Respective contribution of Appl to mushroom body axon growth and long-term memory in *Drosophila*

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Summary

The Amyloid Precursor Protein (APP) is linked to Alzheimer's disease. *Appl* is the single *Drosophila* APP ortholog and is expressed in all neurons throughout development. Appl was previously shown to modulate, cell-autonomously, axon outgrowth in the mushroom bodies (MBs), the fly olfactory memory center. Furthermore, *Appl* knockdown in the MBs results in loss of memory following the association of odorants with electric shocks. Nevertheless, the memory defects of flies devoid of Appl remains unknown because $Appl^{d}$ flies, carrying the only known null allele, show an abnormal response to electric shock. We found that $Appl^{d}$ affects the normal function of *vnd*, the gene just proximal to *Appl*. We report here that *vnd* is required for MB β-branch axon outgrowth. Moreover, *vnd* is expressed in neurons close to, but not within, the MB during development and is required non-cell-autonomously for MB axon outgrowth. To decipher developmental and memory defects specifically due to a loss of only *Appl* function, we generated a precise *Appl* null allele ($Appl^{C2.1}$) by CRISPR/Cas9 genomic engineering. With $Appl^{C2.1}$, we confirmed the partial requirement for *Appl* in MB axon outgrowth but found no defects of electric shock avoidance, allowing us to test for potential memory defects. $Appl^{C2.1}$ flies showed a complete loss of long-term memory which was fully rescued by MB-restricted expression of $Appl^{+}$ only during the adult stage. Therefore, we demonstrate that the complete lack of Appl affects memory independently from structural developmental defects.

Introduction

Alzheimer's disease (AD) is associated with extracellular accumulation of amyloid fibrils derived from the Amyloid Precursor Protein (APP). APPs have therefore been intensely investigated, however their physiological function in the brain remains unclear and controversial [1-3]. Although there are three paralogues in mammals (APP, APLP1 and APLP2), *Drosophila* encodes a

single APP homologue, called *Appl*, that is expressed in all neurons throughout development. It has been shown that the type I transmembrane protein coding gene *Appl* is a conserved neuronal modulator of a Wnt planar cell polarity (Wnt/PCP) pathway, a regulator of cellular orientation within the plane of an epithelium [4]. It has been proposed that Appl is part of the membrane complex formed by the core PCP receptors Fz (*frizzled*) and Vang (*Van Gogh*) [4, 5].

The mushroom bodies (MBs) are two bilaterally symmetric structures in the central brain that are required for learning and memory [6]. Each MB is comprised of 2000 neurons that arise from 4 neuroblasts. Three types of neurons appear sequentially during development: the embryonic/early larval γ, the larval α'β', and the late larval/pupal αβ type. Each αβ neuron projects an axon that branches to send an α branch dorsally, which contributes to the formation of the α lobe, and a β branch medially, which contributes to the formation of the β lobe [7]. So far, $Appl^{d}$ is the only reported null *Appl* allele and it results from a synthetic genomic deletion removing the *Appl* locus [8]. The $Appl^{d}$-bearing chromosome was selected, after γ irradiation, as a translocation of a partial duplication of the X chromosome on the Y chromosome to a X chromosome terminal deficiency (S1 Fig). $Appl^{d}$ flies are viable, fertile and display no gross structural defects in the brain [8]. However, the *Appl* signaling pathway is required for proper axon outgrowth in the MBs since $Appl^{d}$ flies display modestly-penetrant axonal defects in αβ neurons. In particular, Appl is required cell-autonomously for β-branch axon outgrowth [4, 9]. Using *in vivo* inducible RNA interference strategies, it was shown that Appl knockdown in the MBs results in loss of memory following the association of odorants with electric shocks [10]. Nevertheless, the memory defect of *Appl* null flies cannot be assessed for aversive memory because $Appl^{d}$ flies, unlike wild-type flies, show an abnormal response to electric shock [8].

The *ventral nervous system defective* (*vnd*) gene, which is immediately proximal to *Appl*, encodes a Nk2-class homeodomain transcription factor, that acts in a context-dependent manner as an activator or repressor and is essential for the development of the nervous system. The *vnd* gene encodes two proteins: Vnd-A and Vnd-B whose mRNAs arise from two different promoters. These two proteins differ in their aminoterminal domains and are identical in the remainder of their sequences. While Vnd-A is a transcription repressor from promoters containing Nk-2 binding sites, Vnd-B directly activates transcription [11]. Flies bearing a null allele of *vnd* in hemi- or homozygous condition are embryonic lethal [12].

Interestingly, we found that the $Appl^{d}$ chromosome also genetically affects *vnd* function. To genetically dissect *Appl* and *vnd* functions, we generated CRISPR alleles that precisely deletes the *Appl* gene without affecting *vnd* function ($Appl^{C2.1}$) and that precisely deletes each one of the two *vnd* transcripts without affecting *Appl* ($vnd^{C\Delta A}$ and $vnd^{C\Delta B}$). We showed here that *vnd-A,* but not *vnd-B,* is also required for MB β-branch axon outgrowth. Unexpectedly, *vnd* is expressed in neurons close to, but not within, the MB during development and is required non-cell-autonomously, likely by promoting the production of one (or several) secreted factor(s) involved in the MB axon outgrowth. To analyze the exact developmental and memory defects due to the specific loss of the *Appl* function only, we used $Appl^{C2.1}$ and first confirmed the partial requirement of *Appl* in MB β-branch axon outgrowth. Interestingly, $Appl^{C2.1}$ flies, in contrast to $Appl^{d}$ flies, showed a normal response to electric shock but a complete loss of long term memory independently from potential defects during brain development.

Results

86
87 **Generating new *Appl* CRISPR alleles**
88 The complex chromosome structure associated with $Appl^{d}$ complicates its subsequent genetic
89 manipulation (S1 Fig). Therefore, we intended to produce new null *Appl* alleles by removing the
90 entire *Appl* transcriptional unit via CRISPR/Cas9-mediated deletion [13]. We recovered $Appl^{C1.4}$
91 and $Appl^{C2.1}$, two CRISPR *Appl* null alleles (Fig 1 and S2 Fig), following an adaptation of a published
92 protocol in order to produce circa 50kb deletions [14]. $Appl^{d}$ MBs display a modestly-penetrant
93 cell-autonomous axon growth defect of the β-branches which manifests as an absence of the β
94 lobe [4, 5]. Surprisingly, we found a strong difference in the penetrance of the absence of the β
95 lobe phenotype in the two *Appl* CRISPR alleles. Although 9% of $Appl^{C2.1}$ MBs lacked the β lobe ,
96 slightly lower than the 14.5% described for $Appl^{d}$ [15], $Appl^{C1.4}$ MBs displayed a much higher
97 penetrance (66%) of this phenotype (Fig 1). We determined the precise deletions present in the
98 two alleles via sequencing and found that while the $Appl^{C2.1}$ deletion precisely removed the *Appl*
99 transcriptional unit, the $Appl^{C1.4}$ allele also removed a part of the *vnd* transcriptional unit (Fig 1).
100 We then similarly mapped the $Appl^{d}$ deletion and found that, unlike $Appl^{C2.1}$, it removes most of
101 the intergenic region between *Appl* and *vnd* which may influence *vnd* function (Fig 1). We then
102 assessed, by genetic complementation tests, if the different *Appl* null alleles possibly affected *vnd*
103 function. We used vnd^{A} a molecularly-characterized lethal allele which impacts both *vnd-B* and
104 *vnd-A* transcripts (Fig 2) [16]. Although $Appl^{C2.1}/vnd^{A}$ MBs displayed no anatomical MB
105 phenotypes, $Appl^{d}/vnd^{A}$ and $Appl^{C1.4}/vnd^{A}$ MBs displayed 14% and 69% of β lobe absence,
106 respectively (Fig 2). Flies heterozygous for any of the four mutations displayed no MB phenotypes:
107 vnd^{A}/+ (n = 72), $Appl^{C1.4}$/+ (n = 60), $Appl^{C2.1}$/+ (n = 42) and $Appl^{d}$/+ previously described [4].
108 Therefore, $Appl^{d}$ and $Appl^{C1.4}$ but not $Appl^{C2.1}$ affect *vnd* functions in MB development. Taken
109 together, these data strongly suggest that *vnd*, the gene just proximal to *Appl*, is also involved in
110 the MB β-branch axon growth and likely to a much greater extent than *Appl* itself.
111
112 **Generation of new *vnd* CRISPR alleles deleted either for the *vnd-B* or for the *vnd-A* function**
113 There are two *vnd* transcripts, *vnd-A* and *vnd-B* that produce two different Vnd proteins,
114 respectively Vnd-A and Vnd-B (Fig 2). It was proposed that, while Vnd-A has a main role during
115 embryogenesis, Vnd-B is associated with metamorphosis [11]. In order to determine which Vnd
116 isoform is required for MB β-branch axon growth, we produced the new *vnd* alleles $vnd^{C\Delta A}$ and
117 $vnd^{C\Delta B}$ by CRISPR/Cas9 genomic engineering that eliminate either the *vnd-A* or the *vnd-B* isoform,
118 respectively (Fig 3 and S3 Fig). Males bearing a $vnd^{C\Delta B}$ mutant allele ($vnd^{C\Delta B}$/Y), as well as $vnd^{C\Delta B}$/
119 $Appl^{C1.4}$ females, are viable and have essentially wild-type MBs (Fig 3). Males bearing a $vnd^{C\Delta A}$
120 mutant allele ($vnd^{C\Delta A}$/Y) are embryonic lethal similarly to other *vnd* null alleles (vnd^{A}, $vnd^{\Delta 38}$ and
121 vnd^{6}) which affect both isoforms. Also, $Appl^{C1.4}/vnd^{C\Delta A}$ female MBs displayed a strong phenotype
122 of β lobe absence with a penetrance (64%) similar to those of $Appl^{C1.4}/vnd^{A}$ female MBs (Fig 4).
123 Genetically, $Appl^{C1.4}/vnd^{C\Delta A}$; *Dp-*$Appl^{+}$/+ females have two wild-type doses of $Appl^{+}$ and the β lobe
124 absence phenotype (69%) was not distinguishable from that observed in $Appl^{C1.4}/vnd^{C\Delta A}$; +/+
125 females (64%) and therefore be entirely due to *vnd* lack-of-function. Supporting this hypothesis,
126 we observed a complete rescue when an extra dose of vnd^{+} is supplied in $Appl^{C1.4}/vnd^{C\Delta A}$; *Dp-*
127 vnd^{+}/+ females (Fig 4). $Appl^{C1.4}$/Y males have no $Appl^{+}$ function (null allele) and also display
128 reduced vnd^{+} function. Moreover, $Appl^{C1.4}$/Y male MB phenotype is moderately rescued by the
129 presence of an extra dose of $Appl^{+}$ and strongly rescued by an extra dose of vnd^{+} (Fig 4). Taken

