Brain-wide synaptic inputs to aromatase-expressing neurons in the medial amygdala suggest complex circuitry for modulating social behavior

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Brain-wide synaptic inputs to aromatase-expressing neurons in the medial amygdala suggest complex circuitry for modulating social behavior.

Abstract:

Here, we reveal an unbiased view of the brain regions that provide specific inputs to aromatase-expressing cells in the medial amygdala, neurons which play an outsized role in the production of sex specific social behaviors, using rabies tracing and light-sheet microscopy. While the downstream projections from these cells are known, the specific inputs to the aromatase-expressing cells in the medial amygdala remained unknown. We observed established connections to the medial amygdala (e.g., bed nucleus of the stria terminalis and accessory olfactory bulb) indicating that aromatase neurons are a major target cell-type for efferent input including from regions associated with parenting and aggression. We also identified novel and unexpected inputs from areas involved in metabolism, fear and anxiety, and memory and cognition. These results confirm the central role of the medial amygdala in sex specific social recognition and social behavior and point to an expanded role for its aromatase-expressing neurons in the integration of multiple sensory and homeostatic factors, which are likely used to modulate many other social behaviors.

Significance Statement:

Aromatase-expressing neurons in the medial amygdala play a significant role in producing critically important social behaviors including parenting, aggression, and reproduction. We used rabies tracing and light-sheet microscopy to reveal an unbiased view of many brain regions that provide direct synaptic input to aromatase neurons and observe both well-established and previously unknown inputs from areas involved in parenting and aggression, metabolism, fear and anxiety, and memory and cognition. These results confirm the central role of the medial amygdala in social recognition behavior and point to an expanded role for its aromatase-expressing neurons in the integration of multiple sensory and homeostatic factors, which can be used to modulate many other social behaviors.

Introduction:

Social behaviors are necessary for communication, survival, and reproduction in species throughout the animal kingdom (Darwin, 1871; Marler, et al., 1979; Ueda et al., 2020), and depend on the integration of external and internal sensory cues. Nearly all sensory systems have been linked to social behavior (Keller, et al., 2006a; 2006b; 2006c; Pomerantz, et al., 1983; Contreras and Agmo, 1993; Strasser and Dixon, 1986). For example, the diverse, and often beautiful, vocalizations of songbirds signal their species, individual identity, territorial ownership, and readiness to mate (Marler, 1961). In humans, visual cues produced in the face and hands provide information about another's identity and emotional state (Haxby, et al., 2002). For many species, chemosensory cues are particularly important to detect, identify, and respond to social partners (Bradley, et al., 2002; Dulac, et al., 1995; Gonzalez, et al., 2017; Keller, et al., 2006c; Schwanzel-Fukuda, et al., 1991). In mice, chemosensory information, transduced by the main olfactory epithelium and the vomeronasal organ, provides the primary sensory input to a conserved network of brain regions dedicated to executing social behaviors (Newmann, et al., 1999).

The core brain regions that make up the social behavior network (SBN) are well-established and conserved for all vertebrate species examined thus far (Goodson, 2005). However, identifying the specific neural circuits that generate social behaviors has been challenging because of both the heterogeneity of cell populations in these regions and the interwoven and reciprocal nature of both the behaviors themselves and the underlying circuits. Thus, a current goal in neuroscience is to define specific

contributions of well-defined populations of neurons to circuit function and, ultimately, to behaviors. Genetic and viral tools allow precise characterization of the connections made by individual populations of neurons and have been instrumental in defining cell-type-specific wiring diagrams that mediate specific behaviors (Watabe-Uchida, et al., 2012; Menegas, et al., 2015; Kohl, et al., 2018; Wickersham, et al., 2007).

The medial amygdala (MeA), a central node in the SBN, receives sensory input directly from the accessory olfactory bulb (AOB) and the main olfactory bulb (MOB). The MeA integrates chemosensory signals with modulatory input from other brain regions (Ferguson, et al., 2001; Yao, et al., 2017) and circulating hormones (Cooke, et al., 1999; Cooke, et al., 2005) to guide behavioral responses through its projections to efferent behavioral centers (Wu, et al., 2009). MeA neurons in mice display sex differences in sensory responses to social stimuli (Bergan, et al., 2014; Samuelsen & Meredith, 2009; Kim et al., 2017) and robust anatomical sex differences (Cooke, et al., 1999; Wu, et al., 2009; Billing et al., 2020). Social behaviors that are tightly associated with the MeA, including parenting, mate choice, and aggression, also display clear sex differences (Chen, et al., 2020; Vochteloo, et al., 1987; Yao, et al., 2017). Each of these behaviors are critical for survival and reproduction. Their dependence on an animal's sex, age, and neuroendocrine status offers an opportunity to understand how the function of a common neural circuit can be modified to meet the specific behavioral requirements of an individual animal.

A large population of MeA neurons express the enzyme aromatase, which converts testosterone to estradiol, is critical for aggression in both sexes, and is known to shape the pattern of sensory responses in the MeA (Unger et al., 2015; Bergan et al., 2014). To fully understand the role of aromatase neurons in social behavior, however, we must first identify the inputs they receive and the circuits they form. Past experiments have addressed the electrophysiology of MeA neurons (Binns, et al., 2005; Bergan et al., 2014; Yao et al., 2017; Meredith et al., 2004; Li, et al., 2018) as well as the efferent targets of the MeA aromatase population (Wu et al., 2009). Recently, a sex-specific connection from AOB mitral and tufted neurons to aromatase neurons of the MeA was identified using rabies-based viral tracing from aromatase neurons (Billing, et al., 2020). However, the MeA integrates information from a large network of brain regions. Here we use rabies-based circuit mapping in conjunction with whole-brain cleared tissue imaging to exhaustively characterize the sources of synaptic input to aromatase neurons in the MeA, and to identify the information channels that shape aromatase-dependent social behaviors.

Materials and Methods:

Animal Use: All experiments were performed in strict compliance with the National Institute of Health. All animals were handled according to a protocol approved by the UMass Amherst Institutional Animal Care and Use Committee (IACUC; protocol #2018-0014 and #2017-0060).

Fifteen adult mice (2 to 8 months old, both male (n=9) and female (n=6)) from an existing transgenic mouse line (Cyp19a1-Cre: Jax Labs) were housed in a temperature (22°C) and light (12hr: 12hr light: dark) controlled facility, with *ad libitum* access to food and water. The Cyp19a1-Cre transgenic line was generated by BAC recombination (Yao et al., 2017); its expression pattern faithfully recapitulates endogenous aromatase expression (Yao et al., 2017) and displays no known behavioral deficits in either heterozygous or homozygous animals.

Viral injections: We used a retrograde tracing system based on the modified rabies virus (EnvA-SADΔG-EGFP; Wickersham, et al., 2007) that uses two consecutive stereotaxic injections to visualize →MeA^{arom+}.

99 In the first injection, 500 nl of AAV8-FLEX-TVA and AAV8-FLEX-RG-mCherry (mixed 1:1; Watabe-Uchida
100 et al. 2012) were injected into either the left or right MeA (Bregma -1.9, Lateral 1.9, Depth 4.5 to 5.5).
101 After 14 days, 500 nl of SADΔG-EGFP(EnvA) virus (Viral Vector Core, Salk Institute, La Jolla, CA) was
102 injected into the MeA at the same stereotaxic coordinates (Figure 2B; Wickersham et al. 2007). All
103 stereotaxic injections used a cold capillary (20-micron diameter tip) coupled to a Narishige hydraulic
104 manipulator (Wu et al., 2014). All AAV viruses were produced by the UNC Vector Core Facility (Chapel
105 Hill, NC, United States).

106
107 The rabies virus requires the cell-surface expression of TVA to enter a cell and is therefore limited to
108 infecting Cre-expressing neurons (Figure 2A). Once inside a neuron, the modified rabies virus requires
109 co-expression of the envelope glycoprotein (RG) to be packaged for retrograde trans-synaptic spread.
110 The efficiency of viral infection was determined by injecting the same viruses into double-transgenic line
111 that labels all Cre-expressing neurons with the R26-lsl-tdTomato reporter (Figure 2C; Madisen et al.,
112 2010). This control experiment allowed us to estimate the infection rate (percent of the target population
113 labeled by rabies; Figure 2D).

114
115 *Tissue Processing:* Ten days after the final injection, animals were deeply anesthetized with isoflurane
116 and perfused with 50ml cold PBS followed by 25 ml cold PFA (4% in PBS). The brain was extracted and
117 post-fixed in 25 ml hydrogel (4% acrylamide, 4% PFA, 0.05% bis acrylamide, and 0.25% VA-044 initiator
118 suspended in 0.01 M PBS; Isogai, et al., 2017) 4 °C overnight.

119
120 After 12 - 24 hours incubation in hydrogel, oxygen was flushed from the hydrogel by bubbling the liquid
121 hydrogel solution with nitrogen. The tissue container was resealed and transferred to a 37°C water bath
122 until polymerization was complete (at least two hours). Excess hydrogel was removed from the brain
123 manually and the tissue sample was incubated to SDS-clearing solution (10 mM sodium dodecyl sulfate
124 in 0.1 M borate buffer, pH 8.5) for 2 days at 37 °C prior to MHD-accelerated clearing (Dwyer, et al, 2019).

125
126 Active clearing was performed in a 5-gallon container containing SDS-clearing solution using a custom
127 magnetohydrodynamic (MHD) clearing device (Dwyer et al., 2019) that rapidly removed unbound lipids
128 from the tissue sample at 37°C. Brains were cleared until bright white and translucent, which typically
129 took 24-48 hours. Brains were then transferred to 0.01M PBS for 24 hr. Brains were transferred from PBS
130 to an OptiView imaging solution (Isogai et al. 2017) with refractive index 1.45 and incubated at 37°C for 2
131 days before imaging.

132
133 *Image acquisition and processing:* Images were acquired with the Zeiss Z.1 Lightsheet microscope (Carl
134 Zeiss, Jena, Germany). Rabies-labeled eGFP-expressing neurons were excited with a 488 nm laser. A
135 561 nm and/or 647 nm laser was used to produce an autofluorescence image for subsequent background
136 subtraction and isolation of the GFP signal. Images were collected with a 5-times magnification objective
137 lens with PCO-Edge sCMOS cameras (PCO, Kelheim, Germany). The entire brain was imaged in the
138 horizontal orientation from both the dorsal and ventral surfaces. This produced a series of slightly
139 overlapping 3D image stacks for each brain. 3D Image stacks were saved at 1-5 μm resolution and
140 reconstructed to form a 3D image of the entire brain using custom MATLAB scripts (Mathworks, Natick,
141 MA).

142
143 *Cell-counting:* Rabies-labeled cells were identified using a human-trained computer vision algorithm
144 (Ilastik, Heidelberg University). Briefly, a training subset of images were annotated as 'not tissue',
145 'unlabeled tissue', and 'rabies labeled neuron' by a trained user to prepare a machine learning kernel to
146 automatically identify rabies labeled neurons. The resulting kernel was refined over several iterations until
147 it accurately identified rabies labeled cells. Ilastik then automatically classified each pixel in from each

image based on its probability of being a member of each category. The resulting probability map for 'rabies labeled neuron' were segmented with 'regionprops' in MATLAB and the centroids of each identified neuron were identified. Automatically identified cells (ilastik, Heidelberg University) were reviewed and confirmed by a human observer for quality control.

Each identified 'input cell' was assigned to a brain region based on its anatomical location. Thus, each imaged brain was transformed into a list containing the numbers and positions of identified neurons in each brain region and for each experimental animal. The identified populations were interpreted as the afferent synaptic input to the target population. Our past successes with this strategy likely result from three factors: 1) Thousands of input neurons are typically labeled in each brain providing broad coverage of social circuits. 2) The genetic specificity, 'starter neurons', of our approach reduces variability introduced by cell-type heterogeneity and by fibers of passage at the injection site; 3) The automated analysis pipeline allows user to annotate a sample dataset, which is then used to efficiently and accurately segment all subsequent datasets into 'input cells', 'starter cells', and 'unlabeled tissue' in an unbiased manner (Menegas et al., 2015). Because of the intensely bright fluorescence of EGFP driven by the EnvA-SADΔG-EGFP virus, this algorithm can identify rabies labeled neurons with more than 99% accuracy and with very few false positives.

Brain Alignment: Each reconstructed 3D brain was aligned to the common framework Allen Brain Atlas (ccfv3; Wang, et al., 2020) using elastix (Klein, et al., 2010; Shamonin, et al., 2014). Custom MATLAB scripts (Mathworks, Natick, MA) were used to integrate user input and computer processing and produce the alignment. Transformix (Klein, et al., 2010; Shamonin, et al., 2014) was then used to migrate the identified cells in each brain to the position of the accurate brain region in the standard Allen Brain Atlas framework. This allowed us to identify the number of eGFP-expressing cells in each region of the brain in each animal.

Statistical Analysis: Statistical analyses were performed using MATLAB. Means are reported with standard error of the mean. Regressions were performed in MATLAB using the "fitlm" and "predict" functions. Regions identified as providing input to MeA arom+ neurons were determined using a single sample t-test on the observed cell counts in each region with Bonferroni correction for multiple comparisons when appropriate. A second comparison was made using a single sample t-test to determine if the input from a given region exceeded the expected input based on chance using the region volume and an even distribution of cells as the chance rates (see Table 3). Sex differences in synaptic input were first characterized using a repeated measures ANOVA with interactions conducted in MATLAB. Post-hoc analyses for sex differences were conducted using an exact Permutation test comparing the cell counts observed in males versus females for each region (Efron and Tibshirani, 1986). D' was calculated as a sensitivity index for distributions with different SEM by normalizing the difference in cell count means by the standard deviation of the overall distribution. All scripts required to replicate these analyses have been provided as supplementary materials.

Results:

We used a previously described aromatase-cre transgenic mouse line (Yao et al., 2017) crossed with the AI9 tdTomato reporter line (Madison, et al., 2010) to identify aromatase-expressing neurons throughout the brain (Figure 1). Consistent with previous reports, aromatase was expressed in a subset of cells largely restricted to the social behavior network with the largest population located in the posterodorsal MeA (MeApd; Figure 1C; Unger, et al., 2015; Yao, et al., 2017; Morris, et al., 2008; Newman, et al.,

1999). We cleared the intact mouse brain with a modified version of CLARITY (Dwyer et al 2019, Chung et al., 2013), and imaged the whole brain using lightsheet microscopy (Isogai et al., 2017; Menegas et al., 2015). The full brain was digitally reconstructed and aligned to the Allen reference brain to allow automated categorization by region. This approach allowed us to identify labeled neurons throughout the brain and to maintain the macroscopic organization of these cells (Figure 1C).

Population data: broad-scale brain regions

Next, we identified the inputome for aromatase-expressing neurons located in the MeApd. The MeApd of adult male and female aromatase-cre mice was stereotactically injected with double-floxed inverse orientation adeno-associated viruses that selectively express the EnvA receptor (TVA) and rabies glycoprotein (RG) in aromatase-expressing neurons following cre-based recombination (Figure 2A; see methods). Two weeks later, an avian G-deleted rabies virus was injected in the same location (Rabies-ΔG-eGFP). Endogenous tdTomato and eGFP-expressing 'starter neurons' were visible in the MeApd (Figure 2C). As above, rabies-infected brains were cleared, imaged with lightsheet microscopy, and aligned to the Allen reference atlas. GFP-positive neurons were automatically detected using a machine vision algorithm and manually curated to ensure accuracy (see methods; Menegas et al., 2015).

The number of neurons retrogradely labeled by rabies, which synapse directly on aromatase-expressing neurons in the MeApd ($\rightarrow$ MeA^{arom+}), were counted in all brain regions. The number of neurons labeled outside the MeA scaled linearly with the size of the initially infected 'starter neuron' population in the MeApd (Figure 2D; $B = 2.6$, [1.06, 4.1] 95% CI, $R^2 = 0.45$; $F = 12.9$, $p = 0.002$). Injections were performed unilaterally in either the right or left hemisphere and the vast majority of $\rightarrow$ MeA^{arom+} neurons were ipsilateral, indicating that the circuit that provides input to aromatase-expressing neurons in the MeA is largely contained within a single hemisphere (Figure 2E; Table 1; Percentage of Ipsi cells = 98.9 ± 0.24 SEM; t-test: $p = 0.0002$). Consistent with previous descriptions of inputs to the MeA (Scalia, et al., 1975), almost the entire identified inputome was restricted to subcortical regions (99.6%; Figure 2F). Even when looking at finer regions that span the brain (e.g., hippocampal formation), we find nearly all cells confined to the most ventral areas (Figure 7A). Taken together, we found that each 'starter neuron' is associated with more than 100 presynaptic neurons on average, and the overwhelming majority of these neurons were both ipsilateral and subcortical.

Synaptic input: coarse regions

Aligning our whole brain datasets to the Allen reference atlas allowed us to identify the location of each neuron with high specificity. An individual dataset typically had neurons distributed across many subcortical regions. An example of neurons identified in a single animal is shown in Figure 3. We divided the Allen atlas into 10 mutually exclusive brain regions spanning the full volume of the reference brain and used these regions to coarsely classify the inputome for aromatase-expressing MeApd neurons (Figure 4A,B; see methods). Only statistically significant sources of synaptic input are reported, unless otherwise noted. The majority of $\rightarrow$ MeA^{arom+} were located in the cerebral nuclei (59.7 ± 1.4 ; $t(17)=10.8$, $p<0.0001$), with additional significant populations of $\rightarrow$ MeA^{arom+} neurons in the hypothalamus (11 ± 1.1 ; $t(17)=2.5$, $p=0.01$), hippocampus (10 ± 0.8 ; $t(17)=3.26$, $p = 0.0023$), cortical subplate (8.9 ± 0.4 ; $t(17)=5.7$, $p<0.0001$) and olfactory regions (7.2 ± 0.35 ; $t(17)=5.2$, $p<0.0001$; Figure 4 B,C). A small but consistent population of $\rightarrow$ MeA^{arom+} neurons were identified in the thalamus (1.9 ± 0.2 ; $t(17)=2.05$, $p = 0.03$) and midbrain (0.9 ± 0.07 ; $t(17)=3.4$, $p = 0.0016$). Very few neurons were identified in the isocortex (0.36 ± 0.03 ; $t(17)=3.3$, $p=0.002$), even though the isocortex and cerebellum represent the two largest regions of the brain by volume. Inputs from the hindbrain (0.02 ± 0.003 ; $t(17)=1.5$, $p=0.076$) and cerebellum (0.009 ± 0.002 ; $t(17)=1$, $p=0.17$) did not reach statistical significance. This indicates that the densities of neurons in

the isocortex, cerebellum, midbrain, and hindbrain are very low while the densities of labeled neurons was highest in the cerebral nuclei, cortical subplate, and hypothalamus (Figure 4A; Figure 4-1). Because the midbrain, isocortex, hindbrain, and cerebellum each contained less than a single percent of the $\rightarrow\text{MeA}^{\text{arom}+}$ they were excluded from the main dataset. We have included a detailed summary of all inputs from these minor regions in the supplementary materials (see Figures 4-2,4-3,4-4; Table 2). Comparison of the cell counts to cell density is included (Figures 4-1, 5-1, 6-1, 7-1,8-1).

