

**Supplementary Table 5. Functional enrichment in KEGG pathways of the STRING protein-protein interaction network including genes under selective pressure in bat lineages, genes showing bat-specific upregulation with age, and LC3.**

<b>Pathway ID</b>	<b>Pathway description</b>	<b>Observed gene count</b>	<b>FDR</b>	<b>Matching protein in the network</b>
5169	Epstein-Barr virus infection	6	0.000128	Csnk2a1,Eif2ak4,Map3k7,Nedd4,Pik3ca,Tbk1
5162	Measles	5	0.000257	Csnk2a1,Eif2ak4,Map3k7,Pik3ca,Tbk1
4144	Endocytosis	5	0.00138	Nedd4,Sh3glb1,Vps36,Vps4a,Vta1
4140	Regulation of autophagy	3	0.00208	Pik3c3,Pik3r4,Ulk2
4152	AMPK signaling pathway	4	0.00211	Map3k7,Mtor,Pik3ca,Sirt1
4150	mTOR signaling pathway	3	0.00495	Mtor,Pik3ca,Ulk2
5168	Herpes simplex infection	4	0.00832	Csnk2a1,Eif2ak4,Map3k7,Tbk1
4620	Toll-like receptor signaling pathway	3	0.016	Map3k7,Pik3ca,Tbk1
4668	TNF signaling pathway	3	0.0178	Dnm11,Map3k7,Pik3ca
5160	Hepatitis C	3	0.03	Eif2ak4,Pik3ca,Tbk1
5206	MicroRNAs in cancer	3	0.0303	Mtor,Rock1,Sirt1
4145	Phagosome	3	0.0424	Atp6v1c1,Atp6v1h,Pik3c3
5164	Influenza A	3	0.0442	Eif2ak4,Pik3ca,Tbk1
4930	Type II diabetes mellitus	2	0.0498	Mtor,Pik3ca

**Supplementary Table 6. Genes enriched in the parental GO term 'autophagy' that showed correlation with age in M.**

<b>Gene</b>	<b>Bat</b>	<b>Human</b>	<b>Mouse</b>
<i>PIK3CA</i>	0.483	-0.233	-0.568
<i>ROCK1</i>	0.468	-0.091	-0.41
<i>RB1CC1</i>	0.446	-0.143	-0.164
<i>ATP6V1E2</i>	0.438	-0.469	NA
<i>RAB12</i>	0.423	0.075	0.254
<i>CSNK2A1</i>	0.415	-0.015	-0.406
<i>SCFD1</i>	0.385	-0.235	0.027
<i>NEDD4</i>	0.383	-0.043	-0.1
<i>UVRAG</i>	0.36	0.156	0.087
<i>POLR3A</i>	0.343	0.17	-0.185
<i>ATG3</i>	0.341	-0.117	0.508
<i>MTDH</i>	0.318	-0.148	0.586
<i>CISD2</i>	0.314	0.079	0.28
<i>PIK3CB</i>	0.308	-0.14	0.497
<i>ATG4C</i>	0.296	-0.281	0.656
<i>PAFAH1B2</i>	0.293	-0.278	-0.097
<i>MAPK8</i>	0.286	0.099	-0.187
<i>USP33</i>	0.278	-0.237	-0.165
<i>STAM</i>	0.276	0.029	-0.213
<i>FIS1</i>	0.275	0.111	-0.032
<i>MID2</i>	0.274	0.218	0.262
<i>TRAPPC8</i>	0.274	-0.167	-0.066
<i>ULK2</i>	0.271	-0.017	-0.312
<i>FBXW7</i>	0.267	0.074	0.112
<i>TOMM70</i>	0.267	NA	NA
<i>SIRT1</i>	0.243	-0.091	-0.566
<i>HERC1</i>	0.241	0.06	0.086
<i>VPS26A</i>	0.24	0.046	0.367
<i>PRKAB2</i>	0.234	-0.157	0.551
<i>STAM2</i>	0.226	-0.299	0.334
<i>SNX14</i>	0.214	-0.27	-0.158
<i>EP300</i>	0.213	-0.17	0.013
<i>VTA1</i>	0.208	-0.302	-0.327
<i>MAP3K7</i>	0.203	-0.213	-0.247
<i>TBC1D5</i>	0.198	-0.231	0.111
<i>TBK1</i>	0.198	-0.218	-0.215
<i>SNX5</i>	0.19	0.143	-0.653
<i>VPS36</i>	0.179	-0.207	-0.483
<i>NRBF2</i>	0.177	-0.236	-0.361
<i>WDFY3</i>	0.176	-0.134	0.703
<i>DNM1L</i>	0.168	-0.081	-0.245
<i>VTG1A</i>	0.164	0.042	0.482
<i>UBXN2B</i>	0.146	-0.14	-0.179
<i>EIF2AK4</i>	0.141	-0.069	-0.361
<i>WDR41</i>	0.138	-0.121	0.275
<i>RIPK2</i>	0.137	0.232	-0.214

