

Supplementary Table 1. Mice and cage ID used in the study

Age	Mouse ID	Genotype	Cage ID ^a	Housing Condition	
week 24	M-19	<i>Nfkbiz</i> ^{-/-}	1	non-cohoused	
	M-25	<i>Nfkbiz</i> ^{-/-}	2	non-cohoused	
	M-0	<i>Nfkbiz</i> ^{+/+}	3	non-cohoused	
	M-45				
	M-49				
	M-50				
	M-51				
	M-82	<i>Nfkbiz</i> ^{-/-}	4	non-cohoused	
	M-183	<i>Nfkbiz</i> ^{-/-}	5	non-cohoused	
	M-188				
week 3 & week 20	M40	<i>Nfkbiz</i> ^{-/-}	6	cohoused	
	M28	<i>Nfkbiz</i> ^{+/+}			
	M29				
	M31	<i>Nfkbiz</i> ^{+/+}	7	non-cohoused	
	M32				
	M47	<i>Nfkbiz</i> ^{-/-}	8	non-cohoused	
	M48				
	M49				
	M53	<i>Nfkbiz</i> ^{-/-}	9	cohoused	
	M57	<i>Nfkbiz</i> ^{+/+}			
	M55	<i>Nfkbiz</i> ^{+/+}	10	non-cohoused	
	M56				
	M58				
	M59				
	M74	<i>Nfkbiz</i> ^{-/-}	11	cohoused	
	M76				
	M79	<i>Nfkbiz</i> ^{+/+}			
	M82	<i>Nfkbiz</i> ^{-/-}	12	cohoused	
	M83	<i>Nfkbiz</i> ^{+/+}			
	M88	<i>Nfkbiz</i> ^{-/-}	13	non-cohoused	
M89					
M207	<i>Nfkbiz</i> ^{+/+}	14	cohoused		
M213	<i>Nfkbiz</i> ^{-/-}				
M231	<i>Nfkbiz</i> ^{-/-}	15	non-cohoused		

^aThe cage ID is in a chronological order based on the date of birth.

Supplementary Table 2. Differentially expressed genes in the salivary glands of *Nfkbiz*^{-/-} vs. *Nfkbiz*^{+/+} mice.

Gene_Symbol	Description	KO/WT fold change	KO/WT volume	<i>p</i>	<i>q</i>
<i>Jchain</i>	immunoglobulin joining chain	7.36	4.74	0.017	0.957
<i>Oas1a</i>	2-5 oligoadenylate synthetase 1A	3.79	4.12	0.003	0.957
<i>Usp18</i>	ubiquitin specific peptidase 18	3.19	6.02	0.045	0.957
<i>Spi1</i>	spleen focus forming virus (SFFV) proviral integration oncogene	2.82	6.24	0.029	0.957
<i>Znfx1</i>	zinc finger, NFX1-type containing 1	2.75	5.88	0.023	0.957
<i>Lgals9</i>	lectin, galactose binding, soluble 9	2.55	5.52	0.021	0.957
<i>Baiap2</i>	brain-specific angiogenesis inhibitor 1-associated protein 2	2.37	5.60	0.011	0.957
<i>Eif2ak2</i>	eukaryotic translation initiation factor 2-alpha kinase 2	2.34	6.90	0.006	0.957
<i>Xaf1</i>	XIAP associated factor 1	2.25	4.95	0.044	0.957
<i>Insc</i>	Inscuteable homolog	2.23	3.43	0.011	0.957
<i>Sdc3</i>	syndecan 3	2.23	5.46	0.037	0.957
<i>H2-Q7</i>	histocompatibility 2, Q region locus 7	2.20	7.63	0.046	0.957
<i>Fnl1</i>	fibronectin 1	2.15	5.69	0.007	0.957
<i>Elk4</i>	ELK4, member of ETS oncogene family	2.15	7.00	0.007	0.957
<i>Apbb2</i>	amyloid beta (A4) precursor protein-binding, family B, member 2	2.13	8.10	0.040	0.957
<i>H2-K1</i>	histocompatibility 2, K1, K region	2.03	10.24	0.039	0.957
<i>Ino80</i>	INO80 homolog	2.01	6.40	0.032	0.957
<i>Chd7</i>	chromodomain helicase DNA binding protein 7	1.98	7.76	0.037	0.957
<i>Ccr2</i>	chemokine (C-C motif) receptor 2	1.98	2.62	0.035	0.957
<i>Slc44a5</i>	solute carrier family 44, member 5	1.94	1.82	0.029	0.957
<i>Fndc3b</i>	fibronectin type III domain	1.92	8.63	0.024	0.957