Synaptic input: finer-scale regions

Closer investigation of five primary sources of input to the aromatase-expressing neurons in the MeApd revealed a consistent presynaptic circuit. $\rightarrow\text{MeA}^{\text{arom}+}$ neurons in the cerebral nuclei were initially divided into the striatum (48.1 ± 1.2 ; $t(17)=10$, $p<0.0001$) and pallidum (11.6 ± 0.6 ; $t(17)=4.7$, $p<0.0001$; Figure 5A). Within the striatum, the MeA, including the 'starter neuron' population accounts for $20 \pm 1.3\%$ of the total $\rightarrow\text{MeA}^{\text{arom}+}$ neurons in the brain (Figure 5B; $t(17)=3.8$, $p=0.0007$). Regions that border the MeA, including CEA and CP, accounted for an additional (11 ± 0.6 ; $t(17)=4.7$, $p < 0.0001$) and (6.6 ± 0.6 ; $t(17)=2.6$, $p=0.01$) percentage of the overall inputome respectively (Figure 5B). Smaller populations of $\rightarrow\text{MeA}^{\text{arom}+}$ were identified in the IA (0.43 ± 0.04 ; $t(17)=2.7$, $p=0.0078$), nucleus accumbens (0.15 ± 0.014 ; $t(17)=2.6$, $p=0.009$), fundus of the striatum (0.11 ± 0.011 ; $t(17)=2.5$, $p=0.01$), lateral septal nucleus (0.15 ± 0.01 ; $t(17)=3$, $p=0.0037$), and septofimbrial nucleus (0.05 ± 0.006 ; $t(17)=2.0$, $p=0.034$) while the populations of $\rightarrow\text{MeA}^{\text{arom}+}$ in the rest of the striatal regions were not significant (Figure 5D). The largest pallidum projections include the globus pallidus, both external (3.25 ± 0.3 ; $t(17)=2.6$, $p=0.009$) and internal (1.5 ± 0.12 ; $t(17)=3.0$, $p=0.004$) segments; the substantia innominata (2.5 ± 0.2 ; $t(17)=3.2$, $p=0.0025$), the bed nuclei of the stria terminalis (0.61 ± 0.04 ; $t(17)=3.5$, $p=0.001$), and the diagonal band nucleus (0.5 ± 0.03 ; $t(17)=3.6$, $p=0.001$; Figure 5C).

The hypothalamus provided the second largest source of $\rightarrow\text{MeA}^{\text{arom}+}$ neurons with most inputs located in the lateral (4.5 ± 0.4 ; $t(17)=2.6$, $p=0.001$) and medial (3.1 ± 0.4 ; $t(17)=1.9$, $p=0.04$) zones, with a smaller contribution from the periventricular region (1.0 ± 0.06 ; $t(17)=3.9$, $p=0.0006$) and the periventricular zone (0.25 ± 0.03 ; $t(17)=2.4$, $p=0.01$; Figure 6A). The two hypothalamic regions providing the largest number of $\rightarrow\text{MeA}^{\text{arom}+}$ neurons to the inputome are the lateral hypothalamic area (2.0 ± 0.17 ; $t(17)=3.0$, $p=0.004$) and ventromedial hypothalamic nucleus (1.2 ± 0.16 ; $t(17)=1.9$, $p=0.04$; Figure 6A; Table 3).

Both the amygdala and hippocampus are critical for memory and contain large populations of $\rightarrow\text{MeA}^{\text{arom}+}$ neurons. Hippocampal $\rightarrow\text{MeA}^{\text{arom}+}$ neurons are primarily located in field CA3 (6.3 ± 0.6 ; $t(17)=2.7$, $p=0.007$), followed by field CA1 (2.5 ± 0.2 ; $t(17)=3.3$, $p = 0.002$) and CA2 (0.26 ± 0.2 ; $t(17)=2.8$, $p = 0.006$; Figure 7A). We also observed $\rightarrow\text{MeA}^{\text{arom}+}$ cells in the hippocampal-amygdaloid transition area (0.22 ± 0.02 ; $t(17)=2.7$, $p=0.00$). The hippocampus is a large structure that spans nearly the entire dorsal to ventral axis of the brain. The vast majority of $\rightarrow\text{MeA}^{\text{arom}+}$ neurons in the hippocampus were located in the posterior ventral hippocampus (Figure 7A).

The largest proportion of inputs from the cortical subplate originate in amygdalar nuclei (Figure 7B), including the posterior amygdalar nucleus (3.8 ± 0.2 ; $t(17)=4.0$, $p=0.0005$) and lateral amygdala (0.1 ± 0.01 ; $t(17)=2.3$, $p = 0.017$). The anterior and posterior basomedial (1.6 ± 0.1 ; $t(17)=3.3$, $p=0.002$; 1.6 ± 0.1 ; $t(17)=3.4$, $p=0.002$) and anterior and posterior basolateral (0.6 ± 0.06 ; $t(17)=2.6$, $p = 0.009$; 0.3 ± 0.024 ; $t(17)=2.8$, $p=0.006$) nuclei of the amygdala also each showed $\rightarrow\text{MeA}^{\text{arom}+}$ cells.

Within the olfactory areas (Figure 8A), the largest proportion of inputs originate in the cortical amygdalar (4.0 ± 0.3 ; $t(17)=3.8$, $p=0.0007$) and piriform (1.0 ± 0.06 ; $t(17)=4.4$, $p = 0.0002$) areas, as well as the accessory olfactory bulb (1.0 ± 0.1 ; $t(17)=2.4$, $p = 0.014$). Smaller contributions originate in the piriform

amygdalar area (0.38 ± 0.03 ; $t(17)=4.5$, $p=0.00017$), the postpiriform transition area (0.34 ± 0.03 ; $t(17)=2.8$, $p=0.0067$).

The largest proportion of input cells originating in the thalamus (Figure 8B) come from the reticular nucleus (0.9 ± 0.15 ; $t(17)=1.6$, $p=0.07$) though this population was variable between individuals and not statistically significant. Additional input came from the ventral group of the dorsal thalamus (0.33 ± 0.04 ; $t(17)=2.1$, $p=0.025$), with smaller contributions originating from the geniculate groups of the dorsal thalamus (0.2 ± 0.03 ; $t(17)=1.2$, $p=0.1$) ventral thalamus (0.08 ± 0.01 ; $t(17)=2.1$, $p=0.023$), midline group of the dorsal thalamus (0.11 ± 0.01 ; $t(17)=2.7$, $p=0.0002$), and lateral group of the dorsal thalamus (0.04 ± 0.005 ; $t(17)=2.0$, $p=0.03$).

Sex Differences in distribution of observed input cells

Because sex differences in the MeA, and specifically in MeA^{arom+} neurons, are well established (Cooke, et al., 2005; Yao et al., 2017; Billing et al., 2019) we investigated sex differences in synaptic input to MeA^{arom+} neurons. A regression analysis of the cell counts for all male regions against cell counts for all female regions indicated that the major regions providing synaptic input to MeA^{arom+} neurons are largely conserved across sexes (Figure 9; $R^2 = 0.60252$; $F = 39.4127$; $p < 0.00001$; linear regression). No significant difference was observed for sex when considering all regions (ANOVA: $F = 0.04$ $p = 0.83$); however, there was a significant interaction between region and sex (ANOVA: $F = 1.81$, $p = 0.01$) indicating that a subset of brain regions displayed sex differences in projections to MeA^{arom+} neurons. Post-hoc analyses revealed nine regions that provided more input in males and one region that provided more input in females (Figure 9). MeA^{arom+} neurons received more input from the AOB, basolateral amygdala (both anterior and ventral), CA1 region of the hippocampus, piriform areas, diagonal band nucleus, and lateral preoptic area in males and more input from the ventral premammillary nucleus in females ($p < 0.05$: permutation test; Table 4). Additionally, the fraction labeled neurons in the MeA, local to the injection site, was higher in females (29.2 ± 10.7) than males though this trend did not reach significance (13.0 ± 3.5 ; $p=0.08$: permutation test; Figure 9-1).

Discussion:

Social behaviors require an animal to detect and respond to specific stimuli that signal the identity of a conspecific: rivals, potential mates, and offspring each demand different behavioral responses. As a central component of the social behavior network the MeA plays an important role in interpreting chemicals used to convey social information and producing appropriate behavioral responses (Newman, et al., 1999; Bakker, et al., 2002; Yao, et al., 2017). Here, we focus on a population of neurons in the MeA that express the enzyme aromatase (Naftolin et al., 1975), which has been causally linked to social behaviors (Unger et al., 2015; Lee et al., 2014; Ishii et al., 2017). In this study we identify the broad constellation of synaptic inputs that allow aromatase-expressing MeA neurons to integrate social information. We show that these neurons receive input from an unexpectedly wide range of regions, with strong inputs from regions linked to chemosensation, memory, metabolism, and the networks underlying social behaviors and decision-making. (Figure 10)

Two regions that are classically associated with the MeA are the AOB and BNST (Scalia, et al., 1975). The MeA is often illustrated as the third node in the vomeronasal pathway: vomeronasal sensory neurons project to the AOB that in turn projects to the MeA (Scalia et al., 1975). Similarly, the BNST and MeA are together considered the extended amygdala, a collective region that processes sensory and social information (Marino, et al., 2016). Using classical retrograde tracing it has been previously shown that

most AOB neurons project to the MeA (De Olmos, et al., 1978; Bergan, et al., 2014, with aromatase neurons receiving input overwhelmingly from the anterior subdivision of the AOB (Billing, et al., 2019). Our tracing results demonstrate a clear input to aromatase-expressing MeA neurons from both the AOB and the BNST. However, the collective inputs from the AOB and BNST account for less than 2 percent of the overall $\rightarrow\text{MeA}^{\text{arom}+}$ neurons. This result should not be interpreted as evidence that few AOB neurons project to the MeA, but rather, it highlights the larger set of projections coming from areas other than the AOB and BNST. Aromatase-expressing neurons clearly have a wide-ranging role as integrators of information from inputs throughout the brain, illustrating the danger in thinking of the social behavior network as a simple feed-forward network. Moreover, our results indicate that many known *postsynaptic* targets of the MeA are also *presynaptic* inputs to aromatase expressing MeA neurons, suggesting that the MeA forms feedback loops with many regions in the social behavior network, even at the level of the population of aromatase-expressing neurons.

Nearly all $\rightarrow\text{MeA}^{\text{arom}+}$ neurons were located ipsilateral to the site of injection (Figure 1). This is consistent with previous findings (Canteras, et al., 1995; Bressler, et al., 1996; Bergan et al., 2014) and indicates that afferent sensory information from the left and right VNO is kept separate at least to the level of the MeA. The near complete ipsilateral bias seems surprising given the need to integrate both sides of the body in social behavior. One possibility is that chemical compounds activate each VNO similarly, reducing the need for integration between left and right sides. A second possibility is that, like the auditory system (Clemens, et al., 2015, Schnupp, et al., 2009) or visual system (Krapp, et al., 2001), internasal comparisons provide an additional line of sensory information (e.g. spatial location). In the latter case, our data suggests that internasal comparisons are likely done outside the MeA.

Despite representing more than 12.9% of the brain by volume, the cortex contained less than 0.5 percent of the total identified $\rightarrow\text{MeA}^{\text{arom}+}$ neurons. The only exception to this rule was the piriform cortex which processes olfactory information and provided clear input to aromatase neurons in the MeA, indicating an indirect route for arom+ neurons to integrate input from the main olfactory system with 'direct' vomeronasal input from the AOB. There is also a small input from the thalamus, which may represent an alternative pathway of directing cortical information to the arom+ MeA neurons. Indeed, integration between the main olfactory and vomeronasal systems is critical for adaptive social behaviors and these data indicate that inputs from both systems converge on $\text{MeA}^{\text{arom}+}$ with direct input from the AOB and multisynaptic input from the MOB. Consistent with the survival value of sex, parenting, and territorial defense, the brain regions that provide input to aromatase-expressing neurons are evolutionarily old and conserved (O'Connell, et al., 2011).

The vast majority of inputs to the aromatase-expressing MeA neurons were found in cerebral nuclei, hypothalamus, hippocampal formation, cortical subplate, and associated olfactory areas. The remaining regions collectively comprise less than 1.3% of total inputs. Thus, the inputome reported in this study suggests an integration of chemosensory input, emotional processing, memory, and sociosexual behavior regulation by MeA aromatase neurons. A combination of inputs from areas that provide information about the metabolic, reproductive, and attentional status of the animal implies a strong effect of the internal status of the animal on the activity of aromatase-expressing MeA cells that are likely integrated with input from regions involved in voluntary movement and the production of social behaviors. We will briefly discuss these specific inputs by their known functions in the following sections.

Areas involved in detecting chemosensory cues to drive specific sexual discrimination and sociosexual behaviors provide strong input to aromatase-expressing MeA neurons. Inputs from the ventromedial hypothalamus (VMH), posterolateral and posteromedial cortical amygdala (PLCO, PMCO), anterior basomedial amygdala (aBMA), the nucleus of the lateral olfactory tract (LT), and AOB were identified

(Nomoto and Lima 2015; Yang et al 2013; Maras and Petrulis 2008; Melis et al 2009; Hashikawa et al 2016; Moncho-Bogani et al 2005; Guo et al 2018). This result is consistent with previous data from MeA, PLCO, AOB, and LT which are involved in the interpretation of chemosensory signals (Vaz, et al., 2017; Root, et al., 2014; Sosulki, et al., 2011).

Research into aggression, parenting, and sex consistently implicate the ventromedial hypothalamus (Kim, et al., 2019; Wang, et al., 2015) and medial preoptic area (Numan, 1988) as control regions for these behaviors. Recent work highlights the important role of galanin-expressing neurons of the MPOA for parental behavior (Wu, et al., 2014; Kohl, et al., 2018), and a primary source of sensory input for galanin-expressing neurons is the MeA. The MPOA is necessary to produce sex-specific mating and parenting behaviors (Wei, et al., 2018). The MPOA also plays a role in driving positive reinforcement for social interactions (Hu, et al., 2021). By identifying an arom+ MeA neuron-specific interaction between the MPOA and MeA, we can propose a loop between the MeA and MPOA with the potential to mediate positive and negative sex-specific patterns in parental and direct social interaction behaviors. Additional input to arom+ MeA neurons from the perifornical area (PeFA), BNST, and amygdalohippocampal area (AHi) further strengthen the role of the identified MeA arom+ circuitry for parental behavior (Kohl, et al., 2018; Autry, et al., 2019; Lebow, et al., 2016). neurons. Combined with previous data showing afferent inputs from the MeA (Pardo-Bellever, et al., 2012), these data demonstrate that aromatase-expressing MeA neurons have direct access to a parenting circuit.

Activation of VMH neurons causes immediate territorial aggression (Lin, et al., 2011): this is believed to be, at least in part, due to the role of ESR1-expressing neurons in the VMH (Lee, et al., 2014). A distinct aggressive behavior, pup-directed aggression, has been linked to the perifornical area (PeF; Autry, et al., 2019), amygdalohippocampal transition area (HATA), and ventromedial hypothalamus. Each of the aggression-linked regions contain neurons that project to aromatase neurons in the MeA, consistent with the observation that chemical silencing of aromatase-expressing neurons in the MeA directly reduces aggression in both male and female mice (Unger, et al., 2015).

Social interactions can be strongly influenced by fear and anxiety in both animals and people (Beery, et al., 2015; Sarnoff, et al., 1961). We found that several nodes of the amygdalar fear network send direct input to MeA aromatase neurons. The central amygdala (CeA), basomedial amygdalar nucleus (BMA), bed nucleus of the stria terminalis (BNST), and zona incerta (ZI) had some of the densest projections to the MeA in the brain; each is tightly linked to regulating anxiety and fear responses (Adhikari et al 2015; Amano et al 2010; Duvarci, et al., 2011; Chou, et al., 2018). Initially, this might suggest is that aromatase-expressing neurons are directly involved in the fear response to predators. We think this is not the case as the aromatase-expressing neurons receive sensory information from a class of V1R neurons not associated with predator responses (Billing, et al., 2020; Isogai, et al., 2011). Instead, we predict that these inputs are more likely sculpting behaviors directed towards conspecifics (mates, competitors, and pups) based on the proximity of predators (Apfelbach et al., 2005).

MeA aromatase neurons receive direct input from the hippocampus, known for its role in memory formation and consolidation (Scoville, et al., 1957). Hippocampal inputs to the MeA were not evenly distributed throughout the hippocampus, but rather were concentrated in the posterior ventral hippocampus including the HATA, CA1, CA2, and CA3. These are also the hippocampal regions anatomically closest to the MeA. Previous data indicate that region CA2 is particularly involved in memory and spatial processing but is also highly receptive to social state and plays a role in the deduction of social novelty (Dudek, et al., 2016). Similarly, the MeA has been linked to social memory (Ferguson et al., 2001) and MeA aromatase neurons have been directly implicated in social discrimination (Yao et al., 2017). We identified direct input from the ventral tegmental area, and together these sources of input may

help elevate and reinforce responses to emotionally relevant stimuli (Zikopoulos, et al., 2012). We also identified inputs from areas involved in regulation of voluntary movement suggesting a potential for gating aromatase neuron-dependent behaviors.

A broad set of identified inputs to MeA aromatase neurons are associated with metabolic regulation, including the tuberal nucleus (TN), ventral premammillary nucleus (VPM), lateral hypothalamus (LH), and ventromedial hypothalamus (VMH). However, a hallmark of social behavior is that the pattern of social behaviors observed in young animals is different from those observed in adult animals. The transition from juvenile to adult behaviors depends on metabolic constraints including body weight and fat content (Castellano, et al., 2016). The observed input from brain regions that regulate metabolic state (Luo, et al., 2018; Donato, et al., 2010; Nisbett 1972; Berthoud and Munzberg 2011) further supports the role of the MeA as a node responsible for coordinating social behaviors in accord with internal state, reproductive readiness, and environmental contexts (Padilla et al., 2016). This suggests that information about sexual receptivity and readiness are integrated with other relevant cues about conspecifics in the aromatase-expressing cells in the MeA.

In accord with the role of MeA, and aromatase neurons, in sexually dimorphic social behaviors, the MeA displays structural, molecular, and functional sex differences (Nishizuka and Arai, 1981; De Vries et al., 1984; Cooke et al., 1999; Morris et al., 2008; Bergan et al., 2014; Billing et al., 2019). In fact, the domestication process of creating isogenic mouse strains may have accentuated sex-differences in circuit function (Chalfin, et al., 2014; Bansal, et al., 2021). We found that the broad pattern of regional inputs to aromatase-expressing MeA neurons was conserved across males and females; however, a number of regions displayed a quantitative difference in the percentage of inputs observed in males as compared to females. Of the ten regions identified as having a quantitative sex-difference, nine had more labeled neurons in males. One possible explanation for this male bias is that the percentage of connections made by aromatase-expressing neurons inside the MeA is higher in females as compared to males. This hypothesis is partially supported by our data, which indicates more neurons labeled in the female MeA versus the male MeA; however, this trend did not reach significance. To account for variability in the levels of starter neurons infection, our analyses here rely on normalizing cell counts in each region by the overall number of identified neurons, and therefore, we cannot distinguish between a reduction in the number of local connections versus an enhancement of long-range connections.

