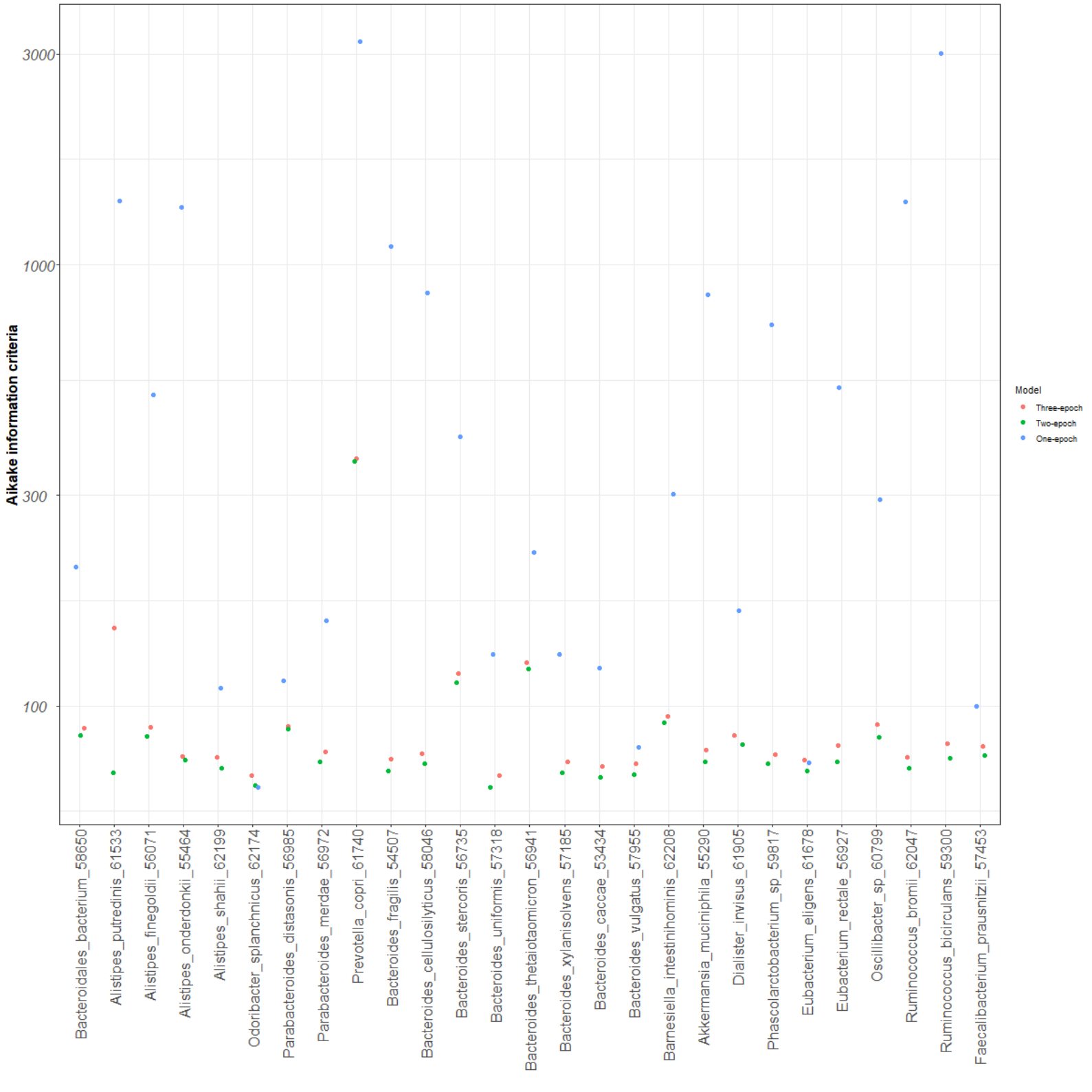
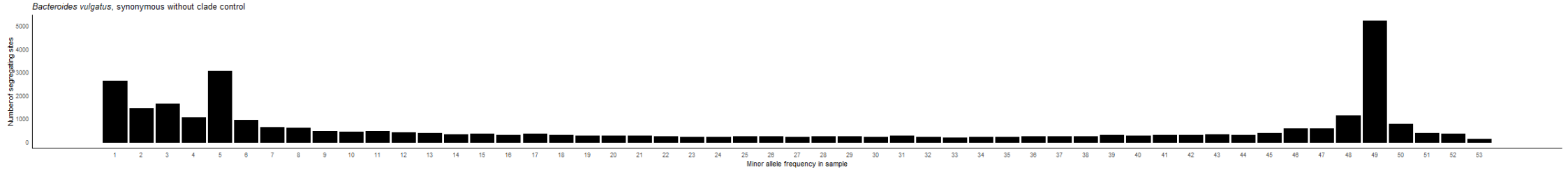
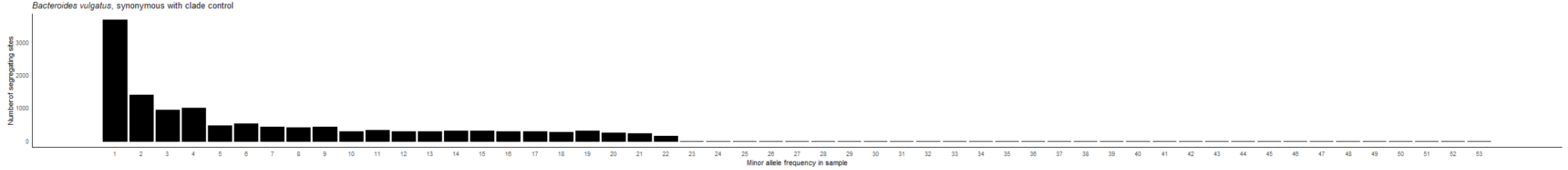
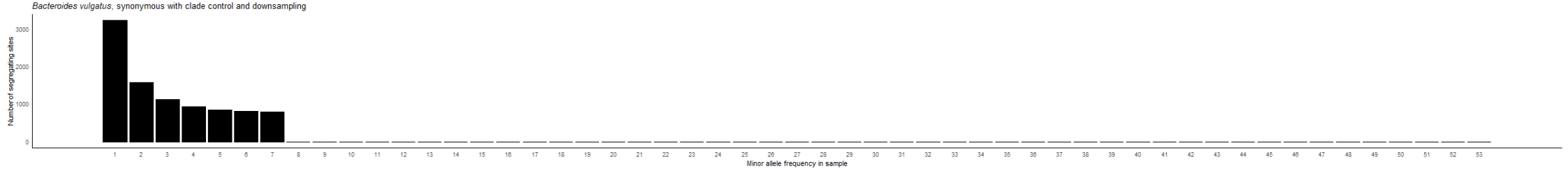
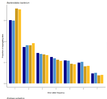

Aikake information criteria
3000
1000
300
100
Model
Three-epoch
Two-epoch
One-epoch
Bacteroidales_bacterium_58650
Alistipes_putredinis_61533
Alistipes_finegoldii_56071
Alistipes_onderdonkii_55464
Alistipes_shahii_62199
Odoribacter_splanchnicus_62174
Parabacteroides_distasonis_56985
Parabacteroides_merdae_56972
Prevotella_copri_61740
Bacteroides_fragilis_54507
Bacteroides_cellulosilyticus_58046
Bacteroides_stercoris_56735
Bacteroides_uniformis_57318
Bacteroides_thetaiotaomicron_56941
Bacteroides_xylanisolvens_57185
Bacteroides_caccae_53434
Bacteroides_vulgatus_57955
Barnesiella_intestinihominis_62208
Akkermansia_muciniphila_55290
Dialister_invisus_61905
Phascolarctobacterium_sp_59817
Eubacterium_eligens_61678
Eubacterium_rectale_56927
Oscillibacter_sp_60799
Ruminococcus_bromii_62047
Ruminococcus_bicirculans_59300
Faecalibacterium_prausnitzii_57453

