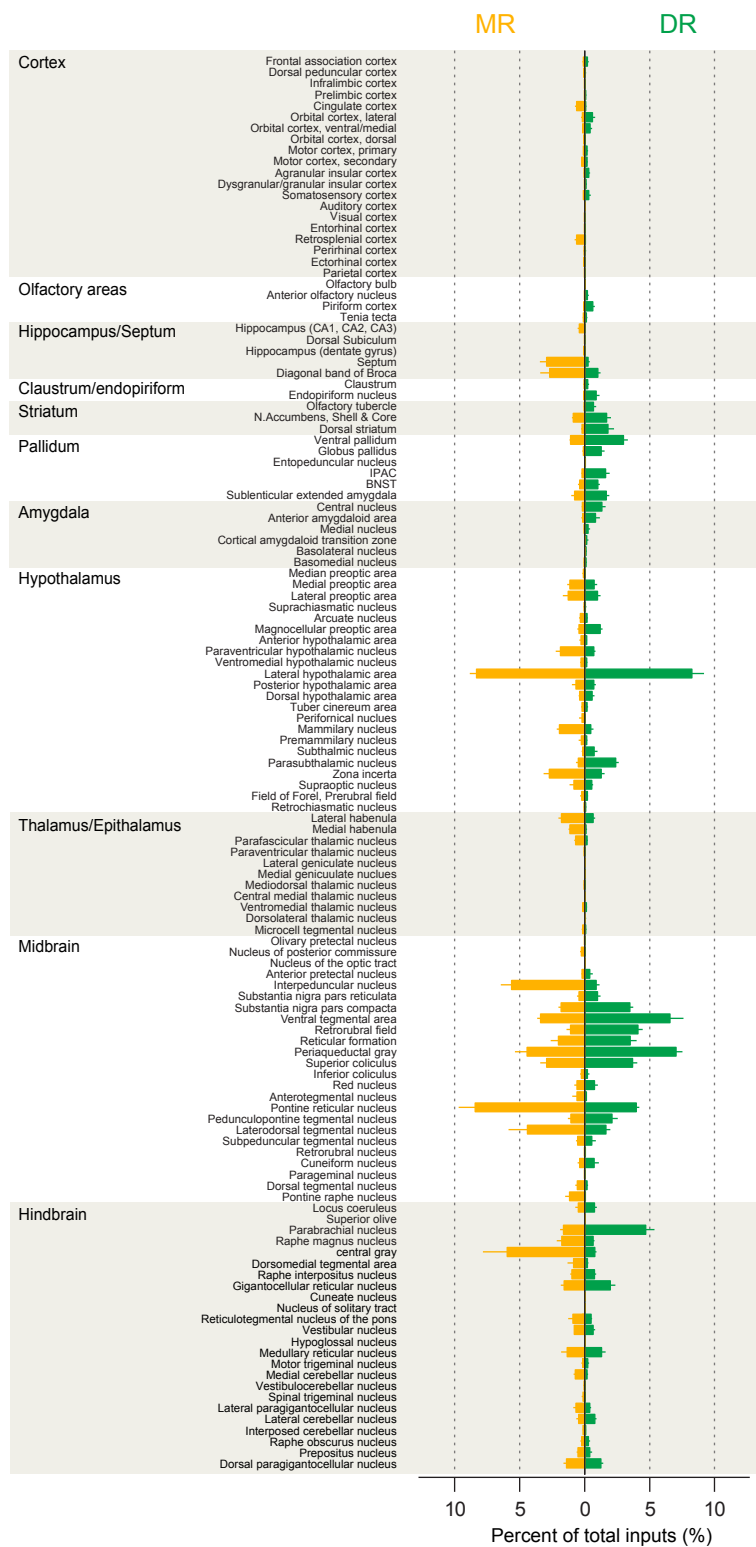


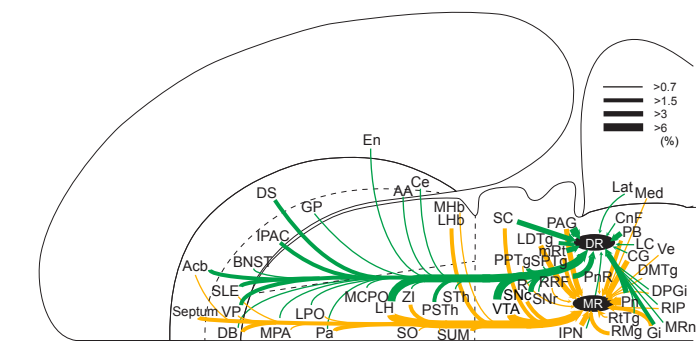
**Figure S1. Percent of total inputs from individual animals (Related to Figure 1)**

Cg, cingulate cortex; RS, retrosplenial granular cortex; LO, lateral orbital cortex; M1, primary motor cortex; M2, secondary motor cortex; S, somatosensory cortex; Septal nucleus; Acb, nucleus accumbens; DS, dorsal striatum; DB diagonal band of broca; VP, ventral pallidum; BNST, bed nucleus of the stria terminalis; SLE, sublenticular extended amygdala; IPAC, interstitial nucleus of the posterior limb of the anterior commissure; GP, globus pallidus; Ce, central nucleus of the amygdala; ZI, zona incerta; Pa, paraventricular hypothalamic nucleus; LH, lateral hypothalamic area; PSTh, parasubthalamic nucleus; MHb, medial habenula; LHb, lateral habenula; SUM, supramammillary nucleus; IPN, interpeduncular nucleus; VTA, ventral tegmental area; SNc, substantia nigra pars compacta; SNr, substantia nigra pars reticulata; RRF, retrorubral field; PAG, periaqueductal gray; mRt, mesencephalic reticular formation; LDTg, laterodorsal tegmental nucleus; Pn, pontine reticular nucleus; PPTg, pedunculotegmental nucleus ; PB, parabrachial nucleus; SC, superior colliculus.

