

Trait-based community assembly and succession in the infant gut microbiome.

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Tables and figures

Trait	Sources	Units	Range of values	Percent coverage
16S gene copies	PICRUSt, NCBI	No. in genome	1 - 12	68
Aggregation	IJSEM	0 or 1	0 - 1	34
B vitamins	Magnusdottir et al. 2015	No. pathways in genome	0 - 8	65
GC content	IJSEM, BacDive	Percent (%)	27 - 71	55
Genes	NCBI	No. in genome	1300 - 6300	53
Genome size	NCBI	Mb	1.3 - 6.7	53
Gram positive	IJSEM, BacDive	0 or 1	0 - 1	33
IgA binding affinity	Palm et al. 2014	$\log ([\text{IgA+}]/[\text{IgA-}] + 1)$	0 - 4.3	59
Length	IJSEM, BacDive	$\log (\mu\text{m})$	-0.8 - 2.2	31
Motility	IJSEM	0 or 1	0 - 1	33
Oxygen tolerance	IJSEM, BacDive	Nominal score (1 - 5)	1 - 5	65
pH optimum	IJSEM, BacDive	pH	4 - 8.3	30
Salt optimum	IJSEM, BacDive	g/l	0 - 8	25
Sporulation	Browne et al. 2016	Continuous score (0 - 1)	0 - 0.72	57
Temperature optimum	IJSEM, BacDive	°C	23 - 40	30
Width	IJSEM, BacDive	$\log (\mu\text{m})$	-1 - 1.3	33

Table 1. Sources of trait data. Percent coverage reflects the percent of sequences with trait information across all community samples. PICRUSt refers to Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (Langille et al. 2013). NCBI refers to the National Center for Biotechnology Information. IJSEM refers to the International Journal of Systematic and Evolutionary Microbiology. BacDive refers to the Bacterial Diversity Metadatabase (Sohnngen et al 2014). Oxygen tolerance nominal scores are: 1: Anaerobe; 2: Facultative aerobe; 3: Facultative anaerobe; 4: Microaerophile; 5: Obligate aerobe.

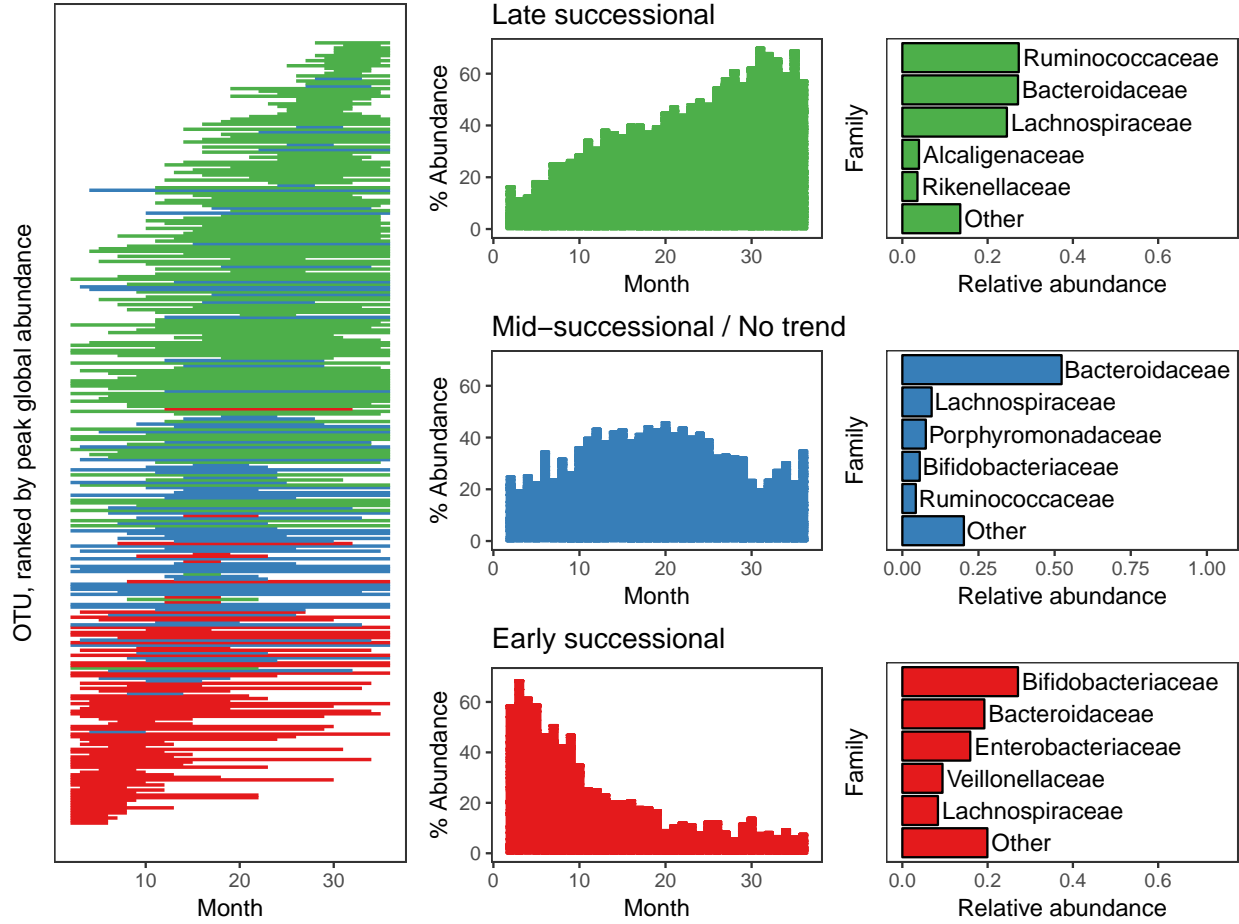


Figure 1. OTU and family-level abundance patterns over time.

Successional ranges of taxa (left), ranked by peak abundance across infants. Colored horizontal lines represent OTUs, and their extents on the x-axis represent the first and last times their mean abundance surpassed 0.1% across infants. Taxa that never attained 0.1% mean abundance are not shown. OTU colors reflect successional status. Taxa were categorized as early (red) or late (green) successional if their global abundances trended significantly ($p < 0.05$) negative or positive over time based on linear regression; OTUs without significant positive or negative trends over time were categorized as mid-successional/no trend (blue). The center column of panels reflects relative abundances of OTUs in each successional category across all infants over time. The right column of panels show barplots of the top five most abundant families and their proportions of the total community.

