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miR-7

71 AAGAAAAUUCUUGUGCCCGCAUUGGUAUUAAAUCCUCG**CAUUCAGUCUUCC**UGCCUCU 128

b

hsa-miR-205/COMMD1 Alignment: mirSVR score:-1.2126 PhastCons score:0.6810

3' gucugaggccacCUUACUUCCu 5' hsa-miR-205 | | | | | | | | 1:5' -----agaugauGUAUGAAGGa 3' COMMD1

hsa-miR-491-5p/COMMD1 Alignment : mirSVR score:-0.5071 PhastCons score:0.5830

3' ggaguaccuucccaAGGGGUGa 5' hsa-miR-491-5p | | | | | | | 39:5' guguccaugaucccUCCCCACu 3' COMMD1

hsa-miR-7/COMMD1 Alignment: mirSVR score:-0.9164 PhastCons score:0.6347

3' uguuguuuuaGUGA----UCAGAAGGu 5' hsa-miR-7 | |: | ||||||| 99:5' uaaauccucgCAUUCAGUCUUCCu 3' COMMD1

Supplementary Figure S1. Analysis of miRNA target sites on 3'-UTR of COMMD1 mRNA using the algorithm miRanda (<u>http://www.microrna.org/</u>). (**a**) Predicted miRNA target sites on the 3'-UTR of COMMD1. (**b**) Sequence alignment and mirSVR scores for the putative target sites.

a COMMD1 3'-UTR wild type and mutant construct schemes

hsa-miR-205 3'-GUCUGAGGCCACCUUACUUCCU-5' I I I I I I I I COMMD1 3'-UTR wt 5'-...AGAUGAUGUAUGAAGGAGUUGGA... COMMD1 3'-UTR mut 5'-...AGAUGAUUUCGUCCUUCGUUGGA...

b miR-205-sponge construct scheme



Supplementary Figure S2. Schematic illustration of (**a**) wild-type (wt) and mutant (mut) COMMD1 3'-UTR reporter constructs, and (**b**) miR-205-sponge construct containing six specific binding sites for miR-205.

Human shCOMMD1-1 TRCN0000167145	Sense:5'-GATCCAAAGTCAACCAAATTCTGAACTCGAGTTCAGAATTTGGTTGACTTTGTTTTTG-3'
	Antisense:5'-AATTCAAAAACAAAGTCAACCAAATTCTGAACTCGAGTTCAGAATTTGGTTGACTTTG-3'
Human shCOMMD1-2 TRCN0000167998	Sense:5'-GATCCAAGCTGCTGTCATTTCCAAACTCGAGTTTGGAAATGACAGCAGCTTGTTTTTG-3'
	Antisense:5'-AATTCAAAAACAAGCTGCTGTCATTTCCAAACTCGAGTTTGGAAATGACAGCAGCTTG-3'
Human shCOMMD1-3	Sense:5'-GATCCGAGGTCAAAGTCAACCAAATCTCGAGATTTGGTTGACTTTGACCTCGTTTTTG-3'
110000108050	Antisense:5'-AATTCAAAAACGAGGTCAAAGTCAACCAAATCTCGAGATTTGGTTGACTTTGACCTCG-3'
Human shCOMMD1-4	Sense:5'-GATCGCTCAAATACACACACCTGTTCTCGAGAACAGGTGTGTGT
1KCN0000168045	Antisense:5'-AATTAAAAAGCTCAAATACACACACCTGTTCTCGAGAACAGGTGTGTGT
Mouse shCOMMD1-1	Sense:5'-GATCGTCTATTGCATCTGCAGACATCTCGAGATGTCTGCAGATGCAATAGACTTTTTG-3'
1RCN0000197798	Antisense:5'-AATTCAAAAAGTCTATTGCATCTGCAGACATCTCGAGATGTCTGCAGATGCAATAGAC-3'
Mouse shCOMMD1-2 TRCN0000350952	Sense:5'-GATCGATGAAGTTAAAGTCAAGCAACTCGAGTTGCTTGACTTTAACTTCATCTTTTTG-3'
	Antisense:5'-AATTCAAAAAGATGAAGTTAAAGTCAAGCAACTCGAGTTGCTTGACTTTAACTTCATC-3'
shLuc TRCN0000072249	Sense:5'-GATCGCGGTTGCCAAGAGGTTCCATCTCGAGATGGAACCTCTTGGCAACCGCTTTTTG -3'
	Antisense:5'-AATTCAAAAAGCGGTTGCCAAGAGGTTCCATCTCGAGATGGAACCTCTTGGCAACCGC -3'
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b



