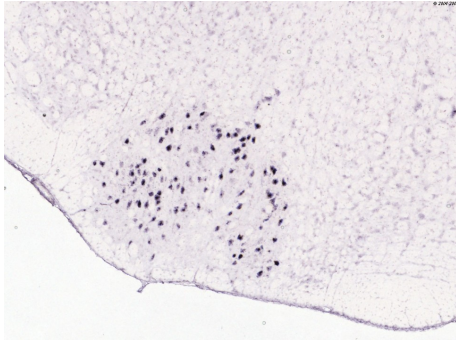
[26.2610019F03Rik](#)



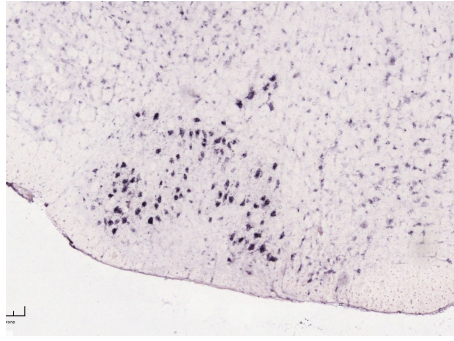
[27.Trim16](#)



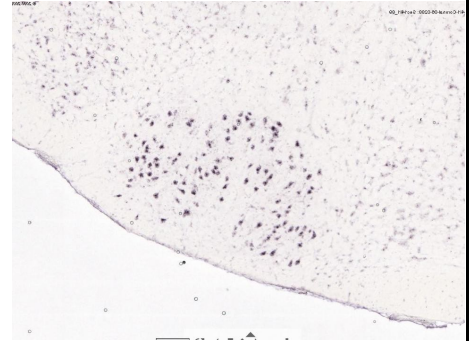
[28.Anxa4](#)



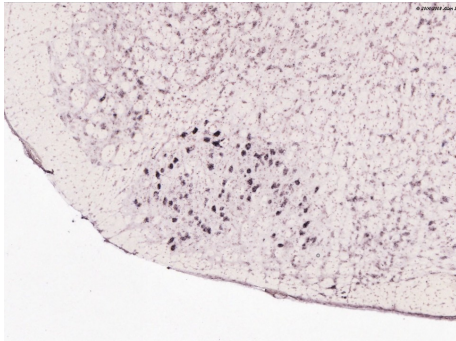
[29.Ankrd6](#)



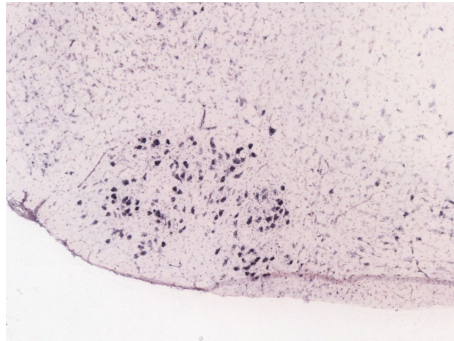
[30.Sec14l1](#)



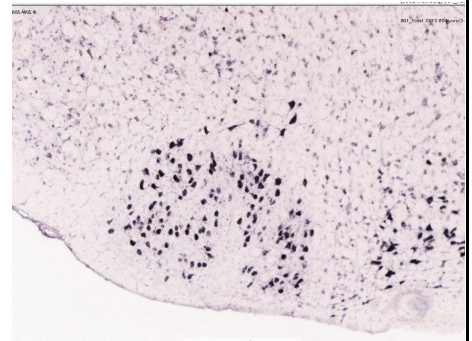
[31.Pip5k1a](#)



[32.Utn](#)

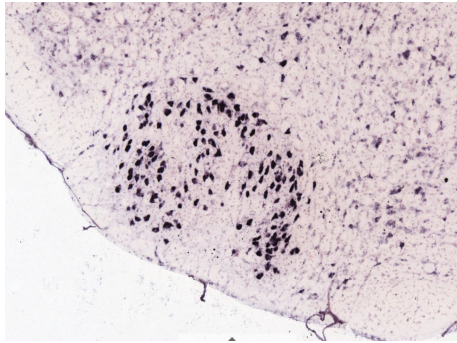


[33.Isoc1](#)

