SUPPLEMENTARY MATERIALS

Gastric vagal afferent signaling to the basolateral amygdala mediates anxiety-like behaviors in experimental colitis mice

Chin-Hao Chen,¹ Tsung-Chih Tsai,¹ Yi-Jen Wu,^{2,3} and Kuei-Sen Hsu^{1,4,*}



Supplemental Figure 1. Gastric vagotomy and targeted ablation of vagal afferent neurons by CCK-SAP injections rescue anxiety-related risk assessment behavioral deficits in DSS-induced colitis mice. (A) Schematic illustration of the experimental timeline. Wild type, Sham, Bilateral gastric vagotomy (GV-Bi), SAP-Blank (Blnk) and CCK-SAP (SAP-Bi) mice received 2% DSS in drinking water for 8 days followed by a maintenance dose of 1% for two days. All groups were subjected to behavioral tests on D9 and D10. (B-E) Comparing the effect of H₂O and DSS treatment on the number of rearing in the open field (OF) test (B), the number of nose pokes in the light dark box (LDB) test (C) and the number of rearing and number of stretches in the elevated plus maze (EPM) test (**D** and **E**) ($H_2O: n = 13$, DSS: n = 12). (F-I) Comparing the effect of sham + DSS and GV-Bi + DSS on the number of rearing in the OF test (F), the number of nose pokes in LDB test (G) and the number of rearing and number of stretches in the EPM test (H and I) (sham-DSS: n = 13, GV-Bi-DSS: n = 14). (J-M) Comparing the effect of Blnk + DSS and SAP-Bi + DSS on the number of rearing in the OF test (J), the number of nose pokes in the LDB test (K) and the number of rearing and number of stretches in the EPM test (L and M) (n = 12 in each group). Data represent the mean \pm SEM. ** P < 0.01, *** P < 0.001 and n.s., not significant by two-tailed Student's ttest and Mann-Whitney U test (D).



Supplemental Figure 2. Gastric vagotomy and targeted ablation of vagal afferent neurons by CCK-SAP injection reduce anxiety level of DSS-induced colitis mice without affecting pain sensitivity and locomotor activity. (A) Schematic illustration of the experimental timeline. Wild type, Sham, Bilateral gastric vagotomy (GV-Bi), SAP-Blank (Blnk) and CCK-SAP (SAP-Bi) mice received 2% DSS in drinking water for 8 days followed by a maintenance dose of 1% for two days. All groups were subjected to behavioral tests on D9 and D10. (B-D) Comparing the effect of H_2O and DSS treatment on (B) novelty suppressed food intake (NSF) test, (C) home cage activity test (HCA) and (D) von Frey test (n = 10 in each group). (E-G) Comparing the effect of sham + DSS and GV-Bi + DSS on (E) novelty suppressed food intake (NSF) test, (F) home cage activity test (HCA) and (G) von Frey test (n = 9 in each group). (H-J) Comparing the effect of Blnk + DSS and SAP-Bi + DSS on (H) novelty suppressed food intake (NSF) test, (I) home cage activity test (HCA) and (J) von Frey test (n = 5in each group). Data represent the mean \pm SEM. * P < 0.05, ** P < 0.01, *** P <0.001 and n.s., not significant by two-way RM ANOVA (D, G, J), two-tailed Student's *t*-test (**B**, **C**, **E**, **H**, **I**) and Mann-Whitney *U* test (**F**).



Supplemental Figure 3. The effect of gastric and subdiaphragmatic vagotomy on **DSS-induced colitis phenotypes.** (A) Schematic of the experimental timeline. Two weeks after surgery, mice received 2% DSS in drinking water for 8 days followed by 1% for two days. All groups were subjected to behavioral tests on D22, D23 and D24 before sacrifice. (B) Body weights recorded during the experimental period (sham-DSS: n = 9, GV-DSS: n = 9, SDV-DSS: n=9). (C) Gross morphology images of sham-DSS, GV-DSS and SDV-DSS group. Arrows indicate: (1) colon; (2) spleen; (3) small intestine; (4) cecum; and (5) stomach. (D, E, G) Quantification of (D) colon length; (E) small intestine length and (G) spleen weight on D25 in sham-DSS, GV-DSS and SDV-DSS groups (n = 9 in each group). (F) H&E staining and histological score of colonic sections were assessed on D25 in sham-DSS, GV-DSS and SDV-DSS groups (n = 4 in each group). M: mucosa layer, SM: submucosa layer, and ML: muscular layer. Scale bar, 200 µm. (H) Quantification of FITC-dextran permeability on D25 in sham-DSS, GV-DSS and SDV-DSS groups (n = 9 in each group). (J) DAI score was used to evaluate the severity of DSS-induced colitis recorded from D14 to D24 (n = 9 in each group). DAI score was calculated total score (body weight + stool consistency + rectal bleeding). Data represent the mean \pm SEM. * P < 0.05, ** P < 0.01, *** P < 0.001 and n.s., not significant by one-way ANOVA with Tukey's multiple comparison test (D, E) and Kruskal-Wallis test with Tukey's multiple comparison test (H).



Supplemental Figure 4. Targeted ablation of vagal afferent neurons by CCK-SAP injection. (A) Schematic illustration of the experimental timeline. Sixteen days after mice received nodal injection of Blank-SAP (Blnk) or CCK-SAP (SAP), Fluorogold (FG, 10 mg/kg) was injected intraperitoneally (i.p.) after behavioral tests. Two weeks after FG injection, mice were sacrificed 90 min after food intake. Mice were food deprived for 20 h prior to food intake. (B) and (C) Representative images and (D) quantitative analysis of c-Fos-labeled cells in Blnk and SAP mice 90 min after food intake within the nucleus tractus solitarius (NTS, n = 5 in each group). Scale bar, 200 μ m. (E) and (F) Representative images and (G) quantitative analysis of FG-labeled cells in nodose ganglia (NDG) 15 days after intraperitoneal injection of FG (n = 5 in each group). Scale bar, 100 μ m. (H) and (I) Representative images and (J) quantitative analysis of FG-labeled cells in dorsal motor nucleus of the vagus (DMV) 15 days after intraperitoneal injection of FG (n = 5 in each group). Scale bar, 200 μ m. Data represent the mean ± SEM. ***P* < 0.01 and n.s., not significant by two-tailed Student's *t*-test.



Supplemental Figure 5. The effect of CCK-SAP nodose injection on DSS-induced colitis phenotypes. (A) Schematic of the experimental timeline. Two weeks after surgery, mice received 2% DSS in drinking water for 8 days followed by a maintenance dose of 1% for two days. All groups were subjected to behavioral tests on D22, D23 and D24 before sacrifice. (B) Body weights recorded during the experimental period of Blank-SAP + DSS (Blnk + DSS) and CCK-SAP + DSS mice (SAP + DSS) (Blnk + DSS: n = 5, SAP + DSS: n = 5). (C) Gross morphology images of Blnk + DSS and SAP + DSS groups. Arrows indicate: (1) colon; (2) spleen; (3) small intestine; (4) cecum; and (5) stomach. (D-F) Quantification of (D) colon length; (E) small intestine length and (F) spleen weight on D25 in Blnk + DSS and SAP + DSS groups (n = 5 in each group). (G) H&E staining and (H) histological score of colonic sections were assessed on D25 in Blnk + DSS and SAP + DSS groups (n = 5 in each group). M: mucosa layer, SM: submucosa layer, and ML: muscular layer. Scale bar, 200 µm. (I) Quantification of FITC-dextran permeability on D25 in Blnk + DSS and SAP + DSS groups (n = 5 in each group). (J) DAI score was used to evaluate the severity of DSS-induced colitis recorded from D14 to D24 (n = 5 in each group). DAI score was calculated total score (body weight + stool consistency + rectal bleeding). Data represent the mean \pm SEM.n.s., not significant by two-tailed unpaired Student's *t*-test (D, E, F, H, I).



Supplemental Figure 6. Gastric vagotomy reduces c-Fos expression in multiple brain regions after the elevated plus maze test in DSS-induced colitis mice. Representative images and quantitative analysis of c-Fos-labeled cells in Sham + DSS and GV + DSS mice 90 min after the EPM test within the nucleus tractus solitarius (NTS, n = 5 in each group) (A and B), locus coeruleus (LC, n = 5 in each group) (C and D) and basolateral amygdala (BLA, n = 5 in each group) (E and F). Scale bar, 200 μ m. AP, area postrema; DMV, dorsal motor nucleus of the vagus; LA, lateral amygdala; CeA, central nucleus of the amygdala. Data represent the mean \pm SEM. **P* < 0.05 and *** *P* < 0.001 by two-tailed unpaired Student's *t*-test (B and F), Mann-Whitney *U* test (D).



Supplemental Figure 7. Targeted ablation of vagal afferent neurons by CCK-SAP injection reduces c-Fos expression in multiple brain regions after the elevated plus maze test in DSS-induced colitis mice. Representative images and quantitative analysis of c-Fos-labeled cells in Blank-SAP-DSS (Blnk + DSS) and CCK-SAP + DSS (SAP + DSS) mice 90 min after the EPM test within the nucleus tractus solitarius (NTS, n = 4 in each group) (A and B), locus coeruleus (LC, n = 4 in each group) (C and D) and basolateral amygdala (BLA, n = 4 in each group) (E and F). Scale bar, 200 µm. AP, area postrema; DMV, dorsal motor nucleus of the vagus; LA, lateral amygdala; CeA, central nucleus of the amygdala. Data represent the mean \pm SEM. **P* < 0.05 by Mann-Whitney *U* test (B), two-tailed unpaired Student's *t*-test (D and F).



Supplemental Figure 8. The effect of DSS treatment on unilateral NTS innervated LC-NET neuronal projection to the BLA. (A) Schematic of the experimental timeline. Mice received AAV_{DJ}-CaMKIIa-mCherry injection into right (or left) NTS and incubated for three weeks followed by 4 % FluoroGold (FG) injection into right (or left) BLA. Three days after FG injection, mice received 2 % DSS in drinking water for 8 days and sacrificed on the last day of DSS treatment. (B) Bar graph comparing the amount of LC neurons (NET⁺) as the relay connecting the NTS to the BLA in both sides of H_2O - and DSS-treated groups (n = 4 in each group). (C and E) Representative image showing tracer injection sites of H₂O- and DSS-treated groups. CaMKIIa (red, mCh) signals in the NTS and FG signals in the BLA. Arrow heads represent FG signals in NTS from BLA. Scale bar, 200 µm. (D and F) Representative image showing FGlabeled LC neurons were immunopositive for NET and CaMKII signals in H₂O- and DSS-treated groups. Scale bar, 200 µm. Augmented figures (Right side) showing NET neurons in rectangle area. Scale bar, 10 µm. AP, area postrema; DMV, dorsal motor nucleus of the vagus; LA, lateral amygdala. Data represent the mean \pm SEM. For statistical analysis, two-way ANOVA for (B).



Supplemental Figure 9. The effect of CNO and saline on DSS-induced colitis phenotypes. (A) Gross morphology images of Saline + DSS and CNO + DSS groups. Arrows indicate: (1) colon; (2) spleen; (3) small intestine; (4) cecum; and (5) stomach. (B) DAI score was used to evaluate the severity of DSS-induced colitis recorded from D1 to D10 (n = 8 in each group). DAI score was calculated total score (body weight + stool consistency + rectal bleeding). (C) Quantification of colon length in Saline + DSS and CNO + DSS groups (n = 8 in each group). (D) Quantification of spleen weight in Saline + DSS and CNO + DSS groups (n = 8 in each group). (E) H&E staining and (F) histological score of colonic sections were assessed in Saline + DSS and CNO + DSS groups (n = 4 in each group). M: mucosa layer, SM: submucosa layer, and ML: muscular layer. Scale bar, 200 μ m. Data represent the mean ± SEM. n.s., not significant by two-tailed unpaired Student's *t*-test (C and D), Mann-Whitney U test (F).



Supplemental Figure 10. Chemogenetic manipulation reduces c-Fos expression in locus coeruleus but not nucleus tractus solitarius after the elevated plus maze test in DSS-induced colitis mice. Representative images and quantitative analysis of c-Fos-labeled cells in Saline + DSS and CNO + DSS mice 90 min after the EPM test within the locus coeruleus (LC, n = 4 in each group) (A and B) and nucleus tractus solitarius (NTS, n = 4 in each group) (C and D). Scale bar, 200 μ m. AP, area postrema; DMV, dorsal motor nucleus of the vagus. Data represent the mean \pm SEM. ** *P* < 0.01 and ns., not significant by two-tailed unpaired Student's *t*-test (B and D).

