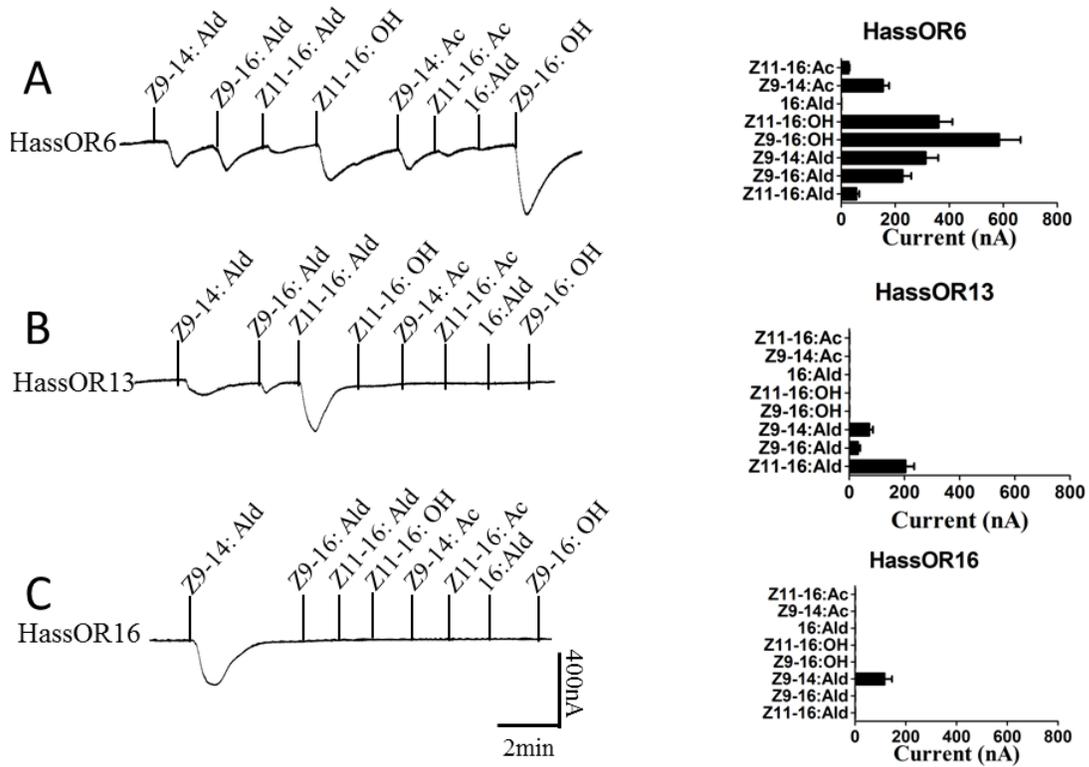


**Sensillar expression and responses of olfactory receptors reveal different peripheral coding in two *Helicoverpa* species using the same pheromone components**

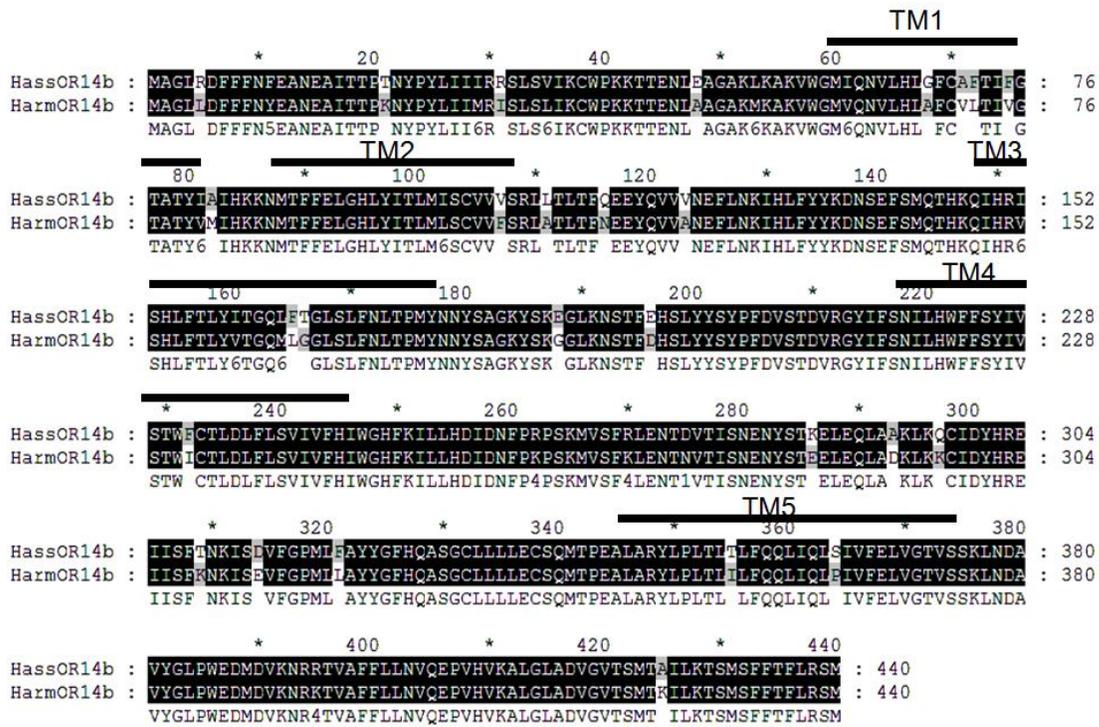
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**Supplementary Table 1. The statistical number of different morphology sensilla on the antenna of *H. assulta* and *H. armigera*.**

	<i>Helicoverpa armigera</i>	<i>Helicoverpa assulta</i>
sensilla trichodea	7810	8300
sensilla basiconica	800	1115
sensilla coeloconica	550	620
sensilla chaetica	486	450
Sensilla auricillica	320	290
sensilla styloconica	81	75
Total NO.	~10137	~10850



**Supplementary Figure 1. Functional analysis of HassOR6 (A), HassOR13 (B) and HassOR16 (C) in *Xenopus* oocytes.** In each panel: (Left) Inward current responses of HassOR/ HassOrco-coexpressed *Xenopus* oocytes to  $10^{-4}$  mol/L sex pheromone components and analogs. (Right) Response profiles of HassORs. Error bars indicate SEM (n=10).



**Supplementary Figure 2. Sequence analysis of the homologous candidate pheromone receptors OR14b of *H. armigera* and *H. assulta***

Five putative trans-membrane domains are indicated with black bar and “TM ‘n’” designation, where ‘n’ designates sequential order of the putative transmembrane domain. Trans-membrane domains were predicted by DNAMAN software.