Comparative study of Hippo pathway genes in cellular conveyor belts of a ctenophore and a cnidarian
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**Additional file 4**
Phylogenetic analyses of core Hippo pathway genes (other than Yorkie)

<table>
<thead>
<tr>
<th>page</th>
<th>Gene family</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Cyclins</td>
</tr>
<tr>
<td>3</td>
<td><em>comment on cyclins tree</em></td>
</tr>
<tr>
<td>4</td>
<td>Salvador (WW domain only)</td>
</tr>
<tr>
<td>5</td>
<td>Salvador (WW + SARAH domains )</td>
</tr>
<tr>
<td>6</td>
<td>Hippo</td>
</tr>
<tr>
<td>7</td>
<td>Warts</td>
</tr>
<tr>
<td>8</td>
<td>Mats</td>
</tr>
<tr>
<td>9</td>
<td>Scalloped</td>
</tr>
</tbody>
</table>
Cyclins
(65 amino-acids)

See comment on next page
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)

**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)

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**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 In this alignment they have been replaced by missing data.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)

outgroup
= kinases most closely related to Hippo in the genome of Branchiostoma floridae
Warts
(325 amino-acids)
Scalloped
(240 amino-acids)