

**Supplementary Table 1. shRNA primers used in this study**

shKRAS-1	FWD	GATCCCCGTTGGAGCTGATGGCGTAGTTCAAGAGACTACGCCATCAGCTCCAACTTTTGGAAA
	REV	AGCTTTTCCAAAAAGTTGGAGCTGATGGCGTAGTCTCTTGAACACTACGCCATCAGCTCCAACGGG
shKRAS-2	FWD	GATCCCCGTTGGAGCTGTTGGCGTAGTTCAAGAGA CTACGCCAACAGCTCCAACTTTTGGAAA
	REV	AGCTTTTCCAAAAAGTTGGAGCTGTTGGCGTAGTCTCTTGAACACTACGCCAACAGCTCCAACGGG
shKRAS-3	FWD	GATCCCCGTTGGAGCTGGTGACGTAGTTCAAGAGACTACGTCACCAGCTCCAACTTTTGGAAA
	REV	AGCTTTTCCAAAAAGTTGGAGCTGGTGACGTAGTCTCTTGAACACTACGTCACCAGCTCCAACGGG
shLAT1 #1	FWD	GATCCCCGCGGCCGAGGAGAAGGAAGTTCAAGAGACTTCCTTCTCCTCGGCCGCTTTTTGGAAA
	REV	AGCTTTTCCAAAAAGCGGCCGAGGAGAAGGAAGTCTCTTGAACACTTCCTTCTCCTCGGCCGCGGG
shSLC38A2 #1	FWD	GATCCCCGGACGATTCAGTATTTCCCTTCAAGAGAGGGAAATACTGAATCGTCTTTTTGGAAA
	REV	AGCTTTTCCAAAAAGGACGATTCAGTATTTCCCTCTCTTGAAGGGAAATACTGAATCGTCCGGG
shASCT2 #1	FWD	GATCCCCCTGGATTATGAGGAATGGATTCAAGAGATCCATTCTCATAATCCAGTTTTGGAAA
	REV	AGCTTTTCCAAAAACTGGATTATGAGGAATGGATCTCTTGAATCCATTCTCATAATCCAGGGG
Scramble shRNA	FWD	GATCCCCGCGAAAGATGATAAGCTAATTCAGAGATTAGCTTATCATCTTTCGCTTTTTGGAAA
	REV	AGCTTTTCCAAAAAGCGAAAGATGATAAGCTAATCTCTTGAATTAGCTTATCATCTTTCGCGGG

