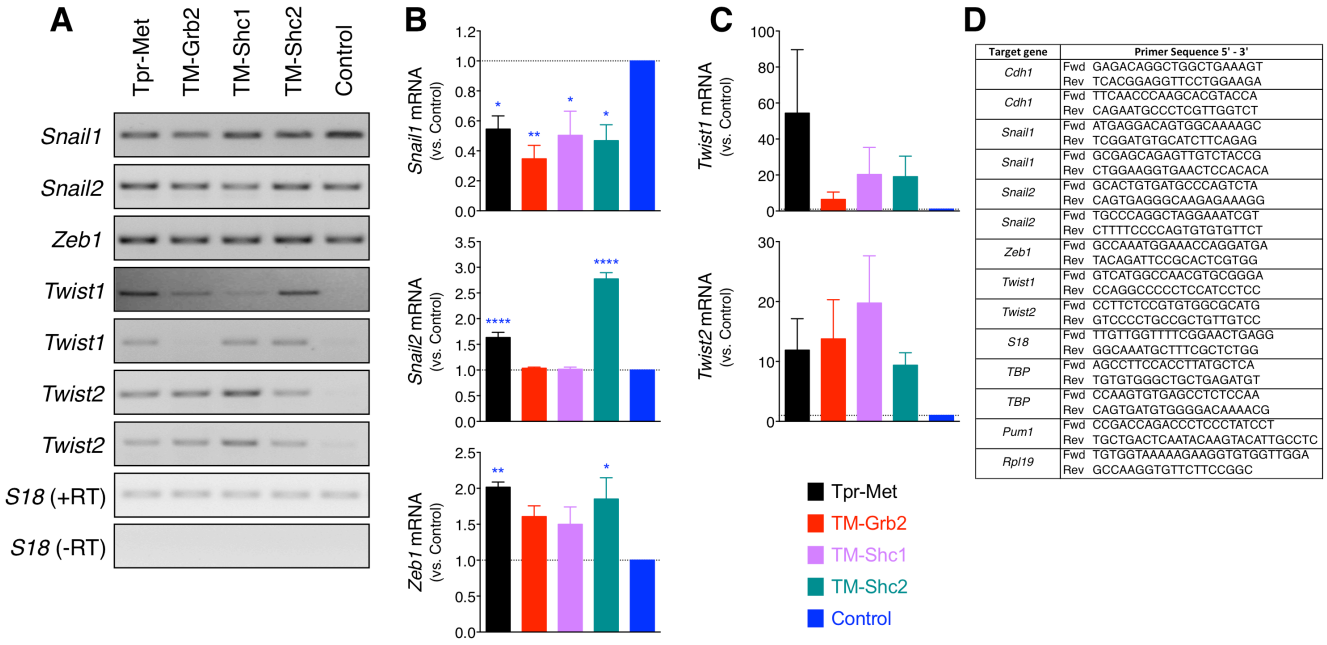

Target gene	Primer Sequence 5' - 3'
Cdh1	Fwd GAGACAGGCTGGCTGAAAGT
	Rev TCACGGAGGTTCCTGGAAGA
Cdh1	Fwd TTCAACCCAAGCACGTACCA
	Rev CAGAATGCCCTCGTTGGTCT
Snail1	Fwd ATGAGGACAGTGGCAAAAGC
	Rev TCGGATGTGCATCTTCAGAG
Snail1	Fwd GCGAGCAGAGTTGTCTACCG
	Rev CTGGAAGGTGAACTCCACACA
Snail2	Fwd GCACTGTGATGCCCAGTCTA
	Rev CAGTGAGGGCAAGAGAAAGG
Snail2	Fwd TGCCCAGGCTAGGAAATCGT
	Rev CTTTTCCCCAGTGTGTGTTCT
Zeb1	Fwd GCCAAATGGAAACCAGGATGA
	Rev TACAGATTCCGCACTCGTGG
Twist1	Fwd GTCATGGCCAACGTGCGGGA
	Rev CCAGGCCCCCTCCATCCTCC
Twist2	Fwd CCTTCTCCGTGTGGCGCATG
	Rev GTCCCCTGCCGCTGTTGTCC
S18	Fwd TTGTTGGTTTTCGGAACTGAGG
	Rev GGCAAATGCTTTCGCTCTGG
TBP	Fwd AGCCTTCCACCTTATGCTCA
	Rev TGTGTGGGCTGCTGAGATGT
TBP	Fwd CCAAGTGTGAGCCTCTCCAA
	Rev CAGTGATGTGGGGACAAAACG
Pum1	Fwd CCGACCAGACCCTCCCTATCCT
	Rev TGCTGACTCAATACAAGTACATTGCCTC
Rpl19	Fwd TGTGGTAAAAAGAAGGTGTGGTTGGA
	Rev GCCAAGGTGTTCTTCCGGC

Additional file 2 – Oncogenic Met, Grb2, and Shc signaling pathways alter the expression of critical E-cadherin transcriptional repressors. E-cadherin mRNA and protein levels were demonstrated to be further reduced in IEC-6 cells expressing the Grb2 or Shc docking-specific oncoproteins, compared to those transformed by Tpr-Met (Figure 1). Thus, the ability of these oncoproteins to alter the expression of E-cadherin transcriptional repressors was evaluated. (**A**) The mRNA levels of *Snail1*, *Snail2*, *Zeb1*, *Twist1,* and *Twist2* were analyzed by semi-quantitative RT-PCR assays performed with total RNA prepared from the indicated serum-starved cells. The *S18* mRNA level is shown as a loading control. (**B**) Relative expression levels of *Snail1*, *Snail2,* and *Zeb1* mRNAs were evaluated by quantitative RT-PCR analyses. The bar graph presents the mean fold-change (± S.E.M.) of the indicated mRNA levels relative to Control-IEC-6 cells, from three independent experiments performed in duplicate. The *TATA-binding protein* (*TBP*), *pumilio RNA-binding family member 1* (*Pum1*), and *ribosomal protein L19* (*Rpl19*) mRNA levels were used for normalization. The levels of *Snail1* mRNA were significantly reduced in all transformed IEC-6 cells (>4-fold relative to Control-IEC-6 cells). The expression of *Snail2* was slightly, but significantly, elevated in Tpr-Met and TM-Shc2-IEC-6 cells, but not in cells transformed by the TM-Grb2 or TM-Shc1 oncoproteins. A slight increase in *Zeb1* mRNA was observed in all transformed IECs when compared to control cells but did reach significance only in Tpr-Met and TM-Shc2 IEC-cells. The basal mRNA levels of *Twist1* and *Twist2* were too low in the Control-IEC-6 cells for reliable quantification by real-time RT-PCR methods. Thus, relative expression levels of *Twist1* and *Twist2* mRNAs were determined by performing semi-quantitative RT-PCR assays, with gel-based densitometric quantification of amplification products. The bar graph shows the mean fold-change (± S.D.) in *Twist1 or Twist2* mRNA levels relative to Control-IEC-6 cells normalized to *S18* mRNA levels, from three independent experiments. *Twist1* and *Twist2* mRNA levels were noticeably elevated in cells transformed by Tpr-Met, and the Grb2 and Shc docking-specific oncoproteins, but the extent of up-regulation of these two genes was highly variable between multiple assays. (**D**) Primer sequences for these RT-PCR analyses are listed. Overall, these data suggest that a combined up-regulation of *Snail2*, *Twist1* or *Twist2* mRNAs, but not of *Snail1* and *Zeb1,* underlies the down-regulation of E-cadherin induced by Met oncogenic signaling pathways and those of Grb2 and Shc in IECs.