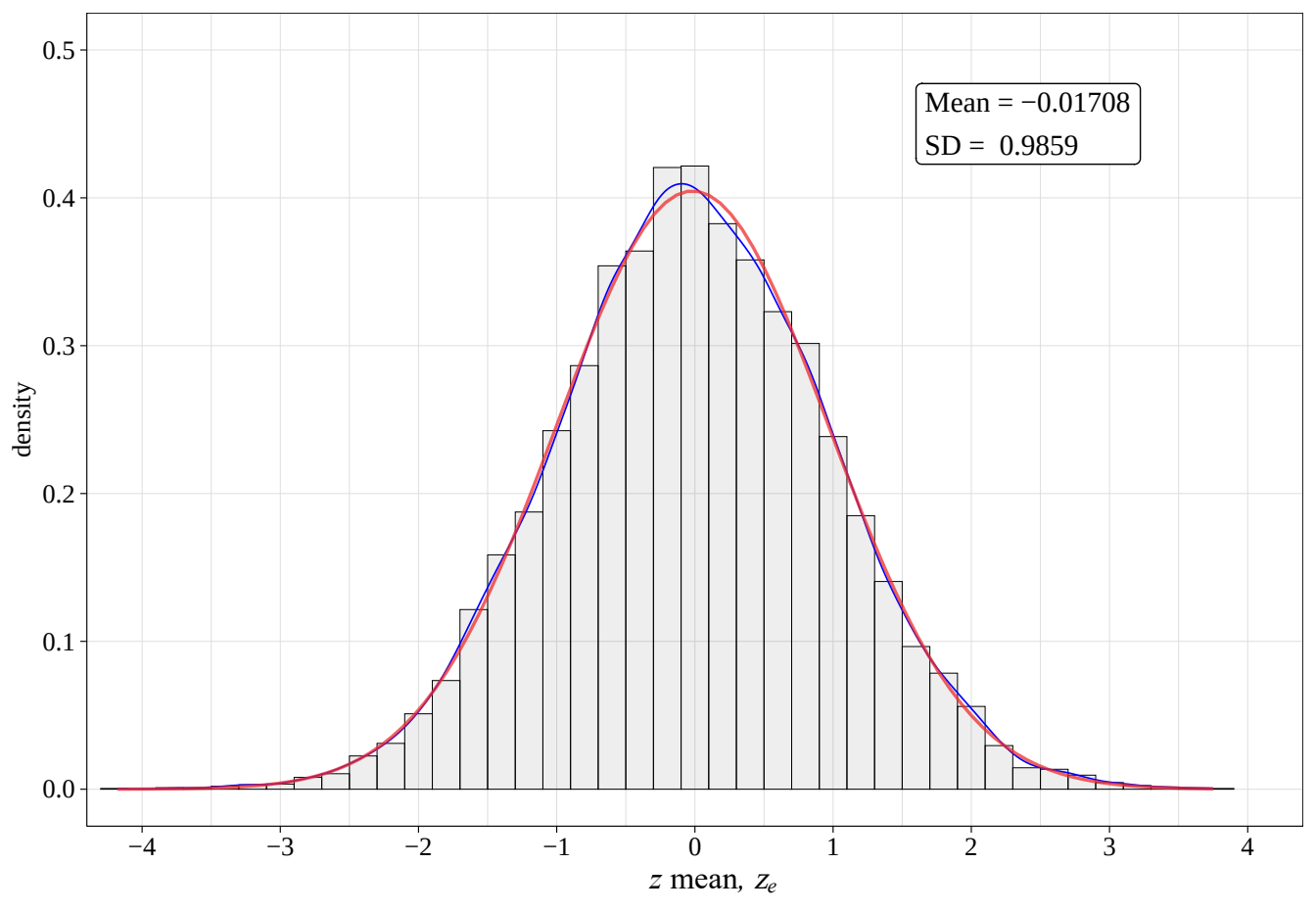


	MGE	MLE	MME
Mean	−0.018807	−0.017084	−0.017084
SD	0.980073	0.985875	0.985875
p(AD)	0.983503	0.963656	0.963656

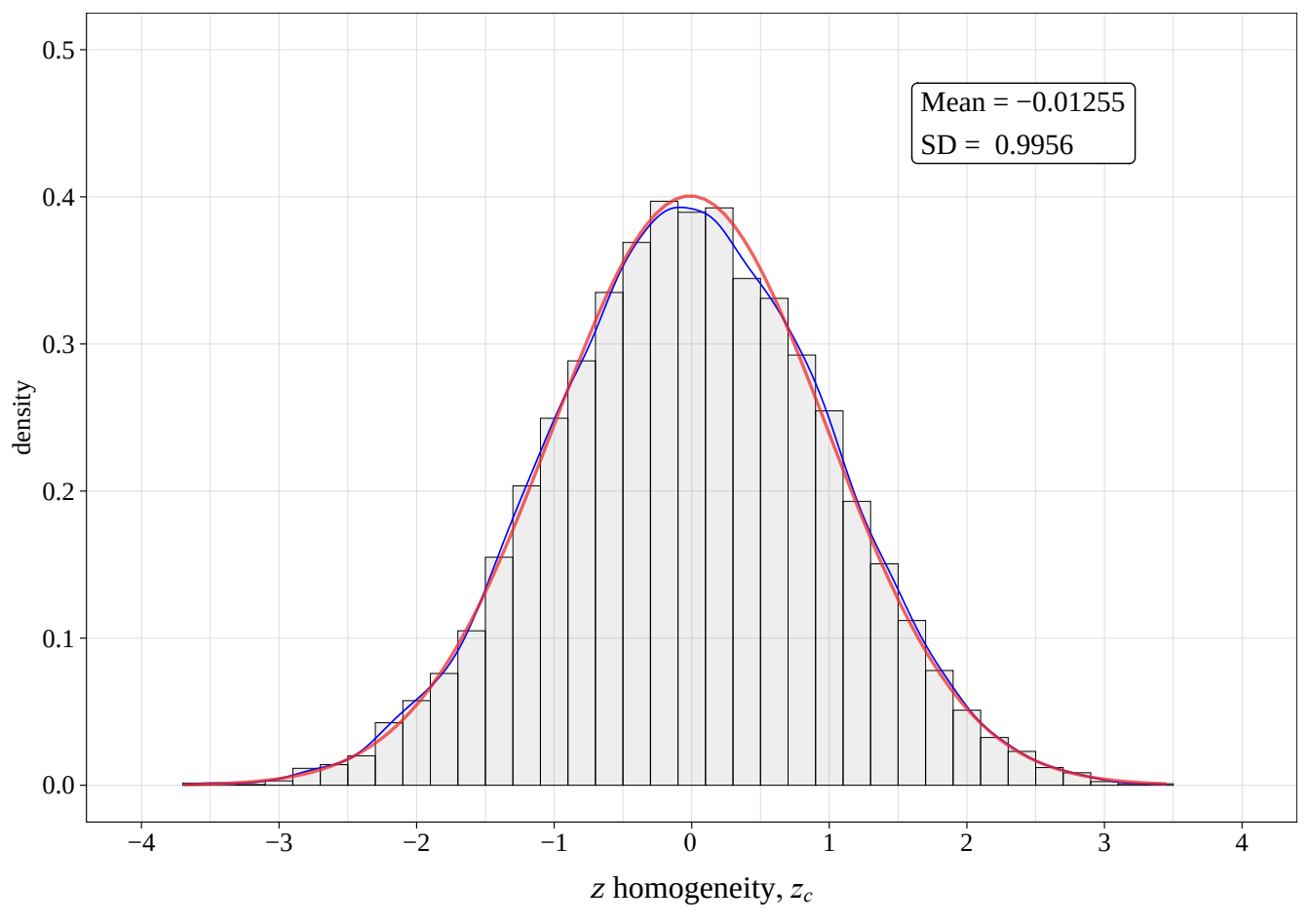
Human-like 1Mbp/40kbp TAD domains, genes-domains model "proportional"

FDR equals to 0.023200 at 10000 permutations

JarqueBera p.value = 0.168730, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.007693, p−value = 0.753480, skewness of normal distribution should be 0

Kurtosis = 3.091130, p−value = 0.062859, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.010854	−0.012552	−0.012552
SD	1.004593	0.995642	0.995642
p(AD)	0.940482	0.891812	0.891812

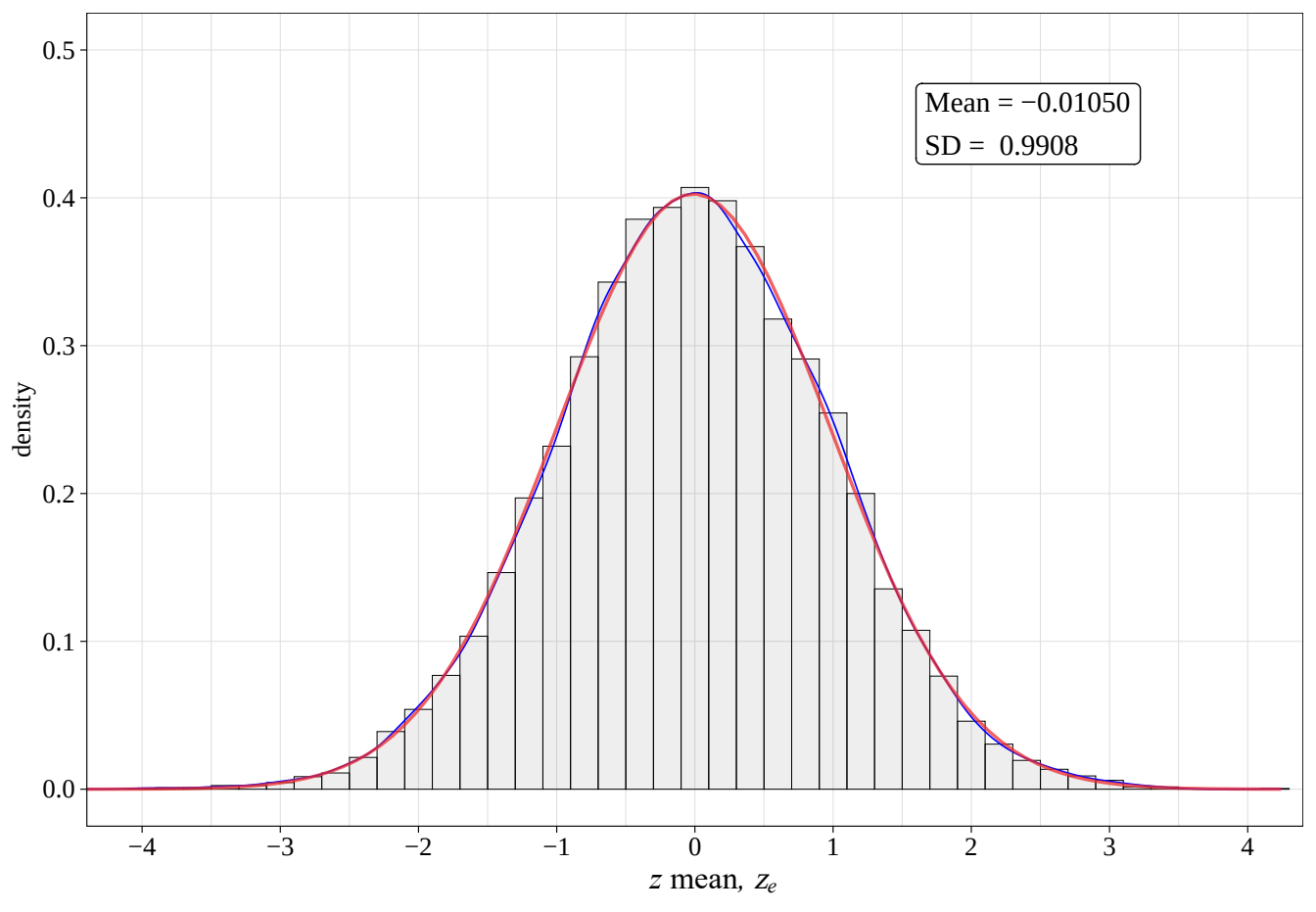
Human-like 1Mbp/40kbp TAD domains, genes-domains model "proportional"

FDR equals to 0.026300 at 10000 permutations

JarqueBera p.value = 0.099717, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.025056, p−value = 0.306343, skewness of normal distribution should be 0

Kurtosis = 2.907508, p−value = 0.059029, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.008583	−0.010497	−0.010497
SD	0.984446	0.990844	0.990844
p(AD)	0.989219	0.938583	0.938583

