**Abstract**

Hox genes in species across the metazoa encode transcription factors (TFs) containing highly-conserved homeodomains that bind target DNA sequences to regulate batteries of developmental target genes. DNA-bound Hox proteins, together with other TF partners, induce an appropriate transcriptional response by RNA Polymerase II (PolII) and its associated general transcription factors. How the evolutionarily conserved Hox TFs interface with this general machinery to generate finely regulated transcriptional responses remains obscure. One major component of the PolII machinery, the Mediator (MED) transcription complex, is composed of roughly 30 protein subunits organized in modules that bridge the PolII enzyme to DNA-bound TFs. Here, we investigate the physical and functional interplay between Drosophila melanogaster Hox developmental TFs and MED complex proteins. We find that the Med19 subunit directly binds Hox homeodomains, in vitro and in vivo. Loss-of-function Med19 mutations act as dose-sensitive genetic modifiers that synergistically modulate Hox-directed developmental outcomes. Using clonal analysis, we identify a role for Med19 in Hox-dependent target gene activation. We identify a conserved, animal-specific motif that is required for Med19 homeodomain binding, and for activation of a specific Ultrabithorax target. These results provide the first direct molecular link between Hox homeodomain proteins and the general PolII machinery. They support a role for Med19 as a PolII holoenzyme-embedded “co-factor” that acts together with Hox proteins through their homeodomains in regulated developmental transcription.

**Introduction**

The finely regulated gene transcription permitting development of pluricellular organisms involves the action of transcription factors (TFs) that bind DNA targets and convey this information to RNA polymerase II (PolII). Hox TFs, discovered through iconic mutations of the *Drosophila melanogaster* Bithorax and Antennapedia Complexes, play a central role in the development of a wide spectrum of animal species [1,2]. Hox proteins orchestrate the differentiation of morphologically distinct segments by regulating PolII-dependent transcription of complex batteries of downstream target genes whose composition and nature are now emerging [3–7]. The conserved 60 amino acid (a.a.) homeodomain (HD), a motif used for direct binding to DNA target sequences, is central to this activity. Animal orthologs of the *Drosophila* proteins make use of their homeodomains to play widespread and crucial roles in differentiation programs yielding the very different forms of sea urchins, worms, flies or humans [8]. They do so by binding simple TAAT-based sequences within regulatory DNA of developmental target genes [9–14]. One crucial aspect of understanding how Hox proteins transform their versatile but low-specificity DNA binding into an exquisite functional specificity involves the identification of functional partners. Known examples include the TALE HD proteins encoded by *extradenticle (exd)*/Pbx and *homothorax (lith)/Meis*, which assist Hox proteins to form stable ternary DNA-protein complexes with much-enhanced specificity. This involves contacts with the conserved Hox Hexapeptide (HX) motif near the HD N-terminus, or alternatively, with the paralog-specific UBD-A motif detected in Ubx and Abdominal-A (Abd-A) proteins [15,16]. Other TFs that can serve as positional Hox partners include the segment-polarity gene products Engrailed (En) and Sloppy-paired, that collaborate with Ubx and Abd-A to repress abdominal...
Autophagy and Hox proteins: a promising therapeutic target for autophagy-dependent diseases

Author Summary

Mutations of Hox developmental genes in the fruit fly Drosophila melanogaster may provoke spectacular changes in form: transformations of one body part into another, or loss of organs. This attribute identifies them as important developmental genes. Insect and vertebrate Hox proteins contain highly related homeodomain motifs used to bind to regulatory DNA and influence expression of developmental target genes. This occurs at the level of transcription of target gene DNA to messenger RNA by RNA polymerase II and its associated protein machinery (>50 proteins). How Hox homeodomain proteins induce fine-tuned transcription remains an open question. We provide an initial response, finding that Hox proteins also use their homeodomains to bind one machinery protein, Mediator complex subunit 19 (Med19) through a Med19 sequence that is highly conserved in animal phyla. Med19 mutants isolated in this work (the first animal mutants) show that Med19 assists Hox protein functions. Further, they indicate that homeodomain binding to the Med19 motif is required for normal expression of a Hox target gene. Our work provides new clues for understanding how the specific transcriptional inputs of the highly conserved Hox class of transcription factors are integrated at the level of the whole transcription machinery.

Results

Hox proteins directly bind Med19 via their homeodomain

To search for MED subunits that contact Hox proteins directly, a Hox/MED binding matrix was established with the in vitro GST-pulldown assay. GST fusions of the eight Drosophila Hox proteins (full-length Labial (Lab), Deformed (Dfd), Scr, Ubx, Abd-A and Abdominal-B (Abd-B), or portions of Pb and Antp) were probed with 35S-labelled MED proteins in standard conditions for 11 MED subunits that are not required for cell viability in yeast and/or that are known to interact physically with TFs in mammalian cells (Materials and Methods). The Med19 subunit stood out, binding strongly to multiple GST-Hox proteins in this assay (mean binding, >5% of input in multiple tests, except for Abd-B, 0.8%; Figure 1A).

To provide an independent and in vivo test for direct Med19/Hox binding, we used the Bimolecular Fluorescence Complementation (BiFC) assay. Auto-fluorescence from the Venus variant of Green Fluorescent Protein (GFP), abolished by truncating Venus protein into N- and C-terminal portions (VN and VC), can be effectively reconstituted when VC and VN fragments are coupled to interacting protein partners that reanimate them in cultured cells [30] or living organisms [31,32]. BiFC tests made use of the Gal4/UAS system [33] to direct co-expression of chimeric VN-Hox and Med-VC proteins. The functional validation of VN-AbdA relative to AbdA has been described [32]. VN-Ubx and VN-Dfd were likewise validated by their gain-of-function (gof) transformations in embryos (Figure S1). Fused Med19-VC was validated by its capacity to rescue lethal Med19 mutants (described below). UAS-directed co-expression of Med19-VC with VN-Ubx, VN-Dfd or VN-AbdA in embryos under engrailed-Gal4 control (en>Med19-VC+VN-Hox) resulted in serial stripes of clear nuclear fluorescent signal for VN-Ubx and VN-Dfd (Figure 1B-C). VN-AbdA was negative in this test (Figure 1D, but see Figure 1H, I below). Nevertheless, the concordant results from GST pulldown and BiFC tests indicate direct Med19 binding to Ubx and Dfd.

The observed direct Med19/Dfd or Ubx binding led us to ask whether these interactions utilize the homeodomain (HD) common to all Hox proteins. Consistent with this possibility, GST fusions containing the HX-HD regions of Pb (middle, a.a. 119–327) and Antp (C-ter, a.a. 279–378) bound Med19 at levels 15- to 50-fold superior to Pb N-ter (a.a. 1–158), Pb C-ter (a.a. 267–782) and Antp N-ter (a.a. 1–90) peptides (Figure 1A). A dissection of the HD-containing C-terminal regions of Ubx, GST-Med19 bound similarly to wild-type and HX-mutated Ubx [15], or to the linker-shortened C-terminal region of crustacean Artemia salina Ubx (Figure S2). Tests with the Antp C-ter peptide (a.a. 279–378) containing its HX, linker and HD, led to the same conclusion (not shown). Confirmation came from binding experiments using immobilized GST-Med19 and Antp, Ubx, Dfd and Abd-B HD peptides, where strong binding was observed for all four homeodomains despite marked divergence of their primary sequences (60% identity of Abd-B and Ubx HD) (Figure 1E). Contrary to the four Hox HD, neither Engrailed HD (43% identity with Ubx HD) nor the TALE class Hth HD (21% identity) bound detectably (Figure 1E). Since Med19 binds Dfd, Antp, Ubx and Abd-B HD but not those of En or Hth, we infer that it is specific and can discriminate among homeodomains.

