

Figure S1. Verification of human oncology array data via Real-Time PCR. Potential GIPR pathway downstream signaling molecules found to be upregulated on protein level upon GIPR overexpression were likewise upregulated on mRNA level in WERI (a) and Y79 RB cells (b). white bar: CTRL= cells transduced with control vector. Colored bars: GIPR overexpressing cells. Values represent means \pm SEM; not significant p-values are not shown. *p<0.05

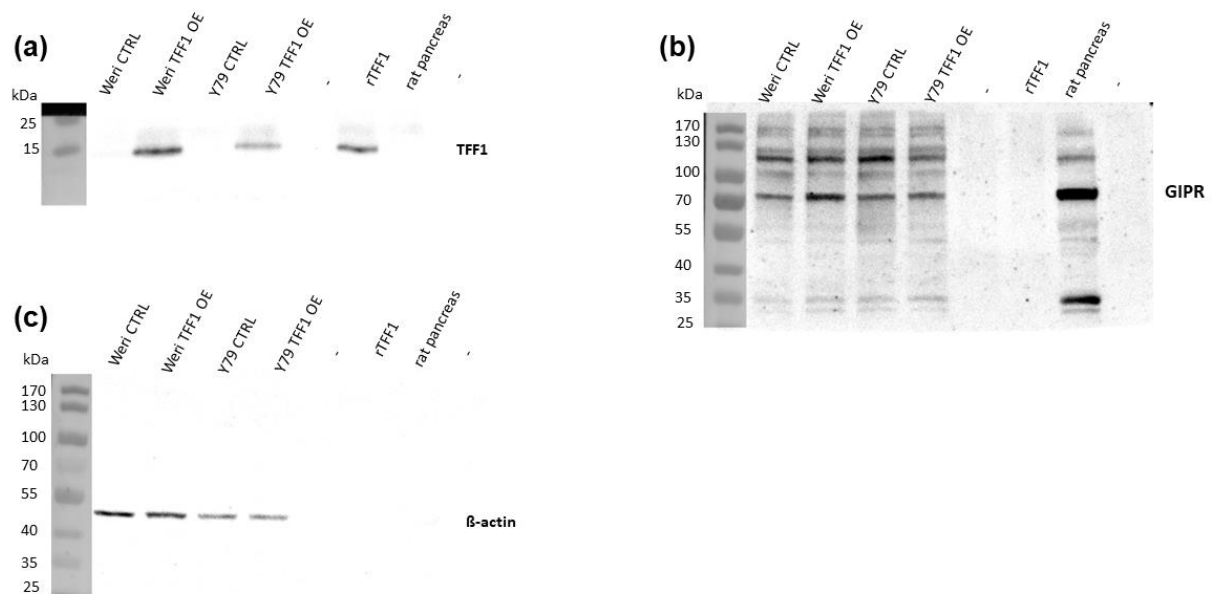


Figure S2. Uncropped Western blots shown in Figure 2c. Uncropped TFF1 (a), GIPR (b) and β -actin (c) Western blots with molecular weight markers (left lanes in KDa) of Weri and Y79 RB cells after lentiviral TFF1 overexpression. Rat pancreas served as a positive control. CTRL= cells transduced with control vector; kDa= kilodalton; rTFF1= recombinant TFF1

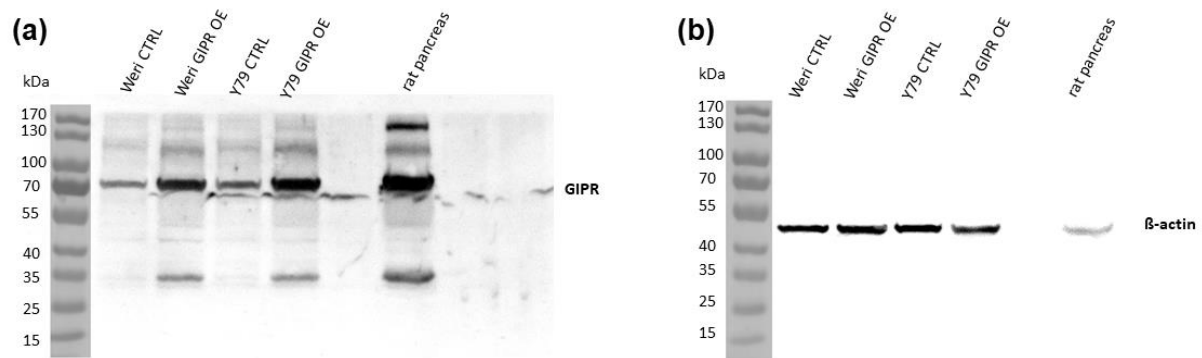


Figure S3. Uncropped Western blots shown in Figure 4b. Uncropped GIPR (a) and β-actin (b) Western blots with molecular weight markers (left lanes in kDa) of Weri and Y79 RB cells after lentiviral GIPR overexpression. Rat pancreas served as a positive control. CTRL= cells transduced with control vector; kDa= kilodalton

