SUPPLEMENTARY INFORMATION

Auto-Regulatory RNA Editing Fine-Tunes mRNA Re-Coding and Complex Behavior in *Drosophila*

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Supplementary Figure S1 | Conserved RNA editing sites. Shown below are the editing sites in the 23 mRNAs analyzed in this study, alongside the surrounding local sequence. Sensitivity to dADAR auto-editing was defined based on data from male heads.

*= intron location
A= editing site
A= non-sensitive site
A= G-sensitive site
A= S- and G-sensitive site

syt (CG3139)

TTGAAGAAGATGGACGTGGGCGGATTGTCTG*ATCCATATGTGAAAA[1]TTGCAATCA
TGCAAAATGGCAAACGTTTGAAAAAGA[2]GAAGACAAGTA[3]TCAA[5]A[6]AAATGCACCC
TCAACCCTTACTATAATGAGTCGTTCTCATTTGAAGTACCATTTGAACAAATA[4]CAA*
AAAATCTGTCTCGTTGTGACCGTCGTGGACTACGATCGTATTGGCACCTCCGAACCC
ATCGGCCGCTG

cap (CG33653)

GACACAAGGTCTAAGCGGTAAACTTA[1]TGTCTGTGCTAGAGTCGACTTTGTC

cpx (CG32490)

AACTGAAAAATCAAATA[1]GAAACGCAAGTAA[2]A[3]TGAGCTAAAAACTCAAATAGAGG
GAAAATGTGTCATGCAGTGA

unc (CG2999)

ACGCAATTGACGCAGTGTTTCGATGTTGTTA[1]GCAAACTCGAGTGTCCTGATCCAGA
AATTTGGA

stn (CG40306)

GTTTACTATGCCCGCCACGCAGGTCTCCCATA[1]CCACCGTGCGCTCGGTGAGTGTCCA
GGATTCGGATGGCGATGAACCGC

lap (CG2520)

ACTAGCAGCGGTGCTGCTGGCGCTAGCGCTGCACTAA[1]CAAATCCATTTCTATCGTC
GCCGCCAGCCGCGCAGGCTGGCCAGCCGATA[2]GTTGATCTGTTCGGTGCCGCGTCGG

dsc (CG34405)

TATGAAGGAGGAGTGTTGGAAA[1]TGTTTCTCACCGAATCTCAAAAACACTA

sbd (CG6798)

GCCCAGCGATTCGGGCGAAAAG*GTTA[1]CGTTA[2]TGTATTTCGATACTCGTGTC

stj (CG12295)

TTCAATGTTGGGACAGAGGCTAGATA[1]TCGCAAAGCATGTTGTCAATACGATATTAG
GTACAAATGACTTTGTGAACA[2]TCTTCACCTTTGATAAGGAAGTGAG

ACTGAAAGAAGGGATTGAACTGTTTA[3]GACCCAAATCGATCGCCAATTATAC

cat (CG15899)

GGTGGCCATTTTGGTTGAGGGATTCA[1]GTTCAGAG*CGAAATGAACGTCGCGA

cad (CG4894)

CAGCGGAATGTGTTATGAAAATTTTA[1]GCATATGGTTTTGTGTTACATA[2]ATGGTGCA
TATCTA[3]A[4]GAAATGGATGGAATTTATTAGATTTTATTAGATTTTACAATTGTAGTTAT
A[5]GG*GGCGATAAGTACTGCACTCTCCC

shb (CG1066)

GGTGGTGCAGGTCTTTCGCATCATGCGCATCCTGCGA[1]A[2]TCCTTAAGCTGG
CCCGTCACTCAACGGGCCTG

TCGTTTCAATACCGGAAA[3]CATTTTGGTGGGCGGGTATTACAATGACAACT
GTTGGCTACGGGGACATCTA[4]TCCCACAACTGCACTGGGAAAGGTTATTGGTA[5]C

CTGTGTGTTGCATATGCGGTGTTCTGGTA[6]A[7]TCGCTTTGCCTATTCCCA
TCATCGTTAACAATTTTGCTGAATTTTATAAGAATCAG

eag (CG10952)

TCGCCGCGGAGACAGACAACGAGAA[1]GGTGTTCACCATCTGCATGATGATC

CTGGATACCGAGAAG*GTACTAAACTA[2]TTGTCCGAAAGATATGAAGGCTGAC
TATGTGTTCATCTAAATCGCAAAGTA[3]TTTA[4]ACGAGCATCCGGCA[5]TTTCGTCTGGCC
TCGGATGGTTGTC

CTCAGACATCGACTGATTTTTCGCAA[6]GGTGGCCGATGTGAAGCGCGAAAAA

GTGATTTGCATGCCATCAAACGTGATA[7]AATTGCTCGAAGTCCTCGATTTCT

slo (CG10693)

GAACTCTGGCGATCCGCTGGATTTTA[1]ATAATGCTCATCGTTTATCGTATTG

CATGATAACAG*AACTGGTCAATGATA[2]GTAACGTGCAGTTTCTCGATCAAGA

rdl (CG10537)

GTCAATTTTGGACCGATCCTCGTTTA[1]GCGTATA[2]GAAAACGACCTGGTGTAGAAACA
CT

CTACATACCCTCTGGACTGATCGTTA[3]TTATATCATGGGTATCATTTTGGCTATGGGT
ATCATTTTGGCTCAATCGCA[4]ATGCAACGCCGGCGCGTGTGGCGCT

GTCGGCTACATGGCAAAACGAATTCAA[5]A[6]TGCGAAAACAAAGATTTATGGCGAT

daf (CG32975)

CTACTTCCGATGCGGTGCCATTGCTGG*GTA[9]CATATTTCAATTGCATAATGTTTATG
GTAGCTTCATCCGTTGTGTCAACGATTTTA[1]A[2]TATTAAATTATCATCATCGAAATGC

