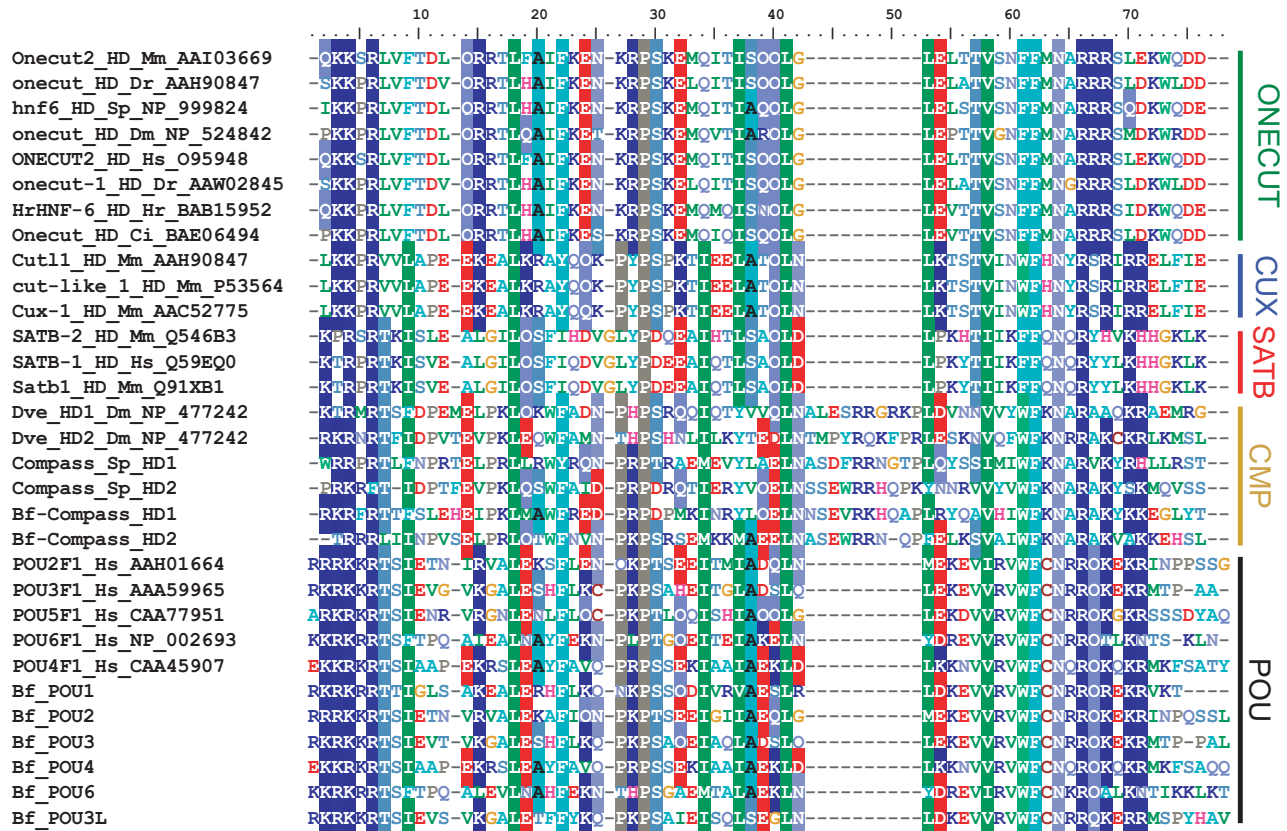


**SUPPLEMENTARY MATERIAL**

**corresponding to:**

**Evolution of *CUT class* homeobox genes: insights from the genome of the amphioxus, *Branchiostoma floridae***

NAOHITO TAKATORI and HIDETOSHI SAIGA\*



## Phylogenetic analysis

### Supplementary Fig. 1. Alignment of amino acid sequences of homeodomain of POU and CUT class proteins generated by CLUSTALW.

Sequence data used for phylogenetic analysis are shown by brown lines. The accession numbers of the sequences used are as follows: Mm\_Cut11: AAH90847; Hs\_CUTL2: O14519; Dm\_cut: NP-524764; Hs\_ONECUT2: O95948; Mm\_Onecut2: AAI03669; Dr\_onecut: AAH90847; Dm\_onecut: NP-524842; Sp\_hnf6: NP-999824; Hr\_HNF-6: BAB15952; Ci\_Onecut: BAE06494; Mm\_SATB-2\_Q546B3; Hs\_SATB-1: Q59EQ0; Mm\_Satb1: Q91XB1; Dm\_Dve: BAA32660; Hs\_POU1F1: NP-000297; Gg\_POU1F1: NP-989650; Hs\_POU2F1: AAH01664; Hs\_POU3F1: AAA59965; Hs\_POU4F1: CAA45907; Hs\_POU5F1: CAA77951; Hs\_POU6F1: NP-002693.