### Tables S1-S3

| Scientific name                               | Abbreviation | Vernacular name          |
|-----------------------------------------------|--------------|--------------------------|
| Heteromunia pectoralis                        | H.p          | Pictorella Finch         |
| Stagonopleura guttata                         | S.g          | Diamond Firetail         |
| Neochmia phaeton phaeton                      | N.p.p        | Crimson Finch            |
| Neochmia phaeton evangelinae                  | N.p.e        | Crimson Finch            |
| Neochmia temporalis                           | E.pi         | Red-browed Finch         |
| Emblema picta                                 | E.pi         | Painted Finch            |
| Neochmia rufcauda                             | N.r          | Star Finch               |
| Neochmia modesta                              | N.m          | Plum-headed Finch        |
| Taeniopygia bichenovii bichenovii             | T.b          | Double-barred Finch      |
| Taeniopygia guttata                           | T.g          | Timor Zebra Finch        |
| Peophila personata                            | P.p          | Masked Finch             |
| Peopephila acuticauda                         | P.a          | Long-tailed Finch        |
| Poephila cincta                               | P.c          | Black-throated Finch     |
| Lonchura cucullata                            | L.c          | Bronze Mannikin          |
| Lonchura fringilloides                        | L.f          | Magpie Mannikin          |
| Lonchura eryzivora                            | L.o          | Java Sparrow             |
| Lonchura punctulata                           | L.p          | Scaly-breasted Munia     |
| Lonchura molucca                              | L.m          | Black-faced Munia        |
| Lonchura castaneothorax                       | L.c          | Chestnut-breasted Mannikin|
| Erythura gouldiae                             | E.g          | Gouldian Finch           |
| Erythura hyperythra                           | E.h          | Tawny-breasted Parrotfinch|
| Erythura prasina                              | E.pr         | Erythura prasina         |
| Erythura psittacea                            | E.ps         | Red-throated Parrotfinch |
| Erythura paeli                                | E.pa         | Fiji Parrotfinch         |
| Erythura tricolor                             | E.tri        | Tricoloured Parrotfinch  |
| Ortygospiza atricollis                        | O.a          | African Quailfinch       |
| Amandina erythracephala                       | A.e          | Red-headed Finch         |
| Amandina fasciata                             | A.f          | Cut-throat Finch         |
| Amandava subflava                             | A.s          | Zebra Waxbill            |
| Amandava amandava                             | A.a          | Red Avadavat             |
| Uraeginthus granatina                         | U.g          | Violet-eared Waxbill     |
| Uraeginthus bengalus                          | U.b          | Red-cheeked Cordon-bleu |
| Pytilia hypogrammica                          | P.h          | Yellow-winged Pytilia    |
| Euscliptospiza dybowskii                      | E.d          | Dybowski's Twinspot      |
| Lagonostica senegala                          | L.s          | Red-billed Firefinch     |
| Estrilda melpoda                              | E.m          | Orange-cheeked Waxbill   |
| Estrilda astrild                              | E.a          | Common Waxbill           |
| Estrilda troglodytes                           | E.tro        | Black-rumped Waxbill     |

### Table S1. Chosen species names

For the 38 species we studied in the Estrildidae family, we list full scientific names, corresponding abbreviations used in Figures and Figure legends, and vernacular names.
### Table S2. Feather types in conserved color domains.

We recorded the presence (noted with 1) of melanin-based, carotenoid-based, structural, or periodic coloration on individual feathers implanted in conserved color domains of the dorsum (i.e. dorsal anterior da, saddle ds, dorsal posterior dp and tail dp) and of the ventrum (breast b, ventral anterior va, flank f, ventral intermediate vi, and ventral posterior vp). Despite trends, color domains displayed a variety of hues and motifs. Ventral domains frequently displayed periodic motifs (20 species, mostly in anterior regions), light melanin coloration (27 species) or carotenoid-based coloration (12 species), but some possessed dark colors (6 species) or structural colors (8 species, mostly anteriorly). Dorsal domains most often displayed brown-grey coloration (31 species), but we also observed carotenoid-based hues (14 species, mostly in posterior regions), structural colors (9 species, mostly anteriorly), and periodic motifs (7 species). Species names abbreviated as in Table 1.
Table S3. Expression profiles and primers for studied candidates.