TGACAGACTGTGCCTTATCATATTCACAATGTTCA[3]CAA[4]TATTA[5]GCCACAATA[6]GCT
GTACTACTA[7]TCA[8]GCACCACATATTATTGTCTCGT

das (CG4128)

GGATTCGATGGCACGTATCACACCAA[1]CA[2]TTGTGGTCAAACATA[3]A[4]CGGCAG
TTGTCTGTACGTGCCCCCT

GTATCTTCAAGAGCACATGCAAGATA[5]GACATCACGTGGTTCCCATTTGATG

GGAAATCAG*TTGGATTTGGTTTTGAA[6]TTCCGAAGATGGAGGGGATCTTTC

ard (CG11348)

AGAATATGACACAAAAAGTTGGAGTA[1]A[2]GATTTGGTTTGGCGTTCGTACAGCT

TAATCAATGTC*AATGAGAAAAATCAA[3]A[4]TTATGAAATCAAACGTTTGGTTACG

sha (CG12348)

ATGTCCCTTTAGACGTATTTAGTGAAGAAATAA[1]A[2]ATTTTATGAATTAGGTGATCAA
GCA

CGAATCAGGCTATGTCCTTGGCAATA[3]TTACGAGTGATACGATTAGTTCGAG

AAAATTGTCGGCTCTTTGTGCGTGA[4]TCGCTGGTGTGCTGACAATCGCACT

TTTCAATTACTTCTATCACCGCGAAA[5]CGGATCA[6]GGAGGAGATGCAGAGCCA

adr (CG12598)

CAGCACCTTGTGGGGATGCACGGATATTTA[1]GTCCTCACGAAAACGACACTGGTGTT
GATAAAC

cac (CG1522)

TTCAACCGATTTGATTGCGTTGTCATTA[1]GTGGTTCGATATTCGAAGTGATCTGGTCC
G

ATGCCCAAGAACTAACAGCAGCCGAAGAGGA[2]ACAA[13]GTCGAA[3]GAGGATAAAGAG
AAACAACTGCAGGAGC

ACCCTGGCAGCTATTTAAGAGAATTCTGGAA[4]TATTATGGATGCTGTGGTCGTTATAT
GCGC

GCGTCGTGAACTCATTGAAAAATGTTGTTAA[5]CATTCTAATCGTGTACATATTGTTTC
AATT

AATGGAAAATTTTTTTATTGTACGGACGAAA[6]GTAAACATACTTCCGCAGAGTGCCA*
GGGCT

CATGATATCGGGTTCTCCGATACCGTATCTA[11]ATGTTGTAGAGATGGTCAAGGAGAC
TCGTC

AGGCATGGCAACAGTCATCCGCGGTATCCAA[12]GAG*GTTCATGGTCAGCATCGACA
AGTCCGG

par (CG9907)

CAATTTACGACTGAAAACTTTTCA[3]A[4]TTAATTGAA[5]A[6]ATAAATATTTTGAAACAGCT
GTTATCACTATG

glu (CG7535)

