

1 **Seven-up acts in neuroblasts to specify adult central complex neuron identity and initiate**
2 **neuroblast decommissioning**

4 Running title: Seven-up specifies neuron identity.

6 Noah R. Dillon¹, Laurina Manning¹, Keiko Hirono¹, and Chris Q. Doe^{1*}

8 NRD: ORCID #0000-0002-6708-4208

9 LM: ORCiD #0000-0003-3730-3702

10 KH: ORCiD #0009-0005-5489-2790

11 CQD: ORCiD #0000-0001-5980-8029

13 ¹Institute of Neuroscience, Howard Hughes Medical Institute, University of Oregon, Eugene,
14 OR 97403

16 * Author for correspondence at cdoe@uoregon.edu

18 Key words: Seven-up, Temporal specification, Central complex, *Drosophila*

20 **Summary**

21 Seven-up acts in Type 2 neuroblasts to specify adult central complex columnar neuron identity
22 and to initiate neuroblast decommissioning.

24 **Abstract**

26 An open question in neurobiology is how diverse neuron cell types are generated from a small
27 number of neural stem cells. In the *Drosophila* larval central brain, there are eight bilateral Type 2
28 neuroblast (T2NB) lineages that express a suite of early temporal factors followed by a different set
29 of late temporal factors and generate the majority of the central complex (CX) neurons. The early-
30 to-late switch is triggered by the orphan nuclear hormone receptor Seven-up (Svp), yet little is
31 known about this Svp-dependent switch in specifying CX neuron identities. Here, we (i) birthdate
32 the CX neurons P-EN and P-FN (early and late, respectively); (ii) show that Svp is transiently
33 expressed in all early T2NBs; and (iii) show that loss of Svp expands the population of early born

34 P-EN neurons at the expense of late born P-FN neurons. Furthermore, in the absence of Svp,
35 T2NBs fail decommissioning and abnormally extend their lineage into week-old adults. We
36 conclude that Svp is required to specify CX neuron identity, as well as to initiate T2NB
37 decommissioning.

38

39 **Introduction**

40

41 Developing a complex brain requires neural stem cells to generate both a large and diverse set of
42 neuron subtypes. *Drosophila* neuroblasts (NBs) are neural stem cells which generate neuronal
43 diversity through the initiation of spatial patterning that establishes lineage identities (Skeath and
44 Thor, 2003; Erclick et al., 2017) and subsequent temporal patterning within a lineage to produce
45 unique neuron subtypes (Doe, 2017; El-Danaf et al., 2022). These processes have been extensively
46 studied in embryonic ventral nerve cord NB lineages (Isshiki et al., 2001; Novotny et al., 2002;
47 Pearson and Doe 2003; Tran and Doe 2008; Moris-Sanz et al., 2014; Grosskortenhaus et al., 2005,
48 2006), but the role of temporal patterning mechanisms in larval central brain NB lineages remains
49 understudied.

50

51 The larval central brain contains ~100 NBs per hemibrain with spatially stereotyped lineages
52 (Pereanu and Hartenstein, 2006). Type 2 neuroblast (T2NB) lineages are generated by eight T2NBs
53 in each hemibrain, with unique spatially defined lineage identities (Pereanu and Hartenstein, 2006;
54 Bello et al., 2008; Boone and Doe, 2008; Bowman et al., 2008). Lineage tracing shows that each
55 T2NB lineage (DM1-6 and DL1-2) produces neurons with lineage-specific morphology (Riebli et al.,
56 2013; Yang et al., 2013; Andrade et al., 2019). T2NBs generate a series of intermediate neural
57 progenitors (INPs), and each INP produces 4-6 ganglion mother cells, which each divide to
58 produce two post-mitotic neurons/glia (Fig. 1A). Notably, the T2NB division pattern is analogous to
59 outer subventricular zone lineages in the primate cortex (Holguera and Desplan, 2018).

60

61 The T2NBs have been shown to express several genes in a temporal-specific manner during larval
62 stages. The IGF-II mRNA-binding protein (Imp) is expressed in a temporal gradient in T2NBs, and
63 other lineages, with high levels of Imp in early NBs and low levels in late NBs; this is inverse to the
64 low-to-high temporal gradient of the RNA-binding protein Syncrip (Liu et al., 2015; Ren et al.,
65 2017; Syed et al., 2017). Previous work has identified the orphan nuclear hormone receptor Seven-
66 up (Svp) as a switching factor to initiate this Imp-to-Syncrip transition within T2NBs (Fig. 1A) (Ren

67 et al., 2017; Syed et al., 2017). Similarly, Svp in ventral nerve cord NB lineages is required to
68 switch Type 1 NBs from producing early born neuron fates to late born fates (Kanai et al., 2005;
69 Mettler et al., 2006; Benito-Sipos et al., 2011; Kowhi et al., 2011). Although Svp is required to
70 switch from early to late temporal gene expression in T2NBs, it is unknown whether this has any
71 effect on the specification of post-mitotic neurons.

72
73 T2NB lineages generate the majority of the central complex (CX) of the *Drosophila* adult brain, with
74 recent connectomes showing the CX containing hundreds of morphologically distinct neuron
75 subtypes (Franconville et al., 2018; Hulse et al., 2021). One group of interest is columnar neurons,
76 which are members of neural circuits responsible for locomotion and spatial navigation behaviors
77 that are integrated in the CX (Giraldo et al., 2018; Green et al., 2019; Turner-Evans et al., 2020);
78 thus, understanding the development of T2NB lineages may shed light on how complex circuits
79 form and drive behavior.

80
81 Here, we characterize the function of Svp in specifying post-mitotic neuron identities within T2NB
82 lineages. We find the birth windows of P-EN and P-FN columnar neurons are from early and late
83 T2NBs respectively. We find that Svp is transiently and asynchronously expressed in all eight larval
84 T2NB lineages. We used CRISPR/Cas9 knockout lines to remove *svp* specifically from T2NB
85 lineages and show that Svp is required for the late born P-FN fate while restricting the early born
86 P-EN fate. Surprisingly, we discover a novel role for Svp in terminating T2NB neurogenesis. We
87 propose that Svp is essential for the early-to-late transition in T2NB lineages, and that these
88 changes propagate down to the level of altered identity in post-mitotic neurons. Finally, we
89 document a novel function of Svp in promoting NB decommissioning.

90
91 **Results**

92
93 Columnar neurons P-EN and P-FN are born from larval T2NBs in different temporal windows.

94
95 Previous birth dating analysis of columnar neuron subtypes only assayed a subset of neurons, for
96 example only 50-65% of the P-FN and P-EN neurons were birth dated (Sullivan et al., 2019). To
97 obtain more complete coverage, we developed a 5-ethynyl-2'-deoxyuridine (EdU) drop out
98 approach to determine the temporal birth window for P-EN and P-FN neurons. Briefly, larvae were
99 fed EdU, a thymidine analog that incorporates into DNA during DNA synthesis. We initiated EdU

100 feeding at different timepoints of larval life and maintained EdU feeding until pupation. By imaging
101 adult brains from larvae fed EdU, we characterized the time of P-EN and P-FN terminal division, as
102 neurons drop out from EdU+ to EdU- at progressively later time points of EdU introduction (Fig.
103 1B,C).

104
105 To account for the differences in the timing of neuron terminal division and the time its parental
106 INP was born from the NB, we took advantage of previous cell cycle data for NBs, INPs, and
107 ganglion mother cells (Homem et al., 2013). Both P-EN and P-FN neurons are derived from young
108 INPs (Sullivan et al., 2019), and neurons from young INPs are born from their parental NB ~12h
109 prior to terminal division (Homem et al., 2013). Therefore, we subtracted 12h to reveal the time of
110 origin from the T2NB. We conclude that P-EN neurons are born from T2NBs between 24h-48h
111 ALH, whereas P-FN neurons are born between 48h-84h ALH (Fig. 1D). Thus, P-EN and P-FN
112 neurons are derived from the same DM1-DM4 T2NB lineages (Yang et al., 2013) and the same
113 young INP lineage (Sullivan et al., 2019), but differ in the timing of their birth window from the
114 T2NB. Next, we use these early and late born neuron identities to determine whether Svp -- known
115 for its role in regulating temporal gene expression in T2NBs (Ren et al., 2017; Syed et al., 2017) --
116 is also required for proper specification of post-mitotic neurons.

117
118 Svp is expressed transiently and asynchronously in all larval T2NB lineages between 18-24h ALH.
119

120 Before assaying neuron identity following Svp knockout, we assayed for Svp protein expression in
121 each of the eight T2NB lineages, primarily to confirm expression in the DM1-DM4 T2NB lineages
122 known to generate the columnar neurons (Riebli et., al 2013; Yang et al., 2013; Andrade et al.,
123 2019). T2NBs were identified by the co-expression of Pnt-Gal4 driving UAS membrane-bound GFP
124 and the pan-neuroblast marker Deadpan in cells ≥ 5 μ m in diameter. Individual T2NB lineages were
125 identified based on spatial position of the T2NBs within the brain lobes (Pereanu and Hartenstein,
126 2006; Izergina et al., 2009). We found that Svp was transiently expressed in all eight lineages with
127 peak occurrence of expression in DM1-3 at 24h ALH (Fig. 2A-C',I) and for lineages DM4-6 and
128 DL1-2 at 18h (Fig. 2D-H',I). Svp protein was restricted to the T2NB and absent in its progeny (Fig.
129 2A-H'). We saw a similar trend of Svp mRNA expression in all early T2NB lineages (Fig. S1). We
130 conclude that Svp is transiently expressed in all T2NB lineages.

131

132 We performed *Svp* loss-of-function with the goal of making the most complete loss- and gain-of-
133 function alterations to the T2NB temporal factor cascade as possible, thereby increasing the
134 chance of seeing changes in P-EN and P-FN neuron identities. We chose to knockout *svp*
135 specifically in T2NB lineages, which has been shown to extend the expression of early NB factors
136 (e.g. Imp, Chinmo) at the expense of late NB factors (e.g. Syncrip, EcRB1, Broad, E93) (Ren et al.,
137 2017; Syed et al., 2017); although changes in neuronal morphology were detected, adult post-
138 mitotic neuron molecular identity was not assayed in these experiments. We hypothesize that if
139 early NB factors play a role in neuronal specification, then loss of *Svp* should result in ectopic P-
140 EN neurons due to failure to switch to late temporal factors, and conversely, *Svp* knockout should
141 reduce or eliminate late born identities such as P-FN neurons.

