

Supplemental Materials:

Supplemental Figure 1: Bayesian analyses of chromosomal make-up across vertebrate taxa. (A) Gecko: *Sphaerodactylus townsendi*, (B) Wall lizard: *Podarcis muralis*, (C) Chinese alligator: *Alligator sinensis*, (D) Human: *Homo sapiens*, (E) Crocodile lizard: *Shinisaurus crocodilurus*, (F) Argentine black and white tegu: *Salvator merianae*, (G) Indian cobra: *Naja naja*, (H) Yellowpond turtle: *Mauremys mutica*, (I) Chicken: *Gallus gallus*, (J) Zebra finch: *Taeniopygia guttata*, (K) Black swan: *Cygnus atratus*, (L) Southern platyfish: *Xiphophorus maculatus*.

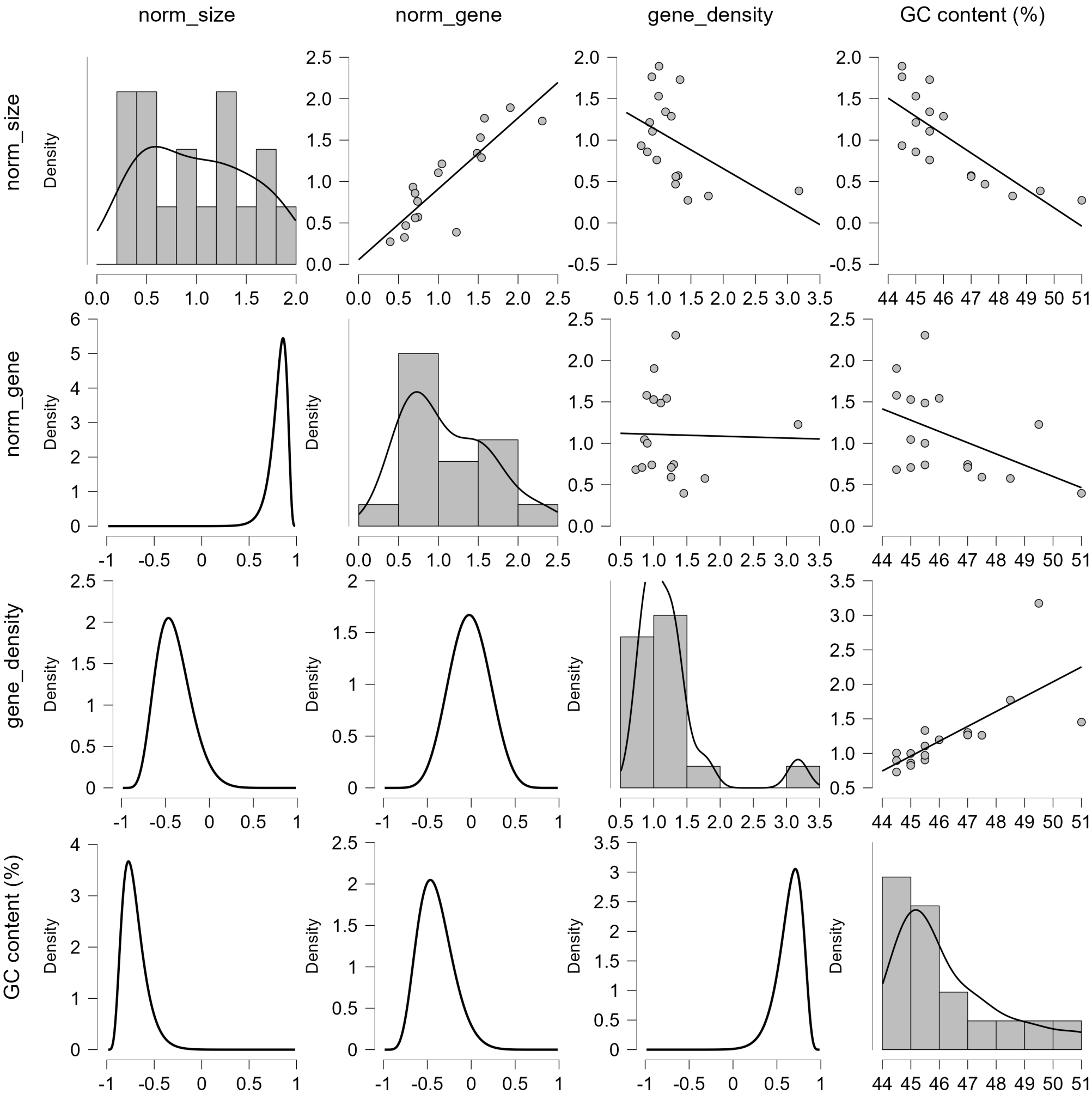
Bayesian Correlation

Bayesian Pearson Correlations

			n	Pearson's r	BF ₁₀
norm_size	-	norm_gene	17	0.865***	2879.882
norm_size	-	gene_density	17	-0.477	1.702
norm_size	-	GC content (%)	17	-0.781***	161.651
norm_gene	-	gene_density	17	-0.024	0.301
norm_gene	-	GC content (%)	17	-0.476	1.688
gene_density	-	GC content (%)	17	0.721**	40.141

* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot



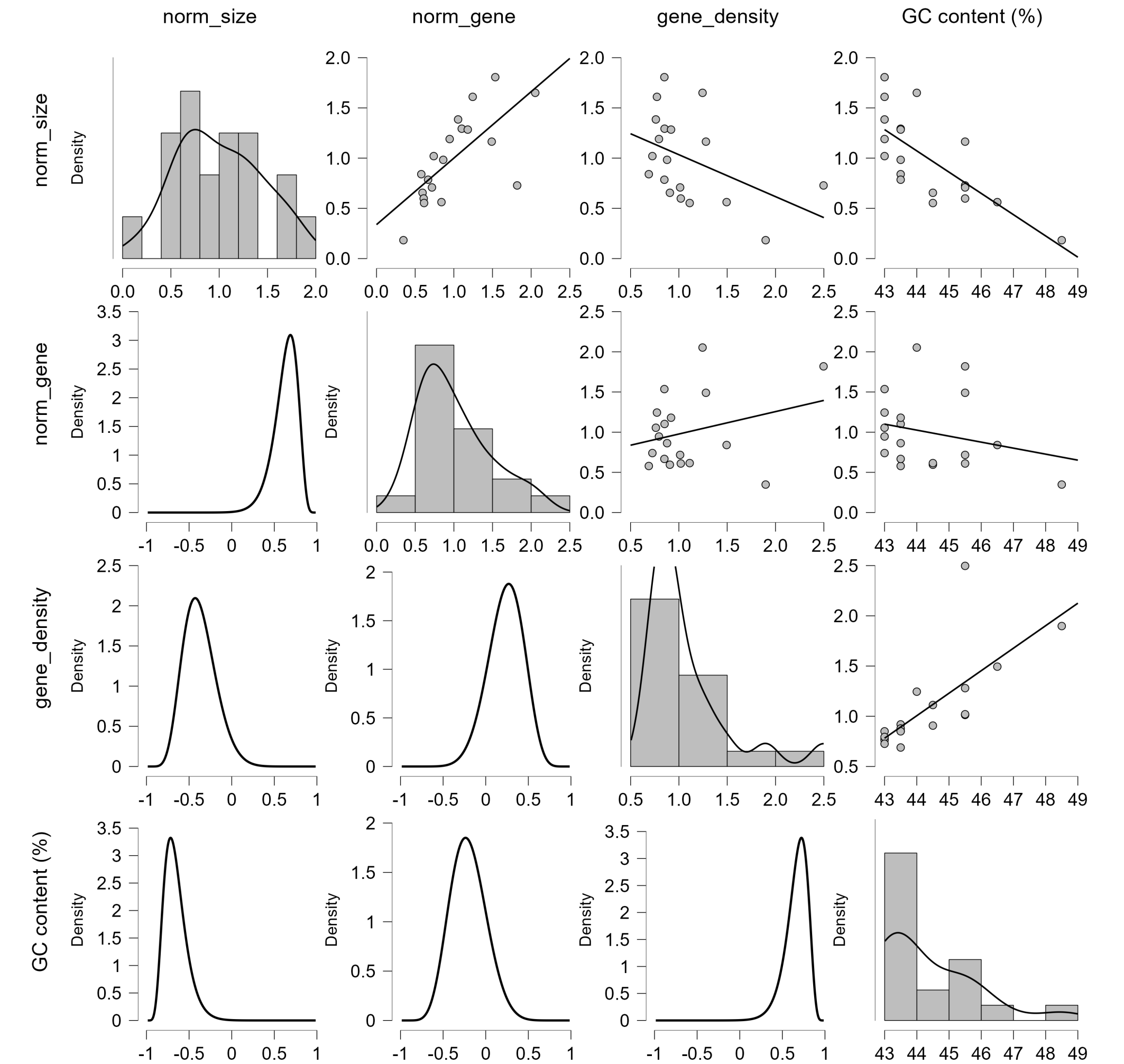
Bayesian Correlation

Bayesian Pearson Correlations

			n	Pearson's r	BF ₁₀
norm_size	-	norm_gene	19	0.699**	48.582
norm_size	-	gene_density	19	-0.438	1.464
norm_size	-	GC content (%)	19	-0.727**	90.447
norm_gene	-	gene_density	19	0.277	0.525
norm_gene	-	GC content (%)	19	-0.243	0.454
gene_density	-	GC content (%)	19	0.734***	105.664

* BF₁₀> 10, ** BF₁₀> 30, *** BF₁₀> 100

Bayesian Correlation Matrix Plot



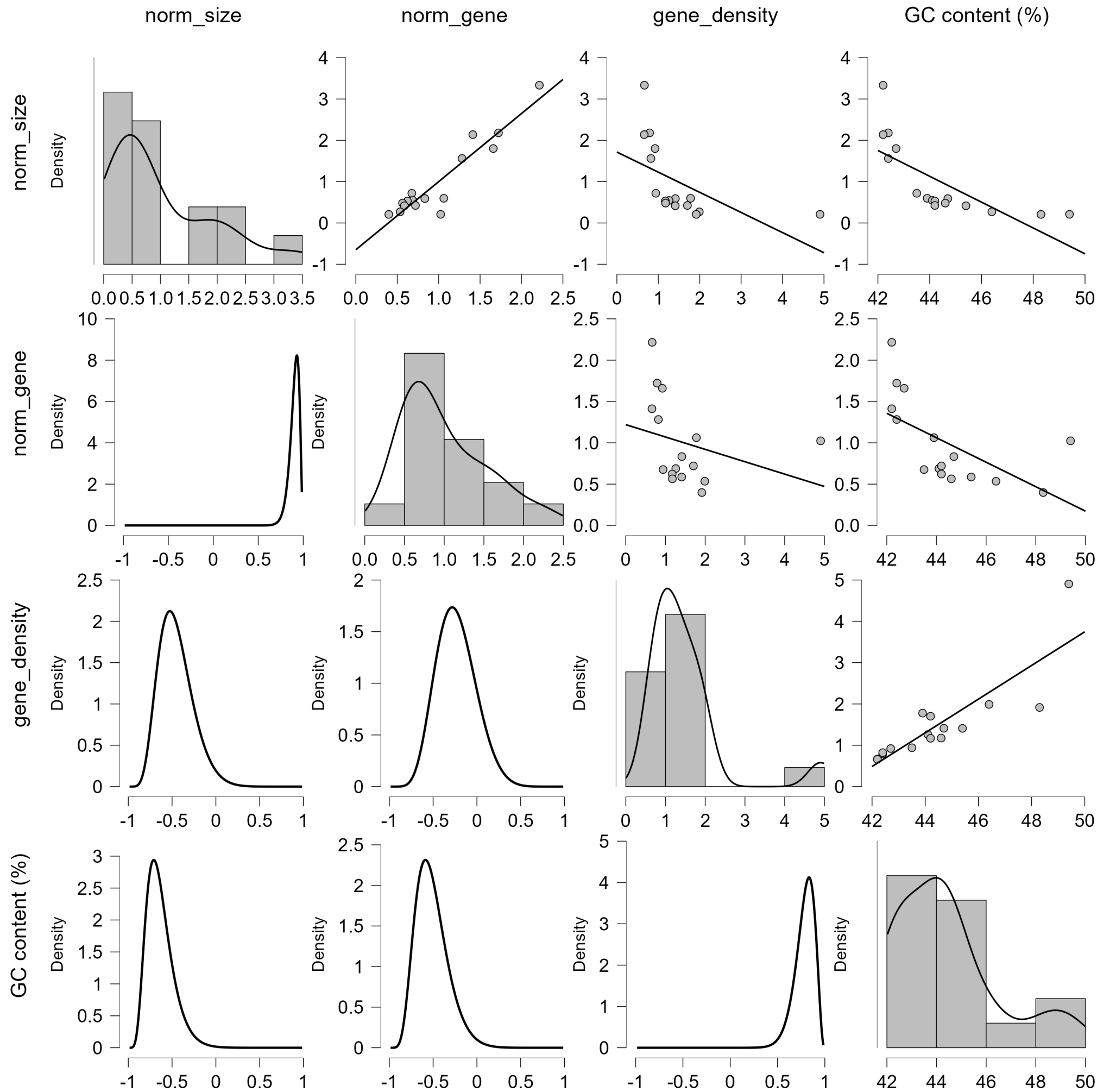
Bayesian Correlation

Bayesian Pearson Correlations

			Pearson's r	BF ₁₀
norm_size	-	norm_gene	0.936***	111257.209
norm_size	-	gene_density	-0.538	2.591
norm_size	-	GC content (%)	-0.720*	28.773
norm_gene	-	gene_density	-0.291	0.536
norm_gene	-	GC content (%)	-0.600	4.958
gene_density	-	GC content (%)	0.850***	847.880

* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot

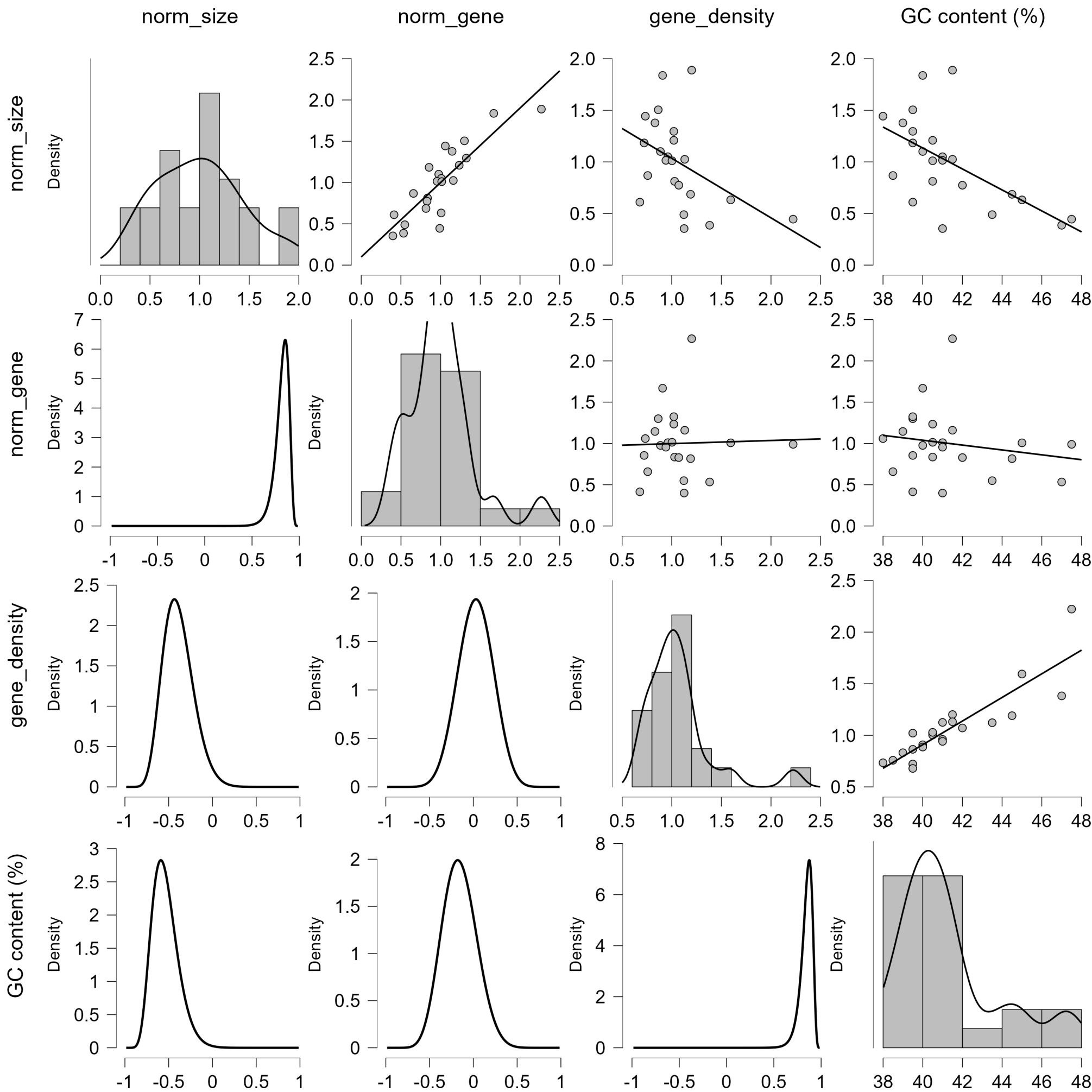


Bayesian Correlation

Bayesian Pearson Correlations			n	Pearson's r	BF ₁₀
norm_size	-	norm_gene	23	0.857***	86563.421
norm_size	-	gene_density	23	-0.443	2.134
norm_size	-	GC content (%)	23	-0.598*	18.642
norm_gene	-	gene_density	23	0.031	0.261
norm_gene	-	GC content (%)	23	-0.183	0.359
gene_density	-	GC content (%)	23	0.879***	402621.999

* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot



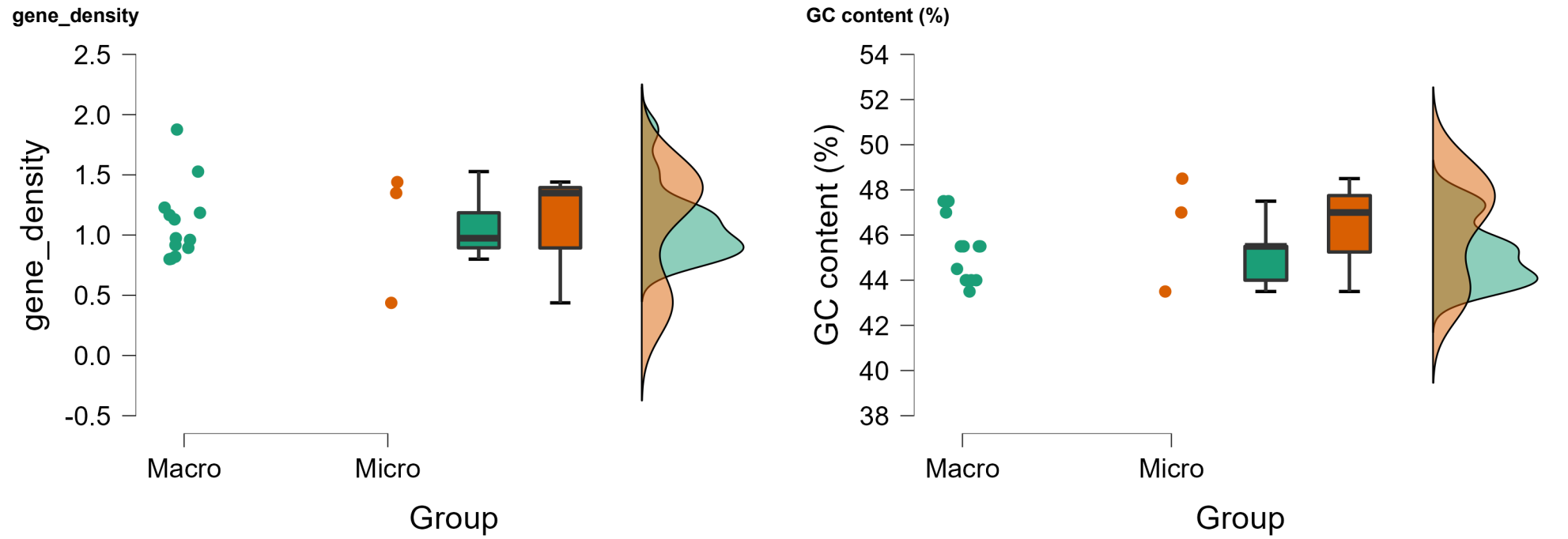
Bayesian Independent Samples T-Test

Bayesian Mann-Whitney U Test			
	BF ₀	W	Rhat
gene_density	0.508	17.000	1.006
GC content (%)	0.703	15.000	1.000

Note. For all tests, the alternative hypothesis specifies that the location of group *Macro* is smaller than the location of group *Micro* .
Note. Result based on data augmentation algorithm with 5 chains of 1000 iterations.

Descriptives

Raincloud Plots

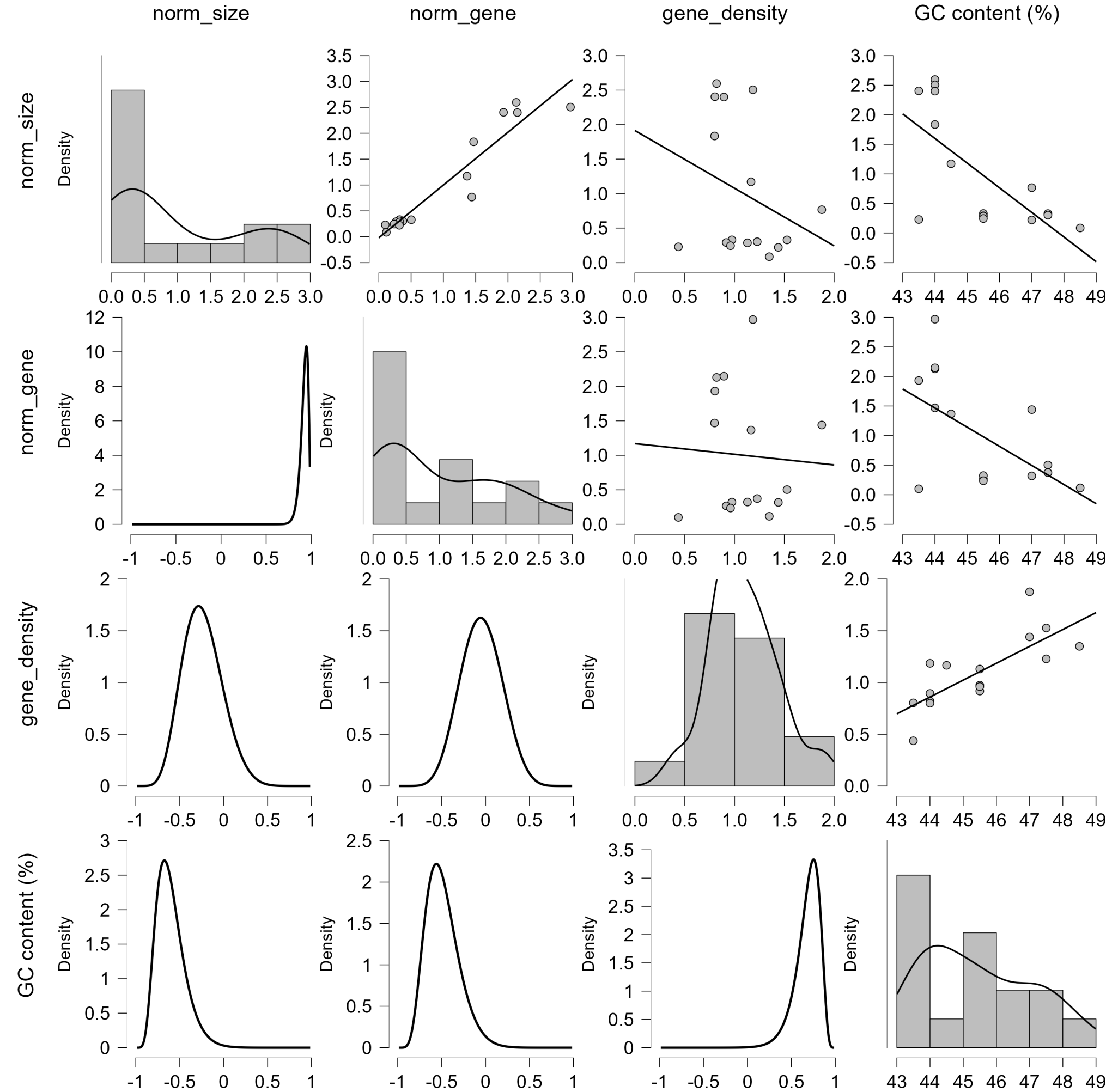


Bayesian Correlation

Bayesian Pearson Correlations					
		n	Pearson's r	BF ₁₀	
norm_size	-	norm_gene	16	0.950***	501947.382
norm_size	-	gene_density	16	-0.294	0.543
norm_size	-	GC content (%)	16	-0.687*	16.134
norm_gene	-	gene_density	16	-0.058	0.315
norm_gene	-	GC content (%)	16	-0.572	3.635
gene_density	-	GC content (%)	16	0.764**	69.420

* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot



Bayesian Independent Samples T-Test

Bayesian Mann-Whitney U Test

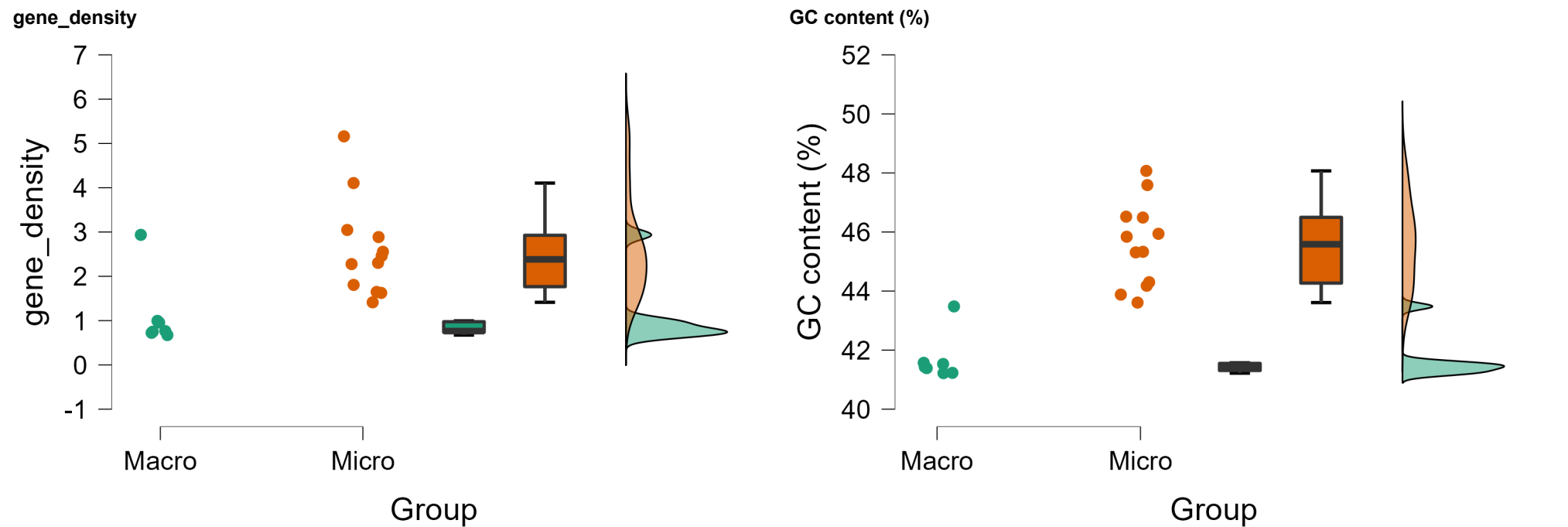
	BF-0	W	Rhat
gene_density	5.712	9.000	1.004
GC content (%)	15.370	0.000	1.001

Note. For all tests, the alternative hypothesis specifies that the location of group *Macro* is smaller than the location of group *Micro* .

Note. Result based on data augmentation algorithm with 5 chains of 1000 iterations.

Descriptives

Raincloud Plots



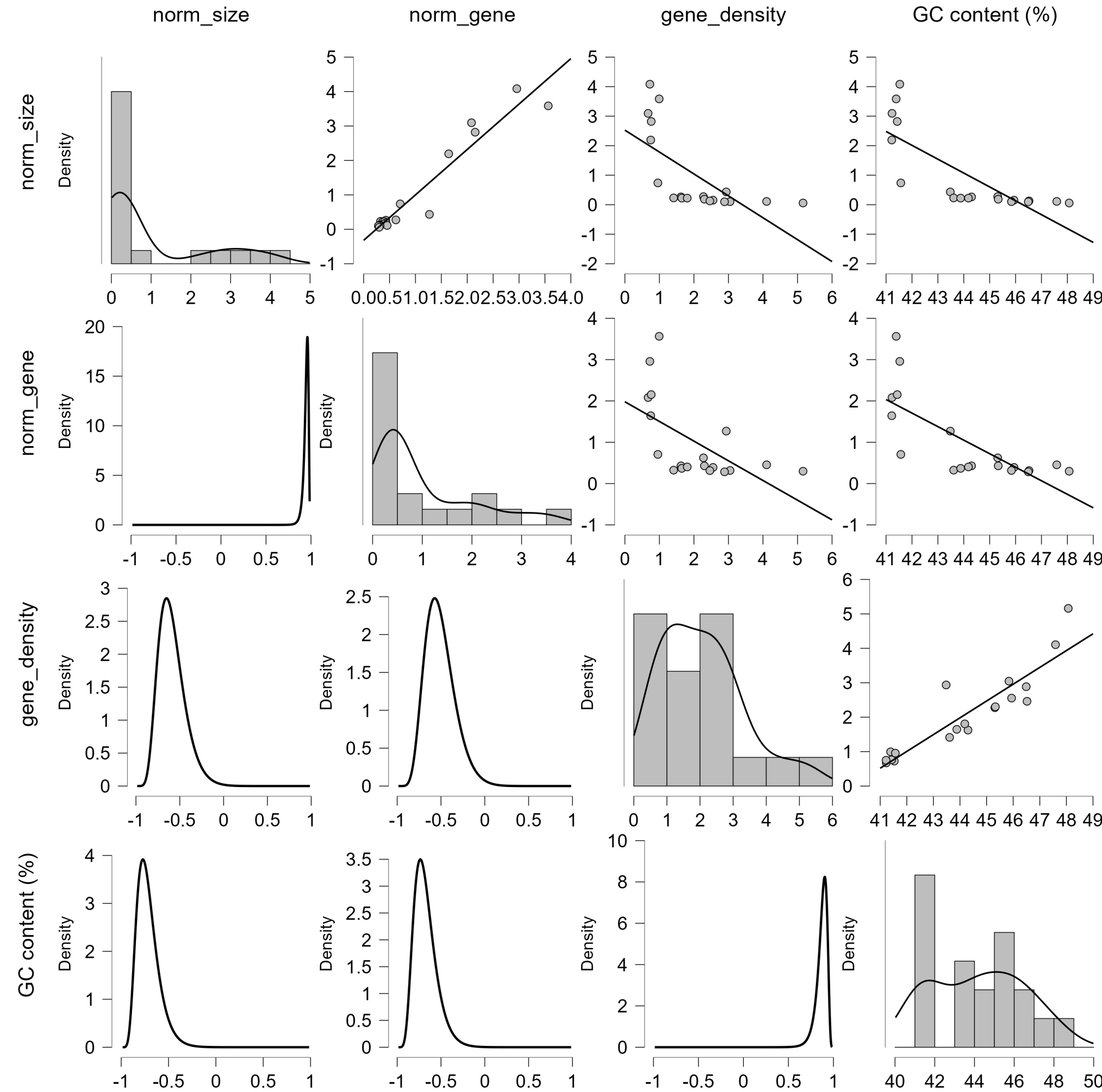
Bayesian Correlation

Bayesian Pearson Correlations

		n	Pearson's r	BF ₁₀
norm_size	- norm_gene	19	0.962***	1.089e+8
norm_size	- gene_density	19	-0.662*	23.654
norm_size	- GC content (%)	19	-0.780***	369.298
norm_gene	- gene_density	19	-0.582	6.845
norm_gene	- GC content (%)	19	-0.745***	140.687
gene_density	- GC content (%)	19	0.908***	162973.383

* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot



Bayesian Independent Samples T-Test

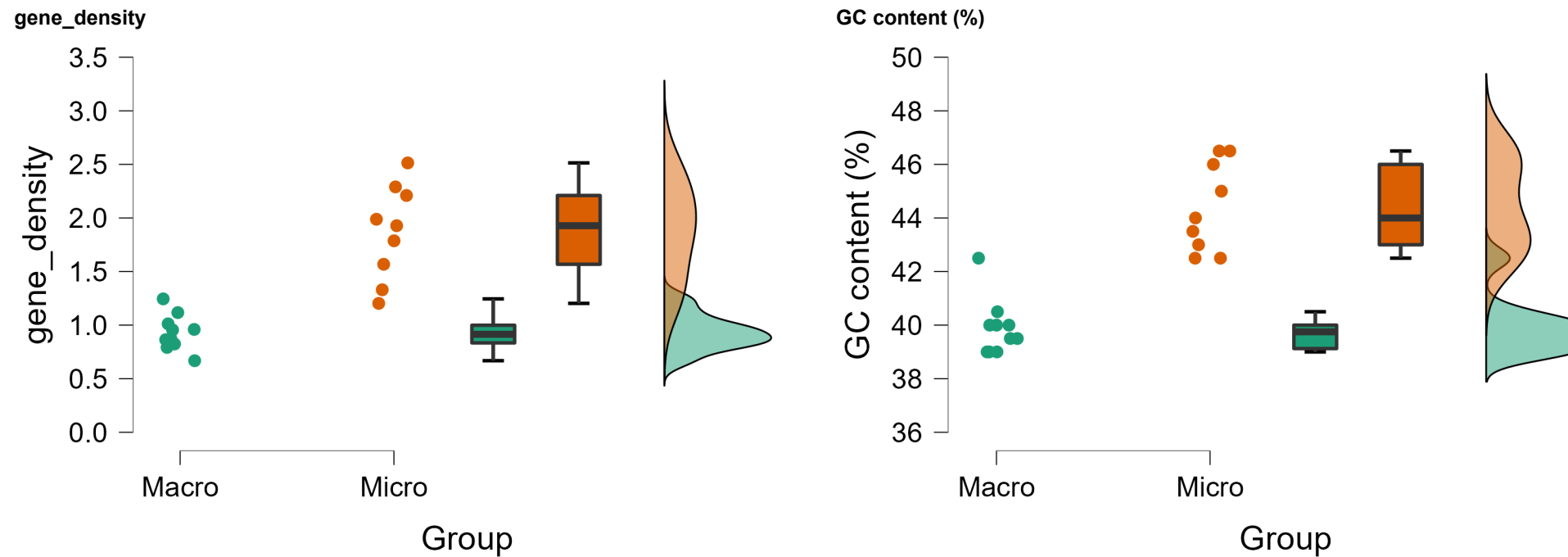
Bayesian Mann-Whitney U Test

	BF ₀	W	Rhat
gene_density	21.345	1.000	1.005
GC content (%)	24.951	1.000	1.000

Note. For all tests, the alternative hypothesis specifies that the location of group *Macro* is smaller than the location of group *Micro* .
Note. Result based on data augmentation algorithm with 5 chains of 1000 iterations.

Descriptives

Raincloud Plots



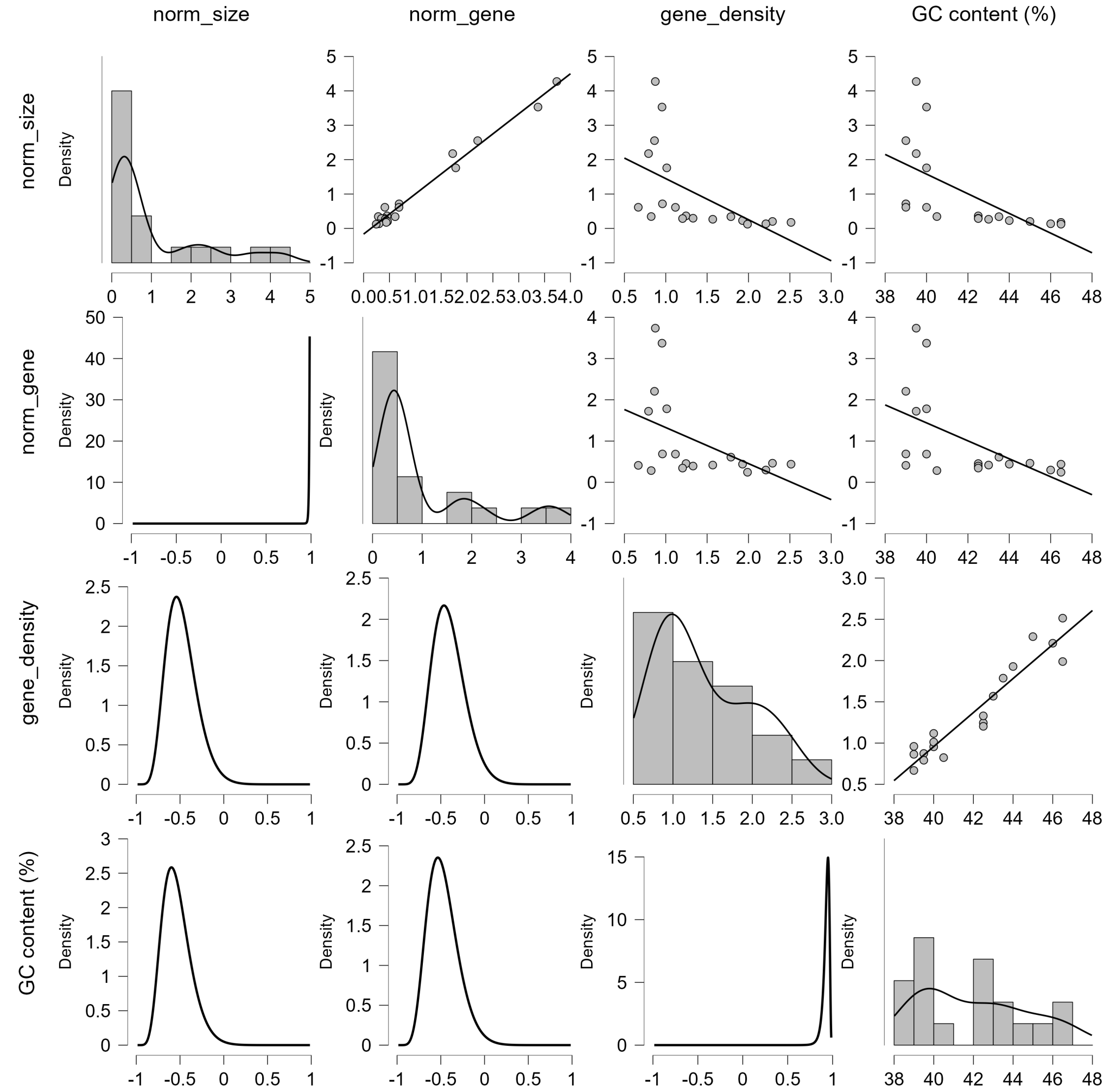
Bayesian Correlation

Bayesian Pearson Correlations

			n	Pearson's r	BF ₁₀
norm_size	-	norm_gene	19	0.992***	7.758e+12
norm_size	-	gene_density	19	-0.551	4.591
norm_size	-	GC content (%)	19	-0.609	9.944
norm_gene	-	gene_density	19	-0.474	2.005
norm_gene	-	GC content (%)	19	-0.545	4.249
gene_density	-	GC content (%)	19	0.952***	1.741e+7

* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot



Bayesian Independent Samples T-Test

Bayesian Mann-Whitney U Test

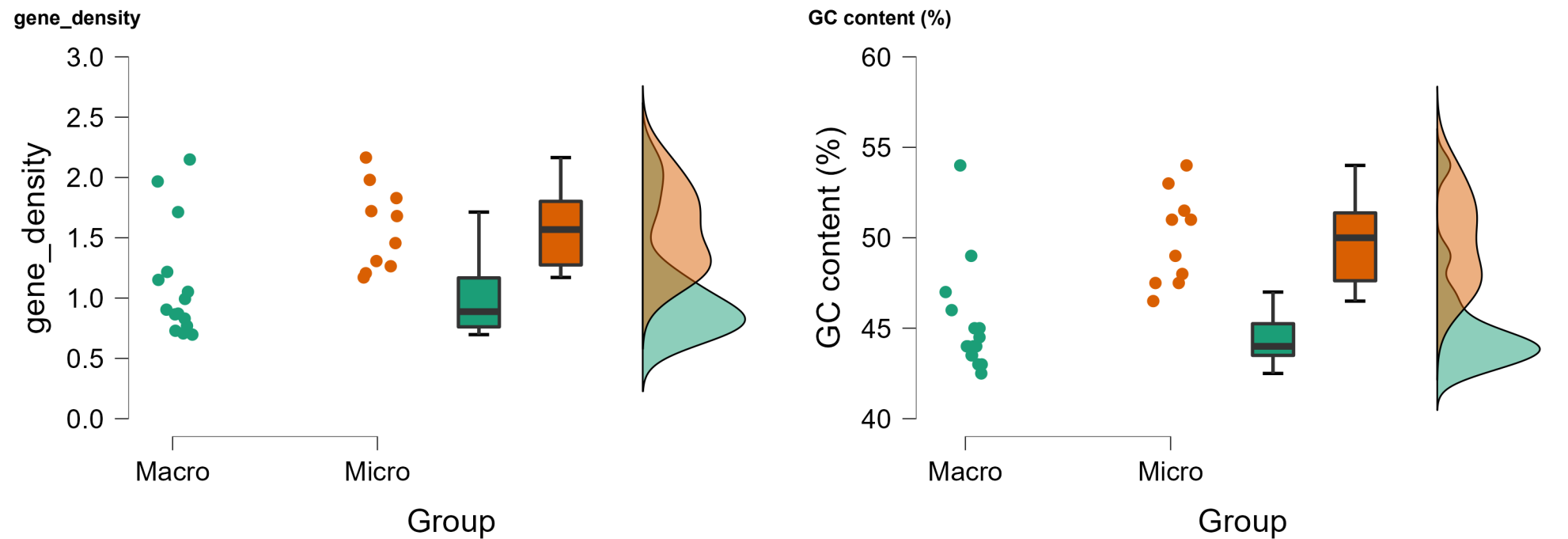
	BF-o	W	Rhat
gene_density	7.625	25.000	1.007
GC content (%)	17.355	15.000	1.003

Note. For all tests, the alternative hypothesis specifies that the location of group *Macro* is smaller than the location of group *Micro* .

Note. Result based on data augmentation algorithm with 5 chains of 1000 iterations.

