Supplementary information for "Sexual size dimorphism in mammals is associated with changes in the size of gene families related to brain development"

Supplementary figures.



Supplementary figure 1. Test of Rensch's rule. Asymmetry for sexual size dimorphism in mammals using logarithm transformed male and female body mass (kg). Red solid line: major-axis regression line; black dash line: slope = 1. The Rensch's rule does apply in the set of 124 species examined in this study as larger male sizes are associated with increasing departure from one-to-one relation in size with females (slope = 1.034, upper – lower confidence intervals: 1.019 - 1.050, p < 0.001). Consistently, we found a significant and positive association between SSD and body mass (r = 0.378; p < 0.001).



Supplementary figure 2. Tissue gene expression ranking in SSD-associated genes. The number on top of the bars represents the mean rank of the tissue. Lighter colours represent significant p-values. a) Expanding SSD-associated genes in adults, b) contracting SSD-associated genes in adults, c) expanding SSD-associated genes in prenatal stages and d) contracting SSD-associated genes in prenatal stages. Source data are provided as a source Data File.



Supplementary figure 3. Brain gene expression rank in SSD-associated genes. The dashed red line shows the mean rank of the SSD-associated gene expression in the brain compared to other tissues. Meanwhile, the solid dark line represents the distribution of 10,000 bootstrapped ranks of SSD-associated genes in the brain. In adults, a) SSD-associated genes under expansion exhibit no statistically significant difference in average gene expression rank compared to bootstrapped results. We observe a significant increase for b) genes under contraction (p < 0.001). In prenatal stages, c) SSD-associated genes under expansion do not display a statistically significant increase but significantly lower ranks compared to bootstrapped results (p < 0.001). d) SSD-associated genes under contraction also demonstrate significantly lower expression ranks than bootstrapped expectations (p < 0.001).



Supplementary figure 4. Temporal patterns of cortical expression of SSD-associated genes. Panels show average gene expression levels for A) SSDassociated under expansion genes in females, B) SSD-associated genes under contraction in females, C) SSD-associated genes under expansion in males and D) SSD-associated genes under contraction in males. The dashed line represents the end of gestation time (nine months). Source data are provided as a source Data File.



Supplementary figure 5. Gene families shared between PGLS with variation and no variation in gene numbers. The numbers in the diagram denote the total gene families that both PGLS share. Numbers in the outer regions of the diagram represent the gene families exclusive to each PGLS.

Structure acronym	Structure name	Brain structure
AMY	amygdaloid complex	Cortex
STC	posterior (caudal) superior temporal cortex (area	Cortex
	22c)	
CGE	caudal ganglionic eminence	Cortex
M1C	primary motor cortex (area M1, area 4)	Cortex
S1C	primary somatosensory cortex (area S1, areas	Cortex
	3,1,2)	
DTH	dorsal thalamus	Cortex
MD	mediodorsal nucleus of thalamus	Cortex
A1C	primary auditory cortex (core)	Cortex
DFC	dorsolateral prefrontal cortex	Cortex
STR	striatum	Cortex
V1C	primary visual cortex (striate cortex, area V1/17)	Cortex
OFC	orbital frontal cortex	Cortex
СВ	cerebellum	Cortex
MFC	anterior (rostral) cingulate (medial prefrontal)	Cortex
	cortex	
TCx	temporal neocortex	Cortex
MGE	medial ganglionic eminence	Cortex
HIP	hippocampus (hippocampal formation)	Subcortex
VFC	ventrolateral prefrontal cortex	Subcortex
ITC	inferolateral temporal cortex (area TEv, area 20)	Subcortex
URL	upper (rostral) rhombic lip	Subcortex
PCx	parietal neocortex	Subcortex
IPC	posteroventral (inferior) parietal cortex	Subcortex
Ocx	occipital neocortex	Cerebellum
CBC	cerebellar cortex	Cerebellum
M1C-S1C	primary motor-sensory cortex (samples)	Cerebellum

Supplementary Table 1. List of terms, abbreviations, and descriptions of brain structures used for sexbiased gene expression in temporal brain analysis.