142
143 We generated *Svp* knockouts specifically in T2NB lineages. We used two independent
144 CRISPR/Cas9 lines (Port et al., 2020) each with two *Svp*-specific sgRNAs to knockout *svp* in
145 T2NBs. To determine the efficiency of our knockouts, we tested these lines for the loss of *Svp*
146 expression and recapitulation of the loss of the late T2NB expression of E93 (Syed et al., 2017).
147 We find that our knockout lines significantly reduce the occurrence of *Svp* expression in T2NBs
148 but with a minority of escaper NBs that have expression levels indistinguishable from wild-type
149 (Fig. S2A-D); these are likely 1-2 T2NB lineages where CRISPR/Cas9-mediated *svp* knockout did
150 not occur. Thus, our *Svp* knockouts had "all or none" effects on *Svp* expression. T2NBs that
151 exhibit loss of *Svp* also show a loss of E93 expression, as previously observed (Syed et al., 2017),
152 further validating the *Svp* knockouts (Fig. S2E-H). We conclude that our CRISPR/Cas9 lines
153 effectively knockout *svp* completely within the majority of T2NB lineages with only a few escapers
154 that show wild-type levels of *Svp* expression. We conclude that these knockout lines can be used
155 to test the role of *Svp* in specifying adult columnar neuron identity.

156
157 Cut expression distinguishes molecular identities of adult P-EN neurons from P-FN neurons.

158
159 P-EN and P-FN neurons were first characterized based on their distinct axon projections into CX
160 neuropils (P-EN sends axons to the EB; P-FN sends axons to the FB) (Wolff et al., 2015). Yet to
161 date no molecular markers have been reported to distinguish these neurons, except for the LexA
162 lines we use here. To address this, we used a single-cell RNA-sequencing atlas of adult T2NB-
163 derived neurons to identify novel molecular markers for P-EN and P-FN neurons (D. Epiney, G.
164 Morales, NRD, S-L. Lai, and CQD; in preparation). We identified that the homeodomain

165 transcription factor Cut was expressed in adult P-EN neurons but not in P-FN neurons (Fig. 3A-
166 B'',C), whereas Svp was in neither adult neuron type (Fig. S3A-B'',C) and Runt was in both neuron
167 types, as previously reported (Sullivan et al., 2017) (Fig. 3A',B'; Fig. S2A-B'). We conclude that Cut
168 distinguishes the molecular identities of adult P-EN and P-FN neurons, and we use this marker in
169 combination with subtype-specific LexA-driven V5 and Runt expression in our analysis of the Svp
170 knockout phenotypes.

171

172 Loss of Svp decreases the number of late born P-FN adult neurons.

173

174 Svp is required for the early-to-late switch in T2NB temporal gene expression (Ren et al., 2017;
175 Syed et al., 2017). Here, we test whether this Svp-dependent switch in the T2NB gene expression
176 extends to the specification of post-mitotic neurons. In this section we asked whether Svp
177 knockout reduces late born P-FN neurons. We found Svp knockout leads to a highly penetrant
178 loss of late born adult P-FN neurons (Fig. 4A-D). We note that there are some P-FN neurons
179 remaining; because the cell bodies are closely clustered, they likely reflect that the Svp knockout
180 failed to remove *svp* within individual T2NB lineages (see Discussion). Further evidence that
181 remaining P-FN neurons derived from Svp escaper NBs include their normal morphology (Fig. 4E-I;
182 S. Movies 1-2) and normal birth date (Fig. 4J). We conclude that Svp is required for the T2NBs to
183 produce the late born P-FN neuron identity, likely due to an extension of early born neuron
184 identities (Fig. 4K).

185

186 Loss of Svp extends the production of early born P-EN adult neurons.

187

188 We next tested whether Svp knockout in T2NBs extends early born P-EN neuron identity, using
189 both molecular and morphological assays. We found that loss of Svp leads to the expansion of
190 adult P-EN neurons, with projections into the protocerebral bridge, ellipsoid body, and noduli (Fig.
191 5A-C). Furthermore, these ectopic P-EN neurons expressed the appropriate P-EN molecular
192 markers: P-EN LexA-driven V5, Runt, and Cut (Fig. 5D-F'',G). We conclude that Svp is required to
193 restrict the production of P-EN neurons.

194

195 The ectopic P-EN neurons could arise from T2NBs generating more P-EN neurons at a normal
196 early time, or they could arise from T2NBs generating P-EN neurons at abnormally late times in
197 their lineage (replacing late born P-FN neurons). To distinguish these models, we performed EdU

198 birth dating of P-EN neurons following Svp knockout. Whereas wild-type P-EN neurons are all
199 born prior to 60h ALH (Fig. 1B), we found that Svp knockout resulted in P-EN neurons still being
200 born at 100h ALH (Fig. 5H). Our data supports a model in which loss of Svp extends the
201 production of early born P-EN neurons at the expense of late born P-FN neurons (Fig. 5I).

202
203 We next wanted to know if the ectopic P-EN neurons showed normal neuropil targeting. We
204 reconstructed CX neuropils from anti-nc82 (Bruchpilot; a presynaptic marker) (Wagh et al., 2006)
205 stains and assayed P-EN neuropil targeting (Fig. 6; S. Movies 3-4). Note that we first quantified all
206 CX neuropil volumes, which includes more neuron subtypes than just the P-EN and P-FN neurons.
207 We found that following loss of Svp in the T2NB lineages, all CX neuropils increased in size (Fig.
208 S4A). This is due in part to ectopic P-EN neurons, which targeted all assayed CX neuropils but
209 with increased targeting volume (Fig. 6A-H'; Fig. S4B-C). The role of neurons in addition to P-EN in
210 generating this neuropil enlargement phenotype is unknown. Next, we assayed neuropil targeting
211 of ectopic P-EN neurons in our T2NB Svp knockouts. We found that ectopic P-EN neurons target
212 all the expected CX neuropils (e.g., protocerebral bridge, ellipsoid body, noduli) but with increased
213 volume, likely reflecting the increase in neurons (Fig. 6A-F'; Fig. S4B). Surprisingly, we observed
214 ectopic P-EN neurons abnormally target the fan-shaped body (Fig. 5G-H',I, Fig. S4B). We
215 conclude that loss of Svp leads to the generation of ectopic P-EN neurons which show targeting to
216 normal neuropil regions with increased volume and off-targeting to the fan-shaped body.

217
218 Loss of Svp extends T2NB lineages into the adult.

219
220 We note above that Svp knockout extended the production of P-EN neurons beyond the later part
221 of larval life at 100h ALH (Fig. 5H), raising the question: Is Svp required for terminating
222 neurogenesis in T2NBs? In wild-type animals, most NBs undergo decommissioning --
223 characterized by loss of molecular markers, cell cycle arrest, death and/or differentiation -- in late
224 larval or early pupal stages (Ito and Hotta, 1992; Maurange et al., 2008; Siegrist et al., 2010; Yang
225 et al., 2017). The time of T2NB decommissioning has not been previously reported. We found that
226 T2NBs normally complete decommissioning by 24h after pupal formation (APF) (Fig. 7A-A'',E). In
227 contrast, Svp knockout in T2NB lineages results in delayed decommissioning with persistence of
228 proliferative T2NBs, marked by pH3, into 7-day old adults (Fig. 7B-D'',E-F). Remarkably, the
229 persistent T2NBs following Svp knockout strongly express the early marker Imp and lack the late
230 marker Syncrip (Fig. 7B-D''), consistent with previous work showing the Imp to Syncrip gradient

231 regulates NB decomposition (Yang et al., 2017). Thus, we conclude that Svp is required to
232 initiate T2NB decomposition (Fig. 7G). How these late functions of Svp, such as T2NB
233 decomposition in pupal stages, are triggered by transient expression of Svp many days earlier
234 in first instar larvae remains an interesting open question.

235

236 Discussion

237 Columnar neurons are born at different times in the T2NB lineage.

238 Our EdU birth dating revealed that P-EN neurons are born from early T2NBs, and P-FN neurons
239 are born from late T2NBs. Previous work showed these neuron identities are both born during the
240 same NB window, conflicting with our results (Sullivan et al., 2017). Our approach tracks the
241 terminal division of cells through EdU labeling, which accounts for all neurons within the
242 population, while previous birth dating relied on a genetic approach that only accounted for 55-
243 65% of the neurons (Sullivan et al., 2017). We propose that EdU birth dating is more
244 comprehensive for assigning neurons to NB birth windows as all neurons are reliably labeled with
245 EdU, providing reproducible tracing of terminal divisions.

247 It remains an open question how T2NBs are patterned to generate birth-order dependent neuronal
248 identities. One hypothesis is that the lineage uses a temporal transcription factor cascade, similar
249 to embryonic Type 1 NBs (Isshiki et al., 2001; Novotny et al., 2002; Pearson and Doe 2003; Tran
250 and Doe 2008; Moris-Sanz et al., 2014). Alternatively, or in combination, the lineage could utilize a
251 temporal gradient of protein expression, like mushroom body NBs (Liu et al., 2015). Several
252 temporally expressed factors are known to cross-regulate in T2NBs (Ren et al., 2017; Syed et al.,
253 2017). Our work with loss of Svp (i.e., changing expression of known temporal factors in T2NBs)
254 shows that temporal patterning at the NB level is required to specify neuron subtypes. This is
255 supported by recent work reporting knockdown of Imp levels in T2NB lineages results in altered
256 CX neurons; however, it is unclear if this is due to the role of Imp at the NB or INP level (Hamid et
257 al., 2023). Additionally, loss of T2NB temporal factors EcR and E93 are required for specifying the
258 CX neuron subtype dFB neurons (Wani et al., 2023). Our data do not distinguish between a model
259 for a temporal transcription factor cascade and/or temporal gradients. Thus, it will be important to
260 test individual temporal factors and expression levels in specifying birth-order dependent fates.

262

263 Svp expression in larval T2NB lineages

264
265 We report a comprehensive characterization of Svp in all eight T2NB lineages at stages that
266 bracket Svp expression. Previous work has only observed Svp expression at either broad temporal
267 windows or limited to a few lineages (Bayraktar and Doe, 2013; Ren et al., 2017; Syed et al., 2017).
268 We show that Svp has a tight expression window between 18-24h ALH in all T2NB lineages with
269 Svp protein restricted to the NB (Fig. 2). This finding is further supported by the Svp mRNA
270 showing a similar expression pattern in the T2NB lineages and restricted to the NB (Fig. S1).
271 Interestingly, *svp* mRNA was expressed before onset of protein expression and remained longer
272 than protein expression (compare Figure 2 to Sup Fig. 1), which suggests post-transcriptional
273 regulation of Svp in the NB. We found evidence that indicates the posterior lineages (DM4-6, DL1-
274 2) express Svp prior to the anterior lineages (DM1-3) (Fig. 2I). We speculate that the distinct onset
275 of Svp expression between lineages may be determined by differential expression of spatial
276 factors. Determining the upstream mechanism that initiates Svp expression remains an open
277 question. A further challenge will be resolving the orphan receptor status of Svp as it remains
278 unknown if Svp requires a ligand for activation.

279
280 Svp is required for late born fates in the T2NB lineages.

