Table S1. Raw data and analysis from graphs in Fig. 1D and 1I.

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Table S2. Raw data and analysis from graphs in Fig. 2D, 2H, 2L, 2P, and 2T.

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Table S3. Raw data and analysis from graphs in Fig. 3D, 3E, 3F, and 3K.

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Table S4. Raw data and analysis from graphs in Fig. S1E, S1H, and S1K.

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Table S5. Raw data and analysis from graph in Fig. S2D-F.

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Table S6. Raw data and analysis from graph in Fig. S3D.

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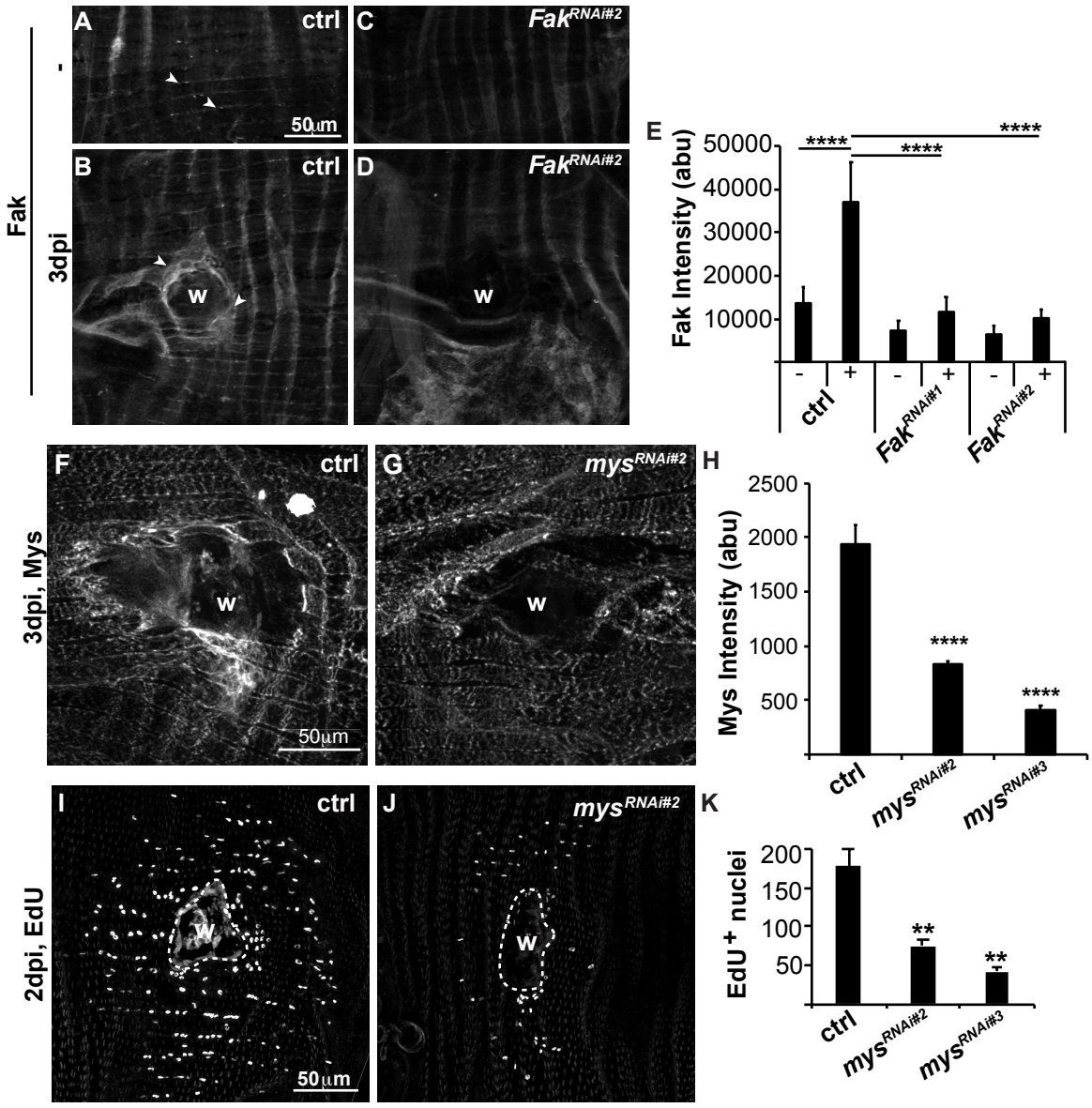

Figure S1. Fak expression, RNAi verification, and mys dependent endoreplication.

