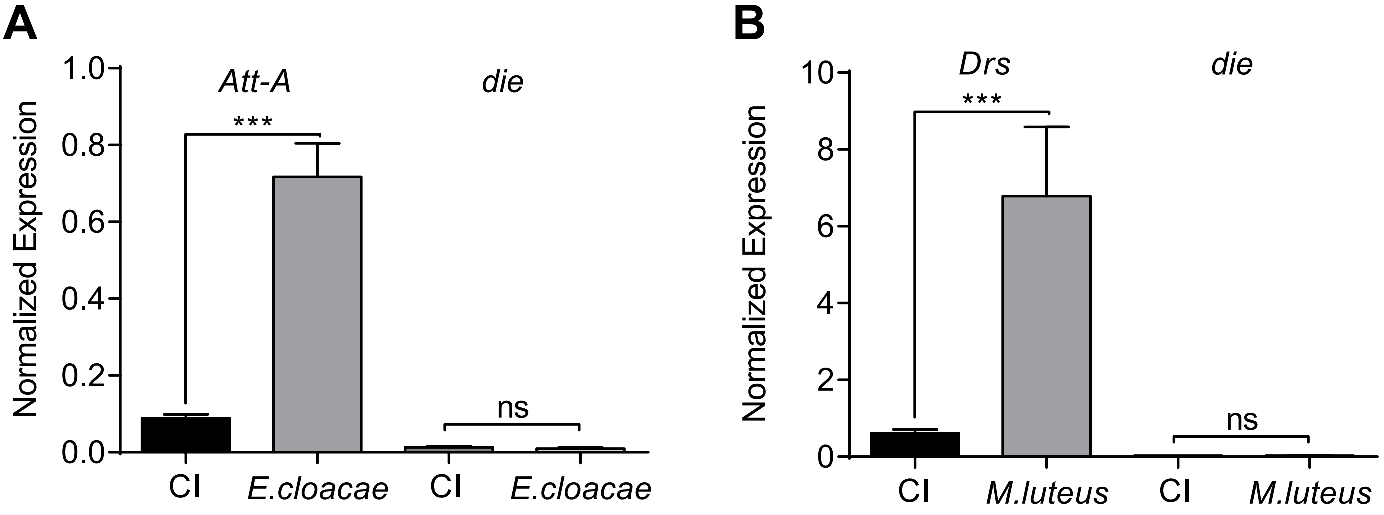


Figure S1: *die* is not induced after infection by *E.cloacae* and *M.luteus* bacteria.
(A, B) Wild-type flies were challenged with the Gram-negative bacteria *E. cloacae* (A) or the Gram positive bacteria *M. luteus* (B), and expression of *die*, *Attacin-A* (an IMD target gene) and *Drosomycin* (a Toll target gene) mRNA was assayed by qRT-PCR at 6h (A) or 24h (B) post-infection. Data represent the mean and s.d. of three independent experiments each containing three groups of 6 flies. t-test: ns $p>0.05$, *** $p<0.001$. CI: clean injury.

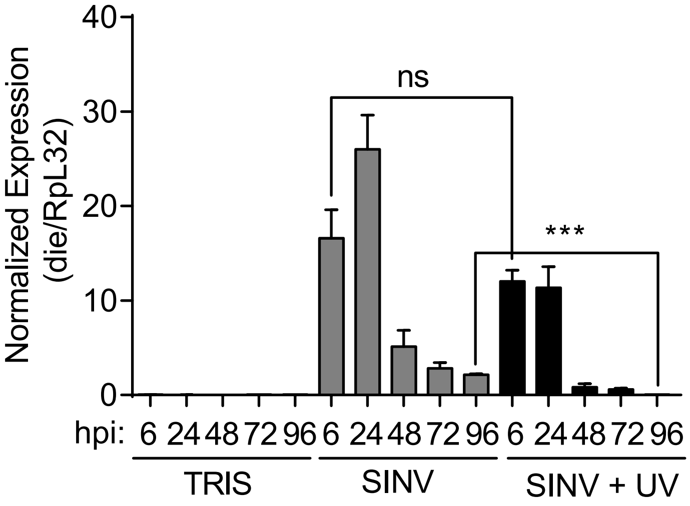


Figure S2: Rapid induction of *die* does not require infectious Sindbis virus.

Wild-type flies were infected with either SINV or UV-inactivated SINV (2500 PFU) and *die* mRNA levels were monitored by qRT-PCR at the indicated timepoints. Mean and s.d. of two independent experiments, each containing three groups of 6 flies, is shown. t-test : ns $p>0.05$, *** $p<0.001$. hpi: hours post-injection. Note that the difference between live and UV-inactivated SINV becomes statistically significant at late time points.

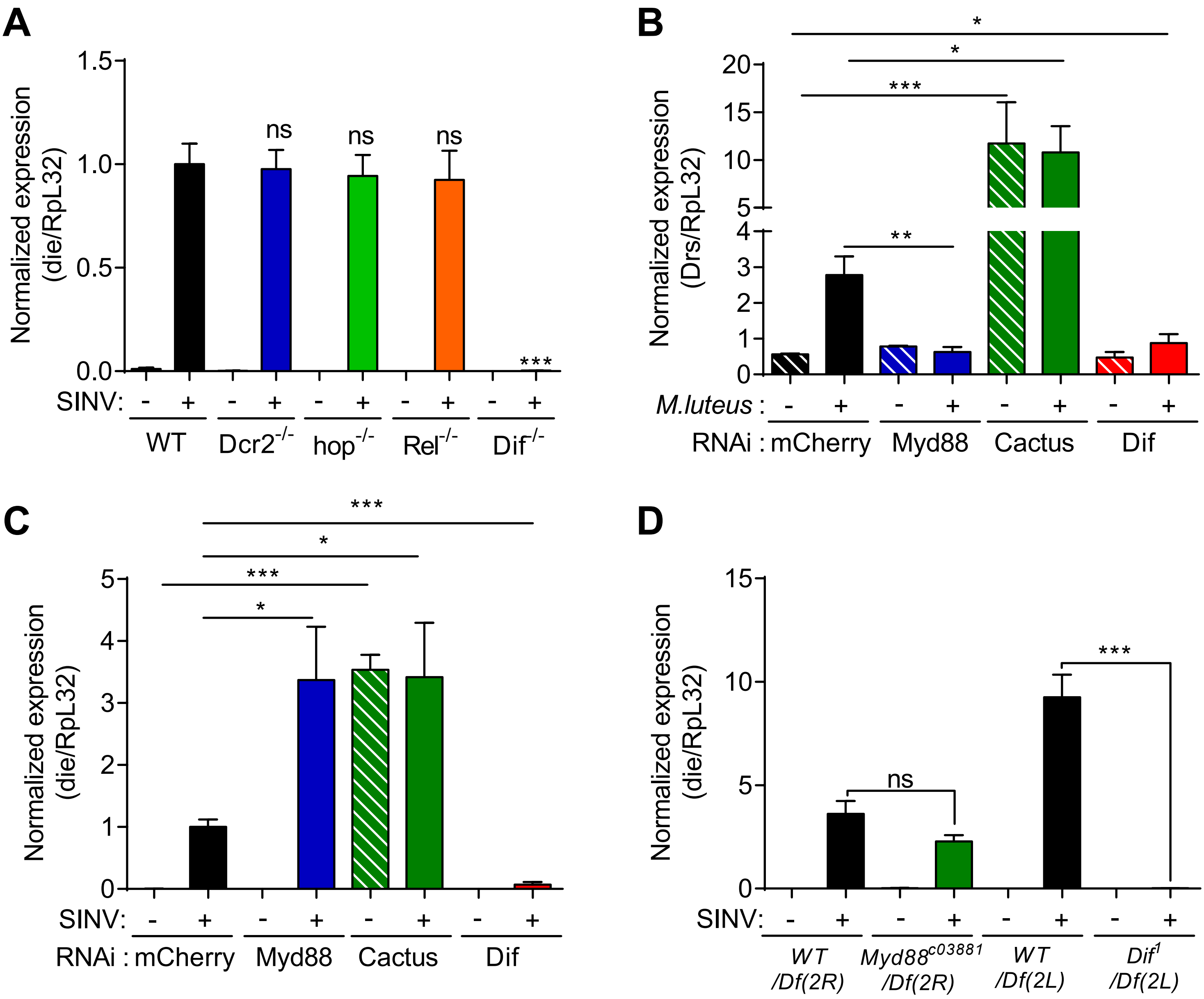
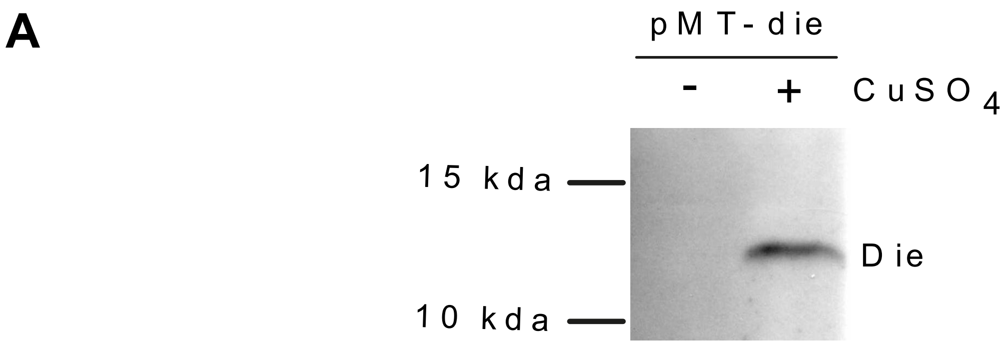


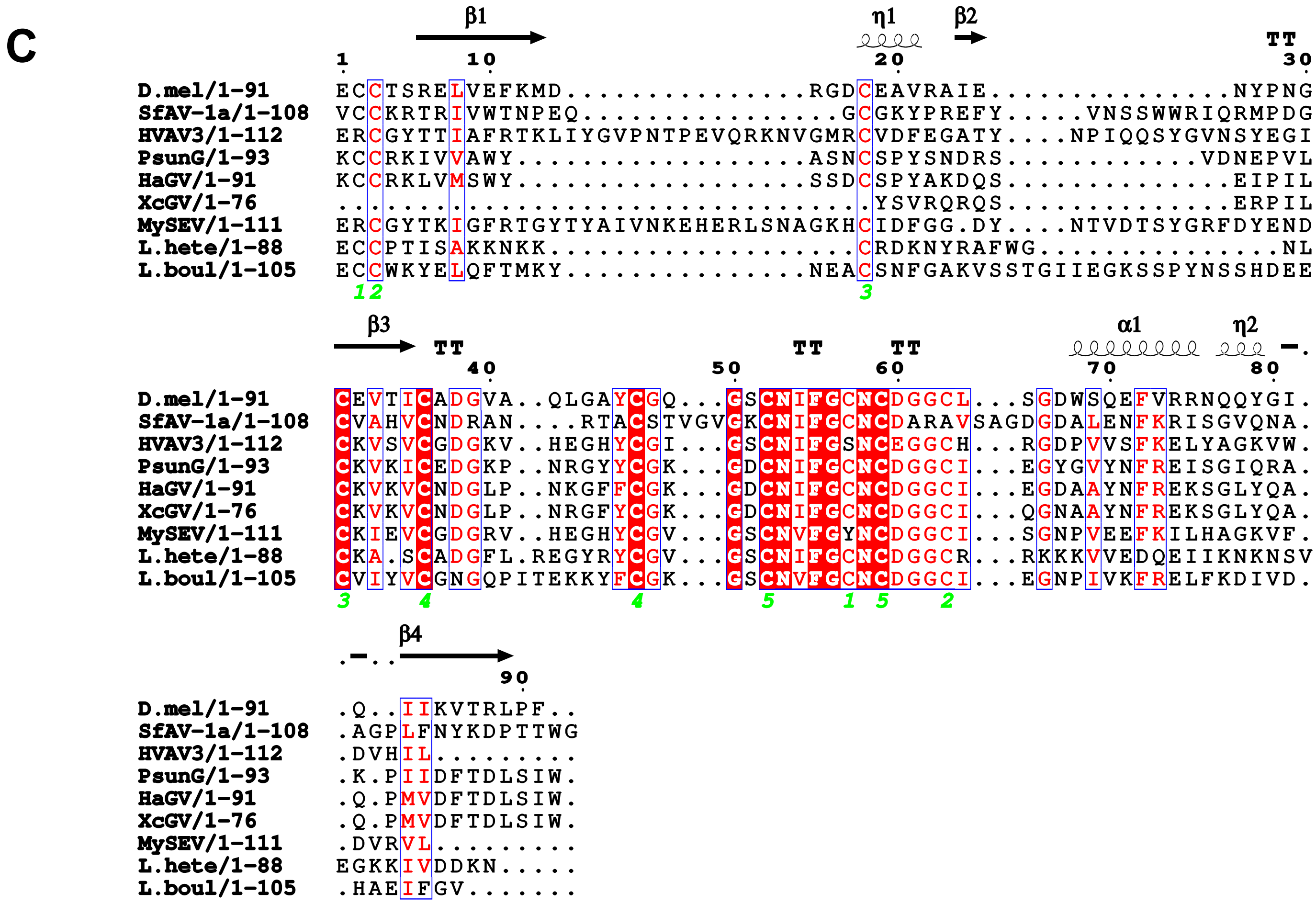
Figure S3: Induction of *die* requires the NF-kappaB transcription factor *Dif* but not *Myd88*

(A) The mutant flies $Dcr2^{L811fsX}$ (Dcr2 $^{-/-}$), $hop^{msv1/M38}$ (hop $^{-/-}$), Rel^{E20} (Rel$^{-/-}$) and Dif^{1} (Dif$^{-/-}$) were injected with TRIS (-) or SINV (+). The expresssion level of *die* mRNA was determined using qRT-PCR at 1 dpi. (B and C) Flies expressing dsRNA (*act-GAL4;UAS-dsRNA*) against *mCherry*, *Myd88*, *Cactus* and *Dif* genes were infected by *M.luteus* (B) or SINV (C). The expression level of *Drosomycin* (*Drs*) (B) or *die* mRNA (C) was determined using qRT-PCR. (D) Hemizygotes flies expressing one (*WT/Df(2R)* and *WT/(Df(2L)*) or zero copy of the *Myd88* ($Myd88^{c03881}$*/Df(2R)*) or *Dif* (Dif^{1}*/Df(2L)*) gene were injected with TRIS (-) or SINV (+). The deficiencies covering *Myd88* and *Dif* genes are Df (2R)BSC279 and Df(2L)Exel7068, respectively. The expression level of *die* mRNA was determined using qRT-PCR at 1 dpi. Data represent the mean and s.d. of three independent experiments, each containing three groups of 6 flies. t-test: ns p>0.05, * p< 0.05, ** p< 0.01, *** p<0.001.



B

Die homolog from:	Name	ID:
Pseudaletia unipuncta granulovirus	ORF109	YP_003422448.1
Helicoverpa armigera granulovirus	HaGV_gp108	YP_001649090.1
Xestia c-nigrum granulovirus	ORF106	NP_059254.1
Spodoptera frugiperda ascovirus 1a	ORF121	YP_762476.1
Heliothis virescens ascovirus 3e	HVAV3e_gp095	YP_001110948
Mythimna separata entomopoxvirus 'L'	MYSEV_165	YP_008003682.1
Leptopilina heterotoma	comp202_c0_seq1	Goecks *et al*., 2013
Leptopilina boulardi	comp479_c0_seq1	Goecks *et al*., 2013



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D.mel/1-91       ECCTSRELVEFKMD...............RGDCEAVRAIE...............NYPNG
SfAV-1a/1-108    VCCKRTRIVWTNPEQ................GCGKYPREFY.....VNSSWWRIQRMPDG
HVAV3/1-112      ERCGYTTIAFRTKLIYGVPNTPEVQRKNVGMRCVDFEGATY....NPIQQSYGVNSYEGI
PsunG/1-93       KCCRKIVVAWY..................ASNCSPYSNDRS............VDNEPVL
HaGV/1-91        KCCRKLVMSWY..................SSDCSPYAKDQS..............EIPIL
XcGV/1-76        .................................YSVRQRQS..............ERPIL
MySEV/1-111      ERCGYTKIGFRTGYTYAIVNKEHERLSNAGKHCIDFGG.DY....NTVDTSYGRFDYEND
L.hete/1-88      ECCPTISAKKNKK...................CRDKNYRAFWG...............NL
L.boul/1-105     ECCWKYELQFTMKY...............NEACSNFGAKVSSTGIIEGKSSPYNSSHDEE

D.mel/1-91       CEVTICADGVA..QLGAYCGQ...GSCNIFGCNCDGGCL...SGDWSQEFVRRNQQYGI.
SfAV-1a/1-108    CVAHVCNDRAN....RTACSTVGVGKCNIFGCNCDARAVSAGDGDALENFKRISGVQNA.
HVAV3/1-112      CKVSVCGDGKV..HEGHYCGI...GSCNIFGSNCEGGCH...RGDPVVSFKELYAGKVW.
PsunG/1-93       CKVKICEDGKP..NRGYYCGK...GDCNIFGCNCDGGCI...EGYGVYNFREISGIQRA.
