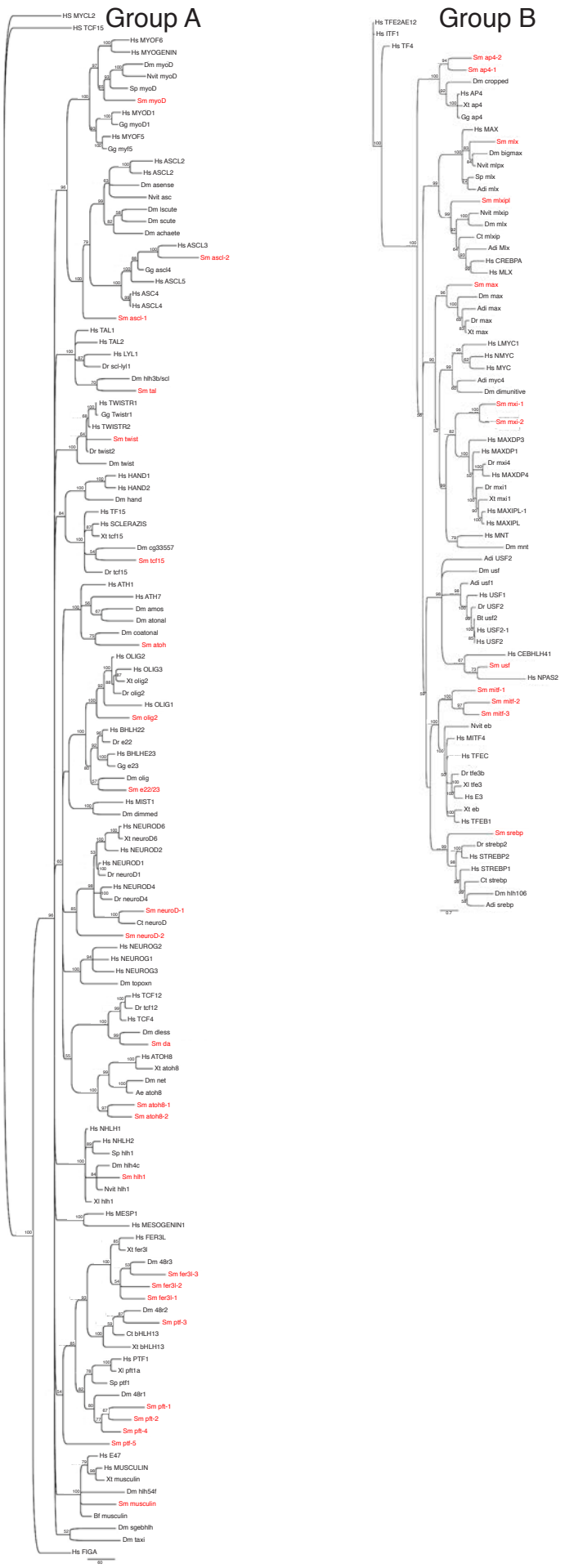

Fig. S1: Bayesian Phylogeny of Groups A and B bHLH transcription factor homologs. Protein sequences used in the phylogenies were obtained from the NCBI Entrez protein database or directly from the genome sequencing projects of included organisms. Sequences were aligned using T-Coffee (Notredame et al., 2000) and the program Geneious (www.geneious.com) was used for Bayesian analyses with the following settings: 1 million replicates, WAG substitution model, 4 heated chains, 25% burnin, and subsample frequency of 1000. Consensus tree images were saved through Geneious and then manipulated in Adobe Photoshop. Only bootstrap values over 50 are shown. Species used: Adi=*Acropora digitifera*; Ag=*Anopheles gambiae*; Bf=*Branchiostoma floridae*; Bt=*Bos taurus*; Ct=*Capitella teleta*; Dm=*Drosophila melanogaster*; Dr=*Danio rerio*; Gg=*Gallus gallus*; Hs=*Homo sapiens*; Nvit=*Nematostella vectensis*; Sp=*Strongylocentrotus purpuratus*; Sm=*Schmidtea mediterranea*; Xl=*Xenopus laevis*; Xt=*Xenopus tropicalis*. *S. mediterranea* homologs are in red fonts.