	containing 3B				
<i>Mast4</i>	microtubule associated serine/threonine kinase family member 4	1.90	8.08	0.043	0.957
<i>Magea6</i>	melanoma antigen, family A, 6	1.89	2.82	0.030	0.957
<i>Mir23b</i>	microRNA 23b	1.89	7.70	0.033	0.957
<i>Zbtb20</i>	zinc finger and BTB domain containing 20	1.89	8.28	0.013	0.957
<i>Tnfrsf1b</i>	tumor necrosis factor receptor superfamily, member 1b	1.88	5.03	0.035	0.957
<i>Iqcf3</i>	IQ motif containing F3	1.87	3.06	0.005	0.957
<i>Prelp</i>	proline arginine-rich end leucine-rich repeat	1.87	5.57	0.010	0.957
<i>Tlr7</i>	toll-like receptor 7	1.86	5.47	0.018	0.957
<i>Ambra1</i>	autophagy/beclin 1 regulator 1	1.86	8.23	0.046	0.957
<i>Rasal1</i>	RAS protein activator like 1	1.83	7.08	0.019	0.957
<i>Sin3a</i>	transcriptional regulator, SIN3A	1.82	8.39	0.026	0.957
<i>Nktr</i>	natural killer tumor recognition sequence	1.82	8.64	0.032	0.957
<i>Fign</i>	fidgetin	1.82	3.60	0.014	0.957
<i>Rptor</i>	regulatory associated protein of MTOR, complex 1	1.82	6.36	0.038	0.957
<i>Lrif1</i>	ligand dependent nuclear receptor interacting factor 1	1.82	5.16	0.011	0.957
<i>Scaf4</i>	SR-related CTD-associated factor 4	1.81	7.95	0.023	0.957
<i>Uvrag</i>	UV radiation resistance associated gene	1.79	6.39	0.005	0.957
<i>Clec4g</i>	C-type lectin domain family 4, member g	1.78	3.94	0.030	0.957
<i>Pld4</i>	phospholipase D family, member 4	1.78	5.85	0.030	0.957
<i>Clip4</i>	CAP-GLY domain containing linker protein family, member 4	1.78	7.84	0.018	0.957
<i>Atxn7</i>	ataxin 7	1.76	6.72	0.020	0.957
<i>Gm11042</i>	predicted gene 11042 [Source:MGI Symbol;Acc:MGI:3779266]	1.76	5.23	0.025	0.957