**Supplementary Table 2. Real time qPCR primers**

SLC1A2 –FWD - GGTGATGTCAGCTCTCGACG  
SLC1A2 – REV – CAGGGAGGGATTGCAAGGTT

SLC1A3 –FWD - TCTTGTTTCTCTGGGGCATCT  
SLC1A3 – REV – TTGCTCAAACAAGCCAAAAC

SLC1A5 – FW - ACCAGGGTGAAGGTGCCCGT  
SLC1A5 – REV-CTTCAGGCCCCAGCTTCCGC

SLC1A6 – FWD - GAGGTCGGGAGAACCAAGTG  
SLC1A6 –REV – TCCTGCTCAGAAAATGTCCCT

SLC1A7 – FWD - TTGTGGCTTCCCTCTAAGGC  
SLC1A7 – REV – CAGGTGGTCGGAGTTGCTAA

SLC3A2 – FWD –ATGCTTGCTGGTGCCGTGGT  
SLC3A2 –REV - TTCAGACCCGCCAGGTTGCC

SLC7A1– FW –CTGGCAGCTCACGGAGGAGGA  
SLC7A1– REV -GCCCCCGACAGGACACCAGA

SLC7A2 – FW - CTCCTCTTCGCGGGACCA  
SLC7A2 – REV- AGACATCGGGCAAAGGTCAG

SLC7A5 – FW –GAGAAGGAAGAGGCGCGG  
SLC7A5 – REV -CCGAGCCGATAATGGTCCC

SLC7A6– FW –TGGCTGCTGCTTGCATATGTCTGC  
SLC7A6– REV –ATGAGCGCTACGACCTTGGCG

SLC7A7– FW –AGGCATTTGTCTGGCCTTCCCTTT  
SLC7A7– REV –TGGCATTGCCTCCTTGGTCCTG

SLC7A8– FW –TCCCCGCCCCATCAAGATCA  
SLC7A8– REV –GTGCAGCAGGAGTGGCTGGG

SLC7A9 – FW - GAGGAAGCCAGCTCCCCTA  
SLC7A9 – REV – CCATGTTTCCTCCTGCTGGT

SLC7A11 – FW - ATGGGACAAGAAACCCAGGTG  
SLC7A11 – REV – TCCCTATTTTGTGTCTCCCCTTG

SLC38A1 – FW -AGCGGCGGTGCATGTGGA  
SLC38A1 – REV –GGAAGCTTGACACCCCTGTTAGC

SLC38A2 – FW - AGCATGAAGAAGGCCGAAAT  
SLC38A2 – REV - TTCAGAGCAGCTTGCTTGG

SLC38A3 – FW – GCTGTTGCAGCCGAGTTC

SLC38A3 – REV – CACTGGTCTCACACCAACAGT

SLC38A4 – FW - CCCCACTCACACAGAACAGAG

SLC38A4 – REV – CAGCGCTTTCTTGTCCACAC

SLC38A6 – FW – CAAGTCGACTCGCTCCTCTC

SLC38A6 – REV - TCTACGAGCCTCTACCCCTG

SLC38A7 – FW- TAGATCCCCGAGGTCTGTGG

SLC38A7 – REV – CTGCAGGGAAAGGGTCTGAG

SLC38A8 – FW - CTGACGGGGGTTTATGGCTT

SLC38A8 – REV – GAGCACGATGGGGTAGACAG

SLC38A9 – FW - CCTGTTTGGACTAGGAGCCC

SLC38A9 – REV – CTCGGTGGACCTCAGTTTCC

SLC38A10 –FW- CTGTGAGAGCCAGCATCCAA

SLC38A10 –REV- TGGACACCAAACAGCATCCA

SLC6A14 –FW-ATCAGGACCGTGGTAACTGGTCCAA

SLC6A14 –REV-TCAAGAAGGCGCCTCCACCATTG

SLC6A15 –FW - AAGACACACTGACGGTGCAT

SLC6A15 –REV – TCGCCGAATTCTTTGACCCA

SLC6A18 – FW - GTCACGCTGTCCTTCCTGAT

SLC6A18 – REV – TGTTCTGTTGAGGTCCGGTG

SLC6A19 – FW - AACCTGGTCACAATCGTCCC

SLC6A19 – REV - TCTGCTGCTGTGGAGTCTTG

GAPDH- FW - GGATTTGGTGGTATTGGG

GAPDH- REV - GGAAGATGGTGATGGGATT

**Supplementary Table 3: GSEA result show differentially expressed pathways in Hke3-KRAS mutant cells.** GSEA summary table show Hke3-KRAS mutant cells upregulated KRAS signaling and several oncogenic pathways, including KRAS, AKT, MEK, MTOR and YAP pathways.