We qualitatively assessed the expression of 60 candidate genes (left column) extracted from RNAseq profiling using in situ hybridization. To do so, we cloned anti-sense probes for 59 candidates using primer sequences listed in right columns (the Tbx5 probe was a kind gift from J. Gros laboratory). For each gene we indicate whether it was spatially-restricted within tracts or found only in a few cells, throughout tracts, or not detected, and Figures where dorsal (D) and ventral (V) expression data is presented.
A 105-species phylogeny of the *Estrildidae* family modified from (28) highlights the position of the 38 studied-species (in bold) shown in Fig. 2 and Fig S3, namely *Heteromunia pectoralis* (*H. p*), *Stagonopleura guttata* (*S. g*), *Neochmia phaeton phaeton* (*N. p. p*), *Neochmia phaeton evanginiae* (*N. p. e*), *Neochmia temporalis* (*N. t*), *Emblema picta* (*E. pi*), *Neochmia ruficauda* (*N. r*), *Neochmia modesta* (*N. m*), *Taeniopygia bichenovii bichenovii* (*T. b*), *Taeniopygia guttata* (*T. g*), *Poephila personata* (*P. p*), *Poephila acuticauda* (*P. a*), *Poephila cincta* (*P. c*), *Lonchura cucullata* (*L. c*), *Lonchura fringilloides* (*L. f*), *Lonchura oryzivora* (*L. o*), *Lonchura punctulata* (*L. p*), *Lonchura Molucca* (*L. m*), *Lonchura castaneothorax* (*L. c*), *Erythrura gouldiae* (*E. g*), *Erythrura hyperythra* (*E. h*), *Erythrura prasina* (*E. pr*), *Erythrura psittacea* (*E. ps*), *Erythrura paelii* (*E. pa*), *Erythrura tricolor* (*E. tri*), *Ortygospiza atricollis* (*O. a*), *Amandina erythrocephala* (*A. e*), *Amandina fasciata* (*A. f*), *Amandava subflava* (*A. s*), *Amandava amandava* (*A. a*), *Uraeginthus granatina* (*U. g*), *Uraeginthus bengalus* (*U. b*), *Pytilia hypogrammica* (*P. h*), *Euschistospiza dybowskii* (*E. d*), *Lagonostica senegala* (*L. s*), *Estrilda melpoda* (*E. m*), *Estrilda astrild* (*E. a*), *Estrilda troglodytes* (*E. tro*). Vernacular species names are listed in Table S1. Numbers of analyzed samples per species are shown in green, species chosen for developmental analyses are shown in orange.
Fig. S2 Feather type classification in the Estrildidae family.

(A) Ventral flat skin preparation of an adult Taeniopygia gutatta (T. g) male showing sparse, spatially random distribution of feathers (arrowheads) outside of tracts (dotted lines). Scale bar: 2 mm. (B) Feathers outside of tracts have downy structure and white distal coloration. (C) Tract feathers and corresponding schematics exemplify feather type classification, based on distal coloration produced by eumelanin (i.e. brown-to-black), phaeomelanin (yellowish-orange), carotenoids (vivid yellow-to-red), structure (blue, green or purple), and/or melanin-based periodic motifs, namely spots, scales, bars and mottled patterns (26). All feathers have a proximal grey basis. Scale bars: 0.3 cm. (D) Feather coloration is represented schematically for
the ventral domains of all studied species, providing color-codes for tract maps also shown in Fig. 2 and Fig. S3. Species names are abbreviated as detailed in Table 1.

**Fig. S3 Dorsal color domains in the *Estrildidae* family.**

Feather coloration recorded on flat skins (upper panels) and color-coded according to methods described in Fig. S4 is represented schematically (bottom panels) for dorsal domains in all
studied species (but for L.m for which flat skin specimens were not available). Species names are abbreviated as detailed in Table S1.

