

NAME	link to category	FDR_logFC_5SA_YAP_A431.top.txt	FDR_logFC_siYAP_siCTRL_A431.bottom.txt	FDR_logFC_siYAP_siCTRL_HaCAT.bottom.txt
YAP signalling				
REACTOME_SIGNALING_BY_HIPPO	http://www.broadinstitute.org/gsea/msig	0.27403983	0.0845902	0.016429855
REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_GENE_EXPRESSION	http://www.broadinstitute.org/gsea/msig	0.09720611	0.27879855	0.2792244
Cell cycle				
REACTOME_G1_S_TRANSITION	http://www.broadinstitute.org/gsea/msig	0.02010638	0	0.000541
REACTOME_MITOTIC_M_M_G1_PHASES	http://www.broadinstitute.org/gsea/msig	0.02990606	0.000957	0
REACTOME_DNA_REPLICATION	http://www.broadinstitute.org/gsea/msig	0.030264564	7.26E-05	0.004145181
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR	http://www.broadinstitute.org/gsea/msig	0.031962935	0	0.01134645
REACTOME_ORC1_RESERVED_FROM_CHROMATIN	http://www.broadinstitute.org/gsea/msig	0.03266372	0.00101811	0.009737373
REACTOME_M_G1_TRANSITION	http://www.broadinstitute.org/gsea/msig	0.033798005	0	0
REACTOME_S_PHASE	http://www.broadinstitute.org/gsea/msig	0.034246594	0	0.005542807
REACTOME_SYNTHESIS_OF_DNA	http://www.broadinstitute.org/gsea/msig	0.04779358	0	0.005340172
REACTOME_CELL_CYCLE_CHECKPOINTS	http://www.broadinstitute.org/gsea/msig	0.06410079	2.78E-05	0
GRAHAM_CM1_DIVIDING_VS_NORMAL_QUIESCENT_UP	http://www.broadinstitute.org/gsea/msig	0.08075432	0	0.001076271
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION	http://www.broadinstitute.org/gsea/msig	0.08450873	0.021575017	0.024000246
BENPORATH_PROLIFERATION	http://www.broadinstitute.org/gsea/msig	0.0936338	0	0.001335144
GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN	http://www.broadinstitute.org/gsea/msig	0.10780007	0	0
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CD	http://www.broadinstitute.org/gsea/msig	0.11104746	0.00605393	0.001100282
SGCGSAAA_V52F1DP2_01	http://www.broadinstitute.org/gsea/msig	0.1132266	0.000446	0.36994377
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	http://www.broadinstitute.org/gsea/msig	0.12175222	0.00714292	0.003874929
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	http://www.broadinstitute.org/gsea/msig	0.123232574	2.74E-05	0.01285284
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OT	http://www.broadinstitute.org/gsea/msig	0.12268792	0.041439086	0.001123692
REACTOME_APC_C_CD20_MEDIATED_DEGRADATION_OF_MITOTIC_PROT	http://www.broadinstitute.org/gsea/msig	0.124558374	0.05772412	0.00103512
V52F1_Q8	http://www.broadinstitute.org/gsea/msig	0.1419023	8.25E-05	0.2755916
REN_ROUND_BY_E2F	http://www.broadinstitute.org/gsea/msig	0.15824489	0	0.000168
V52F1DP2_01	http://www.broadinstitute.org/gsea/msig	0.1583431	0.000461	0.36111528
V52F1DP2_01	http://www.broadinstitute.org/gsea/msig	0.15922602	0.000316	0.308822
E2F1_UP_V1_UP	http://www.broadinstitute.org/gsea/msig	0.16001372	0.07726121	0.13206807
V52F1DP1_01	http://www.broadinstitute.org/gsea/msig	0.1625169	0.000331	0.3450875
V52F1_Q8_01	http://www.broadinstitute.org/gsea/msig	0.1640632	0.004975112	0.37715355
V52F1_Q2	http://www.broadinstitute.org/gsea/msig	0.16427012	0.000364	0.30976173