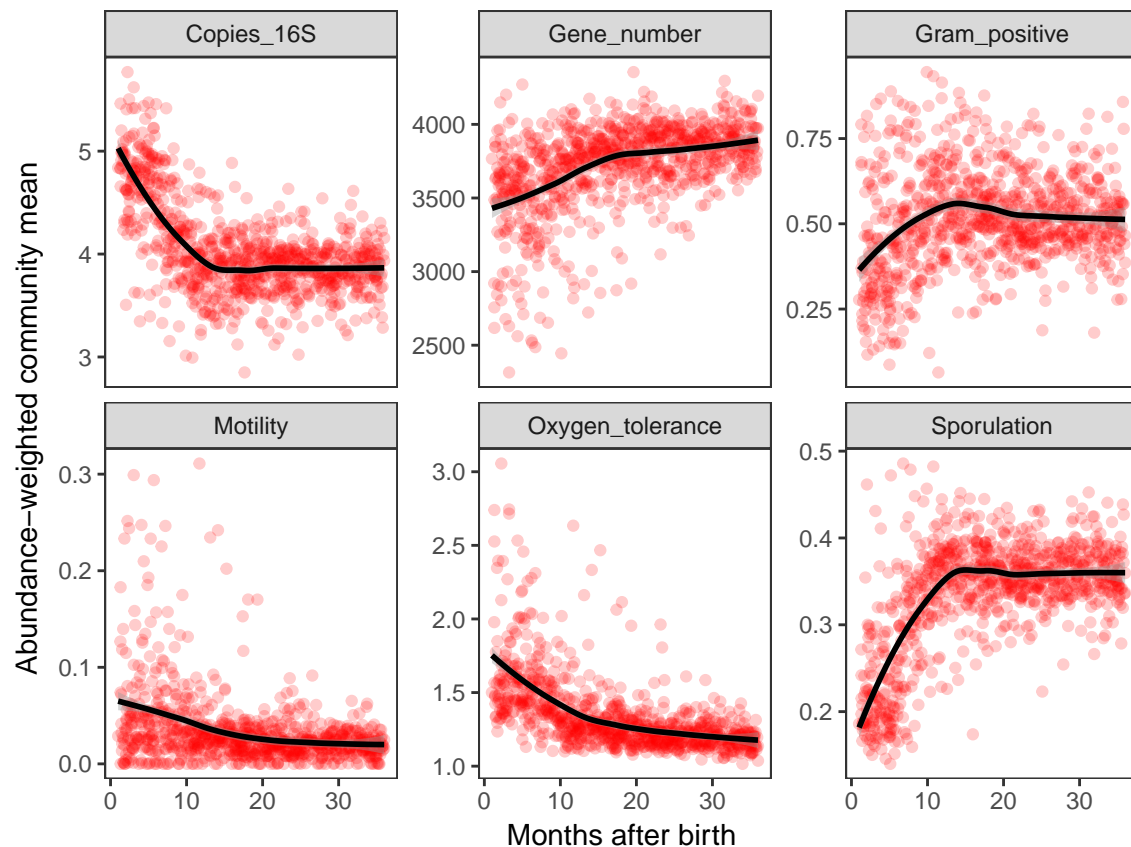


Figure 2. Abundance-weighted trait patterns over time.

Each red circle represents the CWM of one sample for one infant. Solid black lines show community weighted mean (CWM) trait values of gut microbiota over time across all infants. Taxa without trait information were necessarily omitted when calculating CWMs; see Table 1 for coverage statistics. For abundance-weighted patterns for all traits see Fig. S5.

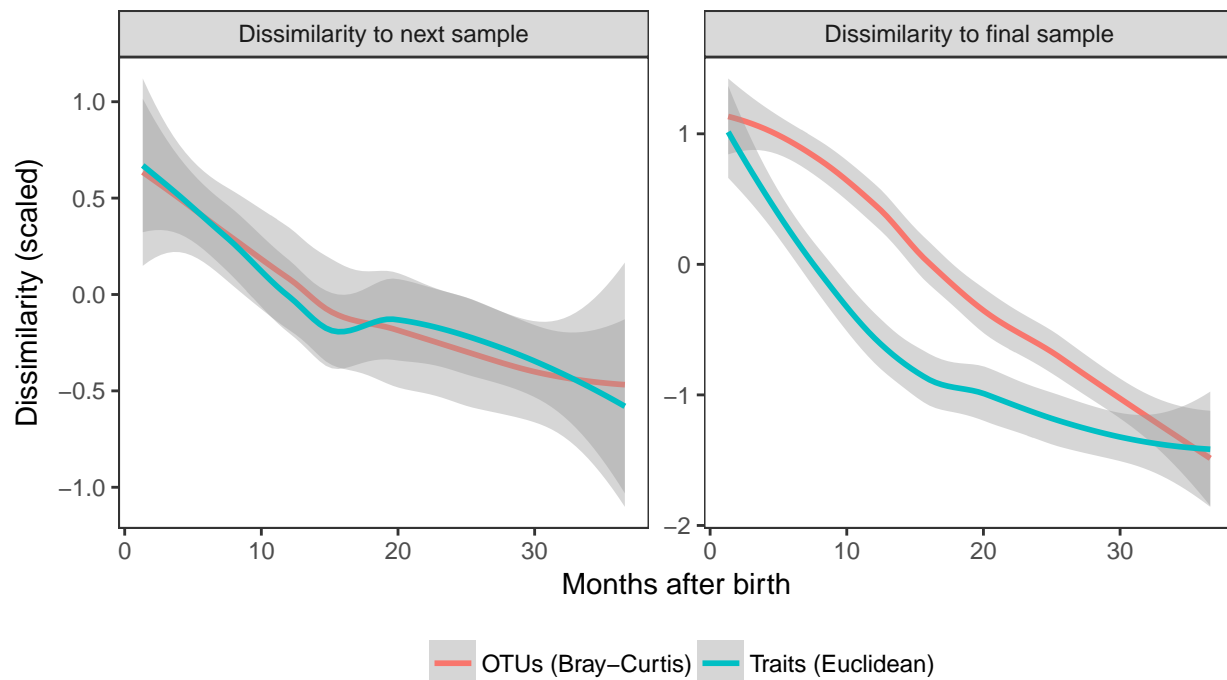


Figure 3. Taxonomic and trait-based rates of community change within infants.

Lines show mean dissimilarities among gut microbiome samples within infants over their development. Trait-based and OTU-based dissimilarities are scaled and plotted together for visual comparison. At left, lines show how dissimilarity between subsequent samples generally decreases over time, highlighting a trend towards compositional stability both in terms of OTUs and traits. At right, lines show dissimilarity between samples and the final community sample for each infant, taken at around 36 months after birth; both OTU-based and trait-based lines decrease over time, illustrating a gradual convergence in composition, but trait-based convergence occurs sooner than OTU-based convergence, suggesting that OTU turnover becomes more functionally redundant over time.