In BiFC assays for Med19/HD association in vivo, comparable signals were observed on co-expressing Med19-VC with full-length VN-Ubx, or its HD alone (VN-HD-Ubx), in the normal Ubx expression domain (Ubx-Gal4; Figure 1F,G). Co-expressing expression of Distal-less [17]. Finally, specific a.a. residues in the HX motif, the HD and the linker separating them play a distinctive role in DNA target specificity, allowing one Hox HD to regulate PolII-dependent transcription [21–28]. Together, these subunits and the MED complex conserved from amoebae to man that serves as an interface between DNA-bound TFs and PolII. MED possesses a conserved, modular architecture characterized by the presence of a Med19-VC was validated by its capacity to rescue lethal Med19 mutants (described below). UAS-directed co-expression of Med19-VC with VN-Ubx, VN-Dfd or VN-AbdA in embryos under engrailed-Gal4 control (en>Med19-VC+VN-Hox) resulted in serial stripes of clear nuclear fluorescent signal for VN-Ubx and VN-Dfd (Figure 1B-C). VN-AbdA was negative in this test (Figure 1D, but see Figure 1H, I below). Nevertheless, the concordant results from GST pulldown and BiFC tests indicate direct Med19 binding to Ubx and Dfd.

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VN-AbdA with Med19-VC under abdA-Gal4 did not give rise to fluorescence (Figure 1D, H). By contrast, AbdA HD (VN-HDabdA) yielded a strong fluorescent signal (Figure 1I), confirming that the Hox HD is sufficient for direct Med19 binding. The differing responses obtained for full-length AbdA versus its HD raise the interesting possibility that AbdA sequences outside the HD limit its access to Med19 in vivo. Taken together, these biochemical and in vivo results indicate that the Hox HD is sufficient for direct binding to Med19.

**Med19 participates in Hox organizing activity**

Apart from yeast, no mutants of Med19 have been described. To address Med19 gene function in vivo, we employed imprecise excision of a viable P element insertion mutant, Med19<sup>P</sup> to generate two loss-of-function (lof) mutations, Med19<sup>1</sup> (a pupal-lethal hypomorphic allele harboring a 14 base pair (bp) upstream deletion), and Med19<sup>2</sup> (deleted for much of its protein coding sequence; see Figure 2A). Homozygotes for the presumptive null mutation Med19<sup>2</sup> die at the end of embryogenesis but do not show

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**Figure 1. Hox proteins bind Med19 through their homeodomains in vitro and in vivo.** (A) GST-pulldown binding assays of 35S-Med19 to immobilized GST-Hox fusions containing full length or protein fragments (below each lane: rectangles represent the entire protein; portions present in GST-Hox chimeric proteins are black, except the HD, represented in red). (B–D) BiFC assays were carried out co-expressing Med19-VC with VN-Ubx (B), VN-Dfd (C) or VN-AbdA (D), from UAS constructs under engravil-Gal4 control (en>). Med19-VC accumulation, detected with antibody against the GFP C-terminal region, is similar in all tests (B’–D’). Gal4-driven Hox protein accumulation is comparable to endogenous, as detected with Ubx, Dfd and AbdA specific antibodies (B’–D’). Relative BiFC fluorescent signals were quantified as in [32]. VN-Ubx signal (B) and VN-Dfd (C) yielded serial rows of nuclear fluorescence; VN-AbdA (D) gave no detectable signal. (E) Direct homeodomain binding to Med19. Pulldowns with immobilized GST or GST-Med19 employed 70 aa-long 35S-labelled peptides centered on the HDs of Antp, Dfd, Ubx, AbdB, En and Hth. (F–I) Direct homeodomain binding to Med19 in BiFC assay. Co-expression of Med19-VC with VN-Ubx (F), or with its HD (VN-HDUbx; G), under Ubx-Gal4 control gives indistinguishable BiFC signals. Expression of Med19-VC under abdA-Gal4 control yielded no fluorescence with VN-AbdA (H) but gave a strong signal with VN-HDabdA alone (I).

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cuticular defects. To remove maternally contributed protein and/or mRNA [34] that might mask early requirements for Med19, we used the Dominant Female Sterile technique to generate mitotic germ-line clones. When clones were induced in females heterozygous for Med19 and for otd<0, egg-laying was observed. Such embryos devoid of maternally contributed Med19 product undergo development (as visualised by nuclear DAPI staining, Figure S3). Though the first nuclear divisions proceed normally (Figure S3, t-1 hr), abnormalities are already visible in pre-cellular blastoderm (Figure S3, t=2 hr), leading to massively disorganised cellular embryos that die soon after (Figure S3). We conclude that a major maternal contribution to embryonic Med19 activity masks its zygoteric roles.

As an alternative approach to examining Med19 function in embryonic development, we made use of Med19-directed RNAi. Ubiquitous RNAi expression under daughtless-Gal4 control gave rise to cuticular defects in the spiracles and head of L2/L3 larvae (Figure S4) reminiscent of the embryonic consequences of Abd-B or mRNA [34] that might mask early requirements for Med19, we or for Ubx-dependent, palps (Figure 3D, arrowhead) require Dfd function in a territory abutting the antennal primordium of the eye-antennal imaginal disc [40], and the palp loss noted above (Figure 2H) suggested a link to Dfd. In interaction tests, palp loss provoked by Dfd-specific RNAi [patched-dsRNAidl] was enhanced in Med19<0 heterozygotes (Figure S6). Conversely, ectopic expression from the gain-of-function (gof) Ubx<0 allele directs a fully penetrant transformation of antenna toward leg (Figure 3A, B) that is partially suppressed in Med19<0 heterozygotes, as shown by the replacement of distal claws by antennal aristae (Figure 3G, Figure S6).

We therefore decided to examine post-embryonic development, making use of partial loss-of-function combinations and of clonal assays. To better characterize the consequences of Med19 loss-of-function, we employed FLP/FRT-mediated mitotic recombination [35] to generate clones of cells homozygous for Med19<0 (t—). In "twin spot" experiments where t— and +/+ cells arise from mitotic recombination in a single t/— cell during mitosis, only t/+ cells were subsequently detected (Figure 2B). This cell lethality is due to loss of Med19, since expressing Med19-VC protein in mutant cells restores viability (Figure 2C); indeed, large Med19/+/Med19<0 clones are observed even though Med19-VC accumulation is less than for wild-type protein in adjacent cells (Figure S5A–A'). Strikingly, Med19/+/Med19<0 cells also survived in the presence of a Minute (M) mutation [36] that slows growth of surrounding heterozygous M+/— cells (Figure 2D). Immune staining with anti-Med19 sera confirmed that Med19 is a protein-null mutation (Figure S5, B–B'). Thus the existence of these clones shows that Med19 is not strictly required for cell viability. The influence of cell environment on cell lethality suggests a role for Med19 in the control of cell competition.

