Supplementary information

YAP induces an oncogenic transcriptional program through TET1-mediated epigenetic remodeling in liver growth and tumorigenesis

Bo-Kuan Wu, Szu-Chieh Mei, Elizabeth H. Chen, Yonggang Zheng, and Duojia Pan

Correspondence to: duojia.pan@utsouthwestern.edu (D.P.)

Supplementary Table 1. GO biological process analysis of up- or down-regulated genes by YAP activation

YAP Tg / CTL	Biological Process Term	nGenes	adjusted *P*
Up regulated	Response to stress	113	4.91E-16
	Regulation of localization	94	1.48E-14
	Response to stimulus	86	1.70E-14
	Regulation of multicellular organismal process	90	1.84E-14
	Regulation of developmental process	91	1.92E-14
	Positive regulation of developmental process	64	4.01E-14
	Embryogenesis and morphogenesis	87	1.46E-13
	Cell motility	64	1.46E-13
	Regulation of cellular component organization	65	1.76E-13
	System development	125	2.05E-13
Down regulated	Small molecule metabolic process	256	1.05E-114
	Organic acid metabolic process	192	2.75E-108
	Carboxylic acid metabolic process	184	4.86E-106
	Oxoacid metabolic process	186	1.00E-104
	Oxidation-reduction process	172	2.80E-80
	Monocarboxylic acid metabolic process	127	3.36E-76
	Lipid metabolic process	168	1.01E-66
	Fatty acid metabolic process	88	1.36E-53
	Small molecule catabolic process	80	3.78E-49
	Drug metabolic process	106	3.80E-44

Note: Over-Representation Analysis was used for statistical analysis and Bonferroni adjusted *P* values are shown.

Supplementary Table 2. GO biological process analysis of genes associated with YAP-induced decrease or increase in DNA methylation

YAPTg / CTL	Biological Process Term	FDR Q-Val	Fold Enrichment
Methylation decrease	Developmental process	0	2.692012
	Cell growth	0	2.58933
	Regulation of localization #	0	2.746334
	Anatomical structure development	0	2.691805
	System development #	0	2.720312
	Cell differentiation	0	2.708641
	Embryogenesis and morphogenesis #	0	2.760538
	Regulation of developmental process #	0	2.732658
	Response to stimulus #	0	2.721302
	Regulation of signaling	0	2.702711
Methylation increase	Small molecule metabolic process *	3.94E-157	2.049202
	Cellular catabolic process	2.46E-112	2.038769
	Organic acid metabolic process *	2.11E-98	2.134464
	Oxoacid metabolic process *	1.64E-96	2.135172
	Carboxylic acid metabolic process *	2.93E-95	2.192601
	Cellular lipid metabolic process	1.45E-76	2.013214
	Small molecule biosynthetic process	1.61E-57	2.372434
	Monocarboxylic acid metabolic process *	2.53E-55	2.151077
	Fatty acid metabolic process *	1.47E-45	2.288306
	Cellular amino acid metabolic process	4.25E-41	2.36484

# indicates that the same biological process term is enriched in up-regulated genes in YAPTg livers (compare with Supplementary Table 1)

* indicates that the same biological process term is enriched in down-regulated genes in YAPTg livers (compare with Supplementary Table 1)

Supplementary Table 3. Overlap of YAP-induced rDMRs and ChIP-seq profile of histone markers from mouse fetal liver

Histone modification (ChIP-seq)	# YAP-induced rDMRs	# overlap between rDMRs and ChIP-seq peaks	% overlap between rDMRs and ChIP-seq peaks	adjusted *P*
H3K4me1	14282	2320	16.24%	< 0.001
H3K4me3	14282	331	2.32%	< 0.001

Note: H3K4me1 is an enhancer marker, H3K4me3 is a promoter marker. Over-Representation Analysis was used for statistical analysis and Bonferroni adjusted *P* values are shown.

