Supplemental Table S1: List of CHD1L putative targets

Fragment No.	Chr. No.	Nearest Gene	Binding Site Location	Distance	Gene_ID	Gene Ontology
4	4p15.2	STIM2	Intragenic(Intron)		57620	Transport; Ion Channel
6	9q34.3	RXRA	3’ end	4,647 bp	6256	Signaling; Metabolism; Transcription
7	14 q21	PELI2	Intragenic (Intron)		57161	Signaling
12(a)	1q23.3	DEDD	5’ end	1,115 bp	9191	Transcription; Apoptosis
12(b)	1q22-q25	SELE	5’ end	1,272 bp	6401	Cell adhesion; Signaling
15	9q22.3	TMOD1	Intragenic (Intron)		7111	Cytoskeleton organization Cell motility
16	22q12.3	SYN3	Intragenic (Intron)		8224	Neurotransmitter secretion
18	7p15.1	CREB5	Intragenic (Intron)		9586	Transcription
19	8p22-p21	TRAILR3	5’ end	6,836 bp	8794	Apoptosis; Signal transduction
20	5p35.2	UNC5A	Intragenic (Intron)		90249	Apoptosis; Signal transduction
22	15q13.1	NDNL2	5’ end	9,323 bp	56160	Cell growth; Transcription
23	3q13.3-q21	TRH	5’ end	35,475 bp	7200	Signal Transduction
25	3q21.1-q21.2	KALRN	Intragenic (Intron)		8997	Transport; signaling transduction
28	5q31	ALDH7A1	Intragenic (Intron)		501	Oxidoreductase activity
30	1p36.21	PDPN	5’ end	16,748 bp	10630	Cell motility and morphogenesis
33	9q33.2	CDK5RAP2	3’ end	66,586 bp	55755	Cell cycle; neuron differentiation
35	6p21	HMGA1	5’ end	17,519 bp	3159	Cell mobility; apoptosis; transcription
36	12q24.1	RPL6	3’ end	6,760 bp	6128	Transcription; translation
37	11q21	PANX1	5’ end	64,186 bp	24145	Receptor binding; transport
38	4q21.23-q21.3	ARHGAP24	5’ end	66.310 bp	83478	cell differentiation; angiogenesis; signaling
40	3p21.1	LIMD1	5’ end	33,787 bp	8994	Signal transduction; transcription
41	10p15	PRKCQ	3’ end	20,644 bp	5588	Signal transduction; transcription; cell growth; apoptosis
42	11q12.1	MS4A8B	Intragenic (Intron)		83661	Signal transduction
49	8p21.3	BIN3	Intragenic (Intron)		55909	Cell cycle; cell growth; cytokinesis
54	1q25.3	RGL1	Intragenic (Intron)		23179	Signal transduction
57	Xq11.1	ARHGEF9	Intragenic (Intron)		23229	Signal transduction

Supplemental Table S2. The top-scoring matrix found in CHD1L-bound DNA sequences

Fragment No.	**Family**	**Matrix**	**Opt. thresh**	**Core Sim.**	**Matrix Sim.**	**Sequence**
CHD1L_1	RUSH	V$SMARCA3.01	0.96	1.0	0.96	**tcCCATgtgcc**
CHD1L_8	RUSH	V$SMARCA3.01	0.96	1.0	0.99	**ttCCATataag**
CHD1L_10	RUSH	V$SMARCA3.01	0.96	1.0	0.99	**ttCCATttgat**
CHD1L_11	RUSH	V$SMARCA3.01	0.96	1.0	0.96	**agCCATataca**
	RUSH	V$SMARCA3.01	0.96	1.0	0.998	**caCCATttatt**
CHD1L_12	RUSH	V$SMARCA3.01	0.96	1.0	0.967	**ctCCATttccc**
CHD1L_15	RUSH	V$SMARCA3.01	0.96	1.0	0.985	**tcCCATttgca**
CHD1L_17	RUSH	V$SMARCA3.01	0.96	1.0	0.99	**ttCCATttgag**
	RUSH	V$SMARCA3.01	0.96	1.0	0.99	**ttCCATttgag**
CHD1L_18	RUSH	V$SMARCA3.01	0.96	1.0	0.992	**ttCCATttatt**
	RUSH	V$SMARCA3.02	0.98	1.0	0.985	**tattACTTtta**
CHD1L_22	RUSH	V$SMARCA3.01	0.96	1.0	0.986	**tgCCATttgtc**
CHD1L_23	RUSH	V$SMARCA3.02	0.98	1.0	0.985	**caggACTTgtt**
CHD1L_27	RUSH	V$SMARCA3.01	0.96	1.0	0.96	**agCCATttggt**
CHD1L_29	RUSH	V$SMARCA3.01	0.96	1.0	0.992	**ctCCATttatg**
CHD1L_35	RUSH	V$SMARCA3.01	0.96	1.0	0.966	**ttCCATttcct**
CHD1L_37	RUSH	V$SMARCA3.02	0.98	1.0	0.985	**tcacACTTatt**
	RUSH	V$SMARCA3.01	0.96	0.96	0.972	**ttACATttgct**
	RUSH	V$SMARCA3.01	0.96	1.0	0.967	**ttCCATgtag**
CHD1L_38	RUSH	V$SMARCA3.01	0.96	0.96	0.965	**tcACATttgct**
	RUSH	V$SMARCA3.02	0.98	1.0	0.992	**t cgcACTTatt**
CHD1L_54	RUSH	V$SMARCA3.02	0.98	1.0	0.987	**atatACTTctc**
CHD1L_57	RUSH	V$SMARCA3.02	0.98	1.0	0.985	**gtgaACTTttg**

