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2 **KEK-6: A TRUNCATED-TRK-LIKE RECEPTOR FOR *DROSOPHILA* NEUROTROPHIN 2**
3 **REGULATES STRUCTURAL SYNAPTIC PLASTICITY**

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28 ABSTRACT

29 Neurotrophism, structural plasticity, learning and long-term memory in mammals critically
30 depend on neurotrophins binding Trk receptors to activate tyrosine kinase (TyrK) signalling,
31 but *Drosophila* lacks full-length Trks, raising the question of how these processes occur in
32 the fly. Paradoxically, truncated Trk isoforms lacking the TyrK predominate in the adult
33 human brain, but whether they have neuronal functions independently of full-length Trks is
34 unknown. *Drosophila* has TyrK-less Trk-family receptors, encoded by the *kekkon* (*kek*)
35 genes, suggesting that evolutionarily conserved functions for this receptor class may exist.
36 Here, we asked whether Keks function together with *Drosophila* neurotrophins (DNTs) at the
37 larval glutamatergic neuromuscular junction (NMJ). Starting with an unbiased approach, we
38 tested the evelen LRR and Ig-containing (LIG) proteins encoded in the *Drosophila* genome
39 for expression in the central nervous system (CNS) and potential interaction with DNTs. Kek-
40 6 was expressed in the CNS, could interact genetically with DNTs and could bind DNT2 both
41 in signaling essays and in co-immunoprecipitations. There is promiscuity in ligand binding, as
42 Kek-6 could also bind DNT1, and Kek-5 could also bind DNT2. In vivo, Kek-6 is found
43 presynaptically in motoneurons, and binds DNT2 produced by the muscle, which functions as
44 a retrograde factor at the NMJ. Kek-6 and DNT2 regulate NMJ growth, bouton formation and
45 active zone homeostasis. Kek-6 does not antagonise the alternative DNT2 receptor Toll-6,
46 but rather the two receptors contribute in distinct manners to NMJ structural plasticity. Using
47 pull-down assays, we identified and validated CaMKII and VAP33A as intracellular partners
48 of Kek-6, and show that together they regulate NMJ growth and active zone formation. These
49 functions of Kek-6 could be evolutionarily conserved, raising the intriguing possibility that a
50 novel mechanism of structural synaptic plasticity involving truncated Trk-family receptors
51 independently of TyrK signaling may also operate in the human brain.

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56 AUTHOR SUMMARY

57 A long-standing paradox had been to explain how brain structural plasticity, learning and
58 long-term memory might occur in *Drosophila* in the absence of canonical Trk receptors for
59 neurotrophin (NT) ligands. NTs link structure and function in the brain enabling adjustments
60 in cell number, dendritic, axonal and synaptic patterns, in response to neuronal activity.
61 These events are essential for brain development, learning and long-term memory, and are
62 thought to depend on the tyrosine-kinase function of the NT Trk receptors. However,
63 paradoxically, the most abundant Trk isoforms in the adult human brain lack the tyrosine
64 kinase, and their neuronal function is unknown. Remarkably, *Drosophila* has kinase-less
65 receptors of the Trk family encoded by the *kekkon* (*kek*) genes, suggesting that deep
66 evolutionary functional conservation for this receptor class could be unveiled. Here, we show
67 that Kek-6 is a receptor for *Drosophila* neurotrophin 2 (DNT2) that regulates structural
68 synaptic plasticity via CaMKII and VAP33A, well-known factors regulating synaptic structure
69 and plasticity, and vesicle release. Our findings suggest that in mammals truncated Trk-
70 family receptors could also have synaptic functions in neurons independently of Tyrosine
71 kinase signalling. This might reveal a novel mechanism of brain plasticity, with important
72 implications for understanding also the human brain, in health and disease.

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84 INTRODUCTION

85 Brain plasticity, neurotrophism in development, structural and synaptic plasticity during
86 learning and long-term memory in humans critically depend on the receptor TrkB binding its
87 neurotrophin (NT) ligand BDNF [1,2]. During development, NTs and Trks regulate neuronal
88 number and connectivity; subsequently BDNF and TrkB establish a reinforcing positive
89 feedback loop promoting synaptic potentiation, and regulate the dynamic generation and
90 elimination of synaptic boutons and dendritic spines in response to activity [1,3-5]. Thus, NTs
91 and Trks are fundamental to linking structure and function in the brain, and this is thought to
92 depend mostly on the tyrosine kinase (TyrK) function of Trks. Through its intracellular TyrK
93 domain, TrkB activates the Ras/MAPKinase, PI3Kinase/ AKT and PLC γ signalling pathways
94 downstream [1,2]. Pre-synaptic targets include Synapsin, to trigger vesicle release [5]. Post-
95 synaptic targets include NMDAR and CREB, essential for long-term potentiation, learning
96 and long-term memory [1,5]. Paradoxically, full-length TrkB decays postnatally and TrkB
97 homodimers are not formed in the adult mammalian brain [6-10]. Instead, the most abundant
98 adult isoform is the truncated TrkB-T1 isoform lacking the TyrK [8-10]. Mutant mice lacking
99 TrkB-T1 have anxiety, and in humans alterations in TrkB-T1 are linked to severe mental
100 health disorders [11-13]. However, the neuronal functions of the truncated Trk isoforms are
101 poorly understood.

102 No canonical, bona fide, full-length, TyrK Trk receptors have been found in
103 *Drosophila*. However, neurotrophism, structural and synaptic plasticity, learning and long-
104 term memory all occur in fruit-flies, implying that either in the course of evolution insects and
105 humans found different molecular solutions to elicit equivalent functions, or that undiscovered
106 mechanisms contribute to brain plasticity in both humans and fruit-flies. Finding out what
107 happened to the Trks in *Drosophila* is important, as it could uncover novel fundamental
108 mechanisms of structure-function relationships in any brain.

109 Trk receptors have long been searched for in *Drosophila*. Trks (TrkA,B,C) bear the
110 unique combination of Cysteine Rich Repeats (CRR), Leucine Rich Repeats (LRR) and
111 Immunoglobulin (Ig) domains extracellularly, and an intracellular TyrK domain (Fig.1A).

112 Original searches focused on the TyrK domain, and identified DTrk and Dror as candidate
113 *Drosophila* Trk homologues, but these are unlikely to bind neurotrophins. DTrk, also known
114 as Off-Track (Otk)[14,15] lacks the LRR and CRR modules, it is kinase-dead and binds
115 Semaphorins (Fig.1A). Dror/Dnrk, like all Ror-family receptors, has an extracellular
116 Frizzled/Kringle module instead [16-18](Fig.1A). Subsequent proteomic analyses found no
117 full-length, canonical Trk orthologues with the combination of LRR, CRR and Ig modules
118 extracellularly and a Trk-family TyrK intracellularly in *Drosophila* [19-21]. However,
119 phylogenetic analysis of the Trk-receptor superfamily identified the *Drosophila* Kekkons
120 (Keks), lacking an intracellular TyrK domain, as closely related to the Trks [22](Fig.1A,B).
121 Trks and Keks both belong to the LIG family of proteins that contain extracellular ligand-
122 binding LRR and Ig motifs [22,23]. There are 38 LIGs in humans, and amongst these are
123 transmembrane proteins with a divergent intracellular domain lacking a TyrK or any
124 conserved motifs [22]. There are 9 LIGs in *Drosophila* and phylogenetic analysis clusters
125 mammalian AMIGO, LINGO, LRIG and LRRC4 in one clade with *Drosophila* Lambik, and
126 mammalian Trks in a separate clade together with *Drosophila* Keks (Kek1-6) [22](Fig.1B).
127 Keks are more similar to the Trks than all other vertebrate LIGs are to each other [22]. Keks
128 have only been found in insects, and thus are remnant, conserved Trk-like receptors in fruit-
129 flies.

130 There are 6 Keks in *Drosophila*, with a cytoplasmic tail lacking any remarkable
131 conservation, except that Kek1, 2, 5 and 6 have a PDZ domain that could bind cytoplasmic
132 effectors [24]. Kek1, 2, 5 and 6 are highly conserved in insects [24]. At least *kek1*, *kek2* and
133 *kek5* are expressed in the CNS [25-27]. Only Kek2 has been investigated in the CNS, where
134 it functions as a neuronal activity dependent modulator of synaptic growth and activity [27].
135 The ligands for the Keks have not been identified.

136 The prime candidates for Kek ligands are the *Drosophila* neurotrophins (DNTs).
137 DNT1 (*Drosophila* neurotrophin 1 also known as Spz2), DNT2 (also known as Spz5) and Spz
138 bear the distinctive and evolutionarily conserved neurotrophin cystine-knot domain of the
139 mammalian neurotrophins [28-36], and they have conserved CNS functions regulating

140 neuronal survival, connectivity and synaptogenesis [35-39]. Spz, DNT2 and DNT1 are known
141 ligands for Toll-1, Toll-6 and Toll-7 receptors of the Toll and Toll-Like Receptor (TLR)
142 superfamily [38,40]. In *Drosophila* Toll-1, Toll-6 and Toll-7 are required for targeting at the
143 embryonic neuromuscular junction (NMJ), Toll-6 and Toll-8 for larval NMJ growth, and Toll-1,
144 Toll-6 and Toll-7 function as neurotrophin receptors regulating neuronal survival and death,
145 connectivity and behaviour [35-38,41-44]. In *Drosophila*, the NMJ is glutamatergic, and
146 undergoes plasticity and potentiation, thus resembling mammalian central synapses, and is
147 the standard context in which to investigate synaptic structural and functional plasticity [45].
148 Given that NT family ligands can bind multiple receptor types, and that receptors and ligands
149 tend to co-evolve [17], conservation of the extracellular ligand-binding domain of Trks and
150 Keks suggested Keks could potentially function as DNT receptors in flies.

151 Here, we investigated whether Kek-6 might function as a DNT receptor in *Drosophila*,
152 at the glutamatergic NMJ synapse.

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154 RESULTS

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156 **Kek6 is a truncated-Trk-like receptor that binds DNTs**

157 To investigate if *Drosophila* LIGs might function as DNT receptors in the CNS, we first looked
158 at their expression in embryos. *CG15744* did not reveal expression above background in the
159 ventral nerve cord (VNC) (Fig.1C); *lambik* and *CG16974* mRNAs were absent from the VNC,
160 but might be expressed in the Peripheral Nervous System (PNS) or muscle, respectively
161 (Fig.1C,D). *kek1* and *kek2* were expressed in VNC cells, and possibly in PNS cells too
162 (Fig.1D), as previously shown [25,27]. *kek3* and *kek4* transcripts were not detected in
163 embryos. *kek5* is expressed in the VNC [26], and we confirmed this with a *kek5-GAL4*
164 reporter, which also revealed PNS expression (Fig.1D). *kek6* transcripts were abundant in
165 the VNC (Fig.1D). Thus, amongst the 9 LIGs, Kek1, 2, 5, and 6 could function in the CNS.

166 To test whether Keks could function downstream of DNTs in vivo, we took advantage
167 of the cold semi-lethality of *DNT1⁴¹ DNT2^{e03444}* double mutants [38], and asked whether it

168 could be rescued with the over-expression of *keks* in neurons. Over-expression of *kek1* and
169 *kek4* in neurons (with *elavGAL4*) did not rescue, and *kek2* and *kek6* did most prominently
170 (Fig.1E, Table S1). Thus, Kek2 and Kek6 could function downstream of DNTs.

171 To ask whether DNT ligands could bind Keks and induce signaling, as Keks lack the
172 TyrK, to enable a signaling readout, we generated chimaeric receptors formed of the
173 extracellular and transmembrane domains of the Keks fused to the intracellular domain of
174 Toll-6 (Fig.2A). Toll-6 uses a conserved TIR domain to activate Dif/NFκB signaling
175 downstream, which can be measured through the activation of *drosomicin-luciferase* (*dros-*
176 *luc*) [38]. We used S2 cells stably transfected with *dros-luc*, transfected them with *kek-Toll-6*
177 chimaeric receptors, and tested whether stimulation with purified cleaved DNT2 (DNT2-CK)
178 could induce Dif/NFκB signaling. The chimaeric receptors targeted correctly to the S2 cell
179 membrane (Fig.2A). Stimulation with DNT2-CK in pDONR transfected controls induced *dros-*
180 *luc*, as S2 cells express multiple Toll receptors [36,38] (Fig.2A). Stimulation with DNT2-CK of
181 cells transfected with *kek3,4,5,6-Toll-6* chimaeras had an effect comparable to the induction
182 by stimulated full-length *Toll-6*, and Kek3-Toll-6 and Kek6-Toll-6 chimaeras responded more
183 robustly (Fig.2A, Table S1). We could not generate Kek1 and Kek2 chimeric receptors, thus
184 a potential interaction with them cannot be ruled out. Thus, DNT2 can interact physically with
185 at least Kek-3 and Kek-6. Together with the above data, this indicated Kek-6 was a strong
186 candidate to interact with DNTs in the CNS.

187 To verify whether Kek-6 could bind DNT2, we carried out co-immunoprecipitations.
188 S2 cells were co-transfected with HA-tagged *kek-6* and V5-tagged full-length *DNT2*.
189 Precipitating Kek6-HA with anti-HA, brought down DNT2-V5 detected with anti-V5 (Fig. 2B).
190 Conversely, precipitating DNT2 with anti-V5, also brought down Kek6 detected with anti-HA
191 (Fig. 2C). Thus, Kek6 can bind DNT2. To test whether Kek6 might also bind DNT1, we co-
192 transfected S2 cells with *kek6-HA* and full-length *DNT1-V5*. Precipitating DNT1 brought down
193 Kek6 (Fig. 2C). Thus, Kek6 can bind both DNT2 and DNT1. To test whether another Kek
194 might also bind the DNTs, S2 cells were co-transfected with *kek5-Flag* and *DNT2-V5*, and

195 we found that precipitating DNT2 also brought down Kek-5 (Fig. 2D). Therefore, Kek-5 can
196 also bind DNT2. These data demonstrate that Keks bind DNT ligands, and that binding is
197 promiscuous.

198 To conclude, Kek-6 was widely expressed in the CNS, rescued the semi-lethality of
199 *DNT1 DNT2* double mutants, and bound DNT ligands in a signaling assay and in co-
200 immunoprecipitations. Thus, Kek-6 could function as a DNT receptor.

201

202 **Kek-6 in motoneurons and DNT2 from the muscle function together at the NMJ**

203 For a functional *in vivo* analysis we focused on Kek-6. *kek-6* CNS expression was examined
204 in larvae using *kek6^{MIMIC13953}* flies bearing a GFP insertion into the *kek-6* coding region
205 (hereafter named *Kek6^{GFP}*). *Kek6^{GFP}* was found in Eve+(Fig.3A) and HB9+(Fig.3B) inter-
206 neurons and motoneurons, and excluded from Repo+ glia (Supplemental Fig.S1) in third
207 instar larval VNCs. *Kek6^{GFP}* was present in motoneuron terminals at the neuro muscular
208 junction (NMJ) of third instar larvae and not in the muscle (Fig.3C,D), revealing NMJ6/7
209 synaptic boutons, surrounded by post-synaptic Dlg (i.e. *Drosophila* PSD95) (Fig.3D,E). Thus,
210 *kek-6* is expressed pre-synaptically in motoneurons.

211 *DNT2* transcripts are expressed in the larval body wall muscles, and localised to post-
212 synaptic boutons [39]. To test if DNT2 could function retrogradely, we generated a tagged
213 form of full-length DNT2 with GFP at the C-terminus, and over-expressed *DNT2-FL-GFP* in
214 the muscle with *MhcGAL4*. DNT2-FL-GFP would result in secretion of mature DNT2-CK-GFP
215 [36], although not all protein might get cleaved and secreted. Over-expression of *DNT2-FL-*
216 *GFP* in muscle resulted in the localization of GFP pre-synaptically in boutons, surrounded by
217 the post-synaptic marker Dlg (Fig.3F). DNT2-FL-GFP also colocalised with the motoneuron
218 marker FasII in boutons (Fig.3G,H,J) and in motoraxons (Fig.3H,I,J). Thus, DNT2 produced
219 in muscle can interact with the receptor Kek-6 in motoneurons, consistent with a retrograde
220 function.