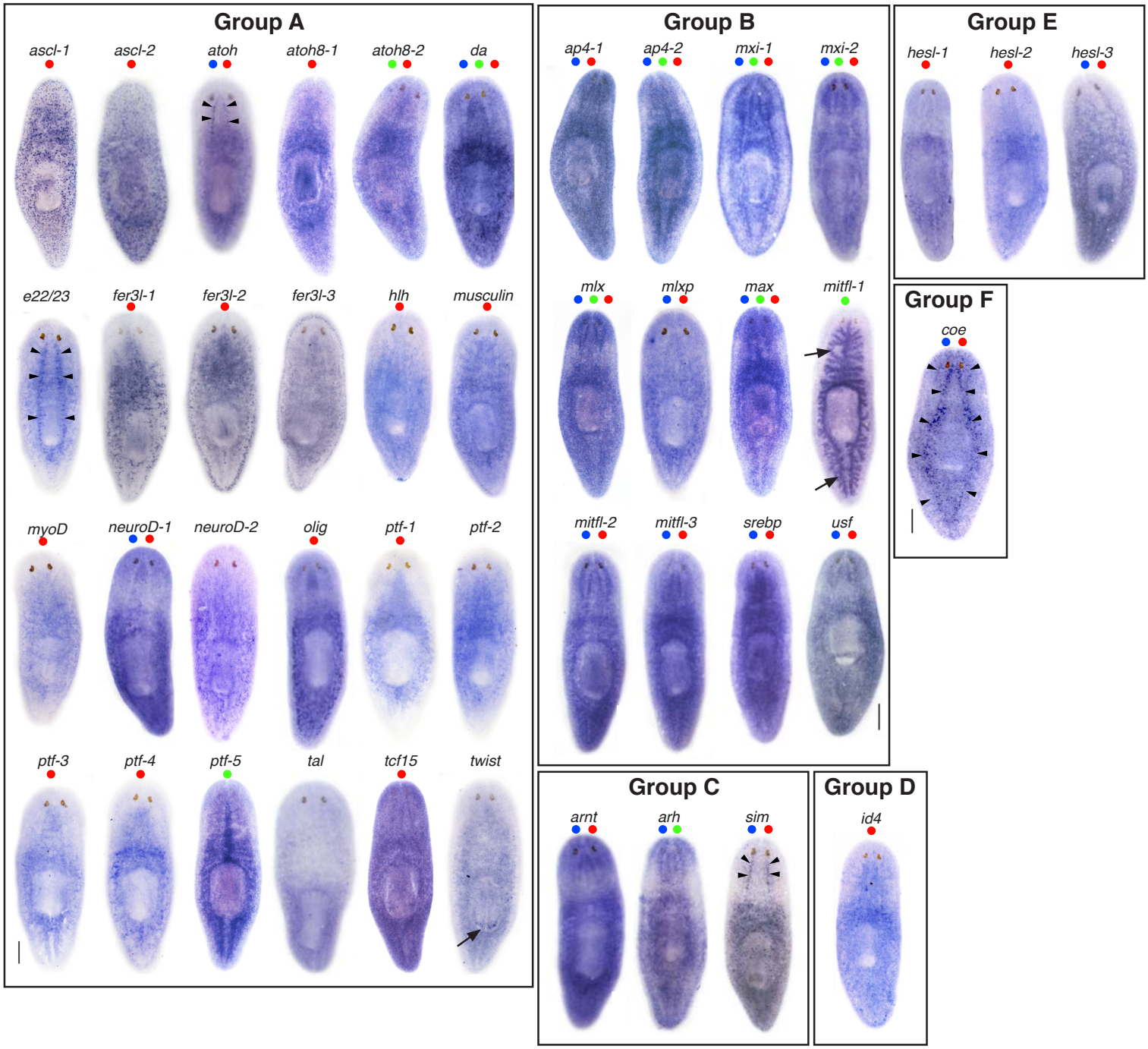

Fig. S2: Expression analysis of bHLH genes in *S. mediterranea*. Intact animals were processed for whole-mount in situ hybridization to bHLH genes. Gene names are indicated above each animal. bHLHs were expressed in a wide range of cells and tissues. *ascl-1* and *ascl-2* were expressed in a punctate pattern throughout the mesenchyme. *atoh*, *e22/23*, *sim*, and *coe* were expressed in distinct cells in the CNS (black arrowheads). *mitfl-1* and *twist* were exclusively detected in the intestine and pharynx (black arrows). Many bHLH genes, including *arnt*, *da*, *ap4-1*, *max* and *srebp*, were detected ubiquitously throughout the animal. *fer3l-1*, *fer3l-2*, and *fer3l-3* exhibited related expression patterns with *fer3l-1* expression detected in the interior mesechyme (stem cell-like) and *fer3l-2* and *fer3l-3* detected more exteriorly (similar to a post-mitotic progeny pattern). No definitive expression pattern was observed for *neuroD-2*. The expression of genes in planarian stem cells and immediate progeny is characterized by parenchymal (mesenchymal) staining ranging from punctate expression in stem cell or progeny to diffuse expression throughout the animal and γ-irradiation sensitive. As expected, most bHLHs displayed reduced expression following γ-irradiation (see Table S1). Blue and green dots above the animals denote expression in the CNS and intestine, respectively; red dots denote genes that were γ-irradiation sensitive. Genes were categorized in bHLH Groups A-F based on their homology. Scale bars = 200 μm.

