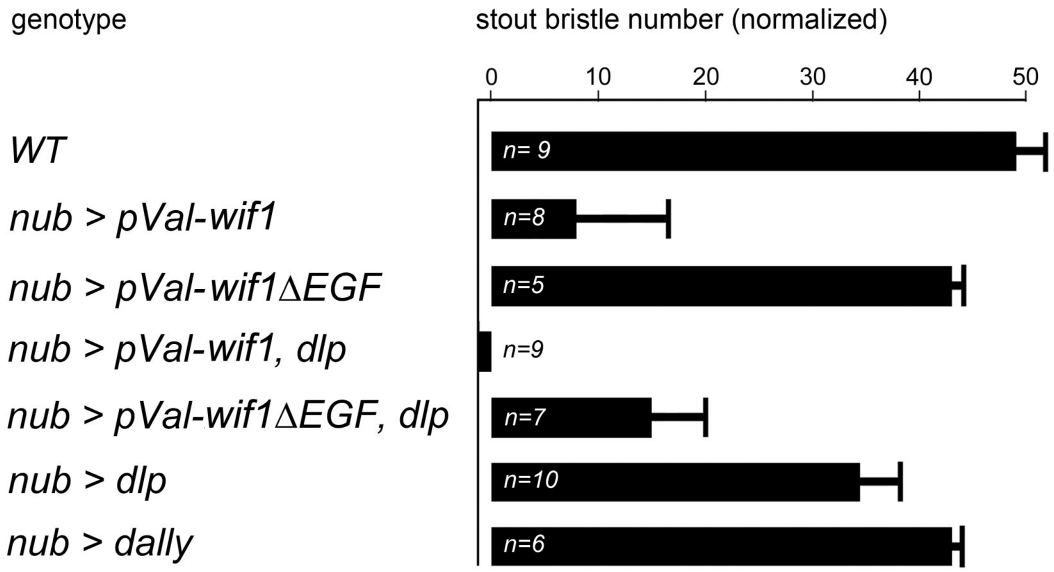

Figure S3. Effects of Wif1 variants and Dlp on stout bristle differentiation

Expression of Dlp together with moderately driven *pVal-wif1* or *pVal-wif1ΔEGF* genomic insertions produced additive reductions in bristle number. Due to slight variability in wing size, stout bristle number was normalized to the length of the sampling area defined in Arbitrary Units (A.U.) The sampling area began at the distal point where L2 intercepts the wing margin (see Figure 7A for L positions) and extended proximally along the anterior margin. The normalized stout bristle numbers were not different between the *nub-gal4, pVal-UAS-wif1* and *nub-gal4, pVal-UAS-wif1ΔEGF, UAS-dlp* conditions. All other differences were statistically significant as determined by the two-tailed Mann-Whitney U Test ($p<0.015$)