**Table S1. List of** **primers used for qPCR approach.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene****Symbol** | **Gene Name** | **Forward Primer****(Sequence 5'-3')** | **Reverse Primer****(Sequence 5'-3')** | **Size****(bp)** | **GenBank****Accession b** | **Eff. (%) c** | **Origin** |
| ***ampk*** | 5' adenosine monophosphate-act. prot. kin. | TGTAGATGGACAGTGGACCCT | GGGCATCAAACACCTCAAAGT | 113 | XM\_014171387.1 | 94.3 | This study d |
| ***apod*** | Apolipoprotein D like | GGAGAAACTGGAGGAGCTGTAC | ACTGAATCATGTCCCTTAGGCC | 130 | XM\_014189629.1 | 97.5 | (Beemelmanns *et al.*, 2020a) |
| ***bax*** | Apoptosis regulator BAX | GACATTTTGTTGTTTAGGGCT | AATAATCACAGACACACACCC | 206 | XM\_014204187 | 86.0 | This study d |
| ***c1ql2*** | Complement c1q-like protein | AACCTGAGCACCTTCAATGGAA | GCGTTGCCATAATTCCCATCAA | 137 | XM\_014172088.1 | 91.0 | (Beemelmanns *et al.*, 2020a) |
| ***c3*** | Complement C3 | TTATTGAAGGAGTGGGCAAAGC | TCTGCTTTCACCATCTCACTCC | 142 | XM\_014131265.1 | 91.5 | (Beemelmanns *et al.*, 2020a) |
| ***calm*** | Calmodulin | GAGATGATCAGAGAAGCCGACA | GCCAGGAGAAGGGTAGGAGA | 104 | BT058660.1 | 92.5 | (Beemelmanns *et al.*, 2020a) |
| ***camp-a*** | Cathelicidin paralog-a | AAGCCAGAAAATGCTCCAGA | ACCCTCAGGACGACCAATTA | 107 | GQ870278.1 | 84.0 | (Beemelmanns *et al.*, 2020a) |
| ***casp8*** | Caspase 8 | TCCTGTCTATATAAGTGGGCGTTC | CTTTCCCGAGTGAGCTAACAGT | 80 | BT072408.1 | 89.5 | (Beemelmanns *et al.*, 2020a) |
| ***cat*** | Catalase | CGACGATAACGTCACACAGG | GCCTGGACCCCGTTTCCATA | 177 | NM\_001140302.1 | 86.0 | (Beemelmanns *et al.*, 2020a) |
| ***cirbp*** | Cold-inducible RNA-binding protein | TTGAGTACACAGCGGTGAATT | ACCAATCTGATGCTATGACGAGA | 132 | BT059171.1 | 98.7 | (Beemelmanns *et al.*, 2020a) |
| ***cldn3*** | Claudin 3 | GCTCACGTTTTTCCCACAGT | CAGTTTGGTGTTGTTCCTCTTCA | 189 | XM\_014214348.1 | 89.5 | (Beemelmanns *et al.*, 2020a) |
| ***ctsh*** | Cathepsin H precursor | AAATGGGTATGGTGGATGCAGT | ACTGTGTCTGTGGTGTTGTGAC | 130 | BT047094.1 | 84.0 | (Beemelmanns *et al.*, 2020a) |
| ***cul3*** | Cullin 3 | TCAGGCCCACTACTCTTCTTACT | GCATTCACATCTTTCCCAAGGG | 127 | XM\_014192069.1 | 89.5 | (Beemelmanns *et al.*, 2020a) |
| ***cyp1a*** | Cytochrome P450 1A | AGGTGGGAATGACTCGTACTC | GATGTATCCTTGACTGTGCAGT | 136 | BT045666.1 | 94.0 | (Beemelmanns *et al.*, 2020a) |
| ***dnmt1*** | DNA (cytosine-5)-methyltransferase 1-like  | TGTGTCTTAGAGCGGATCAAGG | TAGTCCGACACCTCCATCTTCT | 83 | XM\_014203933.1 | 93.5 | (Beemelmanns *et al.*, 2020a) |
| ***egln2*** | Egl nine homolog 2 | TAGTTAAATGTGTGTGTGCGCA | TCTTACCCAGTCTATCTCACACAC | 90 | NM\_001165346.1 | 89.5 | (Beemelmanns *et al.*, 2020a) |
| ***epx*** | Eosinophil peroxidase-like | CCGTGACCCCTTCAGAATC | TCTGCTGTTTGGCCTCTGTA | 116 | BT072012.1 | 108.0 | (Beemelmanns *et al.*, 2020a) |
| ***gr1*** | Glucocorticoid receptor 1 | GAGGCTGCAGGTGTCTTATGA  | CTTCCCCAGCTCCTTTATGTA | 136 | GQ179974 | 99.3 | This study d |
| ***gck*** | Glucokinase  | CTTTGGAGCCAACGGAGA | GCACCAGCTCTCCCATGTA  | 131 | XM\_014171080.1 | 87.0 | Caballero-Solares et al. (2018)  |
| ***gstt1*** | Glutathione S-transferase theta-1 | CAAAGACAAGATGGATGGAGCC | CATGATCTCAACAATGGCCACC | 139 | BT046590.1 | 87.0 | (Beemelmanns *et al.*, 2020a) |
| ***hcn1*** | Potassium sodium hyperpolarization-activated cyclic nucleotide-gated channel 1-like | TGCACAACAGGACAAGGAAGAT | ACCAGTCTACACAGTACCAAGTC | 105 | XM\_014164789.1 | 91.0 | (Beemelmanns *et al.*, 2020a) |
| ***hif1a*** | Hypoxia inducible factor 1-alpha | CCCATGTTCACAACAACAGC | AATGAGAAGGGGCTGAACCT | 100 | NM\_001140022.1 | 88.0 | (Beemelmanns *et al.*, 2020a) |
| ***hsp70*** | Heat shock protein 70 | AGTGATCAACGACTCGACACG | CACTGCATTGGTTATAGTCTTG | 151 | BT045715.1 | 90.0 | (Beemelmanns *et al.*, 2020a) |
