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Supplemental Information

**Long Non-coding RNA PEBP1P2 Suppresses
Proliferative VSMCs Phenotypic Switching
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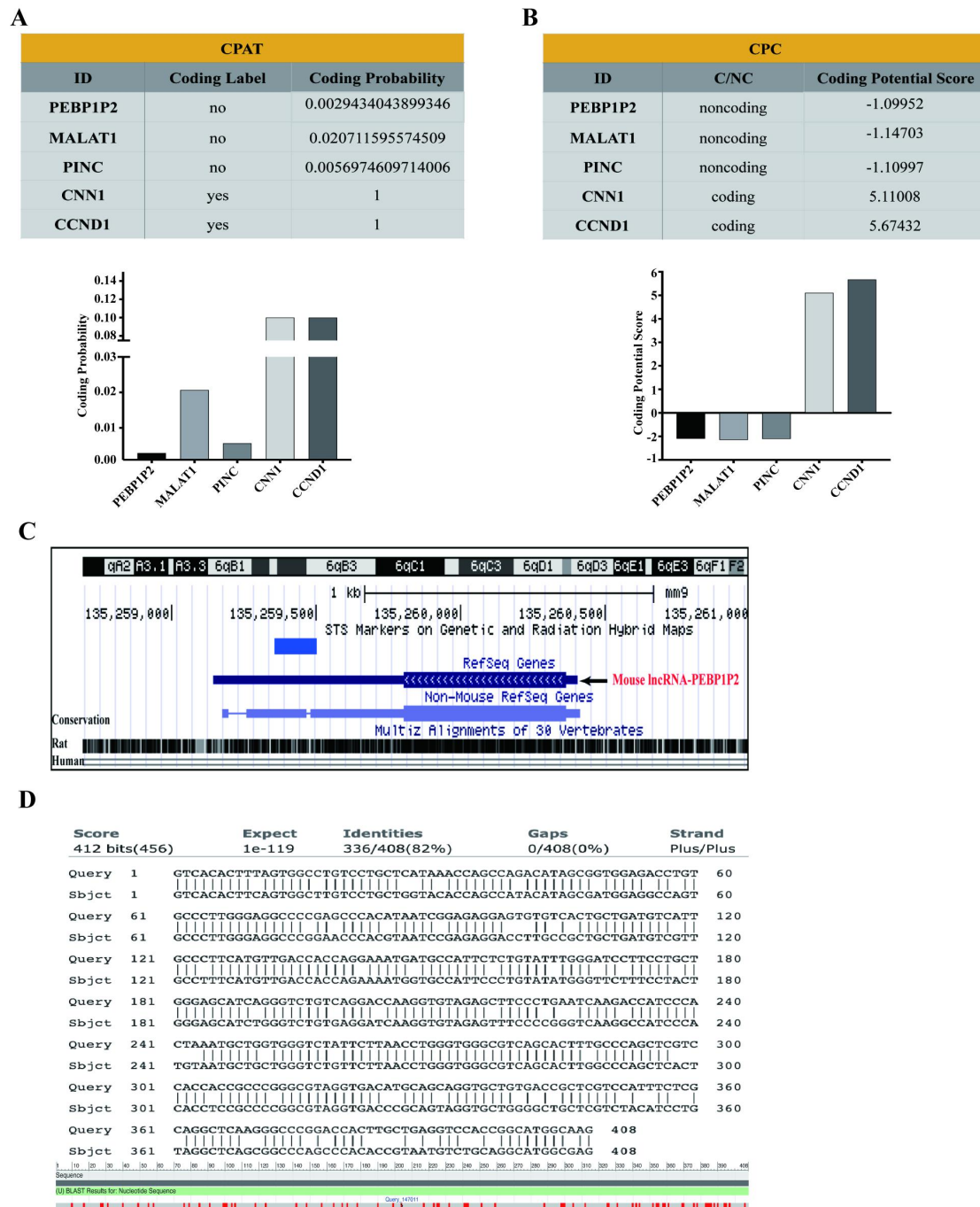


Figure S1. The characterization of PEBP1P2 in coding possibility and conservatism. (A and B) The coding-potential assessment (CPAT, <http://lilab.research.bcm.edu/cpat/index.php>) and coding potential calculator (CPC, <http://cpc.cbi.pku.edu.cn/>) tools were used to predict the coding probability of PEBP1P2. MALAT1 and PINC served as the long non-coding RNA controls, while CNN1 and CCND1 served as the coding RNA controls. (C) Genomic location of PEBP1P2 on mouse assembly (2007) predicted by UCSC LiftOver tool. (D) The NCBI BLAST tool was used to sequence comparison between human and rat PEBP1P2.

