

**OMTN, Volume 35**

**Supplemental information**

**CHD6 eviction of promoter nucleosomes  
maintains housekeeping transcriptional  
program in prostate cancer**

**Lina Bu, Shaodong Huang, Ziyang Rao, Chenyang Wu, Bryan-Yu Sun, Yanhua Liu, Lin He, and Dongyu Zhao**

**Table S1. Summary of available data used in the study.**

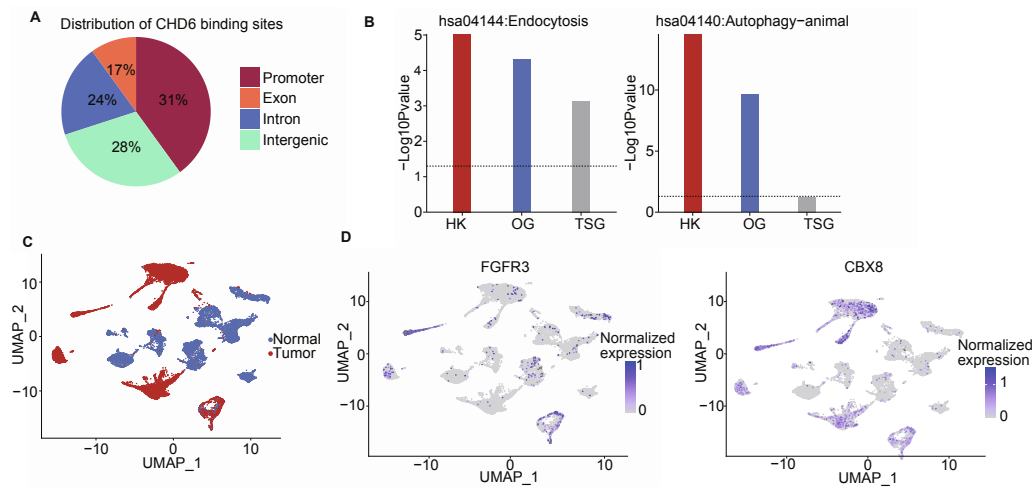
Data name	Data type	Cell	Cell type	ID (GEO database)
HEK293	CUT&Tag	HEK293	Normal	GSE264397
HEK293	CUT&Tag	HEK293	Normal	GSE264397
HEK293	CUT&Tag	HEK293	Normal	GSE264397
Cardiomyocytes	ChIP-seq	Cardiomyocytes	Normal	GSE136057
Cardiomyocytes	ChIP-seq	Cardiomyocytes	Normal	GSE136057
Cardiomyocytes	ChIP-seq	Cardiomyocytes	Normal	GSE136057
Cardiomyocytes	ChIP-seq	Cardiomyocytes	Normal	GSE136057
PolII	ChIP-seq	C4-2	Cancer	GSE55615
H3K4me3	ChIP-seq	C4-2	Cancer	GSE55615
H3K4me1	ChIP-seq	C4-2	Cancer	GSE55615
H3K27ac	ChIP-seq	C4-2B	Cancer	GSE105424
H3K27ac	ChIP-seq	C4-2B	Cancer	GSE105424
H3K36me3	ChIP-seq	C4-2B	Cancer	GSE118629
H3K36me3	ChIP-seq	C4-2B	Cancer	GSE118629
H3K9me3	ChIP-seq	C4-2B	Cancer	GSE118629
H3K9me3	ChIP-seq	C4-2B	Cancer	GSE118629
H3K27me3	ChIP-seq	C4-2B	Cancer	GSE118629
H3K27me3	ChIP-seq	C4-2B	Cancer	GSE118629
MNase	MNase-seq	C4-2	Cancer	GSE214212
MNase	MNase-seq	C4-2	Cancer	GSE214212
MNase	MNase-seq	C4-2	Cancer	GSE214212
MNase	MNase-seq	C4-2	Cancer	GSE214212
MNase	MNase-seq	C4-2	Cancer	GSE214212
MNase	MNase-seq	C4-2	Cancer	GSE214212
MNase	MNase-seq	C4-2	Cancer	GSE214212
ATAC	ATAC-seq	C4-2B	Cancer	GSE145409
BPH1	RNA-seq	BPH1	Normal	GSE210205
BPH1	RNA-seq	BPH1	Normal	GSE210205
BPH1	RNA-seq	BPH1	Normal	GSE210205
BPH1	RNA-seq	BPH1	Normal	GSE210205
PrEC	RNA-seq	PrEC	Normal	GSE70466
PrEC	RNA-seq	PrEC	Normal	GSE70466
PrEC	RNA-seq	PrEC	Normal	GSE70466
RWPE1	RNA-seq	RWPE1	Normal	GSE118629
RWPE1	RNA-seq	RWPE1	Normal	GSE118629
RWPE1	RNA-seq	RWPE1	Normal	GSE118629
DU145	RNA-seq	DU145	Cancer	GSE210205
DU145	RNA-seq	DU145	Cancer	GSE210205
DU145	RNA-seq	DU145	Cancer	GSE210205
DU145	RNA-seq	DU145	Cancer	GSE210205

