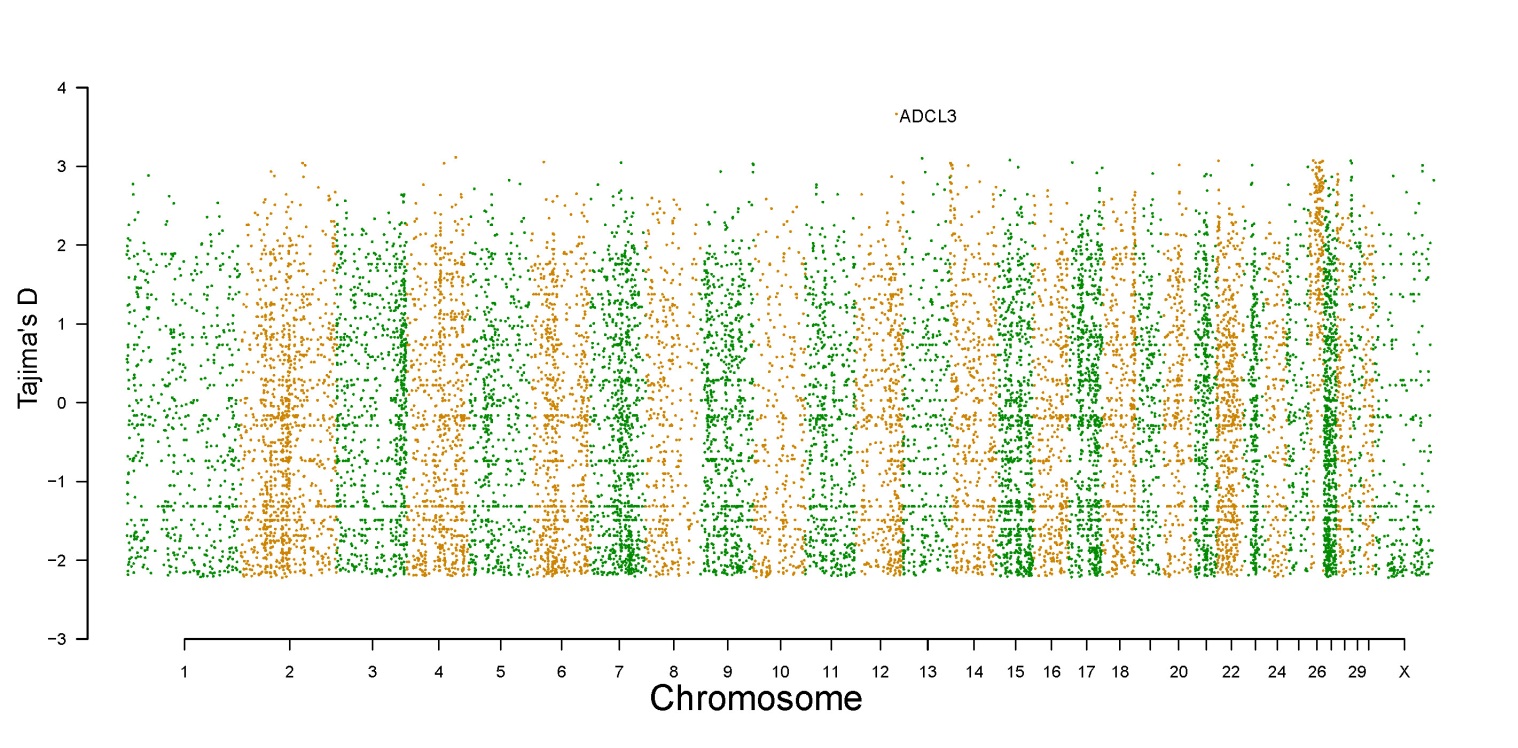
**Supplementary Tables and Figure**s



Supplementary Figure 1. Manhattan plot of the Tajima’s D at the gene level based on SNPs located in coding regions of 6 wild tree shrews. *ADCL3* has a highest value of Tajima’s D (D=3.67), which is marked in the plot.

