

CCCACTT-3'; *WNT2*: 5'-AGAGTGCCAACACCAGTTCC-3' and 5'-TACAGGAGCCACTCACACCA-3'; *WNT3A*: 5'-GCGGGCATCCAGGAGTGCCAG-3' and 5'-CTCTGCACAGGAGCGTGTAC-3'; *WNT4*: 5'-GAGAAAGTGTGGCTGTGACCGG-3' and 5'-ATGTTGTCCGAGCATCCTGACC-3'; *WNT5A*: 5'-TGACAACTGGCAGAAAAACAA-3' and 5'-TCCCTGAATGGAACAACAAA-3'; *WNT5B*: 5'-GCAGTTGACCTGACCTGCTA-3' and 5'-TTCTGTACCTGCTACAGCC-3'; *WNT7A*: 5'-CCAAATGGGCTGGACGAGTG-3' and 5'-CCGGTGGTATGGCCTTGCTE-3'; *WNT7B*: 5'-TCTCTGCTTTGGCGTCTCTAC-3' and 5'-GCCAGGCCAGGAATCTGTG-3'; *WNT9B*: 5'-GGGTGTGTGTGGTGACAATC-3' and 5'-TCCAACAGGTACGAACAGCA-3'; *WNT10A*: 5'-GGCGTCTGTTCTTCTACTGCT-3' and 5'-GATAGCAGAGGCGCCACGTCAGG-3'; *WNT11*: 5'-CTGAATCAGACGCAACACTGTAAAC-3' and 5'-CTCTCTCCAGGTCAAGCAGGTAG-3'.

Assessment of glucagon-mediated Wnt gene expression was performed in primary hepatocytes that were serum-starved overnight. Cells were stimulated with glucagon (100 nM) for 2 hours before RNA isolation and subsequent Wnt isoform analysis.

For the analysis of both G6Pase and PEPCK, the following primers were used: *G6PC*: 5'-ATGAACATTCTCCATGACTTTGGG-3' and 5'-GACAGGAACTGCTTTATTATAGG-3'; *PCK1*: 5'-CATAACGGTCTGACTTCTCTGC-3' and 5'-GAATGGGATGACATACATGGTGCG-3'.

For Wnt target gene analysis, the following primers were used: *AXIN2*: 5'-AACCTATGCCCCGTTTCCTCT-3' and 5'-CTGGTACCCCAACAAGGAGT-3'; *CD1*: 5'-TCTCCTGCTACCGCACAAAC-3' and 5'-TTCCTC-CACTTCCCCCTC-3'; *MYC*: 5'-CTAGTCCGACCAGCGTCAC-3' and 5'-GTACCCCAATCCTGAACCAC-3'; *DKK1*: 5'-GAGGGGAAATTGAGGAAAGC-3' and 5'-GCAGGTGTGGAGCCTAGAAG-3'; *FRZB*: 5'-TCCAACAAGTGATCCGAGCG-3' and 5'-CTCCATACAATTGTAAGCCG-3'; *WISP2*: 5'-ATACAGGTGCCAGGAAGGTG-3' and 5'-CAAGGGCAGAAAGTTGGTGT-3'.

Analysis of gene expression in lipid metabolism was achieved with the following primers: *CPT1A*: 5'-TGACTACGGAGTCCCTGCAA-3' and 5'-GGACAACCTCCATGGCTCAG-3'; *ACOX1*: 5'-GCCTGCTGTGTGGGTATGTCATT-3' and 5'-GTCATGGCGGGTGCAT-3'; *ACCA1*: 5'-ATGCTTCCATGCTGAGATTGT-3' and 5'-TCCATCCTTGAAGCAGGCT-3'.

All gene expression results were normalized to an internal control with the following primer set: *ACTA1*: 5'-TGGCATTGTTACCAACTGGGACG-3' and 5'-GCTTCTCTTTGATGTCACGCACG-3'.

Statistical analysis

For experiments with multiple comparisons, data were first analyzed by analysis of variance (ANOVA) with Bonferroni correction. For single comparisons, a Student's *t* test was performed on data before normalization.

SUPPLEMENTARY MATERIALS

www.sciencesignaling.org/cgi/content/full/4/158/ra6/DC1

Fig. S1. Deletion of hepatic β -catenin does not alter serum insulin concentration.

Fig. S2. Quantification of FoxO1 subcellular localization.

Fig. S3. Insulin tolerance tests (ITTs) in flox/flox β -catenin mice after injection with adenoviruses encoding GFP or Cre recombinase.

Fig. S4. Subcellular localization of FoxO1 in primary hepatocytes after insulin stimulation.

Fig. S5. Deletion of β -catenin decreases the mRNA abundance of FoxO1 transcriptional targets.

Fig. S6. Knockdown of FoxO1 decreases the mRNA abundance of β -catenin transcriptional targets.

Fig. S7. Wnt stimulation increases binding of β -catenin to the *G6PC* promoter.

Fig. S8. Wnt3a stimulates hepatocyte oxygen consumption.

Fig. S9. Effects of glucagon stimulation on the abundance of mRNAs encoding Wnt ligands.

Fig. S10. The effect of β -catenin on the abundance of mRNAs encoding lipid enzymes and on triglyceride concentrations.

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