Supplemental Tables

Table S1. Short tandem repeat (STR) analysis for NCI-N87, NCI-N87TR, SNU216 and SNU216TR.

STR locus	NCI-N87		NCI-N87TR		SNU216		SNU216TR	
	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
Yindel	2		2		-		-	
AMEL	X	Y	X	Y	X		X	
D3S1358	14		14		17		17	
D13S317	8	11	8	11	9		9	
D7S820	10	11	10	11	8	10	8	10
D16S539	9	13	9	13	10	13	10	13
SE33	25.2	29.2	25.2	29.2	25.2		25.2	
D10S1248	13		13		13	15	13	15
D5S818	12	13	12	13	11		11	
D21S11	30		30		30	33.2	30	33.2
TPOX	9	11	9	11	9		9	
D1S1656	16		16		16		16	
D6S1043	12		12		18		18	
DXS6795	10		10		13		13	
D19S433	14	14.2	14	14.2	15.2		15.2	
D22S1045	14	15	14	15	15	17	15	
D8S1179	14		14		13	16	13	16
Penta E	5		5		5		5	
DYS391	10		10		-		-	
D2S441	11	12	11	12	10		10	
D12S391	16	21	16	21	18		18	
D2S1338	23	24	23	24	19		19	
vWA	15	16	15	16	14	20	14	20
Penta D	12		12		9	13	9	13
TH01	9		9		7		7	
D18S51	17		17		16		16	
CSF1PO	8	12	8	12	12		12	
FGA	20	21	20	21	21		21	

Table S2. Primer of genes for quantitative PCR.

Gene	Orientation	Sequence（5‘-3’）
BMAL1	F	CAATCCATACACAGAAGCAAAC
	R	CATCTGCTGCCCTGAGAATGA
CLOCK	F	CTCTACTCATCTGCTGGAAAGTG
	R	ATGGCTCCTTTGGGTCTATTG
PER1	F	ACCTCAGCCAGCATCACCC
	R	GAAGAGTCGATGCTGCCAAAG
PER2	F	TGCAGTGGAGCAGATTCTTT
	R	GGTGGTAGCGGATTTCATTCT
PER3	F	GCCTTACAAGCTGGTTTGC
	R	CTGTGTCTATGGACCGTCCATTT
CRY1	F	GCTCTCAAGGGAGTGGTATTT
	R	CTCTTCCTGACTAGGACGTTTC
CRY2	F	GGGTCCGGGTATTTGATGAG
	R	GTGGAAGAACTGCTGGAAGA
NR1D1	F	GCATGGAGAATTCCGCTTC
	R	CGGTTCTTCAGCACCAGAG
NR1D2	F	CATTTCTATATTTGAAAGTAGCCCAAT
	R	ACTCAATCAAAGAATGTGCTTGTAA
DBP	F	TAGAAGGAGCGCCTTGAGTC
	R	GCAACCCTCCAGTATCCAGA
RORα	F	AAACAAGCAGCGGGAGGTGA
	R	TGGCAAACTCCACCACATAC
HK2	F	ATTGTCCAGTGCATCGCGGA
	R	AGGTCAAACTCCTCTCGCCG
GLUT1	F	CCGCAACGAGGAGAACCG
	R	GTGACCTTCTTCTCCCGCATC
LDHA	F	AGCCCGATTCCGTTACCT
	R	CACCAGCAACATTCATTCCA
PFKFB3	F	CTCGCATCAACAGCTTTGAGG