If Hox/Med19 binding is functionally relevant to homeotic activity, Med19 mutants might provoke Hox-like phenocopies or modify Hox-induced homeotic defects. In light of the strong maternal contribution of Med19 present in embryos, we turned our attention to later developmental stages. Hypomorphic Med19<+/Med19<0 animals, or Med19<+/Med19<0 animals with low-level ubiquitous expression from the Ub-Med19 transgene, survive to the pupal stage and show a fully penetrant loss of anterior spiracles (Figure 2E, F). Rare adult Ub-Med19; Med19<+/Med19<0 survivors showed defects including loss of maxillary palps (Figure 2G, H). Tissue-directed induction of Med19<+/Med19<0 clones in the dorsal compartment of the haltere imaginal disc (apterous-Gal4>UAS-Flp) is associated with disorganization of the distinctive pedicellar sensillae in halteres [37], where these sensory organs are reduced in number and their well-ordered rows disrupted in adult halteres (Figure 2I–I').

All the preceding defects (Figure 2E, I') resemble Hox loss-of-function phenotypes: of Antp for the pupal anterior spiracles [38]; of Dfd for the adult maxillary palps [39,40]; and of Ubx for haltere sensory organs [37]. We therefore asked whether Med19 mutants can act as dose-sensitive modifiers of Hox activity in genetic interaction tests. For Antp, the fully penetrant spiracle loss observed in Med19<+/Med19<0 pupae (Figure 2F) is absent from Med19<0 or Antp<0 heterozygotes but can be detected in Med19<0/Antp<0 double heterozygotes (Figure S6). This synergistic interaction links Med19 to normal Antp function. Conversely, ectopic expression from the gain-of-function (gof) Antp<0 allele directs a fully penetrant transformation of antenna toward leg (Figure 3A, B) that is partially suppressed in Med19<0 heterozygotes, as shown by the replacement of distal claws by antennal aristae (Figure 3G, Figure S6).

Med19 is required for Ubx target gene activation

The intensive attention given to Ubx target gene regulation in the haltere imaginal disc [3–5,41,42] makes it an excellent paradigm for understanding Hox interplay with Med19 in a developmental program. We therefore examined the effect of removing Med19 function on Ubx activity towards selected target genes in the haltere imaginal disc (Figure 4A). Clones of t—/+ cells induced in haltere discs in the presence of a Minute mutation showed Ubx levels comparable to their t+/+ neighbors (Figure 4B–B'). The presence of normal nuclear Ubx signal in mutant cells after several mitotic divisions shows that the Med19 condition has not generally affected transcription. We next examined the effects of Med19<0 mitotic clones on several Ubx target genes in haltere development [41]. Ubx is known for its role in suppressing wing development, and acts to repress a number of prominent wing developmental genes in the haltere imaginal disc [41]. With the combined use of ectopic Hox expression and analysis of the transcriptome, additional Ubx targets have emerged. The first example of a Ubx-activated target was CG13222, which is regulated through an autonomous cis-regulatory region called "edge" for its expression in a band of cells along the posterior border of the haltere disc [42], Expression of the edge-GFP reporter construct, that recapitulates Ubx-dependent CG13222 expression [42] is cell-autonomously abolished in Med19<0 haltere clones (Figure 4C,D; identified with anti-Med19 sera). This shows that Med19 is required for activation of the direct Ubx target CG13222 in the haltere disc. A second positively-regulated target identified in recent whole-genome analyses, bric-a-brac2 (bab2), is induced by ectopic Ubx [5] and correlates with direct Ubx binding to regulatory DNA in vivo [3,4]. Using mitotic recombination, we examined the expression of bab2 in Ubx<0 haltere cells and found that Bab2 accumulation is cell-autonomously abolished (Figure 4E–E'). On examining bab2 expression with respect to Med19 activity, Bab2 accumulation was cell-autonomously down-regulated in Med19<0 cells (Figure 4F–F').

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Figure 2. **Med19 mutations affect cell viability and Hox-related developmental processes.** (A) Mutant alleles were generated by imprecise excision of a viable P element insertion 37 bp upstream of the putative Med19 transcription initiation site (19P). Med191 is a pupal-lethal hypomorph with 14 bp deleted 5' to the Med19 transcription start. Med192 is an embryonic lethal amorph deleted for 1174 bp of DNA spanning exon 1 with its ATG initiation codon. (B–D) Clonal analyses of Med192. (B) ''Twin spot'' analysis. Mitotic recombination induced in hsp70-Flp; Med192 FRT-2A/Ub-GFP FRT-2A larvae (30°C heat shock at 38°C) gave +/+ clones (intense green), but no 2/2 sister clones (GFP-) were observed. (C) Twin spot analysis in rescue conditions. The engrailed-Gal4 driver was used to simultaneously induce mitotic clones (UAS-Flp) and to direct expression of Med19-VC (UAS transgene). Homozygous Med192/2 (2/2) cells (lacking GFP) are now detected. (D) The Med19 condition is not intrinsically cell-lethal. In this wing imaginal disc (genotype, en-Gal4. UAS-Flp/+; Med192 FRT-2A/Ub-GFP M2 FRT-2A), GFP- Med192/- clones are observed. (E–J) Med19 function is required for multiple Hox-related developmental processes. (E,F) Med19 is required for eversion of anterior pupal spiracles. Normal anterior spiracles (E) are absent from Med191/2 hypomorphs (F). (G,H) One maxillary palp (G, arrow) is absent in a surviving Ub-Med19; Med192/- hypomorph (H, arrow). (I,J) Med19 is required for haltere-specific sensory organs. (I) Wild-type haltere, with zone of interest (dotted box) showing rows of pedicellar sensillae...
Med19 activity is required in the haltere disc for normal Ubx-mediated activation of bab2. However, contrary to edge, residual low-level bab2 expression is present in some Med19<sup>−/−</sup> cells (Figure 4F–F’). The responses of these two regulatory sequences to Med19 lof indicate that Med19 is required for Ubx target gene activation.

Several targets whose expression is repressed by Ubx were tested for a requirement for Med19 (Figure 4A). For example, the broad central band of galt<sup>3</sup> (sal) expression in the wing pouch is absent from Ubx-expressing cells of the haltere pouch. sal is derepressed in Ubx<sup>−/−</sup> haltere disc cells [41], as shown by the appearance of Sal protein in Ubx mutant cells (Figure 4G–G’). By contrast, no new expression of Sal is detected in equivalently placed Med19<sup>−/−</sup> clones (Figure 4H–H’). De-repression was likewise not observed for other tested Ubx-repressed targets (not shown), lending molecular support to the interpretation that Med19 is not involved in Ubx repressive activities. While further examples will be required to determine whether this illustrates a general property of Med19 action in transcriptional regulation, these results suggest that Med19 collaboration with Ubx is limited to gene activation.

Med19 binds the Hox homeodomain through a conserved motif

Binding of Hox proteins to Med19 specifically involves their conserved homeodomain. To identify Med19 sequences involved in HD binding, we used GST-pulldown to test full-length or deleted versions of Med19 with GST-HDAnp. Binding was retained on truncating the terminal regions of Med19 (Figure 5A, constructs 1–2), but was abolished on deleting an internal 70 aa region (Figure 5A, constructs 3–4). Smaller deletions confirmed that this region contains sequences required for full binding (Figure 5A, constructs 5–6). This 70 aa Med19 peptide is not only required but also proved sufficient to bind the HD (Figure 5A, construct 7), leading us to call it Homeodomain Interacting Motif (HIM).

