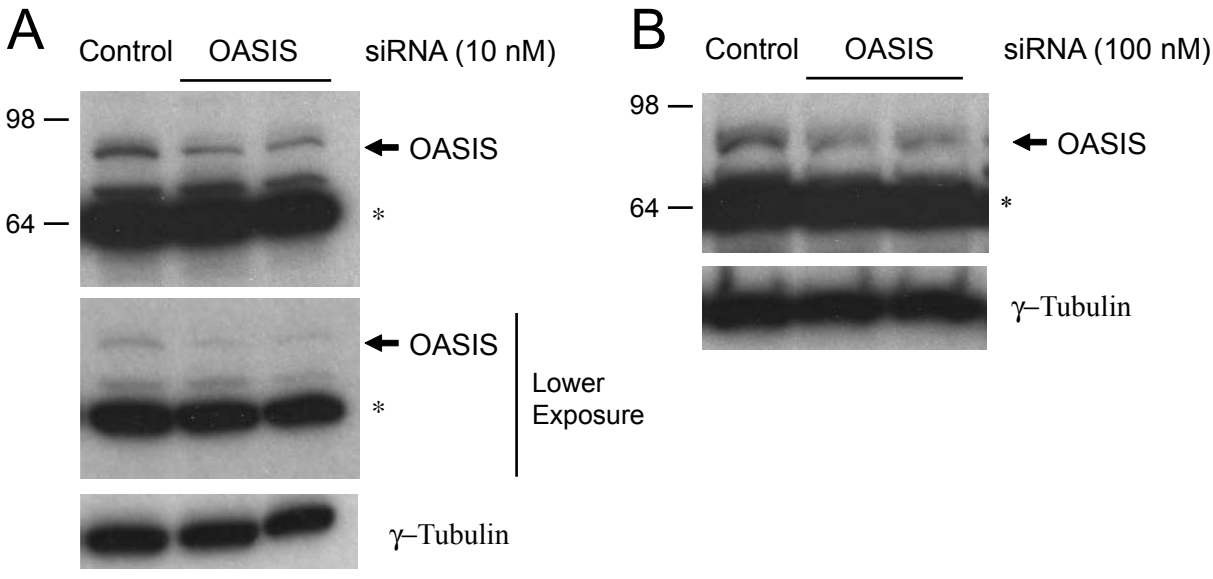

Supplemental Fig. 1. INS-1 831/13 cells were transfected with control (GFP) and OASIS siRNAs at 10 nM (A) or 100 nM (B) using Lipofectamine RNAiMax reagent (Invitrogen). The OASIS siRNA experiments were performed in duplicate. After 72h the cells were lysed in 1% TX-100 lysis buffer (A) or directly in sample buffer (B). 10 µg of protein (A) or 30 µl cell lysate (B) was resolved using 10% SDS-PAGE and immunoblotted for OASIS and γ-tubulin. Note the reduction in the top band migrating at the expected MW for OASIS in the OASIS siRNA transfected cells. The prominant band at 64 kDa is indicated with an asterisk and does not appear to be sensitive to the siRNA treatment. In (A) two different exposures of the anti-OASIS western blot are shown. Only the top OASIS band is sensitive to the siRNA. The siRNA to OASIS was obtained from Invitrogen (GAGAAAUGACUCAGCUGCCAGUGAU) and to GFP as reported previously (Zhang, L. & Volchuk, A. 2010. FEBS Letters. 584:2298)

>gi|53850649|ref|NM_001005562.1| Rattus norvegicus cAMP responsive element binding protein 3-like 1 (Creb3l1), gene-2672 bases