together, these results strongly indicate that the *vnd-A* transcript but not the *vnd-B* transcript is specifically required for MB β-branch axon growth.

Vnd is expressed around the MBs and is not required within the MBs

In order to know where *vnd* is expressed, we employed a *vnd-T2A-GAL4* line where GAL4 is under the control of endogenous *vnd* regulatory sequences via CRISPR gene targeting so that GAL4 and *vnd* are translated from the same mRNA transcript [17, 18]. UAS-GFP labelling revealed a pattern in the ventral ganglion of the third larval instar central nervous system (L3 CNS) similar to that described with immunostaining with antibodies against Vnd [11] thus validating the use of the *vnd-T2A-GAL4* line as a *bona fide vnd* reporter (S4 Fig). GFP was detected, in the developing brain, close to the MBs visualized by anti-Fas2 staining, from L3 to 24 h after puparium formation (APF) (Fig 5A,A'- 5D,D'). Staining reveals two different morphological structures: one organized in a honeycomb pattern and one containing filamentous structures with neurite appearance. To determine the identity of the honeycomb structures, we performed DAPI staining at the L3 stage. We observed a significant DAPI staining in these structures indicating that they likely correspond to cell nuclei (Fig 5EE'). Moreover, these cell nuclei are Vnd positive and Repo negative (Fig 5F,F'- 5G,G') indicating that these cells correspond to neurons, rather than glia. The neurites corresponding to these cell nuclei are very close to the developing MB medial lobe from which the adult β lobe develops (Fig 5). Noticeably, we could not observe any GFP labeling within the MBs themselves. This unexpected expression pattern suggests a non-cell-autonomous role for Vnd in the MB β-branch axon growth. We tested this hypothesis by MARCM mosaic analysis which allows the generation of homozygous *vnd* loss-of-function MB clones in an otherwise heterozygous genetic background and overcome organismal lethality [7, 19]. Mitotic recombination was induced in late-stage embryos/early first instar larvae and the clones were analyzed at the adult stage. We obtained 20 MB $vnd^{A/A}$ clones that include the αβ neurons. All the 20 *vnd* mutant clones displayed a β-branch axon growth that looked identical to that in wild-type clones (S5 Fig). Moreover, we obtained similar results, namely a normal β-branch axon growth, with two additional different null alleles, $vnd^{\Delta 38}$ (8 clones) and vnd^{6} (4 clones) (S5 Fig). Taken together, these results demonstrate that, although *vnd* function is strongly required for MB β-branch axon growth, *vnd* is neither required nor expressed in the MBs themselves. Therefore, it is most likely that Vnd regulates MB axon growth by a non-cell-autonomous mechanism.

***Appl*-null flies have no long-term memory strictly due to the absence of Appl in adult MBs**

Although it is clear that *Appl* function is required for aversive olfactory memory, it has not yet been possible to assess the memory of Appl-null flies , because $Appl^{d}$ flies exhibit impaired electric shock avoidance [8, 20]; In such flies a defect in the aversive memory assay could result from an impairment in electric shock perception during conditioning and therefore not represent true memory defects. We showed here that $Appl^{d}$ also affects *vnd* function (Fig 2) and hence wondered if this impairment in electric shock avoidance was really due to the lack of the *Appl* function itself. In order to test this hypothesis, we evaluated the long-term memory (LTM) performance of $Appl^{C2.1}$/Y flies which are null for *Appl* but wild-type for *vnd*. The electric shock avoidance and olfactory acuity appears wild-type in $Appl^{C2.1}$ flies (Fig 6). Interestingly, $Appl^{C2.1}$ flies showed a complete loss of LTM, and this memory defect was fully rescued by the restricted expression of an *UAS-Appl* transgene in adult MBs (Fig 6). No rescue was detected in the non-induced 18°C

controls (S6 Fig). These results conclusively demonstrate that the specific and complete loss of Appl affects long-term memory independently from any potential defects during brain development.

Discussion

It has been proposed that Appl is part of the membrane complex formed by the core PCP proteins Fz and Vang [4]. *Appl*^{d} was, previous to this report, the only *Appl* null allele described. *Appl*^{d} mutant flies are completely lacking Appl function and exhibit 14.5 % MB β-lobe loss [15] in accordance with what has been reported [4, 5]. This modestly-penetrant axonal phenotype due to the lack of Appl could be due to partially redundant function provided by the other transmembrane receptors of the complex. In particular, flies homozygous for the loss of function allele *Vang*$^{stbm-6}$ exhibit 50% β-lobe loss [5]. As the *Appl*^{d} allele involves complex chromosomic rearrangements [8], we decided to leverage CRISPR in order to produce a definitive deletion of around 50 kb to specifically eliminate the *Appl* transcriptional unit. We recovered two *Appl* complete deletions: *Appl*$^{C1.4}$ and *Appl*$^{C2.1}$ removing around 52 kb and 48 kb and exhibiting 66 % and 9 % β-lobe loss respectively. DNA sequences analysis revealed that, while the *Appl*$^{C2.1}$ deletion removes only *Appl* sequences, the *Appl*$^{C1.4}$ deletion additionally removes a part of the proximally located transcriptional unit corresponding to the *vnd* gene (Fig 1). This indicates that in addition to Appl, *vnd* is likely involved in the β-branch axon outgrowth. Moreover, as can be expected from the extent of the deletions and based on genetic complementation tests, *Appl*$^{C1.4}$ deletion, but not *Appl*$^{C2.1}$ deletion, affects *vnd* function. Most importantly, the *Appl*^{d} deletion, which removes most of the Appl coding sequence and also the intergenic region between *Appl* and *vnd*, also affects *vnd* function (Fig 1 and 2). The role of *vnd* in β-branch axon outgrowth is complicated by the fact that the *vnd* viable mutant alleles (*Appl*^{d} *and Appl*$^{C1.4}$ deletions), are associated with the lack of *Appl* function. Nevertheless, employing a small (less than 100 kb) genomic *Appl*$^{+}$ duplication, we found that flies lacking only *vnd* function exhibit 69% β-lobe loss that is completely rescued by a small genomic *vnd*$^{+}$ duplication (Fig 4). This demonstrates the requirement of *vnd* function for MB β-branch axon outgrowth. To better understand the roles of both Vnd isoforms in the MB β-branch axon outgrowth, we produced two mutations, *vnd*$^{C\Delta B}$ and *vnd*$^{C\Delta A}$, which remove the *vnd-B* and the *vnd-A* transcript respectively (Fig 3 and S3 Fig). Surprisingly, although Vnd-A has a significant role in MB axon growth, apparently Vnd-B plays little to no role in this process. Noticeably, MB phenotype of *Appl*$^{C1.4}$/*vnd*$^{C\Delta A}$ flies is similar in penetrance to the one of *Appl*$^{C1.4}$/*vnd*^{A}, indicating that the lack of *vnd-A* function seems to have the same effect than the complete lack of both *vnd* functions.

