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Supplementary Information for
Drosophila Fezf functions as a transcriptional repressor to direct layer specific synaptic connectivity in the fly visual system

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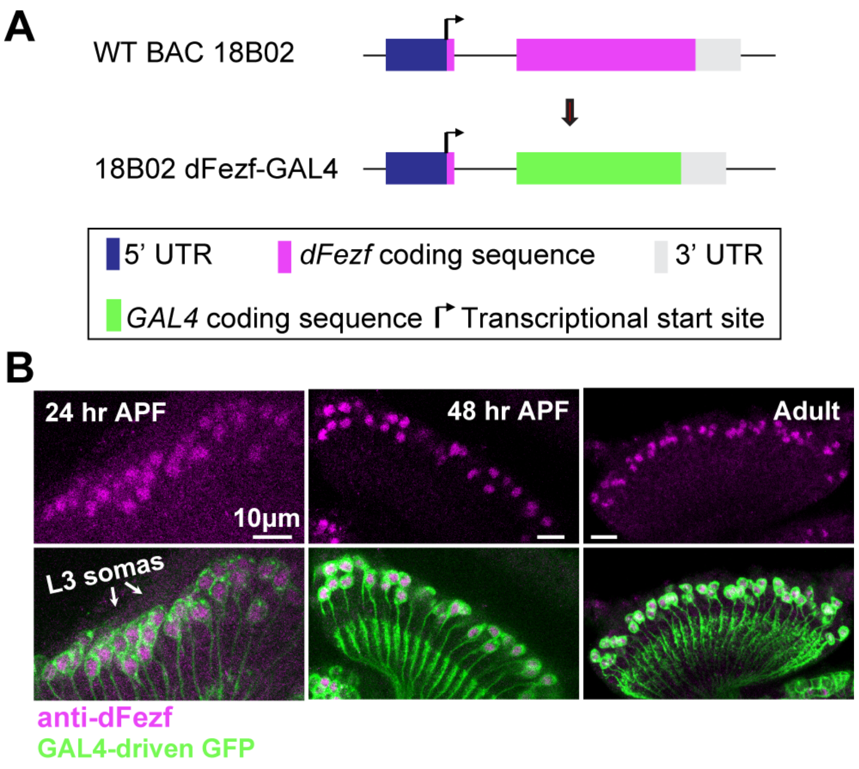

Fig. S1. *dFezf-GAL4* is a new L3-specific driver. As our traditional L3 GAL4 driver *9-9-GAL4* did not label *slp*^{S37A} mutant L3 neurons, we constructed a new L3-specific GAL4 driver using a bacterial artificial chromosome (BAC) harboring the *dFezf* locus. (A) Schematic illustrating the design of the dFezf-GAL4 construct. We modified the original BAC by replacing almost the entire *dFezf* coding region (except the sequence encoding the first three amino acid) with that of GAL4. (B) Confocal images of WT 24 hr APF, 48 hr APF, and adult lamina. To ask whether *dFezf-GAL4* mimics the expression pattern of the endogenous *dFezf* gene, we used this driver to promote expression of a *UAS-myrGFP* reporter (green) and a dFezf antibody (magenta) to identify L3 neurons. As expected, *dFezf-GAL4* labeled L3 neurons in a highly-specific manner within the lamina, as shown by 100% co-localization of myr-GFP-labeled cell bodies and dFezf antibody-labeled nuclei. The specificity of this driver persists throughout development, from 24 hr APF to the adult stage. This driver was used to successfully label *slp*^{S37A} mutant L3 neurons in all experiments in this report. All scale bars = 10 μm.

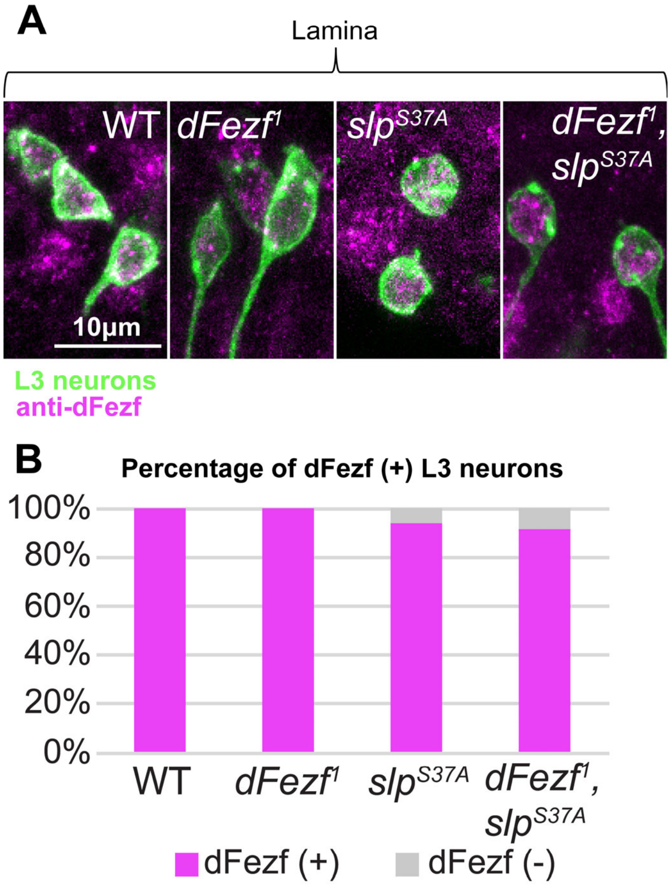

Fig. S2. *dFezf* is expressed in *slp*^{S37A} mutant L3 neurons. We examined the expression of dFezf protein in L3 neurons harboring the *slp*^{S37A} mutation. (A) L3 MARCM clones are labeled with GFP (green). An antibody against dFezf was used to examine presence of dFezf protein. (B) Quantification of dFezf (+) and dFezf (-) cells.

Table S1. 403 differentially expressed (DE) genes in *dFezf*^{1} mutant L3 neurons.