The regions displaying sex differences provide new insights into the function of aromatase-expressing MeA circuits. The ventral premammillary nucleus was the only region identified with more neurons labeled in females and this region has recently been identified as a critical mediator of maternal aggression (Motta, et al., 2013). This is consistent with the role of aromatase-expressing MeA neurons in aggression in female mice (Unger et al., 2015). Regions with more neurons in males are linked to fear and anxiety (Yang, Y, et al., 2017), social and contextual memory (Okuyama, et al., 2016), mate identification and olfaction (Cádiz-Morretti, B., 2016; Wang, L, 2020), regulation of neuropeptide secretion (Brown, 2016), and male-specific sexual behavior (Schmidt, et al., 2000). Still, like the social behaviors mediated by MeA arom+ neurons in mice, the circuits that mediate these behaviors are sculpted differently in males and females, and these differences in circuit connectivity likely support sex differences in social behavior.

Conclusions

We comprehensively identified the inputome of aromatase-expressing MeA neurons, finding the sources of direct synaptic input to aromatase-expressing MeA neurons through rabies-based circuit mapping in the intact brains from transgenic animals expressing cre-recombinase under the control of the aromatase

promoter. Presynaptic inputs were identified through a semiautomated algorithm, which provided an unbiased view of the circuit. Data from each individual is set in a standard reference frame that allows direct comparisons among brains, as well as to future datasets using a similar approach.

Our study confirms that known sources of synaptic input to MeA neurons (e.g., BNST and AOB) synapse specifically on arom+ neurons in the MeA. However, we also identified a broad set of subcortical inputs that have not been previously reported indicating that aromatase neurons in the MeA represent a critical node for integrating an array of internal states for the generation of social behaviors. The broad input to aromatase neurons reveals a framework that allows the aromatase-expressing MeA neurons to occupy a critical position in the social behavior network, with a role in nearly all known social behaviors ranging from parenting and reproduction to aggression and learning. While the overall pattern of inputs was similar in males and females, specific regions displayed sex differences in connectivity with aromatase-expressing MeA neurons further solidifying the role of these neurons as a control center for sex-specific social behaviors that are critical for survival.

Data Availability:

These data have been uploaded to ebrains online repository (Ref. 17110259) for future access and to allow reproducibility.

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Table Captions

Table 1: Ipsilateral bias across brain regions. The average percentage of cells, as well as the absolute count of cells, are shown for each region on the contralateral hemisphere to the injection site.

Table 2: Hypothalamic inputs to aromatase+ cells in the MeA. The hypothalamic regions of the aromatase-expressing MeA cells. The top row describes course hypothalamic àMeAarom+. Each column enumerates the sub-regions in each respective course region àMeAarom+ cells from the top row.

Table 3: Statistical analysis of observed input cells across brain regions. The average percentage of input cells observed in each brain region and the results of two t-tests performed on percentage of cells in each region. 1) T-tests performed to determine if there is any significant input from each brain region. 2) T-tests performed to determine if the input from a given region is larger than expected assuming inputs directly proportional to region volume. The percentage of brain area that each brain region encompasses is also presented for this analysis. Degrees of freedom and standard deviation for each test are also provided.

Table 4: Statistical analysis of sex differences in major input regions. The average percentage of input cells observed in each region for males (mean column 2; SEM column 3) and females (mean column 4; SEM column 5). The p-value obtained from performing a posthoc permutation test comparing the percentage of inputs for each region in male versus female mice (column 6). Posthoc analyses followed an ANOVA with repeated samples.

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Figure Captions

Figure 1. **Identifying aromatase-expressing (arom+) neurons in the mouse brain.** A) The aromatase enzyme mediates the conversion of testosterone into estradiol. B) Crossing aromatase-cre and A19 tdTomato reporter mice ensures that the tdTomato fluorescent protein is coexpressed with aromatase. C) A large population of aromatase-expressing cells is present in the posterodorsal MeA [arrow in (1) horizontal, (2) sagittal and (3) coronal view.

Figure 2. **Mapping the inputome of arom+ neurons in the MeA.** A) Conditional AAV vectors were injected in arom-Cre mice to express TVA, RG, and mCherry in arom+ neurons of the MeA. B) Ten days after AAV injection, G-deleted rabies (GFP) was injected at the same stereotaxic coordinates to infect arom+ 'starter neurons'; followed by 7 days for retrograde movement of rabies from arom+ neurons in the MeA to upstream neurons. C) Infected 'starter neurons' in the MeApd identified by simultaneous tdTomato and eGFP expression. D) The number of neurons labeled by GFP injection outside the MeA scales linearly with the number of 'starter neurons' infected in the MeApd. E) View through the dorsal aspect of the brain showing location of 'starter neurons' (red) and inputome (green) demonstrating that input cells are almost entirely ipsilateral to the injection site (see graph). F) Lateral view of same showing that most inputs originate from subcortical regions.

Figure 3. **Input cell numbers vary across subcortical brain regions.** A sampling of input cells observed in one individual after alignment to the Allen Brain Atlas demonstrates that inputs can be localized to subcortical regions brain-wide and that input cell density varies among brain regions. A) Ventral tegmental area (VTA). B) Bed nucleus of the stria terminalis (BNST). C) Hippocampal formation (HPF). D) Medial preoptic area (MPOA). E) Ventromedial hypothalamic nucleus (VMH). F) Caudoputamen (CP). G) Central amygdalar nucleus (CeA). H) Accessory olfactory bulb (AOB). Each scale bar is 500 μ m.

Figure 4. **Coarse population count of the MeA arom+ inputome.** Each input cell was assigned to one of 10 non-overlapping regions spanning the full volume of the reference brain. Defined regions are: cerebral nuclei (CNU), hypothalamus (H), Hippocampal formation (HPF), Cortical subplate (CTXsp), Olfactory areas (OF), Thalamus (TH), Midbrain (MB), Isocortex, Hindbrain (HB), and Cerebellum (CB). A) Graph showing the percentage of the average total observed input neurons found in each brain region relative to the volume of that brain region shows that some regions have either much higher or much lower density of inputs than would be expected if the cells were evenly distributed across the brain (straight line). B) Percentages of the average total number of input cells found in each defined brain region. C) Pie chart illustrating the proportions of inputome cells found in eight brain regions. Figures 4-1, 4-2, 4-3, and 4-4 are supporting Figure 4.

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Figure 5. **MeA arom+ inputome originating in the cerebral nuclei (CNU).** A) Left, a pie chart indicates the fraction of all labeled neurons in the CNU and the brain atlas depicts the position of hypothalamic regions. Right, bar graph depicts the percentages of input cells found in the striatum (STR) and pallidum (PAL) relative to the whole-brain inputome; pie chart shows the relative proportion of those cells within the cerebral nuclei alone. B) Locations of input neurons within the striatum: line graph shows relative density of cells in subregions of the striatum, bar graph shows relative distribution of inputs relative to the whole-brain inputome; pie chart shows the relative proportion of those cells within parts of the striatum. Regions: Medial amygdala (MEA), Central amygdala (CEA), Caudoputamen (CP), Intercalated amygdalar nucleus (IA), Anterior amygdalar area (AAA), Nucleus accumbens (ACB), Lateral septal nucleus (LS), Fundus of striatum (FS), Olfactory tubercle (OT), Septofimbrial nucleus (SF), Bed nucleus of the accessory olfactory tract (BA), Septohippocampal nucleus (SH). C) Locations of input neurons within the pallidum: bar graph shows relative distribution of inputs relative to the whole-brain inputome; pie chart shows the relative proportion of those cells within parts of the pallidum. Regions: External globus pallidus (GPe), Substantia innominata (SI), Internal globus pallidus (GPi), Bed nucleus of the stria terminalis (BNST), Diagonal band nucleus (NDB), Magnocellular nucleus (MA), Medial septal nucleus (MS), Triangular nucleus of septum (TRS). Figure 5-1 is supporting Figure 5.

Figure 6. **MeA arom+ inputome originating in the hypothalamus (HY).** A) Left, a pie chart indicates the fraction of all labeled neurons in the hypothalamus and the brain atlas depicts the position of hypothalamic regions. Right, bar graph depicts the percentages of input cells found in the five subregions of the hypothalamus relative to the whole-brain inputome; pie chart shows the relative proportion of those cells within those hypothalamic regions. Regions: Lateral zone (LZ), Medial zone (MEZ), Periventricular region (PVR), Periventricular zone (PVZ), Median eminence (ME). B) Locations of input neurons within the lateral zone of the hypothalamus: bar graph shows relative distribution of inputs relative to the whole-brain inputome; pie chart shows the relative proportion of those cells within parts of the medial zone. Regions: Lateral hypothalamic area (LHA), Tuberal nucleus (TU), Zona incerta (ZI), Lateral preoptic area (LPO), Subthalamic nucleus (STN), Paraventricular nucleus (PSTN), Retrochiasmatic area (RCH), Perifornical nucleus (PeF), Preparaventricular nucleus (PST). C) Locations of input neurons within the medial zone of the hypothalamus: bar graph shows relative distribution of inputs relative to the whole-brain inputome; pie chart shows the relative proportion of those cells within parts of the medial zone. Regions: Ventromedial hypothalamic nucleus (VMH), ventral premammillary nucleus (PMv), medial mammillary nucleus (MM), Medial preoptic nucleus (MPN), dorsal premammillary nucleus (PMd), Anterior hypothalamic nucleus (AHN), Posterior hypothalamic nucleus (PH), Tuberomammillary nucleus (TM), Supramammillary nucleus (SUM), Paraventricular hypothalamic nucleus (PVHd), Lateral mammillary nucleus (LM). Figure 6-1 is supporting Figure 6.

Figure 7. **MeA arom+ inputome originating in the hippocampal formation (HPF) and the cortical subplate (CTXsp).** A) Left, a pie chart indicates the fraction of all labeled neurons in the hippocampus and the brain atlas depicts the position of hippocampal regions. Right, bar graph depicts the percentages of input cells found in the regions of the hippocampal formation relative to the whole-brain inputome; pie chart shows the relative proportion of those cells within those regions. The lower inset image illustrates that input cells are located primarily in ventral portions of the HPF. Regions: Field CA1 (CA1), Field CA2 (CA2), Field CA3 (CA3), Entorhinal area (ENT), Hippocampal-amygdalar transition area (HATA), Prosubiculum (ProS), Dentate gyrus (DG), Presubiculum (PRE), Subiculum (SUB), Area prostriata (APr), Postsubiculum (POST), Paraventricular (PAR), Induseum

griseum (IG), Fasciola cinerea (FC). B) Left, a pie chart indicates the fraction of all labeled neurons in the cortical subplate and the brain atlas depicts the position of cortical subplate regions. Right, bar graph depicts the percentages of input cells found in the regions of the cortical subplate relative to the whole-brain inputome; pie chart shows the relative proportion of those cells within those regions. Regions: Posterior amygdalar nucleus (PA), Anterior basomedial amygdalar nucleus (BMAa), Posterior basomedial amygdalar nucleus (BMAp), Anterior basolateral amygdalar nucleus (BLAa), Ventral basolateral amygdalar nucleus (BLAv), Posterior basolateral amygdalar nucleus (BLAp), Lateral amygdalar nucleus (LA), Ventral endopiriform nucleus (EPv), Dorsal endopiriform nucleus (EPd), Claustrum (CLA). Figure 7-1 is supporting Figure 7.

Figure 8. **MeA arom+ inputome originating in the olfactory areas (OLF) and the thalamus (TH).**

A) Left, a pie chart indicates the fraction of all labeled neurons in olfactory areas and the brain atlas depicts the position of olfactory areas. Right, bar graph depicts the percentages of input cells found in subregions of the olfactory area relative to the whole-brain inputome; pie chart shows the relative proportion of those cells within those regions. Regions: Cortical amygdalar area (COA), piriform area (PIR), Accessory olfactory bulb (AOB), Piriform-amygdalar area (PAA), Postpiriform transition area (TR), Nucleus of the lateral olfactory tract (NLOT), Main olfactory bulb (MOB), Taenia tecta (TT), Anterior olfactory nucleus (AON), Dorsal peduncular area (DP). B) Left, a pie chart indicates the fraction of all labeled neurons in the thalamus and the brain atlas depicts the position of thalamic regions. Right, bar graph depicts the percentages of input cells found in subregions of the thalamus relative to the whole-brain inputome; pie chart shows the relative proportion of those cells within those regions. Regions: Reticular nucleus (RT), Ventral group of the dorsal thalamus (VENT), Dorsal geniculate group (GENd), Midline group of the dorsal thalamus (MTN), Ventral geniculate group (GENv), Intralaminar nuclei of the dorsal thalamus (ILM), Peripeduncular nucleus (PP), Lateral group of the dorsal thalamus (LAT), Medial group of the dorsal thalamus (MED), Epithalamus (EPI), Anterior group of the dorsal thalamus (ATN), Subparafascicular area (SPA), Subparafascicular nucleus (SPF). Figure 8-1 is supporting Figure 8.

Figure 9. **Sex differences in the inputome of aromatase-expressing cells in the MeA.** The average percentage of synaptic inputs to aromatase-expressing cells in the MeA compared for each region in males and females. Only regions that provide 0.5% of the overall input are shown and regions identified as having a statistically significant sex difference are shown in color ($p < 0.05$: Permutation post-hoc test following ANOVA with repeated measures on 'sex', 'region', and 'individual'). These regions include field CA1 (CA1), the accessory olfactory bulb (AOB), piriform area (PIR), piriform-amygdalar area (PAA), postpiriform transition area (TA), basolateral amygdalar nucleus- anterior (BLAa), basolateral amygdalar nucleus-ventral (BLAv), diagonal band nucleus (NDB), lateral preoptic area (LPO), and ventral premammillary nucleus (PMv). Regions lying above the line of unity represent a male bias and neurons lying to the right of the unity line indicate a female bias. Error bars indicate the standard errors of the mean (male: vertical; female: horizontal) for each region. Figure 9-1 is supporting Figure 9.

1165 Figure 10. **The inputome of aromatase-expressing cells in the MeA.** A) Illustration showing the
 1166 relative locations of the major inputs to the aromatase-expressing MeA cells throughout the brain as
 1167 defined by our data. Major regions are shaded to demonstrate that the included regions were
 1168 analyzed in groups and are considered components of a larger analysis region. These inputs were
 1169 selected based on their relative abundance in the data and behavioral significance as represented in
 1170 previous literature. B) A Venn diagram showing the relative distribution of the regions displayed in A
 1171 sorted by their reported roles in the production or modulation of Memory, Parenting and Aggression,
 1172 Metabolism, Socio-sexual Behaviors, and Fear and Anxiety behaviors.

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Supplementary Figure Captions

1185 Figure 4-1. **Input cell density in regions brain-wide.** Percentage of input cells in each coarse
 1186 region identified in the Allen Brain Atlas normalized to the volume of that region to determine cell
 1187 densities in each region are presented as A) graph and B) pie chart. The densest concentration of
 1188 input cells is found in the cortical subplate (CTXsp).

1189

1190 Figure 4-2. **MeA arom+ inputome originating in the midbrain (MB).** A) Bar graph depicts the
 1191 percentages of input cells found in major divisions of the midbrain relative to the whole-brain
 1192 inputome; pie chart shows the relative proportion of those cells within those regions. Regions: motor-
 1193 related midbrain regions (MBmot), sensory-related midbrain regions (MBsec), behavior-related
 1194 midbrain regions (MBsta). B) Inputs from motor-related midbrain regions: Bar graph depicts the
 1195 percentages of input cells found in major divisions of these regions relative to the whole-brain
 1196 inputome; pie chart shows the relative proportion of input cells within those regions. Regions:
 1197 Midbrain reticular nucleus (MRN), Superior colliculus [motor] (SCm), Ventral tegmental area (VTA),
 1198 Substantia nigra (SNr), Periaqueductal gray (PAG), Lateral terminal nucleus of accessory optic tract
 1199 (LT), Cuneiform nucleus (CUN), Red nucleus (RN), Retrorubal area of midbrain reticular nucleus
 1200 (RR), Paratrochlar nucleus (Pa4), Pretectal region (PRT), Medial terminal nucleus of accessory optic
 1201 tract (MT), Dorsal terminal nucleus of accessory optic tract (DT), Anterior tegmental nucleus (AT),
 1202 Ventral tegmental nucleus (VTN), Troclear nucleus (IV), Edinger-Westphal nucleus (EW), Medial
 1203 accessory oculomotor nucleus (MA3), Oculomotor nucleus (III), Paranigral nucleus (PN). C) Inputs
 1204 from sensory-related midbrain regions: Bar graph depicts the percentages of input cells found in
 1205 major divisions of these regions relative to the whole-brain inputome; pie chart shows the relative
 1206 proportion of input cells within those regions. Regions: Inferior colliculus (IC), Brachium of inferior
 1207 colliculus (NB), Subcommissural organ (SCO), Midbrain trigeminal nucleus (MEV), Parabigeminal
 1208 nucleus (PBG), Nucleus sagulum (SAG), Superior colliculus [sensory] (SCs).

1209 ****Less than 0.01% of MeA arom+ inputs originate in behavior-related midbrain area; most of those**
 1210 **cells are found in the Dorsal raphe nucleus (DR), Pedunculo pontine nucleus (PPN), and**
 1211 **Interpeduncular nucleus (IPN).**

1212

Figure 4-3. **MeA arom⁺ inputome originating in the Hindbrain (HB).** A) Whole hindbrain: Bar graph depicts the percentages of input cells found in major divisions of the hindbrain relative to the whole-brain inputome; pie chart shows the relative proportion of input cells within those regions. Regions: Motor-related medulla (MY-mot), Sensory-related medulla (MY-sen), Behavioral state medulla (MY-sat), Motor-related pons (P-mot), Sensory-related pons (P-sen), Behavioral state pons (P-sat). B) Only one of the behavior-state portions of the medulla, the nucleus raphe magnus (RM) contains inputs to arom⁺ cells in the MeA. C) Bar graph depicts the percentages of input cells found in major divisions of the motor-related medulla relative to the whole-brain inputome; pie chart shows the relative proportion of input cells within those regions. Two regions of the motor-related medulla provide inputs: the Gigantocellular reticular nucleus (GRN) and the Facial motor nucleus (VII). D) The caudal part of the pontine reticular nucleus (PRNc) is the only part of the motor-related pons to provide inputs to arom⁺ MeA cells. E) In the sensory-related pons, inputs originate from the parabrachial nucleus (PB) and the nucleus of the lateral lemniscus (NLL).

Figure 4-4. **MeA arom⁺ inputome originating in the Isocortex and the Cerebellum (CB).** A) Bar graph depicts the percentages of input cells found in major divisions of the isocortex relative to the whole-brain inputome; pie chart shows the relative proportion of input cells within those regions. Regions: Secondary motor area (MOs), Agranular insular area (AI), Orbital area (ORB), Temporal association area (Tea), Ectorhinal area (ECT), Visceral area (VISC), Anterior cingulate area (ACA), Infralimbic area (ILA), Primary motor area (MOp), Supplementary somatosensory area (SSs), Gustatory areas (GU), Auditory areas (AUD), Visual areas (VIS), Primary somatosensory area (SSp), Prelimbic area (PL), Perirhinal area (PERI), Posterior parietal association areas (PTLp), Retrosplenial area (RSP). B) Inputs from the cerebellum are only found in the cerebellar cortex (CBX).

