

Supplementary

Name	Forward primer	Reverse primer
YAP	5'-TAGCCCTGCGTAGCCAGTTA-3'	5'-TCATGCTTAGTCCACTGTCTGT-3'
AMOTL1	5'-CCATGAATGCCGCAGCCACT-3'	5'-ACCTCCTCCTCCTCTTGCCAGA-3'
AMOTL2	5'-AAGTCGGTGCCATCTGTT-3'	5'-GGTGCTCTGTCTGTAGTCA-3'
AXL	5'-CGCTGCCTGTGTCCTCATCTTG-3'	5'-TCAGTGGTCCGACGACTGTAGG-3'
CTGF	5'-ACCGACTGGAAGACACGTTTG-3'	5'-CCAGGTCAGCTTCGCAAGG-3'
CYR61	5'-TTGGAATGGAGCCTCGCATCCT-3'	5'-AAGGCGGCACTCAGGGTTGT-3'
TEAD1	5'-GGCCCTGGCTATCTATCCACCA-3'	5'-CCTCGTCTTGCTGTCCTGAGT-3'
β -actin	5'-CCCTGGCACCCAGCAC-3'	5'-GCCGATCCACACGGAG-3'

YAP, yes-associated protein; AMOTL1, angiomin-like protein 1; AMOTL2, angiomin-like protein 2; AXL, AXL receptor tyrosine kinase; CTGF, connective tissue growth factor; CYR61, cysteine-rich protein 61; TEAD1, TEA domain transcription factor 1.

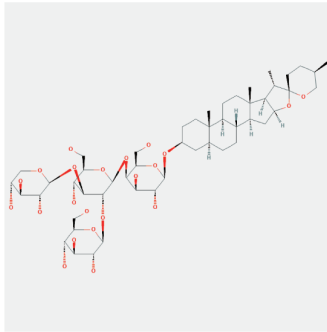
YAP ^{OE} -plasmid sequence	
YAP ^{OE}	<p>ATGGATCCCGGGCAGCAGCCGCCCTCAACCGGCCCCAGGGCCAAAGGGCAGCCGCCCTTCGAGCCCCCGCAGGGGC AGGGCCCCCGCTCCGGACCCGGCAACCGGCACCCGCGGCAGCCAGGCGGCGCCGAGGCACCCCCCGCGGGCATC AGATCGTGCACGTCCGCGGGGACTCGGAGACCGACCTGGAGGCGCTCTTCAACGCGTCATGAACCCCAAGACGGCCAACG TGCCCCAGACCGTGCCCATGAGGCTCCGGAAGCTGCCGACTCCTTCTTCAAGCCGCGGAGCCCAAATCCCACTCCCGAC AGGCCAGTACTGATGCAGGCACTGCAGGAGCCCTGACTCCACAGCATGTTGAGCTCATTCTCTCCAGCTTCTCTGCAGTTG GGAGCTGTTTCTCCTGGGACACTGACCCCACTGGAGTAGTCTCTGGCCCAGCAGCTACACCCACAGCTCAGCATCTTCGAC AGTCTTCTTTGAGATACCTGATGATGTACCTCTGCCAGCAGTTGGGAGATGGCAAAGACATCTTCTGGTCAGAGATACTTCTTA AATCACATCGATCAGACAACAACATGGCAGGACCCCAAGGAAGGCCATGCTGTCCAGATGAACGTCACAGCCCCCACCAGTC CACCAGTGCAGCAGAATATGATGAACTCGGCTTCAGCCATGAACCAGAGAATCAGTCAGAGTGCTCCAGTGAAACAGCCACCA CCCCTGGCTCCCCAGAGCCCACAGGGAGGCGTCATGGGTGGCAGCAACTCCAACCAGCAGCAACAGATGCGACTGCAGCAA CTGCAGATGGAGAAGGAGAGGCTGCGGCTGAAACAGCAAGAAGCTTTCGGCAGGAGTTAGCCCTGCGTAGCCAGTTACCAA CACTGGAGCAGGATGGTGGGACTCAAATCCAGTGTCTTCTCCCGGATGTCTCAGGAATTGAGAACAATGACGACCAATAGCT CAGATCCTTTCTTAACAGTGGCACCTATCACTCTCGAGATGAGAGTACAGACAGTGGACTAAGCATGAGCAGCTACAGTGTCC CTCGAACCCAGATGACTTCTTGAACAGTGTGGATGAGATGGATACAGGTGATACTATCAACCAAAGCACCCTGCCCTCACAGC AGAACCGTTTCCAGACTACCTTGAAGCCATTCTGGGACAAATGTGGACCTTGAACACTGGAAGGAGATGGAATGAACATAG AAGGAGAGGAGCTGATGCCAAGTCTGCAGGAAGCTTTGAGTCTGACATCCTTAATGACATGGAGTCTGTTTTGGCTGCCACCA AGCTAGATAAAGAAAGCTTTCTTACATGGTTATAG</p>