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
KRAS.50_UP.V1_DN	47	0.727041	1.672825	0	0
KRAS.LUNG.BREAST_UP.V1_DN	141	0.590906	1.479416	0	0.029072
LTE2_UP.V1_DN	195	0.577013	1.461095	0	0.027539
KRAS.300_UP.V1_DN	140	0.56784	1.414121	0	0.054492
RPS14_DN.V1_UP	190	0.546408	1.385268	0	0.069131
KRAS.LUNG_UP.V1_DN	142	0.557824	1.379666	0.002	0.061997
CSR_EARLY_UP.V1_DN	126	0.554534	1.376344	0	0.055551
LEF1_UP.V1_DN	187	0.540231	1.360715	0	0.06644
BCAT_GDS748_DN	45	0.591219	1.360629	0.029106	0.059057
PTEN_DN.V2_UP	139	0.555514	1.360524	0.002008	0.053526
KRAS.600.LUNG.BREAST_UP.V1_DN	284	0.531766	1.35987	0	0.049514
MEK_UP.V1_DN	193	0.537247	1.356174	0	0.049454
KRAS.600_UP.V1_DN	279	0.528362	1.35056	0	0.050982
<b>YAP1_UP</b>	47	0.576126	1.323469	0.03617	0.083288
AKT_UP.V1_UP	169	0.51491	1.312728	0.002	0.094015
BCAT_BILD_ET_AL_UP	45	0.561913	1.309766	0.048117	0.093536
KRAS.PROSTATE_UP.V1_DN	141	0.521345	1.308069	0.002012	0.090239
DCA_UP.V1_DN	184	0.520673	1.307438	0.002	0.08627
<b>CORDENONSI_YAP_CONSERVED_SIGNATURE</b>	57	0.553713	1.306511	0.0375	0.084002
RB_DN.V1_UP	117	0.515256	1.292628	0.022222	0.106851
ESC_V6.5_UP_EARLY.V1_DN	161	0.510946	1.284666	0.006036	0.117957
PKCA_DN.V1_DN	154	0.505047	1.274993	0.016064	0.134621
KRAS.BREAST_UP.V1_DN	143	0.51481	1.26997	0.008048	0.142399
RAPA_EARLY_UP.V1_UP	167	0.502631	1.264955	0.016	0.147812
PRC2_SUZ12_UP.V1_UP	184	0.499434	1.255737	0.004008	0.169384
NOTCH_DN.V1_UP	185	0.490813	1.24712	0.018	0.189612
PDGF_UP.V1_DN	132	0.497363	1.242207	0.030181	0.199217
SNF5_DN.V1_UP	173	0.494283	1.241386	0.018	0.195321
EIF4E_DN	100	0.495009	1.229014	0.085366	0.234694
AKT_UP_MTOR_DN.V1_UP	178	0.483054	1.218779	0.024	0.267937
ATM_DN.V1_UP	146	0.484149	1.215959	0.04	0.271283
CAHOY_ASTROGLIAL	100	0.492037	1.20911	0.092929	0.2952
IL2_UP.V1_DN	192	0.47425	1.201629	0.044177	0.324817
CYCLIN_D1_UP.V1_DN	190	0.474798	1.195467	0.042	0.347847
CAHOY_ASTROCYTIC	100	0.487623	1.194946	0.120724	0.340649
IL15_UP.V1_DN	185	0.470222	1.187365	0.054	0.370684
TBK1.DN.48HRS_UP	50	0.512096	1.186988	0.174004	0.363303
JAK2_DN.V1_DN	144	0.475617	1.184571	0.068273	0.366844
NRL_DN.V1_UP	136	0.473472	1.18423	0.088	0.359507
ALK_DN.V1_DN	139	0.473899	1.183517	0.100402	0.354321
IL21_UP.V1_DN	186	0.467553	1.18291	0.066	0.348241
CSR_LATE_UP.V1_DN	147	0.470532	1.179778	0.090361	0.356131
RAPA_EARLY_UP.V1_DN	184	0.464849	1.174293	0.086	0.377339
CRX_NRL_DN.V1_UP	140	0.467575	1.173311	0.118952	0.373372
PTEN_DN.V1_UP	185	0.468173	1.171977	0.076	0.372629
KRAS.DF.V1_DN	192	0.458927	1.168303	0.07014	0.384446
PRC1_BMI_UP.V1_DN	187	0.462202	1.168163	0.068	0.376907
MTOR_UP.N4.V1_DN	183	0.464254	1.168026	0.078	0.369604
VEGF_A_UP.V1_UP	195	0.462448	1.166695	0.082164	0.368077

**Supplementary Table 4: GSEA result show downregulation of major Hallmark pathways in siYAP transfected HCT116 cells.** GSEA summary table show HCT116 cells upregulated mTORC1 signaling and several oncogenic pathways, including E2F, G2M, and MYC, while YAP siRNA transfected cells had a significant downregulation of genes in the E2F, G2M, MTORC1 and MYC pathways.

