Supplemental Materials

Development of a Reporter System for *In Vivo* Monitoring of γ-Secretase Activity in *Drosophila*

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Fig. S1. Phenotypic characterization of wing vein truncations

(A) Length comparison of L3, L4, and L5 veins in wild-type wing. The average L4 to L3 vein length ratio (=b/a) was 0.97±0.0036 (n=23). The average L5 to L3 vein length ratio (=c/a) was 0.58±0.0056 (n=23).

(B) The average percentages of L4 and L5 vein truncations were calculated by the following equations:

L4 vein truncation = [(0.97x-y)/(0.97x)]×100 (%)

L5 vein truncation = [(0.58x-z)/(0.58x)]×100 (%)

Fig. S2. Genetic interactions among N^{TM}-SV^{42m}, *Notch*, and *presenilin* alleles

(A) Females heterozygous for e16E-Gal4 show a normal pattern of five longitudinal veins. Scale bar indicates 50 μm.

(B) Overexpression of N^{TM}-SV^{42m} in the posterior compartment leads to moderate vein truncation (arrows).

(C) In females heterozygous for $N^{Ax\text{-}E2}$, the wing shows mild truncation only in L5 vein (arrow).

(D) One copy of $N^{Ax\text{-}E2}$mutation slightly enhances the GOF phenotype of N^{TM}-SV^{42m} (arrows).

(E) Overexpression of *psn RNAi* in the posterior compartment results in vein thickening (square brackets).

(F) Overexpression of *psn RNAi* completely suppresses the GOF of N^{TM}-SV^{42m}. Square brackets indicate the vein thickening phenotype.

(G) Percentages of wing vein truncations in females with indicated genotypes (***p<0.001, t test). Error bars indicate S.E.M. by t test. n = number of wings scored for each genotype.

Fig. S3. Genetic interactions among *APPL-SV^{82m}*, *Notch*, and *presenilin* alleles

(A) Females heterozygous for e16E-Gal4 show a normal pattern of five longitudinal veins. Scale bar indicates 50 μm.

(B) Overexpression of *APPL-SV^{82m}* in the posterior compartment causes severe vein truncation (arrows). Asterisks indicate a false vein.

(C) In females heterozygous for *N$^{Ax\text{-}E2}$*, the wing shows mild truncation only in L5 vein (arrow).

(D) One copy of *N$^{Ax\text{-}E2}$*mutation hardly enhances the L4 vein GOF phenotype of *APPL-SV^{85m}* (arrows). Asterisks indicate a false vein.

(E) Overexpression of *psn RNAi* in the posterior compartment results in vein thickening (square brackets).

(F) Overexpression of *psn RNAi* in part suppresses the GOF vein phenotype of *APPL-SV^{85m}* (arrows).

(G) Percentages of wing vein truncations in females with indicated genotypes (†p>0.3 and ***p<0.001, t test). Error bars indicate S.E.M. by t test. n = number of wings scored for each genotype.

Fig. S4. Genetic interactions among *p35*, N^{TM}-SV^{42m}, and *APPL*-SV^{82m}

(A) Females heterozygous for e16E-Gal4 show a normal pattern of five longitudinal veins. Scale bar indicates 50 μm.

(B) Overexpression of N^{TM}-SV^{42m} in the posterior compartment results in moderate vein truncation (arrows). Asterisks indicate a false vein.

(C) Overexpression of *APPL*-SV^{82m} in the posterior compartment causes severe vein truncation (arrows).

(D) Overexpression of *p35* in the posterior compartment results in slight vein truncation (arrow).

(E) Coexpression of *p35*in the posterior compartment slightly increases the GOF vein phenotype of N^{TM}-SV^{42m} (arrows).

(F) Coexpression of *p35*in the posterior compartment significantly decreases the L4 vein GOF phenotype of *APPL*-SV^{85m} (arrows).

(G) Percentages of wing vein truncations in females with indicated genotypes (*p<0.05, ***p<0.001, and †not applicable, *t* test). Error bars indicate S.E.M. by *t* test. n = number of wings scored for each genotype.

