## SUPPLEMENTARY FIGURES

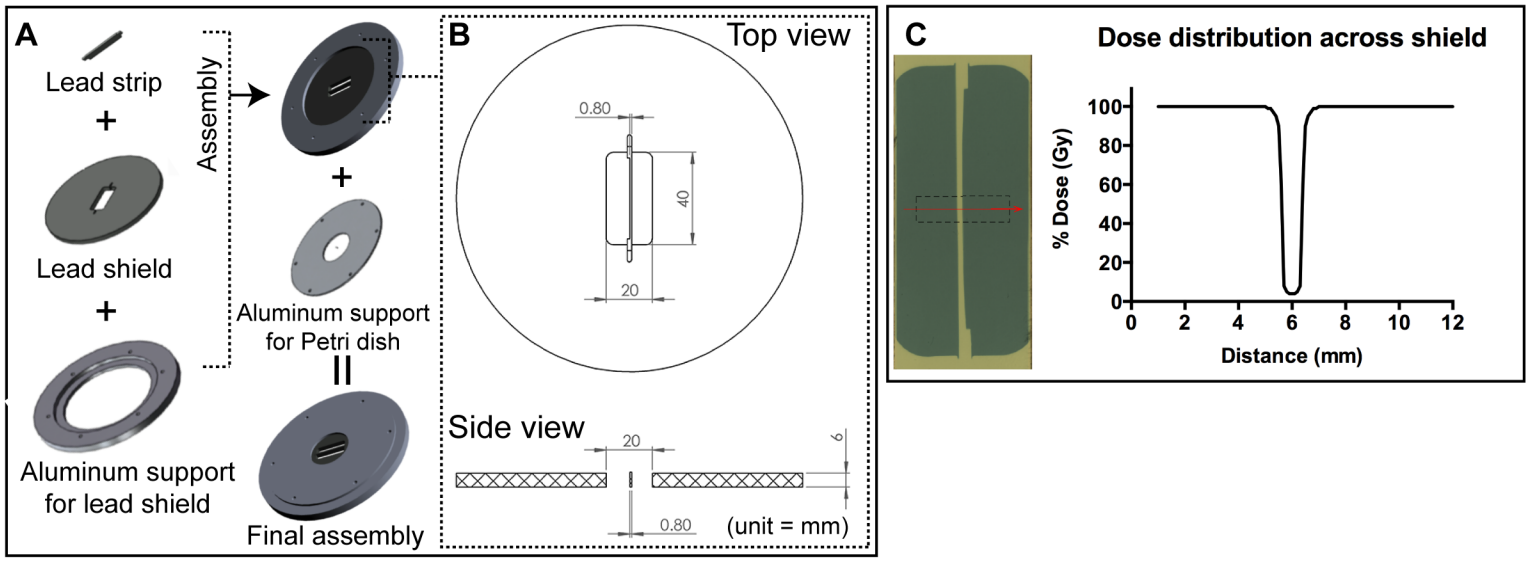
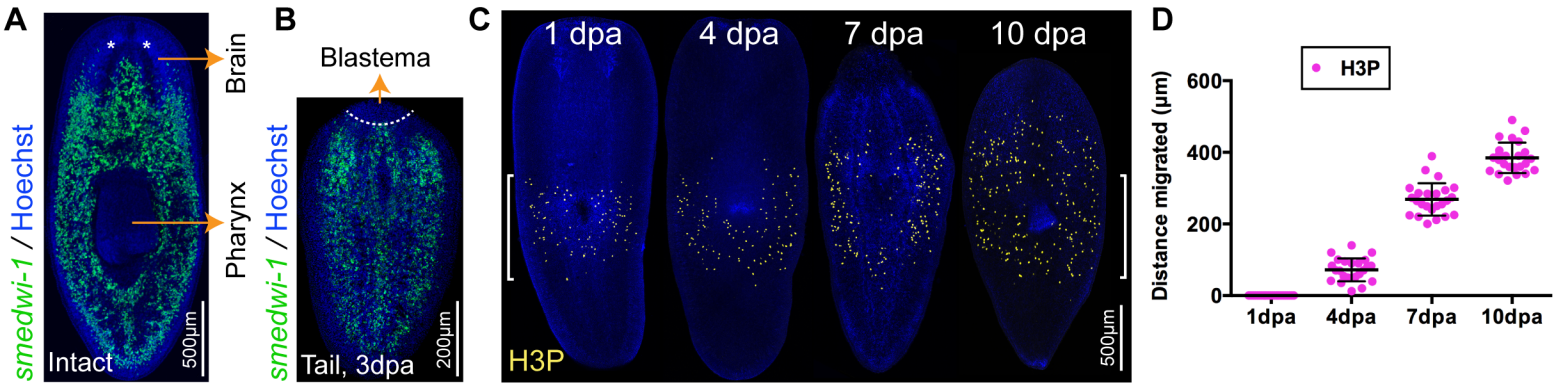


