Pairwise-bias figures for sequencing centers A1, S1, and S2

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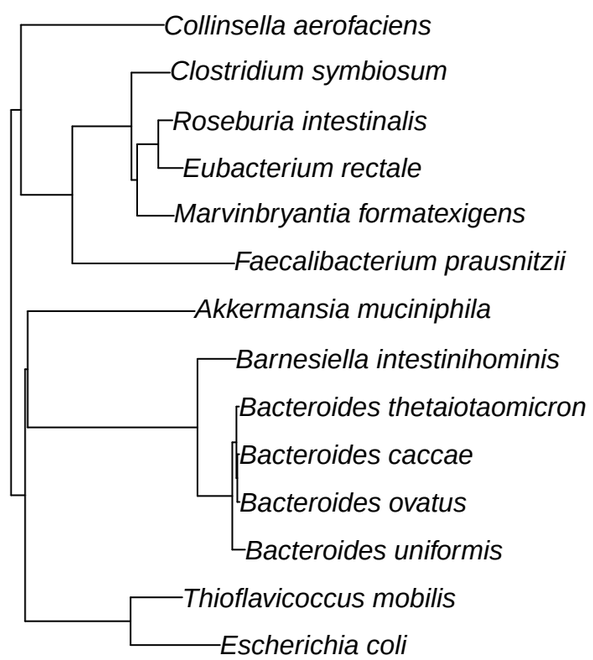
Genome information

Taxa information

taxon	domain	phylum	class	order	family	genus	species
Collinsella aerofaciens	Bacteria	Actinobacteriota	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	Collinsella aerofaciens
Clostridium symbiosum	Bacteria	Firmicutes_A	Clostridia	Lachnospirales	Lachnospiraceae	Clostridium_Q	Clostridium_Q symbiosum
Roseburia intestinalis	Bacteria	Firmicutes_A	Clostridia	Lachnospirales	Lachnospiraceae	Roseburia	Roseburia intestinalis
Eubacterium rectale	Bacteria	Firmicutes_A	Clostridia	Lachnospirales	Lachnospiraceae	Agathobacter	Agathobacter rectalis
Marvinbryantia formatexigens	Bacteria	Firmicutes_A	Clostridia	Lachnospirales	Lachnospiraceae	Marvinbryantia	Marvinbryantia formatexigens
Faecalibacterium prausnitzii	Bacteria	Firmicutes_A	Clostridia	Oscillospirales	Ruminococcaceae	Faecalibacterium	Faecalibacterium prausnitzii_C
Akkermansia muciniphila	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Akkermansiaceae	Akkermansia	Akkermansia muciniphila
Barnesiella intestinihominis	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Barnesiellaceae	Barnesiella	Barnesiella intestinihominis
Bacteroides thetaiotaomicron	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides thetaiotaomicron
Bacteroides caccae	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides caccae
Bacteroides ovatus	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides ovatus
Bacteroides uniformis	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides uniformis
Thioflavicoccus mobilis	Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	Thioflavicoccus	Thioflavicoccus mobilis
Escherichia coli	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia flexneri



T. mobilis, F. prausnitzii, and E. coli are excluded from the bias calculations and figures.

About the figures

There are three "figures", each with 4 sub-figures.

- Figure 1: Bias of (extraction) Protocol 1: Protocol 2
- Figure 2: Bias of (sequencing) Center S1: Center S2
- Figure 3: Bias of (sequencing) Center A1: Center S2

- A. Extraction Batch 1, data points
- B. Extraction Batch 1, mean + bootstrap 95
- C. Extraction Batch 2, data points
- D. Extraction Batch 2, mean + bootstrap 95

Data points are ratios of ratios, representing the (differential) bias of a pair of taxa and a pair of extraction or sequencing protocol; i.e., the efficiency of one taxon relative to another, for one protocol relative to another. Exactly how the data points are generated depends on whether extraction or sequencing bias is being examined, and is described in the figure subtitles.

Figure 1: Extraction bias

Figure 1A. Bias of Protocol 1:Protocol 2 in Batch 1

(row−taxon / col−taxon in aliquot extracted by P. 1) / (row−taxon / col−taxon in aliquot extracted by P. 2), for the same biological specimen