Figure S1

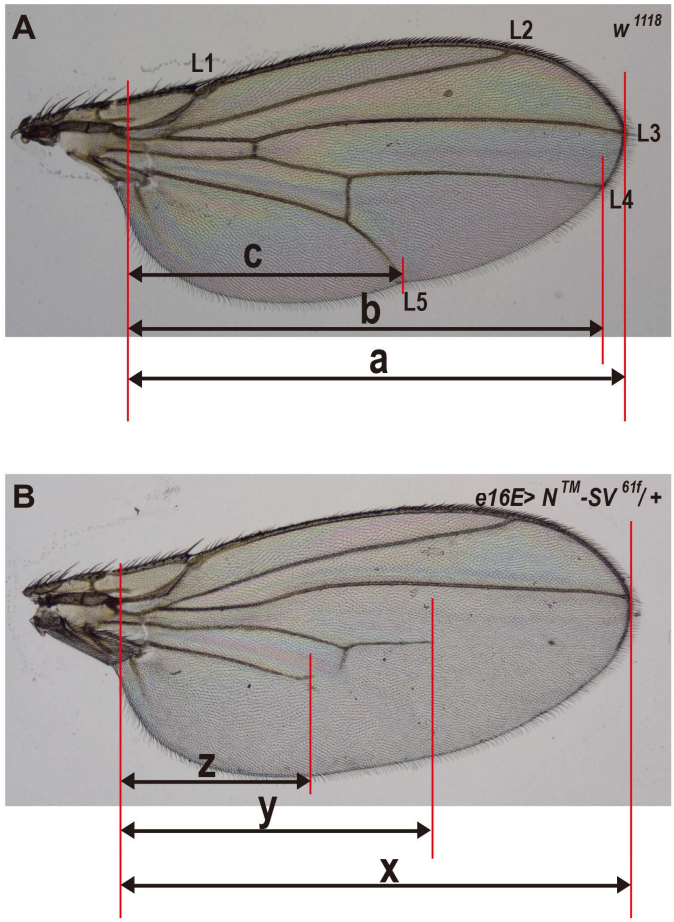


Figure S2

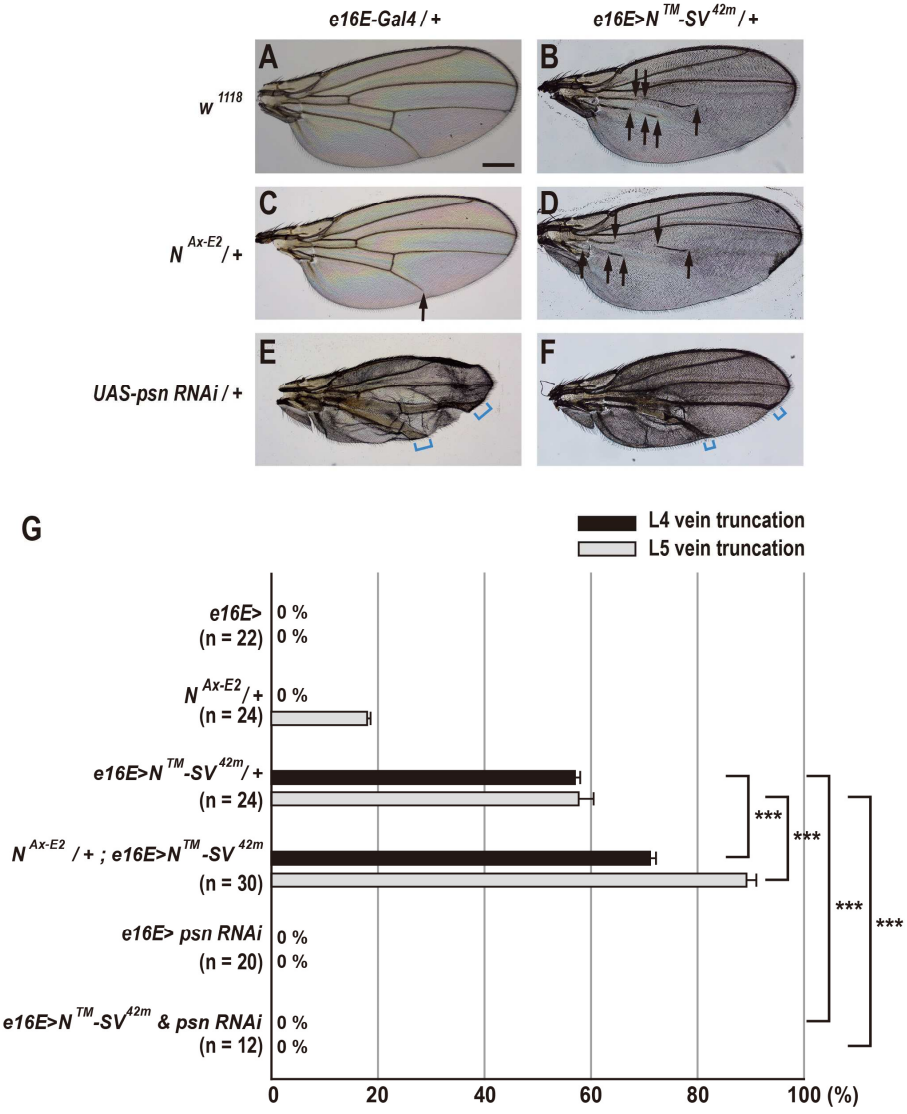

e16E-Gal4 / +
e16E>N TM-SV 42m / +
w 1118
N Ax-E2 / +
UAS-psn RNAi / +
A
B
C
D
E
F
G
L4 vein truncation
L5 vein truncation
e16E>
(n = 22)
0 %
0 %
N Ax-E2 / +
(n = 24)
0 %
