ELECTRONIC SUPPLEMENTARY MATERIAL

Gómez-Robles A, Hopkins WD, Schapiro SJ, Sherwood CC. 2016 The heritability of chimpanzee and human brain asymmetry. Proceedings of the Royal Society B 20161319. http://dx.doi.org/10.1098/rspb.2016.1319

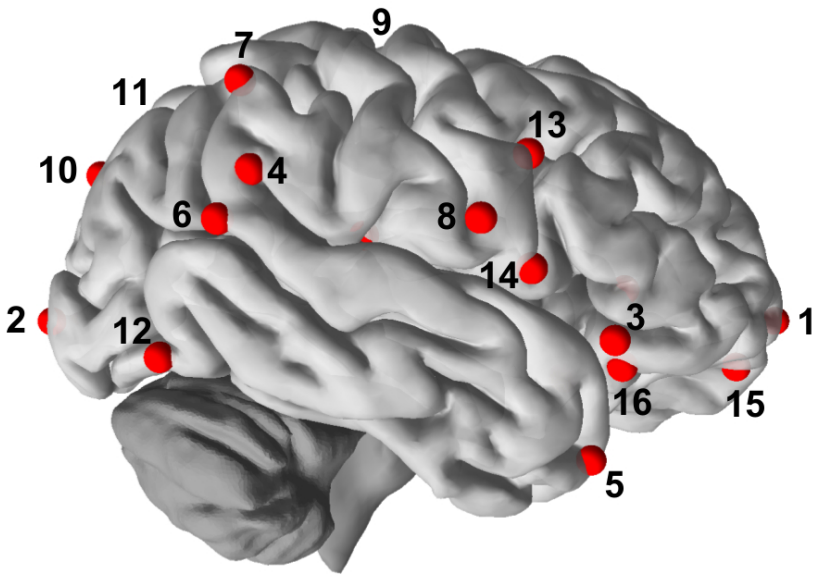

Figure 1. Anatomically homologous landmarks used in this study overlaid on a human brain.

Table S1. Definition of anatomical landmarks.

Landmark	Definition
1	Frontal pole
2	Occipital pole
3	Anterior end of the Sylvian fissure (defined on the pars orbitalis in humans)
4	Posterior end of the Sylvian fissure (following the main course of the fissure when the terminal segment is divided)
5	Anterior end of the superior temporal sulcus (close to the temporal pole)
6	Inflection point between the horizontal segment and the ascending segment of the superior temporal sulcus
7	Most posterior and superior point of the superior temporal sulcus (located between the supramarginal gyrus and the angular gyrus)
8	Inferior termination of the central sulcus
9	Superior termination of the central sulcus (intersection between the central sulcus and the midline)
10	In chimpanzees: intersection between the intraparietal sulcus and the lunate sulcus In humans: intersection between the intraparietal sulcus and the transverse occipital sulcus
11	In chimpanzees: intersection of the lunate sulcus with the midline In humans: intersection of the parieto-occipital sulcus with the midline
12	In chimpanzees: most inferior and lateral point of the lunate sulcus In humans: occipital notch
13	Intersection of the inferior frontal sulcus with the precentral sulcus
14	Inferior end of the precentral sulcus
15	In chimpanzees: superior end of the fronto-orbital sulcus In humans: anterior end of the latero-orbital sulcus
16	In chimpanzees: inferior end of the fronto-orbital sulcus In humans: posterior end of the latero-orbital sulcus

Table S2. Definition of interlandmark distances.

Lobe proportions	
Variable	**Defined between landmarks**
Superior frontal length (SF)	1 and 9
Inferior frontal length (IF)	1 and 8
Temporal length (T)	5 and 10
Superior parietal length (SP)	9 and 11
Inferior parietal length (IP)	8 and 10
Occipital length (O)	2 and 11
Sulcal lengths	
Variable	**Defined between landmarks**
Fronto-orbital (FOS) or latero-orbital sulcus (LOS)	15 and 16
Precentral sulcus (PCS)	13 and 14
Central sulcus (CS)	8 and 9
Sylvian fissure (SyF)	3 and 4
Superior temporal sulcus (STS)	5 and 6, plus 6 and 7
Lunate (LS) or parieto-occipital sulcus (POS)	10 and 11, plus 10 and 12

