Identification of Wnt pathway target genes regulating the division and differentiation of larval seam cells and vulval precursor cells in *C. elegans*

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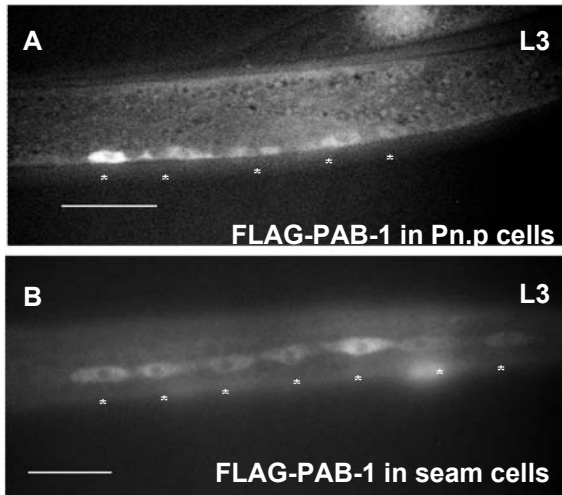1000 Hilltop Circle, Baltimore, MD, 21250

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A L3

FLAG-PAB-1 in Pn.p cells

B L3

FLAG-PAB-1 in seam cells

Figure S1   mRNA tagging method requires FLAG-PAB-1 expression in seam cells and VPCs

FLAG-PAB-1 expressed in the L2/L3 worms can be seen in the VPCs (A) and seam cells (B) of the experimental strain *deIs10; scm::gfp* by antibody staining against the FLAG epitope. The asterisks mark the stained cells. Scale bars represent 50μm.
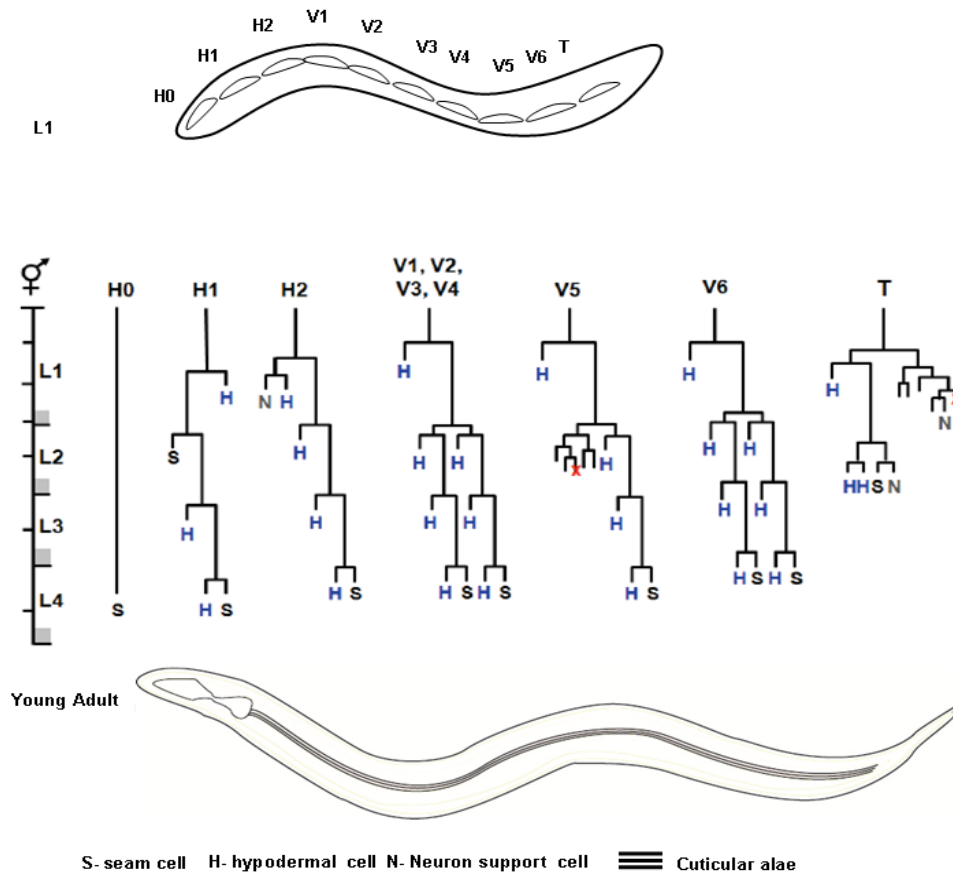
Figure S2 Lineage of larval seam cells

