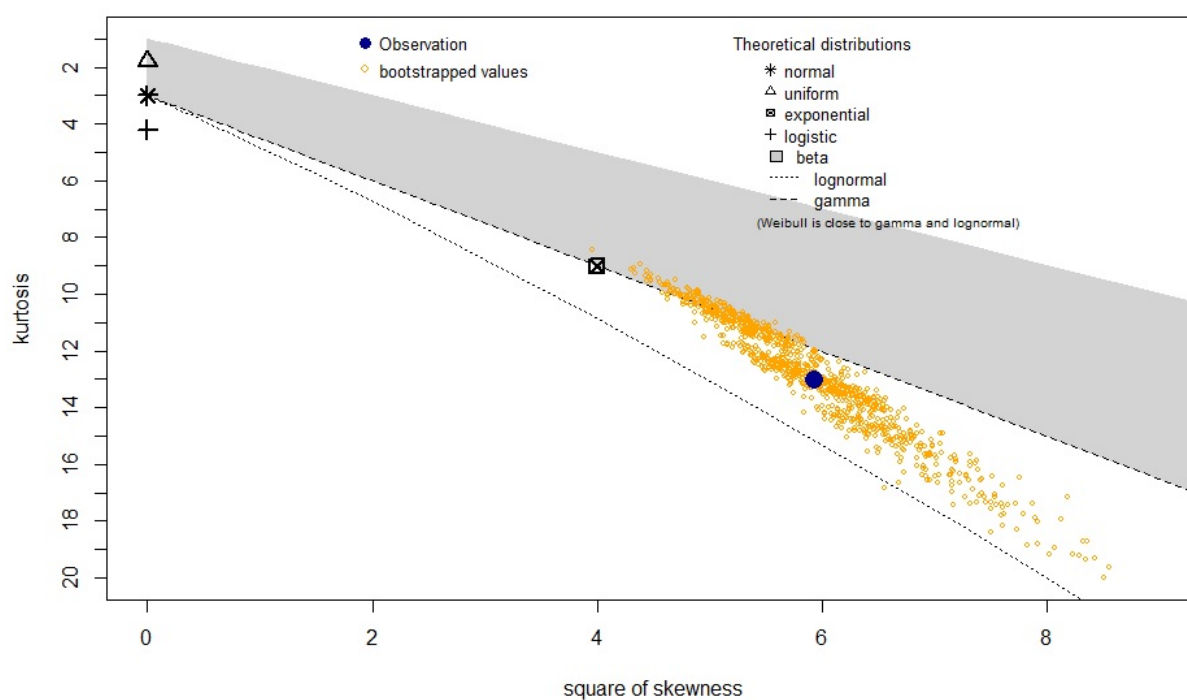


Statistics: percentage variance explained by haplotypes from blocks with LD_0.15 WssGWAS iteration 1 (ssGWAS)

summary statistics

min: 0 max: 0.14619
median: 0.00696
mean: 0.01038186
estimated sd: 0.01104523
estimated skewness: 2.434889
estimated kurtosis: 13.02973

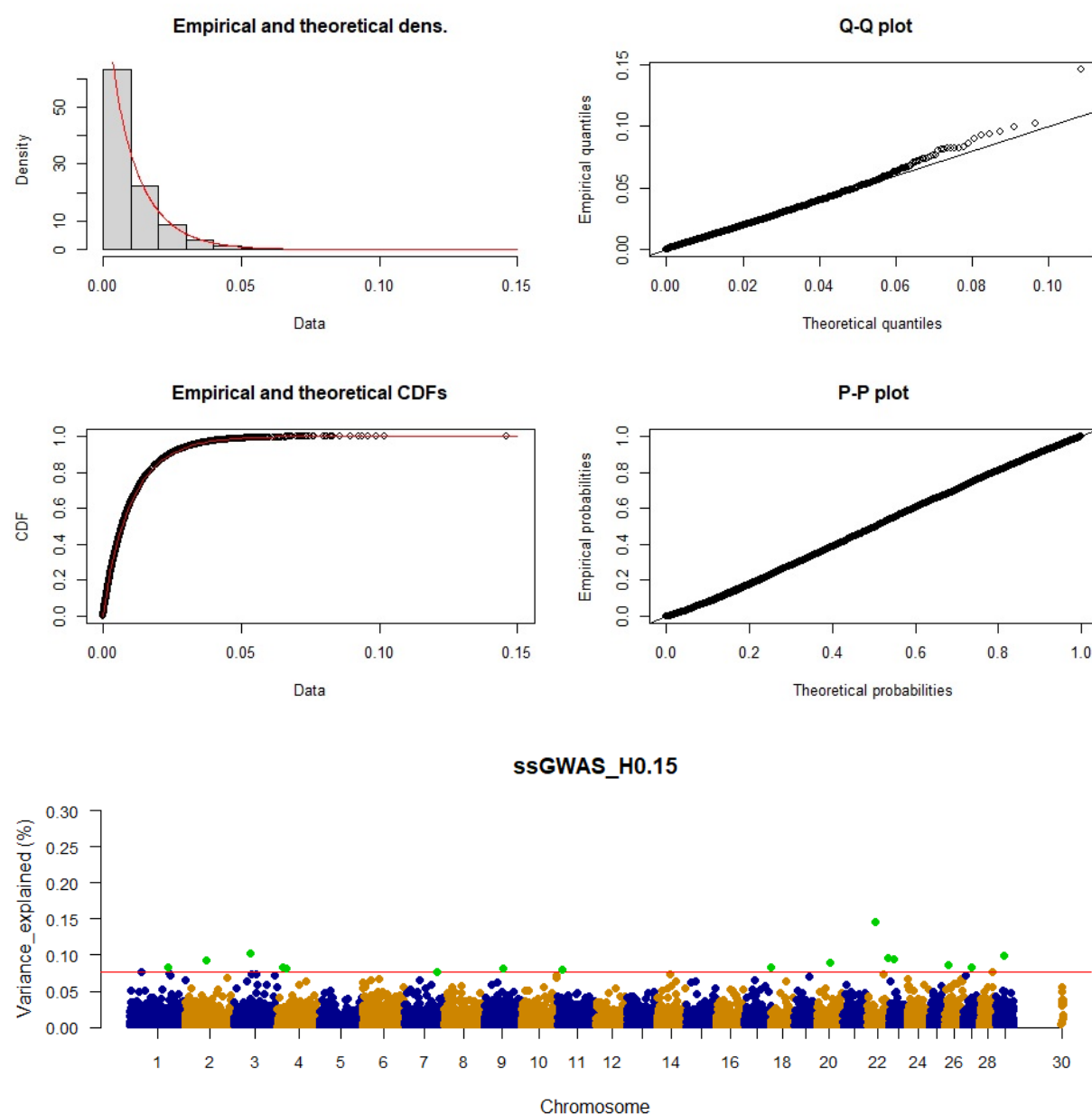
Cullen and Frey graph



Fitting of the distribution 'beta' by matching moments

Parameters :

estimate
shape1 0.8640248
shape2 82.3604749



**Statistics: percentage variance explained by haplotypes from blocks with LD_0.15
WssGWAS iteration 2 (WssGWAS)**

summary statistics

min: 0 max: 0.11174

median: 0.00722

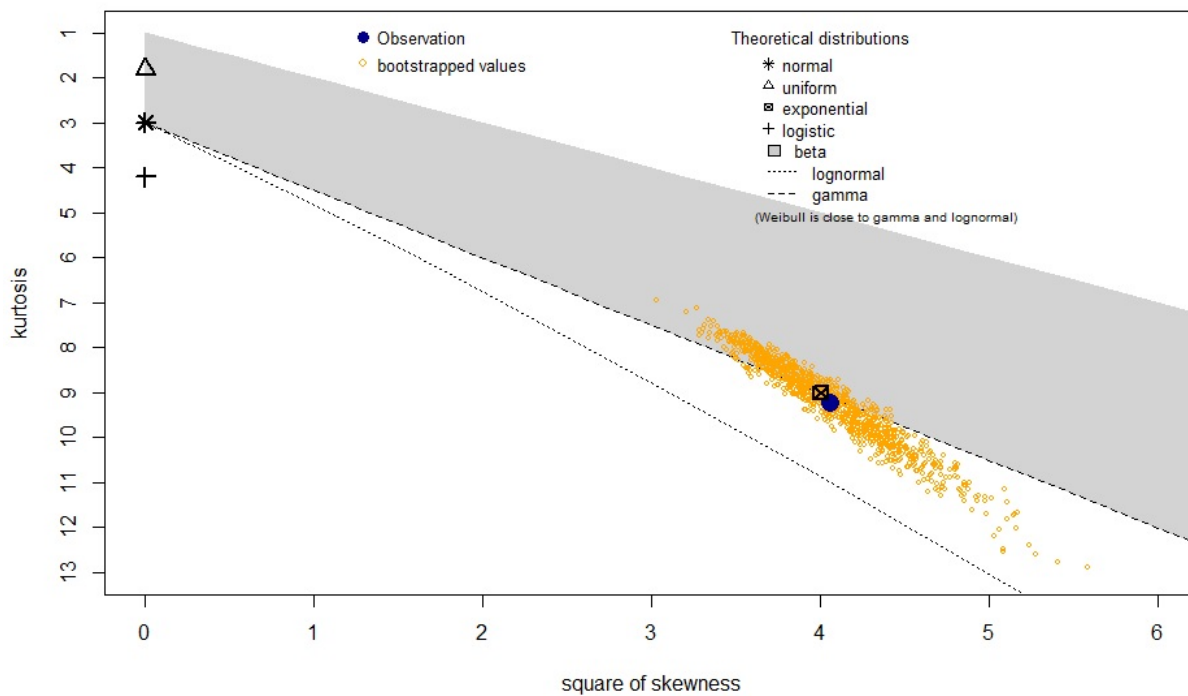
mean: 0.01038182

estimated sd: 0.0103068

estimated skewness: 2.014777

estimated kurtosis: 9.237767

Cullen and Frey graph



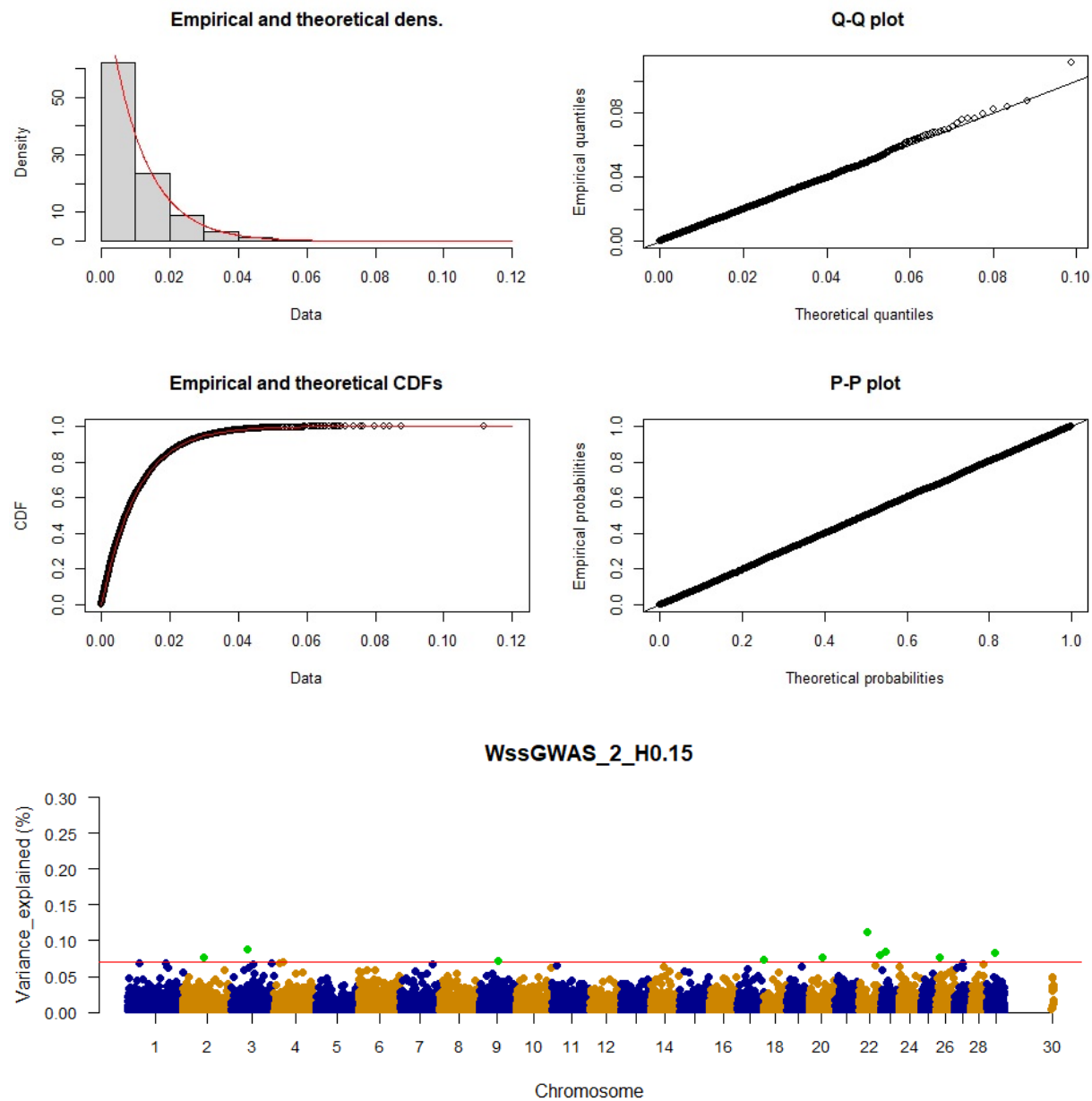
Fitting of the distribution 'beta' by matching moments

Parameters :