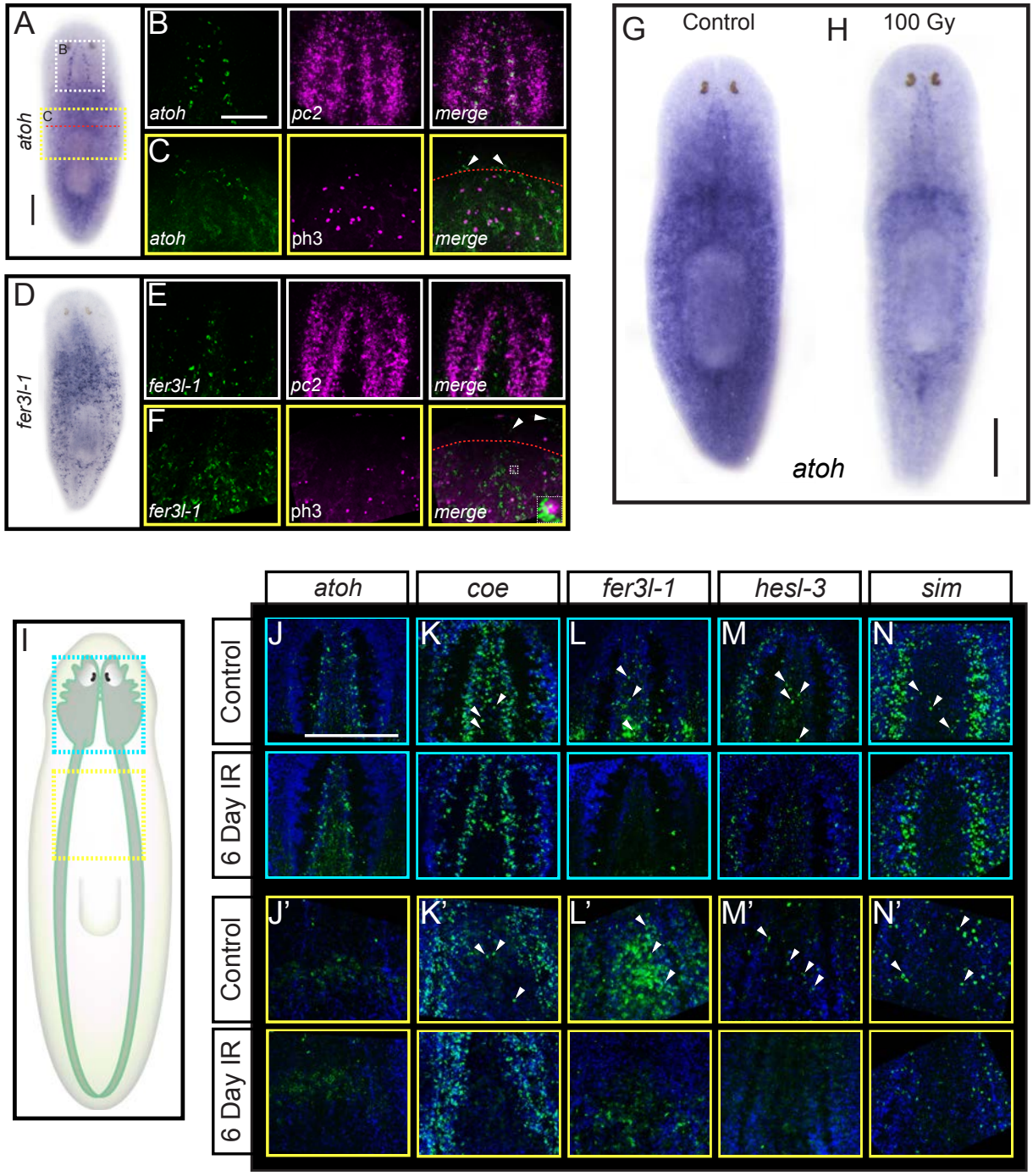

Fig. S3: bHLH genes are expressed in γ-irradiation-sensitive populations near the CNS and stem cell compartment. (A) Expression pattern of atoh. Dashed boxes indicate zoom area of the brain or regeneration blastema shown in B and C, respectively. Dashed red line indicates site of amputation. (B) FISH to *atoh* (green) and *pc2* (magenta). (C) FISH to *atoh* counterstained with anti-phosphohistone-H3 (ph3) to label mitotic cells in 3 day regenerates. Arrowheads denote *atoh*$^{+}$ cells within the blastema. (D-F) show similar analysis for *fer3l-1*. White dashed box in F highlights a bHLH/ph3-positive cells shown at high magnification within the merged image inset. (G and H) WISH to *atoh* in controls or animals 6 days post-irradiation (100 Gy). (I) Cartoon depicting the planarian CNS; blue (head) and yellow (pre-pharyngeal) boxes denote areas of the animal imaged in J-N and J'-N', respectively. (J-N') Control and γ-irradiated animals processed for fluorescent in situ hybridization to *atoh*, *coe*, *fer3l-1*, *hesl-3*, and *sim*, and counterstained with DAPI. Arrowheads denote representative cell populations lost following γ-irradiation. Scale bars = 200 μm.

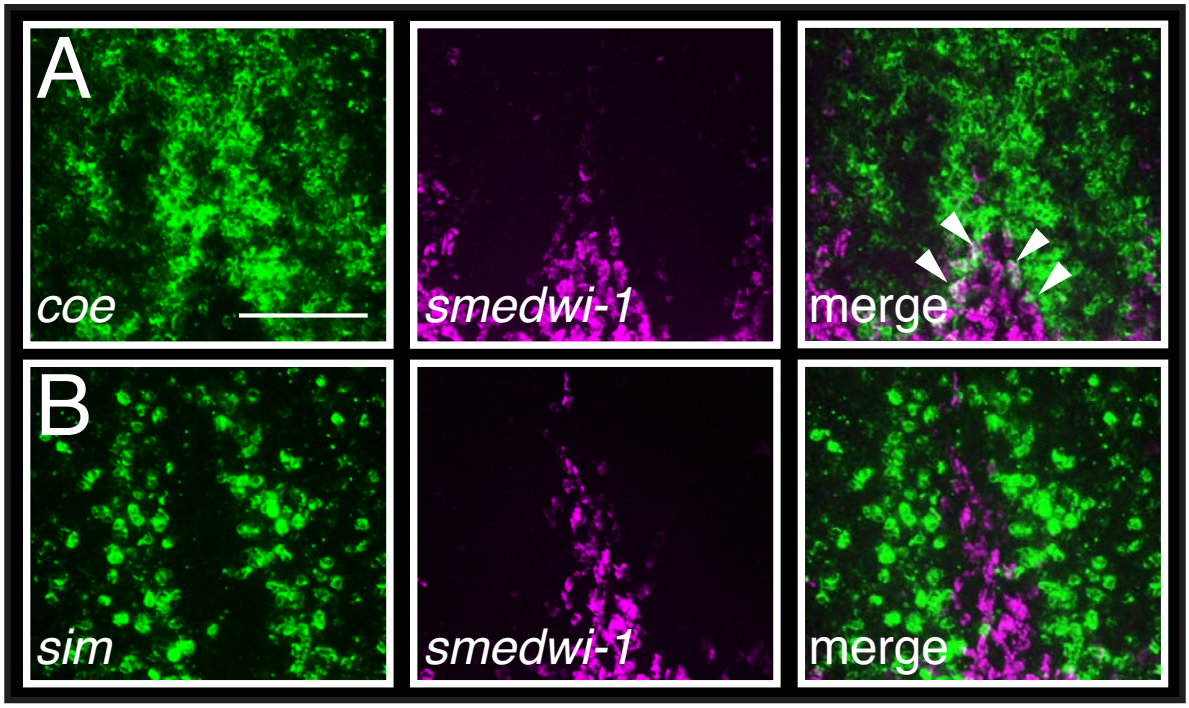

Fig. S4: *coe* and *sim* are not co-expressed with *smedwi-1* in the anterior region of the cephalic ganglia. (A-B) Representative images from the head region of animals processed for double-fluorescent in situ hybridization to *coe* or *sim* and *smedwi-1*. White arrows point to *coe*$^{+}$/*smedwi-1*$^{+}$ cells. Scale bar in A = 100 μm.

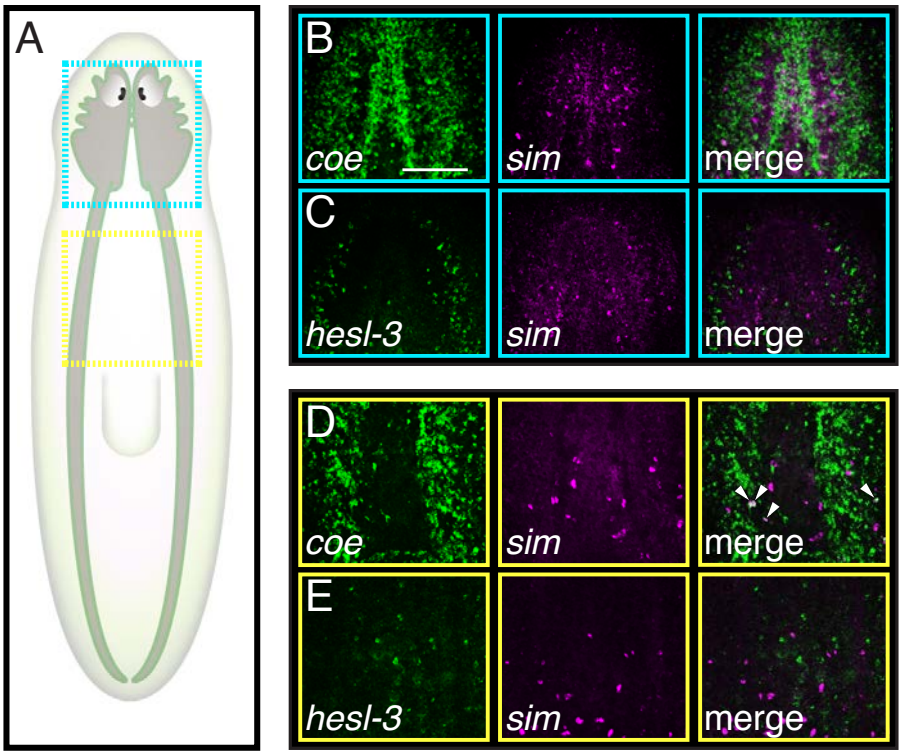

Fig. S5: *coe* and *sim* are co-expressed in cells in the pre-pharyngeal area. (A) Cartoon depicting the planarian CNS. Blue (head) and yellow (pre-pharyngeal) boxes denote the region of the animal imaged in B-D, respectively. (B-E) Images of the brain region of animals processed for double-fluorescent in situ hybridization to *coe* and *sim* or *hesl-3* and *sim*. Scale bar in B = 100 μm.

