

Supplementary Materials

Supplementary Table S1 Quality parameters of RNA extracted from heart tissue of *N. fuscus*, *L. brandtii*, and *M. musculus*.

Sample name	RNA concentration (ng/ μ l)	OD260/280	OD260/230	RNA integrity number (RIN)
CK-NF-1	219	2.07	2.16	8.0
CK-NF-2	307	2.01	2.26	8.1
CK-NF-3	612	2.06	2.31	7.5
HY-NF-1	350	2.02	2.36	8.0
HY-NF-2	362	2.08	2.26	8.0
HY-NF-3	126	2.05	2.27	7.8
CK-LB-1	352	2.06	2.06	7.9
CK-LB-2	332	2.01	2.11	7.8
CK-LB-3	396	2.02	2.23	7.7
HY-LB-1	585	2.01	2.29	8.2
HY-LB-2	926	2.02	2.32	8.1
HY-LB-3	419	2.13	2.32	8.2
CK-MU-1	667	2.01	2.13	8.2
CK-MU-2	434	2.02	2.03	8.2
CK-MU-3	328	2.08	2.17	8.1
HY-MU-1	462	2.01	2.12	8.2
HY-MU-2	531	2.08	2.27	8.8
HY-MU-3	297	2.05	2.24	8.1

Notes: CK: normoxia; HY: hypoxia; NF: *N. fuscus*; LB: *L. brandtii*; MU: *M. musculus*; 1-3 represents the individual number.

Supplementary Table S2 Illumina HiSeq sequencing of analyzed samples in heart tissue.

Sample name	Raw reads number	Clean reads number	Error rate (%)	Clean reads GC content (%)	Clean reads Q30 (%)	Total clean bases (G)
CK-NF-1	68 835 386	67 059 922	0.02	48.16	95.37	10.06
CK-NF-2	67 236 868	66 390 080	0.02	48.36	95.37	9.96
CK-NF-3	72 726 640	72 037 496	0.02	48.48	95.31	10.81
HY-NF-1	58 411 642	57 101 610	0.02	48.09	96.69	8.57
HY-NF-2	57 400 444	55 522 398	0.02	48.29	96.69	8.33
HY-NF-3	60 695 672	59 549 612	0.02	48.58	96.78	8.93
CK-LB-1	58 332 720	57 374 788	0.02	46.59	95.05	8.61
CK-LB-2	53 711 202	52 944 392	0.02	46.62	95.10	7.94
CK-LB-3	45 329 340	44 937 434	0.02	46.16	96.44	6.74
HY-LB-1	55 247 724	53 968 842	0.02	46.57	96.38	8.10
HY-LB-2	52 582 468	52 143 544	0.02	46.53	96.50	7.82
HY-LB-3	63 825 580	63 168 884	0.02	46.49	96.31	9.48
CK-MU-1	47 305 590	46 455 370	0.02	46.51	95.30	6.97
CK-MU-2	47 426 120	46 848 840	0.02	46.72	95.14	7.03
CK-MU-3	45 301 130	44 740 226	0.02	46.74	96.56	6.71
HY-MU-1	64 392 188	63 257 508	0.02	45.92	96.44	9.49
HY-MU-2	53 727 288	52 801 036	0.02	46.34	96.44	7.92
HY-MU-3	62 596 254	61 936 902	0.02	45.67	95.15	9.29
Total	1 035 084 256	1 018 238 884	-	-	-	152.76

Notes: CK: normoxia; HY: hypoxia; NF: *N. fuscus*; LB: *L. brandtii*; MU: *M. musculus*; 1-3 represents the individual number.

Supplementary Table S3 Length distribution of unigenes in *N. fuscus*, *L. brandtii*, and *M. musculus*.

Length range(bp)	<i>N. fuscus</i>	<i>L. brandtii</i>	<i>M. musculus</i>
200-300	5 312	3 596	5 596
300-500	51 257	42 761	46 635
500-1000	56 614	49 862	48 729
1000-2000	21 259	18 401	18 506
> 2000	18 750	17 679	17 570
Total number	153 192	132 299	137 036

Supplementary Table S4 Functional annotation of unigenes in *N. fuscus*, *L. brandtii*, and *M. musculus*.

