

Supplementary figure legends

Supplementary Figure 1 : IRS1 expression in colorectal carcinomas.

A Immunohistochemical staining for IRS1 was performed on tissue microarrays containing normal colonic mucosa and colorectal carcinomas. Representative samples for weakly, moderately and strongly staining colorectal carcinoma specimens, as well as moderately staining colorectal mucosa are shown.

B Analysis of IRS1 expression by IHC in colorectal carcinoma specimens scored in a semiquantitative scale of weak, moderate and strong.

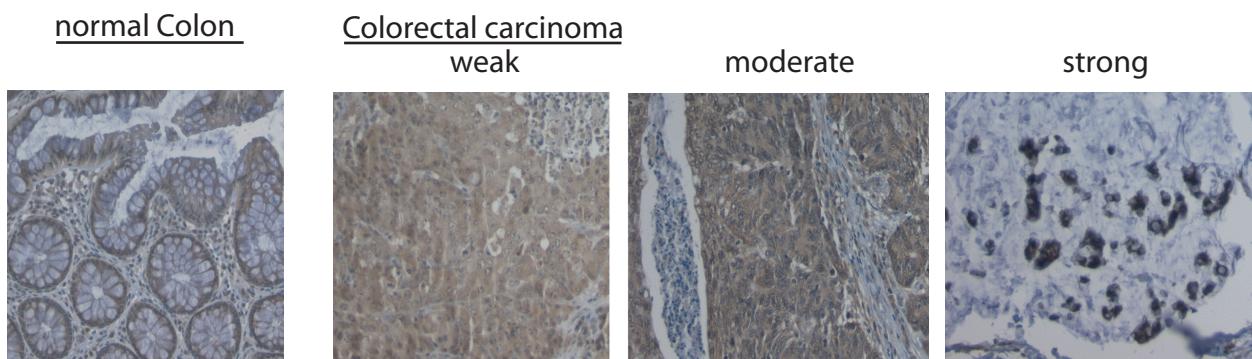
Supplementary Figure 2 : IRS1 knockdown reduces focus formation in RK3E

A Representative images of methylene blue stained plates after focus formation assay in RK3E cell lines expressing control shRNA and two different shRNAs targeting the IRS1 transcript, upon transduction with recombinant retroviruses driving expression of LacZ, wildtype β -catenin and S33Y β -catenin.

Supplementary Figure 3 : Genomic loci analyzed by chromatin immunoprecipitation.

Predicted TCF binding sites are highlighted (CTTGAT) or underlined (CWTTGWW). Mutations introduced into the downstream site 2 reporter construct are indicated in red.