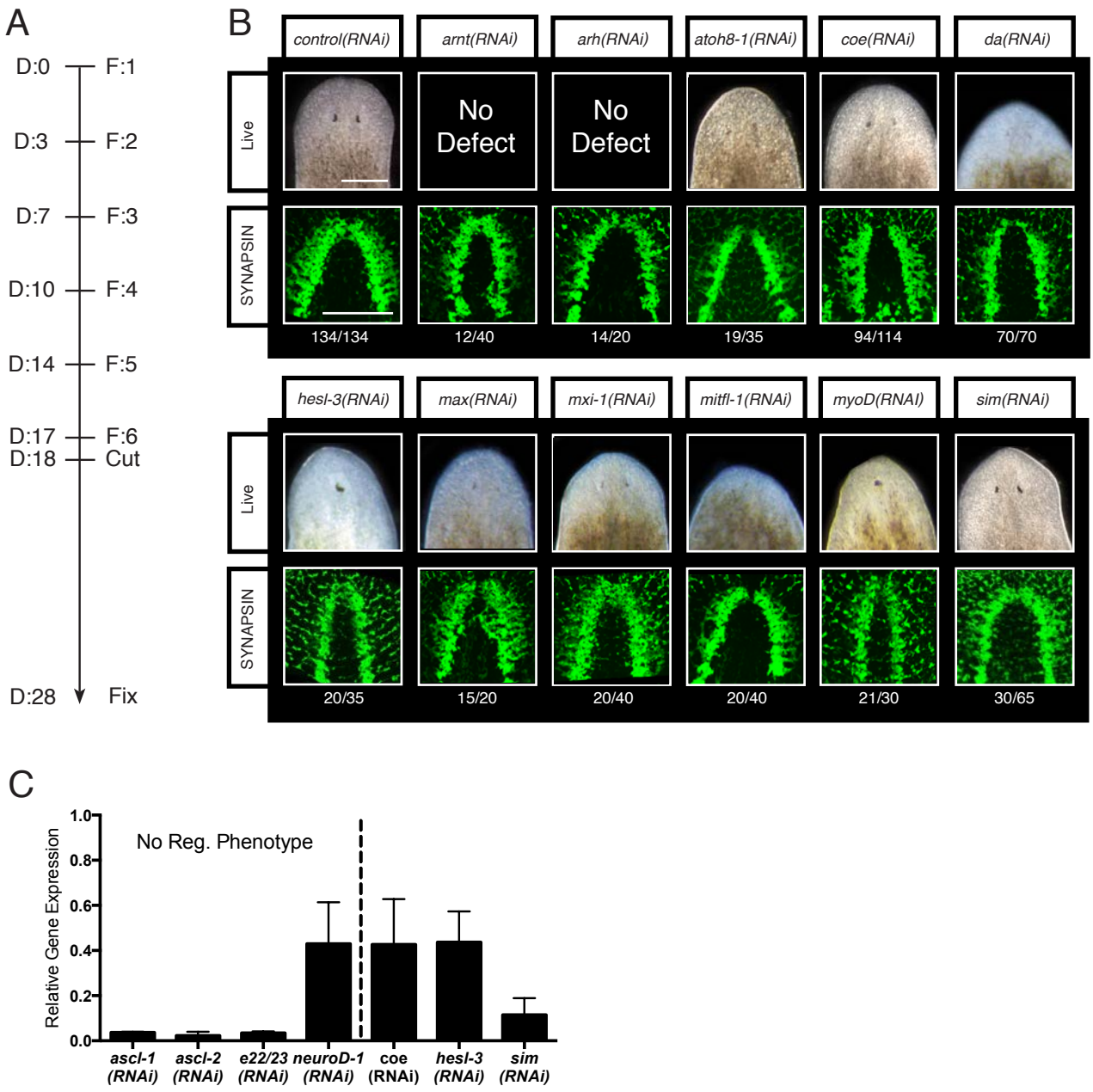

Fig. S6: bHLH RNAi screen for defects in CNS regeneration. (A) Experimental design for RNAi screen; D and F denote days and number of bacterial feedings, respectively. (B) Summary of RNAi phenotypes following bHLH knockdowns. Images shown are of 10-day regenerates. Numbers below images refer to the number of animals with an observable regeneration defect. (C) Quantitative real-time PCR measurements of relative mRNA expression after RNAi knockdown of selected bHLH genes. *ascl-1*, *ascl-2*, *e22/23* and *neuroD-1* did not result in a regeneration phenotype following RNAi. Scale bars = 200 μm