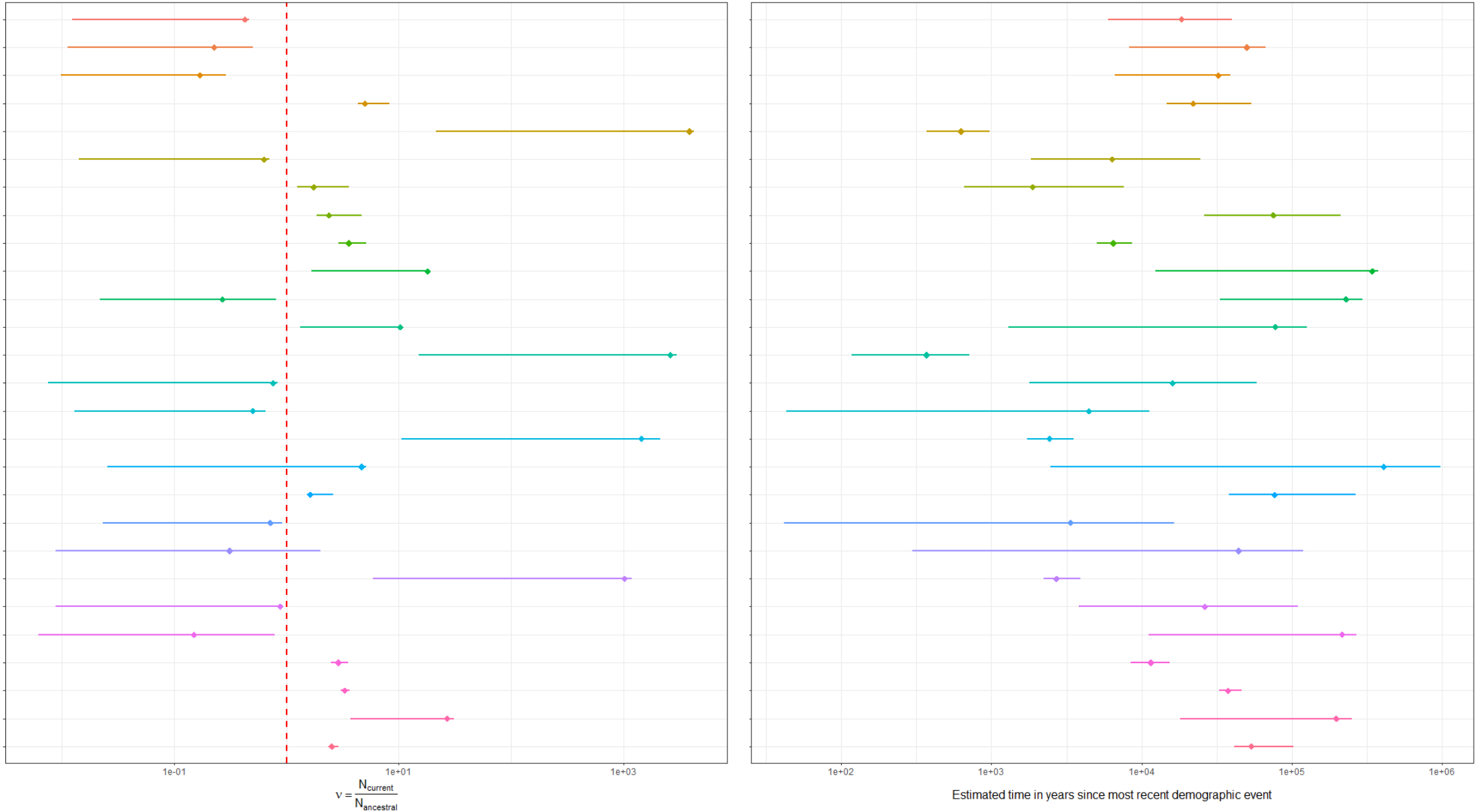

Bacteroides vulgatus, synonymous without clade control
Number of segregating sites
Minor allele frequency in sample


Bacteroides vulgatus, synonymous with clade control
Number of segregating sites
Minor allele frequency in sample


Bacteroides vulgatus, synonymous with clade control and downsampling
Number of segregating sites
Minor allele frequency in sample

Bacillus cereus


Bacillus cereus
Mean ABB Stepness
Bacillus cereus
Bacillus cereus
Bacillus cereus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1e+01
1e+03
$\nu = \frac{N_{current}}{N_{ancestral}}$
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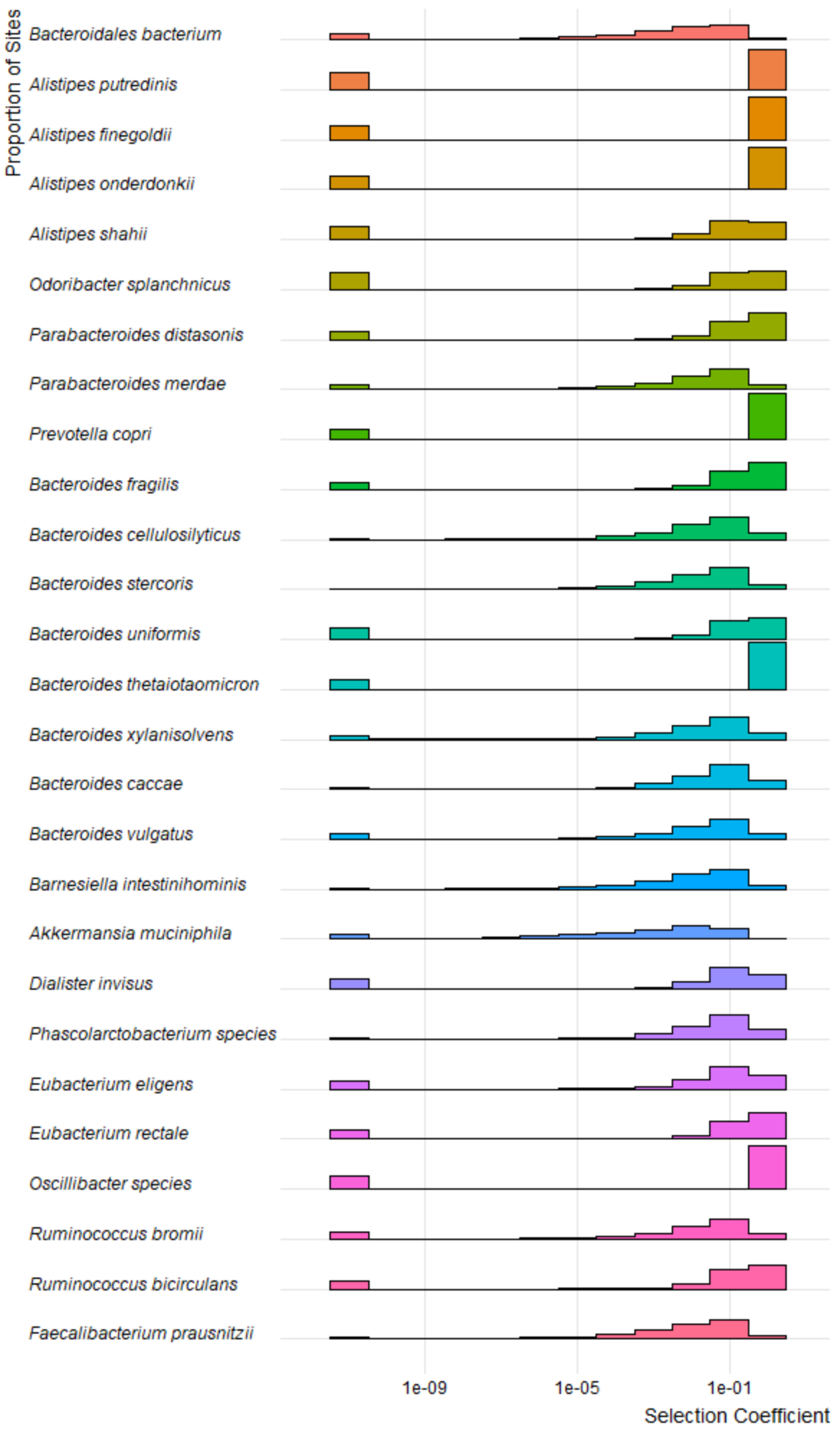
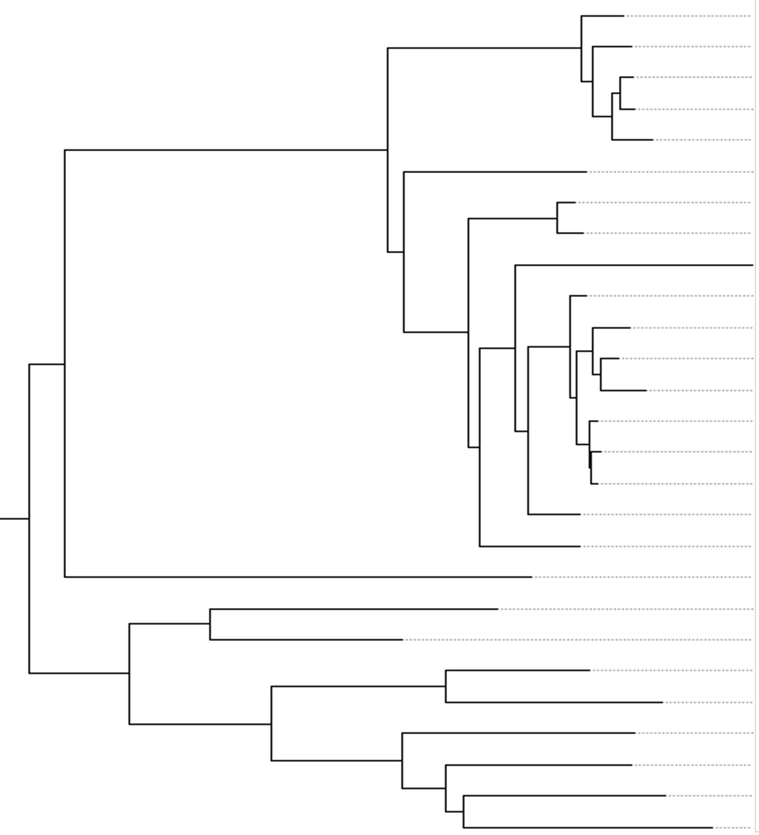
1e+03
1e+04
1e+05
1e+06
Estimated time in years since most recent demographic event

