

Figure Legends for electronic supplementary material

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FGF signaling in gastrulation and neural development in *Nematostella vectensis*, an anthozoan cnidarian

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S1 A Bayesian phylogenetic analysis of FGF ligands. Previous studies have identified eight classes of FGFs within the Metazoa (Popovici et al. 2005). We identified 13 putative genes that possessed FGF core domains within the *N. vectensis* genome (Joint Genome Institute). Of the 13, a Bayesian analysis confirms the orthology for four FGF ligands (*blue arrows*) all within the FGF-D class (FGF8/17/18). The remaining nine ligands (*black arrows*) in the *N. vectensis* genome appear to cluster together and may either represent cnidarian-specific FGF groups or belong to one of the established classes, but the phylogenetic relationship has been obscured. *N. vectensis* sequences are shown in *bold with arrows*. Boxes demark those FGF ligands, where expression patterns have been determined. Numbers above branches indicate posterior probabilities (GIF 20 kb)

S2 A Bayesian phylogenetic analysis of FGFRs. *N. vectensis* possesses 3 putative RTKs that by BLASTX searches were classified as FGFRs. A Bayesian phylogenetic analysis confirms that two of the three are legitimate FGFRs. *NvFGFRa* and *NvFGFRb* are most closely related to an FGFR from a hydrozoan cnidarian, *Hydra FGFR-like (kringelchen)* and the lone FGFR in the *C. elegans* genome, *egl-15*. The third receptor, *NvFGFRc*, groups with a hydrozoan RTK of a different family (*P. carnea VEGFR*) and is likely not a true FGFR. *N. vectensis* FGFRs are indicated by *boxes and arrows*. Numbers above branches indicate posterior probabilities (GIF 13 kb)

S3 A Bayesian phylogenetic analysis of *sprouty* related metazoan genes. The *N. vectensis* genome only contained one potential *sprouty/spred* family member. Bayesian analysis shows that the *NvSprouty* ortholog forms a sister group to vertebrate and *Drosophila sprouty* genes, to the exclusion of *Spred* genes, suggesting that *NvSprouty* is a definitive *sprouty* ortholog. The *N. vectensis sprouty* ortholog is indicated by a *box and an arrow*. Numbers above branches indicate posterior probabilities (GIF 9 kb)

S4 Bayesian phylogenetic analysis of metazoan *Churchill (ChCh)* genes, a zinc finger transcription factor. The *N. vectensis* genome only contained one potential ortholog of *Churchill*, which forms a sister group relationship with the echinoderm, *S. purpuratus Churchill* gene with 100% posterior probability. *N. vectensis NvChurchill* gene is indicated by a *box and an arrow*. Numbers above branches indicate posterior probabilities (GIF 6 kb)

S5 *NvFGF8B* is expressed exclusively at the aboral end during development. Transcripts for *NvFGF8B* were not detectable during cleavage stages (data not shown) and throughout gastrulation (**a**). During planula (**b**) and polyp (**c**) stages, transcripts were detectable in a few endodermal cells at the aboral end, below the apical tuft. All embryo views are lateral with the *asterisk* denoting the site of gastrulation and future mouth (GIF 92 kb)

S6 A complete receptor tyrosine kinase signaling pathway exists in Cnidaria. Besides FGF pathway ligands, receptors, and target genes, cnidarians also appear to possess orthologs to the canonical FGF RTK signal transduction pathway that is conserved throughout Bilateria. Distal to FGFRs, this pathway in vertebrates consists of FRS2, Grb2, SOS, Ras, Raf, MEK, and ERK, operating sequentially to relay intracellular signals from cell surface to nuclear target genes (Eswarakumar et al. 2005). Upon receptor activation, FRS2, an adaptor protein, binds the FGFR phosphorylated cytoplasmic tails and recruits Grb2, also an adaptor protein. Grb2 recruits SOS, a guanine nucleotide exchange factor that binds and activates the small GTPase, Ras. Activated Ras binds Raf, a MAP kinase kinase kinase that phosphorylates and activates MEK, a MAP kinase kinase. MEK subsequently activates Erk, a MAP kinase that phosphorylates and regulates nuclear transcription factors (ETS) and their regulators to affect gene activity. Potential orthologs for nearly all of these components, with the exception of FRS2, were identified by BLAST searches of the assembly of the *N. vectensis* genome (Joint Genome Institute). The existence of this conserved pathway in *N. vectensis* provides further evidence that FGF/RTK signaling is an ancient, conserved pathway (GIF 7 kb)

S7 Nexus file for FGF ligand phylogenetic analysis

S8 Nexus file for FGFR phylogenetic analysis

S9 Nexus file for Sprouty phylogenetic analysis

S10 Nexus file for Churchill phylogenetic analysis