| ***hsp90aa1*** | Heat shock protein hsp 90-alpha | CGAGGACATGAAGAAGAGGCAT | ACACTGTCACCTTCTCCACTTT | 104 | KC150878.1 | 92.5 | (Beemelmanns *et al.*, 2020a) |
| ***hsp90ab1*** | Heat shock protein hsp 90-beta | AGGATTCCAAGGACAAGAAGAAGA | GTCAGGCTCTTGTAGAACTCCC | 145 | KC150883.1 | 93.5 | (Beemelmanns *et al.*, 2020a) |
| ***hspd1*** | 60 kda heat shock mitochondrial  | CGGTCCAAGCCACAAGTTAATG | CAACACTTGAATGCACGGTAGT | 133 | BT071923.1 | 87.5 | (Beemelmanns *et al.*, 2020a) |
| ***igfbp2b1*** | Insulin-like growth factor-binding prot. 2b1 | CTGCTTATGTTACTTGGTCTGCC | TACAGTTGATGGTGAGCTCAGG | 112 | NM\_001123648.1 | 87.5 | (Beemelmanns *et al.*, 2020a) |
| ***il8*** | Interleukin-8 | GAAAGCAGACGAATTGGTAGAC | GCTGTTGCTCAGAGTTGCAAT | 99 | BT046706 | 90.7 | Soto-Dávila et al. (2020)  |
| ***irf2*** | Interferon regulatory factor 2  | TTCATCAGAGCAGTCACAGTCC | GACTGACTGCTCCTCATTCTCC | 107 | NM\_001252351.1 | 107.5 | (Beemelmanns *et al.*, 2020a) |
| ***jak2*** | Tyrosine-protein kinase JAK2-like | ACCGCTCAGATATGTAAGGGTATG | AGCTCACTCTCTACCAGGATGT | 95 | XM\_014171549.1 | 92.0 | (Beemelmanns *et al.*, 2020a) |
| ***jund*** | Transcription factor JUN-D-like | CTGGATTAGGGTAGAATAGGTGCA | ACATTGAGGGATGCAGTTCAGT | 134 | XM\_014190066.1 | 86.5 | (Beemelmanns *et al.*, 2020a) |
| ***mhcii*** | MHC class ii antigen alpha chain | GGGCACTGGACTAGAGAGATCT | TGGCGTACATTGTTGACTGTGA | 110 | XM\_014137044.1 | 94.0 | (Beemelmanns *et al.*, 2020a) |
| ***mmp9*** | Matrix metalloproteinase 9 | GGACCTTGTGACCAGGAAAA | TGGAGGACAGACCCAGTTTC | 110 | NM\_001140457.1 | 90.5 | (Beemelmanns *et al.*, 2020a) |
| ***nckap1l*** | Nck-associated protein 1-like | TCTGCGTCTATGTGTGACCTTC | GGTCATTGAGGTTGCACTGTTC | 95 | XM\_014134027.1 | 100.0 | (Beemelmanns *et al.*, 2020a) |
| ***ndufa1*** | NADH dehydrogenase 1 alpha sub.1  | TGATGGAGAGAGACAGACGAGT | AGGTGAGATCTGGGATTAGTGGA | 89 | BT046880.1 | 91.0 | (Beemelmanns *et al.*, 2020a) |
| ***ndufa4*** | Cytochrome c oxidase subunit NDUFA4 | GCCTCTTTCAACACACAACACT | TCACTTTAGGGTTGGAGAGGGT | 96 | XR\_001319779.1 | 86.0 | (Beemelmanns *et al.*, 2020a) |
| ***pdk3*** | Pyruvate dehydrogenase kinase isozyme 3 | AGTACATTATTTCCCGTGGTGTCA | CCACAGTTTCCATGGTAGCAGA | 116 | NM\_001139694.1 | 88.5 | (Beemelmanns *et al.*, 2020a) |
| ***prdx6*** | Peroxiredoxin-6 | GCGTTCATGTTGCATTTGTTGT | CGCAATTAGAAGTAAGGCAGCA | 126 | BT047207.1 | 92.5 | (Beemelmanns *et al.*, 2020a) |
| ***rraga*** | Ras-related GTP binding A  | GTTGTAGTAAACTGGCAGCCTC | TTAATGAGTGTGGCTGCAAAGG | 145 | XM\_014137442.1 | 89.5 | (Beemelmanns *et al.*, 2020a) |
| ***serpinh1*** | SerpinH1 | GACCATTCAAAAATCAACCTCA | CATGGCTCCATCAGCATTCT | 129 | XM\_014214963.1 | 92.0 | (Beemelmanns *et al.*, 2020a) |
| ***sod1*** | Superoxide dismutase 1 | AGATGGCACTGAAGGCTGTT | GTCAGACCTGCGATCTCTCC | 121 | BT056659 | 91.8 | This study d |
| ***tapbp*** | Tapasin | ATTCCCTGCTGCAATGATCCA | CCTGCTGTGACTTGGTTTCTTC | 83 | BT045317.1 | 90.0 | (Beemelmanns *et al.*, 2020a) |
| ***tnfrsf6b*** | Tumor necrosis factor receptor sup. mem. 6b | CAACTGTCCTAGACCTTCTCACA | TGTCCAGGATATCATGCAATCGA | 87 | XM\_014136455.1 | 100.5 | (Beemelmanns *et al.*, 2020a) |
| ***txn*** | Thioredoxin | AGGATTCCTTCTTCATTGCCCT | TTCCGACAGCCCTTTGAAGAA | 119 | BT125521.1 | 103.5 | (Beemelmanns *et al.*, 2020a) |
| ***ucp2***  | Mitochondrial uncoupling protein 2 | CTGATCTCTGCCGTCACCAT | AGAAGACTGATGAGGTGAAGACA | 89 | XM\_014196911.1 | 87.5 | (Beemelmanns *et al.*, 2020a) |
| ***eif3d* a** | Eukaryotic translation initiation factor 3 sub. D  | CTCCTCCTCCTCGTCCTCTT | GACCCCAACAAGCAAGTGAT | 105 | GE777139 | 91.5 | Eslamloo et al. (2017) |
| ***rpl32* a** | 60S ribosomal protein 32 | AGGCGGTTTAAGGGTCAGAT | TCGAGCTCCTTGATGTTGTG | 119 | BT043656 | 95.5 | Xue et al. (2015)  |

a Primers used for normalization purpose and amplification efficiencies were determined in Beemelmanns *et al.* (2020a).