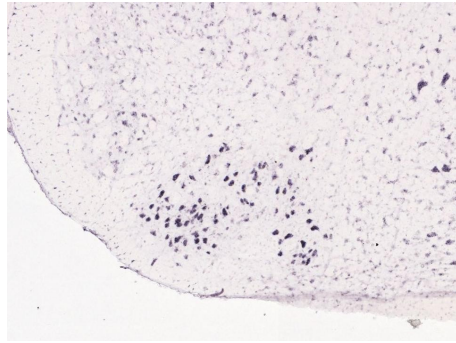


General Expression Pattern

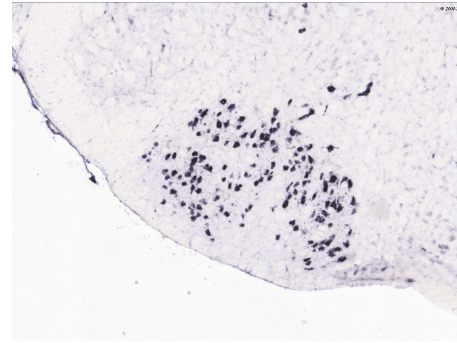
[34.Gfra1](#)



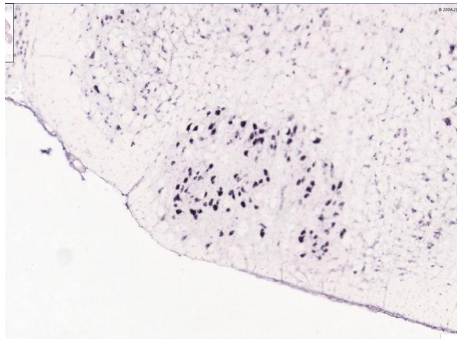
[35.Cd59a](#)



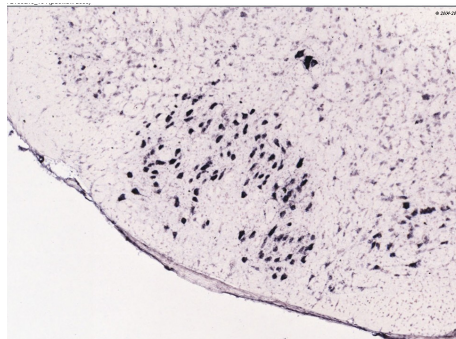
[36.Lgals1](#)



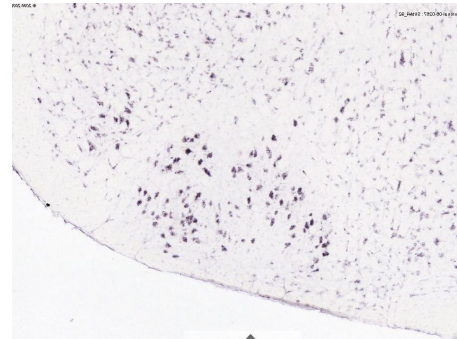
[37.Cast](#)



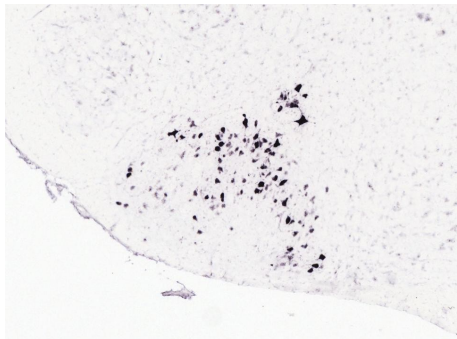
[38.S100a10](#)



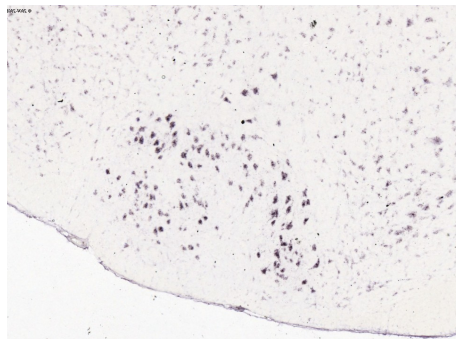
[39.Slitrk4](#)



