**Table S1.** Illumina sequencing data for analyzed samples

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Samples | Raw Reads Number | Clean Reads Number | Base Number (Gbp) | GC Content (%) | %≥Q30 |
| CK1-LM | 28,737,984 | 26,102,782 | 6.57 | 48.81% | 91.71% |
| CK2-LM | 28,679,082 | 26,042,739 | 6.56 | 49.01% | 91.31% |
| CK3-LM | 34,655,748 | 31,035,722 | 7.81 | 49.14% | 91.03% |
| Ahyp1-LM | 34,186,302 | 30,998,199 | 7.81 | 49.38% | 91.60% |
| Ahyp2-LM | 34,271,893 | 31,245,688 | 7.87 | 49.17% | 91.81% |
| Ahyp3-LM | 35,535,955 | 32,083,280 | 8.08 | 49.48% | 91.33% |
| CK1-LB | 39,107,546 | 35,420,510 | 8.92 | 50.01% | 91.43% |
| CK2-LB | 35,050,234 | 32,039,776 | 8.07 | 49.46% | 91.43% |
| CK3-LB | 32,946,493 | 29,979,937 | 7.55 | 49.15% | 91.34% |
| A-hyp1-LB | 32,069,055 | 29,343,366 | 7.39 | 49.53% | 91.70% |
| A-hyp2-LB | 31,701,790 | 28,665,533 | 7.22 | 49.76% | 90.39% |
| A-hyp3-LB | 31,601,342 | 28,718,261 | 7.24 | 49.36% | 91.69% |
| Total | 398,543,424 | 361,675,793 | 91.09 |  |  |

Notes: **Samples**: Sample name; **Raw Reads** **Number**: The reads amount before filtering; **Clean Reads Number**: The reads amount after filtering; **Clean Bases Number**: The total base amount after filtering; **GC Content (%)**: the percentage of G and C bases in all Clean reads; **%≥Q30**: The rate of bases which quality is greater than 30 value in clean reads.

**Table S2.** Length distribution and quality metrics of unigenes from the *L. mandarinus* and *L.* *brandtii*

|  |  |  |
| --- | --- | --- |
| Length Range (bp) | *L. mandarinus* | *L.* *brandtii* |
|  200- 300 | 31,952 | 32,598 |
|  300- 500 | 18,365 | 19,543 |
|  500-1000 | 12,354 | 12,932 |
| 1000-2000 |  8,782 |  8,620 |
| >2000 |  9,525 |  9,751 |
| Total Number | 80,978 | 83,444 |

Notes: **Length Range:** Length distribution of assembled unigenes; **Total Number:** The total number of Unigenes;

**Table S3.** Functional annotation results for *L. mandarinus* and *L.* *brandtii* transcriptomes

|  |  |  |
| --- | --- | --- |
| Database | *L. mandarinus* | *L.* *brandtii* |
| GO | 16165 | 16034 |
| KEGG | 12780 | 12458 |
| KOG | 13105 | 12993 |
| Swissprot | 16700 | 17084 |
| Nr | 21012 | 20126 |
| All | 25316 | 25950 |