b Nucleotide sequences from GenBank were used for primer design as described in Beemelmanns *et al.* (2020a).

c Amplification efficiencies were calculated using a 5-point 1:3 dilution series starting with cDNA representing 10 ng of input total RNA. Presented are values

 determined from cDNA templates of the CT and WH treatment groups (n=6) from Beemelmanns *et al.* (2020a).

d Primers established within the Genomic Applications Partnership Program (GAPP #6604) and quality tested again as described in Beemelmanns *et al.* (2020a).

**Table S2. Complete results of the temperature and hypoxia treatment effects on the first two principal components (PC-1, PC-2) based on the mRNA expression of 27 ‘stress’-related and 15 immune-related genes.**

|  |
| --- |
| **Linear Mixed Effect Models and Post-Hoc Tests for Principal Components (PC-1 and PC-2)** |
|  | ***All ‘Stress’ Genes (27)*** | ***All Immune Genes (15)*** |
|  | **PC-1** | **PC-2** | **PC-1** | **PC-2** |
| **Model** | **DenDF** | **F.value** | **Pr(>F)** |  | **DenDF** | **F.value** | **Pr(>F)** |  | **DenDF** | **F.value** | **Pr(>F)** | **DenDF** | **F.value** | **Pr(>F)** |  |
| **Group** | 4 | 66.61 | **0.001** | \*\* | 4 | 8.52 | **0.042** | \* | 3 | 1.01 | 0.451 | 4 | 21.15 | **0.011** | \* |
| **Temperature** | 101 | 25.74 | **<0.0001** | \*\*\* | 101 | 2.06 | *0.092* |  | 101 | 0.81 | 0.523 | 101 | 15.17 | **<0.0001** | \*\*\* |
| **Condition Factor** | 104 | 8.20 | **0.005** | \*\* | 104 | 0.48 | 0.489 |   | 103 | 0.07 | 0.796 | 104 | 0.87 | 0.354 |   |
| **Group:Temperature** | 101 | 7.08 | **<0.0001** | \*\*\* | 101 | 0.91 | 0.514 |   | 101 | 0.93 | 0.495 | 101 | 5.14 | **<0.0001** | \*\*\* |
| **Variance (%)**  | 33.7 | 21.6 | 27.5 | 22.0 |
| **Variance (%) Residuals** | 99.7 | 99.2 | 96.0 | 99.2 |
| **Variance (%) Random** | 0.3 | 0.8 | 4.0 | 0.8 |
| **Group** | **df** | **t.ratio** | **p.value** |  | **df** | **t.ratio** | **p.value** |  |  |  |  | **df** | **t.ratio** | **p.value** |  |
| **CT vs WN** | 3 | -10.22 | **0.003** | \*\* | 3 | -3.51 | *0.060* |  |   |   |  | 3 | 5.34 | **0.020** | \* |
| **CT vs WH** | 4 | -9.28 | **0.002** | \*\* | 4 | -3.50 | *0.060* |  |   |   |  | 4 | 5.68 | **0.013** | \* |
| **WN vs WH** | 4 | 0.04 | 0.970 |   | 4 | -0.28 | 0.795 |   |   |   |  | 4 | 0.76 | 0.484 |   |
| **Temperature**  | **df** | **t.ratio** | **p.value** |  |  |  |  |  |  |  |  |  |  |  |  |
| **12°C vs 16°C-3d** | 102 | -0.47 | 0.642 |   |   |   |  |   |   |   |  | 102 | -0.57 | 0.573 |   |
| **12°C vs 18°C-3d** | 103 | -1.90 | 0.076 |   |   |   |  |   |   |   |  | 103 | 0.59 | 0.573 |   |
| **12°C vs 20°C-3d** | 103 | -6.41 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 103 | 4.76 | **<0.0001** | \*\*\* |
| **12°C vs 20°C-4wks** | 102 | -5.81 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 102 | 2.50 | **0.024** | \* |
| **16°C-3d vs 18°C-3d** | 101 | -2.01 | 0.068 |   |   |   |  |   |   |   |  | 101 | 1.48 | 0.179 |   |
| **16°C-3d vs 20°C-3d** | 101 | -8.03 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 7.07 | **<0.0001** | \*\*\* |
| **16°C-3d vs 20°C-4wks** | 101 | -6.90 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 3.91 | **2.0eE-04** | \*\*\* |
| **18°C-3d vs 20°C-3d** | 101 | -6.14 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 5.70 | **<0.0001** | \*\*\* |
| **18°C-3d vs 20°C-4wks** | 101 | -4.82 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 2.39 | **0.027** | \* |
| **20°C-3d vs 20°C-4wks** | 101 | 1.26 | 0.234 |   |   |   |  |   |   |   |  | 101 | -3.27 | **0.003** | \*\* |
| **Pair-Wise Comparisons of Control (CT), Warm & Normoxic (WN) and Warm & Hypoxic (WH) Treatment Groups** **at a Particular Temperature (12°C, 16°C-3d, 18°C-3d, 20°C-3d and 20°C-4wks)** |
| **12°C** | **df** | **t.ratio** | **p.value** |  |  |  |  |  |  |  |  | **df** | **t.ratio** | **p.value** |  |
| **CT vs WN** | 47 | 0.89 | 0.379 |   |   |   |  |   |   |   |  | 44 | -0.87 | 0.581 |   |
| **CT vs WH** | 49 | -2.37 | **0.032** | \* |   |   |  |   |   |   |  | 45 | 0.23 | 0.819 |   |
| **WN vs WH** | 50 | -3.23 | **0.007** | \*\* |   |   |  |   |   |   |  | 46 | 1.08 | 0.581 |   |
| **16°C-3d** | **df** | **t.ratio** | **p.value** |  |  |  |  |  |  |  |  | **df** | **t.ratio** | **p.value** |  |
| **CT vs WN** | 47 | -3.64 | **0.002** | \*\* |   |   |  |   |   |   |  | 44 | 0.96 | 0.669 |   |
| **CT vs WH** | 52 | -2.44 | **0.028** | \* |   |   |  |   |   |   |  | 49 | 0.77 | 0.669 |   |
| **WN vs WH** | 52 | 1.04 | 0.303 |   |   |   |  |   |   |   |  | 48 | -0.15 | 0.884 |   |
| **18°C-3d** | **df** | **t.ratio** | **p.value** |  |  |  |  |  |  |  |  | **df** | **t.ratio** | **p.value** |  |
| **CT vs WN** | 48 | -5.55 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 44 | 2.47 | **0.044** | \* |
| **CT vs WH** | 49 | -5.31 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 45 | 2.25 | **0.044** | \* |
| **WN vs WH** | 50 | 0.18 | 0.861 |   |   |   |  |   |   |   |  | 46 | -0.19 | 0.848 |   |
| **20°C-3d** | **df** | **t.ratio** | **p.value** |  |  |  |  |  |  |  |  | **df** | **t.ratio** | **p.value** |  |
| **CT vs WN** | 47 | -7.92 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 44 | 5.48 | **<0.0001** | \*\*\* |
| **CT vs WH** | 51 | -7.21 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 48 | 6.63 | **<0.0001** | \*\*\* |