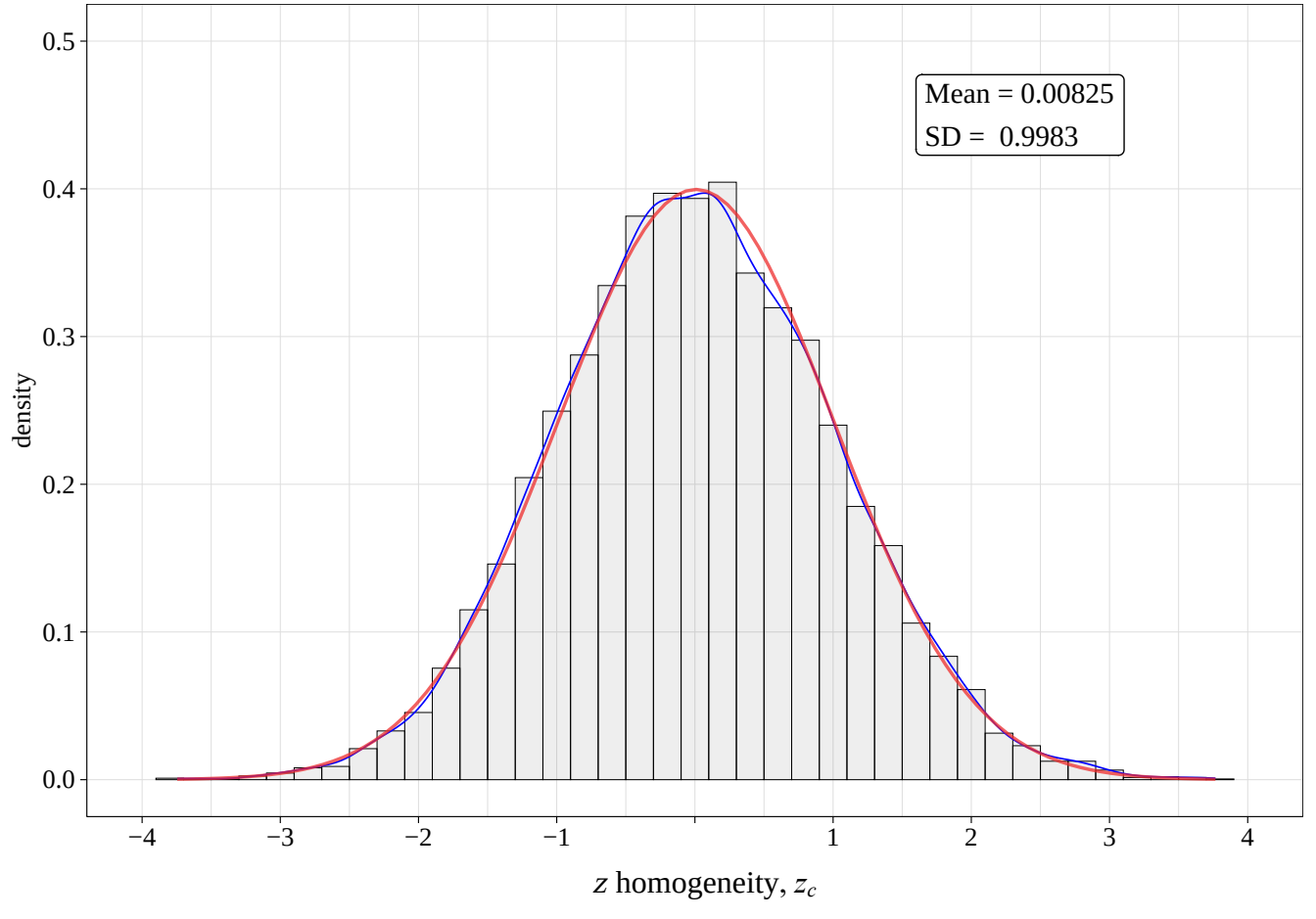
Human-like 1MBp/40kbp TAD domains, genes-domains model "start"

FDR equals to 0.025400 at 10000 permutations

JarqueBera p.value = 0.006224, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.032063, p−value = 0.190552, skewness of normal distribution should be 0

Kurtosis = 3.142367, p−value = 0.003660, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	0.000382	0.008255	0.008255
SD	0.998383	0.998350	0.998350
p(AD)	0.598319	0.539655	0.539655

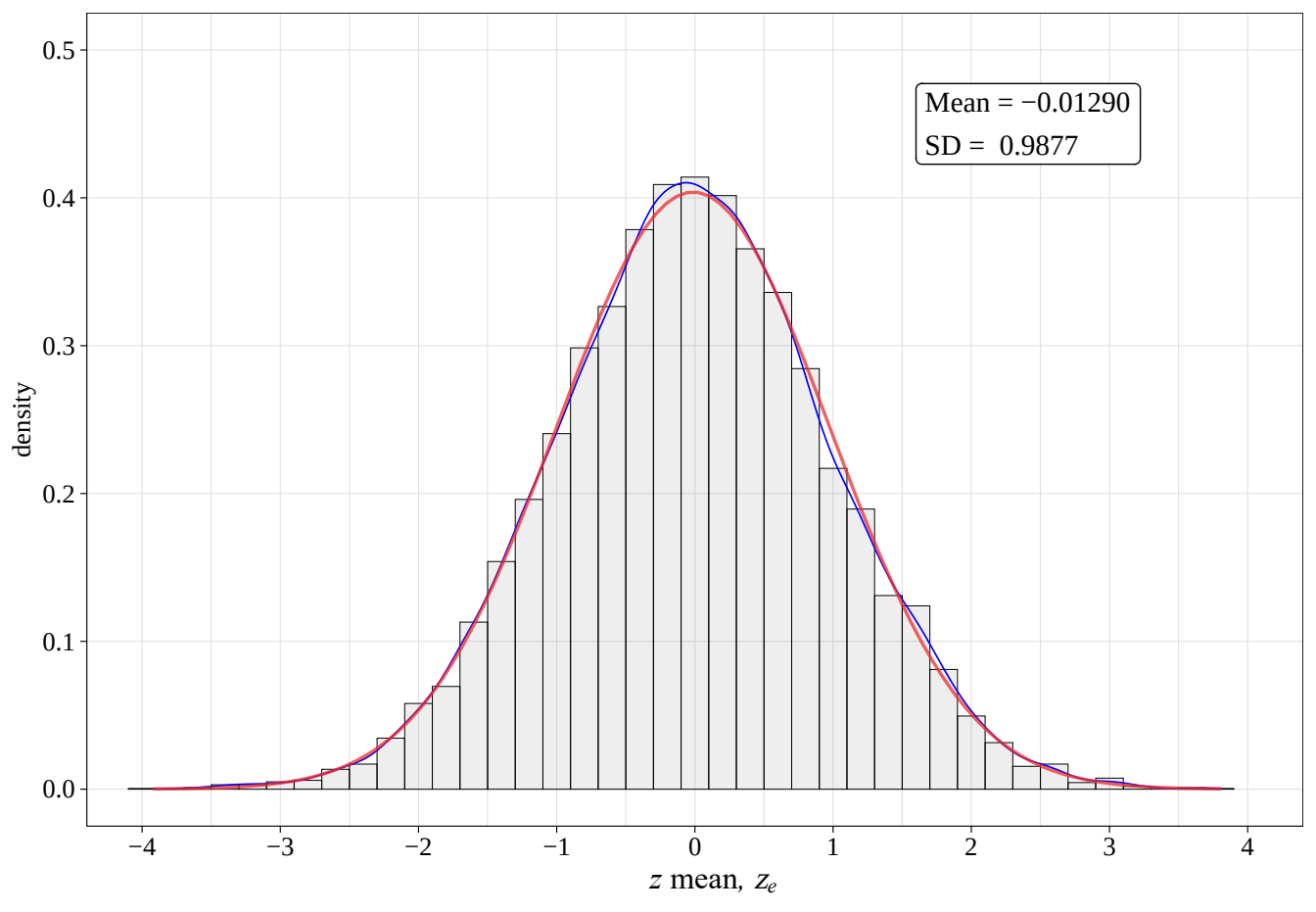
Human-like 1MBp/40kbp TAD domains, genes-domains model "start"

FDR equals to 0.022500 at 10000 permutations

JarqueBera p.value = 0.035481, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.061044, p−value = 0.012699, skewness of normal distribution should be 0

Kurtosis = 3.033477, p−value = 0.494387, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.014512	−0.012896	−0.012896
SD	0.978478	0.987683	0.987683
p(AD)	0.823285	0.818767	0.818767

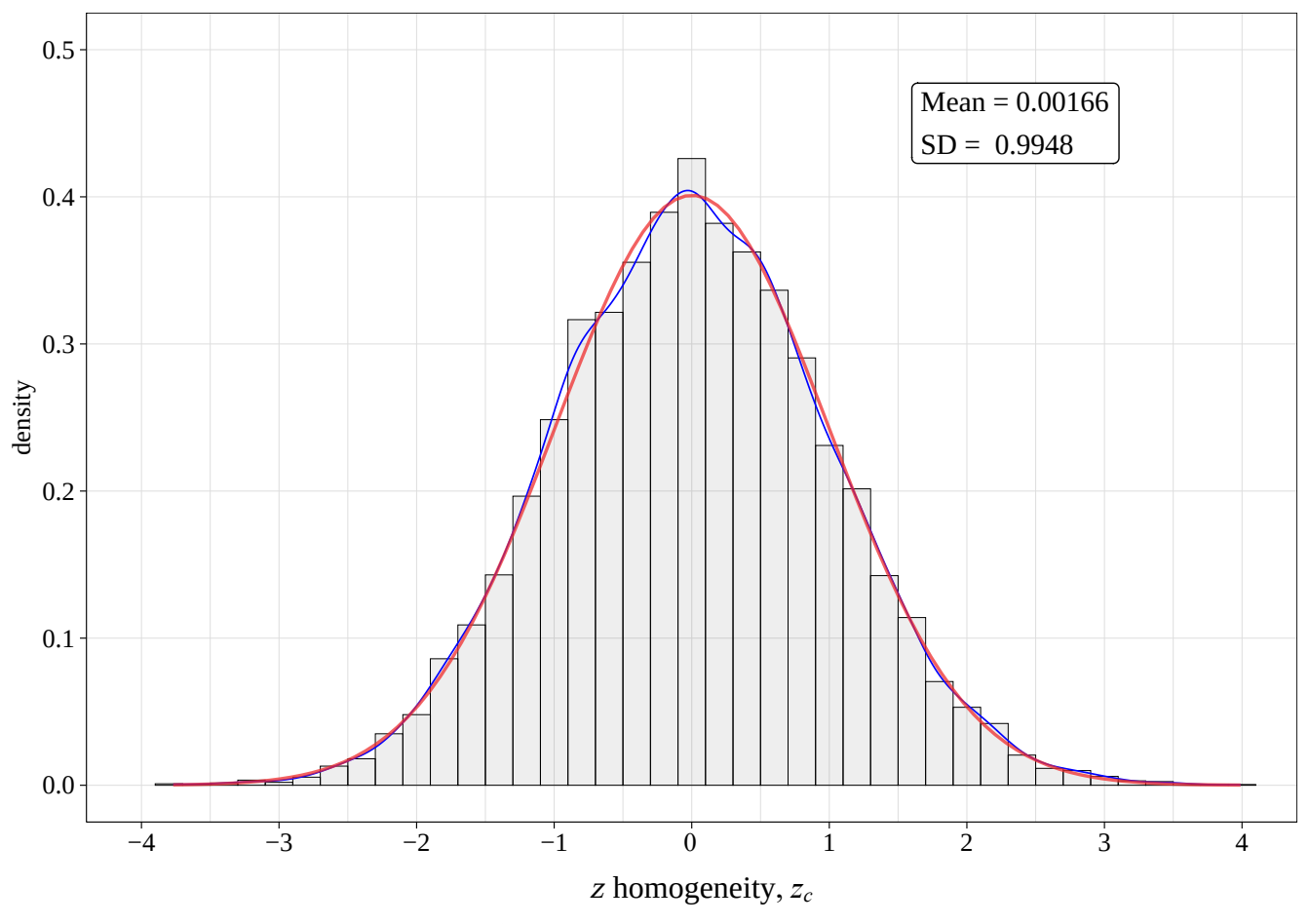
Human-like 1MBp/40kbp TAD domains, genes-domains model "longer part"

FDR equals to 0.023700 at 10000 permutations

JarqueBera p.value = 0.268202, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.003701, p−value = 0.879894, skewness of normal distribution should be 0

Kurtosis = 3.079133, p−value = 0.106246, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.002981	0.001656	0.001656
SD	0.994693	0.994788	0.994788
p(AD)	0.892202	0.845307	0.845307