PC3	RNA-seq	PC3	Cancer	GSE210205
PC3	RNA-seq	PC3	Cancer	GSE210205
PC3	RNA-seq	PC3	Cancer	GSE210205
PC3	RNA-seq	PC3	Cancer	GSE210205
22RV1	RNA-seq	22RV1	Cancer	GSE214585
22RV1	RNA-seq	22RV1	Cancer	GSE214585
22RV1	RNA-seq	22RV1	Cancer	GSE214585
22RV1	RNA-seq	22RV1	Cancer	GSE214585
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
LNcap	RNA-seq	LNcap	Cancer	GSE193468
VCaP	RNA-seq	VCaP	Cancer	GSE136272
VCaP	RNA-seq	VCaP	Cancer	GSE136272
VCaP	RNA-seq	VCaP	Cancer	GSE136272
C4-2	RNA-seq	C4-2	Cancer	GSE214212
C4-2	RNA-seq	C4-2	Cancer	GSE214212
C4-2	RNA-seq	C4-2	Cancer	GSE214212
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829
CRPC	scRNA-seq	CRPC	Cancer	GSE137829

**Table S2. Overlapping genes with sharp CHD6 peaks between HEK293 and cardiomyocytes.**

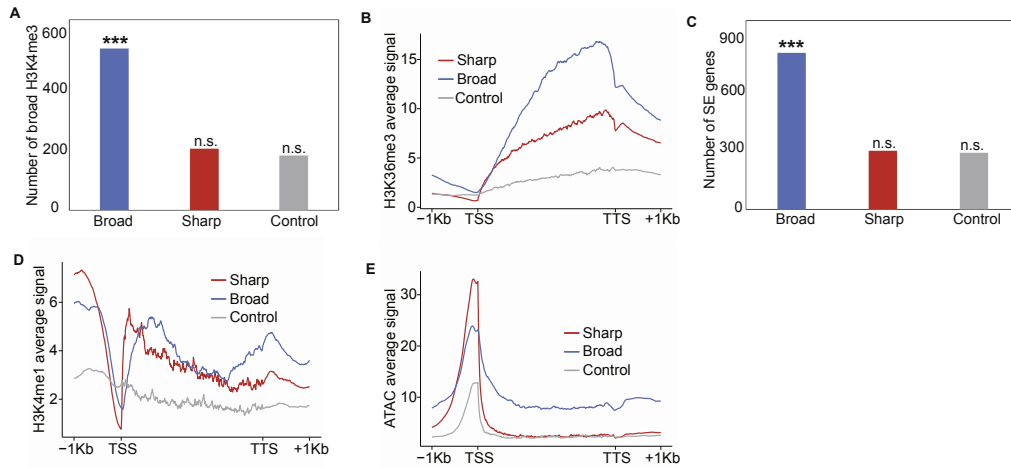
TMEM55B	MRPL54	ELK1	SGTA	ZFYVE16	CC2D1B
BLOC1S3	MLH1	ZNF345	RPS26	ATP6V0B	AP4M1
MRPS18B	SKA2	CAPN10	ATP6V1G1	WDR77	HSPA13
TRAPPC6A	ATP5G1	HSPA9	ARID4A	AATF	UBE2Q1
CALR	EXOC8	CDV3	SLC20A1	CNPY3	DNAJB9
ZBTB37	SERBP1	BUB3	DNAJC16	AHSA1	RMND1
CD164	THAP5	DUS3L	AP4B1	FBXO17	HSP90B1
ASNA1	PRR3	C1orf174	PNISR	SH2B3	ARPC5
USP5	BCLAF1	SFR1	PSMD10	NOL6	UBE2S
SRSF2	ATF2	DCLRE1B	YIF1A	COMMD4	HMGN4
NFKBIB	UBAP2L	TCEANC2	UBE4B	SNX12	THNSL1
ZNF687	CNOT1	UVRAG	M6PR	WDR3	ALDH6A1