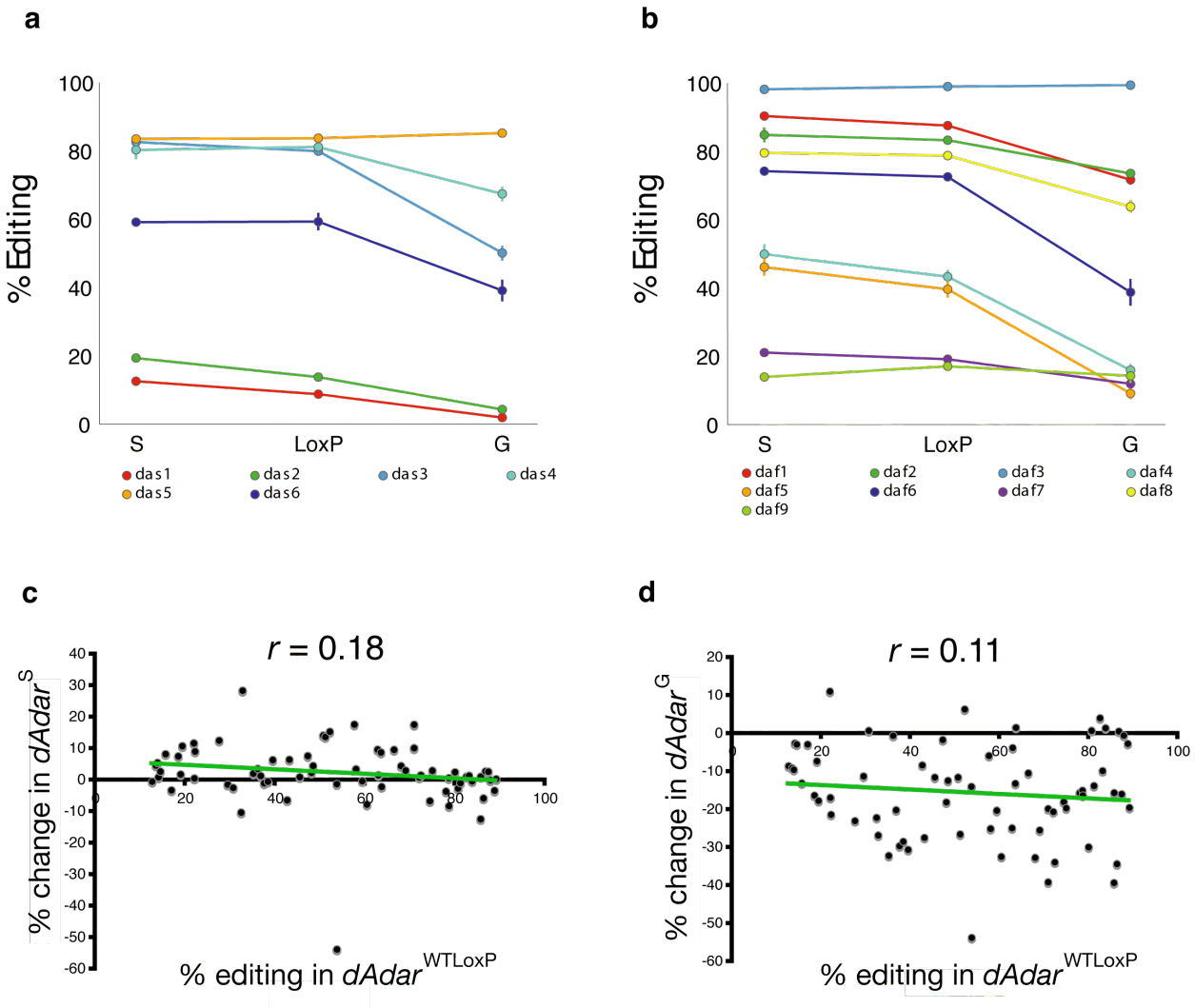
CACTAGCAAATAATGCCAAA[1]A[2]TAAATTTCCGAGAAAAGGAGAAAAAAGTC

GCCTCAAAGTCGATCTACTATTCAA[3]GCGAGAATTCTCATATTACTTAATACAAATT

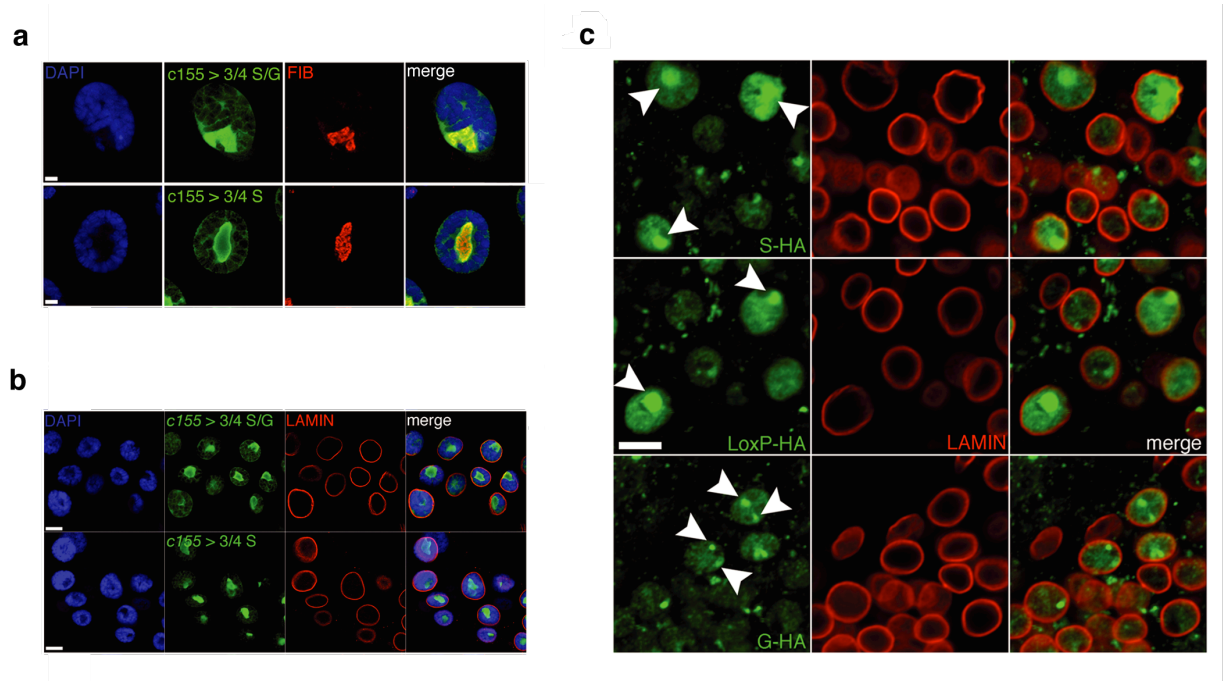
dop (CG18314)

