



**Supplementary Figure 4:** Phylogenetic tree of desaturases after Lienard et al (2014) Nat Comm (in red), and including our *B. anynana* candidate Δ9 and Δ11 desaturases (Ban delta9-like Nieberding and Ban delta11-like Nieberding, highlighted in red and preceded by a red star), comprising a representative set of moth and butterfly desaturases. Sequence abbreviations correspond to species names as described in Lienard et al. (2014 Nat Comm): Ape, *Antheraea pernyi*; Ase, *Agrotis segetum*; Ave, *Argyrotaenia velutinana*; Bmo, *Bombyx mori*; Che, *Choristoneura herana*; Cpa, *Choristoneura parrallela*; Dpu, *Dendrolimus punctatus*; Epo, *Epiphyas postvittana*; Has, *Helicoverpa assulta*; Har, *Helicoverpa armigera*, Hvi, *Heliiothis virescens*; Hsub, *Helicoverpa subflexa*; Lcap, *Lampronia capitella*; Mbr, *Mamestra brassicae*; Obr, *Operophtera brumata*; Onu, *Ostrinia nubilalis* (Ofu, Ola, Onr.za, Opa, Osc, Oza and Oze correspond to other *Ostrinia* species); Pex, *Planotortrix excessana*; Poc, *Planotortrix octo*; Tni, *Trichoplusia ni*; Tpi, *Thaumetopoea pityocampa*; Yev, *Yponomeuta evonymella* (Yro and Ypa correspond to other *Yponomeuta* species). We used maximum likelihood inference to reconstruct the phylogeny using the standalone version of PhyML14 and the WAG+I+G model as determined by performing model selection in Topali v2.515 as described in Lienard et al. (2014) Nat Comm. The cladograms were visualized and prepared using the online tool EvolView v2. Numbers at the nodes indicate bootstrap values for 100 replicates.