| **WN vs WH** | 51 | 0.43 | 0.672 |   |   |   |  |   |   |   |  | 47 | 1.36 | 0.182 |   |
| **20°C-4wks** | **df** | **t.ratio** | **p.value** |  |  |  |  |  |  |  |  | **df** | **t.ratio** | **p.value** |  |
| **CT vs WN** | 48 | -7.22 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 44 | 4.62 | **1.0E-04** | \*\*\* |
| **CT vs WH** | 48 | -5.50 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 44 | 4.45 | **1.0E-04** | \*\*\* |
| **WN vs WH** | 49 | 1.67 | 0.101 |   |   |   |  |   |   |   |  | 45 | -0.15 | 0.882 |   |
| **Pair-Wise Comparisons of Control (CT), Warm & Normoxic (WN) and Warm & Hypoxic (WH) Treatment Groups****Across Temperatures (12°C, 16°C-3d, 18°C-3d, 20°C-3d and 20°C-4wks)** |
| **CT** | **df** | **t.ratio** | **p.value** |  |  |  |  |  |  |  |  | **df** | **t.ratio** | **p.value** |  |
| **12°C vs 16°C-3d** | 102 | 1.11 | 0.448 |   |   |   |  |   |   |   |  | 102 | -1.10 | 0.839 |   |
| **12°C vs 18°C-3d** | 102 | 1.44 | 0.307 |   |   |   |  |   |   |   |  | 102 | -1.19 | 0.839 |   |
| **12°C vs 20°C-3d** | 102 | -0.35 | 0.809 |   |   |   |  |   |   |   |  | 102 | -0.55 | 0.839 |   |
| **12°C vs 20°C-4wks** | 102 | -0.52 | 0.809 |   |   |   |  |   |   |   |  | 102 | -1.31 | 0.839 |   |
| **16°C-3d vs 18°C-3d** | 101 | 0.40 | 0.809 |   |   |   |  |   |   |   |  | 101 | -0.13 | 0.935 |   |
| **16°C-3d vs 20°C-3d** | 101 | -1.63 | 0.266 |   |   |   |  |   |   |   |  | 101 | 0.58 | 0.839 |   |
| **16°C-3d vs 20°C-4wks** | 101 | -1.80 | 0.252 |   |   |   |  |   |   |   |  | 101 | -0.22 | 0.935 |   |
| **18°C-3d vs 20°C-3d** | 101 | -2.04 | 0.221 |   |   |   |  |   |   |   |  | 101 | 0.72 | 0.839 |   |
| **18°C-3d vs 20°C-4wks** | 101 | -2.19 | 0.221 |   |   |   |  |   |   |   |  | 101 | -0.08 | 0.935 |   |
| **20°C-3d vs 20°C-4wks** | 101 | -0.16°C | 0.876 |   |   |   |  |   |   |   |  | 101 | -0.79 | 0.839 |   |
| **WN** | **df** | **t.ratio** | **p.value** |  |  |  |  |  |  |  |  | **df** | **t.ratio** | **p.value** |  |
| **12°C vs 16°C-3d** | 102 | -3.05 | **0.004** | \*\* |   |   |  |   |   |   |  | 102 | 0.59 | 0.557 |   |
| **12°C vs 18°C-3d** | 102 | -4.23 | **1.0E-04** | \*\*\* |   |   |  |   |   |   |  | 102 | 1.78 | 0.111 |   |
| **12°C vs 20°C-3d** | 102 | -8.19 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 102 | 5.13 | **<0.0001** | \*\*\* |
| **12°C vs 20°C-4wks** | 102 | -7.91 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 102 | 3.76 | **0.001** | \*\* |
| **16°C-3d vs 18°C-3d** | 101 | -1.52 | *0.053* |  |   |   |  |   |   |   |  | 101 | 1.39 | 0.186 |   |
| **16°C-3d vs 20°C-3d** | 101 | -5.93 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 5.15 | **<0.0001** | \*\*\* |
| **16°C-3d vs 20°C-4wks** | 101 | -5.41 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 3.51 | **0.001** | \*\* |
| **18°C-3d vs 20°C-3d** | 101 | -4.42 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 3.77 | **0.001** | \*\* |
| **18°C vs 20°C-4wks** | 101 | -3.86 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 2.10 | 0.064 |   |
| **20°C-3d vs 20°C-4wks** | 101 | 0.54 | 0.588 |   |   |   |  |   |   |   |  | 101 | -1.66 | 0.124 |   |
| **WH** | **df** | **t.ratio** | **p.value** |  |  |  |  |  |  |  |  | **df** | **t.ratio** | **p.value** |  |
| **12°C vs 16°C-3d** | 101 | 1.03 | 0.304 |   |   |   |  |   |   |   |  | 101 | -0.60 | 0.548 |   |
| **12°C vs 18°C-3d** | 102 | -1.18 | 0.270 |   |   |   |  |   |   |   |  | 102 | 0.63 | 0.548 |   |
| **12°C vs 20°C-3d** | 102 | -4.95 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 102 | 5.48 | **<0.0001** | \*\*\* |
| **12°C vs 20°C-4wks** | 102 | -3.30 | **0.003** | \*\* |   |   |  |   |   |   |  | 102 | 2.56 | **0.020** | \* |
| **16°C-3d vs 18°C-3d** | 101 | -2.38 | **0.029** | \* |   |   |  |   |   |   |  | 101 | 1.33 | 0.235 |   |
| **16°C-3d vs 20°C-3d** | 101 | -6.54 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 6.68 | **<0.0001** | \*\*\* |
| **16°C-3d vs 20°C-4wks** | 101 | -4.73 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 3.46 | **0.002** | \*\* |
| **18°C-3d vs 20°C-3d** | 101 | -4.15 | **<0.0001** | \*\*\* |   |   |  |   |   |   |  | 101 | 5.38 | **<0.0001** | \*\*\* |
| **18°C-3d vs 20°C-4wks** | 101 | -2.35 | **0.029** | \* |   |   |  |   |   |   |  | 101 | 2.15 | **0.049** | \*  |
| **20°C-3d vs 20°C-4wks** | 101 | 1.81 | *0.092* |   |   |   |  |   |   |   |  | 101 | -3.24 | **0.003** |  \*\* |

The linear mixed effect models (*lmer*) were individually performed on extracted scores of PC-1 and PC-2 to assess the ‘group\*temperature’ interaction, and included the covariate ‘condition factor (CF)’ and the random term ‘tank’. The Principal Component Analysis (PCA) was computed based on log2 RQ-values of *i*) 27 ‘stress’-related genes and *ii*) 15 immune-related genes (Figure 2). The variance explained by each PC is indicated in percentage (%) values. Significant *lmer* models were followed by *emmeans* post-hoc tests with False Discovery Rate (FDR) correction of *p*-values to obtain a pair-wise comparison between Control (CT), Warm & Normoxic (WN) and Warm & Hypoxic (WH) treatments within and between temperature point (12°C, 16°C-3d, 18°C-3d, 20°C-3d and 20°C-4wks). Significant values are marked in bold letters (*p<*0.0001\*\*\*, *p<*0.001\*\*, *p<*0.05\*) and trends in italics (0.05<*p*<0.1).

