ALLEN INSTITUTE *for* BRAIN SCIENCE
*Fueling Discovery*

**ANNOTATION REPORT**

ALLEN BRAIN ATLAS
MOUSE BRAIN

# MOTOR NUCLEUS OF THE TRIGEMINAL NERVE (V)

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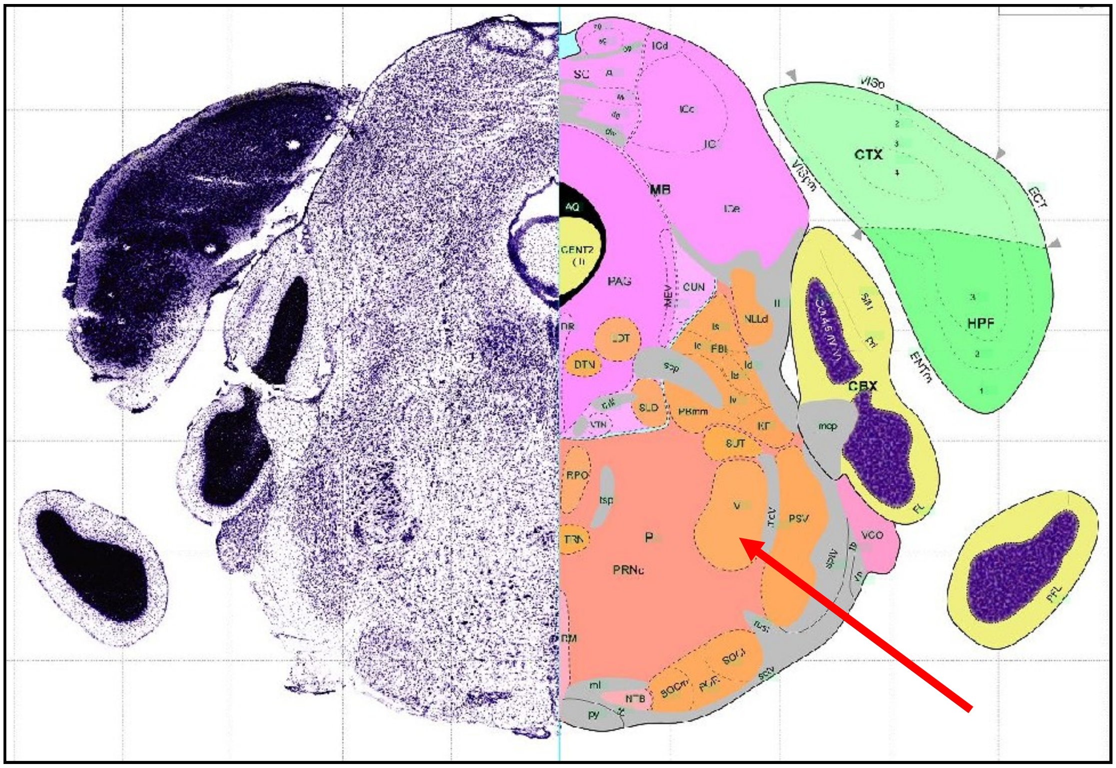
## Introduction

*This report contains a summary of expression patterns for genes that are enriched in the motor nucleus of the trigeminal nerve (V) of the pons. 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 motor nucleus of the trigeminal nerve were compared to the values of its larger parent structure, in this case the pons, 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 motor nucleus of the trigeminal nerve 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: 101-108
Allen Reference Atlas Sagittal Levels: 11-14
Shown below is a plate from the Allen Reference Atlas, depicting the motor nucleus of trigeminal ([level 104](#)):



# *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.*

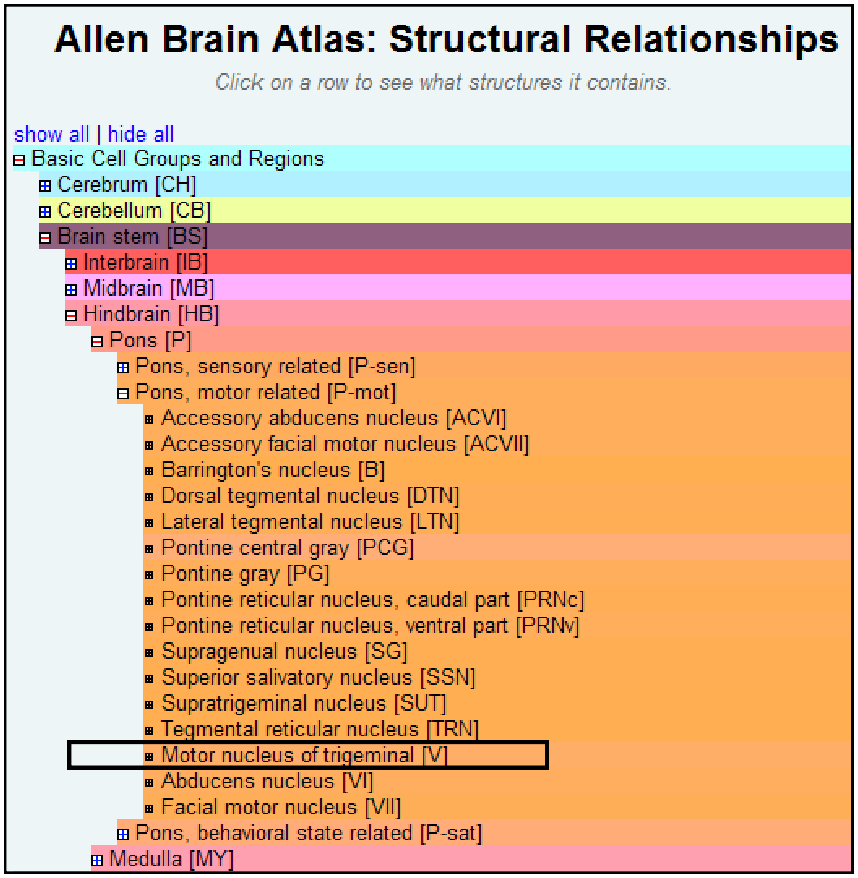
*For additional information please refer to the Allen Reference Atlas white paper.*
*BrainInfo houses a search engine that allows searches for structure name aliases.*

The motor nucleus of the trigeminal nerve (V) is located in the lateral region of the pons, within the lateral aspect of the pontine reticular nucleus (PRN). In the coronal plane, it first emerges at the level at which the trigeminal nerve root exits the pons, and terminates caudally at the border between the pons and the medulla. Laterally, the nucleus is bordered by the motor root of the trigeminal nerve (moV), which separates the motor nucleus from the principal sensory nucleus of the trigeminal nerve (PSV). It is bordered ventrocaudally by the facial motor nerve (VIIn), and dorsally by the supratrigeminal nucleus (SUT).

In the sagittal plane, at medial aspects of the motor nucleus, V sits within the posterior aspect of the PRN, ventral to the SUT. The facial nerve is positioned caudal to the motor nucleus, providing orientation as to the placement of V. At more lateral aspects, prior to the emergence of the SUT, it is located in the rostral portion of the PRN.

The neurons within the motor nucleus are larger than the neurons in the neighboring PSV and PRN. They are more densely packed than the large neurons of the PRN, making it easy to distinguish between these two structures. The motor nucleus of the trigeminal nerve is easily identified in both the coronal and sagittal Nissl-stained sections.

