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SUPPLEMENTARY ONLINE DATA

Holocarboxylase synthetase interacts physically with nuclear receptor co-repressor, histone deacetylase 1 and a novel splicing variant of histone deacetylase 1 to repress repeats

Dandan LIU* and Janos ZEMPLENI*[1]

*Department of Nutrition and Health Sciences, Ruth Leverton Hall, University of Nebraska-Lincoln, Lincoln, NE 68583-0806, U.S.A.

Supplementary Table S1 can be found on the next page.

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[1] To whom correspondence should be addressed (email JZEMPLENI2@UNL.EDU).

Table S1 PCR primers used in the present study

GenBank® entries: CDK3 = cyclin-dependent kinase 3 (NM_001261); Chr1alpha = chromosome 1 alpha satellite repeats (M26919); Chr4alpha = chromosome 4 alpha satellite repeats (M38467); GAPDH = glyceraldehyde-3-phosphate dehydrogenase (NG_007073 for genomic DNA and NM_002046 for complementary DNA); HDAC1 = histone deacetylase 1 (NM_004964); HLCS = holocarboxylase synthetase (NM_000411); LTR15 = intact LTR (AC116309); LTR22 = solitary LTR (AL451165); MDM2 = E3 ubiquitin-protein ligase MDM2 (NM_002392); N-CoR = nuclear receptor corepressor (NM_006311); TP53 = tumour protein p53 (NM_000546). F, forward; gDNA, genomic DNA; P, primer pair; R, reverse; R-U5 = region between R and U5 of LTR of HERV-K families; U5 = U5 region of LTR of HERV-K families.

P	Target; template	Primer sequences 5→3′	F/R
1	HLCS-NT; cDNA	GCCGAATTCCCATGGAAGATAGACTCC	F
		CAGGTCGACCCGAAGGCCTCCATGTTG	R
2	HLCS-CD; cDNA	GCCGAATTCCCTTTGCCGAAGTGACCC	F
		CAGGTCGACCCGTCACTGTAATAAATA	R
3	HLCS-L; cDNA	GCCGAATTCCCACCATCTGCATCAACG	F
		CAGGTCGACCCGTGGACCCAGTATCGG	R
4	HLCS-CT; cDNA	GCCGAATTCACAGTGGTCAGCAAGTCC	F
		CAGGTCGACTCTCAGCATGTCGAAGGA	R
5	HLCS; cDNA	GTCCGAATTCGGGGAGCATGTTGGCAGAG	F
		ATTTCTCGAGCCCGCCGTTTGGGGAG	R
6	N-CoR-NT; cDNA	GCGGAATTCCCTCAAGTTCAGGTTATCCT	F
		GCGGGTACCATCCAAGTCTCTTTCTTTGG	R
7	N-CoR-CD; cDNA	GCGGAATTCCCACCAAAGCTGACTCTGT	F
		GCGGGTACCAGCACTTGCAGCAGCTGC	R
8	N-CoR-CT; cDNA	GCGGAATTCCCCCTGGTACACAGATTACTTT	F
		GCGGGTACCGTCATCACTATCCGACAGG	R
9	CT$_{K2323R}$; cDNA	TCAGGAGGAGTTTGCAGACCAAAGCTGATCAGC	F
		TTTGGTCTGCAAACTCCTCCTGAATGAGGTGAT	R
10	CT$_{K2325R}$; cDNA	GGAGTTTGCAAACCAAGGCTGATCAGCAAGTCA	F
		ATCAGCCTTGGTTTGCAAACTCCTCCTGAATGA	R
11	CT$_{del}$; cDNA	CCATCACCTCATTCAAGCAAGTCAAACAGC	F
		TGCTTGAATGAGGTGATGGGTCCCCTTCCT	R
12	N-CoR-NT; cDNA	GCGGAATTCTCAAGTTCAGGTTATCCTCC	F
		GCGGAGCTCATCCAAGTCTCTTTCTTTGG	R
13	N-CoR-CD; cDNA	GCGGAATTCACCAAAGCTGACTCTGTGG	F
		GCGGAGCTCAGCACTTGCAGCAGCTGC	R
14	N-CoR-CT; cDNA	GCGGAATTCCCTGGTACACAGATTACTTTCC	F
		GCGGAGCTCGTCATCACTATCCGACAGG	R
15	HDAC1 & Δ31; cDNA	GCGGAATTCAAGCGCAGACGCAGGG	F
		GCGGGTACCGGCCAACTTGACCTCCTCCTTG	R
16	HDAC1 & Δ31; cDNA	GCGGAATTCAAGCGCAGACGCAGGG	F
		GCGGAGCTCGGCCAACTTGACCTCCTCCTTG	R
17	NLuc; cDNA	CCCGTCGACCGAAGACGCCAAAAAC	F
		CCCGCGGCCGCTCCATCCTTGTCAAT	R
18	CLuc; cDNA	GCGGGCCATGGAGGCCATGTCCGGT	F
		GCGGAATTCGCACGGCGATCTTTCCG	R
19	TP53; cDNA	CGGCCATGGAGGCCGAGGAGCCGCAGTCA	F
		GCGGTCGACCGTCTGAGTCAGGCCCTTCTGTC	R
20	MDM2; cDNA	GCGGAATTCCCGTGAGGAGCAG	F
		GCGCTCGAGAGGGGAAATAAGTTAGCA	R
21	CDK3; cDNA	GCGGAATTCCCGATATGTTCCAGAA	F
		GCGCTCGAGAATGGCGGAATCGCT	R
22	LTR15; gDNA	TTGTCATTGGTTCTGTGTAGGG	F
		CCTCCATATGCTGAACGCTG	R
23	LTR22; gDNA	ATGGATTCAGCCTGTGTCTTTGGG	F
		CCTCCATATGCTGAACGCTG	R
24	GAPDH; gDNA	ATGACAAGCATGAGGCAGAG	F
		CAACCAGGACCGTTAACCCTTTCT	R
25	HLCS; cDNA	ATGGAAGATAGACTCCACAT	F
		TGAGACCTGATCCTTAACTTCC	R
26	U5; cDNA	AACTCAGAGGCTGGCG	F
		AGACACAGAGACAAAGTATAGAGA	R
27	R-U5; cDNA	GCGGGCAGCAATACTGCTTTGTAA	F
		ACCAGCGTTCAGCATATGGAGGAT	R
28	GAPDH; cDNA	TCCACTGGCGTCTTCACC	F
		GGCAGAGATGATGACCCTTT	R
29	Chr1alpha; cDNA, gDNA	CATCGAATGGAAATGAAAGGAGTC	F
		ACCATTGGATGATTGCAGTCAA	R
30	Chr4alpha; cDNA, gDNA	CTGCACTACCTGAAGAGGAC	F
		GATGGTTCAACACTCTTACA	R

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