Descriptives

Raincloud Plots



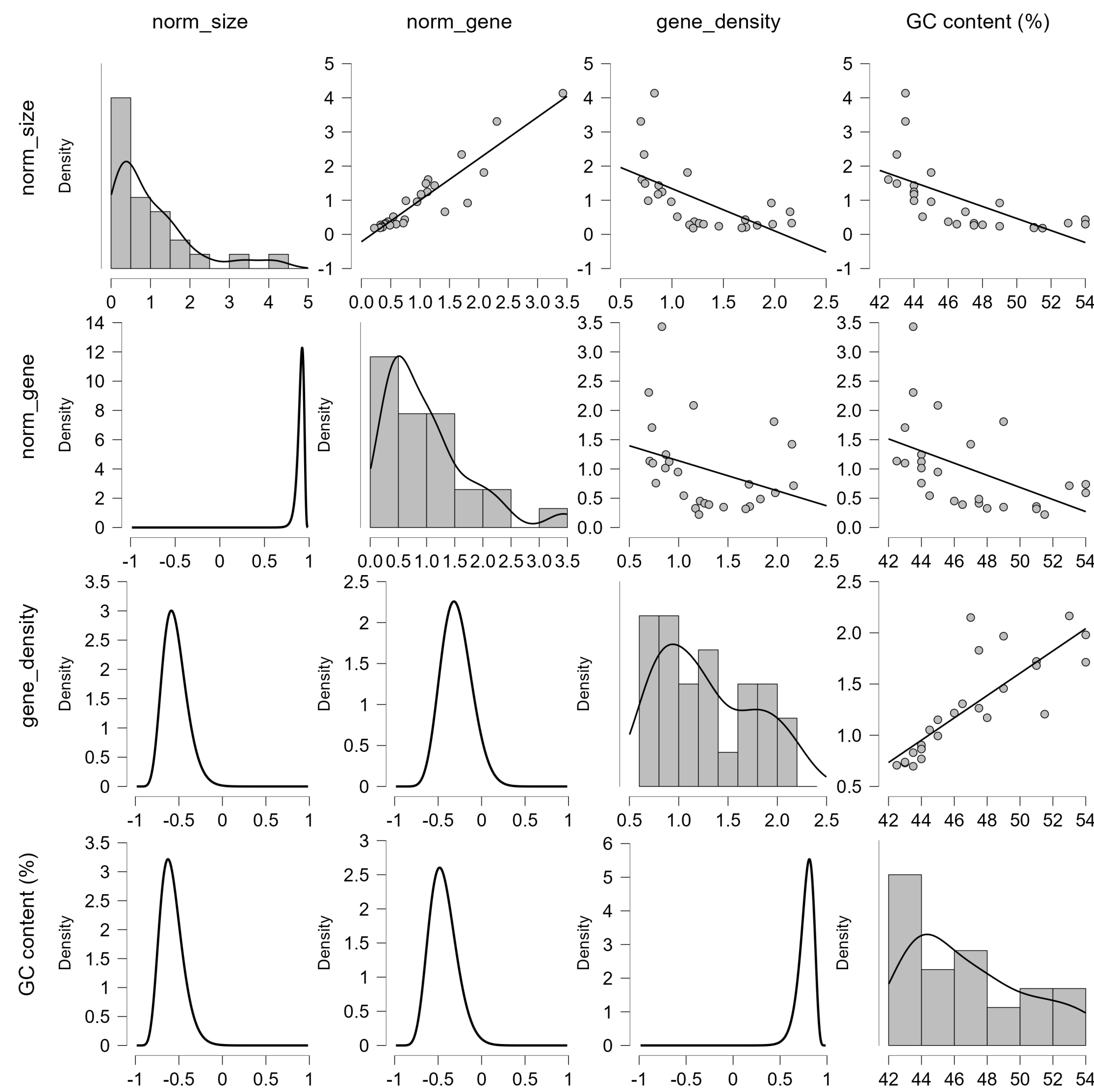
Bayesian Correlation

Bayesian Pearson Correlations

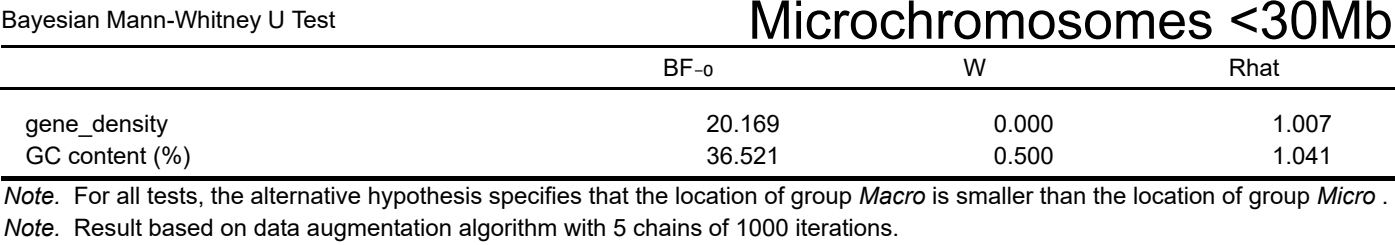
		n	Pearson's r	BF ₁₀
norm_size	- norm_gene	26	0.925***	5.066e+8
norm_size	- gene_density	26	-0.595**	31.421
norm_size	- GC content (%)	26	-0.633**	73.342
norm_gene	- gene_density	26	-0.324	0.836
norm_gene	- GC content (%)	26	-0.490	5.190
gene_density	- GC content (%)	26	0.817***	50912.759

* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot

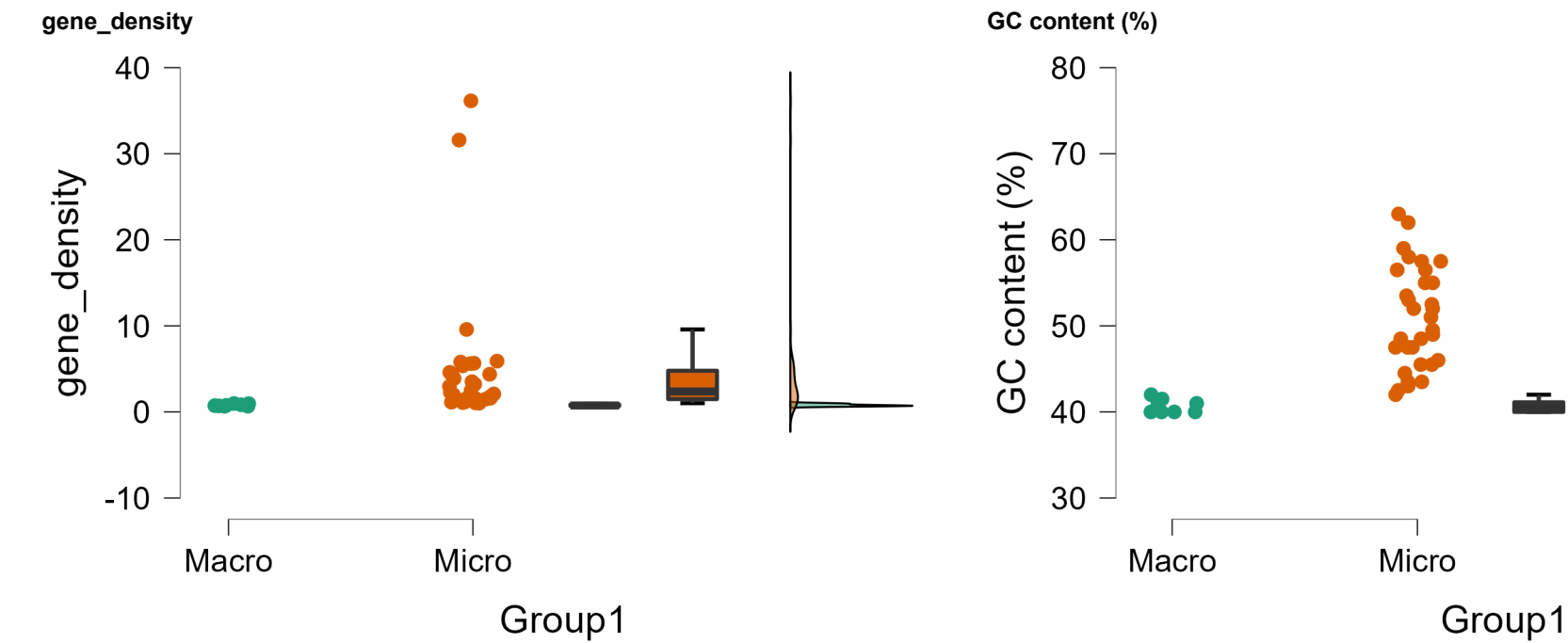


Bayesian Independent Samples T-Test

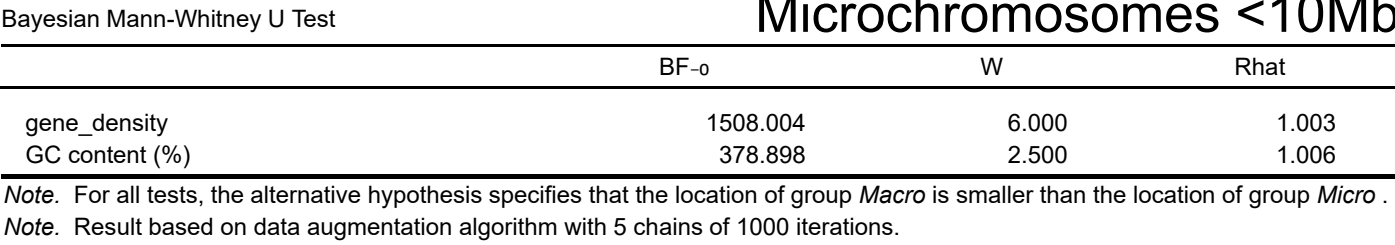


Descriptives

Raincloud Plots

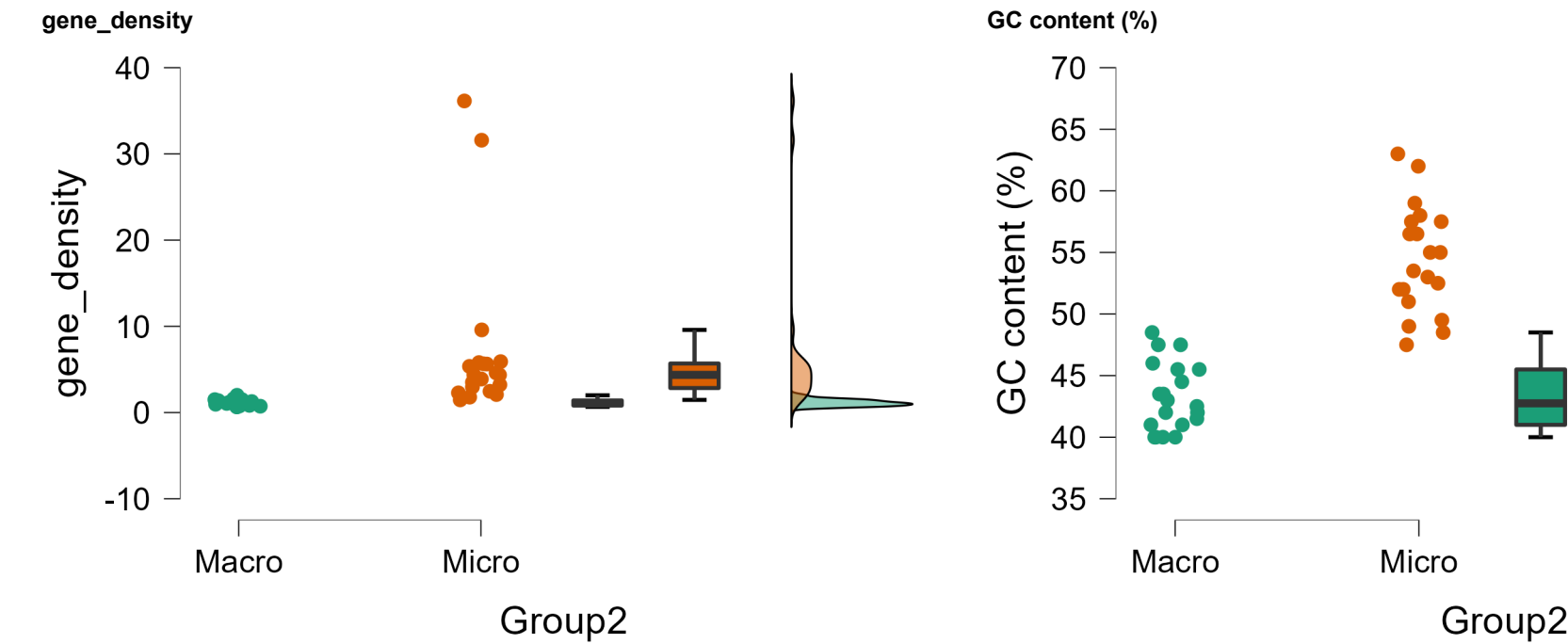


Bayesian Independent Samples T-Test



Descriptives

Raincloud Plots

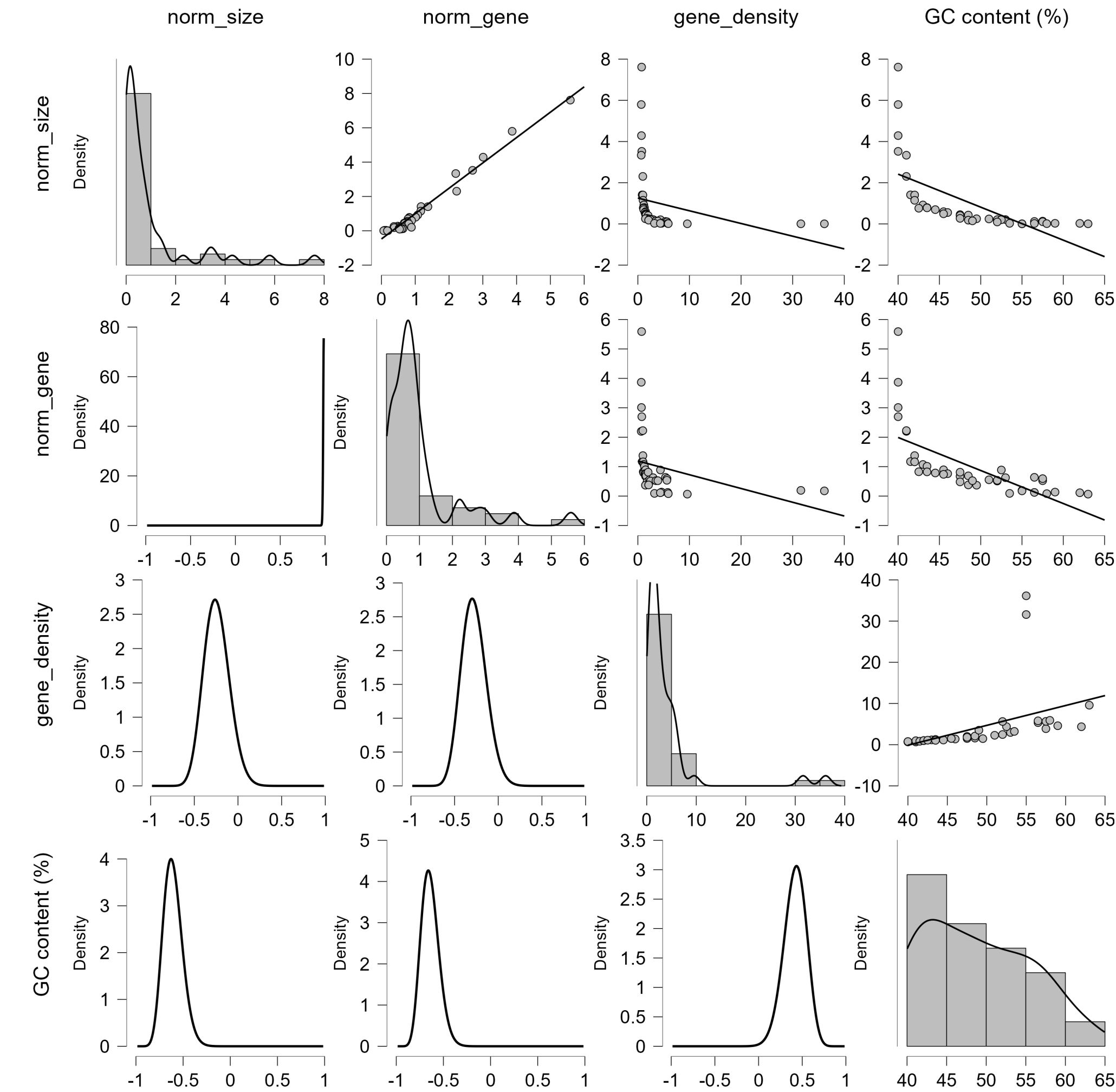


Bayesian Correlation

Bayesian Pearson Correlations				
		n	Pearson's r	BF ₁₀
norm_size	- norm_gene	40	0.986***	2.908e+27
norm_size	- gene_density	40	-0.266	0.744
norm_size	- GC content (%)	40	-0.642***	2921.784
norm_gene	- gene_density	40	-0.302	1.114
norm_gene	- GC content (%)	40	-0.674***	11004.147
gene_density	- GC content (%)	40	0.448*	11.276

* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot



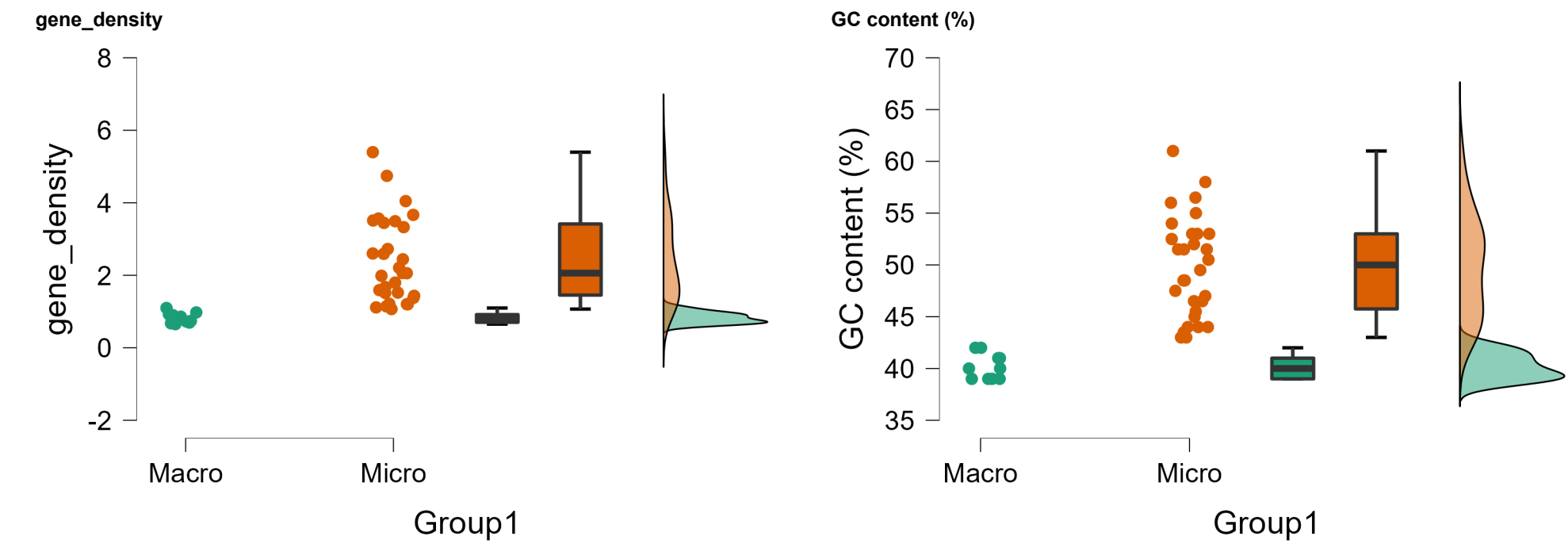
Bayesian Independent Samples T-Test

Bayesian Mann-Whitney U Test			
	BF-o	W	Rhat
gene_density	50.297	1.000	1.062
GC content (%)	217.699	0.000	1.020

Note. For all tests, the alternative hypothesis specifies that the location of group *Macro* is smaller than the location of group *Micro* .
Note. Result based on data augmentation algorithm with 5 chains of 1000 iterations.