Table S1. Details of statistical data

Figure No.	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	p = value
Fig 1D	Dodyweight	H2O	WT	-	Male	10			Time x DSS	n < 0.001
Fig.16	Body weight	DSS	WT	-	Male	10	-	Two-way RIVI ANOVA	$F_{(7,126)} = 42.39$	<i>ρ</i> < 0.001
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	t-distribution t, df	p = value
	Colon longth (cm)	H2O	WT	-	Male	10	7.67 ± 0.11	Mann Whitney II test		n < 0.001
Fig.1D		DSS	WT	-	Male	10	5.20 ± 0.27	Wiann-whitney o test	_	p < 0.001
Fig 1F	Intesting longth (om)	H2O	WT	-	Male	10	42.92 ± 0.69	Two tailed uppoired Student's t test	t	n = 0.000
FIG.1E	intestine length (cm)	DSS	WT	-	Male	10	38.11 ± 1.48	Two-tailed unpaired student's t-test	l(18) = 2.96	p = 0.009
	Sploop weight (g)	H2O	WT	-	Male	10	0.06 ± 0.01	Two tailed uppaired Student's t test	+ = 7.10	n < 0.001
FIG.1F	spieen weight (g)	DSS	WT	-	Male	10	0.12 ± 0.01		t ₍₁₈₎ – 7.19	p < 0.001
	Listal aginal same	H2O	WT	-	Male	6	0.50 ± 0.22	Mann Whitney II test		n = 0.002
Fig.1H	HISLOIOGICAI SCOTE	DSS	WT	-	Male	6	4.33 ± 0.67	Mann-whitney O test	-	p = 0.002
Fig 11	FITC Dovtron (ng/ml)	H2O	WT	-	Male	10	0.64 ± 0.15	Two tailed uppaired Student's t test	+ = 2.80	n = 0.001
FIG.11	FITC-Dextrait (lig/lill)	DSS	WT	-	Male	10	1.45 ± 0.24		t ₍₁₈₎ – 2.89	p = 0.001
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	<i>p</i> = value
Fig. 11	Disease activity index	H2O	WT	_	Male	10			Time x DSS	n < 0.001
гійтті		DSS	WT	-	Male	10	-		F _(9,162) = 71.55	$\mu < 0.001$

Figure	Pai	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	<i>p</i> = value
		total distance	H2O	WT	-	Male	13	44.10 (36.08, 48.96)	Mann Whitney II test		n < 0.001
FIG.2B	OFT	(m)	DSS	WT	-	Male	12	22.35 (18.71, 24.38)	Mann-Whitney O test	-	p < 0.001
Fig 20	OFI	time in center	H2O	WT	-	Male	13	14.00 (10.50, 16.50)	Two tailed wavesized Student's t test		m (0.001
Fig.2C		(sec)	DSS	WT	-	Male	12	5.50 (2.00, 7.00)	Two-tailed unpaired student's t-test	$l_{(23)} = 5.45$	p < 0.001
F:= 2D		duration	H2O	WT	-	Male	13	36.00 (25.00, 50.00)	Two tailed wavesized Student's t test	+ 2.20	m 0.021
FIG.2D	חסו	(sec)	DSS	WT	-	Male	12	18.50 (9.00, 40.75)	Two-talled unpaired student's t-test	$l_{(23)} = 2.30$	p = 0.031
	LDB	ontring	H2O	WT	-	Male	13	13.00 (9.50, 17.50)	Two tailed uppaired Student's t test	+ - 2.02	n = 0.054
FIG.2E		entries	DSS	WT	-	Male	12	8.00 (3.00, 11.50)	Two-talled unpaired student's t-test	$t_{(23)} = 2.03$	p = 0.054
Fig 2C		total distance	H2O	WT	-	Male	13	16.12 (8.84, 18.64)	Mann Whitney II test		n = 0.016
Fig.20		(m)	DSS	WT	-	Male	12	7.59 (5.28, 11.11)	Mann-Whitney O test	-	p = 0.016
		open arms	H2O	WT	-	Male	13	15.20 (4.40, 22.80)	Mann Whitney II test		n - 0.025
FIG.2H	EPIVI	(sec)	DSS	WT	-	Male	12	1.35 (0.53, 6.40)	Mann-Whitney O test	-	p = 0.035
		closed arms	H2O	WT	-	Male	13	60.80 (47.95, 90.35)	00.35) Two tailed uppeired Student's t test	tost t = 2.40	n = 0.025
Fig.21		(sec)	DSS	WT	-	Male	12	89.60 (74.78, 96.73)	Two-talled unpaired Student's t-test	$t_{(23)} = 2.40$	p = 0.025

Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Dunn's test	p = value
		Sham	WT	-	Male	23	0.57 ± 0.02		-	-
		GV-Bi	WT	-	Male	24	0.82 ± 0.04		Sham vs. GV	<i>p</i> < 0.001
Fig.3C Food inta	Food intoko (g)	SDV	WT	-	Male	23	1.03 ± 0.07	Kruskal-Wallis test (p < 0.001)	Sham vs. SDV	<i>p</i> < 0.001
	FOOD INTAKE (g)	GV-R	WT	-	Male	13	0.73 ± 0.04		Sham vs. GV-R	<i>p</i> = 0.033
		SDV-R WT - Male 12 0.83 ± 0.03	Sham vs. SDV-R	<i>p</i> < 0.001						
		V-L	WT	-	Male	13	0.84 ± 0.04)4	Sham vs. V-L	<i>p</i> < 0.001

Figure	Ра	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
	OFT	total distance	Sham	WT	H ₂ O	Male	10	50.35 (39.53, 55.98)	Two tailed uppaired Student's t test	+ _ 0 C 1	n < 0.001
Fig.3D	UFI	(m)	Sham	WT	DSS	Male	13	17.59 (12.91, 23.51)	Two-talled unpaired student's t-test	$l_{(21)} = 8.01$	p < 0.001

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
			Sham	WT	H ₂ O	Male	10	50.35 (39.53, 55.98)			
			GV-Bi	WT	H ₂ O	Male	10	33.50 (28.03, 39.70)		stFixed effects F(DFn,DFd) $p =$ VVADSS x Vagotomy $F_{(1,43)} = 1.91$ $p =$ VVADSS x Vagotomy $F_{(1,42)} = 0.16$ $p =$ VVADSS x Vagotomy $F_{(1,42)} = 0.38$ $p =$ VVADSS x Vagotomy $F_{(1,43)} = 0.67$ $p =$ VVADSS x Vagotomy $F_{(1,43)} = 0.67$ $p =$	m 0175
			Sham	WT	DSS	Male	13	17.59 (12.91, 23.51)	TWO-WAY ANOVA	$F_{(1,43)} = 1.91$	p = 0.175
			GV-Bi	WT	DSS	Male	14	25.38 (16.88, 34.07)			
			Sham	WT	H ₂ O	Male	10	50.35 (39.53, 55.98)			
	OFT	total distance	GV-Bi	WT	H ₂ O	Male	10	33.50 (28.03, 39.70)		DSS x Vagotomy	m 0.699
FIg.5D	OFT	(m)	Sham	WT	DSS	Male	13	17.59 (12.91, 23.51)	Two-way ANOVA	$F_{(1,42)} = 0.16$	p = 0.000
			GV-R	WT	DSS	Male	13	16.20 (11.15, 19.25)			
			Sham	WT	H ₂ O	Male	10	50.35 (39.53, 55.98)			n = 0.542
			GV-Bi	WT	H ₂ O	Male	10	33.50 (28.03, 39.70)		DSS x Vagotomy	
			Sham	WT	DSS	Male	13	13 17.59 (12.91, 23.51) Two-way A 13 9.90 (7.75, 21.15) Two-way A	Two-way ANOVA	$F_{(1,42)} = 0.38$	μ – 0.542
			V-L	WT	DSS	Male	13	9.90 (7.75, 21.15)			
			Sham	WT	H ₂ O	Male	10	50.35 (39.53 <i>,</i> 55.98)	98)		n = 0.417
			Sham SDV-Bi	WT	H ₂ O	Male	10	42.80 (35.95, 55.75)		DSS x Vagotomy	
			Sham	WT	DSS	Male	13	17.59 (12.91, 23.51)	Two-way ANOVA	$F_{(1,43)} = 0.67$	p = 0.417
			SDV-Bi	WT	DSS	Male	13	14.60 (8.95, 17.10)			
			Sham	WT	H ₂ O	Male	10	50.35 (39.53, 55.98)			
	OFT	total distance	SDV-Bi	WT	H ₂ O	Male	10	42.80 (35.95, 55.75)		DSS x Vagotomy	n = 0.127
FIG.5D	OFI	(m)	Sham	WT	DSS	Male	13	17.59 (12.91, 23.51)	Two-way ANOVA	$F_{(1,41)} = 2.42$	p = 0.127
			SDV-R	WT	DSS	Male	12	17.30 (11.18, 23.18)	$ \begin{array}{c} $		
			Sham	WT	H ₂ O	Male	10	50.35 (39.53, 55.98)			
			SDV-Bi	WT	H ₂ O	Male	10	42.80 (35.95, 55.75)		DSS x Vagotomy	p = 0.342
			Sham	WT	DSS	Male	13	17.59 (12.91, 23.51)	TWO-WAY ANOVA	$F_{(1,42)} = 0.92$	
			V-L	WT	DSS	Male	13	9.90 (7.75, 21.15)			

Figure	Pai	rameter	Test specifications	ions Genotype Treatment Sex Number of individuals Median (Q1,Q3)		Statistical test	t-distribution t, df	<i>p</i> = value			
Eig 2E		time in center	Sham	WT	H ₂ O	Male	10	8.45 (7.25, 14.45)	Two tailed uppoired Student's t test	+	n < 0.001
FIg.3E	UFI	(sec)	Sham	WT	DSS	Male	13	2.00 (1.00, 5.00)	Two-talled unpaired student's t-test	$l_{(21)} = 4.27$	p < 0.001

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
			Sham	WT	H ₂ O	Male	10	8.45 (7.25, 14.45)			
			GV-Bi	WT	H ₂ O	Male	10	8.90 (7.45, 10.78)		DSS x Vagotomy	n = 0.192
			Sham	WT	DSS	Male	13	2.00 (1.00, 5.00)	Two-way ANOVA	$F_{(1,43)} = 1.84$	p – 0.182
			GV-Bi	WT	DSS	Male	14	2.50 (1.70, 6.25)			
			Sham	WT	H ₂ O	Male	10	8.45 (7.25, 14.45)			
	OFT	time in center	GV-Bi	WT	H ₂ O	Male	10	8.90 (7.45, 10.78)		DSS x Vagotomy	n = 0.210
FIG.SE	UFI	(sec)	Sham	WT	DSS	Male	13	2.00 (1.00, 5.00)	Two-way ANOVA	$F_{(1,42)} = 1.57$	$\mu = 0.218$
			GV-R	WT	DSS	Male	13	2.80 (1.05, 6.10)			
			Sham	WT	H ₂ O Male 10 8.45 (7.25, 14.45)						
			GV-Bi	WT	H ₂ O	Male	10	8.90 (7.45, 10.78)	, 10.78) DSS x Vago		n = 0.398
			Sham	WT	DSS	Male	13	2.00 (1.00, 5.00)) Iwo-way ANOVA	$F_{(1,42)} = 0.73$	p = 0.398
			V-L	WT	DSS	Male	13	0.80 (0.20, 4.65)			
			Sham	WT	H ₂ O	Male	10	8.45 (7.25, 14.45)			
			SDV-Bi	WT	H ₂ O	Male	10	9.05 (5.28, 10.80)		DSS x Vagotomy	$n = 0.0 \Gamma C$
			Sham	WT	DSS	Male	13	2.00 (1.00, 5.00)	Two-way ANOVA	$F_{(1,43)} = 3.86$	$\mu = 0.050$
Eig 2E		time in center	SDV-Bi	WT	DSS	Male	13	5.40 (1.95, 17.40)			
FIG.SE	OFI	(sec)	Sham	WT	H ₂ O	Male	10	8.45 (7.25, 14.45)			
			SDV-Bi	WT	H ₂ O	Male	10	9.05 (5.28, 10.80)		DSS x Vagotomy	n = 0.045
			Sham	WT	DSS	Male	13	2.00 (1.00, 5.00)	Two-way ANOVA	$F_{(1,41)} = 4.26$	<i>p</i> = 0.045
			SDV-R	WT	DSS	Male	12	4.70 (1.75, 6.90)			

Figure	Par	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
			Sham	WT	H ₂ O	Male	10	8.45 (7.25, 14.45)			
Fig 3F	OFT	time in center	SDV-Bi	WT	H ₂ O	Male	10	9.05 (5.28, 10.80)		DSS x Vagotomy	m 0.241
FIg.3E	OFI	(sec)	Sham	WT	DSS	Male	13	2.00 (1.00, 5.00)	Two-way ANOVA	$F_{(1,42)} = 1.41$	p = 0.241
			V-L	WT	DSS	Male	13	0.80 (0.20, 4.65)			

