



FIGURE S2. —Quantification of wound closure with alternative RNAi lines, dominant-negative transgenes, or mutants. (A) Quantification of wound closure upon epidermal expression of the indicated *UAS-RNAi* transgenes (original RNAi line, open bar; non-overlapping RNAi line, diagonal striped hash; overlapping RNAi line, dotted hash; larval viable mutants, wavy hash; dominant-negative transgenes, diamond hash). (A) JNK pathway candidate genes. Non-overlapping lines targeting *misshapen*, *slipper*, *Tak1*, *Mkk4*, and *DFos/kay* also show open wound phenotypes, as do overlapping lines targeting *Mkk4* and *DJun/Jra* and larval viable mutations in *slipper* and *Tak1*. (B) Actin cytoskeletal dynamics candidate genes. Non-overlapping lines targeting *Ced-12*, *mbc*, *Arp14D*, and *Arp11*, also show open wound phenotypes, as do overlapping lines targeting *Ced-12*, *SCAR*, and *Arp11*, and dominant-negative transgenes targeting *Rac1* and *Cdc42*. Absence of a bar indicates a line, transgene, or mutant was not available or not tested for that gene. The number of scored larvae for each RNAi knockdown using *e22c-Gal4* in A and B was as follows (original RNAi lines see column 3 in Table S1): *n* for non-overlapping RNAi lines: *msn* = 39, *slpr* = 40, *Tak1* = 43, *Mkk4* = 40, *DFos/kay* = 30, *Ced-12* = 37, *mbc* = 43, *Arp14D* = 48; *n* for overlapping RNAi lines: *slpr* = 30, *Mkk4* = 34, *DJun/Jra* = 33, *Ced-12* = 37, *SCAR* = 31; *n* for mutants: *slpr* = 9, *Tak1* = 8; *n* for DN versions: *Rac1* = 36, *Cdc42* = 34. The number of scored larvae for each RNAi knockdown using *Der-2;A58* in B was as follows (original RNA line see legend of Figure 3): *n* for non-overlapping RNAi line: *Arp11* = 36; *n* for overlapping RNAi line: *Arp11* = 42.