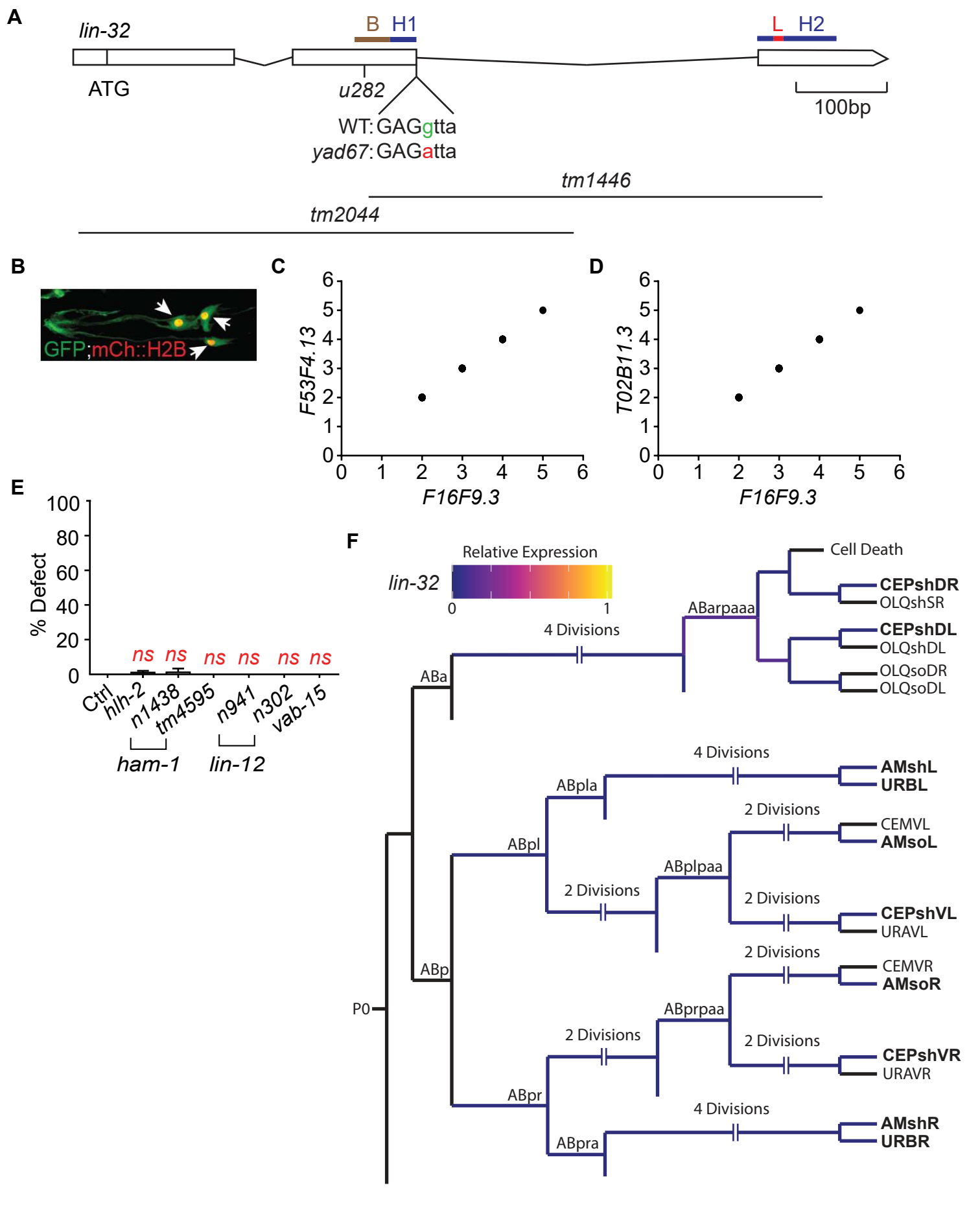
A
lin-32
B H1
L H2
ATG
u282
100bp
WT: GAGgtta
yad67: GAGatta
tm1446
tm2044
B
GFP;mCh::H2B
C
F53F4.13
F16F9.3
D
T02B11.3
F16F9.3
E
% Defect
ns ns ns ns ns ns
Ctrl
hlh-2
n1438
tm4595
n941
n302
vab-15
ham-1
lin-12
F
Relative Expression
lin-32
0
1
Cell Death
CEPshDR
OLQshSR
CEPshDL
OLQshDL
OLQsoDR
OLQsoDL
ABarpaaa
4 Divisions
ABa
4 Divisions
AMshL
URBL
ABpla
2 Divisions
CEMVL
AMsoL
ABpl
ABplpaa
2 Divisions
2 Divisions
CEPshVL
URAVL
2 Divisions
CEMVR
AMsoR
ABp
P0
ABprpaa
2 Divisions
2 Divisions
CEPshVR
URAVR
ABpr
4 Divisions
AMshR
URBR
ABpra

Figure S1. *lin-32* mutants exhibit ectopic AMsh cells (A) The genomic organization of *lin-32*. The point mutation in the *yad67* allele is colored red. Part of the exon and intron at the affected region in *yad67* is highlighted, with the exons in lower case and the introns in upper case. The regions affected in the other alleles used in this study, *tm2044*, *tm1446* and *u282*, are marked. (B) Confocal image of AMsh cells labelled with the *Pf53f4.13::GFP* reporter in green and *Pf16f9.3::mCherry::H2B* in red during the D1 adult stage of *lin-32(yad67)* animals. White arrows indicate AMsh cells. Scale bar, 10 µm. (C) Correlation of the number of cells labelled by the *Pf16f9.3* marker to the *Pf53f4.13* marker. 45 D1 adult animals were quantified. (D) Correlation of the number of cells labelled by the *Pf16f9.3* promoter to the *Pt02b11.3* marker. 45 D1 adult animals were quantified. (E) The proportion of D1 animals with the labelled genotype that possess additional AMsh cells. (F) Cell lineage diagram depicting the expression of *lin-32* in a subset of cells in the AB lineage mentioned in this study. Relative expression data adapted from (Packer *et al.* 2019). Data are represented as mean ± SD. One-way ANOVA, followed by Tukey's HSD test, *$p < 0.05$ **$p < 0.01$. ns, not significant. Each column represents three biological replicates of at least 50 worms each time.