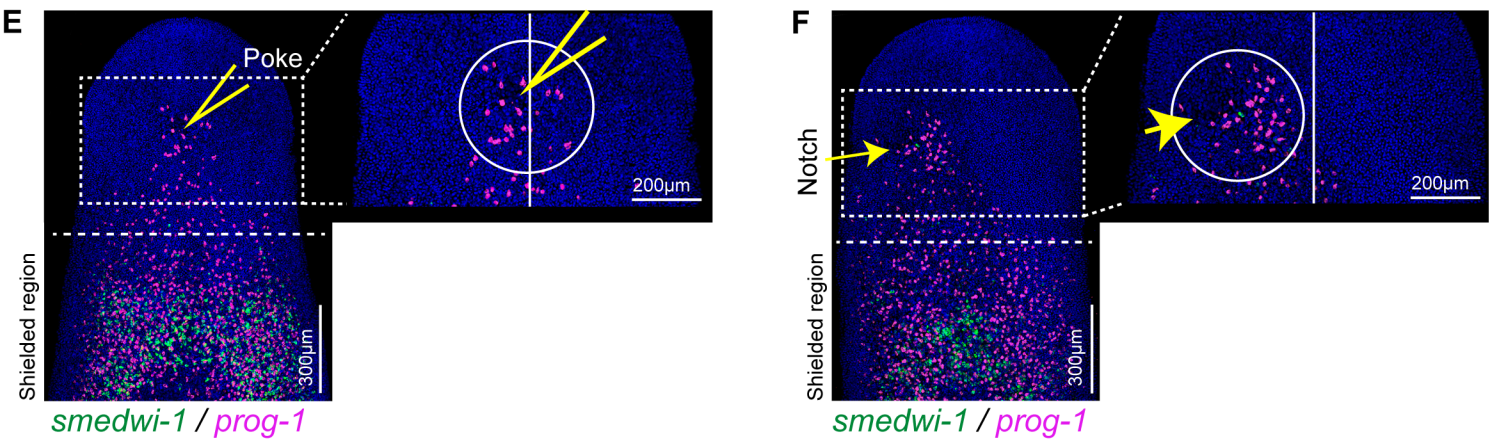

**Figure S1. Parts and dimensions of lead shield assembly**

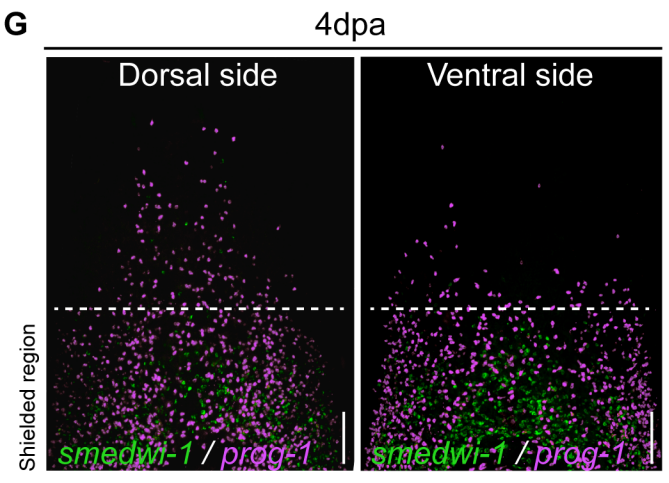
(A) Lead strip and lead shield are assembled with aluminium support which further covered with aluminium disc to support Petri dish in the final lead shield assembly.

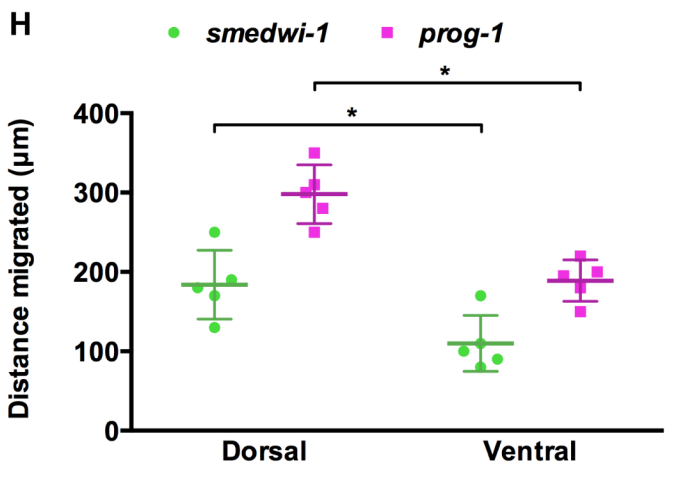
(B) Dimensions of lead shield and lead strip from top and side view. Unit: mm.

