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Choubey L, Collette JC, Smith KM. 2017. Quantitative assessment of fibroblast growth factor receptor 1 expression in neurons and glia. PeerJ 5:e3173 <https://doi.org/10.7717/peerj.3173>

Quantitative assessment of *Fgfr1* expression in Neurons and Glia

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Fibroblast growth factors (FGFs) and their receptors (FGFRs) have numerous functions in the developing and adult CNS. For example, the FGFR1 receptor is important for proliferation of radial glial cells in the cortex and hippocampus, oligodendrocyte proliferation and regeneration, midline glia morphology and soma translocation, Bergmann glia morphology, and cerebellar morphogenesis. In addition, FGFR1 signaling in astrocytes is required for postnatal maturation of interneurons expressing parvalbumin (PV). FGFR1 is implicated in synapse formation in the hippocampus, and alterations in the expression of *Fgfr1* and its ligand, *Fgf2* accompany major depression. Understanding which cell types express *Fgfr1* during development may elucidate its roles in normal development of the brain as well as illuminate possible causes of certain neuropsychiatric disorders. Here, we used a BAC transgenic reporter line to trace *Fgfr1* expression in the developing murine CNS. The specific transgenic line employed was created by the GENSAT project, *tgFGFR1-EGFP338Gsat*, and includes a gene encoding enhanced green fluorescent protein (EGFP) under the regulation of the *Fgfr1* promoter, to trace *Fgfr1* expression in the developing CNS. This model reveals that *Fgfr1* is primarily expressed in glial cells, in both astrocytes and oligodendrocytes, along with some neurons. Dual labeling experiments indicate that the proportion of GFP+ (*Fgfr1*+) cells that are also GFAP+ increases from postnatal day 7 (P7) to 1 month, illuminating dynamic changes in *Fgfr1* expression during postnatal development of the cortex. In postnatal neurogenic areas, GFP expression was also observed in SOX2, doublecortin (DCX), and brain lipid-binding protein (BLBP) expressing cells. *Fgfr1* is also highly expressed in DCX positive cells of the dentate gyrus, but not in the rostral migratory stream. *Fgfr1* driven GFP was also observed in tanycytes and GFAP+ cells of the hypothalamus, as well as in Bergmann glia and astrocytes of the cerebellum. Understanding which cell types express *Fgfr1* may elucidate its role in neuropsychiatric disorders and brain development.

1 **Quantitative assessment of *Fgfr1* expression in Neurons and Glia**

2 Short title: *Fgfr1* expression in Neurons and Glia

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13 **Running head:** *Fgfr1* is expressed in neurons and glia

14 **Key words:** Fibroblast Growth Factor, astrocyte,

15 oligodendrocyte, doublecortin, SOX2, cortex, hippocampus, SVZ

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21 **Abstract**

22 **Background.** Fibroblast growth factors (FGFs) and their receptors (FGFRs) have numerous
23 functions in the developing and adult CNS. For example, the FGFR1 receptor is important for
24 proliferation of radial glial cells in the cortex and hippocampus, oligodendrocyte proliferation
25 and regeneration, midline glia morphology and soma translocation, Bergmann glia morphology,
26 and cerebellar morphogenesis. In addition, FGFR1 signaling in astrocytes is required for
27 postnatal maturation of interneurons expressing parvalbumin (PV). FGFR1 is implicated in
28 synapse formation in the hippocampus, and alterations in the expression of *Fgfr1* and its ligand,
29 *Fgf2* accompany major depression. Understanding which cell types express *Fgfr1* during
30 development may elucidate its roles in normal development of the brain as well as illuminate
31 possible causes of certain neuropsychiatric disorders.

32 **Methods.** Here, we used a BAC transgenic reporter line to trace *Fgfr1* expression in the
33 developing postnatal murine CNS. The specific transgenic line employed was created by the
34 GENSAT project, *tgFGFR1-EGFP338Gsat*, and includes a gene encoding enhanced green
35 fluorescent protein (*EGFP*) under the regulation of the *Fgfr1* promoter, to trace *Fgfr1* expression
36 in the developing CNS. Unbiased stereological counts were performed for several cell types in
37 the cortex and hippocampus.

38 **Results.** This model reveals that *Fgfr1* is primarily expressed in glial cells, in both astrocytes and
39 oligodendrocytes, along with some neurons. Dual labeling experiments indicate that the
40 proportion of GFP+ (*Fgfr1*+) cells that are also GFAP+ increases from postnatal day 7 (P7) to 1
41 month, illuminating dynamic changes in *Fgfr1* expression during postnatal development of the
42 cortex. In postnatal neurogenic areas, GFP expression was also observed in SOX2, doublecortin
43 (DCX), and brain lipid-binding protein (BLBP) expressing cells. *Fgfr1* is also highly expressed

44 in DCX positive cells of the dentate gyrus, but not in the rostral migratory stream. *Fgfr1* driven
45 GFP was also observed in tanycytes and GFAP+ cells of the hypothalamus, as well as in
46 Bergmann glia and astrocytes of the cerebellum.

47 **Conclusions.** The *tgFGFR1-EGFP338Gsat* mouse model expresses GFP that is congruent
48 with known functions of FGFR1, including hippocampal development, glial cell development,
49 and stem cell proliferation. Understanding which cell types express *Fgfr1* may elucidate its role
50 in neuropsychiatric disorders and brain development.

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55 **Introduction**

56 Differential binding of Fgfs to Fgf receptor isoforms may confer a high degree of
57 selectivity leading to signaling events that lead to a multitude of specific cellular responses
58 (Fortin et al., 2005). Multiple *Fgfligands* and three of the *Fgfrs* (*Fgfr1*, *Fgfr2*, and *Fgfr3*) are
59 expressed in the CNS (el-Husseini et al., 1994, Belluardo et al., 1997, Bansal et al., 2003). This
60 complex system of Fgfs and Fgfrs plays a pivotal role in the normal development, maturation,
61 and function of the central nervous system (CNS) (Iwata and Hevner, 2009, Stevens et al.,
62 2010b, Hebert, 2011). FGF signaling is implicated in patterning of the CNS, in determining
63 neuronal and glial cell fate, in influencing cerebral cortex size through maintenance of radial
64 glial stem cells, in cerebellar development, and in regional patterning of the neocortex and
65 midbrain-hindbrain boundaries (Vaccarino et al., 1999, Fukuchi-Shimogori and Grove, 2001,
66 Korada et al., 2002, Storm et al., 2003, Shin et al., 2004, Gutin et al., 2006, Smith et al., 2006,

67 Storm et al., 2006, Cholfin and Rubenstein, 2007, Muller Smith et al., 2008, Kang et al., 2009,
68 Stevens et al., 2010a, Rash et al., 2011, Muller Smith et al., 2012, Rash et al., 2013, Kang et al.,
69 2014, Smith et al., 2014).

70 Loss of FGFR1 function by *hGFAP-Cre*-induced deletion of *Fgfr1^{fllox/fllox}* alleles in the
71 dorsal telencephalon of mice results in decreased hippocampal size and volume, without altering
72 hippocampal patterning, and also results in a reduction in the number of dividing progenitor cells
73 of the ventricular zone and dentate gyrus (Ohkubo et al., 2004). The *hGFAP-Cre* transgene
74 targets the radial glial of the dorsal telencephalon during mid neurogenesis (Ohkubo et al., 2004).
75 *Fgfr1* mutants also exhibit a disruption in corpus callosum and hippocampal commissure due to
76 abnormal midline glia development (Smith et al., 2006, Tole et al., 2006). The midline glial cells
77 fail to undergo soma translocation and formation of the indusium griseum leading to midline
78 commissural axon guidance defects (Smith et al., 2006). Furthermore, these mice exhibit
79 postnatal loss of maturation in GABAergic interneurons expressing parvalbumin (PV) and
80 exhibit behavioral hyperactivity (Muller Smith et al., 2008, Smith et al., 2014). Hyperactivity
81 and a decrease in number of interneurons in the cortex co-occur in patients with schizophrenia,
82 bipolar disorder, and Tourette syndrome (Benes et al., 2000, Volk et al., 2000, Kalanithi et al.,
83 2005, Akbarian and Huang, 2006, Hashimoto et al., 2008, Kataoka et al., 2010, Gonzalez-Burgos
84 et al., 2011, Volk and Lewis, 2013). Interestingly, *Fgfr1* expression was found to be increased in
85 the prefrontal cortex of individuals with schizophrenia (Volk et al., 2016). Dual inactivation of
86 floxed alleles of *Fgfr1* and *Fgfr2* with the *hGFAP-Cre* transgene results in abnormal cerebellar
87 morphogenesis including reduced size of the cerebellum due to a defect in proliferation of both
88 cerebellar glia and granule cell precursors, abnormal orientation and morphology of Bergmann
89 glia, and loss of laminar architecture (Muller Smith et al., 2012). This phenotype is similar to that

90 observed in Fgf9 mutants (Lin et al., 2009). FGFRs are implicated in maintaining astrocytes in a
91 non-reactive state, and in impeding glial scar formation (Kang et al., 2014). *Fgfr1* deletions
92 targeted to oligodendrocyte lineages do not disrupt oligodendrocyte birth, but affect myelin
93 sheath thickness, as well as remyelination and recovery in chronic demyelination models
94 (Furusho et al., 2012, Furusho et al., 2015). Therefore, FGFR1 has important roles in glial
95 function and development including stem cell proliferation, migration, morphology, and support
96 of neural maturation..

97 FGF signaling is implicated as a contributing factor in affective disorders, including
98 depression. Patients with major depressive disorder (MDD) and bipolar disorder have altered
99 gene expression of FGFs and FGFRs (Evans et al., 2004, Gaughran et al., 2006). *In situ*
100 hybridization revealed that mRNA for *Fgfr1*, and its ligand *Fgf2*, were both down regulated in
101 the hippocampus of rats that had undergone the social defeat paradigm (Turner et al., 2008).
102 Microinjections of FGF2 into the lateral ventricles of rats resulted in an increase in *Fgfr1* mRNA
103 in the dentate gyrus within 24 hours post FGF2 injections and was accompanied by acute
104 antidepressant-like effects in the force swim test (Elsayed et al., 2012). Intracerebroventricular
105 infusions of FGF2 into mice were sufficient to block the anhedonia-like behavior caused by
106 chronic unpredictable stress (CUS). Furthermore, intracerebroventricular infusions of FGF2
107 blocked CUS-induced inhibition of proliferating glia in the prefrontal cortex, and produced
108 antidepressant actions in the novelty suppressed feeding test and forced swim test (Elsayed et al.,
109 2012). Furthermore, increased anxiety, dysregulation of the hypothalamic pituitary axis and
110 decreased hippocampal glucocorticoid receptor expression is observed in FGF2 knockout mice.
111 These effects are reversible by administration of FGF2 (Salmaso et al., 2016). FGF22 and FGF7
112 are presynaptic organizing molecules that promote differentiation of excitatory and inhibitory

113 presynaptic terminals in the hippocampal CA3 region through combinatorial signaling of sets of
114 FGFRs (Umemori et al., 2004, Terauchi et al., 2010, Dabrowski et al., 2015). Given the data that
115 FGF2/FGFR1 signaling is important for the regulation of mood and affect, and that FGFR1
116 signaling may participate in synaptogenesis, a better understanding of the cell types expressing
117 *Fgfr1* is important to improving our understanding of its actions.

118 Previous estimates of *Fgfr1* expression have been derived from *in situ* hybridization
119 studies and from immunocytochemistry using antibodies against FGFR1 (Gonzalez et al., 1995,
120 Belluardo et al., 1997, Bansal et al., 2003, Ohkubo et al., 2004, Blak et al., 2005). In embryonic
121 mice, *Fgfr1* is strongly expressed in the hippocampal hem, choroid plexus, cortical ventricular
122 zone, and cortical midline (el-Husseini et al., 1994, Bansal et al., 2003, Ohkubo et al., 2004,
123 Smith et al., 2006). During brain development, expression of *Fgfrs* change within the
124 oligodendrocyte lineage in a spatial and temporal fashion (Bansal et al., 2003). *Fgfr1* is
125 expressed in all three stages: proliferation, migration, and differentiation of oligodendrocytes
126 (OL) (Fortin et al., 2005). An *in situ* hybridization study showed that *Fgfr1* is not expressed
127 where *Olig2*-positive and *Pdgfra*-positive OL progenitors arise in the ventral ventricular zone
128 (Bansal et al., 2003). In adult mice, the strongest *Fgfr1* expression is observed in the
129 hippocampus (Ohkubo et al., 2004). Based on a literature review, Turner and colleagues
130 surmised that neuronal populations in the adult hippocampus and cortex mostly express *Fgfr1*, in
131 contrast to other FGF receptors that are considered to be expressed primarily in glia (Turner et
132 al., 2012a).

