

1 **A molecularly defined neural circuit for cold defense revealed**
2 **by targeted single-nucleus transcriptomic mapping**

3

4 **Supplementary materials**

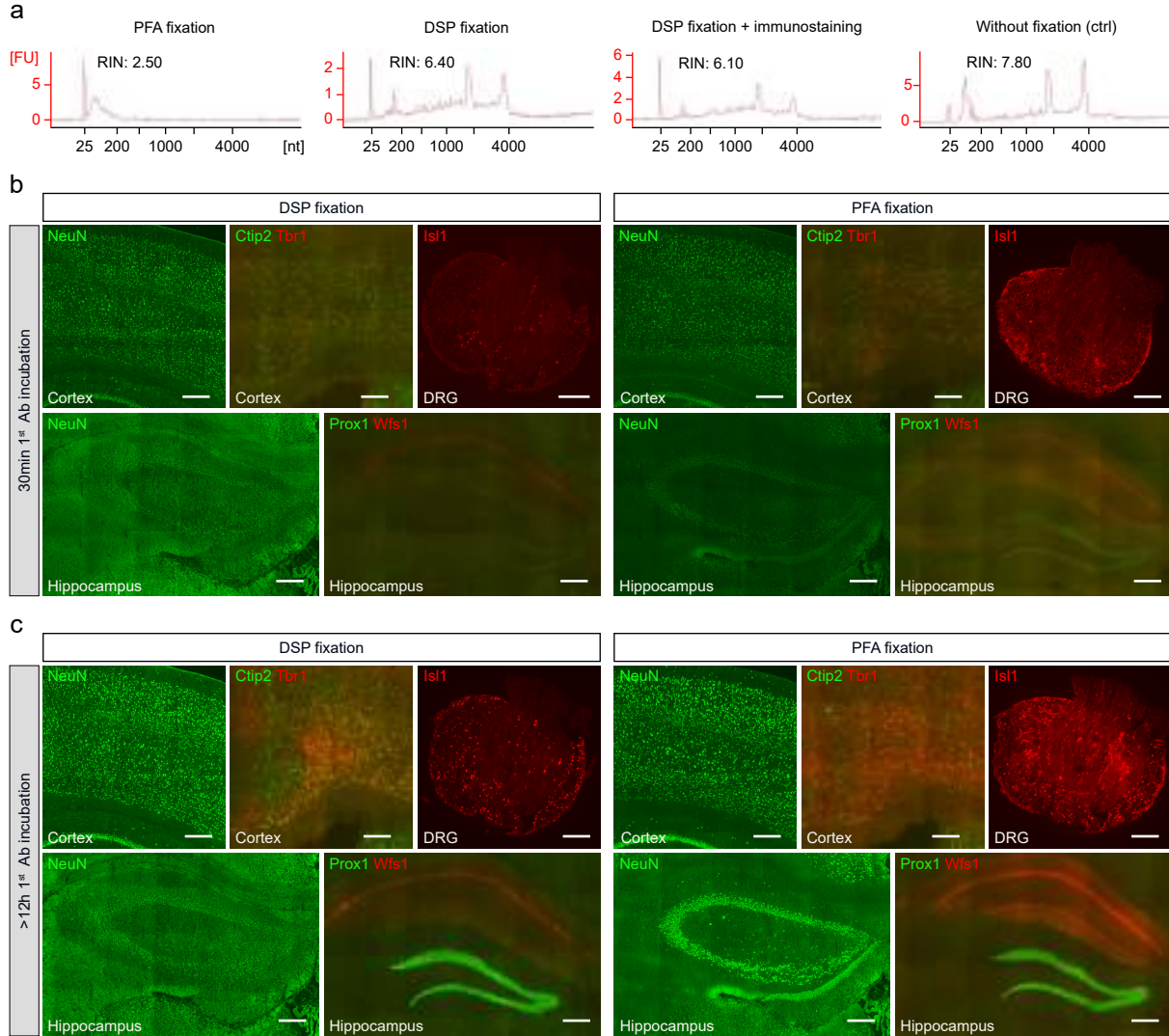
5

6 Contents:

7 (1) Extended Data Figure 1-18 and figure legends

8 (2) Supplementary Table 1-4 and table legends

9 **Extended Data Fig. 1**

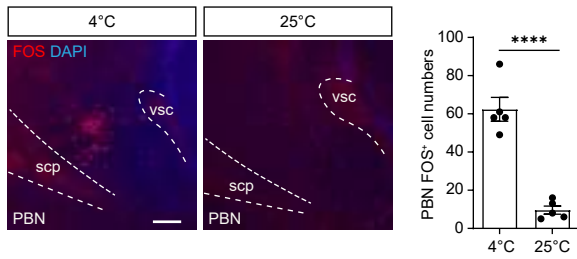


10

11 **Extended Data Fig. 1 Assessment of the modified immunostaining method.**

12 **a**, RNA integrity (RIN) assessment of total RNA samples extracted from consecutive sections of
 13 the same mouse brain fixed with PFA or DSP for comparison. DSP-fixed samples were incubated
 14 with DTT; one of the two DSP-fixed samples was stained with the FOS antibody using the
 15 optimized protocol before RNA extraction. A sample of fresh-frozen sections was taken as a
 16 positive control in RNA integrity analysis. A higher RIN value indicates better RNA integrity. **b-c**,
 17 Detection of various neuronal markers (NeuN, Ctip2, Tbr1, Isl1, Prox1, and Wfs1) expressing in
 18 the peripheral and central nervous systems on the sections fixed by DSP (left panels in **b,c**) or PFA
 19 (right panels in **b,c**), with short (30 min; **b**) or long (>12 h; **c**) primary antibody incubations. Scale
 20 bars in **b,c**: 100 μ m.

21 **Extended Data Fig. 2**



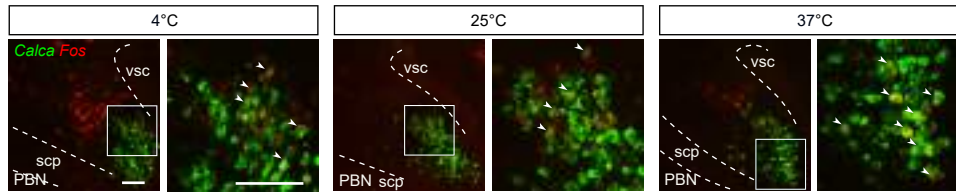
22

23 **Extended Data Fig. 2 Cold-activated neurons in the PBN recognized by FOS immunostaining.**

24 FOS immunostaining in the PBN of wild-type mice exposed to 4°C vs. 25°C. FOS⁺ cell numbers
25 were compared between 4°C and 25°C (n=5 mice per group). Statistical analysis used two-tailed
26 unpaired Student's *t*-test. Scale bar: 200 μm.

29 **Extended Data Fig. 3 Generation of a new PBN cell atlas using high-throughput snRNA-seq.**
30 **a**, tSNE plot of cell populations in the PBN of wild-type mice. **b**, Bubble plot of marker genes
31 defining major PBN cell types. **c**, tSNE plot of *Slc17a6*⁺ neuronal clusters of the PBN and its
32 adjacent areas. **d**, Heatmap of cluster-specific marker genes of *Slc17a6*⁺ neurons (see
33 Supplementary Table 1 for the marker gene list). **e**, Bubble plot of canonical markers for the PBN
34 neurons studied previously.

