Figure S1

z positions

Toll-6 expression

Toll-6^MIMICGFP
Ctxglia-split>mCherry.NLS

z position #1

z position #2

Toll-6^MIMICGFP

Ctxglia-split>mCherry.NLS

brain

ventral nerve cord

dSARM expression
ventral surface

wrapper932iQF2>LacZ.NLS
dSARM>mCherry.NLS

dSARM>mCherry.NLS

wrapper932iQF2>LacZ.NLS

Brain

VNC

FoxO^MIMICGFP
anti-FoxO

FoxO^MIMICGFP
anti-FoxO
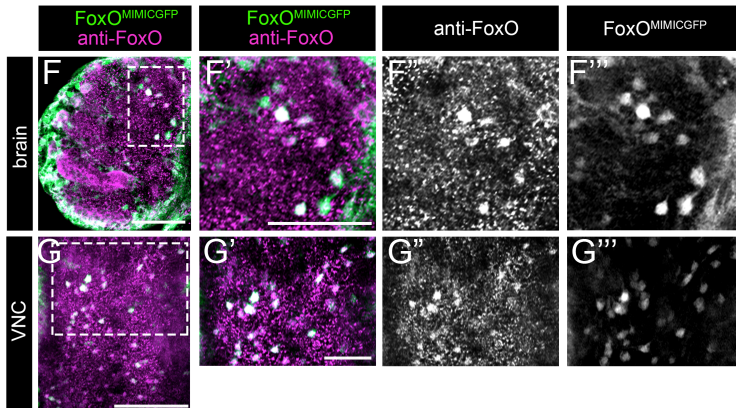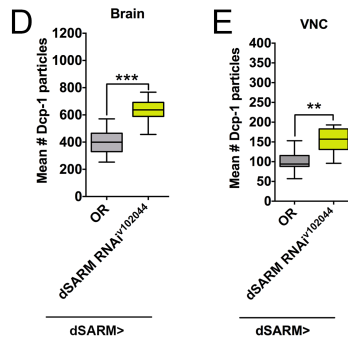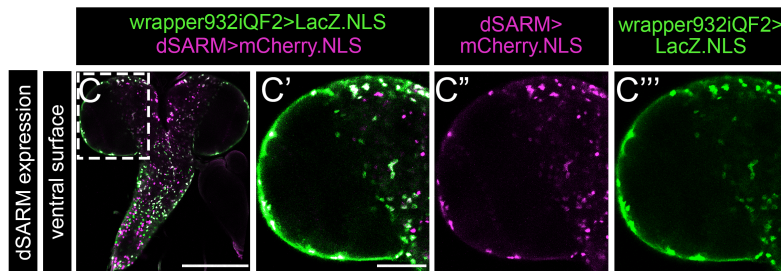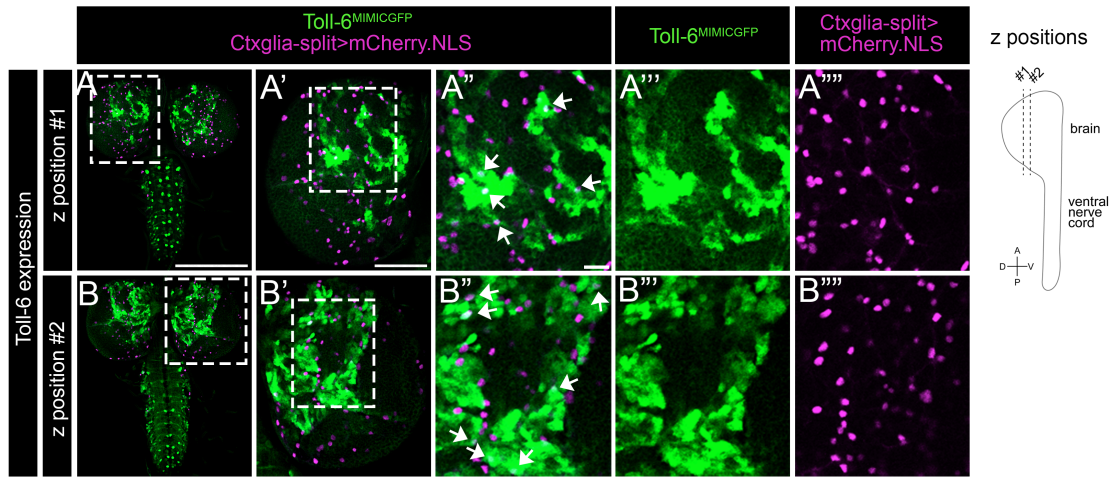
anti-FoxO

FoxO^MIMICGFP

brain

VNC

Figure S1. **Expression and validation of Toll-6, dSARM and FoxO in cortex glia, related to Figure 2.** (A-B) Representative 3 μm z-projections of Ctxglia-split>mCherry.NLS, Toll-6^{MIMICGFP}/+ L3 CNS labeled with anti-GFP (green) and anti-mCherry (magenta). Scale bar is 200 μm. (A', B') Projections of one brain lobe depicting co-labeling of anti-GFP with anti-mCherry. Scale bar is 50 μm. (A', B') Higher magnification projections of cortex glial nuclei (anti-mCherry) labeled with Toll-6^{MIMICGFP} (anti-GFP). Single channel projections of brain lobe labeled with (A''', B''') anti-GFP and (A'''', B'''') anti-mCherry. Scale bar is 10 μm. (C) Representative 3 μm z-projections of wrapper932iQF2>LacZ.NLS; dSARM>mCherry.NLS L3 CNS labeled with anti-ßgal (green) and anti-mCherry (magenta). Scale bar is 200 μm. (C') Higher magnification projection of one brain lobe depicting co-labeling of anti-ßgal and anti-mCherry. Single channel projections of brain lobe labeled with (C'') anti-mCherry and (C''') anti-ßgal. Scale bar is 50 μm. Quantification of total Dcp-1 particles in the (D) brain of: dSARMGal4/+: 396; dSARM>dSARM RNAi^{v102044}: 632; and (E) VNC of: dSARMGal4/+: 100; dSARM>dSARM RNAi^{v102044}: 156. (F) Representative 3 μm z-projections of a FoxO^{MIMICGFP}/+ brain lobe labeled with anti-GFP (green) and anti-FoxO (magenta). Scale bar is 50 μm. (F') Higher magnification projection of brain lobe labeled with anti-GFP and anti-FoxO. Single channel projections of (F'') anti-FoxO and (F''') anti-GFP. Scale bar is 25 μm. (G) Representative 3 μm z-projections of 2 segments of a FoxO^{MIMICGFP}/+ VNC labeled with anti-GFP (green) and anti-FoxO (magenta). Scale bar is 75 μm. (G') Higher magnification projection of anti-GFP and anti-FoxO co-labeling. Single channel projections of (G'') anti-FoxO and (G''') anti-GFP. Scale bar is 25 μm. **, P<0.01; ***, P<0.001.