An L1 worm has 10 seam cells. At L2, six seam cells undergo a proliferative division to increase the number of seam cells to 16. In each larval stage, most seam cells divide asymmetrically to maintain their population as well as contribute to the hypodermal syncytium and to other neuronal support structures. After their final division, seam cells differentiate and undergo homotypic fusion to form a single-celled syncytium which secretes a specialized cuticular structure called alae.

Table S1   239 putative Wnt targets from seam cells and VPCs. Shown are 239 putative Wnt targets identified by microarray analysis: the average fold change and p value in Wnt pathway over-activation conditions is shown for each gene. '*' indicates 24 genes previously known to be expressed in the seam cells (Wormbase release 220). '§' indicates 12 genes previously known to be expressed in the vulval cell lineage (Wormbase release 220) '#' indicates five genes shown to be expressed in seam cells, hypodermal cells and P cells by Jackson et al., 2014.

Gene WB ID	Gene Public Name	p-value Wnt over-activation	fold change Wnt Over-activation
WBGene00000615	col-38[#]	0.000	29.7
WBGene00000626	col-49[#]	0.000	23.5
WBGene00013754	fbxa-116	0.002	16.1
WBGene00006509	tag-164	0.000	14.6
WBGene00007381	C06C6.7	0.000	14.3
WBGene00018295	oac-29	0.002	14.2
WBGene00012046	T26E4.4[#]	0.003	13.3
WBGene00014079	ZK792.7	0.000	12.8
WBGene00022140	Y71G12A.4	0.008	12.1
WBGene00009898	dod-23	0.000	11.8
WBGene00013986	ZK512.7	0.001	11.2
WBGene00001068	dpy-6	0.004	10.7
WBGene00015765	C14C11.1	0.000	10.3
WBGene00022589	ZC317.6	0.000	10.3
WBGene00008211	C49F5.7	0.002	10.3
WBGene00016058	nspd-3	0.001	10.0
WBGene00012783	Y43C5A.3	0.001	10.0
WBGene00003763	nlp-25	0.017	10.0
WBGene00044630	bus-17	0.007	9.6
WBGene00017485	F15E6.4	0.001	9.4
WBGene00017488	dct-7	0.031	8.7
WBGene00016683	C45G9.12	0.004	8.5
WBGene00011226	R11.1	0.001	7.8
WBGene00011624	T08G5.3	0.004	7.8
WBGene00021379	Y37E11B.7	0.034	7.7
WBGene00012591	nspe-1	0.022	7.5
WBGene00015182	B0416.7	0.002	7.4
WBGene00001691	grd-2	0.004	6.9
WBGene00003862	old-1	0.004	6.7
WBGene00003863	old-2	0.004	6.7
WBGene00018380	F43C11.3	0.036	6.6
WBGene00021731	Y49G5A.1	0.000	6.3
WBGene00000647	col-71[#]	0.001	6.2
WBGene00020033	R12E2.7[§*]	0.012	6.2
WBGene00017759	F23H11.3	0.002	6.0
WBGene00008472	E03H4.4	0.000	6.0
WBGene00013514	Y73F4A.1	0.019	6.0

