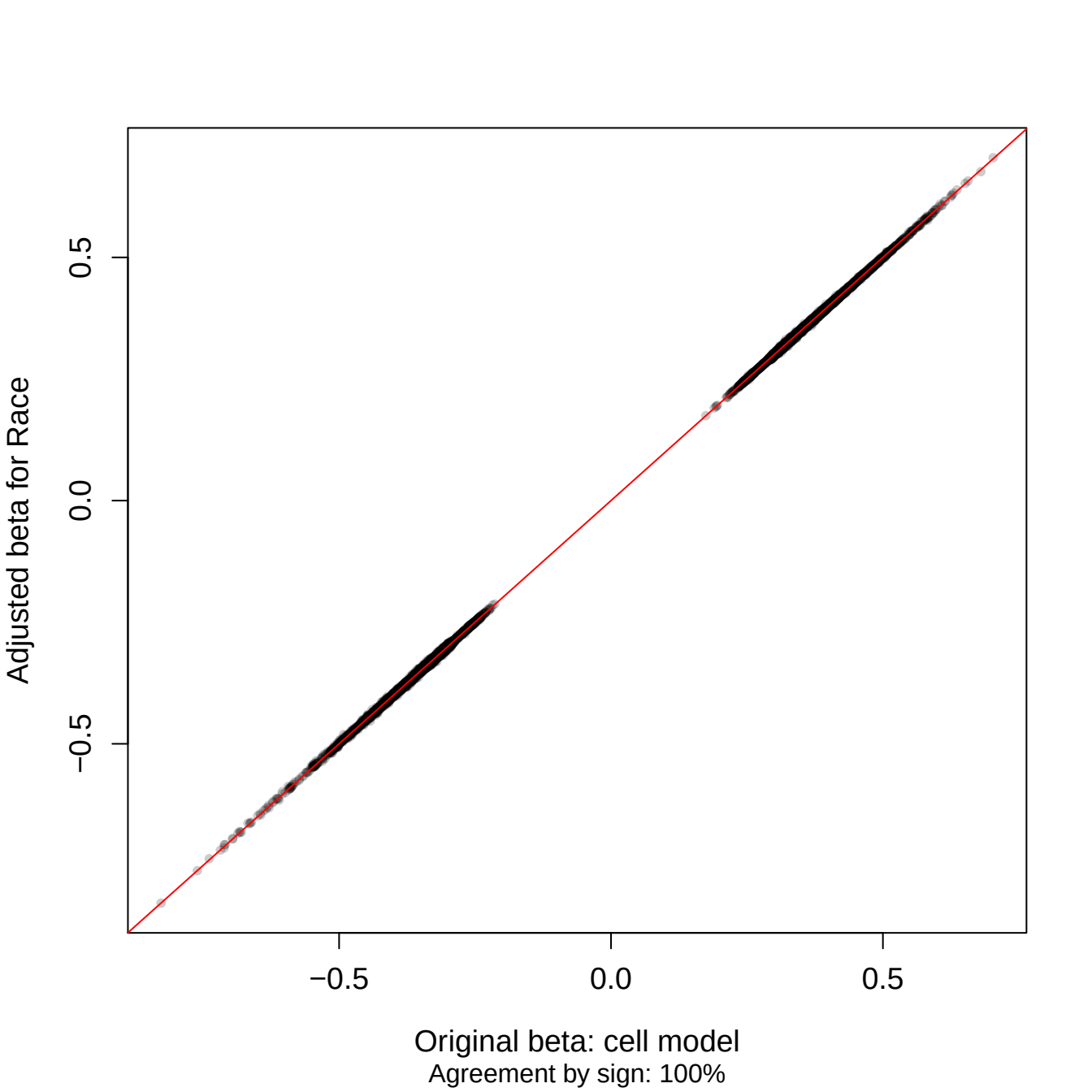
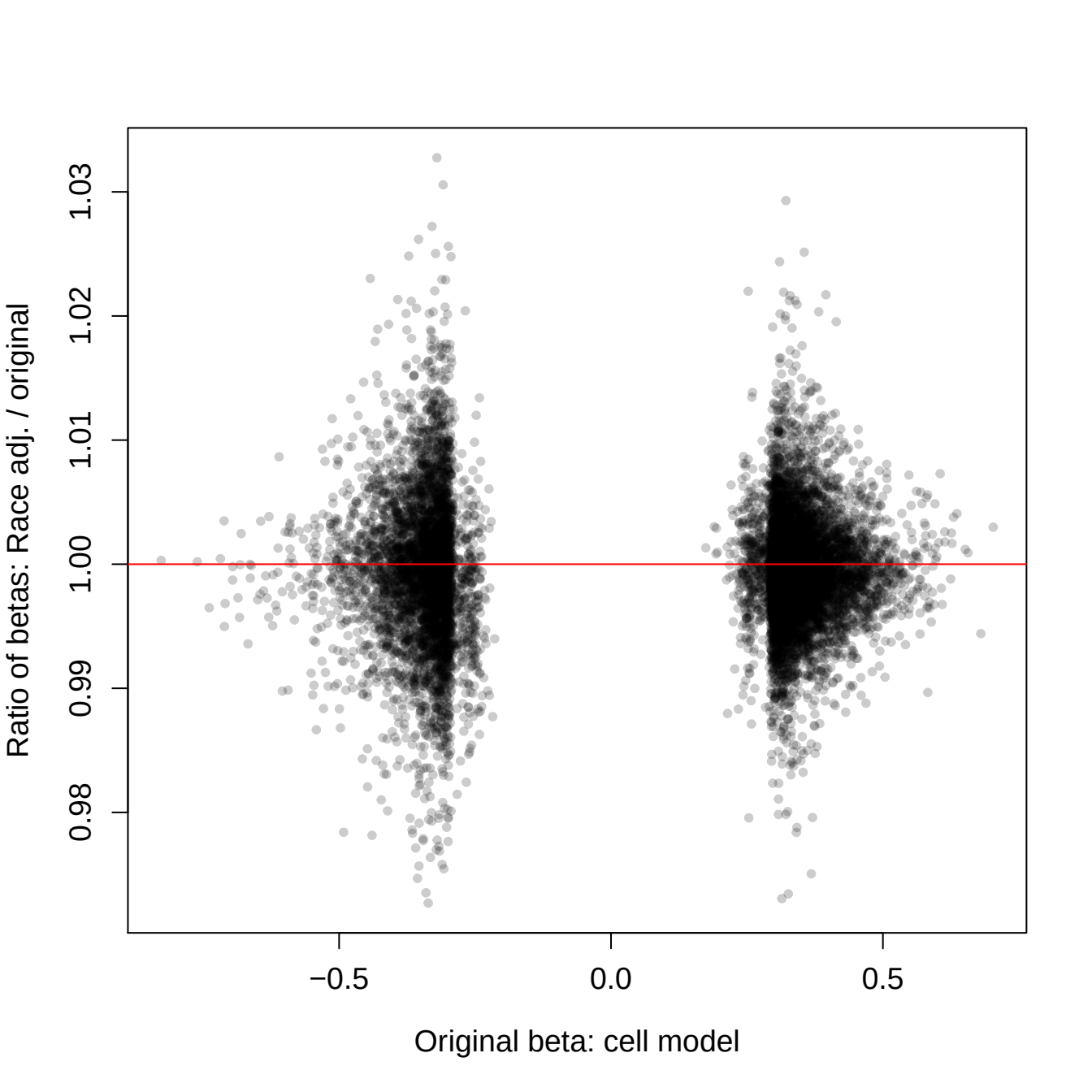
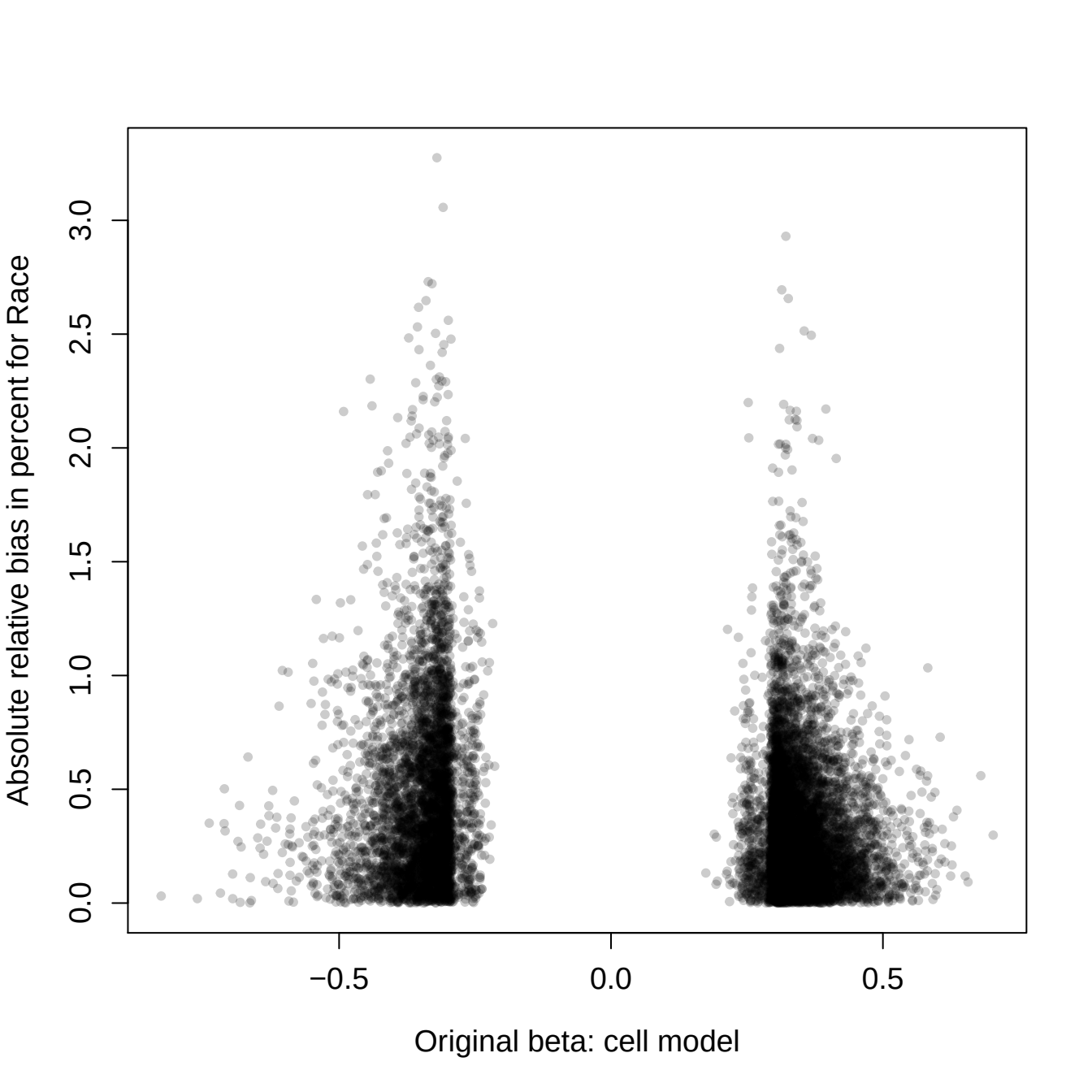
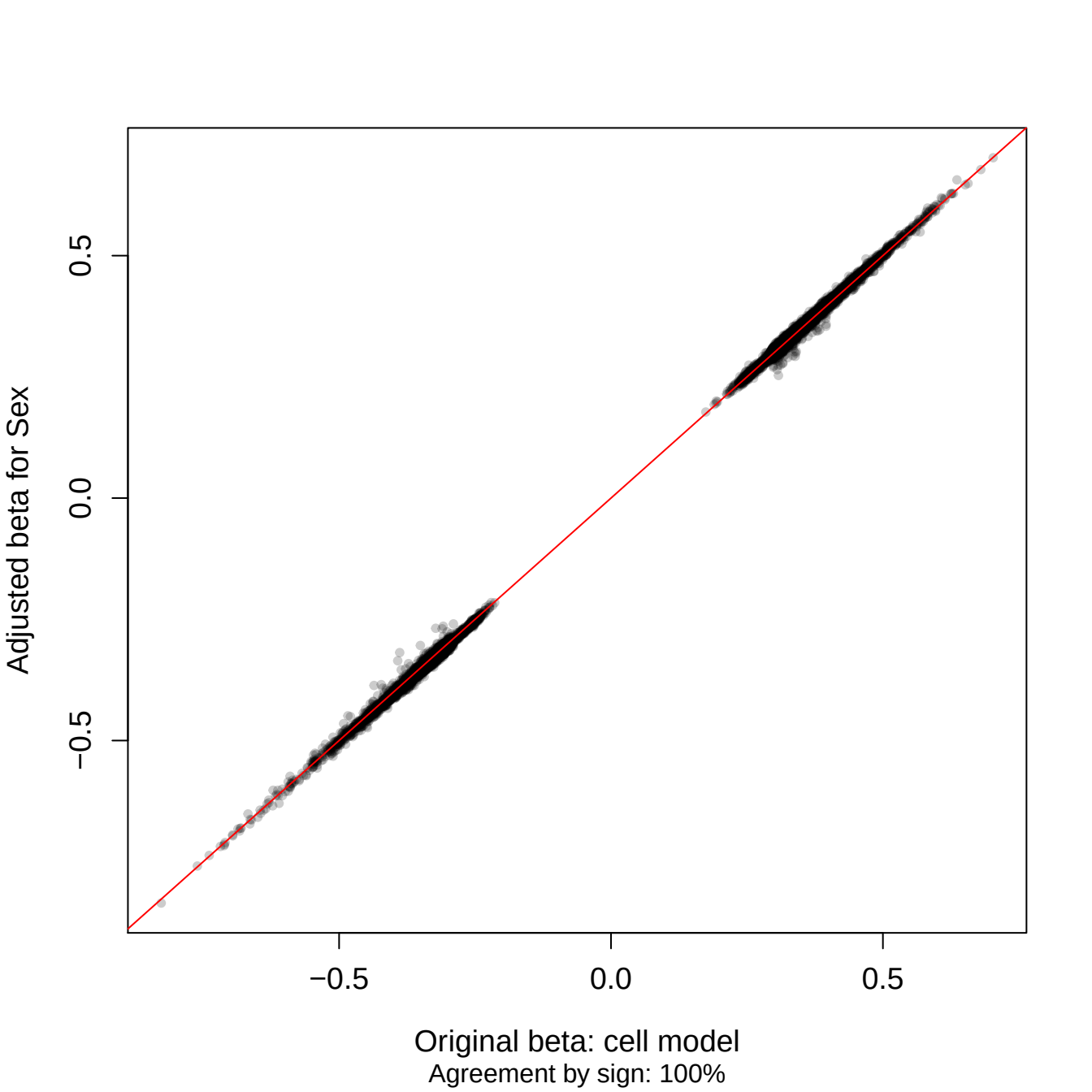
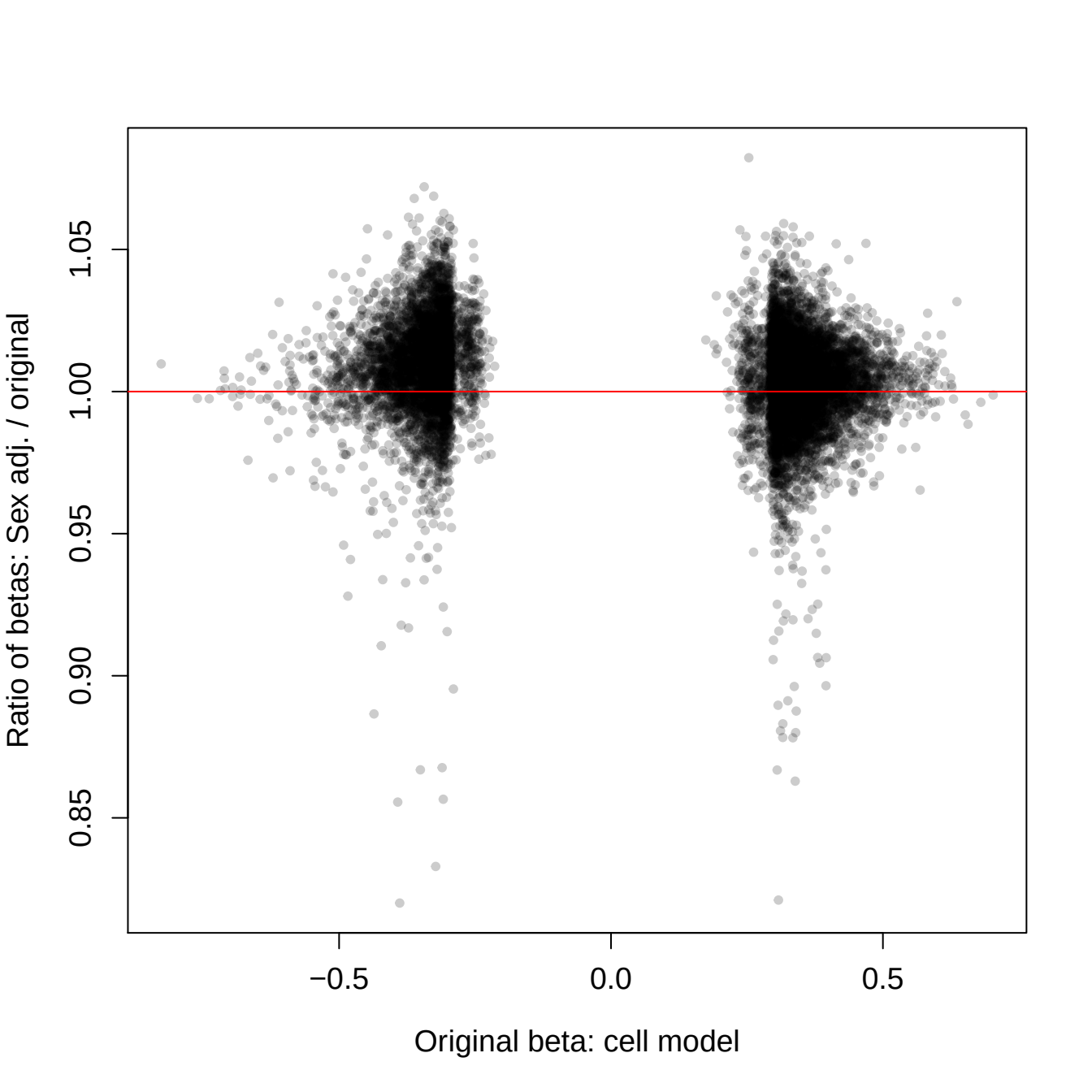
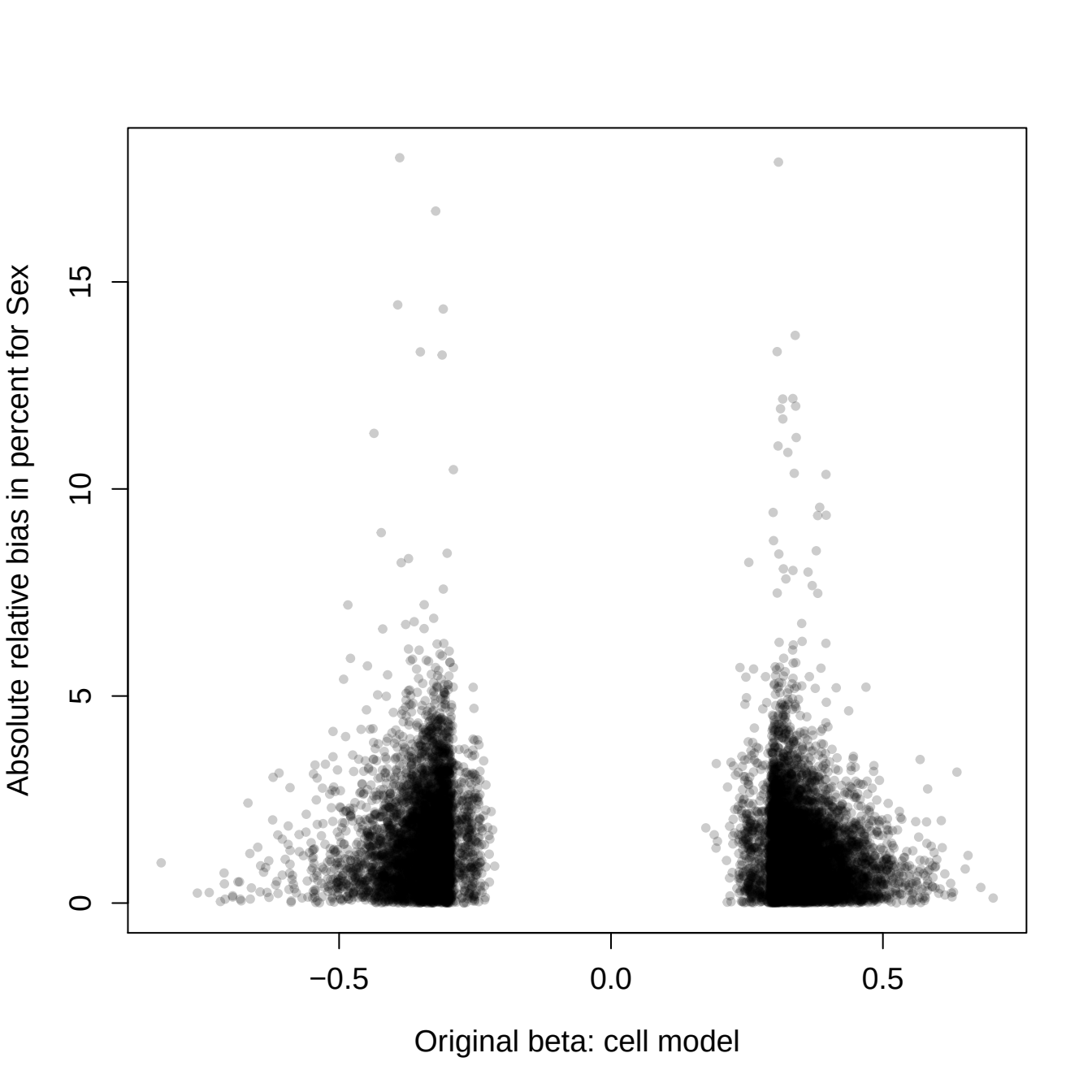