Supplementary Table 4. Motifs and matched transcription factors (TFs) in YAP-induced rDMRs

Motifs (6-mer)	E-value	Matched TFs	Motifs (7-mer)	E-value	Matched TFs
	4.80E-32	STAT2, ZNF384, MECOM		8.50E-30	FOXA1, MEF2A, MEF2C
	1.10E-26	SOX10, SOX15, SOX3		1.00E-26	KLF1, KLF2, KLF6
	2.50E-20	RUNX1, RUNX3, RUNX2		1.30E-18	STAT2, SOX15, SOX3
	4.70E-14	ZBTB7A, GABPA, SPI1		1.40E-18	ZNF384, SOX15, SOX5
	6.90E-13	SOX8, SOX14, NKX3-2		2.90E-14	PRDM4, MEIS1, FOS::JUN
	8.70E-13	GATA1		3.30E-14	PRDM4, FOXO1, FOXP1
	3.60E-12	IRF5, ZNF136, NFYB		3.50E-13	PRDM4, SPI1, OSR2
	7.10E-12	DLX1, RAX, MIXL1		1.80E-12	KLF9, MSANTD3, NKX2-5
	1.10E-11	TEAD4, TEAD1, TEAD2		4.60E-12	STAT2, ZNF384, STAT1::STAT2
	2.50E-11	HOXB13, MEF2C, MEF2A		7.10E-12	PRDM4, PRDM1, SMAD4

Supplementary Table 5. GO biological process analysis of genes associated with TET1-dependent rDMRs

Biological Process Term	FDR Q-Val	Fold Enrichment
Developmental process *	0	2.70819
Multicellular organism development	0	2.724353
Embryogenesis and morphogenesis * #	0	2.702879
System development * #	0	2.740318
Regulation of localization * #	0	2.706329
Cell differentiation *	0	2.73403
Cellular developmental process	0	2.71477
Response to stimulus * #	0	2.717729
Organogenesis	0	2.75136
Regulation of developmental process * #	0	2.732671

* indicates that the same biological process term is enriched in YAP rDMRs-associated genes (compare with Supplementary Table 2).

# indicates that the same biological process term is enriched in both up-regulated genes in YAPTg livers and YAP rDMRs-associated genes (compare with Supplementary Table 1 and 2).

Supplementary Table 6. GO biological process analysis of up-regulated genes in YAPTg livers that were down-regulated by *Tet1*-deletion

Biological Process Term	**nGenes**	**adjusted *P***
Regulation of localization #	127	6.15E-22
Regulation of developmental process #	118	9.38E-19
Response to stress #	135	1.28E-16
Regulation of multicellular organismal process #	123	2.12E-16
Embryogenesis and morphogenesis #	110	2.18E-16
Response to stimulus #	141	2.18E-16
Positive regulation of developmental process #	78	5.79E-16
Cell motility #	79	7.68E-16
Cell adhesion	71	9.88E-16
System development #	75	9.92E-16

# indicates that the same biological process term is enriched in up-regulated genes in YAPTg livers (compare with Supplementary Table 1)

Note: Over-Representation Analysis was used for statistical analysis and Bonferroni adjusted *P* values are shown.