<i>Gm10217</i>	predicted gene 10217 [Source:MGI Symbol;Acc:MGI:3642099]	1.75	10.50	0.032	0.957
<i>Dennd1a</i>	DENN/MADD domain containing 1A	1.75	6.04	0.042	0.957
<i>Map3k13</i>	mitogen-activated protein kinase kinase kinase 13	1.74	5.56	0.029	0.957
<i>Ghrl</i>	ghrelin	1.74	5.68	0.039	0.957
<i>Grn</i>	granulin	1.73	9.13	0.046	0.957
<i>Arhgap26</i>	Rho GTPase activating protein 26	1.72	7.67	0.021	0.957
<i>Traf3ip3</i>	TRAF3 interacting protein 3	1.70	4.55	0.027	0.957
<i>Exoc6b</i>	exocyst complex component 6B	1.70	6.55	0.005	0.957
<i>Kmt2a</i>	lysine (K)-specific methyltransferase 2A	1.70	7.02	0.040	0.957
<i>Pomt1</i>	protein-O-mannosyltransferase 1	1.69	6.93	0.033	0.957
<i>Pik3ap1</i>	phosphoinositide-3-kinase adaptor protein 1	1.69	7.30	0.005	0.957
<i>Olfir692</i>	olfactory receptor 692	1.69	4.06	0.040	0.957
<i>Atp10a</i>	ATPase, class V, type 10A	1.68	4.58	0.024	0.957
<i>Clec3a</i>	C-type lectin domain family 3, member a	1.68	2.73	0.033	0.957
<i>Gm17571</i>	predicted gene, 17571 [Source:MGI Symbol;Acc:MGI:4937205]	1.67	10.93	0.018	0.957
<i>Gbp9</i>	guanylate-binding protein 9	1.67	3.12	0.048	0.957
<i>Arhgap39</i>	Rho GTPase activating protein 39	1.67	6.40	0.028	0.957
<i>Arhgap15</i>	Rho GTPase activating protein 15	1.66	3.68	0.027	0.957
<i>Gm6455</i>	predicted gene 6455	1.65	2.97	0.028	0.957
<i>Tlr9</i>	toll-like receptor 9	1.65	3.94	0.040	0.957
<i>Casz1</i>	castor zinc finger 1	1.65	6.81	0.005	0.957
<i>Zfp248</i>	zinc finger protein 248	1.65	4.61	0.035	0.957
<i>Galnt9</i>	UDP-N-acetyl-alpha-D- galactosamine:polypeptide N- acetylgalactosaminyltransferase 9	1.64	3.89	0.019	0.957
<i>Strada</i>	STE20-related kinase adaptor alpha	1.64	3.79	0.048	0.957
<i>Zfp280c</i>	zinc finger protein 280C	1.64	6.25	0.042	0.957

<i>Efcab9</i>	EF-hand calcium binding domain 9	1.64	2.93	0.014	0.957
<i>Ggcx</i>	gamma-glutamyl carboxylase	1.63	8.20	0.045	0.957
<i>Thbs3</i>	thrombospondin 3	1.62	3.75	0.035	0.957
<i>Clasp1</i>	CLIP associating protein 1	1.62	6.72	0.025	0.957
<i>Zc3h7a</i>	zinc finger CCCH type containing 7 A	1.61	7.04	0.000	0.957
<i>Arsb</i>	arylsulfatase B	1.61	7.44	0.040	0.957
<i>Hdac8</i>	histone deacetylase 8	1.61	5.96	0.028	0.957
<i>Tonsl</i>	tonsoku-like, DNA repair protein	1.60	3.97	0.049	0.957
<i>Hmgxb3</i>	HMG box domain containing 3	1.60	6.28	0.029	0.957
<i>Olf102</i>	olfactory receptor 102	1.59	1.90	0.016	0.957
<i>Gm3414</i>	predicted gene 3414	1.59	4.53	0.011	0.957
<i>Olf1786</i>	olfactory receptor 786	1.58	2.44	0.033	0.957
<i>Cyp2s1</i>	cytochrome P450, family 2, subfamily s, polypeptide 1	1.58	8.64	0.045	0.957
<i>Dpp7</i>	dipeptidylpeptidase 7	1.58	6.51	0.043	0.957
<i>Med27</i>	mediator complex subunit 27	1.58	6.26	0.024	0.957
<i>Cabyr</i>	calcium-binding tyrosine-(Y)- phosphorylation regulated (fibrousheathin 2)	1.57	3.11	0.025	0.957
<i>Secisbp2</i>	SECIS binding protein 2	1.57	6.06	0.010	0.957
<i>Cdk17</i>	cyclin-dependent kinase 17	1.57	6.28	0.000	0.957
<i>Wdr7</i>	WD repeat domain 7	1.57	6.78	0.021	0.957
<i>Vwc2</i>	von Willebrand factor C domain containing 2	1.57	3.74	0.027	0.957
<i>Scd1</i>	stearoyl-Coenzyme A desaturase 1	1.57	10.09	0.008	0.957
<i>Gpr153</i>	G protein-coupled receptor 153	1.57	3.76	0.040	0.957
<i>Olf1987</i>	olfactory receptor 987	1.56	2.39	0.030	0.957
<i>Dnajb13</i>	DnaJ (Hsp40) related, subfamily B, member 13	1.56	3.33	0.047	0.957
<i>Nvl</i>	nuclear VCP-like	1.55	6.60	0.044	0.957
<i>Bnc1</i>	basonuclin 1	1.55	4.35	0.047	0.957
<i>Ndst1</i>	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	1.54	8.83	0.003	0.957

