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EphrinA5 signaling is required for the distinctive targeting of raphe serotonin neurons in the forebrain.

EphrinA signaling directs serotonin raphe projections

Teng Teng^{1,2,3}, Afsaneh Gaillard^{4,5}, Aude Muzerelle^{1,2,3} and Patricia Gaspar^{1,2,3}

¹Inserm UMR-S 839, 75005, Paris, France

²Université Pierre et Marie Curie, Paris, France

³Institut du Fer à Moulin, Paris, France

⁴Inserm 1084, Poitiers, France

⁵Université de Poitiers, Poitiers, France

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Correspondence should be addressed to Patricia Gaspar, INSERM U 839, 17 rue du Fer à Moulin, 75005, Paris, France. Tel: 331 45 87 61 28 Fax: 331 45 87 61 30. Email: patricia.gaspar@inserm.fr

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4 **Author names affiliations:**

5 Teng Teng ^{1, 2, 3}, Afsaneh Gaillard ^{4, 5}, Aude Muzerelle ^{1, 2, 3}, Patricia Gaspar ^{1, 2, 3}

6 1. Inserm UMR-S 839, 75005, Paris, France

7 2. Université Pierre et Marie Curie, Paris, France

8 3. Institut du Fer à Moulin, Paris, France

9 4. Inserm 1084, Poitiers, France

10 5. Université de Poitiers, Poitiers, France

11 **Corresponding author:**

12 Patricia Gaspar, email: patricia.gaspar@inserm.fr

13 Address: INSERM U 839, 17 rue du Fer à Moulin, 75005, Paris, France

14 Tel: 331 45 87 61 28 Fax: 331 45 87 61 30;

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Abstract

Serotonin (5-HT) neurotransmission in the brain relies on a widespread axon terminal network originating from the hindbrain raphe nuclei. These projections are topographically organized such that the dorsal (DR), and median raphe (MnR) nuclei have different brain targets. However, the guidance molecules involved in this selective targeting in development are unknown. Here, we show the implication of ephrinA5 signaling in this process. We find that the *EphA5* gene is selectively expressed in a subset of 5-HT neurons during embryonic and postnatal development. Highest co-expression of *EphA5* and of the 5-HT marker *Tph2* is found in the DR with lower co-expression in the MnR, and hardly any colocalization in the caudal raphe in the medulla. Accordingly, ephrinA induced a dose-dependent collapse response of 5-HT growth cones cultured from rostral but not caudal raphe. Ectopic expression of ephrinA3, after in utero electroporation in the amygdala and piriform cortex, repelled 5-HT raphe fiber ingrowth. Conversely, misplaced DR 5-HT axons were found in ephrin A5 KO mice in brain regions that are normally only targeted by MnR 5-HT axons. This causes an overall increase in the density of 5-HT innervation in the ventromedial hypothalamus, the suprachiasmatic nucleus and the olfactory bulb. All these brain areas have high expression of ephrinAs at the time of 5-HT fiber ingrowth. Present results show for the first time the role of a guidance molecule for the region-specific targeting of raphe neurons. This has important implications to understand how functional parsing of central 5-HT neurons is established during development.

Significance statement: Present results demonstrate a new role of ephrinA signaling for the selective targeting of 5-HT raphe nuclei. The tyrosine kinase EphA5 is differentially expressed across 5-HT neurons from the different raphe nuclei in mice, correlating with a different repulsive action of ephrinA on the growth of 5-HT axons. EphrinA5 loss of function causes a mis-targeting of dorsal raphe 5-HT axons, whereas overexpression of ephrinA inhibits the ingrowth of 5-HT raphe axons in the amygdala and piriform cortex that are main targets of the dorsal raphe 5-HT neurons. Thus Eph-ephrin signaling acts as a repulsive signal to differentially target 5-HT axons originating from different raphe nuclei.

64 Introduction

65 Serotonin (5-Hydroxytryptamine, 5-HT) neurotransmission is implicated in a large
 66 number of physiological functions raising the question of a division of labor among the
 67 different hindbrain nuclei that synthesize 5-HT (Calizo et al., 2011; Hale and Lowry, 2011;
 68 Kiyasova and Gaspar, 2011). The 5-HT synthesizing neurons are distributed into several
 69 raphe nuclei in the hindbrain that have been parsed according to anatomical and physio-
 70 logical criteria. Individual raphe nuclei target different brain regions and consequently, are
 71 involved in different functions. For instance the caudal 5-HT raphe nuclei (the B1-B3 cell
 72 groups) that are located in the medulla, project to the brainstem and spinal cord are im-
 73 plicated in motor control and in neurovegetative functions (Schmidt and Jordan, 2000;
 74 Pflieger et al., 2002; Brust et al., 2014). Conversely, 5-HT neurons of the rostral raphe
 75 which are located in the pontine region of the hindbrain (the B5-B9 cell groups) project to
 76 the forebrain and have been involved in diverse higher brain functions, such as mood,
 77 learning and diverse social behaviors, such as aggression and maternal behavior (Dea-
 78 kin and Graeff, 1991; Lucki, 1998; Fernandez and Gaspar, 2012, Trowbridge et al. 2011).
 79 Within these broad raphe divisions, further anatomical and functional distinctions can be
 80 made ; for instance the rostral raphe cluster comprises neurons of the dorsal raphe (DR
 81 =B6+B7) and the median raphe (MnR= B5+B8) groups that are implicated in different
 82 brain functions (Jacobs and Azmitia, 1992; Fernandez et al., 2015; Teissier et al., 2015)
 83 and innervate complementary targets in the telencephalon (Vertes et al. 99, Muzerelle et
 84 al., 2016). This organization suggests that specific axon guidance molecules could orient
 85 the 5-HT-containing axons to specific targets, although the underlying molecular mecha-
 86 nisms are largely unknown (Kiyasova and Gaspar, 2011).

87 Previous transcriptome profiling of developing 5-HT raphe neurons identified dis-
 88 tinct expression profiles between the rostral pontine and the caudal medullary raphe cell
 89 groups (Wylie et al., 2010). Among these differentially expressed genes a number of ax-
 90 on guidance molecules, such as Eph receptors and their ephrin ligands are potential
 91 candidates for the selective guidance of 5-HT neuron subsets. The properties of EphA
 92 receptors as short-range guidance factors make them attractive candidates for selective
 93 axon targeting (O'Leary and Wilkinson, 1999; Klein and Kania, 2014). Eph-ephrin signal-
 94 ing has indeed been involved in many functions, one of the best known being it's role for
 95 establishing topographic maps in several sensory systems (Prakash et al., 2000; Miko et
 96 al., 2007). Moreover the EphA ligand, ephrinA5 was suggested to be involved in the de-

97 velopment of the dopaminergic neurons, based on its dynamic developmental expression
98 patterns (Deschamps et al., 2009, 2010; Prestoz et al., 2012).

99 In the present study, we demonstrate a role for Eph-ephrinA signaling in develop-
100 ing 5-HT raphe neurons to repel axon growth of a subset of 5-HT neurons. We find that
101 ephrinA5 is required for the exquisite differential targeting of the DR and MnR axons in
102 the olfactory bulb, amygdala and hypothalamus. These observations establish for the first
103 time a role of Eph-ephrinA signaling to organize the broad topography of a monoaminer-
104 gic system.

105 **Material and methods**

106 **Animals**

107 Most experiments (gene expression, cell cultures, electroporations) were performed
108 on mice of the Swiss background (RjOrl:SWISS) purchased from a commercial breeder
109 (Centre d'Elevage R. Janvier). E0 was defined as the plug date and P0 as the date of
110 birth.

111 The Pet1-Cre::RCE-GFP mouse line was used for RT-qPCR analyses. ePet1-Cre
112 mice (Scott et al., 2005) in which the serotonergic specific promoter of the Pet1 gene
113 controls Cre expression were crossed to the RCE-GFP mouse line where enhanced
114 green fluorescent protein is conditionally expressed under the Rosa-26 promoter (Sousa
115 et al., 2009). Pet1-Cre::RCE-GFP mice were bred in our local facility and brains collected
116 from P5, P15 and adult mice.

117 The ephrinA5-KO mouse line (Frisen et al., 1998) was maintained on a C57Black6
118 background (Deschamps et al., 2009). Briefly, these mice have a PGK-neo cassette re-
119 placing the 5' acceptor splice site and the sequences encoding amino acid residues 42–
120 129. The PCR primers for genotype are as follows: primer 1 (TCCAGCTGTGCAG-
121 TTCTCCAAAACA) and primer 2 (ATTCCAGAGGGGTGACTACCACATT) for wild-type
122 sequences (397bp) and primers 1 and primer 3 (AGCCCAGAAAGCGAAGGAG-
123 CAAAGC) for mutant sequences (513bp).

124 All experiments were performed in compliance with the standard ethical guidelines
125 (European Community Guidelines and French Agriculture and Forestry Ministry Guide-
126 lines for Handling Animals decree 87849). All efforts were made to reduce the number of
127 animals used and their suffering. Male and female mice were used indiscriminately in all
128 experiments.

129 Histology

130 **Section preparation** Brains of Swiss mice were collected at embryonic days 12
131 (E12), E14, E16, E17, E18, at postnatal days 0(P0), P5, P10, P15 and from adult aged
132 over 8 weeks.

133 Mice aged P5 or younger were anesthetized on ice. Mice older than P5 were anes-
134 thetized with pentobarbital, 25mg/kg and xylazine, 5mg/kg. Fixation was either with im-
135 mersion (E14, E16) or perfusion (>E16) with 4% PFA (4% paraformaldehyde in 0.12M
136 phosphate buffer, pH 7.4). Dissected brains were post-fixed 2 hours (embryonic ages) or
137 overnight (all postnatal ages) before cryoprotection in 10% sucrose and freezing in iso-
138 pentane cooled with dry ice at -45° to -55°C. In some in situ hybridization (ISH) protocols
139 no post-fixation was performed. Frozen brains were then cut with a cryostat to either cor-
140 onal or sagittal 20µm thick sections and collected as series of 6. Frozen sections were
141 stored at -80°C before immunohistochemistry or ISH. Some brains were processed as
142 floating sections and sectioned with a freezing microtome. In this case, the brains were
143 cryoprotected in 30% sucrose and frozen directly on the platform of the cryotome at -
144 40°C; serial 40µm thick coronal sections were collected in 1X PBS with 0.01% sodium
145 azide. Sections were stored at 4°C before processing.

146 **In situ hybridization** (ISH) was used to analyze EphAs and ephrinAs expression.
147 Digoxigenin-labelled mRNA probes were transcribed from mouse EphA3, EphA4, EphA5,
148 EphA7, and Efna2, Efna3, Efna5, cDNAs. Sense and antisense digest enzymes and pol-
149 ymerases of these probes are listed in Table 1. Sections were air-dried for at least two
150 hours under a hood. Specific antisense RNA probes (0.1-1µg/ml) were mixed with hybrid-
151 ization buffer (50% formamide, 10% dextran sulfate, 1X Denhardt's, 5X SSC and 250
152 µg/ml tRNA) and incubated at 52°C, 58°C or 65°C for 10mins. 350ul of mixed hybridiza-
153 tion buffer was added to each section, covered with a cover-slip, and incubated overnight
154 at the same temperature. The sections were washed with PBS and PBS Triton 0.1% and
155 incubated with anti-Digoxigenin (1/1000) 4° overnight. Sections were washed with 1X
156 PBS and NTMT (Tween 10%; Tris-HCL, pH 9.5, 1M; MgCl2, 1M; NaCl, 5M; H2O) buffer
157 and incubated at 37° with NBT+BCIP or fast red (TR/Naphthol AS-MX Tablets, SIGMA
158 F4523-50 SET) to reveal the reaction. Duration of the revelation (from 2 to 24 hours) was
159 determined empirically according to the sensitivity of the probes and the concentration of
160 the anti-Dig solution. The signal was checked with bright field or fluorescence microscop-
161 y. Duration was kept identical for a given experiment (eg. Time course of expression).

