

Supplementary Figure 1. Downregulation of VGLL4 in CRC. Relative VGLL4 mRNA levels in CRC patients of different tumor stages from GSE14333 dataset. Black bar denotes mean value. *Unpaired t tests* were used to compare the different between groups.

Related to Figure 1.



Supplementary Figure 2. Upregulation of Hippo signaling in CRC. (a-d) mRNA levels of *YAP* and YAP target genes in CRC tissue. Relative mRNA levels of *YAP* (a), *CTGF* (b), *Cyr61* (c) and *CDX2* (d) were analyzed. Experiments we repeated two times. Paired *t* tests were used to compare the different between paired tissue samples. (e) Box plots of *YAP* and YAP target genes levels at different tumor stages. Data are expressed as median and interquartile range (IQR). Experiments were repeated two times. *p < 0.05, significant relative to control. (f) Scatter plot between *VGLL4* and *CTGF* or *YAP* mRNA levels in CRC samples by applying Spearman's correlation. Experiments were repeated two times. (g) Levels of VGLL4 protein in five human colorectal carcinomas and their paired adjacent normal tissues were analyzed. Related to **Figure 2.**



Supplementary Figure 3. Effect of VGLL4 on nuclear translocation of β -catenin. (a) Knockdown efficiency of two parallel VGLL4shRNA. (b,c) Nuclear translocation of β -catenin in cells transfected with VGLL4 or it's mutant. (b) Immunoblotting of nuclear β -catenin in HEK293T cells. (c) Representation images of β -catenin staining in L1 cells. (b,c) Relative activity of TEAD4 luciferase reporter (b), and mRNA levels of YAP target genes.

Related to Figure 3.





vector-transfected group. Related to **Figure 3.**



Supplementary Figure 5. Microarray and GO analyses in HCT116 cells. (a) Heat map of array based genome wide mRNA expression analysis. Hierarchical clustering analysis of significant changed genes that are very different between *n.c.* and *siSUN* groups was carried out. (b) Schematic illustration of the microarray data. *Note:* asterisk indicates that the ratio of VGLL4 negatively regulated Wnt target genes (39 out of 114, 34.2%) is statistically higher than the ratio of VGLL4 negatively regulated total genes expressed in HCT116 cells (305 out of 19992, 1.5%). (c,d) Hierarchy of biological process (BP), molecular function (MF), or cell colocalization (CC) or pathways defined in the GO or KEGG database. Related to Figure 3.



Supplementary Figure 6. Functional interplay between TEADs and TCF4. (a) Knockdown efficiency of TEADs (1-4). **p < 0.01, significant relative to negative control group. (b) ChIP assay showing TCF4/TEAD4 binding to the indicated genes' promoters in 293T cells transfected with control siRNA, TEADs siRNAs or TCF4 siRNA. Left: siTEADs, ChIPed with TCF4 antibody. Right: siTCF4s, ChIPed with TEAD4 antibody. Experiments we repeated two times. Unpaired *t* tests were used to compare the different between groups. *p < 0.05, ** p < 0.01, *** p < 0.001, significant relative to control siRNA group. n.s., no statistical significance. Related to **Figure 4.**



Supplementary Figure 7. Super-TDU Treatment of HCT116 and SW480 Cells. (a) Cell viability of HCT116 cells after treatment with Super-TDU. (b) Cell viability of SW480 cells after treatment with Super-TDU. Data represent the mean \pm S.D. from one experiment. Experiments we repeated three times. To calculate IC₅₀, linear regression was used.

Related to Figure 7.



Supplementary Figure 8. Model for VGLL4 Regulation of TCF4 and TEAD4. TEAD4 directly associates with TCF4 to facilitate its transactivation. VGLL4 regulates Wnt/ β -catenin signaling by targeting the TEAD-TCF4 complex to interfere the transactivation of TCF4 during Wnt3a-induced β -catenin signaling. VGLL4 is downregulated in CRC in which Wnt/ β -catenin signaling is hyperactivated. Related to Figure 7.

Figure 5c



Figure 5g



Supplementary Figure 9. Raw images used in Figure 5c and 5g.