Supplemental Table 1. Primers used to identify transcript expression by RT-PCR or qRT-PCR and double stranded (si)RNA sequences

Gene name	Amplicon Size (RT-PCR)	GenBank Accession #	Primer: Sense 5'→ 3'	Primer: Antisense 5'→ 3'
16S ribosomal RNA gene (*E. chaffeensis*)	430 bp	M73222	GTATTACCGCGGCTGCTGGCAC	CAATTGCTTATAACCTTTTGGTTATAAAT
rp49 (*Drosophila*)	165 bp	U92431	ATCGGTTACGGATCGAACAA	GACAATCTCCTTGCGCTTCT
Gene name	**Real Time Probe (qRT-PCR)**	**GenBank Accession #**	**Primer: Sense 5'→ 3'**	**Primer: Antisense 5'→ 3'**
rp15a (*Drosophila*)	5'-56-FAM/TGGGAGGCAAAATTCTCGGCTTC/36-TAMsp-3'	NM_136772	TGGACCACGAGGAGGCTAGG	GTTGGTGCATGGTCGGTGA
UCK2 (human)	5'-/56FAM/TAGGTTGCCAGAGTTTCATTAGGCCGCT/3IABkFQ/-3'	NM_012474.4	ACTTGGGCTTGGAGCTGGATACTT	TGCACAAGGGCAAGAGAGGTCATA
S14 (human)	5'-/56FAM/CCGGGATAG/ZEN/CTGTCCTGTTAGAATCAGA/3IABkFQ/-3'	NM_001025071.1	TGGCTGATGAAGAAATTGCTGCCC	ACGGGACGTCATAACACACCGATT
HPRT (human)	SYBR green detection	NM_000194.2	AGATGGTCAAGGTCGCAAGC	GGACTCCAGATGTTTCCAAACTCAAC
Gene name	**IDT Catalog ID**	**Location Region/Exon[1]**	**siRNA Sense 5'→ 3'**	**siRNA: Antisense 5'→ 3'**
UCK-2 (human)	HSC.RNAI.N012474.12.1	3'UTR/7	CGUGUAACCAGUUAUAAAUACAUAU	AUAUGUAUUUAUAACUGGUUACACGUU
UCK-2 (human)	HSC.RNAI.N012474.12.2	CDS/2	AGCUUCUACCGUGUCCUUACCUCGG	CCGAGGUAAGGACACGGUAGAAGCUAU
UCK-2 (human)	HSC.RNAI.N012474.12.3	CDS/4-5	CUCUCACGCAGAGUAUUAAGGGACA	UGUCCCUUAAUACUCUGCGUGAGAGCC
HPRT1 (human)	HPRT-S1 DS Transfection Control	NA	GCCAGCUUUGUUGGAUUUGAAAUU	UUCGGUCUGAAACAACCUAAACUUUAA
Scrambled	NC1 Negative Control Duplex	NA	CGUUAAUCGCGUAUAAUACGCGUAU	CAGCAAUUAGCGCAUAUUAUGCGCAUA

[1] Target location in RNA transcript. UTR: Unstranlated region. CDS: Coding sequence. NA: Not applicable.