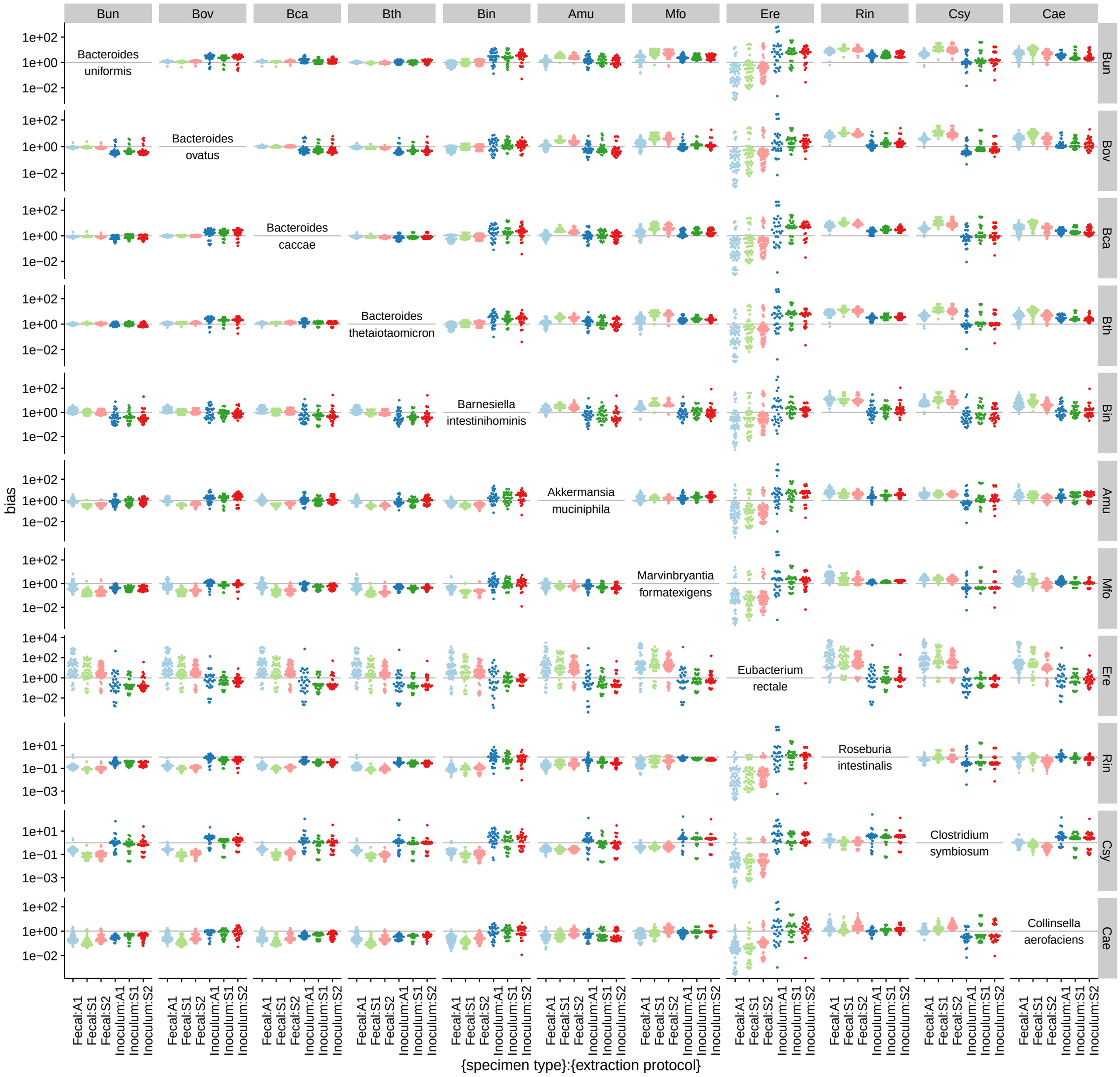


Figure 1B. Bias of Protocol 1:Protocol 2 in Batch 1

(row−taxon / col−taxon in aliquot extracted by P. 1) / (row−taxon / col−taxon in aliquot extracted by P. 2), for the same biological specimen

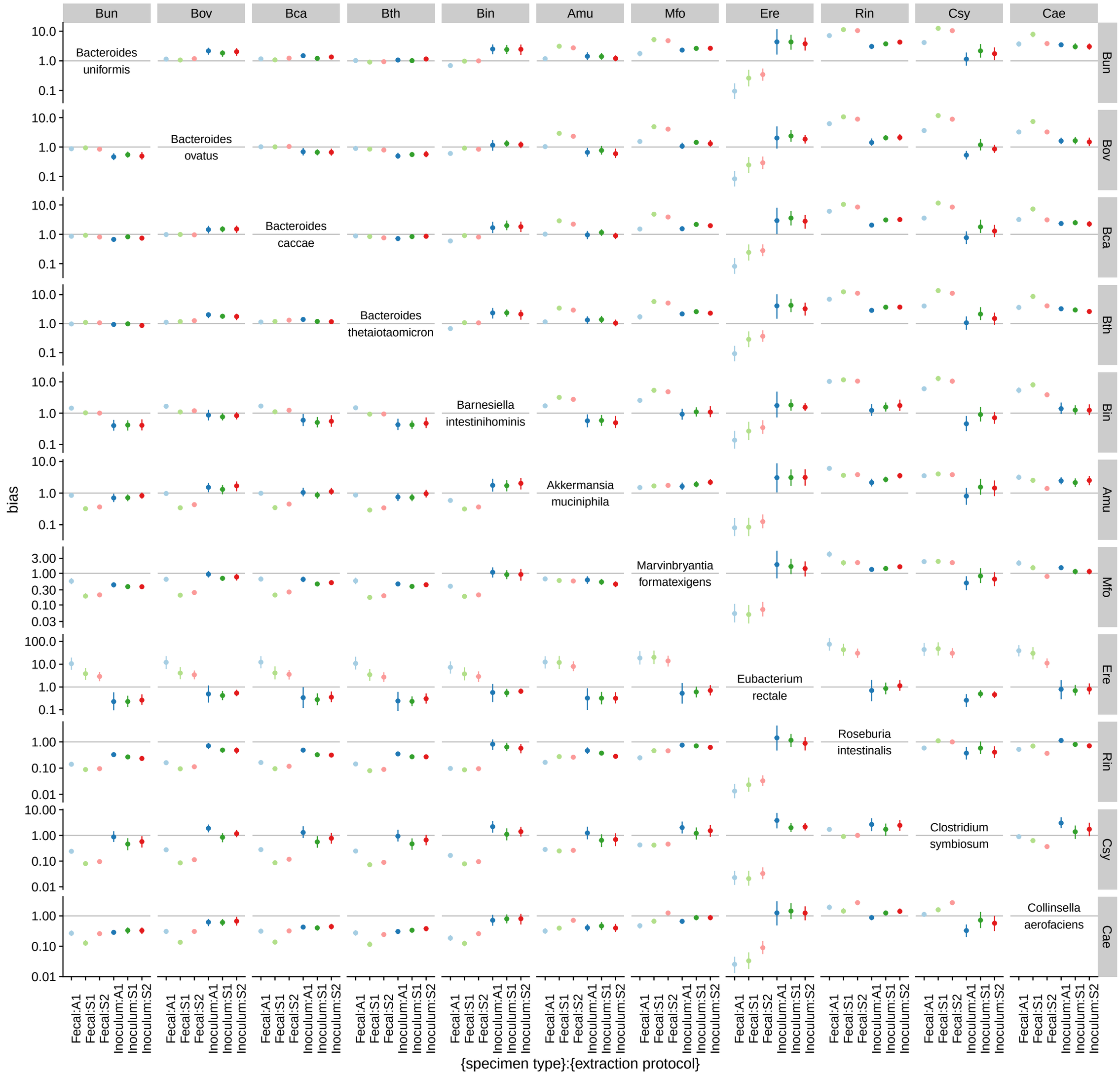


Figure 1C. Bias of Protocol 1:Protocol 2 in Batch 2

(row−taxon / col−taxon in aliquot extracted by P. 1) / (row−taxon / col−taxon in aliquot extracted by P. 2), for the same biological specimen