It may have been anticipated that Vnd, a transcription factor, was required within the MBs and was probably being part of the Appl signaling pathway in order to act on axon growth. Consequently, Vnd should have been expressed within the MBs and the *vnd* function was expected to be cell-autonomous. However, endogenous *vnd* transcription monitored by GAL4 expression that is translated from the same mRNA transcript and validated by an anti-Vnd antibody show no sign of expression within the MBs. Rather, *vnd* is transcribed within a neuronal brain structure in close proximity to the developing MB medial lobe from which the adult β lobe develops (Fig 5). Also, using MARCM mosaic analysis, we show that β axons extended from MB clones null for *vnd* function exhibit wild-type growth patterns (S5 Fig) demonstrating a non-cell-

218 autonomous requirement for Vnd. Therefore, we favor the hypothesis where *vnd* expressed in a
219 MB surrounding brain structure is generating, directly or indirectly, one or several secreted
220 factors that will act on the axon growth of the developing β medial lobe.
221 Prior to this study, it was not possible to evaluate the effects of a complete lack of *Appl* in
222 aversive olfactory memory due to the failure of $Appl^{d}$ mutants to show normal shock reactivity
223 [8, 20]. It was therefore hypothesized that it was the lack of Appl *per se* which was the cause of
224 this impairment in electric shock avoidance. We reevaluated this hypothesis with the $Appl^{C2.1}$
225 allele which removes only the *Appl* function. Flies bearing only a deletion of *Appl* react normally
226 to electric shock and olfactory cues similarly to control flies but show a total lack of 24h memory
227 after a long-term conditioning (Fig 6). Therefore, it is not the lack of *Appl* function in the $Appl^{d}$
228 mutants which is the origin of the impairment in electric shock avoidance. Importantly, the
229 memory defect can be completely rescued by the expression of $Appl^{+}$ solely in the post-
230 development adult MBs. This demonstrates that a complete lack of *Appl* results in a specific
231 memory defect independently of any role that Appl might have in the developing brain.
232 Consequently, the modest mutant MB axonal growth morphological phenotype displayed by the
233 $Appl^{C2.1}$ allele likely has no measurable impact on long-term memory. This is in accordance with
234 the requirement of the vertical lobes but not the median lobes in aversive long-term memory
235 [21].
236 The accumulation of amyloid-β (Aβ) is a hallmark feature of AD [22, 23]. Nevertheless, the
237 production of Aβ peptides is at the expense of the full-length APP protein levels, whose roles in
238 AD are, as yet, unclear. The *Drosophila* memory defect due to the complete lack of *Appl* may
239 therefore be relevant to the memory defects associated with human AD. Therefore, our
240 observation that the memory defect resulting from the complete lack of *Appl* could be completely
241 rescued by the expression of $Appl^{+}$ in a specific adult brain region, thus bypassing any potential
242 role of APPL in development could be of significance to our understanding of the molecular basis
243 of AD.
244

245 ## Materials and methods

246

247 ### *Drosophila* stocks

248 All crosses were performed on standard culture medium at 25˚C. Except where otherwise stated,
249 all alleles and transgenes have been described previously (http://flystocks.bio.indiana.edu/). The
250 following alleles were used: $Appl^{C1.4}$, $Appl^{C2.1}$, $vnd^{C\Delta A}$ and $vnd^{C\Delta B}$ were generated in this study. *Appl-*
251 y^{+} (BL #56073), $Appl^{d}$ (BL #43632), $Vang^{stbm-6}$ (BL #6918) and vnd^{A} (BL #57139), $vnd^{\Delta 38}$ [24](Chu
252 1998), vnd^{6} [12](Jimenez 1995). The following transgenes were used: *UAS-mCD8::GFP* (BL #5137),
253 *UAS-Appl* (BL #38403) and the duplications resulting from genomic transgenes *Dp-Appl*$^{+}$ (BL
254 #32288) and *Dp-vnd*$^{+}$ (BL #30219) both inserted into the same attP site at 65B2. We used three
255 GAL4 lines: *vnd-T2A-GAL4* which reveals *vnd* transcription, *c739-GAL4* (BL #7362) expressed in
256 adult αβ MB neurons [25] and VT30559 expressed in adult MB neurons [26]. Recombinant
257 chromosomes were obtained by standard genetic procedures and were molecularly verified.
258

259 ### CRISPR-Cas9 strategy

260 All guide RNA sequences (single guide RNA (sgRNA)) were selected using the algorithm
261 targetfinder.flycrispr.neuro.brown.edu/ containing 20 nucleotides each (PAM excluded) and are

262 predicted to have zero off-targets. We selected one pair of sgRNA for the *Appl* gene and two pairs
263 of sgRNA for the *vnd* gene. For *Appl*, the pair is targeting the all transcriptional unit (S2 Fig). For
264 *vnd*, each pair is targeting either the A specific region of *vnd* or the B specific region of *vnd* (S3
265 Fig). We used the following oligonucleotide pairs: CRISPR-1 Appl fwd and CRISPR-1 Appl rev to
266 target the all *Appl* region, CRISPR-1 vnd A fwd and CRISPR-1 vnd A rev to target the A region of
267 *vnd*, CRISPR-1 vnd B fwd and CRISPR-1 vnd B rev to target the B region of *vnd* (see the
268 corresponding oligonucleotide sequences in S2 and S3 Fig.). We introduced two sgRNA sequences
269 into pCFD4 [14], a gift from Simon Bullock (Addgene plasmid # 49411) by Gibson Assembly (New
270 England Biolabs) following the detailed protocol at crisprflydesign.org. For PCR amplification, we
271 used the protocol described on that website. Construct injection was performed by Bestgene
272 (Chino Hills, CA) and all the transgenes were inserted into the same attP site (VK00027 at 89E11).
273 Being aware that the DNA excision of nearly 50 kb might be rare, we have decided to use a positive
274 screen before validation by genomic PCR. We have used a stock where the *Appl* gene is marked
275 by a y^+ construct. The deletion of the *Appl* gene should therefore be associated to y^- phenotype.
276 Transgenic males expressing the *Appl* sgRNAs and bearing an isogenized X chromosome (*y Appl-*
277 *y^+ Act-Cas9 w**) were crossed to *FM7c/ph^0 w* females. 180 crosses were set up and only two
278 crosses gave rise to *y $Appl^{deletion?}$ Act-Cas9 w*/FM7c* females indicating 1% of CRISPR efficacy.
279 From each of these two crosses, a single *y $Appl^{deletion}$ Act-Cas9 w* /FM7c* female was crossed with
280 *FM7c* males to make a stock (*$Appl^{C1.4}$* and *$Appl^{C2.1}$* where Cas9 was removed). The deletion were
281 then validated by genomic PCR using two couples of primers: *$Appl^{C1.4}$* fwd
282 (GAGCCAGATACACAAGCACA) / *$Appl^{C1.4}$* rev (GGCTTTGTTTACTTCCTGGC) and *$Appl^{C2.1}$* fwd
283 (TCCTACTACGTTCCACAATC) / *$Appl^{C2.1}$* rev (TAATGCCCAACATATCCAAC). The precise endpoints of
284 the deletion were determined by sequencing (Genewiz, France). Transgenic males expressing the
285 different *vnd* sgRNAs were crossed to *y nos-Cas9 w** females bearing an isogenized X
286 chromosome. 100 crosses were set up for each sgRNA pair, with up to 5 males (because of poor
287 viability) containing both the sgRNAs and *nos-Cas9,* and 5 *FM7c/ph^0 w* females. From each
288 selected cross, a single *y $vnd^{deletion?}$ nos-Cas9 w* /FM7c* female was crossed with *FM7c* males to
289 make a stock which was validated for the presence of an indel by genomic PCR with primers
290 flanking the anticipated deletion and the precise endpoints of the deletion were determined by
291 sequencing (Genewiz, France) using *vnd*-specific primers: *$vnd^{C\Delta A}$* fwd (ccaacaaagccgagagtctct) /
292 *$vnd^{C\Delta A}$* rev (cgggaatttctaagccagggt) and *$vnd^{C\Delta B}$* fwd (cgatttggggcgttgtgagta) / *$vnd^{C\Delta B}$* rev
293 (gttgggctttaatccgggagt). A CRISPR efficacy of at least 5% was obtained in both cases. We kept a
294 single stock from each set of CRISPR experiment: *$vnd^{C\Delta A}$* and *$vnd^{C\Delta B}$* where Cas9 was removed.
295

296 **Brain dissection, immunostaining and MARCM mosaic analysis**

297 Adult fly heads and thoraxes were fixed for 1 h in 3.7% formaldehyde in phosphate-buffered
298 saline (PBS) and brains were dissected in PBS. For larval and pupal brains, brains were first
299 dissected in PBS and then fixed for 15 min in 3.7% formaldehyde in PBS. They were then treated
300 for immunostaining as described [19, 27]. Antibodies, obtained from the Developmental Studies
301 Hybridoma Bank, were used at the following dilutions: Mouse monoclonal anti–Fas2 (1D4) 1:10 ,
302 mouse monoclonal anti-Repo (8D1.2) 1:10 and guinea pig polyclonal anti-vnd (1/1000). Goat
303 secondary antibodies conjugated to Cy3 against mouse or guinea pig IgG (Jackson
304 Immunoresearch laboratory) were used at 1:300 for detection. DAPI (Sigma) was used after
305 secondary antibody washes. Tissues were incubated 10 minutes at room temperature in a 1/1000

solution from a stock containing 1 mg/ml of DAPI solution, then washed. To generate clones in the MB, we used the MARCM technique [19]. First instar larvae were heat-shocked at 37°C for 1 h. Adult brains were fixed for 15 min in 3,7% formaldehyde in PBS before dissection and GFP visualization.