**Table S3. Temperature and hypoxia treatment effects on the mRNA expression of 45 target genes.**

|  |
| --- |
| **Linear Mixed Effect Models per Gene** |
|  |  | **Group** **DF=2** | **Temperature** **DF=4** | **Group:****Temperature** **DF=8** | **Cond. Factor DF=1** |
| **Gene** | **Functional****Category** | **Pr (F) Sign.** | **Pr (F) Sign.** | **Pr (F) Sign.** | **Pr (F) Sign.** |
| **serpinh1** | Temp. Stress  | **0.003** | **\*\*** | **2.2e-16** | **\*\*\*** | **1.0e-15** | **\*\*\*** | 0.371 |   |
| **hsp90aa1** | Temp. Stress  | **0.007** | **\*\*** | **4.6e-4** | **\*\*\*** | **0.001** | **\*\*** | 0.197 |   |
| **hsp70** | Temp. Stress  | **0.003** | **\*\*** | **0.009** | **\*\*** | 0.254 |   | 0.682 |   |
| **hsp90ab1** | Temp. Stress  | *0.082* |  | 0.240 |   | 0.843 |   | 0.424 |   |
| **cirbp** | Temp. Stress  | **0.005** | **\*\*** | **1.3e-12** | **\*\*\*** | **2.7e-10** | **\*\*\*** | 0.124 |   |
| **hspd1** | Temp. Stress  | **2.2e-16** | **\*\*\*** | **8.9e-14** | **\*\*\*** | **4.0e-4** | **\*\*\*** | 0.327 |   |
| **jak2** | Stress, Apoptosis  | **7.1e-7** | **\*\*\*** | **0.005** | **\*\*** | **0.016** | **\*** | 0.739 |   |
| **jund** | Stress, Apoptosis | **0.016** | **\*** | **3.4e-5** | **\*\*\*** | **0.018** | **\*** | 0.161 |   |
| **hcn1** | Oxidative Stress | **0.002** | **\*\*** | **4.1e-6** | **\*\*\*** | **1.8e-5** | **\*\*\*** | **0.023** | **\*** |
| **txn** | Oxidative Stress | **0.003** | **\*\*** | 0.658 |   | 0.724 |   | 0.325 |   |
| **ndufa4** | Oxidative Stress | 0.270 |   | 0.391 |   | 0.222 |   | 0.886 |   |
| **prdx6** | Oxidative Stress | **2.2e-16** | **\*\*\*** | **2.2e-16** | **\*\*\*** | **2.5e-10** | **\*\*\*** | *0.079* |  |
| **ucp2** | Oxidative Stress | **1.1e-13** | **\*\*\*** | **5.4e-7** | **\*\*\*** | **1.0e-7** | **\*\*\*** | 0.860 |   |
| **rraga** | Oxidative Stress | **0.004** | **\*\*** | **2.1e-11** | **\*\*\*** | **3.0e-6** | **\*\*\*** | **0.047** | **\*** |
| **cyp1a** | Oxidative Stress | **0.019** | **\*** | **3.0e-8** | **\*\*\*** | **0.002** | **\*\*** | 0.162 |   |
| **gstt1** | Oxidative Stress | **4.7e-6** | **\*\*\*** | **9.1e-6** | **\*\*\*** | 0.117 |   | **1.7e-5** | **\*\*\*** |
| **ndufa1** | Oxidative Stress | 0.147 |   | **4.1e-4** | **\*\*\*** | **0.001** | **\*\*\*** | 0.266 |   |
| **sod1** | Oxidative Stress | 0.409 |   | **2.4e-4** | **\*\*\*** | 0.392 |   | 1.000 |  |
| **cat** | Oxidative Stress | 0.880 |   | **0.012** | **\*** | 0.694 |   | *0.050* |  |
| **gr1** | Oxidative Stress | 0.776 |   | **0.027** | **\*** | 0.914 |   | 0.483 |   |
| **egln2** | Hypoxia Response | **0.027** | **\*** | **2.5e-5** | **\*\*\*** | **6.8e-7** | **\*\*\*** | 0.256 |   |
| **calm** | Hypoxia Response | **0.017** | **\*** | **3.2e-6** | **\*\*\*** | **0.003** | **\*\*** | **0.005** | **\*\*** |
| **hif1a** | Hypoxia Response | 0.130 |   | **0.003** | **\*\*** | **0.002** | **\*\*** | **4.4e-4** | **\*\*\*** |
| **cldn3** | Hypoxia Response | 0.385 |   | **0.025** | **\*** | **0.027** | **\*** | 0.929 |   |
| **ampk** | Hypoxia Response | 0.170 |   | **5.2e-5** | **\*\*\*** | 0.221 |   | **0.001** | **\*\*\*** |
| **igfbp2b1** | Hypoxia Response | 0.740 |   | *0.081* |  | 0.457 |   | 0.880 |   |
| **cul3** | Hypoxia Response | 0.448 |   | 0.252 |   | 0.304 |   | **0.040** | **\*** |