281
282 We found that Svp knockout resulted in a loss of the late born P-FN neuron identity. The remaining
283 P-FN neurons resemble wild-type neurons in cell body location, numbers, morphology, and birth
284 window. We report that the Svp knockout lineages have a success rate of ~75%, with
285 approximately 1 out of 4 T2NBs completely escaping *svp* knockout (Fig. S2). Wild-type P-FN
286 neurons number ~40 cells, but in Svp knockouts we see ~5-15 cells remaining, which is the
287 expected proportion based on the efficiency of our knockout lines (Fig. 4D). Moreover, the
288 remaining P-FN neurons display lineage-appropriate morphology (Fig. 4E-H) and a wild-type birth
289 window from the T2NBs (Fig. 4J). We conclude that the remaining P-FN neurons are derived from
290 Svp knockout escaping NBs that maintain normal Svp expression and hence develop normally.
291 Thus, our Svp knockout can be described as an "all or none" knockout of Svp in ~75% of the
292 T2NBs.

293
294 Svp specification of other CX neuron subtypes

296 Svp has previously been reported as either a switching factor in embryonic and larval NBs (Kanai
297 et al., 2005; Mettler et al., 2006; Maurange et al., 2008; Benito-Sipos et al., 2011; Kowhi et al.,
298 2011) or as a post-mitotic fate determinate in photoreceptor neuron subtypes (Mlodzik et al., 1990;
299 Hiromi et al., 1993). Our work shows that Svp acts as a switching factor in T2NBs for specifying
300 neuron identities, as Svp was not expressed in post-mitotic P-EN or P-FN neurons (Fig. S3).
301 However, we cannot rule out that Svp is required as a post-mitotic fate determinant for other CX
302 subtypes.

303
304 We show that Svp is required to restrict the early born P-EN identity as loss of Svp resulted in
305 T2NBs extending production of P-EN neurons into an abnormally late temporal window (Fig. 5H).
306 These ectopic P-EN neurons maintain wild-type molecular markers (e.g., LexA, Runt, Cut) (Fig.
307 5G). We note that these ectopic P-EN neurons have ectopic targeting to the fan-shaped body, a
308 neuropil not targeted by wild-type P-EN neurons (Fig. 6G-H',I; Fig. S4B-C). We speculate that this
309 abnormal targeting may be compensation for the loss of P-FN neurons that normally target the
310 region, suggesting that columnar neuron targeting may be promiscuous when subtypes are
311 absent. We note that P-EN neurons are just one fate born from the early temporal window; other
312 neurons born at a similar time are not visible with the P-EN/P-FN LexA markers used here. We
313 hypothesize that these early born populations will also be expanded with the loss of Svp. It will be
314 vital for future work to identify additional CX neuron markers and their birth date from the T2NBs to
315 test for functional temporal patterning factors.

316
317 We find that the loss of Svp resulted in significant changes to CX neuropil volumes. While targeting
318 from ectopic P-EN neurons accounts for a portion of this increase, it does not fully account for the
319 global CX neuropil enlargement we report (Fig. S4B-C). We speculate that either expanded
320 populations of other T2NB-derived neuron subtypes and/or synaptic partners account for the
321 ectopic targeting to these neuropils. For example, P-EN neurons form synapses with the T2NB-
322 derived E-PG neurons (Green et al., 2017; 2019), thus, loss of Svp could lead to either E-PG
323 compensation with increased targeting to ectopic P-EN neurons and/or an expanded E-PG neuron
324 population. We are unable to account for the global CX changes that occurred with the loss of Svp
325 due to the limitation in our assays of just the P-EN and P-FN neurons.

326
327 Svp regulation of Type 2 neuroblast temporal progression
328

329 Svp is expressed in early larval T2NBs prior to the Imp to Syncrip transition (Ren et al., 2017); thus,
330 we were surprised by our findings that Svp is required for terminating neurogenesis in pupae.
331 Previous work has shown the transition in central brain NBs from Imp to Syncrip expression
332 initiates NB decommissioning (Yang et al., 2017). Interestingly, mushroom body NBs remain
333 proliferating into pupal stages, when other NBs have decommissioned, due to sustained Imp
334 expression (Yang et al., 2017). Consistent with our work on T2NBs, previous work has also
335 demonstrated that loss of Svp in ventral nerve cord and central brain NB lineages leads to
336 continued NB proliferation into the adult (Maurange et al., 2008; Narbonne-Reveau et al., 2016).
337 We report that loss of Svp in early larval T2NBs had profound impacts on the lifespan of the NBs,
338 where they survive into 7-day adults manifesting (i) maintained Imp expression; (ii) mitotically
339 active; (iii) maintain low levels of Syncrip (Fig. 7). Thus, we propose that Svp initiating the switch of
340 Imp-to-Syncrip in T2NBs is a NB autonomous mechanism required for terminating neurogenesis
341 within T2NB lineages. This is consistent with previous work showing Svp is required for the
342 progression of Imp to Syncrip expression in T2NBs (Ren et al., 2017). We speculate that Svp may
343 regulate chromatin landscape and/or initiate a temporal cascade to account for the long-term
344 effects Svp has on T2NB temporal progression.

345
346 Recently, Notch signaling has been shown to be required for central brain Type 1 NB
347 decommissioning by disrupting temporal patterning progression; loss of Notch signaling produced
348 prolonged expression of the early factor Imp and reduced expression of the late factor E93 (Sood
349 et al., 2023). Additionally, Notch signaling appeared to be required in terminating expression of the
350 early factors Castor and Svp (Sood et al., 2023). This indicates that Notch signaling acts upstream
351 of NB temporal factors, and thus is likely to act upstream of Svp as well. This is difficult to test as
352 loss of Notch signaling in T2NBs results in loss of neuroblast identity (San-Juan and Baonza, 2011;
353 Zhu et al., 2012; Li et al., 2016; Li et al., 2017).

354
355 Conserved role of Svp in vertebrate temporal patterning
356
357 Our work shows that Svp acts as a switching factor in T2NBs to switch from producing early born
358 to late born neuronal identities. The mammalian orthologs of *svp*, *Coup-tfl/II* have been
359 characterized for a similar role as a switching factor in murine neural stem cells (Naka et al., 2008;
360 Lodato et., al 2011). *Coup-tfl/II* are required for cultured neural stem cells to switch from producing
361 early born neuron cell types to producing late born glia, since a loss of this molecular switch

362 resulted in sustained neurogenesis (Naka et al., 2008). Additionally, *Coup-tfl/II* are required for
363 switching cortical neural stem cells from producing early born interneuron fates to late born
364 interneuron fates (Lodato et., al 2011). These findings, along with ours and others in *Drosophila*,
365 suggest that Svp has a conserved role as a neural stem cell switching factor from fly to mammals
366 (Mettler et al., 2006; Benito-Sipos et al., 2011; Ren et al., 2017).

367

368 Materials and Methods

369 Animal Preparation

370 *Drosophila melanogaster* was used in all experiments. All flies were kept and maintained at 25°C
371 unless stated otherwise. Stocks used can be found in Table S1 and experimental genetic crosses
372 in Table S2.

373

374 *EdU experiments*

375 EDU (5-ethynyl-2'-deoxyuridine; Millipore-sigma #900584-50MG), a thymidine analog, was used
376 to label proliferating cells starting at various sequential larvae ages. Larvae were fed food
377 containing 20ug/ml EdU nonstop from the initial age feeding started until the larvae pupated.
378 Larvae fed on EdU were raised at temperatures between 18°C to 21°C until adults hatched and
379 were dissected.

380

381 *Larval experiments*

382 Embryos were collected on 3% agar apple juice caps with yeast paste for 4 hours and aged for
383 21 hours. After aging, embryos were transferred to a fresh cap and aged 4 hours for hatching.
384 Hatched larvae were collected and dissected at the corresponding time after larval hatching
385 (ALH).

386

387 *Adult experiments*

388 Males and virgin females were introduced in standard yeast medium vials and flipped every two
389 days. 2-5 day old adult flies were dissected for all experiments unless stated otherwise. All
390 animals dissected were a mixture of male and female unless otherwise specified.

391

392 Hybridization Chain Reaction (HCR) RNA fluorescent in situ hybridization

393 Larval brains were dissected in Schneider's insect medium, fixed in 4% PFA (paraformaldehyde;
394 Electron Microscopy Sciences 15710) in PBS (Phosphate buffered saline, Sigma-Aldrich P4417)

395 for 7-15 min at room temperature, and washed in PBST (PBS with 0.3% Triton, Sigma-Aldrich
396 T8787). The fixed brains were stored in 70% Ethanol in water at 4 °C until used. We followed the
397 protocol from [Duckhorn et al. \(2022\)](#). A 20-probe set targeting svp transcripts was synthesized by
398 Molecular Instruments, Inc. and probes were added to a final concentration of 4 nM for
399 hybridization. Amplifier B3-546 was also synthesized by Molecular Instruments, Inc and 6 pmol of
400 each hairpin (h1 and h2), was added for amplification.

401

402 Immunohistochemistry

403 Antibodies used with supporting notes can found in [Table S3](#).

404

405 *Larval brain sample preparation*

406 Larval brains were dissected in PBS and mounted on poly-D-lysine coated coverslips (Neuvitro
407 Corporation GG-12-PDL; primed in 100% ethanol). Samples fixed for 23 minutes in 4% PFA in
408 PBST. Samples were washed in PBST and blocked with 2% normal donkey serum (Jackson
409 ImmunoResearch Laboratories, Inc.) in PBST. Samples incubated in a primary antibody mix diluted
410 in PBST for overnight or 1-2 days at 4°C. Primary antibodies were removed, and samples
411 thoroughly washed with PBST. Samples were incubated in secondary antibodies overnight at 4°C.
412 Secondary antibodies were removed, and samples washed in PBST. Samples were dehydrated
413 with an ethanol series of 30%, 50%, 75%, and 100% ethanol then incubated in xylene (Fisher
414 Chemical X5-1) for 2x10 minutes. Samples were mounted onto slides with DPX (Sigma-Aldrich
415 06552) and cured for 3-4 days then stored at 4°C until imaged.

416

417 *Adult brain sample preparation*

418 Adult brains were prepared similar to larval brains with the exception of 41 minutes for fixation in
419 4% PFA and 2x12 minute xylene incubations.

420

421 *EdU adult brain sample preparation*

422 Adult brains from EdU fed larvae were dissected in HL3.1 then fixed in 4% PFA for 30 minutes and
423 incubated in block at 4°C overnight. Samples were incubated in primary and secondary mixes
424 prior to Click-it-Reaction to label EdU. The Click-it-Reaction mix was comprised of PBS, Copper II
425 sulfate (ThermoFisher 033308.22), 555-Azide (Thermofisher A20012) in DMSO and ascorbic acid
426 (Sigma-Aldrich A4544-25G) for a 2-hour incubation. Samples were dehydrated and washed in
427 xylene before DPX mounted as described above.

428

429 Confocal Microscopy

430 Fixed preparations were imaged with a Zeiss LSM 900 or 800 laser scanning confocal (Carl Zeiss
431 AG, Oberkochen, Germany) equipped with an Axio Imager.Z2 microscope. A 10x/0.3 EC Plan-
432 Neofluar M27 or 40x/1.40 NA Oil Plan-Apochromat DIC M27 objective lens were used. Software
433 program used was Zen 3.6 (blue edition) (Carl Zeiss AG, Oberkochen, Germany).