L. Gorrepati *et al.*

WBGene00018744	*F53B3.6*	0.008	5.9
WBGene00022024	*Y64H9A.2*	0.000	5.9
WBGene00009130	*F25H5.8*	0.012	5.8
WBGene00000656	*col-80*	0.007	5.8
WBGene00001079	*dpy-20*	0.002	5.6
WBGene00007297	*C04F12.1*	0.004	5.5
WBGene00050896	*ttr-56*	0.000	5.4
WBGene00010856	*M04C9.1*	0.001	5.4
WBGene00010743	*K10D6.3*	0.012	5.2
WBGene00001882	*his-8*	0.001	5.2
WBGene00001894	*his-20*	0.001	5.2
WBGene00001896	*his-22*	0.001	5.2
WBGene00001926	*his-52*	0.001	5.2
WBGene00011077	*R07B1.5*	0.007	5.2
WBGene00004394	*rol-1*	0.001	5.2
WBGene00021427	*Y38F2AR.9*	0.006	5.2
WBGene00015758	*nhr-155*	0.001	5.1
WBGene00000930	*dao-4*[#]	0.011	5.0
WBGene00018219	*F40A3.4*	0.003	5.0
WBGene00015865	*C16E9.1*	0.004	4.9
WBGene00016926	*nhr-171*	0.005	4.8
WBGene00011948	*T23F1.5*	0.000	4.8
WBGene00003664	*nhr-74**	0.004	4.8
WBGene00011814	*T16H12.4*	0.011	4.8
WBGene00045387	*K09H9.8*	0.004	4.7
WBGene00021994	*Y59E9AL.4*	0.005	4.7
WBGene00011533	*T06E4.5*	0.010	4.6
WBGene00020380	*T09B4.6*	0.006	4.5
WBGene00020769	*T24D8.6*	0.020	4.5
WBGene00021605	*Y46H3C.5*	0.013	4.5
WBGene00015172	*B0410.3*	0.001	4.5
WBGene00014003	*ZK593.3*	0.050	4.5
WBGene00011023	*R05A10.6*	0.014	4.5
WBGene00015769	*C14C11.7*	0.001	4.5
WBGene00013438	*ztf-29*	0.030	4.4
WBGene00003703	*nhr-113**	0.019	4.3
WBGene00015340	*C02E7.7*	0.000	4.3
WBGene00006534	*tba-8**	0.001	4.3
WBGene00012594	*nspe-5*	0.000	4.3
WBGene00004202	*pry-1*[§*]	0.018	4.2
WBGene00017436	*F13H8.3*	0.029	4.1
WBGene00020613	*T20D4.7*	0.036	4.1
WBGene00000493	*che-14*[§*]	0.037	4.1
WBGene00022816	*fbn-1*	0.027	4.1
WBGene00043147	*nspd-6*	0.004	4.1
WBGene00015339	*C02E7.6*	0.000	4.1
WBGene00009026	*F21G4.5*	0.008	4.0

WBGene00000406	cdk-4§*	0.007	3.9
WBGene00005672	sru-9	0.000	3.9
WBGene00011594	T07G12.3	0.033	3.9
WBGene00001885	his-11	0.005	3.9
WBGene00001889	his-15	0.005	3.9
WBGene00001918	his-44*	0.005	3.9
WBGene00019306	K02E7.1	0.043	3.9
WBGene00018416	retr-1	0.007	3.9
WBGene00009787	F46F2.3	0.018	3.8
WBGene00000516	cki-1§*	0.007	3.8
WBGene00015196	B0454.5	0.011	3.8
WBGene00000072	add-1*	0.009	3.7
WBGene00011033	R05D11.5	0.000	3.7
WBGene00017297	F09E10.7	0.002	3.7
WBGene00000653	col-77	0.001	3.7
WBGene00013661	Y105C5B.23	0.031	3.7
WBGene00001878	his-4	0.003	3.7
WBGene00002393	lpr-1	0.020	3.6
WBGene00017799	F25G6.8	0.015	3.6
WBGene00012324	rhy-1	0.029	3.6
WBGene00009590	ttr-4	0.012	3.6
WBGene00010538	ttr-3	0.012	3.6
WBGene00015051	B0218.7	0.000	3.6
WBGene00006367	sym-2	0.001	3.6
WBGene00003446	msp-53	0.002	3.5
WBGene00006539	tbb-6	0.000	3.5
WBGene00020873	T28A11.6	0.027	3.5
WBGene00011665	T09F5.1	0.010	3.5
WBGene00009160	F26E4.5	0.018	3.5
WBGene00000711	col-138	0.000	3.4
WBGene00011398	qdpr-1	0.021	3.4
WBGene00017783	F25E5.2	0.008	3.4
WBGene00021997	Y59E9AR.1	0.001	3.4
WBGene00022002	Y59E9AR.7	0.001	3.4
WBGene00021927	Y55F3AM.10	0.001	3.4
WBGene00016919	C54E4.4	0.025	3.4
WBGene00015442	C04F1.1	0.050	3.4
WBGene00016641	C44C1.1	0.014	3.3
WBGene00007770	nhr-259	0.038	3.3
WBGene00018689	F52D2.7	0.001	3.3
WBGene00015987	C18G1.9	0.001	3.3
WBGene00012323	oac-54	0.032	3.3
WBGene00018702	F52E4.5	0.002	3.2
WBGene00001984	hog-1	0.018	3.1
WBGene00019234	ugt-8	0.011	3.1