Figure	Pa	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	p = value
										H ₂ O Sham vs. H ₂ O SDV-Bi	<i>p</i> = 0.160
			Sham	WT	H ₂ O	Male	10	8.45 (7.25, 14.45)		H ₂ O Sham vs. DSS Sham	<i>p</i> < 0.001
	OFT	time in center	SDV-Bi	WT	H ₂ O	Male	10	9.05 (5.28, 10.80)	Two-way ANOVA	H_2O Sham vs. DSS SDV-R	<i>p</i> < 0.001
Fig.3E	OFT	(sec)	Sham	WT	DSS	Male	13	2.00 (1.00, 5.00)	Tukey's Multiple Comparisons test	H ₂ O SDV-Bi vs. DSS Sham	<i>p</i> = 0.003
			SDV-R	WT	DSS	Male	12	4.70 (1.75, 6.90)	.90)	H ₂ O SDV-Bi vs. DSS SDV-R	<i>p</i> = 0.022
										DSS Sham vs. DSS SDV-R	<i>p</i> = 0.891

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	<i>p</i> = value
Fig 2E		duration	Sham	WT	H ₂ O	Male	10	32.50 (20.50, 43.25)	Two tailed uppaired Student's t test	+ _ 2.00	n < 0.001
Fig.3F	LDB	(sec)	Sham	WT	DSS	Male	13	10.00 (6.00, 24.00)	Two-talled unpaired student's t-test	$l_{(21)} = 3.89$	p < 0.001

Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
		Sham	WT	H ₂ O	Male	10	32.50 (20.50, 43.25)			
		GV-Bi	WT	H ₂ O	Male	10	26.00 (21.25, 41.00)		DSS x Vagotomy	n = 0.002
		Sham	WT	DSS	Male	13	10.00 (6.00, 24.00)	Two-way ANOVA	F _(1,43) = 9.78	p = 0.003
		GV-Bi	WT	DSS	Male	14	46.85 (20.58, 62.10)			
		Sham	WT	H ₂ O	Male	10	32.50 (20.50, 43.25)			
	duration	GV-Bi	WT	H ₂ O	Male	10	26.00 (21.25, 41.00)		DSS x Vagotomy	n = 0.144
FIG.3F	LDB (sec)	Sham	WT	DSS	Male	13	10.00 (6.00, 24.00)	Two-way ANOVA	$F_{(1,42)} = 2.22$	p = 0.144
		GV-R	WT	DSS	Male	13	15.80 (7.10, 52.25)			
		Sham	WT	H ₂ O	Male	10	32.50 (20.50, 43.25)			n - 0.256
		GV-Bi	WT	H ₂ O	Male	10	26.00 (21.25, 41.00)		DSS x Vagotomy	
		Sham	WT	DSS	Male	13	10.00 (6.00, 24.00)	Two-way ANOVA	F _(1,42) = 0.87	p = 0.356
		V-L	WT	DSS	Male	13	14.30 (9.10, 25.10)			
		Sham	WT	H ₂ O	Male	10	32.50 (20.50, 43.25)			n = 0.019
		SDV-Bi	WT	H ₂ O	Male	10	29.50 (19.00, 38.25)		DSS x Vagotomy	
		Sham	WT	DSS	Male	13	10.00 (6.00, 24.00)	Two-way ANOVA	$F_{(1,43)} = 6.07$	$\mu = 0.018$
		SDV-Bi	WT	DSS	Male	13	21.20 (14.25, 35.85)			
		Sham	WT	H ₂ O	Male	10	32.50 (20.50, 43.25)			
	duration	SDV-Bi	WT	H ₂ O	Male	10	29.50 (19.00, 38.25)		DSS x Vagotomy	n = 0.076
rig.sr	(sec)	Sham	WT	DSS	Male	13	10.00 (6.00, 24.00)	Two-way ANOVA	$F_{(1,41)} = 3.32$	$\mu = 0.076$
		SDV-R	WT	DSS	Male	12	21.75 (8.43, 31.95)	$\frac{1.257}{1.00}$ Two-way ANOVA $F_{(1,41)} = 3.32$		
		Sham	WT	H ₂ O	Male	10	32.50 (20.50, 43.25)			
		SDV-Bi	WT	H ₂ O	Male	10	29.50 (19.00, 38.25)		DSS x Vagotomy	γ p = 0.157
		Sham	WT	DSS	Male	13	10.00 (6.00, 24.00)	I WO-WAY ANOVA	$F_{(1,42)} = 2.08$	
		V-L	WT	DSS	Male	13	14.30 (9.10, 25.10)			

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	p = value
										H_2O Sham vs. H_2O GV-Bi	p = 0.984
			Sham	WT	H ₂ O	Male	10	32.50 (20.50, 43.25)		H₂O Sham vs. DSS Sham	<i>p</i> = 0.022
		duration	GV-Bi	WT	H ₂ O	Male	10	26.00 (21.25, 41.00)	Two-way ANOVA	H₂O Sham vs. DSS GV-Bi	p = 0.737
rig.sr	LUD	(sec)	Sham	WT	DSS	Male	13	10.00 (6.00, 24.00)	Tukey's Multiple Comparisons test	H₂O GV-Bi vs. DSS Sham	<i>p</i> = 0.056
			GV-Bi	WT	DSS	Male	14	46.85 (20.58, 62.10)		H₂O GV-Bi vs. DSS GV-Bi	<i>p</i> = 0.502
										DSS Sham vs. DSS GV-Bi	<i>p</i> < 0.001

Figure	Par	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	<i>p</i> = value
										H ₂ O Sham vs. H ₂ O SDV-Bi	<i>p</i> = 0.592
			Sham	WT	H ₂ O	Male	10	32.50 (20.50, 43.25)		H ₂ O Sham vs. DSS Sham	<i>p</i> < 0.001
		duration	SDV-Bi	WT	H ₂ O	Male	10	29.50 (19.00, 38.25)	Two-way ANOVA	H ₂ O Sham vs. DSS SDV-Bi	<i>p</i> = 0.146
FIg.3F	LDB	(sec)	Sham	WT	DSS	Male	13	10.00 (6.00, 24.00)	Tukey's Multiple Comparisons test	H ₂ O SDV-Bi vs. DSS Sham	<i>p</i> = 0.028
			SDV-Bi	WT	DSS	Male	13	21.20 (14.25, 35.85)		H ₂ O SDV-Bi vs. DSS SDV-Bi	<i>p</i> = 0.847
										DSS Sham vs. DSS SDV-Bi	<i>p</i> = 0.112

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	<i>p</i> = value
		ontrioc	Sham	WT	H ₂ O	Male	10	12.50 (8.75, 15.25)	Mann Whitney II test		n < 0.001
FIg.3G	LDB	entries	Sham	WT	DSS	Male	13	3.00 (2.00, 5.50)	Mann-whitney 0 test	-	p < 0.001

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
			Sham	WT	H ₂ O	Male	10	12.50 (8.75, 15.25)			
			GV-Bi	WT	H ₂ O	Male	10	10.50 (7.75, 15.00)		DSS x Vagotomy	m 0.024
			Sham	WT	DSS	Male	13	3.00 (2.00, 5.50)	TWO-WAY ANOVA	$F_{(1,43)} = 4.80$	p = 0.034
			GV-Bi	WT	DSS	Male	14	6.00 (4.75, 12.00)			
			Sham	WT	H ₂ O	Male	10	12.50 (8.75, 15.25)			
Fig 2C		ontrios	GV-Bi	WT	H ₂ O	Male	10	10.50 (7.75, 15.00)		DSS x Vagotomy	p = 0.790
Fig.3G	LDB	entries	Sham	WT	DSS	Male	13	3.00 (2.00, 5.50)	TWO-WAY ANOVA	$F_{(1,42)} = 0.07$	
			GV-R	WT	DSS	Male	13	3.00 (1.00, 5.00)			
			Sham	WT	H ₂ O	Male	10	12.50 (8.75, 15.25)		DSS x Vagotomy	n = 0.664
			GV-Bi	WT	H ₂ O	Male	10	10.50 (7.75, 15.00)			
		Sham	WT	DSS	Male	13	3.00 (2.00, 5.50)	TWO-WAY ANOVA	$F_{(1,42)} = 0.19$	<i>p</i> = 0.664	
		V-L	WT	DSS	Male	13	3.00 (2.00, 3.50)				
			Sham	WT	H ₂ O	Male	10	12.50 (8.75, 15.25)			
			SDV-Bi	WT	H ₂ O	Male	10	13.50 (10.50, 20.00)		DSS x Vagotomy	n = 0.917
			Sham	WT	DSS	Male	13	3.00 (2.00, 5.50)	TWO-WAY ANOVA	$F_{(1,43)} = 0.05$	$\mu = 0.817$
			SDV-Bi	WT	DSS	Male	13	21.20 (14.25, 35.85)			
			Sham	WT	H ₂ O	Male	10	12.50 (8.75, 15.25)			
Fig 2C		ontrioc	SDV-Bi	WT	H ₂ O	Male	10	13.50 (10.50, 20.00)		DSS x Vagotomy	p = 0.67E
FIg.30	Fig.3G LDB entries	Sham	WT	DSS	Male	13	3.00 (2.00, 5.50)	TWO-WAY ANOVA	$F_{(1,41)} = 0.18$	$\mu = 0.075$	
		SDV-R	WT	DSS	Male	12	3.00 (2.25, 6.75)				
		Sham	WT	H ₂ O	Male	10	12.50 (8.75, 15.25)				
			SDV-Bi	WT	H ₂ O	Male	10	13.50 (10.50, 20.00)		DSS x Vagotomy $F_{(1,42)} = 0.02$ p	p = 0.888
			Sham	WT	DSS	Male	13	3.00 (2.00, 5.50)	.50) Two-way ANOVA		
			V-L	WT	DSS	Male	13	3.00 (2.00, 3.50)			

Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	p = value
									H ₂ O Sham vs. H ₂ O GV-Bi	<i>p</i> = 0.956
		Sham	WT	H ₂ O	Male	10	12.50 (8.75, 15.25)		H ₂ O Sham vs. DSS Sham	<i>p</i> < 0.001
Fig 2C		GV-Bi	WT	H ₂ O	Male	10	10.50 (7.75, 15.00)	Two-way ANOVA	H ₂ O Sham vs. DSS GV-Bi	<i>p</i> = 0.216
Fig.3G	LDB entries	Sham	WT	DSS	Male	13	3.00 (2.00, 5.50)	Tukey's Multiple Comparisons test	H ₂ O GV-Bi vs. DSS Sham	<i>p</i> = 0.002
		GV-Bi	WT	DSS	Male	14	6.00 (4.75, 12.00)		H ₂ O GV-Bi vs. DSS GV-Bi	<i>p</i> = 0.497
									DSS Sham vs. DSS GV-Bi	<i>p</i> = 0.040

Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
	total distance	Sham	WT	H ₂ O	Male	10	14.75 (12.28, 17.15)	Mann Whitney II test		n < 0.001
FIg.3H	(m)	Sham	WT	DSS	Male	13	4.55 (3.50, 5.48)	Mann-Whitney O test	-	p < 0.001

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	
			Sham	WT	H ₂ O	Male	10	14.75 (12.28, 17.15)	
			GV-Bi	WT	H ₂ O	Male	10	11.00 (7.75, 12.43)	
			Sham	WT	DSS	Male	13	4.55 (3.50, 5.48)	
			GV-Bi	WT	DSS	Male	14	10.08 (5.55, 14.20)	
			Sham	WT	H ₂ O	Male	10	14.75 (12.28, 17.15)	
		total distance	GV-Bi	WT	H ₂ O	Male	10	11.00 (7.75, 12.43)	
FIg.3H	EPIVI	(m)	Sham	WT	DSS	Male	13	4.55 (3.50, 5.48)	
			GV-R	WT	DSS	Male	13	4.60 (3.55, 8.90)	
			Sham	WT	H ₂ O	Male	10	14.75 (12.28, 17.15)	
			GV-Bi	WT	H ₂ O	Male	10	11.00 (7.75, 12.43)	
			Sham	WT	DSS	Male	13	4.55 (3.50, 5.48)	
			V-L	WT	DSS	Male	13	6.40 (4.40, 9.85)	
			Sham	WT	H ₂ O	Male	10	14.75 (12.28, 17.15)	
			SDV-Bi	WT	H ₂ O	Male	10	16.00 (12.78, 19.15)	
			Sham	WT	DSS	Male	13	4.55 (3.50, 5.48)	
			SDV-Bi	WT	DSS	Male	13	4.90 (3.35, 7.10)	
			Sham	WT	H ₂ O	Male	10	14.75 (12.28, 17.15)	
		total distance	SDV-Bi	WT	H ₂ O	Male	10	16.00 (12.78, 19.15)	
FIg.3H	EPIVI	(m)	Sham	WT	DSS	Male	13	4.55 (3.50, 5.48)	
			SDV-R	WT	DSS	Male	12	4.55 (3.93, 6.15)	
			Sham	WT	H ₂ O	Male	10	14.75 (12.28, 17.15)	
			SDV-Bi	WT	H ₂ O	Male	10	16.00 (12.78, 19.15)	
			Sham	WT	DSS	Male	13	4.55 (3.50, 5.48)	
			V-L	WT	DSS	Male	13	6.40 (4.40, 9.85)	