Figure S2

Row 1 (A–F): cortex glia membranes (green)

| control | Ctxglia-split> Toll-6 RNAi | Ctxglia-split> dSARM RNAi | Ctxglia-split> FoxO RNAi | Ctxglia-split> Drpr RNAi³ᴮ | Ctxglia-split> Drpr-I RNAi |
| A | B | C | D | E | F |

G–H:
Rab7-YFP / Ctxglia-split> mCD8::Cherry
Rab7-YFP
Ctxglia-split> mCD8::Cherry

I: Percent of Rab7-YFP donuts in cortex glial membranes — control

J–L:
Rab7-YFP / Dcp-1
Rab7-YFP / Elav
Rab7-YFP / Repo
Rab7-YFP
Dcp-1
Elav
Repo

M: Proportion of Rab7 donuts surrounding marker — Dcp-1, Elav, Repo

N: # Rab7+ donuts — control, Toll-6 RNAi ᵛ⁹²⁸, dSARM RNAi ᵛ¹⁰²⁰⁴⁴, FoxO RNAi ᵛ¹⁰⁷⁷⁸⁶, Drpr-I RNAi
Ctxglia-split> mCD8::Cherry
** *** ** ***

O: # Rab7+ donuts / area of cortex region — control, Toll-6 RNAi ᵛ⁹²⁸, dSARM RNAi ᵛ¹⁰²⁰⁴⁴, FoxO RNAi ᵛ¹⁰⁷⁷⁸⁶, Drpr-I RNAi
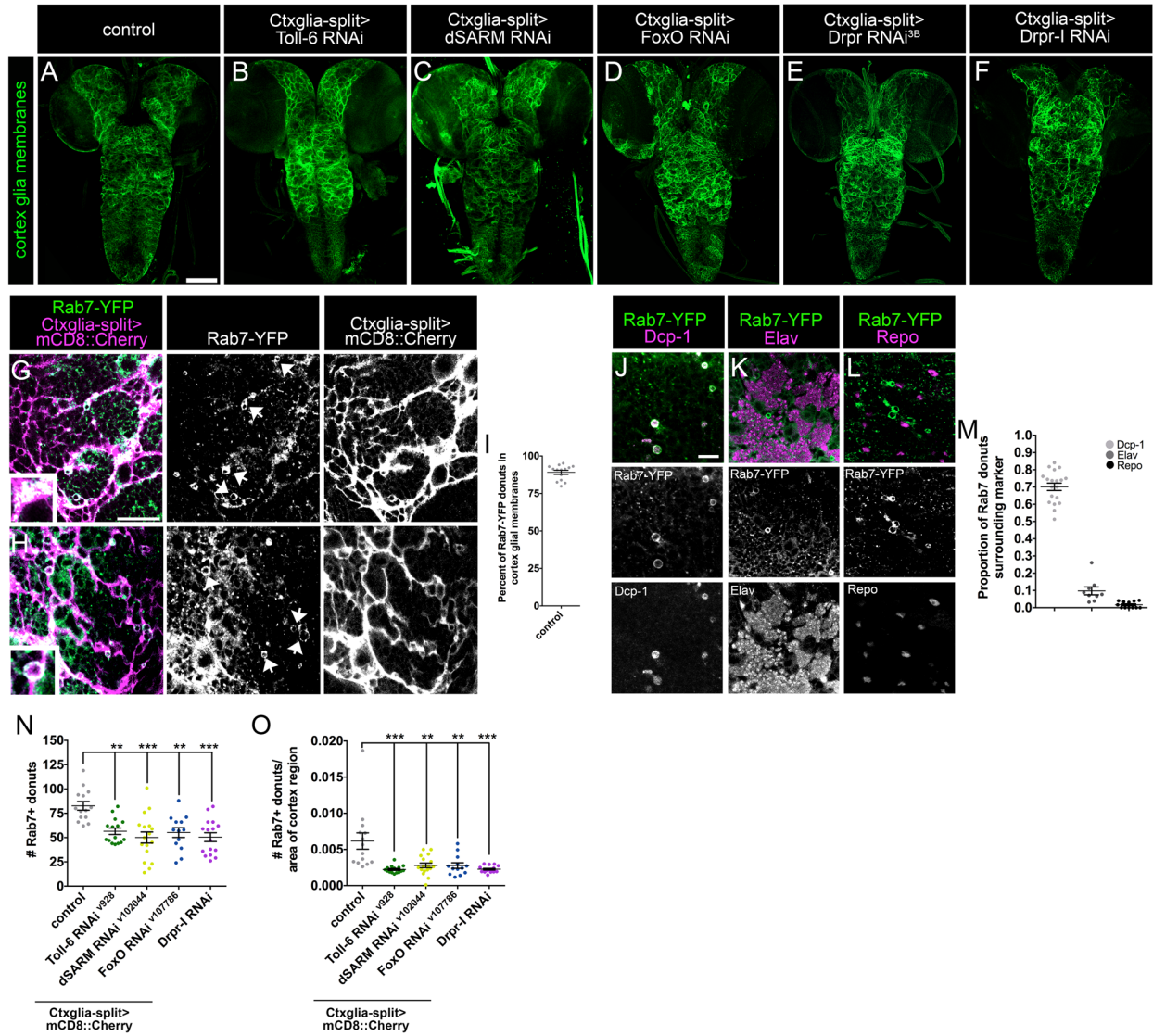Ctxglia-split> mCD8::Cherry
*** ** ** ***