Table S3. Heritability of lobe proportions in chimpanzees

	Left				Right			
	h^2	**HPDI**	**ΔDIC (P)**	**Fixed**	**h^2**	**HPDI**	**ΔDIC (P)**	**Fixed**
SF	**0.45**	0.20-0.70	49.88 (0.003)	scan	**0.55**	0.27-0.77	71.41 (<0.001)	scan
IF	**0.39**	0.17-0.72	48.19 (0.004)	—	**0.62**	0.36-0.87	110.04 (<0.001)	sex, age, sex*age
T	**0.47**	0.20-0.75	60.31 (0.003)	scan	**0.58**	0.26-0.80	76.36 (<0.001)	scan
SP	**0.63**	0.33-0.82	91.23 (<0.001)	sex, scan	**0.42**	0.27-0.77	69.63 (0.001)	sex, scan
IP	**0.65**	0.38-0.86	111.56 (<0.001)	scan	**0.71**	0.41-0.88	136.44 (<0.001)	sex
O	**0.52**	0.28-0.82	85.85 (<0.001)	scan	**0.61**	0.28-0.82	83.04 (<0.001)	—

h^2: heritability; HPDI: highest posterior density interval; ΔDIC (P): difference in the deviance information criterion between the model with and without pedigree information (P-value); Fixed: significant fixed effects. Bold: significant heritability under our simulation-based threshold.

Table S4. Heritability of lobe proportions in humans

	Left				Right			
	h^2	**HPDI**	**ΔDIC (P)**	**Fixed**	**h^2**	**HPDI**	**ΔDIC (P)**	**Fixed**
SF	0.20	0.08-0.39	5.04 (0.419)	—	**0.40**	0.15-0.63	34.22 (0.017)	—
IF	0.20	0.11-0.49	14.03 (0.126)	—	**0.53**	0.27-0.72	64.43 (<0.001)	—
T	**0.36**	0.15-0.57	29.55 (0.024)	—	**0.64**	0.40-0.80	106.38 (<0.001)	—
SP	**0.40**	0.19-0.66	45.46 (0.003)	—	**0.32**	0.13-0.57	25.79 (0.034)	—
IP	**0.42**	0.18-0.62	41.13 (0.005)	—	**0.38**	0.15-0.58	29.98 (0.024)	—
O	**0.65**	0.35-0.84	101.50 (<0.001)	—	**0.52**	0.26-0.73	63.01 (<0.001)	—

h^2: heritability; HPDI: highest posterior density interval; ΔDIC (P): difference in the deviance information criterion between the model with and without pedigree information (P-value); Fixed: significant fixed effects. Bold: significant heritability under our simulation-based threshold.

Table S5. Phenotypic and genetic correlations between corresponding left and right lobe proportions.

	Chimpanzee		Human	
	ρ_P (HPDI)	**ρ_G (HPDI)**	**ρ_P (HPDI)**	**ρ_G (HPDI)**
SF	**0.89** (0.85-0.91)	**0.85** (0.72-0.93)	**0.67** (0.59-0.74)	**0.70** (0.35-0.87)
IF	**0.57** (0.47-0.66)	**0.69** (0.36-0.84)	**0.30** (0.17-0.43)	**0.45** (0.07-0.73)
T	**0.69** (0.61-0.76)	**0.78** (0.57-0.90)	**0.46** (0.35-0.56)	**0.66** (0.40-0.81)
SP	**0.78** (0.71-0.83)	**0.83** (0.64-0.90)	**0.64** (0.55-0.71)	**0.68** (0.40-0.87)
IP	**0.60** (0.49-0.67)	**0.74** (0.54-0.87)	**0.35** (0.21-0.45)	**0.52** (0.18-0.76)
O	**0.84** (0.79-0.88)	**0.87** (0.70-0.92)	**0.72** (0.64-0.78)	**0.81** (0.61-0.89)

ρ_P: phenotypic correlation; ρ_G: genetic correlation; HPDI: highest posterior density interval. Bold: significant correlation as indicated by a HPDI that does not include 0.

Table S6. Heritability of sulcal lengths in chimpanzees

	Left				Right			
	h^2	**HPDI**	**ΔDIC (P)**	**Fixed**	**h^2**	**HPDI**	**ΔDIC (P)**	**Fixed**
FOS	**0.29**	0.15-0.59	28.19 (0.049)	—	**0.34**	0.13-0.61	29.37 (0.044)	—
PCS	0.25	0.10-0.56	20.32 (0.099)	—	0.27	0.10-0.52	16.25 (0.153)	—
CS	**0.43**	0.18-0.69	43.98 (0.007)	—	**0.39**	0.19-0.73	52.14 (0.003)	scan
SyF	**0.38**	0.16-0.62	35.69 (0.020)	—	**0.38**	0.19-0.66	42.29 (0.010)	scan
STS	**0.52**	0.19-0.75	59.53 (0.003)	—	**0.31**	0.14-0.65	32.45 (0.030)	—
LS	0.32	0.13-0.61	26.16 (0.062)	sex, age, scan	**0.34**	0.13-0.64	31.72 (0.032)	scan

h^2: heritability; HPDI: highest posterior density interval; ΔDIC (P): difference in the deviance information criterion between the model with and without pedigree information (P-value); Fixed: significant fixed effects. Bold: significant heritability under our simulation-based threshold.