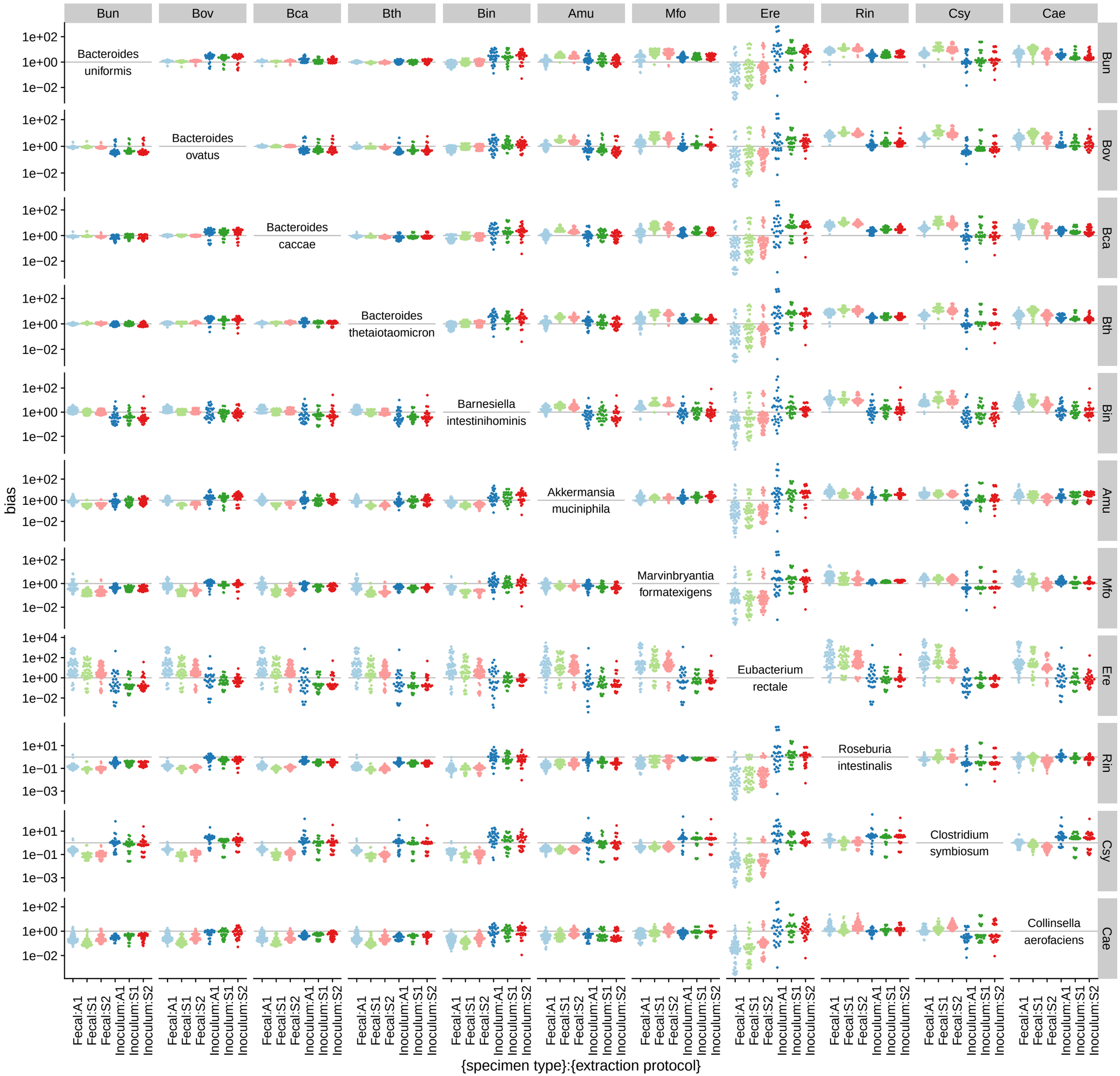


Figure 1D. Bias of Protocol 1:Protocol 2 in Batch 2

(row−taxon / col−taxon in aliquot extracted by P. 1) / (row−taxon / col−taxon in aliquot extracted by P. 2), for the same biological specimen

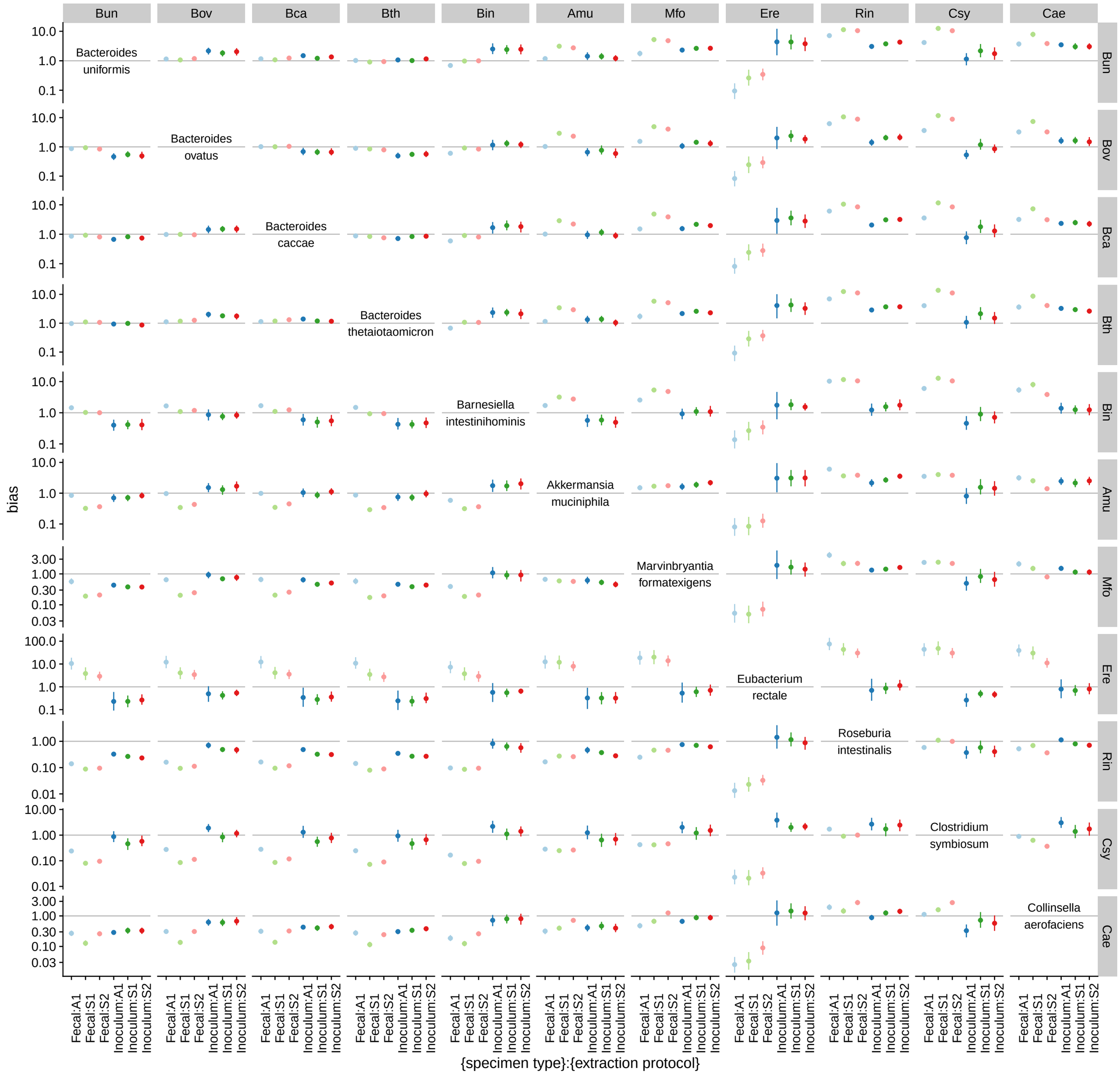


Figure 2: Sequencing bias, S1:S2

Figure 2A. Bias of Center S1:Center S2 in Batch 1

(row−taxon / col−taxon measured by S1) / (row−taxon / col−taxon measured by S2), for the same DNA sample

