

## Supplementary Material

**Table S1** Sequence of LncRNA *SMARCD3-OT1*

GRCg7b (chr2:118054-118633,133484-133684,134874-135641)

GATGGGAAGGTGAGGTGGTTCACCGTTGTTGTGGTCTGGGGACCTTTTCCTGCTTTTCTGGTG  
GTGGTCACATCCACCCCTGAAGCTGATCTGATGCTTCCAGATCCCTCTGCGCTGGTGAGAACCCA  
GGATCCCTCATCAGAGGTGGACCCTTCCAGCACCATGTCCTGGGATGAATGGTGATTTTGACCAT  
CTCCTACCTTGTGCAGACGGACACCCCATGAGGGCCCATATACTCCTCAAACCTTTCTTCTGGAAG  
ATACCACCATCCAAACCTGCGAGAGTGCATCTGCATTGCTGGCCTTCTTCAGGATGGTGGGGAG  
CAGGAGCTGCTTTGATTCTCCTTTCTCCCTTTGGGAAGGACACATACCCACCCCAAGGAGAGTG  
CTCCAGAGGGGATGACATCCCCTTTGCCAGGTCCTGCGGGACAGACTTGCCAGTTTCCCAGGG  
AAGCTGCTGCTCTGTGCTGTCTGCTTGGAAAGTGAGACCAGGTCATGTCCAGTGACCAGTCCAAT  
CTCAGTCTGTGGTATGGGGCTGTCAGCAGTGCCCTTCTTGGAGAATGACTTCAAAGTATGACGTG  
CCTGGAGGAGCCGTGCACCTTCTGAAAAGAACCAGTTTCTTGGTACTGCTTCAGTAGCAATCAA  
CACCCAGCTGTTACCATAGGGACACTGCCATGAGGAGCCAGATCTTTCCAAGCAGGATTCTTG  
CCCTTCGGCCCTAGGGAAGGAATCCCAGCCTGGCCCCGCTCCTTGGGCATCGTGAGGAGCTGG  
ATCCAAATGCATCTTCCGCTGCTCTCTTAGAGCTGCTCCTGCTTCAGGTCAATTAGAATGTCTGC  
TGCTCAGTCATCATGATACAATATCTGGTTTCTACCCCATCTGCTGTGGATAAGGTTGCTGCTCC  
CTCTTGGTCTGCACACATGTGACTGTAGGTGTTTGCCATCTGCCTAGCCTGGCACAGGAGAATGA  
AAAGCTGGAAGGCTTGGAATAATGTCCTACCTGCTGCTATAGGCGTATCACAGCTCCTTCAGGACT  
GACCTTCCACTGCTGCCTTGTGTTTTCCAGCCAAAATCTCCTGATACTTTAATGCCCATTTGATTT  
TTTTTTGTCTTTGACCCAAACGACTGTGAACTTTCCCCGCGTCTTCTCATGTACATCTCTGAA  
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GCCCAGCCATCCCCAGACCTGCTGGCAGCTCCTTGCTTCCACCACTCGTCATCCTTGTGACATTT  
TGTTTACAACCTTTTACTTGCTGTTTGTGTTTGTGGACATTGGGTGTTACAGTCAGAATTCAGAC  
ATGTTTCCCTGCATTACATTCAAGTTGCTTTTGCCATTTTACTTCTGGCTGCCATTTCTCAAAGCTG  
TCGATGTTTGCTGTAATAATGCACTGCCTGAGATGAAAATTCCTTTTCTCAGGGGTCATCTTTTC  
ATAACTTTGTGATTATTTGCCAAATAAAATGATTTAAAAAGTCA