Figure S2. **Loss of Toll-6-FoxO signaling does not alter gross morphology of cortex glia but does lead to defects in phagocytic machinery, related to Figure 3.** (A-F) Ventral z-projections depicting cortex glial processes in the L3 CNS labeled with Ctxglia-split>mCD8::GFP in indicated genotypes. Scale bar is 50 μm. (G-H) Representative confocal projections depicting Rab7-YFP (green) localized within cortex glial membranes (magenta). Insets depict (G) diffuse Rab7-YFP labeling or (H) Rab7-YFP donut within cortex glial membranes. Arrows denote Rab7-YFP donuts. Scale bar is 20 μm. (I) Quantification of the percent of Rab7-YFP donuts within cortex glial membranes in Ctxglia-split>mCD8::Cherry, Rab7-YFP/+ brains mean is 89 ± 1.3 % (n=16). Error bars are SEM. Representative projections of Rab7-YFP donuts (green) associated with (J) Dcp-1 (magenta); (K) Elav (magenta); and (L) Representative projection of Rab7-YFP donuts (green) associated with Repo (magenta) in L3 brains. Scale bar is 15 μm. (M) Quantification of Rab7-YFP donuts surrounding apoptotic (Dcp-1), neuronal (Elav), or glial (Repo) markers in Ctxglia-split>mCD8::Cherry, Rab7-YFP/+ brains means are: Dcp-1: 0.7 ± 0.02 (n=19); Elav: 0.1 ± 0.02 (n=9); Repo: 0.02 ± 0.005 (n=12). Error bars are SEM. (N) Quantification of number of Rab7-YFP donuts within cortex glial membranes in indicated genotypes, means are: Ctxglia-split>mCD8::Cherry, Rab7-YFP/+ (control): 83 ± 4.5 (n=14); Ctxglia-split>Toll-6 RNAi [v928]; mCD8::Cherry, Rab7-YFP/+: 57 ± 3.3 (n=15); Ctxglia-split>dSARM RNAi[v102044]; mCD8::Cherry, Rab7-YFP/+: 50 ± 5.7 (n=17); Ctxglia-split>FoxO RNAi[v107786]; mCD8::Cherry, Rab7-YFP/+: 55 ± 5.0 (n=13); Ctxglia-split>Drpr-I RNAi; mCD8::Cherry, Rab7-YFP/+: 50 ± 4.5 (n=16). (O) Quantification of number of Rab7-YFP donuts normalized to area of cortex region in: Ctxglia-split>mCD8::Cherry, Rab7-YFP/+ (control): 0.0062 ± 0.001 (n=14); Ctxglia-split>Toll-6 RNAi [v928]; mCD8::Cherry, Rab7-YFP/+: 0.0022 ± 0.00013 (n=15); Ctxglia-split>dSARM RNAi [v102044]; mCD8::Cherry, Rab7-YFP/+: 0.0028 ± 0.00032 (n=17); Ctxglia-split>FoxO RNAi [v107786]; mCD8::Cherry, Rab7-YFP/+: 0.0028 ± 0.00038 (n=13); Ctxglia-split>Drpr-I RNAi; mCD8::Cherry, Rab7-YFP/+: 0.0023 ± 0.00011 (n=16). **, $P<0.01$; ***, $P<0.001$.

Figure S3

A

Annexin V particles/
5 µm depth

***

control 10 mM CHX

9 10

B Brain #1
Spg membranes
Dextran-568

C Brain #2
+ Dextran-568

D Brain #3
+ Dextran-568

Spg membranes

Dextran-568

Rab7-YFP
Annexin V | Annexin V | Rab7-YFP | Orthogonal views
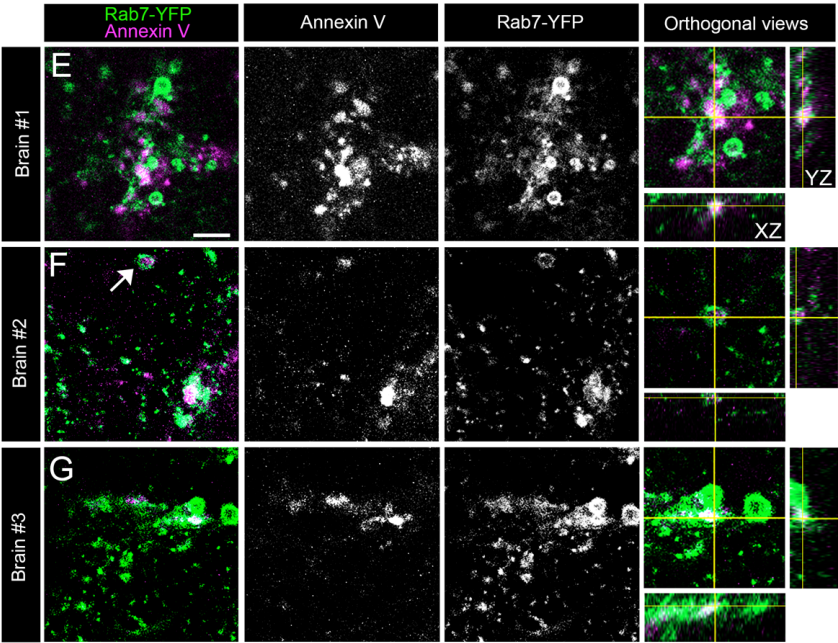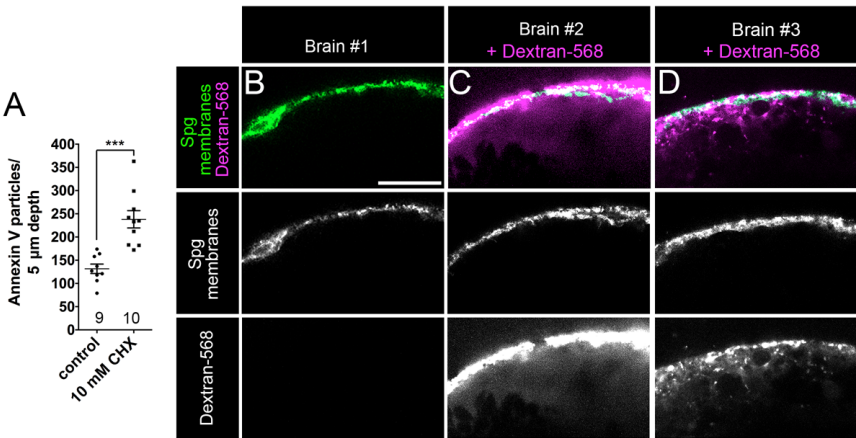
Brain #1

YZ

XZ

Brain #2

Brain #3

Figure S3. **Annexin V crosses the BBB and co-localizes with Rab7-YFP, related to Figure 4.** (A) Quantification of Annexin V particles in the brain of: control treated: 132 ± 10; CHX treated: 238 ± 19. Representative images of L3 brains with subperineurial glia labeled with mCD8::GFP (spg>mCD8::GFP) and (B) not incubated with Dextran-568; (C-D) incubated with 10 kDa Dextran-568 (magenta). Scale bar is 25 µm. (E-G) Representative images of endogenously tagged Rab7-YFP co-localized with Annexin V in cortex region of the L3 brain in live tissue. Arrow indicates a Rab7-YFP donut surrounding an Annexin V particle. Scale bar is 15 µm. *n* is noted at the bottom of each column; ***, P<0.001.