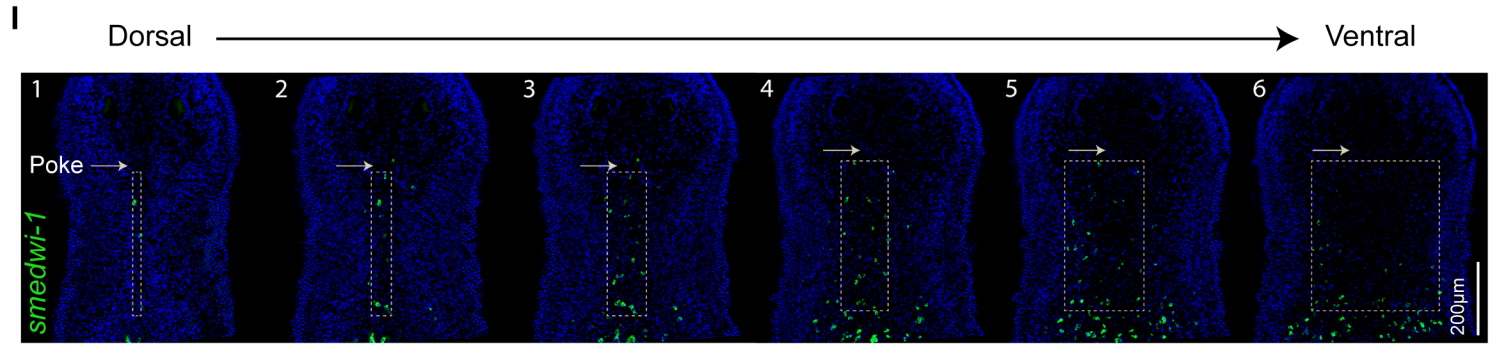
(C) Dose distribution across the lead strip showing greater than 95% attenuation of X-ray dose under the shield protected region.

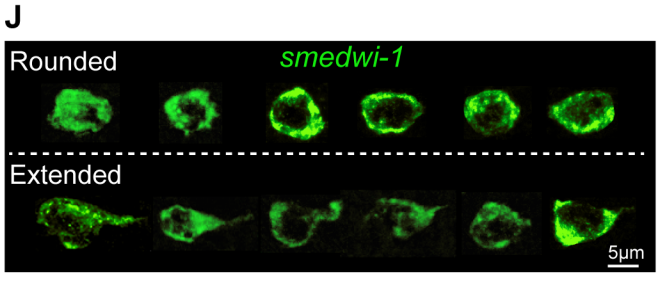


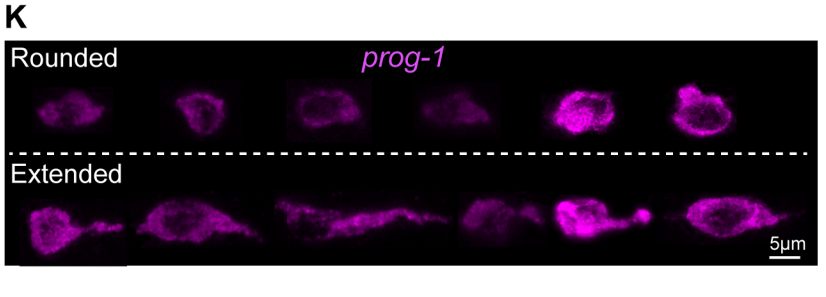



**Figure S2. General features of cell migration and different shapes of migrating and non-migrating cells**

(A) FISH showing distribution of stem cells (green) in intact wild type worm. Stem cells are absent in the pharynx region, in brain region and region anterior to photoreceptors (*). Scale bar: 500µm.

(B) FISH showing that stem cells (green) are absent in the early regenerative blastema in a tail fragment regenerating at 3dpa (n=5). Scale bar: 200µm.

(C) H3P immunostaining shows increase in mitotic cells (yellow) in the migratory region in decapitated animals over the time course, 1dpa, 4dpa, 7dpa and 10dpa (n=5 per time point). "[ ]" represent shielded area. Scale bar: 500µm.

(D) Graph showing increasing distance of mitotic cells (magenta dots) from the shielded region over the time course, 1dpa, 4dpa, 7dpa and 10dpa (n=5 per time point). Each dot represents the distance of individual H3P cell from the shielded region. 5 most distal H3P cells were considered for measurements from each animal. Lines and error bars indicate mean and SD.

(E, F) Stem cells (green) and early progeny (magenta) show directional migration towards the site of poking (E) and notch (F).

(G) Stem cells (green) and early progeny (magenta) from the dorsal side migrate more rapidly than the ventral side. Scale bar: 100µm.

(H) Measurements of distance migrated by stem cells (green) and early progeny (magenta) from dorsal and ventral side in decapitated animal at 4dpa. Each dot represents average the distance migrated by 10 most distal cells in an animal (n=5). Lines and error bars indicate mean and SD.

(I) Montage showing migrating stem cells (green) in different planes from dorsal to ventral side (1 to 6).

(J-K) Different morphology of stem cells (green) (J) and early progeny (magenta) (K) without and with extended processes.