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
HALLMARK_E2F_TARGETS	199	-0.69647	-3.06596	0	0
HALLMARK_G2M_CHECKPOINT	199	-0.6802	-3.0027	0	0
HALLMARK_MITOTIC_SPINDLE	198	-0.54339	-2.34664	0	0
HALLMARK_INTERFERON_ALPHA_RESPONSE	96	-0.55896	-2.23639	0	0
HALLMARK_DNA_REPAIR	150	-0.47329	-2.00096	0	0
HALLMARK_INTERFERON_GAMMA_RESPONSE	200	-0.44235	-1.92045	0	0
HALLMARK_ESTROGEN_RESPONSE_LATE	199	-0.43515	-1.91705	0	0
HALLMARK_UV_RESPONSE_UP	158	-0.44206	-1.88693	0	1.45E-04
HALLMARK_P53_PATHWAY	199	-0.41436	-1.81642	0	5.15E-04
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	112	-0.43743	-1.7759	0.001368	8.48E-04
HALLMARK_UV_RESPONSE_DN	144	-0.42068	-1.77492	0	7.71E-04
HALLMARK_MTORC1_SIGNALING	199	-0.40217	-1.75352	0	8.86E-04
HALLMARK_ESTROGEN_RESPONSE_EARLY	198	-0.38413	-1.68139	0	0.003781
HALLMARK_CHOLESTEROL_HOMEOSTASIS	73	-0.43555	-1.65951	0	0.004252
HALLMARK_APOPTOSIS	161	-0.38847	-1.65605	0	0.003969
HALLMARK_GLYCOLYSIS	200	-0.37827	-1.65468	0	0.003721
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	200	-0.35431	-1.54489	0	0.013719
HALLMARK_ANDROGEN_RESPONSE	100	-0.3693	-1.46835	0.015537	0.028393
HALLMARK_TNFA_SIGNALING_VIA_NFKB	198	-0.32999	-1.45419	0.007692	0.03105
HALLMARK_HYPOXIA	200	-0.32806	-1.4411	0.002497	0.034345
HALLMARK_MYC_TARGETS_V1	200	-0.3252	-1.42694	0.006361	0.037397
HALLMARK_SPERMATOGENESIS	135	-0.34267	-1.42005	0.01626	0.038783
HALLMARK_MYC_TARGETS_V2	58	-0.36894	-1.36655	0.071207	0.063522
HALLMARK_HEME_METABOLISM	200	-0.30494	-1.33308	0.034527	0.084506
HALLMARK_KRAS_SIGNALING_UP	199	-0.30061	-1.31887	0.02799	0.091213
HALLMARK_IL2_STAT5_SIGNALING	197	-0.29384	-1.29437	0.046572	0.108145

**Supplementary Table 5. GSEA result show downregulation of major oncogenic signalling pathways in siYAP transfected HCT116 cells.** GSEA summary table show HCT116 cells upregulated Cordenonsi\_YAP\_conserved\_signature, E2F, EGFR, mTORC1 signaling and several oncogenic pathways, including MEK and MYC, while YAP siRNA transfected cells had a significant downregulation of genes in the Cordenonsi YAP conserved signature, MEK, E2F, MTOR and MYC oncogenic pathways.