HaGV/1-91        CKVKVCNDGLP..NKGFFCGK...GDCNIFGCNCDGGCI...EGDAAYNFREKSGLYQA.
XcGV/1-76        CKVKVCNDGLP..NRGFYCGK...GDCNIFGCNCDGGCI...QGNAAYNFREKSGLYQA.
MySEV/1-111      CKIEVCGDGRV..HEGHYCGV...GSCNVFGYNCDGGCI...SGNPVEEFKILHAGKVF.
L.hete/1-88      CKA.SCADGFL.REGYRYCGV...GSCNIFGCNCDGGCR...RKKKVVEDQEIIKNKNSV
L.boul/1-105     CVIYVCGNGQPITEKKYFCGK...GSCNVFGCNCDGGCI...EGNPIVKFRELFKDIVD.

D.mel/1-91       .Q..IIKVTRLPF..
SfAV-1a/1-108    .AGPLFNYKDPTTWG
HVAV3/1-112      .DVHIL.........
PsunG/1-93       .K.PIIDFTDLSIW.
HaGV/1-91        .Q.PMVDFTDLSIW.
XcGV/1-76        .Q.PMVDFTDLSIW.
MySEV/1-111      .DVRVL.........
L.hete/1-88      EGKKIVDDKN.....
L.boul/1-105     .HAEIFGV.......
```

Figure S4

(A) The C-terminally V5 tagged Die protein is detected by Western blot with anti-V5 antibodies in the supernatant of S2 cells transfected with a metallothionein driven vector expressing the *die* cDNA. (B) The table indicates the origin, name and reference sequence for Die homologs. (C) The Die protein of *D. melanogaster* was aligned to homologous gene products from *Spodoptera frugiperda ascovirus* (SfAV-1a), *Heliothis virescens ascovirus 3e* (HVAV3), *Pseudalatia unipuncta granulovirus* (PsunG), *Helicoverpa armigera granulovirus* (HaGV), *Xestia c-nigrum granulovirus* (XcGV), *Mythimna separata entomopoxvirus L* (MySEV), *Leptopilina boulardi* (L.boul) and *Leptopilina heterotoma* (L.hete). Secondary structure elements as determined in *Drosophila* Die, are indicated below the sequences as arrows and helices, respectively. Conserved residues are boxed, and strictly conserved residues are shown in white with a red background. The figure was generated with ESPript (Gouet *et al.,* 2003)

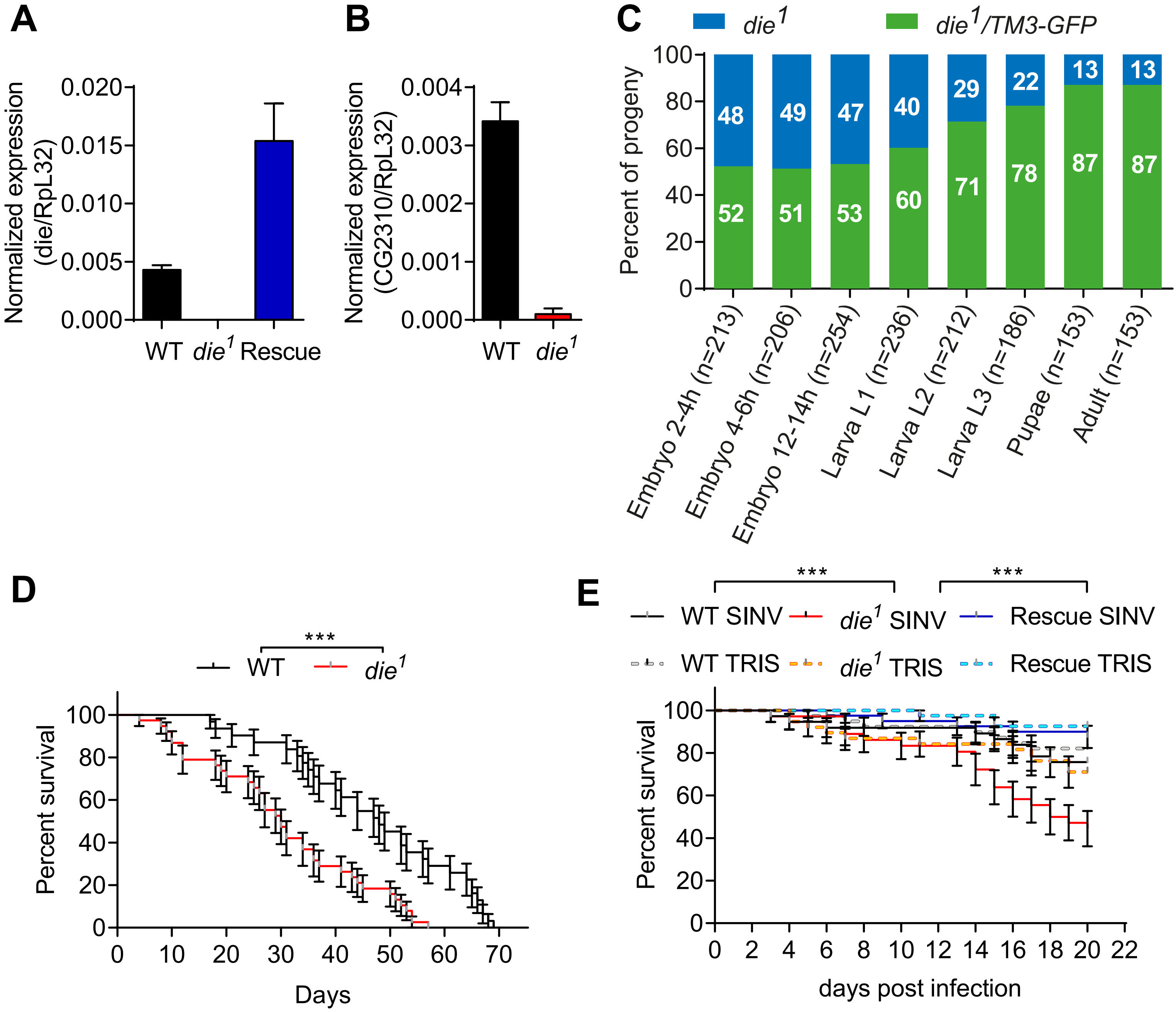

Figure S5: *die* is required for viability during developments and in adults.

(A and B) mRNA levels for *die* and CG2310 were monitored by qPCR in wild-type, *die*^{1} mutant and Rescue (*act-GAL4; UAS-die, die*^{1}) flies. (C) Homozygous *die*^{1} mutant males were crossed to heterozygous *die*^{1}*/TM3-GFP* females, generating 50% of *die*^{1} homozygous embryos and 50% of heterozygous embryos expressing the GFP balancer chromosome. The ratio between homozygous and heterozygous progeny was followed throughout development at 25°C. Data represent the mean of 2 independent experiments and the total number of individuals monitored is indicated. (D) The lifespan of wild-type and *die*^{1} flies was measured daily at 25°C. (E) Flies of the indicated genotype were injected with Tris, SINV and survival was monitored daily at 25°C. Data represent the mean and s.d. (A and B) or s.e (D and F) of 3 independent experiments, each containing 3 groups of 10 (D and E) or 6 (A and B) flies. Log rank test: *** indicate that $p<0.001$.

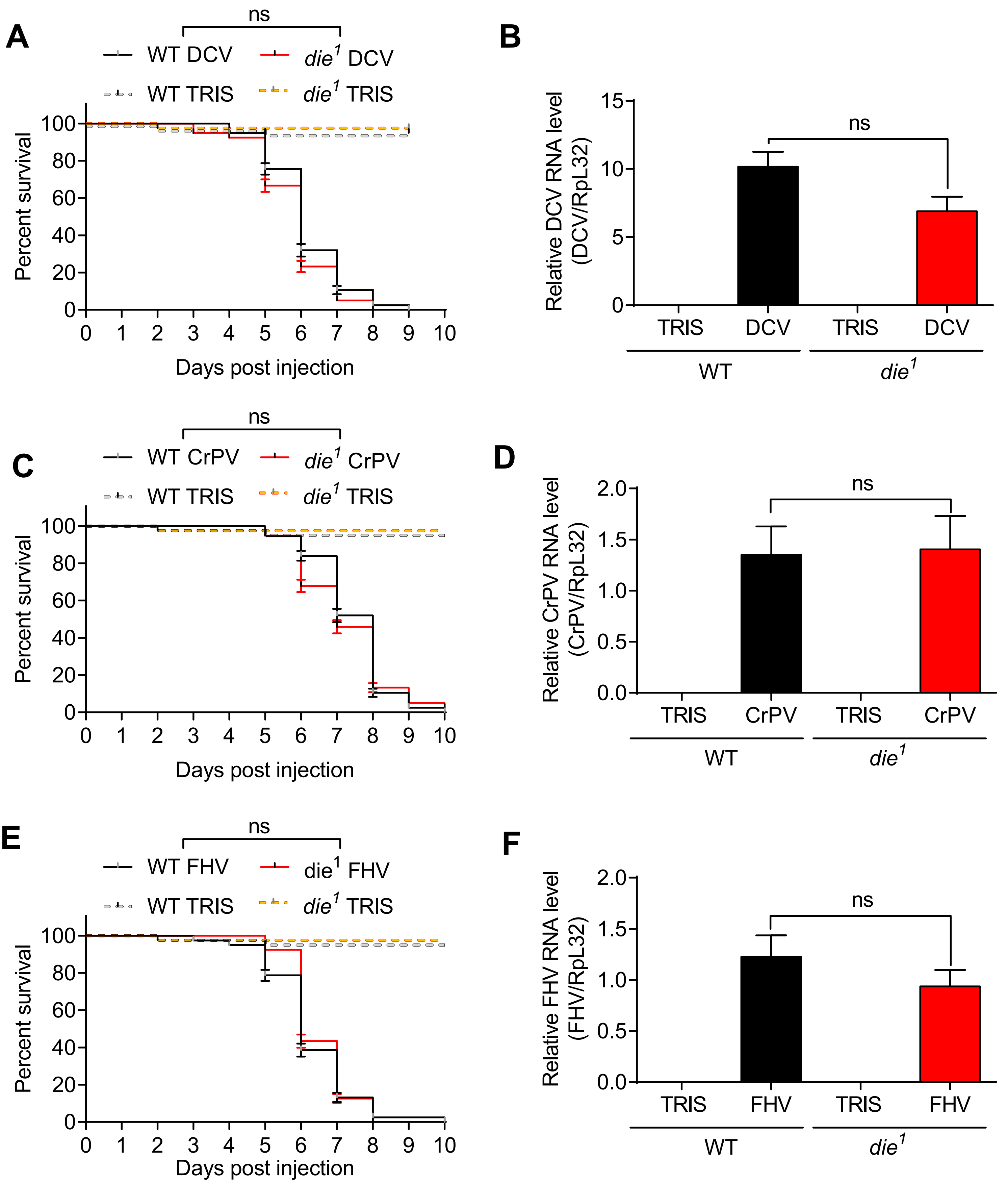

Figure S6: *die^1* mutant flies are not sensitive to DCV, CrPV and FHV.

(A, C, E) Flies of the indicated genotype were injected with TRIS, DCV (A), CrPV (C) or FHV (E) and survival was monitored daily at 25°C. (B, D, F) Analysis of the accumulation of DCV (B), CrPV (D) and FHV (F) RNA in wild-type and *die^1* mutants at 3 dpi. Data represent the mean and s.e. (A, C, E) or s.d. (B, D, F) of 3 independent experiments, each containing 3 groups of 10 (A, C, E) or 6 (B, D, F) flies. Log rank (A, C, E) and t test (B, D, F): ns indicates that $p > 0.05$.

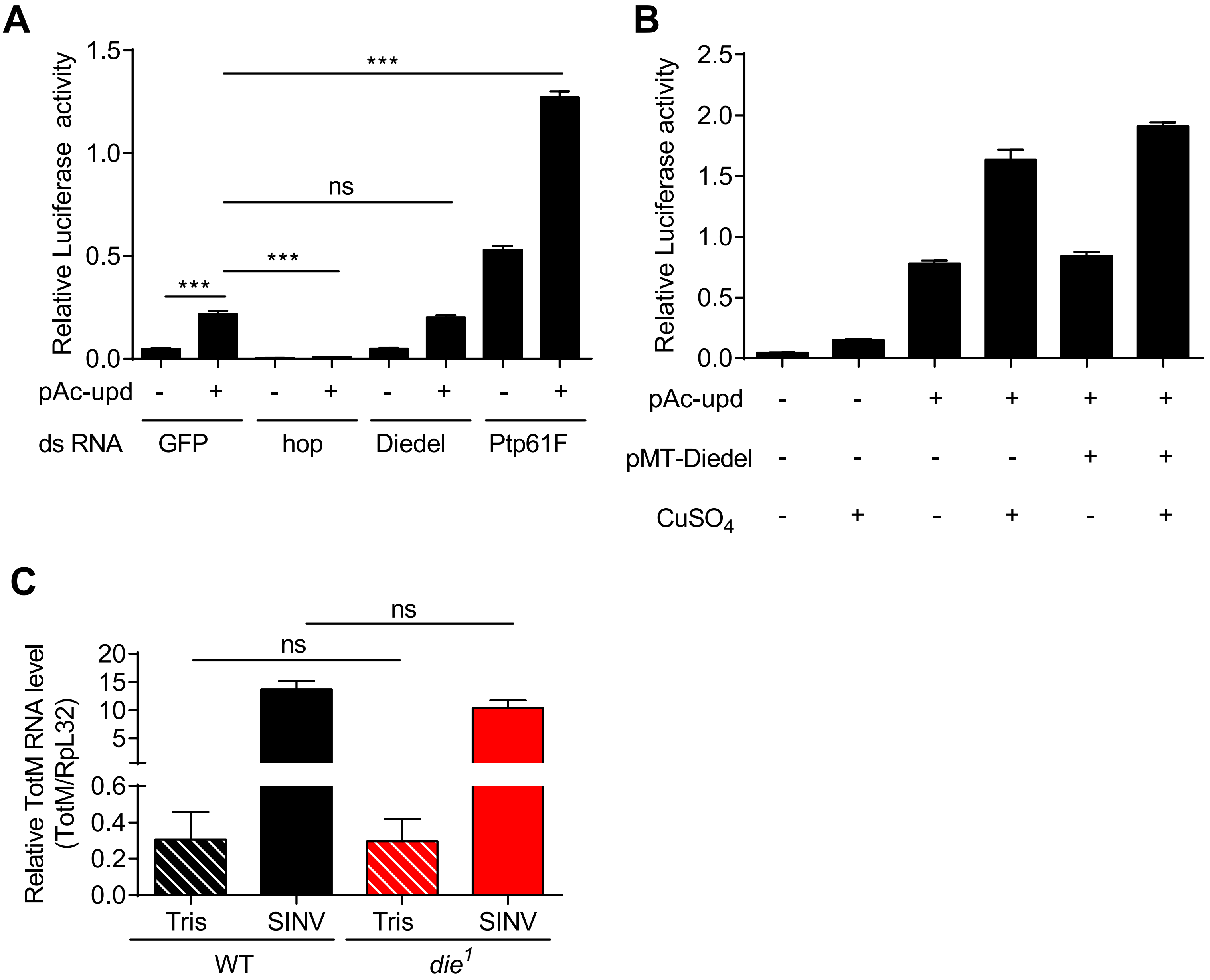

Figure S7: *die* is not a negative regulator of the JAK/STAT pathway.

(A and B) S2 cells were co-transfected with the *Turandot M* (*TotM*) Luciferase reporter and the pAC-upd plasmid. (A) dsRNA against *hopsctoch* (*hop*) or *Ptp61F,* but not *die,* significantly affects the induction of the Luciferase by *Upd*. (B) S2 cells were also co-transfected the pMT-*die* plasmid. CuSO4 were added in order to induce the expression of Die protein. (C) Analysis of the relative TotM RNA level in wild-type and *die*^{1} mutant flies 24 hours post injection. Data represent the mean and s.d. of 3 independent experiments, each containing 3 groups of 6 flies (C). t test (A, C): ns indicate that p> 0.05, *** p< 0,001.

