Table S1. Summary of changes in gene expression in *arnt2*^{m1055} mutant embryos

Category of analyzed gene expression	Gene	Stages analyzed	Altered expression
Proliferation	*mcm5*	36, 60 hpf	No
	pcna	36, 60 hpf	No
Patterning+differentiation	*arnt2*	24 hpf	Yes
	dlx2	32 hpf	No
	dlx4	32 hpf	No
	fezl	48 hpf	No
	foxa2	32 hpf	No
	lim1	32 hpf	No
	nk2.1	32 hpf	No
	nk2.2	32 hpf	No
	nk5.1	32 hpf	No
	otpa	24, 48, 72 hpf	No
	otpb	24, 48, 72 hpf	No
	pou47	24-72 hpf	Yes
	pou50	32 hpf	No
	shh	32 hpf	No
	sim1a	24-72 hpf	No
	sim1b	24-72 hpf	Yes
	sim2	24-72 hpf	No
Neurotransmitter/neurohormone expression	*crh*	3, 4 dpf	Yes
	itnp	3, 4 dpf	Yes
	sst1	3, 4 dpf	Yes
	th	24-120 hpf	Yes
	trh	3, 4 dpf	Yes
	vsnp	3, 4 dpf	Yes
Others	*dat* (*slc6a3*)	78 hpf	Yes
	ddc	78 hpf	Yes
	tphD1	72 hpf	No

Gene expression was analyzed by whole-mount in situ hybridization using embryos derived from a cross of heterozygous carriers of the *arnt2*^{m1055} allele. The tails of the stained embryos were used for genotyping and expression of markers was compared by light microscopy in homozygous mutants and wild-type siblings. All analyzed batches contained at least 50 embryos.