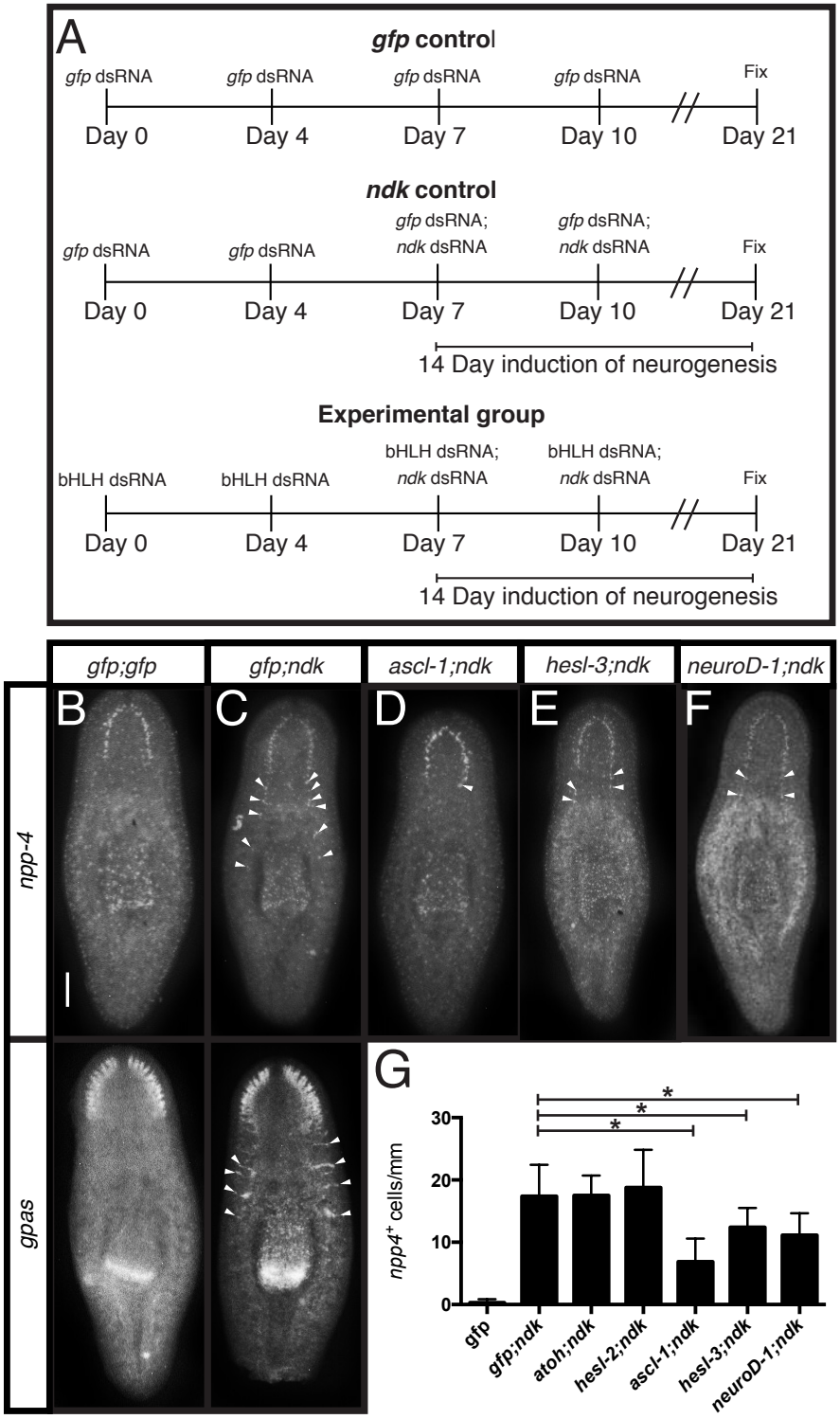

Fig. S7. *ascl-1*, *hesl-3,* and *neuroD-1* suppress ectopic formation of *npp-4*⁺ cells when co-silenced with *ndk*. (A) Schematic of RNAi-based suppression assay. For double knockdown experiments, bacterial pellets containing dsRNA for each gene were mixed 1:1. For select bHLH and ndk co-silencing experiments, planarians were fed dsRNA four times over two weeks. The first two RNAi feedings contained *bHLH* dsRNA and the final two RNAi treatments contained both *bHLH* and *ndk* dsRNA. (B-F) *gfp;gfp(RNAi)*, *gfp;ndk(RNAi)*, *ascl-1;ndk(RNAi), hesl-3;ndk(RNAi)*, and *neuroD-1;ndk(RNAi)* animals were processed for FISH to *npp-4* or *gpas*. (G) Quantification of ectopic *npp-4*⁺ cells (arrowheads in B-F of top row; n > 9 animals per group); neurons were normalized by the length of the animal (mm). Asterisks denote a significant reduction of cells when compared with *gfp;ndk(RNAi)* animals ($p < 0.05$, Student's t-test). The expansion of *gpas* after *ndk* RNAi (arrowheads in B and C of bottom row) was not affected after *bHLH* knockdowns. Scale bar = 200 μm.

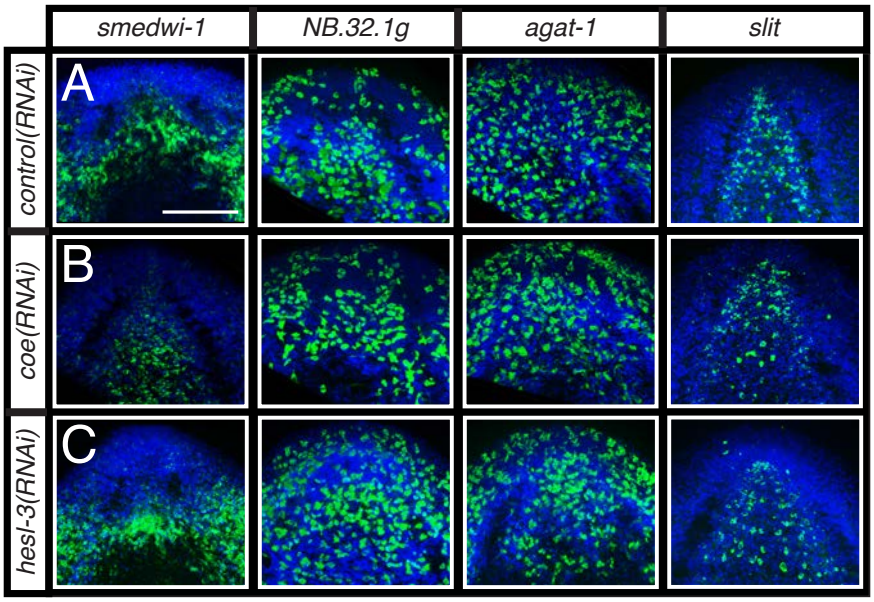

Fig. S8: *coe* and *hesl-3* RNAi phenotypes are not due to a loss of the stem cells, progeny, or midline signals. (A-C) RNAi treated animals were amputated, allowed to regenerate for 5 days, and then processed for fluorescent in situ hybridization to *smedwi-1*, *NB.32.1g*, *agat-1*, or *slit* and counterstained with DAPI. Scale bar = 100 μm.

Movie 1. *control(RNAi)* intact planarians display the stereotypical light avoidance response and glide away from the center of the petri dish.

Movie 2. *coe(RNAi)* intact animals fail to display a robust response to light. Some animals do not show normal locomotion behaviors and appear to be immobilized.

Movie 1

Movie 2

Table S1. Summary of bHLH homologs in S. mediterranea and their expression patterns determined from published RNA-seq data and in situ hybridization.