162 The sections were washed with 1X PBS, and mounted in mowiol-Dabco (25 mg/ml) or
163 processed with Immunohistochemistry.

164 **Immunohistochemistry** was performed either on alternate series of sections or in
165 combination with ISH. Sections were washed in PBS, then in PGT (PBS with 0.2% gela-
166 tin and 0.25% Triton X-100) 4 X 15 mins. Sections were incubated overnight at 4°C with
167 the following primary antibodies: anti-Tph2 (mouse monoclonal, 1/1000, Sigma), anti-5-
168 HT (rabbit polyclonal, 1/1000 Sigma), anti-SERT (rabbit polyclonal, 1/1000, Calbiochem).
169 For fluorescence microscopy, sections were then incubated for 2h at room temperature
170 with the following secondary antibody: donkey anti-rabbit 488 (1/200, Jackson), donkey
171 anti-rabbit Cy3 (1/200, Jackson), donkey anti-mouse 488 (1/200, Jackson), donkey anti-
172 mouse Cy3 (1/200, Jackson), or with phalloidin 594 (1/40 Invitrogen). Then sections were
173 rinsed in PB, mounted in mowiol-Dabco (25 mg/ml) and stored at +4°C.

174 **RT-qPCR** . Brains of Pet1-Cre::RCE-GFP mice were collected at postnatal day 5, 15
175 and adult (6 weeks). Brains were kept in 1X PBS on ice and sectioned in the coronal
176 plane with a tissue chopper to 300µm thick sections. The DR was micro dissected under
177 a fluorescent macroscope (Zeiss-MV10) and collected into 5ml tubes, which contained
178 2ml of cold 1X PBS, a cortical hemisphere was collected as a positive control. To obtain
179 enough tissue for RNA isolation from the raphe, four cases were pooled together for each
180 sample analyzed. Tissue was either directly processed for RNA isolation or fast frozen at
181 -80°C. RNA isolation from tissue was done with Trizol Reagent (Sigma). Samples were
182 weighed (≤ 50 mg) before homogenization, PBS was removed extensively and 1ml of tri-
183 zol was added. Tissue was homogenized and homogenates were transferred to 2ml ep-
184 pendorf tubes with 0.2ml of chloroform, gently mixed for 15 seconds, and centrifuged
185 12000g, for 15mins at 4°C. The upper phase was collected and RNA was precipitated
186 with isopropyl alcohol, 0.5ml, incubating at room temperature (5mins), centrifuged at
187 12000g for 10mins at 4°C. After removal of the supernatant, the RNA pellet was air-dried
188 and dissolved in 100µl Milli-Q water and stored at -80°C.

189 Possible DNA contamination was cleared using DNase I (Thermo) and RT-PCR was
190 done with the SuperScriptII kit (Invitrogen). Quantitative-PCR was performed with the
191 Thermo SYBR Green Mix kit according to the manufacturers' instruction. Primers are
192 listed in Table 2.

193 **Raphe culture and collapse assay.** E12 embryos were collected from Swiss timed-
 194 pregnant dams. Embryonic hindbrains were rapidly dissected as an 'open book' in ice
 195 cold 1X PBS. The rostral and caudal raphe were separated based on anatomical land-
 196 marks. The dissected raphe was further cut into 200µm explants with a tissue chopper.
 197 Explants were placed onto polylysine/laminin-coated glass coverslips (Marlenfield,
 198 0111540) in 4-well culture boxes (Nuncclon, 176740) in DMEM F-12 medium to which BSA
 199 (1%), Pen/strep, Glutamine (200mM), Glucose (50%) were added. Explants were cul-
 200 tured for 3-4 days at 37°C, in 5% CO₂. For the collapse assay ephrinA5 (R&D System,
 201 374-EA) was added at different concentrations (50mM, 250mM, 500mM) for 1h. Explants
 202 were then quickly washed in PBS, fixed in buffered 4% PFA for 30mins, and washed ex-
 203 tensively before 5-HT immunocytochemistry (anti-5-HT rabbit polyclonal, 1/1000 from
 204 Sigma) and phalloidin 594 (1/40 Invitrogen) staining.

205 **Quantification of the collapse assay.** Explants were imaged with a fluorescence
 206 microscope. Only round-shaped explants which contained 5-HT neurons were quantified,
 207 Over 100 growth cones from 3 explants for each condition were counted using a
 208 63X/1.25 objective. The number of collapsed/non collapsed growth cones was counted
 209 for both 5-HT axons and non-5-HT axons, comparing the 5-HT immunostaining with the
 210 phalloidin staining. Results from 3 independent experiments were used to calculate the
 211 mean ratio \pm SEM per condition.

212 **Anterograde Tracing.** We used an adeno-associated virus
 213 (AAV1.CAG.tdTomato.WPRE.SV40 ref: AV-1-PV3365, Penn Vector) to express td-tomato
 214 fluorescence in the DR neurons and projections. A single injection (20nl of the virus non-
 215 diluted) was done in the DR using glass pulled capillaries (5-000-1001-X10, Drummond;
 216 puller model 720, KOPF with a heat of 14.5 and solenoid 2). DR stereotaxic injections
 217 were performed as previously described (Muzerelle et al., 2016). Adult ephrinA5 KO mice
 218 and control littermate (+/+ or +/-) mice were anesthetized with ketamine (150 mg/kg) /
 219 xylazine (10 mg/kg). Animals were positioned on a foam board horizontally, the head was
 220 fixed and kept horizontal, and Bregma coordinates measured to calculate the position of
 221 the injection site and the angle of stereotaxic arm. To target the DR the following coordi-
 222 nates were used: antero-posterior: 0.5mm to lambda; medio-lateral: 1mm; dorsoventral: -
 223 3.2mm. The animals were kept for 3 weeks and were perfused by 4% PFA. Brains were
 224 processed as described above, collecting serial 50µm coronal sections throughout the
 225 brain.

226

227 **In utero electroporation of EphrinA construct** . GFP-Efna3 was sub-cloned into
 228 the vector pCIG-Td-tomato. The pCIG-Td-tomato vector without the insert was used for
 229 the control condition. Both plasmids were purified by Qiagen EndoFree Plasmid Maxi kit,
 230 and stored at a final concentration of 2.5µg/µl.

231 To target gene expression in the amygdala, we followed a previously described in
 232 utero electroporation protocol (Remedios et al., 2004; Huang et al., 2014). The plasmids
 233 (1µg/µl) were mixed with 1% Fast Green (F7252, Sigma-Aldrich) and injected into one of
 234 the lateral ventricles of E12.5 embryos with glass-pulled micropipettes. Then a 3mm di-
 235 ameter electrode (LF650P3, BEX) was placed toward the caudal and ventral part of the
 236 telencephalon. Six electric pulses (30V, 50ms pulse length) with 950-ms intervals were
 237 applied using an electroporator (CUY21, BEX). After delivery, foster mothers delivering at
 238 the same time as the experimental subjects adopted the newborn pups. The electro-
 239 porated pups were perfused at P5 and processed for immunocytochemistry as described
 240 above.

241 **Image acquisition:** For bright field microscopy, histological sections were imaged
 242 using a slide scanner (Nanozoomer 2.0-HT C9600, Hamamatsu, Japan) objective X20 or
 243 captured with a Cool SNAP camera mounted on a bright-field microscope (Provis, Olym-
 244 pus,). For illustration purposes, images from the nanozoomer were exported in Tiff format
 245 using the NDP View2 software (Hamamatsu, Japan).

246 For fluorescence microscopy, images were acquired with a Leica DM 6000B system
 247 using a 40x/0.70 oil objective (tissue cultures), or acquired on a Leica SP5 confocal sys-
 248 tem (co-localization and fiber density analyses), equipped with an Argon laser (for the
 249 488nm excitation), a Diode 561nm and HeNe 633nm. Z-stacks of confocal images were
 250 acquired at 1024 x 1024 pixel resolution, with a pinhole set to one Airy unit and optimal
 251 settings for gain and offset.

252 **Image analyses** ; EphA5-Tph2 co-localization was analyzed on P5 brains processed
 253 from 3 independent experiments. 20µm-thick cryostat sections through the brainstem
 254 were collected as series of 6. One series was processed for combined EphA5 HIS (fast
 255 red chromogen), Tph2 immunohistochemistry (revealed with Alexa 488) and DAPI, and
 256 imaged with a confocal microscope. These 3 fluorochromes were sequentially acquired
 257 with a 40X/1.25 N.A Plan-apochromat objective at 3 different rostrocaudal levels through
 258 the raphe (Paxinos Atlas, levels: Bregma -4.3mm, -4.6mm and -4.9mm). The whole hind-
 259 brain area containing Tph2+ neurons was acquired including the different subdivisions of

the DR in the dorsal part (DRD), the ventral part (DRV) the lateral wings (DR-LW), and the caudal part (DR-C, B6). Acquisitions included the MnR which comprises the B8 and B5 cell groups, and the suprallemniscal B9 cell groups. Confocal stacks were analyzed with image J. A 150 μ m X 150 μ m square mask was used for random selection of counting areas. Three random selections were positioned on each distinct 5-HT sub-nucleus. A cell counter plugin was used to count the Tph2 positive cells on individual confocal sections, EphA5 positive cells and the co-localized neurons. It should be noted that in contrast to BCIP the fast red used as a chromogen for ISH mRNA revelation generally diffuses into the nucleus of labelled cells, in contrast to the Tph2 labelling that remains in the cytoplasm (eg. Figure 2 C, Figure 3).

Fiber density was analyzed in two different ways, in cases in anterograde tracer injections and in utero electroporation. In the olfactory bulb and amygdala, confocal images were acquired at 4 μ m intervals over 20 μ m in z. A maximum Z-projection of the image stacks was performed with image J. Then, a circular mask of 20 μ m diameter was used for random sample selection. All labeled fibers that crossed the edge of the mask were counted with a cell counter to compute linear densities. In the hypothalamus, where there is a high density of 5-HT innervation single confocal images were analyzed. Confocal 16 bit images were copied to Image J with an 8-bit format and processed as described (Kiyasova et al. 2011). Subtraction of the background was done with a 20 pixels rollerball and a binary image was obtained after applying a fixed range threshold for all the images. The nuclear region of interest (ROI) was delimited and the area occupied by the labeled fibers was measured within a circular mask (100 μ m diameter), the mask was randomly placed in 3-5 different locations over the structure, to calculate a mean density value per area and per animal.