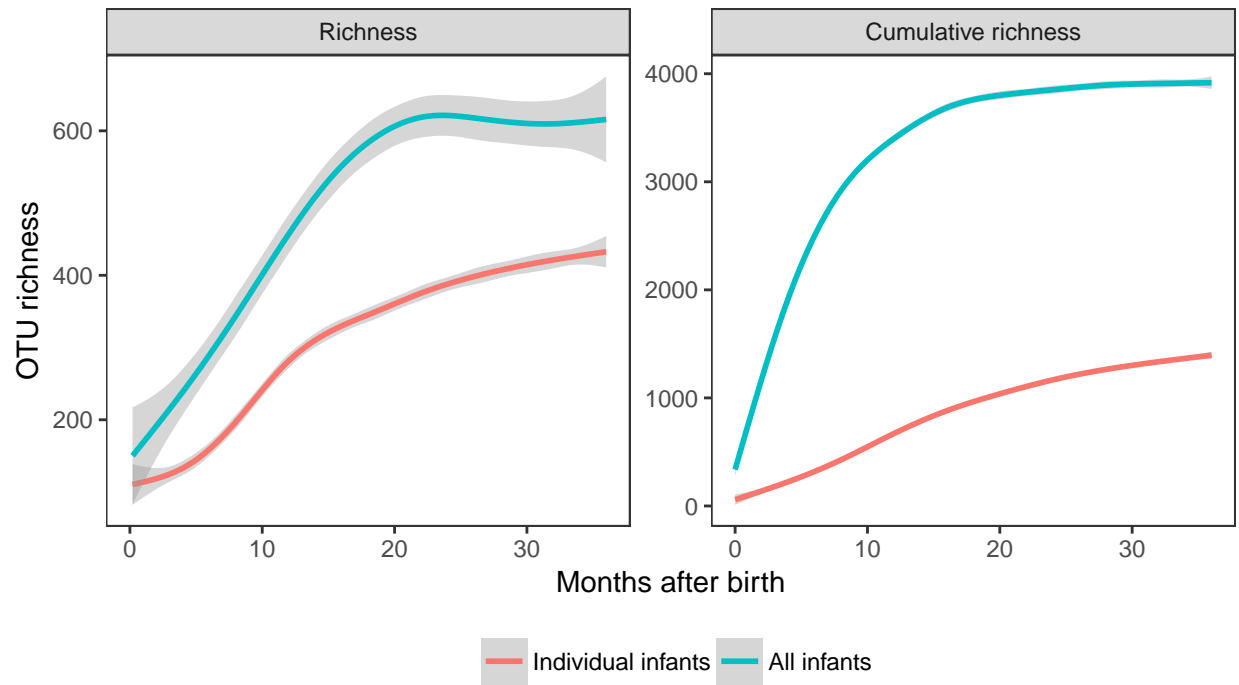


Figure 4. OTU richness in individual infants (left) and across infants (right).

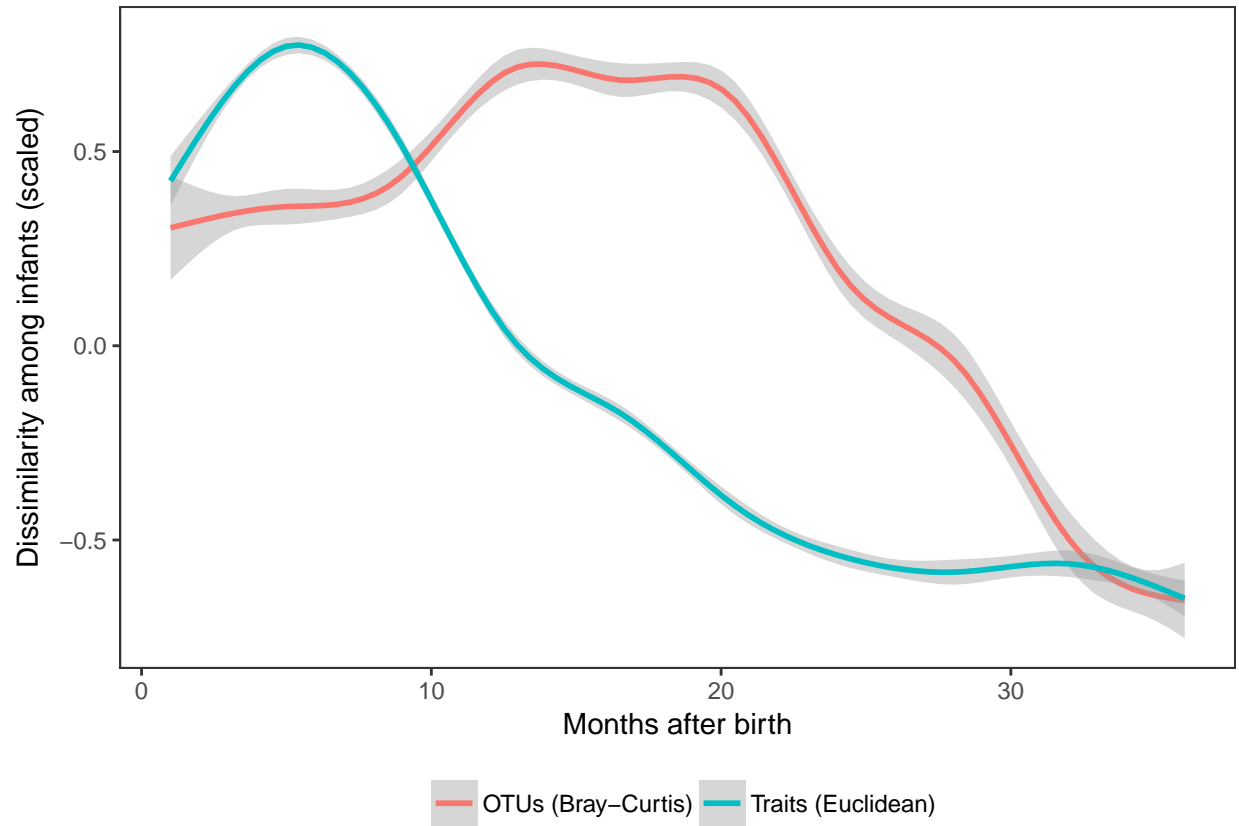


Figure 5. Mean dissimilarity in gut microbiomes across infants over early development.

Community dissimilarity is calculated by grouping samples into one-month slices, and then calculating the average dissimilarity of all pairwise comparisons within each slice (excluding samples from the same infant).