<i>G530012D18Rik</i>	RIKEN cDNA G530012D1 gene [Source:MGI Symbol;Acc:MGI:3642025]	1.53	3.90	0.019	0.957
<i>Ces1a</i>	carboxylesterase 1A	1.53	3.13	0.013	0.957
<i>Gm11060</i>	predicted gene 11060 [Source:MGI Symbol;Acc:MGI:3779284]	1.53	8.03	0.014	0.957
<i>Cul7</i>	cullin 7	1.52	5.55	0.040	0.957
<i>F2rl2</i>	coagulation factor II (thrombin) receptor-like 2	1.52	4.81	0.041	0.957
<i>Psg20</i>	pregnancy-specific glycoprotein 20	1.52	4.60	0.030	0.957
<i>Gtpbp8</i>	GTP-binding protein 8 (putative)	1.52	4.83	0.041	0.957
<i>Tcf4</i>	transcription factor 4	1.52	8.43	0.014	0.957
<i>Znrf3</i>	zinc and ring finger 3	1.51	7.01	0.036	0.957
<i>Gm694</i>	predicted gene 694	1.51	3.52	0.015	0.957
<i>Shisa5</i>	shisa family member 5	1.50	7.09	0.049	0.957
<i>Gbf1</i>	golgi-specific brefeldin A- resistance factor 1	1.50	9.12	0.046	0.957
<i>Sohlh2</i>	spermatogenesis and oogenesis specific basic helix-loop-helix 2	-1.50	2.36	0.009	0.957
<i>Stub1</i>	STIP1 homology and U-Box containing protein 1	-1.50	6.62	0.042	0.957
<i>Snrpf</i>	small nuclear ribonucleoprotein polypeptide F	-1.51	5.37	0.006	0.957
<i>Mapk1</i>	mitogen-activated protein kinase 1	-1.52	6.51	0.014	0.957
<i>1700029H14Rik</i>	RIKEN cDNA 1700029H14 gene	-1.52	6.04	0.043	0.957
<i>Hint1</i>	histidine triad nucleotide binding protein 1	-1.52	7.33	0.015	0.957
<i>Nme2</i>	NME/NM23 nucleoside diphosphate kinase 2	-1.53	8.13	0.036	0.957
<i>Ppp1r11</i>	protein phosphatase 1, regulatory (inhibitor) subunit 11	-1.53	5.86	0.007	0.957
<i>Ipp</i>	IAP promoted placental gene	-1.53	3.60	0.025	0.957
<i>Dcpp3</i>	demilune cell and parotid protein 3	-1.53	12.55	0.038	0.957
<i>Ptov1</i>	prostate tumor over expressed gene 1	-1.53	7.23	0.016	0.957