221 To investigate the *in vivo* functions of Kek6 and DNT2, we generated *kek6* and *DNT2*
222 null mutant alleles by FRT-mediated recombination between PiggyBac insertions [46].
223 Neither *kek6*³⁴/*Df(3R)ED6361* or *DNT2*³⁷/*Df(3L)6092* loss of function mutants, nor
224 *kek6*^{-/-} *DNT2*^{-/-} double mutants, affected viability. We analysed larval locomotion using
225 FlyTracker software to trace trajectories and measure crawling speed [38], and found that
226 *kek6*³⁴/*Df(3R)ED6361* mutant larvae crawled more slowly than controls (Fig.4A, Table S1),
227 and *DNT2*³⁷/*Df(3L)6092* larvae crawled even slower (Fig.4A, Table S1). *kek6*^{-/-} *DNT2*^{-/-}
228 double null larvae crawled at similar speeds as *DNT2*^{-/-} mutants, but travelled shorter
229 distances, moving around the starting spot (Fig.4A, Table S1). The synergistic effect in the
230 double mutants suggested that Kek-6 and DNT2 are functionally linked.

231 Locomotion phenotypes suggested the NMJ might be affected, so we looked at the
232 muscle 6/7 NMJs, which require DNT1 and 2 [39]. Targeting at muscle 6/7 NMJ was affected
233 in *kek6*^{-/-} mutant embryos and upon *kek-6* over-expression in neurons (Supplemental
234 Fig.S2). In wandering third instar larvae, *kek6*^{-/-} and *DNT2*^{-/-} single mutant larvae, and *kek6*^{-/-}
235 *DNT2*^{-/-} double mutants, had smaller NMJs than controls, with fewer Ib boutons and
236 shorter axonal terminal length (Fig.4B, Table S1). Thus, Kek-6 and DNT2 are required for
237 normal NMJ growth. *kek6*^{-/-} and *DNT2*^{-/-} single mutant NMJs had higher active zone density,
238 visualized with anti-Brp (*Drosophila* ELKs) and quantified automatically throughout the NMJ
239 stack of images using DeadEasy Synapse software [39](Fig.4B, Table S1). Since the NMJs
240 were smaller, this suggested that the increase in active zones was a homeostatic
241 compensation of defective synaptic function, to enable adequate behaviour. Homeostatic
242 adjustments in active zones are a common manifestation of structural plasticity at the NMJ
243 [47]. Remarkably, the increase in active zone density did not occur in *kek6*^{-/-} *DNT2*^{-/-} double
244 mutants (Fig.4B, Table S1), meaning that compensation fails in the double mutants. To
245 further test how Kek-6 affects the synapse, we also visualised Synapsin, which
246 phosphorylates components of the SNARE complex to promote neurotransmitter vesicle
247 release [48], and quantified it automatically using DeadEasy Synapse software [39]. *kek6*^{-/-}
248 mutants had reduced Synapsin production (Fig.4B, Table S1), revealing defective synapse

249 composition. Conversely, over-expression of *kek-6* did not alter NMJ size (Fig.5A and
250 Supplemental Fig.S4A), but it increased active zone density (Fig.5A, Table S1), and induced
251 ghost boutons, albeit not significantly (Supplemental Fig.S3C-E, Table S1). Ghost boutons
252 are presynaptic, HRP+ Dlg-negative, immature boutons that fail to get stabilized, and are
253 correlates of increased neuronal activity, thus further indicating that Kek-6 influences
254 structure and/or function. Like Kek-6 gain of function, over-expression of full-length *DNT2-FL*
255 in muscle, and either full-length *DNT2-FL* or mature *DNT2-CK* in motorneurons (with
256 *D42GAL4*), also increased active zones (Fig.5B,C Table S1). Thus both DNT2 and Kek6
257 induce active zone formation. Altogether, these data show that both Kek-6 and DNT2 are
258 required to regulate NMJ growth and for appropriate synaptic structure.

259 Our data suggested that DNT2 functions as a retrograde ligand for Kek-6. Over-
260 expression of *DNT2-FL* in muscle increased axonal terminal size and pre-synaptic active
261 zones (Fig.5B). To verify this, we used epistasis analysis. Over-expression of *kek6* in
262 motorneurons rescued the NMJ mutant phenotypes of bouton number and axonal length of
263 *kek6³⁴/Df(3R)6361* mutants (Fig.6A, Table S1), demonstrating that the *kek6*^{-/-} mutant
264 phenotypes were specific. Over-expression of *kek6* in motorneurons rescued the NMJ
265 phenotypes of *DNT2³⁷/Df(3L)6092* mutants and *kek6^{-/-} DNT2^{-/-}* double mutants (Fig.6B,C,
266 Table S1), demonstrating that Kek-6 functions downstream of DNT2. Over-expression of
267 untagged *DNT2-FL* in muscle (with *MhcGAL4*) increased Dlg+ bouton number (Fig.6B), and
268 importantly, this was rescued by *kek-6* loss of function (Fig.6B, Table S1). Since Kek6
269 functions pre-synaptically, and DNT2 was over-expressed in muscle, this demonstrates that
270 DNT2 is a retrograde ligand for Kek-6. Altogether, our data demonstrate that DNT2 is a
271 retrograde ligand for Kek-6 at the NMJ and that DNT2 and Kek6 are required together for
272 synaptic structure and NMJ growth.

273 Intriguingly, our data also suggested that DNT2 had additional functions compared to
274 *kek-6*. Homeostatic compensation of active zones did not occur in *kek-6^{-/-} DNT2^{-/-}* double
275 mutants (Fig.4B). Furthermore, over-expression of *DNT2* but not *kek-6* increased NMJ size,
276 as both HRP+ axonal terminal length (Fig.5B) and bouton number (Fig.6B) increased when

277 *DNT2-FL* was over-expressed from muscle. DNT2 is also a known ligand of Toll-6 [38], and
278 Toll-6 and -8 are required in motoneurons for NMJ growth and active zone formation[37,43].
279 So this raised two questions: do Toll-6 and Kek-6 interact functionally as DNT2 receptors at
280 the NMJ, and why?

281

282 **Kek-6 and Toll-6 cooperate to modulate NMJ structural homeostasis**

283 LIG proteins and truncated Trk isoforms can function as ligand sinks or dominant negative
284 co-receptors that abrogate signaling, e.g. by full-length Trks [6,7]. Thus, Kek-6 might inhibit
285 Toll-6 function.

286 Although Toll-6 has NMJ functions, its expression here had not been reported [43].
287 Using a MIMIC insertion into the intronless coding region of Toll-6, we generated *Toll-6GAL4*
288 flies by RMCE, and found Toll-6>mCD8-GFP to be distributed at the muscle 6/7 NMJ,
289 colocalising with the motoraxon marker FasII (Fig.7A). Like *kek-6* and *DNT2* mutants, *Toll-*
290 *6^{MIO2.127}/Df(3L)BSC578* mutants had smaller NMJs, with shorter HRP+ axonal length (Fig.6B,
291 Table S1) as previously reported [43], confirming that Toll-6 is required for NMJ growth.
292 Contrary to *kek-6^{-/-}* mutants, *Toll-6^{-/-}* mutants had reduced Brp+ active zones compared to
293 controls (Fig.7B), meaning that Toll-6 is required for active zone formation. *kek-6^{-/-} Toll-6^{-/-}*
294 double mutant larvae still had small NMJs, like each single mutant alone (Fig.7B, Table S1),
295 and Brp+ active zones remained lower than in controls and comparable to the levels of *Toll-*
296 *6^{-/-}* single mutants (Fig.7B). These results reveal that: 1) Since Toll-6 is required for active
297 zone formation, and over-expression of *kek-6* increased active zones, Kek-6 does not
298 function as a DNT2 sink nor as an inhibitor or dominant negative co-receptor for Toll-6. 2)
299 The compensatory increase in active zones observed in *kek-6^{-/-}* and *DNT2^{-/-}* single mutants
300 did not occur in *kek-6^{-/-} DNT2^{-/-}* or *kek-6^{-/-} Toll-6^{-/-}* double mutants, meaning that the
301 concerted functions of Toll-6 and Kek-6 as DNT2 receptors are required for NMJ structural
302 homeostasis.

303 To test whether Kek-6 and Toll-6 might physically interact to form a receptor complex,
304 we carried out co-immunoprecipitations, and to ask if potential interactions were promiscuous

305 or specific, we also tested Toll-7. S2 cells were co-transfected with the active forms *Toll-6^{CY}-*
306 *Flag* or *Toll-7^{CY}-Flag* and *Kek6-HA*, and we found that precipitating Toll-6^{CY} and Toll-7^{CY} with
307 anti-Flag brought down Kek6 detected with anti-HA (Fig.7C). Thus, Kek6 can bind Toll-6 and
308 Toll-7.

309 Altogether, these data showed that retrograde DNT2 can bind two receptor types at
310 the NMJ - Toll-6 and Kek-6 - which can interact pre-synaptically to cooperatively promote
311 NMJ growth and regulate active zone homeostasis. This, however, raised a new question: if
312 Kek-6 did not function simply by modulating Toll-6, and in the absence of a TyrK, how might
313 it function?

314

315 **Kek-6 functions via CaMKII and VAP33A**

316 To find out how Kek-6 might function, we carried out pull-down assays to isolate candidate
317 factors binding its intracellular domain. S2 cells were transfected with *kek6-Flag*, and anti-
318 Flag coated beads were used to expose Kek-6 to cell lysates from either S2 cells or wild-type
319 adult fly heads, and bound proteins were isolated by SDS-PAGE followed by mass
320 spectrometry (Fig.8A,B). Candidates were identified as proteins present in Kek6-Flag
321 samples and absent from non-transfected mock controls, and if identified from multiple
322 peptides (Tables S2 and S3). Prevalent amongst these were proteins involved in vesicle
323 trafficking, axonogenesis, dendrite morphogenesis and synaptic function (Fig.8C). Amongst
324 the top hits were CaMKinase II identified from fly heads, and VAP33A from both S2 cells and
325 heads (Fig.8C). CaMKII functions both as a kinase and a scaffolding protein, to promote
326 structural synaptic plasticity. Post-synaptically, it phosphorylates and recruits AMPAR and
327 NMDAR to the post-synaptic density, leading to post-synaptic potentiation, and pre-
328 synaptically it localizes to active zones and phosphorylates Synapsin and other SNARE
329 complex proteins, triggering neurotransmitter release [48-51]. VAP33A is a Vamp Associated
330 Protein, of the SNARE complex, and also has universal functions in exocytosis and vesicle
331 trafficking [52]. To validate these two candidates as downstream effectors of Kek-6, we
332 carried out co-immunoprecipitations. We co-transfected S2 cells with Kek6-Flag and either

333 CaMKII or VAP33A tagged with HA. Precipitating Kek-6-Flag, brought down CaMKII-HA
334 (Fig.8D). Similarly, precipitating Kek-6-Flag also brought down VAP33A-HA (Fig.8D). Thus,
335 Kek-6 can bind CaMKII and VAP33A.

336 To validate the functional relationship between Kek-6 and CaMKII *in vivo*, we asked
337 whether altering Kek-6 function would affect CaMKII activation in brain. We tested for the
338 constitutively active state of CaMKII, corresponding to phosphorylation at Thr286 (T287 in
339 *Drosophila*), using anti-pCaMKII^{T287} antibodies. In the heads of *kek6³⁴/Df(3R)ED6361* mutant
340 adult flies the relative levels of pCaMKII^{T287}, normalised over non-phosphorylated CaMKII,
341 decreased (Fig.8E Table S1). Conversely, over-expression of *kek-6* in retina (with
342 *GMRGAL4*) increased CaMKII phosphorylation (Fig.8E, Table S1). Over-expressing *DNT2-*
343 *FL* had the same effect (Fig.8E). Thus, Kek-6 is required for CaMKII activation, and both
344 Kek-6 and DNT2 can activate CaMKII downstream.

345 Next we asked whether CaMKII and VAP33A might function downstream of Kek6 at
346 the NMJ. Unfortunately, we were not able to get antibodies to inactive CaMKII to work
347 reliably at the NMJ for normalisation, so we visualised constitutively activated CaMKII with
348 pCaMKII^{T287} and quantified it automatically, using DeadEasy Synapse, which detected the
349 increase in pCaMKII caused by the over-expression of activated CaMKII^{T287} in motoneurons
350 (*D42>CaMKII^{T287D}*, Fig. S4A,C). Pre-synaptic over-expression of *CaMKII^{T287}* increased
351 axonal length, lb bouton number and active zone density, and inhibiting CaMKII activation
352 pre-synaptically by over-expressing the CaMKII phosphorylation inhibitor *Ala* [53] resulted in
353 smaller NMJs and reduced active zones (Fig.S4A-C, Table S1), as previously reported [54].
354 Thus we asked whether Kek-6 influenced CaMKII at the NMJ. Pre-synaptic over-expression
355 of *kek6* increased pCaMKII^{T287} levels (Fig.9A, Table S1). This increase was rescued by the
356 over-expression of *Ala* together with *kek6*, showing that this phenotype was specific (Fig.9A,
357 Table S1). However, over-expression of *Ala* alone did not result in a detectable reduction in
358 pCaMKII in this case (Fig.9A, Table S1). This could be due either to the fact that CaMKII is
359 most abundant post-synaptically, and we were only inhibiting it pre-synaptically, or to limited
360 efficacy of the inhibitor. To try an alternative approach, we knocked-down pre-synaptic

361 *CaMKII* expression with RNAi, and this decreased pCaMKII^{T287} levels, causing a stronger
362 effect than Ala (Fig.9A, Table S1). Like Ala, pre-synaptic *CaMKII-RNAi* knock-down together
363 with *kek-6* over-expression also rescued pCaMKII^{T287} levels, and reduced them further than
364 controls (Fig.9A, Table S1), meaning that CaMKII functions downstream of Kek-6. Together,
365 these data show that Kek-6 activates CaMKII.

366 Pre-synaptic CaMKII localizes to active zones [49,55], so next we asked whether
367 CaMKII was required for the increased active zones caused by *kek-6* gain of function.
368 CaMKII inhibition with Ala or knock-down with RNAi decreased active zones (Fig.S4A,B and
369 Fig.9B, Table S1) and over-expression of *activated CaMKII* in motoneurons increased active
370 zones (Fig.S4A,C, Table S1). Remarkably, over-expression of *Ala* or *CaMKII-RNAi* together
371 with *kek6*, rescued the increase in active zones caused by *kek6* gain of function (Fig.9C,D,
372 Table S1). These showed that CaMKII is required downstream of Kek-6 for active zone
373 formation. Furthermore, in *kek6*^{-/-} mutants and *kek6*^{-/-} *DNT2*^{-/-} double mutants the levels of
374 pCaMKII^{T287} decreased (Fig.10A, Table S1), showing that Kek-6 is required for CaMKII
375 activation at the NMJ. We found no significant effect of *DNT2* loss or gain of function on
376 pCaMKII^{T287} levels at the NMJ. Importantly, over-expressing activated *CaMKII*^{T287D} pre-
377 synaptically rescued the phenotypes of decreased axonal length and reduced lb boutons of
378 *kek6*^{-/-} (Fig.10B) and *DNT2*^{-/-} (Fig.10C) single mutants, and *kek6*^{-/-} *DNT2*^{-/-} double mutants
379 (Fig.10D) (Table S1). This means that the mutant phenotypes were caused, at least partly,
380 by decreased CaMKII activation. Together, these data demonstrate that Kek-6 and DNT2
381 function in concert upstream of CaMKII to regulate NMJ size and active zones.

382 To test the functional link between Kek-6, DNT2 and VAP33A, we used genetic
383 epistasis. Loss of *VAP33A* function in mutants caused a reduction in lb boutons (Fig.11A,B),
384 and pre-synaptic over-expression of *VAP33A* increased lb bouton number (Fig.11A,D,E,
385 Table S1), as previously reported[52]. These phenotypes were also shared with alterations in
386 *kek6* and *DNT2* levels, consistent with common functions. Importantly, over-expression of
387 *VAP33A* in motoneurons rescued bouton number in *kek-6*^{-/-} (Fig.11A,C) and *DNT2*^{-/-}
388 (Fig.11A,D) single mutants (Table S1). Thus, VAP33A functions downstream of Kek-6 and

389 DNT2. Interestingly, *kek-6^{-/-} DNT2^{-/-}* double mutants rescued the increase in Ib boutons
390 caused by *VAP33A* over-expression, restoring bouton number down to control levels
391 (Fig.11A,E, Table S1). This suggests that *VAP33A* may be required both for pre-synaptic
392 vesicle release downstream of *Kek6*, and post-synaptic secretion of *DNT2*.

393 To conclude, altogether these data show that *CaMKII* and *VAP33A* function
394 downstream of *DNT2* and *Kek6* in motoneurons.