Database	<i>N. fuscus</i>	<i>L. brandtii</i>	<i>M. musculus</i>
Nr	39 110 (25.53%)	37 302 (28.20%)	41 306 (30.14%)
SwissProt	33 455 (21.84%)	32 025 (24.21%)	33 001 (24.08%)
KOG	24 113 (15.74%)	23 124 (17.48%)	23 144 (16.89%)
EggNOG	31 573 (20.61%)	30 685 (23.19%)	31 155 (22.73%)
KEGG	22 215 (14.50%)	21 910 (16.56%)	21 515 (15.70%)
GO	28 280 (18.46%)	27 838 (21.04%)	27 480 (20.05%)
Total	44 404 (28.99%)	41 384 (31.28%)	45 967 (33.54%)

Supplementary Table S5 Number of DEGs annotated in Nr, Swiss-Prot, KEGG, and EggNOG databases.

Database	<i>N. fuscus</i>	<i>L. brandtii</i>	<i>M. musculus</i>
Nr	183	186	350
SwissProt	165	171	330
KEGG	169	169	334
EggNOG	114	145	273
All	190	192	380

Supplementary Table S6 Annotated DEGs in *N. fuscus*, *L. brandtii*, and *M. musculus*.

[DEGs annotated information.xlsx](#)

Supplementary Table S7 GO terms enriched in *N. fuscus*, *L. brandtii*, and *M. musculus* DEGs.

[GO enrichment results.xlsx](#)

Supplementary Table S8 KEGG pathways enriched in *N. fuscus*, *L. brandtii*, and *M. musculus* DEGs.

[KEGG enrichment results.xlsx](#)

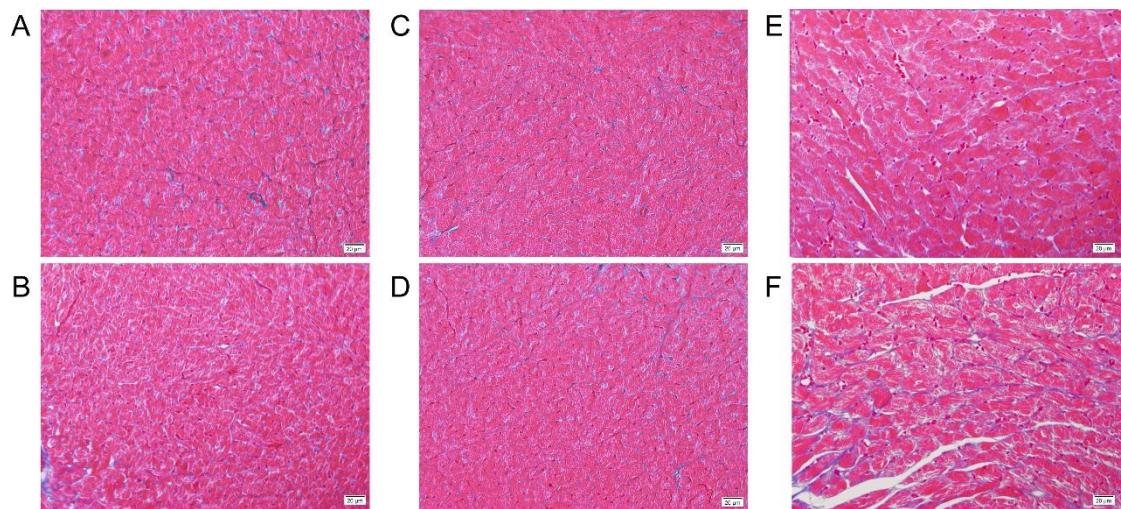
Supplementary Table S9 qRT-PCR primers for validation of RNA-seq data.

Gene	<i>N. fuscus</i> and <i>L. brandtii</i>	<i>M. musculus</i>
<i>Alas2</i>	F: CAGCCCCAGAAGTCCAAG R: ATTACACAGTCTAACACACACGGTA	F: TACCAGCAAGTTCATGTGGA R: CACTGTTGCGAATGCCTT
<i>Ehhad</i>	F: CAGCTCTCCCCAGACTCGT R: CATCAGCGAAAATGCCGTCCA	F: ACTTGTGTCCGTTAGTCAGTCCA R: TTCCAAGCCAAGAACACC
<i>Hba</i>	F: ACTCAGAGCAGACAGGGCAC R: AGACCAACATCAAGACTGCCT	F: TCTGGGAAAGACAAAAGCAACA R: GACCTTCTGCCGTGACCCCTT
<i>Map3k6</i>	F: GATCGCTCTCACAAACGACT R: ACGTGTGTAGAAACTAATAGTACTCT	F: ACCCCTAAAGGACAACGAGA R: AGCTGCCTCCCATTATCCTC
<i>Myoc</i>	F: GTACACAGTCAGCAGCTACTCT R: GTGACCATGTTGAAGTTGTCCC	F: TTTGAGTACAGTCAGATAAGCCAGT R: CTTCTCTGCCTTCACGGTCT
<i>Rsd2</i>	F: TTAGCGTCAACTACCACTTCACC R: CGAGCTTACCCACGTATTCAACC	F: TTGAAACATTCTGGAGCGTCAC R: CATACTTCCGCCACGCTTC
β -actin	F: ACATCGTAAAGACCTCTATGCC R: TACTCCTGCTTGCTGATCCAC	F: ACATCGTAAAGACCTCTATGCC R: TACTCCTGCTTGCTGATCCAC