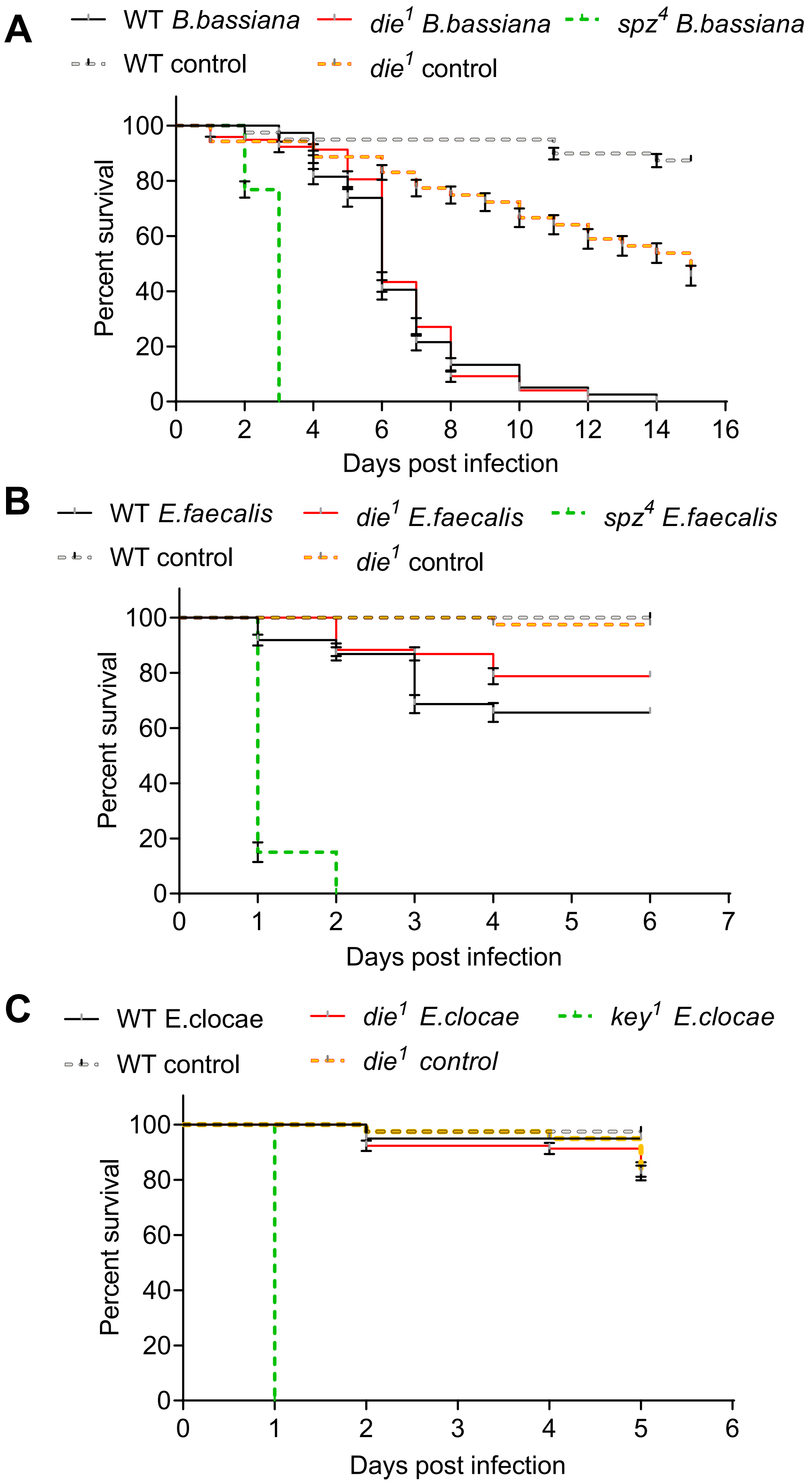

Figure S8: *die*^{1} mutants are not sensitive to bacterial and fungal infections.

(A, B, C) Wild-type, *die*^{1}, *spz*^{4} (A, B), *key*^{1} (C) flies were naturally infected with *B.bassiana* (A), or injected with *E.faecalis* (B) or *E.cloacae* (C) and survival was monitored daily at 29°C. Data represent the mean and s.e. of three independant experiments, each containing 3 groups of 10 flies.

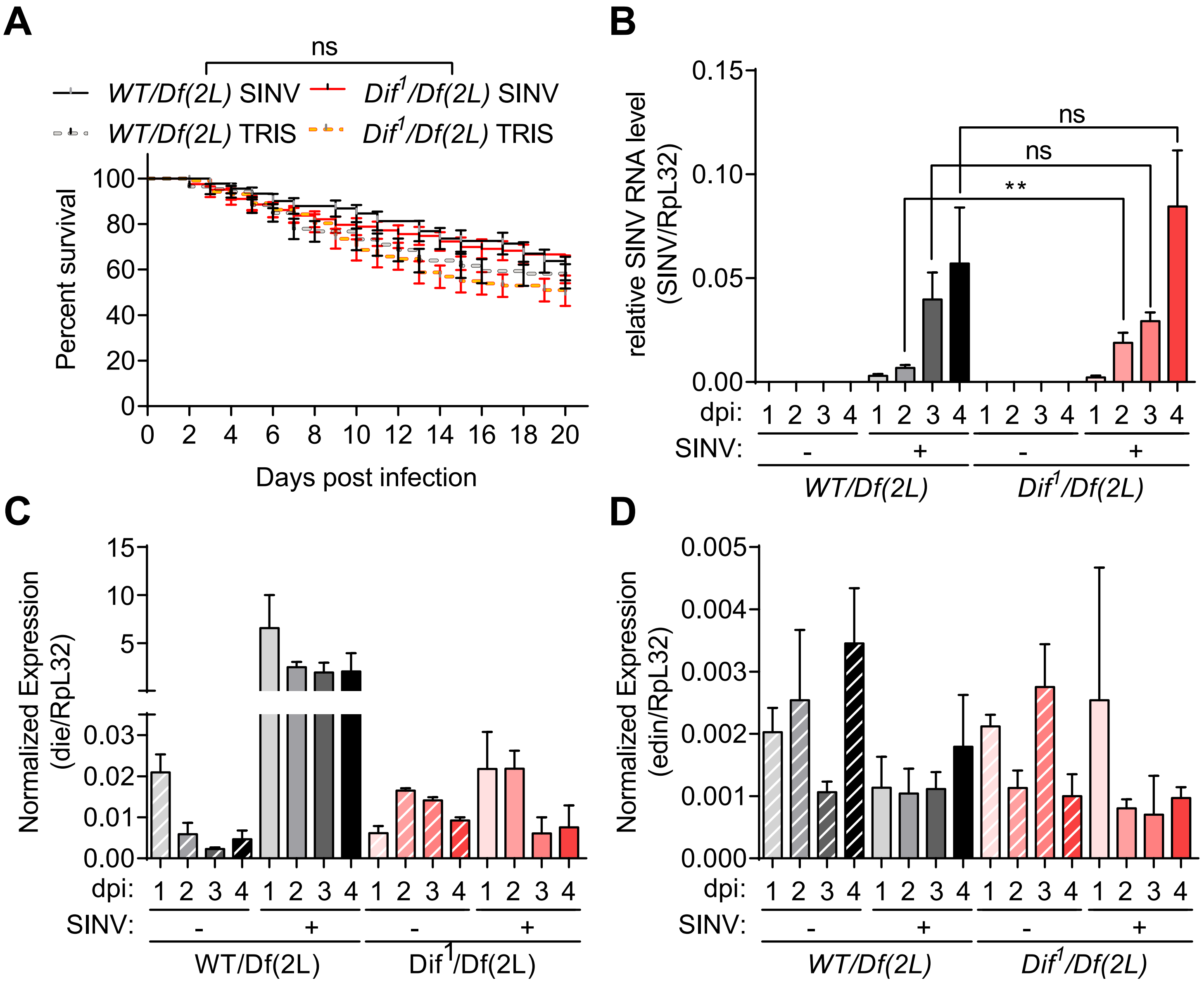

Figure S9: The basal level of *die* is sufficient to protect against SINV infection.

Hemizygotes flies expressing one (*WT/(Df(2L)*) or zero copy of the gene *Dif* (*Dif^1/Df(2L)*) were injected with TRIS (-) or SINV (+). The defiency covering the Dif gene is Df(2L)Exel7068. (A) The survival of these flies was monitored daily at 29°C. (B, C, D) The expression level of SINV (B), *die* (C) and *edin* (D) RNA were determined using qPCR at 1 to 4 dpi. Data represent the mean and s.e. (A) or s.d. (B-D) of three independent experiments, each containing three groups of 10 flies (A) or two group of 6 flies (B-D). Log rank (A) or t-test (B): ns p>0.05, ** p< 0.01.

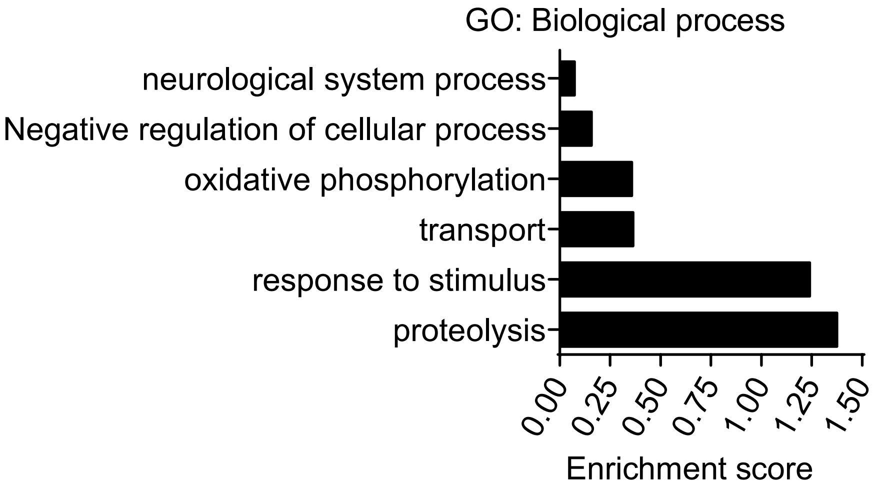

Figure S10: Gene ontology analysis for biological process for the 69 downregulated genes in non infected conditions when *die* is mutated.

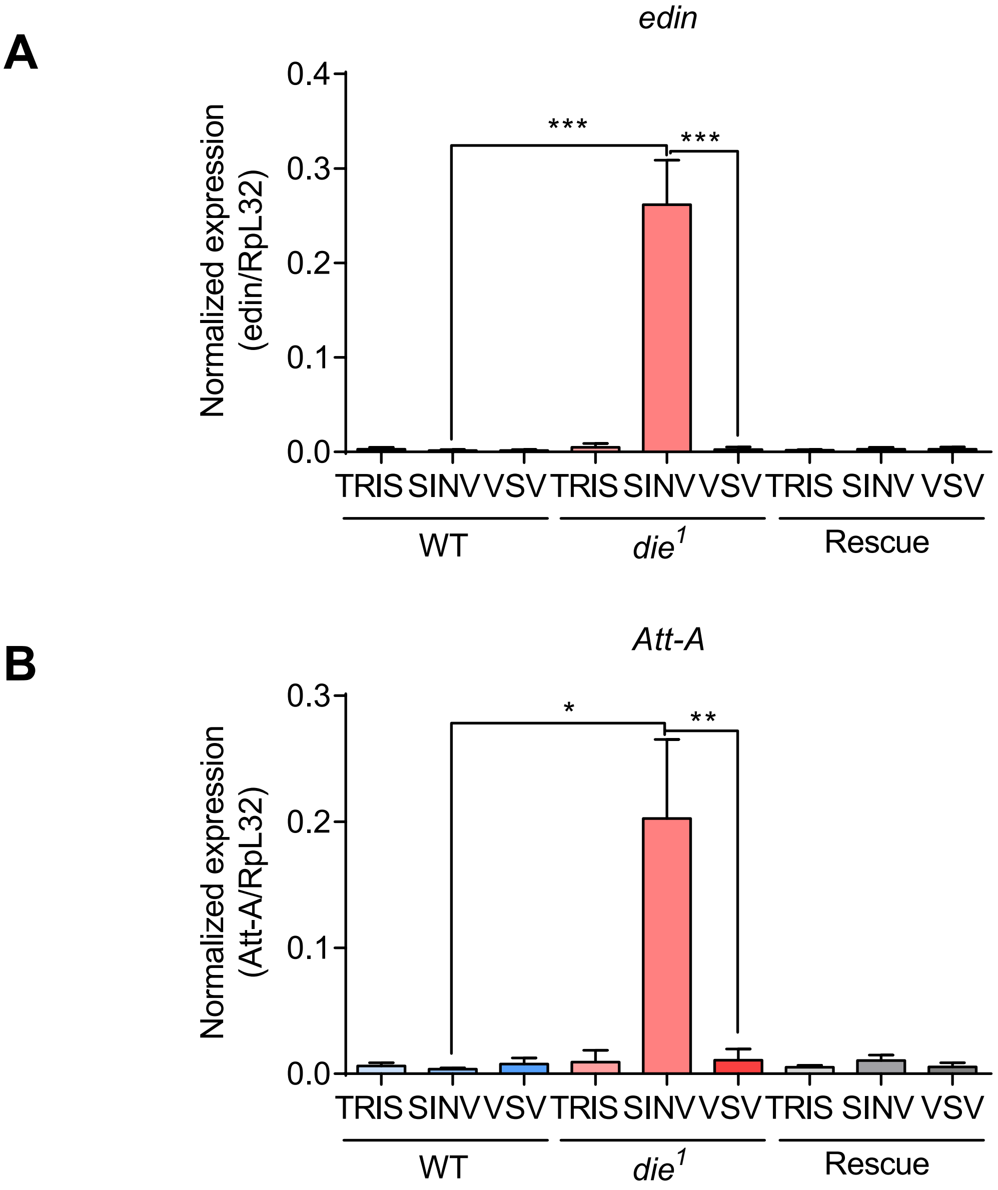

Figure S11: *edin* and *Attacin-A* are not induced by VSV infection in *die*^{1} mutant flies.

(A, B) mRNA levels of *edin* (A) and *Attacin-A* (B) were monitored in wild-type and *die*^{1} flies at 4 days post injection with Tris, SINV or VSV. Data represent the mean and s.d. of three independent experiments, each containing two groups of 6 flies. t-test: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

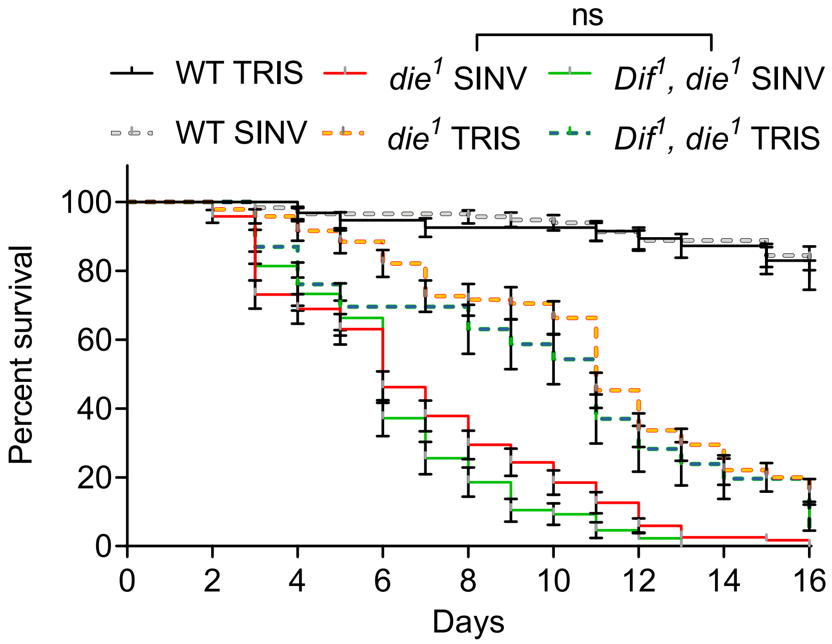

Figure S12: *Dif* mutation cannot rescue the phenotype of *die* mutant flies.

Wild-type, *die*^{1}, and double mutant *Dif*^{1}*; die*^{1} flies were injected with Tris or SINV and survival was monitored daily at 29°C. Data represent the mean and s.e. of 3 independent experiments, each containing 3 groups of 10 flies. Log rank test: ns indicate that $p > 0.05$.

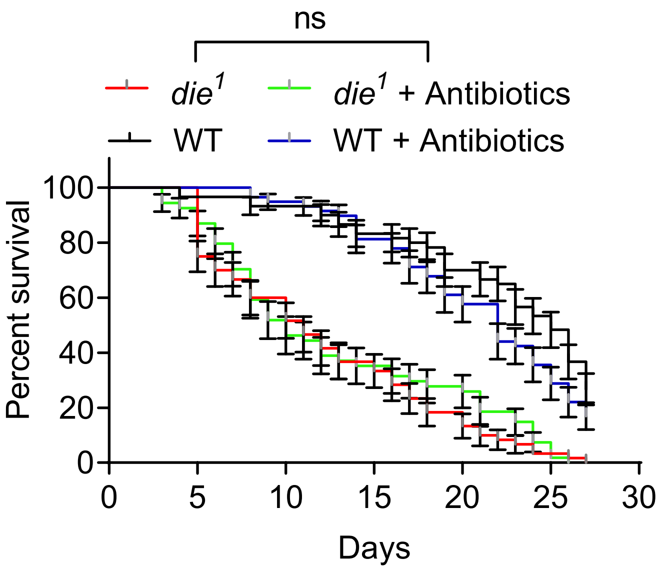

Figure S13: Antibiotics treatment does not restore the survival of *die*^{1} mutant flies.

Survival of WT and *die*^{1} mutant flies on normal and antibiotics media. Data represent the mean and s.e. of three independent experiments, each containing two groups of 10 flies. Log rank test: ns p> 0.05.

