

Supplementary Information

1 Supplemental Methods

1.1 Pipeline optimization

The construction of the pipeline used included considerations of computational time and resources available as well as systematic testing of software and parameter options. Preliminary testing and construction was performed on simple random samples of 100 species obtained from a dataset of 714 fully-sequenced Terrabacteria genomes to reduce the computational time of larger reconstruction steps (i.e., orthology detection, substitution matrix and tree estimation). Once the pipeline was established, further testing and parameter exploration was performed using 714 species. Once finalized, we updated our dataset to include fully-sequenced proteomes for the Terrabacteria that have been added to National Center for Biotechnology Information (NCBI) during the construction of the pipeline. Our final dataset consisted of 766 species.

After evaluating the computational requirements of OrthoMCL (Li Li *et al.*, 2003) and ProteinOrtho (Lechner *et al.*, 2011), we found that the algorithm used to evaluate similarity among species based on results of bidirectional blastp scores for ProteinOrtho, at 0 connectivity, was the most appropriate choice for this study based on speed and similarity of results. Once ortholog identification was mapped through ProteinOrtho, a Perl script designed within our lab filtered homologous groups and identified orthologous groups based on a threshold of desired species represented in each ortholog. We tested multiple values (100%, 99%, 97%, 95%, 90%, and 80%) and found that the 90% threshold optimized the number of orthologs and amount of missing data (30 orthologs) (Tables S1 and S2). Each ortholog was aligned using MUSCLE (Edgar, 2004) for multiple sequence alignments under default parameters. We estimated the best substitution model using ProtTest (Darriba *et al.*, 2011) and found that the LG model had the highest AIC across all simple random samples. In order to reduce the presence of missing data, we filtered alignments based on site coverage. The alignments were filtered to exclude columns with more than 25% gaps. After concatenating each individual aligned ortholog we obtained an alignment of 6,227 sites.

Table S1 Effects of species coverage and connectivity in ProteinOrtho on the the size of the dataset. Based on a dataset of 714 species.

Sp. filter	Alignment length	Connectivity	Ortholog count
none	5772	1	6
100	1673	0.95	21
99	2330	0.75	29
97	2431	0.5	35
95	2462	0.25	53
90	2484	0.1	58
80	2550	0	30

Table S2 Orthologs groups and percent of species coverage in alignment with 25% or less gaps per site. Based on a dataset of 766 species.

Name	% sp. coverage	Description (NCBI taxon. id: 79880) ^a
OG110	90.73	DNA recombination and repair protein RecF
OG175	91.51	DNA repair protein RecN
OG678	92.29	Segregation and condensation protein A
OG133	93.73	16S rRNA processing protein RimM
OG229	94.64	LSU ribosomal protein L21p
OG195	96.99	tRNA pseudouridine synthase B
OG290	97.12	DNA recombination and repair protein RecO
OG244	97.25	Recombination protein RecR
OG321	97.25	LSU ribosomal protein L9p
OG333	98.3	Excinuclease ABC subunit B
OG117	98.43	SSU ribosomal protein S10p (S20e)
OG95	98.82	SSU ribosomal protein S11p (S14e)
OG304	98.82	LSU ribosomal protein L18p (L5e)
OG306	98.82	LSU ribosomal protein L15p (L27Ae)
OG296	99.21	LSU ribosomal protein L22p (L17e)
OG298	99.34	LSU ribosomal protein L16p (L10e)
OG179	99.6	LSU ribosomal protein L19p
OG183	99.6	LSU ribosomal protein L10p (P0)
OG217	99.6	Translation elongation factor Ts
OG218	99.6	SSU ribosomal protein S2p (SAe)
OG295	99.6	LSU ribosomal protein L2p (L8e)
OG302	99.6	SSU ribosomal protein S8p (S15Ae)
OG96	99.73	SSU ribosomal protein S13p (S18e)
OG182	99.73	LSU ribosomal protein L1p (L10Ae)
OG294	99.73	LSU ribosomal protein L4p (L1e)
OG293	99.86	LSU ribosomal protein L3p (L3e)
OG303	99.86	LSU ribosomal protein L6p (L9e)
OG305	99.86	SSU ribosomal protein S5p (S2e)
OG297	100	SSU ribosomal protein S3p (S3e)
OG93	99.08	LSU ribosomal protein L17p

^agene descriptions based on *Bacillus clausii*.