estimate

shape1 0.9938006

shape2 94.7312646



**Statistics: percentage variance explained by haplotypes from blocks with LD_0.15
WssGWAS iteration 3 (WssGWAS)**

summary statistics

min: 0 max: 0.11876

median: 0.0072

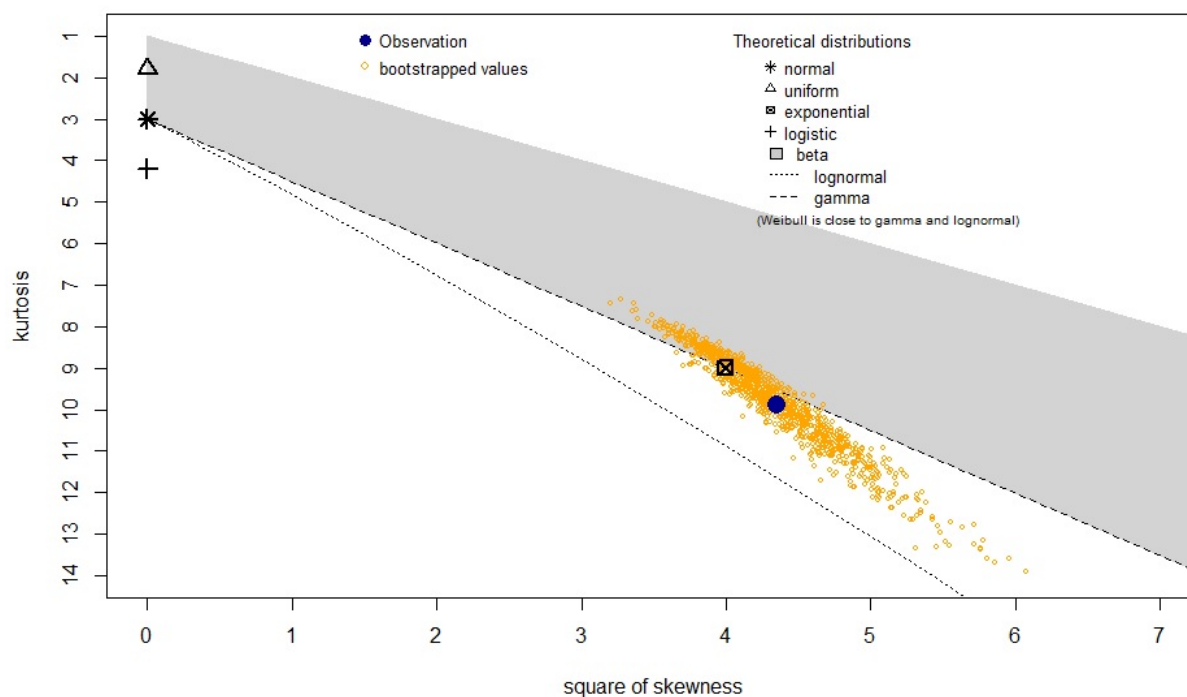
mean: 0.01038177

estimated sd: 0.01039503

estimated skewness: 2.085039

estimated kurtosis: 9.878912

Cullen and Frey graph



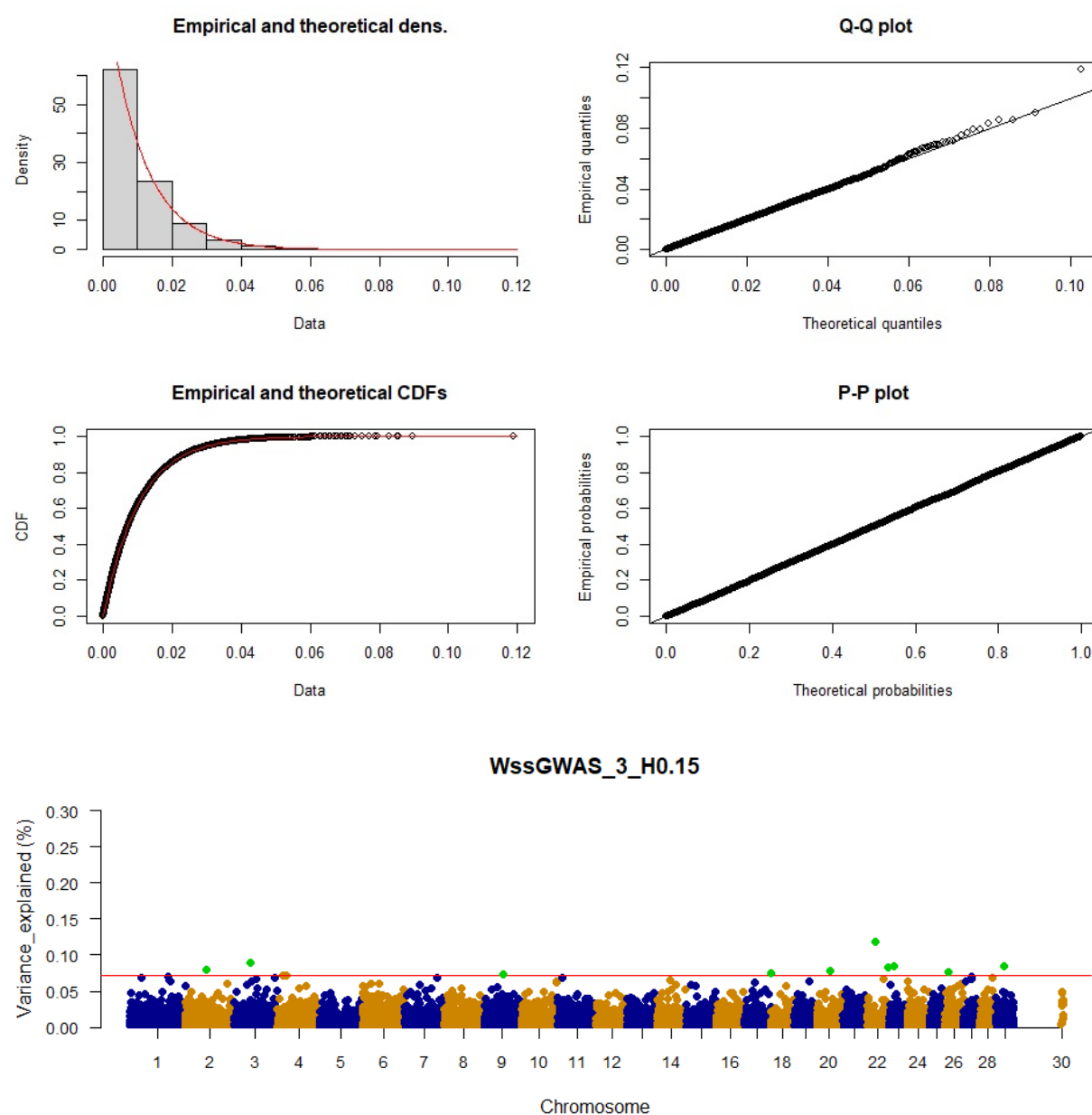
Fitting of the distribution ' gamma ' by matching moments

Parameters :

estimate

shape 0.9975547

rate 96.0871396



**Statistics: percentage variance explained by haplotypes from blocks with LD_0.50
WssGWAS iteration 1 (ssGWAS)**

summary statistics

min: 0 max: 0.1623

median: 0.01234

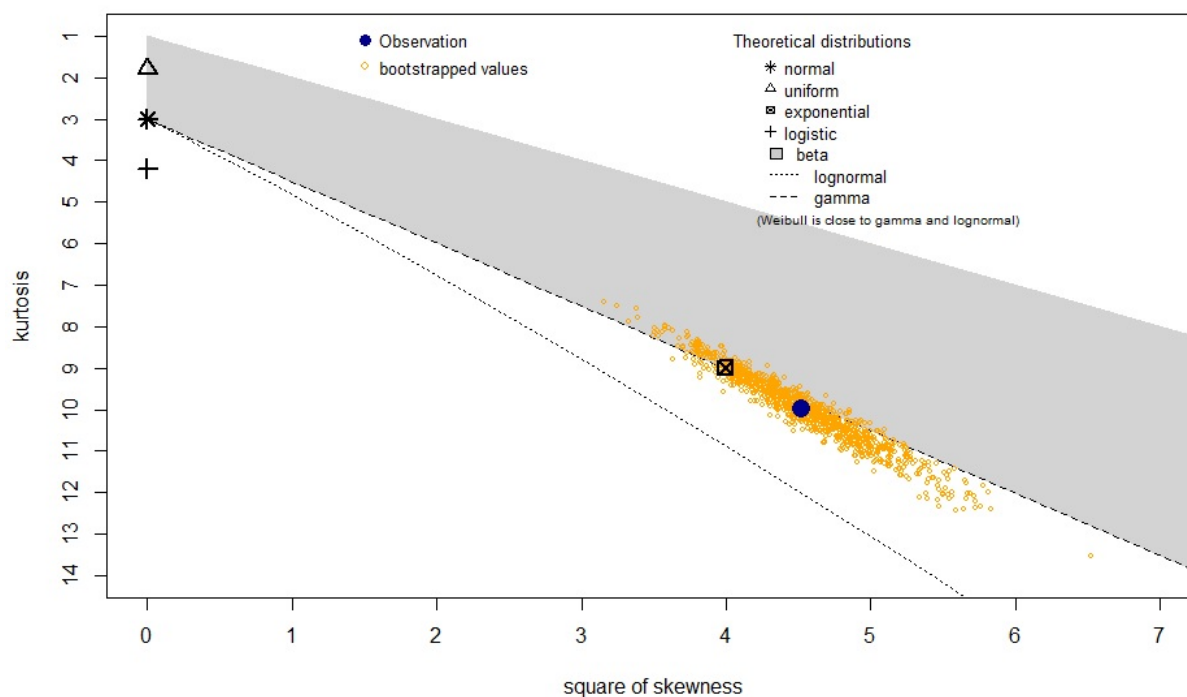
mean: 0.01780299

estimated sd: 0.01780225

estimated skewness: 2.127498

estimated kurtosis: 9.980306

Cullen and Frey graph



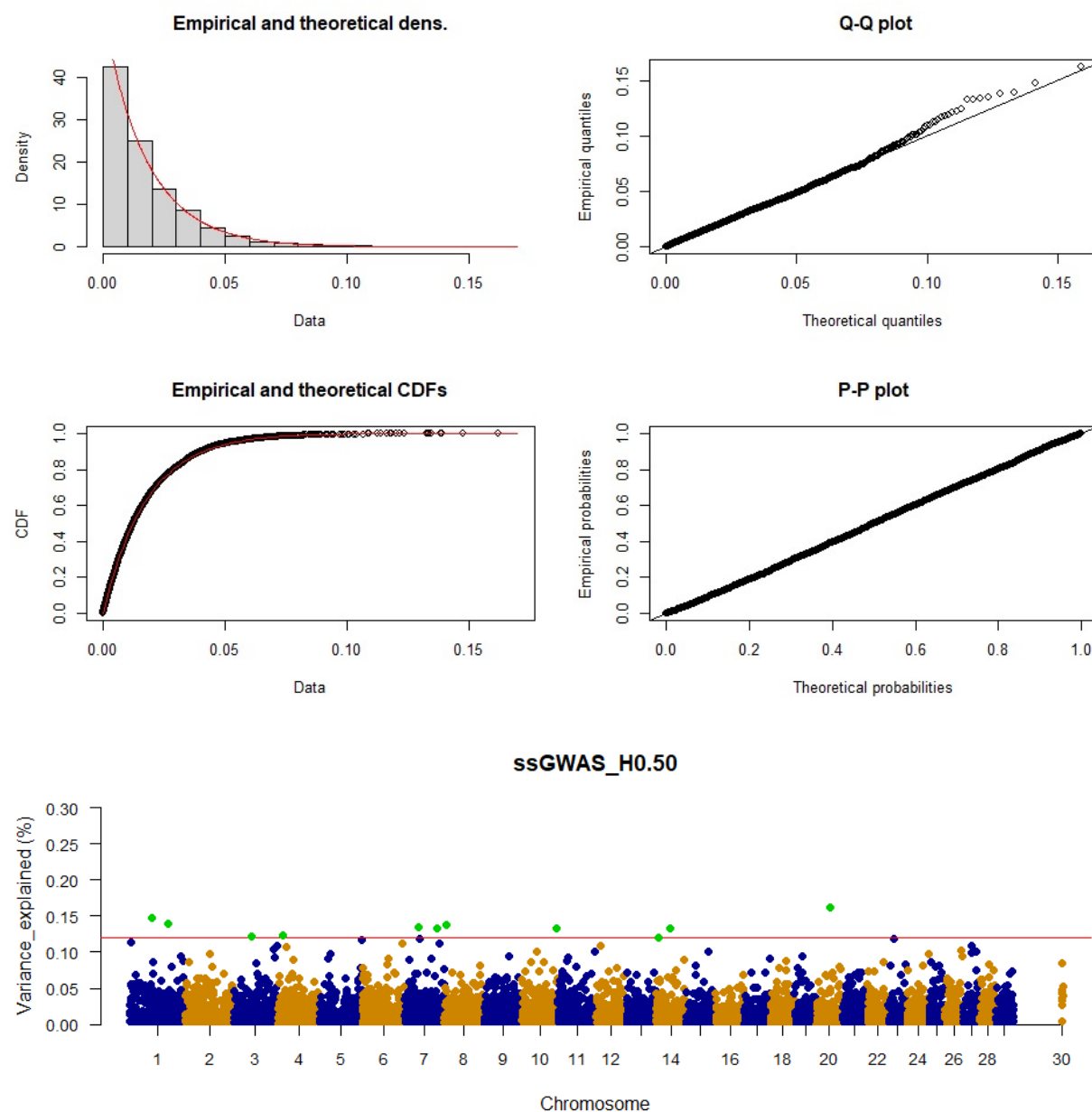
Fitting of the distribution 'beta' by matching moments

Parameters :

estimate

shape1 0.9646514

shape2 53.2201335



**Statistics: percentage variance explained by haplotypes from blocks with LD_0.50
WssGWAS iteration 2 (WssGWAS)**

summary statistics

min: 0 max: 0.13383

median: 0.01303

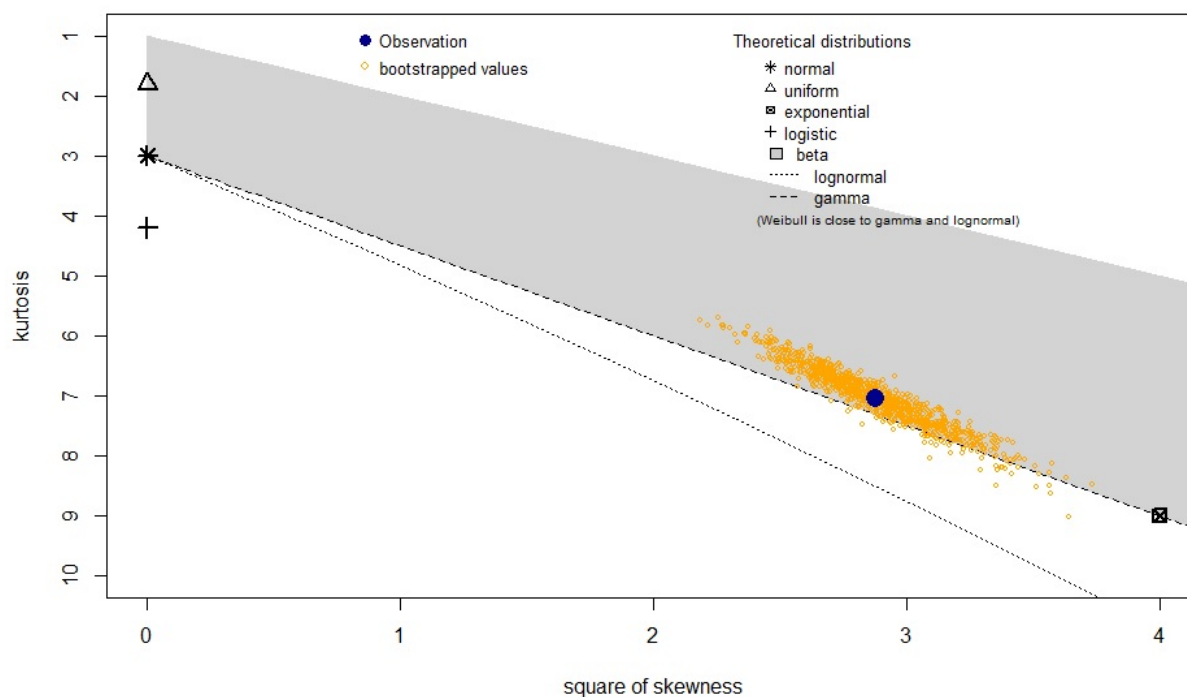
mean: 0.01780287

estimated sd: 0.01635826

estimated skewness: 1.69526

estimated kurtosis: 7.043574

Cullen and Frey graph



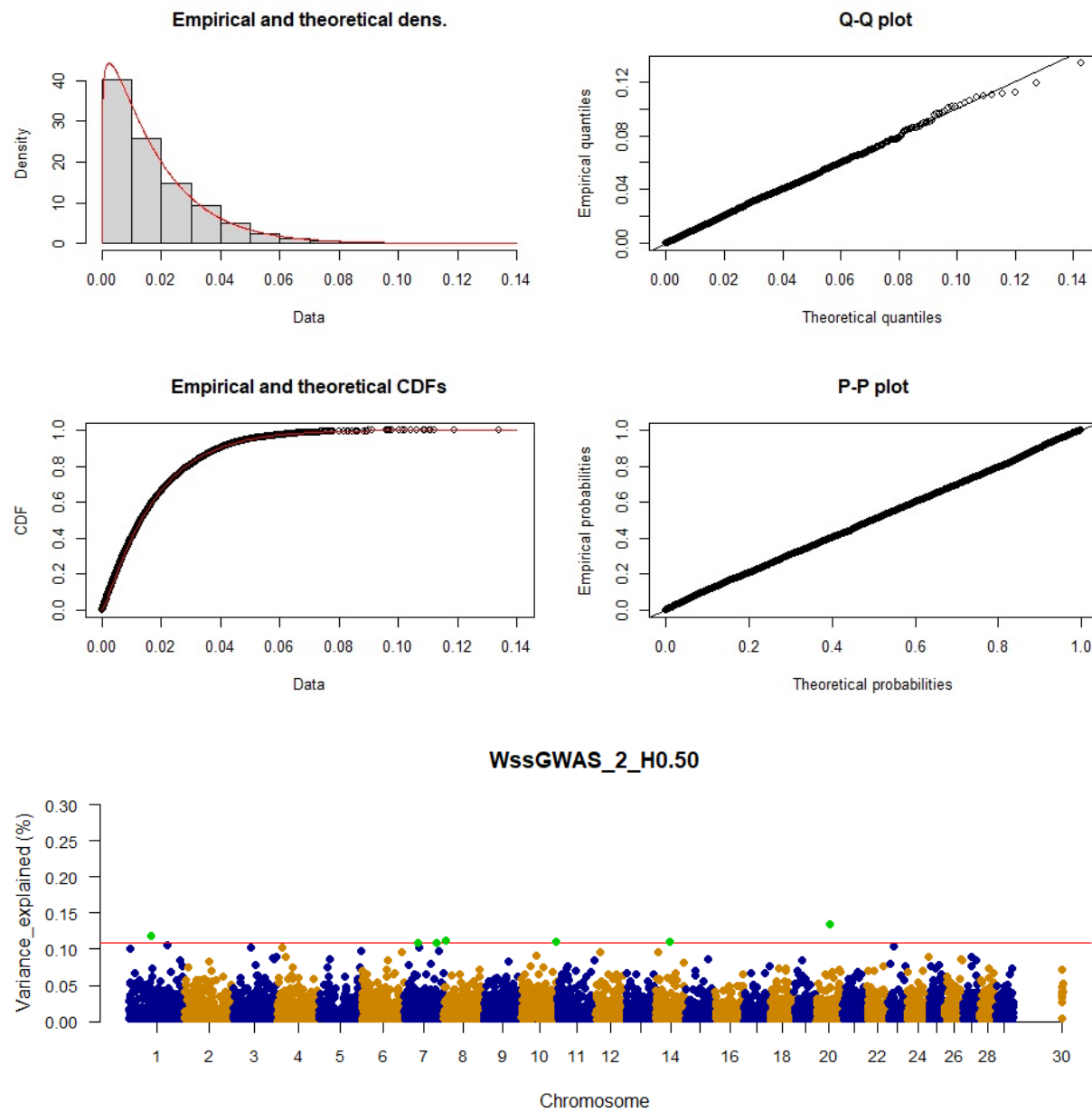
Fitting of the distribution 'beta' by matching moments