35 **Extended Data Fig. 4**



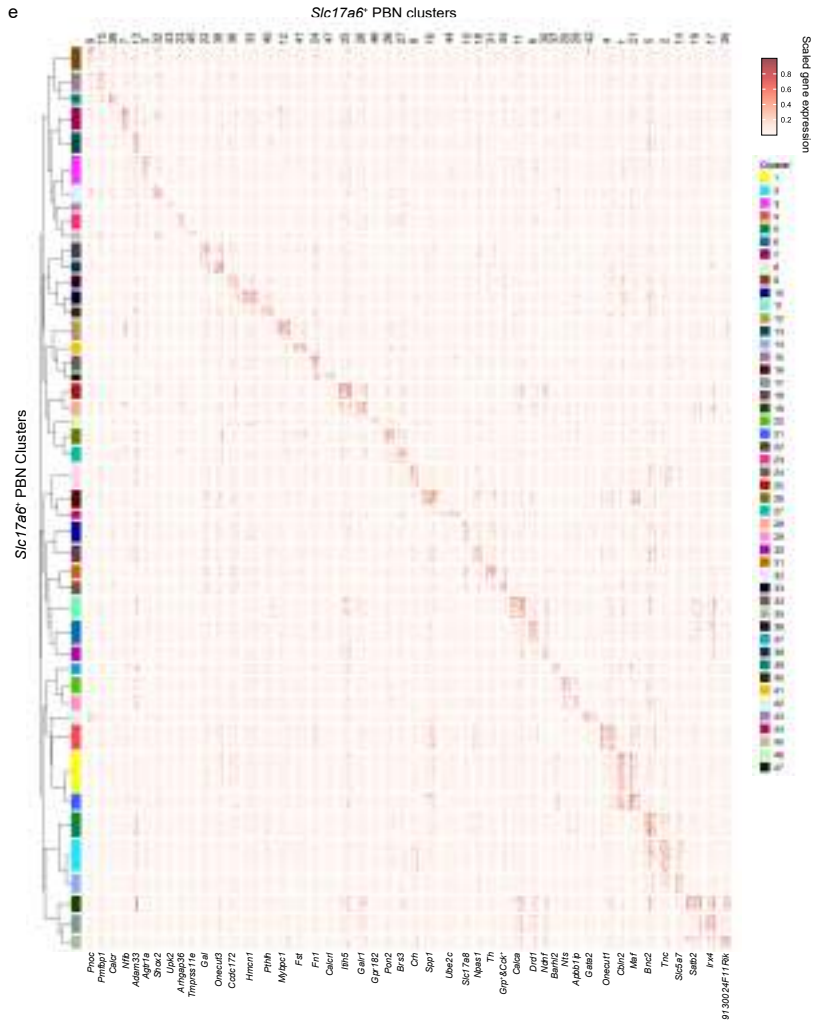
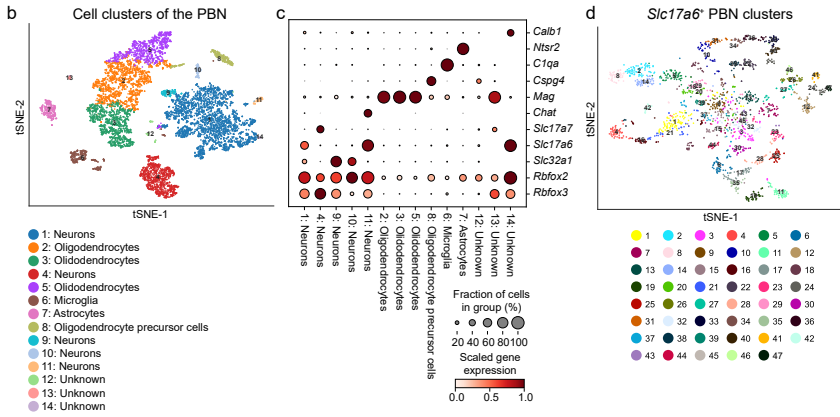
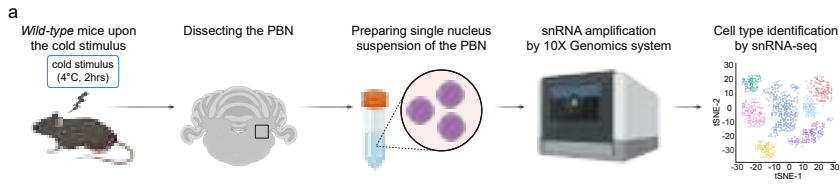
36

37 **Extended Data Fig. 4 Co-expression of *Fos* and *Calca* in the PBN of the mice at different ambient**
38 **temperatures.**

39 smFISH showing *Fos* and *Calca* co-expression in the eLPBN of mice exposed to 4°C, 25°C, and 37°C.

40 Arrowheads indicate the neurons co-expressing *Calca* and *Fos*. Scale bar: 100 μm.

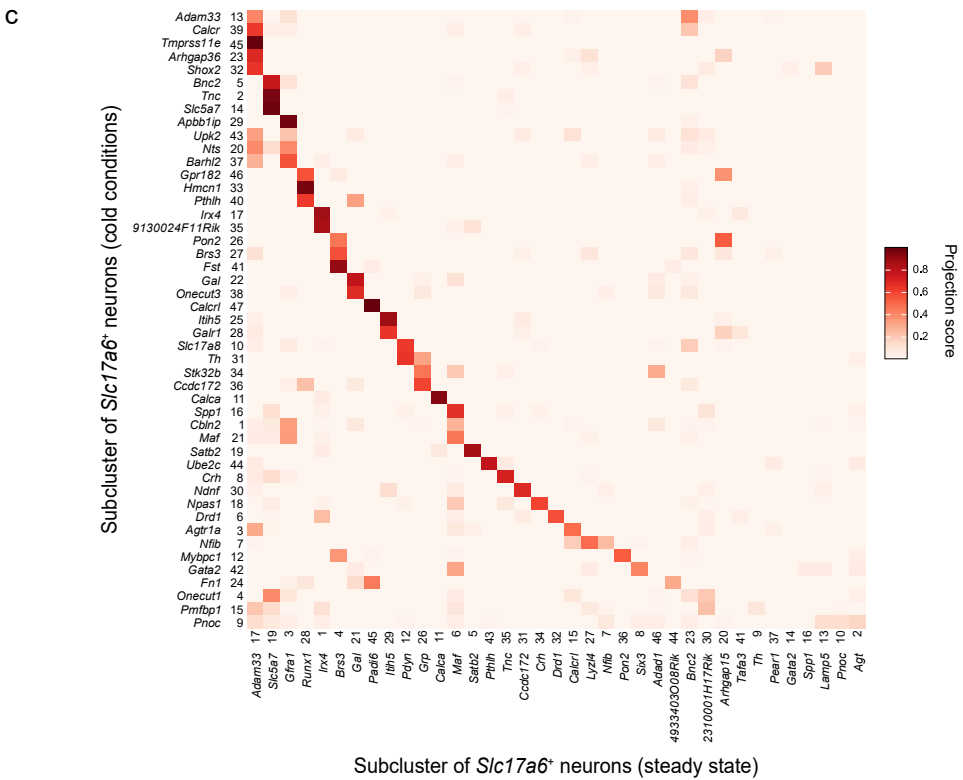
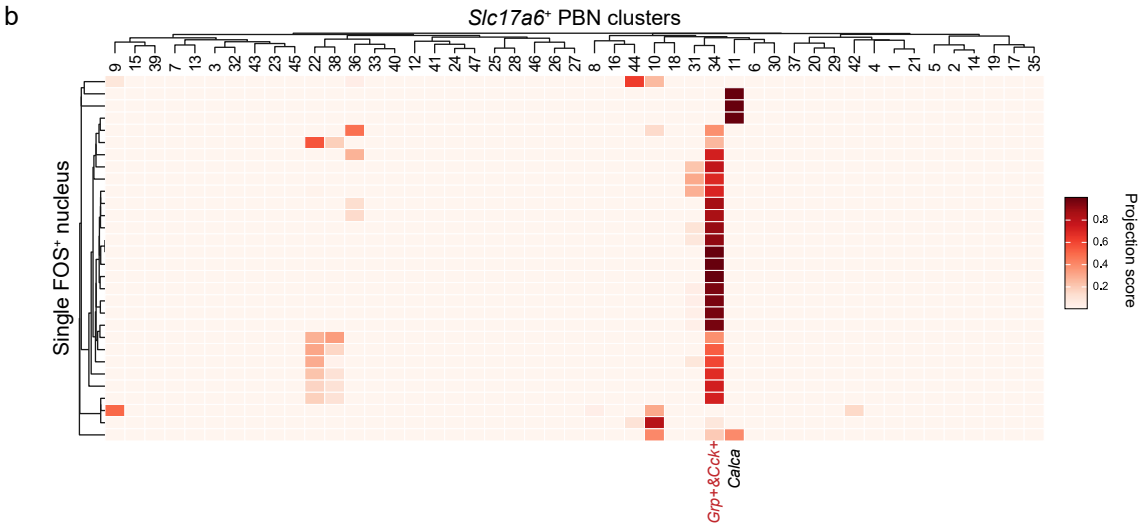
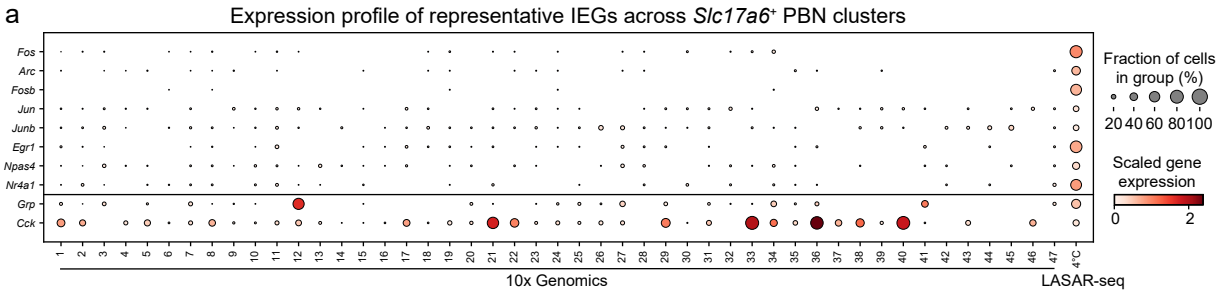
41 Extended Data Fig. 5