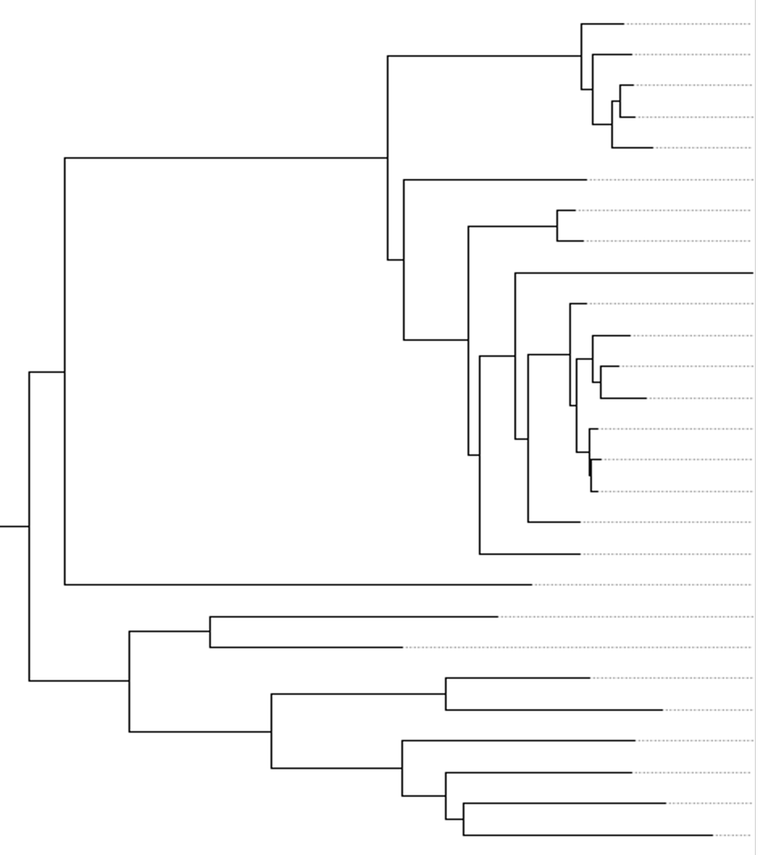

Proportion of Sites
Bacteroidales bacterium
Alistipes putredinis
Alistipes finegoldii
Alistipes onderdonkii
Alistipes shahii
Odoribacter splanchnicus
Parabacteroides distasonis
Parabacteroides merdae
Prevotella copri
Bacteroides fragilis
Bacteroides cellulosilyticus
Bacteroides stercoris
Bacteroides uniformis
Bacteroides thetaiotaomicron
Bacteroides xylanisolvens
Bacteroides caccae
Bacteroides vulgatus
Barnesiella intestinihominis
Akkermansia muciniphila
Dialister invisus
Phascolarctobacterium species
Eubacterium eligens
Eubacterium rectale
Oscillibacter species
Ruminococcus bromii
Ruminococcus bicirculans
Faecalibacterium prausnitzii
1e-09
1e-05
1e-01
Selection Coefficient