The HIM interval of Med19 was then compared with Med19 orthologs from a spectrum of eukaryotes. Sequence alignments reveal a lysine/arginine-rich sequence that is strongly conserved in Med19 orthologs from six vertebrate or insect species (Figure S7). This striking conservation suggests that the contribution of HIM to Med19 function is subject to strong selective pressure.

Med19 is required for Ubx-mediated activation of specific target genes in vivo, and directly binds Hox HDs in vitro through its conserved HIM motif. This suggested that Ubx function passes through Med19, potentially via its HIM sequence. We therefore sought evidence for Med19/Hox binding in cellulo. Cultured Drosophila cells expressing UAS-Med19-VC or UAS-Med19ΔHIM-VC were used for co-immunoprecipitations with anti-GFP (VC). As shown in the Western blot of Figure S8, the three endogenous Med1 isoforms were associated with both Med19-VC and Med19ΔHIM-VC. This is consistent with the incorporation of full-length and HIM-deleted forms into the MED complex.

We next co-expressed these proteins with Ubx-HA and tested for their association in cellulo. As seen in Figure 5B, Ubx-HA co-precipitates with Med19-VC, indicating the association of Ubx transcription factor with Med19. By contrast, less Ubx-HA was detected on co-precipitating with Med19ΔHIM-VC (relative to a non-specific band that serves as a de facto internal loading control, * in Figure 5B). These results indicate that the HIM domain contributes to Ubx-Med19 interaction.

To further investigate the contribution of the HIM domain to HD binding in vivo, we generated transgenic lines containing the same UAS-Med19-VC, -Med19ΔHIM-VC and -HIM-VC constructs used above, and tested each protein’s ability to bind to VN-HDUBx in the BiFC assay. In control experiments, Med19-VC, HIM-VC and Med19ΔHIM-VC accumulated at comparable levels in wing imaginal discs (Figure S8). Med19-VC and HIM-VC are fully nuclear. The Med19ΔHIM-VC protein (lacking the highly basic HIM element) is seen to accumulate in both the cytoplasm and the nucleus (Figure S8). This indicates that the HIM element contributes to nuclear localisation, together with other Med19 sequences. As noted in embryos (Figure 1G), co-expressing Med19-VC with VN-HDUBx under dpp-Gal4 control in wing imaginal discs resulted in clear fluorescent signal (Figure 5C). When HIM-VC was tested for its ability to interact with the Ubx HD, it gave rise to a fluorescent signal stronger than for intact Med19; by contrast, the Med19ΔHIM-VC fusion yielded only a background-level signal with VN-HDUBx (Figure 5C). Taken together, these results of biochemical and BiFC experiments indicate that Med19 HIM is necessary and sufficient for full HD binding.

HIM is required for Ubx target gene activation

While Med19 benefit of its conserved HIM element can be incorporated into MED, as shown above, its functional requirements in vivo remained an open question. Accordingly, we tested whether Drosophila HIM is relevant to Med19 developmental functions. In a genetic rescue test, ubiquitous Med19-VC expression restored adult viability to pupal-lethal Med19<sup>−/−</sup> <i>Med19<sup>−/−</sup></i>/Med19<sup>−/−</sup> hypomorphs, whereas Med19ΔHIM-VC did not. Med19ΔHIM-VC also showed a reduced aptitude to rescue pupal spiracles, adult maxillary palps and haltere sensillae compared with Med19-VC (Figure S6). These results indicate a requirement for Med19 HIM in several Hox-dependent developmental processes.

We therefore sought to test the influence of the Med19 HIM peptide on Ubx-dependent transcriptional activation of the direct target <i>CG13222/edge</i>. To this end, (i) FLP/FRT-mediated mitotic recombination was used to generate cells devoid of wild-type protein, while (ii) UAS/Gal4-directed expression supplied normal or HIM-deleted Med19-VC, and (iii) the edge-GFP reporter was employed to assess Ubx-mediated activation of <i>CG13222</i>. <i>Eve</i>-Gal4-directed UAS-Flp expression in the posterior haltere disc compartment served to induce mitotic recombination there, while en-Gal4 simultaneously directed expression of Med19-VC or Med19ΔHIM-VC in the posterior compartment (Figure 6A–B). These twin-spot experiments provided two important observations. Firstly, large <i>−/−</i> clones (RFP<sup>−</sup>) were observed not only in Med19-VC but also in Med19ΔHIM-VC expressing discs (Figure 6A’, B’). The existence of <i>−/−</i> clones is in marked contrast with their complete absence in Figure 2B. This shows that both Med19-VC and Med19ΔHIM-VC restore cell viability. We conclude that HIM is not necessary for cell viability. Further, it indicates that not only are both forms of Med19-VC incorporated into MED, but they are functional there. Secondly, Med19-VC and Med19ΔHIM-VC differed markedly in their capacities to
ensure activation of the Ubx target gene CG13222. Reporter expression was observed within all appropriately positioned clones of −/− cells expressing Med19-VC (11 of 11 clones; Figure 6A, C). By contrast, edge-GFP expression was entirely absent from most clones expressing Med19ΔHIM-VC (7 of 11 clones; Figure 6B, C). The existence of HIM-independent cell proliferation/survival shows that this cellular function of Med19 can be uncoupled from its Hox-related role. These results also provide clear functional evidence that Ubx-dependent activation of its edge-GFP target requires HIM-endowed Med19.

Figure 3. Synergistic interactions between Med19 and Hox mutations. Dose-sensitivity for Med19 was tested relative to Hox gain-of-function mutations of Antp (A–C), Dfd (D–F), and Ubx (G–I). (A) Wild-type antenna, with distal arista (ar) indicated by an arrowhead; (B) AntpNS−directed transformation of antenna toward leg with distal claw (cl, arrowhead); (C) the transformation is attenuated in AntpNS/Med19− trans-heterozygotes, as shown by the presence of a partial arista (ar, arrowhead). (D) Wild-type head, with the maxillary palp (Mx) indicated by arrowhead. (E) Dfd1 provokes head defects including reduced eyes and the appearance of ectopic Mx (arrowhead), here positioned behind the antenna. (F) In Dfd1/Med19− heterozygotes (or here, Dfd1Med19−/Med19−), no ectopic Mx were observed. (G) Wild-type wing. (H) Homozygote for the UbxCbx1 gof allele that expressed Ubx protein in the posterior compartment of the wing. Note the discrete hemi-haltere induced by Ubx, which is oriented at right-angles relative to the longitudinal wing axis. (I) In UbxCbx1 Med19−/UbxCbx1 Med19− wings, the posterior wing is no longer organized as a hemi-haltere, and the cellular trichomes are reoriented toward the long wing axis (arrow).

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Discussion

Med19, a MED regulatory subunit that binds Hox transcription factors

Hox homeodomain proteins are well-known for their roles in the control of transcription during development. Further, much is known about the composition and action of the PolIII transcription machine. However, virtually nothing is known of how the information of DNA-bound Hox factors is conveyed to PolII in gene transcription. The Drosophila Ultrabithorax-like mutant affecting the large subunit of RNA PolII provokes phenotypes reminiscent of Ubx mutants [43], but the molecular basis of this remains unknown. The lone direct evidence linking Hox TFs to the PolII machine is binding of the Antp HX motif to the TFIID component BIP2 [20]. Here, we undertook to identify physical and functional links between Hox domain TFs and the MED transcription complex. Our results unveil a novel aspect of the evolutionary Hox gene success story, extending the large repertory of proteins able to interact with the HD [44] to include the Drosophila MED subunit Med19. HD binding to Med19 via the conserved HIM suggests this subunit is an ancient Hox collaborator. Accordingly, our loss-of-function mutants reveal that Med19 contributes to normal Hox developmental function and does so at least in part via its HIM element. Thus this analysis reveals a previously unsuspected importance for Med19 in Hox-affiliated developmental functions.