Descriptives

Raincloud Plots



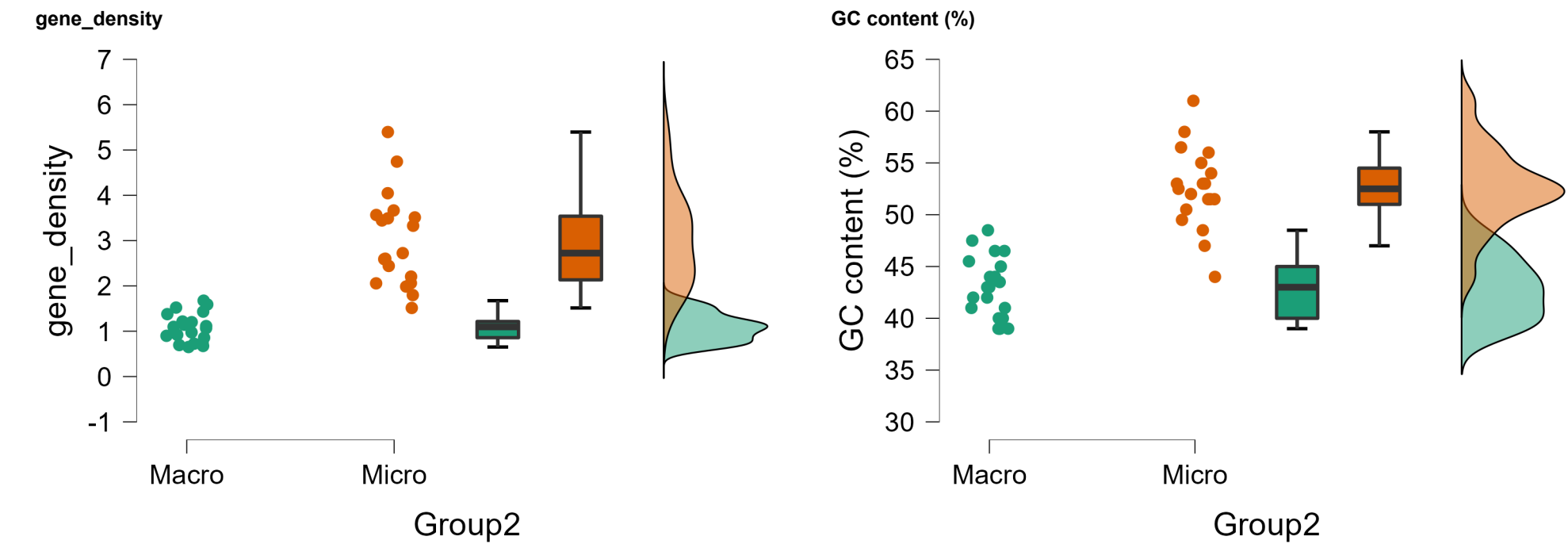
Bayesian Independent Samples T-Test

Bayesian Mann-Whitney U Test			
	BF-o	W	Rhat
gene_density	574.148	3.000	1.005
GC content (%)	631.566	9.500	1.000

Note. For all tests, the alternative hypothesis specifies that the location of group *Macro* is smaller than the location of group *Micro* .
Note. Result based on data augmentation algorithm with 5 chains of 1000 iterations.

Descriptives

Raincloud Plots

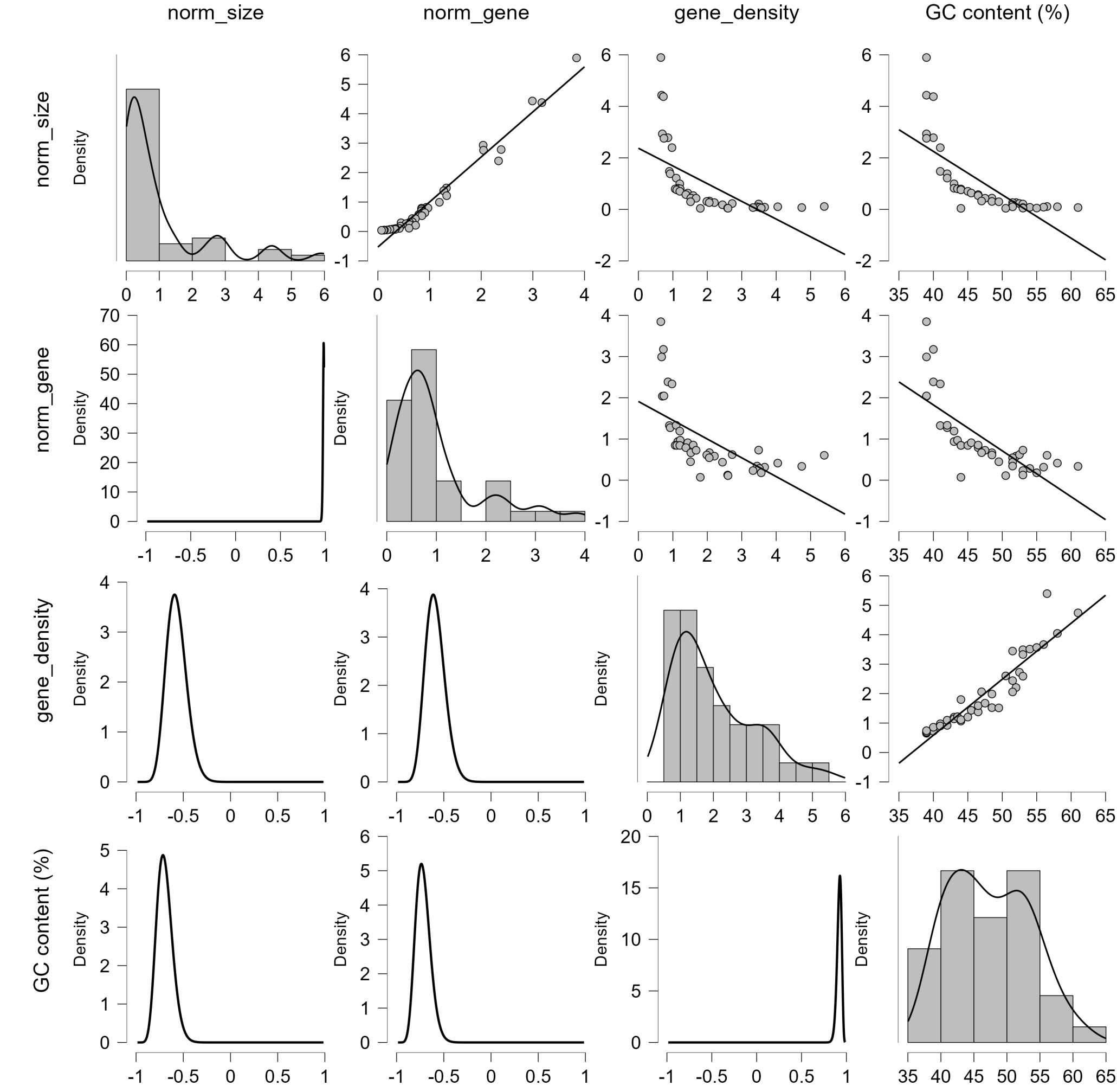


Bayesian Correlation

Bayesian Pearson Correlations					
		n	Pearson's r	BF ₁₀	
norm_size	-	norm_gene	40	0.983***	5.665e+25
norm_size	-	gene_density	40	-0.606***	779.978
norm_size	-	GC content (%)	40	-0.728***	162609.166
norm_gene	-	gene_density	40	-0.626***	1566.868
norm_gene	-	GC content (%)	40	-0.749***	584207.309
gene_density	-	GC content (%)	40	0.932***	1.594e+15

* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot

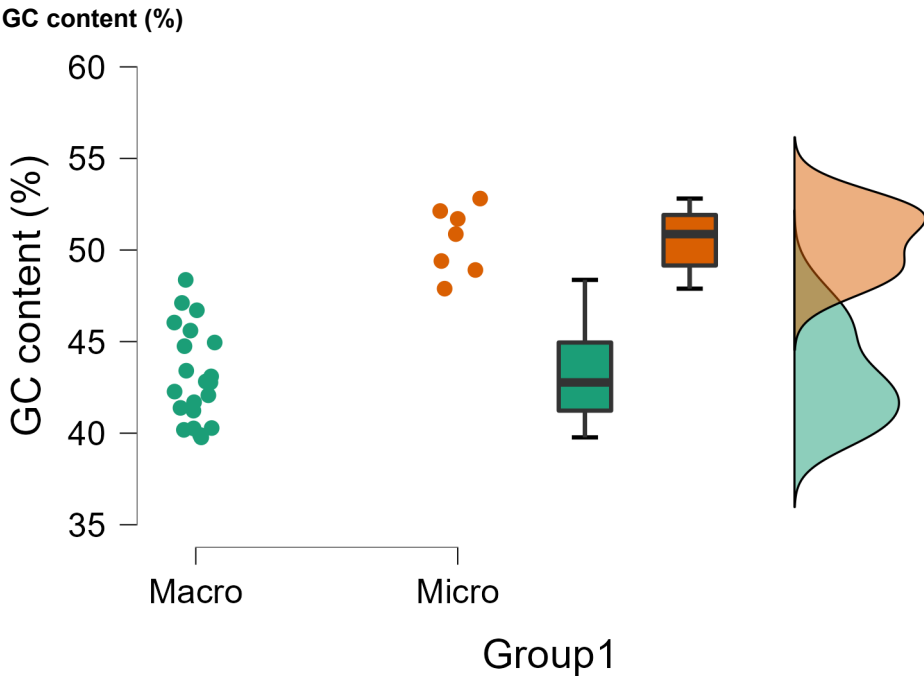


Bayesian Independent Samples T-Test

Bayesian Mann-Whitney U Test		Microchromosomes <30Mb	
	BF _{-o}	W	Rhat
GC content (%)	20.148	1.000	1.005
<i>Note.</i> For all tests, the alternative hypothesis specifies that the location of group <i>Macro</i> is smaller than the location of group <i>Micro</i> . <i>Note.</i> Result based on data augmentation algorithm with 5 chains of 1000 iterations.			

Descriptives

Raincloud Plots

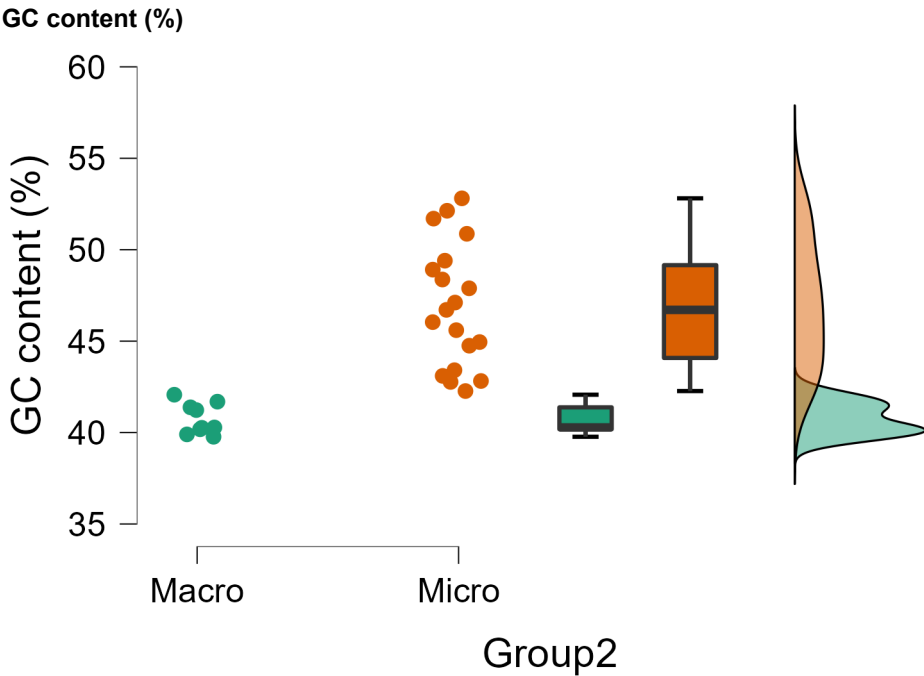


Bayesian Independent Samples T-Test

Bayesian Mann-Whitney U Test		Microchromosomes <10Mb	
	BF _{-o}	W	Rhat
GC content (%)	56.836	0.000	1.010
<i>Note.</i> For all tests, the alternative hypothesis specifies that the location of group <i>Macro</i> is smaller than the location of group <i>Micro</i> . <i>Note.</i> Result based on data augmentation algorithm with 5 chains of 1000 iterations.			