WBGene00000596	*col-7**	**0.010**	**3.1**
WBGene00000638	*col-62*	**0.010**	**3.1**
WBGene00003102	*mab-5§**	**0.013**	**3.1**
WBGene00008290	*C54C8.2**	**0.033**	**3.1**
WBGene00020216	*trap-2*	**0.031**	**3.1**
WBGene00020445	*T12B3.2*	**0.008**	**3.1**
WBGene00015950	*C18A11.4*	**0.000**	**3.1**
WBGene00010225	*ttr-31*	**0.025**	**3.0**
WBGene00010800	*srsx-37*	**0.009**	**3.0**
WBGene00012055	*srsx-36*	**0.009**	**3.0**
WBGene00016192	*C28H8.1*	**0.002**	**3.0**
WBGene00000734	*col-161*	**0.008**	**3.0**
WBGene00000735	*col-162*	**0.008**	**3.0**
WBGene00001480	*fmo-5*	**0.015**	**3.0**
WBGene00014162	*ZK938.6*	**0.006**	**3.0**
WBGene00016294	*C31H2.4*	**0.008**	**2.9**
WBGene00044623	*bus-8**	**0.013**	**2.9**
WBGene00015453	*C04G6.2*	**0.007**	**2.9**
WBGene00077489	*C04G6.13*	**0.007**	**2.9**
WBGene00003444	*msp-51*	**0.026**	**2.9**
WBGene00003448	*msp-55*	**0.026**	**2.9**
WBGene00003450	*msp-57*	**0.026**	**2.9**
WBGene00011434	*T04D3.5*	**0.016**	**2.8**
WBGene00006660	*twk-5*	**0.015**	**2.8**
WBGene00000969	*dhs-5*	**0.013**	**2.8**
WBGene00001253	*elt-6§*	**0.011**	**2.8**
WBGene00021486	*lbp-9*	**0.001**	**2.8**
WBGene00010742	*K10D6.2*	**0.004**	**2.7**
WBGene00016449	*C35D10.13*	**0.002**	**2.7**
WBGene00003622	*nhr-23*	**0.002**	**2.7**
WBGene00000720	*col-147*	**0.050**	**2.7**
WBGene00008435	*glna-2*	**0.022**	**2.6**
WBGene00016011	*C23G10.2*	**0.007**	**2.6**
WBGene00012165	*cutl-6*	**0.049**	**2.6**
WBGene00017348	*F10E7.6*	**0.036**	**2.6**
WBGene00009657	*F43G6.4*	**0.023**	**2.6**
WBGene00001692	*grd-3**	**0.008**	**2.5**
WBGene00012420	*Y7A9D.1*	**0.007**	**2.5**
WBGene00009489	*F36G9.13*	**0.001**	**2.5**
WBGene00009675	*F44A6.3*	**0.034**	**2.5**
WBGene00002070	*ile-1*	**0.004**	**2.5**
WBGene00000990	*dhs-27*	**0.016**	**2.5**
WBGene00016346	*fbxa-120*	**0.006**	**2.5**
WBGene00018252	*F40H3.6*	**0.003**	**2.5**
WBGene00012364	*W09D12.1*	**0.009**	**2.5**