1.2 Alternative Maximum Likelihood (ML) estimation methods

Initially, we considered commonly used RaxML (Stamatakis, 2006), and FastTree (Price *et al.*, 2010) software to construct Maximum-Likelihood phylogenetic trees. FastTree was able to estimate phylogenies for large datasets in a fraction of the time that RaxML required, with comparable likelihoods & topology results (Liu *et al.*, 2011). Therefore, using FastTree instead of RaxML in our pipeline allowed the large-scale production of trees required to perform the planned permutations on taxon sampling. However, FastTree did not have the appropriate

substitution model estimated for our dataset (LG) so we altered the software to include the LG substitution matrix and sent the modified software to the authors for verification. Ultimately, our matrix was accepted and implemented in the subsequent versions of the software (version 2.1.9: March 29, 2016).

The recent widespread use of IQ-Tree (Nguyen *et al.*, 2014; Zhou *et al.*, 2017) as a fast phylogenetic tree-building method prompted a re-analysis of some of our datasets to compare the results with those obtained by FastTree. These analyses were completed manually as IQ-Tree is not implemented yet in our pipeline. The repeated analyses include (i). each permutation scenario (DT, CHF, ACT) under HIGH and LOW sampling and (ii.) ACT permutations scenarios under MID random sampling scenarios. These are the analyses that show the strongest trends in FastTree and, therefore, the best candidates for a re-analysis with IQ-Tree. Just as with the products of FastTree, all trees were analyzed for the discordance produced on both the internal node level as well as at the backbone level (for results see below, Supplementary Results, section 2.1).

1.3 Sampling & permutation scenario example

While a simulation approach would have allowed to fully control variables, it is limited in the complexity of the evolutionary processes that can be modeled. For example, horizontally transferred genes and long-branch attraction are known to affect phylogenetic accuracy but the relative effect they have on a phylogeny are not well understood. Modeling these phenomena under a variety of conditions would be computationally taxing as it would exponentially increase the numbers of scenarios and permutations to explore. Instead, we chose to use empirical data that implicitly already includes this information and compare the effect of taxon resampling on phylogenetic accuracy within a relative framework (total # of trees produced: > 1960). In other words, all our permutations share the same potential confounding factors that may be affecting phylogenetic reconstruction so that the only variable changing is the number of species representing each phylum and the weight of these confounding factors that each species carries within its genome.

Thus, using empirical data, we implemented different sampling scenarios to an alignment by removing a set number of taxa for a chosen phylum (e.g., *Deinococcus-Thermus*) without altering the number of species present in other phyla. We tested three sampling scenarios representing LOW, HIGH and MID level sampling for a given phylum. Within each scenario, all species for a single phylum are then permuted to determine if a specific lineage is more likely to influence the accuracy of phylogenetic reconstruction than others. Under MID level sampling we also explored the possibility that if a set of closely related species (e.g., a monophyletic genus) is chosen instead of a set of randomly selected species the topology might be affected. Thus, we created two MID level sampling scenarios, one ancestry-based (MIDanc) and another, randomly-based (MIDran) that uses the same number of species from MIDanc but performs 20 iterations using randomly selected species.

For example, consider a phylum represented by six species belonging to two different classes (one containing two species and the other containing four species). In the LOW scenario, the resulting permutations create 6 phylogenetic trees each with only one of the six species available for that phylum. Under HIGH sampling, again 6 trees will be created each with five of the six species available. Using this hypothetical example for MID sampling, 2 trees will be created each with the representative species for one of the two classes for the MIDanc scenario. The same number of species used for MIDanc (two and four) would be randomly selected from six species and repeated 20 times resulting in a total of 40 (20 with two species kept and 20 with four species kept) to obtain the trees produced in the MIDran scenario.