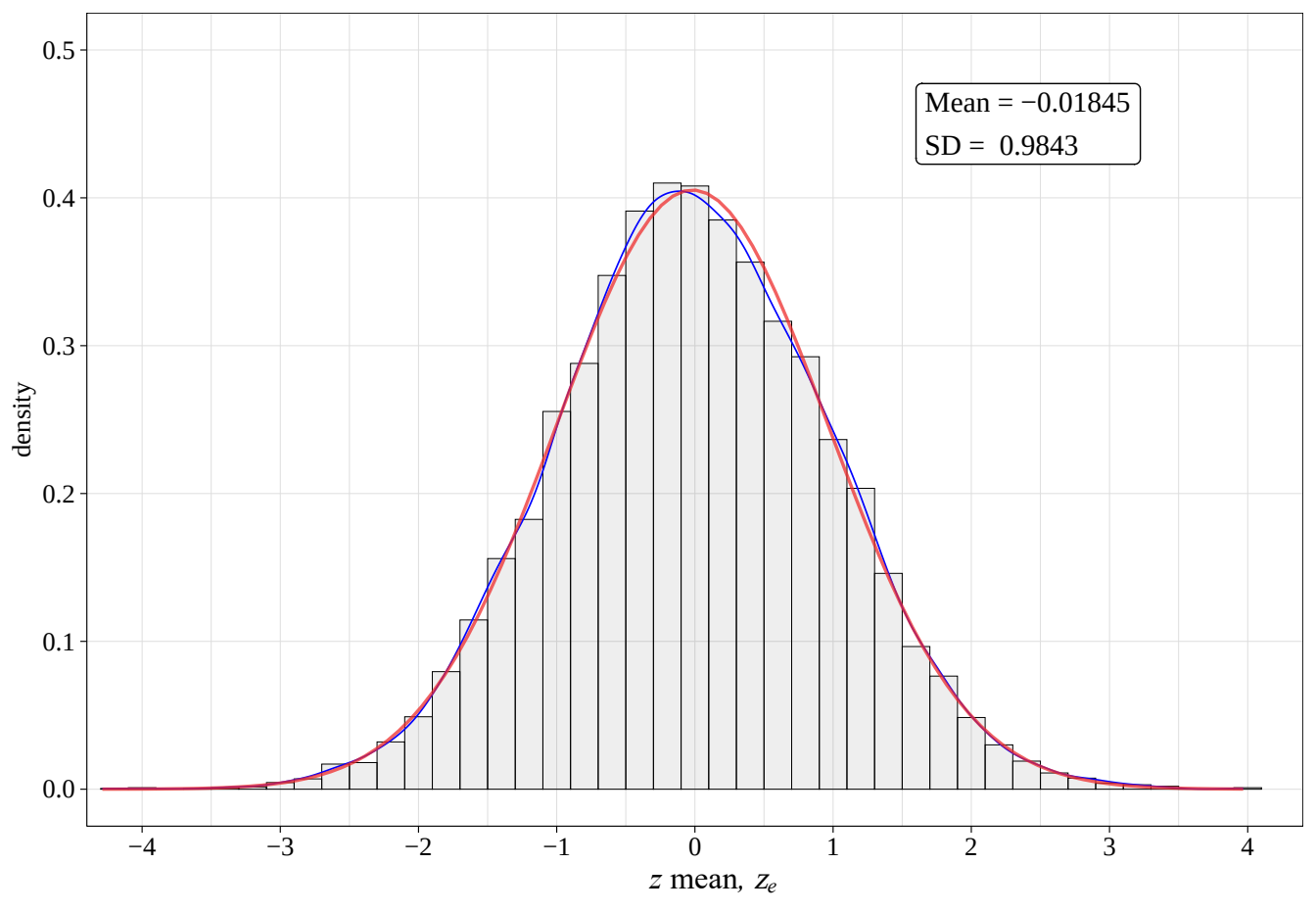
Human-like 1MBp/40kbp TAD domains, genes-domains model "longer part"

FDR equals to 0.022400 at 10000 permutations

JarqueBera p.value = 0.103371, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.048897, p−value = 0.045912, skewness of normal distribution should be 0

Kurtosis = 3.036465, p−value = 0.456672, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.021059	−0.018448	−0.018448
SD	0.982115	0.984279	0.984279
p(AD)	0.922507	0.912524	0.912524

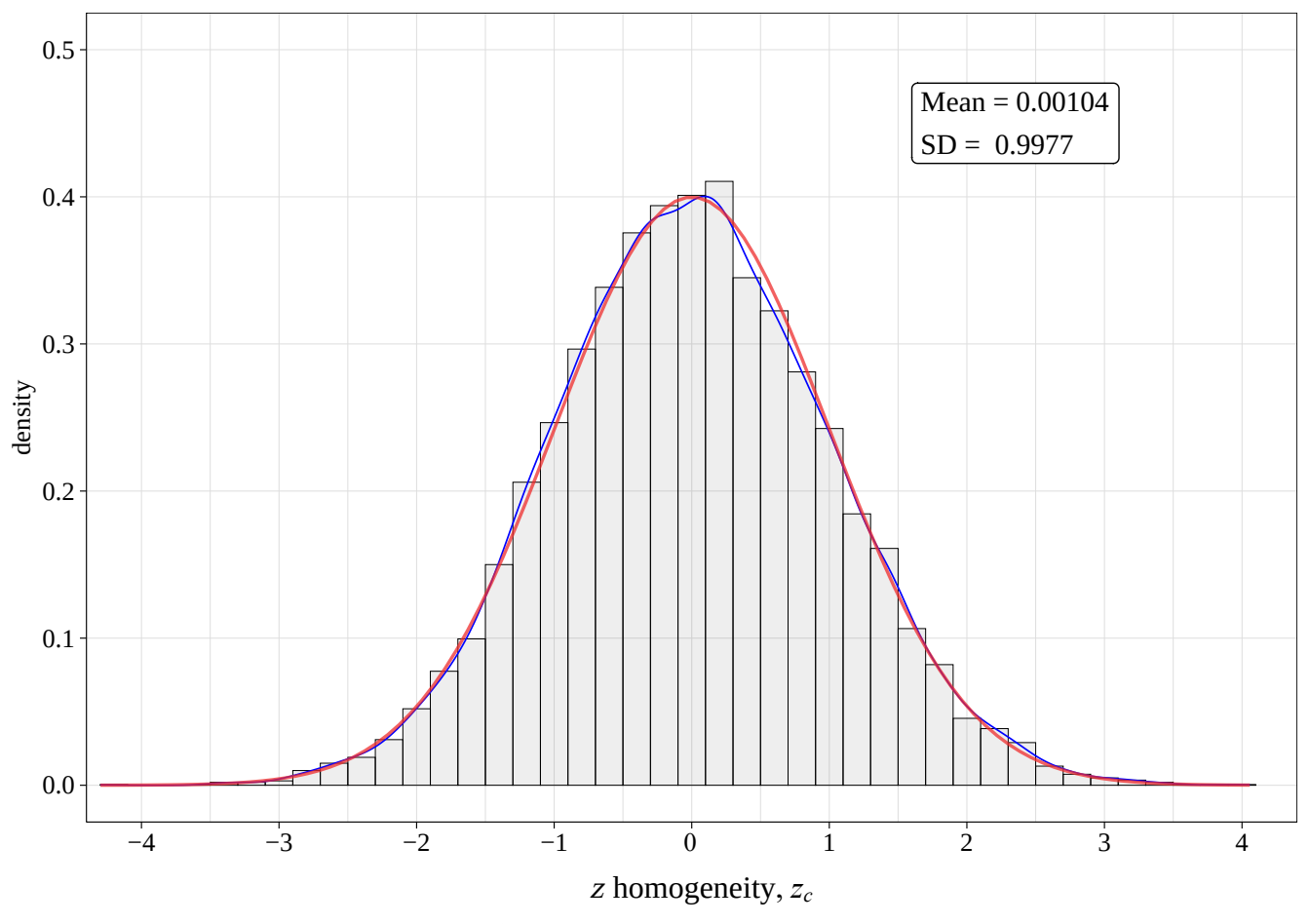
Human-like 1MBp/40kbp TAD domains, genes-domains model "midpoint"

FDR equals to 0.023200 at 10000 permutations

JarqueBera p.value = 0.225491, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.009124, p−value = 0.709532, skewness of normal distribution should be 0

Kurtosis = 3.082562, p−value = 0.091933, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.005822	0.001043	0.001043
SD	0.995999	0.997715	0.997715
p(AD)	0.683332	0.638188	0.638188

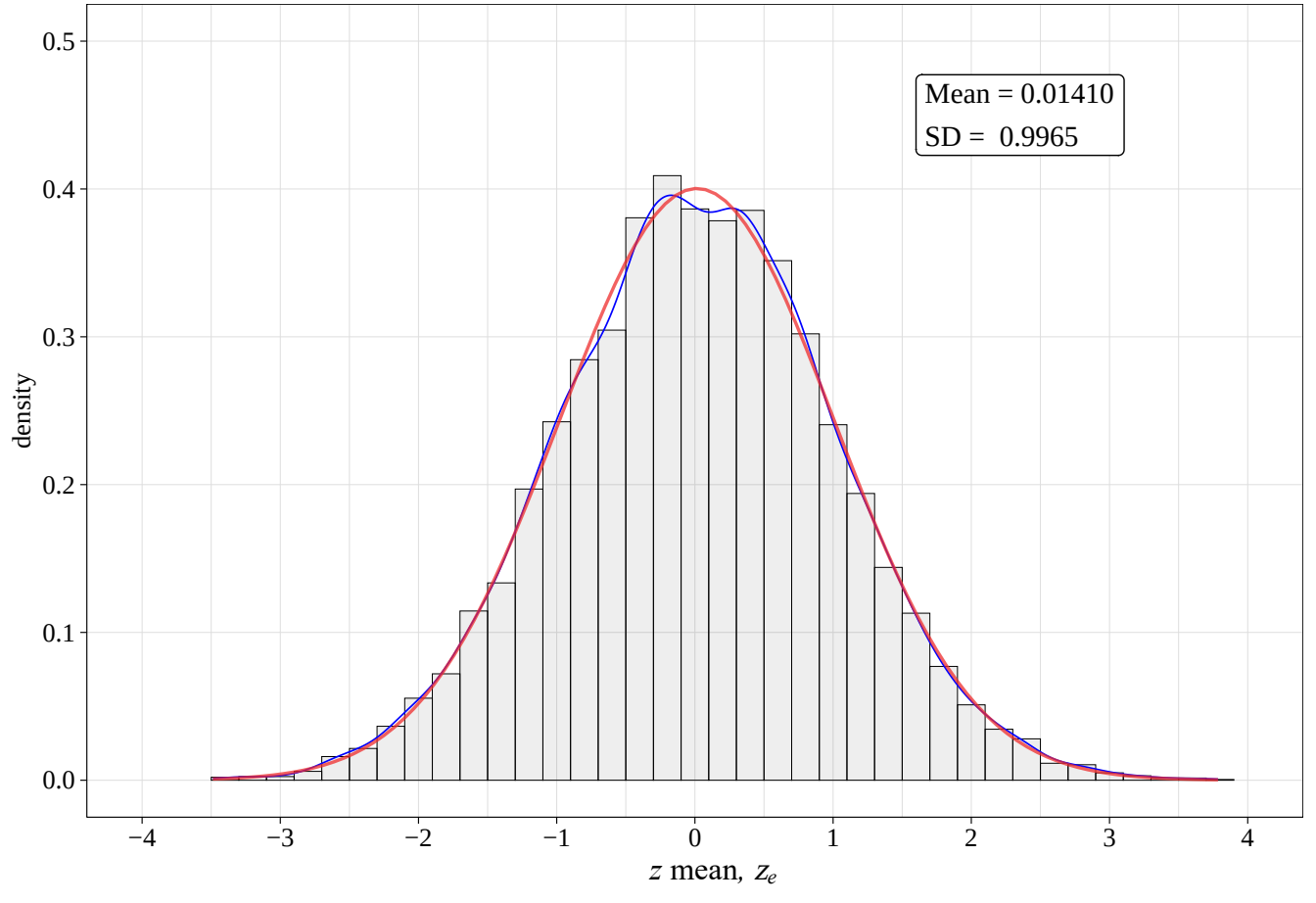
Human-like 1MBp/40kbp TAD domains, genes-domains model "midpoint"

FDR equals to 0.023800 at 10000 permutations

JarqueBera p.value = 0.107264, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.046867, p−value = 0.055704, skewness of normal distribution should be 0

Kurtosis = 3.043928, p−value = 0.369891, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	0.015182	0.014096	0.014096
SD	0.993213	0.996484	0.996484
p(AD)	0.950417	0.944920	0.944920

