

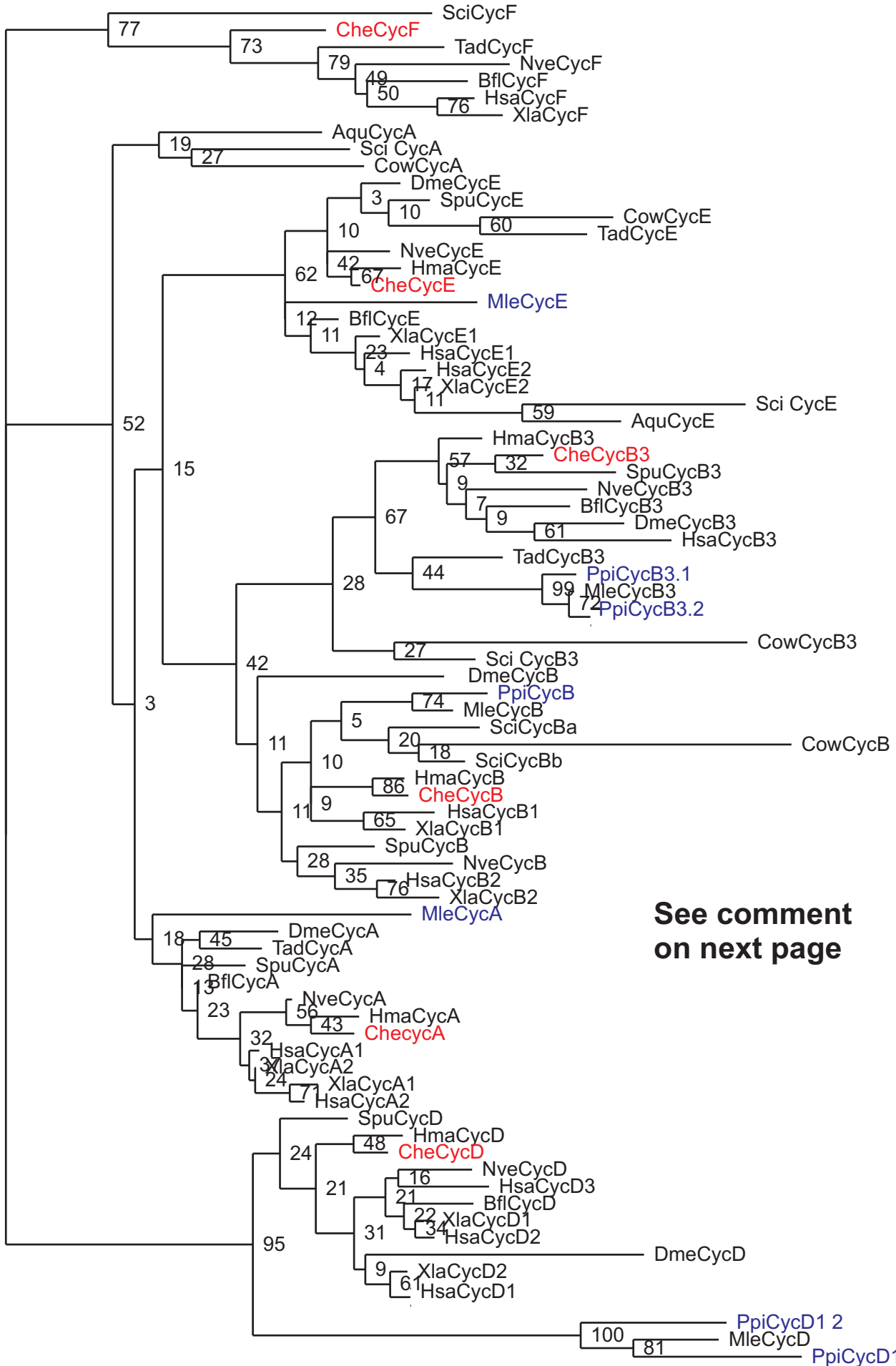
Additional file 4

Phylogenetic analyses of core Hippo pathway genes (other than Yorkie)

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Cyclins

(65 amino-acids)