Supplementary Table 7. List of 1,003 TET1-dependent YAP target genes

1110051M20RIK	ADC	ARHGAP25	CACNA1S	CHAF1B	CYTH4	ENOPH1
1500012F01RIK	ADCY2	ARHGAP27	CADM4	CHEK1	DAB1	ENTPD1
1700011H14RIK	ADCY7	ARHGDIB	CAMP	CHMP4C	DAB2	EPB4.1L3
1700016C15RIK	ADGB	ARHGEF2	CAPNS2	CHP2	DAB2IP	EPB4.1L4A
1700020N01RIK	ADORA1	ARID5A	CARD9	CHST14	DAPK2	EPS8L2
1700030C10RIK	ADRB1	ARL11	CASC5	CHST3	DAPP1	EPS8L3
1700040L02RIK	ADRB2	ARL4C	CASP2	CIB3	DCBLD1	EPSTI1
1700061I17RIK	AEN	ARPC1B	CATSPER4	CIT	DCDC2A	ERC2
1700084C01RIK	AGPAT4	ASAH1	CBLN3	CKB	DCLK3	ESM1
1700113H08RIK	AGRN	ASAP3	CCDC14	CLDN23	DCP1B	ESPN
1810011H11RIK	AHNAK	ASB15	CCDC148	CLEC12A	DDAH2	EVA1B
1810062G17RIK	AI413582	ASF1B	CCDC158	CLEC2I	DDR1	EVL
2010109I03RIK	AI429214	ASPRV1	CCDC64	CLEC4A1	DEFB1	EVPL
2310007B03RIK	AI467606	ASXL3	CCDC68	CLEC4B1	DGKI	EXO1
2510009E07RIK	AIF1	ATF3	CCDC88B	CLEC4F	DIAP3	EZR
2900011O08RIK	AIM2	ATOH8	CCL2	CLIC1	DISC1	F2RL1
4930426L09RIK	AKAP2	ATP13A4	CCL24	CLIP2	DLC1	F2RL3
4930427A07RIK	AKR1B10	ATP1B3	CCL5	CMKLR1	DLG4	F3
4930429B21RIK	AKR1B3	ATP8B2	CCL7	CNBD2	DLGAP5	FA2H
4930550C14RIK	AKR1B7	AXL	CCL9	COL16A1	DNAAF3	FADS3
4933427E11RIK	ALDH18A1	B3GNT8	CCND1	COL23A1	DNM3	FAM105A
5031414D18RIK	ALOX5AP	B4GALNT4	CCND3	CORO2A	DOCK2	FAM110A
5730508B09RIK	AMOTL2	B4GALT6	CCR1	COTL1	DOK1	FAM110C
6330416G13RIK	AMPD3	BAIAP2L2	CCR5	CPEB1	DOK4	FAM111A
8430427H17RIK	ANGPTL1	BASP1	CD2AP	CPNE8	DOS	FAM118A
A4GALT	ANGPTL7	BATF2	CD300A	CRLF2	DUSP2	FAM129A
A530016L24RIK	ANK1	BC021891	CD300LB	CRTAM	DUSP5	FAM132A
A530032D15RIK	ANK3	BC049352	CD300LF	CRYAB	DUSP7	FAM13C
A530064D06RIK	ANKRD27	BC100451	CD37	CRYGS	DYRK4	FAM163A
A630001G21RIK	ANKRD6	BCL2	CD40	CRYM	E230008N13RIK	FAM212B
A730020M07RIK	ANKS6	BCL2A1D	CD44	CSF1	E330021D16RIK	FAM49A
A930004D18RIK	ANLN	BEND6	CD48	CSF1R	ECT2	FAM49B
ABCA13	ANO6	BICC1	CD5L	CSF2RB	EDA	FAM65B
ABCA4	ANXA2	BIN2	CD74	CSF2RB2	EDIL3	FAM72A
ABCA5	ANXA3	BIN3	CD80	CSNK1E	EFCAB4B	FAM73A
ABCC1	ANXA4	BMP6	CD83	CSRNP3	EGR2	FAM78A
ABCC12	ANXA5	BMPER	CD97	CSRP1	EHD4	FAM83B
ABCC5	AOAH	BORA	CDC42EP1	CTGF	EIF4E3	FAM83D
ABCG1	AP1S2	BRCA1	CDCA7L	CTNNAL1	ELL3	FAM84A
ABCG3	APBB1IP	BTBD11	CDCA8	CTPS	ELN	FAM84B
ABI2	APH1B	BTC	CDK1	CTSS	ELOVL7	FANCA
ABI3	APOBEC3	BTG2	CDKL1	CX3CL1	EMB	FBLIM1
ABR	APOL10A	BTLA	CDKN1C	CX3CR1	EME1	FBXO25
ACE	APP	BUB1	CDS1	CXCL16	EMILIN2	FBXO48
ACTA2	ARC	C1QA	CDS2	CXCL17	EMP2	FCGBP
ADAM11	ARF2	C1QB	CEACAM2	CXCR4	EMR1	FCGR1
ADAM12	ARG2	C1QL3	CENPF	CYFIP2	EMR4	FCGR3
ADAM5	ARHGAP11A	C330027C09	CENPN	CYP2A22	ENAH	FCGR4
ADAMTS7	ARHGAP15	C3AR1	CEP72	CYP4F16	ENC1	FCNB
ADAP1	ARHGAP19	C5AR1	CERS6	CYR61	ENGASE	FCRL1