Figure S4
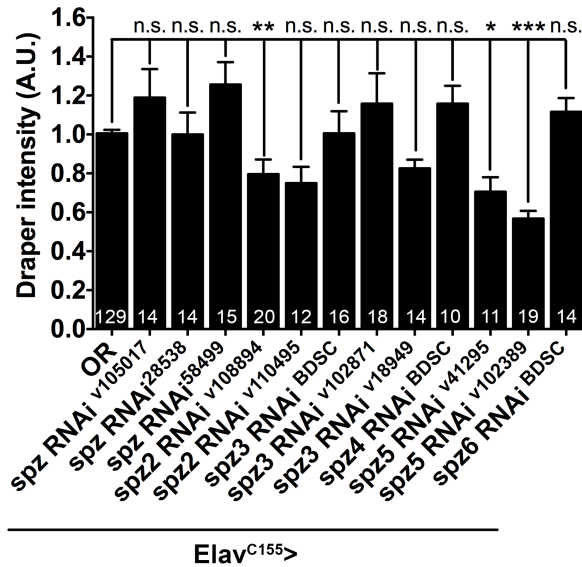
Figure S4. **A neuronal Spätzle protein serves as a Toll-6 ligand, related to Figure 5.**
Quantification of mean Drpr intensity normalized to control: Elav[C155]Gal4/+: 1.0 ± 0.02;
Elav[C155]>Spz RNAi[v105017]: 1.2 ± 0.15; Elav[C155]>Spz RNAi[28538]: 1.0 ± 0.1; Elav[C155]>Spz
RNAi[58499]: 1.3 ± 0.1; Elav[C155]>Spz2 RNAi[v108894]: 0.8 ± 0.08; Elav[C155]>Spz2 RNAi[v110495]:
0.75 ± 0.08; Elav[C155]>Spz3 RNAi[BDSC]: 1.0 ± 0.1; Elav[C155]>Spz3 RNAi[v102871]: 1.2 ± 0.2;
Elav[C155]>Spz3 RNAi[v18949]: 0.83 ± 0.05; Elav[C155]5>Spz4 RNAi[BDSC]: 1.2 ± 0.1;
Elav[C155]>Spz5 RNAi[v41295]: 0.71 ± 0.08; Elav[C155]>Spz5 RNAi[v102389]: 0.57 ± 0.04;
Elav[C155]>Spz6 RNAi[BDSC]: 1.1 ± 0.07. n is noted at the bottom of each column. n.s., not
significantly different. *, P<0.05; **, P<0.01; ***, P<0.001. Error bars are SEM.