WBGene00001703	*grd-14**	0.002	2.4
WBGene00010289	*F58H1.6*	0.015	2.4
WBGene00021845	*rpb-7*	0.000	2.4
WBGene00007592	*C14H10.2*	0.015	2.4
WBGene00012443	*Y15E3A.4*	0.010	2.3
WBGene00009807	*pepm-1*	0.004	2.3
WBGene00015593	*C08E3.1*	0.036	2.3
WBGene00015605	*C08E3.13*	0.036	2.3
WBGene00000601	*col-12*	0.028	2.3
WBGene00003611	*nhr-12*	0.015	2.3
WBGene00005025	*sqv-7*§*	0.007	2.2
WBGene00017082	*DC2.5*	0.004	2.2
WBGene00010051	*F54D5.5*	0.018	2.2
WBGene00011890	*T21C9.1*	0.005	2.2
WBGene00007925	*C34C12.6*	0.022	2.1
WBGene00006476	*rhgf-2*	0.009	2.1
WBGene00000532	*clh-5*	0.031	2.1
WBGene00000602	*col-13*	0.036	2.1
WBGene00019666	*sago-1*§*	0.024	2.1
WBGene00016929	*C54F6.12*	0.024	2.1
WBGene00019331	*dos-3*	0.008	2.1
WBGene00004272	*rab-8*	0.045	2.1
WBGene00044349	*Y71G12B.32*	0.000	2.1
WBGene00000729	*col-156*	0.027	2.1
WBGene00013981	*ZK507.6*	0.036	2.1
WBGene00010470	*cdr-4*	0.027	2.1
WBGene00013292	*Y57G11A.4*	0.017	2.0
WBGene00011561	*ttr-15*	0.009	2.0
WBGene00001073	*dpy-11*	0.026	2.0
WBGene00021789	*nol-6*	0.017	2.0
WBGene00010523	*K03B8.4*	0.040	2.0
WBGene00001971	*hmg-1.1*§*	0.022	2.0
WBGene00019826	*R02E4.1*	0.004	2.0
WBGene00002990	*lin-1*	0.038	1.9
WBGene00018488	*acs-1*	0.048	1.9
WBGene00004164	*pqn-83*	0.015	1.9
WBGene00004702	*rsp-5*	0.004	1.9
WBGene00002261	*ldb-1*	0.047	1.9
WBGene00006543	*tbx-2*	0.039	1.9
WBGene00008571	*F08B12.1*	0.040	1.9
WBGene00020109	*R151.6*	0.013	1.9
WBGene00012186	*mlt-11**	0.043	1.8
WBGene00020263	*T05E8.3*	0.010	1.8
WBGene00011731	*acbp-5*	0.037	1.8
WBGene00018341	*F42A10.5*	0.049	1.8

WBGene00000100	*ajm-1*§*	0.026	1.8
WBGene00000730	*col-157*	0.023	1.8
WBGene00000728	*col-155*	0.030	1.8
WBGene00004701	*rsp-4**	0.006	1.7
WBGene00000727	*col-154*	0.029	1.7
WBGene00022164	*Y71H2AL.1*	0.042	1.7
WBGene00014186	*nhr-244*	0.019	1.7
WBGene00002051	*ifa-3*	0.004	1.7
WBGene00019850	*srt-18*	0.019	1.7
WBGene00009381	*F34H10.4*	0.023	1.7
WBGene00019237	*H24G06.1*	0.021	1.7
WBGene00001928	*his-54*	0.042	1.7
WBGene00003911	*pak-1*	0.025	1.6
WBGene00010317	*idh-1*§*	0.044	1.6
WBGene00003891	*osm-11*§*	0.047	1.6
WBGene00015757	*C14C6.3*	0.009	1.6
WBGene00014098	*ZK836.2*	0.022	1.6
WBGene00011604	*T08A11.1*	0.029	1.5
WBGene00015181	*B0416.5*	0.003	1.5
WBGene00002196	*kin-10*	0.124	1.5

Table S2 24 putative Wnt target genes in common between Jackson et al., 2014 and this work. Of the 239 putative Wnt pathway regulated genes from seam cells and VPCs identified here by mRNA tagging, 24 genes were also identified by Jackson et al., 2014 in a non-tissue specific analysis of Wnt upregulated genes.