A

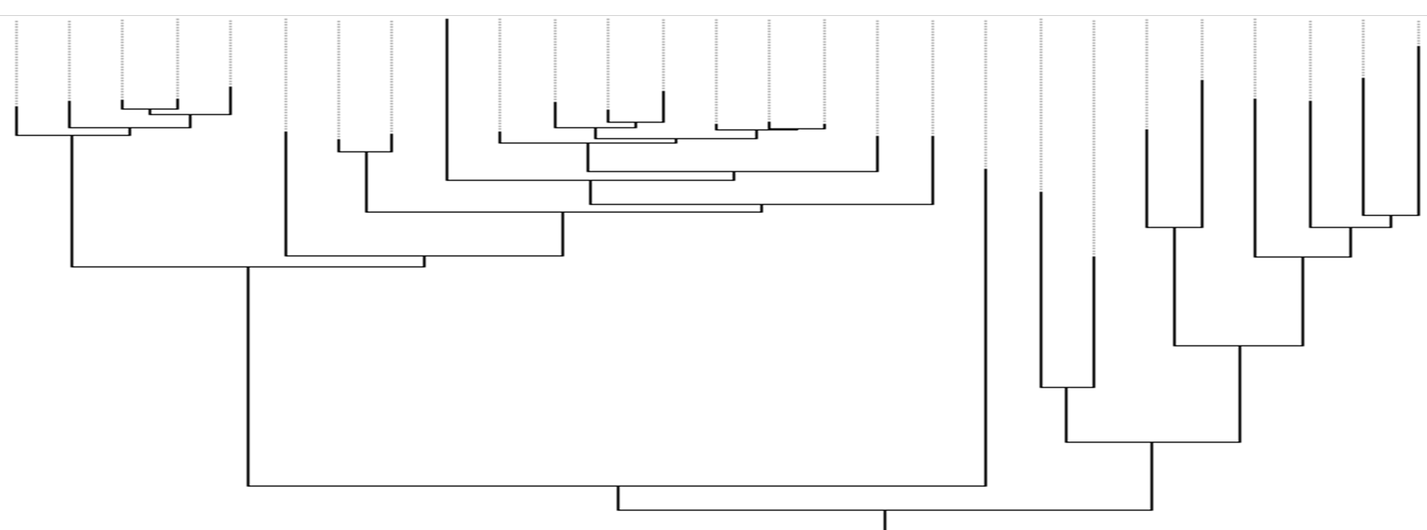


	Bacteroidales bacterium	Alistipes putredinis	Alistipes finegoldii	Alistipes onderdonkii	Alistipes shahii	Odoribacter splanchnicus	Parabacteroides distasonis	Parabacteroides merdae	Prevotella copri	Bacteroides fragilis	Bacteroides cellulosilyticus	Bacteroides stercoris	Bacteroides uniformis	Bacteroides thetaiotaomicron	Bacteroides xylanisolvens	Bacteroides caccae	Bacteroides vulgatus	Barnesiella intestinihominis	Akkermansia muciniphila	Dialister invisus	Phascolarctobacterium species	Eubacterium eligens	Eubacterium rectale	Oscillibacter species	Ruminococcus bromii	Ruminococcus bicirculans	Faecalibacterium prausnitzii
Bacteroidales bacterium	0.0																										
Alistipes putredinis	-7.4	0.0																									
Alistipes finegoldii	-14.7	-0.2	0.0																								
Alistipes onderdonkii	-57.0	-15.1	-16.8	0.0																							
Alistipes shahii	-0.0	-8.1	-16.4	-62.6	0.0																						
Odoribacter splanchnicus	-5.3	-0.4	-1.5	-24.0	-5.9	0.0																					
Parabacteroides distasonis	-43.7	-69.4	-129.2	-240.5	-46.5	-75.4	0.0																				
Parabacteroides merdae	-77.0	-102.6	-164.4	-267.4	-80.6	-110.6	-12.9	0.0																			
Prevotella copri	-5.2	-1.3	-4.2	-40.9	-6.0	-0.2	-113.4	-147.9	0.0																		
Bacteroides fragilis	-130.8	-149.4	-263.2	-411.2	-138.7	-171.4	-35.1	-1.6	-259.9	0.0																	
Bacteroides cellulosilyticus	-80.6	-104.9	-186.4	-312.0	-85.5	-117.2	-9.2	-1.1	-174.4	-7.7	0.0																
Bacteroides stercoris	-35.5	-60.9	-114.3	-220.1	-37.8	-65.4	-0.6	-18.0	-97.6	-45.3	-14.6	0.0															
Bacteroides uniformis	-0.3	-4.2	-8.1	-38.9	-0.3	-2.5	-39.2	-69.7	-1.9	-109.5	-69.6	-32.5	0.0														
Bacteroides thetaiotaomicron	-24.8	-49.2	-91.4	-185.6	-26.3	-51.2	-3.0	-24.1	-73.6	-54.5	-21.2	-0.9	-23.8	0.0													
Bacteroides xylanisolvens	-17.6	-38.8	-63.7	-130.7	-18.3	-38.1	-2.1	-18.4	-47.2	-37.6	-14.7	-0.7	-18.2	-0.0	0.0												
Bacteroides caccae	-74.0	-99.2	-169.8	-283.9	-78.1	-108.9	-8.4	-0.9	-155.0	-6.5	-0.0	-13.1	-65.3	-19.1	-13.8	0.0											
Bacteroides vulgatus	-3.8	-18.6	-32.3	-84.7	-3.8	-16.4	-16.2	-42.2	-19.0	-74.3	-40.0	-11.6	-5.1	-6.5	-4.7	-37.2	0.0										
Barnesiella intestinihominis	-35.3	-60.8	-115.7	-223.9	-37.7	-65.5	-0.9	-19.3	-99.3	-48.6	-16.1	-0.0	-32.2	-0.8	-0.6	-14.4	-11.3	0.0									
Akkermansia muciniphila	-2.3	-2.8	-7.2	-46.3	-2.7	-1.2	-88.4	-124.4	-0.6	-218.4	-142.8	-75.0	-0.6	-55.5	-36.5	-127.8	-12.9	-75.9	0.0								
Dialister invisus	-8.5	-28.7	-56.4	-136.3	-8.9	-27.9	-19.4	-50.5	-39.0	-102.6	-52.4	-13.1	-9.6	-6.4	-3.9	-46.7	-0.3	-12.8	-26.7	0.0							
Phascolarctobacterium species	-82.2	-107.7	-166.2	-263.4	-85.6	-115.2	-17.3	-0.4	-149.0	-0.2	-3.0	-22.8	-75.0	-29.1	-22.8	-2.7	-47.4	-24.2	-127.2	-55.8	0.0						
Eubacterium eligens	-0.0	-7.9	-15.1	-56.4	-0.0	-5.7	-38.1	-70.1	-5.7	-117.4	-71.7	-30.7	-0.4	-21.4	-15.5	-66.3	-3.0	-30.5	-2.7	-6.9	-75.4	0.0					
Eubacterium rectale	-3.9	-20.9	-41.4	-111.4	-4.0	-19.2	-29.1	-62.1	-25.3	-120.3	-66.1	-21.4	-5.2	-12.4	-7.9	-59.1	-0.1	-21.2	-16.2	-1.2	-67.2	-3.0	0.0				
Oscillibacter species	-13.6	-0.0	-0.1	-20.7	-15.3	-1.0	-134.5	-168.9	-3.3	-277.4	-195.0	-118.7	-7.1	-93.9	-63.6	-176.1	-31.3	-120.4	-6.1	-57.0	-169.8	-14.0	-41.2	0.0			
Ruminococcus bromii	-0.5	-5.1	-11.4	-54.1	-0.6	-3.1	-63.7	-99.4	-2.7	-171.0	-109.1	-53.0	-0.0	-38.3	-26.1	-98.9	-7.5	-53.2	-0.7	-16.0	-103.7	-0.7	-8.7	-10.2	0.0		
Ruminococcus bicirculans	-3.0	-19.8	-41.4	-115.8	-3.1	-18.1	-38.5	-73.7	-24.9	-147.3	-82.6	-29.1	-4.3	-17.3	-10.6	-72.6	-0.4	-29.1	-15.2	-2.5	-78.3	-2.2	-0.2	-41.4	-7.6	0.0	
Faecalibacterium prausnitzii	-10.7	-30.9	-56.1	-128.4	-11.2	-30.0	-10.8	-36.7	-39.3	-72.6	-34.9	-6.6	-11.7	-2.6	-1.7	-31.8	-1.1	-6.3	-28.2	-0.4	-42.0	-9.0	-2.7	-56.2	-18.2	-4.4	0.0