Fig. S4 Color pattern characterization in *Taeniopygia guttata*.

(A) Typical feather types found in *Taeniopygia guttata* individuals were classified and color-coded in 5 groups according to their distal coloration, namely entirely black (Bl), striped (S), entirely brown (Br), orange (with or without white spots; O) and beige (Be). (B) In *Taeniopygia guttata* males, we recorded feather types at each position of ventral flat skin preparations (n=5). Graphs show percentages of Bl, S, Br, O, and Be ventral tract feathers along chevrons 11, 16, and 21 (indicated in corresponding tract maps). Compiling quantifications for each chevron of the tract produced precise color maps in which color domains are separated by boundaries with highly reproducible overall mean positions. However, some color domains display a gradient
of periodic motifs (i.e. in the flank f or the breast b and ventral anterior va domains, as defined in Fig. 3). The longitudinal f-vi boundary, most often observed in Estrildidae (see Fig. S5), is also the sharpest: in Taeniopygia guttata males it precisely locates on the fourth feather of each chevron (F4) throughout the length of the ventral tract, such that this feather displays a split pattern (i.e., dorsal half orange and ventral half beige). (C) In Taeniopygia guttata females, the flank f is brown instead of orange, but the color boundary is found at the same location on F4, which displays a brown dorsal half and a beige ventral half (n=3). Error bars: SEM. vm: ventral midline. Scale bars: 2 mm.

Fig. S5 Compilation of color boundaries in the Estrildidae family.

(A) All color boundaries observed in Estrildid finch species chosen for the survey were reported on single dorsal or ventral tract maps (each species is color-coded). (B) Most boundaries were oriented along tract axes: respectively 76% and 74% of dorsal and ventral boundaries were
parallel to tract axes (i.e., longitudinal or transverse but not oblique). Left panels: longitudinal boundaries were sharp while transverse or oblique boundaries frequently formed gradients. Right panels: We identified “main” boundaries by grouping together those with similar positions. This outlined boundary-rich regions of the tracts that we color-coded on tract maps (for each region, lines of darker shades indicate the mean position of observed boundaries and numbers indicate the number of species displaying a boundary). (C) Main boundaries were compiled on single dorsal or ventral tract maps.

**Fig. S6 Tract formation dynamics in *Taeniopygia bichenovii*.**

Stains for β-catenin transcripts (in purple) mark developing feather primordia during ventral and dorsal tract formation in the owl finch *Taeniopygia bichenovii*. The timely sequence of primordia emergence is identical to that described in *Taeniopygia guttata* embryos, consistent
with previous work showing that tracts are conserved throughout the *Estrildidae* family (27).

Scale bars: 500 µm.

**Fig. S7** Extent of *Agouti* expression in *Taeniopygia guttata* and *Gallus gallus*.

(A) In *Taeniopygia guttata* embryos and corresponding schematics at HH28, β-catenin is expressed in a droplet-shaped region, marking early tract emergence. (B) In *Gallus gallus* embryos and corresponding schematics at HH28, β-catenin is expressed in a continuous segment, marking early tract emergence. (C) Double *in situ* stains in *Taeniopygia guttata* embryos and corresponding schematics at HH28 show that *Agouti* (in purple) forms a longitudinal band overlapping with the forming tract marked by β-catenin (in red). On transverse sections (a; white dotted line), the dorsal limit of *Agouti* expression (purple arrow in
schematics) marks the position of the future f-vi boundary (stained with β-catenin, red arrows). *Agouti* is present in the dermis while β-catenin stains the epidermis (the limit between skin layers is shown with black dotted lines). (D) In *Gallus gallus* embryos at HH28, *Agouti* does not overlap with β-catenin in the presumptive f and vi regions. Scale bars: 500 µm (section: 100 µm).
Fig. S9 Neural tube grafts.