Statistical analyses. All the statistical analyses applied were performed with GraphPad Prism 6. One-way ANOVA was performed for the Q-PCR, co-localization and collapse assays. To evaluate difference between any of two samples Tukey's multiple comparisons was performed. Student t-test was performed for intergroup comparisons in the fiber density analyses. Unpaired t-test was used for comparison of independent samples and paired t-test was done for analyses comparing, ipsi and contralateral innervation in the same case. Data are expressed as Means \pm SEM, $P < 0.05$ was considered as significant.

Results

Expression of EphA receptors in the raphe nuclei.

In rodents, 5-HT neurons of the hindbrain start extending axons by embryonic day 12 (E12) reach most of their forebrain targets between E15 and postnatal day 1 (P1) and start arborizing in these targets over the following postnatal days (Lidov and Molliver, 1982 in rats; Kiyasova and Gaspar, 2011, in mice).

We began by screening the expression of the EphA receptors at P5, a time when the 5-HT axons are still actively growing and branching in their targets (Lidov and Molliver, 1982) and where the DR and the MnR can be clearly individualized. Q-PCR analyses were performed on-micro-dissected DR from Pet1-GFP mice (Scott et al., 2005). *EphA3*, *A4*, *A5*, *A6*, *A7*, and *A8* mRNAs using GAPDH as a housekeeping gene. This analysis showed that *EphA5* is the most abundant EphA receptor in the DR at P5, with lower expression of *EphA4*, *EphA6*, and *EphA7*. And no detectable expression of *EphA3* and *EphA8* (Figure 1A). To determine the cellular localization of the *Eph* genes, in situ hybridization (ISH) was performed on consecutive serial coronal sections through the raphe, using specific mRNA probes of EphAs (Table 1) and to the serotonin transporter (SERT) used as a marker of the 5-HT raphe neurons. This showed that among the Ephs genes examined, only *EphA5* was clearly localized in the DR and the MnR containing 5-HT neurons, but with no visible expression in the raphe magnus, obscurus and pallidus (the B1-3 raphe cell groups)(Figure 1B). The other EphA genes, *EphA4* and *EphA7* genes, were not detectable in any of the raphe nuclei but were localized to nuclei, such as the dorsal lateral tegmental nuclei and superior olive, that abut the raphe nuclei (Figure 1B), which likely explains their detection when analyzed by Q-PCR on dissected DR tissue. Sense probes that were used as controls.

Overall, these results indicated a preferential expression of *EphA5* over other EphA receptors in the developing DR and MnR.

EphA5 expression is dynamically regulated during raphe development

To evaluate the possible developmental impact of *EphA5* at different stages of raphe development, we analyzed its expression timeline. Serial sagittal (E14, n=4) and coronal (postnatal and adult) sections were processed for *EphA5* ISH P0 (n>5), P5 (n>5), P10 (n>5), P15 (n>5) and adult (n=2). *EphA5* expression was detectable in the rostral raphe at E14 (Figure 2 B). This expression was maintained at a high level over the first week following birth and subsequently declined by P15 (Figure 2B) up to adulthood where only weak expression is detectable (not shown). To obtain a quantitative evaluation of the time

course of expression Q-PCR measures of EphA5 mRNA were done on DR tissue from P5, P15 and adult brains (Figure 2A). This showed a significant decrease of EphA5 expression between P5 and P15 ($p < 0.05$), consistent with the ISH observation.

These results indicated that EphA5 is dynamically regulated during development with highest expression in early postnatal life with a subsequent decline in expression by P15.

Serotonergic raphe nuclei differ in EphA5 expression pattern

Hindbrain raphe nuclei contain a heterogeneous neuronal population that includes in addition to 5-HT neurons, glutamatergic, GABAergic, and peptide-containing neurons. To determine whether EphA5 is specifically expressed in the serotonergic neurons we combined fluorescent *EphA5* ISH and tryptophan hydroxylase (Tph2) immunocytochemistry (Nguyen et al. 2001) (Figure 2). At E14, 5-HT neurons have not yet achieved their full migration, making it difficult to distinguish clearly all the individual raphe cell groups other than the 2 main rostral and caudal clusters. However a distinction could be made between the dorsal and ventral Tph2+ neurons of the rostral cluster that corresponds to the prospective DR and MnR respectively (Figure 2C). In the dorsal part, a large number of co-localized EphA5-Tph2+ neurons were found (Figure 2C'), whereas rare co-localisation was found in the ventral part. In contrast, in the medulla, the caudal Tph2+ cluster appeared to be entirely segregated from the *EphA5* expressing region.

A more detailed quantitative evaluation of EphA5-Tph2 co-localisation was done at P5, since distinction of these components can be done clearly at this stages (Figure 2 D-E), and this postnatal developmental stage is highly relevant to the ingrowth of 5-HT axons in their targets. Co-localization of Tph2 and was evaluated quantitatively in the different sub-nuclei (Figure 3, tables 3-4). The highest co-localization index was found in the DR (B7- all subcomponents pooled) where more than half of the 5-HT neurons expressed EphA5 ($50.2\% \pm 2.2\%$, $n=3$, Figure 3A, D); while the lowest co-localization ratio was noted in the caudal (B1-B3) raphe cell groups (Figure 3C,D). In the MnR (B5, B8), a strong expression of *EphA5* was visible, but only a minority (14-22% respectively) of the 5-HT neurons expressed *EphA5* (Figure 3B, D). Further heterogeneous expression was observed within the DR where co-localization was compared at 3 different rostro-caudal levels (Figure 3E) and in 3 different DR subdivisions (lateral, dorsal, ventral) (Figure 3E and Table 4); Medially located DR neurons have a higher percentage of co-localized neurons than the laterally located DR neurons (Figure 2B, C; Figure 3E). Overall, this co-localization pattern indicates a clear topography of EphA5 expression in the raphe subgroups with a rostral to caudal decreasing expression that was visible during embryonic

stages (Figure 2C) and maintained at P5 (Figure 3). Such differences in expression of EphA5 between the different 5-HT cell groups suggested that EphA5 signaling could be involved in the differential targeting of these various 5-HT neurons.

Collapse response of 5-HT raphe neurons after the ephrinA application.

To examine the functional role of EphA5 expression on 5-HT axon outgrowth, we took advantage of the clear-cut differential expression of EphA5 between the rostral (B5-B9) and caudal-medullary (B1-B3) clusters of 5-HT neurons at embryonic ages and compared their response to application of the ligand ephrinA5. Raphe explants from E12 hindbrains, were dissected as illustrated (Figure 4A) and cultured 48h on glass coverslips. In explants from the rostral raphe, ephrinA5-FC induced the collapse of a large fraction of 5-HT growth cones (Figure 4-B). A dose dependent effect was noted: 71.3% \pm 4.5% of the 5-HT growth cones were collapsed at the highest concentration tested (500ng/ml) and 45-50% at intermediate concentrations (50-250ng/ml) (Figure 4C). In caudal raphe explants, ephrinA5 application did not induce a significant collapse response compared to controls at any of the concentrations tested (Figure 4 B2, 4D).

Because EphA5 is also expressed in a large number of non-5HT neurons in both the rostral and caudal raphe areas (table 3), we also measured the collapse responses of the non-5-HT axons. The non-5-HT growth cones showed a significant dose-dependent collapse response in both rostral and caudal explants (Figure 4 E, F), thus not displaying the regional selectivity noted for 5-HT growth cones.

Overall, these experiments demonstrated that the pattern of EphA5 expression in 5-HT raphe neurons correlated with a repulsive response to the application of ephrinA5-FC. Interestingly, there was a dose response effect suggesting that differences in the ligand/receptor ratio could contribute to a differential targeting of 5-HT raphe neurons.

5-HT innervation is reduced by ectopic ephrinA expression in the amygdala.

Next, we investigated the effects of ephrinA ligands for *in vivo* 5-HT axon targeting using an over-expression strategy. We focused on the amygdala and piriform cortex which are preferential targets of the DR 5-HT neurons (Muzerelle et al. 2016), and express only very low levels of the main EphA5 ligands, ephrinA2, ephrinA3 and ephrinA5, based on our own observations, confirming previously published reports (Deschamps et al., 2010, Gerstmann et al. 2015) and available public resources (Allen Brain Atlas, <http://developingmouse.brain-map.org/gene/show/13415>, 13416, 13418). This suggested that the amygdala and piriform cortex could be permissive for the ingrowth of DR axons

which express high level of EphA5 receptors. To examine this possibility, we used an in utero electroporation strategy to ectopically express ephrinA3 that has been shown to have the highest affinity for EphA5 (Gale et al. 1996). An ephrinA3 cDNA fragment was sub-cloned into a pCIG-Tdtomato vector; the plasmid with or without the ephrinA3 insert was electroporated into the amygdala and piriform cortex at E12.5 and the brains processed at P5 for 5-HT immunocytochemistry. Not structural changes were observed on the electroporated/non electroporated side, as evaluated by Nissl staining. The electroporated cells were visible in different parts of the amygdala (basolateral and basomedial amygdaloid nucleus), and in the piriform cortex (Figure 5A, B, C). Measures of 5-HT fiber density showed a significant decrease of 5-HT fibers on the electroporated amygdala (0.07 ± 0.01 fibers/ μm) and piriform cortex (0.07 ± 0.01 fibers/ μm) compared to the contralateral non-electroporated amygdala (0.21 ± 0.03 fibers/ μm) and piriform cortex (Figure 5D, 7E.). Conversely, in the cases electroporated with the control vector, the density of 5-HT fibers was unchanged compared to the non-electroporated side. This result indicated that ectopic expression of ephrinA3 during development can specifically reduce the 5-HT raphe-amygdala innervation ($n=5$, $p < 0.005$).

EphrinA5 is required for the differential forebrain targeting of B7/B8 raphe neurons

To investigate the role of endogenous ephrins in 5-HT axon targeting, we investigated the effects of loss of function of one of the major EphA5 ligands, ephrinA5. Using the ephrinA5 KO mouse model. We reasoned that 5-HT neurons with high EphA5 expression in the raphe should avoid innervating brain regions containing high levels of the ligand ephrinA5. ISH of an EfnA5 riboprobe was done on serial sections of P5 brains. We focused on 3 main regions with high ephrinA5 expression, namely the olfactory bulb (OB) (Fig 6C), the ventromedial hypothalamus (VMH) and the suprachiasmatic nucleus (SCN) (Figure 7 A, F). Indeed, previous selective anterograde tracing from these DR and MnR had shown that the DR targets the granule cell layer of the OB and seems arrested by the mitral cell layer, whereas the MnR targets the glomerular layer (GL) of the OB (Figure 6C) (Steinfeld 2015, Muzerelle et al., 2016). Similarly, 5-HT DR axons consistently avoid the VMH and SCN that are instead innervated by MnR raphe neurons (Bang et al. 2012, Muzerelle et al. 2016)

Anterograde tracing of the DR neurons was done with an AAV viral vector expressing Td-tomato comparing ephrinA5 KO and WT mice. We evaluated the extent of anterogradely labeled neurons that are 5-HT-immunopositive in the raphe (Figure 6A) and the

size of the injection site (Figure 6B). Transfection was limited to the DR (Figure 6B) and the number of transfected 5-HT cells was equivalent in the control and mutant mice. Anterogradely labeled axons were further characterized as serotonergic (or not), using 5-HT transporter (SERT) immunohistochemistry (Figure 6 D', E').