Supplementary tables and figures

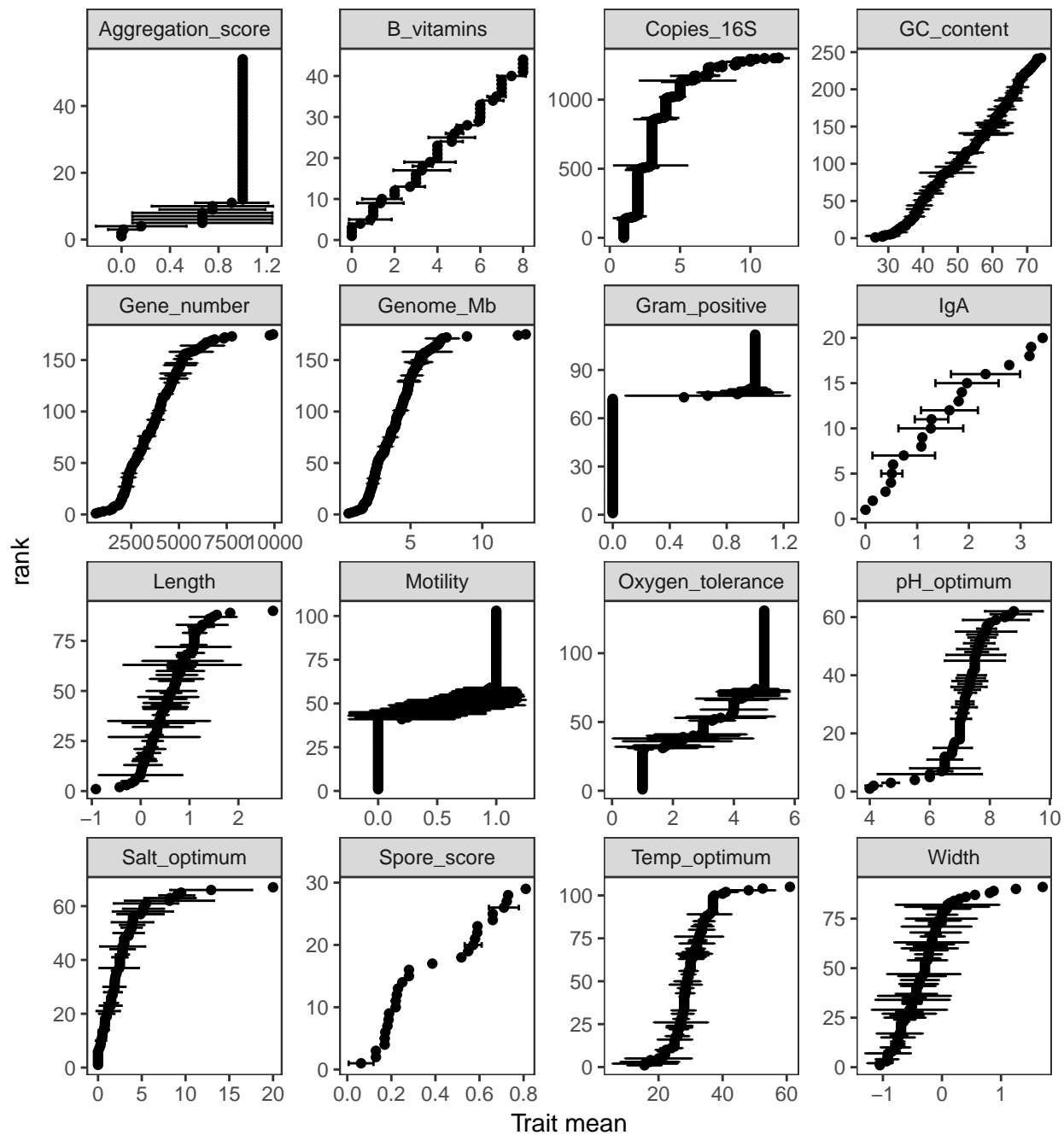


Figure S1. Intragenus trait variation across

All trait data gathered from sources in Table 1, including genera that were not observed in this study. Each row is a genus; filled circles show the mean trait value of the OTUs in that genus (). Horizontal lines show ± 1.0 St. Dev. of trait values for each genus.

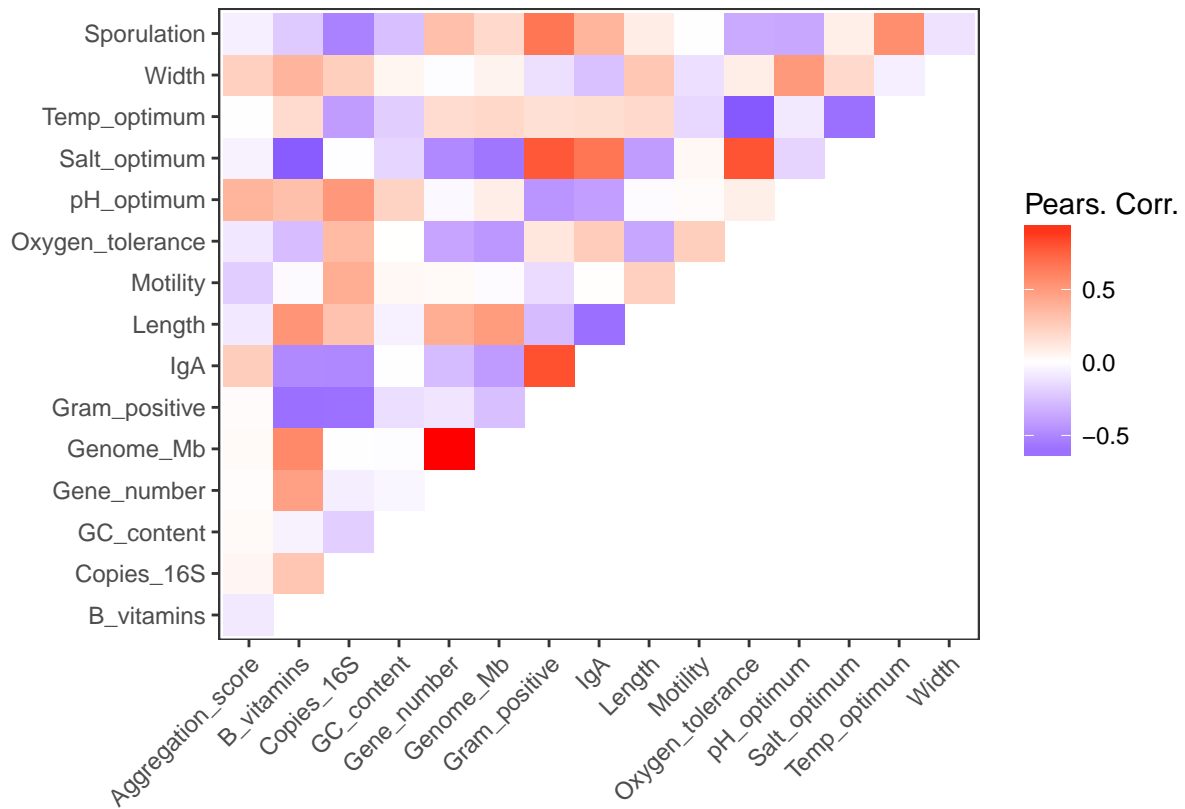


Figure S2. Pearson correlation coefficients among traits.

