Supplementary Materials

Figure S1. Protein sequence alignment of the tree shrew IL7. The red sequence IDs indicate sequences obtained by molecular cloning and deposited in GenBank in our previous study (Yu et al., 2014), and the blue sequence IDs indicate sequences obtained by using the TS_3.0 genome annotation.

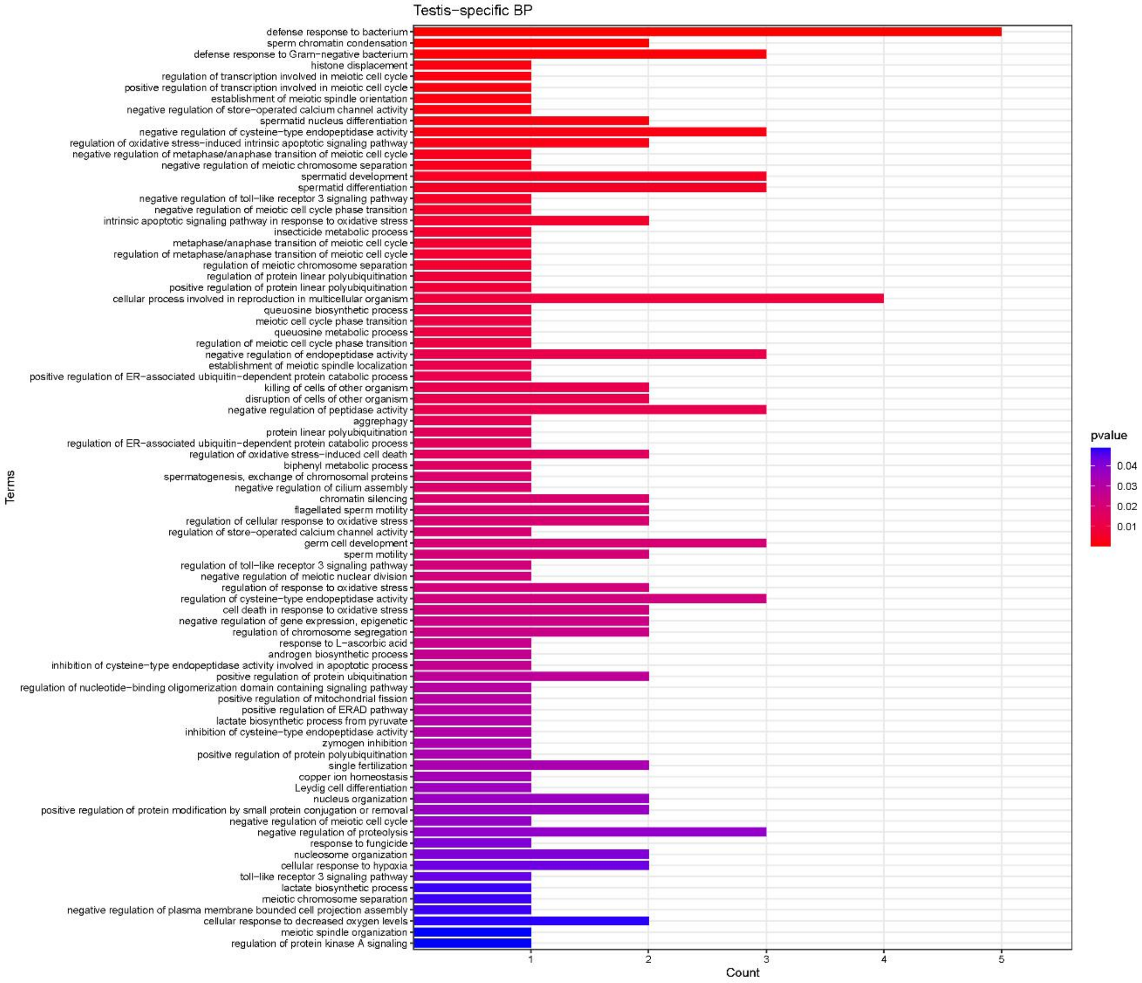

Figure S2. Biological process enrichment of testis-specific genes

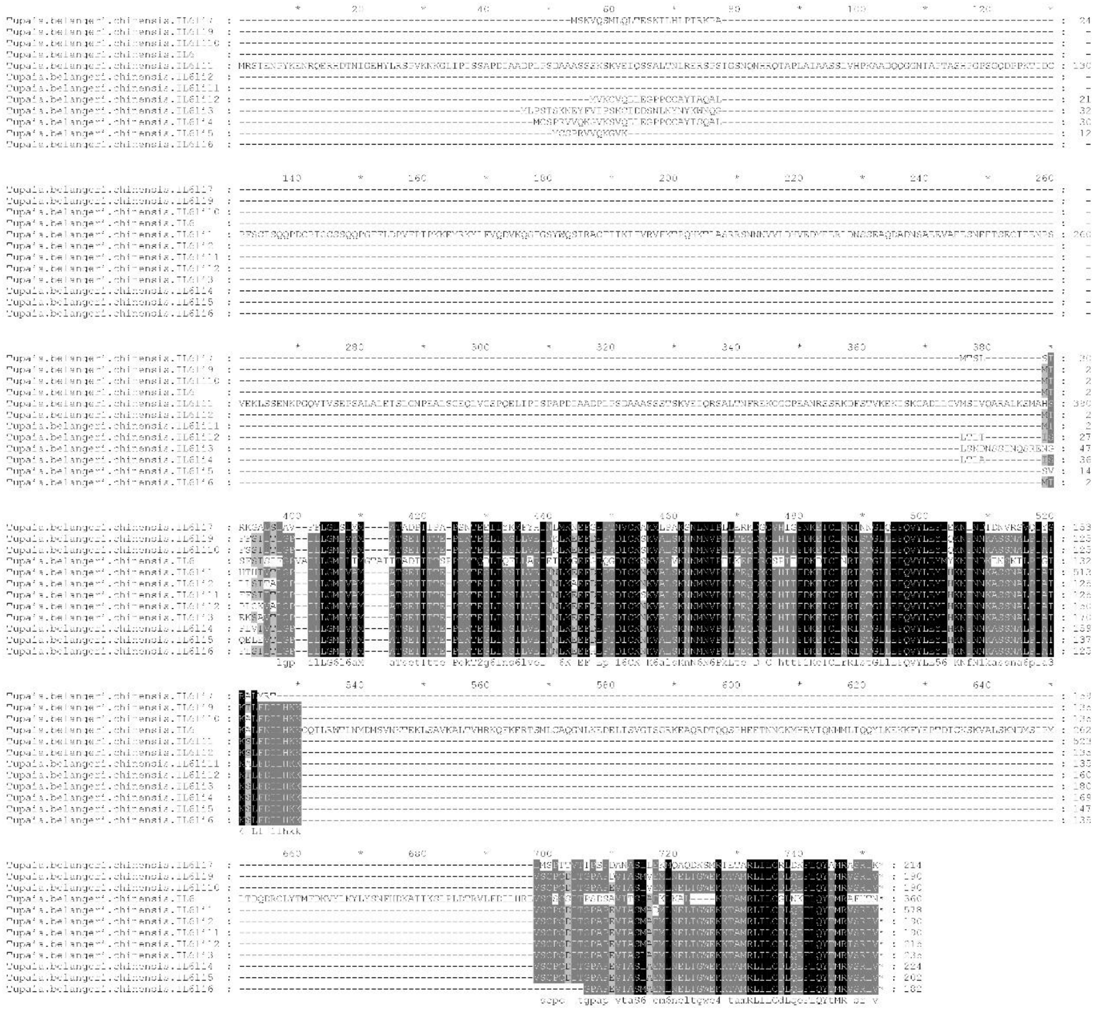

Figure S3. Protein sequence alignment of tree shrew *IL6* gene family. The longest protein sequence for each gene family member was chosen for the alignment.