B



	Bacteroidales bacterium	Alistipes putredinis	Alistipes finegoldii	Alistipes onderdonkii	Alistipes shahii	Odoribacter splanchnicus	Parabacteroides distasonis	Parabacteroides merdae	Prevotella copri	Bacteroides fragilis	Bacteroides cellulosilyticus	Bacteroides stercoris	Bacteroides uniformis	Bacteroides thetaiotaomicron	Bacteroides xylanisolvens	Bacteroides caccae	Bacteroides vulgatus	Barnesiella intestinihominis	Akkermansia muciniphila	Dialister invisus	Phascolarctobacterium species	Eubacterium eligens	Eubacterium rectale	Oscillibacter species	Ruminococcus bromii	Ruminococcus bicirculans	Faecalibacterium prausnitzii
Bacteroidales bacterium	0.0																										
Alistipes putredinis	-33.9	0.0																									
Alistipes finegoldii	-17.1	-6.7	0.0																								
Alistipes onderdonkii	-30.8	-0.2	-7.3	0.0																							
Alistipes shahii	-4.1	-35.0	-11.8	-32.4	0.0																						
Odoribacter splanchnicus	-4.4	-21.5	-12.1	-17.1	-3.6	0.0																					
Parabacteroides distasonis	-0.7	-72.8	-28.5	-86.5	-5.3	-5.7	0.0																				
Parabacteroides merdae	-3.9	-30.0	-14.5	-25.7	-1.3	-3.3	-23.8	0.0																			
Prevotella copri	-10.3	-37.1	-12.6	-34.4	-0.1	-4.0	-34.1	-12.7	0.0																		
Bacteroides fragilis	-15.7	-127.9	-74.9	-166.7	-18.0	-29.8	-44.3	-31.0	-75.7	0.0																	
Bacteroides cellulosilyticus	-35.6	-142.4	-90.1	-175.0	-37.6	-49.3	-21.7	-30.2	-90.9	-5.6	0.0																
Bacteroides stercoris	-26.2	-148.5	-96.2	-190.5	-27.6	-43.3	-11.8	-13.8	-96.9	-6.9	-8.3	0.0															
Bacteroides uniformis	-0.8	-41.7	-16.4	-39.2	-2.4	-2.1	-2.2	-2.4	-4.7	-15.7	-36.1	-23.9	0.0														
Bacteroides thetaiotaomicron	-7.1	-30.9	-12.1	-26.9	-3.6	-1.2	-75.6	-8.6	-5.7	-80.8	-87.8	-66.0	-8.1	0.0													
Bacteroides xylanisolvens	-1.9	-67.1	-20.6	-61.5	-8.3	-4.5	-6.2	-3.9	-15.8	-18.6	-17.1	-6.4	-1.7	-30.0	0.0												
Bacteroides caccae	-16.3	-105.5	-56.1	-126.0	-19.1	-25.6	-15.3	-30.0	-58.2	-7.0	-0.1	-4.7	-17.4	-85.7	-16.1	0.0											
Bacteroides vulgatus	-0.8	-59.6	-20.0	-57.9	-6.7	-3.2	-4.4	-4.8	-13.2	-8.4	-28.7	-11.0	-0.8	-18.2	-0.5	-16.4	0.0										
Barnesiella intestinihominis	-0.0	-0.0	-0.0	-0.0	-0.0	0.0	-0.1	-2.1	-0.7	-0.4	-0.0	-5.6	-0.0	-0.1	-0.8	-0.1	-0.2	0.0									
Akkermansia muciniphila	-1.2	-29.9	-17.8	-23.1	-7.0	-2.0	-2.4	-11.0	-8.9	-31.3	-48.9	-49.1	-0.1	-14.5	-1.7	-22.1	-0.7	-0.0	0.0								
Dialister invisus	-2.2	-66.5	-16.9	-57.2	-10.1	-2.3	-19.4	-9.0	-10.7	-14.6	-36.4	-15.3	-0.2	-25.4	-2.0	-29.3	-0.6	-0.0	-0.1	0.0							
Phascolarctobacterium species	-14.2	-119.5	-67.2	-147.8	-16.8	-27.1	-28.9	-29.5	-68.1	-0.2	-2.1	-8.1	-14.6	-80.9	-20.1	-2.7	-9.1	-0.0	-27.5	-15.8	0.0						
Eubacterium eligens	-1.7	-48.8	-16.9	-47.5	-4.4	-2.0	-4.3	-5.7	-6.6	-15.3	-35.2	-23.0	-0.1	-11.3	-2.1	-17.5	-1.1	-0.0	-0.3	-0.4	-14.4	0.0					
Eubacterium rectale	-2.4	-65.5	-18.8	-61.4	-8.8	-2.2	-11.4	-18.8	-12.2	-21.3	-40.6	-26.1	-0.2	-25.6	-2.4	-29.8	-1.5	-0.2	-0.5	-0.9	-21.3	-0.2	0.0				
Oscillibacter species	-9.4	-20.9	-11.4	-15.9	-4.1	-0.2	-20.1	-5.3	-4.2	-69.7	-85.9	-91.7	-7.9	-3.4	-11.9	-48.5	-11.3	-0.1	-5.3	-8.3	-61.1	-8.3	-10.1	0.0			
Ruminococcus bromii	-1.1	-39.7	-13.0	-38.4	-0.8	-2.3	-2.1	-0.7	-1.3	-20.4	-40.3	-33.9	-1.2	-5.5	-3.2	-18.9	-1.8	-0.0	-1.7	-3.5	-18.0	-2.4	-3.1	-4.8	0.0		
Ruminococcus bicirculans	-1.7	-93.0	-44.5	-109.0	-4.8	-12.3	-2.4	-12.8	-46.4	-13.4	-32.8	-29.1	-2.4	-41.4	-3.4	-14.0	-3.3	-0.0	-9.1	-8.3	-11.6	-2.8	-12.1	-36.8	-4.3	0.0	
Faecalibacterium prausnitzii	-5.8	-66.5	-21.9	-60.0	-12.3	-6.4	-17.2	-3.1	-14.3	-11.3	-33.3	-9.1	-2.5	-24.2	-2.0	-26.1	-0.8	-0.7	-3.7	-1.3	-12.6	-2.9	-4.5	-13.2	-7.6	-7.1	0.0