**Table S2** Sequences of different ORFs of LncRNA *SMARCD3-OT1*

ORFs	sequences
ORF1	ATGGTGGGGAGCAGGAGCTGCTTTGATTCTCCTTTCCTCCCTTTGGGAAGGACA CATACCCAACCCAGGAGAGTGCTCCAGAGGGGATGACATCCCCTTTGCCAGGTCC TGCGGGACAGACTTGCCAGTTTCCCAGGGAAGCTGCTGCTCTGTGCTGTCTGCT TGGAAGTGA
ORF2	ATGTTTCCCTGCATTACATTCAAGTTGCTTTTGCCATTTTACTTCTGGCTGCCATTTT TCAAAGCTGTCGATGTTTGCTGTAATAATGCACTGCCTGAGATGAAAATTCCTTT TCTCAGGGGTCATCTTTTCATAACTTTGTGATTATTTTGCCAAATAAAATGATTTAA
ORF3	ATGAATGGTGATTTTGACCATCTCCTACCTTGTGCAGACGGACACCCCATGAGGG CCCATATACTCCTCAAACCTTCTTCTGGAAGATACCACCATCCAAACCTGCGAGA GTGCATCTGCATTGCTGGCCTTCTTCAGGATGGTGGGGAGCAGGAGCTGCTTTGA
ORF4	ATGATACAATATCTGGTTTCTACCCCATCTGCTGTGGATAAGGTTGCTGCTCCCT

ORFs	sequences
	CTTGGTCTGCACACATGTGACTGTAGGTGTTTGCCATCTGCCTAG
ORF5	ATGCTTCCAGATCCCTCTGCGCTGGTGAGAACCCAGGATCCCTCATCAGAGGTGG ACCTTCCAGCACCATGTCCTGGGATGAATGGTGA
ORF6	ATGACTTCAAAGTATGACGTGCCTGGAGGAGCCGTGCACCTTCTGAAAAGAACC AGTTTCTTGGTACTGCTTCAGTAG
ORF7	ATGTACATCTCTGAAGATGGTAAAAAATGAAAGAAAGAAAGAAACCAGCAAA CAGACAAAAACCTGCCTAG
ORF8	ATGTCCAGTGACCAGTCCAATCTCAGTCTGTGGTATGGGGCTGTCAGCAGTGCCC TTCTTGGAGAATGA
ORF9	ATGCATCTTCCGCCTGCTCTCTTAGAGCTGCTCCTGCTTCAGGTCAATTAG
ORF10	ATGAGGAGCCAGATCTTTCCAAGCAGGATTCTTGCCCTTCGGCCCTAG
ORF11	ATGGTGATTTTGACCATCTCCTACCTTGTGCAGACGGACACCCCATGA
ORF12	ATGGGGCTGTCAGCAGTGCCCTTCTTGGAGAATGACTTCAAAGTATGA
ORF13	ATGAAAAGCTGGAAGGCTTGAAAATGTCCTACCTGCTGCTATAG
ORF14	ATGACGTGCCTGGAGGAGCCGTGCACCTTCTGA