See comment
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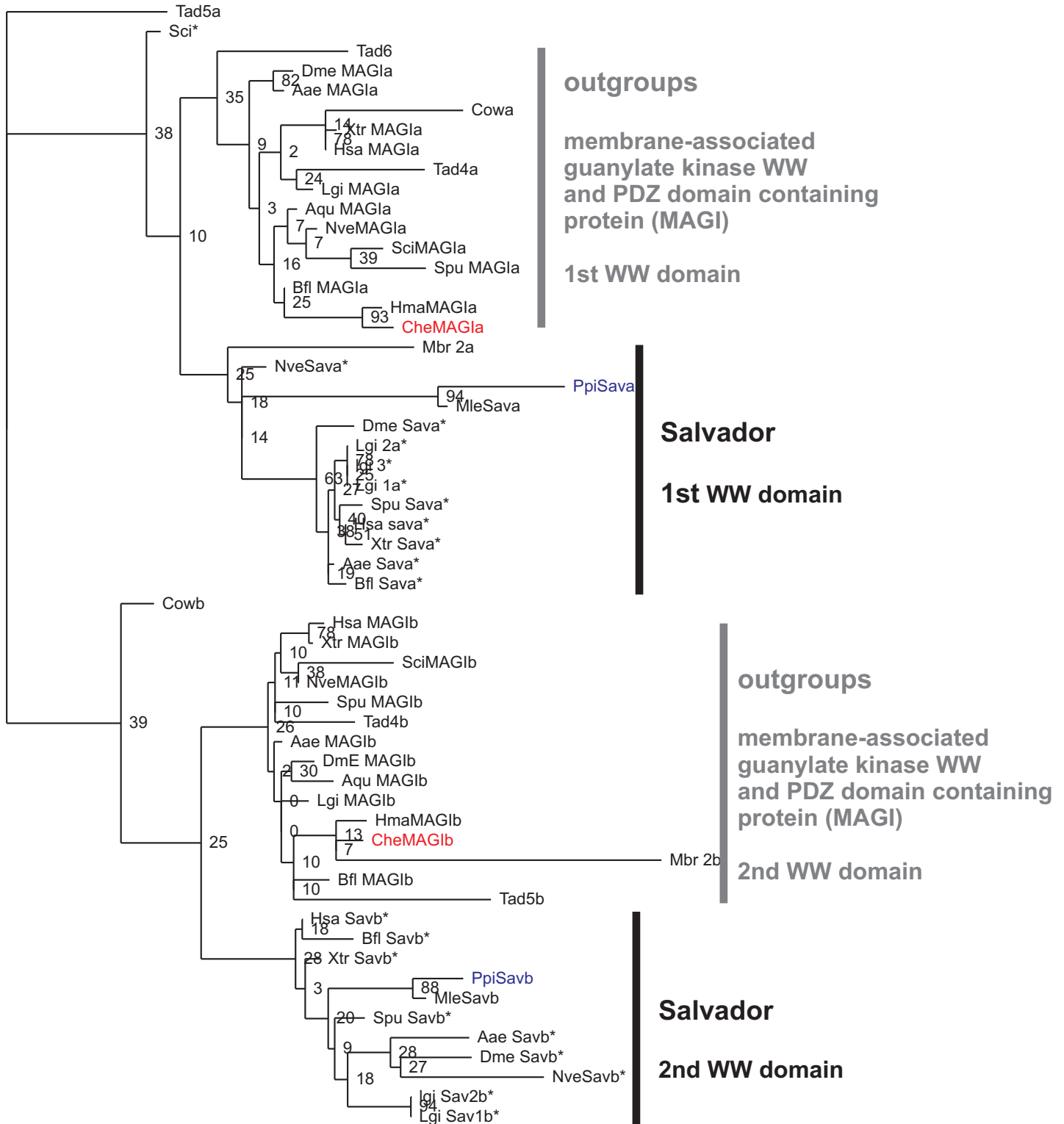
Comment concerning the tree of cyclins

The cyclin subfamilies are strongly conserved at the metazoan level and unsurprisingly, we could detect orthologues of cyclin A, B, B3, D and E in all sampled metazoans including ctenophores. More interestingly, *P. pileus* has two paralogues of cyclin B3 and two paralogues of cyclin D, whereas the other ctenophore *M. leydii* has only one for both subfamilies. In *P. bachei* we found two paralogues of cyclin B3 but only one cyclin D (not shown). In both cases, the tree topology suggests secondary loss of one of the duplicated ctenophore cyclins in *M. leydii*.