<i>SH3GLB1</i>	0.132	-0.149	-0.039
<i>ATG4A</i>	0.121	-0.063	0.094
<i>PIK3R4</i>	0.11	-0.227	-0.457
<i>ATG5</i>	0.108	-0.082	0.227
<i>IFT88</i>	0.104	-0.124	0.268
<i>VIPAS39</i>	0.103	-0.202	NA
<i>ATP6V1H</i>	0.099	-0.172	-0.032
<i>SPTLC1</i>	0.093	-0.2	0.072
<i>PIK3C3</i>	0.077	-0.268	-0.269
<i>ATG10</i>	0.076	-0.105	0.147
<i>PTK2</i>	0.061	0.109	0.484
<i>RAB3GAP1</i>	0.053	-0.013	-0.567
<i>AMBRA1</i>	0.052	0.153	-0.323
<i>EPM2A</i>	0.048	0.025	0.268
<i>ANXA7</i>	0.046	-0.2	0.383
<i>ATP6VIC1</i>	0.03	-0.186	-0.09
<i>U2AF1</i>	0.03	-0.053	-0.207
<i>ATP6V0A1</i>	0.021	0.015	0.181
<i>RHEB</i>	-0.006	-0.018	0.356
<i>VPS4B</i>	-0.023	-0.248	0.202
<i>ACTL6A</i>	-0.066	-0.327	-0.318
<i>SREBF2</i>	-0.074	-0.037	-0.03
<i>TPCN1</i>	-0.08	-0.151	0.112
<i>MTMR3</i>	-0.084	-0.012	0.067

myotis bats. The Spearman's rank correlation coefficients between their expression and age in bat, human and mouse were extracted from Huang et al. (2019). NA – transcript not detected in the blood transcriptome.

**Supplementary Table 7. Taxonomic information: List of species included in the study, their record lifespan from AnAge, source of the samples, age ranges of individuals included in the study and sampling permit details.**

Species	Max. lifespan	Source	Sample	Age range	Permit details for sampling wild bat populations
<i>M. myotis</i>	37.1yrs	Wild population, Brittany, France	wing punches	0 - 7+yrs	Arrêté préfectoral (18/07/2013 and 05/08/2013) issued to Eric Petit, Frédéric Touzalin and Sébastien Puechmaille by Préfet du Morbihan, valid between 15th June - 15th September; 2013-2017 inclusive
<i>P. kuhlii</i>	8yrs	Wild population, Krašnja, Slovenia	wing punches	0 – 7+ yrs	Aut. Prot. N°: 13040, issued to Roberto Toffoli and Andrea Locatelli by the Italian ministry for the territory and sea safeguard (Ministero della tutela del territorio e del mare)
		Wild population, Piemonte, Italy			Aut N°: 35601-35/2010-6, issued to Primož Presetnik by the Slovenian Environment Agency (Agencija Republike Slovenije za okolje)
<i>M. musculus</i> (C57BL/6J strain)	4 yrs	Conboy laboratory (Department of Bioengineering, Berkeley Research, University of California) and O'Neill laboratory (School of Biochemistry and Immunology, Trinity College Dublin)	ear clippings	2 – 22 months	not applicable
<i>M. musculus</i> (NHEJ background)	na	Gorbanova laboratory (Departments of Biology and Medicine, University of Rochester, Rochester, NY 14627, USA)	flank-skin derived primary fibroblasts developed as described in Vaidya et al. (2014)	3 and 28 months	not applicable