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



**Allen Brain Atlas: Structural Relationships**

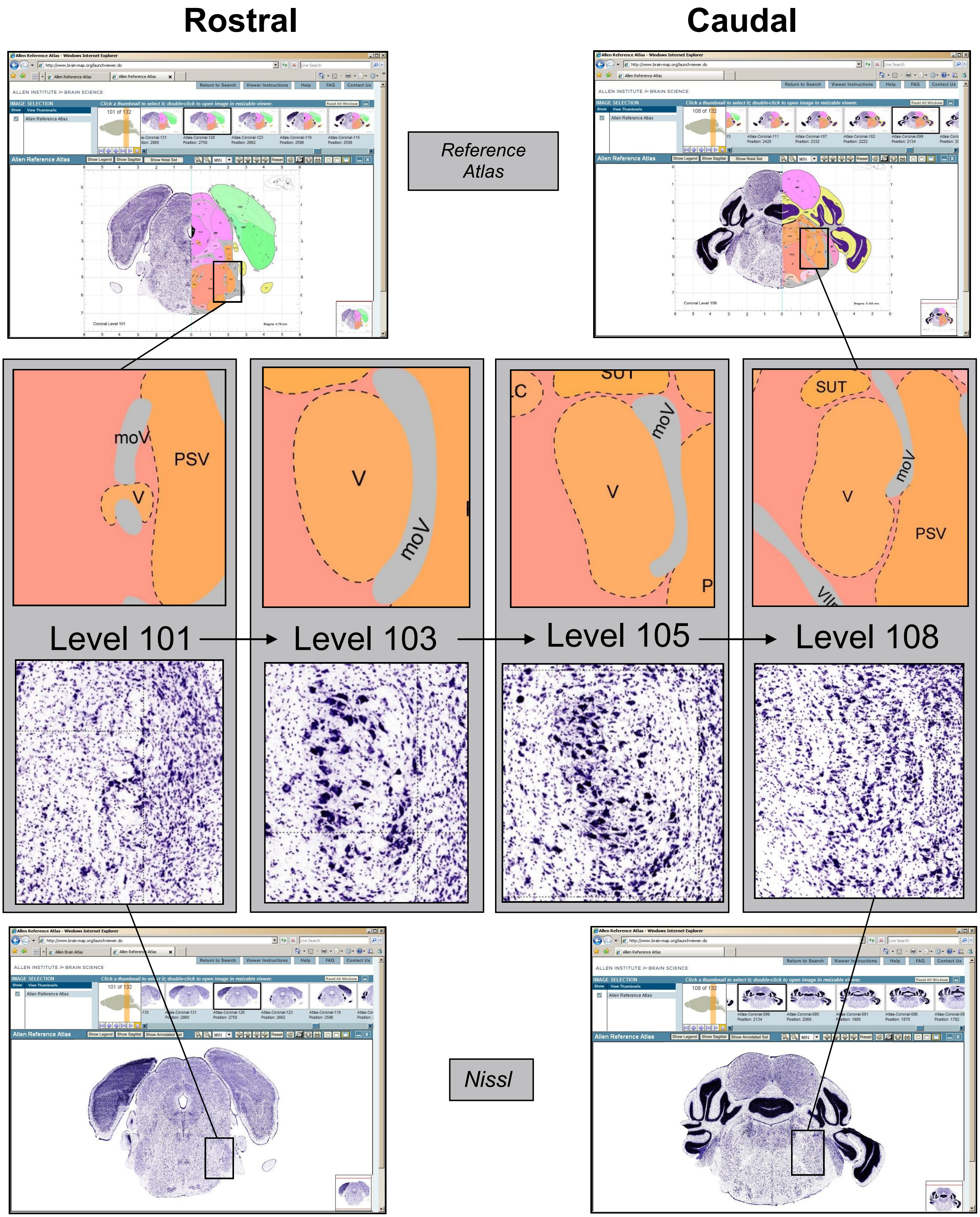
*Click on a row to see what structures it contains.*

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]

# Atlas and Nissl:

## Coronal:

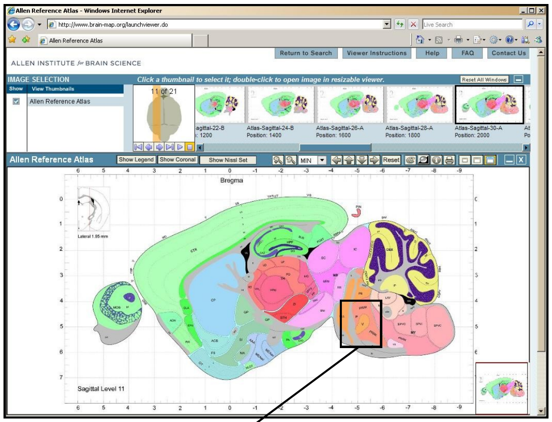


# Atlas and Nissl:

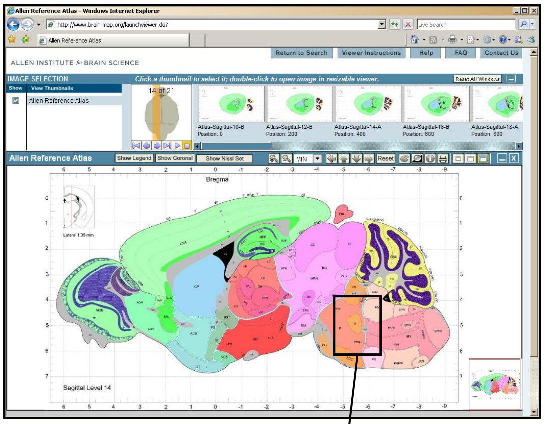
## Sagittal:

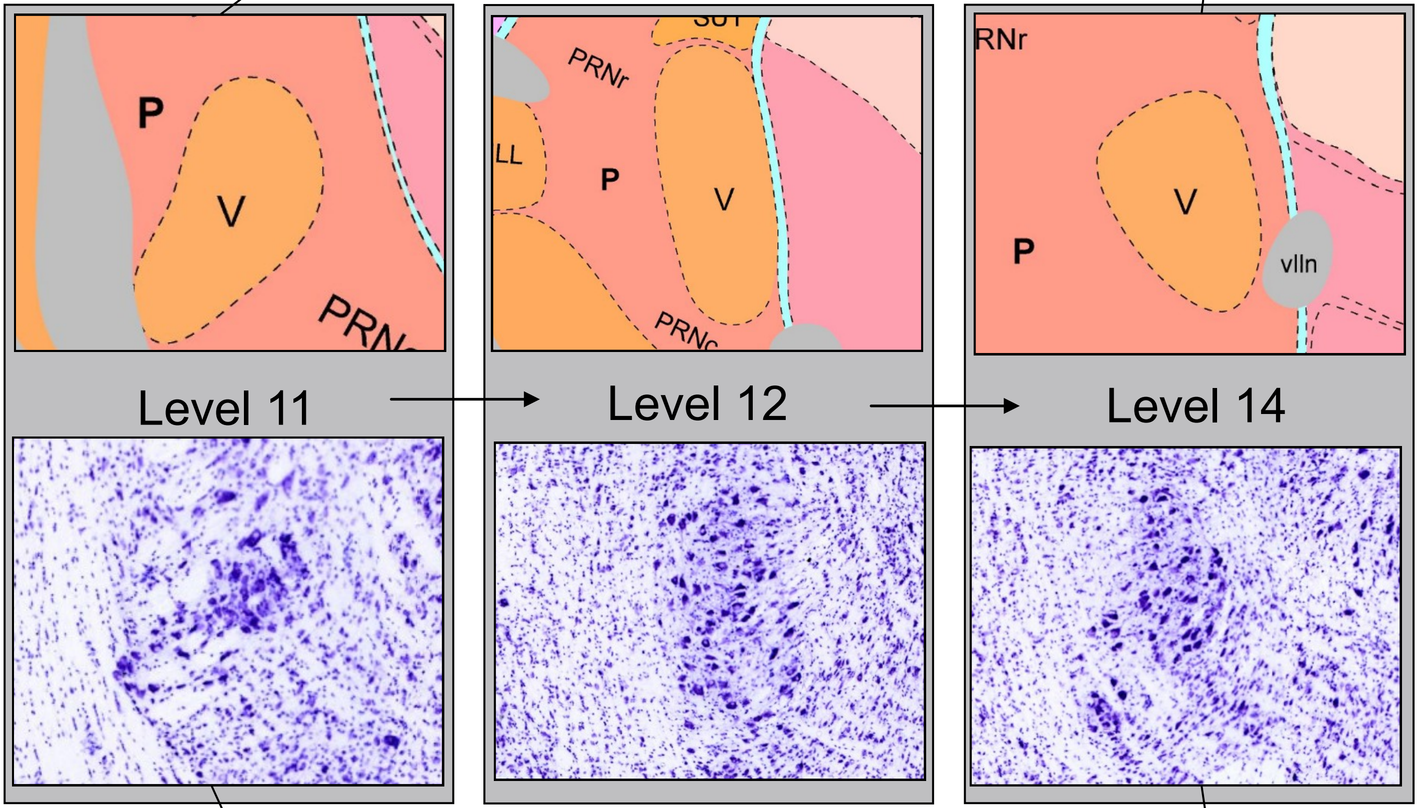
### Lateral

### Medial

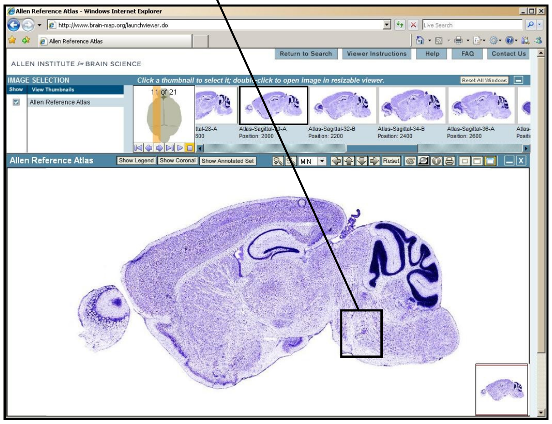


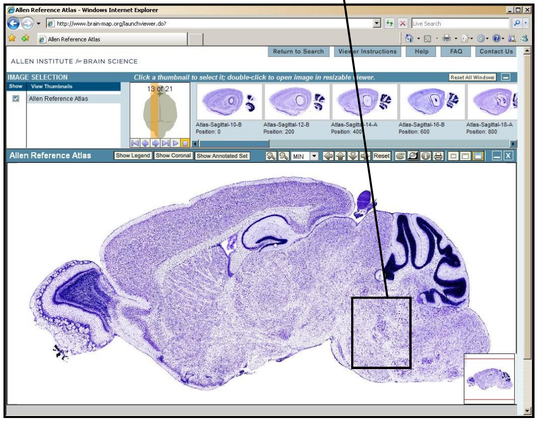
Reference Atlas





Nissl





# *In Situ Hybridization Expression Patterns of 50 Select Genes:*

*The in situ hybridization (ISH) data below presents the motor nucleus of the trigeminal nerve's 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 motor nucleus of the trigeminal nerve. 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.*