FERMT3
FGD3
FGR
FHL2
FIBIN
FLI1
FLT3
FMNL1
FMO2
FOS
FRMD4A
FRY
FSTL3
FUT10
FXYD5
FYB
GADD45A
GAL3ST1
GALK1
GALNT3
GAS6
GATM
GBGT1
GCNT1
GDPD5
GGT1
GIPC2
GJA5
GKAP1
GLIPR2
GLIS2
GLIS3
GLRP1
GM13251
GM13547
GM16432
GM5150
GM5420
GM6484
GM765
GMDS
GMFG
GMIP
GNAI1
GNG2
GNGT2
GNPDA2
GOLM1
GPNMB
GPR114
GPR132
GPR137B
GPR141
GPR160
GPR176
GPR18
GPR183
GPR35
GPR39
GPR56
GPR84
GPX3
GPX7
GRAMD1B
GREB1L
GSG1
GSG2
GSTA1
GYLTL1B
GYPC
GZMK
H2-DMB1
H2-EB1
H2-OB
HAO2
HAVCR2
HBEGF
HCK
HDAC11
HES1
HEY1
HK2
HK3
HMGB2
HN1
HNF1B
HOMER3
HPCAL1
HPGDS
HRH1
HSF2BP
HSPB2
HTRA3
HYDIN
I830077J02RIK
ICOSL
ID2
ID3
ID4
IDH2
IDO1
IFI204
IFI205
IFIT1
IFNGR1
IFNLR1
IGF2
IGF2BP1
IKZF1
IL10RA
IL12A
IL16
IL17RD
IL1B
IL1R2
IL22RA1
IL33
INADL
INCENP
INPP5D
IRF4
IRF8
ISM2
ITGA11
ITGA3
ITGA4
ITGA6
ITGAM
ITGAX
ITPR3
ITPRIPL2
JDP2
KCNA2
KCNAB2
KCNE3
KCNG2
KCNJ16
KCNJ2
KCNJ9
KCNK13
KCNMB1
KCNN4
KCNU1
KCTD12B
KIF11
KIF14
KIF15
KIF18B
KIF20A
KIF20B
KIF21B
KIF22
KIFC1
KIFC3
KL
KLF11
KLF5
KLHDC1
KLHDC7A
KLHL13
KLHL31
KLRA6
KLRG2
KRT4
KRT80
KRTCAP3
LAIR1
LAMA5
LAMC2
LAPTM5
LGALS3
LGR6
LIF
LIG1
LILRA5
LIMCH1
LIMD2
LIMS1
LIPO1
LMCD1
LPCAT2
LPCAT4
LPHN3
LRMP
LRRC1
LRRC25
LRRC39
LST1
LTC4S
LTF
LXN
LY6C2
LY6D
LYNX1
LYZ1
M1AP
MAD2L1
MADCAM1
MAFK
MAGI2
MANBAL
MAP3K14
MAPK13
MARCO
MATN4
MB21D1
MBD4
MBIP
MBLAC1
MBP
MCF2
MCF2L
MCM4
MCM6
MECOM
MERTK
METRNL
MEX3B
MFSD10
MFSD7B
MFSD7C
MGAT4A
MGST2
MICAL1
MIS18A
MKI67
MLLT3
MNS1
MORC4
MPDZ
MPHOSPH6
MPO
MPP7
MRO
MSRB3
MSTO1
MT1
MTAP7D3
MTHFD2L
MTUS2
MUM1L1
MVB12B
MVP
MXD3
MYB
MYBPC1
MYBPC3
MYC
MYH15
MYL12A
MYL12B
MYO1C
MYO5C
MYO9A
MYOT
NAIP1
NAIP5
NAP1L1
NCAPD2
NCAPH
NCF4
NCKAP5L
NCOA7
NEBL
NEDD9
NEIL2
NEK5
NENF
NEU3
NEURL1A
NEURL1B
NEURL3
NFAM1
NFE2L2
NFKB2
NGP
NID2
NKX2-6
NLRC4
NLRP3
NOD2
NOS1
NOS1AP
NOS2
NOXA1
NR4A1
NRADD
NRAP
NRIP2
NRM
NUAK1
NUAK2
NUMBL
OAS2
OIP5
OLFM3
OPTC
ORAI2
ORC1
OSBPL10
OSBPL3
OSBPL7
OSCP1
OTUD1
OXCT1
P2RX5
P2RX7
P2RY12
P2RY13
P4HA2
PAK1
PALMD
PANX1
PAQR6
PARD3B
PARD6B
PARM1
PARVG
PATZ1
PAWR
PCOLCE2
PDE6C
PDGFB
PDLIM2
PDLIM4
PDZK1IP1
PEG3
PF4
PGAP3
PHACTR3
PHIP
PHLDA2
PHLDA3
PHLDB1
PI16
PIK3CD
PIK3R5
PIK3R6
PILRA
PILRB1
PKDCC
PKIA
PKP2
PLA2G5
PLAC8
PLAT
PLAU
PLAUR
PLCG2
PLCL1