Parameters :

estimate

shape1 1.145738

shape2 63.211191



**Statistics: percentage variance explained by haplotypes from blocks with LD_0.50
WssGWAS iteration 3 (WssGWAS)**

summary statistics

min: 0 max: 0.13975

median: 0.01295

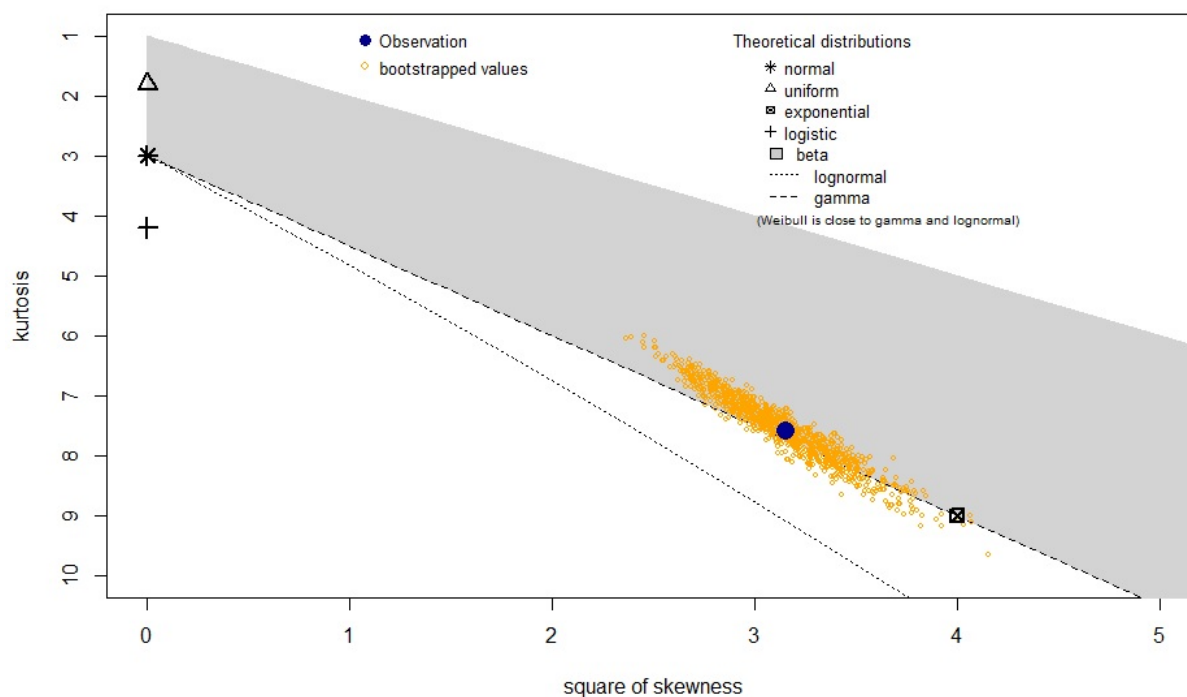
mean: 0.01780288

estimated sd: 0.01654919

estimated skewness: 1.775167

estimated kurtosis: 7.591097

Cullen and Frey graph



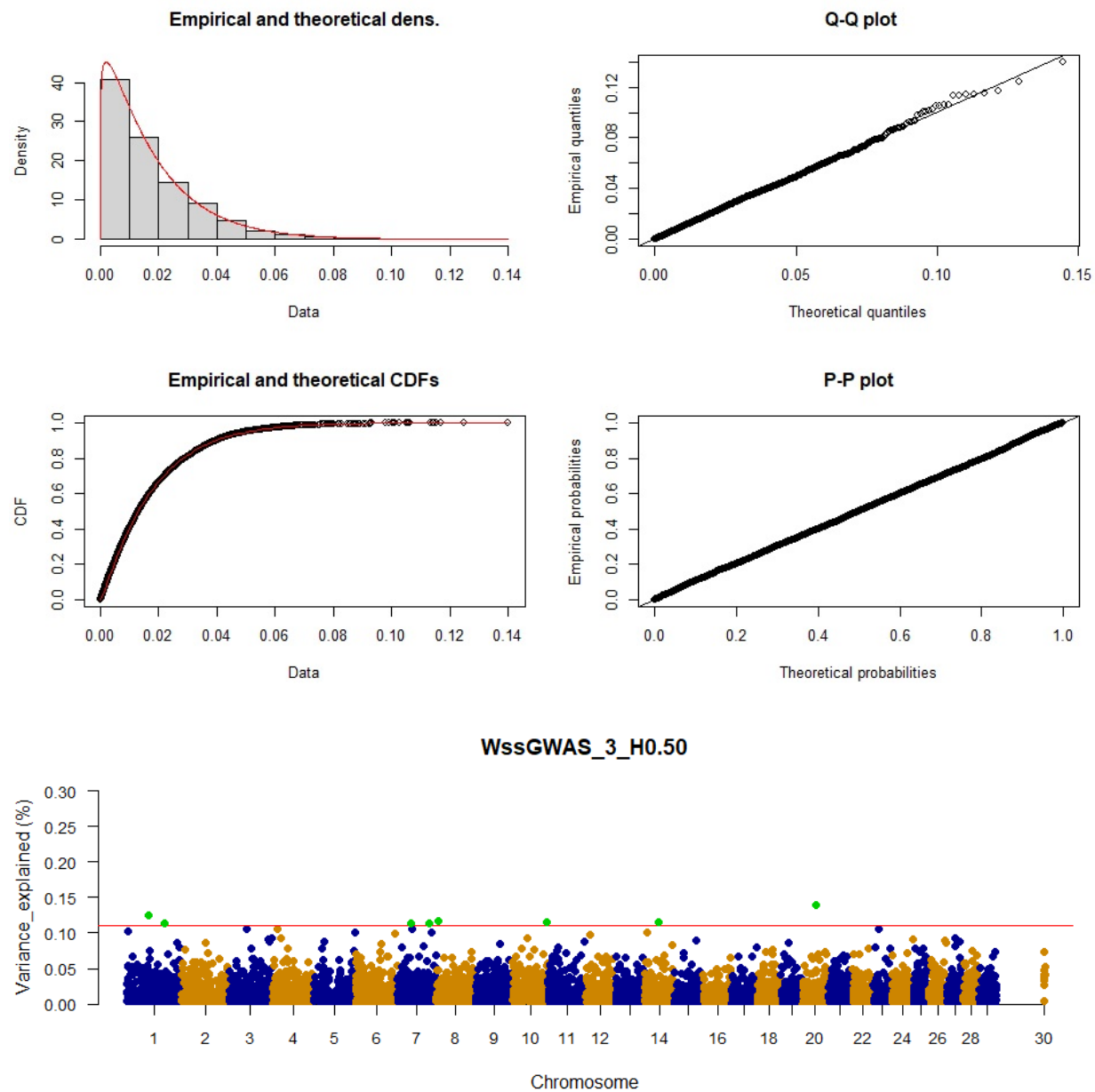
Fitting of the distribution 'beta' by matching moments

Parameters :

estimate

shape1 1.119046

shape2 61.738552



**Statistics: percentage variance explained by haplotypes from blocks with LD_0.80
WssGWAS iteration 1 (ssGWAS)**

summary statistics

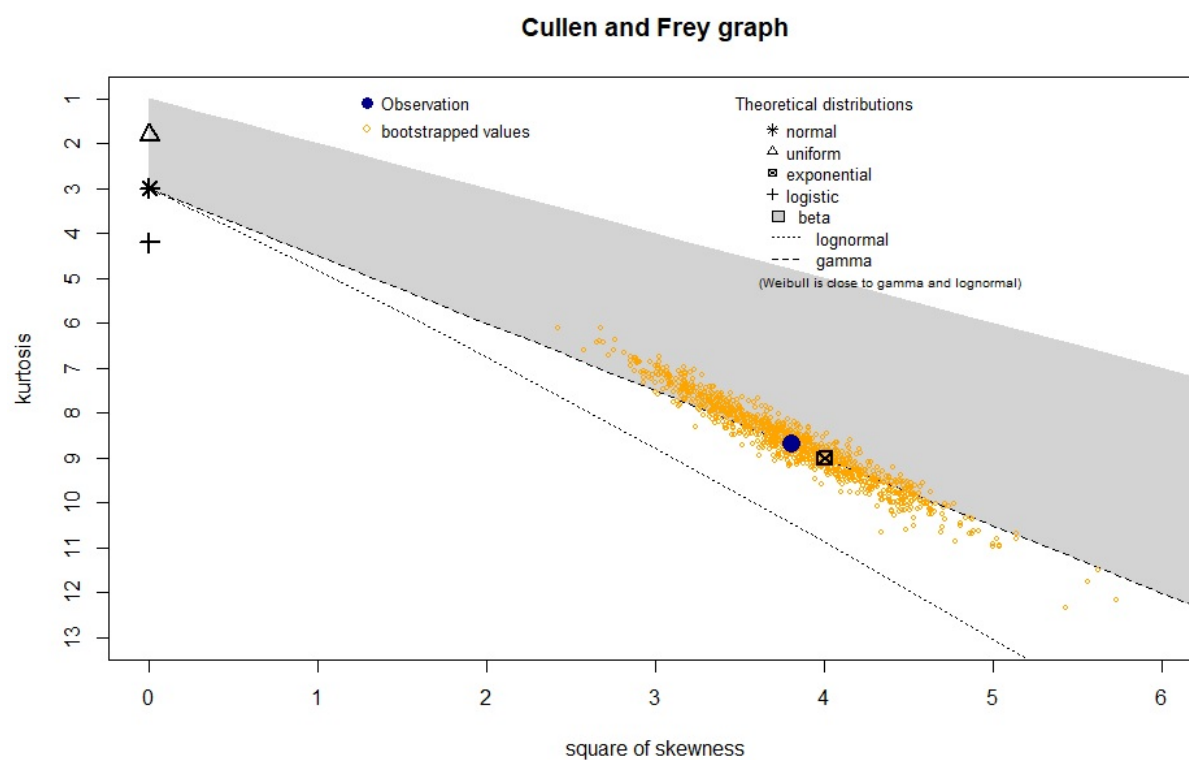
min: 0 max: 0.27178

median: 0.02626

mean: 0.03675104

estimated sd: 0.0349454

estimated skewness: 1.951988



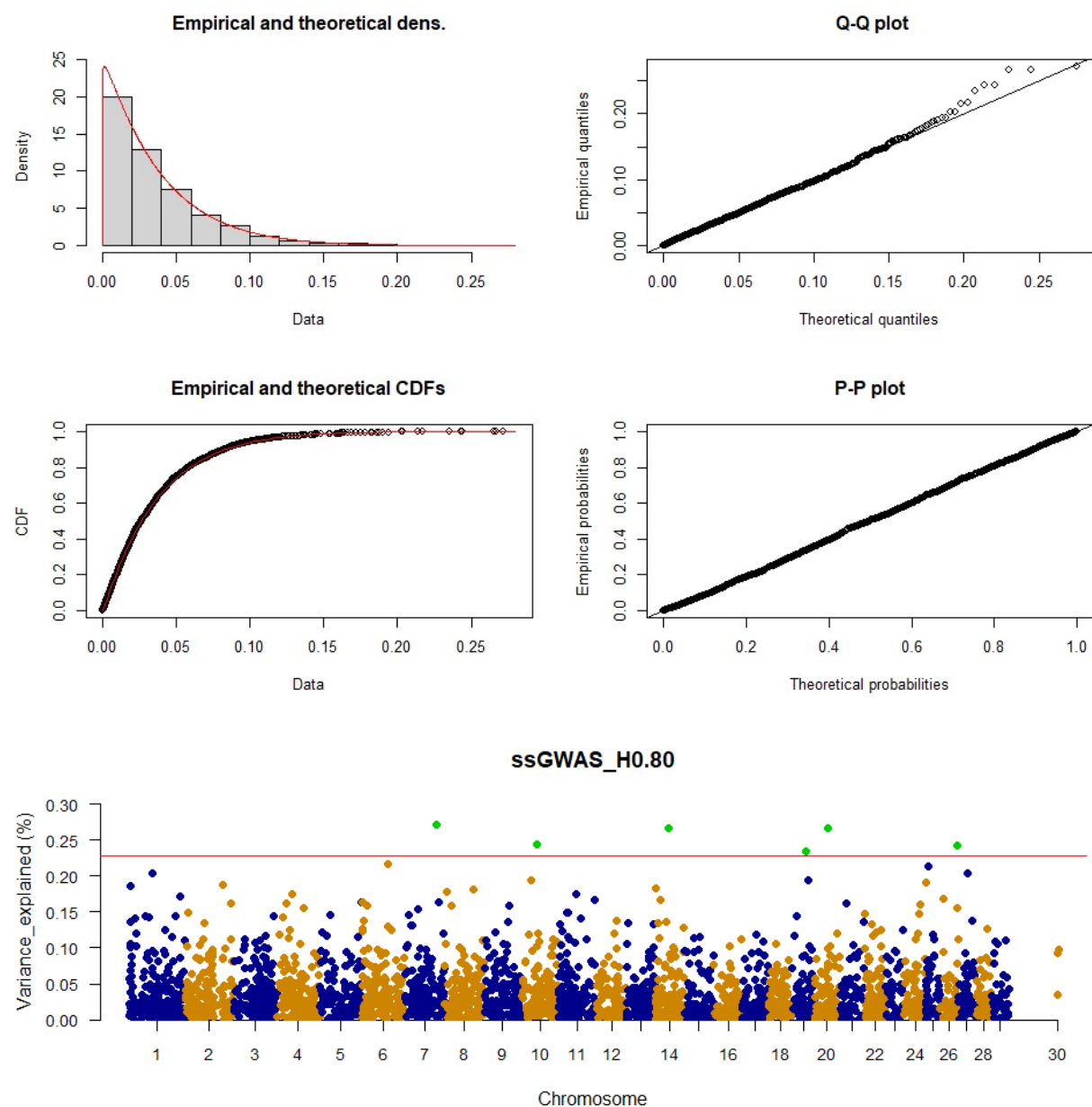
Fitting of the distribution 'beta' by matching moments