133 Despite clear advances in our understanding of FGF signaling derived from *in situ*
134 hybridization, it suffers from poor cell-type resolution. Likewise, although
135 immunocytochemistry using antibodies raised to FGFR1 have proven to be important, cross-

136 reactivity to other FGFRs remains a concern. To circumvent these issues, we investigated *Fgfr1*
137 expression in PV+ interneurons, employing a transgenic reporter line, *tgFGFR1-*
138 *EGFP338Gsat* bacterial artificial chromosome (BAC), that was obtained from GENSAT,
139 <http://www.gensat.org> (Smith et al., 2014). In this transgenic line, the gene encoding enhanced
140 green fluorescent protein (*EGFP*) is regulated under the same promoter as *Fgfr1*. Thus, GFP
141 fluorescence should indicate expression of genes encoding *Fgfr1*. We previously showed that in
142 *tgFGFR1-EGFP338Gsat* mice, PV+ interneurons did not colocalize with GFP+ cells. Thus,
143 the decrease in PV+ interneurons due to inactivation of *Fgfr1* occurs non-cell-autonomously
144 (Smith et al., 2014). We also observed that a large number of glia appeared to express *Fgfr1* in
145 adult mice. In the present study, we extend our studies and present a quantitative analysis of the
146 relative expression of *Fgfr1* in neurons versus glial cells during postnatal development of the
147 telencephalon. We show that *Fgfr1* is differentially expressed, primarily in GFAP+ astrocytes
148 and OLIG2+ cells, with a minority of cells colocalizing with NeuN+ neurons. Furthermore,
149 SOX2+ cells, BLBP+ cells and DCX+ cells in the cortex, hippocampus, subventricular zone
150 (SVZ), and hypothalamus of mice are colocalized with the GFP signal, indicating that these cells
151 also express *Fgfr1*.

152

153 **Methods and Materials**

154 *Animals*

155 Wild type Swiss Webster mice were crossed with mice expressing enhanced green
156 fluorescent protein (EGFP) under the same promoter as *Fgfr1* (*tgFGFR1-EGFP338Gsat*). The
157 transgenic line, *tgFGFR1-EGFP338Gsat* was generated from the GENSAT project
158 (GENSAT.org) by microinjecting bacterial artificial chromosome with *Fgfr1* promoter driving

159 EGFP into the pronucleus of fertilized mouse eggs. GENSAT produces transgenic BAC-EGFP
160 reporter and BAC-Cre recombinase driver mouse lines with the aim to map the expression of
161 genes in the CNS of mice (Heintz, 2004). This line was obtained from the Mutant Mouse
162 Resource Center (MMRRC.org) at UC Davis. This study was conducted in an ethical manner,
163 utilizing the recommendations of The Guide for the Care and Use of Laboratory Animals of the
164 National Institutes of Health. Animals were euthanized under the University of Louisiana at
165 Lafayette IACUC committee APS numbers 2012-8717-046, 2013- 8717-053, 2014-8717 040,
166 2015-8717-033. Tissue collected for this study was performed under ketamine/xylazine cocktail
167 for P7 and older animals.

168 **Genotyping**

169 The mice were genotyped by polymerase chain reaction (PCR) for GFP and through GFP
170 screening with goggles containing a GFP filter (BLS LTD). For PCR based genotyping, tails of
171 mice were collected and DNA was extracted from the tail using 50mM sodium hydroxide (95°C
172 for 30 min), followed by neutralization with 1M TRIS (pH 7.6). Master mix for 1 reaction of
173 PCR for amplifying *GFP* was created using 2.5 µl of 10x PCR buffer, 0.5 µl of 10mM dNTP
174 mix, 1 µl of eGFP forward and reverse primer mix (Forward:AAGTTCATCTGCACCACCG
175 and Reverse: TGCTCAGGTAGTGGT
176 TGTCG), 0.2 µl of 5 units/ µl Hot start Taq Polymerase and 18.8 µl of distilled water. Two
177 microliters of DNA sample were added to 23 µl of Master mix per PCR tube and the samples
178 were amplified in the Applied Biosystems 96 Well Thermocycler. In adult *tgFGRI-*
179 *EGFPGP338Gsat* positive mice, we found we could reliably genotype mice due to GFP
180 expression in the eye, using GFP goggles (available from BLS).

181 **Immunostaining**

182 P7 mice were anesthetized with ketamine/xylazine (100 mg and 10 mg per kg of body
183 weight respectively) and euthanized by cervical dislocation. Brains were dissected out and in 4%
184 PFA overnight. Adult mice were euthanized by cardiac perfusion under deep anesthesia
185 (ketamine/xylazine as above). Mice were perfused with cold 1x Phosphate Buffered Saline
186 (PBS) followed by 4% PFA in 1x PBS. Brains were post fixed overnight and cryoprotected as
187 described above. Brains collected from P7 and one-month ages were cryoprotected in 20%
188 sucrose/1xPBS, and cryopreserved with exposure to dry ice and embedded in optimal cutting
189 temperature (OCT) at the time of sectioning. The tissue was thick sectioned (50 μ m, free
190 floating) in a cryostat (Microm, HM 505 E) in a series of 10 vials containing 1xPBS. Samples
191 were stored in PBS with 0.2% sodium azide at 4°C, and protected from light exposure.

192 Prior to antibody incubation, sections were blocked with 10% serum in PBS with 0.2%
193 triton x (Sigma Aldrich) and 0.1% tween 20 (Sigma Aldrich), except for anti-Gad67 staining
194 which did not include detergents. Primary antibodies (**Table 1**) were detected with Alexa
195 conjugated secondary antibodies (Jackson labs and Abcam) or AMCA conjugated secondary
196 antibodies (Vector) in 5% serum. VECTASHIELD DAPI used for double staining and
197 VECTASHIELD without DAPI used for triple staining when mounting sectioned tissue onto
198 polyprep slides.

199 **Cell Counting**

200 Unbiased estimated counts of astrocytes expressing glial fibrillary acidic protein (GFAP),
201 neurons expressing NeuN, and oligodendrocytes and oligodendrocyte precursors expressing
202 Olig2 were obtained using StereoInvestigator software (Microbrightfield) coupled with a
203 AxioCam MRm on the Zeiss axioimager microscope equipped with an ApoTome.2. Tops of
204 cells were counted in three-dimensional counting boxes, which were set to specific parameters

205 (Table 2). For counts of the cortex and hippocampus, 50 μm sections were sampled every 20th
206 (cortex) and every 10th section (Hippocampus). Fluorescence images were acquired through
207 StereoInvestigator imaging software.

208 To determine the percentage of GFP+ cells that were neuronal stem cells expressing Sox2
209 and neuroblasts expressing DCX, we acquired z stack images of the anterior dentate gyrus
210 hemisphere and a section 500 μm posterior to this first section. The z stack images obtained to
211 count SOX2 markers were 19 μm thick with each slice 1 μm thick. The z stack images acquired
212 to count DCX markers were 10 μm thick with each slice 1 μm thick.

213 Statistical Analysis

214 Data from the StereoInvestigator software were entered into Excel, imported to JMP Pro 11, and
215 analyzed by student t-tests or ANOVA using SAS.

216

217 Results

218 *Fgfr1* is expressed in various cells types of the dentate gyrus, CA, and subventricular zone 219 (SVZ) at P7

220 Previous *in situ* studies indicated high levels of *Fgfr1* mRNA in the hippocampus,
221 including dentate gyrus (DG) and cornu ammonis (CA regions). To investigate the cell types
222 expressing *Fgfr1* in the hippocampus of P7 control and *tgfgfr1-EGFP+* mice, samples were
223 stained by immunocytochemistry for cell-type markers to identify each of the following: GFAP+
224 stem cells and astrocytes, NeuN+ neurons, BLBP+ stem cells, and DCX+ neuroblasts. The cell-
225 type marker staining (red fluorescence) was imaged alongside GFP immunostaining (green
226 fluorescence) to reveal which cell types express *Fgfr1* and with DAPI counterstaining (blue
227 fluorescence) to image nuclei (Fig. 1). The colocalization of a cell type marker and *Fgfr1*

228 expression is indicated by yellow fluorescence caused by overlapping red and green
229 fluorescence. GFAP and GFP immunostaining showed GFP⁺ cells in the GFAP⁺ stem cells of
230 the subgranular zone (SGZ) of the DG of *tgfgfr1-EGFP*⁺ mice (**Fig. 1A-C, Video S1**) with little
231 to no green fluorescence in GFP⁻ controls (**Fig. 1D-F**). In the CA region of the hippocampus,
232 GFAP⁺/GFP⁺ cells were primarily observed surrounding the stratum pyramidale, in the stratum
233 radiatum, stratum oriens, as well as the white matter above the CA region (**Fig. 1 G-I**) with little
234 to no green fluorescence in GFP⁻ littermate controls (**Fig. 1 J-L**). There was strong GFP
235 fluorescence in the stratum pyramidale of the CA region. This GFP staining colocalized with
236 NeuN⁺ cells (neurons) (**Fig. 2A-C**) with little to no green fluorescence in GFP⁻ littermate
237 controls (**Fig. 2D-F**). NeuN⁺ /GFP⁺ cells were also observed in some, but not all, granule cell
238 layer neurons of the developing DG of *tgfgfr1-EGFP*⁺ mice (**Fig. 2G-I**) with little to no green
239 fluorescence in GFP⁻ controls (**Fig. 2J-L**). Stereological analysis of *tgfgfr1-EGFP* expression in
240 GFAP⁺ cells of the dentate gyrus showed that of GFP⁺ cells, 24% ± 8% are GFAP positive, and
241 of GFAP⁺ cells, 50% ± 8% are GFP⁺. Of GFP⁺ cells in the CA, 50% ± 5% are GFAP positive
242 and of GFAP⁺ cells in the CA, 43% ± 9% are GFP positive (**Table 3**). One-way ANOVA
243 statistical analysis revealed that the total number of GFAP⁺ cells in the DG and CA of *tgfgfr1-*
244 *EGFP*⁺ are not significantly different from their littermate controls (**Table 3**). This analysis
245 suggests that the insertion of *tgfgfr1-EGFP* is not lethal to GFAP⁺ stem cells and astrocytes.

246 We further explored *Fgfr1* promoter driven expression of GFP in the postnatal
247 neurogenic niches of the DG and SVZ of the lateral ventricles at P7. Immunostaining for DCX
248 (neuroblasts) and GFP extensively colocalized in the SGZ and granule cell layer (GCL) of the
249 DG (**Fig. 3A and 3B**, low and high magnification respectively) with nearly all DCX positive
250 cells co-expressing GFP. Postnatally, the SVZ of the lateral ventricles gives rise to olfactory bulb

251 interneurons. GFP+ cells were observed in the SVZ, consistent with previous studies of postnatal
252 *Fgfr1* expression (Fagel et al., 2009). However, DCX did not colocalize with GFP staining in the
253 SVZ of the lateral ventricles (**Fig. 3C**), in contrast to what was observed in the DG of the
254 hippocampus. Immunostaining with BLBP (stem cells) and GFP antibodies revealed strong
255 colocalization of *Fgfr1* driven GFP in the subgranular zone (SGZ) of the dentate gyrus (DG)
256 (**Fig. 3D** and **3E**, low and high magnification, respectively) as well as BLBP+ cells of the SVZ
257 (**Fig. 3F**).

258

259 ***Fgfr1* is expressed in cortical GFAP+ astrocytes and NeuN+ neurons at P7**

260 To determine which cortical cells express *Fgfr1*, we stained the cortical tissue of P7
261 *tgfgfr1-EGFP+* and control mice with GFAP and NeuN antibodies. Whereas GFP+ cells
262 colocalized with GFAP+ astrocytes throughout the cortex (**Fig. 4A-C**), GFP+ cells colocalized
263 with NeuN+ cells (neurons) mostly in layers 5 and 6 of the cortex at this age (**Fig. 4D-F**).
264 Stereological analysis of the cortex region revealed that of GFP+ cells in the cortex, $32\% \pm 4\%$
265 are GFAP positive. Of the cortical GFAP+ cells, $93\% \pm 2\%$ are GFP positive. This analysis
266 indicates that most *Gfap* expressing astrocytes also express *Fgfr1*. The total number of cortical
267 GFAP+ cells of *tgfgfr1-EGFP+* mice was not significantly different from the number of cells in
268 littermate controls (**Table 3**), suggesting that the insertion of the transgene does not significantly
269 alter the number of astrocytes expressing *Gfap*.