**Table S3** Sequence of 2,000 bp upstream of *SMARCD3X4*

CTCTTGCACTTACCTTATGCCTCTTAACAAAGAAAACCTCTTTGCAAACCTCTTTTGTGTAAGAG  
TAATGTTGTAGGAGCTTTTTCATACGTTTCTCTACAGAAAATCTTATCTAAGGACTAGGAAGAG  
ATCACTTCCTGTGTGAAACTGCTCAGAGACCTGGAGATTACTGGGCAACATGGGGCCATTTACC  
CCAGTCTGTGGTGAAGAAATGATGCATGAGGTGACGATCTCAGGCTCTGCTAAAAGGGCTAAC  
TTGGTATAATTGGTTTCTTCTGCTTCTGATGAAGGACTCCAACATTCTCAAGTTTTCAGATTTCT  
GCTTGCTTGTATGTGCACACACACATAAAGAGGGAGTACAAACACAGGCTTTTAACTGGACGT  
GACAACAGTGAGAACTGTTACTCTTTACATCTTTCTTATGTTTATGTAGGAGTTTGAGGATCTGC  
TGCCAGTTAAAATGTCAAAGTGTCAATGAGAAATCCTTAATATTGGAGAAATCTGGCTTCTGTG  
CTTGGTCCTTTGATGTATACTTTGCTATTATTATTAGTTACAATCAATGAACAAAAATTTACAGCT  
GGATCATGAGCTTGGAAGCTGAGAGGAGACTGGAAGAAGCTGTGCCAACAGCCAGCCTTTCTC  
TATACAAACATTAAAAATACTTGACAAGATGAACAAGCTGCAGTTCACCGGCTCAATGAAGGA  
GGTTTGTGTTTGGGGTTAAAGTGTGAGAGCCCAGCAGACTGTCAAGAAAGAACAACATAAAGA  
AGTGGAGTGCACGGAGAGCAGAAAGAAGAAAAAATGTGAAAGAGGAAAGGAAGGCCTAGA  
ATTATTTTCAGCAACTCAGTGAAATTGGAAGCAGAAGTAGCAACTTTAATCTGAGAAGAAAGCA  
AACAGCCTGTATAAAAAAAAAAAAAAAAAATCACAAATGTCTACAAAGATAGGCCTGGAATAGA  
GAAGCTCTACCTGGATGGTTATCTAGGAAGTCTCAGCAGATGAGAAAAAATTAATTTTGATTT  
TGAAAAAATAACATCTACACACTTCTGATGGAGGAAAAGCAAGTAGCAATAATAGCAA  
TCATATCTTGTGGTAATAACAAATCCCATGCATGTTACCCCTTCTCTTGGAGCAGCAAAAGAC  
ATGCTGTTTTTCCAGGAATCTGAGAGGAGAAATGCACATTTACTGTTTCAGTTTCTGTTACTTCTT  
CACTTTTCTCAGAGGAAAAAGCCATTGGTGAGTACAGTGCAAAGAATGTGGATAAATACAGAA  
AGAGTTTAGGATGATCATAGGTAGTTCTCTGCAAGGGGAGCTGCAAGGTAGAAGTTACACTAA  
TTTATAGATAGAGTAAATCTGTTATAAAAACTGTGGTAGGGTTCAGCTCGAACTTAAACACAGTC  
AAGGCAGAGCTAATGAGAGCAGCCAAATTTTAAGTCATGACACAGTTGAGCAGCTGAACATAA  
CTACTTCAGGTAAAGTACTTTGCTGTCCGACTCCACCGACCAGACCGCAGGCTTAGACACCT

GGTTCATGTATGTCTACACTTTTTTTTGTCTTCATAAGCAGCCACTTAGGCTATATGTCTTCTGAA  
 ATTTAAGATTGATCATTGCCCACTATTTTGGTCTTCCTTCCCCAACACAGCATACTAGTCACTGT  
 CATTATTGTAAGTATGGGTCTTCGTGACTCACCAGCCTCACATGTAGCTTCCACATCCTGCCCTC  
 GGGCCTAGTGGCTCAATATAAACTCGGGCCTGGGCATGTGGCTTCTGTACAGGTTATATTGCTG  
 GTGTGACCGTTTCTACTTGGCTATAATTATACCTTGGCTGTGGGGCCTGTTGTTTCTGTACAGTAG  
 ACTGACTTTGATGTTTGACTTTAGATGTGCCTCATAACCATGAGCTTTTCTGACGAGTTGGACAC  
 TGAGCACGAGTACCACCTCCTGGTTTGCCTTGCCTTATTCAGAACTGCTGGGCTGGGTCT  
 TGTTGGGGAGCC

**Table S4** Primers used for qRT-PCR

Gene name	Primer sequences (5'-3')	Size(bp)	Annealing temperature (°C)
<i>SMARCD3-OT1</i>	F: CAGTCTGTGGTATGGGGCT R: AGGCGGAAGATGCATTTGG	276	58
<i>SMARCD3X4</i>	F: CAGTTCCTCTCTCAGCAC R: CAAAATCACCATTTCATCC	272	58
<i>GAPDH</i>	F: CAACTTTGGCATTGTGGAGG R: CGCTGGGATGATGTTCTGG	130	58
<i>CDKN1A</i>	F: CGTCTCGGTCTCGAAGTTGA R: CGTCTCGGTCTCGAAGTTGA	133	58
<i>CDKN1B</i>	F: TCGCTGTGCTGGGCTGAA R: CAAGGACGAAAGGATGTGGG	188	58
<i>CCNA1</i>	F: CCCGTAGACCACGAGCAGAT R: TCAGGCAAGGCACAATCTCA	217	58
<i>CCND1</i>	F: CAGAAGTGCGAAGAGGAAGT R: CTGATGGAGTTGTCCGTGTA	158	58
<i>CCNE1</i>	F: CTGCTGGTTCTAACTCCTGCTC R: TGGCGTACTCGATCCATTTCTAT	260	58
<i>MYF5</i>	F: CCTCATGTGGGCTTGCAAA R: CCTTCCGCCGGTCCAT	168	58
<i>MYOD</i>	F: CCTCATGTGGGCTTGCAAA R: CTGGGCTCCACTGTCACTCA	200	58
<i>MYOG</i>	F: CGGAGGCTGAAGAAGGTGAA R: CGGTCCTCTGCCTGGTCAT	320	58
<i>MyHC</i>	F: CTCCTCACGCTTTGGTAA R: CTCCTCACGCTTTGGTAA	213	58
<i>U6</i>	F: CTCGCTTCGGCAGCACA R: AACGCTTCACGAATTTGCGT	189	58
<i>Beta-actin</i>	F: GATATTGCTGCGCTCGTTG R: TTCAGGGTCAGGATACCTCTTT	194	58
<i>TNNC1</i>	F: GTTGAGCAGTTGACAGAAGA R: GAACCATCATAACAAGGAAC	223	58