Supplementary Table 1. Sample information of RNA-seq of tree shrew from GEO or treeshrewdb.org

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample Name | Submission | GEO\_ID/TSDB\_ID | | Reference | Description |
| Brain 1 | KIZ | [SRX157964](https://www.ncbi.nlm.nih.gov/sra/SRX157964%5baccn%5d) |  | [Fan et al., 2013](http://www.mitotool.org/lab/pdf/Nature%20comms%202013%20Fan.pdf) | Brain tissue RNA-seq |
| Brain 2 | KIZ | [SRX3358316](https://www.ncbi.nlm.nih.gov/sra/?term=SRX3358316) |  | [Fan et al., 2018](http://www.mitotool.org/lab/pdf/Fan-2018.pdf) | Brain tissue RNA-seq |
| Brain 3 | KIZ | [SRX3358319](https://www.ncbi.nlm.nih.gov/sra/?term=SRX3358319) |  | [Fan et al., 2018](http://www.mitotool.org/lab/pdf/Fan-2018.pdf) | Brain tissue RNA-seq |
| Cortex 1 | KIZ | [SRX3341772](https://www.ncbi.nlm.nih.gov/sra/?term=SRX3341772) |  | [Fan et al., 2018](http://www.mitotool.org/lab/pdf/Fan-2018.pdf) | Cortex tissue RNA-seq |
| Cortex 2 | KIZ | [SRX3358317](https://www.ncbi.nlm.nih.gov/sra/?term=SRX3358317) |  | [Fan et al., 2018](http://www.mitotool.org/lab/pdf/Fan-2018.pdf) | Cortex tissue RNA-seq |
| Hippocampus 1 | KIZ | [SRX3358315](https://www.ncbi.nlm.nih.gov/sra/?term=SRX3358315) |  | [Fan et al., 2018](http://www.mitotool.org/lab/pdf/Fan-2018.pdf) | Hippocampus tissue RNA-seq |
| Hippocampus 2 | KIZ | [SRX3358318](https://www.ncbi.nlm.nih.gov/sra/?term=SRX3358318) |  | [Fan et al., 2018](http://www.mitotool.org/lab/pdf/Fan-2018.pdf) | Hippocampus tissue RNA-seq |
| Heart | KIZ | [SRX157962](https://www.ncbi.nlm.nih.gov/sra/SRX157962%5baccn%5d) |  | [Fan et al., 2013](http://www.mitotool.org/lab/pdf/Nature%20comms%202013%20Fan.pdf) | Heart tissue RNA-seq |
| Pancreas | KIZ | [SRX157961](https://www.ncbi.nlm.nih.gov/sra/SRX157961%5baccn%5d) |  | [Fan et al., 2013](http://www.mitotool.org/lab/pdf/Nature%20comms%202013%20Fan.pdf) | Pancreas tissue RNA-seq |
| Kidney | KIZ | [SRX157960](https://www.ncbi.nlm.nih.gov/sra/SRX157960%5baccn%5d) |  | [Fan et al., 2013](http://www.mitotool.org/lab/pdf/Nature%20comms%202013%20Fan.pdf) | Kidney tissue RNA-seq |
| Ovary | KIZ | [SRX157966](https://www.ncbi.nlm.nih.gov/sra/SRX157966%5baccn%5d) |  | [Fan et al., 2013](http://www.mitotool.org/lab/pdf/Nature%20comms%202013%20Fan.pdf) | Ovary tissue RNA-seq |
| Testis | KIZ | [SRX157965](https://www.ncbi.nlm.nih.gov/sra/SRX157965%5baccn%5d) |  | [Fan et al., 2013](http://www.mitotool.org/lab/pdf/Nature%20comms%202013%20Fan.pdf) | Testis tissue RNA-seq |
| Liver | KIZ | [SRX157963](https://www.ncbi.nlm.nih.gov/sra/SRX157963%5baccn%5d) |  | [Fan et al., 2013](http://www.mitotool.org/lab/pdf/Nature%20comms%202013%20Fan.pdf) | Liver tissue RNA-seq |
| Liver (control) | KIZ | [SRX1017387](https://www.ncbi.nlm.nih.gov/sra/SRX1017387%5baccn%5d) |  | - | RNA-seq reveal liver changes in the early stage of diabetes in tree shrew, control |
| Liver (diabetes) | KIZ | [SRX1009946](https://www.ncbi.nlm.nih.gov/sra/SRX1009946%5baccn%5d) |  | - | RNA-seq reveal liver changes in the early stage of diabetes in tree shrew |