(A) In the dorsum of HH28 chimeras obtained after grating Taeniopygia guttata neural tube halves in Brown strain Gallus gallus embryos, the expression of Agouti (in purple) was identical to control Gallus gallus embryos (white arrow; see Fig. 5C). (B, C) In the ventrum, neural-tube grafted chimeras displayed host-like patterns of β-catenin (in red) and Agouti (in purple) expression in both the ungrafted-side (B) and the grafted-side (C), compared to control embryos (see Fig. 5E). Scale bars: 500 µm.
**Fig. S9 KEGG pathways analyses for all domain pairs.**

KEGG pathways results displayed for all combinations of domain pairs (abbreviations and color-codes are described in Fig. 6A) along the dorso-ventral axis (left panels) and the antero-posterior axis (right panels) show an enrichment of regulated genes involved in tissue architecture (in green), melanogenesis (in yellow), the Wnt signaling pathway (in blue), the TGF-β signaling pathway (in orange), and other KEGG terms (in grey). Post., posterior; metab., metabolism; sign., signaling; synth., synthesis; ECM, extra-cellular matrix; RI, receptor interaction; unsat., unsaturated.

**Fig. S10 RNA-Seq transcript levels along the dorso-ventral axis.**

Normalized genes counts were plotted as a function of differential expression (log2 fold-change) for combinations of domains in pairs along the dorso-ventral axis. Genes showing
significant differential expression (p-values ≤ 0.05) are shown in red when up-regulated (i.e. higher expression in da, ds, f, or dp + dt domains) or blue when down-regulated. Differentially expressed pigmentation genes, homeobox factors and other relevant candidates are shown in grey boxes.

**Fig. S11 RNA-Seq transcript levels along the antero-posterior axis.**

Normalized genes counts were plotted as a function of differential expression (log2 fold-change) for combinations of domains in pairs along the antero-posterior axis. Genes showing significant differential expression (p-values ≤ 0.05) are shown in red when up-regulated (i.e. higher expression in b + va, f, vi or ds domains) or blue when down-regulated. Differentially
expressed pigmentation genes, homeobox factors and other relevant candidates are shown in grey boxes.

![Alx1 and Fdz4 expression in Taeniopygia guttata embryos](image)

**Fig. S12 Dorsal expression of candidate genes in *Taeniopygia guttata* embryos.**

*In situ* hybridizations for genes indicated in purple in the dorsum of *Taeniopygia guttata* embryos at stage HH28 confirm quantitative RNA-seq data and qualitatively show they possess spatially-restricted expression patterns: profiles of *Alx1* and *Fzd4* create visible boundaries between ds and dp domains. Scale bars: 500 µm.
Fig. S13 Ventral expression of candidate genes in *Taeniopygia guttata* embryos.

*In situ* hybridizations for genes indicated in purple in the ventrum of *Taeniopygia guttata* embryos at stage HH28 confirm quantitative RNA-seq data and qualitatively show they possess spatially-restricted expression patterns (e.g. *Tbx18* marks the f domain). The nascent ventral tract was stained using β-catenin (in red) to assess the extent of expression profiles of candidates encompassing only part of the tract. Scale bars: 500 µm.
Fig. S14 Ventral expression of Tbx15 and Agouti in Taeniopygia guttata embryos.

(A) Double in situ stains and corresponding schematics for Tbx15 (in purple) and β-catenin (in red) on sections corresponding to a show that Tbx15 expression locates in a region directly dorsal to the β-catenin-expressing tract (arrowheads). (B) Tbx15 expression (in purple) is complementary to Agouti (in red), precisely marking the location of the future f-vi boundary (arrowheads). Scale bars: 100 µm.
Fig. S15 Expression of other candidate genes in *Taeniopygia guttata* embryos.

*In situ* hybridizations for genes indicated in purple in the dorsal and ventral regions of *Taeniopygia guttata* embryos at stage HH28 confirm quantitative RNA-seq data and
qualitatively show they are expressed outside of presumptive tracts and/or throughout tract length with varying widths, thus not spatially correlating with conserved color domains (see Fig. 3C). Scale bars: 500 µm.