<i>Yif1a</i>	Yip1 interacting factor homolog A (<i>S. cerevisiae</i>)	-1.53	5.64	0.046	0.957
<i>2410015M20Rik</i>	RIKEN cDNA 2410015M20 gene	-1.53	6.39	0.046	0.957
<i>Rps5</i>	ribosomal protein S5	-1.54	7.61	0.039	0.957
<i>Mpi</i>	mannose phosphate isomerase	-1.54	7.17	0.024	0.957
<i>Nap111</i>	nucleosome assembly protein 1-like 1	-1.54	7.39	0.005	0.957
<i>Dynlt1b</i>	dynein light chain Tctex-type 1B	-1.55	6.48	0.048	0.957
<i>Crygn</i>	crystallin, gamma N	-1.55	5.18	0.015	0.957
<i>Tbx5</i>	T-box 5	-1.55	3.85	0.034	0.957
<i>Cmc2</i>	COX assembly mitochondrial protein 2	-1.55	5.19	0.040	0.957
<i>Angptl4</i>	angiopoietin-like 4	-1.56	4.94	0.041	0.957
<i>Olf1377</i>	olfactory receptor 1377	-1.56	3.29	0.020	0.957
<i>Nt5c</i>	5,3-nucleotidase, cytosolic	-1.56	5.44	0.028	0.957
<i>Nsmce4a</i>	non-SMC element 4 homolog A (<i>S. cerevisiae</i>)	-1.56	5.54	0.045	0.957
<i>Znhit6</i>	zinc finger, HIT type 6	-1.56	5.26	0.024	0.957
<i>Dhrs4</i>	dehydrogenase/reductase (SDR family) member 4	-1.57	7.33	0.038	0.957
<i>Rfx4</i>	regulatory factor X, 4	-1.57	3.96	0.006	0.957
<i>B230217C12Rik</i>	RIKEN cDNA B230217C12 gene	-1.57	3.94	0.002	0.957
<i>Prorsd1</i>	prolyl-tRNA synthetase domain containing 1	-1.58	5.22	0.004	0.957
<i>Dynll2</i>	dynein light chain LC8-type 2	-1.58	4.82	0.026	0.957
<i>Tbx2</i>	T-box 2	-1.58	6.06	0.037	0.957
<i>Cbx3</i>	chromobox 3	-1.58	8.12	0.026	0.957
<i>Sat2</i>	spermidine/spermine N1-acetyl transferase 2	-1.59	4.18	0.009	0.957
<i>Rps20</i>	ribosomal protein S20	-1.59	7.11	0.042	0.957
<i>Snx1</i>	sorting nexin 1	-1.59	4.98	0.019	0.957
<i>Eif3i</i>	eukaryotic translation initiation factor 3, subunit I	-1.59	6.22	0.036	0.957
<i>Dcpp2</i>	demilune cell and parotid protein 2	-1.59	12.10	0.043	0.957
<i>Rpl19</i>	ribosomal protein L19	-1.59	8.65	0.033	0.957

<i>Tlx1</i>	T cell leukemia, homeobox 1	-1.59	6.56	0.012	0.957
<i>Atp5f1</i>	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit B1	-1.60	7.58	0.008	0.957
<i>St3gal5</i>	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	-1.60	5.64	0.033	0.957
<i>Adrb3</i>	adrenergic receptor, beta 3	-1.60	4.03	0.019	0.957
<i>Igbp1</i>	immunoglobulin (CD79A) binding protein 1	-1.60	6.85	0.046	0.957
<i>Hsd12</i>	hydroxysteroid dehydrogenase like 2	-1.61	5.01	0.006	0.957
<i>Gm19659</i>	PREDICTED: predicted gene, 19659 (Gm19659), mRNA.	-1.61	1.94	0.038	0.957
<i>Cklf</i>	chemokine-like factor	-1.61	4.35	0.033	0.957
<i>Ppip5k2</i>	diphosphoinositol pentakisphosphate kinase 2	-1.61	5.64	0.029	0.957
<i>Lipm</i>	lipase, family member M	-1.62	2.31	0.004	0.957
<i>Gnb2l1</i>	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	-1.63	8.08	0.033	0.957
<i>Mrpl22</i>	mitochondrial ribosomal protein L22	-1.64	3.66	0.016	0.957
<i>Il1r2</i>	interleukin 1 receptor, type II	-1.64	4.28	0.030	0.957
<i>Adck3</i>	aarF domain containing kinase 3	-1.64	5.95	0.041	0.957
<i>Bcl2a1d</i>	B cell leukemia/lymphoma 2 related protein A1d	-1.64	3.55	0.049	0.957
<i>Fgf13</i>	fibroblast growth factor 13	-1.65	2.66	0.040	0.957
<i>Rps26</i>	ribosomal protein S26	-1.65	7.57	0.005	0.957
<i>Aldh7a1</i>	aldehyde dehydrogenase family 7, member A1	-1.65	8.15	0.041	0.957
<i>Gm20736</i>	predicted gene, 20736	-1.65	1.85	0.031	0.957
<i>Gucy1a3</i>	guanylate cyclase 1, soluble, alpha 3	-1.65	3.07	0.028	0.957
<i>Hspa2</i>	heat shock protein 2	-1.65	3.76	0.039	0.957
<i>Serp1</i>	stress-associated endoplasmic reticulum protein 1	-1.66	9.53	0.039	0.957
<i>Glr3</i>	glutaredoxin 3	-1.66	6.66	0.047	0.957
<i>Suclg1</i>	succinate-CoA ligase, GDP-	-1.66	7.37	0.036	0.957