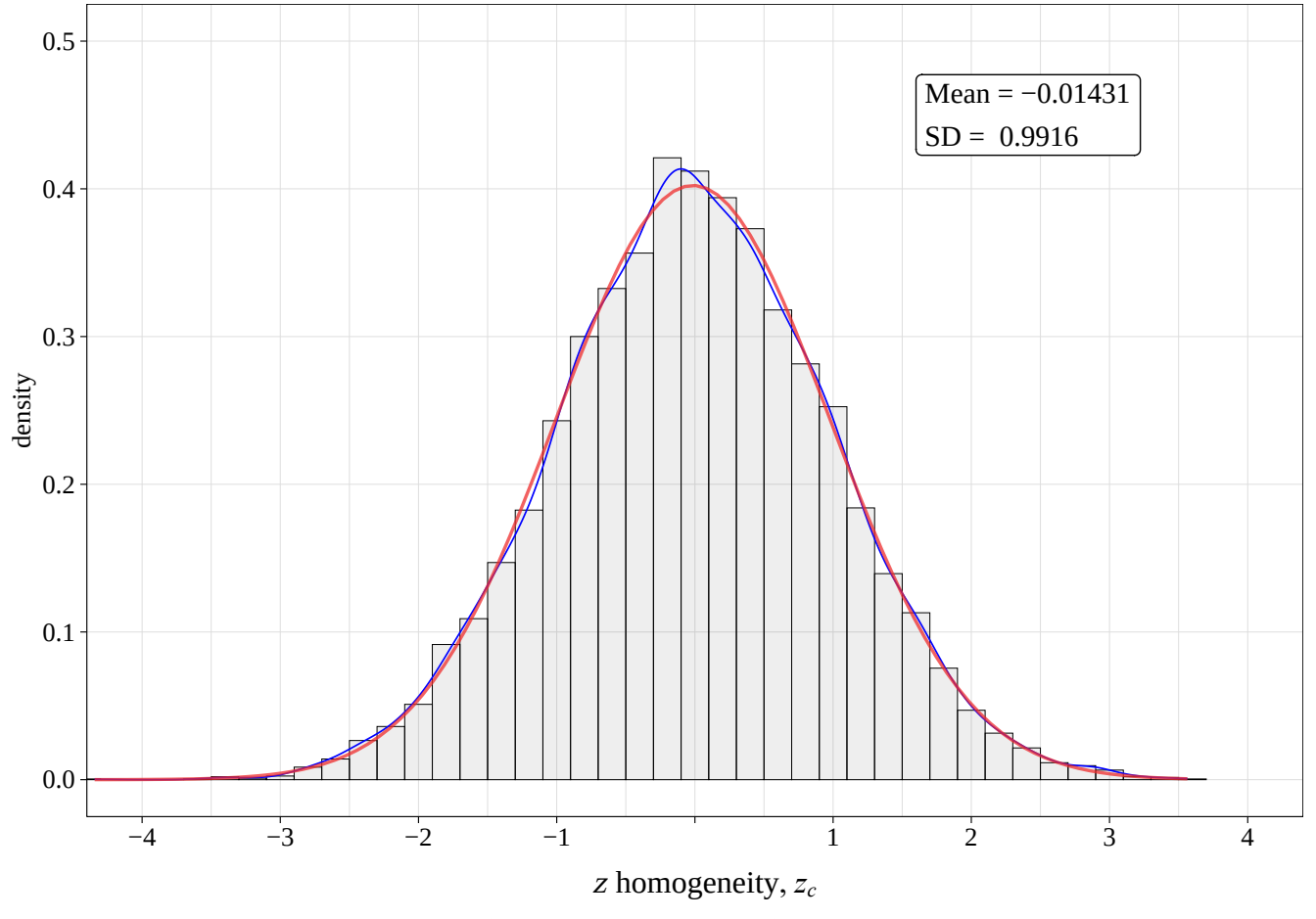
Drosophila-like 140kbp/40kbp TAD domains, genes-domains model "proportional"

FDR equals to 0.024000 at 10000 permutations

JarqueBera p.value = 0.731179, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.011654, p−value = 0.634250, skewness of normal distribution should be 0

Kurtosis = 3.030978, p−value = 0.527165, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.014427	−0.014308	−0.014308
SD	0.986199	0.991626	0.991626
p(AD)	0.940594	0.942630	0.942630

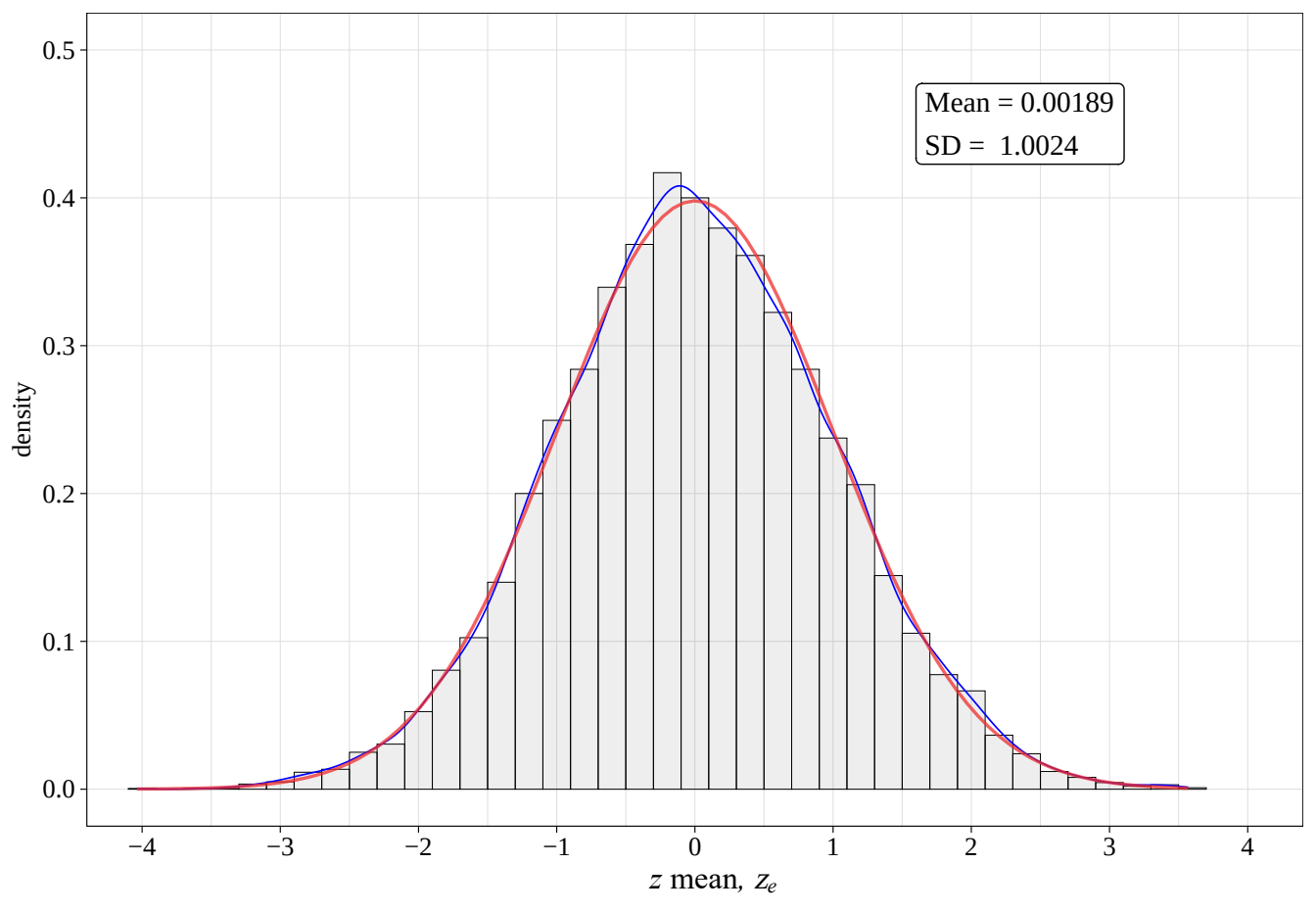
Drosophila-like 140kbp/40kbp TAD domains, genes-domains model "proportional"

FDR equals to 0.025600 at 10000 permutations

JarqueBera p.value = 0.833593, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.003636, p−value = 0.881988, skewness of normal distribution should be 0

Kurtosis = 3.028649, p−value = 0.558686, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.001807	0.001894	0.001894
SD	0.996334	1.002411	1.002411
p(AD)	0.738379	0.738620	0.738620

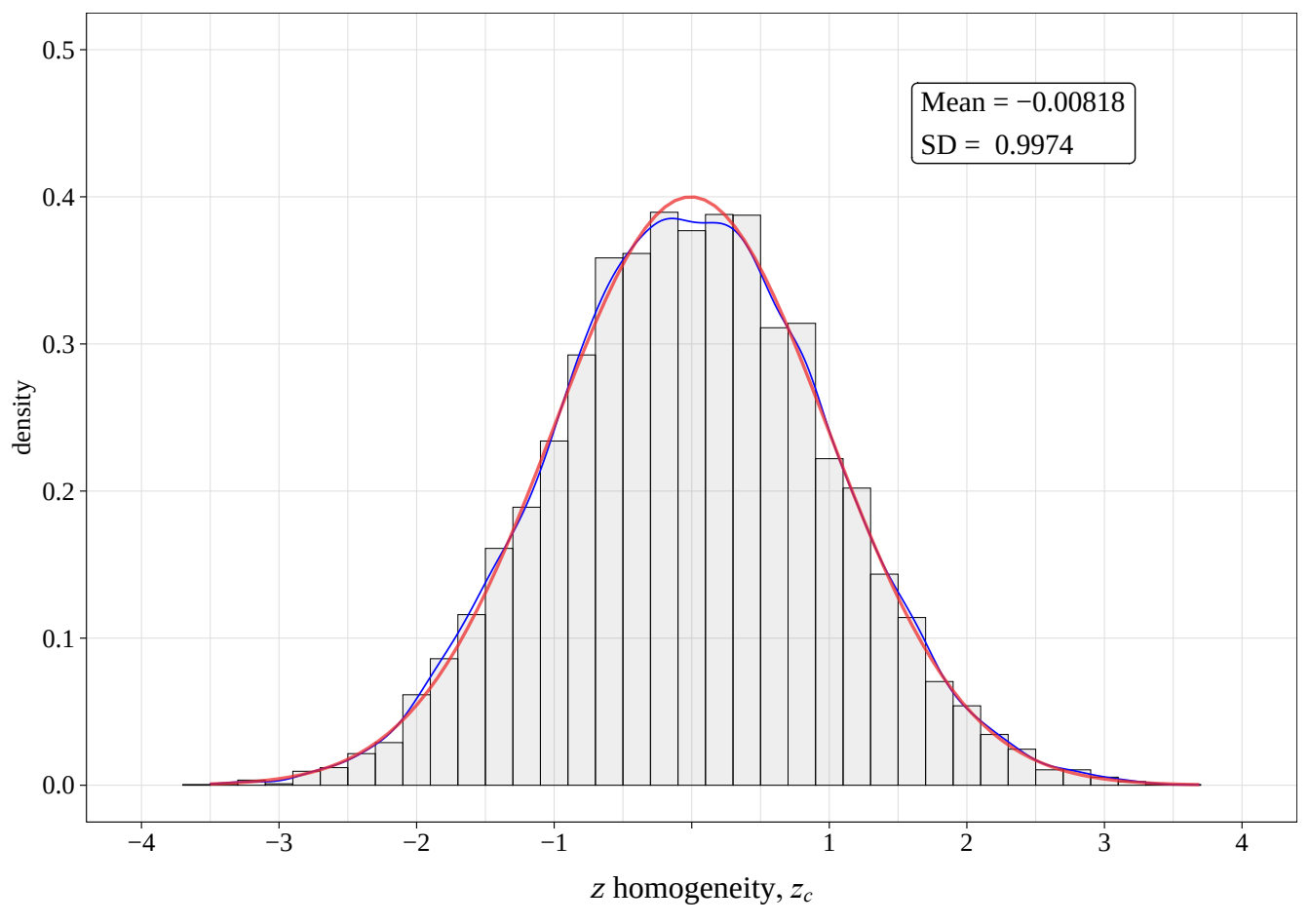
Drosophila-like 140kbp/40kbp TAD domains, genes-domains model "start"

FDR equals to 0.024900 at 10000 permutations

JarqueBera p.value = 0.652692, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.012932, p−value = 0.597527, skewness of normal distribution should be 0

Kurtosis = 3.037134, p−value = 0.448454, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.010026	−0.008181	−0.008181
SD	1.003568	0.997386	0.997386
p(AD)	0.964475	0.941538	0.941538