Table S7. Heritability of sulcal lengths in humans

	Left				Right			
	h^2	**HPDI**	**ΔDIC (P)**	**Fixed**	**h^2**	**HPDI**	**ΔDIC (P)**	**Fixed**
LOS	0.19	0.07-0.34	0.38 (0.667)	—	0.21	0.10-0.46	11.25 (0.187)	—
PCS	0.25	0.09-0.45	9.84 (0.229)	—	0.18	0.08-0.38	4.19 (0.463)	—
CS	**0.44**	0.16-0.64	39.47 (0.008)	sex, sex*age	**0.45**	0.21-0.63	45.32 (0.003)	—
SyF	0.25	0.11-0.47	16.97 (0.090)	—	**0.38**	0.17-0.60	33.36 (0.018)	—
STS	0.29	0.10-0.46	13.48 (0.136)	—	0.17	0.08-0.37	3.96 (0.475)	—
POS	**0.30**	0.11-0.57	22.34 (0.047)	—	0.20	0.10-0.52	15.11 (0.113)	—

h^2: heritability; HPDI: highest posterior density interval; ΔDIC (P): difference in the deviance information criterion between the model with and without pedigree information (P-value); Fixed: significant fixed effects. Bold: significant heritability under our simulation-based threshold.

Table S8. Phenotypic and genetic correlations between corresponding left and right sulcal lengths.

	Chimpanzee		Human	
	ρ_P (HPDI)	**ρ_G (HPDI)**	**ρ_P (HPDI)**	**ρ_G (HPDI)**
FOS/LOS	**0.33** (0.18-0.43)	0.46 (-0.02-0.73)	**0.25** (0.13-0.38)	0.30 (-0.17-0.66)
PCS	**0.30** (0.19-0.43)	0.41 (-0.15-0.71)	**0.38** (0.17-0.41)	0.31 (-0.16-0.64)
CS	**0.59** (0.50-0.68)	**0.76** (0.42-0.87)	**0.34** (0.25-0.48)	**0.64** (0.35-0.80)
SyF	**0.48** (0.37-0.59)	**0.50** (0.12-0.75)	**0.32** (0.19-0.43)	**0.55** (0.23-0.78)
STS	**0.59** (0.50-0.67)	**0.72** (0.38-0.86)	**0.24** (0.09-0.35)	0.14 (-0.28-0.56)
LS/POS	**0.59** (0.46-0.65)	**0.57** (0.12-0.80)	**0.38** (0.25-0.48)	0.40 (-0.08-0.72)

ρ_P: phenotypic correlation; ρ_G: genetic correlation; HPDI: highest posterior density interval. Bold: significant correlation as indicated by a HPDI that does not include 0.

Table S9. Heritability of asymmetry quotients (AQs) for lobe proportions.

	Chimpanzees					Humans				
	AQ (P)	**h^2**	**HPDI**	**ΔDIC (P)**	**Fixed**	**AQ (P)**	**h^2**	**HPDI**	**ΔDIC (P)**	**Fixed**
SF	0.18 (0.153)	0.15	0.06-0.38	1.46 (0.730)	—	-0.17 (0.352)	0.14	0.07-0.32	-1.00 (0.737)	—
IF	**1.13** (0.003)	0.29	0.12-0.59	23.27 (0.075)	—	**2.71** (<0.001)	0.18	0.09-0.44	9.24 (0.244)	—
T	-0.34 (0.100)	0.16	0.07-0.38	1.27 (0.737)	—	-0.39 (0.070)	0.25	0.11-0.47	16.32 (0.096)	—
SP	**1.69** (0.010)	0.23	0.09-0.47	11.25 (0.276)	—	0.70 (0.201)	0.19	0.08-0.39	3.62 (0.488)	—
IP	**-1.67** (<0.001)	0.22	0.08-0.46	9.30 (0.358)	—	**-3.52** (<0.001)	0.25	0.10-0.42	9.96 (0.227)	—
O	**-2.62** (0.001)	0.18	0.10-0.49	11.72 (0.265)	—	0.52 (0.425)	0.19	0.09-0.44	7.63 (0.304)	—

AQ (P): Asymmetry quotient in % of total length and P-value testing if AQs are significantly different from 0. h^2: heritability; HPDI: highest posterior density interval; ΔDIC (P): difference in the deviance information criterion between the model with and without pedigree information (P-value); Fixed: significant fixed effects. Bold: AQs that differ significantly from 0. No heritability is significant under our simulation-based threshold.