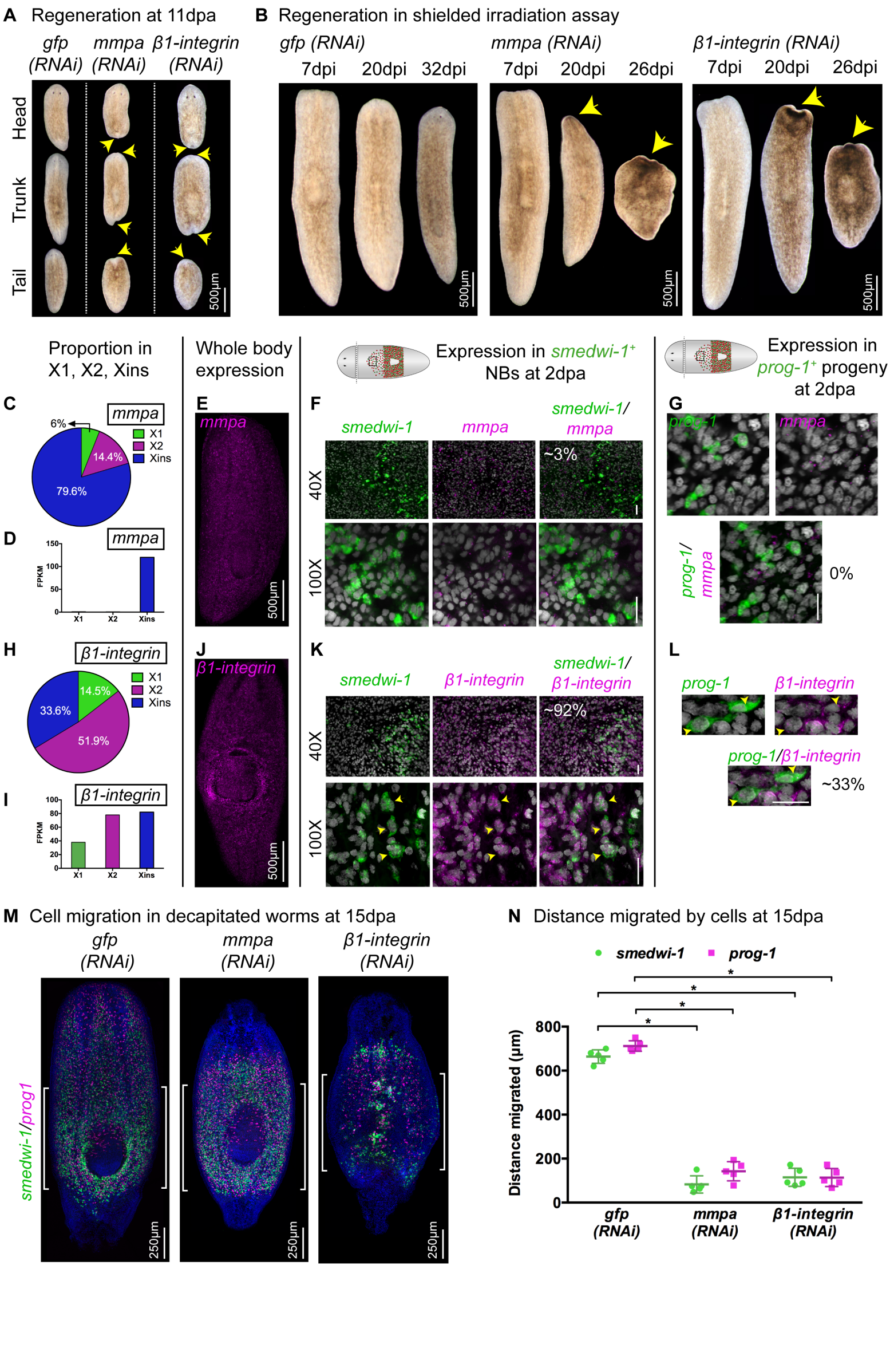

A Regeneration at 11dpa
gfp (RNAi)
mmpa (RNAi)
β1-integrin (RNAi)
Head
Trunk
Tail
500μm
B Regeneration in shielded irradiation assay
gfp (RNAi)
7dpi 20dpi 32dpi
mmpa (RNAi)
7dpi 20dpi 26dpi
β1-integrin (RNAi)
7dpi 20dpi 26dpi
Proportion in X1, X2, Xins
C
mmpa
6%
14.4%
79.6%
X1
X2
Xins
D
mmpa
FPKM
150
100
50
0
X1 X2 Xins
Whole body expression
E
mmpa
500μm
Expression in smedwi-1+ NBs at 2dpa
F
smedwi-1
mmpa
smedwi-1/ mmpa
~3%
40X
100X
Expression in prog-1+ progeny at 2dpa
G
prog-1
mmpa
prog-1/ mmpa
0%
H
β1-integrin
14.5%
33.6%
51.9%
X1
X2
Xins
I
β1-integrin
FPKM
100
80
60
40
20
0
X1 X2 Xins
J
β1-integrin
500μm
K
smedwi-1
β1-integrin
smedwi-1/ β1-integrin
~92%
40X
100X
L
prog-1
β1-integrin
prog-1/β1-integrin
~33%
M Cell migration in decapitated worms at 15dpa
gfp (RNAi)
mmpa (RNAi)
β1-integrin (RNAi)
smedwi-1/prog1
250μm
N Distance migrated by cells at 15dpa
smedwi-1
prog-1
Distance migrated (μm)
800
600
400
200
0
*
gfp (RNAi)
mmpa (RNAi)
β1-integrin (RNAi)

**Figure S3. Regenerative morphology of RNAi animals and expression patterns of *mmpa* and *β1-integrin***

(A) Head, Trunk and Tail fragments regenerated at 11 days post amputation following *gfp(RNAi)*, *mmpa(RNAi)* and *β1-integrin(RNAi)*. (n=10)

(B) Rescue and regeneration of *gfp(RNAi)*, *mmpa(RNAi)* and *β1-integrin(RNAi)* worms following shielded irradiation and decapitation. (n=30)

(C-D) Expression (C) and FPKM (D) profile of *mmpa* in X1, X2 and Xins cell population.