395

396 DISCUSSION

397

398 *Drosophila* homologues of the *Trk* receptor family had long been sought. This was important
399 to find fundamental principles linking structure and function in any brain. Here, we show that
400 *Kek-6* is a *Trk*-family receptor lacking a *TyrK*, for the neurotrophin ligand *DNT2*, regulating
401 structural synaptic plasticity via *CaMKII* and *VAP33A*, in *Drosophila* (Fig.12A,B).

402 Starting with an unbiased approach, we showed that of all *Drosophila* *LIGs* *Keks* are
403 the most likely *DNT* receptors in the *CNS*, and used two assays to demonstrate binding of
404 *Kek-6* to *DNTs*. Using *in vivo* analyses, we demonstrate that motoneurons express *kek-6*,
405 and *Kek-6* binds *DNT2* which is produced by the muscle in post-synaptic boutons, and
406 functions retrogradely. *kek-6* and *DNT2* share mutant phenotypes, *kek6 DNT2* double
407 mutants have synergistic phenotypes, and *kek-6* over-expression can rescue mutant
408 phenotypes of *kek6^{-/-}* and *DNT2^{-/-}* single single and *kek6^{-/-}DNT2^{-/-}* double mutants. *Kek-6* is
409 not a ligand sink or dominant co-receptor for *Toll-6*. Instead, *Kek-6* and *Toll-6* can interact
410 physically and function cooperatively as *DNT2* receptors. *Kek-6* recruits *CaMKII* and
411 *VAP33A* to a pre-synaptic downstream complex and induces *CaMKII* activation. Epistasis
412 analysis demonstrated that *Kek6* functions in motoneurons downstream of *DNT2* and
413 upstream of *CaMKII* and *VAP33A* to promote *NMJ* growth, and active zone formation. We
414 conclude that *DNT2* and its receptors *Kek-6* and *Toll-6* regulate synaptic structural plasticity
415 and homeostasis.

416 Despite abundant evidence that retrograde signals and positive feedback loops
417 regulate structural synaptic plasticity at the *Drosophila* glutamatergic NMJ, the identification
418 of retrograde factors had been scarce [45,56], creating a void for the general understanding
419 of structural synaptic plasticity. BDNF is a key retrograde ligand in mammals, and together
420 with its receptor TrkB they form a positive feedback loop that reinforces synaptic function
421 [1,4]. We have shown the neurotrophin DNT2 is a retrograde ligand for Kek6 (Fig.12B).
422 DNT2 is produced in muscle and over-expression of tagged DNT2 in muscle leads to its
423 distribution in pre-synaptic boutons; over-expression of *DNT2* in muscle induces bouton,
424 active zone formation and axonal terminal growth, pre-synaptically; *DNT2* mutants have
425 smaller NMJs, and pre-synaptic over-expression of either *kek6*, *CaMKII* or *VAP33A* can
426 rescue the *DNT2* loss of function phenotype; and conversely, *kek6* loss of function rescues
427 the phenotype caused by *DNT2* over-expression in muscle. Thus, DNT2 is an evolutionarily
428 conserved retrograde factor at the *Drosophila* synapse.

429 We demonstrate that *keks* are the *Drosophila* *Trk*-family homologues. Previous
430 searches for *Trk*-family receptors in fruitflies had focused on the Tyrosine Kinase domain,
431 and did not identify any bona fide candidates [14-16,18]. Subsequent proteomic analyses
432 confirmed the absence of full-length *Trk* receptors with a conserved tyrosine kinase in
433 fruitflies [19-21]. Since those earlier searches, *Trks* in mammals have been found to encode
434 multiple isoforms, most of which lack the tyrosine kinase domain [6,57]. Human TrkB has 100
435 isoforms, which produce 36 different proteins, of which four are abundant, and the most
436 abundant isoform in the adult human brain is truncated TrkB-T1, which lacks the tyrosine
437 kinase [6,57]. Paradoxically, the function of TrkB-T1 in neurons in the mammalian brain is
438 unknown. Our findings suggest that truncated *Trk* family receptors could have an
439 evolutionarily conserved function regulating structural synaptic plasticity.

440 We also show that Kek-6 functions cooperatively rather than antagonistically with pre-
441 synaptic Toll-6, a known receptor for DNT2, that is also required for synaptic structural
442 plasticity [43]. *LIG* proteins and truncated *Trk* isoforms can function as ‘dominant negative’
443 co-receptors or ‘ligand sinks’. TrkB-T1 can form dimers with TrkB-FL and abrogate signaling,

444 and bind BDNF rendering it unavailable to TrkB-FL [6,7]. This is thought to modulate kinase-
445 signaling levels by TrkB [58]. Similarly, in *Drosophila*, Kek-5 is an inhibitor of BMP signaling
446 [26] and Kek1 an inhibitor of EGFR signaling [59]. Thus, each Kek could function as a
447 specific inhibitor of different signaling pathways. We have shown that Kek-6 and Toll-6 can
448 form a receptor complex for DNT2, as DNT2, as well as binding Toll-6 [38], can also bind
449 Kek-6, and Kek-6 and Toll-6 interact physically. However, our evidence shows that Kek6
450 does not function as an inhibitor of Toll-6, and instead Kek-6 and Toll-6 have distinct
451 functions that positively cooperate to regulate NMJ structure and growth. All *kek-6^{-/-}* and
452 *Toll-6^{-/-}* single mutants, and *kek-6^{-/-} Toll-6^{-/-}* double mutants, have smaller NMJs, ruling out
453 antagonistic functions. Toll-6 is required for active zone formation, and over-expression of
454 *kek-6* also increases active zones, which means Kek-6 does not repress Toll-6. Interactions
455 between DNT2, Kek-6 and Toll-6 are required for homeostatic compensation of active zones,
456 as compensation fails in *kek6^{-/-} DNT2^{-/-}* and *kek-6^{-/-} Toll-6^{-/-}* double mutants. Our data
457 suggest that Kek-6 and Toll-6 influence synaptic structure via alternative, independent
458 pathways. Toll-6 functions in neurons via a canonical pathway to regulate NFκB and JNK
459 [36]; Toll-8 and Toll-6 regulate NMJ plasticity also via an alternative dFOXO pathway[37,43];
460 and we show that Kek-6 functions via CaMKII and VAP33A to regulate synaptic structure
461 independently of Toll-6 (Fig.12B). With our assays, DNTs can bind both Tolls [38] and Keks
462 (this work) promiscuously. The biological significance of this promiscuity is not understood,
463 as ligand-receptor interactions will depend on the availability of each one in different contexts
464 and times. Altogether, our findings strongly suggest that DNTs, Keks and Tolls constitute a
465 novel molecular mechanism that regulates synaptic structural plasticity and homeostasis.

466 We do not yet know how CaMKII gets activated downstream of Kek-6. CaMKII
467 activation and recruitment to active zones depends on the intracellular increase in Ca²⁺
468 levels, both through Ca²⁺ channels, and Ca²⁺ stores through the PLC and IP3 pathways
469 [50,55]. In mammals, TrkB-T1 regulates Ca²⁺ levels in glia and in the heart, two contexts
470 expressing high levels of TrkB-T1 and no TrkB-FL [60-62]. However, the mechanism by
471 which TrkB-T1 raises Ca²⁺ is unknown [60,61], and whether this results in the activation of

472 CaMKII is unclear or may be context dependent [60,62]. CaMKII activation in neurons could
473 depend on the increase in Ca^{2+} with neuronal activity. A potential link of Kek-6 to neuronal
474 activity was revealed by the increase in ghost boutons with *kek-6* gain of function.
475 Furthermore, *kek-2* expression is modulated by neuronal activity, appropriate Kek2 levels at
476 the NMJ are required for normal synaptic structure, and DNT2 can modulate the Na^+/K^+
477 ATPase [27,63]. Thus, Kek-6 could function via a PLC pathway or by influencing membrane
478 channels, to increase Ca^{2+} levels and induce CaMKII activation.

479 The finding that Trk-like receptors can regulate neuronal plasticity independently of
480 kinase signalling is very important. Activation of PLC γ by TrkB TyrK signaling is generally
481 seen as a key mechanism of plasticity [1,5]. Yet CaMKII is necessary and sufficient for
482 synaptic structural plasticity, LTP and long-term memory, and has wide functions in synaptic
483 organization and homeostasis [49-51]. CaMKII can function as a frequency detector, and
484 cause long lasting changes in synaptic strength, structure and brain plasticity [50]. Thus, the
485 regulation of CaMKII and Ca^{2+} by truncated Trk-family receptors and Keks means that they
486 could regulate structural synaptic plasticity independently of the canonical TyrK-dependent
487 PLC γ pathway.

488 Keks are not identical to truncated Trk receptors and may carry out further functions
489 that could be implemented via other routes in mammals. TrkB-T1 has a very short
490 intracellular domain, whereas Keks have longer intracellular fragments including a
491 PSD95/Dlg/ZO1 (PDZ) motif [22,24,25]. PDZ domains are involved in scaffolding, and
492 assembly of post-synaptic complexes that regulate the size and strength of synapses [64].
493 Through its PDZ domain, Kek-6 might recruit synaptic partners and Ca^{2+} channels.
494 Interestingly, truncated TrkC-T1 binds the PDZ-containing protein Tamalin to induce cellular
495 protrusions via Rac[65]. Thus, it is imperative to explore further functional conservation or
496 divergence of signaling mechanisms of Keks vs. truncated Trks.

497 To conclude, evolution may have resolved how to implement structural synaptic
498 plasticity through distinct mechanisms in fruit-flies and humans, or perhaps common

499 molecular principles are shared by both, even if not in every detail. We found that in fruitflies,
500 truncated-Trk-like receptors encoded by the Keks bind neurotrophin ligands to regulate
501 structural synaptic plasticity via CaMKII and VAP33A, and the receptor complex also
502 includes Tolls. It is compelling to consider whether such a non-canonical mechanism of
503 neuronal plasticity, downstream of neurotrophins and Trk receptors but independently of
504 kinase signaling, may also operate in humans, as it could uncover novel mechanisms of
505 brain function and brain disease.

506

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517

518 MATERIALS AND METHODS

519 **Genetics. Mutants:** *Df(3R)ED6361* lacks the *kek-6* locus (Kyoto Stock Centre), *Df(3L)6092*,
520 *Df(3L)ED4342*, *DNT1*⁴¹ and *DNT2*^{e03444} are described in[35], *Df(3L)BSC578* lacks the *Toll-6*
521 locus (Bloomington). Mutant null alleles *kek6*³⁴ and *kek6*³⁵, and *DNT2*³⁷, were generated by
522 FRT mediated recombination of the PiggyBac insertion lines [46]: for *Kek6*:
523 *PBac{RB}kek6*^{e000907} and *PBac{WH}kek6*^{f05733}; for *DNT2*: *PBac{RB}spz5*^{e03444} and
524 *PBac{WH}Shab*^{f05893}. Mutants were selected using genetics and PCR, using primers as
525 recommended in [46]. *kek6*³⁴ is a 41.9 kb deletion that just removes the coding region for
526 *kek6*; *DNT2*³⁷ is a 27 kb deletion that removes the ATG and first exon, most likely resulting in

527 no protein production (Foildi et al, under review). **GAL4 lines:** *kek5GAL4* line
528 *P{GawB}NP5933* (from BSC); *w;;elavGAL4* drives expression in all neurons (insertion on the
529 third chromosome); *Toll-6-GAL4* was generated by RMCE from *MIMICToll-6^{MIO2127}*;
530 *w;;D42GAL4* and *w;Toll-7GAL4* drive expression in motoneurons and have been previously
531 described[38]; *w; MhcRFP MhcGAL4* drives expression in muscle (BSC); *w; GMRGAL4*
532 drives expression in retina. **UAS lines:** to drive expression of each of the *keks* UAS-lines
533 were made as described below. *w;;UAS-DNT2-FL* expresses full length untagged DNT2;
534 *w;;UASDNT2-CK* expresses the mature form of DNT2, i.e. signal peptide+cystine-knot
535 domains; *w; UAS-DNT2-FL-GFP* expresses full-length DNT2 tagged at the COOH end, and
536 were made as described below. *w; 10xUASmyr-Td-Tomato* is membrane tethered (gift of B.
537 Pfeiffer); *w;UASCaMKII^{287D}* expresses constitutively active CaMKII and *w;UASA/a* expresses
538 the CaMKII inhibitor (gifts of J. Hodge); *UASCaMKII-RNAi: y sc v; P{y[+ v+,*
539 *TRiP.GL00237}attP2/TM3, Sb* (BSC); *y[1] w[*]; P{w[+mC]=UAS-FLAG.Vap-33-1.HA}2*
540 (BSC). Double mutant lines were generated by conventional genetics. **MIMIC-GFP lines:** *y*
541 *w; MIMICkek6^{M113953}* and has a GFP insertion in the coding region (BSC). All stocks were
542 balanced over *SM6aTM6B* or *TM6B* to identify balancer chromosomes, and all were
543 generated from a *yw* or *w* mutant background. In all figures, controls are: (1) F1 from *yw* x
544 *Oregon*; (2) *w; GAL4/+*
545
546 **Molecular cloning.** Full length cDNAs for *kek1*, 2, 3, 4, 5 and 6 were obtained either from
547 cDNA clones (*kek1*, *SD01674*; *kek2*, *NB7*), by PCR from cDNA libraries (gift of G. Tear; LD:
548 *kek5*; GH: *kek3*; *kek6*), or by reverse transcription PCR from larvae (*kek4*), using primers
549 designed for Gateway cloning into the pDONR plasmid: *kek1* forward:
550 GGGGACAAGTTTGTAC AAA AAA GCA GGC TCA TCC AGG AAA **ATG** CAT ATC A and
551 reverse: GGGGACCAC TTT GTA CAA GAA AGC TGG GTA GTC AGT TCT TGG TTT GGT
552 TT; *kek2*: forward: GGGGACAAGTTTGTAC AAA AAA GCA GGC TCA **ATG** AGT GGT
553 CTG CCA ATC T and reverse: GGGGACCAC TTT GTA CAA GAA AGC TGG GTA AAT
554 GTC GCT GGT TTC CTG GC; *kek3*: forward: GGGGACAAGTTTGTAC AAA AAA GCA

555 GGC TCA TAT GCG **ATG** GCA GCG GGA A and reverse: GGGGACCAC TTT GTA CAA
556 GAA AGC TGG GTA GCT CTT GAA AAT ATC CTG TC; *kek4*: forward:
557 GGGGACAAGTTTGTAC AAA AAA GCA GGC TCA CTA GAC CTT CCG TTC CTT, and
558 reverse: GGGGACCAC TTT GTA CAA GAA AGC TGG GTA TAT TGA GAT ATC AAC ACC
559 AG; *kek5*: forward: GGGGACAAGTTTGTAC AAA AAA GCA GGC TAG CTA GAC GCA
560 GAC TTA GAG and reverse: GGGGACCAC TTT GTA CAA GAA AGC TGG GTA GAC CTC
561 GGT GCC ATC CTC GC; *kek6*: forward: GGGGACAAGTTTGTAC AAA AAA GCA GGC
562 TCA **ATG** CAT CGC AGC ATG GAT C and reverse: GGGGACCAC TTT GTA CAA GAA
563 AGC TGG GTA GAG CGA CAC GAA CTC GCC AG. *CaMKII* and *VAP33A* full-length cDNAs
564 were cloned using the Gateway System first into *pDONR*, and then into *pAct5-attR-HA*.
565 For expression in flies under UAS/GAL4 control, cDNAs were subcloned to a
566 Gateway *pUAS-attR-mRFP* destination vector for conventional transgenesis, injected by
567 BestGene (www.thebestgene.com). For expression in S2 cells, they were subcloned into
568 tagged *pAct* destination vectors *pAct5c-attR-mCFP*, *pAct5c-attR-FLAG* and *pAct5c-attR-HA*.
569 Constructs used for expression of S2 cells of DNT1 and 2, Toll-6 and 7 were as previously
570 described[38]. Chimaeric Kek-Toll-6 receptors were generated after analyzing the domain
571 composition of the proteins using ProSite (ExpASy), PFAM, SMART, TMHMM and TMPred
572 algorithms and PubMed data. Primers were designed to amplify the sequences that encode
573 the extracellular and transmembrane domains of Kek3–6, including 15 amino acids C-
574 terminal to the Kek transmembrane region, and the intracellular domain of Toll6, at halfway
575 between the transmembrane region and the TIR domain. A unique enzyme site (BamHI or
576 EcoRI) was included in the designed primers to join the *kek* and *Toll-6* sequences, and attB
577 sites were introduced in the primers at the 5' and 3' ends of the chimaeric insert for Gateway
578 cloning into *pAct5c-attR-3xHA* destination vector. Unfortunately, we were not able to
579 generate *kek1-Toll-6* and *kek2-Toll-6* chimaeric receptor constructs. To clone chimaeric
580 *kek3,4,5,6-Toll-6* receptor constructs, reverse primers at the juxtamembrane of *keks* were as
581 follows: *kek3-Toll-6*:_CGAT-GAATTC-AGGTACAGAGTTCCAGAGAC; *kek4-Toll-6*: CGCG-
582 GAATTC-TTGCAAATAAGTGTGCTGGC; *kek5-Toll-6*: CTAT-GGATCC-

583 GCTCATCATGGTGGTGCCT; *kek6-Toll-6*: GTAT-GAATTC-
584 ACGCCGGCCTTGTTGGCATG. *Toll-6* primers from chimaeras were: Forward primers from
585 juxtamembraneCATG-GAATTC-AACTTCTGCTACAAGTCACC (compatible with *kek3*, *kek4*
586 and *kek6* chimaeras) or CATG-GGATCC-AACTTCTGCTACAAGTCACC (compatible with
587 *kek5* chimaera) and reverse from C terminus: GGGGACCAC TTT GTA CAA GAA AGC TGG
588 GTC CGC CCA CAG GTT CTT CTG CT.