**A**



**B**

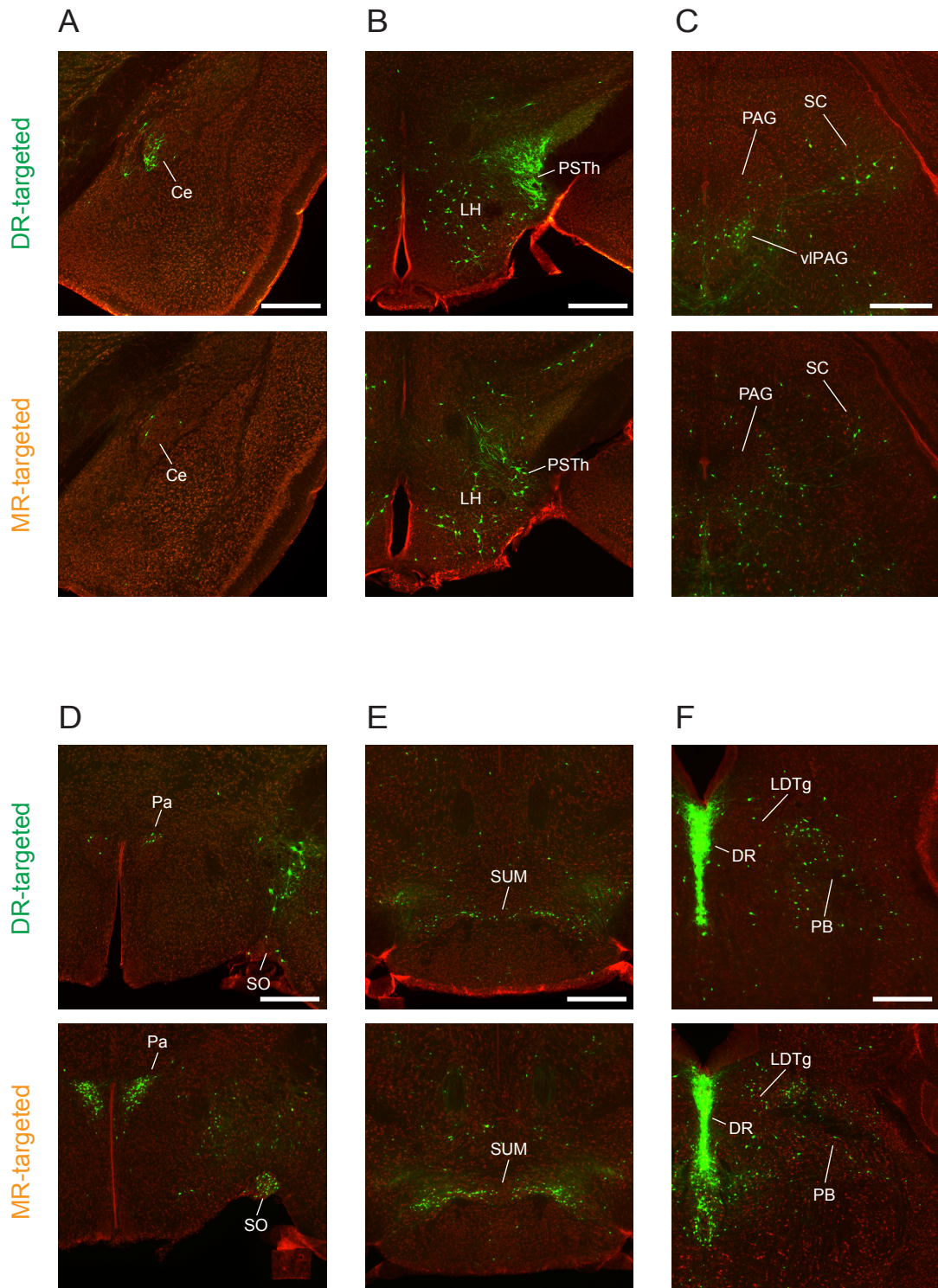


**Figure S2. Summary of monosynaptic inputs to DR and MR serotonin neurons including caudal hindbrain areas (Related to Figure 2)**

(A) Monosynaptic inputs to MR and DR serotonin neurons including caudal hindbrain areas (orange and green, respectively). The values are the percentages of total inputs in each area. Twenty areas of caudal hindbrain are added to Figure 2, and the percentages of total inputs in each area are recalculated based on all brain areas. Mean  $\pm$  SEM (n = 7 and 5 mice for DR and MR groups, respectively). DR and MR areas are excluded from the analysis.

(B) Flatmap summary of monosynaptic inputs to DR and MR serotonin neurons. Green indicates inputs to DR serotonin neurons. Orange indicates inputs to MR serotonin neurons. The thickness of each line indicates the percentage of total inputs in each area as defined at the top right corner. The flatmap representation is after Swanson (2000).





**Figure S3. Comparisons of other major input areas (Related to Figure 3)**

(A) Central nucleus of the amygdala (Ce). Ce projects to DR more than MR serotonin neurons.

Bregma  $-1.70$  mm. Scale bars,  $0.5$  mm.

(B) Lateral hypothalamic area (LH) and paraventricular nucleus (PVH). Serotonin-projecting neurons in LH are sparsely distributed. PVH neurons project to DR more than MR serotonin neurons.