43 **Extended Data Fig. 5 A new PBN cell atlas of cold-treated mice obtained by high-throughput**
44 **single-nucleus RNA-seq.**

45 **a**, Schematic workflow of the single-nucleus RNA-seq experiment to establish a new PBN cell atlas
46 from cold-treated wild-type mice using 10x Genomics platform. **b**, tSNE plot of nuclei isolated
47 from the PBN and adjacent areas in cold-treated mice. **c**, Bubble plot of marker gene expression
48 defining major PBNs cell types. **d**, tSNE plot of *Slc17a6*⁺ neuronal clusters in the PBN and adjacent
49 areas. **e**, Heatmap of marker genes for each subtype of *Slc17a6*⁺ neurons (see Supplementary
50 Table 2 for marker gene list).

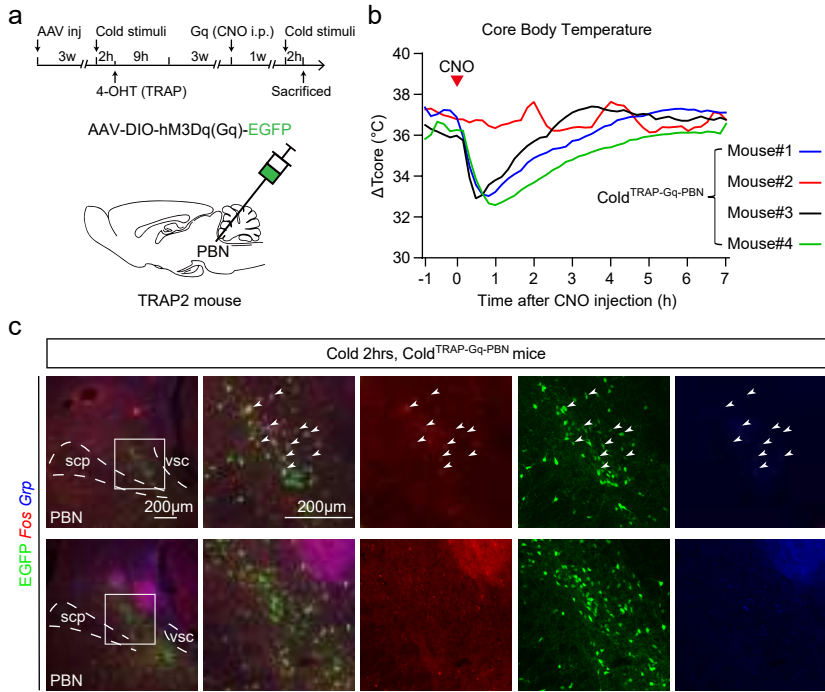
51 Extended Data Fig. 6



53 **Extended Data Fig. 6 Comparison of cold-activation parabrachial neurons analyzed by high-**
54 **throughput snRNA-seq or LASAR-seq.**

55 **a**, Bubble plots showing the expression of immediate-early genes across *Slc17a6*⁺ PBN clusters
56 from cold-treated mice, compared to the cold-induced FOS⁺ neurons identified by LASAR-seq
57 (last column on the right). **b**, Heatmap of mapping the cold-activated neurons analyzed by LASAR-
58 seq to the new PBN atlas from cold-treated mice as reference. **c**, Heatmap showing the
59 transcriptomic similarity between PBN cell atlases from the mice at steady state and stimulated
60 by 4°C cold.

61 **Extended Data Fig. 7**



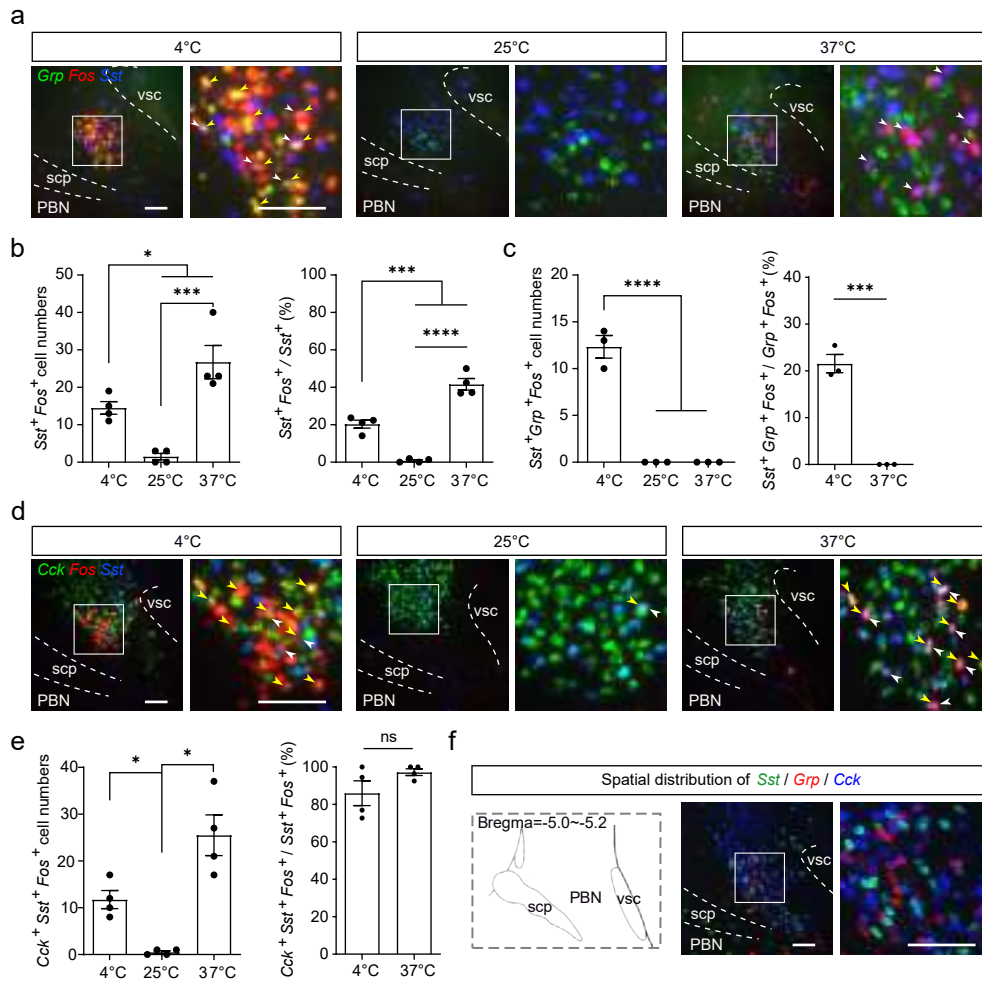
62

63 **Extended Data Fig. 7 Analyzing cold-activated PBN neurons using the FosTRAP2 method.**

64 **a**, Schematic illustration of the TRAP2 experiment to label and re-activate cold-activated neurons
 65 using AAV vectors encoding DIO-hM3Dq(Gq)-EGFP. For cross-validation with the endogenous
 66 FOS expression induced by a cold stimulus, the mice were exposed to 4°C for 2h before sacrifice.