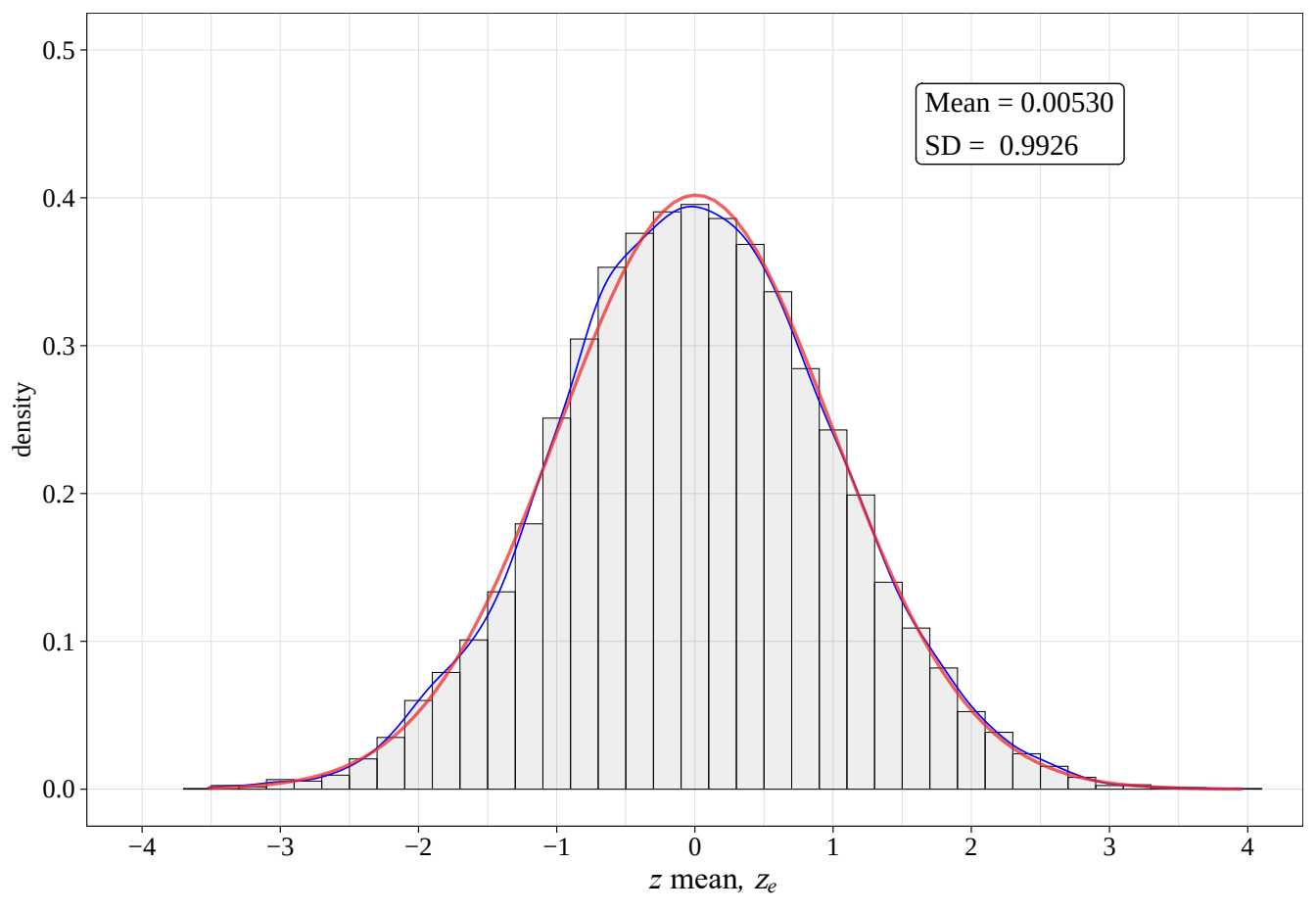
Drosophila-like 140kbp/40kbp TAD domains, genes-domains model "start"

FDR equals to 0.023300 at 10000 permutations

JarqueBera p.value = 0.232496, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.023298, p−value = 0.341537, skewness of normal distribution should be 0

Kurtosis = 2.930491, p−value = 0.155945, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	0.001417	0.005303	0.005303
SD	0.990377	0.992645	0.992645
p(AD)	0.817072	0.808205	0.808205

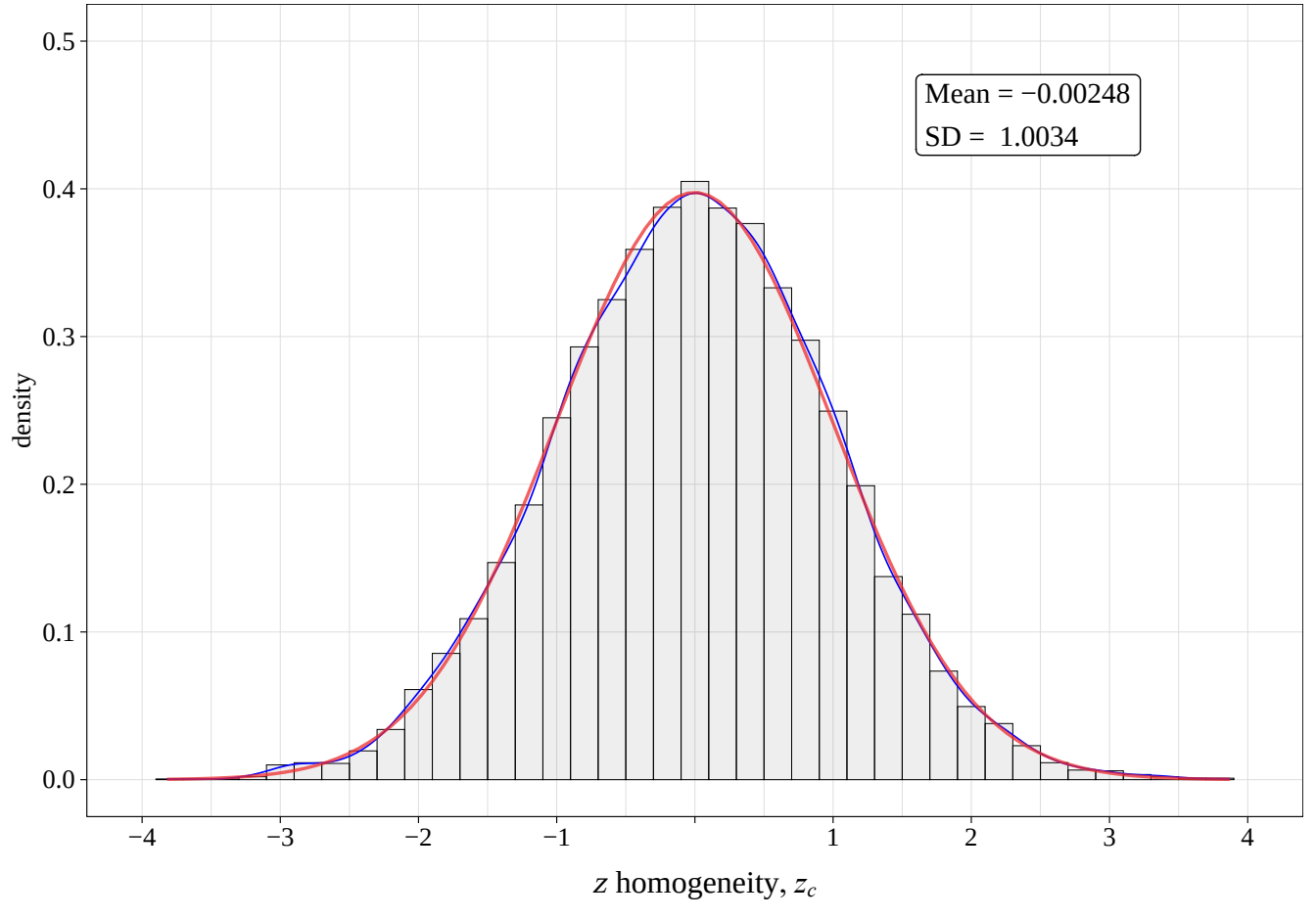
Drosophila-like 140kbp/40kbp TAD domains, genes-domains model "longer part"

FDR equals to 0.024200 at 10000 permutations

JarqueBera p.value = 0.636924, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.021432, p−value = 0.381599, skewness of normal distribution should be 0

Kurtosis = 3.018111, p−value = 0.711619, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	0.001030	−0.002476	−0.002476
SD	0.999191	1.003432	1.003432
p(AD)	0.925675	0.899528	0.899528

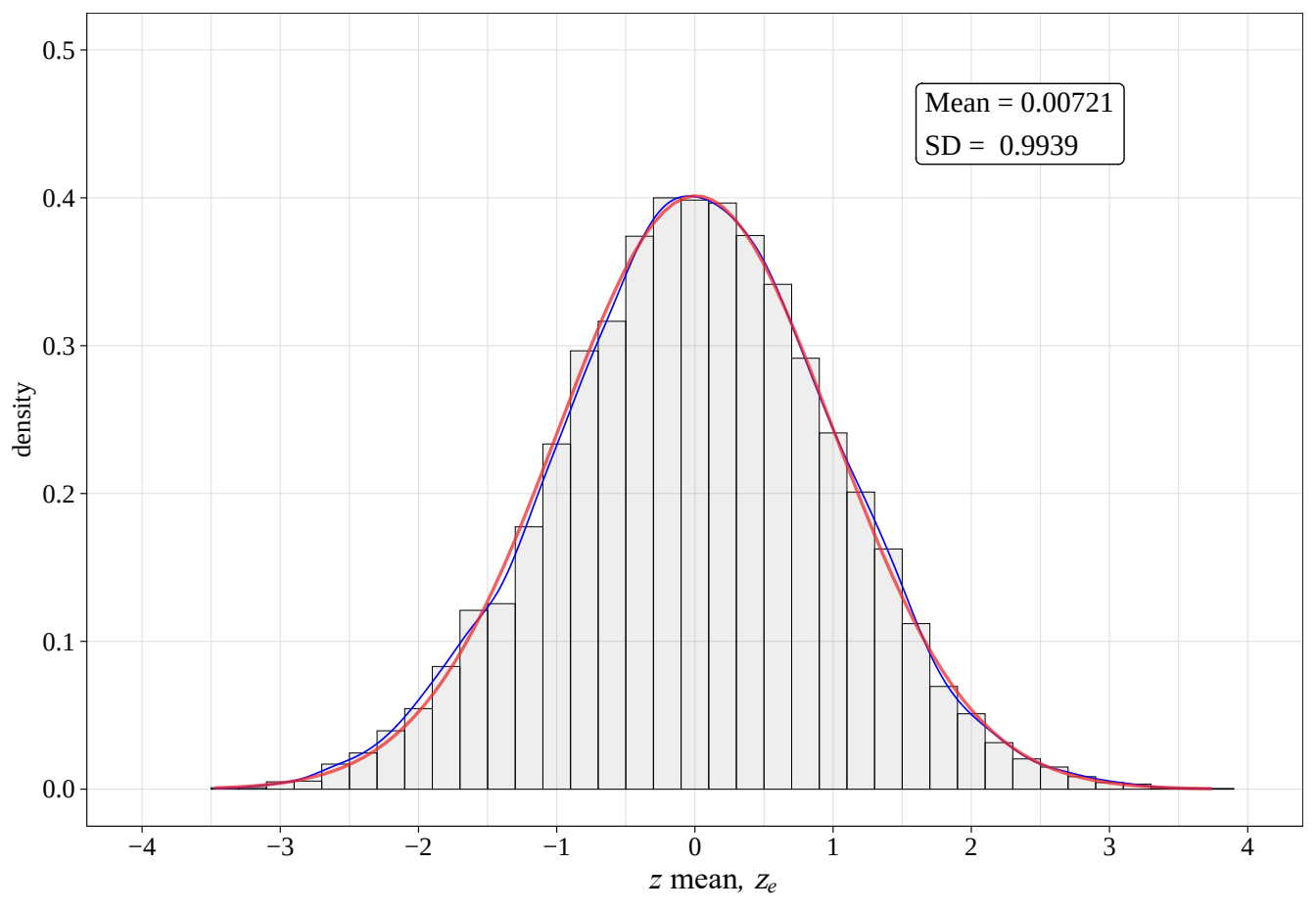
Drosophila-like 140kbp/40kbp TAD domains, genes-domains model "longer part"

FDR equals to 0.026100 at 10000 permutations

JarqueBera p.value = 0.366112, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.011553, p−value = 0.637163, skewness of normal distribution should be 0

Kurtosis = 3.065492, p−value = 0.181272, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	0.012194	0.007212	0.007212
SD	0.990042	0.993927	0.993927
p(AD)	0.683405	0.688281	0.688281