Adjusted beta for Race
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%

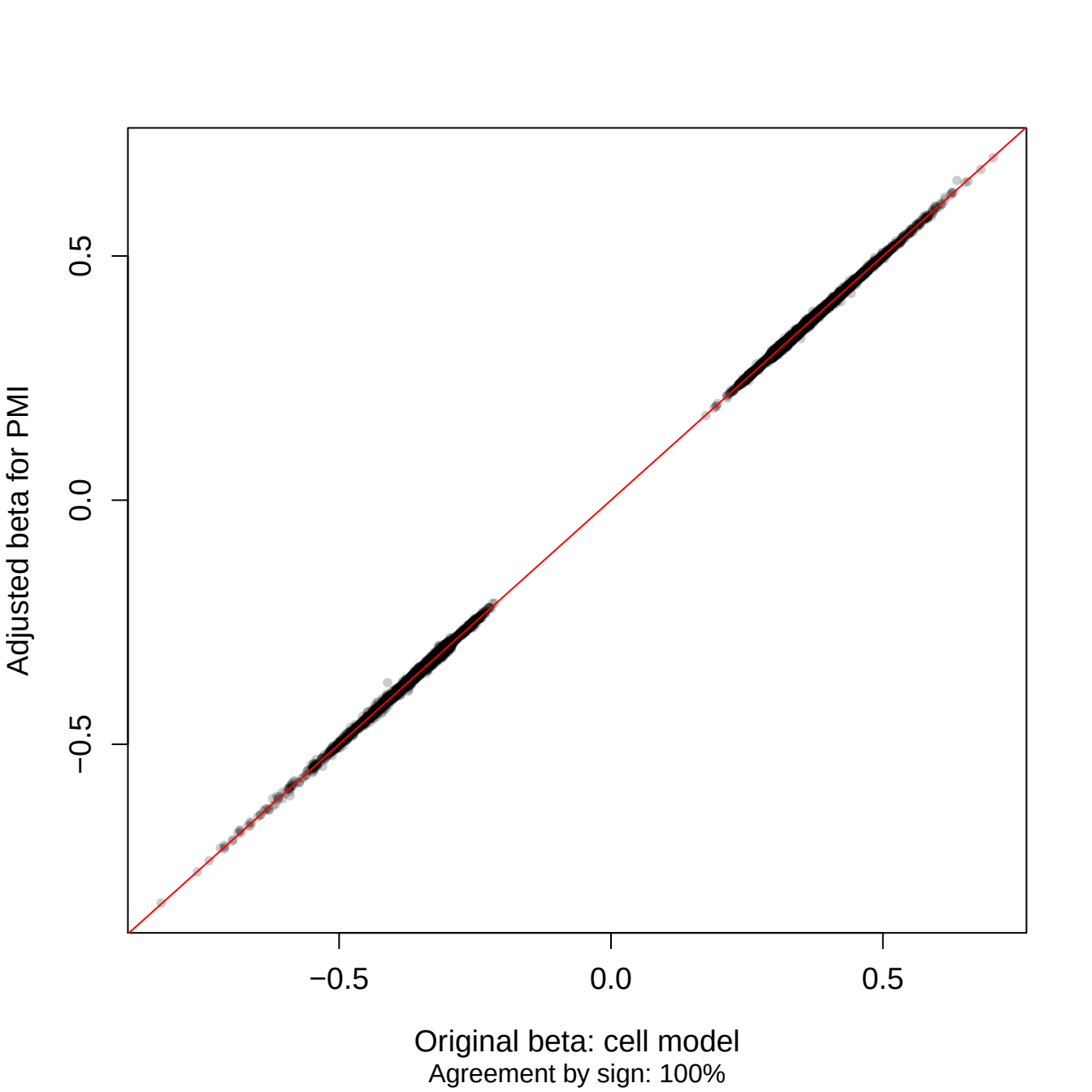

Ratio of betas: Race adj. / original
0.98
0.99
1.00
1.01
1.02
1.03
−0.5
0.0
0.5
Original beta: cell model

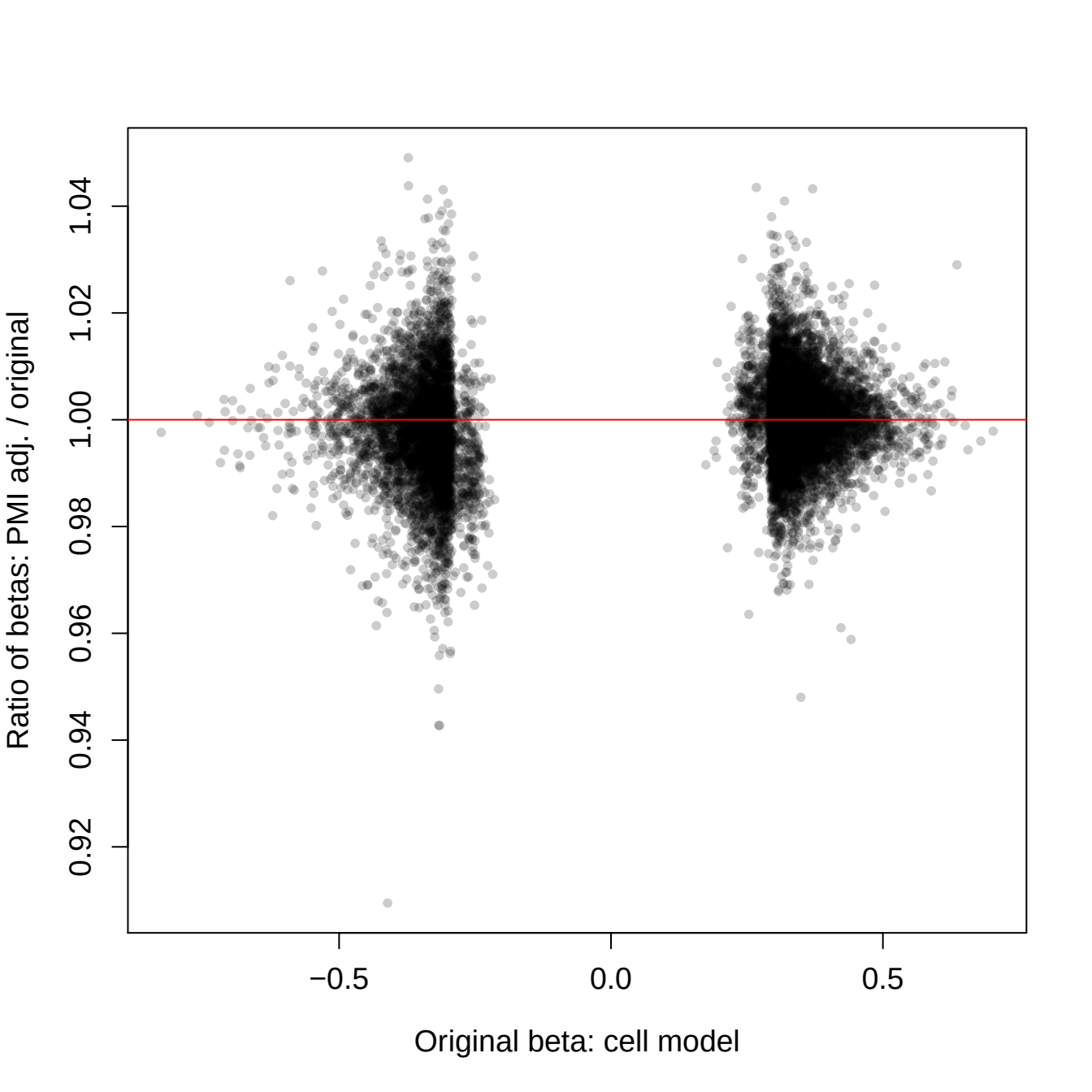

Absolute relative bias in percent for Race
0.0
0.5
1.0
1.5
2.0
2.5
3.0
−0.5
0.0
0.5
Original beta: cell model