Parameters :

estimate

shape1 1.029004

shape2 26.970321



**Statistics: percentage variance explained by haplotypes from blocks with LD_0.80
WssGWAS iteration 2 (WssGWAS)**

summary statistics

min: 0 max: 0.21691

median: 0.02794

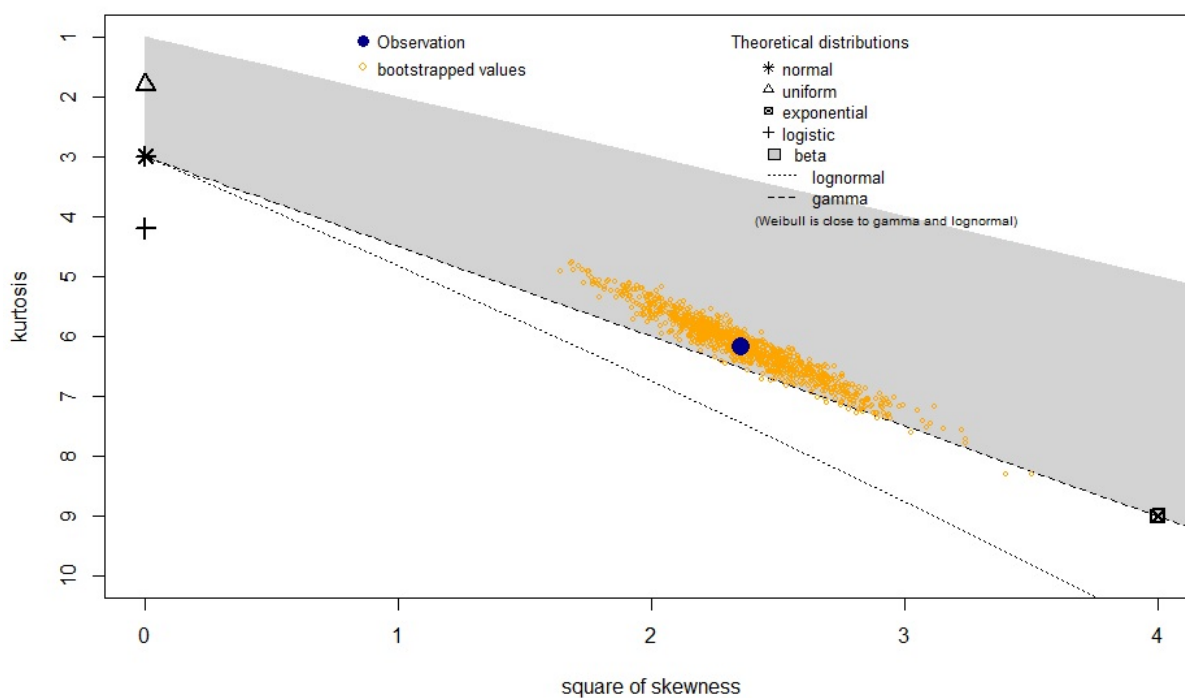
mean: 0.03675115

estimated sd: 0.03164835

estimated skewness: 1.533357

estimated kurtosis: 6.171605

Cullen and Frey graph



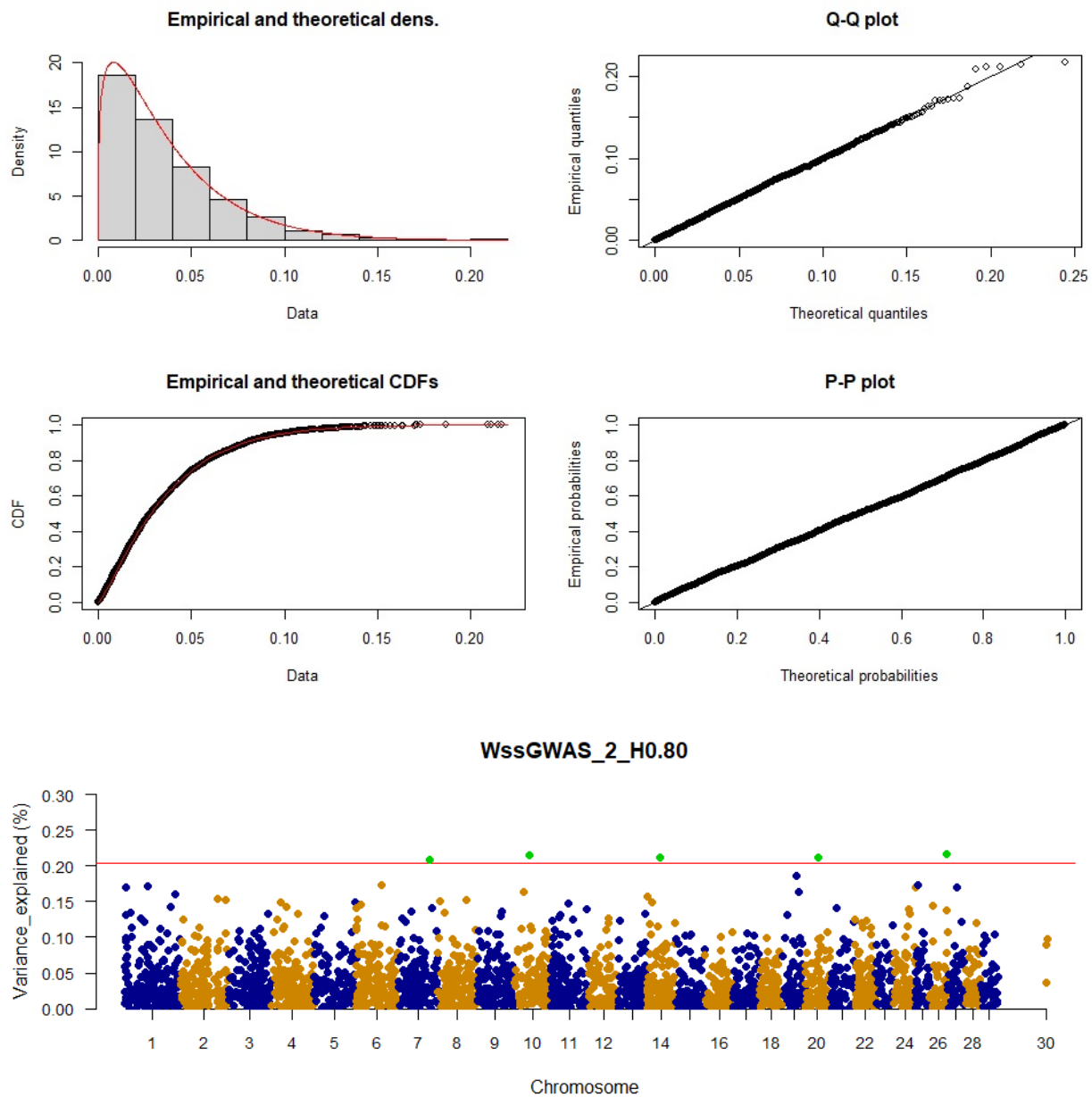
Fitting of the distribution 'beta' by matching moments

Parameters :

estimate

shape1 1.262633

shape2 33.093668



**Statistics: percentage variance explained by haplotypes from blocks with LD_0.80
WssGWAS iteration 3 (WssGWAS)**

summary statistics

min: 0 max: 0.22334

median: 0.02774

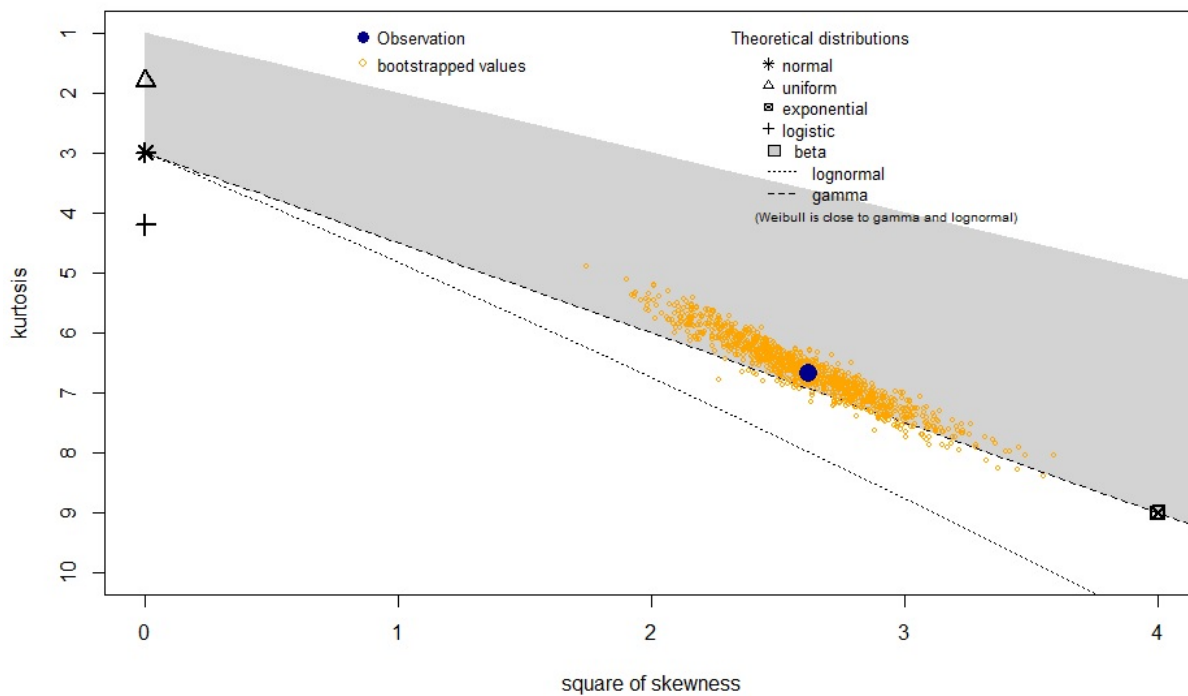
mean: 0.03675105

estimated sd: 0.03212226

estimated skewness: 1.619313

estimated kurtosis: 6.679214

Cullen and Frey graph



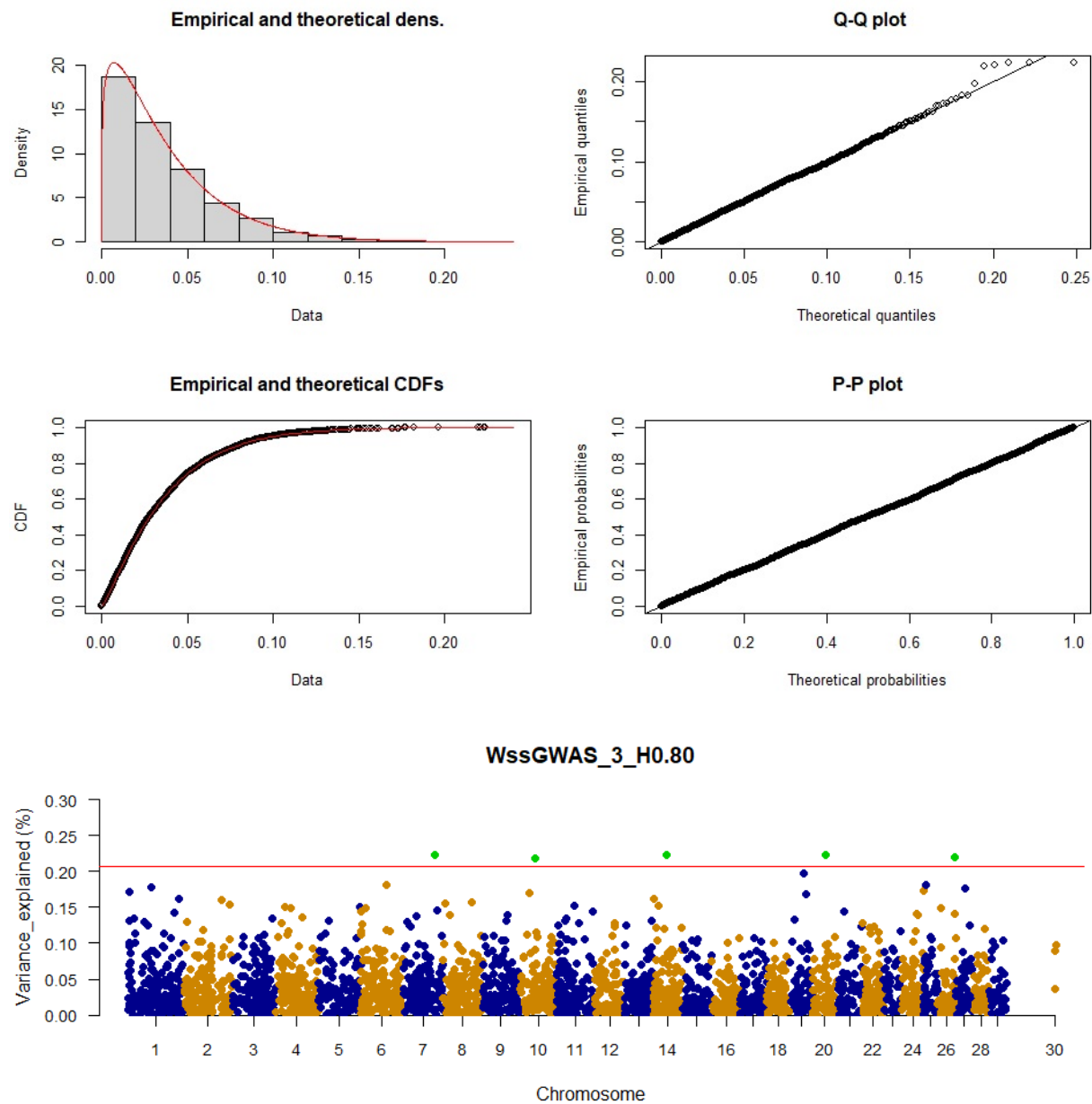
Fitting of the distribution 'beta' by matching moments

Parameters :

estimate

shape1 1.224569

shape2 32.096091



Statistics: percentage variance explained by haplotypes and non-clustered SNPs from blocks with LD_0.15
WssGWAS iteration 1 (ssGWAS)