1.4 Orthology & alignment length investigation

The length of an alignment is known to contribute to phylogenetic accuracy (Som, 2014). In our experimental design changes in alignment length can be caused by two factors: first, when the number of species retained is smaller there is a possibility that the number of orthologs may increase thus increasing the alignment length; second, different species sets can alter the number of gaps in the alignment, with higher gaps more likely to decrease the accuracy of phylogenetic reconstructions. To account for these variables, using *Deinococcus-Thermus* (DT) permutations under the LOW sampling scenario, we reduced the dataset at the start of the pipeline and reran ProteinOrtho (Lechner *et al.*, 2011) (Fig. 2: green box). We found that under the same parameters, reducing the dataset, from 766 species (FULL) to 747 species (DT: LOW), the number of orthologs we obtained increased by one (from 30 (FULL) to 31) in 19 of the 20 trees, resulting in an average 11% (10.57-11.16%) difference in alignment length (Table S3). *Marinithermus hydrothermalis* was the exception with only 0.21% difference (Table 3). If the number of orthologs increased, we then performed a bootstrap analysis to reduce the alignment length to the same number of sites (6,227) as the original concatenation. Fifty bootstrap iterations (bp) were performed for each permutation from which a majority-rule consensus tree (bp consensus tree) was estimated using IQ-TREE (Nguyen *et al.*, 2014).

We compared the backbones of permutation trees produced with the additional orthologs (re-ortholog trees) to the original DT trees produced under LOW sampling using the orthologs obtained from the full dataset (original trees) to evaluate if the change in orthologs would produce different backbone phylogenies. We found that in 60% of the trees with the additional ortholog, and thus longer alignment length, there was no difference in the backbone topology produced (Table S4). We also compared the bp consensus trees to the re-ortholog trees to see if the composition of the randomly selected sites that remained in the bootstrapped alignment affected the phylogeny of the backbone produced. In 80% of permutations, reducing the length of the alignment had no effect on the phylogeny produced (Table S4). Overall, altering the number of orthologs and/or the alignment length has no effect on the topology produced in 55% of the cases (Table S4) (e.g., Tree C before and after the change in variables stays the same). In the remaining 45% of the cases, the topology switched between Trees B, C, and D.

Table S3 Ortholog group re-sampling results. Difference observed when Deinococcus-Thermus permutations under LOW sampling were altered at the start of the pipeline as opposed to altering the supermatrix. Differences are obtained through comparison with the result of the full dataset (30 orthologs, 6227 sites). Dcc.: Deinococcus, Th.: Thermus.

Species	Orthologs	Alignment length	Site diff.	% diff.
Dcc. actinosclerus	31	6948	721	10.94
Dcc. deserti	31	6916	689	10.48
Dcc. geothermalis	31	6922	695	10.57
Dcc. gobiensis	31	6914	687	10.46
Dcc. maricopensis	31	6936	709	10.77
Dcc. peraridilitoris	31	6941	714	10.84
Dcc. proteolyticus	31	6935	708	10.76
Dcc. radiodurans	31	6938	711	10.80
Dcc. soli	31	6936	709	10.77
Dcc. swuensis	31	6938	711	10.80
Marinith. hydrothermalis	30	6240	13	0.21
Meioth. silvanus	31	6942	715	10.86
Oceanith. profundus	31	6949	722	10.96
Th. aquaticus	31	6936	709	10.77
Th. oshimai	31	6939	712	10.82
Th. parvatiensis	31	6944	717	10.89
Th. scotoductus	31	6944	717	10.89
Th. sp. CCB	31	6935	708	10.76
Th. thermophilus	31	6963	736	11.16
Truepera radiovictrix	31	6938	711	10.80
Average	31	6903	676	10.27
Stardard deviation	0.22	156	675	10.25

Table S4 Backbone topology resulting from resampling of orthologs based on those presented in Figure 5, obtained under LOW sampling for Deinococcus-Thermus phylum permutations as explained in section 3.4 of main text. Consensus trees were generated from 50 bootstraps (bp) based on majority rule consensus. Dcc.: Deinococcus, Th.: Thermus.

Species	original	re-ortholog	bp consensus
Dcc. actinosclerus	tree C	tree C	tree C
Dcc. deserti	tree B	tree C	tree C
Dcc. geothermalis	tree B	tree C	tree C
Dcc. gobiensis	tree C	tree C	tree C
Dcc. maricopensis	tree C	tree C	tree D
Dcc. peraridilitoris	tree B	tree C	tree C
Dcc. proteolyticus	tree B	tree C	tree C
Dcc. radiodurans	tree C	tree C	tree C
Dcc. soli	tree C	tree B	tree C
Dcc. swuensis	tree C	tree C	tree C
Marinith. hydrothermalis	tree C	tree C	tree C
Meioth. silvanus	tree D	tree C	tree C
Oceanith. profundus	tree C	tree C	tree C
Th. aquaticus	tree C	tree C	tree C
Th. oshimai	tree C	tree B	tree C
Th. parvatiensis	tree C	tree C	tree C
Th. scotoductus	tree C	tree C	tree C
Th. sp. CCB	tree C	tree C	tree C
Th. thermophilus	tree C	tree C	tree C
Truepera radiovictrix	tree B	tree C	tree D

