**SUPPLEMENTAL FIGURE AND TABLE LEGENDS**

**Table S1. Long non-coding RNAs elevated in CCICs compared to their more differentiated counterpart.** Fold change increases and functions are indicated *as shown*.

**Figure S1. RNA abundance of *WNT*-ligand activated genes from sorted subpopulations of HT-29 cells enriched for the CD24 and CD44 stem cell surface antigens.** Custom IGV tracks were used to visualize the relative abundance of the primary RNA reads from Illumina HiSeq from samples of HT-29 cells gated for CD24 and CD44 enrichment**.**

**Figure S2. Ultraviolet photocrosslinking by PAR-CLIP identifies selective interactions of *RBM5-AS1*/*LUST* with β-catenin and TCF4.** Immunoprecipitation with antibodies against EZH2, β-catenin, TCF4 and CBX7 was performed, followed by isolation of the crosslinked and co-immunoprecipitated RNA in CaCo-2 cells by using Photoactivatable-Ribonucleoside-Enhanced Crosslinking and Immunoprecipitation (PAR-CLIP) application. The isolated RNA was converted into a cDNA library and measured by RT-qPCR**.**

**Figure S3. Mobility of *RBM5-AS1*/*LUST* transcript is retarded by -catenin and TCF4 from CaCo-2 cell nuclear extracts. A)** EMSA was performed using biotin labeled and unlabeled RNA species representing the full-length of *RBM5-AS1*/*LUST* transcript as shown. Nuclear extracts and antibodies used are indicated *above* the lanes. **B)** Direct binding to RNA was assessed with recombinant affinity purified full-length -catenin protein (catalogue number ab63175; AbCam). Essentially as described above the *RBM5-AS1* and sense *RBM5* RNA transcripts, as indicated, were labeled with biotin and used in EMSA studies to compare binding of  catenin to *RBM5-AS1* and *RBM5* sense RNAs.

**Figure S4. Abundance of *RBM5-AS1*/*LUST* and *AKR1B10* corresponds with mortality for patients with resected colon adenocarcinoma**. Public data sets were retrieved using R software analysis for the Cancer Genome Atlas datasets. Kaplan-Meier survival analysis was done in *R* using the ‘survival’ package (*n=187*).

**SUPPLEMENTAL MATERIALS AND METHODS**

*Flow-cytometry analysis and cell sorting*

For FACS analysis, cells were stained using the following concentrations, respectively: 0.1:10 for CD44 and 0.5:10 for CD24, CD133 and CD166. All experiments and analysis were performed as previously described ([1](#_ENREF_1),[2](#_ENREF_2)).

## *Human LncProfiler qPCR array*

LncProfilerTM qPCR array (System Biosciences) was performed according to the manufacturer’s instructions.

*RNA Electrophoretic Mobility Shift Assay (EMSA)*

The RNA EMSA experiments were performed essentially as described ([3](#_ENREF_3)). All RNA probes were gel-purified from a native polyacrylamide gel and eluted for EMSA reactions using 5μg of CaCo2 cell nuclear extract and 1μg of either -catenin (Bethyl Labs) or TCF4 antibodies (AbCam) for supershift analysis.

*Mouse xenograft studies with HT-29 colon adenocarcinoma cells*

Specific volume calculations of tumor sizes were made using the following calculations (V = w2 \* l \* π/6; with w as tumor width and “l” as the tumor length) . All experimental procedures were approved by the Icahn School of Medicine at Mount Sinai Institutional Animal Care and Use committee under protocol LA09-00445 under the guidelines approved for animal use by the NIH.

**SUPPLEMENTAL** **REFERENCES**

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