Gene Name	Top Hit Accession	Top Hit Gene Name	Top Hit Evalue	Category	cRPKM SC *	cRPKM Prog *	cRPKM Diff *	log2(X1/Xins) #	log2(X1/X2) #	log2(X2/Xins) #	Category	Stem Cells/Progeny	CNS	Pharynx	Intestine	Epidermis	Mesenchyme
Smed-achaete scute like-1 (ascl-1)	Q6XD76	ASCL4_HUMAN	4.00E-11	*A*	19.03	34.14	40.22	-2.811263821	-0.481553859	-2.329709962	6	Yes	No	No	No	No	Yes
Smed-achaete scute like-2 (ascl-2)	Q9NQ33	ASCL3_HUMAN	7.00E-19	*A*	1.17	2.77	3.71	0.763645015	0.596177444	0.167467571	2	Yes	No	No	No	No	Yes
Smed-activating enhancer binding protein-like-4-1 (ap4-1)	Q01664	TFAP4_HUMAN	1.00E-15	*B*	4.22	7.75	7.75	-1.723158391	-0.159717879	-1.563440512	6	Yes	Yes	Yes	No	No	Yes
Smed-activating enhancer binding protein-like-4-2 (ap4-2)	Q01664	TFAP4_HUMAN	4.00E-15	*B*	153.27	150.92	17.96	1.814102441	0.554289807	1.259812634	1	Yes	Yes	Yes	Yes	No	Yes
Smed-aryl hydrocarbon receptor (ahr)	Q95LD9	AHR_DELLE	1.00E-95	*C*	0.75	10.49	7.26	-1.699145616	-1.970169379	0.271023763	3	No	Yes	No	No	Yes	Yes
Smed-aryl hydrocarbon receptor nuclear translocator-like (arnt)	O15945	ARNT_DROME	2.00E-149	*C*	31.88	58.94	10.93	2.222109911	0.722122834	1.499987077	1	Yes	Yes	No	No	No	Yes
Smed-atonal homolog (atoh)	P48985	ATOH1_MOUSE	3.00E-15	*A*	NA	NA	NA	2.026679421	-2.047678746	4.074358167	3	Yes	Yes	No	No	No	Yes
Smed-atonal homolog 8-1 (atoh8-1)	Q99NA2	ATOH8_MOUSE	8.00E-21	*A*	9.74	9.03	6.23	1.723287277	0.225953792	1.497333485	1	Yes	No	Yes	No	No	Yes
Smed-atonal homolog 8-1 (atoh8-2)	Q99NA2	ATOH8_MOUSE	2.00E-21	*A*	8.19	16.3	5.1	0.289713827	-0.110414501	0.400128328	3	Yes	No	Yes	Yes	No	Yes
Smed-basic helix-loop-helix family, member e22/23-like (e22/23)	Q8BGW3	BHE23_MOUSE	1.00E-34	*A*	0.93	2.17	17.47	-4.017714699	-4.003735398	-0.0139793	5	No	Yes	No	No	No	Yes
Smed-collier (coe)	Q63398	COE1_RAT	0	*F*	7.27	27.86	11.33	1.493145159	-0.638989339	2.132134498	3	Yes	Yes	Yes	No	No	Yes
Smed-daughterless (da)	P11420	DA_DROME	3.00E-41	*A*	53.33	49.7	19.05	2.52093294	1.485722114	1.035210826	1	Yes	Yes	Yes	Yes	Yes	Yes
Smed-fer3l-1 (fer3l-1)	Q9VGJ5	FER3_DROME	4.00E-31	*A*	31.02	16.89	8.73	1.063803447	2.014550656	-0.950747209	4	Yes	Yes	No	No	No	No
Smed-fer3l-2 (fer3l-2)	Q923Z4	FER3L_MOUSE	3.00E-26	*A*	5.67	16.56	7.59	-0.574771203	0.096606434	-0.671377637	6	Yes	No	No	No	No	Yes
Smed-fer3l-3 (fer3l-3)	Q9VGJ5	FER3_DROME	1.00E-23	*A*	0.08	0.6	11.46	-5.399585334	-1.725750651	-3.673834683	5	No	No	No	No	No	Yes
Smed-hairy and enhancer of split like-1 (hesl-1)	Q00P32	HES2_XENLA	2.00E-07	*E*	3.81	0	0.09	NA	NA	NA	NA	Yes	Yes	No	No	No	Yes
Smed-hairy and enhancer of split like-2 (hesl-2)	Q03062	HES5_RAT	4.00E-15	*E*	4.51	0.92	0.96	3.274606934	2.844104957	0.430501977	2	Yes	No	No	No	No	Yes
Smed-hairy and enhancer of split like-3 (hesl-3)	Q7KM13	HEY_DROME	3.00E-30	*E*	11.96	0.78	0.18	4.684890904	3.447034004	1.237856899	2	Yes	Yes	No	No	No	Yes
Smed-helix-loop-helix 1 (hlh1)	Q02576	HEN1_MOUSE	4.00E-25	*A*	NA	NA	NA	NA	NA	NA	NA	Yes	Yes	No	No	No	Yes
Smed-inhibitor of DNA binding 4 (id4)	P47928	ID4_HUMAN	7.00E-13	*D*	7.7	8.45	17.52	0.102628274	-1.151843339	1.254471613	3	Yes	Yes	No	No	No	Yes
Smed-max-interactor-1 (mxi-1)	P50538	MAD1_MOUSE	6.00E-07	*B*	14.78	31.8	35.8	-0.057960799	-0.965995962	0.908035162	3	Yes	Yes	Yes	Yes	No	Yes
Smed-max-interactor-2 (mxi-2)	P50541	MXI1_DANRE	2.00E-06	*B*	5.62	13.45	48.55	-1.57110712	-0.895675653	-0.675431468	5	Yes	Yes	Yes	Yes	No	Yes
