

Supporting information

Table SI 1: Sequences and characteristics of the primer pairs s used to amplify genes under study by real-time qRT-PCR

Target ^a	Primer Sequence 5'-3' ^b		Length (pb) ^c	Amplification efficiency (R ²) ^c
<i>Antioxidative defense</i>				
<i>Cat</i>	F: 5'- AATGCTCCAGGGCCGCCTTTTGCCTACC	-3'	141	0.995 (99.2%)
	R: 5'- GGTAATAGTTGGGGGCACCACCCTGGTTG	-3'		
<i>Sod1</i>	F: 5'- GAAGGCCAGCATGGGTTCACGTC	-3'	109	0.999 (99.8%)
	R: 5'- TAAGAAACATGGTGGCCCGGCGG	-3'		
<i>Gpx1</i>	F: 5'- GCAGAAGCGTCTGGGACCTCGTG	-3'	101	0.999 (99.9%)
	R: 5'- GGGAACTCAGAATCTCCTCATTCTTGCCA	-3'		
<i>Gpx3</i>	F: 5'- CCCCAGTCTCAAGTATGTTTCGACCAGGTG	-3'	132	0.998 (99.1%)
	R: 5'- GCAGTGGGAGGGCAGGAGTTCTTCAG	-3'		
<i>Prdx1</i>	F: 5'- GTGTGTCCCACGGAGATCATTGCTTTCA	-3'	92	0.995 (99.8%)
	R: 5'- TGAGAATCCACAGAAGCTCCAATCACTTG	-3'		
<i>Prdx6</i>	F: 5'- TGCCTGGAGCAAGGACATCAATGCTTA	-3'	106	1.000 (99.4%)
	R: 5'- AGGGACCTTGCCATCCTTTTGGGC	-3'		
<i>Txn2</i>	F: 5'- GTCCCCTCCCACATCAAAAACTCCCAAC	-3'	108	0.999 (99.99%)
	R: 5'- GGCCACAGGACAGTGTCAAAGGTGC	-3'		
<i>Biotransforming enzymes</i>				
<i>GstA1/2</i>	F: 5'- CCCCCAGACCAAAGAGAAGCCAAGAC	-3'	126	1.004 (98.5%)
	R: 5'- GGTCAGCCTGTTGCCACAAAGGTAG	-3'		
<i>GstM1</i>	F: 5'- CGCTACCTTGCCCGAAAGCACC	-3'	91	1.002 (99.1%)
	R: 5'- GGGTGTCCATGACCTGGTTCTCCAC	-3'		
<i>GstP1</i>	F: 5'- GCGGCAAATATGTCACCCTCATCTACACC	-3'	104	0.999 (99.9%)
	R: 5'- GGACAGCAGGGTCTCAAAAGGCTTCA	-3'		
<i>GstP2</i>	F: 5'- CGGCAAATATGGCACCATGATCTACAGA	-3'	103	0.999 (99.8%)
	R: 5'- GGACAGCAGGGTCTCAAAAGGCTTCA	-3'		
<i>Cyp1A2</i>	F: 5'- TGGTGCCATGTGCTTTGGGAAGAAC	-3'	113	0.998 (99.6%)
	R: 5'- AGTCCACTGCATTCCCTGAGGTGACATT	-3'		
<i>Cyp2B9</i>	F: 5'- ATCGGCTCACACCGGCTACCAACTC	-3'	156	1.002 (99.4%)
	R: 5'- GGGGAGCAGGTACCCTCGGAACAGT	-3'		
<i>Cyp2B10</i>	F: 5'- GGAGAGCGCTTTGAGTACACAGACCGTC	-3'	143	0.998 (99.0%)
	R: 5'- CTGTGGGCACCAGGAAAGTACTTCAGG	-3'		
<i>Cyp2B13</i>	F: 5'- CGGACCATTGCTGCAGCTCAGCTAGTT	-3'	158	0.979 (99.3%)
	R: 5'- GGCCTCCTCCTTTATCCTCTCCTCCACAC	-3'		
<i>Cyp3A11</i>	F: 5'- GGTCAAACGCCTCTCCTTGCTGTCA	-3'	91	1.001 (99.7%)
	R: 5'- CCCGCCGTTTGTGAAGACAGAA	-3'		
<i>Cyp4A10</i>	F: 5'- TTGACCCTTCCAGGTTTGACCAGAC	-3'	139	1.001 (99.7%)
	R: 5'- CGGAGCAGTGTGAGGGCCACAA	-3'		