(A-D) Representative immunofluorescent images of Fak staining in the fly abdomen of the control (epi-Gal4/ w^{1118}) or Fak knockdown (epi-Gal4/UAS-$Fak^{RNAi\#2}$). Uninjured (-) and 3 dpi (+). Examples of epithelial Fak staining (arrowheads). Wound site (w). (E) Quantification of Fak epithelial expression in control (-, n=15 and +, n=11), $Fak^{RNAi\#1}$ (-, n=12 and +, n=7), and $Fak^{RNAi\#2}$ (-, n=9 and +, n=5). Error bars represent mean ± SE and data were analyzed by two-tailed unpaired t-test. (F and G) Representative immunofluorescent images of Mys staining in fly abdomen at 3 dpi in control (epi-Gal/w^{1118}) and $mys^{RNAi\#2}$ (epi-Gal/UAS-$mys^{RNAi\#2}$) strains. Wound site (w). (H) Quantification of Mys intensity in control (n=13), $mys^{RNAi\#2}$ (n=12), and $mys^{RNAi\#3}$ (n=5). Error bars represent mean ± SE and data were analyzed by two-tailed unpaired t-test, $p < 0.001$ (***). (I and J) Representative immunofluorescent images of EdU labeling (S phase cell cycle marker) at 2 dpi. Wound scar (outlined, w). (K) Quantification of EdU^+ epithelial nuclei in control (n= 9), $mys^{RNAi\#2}$ (n=9), $mys^{RNAi\#3}$ (n=9). Error bars represent mean ± SE and data were analyzed by two-tailed unpaired t-test, $p < 0.001$ (***). Also see Source Data 4.