434

435 Image processing and analysis

436 *Cell counting and neuropil target scoring*

437 Confocal image stacks were loaded into FIJI (ImageJ 1.50d, <https://imagej.net/Fiji>). Cells were
438 counted using the Cell Counter plugin. Neuropil targeting was determined by co-localization of
439 LexA expression with neuropil marker that was not a filament bundle passing through the neuropil.

440

441 *Imaris neuropil reconstructions*

442 Confocal image stacks were loaded into Imaris 10.0.0 (Bitplane AG, Zurich, Switzerland). Imaris
443 Surface objects were created for each neuropil using nc82 staining and LexA expression followed
444 by new objects designating overlap between neuropil and neurites. Briefly, the Surface tool was
445 selected, and a region of interest (ROI) was drawn to encompass a whole CX neuropil or LexA
446 expression. The source channel was selected (nc82 in RRX for neuropils or LexA in 647 for
447 neurites) and absolute threshold intensity was manually set slice by slice to outline fluorescent
448 signal and morphologically split to separate regions. All Starting Points and Seed Points were kept
449 ensuring full coverage of signal. Surfaces were rendered and surfaces outside neuropil structures
450 removed. To find the LexA targeting for each neuropil, Surface-Surface Overlap File XTension
451 (Matthew Gastinger, <https://imaris.oxinst.com/oP-EN/view/surface-surface-overlap>) was used to
452 find the volume (μm^3) of overlap. A Smoothing Factor of 0.2 μm was kept for all surfaces.

453

454 *Figure preparation*

455 Images in figures were prepared either in Imaris 10.0.0 or FIJI. Scale bars are given for a single
456 slice in all single slice images and from all stacks within maximum intensity projections images.
457 Pixel brightness was adjusted in images for clearer visualization; all adjustments were made
458 uniformly over the entire image, and uniformly across wild-type samples and corresponding
459 control and experimental samples. Adobe Illustrator 2023 was used for formatting.

460

461 **Statistical analyses**

462 Statistics were computed using Python tests (see supplemental script for specific packages). All
463 statistical tests used are listed in the figure legends. *P*-values are reported in the figure legends.
464 Plots display n.s. = not significant, * is *P* < 0.05, and ** is *P* < 0.01. Plots were generated using
465 Seaborn and Matplotlib packages in Python.

466

467 **Additional files**

468 **Supplementary figures**

469

470 **Supplementary tables**

471

472 **Acknowledgements**

473 We thank fellow lab members Kristen Lee, Peter Newstein, Megan Radler, and Chundi Xu for
474 constructive comments on the manuscript. We also thank Tzumin Lee (University of Michigan), and
475 Mubarak Syed (University of New Mexico) for comments on the manuscript. Antibodies obtained
476 from the Developmental Studies Hybridoma Bank, created by the NICHD of the NIH and
477 maintained at the University of Iowa, Department of Biology, Iowa City, IA were used in this study.
478 Stocks obtained from the Bloomington Drosophila Stock Center (NIH P40OD018537) and Vienna
479 Drosophila Resource Center were used in this study.

480

481 **Author contributions**

482 Conceptualization: NRD, CQD. Design: NRD, LM (EdU drop out), KH (HCR RNA in situ), CQD.
483 Investigation: NRD, LM (EdU drop out), KH (HCR RNA in situ). Analysis: NRD. Writing – original
484 draft: NRD, CQD. Writing – review and editing: NRD, LM, KH, CQD.

485

486 **Competing interests**

487 The authors declare no competing interests.

488

489 **Funding**

490 Funding was provided by the National Institute of Health [HD27056, T32-HD07348] and the
491 Howard Hughes Medical Institute.

492

493 **Data availability**

494 All relevant data can be found within the article and its supplementary information.

495

496

497

References

498

Andrade, I. V., Riebli, N., Nguyen, B.-C. M., Omoto, J. J., Cardona, A. and Hartenstein, V.

499

(2019). Developmentally Arrested Precursors of Pontine Neurons Establish an Embryonic Blueprint of the Drosophila Central Complex. *Current Biology* **29**, 412-425.e3.

500

Bayraktar, O. A. and Doe, C. Q. (2013). Combinatorial temporal patterning in progenitors expands neural diversity. *Nature* **498**, 449–455.

501

Bello, B. C., Izergina, N., Caussinus, E. and Reichert, H. (2008). Amplification of neural stem cell proliferation by intermediate progenitor cells in Drosophila brain development. *Neural Development* **3**, 5.

502

Benito-Sipos, J., Ulvklo, C., Gabilondo, H., Baumgardt, M., Angel, A., Torroja, L. and Thor, S. (2011). Seven up acts as a temporal factor during two different stages of neuroblast 5-6 development. *Development* **138**, 5311–5320.

503

Boone, J. Q. and Doe, C. Q. (2008). Identification of Drosophila type II neuroblast lineages containing transit amplifying ganglion mother cells. *Developmental Neurobiology* **68**, 1185–1195.

504

Bowman, S. K., Rolland, V., Betschinger, J., Kinsey, K. A., Emery, G. and Knoblich, J. A. (2008). The Tumor Suppressors Brat and Numb Regulate Transit-Amplifying Neuroblast Lineages in Drosophila. *Developmental Cell* **14**, 535–546.

505

Doe, C. Q. (2017). Temporal Patterning in the Drosophila CNS. *Annual Review of Cell and Developmental Biology* **33**, 219–240.

506

Duckhorn, J. C., Junker, I. P., Ding, Y. and Shirangi, T. R. (2022). Combined in Situ Hybridization Chain Reaction and Immunostaining to Visualize Gene Expression in Whole-Mount Drosophila Central Nervous Systems. In *Behavioral Neurogenetics* (ed. Yamamoto, D.), pp. 1–14. New York, NY: Springer US.

507

El-Danaf, R. N., Rajesh, R. and Desplan, C. (2023). Temporal regulation of neural diversity in Drosophila and vertebrates. *Seminars in Cell & Developmental Biology* **142**, 13–22.

508

Erclik, T., Li, X., Courgeon, M., Bertet, C., Chen, Z., Baumert, R., Ng, J., Koo, C., Arain, U., Behnia, R., et al. (2017). Integration of temporal and spatial patterning generates neural diversity. *Nature* **541**, 365–370.

509

Franconville, R., Beron, C. and Jayaraman, V. (2018). Building a functional connectome of the Drosophila central complex. *eLife* **7**, e37017.

510

Giraldo, Y. M., Leitch, K. J., Ros, I. G., Warren, T. L., Weir, P. T. and Dickinson, M. H. (2018). Sun Navigation Requires Compass Neurons in Drosophila. *Curr Biol* **28**, 2845–2852.e4.

511

Green, J., Adachi, A., Shah, K. K., Hirokawa, J. D., Magani, P. S. and Maimon, G. (2017). A neural circuit architecture for angular integration in Drosophila. *Nature* **546**, 101–106.

512

Green, J., Vijayan, V., Mussells Pires, P., Adachi, A. and Maimon, G. (2019). A neural heading estimate is compared with an internal goal to guide oriented navigation. *Nat Neurosci* **22**, 1460–1468.

513

Grosskortenhaus, R., Pearson, B. J., Marusich, A. and Doe, C. Q. (2005). Regulation of Temporal Identity Transitions in Drosophila Neuroblasts. *Developmental Cell* **8**, 193–202.

514

Grosskortenhaus, R., Robinson, K. J. and Doe, C. Q. (2006). Pdm and Castor specify late-born motor neuron identity in the NB7-1 lineage. *Genes Dev.* **20**, 2618–2627.

515

Hamid, A., Gattuso, H., Caglar, A. N., Pillai, M., Steele, T., Gonzalez, A., Nagel, K. and Syed, M. H. (2023). The RNA-binding protein, Imp specifies olfactory navigation circuitry and behavior in Drosophila. 2023.05.26.542522.

542 **Hiromi, Y., Mlodzik, M., West, S. R., Rubin, G. M. and Goodman, C. S.** (1993). Ectopic
543 expression of seven-up causes cell fate changes during ommatidial assembly. *Development*
544 **118**, 1123–1135.

545 **Holguera, I. and Desplan, C.** (2018). Neuronal specification in space and time. *Science*.

546 **Homem, C. C. F., Reichardt, I., Berger, C., Lendl, T. and Knoblich, J. A.** (2013). Long-Term Live
547 Cell Imaging and Automated 4D Analysis of Drosophila Neuroblast Lineages. *PLoS One* **8**,
548 e79588.

549 **Hulse, B. K., Haberkern, H., Franconville, R., Turner-Evans, D. B., Takemura, S., Wolff, T.,**
550 **Noorman, M., Dreher, M., Dan, C., Parekh, R., et al.** (2021). A connectome of the Drosophila
551 central complex reveals network motifs suitable for flexible navigation and context-dependent
552 action selection. *eLife* **10**, e66039.

553 **Isshiki, T., Pearson, B., Holbrook, S. and Doe, C. Q.** (2001). Drosophila Neuroblasts Sequentially
554 Express Transcription Factors which Specify the Temporal Identity of Their Neuronal Progeny.
555 *Cell* **106**, 511–521.

556 **Ito, K. and Hotta, Y.** (1992). Proliferation pattern of postembryonic neuroblasts in the brain of
557 *Drosophila melanogaster*. *Developmental Biology* **149**, 134–148.

558 **Izergina, N., Balmer, J., Bello, B. and Reichert, H.** (2009). Postembryonic development of transit
559 amplifying neuroblast lineages in the Drosophila brain. *Neural Dev* **4**, 44.

560 **Kanai, M. I., Okabe, M. and Hiromi, Y.** (2005). seven-up Controls Switching of Transcription
561 Factors that Specify Temporal Identities of Drosophila Neuroblasts. *Developmental Cell* **8**,
562 203–213.

563 **Kohwi, M., Hiebert, L. S. and Doe, C. Q.** (2011). The pipsqueak-domain proteins Distal antenna
564 and Distal antenna-related restrict Hunchback neuroblast expression and early-born neuronal
565 identity. *Development* **138**, 1727–1735.

566 **Li, X., Xie, Y. and Zhu, S.** (2016). Notch maintains *Drosophila* type II neuroblasts by suppressing
567 the expression of the Fez transcription factor Earmuff. *Development* **136**, 184.

568 **Li, X., Chen, R. and Zhu, S.** (2017). bHLH-O proteins balance the self-renewal and differentiation
569 of Drosophila neural stem cells by regulating Earmuff expression. *Dev Biol* **431**, 239–251.

570 **Liu, Z., Yang, C.-P., Sugino, K., Fu, C.-C., Liu, L.-Y., Yao, X., Lee, L. P. and Lee, T.** (2015).
571 Opposing intrinsic temporal gradients guide neural stem cell production of varied neuronal
572 fates. *Science* **350**, 317–320.