Gene name	Primer sequences (5'-3')	Size(bp)	Annealing temperature (°C)
<i>TNNI1</i>	F: GAGGAGTGGGAGCAGGAGAT R: TTCGTCCACAATCTCAACCT	231	58
<i>TNNT1</i>	F: GATATTGCTGCGCTCGTTG R: TTCAGGGTCAGGATACCTCTTT	139	58
<i>SRL</i>	F: CCTCCTCGGGCTGGATGACA R: GTTCTTGCTGCTTGCGGTTT	272	58
<i>TNNC2</i>	F: GAGCAGCAAAGATGGCGTCA R: ATCACCGTGCCCAACTCCTT	151	58
<i>TNNT3</i>	F: AGAGGGAAGAAGCAAACAGC R: GTCCACAGTTCCTTAGCCT	123	58

**Table S5** Primers used for RACE

Primer name	Primer sequences (5'-3')	Annealing temperature (°C)
<i>SMARCD3-OT1</i> 5'RACE outer	CTCACTTCCAAGCAGACAGCACAGAG CA	Step down
<i>SMARCD3-OT1</i> 5'RACE inner	GACAGCACAGAGCAGCAGCTTC	Step down
<i>SMARCD3-OT1</i> 3'RACE outer	CCAGGAGAGTGCTCCAGAGGGGATGA CA	Step down
<i>SMARCD3-OT1</i> 3'RACE inner	CCAAATGCATCTTCCGCCTGCTC	Step down

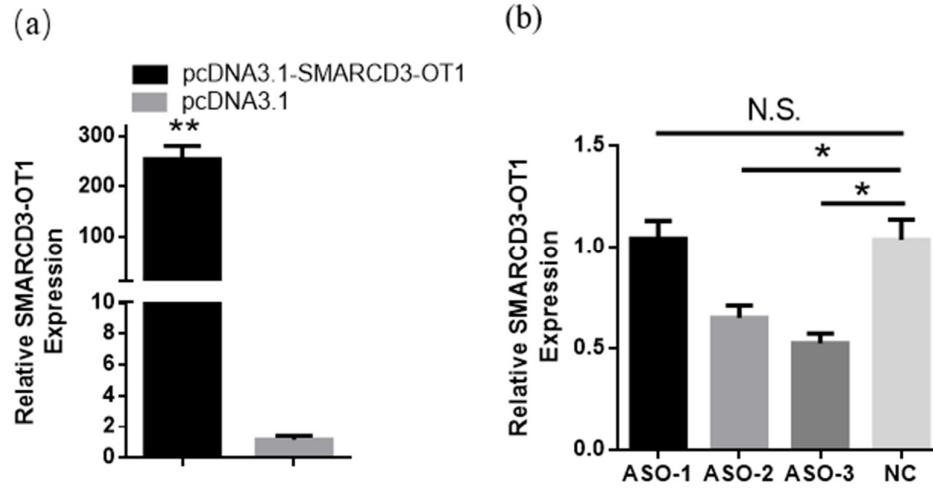
**Table S6** Primers used for plasmid construction