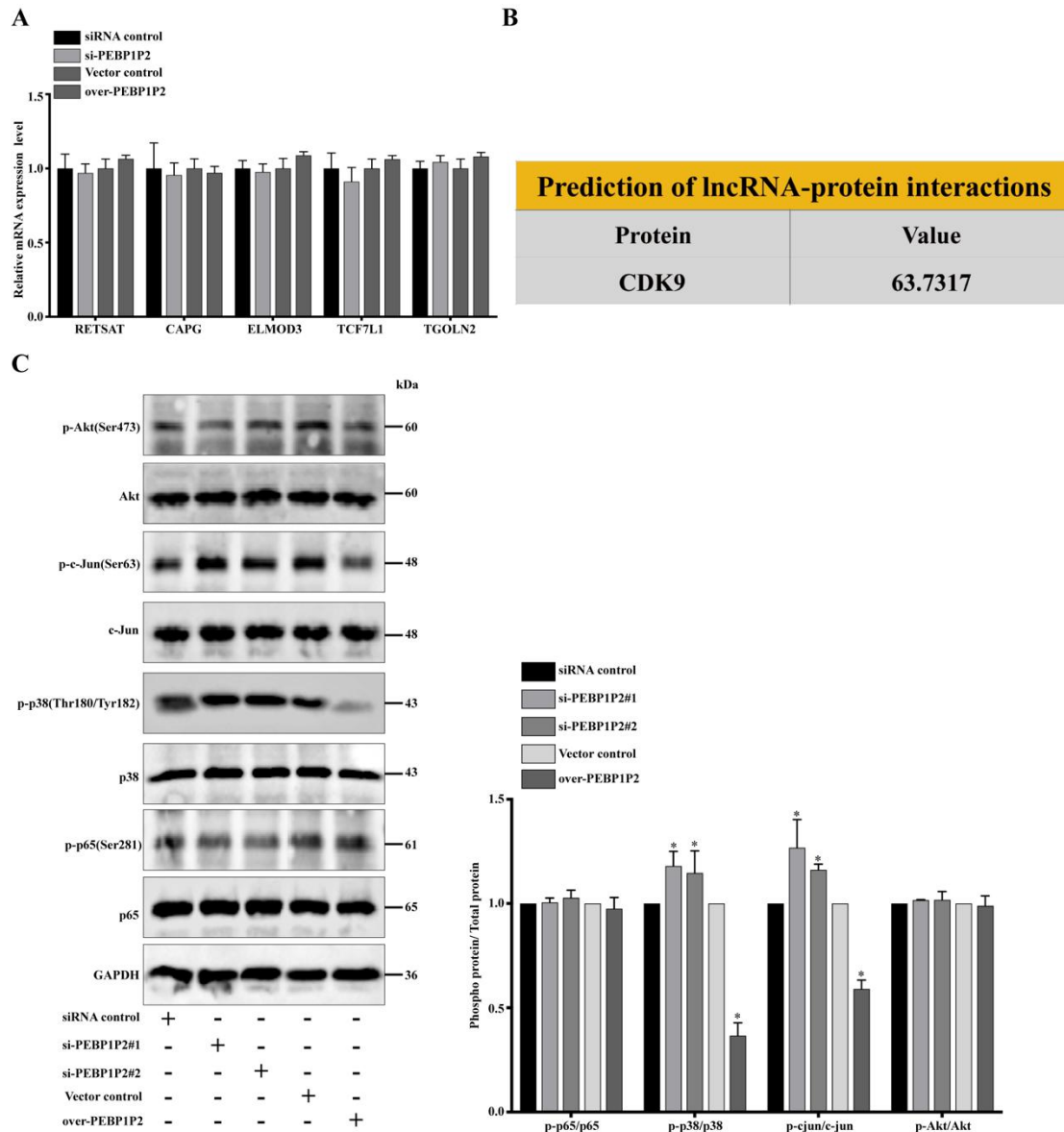


Figure S2. PEBP1P2 may work in trans. (A) The mRNA expression level of PEBP1P2 neighbor genes after PEBP1P2 knockdown or overexpression in VSMCs were measured by qRT-PCR. (B) The prediction of lncRNA-protein interactions tool (<http://bioinfo.bjmu.edu.cn/lncpro/#>) was used to predict the potential PEBP1P2/ CDK9 interaction. (C) Detection of PEBP1P2 knockdown or overexpression on the protein expression of NF- κ B p65, p-NF- κ B p65, p38MAPK, p-p38MAPK, c-Jun, p-c-Jun, Akt, and p-Akt by western blot. Data are presented as mean \pm SD. n=3. * P < 0.05 vs Ctl.

Table S1. General Characteristics of the CHD Patients and Healthy People.