AACTGCTCTGGCTGAAAA[1]TTTA[2]TCGAACCCTA[3]GTCATA[10]TGATGTCATTCGCATTA
[4]GTCTTTGCATTCTGGGTGTCCTGGCTGCCATGGATTCTG

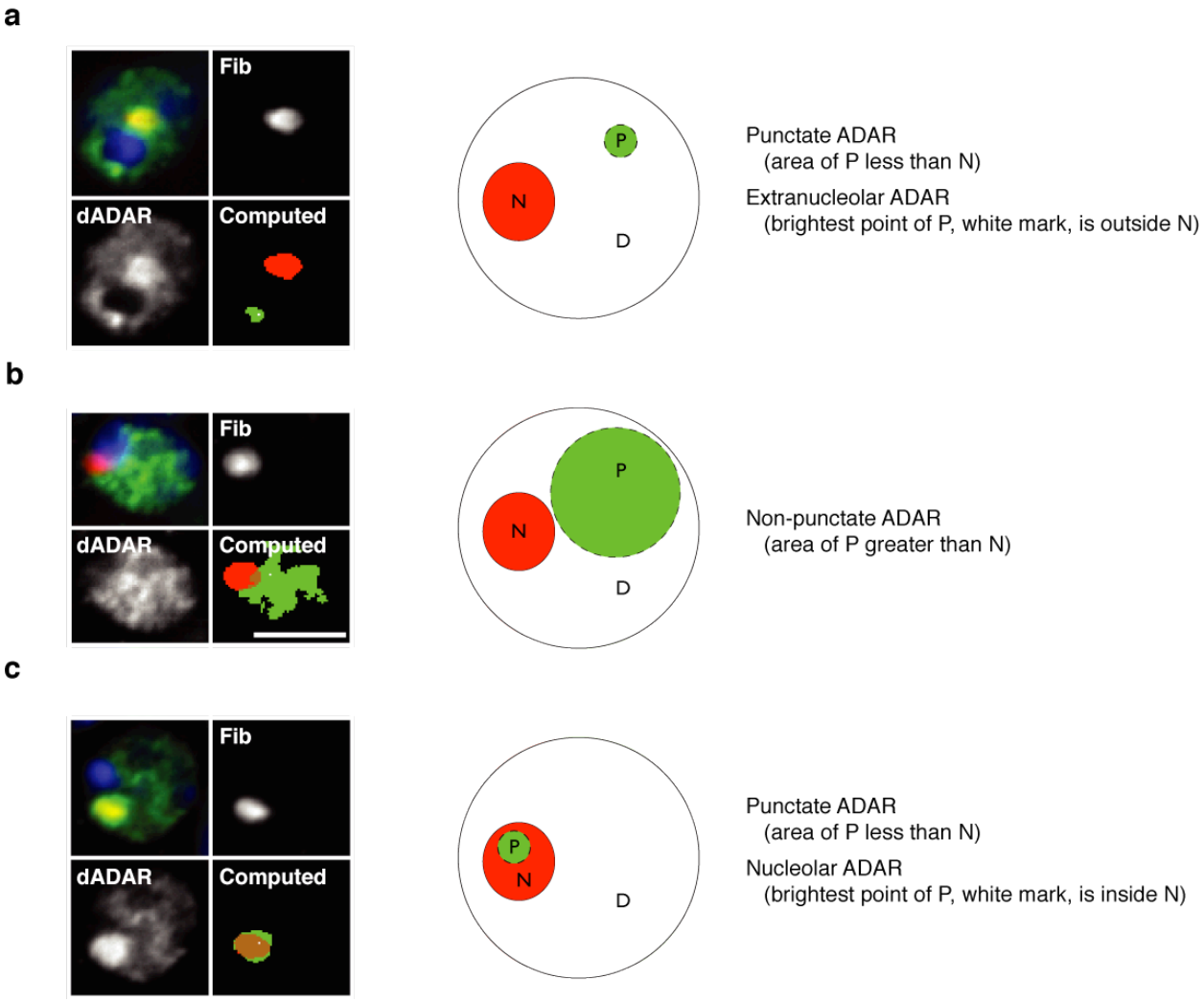
TGCTTAACCATTTGTTGTAAGACTA[5]A[6]GGGCCGTTTGCAAGCAGAGCTA[7]A[8]TCGGGT
TGGACCCAGATGACTA[9]GAGTTAGATTTAGATTTTCATTCTCC



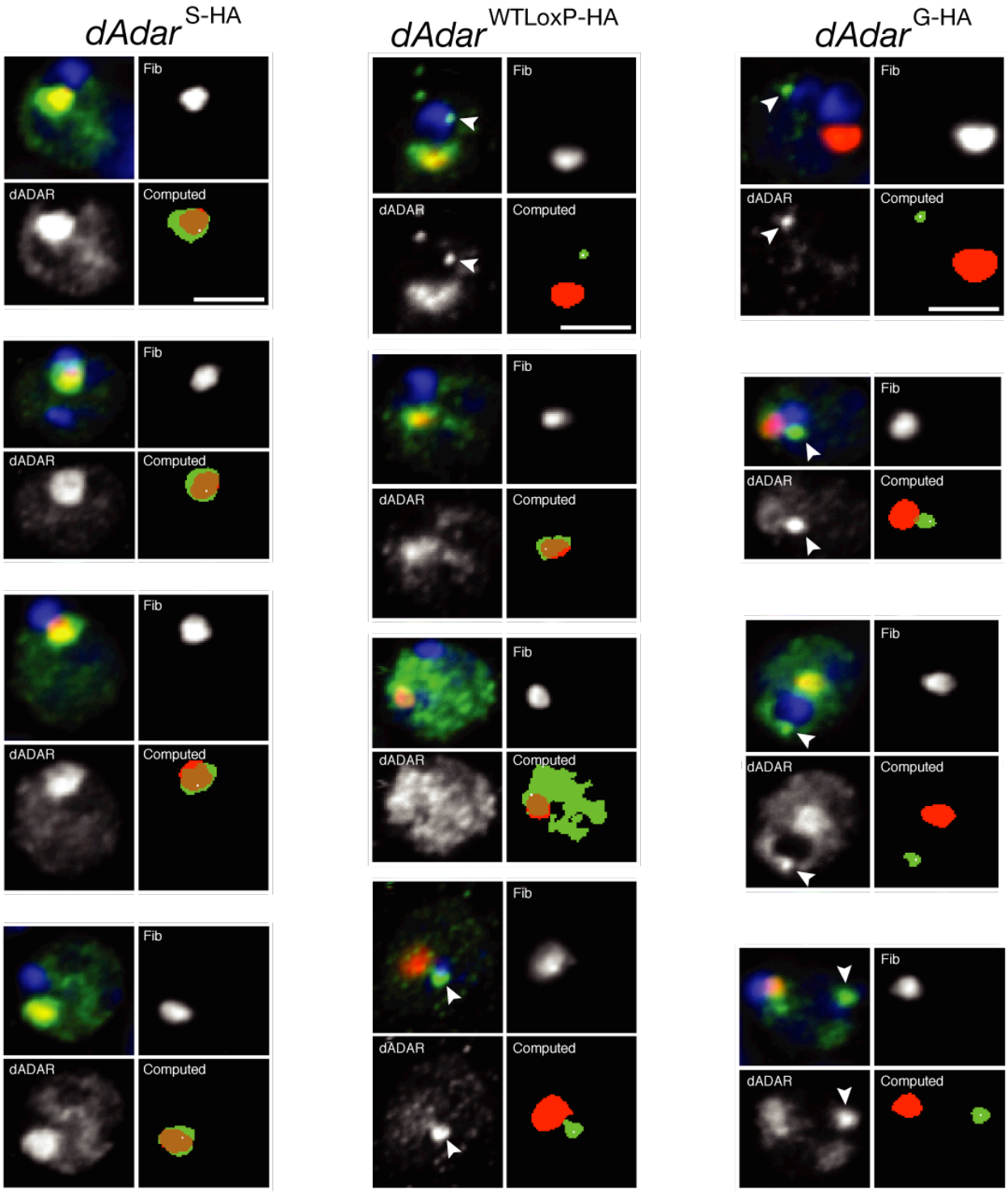
Supplementary Figure S2 | Effects of altering dADAR auto-editing are not biased to sites with high or low editing levels. (**a**) Six editing sites in the *Dα6* acetylcholine receptor transcript show differential regulation in *dAdar*^{S} and *dAdar*^{G} when compared to *dAdar*^{WTLoxP}. One site in *Dα6* shows no alteration, three sites show a mono-directional alteration, and two sites show a bi-directional alteration in response to abolishing or hard-wiring *dAdar* auto-editing. (**b**) Nine editing sites in the *Dα5* acetylcholine receptor transcript show differential regulation in *dAdar*^{S} and *dAdar*^{G} when compared to *dAdar*^{WTLoxP}. Two sites in *Dα5* show no alteration, five sites show a mono-directional, and two sites a bi-directional alteration upon changes in *dAdar* auto-editing. mRNAs were amplified from male head cDNA. Mean values for each site were defined as significantly different ($P < 0.05$) from *dAdar*^{WTLoxP} using one-way ANOVA with Dunnett post-hoc test (n = 3-8 PCRs per site). Error bars, s.e.m. (**c-d**) For all sites analyzed with editing levels between 10-90%, increased editing in *dAdar*^{S} males heads (**c**) and reduced editing in *dAdar*^{G} male heads (**d**) are not correlated with the endogenous level of editing for each site in *dAdar*^{WTLoxP} male heads.