In the OB of WT mice, anterogradely labeled axons, all of which were SERT+, were restricted to the granular cell layer (GCL) and appeared to be arrested at the edge of the mitral cell layer (ML) that expresses high ephrinA5 levels (Figure 6C); only a few fibers entering into the external plexiform layer (EPL) (Figure 6D-D'), confirming previous observations (Steinfeld et al. 2015, Muzerelle et al. 2016). In the ephrinA5 KO mice, DR axons did not seem to be arrested by the ML, which they crossed, arborizing into the EPL (Figure 6E-E'). To obtain quantitative measures normalized to the number of anterogradely labeled axons, we estimated the density of td tomato labeled fibers in the CGL and the EPL, and calculated the EPL/CGL ratio. This ratio was significantly increased in ephrinA5 KO mice compared to WT mice (Figure 6F). To determine whether the overall density of 5-HT labeled axons was modified, we measured the density of SERT-labeled axons in the CGL and the EPL and found an overall increase in the density of 5-HT axons in the EPL but not in the CGL (Figure 6 G, H). This indicates that the increased EPL/CGL ratio in ephrinA5 KO mice is not the consequence of a general increase in the number of 5-HT axons reaching the OB, but rather due to an increase in the fraction of DR axons that cross beyond the ML.

In the same cases, we further analyzed DR anterograde labeling and global 5-HT innervation in two hypothalamic areas that show high ephrinA5 expression: the ventromedial hypothalamus (VMH) (Figure 7A) and the suprachiasmatic nucleus (SCN) (Figure 7F). Both nuclei show a high level of ephrinA5 at P5 (Figure 7A, F). In WT mice, anterograde labeling from the DR shows that both the VMH and the SCN are not targeted by DR axons (Figure 7B', G') confirming previous observations (Bang et al. 2012, Muzerelle et al., 2016). However, these areas contain a very high density of SERT+ labeled terminals that originate mainly from the MnR. In the ephrinA5 KO mice, the density of DR anterograde projection was substantially increased in both the VMH (Figure 7C', E) and the SCN (Figure 7H', J). Double labeling (td-tomato and SERT) showed that both 5-HT and non 5-HT DR axons contributed to this increase (Figure 7C'', H''). However the overall density of SERT+ labeled fibers also showed a significant increase in the VMH (Figure 7E,I).

These experiments indicated a requirement of ephrinA5 for the targeting of the DR axons, showing that the absence of ephrinA5 results in an increased serotonergic innervation of distinctive layers of the OB and of key hypothalamic nuclei resulting in an overall increase of the 5-HT innervation in these areas (Figure 8).

Discussion

Our results demonstrate for the first time a role of ephrinA signaling for the selective targeting of serotonergic raphe nuclei. We show that EphA5 is differentially expressed across the different hindbrain raphe nuclei, and that this correlates with a different repulsive action of ephrinA on 5-HT axon growth. Ectopic expression of ephrinA inhibits the ingrowth of 5-HT raphe axons in main targets of the dorsal raphe 5-HT neurons and ephrinA5 loss of function causes a mis-targeting of dorsal raphe 5-HT axons resulting in localized increases in 5-HT innervation.

The development of raphe neurons has been well outlined by classical morphological studies in rodents (Lidov and Molliver, 1982; Wallace and Lauder, 1983), however, only few insights have been obtained to date into the molecular control of axon guidance in this system. Wnt signals have been implicated in the polarity of 5-HT neurons (Fenstermaker et al., 2010) and Slit/Robo signaling influences 5-HT axon tract organization in the medial forebrain bundle (Bagri et al., 2002), but hardly anything is known about the molecular control of selective 5-HT axon targeting. This knowledge gap is likely due to a prevailing view of 5-HT neurons as a diffuse highly collateralized system with limited specificity (Agnati et al., 2006). However, increasing evidence showed that raphe 5-HT neurons are in fact heterogeneous in their molecular identities (Wylie et al., 2010; Fernandez et al., 2015; Okaty et al., 2015), their physiology (Calizo et al., 2011; Fernandez and Gaspar, 2012), their genetic determinants (Kiyasova et al., 2011), and their connectivity (Azmitia and Segal, 1978; Commons, 2015; Muzerelle et al., 2016). In addition to the established divergence of axons arising from the rostral and caudal 5-HT neuron clusters (directed toward the forebrain and the spinal cord respectively), there is a distinct topographic organization within the ascending forebrain projections. 5-HT axons originating from the DR and MnR occupy complementary terminal territories in the forebrain (Bobillier et al., 1976; Azmitia and Segal, 1978; Jacobs et al., 1978; Vertes et al., 1999; Muzerelle et al., 2016). Coinciding with this topographic anatomical organization, our study revealed a gradient of EphA5 gene expression with higher EphA expression in the DR than in the MnR, and in addition a clear rostral to caudal and medial to lateral ex-

494 pression gradient. Thus, high EphA5 expression in DR neuronal subsets could explain
 495 why DR 5-HT neurons do not innervate brain areas that have high expression of ephrinA,
 496 which are instead innervated by 5-HT neurons from the MnR. This is particularly clear in
 497 the case of the olfactory bulb (OB), where DR and MnR 5-HT neurons are located re-
 498 spectively in the central (GCL) or outer (EPL, GL) layers of the OB (Steinfeld et al 2015;
 499 Muzerelle et al., 2016). The ephrinA3/5 expressing mitral cell layer might then act as a
 500 barrier to prevent DR 5-HT axons from crossing into the outer OB layers. Similarly, hypo-
 501 thalamic nuclei that normally receive all (suprachiasmatic) or a majority (VMH) of their 5-
 502 HT innervation from the MnR (Bang et al., 2012; Muzerelle et al., 2016) show high levels
 503 of ephrinA expression during development. The implication of ephrinA was supported by
 504 altered distribution of DR axons. In both the OB and the hypothalamus, 5-HT innervation
 505 was increased and anterogradely labeled axons from the DR were misplaced as though
 506 an inhibitory barrier was removed. Conversely, when an ephrinA ligand was ectopically
 507 expressed in a structure such as the amygdala, which is a preferential target of the DR 5-
 508 HT innervation (Muzerelle et al., 2016), the ingrowth of 5-HT raphe axons was significant-
 509 ly reduced. Thus, present results indicate that ephrinA5 signaling contributes to the se-
 510 lective targeting of 5-HT axons in the forebrain by repelling the ingrowth of 5-HT axons
 511 originating from the DR, in brain regions that are normally targeted by the MnR.

512 EphrinA signaling may also influence other aspects of the topography of DR; this is
 513 suggested by our observation of a difference of EphA5 expression in the medial lateral
 514 parts of the DR which coincides with differential anatomical projections. 5-HT neurons in
 515 the lateral wings of the DR have a low level of EphA expression and project to regions
 516 with high ephrinA5 expression such as the lateral geniculate nucleus (Muzerelle et al.
 517 2016, Wilks et al. 2010). It will be interesting to determine in the future how the combina-
 518 tion of axon guidance molecules in raphe targets contribute to attracting subsets of 5-HT
 519 axons to defined brain areas/layers. In particular we do not know what factors attract the
 520 MnR 5-HT axons to the areas that are avoided by the DR. Intriguingly 5-HT itself could
 521 contribute to this growth-promoting effects, since a defective innervation of the SCN was
 522 observed in Tph2-KO mice (Migliarini et al., 2013). The mis-targeting of DR axons in the
 523 hypothalamus of ephrinA5 KO mice concerned both 5-HT and non 5-HT neurons of the
 524 DR, indeed as noted in the present study, both cell types express EphA5. These com-
 525 mon axon guidance cues are consistent with shared connectivity profiles; indeed, previ-
 526 ous anatomical tracing studies showed that DR afferents frequently contain a mix of 5-HT

527 and non 5-HT neurons (Steinbusch and Nieuwenhuys, 1981; Kiyasova et al., 2011), the
 528 latter could include glutamatergic Vglut3+ (Hioki et al., 2010) and GABAergic neurons
 529 (Bang et al., 2012). Thus DR neurons could share similar axon guidance mechanisms,
 530 independent of their neurotransmitter content.

531 EphA-ephrinA signaling is involved in several neuronal developmental processes
 532 from cell migration to synaptic maturation (rev. in Cramer and Miko, 2016; Kania and
 533 Klein, 2016) although its best known implication in neural development is for axon guid-
 534 ance, where both repulsive and attractive interactions have been described. Our current
 535 studies indicated a main inhibitory effect of the ephrinA ligands on 5-HT axon growth: *in*
 536 *vitro*, ephrinA5 induced a collapse of the growth cones and *in vivo* ectopic expression of
 537 ephrinA3 inhibited 5-HT axon ingrowth. This corresponds to the classic repulsive forward
 538 signaling of EphA receptor activation (Kania and Klein, 2016), and is most likely due to
 539 the EphA5 receptor according to the present localization studies. However we cannot
 540 exclude the implication of other EphAs since transcriptional profiling of raphe neurons in
 541 embryonic and postnatal brains reported also the presence of other EphA (Wylie et al.,
 542 2010; Okaty et al., 2015), but likely expression is at levels that are too low for our ISH
 543 detection. Moreover, the loose specificity of the EphA5 receptors for ephrinA ligands and
 544 the redundancy of ephrinA expression in several brain targets (such as the mitral cells in
 545 the OB) suggest that the defects of 5-HT axon targeting observed in the ephrinA5 KO
 546 might be more pronounced in double or triple ephrinA KO mice. Such redundancy has
 547 previously been observed in the visual system (Feldheim et al., 2000).

548 In the visual and auditory sensory maps Eph-ephrinA signaling acts to build a contin-
 549 uous topographic map (Cramer and Miko, 2016) however present results do not indicate
 550 that this is the case in the 5-HT raphe system where topography is much looser. Indeed
 551 DR and MnR have different targets but do not display further topographic organization
 552 within their preferred targets. Thus, we propose that as regards the 5-HT systems, Eph-
 553 ephrinA signaling could act in a target selection process, by generating non permissive
 554 boundaries for the ingrowth of DR 5-HT raphe subtypes. This effect would then be more
 555 similar of that observed for the motor neurons when choosing a dorsal/ventral muscle
 556 targets during development (Eberhart et al., 2004).

557 EphA5 expression in 5-HT raphe neurons was dynamically expressed, being max-
 558 imal during axon growth in embryonic life and target reaching during the early postnatal

559 period and showing decreased expression, similarly to what has reported for ephrinA5
560 expression (Deschamps et al., 2010). Given the potential of 5-HT neurons to regenerate
561 and grow, it will be interesting to know whether the present developmental mechanisms
562 are reactivated after a lesion, and whether the propensity of serotonin axons to regrow
563 (Mullner et al., 2008) could be linked to their EphA content.