Figure 5-1. **Input cell density in the cerebral nuclei (CNU).** A) Input cell densities of constituent regions of the cerebral nuclei. B) Input cell densities of constituent regions in the striatum. C) Input cell densities of constituent regions in the pallidum. Results are presented as both bar and pie charts.

Figure 6-1. **Input cell density in the hypothalamus (HY).** A) Input cell densities of constituent regions in the hypothalamus. B) Input cell densities of constituent regions in the lateral zone of the hypothalamus. C) Input cell densities of constituent regions in the medial zone of the hypothalamus. Results are presented as both bar chart and pie charts.

Figure 7-1. **Input cell density in the hippocampal formation (HPF) and the cortical subplate (CTXsp).** A) Input cell densities of constituent regions in the hippocampal formation. B) Input cell densities of constituent regions in the cortical subplate. Results are presented as both bar and pie charts.

Figure 8-1. **Input cell density in the olfactory areas (OLF) and the thalamus (TH).** A) Input cell densities of constituent regions in the olfactory areas. B) Input cell densities of constituent regions in the thalamus. Results are presented as both bar and pie charts.

Figure 9-1. **Comparison of sex differences in observed inputs to MeA^{Arom⁺} Cells.** A) Graph comparing the fraction of labeled neurons in the MeA, local to the injection site, in females and males. B) graph showing the d-prime values for sex differences in the regions presented in Figure 9.

a Cerebral Nuclei (CNU)

% of cells in whole brain

proportion of cells in region

b Striatum (STR)

c Pallidum (PAL)

a Hypothalamus (HY)

% of cells in whole brain

proportion of cells in region

b Lateral zone (LZ)

c Medial zone (MEZ)

+ Periventricular region (PVR): Areas contain 1.1% of MeA arom+ inputs, most cells originate in the DMH and MPO, with smaller contributions from the AVP, PVp, and AVPV.

++ Periventricular zone (PVZ): Areas contain less than 0.5% of MeA arom+ inputs, most cells originate in the ARH and PVi, with smaller contributions from the PVH and SO.

a Hippocampal formation (HPF)

proportion of cells in region

b Cortical subplate (CTXsp)

a Olfactory areas (OLF)

% of cells in whole brain

proportion of cells in region

b Thalamus (TH)

Region name	Contra percentage	Total number
Inferior colliculus	0	0
Basic cell groups and regions	0.770459457	82
Anterior amygdalar area	0	0
Periventricular hypothalamic nucleus, anterior part	85.71428571	6
Anterior cingulate area	75	3
Paraventricular hypothalamic nucleus	6	3
Infralimbic area	0	0
Intralaminar nuclei of the dorsal thalamus	2.631578947	1
Nucleus accumbens	1.538461538	2
Paraventricular hypothalamic nucleus, descending division	0	0
Lateral terminal nucleus of the accessory optic tract	0	0
Anterodorsal preoptic nucleus	4.347826087	1
Anterior hypothalamic nucleus	0	0
Agranular insular area	3.389830508	2
Interpeduncular nucleus	50	1
Periventricular hypothalamic nucleus, intermediate part	48.35164835	44
Periventricular hypothalamic nucleus, posterior part	8.333333333	3
Midbrain reticular nucleus	6.666666667	1
Lateral amygdalar nucleus	0	0
Periventricular hypothalamic nucleus, preoptic part	22.91666667	11
Lateral group of the dorsal thalamus	0	0
Accessory olfactory bulb	0	0
Anterior olfactory nucleus	0	0
Retrochiasmatic area	0	0
Lateral hypothalamic area	0.412654746	6
Nucleus raphe magnus	50	1
Lateral mammillary nucleus	10	1
Red nucleus	0	0
Arcuate hypothalamic nucleus	12.85714286	9
Lateral preoptic area	1.308900524	5
Lateral septal nucleus	1.015228426	2
Midbrain reticular nucleus, retrorubral area	0	0
Auditory areas	0	0
Reticular nucleus of the thalamus	0	0
Anteroventral preoptic nucleus	1.785714286	2
Anteroventral periventricular nucleus	6.25	5
Suprachiasmatic nucleus	66.66666667	2
Bed nucleus of the accessory olfactory tract	0	0
Superior colliculus, motor related	0	0
Magnocellular nucleus	0	0
Basolateral amygdalar nucleus, anterior part	0	0
Septofimbrial nucleus	5.263157895	2
Basolateral amygdalar nucleus, posterior part	0.307692308	1
Primary somatosensory area	0	0
Basomedial amygdalar nucleus, anterior part	0.102092905	2
Accessory supraoptic group	0	0

Basomedial amygdalar nucleus, posterior part	0.064683053	1
Subfornical organ	0	0
Substantia innominata	0	0
Subparaventricular zone	50	3
Bed nuclei of the stria terminalis	0.333889816	2
Preparasubthalamic nucleus	0	0
Parasubthalamic nucleus	0.641025641	1
Substantia nigra, compact part	100	1
Supplemental somatosensory area	75	3
Substantia nigra, reticular part	0	0
Field CA1	0	0
Supraoptic nucleus	0	0
Medial amygdalar nucleus	0.008221656	1
Field CA2	0	0
Medial group of the dorsal thalamus	10	1
Basolateral amygdalar nucleus, ventral part	0.241545894	1
Median preoptic nucleus	33.33333333	1
Field CA3	0.027307482	1
Subthalamic nucleus	0	0
Medial mammillary nucleus	12.40310078	32
Subiculum	0	0
Main olfactory bulb	84.44444444	38
Medial preoptic nucleus	2.459016393	6
Medial preoptic area	1.742160279	5
Supramammillary nucleus	14.66666667	11
Cerebellar cortex	0	0
Central amygdalar nucleus	0.010026068	1
Temporal association areas	6.25	1
Tuberomammillary nucleus	18.75	9
Medial septal nucleus	15.55555556	35
Postpiriform transition area	0.869565217	4
Midline group of the dorsal thalamus	6.140350877	7
Nucleus of the brachium of the inferior colliculus	0	0
Triangular nucleus of septum	0	0
Clastrum	0	0
Taenia tecta	0	0
Diagonal band nucleus	4.625199362	29
Nucleus of the lateral lemniscus	100	1
Tuberal nucleus	1.587301587	7
Cuneiform nucleus	0	0
Nucleus of the lateral olfactory tract	0	0
Cortical amygdalar area	0.138197899	5
Ventral group of the dorsal thalamus	0	0
Facial motor nucleus	0	0
Visual areas	0	0
Caudoputamen	0.095739588	2
Visceral area	0	0

Ventrolateral preoptic nucleus	0	0
Ventromedial hypothalamic nucleus	8.396946565	55
Orbital area	28.57142857	2
Dentate gyrus	0	0
Ventral tegmental area	0	0
Olfactory tubercle	0	0
Posterior amygdalar nucleus	0.062558649	2
Piriform-amygdalar area	0	0
Periaqueductal gray	20	1
Zona incerta	0	0
Dorsal peduncular area	0	0
Dorsomedial nucleus of the hypothalamus	19.7080292	54
Parabrachial nucleus	0	0
Dorsal nucleus raphe	50	1
Ectorhinal area	0	0
Entorhinal area	0	0
Posterodorsal preoptic nucleus	0	0
Perirhinal area	0	0
Posterior hypothalamic nucleus	13.06818182	23
Endopiriform nucleus, dorsal part	0	0
Epithalamus	50	1
Piriform area	0.415973378	5
Endopiriform nucleus, ventral part	0	0
Prelimbic area	0	0
Dorsal premammillary nucleus	9.395973154	14
Primary motor area	40	2
Secondary motor area	90.47619048	19
Fundus of striatum	0	0
Ventral premammillary nucleus	3.816793893	10
Geniculate group, dorsal thalamus	0	0
Geniculate group, ventral thalamus	0	0
Globus pallidus, external segment	0	0
Globus pallidus, internal segment	0	0
Peripeduncular nucleus	0	0
Gigantocellular reticular nucleus	100	1
Pedunculopontine nucleus	0	0
Gustatory areas	0	0
Presubiculum	0	0
Pontine reticular nucleus, caudal part	100	1
Pretectal region	0	0
Intercalated amygdalar nucleus	0	0
Parastrial nucleus	0	0
Prosubiculum	0	0
Ventromedial preoptic nucleus	25	1
Perifornical nucleus	0	0
Hippocampo-amygdalar transition area	0.534759358	1
Paratrochlear nucleus	0	0

of contra cells

Periventricular region	Periventricular zone	Hypothalamic medial zone	Hypothalamic lateral zone
Anterodorsal preoptic nucleus	Paraventricular hypothalamic nucleus	Anterior hypothalamic nucleus	Lateral Hypothalamic area
Anteroventral preoptic nucleus	Periventricular hypothalamic nucleus, anterior	Medial mammillary nucleus	Lateral preoptic area
Anteroventral periventricular nucleus	Periventricular hypothalamic nucleus, intermediate	Supramammillary nucleus	Parasubthalamic nucleus
Dorsomedial nucleus of the hypothalamus	Arcuate hypothalamic nucleus	Tuberomammillary nucleus	Perifornical nucleus
Medial preoptic area		Medial preoptic nucleus	Retrochiasmatic area
Posterodorsal preoptic nucleus		Dorsal premammillary nucleus	Subthalamic nucleus
Parastrial nucleus		Ventral premammillary nucleus	Tuberal nucleus
Periventricular hypothalamic nucleus, posterior		Ventromedial hypothalamic nucleus	Zona incerta
Periventricular hypothalamic nucleus, preoptic		Posterior hypothalamic nucleus	

Ventrolateral preoptic nucleus			
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Superior central nucleus raphe: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Superior central nucleus raphe: ttest pval: NaN; tstat : NaN;
 df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.13627
 Superior central nucleus raphe: ttest pval (scaled--expected based
 on size): 1; tstat : -Inf; df : 17; sd : 0

Locus ceruleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Locus ceruleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.0031612
 Locus ceruleus: ttest pval (scaled--expected based on size): 1;
 tstat : -Inf; df : 17; sd : 0

Laterodorsal tegmental nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Laterodorsal tegmental nucleus: ttest pval: NaN; tstat : NaN;
 df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.044372
 Laterodorsal tegmental nucleus: ttest pval (scaled--expected based
 on size): 1; tstat : -Inf; df : 17; sd : 0

Nucleus incertus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Nucleus incertus: ttest pval: NaN; tstat : NaN; df : 17; sd :
 0
 Test against a Expected # of cells based on region size 0.023008
 Nucleus incertus: ttest pval (scaled--expected based on size): 1;
 tstat : -Inf; df : 17; sd : 0

Pontine reticular nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Pontine reticular nucleus: ttest pval: NaN; tstat : NaN; df :
 17; sd : 0
 Test against a Expected # of cells based on region size 0.54093
 Pontine reticular nucleus: ttest pval (scaled--expected based on
 size): 1; tstat : -Inf; df : 17; sd : 0

Nucleus raphe pontis: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Nucleus raphe pontis: ttest pval: NaN; tstat : NaN; df : 17;
 sd : 0
 Test against a Expected # of cells based on region size 0.020984
 Nucleus raphe pontis: ttest pval (scaled--expected based on size):
 1; tstat : -Inf; df : 17; sd : 0

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Subceruleus nucleus:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Subceruleus nucleus:      ttest  pval:  NaN;    tstat : NaN;    df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.0057519
Subceruleus nucleus:      ttest  pval (scaled--expected based on size):
1;    tstat : -Inf;    df : 17;    sd : 0
-----

Sublaterodorsal nucleus:  Mean:  0 +/- 0 SEM
Test against a mean of 0
Sublaterodorsal nucleus:  ttest  pval:  NaN;    tstat : NaN;    df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.010241
Sublaterodorsal nucleus:  ttest  pval (scaled--expected based on
size): 1;    tstat : -Inf;    df : 17;    sd : 0
-----

Nucleus of the lateral lemniscus:      Mean:  0.00044941 +/- 0.00011216
SEM
Test against a mean of 0
Nucleus of the lateral lemniscus:      ttest  pval:  0.16567;    tstat : 1;
df : 17;    sd : 0.0019067
Test against a Expected # of cells based on region size 0.25004
Nucleus of the lateral lemniscus:      ttest  pval (scaled--expected based
on size): 1;    tstat : -555.3697;    df : 17;    sd : 0.0019067
-----

Principal sensory nucleus of the trigeminal:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Principal sensory nucleus of the trigeminal:      ttest  pval:  NaN;
tstat : NaN;    df : 17;    sd : 0
Test against a Expected # of cells based on region size 0.24141
Principal sensory nucleus of the trigeminal:      ttest  pval (scaled--
expected based on size): 1;    tstat : -Inf;    df : 17;    sd : 0
-----

parabrachial nucleus:      Mean:  0.0017976 +/- 0.00044863 SEM
Test against a mean of 0
parabrachial nucleus:      ttest  pval:  0.16567;    tstat : 1;    df : 17;
sd : 0.0076267
Test against a Expected # of cells based on region size 0.29638
parabrachial nucleus:      ttest  pval (scaled--expected based on size):
1;    tstat : -163.8736;    df : 17;    sd : 0.0076267
-----

Superior olivary complex:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Superior olivary complex:      ttest  pval:  NaN;    tstat : NaN;    df :
17;    sd : 0

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Test against a Expected # of cells based on region size 0.20263
Superior olivary complex: ttest pval (scaled--expected based on
size): 1; tstat : -Inf; df : 17; sd : 0

Abducens nucleus: Mean: 0 +/- 0 SEM
Test against a mean of 0
Abducens nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd :
0
Test against a Expected # of cells based on region size 0.0080405
Abducens nucleus: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Facial motor nucleus: Mean: 0.00059285 +/- 0.00014795 SEM
Test against a mean of 0
Facial motor nucleus: ttest pval: 0.16567; tstat : 1; df : 17;
sd : 0.0025152
Test against a Expected # of cells based on region size 0.20784
Facial motor nucleus: ttest pval (scaled--expected based on size):
1; tstat : -349.5866; df : 17; sd : 0.0025152

Accessory facial motor nucleus: Mean: 0 +/- 0 SEM
Test against a mean of 0
Accessory facial motor nucleus: ttest pval: NaN; tstat : NaN;
df : 17; sd : 0
Test against a Expected # of cells based on region size 0.0011986
Accessory facial motor nucleus: ttest pval (scaled--expected based
on size): 1; tstat : -Inf; df : 17; sd : 0

Nucleus ambiguus: Mean: 0 +/- 0 SEM
Test against a mean of 0
Nucleus ambiguus: ttest pval: NaN; tstat : NaN; df : 17; sd :
0
Test against a Expected # of cells based on region size 0.0093817
Nucleus ambiguus: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Dorsal motor nucleus of the vagus nerve: Mean: 0 +/- 0 SEM
Test against a mean of 0
Dorsal motor nucleus of the vagus nerve: ttest pval: NaN; tstat :
NaN; df : 17; sd : 0
Test against a Expected # of cells based on region size 0.037822
Dorsal motor nucleus of the vagus nerve: ttest pval (scaled--
expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Gigantocellular reticular nucleus: Mean: 0.003247 +/- 0.00081034 SEM
Test against a mean of 0

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Gigantocellular reticular nucleus: ttest pval: 0.16567; tstat : 1; df : 17; sd : 0.013776

Test against a Expected # of cells based on region size 0.60393

Gigantocellular reticular nucleus: ttest pval (scaled--expected based on size): 1; tstat : -184.9991; df : 17; sd : 0.013776

Infracerebellar nucleus: Mean: 0 +/- 0 SEM

Test against a mean of 0

Infracerebellar nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.011742

Infracerebellar nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Inferior olivary complex: Mean: 0 +/- 0 SEM

Test against a mean of 0

Inferior olivary complex: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.11344

Inferior olivary complex: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Intermediate reticular nucleus: Mean: 0 +/- 0 SEM

Test against a mean of 0

Intermediate reticular nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.60413

Intermediate reticular nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Inferior salivatory nucleus: Mean: 0 +/- 0 SEM

Test against a mean of 0

Inferior salivatory nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.0015619

Inferior salivatory nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Linear nucleus of the medulla: Mean: 0 +/- 0 SEM

Test against a mean of 0

Linear nucleus of the medulla: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.013405

Linear nucleus of the medulla: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

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Lateral reticular nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Lateral reticular nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.13335
 Lateral reticular nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Magnocellular reticular nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Magnocellular reticular nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.11764
 Magnocellular reticular nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Medullary reticular nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Medullary reticular nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.44487
 Medullary reticular nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Parvicellular reticular nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Parvicellular reticular nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.49066
 Parvicellular reticular nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Parasolitary nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Parasolitary nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.006139
 Parasolitary nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Paragigantocellular reticular nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Paragigantocellular reticular nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.21407
 Paragigantocellular reticular nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

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-----
Perihypoglossal nuclei:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Perihypoglossal nuclei:      ttest  pval:  NaN;   tstat : NaN;   df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.07651
Perihypoglossal nuclei:      ttest  pval (scaled--expected based on size):
1;   tstat : -Inf;   df : 17;   sd : 0
-----

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-----
Parapyramidal nucleus:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Parapyramidal nucleus:      ttest  pval:  NaN;   tstat : NaN;   df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.02057
Parapyramidal nucleus:      ttest  pval (scaled--expected based on size):
1;   tstat : -Inf;   df : 17;   sd : 0
-----

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-----
Vestibular nuclei:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Vestibular nuclei:      ttest  pval:  NaN;   tstat : NaN;   df : 17;   sd
: 0
Test against a Expected # of cells based on region size 0.74321
Vestibular nuclei:      ttest  pval (scaled--expected based on size):  1;
tstat : -Inf;   df : 17;   sd : 0
-----

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```

-----
Nucleus x:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Nucleus x:      ttest  pval:  NaN;   tstat : NaN;   df : 17;   sd : 0
Test against a Expected # of cells based on region size 0.01238
Nucleus x:      ttest  pval (scaled--expected based on size):  1;   tstat
: -Inf;   df : 17;   sd : 0
-----

```

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-----
Hypoglossal nucleus:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Hypoglossal nucleus:      ttest  pval:  NaN;   tstat : NaN;   df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.061142
Hypoglossal nucleus:      ttest  pval (scaled--expected based on size):
1;   tstat : -Inf;   df : 17;   sd : 0
-----

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-----
Nucleus y:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Nucleus y:      ttest  pval:  NaN;   tstat : NaN;   df : 17;   sd : 0
Test against a Expected # of cells based on region size 0.0050966
Nucleus y:      ttest  pval (scaled--expected based on size):  1;   tstat
: -Inf;   df : 17;   sd : 0
-----

```

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Nucleus raphe magnus: Mean: 0.0010423 +/- 0.00018033 SEM
 Test against a mean of 0
 Nucleus raphe magnus: ttest pval: 0.083673; tstat : 1.4425; df : 17; sd : 0.0030655
 Test against a Expected # of cells based on region size 0.031972
 Nucleus raphe magnus: ttest pval (scaled--expected based on size): 1; tstat : -42.8057; df : 17; sd : 0.0030655