67 **b**, Chemogenetic re-activation of the TRAP2-labeled neurons and T_{core} telemetry recording. **c**,
 68 Fluorescent images of combinatorial immunostaining of EGFP (“cold-trapped” cell marker) and
 69 smFISH of *Fos* and *Grp* for analyzing their colocalization. Enlarged images of the rectangular areas
 70 were shown next to the first column. White arrowheads point to the cells co-expressing EGFP,
 71 *Fos*, and *Grp*. Scale bar: 200 μ m.

72 **Extended Data Fig. 8**

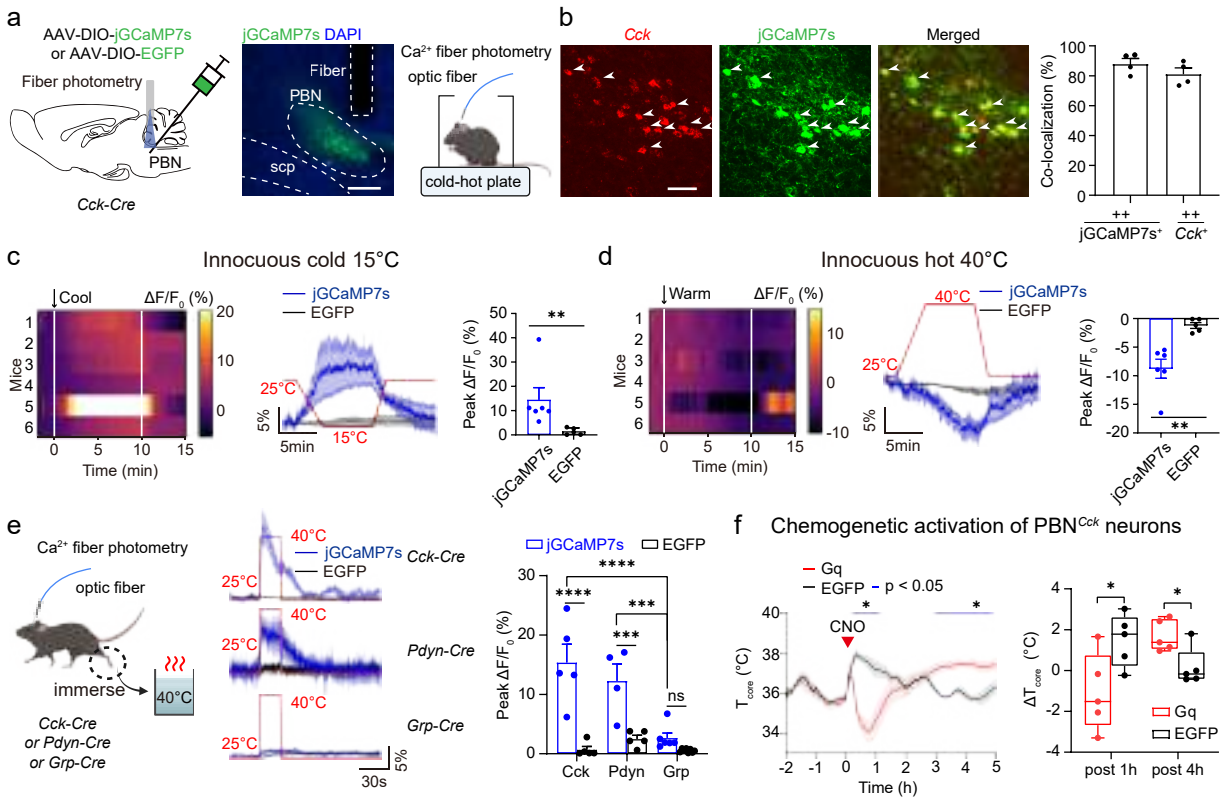


73

74 **Extended Data Fig. 8 *Sst*⁺ PBN neurons respond to both cold and warm stimuli.**

75 **a**, smFISH images showed *Fos*, *Sst*, and *Grp* expression in the PBN of mice exposed to 4°C, 25°C,
 76 or 37°C. White arrowheads point to the neurons co-expressing *Sst* and *Fos*, and the yellow ones
 77 point to the neurons co-expressing *Grp* and *Fos*. **b**, Numbers of *Sst* and *Fos* co-expressing neurons
 78 at 4°C, 25°C, or 37°C; percentages of *Fos*⁺ activated neurons among *Sst*⁺ cells ($Fos^+ Sst^+ / Fos^+$) at
 79 4°C, 25°C, or 37°C (n=4 mice per group). **c**, Numbers of *Sst*, *Grp*, and *Fos* triple co-expressing
 80 neurons at 4°C, 25°C, or 37°C; percentages of *Sst*⁺ neurons among the activated *Grp*⁺ cells (Sst^+
 81 $Grp^+ Fos^+ / Grp^+ Fos^+$) at 4°C or 37°C (n=3 mice per group). **d**, smFISH images showed *Fos*, *Sst*, and
 82 *Cck* in the PBN of mice exposed to 4°C, 25°C, or 37°C. White arrowheads point to the neurons co-
 83 expressing *Sst* and *Fos*, and the yellow ones point to the neurons co-expressing *Cck* and *Fos*. **e**,
 84 Numbers of *Cck*, *Sst*, and *Fos* triple co-expressing neurons at 4°C, 25°C, or 37°C; percentages of
 85 *Cck*⁺ neurons among the activated *Sst*⁺ cells ($Cck^+ Sst^+ Fos^+ / Sst^+ Fos^+$) at 4°C or 37°C (n=4 mice
 86 per group). **f**, Spatial distribution of *Sst*⁺, *Grp*⁺, or *Cck*⁺ neurons in the PBN examined by smFISH.
 87 Statistical analyses used one-way ANOVA followed by Bonferroni's test in **b**, **c**, and **e**. Scale bars
 88 in **a**, **d**, and **f**: 50 μm.