Supplementary Figure S3. Development of short hairpin RNAs (shRNAs) for knockdown COMMD1 expression. Four shRNAs targeting different regions of the COMMD1 mRNA (shCOMMD1-1 to shCOMMD1-4) and a control shRNA targeting luciferase mRNA (shLuc) were designed and lentiviral expression vectors were constructed. (a) Sequences of sense and anti-sense oligonucleotides employed for generating these COMMD1-specific shRNAs. The shRNA sequences were obtained from the Public TRC Portal of the RNAi Consortium (www.broadinstitute.org/rnai/public/gene/search). The TRC identification numbers and oligonucleotide sequences are shown below the name of each shCOMMD1 and in the right column, respectively. (b) The efficiencies of these shRNAs were determined by achieving stable expression in SAS cells and analyzing COMMD1 expression by immunoblot analysis. The four COMMD1-specific shRNAs resulted in effective COMMD1 knockdown, while shLuc had no effect. shCOMMD1-4 (referred to as shCOMMD1 in this paper) was employed in experiments in this study. Samples were from COMMD1 over expressed cells for COMMD1 OE.

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Supplementary Figure S4. COMMD1 regulates NF- κ B activation in D121 cells. Phosphorylation levels of RelA in shLuc and shCOMMD1 stably transfected D121 cells were measured by flow cytometric analysis. Elevated levels of phosphorylated RelA (phospho-RelA) were detected in the COMMD1 knockdown cells. The left panel shows a representative histogram for the right bar figure for phospho-RelA levels in the shLuc and shCOMMD1 stably transfected D121 cells. Data represent mean ± SD from three independent experiments. *P < 0.05

Primers used in microRNA qRT-PCR

miR-205_RT	5'-GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACCAGACT-3'
primer	
U6_RT primer	5'-GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACAAAAATAT-3'
miR-205	forward 5'-GCATCATCCTTCATTCCACCGG-3'
U6	forward 5'-TTCCTCCGCAAGGATGACACGC-3'
Universal reverse	reverse 5'-GTGCAGGGTCCGAGGT-3'
primer	
Primary U6	forward 5'-CTCGCTTCGGCAGCACA-3'
	reverse 5' -AACGCTTCACGAATTTGCGT-3'
Primary	forward 5'-ACAGGCTGAGGTTGACATGC-3'
hsa-miR-205	reverse 5'-CTCCTGAACTTCACTCCACTGAAA-3'
Primary	forward 5'-CTTCACTCCACTGAAATCTGGTTG-3'
mmu-miR-205	reverse 5'-CTACACGAGGAGGCTTAGTAGACA-3'

Synthetic oligonucleotide used to generate 3' UTR reporter constructs

COMMD1 3'	forward 5'-ATGTACGCGTAGATGATGTATGAAGGAGTTGGAGTTGTTG-3'
UTR Wt	reverse 5'-AGACAAGCTTAGAGGCAGGAAGACTGAATGCG-3'
COMMD1 3'	forward 5'-ATGTACGCGTAGATGATTTCGTCCTTCGTTGGAGTTGTTGAA-3'
UTR Mut	