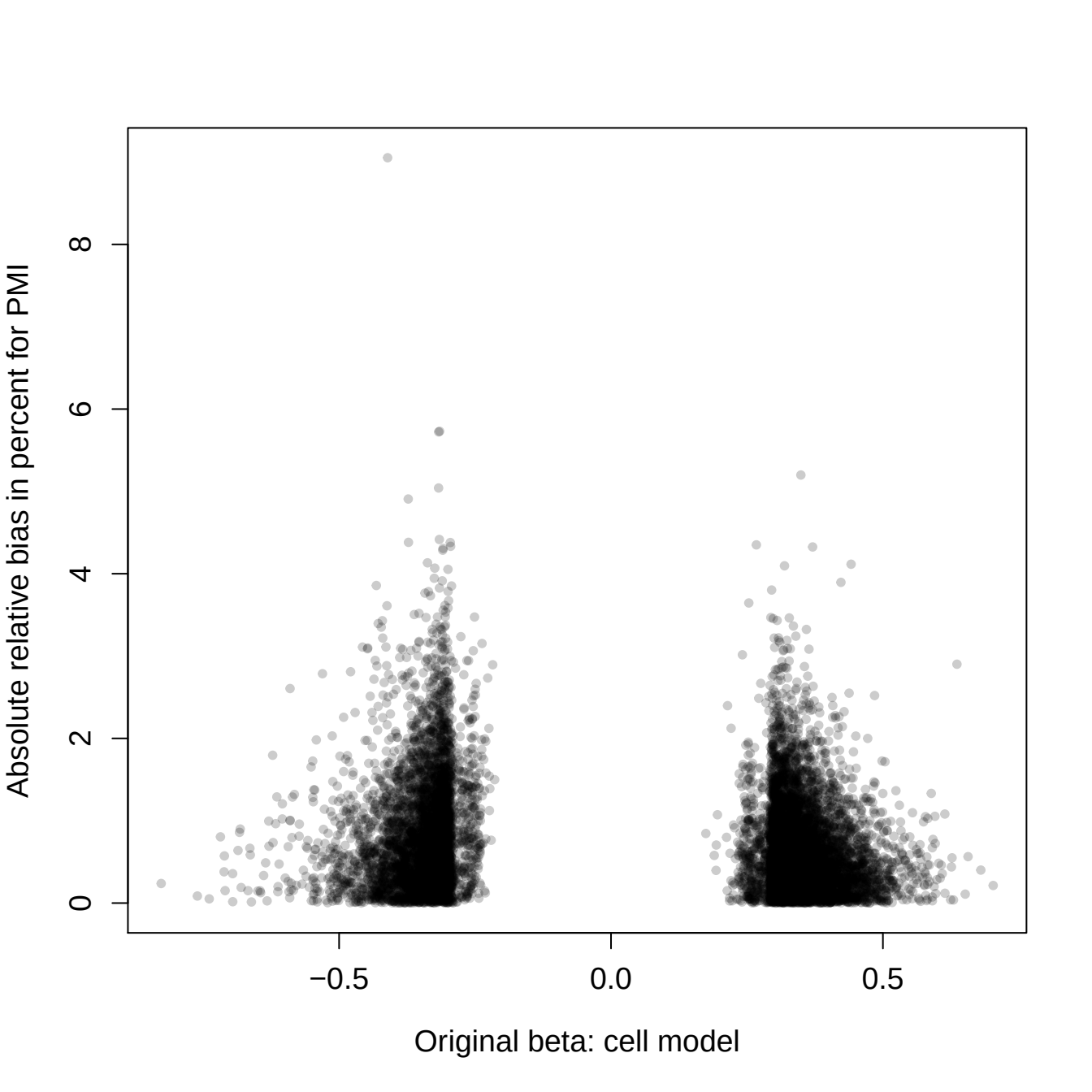

Adjusted beta for Sex
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%

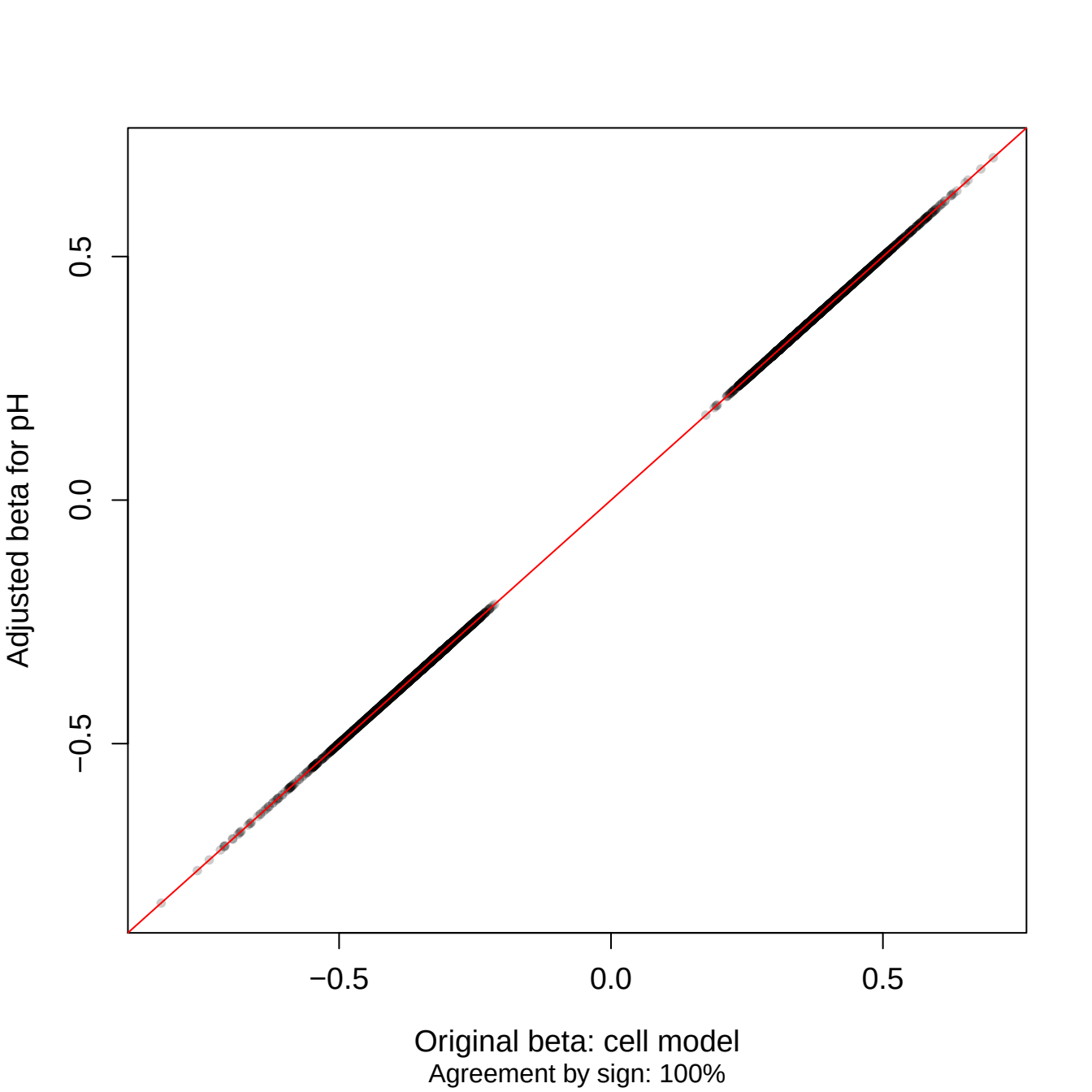

Ratio of betas: Sex adj. / original
0.85
0.90
0.95
1.00
1.05
−0.5
0.0
0.5
Original beta: cell model

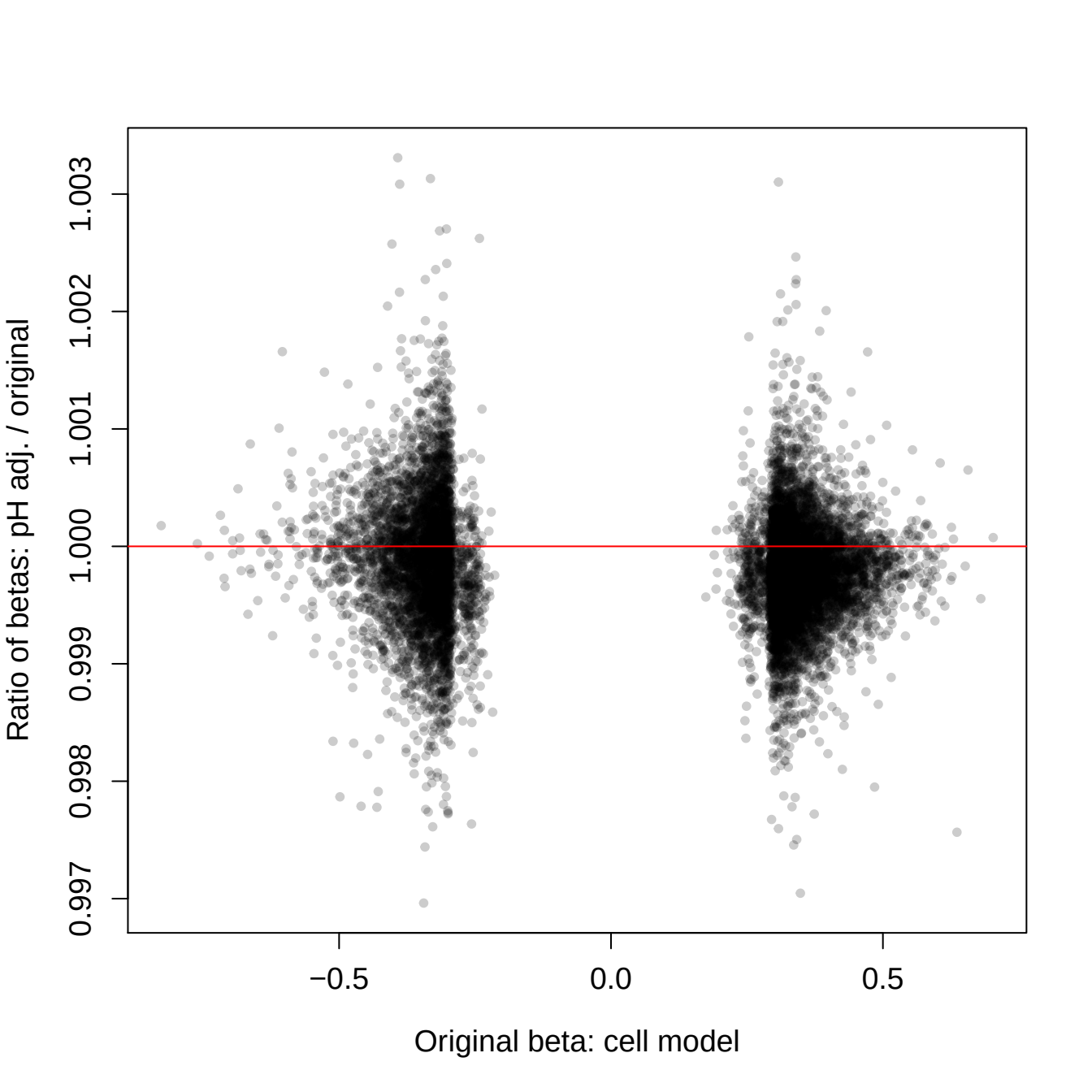

Absolute relative bias in percent for Sex
0
5
10
15
−0.5
0.0
0.5
Original beta: cell model

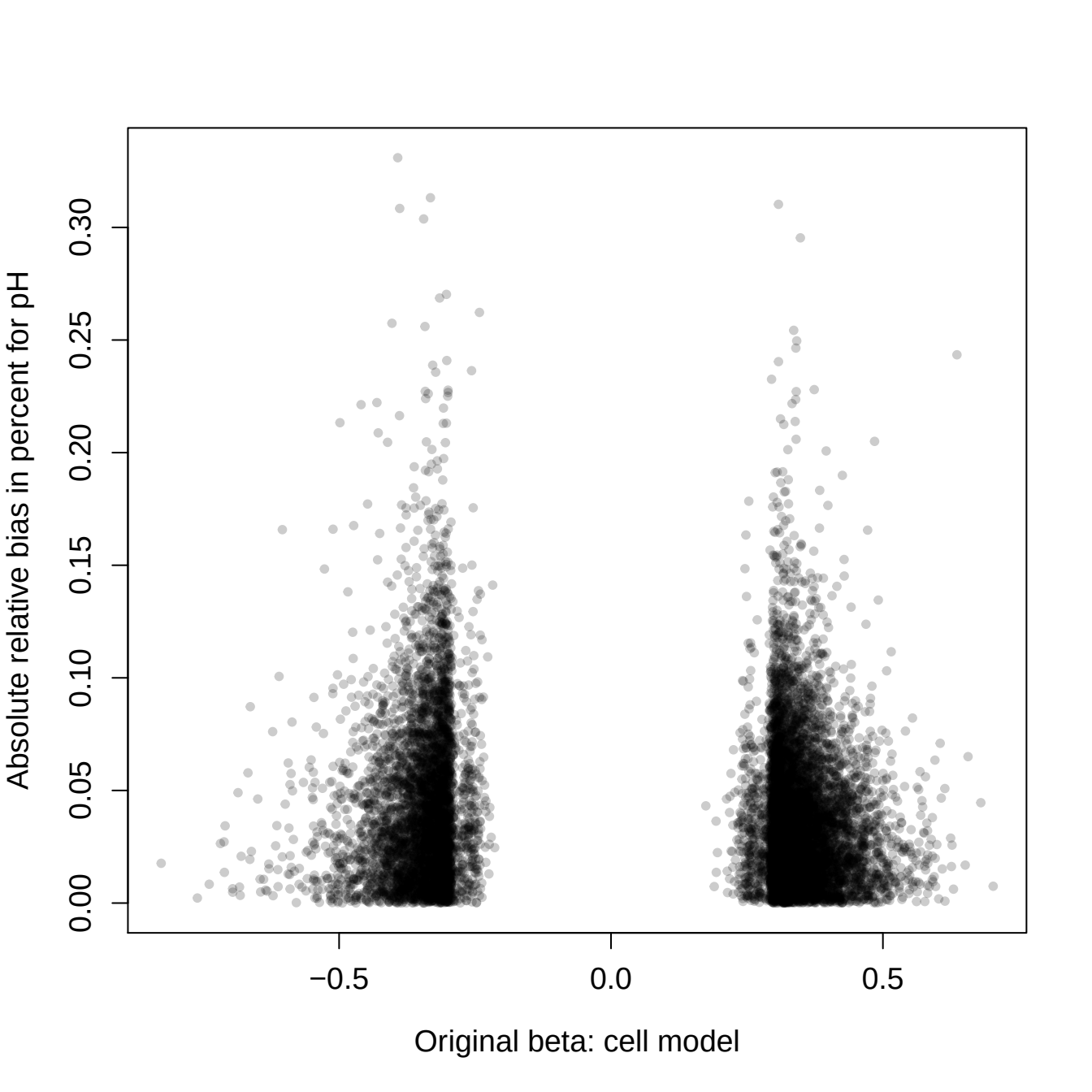

Adjusted beta for PMI
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%

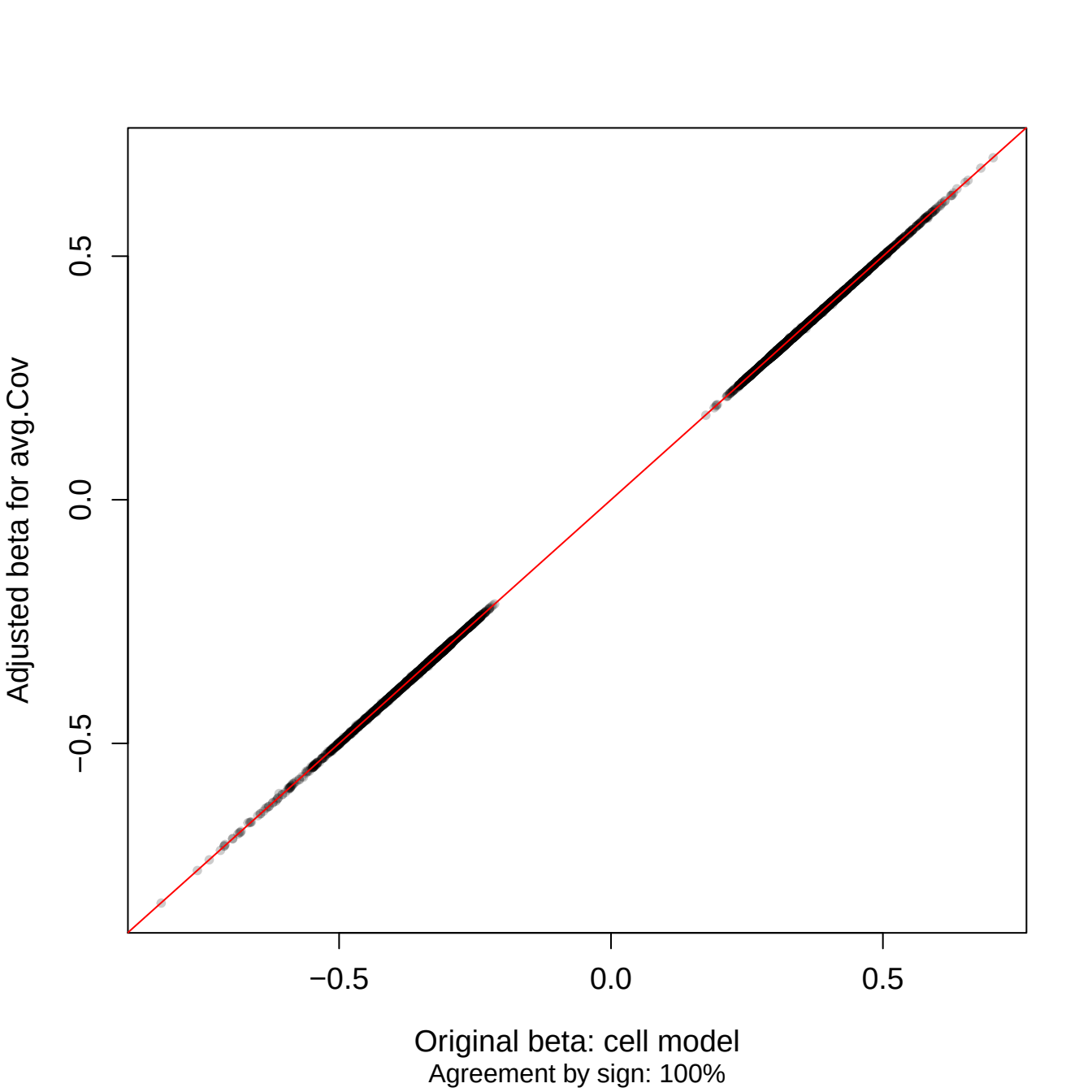

Ratio of betas: PMI adj. / original
0.92
0.94
0.96
0.98
1.00
1.02
1.04
−0.5
0.0
0.5
Original beta: cell model

