**Supplemental Material List**

* Supplemental Table 1

Gene Set enrichment data for Ribosome profiling comparing translation efficiency changes between SW480 cells overexpressing LIN28B and SW480 cells overexpressing LIN28B but with IMP1 deletion.

* Supplemental Table 2

Comparison of fold change of transcripts between the eCLIP studies(Conway et al., 2016) and our TE studies.

* Supplemental Table 3

List of all the qPCR primers used.

* Supplemental Table 4

List of all the genotyping primers used.

* Supplemental Table 5

All the sequencing primers and linkers used for library generation in ribosome profiling

* Supplemental Table 6

Gene Set enrichment data for RNA sequencing comparing mice crypt samples from Imp1 wildtype mice and mice with Imp1 deletion in the intestinal epithelium

* Supplemental Table 7

Numbers and sex distribution of mice used in all the experiments

* Supplemental Table 8

Pathway analysis using DAVID software of the differentially expressed genes from in SW480 cells overexpressing LIN28B to see what signaling/effector pathways are enriched with IMP1 deletion.

* Supplemental Table 9

The list of genes that have differential translation efficiencies in in SW480 cells overexpressing LIN28B with IMP1 deletion that are associated with Wnt signalling.

* Supplemental Table 10

The list of differentially expressed genes in in SW480 cells overexpressing LIN28B with IMP1 deletion that are associated with Wnt signalling.

* Supplemental Table 11

The list of genes differentially expressed at RNA and active translation levels between LIN28B overexpressing SW480 cells with and without CRISPR/Cas9-mediated IMP1 deletion