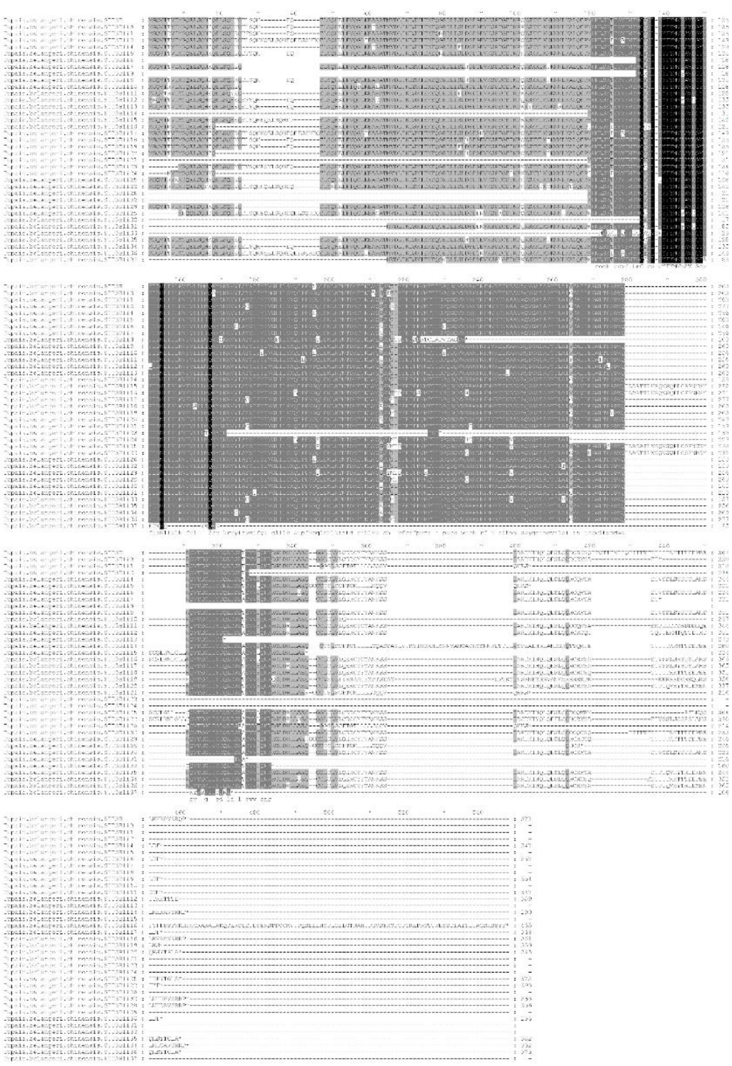

Figure S4. Protein sequence alignment of tree shrew *STT3B* gene family. The longest protein sequence for each gene family member was chosen for the alignment.

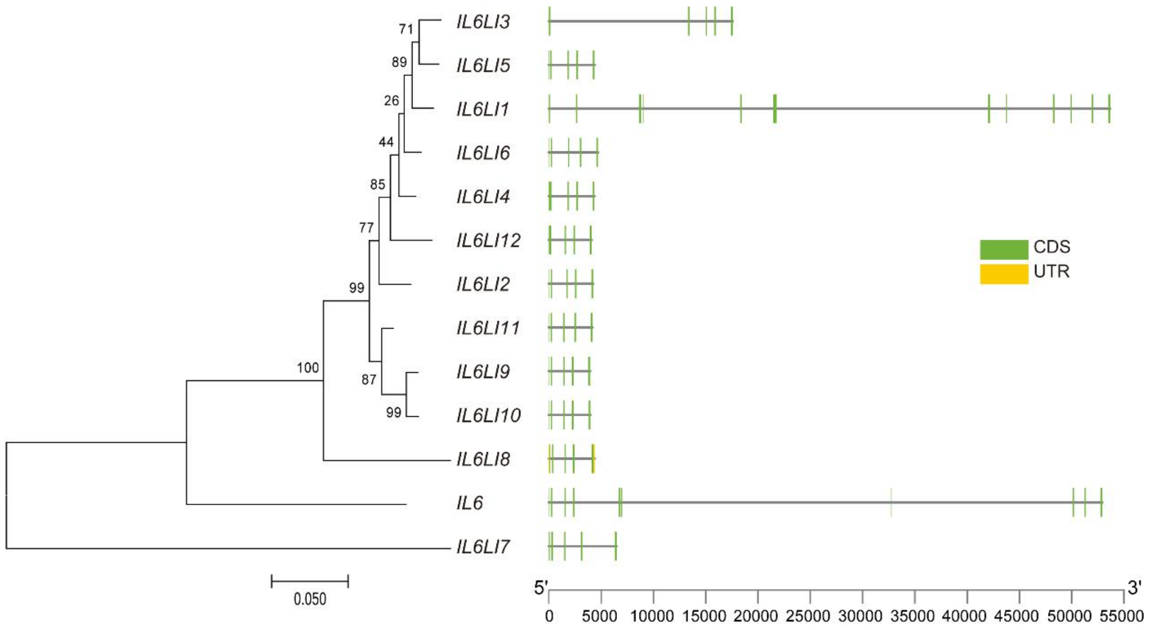

Figure S5. Gene structure and phylogenetic relationship among tree shrew *IL6* gene family members. (*left*) The maximum likelihood tree was constructed using MEGA7, with the ML methods (K2+G model) and 1,000 bootstraps. (*right*) Gene structure based on the TS_3.0 genome annotation. CDS, coding sequence; UTR, untranslated region.