e16E>N TM-SV 42m / +
(n = 24)
N Ax-E2 / + ; e16E>N TM-SV 42m
(n = 30)
e16E> psn RNAi
(n = 20)
0 %
0 %
e16E>N TM-SV 42m & psn RNAi
(n = 12)
0 %
0 %
***
***
***
***
0
20
40
60
80
100 (%)

Figure S3

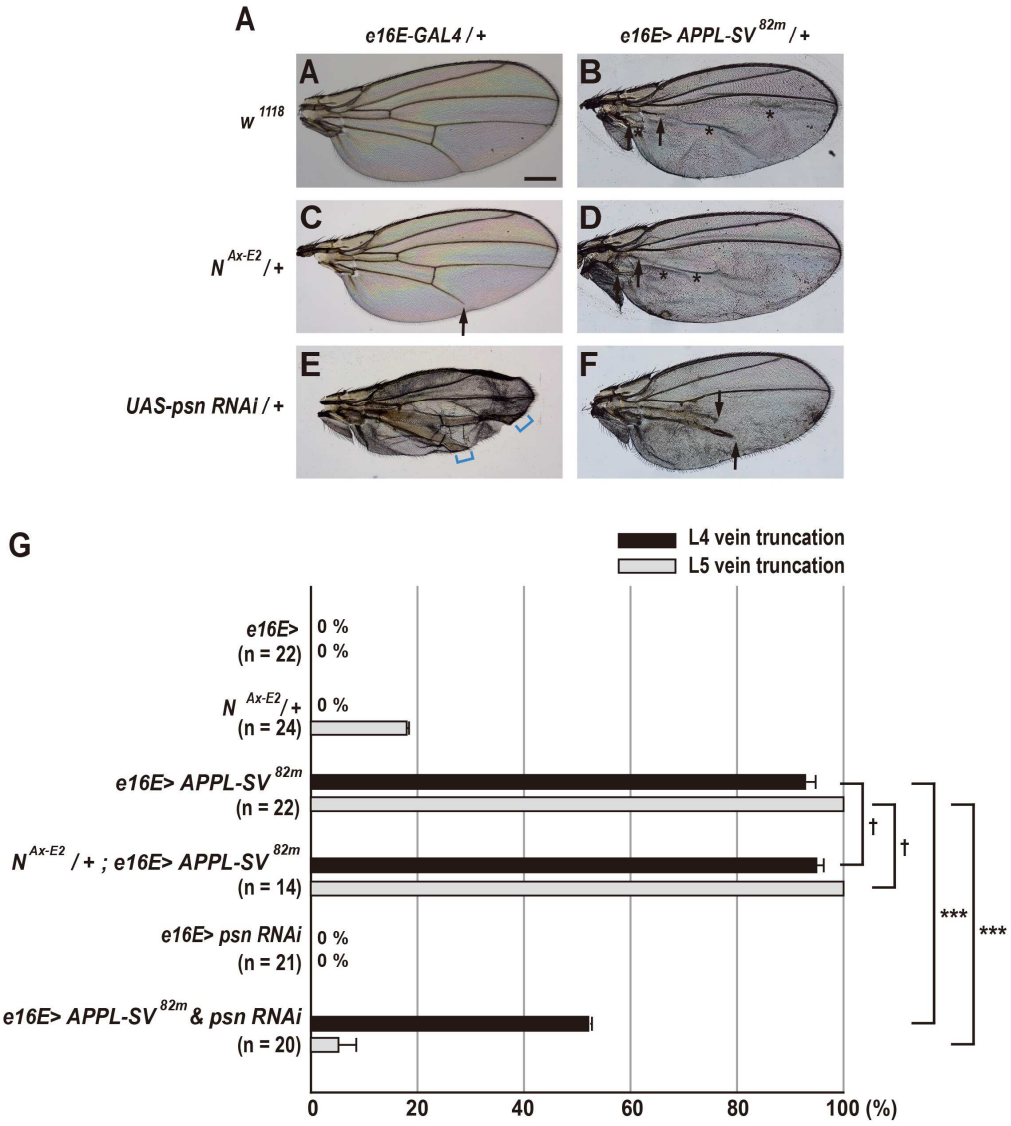
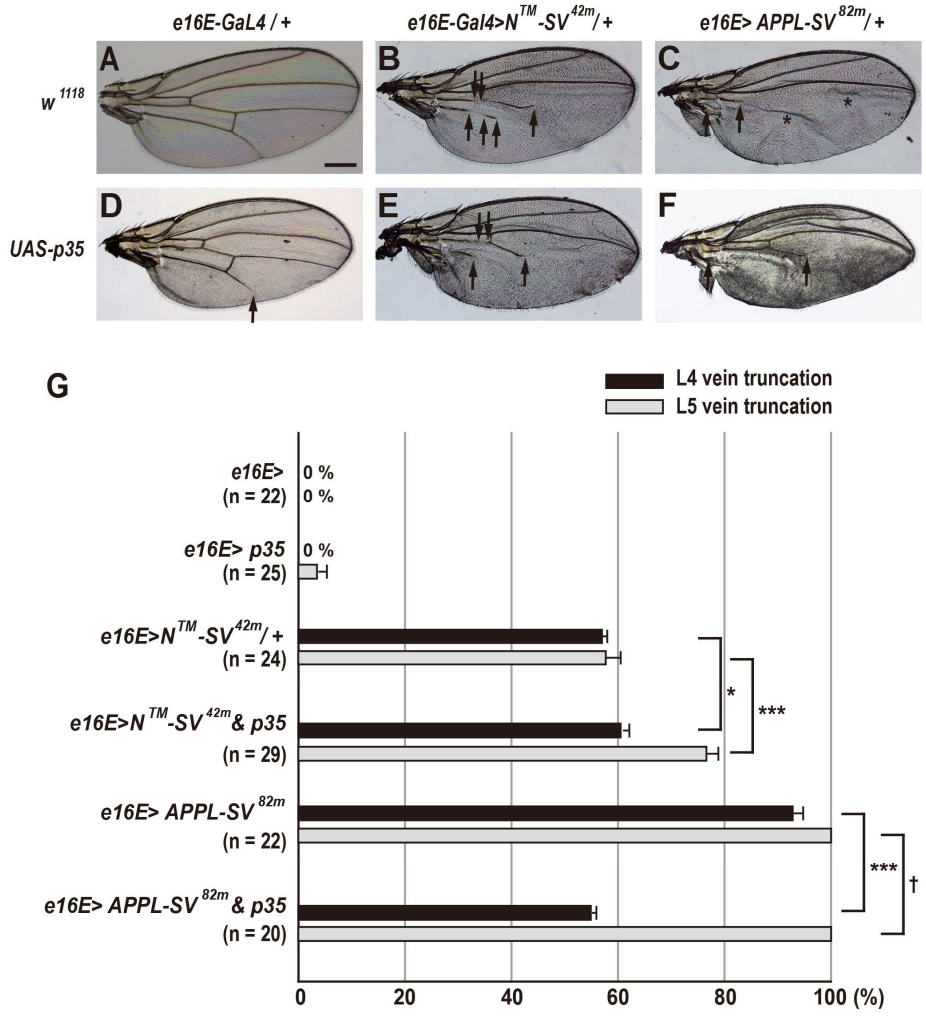