ISHIDA_E2F_TARGETS	http://www.broadinstitute.org/gsea/msig	0.16454798	0	0
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	http://www.broadinstitute.org/gsea/msig	0.17069401	0	0.003772688
REACTOME_CELL_CYCLE_MITOTIC	http://www.broadinstitute.org/gsea/msig	0.18161228	0.001131917	0.024216514
V52F1DP1_01	http://www.broadinstitute.org/gsea/msig	0.18244343	0.000679	0.5290016
V52F1_Q3	http://www.broadinstitute.org/gsea/msig	0.1880097	0.007132111	0.5434143
V52F1_Q4	http://www.broadinstitute.org/gsea/msig	0.18903509	0.000138	0.39689186
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR	http://www.broadinstitute.org/gsea/msig	0.19078194	0.008684116	0.002806893
REACTOME_G2_M_CHECKPOINTS	http://www.broadinstitute.org/gsea/msig	0.19329703	0	0.001109398
V52F1_Q8	http://www.broadinstitute.org/gsea/msig	0.19384018	0.000136	0.3448235
WHITFIELD_CELL_CYCLE_LITERATURE	http://www.broadinstitute.org/gsea/msig	0.20453149	7.48E-05	0.003303728
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	http://www.broadinstitute.org/gsea/msig	0.20505580	6.67E-05	0.030043823
CHANG_CYCLING_GENES	http://www.broadinstitute.org/gsea/msig	0.21735805	0	0.000558
KEGG_DNA_REPLICATION	http://www.broadinstitute.org/gsea/msig	0.21759363	0	0.11667396
REACTOME_DNA_STRAND_ELONGATION	http://www.broadinstitute.org/gsea/msig	0.2220706	0	0.048146147
REACTOME_MITOTIC_G1_G1_S_PHASES	http://www.broadinstitute.org/gsea/msig	0.22380826	0	0.001282028
KONG_E2F_TARGETS	http://www.broadinstitute.org/gsea/msig	0.22829128	0	0.000138
OLSON_E2F_TARGETS_DN	http://www.broadinstitute.org/gsea/msig	0.25124517	0.18841921	0.3222239
KAUFFMANN_DNA_REPLICATION_GENES	http://www.broadinstitute.org/gsea/msig	0.25262678	0	0.059563834
Cell growth				
REACTOME_MRNA_PROCESSING	http://www.broadinstitute.org/gsea/msig	0.012915894	0.002623442	0.001638745
BURTON_ADIPONECTIN_PEAK_AT_16HR	http://www.broadinstitute.org/gsea/msig	0.035835117	0	0.0853237
REACTOME_TRNA_AMINOACYLATION	http://www.broadinstitute.org/gsea/msig	0.046430897	0.1984875	0.004750761
RNA_PROCESSING	http://www.broadinstitute.org/gsea/msig	0.04649598	0.001356013	0.011267367
KEGG_SPLICING	http://www.broadinstitute.org/gsea/msig	0.057477616	0.057894554	0.13498631
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	http://www.broadinstitute.org/gsea/msig	0.06119907	0.028434383	0.005405107
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	http://www.broadinstitute.org/gsea/msig	0.06144109	0.23855021	0.013823001
MRNA_PROCESSING_0006397	http://www.broadinstitute.org/gsea/msig	0.08926187	0.01572194	0.012224521
REACTOME_TRANSCRIPTION	http://www.broadinstitute.org/gsea/msig	0.09406843	0	0.007614609
REACTOME_RNA_POL_I_TRANSCRIPTION	http://www.broadinstitute.org/gsea/msig	0.104830325	0.059167907	0.012420549
RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	http://www.broadinstitute.org/gsea/msig	0.10811508	0.11179424	0.21043202
RNA_HELICASE_ACTIVITY	http://www.broadinstitute.org/gsea/msig	0.120443721	0.2004321	0.08311878
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	http://www.broadinstitute.org/gsea/msig	0.20327962	0.028316427	0.017792491
