Figure S2. Protein sequence alignment of 3′ kinesin. The kinesin protein product from exon 9 to exon 14 is shown. Two representative sequences per species are shown. Residues with amino acid changes are highlighted. Polymorphic residues are indicated by a green asterisk (*), those residues where H. heurippa is different from H. c. cordula and H. m. melpomene are indicated by a blue asterisk (*) and the red asterisk (*) indicates one residue where H. c. cordula is different from H. h. heurippa and H. m. melpomene. We observed five amino acid differences between H. melpomene vs. H. heurippa. This might reflect adaptive change subsequent to formation of H. heurippa, although there was no significant evidence for selection on the locus. Perhaps more likely however, these changes may represent fixation of nearly-neutral variation due to a population bottleneck during the origin of H. heurippa. Only one amino acid difference was found between H. melpomene and H. cydno in a residue also relating H. melpomene with H. heurippa. Although this amino acid replacement might be responsible for a structural protein change causing the red band, several intronic sites show a similar pattern and may have regulatory functions.