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.