Smed-max-like protein x (mlx)	Q9UH92	MLX_HUMAN	4.00E-33	*B*	100.4	142.72	48.91	1.290308875	0.461109763	0.829199113	1	Yes	Yes	Yes	Yes	No	Yes
Smed-microphthalmia-associated transcription factor like-1 (mitfl-1)	Q08874	MITF_MOUSE	5.00E-12	*B*	1.21	2.12	17.32	-3.793499542	-1.403822556	-2.389676985	5	No	No	No	No	No	No
Smed-microphthalmia-associated transcription factor like-2 (mitfl-2)	Q6XBT4	USF1_BOVIN	1.00E-09	*B*	19.43	37.69	19.44	0.77606873	0.36519556	0.41087317	1	Yes	Yes	No	No	No	Yes
Smed-microphthalmia-associated transcription factor like-3 (mitfl-3)	P19484	TFEB_HUMAN	7.00E-08	*B*	21.67	8.28	10.94	1.528466439	1.822857224	-0.294390785	2	Yes	Yes	No	No	No	Yes
Smed-mlx interacting protein-like (mlxipl)	Q99MZ3	MLXPL_MOUSE	5.00E-27	*B*	9.43	19.65	15.04	-0.15075684	-0.033276976	-0.117479864	6	Yes	Yes	No	No	No	Yes
Smed-musculin	A8E5T6	TCF21_XENTR	1.00E-20	*A*	5.1	0.63	0.59	NA	NA	NA	NA	Yes	Yes	No	No	No	Yes
Smed-MYC assciated factor X (max)	P52164	MAX_RAT	2.00E-16	*B*	71.58	160.14	56.55	1.136004411	-0.171197368	1.30720178	1	Yes	Yes	Yes	Yes	Yes	Yes
Smed-myogenic differentiation (myoD)	Q91154	MYF5_NOTVI	2.00E-39	*A*	12.6	11.04	14.73	1.187144093	1.071515453	0.11562864	2	Yes	No	No	No	No	Yes
Smed-neurogenic differentiation-1 (neuroD-1)	Q6NYU3	NDF6A_DANRE	9.00E-41	*A*	12.21	2.97	0.83	3.693436013	2.125430512	1.568005501	1	Yes	Yes	No	No	No	Yes
Smed-neurogenic differentiation-2 (neuroD-2)	Q9HD90	NDF4_HUMAN	4.00E-11	*A*	2.64	1.22	2.03	-0.422627981	-1.837809158	1.415181178	3	NA	NA	NA	NA	NA	NA
Smed-oligodendrocyte lineage transcription factor (olig)	Q90XB3	OLIG2_CHICK	2.00E-30	*A*	8.2	0.38	0.22	NA	NA	NA	NA	Yes	No	No	No	No	Yes
Smed-pancreas specific transcription factor-1 (ptf-1)	Q7RTS3	PTF1A_HUMAN	7.00E-26	*A*	2.5	0.22	2.2	NA	NA	NA	NA	Yes	No	No	No	No	Yes
Smed-pancreas specific transcription factor-2 (ptf-2)	Q4ZHW1	PTF1A_XENLA	9.00E-33	*A*	0.21	0.39	2	NA	NA	NA	NA	No	No	No	No	No	Yes
Smed-pancreas specific transcription factor-3 (ptf-3)	Q20561	HLH13_CAEEL	8.00E-24	*A*	0.26	0	2.46	NA	NA	NA	NA	Yes	No	No	No	No	Yes
Smed-pancreas specific transcription factor-4 (ptf-4)	Q4ZHW1	PTF1A_XENLA	3.00E-33	*A*	0.82	6.1	20.36	-2.246339074	-3.884949246	1.638610172	3	Yes	No	No	No	No	Yes
Smed-pancreas specific transcription factor-5 (ptf-5)	Q8AW52	ATOH7_DANRE	2.00E-12	*A*	0.18	3.23	11.07	-1.764733957	-2.389883365	0.625149408	3	No	No	Yes	Yes	No	Yes
Smed-single minded (sim)	A2T6X9	SIM1_PANTR	6.00E-161	*C*	14.74	6.15	2.52	4.884660416	2.869195938	2.015464478	1	Yes	Yes	Yes	No	No	Yes
Smed-sterol regulatory element binding transcription factor (srebp)	A3KNA7	SRBP2_DANRE	3.00E-15	*B*	17.13	46.46	28.97	0.46831113	-0.298806385	0.767117515	3	Yes	Yes	Yes	No	No	Yes
Smed-T-cell acute lymphocytic leukemia (tal)	P17542	TAL1_HUMAN	9.00E-17	*A*	0.23	3.69	6.45	-4.330872584	-5.062034039	0.731161455	3	No	No	No	No	No	Yes
Smed-transcription factor 15 (tcf15)	P79782	TCF15_CHICK	3.00E-23	*A*	59.67	20.65	14.63	1.723522574	0.927041018	0.796481556	1	Yes	No	Yes	No	No	Yes
Smed-twist	Q9D030	TWST2_MOUSE	1.00E-32	*A*	2.31	1.74	0.25	4.980875731	1.462910913	3.517964818	1	No	No	Yes	No	No	Yes
Smed-upstream transcription factor (usf)	Q15853	USF2_HUMAN	1.00E-09	*B*	32.3	32.87	30.57	1.168698426	0.706880908	0.461817517	1	Yes	Yes	No	No	No	Yes