	forming, alpha subunit				
<i>Veph1</i>	ventricular zone expressed PH domain-containing 1	-1.66	3.21	0.028	0.957
<i>Arl1</i>	ADP-ribosylation factor-like 1	-1.66	8.99	0.017	0.957
<i>Neu2</i>	neuraminidase 2	-1.67	5.79	0.032	0.957
<i>Aven</i>	apoptosis, caspase activation inhibitor	-1.67	5.80	0.015	0.957
<i>Tcf19</i>	transcription factor 19	-1.67	4.16	0.002	0.957
<i>Rpsa</i>	ribosomal protein SA	-1.67	8.56	0.014	0.957
<i>Mtif3</i>	mitochondrial translational initiation factor 3	-1.67	4.60	0.032	0.957
<i>Dynlt1c</i>	dynein light chain Tctex-type 1C	-1.68	5.79	0.023	0.957
<i>Fam174a</i>	family with sequence similarity 174, member A	-1.68	5.97	0.005	0.957
<i>BC031181</i>	cDNA sequence BC031181	-1.69	6.58	0.021	0.957
<i>Tmem42</i>	transmembrane protein 42	-1.70	4.98	0.012	0.957
<i>Hist1h2ac</i>	histone cluster 1, H2ac	-1.70	5.74	0.012	0.957
<i>Pfdn1</i>	prefoldin 1	-1.72	5.68	0.009	0.957
<i>Rps9</i>	ribosomal protein S9	-1.73	7.48	0.015	0.957
<i>Ywhaq</i>	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	-1.73	7.40	0.037	0.957
<i>Vdac1</i>	voltage-dependent anion channel 1	-1.73	7.44	0.042	0.957
<i>Adprh</i>	ADP-ribosylarginine hydrolase	-1.75	4.68	0.033	0.957
<i>Clql4</i>	complement component 1, q subcomponent-like 4	-1.76	2.69	0.040	0.957
<i>Hibadh</i>	3-hydroxyisobutyrate dehydrogenase	-1.77	7.53	0.041	0.957
<i>Hsbp1l1</i>	heat shock factor binding protein 1-like 1	-1.77	4.95	0.046	0.957
<i>Dpm3</i>	dolichyl-phosphate mannosyltransferase polypeptide 3	-1.78	6.83	0.032	0.957
<i>Ndufa9</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	-1.78	6.95	0.009	0.957

<i>Fbxw9</i>	F-box and WD-40 domain protein 9	-1.78	4.85	0.016	0.957
<i>Ntan1</i>	N-terminal Asn amidase	-1.80	5.51	0.004	0.957
<i>Rps4x</i>	ribosomal protein S4, X-linked	-1.80	7.37	0.038	0.957
<i>Abhd3</i>	abhydrolase domain containing 3	-1.81	4.61	0.011	0.957
<i>Tnnc2</i>	troponin C2, fast	-1.83	4.59	0.036	0.957
<i>Blvra</i>	biliverdin reductase A	-1.83	5.22	0.015	0.957
<i>Ccl28</i>	chemokine (C-C motif) ligand 28	-1.83	9.24	0.039	0.957
<i>Hint2</i>	histidine triad nucleotide binding protein 2	-1.85	4.40	0.040	0.957
<i>Ube2a</i>	ubiquitin-conjugating enzyme E2A	-1.85	4.68	0.014	0.957
<i>Cnpy4</i>	canopy 4 homolog (zebrafish)	-1.87	4.01	0.020	0.957
<i>Anapc4</i>	anaphase promoting complex subunit 4	-1.87	4.56	0.045	0.957
<i>Adgrg3</i>	adhesion G protein-coupled receptor G3	-1.87	3.62	0.044	0.957
<i>Moap1</i>	modulator of apoptosis 1)	-1.88	3.58	0.001	0.957
<i>Ndufa6</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	-1.96	6.20	0.023	0.957
<i>Tpt1</i>	tumor protein, translationally-controlled 1	-1.98	9.19	0.014	0.957
<i>Acp1</i>	acid phosphatase 1, soluble	-1.98	5.49	0.030	0.957
<i>Anxa2</i>	annexin A2	-1.99	5.43	0.038	0.957
<i>Etfa</i>	electron transferring flavoprotein, alpha polypeptide	-1.99	7.52	0.045	0.957
<i>Gnmt</i>	glycine N-methyltransferase	-2.00	6.57	0.019	0.957
<i>Insig1</i>	insulin induced gene 1	-2.21	8.25	0.028	0.957
<i>Rpl36al</i>	ribosomal protein L36A-like	-2.63	6.50	0.044	0.957