Figure	Par	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	
			Sham	WT	H ₂ O	Male	10	12.50 (8.75, 15.25)	
		total distance	GV-Bi	WT	H ₂ O	Male	10	10.50 (7.75, 15.00)	
FIg.3H	EPIVI	(m)	Sham	WT	DSS	Male	13	3.00 (2.00, 5.50)	Tukey'
			GV-Bi	WT	DSS	Male	14	6.00 (4.75, 12.00)	
			Sham	WT	H ₂ O	Male	10	14.75 (12.28, 17.15)	
	EDM	total distance	SDV-Bi	WT	H ₂ O	Male	10	16.00 (12.78, 19.15)	
гід.эп	EFIVI	(m)	Sham	WT	DSS	Male	13	4.55 (3.50, 5.48)	Tukey'
			SDV-Bi	WT	DSS	Male	13	4.90 (3.35, 7.10)	
									-
			Sham	WT	H ₂ O	Male	10	14.75 (12.28, 17.15)	-
	EDM	total distance	SDV-Bi	WT	H ₂ O	Male	10	16.00 (12.78, 19.15)	
118.311		(m)	Sham	WT	DSS	Male	13	4.55 (3.50, 5.48)	Tukey'
			SDV-R	WT	DSS	Male	12	4.55 (3.93, 6.15)	
									-
			Sham	WT	H ₂ O	Male	10	14.75 (12.28, 17.15)	-
Fig 2H	FDM	total distance	SDV-Bi	WT	H ₂ O	Male	10	16.00 (12.78, 19.15)	-
118.511		(m)	Sham	WT	DSS	Male	13	4.55 (3.50, 5.48)	Tukey'
			V-L	WT	DSS	Male	13	6.40 (4.40, 9.85)	

Statistical test	Fixed effects F(DFn,DFd)	p = value
Two-way ANOVA	DSS x Vagotomy F _(1,43) = 4.81	p = 0.034
Two-way ANOVA	DSS x Vagotomy F _(1,42) = 0.07	p = 0.797
Two-way ANOVA	DSS x Vagotomy F _(1,42) = 0.44	p = 0.512
Two-way ANOVA	DSS x Vagotomy F _(1,43) = 10.46	p = 0.002
Two-way ANOVA	DSS x Vagotomy F _(1,41) = 9.72	p = 0.003
Two-way ANOVA	DSS x Vagotomy F _(1,42) = 16.21	p < 0.001
Statistical test	Compared Groups	<i>p</i> = value
	H ₂ O Sham vs. H ₂ O GV-Bi	<i>p</i> = 0.964
	H ₂ O Sham Vs. DSS Sham	<i>p</i> < 0.001
I WO-WAY ANOVA	H ₂ O Sham VS. DSS GV-BI	p = 0.028
Multiple Comparisons test		<i>p</i> < 0.001
	H ₂ U GV-BI VS. DSS GV-BI	p = 0.007
	USS Sham vs. USS GV-BI	p = 0.002
	H ₂ O Sham vs. H ₂ O SDV-BI	p = 0.000
	H ₂ O Sham vc DSS SDV Bi	p < 0.001
I WO-Way ANOVA	H_2O SIIdIII VS. DSS SDV-BI	p < 0.001
s multiple compansons test	H_2O SDV-Bi vs. DSS SDV-Bi	p < 0.001
	DSS Sham vs. DSS SDV-Bi	p = 0.007
	Han Sham vs. Han SDV-Bi	p = 0.800
	H_2O Sham vs. DSS Sham	p < 0.001
	H_2O Sham vs. DSS SDV-R	p < 0.001
Multiple Comparisons test	H_2O SDV-Bi vs. DSS Sham	p < 0.001 n < 0.001
	H_2O SDV-Bi vs. DSS SNUT	<i>p</i> < 0.001
	DSS Sham vs. DSS SDV-R	p > 0.999
	H ₂ O Sham vs. H ₂ O SDV-Ri	p = 0.002
	H_2O Sham vs. DSS Sham	<i>p</i> < 0.001
Two-way ANOVA	H ₂ O Sham vs. DSS V-L	<i>p</i> < 0.001
, s Multiple Comparisons test	H ₂ O SDV-Bi vs. DSS Sham	<i>p</i> < 0.001
-	H ₂ O SDV-Bi vs. DSS V-L	<i>p</i> = 0.022

DSS Sham vs. DSS V-L

p = 0.308

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
		open arms	Sham	WT	H ₂ O	Male	10	6.05 (2.33, 15.58)	Mann Whitney II test		n = 0.002
Fig.31	EPIVI	(sec)	Sham	WT	DSS	Male	13	0.40 (0.00, 1.30)	Mann-Whitney O test	-	p = 0.003

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
			Sham	WT	H ₂ O	Male	10	6.05 (2.33, 15.58)			
			GV-Bi	WT	H ₂ O	Male	10	6.25 (1.55, 12.68)		DSS x Vagotomy	n = 0.001
			Sham	WT	DSS	Male	13	0.40 (0.00, 1.30)	TWO-WAY ANOVA	$F_{(1,43)} = 11.90$	p = 0.001
			GV-Bi	WT	DSS	Male	14	10.08 (2.08, 24.25)			
			Sham	WT	H ₂ O	Male	10	6.05 (2.33, 15.58)			
		open arms	GV-Bi	WT	H ₂ O	Male	10	6.25 (1.55, 12.68)		DSS x Vagotomy	p = 0.055
rig.Si	EFIVI	(sec)	Sham	WT	DSS	Male	13	0.40 (0.00, 1.30)	Two-way ANOVA	$F_{(1,42)} = 3.90$	p = 0.055
			GV-R	WT	DSS	Male	13	0.40 (0.00, 5.85)			
			Sham	WT	H ₂ O	Male	10	6.05 (2.33, 15.58)			
			GV-Bi	WT	H ₂ O	Male	10	6.25 (1.55, 12.68)		DSS x Vagotomy	n = 0.044
		Sham	WT	DSS	Male	13	0.40 (0.00, 1.30)	Two-way ANOVA	$F_{(1,42)} = 4.31$	$\mu = 0.044$	
			V-L	WT	DSS	Male	13	1.00 (0.10, 7.50)			
			Sham	WT	H ₂ O	Male	10	6.05 (2.33, 15.58)			
			SDV-Bi	WT	H ₂ O	Male	10	9.05 (4.15, 12.50)		DSS x Vagotomy	n = 0.014
			Sham	WT	DSS	Male	13	0.40 (0.00, 1.30)		$F_{(1,43)} = 6.57$	μ = 0.014
			SDV-Bi	WT	DSS	Male	13	5.20 (1.45, 12.85)			
			Sham	WT	H ₂ O	Male	10	6.05 (2.33, 15.58)			
Eig 21	EDNA	open arms	SDV-Bi	WT	H ₂ O	Male	10	9.05 (4.15, 12.50)		DSS x Vagotomy	n = 0.172
i ig.5i	g.3I EPM (sec)	Sham	WT	DSS	Male	13	0.40 (0.00, 1.30)	Two-way ANOVA	$F_{(1,41)} = 1.93$	p = 0.172	
		SDV-R	WT	DSS	Male	12	0.75 (0.03, 2.15)				
		Sham	WT	H ₂ O	Male	10	6.05 (2.33, 15.58)				
			SDV-Bi	WT	H ₂ O	Male	10	9.05 (4.15, 12.50)		DSS x Vagotomy	n = 0.051
			Sham	WT	DSS	Male	13	0.40 (0.00, 1.30)	(0) Two-way ANOVA	$F_{(1,42)} = 4.03$	p = 0.051
			V-L	WT	DSS	Male	13	1.00 (0.10, 7.50)			

Figure	Pa	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	<i>p</i> = value
										H ₂ O Sham vs. H ₂ O GV-Bi	<i>p</i> = 0.741
			Sham	WT	H ₂ O	Male	10	6.05 (2.33, 15.58)		H ₂ O Sham vs. DSS Sham	<i>p</i> = 0.009
Fig 21	EDM	open arms	GV-Bi	WT	H ₂ O	Male	10	6.25 (1.55, 12.68)	Two-way ANOVA	H ₂ O Sham vs. DSS GV-Bi	p = 0.977
rig.oi	EFIVI	(sec)	Sham	WT	DSS	Male	13	0.40 (0.00, 1.30)	Tukey's Multiple Comparisons test	H ₂ O GV-Bi vs. DSS Sham	<i>p</i> = 0.119
			GV-Bi	WT	DSS	Male	14	10.08 (2.08, 24.25)		H ₂ O GV-Bi vs. DSS GV-Bi	<i>p</i> = 0.443
										DSS Sham vs. DSS GV-Bi	<i>p</i> = 0.001
										H ₂ O Sham vs. H ₂ O GV-Bi	<i>p</i> = 0.423
			Sham	WT	H ₂ O	Male	10	6.05 (2.33, 15.58)		H_2O Sham vs. DSS Sham	<i>p</i> < 0.001
Fig 21	EDM	open arms	GV-Bi	WT	H ₂ O	Male	10	6.25 (1.55, 12.68)	Two-way ANOVA	H ₂ O Sham vs. DSS V-L	<i>p</i> = 0.003
FIB.21	EPIVI	(sec)	Sham	WT	DSS	Male	13	0.40 (0.00, 1.30)	Tukey's Multiple Comparisons test	H ₂ O GV-Bi vs. DSS Sham	<i>p</i> = 0.007
			V-L	WT	DSS	Male	13	1.00 (0.10, 7.50)		H ₂ O GV-Bi vs. DSS V-L	<i>p</i> = 0.152
										DSS Sham vs. DSS V-L	<i>p</i> = 0.512
										H ₂ O Sham vs. H ₂ O SV-Bi	<i>p</i> = 0.860
			Sham	WT	H ₂ O	Male	10	6.05 (2.33, 15.58)	-	H ₂ O Sham vs. DSS Sham	<i>p</i> = 0.021
Fig 21	EDM	open arms	SDV-Bi	WT	H ₂ O	Male	10	9.05 (4.15, 12.50)	Two-way ANOVA	H_2O Sham vs. DSS SDV-Bi	<i>p</i> = 0.993
rig.ji		(sec)	Sham	WT	DSS	Male	13	0.40 (0.00, 1.30)	Tukey's Multiple Comparisons test	H ₂ O SDV-Bi vs. DSS Sham	<i>p</i> = 0.142
			SDV-Bi	WT	DSS	Male	13	5.20 (1.45, 12.85)		H ₂ O SDV-Bi vs. DSS SDV-Bi	<i>p</i> = 0.938
										DSS Sham vs. DSS SDV-Bi	<i>p</i> = 0.022

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	
		closed arms	Sham	WT	H ₂ O	Male	10	79.00 (66.95, 88.78)	
Fig.5J	EPIVI	(sec)	Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)	TWO-Lai

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	<i>p</i> = value
F:- 21		closed arms	Sham	WT	H ₂ O	Male	10	79.00 (66.95, 88.78)		+ 474	
FIg.3J	EPIVI	(sec)	Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)	Two-tailed unpaired student's t-test	$l_{(21)} = 4.74$	<i>p</i> < 0.001
		•					·				
Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
			Sham	WT	H ₂ O	Male	10	79.00 (66.95, 86.78)			
			GV-Bi	WT	H ₂ O	Male	10	72.00 (60.83, 82.48)		DSS x Vagotomy	n = 0.002
			Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)	Two-way ANOVA	$F_{(1,43)} = 10.22$	$\mu = 0.005$
			GV-Bi	WT	DSS	Male	14	80.35 (62.70, 89.93)			
			Sham	WT	H ₂ O	Male	10	79.00 (66.95, 86.78)			
		closed arms	GV-Bi	WT	H ₂ O	Male	10	72.00 (60.83, 82.48)		DSS x Vagotomy	n = 0.116
FIB.51	EPIVI	(sec)	Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)	Two-way ANOVA	$F_{(1,42)} = 2.58$	$\mu = 0.116$
			GV-R	WT	DSS	Male	13	91.00 (82.85, 98.40)	<u>)</u> 8)		
			Sham	WT	H ₂ O	Male	10	79.00 (66.95, 86.78)	36.78) 32.48)DSS x Vagotomy		
			GV-Bi	WT H ₂ O Male 10 72.00 (60.83, 82.48) Two-way ANOVA DSS x		DSS x Vagotomy	n = 0.110				
		Sham V-L	WT	DSS	Male	13	96.00 (90.95, 99.30)) Two-way ANOVA	$F_{(1,42)} = 2.66$	μ 0.110	
			V-L	WT	DSS	Male	13	93.90 (79.35, 96.10)			
			Sham	WT	H ₂ O	Male	10	79.00 (66.95, 86.78)			
			SDV-Bi	WT	H ₂ O	Male	10	78.25 (72.25, 84.75)		DSS x Vagotomy	n < 0.001
			Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)	Two-way ANOVA	$F_{(1,43)} = 14.16$	μ < 0.001
			SDV-Bi	WT	DSS	Male	13	89.20 (74.90, 93.80)			
			Sham	WT	H ₂ O	Male	10	79.00 (66.95, 86.78)			
Eig 21	EDNA	closed arms	SDV-Bi	WT	H ₂ O	Male	10	78.25 (72.25, 84.75)		DSS x Vagotomy	n = 0.016
Fig.5J	EFIVI	(sec)	Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)	Two-way ANOVA	$F_{(1,41)} = 6.31$	p = 0.010
			SDV-R	WT	DSS	Male	12	92.95 (90.13, 96.35)			
			Sham	WT	H ₂ O	Male	10	79.00 (66.95, 86.78)			
			SDV-Bi	WT	H ₂ O	Male	10	78.25 (72.25, 84.75)		DSS x Vagotomy	<i>p</i> = 0.004
			Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)	TWO-WAY ANOVA	$F_{(1,42)} = 9.14$	
			V-L	WT	DSS	Male	13	93.90 (79.35, 96.10)			