Table S10. Heritability of asymmetry quotients (AQs) for sulcal lengths.

	Chimpanzees					Humans				
	AQ (P)	**h^2**	**HPDI**	**ΔDIC (P)**	**Fixed**	**AQ (P)**	**h^2**	**HPDI**	**ΔDIC (P)**	**Fixed**
FOS/ LOS	-1.04 (0.214)	0.22	0.08-0.45	10.17 (0.318)	—	**-6.03** (<0.001)	0.13	0.07-0.34	0.04 (0.682)	—
PCS	3.75 (0.060)	0.23	0.09-0.47	12.09 (0.249)	—	0.08 (0.949)	0.17	0.07-0.34	-0.22 (0.696)	—
CS	-0.36 (0.169)	0.20	0.07-0.38	2.22 (0.688)	scan	-0.65 (0.072)	0.16	0.07-0.36	0.87 (0.639)	Sex, age, sex*age
SyF	**-2.68** (<0.001)	0.27	0.12-0.58	20.89 (0.092)	—	**-7.46** (<0.001)	0.17	0.07-0.33	0.75 (0.649)	—
STS	**-1.20** (0.001)	0.20	0.08-0.42	5.28 (0.524)	—	**-4.00** (<0.001)	0.22	0.09-0.40	6.51 (0.347)	—
LS/ POS	-0.82 (0.130)	0.21	0.09-0.49	9.75 (0.338)	sex, age, sex*age	**2.02** (<0.001)	0.20	0.08-0.43	6.69 (0.341)	—

AQ (P): Asymmetry quotient in % of total length and P-value testing if AQs are significantly different from 0. h^2: heritability; HPDI: highest posterior density interval; ΔDIC (P): difference in the deviance information criterion between the model with and without pedigree information

(P-value); Fixed: significant fixed effects. Bold: AQs that differ significantly from 0. No heritability is significant under our simulation-based threshold.

Table S11. Heritability of principal components of asymmetric shape variation in chimpanzees, which represent major patterns of asymmetric variation in the sample.

	% var	DA α	h^2	HPDI	ΔDIC (P)	Fixed
PC1	13.07	85.52	0.21	0.08-0.44	6.77 (0.457)	—
PC2	9.69	**64.71**	0.17	0.09-0.42	8.83 (0.378)	—
PC3	7.70	**76.25**	0.18	0.07-0.39	1.89 (0.706)	sex, age, sex*age, scan
PC4	6.95	84.97	0.16	0.06-0.37	0.36 (0.780)	—
PC5	5.62	86.52	0.24	0.10-0.53	15.37 (0.168)	—

% var: percentage of variance explained by each principal component; DA α: angle formed between each eigenvector and the directional asymmetry vector (values closer to 0º indicate a stronger relationship, and values closer to 90º indicate total dissimilarity; 78.42º is the significance threshold above which vectors are considered unrelated); h^2: heritability; HPDI: highest posterior density interval; ΔDIC (P): difference in the deviance information criterion between the model with and without pedigree information (P-value); Fixed: significant fixed effects. Bold: PCs that are significantly correlated with DA. No heritability is significant under our simulation-based threshold.

Table S12. Heritability of principal components of asymmetric shape variation in humans, which represent major patterns of asymmetric variation in the sample.

	% var	DA α	h^2	HPDI	ΔDIC (P)	Fixed
PC1	13.48	**36.38**	0.25	0.10-0.50	16.15 (0.096)	—
PC2	8.80	81.75	0.29	0.11-0.49	17.86 (0.081)	sex
PC3	8.08	78.60	0.23	0.10-0.50	14.65 (0.120)	—
PC4	7.34	**71.68**	0.19	0.09-0.41	8.50 (0.274)	—
PC5	5.84	86.28	0.25	0.08-0.44	10.27 (0.219)	—

% var: percentage of variance explained by each principal component; DA α: angle formed between each eigenvector and the directional asymmetry vector (values closer to 0º indicate a stronger relationship, and values closer to 90º indicate total dissimilarity; 78.42º is the significance threshold above which vectors are considered unrelated); h^2: heritability; HPDI: highest posterior density interval; ΔDIC (P): difference in the deviance information criterion between the model with and without pedigree information (P-value); Fixed: significant fixed effects. Bold: PCs that are significantly correlated with DA. No heritability is significant under our simulation-based threshold.