	R	TCAGTGTTTCCTGGAGGAGTC
PKM2	F	TCTGTACCATTGGCCCAGCTT
	R	TGGCTGTGCGCACATTCTTGA
PFK1	F	GGTGCCCGTGTCTTCTTTGT
	R	AAGCATCATCGAAACGCTCTC
GAPDH	F	ACCCAGAAGACTGTGGATGG
	R	TCTAGACGGCAGGTCAGGTC
MCT1	F	CATGCCACCACCAGCGAAG
	R	TGACAAGCAGCCACCAACAATC
CD36	F	GGCTGTGACCGGAACTGTG
	R	AGGTCTCCAACTGGCATTAGAA
PPARγ	F	GTGCCAGTTTCGATCCGTAGA
	R	GGCCAGCATCGTGTAGATGA
β-Actin	F	CATGTACGTTGCTATCCAGGC
	R	CTCCTTAATGTCACGCACGAT

Table S3. Primers of potential E-box regions or binding sites for chromatin immunoprecipitation (ChIP) experiment.

Region or sites	Position	Sequence（5'-3'）
E-box region1	F: -564~-583	ACTTTCCGGCCGTGCTACAA
	R: -472~-491	CCTGTGCGGAGAGACACTGT
E-box region2	F: -746~-766	TCTCAAGCAACCCTCCAACCT
	R: -622~-641	ACAAGAGTCGGCCCATCCTC
E-box region3	F: -787~-806	GGGTCTCACTATGTCGCCCA
	R: -685~-706	AGATGAGGAAATTGAGGCAAGGC
E-box region4	F: -916~-935	TCATAGCTCACTGCAGCCTC
	R: -831~-850	AAATCAGCCGGACATGGTGG
E-box region5	F: -1753~-1772	AAGGAGGGTTGAGGACGTGC
	R: -1673~-1692	CTCCCACTTCAGCGTCCCAA
E-box region6	F: -1956~-1975	CCTCAGAGTGGAGCACTGGT
	R: -1865~-1885	CCCTGCCCTTGTCTTACTCCT
Primer-P1	F: -1979~-1998	GGGGAGTGAGGTTAGCCAGA
	R: -1856~-1875	TCTTCTCTTCCCTGCCCTTG
Primer-P2	F: -1856~-1875	CAAGGGCAGGGAAGAGAAGA
	R: -1754~-1773	CACGTCCTCAACCCTCCTTC
Primer-P3-4	F: -1091~-1110	TGGCTCTTAGAGAGGCAGCA
	R: -915~-934	CGAGGCTGCAGTGAGCTATG

Table S4. siRNA sequence.

Gene	Number	Sequence
BMAL1	Sequence #1	TCACCAAGATGACATAGGA
	Sequence #2	GTCAGAGTTTGTTTGACTA
CLOCK	Sequence #1	GAGCTCGATTGTTGACAGA
	Sequence #2	CCAGCAACTTGCACCTATA
PER1	Sequence #1	CGCTCGCCCTGGCCAATAA
	Sequence #2	TTATTGGCCAGGGCGAGCG
PER2	Sequence #1	GCGCTAAGGTCCAGTGATA
	Sequence #2	GGTCAAACCTCGAGACTCA
PER3	Sequence #1	GCTCACCCTTGCAGTTAAA
	Sequence #2	GTCTCACTGTGGTTGAAAA
CRY1	Sequence #1	GATGCAGATTGGAGCATAA
	Sequence #2	GGATGAAACAGATCTATCA
CRY2	Sequence #1	GGCTTAACATTGAACGAAT
	Sequence #2	TGGCGAGAGTTCTTCTACA
NR1D1	Sequence #1	CATGTCCTATGAACATGTA
	Sequence #2	GCAACTCAAAGAATGTTCT
NR1D2	Sequence #1	GAGAACGGATTCCCAAGAA
	Sequence #2	GATCTTCGATCTTTAAACA
DBP	Sequence #1	GCGATGTGGAGTACGTAGA
	Sequence #2	GAGACCTTTGACCCTCGAA
RORα	Sequence #1	CCCGACGTCTTCAAATCCT
	Sequence #2	CACGACGACCTCAGTAACT
PPARγ	Sequence #1	AGATAAAGCTTCTGGATTT
	Sequence #2	AGGAAAGACAACAGACAAA