summary statistics

min: 0 max: 0.08996

median: 0.00102

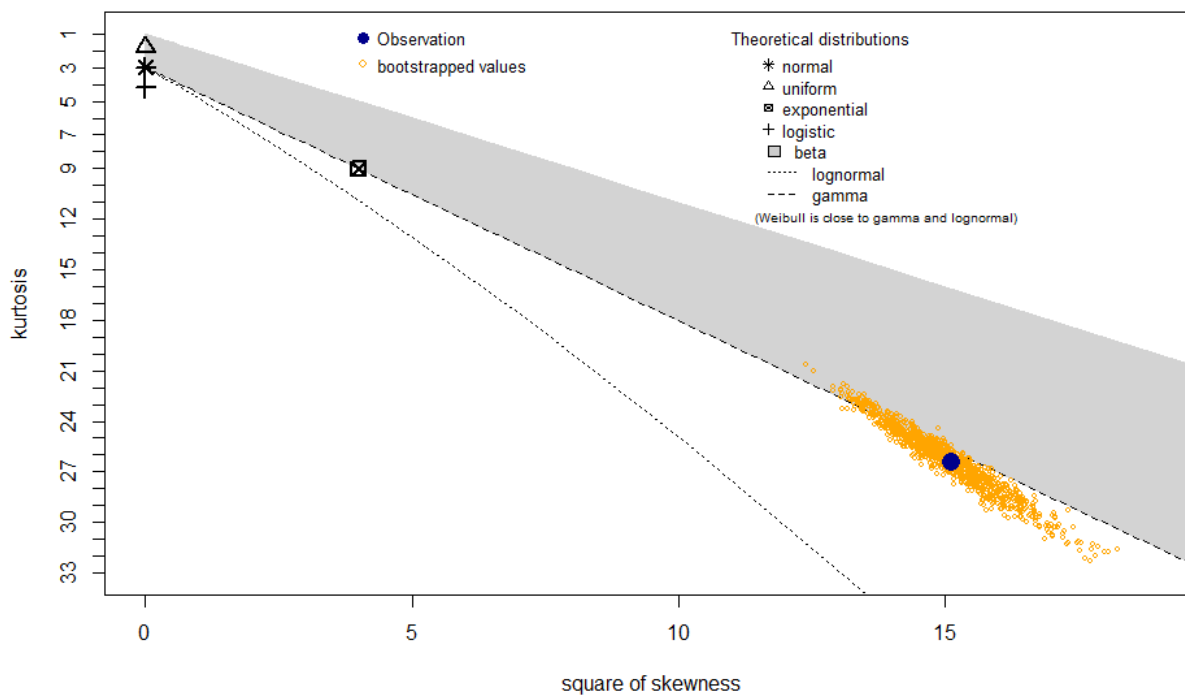
mean: 0.003277807

estimated sd: 0.005750574

estimated skewness: 3.888373

estimated kurtosis: 26.44834

Cullen and Frey graph



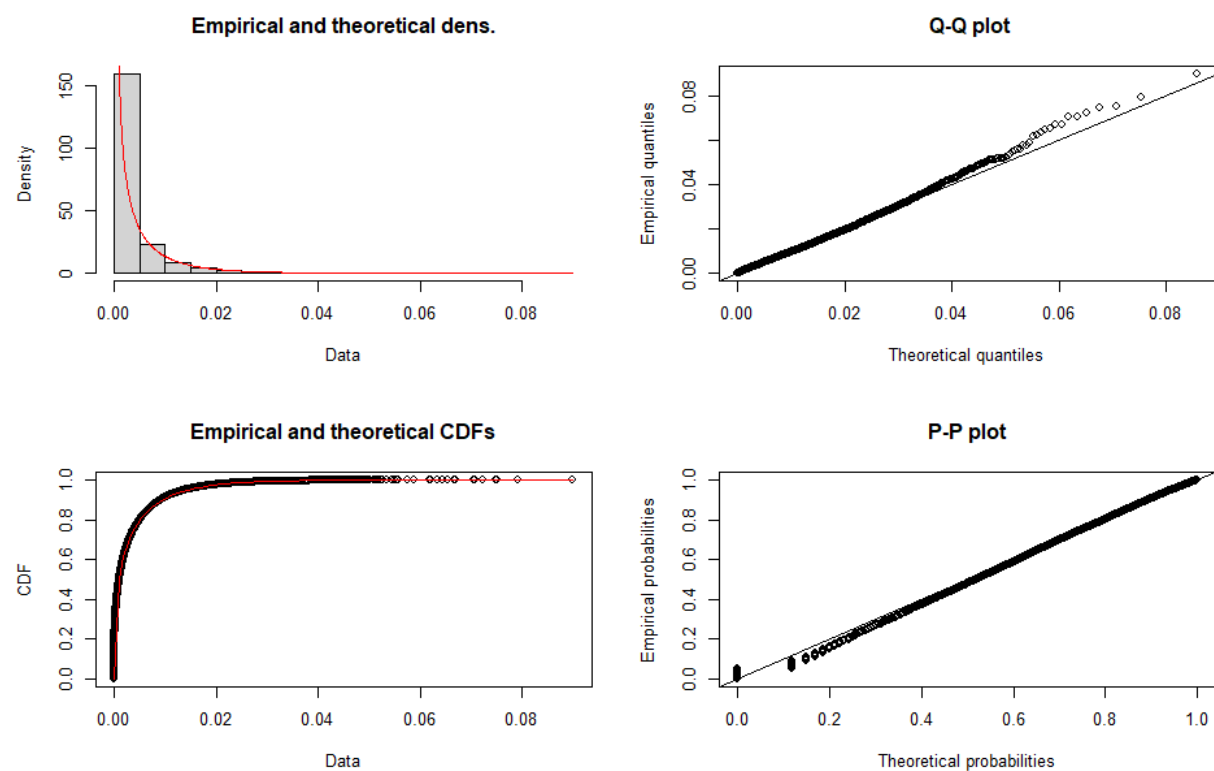
Fitting of the distribution ' gamma ' by matching moments

Parameters :

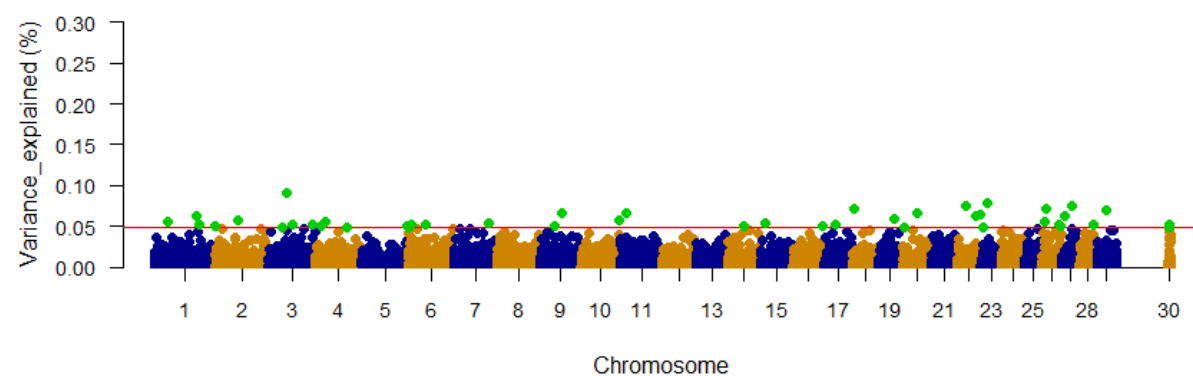
estimate

shape 0.3249067

rate 99.1231862



ssGWAS_NCSNP_H0.15



Statistics: percentage variance explained by haplotypes and non-clustered SNPs from blocks with LD_0.15

WssGWAS iteration 2 (WssGWAS)

summary statistics

min: 0 max: 0.07945

median: 0.00105

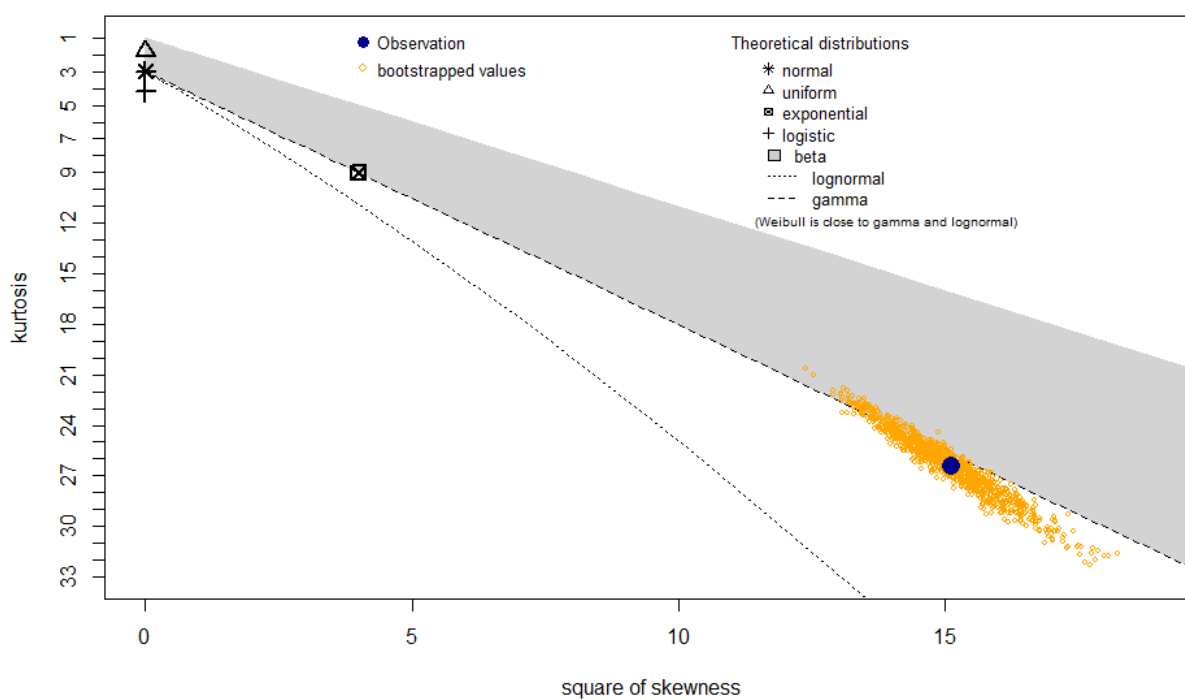
mean: 0.003277817

estimated sd: 0.00553031

estimated skewness: 3.507454

estimated kurtosis: 21.40061

Cullen and Frey graph



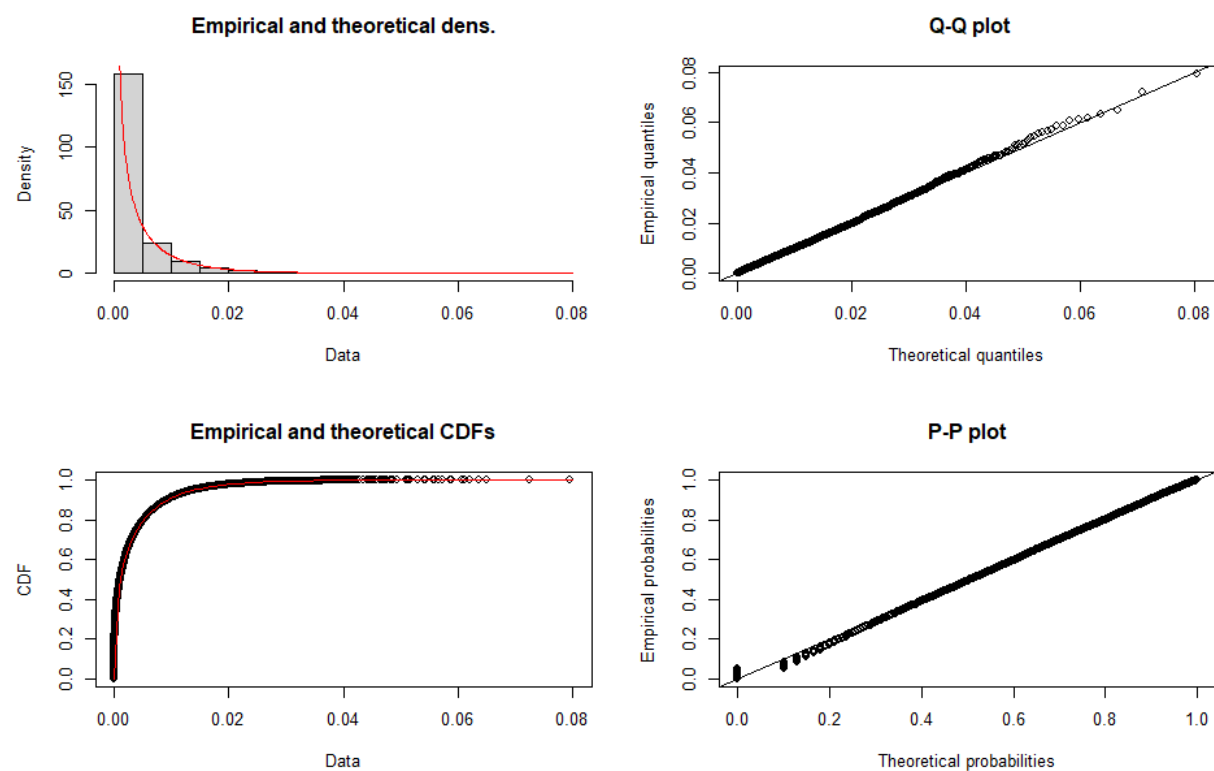
Fitting of the distribution ' gamma ' by matching moments

Parameters :

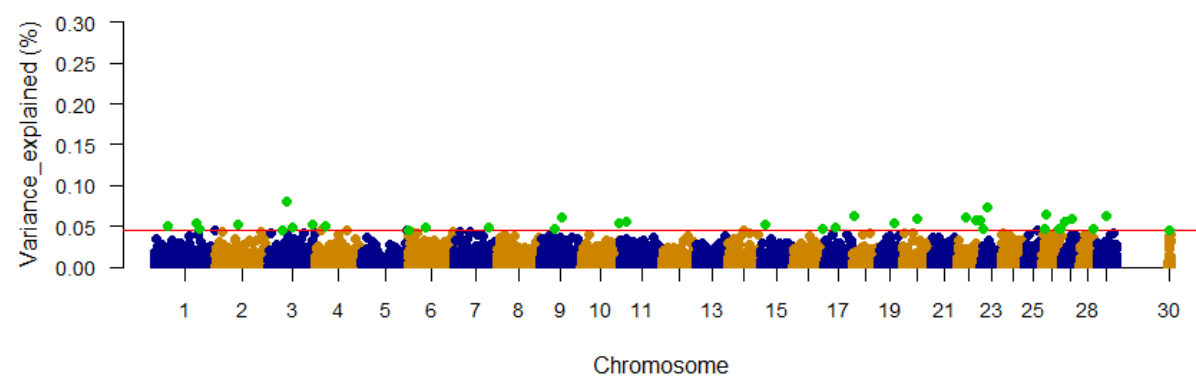
estimate

shape 0.3513052

rate 107.176587



WssGWAS_2_NCSNP_H0.15



Statistics: percentage variance explained by haplotypes and non-clustered SNPs from blocks with LD_0.15

WssGWAS iteration 3 (WssGWAS)