<i>Cyp19A1</i>	F: 5'- GAAAGCATGCGGTACCAGCCTGT	-3'	130	0.997 (99.6%)
	R: 5'- CGAGCCTGTGCATTCTTCCGATG	-3'		
<i>Lipid metabolism and retinoic acid signaling pathway</i>				
<i>Adh1</i>	F: 5'- CCACTCTTTTCCCTCAGTGTGGAGAAT	-3'	168	0.999 (99.1%)
	R: 5'- GAAGGTGCTGGTGCTGATGAAGTTGTGG	-3'		
<i>Akr1b8</i>	F: 5'- GCCATTGACGCTGGGTATCGCCATATC	-3'	139	0.979 (99.2%)
	R: 5'- GCCACAGCTTGCTGACGATGAAGAGGTC	-3'		
<i>Fabp3</i>	F: 5'- CACCAGGCAGGTGGCTAGCATGACCA	-3'	157	1.000 (98.7%)
	R: 5'- GACCTTCCGGTCATCTGCTGTCACCTCG	-3'		
<i>Hmgcr1</i>	F: 5'- GACTGTGGTTTGTGAAGCCGTCATTCCAG	-3'	158	0.999 (98.1%)
	R: 5'- CAATGTTTGCTGCGTGGGCGTTGTAG	-3'		
<i>Rarres1</i>	F: 5'- GCTGAAAACGGATGATGACAGCATCGAC	-3'	157	1.001 (98.9%)
	R: 5'- TTCTGGGCTCTGTTGCTCTTGACAGTGG	-3'		
<i>StAr</i>	F: 5'- TCGGAACTCTCTGCTTGGTTCTCAACTGG	-3'	157	0.999 (99.4%)
	R: 5'- GTCCCCGTTCTCCTGCTGGCTTTCC	-3'		
<i>mTor</i>	F: 5'- CCTGGCGATGGCAGGGGACACTTTCAC	-3'	127	1.000 (99.8%)
	R: 5'- CTCACGGAGAACGAGGACAGCGGCATG	-3'		
<i>Mitochondrial intrinsic apoptosis pathway</i>				
<i>Bcl2l1</i>	F: 5'- AGAAACTGAAGCAGAGAGGGAGACCCC	-3'	152	0.9996 (98.9%)
	R: 5'- GCGCTTGCTTCACTGCTGCCATGGG	-3'		
<i>Bax</i>	F: 5'- CAGGATGCGTCCACCAAGAAGCTGAG	-3'	128	0.9993 (98.9%)
	R: 5'- CGGAAGAAGACCTCTCGGGGGGAGT	-3'		
<i>Apaf1</i>	F: 5'- ACTTCTCCCCCTATGACCATTGGCTGTG	-3'	135	0.9782 (99.2%)
	R: 5'- GAGAAAACATCACACCGTGAACCCAACTCA	-3'		
<i>Casp3</i>	F: 5'- ACATGGGAGCAAGTCAGTGGACTCTGGG	-3'	152	0.998 (99.8%)
	R: 5'- CTGCGTCCACATCCGTACCAGAGCGAG	-3'		
<i>DNA repair</i>				
<i>Apex</i>	F: 5'- CTTCCGGCATCTCTACCCCAACACTGCT	-3'	85	1.000 (98.1%)
	R: 5'- CCAACCAACATTCTTAGAGCGGGCATTCA	-3'		
<i>Ogg1</i>	F: 5'- GCTGAGACAAGACCCCACTGAGTGCCTTT	-3'	159	1.003 (99.1%)
	R: 5'- TGGAGGTTTGGGAAGCCATGATAAGTGACA	-3'		

^a Gene symbols are according to the NCBI Gene database.
^b Sequence of forward (F) and reverse (R) primers.
^c PCR product size in base pair (bp).
^d The real-time PCR efficiencies (E) were calculated from each standard curve according to the equation $E = -10^{(-1/\text{slope})} - 1$. E is in the range from 0 (minimum value) to 1 (maximum and optimum), i.e., E = 1 is equal to 100% efficiency. Numbers in parentheses are correlation coefficient (R²) values obtained for the efficiency curve.