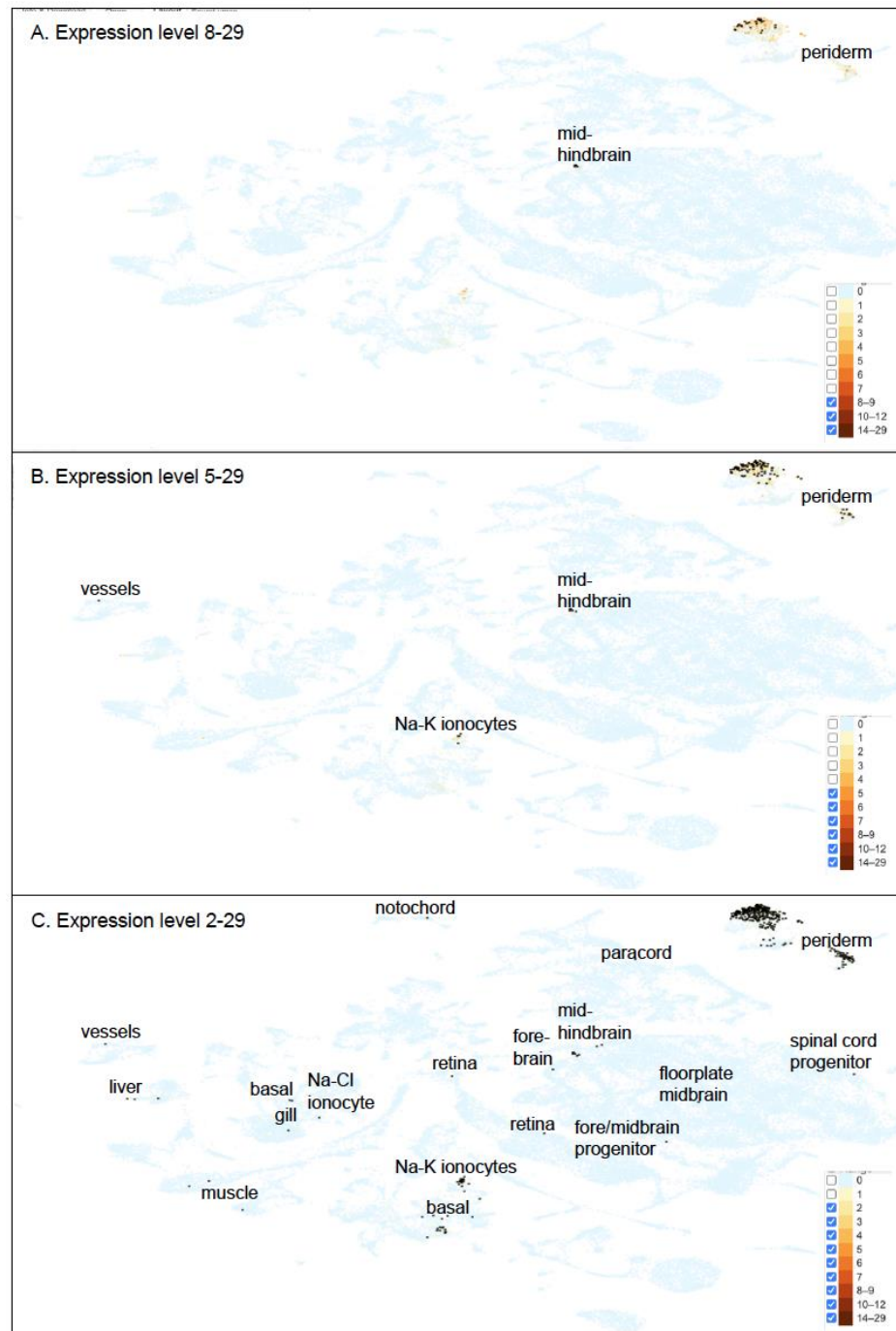


Supplementary Table S1

Primers used to synthesize riboprobe for <i>in situ</i> hybridization.			
Species	Acc. Number	Sequence (5' > 3')	Riboprobe size
<i>Danio rerio</i>	NM_131660	<i>Fw</i> - CAAGCAGCGGGTGTGCAAAC	908 bp
		<i>Rv</i> - CTATGCAAACGTGCTCAGTG	
<i>Oryzias latipes</i>	NM_001104855	<i>Fw</i> - GTATATGGGCACAGAGATCG	953 bp
		<i>Rv</i> - CTTCAAACAGCGTGTCCAC	
<i>Lepisosteus oculatus</i>	XM_015366414	<i>Fw</i> - CGACATGAGCTATGAGAGCG	943 bp
		<i>Rv</i> - GTCCACATGTGCCTTAGAGC	



Supplemental Figure S1. *nos1* expression in scRNA-seq data.

A. At the highest levels of expression (levels 8 to 29), *nos1* was expressed in 30 cells that include periderm cells and a highly specific group of midbrain-hindbrain neurons.

B. At high and midlevel expression (levels 5 to 29), *nos1* was expressed in 112 cells that included the more periderm and midbrain-hindbrain cells, and in addition, several Na-K ionocytes, and strongly in one blood vessel cell.

C. At high, mid-, and low levels (levels 2 to 29), *nos1* transcript was present in additional cells, including muscle, basal skin cells, gill, retina, and in the CNS in the forebrain, floorplate of the midbrain, and in spinal cord progenitor cells.

Data were extracted from the zebrafish gene expression atlas (Farnsworth *et al.*, 2019), and include embryos at 1 and 2 dpf and larvae at 5 dpf. Color scale for expression levels shown at lower right of each panel. Cell identities determined as in Farnsworth *et al.* (2019).

Farnsworth DR, Saunders LM, Miller AC. A single-cell transcriptome atlas for zebrafish development. *Dev. Biol.* (2020) 459: 100-108. doi: 10.1016/j.ydbio.2019.11.008.