

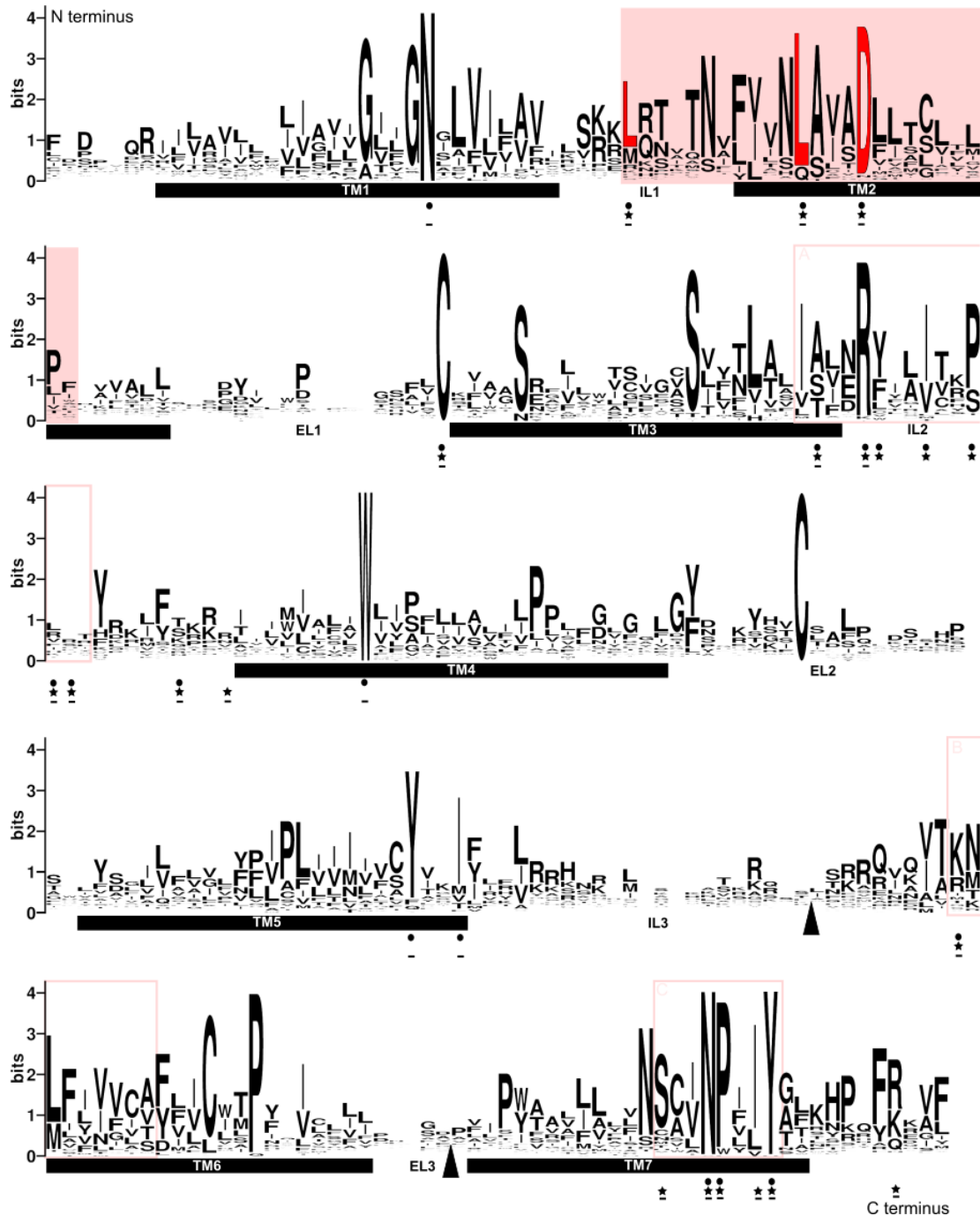
Holothurians have a reduced GPCR and odorant receptor-like repertoire compared to other echinoderms

Nathalie Marquet*, João C.R. Cardoso, Bruno Louro, Stefan A. Fernandes, Sandra C. Silva, Adelino V.M. Canário

CCMAR - Centre of Marine Sciences, University of Algarve, Campus de Gambelas, 8005-139 Faro, Portugal

*Corresponding author: N. Marquet

e-mail: <nmarquet@gmail.com>



Supplementary Figure S1. WebLogo based on the alignment of the entire sea cucumber OR repertoire (*H. arguinensis* and *A. japonicus*). The black bars delimitate the seven transmembrane domains (TM1-7) defined in THMHMM v2.0⁷². The intracellular and extracellular loops are labelled as “IL” and “EL” respectively. Positions with gaps in more than 95% sequences, poorly aligned blocks of sequences (arrows) and N- and C- terminal sequences have been removed. Amino acid positions that are common to fish ORs⁸⁴ are indicated with “●”, and those common to cephalochordates²⁹ and cnidaria²⁸ are indicated with “★” and with “—” respectively. The region of the alignment that contains the motif of interest is highlighted in pink. The pink frames represent the area where other motifs are usually found in ORs (A: M_AxDRYxxxCxPLxY, B: K_AxxTxxxH, C: PxxNPxxY). The height of each symbol indicates the relative frequency of each amino acid at that position.