# Supplementary Material

## Supplementary Figures



**Supplementary Figure 1.**Correlogram showing significant (*p*< 0.05) Spearman correlation (*r*S, colored circles) between baseline expression of 13 genes in northern elephant seal skeletalmuscle. Circle color denotes direction of relationship (brown: positive, green: negative), while size of circles and color intensity denote magnitude of correlation.



**Supplementary Figure 2.**Correlogram showing significant (*p*< 0.05) Spearman correlation (*r*S, colored circles) between baseline expression of 10 genes in northern elephant seal whole blood. Circle color denotes direction of relationship (brown: positive, green: negative), while size of circles and color intensity denote magnitude of correlation.

## Supplementary Tables

**Supplementary Table1.**Age class, fasting state, sex, and year sampled for animals used in the study.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Animal ID** | **Age Class** | **Fasting State** | **Sex** | **Year Sampled** |
| pup1 | pup | early | male | 2020 |
| pup2 | pup | early | female | 2020 |
| pup3 | pup | early | male | 2020 |
| pup4 | pup | early | male | 2020 |
| pup5 | pup | early | female | 2020 |
| pup6 | pup | early | female | 2020 |
| pup7 | pup | early | female | 2020 |
| pup8 | pup | late | male | 2020 |
| pup9 | pup | late | male | 2020 |
| pup10 | pup | late | male | 2020 |
| pup11 | pup | late | female | 2020 |
| pup12 | pup | late | male | 2020 |
| pup13 | pup | late | male | 2020 |
| pup14 | pup | late | male | 2020 |
| pup15 | pup | late | male | 2020 |
| juv2 | juvenile | early | female | 2017 |
| juv15 | juvenile | early | male | 2017 |
| juv16 | juvenile | early | male | 2017 |
| juv18 | juvenile | early | NA | 2017 |
| juv19 | juvenile | early | male | 2017 |
| juv20 | juvenile | early | female | 2017 |
| juv23 | juvenile | early | male | 2017 |
| juv28 | juvenile | early | female | 2017 |
| juv29 | juvenile | early | female | 2017 |
| fem\_early\_6 | adult | early | female | 2020 |
| fem\_early\_7 | adult | early | female | 2020 |
| fem\_early\_8 | adult | early | female | 2021 |
| fem\_early\_9 | adult | early | female | 2021 |
| fem\_early\_10 | adult | early | female | 2021 |
| fem\_early\_11 | adult | early | female | 2021 |
| fem\_late\_2 | adult | late | female | 2020 |
| fem\_late\_3 | adult | late | female | 2020 |
| fem\_late\_4 | adult | late | female | 2020 |
| fem\_late\_5 | adult | late | female | 2020 |
| fem\_late\_6 | adult | late | female | 2020 |
| fem\_late\_7 | adult | late | female | 2021 |
| fem\_late\_8 | adult | late | female | 2021 |
| male\_early\_1 | adult | early | male | 2020 |
| male\_early\_2 | adult | early | male | 2020 |
| male\_early\_3 | adult | early | male | 2020 |
| male\_early\_4 | adult | early | male | 2020 |
| male\_early\_5 | adult | early | male | 2020 |
| male\_late\_6 | adult | late | male | 2020 |
| male\_late\_7 | adult | late | male | 2020 |
| male\_late\_8 | adult | late | male | 2020 |
| male\_late\_10 | adult | late | male | 2020 |
| male\_late\_11 | adult | late | male | 2020 |
| male\_late\_12 | adult | late | male | 2020 |