A fundamental property of the modular MED complex is its great flexibility that allows it to wrap around PolII and to change form substantially in response to contact with specific TFs [45]. Recent work in the yeast X. cernuae places Med19 at the interfaces of the head, middle and CDK8 kinase modules [46,47]. Med19 is thus well-positioned to play a pivotal regulatory role in governing MED conformation (Figure 7). Our results raise the intriguing possibility that MED structural regulation and physical contacts with DNA-bound TFs can pass through the same subunit. In agreement with this idea, recent work identified direct binding between mouse Med19 (and Med26) and RE1 Silencing Transcription Factor (REST) [48]. This binding involves a 460 a.a. region of REST encompassing its DNA-binding Zn fingers [48]. The present work goes further, in identifying a direct link between the conserved Hox homeodomain and Med19 HIM (Figure 7) that, to our knowledge, is the first instance for a direct, functionally relevant contact of MED with a DNA-binding motif rather than an activation domain.

Hox-independent Med19 roles in cell proliferation/survival

Med19 contributes to developmental processes with Antp (spiracle eversion), Dfd (Mx palp), and Ubx (haltere differentiation). Other phenotypes identified with our mutants indicate further, non-Hox related roles for Med19. As shown here, complete loss of Med19 function leads to cell lethality that can be conditionally alleviated when surrounded by weakened, Minute mutation-bearing cells. These observations, that uncouple HIM-dependent functions from the role of Med19 in cell survival/proliferation (Figure 6B), are compatible with reports correlating over-expression of human Med19/Lung Cancer Metastasis-Related Protein 1 (LCMR1) in lung cancer cells with clinical outcome [49]. Further, RNAi-mediated knock-down of Med19 in cultured human tumor cells can reduce proliferation, and tumorigenicity when injected into nude mice [50–58]. A recent whole-genome, RNAi-based screen identified Med19 as an important element of Androgen Receptor activity in prostate cancer cells where gene expression levels also correlated with clinical outcome [59]. It will be of clear interest to examine how, and with what partners, Med19 carries out its roles in cell proliferation/survival.

Transcriptional activation versus repression

The role played by mammalian Med19 and Med26 in binding the REST TF, involved in inhibiting neuronal gene expression in non-neuronal cells [48,60], provides an instance of repressive Med19 regulatory function. We found that Med19 activity is required in the Drosophila haltere disc for transcriptional activation of CG13222/edge and bab2, but is dispensable for Ubx-mediated repression of five negatively-regulated target genes (Figure 4); Ubx can choose to activate or it can repress, at least in part through an identified repression domain at the C-terminus just outside its homeodomain [61]. Conversely Med19, which binds the Ubx homeodomain, appears to have much to do with activation.

Concerning the mechanisms of Ubx-mediated repression, one illuminating example comes from analyses of regulated embryonic Distal-less expression [17]. Ubx can associate combinatorially with Exd and Hh, plus the spatially restricted co-factors Engrailed or Sloppy-paired in repressing Distal-less [17]. Engrailed in turn is able to recruit Groucho co-repressor [62], suggesting that localized repression involves DNA-bound Ubx/Exd/Hh/Engrailed, plus Engrailed-bound Groucho. Groucho has been proposed to function as a co-repressor that actively associates with regulatory proteins and organizes chromatin to block transcription. Wong and Struhl [63] demonstrated that the yeast Groucho homolog Tup1 interacts with DNA-binding factors to mask their activation domains, thereby preventing recruitment of co-activators (including MED) necessary for activated transcription. The number of targets remains too small to be sure Med19 is consecrated to activation. Nonetheless, it will be of interest to determine whether Groucho can play a role in blocking MED/Ubx interactions that could provide an economical means for distinguishing gene activation from repression.

The Hox-MED interface in evolution and development

The conserved Hox proteins and the gene complexes that encode them are well-known and widely used to study development and evolution. As to the evolutionary conservation of the Mediator transcription complex, the presence of MED constituents in far-flung eukaryotic species from unicellular parasites to

Figure 4. Med19 acts as a “co-factor” for Ubx-mediated gene activation. (A) Summary of Ubx target genes analyzed. Ubx can repress (red bars) or activate (green arrows) direct target genes. (B–H) Med19 function in Ubx target gene expression. Images show whole haltere imaginal discs that are wild-type (C), or bear mitotic clones of Med19+ in a Minute background (B, D, F, H) or of Ubx+ (E,G). The other columns contain enlargements of boxed images in the first column, showing genotypic markers to identify clones (B–H*); expression of gene of interest (B–H*); and merged images (B–H**). (B–B) Ubx protein (red) accumulates normally in a Med19+/− clone (GFP-). (C–C*) edge-GFP reporter gene expression (green) is localized in a row of cells at the posterior border of the disc; ubiquitous expression of wild-type Med19 is revealed by anti-Med19 (red). (D–D*) edge-GFP expression (green) is absent in a Med19−/− clone (absence of anti-Med19, red; circled) crossing the line of edge-expressing cells. (E–E*) Bab2 protein (anti-Bab2, red) is absent from Ubx+/− cells (GFP-). (F–F*) Bab2 expression (red) is cell-autonomously down-regulated in Med19−/− cells (GFP-). (G–G*) spalt (sal) expression (anti-Sal, red) appears in centrally positioned cells of Ubx+/− clones (GFP-) in the haltere pouch. (H) Spalt (red) is not repressed in Med19 mutant cells (GFP-) positioned as for the Ubx clone (G*)

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humans [21] indicates that this complex existed well before the emergence of the modern animal Hox protein complexes. The DNA-binding domains are often the most conserved elements of TF primary sequence, and in the case of the Hox HD, recent forays into “synthetic biology” agree that this was the functional heart of the ancestral proto-Hox proteins [64–66]. Indeed, Scr, Antp and Ubx mini-Hox peptides containing HX, linker and HD motifs behave to a good approximation like the full-length forms.
Figure 6. Med19 HIM is required for Ubx target gene activation, but not for cell proliferation/survival. Med19-VC (A) or Med19ΔHIM-VC (B) proteins were expressed (UAS constructs, en-Gal4) in posterior haltere imaginal discs harboring Med19 mutant clones. Med19-VC or Med19ΔHIM-VC were detected with antisera directed against C-terminal GFP (αVC, blue). (A–A′, B–B′) Med19 clones were identified using a ubiquitous RFP marker: −/− (no red), +/+ (red). Activation of the Ubx target edge-GFP at the posterior haltere edge was visualized by GFP (green). Regions containing Med19−/− clones of interest are enlarged (A′–A″, B′–B″). (A–A″) Med19-VC restored expression of edge-GFP. (B–B″) Med19ΔHIM-VC failed to rescue edge-GFP activation here. GFP-expression here is limited to a single wild-type cell that abuts the −/− clone (B′, B″, arrow). (C) Three levels of edge-GFP expression could be discerned: normal, present but reduced, or none. All correctly positioned −/+ clones with Med19-VC showed GFP expression (11 of 11) of which 9/11 were normal. Most clones possessing Med19ΔHIM-VC showed no GFP (7 of 11), and only two of 11 clones showed normal expression.