270 We examined whether *tgfgfr1-EGFP+* was expressed in oligodendrocytes and their
271 precursors by staining for OLIG2 in the cortex. We found that OLIG2+ staining colocalized with
272 GFP in the cortex (**Fig. 4G-I**) and SVZ and subcortical white matter (**Fig. 4J**). At P7, radial glia
273 of the cortex are undergoing soma translocation to become astrocytes, and can be detected with

274 BLBP. BLBP and GFP immunostaining revealed strong colocalization throughout the cortex
275 (**Fig. 4K-M**). At P7, GFP staining colocalized with BLBP+ stem cells and Bergmann Glia in the
276 developing cerebellum (**Fig. 4N**). This finding is consistent with the participation of *Fgfr1*/*Fgfr2*
277 signaling in Bergmann Glia morphology and cerebellar development (Muller Smith et al., 2012).
278 Furthermore, GFP+ cells colocalized with GFAP+ astrocytes of the cerebellum, but not within
279 granule cell layer or molecular layer neurons that stain with NeuN. GFP+ cells likely colocalized
280 with NeuN- Purkinje neurons based on the location and size of GFP+ cells in the Purkinje layer
281 (**Fig. S1 and Video S2**).

282

283 ***Fgfr1* is expressed in specific cell types of the hippocampus and SVZ at 1 month**

284 We next investigated *Fgfr1* expression in 1-month *tgfgfr1-EGFP*+ mice. Immunostaining
285 for SOX2+ cells (stem cells), DCX+ cells (neuroblasts), NeuN+ neurons, GFAP+ astrocytes and
286 stem cells, and OLIG2+ oligodendrocytes was performed in combination with GFP
287 immunostaining to determine which cell types express *Fgfr1* in the dentate gyrus, CA, and SVZ.
288 GFP+ cells colocalized with SOX2+ cells (**Fig. 5A-E**) and DCX+ cells (**Fig. 5F-J**) in the SGZ
289 and granule cell layers. To determine the percentage of GFP+ cells that were SOX-2 positive and
290 DCX positive, we obtained z stack images of an anterior dentate gyrus hemisphere and posterior
291 dentate gyrus hemisphere, and performed counts from these images. Of the GFP+ cells counted
292 in the z stack, 33% ± 2% are SOX2 positive. Conversely, the majority of SOX2+ cells, 71% ±
293 2%, are GFP positive (**Fig. 5E**). Of the GFP+ cells counted in the z stack, 64% ± 0.9% are DCX
294 positive and of DCX+ cells, 86% ± 2% are GFP positive (**Fig. 5J**). Triple staining with GFP,
295 GFAP and NeuN antibodies revealed that GFAP+ cells (stem cells) and NeuN+ cells (neurons)
296 colocalized with GFP+ cells in the SGZ (**Fig. 5K-N**) and in the CA region (**Fig. 5O-R**),

297 respectively. GFP+ cells did not colocalize with OLIG2+ cells (oligodendrocytes) in the dentate
298 gyrus (**Fig. S2**). Taken together, these results indicate that GFP (*Fgfr1*) was expressed in stem
299 cells and neuroblasts of the DG. Stereological analysis of *tgfgfr1-EGFP* expression in NeuN+
300 cells of the dentate gyrus showed that of GFP+ cells, 16% ± 6% are NeuN positive and of
301 NeuN+ cells, 5% ± 0.7% are GFP positive. Of GFP+ cells in the CA, 25% ± 7% are NeuN
302 positive and of NeuN+ cells, 15% ± 6% are GFP positive. Stereological analysis of *tgfgfr1-*
303 *EGFP* expression in GFAP+ cells of the dentate gyrus showed that of GFP+ cells, 51% ± 3% are
304 GFAP positive and of GFAP+ cells, 85% ± 4% are GFP positive. Of GFP+ cells in the CA, 61%
305 ± 9% are GFAP positive and of GFAP+ cells, 81% ± 3% are GFP positive. These findings
306 indicate that most GFAP positive astrocytes express *Fgfr1* at 1 month. The total number of
307 SOX2+ cells, DCX+ cells, NeuN+ cells and GFAP+ cells of *tgfgfr1-EGFP*+ mice were not
308 significantly different from their littermate controls in the DG and CA (Sox2: p=0.23, DCX:
309 p=0.88 and **Table 3**).

310 Many GFAP+ cells also express GFP in the SVZ (**Fig. 6A-H**) of 1 month *tgfgfr1-*
311 *EGFP*+ mice. Colocalized GFP positive cells and GFAP positive fibers were observed both
312 within the SVZ and in the white matter above it (**Fig. 6D, 6G, and 6H**). There was also
313 significant colocalization of GFP with SOX2+ cells (**Fig. 6I-L**) indicating that GFAP+ and
314 SOX2+ stem cells of the SVZ express *Fgfr1*. NeuN+/GFP+ cells were not observed in the SVZ.
315 Similar to what was found at P7, GFP+ cells did not colocalize with DCX+ cells (neuroblasts) in
316 the SVZ (**Fig. 6M-O**) or in the DCX+ cells of rostral migratory stream (RMS) as it enters the
317 olfactory bulb (**Fig. 6P**). In the rostral migratory stream, GFP staining surrounds the DCX+ cells
318 as would be expected from astrocytes surrounding the migrating neuroblasts.
319

320 ***Fgfr1* is expressed in cortical GFAP+ astrocytes, NeuN+ neurons and OLIG2+ cells at 1**
321 **month**

322 To determine which cortical cells express *Fgfr1*, we examined cortical tissue of 1-month
323 old *tgfgfr1-EGFP+* and control mice immunostained with GFAP, NeuN or OLIG2 antibodies
324 alongside GFP antibodies. Analysis of *Fgfr1* expression in the cortex revealed that GFP+ cells
325 colocalized with GFAP+ and NeuN+ cells (**Fig. 7A-E**, compared to control **D**). Of note, GFP
326 immunofluorescence appeared less brightly fluorescent in cells colocalizing with NeuN
327 compared to those colocalizing with GFAP. GFP+ cells also colocalized with OLIG2+ cells (**Fig.**
328 **7G-H**) with little to no green fluorescence occurring in littermate controls (**Fig. 7I**).
329 Stereological analysis of the cortex revealed that of GFP+ cells, $57\% \pm 7\%$ are GFAP positive.
330 Of the GFAP+ astrocytes, $83\% \pm 6\%$ are GFP positive. Of GFP+ cells, $25\% \pm 4\%$ are NeuN
331 positive and of NeuN+ cells, $12\% \pm 2\%$ are GFP positive. Of GFP+ cells, $29\% \pm 0.9\%$ are
332 OLIG2 positive and of OLIG2+ cells, $58\% \pm 0.08\%$ are GFP positive. The total number of
333 cortical GFAP+, NeuN+, and OLIG2+ cells of *tgfgfr1-EGFP+* mice were not significantly
334 different from their littermate controls (**Table 3**).

335

336 ***Fgfr1* is expressed in various cell types of the hypothalamus at P7 and 1 month**

337 Comparing *Fgfr1* expression in different regions of the P7 and 1-month old mice, we
338 observed GFP expression in cells of the hypothalamus and among cells lining the third ventricle,
339 within the arcuate nucleus and medial eminence (**Fig. 8, Fig. S3 and Video S3**). In 1-month
340 *tgfgfr1-EGFP+* mice, GFP+ cells strongly colocalized with SOX2+ cells throughout the
341 hypothalamus and third ventricle and arcuate nucleus (**Fig. 8D-I**). GFAP+ tanycytes, including
342 those of the arcuate nucleus were among the hypothalamic cells observed to express *Fgfr1* both

343 at 1 month and at P7 (**Fig. 8J-L**). Tanycytes participate in neuroendocrine regulation and
344 transport of molecules from the CSF to the hypothalamus, release of gonadotropin-releasing
345 hormone, and production of triiodothyronine (T3) in the brain (Rodriguez et al., 2005). GFP
346 expression was not observed in NeuN⁺ or OLIG2⁺ cells of the hypothalamus (**Fig. 8M-O, Fig.**
347 **S3 A-D**). At P7, we also observed colocalization of BLBP and GFP in the hypothalamus near the
348 third ventricle, but not many in the medial eminence (**Fig. S3 E,F, Video S3**).

349

350 **Calretinin (CR) and somatostatin (SST) neurons express *Fgfr1* in one-month old mice.**

351 The NeuN⁺/GFP⁺ neurons observed at 1 month were not restricted to any specific
352 cortical layer, and a minority population of GFP colocalized with NeuN⁺ neurons. We therefore
353 sought to determine if inhibitory neurons express *Fgfr1*. Tissue from one-month old *tgfgfr1-*
354 *EGFP*⁺ mice and their control littermates was stained for GAD67. Some GAD67⁺ cells
355 colocalized with GFP in the cortex (**Fig. 9A, B**), but not in the hippocampus (**Fig. 9C**) or SVZ
356 (**Fig. 9D**). Our previous investigations determined that GFP was not colocalized with PV⁺
357 interneurons (Smith et al., 2014). This led to the experiments in which staining the one-month
358 old tissue with calretinin (CR) and somatostatin (SST) was performed alongside GFP
359 immunostaining. CR⁺ inhibitory neurons express GFP in the cortex (**Fig. 9E, F**), DG (**Fig. 9G**),
360 and SVZ (**Fig. 9H**). Some SST⁺ inhibitory neurons express GFP in the anterior cingulate of the
361 cortex (**Fig. 9I, J**), but none were observed in the DG (**Fig. 9K**).

362

363 **Discussion**

364 Through immunostaining for GFP in *tgFgfr1-EGFP*⁺ mice of the *tgFGFR1-*
365 *EGFPGP338Gsat* line, we examined the cell specific expression of *Fgfr1* in the cortex,

366 hippocampus, SVZ, hypothalamus, and cerebellum from P7 to one-month of age. In postnatal
367 brains, *Fgfr1* is highly expressed in the hippocampus, SVZ, hypothalamus, and in numerous cells
368 of the cortex. In the hippocampus, *Fgfr1* was expressed in DCX+ neuroblasts, in GFAP+ stem
369 cells and astrocytes, and Sox2+ stem cells of the SGZ, and in neurons of the CA. Furthermore,
370 *Fgfr1* was expressed in astrocytes, neurons, and oligodendrocytes. *Fgfr1* expression in cortical
371 neurons was not restricted to a single layer and colocalized with CR+ and SST+ inhibitory
372 neurons. *Fgfr1* expression was also observed in Bergmann glia and GFAP+ astrocytes of the
373 cerebellum.

374 The *tgFgfr1-EGFP+* line has been shown to be a robust model in identifying which cell
375 types express *Fgfr1*, corroborating the findings of previous *in situ* hybridization studies (el-
376 Husseini et al., 1994, Gonzalez et al., 1995, Belluardo et al., 1997, Bansal et al., 2003, Ohkubo et
377 al., 2004). This transgenic line gives the added benefit of allowing simple identification of the
378 subtype of cells expressing *Fgfr1* by immunofluorescence staining since GFP is regulated by the
379 *Fgfr1* promoter. Unlike the use of antibodies for FGFR1, which may have cross reactivity with
380 similar FGFR family members, we can have greater confidence that we are identifying *Fgfr1*
381 expression accurately within a cell. Total neuronal and glial cell counts were not significantly
382 different between the *tgfgfr1-EGFP+* mice and their control littermates. Therefore, the insertion
383 of this transgene into the host DNA does not cause toxicity amongst the neuronal and glial cells
384 observed.