PLD1	RAC2	SEPN1	SLFN1	TBC1D1	TRPS1	ZFP90
PLD2	RAD51	SEPT6	SLFN2	TBC1D19	TRPV4	ZFP956
PLD6	RANBP3L	SEPT8	SLFN3	TBC1D9	TSPAN15	ZYX
PLEK	RAP1GAP	SERPINB6B	SLFN8	TBXAS1	TSPAN17	
PLEK2	RAP1GAP2	SESTD1	SLIT1	TCEA2	TTC22	
PLEKHA2	RASA3	SETD7	SLPI	TEAD1	TTK	
PLEKHA4	RASAL1	SFRP5	SMAD7	TEAD4	TTLL10	
PLEKHH1	RASGRP1	SGK1	SMC1B	TEKT5	TTLL9	
PLEKHM3	RASGRP3	SH2D1B1	SMCO3	TFEC	TTN	
PLEKHO1	RASL11A	SH2D4A	SMIM6	TGFA	TUBA1B	
PLTP	RBBP8	SH3BP1	SMO	TGIF1	TUBB6	
PMP22	RBL1	SH3D21	SMOC2	TGM2	UBASH3B	
POU2F2	RCAN3	SH3KBP1	SMPD3	THEMIS2	UBTD2	
POU4F1	RELB	SH3TC1	SMPD5	TIFAB	UCK2	
PPBP	REM2	SHANK2	SMTNL2	TIMD4	UMODL1	
PPFIA4	RFTN1	SHC4	SNX20	TIMP2	UNC5B	
PPL	RGCC	SHROOM3	SOAT1	TLX1	UST	
PPM1H	RGS1	SIAH1A	SOCS3	TM6SF1	VASP	
PPP1R36	RGS10	SIGLEC1	SOD3	TMC3	VAV1	
PQLC3	RGS11	SIGLECE	SORBS1	TMCC3	VEPH1	
PRC1	RGS19	SKA1	SORBS2	TMEM117	VGLL3	
PRDM1	RGS9BP	SLA	SOX4	TMEM136	VILL	
PRELP	RHBDF2	SLC11A1	SOX9	TMEM150B	VIM	
PREX1	RHOH	SLC13A5	SPATA7	TMEM191C	VLDLR	
PRKCB	RILPL1	SLC14A1	SPDL1	TMEM194B	VOPP1	
PRKCD	RINL	SLC15A3	SPECC1	TMEM246	WBSCR17	
PRMT2	RNASEL	SLC16A5	SPIC	TMEM41A	WDFY4	
PROCR	RNF145	SLC16A9	SPIRE2	TMEM43	WDR52	
PROM1	RNF180	SLC1A5	SPON2	TMEM65	WEE1	
PRR24	RNF186	SLC22A21	SPP1	TMEM98	WFDC2	
PRR5L	ROR1	SLC22A4	SRC	TMPO	WIPF1	
PRRG4	RPH3AL	SLC25A24	SRGAP3	TMSB4X	WNT9A	
PRUNE2	RPL39L	SLC25A4	SRGN	TNFAIP2	WWC1	
PSTPIP1	RPS6KA4	SLC26A2	ST3GAL2	TNFAIP3	WWC2	
PTGDS	RRAGB	SLC26A8	ST8SIA4	TNFAIP6	XCL1	
PTGS1	RRAS2	SLC27A6	STAMBPL1	TNFAIP8	ZBTB3	
PTP4A3	RTKN2	SLC28A2	STK17B	TNFRSF11	ZC3H7B	
PTPN13	RUNX1	SLC2A3	STMN1	TNFRSF13	ZDHHC23	
PTPN14	S1PR2	SLC35F2	STMND1	TNFRSF19	ZFP113	
PTPN18	SAMD4	SLC38A1	STOML1	TNFRSF25	ZFP248	
PTPN6	SAMSN1	SLC39A13	STRADA	TNFRSF9	ZFP382	
PTPN7	SASH3	SLC40A1	STX3	TPCN2	ZFP449	
PTPRC	SCEL	SLC41A3	SULT2B1	TRAIP	ZFP532	
PTPRH	SCHIP1	SLC44A3	SYNC	TREM1	ZFP608	
PTPRM	SCUBE3	SLC4A3	SYNGR1	TREML2	ZFP618	
R3HCC1	SDK1	SLC4A9	SYNPO	TREML4	ZFP651	
RAB11FIP4	SDPR	SLC5A11	SYT17	TRIM30B	ZFP688	
RAB31	SELPLG	SLC7A8	TAB1	TRIM35	ZFP69	
RAB39	SEMA3B	SLC8A1	TACC3	TRIM36	ZFP747	
RAB44	SEMA4D	SLCO1A5	TAGAP	TRIP6	ZFP810	