(E) FISH showing whole body expression pattern of *mmpa*.

(F-G) FISH showing expression of *mmpa* in *smedwi-1*$^{+}$ NBs (F) and *prog-1*$^{+}$ progeny (G) at 2dpa. Around 3% *smedwi-1*$^{+}$ NBs express *mmpa* and no detectable expression of *mmpa* found in *prog-1*$^{+}$ progeny. Scale bars: 20μm

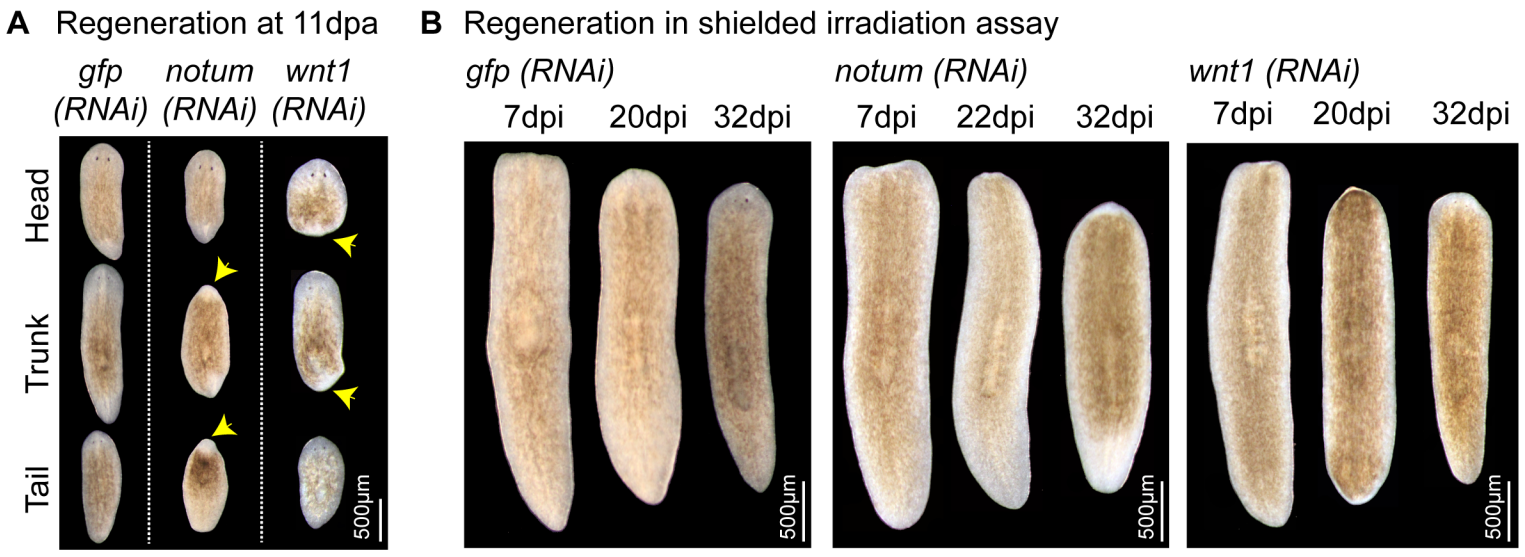
(H-I) Expression (H) and FPKM (I) profile of *β1-integrin* in X1, X2 and Xins cell population.

(J) FISH showing whole body expression pattern of *β1-integrin*.

(K-L) FISH showing expression of *β1-integrin* in *smedwi-1*$^{+}$ NBs (K) and *prog-1*$^{+}$ progeny (L) at 2dpa. Around 92% *smedwi-1*$^{+}$ NBs and 33% *prog-1*$^{+}$ progeny express *β1-integrin*.

(M) FISH shows stem cells (green) and early progeny (magenta) migrate and repopulate the entire migratory region at 15dpa in *gfp(RNAi)* animals but the migration is inhibited in *mmpa(RNAi)* and *β1-integrin(RNAi)* worms that leads to regression of anterior tissue. "[ ]" represent shielded area.

(N) Measurements shows drastic decrease in the distance migrated by stem cells (green) and early progeny (magenta) at 15dpa in *mmpa(RNAi)* and *β1-integrin(RNAi)* animals compared to *gfp(RNAi)* worms (n=5). Each dot represents the average distance migrated by 10 most distal cells from each animal. Lines and error bars indicate mean and SD. Student's t test: *$p<0.05$.