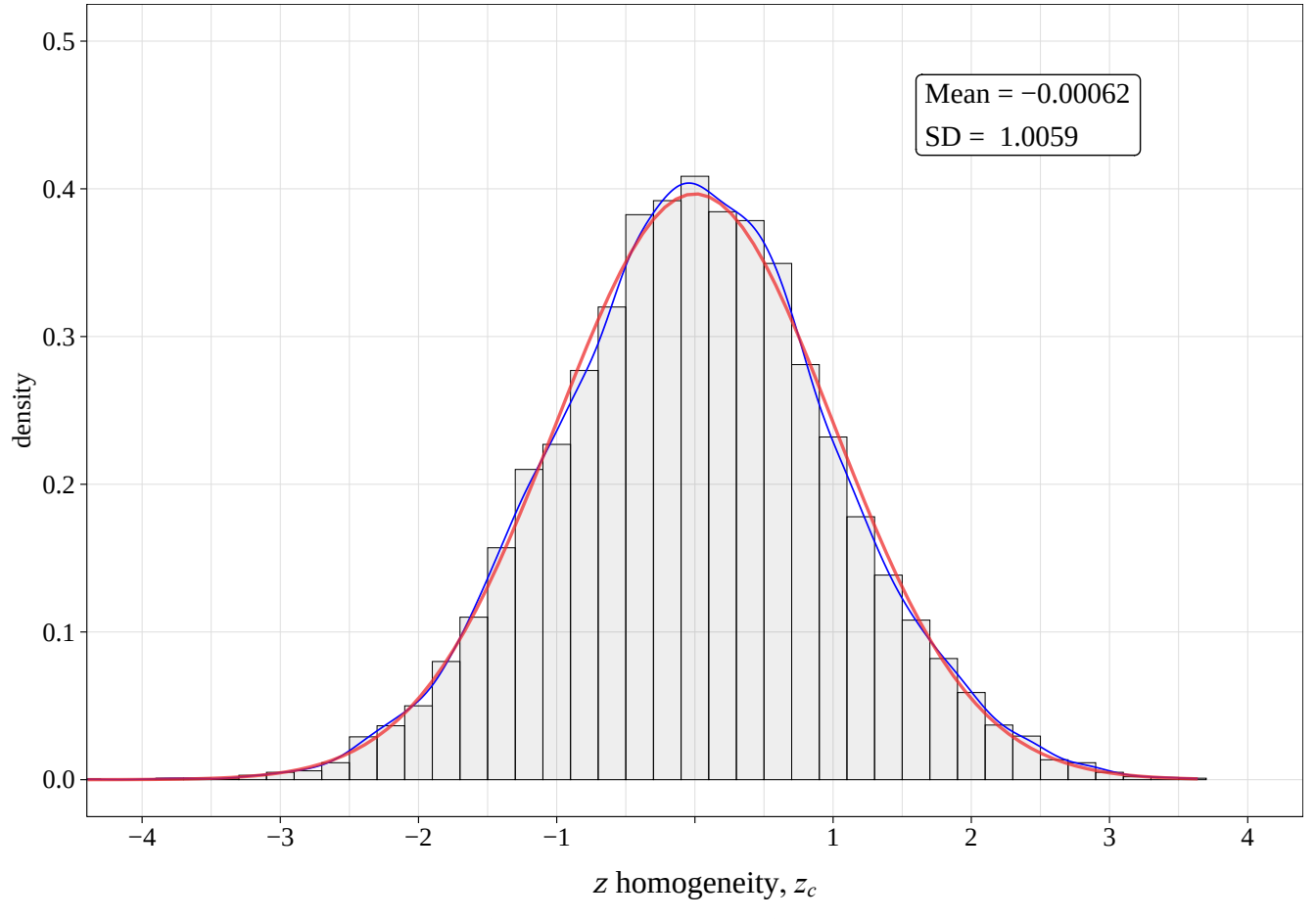
Drosophila-like 140kbp/40kbp TAD domains, genes-domains model "midpoint"

FDR equals to 0.025800 at 10000 permutations

JarqueBera p.value = 0.566412, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.024012, p−value = 0.326944, skewness of normal distribution should be 0

Kurtosis = 2.979453, p−value = 0.674919, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.001525	−0.000619	−0.000619
SD	0.993349	1.005891	1.005891
p(AD)	0.469945	0.480782	0.480782

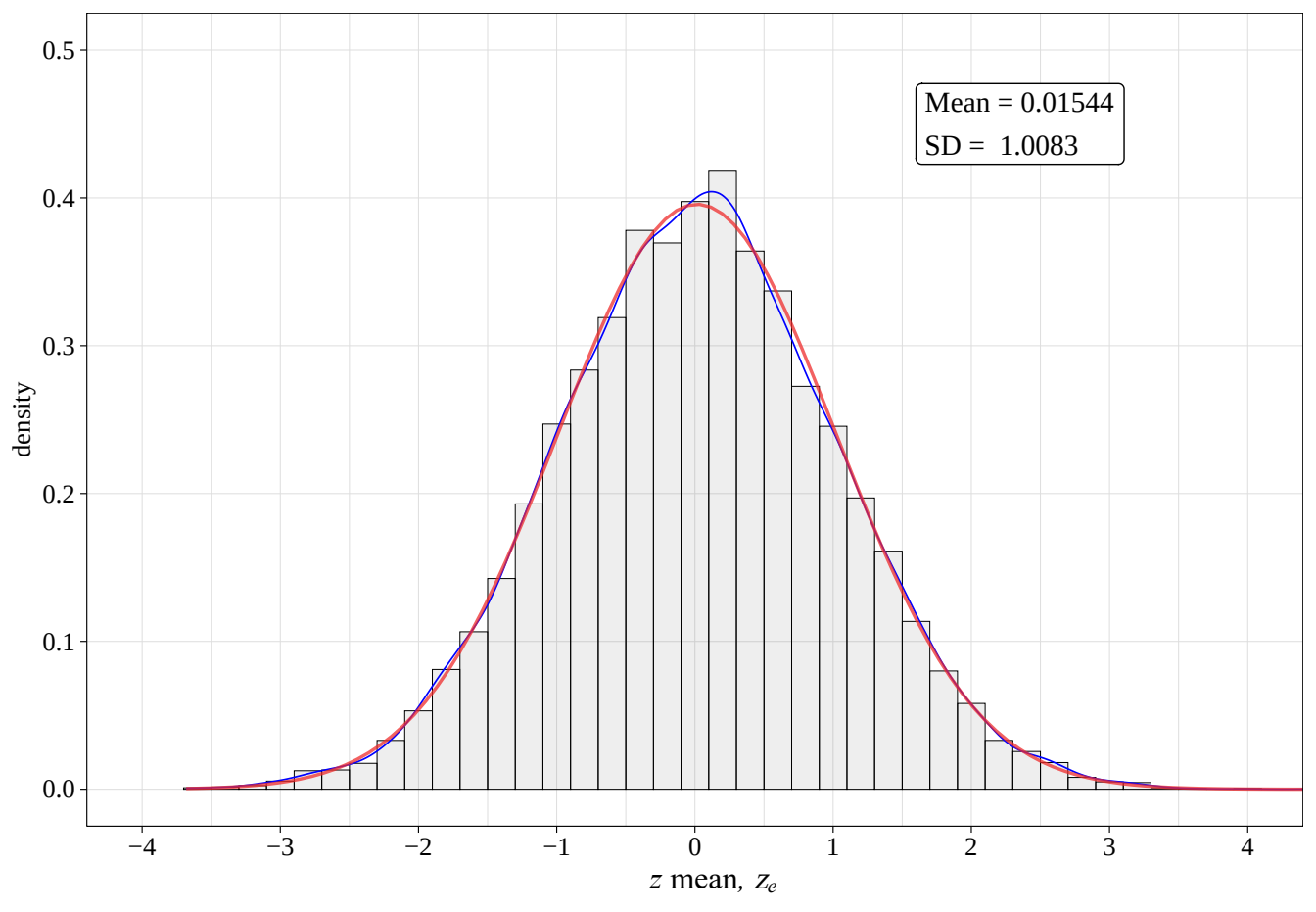
Drosophila-like 140kbp/40kbp TAD domains, genes-domains model "midpoint"

FDR equals to 0.026200 at 10000 permutations

JarqueBera p.value = 0.275481, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.012675, p−value = 0.604847, skewness of normal distribution should be 0

Kurtosis = 3.074470, p−value = 0.128484, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	0.014324	0.015438	0.015438
SD	1.001698	1.008297	1.008297
p(AD)	0.968205	0.955051	0.955051

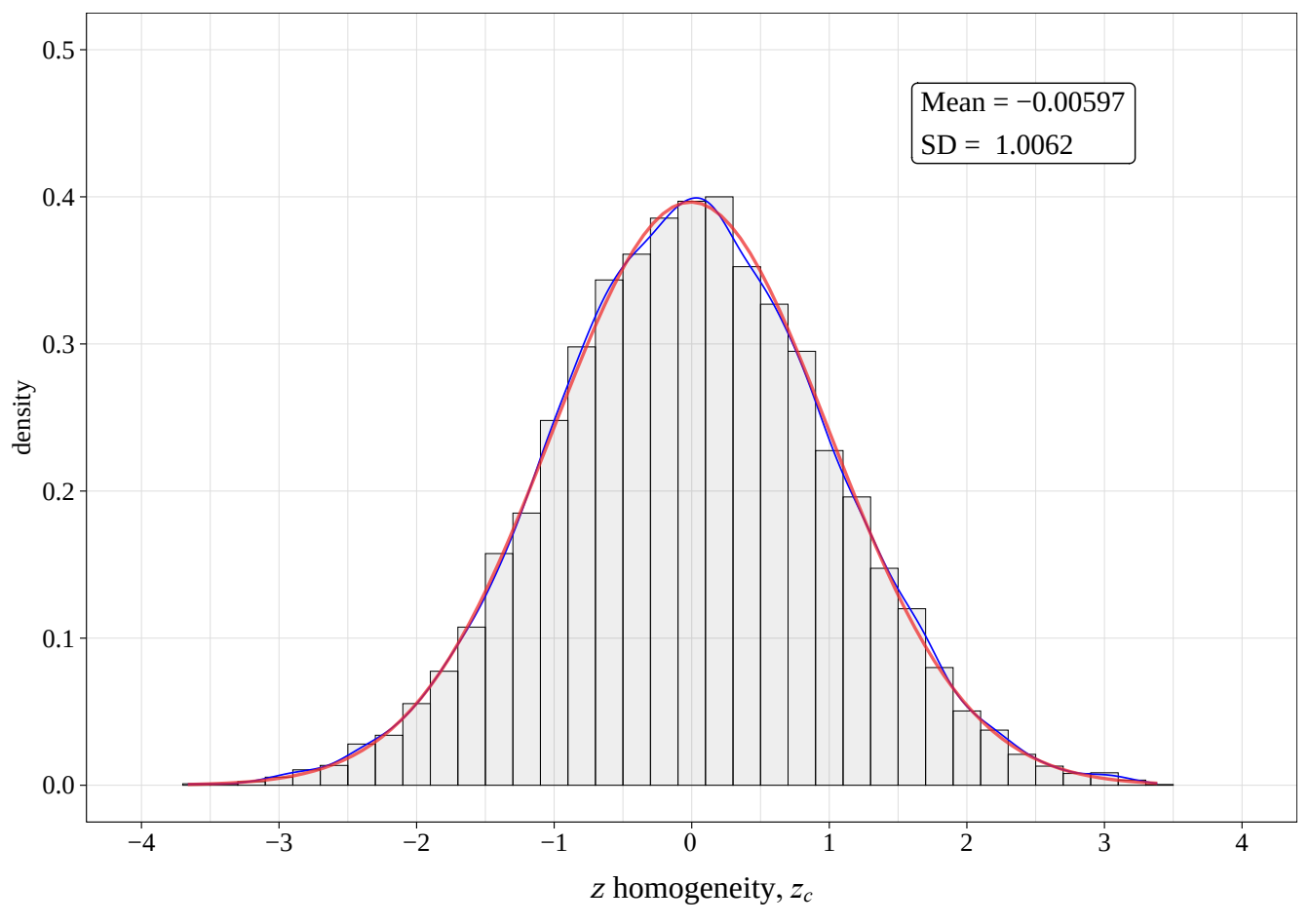
RAFT domains, genes-domains model "proportional"

FDR equals to 0.023700 at 10000 permutations

JarqueBera p.value = 0.325783, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.013144, p−value = 0.591555, skewness of normal distribution should be 0

Kurtosis = 3.068500, p−value = 0.162036, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.008132	−0.005967	−0.005967
SD	1.003922	1.006243	1.006243
p(AD)	0.987741	0.988546	0.988546