Primer name	Primer sequences (5'-3')	Size(bp)	Annealing temperature (°C)
<i>SMARCD3-OT1</i> ORF1	F: ATGAATGGTGATTTTGACCATCTC R: GGGAGCAGGAGCTGCTTTGG	165	58
<i>SMARCD3-OT1</i> ORF2	F: ATGACTTCAAAGTATGACGTGCC R: AGTTTCTTGGTACTGCTTCAGTGG	78	58
<i>SMARCD3-OT1</i> ORF3	F: CGTCTCGGTCTCGAAGTTGA R: TGCTCCTGCTTCAGGTCAATTGG	51	58
<i>SMARCD3-OT1</i> ORF4	F: AATGATACAATATCTGGTTTCCT R: TAGGTGTTTGCCATCTGCCTGG	102	58
<i>SMARCD3-OT1</i> ORF5	F: ATGTACATCTCTGAAGATG R: AAACAGACAAAAACCTGCCTGG	72	58
<i>SMARCD3-OT1</i> ORF6	F: ATGTTTGCTGTAATAAT R: ATAATGCACTGCCTGAGATGG	33	58
	F: ATGGTGATTTTGACCATCT	48	58

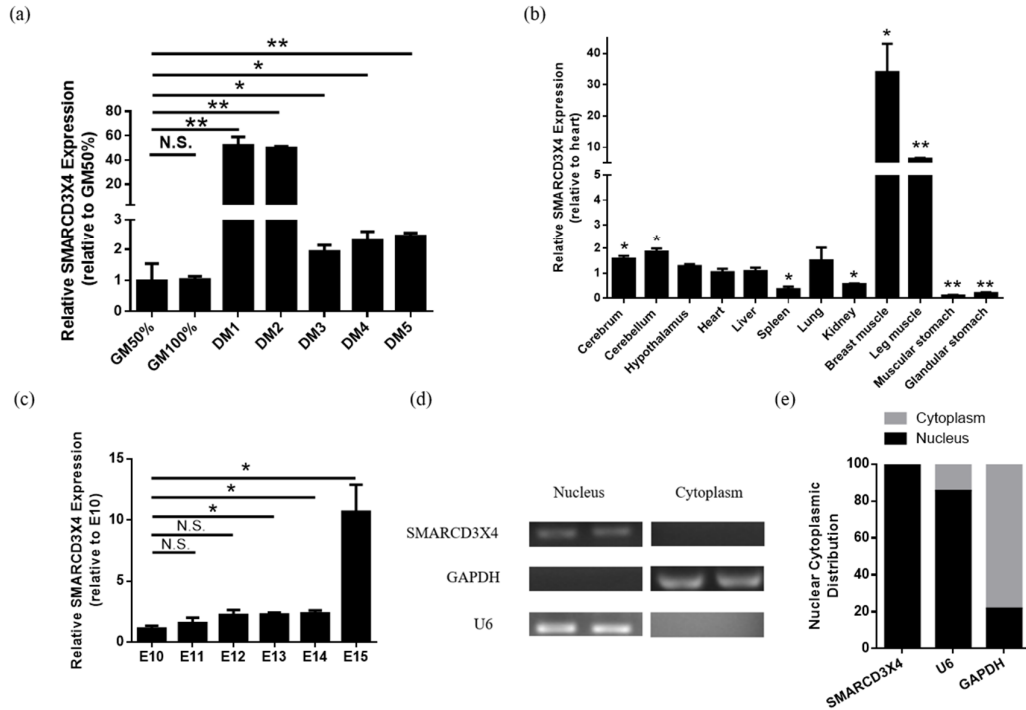
Primer name	Primer sequences (5'-3')	Size(bp)	Annealing temperature (°C)
<i>SMARCD3-OT1</i> ORF7	R: TGTGCAGACGGACACCCCATGG	174	58
<i>SMARCD3-OT1</i> ORF8	F: ATGGTGGGGAGCAGGAGCTGCTT R: TCTGTGCTGTCTGCTTGGAAGTGG		
<i>SMARCD3-OT1</i> ORF9	F: ATGTCCAGTGACCAGTCCAAT R: AGCAGTGCCCTTCTTGGAGAATGG	69	58
<i>SMARCD3-OT1</i> ORF10	F: CGGAGGCTGAAGAAGGTGAA R: GGATTCTTGCCCTTCGGCCCTGG	48	58
<i>SMARCD3-OT1</i> ORF11	F: CTCCTCACGCTTTGGTAA R: TGTCTGGGATGAATGGTGG	90	58
<i>SMARCD3-OT1</i> ORF12	F: ATGGGGCTGTCAGCAGTGC R: TGGAGAATGACTTCAAAGTATGG	48	58
<i>SMARCD3-OT1</i> ORF13	F: ATGAAAAGCTGGAAGGCTTG R: AAAATGTCCTACCTGCTGCTATGG	45	58
<i>SMARCD3-OT1</i> ORF14	F: ATGTTTCCCTGCATTACATTCAAGT R: ATTTTGCCAAATAAAATGATTGG	171	58
pEGFP-N1 mutation	F: CACCGGTCGCCACCATTGTTAGCAAG R: CTTGCTAACAATGGTGGCGACCGGTG	4733	60