GLA	CD3EAP	CEP95	SLC2A4	DCTPP1	SDR39U1
SNRPD2	GIPC1	C1orf43	GANC	S100A1	ILVBL
HNRNPH2	COX14	C7orf25	ZNF318	RRAGC	PIAS4
TRAF7	EPM2AIP1	FAM192A	VPS33A	PPP1R15B	BLOC1S1
MPND	OSGEP	POLR2A	DES11	PRDX6	LAMP1
APEX1	PABPN1	HNRNPDL	LAMTOR4	DNAJC13	IMP4
ZNF576	YBX1	GLYR1	CSTB	PQBP1	DACT3
C5orf51	DOLK	FAM76A	RBM39	ALDH3A2	BAX
CATSPERD	HIST1H4H	RPL19	FOXO1	ZMAT5	TMEM185B
SWSAP1	RPS12	HMBBOX1	RPS28	FAF1	PET100
QPCTL	CD2BP2	TSR3	TSNAX	NBR1	CENPL
CYB5D1	FNIP1	UQCR11	PMVK	TMEM59	FAM179B
C19orf47	HMGN1	CCDC151	RPL9	MDH1	SUPV3L1
SHPK	CDK5	KIAA1009	ZNF706	RPL39	ULK3
CCNYL1	CNPY4	GTF2F1	SOCS5	CCT8	ZNF526
WBP1	MBTD1	PHB	PHF5A	PRELID1	TMEM131
ORC6	KLRG1	WDR75	TMTC3	OTUD1	CHCHD4
RBM42	UVSSA	PSMB3	MTF1	MAX	RUVBL2
LIN37	HPS5	MIEN1	FAM168B	FGFR1OP2	PARP6
ZNF181	GTF2H1	NPAT	FEN1	RPAIN	TXLNG
IER5	ZNF865	SRSF1	RPA1	LCN12	ENKUR
UBTD1	C8orf44	TOP3A	EIF3A	EXOSC1	RPL23
RIBC1	KIF20A	SPAG5	UBE2C	NAGA	ZNF503
DXO	HNRNPD	SIRT1	POLE3	EME1	PRPF38A
ZBTB5	CREB3L4	MLX	PLEKHH3	C12orf49	ALOXE3
C6orf211	CCDC115	RELL1	UBL5	TIMM17B	MMS19
TMEM116	ETF1	AP5Z1	AKR7A2	NGRN	RNF41

TIA1	H2AFV	DERL3	RBM23	RBX1	MRPL55
NTHL1	ZFP91	USO1	PPIP5K2	HINFP	PPP1R3D
UROD	GK	G6PC3	WDR92	B3GALT6	SLC35A5
MYL12A					



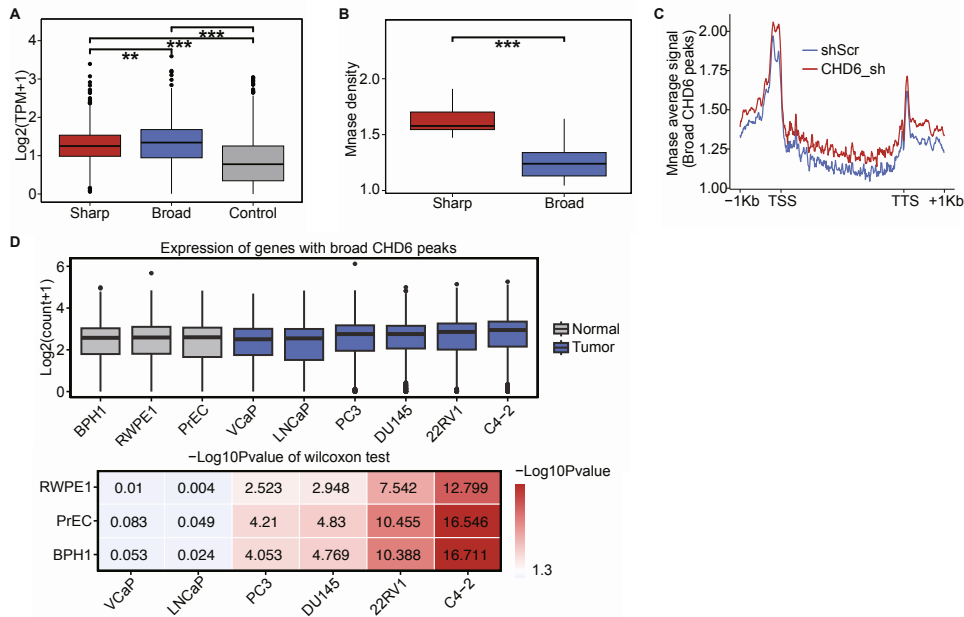
**Figure S1. Distribution characteristics of the CHD6 binding sites.**