Descriptives

Raincloud Plots

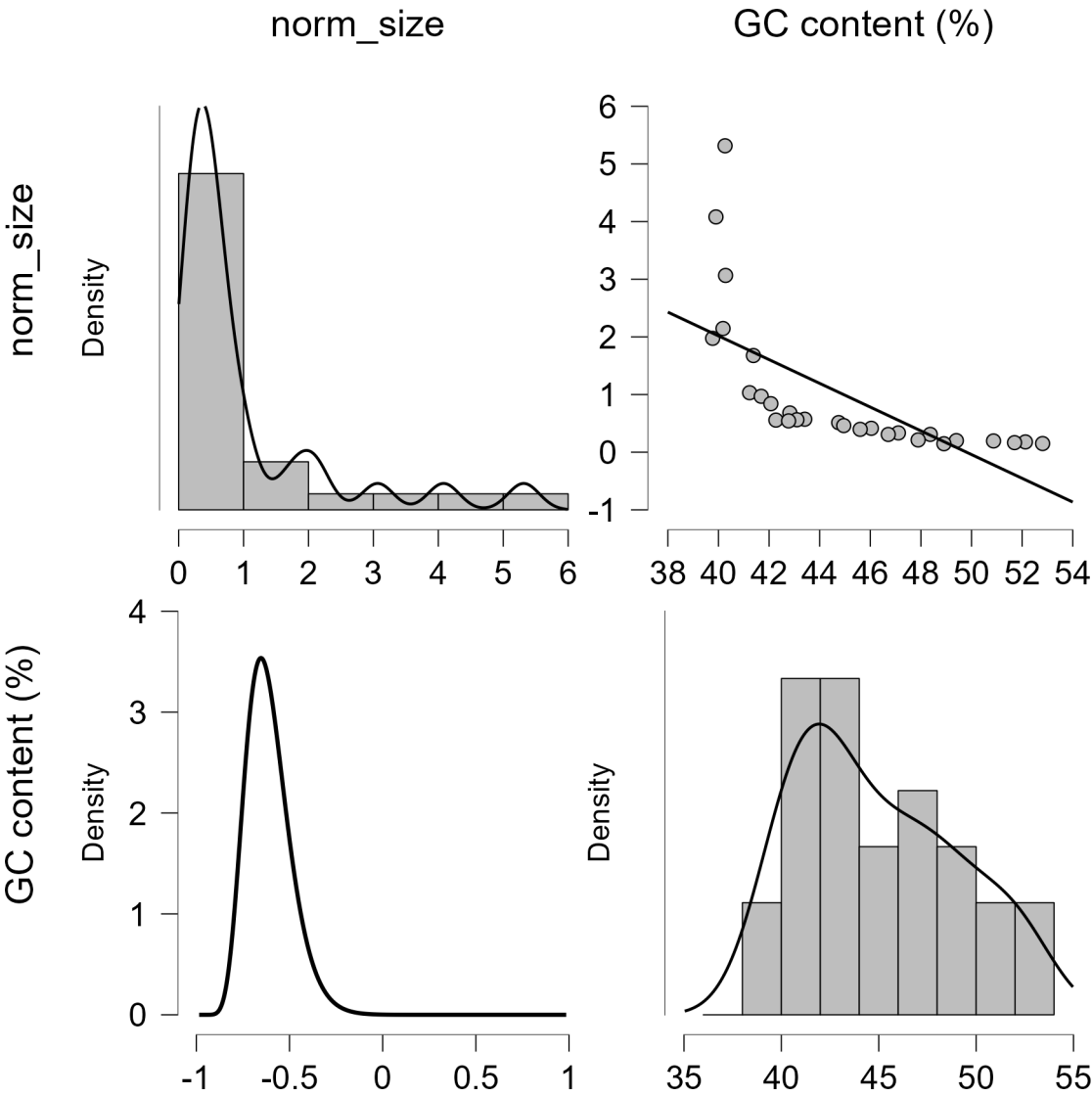


Bayesian Correlation

Bayesian Pearson Correlations				
			Pearson's r	BF ₁₀
norm_size	-	GC content (%)	-0.660***	241.027

* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot



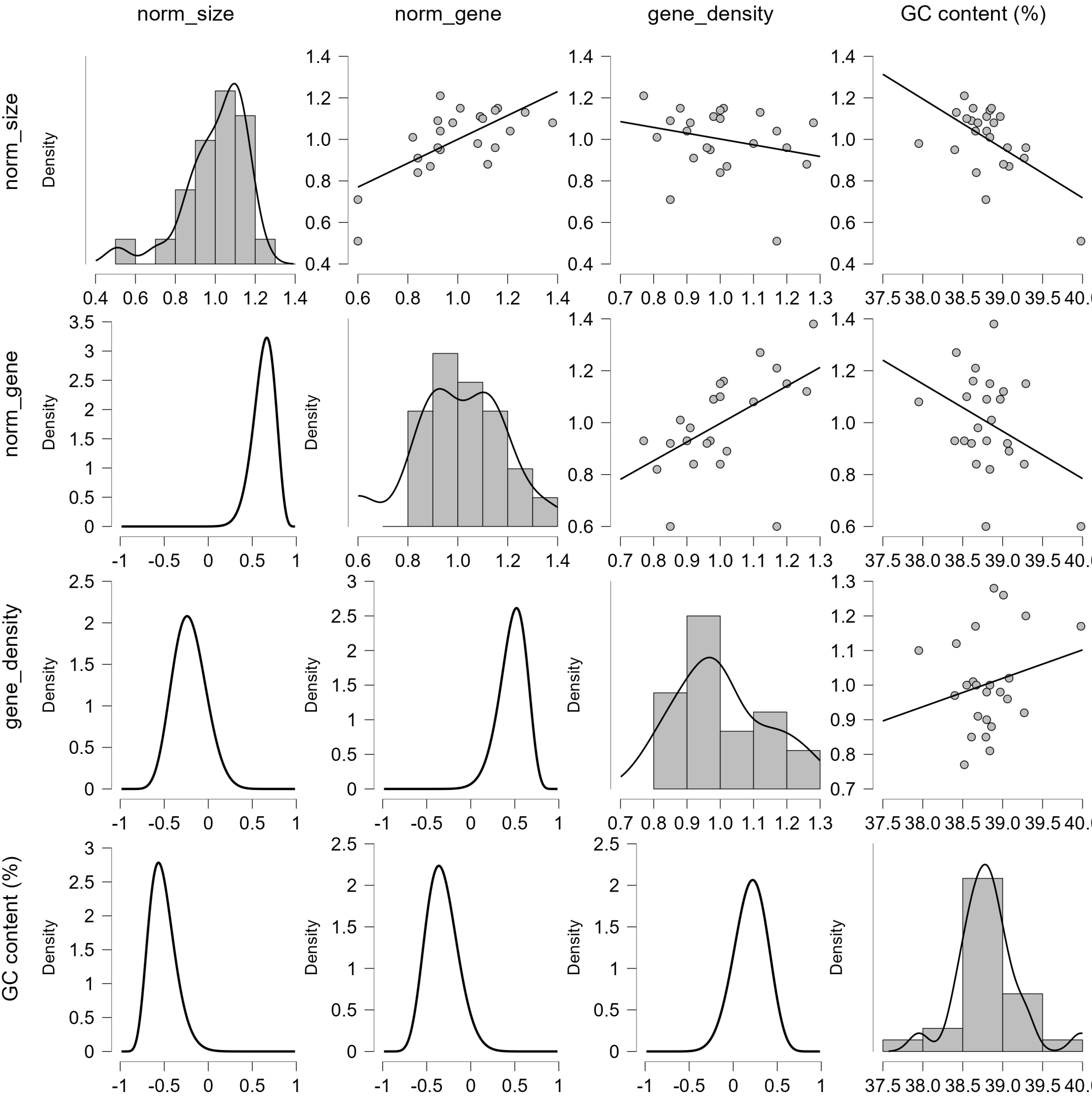
Bayesian Correlation

Bayesian Pearson Correlations

			n	Pearson's r	BF ₁₀
norm_size	-	norm_gene	24	0.685***	156.865
norm_size	-	gene_density	24	-0.245	0.475
norm_size	-	GC content (%)	24	-0.574*	14.579
norm_gene	-	gene_density	24	0.528	7.026
norm_gene	-	GC content (%)	24	-0.369	1.121
gene_density	-	GC content (%)	24	0.226	0.431

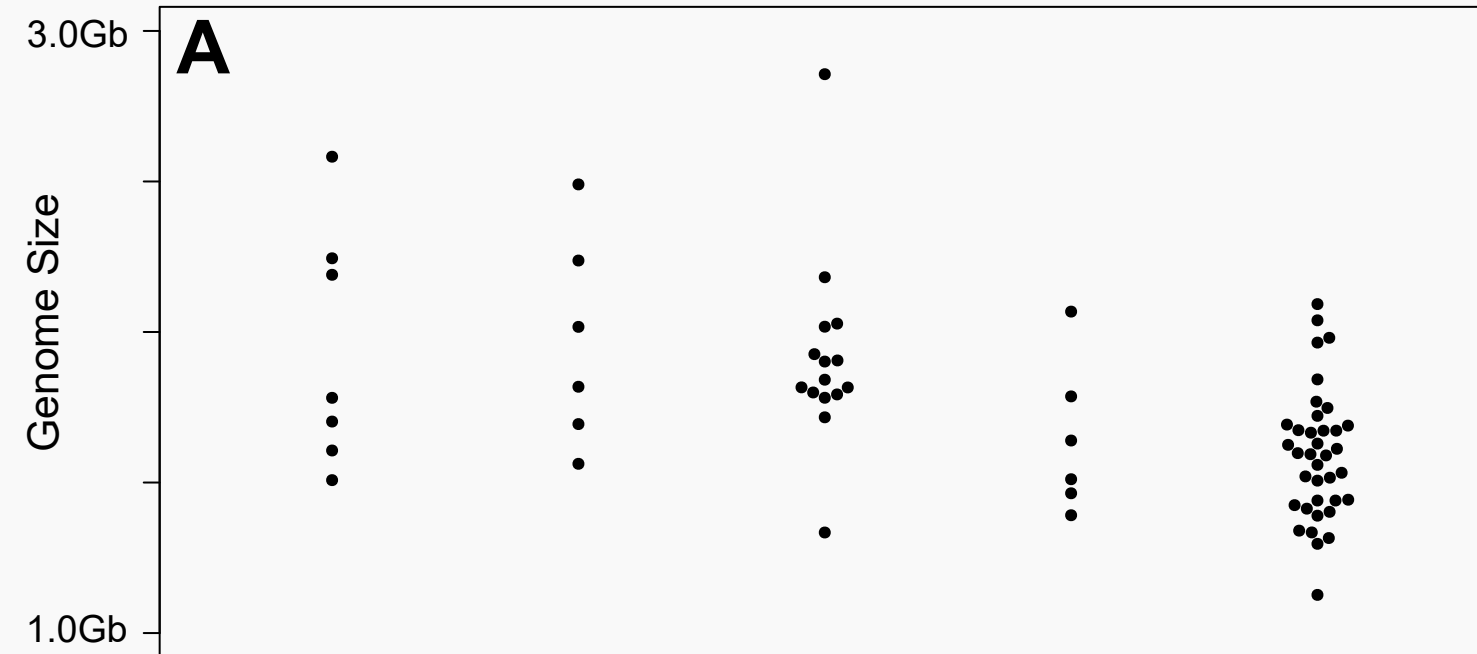
* BF₁₀ > 10, ** BF₁₀ > 30, *** BF₁₀ > 100