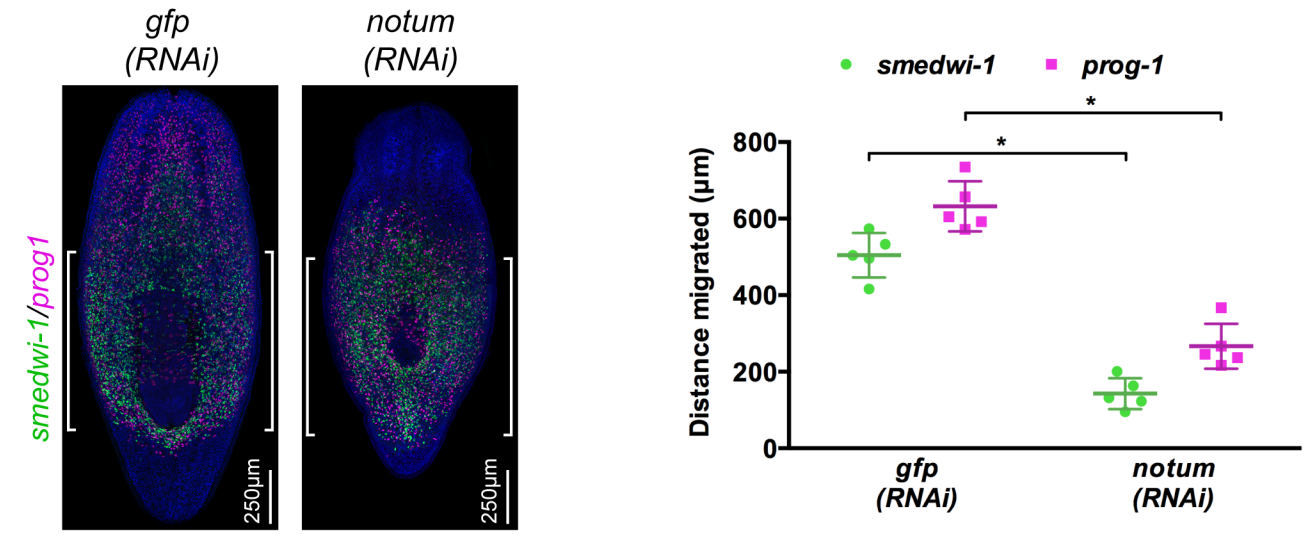



**Figure S4. Regenerative phenotype of *notum* and *wnt1* RNAi animals**

(A) Head, Trunk and Tail fragments regenerated at 11 days post amputation following *gfp(RNAi)*, *notum(RNAi)* and *wnt1(RNAi)*. (n=10)

(B) Rescue and regeneration of *gfp(RNAi)*, *notum(RNAi)* and *wnt1(RNAi)* worms following shielded irradiation and decapitation. (n=30)

(C) Rescue of intact uninjured animals in *gfp(RNAi)* and *notum(RNAi)* worms following shielded irradiation. (n=30)

(D) FISH shows stem cells (green) and early progeny (magenta) migrate anteriorly and repopulate almost entire migratory region at 20dpi in *gfp(RNAi)* animals but the migration is inhibited in *notum(RNAi)* worms that leads to regression of anterior tissue. "[ ]" represent shielded area.

(E) Measurements shows drastic decrease in the distance migrated by stem cells (green) and early progeny (magenta) at 20dpi in *notum(RNAi)* compared to *gfp(RNAi)* worms (n=5). Each dot represents the average distance migrated by 10 most distal cells from each animal. Lines and error bars indicate mean and SD. Student's t test: *$p<0.05$.