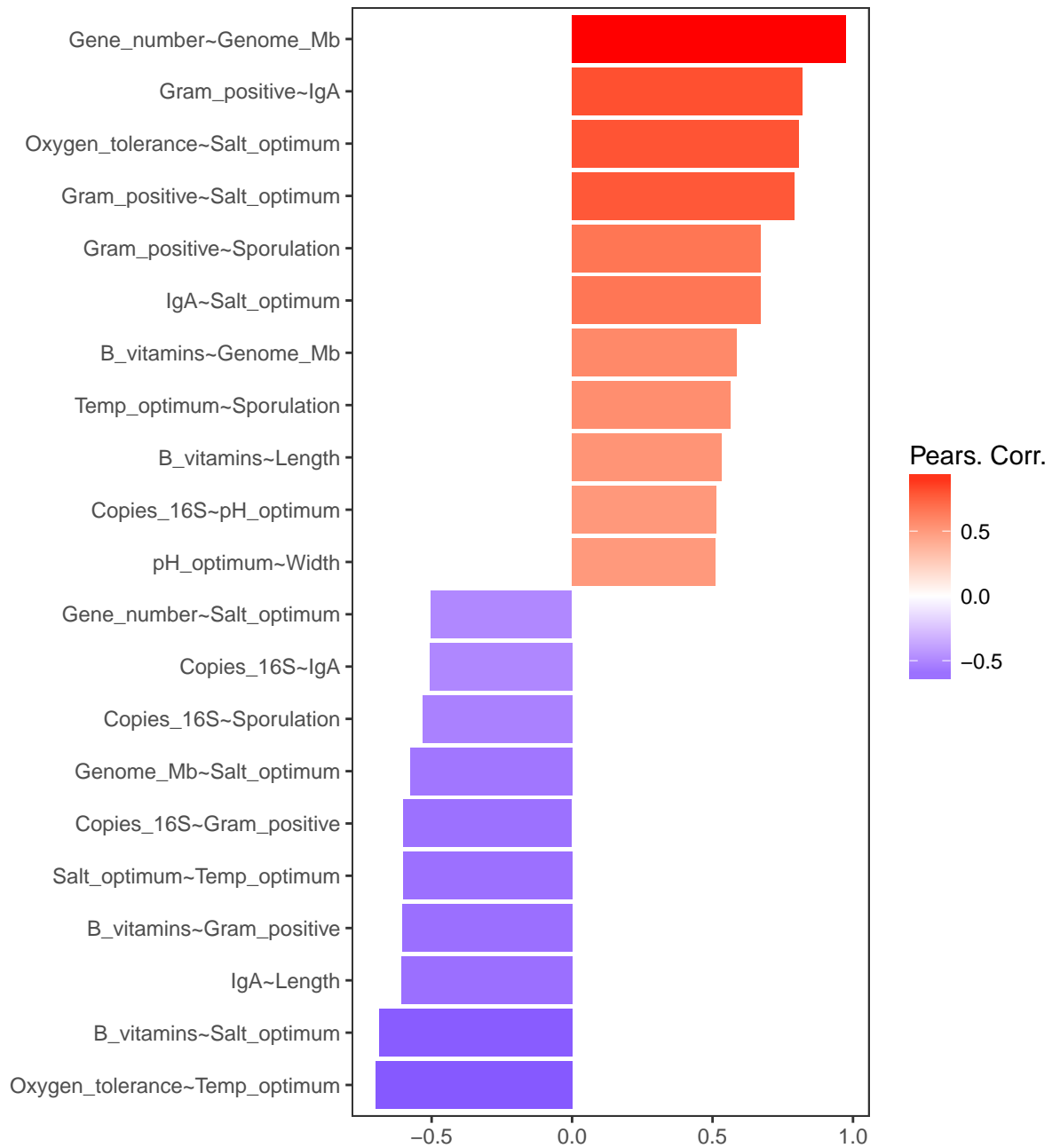


Figure S3. Ranked pairwise Pearson correlations among traits > 0.5.