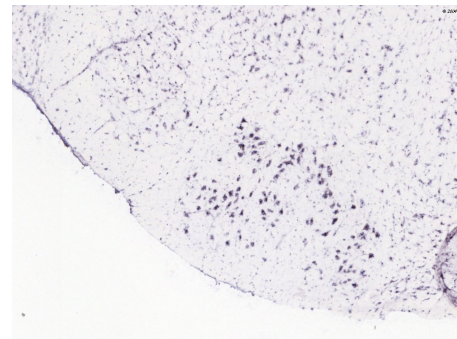
[40.Calca](#)



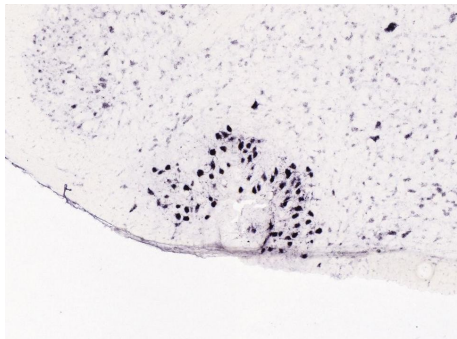
[41.Slc35f3](#)



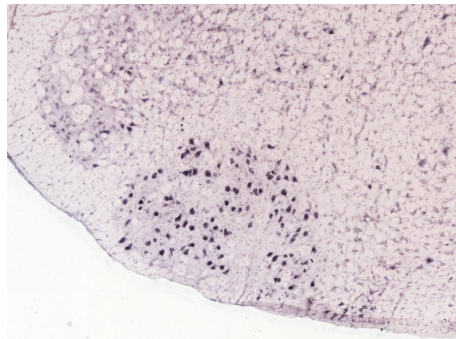
[42.Man2b1](#)



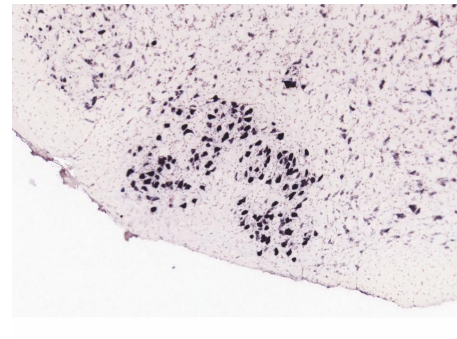
[43.A330043P19Rik*](#)



[44.Gem](#)

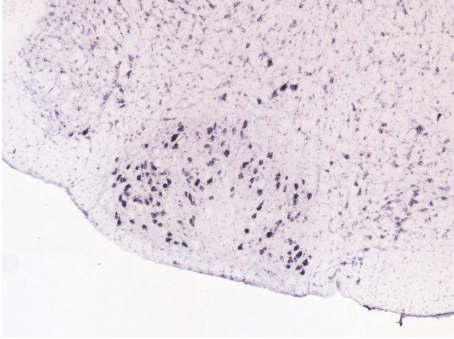


[45.A230083H22Rik](#)

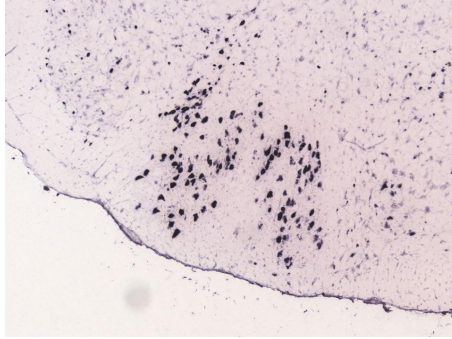


General Expression Pattern

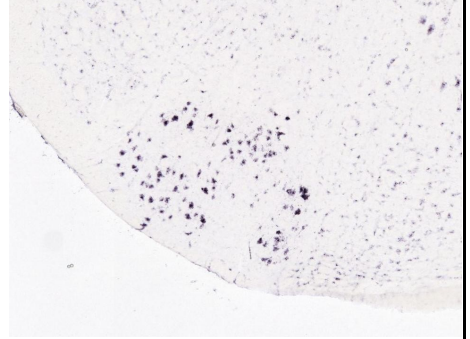
[46.Dnaja4](#)