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPT	http://www.broadinstitute.org/gsea/msig	0.23740312	0	0.04974437
REACTOME_TRANSPORT_OF_MATURING_MRNA_DERIVED_FROM_AN_INTRON	http://www.broadinstitute.org/gsea/msig	0.24279736	0.049280223	0.04197069
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	http://www.broadinstitute.org/gsea/msig	0.26221517	0.05235285	0.04195959
SPLICING	http://www.broadinstitute.org/gsea/msig	0.27259094	0.23129094	0.02454544
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	http://www.broadinstitute.org/gsea/msig	0.27634937	0.23457132	0.042890634
RNA_POLYMERASE_ACTIVITY	http://www.broadinstitute.org/gsea/msig	0.28282723	0.023127701	0.044442423
Cancer/metastasis				
GRADE_COLOR_AND_RECTAL_CANCER_UP	http://www.broadinstitute.org/gsea/msig	0.03838893	0.21228471	0.003991324
KOBAYASHI_EGFR_SIGNALING_24HR_DN	http://www.broadinstitute.org/gsea/msig	0.0505721	0	0.000573
SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM	http://www.broadinstitute.org/gsea/msig	0.030234784	0.021466859	0
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	http://www.broadinstitute.org/gsea/msig	0.033990975	0	0
BOYAUULT_LIVER_CANCER_SUBCLASS_G3_UP	http://www.broadinstitute.org/gsea/msig	0.043235235	0.004435256	0.018923517
NAKAMURA_CANCER_MICROENVIRONMENT_DN	http://www.broadinstitute.org/gsea/msig	0.048736367	0.00668	0.15767501
SABRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP	http://www.broadinstitute.org/gsea/msig	0.06540228	0.06540228	0.031196701
WINNENFENICK_MELANOMA_METASTASIS_UP	http://www.broadinstitute.org/gsea/msig	0.0807091	0.000266	0.001537526
RHODES_UNDIFFERENTIATED_CANCER	http://www.broadinstitute.org/gsea/msig	0.10512301	0.001352914	0.00111937
KAUFFMANN_MELANOMA_RELAPSE_UP	http://www.broadinstitute.org/gsea/msig	0.105220415	0	0.007739451
TOMIDA_METASTASIS_UP	http://www.broadinstitute.org/gsea/msig	0.10571032	0.041445088	0.21375494
VECCO_GASTRIC_CANCER_EARLY_UP	http://www.broadinstitute.org/gsea/msig	0.207774	0.207774	0.05323398
ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN	http://www.broadinstitute.org/gsea/msig	0.26681277	0.001433474	0.028167572
CRONQUIST_NRAS_SIGNALING_DN	http://www.broadinstitute.org/gsea/msig	0.29664127	0	0.000191
DANG_MYC_TARGETS_UP	http://www.broadinstitute.org/gsea/msig	0.29295662	0.16562039	0
BORCEKUX_MALIGNANT_MESOTHELIOMA_UP	http://www.broadinstitute.org/gsea/msig	0.2960386	0.25912035	0.17807612
RHODES_CANCER_METASTASIS_SIGNATURE	http://www.broadinstitute.org/gsea/msig	0.2927492	0.15227412	0.024029912
DANG_MYC_TARGETS_UP	http://www.broadinstitute.org/gsea/msig	0.29295662	0.16562039	0
BOYAUULT_LIVER_CANCER_SUBCLASS_G123_UP	http://www.broadinstitute.org/gsea/msig	0.29370321	0.08395546	0.049637258
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	http://www.broadinstitute.org/gsea/msig	0.29377588	0.000135	0.01669378
PUANA_BREAST_CANCER_UT_NETWORK	http://www.broadinstitute.org/gsea/msig	0.27327272	0.003610279	0.024503974
DAIRKEE_CANCER_PHONE_RESPONSE_BPA	http://www.broadinstitute.org/gsea/msig	0.2751443	0.22182393	0.052520353
SMID_BREAST_CANCER_LUMINAL_A_DN	http://www.broadinstitute.org/gsea/msig	0.29719597	0.020338075	0.005284015