Supplementary Figure S3 | dADAR localization in 3rd instar larval salivary glands and adult neurons. (**a**) Two separate transgenes representing the predominant adult-stage isoforms of dADAR, which lacks the alternatively spliced 3a exon[23] (termed '3/4') were expressed in larval salivary glands using the *elav*^{c155}-Gal4 driver. At the auto-editing site, the serine codon was either wild-type (AGT) ('S/G') and is capable of being edited by the dADAR transgene, or was mutated to an un-editable synonymous TCT codon ('S'). When expressed in the *dAdar* null adult nervous system, the wild-type dADAR transgene is robustly auto-edited[23]. Both the 3/4 S/G (upper panels) and the 3/4 S transgene (lower panels) primarily co-localized with the nucleolus, labeled with an anti-fibrillarin (FIB) antibody. Scale bar, 5 μm. (**b**) Both the 3/4 S/G (upper panel) and the 3/4 S (lower panel) transgenes localize internally to the nuclear envelope (labeled with an anti-Lamin antibody) in 3rd instar larval salivary glands. Scale bars, 20 μm. (**c**) In adult neuronal nuclei, WTLoxP-HA, S-HA and G-HA dADARs also localize to within the nuclear envelope. Arrows indicate the primary concentrations of nuclear dADAR. Note the presence of multiple punctae within the nucleus in neurons expressing G-HA dADAR, but not S-HA dADAR. Scale bar, 5 μm.

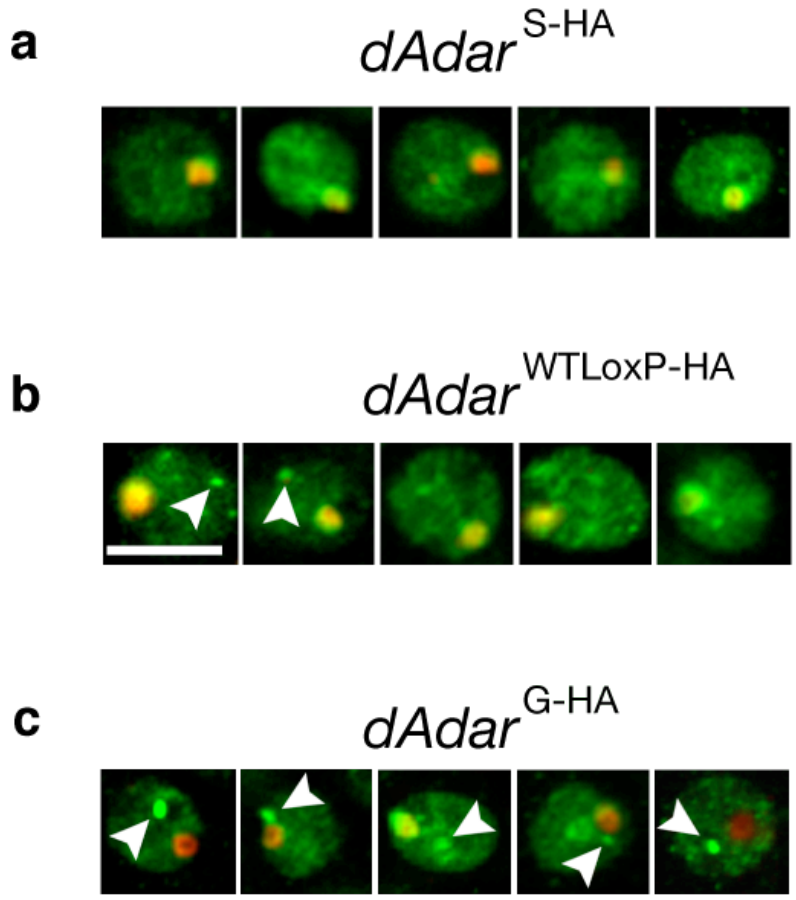


Supplementary Figure S4 | Computational analysis of dADAR localization in adult neurons. Automated categorization of extranucleolar punctate dADAR staining. Each category contains an example image, a model of its category, and the definition of the category. The tetrad of images show a merged image with DAPI (blue), dADAR (green), and fibirillarin (red), the individual dADAR and fibrillarin channels, and the computer's identification of the nucleolus and punctae. The computer's identification shows measures A (white), P (green), and N (red) as described in the methods. Next is a model of the computer's categorization of the cell followed by the definitions of that category. (**a**) Extranucleolar punctate dADAR staining. (**b**) Non-punctate dADAR staining. (**c**) Punctate non-extranucleolar dADAR staining. Scale bar, 5 μm.