| Hepatocyte | NIBS | [SRX125163](https://www.ncbi.nlm.nih.gov/sra/SRX125163%5baccn%5d) |  | [Yan et al., 2012](https://www.ncbi.nlm.nih.gov/pubmed/23150796) | Hepatocyte RNA-seq |
| DGC-enriched Thy1- cells 1 | KIZ | [TSDB2017R01](http://www.treeshrewdb.org/data/CR_SSC/TS1_Thy1-N.fq.gz) |  | [Li et al., 2017](http://www.mitotool.org/lab/pdf/2016-LCH-cell_research.pdf) | differentiating germ cell (DGC) -enriched Thy1− cells |
| DGC-enriched Thy1- cells 2 | KIZ | [TSDB2017R02](http://www.treeshrewdb.org/data/CR_SSC/TS2_Thy1-N.fq.gz) |  | [Li et al., 2017](http://www.mitotool.org/lab/pdf/2016-LCH-cell_research.pdf) | differentiating germ cell (DGC) -enriched Thy1− cells |
| SSC-enriched Thy1+ cells 1 | KIZ | [TSDB2017R03](http://www.treeshrewdb.org/data/CR_SSC/TS1_Thy1-P.fq.gz) |  | [Li et al., 2017](http://www.mitotool.org/lab/pdf/2016-LCH-cell_research.pdf) | spermatogonial stem cells (SSC) -enriched Thy1+ cells |
| SSC-enriched Thy1+ cells 2 | KIZ | [TSDB2017R04](http://www.treeshrewdb.org/data/CR_SSC/TS2_Thy1-P.fq.gz) |  | [Li et al., 2017](http://www.mitotool.org/lab/pdf/2016-LCH-cell_research.pdf) | spermatogonial stem cells (SSC) -enriched Thy1+ cells |
| Thy1+ cells P0 1 | KIZ | [TSDB2017R05](http://www.treeshrewdb.org/data/CR_SSC/TS3_BeadsP0.R1.fq.gz) | [TSDB2017R06](http://www.treeshrewdb.org/data/CR_SSC/TS3_BeadsP0.R2.fq.gz) | [Li et al., 2017](http://www.mitotool.org/lab/pdf/2016-LCH-cell_research.pdf) | Thy1+ cells cultured for passages 0 (P0), 1 week for each passage |
| Thy1+ cells P0 2 | KIZ | [TSDB2017R07](http://www.treeshrewdb.org/data/CR_SSC/TS4_BeadsP0.R1.fq.gz) | [TSDB2017R08](http://www.treeshrewdb.org/data/CR_SSC/TS4_BeadsP0.R2.fq.gz) | [Li et al., 2017](http://www.mitotool.org/lab/pdf/2016-LCH-cell_research.pdf) | Thy1+ cells cultured for passages 0 (P0), 1 week for each passage |
| Thy1+ cells P1 1 | KIZ | [TSDB2017R09](http://www.treeshrewdb.org/data/CR_SSC/TS3_BeadsP1.R1.fq.gz) | [TSDB2017R10](http://www.treeshrewdb.org/data/CR_SSC/TS3_BeadsP1.R2.fq.gz) | [Li et al., 2017](http://www.mitotool.org/lab/pdf/2016-LCH-cell_research.pdf) | Thy1+ cells cultured for passages 1 (P1), 1 week for each passage |
| Thy1+ cells P1 2 | KIZ | [TSDB2017R11](http://www.treeshrewdb.org/data/CR_SSC/TS4_BeadsP1.R1.fq.gz) | [TSDB2017R12](http://www.treeshrewdb.org/data/CR_SSC/TS4_BeadsP1.R1.fq.gz) | [Li et al., 2017](http://www.mitotool.org/lab/pdf/2016-LCH-cell_research.pdf) | Thy1+ cells cultured for passages 1 (P1), 1 week for each passage |
| Thy1+ cells P2 1 | KIZ | [TSDB2017R13](http://www.treeshrewdb.org/data/CR_SSC/TS3_BeadsP2.R1.fq.gz) | [TSDB2017R14](http://www.treeshrewdb.org/data/CR_SSC/TS3_BeadsP2.R2.fq.gz) | [Li et al., 2017](http://www.mitotool.org/lab/pdf/2016-LCH-cell_research.pdf) | Thy1+ cells cultured for passages 2 (P2), 1 week for each passage |
| Thy1+ cells P2 2 | KIZ | [TSDB2017R15](http://www.treeshrewdb.org/data/CR_SSC/TS4_BeadsP2.R1.fq.gz) | [TSDB2017R16](http://www.treeshrewdb.org/data/CR_SSC/TS4_BeadsP2.R2.fq.gz) | [Li et al., 2017](http://www.mitotool.org/lab/pdf/2016-LCH-cell_research.pdf) | Thy1+ cells cultured for passages 2 (P2), 1 week for each passage |

