

Supplemental Table 1. Affymetrix (Rat Genome Array) expression profiling comparing un-induced cells to cells expressing active fragment of human OASIS for 48 h. Common genes induced in three independent experiments greater than 2-fold are shown. * genes induced in 2 of 3 experiments

Gene ID	Fold Change (Mean)	Description/ Putative Function
294103	41.42	Papss2, sulfate conjugation
25107	40.04*	Avrp1A, inositol-calcium signaling
360959	14.86	HtrA3, inhibitor of TGF- β signaling, Apoptosis
312607	12.27	Pdzrf3, ubiquitin protein ligase activity
287877	8.21	P5cr1, arginine and proline metabolism
294048	7.76	Pi3kap, signaling
171041	6.49*	Kns2, Kinesin 2
360611	5.88	Cop ζ 2, protein transport
498609	5.68	Lpar2, signal transduction
297894	5.56*	Matn1, cartilage matrix protein
29241	5.304*	Adcy8, adenylyl cyclase 8
79247	5.082*	Htr5b, serotonin receptor
315131	4.89	KDEL Erd3, protein transport
25027	4.75	Slc16a1, transporter
282712	3.78	Slc6a15, transporter
690050	3.55	Tpmt, thiopurine methylation
304322	3.45*	Chst12, Carbohydrate sulfotransferase
316842	3.27*	Metrn1, glial cell differentiation
64313	3.2	Oat, proline metabolism
29643	3.25	Sv2c, protein secretion/transport
171044	2.7*	Sstr3, neurotransmitter
64157	2.64	Ddah1, transcriptional regulation
308836	2.61	Kctd14, ubiquitination
291444	2.54*	Prrc1, proline-rich coiled-coil 1
406166	2.47	Agpat1, biosynthesis of glycerolipids
306344	2.46	Arrdc2, adrenergic receptor signaling
680493	2.43	Cd3 ϵ ap, Notch signaling
114519	2.4	Nfil3, transcription factor
362204	2.3	Casc4, cancer
300211	2.23	Fkbp11, protein folding
83425	2.36	Prka, adrenergic receptor signaling
362368	2.35*	Ggct, gamma-glutamyl cyclotransferase
24561	2.33*	Mpg, N-methylpurine-DNA glycosylase
314879	2.16	Xpot, nuclear receptor for tRNAs
64475	2.13	P4ha1, proline metabolism