Supplementary Table 3. The summary of sequencing characteristics

	Number of raw reads	Number of valid reads	Average read length	Coverage %
24 week old <i>Nfkbiz</i> ^{+/+} (n=5)	76,586 ± 10,119	63,527 ± 8,614	426 ± 1.5	99.97 ± 0.01
24 week old <i>Nfkbiz</i> ^{-/-} (n=5)	88,757 ± 14,443	72,844 ± 12,437	425 ± 1.1	99.97 ± 0.01
3 week old non-cohoused <i>Nfkbiz</i> ^{+/+} (n=6)	40,673 ± 15,750	37,962 ± 15,032	425 ± 2.2	99.94 ± 0.05
3 week old cohoused <i>Nfkbiz</i> ^{+/+} (n=6)	67,115 ± 18,277	52,360 ± 18,837	425 ± 1.5	99.91 ± 0.09
3 week old cohoused <i>Nfkbiz</i> ^{-/-} (n=6)	75,172 ± 25,495	65,805 ± 21,319	425 ± 0.8	99.93 ± 0.07
3 week old non-cohoused <i>Nfkbiz</i> ^{-/-} (n=6)	77,651 ± 31,487	67,109 ± 22,892	426 ± 0.4	99.96 ± 0.01
20 week old non-cohoused <i>Nfkbiz</i> ^{+/+} (n=6)	47,015 ± 13,615	43,618 ± 12,109	426 ± 0.5	99.93 ± 0.01
20 week old cohoused <i>Nfkbiz</i> ^{+/+} (n=6)	54,692 ± 43,660	43,526 ± 25,561	426 ± 1.0	99.89 ± 0.08
20 week old cohoused <i>Nfkbiz</i> ^{-/-} (n=6)	48,650 ± 21,020	44,026 ± 19,188	426 ± 0.6	99.93 ± 0.05
20 week old non-cohoused <i>Nfkbiz</i> ^{-/-} (n=6)	51,059 ± 30,985	44,182 ± 26,252	426 ± 0.9	99.93 ± 0.05

NR_117375.1	315	AGGGAATCTTCGGCAATGGGGCAACCCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGT	374
Current study	1	60
NR_117375.1	375	TTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACGTGTGTGAGAGTGGAAGTTCACAC	434
Current study	61	120
NR_117375.1	435	AGTGACGGTAACTTACCAGAAAGGGACGGCTAACTACGTGCCAGCAGCCGCGGTAATACG	494
Current study	121	180
NR_117375.1	495	TAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCCGTTGGATAAG	554
Current study	181	240
NR_117375.1	555	TCTGAAGTTAAAGGCTGTGGCTCAACCATAGTATGCTTTGGAACTGTTCAACTTGAGTG	614
Current study	241 T	300
NR_117375.1	615	CAGAAGGGGAGAGTGGAATTCATGTGTAGCGGTGGAATGCGTAGATATATGGAGGAACA	674
Current study	301	360
NR_117375.1	675	CCGGTGGCGAAAGCGGCTCTCTGGTCTGTAACGTGACGCTGAGGCTCGAAAGCGTGGGTAG	734
Current study	361	420
NR_117375.1	735	CGAAC	739
Current study	421	425

Supplementary Figure 1. The sequence of 16S rRNA gene of *Streptococcus danieliae* The sequence of a dominant amplified sequence variant assigned to *S. danieliae* in the current study was compared to the sequence of 16S rRNA gene of *S. danieliae* strain ERD01G reported by Clavel et al.²¹