**Table S4.** Annotated DEGs for *L. mandarinus* and *L.* *brandtii*



**Table S5.** GO terms significant enriched for up- and downregulated DEGs in *L. mandarinus* and *L.* *brandtii*

|  |  |
| --- | --- |
| ***L. mandarinus*** | ***L. brandtii*** |
| **Up-regulated** | **Up-regulated** |
| **GO terms** | **Ontology** | **GO ID** | ***P* value** | **GO terms** | **Ontology** | **GO ID** | ***P* value** |
| Extracellular region | CC | 0005576 | 0.000 | Extracellular region part | CC | 0044421 | 0.000 |
| Extracellular region part | CC | 0044421 | 0.000 | Extracellular region | CC | 0005576 | 0.000 |
| Extracellular matrix  | CC | 0031012 | 0.003 | Extracellular matrix | CC | 0031012 | 0.001 |
| Response to stimulus | BP | 0050896 | 0.001 | Immune system process | BP | 0002376 | 0.002 |
| Biological regulation | BP | 0065007 | 0.001 | Cellular response to stimulus | BP | 0051716 | 0.025 |
| Cell communication | BP | 0007154 | 0.002 | Response to stimulus | BP | 0050896 | 0.037 |
| Cellular response to stimulus | BP | 0051716 | 0.002 | Biological regulation | BP | 0065007 | 0.045 |
| Response to stress | BP | 0006950 | 0.004 | Catalytic activity, acting on aprotein | MF | 0140096 | 0.002 |
| Growth | BP | 0040007 | 0.026 | DNA-binding transcription factor activity | MF | 0003700 | 0.005 |
| DNA-binding transcriptionfactor activity | MF | 0001071 | 0.013 |  |  |  |  |
| Helicase activity | MF | 0004386 | 0.027 |  |  |  |  |
| **Down-regulated** | **Down-regulated** |
| Cell proliferation | BP | 0008283 | 0.013 | Locomotion | BP | 0040011 | 0.002 |
| Transmembrane transport | BP | 0055085 | 0.013 | Anatomical structure development | BP | 0048856 | 0.003 |
| DNA binding | MF | 0003677 | 0.001 | Developmental process | BP | 0032502 | 0.003 |
| Transmembrane transporter activity | MF | 0022857 | 0.001 | Anatomical structure morphogenesis | BP | 0009653 | 0.020 |
| Nucleic acid binding  | MF | 0003676 | 0.001 | Multicellular organism development | BP | 0007275 | 0.023 |
| Transcription factor binding | MF | 0008134 | 0.036 | Cell motility | BP | 0048870 | 0.039 |
| DNA-binding transcription factor activity | MF | 0003700 | 0.003 | DNA-binding transcription factor activity | MF | 0003700 | 0.002 |
|  |  |  |  | DNA binding | MF | 0003677 | 0.000 |
|  |  |  |  | Binding | MF | 0005488 | 0.002 |
|  |  |  |  | Nucleic acid binding | MF | 0003676 | 0.003 |
|  |  |  |  | Ion binding | MF | 0043167 | 0.024 |
|  |  |  |  | Nuclease activity | MF | 0004518 | 0.030 |
|  |  |  |  | Hydrolase activity, acting on ester bonds | MF | 0016788 | 0.046 |
|  |  |  |  | Extracellular space | CC | 0005615 | 0.007 |

Notes: Terms with *P* < 0.05 are shown, with a Benjamini-Hochberg correction or false discovery rate. BP: biological process; CC: cellular component; MF: molecular function.

**Table S6.** KEGG pathways enriched for up- and downregulated DEGs in *L. mandarinus* and *L.* *brandtii* under acute hypoxia

|  |  |
| --- | --- |
| ***L. mandarinus*** | ***L. brandtii*** |
| **Up-regulated** | **Up-regulated** |
| **Pathway** | **Map ID** | ***adj.P value*** | **Pathway** | **Map ID** | ***adj.P value*** |
| HTLV-I infection | 05166 | 0.038 | Proteoglycans in cancer | 05205 | 0.000 |
| Proteoglycans in cancer | 05205 | 0.040 | HIF-1 signaling pathway | 04066 | 0.000 |
| Hippo signaling pathway | 04390 | 0.040 | Transcriptional misregulation in cancers | 05202 | 0.000 |
| p53 signaling pathway | 04115 | 0.040 | MicroRNAs in cancer | 05206 | 0.000 |
|  |  |  | TNF signaling pathway | 04668 | 0.000 |
|  |  |  | HTLV-I infection | 05166 | 0.004 |
|  |  |  | NF-kappa B signaling pathway | 04064 | 0.004 |
|  |  |  | Pathways in cancer | 05200 | 0.007 |
|  |  |  | p53 signaling pathway | 04115 | 0.008 |
|  |  |  | NOD-like receptor signaling pathway | 04621 | 0.007 |
|  |  |  | Basal cell carcinoma | 05217 | 0.010 |
|  |  |  | PI3K-Akt signaling pathway | 04151 | 0.010 |
|  |  |  | Bladder cancer | 05219 | 0.010 |
|  |  |  | Central carbon metabolism in cancer | 05230 | 0.023 |
|  |  |  | Hippo signaling pathway | 04390 | 0.023 |
|  |  |  | Hypertrophic cardiomyopathy (HCM) | 05410 | 0.024 |
|  |  |  | Melanogenesis | 04916 | 0.030 |
|  |  |  | Signaling pathways regulating pluripotency of stem cells | 04550 | 0.038 |
| **Down-regulated** | **Down-regulated** |
| Amyotrophic lateral sclerosis (ALS) | 05014 | 0.018 | Transcriptional misregulation in cancers | 05202 | 0.034 |

Notes: Pathways with *adj.P value* < 0.05 are shown, with a Benjamini-Hochberg correction or false discovery rate.