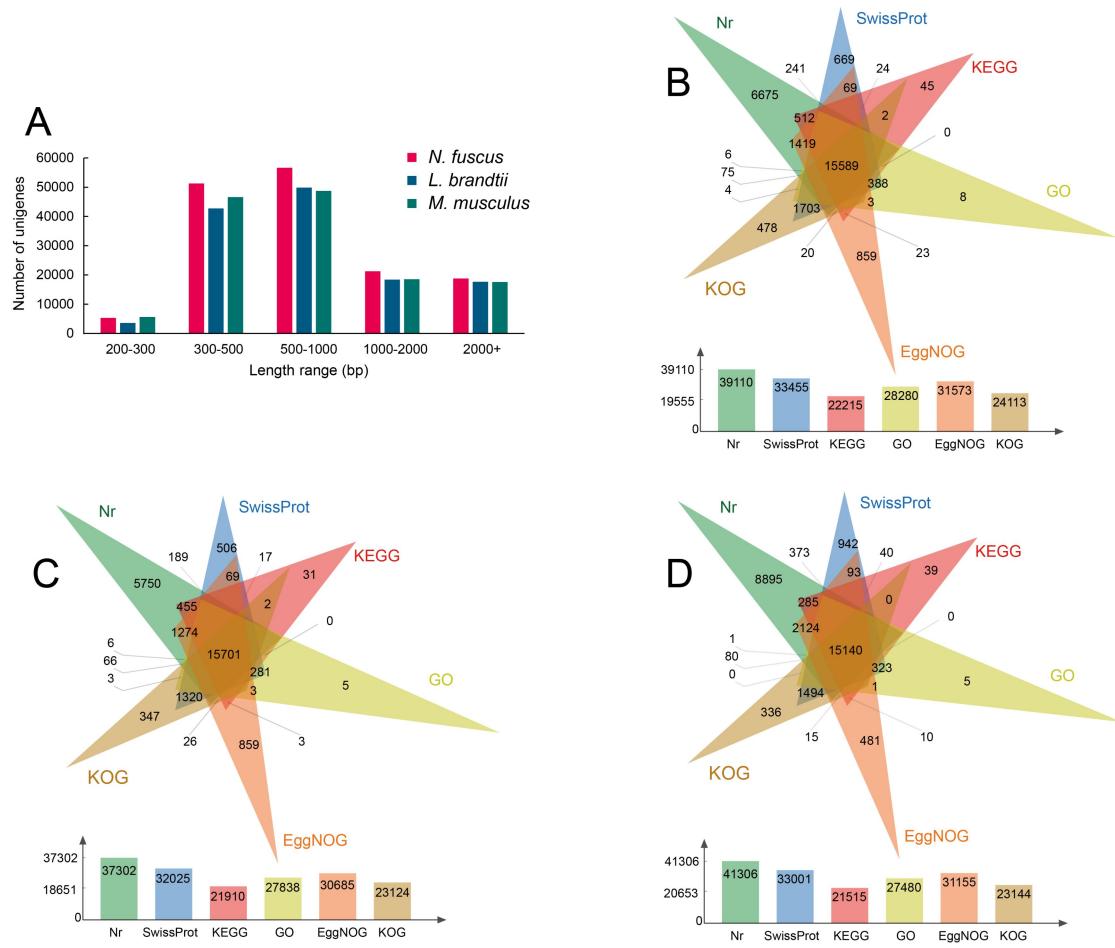
Supplementary Table S10 PPI network functional clusters of DEGs in *N. fuscus*, *L. brandtii*, and *M. musculus*.