Salvador

Alignment of WW domains only (34 amino-acids)

* proteins which contain a SARAH domain (the Hippo-interacting domain of Sav)

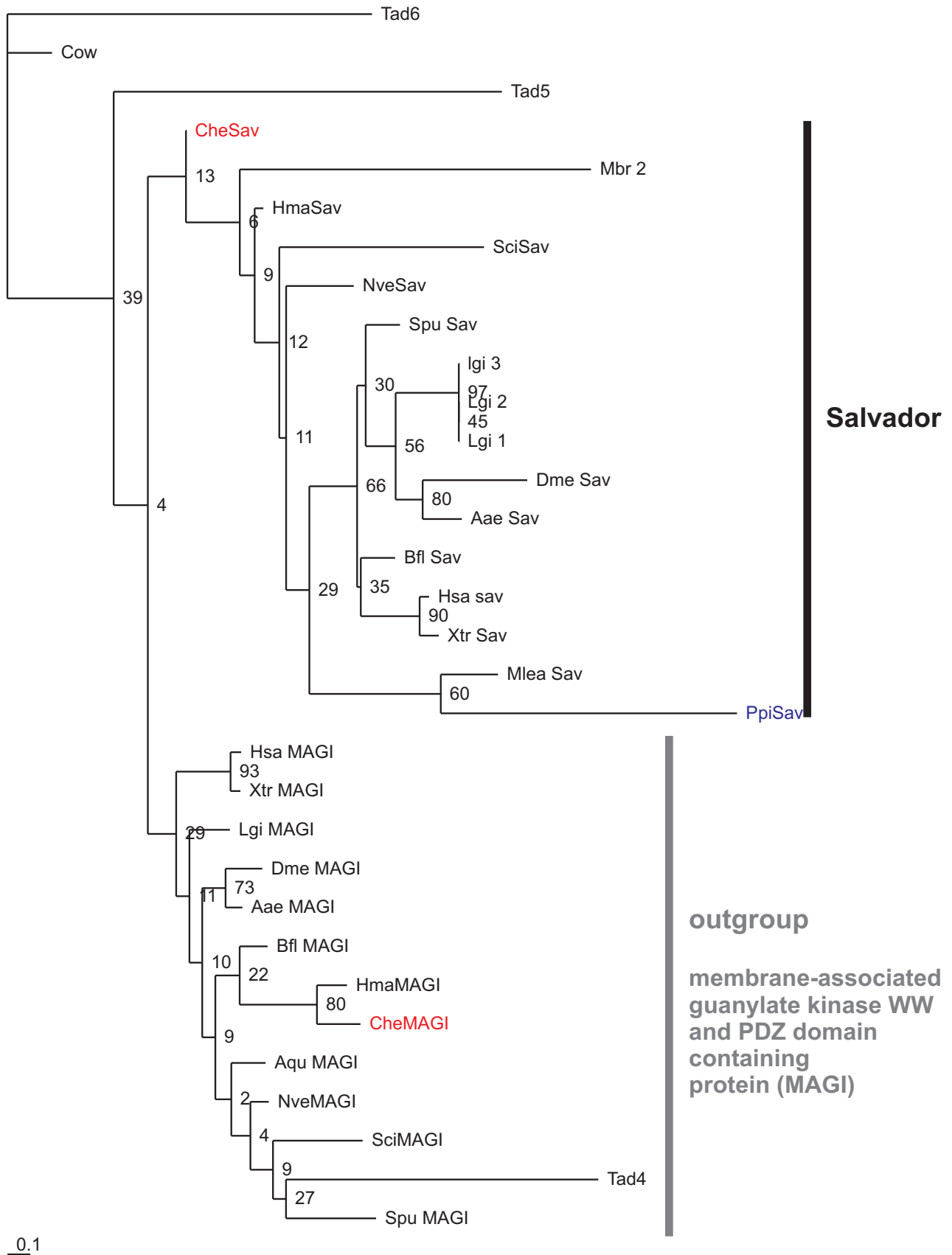


0.1

Note: WW domains are absent in the Salvador proteins of hydrozoans (*Clytia hemisphaerica* and *Hydra magnipapillata*).