Figure S5

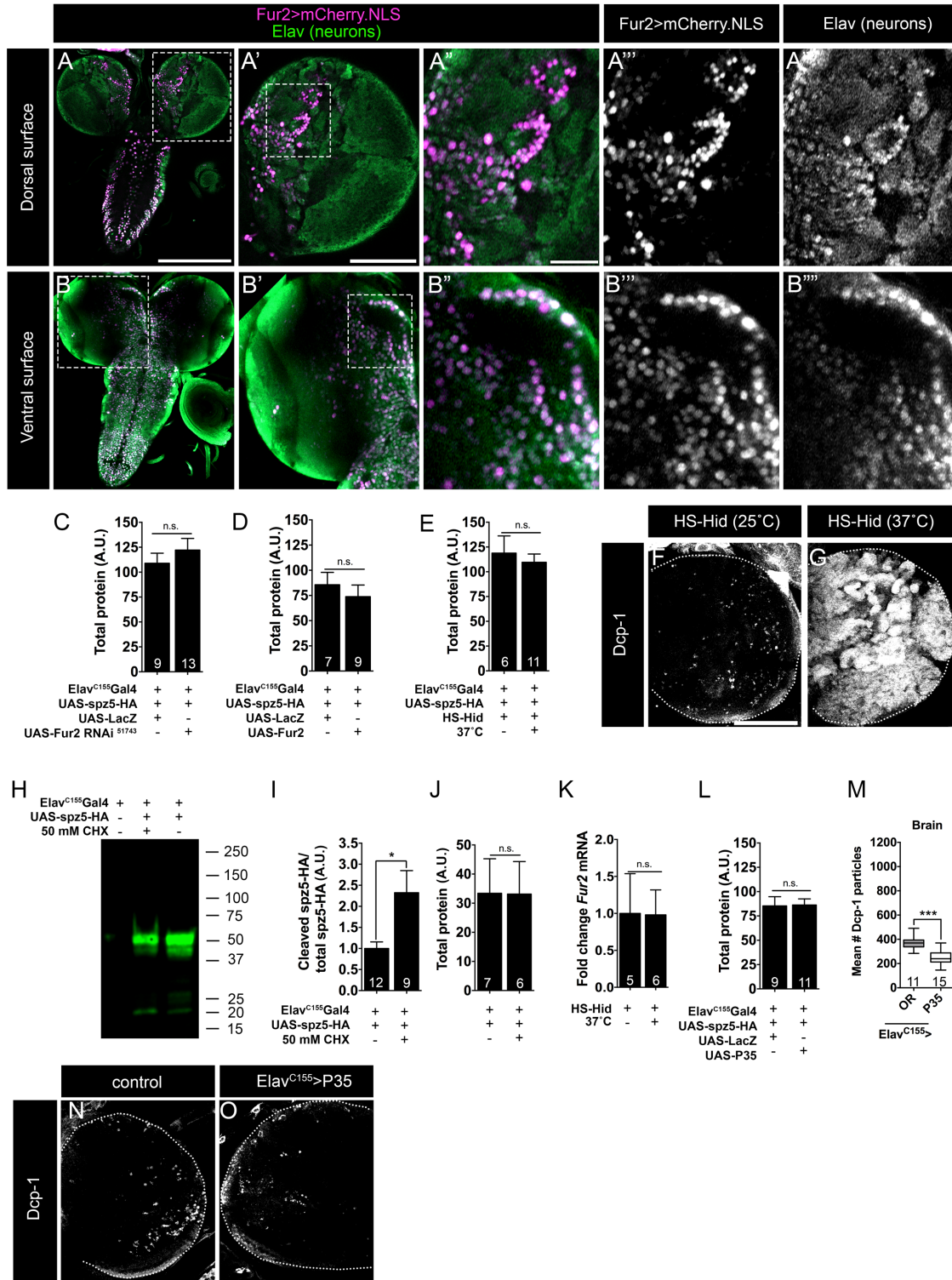Figure S5. **Fur2 is expressed in neurons and cleaves Spz5 in response to elevated apoptosis, related to Figure 6.** (A,B) Projection of Fur2>mCherry.NLS L3 CNS labeled with anti-Elav (green) and anti-mCherry (magenta). Scale bar is 150 µm. (A', B') Projection of one brain lobe labeled with anti-Elav (green) and anti-mCherry (magenta). Scale bar is 60 µm. (A", B") Higher magnification projection of region of brain lobe depicting Fur2+ neurons. Single channel projections of region of brain lobe labeled with (A''', B''') anti-mCherry or (A"", B"") anti-Elav. Scale bar is 20 µm. (C) Quantification of total protein in: Elav^{C155}>LacZ, Spz5-HA: 109 ± 10; Elav^{C155}>Fur2 RNAi [51743]; Spz5-HA: 122 ± 12. (D) Quantification of total protein in: Elav^{C155}>LacZ, Spz5-HA: 86 ± 12; Elav^{C155}>Fur2, Spz5-HA: 74 ± 12. (E) Quantification of total protein in: Elav^{C155}>Spz5-HA; HS-Hid (25ºC): 119 ± 17; Elav^{C155}>Spz5-HA; HS-Hid (37ºC): 110 ± 8.4. (F-G) Representative confocal projections of indicated genotypes labeled with anti-Dcp-1. Scale bar is 50 µm. (H) Representative Western blot of Spz5-HA cleavage in indicated genotypes. (I) Quantification of cleaved Spz5-HA to total Spz5-HA normalized to control in: Elav^{C155}>Spz5-HA (PBS): 1.0 ± 0.2; Elav^{C155}>Spz5-HA (CHX): 2.3 ± 0.5. (J) Quantification of total protein in: Elav^{C155}>Spz5-HA (PBS): 33 ± 12; Elav^{C155}>Spz5-HA (CHX): 33 ± 11. (K) qRT-PCR analysis of relative *Fur2* mRNA levels in: HS-Hid (25ºC): 1.0 ± 0.54; HS-Hid (37ºC): 0.98 ± 0.34. (L) Quantification of total protein in: Elav^{C155}>LacZ; Spz5-HA: 85 ± 9.5; Elav^{C155}> P35; Spz5-HA: 86 ± 6.2. (M) Quantification of Dcp-1 particles in indicated genotypes. Means are: Elav^{C155}/+: 376; Elav^{C155}>P35: 248. (N-O) Representative confocal projections of indicated genotypes labeled with anti-Dcp-1. Error bars for bar graphs are SEM. Error bars for box and whisker plots are minimum and maximum values. n is noted at the bottom of each column. n.s., not significantly different; *, P<0.05; ***, P<0.001.
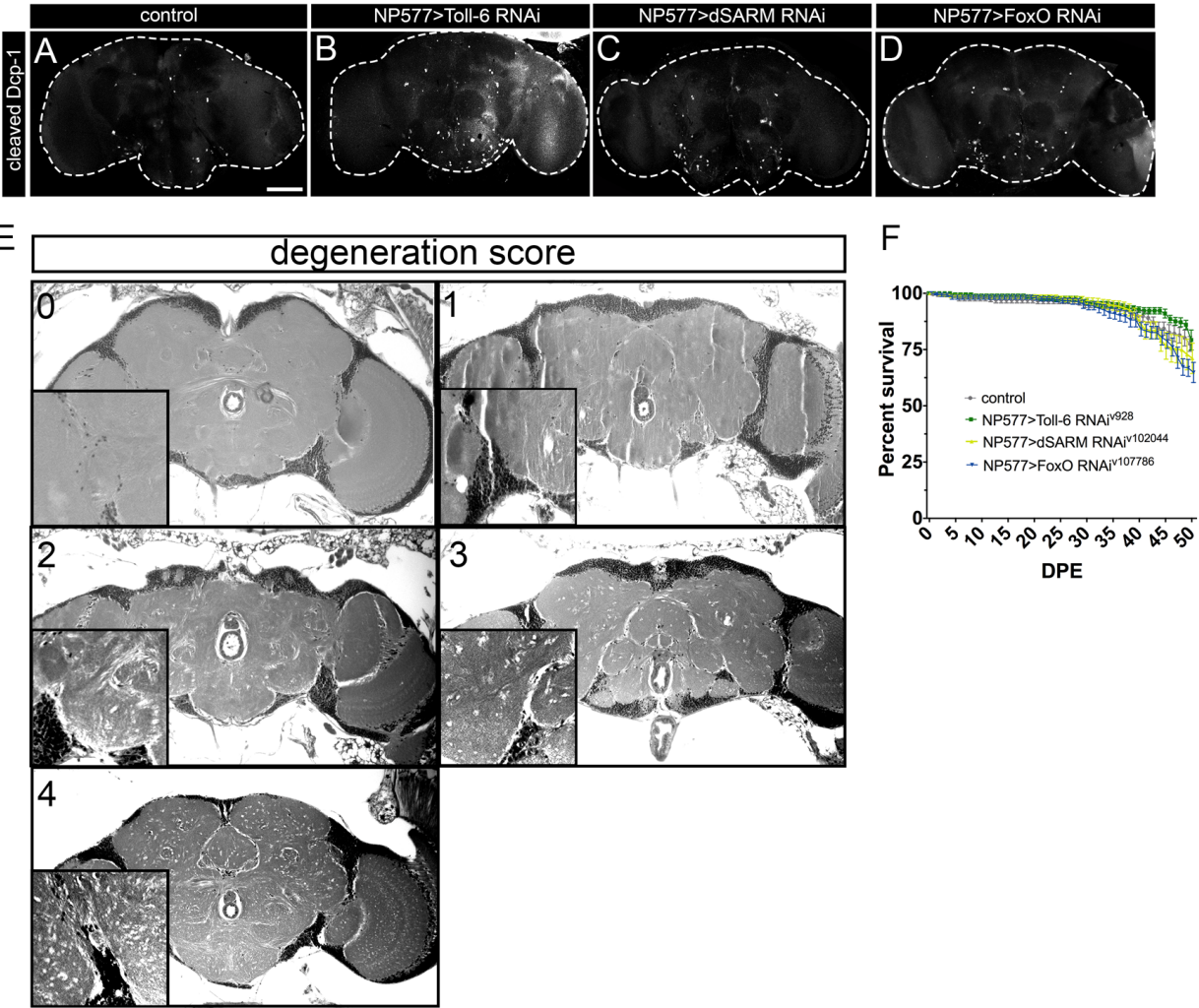
Figure S6

Figure S6. **Apoptotic debris and neurodegeneration phenotypes, related to Figure 7.** (A-D) Representative z-projections of adult brains of indicated genotypes labeled with anti-Dcp-1. Scale bar is 100 μm. (E) Neurodegeneration index. (F) Lifespan analysis of adult flies of indicated genotypes.