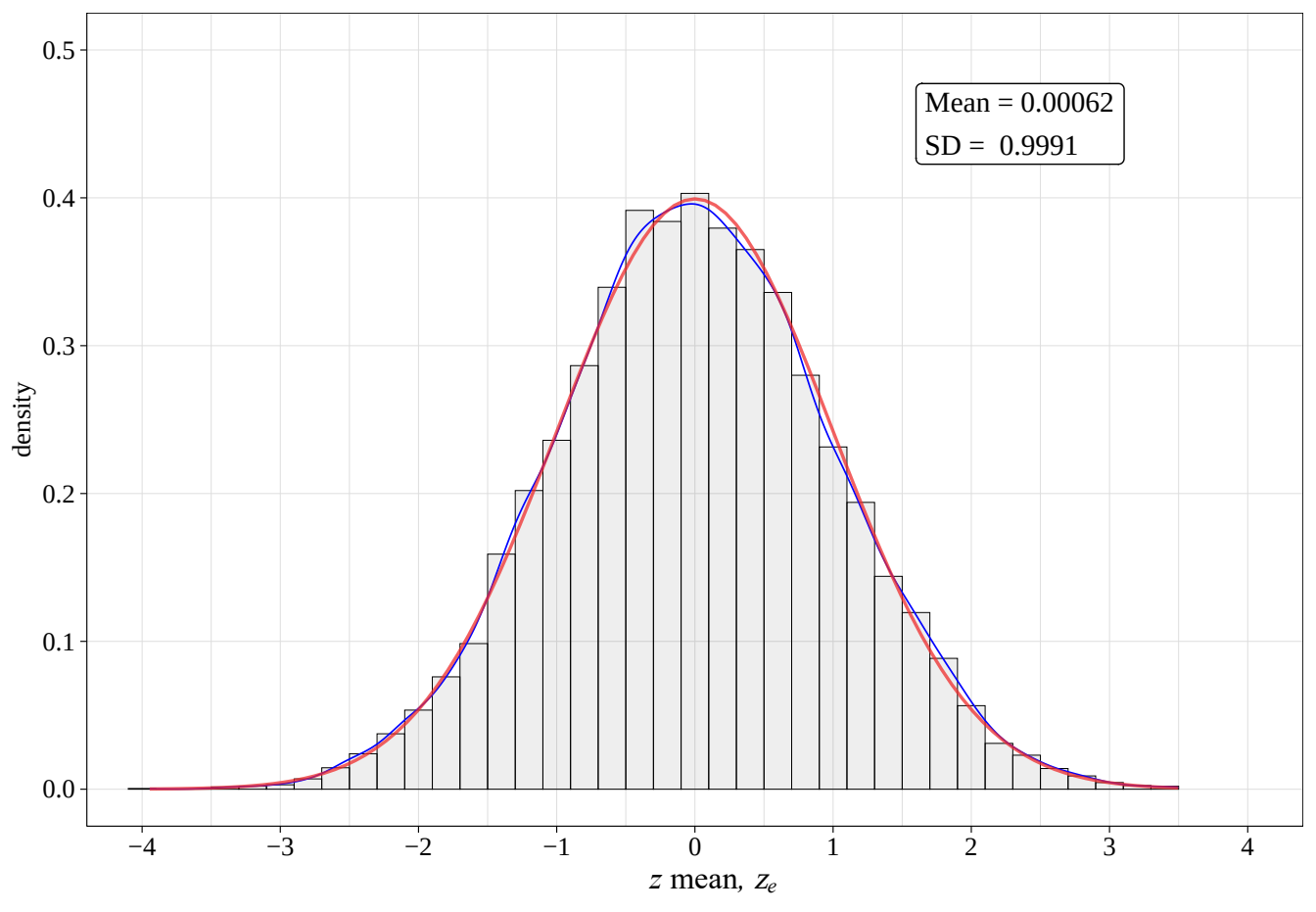
RAFT domains, genes-domains model "proportional"

FDR equals to 0.026400 at 10000 permutations

JarqueBera p.value = 0.967455, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.006023, p−value = 0.805778, skewness of normal distribution should be 0

Kurtosis = 2.996296, p−value = 0.939727, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.003991	0.000624	0.000624
SD	0.998695	0.999103	0.999103
p(AD)	0.850339	0.845242	0.845242

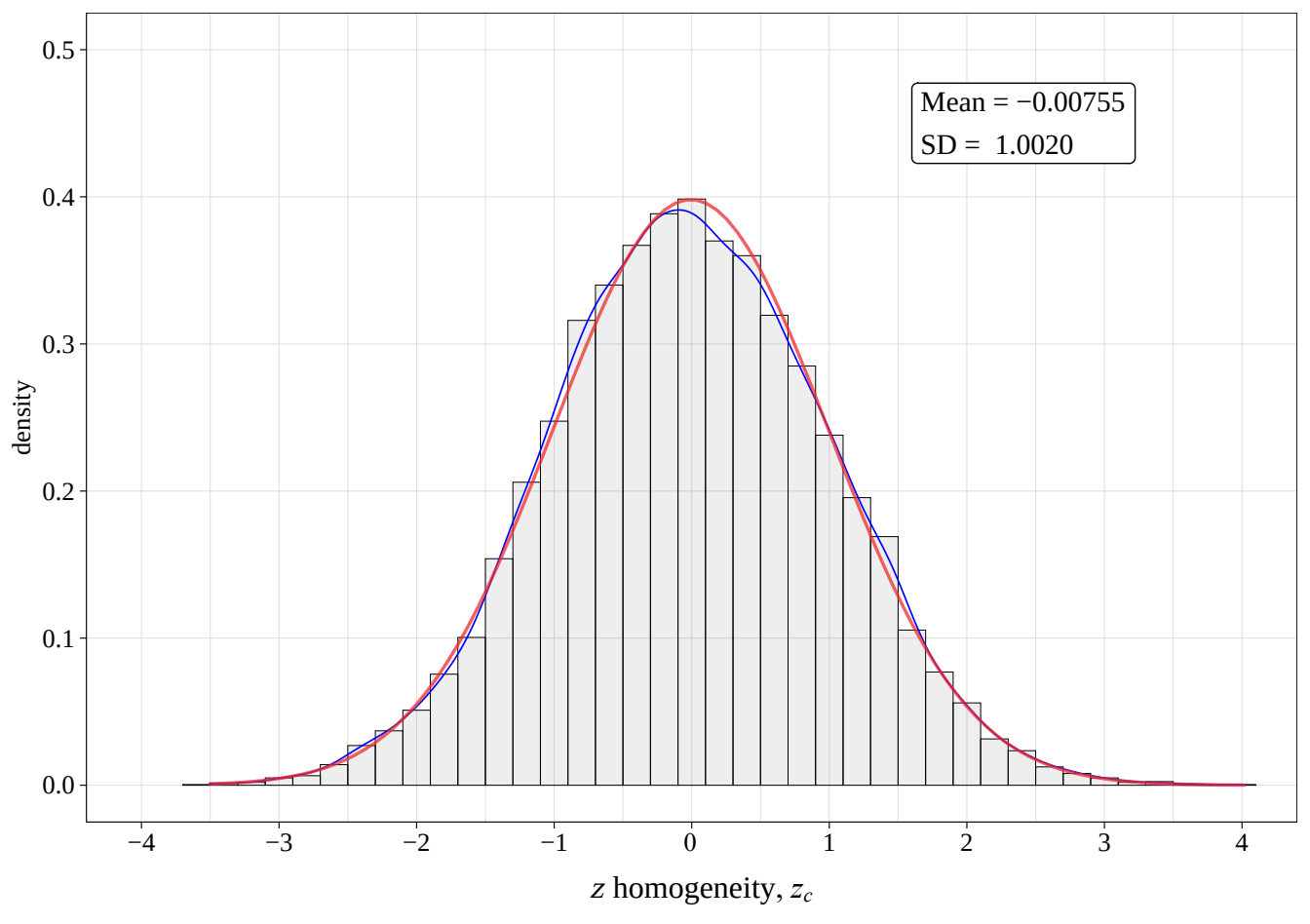
RAFT domains, genes-domains model "gene start"

FDR equals to 0.025400 at 10000 permutations

JarqueBera p.value = 0.435884, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.025550, p−value = 0.296915, skewness of normal distribution should be 0

Kurtosis = 2.962924, p−value = 0.449164, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.012962	−0.007552	−0.007552
SD	1.008330	1.002012	1.002012
p(AD)	0.525438	0.539032	0.539032

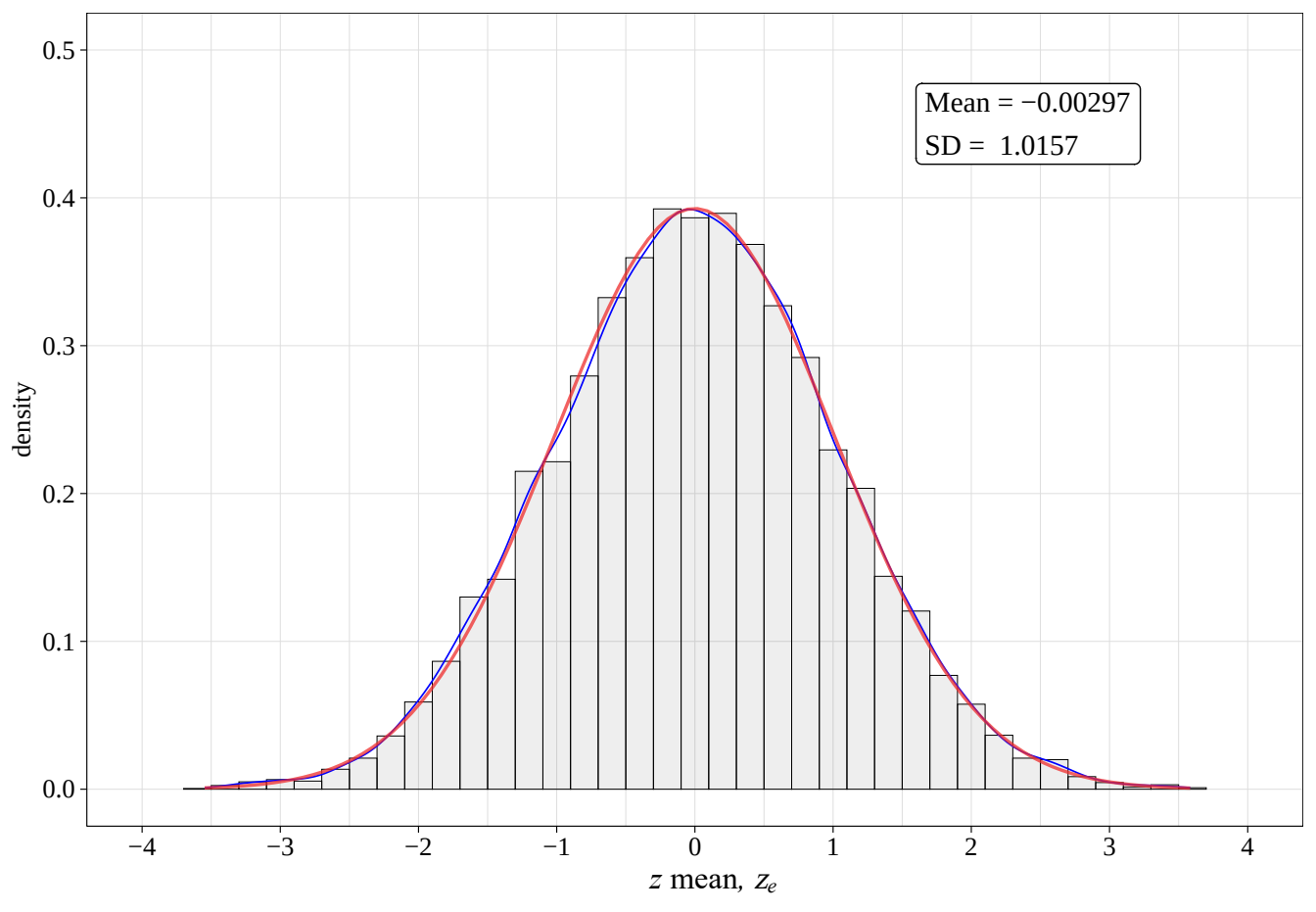
RAFT domains, genes-domains model "gene start"

FDR equals to 0.025700 at 10000 permutations

JarqueBera p.value = 0.358991, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.033646, p−value = 0.169562, skewness of normal distribution should be 0

Kurtosis = 2.980275, p−value = 0.687223, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.001593	−0.002968	−0.002968
SD	1.016628	1.015743	1.015743
p(AD)	0.987740	0.987914	0.987914