Bayesian Correlation Matrix Plot

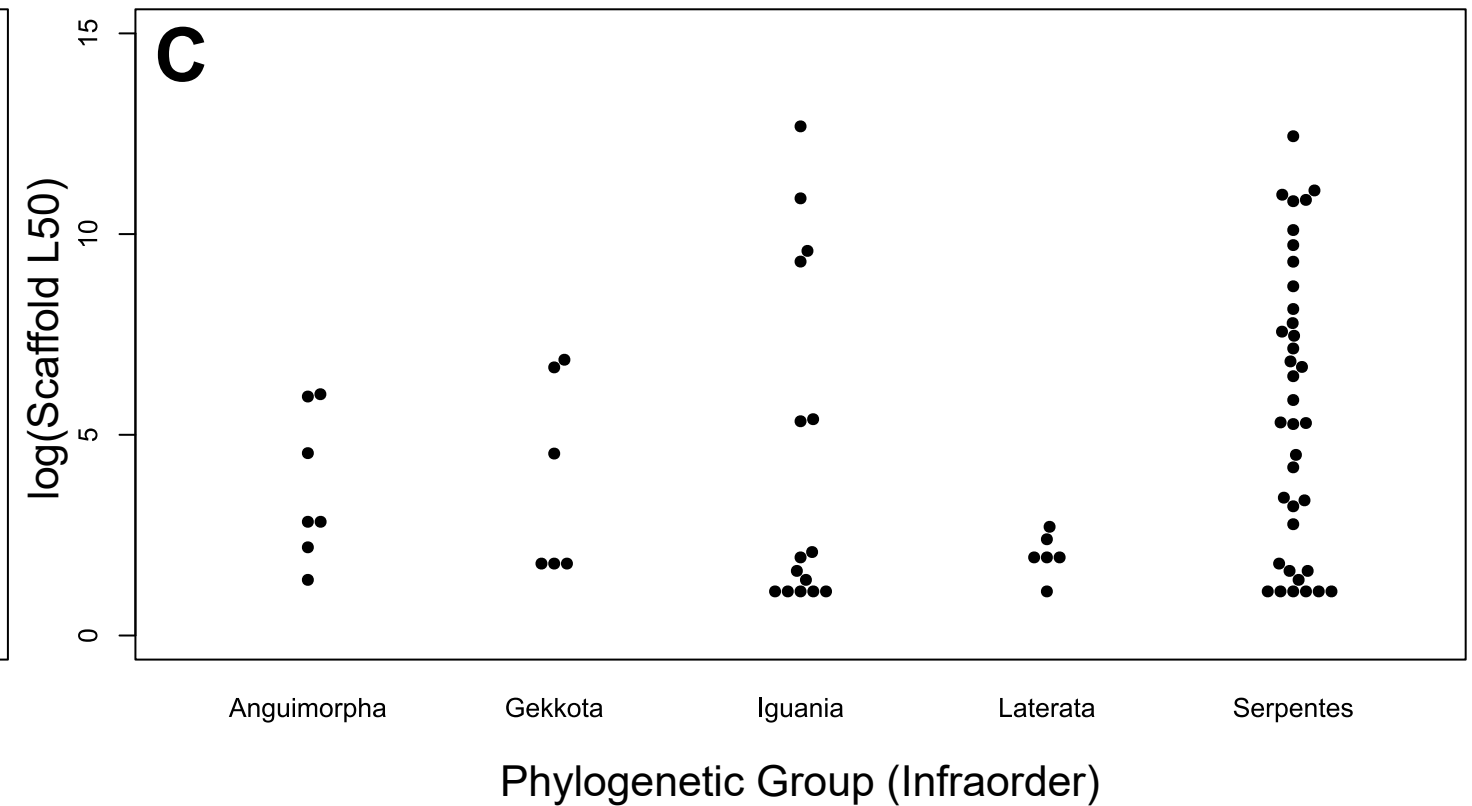
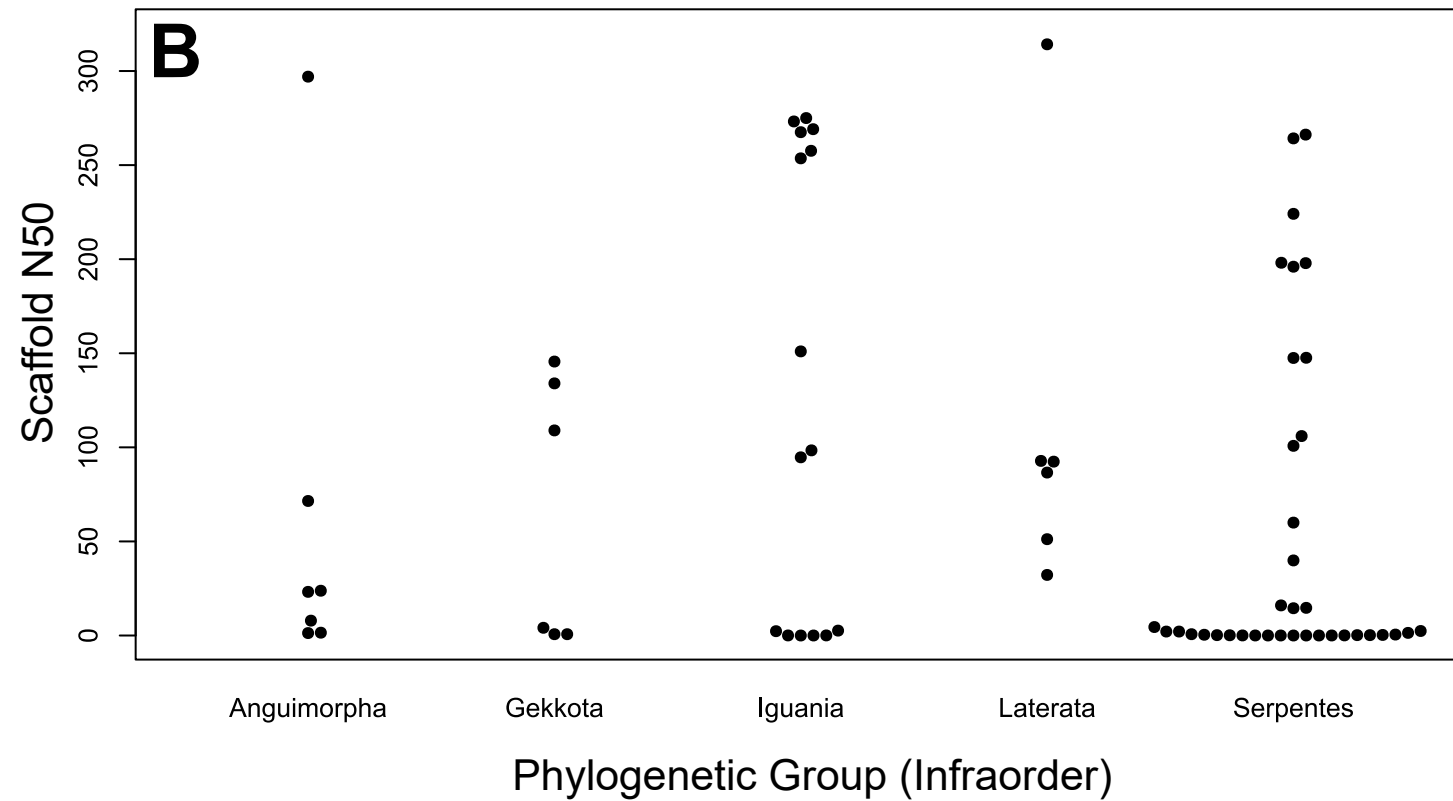
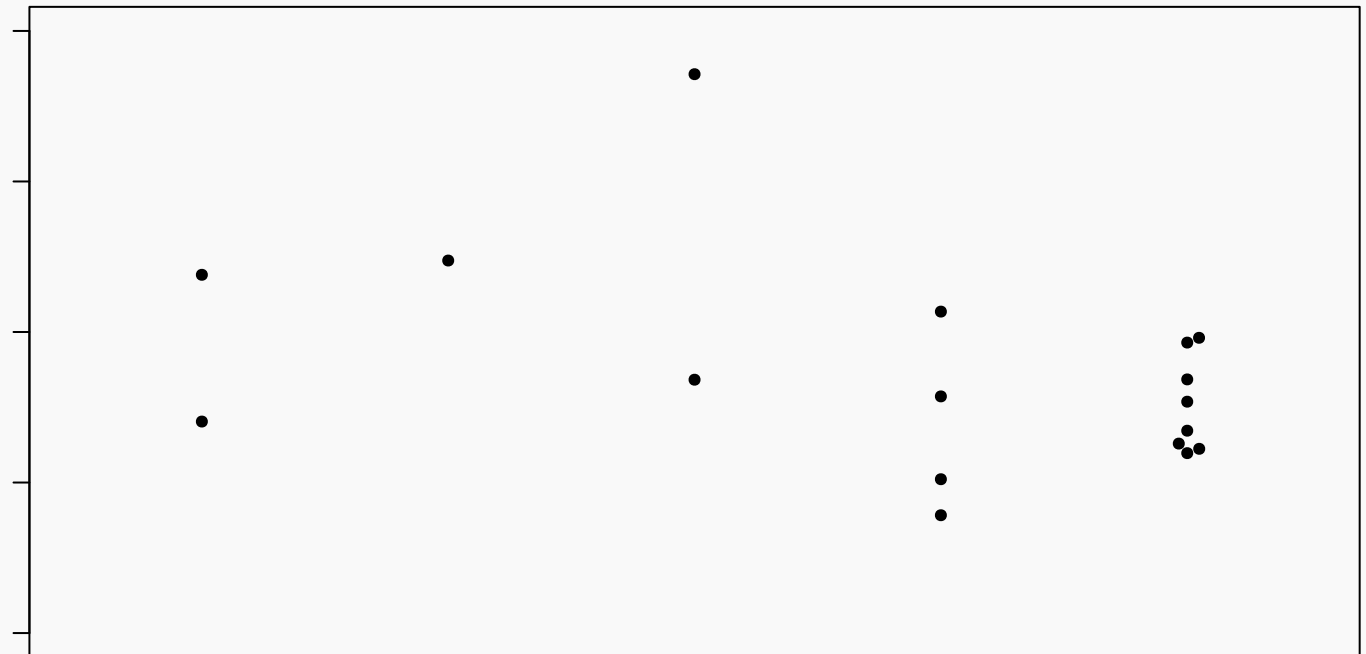


Supplemental Figure 2: Beeswarm plots splitting genome assemblies by phylogenetic group (Infraorder). (A) Genome size per group for all assemblies (left panel) and long-read only assemblies (right panel). (B) Scaffold N50 and (C) scaffold L50 for all assemblies in each group. Scaffold N50/L50 statistics are capped by physical chromosome sizes within the species in high-quality assemblies, i.e. taxa with macro-/microchromosomes have larger potential N50's and lower potential L50's.

Genome Size by Phylogenetic Group

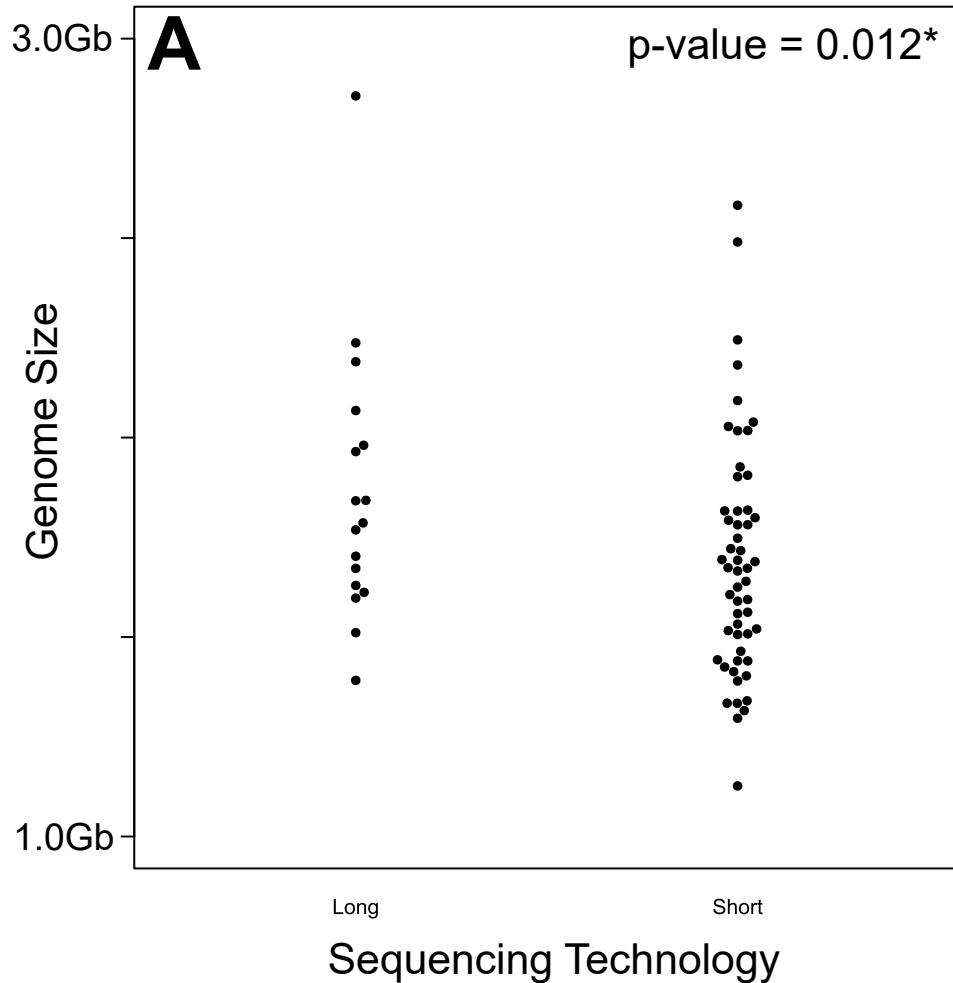


Long-read Genomes Only

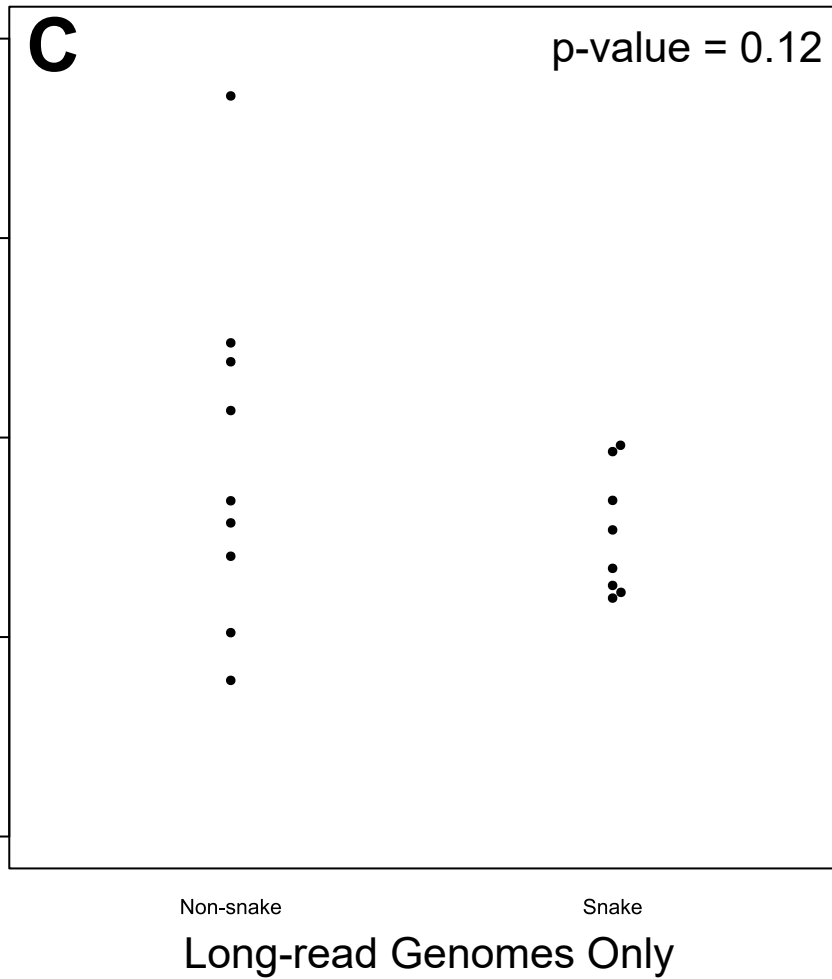
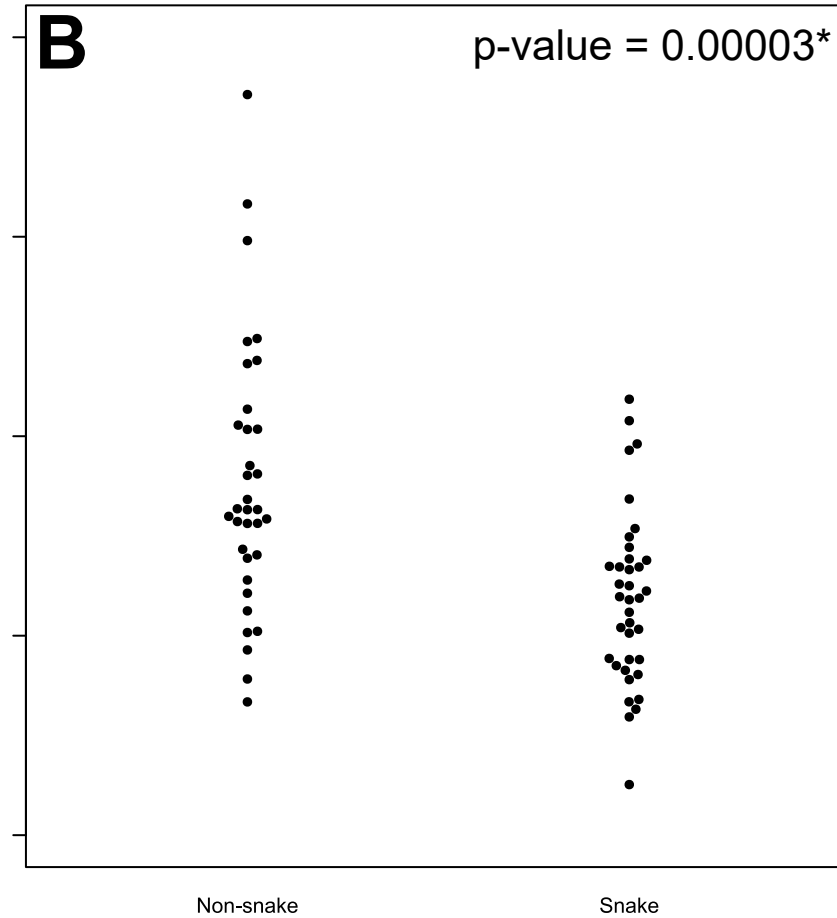


Supplemental Figure 3: Beeswarm plots splitting genome sizes by technology used to generate the primary assembly (contigs). According to total assembly data (B), snakes appear to have significantly smaller genomes than other squamates. However, (C) when accounting for the extreme bias of short-read assemblies in snakes, this difference disappears. *Long = PacBio and/or ONT, Short = Illumina, Sanger, 454, etc.*

Genome Size by Sequencing Technology



Genome Size: Snakes vs. Non-snakes



Supplemental Table 1: Squamates vs mammal funding source comparison. (A) Most high-quality squamate genomes are generated using soft money from start-up/personal funds or (generally smaller) basic science foundation grants, compared to mammals that receive most of their funding from health and agricultural funding agencies rather than basic/personal funding sources. (B) Breakdown of genomes and references used to generate the funding information shown in A.

