



Figure 2—figure supplement 2. Phylogenetic analysis of SMED-FGFR proteins. Top right: Domain diagram of FGFR and FGFR proteins. IG, immunoglobulin domain; TM, transmembrane domain; TyrKc, Tyrosine kinase. Tree showing 54 FGFR proteins from diverse organisms, which were aligned using MUSCLE with default settings and trimmed with Gblocks. Maximum likelihood analyses were run using PhyML with 100 bootstrap replicates, the WAG model of amino acid substitution, 4 substitution rate categories and the proportion of invariable sites estimated from the dataset. All ML bootstrap values are shown above or below respective branch. Hs, *Homo sapiens*; Mm, *Mus musculus*; Xt, *Xenopus tropicalis*; Sp, *Strongylocentrotus purpuratus*; Cs, *Capitella sp. I*; Lg, *Lottia gigantea*; Ci, *Ciona intestinalis*; Sm, *Schistosoma mansoni*; Smed, *Schmidtea mediterranea*; Dj, *Dugesia japonica*; Dl, *Dendrocoelum lacteum*; Ptor, *Planaria torva*; Pt, *Polycelis tenuis*; Pn, *Polycelis nigra*; Nv, *Nematostella vectensis*. Right, ISH of the 6 *Schmidtea mediterranea* FGFR genes shown in tree. Images are representative of $n > 10$ animals. Anterior, left.