YAP^{OE}, yes-associated protein (YAP) overexpression.

Figure 1 Primer and plasmid sequences.

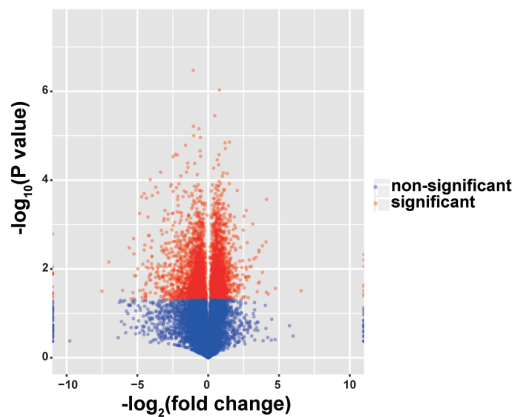
A

Chemical Structure of Degalactotigonin



(National Center for Biotechnology Information. PubChem Database. Source=Sigma-Aldrich, SID=329770112, <https://pubchem.ncbi.nlm.nih.gov/substance/329770112>.)

B



C

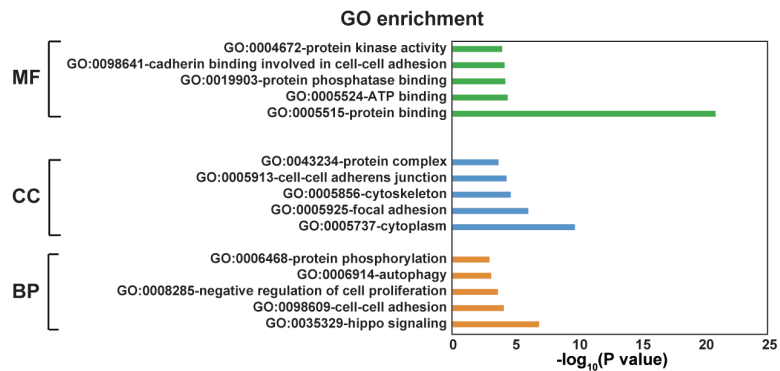


Figure S2 (A) The chemical structure of degalactotigonin is presented (available at the website <https://pubchem.ncbi.nlm.nih.gov/substance/329770112>). (B) Scatter plot of significantly differentially expressed genes in 786-O cells with or without degalactotigonin treatment. (C) Gene ontology (GO) analysis was used to classify differentially expressed genes in 786-O cells with or without degalactotigonin treatment.

Table S1 Signaling pathway analysis of significantly differentially expressed genes in control or degalactotigonin (DGT) treated 786-O cells

Pathway identifier	Pathway name	#-log ₁₀ (P)	Entities P value
R-HSA-2028269	Signaling by Hippo	4.136430337	0.000073
R-HSA-69560	Transcriptional activation of p53 responsive genes	1.796568943	0.015974639
R-HSA-69895	Transcriptional activation of cell cycle inhibitor p21	1.796568943	0.015974639
R-HSA-428359	Insulin-like growth factor-2 mRNA binding proteins (IGF2BPs/IMPs/ VICKZs) bind RNA	1.500466138	0.031588853
R-HSA-381119	Unfolded protein response (UPR)	1.472127309	0.033718845
R-HSA-381070	IRE1alpha activates chaperones	1.439299463	0.036366419
R-HSA-381038	XBP1 (S) activates chaperone genes	1.369382435	0.042718654
R-HSA-6804754	Regulation of TP53 expression	1.343186	0.045374724

R, Reactome; HSA, Homo sapiens.