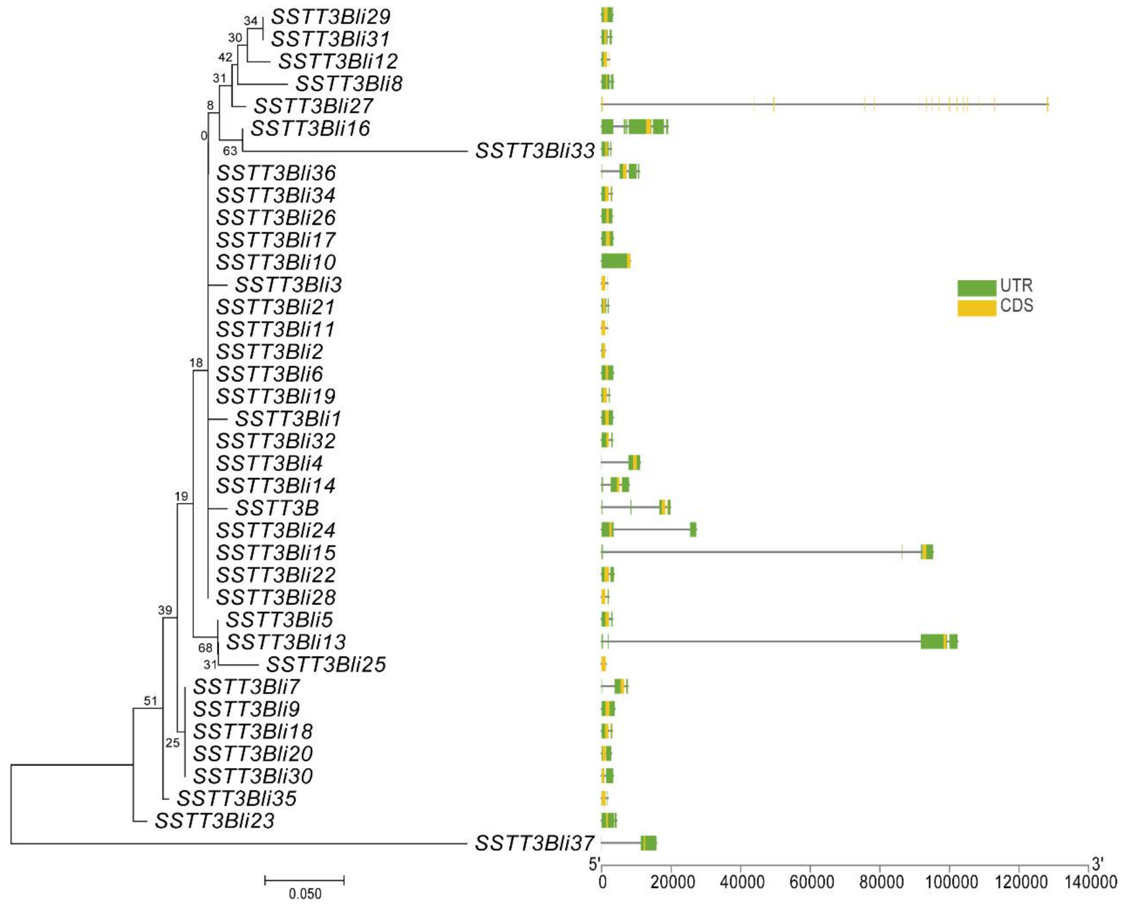

Figure S6. Gene structure and phylogenetic relationship among tree shrew *STT3B* family members. (*left*) The maximum likelihood tree was constructed using MEGA7, with the ML methods (K2+G model) and 1,000 bootstraps. (*right*) Gene structure based on the TS_3.0 genome annotation. CDS, coding sequence; UTR, untranslated region.

Table S1. Information of publicly available tree shrew RNA-seq datasets

Library type	Description	No. of datasets	Source	Accession number	No. of datasets after QC	Reference
Poly(A)$^+$	Pancreatic cancer tissues	3	GEO	PRJNA434450	3	(Tu et al., 2019)
Poly(A)$^+$	Tree shrew adipose tissues	12	GEO	PRJNA310673	12	(Han et al., 2020)
Poly(A)$^+$	Tree shrew liver tissues	2	GEO	PRJNA282350	2	(Wu et al., 2016)
Poly(A)$^+$	Tree shrew PBMC	6	GEO	PRJNA473782	6	-
Poly(A)$^+$	Tree shrew brain RNA-seq	6	GEO	PRJNA416241	6	(Fan et al., 2018)
Poly(A)$^+$	Tree shrew multi organ RNA-seq	7	GEO	PRJNA170104	7	(Fan et al., 2013)

Poly(A)$^+$	Tree shrew immortalized hepatocytes cell lines	21	GSA	PRJCA002538	21	(Zhang et al., 2020)
Poly(A)$^+$	Tree shrew hepatocytes RNA-seq	7	GEO	PRJNA87013	7	(Yan et al., 2012)
Poly(A)$^+$	differentiating germ cell and cell line	10	TSDB	TSDB2017R01-TSDB2017R15	6	(Li et al., 2017)
Poly(A)$^+$	Mixed tissues	1	GEO	PRJNA200450	1	(Lin et al., 2014)
Poly(A)$^+$ & Ribo$^-$	HBV infected tree shrew liver	21	DDBJ	DRR155071-DRR155099	21	(Sanada et al., 2019)
Poly(A)$^+$	Tree shrew glioblastoma	5	GSA	PRJCA000125	5	(Tong et al., 2017)

Poly(A)$^+$, poly A enriched library construction; Ribo$^-$, ribosome depletion library construction. PBMC, peripheral blood mononuclear cell; HBV, hepatitis B virus; GEO, gene expression omnibus (https://www.ncbi.nlm.nih.gov/geo/); GSA, genome sequence archive (https://ngdc.cncb.ac.cn/gsa/); TSDB, tree shrew database (http://www.treeshrewdb.org/); DDBJ, DNA Data Bank of Japan (https://www.ddbj.nig.ac.jp/index-e.html).

