

## **Supplemental Material to:**

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**Formin' cellular structures: Physiological roles of  
Diaphanous (Dia) in actin dynamics**

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## 1 **Supplementary information**

2 Metazoan and fungal sequences were extracted from Ensembl (<http://www.ensembl.org>),  
3 *Monosiga brevicollis* from the Joint Genome Institute (<http://genome.jgi.doe.gov>) and  
4 *Capsaspora owczarzakii* from the Broad Institute (<http://www.broadinstitute.org>). The  
5 sequences had to contain a GTPase binding (Pfam PF06371), a FH3 (PF06367) and a FH2  
6 domain (PF02181) <sup>172</sup>. To avoid edge effects caused by PFAMs local domain detection,  
7 SMART<sup>9</sup> was used to delineate the position of the domains in the extracted sequences. To  
8 focus the tree reconstruction on conserved positions, domain sequences were extracted and  
9 concatenated. An alignment was calculated using MUSCLE with default parameters <sup>10</sup>.  
10 Models for the phylogenetic tree reconstruction were estimated by ProtTest resulting in  
11 LG+I+G+F <sup>11</sup>. The tree was calculated with PHYML <sup>173</sup> and robustness estimated by  
12 approximate likelihood ratio tests <sup>174</sup>. Diaphanous Sequences: *Homo sapiens*:  
13 ENSG00000131504 DIAPH1; ENSG00000147202 DIAPH2; ENSG00000139734 DIAPH3.  
14 *Ciona savignyi*: ENSCSAVG00000008096. *Drosophila melanogaster*: FBgn0011202 dia.  
15 *Caenorhabditis elegans*: F11H8.4 Cyk-1. *Amphimedon queenslandica*: Aqu1.221683.  
16 *Trichoplax adherens*: TriadG60005. *Monosiga brevicollis*: A9UVG5.1. *Capsaspora*  
17 *owczarzakii*: E9CGJ0.1, E9C1Z5.1

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## 19 **Supplementary Table 1**

Table A - Differentially conserved sites between Dia1 and Dia2 / 3

Position in mDia1	Z-score	AA in Dia1	AA in Dia2 and 3
41	5,47	E	D
91	5,2	L	M
101	5,86	Q	K
125	5,34	A	K
138	5,54	M	E
164	6,24	N	T
165	6,23	N	S
187	6,6	K	E
207	6,6	E	K
210	6,61	R	Q
225	6,61	M	I
232	5,89	I	L
262	5,88	Q	E
302	5,9	K	Q
313	5,87	I	V
327	5,89	S	N
351	5,26	V	I
487	6,62	H	Q
762	5,89	L	M

Table B - Differentially conserved sites between Dia2 and Dia3. Sites identical to Dia1 in bold.

Position in mDia1	Z-score	AA in Dia1	AA in Dia2	AA in Dia3
249	5,46	D	E	<b>D</b>
323	5,42	V	I	L
330	5,47	M	L	<b>M</b>
359	5,48	Q	N	H
422	5,46	Y	<b>Y</b>	F
756	5,46	Y	<b>Y</b>	F
833	5,08	K	R	<b>K</b>
986	5,12	F	<b>F</b>	S

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