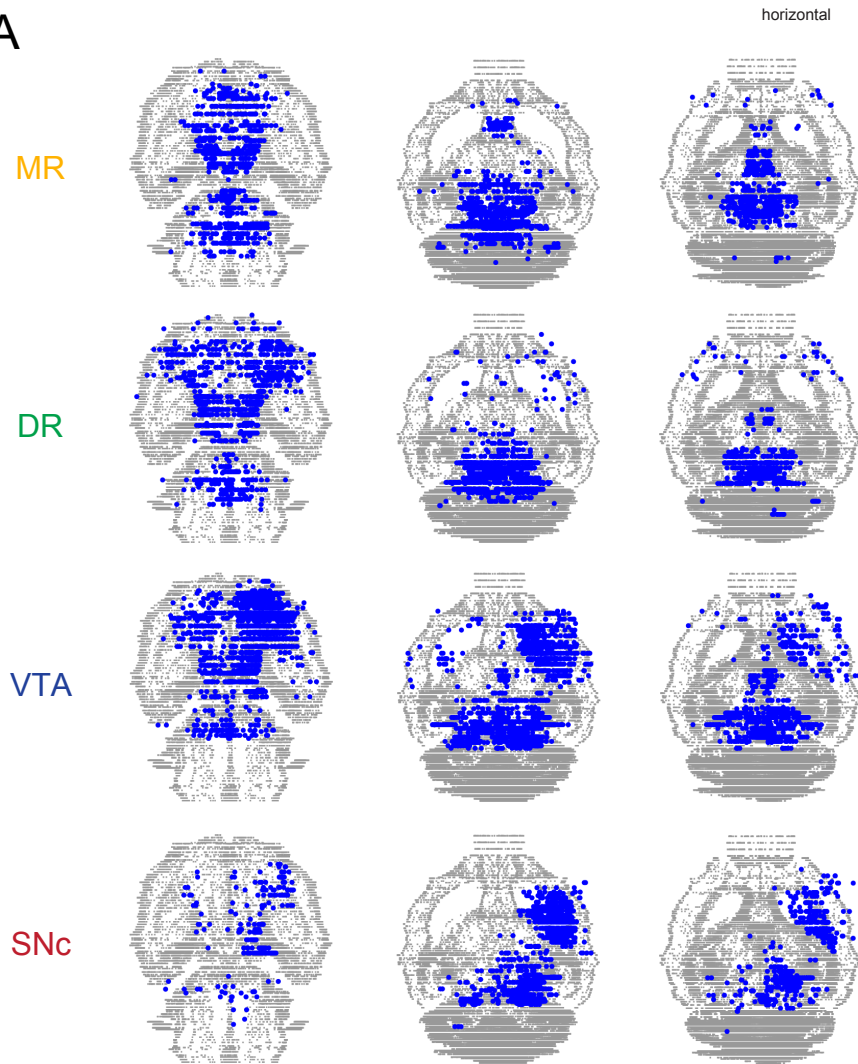
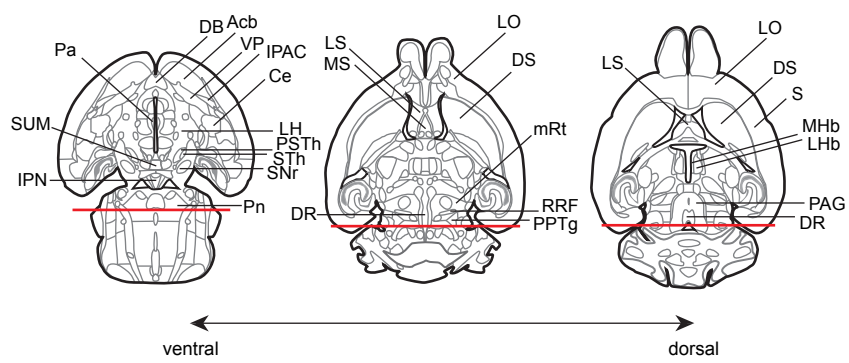
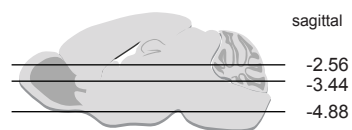
Bregma  $-2.30$  mm. Scale bars,  $0.5$  mm.

(C) PAG, periaqueductal gray and SC, superior colliculus. DR serotonin-projecting neurons are clustered in the ventrolateral part of the PAG (vlPAG) and ventral part of SC, whereas MR serotonin-projecting neurons are sparsely distributed in these areas. Bregma  $-4.04$  mm. Scale bars,  $0.5$  mm.

(D) Paraventricular hypothalamic nucleus (Pa) and supraoptic nucleus (SO). Pa projects to MR more than DR serotonin neurons. Bregma  $-0.82$  mm. Scale bars,  $0.5$  mm.