Table S2. Sample information for different tree shrew transcriptome datasets

ID	Gender	Age (months)	Tissues	Sequencing strategy	No. of datasets
27d2	female	21	Brain, Cortex, Hippocampus, Heart, Liver, Spleen, Kidney, Small intestine, Ovary	RNA-seq & ISO-seq (pooled samples)	9
U23	male	29	Testis	RNA-seq	1
U22	female	17	Brain, Cortex, Hippocampus, Heart, Liver, Spleen, Lung, Kidney, Small intestine, Muscle, Ovary	RNA-seq & ISO-seq (pooled samples)	11
16c7	male	32	Brain, Cortex,	RNA-seq	11

			Hippocampus, Heart, Liver, Spleen, Lung, Kidney, Small intestine, Muscle, Testis		
16c	male	28	Brain, Cortex, Hippocampus, Heart, Liver, Spleen, Lung, Kidney, Small intestine, Muscle, Testis	RNA-seq	119
21	male	67	Liver	Ribo$^-$ RNA-seq	1
28a	male	63	Liver	Ribo$^-$ RNA-seq	14
U31	male	6	Liver	Ribo$^-$ RNA-seq	1
U32	male	7	Liver	Ribo$^-$ RNA-seq	1

ISO-seq, long-read isoform sequencing; Ribo$^-$, ribosome depletion RNA-SEQ library construction.

Table S3. Information of RNA-seq datasets of virus-infected cells and tissues

Library type	Description	No. of datasets	Experiment design
Poly(A)$^+$	HCV infected TPH	18	HCV infected and uninfected (NC) samples were collected at 24, 48, and 72 hours post infection
Poly(A)$^+$	NDV infected TSPRC	18	NDV infected and uninfected (NC) samples were collected at 3, 9, and 12 hours post infection
Poly(A)$^+$	EMCV infected TSPRC	9	EMCV infected and uninfected (NC) samples were collected at 3, 9, and 12 hours post infection
Poly(A)$^+$	HSV-1 infected TSPRC	8	HSV-1 infected and uninfected (NC) samples was collected at 6 and 12 hours post infection
Poly(A)$^+$	SeV infected TSPRC	9	SeV infected and uninfected (NC) samples were collected at 3, 9, and 12 hours post infection
Ribo$^-$	IAV infected lung	24	Sample were collected at 0, 3, and 5 days post IAV infection

Poly(A)$^+$, poly A enriched library construction; Ribo$^-$, ribosome depletion library construction.

TSPRC, tree shrew primary renal cells. TPH, Tree shrew primary hepatocytes.

HCV, Hepatitis C virus; NDV, Newcastle disease virus; EMCV, Encephalomyocarditis virus; HSV-1, herpes simplex virus type 1; SeV, Sendai virus; IAV, influenza A virus.

Table S4. Sequences obtained by molecular cloning

Gene	GenBank accession number	Reference
GBP1	AG214685.1	(Gu et al., 2019)
GBP2	AG214686.1	
GBP4	AG214687.1	
GBP5	AG214688.1	
GBP7	AG214689.1	
IL7 (variant 1)	AFA42954.1	(Yu et al., 2014)
IL7 (variant 2)	AFA42955.1	
IL7 (variant 3)	AFA42956.1	
IL7 (variant 4)	AFA42957.1	
IL7 (variant 5)	AFA42958.1	
IL7 (variant 6)	AFA42959.1	
TLR1	GT354316.1	(Yu et al., 2016)
TLR2	GT354317.1	
TLR3	GT354318.1	
TLR4	GT354319.1	
TLR5	GT354320.1	
TLR6	GT354321.1	
TLR7	GT354322.1	
TLR8	GT354323.1	
TLR9	GT354324.1	
TLR11	GT354325.1	
TLR12	GT354326.1	
OAS1	MH512001	(Yao et al., 2019)
OAS2	MH512002	
OASL1	MH512003	
OASL2	MH512004	

APOBEC3_A3A	KU053484.1	(Luo et al., 2018)
APOBEC3_A3C	KU053485.2	
APOBEC3_A3F	KU053486.3	
APOBEC3_A3G	KU053487.4	

GBP, guanylate binding protein; *IL7*, interleukin 7; *TLR*, toll like receptor; *OAS*, 2'-5'-oligoadenylate synthetase; *OASL*, 2'-5'-Oligoadenylate synthetase like; *APOBEC3*, apolipoprotein b mRNA editing enzyme catalytic subunit 3.