564 What could be the pathophysiological consequences of targeting defects of raphe
565 neurons in the olfactory bulb or the hypothalamus? Our observations in ephrinA5 KO
566 showed that mis-targeting of the DR axons was correlated with a general increase of 5-
567 HT innervation in these regions, suggesting that excitatory/inhibitory balance is compro-
568 mised in these brain nuclei. Interestingly, behavioral observations conducted in the
569 ephrinA5 and EphA5 KO mice showed some common phenotypes that could relate to
570 our observations. Both studies report a reduction in inter-male aggression (Mamiya et al.,
571 2008; Sheleg et al., 2015) and increase of 5-HT levels in the hypothalamus was shown in
572 the EphA5 KO (Mamiya et al., 2008) consistent with our observations of increased 5-HT
573 innervation in this brain region. Interestingly the increased 5-HT innervation that we ob-
574 served in the ephrinA5 KO was concentrated in the ventrolateral part (VMHVL), which
575 has been specifically implicated in modulating aggression (Martinez et al 2008; Silva et
576 al. 2016). Clearly, the possible pathophysiological consequences of SCN hyper-
577 innervation calls for further studies on the circadian rhythms of these mutants, given the
578 implication of 5-HT innervation to the SCN in entraining circadian rhythmicity (Versteeg et
579 al., 2015)

580 Given the implication of 5-HT in a wide range of behaviors, and psychiatric disorders, our
581 study point to new gene targets that may indirectly affect 5-HT functions by changing the
582 targeting of raphe neurons and inducing modifications of 5-HT inputs in selected brain
583 regions.

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760

761 **Figure Legends**

762 **Figure 1 - EphA receptor gene expression in the developing mouse raphe.**

763 A, Q-PCR of EphA3, EphA4, EphA5, EphA6, EphA7 and EphA8 mRNAs in DR extracts
764 from P5 mice (n=4 mice /experiment) Relative mRNA expression was calculated as $2^{-\Delta Ct}$
765 (delta of cycle threshold) Data are presented as mean \pm SEM from 3 independent ex-
766 periments.

767 B, In situ hybridization of SERT, EphA3, EphA4, EphA5 and EphA7 mRNAs is shown at 3
768 different rostro-caudal levels of the raphe nuclei, including the DR (B7), the caudal DR
769 (B6), the rostral MnR (B8), the caudal MnR (B5), the raphe pallidus (B1), obscurus (B2),
770 and magnus (B3). Coronal serial sections (20 μ m thick) were labeled with the 5 different
771 probes. The localization of the 5-HT neurons as revealed by SERT expression was out-
772 lined with dashed yellow lines that were transferred to the consecutive sections on the
773 series. This shows that only EphA5 labeling coincides clearly with the contours of B7
774 and B8. EphA4 and EphA7 are also strongly expressed in the brainstem but signal is
775 mainly detected in cell groups such as the dorsal anterior tegmental nucleus (atg) or the
776 dorsal tegmental nucleus (dtg) or the inferior olive (io) that come very close to the raphe.
777 Scale bar= 250 μ m

778 **Figure 2- EphA5 is expressed in serotonergic neurons during embryonic and post-
779 natal development.**

780 A- Q-PCR of EphA5 mRNAs in DR extracts from P5 (n=3), P15 (n=3) and adult (n=3).
781 Relative mRNA expression was calculated as $2^{-\Delta Ct}$. Data are presented as mean \pm SEM
782 from 3 independent experiments,

783 B- Time course of EphA5 expression in the developing raphe was analyzed on sagittal
784 (E14) and coronal (P0, P5, P10, P15) sections through the raphe nuclei. Note the de-
785 crease in EphA5 expression by P15. No expression is detected using the sense probe of
786 EphA5, Scale bar=500 μ m.

787 C- Co-localization was visualized on confocal images after Tph2-immunostaining (green)
788 and EphA5 ISH (red). Sagittal section of E14 mouse brain through the rostral (R) and
789 caudal (C) raphe clusters that are indicated with arrows. Note that the dorsal part of the
790 rostral cluster overlaps with EphA5 labeling, whereas the ventral part does not. C',
791 shows a higher power image of the boxed area in 2A. Arrows indicate co-localized neu-
792 rons (red nuclear labeling for EphA5 and green cytoplasmic labeling for Tph2); the as-

793 terisk shows Tph2 + neurons with no EphA5 expression. Scale bar=1 mm (A), 100 μ m
794 (A')

795 D, E, F, Coronal sections of a P5 mouse hindbrain at 3 a rostral (B), intermediate (C) and
796 caudal (C) levels of the raphe. Sections were counter-stained with DAPI. Scale bar=500
797 μ m

798 **Figure 3- Quantification of EphA5-Tph2 co-localization in distinct raphe nucleus.**

799 A-C, High power confocal images in B7, B8 and B2, showing the difference in co-
800 localization of EphA5 and Tph2 in different raphe nuclei. White arrows point to
801 Tph2+EphA5 co-localized neurons whereas the arrowheads show neuron containing
802 only EphA5. Scale bar=50 μ m

803 D, E, Histograms summarizing the % co-localization among the different raphe nuclei,
804 subdivided as the B1-B9 cell groups (D) and within the DR where co-localization was
805 compared at 3 different rostro-caudal levels : caudal DR DR-C), middle DR (DR-M),
806 rostral DR (DR-R) and in 3 different DR subdivisions: DR lateral (DR-L), DR-dorsal (DR-
807 D), and DR ventral (DR-V). Data are presented as mean \pm SEM (n=3), one-way Anova,
808 ***p<0.005 and ****p<0.001.

809 **Figure 4- EphrinA5 induces collapse of rostral raphe serotonin axons in vitro.**

810 A, Explant preparation: hindbrain was dissected as an 'open book' from E12 embryos;
811 the rostral and caudal raphe were dissected as depicted on a whole mount E12 hind-
812 brain stained for 5-HT. Scale bar=2mm.

813 B; Raphe explants (3DIV) were stained for 5-HT (green) and phalloidin (red). B1- shows
814 the 5-HT+ axons emerging from the explant; B2-5 shows 5-HT-labelled growth cones
815 displaying either a normal fan-like morphology (B2, B3) or collapsed growth cone that
816 have branch-like morphology (B4) or a long trailing process and an actin rich retraction
817 bulb . Scale bar=100 μ m (B1), 10 μ m (B2-B5)

818 C, D, E, F, Histograms show the % of collapsed growth cones when explants are ex-
819 posed to different concentrations of ephrinA5. C-D) 5-HT-labeled axons from rostral (C)
820 and caudal (D) explants; E-F) non-5-HT axons from rostral (E) and caudal (F) explants.
821 (> 5 explants and >100 growth cones per condition). Data are presented as mean \pm
822 SEM, one-way anova, *p<0.05, **p<0.01, ***p<0.005 and ****p<0.001.

823 **Figure 5- Overexpression of ephrinA3 down regulates serotonergic innervation in**

824 **the amygdala and piriform cortex.**

825 A-A", B-B", Electroporated neurons were revealed by td-tomato with the ephrinA3 plas-
826 mid in the targets of Am (A) and Pir (B). Corresponding 5-HT immunocytochemistry from
827 the electroporated (A', A') and non electroporated (A", A") sides. Note the decrease of 5-
828 HT fibers in the outlined area compared to the control side. Scale bar=100μm

829 C, Target of electroporation (td-tomato) on a coronal section of P5 mouse brain at the
830 level of amygdala. Arrows show electroporated Am and Pir. Scale bar=1000μm

831 D, E, Scatterogram shows serotonergic fiber density in the electroporated (red) versus
832 non electroporated (blue) amygdala (D) and piriform cortex (E). Overexpression of
833 ephrinA3 resulted in a significant decrease of 5-HT fiber density compared to the control
834 groups, (n=5). Data are presented as mean ± SEM, paired t test was used for ipsi vs.
835 contra, ***p<0.005.

836 **Figure 6- Anterograde tracing from dorsal raphe to olfactory bulb in ephrinA5-/-**
837 **mice.**

838 A, AAV-tdtomato virus was injected in the DR. Injection sites were checked with 5-HT
839 immunohistochemistry on the coronal raphe sections, showing 5-HT and td-tomato la-
840 beling in the DR but not in the MnR (A). Scale bar=500μm (A left), 50μm (A right)

841 B, The scheme shows the extent of AAV transfection in the WT (n=5) and ephrinA5 (n=5)
842 cases; iThe injection site was reconstructed for each case, and were drawn manually on
843 representative coronal raphe sections (Bregma: -4.60mm) using a different color code
844 for each case.

845 C, Sagittal mouse brain scheme showing the projections from the DR and MnR to the
846 olfactory bulb (OB) targeting the inner (GCL) or outer (GL) layers respectively.

847 C', In situ hybridization of ephrinA5 (EfnA5) mRNA on OB coronal section. A selective
848 expression of ephrinA5 is observed in the mitral layer (ML). Scale bar=250μm

849 D-E', Anterogradely labeled axons (td-tomato) and SERT+ fibers in the OB of WT (D, D')
850 and ephrinA5 KO mice (E, E'). Most of the td-tomato were co-labeled with SERT. More
851 co-labeled fibers were detected in the EPL of ephrinA5 -/- mice, compared to WT. Scale
852 bar=50μm.

853 F-H, Histograms show the fiber densities of anterogradely labeled and SERT-labeled ax-
854 ons. (F) The density of td-tomato fibers was normalized by calculating the EPL/GCL fi-

ber density ratio. The density of 5-HT axons was measured as linear density of SERT labelled axons (fibers/ μm) in the EPL (G) and CGL (H) (** $p < 0.005$)

Figure 7- EphrinA5 expression modulates the DR innervation in forebrain target.

A, F, Expression of ephrinA5 (Efna5) in the ventromedial hypothalamus (VMH) (A), and the suprachiasmatic nucleus (SCN) (F) in coronal brain section of P5 mice. High level of ephrinA5 were detected in the VL and DM part of VMH. Scale bar=500 μm .

B-B", C-C", G-G", H-H', immunofluorescence images show SERT labeling and antero-grade labeling of DR in adult in control (B-B", G-G") and ephrinA5 KO mice (C-C", H-H"). Few fibers were detected in VMH and SCN of the control cases whereas labeled fibers were detected in larger amounts in the VMH and SCN of the ephrinA5 KO (see arrows to compare between pictures). Scale bar=100 μm (B-C"), 50 μm (G-H").

D, E, I, J,) Histograms show the fiber densities anterogradely labeled and SERT+ axons. Fiber density was calculated as pixels per μm^2 and the data are presented as mean \pm SEM, unpaired t test, * $p < 0.05$, ** $p < 0.01$ and *** $p < 0.005$.

Figure 8-Summary diagram. This scheme shows the expression level of EphA5 in the different 5-HT raphe nuclei, indicated with different shades of green, the maximal being in the DR-V, and lowest in B1, B2. The projections of the DR 5-HT neurons to the amygdala and to the granular cell layer (GCL) of the olfactory bulb are indicated with solid lines. In the ephrinA5 knock out mice, additional projections to the ventromedial hypothalamus (VMH) and to the external plexiform layer (EPL) are visible; these are indicated with dotted lines. High ephrinA5-expression in the mitral cell layer (ML) and the VMH is indicated in orange.