Gene	WT (TPM)	*dFezf*^{1} (TPM)	padj	Biocategory
CG34113	11.88353	0.012234	6.40E-61	cell_surface
CG2082	0.289713	70.00823	1.37E-44	NA
CG32052	195.2752	0	9.60E-40	cell_surface
CG45263	0.030555	18.84248	3.83E-38	cell_surface
CG15465	0	18.31327	1.50E-37	NA
dpr10	0.708601	18.66119	1.51E-37	cell_surface
danr	2.534069	80.55821	4.22E-34	TF
CG10384	0.087786	14.9419	8.07E-34	RNA_binding
CG6154	0	21.26582	3.74E-29	NA
dpr13	0.008986	9.62952	1.93E-26	cell_surface
pog	18.28413	0.671769	6.91E-25	NA
NetB	31.48418	0.118607	1.87E-24	cell_surface
CG13579	8.772826	0.005361	3.43E-24	cell_surface
unc-13-4A	0.002997	3.748376	6.00E-22	NA
aPKC	30.70797	1.339071	7.25E-22	kinase_activity,microtubule
Cyp6a2	0	21.61973	6.30E-19	ecdysone_inducible
Eip63F-1	0	5.551063	6.84E-19	ecdysone_inducible
mthl5	24.32956	1.675455	1.17E-17	cell_surface
tna	14.6588	81.06448	2.60E-17	TF
alpha-Man-IIb	0	2.731062	3.63E-17	NA
Fas3	253.1028	67.58279	3.64E-15	cell_surface
Dscam4	0.108643	9.649883	8.14E-15	cell_surface
CG11357	0	4.282307	3.99E-14	cell_surface
Pvf3	34.85952	4.74629	6.26E-14	cell_surface
CG31760	0.540704	19.58649	6.26E-14	NA
CG42346	0.05089	2.506987	6.80E-13	cell_surface
I-3	0	18.5529	1.19E-12	NA
kek1	32.52628	3.737976	2.25E-12	cell_surface
TrissinR	0	2.420962	4.79E-12	cell_surface
Zasp67	9.091009	0.061124	1.06E-11	NA
noc	12.40134	1.146227	1.34E-11	TF
dnr1	0.013647	4.781081	1.39E-11	NA
sick	2.272182	33.47358	1.52E-11	NA
dpr12	0.016191	5.152015	7.48E-11	cell_surface
Ilp1	24.31122	0	1.11E-10	cell_surface
CG33639	0	2.084802	1.95E-10	cell_surface
CG3014	6.385718	0	2.64E-10	NA
Ziz	2.876359	24.26394	2.81E-10	gef,gef
CG15236	10.64867	46.84581	3.01E-10	NA
G6P	6.923471	0	6.32E-10	phosphatase_activity
ATP8B	0	1.135664	7.45E-10	membrane_transporter
CG44422	1.452494	17.40857	1.29E-09	NA
Vha100-3	0	2.845595	2.06E-09	membrane_transporter
dpr20	0	2.539965	4.20E-09	cell_surface
dpr3	15.18489	2.391386	8.30E-09	cell_surface
CG5062	0.004529	4.513476	9.81E-09	NA
aos	3.804452	33.64292	1.06E-08	cell_surface
CG34370	9.627797	0.914704	1.19E-08	cell_surface
nAChRalpha7	16.96315	73.35559	1.19E-08	membrane_transporter
stai	325.6439	117.1967	1.51E-08	NA
CG7627	0	1.121038	1.66E-08	membrane_transporter
CG9331	0.142324	7.730927	3.70E-08	NA
CG42324	6.936311	32.33093	4.64E-08	NA
MESR3	55.91881	2.245028	7.63E-08	NA
ZnT33D	0	1.95866	9.27E-08	membrane_transporter
fas	31.87103	7.244237	1.10E-07	cell_surface

rdo	11.5939	41.29886	1.28E-07	cell surface
Ptp99A	26.63526	110.3687	1.86E-07	cell surface,phosphatase activity
SP2353	43.02196	10.61129	2.92E-07	cell surface
CG15097	29.68088	74.82531	3.53E-07	actin binding
sm	7.452186	34.04271	3.58E-07	RNA binding
sano	1.991947	14.8792	6.35E-07	NA
dpr11	0.527716	5.672138	6.86E-07	cell surface
CycD	0.010709	3.291448	7.72E-07	NA
CG13559	0	1.669519	7.72E-07	NA
CG34334	0	0.730676	7.72E-07	RNA binding
CG1208	0	0.595205	7.72E-07	membrane transporter
CG7813	0	0.50936	8.97E-07	membrane transporter
CG43092	0	1.640524	9.09E-07	NA
Drl-2	0.00186	1.272309	1.12E-06	cell surface,kinase activity
Tsp33B	0	1.509015	1.17E-06	cell surface
CG14000	0	1.022056	1.17E-06	NA
Hr51	0	0.708187	1.17E-06	TF
CG42343	0	1.06681	1.20E-06	cell surface
shakB	0.173288	78.15027	1.27E-06	membrane transporter
CG42750	2.592332	17.26361	1.27E-06	NA
ETHR	0	0.508349	1.28E-06	cell surface
CG11289	0	0.68623	1.28E-06	NA
olf413	6.841745	0.63698	1.28E-06	NA
mab-21	0.047498	4.568228	1.37E-06	NA
comm2	0	0.654127	1.46E-06	cell surface
CG34155	0.094695	9.273065	1.47E-06	cell surface
CG13739	0.010091	8.467423	1.60E-06	cell surface
CG4743	5.999717	0	1.80E-06	membrane transporter
CG43295	0	2.061151	1.80E-06	NA
amos	0	1.783501	1.80E-06	TF
clumsy	0	0.079446	1.88E-06	membrane transporter
CG10357	0	0.272485	2.03E-06	NA
CG1402	19.14221	3.298207	2.04E-06	NA
CG13766	3.293198	0	2.38E-06	NA
Ten-a	0.200026	5.259921	2.56E-06	cell surface
CG31278	7.947684	0	3.59E-06	NA
Ir76b	0	0.173213	4.16E-06	membrane transporter
CG2750	0	0.038909	4.16E-06	NA
CG33143	0	0.063181	4.33E-06	cell surface
CG4951	6.522151	0	4.33E-06	NA
Sfp33A2	0	2.544466	4.33E-06	NA
CG3709	2.236691	0	5.48E-06	RNA binding
CG9932	15.85899	52.20831	6.62E-06	TF
CG31808	0	2.051001	7.34E-06	NA
CG4496	0.136155	3.107705	9.52E-06	TF
CG4935	5.246885	0.02021	1.12E-05	NA
Nrx-IV	11.33556	2.280907	1.70E-05	cell surface
Or45a	0.0091	2.510192	1.82E-05	cell surface
CG5705	5.43729	0.026808	2.17E-05	RNA binding
sbb	22.61916	93.79258	2.17E-05	TF
Nedd4	2.05424	12.66206	2.51E-05	NA
bru-3	88.54569	22.73377	2.72E-05	RNA binding,translation regulation
Dop2R	1.064735	0	4.68E-05	cell surface
CG43783	5.386204	0.619699	4.82E-05	NA
Ih	0.058099	15.50847	5.20E-05	membrane transporter
Lrch	15.90225	0.855465	5.42E-05	cell surface
pyd	0.919407	8.7705	5.52E-05	kinase activity
CG15473	0.066088	3.494454	5.62E-05	cell surface
Liprin-gamma	0.649271	8.280584	6.08E-05	NA