Production of the anti-Vnd antiserum

Full length vnd-RA was amplified via PCR from cDNA and cloned into a pRSET bacterial expression vector (ThermoFisher) in frame with an N-terminal 6x-His tag, amplified in DH5alpha and transformed into BL21 competent cells for protein production. His-tagged VndA was purified over a Nickel-NTA agarose resin (Qiagen) according to manufacturer's recommendation. Purified protein was injected into guinea pigs by Squarix GmbH (Marl, Germany, www.squarix.de), selected by assuring that pre-bleeds did not produce signal in Western blots of fly extracts. Successive bleeds were screened for distinct signal in Western blots using embryo extracts and by immunohistochemistry, where signal was expected post 2.5hrs AED.

Behavior experiments

For behavior experiments, flies were raised on standard medium at 18°C and 60% humidity in a 12-h light/dark cycle. We used the TARGET system [28] to inducibly express UAS-*Appl*$^{+}$ construct exclusively in adult flies and not during development. 0-3 day old flies were transferred to fresh bottles containing standard medium and kept at 30.5°C for 2 days before conditioning. For non-induced experiments, flies were transferred to fresh bottles containing standard medium and kept at 18°C before conditioning. All the behavior experiments, including the sample sizes, were conducted similarly to other studies [29]. Groups of 20-50 flies were subjected to olfactory conditioning protocol consisting of five associative cycles spaced by 15min inter-trial intervals (5x spaced training). Conditioning was performed at 25°C using previously described barrel-type machines that allow the parallel training of up to 6 groups [21]. Throughout the conditioning protocol, each barrel was plugged into a constant air flow at 2 L/min. For a single cycle of associative training, flies were first exposed to an odorant (the CS+) for 1 min while 12 pulses of 5s long 60 V electric shocks were delivered; flies were then exposed 45 s later to a second odorant without shocks (the CS-) for 1 min. The odorants 3-octanol (Fluka 74878, Sigma-Aldrich) and 4-methylcyclohexanol (Fluka 66360, Sigma-Aldrich), diluted in paraffin oil to a final concentration of 2.79·10-1 g/L, were alternately used as conditioned stimuli. During unpaired conditionings, the odor and shock stimuli were delivered separately in time, with shocks occurring 3 min before the first odorant. Flies were kept at 18°C on standard medium between conditioning and the memory test. The memory test was performed at 25°C in a T-maze apparatus [30](Tully 1985), 24 h after spaced training. Each arm of the T-maze was connected to a bottle containing 3-octanol and 4-methylcyclohexanol, diluted in paraffin oil to a final concentration identical to the one used for conditioning. Flies were given 1 min to choose between either arm of the T-maze. A performance score was calculated as the number of flies avoiding the conditioned odor minus the number of flies preferring the conditioned odor, divided by the total number of flies. A single performance index value is the average of two scores obtained from two groups of genotypically identical flies conditioned in two reciprocal experiments, using either odorant (3-octanol or 4-methylcyclohexanol) as the CS^{+}. The indicated 'n' is the number of independent performance index values for each genotype. The shock response tests were performed at 25°C by placing flies

350 in two connected compartments; electric shocks were provided in only one of the compartments.
351 Flies were given 1 min to move freely in these compartments, after which they were trapped,
352 collected, and counted. The compartment where the electric shocks were delivered was
353 alternated between two consecutive groups. Shock avoidance was calculated as for the memory
354 test. Because the delivery of electric shocks can modify olfactory acuity, our olfactory avoidance
355 tests were performed at 25°C on flies that had first been presented another odor paired with
356 electric shocks. Innate odor avoidance was measured in a T-maze similar to those used for
357 memory tests, in which one arm of the T-maze was connected to a bottle with odor diluted in
358 paraffin oil and the other arm was connected to a bottle with paraffin oil only. Naive flies were
359 given the choice between the two arms during 1 min. The odor-interlaced side was alternated for
360 successively tested groups. Odor concentrations used in this assay were the same as for the
361 memory assays. At these concentrations, both odorants are innately repulsive.
362
363 **Microscopy and image processing**
364 Images were acquired at room temperature using a Zeiss LSM 780) equipped with a 40x PLAN
365 apochromatic 1.3 oil-immersion differential interference contrast objective lens and a Leica SP8
366 laser scanning confocal microscopes (MRI Platform, Institute of Human Genetics, Montpellier,
367 France. The immersion medium used was Immersol 518F. The acquisition software used was Zen
368 2011 (black edition) for the Zeiss and LasX for the Leica. Contrast and relative intensities of the
369 green (GFP), of the red (Cy3) and of the DAPI channels were processed with ImageJ (Fiji) software.
370 Settings were optimized for detection without saturating the signal.
371
372 **Statistics**
373 Comparison between two groups expressing a qualitative variable was analyzed for statistical
374 significance using the Chi^2 test. (BiostaTGV: http://biostatgv.sentiweb.fr/?module=tests). For
375 behavior experiments, all data are presented as mean ± SEM. 2 groups of about 30 flies were
376 reciprocally conditioned, using respectively octanol or methylcyclohexanol as the CS^+. The
377 memory score was calculated from the performance of two groups as described above, which
378 represents a single experimental replicate. Comparisons of the data series between two
379 conditions were achieved by a two-tailed unpaired t-test. Comparisons between more than two
380 distinct groups were made using a one-way ANOVA test, followed by Tukey pairwise comparisons
381 between the experimental groups and their controls. ANOVA results are presented as the value
382 of the Fisher distribution F(x,y) obtained from the data, where x is the number of degrees of
383 freedom between groups and y is the total number of degrees of freedom for the distribution. In
384 the figures, asterisks illustrate the significance level of the t-test, or of the least significant
385 pairwise comparison following an ANOVA. Values of $p < 0.05$ were considered to be significant.
386 Statistical significance was defined as: ns = not statistically different, **p<0.01 and****p<0.0001.
387
388
389 ## Figure legends
390
391 **Fig 1. Generating new *Appl* CRISPR alleles.**
392 (A) Schematic representation of *Appl* (blue) and *vnd* (green) genes and transcripts. White boxes
393 represent 5'UTR and 3'UTR, blue and green boxes represent *Appl* and *vnd* coding sequences