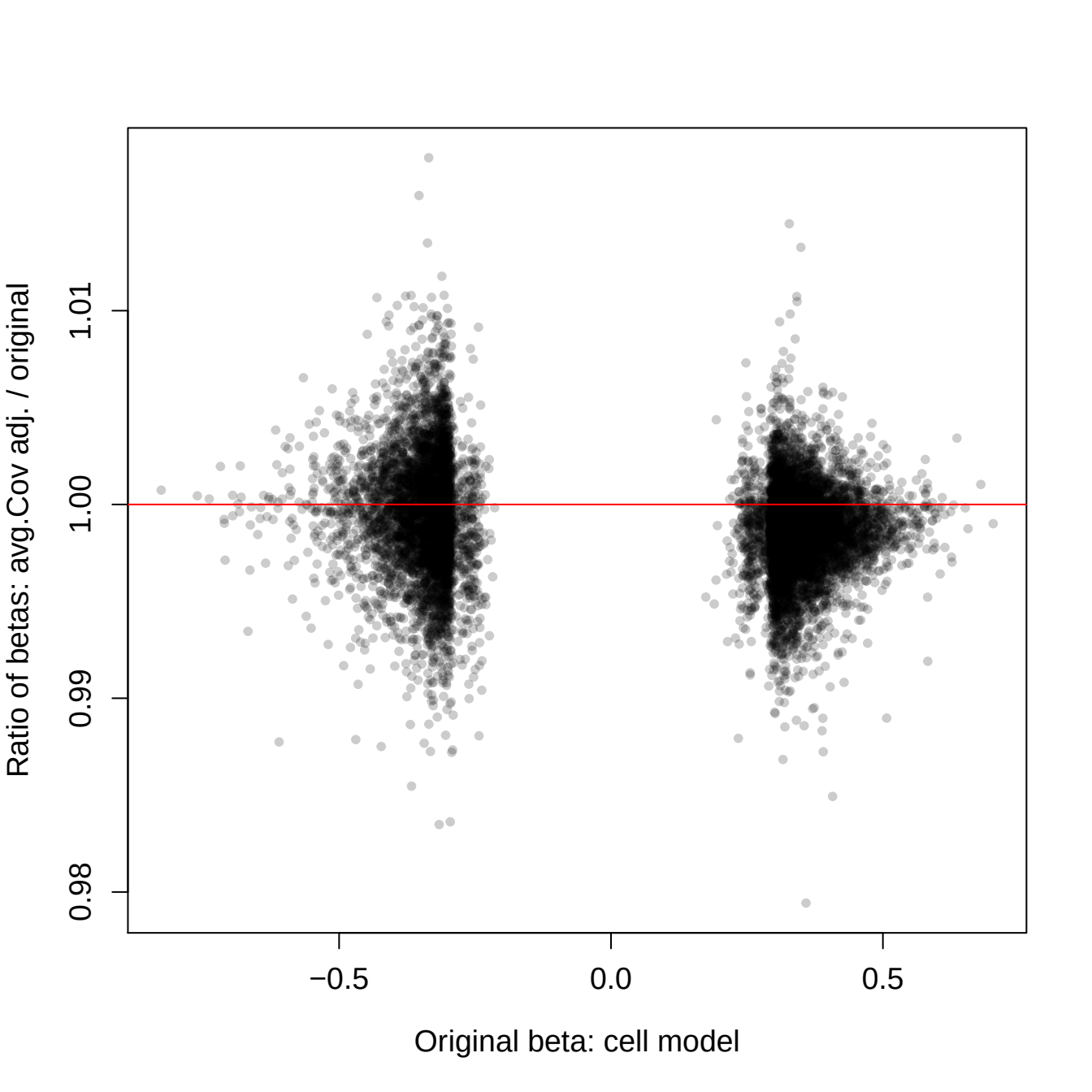

Absolute relative bias in percent for PMI
0
2
4
6
8
−0.5
0.0
0.5
Original beta: cell model

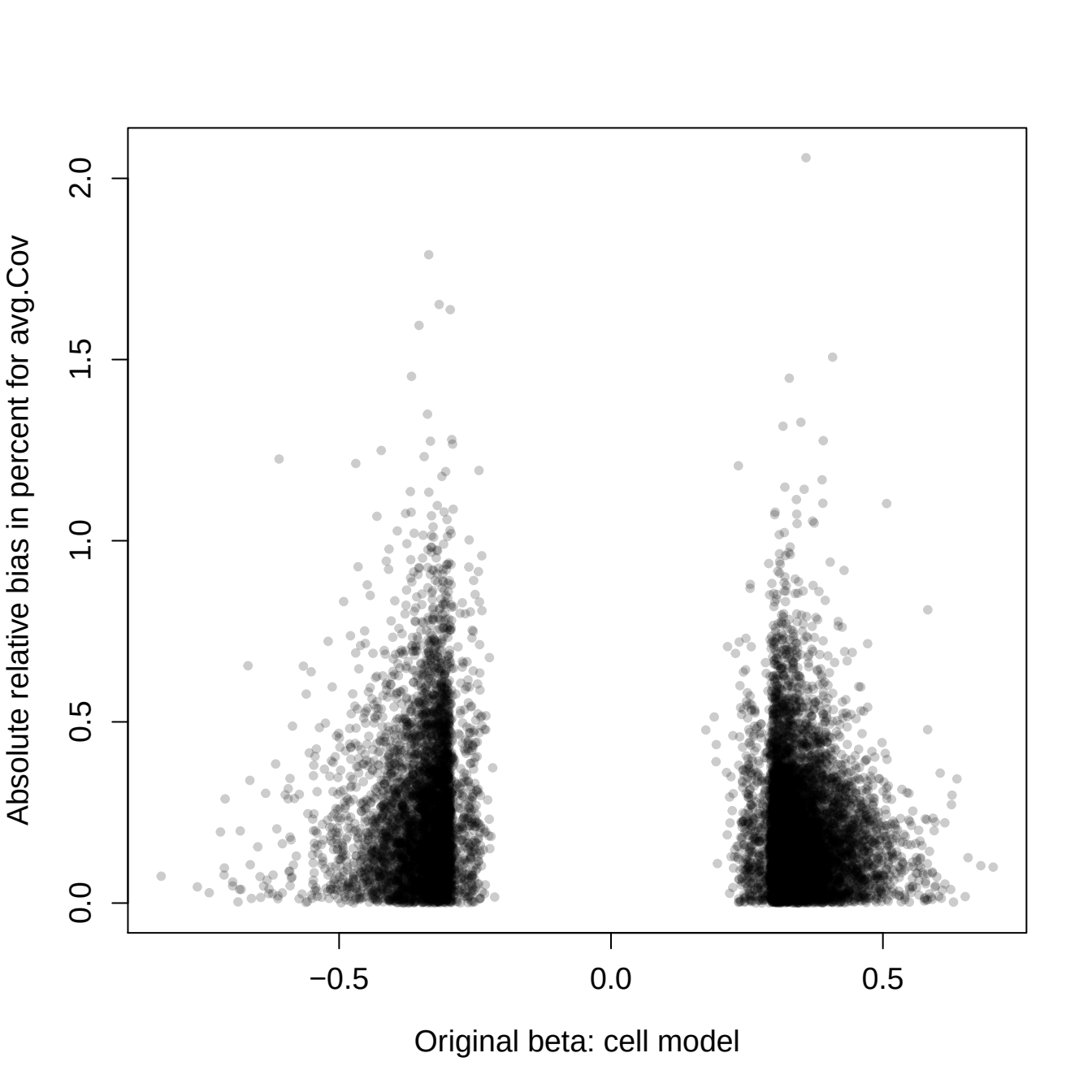

Adjusted beta for pH
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%

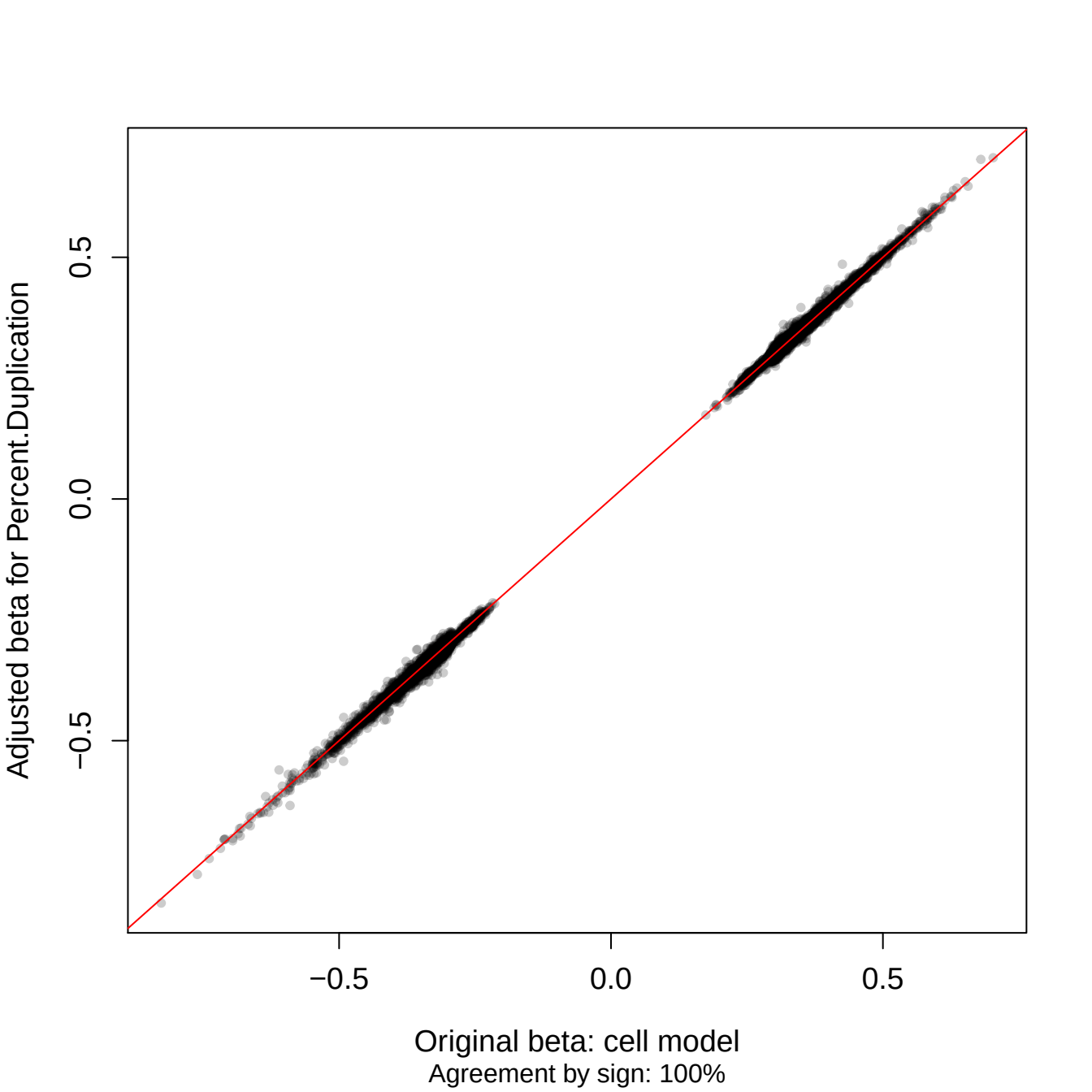

Ratio of betas: pH adj. / original
0.997
0.998
0.999
1.000
1.001
1.002
1.003
−0.5
0.0
0.5
Original beta: cell model

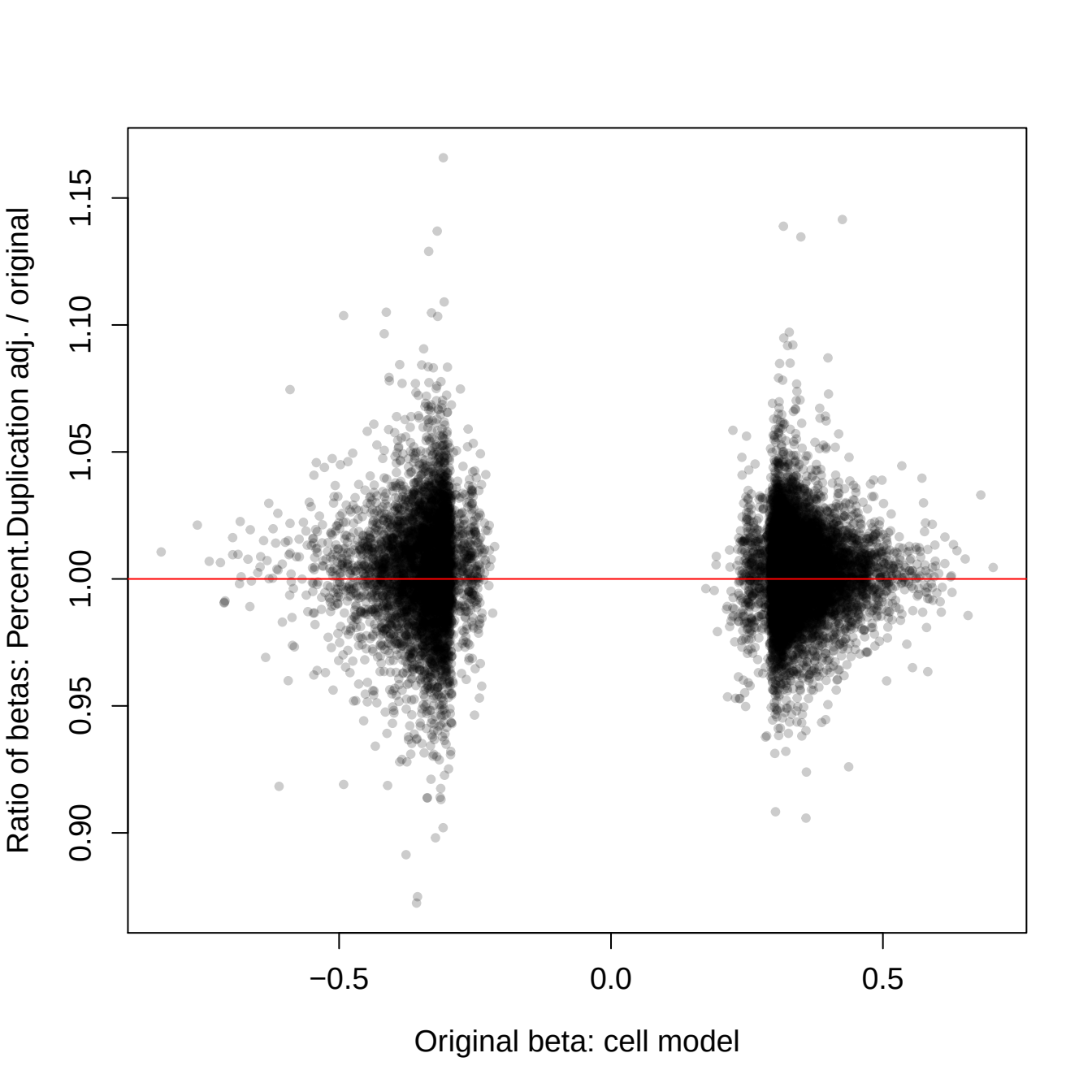

Absolute relative bias in percent for pH
0.00
0.05
0.10
0.15
0.20
0.25
0.30
−0.5
0.0
0.5
Original beta: cell model

