Table S1. Sequences of primers used for RT-PCR and quantitative RT-PCR (qRT-PCR)

Gene	Accession No		Sequences (5' - 3')	Length (bp)	Efficiency[C]	(R^2)[D]
RN18S1[A]	NR_036642.1	F	AGTACGCACGGCCGGTACAGT	130	-	-
		R	CAGCGCCCGTCGGCATGTATT			
GAK[B]	NM_001046084.2	F	TCTGGGAAGTGGCAGAGAGT	294	1.85	0.99
		R	CGGCACGTCTGGTAGAAGAT			
VPS4A[B]	NM_001046615.1	F	CAAAGCCAAGGAGAGCATTC	222	1.92	0.97
		R	ATGTTGGGCTTCTCCATCAC			
ACTB[B]	NM_173979.3	F	GAATCCTGCGGCATTCACGA	192	1.94	0.99
		R	AGGGGGCGCGATGATCTTG			
RARRES2[B]	NM_001046020.2	F	GTTTGTGAGGCTGGAGTTC	173	1.95	0.99
		R	GAGTCTGTATGGGACAGTGC			
CMKLR1[B]	NM_001145235.1	F	CATCGTCGTTCTGGAGGAGT	169	2.00	0.97
		R	GTTGAGGAACCAGACGGTGT			
CCRL2[B]	NM_001075732.2	F	CCAGGGGGATAAACAGTGGT	266	2.04	0.98
		R	ATCTTGGGGTCGTATGGGGT			
GPR1[B]	NM_001206545.1	F	GGTCTCCTTGGTGTTGTGCT	291	1.97	0.98
		R	TAGCGGTCCAGGCTTATCAC			
CD68	NM_001045902.1	F	AGGTTGGCTGTGTTCTTCTCT	183	1.92	0.99
		R	GGTTCTGTGGCTCTTGGTAGT			
CSN1S1	NM_181029.2	F	TGTCTTGTGGCTGTTGCTCT	76	1.94	0.97
		R	CATTGAGGACTTCTTGAGGGA			

A: 18S rRNA was not used for qRT-PCR. Thus, primer efficiency and R^2 were not determined.

B: These primer pairs were incorporated from Suzuki *et al*., 2016

C: Primer efficiency = $10^{(-1/\text{Slope})}$; the slope was calculated from a standard curve constructed using a 5 points dilution series of pooled cDNA

B: R^2 represents the coefficient of determination for the standard curve.