nw	0.00192	1.603292	6.08E-05	NA
CG30015	0.061651	2.736231	6.70E-05	NA
CG43795	0.005174	1.469088	6.76E-05	NA
kek3	21.10725	6.356945	8.46E-05	cell surface
SK	5.047885	30.4037	8.64E-05	membrane transporter
CG32655	0	3.267332	8.83E-05	NA
slp1	51.27967	143.8324	0.000102	TF
dpr6	18.89109	2.253075	0.000105	cell surface
CG34215	0	9.586342	0.000108	NA
Indy-2	1.089373	0	0.000124	membrane transporter
Side	5.433166	25.12469	0.000129	TF
CG42594	1.202565	9.387816	0.000157	membrane transporter
CG32507	0	5.566355	0.000157	NA
CG11961	0	3.072836	0.000163	NA
CG15317	3.955568	0	0.000186	NA
CG17744	0.025347	2.693683	0.000196	NA
muc	1.376628	8.563522	0.000204	NA
Rgk3	9.360697	1.301388	0.000213	NA
mam	3.995281	16.36035	0.000251	TF
CG30184	5.196979	0	0.000259	NA
rho	114.7532	47.28392	0.000265	NA
CG31221	0.002772	0.717653	0.000266	cell surface
CG6428	0.001755	2.430037	0.000283	NA
NK7.1	2.49552	25.38103	0.000301	TF
drpr	9.732045	28.83272	0.000302	cell surface
CG31705	9.296062	0.114256	0.000322	NA
Unc-76	40.66872	16.85176	0.000355	NA
Btk29A	31.29116	62.89473	0.000395	kinase activity
ush	0.712367	6.161281	0.000399	TF
Mur89F	1.650626	0.003267	0.000408	cell surface
CG34114	0.037523	2.456051	0.000408	cell surface
CG10089	1.747408	8.860604	0.000419	phosphatase activity
dare	1.966962	0	0.000435	NA
klar	12.11855	28.68106	0.000443	actin binding,microtubule
CG5262	3.429154	0.048678	0.000621	NA
dan	0.024197	2.342296	0.000624	TF
Ilp2	6.339661	0	0.000654	cell surface
fu12	1.640849	0	0.000654	NA
Pde9	0.299137	2.558201	0.000654	NA
plum	15.04375	47.7598	0.000749	cell surface
alpha-Est9	0.939542	0.018438	0.000756	NA
wry	0.031527	1.058439	0.000806	cell surface
mtg	0	1.129485	0.000844	cell surface
igl	29.87984	7.392818	0.000849	NA
Ts	0.014559	4.586853	0.000868	NA
ECSIT	10.23323	0.36016	0.000899	NA
sNPF	22.18991	54.93198	0.000901	cell surface
CG9445	0.479496	32.061	0.000929	NA
CG32137	0	0.832268	0.000996	NA
CG11498	0	3.081135	0.001046	NA
CG44434	0	1.004428	0.001052	NA
l(2)35Bd	5.320604	0.231082	0.001052	RNA binding
Cad87A	0.053042	2.65702	0.001055	cell surface
CG4661	0	1.178651	0.001055	NA
CG17211	0	0.650492	0.001073	cell surface
CG5004	0.058175	2.095606	0.001094	NA
tutl	25.60418	63.76552	0.001248	cell surface
CG3961	1.970823	8.25702	0.001392	NA
CG42788	2.391869	7.039228	0.001395	NA

CG9643	10.57771	0.158029	0.001405	cell surface
CG34174	4.336961	0.017949	0.001405	NA
Pkc53E	0.019979	1.590975	0.001458	kinase activity
jigr1	17.8165	3.793237	0.00153	NA
sel	0	1.967713	0.001585	NA
w	16.37636	4.816572	0.001611	membrane transporter
CG14684	6.803023	0	0.001624	NA
CG15725	0.03263	2.178538	0.001656	TF
cdi	11.66652	25.15858	0.00169	kinase activity
crol	28.4974	52.49805	0.001863	ecdysone inducible,TF
Octbeta2R	0.268203	1.858324	0.001951	cell surface,TF
CG13298	345.429	99.81175	0.002066	RNA binding
CG4168	0	0.261544	0.002142	cell surface
Nipsnap	9.571332	1.176855	0.002206	NA
RhoGEF64C	0.001416	1.340452	0.002239	gef
pyr	0.068604	1.650445	0.002241	cell surface
CG32500	7.483209	0	0.002269	NA
CG1314	0	1.893886	0.002277	NA
CG2906	3.771692	0.100309	0.002277	NA
ths	6.151339	1.964513	0.00231	cell surface
Rpp30	0	3.600033	0.002343	RNA binding
glob1	0	3.736831	0.002359	NA
MFS10	0.031963	4.165587	0.002497	membrane transporter
CG1492	0.002777	2.054897	0.002497	NA
CG16749	0	3.62725	0.002497	NA
Nup93-2	2.737992	0.067742	0.002497	NA
fus	0.002051	1.767706	0.002727	RNA binding
CG43759	1.891388	0.119946	0.002744	NA
mt:ATPase6	57.3718	196.5914	0.002748	membrane transporter
ttm2	0	1.116157	0.002773	NA
CG4576	0	0.988477	0.002951	NA
Ppt1	5.253235	0	0.002976	NA
GstT4	0.648577	6.536605	0.003058	NA
Prosalpha1	0.185595	12.88403	0.00306	NA
key	0.006933	4.460765	0.003061	kinase activity
140up	5.519082	0.147948	0.003097	NA
Lpt	0.217676	2.719038	0.003112	ecdysone inducible
kek2	7.966364	22.70594	0.003526	cell surface
modSP	0.016751	2.049717	0.003726	cell surface
vri	0	0.465464	0.003726	TF
Vps16B	1.697374	0	0.003726	NA
Nhe2	4.865311	14.93779	0.003731	membrane transporter
CG5151	13.15818	26.26578	0.003823	NA
CG5850	0.541589	4.725566	0.003912	cell surface
CG5910	36.11484	9.06996	0.003978	NA
Ski6	17.60152	2.272964	0.004007	RNA binding
CG15803	0.398645	0	0.004116	NA
cac	7.155048	21.29769	0.00412	membrane transporter,synapse
Con	0.003263	0.556177	0.004174	cell surface
syd	11.5023	29.91982	0.004174	NA
ck	0.002448	0.420985	0.004288	actin binding
CG42339	9.374411	2.055216	0.004288	NA
Toll-7	9.611343	1.829991	0.004694	cell surface
PyK	0	2.010359	0.004706	kinase activity
Cyp310a1	2.68233	0	0.004712	NA
Aats-glupro	1.322814	8.382317	0.00503	NA
CG12868	8.37536	0.096834	0.005604	NA
CG32333	0.370235	4.504435	0.005693	NA
CG18171	0.064644	1.495754	0.005701	NA