Synthetic oligonucleotide used to generate miR-205 sponge constructs

S1_Xba1	5'-CTAGATAACAGACTCCGACCAATGAAGGACGATCAGACTCCGACCAATGA AGGAG -3'
AS1_NheI	5'-CTAGCTCCTTCATTGGTCGGAGTCTGATCGTCCTTCATTGGTCGGAGTCTGTTAT-3'
S2_NheI	5'-CTAGCATAACAGACTCCGACCAATGAAGGACGATCAGACTCCGACCAATGAAGGAG-3'
AS2_EcoRI	5'-AATTCTCCTTCATTGGTCGGAGTCTGATCGTCCTTCATTGGTCGGAGTCTGTTATG-3'
S3_EcoRI	5'-AATTCATAACAGACTCCGACCAATGAAGGACGATCAGACTCCGACCAATGAAGGAG-3'
AS3_BamHI	5'-GATCCTCCTTCATTGGTCGGAGTCTGATCGTCCTTCATTGGTCGGAGTCTGTTATG-3'

Synthetic oligonucleotide used to generate precursor miR-205 construct

Pre hsa-miR-205	forward 5'-CATCGAATTCGGTCCTTGACATCTCCCAAA-3'
	reverse 5'-AGCAGGATCCCTGAAGAAGCACGCACACTC-3'

Supplementary Table S1. Sequences of primers employed for microRNA, RT-qPCR, and generation of COMMD1 3'-UTR reporter, miR-205-sponge, and miR-205 overexpression constructs.

COMMD1	forward 5'-CGGAGCCAGCTATATCCAGA-3'
	reverse 5'-TTGGAAATGACAGCAGCTTG-3'
АСТВ	forward 5'-TCCCTGGAGAAGAGCTACGA-3'
	reverse 5'-AGCACTGTGTTGGCGTACAG-3'
GAPDH	forward 5'-GAGTCAACGGATTTGGTCGT-3'
	reverse 5'-GACAAGCTTCCCGTTCTCAG-3'
c-MYC	forward 5'-TTCGGGTAGTGGAAAACCAG-3'
	reverse 5'-CAGCAGCTCGAATTTCTTCC-3'
SOX-2	forward 5'-ACACCAATCCCATCCACACT-3'
	reverse 5'-GCAAACTTCCTGCAAAGCTC-3'
OCT-4	forward 5'-GAAGGATGTGGTCCGAGTGT-3'
	reverse 5'-GTGAAGTGAGGGCTCCCATA-3'
KLF-4	forward 5'-ACCCACACAGGTGAGAAACC-3'
	reverse 5'-ATGTGTAAGGCGAGGTGGTC-3'
NANOG	forward 5'-TTCCTTCCATGGATCTG-3'
	reverse 5'-ATCTGCTGGAGGCTGAGGTA-3'
ALDH1	forward 5'-TGTTAGCTGATGCCGACTTG-3'
	reverse 5'-CTTCTTAGCCCGCTCAACAC-3'
ABCG2	forward 5'-GTGGCCTTGGCTTGTATGAT-3'
	reverse 5'-AACAATTGCTGCTGTGCAAC-3'
CD44	forward 5'-AAGGTGGAGCAAACACAACC-3'
	reverse 5'-AGCTTTTTCTTCTGCCCACA-3'
CD117	forward 5'-AGAGACTTGGCAGCCAGAAA-3'
	reverse 5'-AGGGGCTGCTTCCTAAAGAG-3'
CD133	forward 5'-GCCACCGCTCTAGATACTGC-3'
	reverse 5'-TGTTGTGATGGGCTTGTCAT-3'
TNF- α	forward 5'-AACCTCCTCTGCCATCAA-3'
	reverse 5'-CCAAAGTAGACCTGCCCAGA-3'
IL-1β	forward 5'-ACGATGCACCTGTACGATCA-3'
P.	reverse 5'-TCTTTCAACACGCAGGACAG-3'
IL-6	forward 5'-TACCCCCAGGAGAAGATTCC-3'
	reverse 5'-TTTTCTGCCAGTGCCTCTTT-3'
IL-8	forward 5'-GTGCAGTTTTGCCAAGGAGT-3'
	reverse 5'-CTCTGCACCCAGTTTTCCTT-3'
CXCL1	forward 5'-AGGGAATTCACCCCAAGAAC-3'
	reverse 5'-CACCAGTGAGCTTCCTCCTC-3'
CCL2	forward 5'-CCCCAGTCACCTGCTGTTAT-3'
	reverse 5'-TGGAATCCTGAACCCACTTC-3'
MMP9	forward 5'-CTCGAACTTTGACAGCGACA-3'
	reverse 5'-GCCATTCACGTCGTCCTTAT-3'
NOS2	forward 5'-ACAAGCCTACCCCTCCAGAT-3'
	reverse 5'-TCCCGTCAGTTGGTAGGTTC-3'

Supplementary Table S2. Sequences of forward and reverse primers employed for PCR amplification of human genes.