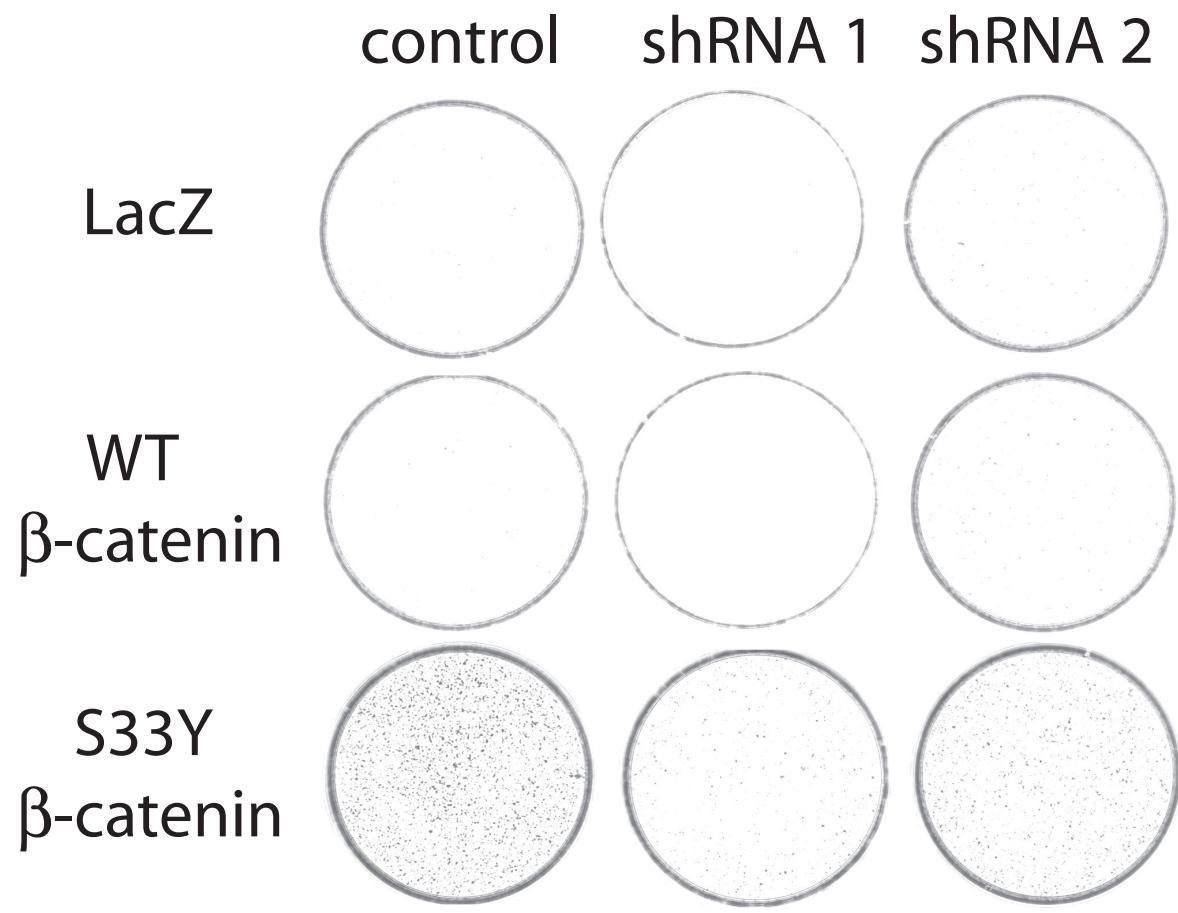
A



B

	weak	moderate	strong
colorectal cancer	16	21	7
normal mucosa	1	2	0

Bommer et al Supplementary figure 1:



Bommer et al Supplementary Figure 2

Supplementary figure 3

Genomic fragments encompassing the ChIP sites in the IRS1 locus

CTTGAT sites are shaded and underlined

CWTTGWW sites are underlined

Intronic site

AGAATACCGTAGAGGTCTGTAGCTAATGACCTATGTAACACTAGCTGGACTATTCTGGAAA
CTTGAAACAAAGGCCATTGGCAGATATATTCCTGTTTAGTATCAGTTATAAAGGA
ACATAAGGTTGTTCAGGTTAGTTAATATTAAACAATTAAAAACAACCTTTGCAAAGA
TTCATTTGGTGAATAGGATGTATATAGAAACAGCTGGTTCTGTGAAACAACCT
TCTGGGGCCCTCACAGTCAACAAGTACAGACAGCCAACTGATTATAAGGGAAAGGTGTTG
AAATATTACACATGAAACTCTAAATATGGAGAACACATACATACACACTGGTATAAAA
GAAGCCTCACTGTAATCTGTATGATCTAGCATGTCAGGAATTCTACTGCAAGAATTACAA
CAAGCTGAGACAATT CGGTGAGAGAGAAAGAAAA**ATCAATG**TCTGTGTTAAAAGAAA

downstream site 1

AAGCCATCTATTAAATTGGTATCCCAGTAAGTGTGAGTTGAGCTGCCT
TTCACTTAACCTACCATGAGCTTAAATTAAATAAAATTGTAAGAAG**ATCAAAG**TTC
CTTCTTTAATTCTTCTAGATCCTTGGGGAGACCCTGTTATCTCTGTAAAGTTCAAGTC
TGCCTAACTCTAACAGCCTAACATCTGACATCCAACCATGGAATCTGCGGAGACCATTCC
TCCTCCTTCTCAGTCTCATATTCCCATTCCCTGCCAGACTACAGTTGGAAGTTGTTGA
ATGAATTACAAGTACTACCATTGCACTTCACACACTGTTAAAGGCAGAAGTATCAGAT
TTCTCAGCACTGTGAAGAAGTTGGCAACT**TTCAAAG**CAATTGCAAGCATCTATTACATT
ATTAAGCAAGGGCAATAATGATCTACAAACTGCCAACAGCTCATG