Species	Genome version	Weblink
Homo sapiens	GRCh38.p13	https://asia.ensembl.org/Homo_sapiens/Info/Index
Pan troglodytes	Pan_tro_3.0	https://asia.ensembl.org/Pan_troglodytes/Info/Index
Gorilla gorilla gorilla	gorGor4	https://asia.ensembl.org/Gorilla_gorilla/Info/Index
Macaca mulatta	Mmul_10	https://asia.ensembl.org/Macaca_mulatta/Info/Index
Rattus norvegicus	Rnor_6.0	https://asia.ensembl.org/Rattus_norvegicus/Info/Index
Mus musculus	GRCm39	https://asia.ensembl.org/Mus_musculus/Info/Index
Sus scrofa	Sscrofa11.1	https://asia.ensembl.org/Sus_scrofa/Info/Index?db=core
Bos taurus	ARS-UCD1.2	https://asia.ensembl.org/Bos_taurus/Info/Index
Canis lupus familiaris	CamFam3.1	https://asia.ensembl.org/Canis_lupus_familiaris/Info/Index
Oryctolagus cuniculus	OryCun2.0	https://asia.ensembl.org/Oryctolagus_cuniculus/Info/Index

Table S5. Genome information of 11 vertebrate species used in this study

Table S6. Assessment of annotation completeness in Chinese tree shrew using *Eukaryota* BUSCOs and *mammalian* BUSCOs

Version	Complete BUSCOs	Complete and single-copy BUSCOs	Complete and duplicated BUSCOs	Fragmented BUSCOs	Missing BUSCOs
***Eukaryota* BUSCOs**					
TS_1.0	221	210	11	20	14
TS_2.0	235	228	7	8	12
TS_3.0	250	236	14	4	1
Tupchi_1.0	216	207	9	16	23
TupaiaBase	195	187	8	30	30
Human	253	246	7	1	1
Mouse	250	244	6	2	3
***mammalian* BUSCOs**					
TS_1.0	7568	7484	84	666	992
TS_2.0	7519	7457	62	332	1375
TS_3.0	8559	8250	177	304	363

Tupchi_1.0	7884	7814	70	453	889
TupaiaBase	6080	6023	57	640	2506
Human	8931	8810	121	31	264
Mouse	8916	8839	77	18	292

BUSCO: Benchmarking with Universal Single-Copy Orthologs (Seppey et al., 2019; Simão et al., 2015; Waterhouse et al., 2018). A total of 255 benchmarking universal single-copy orthologs of the *Eukaryota* dataset were retrieved from BUSCO. The three versions of tree shrew genome annotation were established by our group: TS_1.0 (Fan et al., 2013), TS_2.0 (Fan et al., 2019), and TS_3.0 (current version of tree shrew annotation). Tupchi_1.0, NCBI version of tree shrew annotation (https://www.ncbi.nlm.nih.gov/assembly/GCF_000334495.1/). The TupaiaBase was established by (Sanada et al., 2019). Human (https://asia.ensembl.org/Homo_sapiens/Info/Index) and Mouse (https://asia.ensembl.org/Mus_musculus/Info/Index/) datasets were taken from the public sources.

Table S7. Number of orthologs among 11 species

	Chimpanzee	Cattle	Dog	Gorilla	Human	Rhesus monkey	Mouse	Pig	Rabbit	Rat	Tree shrew
Chimpanzee	-	19 574	19 597	22 487	20 380	20 370	19 930	20 034	19 098	19 656	19 268
Cattle	14 367	-	17 658	17 541	17 835	16 615	18 014	18 246	17 129	17 717	17 201
Dog	14 323	15 187	-	17 385	17 568	16 595	17 689	17 749	16 879	17 413	17 009
Gorilla	17 545	14 445	14 430	-	19 583	19 696	19 417	19 545	18 646	19 142	18 696
Human	16 616	15 313	15 286	16 580	-	17 761	18 291	17 981	17 008	17 791	17 299
Rhesus monkey	15 359	13 991	13 952	15 395	15 366	-	17 961	18 139	17 347	17 744	17 435
Mouse	14 649	15 377	15 199	14 729	15 746	14 175	-	18 401	17 552	20 047	17 736

Pig	14 198	14 916	14 695	14 296	15 085	13 832	14 941	-	19 818	20 105	19 570
Rabbit	13 147	13 985	13 851	13 234	14 061	12 887	14 245	13 502	-	16 820	16 333
Rat	14 149	14 862	14 665	14 171	15 055	13 705	16 579	14 445	13 758	-	17 650
Tree shrew	13 791	14 246	14 165	13 830	14 549	13 390	14 530	13 873	13 040	14 015	-

Below the diagonal, number of one-one orthologue between each species pair; above the diagonal, number of total orthologues between each species pair (one-one, one-many, many-one). The data sources for Chimpanzee (*Pan troglodytes*), Cattle (*Bos taurus*), Dog (*Canis lupus familiaris*), Gorilla (*Gorilla gorilla gorilla*), Human (*Homo sapiens*), Rhesus monkey (*Macaca mulatta*), Mouse (*Mus musculus*), Pig (*Sus scrofa*), Rabbit (*Oryctolagus cuniculus*), and Rat (*Rattus norvegicus*) are listed in Table S5. The Chinese tree shrew (*Tupaia belangeri chinensis*) data are generated in this study.