Table legends

Table 1. List of mRNA probes

Table 2. List of RT-QPCR primers

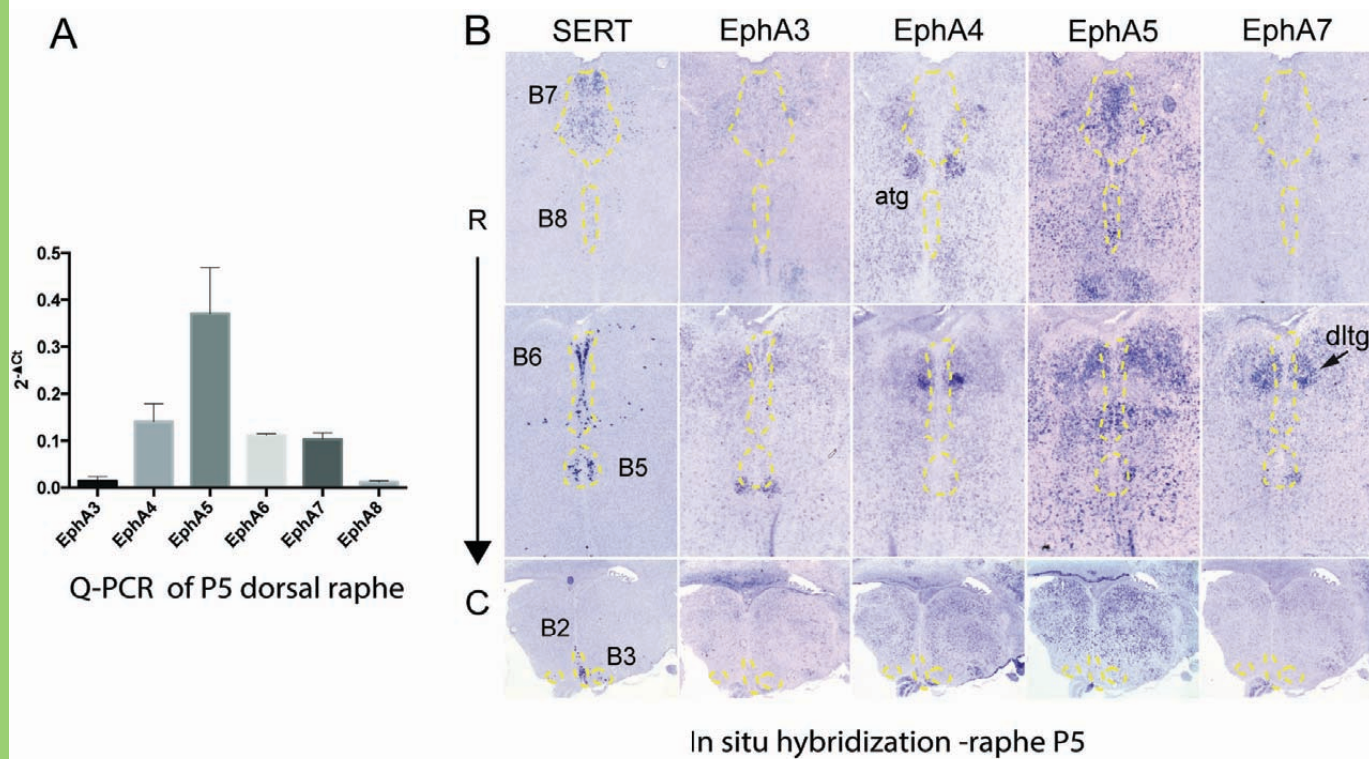
Table 3. Counts of Tph2-immunopositive and EphA5 expressing neurons and colocalized neurons in different raphe nuclei

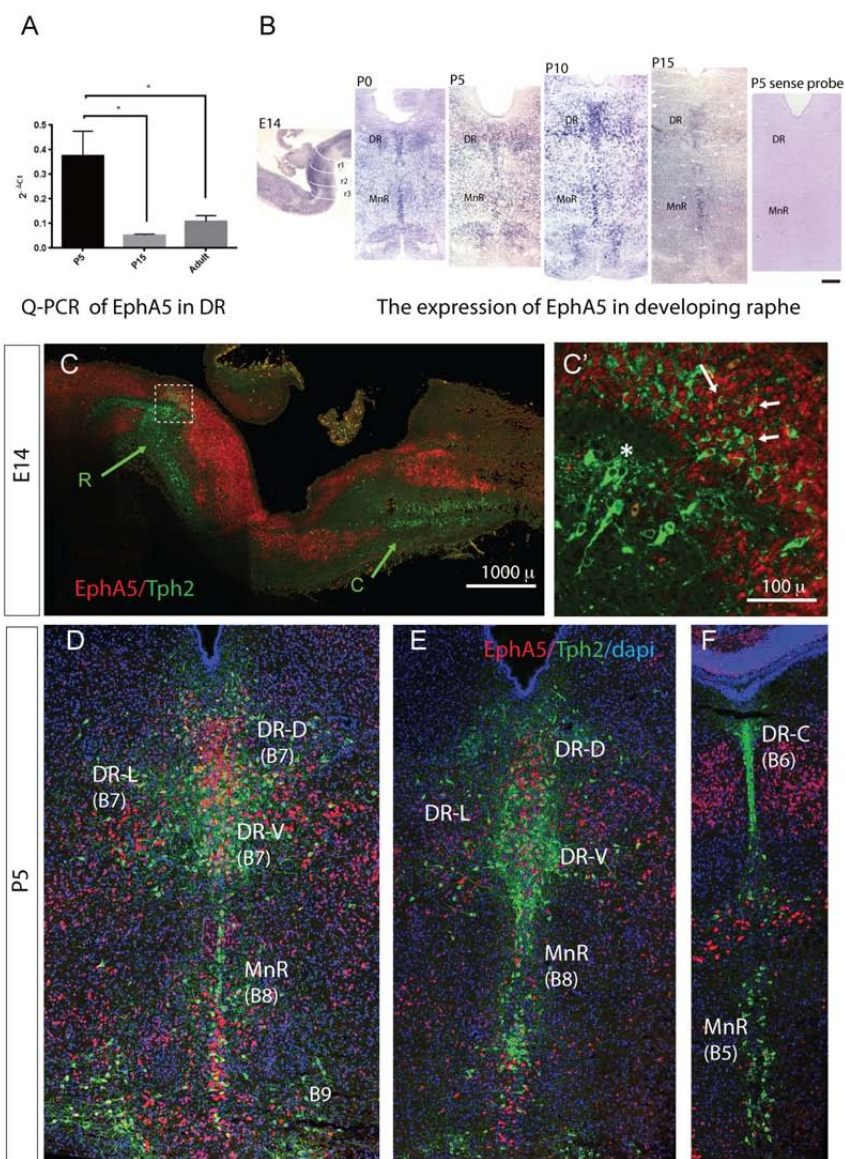
Figures are the mean cell numbers \pm SEM / area obtained from counts done in 3 cases in regions of interest (ROI) covering the different raphe nuclei (B1 to B9). All cells (validated by DAPI staining) immunolabeled for Tph2, for EphA5 and double-labeled for Tph2 and EphA5 were counted in 3 different ROI (dimension 0,225 mm^2) for each structures

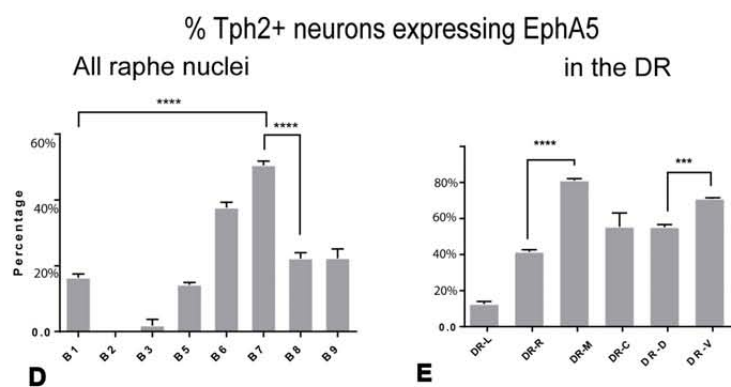
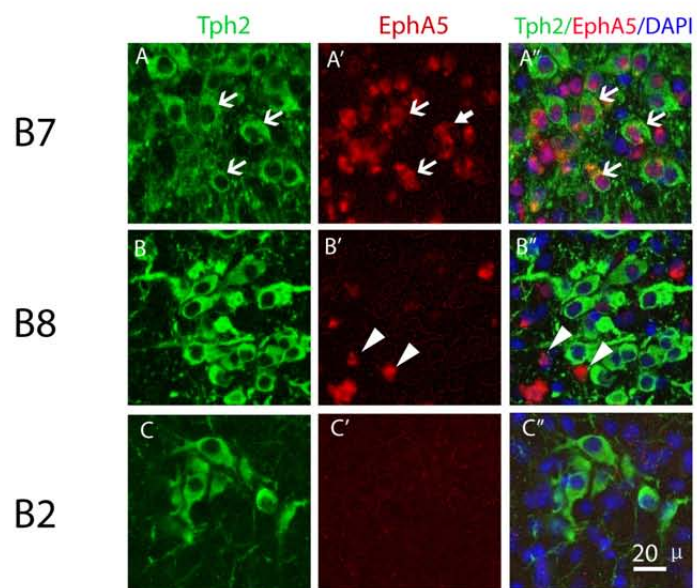
886 and for each case and checked for co-localization % of the co-labeled Tph2 neurons is
887 indicated.

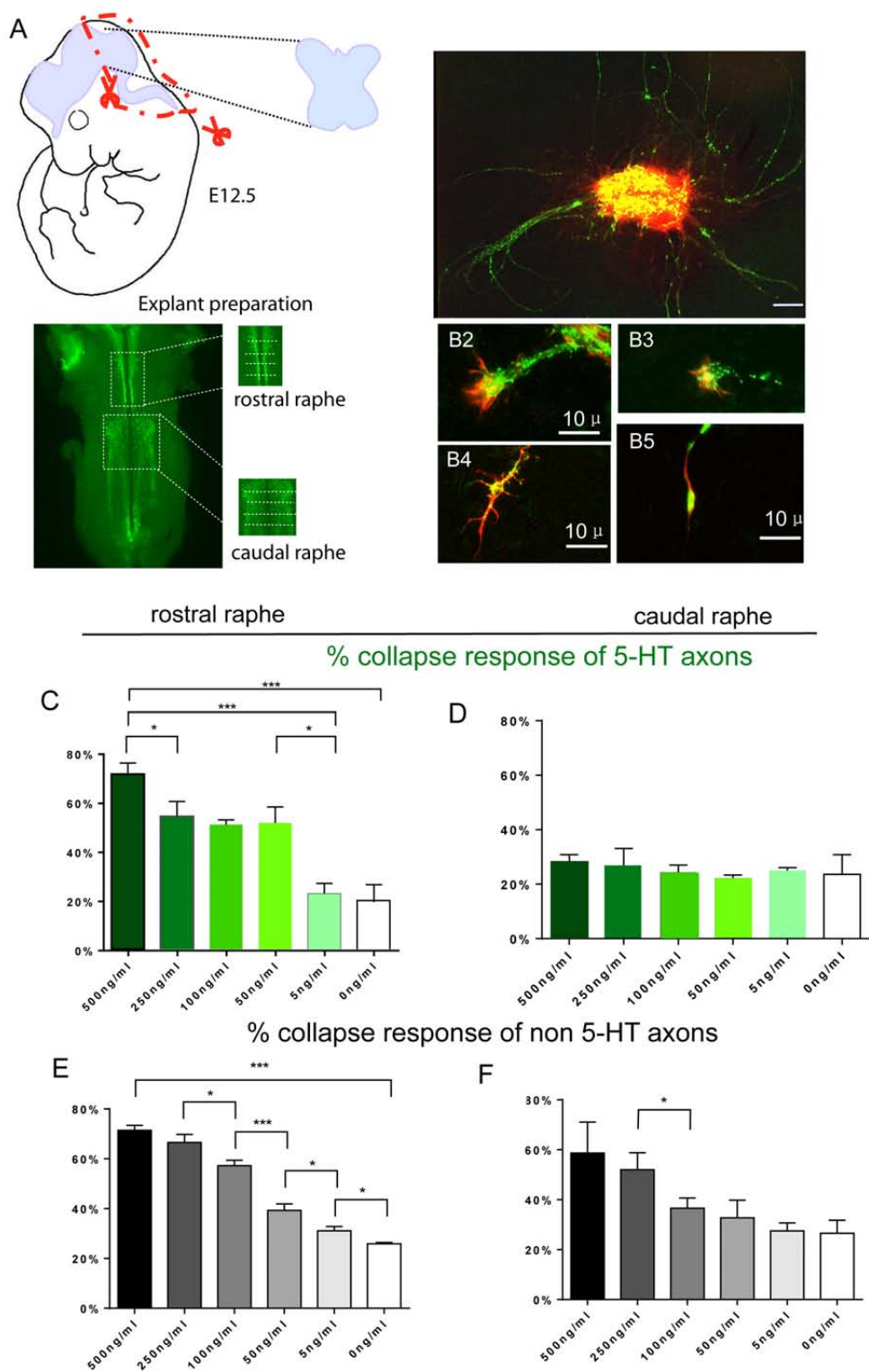
888 **Table 4. Counts of Tph2-immunopositive and EphA5 expressing neurons and colo-**
889 **calized neurons in the dorsal raphe (B7) (mean \pm SEM, n=3).**