Table S1

	# Dcp-1 particles (brain)				# Dcp-1 particles (VNC)			
	Mean	SEM	n	Significant?	Mean	SEM	n	Significant?
wild type (OregonR; OR)	353	19	9	n/a	113	5.5	9	n/a
Toll-6^{EX13}	641	52	10	***	170	6.5	10	**
FoxO$^{\Delta 94}$	613	32	14	***	182	15	14	***
Toll-6^{EX13}, FoxO$^{\Delta 94}$	563	31	8	*	169	8.6	8	*
dSARM$^{4621/4705}$	594	31	14	***	174	8.4	15	***
Toll-6^{EX13}/+	422	30	12	ns	132	6.6	12	ns
dSARM^{4621}/+	418	24	16	ns	132	7.1	16	ns
dSARM^{4621}/+, Toll-6^{EX13}/+	666	23	16	***	209	6.6	16	***
FoxOΔ^{94}/+	381	24	11	ns	131	9.2	11	ns
dSARM^{4621}/+, FoxOΔ^{94}/+	713	23	11	***	186	8.9	11	***
Toll-7^{g1-1}	378	37	9	ns	110	4.7	0	ns
Toll-7^{AWI}	402	33	9	ns	146	5.3	10	ns
Rel^{E20}	395	40	11	ns	125	8.5	11	ns
MyD88^{C03881}	375	37	12	ns	112	5.1	13	ns
Df(2R)BDSC279/+	569	34	11	**	178	15	11	**
Df(2R)BDSC280/+	432	32	8	ns	130	11	8	ns
MyD88^{C03881}/Df(2R)BDSC 280	446	34	14	ns	151	6.9	14	ns
Elav^{C155}Gal4/+	386	16	15	n/a	123	8.5	16	ns
Elav^{C155}>Toll-6 RNAi^{v928}	383	23	15	ns	115	6.6	16	ns
Elav^{C155}>dSARM RNAi$_{v102044}$	400	28	18	ns	107	4.4	14	ns
Elav^{C155}>FoxO RNAi$_{v107786}$	382	29	11	ns	106	6.3	12	ns
RepoGal4/+	388	28	11	n/a	109	5	13	n/a
Repo>Toll-6 RNAi^{v928}	631	29	12	***	187	5.7	14	***
Repo>dSARM RNAi$_{v102044}$	593	29	9	**	184	10	12	***
Repo>FoxO RNAi^{v107786}	599	41	13	**	160	11	11	*
Nrv2>Toll-6 RNAi^{v928}	722	31	10	***	192	15	12	***
Inx2>Toll-6 RNAi^{v928}	681	72	13	**	194	12	14	***
NP577>Toll-6 RNAi^{v928}	600	27	12	**	189	6.6	16	***
Alrm>Toll-6 RNAi^{v928}	403	27	10	ns	120	8.3	10	ns
Mz0709>Toll-6 RNAi^{v928}	381	23	12	ns	115	9.3	12	ns
NP6293>Toll-6 RNAi^{v928}	445	36	11	ns	111	12	11	ns
Spg>Toll-6 RNAi^{v928}	412	18	10	ns	134	11	10	ns
NP577Gal4/+	350	18	17	n/a	121	5.1	18	n/a
NP577>Toll-6 RNAi^{v928}	600	27	12	***	189	6.4	14	***
NP577>Toll-6 RNAi^{BDSC}	637	28	9	***	185	8.6	10	***
NP577>dSARM RNAi$_{v102044}$	614	28	10	***	196	8.6	10	***
NP577>dSARM RNAi$_{v105369}$	617	24	9	***	201	8.8	10	***
NP577>FoxO RNAi^{v107786}	628	25	12	***	183	8.4	13	***
NP577>FoxO RNAi^{BDSC}	607	42	9	**	174	11	10	*
NP577>Toll-6	228	14	20	*	79	3.9	19	***
NP577>Toll-6^{TIRdead}	379	16	12	ns	127	5.1	12	ns
NP577>Toll-6, dSARM^{4621}	687	31	9	*	240	14	8	*
NP577>Toll-6, FoxO$^{\Delta 94}$	709	27	11	***	163	12	11	ns
NP577>dSARM	284	13	26	ns	108	6.8	11	ns

NP577>FoxO	225	15	21	*	70	4	21	***
Ctxglia-splitGal4/+	373	27	17	n/a	153	4.4	17	n/a
Ctxglia-split>Toll-6 RNAi[v928]	729	34	16	***	211	10	15	*
Ctxglia-split>dSARM RNAi[v102044]	730	28	14	***	259	13	16	***
Ctxglia-split>FoxO RNAi[v107786]	617	26	17	***	212	11	17	**
Ctxglia-split>Dorsal RNAi[BDSC27650]	417	29	12	ns	136	12	12	ns
Ctxglia-split> Dorsal RNAi[BDSC34938]	418	32	11	ns	133	15	11	ns

Table S1. **Toll-6-FoxO signaling functions in cortex glia to regulate apoptotic debris, related to Figure 1.** Quantification of Dcp-1 particles in the brain and VNC of indicated genotypes. n.s., not significantly different. *, P<0.05; **, P<0.01; ***, P<0.001.

Table S2

Even-skipped (Eve) dorsally projecting motor and interneurons

Genotype	Mean # Eve + cells (abdominal VNC)	SEM	n	Significant?
OR	33	0.52	24	n/a
Toll-6^{EX13}	34	0.89	15	n.s.
dSARM$^{4621/4705}$	34	0.96	19	n.s.
FoxO$^{\Delta94}$	33	0.71	24	n.s.
NP577Gal4/+	34	0.79	13	n.s.
NP577>Toll-6 RNAi^{v928}	35	0.77	15	n.s.
NP577>dSARM RNAi^{v102044}	33	0.65	20	n.s.
NP577>FoxO RNAi^{v107786}	33	0.84	28	n.s.
Elav^{C155}Gal4/+	34	0.85	30	n.s.
Elav^{C155}>spz5 RNAi^{102389}	36	0.85	19	n.s.
Elav^{C155}>spz5 RNAi^{41295}	35	1.0	15	n.s.

Hb9 ventrally projecting motor and interneurons

Genotype	Mean # Hb9 + cells (thoracic VNC)	SEM	n	Significant?	Mean # Hb9+ cells/lobe	SEM	n	Significant?
OR	123	6.1	7	n/a	119	2.9	13	n/a
Toll-6^{EX13}	120	4.1	23	n.s.	123	3.2	21	n.s.
dSARM$^{4621/4705}$	118	3.8	17	n.s.	114	3.5	11	n.s.
FoxO$^{\Delta94}$	118	3.6	27	n.s.	117	4.7	11	n.s.
NP577Gal4/+	109	2.5	18	n.s.	114	3.3	17	n.s.
NP577>Toll-6 RNAi^{v928}	114	3.3	23	n.s.	111	3.0	17	n.s.
NP577>dSARM RNAi^{v102044}	119	3.3	23	n.s.	118	2.6	19	n.s.
NP577>FoxO RNAi^{v107786}	114	2.6	17	n.s.	118	3.9	10	n.s.
Elav^{C155}Gal4/+	131	3.8	21	n.s.	131	3.3	18	n.s.
Elav^{C155}>spz5 RNAi^{102389}	132	3.1	18	n.s.	139	4.0	15	n.s.
Elav^{C155}>spz5 RNAi^{41295}	126	4.4	14	n.s.	125	4.4	10	n.s.