**Table S7** Oligonucleotide used for interference

Fragment name	Sequences (5'-3')
<i>ASO-SMARCD3-OT1</i>	AAACCTGCCTAGAACAGCCC
<i>ASO-SMARCD3X4</i>	GGGAAAGACCAGCACAAAT



**Figure S1** The fold-changes of lncRNA *SMARCD3-OT1* after overexpression and knockdown. (a) Relative *SMARCD3-OT1* expression after introducing overexpression vector of *SMARCD3-OT1* into CPMs (n = 6). (b) Relative *SMARCD3-OT1* expression after introducing ASO of *SMARCD3-OT1* into CPMs (n = 6). Data are expressed as a fold change relative to the control. Results are shown as mean  $\pm$  SEM. Statistical significances of differences between means were assessed using an independent sample t-test. \* $p < 0.05$ , \*\* $p < 0.01$ .



**Figure S2** The expression pattern of *SMARCD3X4*. **(a)** Expression levels of *SMARCD3X4* in CPMs cultured in growth medium at 50% and 100% cell confluency (50%GM and 100%GM) and differentiation medium from 1 to 5 days (DM1 to DM5) (n = 6). **(b)** Tissue expression profiles of *SMARCD3X4* in 7-week-old chickens (n = 6). **(c)** Expression levels of *SMARCD3X4* from embryonic day 10 (E10) to E15 (n = 6). **(d, e)** Distribution of *SMARCD3X4* in the cytoplasm and nuclei of CPMs was determined by PCR and qRT-PCR. Data are presented as mean  $\pm$  SEM. Statistical significance of differences between means was assessed using an independent sample t-test. \* $p < 0.05$ , \*\* $p < 0.01$ .

(a)

TF	Pattern name	Source	Sequence name	Start	Stop	Strand	Score	P value	Q value	Matched motif
SP2		database	SMARCD3X4	378	392	-	18.3965	2.29e-07	0.000764	CCCCCGCCCCCGCT
SP2		database	SMARCD3X4	726	734	-	13.6735	1.11e-05	0.0285	AGCCGGGCG
SP2		database	SMARCD3X4	372	388	-	13.6379	1.2e-05	0.0135	CCCCCGCTCCAGGA
SP2		database	SMARCD3X4	28	42	-	13.6207	1.21e-05	0.0135	CCCCCGCCCCAGAC
SP2		database	SMARCD3X4	760	776	+	13.2921	1.31e-05	0.00968	GCTGGGCGGAGCTGG
SP2		database	SMARCD3X4	688	704	-	13.2247	1.39e-05	0.00968	CCCCCGCGGAGGCGC
SP2		database	SMARCD3X4	205	221	+	12.809	1.94e-05	0.00968	AGGGCGGCGGTCGGA
SP2		database	SMARCD3X4	692	708	-	12.7079	2.09e-05	0.00968	GCTGGGCGGCGGAG
SP2		database	SMARCD3X4	390	396	+	12.6995	2.11e-05	0.00968	GGGGGGGGGGCGCT

(b)