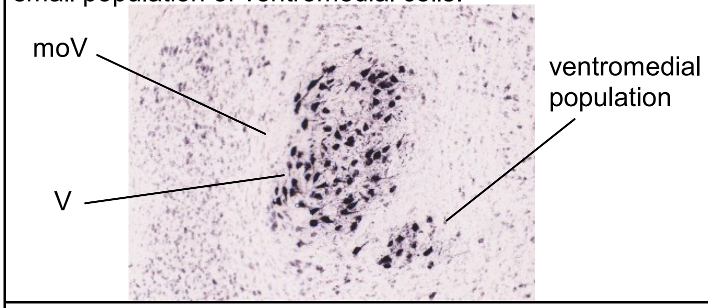
The majority of the 50 Select Genes express with high density and high intensity throughout the motor nucleus of the trigeminal nerve. This type of expression, combined with the large motor neurons that comprise the nucleus, make it a readily discernable structure. For these 50 genes, expression was seen in almost all cells within the motor nucleus, with no evidence of either gradients or additional subdivisions of the nucleus itself. A small population of cells that only span a few coronal sections appear ventromedially to the main body of the nucleus and the vast majority of the 50 Select Genes express in this area.

| **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 |

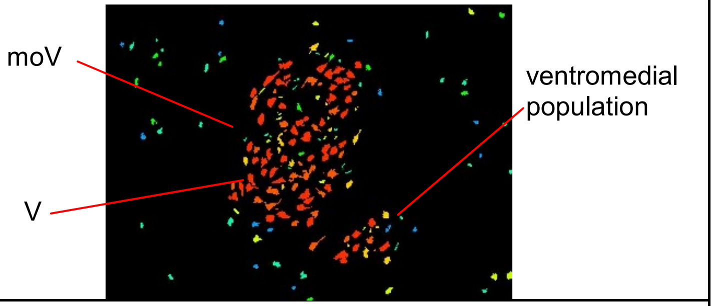
To view heat map at brain-map.org, right click on the ISH image and select "Show Expression Analysis."

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

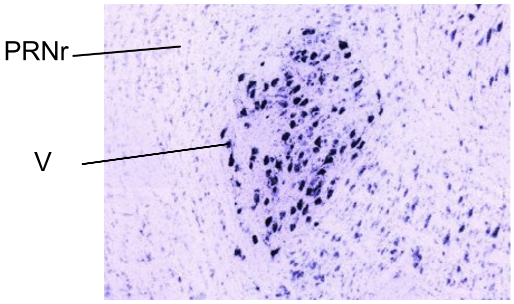
**ISH**
**Dffa**
**Coronal:** Expression of *Dffa* is widespread and intense, demonstrating the oblong shape of the nucleus. Note the small population of ventromedial cells.



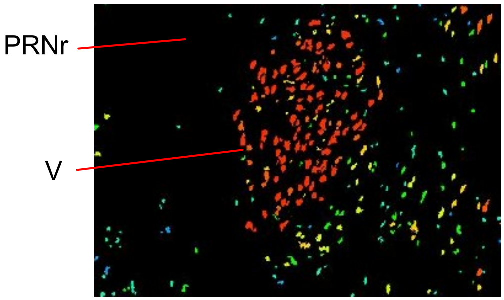
**Heat map**
**Dffa**
**Coronal:** Very high intensity labeling is obvious in the heat map image.



**ISH**
**Dffa**
**Sagittal:** *Dffa* expression show no anterior to posterior gradients or divisions of V.



**Heat map**
**Dffa**
**Sagittal:** Very high intensity is noted in the sagittal section as well.



**50 SELECT GENES:**

*This gene list was generated by manual curation of an algorithmically derived list that compared gene expression values of the motor nucleus of the trigeminal nerve to those of the pons. Categories of expression are subjectively grouped by relative expression characteristics.*

*Curation of 50 Select Genes List: July 2008*

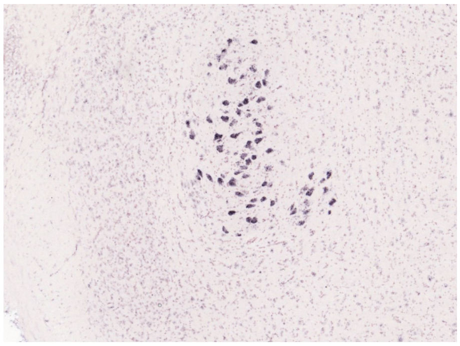
## Widespread Expression Pattern

| Number | Gene Symbol | Gene Name | Expression Pattern |
|---|---|---|---|
| 1 | Hspb1 | heat shock protein 1 | High density, medium intensity |
| 2 | Adam19 | a disintegrin and metallopeptidase domain 19 (meltrin beta) | High density, medium intensity |
| 3 | Layn | layilin | High density, very high intensity |
| 4 | Pacrg | Park2 co-regulated | High density, high intensity |
| 5 | Kcnj14 | potassium inwardly-rectifying channel, subfamily J, member 14 | High density, very high intensity |
| 6 | Calcb | calcitonin-related polypeptide, beta | High density, very high intensity |
| 7 | Ninj1 | ninjurin 1 | High density, medium intensity |
| 8 | Chrna3 | cholinergic receptor, nicotinic, alpha polypeptide 3 | High density, high intensity |
| 9 | Trhr | thyrotropin releasing hormone receptor | High density, medium intensity |
| 10 | Pappa | pregnancy-associated plasma protein A | High density, high intensity |
| 11 | Serpina3k | serine (or cysteine) peptidase inhibitor, clade A, member 3K | High density, medium intensity |
| 12 | Rspo2 | R-spondin 2 homolog (Xenopus laevis) | High density, high intensity |
| 13 | Slc5a7 | solute carrier family 5 (choline transporter), member 7 | High density, very high intensity |
| 14 | Prss12 | protease, serine, 12 neurotrypsin (motopsin) | High density, high intensity |
| 15 | Lgals1 | lectin, galactose binding, soluble 1 | High density, very high intensity |
| 16 | Dmp1 | dentin matrix protein 1 | High density, medium intensity |
| 17 | Serpinb6a | serine (or cysteine) peptidase inhibitor, clade B, member 6a | High density, very high intensity |
| 18 | Serpina3c | serine (or cysteine) peptidase inhibitor, clade A, member 3C | High density, medium intensity |
| 19 | Gm528 | gene model 528, (NCBI) | High density, high intensity |
| 20 | Cyb5r1 | cytochrome b5 reductase 1 | High density, high intensity |
| 21 | Kcnmb4 | potassium large conductance calcium-activated channel, subfamily M, beta member 4 | High density, high intensity |
| 22 | Tex261 | testis expressed gene 261 | Medium density, medium intensity |
| 23 | Slc41a3 | solute carrier family 41, member 3 | High density, very high intensity |
| 24 | Nrp1 | neuropilin 1 | High density, medium intensity |
| 25 | Entpd3 | ectonucleoside triphosphate diphosphohydrolase 3 | High density, high intensity |
| 26 | Anxa2 | annexin A2 | High density, high intensity |
| 27 | Trim16 | tripartite motif protein 16 | High density, medium intensity |
| 28 | Dffa | DNA fragmentation factor, alpha subunit | High density, very high intensity |
| 29 | Cda | cytidine deaminase | High density, medium intensity |
| 30 | Cd59a | CD59a antigen | High density, high intensity |
| 31 | 2610019F03Rik | RIKEN cDNA 2610019F03 gene | High density, high intensity |
| 32 | Sox14 | SRY-box containing gene 14 | Medium density, low intensity |
| 33 | Calca | calcitonin/calcitonin-related polypeptide, alpha | High density, very high intensity |
| 34 | Tmem74 | transmembrane protein 74 | High density, medium intensity |
| 35 | Gem | GTP binding protein (gene overexpressed in skeletal muscle) | High density, high intensity |
| 36 | Lxn | latexin | High density, very high intensity |
| 37 | Paqr8 | progestin and adipoQ receptor family mem- | High density, medium intensity |

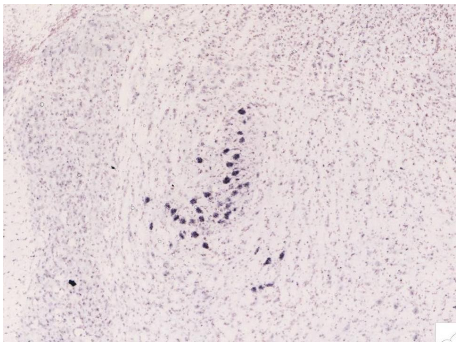
## Widespread Expression Pattern

| Number | Gene Symbol | Gene Name | Expression Pattern |
|---|---|---|---|
| 38 | Loh11cr2a | loss of heterozygosity, 11, chromosomal region 2, gene A homolog (human) | Medium density, high intensity |
| 39 | Dpysl3 | dihydropyrimidinase-like 3 | High density, high intensity |
| 40 | Msn | moesin | High density, very high intensity |
| 41 | Ibrdc2 | IBR domain containing 2 | Medium density, medium intensity |
| 42 | Wfs1 | Wolfram syndrome 1 homolog (human) | High density, high intensity |
| 43 | Slc18a3 | solute carrier family 18 (vesicular monoamine), member 3 | High density, very high intensity |
| 44 | D930040M24Rik | RIKEN cDNA D930040M24 gene | Medium density, low intensity |
| 45 | A330043P19Rik* | RIKEN cDNA A330043P19 gene (non-RefSeq) | High density, very high intensity |
| 46 | D13Bwg1146e | DNA segment, Chr 13, Brigham & Women's Genetics 1146 expressed | High density, medium intensity |
| 47 | Slc35f3 | solute carrier family 35, member F3 | High density, high intensity |
| 48 | Rrad | Ras-related associated with diabetes | High density, low intensity |
| 49 | Tmem63c | transmembrane protein 63c | High density, high intensity |
| 50 | Slitrk4 | SLIT and NTRK-like family, member 4 | High density, high intensity |