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
CORDENONSI_YAP_CONSERVED_SIGNATURE	57	-0.70353	-2.59526	0	0	0
RPS14_DN.V1_DN	186	-0.55987	-2.43561	0	0	0
CSR_LATE_UP.V1_UP	163	-0.56055	-2.41421	0	0	0
RB_P107_DN.V1_UP	129	-0.57326	-2.36787	0	0	0
E2F1_UP.V1_UP	188	-0.52359	-2.28718	0	0	0
E2F3_UP.V1_UP	185	-0.50543	-2.20597	0	0	0
VEGF_A_UP.V1_DN	193	-0.49335	-2.17613	0	0	0
TBK1.DF_UP	286	-0.47382	-2.17589	0	0	0
PRC2_EZH2_UP.V1_DN	191	-0.49764	-2.17092	0	0	0
GCNP_SHH_UP_LATE.V1_UP	178	-0.46995	-2.02557	0	9.72E-05	0.001
PRC2_EED_UP.V1_DN	193	-0.45341	-1.96481	0	8.83E-05	0.001
LTE2_UP.V1_DN	195	-0.44528	-1.95101	0	8.10E-05	0.001
SIRNA_EIF4GI_DN	97	-0.47526	-1.89752	0	3.80E-04	0.005
RAF_UP.V1_UP	193	-0.43187	-1.88164	0	4.17E-04	0.006
TBK1.DN.48HRS_DN	49	-0.52467	-1.85378	0	5.14E-04	0.008
EGFR_UP.V1_DN	196	-0.42149	-1.83506	0	7.79E-04	0.013
TBK1.DF_DN	284	-0.40633	-1.8347	0	7.33E-04	0.013
HOXA9_DN.V1_DN	189	-0.42084	-1.82853	0	8.50E-04	0.016
GCNP_SHH_UP_EARLY.V1_UP	168	-0.42573	-1.82342	0	8.05E-04	0.016
ERBB2_UP.V1_DN	197	-0.39968	-1.76638	0	0.001574	0.033
P53_DN.V1_UP	192	-0.40365	-1.74736	0	0.001869	0.041
CAMP_UP.V1_UP	195	-0.40009	-1.74202	0	0.001913	0.044
EGFR_UP.V1_UP	189	-0.40217	-1.73773	0	0.00196	0.047
MEK_UP.V1_DN	192	-0.39162	-1.71497	0	0.002561	0.064
LTE2_UP.V1_UP	187	-0.3932	-1.70345	0	0.00308	0.08
PTEN_DN.V2_UP	137	-0.40842	-1.70028	0	0.003032	0.08
RB_DN.V1_UP	117	-0.40978	-1.68945	0.001383	0.003358	0.091
KRAS.DF.V1_UP	190	-0.39158	-1.68098	0	0.003544	0.099
AKT_UP.V1_UP	167	-0.3894	-1.66847	0	0.00399	0.114
SNF5_DN.V1_UP	170	-0.38692	-1.66487	0	0.003955	0.117
STK33_DN	276	-0.36071	-1.65047	0	0.004616	0.139
RAF_UP.V1_DN	192	-0.3743	-1.64854	0	0.004502	0.139
RB_P130_DN.V1_UP	127	-0.39573	-1.64136	0	0.004689	0.15
BMI1_DN.V1_UP	145	-0.39015	-1.64036	0	0.004612	0.152
MEK_UP.V1_UP	195	-0.36772	-1.61756	0	0.005899	0.195
EIF4E_DN	100	-0.39046	-1.56786	0.001399	0.010991	0.335
MTOR_UP.N4.V1_UP	194	-0.3589	-1.5646	0	0.011169	0.35
LEF1_UP.V1_UP	191	-0.3582	-1.55002	0.001321	0.012911	0.407
STK33_NOMO_DN	276	-0.34082	-1.54662	0	0.013058	0.416
MTOR_UP.V1_UP	164	-0.36071	-1.53829	0.002663	0.014223	0.45
CAHOY_OLIGODENDROCUTIC	96	-0.38781	-1.5323	0.01273	0.014851	0.472
BCAT_GDS748_UP	48	-0.41912	-1.48121	0.041411	0.026466	0.681