Gene WB ID	Gene
WBGene00000615	*col-38*
WBGene00000626	*col-49*
WBGene00000647	*col-71*
WBGene00000930	*dao-4*
WBGene00001984	*hog-1*
WBGene00004202	*pry-1*
WBGene00006509	*tag-164*
WBGene00006539	*tbb-6*
WBGene00008472	*E03H4.4*
WBGene00009898	*dod-23*
WBGene00010470	*cdr-4*
WBGene00011077	*R07B1.5*
WBGene00011594	*T07G12.3*
WBGene00011624	*T08G5.3*
WBGene00012046	*T26E4.4*
WBGene00012783	*Y43C5A.3*
WBGene00013754	*fbxa-116*
WBGene00015442	*C04F1.1*
WBGene00016058	*nspd-3*
WBGene00017485	*F15E6.4*
WBGene00018295	*oac-29*
WBGene00018416	*retr-1*
WBGene00019234	*ugt-8*
WBGene00043147	*nspd-6*

L. Gorrepati *et al.*

Table S3   Genes in common between van der Bent et al., 2014 and this work. Of the 239 putative Wnt pathway regulated genes from seam cells and VPCs identified here by mRNA tagging, 35 genes were also identified by van der Bent et al., 2014 as genes that were differentially expressed between a wild type strain and a strain carrying a loss-of-function mutation in *bar-1*. The third column indicates whether expression of the gene was decreased or increased in the *bar-1(ga80)* strain relative to wild type. Genes with an asterisk (*) were identified as downregulated upon loss of *bar-1* in van der Bent et al. 2014 and upregulated upon expression of an activated BAR-1 protein in this work and in Jackson et al . 2014.

Gene WB ID	Gene	*bar-1(ga80)* expression
WBGene00000493	*che-14*	decreased
WBGene00000615	*col-38**	decreased
WBGene00000626	*col-49**	decreased
WBGene00000647	*col-71**	decreased
WBGene00000711	*col-138**	decreased
WBGene00000735	*col-162*	decreased
WBGene00000930	*dao-4**	decreased
WBGene00001073	*dpy-11**	decreased
WBGene00001691	*grd-2**	decreased
WBGene00001885	*his-11*	decreased
WBGene00001984	*hog-1**	decreased
WBGene00002393	*lpr-1*	decreased
WBGene00004394	*rol-1*	decreased
WBGene00011077	*R07B1.5**	decreased
WBGene00011594	*T07G12.3**	decreased
WBGene00011665	*T09F5.1*	decreased
WBGene00012186	*mlt-11*	decreased
WBGene00013514	*Y73F4A.1*	decreased
WBGene00015172	*B0410.3*	decreased
WBGene00015442	*C04F1.1**	decreased
WBGene00015453	*C04G6.2*	decreased
WBGene00015950	*C18A11.4**	decreased
WBGene00017783	*F25E5.2**	decreased
WBGene00022024	*Y64H9A.2*	decreased
WBGene00077489	*C04G6.13*	decreased
WBGene00000720	*col-147*	increased
WBGene00006539	*tbb-6*	Increased
WBGene00007297	*C04F12.1*	Increased
WBGene00010051	*F54D5.5*	Increased
WBGene00011434	*T04D3.5*	Increased
WBGene00011561	*ttr-15*	Increased
WBGene00012783	*Y43C5A.3*	Increased
WBGene00015865	*C16E9.1*	Increased
WBGene00016919	*C54E4.4*	Increased
WBGene00021379	*Y37E11B.7*	increased

Table S4   DAVID analysis identifies four functionally related groups among cell type specific Wnt targets. DAVID analysis of the seam cell/VPC Wnt regulated genes identified four functionally related gene groups. The microarray fold change in the Wnt over-activation condition for each gene is indicated. The enrichment score for each gene group is indicated in parenthesis (column 2). The enrichment score is the geometric mean of the modified Fisher's exact p-value (EASE score) of each gene in a given gene group. A higher enrichment score indicates a higher rank in functional importance (Huang et al. 2009a, 2009b). Of these 57 genes grouped by DAVID, seven genes are expressed in seam (indicated by '#', column 2), two genes in the vulva (indicated by 'Δ') and five in the seam and vulva (indicated by '§') (Wormbase release 220). '*' indicates genes in this list that were characterized further in this work.