589 Un-tagged full-length DNT2 was cloned into the pUAS-attB vector by conventional
590 cloning, DNT2-full length (DNT2-FL) was PCR-amplified from cDNA libraries, and cloned into
591 pUAS-attB for Φ C31 transgenesis [66]. UAS-DNT2-FL-GFP was cloned by Gateway cloning
592 into pUAS-GW-GFP, followed by conventional transgenesis.

593

594 **Luciferase signaling in S2 cells.** For Dif signaling assays using chimaeric *kek-Toll-6*
595 receptors, S2 cells stably transfected with *drosomycin-luciferase* were maintained at 27°C in
596 air in Insect-Xpress medium (Lonza) supplemented with penicillin/streptomycin/L-glutamine
597 mix (Lonza) and 10% foetal bovine serum (Lonza). 1ml suspended cells were passaged
598 every two days into 4ml fresh medium. 3×10^6 cells in 2ml media were seeded per well of a 6-
599 well plate 24 hours prior to transfection. Per well of experiment, 250 μ l serum-free media, 3 μ l
600 TransIT-2020 (Mirus), 2 μ g of HA tagged chimaeric receptors *kek-toll6-HA* plus 1 μ g of *pAct-*
601 *renilla-luciferase* were incubated at room temperature for 30 minutes, supplemented with
602 350 μ l serum-free media and added to aspirated cells. After 4 hours, transfection mixture was
603 removed and 2ml supplemented medium added. All experiments were conducted 48 hours
604 after transfection; for imaging membrane targeting of *Kek-Toll6-HA* protein S2 cells were
605 starved for 6h prior to fixation.

606 For signaling assays, S2 cells were stimulated with 50nM/well of purified baculovirus
607 DNT2 protein (generated as previously described[38]) and Dif signalling quantified by
608 luminescence. DNT2 was added 48 hours after transfection and luminescence quantified 24
609 hours after DNT stimulation. Transfected and stimulated cells were pelleted from single
610 wells, resuspended in 400 μ l media and separated into three 50 μ l aliquots in an opaque 96-

611 well plate. 40µl of Firefly Luciferase Substrate (Dual-Glo Luciferase Assay System;
612 Promega) was added per 50µl aliquot, incubated for 10 minutes, and luminescence
613 measured using a Mithras LB 940 Multimode Microplate Reader (Berthold). 40µl Stop & Glo
614 substrate (Dual-Glo Luciferase Assay System; Promega) was added to quench Dif signal
615 and activate Renilla Luciferase. Renilla luminescence data was used to normalize Firefly
616 Luciferase data.

617

618 **Co-immunoprecipitations.** Coimmunoprecipitations were carried out as previously
619 described[38], after transfecting standard S2 cells with the following constructs: (1) Co-IP
620 Kek6-DNT2: *pAct5C-Pro-TEV6HisV5-DNT2-CK* and *pAct5C-Kek6-3xHA*; (2) Co-IP Kek6-
621 DNT2 or Kek6-DNT1: *pAct5C-Kek6-3xHA*, *pAct5C-Pro-TEV6HisV5-DNT1-CK-CTD*, *pAct5C-*
622 *Pro-TEV6HisV5-DNT2-CK*; (3) Co-IP Kek5-DNT2: *pAct5C-Kek5-3xFlag* and *pAct5C-Pro-*
623 *TEV6HisV5-DNT2-CK*. (4) Co-IP kek6-Toll-6: *pAct5C-Kek6-HA* and *pAct5C-Toll-6^{CY}-3xFlag*,
624 *pAct5C-Toll-7^{CY}-3xFlag* . (5) Co-IP Kek6-CaMKII: *pAct5-CaMKII-HA* and *pAct-kek-6-FLAG*.
625 (6) Co-IP kek6-VAP33A: *pAct5-Vap33A-HA* and *pAct-kek-6-FLAG*. 48h after transfection
626 cells were harvested and washed in PBS. Final cell pellets were lysed in 600 µL NP-40
627 buffer (50 mM Tris-HCl pH:8.0, 150 mM NaCl, 1% Igepal-630) supplemented with protease
628 inhibitor cocktail (Pierce). For V5 and HA immuno-precipitations, 500 µL of lysates from single
629 or co-transfected cells were incubated with 1 µg of mouse anti-V5 or 1 µg of mouse anti-HA
630 antibodies overnight at 4 °C, then the lysate plus antibody mixtures were supplemented with
631 25 µL of protein-A/G magnetic beads (Pierce) and incubated for 1 h at room temperature.
632 For Flag immunoprecipitations, lysates were incubated with anti-Flag antibody conjugated
633 magnetic beads (Sigma-Aldrich) overnight at 4 °C. In both cases, beads were washed
634 thoroughly in NP-40 buffer and/or PBS. Proteins were eluted in 40 µL of 2x Laemmli-buffer
635 and analysed by Western blot following standard procedures.

636

637 **Pull-down assays and proteomics.** S2 cells were transfected with 4 µg *pAct5C-Kek6-*
638 *3xFlag* expression construct. For controls mock-transfected cells (i.e. no construct) were

639 used. After transfection cells were processed as described above for co-immunoprecipitation.
640 600 μ L of cell lysates were incubated with 20 μ L of anti-Flag conjugated magnetic beads
641 overnight at 4 °C. Beads were washed thoroughly in PBS, then proteins were eluted in 40 μ L
642 2x Laemmli-buffer for 10 min at room temperature. Eluted proteins were loaded onto 10%
643 polyacrylamide gels. Alternatively, proteins were not eluted after overnight incubation with
644 anti-Flag beads, but they were re-incubated with whole fly (OregonR) head lysates. Here, 60
645 heads were lysed in 600 μ L of NP-40 buffer. After overnight incubation at 4 °C, proteins were
646 eluted and analysed as for S2 cell lysate proteins. Thus, eluted proteins were loaded onto
647 10% polyacrylamide gels, and the gels were stained with Coomassie Blue and cut into
648 several pieces. Gel pieces were subjected to in-gel digestion with trypsin using a standard
649 protocol. Tryptic peptides were analysed by LC-MS/MS using Ultimate 3000 HPLC coupled
650 to a LTQ Orbitrap Velos ETD mass-spectrometer. Peptide separation, mass spectrometric
651 analysis and database search were carried out as specified at the University of Birmingham
652 Proteomics Facility. Candidate binding proteins were identified on these criteria: (1) Proteins
653 were accepted only if they were identified with at least two high confident peptides. (2) Mock-
654 transfected controls and Kek6-3xFlag samples were compared, and only proteins identified
655 from Kek6-3xFlag lysates or heads, but absent from controls, were considered as possible
656 interacting partners for Kek6.

657

658 **Western blotting.** Western blot was carried out following standard procedures using
659 antibodies listed here: mouse anti-V5 (1:5000, Invitrogen), mouse anti-HA (1:2000, Roche),
660 chicken anti-HA (1:2000, Aves), rabbit anti-Flag (1:2000, Sigma-Aldrich), HRP-conjugated
661 anti-mouse IgG (1:5000-1:10000, Vector), HRP-conjugated anti-chicken IgG (1:5000,
662 Jackson Immunoresearch), HRP-conjugated anti-rabbit IgG (1:1000-1:5000, Vector), mouse
663 dCaMKII (Cosmo CAC-TNL-001-CAM 1:1000), rabbit α -p-CaMKII α (Thr 286) (Santa Cruz sc-
664 12886-R 1:1000), mouse Tubulin DM1A (Abcam ab7291 1:10000).

665

666 **NMJ dissections and preparation**

667 NMJ preparations were carried out according to [67]. For GFP stainings in *MhcGAL4>UAS-*
668 *DNT2-FL-GFP*, L3 larvae were placed in agar plates (2%) and left at 29°C for 90 minutes to
669 potentiate the NMJ before dissections [68]. A hundred and twenty female flies and 50 males
670 were placed in a cage with a removable agar and grape juice plate. On the second day,
671 plates were changed for new ones in the morning and evening, and discarded. On the third
672 day, the plates were changed every 1h 30min and discarded. On the fourth day, the plates
673 were changed every 1h 30min and kept in a 25°C incubator for larvae collection. The next
674 day, hatched L1 larvae from each plate were transferred to a vial, and exactly 40 larvae were
675 placed in each vial. When larvae reached L3 stage (5 days after egg laying), they were
676 dissected in low calcium saline as previously described[67], and fixed for 10 minutes in
677 Bouin's solution (HT10132 SIGMA). Samples were washed 6 times for 10 minutes in PBT
678 (0.1% of Triton in 1M PBS) to remove fixative solution and kept overnight in blocking solution
679 (10% normal goat serum in 0.1% Triton in PBS 1M). Primary antibodies were incubated
680 overnight at 4°C and samples were washed the following day 8 times for 10 minutes in PBT.
681 Secondary antibodies were incubated for 2h at room temperature and samples were washed
682 8 times for 10 minutes in PBT. Samples were mounted in Vectashield anti-bleaching medium
683 (Vector Labs) in No.0 coverslips. NMJs were analysed for muscle 6/7 only; segments A3 and
684 A4 were analysed in each larva.

685

686 **Immuno-stainings and in situ hybridisations.** Antibody stainings in embryos and S2 cells
687 were carried out following standard procedures, using the following primary antibodies at the
688 indicated dilutions: mouse anti-FasII at 1:5 (ID4, Developmental Studies Hybridoma Bank,
689 Iowa); rabbit anti-GFP 1:1000 (Molecular Probes); mouse anti-Dlg 1:20 (4F3, Developmental
690 Studies Hybridoma Bank, Iowa); rabbit anti-HRP 1:250 (Jackson Immunoresearch); mouse
691 anti-Brp 1:100 (nc82, Developmental Studies Hybridoma Bank, Iowa); rabbit anti-p-
692 CaMKII^{T287} 1:150 (Santa Cruz), detects phosphorylation at Thr286 (T287 in *Drosophila*),
693 constitutively active form; mouse plain anti-Synapsin at 1:25 (DSHB 3C11). Secondary
694 antibodies were: anti-guinea pig-Alexa 488 at 1:250 (Molecular Probes); biotinylated anti-

695 mouse at 1:300 (Jackson Labs) followed by the ABC Elite Kit (Vector Labs); biotinylated anti-
696 guinea pig at 1:300 (Jackson Labs) followed by Streptavidin-Alexa-488 at 1:400 (Molecular
697 Probes); anti-rabbit-Alexa 488 at 1:250 (Molecular Probes); anti-mouse-Alexa 488 1:250
698 (Molecular Probes); anti-rabbit-Alexa 647 at 1:250 (Molecular Probes); anti-mouse-Alexa 647
699 1:250 (Molecular Probes).

700 In situ hybridizations were carried out following standard procedures, using antisense
701 mRNA probes from 5' linearised plasmids and transcribed as follows: *lambik*: a 551
702 nucleotides fragment was cloned into pDONR with primers: forward
703 GGGGACAAGTTTGTAC AAA AAA GCA GGC TAG AAA CTA CGC ATG AGC CTG and
704 reverse GGGGACCAC TTT GTA CAA GAA AGC TGG GTA CCG CTC AAA TGT CCA CTG
705 T; then linearised with HpaI and transcribed with T7 RNA polymerase. *CG15744*: a 569
706 nucleotides fragment was cloned into pDONR with primers: forward
707 GGGGACAAGTTTGTAC AAA AAA GCA GGC TGG ATT GGA TAG CCT TGG TGA and
708 reverse GGGGACCAC TTT GTA CAA GAA AGC TGG GTT TCG CTT CCA TCT CCA TCT
709 C (linearised with HpaI, transcribed with T7); *CG16974*: a 548 nucleotides fragment was
710 cloned into pDONR with primers: forward GGGGACAAGTTTGTAC AAA AAA GCA GGC
711 TTA TAT GAA TCC CGA AGG CGC and reverse GGGGACCAC TTT GTA CAA GAA AGC
712 TGG GTT TGG GGG GAG TAG ATG GTA A_(linearised with HPA1, transcribed with T7);
713 *kek1* (*SD01674+pOT2* cDNA clone; linearised with EcoRI, transcribed with SP6 RNA
714 polymerase); *kek2* (*NB7+pNB40*; HindIII; T7); *kek3* (HpaI; T7); *kek4* (*GH27420+pOT2*;
715 EcoRI; SP6); *kek6* (in *pDONR*, HpaI; T7); *CG15744* (in pDNOR, HpaI; T7); *CG16974* (in
716 pDNOR, HpaI; T7); *lambik* (in pDONR, HpaI; T7). Colorimetric reaction was using Alkaline
717 Phosphatase conjugated anti-DIG conjugated.

718

719 **Microscopy and Imaging.** Wide-field Nomarski optics images were taken with a Zeiss
720 Axioplan microscope, 63x lens and JVC 3CCD camera and Image Grabber graphics card
721 (Neotech) and a Zeiss AxioCam HRc camera and Zen software. Laser scanning confocal
722 microscopy was carried out using a Leica SP2 AOBS inverted confocal microscope, 40x

723 lens, at 1024 x 1024 resolution, and a Zeiss LSM710 inverted laser scanning confocal
724 microscope with a 40x lens, 1024 x 1024 resolution, 0.25 μ m step for anti-Brp, and 0.5 μ m
725 step for the rest. Images were compiled using ImageJ, Adobe Photoshop and Illustrator.

726 For NMJ data, all images provided in the figures are projections from Z stacks; all the
727 quantitative analyses were carried out in the raw stacks, not in projections. Muscle surface
728 area was measured from bright field images using ImageJ. Anti-HRP was used to measure
729 total terminal axonal length using ImageJ. Boutons were visualized with anti-Dlg, and total
730 boutons as well as separately Ia and Ib boutons, were counted manually with the aid of the
731 ImageJ Cell Counter plug-in. Automatic quantification of active zones labeled with anti-Brp,
732 and anti-pCaMKII^{T287}, were carried out in 3D throughout the stacks of images using the
733 DeadEasy Synapse ImageJ plug-in that we previously validated [39], and anti-Synapsin was
734 analysed with a slightly modified version. DeadEasy Synapse first reduces the Poisson
735 noise, characteristic of confocal microscopy images, of each slice in the stack using a
736 median filter. Subsequently, in order to separate signal (e.g. Brp+ active zones) from the
737 background, images are segmented. Since the intensity of the staining varied within each
738 image and from image to image, the maximum entropy threshold method [69] was used to
739 find a local optimal threshold value for each pixel. For this, we used a square window of size
740 15x15, sufficient to find the local optimal threshold around each pixel in an image. In this
741 way, each pixel is considered part of an active zone if the value of the pixel is higher than the
742 local threshold, otherwise assigned to the background. Since this method is computationally
743 expensive and very low intensity pixels correspond to background, it was possible to reduce
744 the computation time by assigning pixels whose intensity was lower or equal than 20 directly
745 as part of the background and only applying the thresholding method to pixels whose
746 intensity was higher than 20. Finally the volume of the active zones is measured. This
747 method worked just as accurately with Brp, pCaMKII^{T287} and Synapsin stainings. Data were
748 normalized to muscle surface area or axonal length.