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	p = value
										H ₂ O Sham vs. H ₂ O GV-Bi	<i>p</i> = 0.906
			Sham	WT	H ₂ O	Male	10	79.00 (66.95, 86.78)		H₂O Sham vs. DSS Sham	<i>p</i> < 0.001
		closed arms	GV-Bi	WT	H ₂ O	Male	10	72.00 (60.83, 82.48)	Two-way ANOVA	H₂O Sham vs. DSS GV-Bi	<i>p</i> = 0.472
FIB.31	EPIVI	(sec)	Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)	Tukey's Multiple Comparisons test	H_2O GV-Bi vs. DSS Sham	<i>p</i> < 0.001
			GV-Bi	WT	DSS	Male	14	80.35 (62.70, 89.93)		H ₂ O GV-Bi vs. DSS GV-Bi	<i>p</i> = 0.886
										DSS Sham vs. DSS GV-Bi	<i>p</i> = 0.001
										H ₂ O Sham vs. H ₂ O SDV-Bi	p = 0.157
			Sham	WT	H ₂ O	Male	10	79.00 (66.95, 86.78)		H_2O Sham vs. DSS Sham	<i>p</i> < 0.001
		closed arms (sec)	SDV-Bi	WT	H ₂ O	Male	10	78.25 (72.25, 84.75)	Two-way ANOVA	H ₂ O Sham vs. DSS SDV-Bi	<i>p</i> = 0.046
FIB.31	EPIVI		Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)	0) Tukey's Multiple Comparisons test	H ₂ O SDV-Bi vs. DSS Sham	<i>p</i> = 0.008
			SDV-Bi	WT	DSS	Male	13	89.20 (74.90, 93.80)		H ₂ O SDV-Bi vs. DSS SDV-Bi	p = 0.979
										DSS Sham vs. DSS SDV-Bi	<i>p</i> = 0.011
										H ₂ O Sham vs. H ₂ O SDV-Bi	<i>p</i> = 0.025
		√l closed arms (sec)	Sham	WT	H ₂ O	Male	10	79.00 (66.95, 86.78)		H₂O Sham vs. DSS Sham	<i>p</i> < 0.001
			SDV-Bi	WT	H ₂ O	Male	10	78.25 (72.25, 84.75)	86.78)Two-way ANOVA99.30)Tukey's Multiple Comparisons test96.35)	H ₂ O Sham vs. DSS SDV-R	<i>p</i> < 0.001
F18.21	EPIVI		Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)		H ₂ O SDV-Bi vs. DSS Sham	<i>p</i> < 0.001
			SDV-R	WT	DSS	Male	12	92.95 (90.13, 96.35)		H ₂ O SDV-Bi vs. DSS SDV-R	<i>p</i> < 0.001
										DSS Sham vs. DSS SDV-R	<i>p</i> = 0.969

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	p = value
										H ₂ O Sham vs. H ₂ O SV-Bi	<i>p</i> = 0.069
			Sham	WT	H ₂ O	Male	10	79.00 (66.95, 86.78)		H_2O Sham vs. DSS Sham	<i>p</i> < 0.001
Fig 21	Fig.3J EPM C	closed arms	SDV-Bi	WT	H ₂ O	Male	10	78.25 (72.25, 84.75)	34.75)Two-way ANOVA99.30)Tukey's Multiple Comparisons test96.10)	H ₂ O Sham vs. DSS V-L	<i>p</i> < 0.001
FIg.5J		(sec)	Sham	WT	DSS	Male	13	96.00 (90.95, 99.30)		H ₂ O SDV-Bi vs. DSS Sham	<i>p</i> = 0.001
			V-L	WT	DSS	Male	13	93.90 (79.35, 96.10)		H ₂ O SDV-Bi vs. DSS V-L	<i>p</i> = 0.084
										DSS Sham vs. DSS V-L	<i>p</i> = 0.340

Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Dunnett's test	p = value
		SAP-Blank	WT	-	Male	21	0.59 ± 0.04		-	-
	Food intoko (g)	CCK-SAP-Bi	WT	-	Male	21	0.80 ± 0.05	One-way ANOVA (p = 0.016)	SAP-Blank vs. CCK-SAP-Bi	<i>p</i> = 0.001
Fig.4C	FOOD INTAKE (g)	CCK-SAP-R	WT	-	Male	10	0.79 ± 0.05	(<i>p</i> = 0.016)	SAP-Blank vs. CCK-SAP-R	<i>p</i> = 0.015
		CCK-SAP-L	WT	-	Male	10	0.76 ± 0.03		SAP-Blank vs. CCK-SAP-L	<i>p</i> = 0.045

Figure	Ра	arameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
	OFT	total distance	SAP-Blank	WT	H ₂ O	Male	9	33.90 (28.65, 36.55)	Two tailed upperived Student's treat	+ 10	m (0,001
Fig.4D	UFI	(m)	SAP-Blank	WT	DSS	Male	12	18.15 (13.38, 25.73)	Two-talled unpaired Student's t-test	$t_{(19)} = 5.19$	p < 0.001

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	<i>p</i> = value
			SAP-Blank	WT	H ₂ O	Male	9	33.90 (28.65, 36.55)			
			CCK-SAP-Bi	WT	H ₂ O	Male	9	34.10 (30.10, 40.95)		DSS x Nodose CCK-SAP	n = 0.002
			SAP-Blank	WT	DSS	Male	12	18.15 (13.38, 25.73)	Two-way ANOVA	$F_{(1,38)} = 0.28$	p = 0.603
			CCK-SAP	WT	DSS	Male	12	16.85 (12.90, 21.45)			
			SAP-Blank	WT	H ₂ O	Male	9	33.90 (28.65, 36.55)			
	OFT	total distance	CCK-SAP-Bi	WT	H ₂ O	Male	9	34.10 (30.10, 40.95)	3.90 (28.65, 36.55) 4.10 (30.10, 40.95) 8.15 (13.38, 25.73) 8.15 (14.83, 20.90)	DSS x Nodose CCK-SAP $F_{(1,36)} = 0.10$	p = 0.750
FIg.4D	Fig.4D OFT	total distanceCCK-SAP-Bi(m)SAP-BlankCCK-SAP-R	SAP-Blank	WT	DSS	Male	12	18.15 (13.38, 25.73)			
			WT	DSS	Male	10	18.15 (14.83, 20.90)				
			SAP-Blank WT H ₂ O Male 9 33.90 (28.65, 36.55)								
		CC SA	CCK-SAP-Bi	WT	H ₂ O	Male	9	34.10 (30.10, 40.95)		DSS x Nodose CCK-SAP	n = 0.084
			SAP-Blank	WT	DSS	Male	12	18.15 (13.38, 25.73)	, 25.73) Two-way ANOVA	$F_{(1,36)} = 3.16$	<i>p</i> = 0.084
			CCK-SAP-L	WT	DSS	Male	10	12.00 (9.90, 16.33)			

Figure	Pa	arameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
	OFT	time in center	SAP-Blank	WT	H ₂ O	Male	9	9.10 (4.60, 15.95)	Two tailed warsings (Student's t test	t(10) - 1 27	n < 0.001
Fig.4E	UFI	(sec)	SAP-Blank	WT	DSS	Male	12	1.80 (0.60, 3.98)	i wo-talled unpaired Student's t-test	$l_{(19)} = 4.27$	p < 0.001

Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
		SAP-Blank	WT	H ₂ O	Male	9	9.10 (4.60, 15.95)			
		CCK-SAP-Bi	WT	H ₂ O	Male	9	7.90 (6.25, 14.55)		DSS x Nodose CCK-SAP	n = 0.110
		SAP-Blank	WT	DSS	Male	12	1.80 (0.60, 3.98)	TWO-WAY ANOVA	$F_{(1,38)} = 2.68$	p = 0.110
		CCK-SAP	WT	DSS	Male	12	1.60 (0.60, 3.35)			
		SAP-Blank	WT	H ₂ O	Male	9	9.10 (4.60, 15.95)			
Fig /F	time in center	CCK-SAP-Bi	WT	H ₂ O	Male	9	1.80 (0.60, 3.98) 1.00 (0.60, 3.98) 1.60 (0.60, 3.35) 9.10 (4.60, 15.95) 7.90 (6.25, 14.55) Two-way ANOVA 1.80 (0.60, 3.98) 1.35 (0.38, 2.85) 9.10 (4.60, 15.95) 9.10 (4.60, 15.95)	DSS x Nodose CCK-SAP	n = 0.119	
FIG.4C	(sec)	SAP-Blank	WT	DSS	Male	12	1.80 (0.60, 3.98)	I wo-way ANOVA	$F_{(1,36)} = 2.55$	p = 0.119
		CCK-SAP-R	WT	DSS	Male	10	1.35 (0.38, 2.85)			
		SAP-Blank	WT	H ₂ O	Male	9	9.10 (4.60, 15.95)			
		CCK-SAP-Bi	WT	H ₂ O	Male	9	7.90 (6.25, 14.55)	5, 14.55) Two-way ANOVA DSS x No 50, 3.98) F(1)	DSS x Nodose CCK-SAP	n = 0.116
		SAP-Blank	WT	DSS	Male	12	1.80 (0.60, 3.98)		$F_{(1,36)} = 2.59$	<i>p</i> = 0.116
		CCK-SAP-L	WT	DSS	Male	10	1.95 (0.55, 3.00)			

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
		duration	SAP-Blank	WT	H ₂ O	Male	9	33.50 (22.90, 40.75)	Mann M/hitnov/11 tast		n < 0.001
Fig.4F	LDB	(sec)	SAP-Blank	WT	DSS	Male	12	3.90 (0.00, 9.50)	Wann-Whitney O test	-	<i>ρ</i> < 0.001

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
			SAP-Blank	WT	H ₂ O	Male	9	33.50 (22.90, 40.75)			
			CCK-SAP-Bi	WT	H ₂ O	Male	9	36.30 (16.85, 39.10)		'ADSS x Nodose CCK-SAP $F_{(1,38)} = 35.09$ 'ADSS x Nodose CCK-SAP $F_{(1,36)} = 2.31$ /ADSS x Nodose CCK-SAP $F_{(1,36)} = 2.57$	a (0.001
			SAP-Blank	WT	DSS	Male	12	3.90 (0.00, 9.50)	Two-way ANOVA	$F_{(1,38)} = 35.09$	<i>p</i> < 0.001
			CCK-SAP	WT	DSS	Male	12	42.60 (27.80, 50.38)			
			SAP-Blank	WT	H ₂ O	Male	9	33.50 (22.90, 40.75)			
	Fig.4F LDB	duration	CCK-SAP-Bi	WT	/T H ₂ O Male 9 36.30 (16.85, 39.10)		DSS x Nodose CCK-SAP	n = 0.127			
FIg.4F		(sec)	(sec) SAP-Blank WT DSS Male 57 50.50 (10.85, 55.10)	Two-way ANOVA	$F_{(1,36)} = 2.31$	p = 0.137					
		CCK-SAP-R WT DSS Male 12 S.90 (0.00, 9.50) SAP-Blank WT DSS Male 10 9.50 (0.75, 18.75) SAP-Blank WT H ₂ O Male 9 33.50 (22.90, 40.75)	CCK-SAP-R	WT	DSS	Male	10	9.50 (0.75, 18.75)			
			CCK-SAP-Bi	WT	H ₂ O	Male	9	36.30 (16.85, 39.10)	B0, 40.75) DSS x Nodose CCK-SA 85, 39.10) Two-way ANOVA 90, 9.50) F _(1,36) = 2.57	DSS x Nodose CCK-SAP	n = 0.110
			SAP-Blank	WT	DSS	Male	12	3.90 (0.00, 9.50)		$F_{(1,36)} = 2.57$	<i>p</i> = 0.118
			CCK-SAP-L	WT	DSS	Male	10	9.45 (0.53, 19.05)			