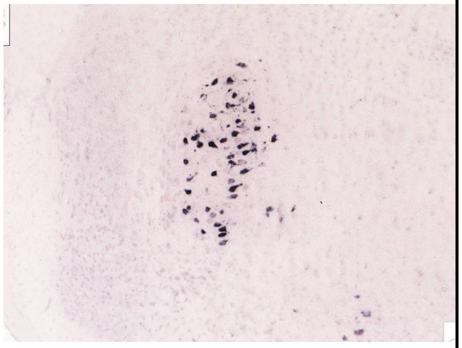
1.Hspb1



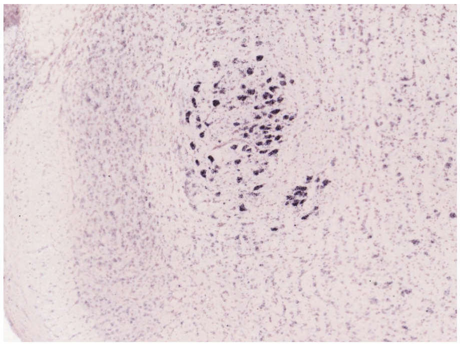
2.Adam19



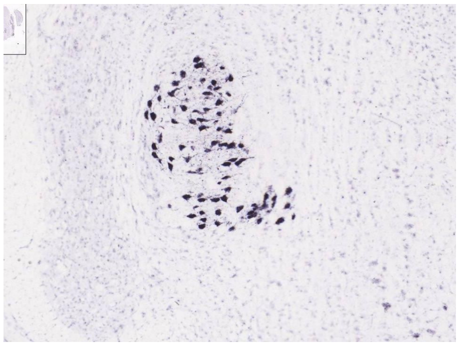
3.Layn



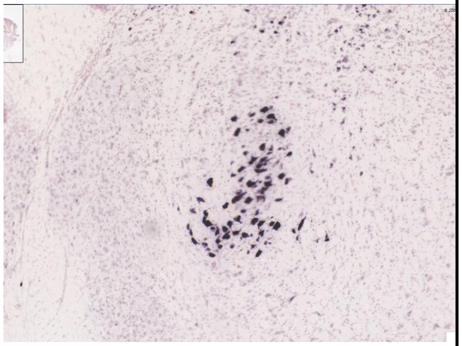
4.Pacrg



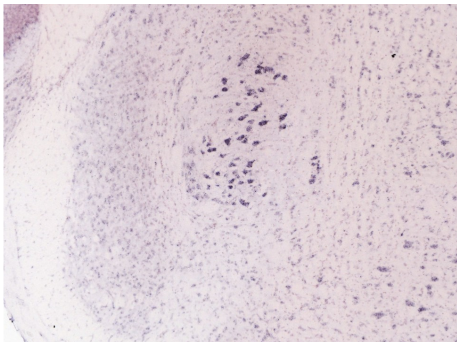
5.Kcnj14



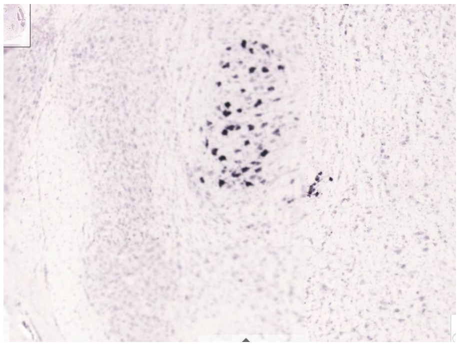
6.Calcb



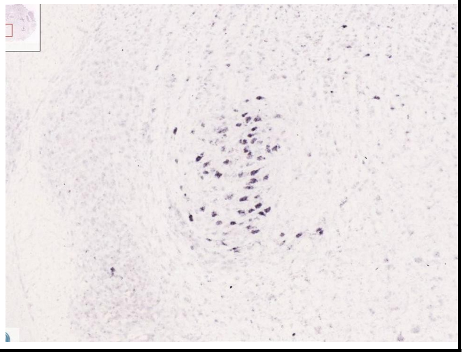
7.Ninj1



8.Chrna3

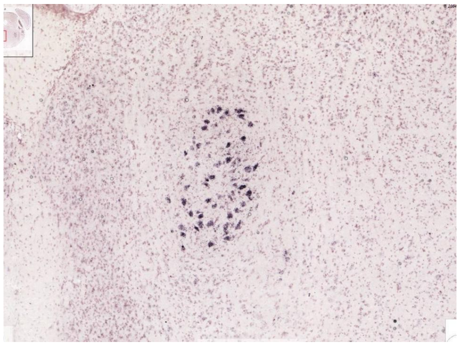


9.Trhr

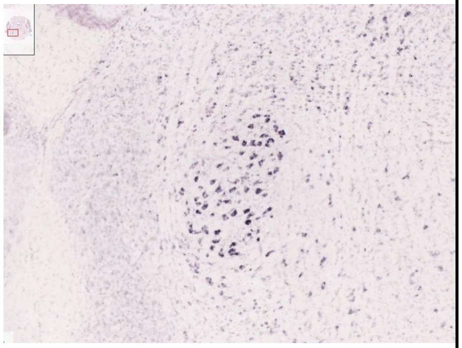


## Widespread Expression Pattern

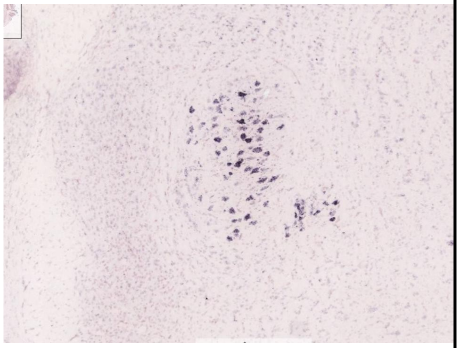
10.Pappa



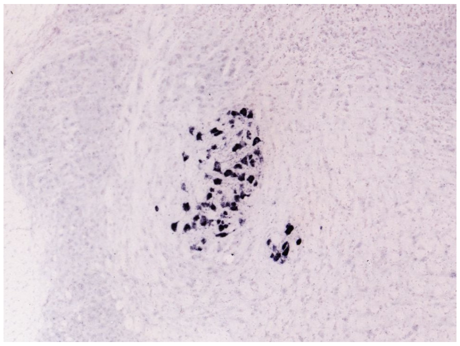
11.Serpina3k



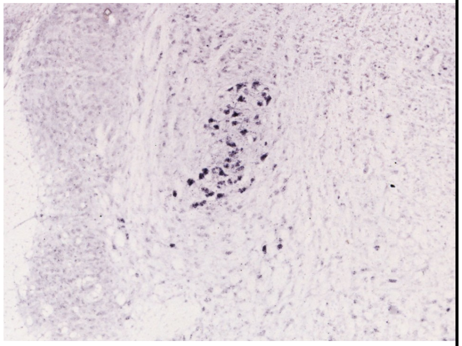
12.Rspo2



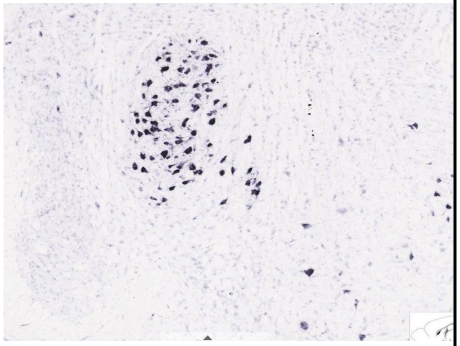
13.Slc5a7



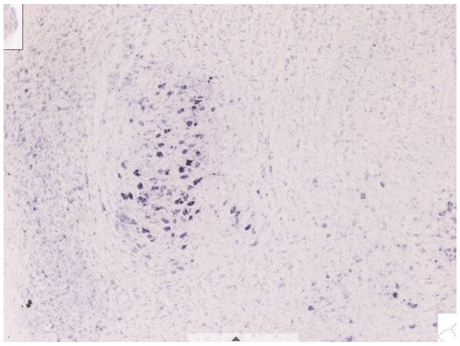
14.Prss12



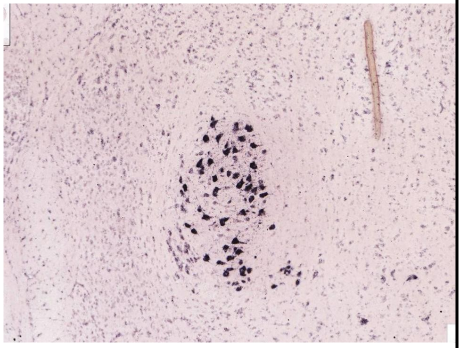
15.Lgals1



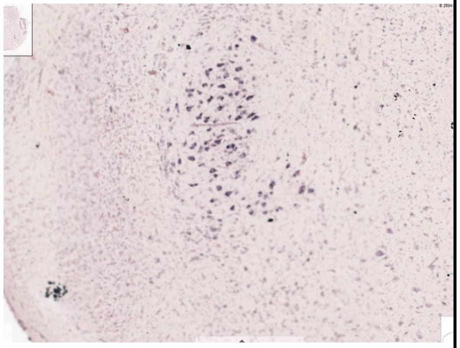
16.Dmp1



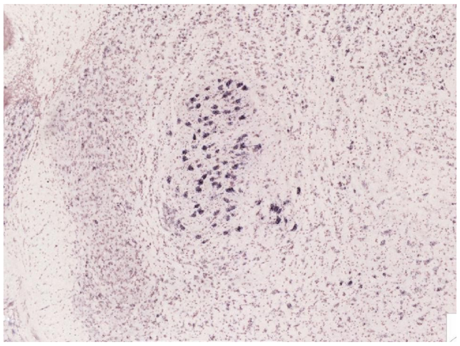
17.Serpinb6a



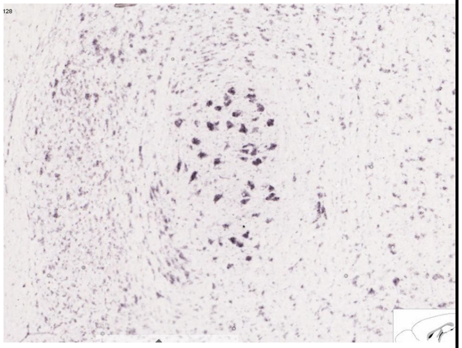
18.Serpina3c



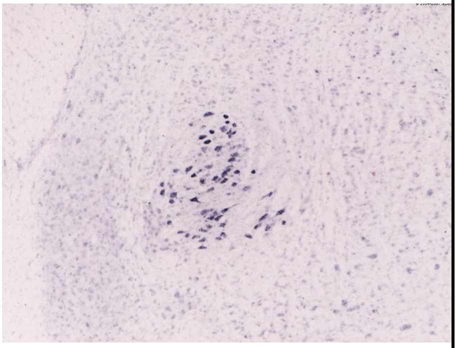