Supplemental Table S3. In Vivo Tumor Development Experiments of Vector and CHD1L-Transfected HCC Cell Lines in Nude Mice

Cell type[a]	**Cell numbers injected**	**Tumor incidence**[b]	**Average volume (mm^3)**[c]
Vec-7703	4000,000	1/5	32
CHD1L-7703	4000,000	4/5	512
Vec-LO2	2000,000	1/5	75
CHD1L-LO2	2000,000	5/5	672

[a] Vec-7703 and CHD1L-7703, Vec-LO2 and CHD1L-LO2 cells were maintained subcutaneously in nude mice.

[b] The number of tumors detected/number of injections.

[c] The average volumes of tumors detected.

Supplemental Table S4. IHC scores of CHD1L in 50 pairs of primary HCCs and matched metastatic HCCs.

		IHC scores of Metastati HCCs (no. of sections)				Total
		0	**1**	**2**	**3**	
IHC scores of	**0**	3	8	2	0	13 (26%)
Primary HCCs	**1**	1	2	10	2	15 (30%)
(No. of sections)	**2**	1	1	8	12	22 (44%)
Total		5(10%)	11 (22%)	20 (40%)	14 (28%)	50

Supplemental Table S5. The DNA sequence of ChIP-PCR primers

Fragment No.	**Gene**	**Primer**	**DNA sequence**
37	PANX1	Forward	5'-TTCTCAGCACCACATCACAC-3'
		Reverse	5'- GGAGCAGGTTGTTCAGTTTC-3'
22	NDNL2	Forward	5'-CAGGCTCAAGAGGGAAGAGC-3'
		Reverse	5'-ATCATTTGCCCAGGACAGG-3
35	HMGA1	Forward	5'-GCACCCTTTGGTTGGATT-3'
		Reverse	5'-AAGCAGGATGATGATGGTAAGA-3'
12(a)	SELE	Forward	5'-CTGCAACCTCCATTTCCC-3'
		Reverse	5'-GCCTGTAATCCCAGCTACTT-3
15	TMOD1	Forward	5'-GTCACCCAAATGCAAACG-3'
		Reverse	5'-CCCCTCTTAAAGGCTCCC-3'
27	MTHFS	Forward	5'-AGCCATTTGGTAGGAAGTTG-3'
		Reverse	5'-GAAGCAATGTGGGCAGAG-3'
57	ARHGEF9	Forward	5'-ATTGCTGTGAACTTTTGTCTT-3'
		Reverse	5'-AGAGGAGGAGATGGGAAGA-3'
18	CREB5	Forward	5'-ATTGTAAATGACTGGAAAACTG-3
		Reverse	5'-CTGAAATAATAGGGGAAAGG-3'
38	ARHGAP24	Forward	5'-TTTGCTGAGGAGTGCTTTA-3'
		Reverse	5'-CACCACATCgCACTTATTC-3'
23	TRH	Forward	5'-CAGCAGGACTTGTTTTC-3'
		Reverse	5'-ATAATGACTAATGAGGGTAA-3'