Ripalpha	1.955636	0	0.005714	NA
px	3.731004	13.70352	0.005764	TF
Octbeta1R	0.092414	7.683934	0.005795	cell surface
klg	201.6309	107.0528	0.005823	cell surface
pnt	0	1.192648	0.005983	TF
CG1137	0	0.980164	0.006193	NA
spn-B	0	1.654225	0.006208	translation regulation
CG32547	0.279454	3.480328	0.00658	cell surface
dp	0.001299	0.241688	0.006655	cell surface
CG3921	1.25069	5.18644	0.006855	cell surface
CG12672	2.618133	0.024631	0.00708	NA
CG42524	5.563916	27.72147	0.00708	NA
Syn	2.720516	7.481271	0.00708	synapse
CG13229	26.66609	11.07835	0.007426	cell surface
CG3726	2.087591	6.600127	0.007438	TF
Chd64	11.79513	34.15003	0.007749	actin binding
CG31523	0.003366	0.926782	0.007749	cell surface
CG18273	0.004251	0.969175	0.007814	NA
CG43679	17.46826	0	0.008203	NA
cuff	1.802207	0.003284	0.008451	NA
elB	8.902629	0.69454	0.008469	TF
Ilp3	3.141261	0	0.008702	cell surface
mtd	9.194649	20.97012	0.008764	cell surface
CG10527	2.146003	0	0.009116	NA
mld	0.26037	4.228694	0.009477	TF
bchs	1.444104	3.467059	0.009601	NA
CG31538	0	1.58555	0.009601	NA
mt:CoI	116.564	373.9999	0.010031	membrane transporter
CG31213	0	0.265049	0.010146	membrane transporter
CG5726	1.364513	0.03849	0.010146	NA
DNApol-eta	0.976527	6.055668	0.010948	NA
chinmo	0.122158	9.890789	0.011433	TF
Cpr51A	0	8.753699	0.011438	NA
mt:ND5	0.049428	0.936789	0.011644	NA
CG42362	3.790737	0.189859	0.011987	NA
how	0	0.781891	0.012248	splicing regulator
CG10804	0.526245	4.630309	0.012296	membrane transporter
Moe	27.56902	69.76339	0.01236	actin binding
CG11261	0	0.637654	0.012972	NA
CG32982	0.079739	3.378639	0.012972	NA
CG34136	2.054602	15.53229	0.013359	cell surface
Acph-1	2.450602	0.220413	0.013359	phosphatase activity
dpr8	19.5185	7.108928	0.014657	cell surface
Ir56c	0	0.997723	0.015115	membrane transporter
CkIIalpha-i1	1.950304	0.007318	0.015115	NA
tefu	0.232075	0.00488	0.015364	kinase activity
Tl	6.458853	17.16347	0.015368	cell surface
CG42732	0.03303	0.592502	0.015368	membrane transporter
Muc14A	0.018428	0.182703	0.015387	cell surface
CG11191	197.4638	88.94273	0.015387	NA
CG7747	0.749976	4.86659	0.015432	NA
CG8549	3.913136	0.18907	0.015478	NA
Hsp70Ab	6.317599	30.21186	0.015644	NA
sNPF-R	15.68864	4.725437	0.016254	cell surface
Ppa	13.52097	4.216238	0.016254	NA
Rab27	1.817198	0	0.016416	NA
CG45062	0	0.59926	0.016488	cell surface
mt:Cyt-b	6.531044	23.76314	0.016711	membrane transporter
2mit	2.171556	5.962078	0.01683	cell surface

Prp31	7.185817	0.587923	0.01686	splicing regulator
pst	1.270857	0.026401	0.017246	NA
CG4968	31.7879	8.619606	0.017363	NA
mt:CoII	61.87347	188.2845	0.017607	membrane transporter
rudhira	8.036488	23.55901	0.017797	NA
CG43779	0	4.820871	0.01884	cell surface
ventrally-	53.82839	14.37659	0.019367	NA
His1:CG33822	2.04131	0.047294	0.020395	chromatin assembly
CG16710	0	3.262391	0.021843	NA
Rtnl1	90.71359	46.48522	0.021917	NA
His1:CG33810	2.015965	0.046254	0.021934	chromatin assembly
mav	5.228678	15.50696	0.022482	cell surface
CG7849	0.023463	3.514635	0.023209	RNA binding
CG2269	0.480491	6.091315	0.023339	cell surface
SkpB	4.0473	0	0.023649	NA
Vap-33B	24.137	7.294472	0.023755	NA
CG14040	2.922456	0.091737	0.02376	membrane transporter
CG18478	3.222709	0.070089	0.024035	NA
Rh7	2.008626	0.181879	0.024405	NA
CG30195	0	6.818133	0.024893	NA
dpr	13.64361	0.19228	0.024913	cell surface
Ack	2.369281	6.079788	0.025101	kinase activity
Oatp33Eb	0	0.743513	0.025101	membrane transporter
Trs31	28.36093	6.686111	0.025101	NA
5-HT2A	5.107504	0.480053	0.02525	NA
CG32845	1.385386	0.006739	0.025305	NA
trn	6.170248	0.314919	0.025444	cell surface
Pif1A	0.722761	4.212382	0.025478	TF
Zasp52	0.522896	0	0.026743	NA
rau	2.673462	15.05731	0.027305	NA
CG1532	3.457714	0	0.027376	NA
CG9328	1.712064	7.320045	0.027393	TF
PK2-R1	0.890775	0.012796	0.027399	cell surface
DJ-1alpha	1.177093	14.63657	0.027399	NA
GluRIB	0.000911	0.167749	0.027503	membrane transporter
CG1319	4.009723	0.029842	0.027944	NA
Nrt	110.4285	210.8207	0.029414	cell surface
SMC2	0.067484	1.212677	0.029466	NA
na	1.147109	4.594127	0.029567	membrane transporter
svp	0.040818	2.016238	0.029706	ecdysone inducible,TF
aru	0.092745	1.952906	0.029706	NA
Ext2	1.592178	0.049378	0.030206	cell surface
CG43338	1.298854	0	0.030206	NA
CG6424	18.43552	32.12712	0.030358	NA
CG32432	0	0.377711	0.030598	cell surface
Hrd3	2.950074	0.283974	0.030793	cell surface
Fancd2	0.371149	1.776016	0.031225	kinase activity
pan	25.05157	49.35103	0.031225	TF
CG3407	1.882535	0.015321	0.031285	TF
Samuel	0.022538	1.663904	0.031542	NA
Lcch3	12.8271	24.62466	0.032211	membrane transporter
para	1.522495	4.555882	0.032211	membrane transporter
Pbp45	0.046439	2.784306	0.032211	TF
CG18858	11.34784	1.400248	0.033145	NA
Cks30A	2.138376	0	0.033174	kinase activity
CG34140	7.279229	0.187032	0.033174	RNA binding
CG33234	1.604583	0.011646	0.033288	NA
CG8005	3.552104	0.008381	0.033803	NA
CG3626	0.065686	1.534186	0.033954	NA

