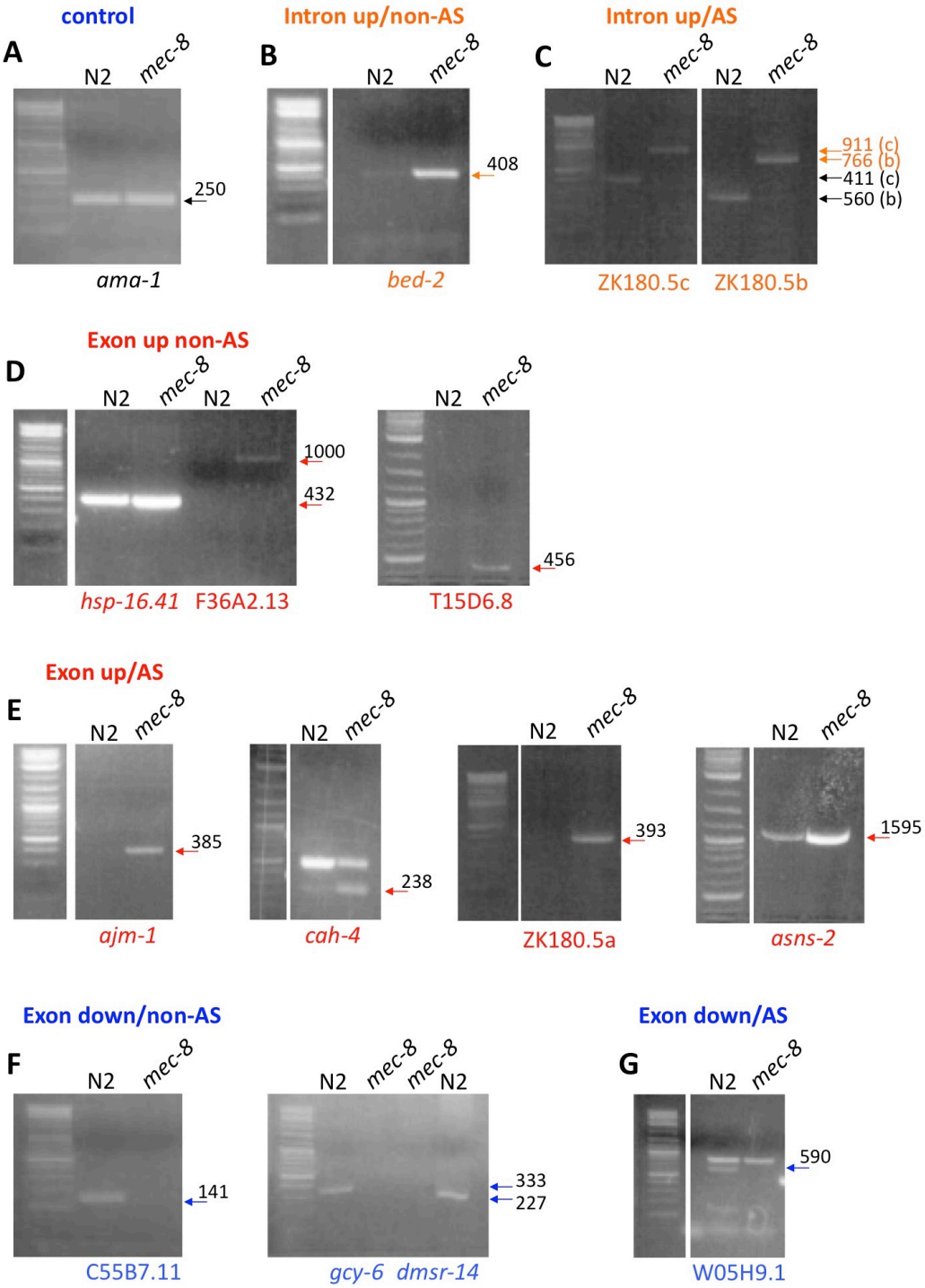

Figure 4–figure supplement 1. **Examples of gene regions differentially expressed in *mec-8* mutants and confirmed by RT-PCR.** Total RNA used for tilling arrays was reverse transcribed using oligo-dT primers and amplified by PCR using specific primers for each gene region (see Supplemental File 5). Each gene region was amplified using 30 cycles. Sizes are indicated in base pairs; arrows indicate bands that correspond to the expected sizes in *mec-8* mutants based on tiling array results. For size reference, a 2-log DNA ladder (NEB) was used. (A) Control PCR with *ama-1*. (B) A gene (*bed-2*) with up-regulated introns (intron up) and that is not alternatively spliced (non-AS). (C) Intron up, AS gene (ZK180.5c and b). (D) Exon up, non-AS genes (*hsp-16.41*, F36A2.13, T15D6.8). (E) Exon up, AS genes (*ajm-1*, *cah-4*, ZK180.5a, *asns-2*). (F) Exon down, non-AS genes (C55B7.11, *gcy-6*, *dmsr-14*). (G) Exon down, AS gene (W05H9.1).