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	p = value
										H ₂ O SAP-B vs. H ₂ O CCK-SAP	<i>p</i> = 0.841
			SAP-Blank	WT	H ₂ O	Male	9	33.50 (22.90, 40.75)		H ₂ O SAP-B vs. DSS SAP-B	<i>p</i> < 0.001
	Fig.4F LDB duration (sec)	LDB duration (sec)	CCK-SAP-Bi	WT	H ₂ O	Male	9	36.30 (16.85, 39.10)	.10) Two-way ANOVA 0) Tukey's Multiple Comparisons test	H ₂ O SAP-B vs. DSS CCK-SAP	<i>p</i> = 0.681
rig.4r			SAP-Blank	WT	DSS	Male	12	3.90 (0.00, 9.50)		H ₂ O CCK-SAP vs. DSS SAP-B	<i>p</i> < 0.001
			CCK-SAP	WT	DSS	Male	12	42.60 (27.80, 50.38)		H ₂ O CCK-SAP vs. DSS CCK-SAP	<i>p</i> = 0.205
										DSS SAP-B vs. DSS CCK-SAP	<i>p</i> < 0.001

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
Fig 4C		ontrioc	SAP-Blank	WT	H ₂ O	Male	9	8.50 (3.00, 12.00)	Two tailed uppaired Student's t test	+ - 4.08	m < 0.001
FIg.4G	LDB	entries	SAP-Blank	WT	DSS	Male	12	1.00 (0.00, 3.00)	Two-talled unpaired student's t-test	$l_{(19)} = 4.98$	p < 0.001

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
			SAP-Blank	WT	H ₂ O	Male	9	8.50 (3.00, 12.00)			
			CCK-SAP-Bi	WT	H ₂ O	Male	9	7.00 (5.00, 11.00)		DSS x Nodose CCK-SAP	m 0.000
			SAP-Blank	WT	DSS	Male	12	1.00 (0.00, 3.00)	Two-way ANOVA	F _(1,38) = 8.53	p = 0.006
			CCK-SAP	WT	DSS	Male	12	8.00 (6.00, 10.00)			
			SAP-Blank	WT	H ₂ O	Male	9	8.50 (3.00, 12.00)			
	Fig.4G LDB	entries	CCK-SAP-Bi	WT	H ₂ O	Male	9	7.00 (5.00, 11.00)	Two-way ANOVA	DSS x Nodose CCK-SAP F _(1,36) = 0.004	p = 0.948
FIg.4G			SAP-Blank	WT	DSS	Male	12	1.00 (0.00, 3.00)			
			CCK-SAP-R	WT	DSS	Male	10	0.75 (0.00, 2.50)			
			SAP-Blank	WT	H ₂ O	Male	9	8.50 (3.00, 12.00)			
			CCK-SAP-Bi	WT	H ₂ O	Male	9	7.00 (5.00, 11.00)		DSS x Nodose CCK-SAP	m 0.02C
			SAP-Blank	WT	DSS	Male	12	1.00 (0.00, 3.00)	.00) Two-way ANOVA	$F_{(1,36)} = 0.008$	p = 0.926
			CCK-SAP-L	WT	DSS	Male	10	0.75 (0.00, 3.00)			

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	p = value
										H ₂ O SAP-B vs. H ₂ O CCK-SAP	p = 0.995
Fig 4G		optrios	SAP-Blank	WT	H ₂ O	Male	9	H2O S 8.50 (3.00, 12.00) Two-way ANOVA H2O S 7.00 (5.00, 11.00) Tukey's Multiple Comparisons test H2O S	H ₂ O SAP-B vs. DSS SAP-B	<i>p</i> < 0.001	
Fig.40	Fig.4G LDB	entries	CCK-SAP-Bi	WT	H ₂ O	Male	9	7.00 (5.00, 11.00))	H ₂ O SAP-B vs. DSS CCK-SAP	p = 0.722
			SAP-Blank	WT	DSS	Male	12	1.00 (0.00, 3.00)		H ₂ O CCK-SAP vs. DSS SAP-B	<i>p</i> < 0.001

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	p = value
Fig 4G		antriaa	CCK-SAP	WT	DSS	Male	12	8.00 (6.00, 10.00)		H ₂ O CCK-SAP vs. DSS CCK-SAP	p = 0.559
Fig.4G	LDB	entries								DSS SAP-B vs. DSS CCK-SAP	<i>p</i> < 0.001

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
Fig 4H		total distance	SAP-Blank	WT	H ₂ O	Male	9	11.80 (9.30, 14.60)	Two tailed uppaired Student's t test	+ _ 4.08	n = 0.020
Fig.4H	EPIVI	(m)	SAP-Blank	WT	DSS	Male	12	8.65 (5.63, 10.45)	Two-talled unparted student's t-test	$t_{(19)} = 4.98$	p = 0.036

Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
		SAP-Blank	WT	H ₂ O	Male	9	11.80 (9.30, 14.60)			
		CCK-SAP-Bi	WT	H ₂ O	Male	9	13.50 (10.50, 17.90)		DSS x Nodose CCK-SAP	n = 0.100
		SAP-Blank	WT	DSS	Male	12	8.65 (5.63, 10.45)	TWO-WAY ANOVA	$F_{(1,38)} = 1.71$	p = 0.198
		CCK-SAP	WT	DSS	Male	12	12.45 (10.78, 19.38)			
		SAP-Blank	WT	H ₂ O	Male	9	11.80 (9.30, 14.60)			
	EPM total distance (m)	CCK-SAP-Bi	WT	H ₂ O	Male	9	13.50 (10.50, 17.90)		DSS x Nodose CCK-SAP	n = 0.002
FIg.4H	EPIVI (m)	SAP-Blank	WT	WI H2O Male 9 WT DSS Male 12 WT DSS Male 12 WT DSS Male 9 WT H2O Male 9 WT H2O Male 9 WT H2O Male 9 WT DSS Male 12 WT DSS Male 9 WT DSS Male 12 WT DSS Male 12 WT H2O Male 9 WT DSS Male 12	8.65 (5.63, 10.45)	Two-way ANOVA	$F_{(1,36)} = 3.72$	p = 0.062		
		CCK-SAP-R	WT	DSS	Male	10	4.30 (3.80, 6.28)	Two-way ANOVA DSS x Nodose CCK-SAP F(1,36) = 3.72		
		SAP-Blank	WT	H ₂ O	Male	9	11.80 (9.30, 14.60)			
		CCK-SAP-Bi	WT	H ₂ O	Male	9	13.50 (10.50, 17.90)	The ANOVA	DSS x Nodose CCK-SAP	- 0.011
		SAP-Blank	WT	DSS	Male	12	8.65 (5.63, 10.45)	i wo-way ANOVA	$F_{(1,36)} = 7.14$	<i>p</i> = 0.011
		CCK-SAP-L	WT	DSS	Male	10	4.15 (2.70, 5.43)			

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
Fig. 41		open arms	SAP-Blank	WT	H ₂ O	Male	9	1.80 (0.05, 3.75)	Two tailed uppaired Student's t test	+ - 2.10	m = 0.050
Fig.4i	EPIVI	(sec)	SAP-Blank	WT	DSS	Male	12	0.40 (0.15, 0.75)	Two-talled unpared student's t-test	$l_{(19)} = 2.10$	p = 0.050

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	p = value
			SAP-Blank	WT	H ₂ O	Male	9	1.80 (0.05, 3.75)			
			CCK-SAP-Bi	WT	H ₂ O	Male	9	2.40 (0.85, 8.50)		DSS x Nodose CCK-SAP	n = 0.002
			SAP-Blank	WT	DSS	Male	12	0.40 (0.15, 0.75)	TWO-Wdy ANOVA	$F_{(1,38)} = 10.07$	p = 0.005
			CCK-SAP	WT	DSS	Male	12	8.15 (3.53, 12.68)			
			SAP-Blank	WT	H ₂ O	Male	9	1.80 (0.05, 3.75)			
Fig 41		open arms	CCK-SAP-Bi	WT	H ₂ O	Male	<u>9</u> 1.80 (0.05, 3.75) <u>9</u> 2.40 (0.85, 8.50) <u>12</u> 0.40 (0.15, 0.75) Two-way ANOVA	DSS x Nodose CCK-SAP	n = 0.276		
Fig.4I EF	EPIVI	(sec)	SAP-Blank	WT	DSS	Male	12	0.40 (0.15, 0.75)	TWO-Wdy ANOVA	ay ANOVADSS x Nodose CCK-SAP $F_{(1,38)} = 10.07$ ay ANOVADSS x Nodose CCK-SAP $F_{(1,36)} = 1.23$ ay ANOVADSS x Nodose CCK-SAP $F_{(1,36)} = 1.85$	<i>p</i> = 0.276
			CCK-SAP-R	WT	DSS	Male	10	0.80 (0.38, 2.00)	$\frac{5}{0}$ F(1,36) = 1.23		
			SAP-Blank	WT	H ₂ O	Male	9	1.80 (0.05, 3.75)		F(1,36) = 1.23	
			CCK-SAP-Bi	WT	H ₂ O	Male	9	2.40 (0.85, 8.50)		DSS x Nodose CCK-SAP	n = 0.192
			SAP-Blank	WT	DSS	Male	12	0.40 (0.15, 0.75)	0.75) Two-way ANOVA	$F_{(1,36)} = 1.85$	<i>p</i> = 0.182
			CCK-SAP-L	WT	DSS	Male	10	0.15 (0.00, 2.80)			

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	p = value
										H ₂ O SAP-B vs. H ₂ O CCK-SAP	<i>p</i> = 0.857
			SAP-Blank	WT	H ₂ O	Male	9	1.80 (0.05, 3.75)		H ₂ O SAP-B vs. DSS SAP-B	<i>p</i> = 0.063
	Fig.4I EPM open arms (sec)	open arms	CCK-SAP-Bi	WT	H ₂ O	Male	9	2.40 (0.85, 8.50)	50)Two-way ANOVA75)Tukey's Multiple Comparisons test68)	H ₂ O SAP-B vs. DSS CCK-SAP	<i>p</i> = 0.719
FIB.41		(sec)	SAP-Blank	WT	DSS	Male	12	0.40 (0.15, 0.75)		H ₂ O CCK-SAP vs. DSS SAP-B	<i>p</i> = 0.319
			CCK-SAP	WT	DSS	Male	12	8.15 (3.53, 12.68)		H ₂ O CCK-SAP vs. DSS CCK-SAP	<i>p</i> = 0.245
										DSS SAP-B vs. DSS CCK-SAP	<i>p</i> = 0.002

Figure	Par	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
Fig. 41		closed arms	SAP-Blank	WT	H ₂ O	Male	9	86.00 (77.15, 92.20)	Two tailed uppaired Student's t test	$t_{(10)} = 3.34$	n = 0.002
FIB.41	EPIVI	(sec)	SAP-Blank	WT	DSS	Male	12	93.05 (91.05, 94.73)	i wo-talled unpailed Student's t-test	ι(19) – 3.34	$\mu = 0.003$

Figure	Par	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Fixed effects F(DFn,DFd)	<i>p</i> = value
			SAP-Blank	WT	H ₂ O	Male	9	86.00 (77.15, 92.20)			
			CCK-SAP-Bi	WT	H ₂ O	Male	9	77.20 (70.70, 86.25)		DSS x Nodose CCK-SAP	n = 0.009
			SAP-Blank	WT	DSS	Male	12	93.05 (91.05, 94.73)	Two-way ANOVA	F _(1,38) = 7.72	p = 0.008
			CCK-SAP	WT	DSS	Male	12	78.45 (68.35, 85.48)			
			SAP-Blank	WT	H ₂ O	Male	9	86.00 (77.15, 92.20)			
	Fig.4J EPM	closed arms (sec)	CCK-SAP-Bi	WT	H ₂ O	Male	9	77.20 (70.70, 86.25)	5) 3) Two-way ANOVA	DSS x Nodose CCK-SAP	<i>p</i> = 0.974
FIg.4J			SAP-Blank	WT	DSS	Male	12	93.05 (91.05, 94.73)		$F_{(1,36)} = 0.001$	
			CCK-SAP-R	WT	DSS	Male	10	94.25 (89.20, 95.78)			
		-	SAP-Blank	WT	H ₂ O	Male	9	86.00 (77.15, 92.20)			
			CCK-SAP-Bi	WT	H ₂ O	Male	9	77.20 (70.70, 86.25)		DSS x Nodose CCK-SAP	n = 0.002
		SAP-Blank	WT	DSS	Male	12	93.05 (91.05, 94.73)	J4.73) Two-way ANOVA	$F_{(1,36)} = 0.002$	<i>p</i> = 0.962	
			CCK-SAP-L	WT	DSS	Male	10	96.05 (91.48, 98.38)			

Figure	Para	ameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	Compared Groups	p = value
										H ₂ O SAP-B vs. H ₂ O CCK-SAP	<i>p</i> > 0.999
			SAP-Blank	WT	H ₂ O	Male	9	86.00 (77.15, 92.20)		H ₂ O SAP-B vs. DSS SAP-B	<i>p</i> = 0.001
		EPM closed arms (sec)	CCK-SAP-Bi	WT	H ₂ O	Male	9	77.20 (70.70, 86.25)	36.25)Two-way ANOVA34.73)Tukey's Multiple Comparisons test35.48)	H ₂ O SAP-B vs. DSS CCK-SAP	<i>p</i> = 0.940
FIg.4J	Fig.4J EPM		SAP-Blank	WT	DSS	Male	12	93.05 (91.05, 94.73)		H ₂ O CCK-SAP vs. DSS SAP-B	<i>p</i> = 0.011
			CCK-SAP	WT	DSS	Male	12	78.45 (68.35, 85.48)		H ₂ O CCK-SAP vs. DSS CCK-SAP	<i>p</i> = 0.933
										DSS SAP-B vs. DSS CCK-SAP	<i>p</i> < 0.001