Downstream site 2

GGGCCATATGCCAAGAATAACAGATTGAACCTTAACCTCAAGTCTGAAAAGTTCTTTAC
TGACTAGAGTTCAACCCCAGTCTATTATCCTAAACTAATGATAAGCAATC**CTTGAT**GCTG
TCCTTGAACAAGTTGTGAAGCTAAACTCAGTGAGAAAGAAAAAGCAGCATATAAAGGA
AGCTTTGAGTTAGCAGCTATGCTAATTCTTAATTGCAGACATAGTACAAACATTCACACC
TTAAGGTTGCAATAACAAGACCCA

Mutant construct for site 2 :

GGGCCATATGCCAAGAATAACAGATTGAACCTTAACCTCAAGTCTGAAAAGTTCTTTAC
TGACTAGAGTTCAACCCCAGTCTATTATCCTAAACTAATGATAAGCAATC**CTGCAT**GCTG
TCCTTGAACAAGTTGTGAAGCTAAACTCAGTGAGAAAGAAAAAGCAGCATATAAAGGA
AGCTTTGAGTTAGCAGCTATGCTAATTCTTAATTGCAGACATAGTACAAACATTCACACC
TTAAGGTTGCAATAACAAGACCCA

Downstream site 3

TATGTAAGGAAAGAACACAAGTGCCTTATCAAGCACCTGCAATTAAACACACAGCCAACG
TATATTGCAAAAGAGCATCTTATTACAAGGATACAGATACTTATCTTTAAATTAGTAGT
TATTCTAACACATACTCCCTAAGCATTCTGAATTAGAACAGGAAACAGGACTGCAAAACAGCCT
ACTTAAAAGAGAACAGCATTCTACTCTGAATTAGAACAGGAAACAGGACTGCAAAACAGCCT
AGAGACTCCTGAGCATACCTCTAGGAGAAATTTAAAGCTTTATTTACCTGAAAATACTG
ACAACAAAAGCCAATAACCTGCTGTATTACTGAGTAGTTACAATTATAGAAAAAACATT
TTTACATAATGATTGGTAAATGTCATCAT**CTTGTT**ATATTTACTTCGCCCTATATTGT
ACAAGGGCACTAAGTATTAATAACCCAATCACAGACTTCTTATTGTAAATCATTCAATT

Downstream site 4

TGTGGCTATGACTTGGAAATTATTGGTATCACTTAGTAAACACTGTTGATCTAGCATTGCC
TTCTCTCCAATTAAAAATAGAGTCTGGCC**AACAATG**ACAGGTCCCCACCACCAGGTATTGG
CCTCAGTCTGTTAGTGAAGCATTACAGCCTCTAATTGGCATTCTCTTCAGAATTGG
CAAATTGGTCAAAGCAGACCAGCACTATAGTAAACCTTCATT**ATCAATG**CAAATCCTAACAA
GAAAAGCATTCCATTCTCTTA**CATTGTA**CGTCATAATGAAACACAATAAATTATTGTG
AACACCTCTAGGAAGACATTGAAATAGACAAAGCAGAAAATGCTTGCA

Downstream site 5

AGCTTGTGATCTGAGGTGAACGACTTTATCTCCCTATTCTGCTCTTCAGCTATGAAAG
ACCTAATACACTTCTAAAAGTGAACAGGCACACATCC**CTTGAT**AACCTGTTCTCAGTTTA
GCTTGCCAGAAGTTATAACCTTATTCTTACTACAATTAAATCTTTCTTGTTAGTG
GGAGGAGAACATAATGATGTACATGCAAAACCAATATGCCAAAGAATGCATGTATTTC
CCTCTGGAAGGAGTGCATGAAAGTTAGGCATGGTAGTAAACCCGACTGATTAACCTACCA
CTGATTAGAACACTGACTCACCATACTGACTAACACACATCAGATATTATCTGGGCCAAC
CCTGGTTGACTCATAATCTATGGTTAAGATGAAGATCGGAGCTACTTTGATCTCTTCTT
GCAAGCAT**TACAAAG**AAGATAATACCTGTGACTAGCAGAGCCAACCTTACTGCCACAGAG