573 **Lodato, S., Tomassy, G. S., De Leonibus, E., Uzcategui, Y. G., Andolfi, G., Armentano, M.,**
574 **Touzot, A., Gaztelu, J. M., Arlotta, P., Menendez de la Prida, L., et al.** (2011). Loss of
575 COUP-TFI Alters the Balance between Caudal Ganglionic Eminence- and Medial Ganglionic
576 Eminence-Derived Cortical Interneurons and Results in Resistance to Epilepsy. *J Neurosci* **31**,
577 4650–4662.

578 **Maurange, C., Cheng, L. and Gould, A. P.** (2008). Temporal Transcription Factors and Their
579 Targets Schedule the End of Neural Proliferation in Drosophila. *Cell* **133**, 891–902.

580 **Mettler, U., Vogler, G. and Urban, J.** (2006). Timing of identity: spatiotemporal regulation of
581 hunchback in neuroblast lineages of Drosophila by Seven-up and Prospero. *Development*
582 **133**, 429–437.

583 **Mlodzik, M., Hiromi, Y., Weber, U., Goodman, C. S. and Rubin, G. M.** (1990). The Drosophila
584 seven-up gene, a member of the steroid receptor gene superfamily, controls photoreceptor
585 cell fates. *Cell* **60**, 211–224.

586 **Moris-Sanz, M., Estacio-Gómez, A., Alvarez-Rivero, J. and Díaz-Benjumea, F. J.** (2014).
587 Specification of neuronal subtypes by different levels of Hunchback. *Development* **141**, 4366–
588 4374.

589 **Naka, H., Nakamura, S., Shimazaki, T. and Okano, H.** (2008). Requirement for COUP-TFI and II
590 in the temporal specification of neural stem cells in CNS development. *Nat Neurosci* **11**, 1014–
591 1023.

592 **Narbonne-Reveau, K., Lanet, E., Dillard, C., Foppolo, S., Chen, C.-H., Parrinello, H., Rialle, S.,**

593 **Sokol, N. S. and Maurange, C.** (2016). Neural stem cell-encoded temporal patterning
594 delineates an early window of malignant susceptibility in Drosophila. *eLife* **5**, e13463.

595 **Novotny, T., Eiselt, R. and Urban, J.** (2002). Hunchback is required for the specification of the
596 early sublineage of neuroblast 7-3 in the Drosophila central nervous system. *Development*
597 **129**, 1027–1036.

598 **Pearson, B. J. and Doe, C. Q.** (2003). Regulation of neuroblast competence in Drosophila. *Nature*
599 **425**, 624–628.

600 **Pereanu, W. and Hartenstein, V.** (2006). Neural Lineages of the Drosophila Brain: A Three-
601 Dimensional Digital Atlas of the Pattern of Lineage Location and Projection at the Late Larval
602 Stage. *J Neurosci* **26**, 5534–5553.

603 **Port, F., Strein, C., Stricker, M., Rauscher, B., Heigwer, F., Zhou, J., Beyersdörffer, C., Frei, J.,**

604 **Hess, A., Kern, K., et al.** (2020). A large-scale resource for tissue-specific CRISPR
605 mutagenesis in Drosophila. *eLife* **9**, e53865.

606 **Ren, Q., Yang, C.-P., Liu, Z., Sugino, K., Mok, K., He, Y., Ito, M., Nern, A., Otsuna, H. and Lee,**

607 **T.** (2017). Stem Cell-Intrinsic, Seven-up-Triggered Temporal Factor Gradients Diversify
608 Intermediate Neural Progenitors. *Current Biology* **27**, 1303–1313.

609 **Riebli, N., Viktorin, G. and Reichert, H.** (2013). Early-born neurons in type II neuroblast lineages
610 establish a larval primordium and integrate into adult circuitry during central complex
611 development in Drosophila. *Neural Development* **8**, 6.

612 **San-Juán, B. P. and Baonza, A.** (2011). The bHLH factor deadpan is a direct target of Notch
613 signaling and regulates neuroblast self-renewal in Drosophila. *Dev Biol* **352**, 70–82.

614 **Siegrist, S. E., Haque, N. S., Chen, C.-H., Hay, B. A. and Hariharan, I. K.** (2010). Inactivation of
615 Both foxo and reaper Promotes Long-Term Adult Neurogenesis in Drosophila. *Current Biology*
616 **20**, 643–648.

617 **Skeath, J. B. and Thor, S.** (2003). Genetic control of Drosophila nerve cord development. *Current*
618 *Opinion in Neurobiology* **13**, 8–15.

619 **Sood, C., Nahid, M. A., Branham, K. R., Pahl, M. C., Doyle, S. E. and Siegrist, S. E.** (2023).
620 Delta-dependent Notch activation closes the early neuroblast temporal program to promote
621 lineage progression and neurogenesis termination in Drosophila. *eLife* **12**.

622 **Sullivan, L. F., Warren, T. L. and Doe, C. Q.** (2019). Temporal identity establishes columnar
623 neuron morphology, connectivity, and function in a Drosophila navigation circuit. *eLife* **8**,
624 e43482.

625 **Syed, M. H., Mark, B. and Doe, C. Q.** (2017). Steroid hormone induction of temporal gene
626 expression in Drosophila brain neuroblasts generates neuronal and glial diversity. *eLife* **6**,
627 e26287.

628 **Tran, K. D. and Doe, C. Q.** (2008). Pdm and Castor close successive temporal identity windows in
629 the NB3-1 lineage. *Development* **135**, 3491–3499.

630 **Turner-Evans, D. B., Jensen, K. T., Ali, S., Paterson, T., Sheridan, A., Ray, R. P., Wolff, T.,**

631 **Lauritzen, J. S., Rubin, G. M., Bock, D. D., et al.** (2020). The Neuroanatomical Ultrastructure
632 and Function of a Biological Ring Attractor. *Neuron* **108**, 145–163.e10.

633 **Wagh, D. A., Rasse, T. M., Asan, E., Hofbauer, A., Schwenkert, I., Dürrbeck, H., Buchner, S.,**

634 **Dabauvalle, M.-C., Schmidt, M., Qin, G., et al.** (2006). Bruchpilot, a protein with homology to
635 ELKS/CAST, is required for structural integrity and function of synaptic active zones in
636 Drosophila. *Neuron* **49**, 833–844.

637 **Wani, A. R., Chowdhury, B., Luong, J., Chaya, G. M., Patel, K., Isaacman-Beck, J., Shafer, O.,**
638 **Kayser, M. S. and Syed, M. H. (2023). Stem cell-specific ecdysone signaling regulates the**
639 **development and function of a Drosophila sleep homeostat. 2023.09.29.560022.**

640 **Wolff, T., Iyer, N. A. and Rubin, G. M. (2015). Neuroarchitecture and neuroanatomy of the**
641 **Drosophila central complex: A GAL4-based dissection of protocerebral bridge neurons and**
642 **circuits. *J Comp Neurol* **523**, 997–1037.**

643 **Yang, J. S., Awasaki, T., Yu, H.-H., He, Y., Ding, P., Kao, J.-C. and Lee, T. (2013). Diverse**
644 **neuronal lineages make stereotyped contributions to the Drosophila locomotor control center,**
645 **the central complex. *Journal of Comparative Neurology* **521**, 2645–2662.**

646 **Yang, C.-P., Samuels, T. J., Huang, Y., Yang, L., Ish-Horowicz, D., Davis, I. and Lee, T. (2017).**
647 **Imp and Syp RNA-binding proteins govern decommissioning of Drosophila neural stem cells.**
648 ***Development* **144**, 3454–3464.**

649 **Zhu, S., Wildonger, J., Barshow, S., Younger, S., Huang, Y. and Lee, T. (2012). The bHLH**
650 **Repressor Deadpan Regulates the Self-renewal and Specification of Drosophila Larval Neural**
651 **Stem Cells Independently of Notch. *PLOS ONE* **7**, e46724.**