A. aspersum

Cicadella

Empoasca

LEPIDOPTERA

A. ulmi

Lepidoptera

Acalypta

A. ulmi

Acalypta

Aphrophora

Aphrophora

A. ulmi

A. ulmi

Aphis

Aphrophoridae

Lathridiidae

Aphis

Aphis

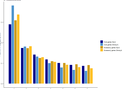
Aphrophoridae

Acanthosoma

Aphis

Aphrophoridae

Acanthosoma

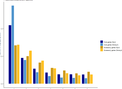


Aphis

Aphrophoridae

Acanthosoma

Aphis



Phaenacoleucaspis species

Aphis

Aphis

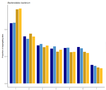
Pterothrella species

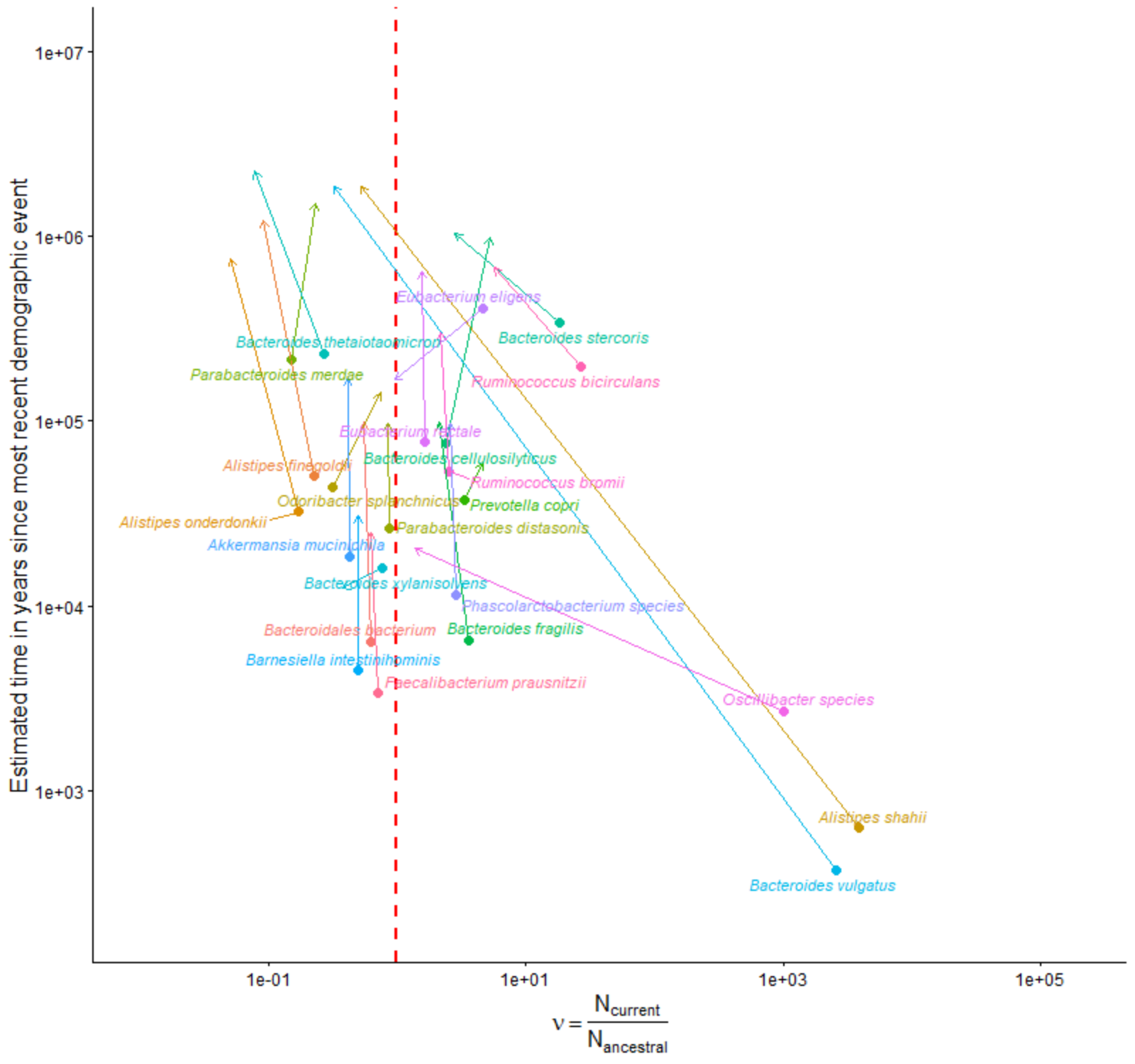
Rhyzobrotus tortrix

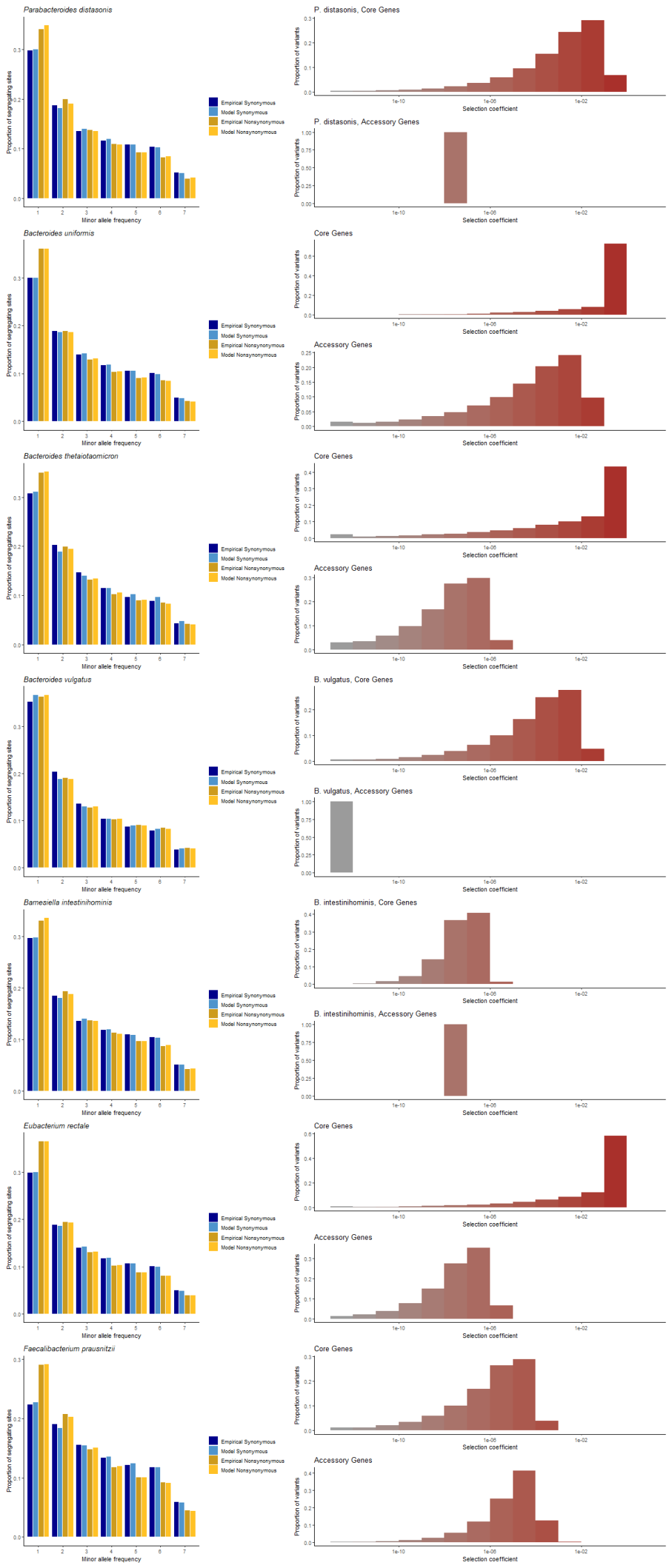
Rhyzobrotus tortrix

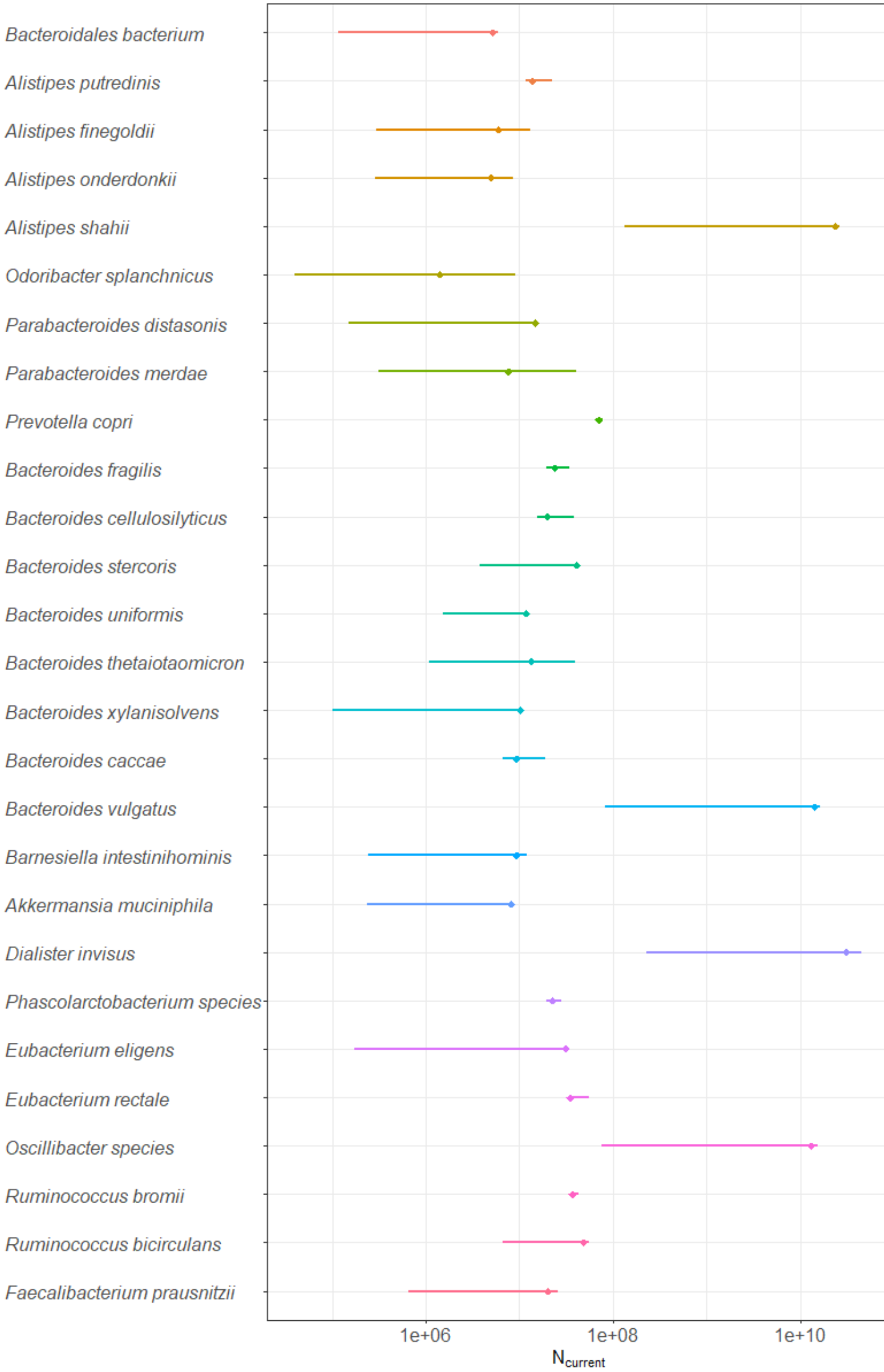
Aphrophoridae

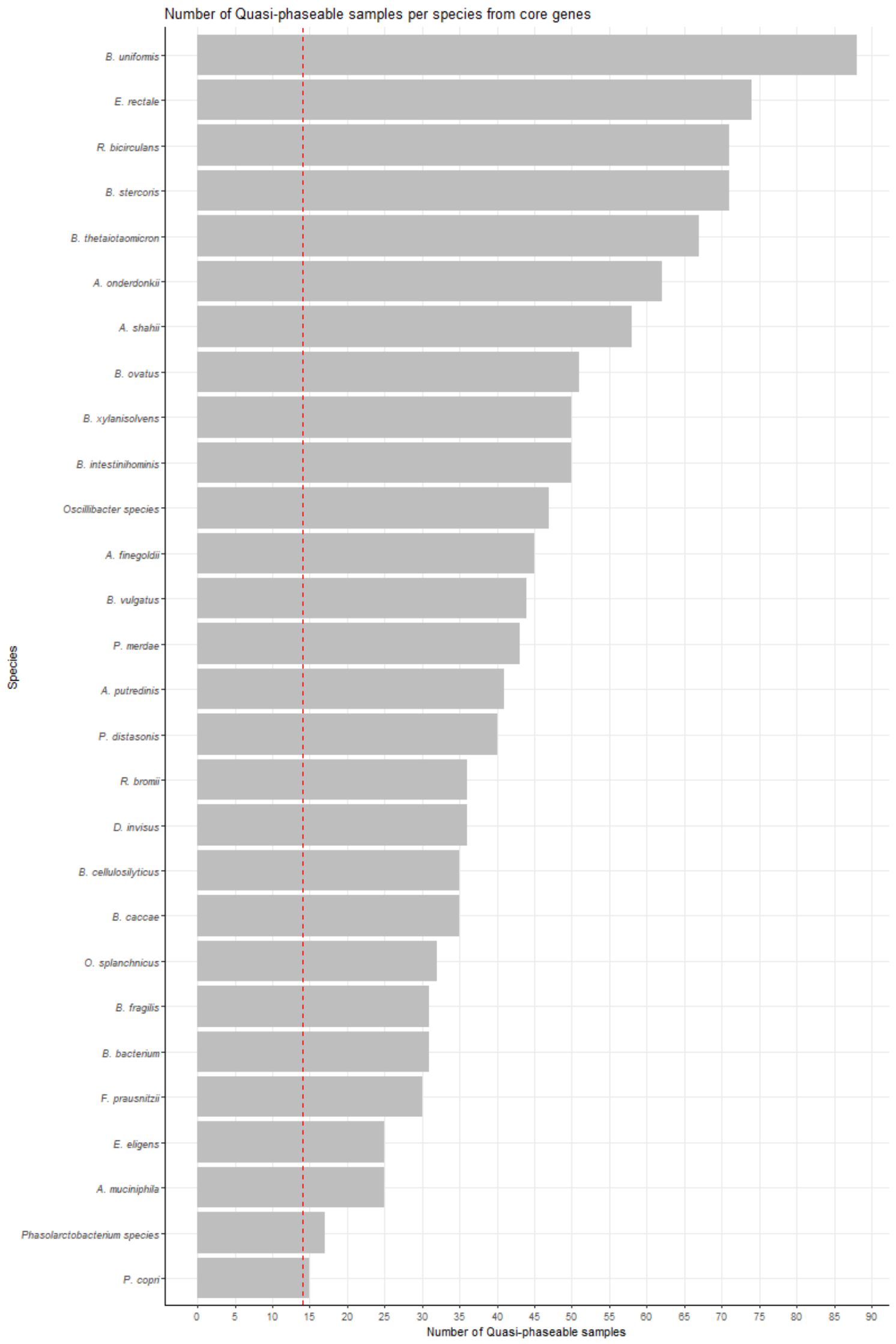
Rhynchostele cervantesii

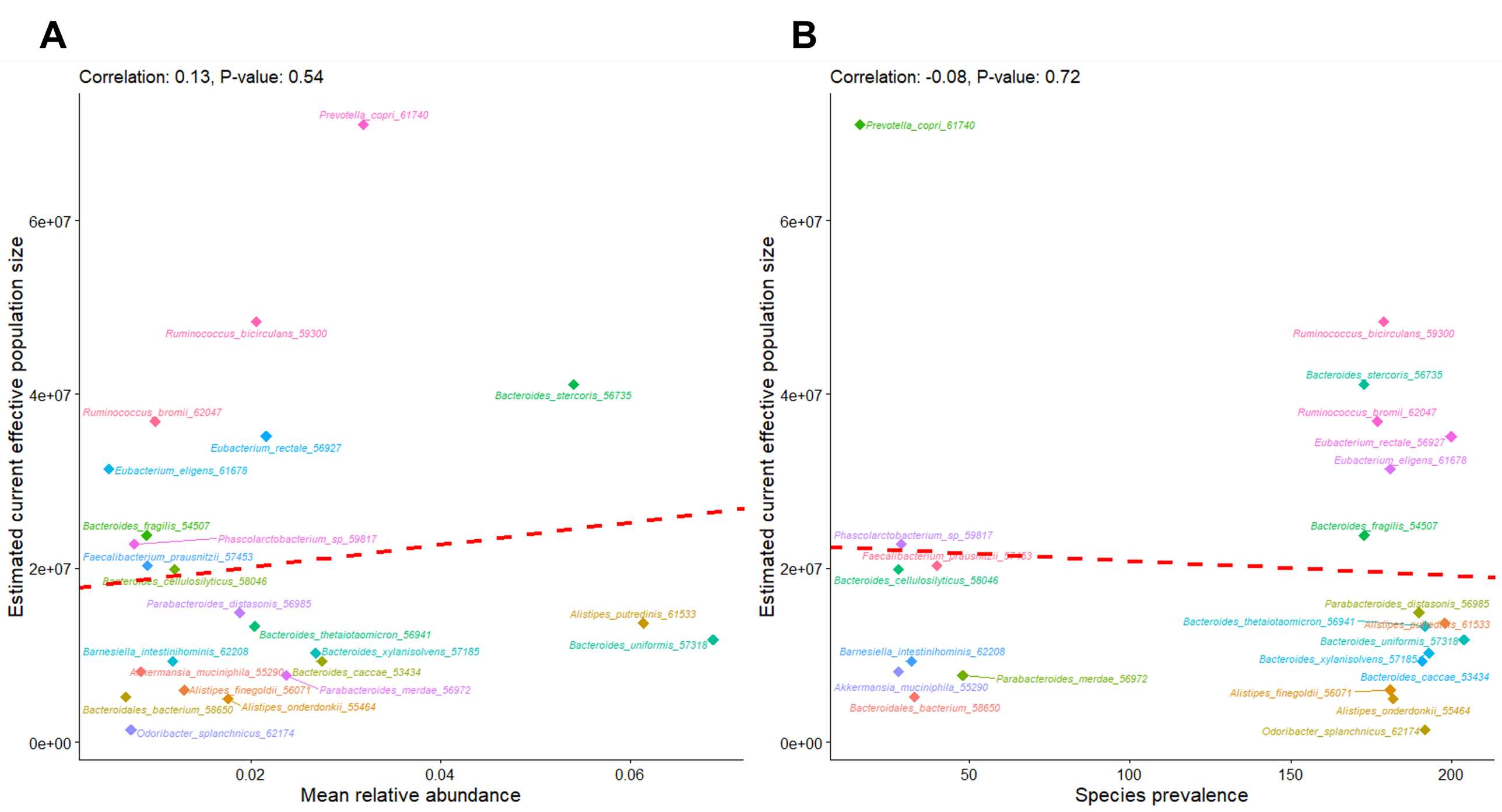

Rhynchostele cervantesii
Rhynchostele cervantesii
Rhynchostele cervantesii

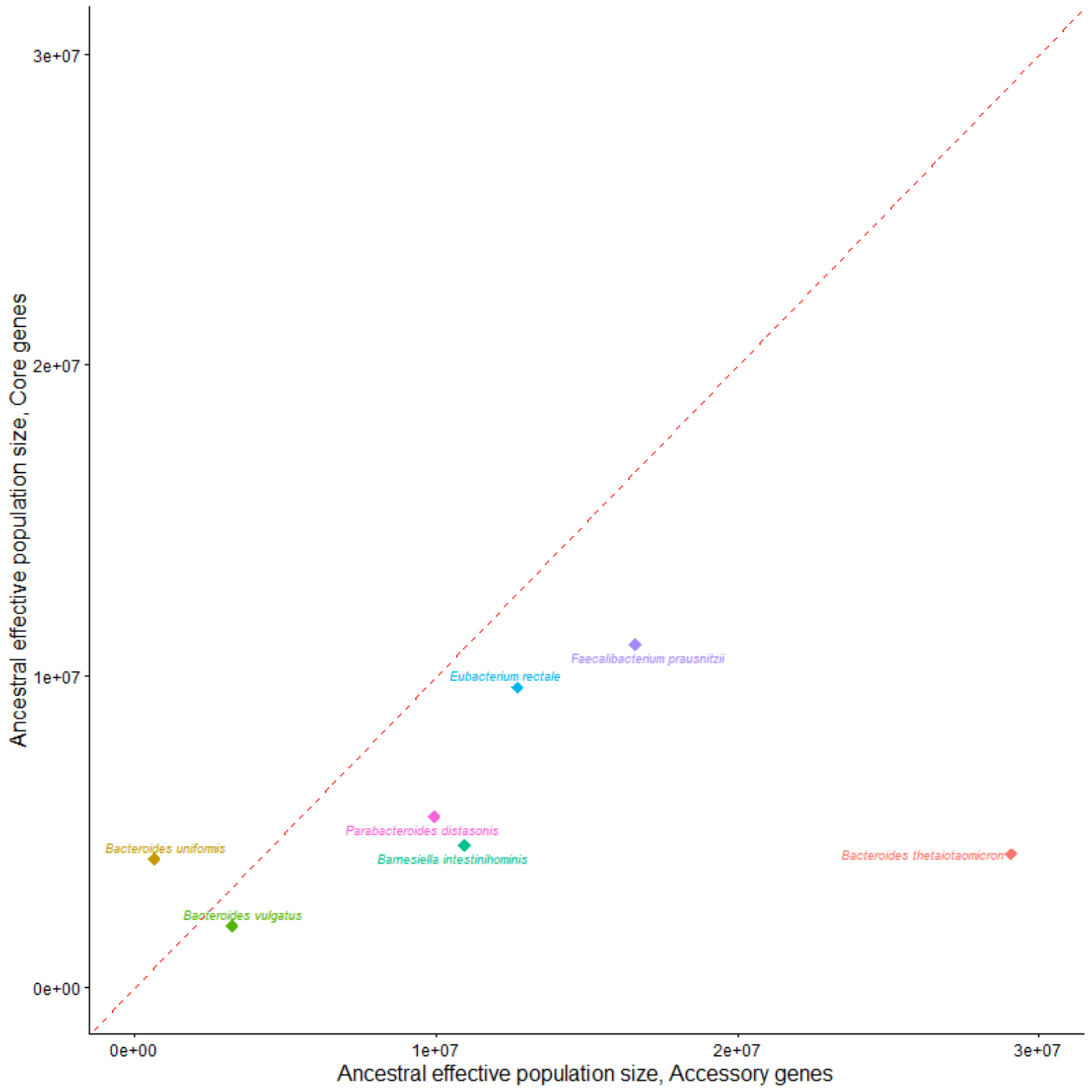

Estimated time in years since most recent demographic event
1e+07
1e+06
1e+05
1e+04
1e+03
1e-01
1e+01
1e+03
1e+05
$\nu = \frac{N_{current}}{N_{ancestral}}$
Eubacterium eligens
Bacteroides stercoris
Bacteroides thetaiotaomicron
Parabacteroides merdae
Ruminococcus bicirculans
Eubacterium rectale
Bacteroides cellulosilyticus
Alistipes finegoldii
Ruminococcus bromii
Odoribacter splanchnicus
Prevotella copri
Alistipes onderdonkii
Parabacteroides distasonis
Akkermansia muciniphila
Bacteroides xylanisolvens
Phascolarctobacterium species
Bacteroidales bacterium
Bacteroides fragilis
Barnesiella intestinihominis
Faecalibacterium prausnitzii
Oscillibacter species
Alistipes shahii
Bacteroides vulgatus


Parabacteroides distasonis
P. distasonis, Core Genes
P. distasonis, Accessory Genes
Bacteroides uniformis
Core Genes
Accessory Genes
Bacteroides thetaiotaomicron
Core Genes
Accessory Genes