749

750 **Locomotion assays.** L3 wandering larvae were placed one at a time on an agar plate (2%)
751 and left it crawl for 40 seconds. Larvae were filmed crawling across the agar plate and then
752 discarded. Plates were cleared before placing another larva. At least 50 larvae were filmed
753 per genotype, and the test was always done in the morning. Films of 400 frames per larva
754 were analysed using FlyTracker software developed in our lab to obtain the trajectory and
755 speed, as previously described[38].

756

757 **Statistical analysis.** Data were analysed in SPSS Statistics 21 (IBM) and GraphPad Prism
758 6. Confidence interval was 95% ($p < 0.05$). Categorical data were tested using χ^2 , and a
759 Bonferroni correction was applied for multiple comparisons. Continuous data were first tested
760 for normality by determining the kurtosis and skewness, and a Levene's Test was applied to
761 test for homogeneity of variance. Data were considered not normally distributed if absolute
762 kurtosis and skewness values for each genotype were greater than 1.96 x standard error of
763 kurtosis/skewness. Variance of the populations of different samples were considered
764 unequal if Levene's test for homogeneity of variance gave a p value of < 0.05 . If samples
765 were normally distributed and variances were equal, Student-t tests were applied for 2-
766 sample type graphs, and One-Way ANOVA was used to compare means from > 2 samples.
767 When data were normally distributed, but variances were unequal, Welch ANOVA was used
768 instead. Multiple comparison corrections to normal data were applied using a post-hoc
769 Dunnett test of comparisons to a control, Games-Howell or Bonferroni post-hoc comparing all
770 samples. Non-parametric continuous data were compared using a Mann-Whitney U-test
771 when 2 sample types were being analysed, and a Kruskal-Wallis test for > 2 samples, and
772 multiple comparison corrections were applied using a post-hoc Dunn test. See Table S1 for
773 all statistical sample sizes, applied tests and p values.

774

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963

964 FIGURE LEGENDS

965

966 **Fig.1 Keks are Trk-like receptors expressed in the CNS.** (A) Modular composition of TrkB,
967 TrkB-T1, Dror, Otk and *Drosophila* LIGs. (B) Amongst the LIGs, Keks are closer to the Trks
968 than any other mammalian or *Drosophila* LIGs, adapted from the phylogeny of Mandai et
969 al.[22]. (C-D) mRNA distribution in embryos: (C) *CG15744*, *lambik* and *CG16974* are not
970 expressed in the VNC (arrows) above background, but *lambik* is in PNS and *CG16974* in
971 muscle precursors (arrowheads); (D) *kek-1*, *kek-2* and *kek-6* transcripts are found in the
972 VNC, and *kek5GAL4>tdTomato* drives expression in VNC and PNS (right) neurons. (E)
973 Over-expression of *keks* – most prominently *kek2* and 6 - in all neurons with *elavGAL4*
974 rescued the cold semi-lethality of *DNT1⁴¹ DNT2^{e03444}* double mutants. Chi-square and
975 Bonferroni multiple comparisons correction. * $p < 0.05$, *** $p < 0.001$. For statistical details see
976 Table S1.

977

978 **Fig.2 Keks bind DNTs.** (A) Diagram of Chimaeric Kek-Toll-6-HA receptors, bearing the
979 extracellular and transmembrane domains of Keks and the intracellular signaling domain of
980 Toll-6 (left). Chimaeric receptors visualized with anti-HA antibodies are distributed to the cell
981 membrane in S2 cells (middle). Binding of purified mature DNT2-CK to the extracellular
982 domain of Kek-Toll-6 receptors activates the *drosomycin-luciferase* reporter (right). Black
983 asterisks denote comparisons to empty vector (pDONR) control, and red asterisks refer to
984 no-stimulation controls. Welch ANOVA $p < 0.001$; asterisks refer to post-hoc Games-Howell
985 * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. (B-D) Western blots showing co-immunoprecipitations from
986 co-transfected S2 cells: (B) precipitation of Kek6-HA with anti-HA brings down DNT2-V5
987 detected with anti-V5. (C) Reverse co-IP for Kek6 and DNT2. Precipitation of DNT1-V5 also
988 brings down Kek6-HA. (D) Precipitation of DNT2-V5 brings down Kek5-Flag. Black asterisks
989 indicate the relevant control bands, red arrows indicate co-IPs. Input controls: cell lysate from
990 co-transfected cells express both proteins. IP: immunoprecipitation; WB: western blot; FL: full
991 length; CK: cystine-knot cleaved form. DNTs can be spontaneously cleaved following
992 expression from these constructs in S2 cells.

993

994 **Fig.3 Kek-6 is expressed pre-synaptically in motoneurons and binds post-synaptic**

995 **DNT2.** (A-B) Kek-6^{GFP} GFP colocalises with the neuronal markers Eve (A) and HB9 (B) in
996 the larval VNC (arrows show examples). (C) Kek-6^{GFP} was found in third instar larval muscle
997 6/7 NMJ and synaptic boutons (higher magnification). (D) Kek-6^{GFP} was found in the
998 motorneuron axonal terminal (arrows), and in pre-synaptic bouton lumen (higher
999 magnification on the right), not colocalising with the post-synaptic marker anti-Dlg (arrows).
1000 (E) Illustration. (F-J) Over-expression of GFP tagged full-length DNT2 in muscle
1001 (*MhcGAL4>UAS-DNT2-FL-GFP*) revealed: (F) DNT2-GFP distribution within the pre-synaptic
1002 bouton lumen (arrows), boutons labeled post-synaptically with anti-Dlg; (G-J) DNT2-GFP
1003 along the motoraxon and within the pre-synaptic bouton lumen, both labeled with FasII
1004 (arrows).

1005

1006 **Fig. 4 *kek6* and *DNT2* mutants have smaller NMJs.** (A) Plotted trajectories of filmed
1007 larvae (left), and histograms (right) of frames vs. speed analysed with FlyTracker. Kruskal-
1008 Wallis $p < 0.0001$ and $***p < 0.001$ post-hoc Dunn test. (B) NMJs (left) and box-plot graphs
1009 (right) showing: *kek6*^{-/-} and *DNT2*^{-/-} single mutants and *kek6*^{-/-} *DNT2*^{-/-} double mutants
1010 have fewer Dlg+ boutons and smaller HRP+ axonal terminals (normalized to muscle area,
1011 MSA). Dlg: Kruskal-Wallis $p < 0.0001$, and $*p < 0.05$, $**p < 0.01$, $***p < 0.001$ post-hoc Dunn;
1012 HRP: One Way ANOVA $p < 0.0001$, and $**p < 0.01$, $***p < 0.001$ post-hoc Dunnett. *kek6* and
1013 *DNT2* single mutants, but not the double mutants, have increased active zone density
1014 (Brp+/HRP+axonal length). Brp: Kruskal-Wallis $p = 0.0012$, and $**p < 0.01$, $***p < 0.001$ Dunn's
1015 post-hoc. *Kek6* mutants have reduced Synapsin, Mann-Whitney U test $***p < 0.001$. For
1016 statistical details, see Table S1. Mutant genotypes throughout figures: Control: *yw/+*;
1017 Mutants: *kek6*^{-/-}: *kek6*³⁴/*Df(3R)6361*; *DNT2*^{-/-}: *DNT2*³⁷/*Df(3L)6092*; *kek6*^{-/-} *DNT2*^{-/-}:
1018 *kek6*³⁴/*Df(3L)6092*/*Df(3R)6361* *DNT2*³⁷.

1019

1020 **Fig. 5 Kek-6 and DNT2 can induce active zones and NMJ growth.** Confocal images of
1021 NMJs from A3-4 muscle 6/7 (left), and box-plot graphs (right), showing: (A) Over-expression
1022 of *kek6* in motoneurons had not effect on HRP+ NMJ size, but it increased Brp+ active
1023 zones. HRP: Student t test n.s. $p=0.07$; Brp: Mann-Whitney U test $***p<0.001$. (B) Over-
1024 expression of full-length DNT2 in muscle increased NMJ size (HRP) and active zones (Brp),
1025 revealing a retrograde function. HRP: Mann-Whitney U test $*p<0.05$; Brp: Student t test
1026 $**p<0.01$. (C) Over-expression of both full-length DNT2 and mature DNT2-CK in
1027 motoneurons induced active zone formation. Brp DNT2-CK: Student t test $**p<0.01$, and Brp
1028 DNT2-FL: Mann-Whitney U test $***p<0.001$. See Table S1. *MN=D42GAL4*.

1029

1030 **Fig. 6 Kek-6 functions downstream of DNT2.** Confocal images of NMJs from A3-4 muscle
1031 6/7 (left), and box-plot graphs (right), showing: (A) Over-expression of *kek-6* in motoneurons
1032 rescued the phenotypes of *kek-6* mutants. Dlg: One Way ANOVA $p<0.0001$ and post-hoc
1033 Bonferroni $*p<0.05$, $***p<0.001$. HRP: One Way ANOVA $p<0.001$ and post-hoc Bonferroni
1034 $**p<0.01$, $**p<0.01$. (B) Left: Over-expression of *kek-6* in neurons rescued the phenotype of
1035 *DNT2* mutants. Dlg: Kruskal-Wallis $p=0.001$, and post-hoc Dunn test $**p<0.01$, $***p<0.001$.
1036 Right: *kek-6* loss of function rescued the increase in boutons caused by the muscle over-
1037 expression of *DNT2*. Dlg: Welch ANOVA $p<0.01$ and post-hoc Games-Howell $*p<0.05$,
1038 $**p<0.01$. (C) Over-expression of *kek-6* in motoneurons rescued the phenotypes of *kek-6*
1039 *DNT-2* double mutants. Dlg: Kruskal-Wallis $p=0.001$ and post-hoc Dunn's test $*p<0.05$,
1040 $**p<0.01$. HRP: Welch ANOVA $p=0.000$, post-hoc Games Howell $**p<0.01$. See Table S1.
1041 GAL4 drivers: Muscle: *MhcGAL4*; Neurons: *elavGAL4*; MN: *D42* or *Toll-7GAL4*. Controls:
1042 white boxes: *yw/+*; grey boxes: *GAL4/+*; mutant genotypes as in Fig.4. Rescue genotypes:
1043 (A) *w; UASkek6RFP/+; Df(3R)6361/kek6³⁴D42GAL4*. (B) *w; UASkek6RFP/+; elavGAL4*
1044 *Df(3L)6092/ DNT2³⁷*; and *w; UASDNT2-FL/+; Df(3R)6361/kek6³⁴D42GAL4*. (C) *w; Toll-*
1045 *7GAL4/UASkek6RFP; kek6³⁴Df(3L)6092/ Df(3R)6361 DNT2³⁷*.

1046

1047 **Fig.7 Kek-6 and Toll-6 interact for NMJ structural homeostasis.** (A) *Toll-6GAL4>mCD8-*
1048 *GFP* revealed expression in motoneurons at the muscle 6/7 NMJ, colocalising with FasII
1049 presynaptically. (B) Muscle 6/7 NMJs (left) and box-plot graphs (right) showing: *Toll-*
1050 *6^{MIO2127}/Df(3L)BSC578* mutants and *Toll-6^{MIO2127}Df(3R)6361/kek6³⁵ Df(3L)BSC578* double
1051 mutants had smaller NMJs (HRP, Kruskal-Wallis p=0.0001), and reduced active zones (Brp,
1052 Kruskal-Wallis p=0.0055), post-hoc Dunn for both *p<0.05, ***p<0.001. (C) Co-
1053 immunoprecipitation from co-transfected S2 cells: Precipitating Toll-6 and Toll-7 with anti-Flag
1054 brought down Kek-6 detected with anti-HA. IP: immuno-precipitation; WB: western blot;
1055 asterisk: co-IP. See Table S1.

1056

1057 **Fig.8 Kek-6 physically interacts with synaptic factors.** (A) Diagram of pull-down
1058 workflow and (B) coomassie-stained gel showing proteins from S2 cell or adult fly head
1059 lysate bound to Kek-6-Flag or mock control. Red boxes indicate fractions used for mass
1060 spectrometry. Hits that appeared in mock controls, or with only one peptide, were dis-
1061 regarded. (C) Selection of candidate interacting proteins, see Tables S2 and S3. (D) Co-
1062 immunoprecipitations from co-transfected S2 cells: precipitating Kek-6-Flag brought down
1063 CaMKII-HA and VAP33A-HA. IP: immunoprecipitation, WB: western blot. (E) Western blots
1064 with anti-activated pCaMKII^{T287}, non-phosphorylated plain CaMKII and Tubulin, from adult fly
1065 heads, GMRGAL4 drives expression in retina. Graphs show pCaMKII^{T287} levels normalized
1066 over non-phosphorylated CaMKII. Student paired t-tests. *p<0.05, **p<0.01, see Table S1.

1067

1068 **Fig. 9 Kek6 activates CaMKII at the NMJ.** NMJs from A3-4 muscle 6/7 (left), and box-plot
1069 graphs (right), NMJs, labeled with anti-pCaMKII^{T287} for the constitutively active form; anti-Dlg
1070 for post-synaptic boutons; anti-HRP for pre-synaptic axonal terminal length; anti-Brp for
1071 active zones. Brp and pCaMKII^{T287} were quantified automatically with DeadEasy Synapse.
1072 (A, B) Over-expression of *kek-6* in motoneurons increased pCaMKII^{T287} levels, which was
1073 rescued with the over-expression of the CaMKII inhibitor Ala (A) or CaMKII RNAi knock-down
1074 (B) pre-synaptically. Kruskal-Wallis p<0.0001 and **p<0.01, ***p<0.001 post-hoc Dunn for

1075 both graphs. (C,D) CaMKII inhibition with Ala (C) or knock-down with CaMKII-RNAi (D)
1076 rescued the increase in active zones caused by *kek-6* over-expression. (C) Welch ANOVA
1077 $p < 0.000$ and $***p < 0.001$ post-hoc Games-Howell, (D) Kruskal-Wallis $p < 0.0001$ and $**p < 0.01$,
1078 $***p < 0.001$ post-hoc Dunn's. See Table S1. MN=motoneurons. Genotypes: (A-D) Control: *w*;
1079 *D42GAL4/+*. (A, C) *w*; *D42GAL4/UASkek6RFP*. *w*; *D42GAL4/UASAla*; *w*;
1080 *D42GAL4/UASkek6RFP UASAla*. (B, D) *D42GAL4/UASCaMKIIRNAi*. *w*;
1081 *D42GAL4/UASkek6RFP UASCaMKIIRNAi*.

1082

1083 **Fig. 10 CaMKII functions downstream of Kek6 and DNT2 at the NMJ.** Confocal images
1084 showing A3-4 muscle 6/7 NMJs, labeled as in Figure 9. (A) Reduced pCaMKII^{T287} levels in
1085 *kek-6* mutants, and *kek-6 DNT2* double mutants. Kruskal-Wallis $p = 0.0009$, and post-hoc
1086 Dunn. (B-D) Over-expression of activated CaMKII^{T287D} in motoneurons rescued the NMJ
1087 phenotypes of (B) *kek-6* mutants, Kruskal-Wallis $p = 0.0081$, post-hoc Dunn; (C) *DNT2*
1088 mutants, Kruskal-Wallis $p = 0.0001$, post-hoc Dunn, and (D) *kek-6 DNT2* double mutants .
1089 Welch ANOVA $p < 0.000$, post-hoc Games-Howell. $*p < 0.05$, $**p < 0.01$, $***p < 0.001$ see Table
1090 S1. Genotypes: MN=motoneurons, *D42GAL4*; Neurons: *elavGAL4*. Different neuronal drivers
1091 were used due to genetic constraints. Control: wild-type: *yw/+*; grey boxes: *D42GAL4/+*. (A)
1092 Mutant genotypes as in Fig.4; Rescues: (B) *w; UASCaMKIIT287/+; D42GAL4 kek6³⁴/*
1093 *Df(3R)6361*. (C) *w; UASCaMKIIT287D/+; elavGAL4 Df(3L)6092/DNT2³⁷*. (D) *w*;
1094 *UASCaMKIIT287D/Toll-7GAL4; kek6³⁴Df(3L)6092/ Df(3R)6361 DNT2³⁷*.