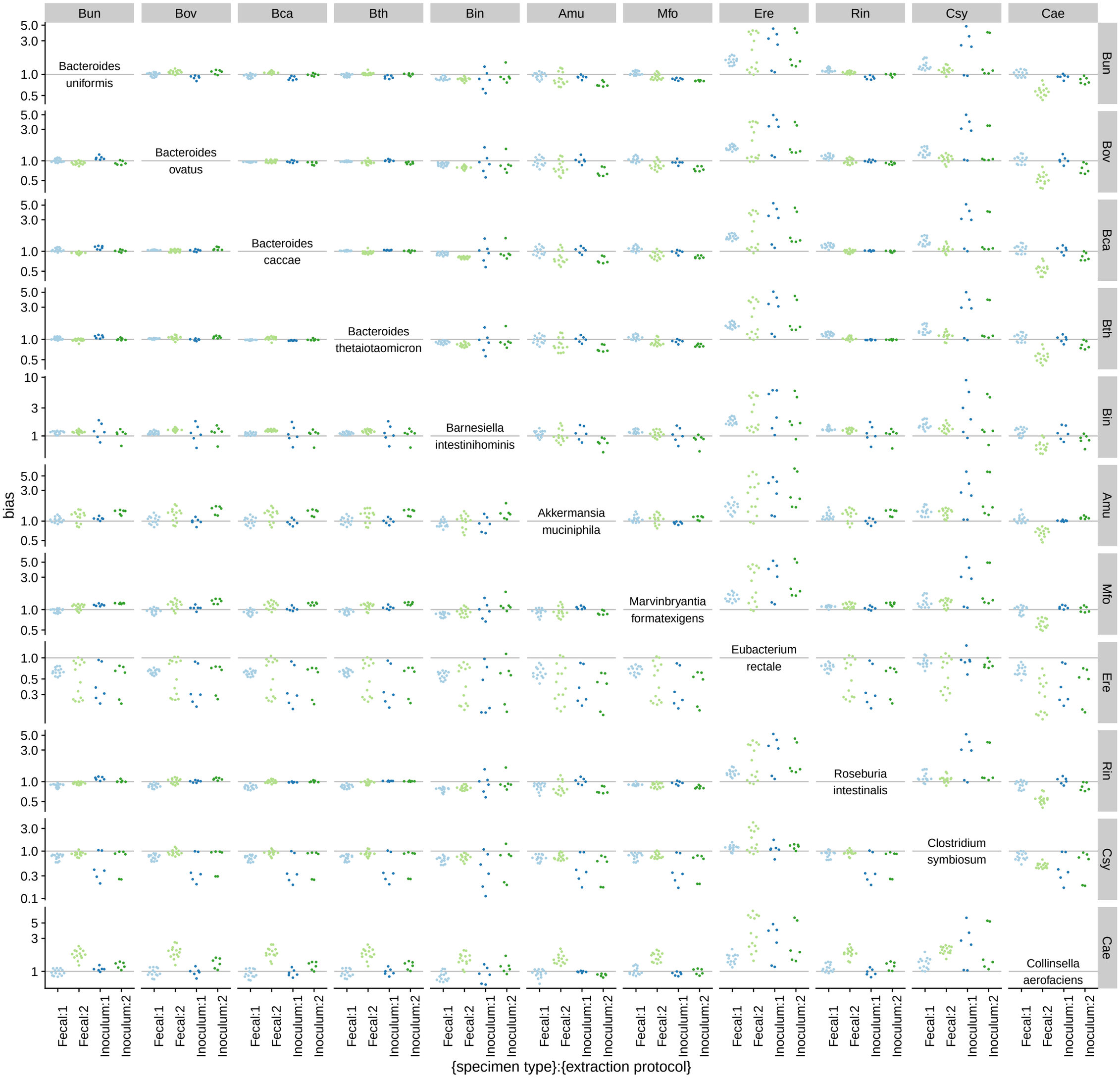


Figure 2B. Bias of Center S1:Center S2 in Batch 1

(row−taxon / col−taxon measured by S1) / (row−taxon / col−taxon measured by S2), for the same DNA sample