Bacteroides vulgatus
B. vulgatus, Core Genes
B. vulgatus, Accessory Genes
Bamesiella intestinihominis
B. intestinihominis, Core Genes
B. intestinihominis, Accessory Genes
Eubacterium rectale
Core Genes
Accessory Genes
Faecalibacterium prausnitzii
Core Genes
Accessory Genes
Empirical Synonymous
Model Synonymous
Empirical Nonsynonymous
Model Nonsynonymous
Proportion of segregating sites
Minor allele frequency
Proportion of variants
Selection coefficient
1e-10
1e-06
1e-02


Bacteroidales bacterium
Alistipes putredinis
Alistipes finegoldii
Alistipes onderdonkii
Alistipes shahii
Odoribacter splanchnicus
Parabacteroides distasonis
Parabacteroides merdae
Prevotella copri
Bacteroides fragilis
Bacteroides cellulosilyticus
Bacteroides stercoris
Bacteroides uniformis
Bacteroides thetaiotaomicron
Bacteroides xylanisolvens
Bacteroides caccae
Bacteroides vulgatus
Barnesiella intestinihominis
Akkermansia muciniphila
Dialister invisus
Phascolarctobacterium species
Eubacterium eligens
Eubacterium rectale
Oscillibacter species
Ruminococcus bromii
Ruminococcus bicirculans
Faecalibacterium prausnitzii
1e+06
1e+08
1e+10
N current


Number of Quasi-phaseable samples per species from core genes
B. uniformis
E. rectale
R. bicirculans
B. stercoris
B. thetaiotaomicron
A. onderdonkii
A. shahii
B. ovatus
B. xylanisolvens
B. intestinihominis
Oscillibacter species
A. finegoldii
B. vulgatus
P. merdae
A. putredinis
P. distasonis
R. bromii
D. invisus
B. cellulosilyticus
B. caccae
O. splanchnicus
B. fragilis
B. bacterium
F. prausnitzii
E. eligens
A. muciniphila
Phasolarctobacterium species
P. copri
Species
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
Number of Quasi-phaseable samples


A
Correlation: 0.13, P-value: 0.54
Estimated current effective population size
Mean relative abundance
0e+00