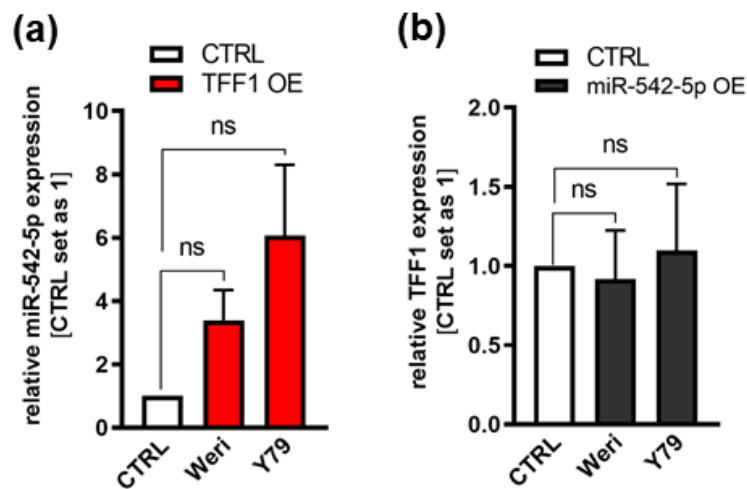


Figure S4. Hypothetical TFF1-miR-542-5p or miR-542-5p-TFF1 signaling axis. (a) Effect of TFF1 overexpression (TFF1 OE) on miR-542-5p expression levels as revealed by Real-Time PCR. (b) Effect of miR-542-5p overexpression (miR-542-5p OE) on TFF1 expression levels as revealed by Real-Time PCR. Values represent means ± SEM; ns= not significant compared to not overexpressing control (CTRL) cells.

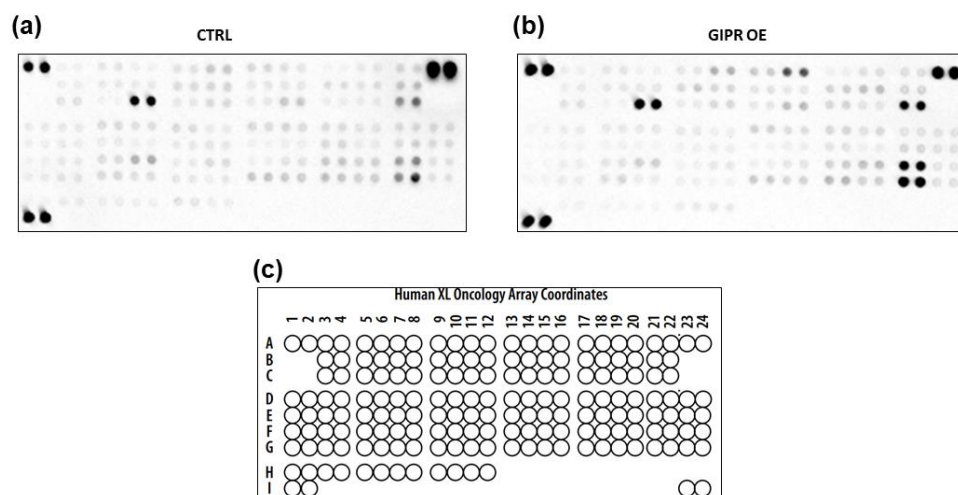


Figure S5. Uncropped human oncology array shown in Figure 10. Uncropped human oncology array of control cells (CTRL; **a**) and after GIPR overexpression (GIPR OE, **b**) in Weri Rb cells. The individual spots can be aligned according to a template (**c**) and the manufacturer's data sheet at https://resources.rndsystems.com/pdfs/datasheets/ary026.pdf?v=20240424&_ga=2.25752637.1453456629.1714036456-411853202.1714036456

Table S1. Significantly enriched GO-terms of genes differentially expressed after GIPR overexpression in Weri RB cells. count: gene numbers enriched in a specific GO-term.

GO-term	count	p-value
GO:0043066~negative regulation of apoptotic process	5	0.0000084
GO:0008284~positive regulation of cell proliferation	5	0.0000087
GO:0001934~positive regulation of protein phosphorylation	4	0.00003
GO:0051726~regulation of cell cycle	4	0.00005
GO:0042981~regulation of apoptotic process	3	0.0023
GO:0009410~response to xenobiotic stimulus	3	0.0029
GO:0008285~negative regulation of cell proliferation	3	0.0079
GO:0010628~positive regulation of gene expression	3	0.0099
GO:0045892~negative regulation of transcription	3	0.0127
GO:0006915~apoptotic process	3	0.0139

Table S2. Significantly enriched KEGG-pathways of genes differentially expressed after GIPR overexpression in Weri RB cells. count: gene numbers enriched in a specific GO-term.

KEGG-pathway	count	p-value
hsa05200:pathways in cancer	6	0.0000005
platinum drug resistance	4	0.000011
hsa04151:PI3K-Akt signaling pathway	5	0.000041
hsa05226:gastric cancer	4	0.000096
hsa05212:pancreatic cancer	3	0.0012
hsa05220:chronic myeloid leukemia	3	0.0012
hsa01521:EGFR tyrosine kinase inhibitor resistance	3	0.0012
hsa05222:small cell lung cancer	3	0.0016
hsa05215:prostate cancer	3	0.0018
hsa01522:endocrine resistance	3	0.0018
hsa04066:HIF-1 signaling pathway	3	0.0022
hsa04210:apoptosis	3	0.0035
hsa05162:measles	3	0.0036
hsa05224:breast cancer	3	0.0041
hsa05202:transcriptional misregulation in cancer 3	3	0.0070
hsa05205:proteoglycans in cancer	3	0.0078
hsa04010:MAPK signaling pathway	3	0.0165
hsa05206:microRNAs in cancer	3	0.0174