

## SUPPLEMENTARY TABLES

Supplementary Table 3. Information of *M. myotis* and *M. molossus* RNA-Seq samples.

Species	Sample ID	Age	Sex	Raw reads	Clean reads
<i>M. molossus</i>	AHKX-1	Adult	Female	32,087,001	29,122,203
	AHKX-2	Adult	Male	39,138,864	35,776,979
	AHKX-3	Adult	Female	34,994,963	32,206,385
	AHKX-4	Adult	Male	42,599,132	38,612,182
	AHKX-5	Adult	Female	44,567,553	40,710,399
	AHKX-6	Adult	Female	39,533,956	36,065,884
	AHKX-7	Adult	Male	41,315,334	38,443,201
	AHKX-8	Adult	Female	41,544,292	38,563,116
<i>M. myotis</i>	AJCC-7	Adult	Female	69,608,563	63,479,697
	AJCC-9	Adult	Female	56,347,739	50,896,083
	AJCC-11	Adult	Female	57,600,266	54,034,263
	AJCC-13	Adult	Female	75,867,273	70,421,670
	AJCC-17	Adult	Female	61,537,380	55,193,047
	AJCC-18	Adult	Female	66,857,830	60,145,110
	AJCC-22	Adult	Female	60,840,476	55,478,542
	AJCC-27	Adult	Female	69,521,460	63,916,035

**Supplementary Table 4. The expression of anti- and pro-longevity genes in *M. myotis* and *M. molossus*.**

<b>TMM normalized expression of anti-longevity genes</b>			
<b>Gene</b>	<b>Description</b>	<b><i>M. myotis</i></b>	<b><i>M. molossus</i></b>
<i>INSR</i>	Insulin receptor	2792.163	5929.826
<i>GSTA4</i>	Glutathione S-transferase Alpha 4	89.007	1284.609
<i>TERF2</i>	Telomeric repeat binding factor 2	251.694	31.528
<i>COQ7</i>	Coenzyme Q7, Hydroxylase	57.091	328.937
<i>EIF5A2</i>	Eukaryotic translation initiation factor 5A2	27.979	21.402
<i>EEF1E1</i>	Eukaryotic translation elongation factor 1 Epsilon 1	20.796	5.661
<i>EPS8</i>	Epidermal growth factor receptor pathway substrate 8	139.443	1.307
<i>CDKN1A</i>	Cyclin dependent kinase inhibitor 1A	10.976	43.224
<i>MTOR</i>	Mechanistic target of rapamycin kinase	279.099	285.992
<i>BAX</i>	BCL2 associated X, apoptosis regulator	14.122	22.982
<i>PARP1</i>	Poly(ADP-ribose) polymerase 1	74.309	233.679
<i>SHC1</i>	SHC adaptor protein 1	25.109	57.983
<i>KCNA3</i>	Potassium voltage-gated channel subfamily A member 3	15.122	36.579
<i>IGF1R</i>	Insulin like growth factor 1 receptor	22.789	540.124
<i>MYC</i>	MYC proto-oncogene, BHLH transcription factor	12.103	8.237
<i>ADCY5</i>	Adenylate cyclase 5	19.26	0
<i>DGAT1</i>	Diacylglycerol O-acyltransferase 1	3.479	80.706
<i>MIF</i>	Macrophage migration inhibitory factor	0	5.14
<i>GHR</i>	Growth hormone receptor	3.1	0
<b>TMM normalized expression of pro-longevity genes</b>			
<b>Gene</b>	<b>Description</b>	<b><i>M. myotis</i></b>	<b><i>M. molossus</i></b>
<i>RICTOR</i>	RPTOR independent companion of MTOR complex 2	12869.042	595.476
<i>ARHGAP1</i>	Rho GTPase activating protein 1	43.247	38.333
<i>BUB1B</i>	BUB1 mitotic checkpoint serine/threonine kinase	7222.727	4630.683
<i>PTEN</i>	Phosphatase and tensin homolog	1830.856	0
<i>ZMPSTE24</i>	Zinc metalloproteinase STE24	1628.613	393.672
<i>UCP2</i>	Uncoupling protein 2	577.02	2683.561
<i>TPP2</i>	Tripeptidyl peptidase 2	2404.549	955.757
<i>PPM1D</i>	Protein Phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> dependent 1D	1184.73	7689.797
<i>CDK7</i>	Cyclin dependent kinase 7	552.9	146.54
<i>CISD2</i>	CDGSH iron sulfur domain 2	150.344	216.23
<i>SQSTM1</i>	Sequestosome 1	456.844	361.879
<i>PRDX1</i>	Peroxiredoxin 1	184.507	58.715
<i>SOD2</i>	Superoxide dismutase 2	103.747	353.785
<i>STUB1</i>	STIP1 homology and U-box containing protein 1	166.509	44.34
<i>GRN</i>	Granulin precursor	261.758	33.561
<i>SIRT1</i>	Sirtuin 1	372.305	509.23
<i>GSK3A</i>	Glycogen synthase kinase 3 Alpha	148.867	300.306
<i>ATM</i>	ATM serine/threonine kinase	1244.425	5006.536
<i>CLOCK</i>	Clock circadian regulator	203.001	22.427
<i>XRCC5</i>	X-ray repair cross complementing 5	137.304	190.863
<i>CAT</i>	Catalase	0	10.697
<i>FOXM1</i>	Forkhead box M1	107.912	225.901
<i>RAE1</i>	Ribonucleic acid export 1	36.031	293.434
<i>MSRA</i>	Methionine sulfoxide reductase A	11.906	4.044
<i>TOP3B</i>	DNA topoisomerase III Beta	50.827	61.747
<i>ARNTL</i>	Aryl hydrocarbon receptor nuclear translocator like	28.035	13.074
<i>NUDT1</i>	Nudix hydrolase 1	0	57.421
<i>SIRT6</i>	Sirtuin 6	0.381	5.36

Note: for each species, gene expression value is represented by the median of TMM normalized expression across all samples (n=8)

Gene expression values were normalized using Trimmed Mean of M-value (TMM) method.