TEAD binding site analysis:

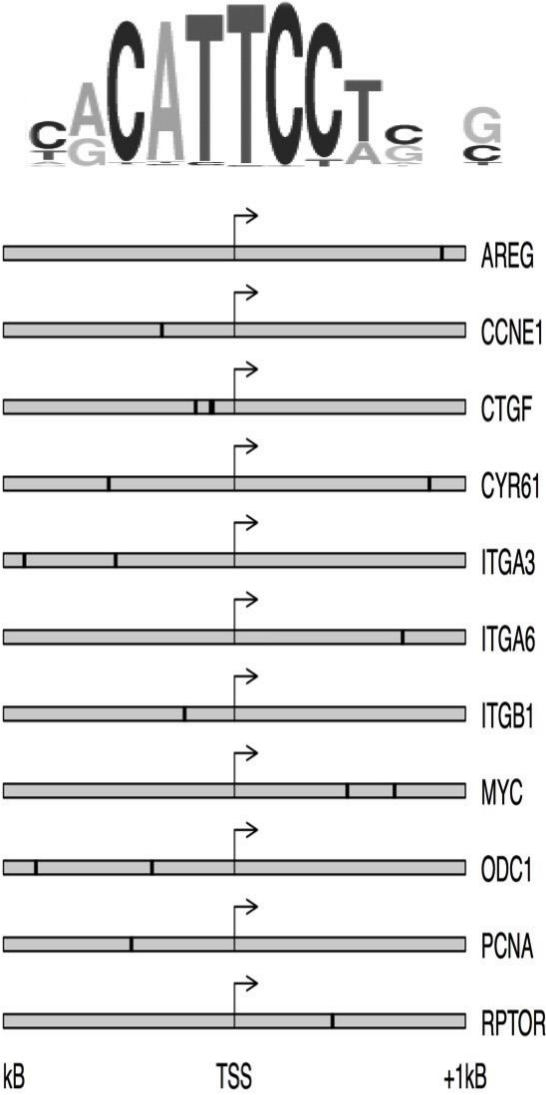


Fig. S1. Gene set enrichment analysis of YAP target genes in keratinocytes. RNAseq analysis was performed on A431 keratinocytes transfected with YAP5SA or siRNA against YAP. Results were compared to HaCaT keratinocytes. Gene sets induced upon YAP5SA expression and decreased upon YAP siRNA are listed in the table. Individual genes that are crucial regulators of each gene set contain several TEAD-specific binding motifs within 1kb of their transcription start sites.

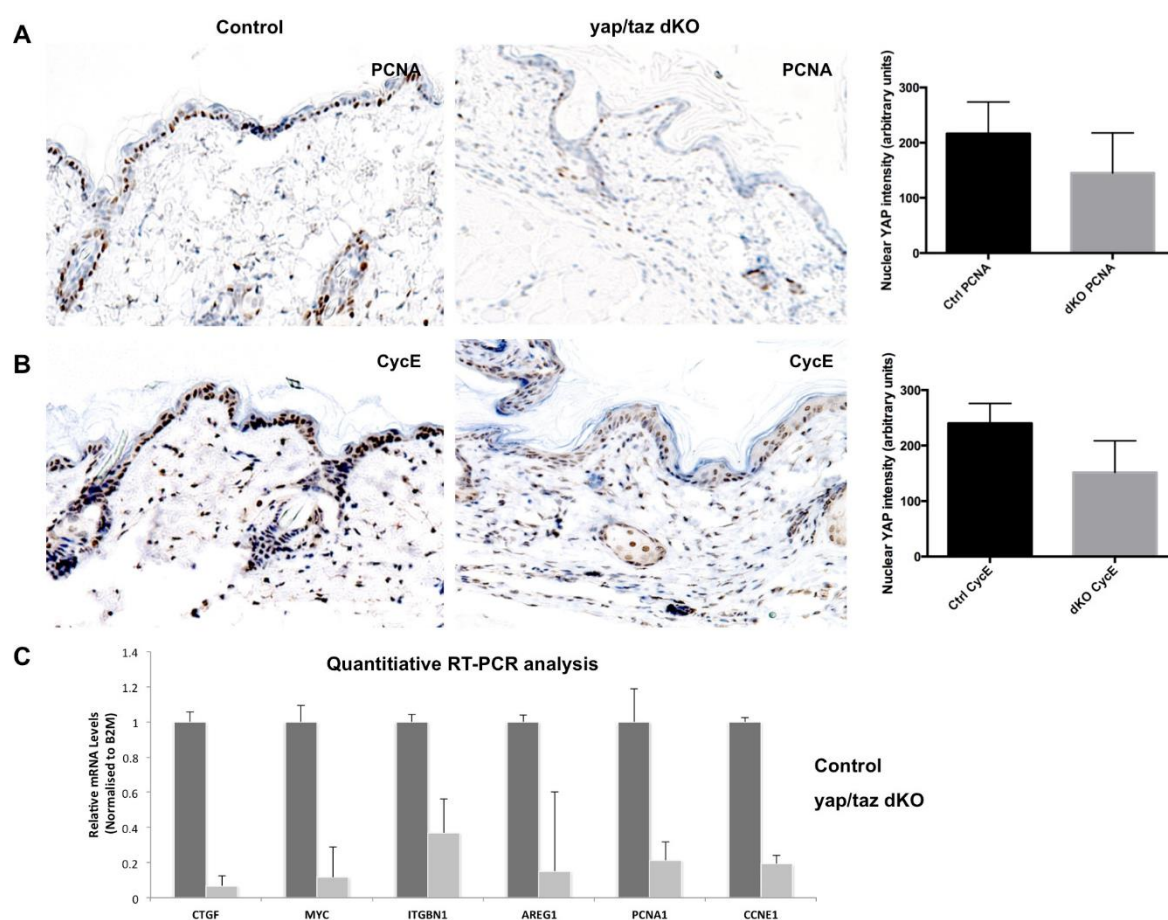


Fig. S2. Reduction in YAP/TAZ target gene expression in yap/taz double knockout skin. Several YAP-dependent genes identified in RNAseq experiments were selected for analysis in wild type versus yap/taz double conditional knockout skin. (A) We find downregulation of PCNA at the protein level by immunostaining. Quantitation was performed on $n=300$ cells from at least 3 different mice. (B) We find downregulation of CyclinE at the protein level by immunostaining. Quantitation was performed on $n=300$ cells from at least 3 different mice. (C) We find downregulation of multiple YAP-dependent genes at the mRNA level by quantitative RT-PCR.