1095

1096 **Fig. 11 VAP33A functions downstream of Kek-6.** (A) Confocal images of NMJs from
1097 segments A3-4, muscle 6/7. (B-E) Box-plot graphs. (A) *VAP33A^{G0231}* mutants have reduced
1098 bouton number, Mann-Whitney U test $***p < 0.001$. (C,D) Pre-synaptic over-expression of
1099 *VAP33A* rescues bouton number in (C) *kek-6* mutants and (D) *DNT2* single mutants,
1100 Kruskal-Wallis $p < 0.0001$ and $*p < 0.05$, $***p < 0.001$ post-hoc Dunn for both. (E) *kek-6 DNT2*
1101 double mutants rescue the bouton number phenotype caused by *VAP33A* gain of function,
1102 Kruskal-Wallis $p < 0.0001$ and $**p < 0.01$, $***p < 0.001$ post-hoc Dunn. See Table S1.

1103 MN=motoneuron, *D42GAL4* (D) or *Toll-7GAL4* (E). Rescue genotypes: (C) *UASVAP33A*;
1104 *D42GAL4 kek6³⁴/Df(3R)6361*. (D) *UASVAP33A/+; elavGAL4 Df(3L)6092/DNT2³⁷*. (E)
1105 *UASVAP33A/Toll-7GAL4; kek6³⁴Df(3L)6092/ Df(3R)6361 DNT2³⁷*

1106

1107 **Fig.12 Retrograde DNT2 binds pre-synaptic Kek-6 activating CaMKII and regulating**

1108 **structural synaptic plasticity.** (A) Illustration of Kek-6 compared to Trk isoforms, and

1109 showing that DNT2 binds Kek-6, which functions via CaMKII and VAP33A downstream. (B)

1110 Pre-synaptic motorneuron terminal at the NMJ: DNT2 is produced at the muscle and

1111 secreted, binds pre-synaptic Kek-6, functioning via CaMKII and VAP33A downstream to

1112 regulate NMJ growth and active zones. DNT2 also binds Toll-6 and interactions between

1113 Kek-6 and Toll-6 regulate NMJ structural homeostasis.

1114

1115 SUPPORTING INFORMATION

1116 **Fig. S1 Kek-6 is expressed is not expressed in glia.** Confocal images of the VNC

1117 neuropile of third instar *Kek-6^{MIMIC-GFP}* larvae, stained with anti-GFP and the pan-glial nuclear

1118 marker anti-Repo. Repo does not colocalise with GFP in any cells, arrows point to examples

1119 of Repo+, GFP-negative cells.

1120

1121 **Fig. S2 Altered *kek-6* function affects motoraxon targeting at embryonic NMJ.**

1122 The motoneuron marker FasII reveals motoraxon targeting phenotypes at muscle 6,7,12,13

1123 in stage 17 embryos, in *kek-6* mutants and upon over-expression of *kek-6* in all neurons (with

1124 *elavGAL4*). Arrows indicate stereotypic projections in wild-type, and mistargeting in other

1125 genotypes. Chi-square $p < 0.0001$ and *** $p < 0.001$ Boferroni corrections, see Table S1.

1126

1127 **Fig. S3 *kek-6* over-expression induces ghost boutons.** (A,B) Over-expression of

1128 *kek-6* in motorneurons (MN) with *D42GAL4* did not affect bouton number (DIg, Mann-

1129 Whitney U-test not significant). (C-E) Over-expression of *kek-6* induced pre-synaptic ghost

1130 boutons lacking a post-synaptic component (arrows: HRP+, presynaptic and DIg-negative,

1131 post-synaptic), (D) higher magnification; (E) quantification. Both bouton number and area
1132 increased, albeit not significantly. Mann-Whitney U-tests. See Table S1. *Genotypes*: Control:
1133 *D42GAL4/+*; *kek6^{-/-}*; *kek6³⁴/Df(3R)6361*; *MN>kek6: D42GAL4>UAS-kek6-RFP* (with one or
1134 two copies of *UAS-kek6*).

1135

1136 **Fig. S4 Loss and gain of CaMKII function affect the NMJ.** (A) Confocal images of
1137 muscle 6/7 NMJs, in A3-4, labeled with anti-HRP for the pre-synaptic terminal, anti-Brp for
1138 active zones, anti-Dlg for post-synaptic boutons and anti-pCaMKII^{T287D} for the constitutively
1139 active form. (B,C) Quantification. (A,B) Inhibiting CaMKII function with Ala in motoneurons
1140 (*D42GAL4>UASAla*) decreased NMJ terminal axonal length (HRP,t-test), and active zones.
1141 Student t-tests, $p<0.005$, $**p<0.01$. (A,C) Pre-synaptic over-expression of constitutively active
1142 CaMKII (*D42GAL4>UASCaMKII^{T287D}*) increased pCaMKII levels (pCaMKII^{T287D}, Student t-test
1143 $**p<0.001$), axonal length (HRP, Student t-test $**p<0.001$), lb bouton number (Dlg, Mann-
1144 Whitney U-test $***p<0.001$), and active zones (Brp, Mann-Whitney U-test $**p<0.01$). See
1145 Table S1.

1146

1147 **Table S1 Statistical Analysis Details.** For all genotypes, sample sizes, tests and p
1148 values, see this table.

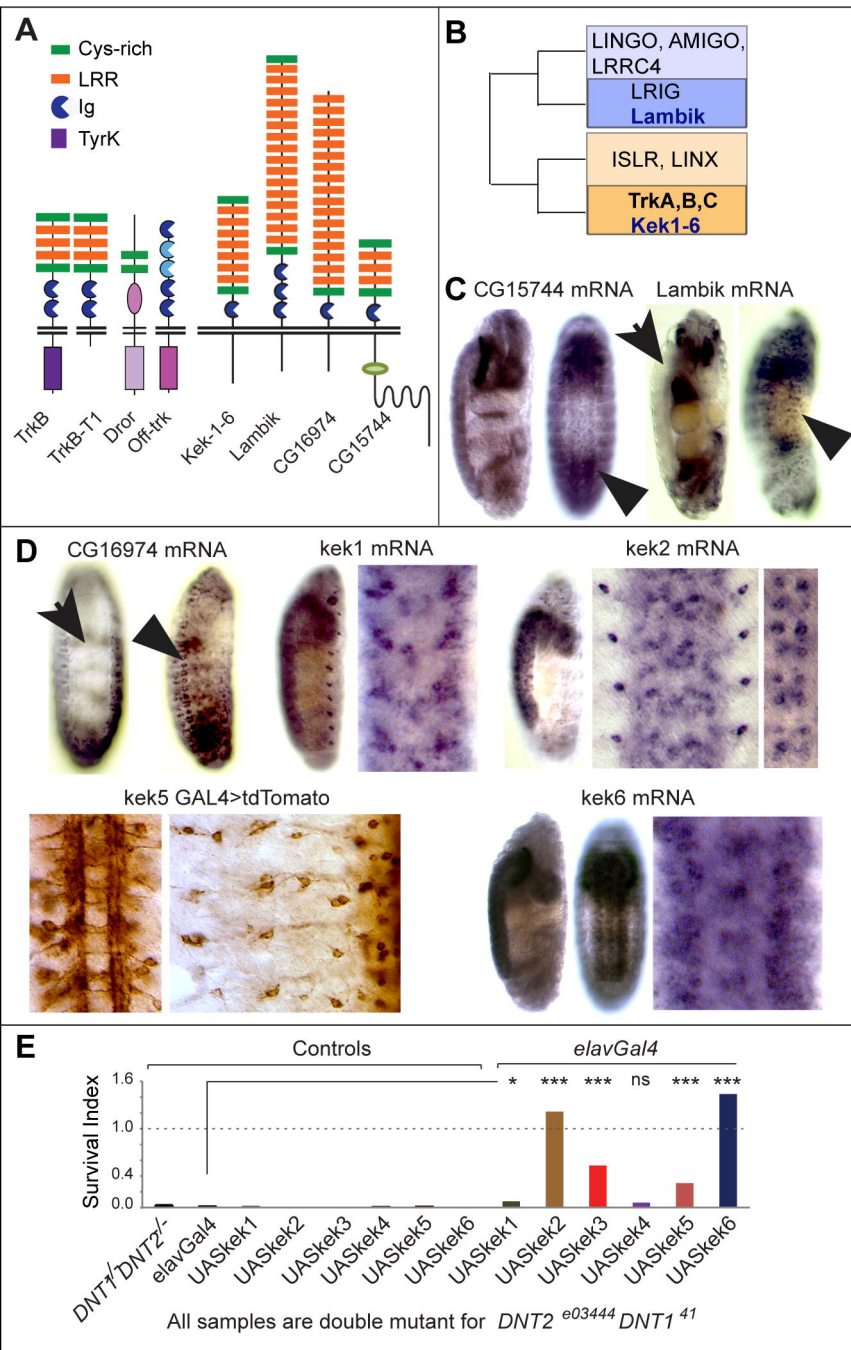
1149

1150 **Table S2 Kek6 pull-down from S2 cells.** List of S2 cell lysate proteins binding Kek6-
1151 Flag, but not mock-transfection controls, and detected with more than one peptide.

1152

1153 **Table S3 Kek6 pull down from adult fly heads.** List of adult fly head proteins binding
1154 Kek6-Flag, but not mock controls, and detected with more than one peptide.

Figure 1 Keks are Trk-like receptors expressed in the CNS



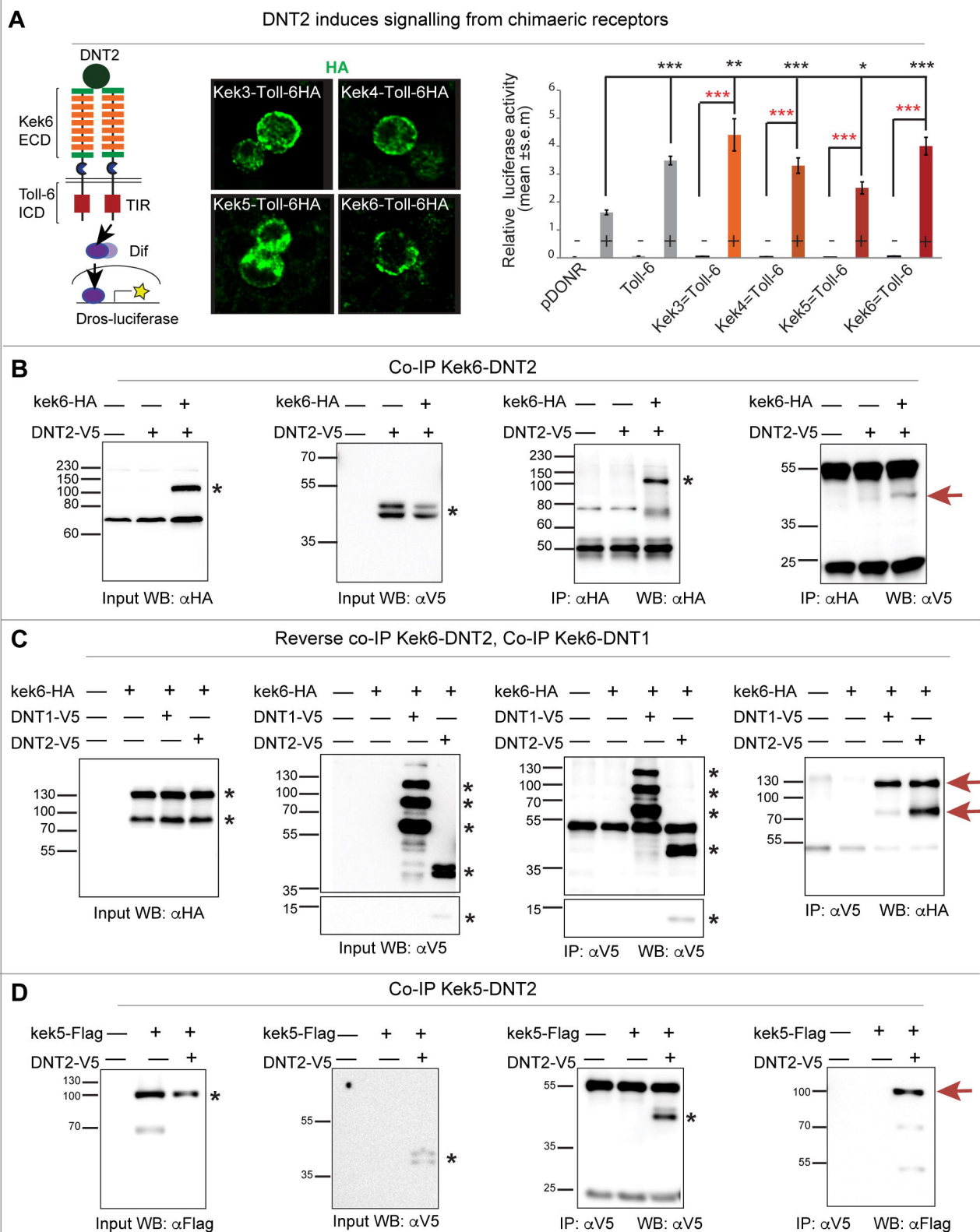
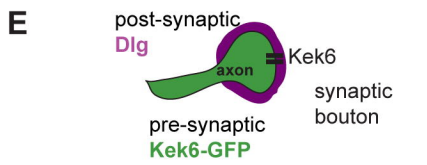
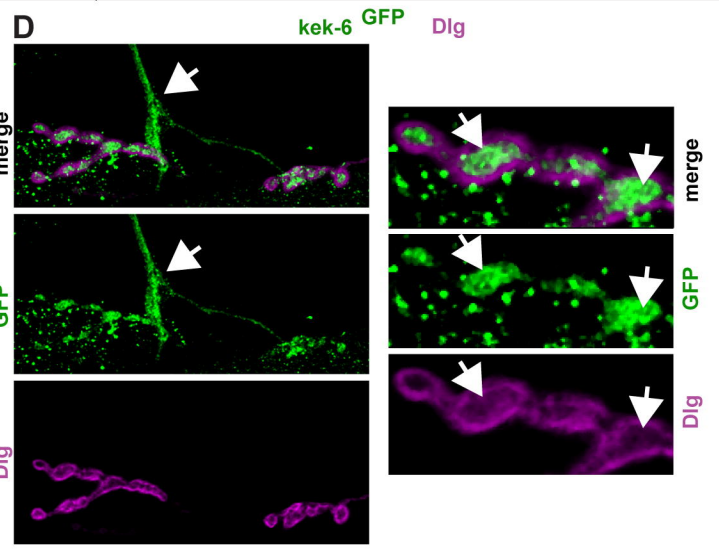
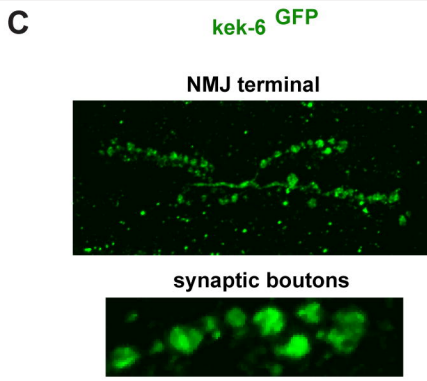
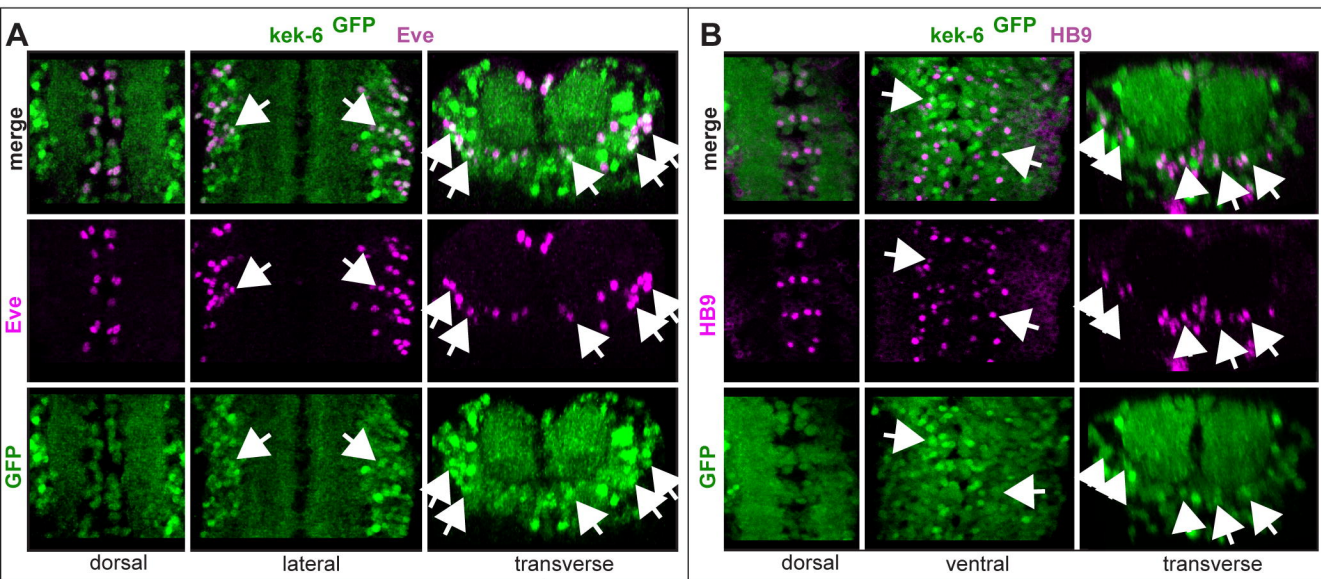