19.Gm528



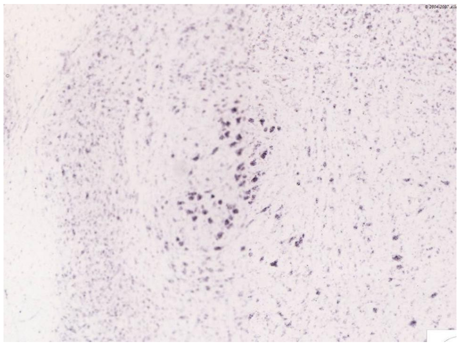
20.Cyb5r1



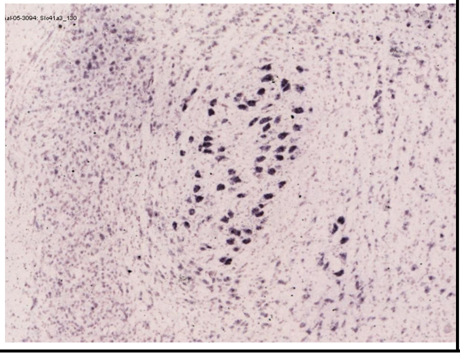
21.Kcnmb4



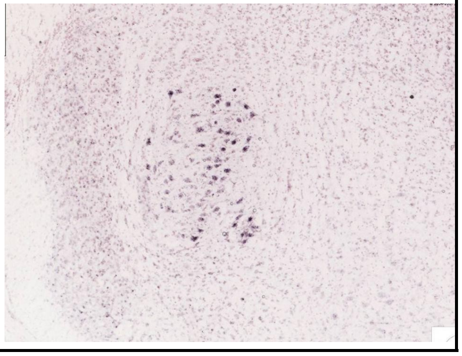
22.Tex261



23.Slc41a3

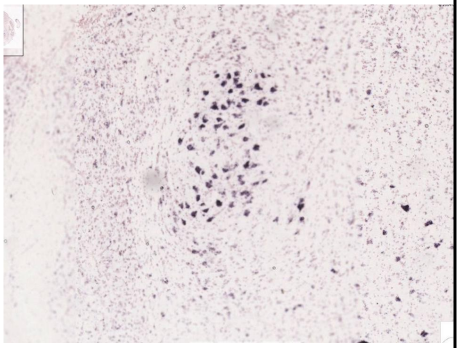


24.Nrp1

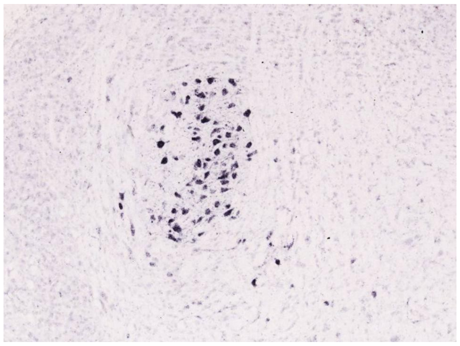


## Widespread Expression Pattern

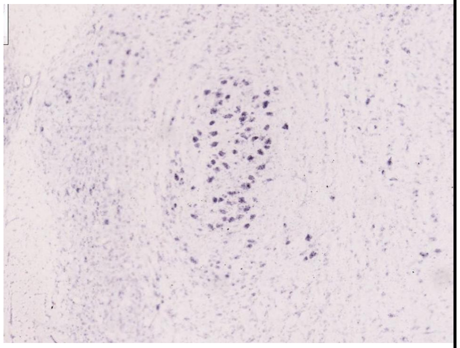
25.Entpd3



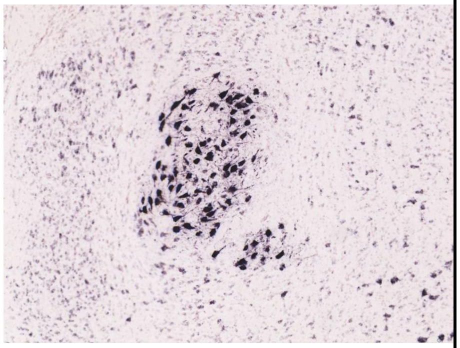
26.Anxa2



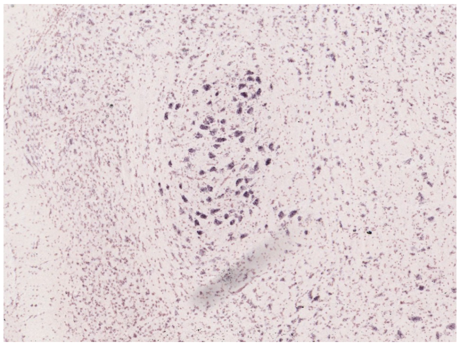
27.Trim16



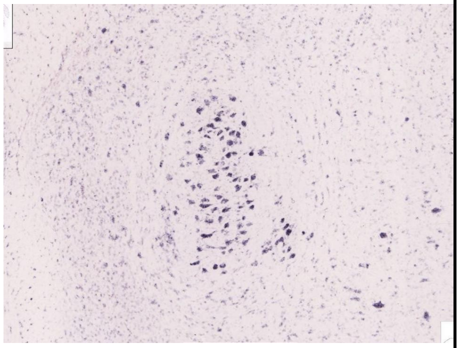
28.Dffa



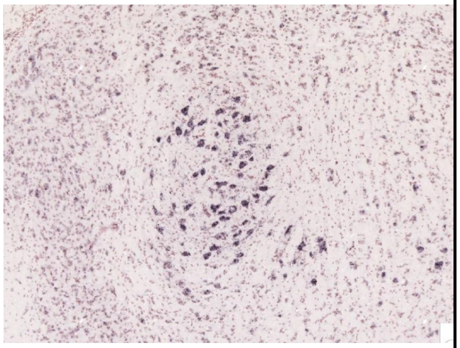
29.Cda



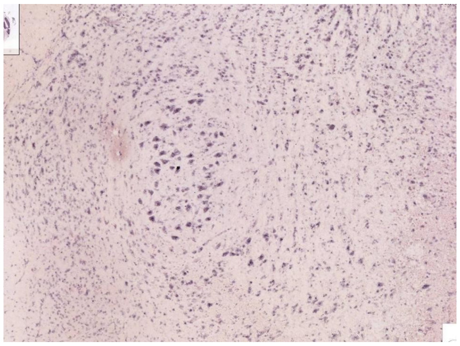
30.Cd59a



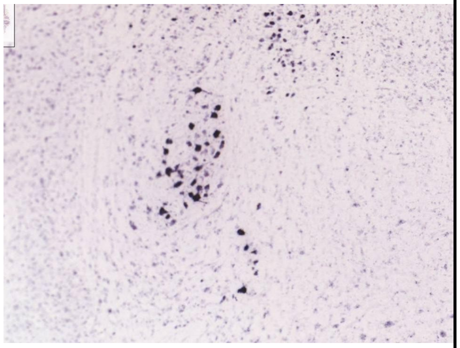
31.2610019F03Rik



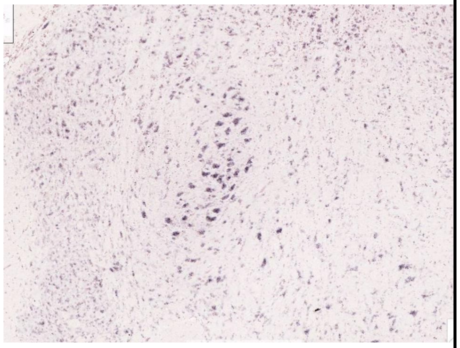
32.Sox14



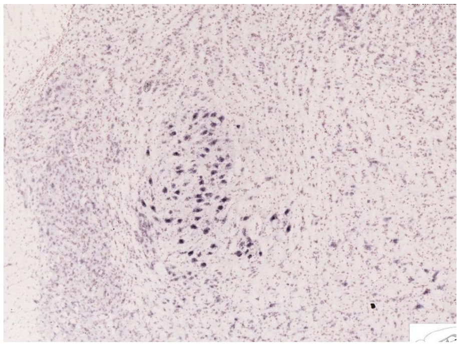
33.Calca



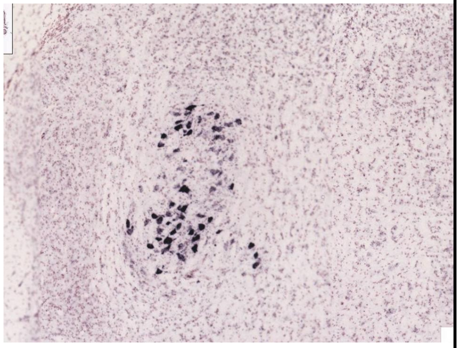
34.Tmem74



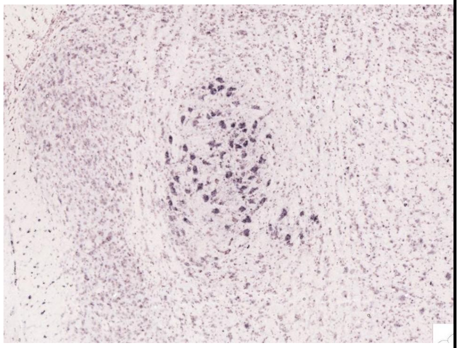
35.Gem



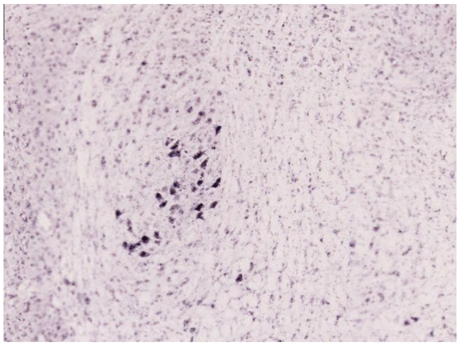
36.Lxn



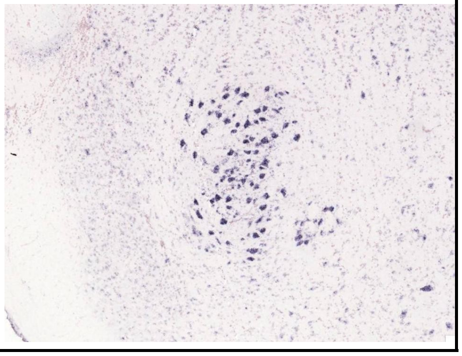
37.Paqr8



38.Loh11cr2a