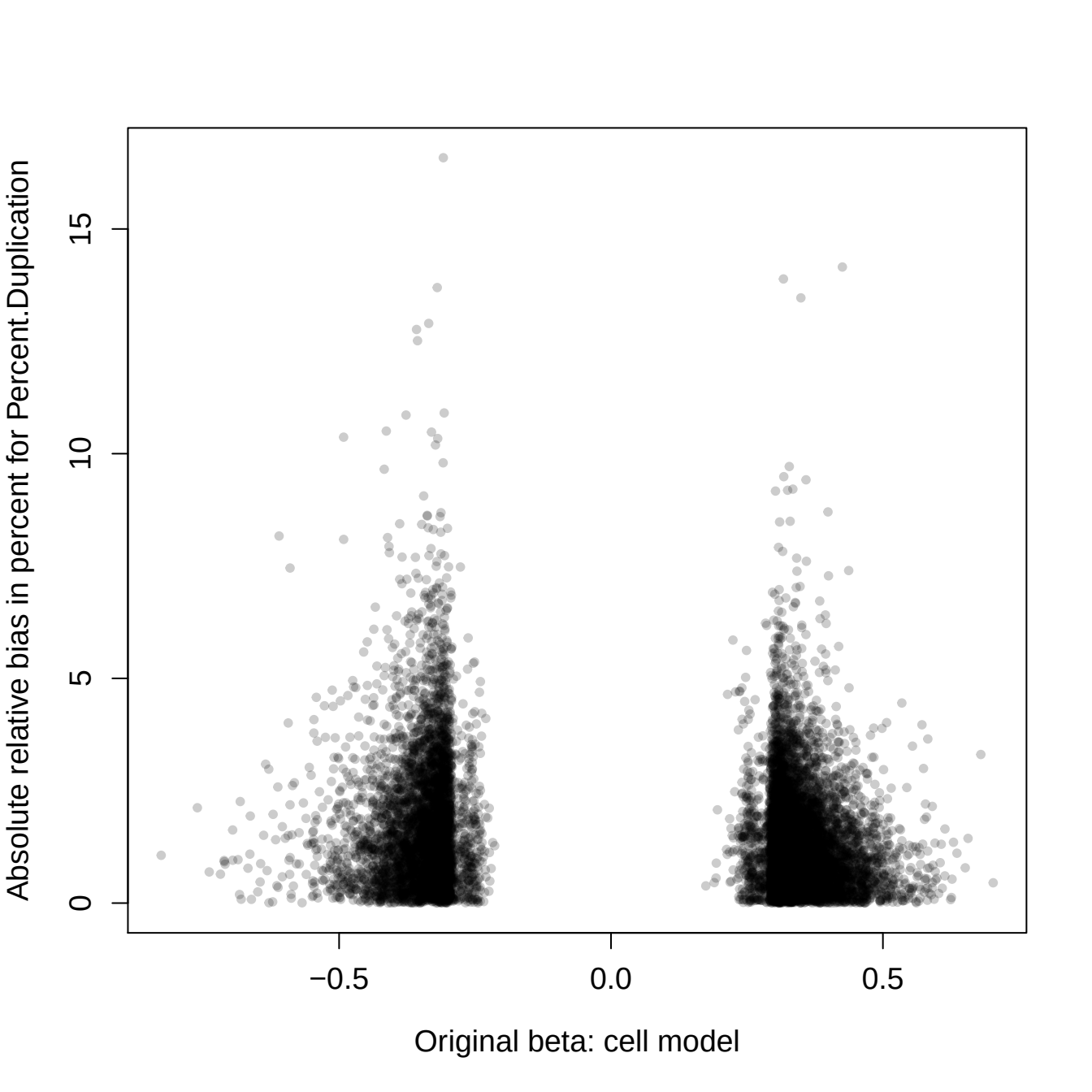

Adjusted beta for avg.Cov
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%

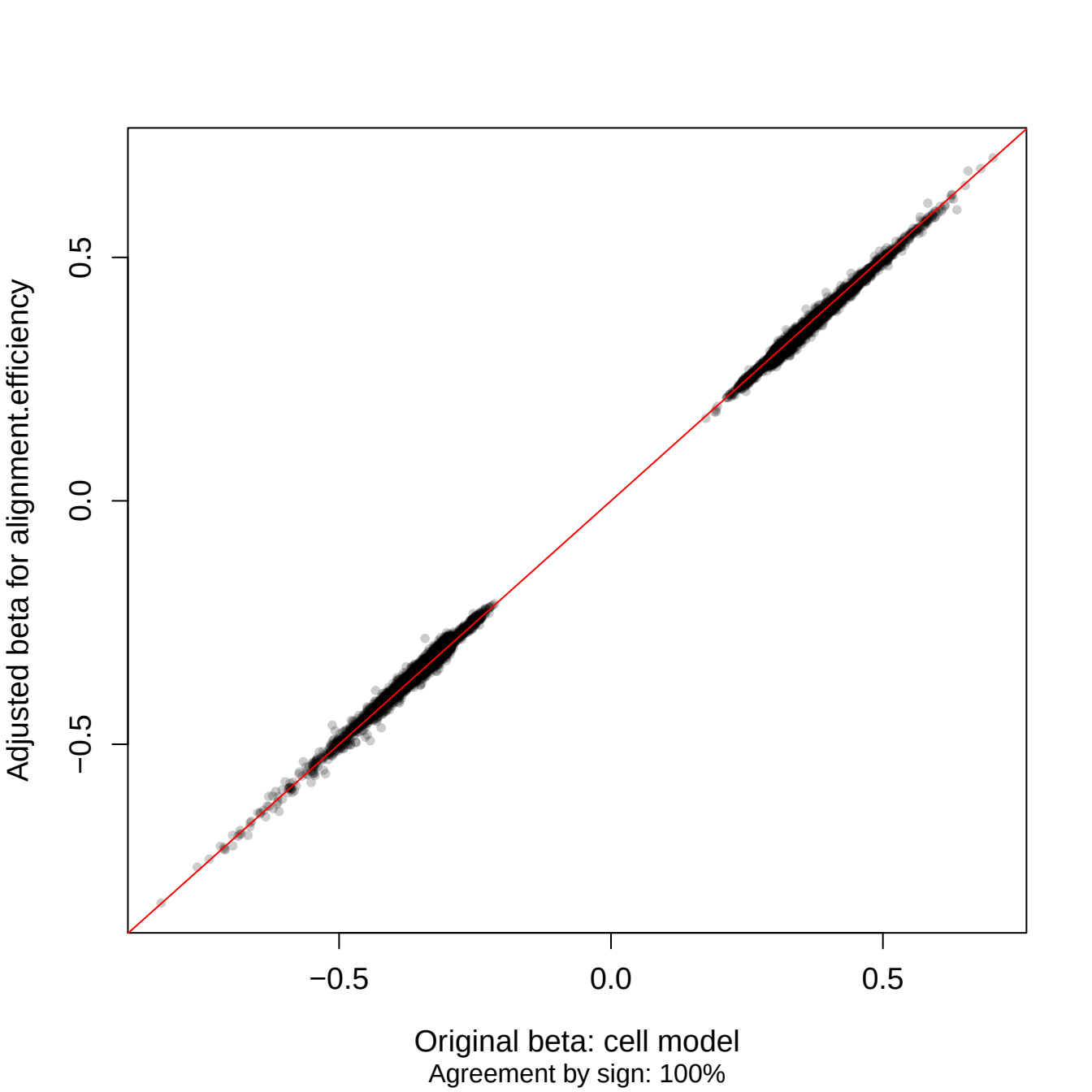

Ratio of betas: avg.Cov adj. / original
0.98
0.99
1.00
1.01
−0.5
0.0
0.5
Original beta: cell model

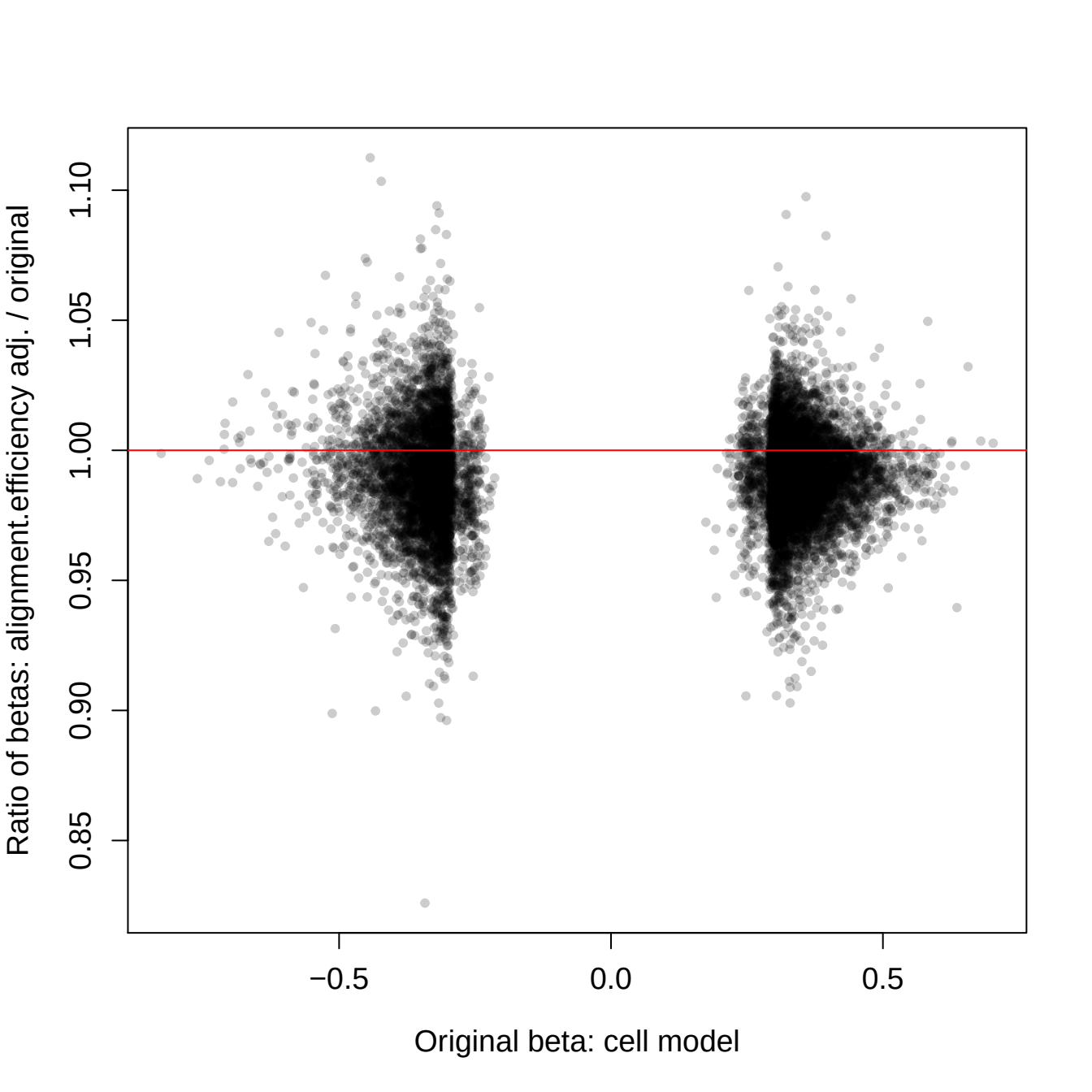

Absolute relative bias in percent for avg.Cov
0.0
0.5
1.0
1.5
2.0
−0.5
0.0
0.5
Original beta: cell model

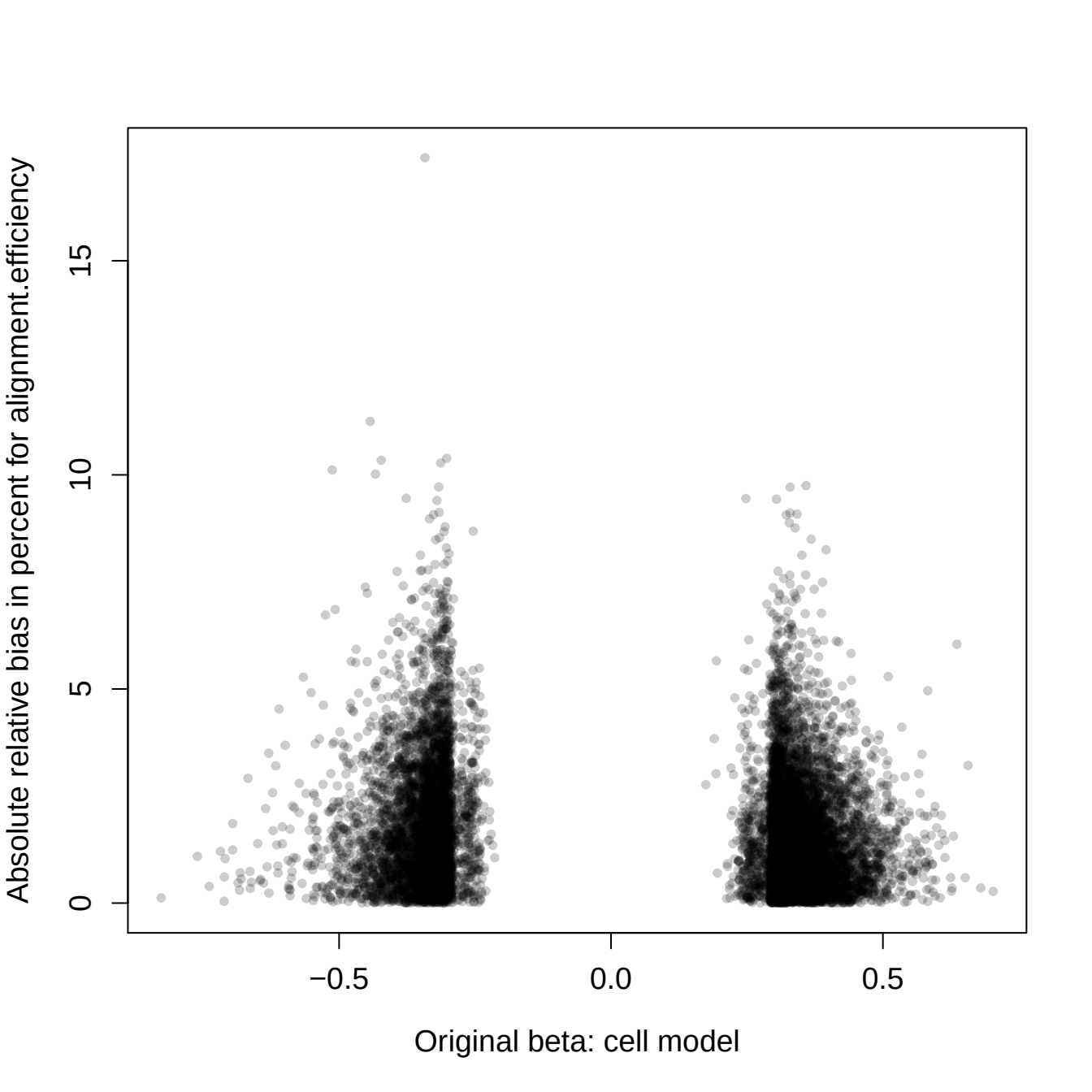

Adjusted beta for Percent.Duplication
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%

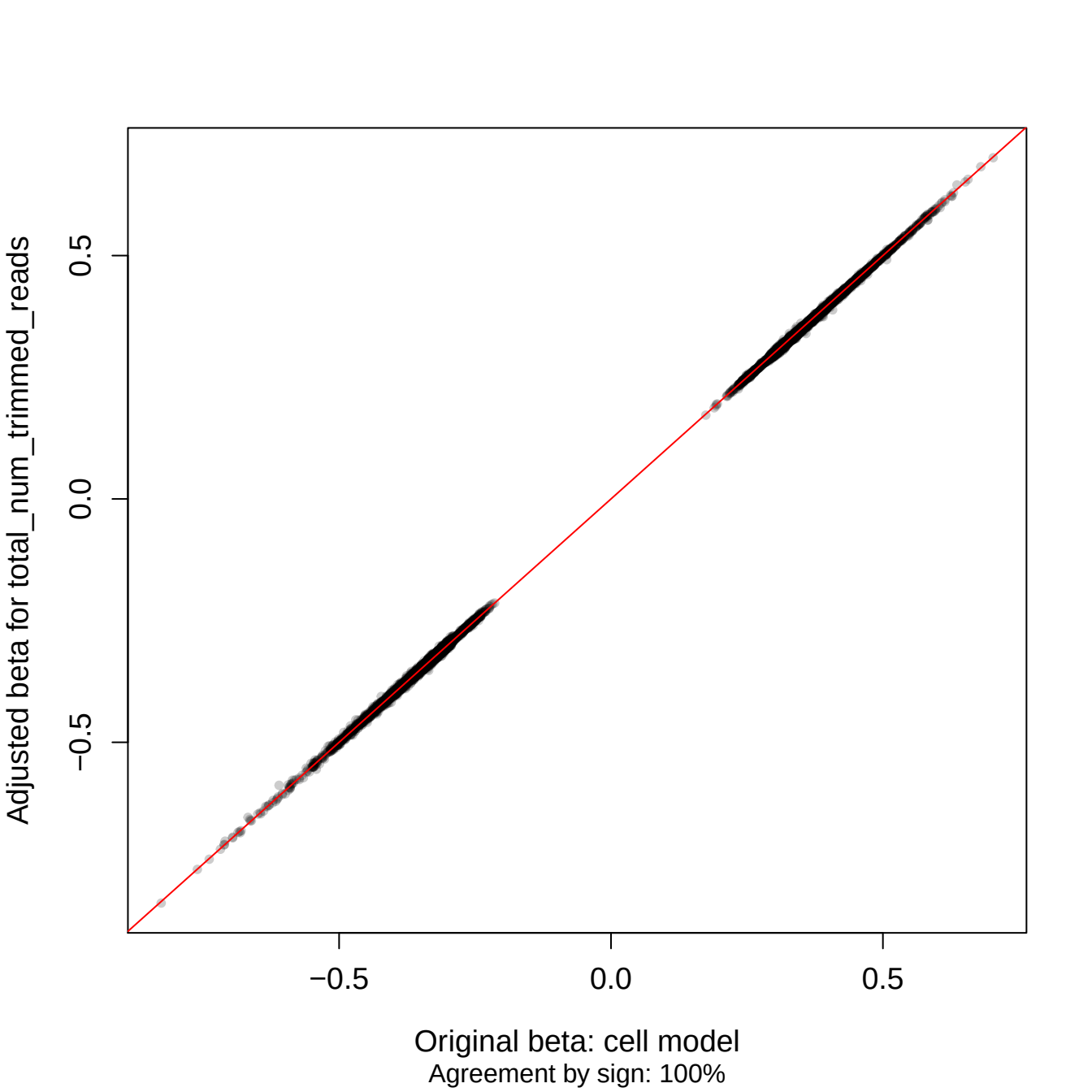

Ratio of betas: Percent.Duplication adj. / original
0.90
0.95
1.00
1.05
1.10
1.15
−0.5
0.0
0.5
Original beta: cell model