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directing appropriate gene activation and repression resulting in genetic transformations [64–66]. Our results showing direct HD binding to Med19 HIM, and thus access to the PolII machinery, allow the activity of these mini-Hox proteins to be rationalized. We surmise that at the time when the Hox HD emerged to become a major developmental transcription player, its capacity to connect with MED through specific existing sequences was a prerequisite for functional success. One expected consequence of this presumed initial encounter with Med19 – a selective pressure on both partners and subsequent refinement of binding sequences – is in agreement with the well-known conservation of Hox homeodomains, and with the observed conservation of the newly-identified HIM element in Hox-containing eumetazoans. We imagine that subsequent evolution over the several hundred million years separating flies and mammals will have allowed this initial contact to be consolidated through subsequent binding to other MED subunits, ensuring versatile but reliable interactions at the MED-TF interface (Figure 7).

A functional Hox-MED interface

Hox homeodomain proteins are traditionally referred to as selector or “master” genes that determine developmental transcription programs. The low sequence specificity of Hox HD transcription factors is enhanced by their joint action with other TFs, of which prominent examples, the TALE homeodomain proteins Extrathorax/Phx and Homothorax/Mei are considered to be Hox co-factors. However, a Hox TF in the company of Exd and Hth could still not be expected to shoulder all the regulatory tasks necessary to make a segment with all the coordinated cell-types it is made up of, and collaboration with cell-type specific TFs appears to be requisite. A useful alternative conception visualizes Hox proteins not as “master-selectors” that act with co-factors, but as highly versatile co-factors in their own right that can act with diverse cell-specific identity factors to generate the cell types of a functional segment [67]. We envisage a model where a Hox protein would be central to assembling cell-specific transcription factors into TF complexes that interface with MED (Figure 7).

Such Hox-anchored TF complexes could make use of selective HD binding to Med19 as a beach-head for more extensive access to MED, such that loss of the Hox protein would incapacitate the complex: in the case of Ubx− cells, inactivating bab2 or derepressing sal. Accordingly, three observations suggest that binding of Hox-centered TF complexes involves additional MED subunits surrounding Med19 (Figure 7): (i) bab2 target gene expression is entirely lost in Ubx-deficient cells but can persist in some Med19− cells; (ii) edge-GFP in Med19− cells expressing Med19ΔHIM-VC was not altogether refractory to Ubx-activated edge-GFP expression (Figure 6); and (iii) Med19ΔHIM-VC is not entirely impaired for Ubx binding, as seen in co-immunoprecipitations (Figure 5). Thus Hox protein input conveyed through Med19-HIM at the head-middle-Cdk8 module hinge might provide an economical contribution toward organizing TF complexes that influence overall MED conformation [45] and hence transcriptional output. Decoding how the information-rich MED interface including Med19 accomplishes this will be an important part of understanding transcriptional specificity in evolution, development and pathology.

Materials and Methods

Ethics statement

Our work using Drosophila was performed in conditions in conformity with French and international standards.

GST pulldowns

Culture and preparation of GST-fusion proteins, preparation of 35S protein probes, and pulldowns were carried out essentially as
Figure 7. Model for the role of Med19 at the interface of Hox and MED. The Mediator complex, composed of four modules – tail, middle, head and CDK8 –, binds physically to PolII, principally through its head module. Hox transcription factors (HD in blue, its three α-helices indicated as cylinders) bind to regulatory DNA sequences distant from the transcription start site (grey arrow), together with unknown numbers of other TFs (here, Hox co-factors Exd and Hth plus cell-specific factors TF1 and TF2). We propose that the DNA-bound Hox homeodomain serves to recruit MED directly through Med19 HIM (green hook). This Hox-MED association then permits the general PolII transcription machinery (PolII-GTF) to be recruited to the Hox target promoter. This link to a MED subunit situated at the interface of the head, middle and CDK8 modules could modify overall MED conformation, favoring additional contacts between the TF complex and MED that modulate transcriptional activity.

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described in [68]. Chimeric GST-Hox constructs fused GST to Hox cDNAs. Full-length Hox fusions were used for Labial, Deformed, Sex combs reduced, Ultrabithorax, Abdominal-A and Abdominal-B. Fragments of Pb and Antp were present in the fusion proteins: Pb1 (N-ter, a.a. 1–130), Pb2 (middle with HD, a.a. 119–327) and Pb3 (C-ter, a.a. 267–782). For Antp, two GST fusions were used: Antp1 (N-ter, 1–90) and Antp4 (C-ter with HD, 279–378). Eleven MED putative surface subunits [21] could be expressed at useable levels in coupled in vitro transcription/translation reactions: Med1/Trap220, Med2/Med29/Ix, Med6, Med12/Kto, Med13/Skd, Med15/Arc105, Med19, Med25, Med30, Cdk8 and CycC.

Co-immunoprecipitations

Cultured Drosophila S2 cells were transfected using FuGENE HD transfection reagent (Roche) with pActin-V5 (negative control; pActin-GAL4 driver with either pUAS-Med19-VC or pUAS-Med19HIM-VC (MED co-IP); or adding pUAS-Ubx-HA (Med19-Ubx co-IP). 10⁷ cells were transfected with driver plasmid plus the UAS responder plasmid(s). After 72 hr, cells were harvested by scraping and pooled, collected by centrifuging then washed with 1x PBS. All subsequent steps until Western blotting were carried out at 4°C. Cell pellets were resuspended in IP buffer (50 mM TrisHCl, pH = 8, 150 mM NaCl, 0.5% NP40, 1 mM EGTA and Roche complete protease inhibitor cocktail), lysed by four-fold passage through a 27G needle, then centrifuged for 10 min at 14,300 rpm. Immunoprecipitation from 1.5 mg of total protein extract (5 μg/μl in IP buffer) was performed with mouse anti-GFP (ROCHE 4 μg/IP), with gentle agitation overnight. 15 μl of G-protein-coupled Sepharose beads (SIGMA, P3296) were then added, gently agitated for 2 hr. The non-bound fraction was discarded. Beads were washed 4 times with fresh IP buffer, taken up in 2X Laemmli buffer containing DTT and SDS, heated to 95°C, and centrifuged. Supernatants were then submitted to polyacrylamide gel electrophoresis. Med1 and Med19 were revealed using polyclonal sera from guinea-pig (diluted 1:500), while Ubx-HA was detected with rabbit anti-HA (SIGMA) diluted 1:1000.