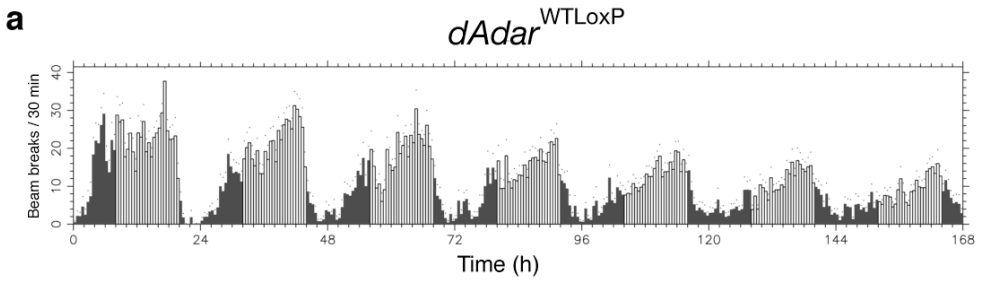

dAdar S-HA
dAdar WTLoxP-HA
dAdar G-HA
Fib
dADAR
Computed

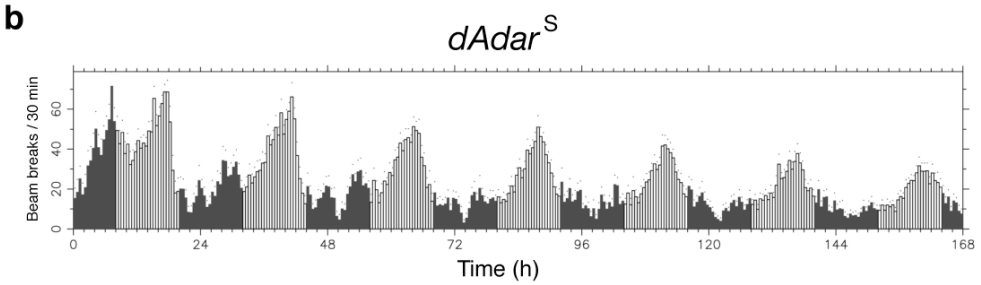
(on previous page)

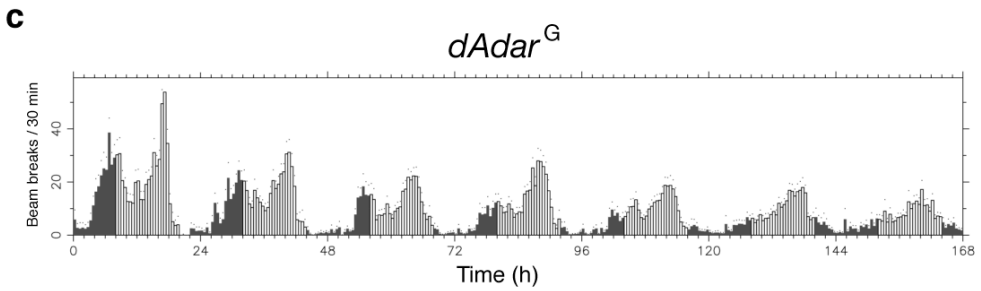
Supplementary Figure S5 | Examples of dADAR localization in *dAdar*$^{S\text{-}HA}$, *dAdar*$^{WTLoxP\text{-}HA}$ and *dAdar*$^{G\text{-}HA}$ adult neurons. For each example, confocal slices showing individual dADAR (green) and Fibrillarin (red) signals, alongside merged image with DAPI (blue), are shown, as well as the computed signals for dADAR and Fibrillarin. dADAR in *dAdar*$^{S\text{-}HA}$ neurons is predominantly localized to the nucleolus and extranucleolar puncta are rarely observed, while in *dAdar*$^{G\text{-}HA}$ neurons, strong extranucleolar puncta are frequently observed (arrowheads). Wild-type *dAdar*$^{WTLoxP\text{-}HA}$ controls exhibit an intermediate phenotype, although dADAR is mainly non-punctal. Scale bars, 5 μm.



Supplementary Figure S6 | Additional images of differences in dADAR localization following manipulation of dADAR auto-editing. In each case, 5 representative adult neuronal nuclei are shown. dADAR (green) was visualized using a mouse anti-HA antibody, rather than the rabbit anti-HA antibody used for all other confocal experiments in the adult brain. (**a**) Consistent with the data obtained using the rabbit anti-HA antibody, dADAR$^{S\text{-}HA}$ stained with mouse anti-HA shows a generally diffuse pattern of expression within the nucleus, and co-localizes with fibrillarin (red). (**b**) This pattern was also predominantly observed in dADAR$^{WTLoxP\text{-}HA}$ neurons, although small puncta were sometimes observed. (**c**) In dADAR$^{G\text{-}HA}$ neurons, we additionally observed strong extranucleolar puncta (arrowheads), as was similarly seen using the rabbit anti-HA antibody. Scale bar, 5 μm.