A

		Signal				Ratio			
Probe name	**Gene name**	**WT NI**	***die*^{1} NI**	**WT SINV**	***die*^{1} SINV**	**die^1/WT NI**	**WT SINV**	**die^1 SINV**	**die^1/WT SINV**
A_09_P008151	*Caspar*	1287,66	1240,07	1220,54	1076,88	0,96	0,95	0,87	0,88
A_09_P021456	*CYLD*	1481,61	1280,96	1350,88	1338,88	0,86	0,91	1,05	0,99
A_09_P026511	dnr1	1902,61	1820,80	1784,27	1834,83	0,96	0,94	1,01	1,03
A_09_P026606	RYBP	734,28	744,73	775,03	752,98	1,01	1,06	1,01	0,97
A_09_P053031	*dUSP36*	2941,69	2658,60	2777,50	2634,91	0,90	0,94	0,99	0,95
A_09_P011671	faf	458,70	408,39	470,86	420,42	0,89	1,03	1,03	0,89
A_09_P073846	PGRP-LB	1670,96	1530,69	2560,27	2384,58	0,92	1,53	1,56	0,93
A_09_P054296	PGRP-LF	713,69	1046,35	973,59	1759,83	1,47	1,36	1,68	1,81
A_09_P056556	PGRP-SC1a	16811,67	16952,60	46478,80	15660,72	1,01	2,76	0,92	0,34
A_09_P025276	PGRP-SC1b	41366,88	52970,67	103938,70	49596,30	1,28	2,51	0,94	0,48
A_09_P110955	PGRP-SC2	67477,00	76402,20	105704,95	136942,50	1,13	1,57	1,79	1,30
A_09_P207530	pirk	2164,10	3135,85	5203,66	6293,94	1,45	2,40	2,01	1,21
A_09_P062616	POSH	494,69	539,00	537,69	581,31	1,09	1,09	1,08	1,08
A_09_P073176	trbd	3294,05	2888,56	2853,13	2775,30	0,88	0,87	0,96	0,97
A_09_P074691	wntD	100,66	68,00	80,00	84,78	0,68	0,79	1,25	1,06

B

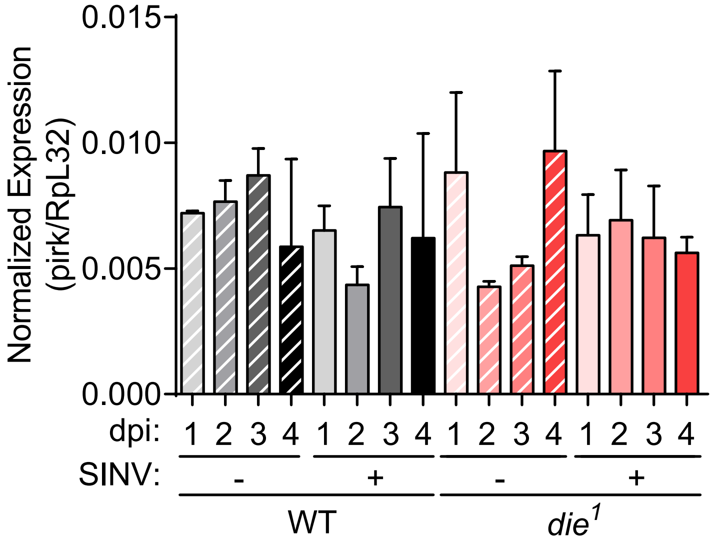

Figure S14: The *die*^{1} mutation does not affect expression of known inhibitors of the IMD pathway.

(A) This table represent the signal and the fold change for the expression of known negative regulators of the IMD pathway in a microarray experiment. Genes colored in red have more than 25% of difference between biological duplicates. (B)The expresssion level of pirk mRNA was determined in WT and *die*^{1} flies injected by TRIS (-) or SINV (+) using qRT-PCR at 1 to 4 dpi. Data represent the mean and s.d. of two independent experiments, each containing two groups of 6 flies.

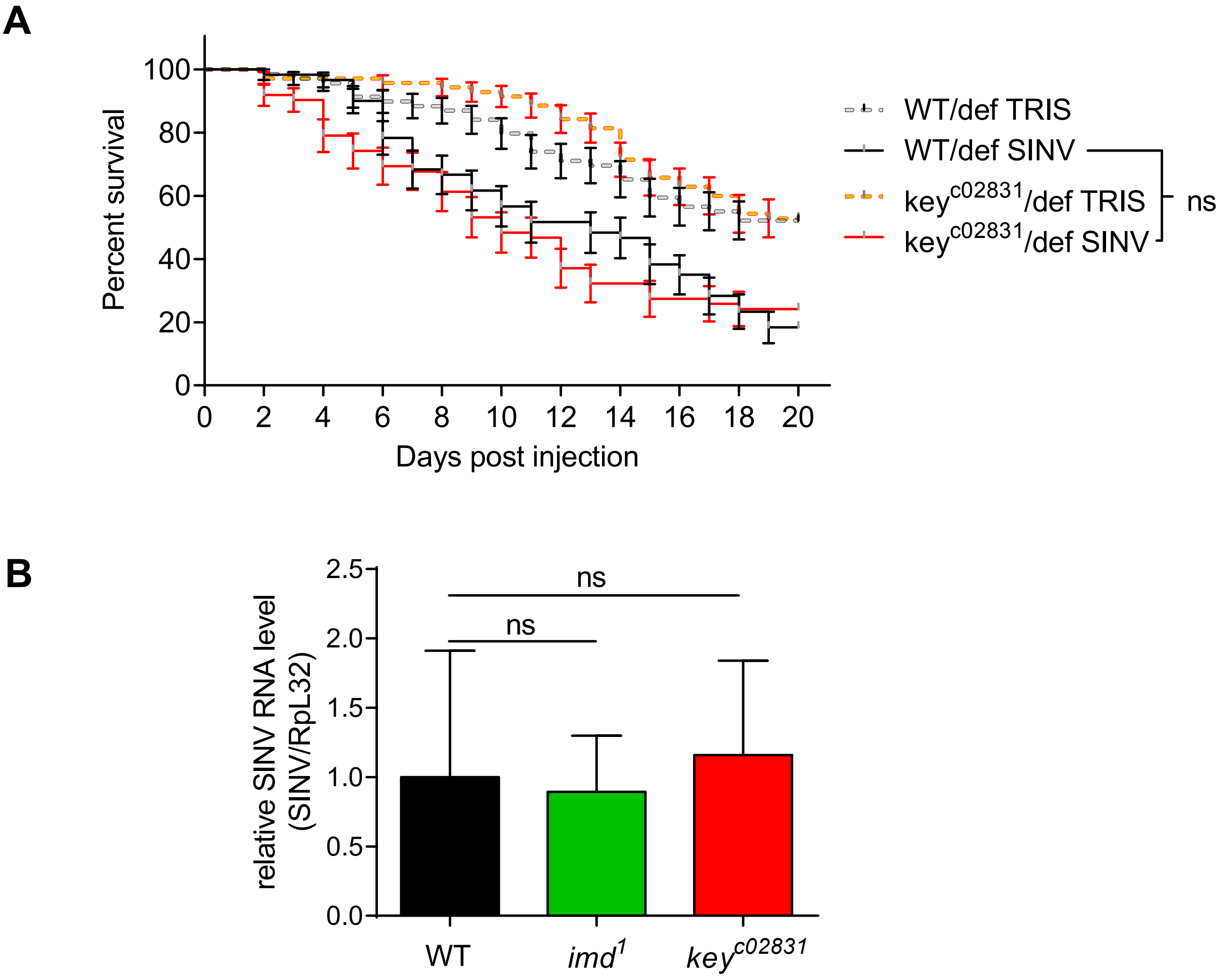

Figure S15: IMD pathway mutant flies are not sensitive to SINV infection.

(A) Survival of WT (w^{1118}) and key null flies (key^{c02831}) crossed with flies carrying the deficiency Df (2R)BSC856 covering the *key* gene (def) after TRIS and SINV injection at 29°C. (B) Viral load of WT (w^{1118}), imd^{1} and key^{c02831} flies infected with SINV at 4dpi (29°C). Data represent the mean and s.e. (A) or s.d. (B) of three independent experiments, each containing three groups of 10 (A) or 6 flies (B). Log rank test (A) and t-test (B): ns indicates that p>0.05.

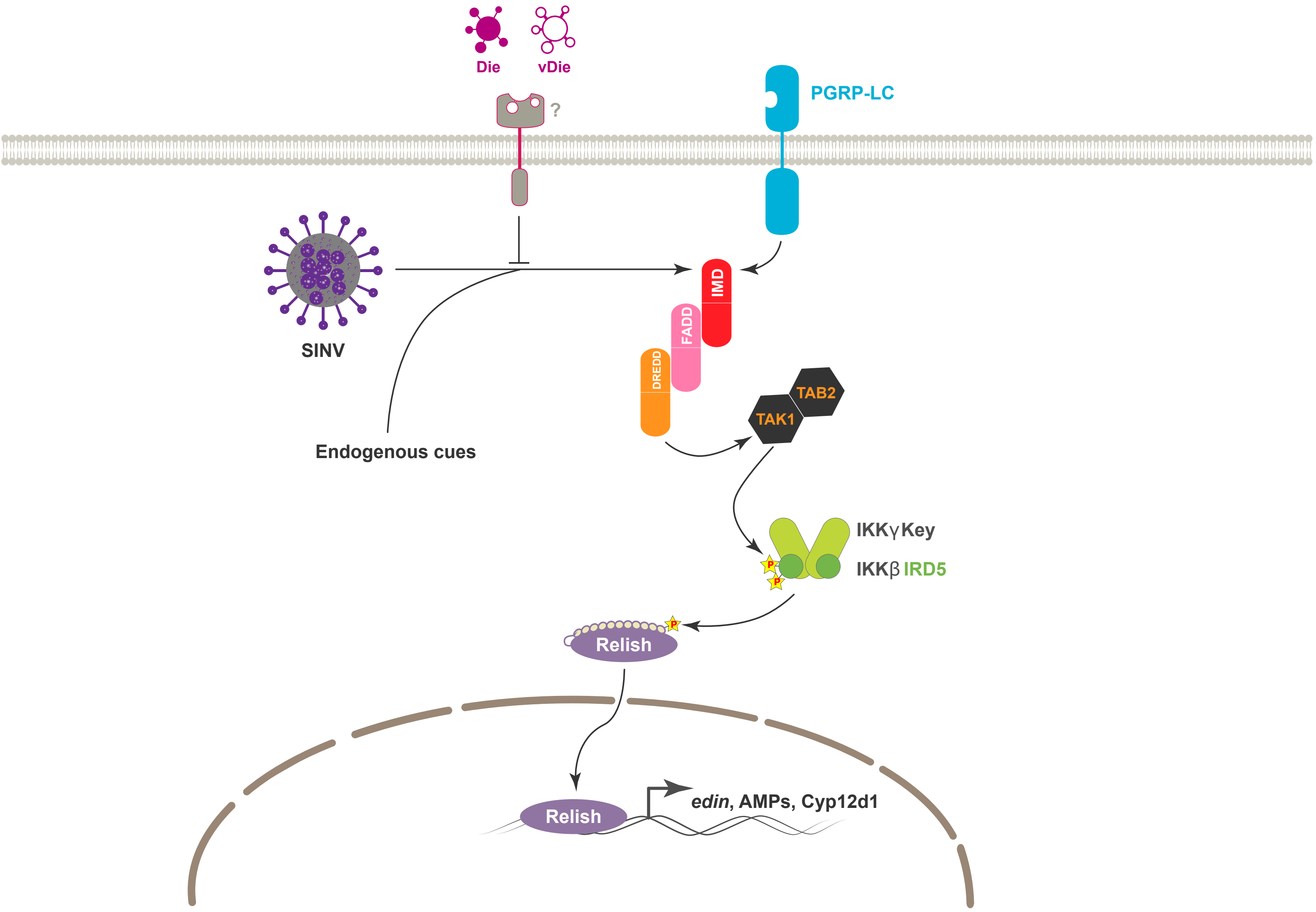

Figure S16: A model for the regulation of the IMD pathway by Diedel.

We propose that Diedel, acting through an uncharacterized membrane receptor, prevents activation of IMD independently of PGRP receptors. This model accounts for the fact that (i) the phenotype of *die*^{1} mutant is reverted in an imd mutant context, placing *die* upstream of *imd*, and (ii) *die*^{1} mutant flies resist normally to bacterial infections, and upregulation of IMD target genes in *die*^{1} mutant flies is not affected by antibiotic treatment.