385 Previous studies have shown that inactivation of FGFR1/FGFR2 and
386 FGFR1/FGFR2/FGFR3 signaling in the developing dorsal VZ results in premature depletion of
387 radial glial stem cells and a smaller cortex, whereas loss of *Fgfr1* alone is sufficient to result in
388 reduced hippocampal volume and reduced hippocampal stem cell proliferation during

389 embryogenesis and the early postnatal period (Ohkubo et al., 2004, Kang et al., 2009, Stevens et
390 al., 2010b, Rash et al., 2011). Our studies of *Fgfr1* expression in embryos and at P1 will be
391 described elsewhere. At P7, *Fgfr1* was expressed in BLBP positive cells. At this age, the BLBP+
392 radial glial cells are undergoing soma translocation and differentiating into astrocytes of the
393 cortical parenchyma. BLBP is also expressed in Bergmann glia of the cerebellum, which are
394 cells that have dual roles as stem cells and as a scaffold for granule cell neuron migration and
395 alignment of Purkinje neuron dendrites. At P7, BLBP positive cells expressed *Fgfr1* in stem cells
396 and Bergmann Glia of the cerebellum. These findings are consistent with the demonstrated
397 occurrence of cooperative signaling between FGFR1 and FGFR2 in the formation of the
398 cerebellum, and specifically, in the morphology and pial attachment of Bergmann glia of the
399 cerebellar anlage (Lin et al., 2009, Muller Smith et al., 2012).

400 At P7, and one-month, *Fgfr1* was expressed in the dentate gyrus and CA regions of the
401 hippocampus, as well as in the SVZ, hypothalamus, and all layers of the cortex. At P7, *Fgfr1* was
402 expressed in the granule cell layer of the dentate gyrus, whereas at 1 month, *Fgfr1* was expressed
403 primarily in the subgranular zone or in the granule zone adjacent to it. The *Fgfr1* expressing cells
404 in the granule cell layer of P7 mice sparsely colocalized with GFAP positive astrocytes and
405 NeuN positive neurons, and the majority colocalized with DCX positive neuroblasts, of which
406 there are many more at P7 than in the more mature brain of a 1-month old mouse. At one month,
407 the *Fgfr1* expressing cells in the subgranular zone colocalized with SOX2+ and GFAP+ stem
408 cells, as well as in the DCX positive neuroblasts. The expression of *Fgfr1* seems to be
409 downregulated from DCX+ cells as they mature into NeuN expressing neurons. The *Fgfr1*
410 expressing cells in the CA region at P7 and 1 month colocalize with GFAP positive astrocytes
411 and NeuN positive neurons in the stratum pyramidale.

412 GFAP positive astrocytes and BLBP stem cells in the SVZ at P7 are expressing *Fgfr1*,
413 indicating that stem cells of the SVZ express *Fgfr1*. GFAP positive astrocytes at 1 month also
414 express *Fgfr1*. At P7 and 1 month, *Fgfr1* expressing cells in the SVZ do not colocalize with
415 DCX positive neuroblasts and NeuN positive neurons. Thus, DCX positive cells express *Fgfr1* in
416 one of the postnatal neurogenic regions – dentate gyrus. The difference in *Fgfr1* expression
417 observed between DCX positive cells of the DG and SVZ implies that the staining in DCX
418 positive cells of the hippocampus is not due to residual GFP protein that has not been degraded
419 once a daughter cell born from a stem cell stops expressing *Fgfr1*. Therefore, we can further
420 accurately identify *Fgfr1* expression within cells using this transgenic model. *Fgfr1* expressing
421 cells were also colocalized with SOX2 positive cells at 1 month. In the SVZ, there may be
422 additional cell types not investigated in the current study, including glial progenitor cells such as
423 O4 or Nestin, which may colocalize with *Fgfr1* expression.

424 FGFR signaling participates in development of hippocampal synaptic transmission and
425 synaptogenesis (Cambon et al., 2004, Umemori et al., 2004, Terauchi et al., 2010). Activation of
426 FGFR1 promotes synapse formation in hippocampal neurons (Cambon et al., 2004, Terauchi et
427 al., 2010, Dabrowski et al., 2015). Changes in *Fgfr1* expression, and FGF2 levels in the
428 hippocampus are linked to major depression and anxiety, as well as to responses to
429 antidepressants (Evans et al., 2004, Newton and Duman, 2004, Gaughran et al., 2006, Turner et
430 al., 2008, Elsayed et al., 2012). It is hypothesized that *Fgf2* and *Fgfr1* are downregulated in
431 depression and anxiety, and this downregulation can be partially reversed by antidepressant
432 treatment (Turner et al., 2012b, a). The chronic unpredictable stress model causes anhedonia and
433 is a model of depression that results in decreased (mRNA) *Fgfr1* levels in the prefrontal cortex
434 (Elsayed et al., 2012). Antidepressant treatment resulted in increased (mRNA) *Fgf2* levels, and

435 the antidepressant effects could be blocked by an FGFR1 inhibitor. These authors further showed
436 that FGF2 administration also had an antidepressant effect (Elsayed et al., 2012).

437 Most GFAP positive astrocytes in the cortex coexpressed *Fgfr1*, and the majority of the
438 *Fgfr1* expressing cells were GFAP+ astrocytes. A minority of *Fgfr1* expressing cells were NeuN
439 positive neurons at P7 and one month. While it was previously believed that *Fgfr2* is expressed
440 in glia and that *Fgfr1* is mostly expressed by neuronal populations in the adult cortex, our
441 findings support the view that most of the cortical cells expressing *Fgfr1* in the adult brain are, in
442 fact, astrocytes or oligodendrocytes (Turner et al., 2012a). In this study we see that most GFAP
443 positive astrocytes express *Fgfr1* and a small proportion of NeuN positive neurons express *Fgfr1*
444 in one month old mice. A higher percentage of *Fgfr1* expressing cells are GFAP positive
445 astrocytes than NeuN positive neurons. Thus, astrocytes constitute a majority of *Fgfr1*
446 expressing cells in the adult brain. This idea is consistent with previous mRNA profiling of
447 astrocytes in which *Fgfr1* was identified as a gene with enriched expression in astrocytes as
448 compared to other cell types in the brain (Lovatt et al., 2007, Cahoy et al., 2008, Doyle et al.,
449 2008).

450 An imbalance of excitatory and inhibitory neurons, along with hyperactivity has been
451 documented in certain neurological disorders (Benes et al., 2000, Volk et al., 2000, Kalanithi et
452 al., 2005, Akbarian and Huang, 2006, Hashimoto et al., 2008, Kataoka et al., 2010, Gonzalez-
453 Burgos et al., 2011, Volk and Lewis, 2013). Inactivation of *Fgfr1* leads to a decrease in the
454 abundance of parvalbumin interneurons and is associated with an increase in hyperactivity
455 (Muller Smith et al., 2008). A subsequent study demonstrated that in these individuals, a
456 decrease in interneurons occurs postnatally and that *Fgfr1* expression does not occur in
457 parvalbumin expressing interneurons (Smith et al., 2014). Thus the decrease in *Fgfr1* expression

458 and decrease in parvalbumin interneurons occurs in a non-cell autonomous manner. Here, we
459 tested other interneuron markers, including GAD67, calretinin, and somatostatin. At one month,
460 GAD67, a marker for inhibitory neurons, colocalizes with *Fgfr1* expressing cells in the cortex
461 and not in the dentate gyrus. Calretinin interneurons express *Fgfr1* throughout the cortex, and in
462 the dentate gyrus, whereas somatostatin interneurons express *Fgfr1* at the anterior cingulate of
463 the cortex. Brandt et al., 2003 demonstrated newborn calretinin positive cells in the dentate gyrus
464 do not express GABA (Brandt et al., 2003), offering a probable explanation as to why GAD67 is
465 not observed colocalizing with *Fgfr1* expressing cells in the DG.

466 The hypothalamus, responsible for controlling hormonal production, stress regulation,
467 and feeding behaviors, has been found to contain a neural stem/progenitor cell niche (Robins et
468 al., 2013). Our results show that GFAP positive astrocytes are *Fgfr1* expressing cells. The
469 morphology and location of the *Fgfr1* expressing cells are consistent with the cells being
470 tanycytes of the hypothalamus (Robins et al., 2013). The medial eminence of the hypothalamus
471 contains *Fgfr1* expressing cells that also express SOX2. *Fgfr1* expressing cells that were not
472 identified are similar in morphology and location to the neurons that release gonadotropin-
473 releasing hormone (GNRH1). These results are in congruence with a study, which demonstrated
474 FGFR1's role in targeting of GNRH1 axons to the medial eminence (Gill and Tsai, 2006, Ojeda
475 et al., 2008). Therefore, understanding FGFR signaling can give further insight to the
476 hypothalamic regulation of homeostasis.

477

478 **Conclusion**

479 FGFR1 has been implicated as having multiple functions in CNS development,
480 homeostasis, and behavior, but defining the cellular basis of its functions depends on having a

481 clear understanding of which cell types the *Fgfr1* gene is expressed in, and when. The GENSAT
482 project was envisioned as a resource that would provide the tools for such detailed studies
483 (Heintz, 2004). Here, we have extended the previously published *in situ* based studies and online
484 resources with a detailed examination of the *tgFGFR1-EGFP338Gsat* line. Our data are
485 congruent with *in situ* studies, but with the added feature of double immunofluorescence with
486 glial and neuronal markers, and a quantification of the relative expression in glial versus
487 neuronal cells in the young adult brain. We here find *Fgfr1* promoter driven GFP expression in a
488 variety of stem cells of the CNS including the young adult SVZ, young adult SGZ, cerebellar
489 Bergmann Glia, and SOX2+ cells of the hypothalamus. An additional study of *Fgfr1* expression
490 in embryonic and perinatal stem cells will be described elsewhere. We also find that *Fgfr1* is
491 expressed predominantly in glia in the young adult brain, although significant expression in
492 DCX+ positive neuroblasts of the hippocampus was also observed. This was in stark contrast to
493 DCX+ neuroblasts of the RMS. Our findings may shed light on the participation of
494 FGF2/FGFR1 signaling in determining anxiety and mood, where a neuronal role for FGFR1 has
495 been hypothesized (Turner et al., 2012a). Future studies are needed to determine whether *Fgfr1*
496 expression colocalizes with other markers, such as S100 β , O4, and NG2 at embryonic and
497 postnatal time points. Since *Gfap* is not expressed in all astrocytes, S100 β (glial specific marker
498 primarily expressed in astrocytes, but also in some ependymal cells) would be a good marker to
499 further explore *Fgfr1* expression. The *tgFgfr1-EGFP+* model can also be used to study
500 additional stages in development, or *Fgfr1* expression after environmental manipulations
501 previously shown to alter *Fgfr1* expression, including animal models for induced depression
502 such as social defeat stress.
503

504 **Acknowledgements**

505 The authors wish to thank Darryl Williams, Deborah June Rogers, Lori Rubin and Marques
506 Jackson, for technical assistance, and Glen Watson and Caryl Chlan for manuscript review.

507

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Table 1. Antibodies used for Immunofluorescence Detection

Antigen	Raised In	Dilution	Source	Marker of
NueN	Mouse	1:125	Millipore	Neuron
GFAP	Rabbit	1:500	Dako Cytomation	Astrocyte
GFP	Chicken	1:250	Abcam Inc.	GFP
Sox2	Rabbit	1:250	Millipore	Neuronal precursor
Olig2	Mouse	1:1000	Millipore	Oligodendrocyte
DCX	Mouse	1:250	Abcam Inc	Neuroblast
GAD67	Mouse	1:1000	Millipore	Inhibitory neuron
Calretinin	Rabbit	1:1000	Millipore	Inhibitory neuron
Somatostatin	Rat	1:200	Millipore	Inhibitory neuron
BLBP	Rabbit	1:1000	Abcam Inc.	Stem cells
Tbr2	Rabbit	1:500	Abcam Inc.	Excitatory neuron

Table 2. Parameters used for Stereological Cell Counts

Time Point	Area	Counting Frame (µm)	Grid Size (µm)	Dissector Height (µm)	Guard Zone Height (µm)	Section Thickness (µm)
P7	Cortex	75 x 75	650 x 700	15	1	50
	DG	75 x 75	250 x 250	15	1	50
	CA	75 x 75	500 x 500	15	1	50
1 month	Cortex	75 x 75	1000 x 1000	15	1	50
	DG	75 x 75	275 x 200	15	1	50
	CA	75 x 75	350 x 250	15	1	50