1.5 Hug et al. (2016) Deinococcus-Thermus permutations

Using the 3083 species concatenated ribosomal protein alignment provided by Hug et al. (2016), we implemented our methods, using the same software and parameters, for the 6 Deinococcus-Thermus (DT) species (*Deinococcus geothermalis*, *Truepera radiovictrix*, *Meiothermus ruber*, *Thermus oshimai*, *Marinithermus hydrothermalis*, *Oceanithermus profundus*) in the alignment. We also re-analyzed our own 766 species dataset after eliminating all DT species except for the 6 used in the Hug et al. study. Resulting trees from both re-analyses were compared to obtain the normalized Robinson-Foulds metric (Table S23 and Table S24, respectively).

2. Supplemental Results

2.1 IQ-TREE vs FastTree

In addition to estimating the FULL (766 species) dataset using IQ-TREE (Nguyen *et al.*, 2014), we also reanalyzed 100% of our alignments under various sampling scenarios for each of the three phyla analyzed (DT, CHF, ACT). We then analyzed all IQ-Tree results following the same methodology used for the FastTree results. The FULL tree produced by IQ-TREE differed from the tree produced by FastTree in 122 branches ($nRF > 0.08$) and resulted in backbone tree B (as shown in Fig. 6 of main text).

Comparing permuted trees produced from IQ-TREE under LOW and HIGH sampling showed much higher discordance ($> 3x$) among the internal nodes than trees produced by FastTree across all three phyla (Table 5). The results of the backbone frequency recovered using FastTree showed consistency in HIGH sampling always recovering the same backbone as the FULL phylogeny but LOW sampling resulted in high variance among backbones reconstructed. IQ-TREE also recovered the reference trees for all trees produced under HIGH sampling and showed more variance among LOW permutations, although in 50% of the cases for DT it reconstructed the FULL tree topology (table 6).

Although nearly 95% of the IQ-Tree trees produced topologies shown in Fig. 6a in the main text, 6 of the 108 trees produced were unique. Keeping *Thermus parvatiensis* as the only DT representative resulted in a backbone topology similar to tree C except that this species grouped between *Coprothermobacter proteolyticus* (CTP) and *Thermodesulfobium narugense* (TSN) (referred to as tree C*). The other 5 trees resulted from LOW permutations within Chloroflexi. Four permutations showed a topology where the permuted species grouped with CTP/TSN and placed the rest of the Firmicutes and Tenericutes with the sister clade of Actinobacteria and Deinococcus-Thermus (Tree H: add the newick style backbone tree here). Keeping only *Roseiflexus castenholzii* resulted in the last unique topology which is similar to the topology shown in tree E but CHF and FT branches are flipped (tree I: add nwk backbone tree). Surprisingly, 90% of the permutations of Actinobacteria under LOW sampling recovered the reference tree (tree B) and in only 2 of the 20 samples was tree A recovered instead.

Table S5 Summary of normalized Robinson-Foulds (nRF) scores produced for each phylum analyzed (DT: Deinococcus-Thermus, CHF: Chloroflexi, ACT: Actinobacteria) for a given sampling scenario (HIGH or LOW).

		DT		CHF		ACT	
		HIGH	LOW	HIGH	LOW	HIGH	LOW
FastTree	ΣnRF	0.538	2.202	0.423	0.741	0.974	1.327
	μ_{nRF}	0.027	0.110	0.030	0.053	0.049	0.066
	σ_{nRF}	0.011	0.077	0.018	0.020	0.025	0.028
IQ-TREE	ΣnRF	7.160	8.546	2.619	3.845	4.141	3.437
	μ_{nRF}	0.358	0.427	0.187	0.275	0.207	0.172
	σ_{nRF}	0.079	0.107	0.046	0.049	0.049	0.042

Table S6 Backbone topology produced for Deinococcus-Thermus (left) and Chloroflexi (right) permutations under LOW sampling scenario (* denotes paraphyletic CTP/TSN).