394 respectively. Schematic representations of the *Appl*^{d}, *Appl*$^{C1.4}$ and *Appl*$^{C2.1}$ mutant alleles where
395 the deleted sequences are represented in light blue. The hatched black segment represents the
396 uncertainty where the deletion of *Appl*^{d} starts in 5'. (B) Representation of the 3' limit of the *Appl*^{d},
397 *Appl*$^{C1.4}$ and *Appl*$^{C2.1}$ mutant alleles (light blue). The hatched black segment represents the
398 uncertainty where the *Appl*^{d} deletion ends in 3'. The orange star represents the position of the 3'
399 sgRNA used to create the two CRISPR deletions. (C) Wild-type (WT) MB revealed by an anti-Fas2
400 staining. The pink and yellow arrowheads show respectively the α and β lobe (n=216 MBs). (D-E)
401 Anti-Fas2 staining reveals the loss of β lobe on a representative *Appl*$^{C1.4}$ brain (n=147 MBs) (D)
402 and on *Appl*$^{C2.1}$ brain (n=253 MBs) (E). The % represents the proportion of loss of β lobe for each
403 genotype. Scale bar = 50 µm.
404
405 **Fig 2. *Appl*^{d} and *Appl*$^{C1.4}$, but not *Appl*$^{C2.1}$, are impaired for *vnd* function.**
406 A) Schematic representation of *vnd* gene and transcripts. White boxes represent 5'UTR and 3'UTR,
407 green boxes represent coding sequences. Red star represents point mutation on *vnd*^{A} allele.
408 Schematic representation of *vnd-B* and *vnd-A* transcripts. The *vnd*^{A} mutation affects both
409 transcripts. (B-D) Anti-Fas2 staining reveals the loss of β lobe on a representative *Appl*^{d}/ *vnd*^{A} brain
410 (n=214 MBs) (B), *Appl*$^{C1.4}$/ *vnd*^{A} brain (n=147 MB) (C) but not on *Appl*$^{C2.1}$/ *vnd*^{A} brain (n=248 MBs)
411 (D). The % represents the proportion of loss of β lobe for each genotype. Scale bar = 50 µm.
412
413 **Fig 3. Generating new *vnd* CRISPR alleles deleted either for the *vnd-B* or the *vnd-A* function.**
414 (A) Schematic representation of *vnd* gene and transcripts. White boxes represent 5'UTR and
415 3'UTR, green boxes represent coding sequences. The hatched black boxes represent the deleted
416 region of *vnd*$^{C\Delta A}$ and *vnd*$^{C\Delta B}$ (B-C) Anti- Fas2 staining reveals essentially wild-type looking MBs on
417 a representative *vnd*$^{C\Delta B}$ brain (n=146 MBs) (B) and *Appl*$^{C1.4}$/ *vnd*$^{C\Delta B}$ brain (n=159 MB) (C). The %
418 represents the proportion of loss of β lobe for each genotype. Scale bar = 50 µm.
419
420 **Fig 4. Vnd-A is required for MB β-branch axon outgrowth.**
421 (A) Quantitation of the rescue of MB β lobe absence of *Appl*$^{C1.4}$/Y (66%; n= 147 MBs, see a
422 representative brain in Fig.1D) and *Appl*$^{C1.4}$/*vnd*$^{C\Delta A}$ (64%; n=198 MBs) (light blue) by an *Appl*
423 duplication (dark blue) (50%; n=150 MBs, 69%; n=89 MBs) and by a *vnd* duplication (green) (3%;
424 n=191 MBs ; 0%; n=164 MBs). **p<0.01 and ****p<0.0001. (B-D) Anti-Fas2 staining on a
425 representative rescued *Appl*$^{C1.4}$/Y; *Dp-vnd*$^{+}$/+ brain (B), *Appl*$^{C1.4}$/*vnd*$^{C\Delta A}$; +/+ brain (C) and on
426 *Appl*$^{C1.4}$/*vnd*$^{C\Delta A}$; *Dp-vnd*$^{+}$/+ brain (D). The % represents the proportion of loss of β lobe for each
427 genotype. Scale bar = 50 µm.
428
429 **Fig 5. *vnd* is expressed close to the developing MB medial lobe.**
430 (A-D) Visualization of *vnd* expression in brain using *vnd-GAL4* driven *UAS-GFP* at L3, 0h, 6h, and
431 24h APF. GFP was visualized on green and anti-FasII staining labelling of MB axons on red. A-D are
432 confocal z stacks taken the whole MB and A'-D' are stacks of five plans from A-D respectively
433 comprising GFP^{+} regions surrounding MB. Arrowheads point to *vnd-GAL4* driven *UAS-GFP*
434 filamentous structures that surround MB medial lobes, which correspond to γ lobes from L3 to 6
435 h APF (A'-C') and β lobes at 24 h APF (D'). n $\geq$ 10 for each time point. (E-G) show single confocal
436 plans showing *vnd* expression using *vnd-GAL4* driven *UAS-GFP* (single channel) at L3. E' to G' are
437 merges of single channel E to G respectively and DAPI staining (red on E'), anti-vnd (red on F') and

anti-Repo (red on G'). DAPI labelled nuclei in honeycomb GFP^+ structures are pointed by arrows in E'. These nuclei were also vnd^+ (arrows in F') and they were not labelled by an anti-repo (white arrow in G') which labels glia nuclei (red dots pointed by a yellow arrow in G'). Scale bars are 50 μm. n $\geq$ 5 brains for each type of staining.

Fig 6. The long-term memory defect of *Appl*$^{C2.1}$/Y flies is rescued by *Appl*$^+$ expression in the adult mushroom body.

(A) Olfactory acuity was normal in *Appl*$^{C2.1}$/Y flies. For octanol**,** data presented as mean ± SEM. *t*-test n=12, t_{22} = 1.12, P = 0.26, ns: not significant. For methylcyclohexanol, data presented as mean ± SEM. *t*-test n=12, t_{22} = 1.51, P = 0.15, ns: not significant. (B) Shock reactivity was normal in *Appl*$^{C2.1}$/Y flies**.** Data presented as mean ± SEM. *t*-test. n=12, t_{22} = 1.47, P = 0.16, ns: not significant. (C) Flies only null for *Appl* have no measurable LTM which is fully rescued by the restricted expression of *Appl* in adult MBs. Data presented as mean ± SEM. n = 22-23, $F_{(4, 108)}$ = 16,41, P < 0.0001. Significance level of *t*-test or least significant pairwise comparison following ANOVA: ****p < 0.0001, ns: not significant.

Supporting information

S1 Fig. Scheme of *Appl*^{d} chromosomic organization

(A) Schematic representation of *Appl*^{d} mutant allele. The upper panel represents the wild-type (WT) X (black) and Y (orange) chromosomes. The *elav*, *Appl* and *vnd* genes are represented respectively in yellow, blue, and green boxes. The middle panel represents the deficiency Df (1)RT518 on the X chromosome deleting the distal part of the chromosome including the *elav* and *Appl* genes. The X Dup Y chromosome represents a duplication of the X chromosome linked to the Y chromosome including the distal part of the X chromosome including the *elav* gene. The lower panel represents a proposed structure of the *Appl*^{d} chromosome where the deficiency bearing X chromosome had been linked by gamma rays to the X Dup Y chromosome (adapted from [8]).

S2 Fig. Structure of the *Appl*$^{C1.4}$ and *Appl*$^{C2.1}$ CRISPR alleles

(A) Schematic representation of *Appl* (blue) and *vnd* (green) genes and transcripts. White boxes represent 5'UTR and 3'UTR, blue and green boxes represent *Appl* and *vnd* coding sequences respectively. The yellow stars in *Appl* 5' region and the orange star in *Appl* 3' region represent the position of the sgRNA used to create *Appl*$^{C1.4}$ and *Appl*$^{C2.1}$ mutants. The red and blue boxes represent respectively the regions magnified in B and C. (B) Representation of the 5' sequence targeted by the sgRNA (yellow) and the PAM domain (magenta) in the WT chromosome *Appl* (blue) (upper line). The lower line is the sequence of the *Appl*$^{C1.4}$ mutant showing the beginning of the deletion about 1kb after the region targeted by the sgRNA. (C) Representation of the 3' sequence targeted by the sgRNA (orange) and the PAM domain (magenta) in the WT chromosome *Appl* (blue) and *vnd* (green) (upper line). The lower line is the sequence of the *Appl*$^{C1.4}$ mutant showing the end of the deletion about 6kb after the region targeted by the sgRNA. (D) Representation of the 5' and 3' sequences targeted by the sgRNA (yellow in 5' and orange in 3') and the PAM domain (magenta) in the WT chromosome *Appl* (blue) (upper line). The lower line