Table S8. Gene family size changes along the phylogenic tree of 11 mammal species

Nodes	Expansions	Gene gain	Equals	Contractions	Gene loss	Sig Exp	Sig Contra
<11>	582	911	20746	866	1011	86	15
Pan troglodytes <6>	1591	2978	19996	607	657	329	27
Oryctolagus cuniculus <20>	866	1906	14980	6348	6537	53	13
Bos taurus <0>	679	1397	19613	1902	2072	51	16
Macaca mulatta <12>	1113	2179	17956	3125	3192	129	19
Gorilla gorilla gorilla <10>	1408	2518	19612	1174	1235	255	30
<3>	46	52	18533	3615	3632	3	7
<1>	205	323	21609	380	398	32	5
<13>	69	87	21180	945	958	4	8
Tupaia belangeri chinensis <14>	1610	5217	16307	4277	4553	120	22
<17>	468	1140	17649	4077	4216	104	20
Homo sapiens <8>	527	920	19065	2602	3094	76	260
<7>	137	217	21514	543	587	28	29

Sus scrofa <2>	1990	4951	19435	769	871	215	7
<19>	26	34	22146	22	24	6	1
<15>	0	0	21574	620	620	0	0
Canis lupus familiaris <4>	779	1316	19088	2327	2576	20	17
*Mus musculu*s <18>	650	2088	21037	507	628	122	35
<9>	563	703	21285	346	368	65	9
Rat<16>	924	1842	20486	784	908	105	41

Expansions, equal, and contractions: Total number of gene families that experienced expansions, equal and contraction along each branch of the phylogenic tree of the 11 vertebrate species described in the main text, respectively. Gene gain and gene loss, number of genes that gained or lost along each branch of the species tree. Sig Exp: number of gene families that undergone significantly expansion. Sig contra: number of gene families that undergone significantly contraction.

Table S9. Tree shrew gene families that undergone significant size changes

Orthogroups	Count	Rep ID	Orthogroups	Count	Rep ID	Orthogroups	Count	Rep ID
OG0000001	-20	*IGHV3-35*	OG0000176	6	*RPL7A*	OG0001667	15	*NSA2*
OG0000002	-12	*IGKV3-11*	OG0000460	7	*MORF4L1*	OG0000107	16	*RPS6*
OG0000008	-11	*H2BC4*	OG0000782	7	*RPL18*	OG0000801	16	*RPL23A*
OG0000012	-8	*IGKV2-28*	OG0016792	7	*GOLGA2*	OG0000904	16	*NPM1*
OG0000013	-7	*OR4F3*	OG0013864	7	*GAPDH*	OG0000441	16	*PUM3*
OG0000027	-7	*H4*	OG0000095	7	*SETMAR*	OG0001300	17	*MIA3*
OG0000046	-6	*IFNA14*	OG0017249	7	*CBX3*	OG0000102	18	*RPS3A*

Orthogroups	**Count**	**Rep ID**	**Orthogroups**	**Count**	**Rep ID**	**Orthogroups**	**Count**	**Rep ID**
OG0000037	-6	*CYP2C19*	OG0000135	7	*HMGN1*	OG0001301	18	*RPL17*
OG0000045	-5	*Novel gene*	OG0000696	7	*HSP90AB3P*	OG0001170	19	*ENV*
OG0000029	-5	*PCDHB1*	OG0000518	7	*UBE2L3*	OG0000071	19	*OR4C6*
OG0000094	-5	*OR10A2*	OG0017248	7	*GAG*	OG0001045	20	*RPL21*
OG0000066	-5	*UGT2B31*	OG0016814	8	*KBTBD7*	OG0000202	21	*KPNA2*
OG0000028	-5	*OR5B12*	OG0000276	8	*BTN1A1*	OG0000054	21	*EIF4A2*
OG0000064	-5	*OR4C12*	OG0000476	8	*HSPD1*	OG0000018	21	*HNRNPA1*
OG000002	-5	*IGHV1-24*	OG001681	8	*HMGB2*	OG00004	23	*LORF2*