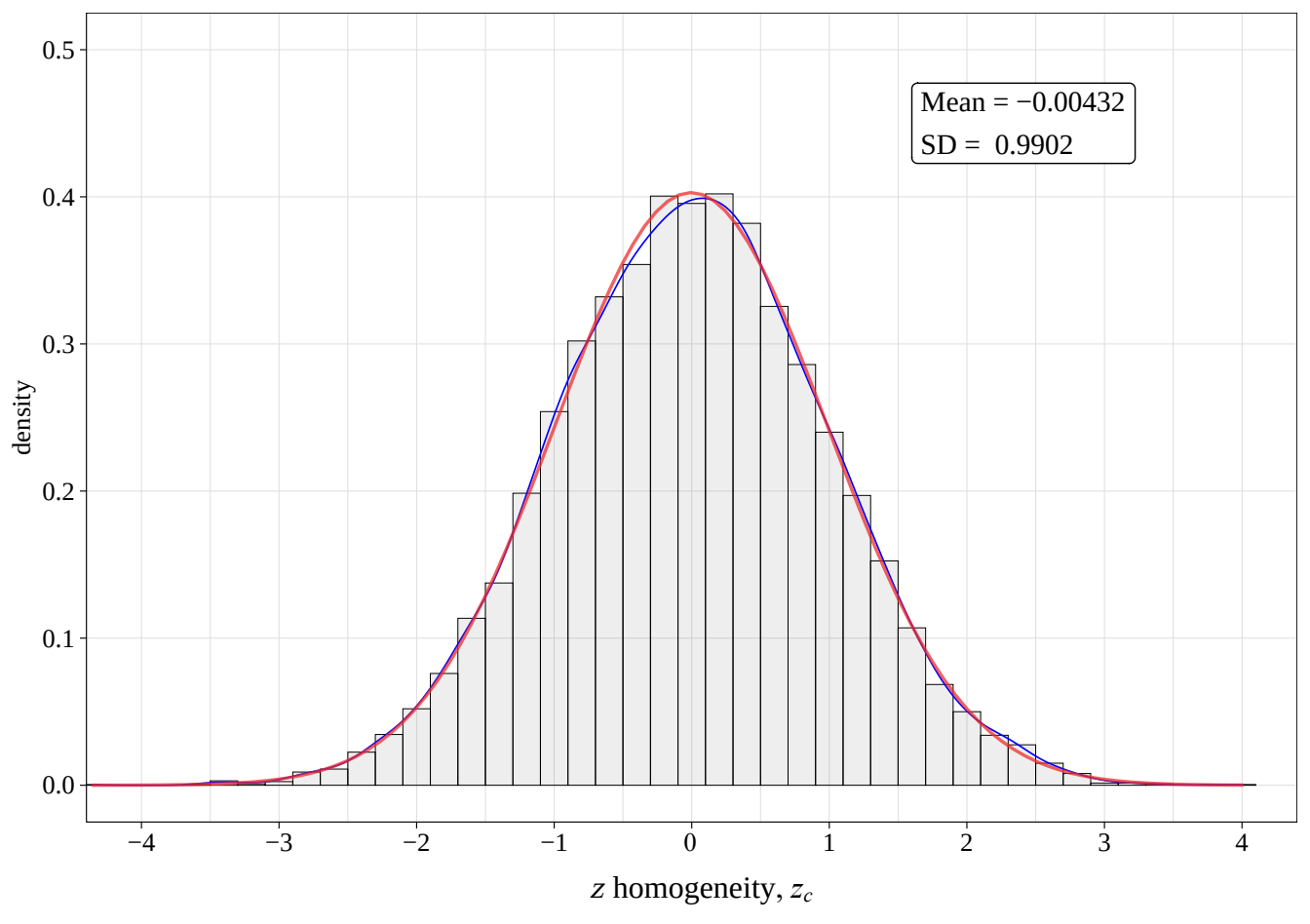
RAFT domains, genes-domains model "longer part"

FDR equals to 0.026300 at 10000 permutations

JarqueBera p.value = 0.879795, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.001631, p−value = 0.946910, skewness of normal distribution should be 0

Kurtosis = 2.975422, p−value = 0.615882, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.003861	−0.004319	−0.004319
SD	0.991700	0.990217	0.990217
p(AD)	0.999014	0.999156	0.999156

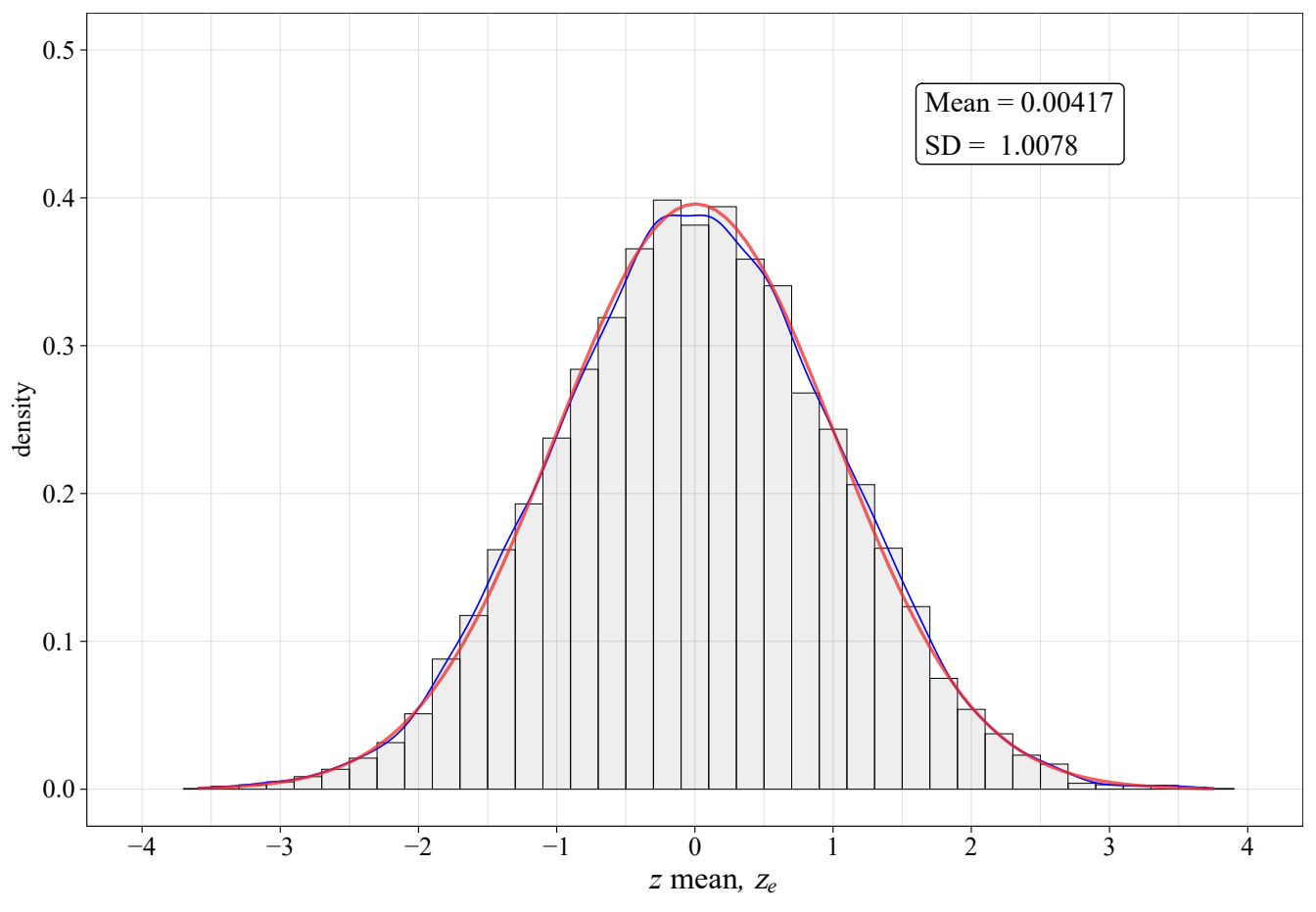
RAFT domains, genes-domains model "longer part"

FDR equals to 0.023800 at 10000 permutations

JarqueBera p.value = 0.950431, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.006671, p−value = 0.785369, skewness of normal distribution should be 0

Kurtosis = 3.008127, p−value = 0.868250, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	0.004646	0.004175	0.004175
SD	1.014154	1.007789	1.007789
p(AD)	0.968996	0.952570	0.952570

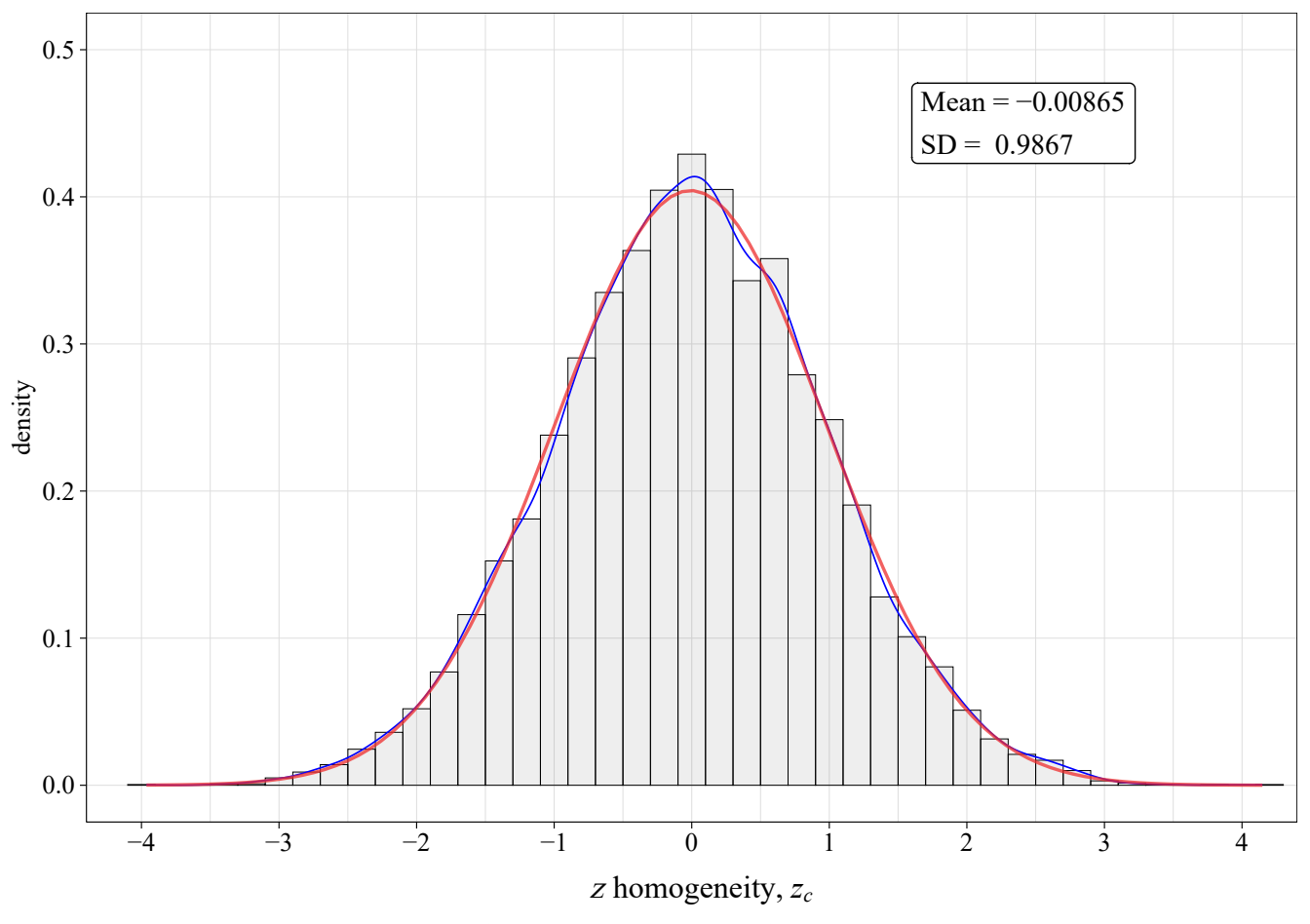
RAFT domains, genes-domains model "gene midpoint"

FDR equals to 0.023000 at 10000 permutations

JarqueBera p.value = 0.602495, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.003768, p−value = 0.877745, skewness of normal distribution should be 0

Kurtosis = 2.951263, p−value = 0.319818, kurtosis of normal distribution should be 3.0



	MGE	MLE	MME
Mean	−0.007651	−0.008645	−0.008645
SD	0.978039	0.986746	0.986746
p(AD)	0.810053	0.812725	0.812725

RAFT domains, genes-domains model "gene midpoint"

FDR equals to 0.024900 at 10000 permutations

JarqueBera p.value = 0.621631, if p−value<0.05 then the distribution is NOT normal

Skewness = 0.003672, p−value = 0.880827, skewness of normal distribution should be 0

Kurtosis = 3.047202, p−value = 0.335295, kurtosis of normal distribution should be 3.0