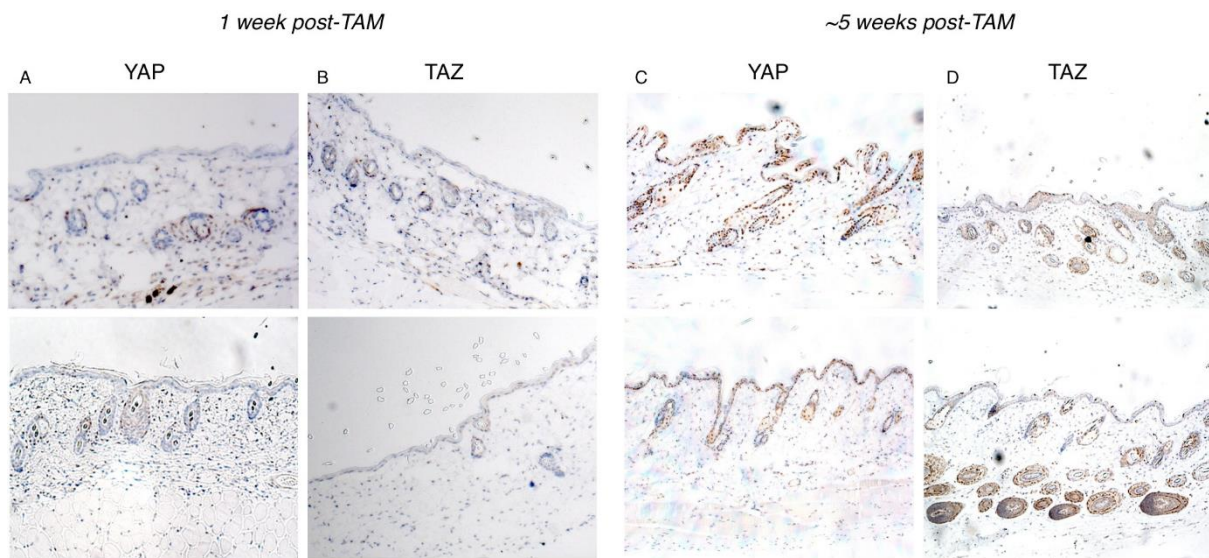


Fig. S3. Repopulation of YAP/TAZ dKO skin by cells escaping Cre-mediated recombination. (A) YAP staining is low in backskin 1 week post-tamoxifen administration (note mosaic deletion). (B) TAZ staining is low in backskin 1 week post-tamoxifen administration. (C) YAP staining is increased in the basal cells of the epidermis, similar to wild type levels, in backskin ~5 week post-tamoxifen administration. (D) TAZ staining is increased in the basal cells of the epidermis, similar to wild type levels, in backskin ~5 week post-tamoxifen administration.