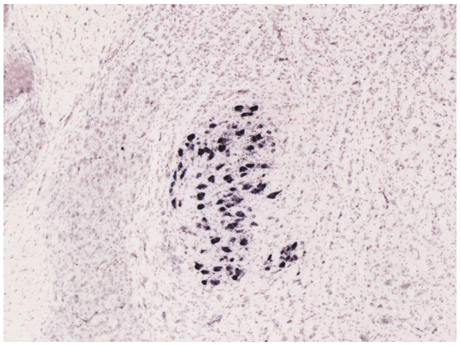


39.Dpysl3

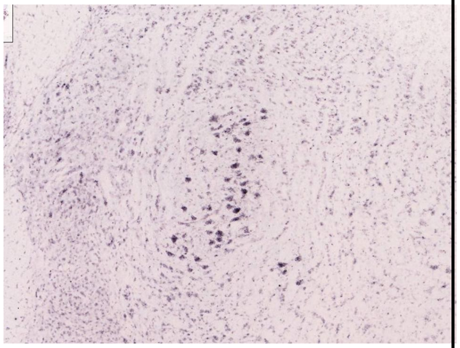


## Widespread Expression Pattern

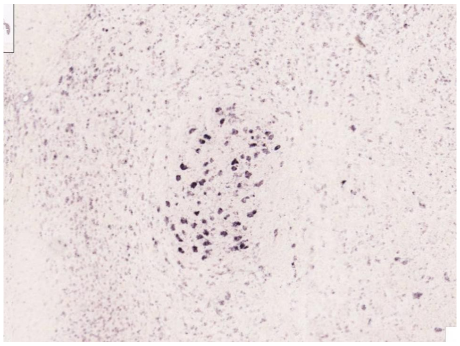
40.Msn



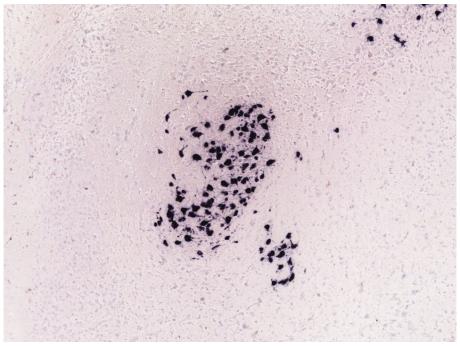
41.Ibrdc2



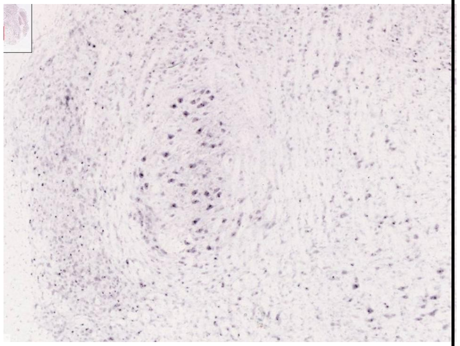
42.Wfs1



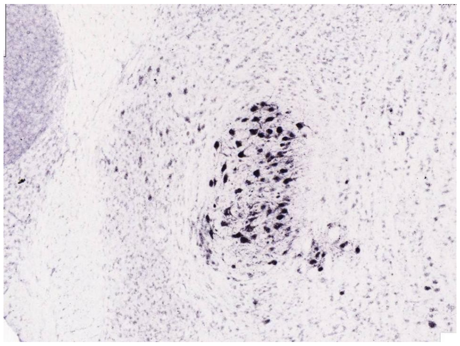
43.Slc18a3



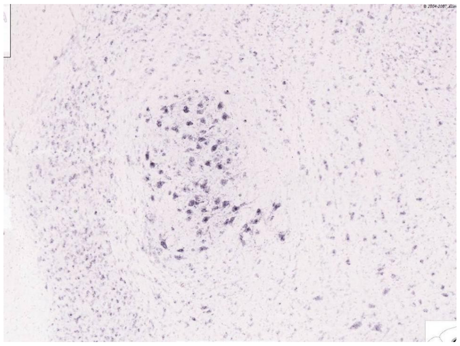
44.D930040M24Rik



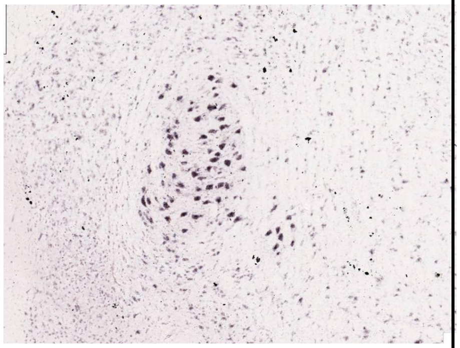
45.A330043P19Rik*



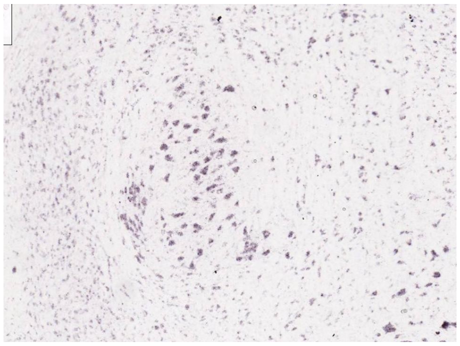
46.D13Bwg1146e



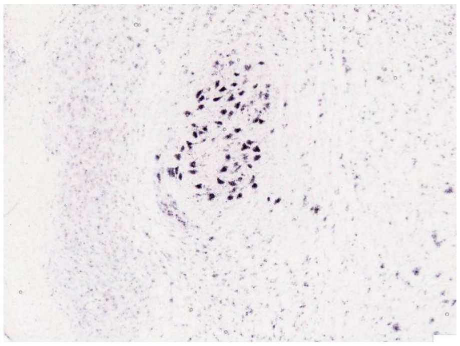
47.Slc35f3



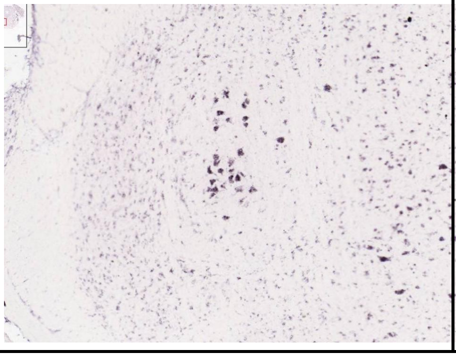
48.Rrad



49.Tmem63c



50.Slitrk4



# *Correlated Expression:*

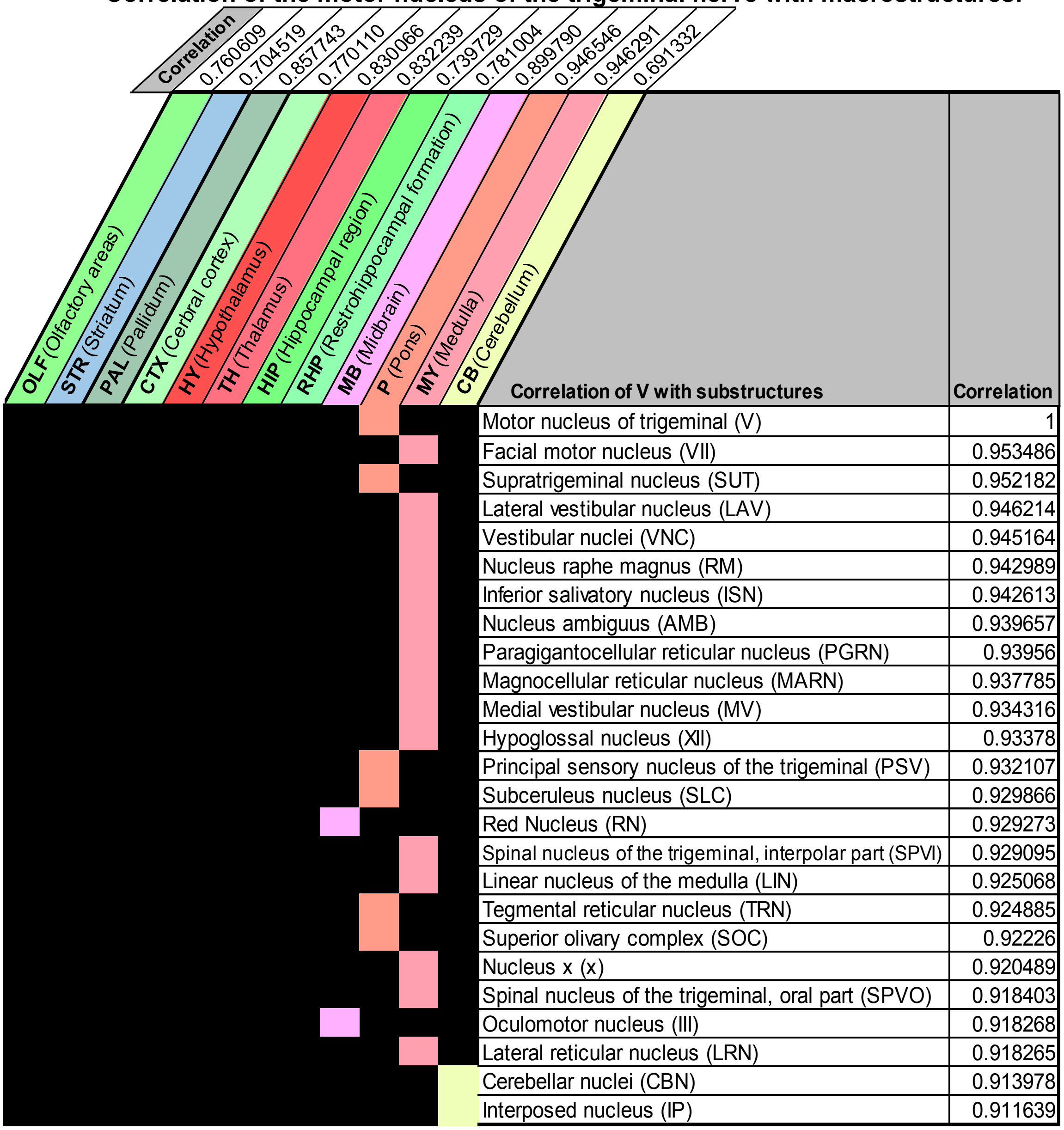
*The ABA coronal set contains many genes of known scientific interest as well as genes exhibiting combinatorial or unique expression patterns. A correlation analysis of all available ABA coronal experiments (4376) was performed by comparing the expression value of the motor nucleus of the