KIZ: Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China.

NIBS: National Institute of Biological Sciences, Beijing, China.

GEO: Gene Expression Omnibus (https://www.ncbi.nlm.nih.gov/gds)

TSDB: TreeshrewDB database (http://www.treeshrewdb.org)

Supplementary Table 2. Genomic structure variants (SVs) of the tree shrew

Supplementary Table 3. Genomic structure variants (SVs) of monkey

Supplementary Table 4. Genomic structure variants (SVs) of mouse

These three tables were listed as a separate Excel file, because each table is too big.

**Supplementary References**

Fan Y, Huang ZY, Cao CC, Chen CS, Chen YX, Fan DD, He J, Hou HL, Hu L, Hu XT, Jiang XT, Lai R, Lang YS, Liang B, Liao SG, Mu D, Ma YY, Niu YY, Sun XQ, Xia JQ, Xiao J, Xiong ZQ, Xu L, Yang L, Zhang Y, Zhao W, Zhao XD, Zheng YT, Zhou JM, Zhu YB, Zhang GJ, Wang J, Yao YG. 2013. Genome of the Chinese tree shrew. *Nature Communications* **4**: 1426.

Fan Y, Luo RC, Su LY, Xiang Q, Yu DD, Xu L, Chen JQ, Bi R, Wu DD, Zheng P, Yao YG. 2018. Does the genetic feature of the Chinese tree shrew (*Tupaia belangeri chinensis*) support its potential as a viable model for Alzheimer's disease research? *Journal of Alzheimers Disease* **61**(3): 1015-1028.

Li CH, Yan LZ, Ban WZ, Tu Q, Wu Y, Wang L, Bi R, Ji S, Ma YH, Nie WH, Lv LB, Yao YG, Zhao XD, Zheng P. 2017. Long-term propagation of tree shrew spermatogonial stem cells in culture and successful generation of transgenic offspring. *Cell Research* **27**(2): 241-252.

Yan H, Zhong G, Xu G, He W, Jing Z, Gao Z, Huang Y, Qi Y, Peng B, Wang H, Fu L, Song M, Chen P, Gao W, Ren B, Sun Y, Cai T, Feng X, Sui J, Li W. 2012. Sodium taurocholate cotransporting polypeptide is a functional receptor for human hepatitis B and D virus. *Elife* **1**:e00049