CG15436	0	1.742685	0.033954	NA
CG32228	0	0.316897	0.034043	NA
CG45081	0	3.388061	0.034043	NA
CG12984	0	2.543189	0.034094	NA
Cks85A	0.023335	5.058845	0.034171	NA
Cpr92A	0	2.032109	0.0344	NA
CG4297	0	0.146499	0.036892	NA
CG5969	34.36593	8.434366	0.038002	NA
Elk	0	0.466672	0.038105	kinase_activity,membrane_transporter,TF
mys	9.040585	19.60377	0.038288	cell_surface
Ndc80	1.387466	0	0.038288	NA
Rph	5.336532	16.3628	0.038288	synapse
beat-VII	0	0.120568	0.03839	cell_surface
CG30089	1.562434	0.05793	0.03839	NA
CG31793	1.819587	0.028621	0.038643	membrane_transporter
Eip78C	19.53794	8.909325	0.038892	ecdysone_inducible,TF
CG43333	0.001054	0.753352	0.038901	cell_surface
CG11796	1.303475	0.005615	0.039089	NA
Tsp42Ef	18.39219	4.01385	0.03929	cell_surface
Shawl	9.217548	2.662528	0.039343	membrane_transporter
CG42342	0.473889	24.47434	0.039561	cell_surface
PIG-V	2.321372	0.069082	0.039638	NA
CG13902	7.4336	1.564371	0.039773	NA
CG42388	0.066447	1.216795	0.039839	NA
CG31038	12.57292	4.986907	0.039938	NA
CG44245	1.003009	10.05294	0.039942	NA
CG5110	50.59477	12.38283	0.040974	NA
CG42265	2.035905	5.463429	0.042426	NA
mamo	30.59669	82.8093	0.042995	TF
Fpps	16.26683	4.722603	0.043014	NA
CG33722	11.4544	2.42981	0.043014	NA
sty	25.71359	44.61492	0.043037	cell_surface
sprt	0	0.573689	0.044784	NA
EDTP	0.009125	1.163094	0.045064	phosphatase_activity
rdhB	0.024827	1.910523	0.045094	NA
jp	1.118624	0.014308	0.045749	NA
CG14966	0	7.24284	0.046009	NA
CG42673	0	0.444487	0.046731	NA
SPR	0.613187	0.009321	0.046798	NA
CG14367	0.505035	9.437672	0.047328	NA
CG41099	2.251188	6.372262	0.047407	TF
CG14022	2.746476	0	0.047637	NA
CG45186	69.97685	37.59366	0.048026	NA
scaf	0	0.528536	0.048038	cell_surface
Sap47	24.58628	46.68885	0.04833	TF
CG2519	8.475299	14.75409	0.048395	NA
CG3011	5.138444	0.539375	0.048809	NA
rn	0.00129	0.302531	0.048809	TF
Xe7	13.58724	34.08751	0.049793	NA
CG13053	54.5563	134.2464	0.049902	NA
CG18769	7.085285	2.000946	0.049981	NA
mgl	0.205233	0.962576	0.049983	cell_surface

Table S2. FlyMine enrichment analysis of the 403 DE genes.

Protein domain name	Adjusted P-value	Gene DB identifier	Protein domain DB identifier
Immunoglobulin-like domain superfamily	2.90E-09	FBgn0000633,FBgn0000636,FBgn0004369,FBgn0010473,FBgn0015399,FBgn0015400,FBgn0016061,FBgn0017590,FBgn0028370,FBgn0034286,FBgn0035170,FBgn0039431,FBgn0040726,FBgn0040823,FBgn0052057,FBgn0052600,FBgn0053202,FBgn0053516,FBgn0083949,FBgn0083950,FBgn0085414,FBgn0250908,FBgn0259245,FBgn0263219,FBgn0266801	IPR036179
Immunoglobulin subtype 2	1.52E-08	FBgn0000633,FBgn0010473,FBgn0015399,FBgn0015400,FBgn0016061,FBgn0017590,FBgn0028370,FBgn0034286,FBgn0035170,FBgn0039431,FBgn0040726,FBgn0040823,FBgn0052057,FBgn0052600,FBgn0053202,FBgn0053516,FBgn0083949,FBgn0083950,FBgn0085414,FBgn0259245,FBgn0263219,FBgn0266801	IPR003598
Immunoglobulin-like domain	1.87E-08	FBgn0000633,FBgn0000636,FBgn0010473,FBgn0015399,FBgn0015400,FBgn0016061,FBgn0017590,FBgn0028370,FBgn0034286,FBgn0035170,FBgn0039431,FBgn0040726,FBgn0040823,FBgn0052057,FBgn0052600,FBgn0053202,FBgn0053516,FBgn0083949,FBgn0083950,FBgn0085414,FBgn0250908,FBgn0259245,FBgn0263219,FBgn0266801	IPR007110
Immunoglobulin subtype	2.71E-08	FBgn0000633,FBgn0010473,FBgn0015399,FBgn0015400,FBgn0016061,FBgn0017590,FBgn0028370,FBgn0034286,FBgn0035170,FBgn0039431,FBgn0040726,FBgn0040823,FBgn0052057,FBgn0052600,FBgn0053202,FBgn0053516,FBgn00	IPR003599