| **c1ql2** | Immune Response | **7.3e-7** | **\*\*\*** | **2.9e-9** | **\*\*\*** | **6.4e-5** | **\*\*\*** | 0.144 |   |
| **casp8** | Immune Apoptosis | *0.079* |  | **0.043** | **\*** | **4.5e-5** | **\*\*\*** | 0.623 |   |
| **tnfrsf6b** | Immune Apoptosis | **0.041** | **\*** | **0.005** | **\*\*** | 0.433 |   | 0.775 |   |
| **apod** | Immune Response | **5.2e-7** | **\*\*\*** | 0.217 |   | 0.239 |   | **0.009** | **\*\*** |
| **epx** | Immune Response | **1.9e-5** | **\*\*\*** | 0.559 |   | *0.080* |  | 0.691 |   |
| **camp-a** | Immune Response | **0.003** | **\*\*** | 0.160 |   | *0.078* |  | 0.694 |   |
| **il8** | Immune Response | **0.014** | **\*** | 0.709 |   | 0.463 |   | 0.654 |   |
| **bax** | Immune Apoptosis | 0.463 |   | *0.082* |  | 0.191 |   | **0.022** | **\*** |
| **mhcii** | Immune Response | 0.162 |   | 0.867 |   | 0.383 |   | 0.718 |  |
| **mmp9** | Immune Response | 0.157 |   | 0.566 |   | 0.414 |   | 0.588 |  |
| **ctsh** | Immune Response | **0.003** | **\*\*** | **7.1e-12** | **\*\*\*** | **1.8e-6** | **\*\*\*** | **0.002** | **\*\*** |
| **nckap1l** | Immune Response | 0.225 |   | **0.012** | **\*** | **0.008** | **\*\*** | 0.286 |   |
| **c3** | Immune Response | 0.418 |   | **3.8e-5** | **\*\*\*** | 0.266 |   | 0.188 |   |
| **irf2** | Immune Response | 0.922 |   | 0.318 |   | 0.848 |   | 0.933 |   |
| **tapbp** | Immune Response | 0.736 |   | 0.726 |   | 0.703 |   | 0.806 |   |
| **gck** | Metabolism | **2.6e-4** | **\*\*\*** | **0.016** | **\*** | 0.106 |   | 0.111 |   |
| **pdk3** | Metabolism | **9.9e-5** | **\*\*\*** | **2.1e-7** | **\*\*\*** | **0.002** | **\*\*** | **0.005** | **\*\*** |
| **dnmt1** | Epigenetics | **2.2e-16** | **\*\*\*** | **1.9e-13** | **\*\*\*** | **1.8e-5** | **\*\*\*** | 0.223 |   |

Linear mixed effect models (*lmer*) were performed individually for each target gene to assess the effect and interaction of the fixed factors ‘group\*temperature’ and the covariate ‘condition factor (CF)’, and included `tank´ as a random term. Significant values are marked in bold letters (*p<*0.0001\*\*\*, *p<*0.001\*\*, *p<*0.05\*) and trends in italics (0.05<*p*<0.1).

**Table S4.** **Fold-change (FC) ratios with the standard error of means (SEM) for 45 target genes.**

|  |
| --- |
| Fold-Change (FC) Ratios |
|  | **12°C-3d** | **16°C-3d** | **18°C-3d** | **20°C-3d** | **20°C-4wks** |
|  | **WN** | **SEM** | **WH** | **SEM** | **WN** | **SEM** | **WH** | **SEM** | **WN** | **SEM** | **WH** | **SEM** | **WN** | **SEM** | **WH** | **SEM** | **WN** | **SEM** | **WH** | **SEM** |
| *ampk* | 1.06 | 0.07 | -1.19 | 0.08 | -1.18 | 0.06 | -1.10 | 0.06 | -1.14 | 0.04 | -1.22 | 0.06 | -1.25 | 0.06 | -1.23 | 0.05 | -1.08 | 0.04 | -1.14 | 0.03 |
| *apod* | 8.36 | 5.35 | 2.62 | 0.83 | 6.38 | 3.05 | 4.60 | 3.23 | 13.24 | 5.55 | 3.85 | 2.25 | 5.30 | 0.56 | 9.39 | 3.10 | 5.91 | 2.63 | 10.55 | 6.37 |
| *bax* | 1.07 | 0.08 | -1.18 | 0.10 | -1.12 | 0.07 | 1.06 | 0.10 | -1.11 | 0.02 | 1.03 | 0.10 | 1.10 | 0.07 | 1.09 | 0.06 | -1.04 | 0.11 | 1.10 | 0.05 |
| *c1ql2* | -1.01 | 0.29 | -1.69 | 0.10 | 1.71 | 0.50 | 1.86 | 0.32 | 3.27 | 1.49 | 2.56 | 0.59 | 6.39 | 0.78 | 12.20 | 4.47 | 1.97 | 0.71 | 2.12 | 0.54 |
| *c3* | 1.28 | 0.15 | 1.07 | 0.13 | 1.00 | 0.23 | 1.23 | 0.18 | 1.09 | 0.16 | -1.01 | 0.09 | -1.67 | 0.11 | -1.61 | 0.12 | -1.56 | 0.10 | -1.64 | 0.08 |