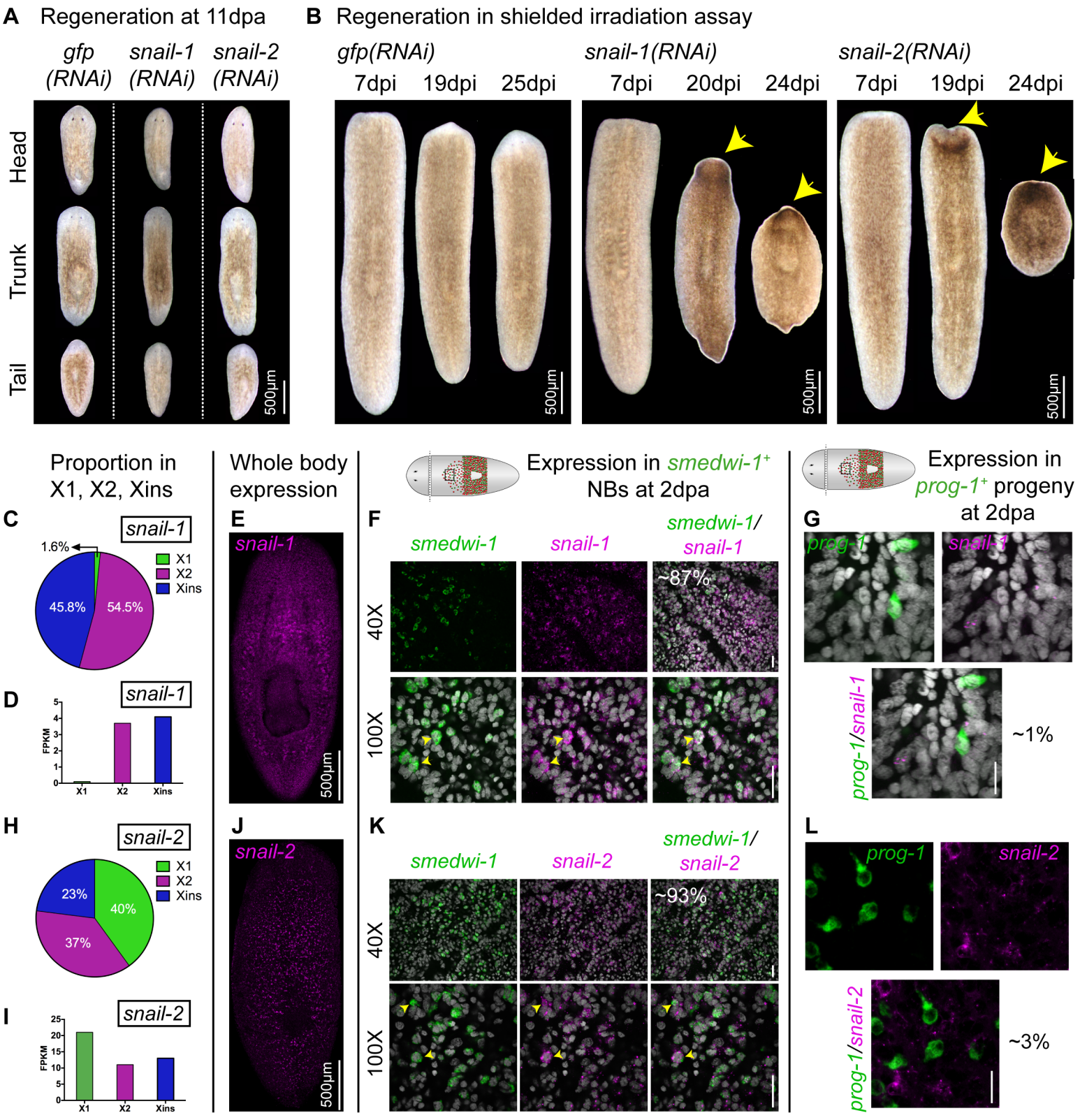


**Figure S5. Regenerative morphology of RNAi animals and expression patterns of *snail-1* and *snail-2***

(A) Head, Trunk and Tail fragments regenerated at 11 days post amputation following *gfp(RNAi)*, *snail-1(RNAi)* and *snail-2(RNAi)*. (n=10)

(B) Rescue and regeneration of *gfp(RNAi)*, *snail-1(RNAi)* and *snail-2(RNAi)* worms following shielded irradiation and decapitation. (n=30)

(C-D) Expression (C) and FPKM (D) profile of *snail-1* in X1, X2 and Xins cell population.

(E) FISH showing whole body expression pattern of *snail-1*.

(F-G) FISH showing expression of *mmpa* in *smedwi-1*$^{+}$ NBs (F) and *prog-1*$^{+}$ progeny (G) at 2dpa. Around 87% *smedwi-1*$^{+}$ NBs express *snail-1* and very little (~1%) expression of *snail-1* found in *prog-1*$^{+}$ progeny. Scale bars: 20μm.

(H-I) Expression (H) and FPKM (I) profile of *snail-2* in X1, X2 and Xins cell population.

(J) FISH showing whole body expression pattern of *snail-2*.

(K-L) FISH showing expression of *snail-2* in *smedwi-1*$^{+}$ NBs (K) and *prog-1*$^{+}$ progeny (L) at 2dpa. Around 93% *smedwi-1*$^{+}$ NBs and less than 3% *prog-1*$^{+}$ progeny express *snail-2*. Scale bars: 20μm.

(M) FISH shows stem cells (green) and early progeny (magenta) migrate and repopulate the entire migratory region at 15dpa in *gfp(RNAi)* animals but the migration is inhibited in *snail-1(RNAi)* and *snail-2(RNAi)* worms that leads to regression of anterior tissue. "[ ]" represent shielded area.

(N) Measurements shows drastic decrease in the distance migrated by stem cells (green) and early progeny (magenta) at 15dpa in *snail-1(RNAi)* and *snail-2(RNAi)* animals compared to *gfp(RNAi)* worms (n=5). Each dot represents the average distance migrated by 10 most distal cells from each animal. Lines and error bars indicate mean and SD. Student's t test: *p<0.05.