481 is the sequence of the *Appl*$^{C2.1}$ mutant showing the beginning of the deletion in the sequence
482 targeted by the 5' sgRNA (yellow) and the end of the deletion in the sequence targeted by the 3'
483 sgRNA (orange).
484
485 **S3 Fig. Structure of the *vnd*$^{C\Delta B}$ and *vnd*$^{C\Delta A}$ CRISPR alleles**
486 (A) Schematic representation of *vnd* (green) gene and transcripts. White boxes represent 5'UTR
487 and 3'UTR, green boxes represent *vnd* coding sequences. The yellow stars represent the position
488 of the sgRNA used to create *vnd*$^{C\Delta B}$ mutant. The orange stars represent the position of the sgRNA
489 used to create *vnd*$^{C\Delta A}$ mutant. (B) Representation of the sequences targeted by the sgRNA (yellow)
490 and the PAM domain (blue) in the WT chromosome *vnd* (green) (upper line). The lower line is the
491 sequence of the *vnd*$^{C\Delta B}$ mutant showing the beginning of the deletion in the sequence targeted
492 by the 5' sgRNA (yellow) and the end of the deletion in the sequence targeted by the 3' sgRNA
493 (yellow). (C) Representation of the sequences targeted by the sgRNA (orange) and the PAM
494 domain (blue) in the WT chromosome *vnd* (green) (upper line). The lower line is the sequence of
495 the *vnd*$^{C\Delta A}$ mutant showing the beginning of the deletion at one nucleotide from the sequence
496 targeted by the 5' sgRNA (orange) and the end of the deletion withinin the sequence targeted by
497 the 3' sgRNA (orange).
498
499 **S4 Fig. Vnd L3 CNS labelling**
500 (A-C) Visualization of *vnd* expression in VNC using both *vnd-GAL4* driven *UAS-GFP* (green) and an
501 anti-vnd antibody (red) at L3 stages. Images A-C and A'-C' are the same confocal z-projection.
502 Laser intensities leading to the green color were increased from B, C to B', C' in order to illustrate
503 the perfect colocalization between the two markers. Low laser intensity allowed us to show red
504 nuclear vnd staining in only some GFP$^+$ cell bodies (white arrowheads in A- C). Soma containing
505 vnd$^+$ positive nuclei that do not seem to be surrounded by GFP in A-C, can be visualized by
506 increased green laser intensity A'- C' (yellow arrowheads), which saturates somas visualized in A-
507 C. Scale bars are 50 μm. n $\geq$ 5 brains.
508
509 **S5 Fig. *vnd* null mutant clones**
510 (A-B) A representative neuroblast MARCM clone in a wild-type (WT) brain (A) and in a *vnd*^{A} brain
511 (B). Scale bar = 50 μm. (C) Number of clones obtained in WT , *vnd*^{A} , *vnd*^{6} and *vnd*$^{\Delta 38}$. Full
512 genotypes: (A) *w* tubP-GAL80 hsFLP122 FRT19A/w*^{1118} *sn FRT19A; c739-GAL4 UAS-mCD8-GFP/*+
513 (also control hsFLP122 in C). (B) *w* tubP-GAL80 hsFLP122 FRT19A/y vnd*^{A} *w FRT19A; c739-GAL4*
514 *UAS-mCD8-GFP/*+ (also vnd^A in C). (C) control hsFLP1: *w tubP-GAL80 hsFLP1 FRT19A* (from the
515 Bloomington stock 5133)/*w UAS-mCD8-GFP sn FRT19A*; *c739-GAL4 UAS-mCD8-GFP/*+. vnd^6: *w*
516 *tubP-GAL80 hsFLP1 FRT19A/y vnd*^{6} *w UAS-mCD8-GFP sn FRT19A*; *c739-GAL4 UAS-mCD8-GFP/*+.
517 vnd$^{\Delta 38}$: *w tubP-GAL80 hsFLP1 FRT19A/vnd*$^{\Delta 38}$ *w UAS-mCD8-GFP FRT19A*; *c739-GAL4 UAS-mCD8-*
518 *GFP/*+.
519
520 **S6 Fig. In absence of *Appl*$^+$ induction, *Appl*$^{C2.1}$/Y flies display a long-term memory defect**. Data
521 presented as mean ± SEM. n = 15, $F_{(4, 70)} = 17.62$, $P < 0.0001$. Significance level of *t*-test or least
522 significant pairwise comparison following ANOVA: ****p < 0.0001.
523
524

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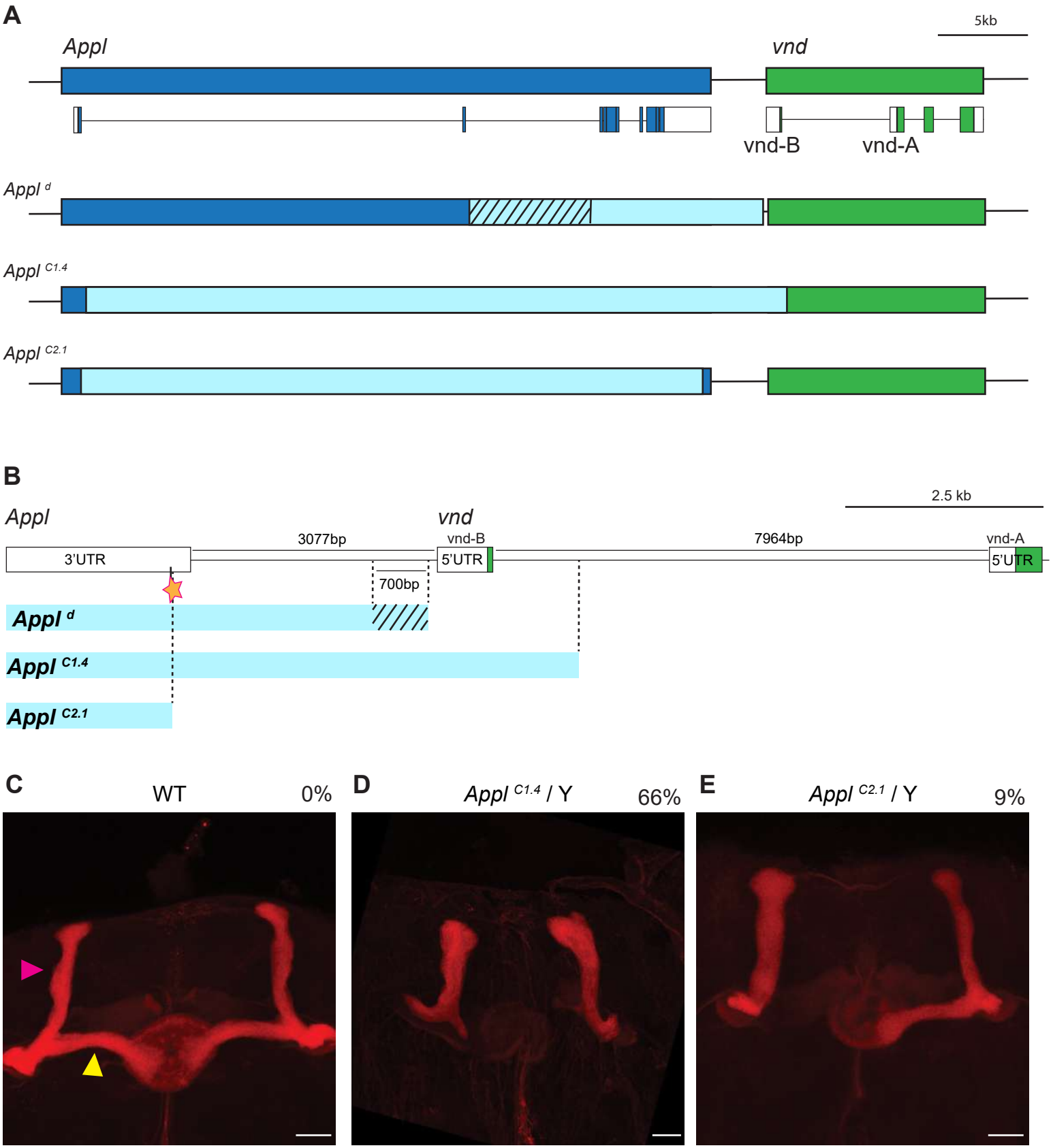
647

Figure 1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3'UTR
5'UTR
5'UTR
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Appl C1.4
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E
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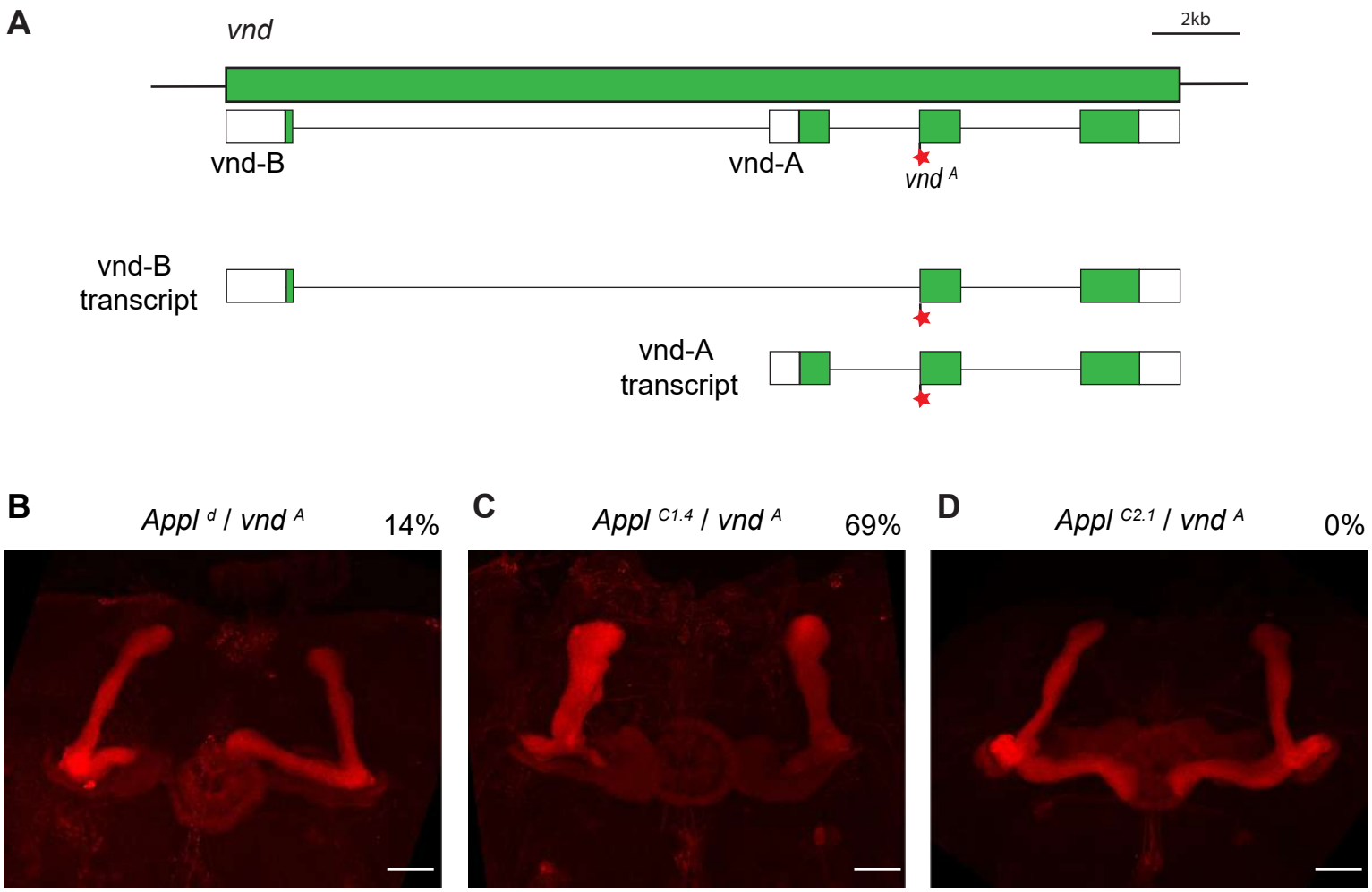
9%