trigeminal nerve 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$\mu$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 motor nucleus of the trigeminal nerve and other brain regions, expression values from all voxels within the motor nucleus of the trigeminal nerve were aggregated to form a single expression value. Two types of comparisons were then made. First, the aggregate expression values of the motor nucleus of the trigeminal nerve 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 motor nucleus of the trigeminal nerve 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 motor nucleus of the trigeminal nerve 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 motor nucleus of the trigeminal nerve and macro/parent-structures are presented, as well as correlation between the motor nucleus of the trigeminal nerve 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.*

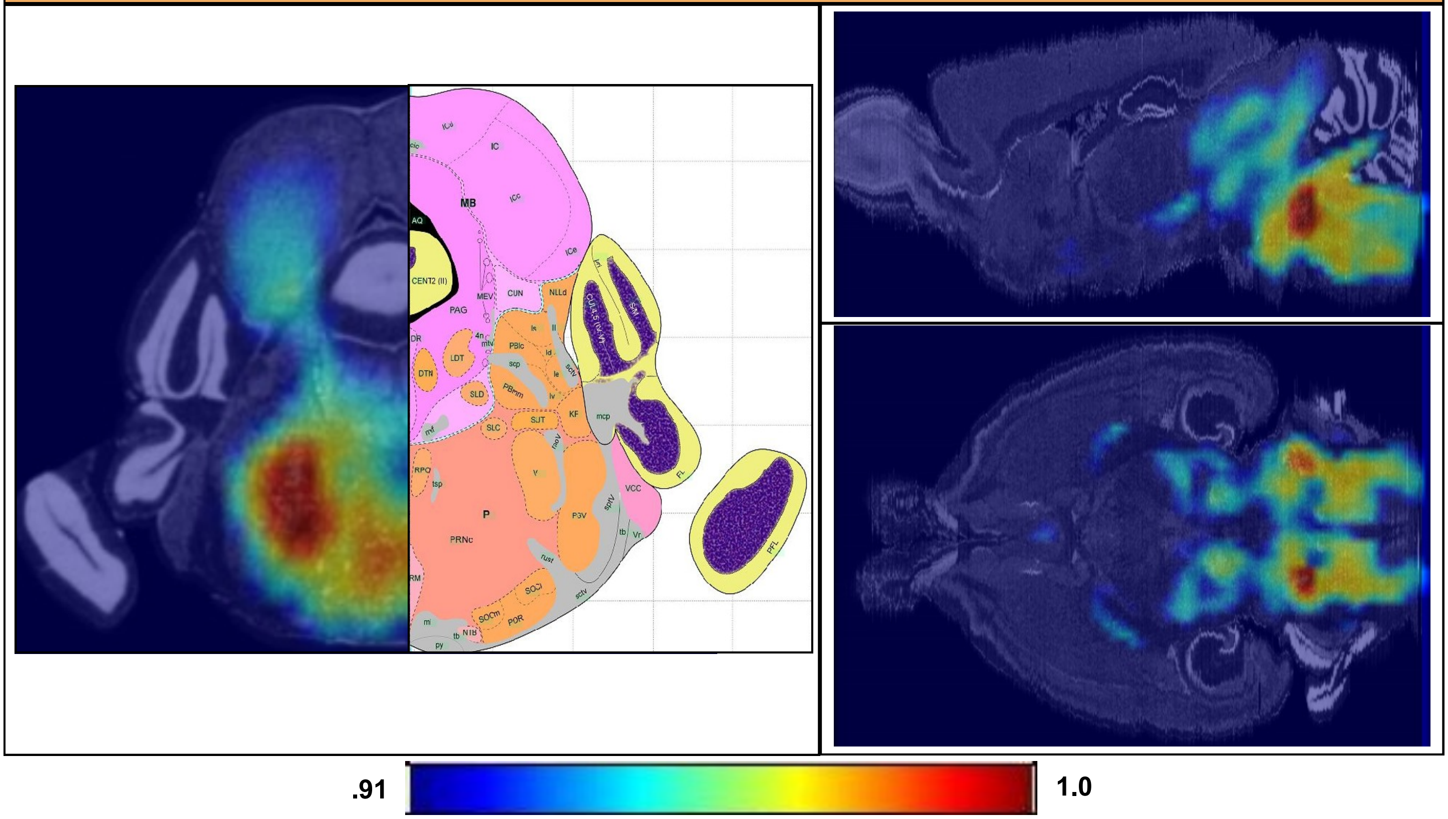
### Correlation of the motor nucleus of the trigeminal nerve with macrostructures:



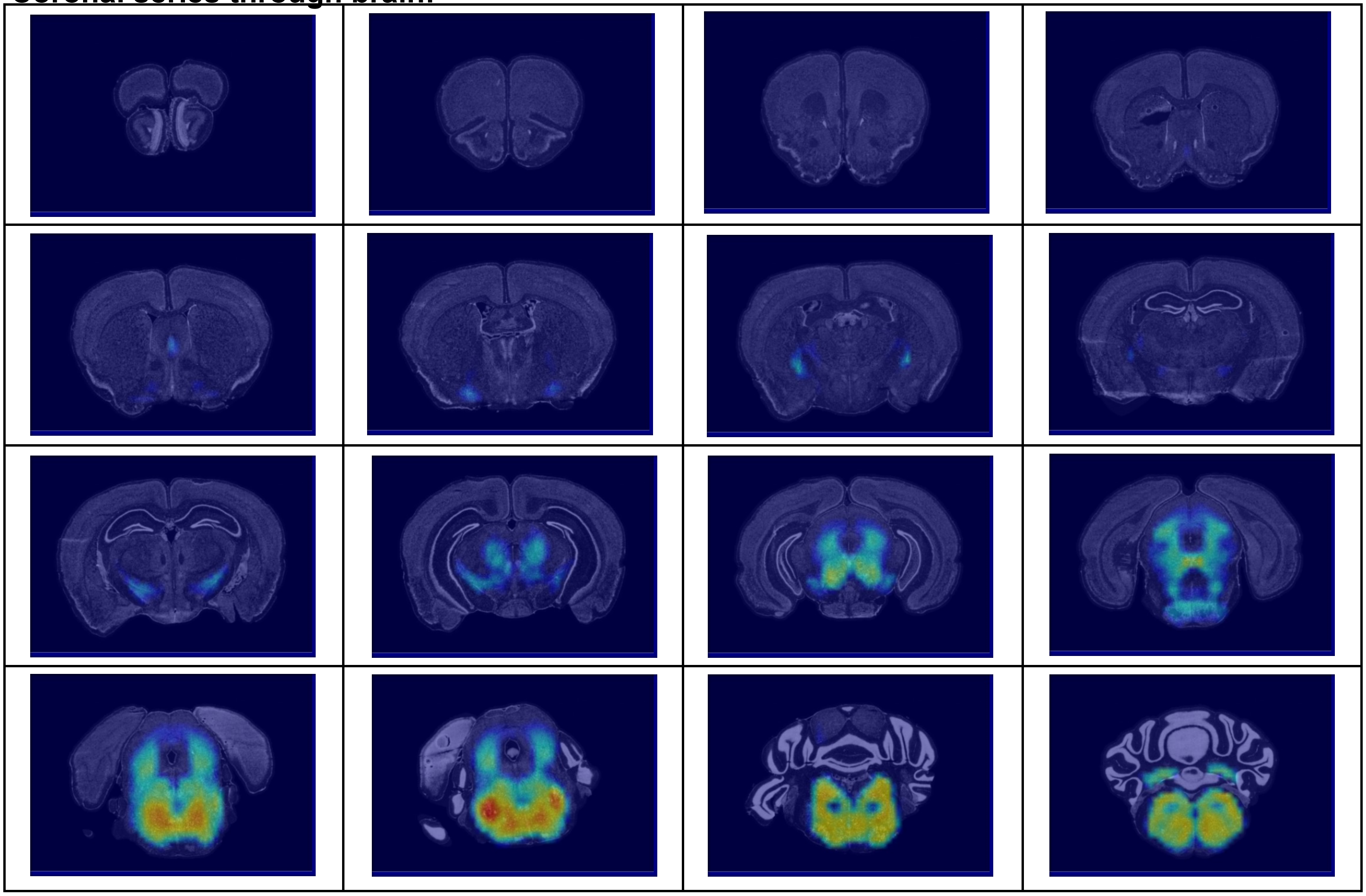
| | Correlation |
|---|---|
| **OLF** (Olfactory areas) | 0.760609 |
| **STR** (Striatum) | 0.704519 |
| **PAL** (Pallidum) | 0.857743 |
| **CTX** (Cerbral cortex) | 0.770110 |
| **HY** (Hypothalamus) | 0.830066 |
| **TH** (Thalamus) | 0.832239 |
| **HIP** (Hippocampal region) | 0.739729 |
| **RHP** (Restrohippocampal formation) | 0.781004 |
| **MB** (Midbrain) | 0.899790 |
| **P** (Pons) | 0.946546 |
| **MY** (Medulla) | 0.946291 |
| **CB** (Cerebellum) | 0.691332 |

| Correlation of V with substructures | Correlation |
|---|---|
| Motor nucleus of trigeminal (V) | 1 |
| Facial motor nucleus (VII) | 0.953486 |
| Supratrigeminal nucleus (SUT) | 0.952182 |
| Lateral vestibular nucleus (LAV) | 0.946214 |
| Vestibular nuclei (VNC) | 0.945164 |
| Nucleus raphe magnus (RM) | 0.942989 |
| Inferior salivatory nucleus (ISN) | 0.942613 |
| Nucleus ambiguus (AMB) | 0.939657 |
| Paragigantocellular reticular nucleus (PGRN) | 0.93956 |
| Magnocellular reticular nucleus (MARN) | 0.937785 |
| Medial vestibular nucleus (MV) | 0.934316 |
| Hypoglossal nucleus (XII) | 0.93378 |
| Principal sensory nucleus of the trigeminal (PSV) | 0.932107 |
| Subceruleus nucleus (SLC) | 0.929866 |
| Red Nucleus (RN) | 0.929273 |
| Spinal nucleus of the trigeminal, interpolar part (SPVI) | 0.929095 |
| Linear nucleus of the medulla (LIN) | 0.925068 |
| Tegmental reticular nucleus (TRN) | 0.924885 |
| Superior olivary complex (SOC) | 0.92226 |
| Nucleus x (x) | 0.920489 |
| Spinal nucleus of the trigeminal, oral part (SPVO) | 0.918403 |
| Oculomotor nucleus (III) | 0.918268 |
| Lateral reticular nucleus (LRN) | 0.918265 |
| Cerebellar nuclei (CBN) | 0.913978 |
| Interposed nucleus (IP) | 0.911639 |

**STRUCTURE vs. VOXEL:**
*Correlation between the motor nucleus of the trigeminal nerve and all other (200$\mu$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 ≤ 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 DAVID gene IDs/ 50 input genes |

***Date of table completion: July 2008***

| GO Category | GO Term | Gene Count | % of Genes | p-value |
|---|---|---|---|---|
| GOTERM_MF_ALL | enzyme inhibitor activity | 6 | 12.24% | 2.55E-04 |
| GOTERM_MF_ALL | endopeptidase inhibitor activity | 5 | 10.20% | 6.85E-04 |
| GOTERM_MF_ALL | protease inhibitor activity | 5 | 10.20% | 7.31E-04 |
| GOTERM_BP_ALL | developmental process | 15 | 30.61% | 0.003049 |
| GOTERM_BP_ALL | anatomical structure development | 12 | 24.49% | 0.003393 |
| GOTERM_CC_ALL | membrane | 30 | 61.22% | 0.005016 |
| GOTERM_BP_ALL | system development | 10 | 20.41% | 0.011239 |
| GOTERM_BP_ALL | anatomical structure morphogenesis | 8 | 16.33% | 0.013500 |
| GOTERM_CC_ALL | plasma membrane | 12 | 24.49% | 0.017106 |
| GOTERM_CC_ALL | cell projection | 5 | 10.20% | 0.020549 |
| GOTERM_BP_ALL | multicellular organismal development | 11 | 22.45% | 0.020719 |
| GOTERM_MF_ALL | enzyme regulator activity | 6 | 12.24% | 0.025659 |
| GOTERM_MF_ALL | cation transmembrane transporter activity | 5 | 10.20% | 0.032803 |
| GOTERM_CC_ALL | extracellular region | 12 | 24.49% | 0.035155 |
| GOTERM_BP_ALL | cell development | 7 | 14.29% | 0.049930 |

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.

## *MOTOR NUCLEUS OF THE TRIGEMINAL NERVE Summary:*

### Anatomy

- The motor nucleus of the trigeminal nerve (V) is located in the lateral region of the pons, and is bordered by the pontine reticular nucleus (PRNc), the supratrigeminal nucleus (SUT), and the motor root of the trigeminal nerve (moV).
- The proximity of the motor nucleus of trigeminal to the facial nerve (VIIn) can be appreciated in the sagittal plane.
- Large, densely packed motor neurons comprise the motor nucleus of the trigeminal nerve and aid in distinguishing it from surrounding structures.

### Expression Patterns of the 50 Select Genes

- All fifty genes examined showed widespread expression throughout the nucleus.
- Some genes, such as *Tex261* and *Loh11cr2a*, were expressed at a lower density, (i.e. scattered population of cells); however, no gradients or obvious subdivisions of the nucleus are revealed by this gene set.

### Correlation

- The motor nucleus of the trigeminal nerve shows highest correlation with nuclei of the midbrain, the pons, the medulla, and the cerebellum.
- Additionally, within these areas, there is correlation with regions of the periaqueductal grey matter and subregions of the superior colliculus.
- Correlation of the motor nucleus of the trigeminal nerve with individual voxels throughout the cerebrum reveals gene expression in the globus pallidus and the zona incerta.

*We encourage you to reply with any comments or questions by email to !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.*