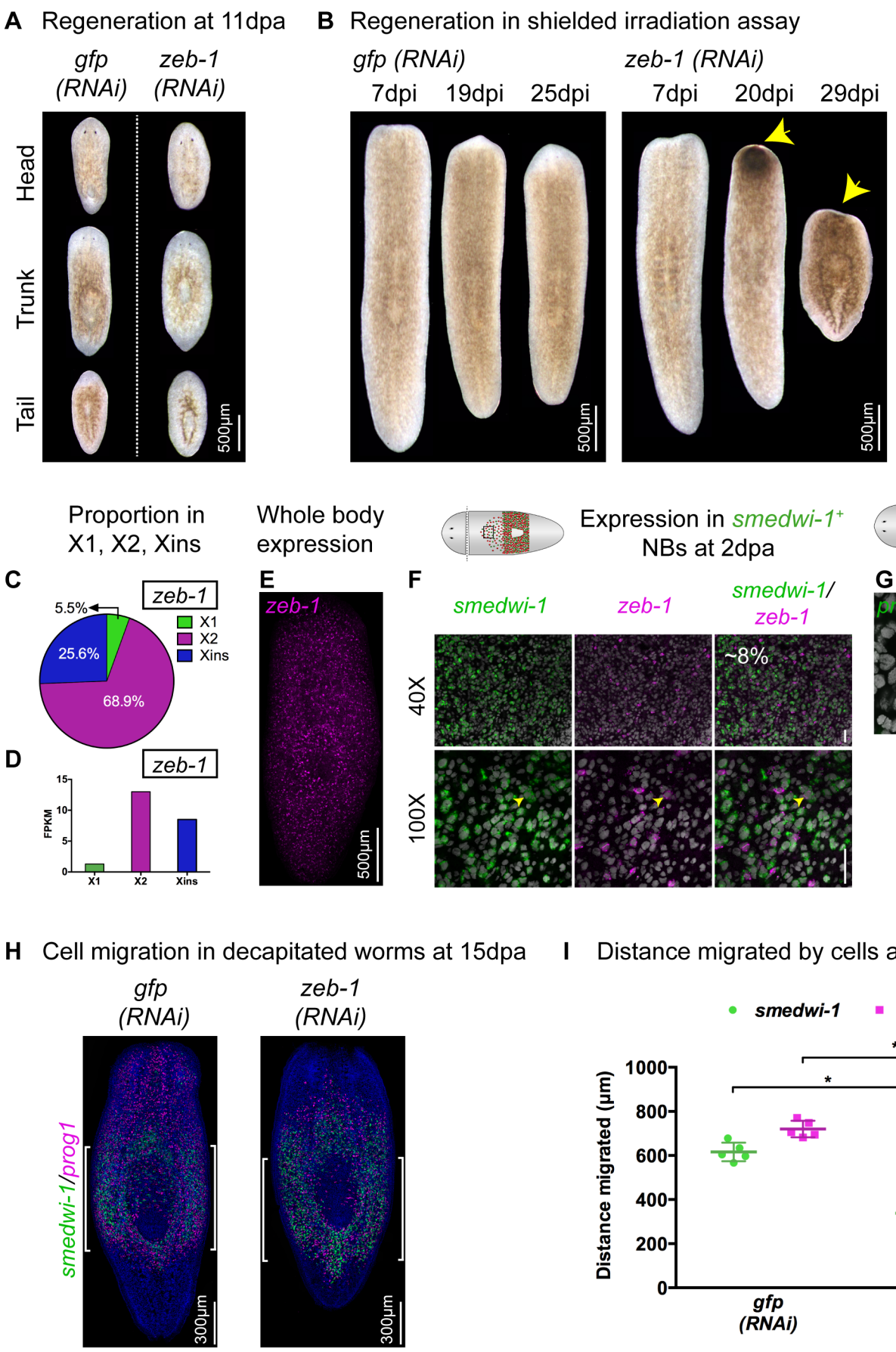


**Figure S6. Effect of *zeb-1* RNAi on regeneration and it's expression in different cell population**

(A) Head, Trunk and Tail fragments regenerated at 11 days post amputation following *gfp(RNAi)* and *zeb-1(RNAi)* animals. (n=10)

(B) Rescue and regeneration of *gfp(RNAi)* and *zeb-1(RNAi)* worms following shielded irradiation and decapitation. (n=30)

(C-D) Expression (C) and FPKM (D) profile of *zeb-1* in X1, X2 and Xins cell population.

(E) FISH showing whole body expression pattern of *zeb-1*.

(F-G) FISH showing expression of *zeb-1* in *smedwi-1*$^{+}$ NBs (F) and *prog-1*$^{+}$ progeny (G) at 2dpa. Around 8% *smedwi-1*$^{+}$ NBs express *zeb-1* and very little (~1%) expression of *zeb-1* found in *prog-1*$^{+}$ progeny. Scale bars: 20μm.

(H) FISH shows stem cells (green) and early progeny (magenta) migrate and repopulate the entire migratory region at 15dpa in *gfp(RNAi)* animals but the migration is inhibited in *zeb-1(RNAi)* worms that leads to regression of anterior tissue. "[ ]" represent shielded area.

(I) Measurements shows drastic decrease in the distance migrated by stem cells (green) and early progeny (magenta) at 15dpa in *zeb-1(RNAi)* animals compared to *gfp(RNAi)* worms (n=5). Each dot represents the average distance migrated by 10 most distal cells from each animal. Lines and error bars indicate mean and SD. Student's t test: *$p<0.05$.