Figure 2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D
Appl C2.1 / vnd A
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Figure 3

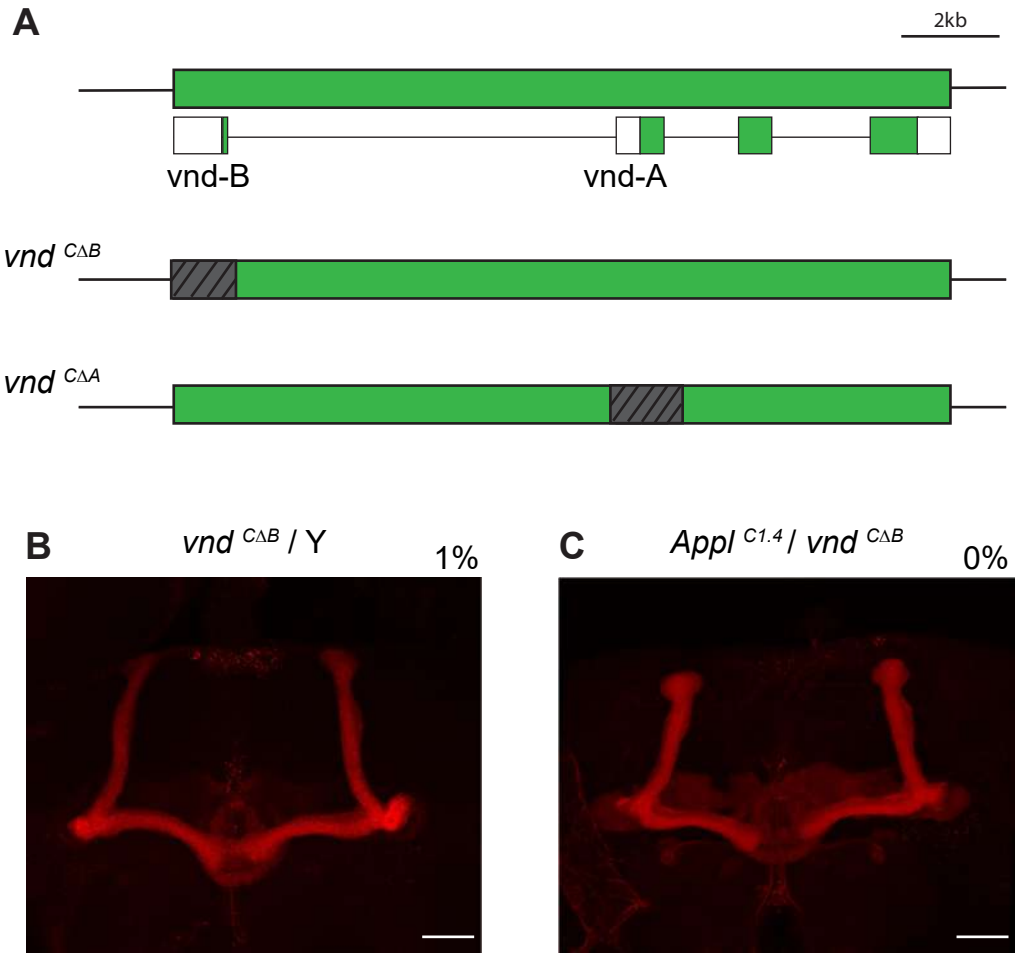


Figure 4

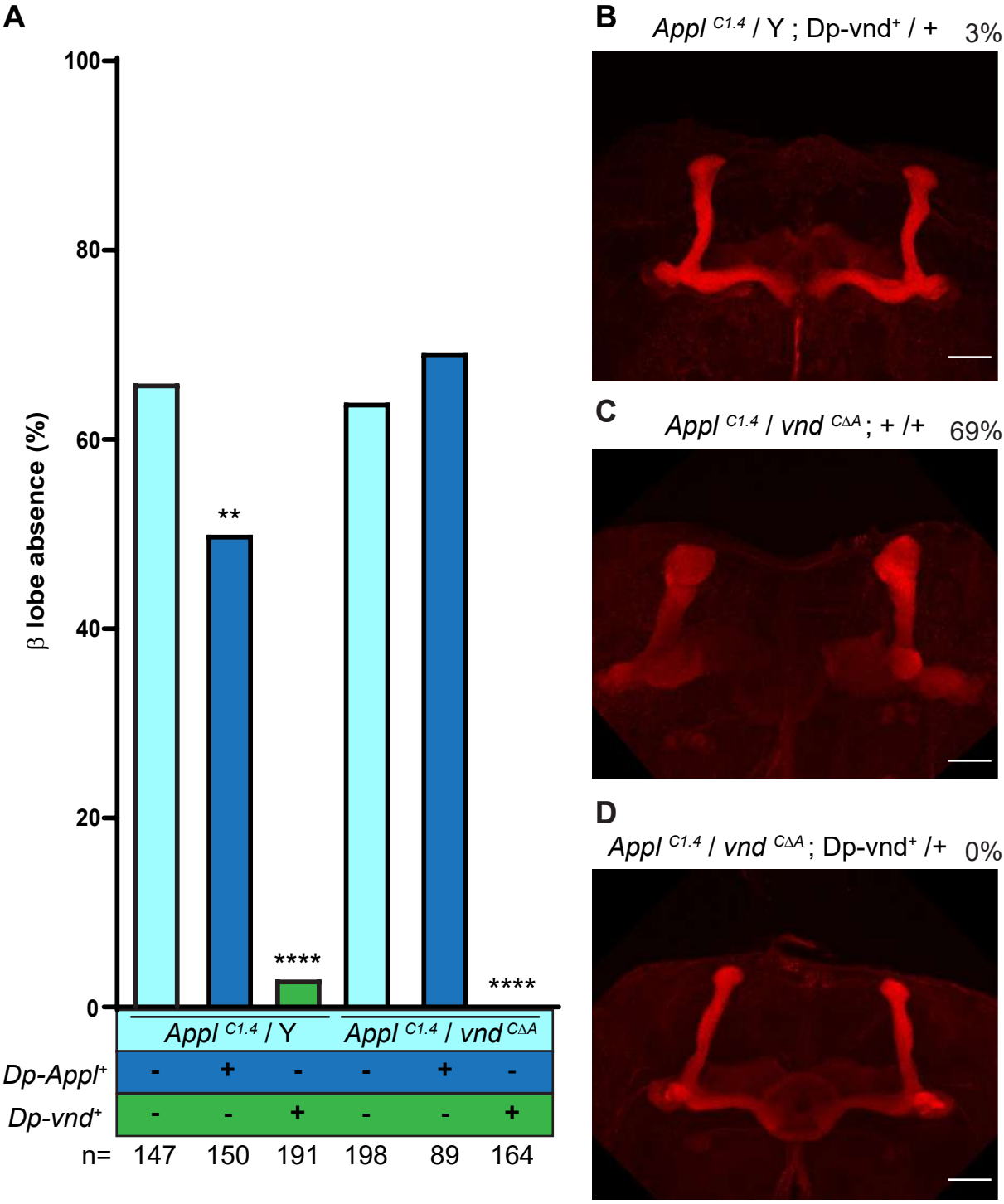

A
100
80
60
40
20
0
β lobe absence (%)
**
****
****
Appl C1.4 / Y
Appl C1.4 / vnd CΔA
Dp-Appl+
Dp-vnd+
- + - - + -
- - + - - +
n= 147 150 191 198 89 164
B
Appl C1.4 / Y ; Dp-vnd+ / +
3%
C
Appl C1.4 / vnd CΔA ; + /+
69%
D
Appl C1.4 / vnd CΔA ; Dp-vnd+ /+
0%