A
e16E-GAL4 / +
e16E> APPL-SV 82m / +
w 1118
N Ax-E2 / +
UAS-psn RNAi / +
A
B
C
D
E
F
G
L4 vein truncation
L5 vein truncation
e16E>
(n = 22)
0 %
0 %
N Ax-E2 / +
(n = 24)
0 %
e16E> APPL-SV 82m
(n = 22)
N Ax-E2 / + ; e16E> APPL-SV 82m
(n = 14)
e16E> psn RNAi
(n = 21)
0 %
0 %
e16E> APPL-SV 82m & psn RNAi
(n = 20)
†
†
***
***
0
20
40
60
80
100 (%)

Figure S4


e16E-GaL4 / +
e16E-Gal4>N TM -SV 42m / +
e16E> APPL-SV 82m / +
w 1118
UAS-p35
A
B
C
D
E
F
G
L4 vein truncation
L5 vein truncation
e16E>
(n = 22)
0 %
0 %
e16E> p35
(n = 25)
0 %
e16E>N TM -SV 42m / +
(n = 24)
e16E>N TM -SV 42m & p35
(n = 29)
e16E> APPL-SV 82m
(n = 22)
e16E> APPL-SV 82m & p35
(n = 20)
*
***
***
†
0
20
40
60
80
100 (%)