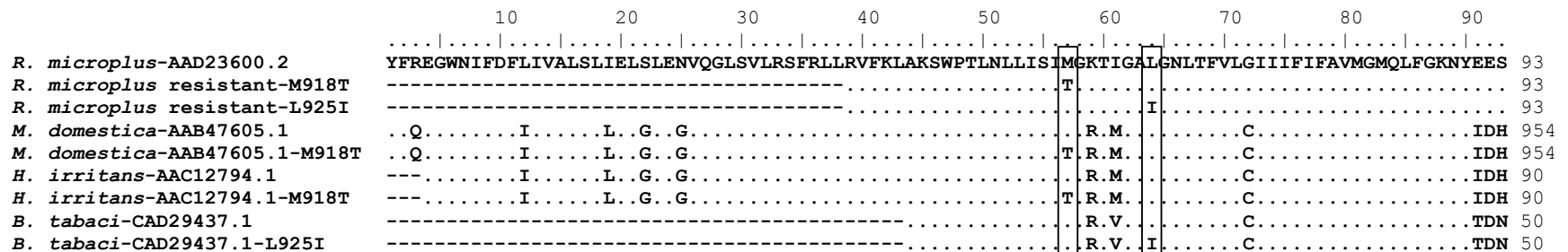


Additional file 5: Figure S3. Amino acid sequence alignment for domain II from *Rhipicephalus microplus* (putative sodium channel accession number: AAD23600.2) with two resistance alleles and three additional fly species that are known to harbour L925I (*kdr*) and M918T (*super-kdr*) substitutions. Amino acid sequences for *R. microplus* resistance alleles were translated from the nucleotide sequences shown in Additional file 4: Figure S2. The *R. microplus* methionine to threonine (putative *super-kdr*) and leucine to isoleucine (*kdr*) substitutions are boxed and show the precise alignment of the putative *super-kdr* substitution to M918T, which is known to correlate with *super-kdr* in two fly species (*Musca domestica* and *Haemotobia irritans*) and the *kdr* substitution to T925I in the white fly (*Bemisia tabaci*). The horizontal ruler represents amino acid positions for *R. microplus* accession number [GenBank: AAD23600.2], while the vertical numbers represents amino acid positions for each individual species according to their respective accession numbers. Amino acid substitution locations are based on previous publications from Williamson et al. [1], Guerrero et al. [2], and Morin et al. [3]. Accession numbers are as follows: *M. domestica* [GenBank: AAB47605.1], *H. irritans* [GenBank: AAC12794.1], and *B. tabaci* [GenBank: CAD29437.1].



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3. Morin S, Williamson MS, Goodson SJ, Brown JK, Tabashnik BE, Dennehy TJ: **Mutations in the *Bemisia tabaci para* sodium channel gene associated with resistance to a pyrethroid plus organophosphate mixture.** *Insect Biochem Molec* 2002, **32**(12):1781-1791.