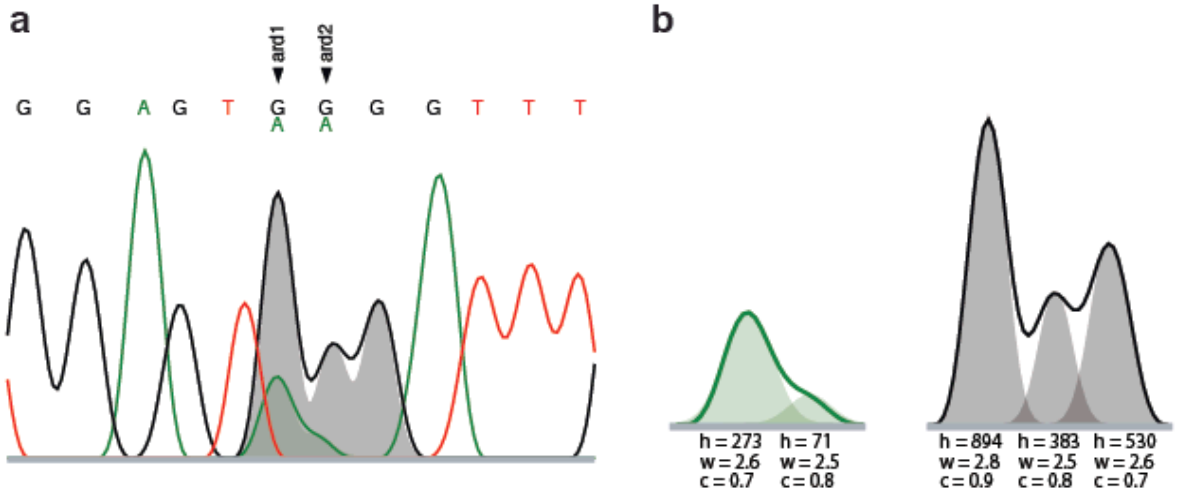




d

	dAdar^{WTLoxP}	*dAdar*^{S}	*dAdar*^{G}
% Rhythmic	100	93.8	100
Period	24.3 ± 0.07	24.0 ± 0.21	24.2 ± 0.07
Power	119.8 ± 7.29	129.4 ± 9.29	117.3 ± 9.39
n	32	32	32

Supplementary Figure S7 | Altering *dAdar* auto-editing does not result in arrhythmic behavior in constant-dark (DD) conditions. (a-c) For each genotype indicated, activity plots were averaged over seven days in DD. Males bearing all *dAdar* alleles exhibited rhythmic locomotor patterns. Light bars - subjective day, dark bars – subjective night. Dots represent s.e.m. (**d**) Table indicating % rhythmicity, period and the power of rhythmicity for all genotypes. Values are presented as mean ± s.e.m. *n*-values are also indicated.



Supplementary Figure S8 | Computational methods to determine editing levels. (**a**) Example electropherogram showing the edited adenosines ard1 and ard2 (sites 1 and 2 of the *ard* acetylcholine receptor), in which the best fit Gaussian curves for the A and G residues are shown as filled green and black, respectively. (**b**) A and G chromatograms on the left and right in which each best fit Gaussian curve and its parameters are shown.

Supplementary Table S1 | Nomenclature for the 23 transcripts analyzed in various *dAdar* allelic backgrounds. Sites (1, 2...) are labeled in a 5' to 3' order within the transcript.

Abbreviation	Locus	Synonyms/ full name	Molecular function
adr	*dAdar*	*Drosophila adenosine deaminase acting on RNA*	RNA editing enzyme
ard	*Ard*	nAcRβ-64B	Nicotinic acetylcholine receptor α-subunit
cac	*cacophony*	Dmcα1A	Voltage-gated calcium channel α-subunit
cad	*Ca-alpha1D*	Dmcα1D	Voltage-gated calcium channel α-subunit
cap	*caps*	Calcium activated protein for secretion	Regulator of exocytosis
cat	*Ca-alpha1T*	Dmcα1T	Voltage-gated calcium channel α-subunit
cpx	*complexin*		Regulator of exocytosis
daf	*Dα5*	nAcRα-34E	Nicotinic acetylcholine receptor α-subunit
das	*Dα6*	nAcRα-30D	Nicotinic acetylcholine receptor α-subunit
dop	*DopEcR*		Dopamine/Ecdysteroid receptor
dsc	*dsc1*	NaCP60E	Voltage-gated sodium channel
eag	*Eag*	*Ether-a-go-go*	Voltage-gated potassium channel α-subunit
glu	*GluClα*		Glutamate-gated chloride channel
lap	*Lap*	like-AP180	Regulator of endocytosis
par	*para*	*paralytic*	Voltage-gated sodium channel α-subunit
rdl	*Rdl*	*resistance to dieldrin*	GABA receptor α-subunit
sbd	*Sbd*	nAcRβ-96A	Nicotinic acetylcholine receptor β-subunit
sha	*shaker*		Voltage-gated potassium channel α –subunit
shb	*shab*		Voltage-gated potassium channel α –subunit
slo	*slowpoke*		Ca^{2+}-activated potassium channel
stj	*straightjacket*	α 2δ	Voltage-gated calcium channel
stn	*stoned-B*		Regulator of endocytosis
syt	*synaptotagmin-1*		Regulator of exocytosis
unc	*unc-13*		Regulator of exocytosis

Supplementary Table S2 | Primers used in this study

Gene	CG Number	Sites	Primer Type	Se quence (5' - 3')
syt	CG3139	1 to 6	Forward	GCTGCGCTACGTGCCGACCGCCGG
			Reverse	GTAGTCCACGACGGTCACAACGAG
			Sequencing	GCTGCGCTACGTGCCGACCGCCGG
cap	CG33653	1	Forward	GATTTGAAAAAGAACGATGGGAAAG
			Reverse	CAGCATATTAATCTGCTGCGAATACC
			Sequencing	CGGGTGTGCCACTTCTGAAGATTTAT
cpx	CG32490	1 to 3	Forward	AGCTAAGCAGATGGTTGGAAA
			Reverse	TGCATGACACATTTTCCCTCT
			Sequencing	CCCCAAGAAGAGCCCAAT
unc	CG2999	1	Forward	TGGACAGTTATCAGCATCTTCAA
			Reverse	ATTCGTGGCTCCAAACTGAT
			Sequencing	GCTGTGGACATGAAGTACGC
stn	CG12473	1	Forward	TCAAGGGTATCGAGCGAATC
			Reverse	GGCCAAGATGCCTTTGATAA
			Sequencing	TGCATACACCACACATCAGC
lap	CG2520	1 and 2	Forward	CGATGCGTTGGATCTTTACA
			Reverse	GGACAGCCAAGTATGATGGG
			Sequencing	TTGTTAGATGCCTTGGAGCA
dsc	CG34405	1	Forward	GCAAGGAATGCGGATTGTAG
			Reverse	GCGTTGCTCACTTCCAGAAT
			Sequencing	CGGATCGTTCTTCACACTGA
sbd	CG6798	1 and 2	Forward	GACCTACAATGGTGCCCAAG
			Reverse	CACATCGATCTCGTTGGTGT
			Sequencing	CCCAAGTGGATCTGAAGCAT
stj	CG12295	1 to 3	Forward	CGTCCGGAATTCCACAATAC
			Reverse	CCTCCTTGCCAATCAGGTAG
			Sequencing	CGACGAGTCCGAAGGATATT
cat	CG15899	1	Forward	GTTGCTGCGAATCCTCAAAT
			Reverse	GTTGGTGGTCGAGGAGTCTG
			Sequencing	TGTGGCACTAATGACGTTCG
cad	CG4894	1 to 5	Forward	GCATCGATTCTATGGGCATT