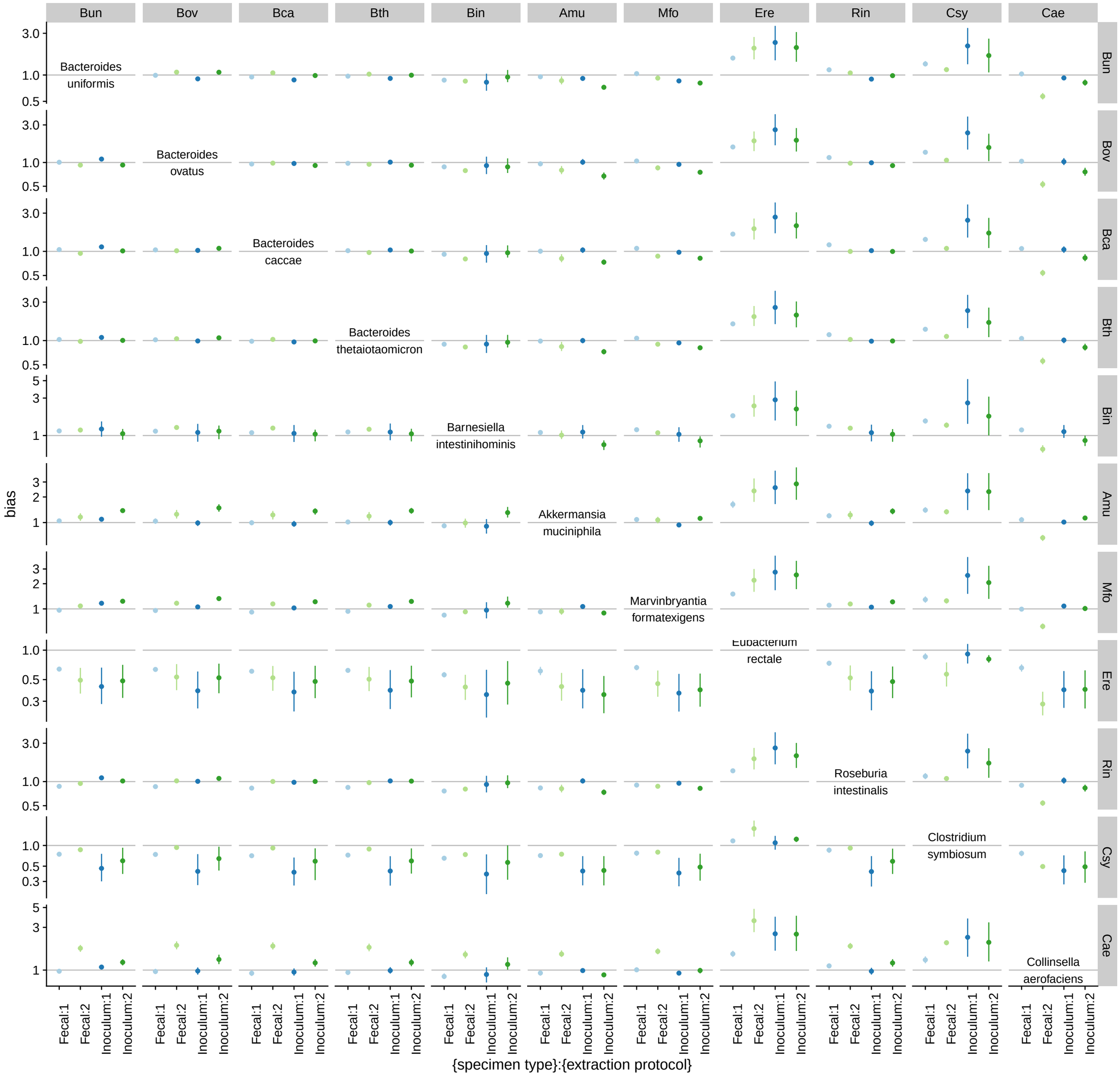


Figure 2C. Bias of Center S1:Center S2 in Batch 2

(row−taxon / col−taxon measured by S1) / (row−taxon / col−taxon measured by S2), for the same DNA sample

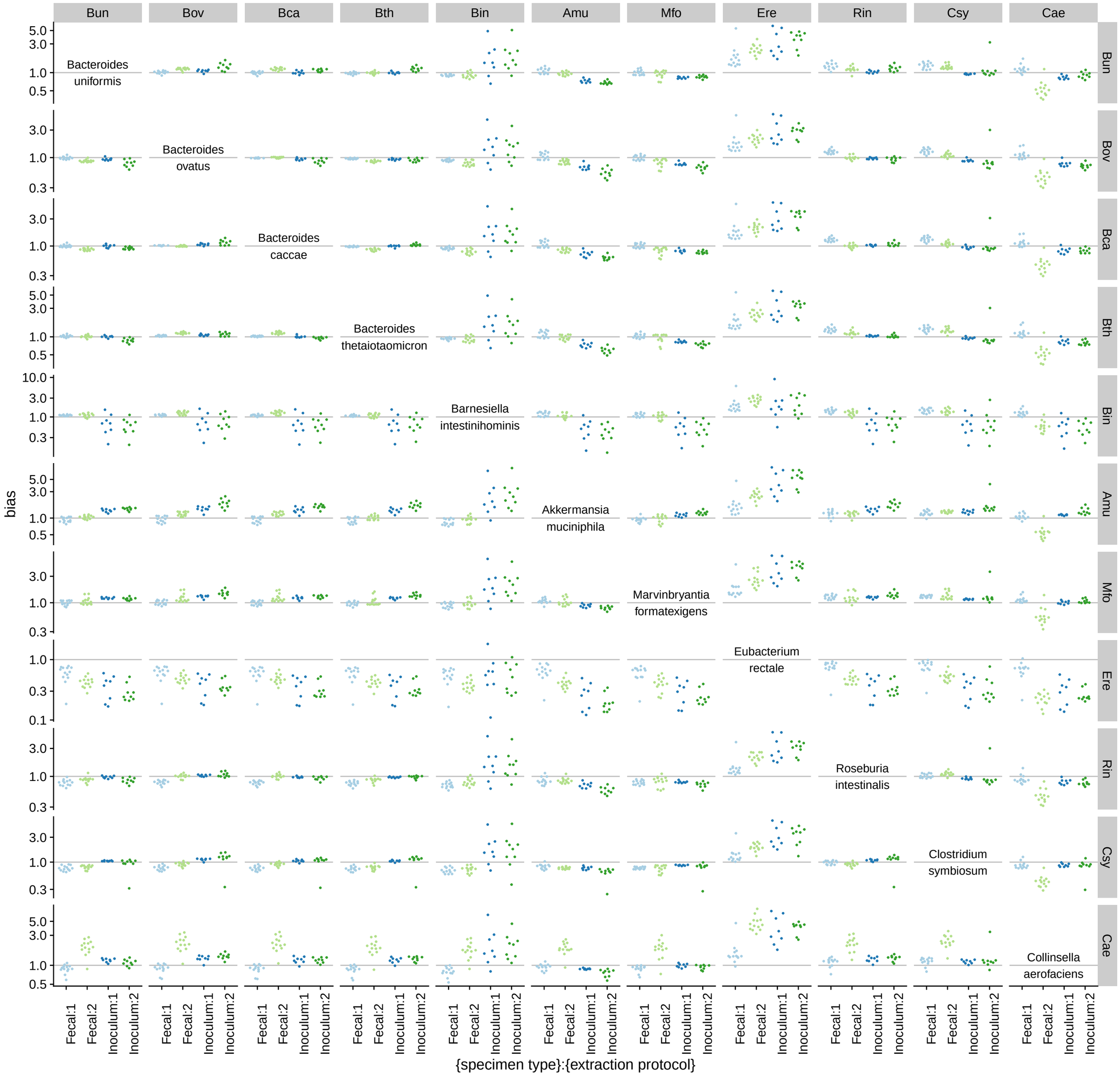


Figure 2D. Bias of Center S1:Center S2 in Batch 2

(row−taxon / col−taxon measured by S1) / (row−taxon / col−taxon measured by S2), for the same DNA sample