Supplementary Table 8. GO biological process analysis of 1,003 TET1-dependent YAP target genes (genes with both TET1-dependent DNA demethylation and TET1-dependent mRNA induction upon YAP activation)

Biological Process Term	**nGenes**	**adjusted *P***
Regulation of localization	69	1.68E-14
Regulation of developmental process	63	6.76E-12
Cell motility	45	3.31E-11
Cellular developmental process	81	3.50E-11
Regulation of transport	50	4.12E-11
Regulation of cell motility	34	5.77E-11
Embryogenesis and morphogenesis	58	1.61E-10
Cell migration	41	1.61E-10
Response to stimulus	40	2.36E-10
System development	38	2.41E-10

Note: Over-Representation Analysis was used for statistical analysis and Bonferroni adjusted *P* values are shown.

Supplementary Table 9. Primer sets

mRNA	**Primer forward**	**Primer reverse**
Tet1	AGAGGAAATGCGAGGTGCTC	CCCCATGACCACGTCTACTG
Gapdh	GGTGTGAACGGATTTGGCCG	GACAAGCTTCCCATTCTCGG
Myc	CCTTTGGGCGTTGGAAACC	CGTCGCAGATGAAATAGGG
Cyr61	CCGAACCGCGAGTTCTTTTC	TCGTGTGGAGATGCCAGTTC
Ctgf	AGTGTGCACTGCCAAAGATG	CCAGGCAAGTGCATTGGTAT
Yap	TGCCGTCATGAACCCCAAGAC	GTCAGAGCTCCCGCAGTACC
Taz	AGCAGTCCTATGACGTGACC	GTGGAAGTGATGGACGGGTG
Tead1	AGCAGAGAGACCCAGACTCG	TCCACAGATTCGAGCAACGG
Tead4	GAGCCCCGAAATTGAGCGAA	CTGGAGACCTGCTTCCTTGT
Mst1	TCCCTCAGGATGGAGACTATGA	TGGGCTGGTGTTGTCAGAAGT
Mst2	GCGGCTAAAAGCACTAGACC	CTGGTCATCCTGAGACAGAGG
Lats1	TGCGAACAGGATATACACAGC	CAGCTTAGCTTGAGGAGGG
Lats2	GTACACGCAGCTCTGTGACT	TAGGGATATGCAGCGTGCTC
Nf2	GCCCAAGGCAGAAGACCTATC	CCATCCTGTTGGTGTCAGGAG
Sav1	GATCAGCCTCCACCCATCAC	TCAGCATTCCCTGGTACGTG
Kibra	AGAGGAGTGTCTGGGAGGTG	CCACGGCTGTCTGTTCTAGC
Amotl2	ACTGTACCTAAGCCGAACCG	CATGCTTCTCTGGCTTGCAC
MBD/ hMeDIP/ ChIP/ FAIRE	**Primer-1**	**Primer-2**
Tet1	CAGTTTAGGGTGAGCTGGGG	GTGCAAAGTCCTAGCCCGAT
Myc	CCAGGACTGTATGTGGAGCG	TCAGGCTGGTGCTGTCTTTG