Dbx interneurons

Genotype	Mean # Dbx + cells (thoracic VNC)	SEM	n	Significant?	Mean # Dbx+ cells/lobe	SEM	n	Significant?
OR	125	2.8	17	n/a	332	4.4	16	n/a
Toll-6^{EX13}	124	3.5	9	n.s.	345	5.9	8	n.s.
dSARM$^{4621/4705}$	124	4.4	7	n.s.	330	7	7	n.s.
FoxO$^{\Delta94}$	128	3.1	9	n.s.	331	7.1	11	n.s.
NP577Gal4/+	125	3	15	n.s.	353	9.3	13	n.s.
NP577>Toll-6 RNAi^{v928}	125	3.9	13	n.s.	349	12	14	n.s.
NP577>dSARM RNAi^{v102044}	125	2.2	12	n.s.	333	5	12	n.s.
NP577>FoxO RNAi^{v107786}	125	3.9	9	n.s.	340	9	9	n.s.

NP577+ cortex glia (and small subset of neurons)

Genotype	Mean # NP577 + cells (abdominal VNC)	SEM	n	Significant?	Mean # NP577 + cells/lobe	SEM	n	Significant?
NP577>GFP.NLS/+	102	4.3	16	n/a	233	5.8	21	n/a
NP577>GFP.NLS; Toll-6^{EX13}	110	6.2	12	n.s.	243	8.3	13	n.s.

NP577>GFP.NLS; dSARM$^{4621/4705}$	111	4.2	13	n.s.	239	5.2	14	n.s.
NP577>GFP.NLS; FoxO$^{\Delta94}$	102	2.5	8	n.s.	232	5.6	13	n.s.
NP577>GFP.NLS; Toll-6 RNAi^{v928}	113	3.6	12	n.s.	235	8.8	8	n.s.
NP577>GFP.NLS; dSARM RNAi^{v102044}	105	4.4	12	n.s.	232	4.1	11	n.s.
NP577>GFP.NLS; FoxO RNAi^{v107786}	120	6.4	10	n.s.	241	7.3	12	n.s.

Table S2. **Cortex glial Toll-6-FoxO signaling does not regulate neuronal survival, related to Figure 3.**

Quantification of number of Hb9, Eve, Dbx, or NP577-positive cells in the brain or VNC of indicated genotypes. n.s., not significantly different.

Table S3

Genotype	Mean Drpr immunofluorescence (A.U.)			
	Mean	SEM	n	Significant?
Ctxglia-split> mCD8::GFP/+	1.0	0.03	16	n/a
Ctxglia-split>Drpr RNAi[BDSC]; mCD8::GFP	0.51	0.06	8	***
Ctxglia-split> Drpr-I RNAi; mCD8::GFP	0.47	0.04	18	***
Ctxglia-split>mCD8::GFP/+	1.0	0.02	96	n/a
Ctxglia-split>Toll-6 RNAi[v928]; mCD8::GFP	0.61	0.07	14	***
Ctxglia-split>Toll-6 RNAi[BDSC], mCD8::GFP	0.69	0.05	12	**
Ctxglia-split> dSARM RNAi[v102044]; mCD8::GFP	0.84	0.06	25	***
Ctxglia-split>dSARM RNAi[v105369]; mCD8::GFP	0.65	0.05	26	***
Ctxglia-split>FoxO RNAi[v107786]; mCD8::GFP	0.71	0.09	15	***
Ctxglia-split> FoxO RNAi[BDSC], mCD8::GFP	0.75	0.04	18	**
NP577>mCD8::GFP/+	1.0	0.02	42	n/a
NP577> Toll-6 RNAi[v928]; mCD8::GFP	0.73	0.02	9	***
NP577> dSARM RNAi[v102044]; mCD8::GFP	0.67	0.05	12	***
NP577> FoxO RNAi[v107786]; mCD8::GFP	0.66	0.07	7	***
NP577>mCD8::GFP/+	1.0	0.03	54	n/a
NP577>mCD8::GFP; Toll-6[EX13]	0.64	0.07	10	***
NP577>mCD8::GFP; dSARM[4621/4705]	0.69	0.09	15	***
NP577>mCD8::GFP; FoxO[Δ94]	0.77	0.05	16	**

	# Dcp-1 particles (brain)				# Dcp-1 particles (VNC)			
	Mean	SEM	n	Significant?	Mean	SEM	n	Significant?
Ctxglia-split/+	373	27	17	n/a	153	4.4	17	n/a
Ctxglia-split> Drpr RNAi[BDSC]	1106	93	10	***	594	60	10	***
Ctxglia-split>Drpr RNAi[3B]	944	74	8	**	307	25	8	**
Ctxglia-split>Drpr-I RNAi	905	100	11	***	285	29	11	*
NP577Gal4/+	350	18	17	n/a	121	5.1	18	n/a
NP577>Drpr-I	385	17	11	n.s.	111	5.4	11	n.s.
NP577Gal4/+;; Toll-6[EX13]	682	32	11	***	179	10	9	**
NP577>Drpr-I; Toll-6[EX13]	423	14	27	n.s.	122	6.1	20	n.s.
NP577Gal4/+;; dSARM[4621/4705]	589	33	11	***	215	10	11	***
NP577>Drpr-I; dSARM[4621/4705]	367	18	10	n.s.	126	8.3	11	n.s.
NP577Gal4/+;; FoxO[Δ94]	609	26	10	***	192	10	10	***
NP577>Drpr-I; FoxO[Δ94]	413	22	17	n.s.	137	8.9	17	n.s.

Table S3 (accompanies Figure 3). Quantification of mean Drpr intensity and Dcp-1 particles in indicated genotypes. Statistical comparisons depicted here are compared to control. n.s., not significantly different. *, P<0.05; **, P<0.01; ***, P<0.001.

Table S4

Genotype	# Annexin V particles in the brain/ 5 µm depth				Proportion of engulfed Annexin V particles			
	Mean	SEM	n	Significant?	Mean	SEM	n	Significant?
Ctxglia-split>LacZ; mCD8::GFP	113	7.3	20	n/a	0.75	0.02	20	n/a
Ctxglia-split>Toll-6 RNAi[v928]; mCD8::GFP	190	8.3	19	***	0.54	0.03	27	***
Ctxglia-split>dSARM RNAi[v102044]; mCD8::GFP	188	6.6	17	***	0.56	0.02	22	***
Ctxglia-split>FoxO RNAi[v107786]; mCD8::GFP	180	9.1	18	***	0.54	0.03	22	***
Ctxglia-split>Drpr-I RNAi; mCD8::GFP	177	10	19	***	0.48	0.02	27	***

Table S4 (accompanies Figure 4). Quantification of number of Annexin V particles and proportion of engulfed Annexin V particles in indicated genotypes. ***, P<0.001.