Nucleus raphe pallidus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Nucleus raphe pallidus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.01641
 Nucleus raphe pallidus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Nucleus raphe obscurus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Nucleus raphe obscurus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.013928
 Nucleus raphe obscurus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Area postrema: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Area postrema: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.012733
 Area postrema: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Cochlear nuclei: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Cochlear nuclei: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.41049
 Cochlear nuclei: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Dorsal column nuclei: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Dorsal column nuclei: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.09435
 Dorsal column nuclei: ttest pval (scaled--expected based on size):

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1; tstat : -Inf; df : 17; sd : 0

External cuneate nucleus: Mean: 0 +/- 0 SEM
Test against a mean of 0
External cuneate nucleus: ttest pval: NaN; tstat : NaN; df :
17; sd : 0
Test against a Expected # of cells based on region size 0.052097
External cuneate nucleus: ttest pval (scaled--expected based on
size): 1; tstat : -Inf; df : 17; sd : 0

Nucleus of the trapezoid body: Mean: 0 +/- 0 SEM
Test against a mean of 0
Nucleus of the trapezoid body: ttest pval: NaN; tstat : NaN; df
: 17; sd : 0
Test against a Expected # of cells based on region size 0.0397
Nucleus of the trapezoid body: ttest pval (scaled--expected based on
size): 1; tstat : -Inf; df : 17; sd : 0

Nucleus of the solitary tract: Mean: 0 +/- 0 SEM
Test against a mean of 0
Nucleus of the solitary tract: ttest pval: NaN; tstat : NaN; df
: 17; sd : 0
Test against a Expected # of cells based on region size 0.19355
Nucleus of the solitary tract: ttest pval (scaled--expected based on
size): 1; tstat : -Inf; df : 17; sd : 0

Spinal nucleus of the trigeminal, caudal part: Mean: 0 +/- 0 SEM
Test against a mean of 0
Spinal nucleus of the trigeminal, caudal part: ttest pval: NaN;
tstat : NaN; df : 17; sd : 0
Test against a Expected # of cells based on region size 0.3686
Spinal nucleus of the trigeminal, caudal part: ttest pval (scaled--
expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Spinal nucleus of the trigeminal, interpolar part: Mean: 0 +/- 0 SEM
Test against a mean of 0
Spinal nucleus of the trigeminal, interpolar part: ttest pval: NaN;
tstat : NaN; df : 17; sd : 0
Test against a Expected # of cells based on region size 0.4143
Spinal nucleus of the trigeminal, interpolar part: ttest pval
(scaled--expected based on size): 1; tstat : -Inf; df : 17; sd :
0

Spinal nucleus of the trigeminal, oral part: Mean: 0 +/- 0 SEM
Test against a mean of 0
Spinal nucleus of the trigeminal, oral part: ttest pval: NaN;

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tstat : NaN; df : 17; sd : 0
Test against a Expected # of cells based on region size 0.21959
Spinal nucleus of the trigeminal, oral part: ttest pval (scaled--
expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Paratrigeminal nucleus: Mean: 0 +/- 0 SEM
Test against a mean of 0
Paratrigeminal nucleus: ttest pval: NaN; tstat : NaN; df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.029041
Paratrigeminal nucleus: ttest pval (scaled--expected based on size):
1; tstat : -Inf; df : 17; sd : 0

Barrington's nucleus: Mean: 0 +/- 0 SEM
Test against a mean of 0
Barrington's nucleus: ttest pval: NaN; tstat : NaN; df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.0033751
Barrington's nucleus: ttest pval (scaled--expected based on size):
1; tstat : -Inf; df : 17; sd : 0

Dorsal tegmental nucleus: Mean: 0 +/- 0 SEM
Test against a mean of 0
Dorsal tegmental nucleus: ttest pval: NaN; tstat : NaN; df :
17; sd : 0
Test against a Expected # of cells based on region size 0.022536
Dorsal tegmental nucleus: ttest pval (scaled--expected based on
size): 1; tstat : -Inf; df : 17; sd : 0

Posterodorsal tegmental nucleus: Mean: 0 +/- 0 SEM
Test against a mean of 0
Posterodorsal tegmental nucleus: ttest pval: NaN; tstat : NaN;
df : 17; sd : 0
Test against a Expected # of cells based on region size 0.010397
Posterodorsal tegmental nucleus: ttest pval (scaled--expected based
on size): 1; tstat : -Inf; df : 17; sd : 0

Pontine central gray: Mean: 0 +/- 0 SEM
Test against a mean of 0
Pontine central gray: ttest pval: NaN; tstat : NaN; df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.14153
Pontine central gray: ttest pval (scaled--expected based on size):
1; tstat : -Inf; df : 17; sd : 0

Pontine gray: Mean: 0 +/- 0 SEM

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Test against a mean of 0
Pontine gray:      ttest  pval: NaN;   tstat : NaN;   df : 17;   sd : 0
Test against a Expected # of cells based on region size 0.21287
Pontine gray:      ttest  pval (scaled--expected based on size):  1;
tstat : -Inf;   df : 17;   sd : 0
-----

Pontine reticular nucleus, caudal part:      Mean:  0.003247 +/-
0.00081034 SEM
Test against a mean of 0
Pontine reticular nucleus, caudal part:      ttest  pval:  0.16567;
tstat : 1;   df : 17;   sd : 0.013776
Test against a Expected # of cells based on region size 0.54369
Pontine reticular nucleus, caudal part:      ttest  pval (scaled--expected
based on size):  1;   tstat : -166.4446;   df : 17;   sd : 0.013776
-----

Supragenua nucleus:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Supragenua nucleus:      ttest  pval:  NaN;   tstat : NaN;   df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.0037724
Supragenua nucleus:      ttest  pval (scaled--expected based on size):
1;   tstat : -Inf;   df : 17;   sd : 0
-----

Supratrigeminal nucleus:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Supratrigeminal nucleus:      ttest  pval:  NaN;   tstat : NaN;   df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.056501
Supratrigeminal nucleus:      ttest  pval (scaled--expected based on
size):  1;   tstat : -Inf;   df : 17;   sd : 0
-----

Tegmental reticular nucleus:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Tegmental reticular nucleus:      ttest  pval:  NaN;   tstat : NaN;   df :
17;   sd : 0
Test against a Expected # of cells based on region size 0.18094
Tegmental reticular nucleus:      ttest  pval (scaled--expected based on
size):  1;   tstat : -Inf;   df : 17;   sd : 0
-----