Table S1: List of genes induced and repressed in non infected *die*^{1} mutant flies

Probe number	**SYMBOL**	**Gene name**	**Flybase ID**	**GO_Biological Process**	***die*^{1}/WT: non infected**	**WT: SINV/non infected**	***die*^{1} : SINV/Non infected**	***die*^{1}/WT SINV**
Induced in *Die*^{1} mutant non infected								
A_09_P134045	Cyp12d1-d	Cyp12d1-d	FBgn0053503	oxidation-reduction process	55,60	1,13	0,93	46,00
A_09_P028156	CG13905	-	FBgn0035176	-	51,47	1,75	0,98	28,72
A_09_P040931	CG1304	-	FBgn0031141	proteolysis	48,76	1,11	1,20	52,68
A_09_P005646	Cyp4p2	Cyp4p2	FBgn0033395	oxidation-reduction process	45,42	1,26	1,20	43,42
A_09_P060946	CG7567	-	FBgn0039670	-	19,03	1,57	0,98	11,82
A_09_P129245	CG16762	-	FBgn0035343	-	14,34	0,72	0,96	18,97
A_09_P029476	Ser6	Serine protease 6	FBgn0011834	proteolysis	8,55	1,12	1,25	9,55
A_09_P112030	CG10140	-	FBgn0036363	chitin metabolic process	7,60	1,24	0,91	5,61
A_09_P019026	Sr-CIV	Scavenger receptor class C, type IV	FBgn0031547	defense response	6,60	1,17	1,21	6,86
A_09_P129495	CG7912	-	FBgn0039736	sulfate transport	6,41	0,83	0,99	7,67
A_09_P045016	LysX	Lysozyme X	FBgn0004431	defense response	5,74	1,49	1,18	4,55
A_09_P015351	CG32368	-	FBgn0052368	-	5,58	3,12	1,07	1,92
A_09_P007351	CG42807	-	FBgn0261989	-	5,48	2,24	1,26	3,08
A_09_P197010	CG34391	-	FBgn0085420	-	5,21	0,87	0,82	4,91
A_09_P004846	CG42666	-	FBgn0261548	-	5,10	1,18	0,88	3,79
A_09_P007126	CG13324	-	FBgn0033789	-	4,90	1,32	1,08	4,00
A_09_P045891	DptB	Diptericin B	FBgn0034407	antibacterial humoral response	4,79	2,94	6,36	10,36
A_09_P030936	veg	vegetable	FBgn0265195	peripheral nervous system development	4,79	0,98	1,01	4,95
A_09_P025181	Cyp6a14	Cyp6a14	FBgn0033302	-	4,40	1,03	1,09	4,64
A_09_P041636	CecC	Cecropin C	FBgn0000279	response to bacterium	4,36	1,92	2,36	5,36
A_09_P030406	Mtk	Metchnikowin	FBgn0014865	response to bacterium	4,02	3,06	4,70	6,17
A_09_P114595	Def	Defensin	FBgn0010385	response to bacterium	4,00	1,19	1,41	4,74
A_09_P113770	CG12780	-	FBgn0033301	defense response to virus	3,92	1,05	0,87	3,28
A_09_P056566	PGRP-SB1	PGRP-SB1	FBgn0043578	immune response	3,80	3,83	4,60	4,57
A_09_P204936	CG11504	-	FBgn0039733	-	3,78	1,43	1,04	2,76
A_09_P045121	sls	sallimus	FBgn0086906	regulation of hemocyte proliferation	3,77	0,88	0,60	2,57
A_09_P215425	CG32198	-	FBgn0052198	-	3,68	0,34	0,54	5,86
A_09_P053436	CG15829	-	FBgn0035743	cellular acyl-CoA homeostasis	3,58	2,27	1,12	1,77
A_09_P195390	A2bp1	Ataxin-2 binding protein 1	FBgn0052062	oogenesis	3,41	1,33	0,85	2,18
A_09_P113810	GstE10	Glutathione S transferase E10	FBgn0063499	glutathione metabolic process	3,24	0,96	0,81	2,74
A_09_P079516	rgn	regeneration	FBgn0261258	tissue regeneration	3,21	1,06	0,82	2,49
A_09_P104130	CG1698	-	FBgn0033443	neurotransmitter transport	3,16	1,52	1,25	2,61
A_09_P180200	CG13795	-	FBgn0031937	neurotransmitter transport	3,14	1,70	1,62	2,99
A_09_P073141	Fst	Frost	FBgn0037724	response to cold	3,11	2,37	1,33	1,75
A_09_P056576	CG8147	-	FBgn0043791	metabolic process	3,10	0,78	0,94	3,76
A_09_P000871	CG33965	-	FBgn0053965	transport	3,08	0,97	0,90	2,86
A_09_P063516	CG13177	-	FBgn0040759	-	3,07	1,46	1,29	2,72
A_09_P075531	CG5399	-	FBgn0038353	-	3,05	0,98	0,93	2,91
A_09_P024916	CG12824	-	FBgn0033222	-	3,05	1,34	0,87	1,99
A_09_P022221	Phae2	Phaedra 2	FBgn0263235	proteolysis	3,03	3,22	1,12	1,05
A_09_P018931	CG8837	-	FBgn0031520	transmembrane transport	3,01	1,05	0,99	2,84
A_09_P037756	PGRP-SA	Peptidoglycan recognition protein SA	FBgn0030310	immune response	2,90	2,40	1,44	1,74
A_09_P129300	CG18609	-	FBgn0034382	fatty acid elongation	2,90	1,61	0,70	1,26
A_09_P059486	CG31272	-	FBgn0051272	transport	2,90	0,85	1,06	3,63
A_09_P168525	phr	photorepair	FBgn0003082	DNA repair	2,87	0,88	1,11	3,60
A_09_P042021	Cyp6a2	Cytochrome P450-6a2	FBgn0000473	oxidation-reduction process	2,87	1,03	1,01	2,81
A_09_P003596	CG34284	-	FBgn0085313	-	2,86	1,09	0,90	2,37
A_09_P028636	CG1139	-	FBgn0035300	growth	2,81	1,13	0,95	2,37
A_09_P040116	CG15043	-	FBgn0030929	-	2,78	1,20	0,84	1,95
A_09_P035761	CG11425	-	FBgn0037167	dephosphorylation	2,78	1,34	1,31	2,71
A_09_P027001	CG10332	-	FBgn0260455	-	2,76	3,08	5,39	4,82
A_09_P048671	spn-F	spn-F	FBgn0086362	oocyte microtubule cytoskeleton organization	2,70	0,94	1,03	2,95
A_09_P171450	Gr98a	Gustatory receptor 98a	FBgn0039520	sensory perception of taste	2,70	0,98	0,84	2,33
A_09_P021706	CG17107	-	FBgn0032281	-	2,67	1,71	1,19	1,87
A_09_P016591	Dh31-R	Diuretic hormone 31 Receptor	FBgn0052843	G-protein coupled receptor signaling pathway	2,65	0,97	0,92	2,54
A_09_P072481	CG11671	-	FBgn0037562	neuromuscular process	2,65	1,52	1,01	1,76
A_09_P042786	Hsp22	Heat shock protein 22	FBgn0001223	response to heat	2,65	0,94	0,74	2,07
A_09_P174270	Bacc	Bacchus	FBgn0031453	behavioral response to ethanol	2,63	1,21	0,95	2,06
A_09_P194406	Tsp2A	Tetraspanin 2A	FBgn0024361		2,60	1,14	0,90	2,06
A_09_P052846	CG13704	-	FBgn0035583	-	2,58	1,09	0,96	2,27
A_09_P146530	CG15210	-	FBgn0040850	-	2,58	1,30	1,02	2,01
A_09_P064591	CG18853	-	FBgn0042173	DNA repair	2,56	0,83	0,96	2,98
A_09_P014306	CG32024	-	FBgn0052024	chitin metabolic process	2,56	1,06	0,80	1,93
A_09_P050676	CG15160	-	FBgn0032688	-	2,55	1,31	1,29	2,51
A_09_P078261	prominin-like	prominin-like	FBgn0026189	neuron projection morphogenesis	2,55	1,11	0,97	2,23
A_09_P044716	shi	shibire	FBgn0003392	vesicle-mediated transport	2,54	1,20	0,72	1,51
A_09_P047886	Khc-73	Kinesin heavy chain 73	FBgn0019968	microtubule-based movement	2,53	0,88	0,89	2,56
A_09_P076236	AttD	Attacin-D	FBgn0038530	defense response to Gram-positive bacterium	2,52	2,18	2,93	3,39
A_09_P121465	Pvf2	PDGF- and VEGF-related factor 2	FBgn0031888	hemocyte migration	2,51	1,42	1,32	2,33
A_09_P007121	CG13323	-	FBgn0033788	-	2,50	1,25	1,05	2,10
A_09_P017326	CG33258	-	FBgn0053258	chitin metabolic process	2,50	0,92	1,19	3,24
A_09_P108115	Arpc3B	Actin-related protein 2/3 complex, subunit 3B	FBgn0065032	actin filament organization	2,45	1,06	0,91	2,10

A_09_P006576	Damm	Death associated molecule related to Mch2 caspase	FBgn0033659	programmed cell death	2,44	0,87	0,98	2,74
A_09_P064786	MESK4	Misexpression suppressor of KSR 4	FBgn0043069	positive regulation of Ras protein signal transduction	2,44	1,08	0,99	2,23
A_09_P026601	CG4250	-	FBgn0034761	-	2,43	2,98	1,79	1,46
A_09_P010311	Dpt	Diptericin	FBgn0004240	response to bacterium	2,42	2,09	6,79	7,87
A_09_P043736	MtnB	Metallothionein B	FBgn0002869	response to metal ion	2,40	1,32	0,63	1,15
A_09_P126820	CG32523	-	FBgn0052523	proteolysis	2,38	1,24	0,91	1,74
A_09_P065776	CSN8	COP9 signalosome subunit 8	FBgn0261437	defense response to bacterium	2,38	1,46	1,05	1,71
A_09_P018246	CG42329	-	FBgn0259229	-	2,37	0,83	0,92	2,61
A_09_P209075	fuss	fussel	FBgn0039932	negative regulation of BMP signaling pathway	2,36	1,44	0,75	1,22
A_09_P033006	Cht4	Chitinase 4	FBgn0022700	chitin catabolic process	2,35	1,22	1,10	2,12
A_09_P007646	Arc2	Arc2	FBgn0033928	-	2,35	4,66	2,32	1,17
A_09_P043361	Lsp1alpha	Larval serum protein 1 alpha	FBgn0002562	-	2,34	1,10	1,13	2,43
A_09_P014056	Mur29B	Mucin related 29B	FBgn0051901	-	2,34	1,18	1,23	2,45
A_09_P069016	CG14292	-	FBgn0038658	-	2,33	1,01	0,99	2,29
A_09_P100340	CG34198	-	FBgn0085227	-	2,33	1,58	1,10	1,62
A_09_P216475	CG15127	-	FBgn0040730	-	2,33	1,13	0,77	1,59
A_09_P075961	CG18622	-	FBgn0038460	-	2,33	1,99	0,97	1,14
A_09_P012906	Bsg	Basigin	FBgn0261822	localization	2,32	1,68	0,85	1,17
A_09_P017061	MtnD	Metallothionein D	FBgn0053192	response to metal ion	2,30	1,85	0,70	0,87
A_09_P163340	CG43693	-	FBgn0263776	-	2,30	1,72	0,82	1,09
A_09_P019556	TotM	Turandot M	FBgn0031701	response to bacterium	2,29	115,21	50,82	1,01
A_09_P128930	CG13075	-	FBgn0036563	chitin metabolic process	2,28	1,31	1,37	2,37
A_09_P008496	CG5550	-	FBgn0034160	-	2,28	1,48	1,25	1,91
A_09_P039921	CG15814	-	FBgn0030873	-	2,27	1,07	0,97	2,05
A_09_P075866	Der-2	Derlin-2	FBgn0038438	defense response to bacterium	2,26	2,27	1,05	1,04
A_09_P206230	CG42728	-	FBgn0261681	chitin metabolic process	2,26	1,22	0,87	1,61
A_09_P041161	Act88F	Actin 88F	FBgn0000047	cytoskeleton organization	2,25	1,87	0,84	1,02
A_09_P153830	CG33470	-	FBgn0053470	-	2,24	2,24	1,99	1,99
A_09_P008901	CG18635	-	FBgn0034279	-	2,22	1,02	1,05	2,27
A_09_P024961	CG14764	-	FBgn0033236	-	2,21	1,07	1,03	2,13
A_09_P024951	CG8791	-	FBgn0033234	transmembrane transport	2,21	1,16	0,85	1,61
A_09_P054476	CG8329	-	FBgn0036022	proteolysis	2,20	1,04	0,71	1,51
A_09_P068056	CG15330	-	FBgn0029987	lateral inhibition	2,20	1,27	0,82	1,41
A_09_P032386	Fak	Focal adhesion kinase	FBgn0020440	negative regulation of MAP kinase activity	2,18	2,11	0,89	0,92
A_09_P026526	CG4269	-	FBgn0034741	-	2,16	1,59	1,25	1,71
A_09_P031241	Rab19	Rab19	FBgn0015793	protein transport	2,13	2,30	1,06	0,99
A_09_P035511	CapaR	Capability receptor	FBgn0037100	neuropeptide signaling pathway	2,13	0,96	1,04	2,32
A_09_P050506	CG15282	-	FBgn0028855	-	2,13	1,32	1,51	2,44
A_09_P023311	Swip-1	Swiprosin-1	FBgn0032731	mesoderm development	2,12	1,24	1,10	1,89
A_09_P028546	Cpr62Bb	Cuticular protein 62Bb	FBgn0035280	chitin-based cuticle development	2,12	1,28	1,08	1,79
A_09_P218475	Ady43A	Ady43A	FBgn0026602	-	2,12	1,27	0,87	1,45
A_09_P075741	Zip89B	Zinc/iron regulated transporter-related protein 89B	FBgn0038412	metal ion transport	2,12	1,14	1,20	2,23
A_09_P068806	CG7142	-	FBgn0038595	proteolysis	2,12	1,06	0,85	1,69
A_09_P170670	Sr-CI	Scavenger receptor class C, type I	FBgn0014033	immune response	2,11	2,01	1,33	1,40
A_09_P176135	PlexA	Plexin A	FBgn0025741	axon guidance	2,11	1,33	0,83	1,32
A_09_P053051	Tektin-C	Tektin C	FBgn0035638	microtubule-based process	2,10	0,76	0,99	2,72
A_09_P025411	PPO2	Prophenoloxidase 2	FBgn0033367	defense response to Gram-positive bacterium	2,10	2,57	1,98	1,62
A_09_P045161	IM2	Immune induced molecule 2	FBgn0025583	defense response	2,10	3,33	1,93	1,22
A_09_P120937	Ssk	Snakeskin	FBgn0036945	intestinal epithelial cell development	2,09	1,13	1,02	1,89
A_09_P216700	CG15369	-	FBgn0030105	-	2,08	5,68	3,19	1,17
A_09_P058261	CG30380	-	FBgn0050380	-	2,08	1,22	1,17	1,99
A_09_P054446	CG3088	-	FBgn0036015	proteolysis	2,07	1,02	0,73	1,49
A_09_P152045	CG44251	-	FBgn0265186		2,07	1,14	0,90	1,64
A_09_P003231	CG34211	-	FBgn0085240		2,07	1,06	0,82	1,60
A_09_P015191	CG32284	-	FBgn0052284	chitin metabolic process	2,07	1,45	1,04	1,48
A_09_P026631	CG13526	-	FBgn0034774	-	2,06	0,91	0,74	1,68
A_09_P144890	CG12012	-	FBgn0035444	-	2,06	1,51	1,07	1,46
A_09_P053661	PGRP-SD	PGRP-SD	FBgn0035806	immune response	2,05	2,41	3,47	2,95
A_09_P129460	CG8197	-	FBgn0033369	neurogenesis	2,04	0,86	0,80	1,91
A_09_P111940	CG10352	-	FBgn0030348	-	2,04	1,43	1,02	1,46
A_09_P128985	CG32109	-	FBgn0052109	-	2,04	2,10	0,94	0,91
A_09_P041416	PPO1	Prophenoloxidase 1	FBgn0261362	defense response to Gram-positive bacterium	2,04	2,44	1,67	1,39
A_09_P019126	CG43773	-	FBgn0264295	-	2,03	1,57	0,80	1,03
A_09_P035756	CG11426	-	FBgn0037166	dephosphorylation	2,03	1,12	0,98	1,78
A_09_P055911	CG13482	-	FBgn0036419	-	2,03	1,49	0,78	1,06
A_09_P010081	Yp3	Yolk protein 3	FBgn0004047	vitellogenesis	2,02	1,48	0,90	1,23
A_09_P060361	CG31664	-	FBgn0051664	-	2,02	2,59	2,13	1,66
A_09_P079686	CG4757	-	FBgn0027584	-	2,01	3,33	2,80	1,69
A_09_P121665	CG16836	-	FBgn0040735	-	2,00	3,99	1,95	0,98
A_09_P067236	CG15784	-	FBgn0029766	-	2,00	1,99	1,40	1,40

Repressed in *Die*^{1} mutant non infected								
A_09_P062366	lectin-28C	lectin-28C	FBgn0040099	-	0,07	2,39	2,59	0,07
A_09_P018296	CG10869	-	FBgn0031347	-	0,10	0,54	1,34	0,25
A_09_P043321	Lcp1	Larval cuticle protein 1	FBgn0002531	chitin-based cuticle development	0,11	0,98	0,63	0,07

A_09_P137560	CG6484	-	FBgn0034247	transmembrane transport	0,12	1,38	1,00	0,09
A_09_P170880	RhoGAP100F	Rho GTPase activating protein at 100F	FBgn0039883	synaptic vesicle localization	0,13	0,84	0,85	0,13
A_09_P072161	CG17192	-	FBgn0039472	lipid catabolic process	0,14	0,74	1,27	0,24
A_09_P147255	CG4398	-	FBgn0034126	-	0,15	1,41	1,87	0,20
A_09_P022396	Vha68-3	Vacuolar H[+] ATPase 68kD subunit 3	FBgn0032464	ATP metabolic process	0,15	0,64	0,86	0,21
A_09_P062376	lectin-24A	lectin-24A	FBgn0040104	-	0,16	1,49	7,12	0,77
A_09_P032116	sfl	sulfateless	FBgn0020251	Wnt signaling pathway	0,17	1,05	1,00	0,16
A_09_P074191	CG4830	-	FBgn0037996	metabolic process	0,19	0,51	0,95	0,35
A_09_P192645	CG42847	-	FBgn0262036	-	0,19	0,75	0,87	0,22
A_09_P217215	CG14957	-	FBgn0035412	chitin metabolic process	0,19	1,68	0,79	0,09
A_09_P028306	CG12090	-	FBgn0035227	-	0,20	1,08	0,94	0,17
A_09_P042926	Jon44E	Jonah 44E	FBgn0001285	proteolysis	0,20	1,11	0,96	0,18
A_09_P078756	Fie	Fire exit	FBgn0026592	-	0,20	1,02	0,97	0,19
A_09_P020981	CG9515	-	FBgn0032077	-	0,21	1,40	1,27	0,19
A_09_P058781	CG31030	-	FBgn0051030	ATP hydrolysis coupled proton transport	0,26	0,88	0,98	0,29
A_09_P010541	LysB	Lysozyme B	FBgn0004425	antimicrobial humoral response	0,26	0,93	0,78	0,22
A_09_P020401	Cyp4d21	Cyp4d21	FBgn0031925	oxidation-reduction process	0,29	1,04	1,39	0,39
A_09_P111285	CG9259	-	FBgn0032913	-	0,30	0,88	1,02	0,34
A_09_P028151	CG13907	-	FBgn0035173	transmembrane transpor	0,30	1,02	1,10	0,32
A_09_P032651	Jon25Bi	Jonah 25Bi	FBgn0020906	proteolysis	0,32	0,93	1,23	0,42
A_09_P015131	CG32267	-	FBgn0052267	-	0,32	1,06	0,99	0,30
A_09_P007686	Oaz	O/E-associated zinc finger protein	FBgn0261613	spiracle morphogenesis, open tracheal system	0,34	0,56	0,67	0,41
A_09_P030671	Rala	Ras-like protein A	FBgn0015286	innate immune response	0,34	1,13	1,03	0,31
A_09_P203445	CG14499	-	FBgn0034317	-	0,35	2,54	1,75	0,24
A_09_P034876	Ir76b	Ionotropic receptor 76b	FBgn0036937	cellular response to salt	0,35	0,54	0,75	0,49
A_09_P008251	Tsf3	Transferrin 3	FBgn0034094	response to bacterium	0,36	1,48	1,40	0,34
A_09_P148025	FucTD	FucTD	FBgn0035217	protein glycosylation	0,36	0,77	0,99	0,46
A_09_P061721	CG11550	-	FBgn0039864	-	0,37	0,88	1,07	0,44
A_09_P007056	CG12374	-	FBgn0033774	proteolysis	0,37	0,63	0,74	0,44
A_09_P053136	Jon65Aii	Jonah 65Aii	FBgn0035666	proteolysis	0,37	0,94	0,64	0,25
A_09_P149115	RpL17	Ribosomal protein L17	FBgn0029897	mitotic spindle organization	0,38	1,11	1,01	0,35
A_09_P008081	CG8299	-	FBgn0034052	proteolysis	0,39	0,72	1,07	0,58
A_09_P006826	CG13155	-	FBgn0033723	-	0,39	1,35	1,15	0,33
A_09_P010556	LysE	Lysozyme E	FBgn0004428	antimicrobial humoral response	0,41	1,16	0,79	0,28
A_09_P063696	CG15213	-	FBgn0040843	-	0,41	1,07	0,85	0,33
A_09_P000766	His4:CG33891	His4:CG33891	FBgn0053891	nucleosome assembly	0,41	0,49	0,69	0,58
A_09_P015161	CG32278	-	FBgn0052278	-	0,42	1,04	1,06	0,43
A_09_P022456	CG5458	-	FBgn0032478	-	0,42	0,71	0,97	0,58
A_09_P030521	Cyp4e1	Cytochrome P450-4e1	FBgn0015034	oxidation-reduction process	0,42	0,94	1,07	0,48
A_09_P033901	rogdi	rogdi	FBgn0036697	olfactory learning	0,42	0,57	0,76	0,57
A_09_P058216	CG30371	-	FBgn0050371	proteolysis	0,46	1,14	0,92	0,37
A_09_P140170	ND-B14	NADH dehydrogenase (ubiquinone) B14 subunit	FBgn0033570	mitochondrial electron transport, NADH to ubiquinone	0,43	1,09	0,91	0,36
A_09_P061851	Syt7	Synaptotagmin 7	FBgn0039900	exocytosis	0,44	0,95	1,11	0,51
A_09_P053151	CG10472	-	FBgn0035670	proteolysis	0,44	0,78	0,70	0,40
A_09_P064576	CG18814	-	FBgn0042137	oxidation-reduction process	0,45	1,07	1,08	0,45
A_09_P215770	Jon65Aiv	Jonah 65Aiv	FBgn0250815	proteolysis	0,45	0,92	0,90	0,44
A_09_P177020	CG33235	-	FBgn0030307		0,45	0,56	0,72	0,57
A_09_P053566	CG8560	-	FBgn0035781	proteolysis	0,45	0,82	0,87	0,48
A_09_P112630	CG18301	-	FBgn0032265	lipid metabolic process	0,47	0,87	1,10	0,59
A_09_P060931	CG2010	-	FBgn0039667	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	0,47	1,04	0,90	0,41
A_09_P019386	Jon25Bii	Jonah 25Bii	FBgn0031654	proteolysis	0,47	1,02	1,10	0,51
A_09_P067501	CG5928	-	FBgn0029836	-	0,47	0,80	1,01	0,60
A_09_P025106	CG14759	-	FBgn0033278	-	0,47	0,88	0,72	0,39
A_09_P029371	Dsp1	Dorsal switch protein 1	FBgn0011764	chromatin remodeling	0,47	0,59	0,65	0,52
A_09_P064951	TotA	Turandot A	FBgn0028396	response to bacterium	0,48	199,69	419,30	1,01
A_09_P031021	Acp76A	Accessory gland protein 76A	FBgn0015586	regulation of proteolysis	0,48	0,73	1,18	0,77
A_09_P066296	Spn28F	Serpin 28F	FBgn0028987	regulation of proteolysis	0,48	0,78	1,09	0,68
A_09_P007476	DJ-1alpha	DJ-1alpha	FBgn0033885	response to oxidative stress	0,48	0,88	0,92	0,51
A_09_P217155	CG6675	-	FBgn0032973	lipid catabolic process	0,48	0,63	1,24	0,96
A_09_P137505	Cyp4e3	Cytochrome P450-4e3	FBgn0015035	oxidation-reduction process	0,48	2,40	1,53	0,31
A_09_P001931	CG16984	-	FBgn0062517	-	0,49	0,68	0,91	0,65
A_09_P090700	Gad1	Glutamic acid decarboxylase 1	FBgn0004516	neurotransmitter receptor metabolic process	0,49	0,80	1,01	0,62
A_09_P124240	CG33230	-	FBgn0053230	-	0,49	1,09	1,10	0,49
A_09_P025351	FANCI	Fanconi anemia complementation group I homologue	FBgn0033354	DNA repair	0,50	0,67	0,78	0,58
A_09_P177435	CG13526	-	FBgn0034774	-	0,50	0,86	1,02	0,59
A_09_P061396	Jon99Fii	Jonah 99Fii	FBgn0039777	proteolysis	0,50	0,93	1,14	0,61

Table S2: List of genes induced and repressed by SINV infection in WT and *die*^{1} flies.