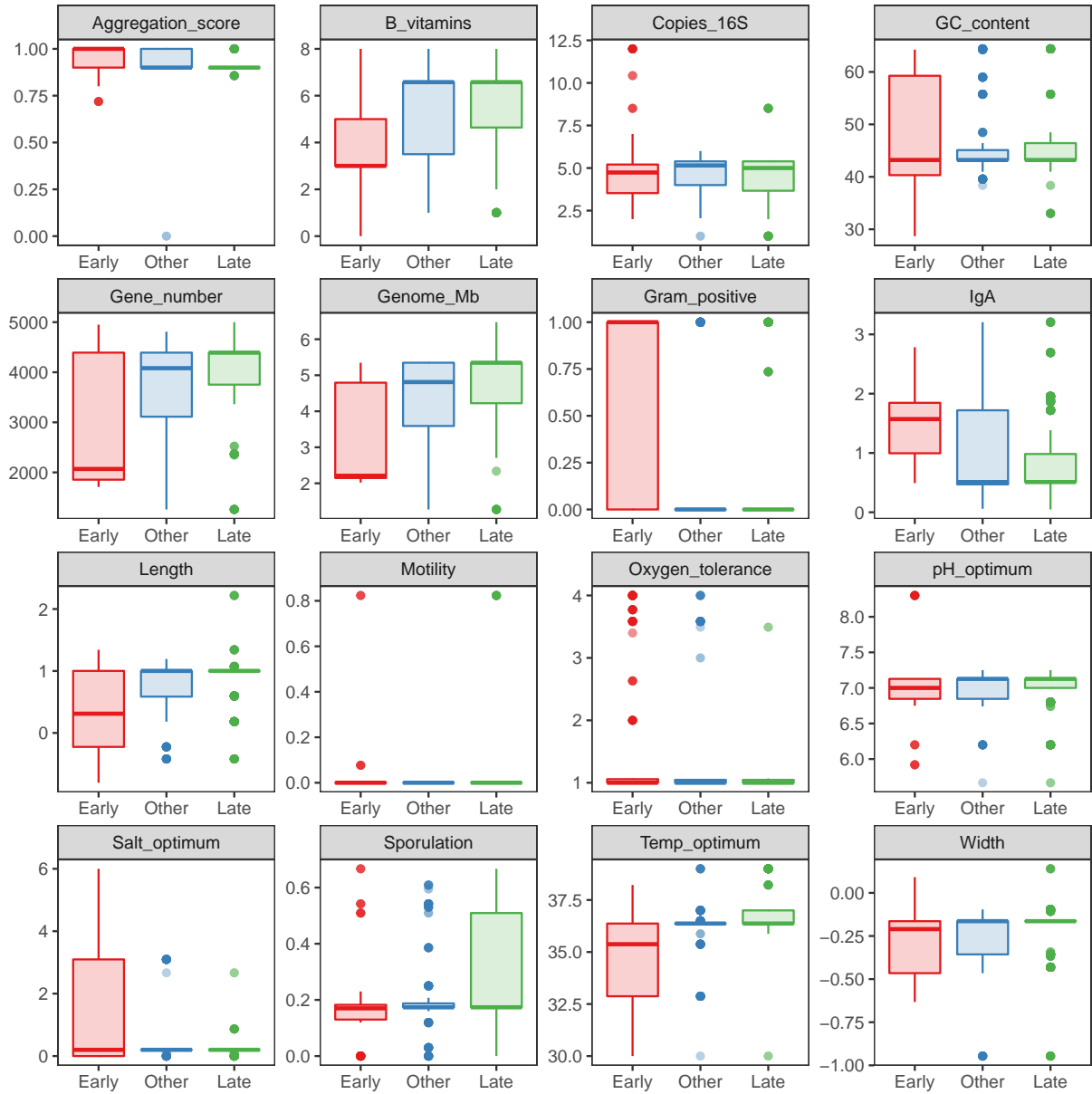


Figure S4. Trait-based differences among OTUs, grouped by successional stage and not weighted by abundance.

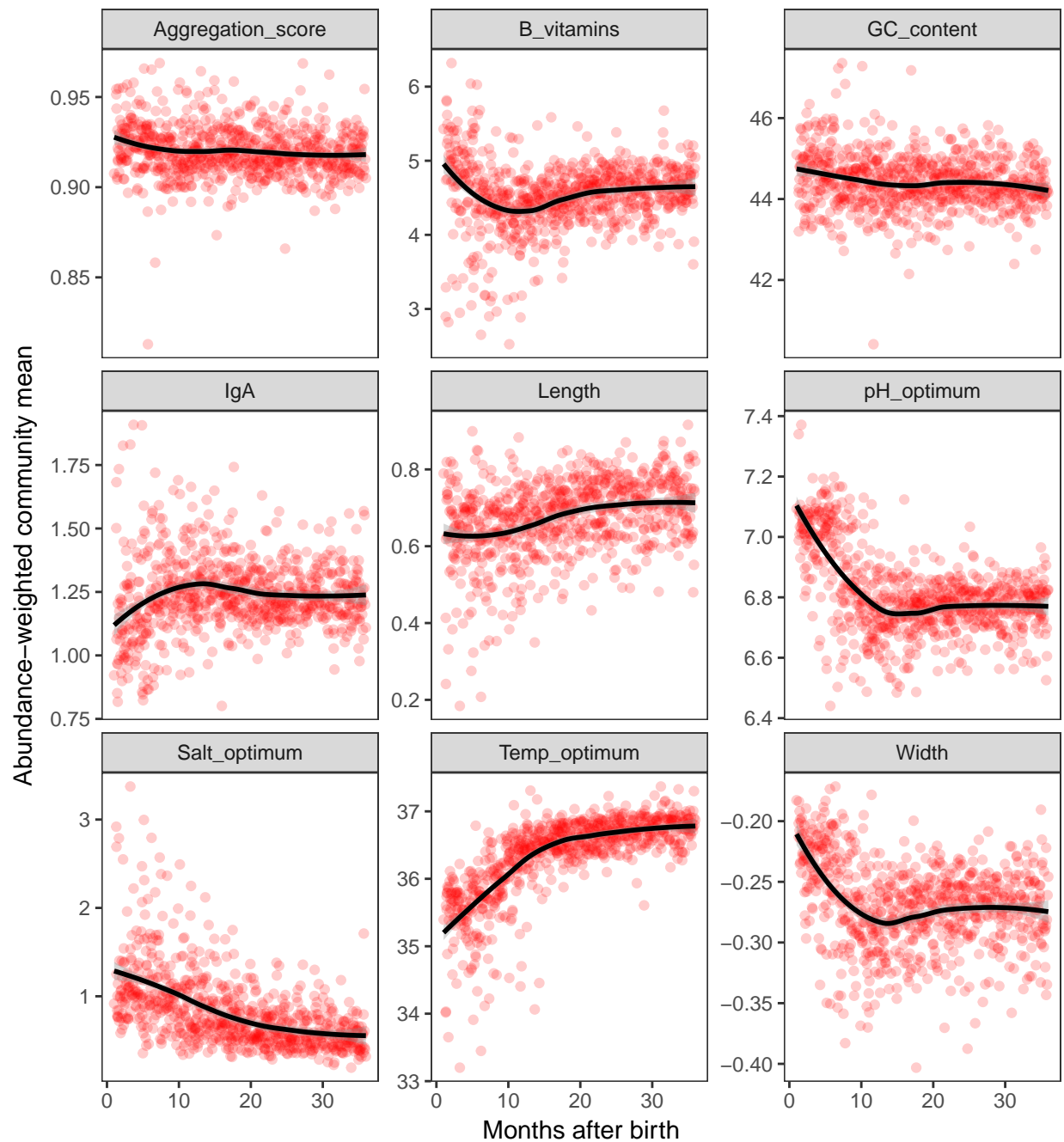


Figure S5. Abundance-weighted trait patterns over time.

Each red circle represents the CWM of one sample for one infant. Solid black lines show community weighted mean (CWM) trait values of gut microbiota over time across all infants. Taxa without trait information were necessarily omitted when calculating CWMs; see Table 1 for coverage statistics. Refer to Figure 2 for abundance-weighted patterns for mean 16S rRNA operon copy number, gene number, Gram status, motility, oxygen tolerance, and sporulation score.