Commd1	forward 5'-GCTCAAACCAAAAAGCAAGG-3'
	reverse 5'-GTTGAGTGCCGTGACTGAGA-3'
Actb	forward 5'-AGCCATGTACGTAGCCATCC-3'
	reverse 5'-CTCTCAGCTGTGGTGGTGAA-3'
Gapdh	forward 5'-ACCCAGAAGACTGTGGATGG-3'
	reverse 5'-CACATTGGGGGTAGGAACAC-3'
c-Myc	forward 5'-ACACGGAGGAAAACGACAAG-3'
	reverse 5'-TCGTCTGCTTGAATGGACAG-3'
Sox-2	forward 5'-AAGGGTTCTTGCTGGGTTTT-3'
	reverse 5'-AGACCACGAAAACGGTCTTG-3'
Oct-4	forward 5'-AAGCCCTCCCTACAGCAGAT-3'
	reverse 5'-CTGGGAAAGGTGTCCCTGTA-3'
Klf-4	forward 5'-GCAGTCACAAGTCCCCTCTC-3'
	reverse 5'-CTGTGTGAGTTCGCAGGTGT-3'
Nanog	forward 5'-CCAGTGGAGTATCCCAGCAT-3'
	reverse 5'-GAAGTTATGGAGCGGAGCAG-3'
Aldh1	forward 5'-GCACTCAATGGTGGGAAAGT-3'
	reverse 5'-TTTGGCCACACACTCCAATA-3'
Abcg2	forward 5'-CCATTCATCAGCCTCGGTAT-3'
	reverse 5'-AATCCGCAGGGTTGTTGTAG-3'
Cd44	forward 5'-TGGATCCGAATTAGCTGGAC-3'
	reverse 5'-AGCTTTTCTTCTGCCCACA-3'
Cd117	forward 5'-GGGCTAGCCAGAGACATCAG-3'
	reverse 5'-AGGAGAAGAGCTCCCAGAGG-3'
Cd133	forward 5'-GAAAAGTTGCTCTGCGAACC-3'
	reverse 5'-TCTCAAGCTGAAAAGCAGCA-3'
Tnf- α	forward 5'-AGCCCCAGTCTGTATCCTT-3'
	reverse 5'-CTCCCTTTGCAGAACTCAGG-3'
Il-1β	forward 5'-CAGGCAGGCAGTATCACTCA-3'
	reverse 5'-AGCTCATATGGGTCCGACAG-3'
Il-6	forward 5'-AGTTGCCTTCTTGGGACTGA-3'
	reverse 5'-TCCACGATTTCCCAGAGAAC-3'
II-8	forward 5'-CGTCCCTGTGACACTCAAGA-3'
•	reverse 5'-TAATTGGGCCAACAGTAGCC-3'
Cxcl1	forward 5'-GCTGGGATTCACCTCAAGAA-3'
	reverse 5'-CTTGGGGACACCTTTTAGCA-3'
Ccl2	forward 5'-CAGGTCCCTGTCATGCTTCT-3'
	reverse 5'-TCTGGACCCATTCCTTG-3'
Mmp9	forward 5'-GAAGGCAAACCCTGTGTGTT-3'
	reverse 5'-AGAGTACTGCTTGCCCAGGA-3'
Nos2	forward 5'-CACCTTGGAGTTCACCCAGT-3'
	reverse 5'-ACCACTCGTACTTGGGATGC-3'

Supplementary Table S3. Sequences of forward and reverse primers employed for PCR amplification of mouse genes.