summary statistics

min: 0 max: 0.07761

median: 0.00106

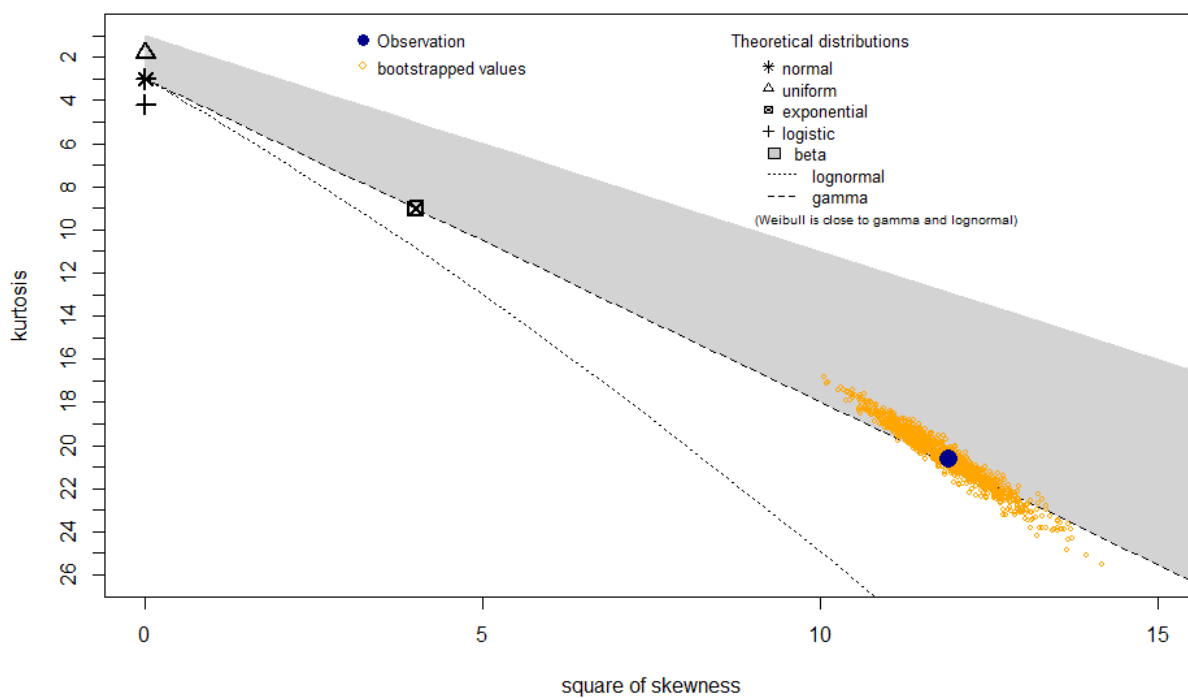
mean: 0.003277773

estimated sd: 0.005503608

estimated skewness: 3.448596

estimated kurtosis: 20.62088

Cullen and Frey graph



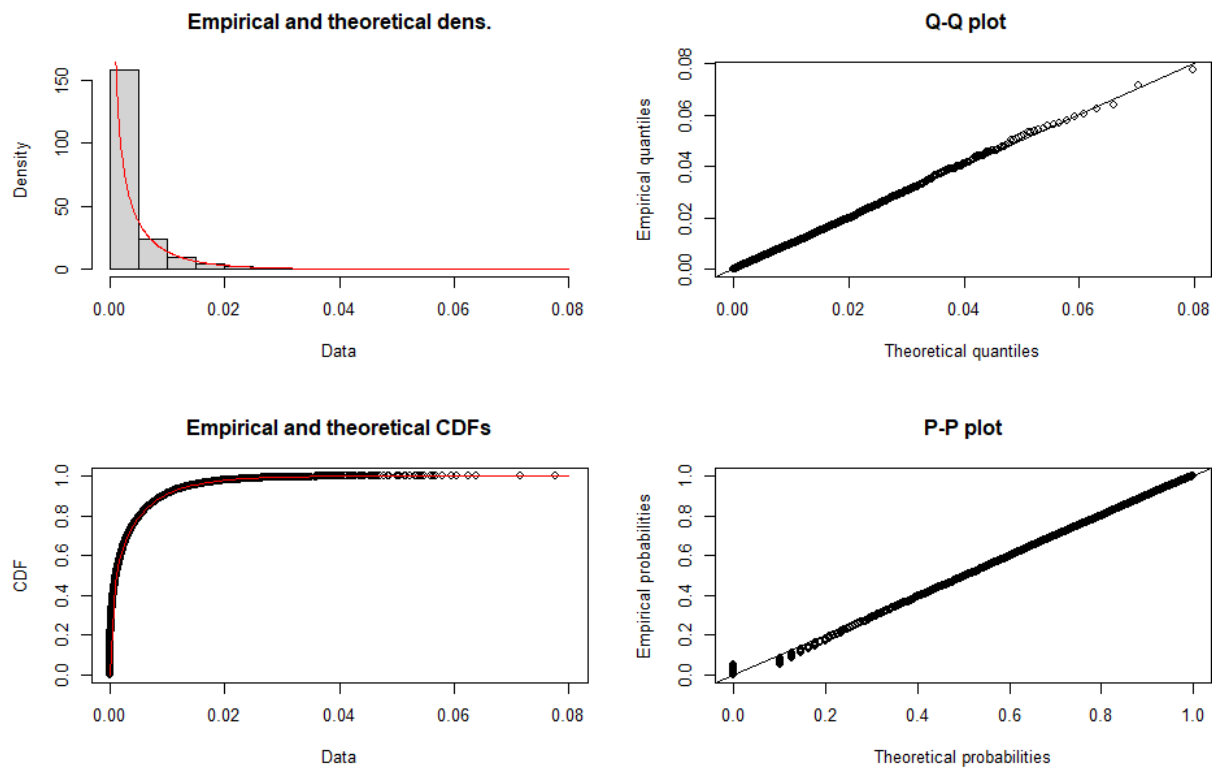
Fitting of the distribution ' gamma ' by matching moments

Parameters :

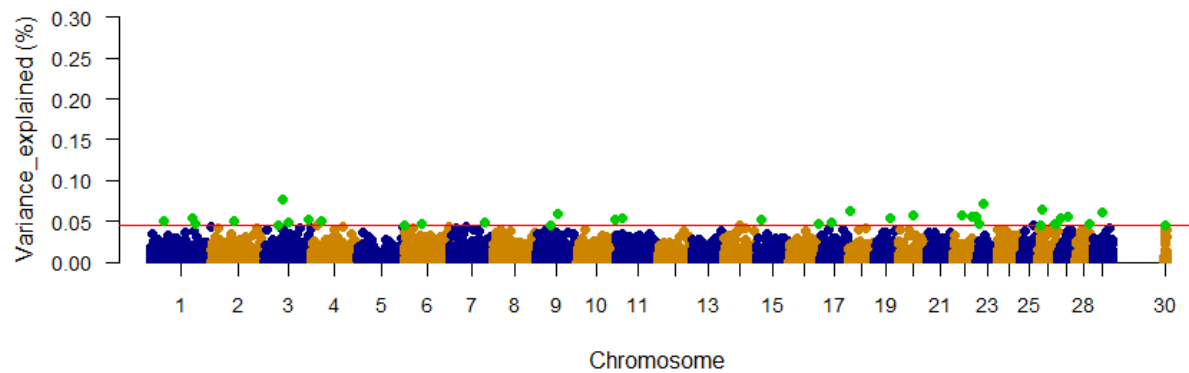
estimate

shape 0.3547129

rate 108.2176497



WssGWAS_3_NCSNP_H0.15



Statistics: percentage variance explained by haplotypes and non-clustered SNPs from blocks with LD_0.50
WssGWAS iteration 1 (ssGWAS)

summary statistics

min: 0 max: 0.09132

median: 8e-04

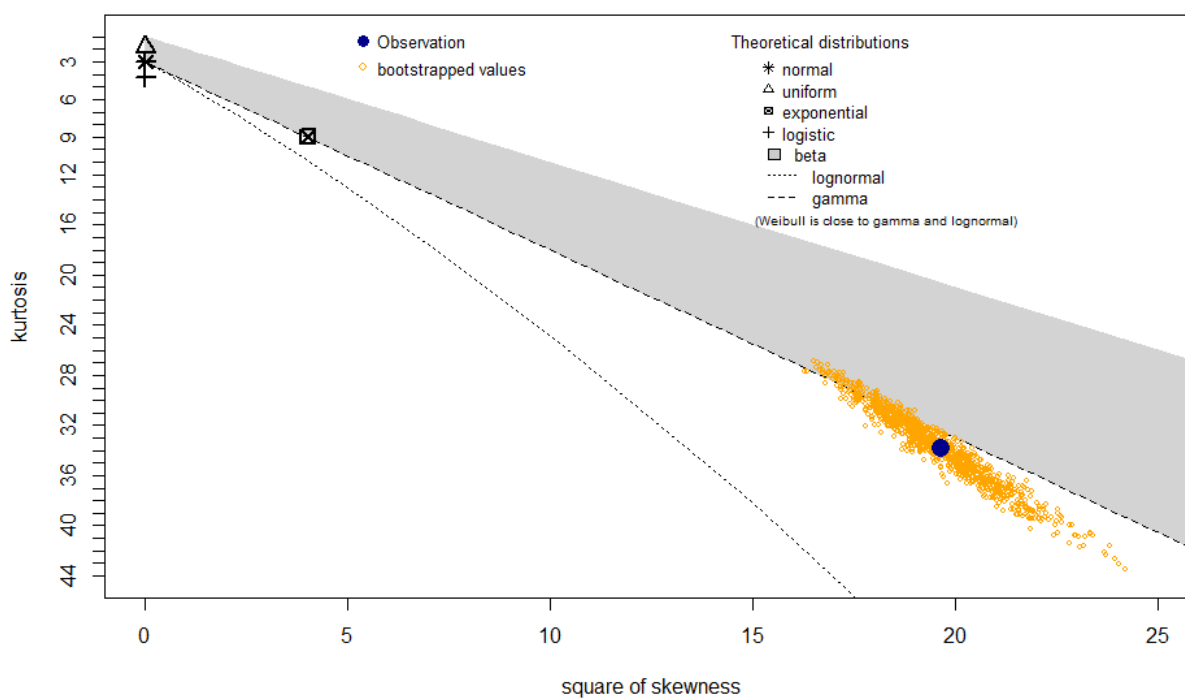
mean: 0.002766918

estimated sd: 0.0051877

estimated skewness: 4.430503

estimated kurtosis: 33.8731

Cullen and Frey graph



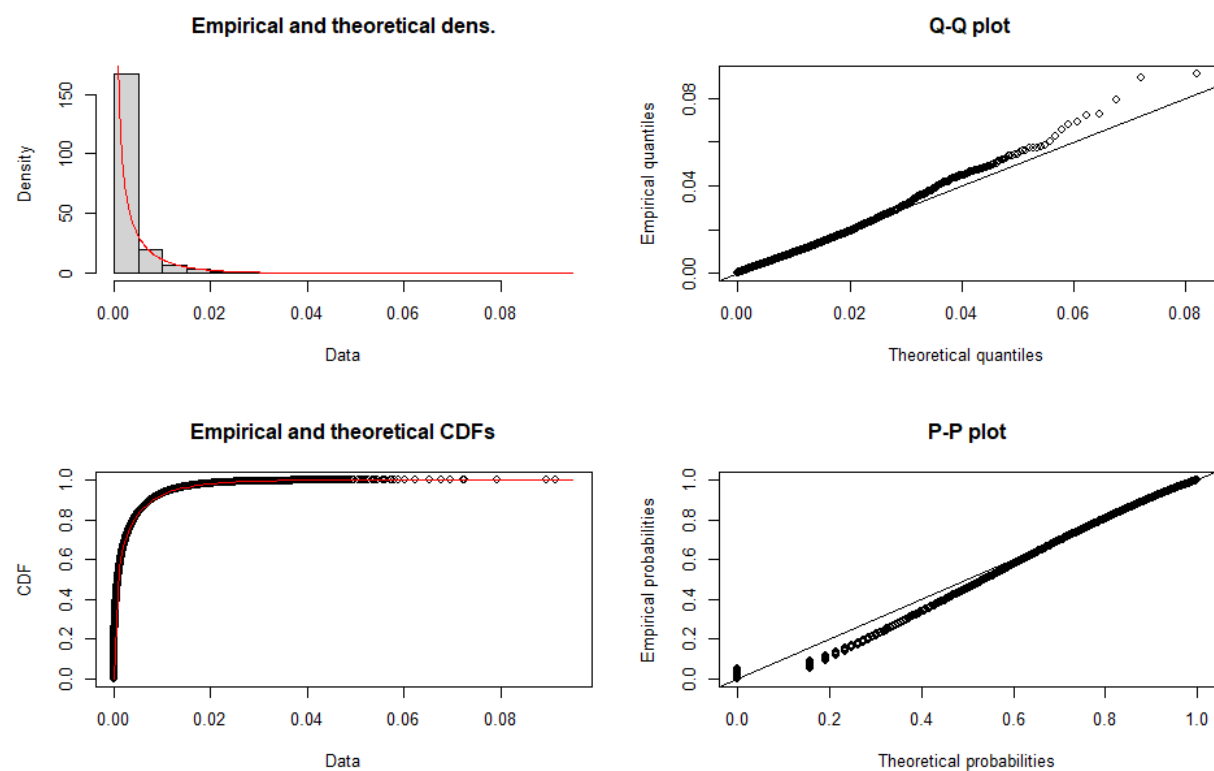
Fitting of the distribution ' gamma ' by matching moments

Parameters :

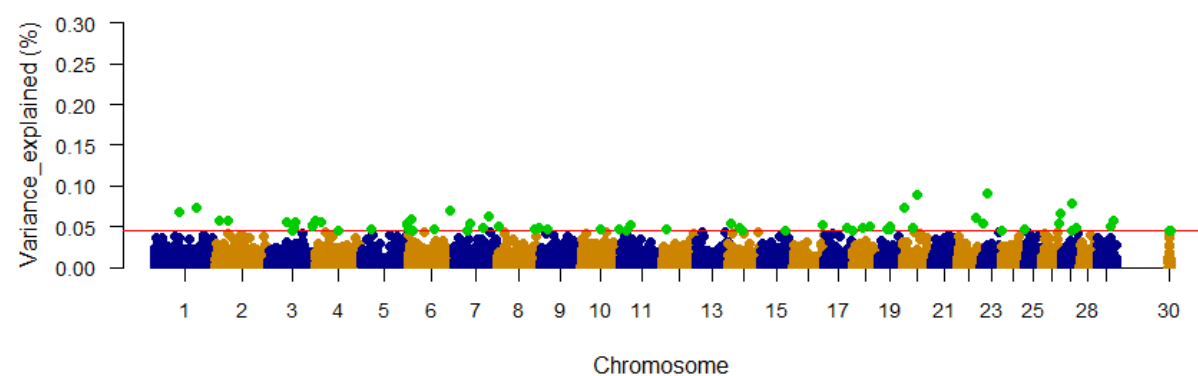
estimate

shape 0.284482

rate 102.815498



ssGWAS_NCSNP_H0.50



Statistics: percentage variance explained by haplotypes and non-clustered SNPs from blocks with LD_0.50

WssGWAS iteration 2 (WssGWAS)

summary statistics

min: 0 max: 0.0786

median: 0.00084

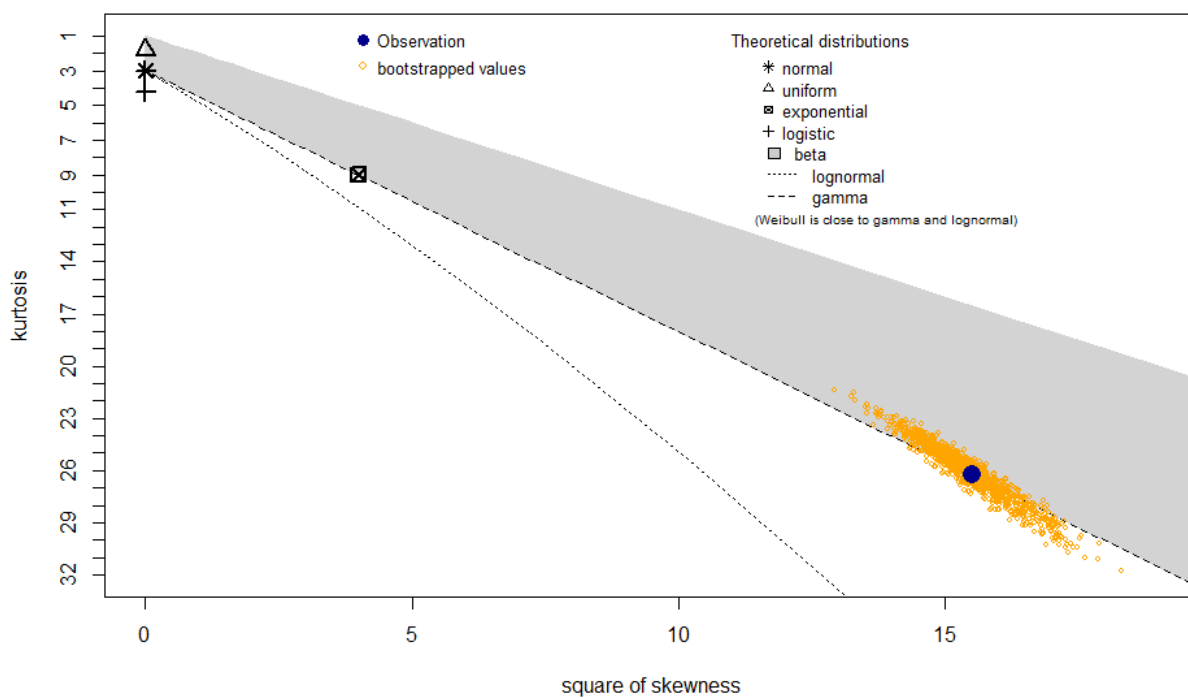
mean: 0.002766926

estimated sd: 0.004962761

estimated skewness: 3.939182

estimated kurtosis: 26.22129

Cullen and Frey graph



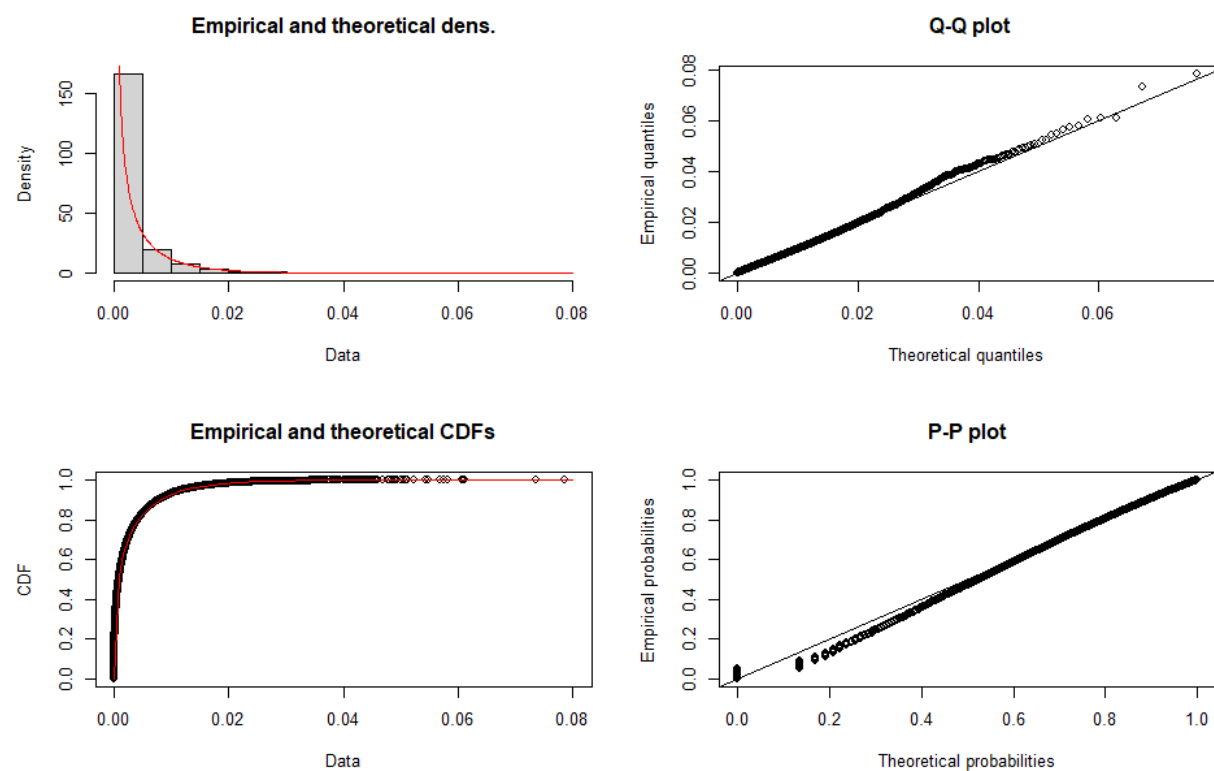
Fitting of the distribution ' gamma ' by matching moments

