

Fig. S1. Eve and Runt expression in dorsal muscles in *tup* mutant embryos. Dorsolateral views of three abdominal segments of stage 15 embryos are shown. (A) Wild-type embryo. Eve (red) and Col (green) are expressed in the DA1 (dotted circled in one segment) and DA3 muscles, respectively. (B) DA1 Eve expression is preserved in *tup^{ex4}* embryos. (C) Wild-type Runt expression in two rows of nuclei in the DO2 muscle (white-dotted circled in one segment). (D) Runt expression reveals an abnormal clustering of the DO2 nuclei.

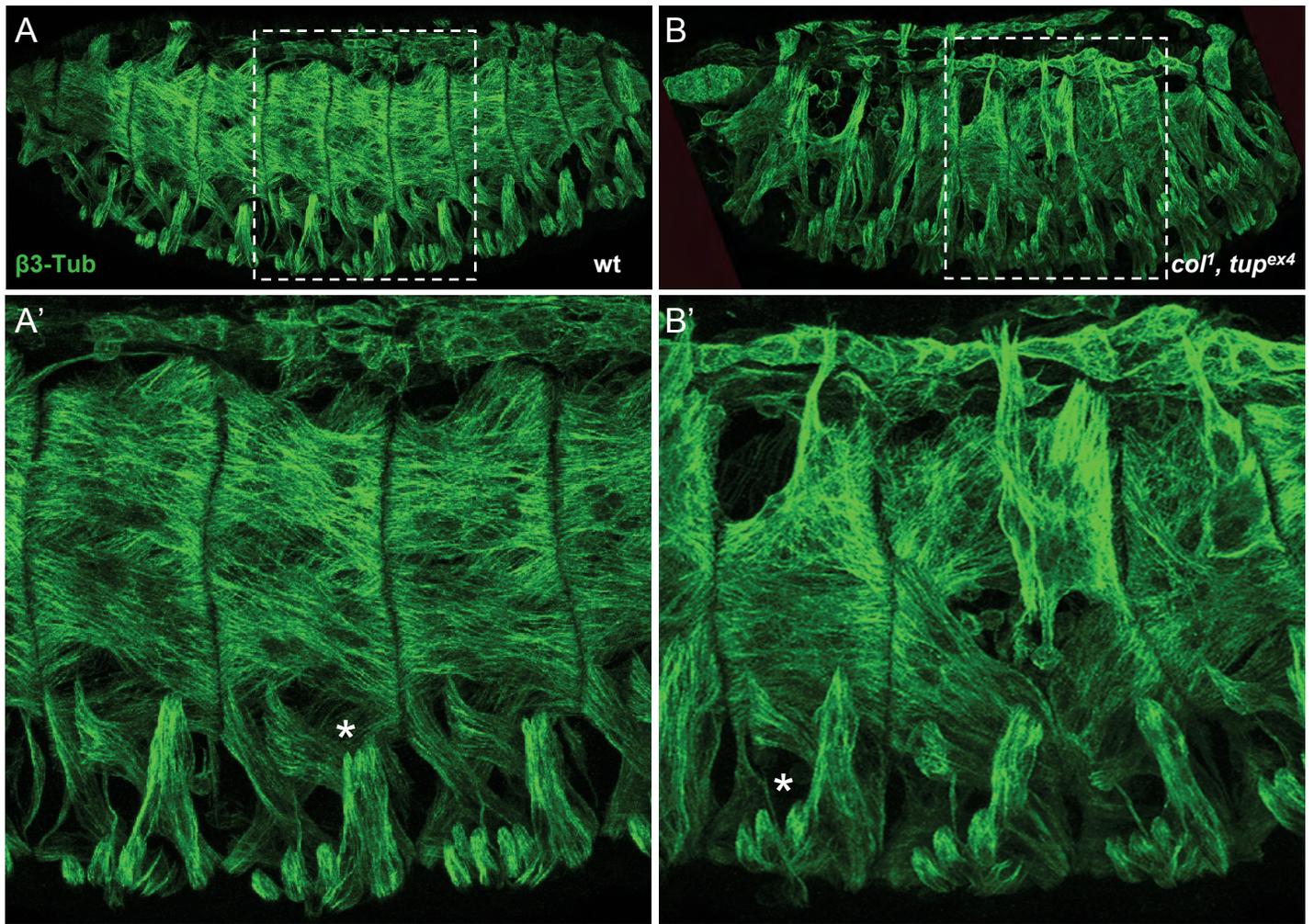


Fig. S2. Cumulative muscle defects in double *col¹, tup^{ex4}* mutant embryos. (A,B) $\beta 3$ -Tubulin staining of stage 16 wild-type (A) and *col¹, tup^{ex4}* (B) embryos. (A',B') High-magnification views of the dorsal and dorsolateral muscles in three segments (framed region in A,B). (B,B') Major disorganization of the dorsal musculature and lack of muscle at the DA3 position (white asterisk) are observed.