		83949,FBgn0083950,FBgn0085414,FBgn0259245,FBgn0263219,FBgn0266801	
Immunoglobulin-like fold	4.85E-07	FBgn0000633,FBgn0000636,FBgn0004369,FBgn0010473,FBgn0015399,FBgn0015400,FBgn0016061,FBgn0017590,FBgn0028370,FBgn0034286,FBgn0035170,FBgn0039431,FBgn0040726,FBgn0040823,FBgn0052057,FBgn0052600,FBgn0053143,FBgn0053202,FBgn0053516,FBgn0053523,FBgn0083949,FBgn0083950,FBgn0085414,FBgn0250908,FBgn0259245,FBgn0263219,FBgn0266801	IPR013783
Zwei Ig domain protein zig-8	4.63469E-05	FBgn0034286,FBgn0035170,FBgn0040726,FBgn0040823,FBgn0052057,FBgn0052600,FBgn0053202,FBgn0053516,FBgn0085414	IPR037448
Immunoglobulin I-set	0.000307832	FBgn0010473,FBgn0015399,FBgn0017590,FBgn0028370,FBgn0035170,FBgn0040726,FBgn0040823,FBgn0052057,FBgn0052600,FBgn0053202,FBgn0053516,FBgn0085414,FBgn0259245,FBgn0263219	IPR013098
G protein-coupled receptor, rhodopsin-like	0.000531042	FBgn0029768,FBgn0033579,FBgn0035010,FBgn0036260,FBgn0036934,FBgn0038063,FBgn0038140,FBgn0038874,FBgn0038980,FBgn0052547,FBgn0053517,FBgn0053639,FBgn0085410,FBgn0087012	IPR000276
GPCR, rhodopsin-like, 7TM	0.000632946	FBgn0029768,FBgn0033579,FBgn0035010,FBgn0036260,FBgn0036934,FBgn0038063,FBgn0038140,FBgn0038874,FBgn0038980,FBgn0052547,FBgn0053517,FBgn0053639,FBgn0085410,FBgn0087012	IPR017452
Cysteine-rich flanking region, C-terminal	0.019211256	FBgn0005775,FBgn0010452,FBgn0015399,FBgn0015400,FBgn0028370,FBgn0034476,FBgn0262473	IPR000483

Immunoglobulin V-set domain	0.03073279	FBgn0010473,FBgn0016061,FBgn0034286,FBgn0035170,FBgn0040823,FBgn0052600,FBgn0053516,FBgn0083949	IPR013106
Leucine-rich repeat, typical subtype	0.040874913	FBgn0005775,FBgn0010452,FBgn0015399,FBgn0015400,FBgn0028370,FBgn0028888,FBgn0032633,FBgn0034476,FBgn0243486,FBgn0259677,FBgn0260793,FBgn0262473	IPR003591

Table S3. List of DE genes that are putative direct dFezf targets.

Gene	bioCategory
Ack	kinase activity
alpha-Man-IIb	enzyme
Blimp-1	TF
bru3	RNA binding
CG12974	unknown
CG15097	actin binding
CG31213	membrane transporter
CG34155	unknown
CG42732	membrane transporter
CG44245	unknown
CG45263	cell surface
CG4753	enzyme
CG5969	unknown
CG6424	unknown
CG8065	unknown
CG9328	nuclear protein
Cyp310a1	metal ion binding
dan	TF
danr	TF
dpr8	cell surface
Drl-2	cell surface
Dscam4	cell surface
Fas1	cell surface
Fas3	cell surface
Lrch	cell surface
mam	TF
mtd	cell surface
na	ion channel
Nrt	cell surface
pbl	gef
pog	unknown
Ptp99A	cell surface
Pvf3	cell surface
px	nuclear protein
Rtnl1	endomembrane protein
sano	cytosolic protein
sm	RNA binding
Syn	synapse
Ten-a	cell surface
tutl	cell surface

Upregulated/**downregulated**

Table S4. List of UAS-cDNA constructs used in mis-expression screen for upregulated candidate genes.

Gene	Line	Source	Stock No.	🟦	🟥
Cell surface genes					
plum	*U02:10.3 y,w;UAS-Plum-FL-Flag(w+)@Attp40(*$y^{+)}$*)Cyo*	Schuldiner Lab		X	X
	U02:45 y,w;UAS-Plum-RFP(w+)@attp40,y^{+}*/Cyo;Sb/Tm6,Tb*	Schuldiner Lab		X	X
	U02:12 y,w;UAS-Plum-FL:Flag(w+)@Attp40(y^{+}*)/Cyo;DH/Tm6,Tb*	Schuldiner Lab		X	X
Tl	*w*; P{UASp-Tl.Venus}1*	BDSC	30899	X	X
	w; P{UASp-Tl.Venus}4*	BDSC	30898	X^	X
	w; P{UASp-Tl.PA-GFP}10*	BDSC	30901	X^	X
	w**; P{UASp-Tl.PA-GFP}3/CyO*	BDSC	30900	X	X
comm	*P{UAS-comm.MYC}1, w**	BDSC	66891	X	
	y^{1} *w***; P{UAS-comm.MYC}2*	BDSC	66887	X	
	y^{1} *w*^{67c23}*; P{EPgy2}comm*^{EY10154}*/TM3, Sb*^{1} *Ser*^{1}	BDSC	17644	X	
	w; UAS-Comm w+ (HA)/CyO-GFP; Comm-delta e^{39} */ TM3Ser-GFP*	Rotin Lab		X	
*Ten-a**	*w*; P{UAS-Ten-a.H}attP24*	BDSC	42018	X	X
	y^{1} *w***; M{UAS-Ten-a.H}ZH-86Fb*	BDSC	41564	X^	X
	w P(48)Ten-aGE1914*	BDSC	41563	X	X
	UAS-Ten-a-PL	Liu Lab		X	X^
	w; LexAop-myrGFP; UAS-Ten-a-PL	Liu Lab			X
	w; LexAop-myrGFP; UAS-Ten-a [86Fb]	Mosca Lab			X^
dpr20	*20xUAS-dpr20-RA [VK13]*	Pecot Lab		X	X
	20xUAS-dpr20-RA [su(Hw)attP2]	Pecot Lab		X^	X^
dpr13	*20xUAS-UAS-dpr13*	Pecot Lab			X
	20xUAS-dpr13 (76A2)	Pecot Lab		X^	
dpr13 + dpr20	*w; 20XUAS-dpr13; 20XUAS-dpr20*	Pecot Lab			X^
dpr10	*20xUAS-dpr10-RA [su(Hw)attP2]*	Pecot Lab		X^	
kek5	*y*^{1} *w*^{67c23} *P{EPgy2}kek5*^{EY05915}	BDSC	16686	X	X

