

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