Motor nucleus of trigeminal:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Motor nucleus of trigeminal:      ttest  pval:  NaN;   tstat : NaN;   df :
17;   sd : 0
Test against a Expected # of cells based on region size 0.07705
Motor nucleus of trigeminal:      ttest  pval (scaled--expected based on
size):  1;   tstat : -Inf;   df : 17;   sd : 0
-----

```

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Peritrigeminal zone: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Peritrigeminal zone: ttest pval: NaN; tstat : NaN; df : 17;
 sd : 0
 Test against a Expected # of cells based on region size 0.069662
 Peritrigeminal zone: ttest pval (scaled--expected based on size):
 1; tstat : -Inf; df : 17; sd : 0

Accessory trigeminal nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Accessory trigeminal nucleus: ttest pval: NaN; tstat : NaN; df
 : 17; sd : 0
 Test against a Expected # of cells based on region size 0.0031035
 Accessory trigeminal nucleus: ttest pval (scaled--expected based on
 size): 1; tstat : -Inf; df : 17; sd : 0

Parvicellular motor 5 nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Parvicellular motor 5 nucleus: ttest pval: NaN; tstat : NaN; df
 : 17; sd : 0
 Test against a Expected # of cells based on region size 0.018285
 Parvicellular motor 5 nucleus: ttest pval (scaled--expected based on
 size): 1; tstat : -Inf; df : 17; sd : 0

Intertrigeminal nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Intertrigeminal nucleus: ttest pval: NaN; tstat : NaN; df : 17;
 sd : 0
 Test against a Expected # of cells based on region size 0.0095718
 Intertrigeminal nucleus: ttest pval (scaled--expected based on
 size): 1; tstat : -Inf; df : 17; sd : 0

Field CA1: Mean: 2.4885 +/- 0.18631 SEM
 Test against a mean of 0
 Field CA1: ttest pval: 0.0019677; tstat : 3.3334; df : 17; sd
 : 3.1672
 Test against a Expected # of cells based on region size 2.6586
 Field CA1: ttest pval (scaled--expected based on size): 0.58877;
 tstat : -0.22787; df : 17; sd : 3.1672

Field CA2: Mean: 0.25768 +/- 0.023006 SEM
 Test against a mean of 0
 Field CA2: ttest pval: 0.0062132; tstat : 2.7953; df : 17; sd
 : 0.3911
 Test against a Expected # of cells based on region size 0.12892
 Field CA2: ttest pval (scaled--expected based on size): 0.090217;

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tstat : 1.3968; df : 17; sd : 0.3911

FieldCa3: Mean: 6.3221 +/- 0.57746 SEM

Test against a mean of 0

FieldCa3: ttest pval: 0.0070927; tstat : 2.7323; df : 17; sd : 9.8169

Test against a Expected # of cells based on region size 1.8646

FieldCa3: ttest pval (scaled--expected based on size): 0.035471;
tstat : 1.9264; df : 17; sd : 9.8169

Dentate Gyrus: Mean: 0.018308 +/- 0.0028243 SEM

Test against a mean of 0

Dentate Gyrus: ttest pval: 0.06206; tstat : 1.6177; df : 17; sd : 0.048013

Test against a Expected # of cells based on region size 1.5904

Dentate Gyrus: ttest pval (scaled--expected based on size): 1;
tstat : -138.9174; df : 17; sd : 0.048013

Fasciola cinerea: Mean: 0 +/- 0 SEM

Test against a mean of 0

Fasciola cinerea: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.051896

Fasciola cinerea: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Induseum griseum: Mean: 0 +/- 0 SEM

Test against a mean of 0

Induseum griseum: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.052127

Induseum griseum: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Entorhinal area: Mean: 0.25717 +/- 0.026799 SEM

Test against a mean of 0

Entorhinal area: ttest pval: 0.014209; tstat : 2.3949; df : 17; sd : 0.45559

Test against a Expected # of cells based on region size 2.4996

Entorhinal area: ttest pval (scaled--expected based on size): 1;
tstat : -20.8826; df : 17; sd : 0.45559

Parasubiculum: Mean: 0 +/- 0 SEM

Test against a mean of 0

Parasubiculum: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
Test against a Expected # of cells based on region size 0.20365

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Parasubiculum: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Postsubiculum: Mean: 0 +/- 0 SEM
Test against a mean of 0
Postsubiculum: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
Test against a Expected # of cells based on region size 0.26263
Postsubiculum: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Presubiculum: Mean: 0.0087044 +/- 0.0014084 SEM
Test against a mean of 0
Presubiculum: ttest pval: 0.070691; tstat : 1.5424; df : 17;
sd : 0.023943
Test against a Expected # of cells based on region size 0.22907
Presubiculum: ttest pval (scaled--expected based on size): 1;
tstat : -39.0475; df : 17; sd : 0.023943

Subiculum: Mean: 0.0026964 +/- 0.00067294 SEM
Test against a mean of 0
Subiculum: ttest pval: 0.16567; tstat : 1; df : 17; sd :
0.01144
Test against a Expected # of cells based on region size 0.56318
Subiculum: ttest pval (scaled--expected based on size): 1; tstat
: -207.8597; df : 17; sd : 0.01144

Prosubiculum: Mean: 0.09977 +/- 0.012787 SEM
Test against a mean of 0
Prosubiculum: ttest pval: 0.034105; tstat : 1.9473; df : 17;
sd : 0.21737
Test against a Expected # of cells based on region size 0.31964
Prosubiculum: ttest pval (scaled--expected based on size): 0.99975;
tstat : -4.2914; df : 17; sd : 0.21737

Hippocampo-amygdalar transition area: Mean: 0.21843 +/- 0.020456 SEM
Test against a mean of 0
Hippocampo-amygdalar transition area: ttest pval: 0.0081639;
tstat : 2.6649; df : 17; sd : 0.34776
Test against a Expected # of cells based on region size 0.092798
Hippocampo-amygdalar transition area: ttest pval (scaled--expected
based on size): 0.07187; tstat : 1.5327; df : 17; sd : 0.34776

Area prostriata: Mean: 0 +/- 0 SEM
Test against a mean of 0
Area prostriata: ttest pval: NaN; tstat : NaN; df : 17; sd :
0

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Test against a Expected # of cells based on region size 0.071492
 Area prostriata: ttest pval (scaled--expected based on size): 1;
 tstat : -Inf; df : 17; sd : 0

Median eminence: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Median eminence: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.018196
 Median eminence: ttest pval (scaled--expected based on size): 1;
 tstat : -Inf; df : 17; sd : 0

Anterodorsal preoptic nucleus: Mean: 0.015989 +/- 0.0016003 SEM
 Test against a mean of 0
 Anterodorsal preoptic nucleus: ttest pval: 0.01163; tstat : 2.4934; df : 17; sd : 0.027206
 Test against a Expected # of cells based on region size 0.021989
 Anterodorsal preoptic nucleus: ttest pval (scaled--expected based on size): 0.81873; tstat : -0.93569; df : 17; sd : 0.027206

Anteroventral preoptic nucleus: Mean: 0.070683 +/- 0.0059333 SEM
 Test against a mean of 0
 Anteroventral preoptic nucleus: ttest pval: 0.0042651; tstat : 2.9731; df : 17; sd : 0.10087
 Test against a Expected # of cells based on region size 0.02003
 Anteroventral preoptic nucleus: ttest pval (scaled--expected based on size): 0.024012; tstat : 2.1306; df : 17; sd : 0.10087

Anteroventral periventricular nucleus: Mean: 0.051614 +/- 0.0055466 SEM
 Test against a mean of 0
 Anteroventral periventricular nucleus: ttest pval: 0.016441; tstat : 2.3224; df : 17; sd : 0.094292
 Test against a Expected # of cells based on region size 0.070762
 Anteroventral periventricular nucleus: ttest pval (scaled--expected based on size): 0.79953; tstat : -0.86153; df : 17; sd : 0.094292

Dorsomedial nucleus of the hypothalamus: Mean: 0.4397 +/- 0.047233 SEM
 Test against a mean of 0
 Dorsomedial nucleus of the hypothalamus: ttest pval: 0.016412; tstat : 2.3233; df : 17; sd : 0.80295
 Test against a Expected # of cells based on region size 0.081722
 Dorsomedial nucleus of the hypothalamus: ttest pval (scaled--expected based on size): 0.037863; tstat : 1.8915; df : 17; sd : 0.80295

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Median preoptic nucleus: Mean: 0.001908 +/- 0.00032727 SEM
 Test against a mean of 0
 Median preoptic nucleus: ttest pval: 0.081943; tstat : 1.455;
 df : 17; sd : 0.0055635
 Test against a Expected # of cells based on region size 0.01748
 Median preoptic nucleus: ttest pval (scaled--expected based on
 size): 1; tstat : -11.8748; df : 17; sd : 0.0055635

Medial preoptic area: Mean: 0.25786 +/- 0.019784 SEM
 Test against a mean of 0
 Medial preoptic area: ttest pval: 0.0023415; tstat : 3.2528; df
 : 17; sd : 0.33633
 Test against a Expected # of cells based on region size 0.12125
 Medial preoptic area: ttest pval (scaled--expected based on size):
 0.051482; tstat : 1.7233; df : 17; sd : 0.33633

Vascular organ of the lamina terminalis: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Vascular organ of the lamina terminalis: ttest pval: NaN; tstat :
 NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.0030865
 Vascular organ of the lamina terminalis: ttest pval (scaled--
 expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Posterodorsal preoptic nucleus: Mean: 0.0086461 +/- 0.00093346 SEM
 Test against a mean of 0
 Posterodorsal preoptic nucleus: ttest pval: 0.0168; tstat :
 2.3116; df : 17; sd : 0.015869
 Test against a Expected # of cells based on region size 0.0025228
 Posterodorsal preoptic nucleus: ttest pval (scaled--expected based
 on size): 0.059994; tstat : 1.6371; df : 17; sd : 0.015869

Parastrial nucleus: Mean: 0.012037 +/- 0.0015809 SEM
 Test against a mean of 0
 Parastrial nucleus: ttest pval: 0.037248; tstat : 1.9003; df :
 17; sd : 0.026875
 Test against a Expected # of cells based on region size 0.02096
 Parastrial nucleus: ttest pval (scaled--expected based on size):
 0.91151; tstat : -1.4086; df : 17; sd : 0.026875

Periventricular hypothalamic nucleus, posterior part: Mean: 0.069225
 +/- 0.0081592 SEM
 Test against a mean of 0
 Periventricular hypothalamic nucleus, posterior part: ttest pval:
 0.024635; tstat : 2.1174; df : 17; sd : 0.13871
 Test against a Expected # of cells based on region size 0.031252

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Periventricular hypothalamic nucleus, posterior part: ttest pval
(scaled--expected based on size): 0.13074; tstat : 1.1615; df : 17;
sd : 0.13871

Periventricular hypothalamic nucleus, preoptic part: Mean: 0.035883
+/- 0.0042756 SEM
Test against a mean of 0
Periventricular hypothalamic nucleus, preoptic part: ttest pval:
0.025751; tstat : 2.0945; df : 17; sd : 0.072685
Test against a Expected # of cells based on region size 0.045852
Periventricular hypothalamic nucleus, preoptic part: ttest pval
(scaled--expected based on size): 0.71587; tstat : -0.5819; df :
17; sd : 0.072685

Subparaventricular zone: Mean: 0.0041656 +/- 0.00060095 SEM
Test against a mean of 0
Subparaventricular zone: ttest pval: 0.050878; tstat : 1.7299;
df : 17; sd : 0.010216
Test against a Expected # of cells based on region size 0.023795
Subparaventricular zone: ttest pval (scaled--expected based on
size): 1; tstat : -8.152; df : 17; sd : 0.010216

Suprachiasmatic nucleus: Mean: 0.0046598 +/- 0.0010502 SEM
Test against a mean of 0
Suprachiasmatic nucleus: ttest pval: 0.14178; tstat : 1.1074;
df : 17; sd : 0.017853
Test against a Expected # of cells based on region size 0.02074
Suprachiasmatic nucleus: ttest pval (scaled--expected based on
size): 0.99932; tstat : -3.8213; df : 17; sd : 0.017853

Subfornical organ: Mean: 0.0011857 +/- 0.00029591 SEM
Test against a mean of 0
Subfornical organ: ttest pval: 0.16567; tstat : 1; df : 17;
sd : 0.0050305
Test against a Expected # of cells based on region size 0.025211
Subfornical organ: ttest pval (scaled--expected based on size): 1;
tstat : -20.263; df : 17; sd : 0.0050305

Ventromedial preoptic nucleus: Mean: 0.0059082 +/- 0.0010758 SEM
Test against a mean of 0
Ventromedial preoptic nucleus: ttest pval: 0.094157; tstat :
1.3706; df : 17; sd : 0.018288
Test against a Expected # of cells based on region size 0.023541
Ventromedial preoptic nucleus: ttest pval (scaled--expected based on
size): 0.99962; tstat : -4.0906; df : 17; sd : 0.018288

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Ventrolateral preoptic nucleus: Mean: 0.012442 +/- 0.0026021 SEM
 Test against a mean of 0
 Ventrolateral preoptic nucleus: ttest pval: 0.12458; tstat : 1.1933; df : 17; sd : 0.044236
 Test against a Expected # of cells based on region size 0.02605
 Ventrolateral preoptic nucleus: ttest pval (scaled--expected based on size): 0.89539; tstat : -1.3052; df : 17; sd : 0.044236

Supraoptic nucleus: Mean: 0.0081396 +/- 0.0014333 SEM
 Test against a mean of 0
 Supraoptic nucleus: ttest pval: 0.087242; tstat : 1.4172; df : 17; sd : 0.024367
 Test against a Expected # of cells based on region size 0.030766
 Supraoptic nucleus: ttest pval (scaled--expected based on size): 0.99947; tstat : -3.9397; df : 17; sd : 0.024367

Accessory supraoptic group: Mean: 0.0012484 +/- 0.00031157 SEM
 Test against a mean of 0
 Accessory supraoptic group: ttest pval: 0.16567; tstat : 1; df : 17; sd : 0.0052967
 Test against a Expected # of cells based on region size 0.0013174
 Accessory supraoptic group: ttest pval (scaled--expected based on size): 0.52172; tstat : -0.055272; df : 17; sd : 0.0052967

Paraventricular hypothalamic nucleus: Mean: 0.03159 +/- 0.0059345 SEM
 Test against a mean of 0
 Paraventricular hypothalamic nucleus: ttest pval: 0.10079; tstat : 1.3285; df : 17; sd : 0.10089
 Test against a Expected # of cells based on region size 0.044498
 Paraventricular hypothalamic nucleus: ttest pval (scaled--expected based on size): 0.70285; tstat : -0.54283; df : 17; sd : 0.10089

Periventricular hypothalamic nucleus, anterior part: Mean: 0.0051395 +/- 0.00090238 SEM
 Test against a mean of 0
 Periventricular hypothalamic nucleus, anterior part: ttest pval: 0.086644; tstat : 1.4214; df : 17; sd : 0.015341
 Test against a Expected # of cells based on region size 0.014353
 Periventricular hypothalamic nucleus, anterior part: ttest pval (scaled--expected based on size): 0.9896; tstat : -2.548; df : 17; sd : 0.015341

Periventricular hypothalamic nucleus, intermediate part: Mean: 0.082574 +/- 0.0049426 SEM
 Test against a mean of 0
 Periventricular hypothalamic nucleus, intermediate part: ttest pval:

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0.00032136; tstat : 4.1694; df : 17; sd : 0.084025
Test against a Expected # of cells based on region size 0.056755
Periventricular hypothalamic nucleus, intermediate part: ttest pval
(scaled--expected based on size): 0.10487; tstat : 1.3037; df : 17;
sd : 0.084025

Arcuate hypothalamic nucleus: Mean: 0.12561 +/- 0.023991 SEM
Test against a mean of 0
Arcuate hypothalamic nucleus: ttest pval: 0.10435; tstat :
1.3067; df : 17; sd : 0.40784
Test against a Expected # of cells based on region size 0.066881
Arcuate hypothalamic nucleus: ttest pval (scaled--expected based on
size): 0.27464; tstat : 0.61099; df : 17; sd : 0.40784

Lateral hypothalamic area: Mean: 2.007 +/- 0.16859 SEM
Test against a mean of 0
Lateral hypothalamic area: ttest pval: 0.0042832; tstat : 2.9711;
df : 17; sd : 2.866
Test against a Expected # of cells based on region size 0.47743
Lateral hypothalamic area: ttest pval (scaled--expected based on
size): 0.018459; tstat : 2.2643; df : 17; sd : 2.866

Lateral preoptic area: Mean: 0.35671 +/- 0.022095 SEM
Test against a mean of 0
Lateral preoptic area: ttest pval: 0.00043528; tstat : 4.0291;
df : 17; sd : 0.37562
Test against a Expected # of cells based on region size 0.12063
Lateral preoptic area: ttest pval (scaled--expected based on size):
0.0081346; tstat : 2.6666; df : 17; sd : 0.37562

Preparasubthalamic nucleus: Mean: 0.017012 +/- 0.0018394 SEM
Test against a mean of 0
Preparasubthalamic nucleus: ttest pval: 0.016913; tstat : 2.3082;
df : 17; sd : 0.031269
Test against a Expected # of cells based on region size 0.0039048
Preparasubthalamic nucleus: ttest pval (scaled--expected based on
size): 0.04661; tstat : 1.7784; df : 17; sd : 0.031269

Parasubthalamic nucleus: Mean: 0.29958 +/- 0.034813 SEM
Test against a mean of 0
Parasubthalamic nucleus: ttest pval: 0.023226; tstat : 2.1477;
df : 17; sd : 0.59182
Test against a Expected # of cells based on region size 0.041815
Parasubthalamic nucleus: ttest pval (scaled--expected based on
size): 0.041046; tstat : 1.8479; df : 17; sd : 0.59182

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Perifornical nucleus: Mean: 0.065641 +/- 0.0075548 SEM
 Test against a mean of 0
 Perifornical nucleus: ttest pval: 0.022304; tstat : 2.1684; df : 17; sd : 0.12843
 Test against a Expected # of cells based on region size 0.054823
 Perifornical nucleus: ttest pval (scaled--expected based on size): 0.36262; tstat : 0.35734; df : 17; sd : 0.12843

Retrochiasmatic area: Mean: 0.093526 +/- 0.023105 SEM
 Test against a mean of 0
 Retrochiasmatic area: ttest pval: 0.16327; tstat : 1.0102; df : 17; sd : 0.39278
 Test against a Expected # of cells based on region size 0.055445
 Retrochiasmatic area: ttest pval (scaled--expected based on size): 0.34298; tstat : 0.41134; df : 17; sd : 0.39278

Subthalamic nucleus: Mean: 0.31615 +/- 0.033088 SEM
 Test against a mean of 0
 Subthalamic nucleus: ttest pval: 0.01451; tstat : 2.3845; df : 17; sd : 0.5625
 Test against a Expected # of cells based on region size 0.088897
 Subthalamic nucleus: ttest pval (scaled--expected based on size): 0.052349; tstat : 1.714; df : 17; sd : 0.5625

Tuberal nucleus: Mean: 0.88995 +/- 0.21065 SEM
 Test against a mean of 0
 Tuberal nucleus: ttest pval: 0.15323; tstat : 1.0544; df : 17; sd : 3.581
 Test against a Expected # of cells based on region size 0.14193
 Tuberal nucleus: ttest pval (scaled--expected based on size): 0.19393; tstat : 0.88623; df : 17; sd : 3.581

Zona incerta: Mean: 0.43925 +/- 0.044104 SEM
 Test against a mean of 0
 Zona incerta: ttest pval: 0.011818; tstat : 2.4856; df : 17; sd : 0.74977
 Test against a Expected # of cells based on region size 0.41362
 Zona incerta: ttest pval (scaled--expected based on size): 0.44319; tstat : 0.14505; df : 17; sd : 0.74977

Anterior hypothalamic nucleus: Mean: 0.16055 +/- 0.010375 SEM
 Test against a mean of 0
 Anterior hypothalamic nucleus: ttest pval: 0.00062553; tstat : 3.8619; df : 17; sd : 0.17638
 Test against a Expected # of cells based on region size 0.15438
 Anterior hypothalamic nucleus: ttest pval (scaled--expected based on size): 0.44188; tstat : 0.14841; df : 17; sd : 0.17638

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Lateral mammillary nucleus:      Mean:  0.011553 +/- 0.0016939 SEM
Test against a mean of 0
Lateral mammillary nucleus:      ttest  pval:  0.053473;   tstat : 1.7021;
df : 17;   sd : 0.028796
Test against a Expected # of cells based on region size 0.020234
Lateral mammillary nucleus:      ttest  pval (scaled--expected based on
size):  0.89096;   tstat : -1.279;   df : 17;   sd : 0.028796
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Medial mammillary nucleus:      Mean:  0.39412 +/- 0.050426 SEM
Test against a mean of 0
Medial mammillary nucleus:      ttest  pval:  0.033895;   tstat : 1.9506;
df : 17;   sd : 0.85724
Test against a Expected # of cells based on region size 0.13169
Medial mammillary nucleus:      ttest  pval (scaled--expected based on
size):  0.10567;   tstat : 1.2988;   df : 17;   sd : 0.85724
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Supramammillary nucleus:      Mean:  0.074357 +/- 0.010899 SEM
Test against a mean of 0
Supramammillary nucleus:      ttest  pval:  0.053429;   tstat : 1.7026;
df : 17;   sd : 0.18529
Test against a Expected # of cells based on region size 0.066235
Supramammillary nucleus:      ttest  pval (scaled--expected based on
size):  0.42733;   tstat : 0.18597;   df : 17;   sd : 0.18529
-----

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Tuberomammillary nucleus:      Mean:  0.081479 +/- 0.010209 SEM
Test against a mean of 0
Tuberomammillary nucleus:      ttest  pval:  0.031348;   tstat : 1.9919;
df : 17;   sd : 0.17355
Test against a Expected # of cells based on region size 0.040192
Tuberomammillary nucleus:      ttest  pval (scaled--expected based on
size):  0.16348;   tstat : 1.0093;   df : 17;   sd : 0.17355
-----

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Medial preoptic nucleus:      Mean:  0.27183 +/- 0.032809 SEM
Test against a mean of 0
Medial preoptic nucleus:      ttest  pval:  0.027118;   tstat : 2.0677;
df : 17;   sd : 0.55775
Test against a Expected # of cells based on region size 0.087929
Medial preoptic nucleus:      ttest  pval (scaled--expected based on
size):  0.089916;   tstat : 1.3989;   df : 17;   sd : 0.55775
-----

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Dorsal premammillary nucleus:      Mean:  0.23528 +/- 0.032657 SEM
Test against a mean of 0
Dorsal premammillary nucleus:      ttest  pval:  0.044981;   tstat :
1.798;   df : 17;   sd : 0.55517
Test against a Expected # of cells based on region size 0.028634
-----

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Dorsal premammillary nucleus: ttest pval (scaled--expected based on size): 0.066362; tstat : 1.5792; df : 17; sd : 0.55517

Ventral premammillary nucleus: Mean: 0.49484 +/- 0.11132 SEM
Test against a mean of 0
Ventral premammillary nucleus: ttest pval: 0.14135; tstat : 1.1094; df : 17; sd : 1.8924
Test against a Expected # of cells based on region size 0.043666
Ventral premammillary nucleus: ttest pval (scaled--expected based on size): 0.16298; tstat : 1.0115; df : 17; sd : 1.8924

Paraventricular hypothalamic nucleus, descending division: Mean: 0.013922 +/- 0.0012852 SEM
Test against a mean of 0
Paraventricular hypothalamic nucleus, descending division: ttest pval: 0.0075325; tstat : 2.7035; df : 17; sd : 0.021848
Test against a Expected # of cells based on region size 0.028634
Paraventricular hypothalamic nucleus, descending division: ttest pval (scaled--expected based on size): 0.99454; tstat : -2.8569; df : 17; sd : 0.021848

Ventromedial hypothalamic nucleus: Mean: 1.2151 +/- 0.16121 SEM
Test against a mean of 0
Ventromedial hypothalamic nucleus: ttest pval: 0.038606; tstat : 1.881; df : 17; sd : 2.7406
Test against a Expected # of cells based on region size 0.11942
Ventromedial hypothalamic nucleus: ttest pval (scaled--expected based on size): 0.054046; tstat : 1.6962; df : 17; sd : 2.7406

Posterior hypothalamic nucleus: Mean: 0.13119 +/- 0.011118 SEM
Test against a mean of 0
Posterior hypothalamic nucleus: ttest pval: 0.0045287; tstat : 2.9449; df : 17; sd : 0.189
Test against a Expected # of cells based on region size 0.15853
Posterior hypothalamic nucleus: ttest pval (scaled--expected based on size): 0.72627; tstat : -0.61383; df : 17; sd : 0.189

Substantia nigra, reticular part: Mean: 0.037884 +/- 0.0052302 SEM
Test against a mean of 0
Substantia nigra, reticular part: ttest pval: 0.044192; tstat : 1.8077; df : 17; sd : 0.088913
Test against a Expected # of cells based on region size 0.43287
Substantia nigra, reticular part: ttest pval (scaled--expected based on size): 1; tstat : -18.8472; df : 17; sd : 0.088913

Ventral tegmental area: Mean: 0.045944 +/- 0.0064395 SEM

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Test against a mean of 0
Ventral tegmental area:      ttest  pval:  0.046427;    tstat : 1.7806;
df : 17;    sd : 0.10947
Test against a Expected # of cells based on region size 0.11082
Ventral tegmental area:      ttest  pval (scaled--expected based on size):
0.98886;    tstat : -2.5143;    df : 17;    sd : 0.10947
-----

Paranigral nucleus:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Paranigral nucleus:      ttest  pval:  NaN;    tstat : NaN;    df : 17;    sd
: 0
Test against a Expected # of cells based on region size 0.004774
Paranigral nucleus:      ttest  pval (scaled--expected based on size):  1;
tstat : -Inf;    df : 17;    sd : 0
-----

Midbrain reticular nucleus, retrorubral area:      Mean:  0.0012484 +/-
0.00031157 SEM
Test against a mean of 0
Midbrain reticular nucleus, retrorubral area:      ttest  pval:  0.16567;
tstat : 1;    df : 17;    sd : 0.0052967
Test against a Expected # of cells based on region size 0.030233
Midbrain reticular nucleus, retrorubral area:      ttest  pval (scaled--
expected based on size):  1;    tstat : -23.2169;    df : 17;    sd :
0.0052967
-----

Midbrain reticular nucleus:      Mean:  0.10224 +/- 0.018492 SEM
Test against a mean of 0
Midbrain reticular nucleus:      ttest  pval:  0.092747;    tstat : 1.3799;
df : 17;    sd : 0.31436
Test against a Expected # of cells based on region size 1.1584
Midbrain reticular nucleus:      ttest  pval (scaled--expected based on
size):  1;    tstat : -14.2545;    df : 17;    sd : 0.31436
-----

Superior colliculus, motor related:      Mean:  0.13275 +/- 0.022439 SEM
Test against a mean of 0
Superior colliculus, motor related:      ttest  pval:  0.079047;    tstat :
1.4765;    df : 17;    sd : 0.38146
Test against a Expected # of cells based on region size 1.2407
Superior colliculus, motor related:      ttest  pval (scaled--expected
based on size):  1;    tstat : -12.3225;    df : 17;    sd : 0.38146
-----

Periaqueductal gray:      Mean:  0.0050446 +/- 0.00090285 SEM
Test against a mean of 0
Periaqueductal gray:      ttest  pval:  0.090573;    tstat : 1.3944;    df :
17;    sd : 0.015348
Test against a Expected # of cells based on region size 1.0825
Periaqueductal gray:      ttest  pval (scaled--expected based on size):

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1; tstat : -297.8342; df : 17; sd : 0.015348

Pretectal region: Mean: 0.00044941 +/- 0.00011216 SEM

Test against a mean of 0

Pretectal region: ttest pval: 0.16567; tstat : 1; df : 17; sd : 0.0019067

Test against a Expected # of cells based on region size 0.47598

Pretectal region: ttest pval (scaled--expected based on size): 1; tstat : -1058.1259; df : 17; sd : 0.0019067

Cuneiform nucleus: Mean: 0.003247 +/- 0.00081034 SEM

Test against a mean of 0

Cuneiform nucleus: ttest pval: 0.16567; tstat : 1; df : 17; sd : 0.013776

Test against a Expected # of cells based on region size 0.1289

Cuneiform nucleus: ttest pval (scaled--expected based on size): 1; tstat : -38.6973; df : 17; sd : 0.013776

Red nucleus: Mean: 0.0024969 +/- 0.00062314 SEM

Test against a mean of 0

Red nucleus: ttest pval: 0.16567; tstat : 1; df : 17; sd : 0.010593

Test against a Expected # of cells based on region size 0.17216

Red nucleus: ttest pval (scaled--expected based on size): 1; tstat : -67.9517; df : 17; sd : 0.010593

Oculomotor nucleus: Mean: 0 +/- 0 SEM

Test against a mean of 0

Oculomotor nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.0070762

Oculomotor nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Medial accessory oculomotor nucleus: Mean: 0 +/- 0 SEM

Test against a mean of 0

Medial accessory oculomotor nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.0035313

Medial accessory oculomotor nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Edinger-Westphal nucleus: Mean: 0 +/- 0 SEM

Test against a mean of 0

Edinger-Westphal nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

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Test against a Expected # of cells based on region size 0.0056501
 Edinger-Westphal nucleus: ttest pval (scaled--expected based on
 size): 1; tstat : -Inf; df : 17; sd : 0

Trochlear nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Trochlear nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd
 : 0
 Test against a Expected # of cells based on region size 0.0015415
 Trochlear nucleus: ttest pval (scaled--expected based on size): 1;
 tstat : -Inf; df : 17; sd : 0

Paratrochlear nucleus: Mean: 0.00044941 +/- 0.00011216 SEM
 Test against a mean of 0
 Paratrochlear nucleus: ttest pval: 0.16567; tstat : 1; df : 17;
 sd : 0.0019067
 Test against a Expected # of cells based on region size 0.0034804
 Paratrochlear nucleus: ttest pval (scaled--expected based on size):
 1; tstat : -6.7444; df : 17; sd : 0.0019067

Ventral tegmental nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Ventral tegmental nucleus: ttest pval: NaN; tstat : NaN; df :
 17; sd : 0
 Test against a Expected # of cells based on region size 0.0082103
 Ventral tegmental nucleus: ttest pval (scaled--expected based on
 size): 1; tstat : -Inf; df : 17; sd : 0

Anterior tegmental nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Anterior tegmental nucleus: ttest pval: NaN; tstat : NaN; df :
 17; sd : 0
 Test against a Expected # of cells based on region size 0.0093647
 Anterior tegmental nucleus: ttest pval (scaled--expected based on
 size): 1; tstat : -Inf; df : 17; sd : 0

Lateral terminal nucleus of the accessory optic tract: Mean:
 0.0042103 +/- 0.0010508 SEM
 Test against a mean of 0