A = 24
B = 12
C = 3
D = 1
E = 3
F = 1

* Labbe et al. 2012

\# Onal et al. 2012

35/43 in Stem Cells
25/43 in CNS
33/43 in Stem Cells or CNS
23/43 in Stem Cells and CNS
NA: Unable to detect by WISH

Table S2. Accession numbers and oligonucleotide sequences to clones used in this study.

bHLH Clones

Gene Name	Accession Number	Forward Primer	Reverse Primer
Smed-achaete scute like-1 (ascl-1)	DN307058	NA	NA
Smed-achaete scute like-2 (ascl-2)	KF487091	CCGCTCGAGTGGGTTGCTTATCCAGAAATG	ATAAGAATGCGGCCGCGACTCGTCGATATCTTGTTCTTT
Smed-activating enhancer binding protein-like-4-1 (ap4-1)	DN305431	NA	NA
Smed-activating enhancer binding protein-like-4-2 (ap4-2)	HO007476	NA	NA
Smed-aryl hydrocarbon receptor (ahr)	KF487107	CATTACCATCCCGCCCGACACAGGAATCAACTG	
Smed-aryl hydrocarbon receptor nuclear translocator (arnt)	KF487108	CATTACCATCCCGCCGATAGAGACCAAGAGCAAATAG	
Smed-atonal homolog (atoh)	Sequence Below	CCGCTCGAGAAACAACCAGCCGACTCAAC	ATAAGAATGCGGCCGCCGTTTGAGCCATTAATAGAGTTTC
Smed-atonal homolog 8-1 (atoh8-1)	DN306140	NA	NA
Smed-atonal homolog 8-2 (atoh8-2)	HO006843	NA	NA
Smed-basic helix-loop-helix family, member e22/23-like (e22/23)	KF487092	CCGCTCGAGAGACTGTTGCGGCTCGAC	ATAAGAATGCGGCCGCTGCGACATAAAATACAAATTGC
Smed-collier (coe)	KF487109	CATTACCATCCCGCGTTTTGAACCATGCTTCG	
Smed-daughterless (da)	KF487093	CCGCTCGAGCGAAGAGCAGACAACAGCAC	ATAAGAATGCGGCCGCTTTTACCAACACCCGATTGC
Smed-fer3l-1 (fer3l-1)	KF487094	CCGCTCGAGTTAAGTCAAATCAGGAACCTC	ATAAGAATGCGGCCGCTGCCGTTCAAAAGTTCAGTC
Smed-fer3l-2 (fer3l-2)	KF487095	CCGCTCGAGATTCGACTGAAATGACTGAAATC	ATAAGAATGCGGCCGCCAACCGCAATGTTTCAATTC
Smed-fer3l-3 (fer3l-3)	KF487096	CCGCTCGAGAGAAACCCCAGCCATTTTTC	ATAAGAATGCGGCCGCAATTTGTCGATCATTTTTCAGG
Smed-hairy and enhancer of split like-1 (hesl-1)	KF487110	CATTACCATCCCGGAAATGGAAAGACGACGAAGGGCG	
Smed-hairy and enhancer of split like-2 (hesl-2)	KF487111	CATTACCATCCCGTCGCCGACAGAGAATAAATTTCGC	
Smed-hairy and enhancer of split like-3 (hesl-3)	KF487112	CATTACCATCCCGCTTGAGCCAGATCAATATCACAGC	
Smed-helix-loop-helix 1 (hlh1)	KF487113	CATTACCATCCCGGATGAATCGTGGTCGAAATTGAGC	
Smed-inhibitor of DNA binding 4 (id4)	KF487114	CATTACCATCCCGAAACTCGTTCCAACGATTCC	
Smed-max-interactor-1 (mxi-1)	KF487115	CATTACCATCCCGAGATTCCGTACCCTGTCGAATTAC	
Smed-max-interactor-2 (mxi-2)	KF487116	CATTACCATCCCGACCCTGGAAGGATCAGAATTGGAC	
Smed-max-like protein x (mlx)	HO006087	NA	NA
Smed-microphthalmia-associated transcription factor like-1 (mitfl-1)	KF487117	CATTACCATCCCGCGCACTCGAAAGCAATTATC	
Smed-microphthalmia-associated transcription factor like-2 (mitfl-2)	KF487118	CATTACCATCCCGTGAAGTCTCGCACAAATGCTCAAC	
Smed-microphthalmia-associated transcription factor like-3 (mitfl-3)	KF487119	CATTACCATCCCGTAAAACGACGACGATCACACAGTC	
Smed-mlx interacting protein-like (mlxipl)	KF487097	CCGCTCGAGAGTTTCGGGACAGTCGTTC	ATAAGAATGCGGCCGCACGGGTTTATTTGTTGCTG
Smed-musculin	KF487098	CCGCTCGAGAAACGTCGTGGTCGTAAACC	ATAAGAATGCGGCCGCCCTCCAGGAACTAATTGACATCG
Smed-MYC asscciated factor X (max)	DN308448	NA	NA
Smed-myogenic differentiation (myoD)	KF487099	CCGCTCGAGTTTCCAGGTTCCACTTGTCC	ATAAGAATGCGGCCGCTCCTAGTCGTCGGGAGTTTG
Smed-neurogenic differentiation-1 (neuroD-1)	DN305764	NA	NA
Smed-neurogenic differentiation-2 (neuroD-2)	KF487120	CATTACCATCCCGGATTTAGGGAAACTCATTGC	
Smed-oligodendrocyte lineage transcription factor 2 (olig2)	KF487100	CCGCTCGAGACCTGAATTCGGCATTGGAC	ATAAGAATGCGGCCGCCCAATAGGAAACTCTTTCAAG
Smed-pancreas specific transcription factor-1 (ptf-1)	KF487101	CCGCTCGAGAGCCGCAAACATGAGAGAAC	ATAAGAATGCGGCCGCGCCAAAGAATAAGGCAGATGG
Smed-pancreas specific transcription factor-2 (ptf-2)	KF487102	CCGCTCGAGCTGATGGAGCCTTTCGGATT	ATAAGAATGCGGCCGCTCATTCCTTTCAACAACACGA
Smed-pancreas specific transcription factor-3 (ptf-3)	KF487103	CCGCTCGAGCGTTTACTTATCAAAATCCTTCTACG	ATAAGAATGCGGCCGCAATGCTGTCGTTGGGTTCAC
Smed-pancreas specific transcription factor-4 (ptf-4)	KF487104	CCGCTCGAGCACTTGCGATTCGTCATAACAG	ATAAGAATGCGGCCGCTCGGTTCCCTGATATTCCTC
Smed-pancreas specific transcription factor-5 (ptf-5)	DN303577	NA	NA
Smed-single minded (sim)	KF487121	CATTACCATCCCGGCGTCTATTATTCGACTGACATCG	
Smed-sterol regulatory element binding transcription factor (srebp)	KF487122	CATTACCATCCCGAAATTCCCCACCCAATGAAC	
Smed-T-cell acute lymphocytic leukemia (tal)	KF487105	CCGCTCGAGTTGTAGGAAACCAATCTCAACG	ATAAGAATGCGGCCGCTTCAAGATTTCTTCCAGAATCC
Smed-transcription factor 15 (tcf15)	AFD29618	NA	NA
Smed-twist	KF487106	CCGCTCGAGCAAGAAAGAACAGAATCATATTTGG	ATAAGAATGCGGCCGCCCCAAGCTCCTTCCATTCTC
Smed-upstream transcription factor (usf)	KF487123	CATTACCATCCCGTGTTTCGATTTGTTCCCGTG	

Other Clones

Gene Name	Accession Number
Smed-agat-1	DN290976
Smed-ChAT	FG310880
Smed-cpp-1	BK007012
Smed-gpas	HQ121519
Smed-h2b	DN298006
Smed-npp-4	BK007037
Smed-npy-2	BK007019
Smedwi-1	DN309285
NB.32.1g	DN298711
Smed-pc2	BK007043

qPCR Primers

Target	Forward Primer	Reverse Primer
Smed-β-tubulin	TGGCTGCTTGTGATCCAAGA	AAATTGCCGCAACAGTCAAATA
Smed-ascl-1	TCTCAATACCCCTTCAATCATG	TGCAGTCGTAACCCGATTTC
Smed-ascl-2	TTTCAATTACCCAGTTCCCTTTC	CGTTCTCTTTCATTGCGTCTC
Smed-coe	CTGCAACGCTGGATCAACTA	TGGCTGATTGCTTCTTCCTT
Smed-e22/23	CGTATGCTCACAGTCCATCG	ATATCCTCGGGACTGGAACC
Smed-hesl-3	CAAAACCAGCCGATTCATTATC	TCGCAATGTTTGTCGGATAC
Smed-neuroD-1	CTCTAATCAAACCGGGCAAG	ATGGAAATGGACCTTGGATG
Smed-sim	AGTCGAATTAACCGGCAATAG	GCTTGGTACTGGTGATGGTAAG

>Smed-atonal homolog (atoh)

AAACAACCAGCCGACTCAACTTACCAAATCGAATCCTATCAAACGGACCGCAGCCAACGACAGAGAACGAAAACGAATGTATTGTTTGAACCGAGCCTTTGACCAACTGAGAGATGTCGTTCCTTACTCTTCT
AATCAAAAGAAAATGTCAAAGTTTGAAACTCTATTAATGGCTCAAACG