2e+07
4e+07
6e+07
0.02
0.04
0.06
Prevotella_copri_61740
Ruminococcus_bicirculans_59300
Bacteroides_stercoris_56735
Ruminococcus_bromii_62047
Eubacterium_rectale_56927
Eubacterium_eligens_61678
Bacteroides_fragilis_54507
Phascolarctobacterium_sp_59817
Faecalibacterium_prausnitzii_57453
Bacteroides_cellulosilyticus_58046
Parabacteroides_distasonis_56985
Bacteroides_thetaiotaomicron_56941
Alistipes_putredinis_61533
Bacteroides_uniformis_57318
Barnesiella_intestinihominis_62208
Bacteroides_xylanisolvens_57185
Akkermansia_muciniphila_55290
Bacteroides_caccae_53434
Alistipes_finegoldii_56071
Parabacteroides_merdae_56972
Bacteroidales_bacterium_58650
Alistipes_onderdonkii_55464
Odoribacter_splanchnicus_62174
B
Correlation: -0.08, P-value: 0.72
Estimated current effective population size
Species prevalence
0e+00
2e+07
4e+07
6e+07
50
100
150
200
Prevotella_copri_61740
Ruminococcus_bicirculans_59300
Bacteroides_stercoris_56735
Ruminococcus_bromii_62047
Eubacterium_rectale_56927
Eubacterium_eligens_61678
Bacteroides_fragilis_54507
Phascolarctobacterium_sp_59817
Bacteroides_cellulosilyticus_58046
Parabacteroides_distasonis_56985
Bacteroides_thetaiotaomicron_56941
Bacteroides_uniformis_57318
Barnesiella_intestinihominis_62208
Bacteroides_xylanisolvens_57185
Parabacteroides_merdae_56972
Bacteroides_caccae_53434
Akkermansia_muciniphila_55290
Alistipes_finegoldii_56071
Bacteroidales_bacterium_58650
Alistipes_onderdonkii_55464
Odoribacter_splanchnicus_62174


3e+07
2e+07
1e+07
0e+00
Ancestral effective population size, Core genes
Faecalibacterium prausnitzii
Eubacterium rectale
Parabacteroides distasonis
Bacteroides uniformis
Barnesiella intestinihominis
Bacteroides thetaiotaomicron
Bacteroides vulgatus
0e+00
1e+07
2e+07
3e+07
Ancestral effective population size, Accessory genes