[Functional cluster results of proteins encoded by DEGs.xlsx](#)

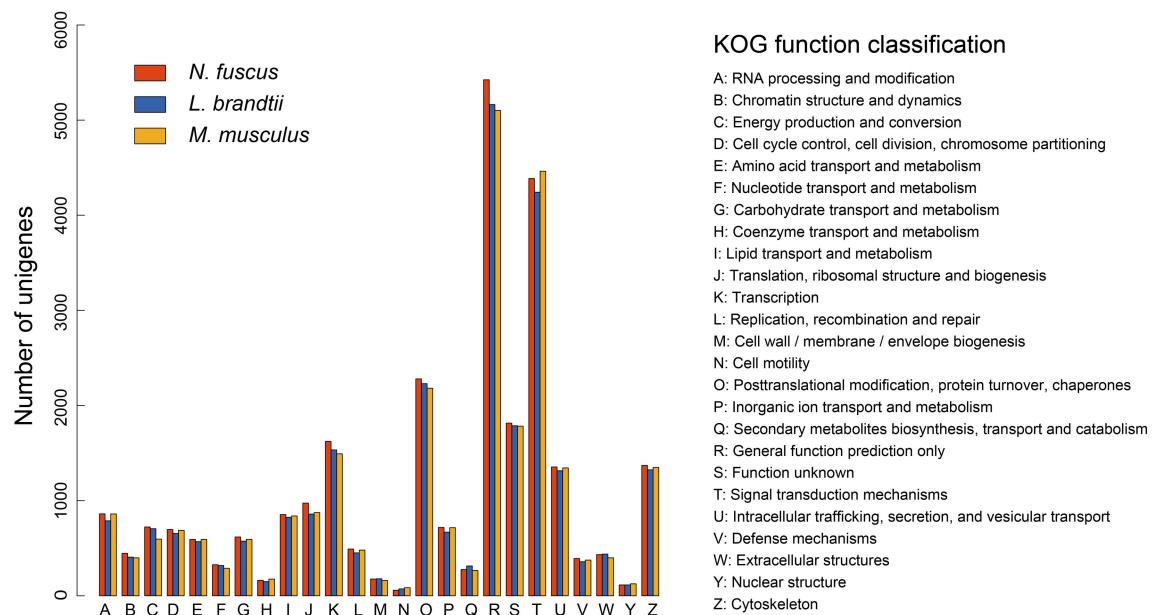
Supplementary Tables S6, S7, S8, S10 are listed as separate excel files due to their large size.



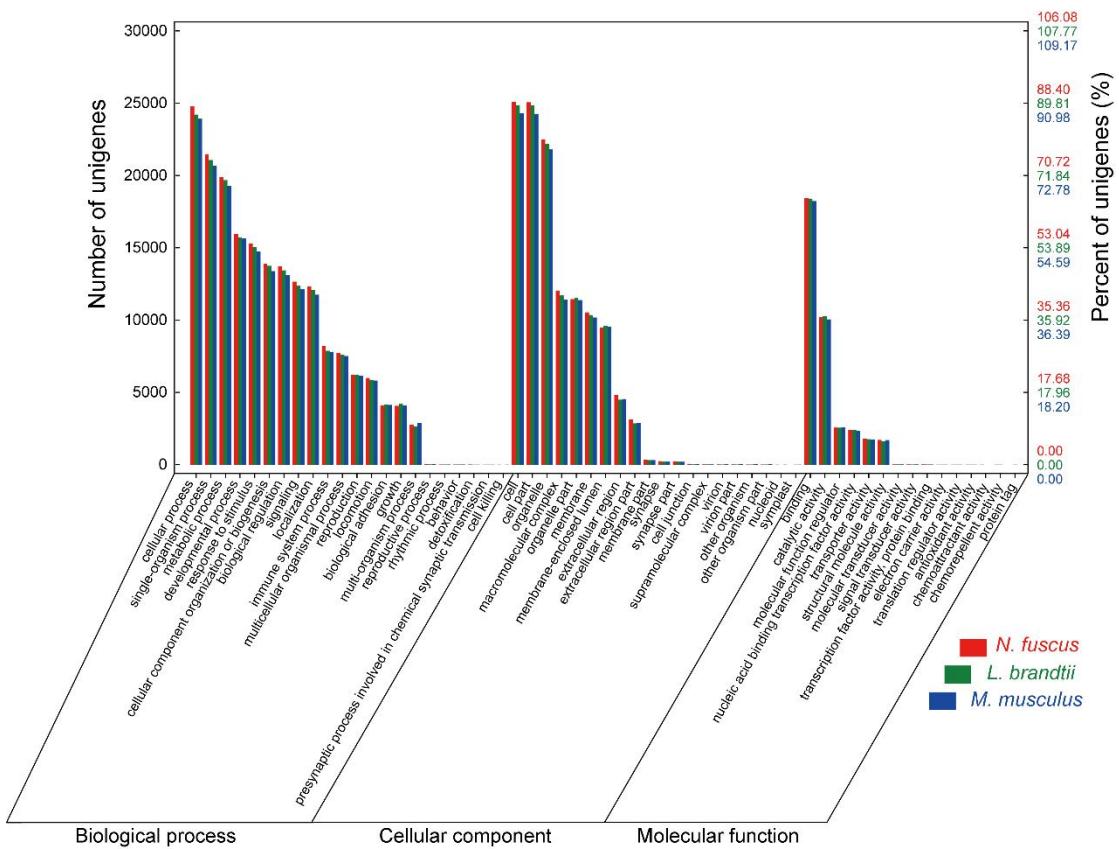
Supplementary Figure S1 Masson staining of heart tissue in *N. fuscus* (A, B), *L. brandtii* (C, D), and *M. musculus* (E, F). Heart tissue morphology of three species under normoxia (A, C, E) and hypoxia (B, D, F). 400 \times magnification.