Gene	Gene description	fold change Wnt over-activation
Gene group 1	*Structural constituents of cuticle (enrichment score 7.3)*	
che-14*	abnormal CHEmotaxis§	4.1
col-7	COLlagen#	3.1
col-12	COLlagen	2.3
col-13	COLlagen	2.1
col-38	COLlagen	29.7
col-49*	COLlagen	23.5
col-62	COLlagen	3.1
col-71	COLlagen	6.2
col-77	COLlagen	3.7
col-80	COLlagen	5.8
col-138	COLlagen	3.4
col-147	COLlagen	2.7
col-154	COLlagen	1.7
col-155	COLlagen	1.8
col-156	COLlagen	2.1
col-157	COLlagen	1.8
col-161	COLlagen	3.0
col-162	COLlagen	3.0
pqn-83	Prion-like-(Q/N-rich)-domain protein	1.9
rol-1	ROLler/collagen	5.2
F54D5.5	F54D5.5	2.2
K03B8.4	K03B8.4	2.0
T04D3.5	T04D3.5	2.8
T06E4.5	T06E4.5	4.6
C44C1.1	C44C1.1	3.3
Gene group 2	*Transcription factors (enrichment score 0.64)*	
dpy-20	DumPY	5.6
elt-6*	Erythroid-Like Transcription factor family§	2.8
nhr-12	Nuclear Hormone Receptor family	2.3
nhr-23*	Nuclear Hormone Receptor family#	2.7
nhr-74*	Nuclear Hormone Receptor family#	4.8

L. Gorrepati *et al.*

*nhr-113**	**Nuclear Hormone Receptor family#**	**4.3**
nhr-259	**Nuclear Hormone Receptor family**	**3.3**
F21G4.5	**F21G4.5**	**4.0**
T16H12.4	**General transcription factor IIH subunit 2**	**4.8**
ztf-29	**Y66D12A.12**	**4.4**
nhr-244	**Nuclear Hormone Receptor family**	**1.7**
nhr-155	**Nuclear Hormone Receptor family**	**5.1**
nhr-171	**Nuclear Hormone Receptor family**	**4.8**
Gene group 3	*Signaling proteins (enrichment score 0.21)*	
ajm-1	**Apical Junction Molecule§**	**1.8**
dpy-6	**DumPY : shorter than wild-type**	**3.8**
*grd-3**	**GRounDhog (hedgehog-like family)#**	**2.5**
*grd-14**	**GRounDhog (hedgehog-like family)#**	**2.4**
*hog-1**	**HOG only (Hedgehog Hog domain alone)**	**3.1**
*ldb-1**	**LIM domain Binding Protein△**	**1.9**
*osm-11**	**OSMotic avoidance abnormal§**	**1.6**
F54D5.5	**F54D5.5**	**2.2**
cdr-4	**CaDmium Responsive**	**2.1**
T08A11.1	**T08A11.1**	**1.5**
B0416.5	**Uncharacterized protein**	**1.5**
C35D10.13	**C35D10.13**	**2.7**
C44C1.1	**C44C1.1**	**3.3**
F10E7.6	**F10E7.6**	**2.6**
*Y71H2AL.1**	**Y71H2AL.1**	**1.7**
*bus-8**	**Bacterially Un-Swollen (M. nematophilum resistant)#**	**2.9**
Gene group 4	*Kinases (enrichment score 0.21)*	
*cdk-4**	**Cyclin-Dependent Kinase family§**	**3.9**
old-1	**Overexpression Longevity Determinant**	**6.7**
*old-2**	**Overexpression Longevity Determinant**	**6.7**
*pak-1**	**P21-Activated Kinase family△**	**1.6**
*F26E4.5**	**F26E4.5**	**3.5**

Table S5   27 seam cell/VPC Wnt regulated genes validated by qPCR. 105 genes (~44%) of 239 putative Wnt target genes were tested by qRT-PCR to validate the directional change observed by microarray, and 27 (26%) genes passed the verification screen (were upregulated ≥1.5 fold in response to Wnt pathway over-activation). Twelve genes (shown in the bottom half of the table) were also downregulated ≥ 1.5 fold in response to Wnt pathway under-activation. *gpd-2* was the reference gene. Biological triplicates of control (*deIs10*) and experimental samples (*deIs10; huIs1* and *deIs10; deIs26*) were analyzed.