(E) Supramammillary nucleus (SUM). SUM projects to MR more than DR serotonin neurons. Bregma  $-2.70$  mm. Scale bars,  $0.5$  mm.

(F) Laterodorsal tegmental nucleus (LDTg) and parabrachial nucleus (PB). LDTg projects to MR more than DR serotonin neurons. Bregma  $-4.96$  mm. Scale bars,  $0.5$  mm.

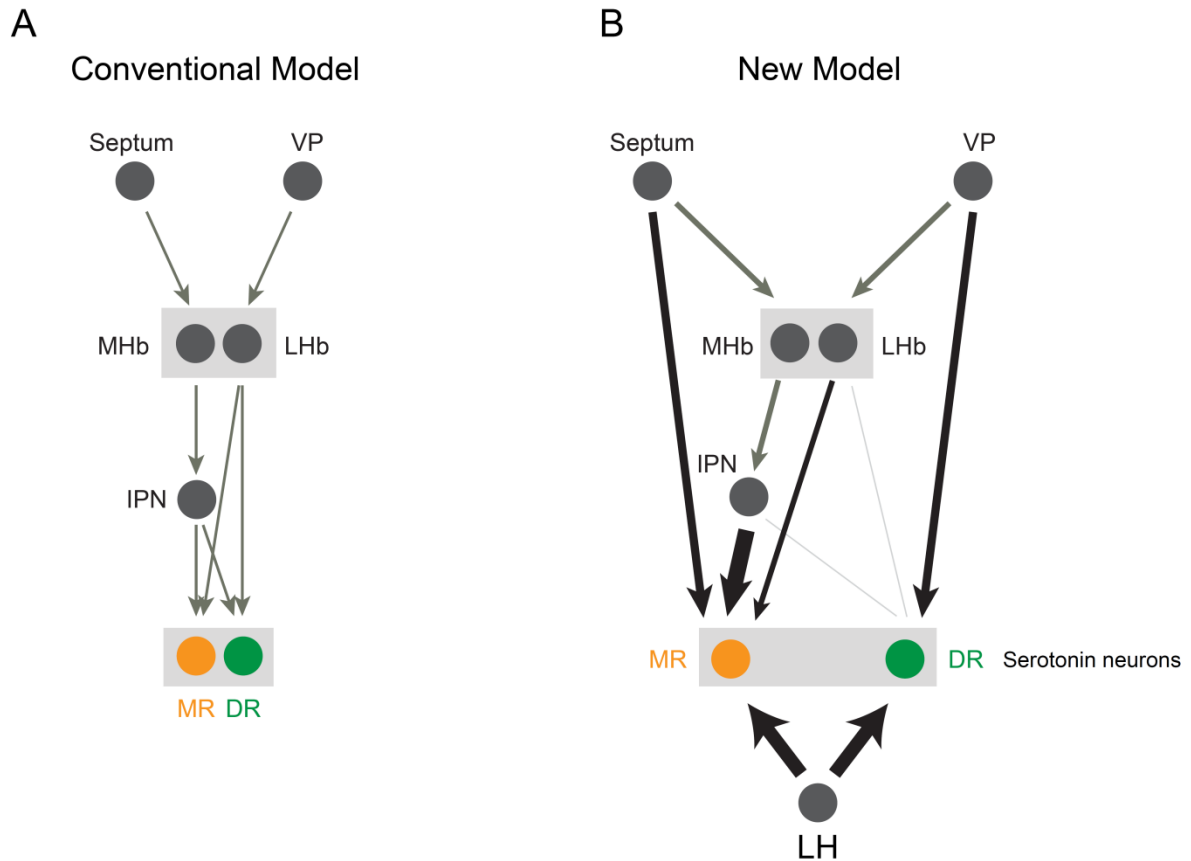
**A****B****C**

**Figure S4. Distributions of monosynaptic inputs projected onto reconstructed horizontal slices**

(A) Data obtained from coronal slices were projected onto a 3D standard brain atlas. Each image represents a horizontal slice of the standardized brain (500  $\mu\text{m}$  thick). Blue dots represent input neurons from two mice each (MR; MR12 and MR13, DR; DR1 and DR6, VTA; v009 and v010, and SNc; s003 and s006). Note that the starter neurons for MR and DR are in both hemispheres while starter neurons in VTA and SNc are in one hemisphere.

