Table S9. *M. brevicollis* presents a key intermediate in the evolution of MAPK signaling.

		Animal		Choanoflagellate	Fungi		Dictyostelia
Kinase		*H.sap*	*N.vec*	*M.bre*	*S.cer*	*N.cra*	*D.dis*
MAPKKK	MEKK1	●	●	●			
	MEKK2	●	●	●			
	MTK1(MEKK4)	●	●				
	ASK (MEKK5-7)	●	●	●			
	MEKK15	●	●				●
	Mos	●	●				
	Raf	●	●				
	LZK (MEKK12-13)	●	●	●			
	MLK (MEKK9-11)	●	●	●			
	TAO	●	●	●			
	UNCLASSIFIABLE		●	●	●	●	●
MAPKK	MKK1	●	●	●	●	●	●
	MKK5	●	●	●			
	MKK3	●	●				
	MKK4	●	●				
	TOPK	●	●	●			
	UNCLASSIFIABLE			●	●	●	
MAPK	ERK	●	●	●	●	●	●
	ERK5	●	●	●			
	p38	●	●	●	●	●	
	JNK	●	●				
	ERK3	●	●				
	ERK7	●	●	●			●
	NMO	●	●				
	UNCLASSIFIABLE				●	●	

Sequence analysis of the three tiers of kinases from the MAPK module in metazoans (human, sea anemone (*Nvec*; *Nematostella vectensis*), choanoflagellate (*M. brevicollis*), fungi (*S.cer*: *Saccharomyces cerevisiae*; *N.cra*: *Neurospora crassa*) and slime mold (*Dictyostelium discoideum*) shows the emergence of MAPK modules in choanoflagellates and lower meatzoans. Kinase subfamilies on the left are from the classification given at kinase.com, based on human kinases.