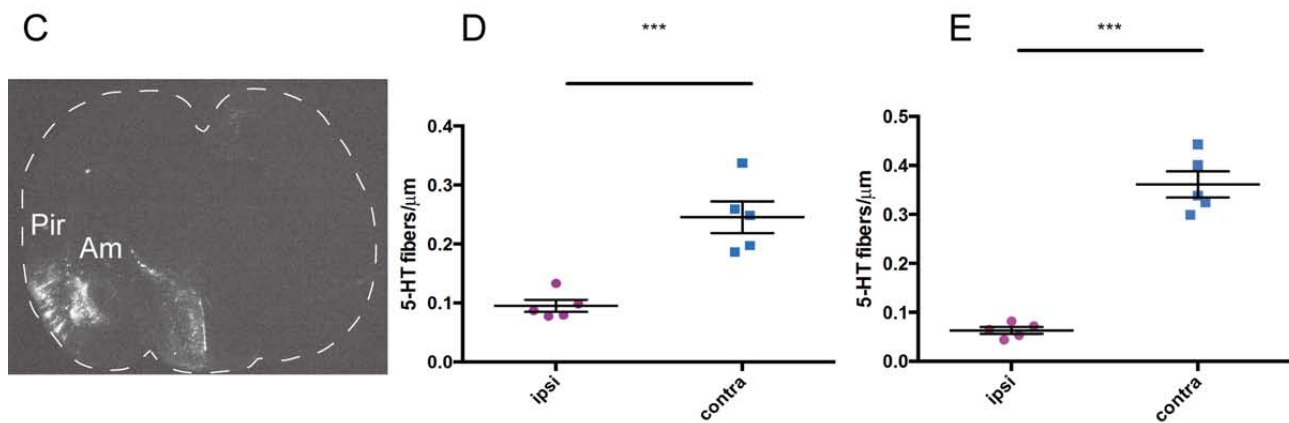
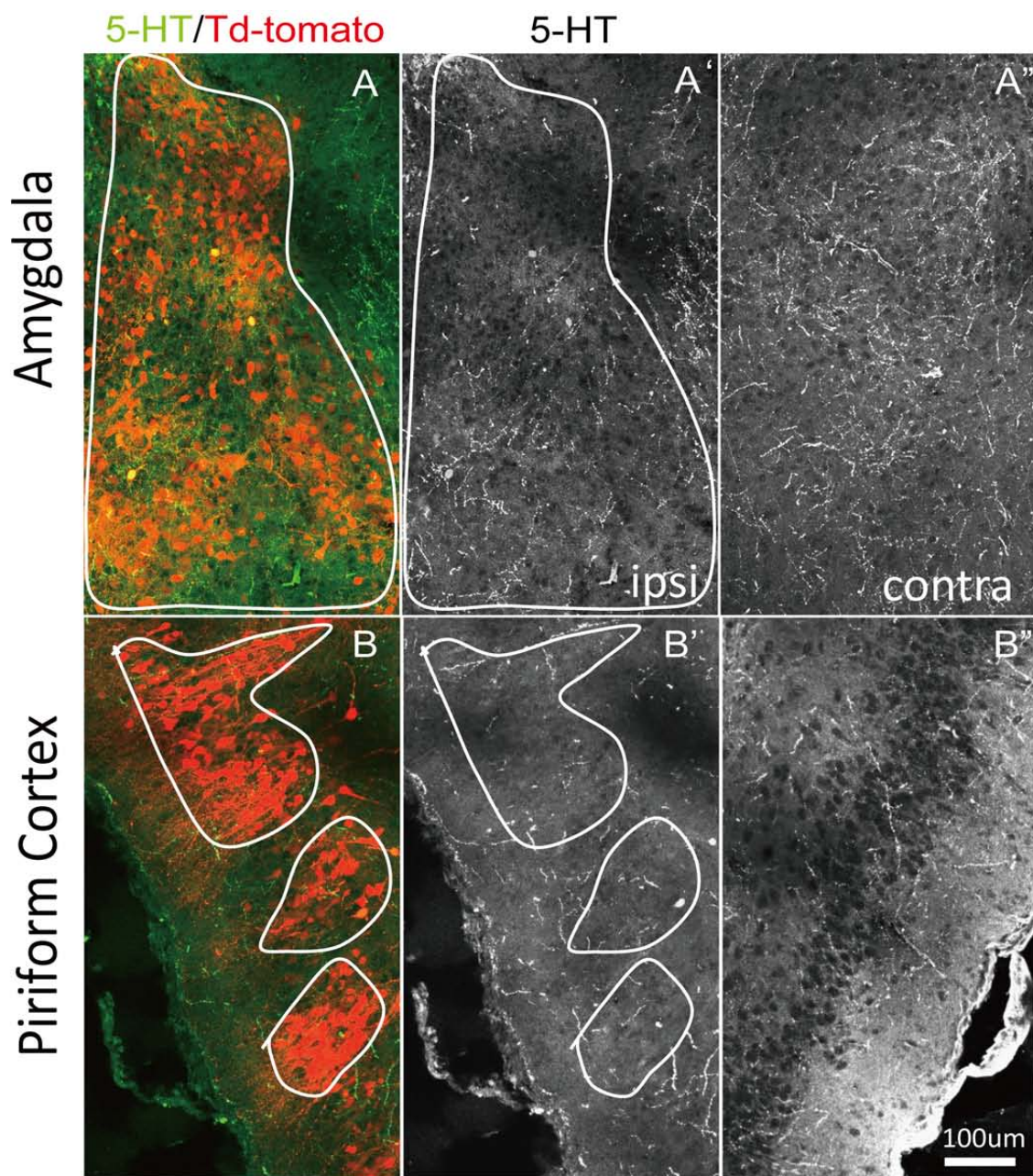
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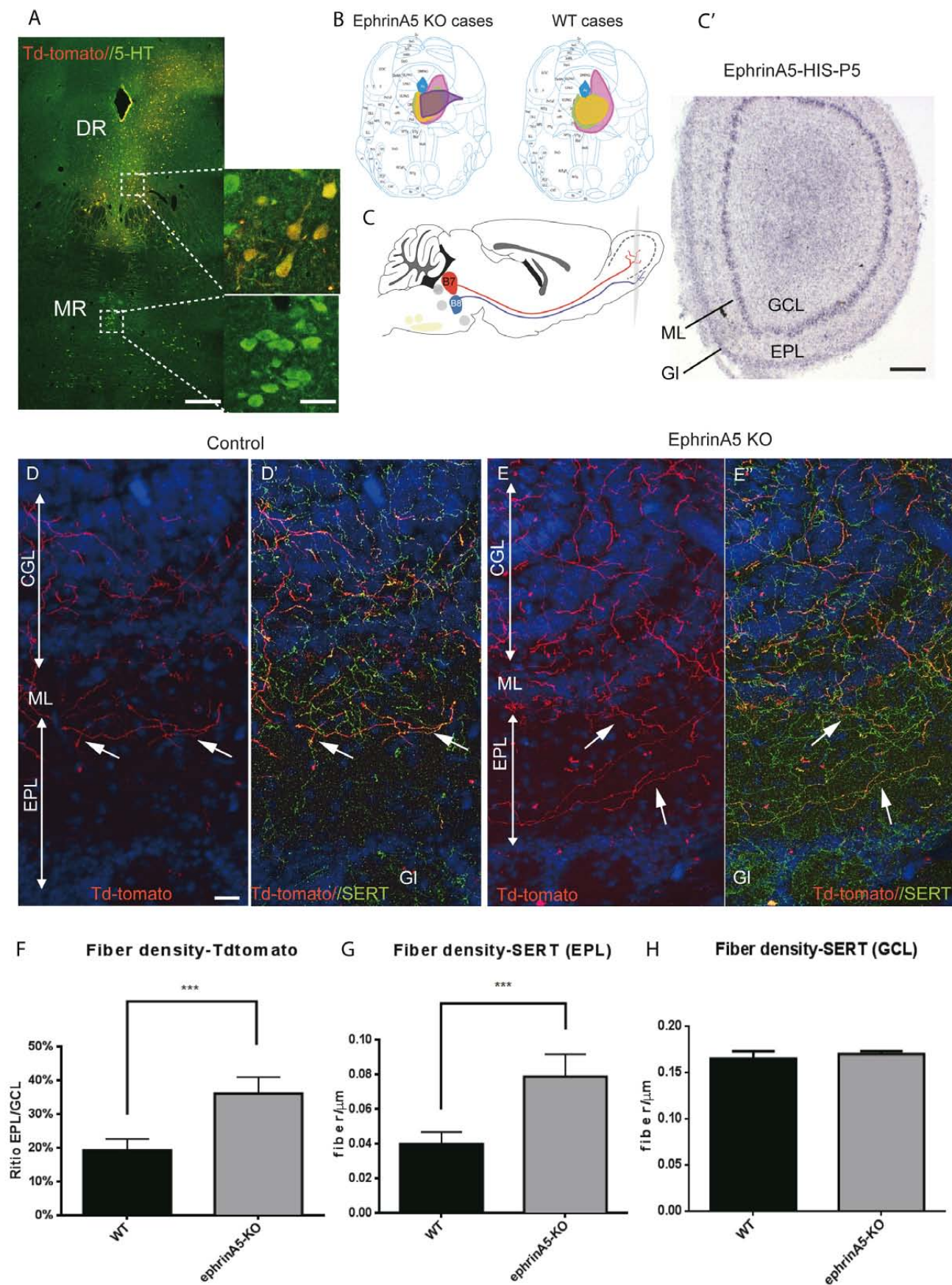