| *calm* | 1.29 | 0.19 | -1.45 | 0.06 | -1.43 | 0.08 | -1.35 | 0.06 | -1.41 | 0.04 | -1.47 | 0.05 | -2.22 | 0.06 | -2.27 | 0.05 | -1.89 | 0.05 | -1.75 | 0.06 |
| *casp8* | -1.15 | 0.05 | -1.12 | 0.10 | -1.18 | 0.06 | 1.06 | 0.08 | 1.11 | 0.12 | 1.19 | 0.08 | 1.71 | 0.12 | 1.57 | 0.11 | 1.54 | 0.08 | 1.56 | 0.10 |
| *cat* | 1.14 | 0.08 | -1.30 | 0.06 | -1.11 | 0.07 | -1.04 | 0.09 | 1.02 | 0.07 | 1.00 | 0.05 | 1.01 | 0.14 | -1.05 | 0.11 | -1.19 | 0.07 | -1.16 | 0.06 |
| *camp-a* | 1.50 | 0.83 | 1.28 | 0.60 | -1.15 | 0.42 | 2.65 | 1.05 | 4.29 | 2.13 | 7.92 | 5.90 | 1.30 | 0.29 | 4.47 | 1.33 | 4.72 | 1.01 | 4.93 | 2.19 |
| *cldn3* | -1.11 | 0.15 | -1.79 | 0.04 | 1.09 | 0.13 | 1.07 | 0.14 | -1.04 | 0.13 | 1.02 | 0.09 | -1.33 | 0.07 | 1.01 | 0.10 | -1.47 | 0.07 | 1.01 | 0.15 |
| *cirbp* | 1.00 | 0.06 | -1.41 | 0.08 | -1.67 | 0.02 | -1.47 | 0.04 | -2.04 | 0.03 | -2.13 | 0.03 | -2.70 | 0.03 | -2.94 | 0.03 | -2.56 | 0.04 | -2.50 | 0.05 |
| *ctsh* | 1.17 | 0.15 | -1.12 | 0.11 | -1.82 | 0.06 | -1.33 | 0.10 | -2.08 | 0.04 | -2.13 | 0.04 | -3.03 | 0.03 | -2.86 | 0.03 | -2.78 | 0.03 | -2.17 | 0.06 |
| *cul3* | 1.04 | 0.05 | 1.03 | 0.06 | -1.05 | 0.04 | 1.08 | 0.08 | 1.03 | 0.04 | 1.15 | 0.06 | 1.17 | 0.08 | 1.01 | 0.06 | 1.02 | 0.08 | -1.03 | 0.07 |
| *cyp1a* | 1.12 | 0.31 | -1.96 | 0.10 | -1.96 | 0.10 | -1.47 | 0.13 | -2.56 | 0.06 | -3.45 | 0.06 | -5.26 | 0.05 | -6.67 | 0.04 | -4.76 | 0.04 | -4.35 | 0.06 |
| *dnmt1* | 1.08 | 0.11 | -2.13 | 0.08 | -1.85 | 0.03 | -1.54 | 0.08 | -2.04 | 0.04 | -2.00 | 0.05 | -1.89 | 0.02 | -1.67 | 0.11 | -2.04 | 0.03 | -1.85 | 0.08 |
| *egln2* | -1.23 | 0.05 | 1.03 | 0.11 | -1.27 | 0.06 | -1.19 | 0.08 | -1.54 | 0.06 | -1.33 | 0.06 | -2.56 | 0.03 | -2.70 | 0.05 | -2.78 | 0.03 | -2.27 | 0.04 |
| *epx* | 3.49 | 2.29 | 1.68 | 0.60 | -1.06 | 0.19 | 2.36 | 0.83 | 1.52 | 0.25 | 1.07 | 0.14 | 3.09 | 0.85 | 2.28 | 0.57 | 2.68 | 0.50 | 2.62 | 0.58 |
| *gck* | -1.45 | 2.37 | -6.25 | 0.05 | -7.69 | 0.08 | -10.00 | 0.05 | -5.26 | 0.07 | -7.14 | 0.04 | -2.08 | 0.25 | -1.32 | 0.30 | -1.41 | 0.43 | -1.52 | 0.21 |
| *gr1* | 1.12 | 0.12 | -1.18 | 0.12 | -1.02 | 0.15 | 1.15 | 0.12 | 1.05 | 0.11 | 1.07 | 0.08 | 1.23 | 0.17 | 1.15 | 0.12 | 1.01 | 0.14 | 1.06 | 0.15 |
| *gstt1* | 1.02 | 0.17 | -1.02 | 0.08 | -1.20 | 0.07 | -1.35 | 0.07 | -1.30 | 0.06 | -1.47 | 0.08 | -1.69 | 0.09 | -1.89 | 0.09 | -1.75 | 0.11 | -1.72 | 0.10 |
| *hcn1* | 1.38 | 0.15 | -1.41 | 0.23 | -1.59 | 0.10 | -1.33 | 0.12 | 1.32 | 0.18 | 1.20 | 0.32 | 5.40 | 1.27 | 5.68 | 1.06 | 1.76 | 0.39 | 1.91 | 0.37 |
| *hif1α* | 1.19 | 0.17 | -1.45 | 0.09 | -1.20 | 0.10 | -1.14 | 0.08 | -1.10 | 0.05 | -1.19 | 0.07 | -1.67 | 0.06 | -1.75 | 0.06 | -1.59 | 0.06 | -1.52 | 0.07 |
| *hspd1* | 1.06 | 0.14 | -1.82 | 0.08 | -2.08 | 0.07 | -2.08 | 0.11 | -2.94 | 0.02 | -3.03 | 0.03 | -3.45 | 0.02 | -2.63 | 0.04 | -2.70 | 0.02 | -2.00 | 0.08 |
| *hsp70* | -1.08 | 0.21 | 3.18 | 1.58 | -1.37 | 0.13 | 1.26 | 0.25 | 1.76 | 0.29 | 1.45 | 0.26 | 2.04 | 0.37 | 2.18 | 0.55 | 1.67 | 0.18 | 1.78 | 0.27 |
| *hsp90aa1* | 1.21 | 0.10 | 1.40 | 0.14 | 1.11 | 0.18 | 1.52 | 0.28 | 1.51 | 0.08 | 1.73 | 0.19 | 3.08 | 0.31 | 3.68 | 0.67 | 2.27 | 0.23 | 2.31 | 0.25 |
| *hsp90ab1* | 1.24 | 0.06 | 1.17 | 0.17 | -1.11 | 0.09 | 1.15 | 0.07 | 1.24 | 0.16 | 1.10 | 0.08 | 1.29 | 0.19 | 1.39 | 0.22 | 1.23 | 0.16 | 1.19 | 0.09 |