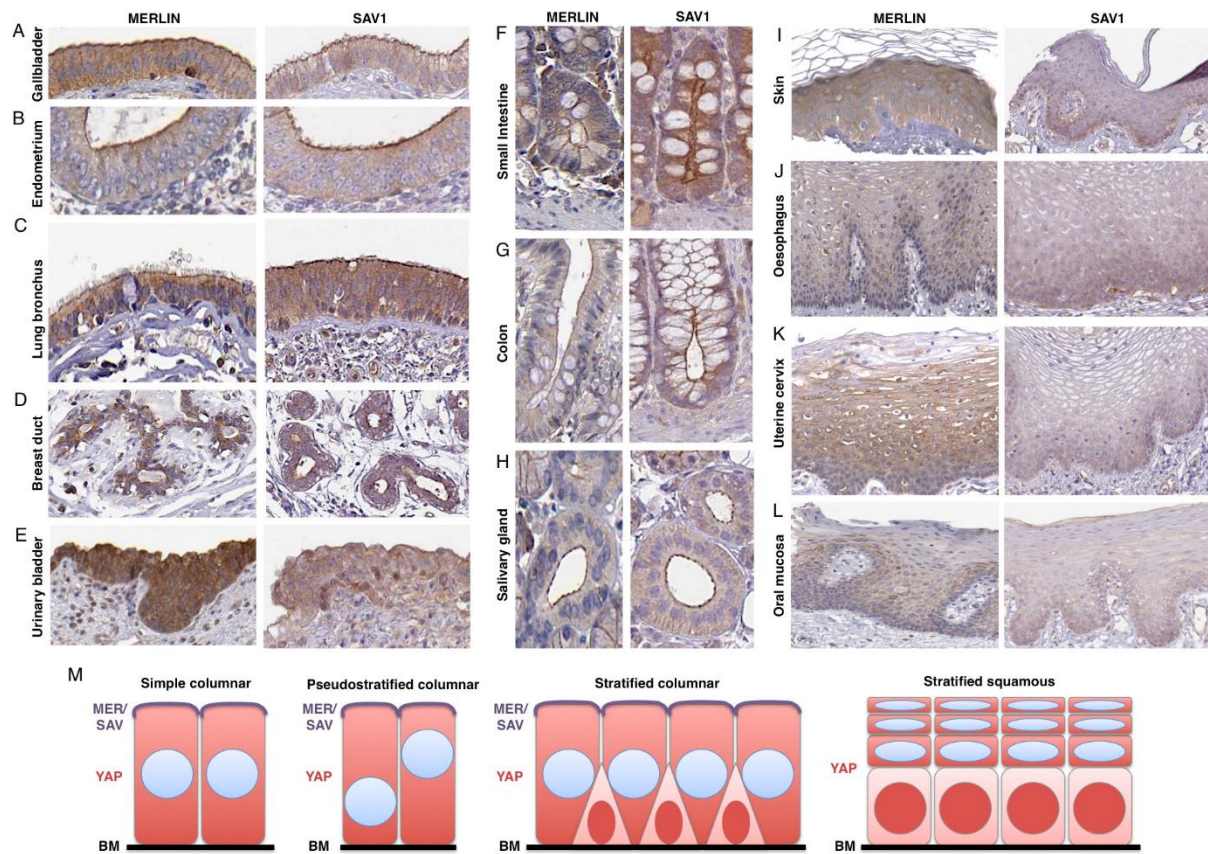


Fig. S4. Merlin and Sav localise in the same manner as Crb3. (A-L) MERLIN and SAV1 localise in the same apical manner as CRB3 in columnar cells of various epithelia. Compare with Fig 3. (M) Schematic diagram of MER/SAV localisation in various epithelial types.