Figure 5

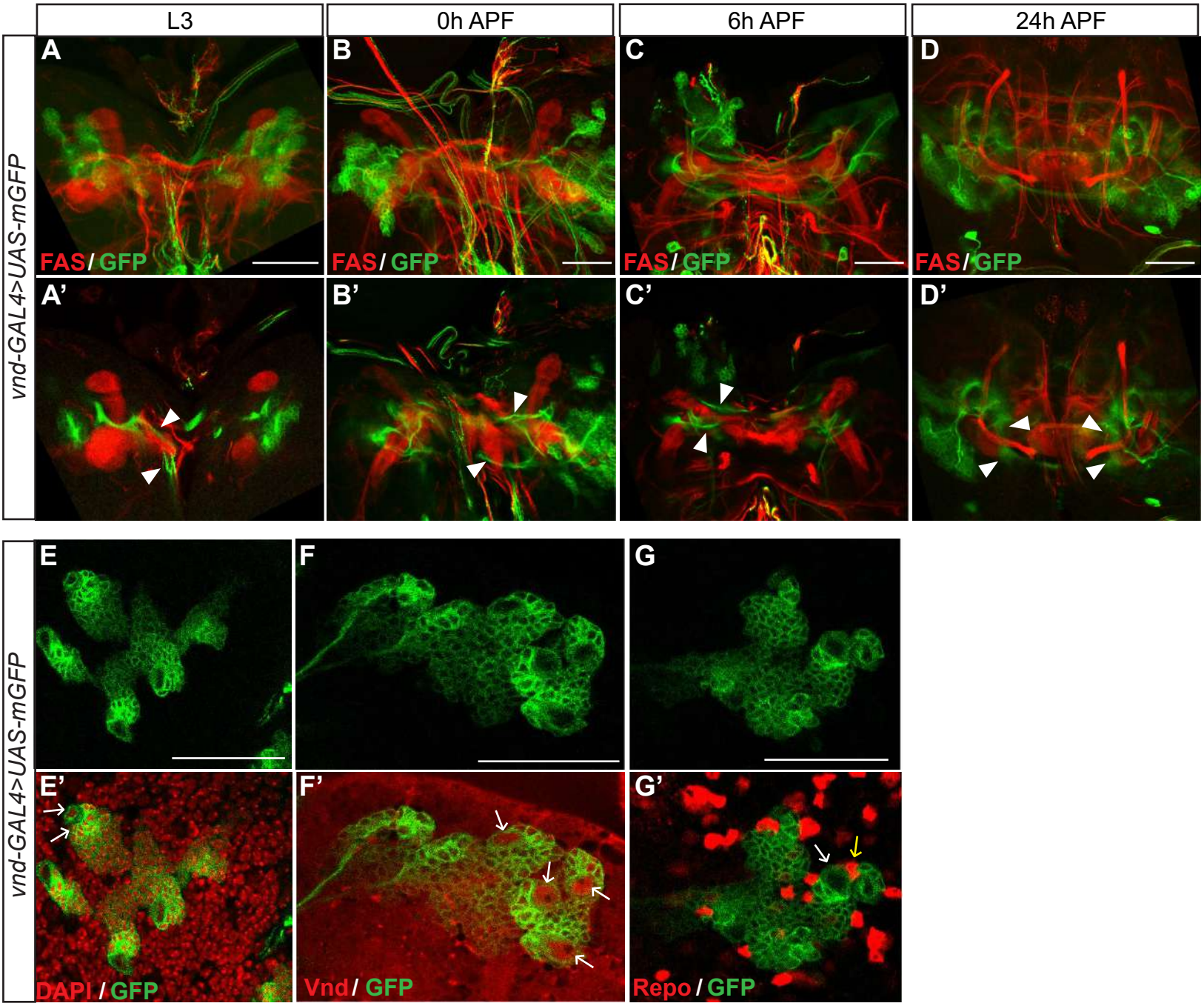
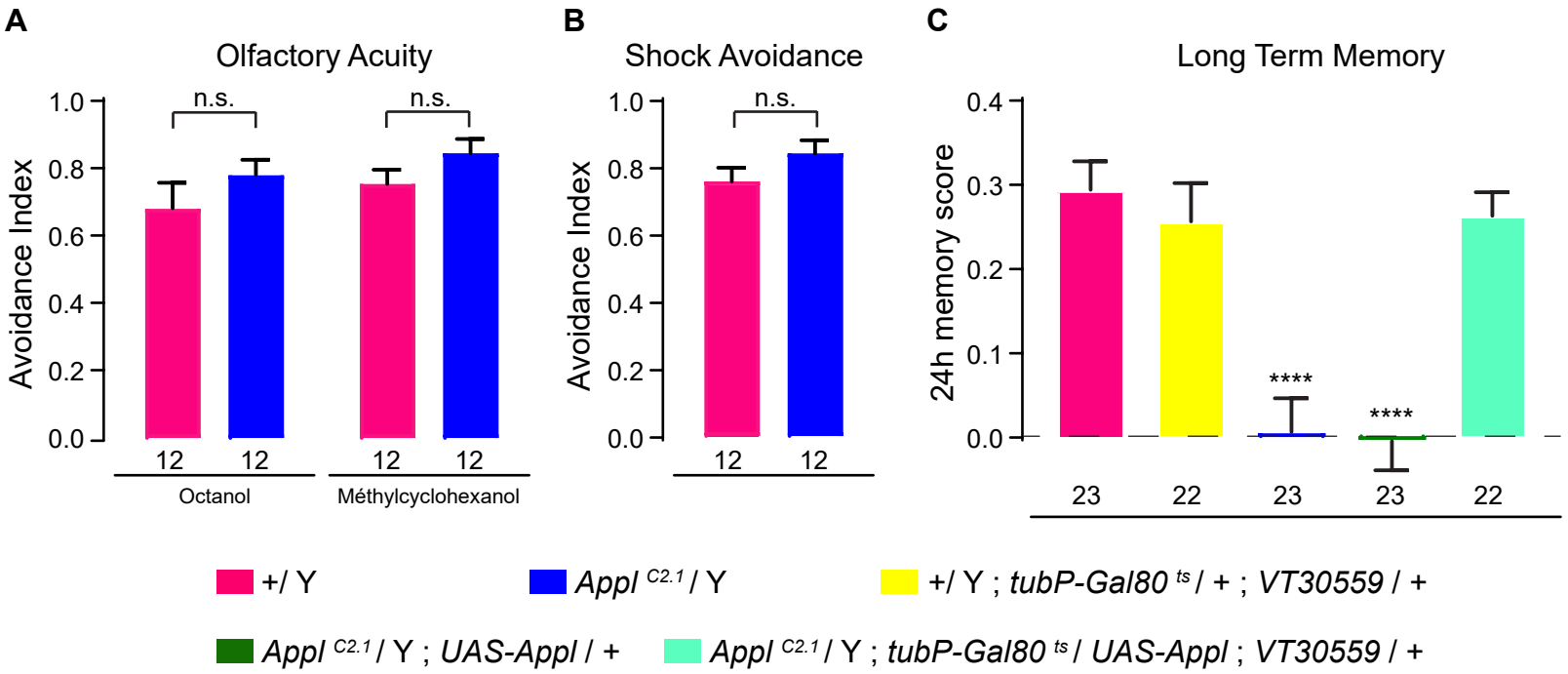

L3
0h APF
6h APF
24h APF
vnd-GAL4>UAS-mGFP
A
B
C
D
FAS / GFP
A'
B'
C'
D'
E
F
G
E'
F'
G'
DAPI / GFP
Vnd / GFP
Repo / GFP

Figure 6


A
Olfactory Acuity
Avoidance Index
1.0
0.8
0.6
0.4
0.2
0.0
n.s.
n.s.
12
12
12
12
Octanol
Méthylcyclohexanol
B
Shock Avoidance
Avoidance Index
n.s.
12
12
C
Long Term Memory
24h memory score
0.4
0.3
0.2
0.1
0.0
****
****
23
22
23
23
22
+/ Y
Appl C2.1 / Y
+/ Y ; tubP-Gal80 ts / + ; VT30559 / +
Appl C2.1 / Y ; UAS-Appl / +
Appl C2.1 / Y ; tubP-Gal80 ts / UAS-Appl ; VT30559 / +