			Reverse	CAGTGGACGTAGCACTCGAA
			Sequencing	TTGCCAACTGTATTGCCTTG
shb	CG1066	1 to 7	Forward	GAAGGTAAATGCGCCGAGTA
			Reverse	GTCCGTTTGCGAGAGATTGT
			Sequencing	GGAAACGAATAAGAATGCAACG
eag	CG10952	1 to 5	Forward	CAATACAGCTGGCTGTGGAA
			Reverse	TCACCCTTCTCGACATCACTT
			Sequencing	GACGGCCCTATATTTCACCA
		6 to 7	Forward	CAATACAGCTGGCTGTGGAA
			Reverse	TCACCCTTCTCGACATCACTT
			Sequencing	GCGACGAAATTTGGAGAAGA
slo	CG10693	1	Forward	CAGCATTGCATCCCTCATTA
			Reverse	TGGTTCCTTGGAAGAACTCC
			Sequencing	CGGTCTTCGATTTCTTCGAG
		2	Forward	CTACCACGAGCTGAAACACG
			Reverse	CGGGTGGGTTGGTTATTACA
			Sequencing	GATGACCTTTGACGACACGA
rdl	CG10537	1 and 2	Forward	CATGCTGGGTGACGTAAACA
			Reverse	CATACCGACGCCCACATT
			Sequencing	CGGAGTCACCATGTATGTGC
		3 to 6	Forward	CATGCTGGGTGACGTAAACA
			Reverse	CATACCGACGCCCACATT
			Sequencing	TGCCCCAATTTAAGGTCTTG
daf	CG32975	1, 2 and 9	Forward	CACTGGGTGTTACCATCTTGC
			Reverse	CTACGAGACAATAATATGTGGTG
			Sequencing	ACTGGGTGTTACCATCTTGC
		3 to 8	Forward	CACTGGGTGTTACCATCTTGC
			Reverse	CTACGAGACAATAATATGTGGTG
			Sequencing	CGTGCATCAAATCATCAACT
das	CG4128	1 to 6	Forward	AATCTGCGCTGGAATGAAAC
			Reverse	CAATGTGAAGCCCAGTAGGG
			Sequencing	TGGAATGAAACGGAATACGG
ard	CG11348	1 to	Forward	GACCTACAATGGTGCCCAAG

		4		
			Reverse	CACATCGATCTCGTTGGTGT
			Sequencing	CCCAAGTGGATCTGAAGCAT
sha	CG12348	1 and 2	Forward	CTGGTCATGGCTTTGGTGGCGGACC
			Reverse	CCGTGTGATCAGTCAGACCTGGCG
			Sequencing	GGATCTGTGATGTCAGGCACCTCG
		3 to 6	Forward	CTGGTCATGGCTTTGGTGGCGGACC
			Reverse	CCGTGTGATCAGTCAGACCTGGCG
			Sequencing	CGAGGTGCCTGACATCACAGATCC
adr	CG12598	1	Forward	CCACAGCATATCAGTCGATTT
			Reverse	TGGAATCGTCCCCTCACCGGAC
			Sequencing	CCACAGCATATCAGTCGATTT
cac	CG1522	1	Forward	GCGGAGAAAAGGTTTCGTTT
			Reverse	GAGTGTTGCAAGACCTGTGG
			Sequencing	TCAACAGTGCTATCGGGAAA
		2 to 5	Forward	CCACAGCATATCAGTCGATTT
			Reverse	TGGAATCGTCCCCTCACCGGAC
			Sequencing	ATGCATTTACCGGCGTATTC
		6	Forward	GTACGAGGAGGAGGACGAACTGC
			Reverse	CTGAAGTCTAGCGGGACTCG
			Sequencing	GTACGAGGAGGAGGACGAACTGC
		11	Forward	GTACGAGGAGGAGGACGAACTGC
			Reverse	CTGAAGTCTAGCGGGACTCG
			Sequencing	CACTGGCCTACGCCTACTTC
		12	Forward	GTACGAGGAGGAGGACGAACTGC
			Reverse	CTGAAGTCTAGCGGGACTCG
			Sequencing	CTCCAGTGGCCAGATCTCC
par	CG9907	1 to 4	Forward	CATTGGTGCAAATCGAACAA
			Reverse	GCTCCGAATGGACATCTTCT
			Sequencing	CATTATTCATGCACACGACGA
glu	CG7535	1 to 2	Forward	GGCAGCGGACACTATTTCTG
			Reverse	GCATCTAAACTGGCCTGCTC
			Sequencing	CTGACTATGGCGGGACCA
		3	Forward	GGCAGCGGACACTATTTCTG
			Reverse	GCATCTAAACTGGCCTGCTC
			Sequencing	CCTACCTCGCTTCACACTGG

dop	CG18314	1 to 9	Forward	GGTGCCCTTCTCCGTGTAT
			Reverse	TTGAGGAGAATGAAAATCTAAATCTAA
			Sequencing	GACCGGAGAATGGATGTACG