**Protein:**

MVNILAADWPQLQAGQGLRRPGRVAGGGARAAPPEEDGAVRGSEPPPPPPRPVSGG  
RRFRGPGGGGPGASSRLPGESGRCCRAGGEGGEVDPGTWRGCPGWGLCGWSPEAFLGPRV  
PRELRFAPLRVPGVGRAGNTRSLSDSMAATAAVSPSEYLQPAASTAQDSQPSPLALLAA  
TCSKIGPPAVEAAVTPAPPQPTPRKLVPIKAPLPLGSGKNFGLSSKGNLFQIQGSG  
VGTSYPGGQLVFAIQNPTVISKGRSSANIQYQAVPQIAAGGQTQIQVQNLTNQIQIP  
GTNQAILTPSSSSHKVPVKKPAPAKSGASPVQSSNVVLTGGSNVTLTLPNNLVNTT  
ESSTQAQVIAESPSKPGKKTRKAMSPSPSTVAVAEQVETVLIETAEINIQAGNNLLI  
VQSPGSGQPAVVQGVVQPKQESQVQIPQALRVVQAASATLPTVPQKSSNIQIQT  
ESTPTQVYFKTPSGELQTVLLQEAFAVTVAPSTSCSSPVSRNSGTVTSKKPTARKERP  
LPKIAPAGGVISLAAQLAAQAIAQTININGVQGVPTITNAGGQQQLTVGNVSGNN  
LTISGLSPTQQLQMEQALSGELPQGEKRRRMACTCPNCKDGEKRPDQGGKKHICHIFE  
CGRTRFKTSLRAHVRLHTGERPFVCNWVFCGRFTRSDQLRHARTHTGDKRFECAQCQ  
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**RNA:**

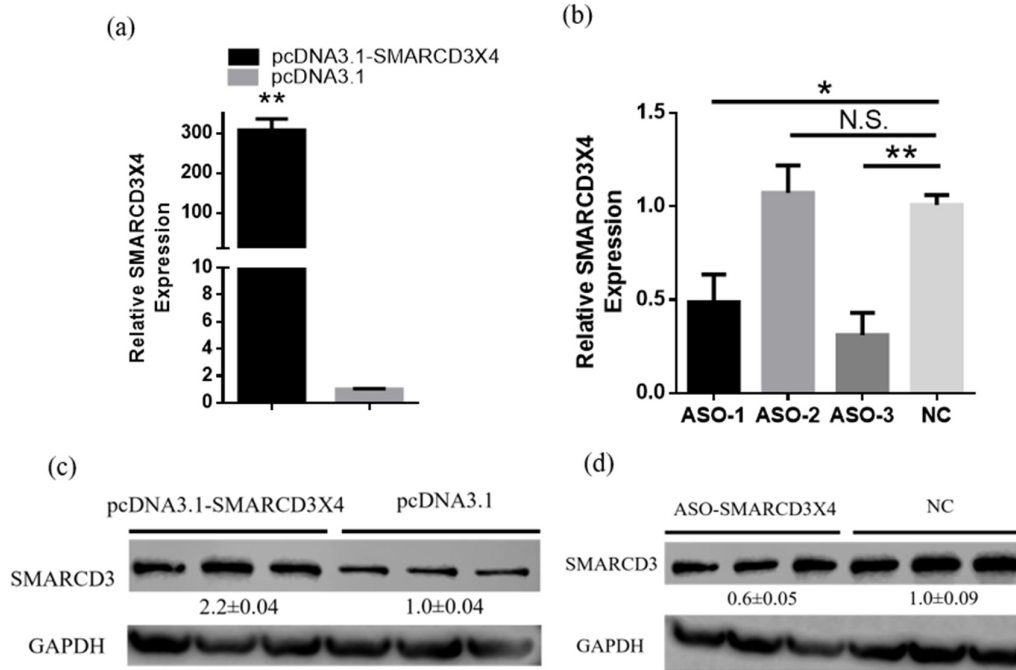
CCACGUGUGGGCUGCAGAAGCCGUCGGGAGCCCUUCCUUCGUGGGCUGAGCUUCCCG  
GGGGCGUGGAGCGCUGCUGCAGCGCUCUGGAGGGGAACUCCCGCUGUCCUCCUG  
AGGCACCCGGUGCUGCCCGCAGUCGGCUCGGGCGUGUCUCCGGCGUGCCUUGGACUG  
CACC CGGCGUGUUCUCAGAGGGAACGCAUCGCCCGGGUGUCUCAGUACAGAGUG  
CUCGCAUCUGACCGCUGCUCUACGCGAGCGCGUGCCGCGUGCUUUGGACAGCGGUUC  
UCCUCCUCCUCCUCCGUUUCUUGCAUCCCGAGCUCUCCUCCAGUCCUCCUCUCAGCA  
CCACCUUGGAGGAGCCUUGGGGUAAGCUGCUGGAAAGACCAGCACAAUUAUUGUG  
AGAGUGAUGGGAAGGUGAGGUGGUUACCCGUUUGUUGGUGUGGGGACCUUUUCCUGC  
UUUUCUGGUGUGGUCACAUCCACCCUGAAGCUGAUCUGAUCUCCAGAUCCUCCUGC  
GCUGGUGAGAACCCAGGAUCCUCAUCAGAGGUGGACCCUCCAGCACCAUUGCUGGGA  
UGAAUGGUGAUUUUGACCAUCUCCUACCUUGUGCAGAGCGACACCCCAUGAGGGCCCAUA  
UACUCCUCAACUUCUUCUGGAAGAUACCAUCCAAACUCCGAGAGUGCAUCUGCA  
UUUGGCGCCUUCUUCAGGAUGGUGGGGAGCAGGAGCUGUUGAUUCUCCUUCUCCCG  
UUUGGGAAGGACACAUACCCACCCAGGAGAGUCCUCCAGAGGGGAUGACAUCUCCUUG  
CCAGGUCCUGCGGGACAGACUUGCCAGUUCUCCAGGGAAGCUGCUGCUGUGCUGUCU  
GCUUGGAAGUGAGACCAGGUCUUGCAGUGACCAUCCAGUCCUGUGGUAUUGGG  
GCUUGCAGCAGUGCCUUCUUGGAGAAUGACUUCAGUAGCUGCCUGGAGGAGCGCG  
UGCACCUCUUGAAGAAAGCAUUCUUGGUGUACUGCUCAGUACUACCAACCCAGCU  
GUUCACCAUAGGGACUGCCAUAGGAGGCCAGAUUCUCCAAAGCAGGAUUCUUGCCU  
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UCCAAUUGCAUCUCCCGCUGCUCUUGAGCUGCUCUUCAGGUAUUAUAGAUUG  
UCUGCUGCUCAGUCAUCAUGAUACAUAUCUGGUUCCUACCCCAUUCUGUGGAUAA  
GGUUGCUGCUCUCCUUGGUGCAGACAUUGAGCUGUAGGUGUUGGCAUUGCCUAGC  
CUGGCACAGGAGAAUGAAAAGCUGGAAGCUGGAAUUGUCCUACCUAGCUGUAUAGC  
GUUAUCACAGCUCUUCAGGACUGACCUUCCACUGCUGCUUGUUGUUCUCCAGCCAAAU  
CUCUGAUACUUAUUGCCCAUUGAUUUUUUUUUGUCUUCGACCCAAACGACUGGA  
AACUUUCCCGCGUCUUCUAGUACAUUCUGAAGAUUGUAAAAAUAAGAAAGAA  
AGAAACCAAGCAACAGAC