 Lateral terminal nucleus of the accessory optic tract: ttest pval:
 0.16567; tstat : 1; df : 17; sd : 0.017863
 Test against a Expected # of cells based on region size 0.004044
 Lateral terminal nucleus of the accessory optic tract: ttest pval
 (scaled--expected based on size): 0.48447; tstat : 0.039508; df :
 17; sd : 0.017863

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Dorsal terminal nucleus of the accessory optic tract: Mean: 0 +/- 0 SEM

Test against a mean of 0

Dorsal terminal nucleus of the accessory optic tract: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.0029235

Dorsal terminal nucleus of the accessory optic tract: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Medial terminal nucleus of the accessory optic tract: Mean: 0 +/- 0 SEM

Test against a mean of 0

Medial terminal nucleus of the accessory optic tract: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.0094734

Medial terminal nucleus of the accessory optic tract: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Superior colliculus, sensory related: Mean: 0 +/- 0 SEM

Test against a mean of 0

Superior colliculus, sensory related: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.47634

Superior colliculus, sensory related: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Inferior colliculus: Mean: 0.020925 +/- 0.0052222 SEM

Test against a mean of 0

Inferior colliculus: ttest pval: 0.16567; tstat : 1; df : 17; sd : 0.088777

Test against a Expected # of cells based on region size 0.96665

Inferior colliculus: ttest pval (scaled--expected based on size): 1; tstat : -45.1962; df : 17; sd : 0.088777

Nucleus of the brachium of the inferior colliculus: Mean: 0.010462 +/- 0.0026111 SEM

Test against a mean of 0

Nucleus of the brachium of the inferior colliculus: ttest pval: 0.16567; tstat : 1; df : 17; sd : 0.044388

Test against a Expected # of cells based on region size 0.029602

Nucleus of the brachium of the inferior colliculus: ttest pval (scaled--expected based on size): 0.95753; tstat : -1.8293; df : 17; sd : 0.044388

Nucleus sagulum: Mean: 0 +/- 0 SEM

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Test against a mean of 0
Nucleus sagulum: ttest pval: NaN; tstat : NaN; df : 17; sd : 0

Test against a Expected # of cells based on region size 0.021344
Nucleus sagulum: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Parabigeminal nucleus: Mean: 0 +/- 0 SEM

Test against a mean of 0

Parabigeminal nucleus: ttest pval: NaN; tstat : NaN; df : 17;
sd : 0

Test against a Expected # of cells based on region size 0.0096839

Parabigeminal nucleus: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Midbrain trigeminal nucleus: Mean: 0 +/- 0 SEM

Test against a mean of 0

Midbrain trigeminal nucleus: ttest pval: NaN; tstat : NaN; df : 17;
sd : 0

Test against a Expected # of cells based on region size 0.0022003

Midbrain trigeminal nucleus: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Subcommissural organ: Mean: 0 +/- 0 SEM

Test against a mean of 0

Subcommissural organ: ttest pval: NaN; tstat : NaN; df : 17;
sd : 0

Test against a Expected # of cells based on region size 0.0092832

Subcommissural organ: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Substantia nigra, compact part: Mean: 0.00044941 +/- 0.00011216 SEM

Test against a mean of 0

Substantia nigra, compact part: ttest pval: 0.16567; tstat : 1;
df : 17; sd : 0.0019067

Test against a Expected # of cells based on region size 0.043051

Substantia nigra, compact part: ttest pval (scaled--expected based on size): 1;
tstat : -94.7958; df : 17; sd : 0.0019067

Pedunculo pontine nucleus: Mean: 0.0012484 +/- 0.00031157 SEM

Test against a mean of 0

Pedunculo pontine nucleus: ttest pval: 0.16567; tstat : 1; df : 17;
sd : 0.0052967

Test against a Expected # of cells based on region size 0.2086

Pedunculo pontine nucleus: ttest pval (scaled--expected based on size): 1;
tstat : -166.0893; df : 17; sd : 0.0052967

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Interfascicular nucleus raphe: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Interfascicular nucleus raphe: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.020156
 Interfascicular nucleus raphe: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Interpeduncular nucleus: Mean: 0.00089881 +/- 0.00022431 SEM
 Test against a mean of 0
 Interpeduncular nucleus: ttest pval: 0.16567; tstat : 1; df : 17; sd : 0.0038133
 Test against a Expected # of cells based on region size 0.079699
 Interpeduncular nucleus: ttest pval (scaled--expected based on size): 1; tstat : -87.671; df : 17; sd : 0.0038133

Rostral linear nucleus raphe: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Rostral linear nucleus raphe: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.016071
 Rostral linear nucleus raphe: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Central linear nucleus raphe: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Central linear nucleus raphe: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
 Test against a Expected # of cells based on region size 0.020332
 Central linear nucleus raphe: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Dorsal nucleus raphe: Mean: 0.0036964 +/- 0.0008115 SEM
 Test against a mean of 0
 Dorsal nucleus raphe: ttest pval: 0.1357; tstat : 1.1368; df : 17; sd : 0.013795
 Test against a Expected # of cells based on region size 0.033422
 Dorsal nucleus raphe: ttest pval (scaled--expected based on size): 1; tstat : -9.1417; df : 17; sd : 0.013795

Primary motor area: Mean: 0.006686 +/- 0.0012921 SEM
 Test against a mean of 0
 Primary motor area: ttest pval: 0.10693; tstat : 1.2913; df : 17; sd : 0.021966
 Test against a Expected # of cells based on region size 2.6186
 Primary motor area: ttest pval (scaled--expected based on size): 1;

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tstat : -504.4714; df : 17; sd : 0.021966

Secondary motor area: Mean: 0.074756 +/- 0.016114 SEM
Test against a mean of 0
Secondary motor area: ttest pval: 0.13147; tstat : 1.1578; df :
17; sd : 0.27393
Test against a Expected # of cells based on region size 2.9481
Secondary motor area: ttest pval (scaled--expected based on size):
1; tstat : -44.5026; df : 17; sd : 0.27393

primary somatosensory area: Mean: 0.0027917 +/- 0.0004482 SEM
Test against a mean of 0
primary somatosensory area: ttest pval: 0.069247; tstat : 1.5545;
df : 17; sd : 0.0076194
Test against a Expected # of cells based on region size 5.5681
primary somatosensory area: ttest pval (scaled--expected based on
size): 1; tstat : -3098.8479; df : 17; sd : 0.0076194

Supplemental somatosensory area: Mean: 0.0063329 +/- 0.0011044 SEM
Test against a mean of 0
Supplemental somatosensory area: ttest pval: 0.085266; tstat :
1.4311; df : 17; sd : 0.018775
Test against a Expected # of cells based on region size 2.0429
Supplemental somatosensory area: ttest pval (scaled--expected based
on size): 1; tstat : -460.2201; df : 17; sd : 0.018775

Gustatory areas: Mean: 0.0050837 +/- 0.00097392 SEM
Test against a mean of 0
Gustatory areas: ttest pval: 0.10502; tstat : 1.3027; df : 17;
sd : 0.016557
Test against a Expected # of cells based on region size 0.38663
Gustatory areas: ttest pval (scaled--expected based on size): 1;
tstat : -97.7722; df : 17; sd : 0.016557

Visceral area: Mean: 0.013856 +/- 0.0013483 SEM
Test against a mean of 0
Visceral area: ttest pval: 0.010045; tstat : 2.5647; df : 17;
sd : 0.022921
Test against a Expected # of cells based on region size 0.52504
Visceral area: ttest pval (scaled--expected based on size): 1;
tstat : -94.6193; df : 17; sd : 0.022921

Auditory areas: Mean: 0.0047348 +/- 0.00071797 SEM
Test against a mean of 0
Auditory areas: ttest pval: 0.05908; tstat : 1.6458; df : 17;
sd : 0.012206

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Test against a Expected # of cells based on region size 1.3473
Auditory areas: ttest pval (scaled--expected based on size): 1;
tstat : -466.6904; df : 17; sd : 0.012206

Visual areas: Mean: 0.008255 +/- 0.0014136 SEM
Test against a mean of 0
Visual areas: ttest pval: 0.081613; tstat : 1.4574; df : 17;
sd : 0.024031
Test against a Expected # of cells based on region size 3.1429
Visual areas: ttest pval (scaled--expected based on size): 1;
tstat : -553.4224; df : 17; sd : 0.024031

Anterior cingulate area: Mean: 0.010989 +/- 0.0024326 SEM
Test against a mean of 0
Anterior cingulate area: ttest pval: 0.13762; tstat : 1.1274;
df : 17; sd : 0.041355
Test against a Expected # of cells based on region size 1.3819
Anterior cingulate area: ttest pval (scaled--expected based on
size): 1; tstat : -140.646; df : 17; sd : 0.041355

Prelimbic area: Mean: 0.0012484 +/- 0.00031157 SEM
Test against a mean of 0
Prelimbic area: ttest pval: 0.16567; tstat : 1; df : 17; sd :
0.0052967
Test against a Expected # of cells based on region size 0.54511
Prelimbic area: ttest pval (scaled--expected based on size): 1;
tstat : -435.6325; df : 17; sd : 0.0052967

Infralimbic area: Mean: 0.014772 +/- 0.0015668 SEM
Test against a mean of 0
Infralimbic area: ttest pval: 0.01546; tstat : 2.3531; df : 17;
sd : 0.026635
Test against a Expected # of cells based on region size 0.20061
Infralimbic area: ttest pval (scaled--expected based on size): 1;
tstat : -29.6022; df : 17; sd : 0.026635

Orbital area: Mean: 0.030667 +/- 0.0049647 SEM
Test against a mean of 0
Orbital area: ttest pval: 0.070793; tstat : 1.5416; df : 17;
sd : 0.0844
Test against a Expected # of cells based on region size 1.3105
Orbital area: ttest pval (scaled--expected based on size): 1;
tstat : -64.3337; df : 17; sd : 0.0844

Agranular insular area: Mean: 0.074015 +/- 0.0062399 SEM
Test against a mean of 0

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Agranular insular area: ttest pval: 0.0043832; tstat : 2.9602;
df : 17; sd : 0.10608
Test against a Expected # of cells based on region size 1.7341
Agranular insular area: ttest pval (scaled--expected based on size):
1; tstat : -66.3957; df : 17; sd : 0.10608

Retrosplenial area: Mean: 0 +/- 0 SEM
Test against a mean of 0
Retrosplenial area: ttest pval: NaN; tstat : NaN; df : 17; sd
: 0
Test against a Expected # of cells based on region size 2.5553
Retrosplenial area: ttest pval (scaled--expected based on size): 1;
tstat : -Inf; df : 17; sd : 0

Posterior parietal association areas: Mean: 0 +/- 0 SEM
Test against a mean of 0
Posterior parietal association areas: ttest pval: NaN; tstat :
NaN; df : 17; sd : 0
Test against a Expected # of cells based on region size 0.57144
Posterior parietal association areas: ttest pval (scaled--expected
based on size): 1; tstat : -Inf; df : 17; sd : 0

Temporal association areas: Mean: 0.033418 +/- 0.0048174 SEM
Test against a mean of 0
Temporal association areas: ttest pval: 0.05076; tstat : 1.7312;
df : 17; sd : 0.081896
Test against a Expected # of cells based on region size 0.71655
Temporal association areas: ttest pval (scaled--expected based on
size): 1; tstat : -35.3897; df : 17; sd : 0.081896

Perirhinal area: Mean: 0.00044941 +/- 0.00011216 SEM
Test against a mean of 0
Perirhinal area: ttest pval: 0.16567; tstat : 1; df : 17; sd
: 0.0019067
Test against a Expected # of cells based on region size 0.17514
Perirhinal area: ttest pval (scaled--expected based on size): 1;
tstat : -388.7036; df : 17; sd : 0.0019067

Ectorhinal area: Mean: 0.02416 +/- 0.0046767 SEM
Test against a mean of 0
Ectorhinal area: ttest pval: 0.10728; tstat : 1.2893; df : 17;
sd : 0.079503
Test against a Expected # of cells based on region size 0.39531
Ectorhinal area: ttest pval (scaled--expected based on size): 1;
tstat : -19.8065; df : 17; sd : 0.079503

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cerebellar cortex: Mean: 0.0087391 +/- 0.002181 SEM
 Test against a mean of 0
 cerebellar cortex: ttest pval: 0.16567; tstat : 1; df : 17;
 sd : 0.037077
 Test against a Expected # of cells based on region size 12.5699
 cerebellar cortex: ttest pval (scaled--expected based on size): 1;
 tstat : -1437.3559; df : 17; sd : 0.037077

Fastigial nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Fastigial nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd
 : 0
 Test against a Expected # of cells based on region size 0.19496
 Fastigial nucleus: ttest pval (scaled--expected based on size): 1;
 tstat : -Inf; df : 17; sd : 0

Interposed nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Interposed nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd
 : 0
 Test against a Expected # of cells based on region size 0.30222
 Interposed nucleus: ttest pval (scaled--expected based on size): 1;
 tstat : -Inf; df : 17; sd : 0

Dentate nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Dentate nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd :
 0
 Test against a Expected # of cells based on region size 0.13733
 Dentate nucleus: ttest pval (scaled--expected based on size): 1;
 tstat : -Inf; df : 17; sd : 0

Vestibulocerebellar nucleus: Mean: 0 +/- 0 SEM
 Test against a mean of 0
 Vestibulocerebellar nucleus: ttest pval: NaN; tstat : NaN; df :
 17; sd : 0
 Test against a Expected # of cells based on region size 0.018814
 Vestibulocerebellar nucleus: ttest pval (scaled--expected based on
 size): 1; tstat : -Inf; df : 17; sd : 0

Ventral group of the dorsal thalamus: Mean: 0.33454 +/- 0.039723 SEM
 Test against a mean of 0
 Ventral group of the dorsal thalamus: ttest pval: 0.025392; tstat
 : 2.1018; df : 17; sd : 0.6753
 Test against a Expected # of cells based on region size 1.0937
 Ventral group of the dorsal thalamus: ttest pval (scaled--expected
 based on size): 0.99991; tstat : -4.7692; df : 17; sd : 0.6753

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Subparafascicular nucleus:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Subparafascicular nucleus:      ttest  pval:  NaN;   tstat : NaN;   df :
17;   sd : 0
Test against a Expected # of cells based on region size 0.044905
Subparafascicular nucleus:      ttest  pval (scaled--expected based on
size):  1;   tstat : -Inf;   df : 17;   sd : 0
-----

Subparafascicular area:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Subparafascicular area:      ttest  pval:  NaN;   tstat : NaN;   df : 17;
sd : 0
Test against a Expected # of cells based on region size 0.028753
Subparafascicular area:      ttest  pval (scaled--expected based on size):
1;   tstat : -Inf;   df : 17;   sd : 0
-----

Peripeduncular nucleus:      Mean:  0.058784 +/- 0.010232 SEM
Test against a mean of 0
Peripeduncular nucleus:      ttest  pval:  0.084889;   tstat : 1.4338;
df : 17;   sd : 0.17395
Test against a Expected # of cells based on region size 0.01455
Peripeduncular nucleus:      ttest  pval (scaled--expected based on size):
0.14785;   tstat : 1.0789;   df : 17;   sd : 0.17395
-----

Geniculate group, dorsal thalamus:      Mean:  0.16823 +/- 0.033751 SEM
Test against a mean of 0
Geniculate group, dorsal thalamus:      ttest  pval:  0.1152;   tstat :
1.244;   df : 17;   sd : 0.57377
Test against a Expected # of cells based on region size 0.35506
Geniculate group, dorsal thalamus:      ttest  pval (scaled--expected
based on size):  0.90749;   tstat : -1.3815;   df : 17;   sd : 0.57377
-----

Lateral group of the dorsal thalamus:      Mean:  0.041493 +/- 0.0052111
SEM
Test against a mean of 0
Lateral group of the dorsal thalamus:      ttest  pval:  0.031631;   tstat
: 1.9872;   df : 17;   sd : 0.088588
Test against a Expected # of cells based on region size 0.68209
Lateral group of the dorsal thalamus:      ttest  pval (scaled--expected
based on size):  1;   tstat : -30.6791;   df : 17;   sd : 0.088588
-----

Anterior group of the dorsal thalamus:      Mean:  0 +/- 0 SEM
Test against a mean of 0
Anterior group of the dorsal thalamus:      ttest  pval:  NaN;   tstat :
NaN;   df : 17;   sd : 0

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Test against a Expected # of cells based on region size 0.57039
 Anterior group of the dorsal thalamus: ttest pval (scaled--expected
 based on size): 1; tstat : -Inf; df : 17; sd : 0

Medial group of the dorsal thalamus: Mean: 0.00711 +/- 0.00096338
 SEM
 Test against a mean of 0
 Medial group of the dorsal thalamus: ttest pval: 0.041505; tstat
 : 1.8419; df : 17; sd : 0.016378
 Test against a Expected # of cells based on region size 0.45517
 Medial group of the dorsal thalamus: ttest pval (scaled--expected
 based on size): 1; tstat : -116.072; df : 17; sd : 0.016378

Midline group of the dorsal thalamus: Mean: 0.11222 +/- 0.010624 SEM
 Test against a mean of 0
 Midline group of the dorsal thalamus: ttest pval: 0.0086697;
 tstat : 2.6359; df : 17; sd : 0.18062
 Test against a Expected # of cells based on region size 0.28566
 Midline group of the dorsal thalamus: ttest pval (scaled--expected
 based on size): 0.99961; tstat : -4.0743; df : 17; sd : 0.18062

Intralaminar nuclei of the dorsal thalamus: Mean: 0.074545 +/-
 0.012797 SEM
 Test against a mean of 0
 Intralaminar nuclei of the dorsal thalamus: ttest pval: 0.082118;
 tstat : 1.4537; df : 17; sd : 0.21756
 Test against a Expected # of cells based on region size 0.36311
 Intralaminar nuclei of the dorsal thalamus: ttest pval (scaled--
 expected based on size): 0.99998; tstat : -5.6275; df : 17; sd :
 0.21756

Reticular nucleus of the thalamus: Mean: 0.87295 +/- 0.14077 SEM
 Test against a mean of 0
 Reticular nucleus of the thalamus: ttest pval: 0.070059; tstat :
 1.5477; df : 17; sd : 2.3931
 Test against a Expected # of cells based on region size 0.49022
 Reticular nucleus of the thalamus: ttest pval (scaled--expected
 based on size): 0.25328; tstat : 0.67855; df : 17; sd : 2.3931

Geniculate group, ventral thalamus: Mean: 0.076796 +/- 0.0089385 SEM
 Test against a mean of 0
 Geniculate group, ventral thalamus: ttest pval: 0.023384; tstat :
 2.1442; df : 17; sd : 0.15195
 Test against a Expected # of cells based on region size 0.17279
 Geniculate group, ventral thalamus: ttest pval (scaled--expected
 based on size): 0.99209; tstat : -2.6803; df : 17; sd : 0.15195

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Epithalamus: Mean: 0.00089881 +/- 0.00022431 SEM

Test against a mean of 0

Epithalamus: ttest pval: 0.16567; tstat : 1; df : 17; sd : 0.0038133

Test against a Expected # of cells based on region size 0.22435

Epithalamus: ttest pval (scaled--expected based on size): 1; tstat : -248.6063; df : 17; sd : 0.0038133

Caudoputatum: Mean: 6.5636 +/- 0.63899 SEM

Test against a mean of 0

Caudoputatum: ttest pval: 0.010071; tstat : 2.5635; df : 17; sd : 10.8628

Test against a Expected # of cells based on region size 6.55

Caudoputatum: ttest pval (scaled--expected based on size): 0.49791; tstat : 0.0053252; df : 17; sd : 10.8628

Nucleus accumbens: Mean: 0.14857 +/- 0.014201 SEM

Test against a mean of 0

Nucleus accumbens: ttest pval: 0.0091294; tstat : 2.611; df : 17; sd : 0.24141

Test against a Expected # of cells based on region size 0.99813

Nucleus accumbens: ttest pval (scaled--expected based on size): 1; tstat : -14.9302; df : 17; sd : 0.24141

Fundus of striatum: Mean: 0.11367 +/- 0.011312 SEM

Test against a mean of 0

Fundus of striatum: ttest pval: 0.011294; tstat : 2.5077; df : 17; sd : 0.19231

Test against a Expected # of cells based on region size 0.093834

Fundus of striatum: ttest pval (scaled--expected based on size): 0.33359; tstat : 0.43761; df : 17; sd : 0.19231

Olfactory Tubercle: Mean: 0.22479 +/- 0.044624 SEM

Test against a mean of 0

Olfactory Tubercle: ttest pval: 0.11284; tstat : 1.2572; df : 17; sd : 0.75861

Test against a Expected # of cells based on region size 0.84157

Olfactory Tubercle: ttest pval (scaled--expected based on size): 0.99847; tstat : -3.4494; df : 17; sd : 0.75861

Lateral septal nucleus: Mean: 0.14769 +/- 0.012135 SEM

Test against a mean of 0

Lateral septal nucleus: ttest pval: 0.0037178; tstat : 3.0375; df : 17; sd : 0.20629

Test against a Expected # of cells based on region size 0.79092

Lateral septal nucleus: ttest pval (scaled--expected based on size):

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1; tstat : -13.2287; df : 17; sd : 0.20629

Septofimbrial nucleus: Mean: 0.046789 +/- 0.0060092 SEM
Test against a mean of 0
Septofimbrial nucleus: ttest pval: 0.034372; tstat : 1.9432; df : 17; sd : 0.10216
Test against a Expected # of cells based on region size 0.17297
Septofimbrial nucleus: ttest pval (scaled--expected based on size): 0.99997; tstat : -5.2403; df : 17; sd : 0.10216

Septohippocampal nucleus: Mean: 0 +/- 0 SEM
Test against a mean of 0
Septohippocampal nucleus: ttest pval: NaN; tstat : NaN; df : 17; sd : 0
Test against a Expected # of cells based on region size 0.0097178
Septohippocampal nucleus: ttest pval (scaled--expected based on size): 1; tstat : -Inf; df : 17; sd : 0

Anterior amygdalar area: Mean: 0.25848 +/- 0.021208 SEM
Test against a mean of 0
Anterior amygdalar area: ttest pval: 0.003685; tstat : 3.0416; df : 17; sd : 0.36054
Test against a Expected # of cells based on region size 0.10747
Anterior amygdalar area: ttest pval (scaled--expected based on size): 0.046736; tstat : 1.7769; df : 17; sd : 0.36054

Bed nucleus of the accessory olfactory tract: Mean: 0.0012484 +/- 0.00031157 SEM
Test against a mean of 0
Bed nucleus of the accessory olfactory tract: ttest pval: 0.16567; tstat : 1; df : 17; sd : 0.0052967
Test against a Expected # of cells based on region size 0.0054463
Bed nucleus of the accessory olfactory tract: ttest pval (scaled--expected based on size): 0.99815; tstat : -3.3625; df : 17; sd : 0.0052967

Central amygdalar nucleus: Mean: 11.3864 +/- 0.59917 SEM
Test against a mean of 0
Central amygdalar nucleus: ttest pval: 9.4177e-05; tstat : 4.7427; df : 17; sd : 10.1858
Test against a Expected # of cells based on region size 0.2958
Central amygdalar nucleus: ttest pval (scaled--expected based on size): 0.00012234; tstat : 4.6195; df : 17; sd : 10.1858

Intercalated amygdalar nucleus: Mean: 0.43087 +/- 0.039931 SEM
Test against a mean of 0

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Intercalated amygdalar nucleus: ttest pval: 0.0077006; tstat : 2.6929; df : 17; sd : 0.67883
 Test against a Expected # of cells based on region size 0.039897
 Intercalated amygdalar nucleus: ttest pval (scaled--expected based on size): 0.012874; tstat : 2.4436; df : 17; sd : 0.67883

Medial amygdalar nucleus: Mean: 20.0323 +/- 1.3142 SEM
 Test against a mean of 0
 Medial amygdalar nucleus: ttest pval: 0.00070912; tstat : 3.8041; df : 17; sd : 22.3418
 Test against a Expected # of cells based on region size 0.5476
 Medial amygdalar nucleus: ttest pval (scaled--expected based on size): 0.00088875; tstat : 3.7001; df : 17; sd : 22.3418

Globus pallidus, external segment: Mean: 3.2419 +/- 0.30863 SEM
 Test against a mean of 0
 Globus pallidus, external segment: ttest pval: 0.0089331; tstat : 2.6215; df : 17; sd : 5.2467
 Test against a Expected # of cells based on region size 0.40648
 Globus pallidus, external segment: ttest pval (scaled--expected based on size): 0.017442; tstat : 2.2928; df : 17; sd : 5.2467

Globus pallidus, internal segment: Mean: 1.4163 +/- 0.11891 SEM
 Test against a mean of 0
 Globus pallidus, internal segment: ttest pval: 0.004272; tstat : 2.9723; df : 17; sd : 2.0215
 Test against a Expected # of cells based on region size 0.1381
 Globus pallidus, internal segment: ttest pval (scaled--expected based on size): 0.00787; tstat : 2.6825; df : 17; sd : 2.0215

Substantia innominata: Mean: 2.5134 +/- 0.19436 SEM
 Test against a mean of 0
 Substantia innominata: ttest pval: 0.0024738; tstat : 3.2273; df : 17; sd : 3.3041
 Test against a Expected # of cells based on region size 0.65833
 Substantia innominata: ttest pval (scaled--expected based on size): 0.014584; tstat : 2.382; df : 17; sd : 3.3041

Magnocellular nucleus: Mean: 0.27731 +/- 0.021054 SEM
 Test against a mean of 0
 Magnocellular nucleus: ttest pval: 0.0021749; tstat : 3.2871; df : 17; sd : 0.35792
 Test against a Expected # of cells based on region size 0.079227
 Magnocellular nucleus: ttest pval (scaled--expected based on size): 0.015619; tstat : 2.348; df : 17; sd : 0.35792

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Medial septal nucleus: Mean: 0.18787 +/- 0.018921 SEM
 Test against a mean of 0
 Medial septal nucleus: ttest pval: 0.012004; tstat : 2.4779; df : 17; sd : 0.32167
 Test against a Expected # of cells based on region size 0.09107
 Medial septal nucleus: ttest pval (scaled--expected based on size): 0.10943; tstat : 1.2767; df : 17; sd : 0.32167

Diagonal band nucleus: Mean: 0.48947 +/- 0.033737 SEM
 Test against a mean of 0
 Diagonal band nucleus: ttest pval: 0.0010556; tstat : 3.6208; df : 17; sd : 0.57353
 Test against a Expected # of cells based on region size 0.16087
 Diagonal band nucleus: ttest pval (scaled--expected based on size): 0.013211; tstat : 2.4308; df : 17; sd : 0.57353

Triangular nucleus of septum: Mean: 0.0064051 +/- 0.00088501 SEM
 Test against a mean of 0
 Triangular nucleus of septum: ttest pval: 0.044312; tstat : 1.8062; df : 17; sd : 0.015045
 Test against a Expected # of cells based on region size 0.11501
 Triangular nucleus of septum: ttest pval (scaled--expected based on size): 1; tstat : -30.6272; df : 17; sd : 0.015045

BNST: Mean: 0.61112 +/- 0.043287 SEM
 Test against a mean of 0
 BNST: ttest pval: 0.0013042; tstat : 3.5234; df : 17; sd : 0.73588
 Test against a Expected # of cells based on region size 0.33723
 BNST: ttest pval (scaled--expected based on size): 0.066372; tstat : 1.5791; df : 17; sd : 0.73588

MainOlfactoryBulb: Mean: 0.25171 +/- 0.038879 SEM
 Test against a mean of 0
 MainOlfactoryBulb: ttest pval: 0.062276; tstat : 1.6158; df : 17; sd : 0.66094
 Test against a Expected # of cells based on region size 4.2909
 MainOlfactoryBulb: ttest pval (scaled--expected based on size): 1; tstat : -25.9276; df : 17; sd : 0.66094

AccessoryOlfactoryBulb: Mean: 0.92978 +/- 0.097154 SEM
 Test against a mean of 0
 AccessoryOlfactoryBulb: ttest pval: 0.014397; tstat : 2.3884; df : 17; sd : 1.6516
 Test against a Expected # of cells based on region size 0.16047
 AccessoryOlfactoryBulb: ttest pval (scaled--expected based on size): 0.032296; tstat : 1.9762; df : 17; sd : 1.6516

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AnteriorOlfactoryNucleus:      Mean:  0.0037733 +/- 0.00069434 SEM
Test against a mean of 0
AnteriorOlfactoryNucleus:      ttest  pval:  0.096383;   tstat : 1.3562;
df : 17;   sd : 0.011804
Test against a Expected # of cells based on region size 1.168
AnteriorOlfactoryNucleus:      ttest  pval (scaled--expected based on
size):  1;   tstat : -418.465;   df : 17;   sd : 0.011804
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Taenia tecta:      Mean:  0.003908 +/- 0.00062019 SEM
Test against a mean of 0
Taenia tecta:      ttest  pval:  0.06712;   tstat : 1.5726;   df : 17;
sd : 0.010543
Test against a Expected # of cells based on region size 0.31398
Taenia tecta:      ttest  pval (scaled--expected based on size):  1;
tstat : -124.7746;   df : 17;   sd : 0.010543
-----

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Dorsal peduncular area:      Mean:  0.001602 +/- 0.0002845 SEM
Test against a mean of 0
Dorsal peduncular area:      ttest  pval:  0.088968;   tstat : 1.4053;
df : 17;   sd : 0.0048365
Test against a Expected # of cells based on region size 0.12319
Dorsal peduncular area:      ttest  pval (scaled--expected based on size):
1;   tstat : -106.657;   df : 17;   sd : 0.0048365
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Piriform area:      Mean:  1.0382 +/- 0.05887 SEM
Test against a mean of 0
Piriform area:      ttest  pval:  0.00019501;   tstat : 4.4014;   df : 17;
sd : 1.0008
Test against a Expected # of cells based on region size 2.6015
Piriform area:      ttest  pval (scaled--expected based on size):  1;
tstat : -6.6274;   df : 17;   sd : 1.0008
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Nucleus of the lateral olfactory tract:      Mean:  0.21477 +/- 0.033776
SEM
Test against a mean of 0
Nucleus of the lateral olfactory tract:      ttest  pval:  0.06548;
tstat : 1.5869;   df : 17;   sd : 0.5742
Test against a Expected # of cells based on region size 0.070684
Nucleus of the lateral olfactory tract:      ttest  pval (scaled--expected
based on size):  0.15097;   tstat : 1.0646;   df : 17;   sd : 0.5742
-----

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Cortical amygdalar area:      Mean:  3.9576 +/- 0.26051 SEM
Test against a mean of 0
Cortical amygdalar area:      ttest  pval:  0.0007289;   tstat : 3.7914;
df : 17;   sd : 4.4286