Probe number	SYMBOL	Gene Name	Flybase ID	GO_Biological Process	WT SINV/non infected	*die*^{1} SINV/Non infected	*die*^{1}/WT non infected	*die*^{1}/WT SINV
Induced (≥2 fold) by SINV infection in WT and *die*^{1} flies								
A_09_P064951	TotA	Turandot A	FBtr0083971	response to bacterium	199,69	419,30	0,48	1,01
A_09_P019556	TotM	Turandot M	FBtr0079073	response to bacterium	115,21	50,82	2,29	1,01
A_09_P056771	TotC	Turandot C	FBtr0083972	response to bacterium	78,54	128,07	0,60	0,99
A_09_P057631	CG30098	-	FBtr0087168	defense response to Gram-positive bacterium	40,16	24,98	2,22	1,38
A_09_P069721	TotB	Turandot B	FBtr0083973	response to bacterium	37,34	27,77	0,99	0,74
A_09_P022946	CG6639	-	FBtr0081004	proteolysis | NOT inferred from key residues	36,83	10,10	3,44	0,94
A_09_P022951	CG18563	-	FBtr0300902	proteolysis	23,56	9,77	2,28	0,95
A_09_P036621	CG11459	-	FBtr0078623	proteolysis	20,43	25,29	0,76	0,94
A_09_P056761	TotX	Turandot X	FBtr0083985	response to bacterium	17,92	17,74	0,73	0,72
A_09_P056756	TotZ	Turandot Z	FBtr0083974	response to bacterium	14,20	8,84	0,95	0,59
A_09_P025346	CG13749	-	FBtr0300706	-	12,92	19,95	1,09	1,68
A_09_P018756	CG3117	-	FBtr0300356	proteolysis | NOT inferred from key residues	12,52	11,58	0,86	0,80
A_09_P057591	CG30088	-	FBtr0273296	proteolysis	10,41	15,26	0,99	1,45
A_09_P057606	CG30091	-	FBtr0087277	proteolysis	10,10	6,18	2,30	1,41
A_09_P058041	CG30287	-	FBtr0071695	proteolysis	9,53	6,07	1,14	0,73
A_09_P071581	CG11893	-	FBtr0084827	wing disc development	7,08	3,16	1,32	0,59
A_09_P070001	fit	female-specific independent of transformer	FBtr0084153	-	6,87	3,82	0,88	0,49
A_09_P076441	Lip3	Lip3	FBtr0082771	lipid metabolic process	6,18	2,17	1,99	0,70
A_09_P059791	Npc2e	Niemann-Pick type C-2e	FBtr0273369	peptidoglycan recognition protein signaling pathway	5,74	2,58	1,77	0,80
A_09_P216700	CG15369	-	FBtr0071309	-	5,68	3,19	2,08	1,17
A_09_P026161	CG42365	-	FBtr0299964	-	5,32	3,13	1,25	0,74
A_09_P191735	CG42362	-	FBtr0299961	-	5,28	3,99	1,21	0,91
A_09_P005786	CG1773	-	FBtr0088467	proteolysis	4,84	3,47	1,10	0,79
A_09_P060656	Sid	Stress induced DNase	FBtr0085307	response to bacterium	4,83	3,95	1,31	1,07
A_09_P007646	Arc2	Arc2	FBtr0087547	-	4,66	2,32	2,35	1,17
A_09_P017611	CG33460	-	FBtr0100642	proteolysis	4,15	3,46	1,46	1,22
A_09_P018421	CG4259	-	FBtr0077854	proteolysis | NOT inferred from key residues	4,13	2,74	1,34	0,89
A_09_P013876	CG31832	-	FBtr0080726	-	4,13	2,87	0,59	0,41
A_09_P070621	CG4408	-	FBtr0084431	proteolysis	4,11	2,12	1,28	0,66
A_09_P018751	CG18557	-	FBtr0077689	proteolysis | NOT inferred from key residues	4,05	5,99	0,51	0,75
A_09_P056566	PGRP-SB1	PGRP-SB1	FBtr0075348	immune response	3,83	4,60	3,80	4,57
A_09_P057576	CG30083	-	FBtr0300381	proteolysis	3,75	2,48	1,52	1,01
A_09_P065881	CG18477	-	FBtr0080756	proteolysis | NOT inferred from key residues	3,67	2,12	1,39	0,80
A_09_P065926	NimC4	Nimrod C4	FBtr0080592	phagocytosis	3,66	2,10	1,75	1,00
A_09_P057301	CG30002	-	FBtr0088466	proteolysis	3,62	3,25	0,91	0,82
A_09_P063056	CG7763	-	FBtr0088135	-	3,50	4,08	1,18	1,37
A_09_P079656	CG14526	-	FBtr0301945	proteolysis	3,41	2,64	1,17	0,90
A_09_P135325	CG14527	-	FBtr0336460	proteolysis	3,40	2,51	1,21	0,90
A_09_P101215	edin	elevated during infection	FBtr0075174	immune response	3,36	16,15	1,88	9,03
A_09_P202245	CG7997	-	FBtr0087172	oligosaccharide metabolic process	3,30	2,78	0,78	0,66
A_09_P007711	CG12868	-	FBtr0301735	-	3,28	2,20	1,32	0,89
A_09_P133305	Cys	Cystatin-like	FBtr0072487	multicellular organism reproduction	3,13	2,42	1,17	0,90
A_09_P010831	zfh1	Zn finger homeodomain 1	FBtr0085701	antimicrobial humoral response	3,11	2,14	1,39	0,96
A_09_P212320	CG4250	-	FBtr0309802	-	3,10	2,33	1,50	1,12
A_09_P037556	Vago	Vago	FBtr0100644	defense response to virus	3,09	2,04	1,74	1,15
A_09_P027001	CG10332	-	FBtr0072109	-	3,08	5,39	2,76	4,82
A_09_P030406	Mtk	Metchnikowin	FBtr0087386	antimicrobial humoral response	3,06	4,70	4,02	6,17
A_09_P011881	GstD2	Glutathione S transferase D2	FBtr0082569	glutathione metabolic process	3,06	2,03	1,77	1,17
A_09_P144210	CG34054	-	FBtr0100109	-	3,04	2,05	1,55	1,05
A_09_P017981	nAcRbeta-21C	nicotinic Acetylcholine Receptor β3	FBtr0078065	ion transport	3,00	2,11	1,68	1,18
A_09_P045891	DptB	Diptericin B	FBtr0086621	antimicrobial humoral response	2,94	6,36	4,79	10,36
A_09_P112520	CG31664	-	FBtr0303377	-	2,87	2,38	1,93	1,60
A_09_P052991	mthl2	methuselah-like 2	FBtr0077088	G-protein coupled receptor signaling pathway	2,87	2,18	2,31	1,75
A_09_P071301	CG13641	-	FBtr0084729	-	2,85	2,65	1,95	1,82
A_09_P075261	CG6912	-	FBtr0083038	-	2,82	2,55	1,29	1,16
A_09_P169575	Tsf1	Transferrin 1	FBtr0074559	response to fungus	2,77	2,58	1,19	1,11
A_09_P060181	CG31606	-	FBtr0079577	-	2,68	2,21	0,54	0,45
A_09_P111540	CG9616	-	FBtr0300059	-	2,68	2,01	1,16	0,87
A_09_P164825	CG3397	-	FBtr0082504	potassium ion transport	2,67	2,74	1,00	1,03
A_09_P015151	Drs-l	Drosomycin-like 1	FBtr0073081	defense response to fungus	2,63	2,37	1,36	1,23
A_09_P130780	Gnmt	Glycine N-methyltransferase	FBtr0082651	triglyceride homeostasis	2,58	3,33	0,97	1,25
A_09_P167250	GstE1	Glutathione S transferase E1	FBtr0086669	response to oxidative stress	2,57	2,18	1,27	1,08
A_09_P007281	IM10	Immune induced molecule 10	FBtr0087655	antibacterial humoral response	2,56	2,62	1,24	1,27
A_09_P061326	CG9733	-	FBtr0085638	proteolysis	2,56	2,01	1,57	1,24
A_09_P006831	CG8501	-	FBtr0087915	-	2,53	2,05	1,39	1,13
A_09_P029506	AttA	Attacin-A	FBtr0087437	antimicrobial humoral response	2,51	7,82	1,73	5,39
A_09_P075311	Spn88Eb	Serpin 88Eb	FBtr0083140	negative regulation of proteolysis	2,49	3,50	1,03	1,45
A_09_P064326	AsnS	Asparagine synthetase	FBtr0089463	asparagine biosynthetic process	2,45	2,08	1,18	1,01
A_09_P034316	Cyp12c1	Cyp12c1	FBtr0075091	oxidation-reduction process	2,44	2,00	1,10	0,89

A_09_P053661	PGRP-SD	PGRP-SD	FBtr0076807	defense response to Gram-positive bacterium	2,41	3,47	2,05	2,95
A_09_P064281	AttC	Attacin-C	FBtr0305795	antibacterial humoral response	2,37	5,82	1,94	4,77
A_09_P187755	CG11395	-	FBtr0086987	signal transduction	2,36	2,05	1,12	0,98
A_09_P025711	GNBP-like3	GNBP-like 3	FBtr0086214	response to fungus	2,32	2,27	1,08	1,06
A_09_P057376	CG30026	-	FBtr0300922	-	2,29	2,17	1,16	1,10
A_09_P064071	TepII	Thioester-containing protein 2	FBtr0079510	antibacterial humoral response	2,28	2,72	0,61	0,73
A_09_P164330	CG6415	-	FBtr0080108	glycine catabolic process	2,24	2,11	1,00	0,94
A_09_P009861	tsl	torso-like	FBtr0084164	torso signaling pathway	2,20	2,10	1,26	1,20
A_09_P076236	AttD	Attacin-D	FBtr0083470	antibacterial humoral response	2,18	2,93	2,52	3,39
A_09_P209530	GstD10	Glutathione S transferase D10	FBtr0082609	glutathione metabolic process	2,15	2,39	0,94	1,04
A_09_P023551	CG13077	-	FBtr0081257	-	2,13	2,25	0,94	0,99
A_09_P010311	Dpt	Diptericin	FBtr0086620	antibacterial humoral response	2,09	6,79	2,42	7,87
A_09_P025801	CG16799	-	FBtr0086249	antimicrobial humoral response	2,07	2,16	0,95	1,00
A_09_P064286	AttB	Attacin-B	FBtr0087438	antibacterial humoral response	2,06	5,27	1,85	4,73
A_09_P075266	CG3984	-	FBtr0083025	-	2,02	2,53	0,85	1,06
Induced (≥2 fold) by SINV infection only in WT flies								
A_09_P060926	die	Diedel	FBtr0085426	response to bacterium	323,47	0,99	0,11	0,00
A_09_P171285	CG14499	-	FBtr0347601	-	7,03	1,86	0,65	0,17
A_09_P121665	CG16836	-	FBtr0086666	-	3,99	1,95	2,00	0,98
A_09_P074491	CG5999	-	FBtr0302379	metabolic process	3,55	1,73	1,43	0,70
A_09_P045336	CG15067	-	FBtr0300844	neurogenesis	3,52	1,70	1,69	0,81
A_09_P045161	IM2	Immune induced molecule 2	FBtr0086664	response to bacterium	3,33	1,93	2,10	1,22
A_09_P022221	CG16997	Phaedra 2	FBtr0302854	proteolysis	3,22	1,12	3,03	1,05
A_09_P015351	CG32368	-	FBtr0076749	-	3,12	1,07	5,58	1,92
A_09_P063316	IM4	Immune induced molecule 4	FBtr0071559	response to bacterium	3,10	1,88	1,80	1,09
A_09_P033651	CG4680	Gag-related	FBtr0075388	-	2,75	1,49	1,88	1,02
A_09_P033466	CG4950	-	FBtr0290260	-	2,70	1,77	1,67	1,10
A_09_P017646	CG33468	-	FBtr0087503	-	2,66	1,94	1,41	1,03
A_09_P052171	Cyp4e3	Cytochrome P450-4e3	FBtr0079925	oxidation-reduction process	2,64	1,65	0,58	0,36
A_09_P009081	IM1	Immune induced molecule 1	FBtr0086662	response to bacterium	2,59	1,88	1,57	1,14
A_09_P009086	CG18107	-	FBtr0086663	-	2,59	1,51	1,88	1,09
A_09_P063186	CG5791	-	FBtr0084180	-	2,57	1,61	1,52	0,95
A_09_P025411	CG8193	Prophenoloxidase 2	FBtr0088663	defense response to Gram-positive bacterium	2,57	1,98	2,10	1,62
A_09_P000201	lectin-37Da	lectin-37Da	FBtr0091498	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	2,53	1,13	1,95	0,87
A_09_P128140	PGRP-SA	Peptidoglycan recognition protein SA	FBtr0073509	defense response to Gram-positive bacterium	2,52	1,54	2,83	1,73
A_09_P012026	Nmdmc	NAD-dependent methylenetetrahydrofolate dehydrogenase	FBtr0081996	oxidation-reduction process	2,49	1,80	1,80	1,30
A_09_P055856	upSET	upSET	FBtr0075768	establishment of chromatin silencing	2,53	1,65	1,11	0,73
A_09_P115030	lectin-28C	lectin-28C	FBtr0343418	-	2,47	1,56	0,09	0,06
A_09_P043376	Lsp2	Larval serum protein 2	FBtr0089324	synaptic target inhibition	2,46	1,42	1,11	0,64