**Interaction probabilities**

Prediction using RF classifier 0.7  
Prediction using SVM classifier 0.65

**Figure S3** Prediction results of the htTFtarget database and RIPseq website. (a) The SP2 transcriptional factor may combine with the 2000 bp upstream of the functional gene *SMARCD3X4*. (b) The SP2 transcriptional factor is predicted to be combined with *SMARCD3-OT1*.





**Figure S4** The fold-changes of *SMARCD3X4* in mRNA and protein levels after overexpression and knockdown. **(a)** Relative *SMARCD3X4* expression in mRNA level after introducing overexpression vector of *SMARCD3X4* into CPMs (n = 6). **(b)** Relative *SMARCD3X4* expression in mRNA level after introducing ASO of *SMARCD3X4* into CPMs (n = 6). **(c)** Relative *SMARCD3X4* expression in protein level after introducing overexpression vector of *SMARCD3X4* into CPMs (n = 3). **(d)** Relative *SMARCD3X4* expression in protein level after introducing ASO of *SMARCD3X4* into CPMs (n = 3). The numbers shown below the bands were folds of band intensities relative to control. Band intensities were quantified by ImageJ and normalized to GAPDH. Data are expressed as a fold change relative to the control. Results are shown as mean ± SEM. Statistical significances of differences between means were assessed using an independent sample t-test. \* $p < 0.05$ , \*\* $p < 0.01$ .