Clinical parameters	Control (n=29)	CHD (n=27)	P
Age, year	24.21 ± 2.04	69.67 ± 8.85*	< 0.001
Male, %	15 (51.7)	18 (66.7)	0.26
BMI, kg/m ²	21.41 ± 2.42	23.15 ± 2.93*	0.019
SBP, mmHg	118 ± 8.96	142.15 ± 23.82*	< 0.001
DBP, mmHg	62.97 ± 3.28	85.26 ± 15.72*	< 0.001
CHO, mmol/L	3.72 ± 0.94	4.60 ± 1.28*	0.005
HDL, mmol/L	2.20 ± 0.34	1.20 ± 0.35*	< 0.001
LDL, mmol/L	0.92 ± 0.49	2.84 ± 1.00*	< 0.001
TG, mmol/L	1.20 ± 1.00	1.71 ± 0.91	0.050
Hypertension, %	0 (0)	16 (59.3) [#]	< 0.001
Smoking, %	8 (27.6)	15 (55.6) [#]	0.035

BMI, body mass index; SBP, systolic blood pressure; DBP, diastolic blood pressure; CHO, cholesterol; HDL, high-density lipoprotein; LDL, low-density lipoprotein; TG, triglyceride. P value is calculated with t-test (*) or Mann-Whitney test (#) to compare continuous variables (presented as mean ± SD) or categorical variables (presented as no. (%)), respectively. **p* < 0.05 vs Ctl, #*p* < 0.05 vs Ctl.

Table S2. siRNA sequences.

siRNA Names	Sequences (5'→3')
siRNA Control sense	UUCUCCGAACGUGUCACGUTT
siRNA Control antisense	ACGUGACACGUUCGGAGAATT
si-PEBP1P2 #1 sense	GCUCAUAAACCAGCCAGACTT
si-PEBP1P2 #1 antisense	GUCUGGCUGGUUUAUGAGCTT
si-PEBP1P2 #2 sense	CCAUUUCUCGCAGGCUCAATT
si-PEBP1P2 #2 antisense	UUGAGCCUGCGAGAAAUGGTT
si-CDK9 #1 sense	GGGAGAUCAAGAUCUUCATT
si-CDK9 #1 antisense	UGAAGGAUCUUGAUCUCCCTT
si-CDK9 #2 sense	GCUGCAAGGGUAGUAUAUATT
si-CDK9 #2 antisense	UAUAUACUACCCUUGCAGCTT

Table S3. Primer Sequences for qRT-PCR

Primer Names	Sequences (5'→3')
Hu-GAPDH Forward	GTCTCCTCTGACTTCAACAGCG
Hu-GAPDH Reverse	ACCACCCTGTTGCTGTAGCCAA
Ra-Gapdh Forward	GCCCATCACCATCTTCCAGGAG
Ra-Gapdh Reverse	GAAGGGGCGGAGATGATGAC
Hu/Ra-PEBP1P2 Forward	ACTTTAGTGGCCTGTCCTGCTCA
Hu/Ra-PEBP1P2 Reverse	TGACGCCACCCAGGTTAAGAATA
Hu-CCDN1 Forward	TCTACACCGACA ACTCCATCCG
Hu-CCDN1 Reverse	TCTGGCATT TTTGGAGAGGAAGTG
Hu- α -SMA Forward	GTGTTGCCCTGAAGAGCAT
Hu- α -SMA Reverse	GCTGGGACATTGAAAGTCTCA
Hu-CNN1 Forward	CCAACGACCTGTTTGAGAACACC
Hu-CNN1 Reverse	ATTTCCGCTCCTGCTTCTCTGC
Hu-SMHC Forward	CGCCAAGAGACTCGTCTGG
Hu-SMHC Reverse	TCTTTCCAACCGTGACCTTC
Hu-CDK9 Forward	CCATTACAGCCTTGCGGGAGAT
Hu-CDK9 Reverse	CAGCAAGGTCATGCTCGCAGAA
Hu-RETSAT Forward	GAAGAGGCTGCGGAACACATCC
Hu-RETSAT Reverse	CCTCAAACCACTCGTAGGCAGT
Hu-CAPG Forward	CAGGTGGAGATTGTCACTGATGG
Hu-CAPG Reverse	CTGGGCATTTGCCTTGT CAGCT
Hu-ELMOD3 Forward	CGGCTCCAAGTTT GACTGTGCC
Hu-ELMOD3 Reverse	GAGTCCATCACCAGGTAGAGCA
Hu-TCF7L1 Forward	TCGTCCCTGGTCAACGAGT
Hu-TCF7L1 Reverse	ACTTCGGCGAAATAGTCCCG
Hu-TGOLN2 Forward	GGAGAGCAGCCACTTCTTTGCA
Hu-TGOLN2 Reverse	CCAAACGTTGGTAGTCACTGGC