Figure	Parameter	Brain region	Test specifications	Genotype	Treatment	Sex	Number (sections)	Mean ± SEM	Statistical test	t-distribution t, df	p = value
Fig 5R	c-Fos	NITS	H2O	WT	-	Male	5 (37)	3.58 ± 0.48	Two tailed uppaired Student's t test	$t_{c} = 2.20$	n < 0.001
TIg.JD	neurons	6171	DSS	WT	-	Male	5 (43)	13.02 ± 0.95		$C_{(8)} = 0.05$	p < 0.001
Fig 5D	c-Fos		H2O	WT	-	Male	5 (21)	19.92 ± 2.10	Two tailed uppaired Student's t test	t = 11 92	p < 0.001
FIg.3D	neurons	LC	DSS	WT	-	Male	5 (26)	61.14 ± 2.78	Two-talled dripalled student's t-test	l(8) - 11.85	p < 0.001
	c-Fos		H2O	WT	-	Male	5 (39)	9.16 ± 1.42	Two tailed uppaired Student's t test	+ _ 2.01	n = 0.017
FIB.SF	Fig.5F neurons	BLA –	DSS	WT	-	Male	5 (35)	14.62 ± 1.13	Two-tailed unpaired Student's t-test	$l_{(8)} = 3.01$	p = 0.017

Figure	Pa	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	<i>p</i> = value
Fig 7C		total distance	Saline	DBH-Cre	DSS	Male	10	22.65 (10.79, 28.70)	Two tailed uppaired Student's t test	t 0.4F	
Fig.7C	OFT	(m)	CNO	DBH-Cre	DSS	Male	10	24.49 (20.90, 30.98)	Two-talled unpaired student's t-test	$t_{(18)} = 0.45$	$\mu = 0.050$
	UFI	time in center	Saline	DBH-Cre	DSS	Male	10	1.65 (0.35, 5.38)	Two tailed waranized Student's thest	+ 2.24	m 0.001
Fig. /D		(sec)	CNO	DBH-Cre	DSS	Male	10	8.10 (7.00, 13.28)	Two-tailed unpaired Student's t-test	test t ₍₁₈₎ = 3.34	<i>p</i> = 0.004

Figure	Ра	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
Fig 7F		duration	Saline	DBH-Cre	DSS	Male	10	29.00 (20.75, 46.50)	Two tailed uppaired Student's t test	t 2.00	n = 0.000
FIg.7E		(sec)	CNO	DBH-Cre	DSS	Male	10	53.50 (44.00, 62.00)	Two-talled unpaired student's t-test	$l_{(18)} = 3.09$	p = 0.006
Fig 7F	LDB	optrios	Saline	DBH-Cre	DSS	Male	10	6.50 (5.00, 9.25)	Two tailed uppaired Student's t test	+ _ 2.25	n = 0.004
Fig. /F	entries	CNO	DBH-Cre	DSS	Male	10	13.00 (8.50, 18.00)	Two-talled unpaired student's t-test	$t_{(18)} - 5.25$	ρ = 0.004	
Fig 7C		total distance	Saline	DBH-Cre	DSS	Male	10	7.61 (6.73, 11.94)	Two tailed uppaired Student's t test	+	n = 0.01
Fig.7G		(m)	CNO	DBH-Cre	DSS	Male	10	11.54 (8.48, 20.31)	Two-tailed unpaired student's t-test	$l_{(18)} = 2.12$	p = 0.04
C:- 711	EPIVI	open arms	Saline	DBH-Cre	DSS	Male	10	6.90 (0.73 <i>,</i> 15.70)		± 2.70	- 0.012
Fig. /H	(sec)	CNO	DBH-Cre	DSS	Male	10	21.45 (9.63, 42.85)	Two-tailed unpaired Student's t-test 2.85)	$l_{(18)} = 2.78$	p = 0.012	

Figure	Parameter		Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
		EPM closed arms	Saline	DBH-Cre	DSS	Male	10	74.95 (53.73, 87.48)) Two tailed uppaired Student's t test	+(18) - 2.02	n = 0.057
Fig. / I	EPIVI	(sec)	CNO	DBH-Cre	DSS	Male	10	53.95 (35.80, 81.05)	Two-talled unpaired student's t-test	l(18) = 2.03	p = 0.057

Figure	Р	arameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
Supplementary		Number of	H ₂ O	WT	-	Male	13	44.0 (39.50, 61.00)	Two tailed warmained Chudant's t test	+	n (0.001
Fig.1B	ÛF	rearings	DSS	WT	-	Male	12	18.0 (10.75, 22.00)	Two-tailed unpaired student's t-test	$l_{(23)} = 0.00$	<i>p</i> < 0.001
Supplementary		Number of nose	H ₂ O	WT	-	Male	13	5.0 (4.00, 7.00)	Two tailed warsing of Chudent's theat	+ 0.69	m 0.504
Fig.1C	LDR	pokes	DSS	WT	-	Male	12	4.0 (2.25, 6.75)	I wo-tailed unpaired Student's t-test	$t_{(23)} = 0.68$	p = 0.504
Supplementary		Number of	H ₂ O	WT	-	Male	13	14.0 (10.50, 16.00)	Mann Whitney II test		n < 0.001
Fig.1D	EPIVI	rearings	DSS	WT	-	Male	12	4.0 (1.25, 6.75)	Mann-whitney 0 test	-	p < 0.001
Supplementary	FDN	Number of	H ₂ O	WT	-	Male	13	9.0 (8.00, 12.00)	Two-tailed unpaired Student's t-test	$t_{res} = 5.46$	n < 0.001
Fig.1E		stretches	DSS	WT	-	Male	12	3.5 (2.00, 5.75)		t ₍₂₃₎ – 5.40	ρ<0.001
Supplementary	OE	Number of	Sham	WT	DSS	Male	13	7.0 (2.00, 11.50)	Two tailed uppaired Student's t test	$t_{\rm (ec)} = 4.44$	n < 0.001
Fig.1F	01	rearings	GV-Bi	WT	DSS	Male	14	21.5 (16.50, 29.25)	Two-tailed unpailed student's t-test	C(25) = 4.44	p < 0.001
Supplementary	חחו	Number of nose	Sham	WT	DSS	Male	13	4.0 (2.00, 5.00)	Two tailed uppaired Student's t test	t 0.24	n = 0.911
Fig.1G	LDB	pokes	GV-Bi	WT	DSS	Male	14	4.0 (3.00, 6.00)	Two-talled unparred student's t-test	$l_{(25)} = 0.24$	p = 0.811
Supplementary		Number of	Sham	WT	DSS	Male	13	2.0 (0.00, 4.50)	Two tailed uppaired Student's t test	+ – E 70	n < 0.001
Fig.1H	EPIVI	rearings	GV-Bi	WT	DSS	Male	14	13.5 (7.50, 16.50)	Two-talled unpaired student's t-test	$t_{(25)} = 5.79$	p < 0.001
Supplementary	FDN	Number of	Sham	WT	DSS	Male	13	4.0 (1.00, 4.00)	Two-tailed unpaired Student's t-test	$t_{(25)} = 4.47$	n < 0.001
Fig.1I		stretches	GV-Bi	WT	DSS	Male	14	6.0 (5.00, 9.50)		C(25) - 4.47	<i>p</i> < 0.001
Supplementary	OE	Number of	SAP-Blank	WT	DSS	Male	12	14.5 (5.50, 20.75)	Two tailed uppaired Student's t test	$t_{cov} = 2.05$	n < 0.001
Fig.1J	01	rearings	CCK-SAP	WT	DSS	Male	12	26.0 (14.25, 39.25)	Two-tailed unpailed student's t-test	$t_{(22)} = 2.95$	p < 0.001
Supplementary		Number of nose	SAP-Blank	WT	DSS	Male	12	3.0 (0.25, 5.25)	Two tailed warsing of Chudent's theat	+ 0.21	n 0.700
Fig.1K	LDR	pokes	CCK-SAP	WT	DSS	Male	12	2.5 (1.25, 5.75)	Two-tailed unpaired student's t-test	$l_{(22)} = 0.31$	p = 0.760
Supplementary		Number of	SAP-Blank	WT	DSS	Male	12	1.5 (1.00, 3.75)	Two tailed warmained Chudentlat test	+ 4.20	n (0.001
Fig.1L	EPIVI	rearings	CCK-SAP	WT	DSS	Male	12	8.0 (6.00, 13.00)	i wo-talled unpaired Student's t-test	$l_{(22)} = 4.30$	<i>p</i> < 0.001
Supplementary		Number of	SAP-Blank	WT	DSS	Male	12	3.0 (2.00, 6.50)	Two tailed uppaired Student's t test	t() - 5 1/	p < 0.001
Fig.1M	ELIN	stretches	CCK-SAP	WT	DSS	Male	12	9.5 (7.00, 14.25)	i wo-talleu unpaileu student sit-test	L(22) - 5.14	$\mu < 0.001$

Figure	Ра	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	p = value
Supplementary		(al threads ald (a)	H2O	WT	-	Male	10			Time x DSS	m < 0.001
Fig.2B	withdraw	/ai threshold (g)	DSS	WT	-	Male	10	-	Two-way RIVI ANOVA	$F_{(9,162)} = 5.68$	<i>p</i> < 0.001
Figure	Ра	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	<i>p</i> = value
Supplementary	NCE	Latency to eat	H2O	WT	-	Male	10	134.5 (99.50, 239.3)	Two tailed warmained Chudent's t test	+ 1	m 0.048
Fig.2C	INSF	(sec)	DSS	WT	-	Male	10	240.5 (173.5, 357.8)	Two-talled unpaired student's t-test	$L_{(18)} = 2.12$	<i>p</i> = 0.048
Supplementary		total distance	H2O	WT	-	Male	10	25.65 (20.93, 29.98)		+ 170	
Fig.2D	HCA (m)		DSS	WT	-	Male	10	18.90 (14.38, 25.00)	Two-tailed unpaired Student's t-test	$t_{(18)} = 1.78$	<i>p</i> = 0.093
Figure	Ра	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	<i>p</i> = value
Supplementary			Sham	WT	DSS	Male	9			Time x DSS	
Fig.2E	withdraw	/ai threshold (g)	GV	WT	DSS	Male	9	-	Two-way RIVI ANOVA	$F_{(9,144)} = 1.06$	p = 0.393
Figure	Ра	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	<i>p</i> = value
Supplementary		Latency to eat	Sham	WT	DSS	Male	9	197.0 (144.0, 371.5)			m 0.00C
Fig.2F	NSF	(sec)	GV	WT	DSS	Male	9	117.0 (100.5, 138.0)	Mann-whitney O test	-	p = 0.006
Supplementary	total distance	Sham	WT	DSS	Male	9	13.50 (8.95, 16.50)	95, 16.50)	t 0.10	n - 0.860	
Fig.2G	HCA	(m)	GV	WT	DSS	Male	9	11.50 (8.50, 17.70)	i wo-talled unpaired Student S t-test	$l_{(16)} = 0.18$	<i>p</i> = 0.860

Figure	Par	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	p = value
Supplementary	W/ithdraw	al thrachold (a)	SAP-Blank	WT	DSS	Male	5			Time x DSS	n = 0.777
Fig.2H	Withdrawai threshold (g)		CCK-SAP	WT	DSS	Male	5	-	Two-way Rivi ANOVA	$F_{(9,72)} = 0.62$	p = 0.777
Figure	Par	rameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Median (Q1,Q3)	Statistical test	t-distribution t, df	p = value
Supplementary	ИСГ	Latency to eat	SAP-Blank	WT	DSS	Male	5	166.0 (149.5, 499.0)	Two tailed uppaired Student's t test	t 2 10	r = 0.050
Fig.21	INSF	(sec)	CCK-SAP	WT	DSS	Male	5	103.0 (88.00, 120.0)	Two-talled unpaired student's t-test	$l_{(18)} = 2.19$	p = 0.059
Supplementary Fig.2J	HCA	total distance (m)	SAP-Blank	WT	DSS	Male	5	11.30 (8.75, 15.90)	Two-tailed unpaired Student's t-test	t ₍₁₈₎ = 0.42	<i>p</i> = 0.683

Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	p = value
		Sham	WT	DSS	Male	9			T: Doc	
	Body weight	GV	WT	DSS	Male	9	-	Two-way RM ANOVA	Time x DSS	<i>p</i> = 0.017
FIg.3D		SDV	WT	DSS	Male	9			F(14,168) - 2.05	
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Compared Groups	p = value
		Sham	WT	DSS	Male	9			Sham DSS vs. GV DSS	<i>p</i> = 0.113
	Body weight	GV	WT	DSS	Male	9	-	Tukey's Multiple Comparisons test	Sham DSS vs. SDV DSS	<i>p</i> = 0.547
Tig.30		SDV	WT	DSS	Male	9			GV DSS vs. SDV DSS	<i>p</i> = 0.642
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Tukey's Multiple Comparisons	p = value
Cumulantantan		Sham	WT	DSS	Male	9	5.90 ± 0.25		Sham DSS vs. GV DSS	<i>p</i> = 0.026
	Colon length (cm)	GV	WT	DSS	Male	9	5.17 ± 0.13	(n < 0.001)	Sham DSS vs. SDV DSS	<i>p</i> < 0.001
Fig.3D		SDV	WT	DSS	Male	9	4.48 ± 0.15	(<i>p</i> < 0.001)	GV DSS vs. SDV DSS	<i>p</i> = 0.038
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Tukey's Multiple Comparisons	p = value
Cumulantantan		Sham	WT	DSS	Male	9	38.44 ± 0.77		Sham DSS vs. GV DSS	<i>p</i> = 0.740
	Intestine length (cm)	GV	WT	DSS	Male	9	36.82 ± 0.80	(n < 0.001)	Sham DSS vs. SDV DSS	<i>p</i> < 0.001
TIB.3L	·	SDV	WT	DSS	Male	9	27.63 ± 2.43	(<i>p</i> < 0.001)	GV DSS vs. SDV DSS	<i>p</i> < 0.001
Cumplementer		Sham	WT	DSS	Male	4	5.00 ± 0.41	Knuckel Mellie test		
Supplementary	Histological score	GV	WT	DSS	Male	4	5.50 ± 0.50	(n = 0.430)	-	-
TIB.51		SDV	WT	DSS	Male	4	5.75 ± 0.25	(p -0.430)		
Cumplementer		Sham	WT	DSS	Male	9	0.15 ± 0.05	Knuckel Mellie test		
	Spleen weight (g)	GV	WT	DSS	Male	9	0.19 ± 0.09	(p = 0.059)	-	-
Fig.50		SDV	WT	DSS	Male	9	0.16 ± 0.01	(p =0.055)		
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Tukey's Multiple Comparisons	p = value
Cumplementer		Sham	WT	DSS	Male	9	2.78 ± 0.51	Knuckel Mellie test	Sham DSS vs. GV DSS	p > 0.999
	FITC-Dextran (ng/ml)	GV	WT	DSS	Male	9	2.00 ± 0.28	(n = 0.004)	Sham DSS vs. SDV DSS	<i>p</i> =0.047
1 lg.311		SDV	WT	DSS	Male	9	21.33 ± 6.29	(p -0.004)	GV DSS vs. SDV DSS	<i>p</i> =0.004
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	p = value
Cumplementer		Sham	WT	DSS	Male	9				
	Disease activity index	GV	WT	DSS	Male	9	-	(n < 0.001)	$F_{(40,245)} = 3.96$	<i>p</i> = 0.017
TIB:21	·Ig.31 ,	SDV	WT	DSS	Male	9		(<i>p</i> < 0.001)	1 (18,216) = 3.50	
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Compared Groups	<i>p</i> = value
Supplomenter		Sham	WT	DSS	Male	9			Sham DSS vs. GV DSS	<i>p</i> = 0.331
	Disease activity index	GV	WT	DSS	Male	9	-	Tukey's Multiple Comparisons test	Sham DSS vs. SDV DSS	<i>p</i> = 0.479
Fig.3I		SDV	WT	DSS	Male	9			GV DSS vs. SDV DSS	<i>p</i> = 0.989

Figure	Parameter	Brain region	Test specifications	Genotype	Treatment	Sex	Number (sections)	Mean ± SEM	Statistical test	t-distribution t, df	p = value
Supplementary	c-Fos	ΝΤς	B-SAP	WT	-	Male	5 (26)	33.70 ± 1.12	Two tailed uppaired Student's t test	t	n = 0.002
Fig.4D	neurons	CTNT	CCK-SAP	WT	-	Male	5 (21)	23.36 ± 1.95		$t_{(8)} = 4.00$	p = 0.002

Figure	Parameter	Brain region	Test specifications	Genotype	Treatment	Sex	Number (sections)	Mean ± SEM	Statistical test	t-distribution t, df	p = value
Supplementary	FG ⁺	Nodoso Conglion	B-SAP	WT	-	Male	5	9.63 ± 0.68	Two tailed uppaired Student's t test	t(a) = 1.66	n = 0.002
Fig.4G	neurons	Vodose Ganglion	CCK-SAP	WT	-	Male	5	6.75 ± 0.65	Two-talled unpailed student's t-test	$t_{(8)} = 4.00$	<i>p</i> = 0.002
Supplementary	FG ⁺		B-SAP	WT	-	Male	5 (24)	38.52 ± 3.83	Two tailed uppaired Student's t test	+ - 0.28	$n = 0.79\Gamma$
Fig.4J	neurons	DMV	CCK-SAP	WT	-	Male	5 (21)	36.46 ± 6.19	Two-tailed unpaired Student's t-test	t t ₍₈₎ = 0.28	p = 0.785

Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	p = value
Supplementary	Podywoight	SAP-Blank	WT	DSS	Male	5			Time x DSS	n = 0.504
Fig.5B	bouy weight	CCK-SAP	WT	DSS	Male	5	-	Two-way KIVI ANOVA	$F_{(7,56)} = 0.91$	μ – 0.504
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	t-distribution t, df	p = value
Supplementary	Colon longth (cm)	SAP-Blank	WT	DSS	Male	5	5.10 ± 0.29	Two tailed uppaired Student's t test	t = 0.20	n = 0.771
Fig.5D	Colon length (cm)	CCK-SAP	WT	DSS	Male	5	4.98 ± 0.27	Two-talled unparted student's t-test	$l_{(8)} = 0.30$	p = 0.771
Supplementary	Intecting longth (am)	SAP-Blank	WT	DSS	Male	5	34.14 ± 0.72	Two tailed uppaired Student's t test	t 1.01	n = 0.242
Fig.5E	intestine length (cm)	CCK-SAP	WT	DSS	Male	5	33.26 ± 0.49	Two-talled unparted student's t-test	$l_{(8)} = 1.01$	p = 0.342
Supplementary	Spleen weight (g)	SAP-Blank	WT	DSS	Male	5	0.14 ± 0.02	Two tailed uppaired Student's t test	+ -0.20	n = 0.700
Fig.5F		CCK-SAP	WT	DSS	Male	5	0.13 ± 0.02	Two-tailed unpaired Student's t-te	$L_{(8)} = 0.39$	p = 0.709
Supplementary	Listological score	SAP-Blank	WT	DSS	Male	5	4.40 ± 0.51	Two tailed uppaired Student's t test	t 0 5 2	n = 0.020
Fig.5H	HISTOIOBICAL SCOLE	CCK-SAP	WT	DSS	Male	5	4.80 ± 0.58	Two-talled unparted student's t-test	$l_{(8)} = 0.52$	p = 0.620
Supplementary	FITC Doutron (ng/ml)	SAP-Blank	WT	DSS	Male	5	17.04 ± 4.11	Two tailed uppaired Student's t test	+ -0.02	n - 0.02F
Fig.51	FITC-Dextran (ng/mi)	CCK-SAP	WT	DSS	Male	5	17.56 ± 4.58	Two-talled unparted student's t-test	$L_{(8)} = 0.08$	p = 0.935
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	p = value
Supplementary	Disease activity index	SAP-Blank	WT	DSS	Male	5	- Two-way RM ANOVA	Time x DSS	<i>p</i> = 0.833	
Fig.5J		CCK-SAP	WT	DSS	Male	5		$F_{(9,72)} = 0.55$		

Figure	Parameter	Brain region	Test specifications	Genotype	Treatment	Sex	Number (sections)	Mean ± SEM	Statistical test	t-distribution t, df	p = value
Supplementary	c-Fos	ΝΤΟ	Sham	WT	DSS	Male	5 (31)	31.06 ± 3.15	Two tailed uppaired Student's t test	+ = 2 2E	n = 0.01
Fig.6B	neurons		GV	WT	DSS	Male	5 (27)	18.46 ± 2.05	Two-talled unpailed student's t-test	l(8) – 5.55	p= 0.01
Supplementary	c-Fos		Sham	WT	DSS	Male	5 (15)	48.30 ± 5.01	Mann Whitney II test		p = 0.016
Fig.6D	neurons	LC	GV	WT	DSS	Male	5 (17)	15.00 ± 7.47	Mann-Whitney O test	-	p = 0.010
Supplementary	c-Fos		Sham	WT	DSS	Male	5 (36)	16.66 ± 1.10	Two tailed uppaired Student's t test	+ – Г 27	m < 0.001
Fig.6F	neurons	BLA	GV	WT	DSS	Male	5 (38)	8.68 ± 1.00	Two-tailed unpaired Student's t-test	st t ₍₈₎ = 5.37	<i>p</i> < 0.001

Figure	Parameter	Brain region	Test specifications	Genotype	Treatment	Sex	Number (sections)	Mean ± SEM	Statistical test	t-distribution t, df	p = value
Supplementary	c-Fos	ΝΤΟ	B-SAP	WT	DSS	Male	4 (24)	33.38 ± 6.02	Mapp Whitney II test		n= 0.02
Fig.7B	neurons		CCK-SAP	WT	DSS	Male	4 (24)	15.73 ± 1.61		-	p = 0.05
Supplementary	c-Fos		B-SAP	WT	DSS	Male	4 (13)	44.70 ± 5.59	Two tailed uppaired Student's t test	+ 2 07	n = 0.02
Fig.7D	neurons	LC	CCK-SAP	WT	DSS	Male	4 (14)	26.85 ± 2.73	Two-tailed unpaired student's t-test	$l_{(6)} = 2.87$	p = 0.03
Supplementary	c-Fos		B-SAP	WT	DSS	Male	4 (28)	9.63 ± 0.68	Two tailed uppaired Student's t test	+ _ 2.00	n = 0.02
Fig.7F	neurons	BLA	CCK-SAP	WT	DSS	Male	4 (29)	6.75 ± 0.65	Two-tailed unpaired Student's t-test	est t ₍₆₎ = 3.06	<i>p</i> = 0.02

Figure	Parameter	Brain region	Test specifications	Genotype	Treatment	Sex	Number	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	<i>p</i> = value
Supplementary Fig.8B	FG⁺mCh⁺ NET⁺ of NET⁺	LC	Right	WT	H ₂ O	Male	5	11.00 ± 2.11	Two-way ANOVA	DSS x Right and Left $F_{(1,12)} = 0.04$	<i>p</i> = 0.841
			Left	WT	H ₂ O	Male	5	14.68 ± 3.82			
			Right	WT	DSS	Male	5	13.08 ± 2.29			
			Left	WT	DSS	Male	5	15.70 ± 1.33			

Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	Fixed effects F(DFn,DFd)	p = value
Supplementary	Disease estivity index	Saline	DBH-Cre	DSS	Male	8	-	Two-way RM ANOVA	Time x DSS	p = 0.501
Fig.9B	9B	CNO	DBH-Cre	DSS	Male	8			$F_{(9,126)} = 0.93$	
Figure	Parameter	Test specifications	Genotype	Treatment	Sex	Number of individuals	Mean ± SEM	Statistical test	t-distribution t, df	p = value
Supplementary Fig.9C	Colon length (cm)	Saline	DBH-Cre	DSS	Male	8	5.46 ± 0.13	- Two-tailed unpaired Student's t-test	t ₍₁₄₎ = 1.44	p = 0.172
		CNO	DBH-Cre	DSS	Male	8	5.18 ± 0.15			
Supplementary	Calcon weight (g)	Saline	DBH-Cre	DSS	Male	8	0.01 ± 0.01	- Two-tailed unpaired Student's t-test	t ₍₁₄₎ = 0.39	<i>p</i> = 0.701
Fig.9D	Spieen weight (g)	CNO	DBH-Cre	DSS	Male	8	0.09 ± 0.01			
Supplementary	Histological score	Saline		DEE	DSS Male	4	5.00 ± 0.41	- Mann-Whitney U test	-	<i>p</i> = 0.371
Fig.9F		CNO	DBH-Cle	DSS		4	5.75 ± 0.25			

Figure	Parameter	Brain region	Test specifications	Genotype	Treatment	Sex	Number (sections)	Mean ± SEM	Statistical test	t-distribution t, df	<i>p</i> = value
Supplementary	c-Fos	s LC	Saline	DBH-Cre	DSS	Male	5 (9)	74.76 ± 4.47	Two-tailed unpaired Student's t-test	t ₍₈₎ = 4.56	<i>p</i> = 0.002
Fig.10B	10B neurons		CNO	DBH-Cre	DSS	Male	5 (9)	43.36 ± 5.25			
Supplementary	c-Fos	NTS	Saline	DBH-Cre	DSS	Male	5 (14)	30.20 ± 2.83	Two-tailed unpaired Student's t-test	$t_{(8)} = 0.41$	<i>p</i> = 0.696
Fig.10D	neurons		CNO	DBH-Cre	DSS	Male	5 (13)	32.00 ± 3.41			