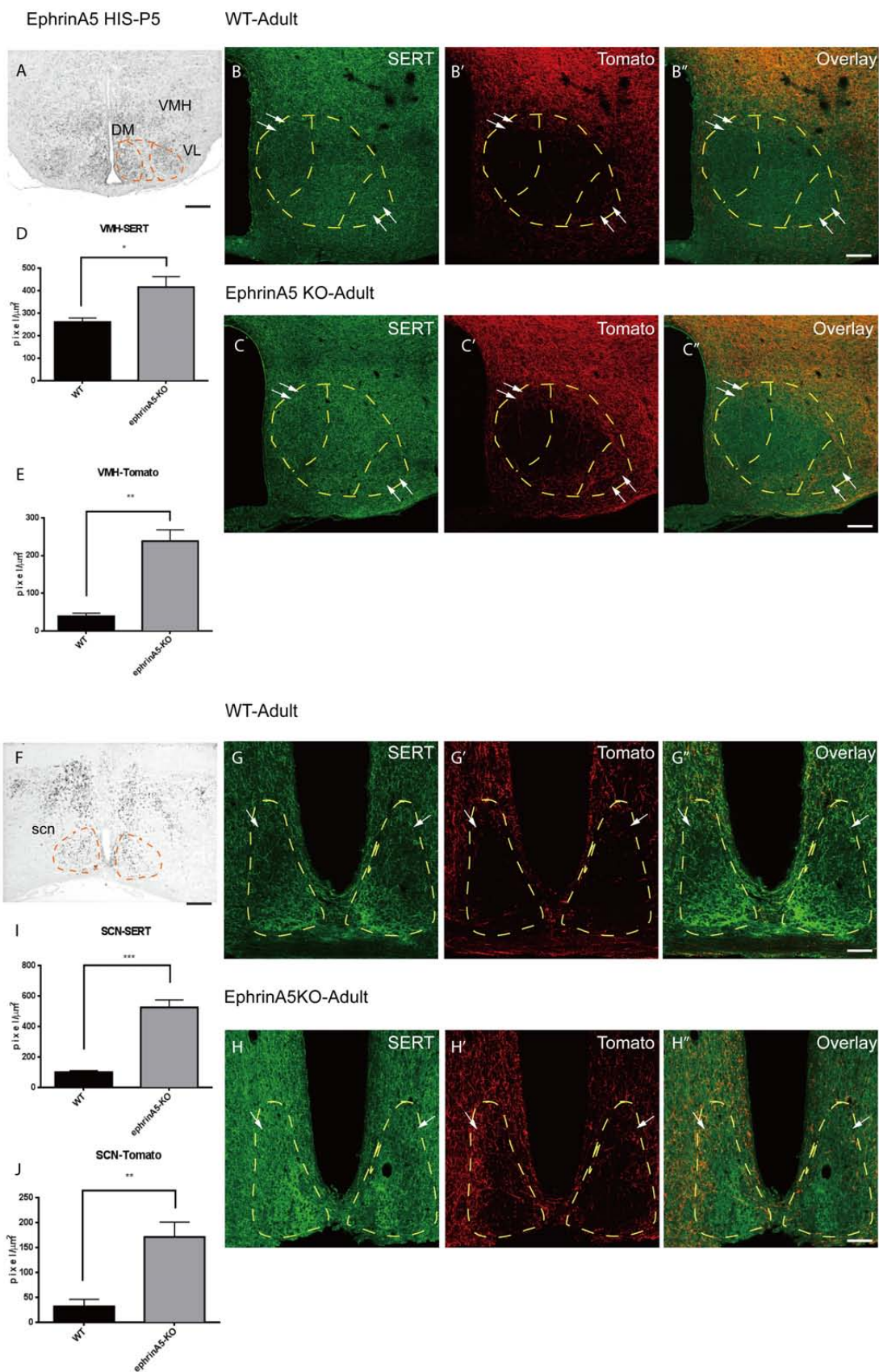












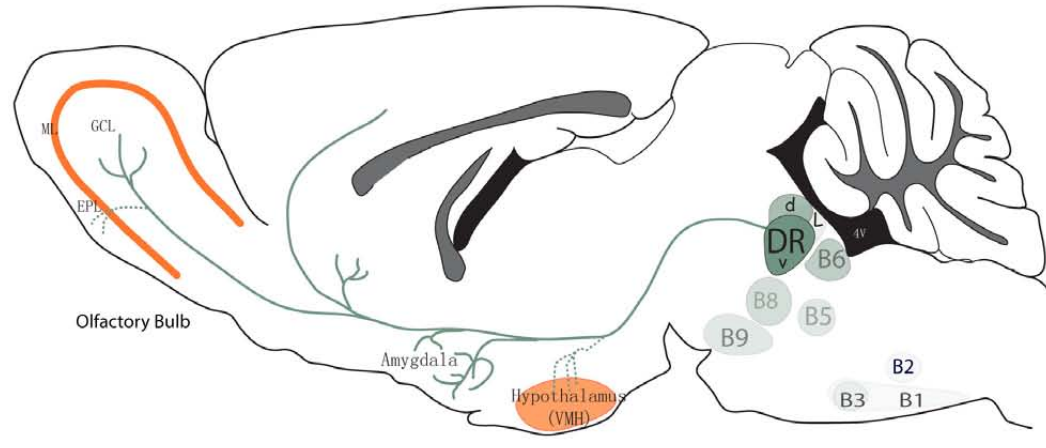


Table 1 Primers for mRNA probe synthesis

	Restriction enzyme		Polymerase	
	Sense	anti-sense	Sense	anti-sense
EphA3	HindIII	EcoRI	T7	T3
EphA4	SacI/SacII	XhoI/BamHI	T7	T3
EphA5	XbaI	BamHI		T7
EphA7	BamHI	XhoI	T7	SP6
Efna2	HindIII	EcoRV	SP6	T7
Efna3	XhoI	BamHI	T7	SP6
Efna5	HindIII	XbaI	T3	T7

Table2 RT-QPCR primers

	mRNA Variant 1	Primer info	Forward primer	Reverse primer
EphA3	NM_010140	Product length 116	TGCGGGACTGTAACAGCATT	CGTGAAGTATGCTCTCGGA
EphA4	NM_007936	Product length 90	GAGGCTCCTGTGTCAACAACT	AGTTGCCAATGGGTACCAGC
EphA5	NM_007937	Product length 98	TTGGCTGTTGACCAGTTGGA	GTCCTCCAGGAAGGCTGTTG
EphA6	NM_007938	Product length 90	ACTGAAATCCGTGAGGTGGG	GACTGAGACCAGAGCGATGC
EphA7	NM_010141	Product length 98	TCCTCCTTAGTCGAGGTCCG	GCCACTCTCCTTCTGCACTG
EphA8	NM_007939	Product length 95	CATTGCTTTCCGCACGTTCT	TCCAGTAGGGTCGTTACCA

Table 3 Measures of EphA5-Tph2 co-localization in the B1-B9 cell groups

	B1	B2	B3	B5	B6	B7	B8	B9
Tph2+	8,2±0,9	2,8±0,1	7,4±0,9	5,1±0,1	30,7±1,9	11,2±0,9	5±0,4	7,3±0,5
EphA5+	19,3±3,3	3,3±1,7	2,9±1,5	8,9±0,2	41,2±2,9	23,3±2,2	18,9±1,6	16,9±0,8
Tph2+/EphA5+	1,3±0,2	0	0,1±0,1	0,7±0,1	11,5±0,6	5,7±0,4	1,1±0,1	1,6±0,2
% Tph2 colocalized	16,4± 1%	0	1,8 ±1,9%	14,3± 0,7%	37,6%± 1,6%	50,5± 1,2%	22,3± 0,2%	22,3±2,8%

Table 4 Measures of EphA5-Tph2 co-localization in the DR cell groups

	DR-LW	DR-C	DR-M	DR-R	DR-D	DR-V
Tph2+	4,5±0,6	17,8±2,3	20,2±1,6	21±2	20,1±2,1	17,9±1,8
EphA5+	20±1,2	20,6±3,6	38,3±4,3	18,6±3,1	32,8±3,5	26,2±4,5
Tph2+/EphA5+	0,6±0,1	7,4±1,1	16,4±1,4	11,3±0,7	11,1±1,4	12,7±1,2
% Tph2 colocalized	12,6% ± 1,5%	41,5±1,2	81,1% ± 1%	44,4% ± 7,7%	55,2% ± 1,4%	70,9% ± 0,6%

Line	Data structure	Type of test	Power
a, Qpcr analysis of EphA5 expression during development (Figure 2A)	Homocedacy	One way ANOVA Tukey's multiple comparisons test	0.7792
b1, Quantification of EphA5-Tph2 co-localization in distinct raphe nucleus (Figure 3D)	Homocedacy	One way ANOVA Tukey's multiple comparisons test	0.8335
b2, Quantification of EphA5-Tph2 co-localization in dorsal raphe nucleus (Figure 3E)	Homocedacy	One way ANOVA Tukey's multiple comparisons test	0.7097
c1, Quantification of percentage of collapsed growth cones (Figure C)	Homocedacy	One way ANOVA Tukey's multiple comparisons test	0.9714
c2, Quantification of percentage of collapsed growth cones (Figure D)	Homocedacy	One way ANOVA Tukey's multiple comparisons test	0.9783
c3, Quantification of percentage of collapsed growth cones (Figure E)	Homocedacy	One way ANOVA Tukey's multiple comparisons test	0.266
c4, Quantification of percentage of collapsed growth cones (Figure F)	Homocedacy	One way ANOVA Tukey's multiple comparisons test	0.934
d1, Quantification of fiber density in amygdala after Efna3 overexpressed (Figure 5D)	Homocedacy	Paired t test (two tailed)	1
d2, Quantification of fiber density in amygdala after Efna3 overexpressed (Figure 5E)	Homocedacy	Paired t test (two tailed)	1
e1, Quantification of fiber density WT vs Efna5 ^{-/-} , OB (Figure 6F)	Homocedacy	Unpaired t test (two tailed)	1
e2, Quantification of fiber density WT vs Efna5 ^{-/-} , OB (Figure 6G)	Homocedacy	Unpaired t test (two tailed)	1
e3, Quantification of fiber density WT vs Efna5 ^{-/-} , OB (Figure 6H)	Homocedacy	Unpaired t test (two tailed)	0.052

f1, Quantification of fiber density WT vs Efna5 ^{-/-} , VMH (Figure 7D)	Homocedacy	Unpaired t test (two tailed)	1
f2, Quantification of fiber density WT vs Efna5 ^{-/-} , VMH (Figure 7E)	Homocedacy	Unpaired t test (two tailed)	1
g1, Quantification of fiber density WT vs Efna5 ^{-/-} , SCN	Homocedacy	Unpaired t test (two tailed)	1
g2, Quantification of fiber density WT vs Efna5 ^{-/-} , SCN	Homocedacy	Unpaired t test (two tailed)	1

Statistical Table

Statistical Calculations were done with scientific software Graphpad Prism 6, published by GraphPad Software, Inc. CA 92037 USA

Powers of each experiment were calculated by an online power calculator

<https://www.anzmtg.org/stats/PowerCalculator>