SUPPLEMENTAL MATERIAL

Malle et al., http://www.jem.org/cgi/content/full/jem.20150218/DC1

Table S1. Differentially expressed genes in βTRAF2 and βTRAF3 islets (chow and DIO)

Gene[a]	Log FC[b]				Associated function[c]
	βTRAF2 chow	βTRAF3 chow	βTRAF2 DIO	βTRAF3 DIO	
Tph1 (tryptophan hydroxylase)	-	-	6.88	6.33	aromatic amino acid family metabolic process, bone remodeling, neuron projection, serotonin synthesis
Lrrc55 **(leucine rich repeat containing 55)**	3.78	2.90	5.00	5.04	potassium ion transport, BK channel auxiliary subunit
Sftpd **(surfactant associated protein D)**	3.12	2.28	4.07	3.15	phospholipid homeostasis, regulation of phagocytosis, LPS binding
Gbp8 (guanylate-binding protein 8)	3.16	-	3.59	3.36	large IFN-γ-induced GTPase
Syt10 (synaptotagmin X)	3.20	-	3.53	3.24	regulation of Ca^{2+}-dependent exocytosis, cytoplasmic vesicle
Crispld2 (cysteine-rich secretory protein LCCL domain containing 2)	3.36	3.33	-	2.68	extracellular matrix (ECM) component, heparin binding, LPS binding, vesicle transport
Hcn1 **(hyperpolarization-activated, cyclic nucleotide-gated K^+ 1)**	2.75	2.40	3.36	3.24	potassium ion transport; voltage-gated potassium channel, sensitivity to cAMP
Fbxw24 **(F-box and WD-40 domain protein 24)**	2.91	1.82	3.48	2.99	protein coding gene, unknown function
Tnfrsf11b (tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin))	-	-	3.20	3.19	osteoprotegerin (OPG), ECM organization, regulation of differentiation, negative regulation of bone resorption, decoy receptor for RANKL
Matn2 (matrilin 2)	-	-	3.42	2.92	ECM, formation of filamentous networks, neuron cell migration,Ca^{2+}-binding,
Rerg **(RAS-like, estrogen-regulated, growth-inhibitor)**	2.13	1.56	3.30	3.04	RAS superfamily of GTPases, negative regulator of cell growth/proliferation
Rasgrp1 (RAS guanyl releasing protein 1)	3.16	3.07	-	2.93	GEF activity: activation of Ras and Rho GTPases, Ca^{2+} binding
Fmo1 (flavin containing monooxygenase 1)	-	-	3.16	2.55	drug metabolic process; oxidation-reduction process; NADPH oxidation; organic acid metabolic process
Grem2 **(gremlin 2 homolog, cysteine knot superfamily (*Xenopus laevis*))**	2.19	1.49	2.54	2.28	regulator of osteoblast differentiation and osteogenesis; cytokine, heparin binding, negative regulation of BMP signaling pathway
Gbp4 (guanylate binding protein 4)	2.29	2.44	-	-	large IFNγ-induced GTPase negative regulation of protein ubiquitination
Krtap13-1 (keratin associated protein 13-1)	2.57	1.96	-	2.26	intermediate filament
Gbp10 (guanylate-binding protein 10)	1.70	2.73	-	-	large IFNγ-induced GTPase
Srbd1 (S1 RNA binding domain 1)	1.74	-	2.34	2.05	nucleobase-containing compound metabolic process, hydrolase activity, nucleic acid binding
Gpr110 (G protein-coupled receptor 110)	-	-	2.61	1.74	adhesion GPCR
Fam69a (family with sequence similarity 69, member A)	2.06	2.20	-	-	ER associated, transmembrane, Ca^{2+} dependent (suspected)
Gfra3 **(glial cell line derived neurotrophic factor family receptor alpha 3)**	2.41	1.57	2.24	1.84	neuron development, embryonic development, apoptosis, artemin receptor