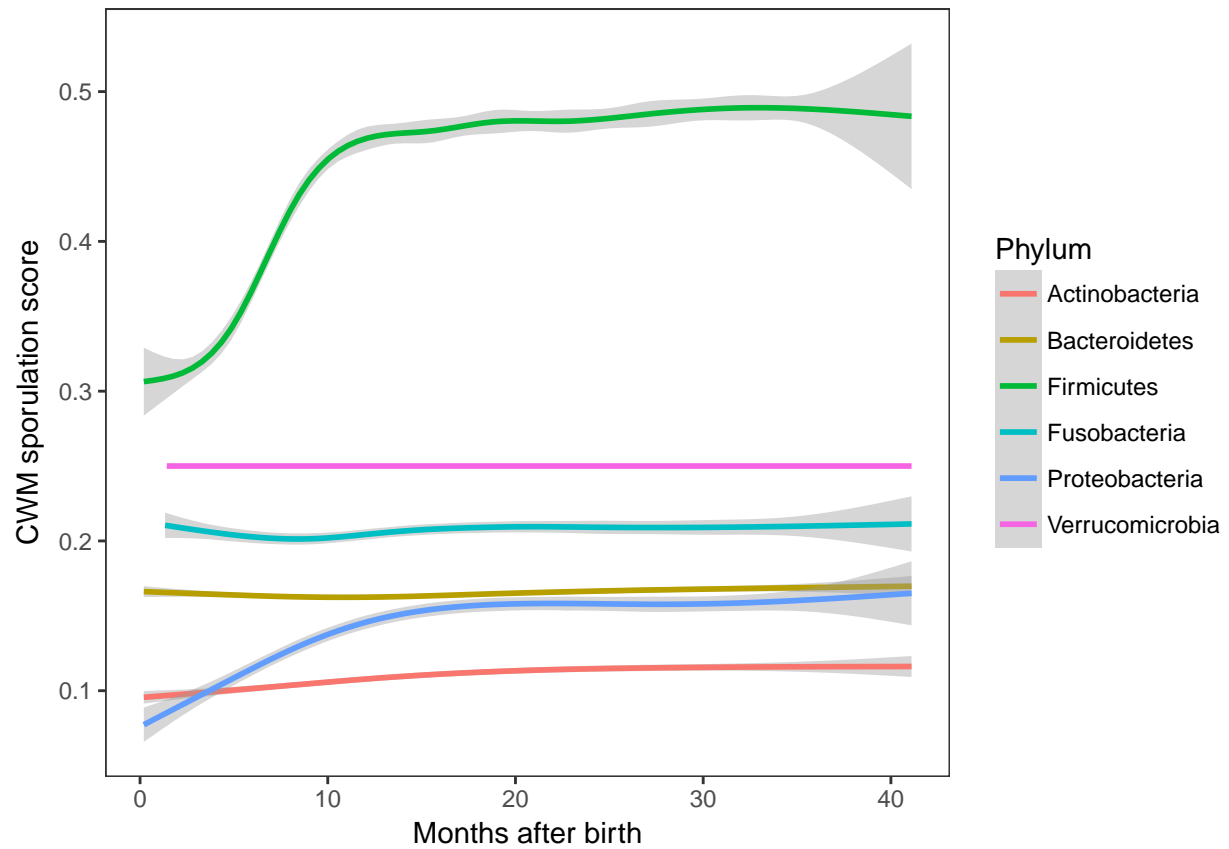


Figure S5. Changes in abundance-weighted mean sporulation scores over time, by Phylum.

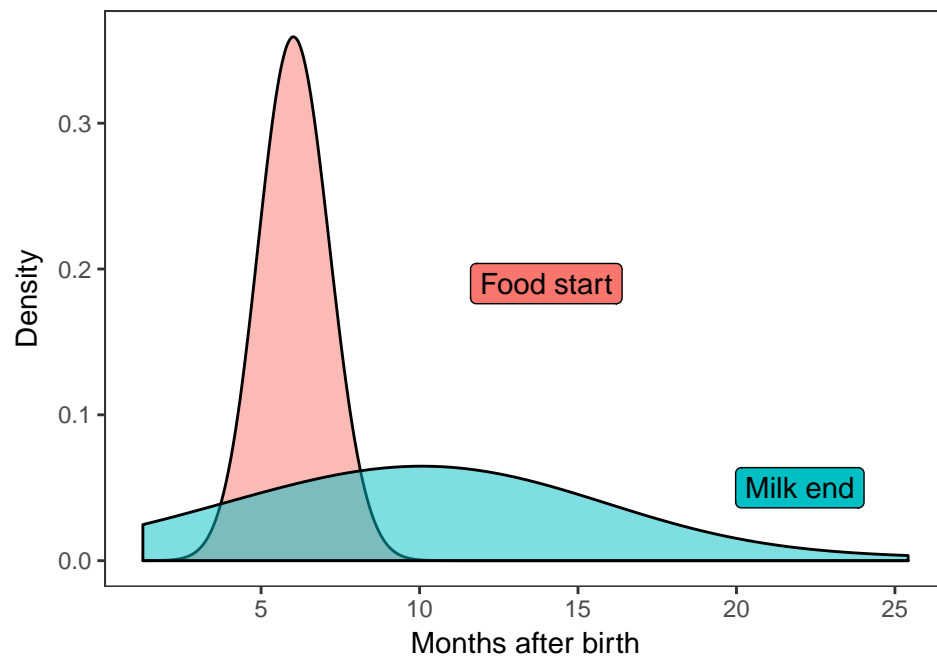


Figure S6. Density of dietary transition times across infants.

Note: For ‘Milk’, I included both formula and breastmilk.

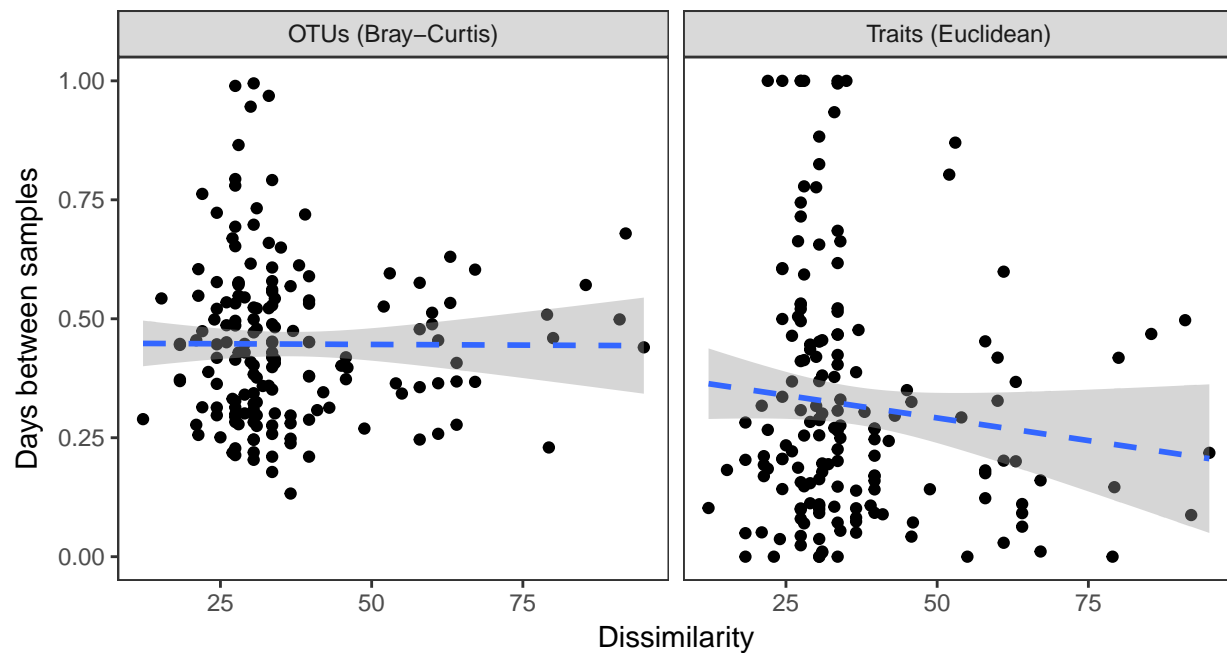


Figure S7. Dissimilarity in community composition plotted by the number of days between samples (up to 100).