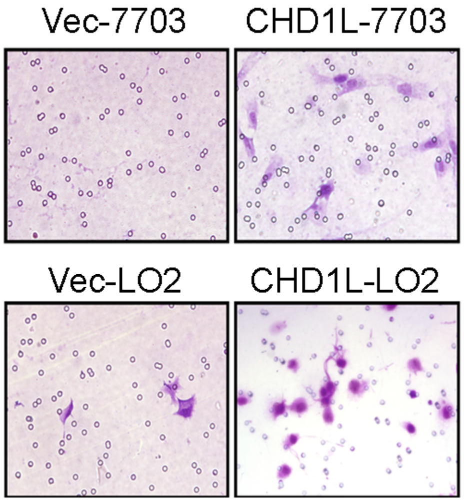
Supplemental Table S6. The DNA sequence of PCR primers

Gene	**Primer**	**DNA sequence**
SCYL1BP1	Forward	5'-TTGGGCACTTTTGGGGGTG -3'
	Reverse	5'-CGCTGTGGTTCAAATGGATCT -3'
P53	Forward	5'-CCGCAGTCAGATCCTAGCG -3'
	Reverse	5'-AATCATCCATTGCTTGGGACG -3'
CHD1L	Forward	5'-TTACTGCGGCTTCATACTGAGG -3'
	Reverse	5'-GGTAAGAGCGTAGGTGAATCCC -3'
18S	Forward	5'-CTCTTAGCTGAGTGTCCCGC-3'
	Reverse	5'-CTGATCGTCTTCGAACCTCC-3'

Supplemental Figures and Figure Legends

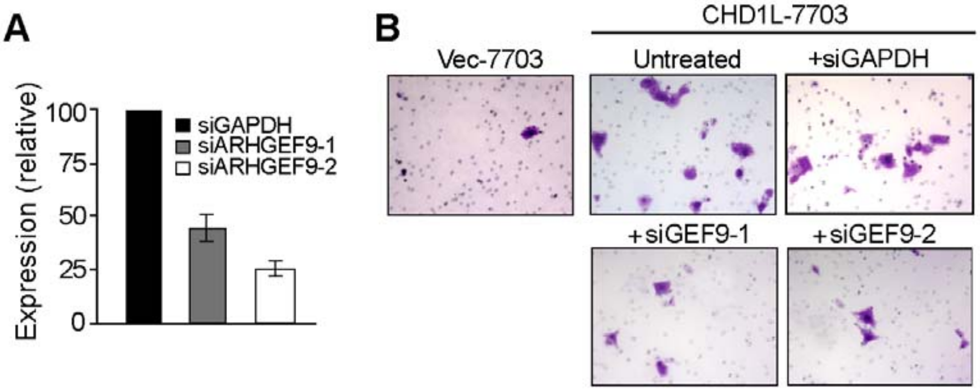
Chen et al. Figure S1

Supplementary Figure S1. DNA sequences of CHD1L binding sites. (**A**) Expression of the GFP/CHD1L fusion protein and GFP alone were detected by western blot analysis in two stable GFP/CHD1L transfectants (CHD1L-C3 and C6) and two GFP empty vector-transfectants (GFP-C3 and C4). (**B**) A subset of sequences (n=17) derived from the CHD1L binding sites is shown with the potential CHD1L-binding motif of 11 bp in length highlighted in gray and the hexameric core sequences are marked in red bold font.



Chen et al .Figure S2

Supplemental Figure S2. Representative images of the Matrigel invasion assays for cells transfected with empty vector or CHD1L-expression plasmid. The cells that invaded through the Matrigel were fixed and stained with crystal violet (200× magnification).



Chen et al. Figure S3

Supplementarl Figure S3. Silencing ARHGEF9 expression inactivates Cdc42 and inhibits cell invasion. (**A**) After silencing of ARHGEF9 expression in CHD1L-7703 cells treated with siARHGEF9-1 or siARHGEF9-2 (but not untreated or siGAPDH) detected by qPCR. The bars represent the mean ± SD of three independent experiments. (**B**) The invasive ability of CHD1L-7703 cells was inhibited in CHD1L-7703 cells treated with siARHGEF9-1 or siARHGEF9-2, rather than untreated or siGAPDH, as detected using Matrigel invasion assays (200× magnification).