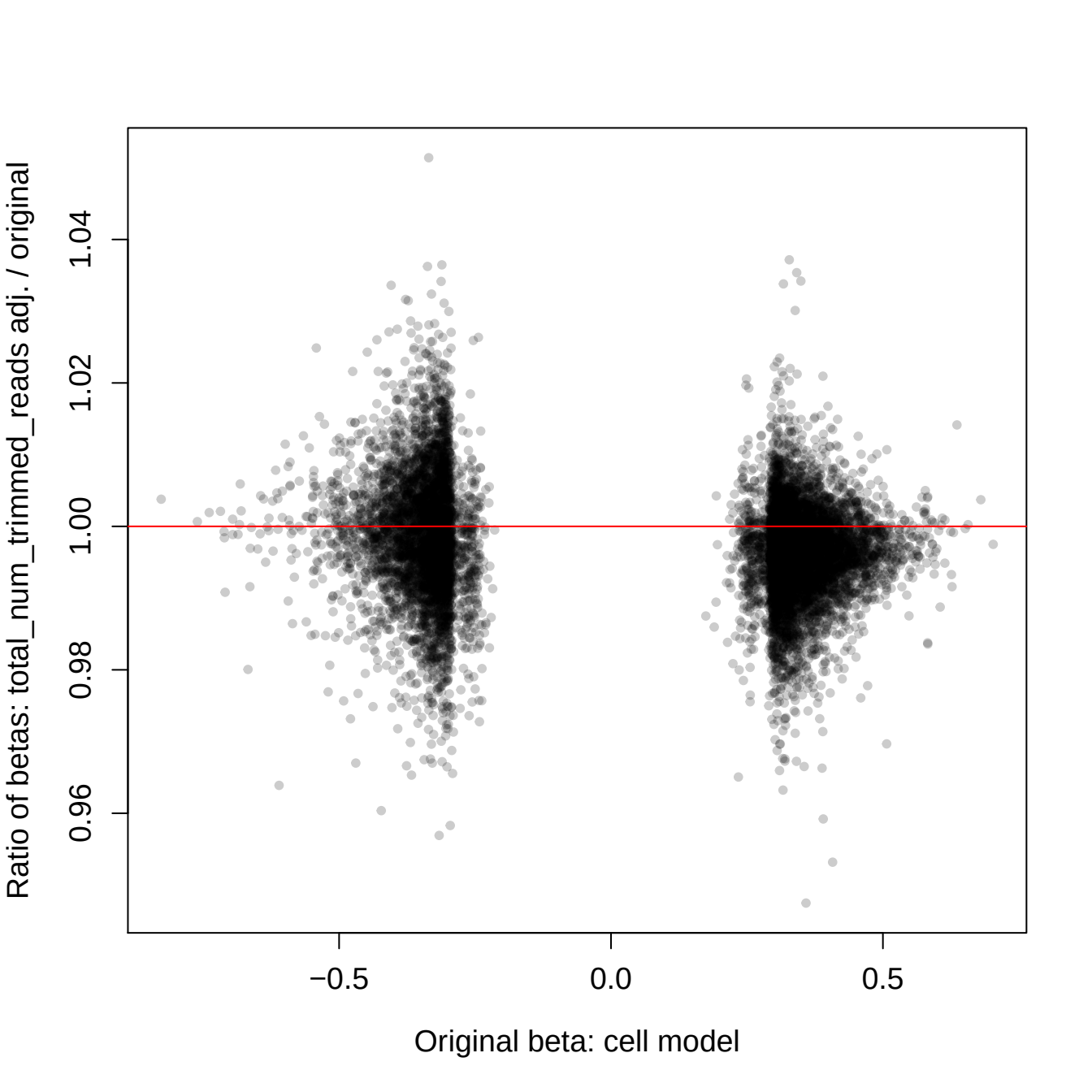

Absolute relative bias in percent for Percent.Duplication
0
5
10
15
−0.5
0.0
0.5
Original beta: cell model

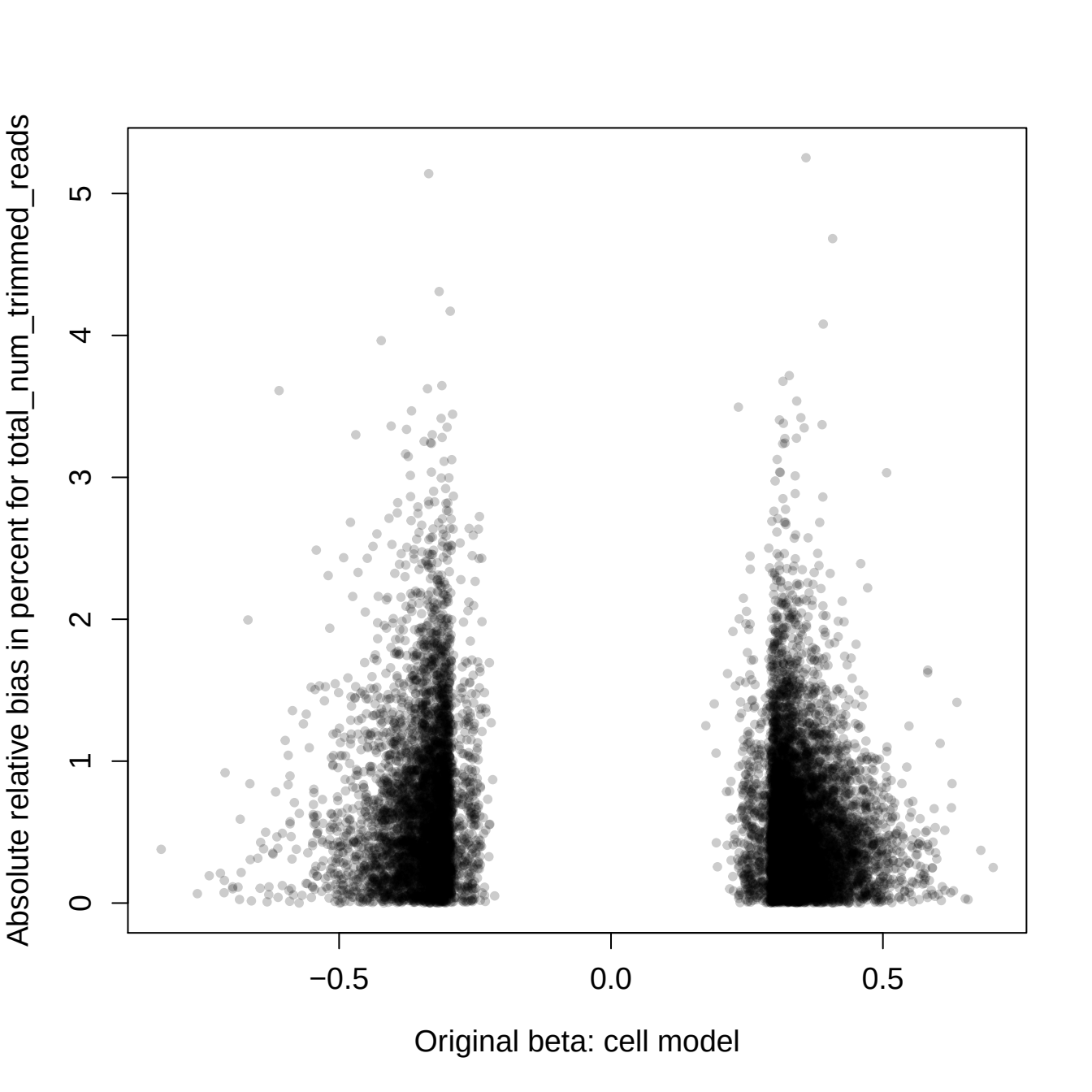

Adjusted beta for alignment.efficiency
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%

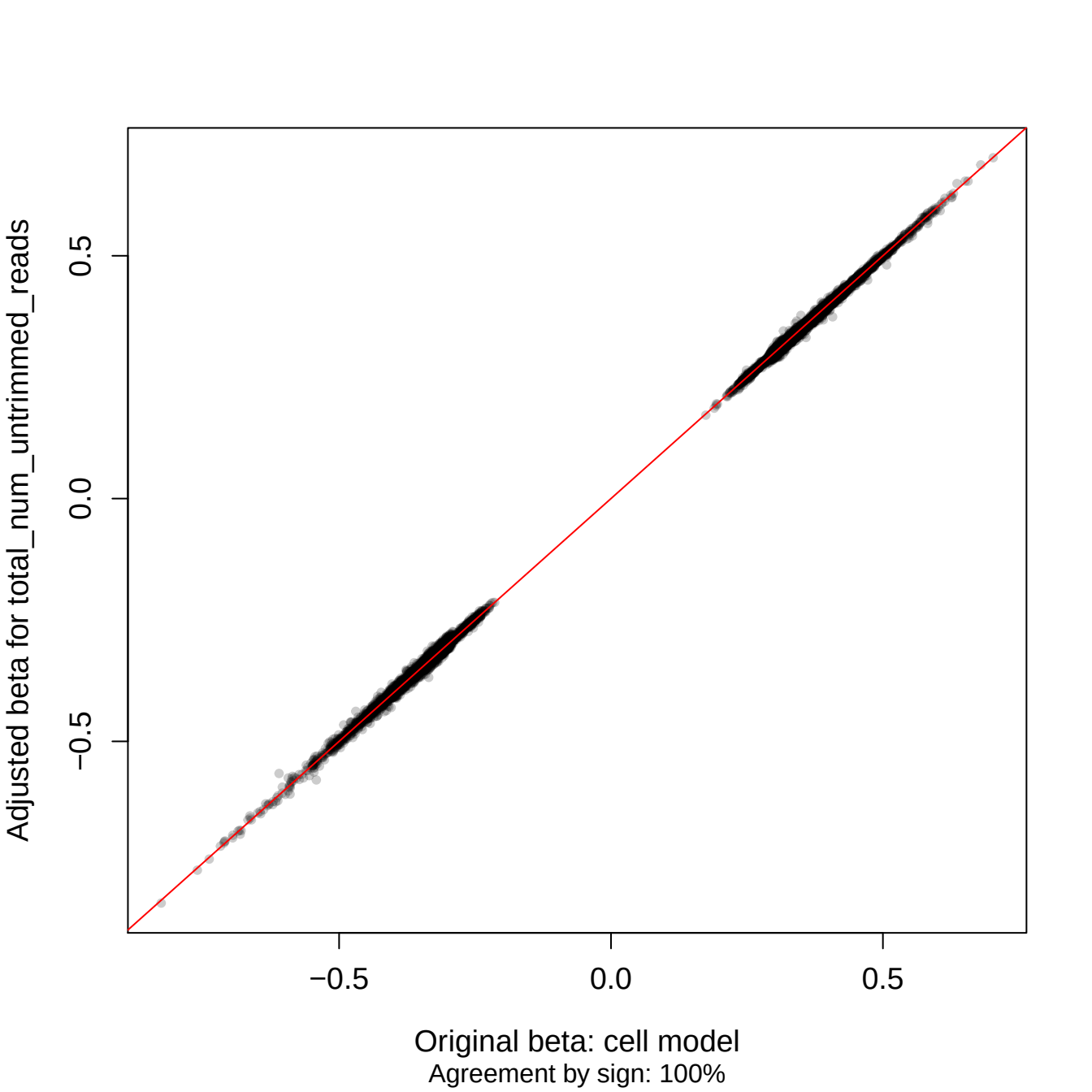

Ratio of betas: alignment.efficiency adj. / original
0.85
0.90
0.95
1.00
1.05
1.10
−0.5
0.0
0.5
Original beta: cell model

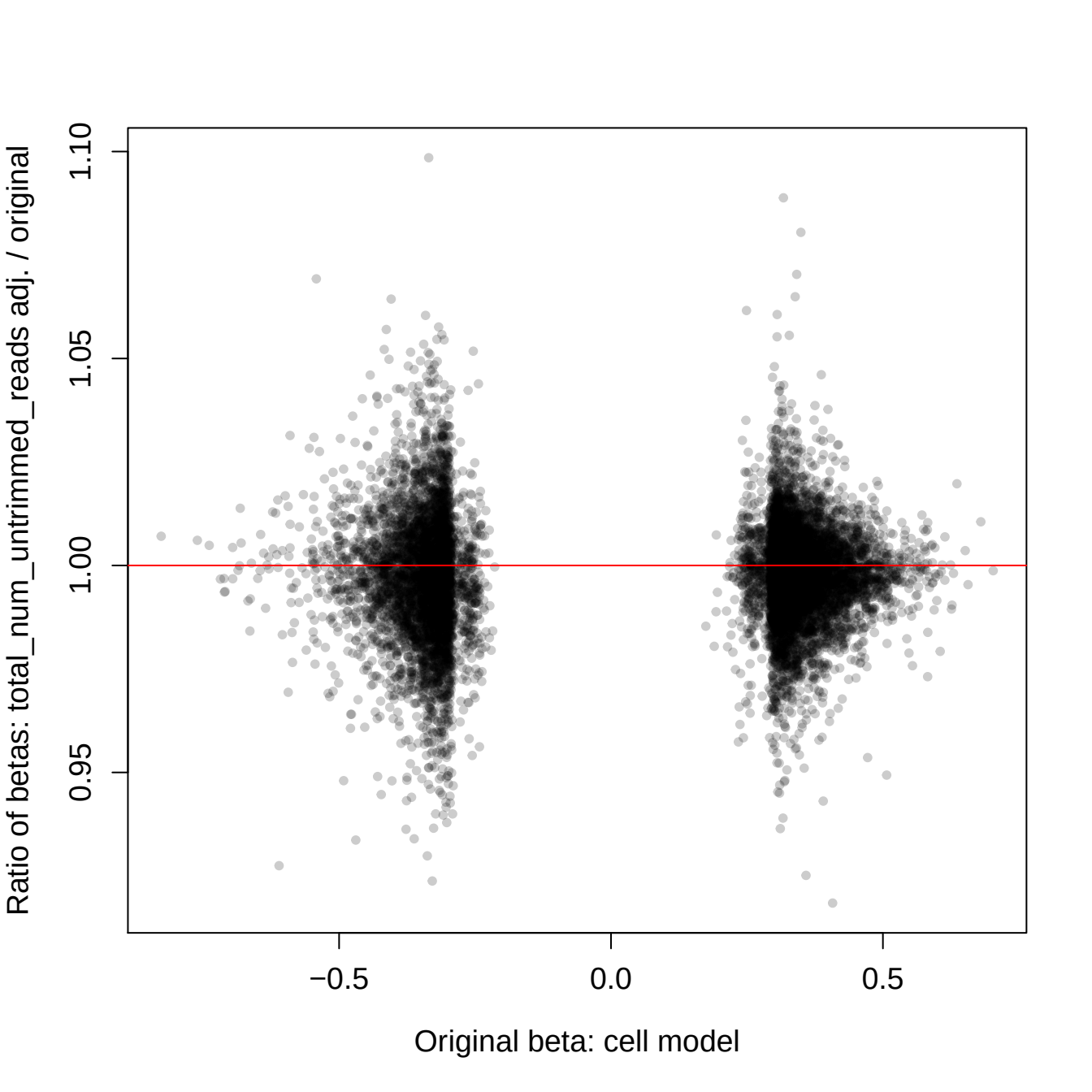

Absolute relative bias in percent for alignment.efficiency
0
5
10
15
−0.5
0.0
0.5
Original beta: cell model

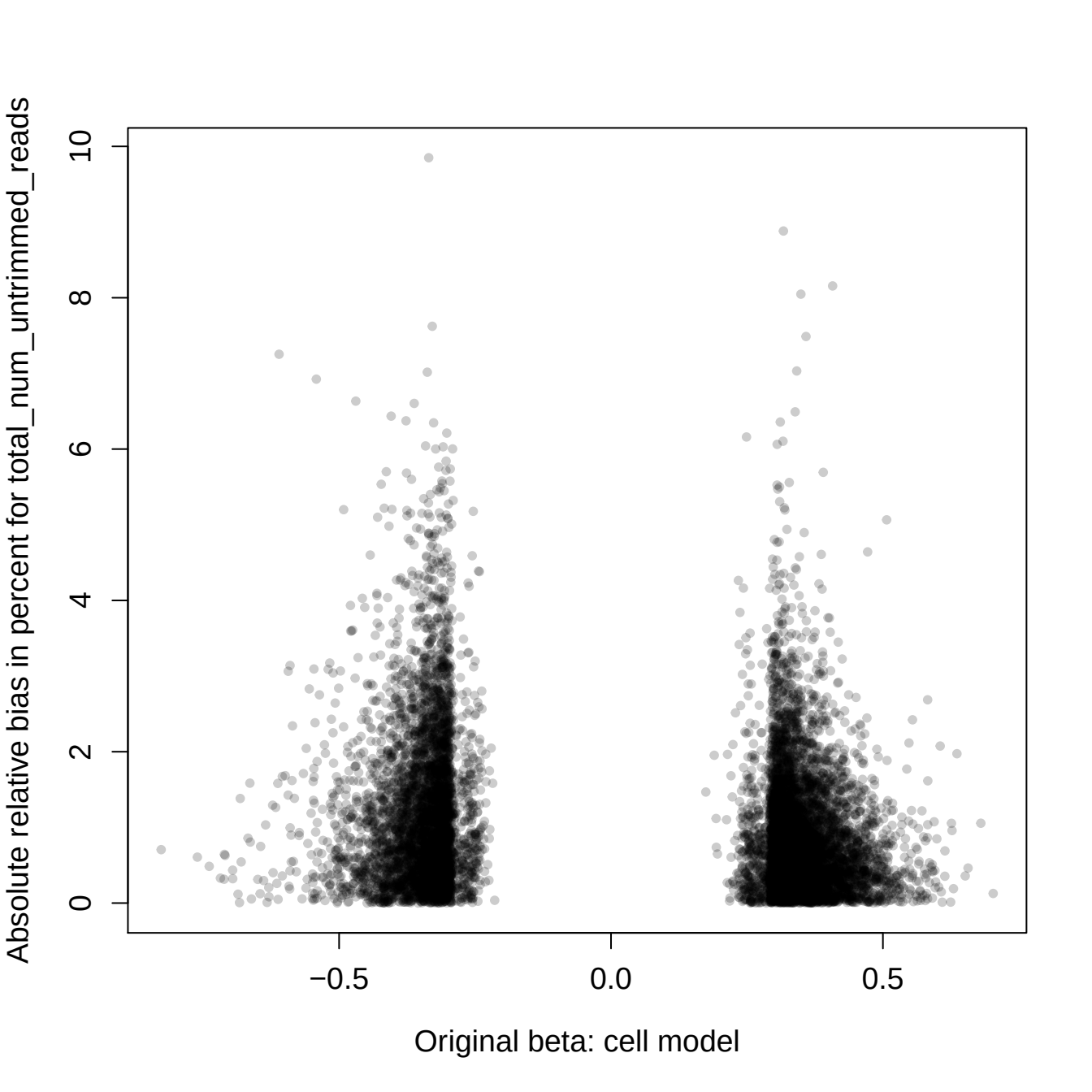

Adjusted beta for total_num_trimmed_reads
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%

