

**Supplementary Table S4.** Genes down regulated by OxR with a fold change <-1.25 and p< 0.01

Gene symbol	Gene name	FC	P-value
<b><i>Adipocyte cytoskeleton and matrix proteins</i></b>			
<i>1100001G20Rik</i>	RIKEN cDNA 1100001G20 gene	-2.1	0.0073
<i>A2ld1</i>	Gamma-glutamylamine cyclotransferase	-1.3	0.0033
<i>Acta1</i>	Actin, alpha 1, skeletal muscle	-1.7	0.0022
<i>Col4a5</i>	Collagen, type IV, alpha 5	-1.3	0.0070
<i>Gkn3</i>	Gastrokine 3	-1.5	0.0003
<i>Hapln3</i>	Hyaluronan and proteoglycan link protein 3	-1.3	0.0058
<i>Itgbl1</i>	Integrin, beta-like 1	-1.4	0.0030
<i>Krtap11-1</i>	Keratin associated protein 1-1	-1.4	0.0013
<i>Lctf</i>	Lactase-like	-1.6	0.0019
<i>Lrtm1</i>	Leucine richrepeats and transmembrane domains 1	-1.6	0.0004
<i>Maoa</i>	Monoamine oxidase A	-1.3	0.0008
<i>Mme</i>	Membrane metallo endopeptidase	-1.5	0.0009
<i>Myom1</i>	Myomesin 1	-1.3	0.0057
<i>Serpina3b</i>	Serine (or cysteine) peptidase inhibitor, clade A, member 3B	-1.4	0.0071
<i>Serpina3m</i>	Serine (or cysteine) peptidase inhibitor, clade A, member 3M	-1.7	0.0004
<i>Tinag</i>	Tubulointerstitial nephritis antigen	-1.8	0.0013
<i>Tpm1</i>	Tropomyosin 1, alpha	-1.4	0.0026
<i>Trdn</i>	Triadin	-1.9	0.0082
<b><i>Metabolism</i></b>			
<i>Acox1</i>	Acyl-Coenzyme A oxidase-like	-1.4	0.0061
<i>Aldh1a7</i>	Aldehyde dehydrogenase family1, subfamily A7	-1.7	0.0095
<i>Apoc4</i>	Apolipoprotein C-IV	-1.4	0.0005
<i>Atp1a4</i>	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, alpha 4 polypeptide	-1.7	0.0087
<i>Bcat1</i>	Branched chain aminotransferase 1, cytosolic	-1.3	0.0066
<i>Cox8b</i>	Cytochrome c oxidase subunit VIIIb	-1.9	0.0055
<i>Fabp12</i>	Fatty acid binding protein 12	-1.4	0.0042
<i>Glul</i>	Glutamate-ammonia ligase (glutamine synthetase)	-1.3	0.0026
<i>Grb14</i>	Growth factor receptor bound protein 14	-1.6	0.0003
<i>Gys2</i>	Glycogen synthase 2	-1.8	0.0029
<i>Lrpap1</i>	Low density lipoprotein receptor –related protein associated protein 1	-1.3	0.0031
<i>Mpst</i>	Mercaptopyruvate sulfurtransferase	-1.5	0.0020
<i>Nudt14</i>	Nudix (nucleoside diphosphate linked moiety X)-type motif 14	-1.3	0.0001
<i>Ppic</i>	Peptidylprolyl isomerase C	-1.3	0.0028
<i>Rwdd3</i>	RWD-domain containing 3	-1.4	0.0009
<i>Sfxn5</i>	Sideroflexin 5	-1.3	0.0011
<i>Tph2</i>	Tryptophan hydroxylase 2	-2.7	0.0033
<i>Tst</i>	Thiosulfate sulfurtransferase, mitochondrial	-1.4	0.0065
<b><i>Lipid mediators</i></b>			
<i>Cyp2c44</i>	Cytochrome P450, family 2, subfamily c polypeptide 44	-1.8	0.0003
<i>D3Bwg0562e</i>	DNA segment, Chr3, Brigham & Women's Genetics 0562 expressed	-1.9	0.0096
<i>Enpp5</i>	Ectonucleotide pyrophosphatase/phosphodiesterase 5	-1.4	0.0099
<i>Hpgd</i>	Hydroxyprostaglandin dehydrogenase 15 (NAD)	-1.3	0.0004
<i>Mgst2</i>	microsomal glutathione S-transferase 2	-1.5	0.0033

Gene symbol	Gene name	FC	P-value
<i>Pemt</i>	Phosphatidylethanolamine N-methyltransferase	-1.3	0.0075
<i>Pla2g2e</i>	Phospholipase A2, group IIE	-2.5	0.0001
<i>Pla2g5</i>	Phospholipase A2, group V	-1.9	0.0056
<i>Slco3a1</i>	Solute carrier organic anion transport family, member 3a1	-1.5	0.0003
<b>Inflammation</b>			
<i>Ccl8</i>	Chemokine (C-C motif) ligand 8	-1.8	0.0002
<i>Clec9a</i>	C-type lectin domain family 9, member a	-1.4	0.0014
<i>S100a8</i>	S100 calcium binding protein A8 (calgranulin A)	-2.8	0.0001
<i>Saa1</i>	Serum amyloid A 1	-1.8	0.0077
<i>Saa3</i>	Serum amyloid A 3	-2	0.0025
<b>Cholesterol</b>			
<i>Dhcr24</i>	24-dehydrocholesterol reductase	-1.6	0.0006
<i>Nsdhl</i>	NAD(P) dependent steroid dehydrogenase-like	-1.3	0.0078
<i>Tm7sf2</i>	Transmembrane 7 superfamily member 2	-1.3	0.0001
<b>Histone regulation/modification</b>			
<i>H2-K1</i>	Histocompatibility 2, K1, K region	-1.3	0.0037
<i>H2-Q10</i>	Histocompatibility 2, Q region locus 10	-1.3	0.0060
<i>Zmynd15</i>	Zinc finger, MYND-type containing 15	-1.4	0.0002
<b>Miscellaneous</b>			
<i>Ccdc3</i>	Coiled coil domain containing 3	-1.4	0.0094
<i>Cck</i>	Cholecystokinin	-4.4	0.0041
<i>Hfe</i>	Hemochromatosis	-1.4	0.0034
<b>Unknown</b>			
<i>6030419C18Rik</i>			
<i>9130204L05Rik</i>		-1.8	0.0047
<i>A_55_P1981992</i>		-1.3	0.0018
<i>B230311B06Rik</i>		-1.3	0.0032
<i>BC054084</i>		-1.4	0.0023
<i>Chr1:138579972-138587381_F</i>		-1.5	0.0026
<i>Chr10:93819821-93976621_F</i>		-1.3	0.0008
<i>chr8:89996710-90049453_F</i>		-1.3	0.0050
<i>ENSMUST00000090166</i>		-1.4	0.0007
<i>NAP060515-1</i>		-1.3	0.0019

Processes are shown in the order as presented in Figure 3. Categorized transcripts per process were subsequently sorted based on alphabetical order.