**Figure S1** Molecular phylogeny of the *kitlg* gene in teleosts. The predicted amino acid sequences of *kitlg* genes of various species were downloaded from GenBank or Ensembl for construction of a phylogenic tree by the maximum likelihood method with 1000-bootstrap replication. Spotted gar was examined as an outlier. The numbers at each node indicate bootstrap probability. Gene names, species, GenBank accession numbers or Ensembl IDs, and amino acid sequences are provided in Table S1.

**Figure S2** Reduced expression of pigmentation-related genes in larvae of *fm* and *kitlga* KO medaka at 3 dph. Total RNA isolated from WT, *fm het*, *fm*, and *kitlga* KO larvae was subjected to RT and real-time PCR analysis of *pax7a* (A), *sox5* (B), *pax3a* (C), and *mitfa* (D) expression. Data were normalized by the amount of GAPDH mRNA and Data are means ± 95% confidence interval from three independent experiments. The *p* values were determined by one-way ANOVA followed by Tukey’s post hoc test.

**Figure S3** Model for chromatophore differentiation, proliferation, and migration from the neural crest. Melanophores and iridophores develop from a shared progenitor, as do xanthophores and leucophores. We propose that the proliferation and migration of leucophores and melanophores are regulated by c-Kit signaling, whereas the development of iridophores and xanthophores are thought to be regulated by Alk-Ltk signaling and Csf1 signaling, respectively.