(A) Distribution of CHD6 binding sites. (B) housekeeping genes (HK), oncogenes (OG) and tumor suppressors genes (TSG) are equally enriched in the KEGG pathways in endocytosis (left), and HK genes, and OG are equally enriched in the KEGG Pathways in autophagy-animal (right). (C) Distribution of tumor and normal cells using scRNA-seq. (D) Expression levels of the oncogene *FGFR3* and *CBX8* in tumor and normal cells. The P values determined using one tail Wilcoxon test.



**Figure S2. Binding models of CHD6 that differ in epigenetic modifications.**

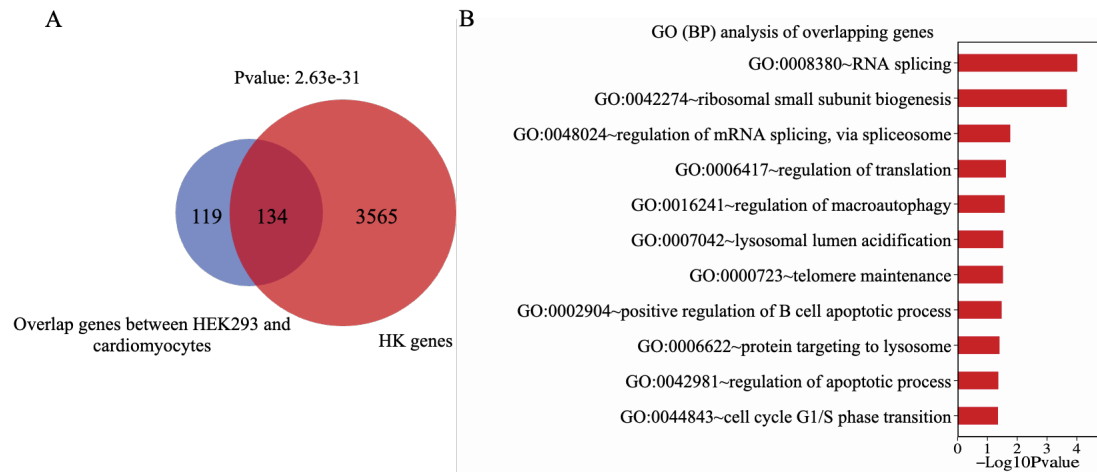
(A) Comparison of the overlap of different genes with broad H3K4me3. (B) Average ChIP-Seq signal value of H3K36me3 plotted around groups. (C) Comparison of the overlap of different genes with super enhancer genes. (D) Average ChIP-Seq signal value of H3K4me1 plotted around different genes. (E) Average ATAC signal value plotted around different groups. P values determined using one tail Wilcoxon test.  $*p < 0.05$ ;  $**p < 0.01$ ;  $***p < 0.001$ . n.s., not significant.



**Figure S3. Higher nucleosome density of the genes with sharp CHD6 peaks than that of the genes with broad CHD6 peaks.**

(A) Expression levels of genes determined from the GTEx tissue dataset. (B) The nucleosome density of the genes with sharp CHD6 peaks is significantly higher than those of the genes with broad CHD6 peaks. (C) Nucleosomes density of broad CHD6 peaks in both the C4-2 control cells and CHD6 knockdown cells. (D) Gene expression levels showing notable variations and significant differences between normal and cancer cell lines. P values determined using one tail Wilcoxon test.  $*p < 0.05$ ;  $**p < 0.01$ ;  $***p < 0.001$ .





**Figure S4. Detailed information on the overlap of genes with sharp CHD6 peaks between HEK293 and cardiomyocytes.**

(A) Analysis of overlapping genes with enrichment in HK genes. (B) GO analysis of overlapping genes.