Figure 3 Kek6 is expressed pre-synaptically in motoneurons and binds post-synaptic DNT2



Muscle expression of DNT2:Mhc>DNT2-FL-GFP

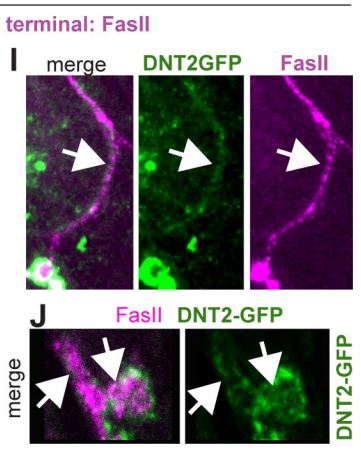
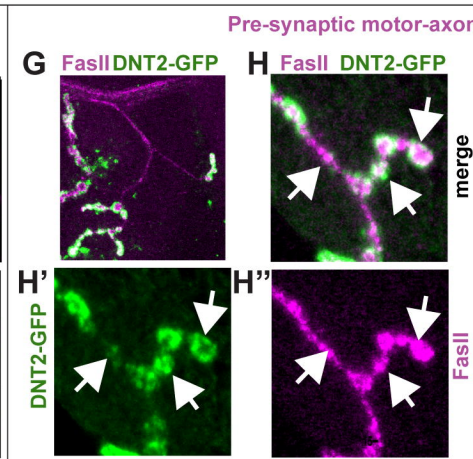
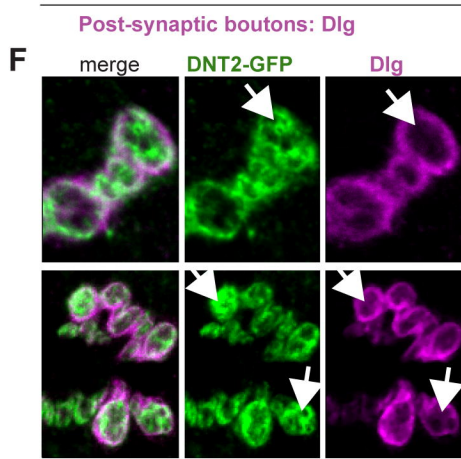


Figure 4 *kek6* and *DNT2* mutants have smaller NMJs

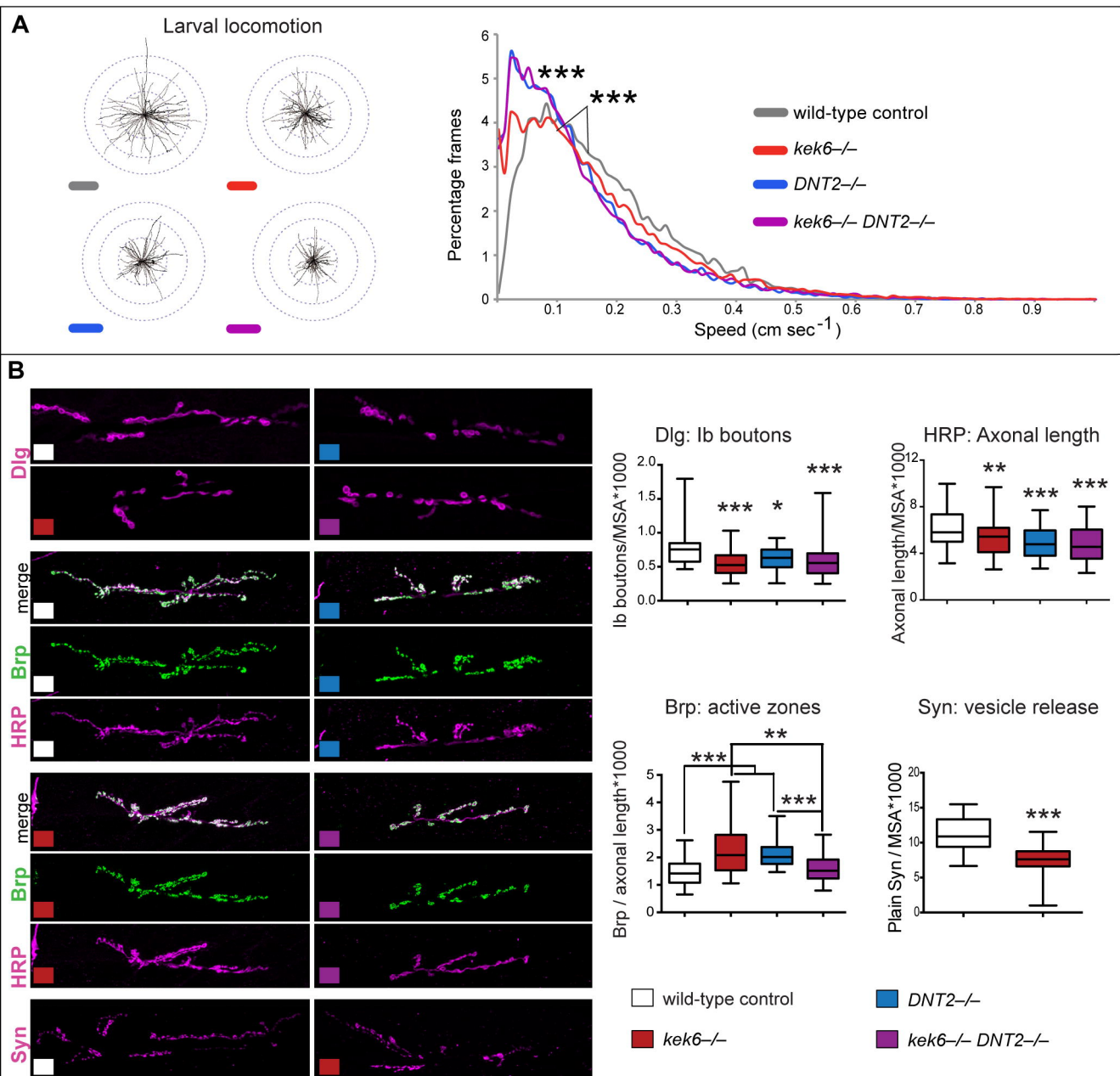


Figure 5 Kek-6 and DNT2 can induce active zones and NMJ growth

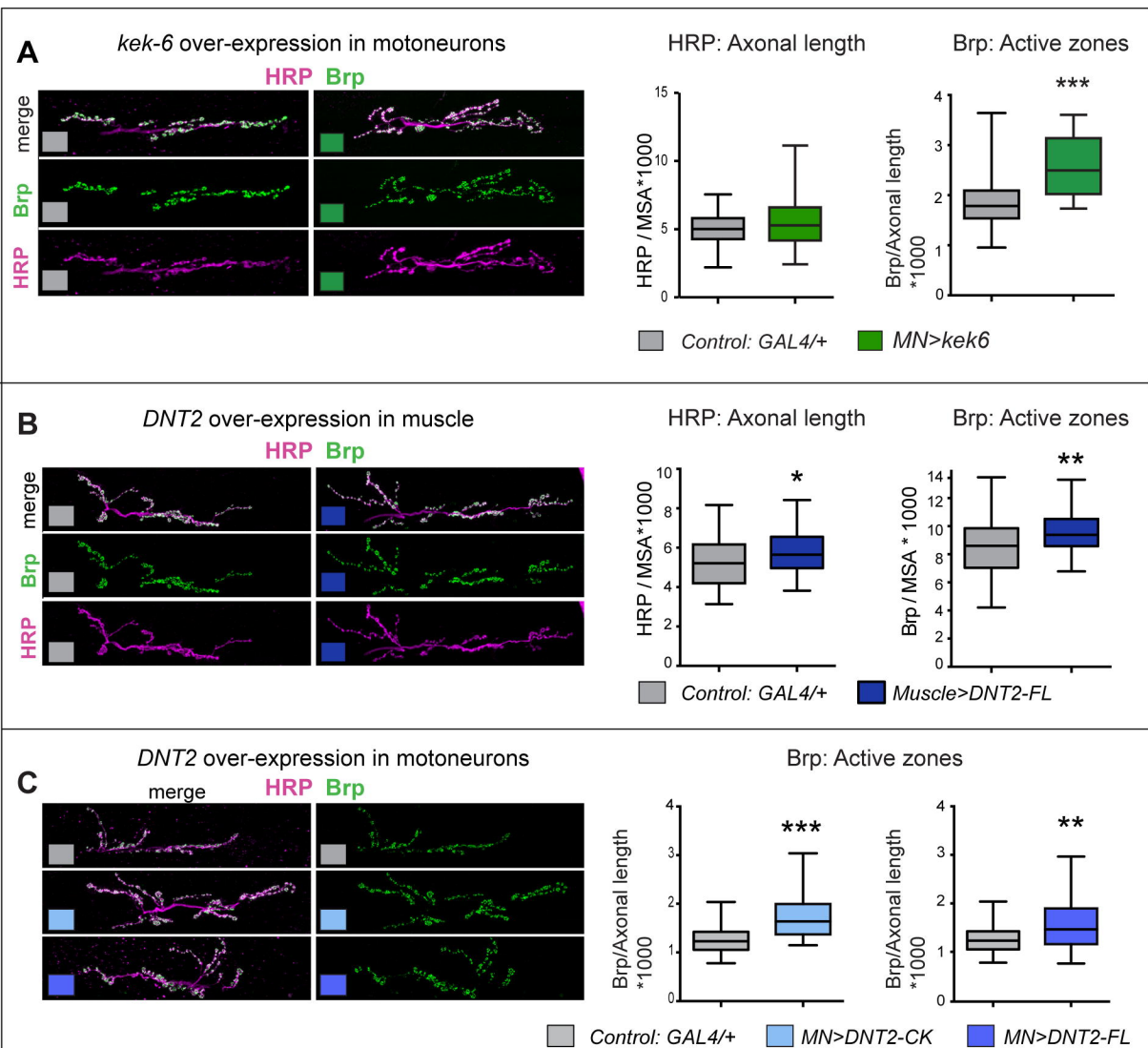
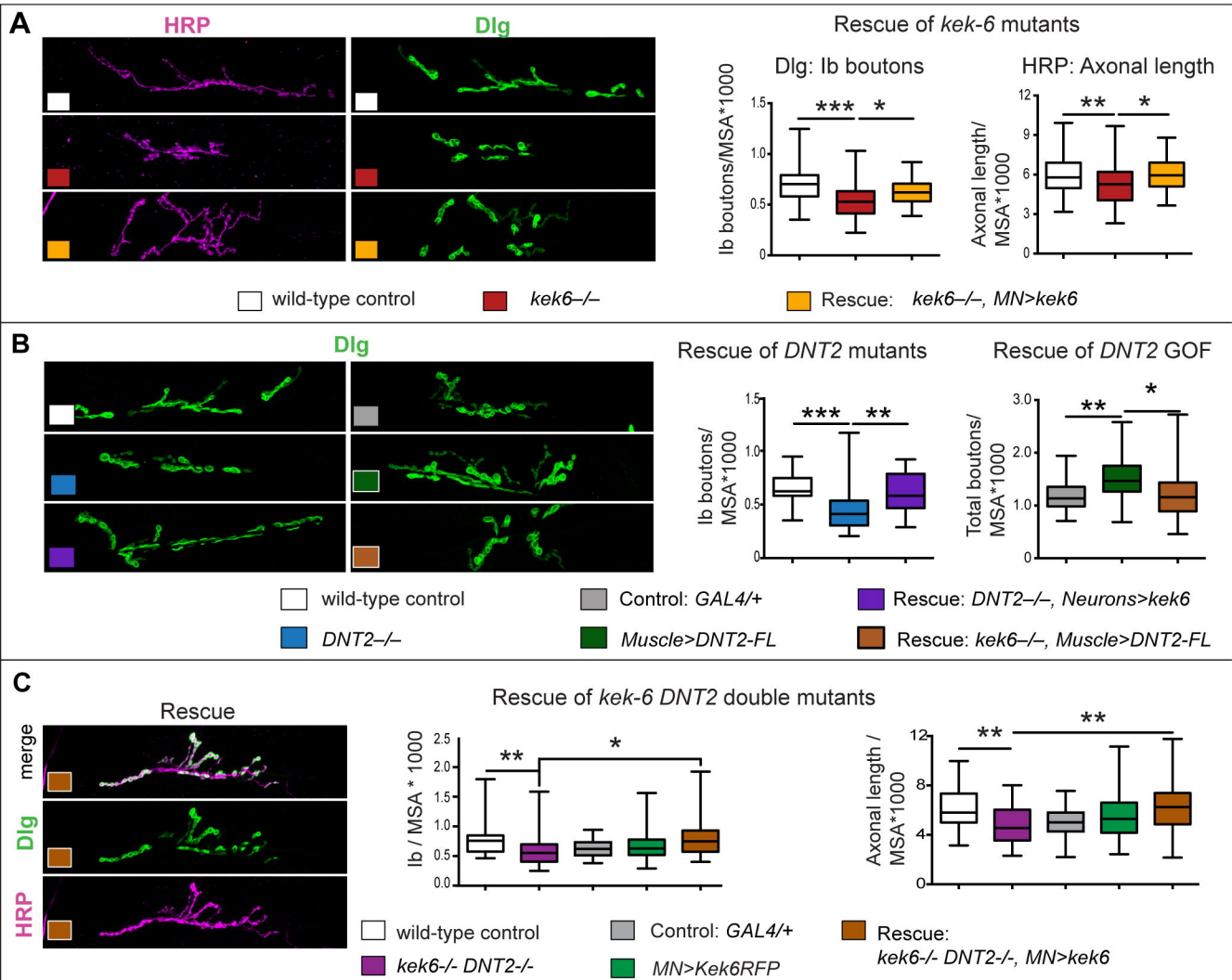


