

Table 1: Gene names, abbreviations, accession number (AN) and gene ontology (GO) of genes considered in this work. Primer sequences, amplicon size (AS, in bp) and calculated reaction efficiencies for RT-qPCR experiments are also reported. Newly identified genes in *O. vulgaris* are marked by an asterisk.

Gene product	AN	GO ^a	Primer	Primer sequence 5' - 3'	AS	Efficiency ^b
α-tubulin	X15845	microtubule (C) GO: 0005874	F	ACTGGTGTCCAACTGGCTTC	105	2.00
			R	TGCTTAACATGCACACAGCA		
β-actin	AB053937	structural constituent of cytoskeleton (F) GO:0005200	F1	TGATGGCCAAAGTTATCACCA	103	1.90
			R1	TGGTCTCATGGATACCAAGCA		
			F2	TCCAGGCTGTGTTGTCCTG		
			R2	AGATCACGACCAAGCCAAAGTC		
CREB	FJ617443*	transcription factor activity (F) GO: 0003700	F	ACAGTATGCCCAAGGTCCTG	122	1.80
			R	TTCCAGTGGTTGCCATAACA		
Dopamine transporter	FJ617441*	dopamine transmembrane transporter activity (F) GO: 0005329	F	GCCCTAGACGGGCATCAAATA	109	2.00
			R	ATCCTGGTCCAAGGGAAAAG		
Elongation factor	AY651883	translational elongation (P) GO: 0006414	F	ACGAAGGCTGGGAAATTGA	104	2.00
			R	TGGTCTCTCCGTTGGTCTCT		
Forkhead box protein P	FJ617444*	transcription factor activity (F) GO: 0003700	F	TCCACACCTGCCATGAGTT	149	2.00
			R	GATTGGTCCCACACTGCTG		
Tyrosine hydroxylase	FJ617442*	Peptidyl-tyrosine hydroxylation (P) GO: 0018336	F	CTCAATTGCAGACATGGCATT	128	1.70
			R	GCGTGAGTCGGAAAACAGATT		
Ubiquitin/ribosomal protein S27a	FJ617440*	protein ubiquitination (P) GO: 0016567	F	TCAAAACCCGCCAACTTAACC	113	1.90
			R	CCTTCAATTGGTCCTTCGTC		
16S	AJ616309	structural constituent of ribosome (F) GO:0005200	F	TTGGGGCTAGAATGAATGGT	112	1.90
			R	GGTCTTTTTCGTCCCTTTAAACA		
18S	FJ617439*	structural constituent of ribosome (F) GO:0005200	F	AGTTCGCAACCGTAAACGATG	142	1.80
			R	CCCTTCCGTCCAATTCCCTTA		

a. According to Gene Ontology (<http://www.geneontology.org/>, last visited Aug, 2008) for each gene is listed a GO number and the corresponding classification: biological function (F), molecular process (P), cellular components (C).

b. Efficiency for each primer pair was derived from standard curves using five serial dilutions of cDNA samples, as described in Methods.