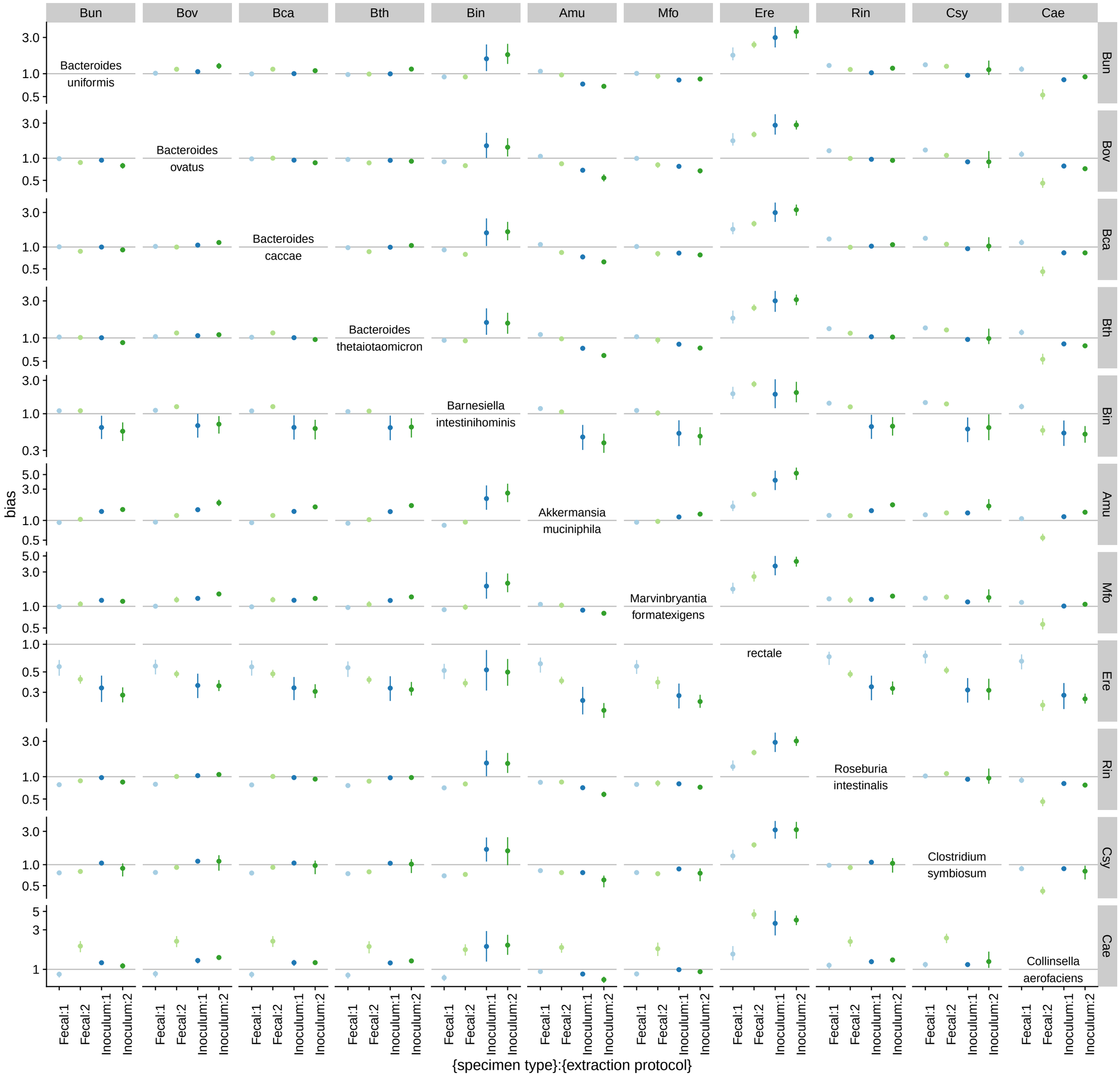


Figure 3: Sequencing bias, A1:S2

Figure 3A. Bias of Center A1:Center S2 in Batch 1

(row−taxon / col−taxon measured by A1) / (row−taxon / col−taxon measured by S2), for the same DNA sample