A. Total Numbers			
Taxon	Basic Science*	Applied Science**	Private/Personal***
Squamate	10	4	6
Mammal	2	18	0
B. Numbers Breakdown			
Squamates	Funding	Citation	
<i>Sphaerodactylus townsendi</i>	Personal***	Pinto et al. 2022	
<i>Eublepharis macularius</i>	Personal***	Pinto et al. 2022	
<i>Paroedura picta</i>	Personal***	Hara et al. 2018	
<i>Pogona vitticeps</i>	Personal***	Georges et al. 2015	
<i>Phrynosoma platyrhinos</i>	Personal***	Koochekian et al. 2022	
<i>Pantherophis guttatus</i>	Personal***	Ullate-Agote and Tzika, 2020	
<i>Anolis carolinensis</i>	Applied**	Alföldi et al. 2011	
<i>Lacerta agilis</i>	Applied**	VGP, <i>unpublished</i>	
<i>Python bivittatus</i>	Applied**	Castoe et al. 2013	
<i>Thamnophis elegans</i>	Applied**	VGP, <i>unpublished</i>	
<i>Shinisaurus crocodilurus</i>	Basic*	Xie et al. 2022	
<i>Sceloporus tristichus</i> (SNOW)	Basic*	Bedoya & Leache, 2021	
<i>Sceloporus tristichus</i> (HOL)	Basic*	Bedoya & Leache, 2021	
<i>Sceloporus undulatus</i>	Basic*	Westfall et al. 2021	
<i>Anolis sagrei</i>	Basic*	Geneva et al. 2021	
<i>Podarcis muralis</i>	Basic*	Andrade et al. 2019	
<i>Zootoca vivipara</i>	Basic*	Yurchenko et al. 2020	
<i>Crotalus viridis</i>	Basic*	Schield et al. 2019	
<i>Hydrophis cyanocinctus</i>	Basic*	Li et al. 2021	
<i>Hydrophis curtus</i>	Basic*	Li et al. 2021	
Mammals	Funding	Citation	
<i>Ochotona princeps</i>	Basic*	Sjodin et al. 2021	
<i>Ursus arctos</i>	Basic*	Armstrong et al. 2022	
<i>Odocoileus virginianus</i>	Applied**	London et al. 2022	
<i>Bos taurus</i>	Applied**	Zimin et al. 2009	
<i>Mus musculus</i>	Applied**	European Bioinformatics Institute, 2002	
<i>Homo sapiens</i>	Applied**	Nurk et al. 2022	
<i>Rattus norvegicus</i>	Applied**	Weiss et al. 2004	
<i>Oryctolagus cuniculus</i>	Applied**	Carneiro et al. 2014	
<i>Equus caballus</i>	Applied**	Wade et al. 2009	
<i>Canis lupus</i>	Applied**	Lindblad-Toh et al. 2005	
<i>Felis catus</i>	Applied**	Pontius et al. 2007	
<i>Pan troglodytes</i>	Applied**	Chimpanzee Sequencing and Analysis Consortium, 2005	
<i>Macaca mulatta</i>	Applied**	Gibbs et al. 2007	
<i>Ovis aries</i>	Applied**	Jiang et al. 2014	

<i>Sus scrofa</i>	Applied**	Groenen et al. 2012
<i>Monodelphis domestica</i>	Applied**	Mikkelsen et al. 2007
<i>Peromyscus maniculatus</i>	Applied**	Harringmeyer and Hoekstra, 2022
<i>Capra hircus</i>	Applied**	Bickhart et al. 2017
<i>Pongo abelii</i>	Applied**	Kronenberg et al. 2018
<i>Microcebus murinus</i>	Applied**	Larsen et al. 2017

Key:

* National Science Foundation, USA (NSF) or equivalent.

** National Institutes of Health (NIH)/United States department of Agriculture (USDA) or equivalent.

*** Laboratory startup funds, private granting agencies, or equivalent.

Table References:

Alföldi, J., Di Palma, F., Grabherr, M., Williams, C., Kong, L., Mauceli, E., ... & Lindblad-Toh, K. (2011). The genome of the green anole lizard and a comparative analysis with birds and mammals. *Nature*, 477(7366), 587-591.

Andrade, P., Pinho, C., Pérez i de Lanuza, G., Afonso, S., Brejcha, J., Rubin, C.-J., Wallerman, O., Pereira, P., Sabatino, S. J., Bellati, A., Pellitteri-Rosa, D., Bosakova, Z., Bunikis, I., Carretero, M. A., Feiner, N., Marsik, P., Paupério, F., Salvi, D., Soler, L., ... Carneiro, M. (2019). Regulatory changes in pterin and carotenoid genes underlie balanced color polymorphisms in the wall lizard. *Proceedings of the National Academy of Sciences*, 116(12), 5633–5642. <https://doi.org/10.1073/pnas.1820320116>

Armstrong, E. E., Perry, B. W., Huang, Y., Garimella, K. V., Jansen, H. T., Robbins, C. T., ... & Kelley, J. L. (2022). A beary good genome: Haplotype-resolved, chromosome-level assembly of the brown bear (*Ursus arctos*). *Genome biology and evolution*, 14(9), evac125.

Bedoya, A. M., & Leaché, A. D. (2021). Characterization of a pericentric inversion in plateau fence lizards (*Sceloporus tristichus*): evidence from chromosome-scale genomes. *G3*, 11(2), jkab036.

Bedoya, A. M., & Leaché, A. D. (2021). Characterization of a pericentric inversion in plateau fence lizards (*Sceloporus tristichus*): evidence from chromosome-scale genomes. *G3*, 11(2), jkab036.

Bickhart, D. M., Rosen, B. D., Koren, S., Sayre, B. L., Hastie, A. R., Chan, S., ... & Smith, T. P. (2017). Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. *Nature genetics*, 49(4), 643-650.

Carneiro, M., Rubin, C. J., Di Palma, F., Albert, F. W., Alföldi, J., Barrio, A. M., ... & Andersson, L. (2014). Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. *Science*, 345(6200), 1074-1079.

Castoe, T. A., De Koning, A. J., Hall, K. T., Card, D. C., Schield, D. R., Fujita, M. K., ... & Pollock, D. D. (2013). The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. *Proceedings of the National Academy of Sciences*, 110(51), 20645-20650.

Chimpanzee Sequencing and Analysis Consortium. (2005). Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature*, 437(7055), 69-87.

European Bioinformatics Institute. (2002). Initial sequencing and comparative analysis of the mouse genome. *Nature*, 420(6915), 520-562.

Geneva, A. J., Park, S., Bock, D., de Mello, P., Sarigol, F., Tollis, M., ... & Losos, J. B. (2021). Chromosome-scale genome assembly of the brown anole (*Anolis sagrei*), a model species for evolution and ecology. *bioRxiv*.

Georges, A., Li, Q., Lian, J., O'Meally, D., Deakin, J., Wang, Z., ... & Zhang, G. (2015). High-coverage sequencing and annotated assembly of the genome of the Australian dragon lizard *Pogona vitticeps*. *Gigascience*, 4(1), s13742-015.

Gibbs, R. A., Rogers, J., Katze, M. G., Bumgarner, R., Weinstock, G. M., Mardis, E. R., ... & Smith, D. G. (2007). Evolutionary and biomedical insights from the rhesus macaque genome. *science*, 316(5822), 222-234.

Groenen, M. A., Archibald, A. L., Uenishi, H., Tuggle, C. K., Takeuchi, Y., Rothschild, M. F., ... & Schook, L. B. (2012). Analyses of pig genomes provide insight into porcine demography and evolution. *Nature*, 491(7424), 393-398.

Hara Y, Takeuchi M, Kageyama Y, Tatsumi K, Hibi M, Kiyonari H, Kuraku S. 2018. Madagascar ground gecko genome analysis characterizes asymmetric fates of duplicated genes. *BMC Biology*. 16: 40.

Harrington, O. S., & Hoekstra, H. E. (2022). Chromosomal inversion polymorphisms shape the genomic landscape of deer mice. *Nature ecology & evolution*, 1-15.

Jiang, Y., Xie, M., Chen, W., Talbot, R., Maddox, J. F., Faraut, T., ... & Dalrymple, B. P. (2014). The sheep genome illuminates biology of the rumen and lipid metabolism. *Science*, 344(6188), 1168-1173.

Koochekian, N., Ascanio, A., Farleigh, K., Card, D. C., Schield, D. R., Castoe, T. A., & Jezkova, T. (2022). A chromosome-level genome assembly and annotation of the desert horned lizard, *Phrynosoma platyrhinos*, provides insight into chromosomal rearrangements among reptiles. *GigaScience*, 11.

Kronenberg, Z. N., Fiddes, I. T., Gordon, D., Murali, S., Cantsilieris, S., Meyerson, O. S., ... & Eichler, E. E. (2018). High-resolution comparative analysis of great ape genomes. *Science*, 360(6393), eaar6343.

Larsen, P. A., Harris, R. A., Liu, Y., Murali, S. C., Campbell, C. R., Brown, A. D., ... & Worley, K. C. (2017). Hybrid de novo genome assembly and centromere characterization of the gray mouse lemur (*Microcebus murinus*). *BMC biology*, 15(1), 1-17.

Li, A., Wang, J., Sun, K., Wang, S., Zhao, X., Wang, T., Xiong, L., Xu, W., Qiu, L., Shang, Y., Liu, R., Wang, S., & Lu, Y. (2021). Two Reference-Quality Sea Snake Genomes Reveal Their Divergent Evolution of Adaptive Traits and Venom Systems. *Molecular Biology and Evolution*, 38(11), 4867–4883. <https://doi.org/10.1093/molbev/msab212>

Li, A., Wang, J., Sun, K., Wang, S., Zhao, X., Wang, T., Xiong, L., Xu, W., Qiu, L., Shang, Y., Liu, R., Wang, S., & Lu, Y. (2021). Two Reference-Quality Sea Snake Genomes Reveal Their Divergent Evolution of Adaptive Traits and Venom Systems. *Molecular Biology and Evolution*, 38(11), 4867–4883. <https://doi.org/10.1093/molbev/msab212>

Lindblad-Toh, K., Wade, C. M., Mikkelsen, T. S., Karlsson, E. K., Jaffe, D. B., Kamal, M., ... & Lander, E. S. (2005). Genome sequence, comparative analysis and haplotype structure of the domestic dog. *Nature*, 438(7069), 803-819.

London, E. W., Roca, A. L., Novakofski, J. E., & Mateus-Pinilla, N. E. (2022). A De Novo Chromosome-level Genome Assembly of the White-tailed Deer, *Odocoileus virginianus*. *Journal of Heredity*.

Mikkelsen, T. S., Wakefield, M. J., Aken, B., Amemiya, C. T., Chang, J. L., Duke, S., ... & Lindblad-Toh, K. (2007). Genome of the marsupial *Monodelphis domestica* reveals innovation in non-coding sequences. *Nature*, 447(7141), 167-177.

Nurk, S., Koren, S., Rhie, A., Rautiainen, M., Bzikadze, A. V., Mikheenko, A., ... & Phillippy, A. M. (2022). The complete sequence of a human genome. *Science*, 376(6588), 44-53.

Pinto, B. J., Gamble, T., Smith, C.H., Keating, S.E., Havird, J., Chiari, Y. (2022). The revised leopard gecko (*Eublepharis macularius*) reference genome 'raises the bar' for squamate genomics. In prep.

Pinto, B. J., Keating, S. E., Nielsen, S. V., Scantlebury, D. P., Daza, J. D., & Gamble, T. (2022). Chromosome-level genome assembly reveals dynamic sex chromosomes in Neotropical leaf-litter geckos (Sphaerodactylidae: *Sphaerodactylus*). *Journal of Heredity*.

Pontius, J. U., Mullikin, J. C., Smith, D. R., Team, A. S., Lindblad-Toh, K., Gnerre, S., ... & NISC Comparative Sequencing Program. (2007). Initial sequence and comparative analysis of the cat genome. *Genome research*, 17(11), 1675-1689.

Rhie, A., McCarthy, S. A., Fedrigo, O., Damas, J., Formenti, G., Koren, S., Uliano-Silva, M., Chow, W., Fungtammasan, A., Kim, J., Lee, C., Ko, B. J., Chaisson, M., Gedman, G. L., Cantin, L. J., Thibaud-Nissen, F., Haggerty, L., Bista, I., Smith, M., ... Jarvis, E. D. (2021). Towards complete and error-free genome assemblies of all vertebrate species. *Nature*, 592(7856), 737–746. <https://doi.org/10.1038/s41586-021-03451-0>

Rhie, A., McCarthy, S. A., Fedrigo, O., Damas, J., Formenti, G., Koren, S., Uliano-Silva, M., Chow, W., Fungtammasan, A., Kim, J., Lee, C., Ko, B. J., Chaisson, M., Gedman, G. L., Cantin, L. J., Thibaud-Nissen, F., Haggerty, L., Bista, I., Smith, M., ... Jarvis, E. D. (2021). Towards complete and error-free genome assemblies of all vertebrate species. *Nature*, 592(7856), 737–746. <https://doi.org/10.1038/s41586-021-03451-0>

Schild, D. R., Card, D. C., Hales, N. R., Perry, B. W., Pasquesi, G. M., Blackmon, H., Adams, R. H., Corbin, A. B., Smith, C. F., Ramesh, B., Demuth, J. P., Betrán, E., Tollis, M., Meik, J. M., Mackessy, S. P., & Castoe, T. A. (2019). The origins and evolution of chromosomes, dosage compensation, and mechanisms underlying venom regulation in snakes. *Genome Research*, 29(4), 590–601. <https://doi.org/10.1101/gr.240952.118>

Sjodin, B. M., Galbreath, K. E., Lanier, H. C., & Russello, M. A. (2021). Chromosome-level reference genome assembly for the American pika (*Ochotona princeps*). *Journal of Heredity*, 112(6), 549-557.

Ullate-Agote, A., & Tzika, A. C. (2021). Characterization of the Leucistic Texas Rat Snake *Pantherophis obsoletus*. *Frontiers in Ecology and Evolution*, 9. <https://doi.org/10.3389/fevo.2021.583136>

Wade, C. M., Giulotto, E., Sigurdsson, S., Zoli, M., Gnerre, S., Imsland, F., ... & Lindblad-Toh, K. (2009). Genome sequence, comparative analysis, and population genetics of the domestic horse. *Science*, 326(5954), 865-867.

Weiss Robert B., Dunn Diane M., Green Eric D., Blakesley Robert W., Bouffard Gerard G., de Jong, P. J., Osoegawa, K., Zhu, B., Marra, M., ... & Collins, F. (2004). Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, 428(6982), 493-521.

Westfall, A. K., Telemeco, R. S., Grizante, M. B., Waits, D. S., Clark, A. D., Simpson, D. Y., ... & Schwartz, T. S. (2021). A chromosome-level genome assembly for the Eastern Fence Lizard (*Sceloporus undulatus*), a reptile model for physiological and evolutionary ecology. *GigaScience*, 10(10), giab066.

Xie HX, Liang XX, Chen ZQ, Li WM, Mi CR, Li M, ... & Du WG. 2022. Ancient demographics determine the effectiveness of genetic purging in endangered lizards. *Mol Biol Evol*. 39: msab359.

Yurchenko, A. A., Recknagel, H., & Elmer, K. R. (2020). Chromosome-Level Assembly of the Common Lizard (*Zootoca vivipara*) Genome. *Genome Biology and Evolution*, 12(11), 1953–1960. <https://doi.org/10.1093/gbe/evaa161>

Zimin, A. V., Delcher, A. L., Florea, L., Kelley, D. R., Schatz, M. C., Puiu, D., ... & Salzberg, S. L. (2009). A whole-genome assembly of the domestic cow, *Bos taurus*. *Genome biology*, 10(4), 1-10.