Table 3. Stereology Results for Hippocampal DG, CA, and Cortex

Age	Area	Marker	# of Marker + cells	P-value	# of GFP+ cells	% of GFP+ cells expressing Marker	% of Marker+ cells expressing GFP
P7	DG	GFAP	5614 ± 467	0.37	15974 ± 7447	24% ± 8%	50% ± 8%
	CA	GFAP	51258 ± 1741	0.42	46413 ± 14851	50% ± 5%	43% ± 9%
	Cortex	GFAP	412147 ± 22494	0.25	1220518 ± 53849	32% ± 4%	93% ± 2%
1 Month	DG	NeuN	755542 ± 228698	0.52	243542 ± 12945	16% ± 6%	5% ± 0.7%
		GFAP	149161 ± 22540	0.53	243542 ± 12945	51% ± 3%	85% ± 4%
	CA	NeuN	670709 ± 59607	0.27	379768 ± 27634	25% ± 7%	15% ± 6%
		GFAP	286614 ± 39645	0.86	379768 ± 27634	61% ± 9%	81% ± 3%
	Cortex	GFAP	1777872 ± 876236	0.66	2321696 ± 1056829	57% ± 7%	83% ± 6%
		NeuN	4962422 ± 2264757	0.97	2321696 ± 1056829	25% ± 4%	12% ± 2%
Olig2		800755 ± 137359	0.85	1574962 ± 195563	29% ± 0.9%	58% ± 0.08%	

Table 4. Qualitative comparison of *Fgfr1* expression

Time Point	Area	<i>Fgfr1</i> Expression in Cell Types					
		BLBP	GFAP	SOX2	DCX	NeuN	Olig2
P7	DG	++	++	NA	+++	+	
	CA		++	NA		++	
	SVZ	+++	+	NA			++
	Cortex	+++	++	NA		+	++
	Hypothalamus		++	NA			
	1 month	DG		++	++	++	
	CA		+			+	
	SVZ		++	++			
	Cortex		++			+	+
	Hypothalamus		++	++			

NA = not analyzed

Figure 1. *Fgfr1* expression in GFAP+ cells of the hippocampus at P7. GFAP (A,D) GFP (B,E) immunostaining of the DG in P7 *tgfgfr1*-EGFP+ mice (A-C, n=3) and *tgfgfr1*-EGFP-littermate controls (D-F, n=3) demonstrated strong GFAP/GFP colocalization in cells of the SGZ (arrowheads) and their radial fibers into the GCL (small arrows). GFAP and GFP immunostaining of the CA region in *tgfgfr1*-EGFP+ mice (G-I, n=3) and *tgfgfr1*-EGFP-controls (J-L, n=3). GFP+ staining was observed in stratum pyramidale (SP) as well as in cells above (stratum oriens, SO) and below (stratum radiatum, SR) this layer (H). GFAP+/GFP+ colabeling (arrowheads) was observed in primarily in the SO and SR within the CA region, and in the white matter dorsal to the hippocampus. Scale bar is 25 μ m. SGZ = subgranular zone, GCL = granule cell layer, SP=stratum pyramidale.

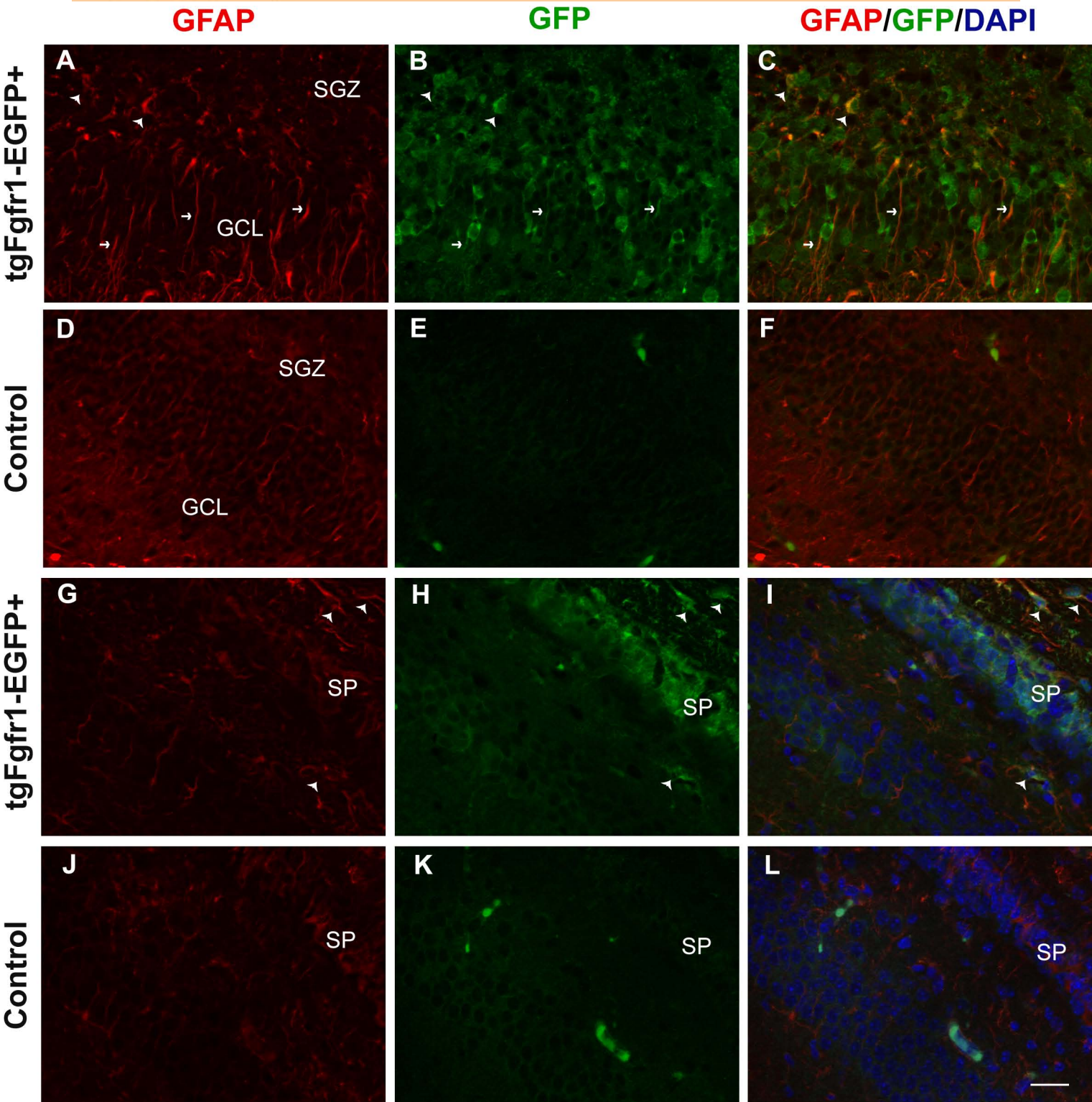


Figure 2. *Fgfr1* expression in NeuN+ cells of the hippocampus at P7. NeuN (A,D) and GFP (B,E) immunostaining of the CA region in *tgfgfr1*-EGFP+ mice (A-C, n=3) and *tgfgfr1*-EGFP- controls (D-F, n=3). NeuN+/GFP+ staining was observed in stratum pyramidale (SP) of the CA region. NeuN (G, J) and GFP (H, K) immunostaining of the DG in *tgfgfr1*-EGFP+ mice (G-I, n=3) and *tgfgfr1*-EGFP- controls (J-L, n=3). There was some colabeling in the granule cell layer between GFP+ and NeuN+ cells. Scale bar is 25 μ m in A-D and 50 μ m in G-L. SP=stratum pyramidale.

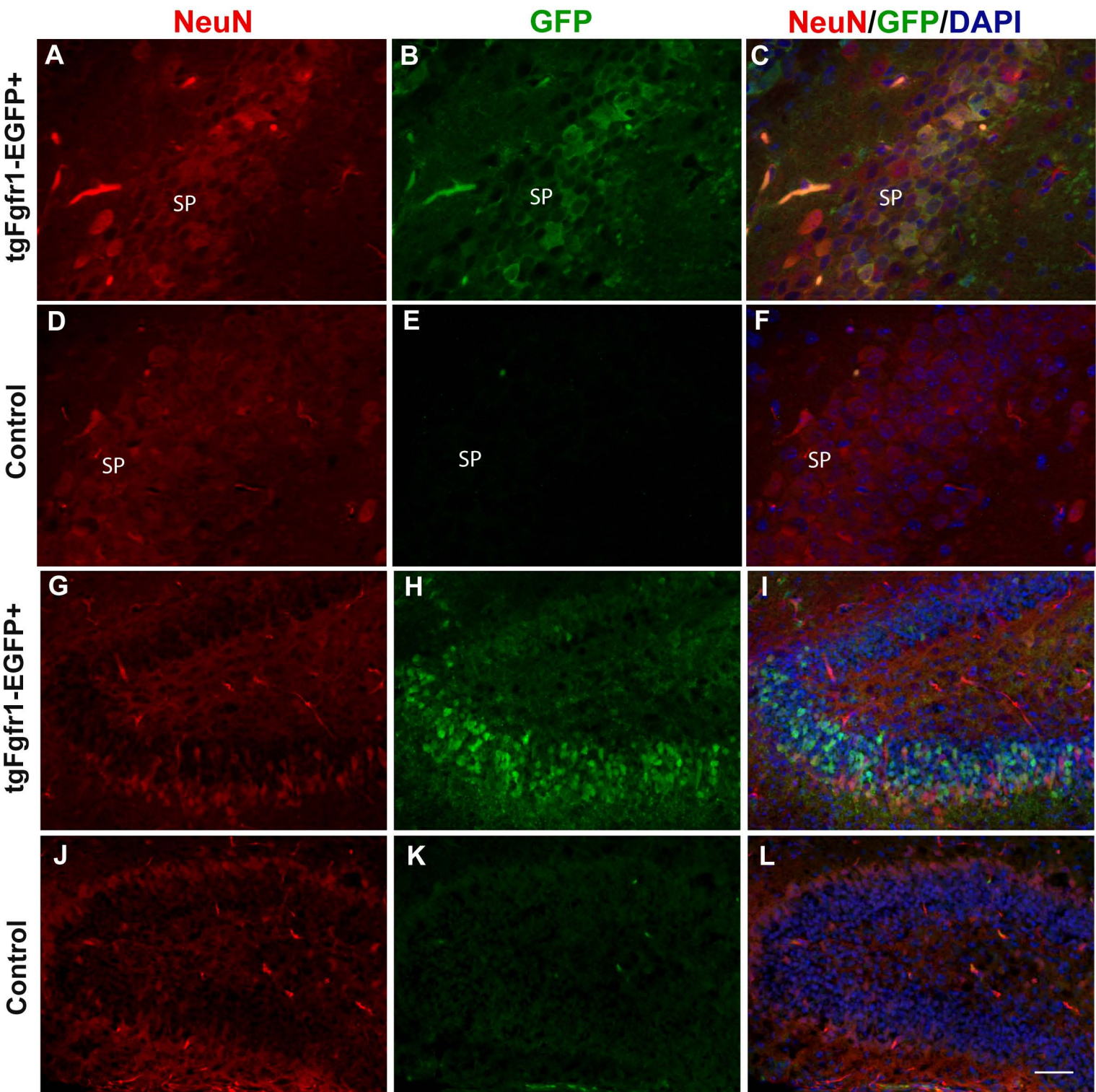


Figure 3. *Fgfr1* expression in neuroblasts of the hippocampus, and stem cells of the hippocampus and SVZ at P7. DCX and GFP colocalize in neuroblasts of the P7 mice in the granule cell layer of the DG in the hippocampus (**A**, low magnification, and **B**, high magnification), but not in the SVZ of the lateral ventricles (**C**). Many of the BLBP+ cells colocalize with GFP in the stem cells of the SGZ of the DG (**D**, low magnification, and **E**, high magnification), as well as stem cell in the SVZ (**F**). Scale bar is 50 μ m in **A,C,D,F** and 25 μ m in **B** and **E**.