Gene	Line	Source	Stock No.	🟦	🟥
	20xUAS-kek5-RB [VK13]	Pecot Lab		X	X
CG45263*	*20xUAS-CG45263-RF [su(Hw)attP2]*	Pecot Lab		X^	
Transcription Factors					
ush	*M{UAS-ush.ORF.3xHA.GW}ZH-86Fb*	FlyORF	F001800	X	X^
	M{UAS-ush.ORF}ZH-86Fb	FlyORF	F001549	X	X
	w; LexAop-myrGFP; M{UAS-ush.ORF.3xHA.GW}ZH-86Fb	FlyORF	F001800		X
	w; LexAop-myrGFP; M{UAS-ush.ORF}ZH-86Fb	FlyORF	F001549		X
slp1	*27-13 y w; UAS.slp1[1F]/CyO; TM2/TM6B*	Tomlinson Lab		X	X
	yw;UAS-sl159.4p	Gebelein Lab		X^	X
	sp/CyO;UAS-slp31c	Gebelein Lab		X^	X
	w; LexAop-myrGFP; M{UAS-slp1.ORF.3xHA.GW}ZH-86Fb	FlyORF	F001900		X^
slp2	*20xUAS-slp2-RA [VK13]*	Pecot Lab		X	X
slp1 + slp2	*yw, hsFLP122; UAS-slp2/CyO; UAS-slp1-3f/TM6B*	Desplan Lab			X
	yw; UAS-slp1/CyO; FRT82B/TM6B	Desplan Lab			X
	yw, hsFLP122; sp/CyO; UAS-slp1/TM2	Desplan Lab			X
	w; UAS.slp1[1F]; 20XUAS-Slp2-RA	Desplan + Pecot Labs			X
*danr**	*w1118; P(48)danrG18430*	BDSC	32030	X	X^
	20xUAS-danr-RA [VK13] (M1)	Pecot Lab		X	X
Other gene types					
mbl	*UAS-mbl (A)*	Perez-Alonso Lab			X
	w; UAS-mbl (C)	Perez-Alonso Lab			X
	yw;mbl[E16]/CyO, GFP (w+) [UAS-mbl(C)-GFP]	Llamusi Lab			X
sick	*UAS-sickieWT SRB3 (2nd)*	Tabata Lab		X	
	UAS-mCherry::sickie(WT) 6264/1/5 (2nd)	Tabata Lab		X	
	UAS-mCherry::sickie(WT) 6264/1/2 (3rd)	Tabata Lab		X	
	UAS-sickie(WT) 4844-1-8-M, strong (3rd)	Tabata Lab		X	
	y^{1} w^{67c23}; *P{EPgy2}sick*^{EY00205}	BDSC	14816	X	
	w^{1118}; *P{EPgy2}sick*^{EY08088}*/CyO, P{sevRas1.V12}FK1*	BDSC	17429	X	

Gene	**Line**	**Source**	**Stock No.**	🟦	🟥
sli	*P{UAS-sli.D}1, w*	BDSC	67687	X	
	w; P{UAS-sli.D}2	BDSC	67688	X	
	w; P{UAS-sli.D}3	BDSC	67689	X	
	y^1 *w; P{UAS-sli.B}3*	BDSC	6472	X	
	w;;UAS-Slit$_{T1}$ *(III) [E14]*	Bashaw Lab		X	X
	w;UAS-Slit$_{T2}$ *(II) [E16]*	Bashaw Lab		X	X
	y^1 *w*^{67c23}*; P{EPgy2}sli*^{EY10695}*/CyO*	BDSC	20202	X	X

1. Blue column: X indicates line crossed to *UAS-Dcr2; 22E09-LexA, LexAop-myr-tdT; 9B08-GAL4*
2. Red column: X indicates line crossed to *22E09-LexA, LexAop-myr-tdT; R9D03-GAL4, UAS-MCFO*
3. ^ indicates strategy also attempted in the *dFezf*^{1} heterozygote background
4. * indicates putative dFezf direct target

Table S5. List of UAS-RNAi constructs used in screens for upregulated and downregulated candidate genes.

Downregulated		
Multiple genes in combination		
Gene	**Source**	**Stock No.**
Cell surface genes		
side-III	VDRC	22742
side-VIII	BDSC	62897
dpr1	VDRC	33816
dpr3	VDRC	106517
dpr6	VDRC	103521
*dpr8**	BDSC	28744
kek1	BDSC	57000
kek3	VDRC	6354
kek1	VDRC	36252
kek3	BDSC	77354
caps	BDSC	28020
trn	VDRC	107883
Toll-7	BDSC	30488
Tl	VDRC	100078
Transcription factors		
noc	VDRC	108422
elb	BDSC	41960
Single gene w/ multiple constructs		
Gene	**Source**	**Stock No.**
Cell surface genes		
CG32052	VDRC	105824
	BDSC	36763
*Fas3**	BDSC	77396
	VDRC	940
CG17716	VDRC	102073
	VDRC	42236
Nrx-IV	BDSC	32424
	BDSC	38192
RNA binding		
*bru3**	VDRC	102442
	BDSC	50734
Other gene types		
*Rtnl1**	VDRC	110545
	VDRC	7866
*Pvf3**	BDSC	38962
	VDRC	50225
*Lrch**	BDSC	50901
	BDSC	41827
*pog**	BDSC	51705
	BDSC	43135
Upregulated		
Knocked down with *dFezf*		
Gene	**Source**	**Stock No.**
Cell surface genes		

dpr10	VDRC	103511
dpr13	VDRC	107676
dpr12	VDRC	106788
dpr20	VDRC	101673
dpr11	VDRC	107548
kek2	VDRC	42449
	VDRC	42450
Fili	VDRC	106055
	VDRC	34784
*Ten-a**	VDRC	103298
*CG45263**	BDSC	62468
*Dscam4**	VDRC	23488
	VDRC	25365
Transcription Factors		
NK7.1	VDRC	108177
ush	BDSC	44041
*danr**	BDSC	65125
*dan**	VDRC	37752
tna	VDRC	28071
Sidpn	VDRC	3066
mld	BDSC	43145
Ptp99A	BDSC	57299
CG9932	VDRC	107846
sbb	VDRC	41845
slp1	VDRC	107562
chinmo	BDSC	62873
Other gene types		
*Drl-2**	VDRC	102192
*sano**	VDRC	104288
*sm**	VDRC	108351
*CG9328**	VDRC	102346
*mam**	BDSC	63601
*CG15097**	VDRC	109428
*tutl**	BDSC	54850
*Ack**	VDRC	39857
*mtd**	BDSC	36638
*Blimp-1**	BDSC	57479
*Nrt**	VDRC	106080
*CG6424**	VDRC	107963

1. * indicates putative dFezf direct target

Table S6. CRISPR/Cas9 screen

Cell surface genes
dpr1 + dpr3
*dpr6 + dpr8**
dpr15, dpr16 +dpr17
dpr6, dpr16 +dpr17
beat-IIb + beat-IIa
kek1 + kek3
18w + Toll-7
dpr2
DIP-β
Ten-m
klg
robo3
Dscam3
*Fas3**
*Fas1**
nrm
Gene expression regulators
*bru3**
elB
noc
msi
nvy