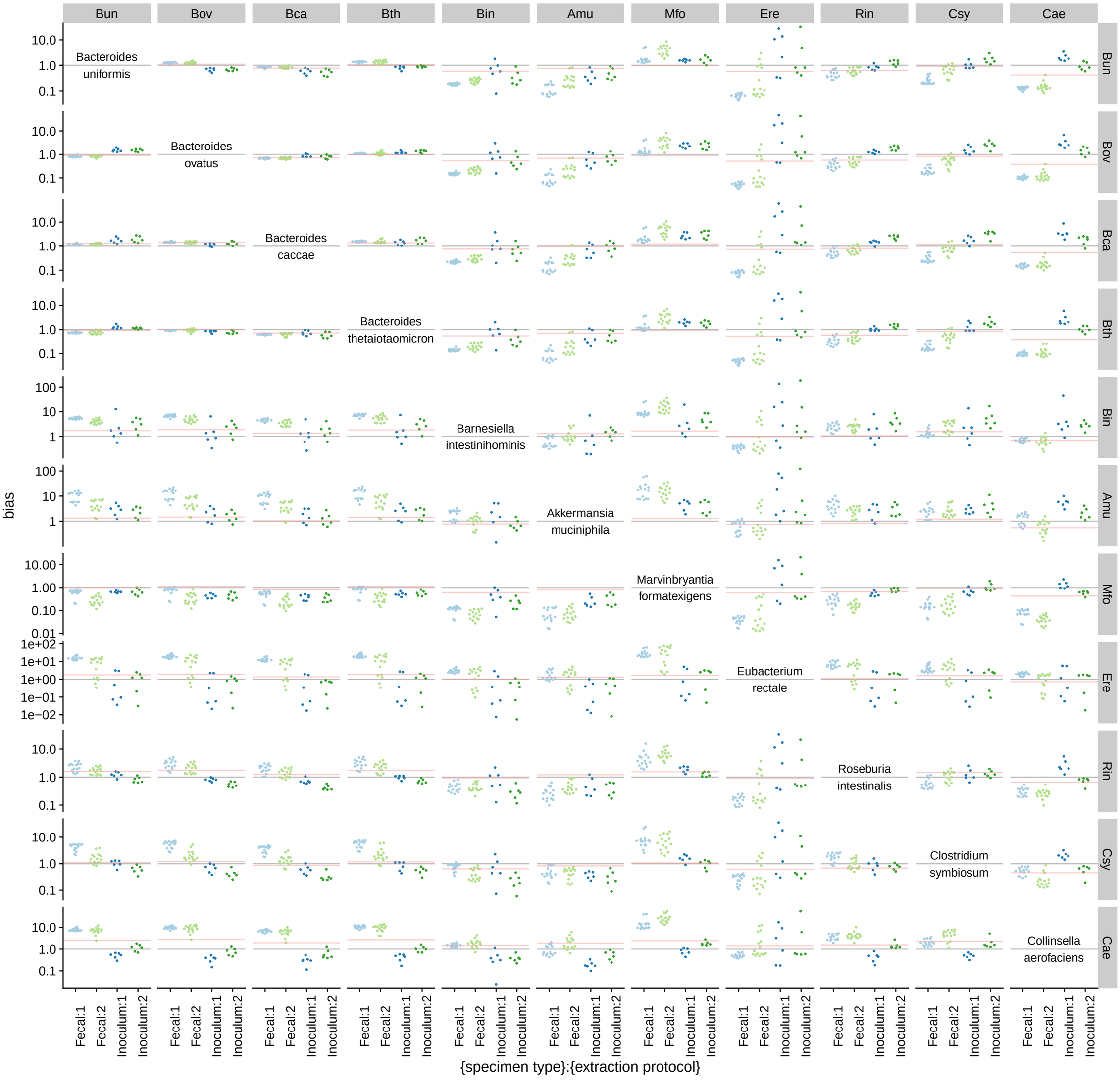


Figure 3B. Bias of Center A1:Center S2 in Batch 1

(row−taxon / col−taxon measured by A1) / (row−taxon / col−taxon measured by S2), for the same DNA sample

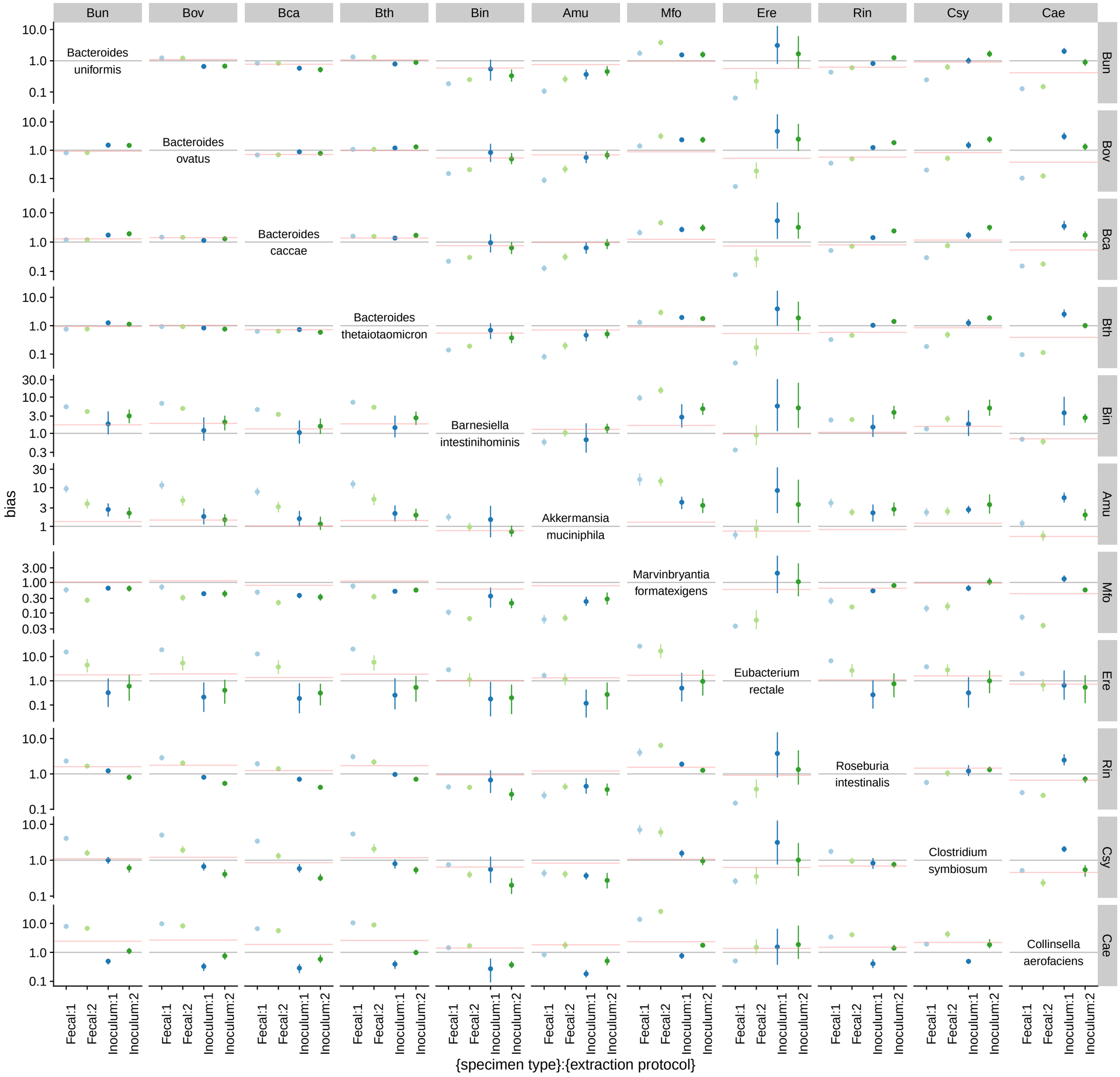


Figure 3C. Bias of Center A1:Center S2 in Batch 2

(row−taxon / col−taxon measured by A1) / (row−taxon / col−taxon measured by S2), for the same DNA sample