Figure 3

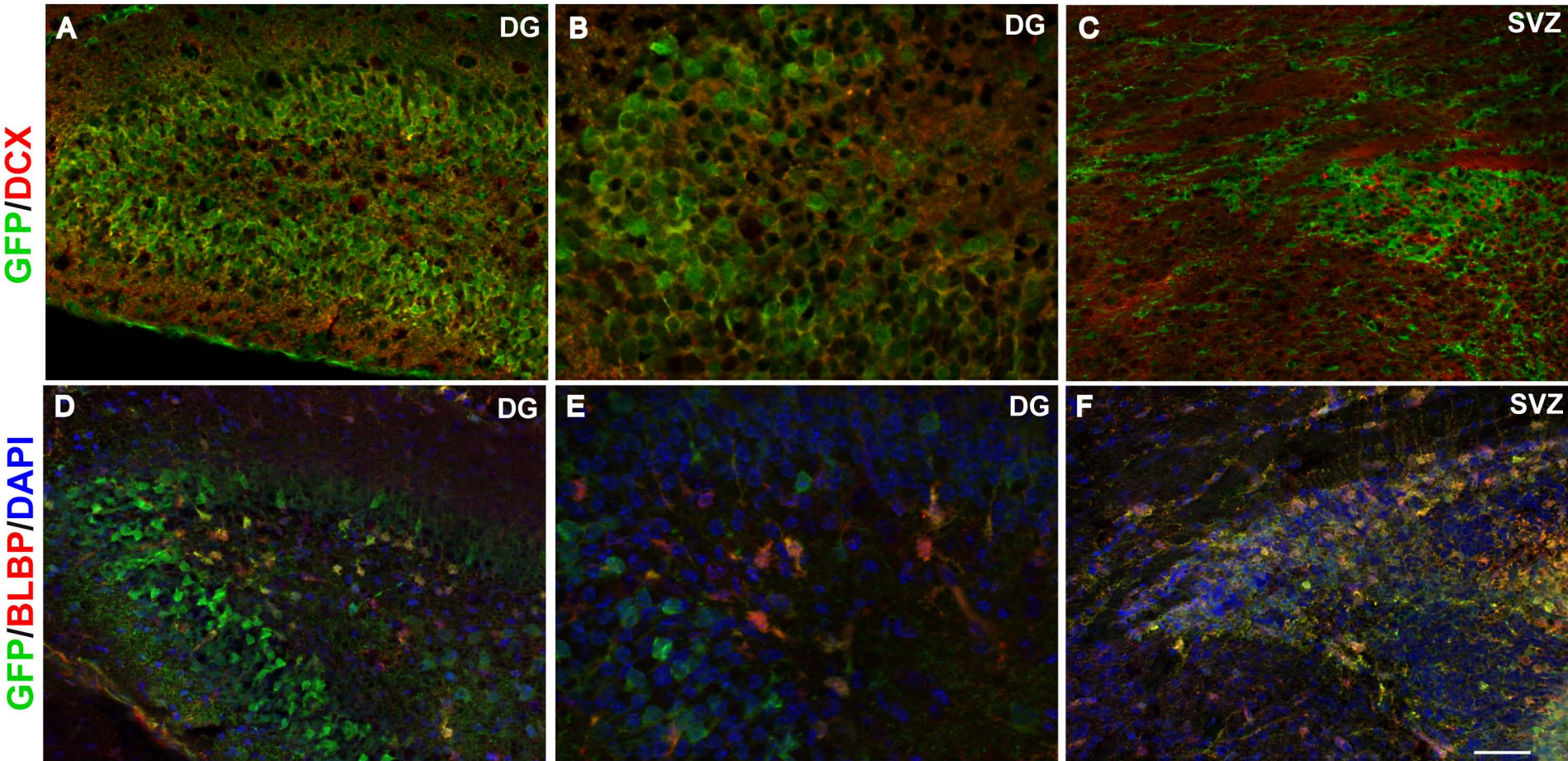
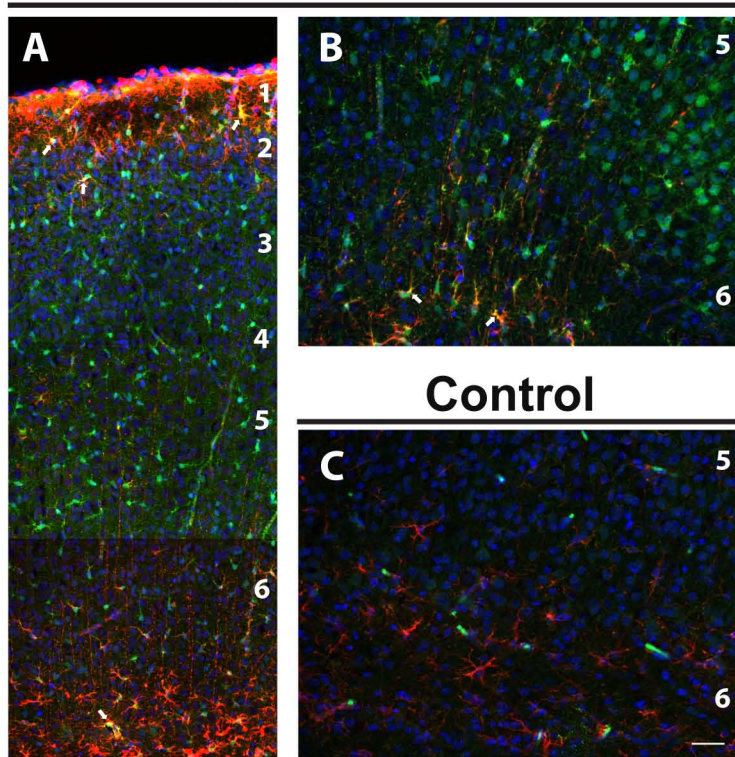


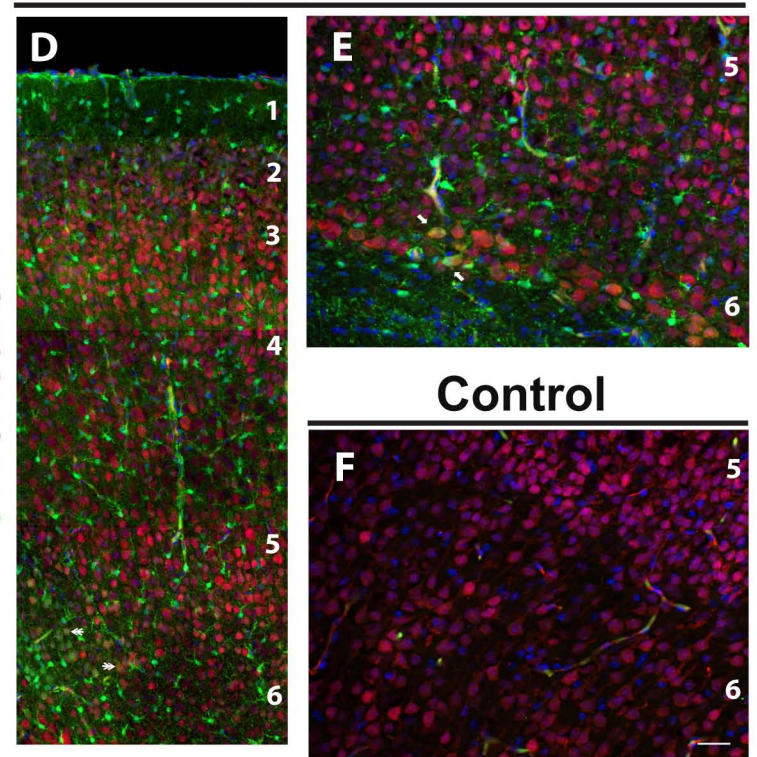
Figure 4. *Fgfr1* expression in cortex of P7 mice. Cortical GFAP, NeuN, BLBP and GFP immunostaining in P7 *tgfgfr1-EGFP+* mice (**A, B, D, E, G-J**, n=3) and *tgfgfr1-EGFP-* controls (**C, F**, n=3). GFP+ cells colocalize with GFAP+ cells (**A, B**). GFP+ cells weakly colocalize with NeuN+ at layers 5 and 6 of the cortex (**D, E**). GFP+ cells colocalize with Olig2+ cells in the cortex (**G-I**) and the subcortical white matter and SVZ (**J**). GFP+ cells colocalize with BLBP+ cells throughout the layers of the cortex (**K-M**) as well as the BLBP+ cells and Bergmann glia of the cerebellum (**N**). Scale bar is 50 μ m. 1, 2, 3, 4, 5, 6 = layers of the cortex.

Peer Preprints
tgFgfr1-EGFP+NOT REE-REVIEWED
tgFgfr1-EGFP+

GFP/GFAP/DAPI

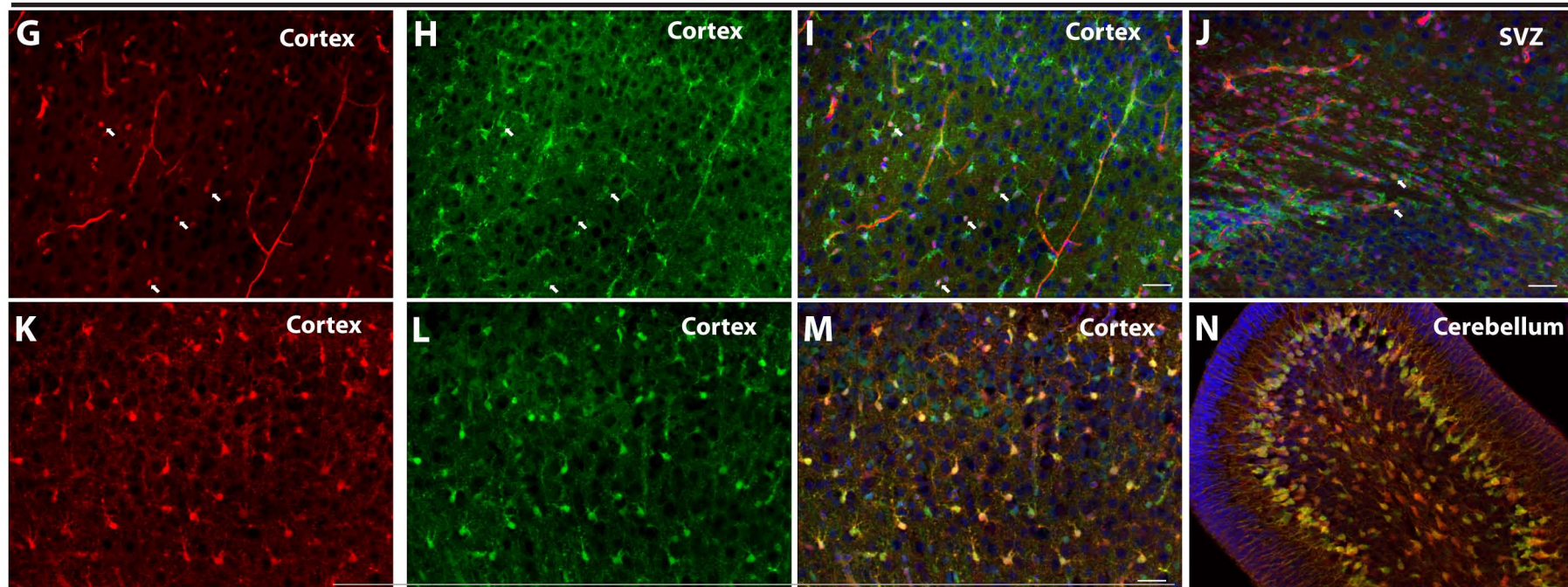


GFP/NeuN/DAPI



tgFgfr1-EGFP+

GFP/OLIG2/DAPI



GFP/BLBP/DAPI

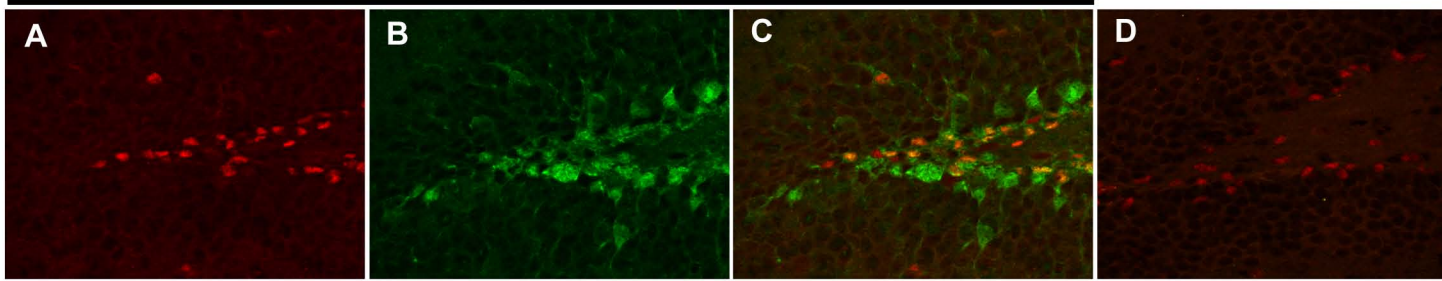
Figure 5. *Fgfr1* expression in the dentate gyrus and CA of 1-month mice. A majority of SOX2⁺ cells (**A, C**) in the DG of *tgfgfr1-EGFP*⁺ mice colocalize with GFP (**B, C**) compared to GFP⁻ controls (**D**). Counts of SOX2⁺ and GFP⁺ cells were made directly from Z stack images (19µm thick, 1 µm steps, from Z stack images using StereoInvestigator software from MBF). The relative proportions of single, and double-labeled cells in the DG were quantified (**E**), with 71% of SOX2 positive cells expressing GFP. A majority of DCX⁺ (**F, H**) cells in the DG also express GFP (**G, H**) compared to GFP⁻ controls (**I**). Counts for DCX⁺ and GFP⁺ were performed on 10µm thick, 1µm step size, Z stack images using Image J (n=3) of the dentate gyrus. The relative proportions of single, and double-labeled cells in the DG were quantified (**J**) with 85% of DCX⁺ cells expressing GFP. GFAP (Red), NeuN (Blue), and GFP triple immunolabeling was performed on 1-month old mice. We observed GFAP and GFP colabeling in both the SGZ of the DG (**K-N**), as well as in the CA region (**O-R**) where most GFAP⁺ cells are present in the stratum oriens or stratum radiatum. NeuN⁺/GFP⁺ double positive cells were primarily observed in the stratum pyramidale (SP) of the CA region in the hippocampus. These cells were quantified by unbiased stereology with the StereoInvestigator (Table 3). Scale bar in **I** is 25 µm for images **A-D** and **F-I**, Scale bar in **R** is 50 µm for images **K-R**.