A_09_P026576	Cyp6d2	Cyp6d2	FBtr0071928	oxidation-reduction process	2,45	1,62	1,53	1,02
A_09_P041416	PPO1	Prophenoloxidase 1	FBtr0302291	defense response to Gram-positive bacterium	2,44	1,67	2,04	1,39
A_09_P141245	Cyp309a1	Cyp309a1	FBtr0077749	oxidation-reduction process	2,40	1,75	1,12	0,82
A_09_P063476	IM3	Immune induced molecule 3	FBtr0086665	antibacterial humoral response	2,39	1,58	1,77	1,17
A_09_P025161	CG8693	Maltase A4	FBtr0088748	carbohydrate metabolic process	2,38	1,42	0,70	0,42
A_09_P213940	CG15068	-	FBtr0086727	-	2,38	1,31	1,50	0,82
A_09_P007636	Arc1	Activity-regulated cytoskeleton associated protein 1	FBtr0087560	behavioral response to starvation	2,37	1,84	1,27	0,98
A_09_P073141	Fst	Frost	FBtr0082101	response to cold	2,37	1,33	3,11	1,75
A_09_P053606	CG8539	-	FBtr0076831	proteolysis	2,37	1,87	1,26	1,00
A_09_P057601	CG30090	-	FBtr0087279	proteolysis	2,37	1,98	1,26	1,05
A_09_P045976	Socs36E	Suppressor of cytokine signaling at 36E	FBtr0081040	negative regulation of JAK-STAT cascade	2,36	1,52	2,00	1,28
A_09_P037576	CG11122	-	FBtr0073481	-	2,34	1,74	0,94	0,70
A_09_P019961	CG42370	-	FBtr0299969	proteolysis	2,32	1,62	0,86	0,60
A_09_P031241	Rab19	Rab19	FBtr0076705	vesicle-mediated transport	2,30	1,06	2,13	0,99
A_09_P062371	lectin-24Db	lectin-24Db	FBtr0077469	-	2,29	1,61	1,51	1,06
A_09_P075866	Der-2	Derlin-2	FBtr0083307	defense response to bacterium	2,27	1,05	2,26	1,04
A_09_P019376	jet	jetlag	FBtr0079057	circadian behavior	2,27	1,05	1,87	0,87
A_09_P153830	CG33470	-	FBtr0087656	-	2,24	1,99	2,24	1,99
A_09_P007351	CG42807	-	FBtr0303819	-	2,24	1,26	5,48	3,08
A_09_P056666	Spn43Ad	Serpin 43Ad	FBtr0089053	-	2,23	1,67	1,84	1,38
A_09_P011906	GstD7	Glutathione S transferase D7	FBtr0082574	glutathione metabolic process	2,22	1,74	0,84	0,66
A_09_P054056	Zasp66	Z band alternatively spliced PDZ-motif protein 66	FBtr0089564	myofibril assembly	2,22	1,65	1,24	0,92
A_09_P065406	NimC1	-	FBtr0080615	phagocytosis	2,21	1,78	1,61	1,30
A_09_P053696	CG7409	-	FBtr0076810	protein folding	2,20	0,96	1,67	0,73
A_09_P065391	NimB4	Nimrod B4	FBtr0080617	defense response to bacterium	2,17	1,77	1,17	0,96
A_09_P102720	spen	split ends	FBtr0078121	Wnt signaling pathway	2,17	1,19	1,16	0,63

A_09_P007231	CG10799	-	FBtr0087748	-	2,16	1,80	0,89	0,74
A_09_P014436	A2bp1	Ataxin-2 binding protein 1	FBtr0305093	nervous system development	2,16	0,99	1,93	0,88
A_09_P061016	Obp99b	Odorant-binding protein 99b	FBtr0085462	sensory perception of chemical stimulus	2,16	0,92	1,54	0,65
A_09_P036451	CG12171	-	FBtr0078708	metabolic process	2,15	1,50	1,17	0,82
A_09_P007721	CG10131	-	FBtr0087499	oxidation-reduction process	2,13	1,76	1,54	1,27
A_09_P042026	DNaseII	Deoxyribonuclease II	FBtr0083538	DNA metabolic process	2,13	1,72	1,18	0,95
A_09_P017651	CG33469	-	FBtr0087504	-	2,13	1,41	1,59	1,05
A_09_P178620	CG3011	-	FBtr0290235	behavioral response to ethanol	2,12	1,83	1,11	0,95
A_09_P055116	CG10361	-	FBtr0076084	cellular amino acid metabolic process	2,12	1,74	1,52	1,25
A_09_P207753	Obp99c	Odorant-binding protein 99c	FBtr0085463	sensory perception of chemical stimulus	2,12	1,66	1,15	0,91
A_09_P217000	CG13794	-	FBtr0079507	neurotransmitter transport	2,11	1,91	1,43	1,29
A_09_P032386	Fak	Focal adhesion kinase	FBtr0086542	negative regulation of MAP kinase activity	2,11	0,89	2,18	0,92
A_09_P170745	Ten-m	Tenascin major	FBtr0078509	synaptic target attraction	2,11	1,73	1,29	1,06
A_09_P107605	Karl	Karl	FBtr0073557	imaginal disc-derived wing morphogenesis	2,10	1,61	1,69	1,29
A_09_P128985	CG32109	-	FBtr0075918	-	2,10	0,94	2,04	0,91
A_09_P197075	Gadd45	Gadd45	FBtr0089049	JNK cascade	2,09	1,38	1,65	1,09
A_09_P035981	CG1092	-	FBtr0078978	neurogenesis	2,07	1,63	1,32	1,04
A_09_P048106	CG4716	-	FBtr0087746	-	2,07	1,94	0,93	0,88
A_09_P055431	ver	verrocchio	FBtr0075960	neurogenesis	2,07	1,48	1,14	0,81
A_09_P008416	CG4927	-	FBtr0100547	proteolysis	2,07	1,41	1,18	0,80
A_09_P059146	CG31148	-	FBtr0084441	cellular response to unfolded protein	2,07	1,88	1,33	1,22
A_09_P189400	Eip93F	Ecdysone-induced protein 93F	FBtr0084169	autophagy	2,07	1,35	1,15	0,75
A_09_P057206	Obp83cd	Odorant-binding protein 83cd	FBtr0078584	sensory perception of chemical stimulus	2,06	1,61	1,11	0,87
A_09_P060461	CG31694	-	FBtr0077685	positive regulation of JAK-STAT cascade	2,06	1,90	0,95	0,88
A_09_P199445	CG33307	-	FBtr0080565	-	2,05	1,53	1,11	0,83
A_09_P007456	CG6553	-	FBtr0087642	-	2,04	1,66	0,99	0,80
A_09_P057746	CG30148	-	FBtr0086266	-	2,04	1,84	1,90	1,72
A_09_P009171	CG5493	-	FBtr0086713	oxidation-reduction process	2,02	1,43	1,40	0,98
A_09_P113980	CG14659	-	FBtr0078873	-	2,02	0,84	1,91	0,79
A_09_P219880	Gel	Gelsolin	FBtr0078969	phagocytosis	2,02	1,79	1,04	0,92
A_09_P046041	Hn	Henna	FBtr0100225	phagocytosis	2,02	1,78	0,94	0,83
A_09_P166370	pncr016:2R	putative noncoding	FBtr0091953	-	2,01	1,16	1,41	0,81
A_09_P170670	Sr-CI	Scavenger receptor class C, type I	FBtr0077467	phagocytosis	2,01	1,33	2,11	1,40
A_09_P009016	CG10916	-	FBtr0086749	determination of adult lifespan	2,01	1,46	1,66	1,21
A_09_P062776	CG3699	-	FBtr0070186	metabolic process	2,01	1,01	0,85	0,43
A_09_P147180	Npc2h	Niemann-Pick type C-2h	FBtr0085722	hemolymph coagulation	2,01	1,51	0,81	0,61
A_09_P002051	Idgf5	Imaginal disc growth factor 5	FBtr0086668	chitin catabolic process	2,00	1,60	1,40	1,11
A_09_P160105	CG2233	-	FBtr0071123	-	2,00	1,37	1,56	1,06
Induced (≥2 fold) by SINV infection only in *die*^{1} mutants								
A_09_P062376	lectin-24A	lectin-24A	FBtr0077539	-	1,49	7,12	0,16	0,77
A_09_P219460	CecA2	Cecropin A2	FBtr0085614	antibacterial humoral response	1,82	4,32	1,29	3,04
A_09_P079521	CG2217	-	FBtr0085630	-	1,68	2,87	0,62	1,07
A_09_P061546	CG15553	-	FBtr0290201	transmembrane transport	1,91	2,78	1,49	2,16
A_09_P041636	CecC	Cecropin C	FBtr0085616	antibacterial humoral response	1,89	2,38	4,33	5,48
A_09_P074121	Ect3	Ectoderm-expressed 3	FBtr0082487	autophagic cell death	1,45	2,38	1,51	2,48
A_09_P012336	Drs	Drosomycin	FBtr0073073	antifungal humoral response	1,65	2,33	1,22	1,72
A_09_P079551	CG6495	-	FBtr0080114	-	1,95	2,24	0,99	1,14
A_09_P010041	wb	wing blister	FBtr0302731	imaginal disc-derived wing morphogenesis	1,66	2,16	1,22	1,60
A_09_P040616	et	eye transformer	FBtr0074757	negative regulation of JAK-STAT cascade	1,66	2,11	1,03	1,32
A_09_P067431	CG4020	-	FBtr0070824	-	1,53	2,05	0,77	1,04
A_09_P004656	CG40801	-	FBtr0113933	-	1,78	2,05	1,12	1,29
A_09_P181540	CG3246	-	FBtr0077572	-	1,80	2,02	0,93	1,04
A_09_P006346	Listericin	Listericin	FBtr0088191	defense response to bacterium	1,64	2,00	1,17	1,42
Repressed (≤0,5 fold) by SINV infection in WT and *die*^{1} mutants								
A_09_P043366	Lsp1beta	Larval serum protein 1 beta	FBgn0002563	lateral inhibition	0,31	0,45	0,95	1,35
Repressed (≤0,5) by SINV infection only in WT								
A_09_P026876	CG9861	-	FBgn0034844	-	0,44	0,89	0,64	1,28
A_09_P167915	CG4836	-	FBgn0270925	oxidation-reduction process	0,46	0,78	0,61	1,04
A_09_P016281	Erk7	Extracellularly regulated kinase 7	FBgn0052703	cellular response to amino acid starvation	0,46	0,71	0,66	1,02
A_09_P026816	Klp59D	Kinesin-like protein at 59D	FBgn0034827	microtubule-based movement	0,46	0,81	0,67	1,19
A_09_P019016	CG3213	-	FBgn0031545	-	0,46	0,76	0,58	0,96
A_09_P056826	CG33992	-	FBgn0264086	-	0,47	0,76	0,63	1,02
A_09_P026546	CG4329	-	FBgn0034745	sensory perception of sound	0,47	0,77	0,68	1,11
A_09_P029441	Pen	Pendulin	FBgn0267727	cytoplasmic transport	0,48	0,76	0,66	1,04
A_09_P025481	CG16716	-	FBgn0034459	cellular protein modification process	0,48	0,77	0,64	1,04
A_09_P074866	CG9297	-	FBgn0038181	calcium ion transport	0,48	0,65	0,83	1,12
A_09_P019236	CG15635	-	FBgn0031617	multicellular organism reproduction	0,49	0,56	0,70	0,81
A_09_P068846	hmw	hemingway	FBgn0038607	spermatogenesis	0,49	0,76	0,68	1,07
A_09_P065951	CG4892	-	FBgn0028884	-	0,49	0,77	0,78	1,22
A_09_P136850	CG4945	-	FBtr0087100	protein phosphorylation	0,50	0,83	0,90	1,12
A_09_P029571	Hsp70Aa	Heat-shock-protein-70Aa	FBtr0082512	response to heat	0,50	0,76	0,68	1,18

Table S2: List of genes induced and repressed by SINV infection in WT and die$_1$ flies.

Repressed (≤0,5 fold) by SINV infection only in *die*^{1} mutants								
A_09_P192275	Cyp4g1	Cytochrome P450-4g1	FBgn0010019	lipid metabolic process	0,62	0,47	0,87	0,66
A_09_P113025	Cpr67Fb	Cuticular protein 67Fb	FBgn0036110	multicellular organism reproduction	0,70	0,48	1,83	1,25
A_09_P045821	Strn-Mlck	Stretchin-Mlck	FBgn0265045	protein phosphorylation	0,63	0,49	1,00	0,78
A_09_P068471	CG12057	-	FBgn0030098	-	0,83	0,49	1,11	0,66
A_09_P171760	CG34324	-	FBtr0112526	chitin metabolic process	0,65	0,50	0,86	0,68
A_09_P049596	sls	sallimus	FBtr0072849	sarcomere organization	0,85	0,50	1,71	1,06
A_09_P056531	Obp57a	Odorant-binding protein 57a	FBtr0086294	sensory perception of chemical stimulus	0,55	0,50	0,58	0,70
A_09_P116830	nrm	neuromusculin	FBtr0304833	synaptic target recognition	0,58	0,50	1,01	0,94
A_09_P003751	CG34324	-	FBtr0112526	chitin metabolic process	0,68	0,50	0,87	0,71

Table S3: List of genes induced and repressed in *die*^{1} compared to WT flies during SINV infection. Genes that are also induced by SINV are highlighted.