Orthogroups	**Count**	**Rep ID**	**Orthogroups**	**Count**	**Rep ID**	**Orthogroups**	**Count**	**Rep ID**
0			2			24		
OG0000080	-5	*CYP4F11*	OG0016813	8	*RPSA*	OG0000491	25	*ENV*
OG0000099	-4	*RPL39L*	OG0000330	9	*KRT18*	OG0000606	25	*TXNRD1*
OG0000067	-4	*USPL12*	OG0016080	9	*TSORF*	OG0000553	26	*RALGDS*
OG0000082	-4	*PCDHA1*	OG0000306	9	*JAM3*	OG0000030	39	*RPL31*
OG0000019	-4	*CEACAM1*	OG0003475	9	*KRT8*	OG0000425	28	*EEF1A1P5*
OG0000118	-4	*ZNF607*	OG0000009	9	*HLA-E*	OG0000026	29	*HVM45*
OG0000041	-5	*GBP1*	OG0000011	9	*IGLV2-8*	OG0000121	30	*NSA2*

Orthogroups	**Count**	**Rep ID**	**Orthogroups**	**Count**	**Rep ID**	**Orthogroups**	**Count**	**Rep ID**
OG0003812	3	*HMGN2*	OG0013871	10	*ANKRD26*	OG0000370	30	*HMGB1*
OG0017921	3	*ST13*	OG0000365	10	*LDHB*	OG0000016	30	*EEF1A1*
OG0017511	3	*OR2I1P*	OG0013872	10	*GAG*	OG0000196	31	*RPL21*
OG0000892	3	*DMD*	OG0005633	10	*RPS3A*	OG0000143	31	*DNAJA1*
OG0001266	3	*LARP7*	OG0013870	10	*TSORF*	OG0000049	32	*HMGN2*
OG0002890	3	*RPS23*	OG0000648	11	*MORF4L2*	OG0000342	33	*HMGB1*
OG0000408	4	*RPL37A*	OG0003756	11	*POL*	OG0000222	35	*GAG-PRO-POL*
OG000289	4	*LORF2*	OG000115	11	*VMN2R116*	OG00000	36	*HMGB1*

Orthogroups	Count	Rep ID	Orthogroups	Count	Rep ID	Orthogroups	Count	Rep ID
6			5			83		
OG0016263	4	*TSORF*	OG0000252	11	*BTN1A1*	OG0000253	38	*RPL21*
OG0000637	4	*NLRP1*	OG0005646	11	*RPS3A*	OG0000032	39	*RPL21*
OG0000963	4	*ATP5F1C*	OG0000201	11	*HSP90AB1*	OG0000092	43	*RPL5*
OG0000293	4	*ZNF705A*	OG0000163	11	*RPS4X*	OG0000114	46	*POL*
OG0000709	4	*POL*	OG0003759	12	*IL6*	OG0000005	47	*OR5B3*
OG0000610	4	*EEF1A1*	OG0001945	12	*POL*	OG0000152	38	*STT3B*
OG0000508	4	*RPL7L1*	OG0000601	12	*CACYBP*	OG0000146	51	*LORF2*

Orthogroups	Count	Rep ID	Orthogroups	Count	Rep ID	Orthogroups	Count	Rep ID
OG0000156	5	*RPL17*	OG0003758	12	*RPS3A*	OG0000059	65	*NCL*
OG0000173	5	*NUTM2G*	OG0000050	13	*HSPA1L*	OG0000057	76	*LORF2*
OG0000275	5	*GCSH*	OG0000141	13	*HNRNPC*	OG0000021	84	*ZNF589*
OG0000692	5	*MRPL42*	OG0002899	13	*ENV*	OG0000043	86	*LIN1*
OG0000911	5	*IGLV1-40*	OG0000413	14	*SSB*	OG0000024	129	*LORF2*
OG0016914	5	*SLAMF6*	OG0000077	14	*RPS2*	OG0000022	138	*L1RE1*
OG0000278	5	*IGHV2-5*	OG0000093	14	*VPREB1*	OG0000014	154	*CASR*
OG000012	6	*RPL36*	OG000147	15	*ENV*	OG00000	158	*RPL7*

Orthogroups	**Count**	**Rep ID**	**Orthogroups**	**Count**	**Rep ID**	**Orthogroups**	**Count**	**Rep ID**
9			3			04		
OG0000294	6	*RPS20*	OG0001948	15	*RNF167*	OG0000007	180	*L1RE1*
OG0017243	6	*RPL9*	OG0001947	15	*GAG*	-	-	-
OG0000920	6	*MICB*	OG0000084	15	*RPL9*	-	-	-

Orthogroups: Group of orthologs among species that were highly identical. The orthogroups were identified by OrthoFinder software (Emms & Kelly, 2019). Count: number of gene family member that undergone changes; minus means number of genes that contracted in a gene family.

Rep ID: the gene symbols that represented the orthogroups. Note that gene Rep ID may represent multiple orthogroups.

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