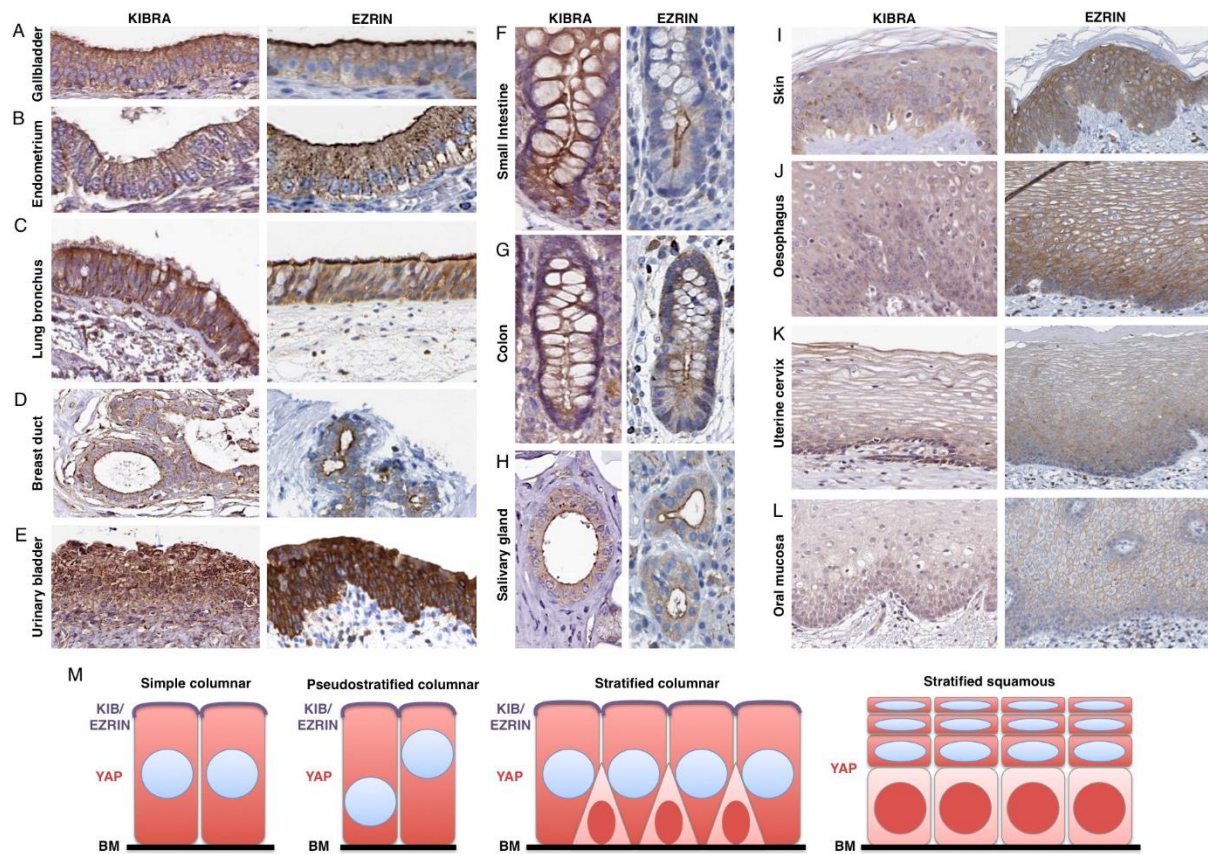


Fig. S5. Kibra and Ezrin localise in the same manner as Crb3. (A-L) KIB and EZR localise in the same apical manner as CRB3 in columnar cells of various epithelia. Compare with Fig 3. (M) Schematic diagram of KIB/EZR localisation in various epithelial types.

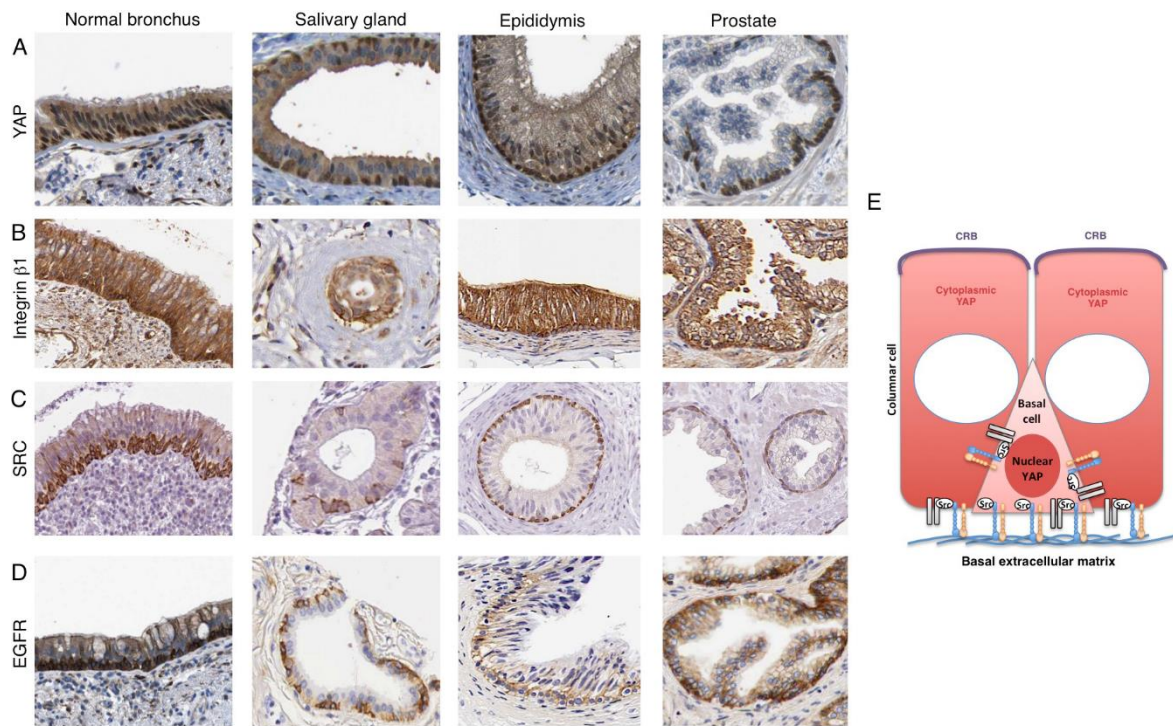


Fig. S6. Integrin-Src-EGFR-YAP localisation in stratified columnar epithelia. Human Protein Atlas data were mined to examine the localisation and expression of YAP, ITGB1, SRC and EGFR. (A) YAP localises to the nucleus in basal layer stem/progenitor cells of bronchus, salivary gland, epididymis and prostate. (B) ITGB1 is expressed in the basal layer stem/progenitor cells of bronchus, salivary gland, epididymis and prostate. (C) SRC is expressed in the basal layer stem/progenitor cells of bronchus, salivary gland, epididymis and prostate. (D) EGFR is expressed in the basal layer stem/progenitor cells of bronchus, salivary gland, epididymis and prostate. (E) Schematic diagram of YAP regulation in stratified columnar epithelia.