Bimolecular Fluorescence Complementation (BiFC)

Constructions corresponding to UAS-VN-Ubx, UAS-VN-AbdA and UAS-VN-HDAbdA transgenic lines are described in [32]. UAS-VN-Dfd, UAS-VN-HD-Ubx: Dfd and Ubx HD sequences were cloned into Xhol-XbaI sites downstream of the Venus VN fragment into the pUAST or pUASTattB plasmids described in [32]. UAS-Med19-VC, UAS-HIM-VC: Full-length Med19 coding sequences, or the internal HIM sequence generated from Med19 cDNA by PCR, were introduced as EcoRI-Xhol fragments to replace Hth coding sequences of pUaHth-VC [32]. For UAS-Med19HIM-VC, internally deleted Med19 was generated from the full-length construct by double PCR, using the overlap extension method. The PCR-derived internal deletion product was cleaved by RsrII and XhoI, then cloned in place of the equivalent fragment of UAS-Med19-VC. All constructs were sequence-verified before fly transformation. Transgenic lines were established by classical P-element mediated germ line transformation or by site-specific integration using the FLC-31 integrase. Embryos were analysed as described in [32]. For BiFC in imaginal discs, late-third-instar larvae of appropriate genotypes were cultured in parallel in the same environmental conditions of temperature and larval density, then were dissected at the same time and fixed in the same solution (2% para-formaldehyde, 0.5M EGTA, 1X PBS). Wing and haltere imaginal discs were dissected and mounted in Vectashield (Vector Labs). Image acquisition was performed on a Leica SP5 using the same laser excitation, brightness/contrast and z settings. Confocal projections from at least 10 distinct wing discs per genotype were analyzed with ImageJ software.

Fly strains

Stocks and crosses were maintained at 25°C on standard yeast-agar-cornmeal medium. Mutant stocks harboring AntpN, Dfdz,
**Ubx** and **Df(3L)BSC8** were from the Bloomington *Drosophila* Stock Collection. **En** was provided by R. Mann. Edge-GFP and **ig** were from the S. Carroll lab. The Ub-Med19 transgenic line expressing full-length Med19 cDNA under **ubi** control is a homozygous-viable insertion on the X chromosome at attP site **ZH 2A**. These transgenic elements carry the visible marker mini-white. **UAS-RNAi** against Med19 is from a non-directed insertion on chromosome 2 (Vienna *Drosophila* Research Collection stock 50110). **UAS-RNAI** lines against Med19 are stocks 27559 and 33710 from the Bloomington collection. **Gal4**-expressing driver lines used were: **en** and **abdA** (dorsal compartment of abdominal segment 1 (A1)), **en**-**Gal4** (posterior compartment), **en**-**Gal4** (ubiquitous), **en**-**Gal4** (posterior compartment), **ap**-**Gal4** (dorsal compartment of wing and haltere discs), **Ubx**-**Gal4** and **abdA**-**Gal4** (abdominal expression under Ubx or abdA control, respectively).

**Generation of Med19 mutants**

Loss-of-function Med19 alleles were generated by imprecise excision, mobilizing the viable P**[(Epany2)EY16159]** insertion marked with mini-white. **UAS-RNAI** against Med19 is from a non-directed insertion on chromosome 2 (**Vienna Drosophila** Research Collection stock 50110). **UAS-RNAI** lines against Med19 are stocks 27559 and 33710 from the Bloomington collection. **Gal4**-expressing driver lines used were: **en**-**Gal4** (imaginal disc-specific, AP boundary, anterior compartment), **en**-**Gal4** (AP boundary, anterior compartment), **en**-**Gal4** (posterior compartment), **ap**-**Gal4** (dorsal compartment of wing and haltere discs), **Ubx**-**Gal4** and **abdA**-**Gal4** (abdominal expression under Ubx or abdA control, respectively).

**Rescue experiments**

The following stocks were employed for rescue tests: **Ubx-Med19**, **Med19**/TM6B, **Hu Tb**; **Med19**/TM6B, **Hu Tb**; **Med19**/TM6B, **Hu Tb**; **Am-Gal4**, **Med19**/TM6B, **Hu Tb**; **UAS-Med19**-**VC**, **Med19**/TM6B, **Hu Tb**; **UAS-Med19-HIM-VC**, **Med19**/TM6B, **Hu Tb**.

**Clonal analyses**

Mittotic clones were induced by Flp recombinase expressed from a hsp70-Flp transgene on heat induction (30' at 38°C), or from a UAS-Flp element under Gal4 control as indicated above (en>Flp, ap>Flp). Clones were generated and identified in marked progeny from crosses using the following stocks: **en**>**Flp**: **Med19**>**FRT-2A**/TM6B, **Hu Tb**; **hsp70-Flp**: **Ub-GFP**>**FRT-2A**/TM6B, **Hu Tb**; **Ub-Med19**: **Ub-GFP**>**FRT-2A**/TM6B, **Hu Tb**; **UAS-Med19**-**VC**: **Ub-GFP**>**FRT-2A**/TM6B, **Hu Tb**; **en**>**Flp**: **Med19**>**FRT-2A**/TM6B, **Hu Tb**: **Ub-GFP**>**FRT-2A**/TM6B, **Hu Tb**; **ap**>**Flp**: **Med19**>**FRT-2A**/TM6B, **Hu Tb**: **hsp70-Flp**: **Ub-GFP**>**FRT-2A**/TM6B, **Hu Tb**; **edge-GFP/CyO, Gy**; **M**-**FRT-2A**/TM6B, **Hu Tb**: **edge-GFP/CyO, Gy**; **M**-**FRT-2A**/TM6B, **Hu Tb**: **edge-GFP/CyO, Gy**; **His2Av-mRFP1**>**FRT-2A**/TM6B, **Hu Tb**: **edge-GFP, UAS-Med19-VC/CyO, Gy**; **His2Av-mRFP1**>**FRT-2A**/TM6B, **Hu Tb**.

**Germ-line clones**

After crossing **y**>**hsp70-Flp**: **Med19**>**FRT-2A**/TM6B, **Hu Tb** females with **w; P**>**FRT-2A**/TM6B, **Sb** males, progeny at L3/early pupal stages were subjected to heat shocks (1 hr, 37°C) on two successive days. Resulting **y**>**hsp70-Flp**: **w; Med19**>**FRT-2A**/TM6B, **Hu Tb** adult females were crossed with **Med19**>**FRT-2A**/TM6B, **Sb** males to generate **soar**-GFP embryos. Embryos resulting from germ-line clones were collected on egg lay plates, then analysed by confocal microscopy after mounting in DAPI-containing Vectashield medium. In positive controls where Med19 was replaced with Med19**, all expected zygotic classes were obtained as viable, fertile adults. In the absence of heat shock, no eggs were laid.

**Antibody staining**

Performed as described in [40]. Antibodies used were: rat anti-Bau2** [J-L Couderc](#), used at 1:3000; mouse anti-GFP (VC) (**Roche**, 1:200) or chicken anti-GFP (VC) (**Invitrogen**); rabbit anti-Spalt** [R. Barrio, 1:100]; mouse anti-Col** [M. Crozatier/A. Vincent, 1:200]; mouse anti-dsRF** [M. Aflolter, 1:1000]; rabbit anti-**β-Gal** (Cappel 1:2500); mouse anti-Wg (1:200) and anti-Ubx (1:50) from the Developmental Studies Hybridoma Bank, University of Iowa.

**Anti-Med19 and -Med1 sera**

Guinea pigs were immunized (Eurogentec) with GST-Med19 or GST-Med1 proteins extracted from *E. coli* and enriched by affinity chromatography. Anti-Med19 sera from terminal bleeds was used for immunocytology without purification at a 1:500 dilution after prior pre-absorption on wild type larvae.

**Phenotypic analyses**

Adult phenotypes were analyzed by light microscopy (**Zeiss Axioshot**) of dissected samples mounted in Hoyer’s medium or by scanning electron microscopy (**Hitachi TM-1000 Tabletop model**) of frozen adults.

**Sequence alignments**

These were generated with the T-Coffee Program, employing the methodology described by [21].