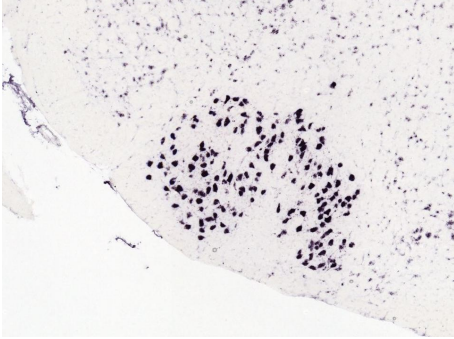
[47.Ecel1](#)



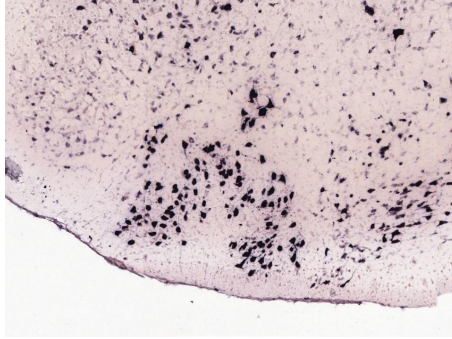
[48.Tmem63c](#)



[49.Susd2](#)



[50.Sncg](#)



Correlated Expression:

The ABA coronal set contains many genes of known scientific interest as well as genes exhibiting combinatorial or unique expression patterns. A correlation analysis of all available ABA coronal experiments (4376) was performed by comparing the expression value of the facial motor nucleus to expression values in other regions of the brain. Following [image analysis](#), the data values for each experiment were mapped to a 3-D reference brain at $(200\mu\text{m})^3$ voxel resolution. Then, each voxel was assigned a single expression value based on the product of density and intensity of expression. Values from all 4376 experiments were computed, and the likelihood of co-expression between any two voxels or regions are reported as a Pearson's correlation coefficient.

For the purposes of determining correlated expression between the facial motor nucleus and other brain regions, expression values from all voxels within the facial motor nucleus were aggregated to form a single expression value. Two types of comparisons were then made. First, the aggregate expression values of the facial motor nucleus and those of other anatomically defined regions (~200 structures) were compared within the 3-D reference brain (structure vs. structure; table below). Second, a color map was then generated to display the correlation between the facial motor nucleus and each of the ~53,000 voxels of the reference volume (structure vs. voxel; correlation map on the following page).

STRUCTURE vs. STRUCTURE

The expression value of the facial motor nucleus was compared to expression values for all other defined atlas regions. Degree of correlation is displayed as a comparative fraction, with self-correlation = 1.000. Correlation between the facial motor nucleus and macro/parent-structures are presented, as well as correlation between the facial motor nucleus and the 25 highest ranking substructures. The most highly correlated macro/parent-structures don't always contain the 25 top most correlated substructures. Columns match the Allen Reference Atlas palette.

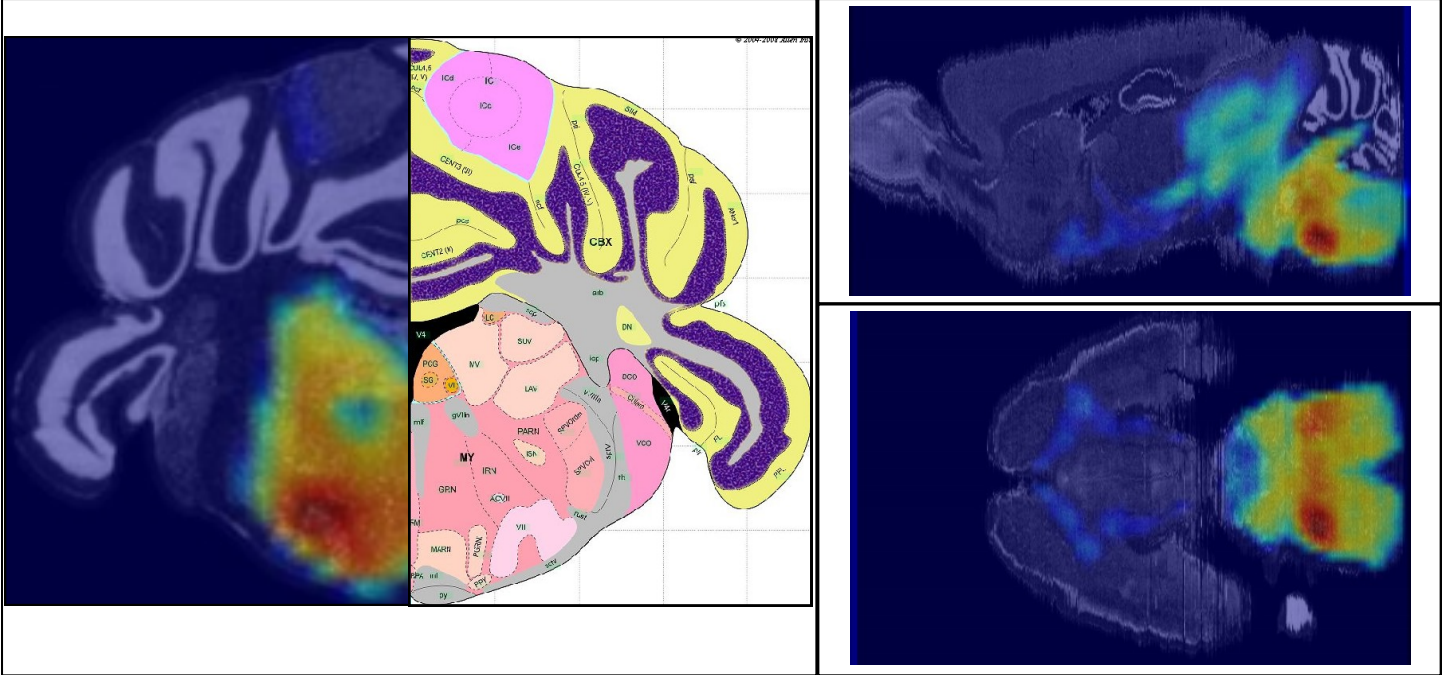
Correlation of VII with macrostructures:

Macrostructure	Correlation
OLF (Olfactory areas)	0.775551
STR (Striatum)	0.720319
PAL (Pallidum)	0.87027
CTX (Cerebral cortex)	0.776963
HY (Hypothalamus)	0.843854
TH (Thalamus)	0.83522
HIP (Hippocampal region)	0.735425
RHP (Retrohippocampal formation)	0.789345
MB (Midbrain)	0.809695
P (Pons)	0.944025
MY (Medulla)	0.953337
CB (Cerebellum)	0.703163

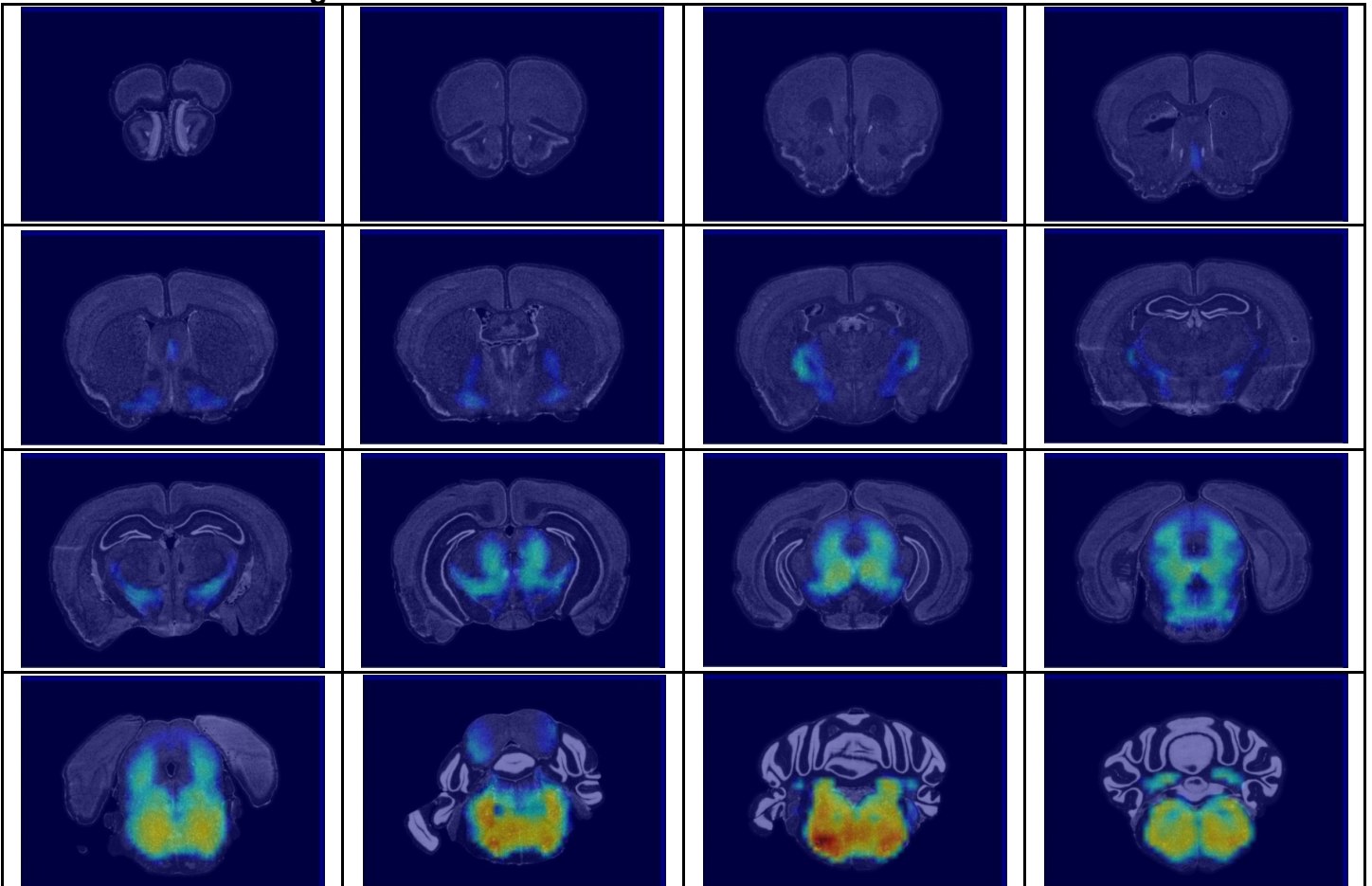
Substructure	Correlation
Facial motor nucleus (VII)	1
Paragigantocellular reticular nucleus (PGRN)	0.956396
Motor nucleus of trigeminal (V)	0.953486
Magnocellular reticular nucleus (MARN)	0.950127
Spinal nucleus of the trigeminal, oral part (SPVO)	0.946556
Lateral vestibular nucleus (LAV)	0.945507
Inferior salivatory nucleus (ISN)	0.94541
Nucleus ambiguus (AMB)	0.942359
Nucleus raphe magnus (RM)	0.938412
Parapyramidal nucleus (PPY)	0.938166
Vestibular nuclei (VNC)	0.937087
Nucleus x (x)	0.936387
Spinal nucleus of the trigeminal, interpolar part (SPVI)	0.929712
Principal sensory nucleus of the trigeminal (PSV)	0.928171
Abducens nucleus (VI)	0.92664
Supratrigeminal nucleus (SUT)	0.924772
Superior olivary complex (SOC)	0.92476
Lateral reticular nucleus (LRN)	0.923036
Hypoglossal nucleus (XII)	0.921764
Medial vestibular nucleus (MV)	0.920406
Red Nucleus (RN)	0.918499
Linear nucleus of the medulla (LIN)	0.914526
Interposed nucleus (IP)	0.909372
Nucleus of the lateral lemniscus (NLL)	0.908286
Subceruleus nucleus (SLC)	0.90695

STRUCTURE vs. VOXEL:

Correlation between the facial motor nucleus and all other $(200\mu\text{m})^3$ voxels in the brain. Degree of correlation assessed for each voxel is provided visually (lower value = the correlation value of the 25th ranked substructure reported on the previous page) using the "jet" color scale at rostrocaudal levels throughout the brain.



Coronal series through brain:



Gene Ontology (GO) Analysis:

GO TABLE:

Below is an ontological analysis of the 50 Select Genes, using [DAVID](#) Bioinformatics Resources. The functional terms that follow were returned using these constraints:

Category	Definition	Constraints
P-value	Probability that the term is over-represented in this 50 Select Genes list relative to the mouse genome	when $p \leq 0.05$
Gene Count	The minimum number of genes that must fall into an ontological category to be considered a group	5 genes per term group
GO Level	The level of functional specificity for GO functional categories: Molecular Function (mf), Biological Process (bp) and Cellular Components (cc)	Level GO_All
# of DAVID IDs	Number of unique DAVID gene IDs from user's input list	49 of DAVID gene IDs/ 50 input genes