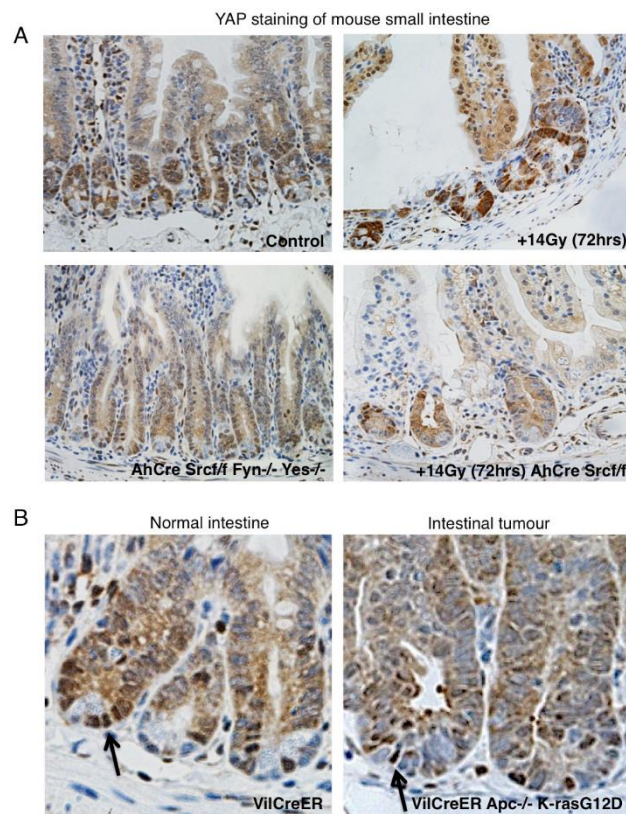


Fig. S7. Src is required for YAP activation after intestinal irradiation. (A) Mouse small intestines stained for YAP before and after 72hrs of gamma-irradiation with 14Gy. Note elevation of YAP levels in crypt progenitor cells. Note decreased YAP levels and nuclear localisation in Src, Fyn, Yes triple knockout intestines or in Src single knockout intestines after 14Gy irradiation. (B) Mouse small intestines from control (Villin-CreER) and Apc K-RasG12D intestines featuring hyperproliferative crypt progenitor expansion. Note that only basal crypt cells feature nuclear YAP, while columnar epithelial cells feature mostly cytoplasmic YAP localisation. Thus, loss of Apc or gain of Ras signalling is not sufficient to induce YAP nuclear localisation *in vivo*.

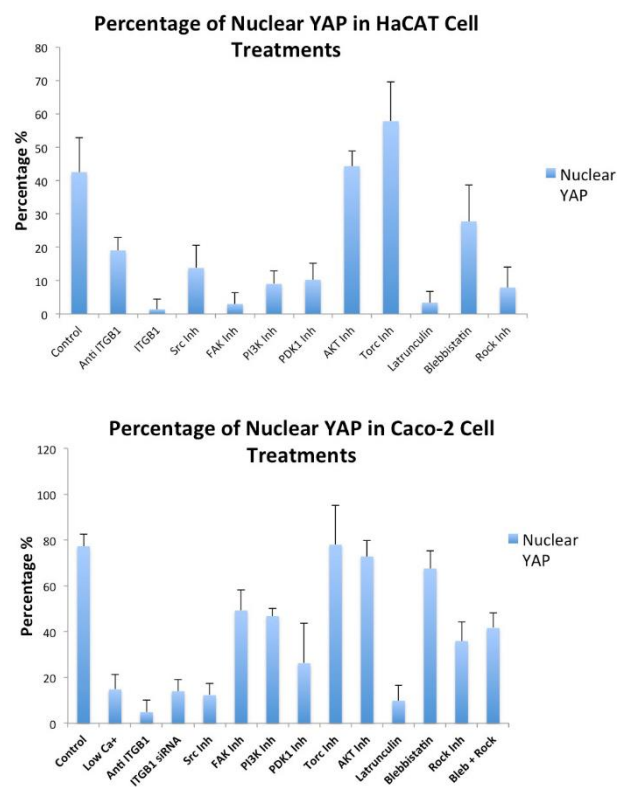


Fig. S8. Comparison of YAP perturbation in HaCAT and Caco-2 cells. Data from Fig 4E and 7G are reproduced to enable direct comparison.