**Supporting Information**

**Figure S1** Venus fusion proteins VN-Ubx and VN-Dfd are functional in the *Drosophila* embryo. Cuticles of wild-type embryos, or of embryos ectopically expressing Hox proteins. First line: left, wild-type embryo showing anterior cuticle from the head to abdominal segment 1 (A1). The three thoracic belts of fine denticles and the first band of denser abdominal denticles are indicated (T1, T2 and T3 and A1, respectively); middle and right, similar transformations of T1, T2 and T3 denticles belts to A1 are induced by the ubiquitous expression of Ubx or of chimeric VN-Ubx, respectively, from UAS enhancers under arm-Gal4 control (arm>). Second line: left, wild-type embryonic head with cephalopharyngeal cuticle. Middle and right: arm-Gal4 driver-directed expression of Dfd or VN-Dfd from a UAS enhancer (arm>) results in similar, major defects of normal head structures, accompanied by the appearance of ectopic maxillary cirri (arrows and inset) typical of Dfd function. (TIF)

**Figure S2** Hexapeptide and linker region are dispensable for interaction with Med19. Bar drawings on the left represent (top) the HD region of *Drosophila* Ubx, with its hexapeptide (HX), linker region and HD; (middle) the HD region of *Drosophila* Ubx, but with its hexapeptide mutated (HXm) as described in Hudry et al. (34); (right) the HD region of crustacean Artemia Ubx, whose HD is identical to the *Drosophila* sequence but whose linker region is much shorter. On the right, GST pulldowns show similar binding to wild-type Ubx (7% of input), Ubx whose HX is mutated (5%), and Ubx, but much shorter. On the right, GST pulldowns show similar binding to wild-type Ubx (7% of input), Ubx whose HX is mutated (5%), or Artemia Ubx with shortened linker (5%). (TIF)

**Figure S3** Strong maternal effect of Med19 mutant germline clones. The photos in A, B and C present the cellular progression of frozen adults.
of embryos lacking maternally contributed Med19 (as seen by DAPI staining of nuclear DNA). (A,B) These embryos are pre-cellular, aged ≈1 hr and ≈2 hr, with the latter corresponding to the onset of zygotic transcription. (C) This embryo, seen shortly after cellularisation, shows massive disorganisation.

**Figure S4** Med19 dsRNA affects the differentiation of larval posterior spiracles and mouthparts. Left column photos: wild-type larval posterior spiracles (top) and mouthparts (bottom). Right column photos: L3 larvae expressing UAS-dsRNA directed against Med19 under daughterless-Gal4 control (da>dsMed19<27>30). These photos reveal defects of posterior spiracles (above) or of larval mouthparts (bottom), resembling the embryonic defects of Hox mutants (noted to the right).

**Figure S5** Med19 null clones can be rescued by UAS-Med19 transgene expression or in a Minute context. Mitotic clones homozygote for Med19<sup>2</sup> were induced in wing imaginal discs by en-Gal4 coupled with UAS-Flp (en>Flp) as described in text. (A, A', A''): en-Gal4 also directed UAS-Med19-VC expression (en>Flp>Med19VC). A large −/− clone is detected by the absence of green GFP (A); Med19 and Med19-VC proteins are both detected by anti-Med19 sera (red, A'); the merged image is shown in A''. (B, B', B''): Mitotic clones were induced as for A-A''. Rather than supply transgenic Med19, clones were induced in the presence of a Minute mutation on the homologous chromosome. (B) −/+ clones are detected on the right-hand side of this wing imaginal disc by the absence of green GFP marker. (B'') Anti-Med19 sera (red) showed no signal in mutant cells. (B'') Merged images confirm the absence of red signal in mutant cells.

**Figure S6** Table 1, interaction data. Phenotypic analyses indicate interactions of Med19 lof mutations with the Antp gof allele Antp<sup>92</sup>; with the Antp lof allele Antp<sup>AvRC3</sup>; with the Dfd gof allele Dfd<sup>2</sup>; and with a lof combination for Dfd [ptc-Gal4>UAS-RNAi (Dfd)]. The heterozygous presence of Med19<sup>2</sup> significantly altered the phenotypic outcome in each case.

**Figure S7** The Med19 Hox “Homeodomain Interacting Motif” (HIM) is conserved across the animal kingdom. At top, a block (TIF) of the HIM element. Sequence alignments are shown for the species listed at the bottom.

**Figure S8** Med19 variant incorporation into MED, expression levels and nuclear location. (A) Co-immunoprecipitation experiment. Extracts of Drosophila S2 cells transfected with act5C-Gal4 driver alone (control), with UAS-Med19-VC or -ΔHIM-VC plasmid, were immunoprecipitated with anti-GFP directed against the VC tag. Western blots of these precipitates tested with anti-Med1 revealed association of the three known Med1 isoforms (Input) with both Med19-VC and ΔHIM-VC in the presence of anti-GFP (IP GFP) but not in controls (IP). (B) Characterisation of expression levels and cellular localisation for Med19-VC, ΔHIM-VC and HIM-VC. (C,D,E) The three proteins are accumulated at similar levels when expressed under dpp-Gal4 control in wing imaginal discs, as seen with anti-GFP. (C) Med19-VC is expressed as a band in the wing imaginal disc under dpp-Gal4 control, detected here with anti-GFP. (F) Enlargement of the boxed region of C. reveals nuclear Med19-VC (arrow), that coincides with anti-Med19 staining (F') and DAPI staining of nuclear DNA (F'). F'' presents the merged signals. (D) ΔHIM-VC expressed in the wing imaginal disc under dpp-Gal4 control is detected with anti-GFP. (G-G'') G, enlargement of the boxed region of D. A single representative cell (arrow) shows co-localisation for anti-GFP (G) and anti-Med19 (G'). As shown by DAPI (G'') and in the merged image (H''), ΔHIM-VC is present both in the nucleus and the cytoplasm. (E) Expression of HIM-VC under dpp-Gal4 control, visualised in a wing imaginal disc with anti-GFP. (H) Enlargement of the boxed region of E. Nuclear HIM localisation (arrow) is confirmed in H' (anti-Med19), H'' (DAPI) and in the merged image (H'''').

**Figure S9** Table 2, phenotypic rescue by Med19-VC and ΔHIM-VC constructs. These forms of Med19 were employed to rescue effects of Med19 mutant combinations. Top: arm-Gal4 driver directed expression of UAS-Med19-VC and -ΔHIM-VC, in the pupal-lethal Med19<sup>2</sup>/Med19<sup>2</sup> context. Culture temperatures are noted. Adult viability was partially restored by Med19-VC, but not by ΔHIM-VC. Spiracle eversion and maxillary formation (where Mx* indicates a mal-formed adult palp) were rescued to a greater extent by Med19-VC. Bottom: −/+ haltere clones were induced in the presence of a Minute mutation by apterous-Flp (ap-Flp), alone or in the presence of UAS-Med19-VC or -ΔHIM-VC. Only Med19-VC yielded apparent rescue.

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**Author Contributions**

Conceived and designed the experiments: MB BH SM YG HMB DLC. Performed the experiments: MB BH CI YC SBF HMB DLC. Analyzed the data: MB BH CI YC SBF SM YG HMB DLC. Contributed reagents/materials/analysis tools: MB BH YC SBF SM YG HMB DLC. Wrote the paper: MB DLC.

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