Salvador

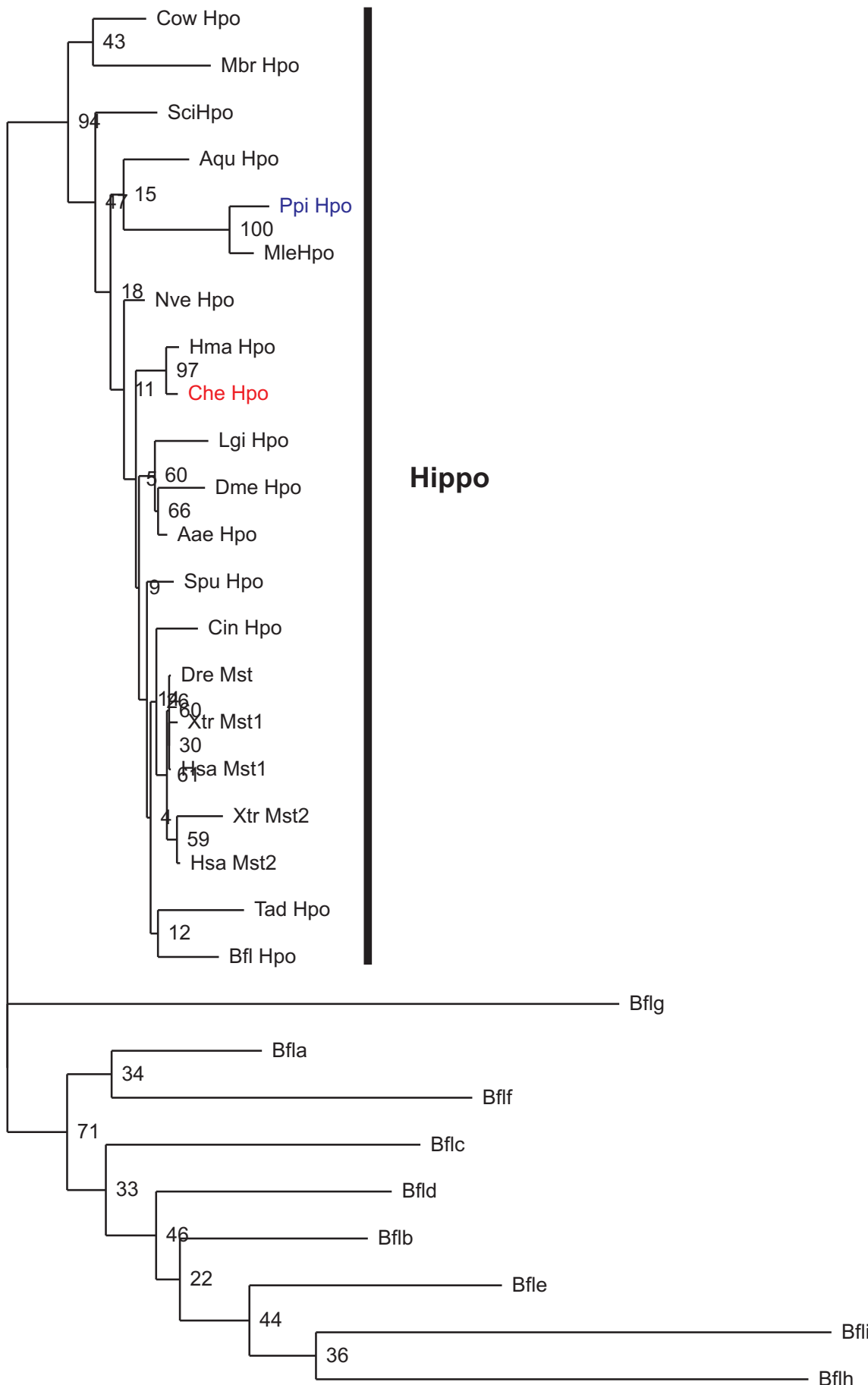
Combined analysis of the two WW domains and the SARAH domain
(116 amino-acids)



Note: WW domains are absent in the Salvador proteins of hydrozoans (*Clytia hemisphaerica* and *Hydra magnipapillata*). In this alignment they have been replaced by missing data.