652

653

654

655

656

657

658

659

660

661

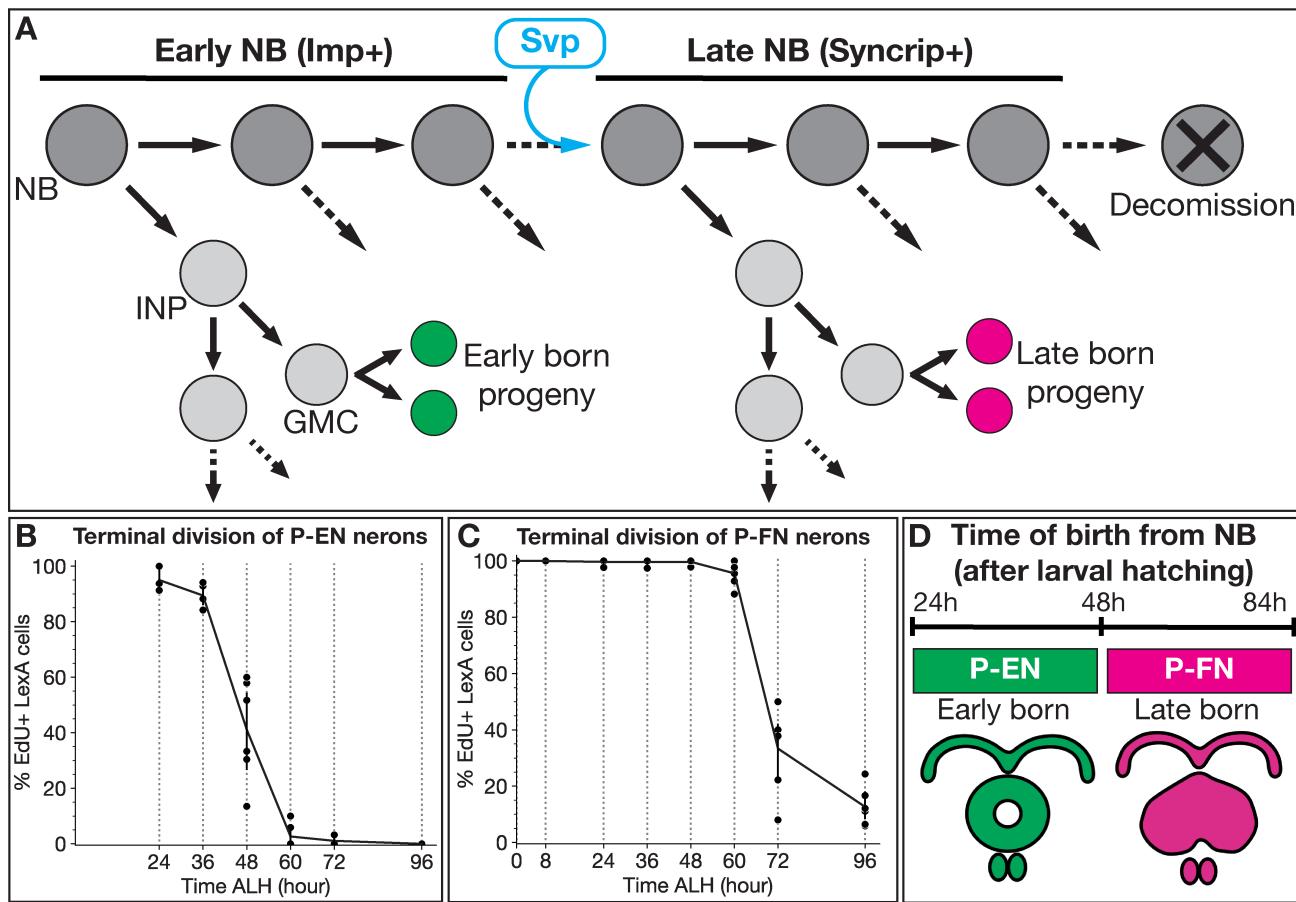
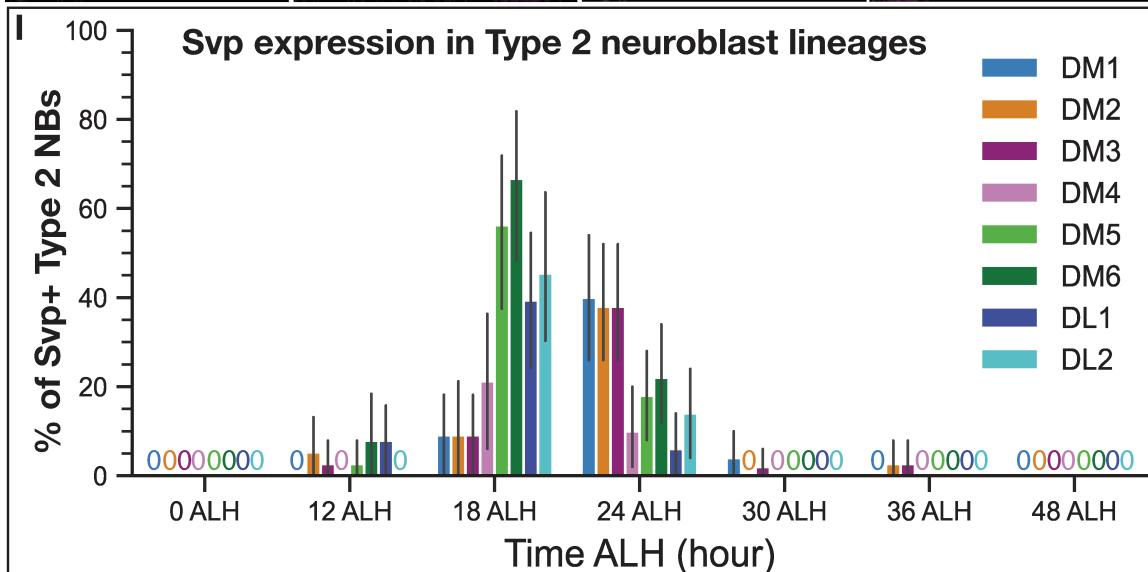
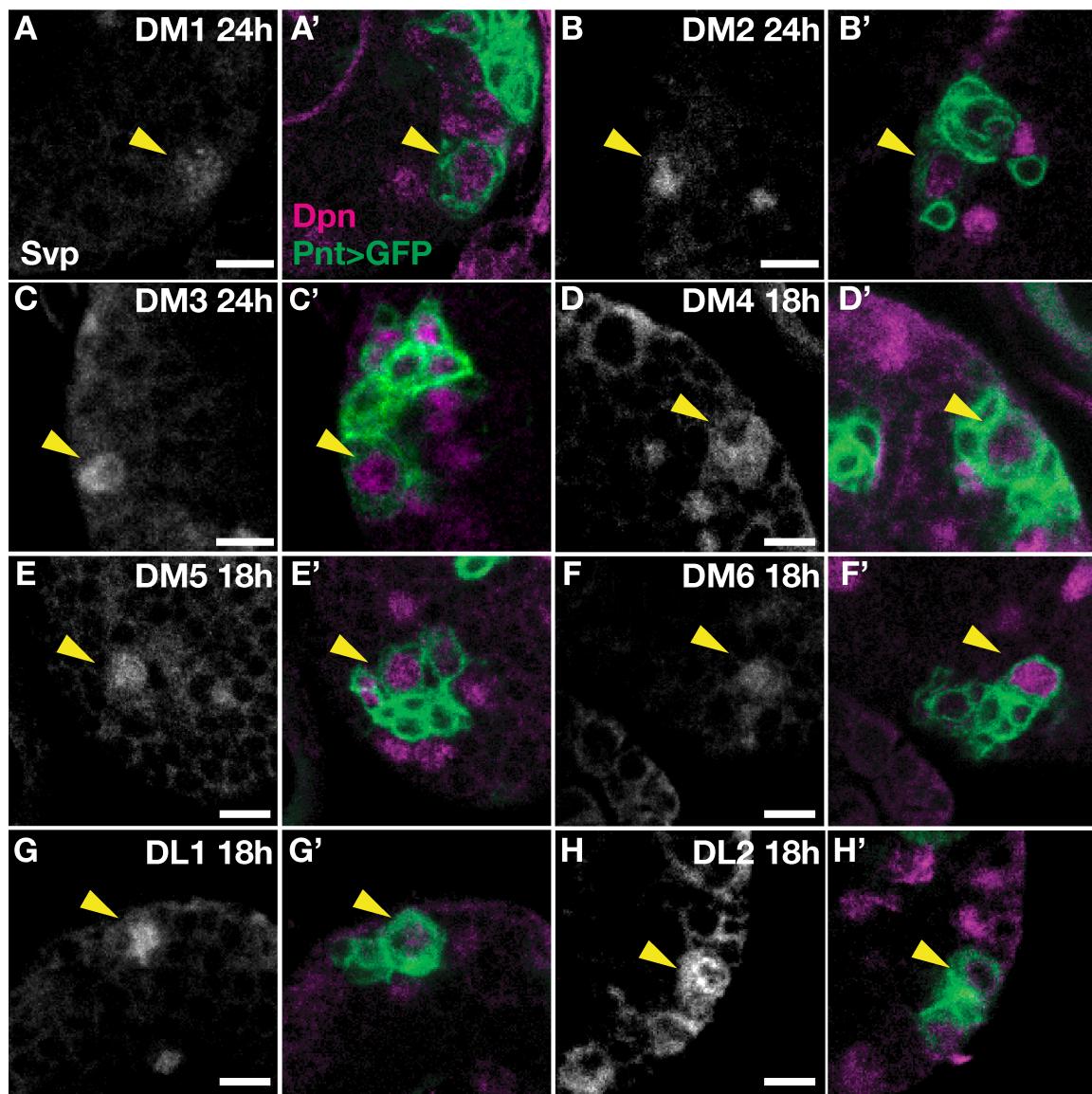


Figure 1. Columnar neuron subtypes are born from larval T2NBs at distinct temporal windows. (A) T2NBs express Imp during early larval stages and transition to Syncrip expression in late larvae due to Svp expression (Ren et al., 2017). All non-mushroom body NBs enter decommissioning in the early pupae (Ito and Hotta, 1992; Maurange et al., 2008; Siegrist et al., 2010; Yang et al., 2017). (B-C) Terminal division by EdU drop out for P-EN neurons (B) and P-FN neurons (C) shown by percent neurons labeled by EdU. Each dot represents one adult brain. For both P-EN and P-FN neurons at each timepoint, $n = 3-7$ brains. (E) Summary of P-EN and P-FN birth windows from larval T2NBs.



673 **Figure 2. Svp is expressed early in all larval T2NB lineages.** (A-C') Svp is expressed at 24h after
674 larval hatching (ALH) in T2NB lineages DM1-3. (D-H') Svp is expressed at 18h ALH in T2NB
675 lineages DM4-6 and DL1-DL2. (A-H) In all images, Svp is in white and T2NBs identified with Pnt-
676 Gal4>GFP and Dpn. Yellow arrowhead, T2NB. (I) Quantification of Svp expression in T2NBs across
677 0h-48h ALH shown as a bar plot with 95% confidence interval. For each lineage, 0 ALH, n = 34; 12
678 ALH, n = 38; 18h ALH, n = 33; 24h ALH, n = 50; 30h ALH, n = 50; 36h ALH, n = 38; 48h ALH, n =
679 49 (DM lineages) or 42 (DL lineages) lobes. Scale bars: 5 μ m.

680

681

682

683

684

685

686

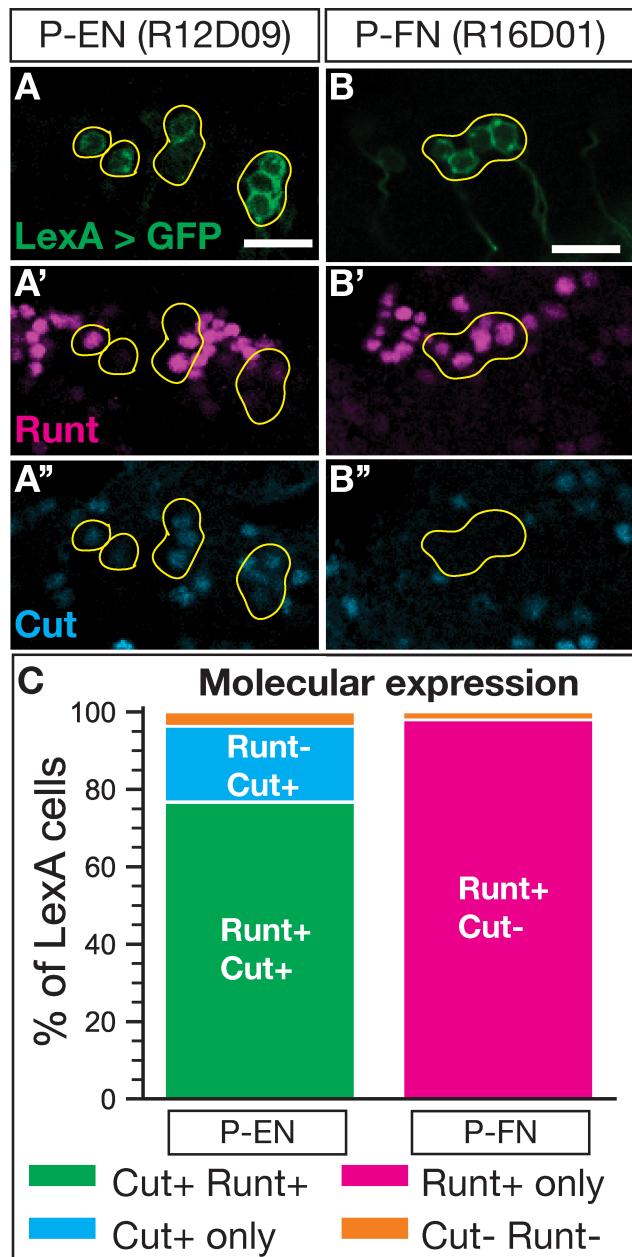


Figure 3. Cut expression distinguishes P-EN and P-FN molecular identities. (A-A') P-EN neurons labeled by LexA driver co-express Runt and Cut. (B-B'') P-FN neurons labeled by LexA driver express Runt but not Cut. (C) Quantification of molecular expression in P-EN and P-FN neurons. P-EN, n = 13; P-FN, n = 6 brains. In all panels, LexA+ neurons in green, Runt in magenta, and Cut in cyan. Yellow outline, neurons of interest. Scale bars: 10 μ m.