89 **Extended Data Fig. 9**

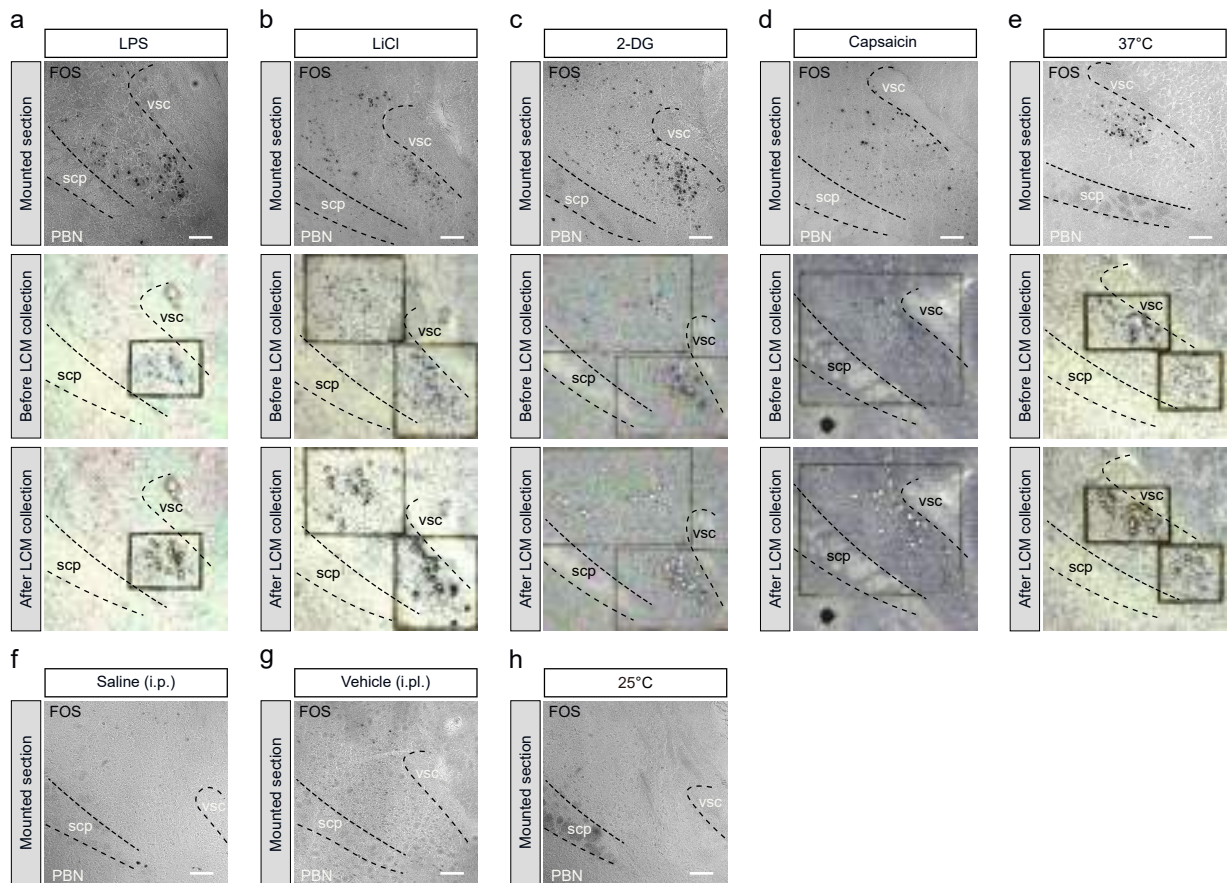


90

91 **Extended Data Fig. 9 *Cck*⁺ PBN neurons respond to both cold and warm stimuli.**

92 **a**, Scheme of Ca²⁺ fiber photometry experiment in *Cck-Cre* mice stimulated by different
 93 temperatures using a cold-hot plate. jGCaMP7s or EGFP was introduced in *Cck*^{PBN} neurons via
 94 AAV injection. **b**, Representative images and quantitative analysis showing jGCaMP7s expression
 95 in *Cck*^{PBN} neurons. Arrowheads point to the neurons co-expressing jGCaMP7s and *Cck*. The bar
 96 plot shows co-expression ratios among jGCaMP7s⁺ or *Cck*⁺ neurons (n=4 mice). **c-d**, Heatmap of
 97 Ca²⁺ signals, averaged Ca²⁺ traces, and bar plot of peak ΔF/F₀ for *Cck*^{PBN} neurons during 15°C (**c**)
 98 or 40°C (**d**) innocuous stimuli (jGCaMP7s: n=6 mice; EGFP: n=5 mice). The stimulating duration is
 99 indicated between two vertical white lines in the heatmaps. **e**, Scheme and results of Ca²⁺ fiber
 100 photometry experiment upon another paradigm of warm stimuli induced by immersing one hind
 101 limb of *Cck-Cre*, *Pdyn-Cre*, or *Grp-Cre* mice expressing jGCaMP7s or EGFP (control) into 40°C water
 102 for 20 s. Averaged Ca²⁺ traces and peak ΔF/F₀ for jGCaMP7s-expressing *Cck*⁺, *Pdyn*⁺, or *Grp*⁺ PBN
 103 neurons and EGFP controls were compared upon 40°C warm stimulus (n=5, 4, 6 for jGCaMP7s
 104 group; n=5, 5, 8 for EGFP group in *Cck-Cre*, *Pdyn-Cre*, and *Grp-Cre* mice). **f**, T_{core} traces of *Cck-Cre*
 105 mice expressing Gq or EGFP in the PBN upon chemogenetic activation by CNO injection at t=0 hr.
 106 ΔT_{core} at t=1 hr and t=4 hr were quantified and shown in the box plot (n=5 mice per group).
 107 Statistical significance was analyzed using two-tailed Mann-Whitney test in **c-e**, and two-tailed
 108 unpaired Student's *t*-test in **f**. Scale bars in **a**: 200 μm; in **b**: 50 μm.

109 **Extended Data Fig. 10**

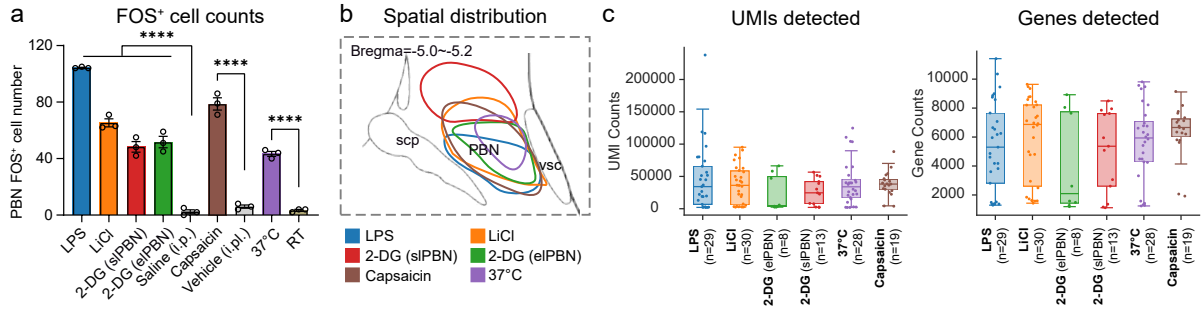


110

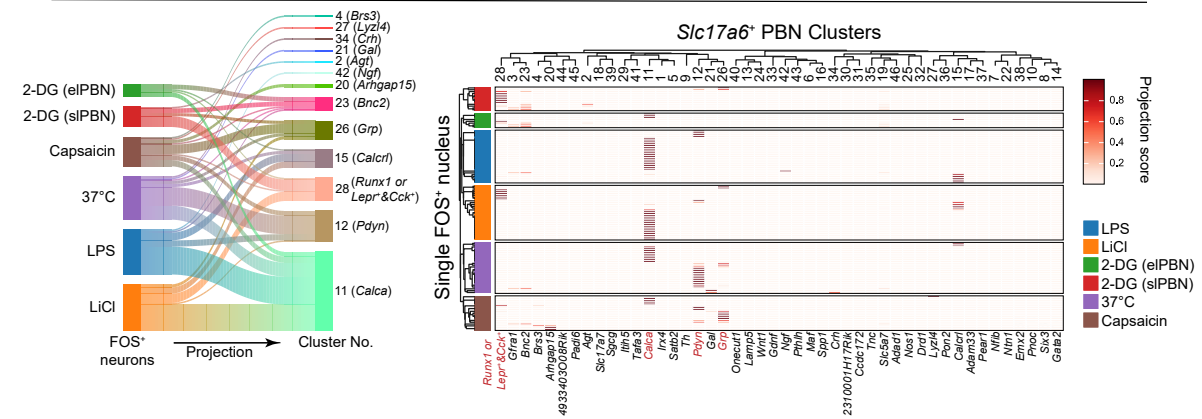
111 **Extended Data Fig. 10 FOS immunostaining and laser microdissection of individual activated**
 112 **neurons in the PBN upon different stimuli.**

113 **a-h** DAB chromogenic FOS immunostaining of PBN in wild-type mice after different stimuli: LPS
 114 i.p. (a), LiCl i.p. (b), 2-DG i.p. (c), capsaicin i.pl. (d), 37°C warm exposure (e) or controls: saline i.p.
 115 injection (f), 20% ethanol vehicle i.pl. injection (g), 25°C exposure (h). Images show brain sections
 116 on standard slides (1st and 4th rows), and on PEN membrane slides before (2nd row) and after (3rd
 117 row) microdissection of the FOS⁺ nuclei. Scale bars: 100 μm.