```

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Test against a Expected # of cells based on region size 0.70976
Cortical amygdalar area: ttest pval (scaled--expected based on
size): 0.0031734; tstat : 3.1114; df : 17; sd : 4.4286

Piriform-amygdalar area: Mean: 0.37813 +/- 0.021107 SEM
Test against a mean of 0
Piriform-amygdalar area: ttest pval: 0.00016796; tstat : 4.4711;
df : 17; sd : 0.35881
Test against a Expected # of cells based on region size 0.25921
Piriform-amygdalar area: ttest pval (scaled--expected based on
size): 0.088843; tstat : 1.4062; df : 17; sd : 0.35881

Postpiriform transition area: Mean: 0.33813 +/- 0.030562 SEM
Test against a mean of 0
Postpiriform transition area: ttest pval: 0.0066758; tstat :
2.7612; df : 17; sd : 0.51955
Test against a Expected # of cells based on region size 0.30535
Postpiriform transition area: ttest pval (scaled--expected based on
size): 0.3961; tstat : 0.26765; df : 17; sd : 0.51955

Clastrum: Mean: 0.0042561 +/- 0.00083431 SEM
Test against a mean of 0
Clastrum: ttest pval: 0.11005; tstat : 1.2731; df : 17; sd :
0.014183
Test against a Expected # of cells based on region size 0.12164
Clastrum: ttest pval (scaled--expected based on size): 1; tstat
: -35.113; df : 17; sd : 0.014183

Endopiriform nucleus-dorsal: Mean: 0.039201 +/- 0.0035084 SEM
Test against a mean of 0
Endopiriform nucleus-dorsal: ttest pval: 0.0063029; tstat :
2.7885; df : 17; sd : 0.059643
Test against a Expected # of cells based on region size 0.43775
Endopiriform nucleus-dorsal: ttest pval (scaled--expected based on
size): 1; tstat : -28.3509; df : 17; sd : 0.059643

Endopiriform nucleus-ventral: Mean: 0.085026 +/- 0.0061553 SEM
Test against a mean of 0
Endopiriform nucleus-ventral: ttest pval: 0.0015377; tstat :
3.4474; df : 17; sd : 0.10464
Test against a Expected # of cells based on region size 0.21637
Endopiriform nucleus-ventral: ttest pval (scaled--expected based on
size): 0.99997; tstat : -5.3255; df : 17; sd : 0.10464

Lateral amygdalar nucleus: Mean: 0.096562 +/- 0.010483 SEM
Test against a mean of 0

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Lateral amygdalar nucleus: ttest pval: 0.017234; tstat : 2.2988;
df : 17; sd : 0.17821

Test against a Expected # of cells based on region size 0.20089

Lateral amygdalar nucleus: ttest pval (scaled--expected based on
size): 0.98814; tstat : -2.4838; df : 17; sd : 0.17821

Basolateral amygdalar nucleus-anterior: Mean: 0.59024 +/- 0.056393
SEM

Test against a mean of 0

Basolateral amygdalar nucleus-anterior: ttest pval: 0.0091088;
tstat : 2.6121; df : 17; sd : 0.95868

Test against a Expected # of cells based on region size 0.17252

Basolateral amygdalar nucleus-anterior: ttest pval (scaled--expected
based on size): 0.040991; tstat : 1.8486; df : 17; sd : 0.95868

Basolateral amygdalar nucleus-posterior: Mean: 0.26929 +/- 0.023909
SEM

Test against a mean of 0

Basolateral amygdalar nucleus-posterior: ttest pval: 0.0060123;
tstat : 2.811; df : 17; sd : 0.40645

Test against a Expected # of cells based on region size 0.15594

Basolateral amygdalar nucleus-posterior: ttest pval (scaled--
expected based on size): 0.1265; tstat : 1.1833; df : 17; sd :
0.40645

Basolateral amygdalar nucleus-ventral: Mean: 0.30243 +/- 0.0294 SEM
Test against a mean of 0

Basolateral amygdalar nucleus-ventral: ttest pval: 0.0099945;
tstat : 2.5672; df : 17; sd : 0.4998

Test against a Expected # of cells based on region size 0.091039

Basolateral amygdalar nucleus-ventral: ttest pval (scaled--expected
based on size): 0.045276; tstat : 1.7944; df : 17; sd : 0.4998

Basomedial amygdalar nucleus -anterior: Mean: 1.5901 +/- 0.12207 SEM
Test against a mean of 0

Basomedial amygdalar nucleus -anterior: ttest pval: 0.0023508;
tstat : 3.251; df : 17; sd : 2.0751

Test against a Expected # of cells based on region size 0.16715

Basomedial amygdalar nucleus -anterior: ttest pval (scaled--expected
based on size): 0.0048844; tstat : 2.9093; df : 17; sd : 2.0751

Basomedial amygdalar nucleus-posterior: Mean: 1.623 +/- 0.12082 SEM
Test against a mean of 0

Basomedial amygdalar nucleus-posterior: ttest pval: 0.0018883;
tstat : 3.3525; df : 17; sd : 2.054

Test against a Expected # of cells based on region size 0.15629

Basomedial amygdalar nucleus-posterior: ttest pval (scaled--expected

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based on size): 0.0037805;    tstat : 3.0296;    df : 17;    sd : 2.054
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Posterior amygdalar nucleus:    Mean: 3.7539 +/- 0.23612 SEM
Test against a mean of 0
Posterior amygdalar nucleus:    ttest  pval: 0.00049723;    tstat :
3.9677;    df : 17;    sd : 4.014
Test against a Expected # of cells based on region size 0.21998
Posterior amygdalar nucleus:    ttest  pval (scaled--expected based on
size): 0.00082354;    tstat : 3.7352;    df : 17;    sd : 4.014
-----
```

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Region	Male average (%)	Male SEM	Female average (%)
Field CA1	3.75	1.26	0.68
FieldCa3	6.79	3.24	2.53
Dorsomedial nucleus of the hypothalamus	0.59	0.36	0.32
Lateral hypothalamic area	2.15	0.83	2.01
Lateral preoptic area	0.55	0.14	0.19
Tuberal nucleus	0.02	0.01	1.98
Medial mammillary nucleus	0.23	0.10	0.57
Ventral premammillary nucleus	0.03	0.01	1.08
Ventromedial hypothalamic nucleus	0.52	0.21	2.15
Reticular nucleus of the thalamus	0.27	0.15	1.66
Caudoputatum	5.78	3.21	8.27
Central amygdalar nucleus	14.61	3.79	9.04
Medial amygdalar nucleus	12.95	3.51	29.19
Globus pallidus, external segment	2.49	1.08	4.49
Globus pallidus, internal segment	1.14	0.53	1.90
Substantia innominata	3.61	1.37	1.58
Diagonal band nucleus	0.74	0.22	0.24
BNST	0.86	0.28	0.40
AccessoryOlfactoryBulb	1.68	0.70	0.19
Piriform area	1.70	0.32	0.29
Cortical amygdalar area	4.13	1.42	2.90
Piriform-amygdalar area	0.60	0.12	0.16
Postpiriform transition area	0.58	0.22	0.06
Basolateral amygdalar nucleus-anterior	1.13	0.38	0.05
Basolateral amygdalar nucleus-ventral	0.54	0.21	0.08
Basomedial amygdalar nucleus -anterior	1.98	0.82	1.27
Basomedial amygdalar nucleus-posterior	1.52	0.43	1.83
Posterior amygdalar nucleus	3.80	1.33	2.56

Female SEM	p-value
0.32	0.0102
1.24	0.1272
0.15	0.3453
1.25	0.4462
0.08	0.0209
1.89	0.0625
0.45	0.3629
1.00	0.0375
1.41	0.1245
1.24	0.1364
4.62	0.2967
2.94	0.1303
10.68	0.0807
2.52	0.2509
0.89	0.2411
0.70	0.1146
0.14	0.0413
0.20	0.0962
0.12	0.0362
0.13	0.0002
1.52	0.2642
0.07	0.0038
0.04	0.0041
0.03	0.0007
0.04	0.01
0.63	0.251
1.01	0.3791
0.97	0.2437