| *igfbp2b1* | 1.35 | 0.11 | 1.14 | 0.17 | 1.01 | 0.23 | 1.15 | 0.16 | 1.13 | 0.21 | -1.14 | 0.10 | -1.64 | 0.14 | -1.67 | 0.15 | -1.28 | 0.11 | -1.41 | 0.10 |
| *il8* | 1.25 | 0.23 | 1.25 | 0.46 | 1.04 | 0.26 | 1.72 | 0.42 | 1.30 | 0.32 | 1.44 | 0.38 | 1.38 | 0.33 | 2.63 | 0.73 | 1.90 | 0.37 | 2.10 | 0.61 |
| *irf2* | 1.32 | 0.09 | 1.04 | 0.15 | 1.08 | 0.23 | 1.14 | 0.16 | 1.12 | 0.15 | 1.09 | 0.06 | -1.25 | 0.15 | -1.23 | 0.17 | -1.08 | 0.12 | -1.18 | 0.11 |
| *jak2* | -1.03 | 0.05 | -1.06 | 0.07 | 1.37 | 0.17 | 1.56 | 0.13 | 1.60 | 0.13 | 1.94 | 0.24 | 1.73 | 0.22 | 1.47 | 0.16 | 1.90 | 0.16 | 1.28 | 0.10 |
| *jund* | 1.90 | 0.58 | 1.26 | 0.26 | 1.36 | 0.29 | 2.27 | 0.71 | 2.89 | 0.43 | 3.59 | 0.51 | 3.18 | 0.53 | 3.03 | 0.35 | 2.02 | 0.40 | 1.27 | 0.21 |
| *mhcii* | 1.16 | 0.21 | 1.02 | 0.35 | -1.05 | 0.09 | 1.48 | 0.34 | 1.05 | 0.15 | 1.17 | 0.22 | 1.04 | 0.16 | 1.46 | 0.32 | 2.00 | 0.21 | 1.78 | 0.28 |
| *mmp9* | 1.84 | 0.43 | 2.18 | 0.59 | -1.16 | 0.28 | 1.21 | 0.33 | 1.17 | 0.29 | -1.16 | 0.15 | 2.01 | 0.54 | 1.43 | 0.25 | 1.77 | 0.30 | 1.83 | 0.51 |
| *nckap1l* | 1.15 | 0.10 | -1.19 | 0.16 | -1.09 | 0.10 | 1.16 | 0.09 | -1.15 | 0.08 | -1.05 | 0.09 | -1.67 | 0.05 | -1.82 | 0.04 | -1.43 | 0.03 | -1.56 | 0.08 |
| *ndufa4* | 1.00 | 0.19 | 1.43 | 0.22 | 1.09 | 0.20 | 1.36 | 0.35 | 1.66 | 0.35 | 1.36 | 0.22 | 2.16 | 0.43 | 1.26 | 0.45 | 1.13 | 0.39 | -1.67 | 0.09 |
| *ndufa1* | 1.13 | 0.04 | -1.15 | 0.05 | -1.11 | 0.05 | -1.01 | 0.04 | -1.20 | 0.03 | -1.15 | 0.04 | 1.02 | 0.05 | 1.02 | 0.02 | -1.14 | 0.08 | -1.01 | 0.03 |
| *pdk3* | -1.20 | 0.08 | -1.69 | 0.05 | 1.16 | 0.14 | 1.26 | 0.10 | 1.23 | 0.11 | 1.33 | 0.12 | 1.80 | 0.15 | 1.34 | 0.11 | 1.54 | 0.10 | 1.24 | 0.13 |
| *prdx6* | 1.05 | 0.09 | -1.75 | 0.05 | -1.67 | 0.03 | -1.64 | 0.06 | -2.04 | 0.02 | -2.08 | 0.03 | -2.63 | 0.01 | -2.63 | 0.02 | -2.86 | 0.02 | -2.56 | 0.06 |
| *rraga* | 1.09 | 0.06 | -1.22 | 0.09 | -1.56 | 0.05 | -1.54 | 0.04 | -1.72 | 0.03 | -1.69 | 0.03 | -1.89 | 0.04 | -2.08 | 0.03 | -2.08 | 0.04 | -1.89 | 0.05 |
| *serpinh1* | -1.05 | 0.13 | 1.20 | 0.20 | 1.21 | 0.11 | 2.00 | 0.26 | 3.61 | 0.39 | 3.48 | 0.37 | 5.51 | 0.89 | 6.32 | 0.78 | 4.77 | 0.50 | 5.50 | 0.66 |
| *sod1* | 1.35 | 0.18 | -1.27 | 0.08 | 1.08 | 0.19 | 1.06 | 0.14 | -1.15 | 0.14 | -1.27 | 0.09 | -1.39 | 0.13 | -1.18 | 0.16 | -1.35 | 0.12 | -1.16 | 0.11 |
| *tapbp* | 1.44 | 0.17 | -1.06 | 0.21 | 1.03 | 0.26 | 1.34 | 0.21 | 1.23 | 0.22 | 1.06 | 0.12 | -1.33 | 0.17 | -1.08 | 0.21 | 1.11 | 0.15 | 1.00 | 0.11 |
| *txn* | 2.46 | 1.01 | 1.23 | 0.30 | -1.12 | 0.13 | 1.41 | 0.44 | 1.77 | 0.33 | 1.72 | 0.59 | -1.64 | 0.15 | -1.72 | 0.10 | 1.72 | 0.20 | 2.01 | 0.41 |
| *tnfrsf6b* | 1.28 | 0.27 | 1.33 | 0.21 | 2.18 | 0.46 | 4.33 | 1.48 | 4.01 | 0.93 | 3.92 | 1.10 | 1.67 | 0.46 | 2.91 | 0.74 | 2.84 | 0.89 | 2.46 | 0.62 |
| *ucp2* | 1.45 | 0.13 | 1.05 | 0.15 | -1.79 | 0.09 | -1.79 | 0.07 | -2.33 | 0.06 | -2.50 | 0.05 | -5.88 | 0.04 | -6.25 | 0.03 | -4.17 | 0.04 | -3.57 | 0.05 |

The fold-change (FC) ratios with the standard errors of means (SEM) for the Warm & Normoxic (WN) and Warm & Hypoxic (WH) treatment groups in comparison to the control group (CT) within each temperature point (12°C, 16°C-3d, 18°C-3d, 20°C-3d and 20°C-4wks) are listed for each gene in alphabetical order.