Table S2 Significantly differentially expressed genes in control and degalactotigonin (DGT) treated 786-O cells

Gene	Control-1	Control-2	Control-3	DGT-1	DGT-2	DGT-3	P value	Fold change
AMOT	2.29211	1.36983	1.79556	0.712478	0.523156	0.481717	0.035449	0.314677
AMOTL1	51.26012	45.809	52.51294	30.82607	29.53478	32.32062	0.005641	0.619603
AMOTL2	25.0911	19.8289	22.3164	14.8918	10.8842	10.6842	0.007631	0.542269
DVL2	10.0039	9.79907	9.2591	13.263	13.5092	13.0765	0.00059	1.371158
LATS1	16.71751549	15.69582851	13.40665365	30.11242179	33.83888394	32.42822804	0.000343	2.103438
MOB1A	15.38069089	13.32144837	12.64070767	25.61937594	24.69038453	23.12892559	0.000671	1.776334
NPHP4	22.87434157	20.0189737	22.36269368	14.94007595	11.31860782	10.97879836	0.005416	0.570637
SAV1	5.321448365	6.658760605	6.548151196	25.79626637	25.40660827	25.39801236	0.000172	4.134251
STK4	11.06159152	11.68175134	11.76547222	23.92575897	19.99353092	23.06959611	0.009991	1.941211
WWC1	14.98695021	13.25237294	15.69304783	42.14629624	40.12990884	42.60605873	0.0000139	2.842602
YAP	18.8626	14.658	19.3661	2.59283	1.91762	1.76988	0.007723	0.118751
YWHAE	14.8928829	10.98269657	11.06684049	25.58243226	20.3183913	22.64409517	0.006653	1.855453

AMOT, angiotenin; AMOTL1, angiotenin-like protein 1; AMOTL2, angiotenin-like protein 2; DVL2, dishevelled 2; LATS1, large tumor suppressor 1; MOB1A, MOB kinase activators 1A; NPHP4, nephrocystin-4; SAV1, salvador homolog-1; STK4, serine/threonine-protein kinase 4; WWC1, WW and C2 domain containing 1; YAP, yes-associated protein; YWHAE, 14-3-3 epsilon.

Table S3 Gene Ontology (GO) analysis of significantly differentially expressed genes in control or degalactotigonin (DGT) treated 786-O cells

Category	Term	#-log ₁₀ (P value)	P value
GOTERM_BP_DIRECT	GO:0035329-hippo signaling	6.85206407	1.41E-07
GOTERM_BP_DIRECT	GO:0098609-cell-cell adhesion	4.058356326	8.74E-05
GOTERM_BP_DIRECT	GO:0008285-negative regulation of cell proliferation	3.594999918	2.54E-04
GOTERM_BP_DIRECT	GO:0006914-autophagy	3.05960331	8.72E-04
GOTERM_BP_DIRECT	GO:0006468-protein phosphorylation	2.915874225	1.21E-03
GOTERM_CC_DIRECT	GO:0005737-cytoplasm	9.690401372	2.04E-10
GOTERM_CC_DIRECT	GO:0005925-focal adhesion	5.998075054	1.00E-06
GOTERM_CC_DIRECT	GO:0005856-cytoskeleton	4.60582154	2.48E-05
GOTERM_CC_DIRECT	GO:0005913-cell-cell adherens junction	4.27922899	5.26E-05
GOTERM_CC_DIRECT	GO:0043234-protein complex	3.633268158	2.33E-04
GOTERM_MF_DIRECT	GO:0005515-protein binding	20.82728188	1.49E-21
GOTERM_MF_DIRECT	GO:0005524-ATP binding	4.37081345	4.26E-05
GOTERM_MF_DIRECT	GO:0019903-protein phosphatase binding	4.178596409	6.63E-05
GOTERM_MF_DIRECT	GO:0098641-cadherin binding involved in cell-cell adhesion	4.117277804	7.63E-05
GOTERM_MF_DIRECT	GO:0004672-protein kinase activity	3.925027976	1.19E-04

BP, biological process; CC, cellular component; MF, molecular function.