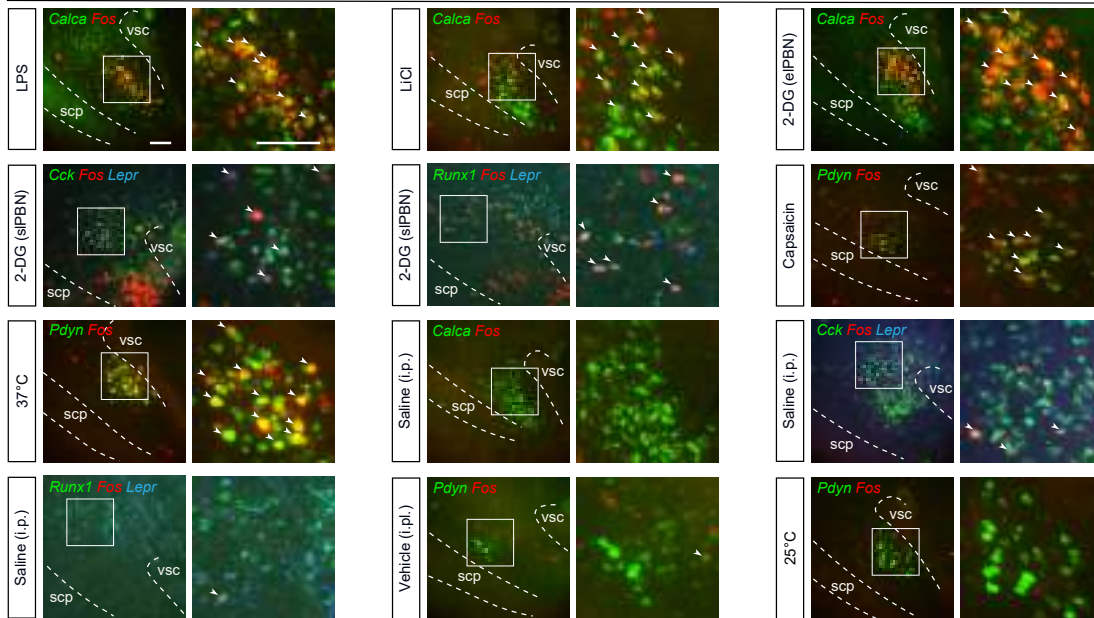
118 **Extended Data Fig. 11**



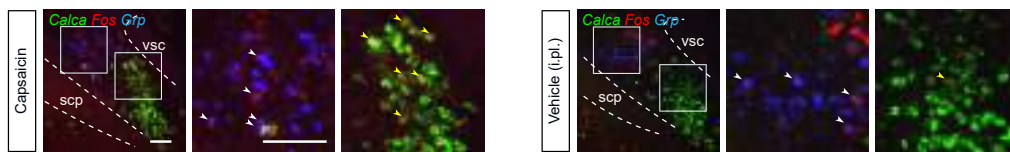
d Mapping the molecular identity of FOS⁺ neurons



e Validation by smFISH in the PBN



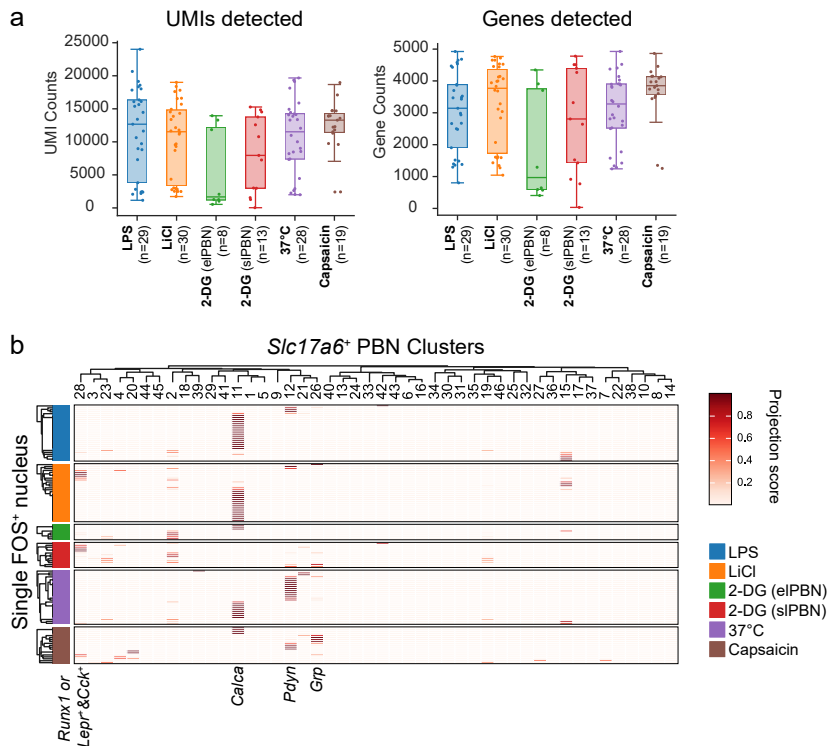
f



120 **Extended Data Fig. 11 Methodological assessment for LASAR-seq.**

121 **a**, FOS⁺ cell numbers in the PBN across different stimuli (RT: 25°C; n=3 mice per stimulus). **b**,
122 Diagrammatic spatial distribution of sparse FOS⁺ neurons in the PBN in response to different
123 stimuli (Bregma: -5.0 to -5.2), with scp (superior cerebellar peduncle) and vsc (ventral
124 spinocerebellar tract) as the anatomical landmarks. **c**, UMI and gene counts of individual FOS⁺
125 neurons; cell numbers passing the quality check are shown in the brackets. **d**, Label transfer
126 analysis of LASAR-seq identifying activated neuronal types with specific molecular markers
127 (Sankey plot, left; heatmap, right); representative marker genes are shown in the brackets of the
128 Sankey plot or at the bottom of the heatmap. The projection scores reflect the correlation
129 between the mapped clusters and the query cells. Marker genes of the activated populations are
130 marked in red in the heatmap. **e-f**, smFISH validation of *Fos* and marker gene co-expression in
131 the PBN after stimuli vs. controls; arrowheads point to the neurons showing co-expression of *Fos*
132 and the corresponding markers. Statistical analysis was performed using one-way ANOVA
133 followed by Bonferroni's test in **b**. Scale bars in **e** and **f**: 100 μm.