Probe number	**SYMBOL**	**Gene Name**	**Flybase ID**	**GO_Biological Process**	***die*^{1}/WT SINV**	***die*^{1}/WT non infected**	***die*^{1} SINV/Non infected**	**WT SINV/non infected**
Induced (≥2 fold) in *die*^{1} compared to WT flies SINV								
A_09_P040931	CG1304	-	FBgn0031141	proteolysis	52,68	48,76	1,20	1,11
A_09_P134045	Cyp12d1-d	Cyp12d1-d	FBgn0053503	oxidation-reduction process	46,00	55,60	0,93	1,13
A_09_P005646	Cyp4p2	Cyp4p2	FBgn0033395	oxidation-reduction process	43,42	45,42	1,20	1,26
A_09_P028156	CG13905	-	FBgn0035176	-	28,72	51,47	0,98	1,75
A_09_P129245	CG16762	-	FBgn0035343	-	18,97	14,34	0,96	0,72
A_09_P194370	CG43089	-	FBtr0304872	ubiquitin-dependent protein catabolic process	14,48	18,29	0,77	0,97
A_09_P060946	CG7567	-	FBgn0039670	-	11,82	19,03	0,98	1,57
A_09_P045891	DptB	Diptericin B	FBtr0086621	antimicrobial humoral response	10,36	4,79	6,36	2,94
A_09_P029476	Ser6	Serine protease 6	FBgn0011834	proteolysis	9,55	8,55	1,25	1,12
A_09_P101215	edin	elevated during infection	FBtr0075174	immune response	9,03	1,88	16,15	3,36
A_09_P010311	Dpt	Diptericin	FBtr0086620	antibacterial humoral response	7,87	2,42	6,79	2,09
A_09_P129495	CG7912	-	FBgn0039736	sulfate transport	7,67	6,41	0,99	0,83
A_09_P019026	Sr-CIV	Scavenger receptor class C, type IV	FBgn0031547	defense response	6,86	6,60	1,21	1,17
A_09_P030406	Mtk	Metchnikowin	FBtr0087386	antimicrobial humoral response	6,17	4,02	4,70	3,06
A_09_P112030	CG10140	-	FBgn0036363	chitin metabolic process	5,61	7,60	0,91	1,24
A_09_P041636	CecC	Cecropin C	FBtr0085616	antibacterial humoral response	5,48	4,33	2,38	1,89
A_09_P029506	AttA	Attacin-A	FBtr0087437	antimicrobial humoral response	5,39	1,73	7,82	2,51
A_09_P012351	Def	Defensin	FBtr0088432	antibacterial humoral response	5,24	3,56	1,80	1,22
A_09_P030936	veg	vegetable	FBgn0265195	peripheral nervous system development	4,95	4,79	1,01	0,98
A_09_P197010	CG34391	-	FBgn0085420	-	4,91	5,21	0,82	0,87
A_09_P027001	CG10332	-	FBtr0072109	-	4,82	2,76	5,39	3,08
A_09_P064281	AttC	Attacin-C	FBtr0305795	antibacterial humoral response	4,77	1,94	5,82	2,37
A_09_P064286	AttB	Attacin-B	FBtr0087438	antibacterial humoral response	4,73	1,85	5,27	2,06
A_09_P056566	PGRP-SB1	PGRP-SB1	FBtr0075348	immune response	4,57	3,80	4,60	3,83
A_09_P007126	CG13324	-	FBgn0033789	-	4,00	4,90	1,08	1,32
A_09_P056576	CG8147	-	FBgn0043791	metabolic process	3,76	3,10	0,94	0,78
A_09_P059486	CG31272	-	FBgn0051272	transport	3,63	2,90	1,06	0,85
A_09_P168525	phr	photorepair	FBgn0003082	DNA repair	3,60	2,87	1,11	0,88
A_09_P076236	AttD	Attacin-D	FBtr0083470	antibacterial humoral response	3,39	2,52	2,93	2,18
A_09_P113770	CG12780	-	FBgn0033301	defense response to virus	3,28	3,92	0,87	1,05
A_09_P015226	CG32302		FBtr0072881	chitin metabolic process	3,26	1,30	1,25	0,50
A_09_P017326	CG33258	-	FBgn0053258	chitin metabolic process	3,24	2,50	1,19	0,92
A_09_P007351	CG42807	-	FBgn0261989	-	3,08	5,48	1,26	2,24
A_09_P219460	CecA2	Cecropin A2	FBtr0085614	antibacterial humoral response	3,04	1,29	4,32	1,82
A_09_P019926	CG9498	-	FBtr0079282	-	2,99	1,94	1,66	1,07
A_09_P064591	CG18853	-	FBgn0042173	DNA repair	2,98	2,56	0,96	0,83
A_09_P180200	CG13795	-	FBtr0300709	neurotransmitter transport	2,97	2,87	1,63	1,57
A_09_P053661	PGRP-SD	PGRP-SD	FBtr0076807	defense response to Gram-positive bacterium	2,05	2,41	2,95	3,47
A_09_P048671	spn-F	spn-F	FBgn0086362	oocyte microtubule cytoskeleton organization	2,95	2,70	1,03	0,94
A_09_P075531	CG5399	-	FBgn0038353	-	2,91	3,05	0,93	0,98
A_09_P000871	CG33965	-	FBgn0053965	transport	2,86	3,08	0,90	0,97
A_09_P018931	CG8837	-	FBgn0031520	transmembrane transport	2,84	3,01	0,99	1,05
A_09_P042021	Cyp6a2	Cytochrome P450-6a2	FBgn0000473	oxidation-reduction process	2,81	2,87	1,01	1,03
A_09_P006576	Damm	Death associated molecule related to Mch2 caspase	FBgn0033659	programmed cell death	2,74	2,44	0,98	0,87
A_09_P113810	GstE10	Glutathione S transferase E10	FBgn0063499	glutathione metabolic process	2,74	3,24	0,81	0,96
A_09_P053051	Tektin-C	Tektin C	FBgn0035638	microtubule-based process	2,72	2,10	0,99	0,76
A_09_P063516	CG13177	-	FBgn0040759	-	2,72	3,07	1,29	1,46
A_09_P035761	CG11425	-	FBgn0037167	dephosphorylation	2,71	2,78	1,31	1,34
A_09_P045121	sls	sallimus	FBgn0086906	regulation of hemocyte proliferation	2,57	3,77	0,60	0,88
A_09_P016591	Dh31-R	Diuretic hormone 31 Receptor	FBgn0052843	G-protein coupled receptor signaling pathway	2,54	2,65	0,92	0,97
A_09_P026381	Alp2	Alkaline phosphatase 2	FBtr0071782	dephosphorylation	2,52	1,84	1,03	0,75
A_09_P079516	rgn	regeneration	FBgn0261258	tissue regeneration	2,49	3,21	0,82	1,06
A_09_P074121	Ect3	Ectoderm-expressed 3	FBtr0082487	autophagic cell death	2,48	1,51	2,38	1,45
A_09_P036976	CG14606	-	FBtr0081603	phagocytosis	2,47	1,70	1,21	0,84
A_09_P026396	Oatp58Db	Organic anion transporting polypeptide 58Db	FBtr0071778	organic anion transport	2,46	1,77	1,02	0,73
A_09_P014056	Mur29B	Mucin related 29B	FBgn0051901	-	2,45	2,34	1,23	1,18
A_09_P050506	CG15282	-	FBgn0028855	-	2,44	2,13	1,51	1,32
A_09_P043361	Lsp1alpha	Larval serum protein 1 alpha	FBgn0002562	-	2,43	2,34	1,13	1,10
A_09_P028636	CG1139	-	FBgn0035300	growth	2,37	2,81	0,95	1,13
A_09_P128930	CG13075	-	FBgn0036563	chitin metabolic process	2,37	2,28	1,37	1,31
A_09_P003596	CG34284	-	FBgn0085313	-	2,37	2,86	0,90	1,09
A_09_P121465	Pvf2	PDGF- and VEGF-related factor 2	FBgn0031888	hemocyte migration	2,33	2,51	1,32	1,42
A_09_P035511	CapaR	Capability receptor	FBgn0037100	neuropeptide signaling pathway	2,32	2,13	1,04	0,96
A_09_P114005	CG33109	-	FBtr0082900	-	2,29	1,87	1,30	1,07
A_09_P069016	CG14292	-	FBgn0038658	-	2,29	2,33	0,99	1,01
A_09_P008901	CG18635	-	FBgn0034279	-	2,27	2,22	1,05	1,02
A_09_P052846	CG13704	-	FBgn0035583	-	2,27	2,58	0,96	1,09
A_09_P043391	Mal-A2	Maltase A2	FBtr0088747	carbohydrate metabolic process	2,24	1,74	1,25	0,97
A_09_P075741	Zip89B	Zinc/iron regulated transporter-related protein 89B	FBgn0038412	metal ion transport	2,23	2,12	1,20	1,14

Table S3: List of genes induced and repressed in *die* $_1$ compared to WT flies during SINV infection.

A_09_P078261	prominin-like	prominin-like	FBgn0026189	neuron projection morphogenesis	2,23	2,55	0,97	1,11
A_09_P064786	MESK4	Misexpression suppressor of KSR 4	FBgn0043069	positive regulation of Ras protein signal transduction	2,23	2,44	0,99	1,08
A_09_P189326	CR41606	-	FBtr0114204	-	2,20	2,69	0,79	0,97
A_09_P021191	CG13117	-	FBtr0079864	-	2,20	2,79	1,05	1,33
A_09_P118470	Dgp-1	Dgp-1	FBtr0086773	-	2,20	2,01	1,03	0,94
A_09_P049331	Cbp53E	Calbindin 53E	FBtr0087056	ative regulation of response to woun	2,18	1,90	1,00	0,87
A_09_P195390	A2bp1	Ataxin-2 binding protein 1	FBgn0052062	oogenesis	2,18	3,41	0,85	1,33
A_09_P073381	CG5361		FBtr0082201	metabolic process	2,17	1,68	1,17	0,91
A_09_P061546	CG15553	-	FBtr0290201	transmembrane transport	2,16	1,49	2,78	1,91
A_09_P100315	CG34269		FBtr0112464		2,16	1,88	0,94	0,82
A_09_P018246	CG42329		FBtr0299796		2,13	2,26	0,92	0,98
A_09_P024961	CG14764	-	FBgn0033236	-	2,13	2,21	1,03	1,07
A_09_P034006	CG7589		FBtr0075221	phagocytosis	2,11	1,80	0,95	0,82
A_09_P007121	CG13323	-	FBgn0033788	-	2,10	2,50	1,05	1,25
A_09_P108115	Arpc3B	Actin-related protein 2/3 complex, subunit 3B	FBgn0065032	actin filament organization	2,10	2,45	0,91	1,06
A_09_P180030	CG11334	-4	FBtr0085808	wing disc development	2,09	1,64	1,31	1,02
A_09_P026401	Oatp58Dc	Organic anion transporting polypeptide 58Dc	FBtr0071777	response to methotrexate	2,09	1,73	0,96	0,80
A_09_P002691	CG17672	-	FBtr0110982	-	2,09	1,94	1,00	0,93
A_09_P020306	Ndae1	Na+-driven anion exchanger 1	FBtr0299538	anion transport	2,08	1,68	1,27	1,03
A_09_P061746	salt	salty dog	FBtr0300915	transmembrane transport	2,08	1,41	1,26	0,86
A_09_P019071	CG3604		FBtr0077545		2,07	1,85	1,29	1,15
A_09_P042786	Hsp22	Heat shock protein 22	FBgn0001223	response to heat	2,07	2,65	0,74	0,94
A_09_P007136	CG13325	-	FBtr0087722	-	2,07	1,76	1,73	1,47
A_09_P194406	Tsp2A	Tetraspanin 2A	FBgn0024361		2,06	2,60	0,90	1,14
A_09_P039921	CG15814	-	FBgn0030873	-	2,05	2,27	0,97	1,07
A_09_P210360	CG32024		FBtr0076580	chitin metabolic process	2,02	2,44	0,84	1,02
A_09_P146530	CG15210	-	FBgn0040850	-	2,01	2,58	1,02	1,30
A_09_P218200	CG5527	-	FBtr0085255	proteolysis	2,01	1,26	1,65	1,03
A_09_P126515	PGRP-LD	Peptidoglycan recognition protein LD	FBtr0091709	immune response	2,00	1,63	1,12	0,91
A_09_P027951	mthl9	methuselah-like 9	FBtr0072574	G-protein coupled receptor signaling pathway	2,00	1,93	1,15	1,11
A_09_P040116	CG15043	-	FBtr0074626	-	2,00	2,72	0,86	1,17
A_09_P008051	CG8249		FBtr0087310		2,00	1,46	1,22	0,89
A_09_P058261	CG30380	-	FBgn0050380	-	1,99	2,08	1,17	1,22

Repressed (≥2 fold) in *die1* compared to WT flies_SINV								
A_09_P060926	die	Diedel	FBtr0085426	response to bacterium	0,00	0,11	0,99	323,47
A_09_P062366	lectin-28C	lectin-28C	FBtr0079527	-	0,07	0,07	2,59	2,39
A_09_P043321	Lcp1	Larval cuticle protein 1	FBtr0088763	chitin-based cuticle development	0,07	0,11	0,63	0,98
A_09_P060921	CG2310	-	FBtr0085434	-	0,08	0,11	1,05	1,52
A_09_P217215	CG14957	-	FBtr0073038	chitin metabolic process	0,09	0,19	0,79	1,68
A_09_P032116	sfl	sulfateless	FBtr0076968	Wnt signaling pathway	0,16	0,17	1,00	1,05
A_09_P038731	CG14410	-	FBtr0073948	-	0,16	0,16	1,15	1,13
A_09_P042926	Jon44E	Jonah 44E	FBtr0088704	proteolysis	0,18	0,20	0,96	1,11
A_09_P028306	CG12090	-	FBtr0072703	-	0,17	0,20	0,94	1,08
A_09_P078756	Fie	Fire exit	FBtr0073157	-	0,19	0,20	0,97	1,02
A_09_P020981	CG9515	-	FBtr0079791	-	0,19	0,21	1,27	1,40
A_09_P010541	LysB	Lysozyme B	FBtr0072628	antimicrobial humoral response	0,22	0,26	0,78	0,93
A_09_P022396	Vha68-3	Vacuolar H+ ATPase 68kD subunit 3	FBtr0080421	ATP metabolic process	0,22	0,17	0,85	0,64
A_09_P147255	CG4398	-	FBtr0087157	-	0,20	0,15	1,87	1,41
A_09_P192645	CG42847	-	FBtr0303932	-	0,22	0,19	0,87	0,75
A_09_P072161	CG17192	-	FBtr0085153	lipid catabolic process	0,24	0,14	1,27	0,74
A_09_P018296	CG10869	-	FBtr0077917	-	0,25	0,10	1,34	0,54
A_09_P053136	Jon65Aii	Jonah 65Aii	FBtr0077042	proteolysis	0,25	0,37	0,64	0,94
A_09_P058781	CG31030	-	FBtr0085579	ATP hydrolysis coupled proton transport	0,29	0,26	0,98	0,88
A_09_P015131	CG32267	-	FBtr0073142	-	0,30	0,32	0,99	1,06
A_09_P143990	CG9531	-	FBtr0079270	protein methylation	0,32	0,33	0,98	1,01
A_09_P030671	Rala	Ras-like protein A	FBtr0070583	innate immune response	0,31	0,34	1,03	1,13
A_09_P028151	CG13907	-	FBtr0072593	transmembrane transpor	0,32	0,30	1,10	1,02
A_09_P063696	CG15213	-	FBtr0077182	-	0,33	0,41	0,85	1,07
A_09_P006826	CG13155	-	FBtr0087956	-	0,33	0,39	1,15	1,35
A_09_P008251	Tsf3	Transferrin 3	FBtr0087130	response to bacterium	0,34	0,36	1,40	1,48
A_09_P111285	CG9259	-	FBtr0081464	-	0,34	0,30	1,02	0,88
A_09_P149115	RpL17	Ribosomal protein L17	FBtr0070982	mitotic spindle organization	0,35	0,38	1,01	1,11
A_09_P074191	CG4830	-	FBtr0082625	metabolic process	0,35	0,19	0,95	0,51
A_09_P140170	ND-B14	NADH dehydrogenase (ubiquinone) B14 subunit	FBtr0088238	mitochondrial electron transport, NADH to ubiquinone	0,36	0,43	0,91	1,09
A_09_P052171	Cyp4e3	Cytochrome P450-4e3	FBtr0079925	oxidation-reduction process	0,36	0,58	1,65	2,64
A_09_P058216	CG30371	-	FBtr0088798	proteolysis	0,37	0,46	0,92	1,14
A_09_P025106	CG14759	-	FBtr0088796	-	0,39	0,47	0,72	0,88
A_09_P020401	Cyp4d21	Cyp4d21	FBtr0079471	oxidation-reduction process	0,39	0,29	1,39	1,04
A_09_P025456	CG15120	-	FBtr0086463	-	0,40	0,52	1,19	1,55
A_09_P053151	CG10472	-	FBtr0077066	proteolysis	0,40	0,44	0,70	0,78
A_09_P060931	CG2010	-	FBtr0085427	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	0,41	0,47	0,90	1,04
A_09_P013876	CG31832	-	FBtr0080726	-	0,42	0,58	2,91	4,06
A_09_P032651	Jon25Bi	Jonah 25Bi	FBtr0079054	proteolysis	0,42	0,32	1,23	0,93
A_09_P025161	Mal-A4	Maltase A4	FBtr0088748	carbohydrate metabolic process	0,42	0,70	1,42	2,38
A_09_P196520	CG42540	-	FBtr0301097	-	0,42	0,42	0,94	0,95
A_09_P063456	CG16926	-	FBtr0086499	-	0,42	0,54	0,90	1,16
A_09_P007686	Oaz	O/E-associated zinc finger protein	FBtr0302927	spiracle morphogenesis, open tracheal system	0,41	0,34	0,67	0,56
A_09_P015161	CG32278	-	FBtr0073033	-	0,43	0,42	1,06	1,04

Table S3: List of genes induced and repressed in *die* $_1$ compared to WT flies during SINV infection.

A_09_P062776	CG3699	-	FBtr0070186	fatty acid beta-oxidation	0,43	0,85	1,01	2,01
A_09_P071671	CG5107	-	FBtr0084879	-	0,43	0,60	0,58	0,79
A_09_P060181	CG31606	-	FBtr0079577	-	0,43	0,55	2,10	2,67
A_09_P024031	CG17571	-	FBtr0081376	proteolysis	0,44	0,73	0,70	1,15
A_09_P061721	CG11550	-	FBtr0085867	-	0,44	0,37	1,07	0,88
A_09_P028401	CG13919	-	FBtr0072759	-	0,45	0,58	1,01	1,32
A_09_P007056	CG12374	-	FBtr0087854	proteolysis	0,44	0,37	0,74	0,63
A_09_P209330	LSm7	-	FBtr0080934	neurogenesis	0,45	0,53	0,95	1,10
A_09_P034876	Ir76b	Ionotropic receptor 76b	FBtr0074869	cellular response to salt	0,49	0,35	0,75	0,54
A_09_P053941	Jon66Cii	Jonah 66Cii	FBtr0076666	proteolysis	0,46	0,57	0,86	1,08
A_09_P063381	CG14974	-	FBtr0073140	-	0,46	0,53	0,78	0,90
A_09_P148025	FucTD	FucTD	FBtr0072693	protein glycosylation	0,46	0,36	0,99	0,77
A_09_P064576	CG18814	-	FBtr0075385	oxidation-reduction process	0,45	0,45	1,08	1,07
A_09_P004316	CG34417	-	FBtr0112704	mesoderm development	0,47	0,54	0,82	0,94
A_09_P170880	RhoGAP100F	Rho GTPase activating protein at 100F	FBtr0302181	synaptic vesicle localization	0,13	0,13	0,85	0,84
A_09_P053566	CG8560	-	FBtr0076868	proteolysis	0,48	0,45	0,87	0,82
A_09_P060291	CG31639	-	FBtr0079208	ubiquitin-dependent protein catabolic process	0,48	0,64	0,67	0,89
A_09_P030521	Cyp4e1	Cytochrome P450-4e1	FBtr0088746	oxidation-reduction process	0,48	0,42	1,07	0,94
A_09_P063371	CG12483	-	FBtr0072540	-	0,49	0,76	0,61	0,95
A_09_P017921	CG11912	-	FBtr0078099	proteolysis	0,49	1,18	0,78	1,87
A_09_P061851	Syt7	Synaptotagmin 7	FBtr0089139	exocytosis	0,50	0,44	1,11	0,95
A_09_P061981	Sox102F	Sox102F	FBtr0100600	positive regulation of heart contraction	0,50	0,47	1,38	1,30
A_09_P109095	CG16704	-	FBtr0077550	-	0,50	0,78	1,21	1,89
A_09_P027391	mRpS17	mitochondrial ribosomal protein S17	FBtr0072277	translation	0,50	0,58	1,02	1,20
A_09_P007476	DJ-1alpha	DJ-1alpha	FBtr0087615	response to oxidative stress	0,50	0,48	0,92	0,88
A_09_P029371	Dsp1	Dorsal switch protein 1	FBgn0011764	chromatin remodeling	0,50	0,47	0,65	0,59