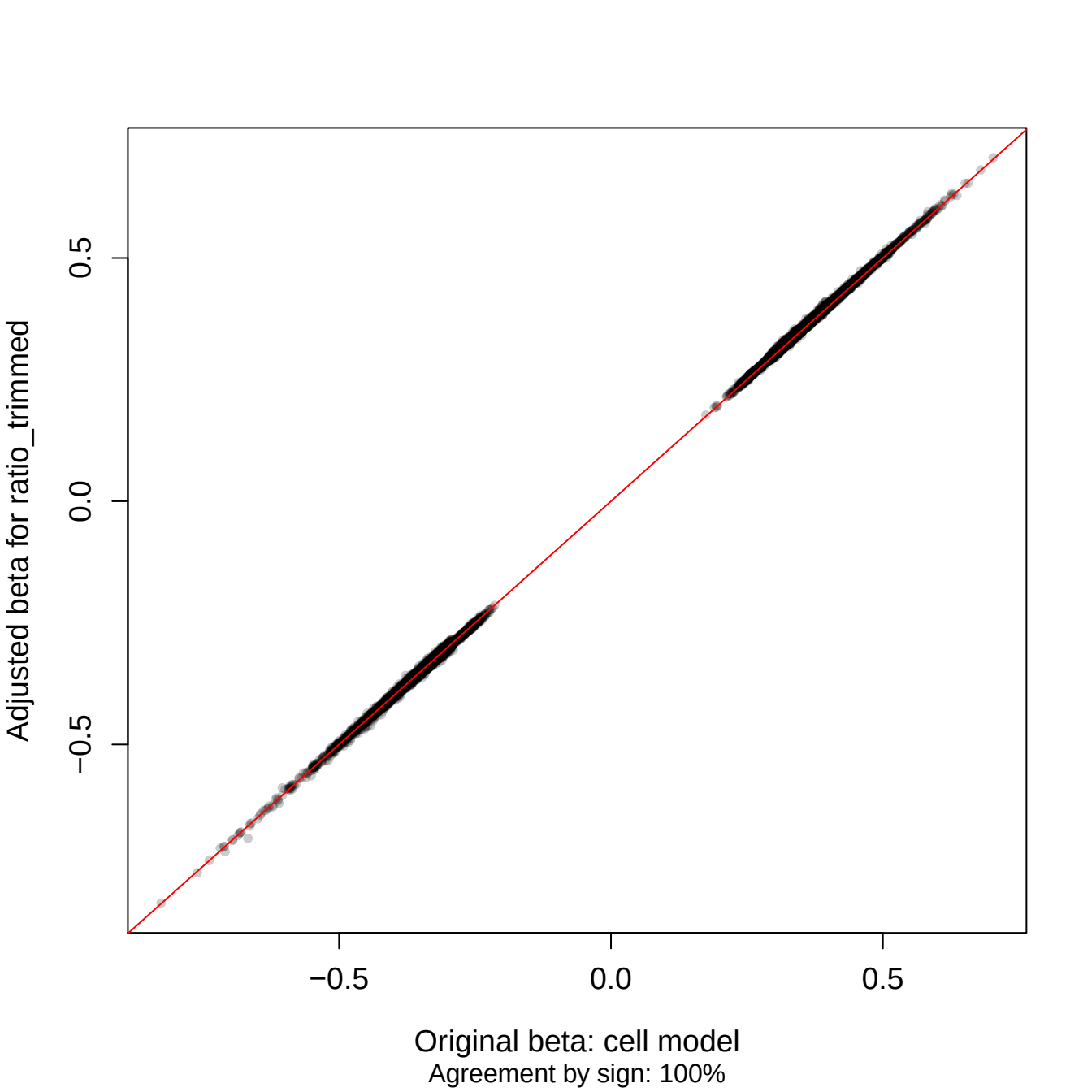

Ratio of betas: total_num_trimmed_reads adj. / original
0.96
0.98
1.00
1.02
1.04
−0.5
0.0
0.5
Original beta: cell model

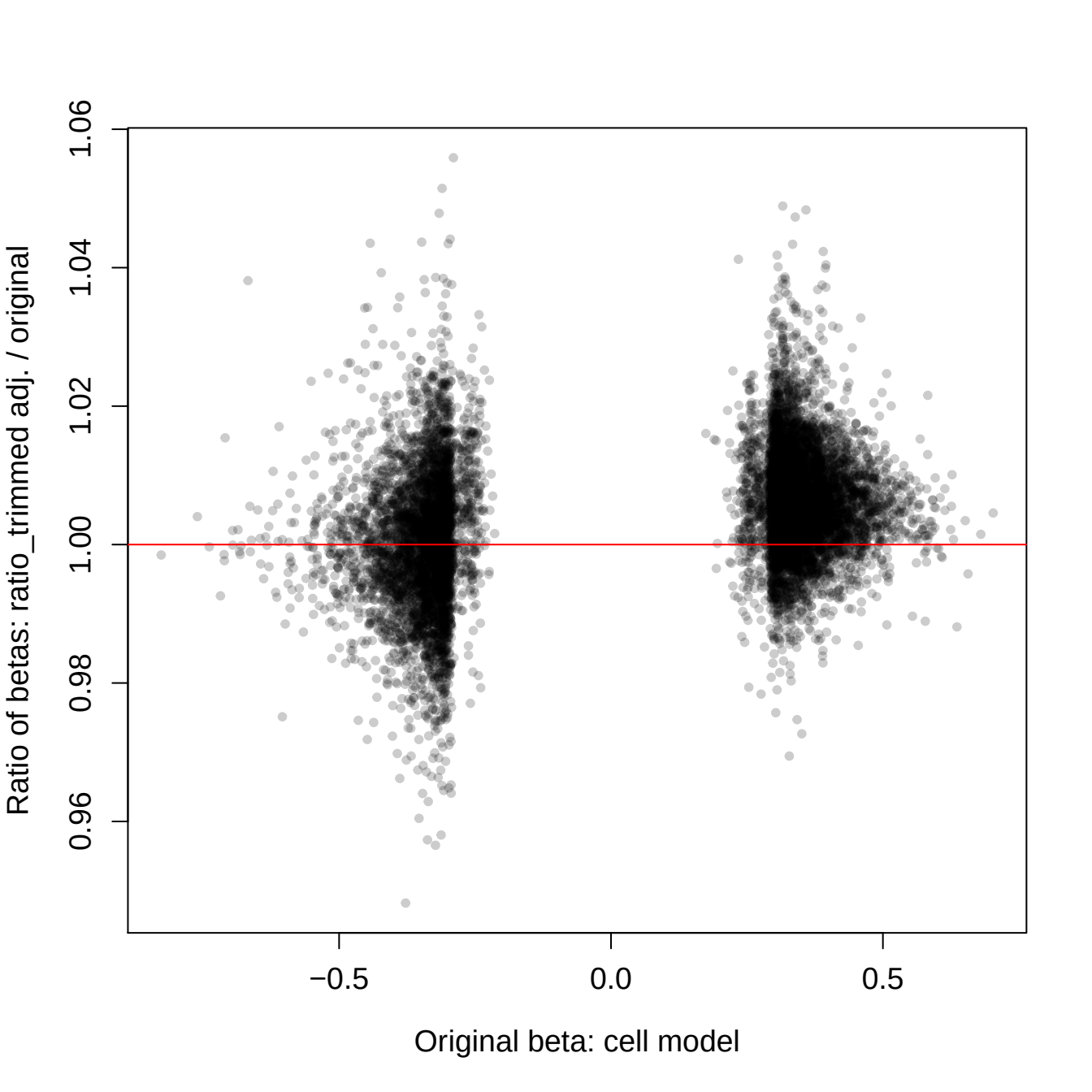

Absolute relative bias in percent for total_num_trimmed_reads
0
1
2
3
4
5
−0.5
0.0
0.5
Original beta: cell model

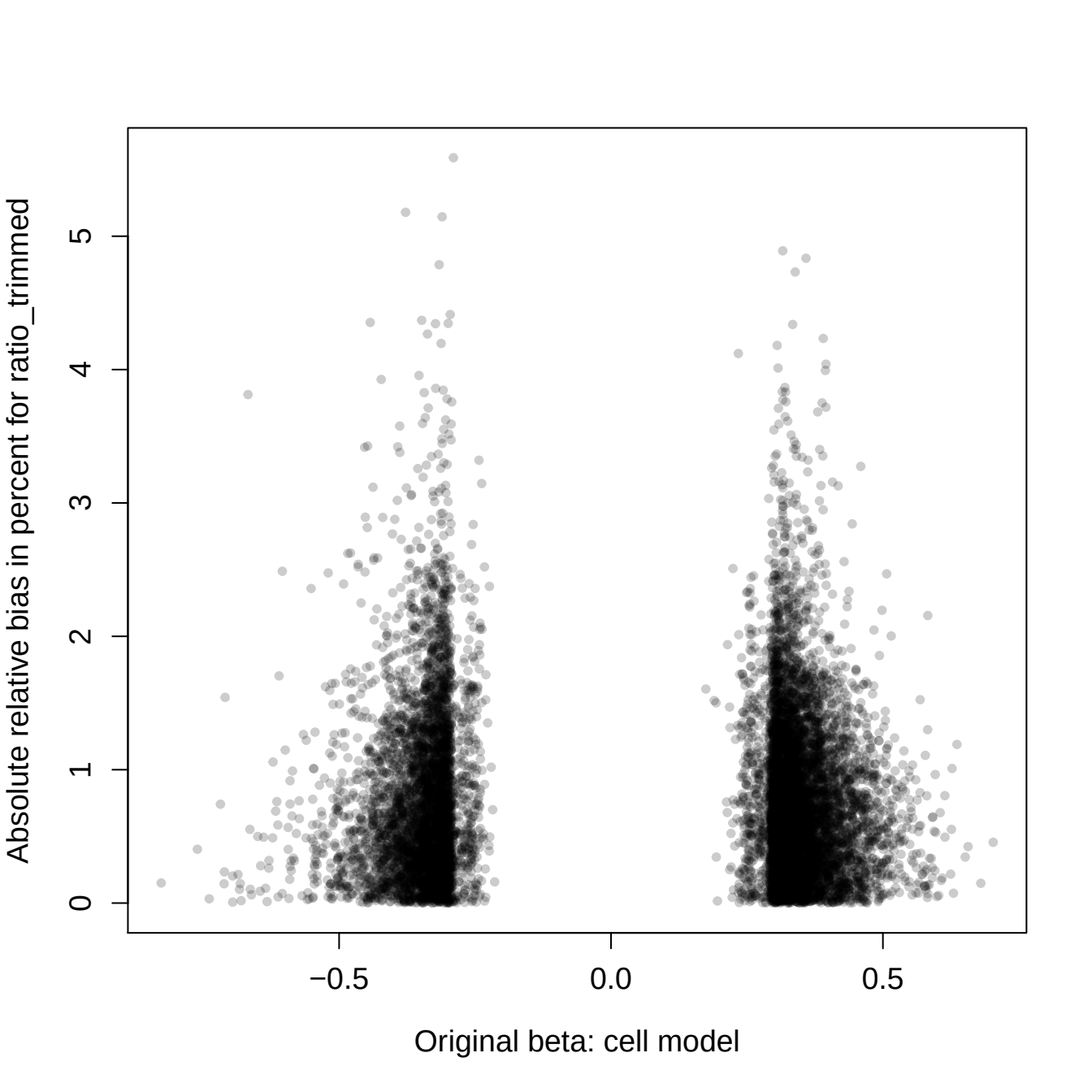

Adjusted beta for total_num_untrimmed_reads
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%

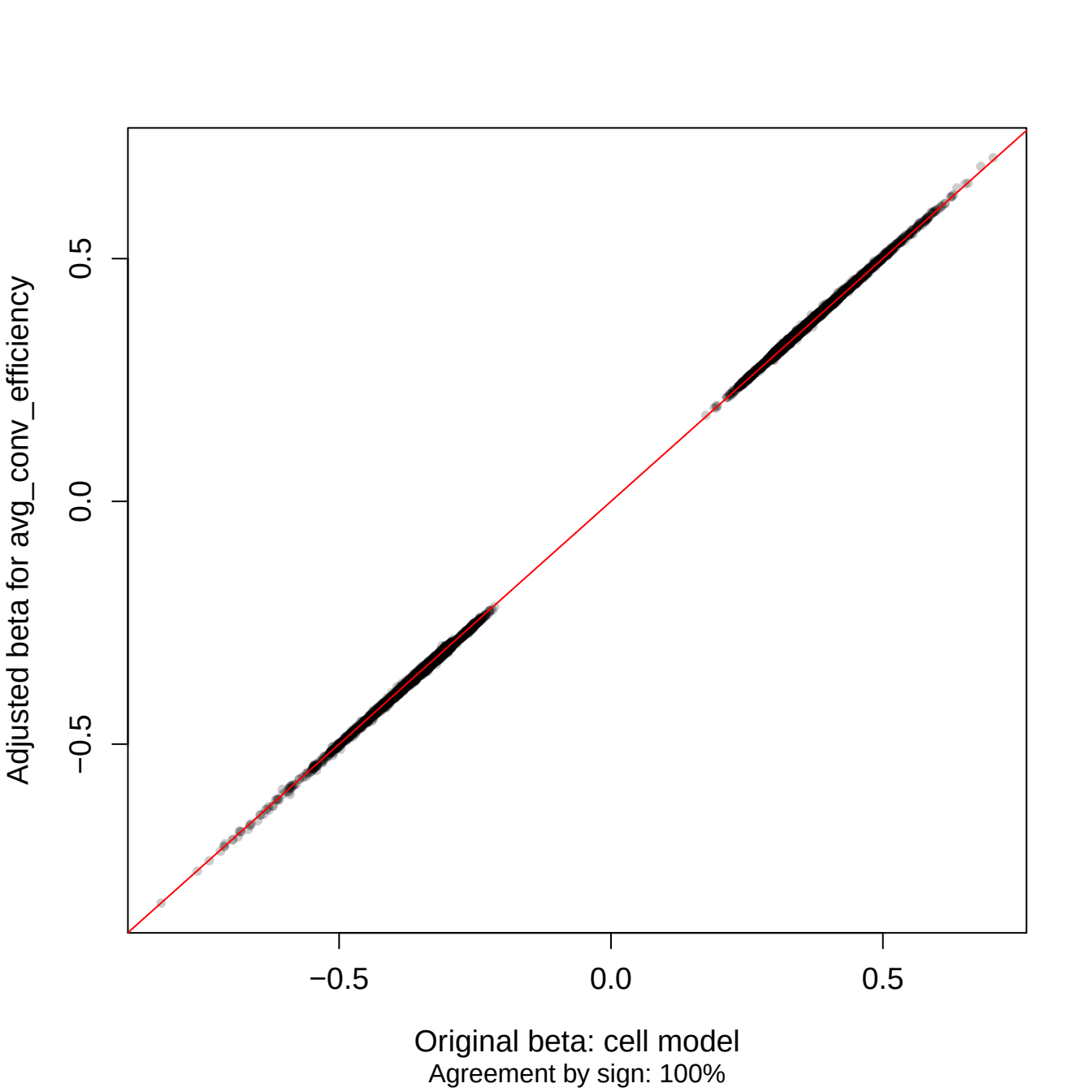

Ratio of betas: total_num_untrimmed_reads adj. / original
1.10
1.05
1.00
0.95
−0.5
0.0
0.5
Original beta: cell model