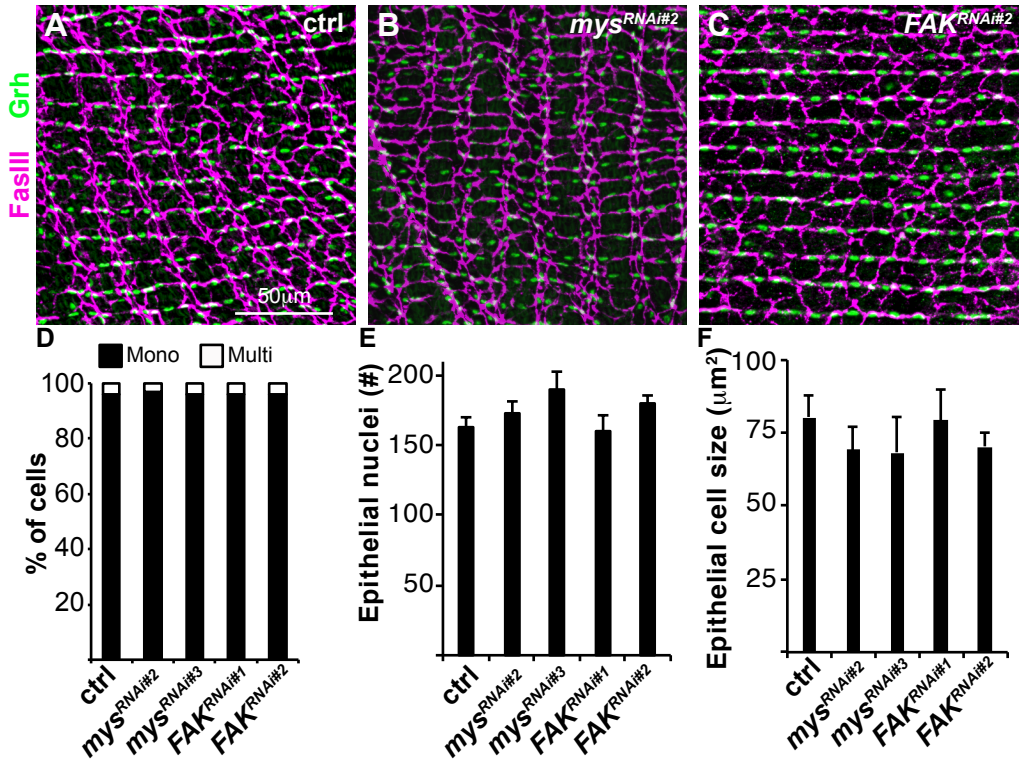

Figure S2. Focal adhesion gene RNAi does not cause ectopic cell fusion. (A-C) Representative immunofluorescent images of FasIII and Grh staining in the uninjured fly abdomen from control, *mys*^{RNAi}, and *Fak*^{RNAi}. (D-F) Quantification of the number nuclei per cell (D), total number of epithelial nuclei (E), and epithelial cell size (F) for control (n=9), *mys*$^{RNAi\#3}$(n=9), *Fak*$^{RNAi\#1}$(n=9), *Fak*$^{RNAi\#2}$ (n=8). There is no significant difference in the number of multinucleated cells, epithelial nuclei, or epithelial cell size. Error bars represent mean $\pm$ SE and data were analyzed by two-tailed unpaired t-test. Also see Source Data 5.

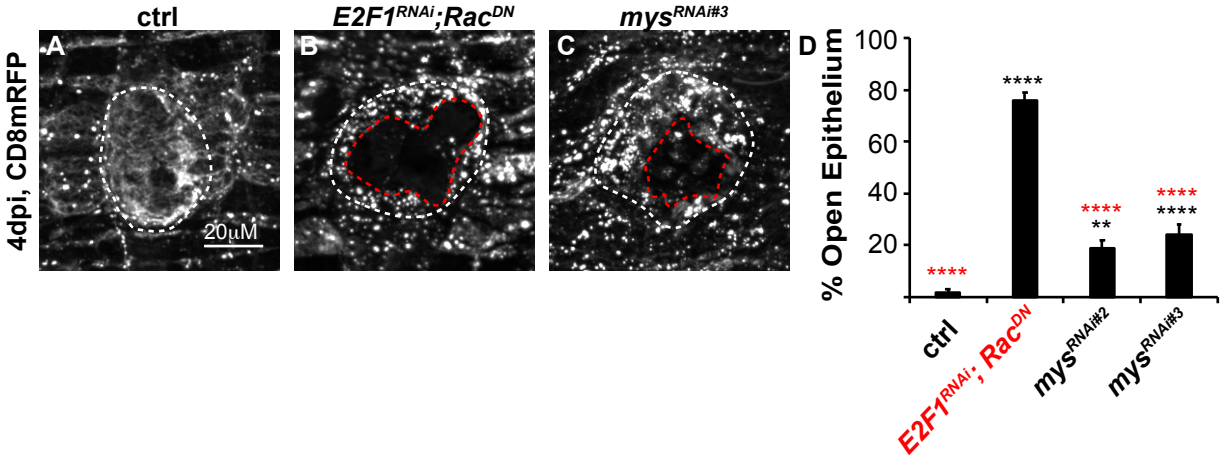

Figure S3. *Mys* knockdown delays wound closure. Re-epithelization during wound repair is detected by expression of a membrane-linked RFP (UAS-mCD8-RFP) under epi-Gal4 control. Representative immunofluorescent images for (A) control (epi-Gal4/+), (B) $E2F1^{RNAi}$; Rac^{DN}, and (C) $mys^{RNAi\#3}$ at 4 dpi. Outlined are wound scar (dashed white line) and open epithelial area (dashed red line). (C) Percent open area (open epithelial area/ wound scar size) at 4 dpi for control (n=21), $E2F1^{RNAi}$, Rac^{DN} (n=15), $mys^{RNAi\#2}$ (n=20), and $mys^{RNAi\#3}$ (n=20). Data were analyzed by 1-way ANOVA with Tukey's multiple comparisons test ** ($p<0.01$) and ****($p<0.0001$). Comparisons to control (black *) and $E2F1^{RNAi}$, Rac^{DN} (red *). Also see Source Data 6.