Date of table completion: May 2008

GO Category	GO Term	Gene Count	% of Genes	p-value
GOTERM_MF_ALL	enzyme inhibitor activity	6	12.24%	2.89E-04
GOTERM_MF_ALL	endopeptidase inhibitor activity	5	10.20%	7.57E-04
GOTERM_MF_ALL	protease inhibitor activity	5	10.20%	8.07E-04
GOTERM_MF_ALL	enzyme regulator activity	7	14.29%	0.007086
GOTERM_MF_ALL	cation transmembrane transporter activity	6	12.24%	0.007839
GOTERM_BP_ALL	cation transport	6	12.24%	0.00895
GOTERM_CC_ALL	membrane	26	53.06%	0.012862
GOTERM_CC_ALL	cell projection	5	10.20%	0.013206
GOTERM_BP_ALL	metal ion transport	5	10.20%	0.020303
GOTERM_MF_ALL	transmembrane transporter activity	7	14.29%	0.022028
GOTERM_MF_ALL	ion transmembrane transporter activity	6	12.24%	0.024084
GOTERM_BP_ALL	response to external stimulus	5	10.20%	0.030318
GOTERM_BP_ALL	ion transport	6	12.24%	0.038123
GOTERM_MF_ALL	transporter activity	8	16.33%	0.041046
GOTERM_MF_ALL	substrate-specific transmembrane transporter activity	6	12.24%	0.041322

Glynn Dennis Jr., Brad T. Sherman, Douglas A. Hosack, Jun Yang, Michael W. Baseler, H. Clifford Lane, Richard A. Lempicki. "DAVID: Database for Annotation, Visualization, and Integrated Discovery." *Genome Biology*. 2003 4(5): P3.

FACIAL MOTOR NUCLEUS Summary:

Anatomy

- The facial motor nucleus is located ventrally at the junction of the pons and the medulla and is surrounded by various reticular nuclei as well as the rubrospinal and spinocerebellar tracts.
- In the coronal view, the cells are arranged in such a way that subdivisions within the nucleus can be seen; however, the motor neurons that comprise the subdivisions are of the same size and shape.
- The size of the motor neurons relative to the surrounding tissue as well as its distinct horseshoe shape in the coronal plane, make it easy to distinguish from surrounding structures.

Expression Patterns of the 50 Select Genes

- The 50 genes examined in this report labeled all subdivisions of the motor nucleus of the facial nerve.
- The intensity of labeling, and the density of the labeled cells ranged from moderate to very high, but these differences did not target a specific subdivision of the nucleus.

Correlation

- The facial motor nucleus was found to be highly correlated with various motor related nuclei of the medulla, pons and is also correlated with the interposed nucleus of the cerebellum.
- Correlation of gene expression in the facial motor nucleus with individual voxels throughout the mouse brain revealed correlation with the globus pallidus and zona incerta, portions of the thalamus (reticular nucleus and ventral posterior complex), and additional areas of the midbrain not noted in the structure to structure analysis, including regions within the superior colliculus.

We encourage you to reply with any comments or questions by email to [!Annotation@alleninstitute.org](mailto:Annotation@alleninstitute.org). To further explore the gene expression data and analytical tools referred to in this report, please access our genome-wide data set at brain-map.org.

Other Tools:

NEUROBLAST:

Many of the 50 genes listed in this report can be used to explore the NeuroBlast tool. This unique mining tool works seamlessly from within brain-map.org to produce a list of genes that share similar expression patterns to any gene in the coronal data set. Search for and select any gene, then select one of several brain regions from the NeuroBlast drop-tab to explore a ranked list of similarly expressed genes for that region.

To learn more about this function, please refer to the [NeuroBlast white paper](#).

BRAIN EXPLORER:

To compare gene expression levels across anatomical structures in 3-D detail, download the [Brain Explorer](#) desktop application. This program is used to view gene expression in 3-D view (coronal, sagittal, horizontal and everywhere in between) across all brain structures and allows for simultaneous viewing of multiple expression profiles.

The NeuroBlast spatial homology function and an anatomic search tool are also available from within Brain Explorer to allow the user to search for and visualize genes with similar expression patterns.