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Gene[a]	Log FC[b]				Associated function[c]
	βTRAF2 chow	βTRAF3 chow	βTRAF2 DIO	βTRAF3 DIO	
Adarb2 (adenosine deaminase, RNA-specific, B2)			2.23	1.81	RED2, RNA-editing deaminase
Tnfrsf9 (tumor necrosis factor receptor superfamily, member 9)	2.05	1.93	-	-	4-1BB, negative regulation of IL10 and IL12 secretion
***Gpr126* (G protein–coupled receptor 126)**	2.29	1.45	2.06	1.85	signal transduction, heart development, mitochondrial function
Tmem47 (transmembrane protein 47)	1.91	-	2.05	1.86	cell-cell junction
B3galt1 (UDP-Gal: betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1)	-	-	1.90	1.93	globo-series glycosphingolipid synthesis
Myo3a (myosin IIIA)	-	-	2.13	1.70	actin filament binding, microfilament motor activity, actin -dependent ATPase activity, S/T phosphorylation, actin catabolic process
Rph3a (rabphilin 3A)	-	-	1.97	1.81	calcium-dependent phospholipid binding, secretory granule associated
Dnahc8 (dynein, axonemal, heavy chain 8)	-	-	1.95	1.83	microtubule-associated; motor activity
Mapk4 (mitogen-activated protein kinase 4)	1.92	1.83	-	1.23	ERK4, kinase activity
Pde7b (phosphodiesterase 7B)	-	-	1.90	1.78	metabolic process, 3′,5′-cyclic-AMP phosphodiesterase activity (cAMP to AMP)
Kcnj5 (potassium inwardly rectifying channel, subfamily J, member 5)	1.81	-	1.89	1.80	potassium ion transport
Cym (chymosin)	-	-	1.87	1.45	peptidase
Gm15577 (predicted gene 15577)	1.68	1.17	1.68	-	unclassified gene
***Kcnk10* (potassium channel, subfamily K, member 10)**	1.72	1.27	1.94	1.85	potassium ion transmembrane transport
Penk (preproenkephalin)	1.47	1.12	1.60	-	neuropeptide signaling pathway, opiod peptide activity
Slc2a13 (solute carrier family 2 (facilitated glucose transporter), member 13)	-	-	1.45	1.31	
Tmem2 (transmembrane protein 2)	-	-	1.34	1.35	multicellular organismal development, extracellular vesicular exosome, morphogenesis
Bcat1 (branched chain aminotransferase 1, cytosolic)	1.68	1.22	-	1.10	metabolic process cell proliferation, transaminase: valine, leucine and isoleucine metabolism
Ogdhl (oxoglutarate dehydrogenase-like)	1.45	1.20	-	-	negative regulator of cell proliferation, modification of AKT/PKB signaling; modification of NF-κB signaling
Gpr182 (G protein-coupled receptor 182)	1.02	1.62	-	-	signal transduction, adrenomedullin receptor activity (suspected)
Igfbp5 (insulin-like growth factor binding protein 5)	1.55	-	1.29	1.06	glucose homeostasis, glucose metabolic process, muscle cell differentiation, regulation of growth, positive regulation of PKB signaling
B3galnt1 (UDP-GalNAc: betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 1)	-	-	1.52	1.06	globo-series glycosphingolipid synthesis

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Gene[a]	Log FC[b]				Associated function[c]
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Ngfr (nerve growth factor receptor (TNFR superfamily,member 16)	-	1.08	1.32	1.30	regulation of cell death, axon guidance, clathrin-coated endocytic vesicle, beta-amyloid binding, ubiquitin protein ligase binding, regulation of reactive oxygen species metabolic process
Gm19510 (predicted gene, 19510)	1.35	1.11	-	-	unclassified non-coding RNA gene
Cish (cytokine inducible SH2-containing protein)	1.23	-	1.35	1.06	regulation of growth, PKC-activating, SOCS family protein
Prok1 (prokineticin 1)	-	-	1.37	1.05	positive regulation of cell proliferation, regulation of angiogenesis, activation of MAPK activity
Ivd (isovaleryl coenzyme A dehydrogenase)	1.23	-	1.17	1.19	leucine catabolic process, acyl-CoA dehydrogenase activity, flavin adenine dinucleotide binding
Socs2 (suppressor of cytokine signaling 2)	1.42	1.05		1.05	positive regulation of differentiation; insulin-like growth factor receptor binding
Lrp8 (low density lipoprotein receptor-related protein 8, apolipoprotein e receptor)	-	-	1.09	1.23	positive regulation of CREB transcription factor activity; calcium ion binding
Wipi1 (WD repeat domain, phosphoinositide interacting 1)	1.21	1.05	-	-	autophagic vacuole assembly, vesicle targeting, estrogen receptor binding, phosphatidylinositol-3-phosphate binding/GSK3β inhibition
Adora1 (adenosine A1 receptor)	-1.27	-1.35	-	-	GPCR, lipid catabolic process, MAPKK activation, negative regulation of inflammatory response, negative regulation of cell proliferation adenylyl cyclase inhibitor; positive regulation of K^+ transport, negative regulation of glutamate secretion

[a] Gene symbol and gene name.

[b] Log-fold change of differential gene expression in chow and DIO βTRAF2 and βTRAF3 islets.

[c] Associated gene function according to DAVID Bioinformatics Database and Mouse Genome Database (MGD) at http://www.informatics.jax.org (Sep 2014).