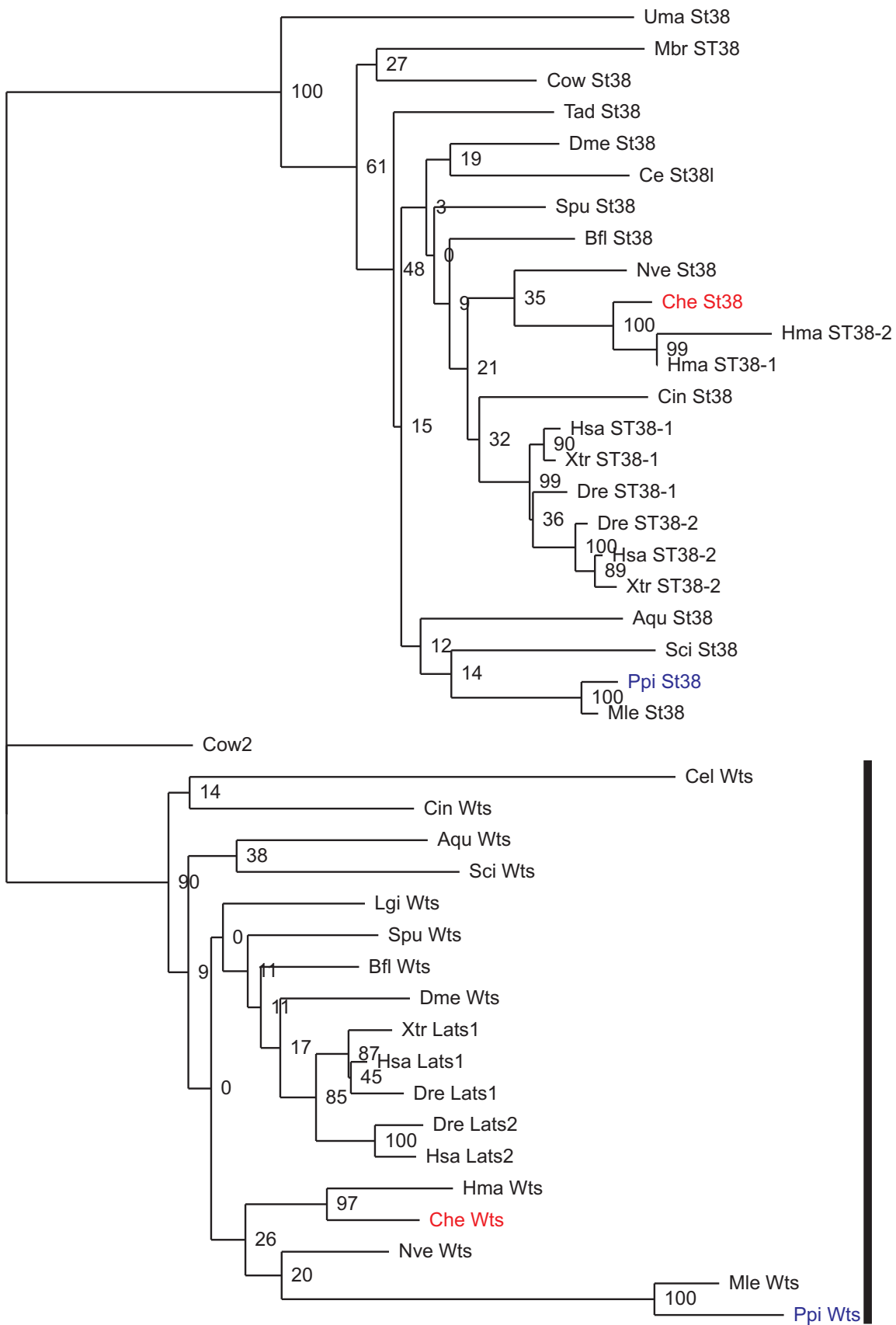
Hippo

(234 amino-acids)



