Figure S6. Map of *Sesamia nonagrioides IMP*. The exon/intron structure of *S. nonagrioides IMP* (*SnIMP* on top), as inferred from our tblastn search and automatic gene prediction, is compared to that of *Bombyx mori IMP* (*BmIMP* bottom). Coding exons are in green and non-coding exons are in red. Coding exons are in green and non-coding exons are in red. Introns and exons are drawn to scale. Introns interrupted with two parallel bars have a scale divided by ten. The BmIMP protein is between 506 and 615-aa long, depending on its five isoforms, and its gene lies on a region of about 80kb with 14 exons (Ncbi: LOC101745047). We chose to represent the closest isoform to *SnIMP*, X1, which has 10 exons. *SnIMP* is on two scaffolds: scf7180000016565_1 for the first three exons (from position 1 to 17,502) and scf7180000018929_1 for the rest of the gene (from position 1,008,067 to 907,985). These two locations correspond to the predicted genes SNONA2_00006561 and SNONA2_00009401 reciprocally, both annotated as *Insulin-like_growth_factor_2_mRNA-binding_protein*. SNONA2_00006561 includes two out the three exons found by tblastn search and it is 98aa long and it maps on the first three exons of BmIMP X1 protein with 68.42% of identity, including a gap corresponding to the second exon. SNONA2_00009401 is 567aa long with eight exons and it maps on the rest of *BmIMP X1* gene with 92.75% identity.