



Figure S5 RNA-seq reads coverage (A) and RT-PCR primers position (B,C) in the three *Ae. aegypti* strain tested for transcript AEEL009166-RA and AEEL001621-RA. In each read (gray raw), mismatches with respect to the reference *Ae. aegypti* genome sequence are shown in colors within the gray raw. RNA-seq reads were mapped to the *Ae. aegypti* genome reference sequence requiring unique match with a maximum of two mismatches. As a consequence, the absence of coverage along a transcript can be interpreted as not-unique sequence within the *Ae. aegypti* genome and/or sequence with high variation (i.e. more than 2 mismatches, insertions, deletions).