Parameters :

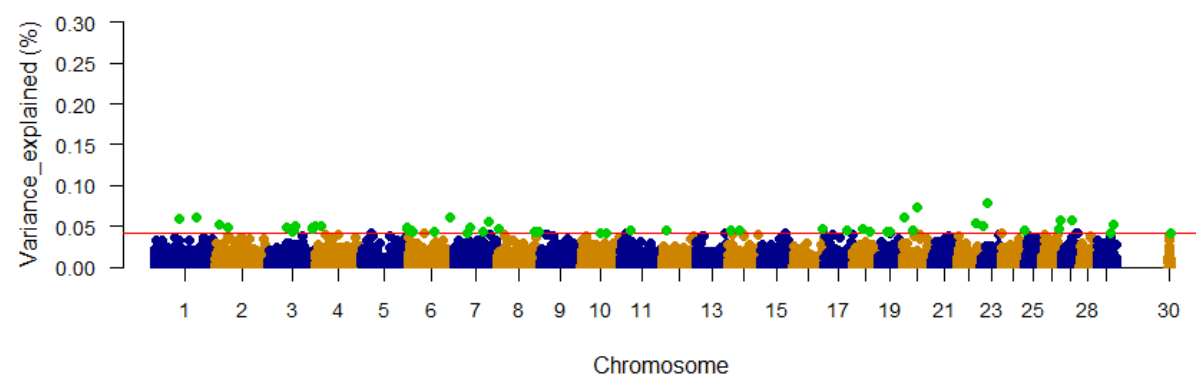
estimate

shape 0.3108569

rate 112.3473688



WssGWAS_2_NCSNP_H0.50



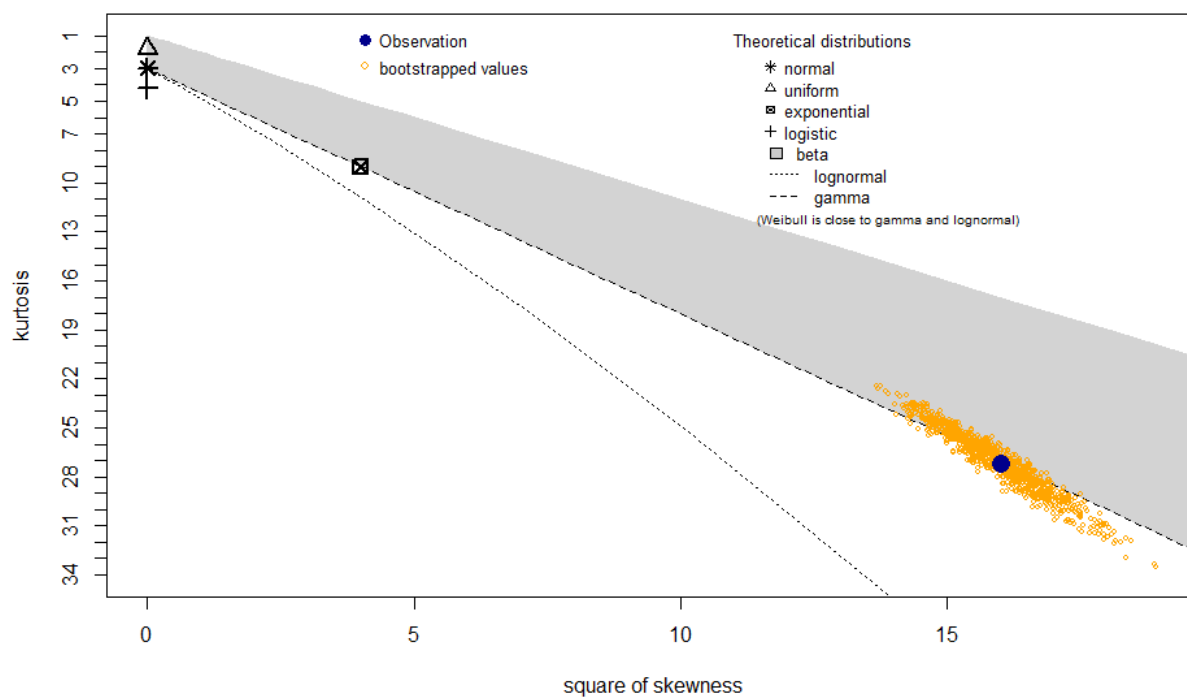
Statistics: percentage variance explained by haplotypes and non-clustered SNPs from blocks with LD_0.50

WssGWAS iteration 3 (WssGWAS)

summary statistics

 min: 0 max: 0.08061
 median: 0.00084
 mean: 0.002766898
 estimated sd: 0.004986442
 estimated skewness: 4.002927
 estimated kurtosis: 27.19834

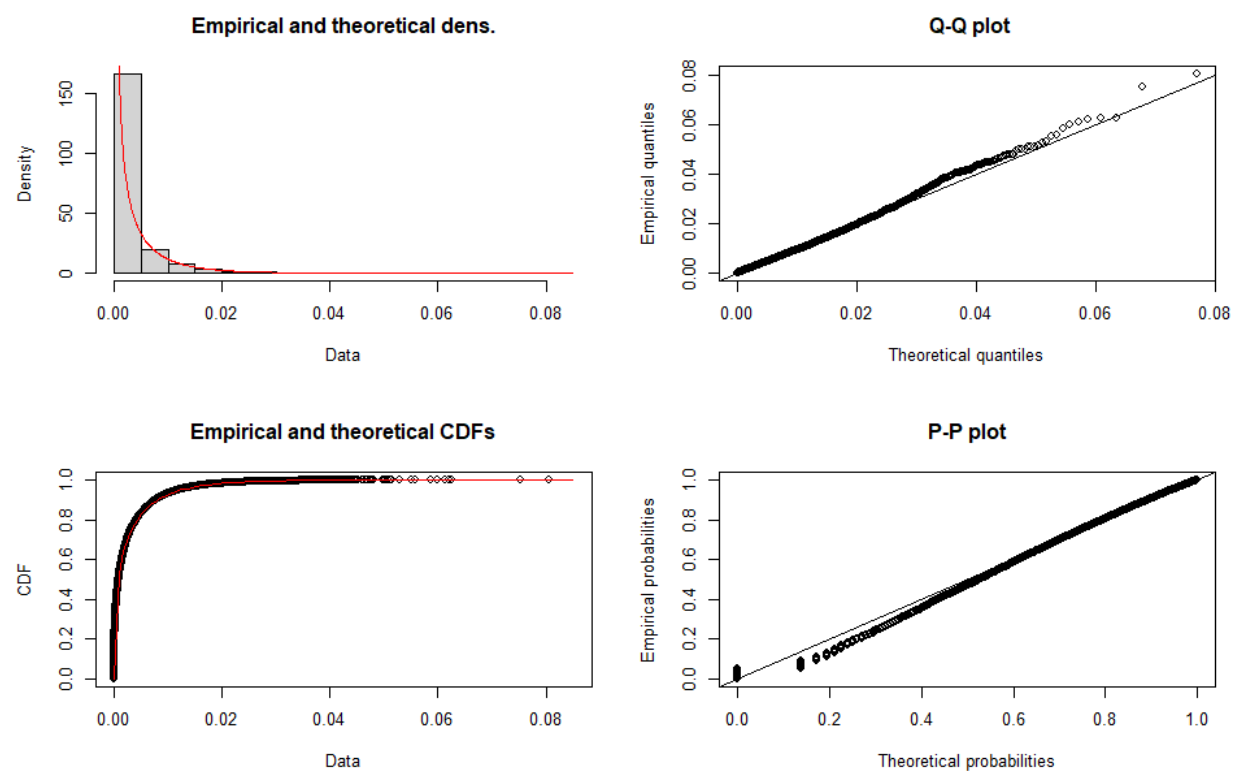
Cullen and Frey graph



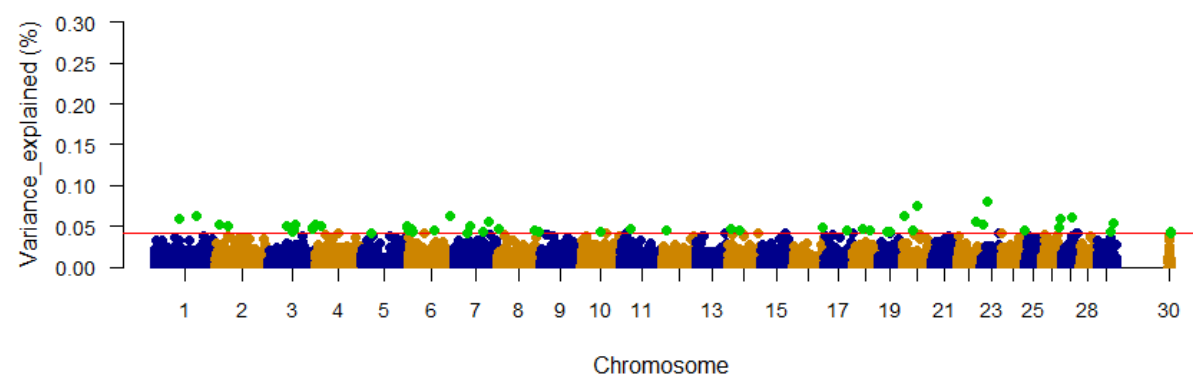
Fitting of the distribution 'gamma' by matching moments

Parameters :

estimate
 shape 0.3079051
 rate 111.2816717



WssGWAS_3_NCSNP_H0.50



Statistics: percentage variance explained by haplotypes and non-clustered SNPs from blocks with LD_0.80
WssGWAS iteration 1 (ssGWAS)

summary statistics

min: 0 max: 0.08546

median: 0.00076

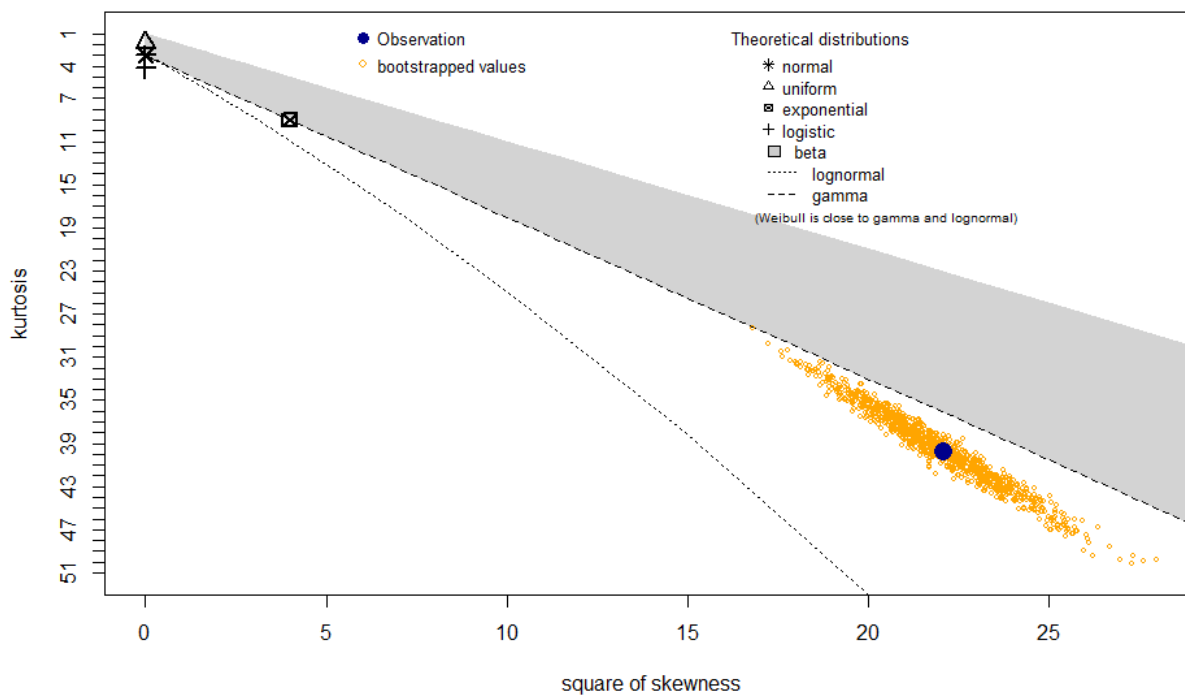
mean: 0.002527993

estimated sd: 0.004725019

estimated skewness: 4.697957

estimated kurtosis: 39.72729

Cullen and Frey graph



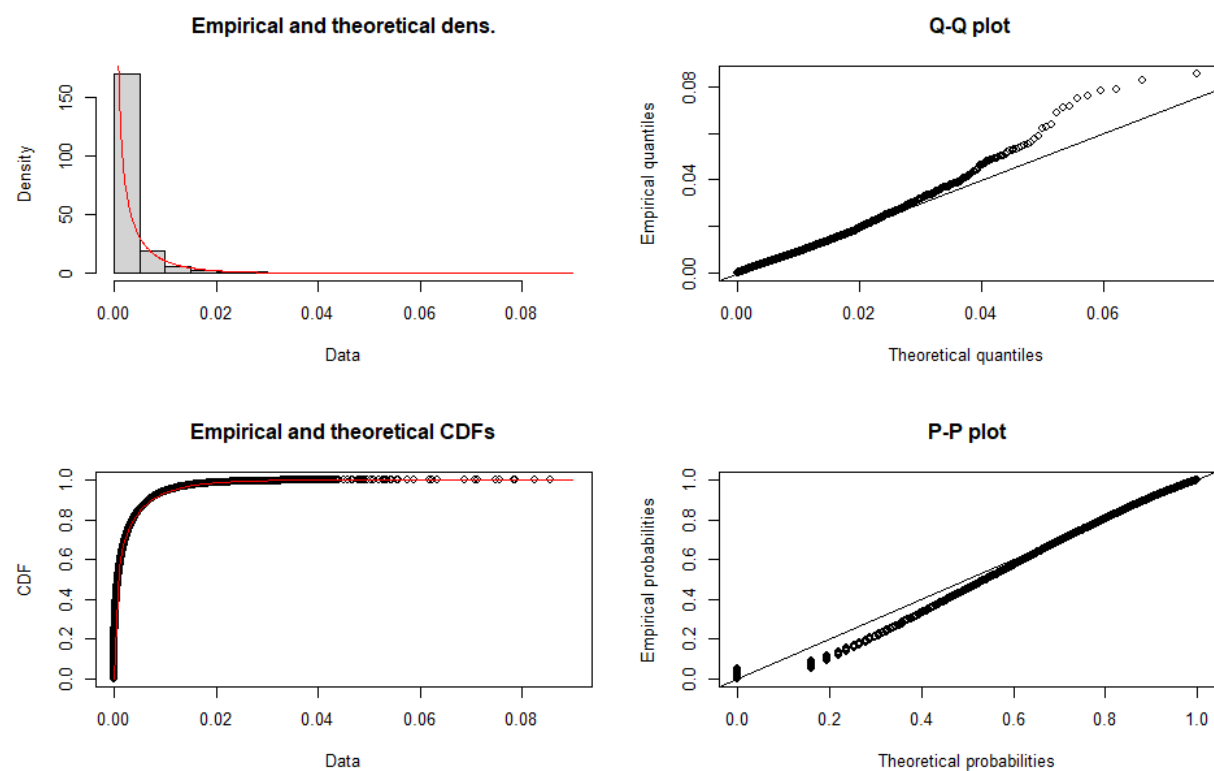
Fitting of the distribution ' gamma ' by matching moments