Warts

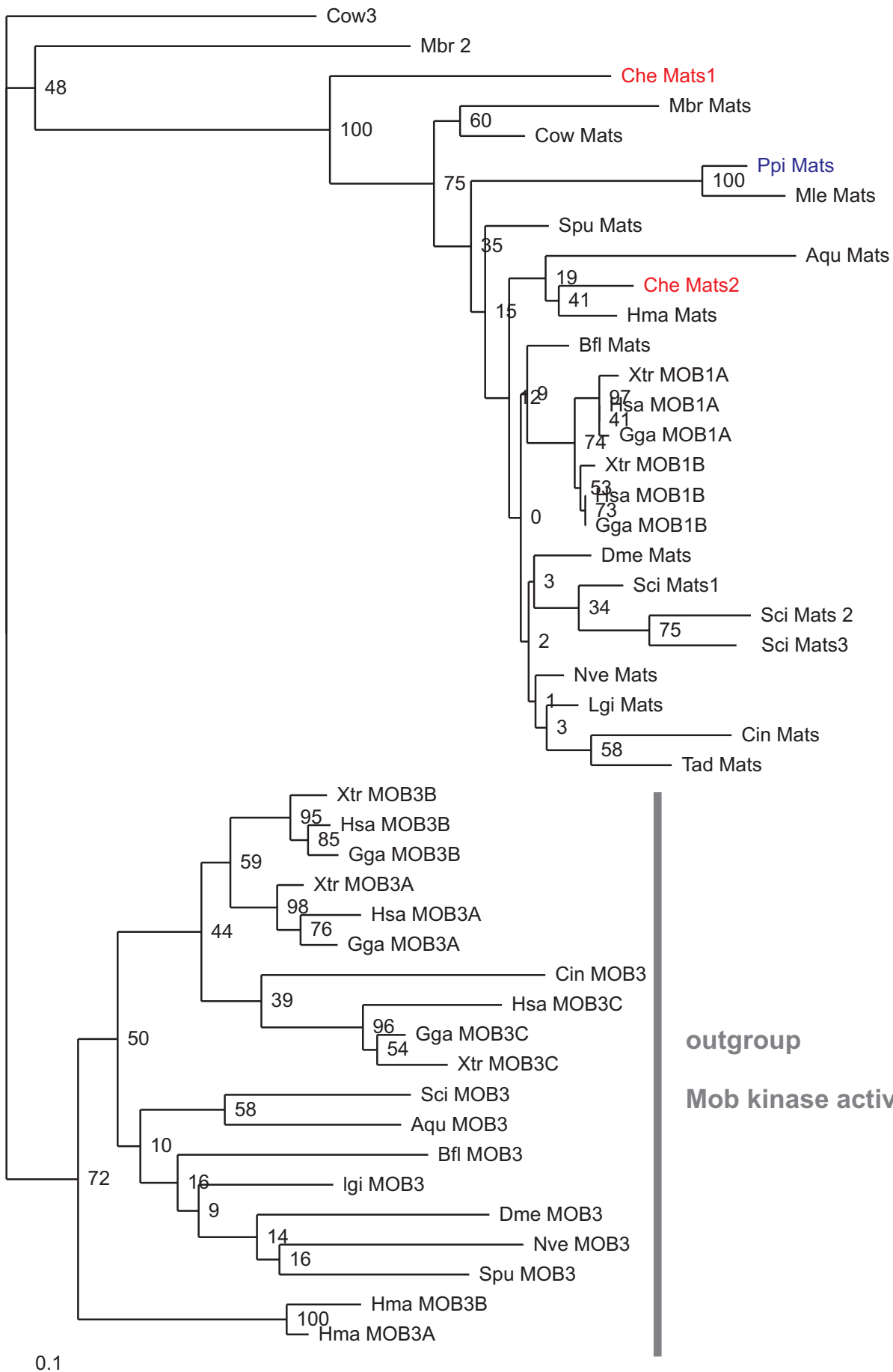
(325 amino-acids)



0.1

Mats

(182 amino-acids)



Scalloped

(240 amino-acids)