Figure 6 Kek-6 functions downstream of DNT2



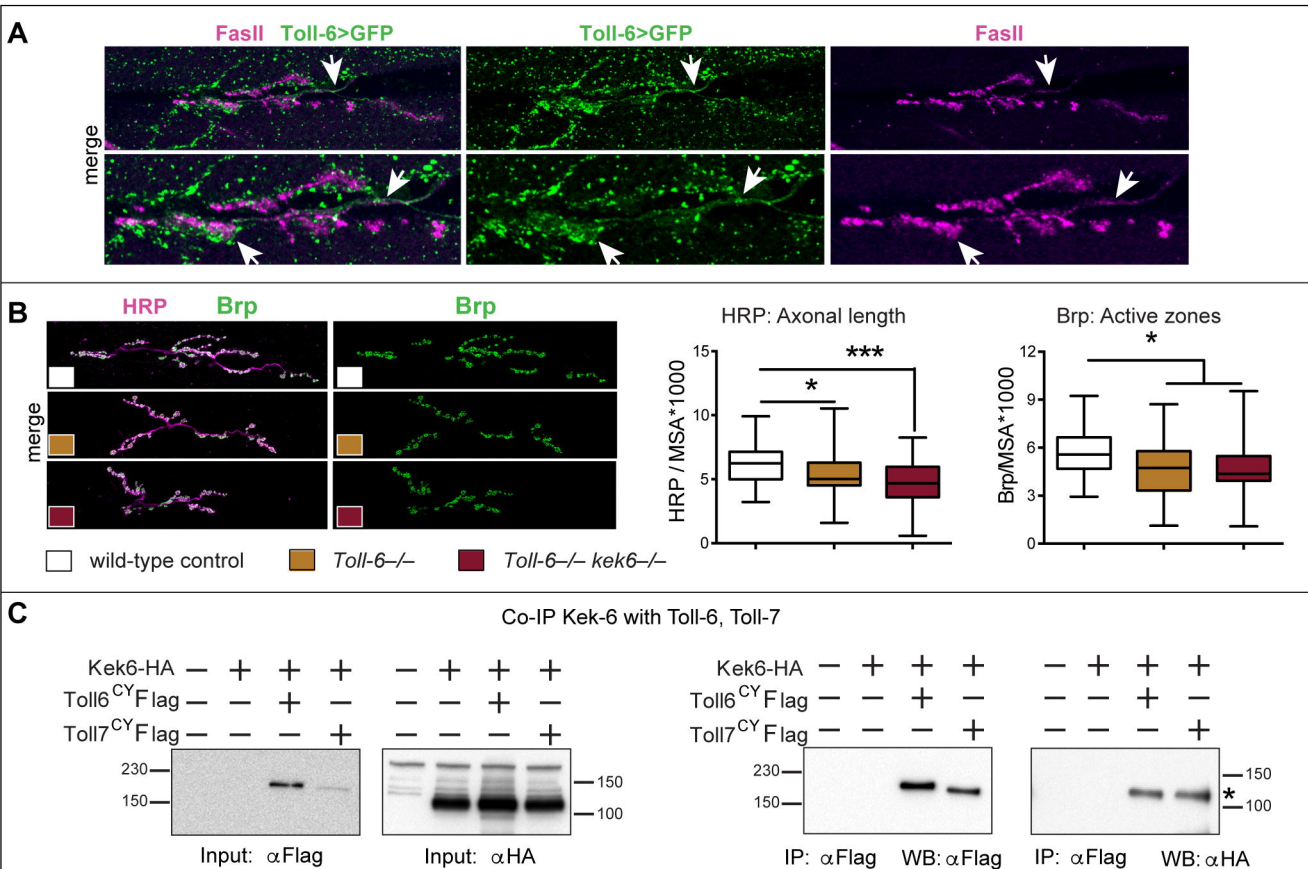
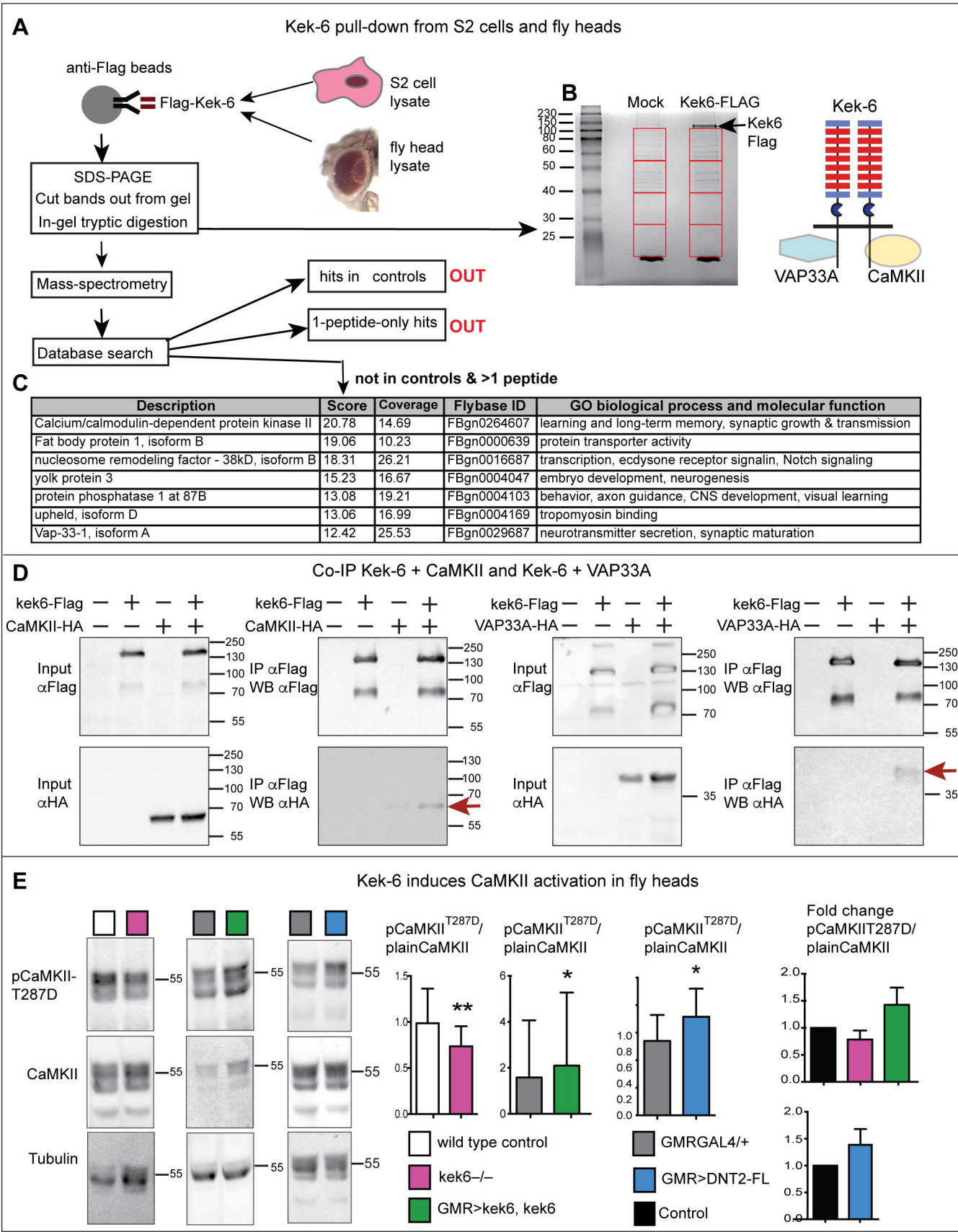


Figure 8 Kek6 physically interacts with synaptic factors.



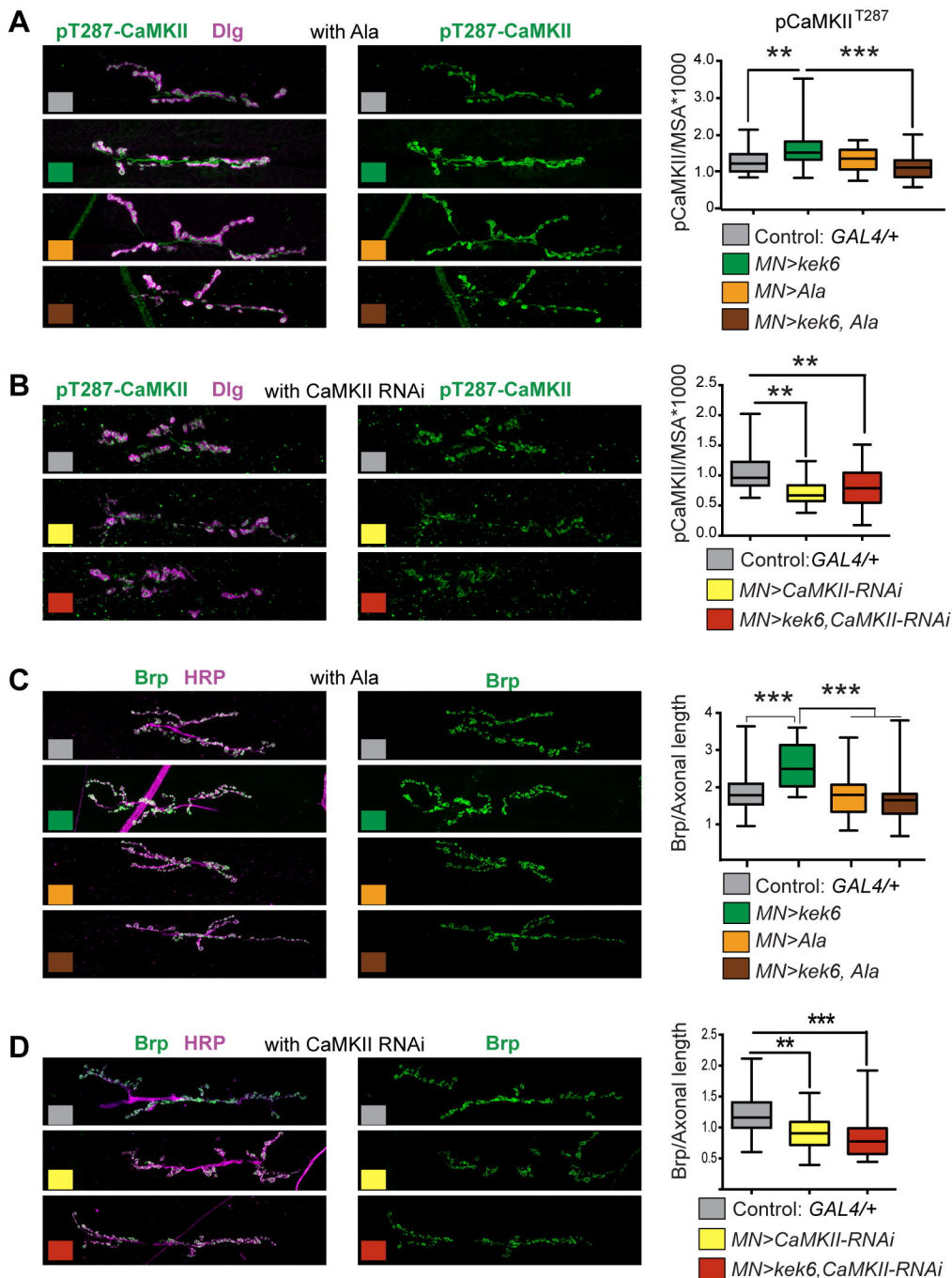


Figure 10 CaMKII functions downstream of *Kek6* and *DNT2* at the NMJ

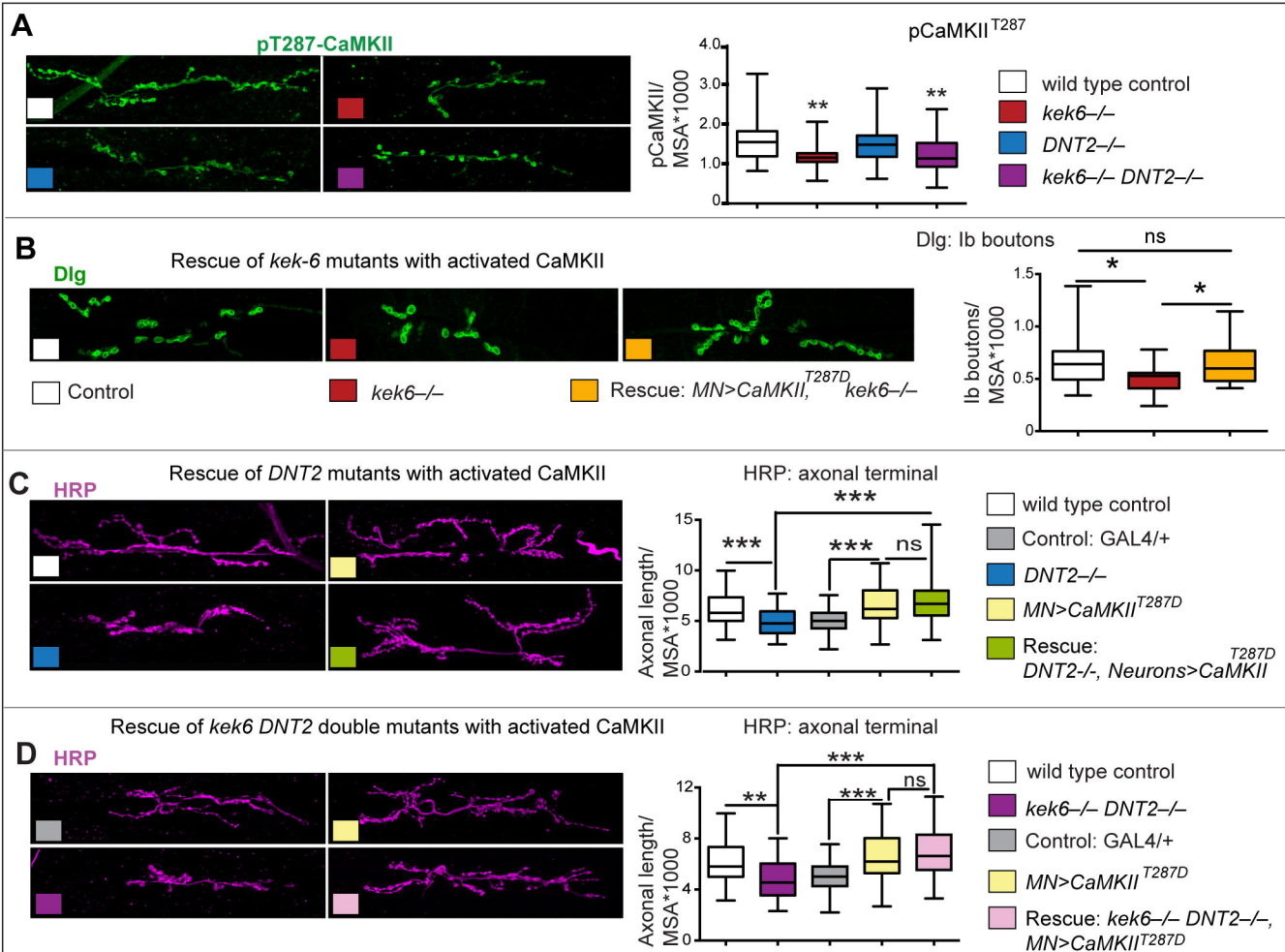


Figure 11 VAP33A functions downstream of Kek-6

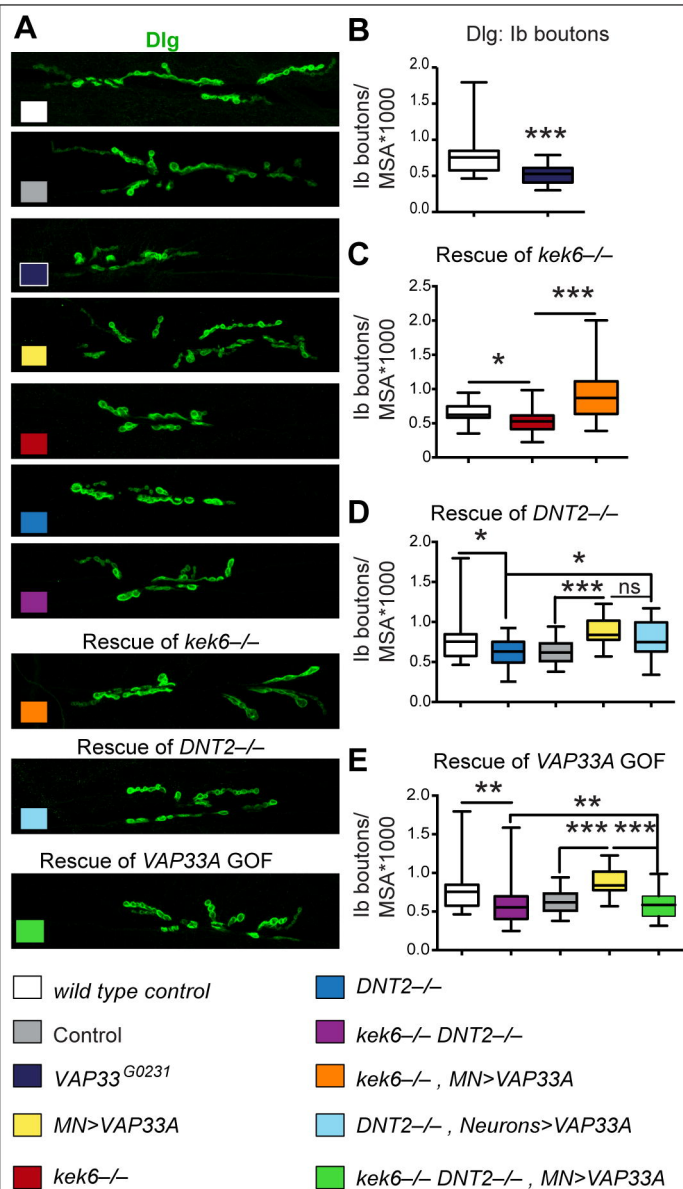
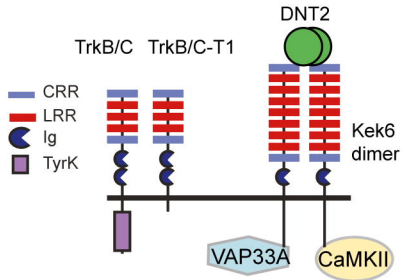


Figure 12 Retrograde DNT2 binds pre-synaptic Kek-6 activating CaMKII and regulating structural synaptic plasticity

A



B