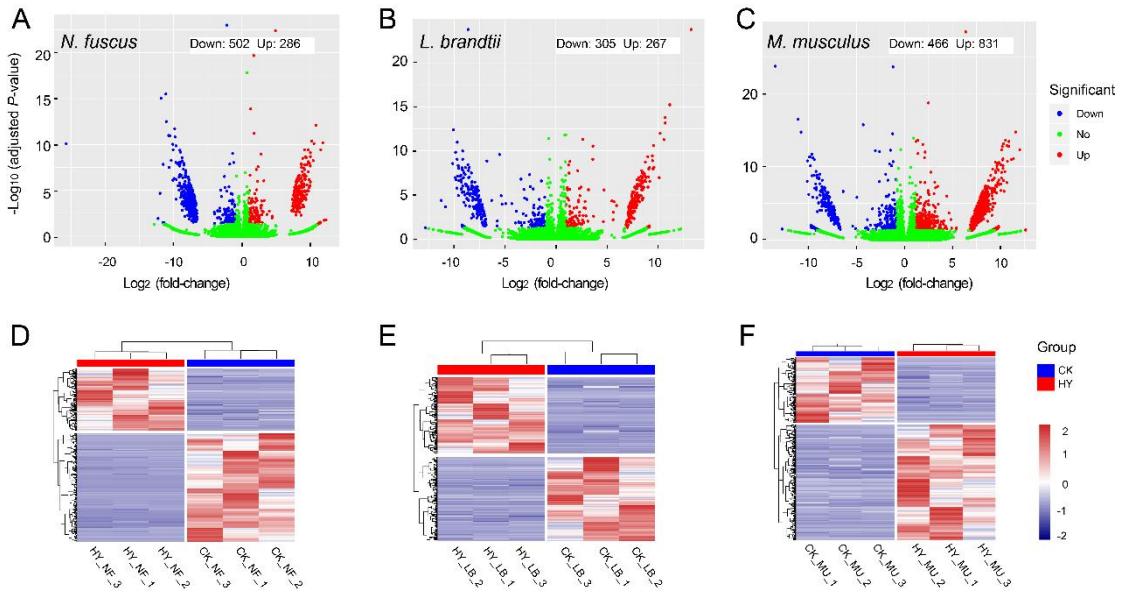
Supplementary Figure S2 Length distribution (A) and annotation of unigenes in *N. fuscus* (B), *L. brandtii* (C), and *M. musculus* (D).



Supplementary Figure S3 KOG functional classification of unigenes in *N. fuscus*, *L. brandtii*, and *M. musculus*.



Supplementary Figure S4 GO functional classification of unigenes in *N. fuscus*, *L. brandtii*, and *M. musculus*.



Supplementary Figure S5 Volcano plots (A, B, C) and heatmap (D, E, F) of DEGs (adjusted $P < 0.05$ and $|\log_2(\text{fold-change})| \geq 1$) in *N. fuscus*, *L. brandtii*, and *M. musculus* under normoxic and hypoxic conditions.