134 **Extended Data Fig. 12**

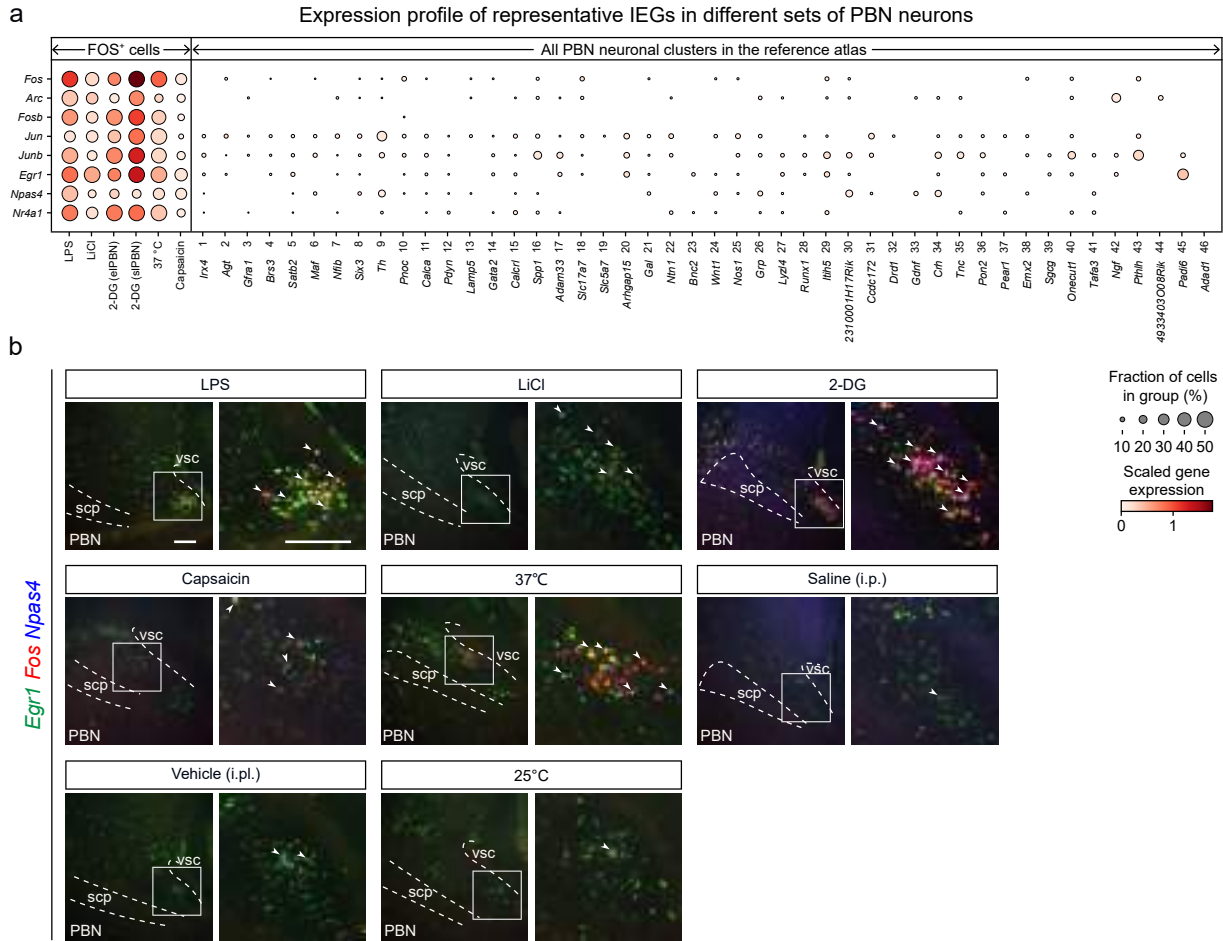


135

136 **Extended Data Fig. 12 Downsampling the LASAR-seq data recapitulates the cell-type mapping**
 137 **results.**

138 **a**, UMI and gene counts of the microdissected FOS⁺ neurons in the PBN upon different stimuli
 139 after downsampling the LASAR-seq data to match the high-throughput snRNA-seq depth of
 140 parabrachial neurons using 10x Genomics platform; cell numbers passing the quality check are
 141 shown in the brackets. **b**, Heatmap showed cell-type identification of sparsely activated neurons
 142 based on the downsampled LASAR-seq data with representative marker genes of the selective
 143 clusters labeled at the bottom.

144 **Extended Data Fig. 13**

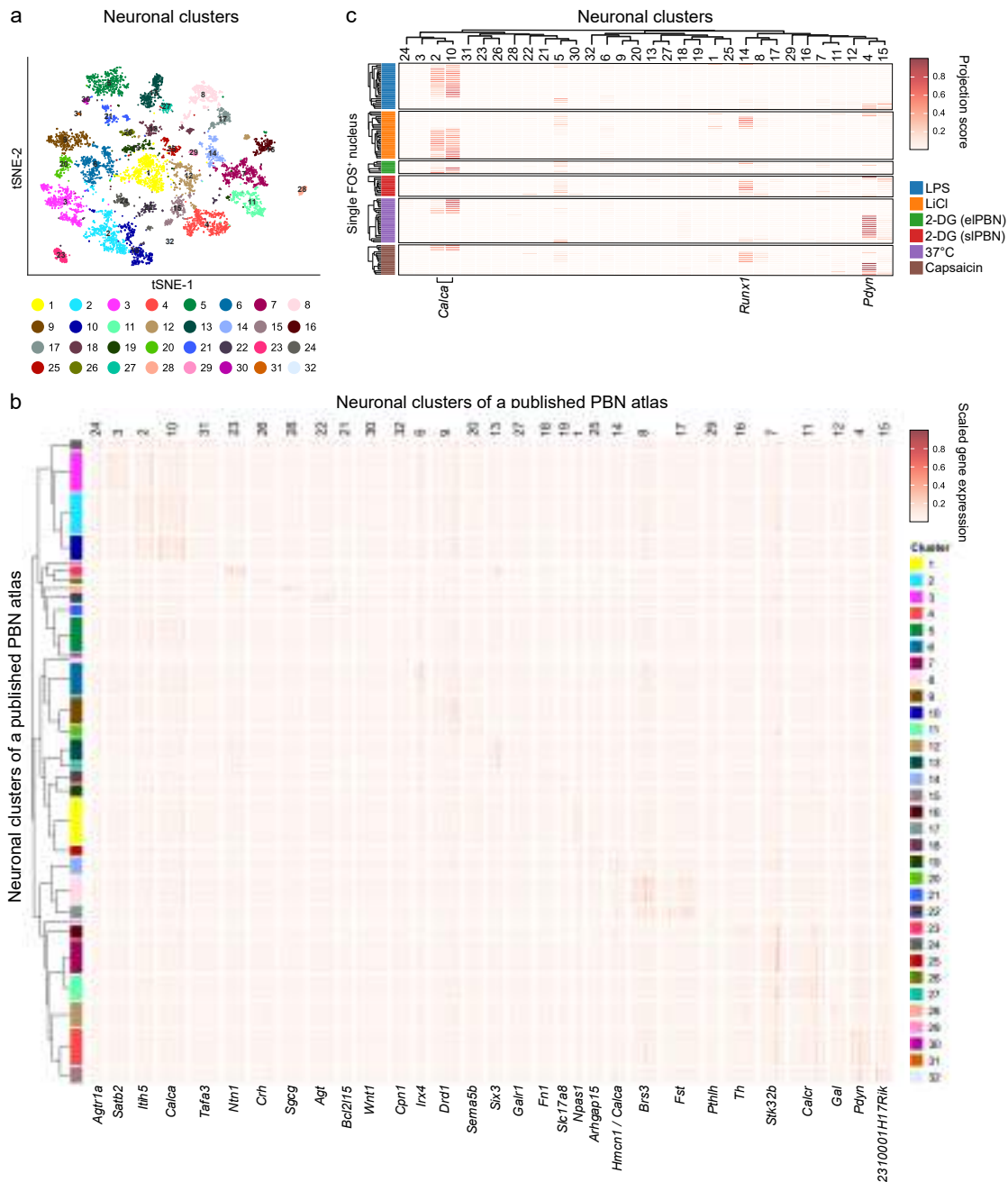


145

146 **Extended Data Fig. 13 Expression of distinct IEGs in activated PBN neurons.**

147 **a**, Bubble plot of immediate-early gene expression in distinct sets of activated neurons studied
 148 by LASAR-seq experiment and by high-throughput snRNA-seq of all PBN neurons (reference atlas,
 149 unstimulated). Stimuli or marker genes are listed at the bottom. **b**, smFISH showed co-expression
 150 of *Fos*, *Egr1*, and *Npas4* in the PBN across different stimulation conditions. Arrowheads point to
 151 the neurons co-expressing *Fos* and corresponding markers. Scale bars in **b**: 100 μ m.