(B) Atlas corresponding to each horizontal section. Input neurons were collected anterior to red lines. Bregma -5.34 mm.

(C) Approximate positions of horizontal images shown in (A) and (B).



**Figure S5. Models of information flow from forebrain to MR/DR serotonin neurons**

(A) Conventional model. The major forebrain projections to both MR and DR, serotonin neurons are believed to come from MHb via IPN and LHb, although there are observations of projections from other areas (Herkenham and Nauta, 1979; Hikosaka et al., 2008; Klemm, 2004; Lecourtier and Kelly, 2007).

(B) New model. Whereas MR serotonin neurons receive projections from the forebrain through MHb and LHb, in addition to direct projections from the septum, DR serotonin neurons receive direct projections from the basal ganglia and the extended amygdale. LH provides the largest inputs to both MR and DR serotonin neurons. The thickness of each black arrow to serotonin neurons indicates the percentage of total inputs in each area. Light grey lines indicate small projections (less than 1 % of total inputs). Some connections are omitted for simplicity.

## SUPPLEMENTAL NOTE

Previous studies found that some TVA-negative (or Cre-negative) neurons were infected nonspecifically by the rabies virus (Miyamichi et al., 2013; Wall et al., 2013; Watabe-Uchida et al., 2012). This is likely due to the extremely high infection efficiency of the rabies virus (very minute expression of TVA is sufficient for rabies infection) and due to a very low level of TVA expression that inevitably occurs in the absence of Cre (i.e., “leak” expression). However, these neurons express negligible levels of RG, a high level of which is required for transsynaptic spread of the rabies virus. Thus, these neurons are very unlikely to contribute significantly to transsynaptic labeling outside injection sites (Miyamichi et al., 2013; Wall et al., 2013; Watabe-Uchida et al., 2012). To test whether Cre-negative cells contributed as starter neurons, we performed control experiments using wild-type mice that had no Cre expression (**Figure 1A**). Consistent with a previous study (Watabe-Uchida et al., 2012), injections of the three viruses in DR resulted in a noticeable number of EGFP-positive neurons at the injection sites ( $29.7 \pm 15.6$  neurons in DR). However, a very small number of EGFP-labeled neurons were found outside injection sites ( $1.67 \pm 0.88$  neurons outside DR; mean  $\pm$  SEM,  $n = 3$  mice), many fewer than those found in experimental animals ( $3,577 \pm 827$  neurons outside DR; mean  $\pm$  SEM,  $n = 7$  mice). Thus, only a negligible number of neurons (0.05% of total input neurons) was non-specifically labeled outside the injection site. Because injection sites contained some non-specifically-labeled neurons in control animals (about 7.78% of the number of starter neurons in experimental animals), our analysis focuses on neurons outside injection sites. No mCherry-positive neurons were found outside injection sites (except in adjacent nuclei that contain serotonin neurons, as discussed above), whereas a large number of EGFP-positive neurons were found (**Figure 1G**).

## **SUPPLEMENTAL EXPERIMENTAL PROCEDURE**

### **Image Analysis**

To compare horizontal distributions of inputs using standardized coordinates, brains of individual animals were fit to a standard atlas (Franklin and Paxinos, 2008). The following brains were used for this analysis: DR1, DR6, MR12, MR13, v009, v010, s003, and s006. Each coronal section in the standard atlas and its matching section in our data was manually landmarked with five points: four peripheral and one central. Next, affine transformations warped the section in our data to the corresponding section in the atlas using the landmarks. We then made horizontal projections of the atlas and the data based on those points in 3-dimensional space (**Figure S4**).

## **SUPPLEMENTAL REFERENCES**

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