**Supplementary Table 2.**Sequences and amplification efficiencies for qPCR primers used in the study. Primers were designed using sequences from NES muscle and blubber transcriptomes (Khudyakov et al., 2015; Deyarmin et al., 2019).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  **Gene**  |  **Transcript ID** |  **Protein name** |  **Primer sequence (5' to 3')** |  **E%** |
|  *HMOX1* |  TRINITY\_DN582021\_c0\_g5 | Heme oxygenase 1  | F: CTGGTGATGGCCTCTCTTTACC R: GCGTAGACCGGGTTGTCC | 97.8 |
|  *HMOX2* |  TRINITY\_DN573552\_c5\_g3 | Heme oxygenase 2 | F: CACACTCGGCAACGATGTCAR: CTCAGAGAGGTCAGCCATCCT | 99.5 |
|  *BVR* |  tr486081 | Biliverdin reductase | F: CTGGGTCTCTGGAGAATATGCCR: GCCCAGGAGTTTCTGGACAA | 93.3 |
|  *GPX3* |  tr295337 | Glutathione peroxidase 3 | F: TAGCTGGCCACGTTGACAAAR: GTGAGCGGCACCATCTATGA | 95.9 |
|  *NRF2* |  tr11361 | Nuclear factor erythroid 2-related factor | F: GCTGCGTTTCAGTCACTTGTTR: GTTTGAGGTGACTGAGCCTGA | 96.9 |
|  *PGC1A* |  tr433035 | Peroxisome proliferator activated receptor gamma coactivator 1-alpha | F: GAGGAGGAGTTGTGGGTGGA R: ACCCCAAGGGTTCCCCATTT | 87.3 |
|  *IL1B* |  tr50419 | Interleukin-1 beta  | F: CCGTCGTCTGTGAGGTGTATR: ACAGCACCAGGGATTTTTGG | 101.6 |
|  *ESRRA* |  tr210045 | Estrogen-related receptor alpha | F: CACACCCAACACCAAGACCTR: CAGGCTTCTCGTCACTGTCA | 84.0 |
|  *ESRRG* |  tr348270 | Estrogen-related receptor gamma | F: GTCCCCGACAGTGACATCAAR: CCTGGAATATGCTTCGCCCA | 106.9 |
|  *EF2* |  tr388769 | Elongation factor 2 | F: TGGCCAAATTTGCTGCCAAGR: CTTGCTGAATTTGCCGTTGG | 100.7 |
|  *GAPDH* |  tr223210 | Glyceraldehyde 3 phosphate dehydrogenase | F: CAGAACATCATCCCTGCCTCR: TGCTTCACCACCTTCTTGA | 97.2 |
|  *SIRT1* | tr23215 | NAD-dependent protein deacetylase sirtuin-1 | F: ACCACCAGATTCTTCAGCGATR: TTTGATTCGGACACACCAGGA | 90.6 |
|  *PRDX1* | tr139285 | Peroxiredoxin 1 | F: GCTCTTCTGGACATCAGGCTR: TGGTTCAGGCCTTCCAGTTT | 90.2 |
|  *PRDX6* | tr94909 | Peroxiredoxin 6 | F: GCACCACAGAGCTTGGCAGAR: AGGATGGCAAGGTCCCGATT | 95.6 |
|  *GPX4* | tr448784 | Phospholipid hydroperoxide glutathione peroxidase | F: AAGTACCGGGGCTTCGTGTGR: CCAGCGGCGAACTCTTTGAT | 93.8 |
|  *IL10* | tr225261 | Interleukin 10 | F: AGAGGTGTCTACAAAGCCATGAR: GTTTTGTTCCCCAGCCTGTTT | 100.8 |
|  *CCL4* | TRINITY\_DN588869\_c10\_g1 | C-C motif chemokine 4  | F: CACCGCCTGCTGCTTTTCTTR: AGAGGCTGCTCGTCTCGAAG | 104.6 |
|  *TLR4* | tr82854 | Toll-like receptor 4 | F: GGTGGCATTTGGCTCACTTCR: TTGGAGGGAGAGGAGAGGTT | 92.8 |
|  *TNFA* | TRINITY\_DN591924\_c5\_g5 |  Tumor necrosis factor  | F: TGGAATCATTGCCCTGTGAGGR: CTAAGCCAGAAGGGGATGAGG | 95.0 |

**Supplementary Table3.**PCA diagnostics (Field et al., 2012) for skeletal muscle and whole blood gene expression datasets.

|  |  |  |
| --- | --- | --- |
|  | Muscle PCA | Blood PCA |
| Number of genes | 13 | 10 |
| Determinant  | 0.0001 | 0.0002 |
| Barlett’s test  | 𝛘2 (78) = 364.03p < 0.0001 | 𝛘2 (45) = 237.91p < 0.0001 |
| KMO test | overall MSA = 0.73 | overall MSA = 0.73 |
| Mean communality | 0.77 | 0.79 |