152 **Extended Data Fig. 14**

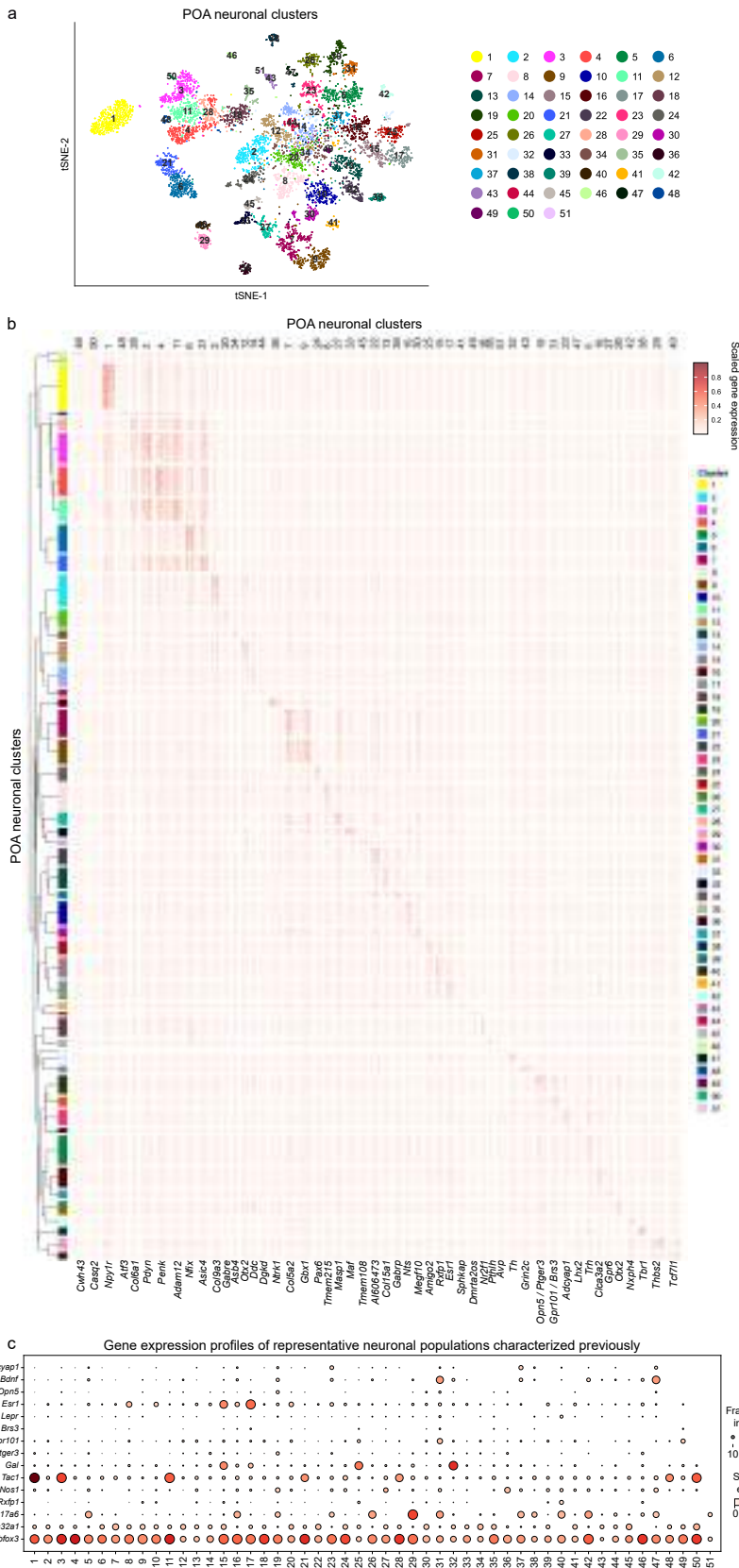


153

154 **Extended Data Fig. 14 Identification of sparsely activated PBN neurons by LASAR-seq using a**
 155 **published PBN atlas as reference.**

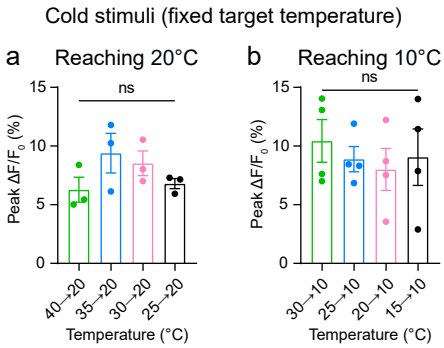
156 **a**, tSNE plot of PBN neuronal clusters from a published scRNA-seq dataset. **b**, Heatmap of cluster-
 157 cluster-specific marker genes of PBN neurons (see Supplementary Table 3 for marker gene list). **c**, Label
 158 transfer analysis of LASAR-seq identifying activated neuronal types in response to different
 159 stimuli (heatmap with key marker genes labeled at the bottom).

160 Extended Data Fig. 15



162 **Extended Data Fig. 15 Single-nucleus atlas of POA neurons served as reference.**
163 **a**, tSNE plot of POA neuronal clusters. **b**, Heatmap of cluster-specific marker genes (see
164 Supplementary Table 4 for marker gene list). **c**, Bubble plot showing previously reported major
165 neuronal types in the POA with representative markers and dedicated functions.

166 **Extended Data Fig. 16**

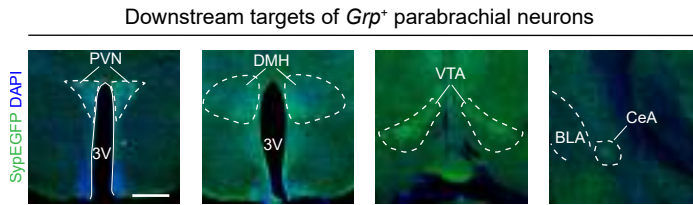


167

168 **Extended Data Fig. 16** Ca^{2+} responses of *Gpr101*⁺ preoptic neurons to the cold stimuli with
169 different fixed target temperatures.

170 **a-b**, Bar plot of peak $\Delta F/F_0$ values of Ca^{2+} response in *Gpr101*⁺ preoptic neurons during the cold
171 stimuli with target temperature at 20°C (**a**, n=3 mice per group) or 10°C (**b**, n=4 mice per group).
172 Mean \pm SEM is shown in the bar plots. Statistical significance was analyzed using two-tailed
173 Mann-Whitney test in **a** and **b**.

174 **Extended Data Fig. 17**

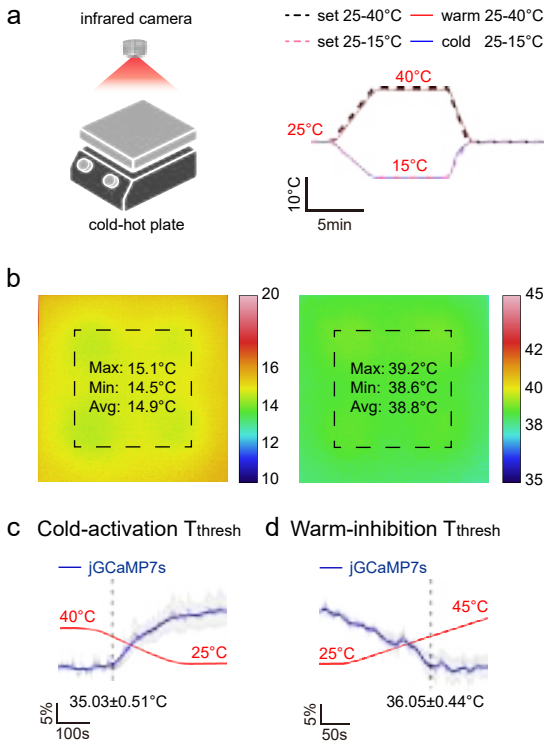


175

176 **Extended Data Fig. 17 Downstream targets of *Grp*^{PBN} neurons in the brain.**

177 Downstream targets of *Grp*^{PBN} neurons in the brain were studied by examining the AAV-
178 introduced SypEGFP expression in *Grp-Cre* mice (as shown in **Fig. 4a**). EGFP immunostaining
179 revealed presynaptic terminals of the *Grp*^{PBN} neurons in the PVN (paraventricular nucleus), DMH
180 (dorsomedial hypothalamus), VTA (ventral tegmental area), and CeA (central nucleus of the
181 amygdala). Scale bar: 500 μ m.

182 **Extended Data Fig. 18**



183

184 **Extended Data Fig. 18 Estimation of temperature thresholds of *Grp*^{PBN} neurons.**

185 **a**, Scheme of a cold-hot plate, and an infrared camera used to evaluate the spatial temperature
 186 distribution in the plate (left panel). Calibration of the cold-hot plate setting vs. actual floor
 187 temperatures measured by a BAT-12 Physitemp thermal probe (right panel, n=4). **b**, Infrared
 188 thermal imaging showed spatial temperature homogeneity in the cold-hot plate. Mice under
 189 anesthesia were positioned centrally (within the area marked by dashed lines), where the spatial
 190 temperature was homogeneous. **c-d**, Estimation of the temperature thresholds to activate (**c**) or
 191 inhibit (**d**) the *Grp*⁺ neurons in the PBN (n=8 mice). The actual averaged floor temperature was
 192 measured by a thermal probe (red traces).

193 **Supplementary table legends**

194 **Supplementary Table 1. A marker gene list of *Slc17a6*⁺ parabrachial neuronal types classified**
195 **using the snRNA-seq dataset of the PBN of mice at unstimulated status in this paper.**

196 **Supplementary Table 2. A marker gene list of *Slc17a6*⁺ parabrachial neuronal types classified**
197 **using the snRNA-seq dataset of the PBN in cold-stimulated mice in this paper.**

198 **Supplementary Table 3. A marker gene list of *Slc17a6*⁺ parabrachial neuronal types classified**
199 **using a published snRNA-seq dataset of the PBN. (Pauli, J.L., *et al.* eLife 2022, 11, e81868.)**

200 **Supplementary Table 4. A marker gene list of neuronal types classified using the snRNA-seq**
201 **dataset of the POA in this paper.**