687

688

689

690

691

692

693

694

695

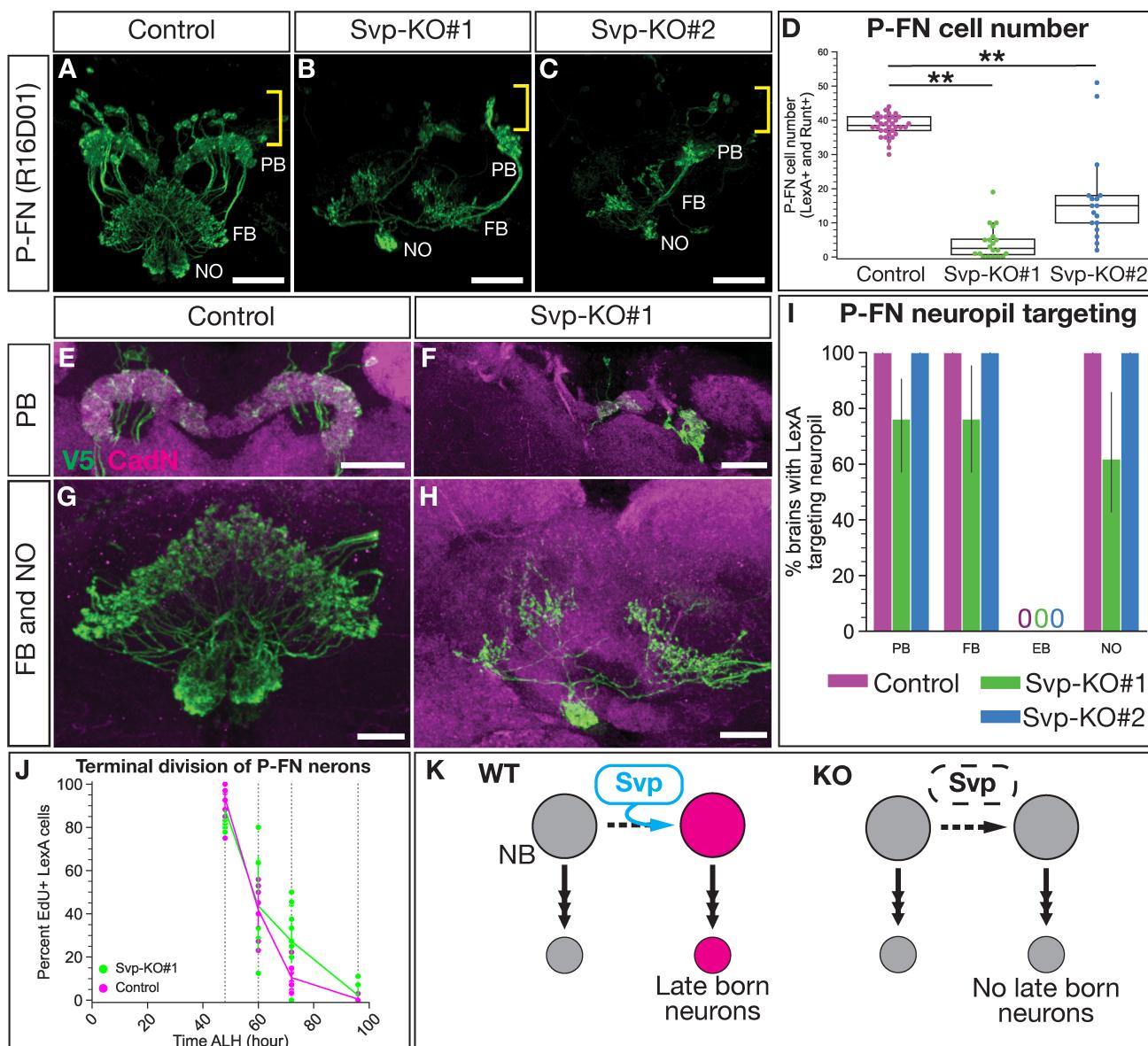


Figure 4. Svp is required for the late born P-FN neuron identity. (A-C) P-FN neurons labeled by LexA driver expressing membrane bound V5 show loss of Svp leads to the loss of P-FN neurons. Yellow brackets show cell body region and white labels of neuropils: Protocerebral bridge (PB), fan-shaped body (FB), and noduli (NO). (D) Quantification of P-FN cell number identified with co-expression of LexA and Runt. Each dot represents one adult brain with box and whisker plot showing distribution. Control, n = 34; Svp-KO#1, n = 20; Svp-KO#2, n = 17. P-values determined by One-way ANOVA, $P < 0.001$, with Tukey post-hoc test: Control versus Svp-KO#1 $P < 0.001$, Control versus Svp-KO#2 $P < 0.001$. (E-F) P-FN neuron PB morphology shows lack of targeting with loss of Svp. (G-H) P-FN neuron FB and NO morphology shows lack of targeting with loss of Svp. (I) Quantification of P-FN neuropil targeting scored based on LexA targeting to neuropils

707 identified with nc82 or CadN shown as a bar plot with 95% confidence interval. Control, n = 35;
708 Svp-KO#1, n = 21; Svp-KO#2, n = 13; 95% confidence interval. (J) P-FN EdU dropout shows P-FN
709 neurons born for Svp-KO escaper neuroblasts are born in a normal NB birth window as shown by
710 percent P-FN neurons labeled by EdU. Each dot represents one adult brain. For all timepoints,
711 Control, n = 11-12; Svp-KO#1 = 5-12 brains. (K) Summary of Svp required for P-FN identity. In all
712 images, LexA+ neurons driving V5 in green and CadN in magenta. Scale bars: (A-C) 20 μ m, (E) 30
713 μ m, (F) 20 μ m, (G-H) 10 μ m.

714

715

716

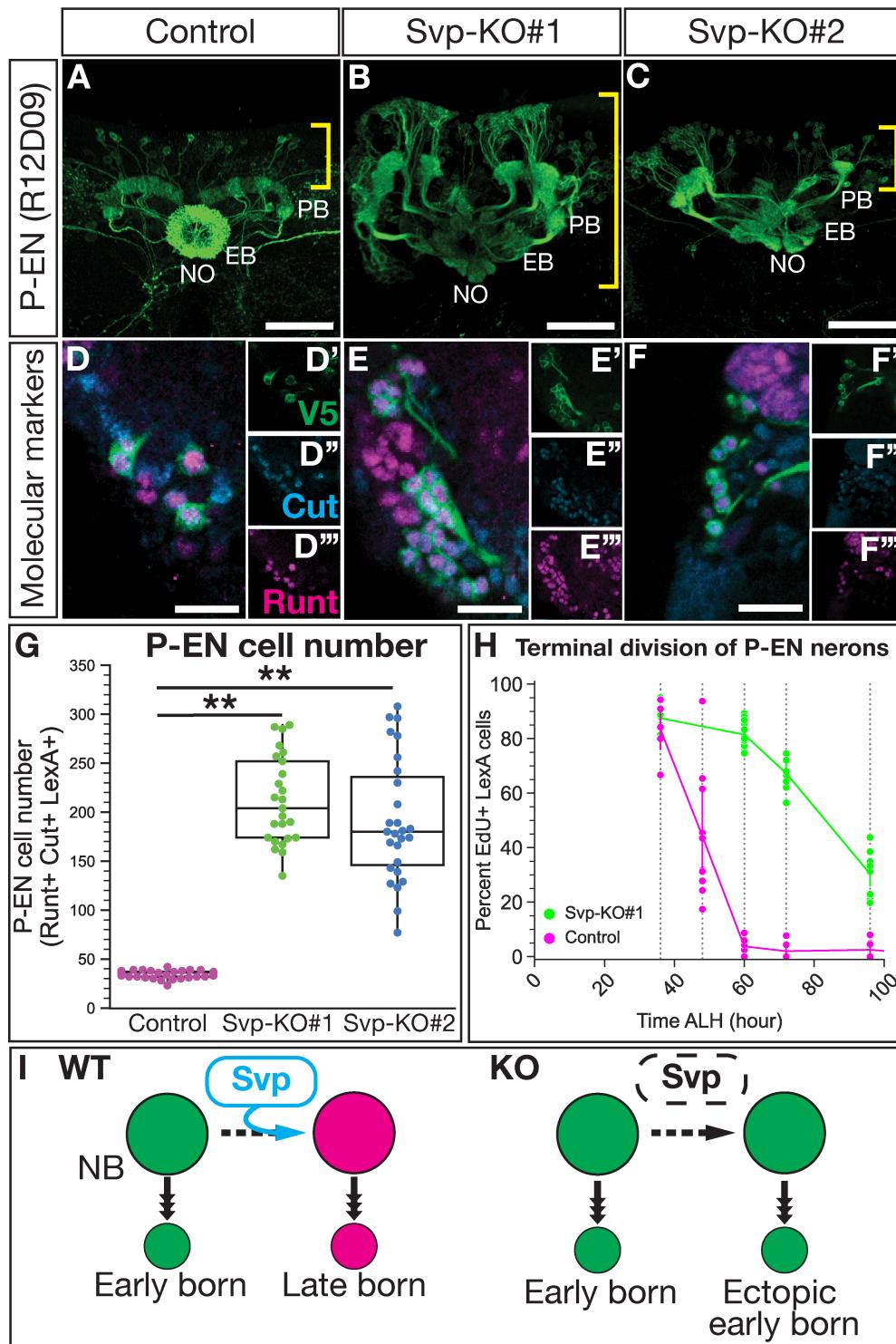


Figure 5. Svp restricts the early born P-EN neuron molecular identity and birth window. (A-C)
 P-FN neurons labeled by LexA drivers show loss of Svp produces ectopic P-EN neurons. Yellow brackets show cell body region and white labels of neuropils: Protocerebral bridge (PB), ellipsoid-body (EB), and noduli (NO). (D-F'') Ectopic neurons maintain expression of P-EN LexA, Cut and

717

718

719

720

721

722 Runt. (G) Quantification of P-EN cell numbers from A-F. Each dot represents one adult brain with
723 box and whisker plot showing distribution. Control, n = 35; Svp-KO#1, n = 25; Svp-KO#2, n = 27
724 brains. *P*-values determined by One-way ANOVA, *P* < 0.001, with Tukey post-hoc test: Control
725 versus Svp-KO#1 *P* < 0.001, Control versus Svp-KO#2 *P* < 0.001. (H) EdU dropout of P-EN
726 neurons show an extended birth window with loss of Svp shown by percent P-EN neurons labeled
727 by EdU. Each dot represents one adult brain. Control, n = 6-10; Svp-KO#1, n = 8-13. (I) Summary
728 of Svp restricting P-EN neuron molecular identity and birth window. In all images, LexA+ neurons
729 driving V5 in green, Runt in magenta, and Cut in cyan. Scale bars: (A-C) 40 μ m, (D-F'') 10 μ m.