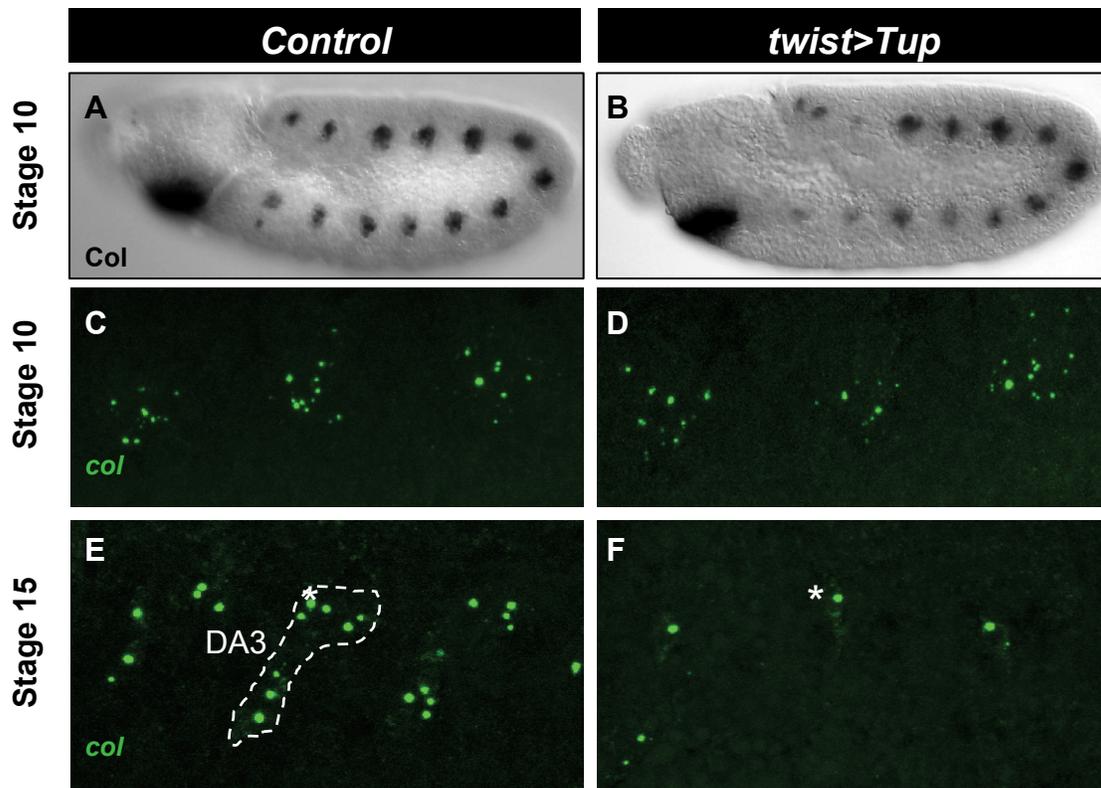


Fig. 3. Tup does not repress *col* transcription prior to the PC stage. (A,B) Col expression in wild-type (A) and *twi>tup* (B) embryos at stage 10. (C-F) *col* transcription in wild-type (C,E) and *twi>tup* (D,F) embryos. (A-D) Promuscular *col* expression is unaffected in *twi>tup* conditions; (E,F) DA3 *col* transcription is fully repressed at stage 15. The DA3 muscle is dotted circled in one wild-type segment. The white asterisk indicates *col* transcription in multidendritic neurons.

GGAAATGCAgcgcggcTCGTCAGTGTCAgtGTCAaaagtcgacatcggaactgaggCATTACAgAAATATCT 75
TGATAACTCAATCTccgAATCTTAAAAGgggggaggatactgaggAAAAcgCCAgCGTCAtggaagtccagccTGT 150
CAGTCagctcaGATCccagcggGATCATGACttcgcagttcaatggagcaggagcgggtggaatatattgccacaaag 225
ccgtggccacAAATTGGCTtGATCGgTGCCGGCTTGAAGTCAATTTGCgaCgGCTTAGGcccacggatcgttoga 300
tcgatcgatcgattggcatcagctgactctcatctgactgaaaactcgaaaactgacttggcagactgacggact 375
aaatctgcccagcaagtACTAAGTAcctggggaTGAGgGACAAACGAgCcgGAAagtGCTccacaAAA**CATATG** 450 **Twist**
GCaCACAATTAccaacTGACAGt**ACGATGTGTTA**aGAAATGCCaAAAtacaagcgagtttctgaggttgagaa 525
ctaggtgatactgtggaaatgttgttttagtactttaagtaaagtaaagtaaagtttcogattaacctttatataac 600
taataactaactagtttcagaaacaattaaatatgtagaaaccaatgcggtcacattgaagcctccgaaaaccg 675
cgagatgcaatacaccgcttgataccctttctcctacaaaaacaaacaccgaataatggaatatgaaatgatg 750
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gcagcggatcccagggaaccagagggcg**GCACATGG**-GCCccctgtgc**GGCATT**TATCAtggggctccg**GaGCA****C** 900 **Mef2**
TATATTTAGACgacg**GGCTAATGGATG**a**Ag**Cagggaaaaatagaggcagataggtacaatgggtgagggagcggg 975
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GCAGGAAGATGAACATTTAgct**GGATAACCCAATC**ctctt**GCCA**c**Gcc****TGATTGCCCGC**caatgtgg 3300

Fig. S4. Nucleotide sequence of *D. melanogaster* Tup-DME. FlyBase positions (release: r5.42) 2L: 18897397..18900688. Conserved sequences in *D. melanogaster*, *D. sechellia*, *D. simulans*, *D. yakuba*, *D. erecta*, *D. pseudoobscura*, *D. persimilis*, *D. ananassae* and *D. willistoni* are in black bold characters. Putative binding sites for Mef2 (purple) and Twi (yellow) were positioned using Jaspar, Consite and Genomatix (MatInspector) matrix models. Their position is indicated in the margin. Only matrix similarities greater than 0.9 were considered. In grey is region corresponding to the ChIP-ChIP data from E. E. Furlong laboratories (http://furlonglab.embl.de/data/browse_chip_mod/). This region includes late binding sites for twist (6-8 hours) and for Mef2 (6-8 hours, 8-10 hours and 10-12 hours).