There is no significant relationship.

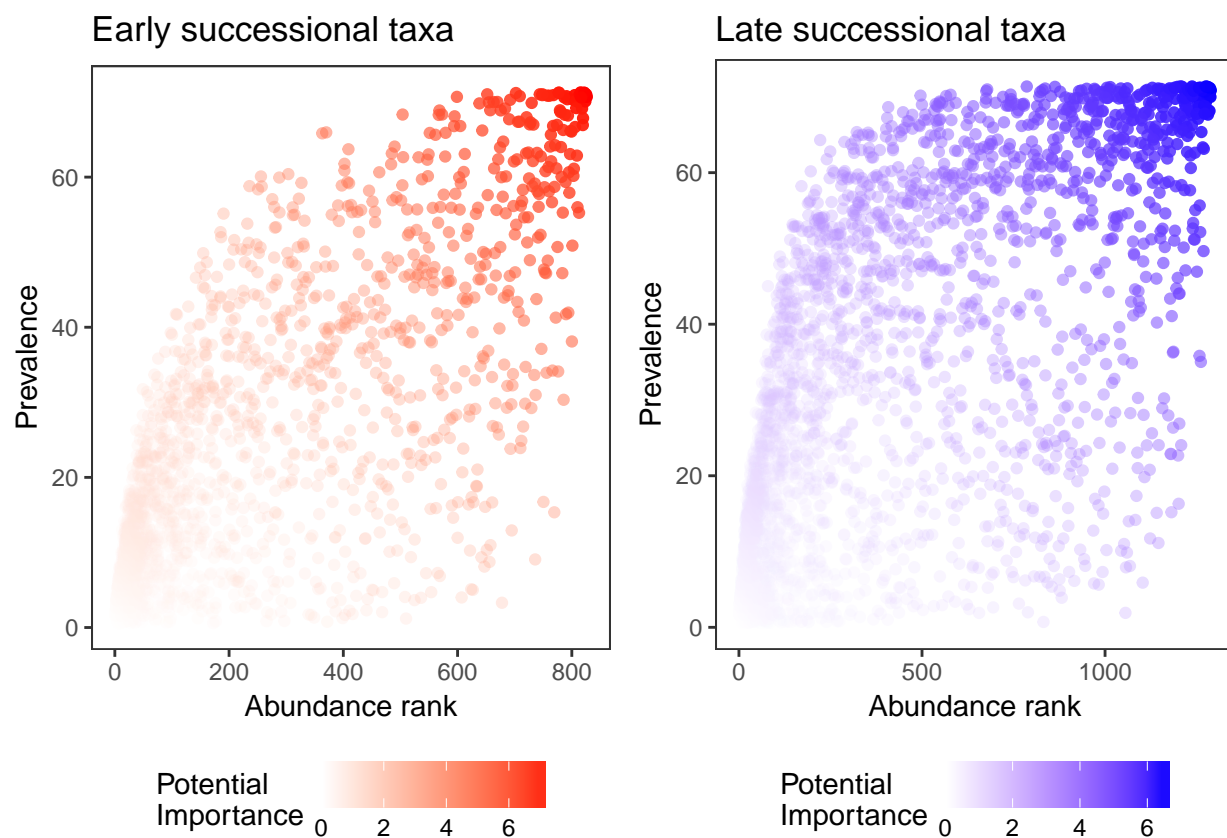


Figure S8. Taxa abundance by prevalence: a measure of importance.

Family	Genus	Species	OTU	Importance
Bifidobacteriaceae	Bifidobacterium	longum	otu72820	7.47
Bacteroidaceae	Bacteroides	unclassified	otu4381553	7.46
Lachnospiraceae	unclassified	unclassified	otu2724175	7.45
Bacteroidaceae	Bacteroides	unclassified	otu3600504	7.45
Enterobacteriaceae	unclassified	unclassified	otu782953	7.45
Bifidobacteriaceae	Bifidobacterium	unclassified	otu825808	7.43
Veillonellaceae	Veillonella	dispar	otu4388775	7.42
Veillonellaceae	Veillonella	dispar	otu4453501	7.42
Pasteurellaceae	Haemophilus	parainfluenzae	otu4477696	7.41
Bacteroidaceae	Bacteroides	fragilis	otu4343627	7.40
Bifidobacteriaceae	Bifidobacterium	adolescentis	otu4347159	7.40
Enterobacteriaceae	unclassified	unclassified	otu4425571	7.38
Enterobacteriaceae	unclassified	unclassified	otu2119418	7.35
Veillonellaceae	Veillonella	unclassified	otu4458959	7.33
Ruminococcaceae	unclassified	unclassified	otu265871	7.32
Erysipelotrichaceae	unclassified	unclassified	otu4390365	7.31
Streptococcaceae	Streptococcus	unclassified	otu4425214	7.31
Clostridiaceae	unclassified	unclassified	otu4434334	7.30
Enterobacteriaceae	unclassified	unclassified	otu668514	7.28
Clostridiaceae	Clostridium	neonatale	otu73000	7.28

Table S1. Early successional taxa, by importance.

Family	Genus	Species	OTU	Importance
Bacteroidaceae	Bacteroides	unclassified	otu3600504	6.60
Lachnospiraceae	unclassified	unclassified	otu289734	6.59
Bacteroidaceae	Bacteroides	unclassified	otu4381553	6.59
Bifidobacteriaceae	Bifidobacterium	longum	otu72820	6.58
Bacteroidaceae	Bacteroides	uniformis	otu3327894	6.57
Lachnospiraceae	unclassified	unclassified	otu2724175	6.56
Bacteroidaceae	Bacteroides	unclassified	otu4439360	6.56
Bifidobacteriaceae	Bifidobacterium	unclassified	otu825808	6.56
Ruminococcaceae	unclassified	unclassified	otu265871	6.55
Bacteroidaceae	Bacteroides	fragilis	otu4343627	6.55
Bacteroidaceae	Bacteroides	caccae	otu193528	6.54
Pasteurellaceae	Haemophilus	parainfluenzae	otu4477696	6.54
Lachnospiraceae	Coprococcus	unclassified	otu182289	6.53
Bacteroidaceae	Bacteroides	uniformis	otu328617	6.53
Verrucomicrobiaceae	Akkermansia	muciniphila	otu4306262	6.52
Bifidobacteriaceae	Bifidobacterium	adolescentis	otu4347159	6.52
Enterobacteriaceae	unclassified	unclassified	otu782953	6.51
Streptococcaceae	Streptococcus	unclassified	otu4425214	6.50
Bacteroidaceae	Bacteroides	unclassified	otu175485	6.49
Lachnospiraceae	Roseburia	unclassified	otu3926480	6.49

Table S2. Late successional taxa, by importance.