Cyr61	GCAAGTAGAGGTGGGGAACC	GTCCCAGGAATTTCCCCTCG
Ctgf	GGTCACTTCCCCATGGTCTC	GTAGAATGGGTCGTGAGCCT
Tead1	TGGAAGGGGAACTCCTAGCC	CAGGCCTCACCACGTGATTC
Tead4	TTTCTTTCAGCGTCTCCCCG	CTCGGGCCAGCAGTAAATCT
Bisulfite sequencing	**Primer-1**	**Primer-2**
Myc	GGGTTTTGTTTTTTATTTTATGTTG	AAACCACTAAAAAATCAATACACTC
Tead1	ATTTTGTTTTTTTTGGAATGTTTGT	CTACCAACAACCTACTCCTCTTCAT
Tead4	TATGTGAATGGGATGTGATTAGGT	CTCCCAACCAAAACTAATAAAACAA
Cyr61	GTGAATTGTTAGGAAAGTGGTTGTT	CAACCCTAACCCTTTAACAACTAAA
Ctgf	TGTAAGTAGTTTTGTGATTATTTTGTT	ACTACAACTTTATATCTTTTAATAAACTCC
Amotl2	TGGTTTTGTTGGTTTTTTAGGTTAT	TCAAAATATTCATCAAAACTACTAC
Kibra	GTTTTTGTTGTTGAGGGTGTATTTA	AAATCTACAATTCTAACCTACTTCTTCTCT
Slc1a5	TGAGATAGGTAGATTAGGTTGAGTT	TTTTATCCATCCCTATAACCAAAAA
Clone rDMR for enhancer assay	**Primer-1**	**Primer-2**
Myc	GGTACCGAGCTCTTACGCGTGGTTTCCGCACCAACCAG	TGCAGATCGCAGATCTCGAGTGAGGGGTCAATGCACTC
Cyr61	GGTACCGAGCTCTTACGCGTAGAACTACTCTAGGTGCC	TGCAGATCGCAGATCTCGAGCCTTGAAATTCCTCACTG
Ctgf	GGTACCGAGCTCTTACGCGTAGCAGCATCCATGAGGAAC	TGCAGATCGCAGATCTCGAGGACTGACGGGCTGATGGAATTTTTAAAAATAATTG
TEAD motif deletion	**Primer-1**	**Primer-2**
Myc	CCGTACAGCCCTCTGCGACGAGGAAGAGAATTTC	TCGTCGCAGAGGGCTGTACGGAGTCGTAGTC
Cyr61	TTACAAGGATAAAGCCTAAGAGTTACCCC	CTTAGGCTTTATCCTTGTAAAAATAAATCATTG
Ctgf	GAATTTCACACTTCTTACACCTAAACCTTG	AGGTGTAAGAAGTGTGAAATTCTCTCAGATTG
Clone rDMR for pCpGfree-promoter	**Primer-1**	**Primer-2**
Myc	CCTAGGATGCATAGTACTAGAGACTTGCTTCCCTTGCTGT	TCTCCACTAGTTACATGTTGCCTACCCTGCTGTGAATGGG
Cyr61	CCTAGGATGCATAGTACTAGCCAGGCAATCAGGAACAACTG	TCTCCACTAGTTACATGTTGGTGCAGCTGTCTCTACCTCTC
***Tet1* shRNA**	**Primer**	
sh*Tet1* -a	TGCTGTTGACAGTGAGCGCCAGGTTCACAATGTTGCTCTATAGTGAAGCCACAGATGTATAGAGCAACATTGTGAACCTGTTGCCTACTGCCTCGGA	
sh*Tet1* -b	TGCTGTTGACAGTGAGCGACAGGTACTAAAGAGACTGTTATAGTGAAGCCACAGATGTATAACAGTCTCTTTAGTACCTGGTGCCTACTGCCTCGGA	