730

731

732

733

734

735

736

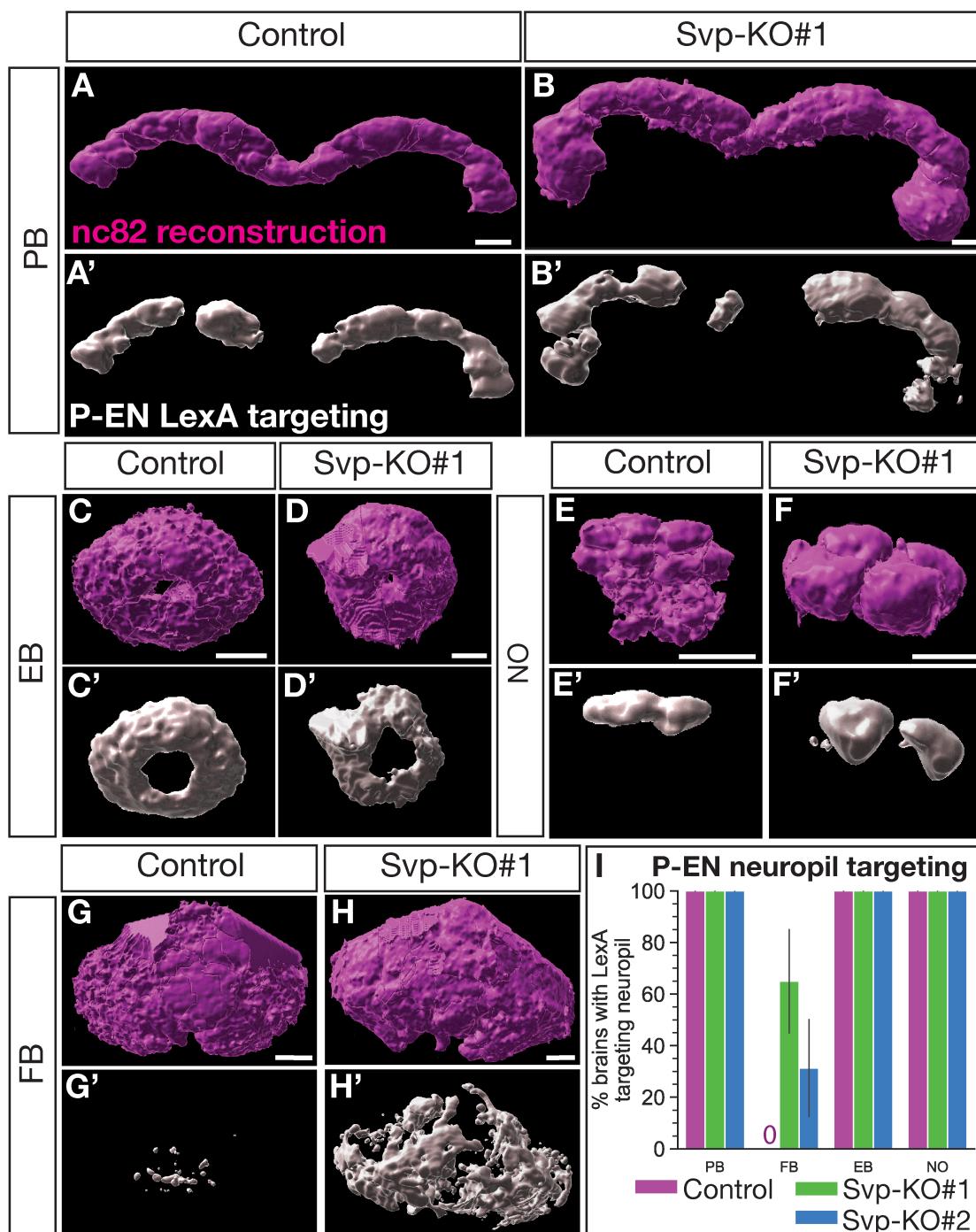


Figure 6. Svp regulates the early born P-EN adult neuron morphology. (A-H') Reconstruction of CX neuropils and P-EN neuron targeting for the protocerebral bridge (PB; A-B'), ellipsoid body (EB; C-D'), noduli (NO; E-F'), and fan-shaped body (FB; G-H'). (I) Quantification of P-EN neuropil targeting scored based on LexA targeting to neuropils identified with nc82 or CadN shown as a bar plot with 95% confidence interval. Control, n = 8; Svp-KO#1, n = 20; Svp-KO#2, n = 16 brains. In all panels, nc82 reconstruction in magenta and P-EN LexA targeting in white. Scale bars: 10 μ m.

737

738

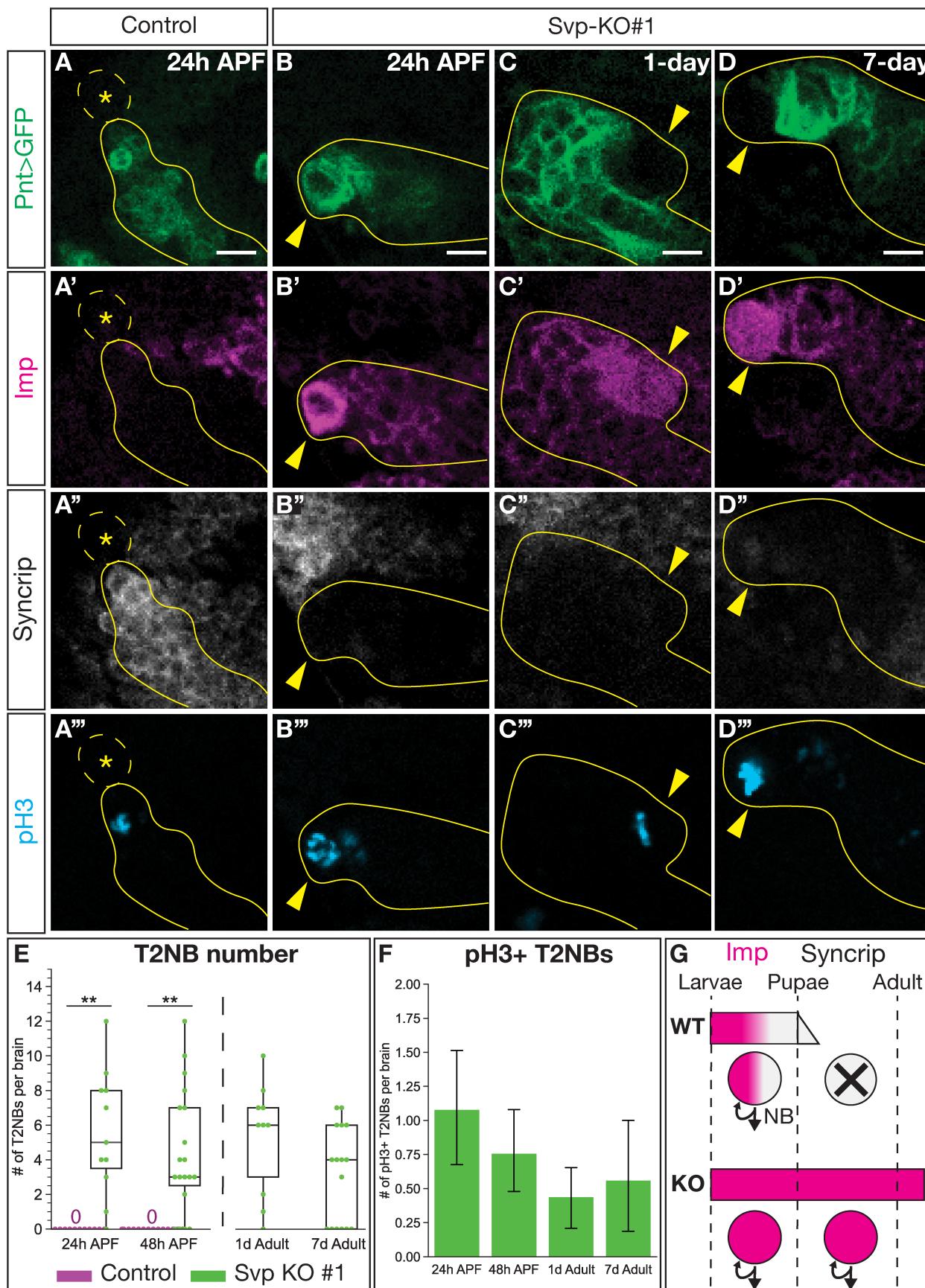
739 CX neuropils and P-EN neuron targeting for the protocerebral bridge (PB; A-B'), ellipsoid body (EB;

740 C-D'), noduli (NO; E-F'), and fan-shaped body (FB; G-H'). (I) Quantification of P-EN neuropil

741 targeting scored based on LexA targeting to neuropils identified with nc82 or CadN shown as a

742 bar plot with 95% confidence interval. Control, n = 8; Svp-KO#1, n = 20; Svp-KO#2, n = 16 brains.

743 In all panels, nc82 reconstruction in magenta and P-EN LexA targeting in white. Scale bars: 10 μ m.



745 **Figure 7. Svp is required for timely onset of T2NB decommissioning.** (A-A'') T2NBs have
746 decommissioned by 24h after pupal formation (APF). (B-D'') Loss of Svp lead to T2NBs remaining
747 with expression of the early factor Imp and no expression of the late factor Syncrip while being
748 mitotically active with expression of pH3 at 24h APF (B-B''), 1-day adult (C-C'') and 7-day adult
749 (D-D''). (A-D) In all images, Type 2 lineage identified with Pnt-Gal4 in green, Imp in magenta,
750 Syncrip in white, and pH3 in cyan. Dashed outline and asterisk, lack of T2NB. Solid yellow outline,
751 Type 2 lineage. Yellow arrowhead, T2NB. (E) Quantification of T2NB number per brain. Each dot
752 represents one brain with box and whisker plot showing distribution. Control 24h APF, n = 16;
753 Svp-KO#1 24h APF, n = 11; Control 48h APF, n = 18; Svp-KO#1 48h APF, n = 19; Svp-KO#1 1d
754 adult, n = 10; Svp-KO#1 7d adult = 16. *P*-values determined by an independent t-test: Control
755 versus Svp-KO#1 at 24h APF $P < 0.001$, at 48h APF $P < 0.001$. (F) Quantification for number of
756 pH3+ ectopic T2NBs remaining in the pupae and adult stages shown as a bar plot with 95%
757 confidence interval. Svp-KO#1 24h APF, n = 37; Svp-KO#1 48h APF n = 25; Svp-KO#1 1d adult, n
758 = 26; Svp-KO#1 7d adult, n = 16. (G) Summary of Svp required for transition of Imp to Syncrip
759 expression in T2NBs for onset of neuroblast decommission. Scale bars: 5 μ m.