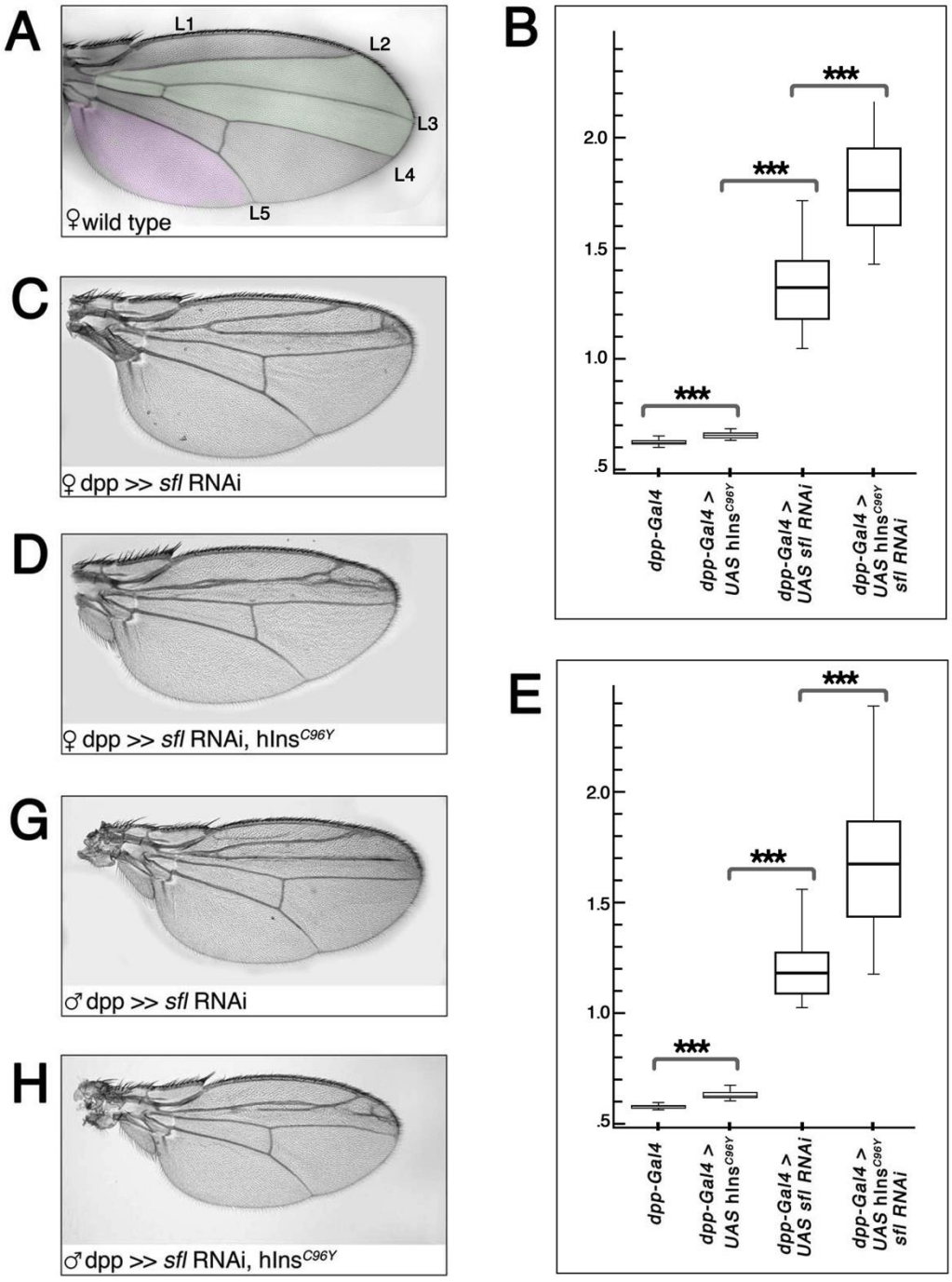

Figure S8 Depletion of *sfl* by RNAi in the developing wing expressing hINS^{C96Y} driven by dpp-Gal4. For both females and males, dpp >> hINS^{C96Y} or Dpp >> *sfl* RNAi expression alone reduces wing area between the L2 and L4 longitudinal veins relative to the posterior-most sector of the wing (bordered by L5). This reduction is more severe in the *sfl* knockdown genotype than in the hINA^{C96Y}-expressing genotype. Co-expression of *sfl* RNAi and hINS ^{C96Y} by dpp-Gal4 results in the obliteration of the L3 vein and further relative reduction of the L2-L4 area.
(A): Wild type wing showing the measured regions of wing used to quantify the effects of both *sfl* RNAi and hINS^{C96Y} expression in dpp-Gal4 domain (L3-L4 intervein sector). Quantification of the (B) female or (E) male wing phenotypes generated by transgenes dpp-Gal4; dpp-Gal4 >UAS-hINS^{C96Y}; (C, G) dpp-Gal4 >> UAS-*sfl* RNAi; and (D, H) dpp-Gal4

>>UAS-*sfl* RNAi; UAS-hINS^{C96Y}. The values represent the ratio of the third posterior cell (in pink color) divided by the L2-L4 intervein sector (in green color) wing area. ***, P < 0.001; Mann-Whitney U test.
Females: dpp-Gal4 (n= 15; Mean= 0.62), dpp-Gal4 >UAS-hINS^{C96Y} (n= 15; Mean=0.65), dpp-Gal4 >> UAS-*sfl* RNAi (n= 23; Mean=1.3) and dpp-Gal4 >>UAS-*sfl* RNAi; UAS-hINS^{C96Y} (n= 22; Mean=1.76).
Males: dpp-Gal4 (n= 15; Mean=0.59), dpp-Gal4 >UAS-hINS^{C96Y} (n= 15; Mean=0.64), dpp-Gal4 >> UAS-*sfl* RNAi (n=23; Mean=1.2) and dpp-Gal4 >>UAS-*sfl* RNAi; UAS-hINS^{C96Y} (n= 29; Mean=1.68).