Figure 5

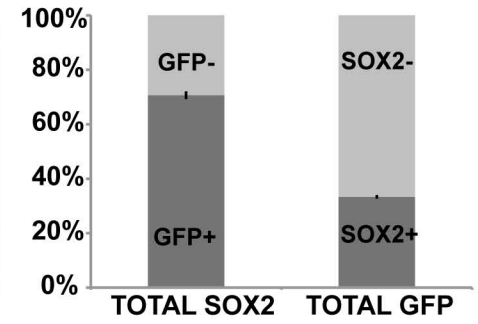
tgFgfr1-EGFP+

Control

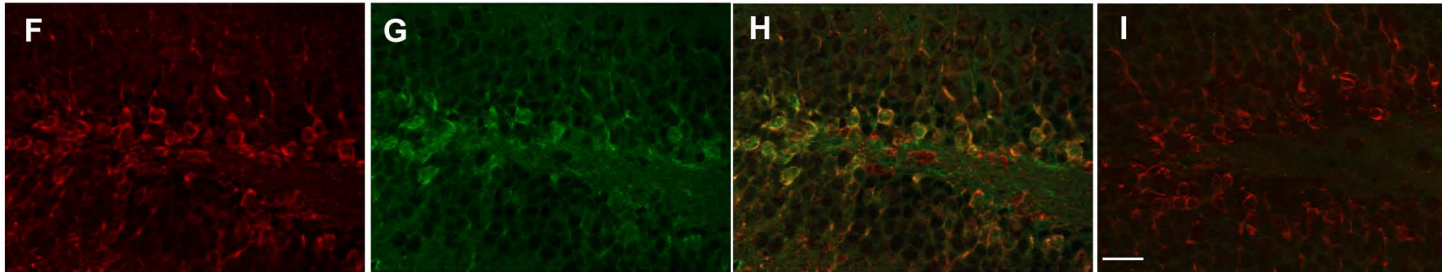
SOX2/GFP



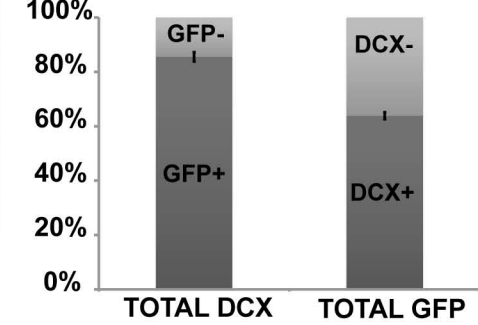
E SOX2 and GFP Co-localization



DCX/GFP



J DCX and GFP Co-localization



GFAP/GFP/NeuN

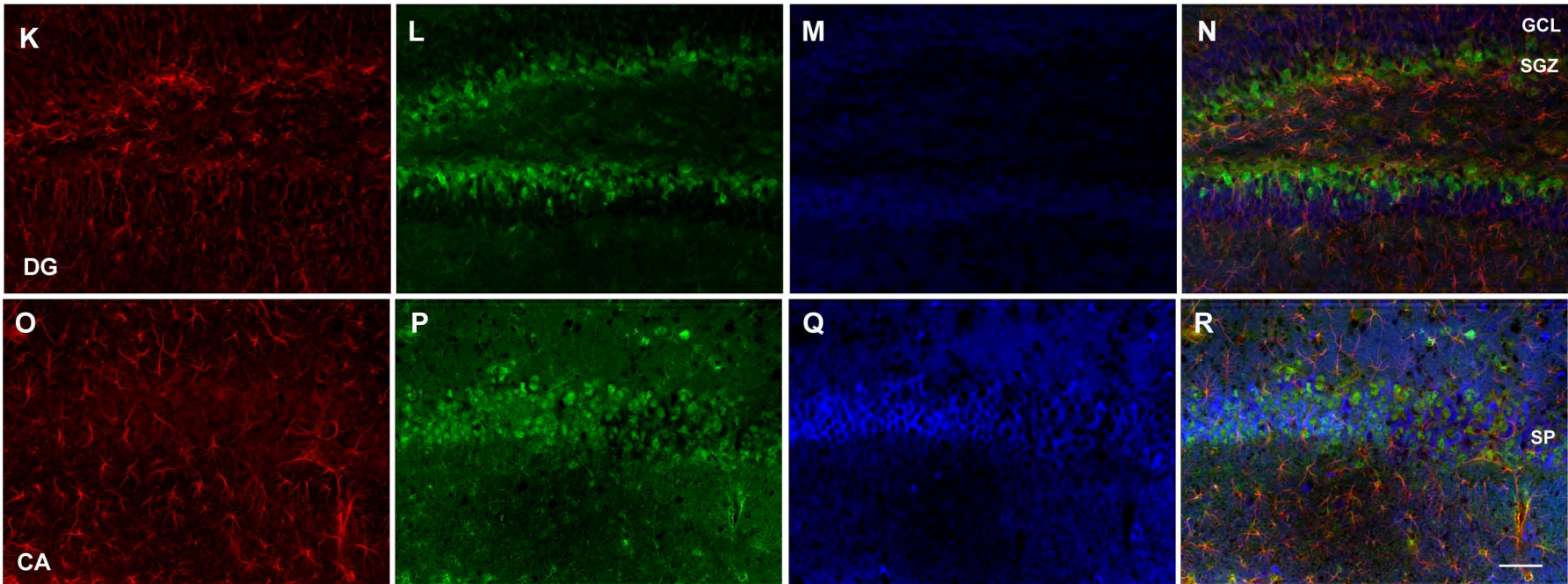


Figure 6. *Fgfr1* expression in the SVZ and rostral migratory stream of 1-month mice. GFP (A,E), GFAP (B,F), NeuN (C), immunostaining of the SVZ in 1-month *tgfgfr1-EGFP*⁺ mice (A-H, n=3). GFP⁺ cells of the SVZ colocalized with GFAP⁺ cells (D, high magnification in G and H. Arrowheads in E-H=GFAP/GFP⁺ cells) and GFAP⁺ fibers. GFP (I) and SOX2 (J) staining demonstrated that many, but not all SOX2⁺ cells also colabel with GFP⁺ (K and L, DAPI staining included in L). In contrast, DCX⁺ neuroblasts in the SVZ and rostral migratory stream did not colabel with GFP (L-O). Scale bar is 50µm in A-D and M-P and 25µm in E-L.

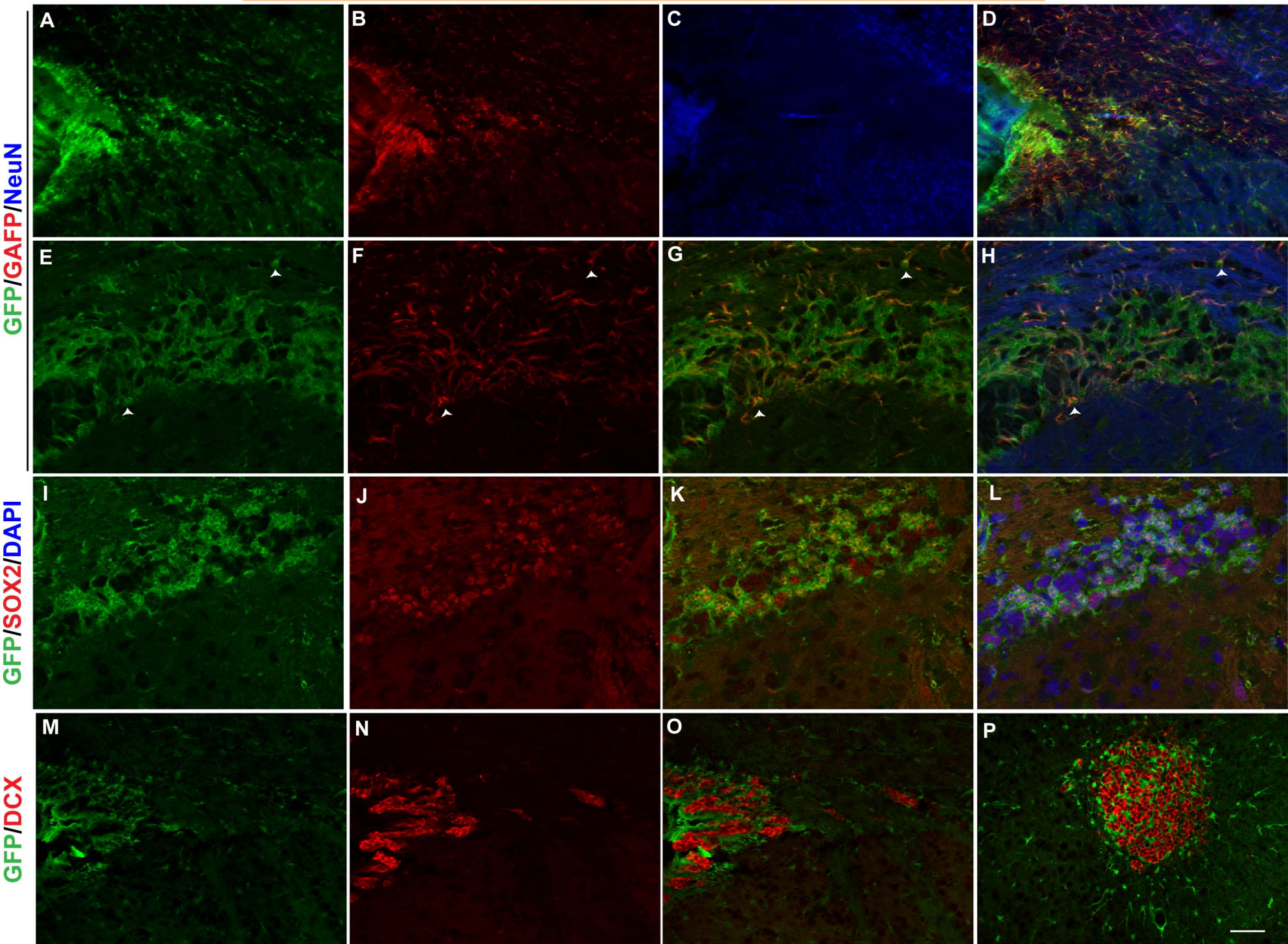


Figure 7. *Fgfr1* expression in the cortex of 1-month mice. Cortical GFAP (Red), NeuN (Blue), and GFP immunostaining in 1-month *tgfgfr1-EGFP+* mice (**A-E**, n=3) and *tgfgfr1-EGF-* mice (**F**, n=3). GFP+ cells colocalized with GFAP+ (arrows) (**A**, **B**, merged in **D**, low magnification in **E**), and some NeuN+ (double arrows) (**B**, **C**, merged in **D**, **lower** magnification in **E**). Immunostaining for Olig2+ in *tgfgfr1-EGFP+* mice (**G**, **H**) compared to *tgfgfr1-EGF-* mice (**I**) demonstrated that many Olig2+ cells colocalized with GFP. Scale bars are 50 μ m.