Table S5

Genotype	Quantification of Dcp-1 particles				Mean Drpr immunofluorescence (A.U.)			
	Mean	SEM	n	Significant?	Mean	SEM	n	Significant?
Elav^{C155}Gal4/+	376	19	11	n/a	0.99	0.04	18	n/a
Elav^{C155}> Spz5 RNAi^{v102389}	683	44	14	***	0.57	0.04	19	***
Elav^{C155}> Spz5 RNAi^{v41295}	731	49	13	***	0.71	0.08	11	*
Elav^{C155}>Spz5 RNAi^{BDSC}	724	40	14	***				
wild type (OR)	435	13	8	n/a	1.0	0.03	36	n/a
Spz5^{AW18}	699	43	13	**	0.73	0.05	37	***
Spz5^{AW18}/+	441	19	15	n.s.				
Spz5^{AW18}/+, Toll-6^{EX13}/+	736	33	12	***				
Spz5^{AW18}/+, dSARM^{4621}/+	710	37	13	***				
Spz5^{AW18}/+, FoxO^{Δ94}/+	669	29	11	**				
Elav^{C155}>P35	248	16	15	n/a				
Elav^{C155}/+;; Toll-6^{EX13}	730	38	9	***				
Elav^{C155}>P35; Toll-6^{EX13}	320	18	12	n.s.				
NP577Gal4/+	524	47	5	n/a				
NP577Gal4/+;; Spz5^{AW18}	786	46	11	*				
NP577>Drpr-I; Spz5^{AW18}	543	27	12	n.s.				
Elav^{C155}Gal4/+	376	19	11	n/a				
Elav^{C155}>Spz5-HA	399	32	9	n.s.				
Elav^{C155}Gal4/+;; Spz5^{AW18}	735	41	8	***				
Elav^{C155}>Spz5-HA, Spz5^{AW18}	471	22	15	n.s.				
Ctxglia-splitGal4/+	373	27	17	n/a				
Ctxglia-split>Spz5 RNAi^{v102389}	377	28	11	n.s.				
Ctxglia-split>Spz5 RNAi^{v41295}	432	33	10	n.s.				

Table S5 (accompanies Figure 5). Quantification of Dcp-1 particles and Drpr immunofluorescence in indicated genotypes. Statistical comparisons depicted here are compared to controls. n.s., not significantly different. *, P<0.05; **, P<0.01; ***, P<0.001.

Table S6.

Genotype	Quantification of Dcp-1 particles				Mean Drpr immunofluorescence (A.U.)			
	Mean	SEM	n	Significant?	Mean	SEM	n	Significant?
$Elav^{C155}Gal4/+$	451	21	14	n/a	1.0	0.02	60	n/a
$Elav^{C155}$>Fur1 RNAi [41914]	640	50	17	*	0.87	0.08	27	*
$Elav^{C155}$> Fur1 RNAi [42481]	631	26	17	**	0.84	0.05	17	*
$Elav^{C155}$>Fur2 RNAi [51743]	785	53	12	***	0.72	0.03	18	***
$Elav^{C155}$>Fur2 RNAi [42577]	694	36	21	***	0.72	0.05	25	***
$Elav^{C155}$>Fur2 RNAi [25959]	642	45	15	*	0.59	0.04	16	***
$Elav^{C155}Gal4/+$	451	21	14	n/a	1.0	0.04	18	n/a
$Elav^{C155}$>Fur1^R	479	40	10	n.s.				
$Elav^{C155}$>Fur1^X	504	60	8	n.s.				
$Elav^{C155}$>Fur2	345	26	15	*	1.3	0.06	16	***
	Cleaved Spz5-HA/total Spz5-HA (A.U.)							
	Mean	SEM	n	Significant?				
$Elav^{C155}$>LacZ; Spz5-HA	1.0	0.2	9	n/a				
$Elav^{C155}$>Fur2 RNAi^{51743}, Spz5-HA	0.47	0.07	13	**				
$Elav^{C155}$>LacZ; Spz5-HA	1.0	0.12	7	n/a				
$Elav^{C155}$>Spz5-HA, Fur2	3.8	1.2	9	*				
$Elav^{C155}$>Spz5-HA; HS-Hid (25ºC)	1.0	0.09	6	n/a				
$Elav^{C155}$>Spz5-HA; HS-Hid (37ºC)	2.1	0.41	11	*				
$Elav^{C155}$>LacZ; Spz5-HA	1.0	0.07	9	n/a				
$Elav^{C155}$> P35; Spz5-HA	0.6	0.09	11	**				

Table S6 (accompanies Figure 6). Quantification of Dcp-1 particles, mean Drpr immunofluorescence, and Spz-5 cleavage in indicated genotypes. Statistical comparisons depicted here are compared to controls. n.s., not significantly different. *, P<0.05; **, P<0.01; ***, P<0.001.

Table S7

Genotype	Quantification of Dcp-1 particles												
	Mean	SEM	n	Significant?									
wild type	41	5.7	8	n/a									
Toll-6^{EX13}	73	4.3	13	**									
FoxO$^{\Delta94}$	80	8.4	10	**									
NP577Gal4/+	41	4.2	10	n/a									
NP577>Toll-6 RNAi^{v928}	75	2.7	14	***									
NP577>Toll-6 RNAi^{BDSC}	78	6.4	14	**									
NP577>dSARM RNAi^{v102044}	83	3.1	10	***									
NP577>dSARM RNAi^{v105369}	75	3.2	9	**									
NP577>FoxO RNAi^{v107786}	75	3.5	11	**									
NP577>FoxO RNAi^{BDSC}	74	4.6	10	**									
Elav^{C155}Gal4/+	44	3.8	9	n/a									
Elav^{C155}> Toll-6 RNAi^{v928}	48	5.0	11	n.s.									
Elav^{C155}>dSARM RNAi^{v102044}	42	1.8	9	n.s.									
Elav^{C155}>FoxO RNAi^{v107786}	42	4.6	10	n.s.									
	5 DPE neurodegeneration index				10 DPE neurodegeneration index				35 DPE neurodegeneration index			
	Mean	SEM	n	Significant?	Mean	SEM	n	Significant?	Mean	SEM	n	Significant?
NP577Gal4/+	1.4	0.2	27	n/a	1.2	0.4	10	n/a	2.7	0.3	11	n/a
NP577>Toll-6 RNAi^{v928}	2.1	0.4	14	n.s	3.5	0.2	11	***	3.4	0.3	8	n.s.
NP577>dSARM RNAi^{v102044}	2.0	0.3	12	n.s.	2.9	0.4	11	**	2.8	0.2	16	n.s.
NP577>FoxO RNAi^{v107786}	2.1	0.4	11	n.s.	2.6	0.3	22	**	2.3	0.4	12	n.s.

Table S7 (accompanies Figure 7). Quantification of Dcp-1 particles and neurodegeneration phenotypes in adult brains of indicated genotypes. n.s., not significantly different. **, P<0.01; ***, P<0.001.