**Table S7**.Results of RNA extraction from *L. mandarinus* and *L. brandtii* brain tissue

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample | RNA Concentration (ng/μl) | OD260/280 | OD260/230 | 28S/18S | RNA Integrity Number(RIN) |
| M1 | 398 | 2.010 | 2.095 | 1.4 | 9.2 |
| M2 | 556 | 2.059 | 2.000 | 1.2 | 9.1 |
| M3 | 498 | 2.041 | 1.886 | 1.1 | 7.7 |
| M4 | 622 | 2.033 | 2.073 | 1.2 | 8.9 |
| M5 | 616 | 2.026 | 2.110 | 1.4 | 9.2 |
| M6 | 612 | 2.068 | 2.155 | 1.2 | 9.0 |
| B1 | 934 | 2.066 | 1.639 | 1.2 | 8.9 |
| B2 | 516 | 2.048 | 1.623 | 1.2 | 8.9 |
| B3 | 412 | 2.124 | 2.124 | 1.2 | 8.8 |
| B4 | 540 | 2.045 | 2.143 | 1.4 | 8.9 |
| B5 | 674 | 2.055 | 1.926 | 1.3 | 8.8 |
| B6 | 834 | 2.085 | 2.183 | 1.4 | 9.1 |

Notes: M: *L. mandarinus*; B: *L. brandtii*; The numbers 1, 2, 3 represent samples from the control group, and the numbers 4, 5, and 6 represent samples from the acute hypoxic treatment group.

**Table S8.** RT-qPCR primers for validation of RNA-Seq data

|  |  |  |  |
| --- | --- | --- | --- |
| Gene | Primer-Forward | Primer-Reverse | Efficiency |
| PER3 | GCATTGCAGGCAAGACTGAG | CAAGACCAGTATGCAGGAGT | 1.28 |
| TIMP3 | GCAAGGACCTCAATTACCG | AGGCGTAGTGTATGGACTGATA | 0.98 |
| THBS1 | GGAGATAACGGTGTGTTTG | CGGAGATCAGGTTGGCAT | 1.13 |
| HK1 | GAGTCTGAGGTCTACGACACC | CCCACGGGTAATTTCTTGTCC | 1.24 |
| EGR1 | GGCCCCTGGTGCTACATAATG | AGGAAGCTACAAATCGGGCAT | 1.08 |
| SERPINE1 | AGCAAGCGGGAAGAAGAGTC | CAGGGTGAGGCAAGCTAGTG | 0.88 |
| *β*-actin | GTCGTACCACTGGCATTGTG | CCATCTCTTGCTCGAAGTCC | 1.05 |

**Table S9.** Characteristics of *L. mandarinus* and *L. brandtii* samples

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample | Age/weeks | Gender | Body length/cm | Weight/g | Brain weight/g |
| M1 | 12 | Male | 9.5 | 40.47 | 0.5203 |
| M2 | 12 | Male | 8.5 | 40.29 | 0.5135 |
| M3 | 12 | Male | 9.0 | 41.72 | 0.5278 |
| M4 | 12 | Male | 8.9 | 43.21 | 0.5425 |
| M5 | 12 | Male | 8.2 | 40.92 | 0.5267 |
| M6 | 12 | Male | 7.9 | 40.27 | 0.5262 |
| B1 | 12 | Male | 8.4 | 42.41 | 0.5531 |
| B2 | 12 | Male | 8.9 | 40.35 | 0.5141 |
| B3 | 12 | Male | 8.0 | 43.48 | 0.5215 |
| B4 | 12 | Male | 9.8 | 40.75 | 0.5112 |
| B5 | 12 | Male | 8.4 | 43.12 | 0.5214 |
| B6 | 12 | Male | 8.9 | 43.39 | 0.5177 |

Notes: M: *L. mandarinus*; B: *L. brandtii*; The numbers 1, 2, 3 represent samples from the control group, and the numbers 4, 5, and 6 represent samples from the severe hypoxic treatment group.