CAGAAGCTGCGCGGAGGAAGAGACCTAGAGAGATCTCTGCGACTCGGCAGCCACCCATCCTCGGGGGAGC
ATTGAGCTCCCCCACCCCCGGCTCCCACCCGGCCCGGGGGGCTCCTCCAGCATCGGCCCCACCCCCGGGC
TCCCCATGGAAGCCAGCTGCGCCCCGGGAGGAGCAGGAGGAGGAGTCGGCTGAAAGCCCACGGTGCTTTC
GGCGCCGCTGCCCTAAGGCCCCCCAGCGCCCCCGACCCGCGCCACCCCCACCGCTCCTCCCCCCGGGCTC
GCCGGGACCTGCCCCCGGGCCGCCTGCCCGCGCCCAGCCGCAGCCTGGTGCGGGGATCCTCGCCGCCCTG
GAGTGAGGGAAGCGCAGCCCGAAGGGGTCCCCTGGAACCCGGCGCGATGGACGCCGTCTTGGAACCTTTC
CCGGCCGACAGGCTGTTCCCGGGATCCAGCTTCCTGGACTTGGGAGACCTGAATGAGTCGGATTTCCTCA
ACAATGCGCACTTCCCGGAGCACCTGGACCACTTTGTGGAGAACATGGAGGACTTCTCCAATGACCTGTT
CAGCAGCTTCTTTGATGACCCTGTGCTGGATGAGAAGAGCCCTCTGCTGGACATGGAACTGGATTCCCCT
GCTCCAGGCATCCAGGCTGAGCACAGCTACTCCCTGAGTGGGGATTCTGCACCCCAGAGCCCCCTTGTGC
CTGTCAAAATGGAGGATACCACCCAAGATATGGAACACGGAGCATGGGCACTGGGAAACAAACTGTGCTC
CATTATGGTGAAGCAGGAGCAGAGCCCGGAGCTTCCGGTTGACCCCCTGGCTGCCTCCTCCGCCATGGCT
GCTGCTACCATGGCCACCCCACCACTGCTGGGCCTCAGCCCCATCTCCAGGCTGCCCATCCCTCACCAGG
CCCCAGGAGAAATGACTCAGCTGCCAGTGATCAAAGCAGAGCCCCCGGAAATGAGCCAGTTTCTCAAAGT
GACACAAGAGGACCTCGTACAGATGCCTCCAACACCCCCCAGCAGCCATGGCAGTGACAGTGACGGCTCC
CAGAGTCCCCGCTCTCTTCCCCCCTCCAGCCCTGTCCGGCCCATGGCCCGCTCCTCCACGGCCATTTCCA
CCTCTCCGCTCCTCACTGCCCCTCACAAACTGCAGGGGACATCAGGGCCACTGCTCTTGACAGAAGAGGA
GAAGCGAACTTTGATCGCCGAGGGTTATCCCATCCCCACCAAACTCCCCCTCACCAAGGCTGAGGAGAAG
GCCCTGAAGAGAGTGCGCAGGAAAATTAAGAACAAGATCTCTGCCCAGGAGAGCCGCCGCAAAAAGAAGG
AGTATGTGGAGTGTCTAGAGAAGAAGGTGGAGACATATACATCAGAGAACAATGAACTGTGGAAGAAGGT
GGAAACCCTAGAGACTGCCAACAGGACCCTGCTCCAGCAGCTGCAGAAACTCCAGACTCTGGTCACCAGC
AAGATCTCCAGACCTTACAAGATGGCGGCCACACAGACTGGCACTTGCCTCATGGTGGCAGCCTTGTGCT
TTGTTCTGGTGCTGGGCTCACTTGCGCCCTGCCTTCCTGCATTCTCTTCTGGCTCAAAGACTGTGAAAGA
AGACCCCGTCGCAGCTGACAGTGTCTACGCAGCCAGTCAGATGCCTTCCCGAAGCCTGCTGTTTTATGAT
GATGGGGCAGGCTCCTGGGAAGATGGCCACCGAGGTGCTCTACTGCCTGTGGAGCCCCCAGAAGGCTGGG
AGCTCAAACCCGGGGGACCAGCAGAGCCGAGGCCCCAGGACCACCTCCGACATGACCATGCGGACAGCAT
CCACGAGACAACCAAGTACTTGAGAGAGACCTGGCCAGAGGATACCGAGGACAATGGCGCCAGCCCCAAT
TTCTCCCACCCCAAGGAGTGGTTCCACGACAGGGATCTGGGCCCCAACACCACCATCAAACTCTCCTAGG
CCACTCCGAGACCCAGGACACAGGACGGACACCCTGGCACCCAGAAGAGGCGTTCTCTTGCTCACTGACC
CAGATCCAGCTCACACCCCTGCCCTGGGGCCCTCTGCCCCAGGAGAAAGGGTCTTTCTTCTCCCCAGCCC
TCCAGCTTCCTGTAGTGCCTGGGGTCCCTCTATGTCCCCGGACACTTGGACTGCTCCCCTGGGCCGACCA
CTCTGTTCCCACTTTTTCCTCCCACAACTATCCGTCCTCCTCCAATCAACCACTCACTGGGCCACCCCTG
miR-140 (259)
TTTCCTTTCCATAGTGACCAACGCAACCACTGTTCCTGGCCCCCTCATATACATACACACAAGCAGACAT
miR-140 (306)
GCACACACAAACACACACCCCCACTTCCTACTGTACAGAGACCAAGAACAGAAATCGTTTGTAAATAATG
AACCTTATTTTTTATTATTGCCGACCCCCTAAGATATTGTATTTTACAAATCTCCCTCCCGTCACCTCTC
CCTTATTTTGTATTTTATGAAGTTAGTGCGGGCTTTGCTACCCCTTGGCCTGGGACAGAGGGACACCCCA
CCCTCACCAGGCCTCCCCGTGCCGCTGCCCAAGCTGCTGGGCCTTTTTAACTGCTCCTCCACCAGCTCAG
CACACGCTTTAAGAAAGCAAAATTAAAAAAAAAAAAAAAAGATTCAGCATCAAAAAAAAAAAAAAAAAA
AAAAAAAAAAA

Yellow: cDNA (ATG-TAG); Underline: 3’ UTR of CREB3L1 gene,
Green: rno-miR-140 micro RNA target binding region.
Pink: rno-miR-140 micro RNA “Seed” regions (7mer-m8) at 259 and 306 base position of 3’ UTR

Supplemental Fig. 2. Analysis of potential micro RNA target sites in the OASIS mRNA

MicroRNA target analysis for the OASIS gene was performed with Targetscan (www. targetscan.org), miRanda/ MiRBase (http://microrna.sanger.ac.uk) and MiRtaget2 (http://

mirdb.org) programs. MicroRNAs (miRNAs) are short (21–23 nucleotides) noncoding RNA molecules that can regulate the expression of protein-coding genes. All three programs predicted that the rat microRNA, rno-miR-140 has target sites in the 3'UTR of rat OASIS mRNA. The "seed sequence" refers to the conserved 6–8mer region of the microRNA. The microRNA, rno-miR-140 (7mer-8) target seed site is detected in the 3'UTR. The seed sequence present in the 3' UTR is conserved between human, mouse and rat OASIS. By the Targetscan program the probability of conserved targeting (P_{CT}) at 0.42 is statistically significant, indicating that the conserved site is likely a miRNA target site. The seed match of 7mer-8 refers to an exact match to positions 2-8 of the mature miRNA (the seed + position 8) (Friedman et al., 2009)

Friedman RC, Farh KK, Burge CB, Bartel DP. Most mammalian mRNAs are conserved targets of microRNAs. Genome Res. 2009; 19(1):92-105.