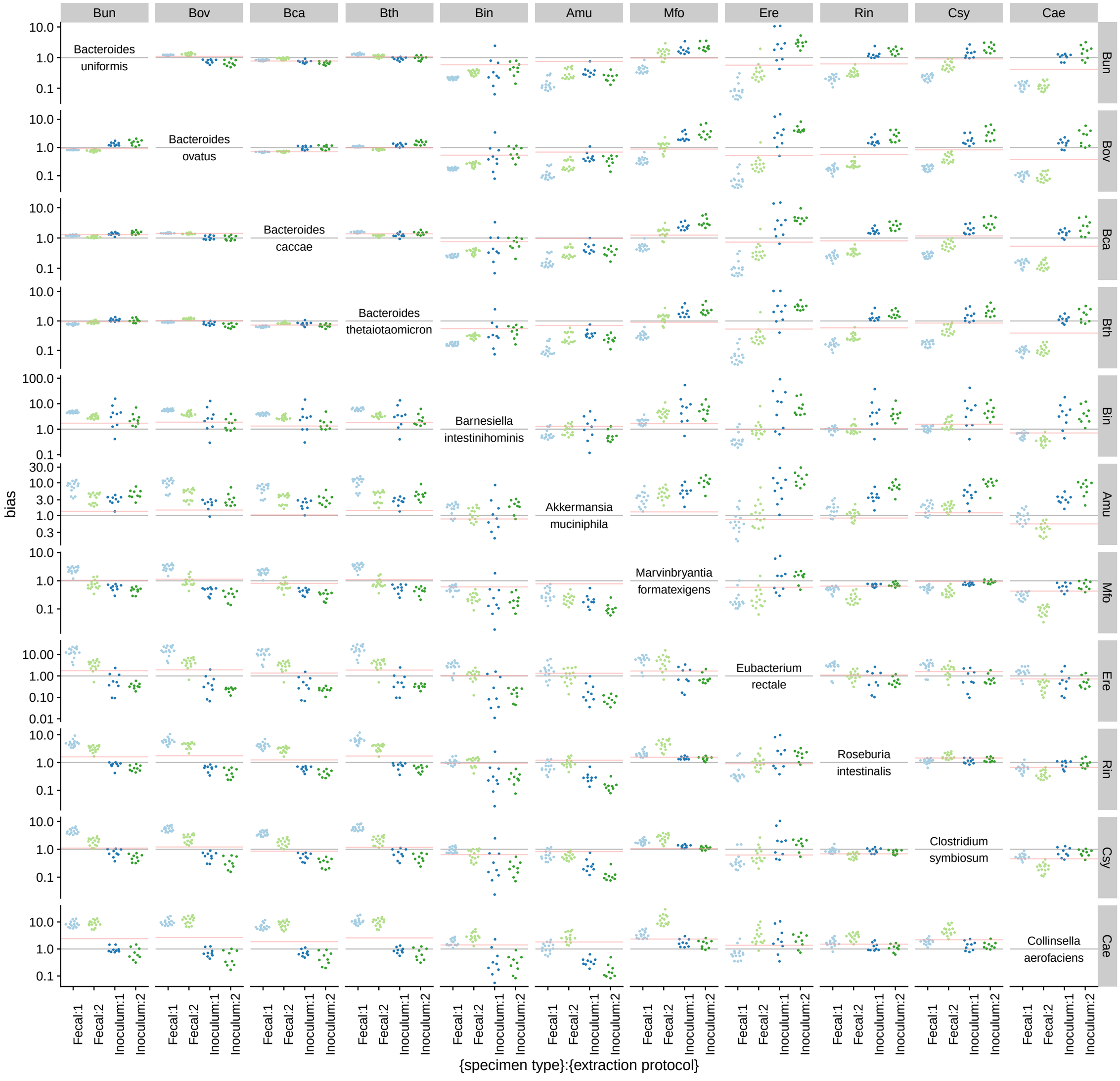
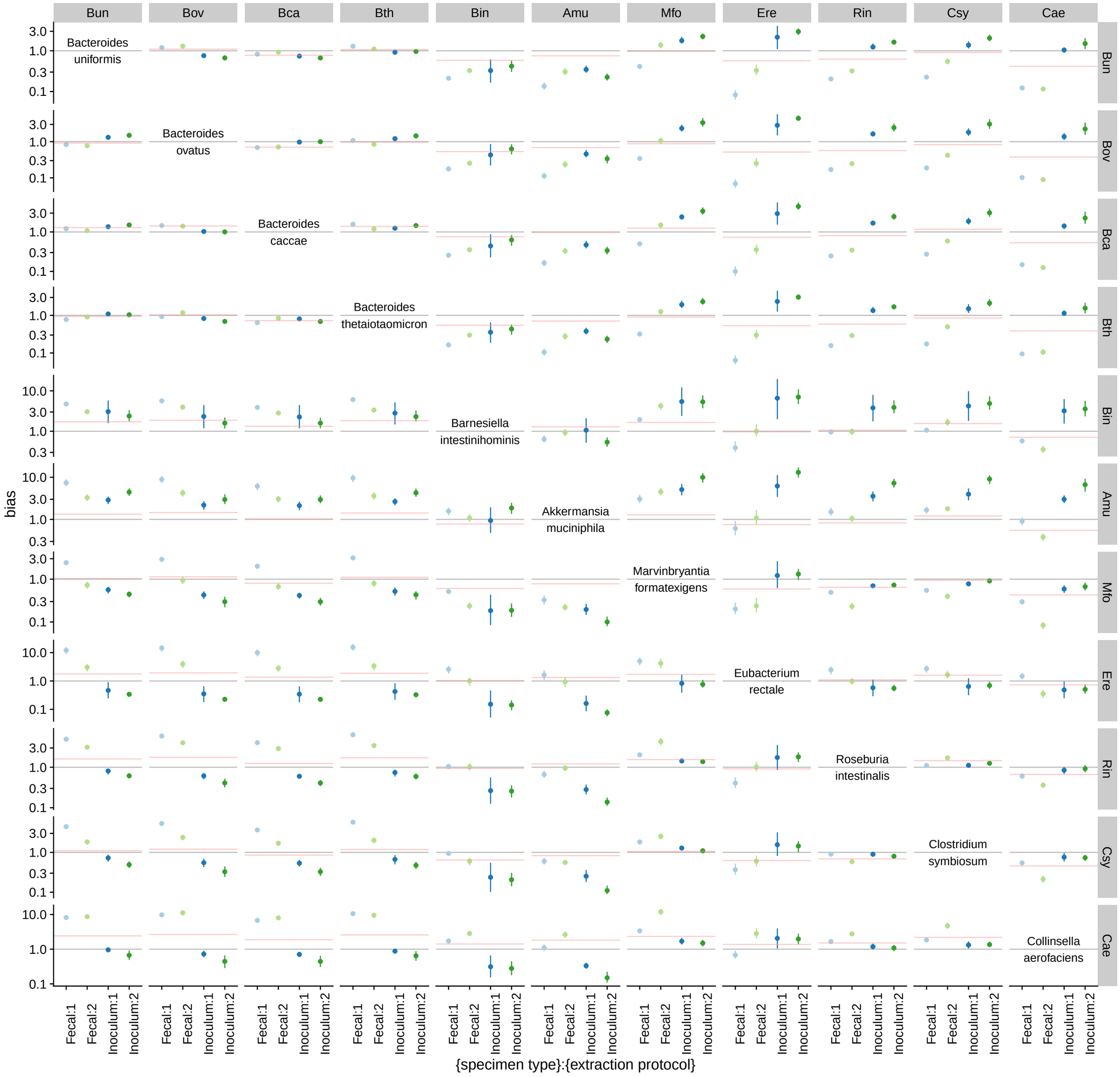


Figure 3D. Bias of Center A1:Center S2 in Batch 2

(row−taxon / col−taxon measured by A1) / (row−taxon / col−taxon measured by S2), for the same DNA sample