Parameters :

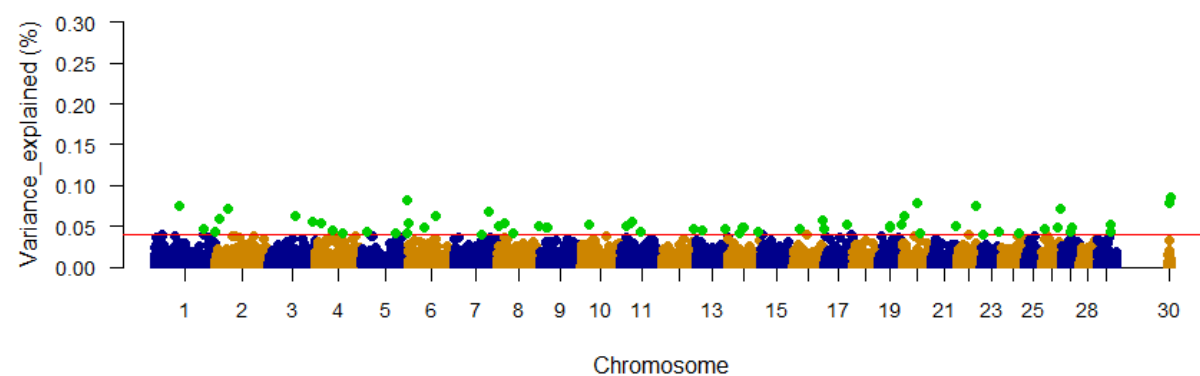
estimate

shape 0.2862567

rate 113.2347650



ssGWAS_NCSNP_H0.80



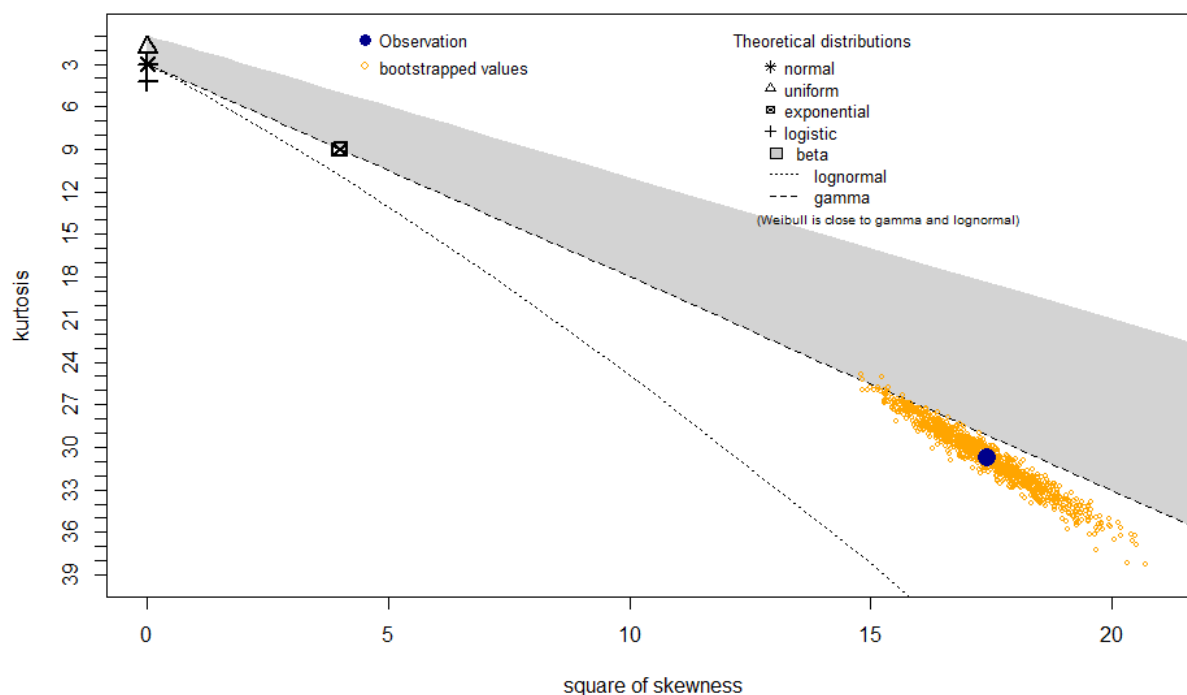
Statistics: percentage variance explained by haplotypes and non-clustered SNPs from blocks with LD_0.80

WssGWAS iteration 2 (WssGWAS)

summary statistics

 min: 0 max: 0.07488
 median: 8e-04
 mean: 0.002527975
 estimated sd: 0.00451904
 estimated skewness: 4.172307
 estimated kurtosis: 30.74078

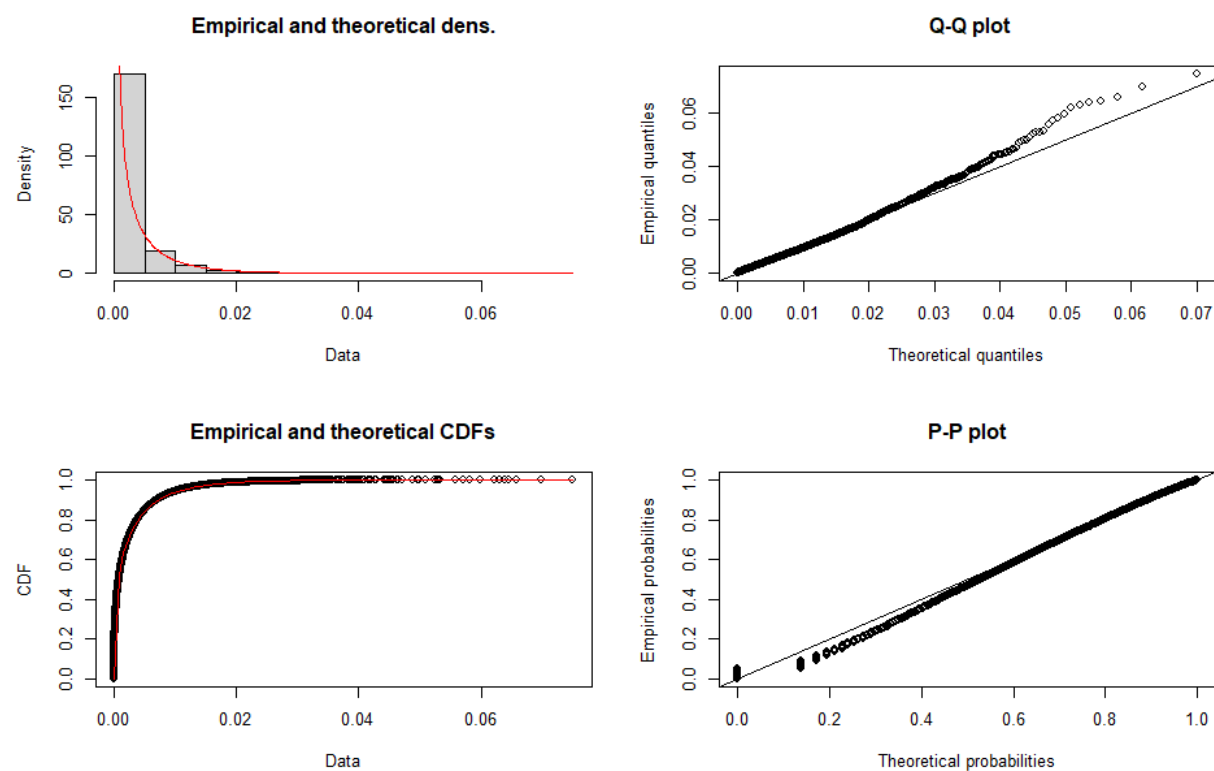
Cullen and Frey graph



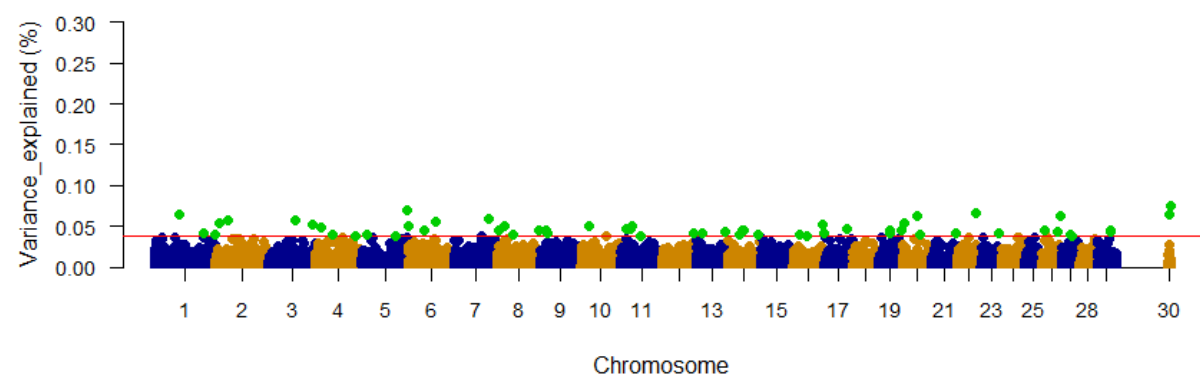
Fitting of the distribution ' gamma ' by matching moments

Parameters :

estimate
 shape 0.3129423
 rate 123.7916759



WssGWAS_2_NCSNP_H0.80



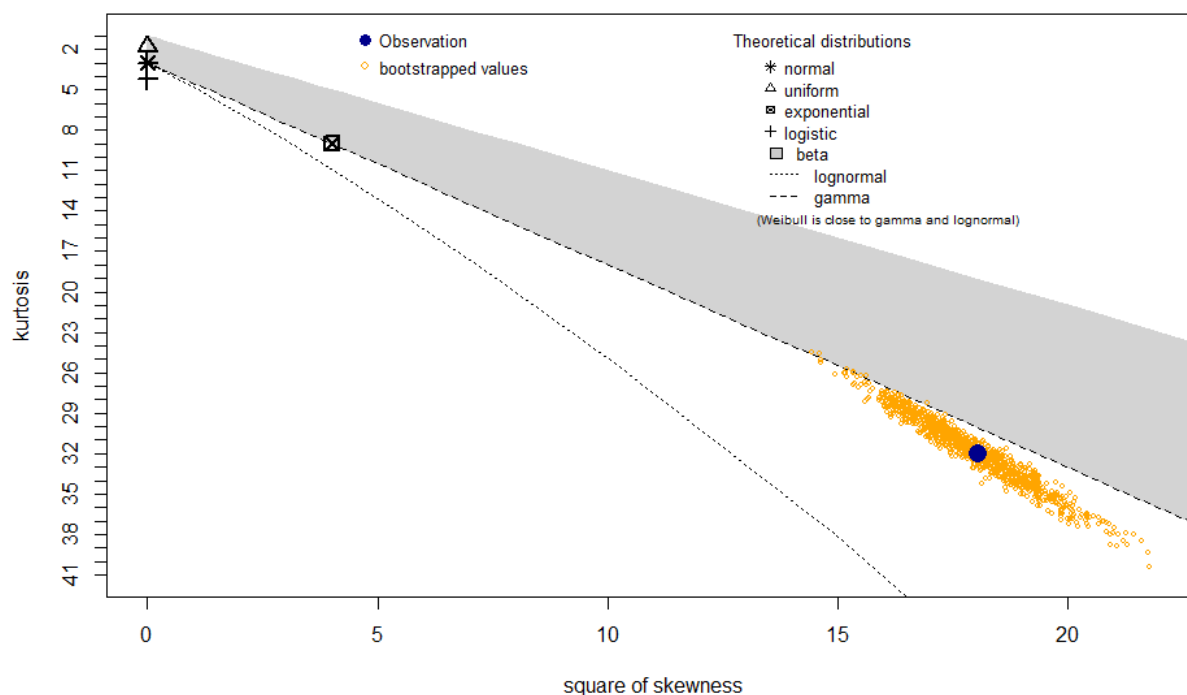
Statistics: percentage variance explained by haplotypes and non-clustered SNPs from blocks with LD_0.80

WssGWAS iteration 3 (WssGWAS)

summary statistics

 min: 0 max: 0.07663
 median: 0.00079
 mean: 0.002527986
 estimated sd: 0.004541451
 estimated skewness: 4.247386
 estimated kurtosis: 32.06017

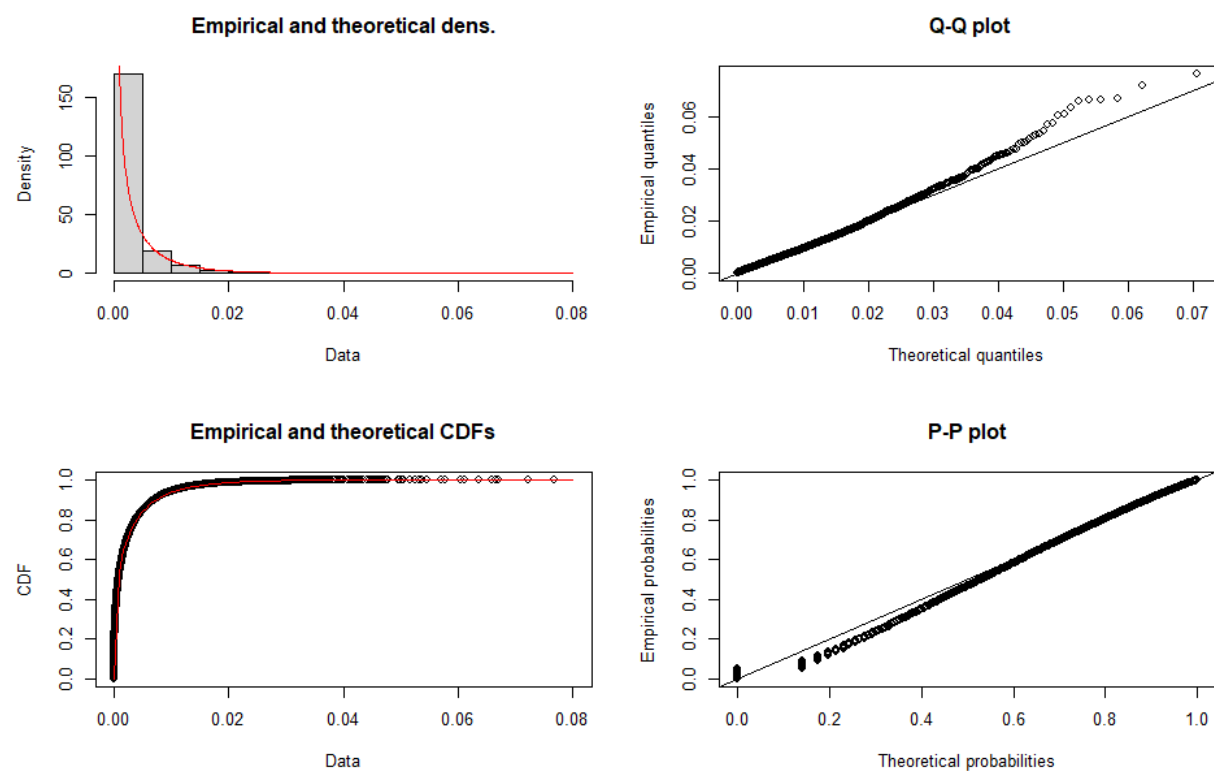
Cullen and Frey graph



Fitting of the distribution ' gamma ' by matching moments

Parameters :

estimate
 shape 0.3098641
 rate 122.5734789



WssGWAS_3_NCSNP_H0.80