Figure 7

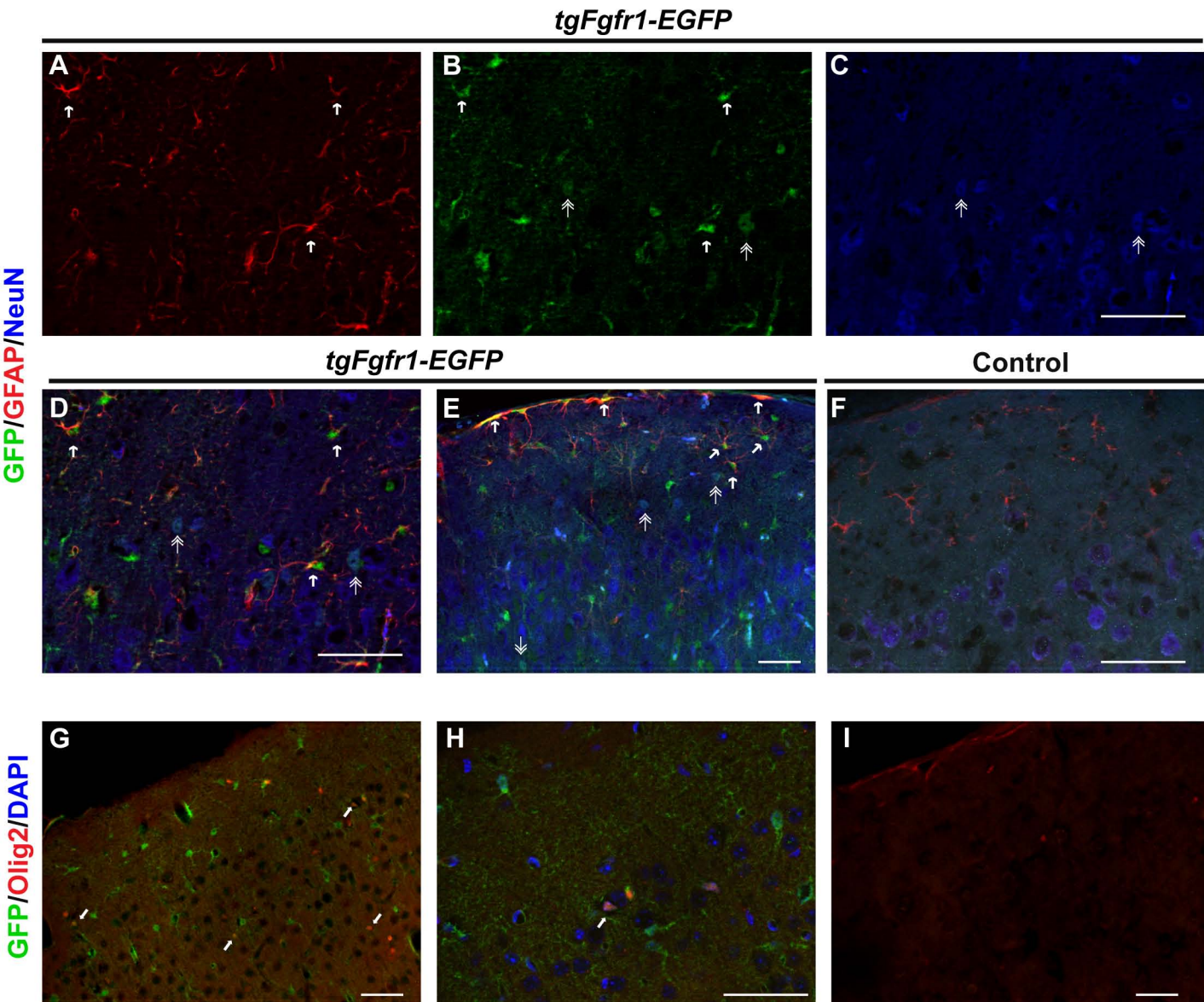
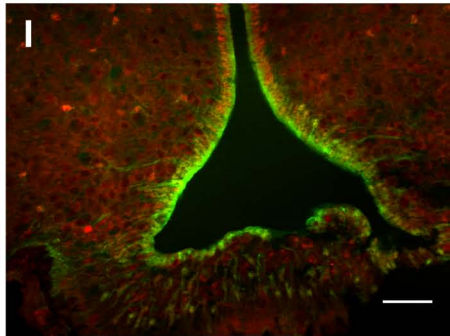
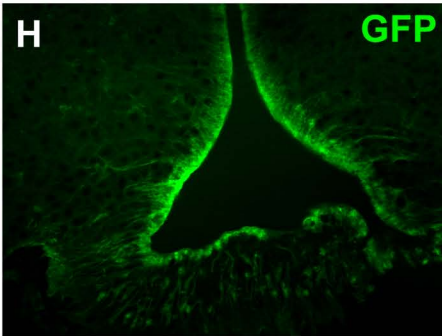
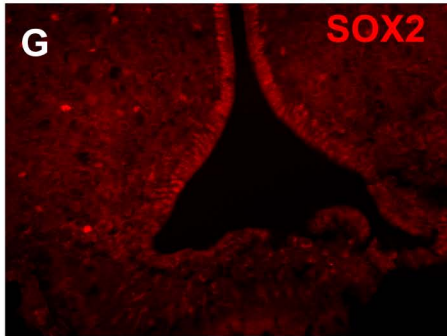
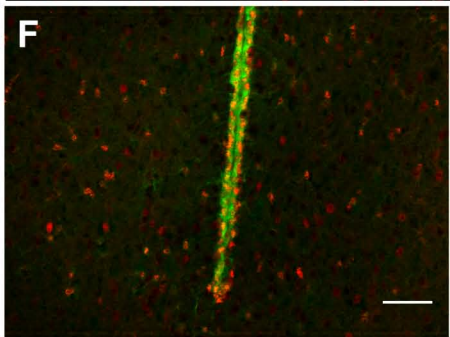
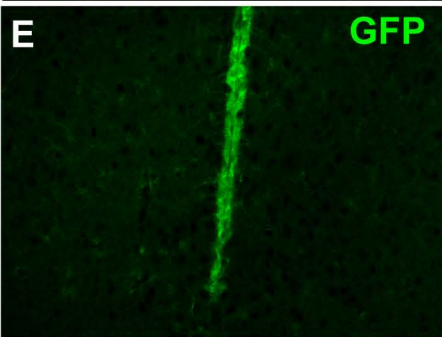
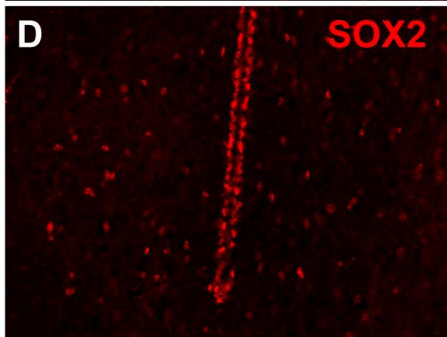
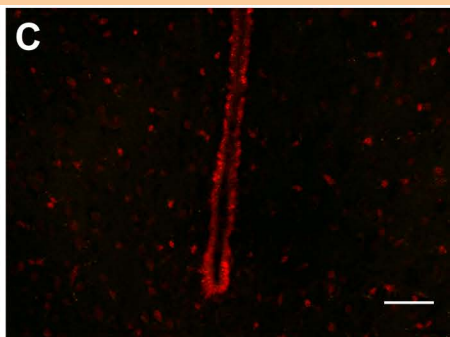
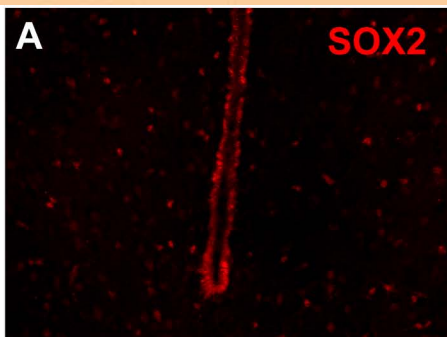


Figure 8. *Fgfr1* expression in the hypothalamus. Sox2+ positive cells were observed along the third ventricle of *tgfgfr1-EGF*- control mice (**A-C**) and *tgfgfr1-EGF*+ mice (**D-I**). These SOX2+ cells also express GFP under the *Fgfr1* promoter (**D-I**). GFAP+ tanocytes along the third ventricle and arcuate nucleus also colocalize with GFP, as do GFAP+ cells within the hypothalamus (**J-L**). NeuN+ cells in the hypothalamus do not colocalize with GFP (**M-O**). **A-L**, 1 month; **M-O**, P7. Scale bar is 50µm.

Control



tgFgfr1-EGFP+

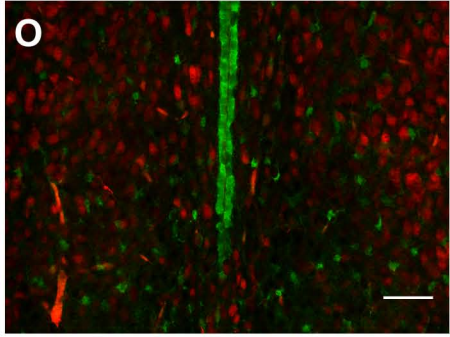
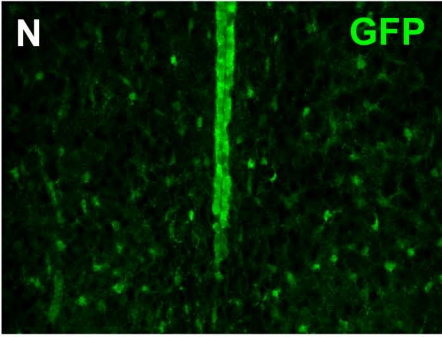
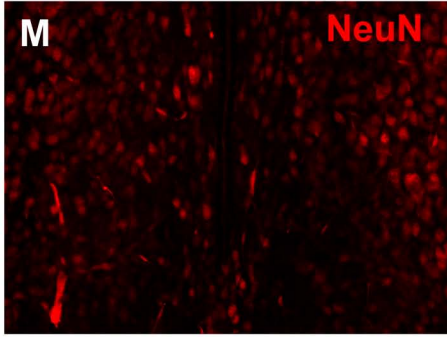
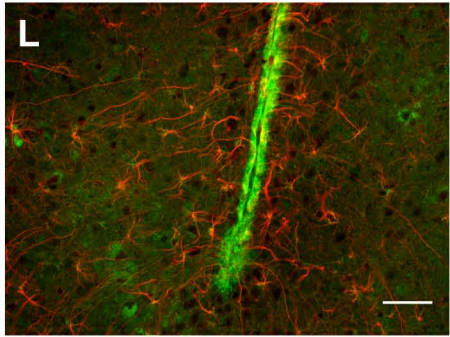
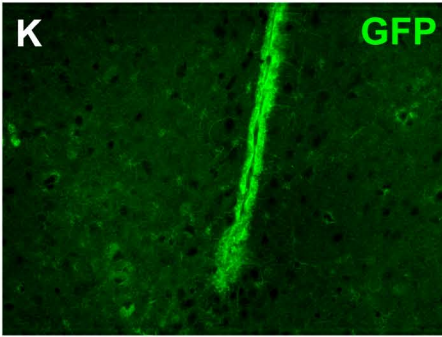
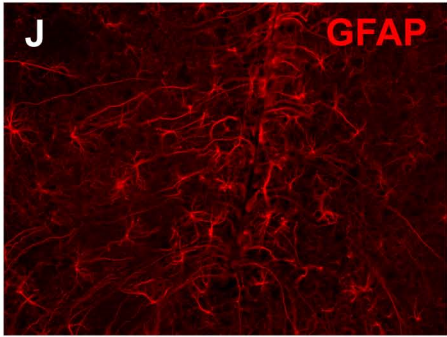


Figure 9. *Fgfr1* expression in the 1-month interneurons. GAD67, CR, SST, and GFP

immunostaining of the cortex, DG, and SVZ in one-month old *tgfgfr1-EGFP-* controls (**A, E, I**, n=2 SST, n=3 GAD67, CR) and *tgfgfr1-EGFP+* mice (**B-D, F-H, J, K**, n=2 SST, n=3 GAD67, CR). GFP+ cells colocalized with GAD67+ cells in the cortex (**B**), but not in the DG (**C**) and SVZ (**D**). Some CR+ cells express GFP in the cortex (**F**), DG (**G**) and SVZ (**H**). Some SST+ cells express GFP in the anterior cingulate of the cortex (**J**), but not in the DG (**K**). Scale bars are 50 μ m. AC = anterior cingulate.

Figure 9