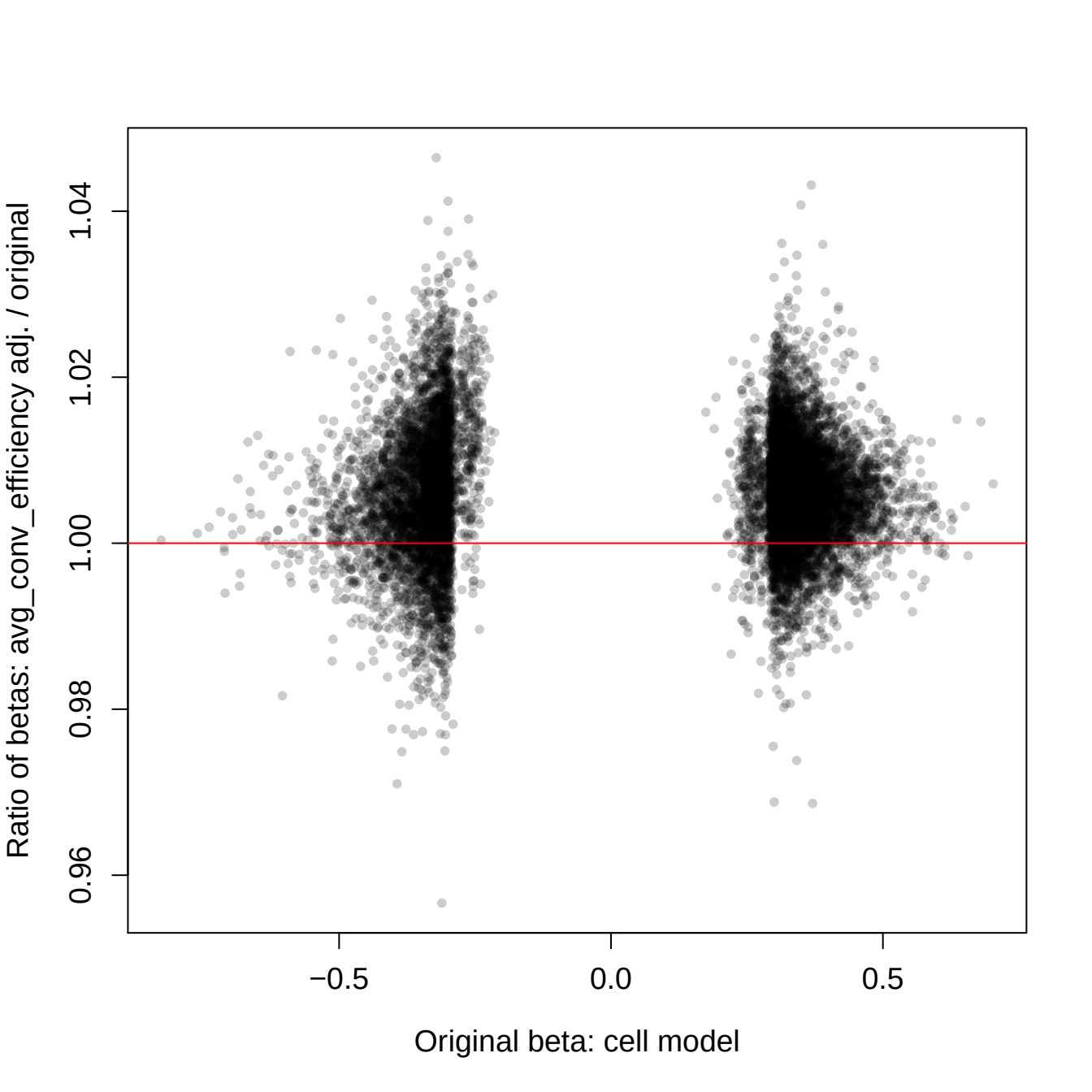

Absolute relative bias in percent for total_num_untrimmed_reads
0
2
4
6
8
10
−0.5
0.0
0.5
Original beta: cell model

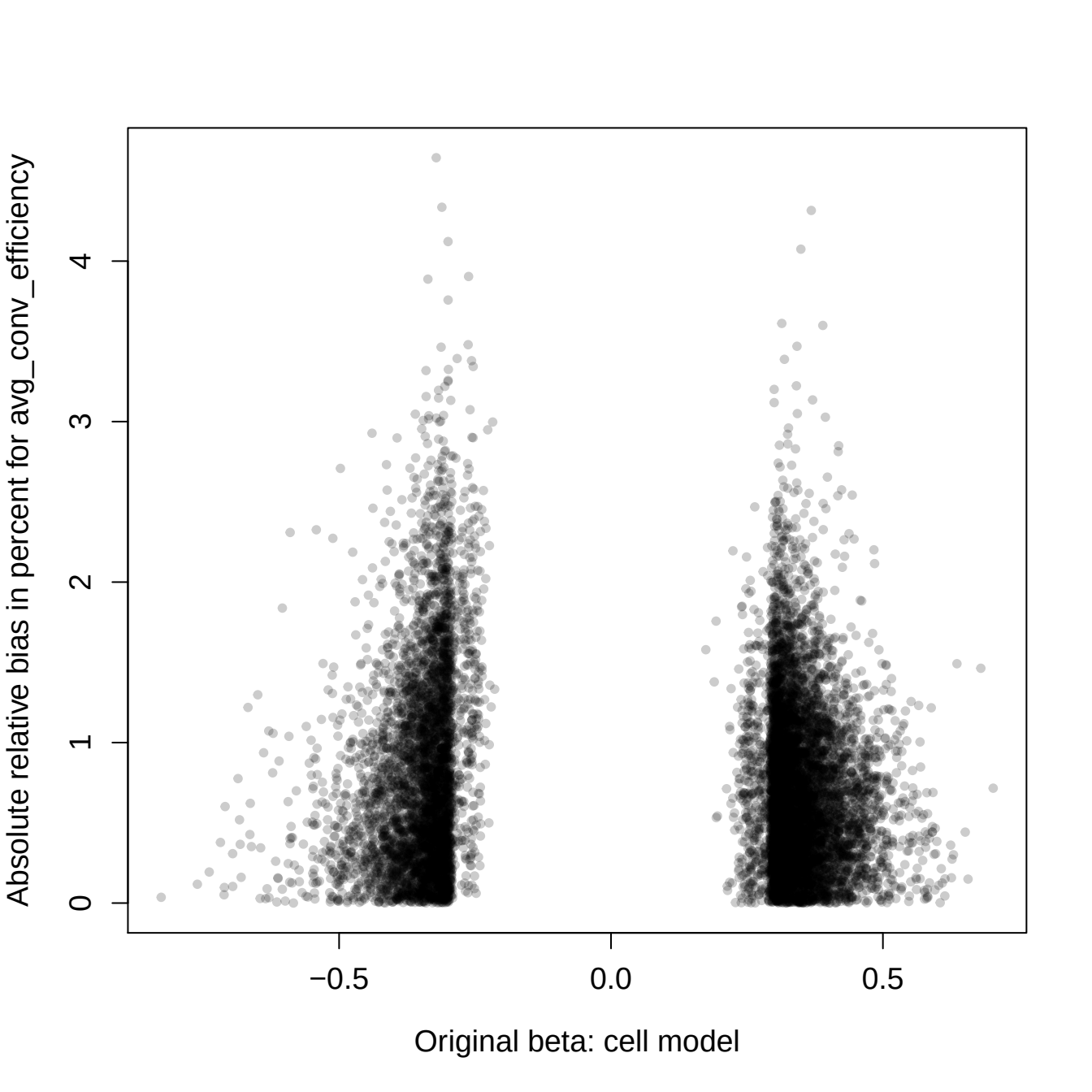

Adjusted beta for ratio_trimmed
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%

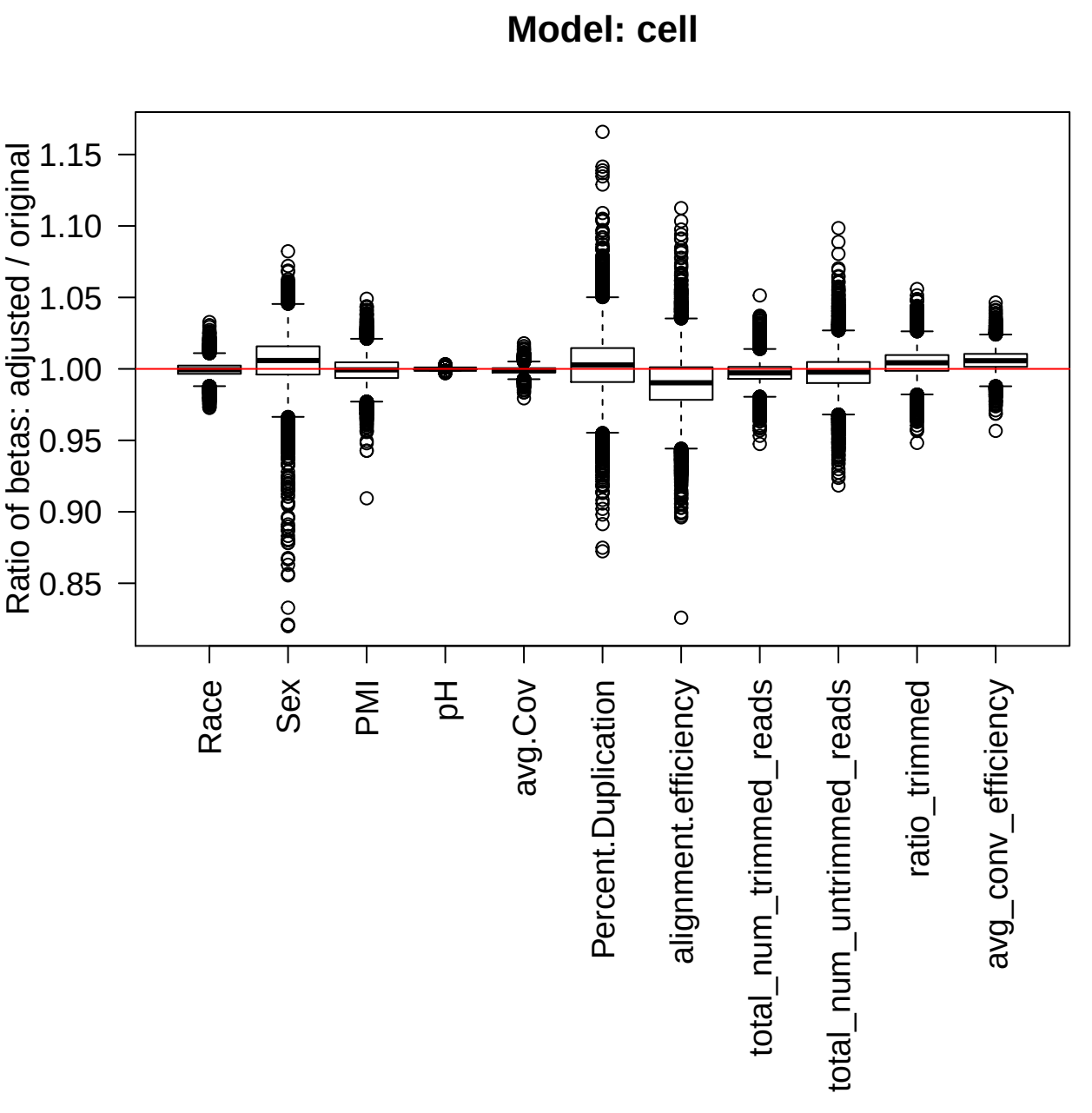

Ratio of betas: ratio_trimmed adj. / original
1.06
1.04
1.02
1.00
0.98
0.96
−0.5
0.0
0.5
Original beta: cell model

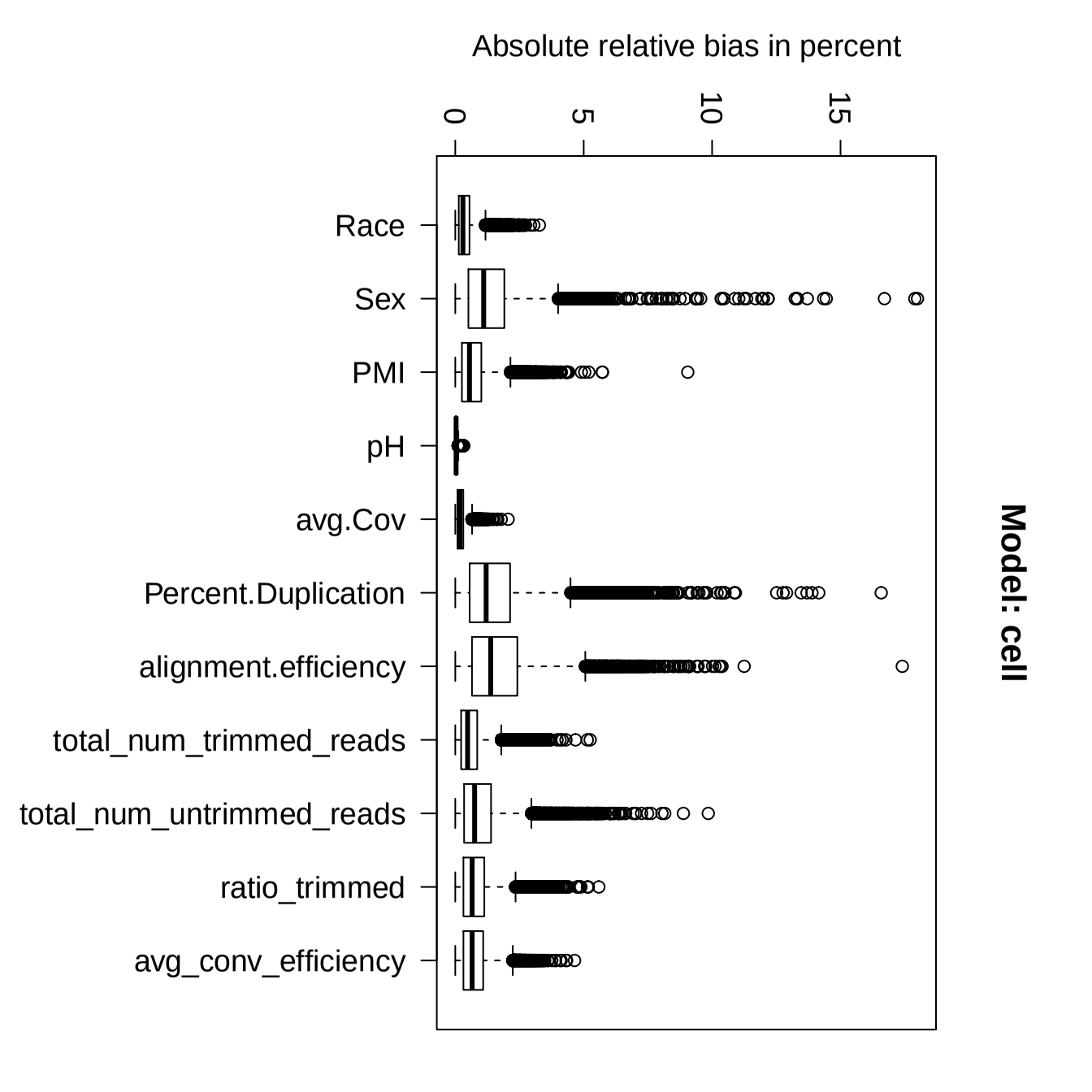

Absolute relative bias in percent for ratio_trimmed
0
1
2
3
4
5
−0.5
0.0
0.5
Original beta: cell model


Adjusted beta for avg_conv_efficiency
0.5
0.0
−0.5
−0.5
0.0
0.5
Original beta: cell model
Agreement by sign: 100%


Ratio of betas: avg_conv_efficiency adj. / original
0.96
0.98
1.00
1.02
1.04
−0.5
0.0
0.5
Original beta: cell model


Absolute relative bias in percent for avg_conv_efficiency
0
1
2
3
4
−0.5
0.0
0.5
Original beta: cell model


Model: cell
Ratio of betas: adjusted / original
1.15
1.10
1.05
1.00
0.95
0.90
0.85
Race
Sex
PMI
pH
avg.Cov
Percent.Duplication
alignment.efficiency
total_num_trimmed_reads
total_num_untrimmed_reads
ratio_trimmed
avg_conv_efficiency


Absolute relative bias in percent
0
5
10
15
Race
Sex
PMI
pH
avg.Cov
Percent.Duplication
alignment.efficiency
total_num_trimmed_reads
total_num_untrimmed_reads
ratio_trimmed
avg_conv_efficiency
Model: cell