1. * indicates putative dFezf direct target

Table S7. Putative TF binding sites in screened genes

Gene	Bio Category	dFezf binding	slp1 binding
18w	Cell surface		
beat-IIa	Cell surface		
beat-IIb	Cell surface		
caps	Cell surface		■
CG32052	Cell surface		■
CG45263	Cell surface	■	■
comm	Cell surface		
DIP-β	Cell surface		
dpr1	Cell surface		
dpr10	Cell surface		■
dpr11	Cell surface		■
dpr12	Cell surface		■
dpr13	Cell surface		■
dpr15	Cell surface		
dpr16	Cell surface		
dpr17	Cell surface		
dpr2	Cell surface		
dpr20	Cell surface		■
dpr3	Cell surface		■
dpr6	Cell surface		■
dpr8	Cell surface	■	■
Drl-2	Cell surface	■	■
Dscam3	Cell surface		
Dscam4	Cell surface	■	
Fas1	Cell surface	■	
Fas3	Cell surface	■	■
Fili	Cell surface		■
kek1	Cell surface		■
kek2	Cell surface		■
kek3	Cell surface		
kek5	Cell surface		
klg	Cell surface		■
Lrch	Cell surface	■	
mtd	Cell surface	■	■
nrm	Cell surface		
Nrt	Cell surface	■	■
Nrx-IV	Cell surface		■
plum	Cell surface		■
Ptp99A	Cell surface	■	■
Pvf3	Cell surface	■	■
robo3	Cell surface		
side-III	Cell surface		
side-VIII	Cell surface		
Ten-a	Cell surface	■	
Ten-m	Cell surface		
Tl	Cell surface		■
Toll-7	Cell surface		■
trn	Cell surface		
tutl	Cell surface		■
sick	Cytoskeleton		
sano	Cytosolic protein	■	■
Rtnl1	Endomembrane	■	■
Ack	kinase activity	■	■
CG9328	Nuclear protein	■	■
bru3	RNA binding	■	
mbl	RNA binding		

Gene	Bio Category	dFezf binding	slp1 binding
msi	RNA binding		
sm	RNA binding		🟦
CG17716	Secreted factor		
sli	Secreted factor		
Blimp-1	TF	🟦	🟦
CG9932	TF		🟦
Chinmo	TF		🟦
dan	TF	🟦	🟦
danr	TF	🟦	🟦
elB	TF		🟦
mam	TF	🟦	🟦
mld	TF		
NK7.1	TF		🟦
noc	TF		🟦
nvy	TF		
sbb	TF		
Sidpn	TF		
slp1	TF		🟦
slp2	TF		
tna	TF		
ush	TF		
CG15097	unknown	🟦	
CG6424	unknown	🟦	🟦
pog	unknown	🟦	

Upregulated/**Downregulated**

* putative dFezf direct target

Table S8. Fly stocks used in this study

Stock name	Source or reference
9–9 GAL4	Gift from U. Heberlein (Nern et al., 2008)
P{10XUAS-IVS-myr::GFP}attP2	Bloomington Drosophila Stock Center (BDSC_32197)
P{tubP-GAL80}LL10 *P{neoFRT}40A*	Bloomington Drosophila Stock Center (BDSC_5192)
P{R27G05-FLPG5.PEST}attP40	Bloomington Drosophila Stock Center (BDSC_55765)
P{10XUAS-IVS-myr::tdTomato}attP2	Bloomington Drosophila Stock Center (BDSC_32221)
dFezf^{1}	C.Y. Lee (Weng et al., 2010)
slp^{S37A}	A. Tomlinson (Sato and Tomlinson, 2007)
UAS-H2A-GFP	S.L. Zipursky (Tan et al., 2015)
UAS-dFezf^{WT}*-HA*	C.Y. Lee (Janssens et al., 2014)
UAS-dFezf^{ERD}*-HA*	C.Y. Lee (Janssens et al., 2014)
UAS-dFezf^{VP16}*-HA*	C.Y. Lee (Janssens et al., 2014)
18B02 dFezf-GAL4	This study

Table S9. Full genotypes of flies used for experiments reported in the listed figure.

Relevant figures	**Abbreviated names**	**Genotypes**
Figure 2		
	WT	*w; tubP-GAL80, FRT40A, 27G05-FLP/FRT40A; 9-9-GAL4, UAS-myr::tdTomato/UAS-H2A-GFP*
	dFezf^{1}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, FRT40A; 9-9-GAL4, UAS-myr::tdTomato/UAS-H2A-GFP*
Figure 3		
	WT	*w; UAS-FRT-stop-FRT-myr::GFP/27G05-FLP; 9-9-GAL4/+*
Figure 4		
A, B, C, D	WT	*w; tubP-GAL80, FRT40A, 27G05-FLP/FRT40A; 9-9-GAL4, UAS-myr::GFP/TM2*
	dFezf^{1}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, FRT40A; 9-9-GAL4, UAS-myr::GFP/MKRS*
	dFezf^{1}*+dFezf*^{WT}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, FRT40A; 9-9-GAL4, UAS-myr::GFP/UAS-dFezf*^{WT}*-3xHA*
	dFezf^{1}*+dFezf*^{ERD}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, FRT40A; 9-9-GAL4, UAS-myr::GFP/UAS-dFezf*^{ERD}*-3xHA*
	dFezf^{1}*+dFezf*^{VP16}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, FRT40A; 9-9-GAL4, UAS-myr::GFP/UAS-dFezf*^{VP16}*-3xHA*
Figure 5		
A	WT	*w; tubP-GAL80, FRT40A, 27G05-FLP/FRT40A; 9-9-GAL4, UAS-myr::tdTomato/UAS-H2A-GFP*
	dFezf^{1}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, FRT40A; 9-9-GAL4, UAS-myr::tdTomato/UAS-H2A-GFP*
B, C, D, E	WT	*w; tubP-GAL80, FRT40A, 27G05-FLP/FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
	slp^{S37A}	*w; tubP-GAL80, FRT40A, 27G05-FLP/slp*^{S37A}*, FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
	dFezf^{1}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
	dFezf^{1}*, slp*^{S37A}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, slp*^{S37A}*, FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
Figure 6		

B, C, D, E	WT	*w; tubP-GAL80, FRT40A, 27G05-FLP/FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
	slp^{S37A}	*w; tubP-GAL80, FRT40A, 27G05-FLP/slp*^{S37A}*, FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
	dFezf^{1}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
	dFezf^{1}*, slp*^{S37A}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, slp*^{S37A}*, FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
Figure S1		
		w; Bl/CyO, Kr-GAL4, UAS-GFP; UAS-myr::GFP/18B02 dFezf-GAL4
Figure S2		
	WT	*w; tubP-GAL80, FRT40A, 27G05-FLP/FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
	slp^{S37A}	*w; tubP-GAL80, FRT40A, 27G05-FLP/slp*^{S37A}*, FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
	dFezf^{1}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*
	dFezf^{1}*, slp*^{S37A}	*w; tubP-GAL80, FRT40A, 27G05-FLP/dFezf*^{1}*, slp*^{S37A}*, FRT40A; UAS-myr::GFP/18B02 dFezf-GAL4*