Gene WB ID	Gene	fold change Wnt over-activation	fold change Wnt under-activation
WBGene00000626	*col-49*	947.5	1.3
WBGene00012046	*T26E4.4*	190.1	1.6
WBGene00010743	*K10D6.3*	151.0	0.9
WBGene00021997	*Y59E9AR.1*	6.8	1.2
WBGene00010538	*ttr-3*	5.7	1.2
WBGene00000516	*cki-1*	4.5	1.2
WBGene00009590	*ttr-4*	4.5	1.0
WBGene00015769	*C14C11.7*	4.1	1.2
WBGene00010856	*M04C9.1*	3.0	0.8
WBGene00015605	*C08E3.13*	2.8	0.8
WBGene00003102	*mab-5*	2.0	0.9
WBGene00021379	*Y37E11B.7*	1.9	1.1
WBGene00002990	*lin-1*	1.6	0.6
WBGene00021927	*Y55F3AM.10*	1.6	1.1
WBGene00003763	*nlp-25*	1.5	0.7
WBGene00011561	*ttr-15*	1.5	0.8
WBGene00009807	*pepm-1*	10.4	0.3
WBGene00004202	*pry-1*	4.1	0.1
WBGene00008435	*glna-2*	3.8	0.5
WBGene00000072	*add-1*	2.2	0.1
WBGene00001692	*grd-3*	1.8	0.1
WBGene00006660	*twk-5*	1.7	0.5
WBGene00012783	*Y43C5A.3*	1.7	0.4
WBGene00015196	*B0454.5*	1.6	0.2
WBGene00000406	*cdk-4*	1.6	0.4
WBGene00012591	*nspe-1*	1.6	0.3
WBGene00005025	*sqv-7*	1.5	0.5

Table S6 Reduction of function for molting genes *mlt-7* and *mlt-11* causes a reduction in terminal seam cell number. Strains carrying the indicated seam cell marker were grown on bacteria expressing double stranded RNA for each indicated gene and the number of GFP-expressing seam cells per side was scored in young adults. Either larva were grown on bacteria and their F1 progeny were scored as adults ('P0' feeding) or newly hatched L1 larvae were grown on bacteria and the same animals were scored as adults ('L1' feeding). *rrf-3(lf)* renders animals hypersensitive to RNAi. The number of animals scored, average number of seam cells per side, and range of seam cells is indicated.

RNAi	Strain	Method	N	Seam cells number	Seam cells range	P value
vector	*rrf-3(lf); grd-10p::GFP*	P0	30	15.9	15-16	
acn-1	*rrf-3(lf); grd-10p::GFP*	P0	60	14.3	12-19	NS
bli-5	*rrf-3(lf); grd-10p::GFP*	P0	30	14.7	13-16	<.005
fbn-1	*rrf-3(lf); grd-10p::GFP*	P0	30	15.2	14-16	NS
mam-1	*rrf-3(lf); grd-10p::GFP*	P0	30	14.9	13-16	NS
mlt-8	*rrf-3(lf); grd-10p::GFP*	P0	30	14.5	12-17	<.005
mlt-9	*rrf-3(lf); grd-10p::GFP*	P0	30	13.5	11-16	<.001
mlt-10	*rrf-3(lf); grd-10p::GFP*	P0	30	15.4	14-16	NS
nas-36	*rrf-3(lf); grd-10p::GFP*	P0	30	17.1	16-29	<.005
nas-37	*rrf-3(lf); grd-10p::GFP*	P0	30	14.3	11-16	<.005
pan-1	*rrf-3(lf); grd-10p::GFP*	P0	30	13.8	13-16	<.001
ptr-23	*rrf-3(lf); grd-10p::GFP*	P0	30	15.4	13-16	NS
mlt-7	*rrf-3(lf); grd-10::GFP*	P0	90	10.9	3-16	<.001
mlt-7	*wrt-2p::GFP*	P0	90	12.8	8-16	<.001
mlt-7	*scm::GFP*	P0	60	12.3	9-15	<.001
mlt-11	*rrf-3(lf); grd-10p::GFP*	P0	60	10.5	7-13	<.001
mlt-11	*rrf-3(lf); grd-10p::GFP*	L1	60	10.1	6-14	<.001
mlt-11	*wrt-2p::GFP*	P0	60	11.6	8-16	<.001
mlt-11	*wrt-2p::GFP*	L1	90	12.3	8-17	<.001

Table S7   Oligonucleotide sequences

Available for download as an Excel file at www.g3journal.org/lookup/suppl/doi:10.1534/g3.115.017715/-/DC1

L. Gorrepati *et al.*