	FastTree	IQ-TREE		FastTree	IQ-TREE
Deinococcus_actinosclerus	C	D	Anaerolinea_thermophila_UNI-1	E	H
Deinococcus_deserti_VCD115	B	B	Caldiilinea_aerophila_DSM_14535__NBRC_104270	F	F
Deinococcus_geothermalis_DSM_11300	B	B	Chloroflexus_aggregans_DSM_9485	F	F
Deinococcus_gobiensis_I-0	C	B	Chloroflexus_aurantiacus_J-10-fl	F	F
Deinococcus_maricopensis_DSM_21211	C	B	Chloroflexus_sp._Y-400-fl	F	F
Deinococcus_peraridilitoris_DSM_19664	B	B	Dehalococcoides_mccartyi_195	B	H
Deinococcus_proteolyticus_MRP	B	B	Dehalococcoides_sp._UCH007	B	H
Deinococcus_radiodurans_R1	C	B	Dehalogenimonas_lykanthroporepellens_BL-DC-9	F	F
Deinococcus_soli__Cha_et_al	C	B	Dehalogenimonas_sp._WBC-2	B	B
Deinococcus_swuensis	C	B	Herpetosiphon_aurantiacus_DSM_785	F	F
Marinithermus_hydrothermalis_DSM_14884	C	A	Roseiflexus_castenholzii_DSM_13941	F	I
Meiothermus_silvanus_DSM_9946	D	C	Roseiflexus_sp._RS-1	F	B
Oceanithermus_profundus_DSM_14977	C	A	Sphaerobacter_thermophilus_DSM_20745	F	F
Thermus_aquaticus_Y51MC23	C	A	Thermomicrobium_roseum_DSM_5159	F	H
Thermus_oshimai_JL-2	C	C			
Thermus_parvatiensis	C	C*			
Thermus_scutoductus_SA-01	C	A			
Thermus_sp	C	C			
Thermus_thermophilus_JL-18	C	A			
Truepera_radiovictrix_DSM_17093	B	B			

We also compared the results of trees produced by MID sampling using randomly selected species (MIDran) for FastTree to trees produced in the same way by IQ-TREE. Again, among the internal nodes within Actinobacteria, overall we found that FastTree averaged lower nRF scores than IQ-TREE (Table S7), however the differences were not as extreme as seen among trees under HIGH and LOW sampling (Table S5). Further, the results of backbone show higher consistency under IQ-TREE with at least 90% of the trees recovering the same backbone as the FULL tree (Table S8).

Table S7 Summary of normalized Robinson-Foulds (nRF) scores produced for Actinobacteria (ACT) permutations under MIDran sampling using 20 replicates of randomly selected species. The number of species kept is shown in each column.

		ACT				
		86	32	19	17	10
FastTree	$\sum nRF$	2.445	4.060	3.230	2.509	1.161
	μ_{nRF}	0.122	0.203	0.162	0.125	0.058
	σ_{nRF}	0.044	0.104	0.060	0.046	0.045
IQ-TREE	$\sum nRF$	3.808	4.792	3.520	2.753	3.102
	μ_{nRF}	0.190	0.240	0.176	0.138	0.155
	σ_{nRF}	0.051	0.057	0.047	0.046	0.087

Table S8 Backbone topology produced by Actinobacteria (ACT) permutations under MID sampling using 20 replicates of randomly selected species. The number of species kept is shown for each column.

		ACT				
		86	32	19	17	10
FastTree	treeA	0.75	0.45	0.3	0.3	0.1
	treeB	0.25	0.4	0.6	0.55	0.9
	treeC		0.1	0.1	0.1	
	treeD		0.05			
	treeE					
	treeF				0.05	
IQ-TREE	treeA	0.1	0.05	0.05	0.1	
	treeB	0.9	0.95	0.95	0.9	0.95
	treeC					
	treeD					0.05
	treeE					
	treeF					

Overall, the results from IQ-Tree and FastTree produce a similar trend that shows multiple topologies obtained by datasets with few species (LOW sampling) and with different species identities (permutations of LOW sampling). However, IQ-Tree shows higher internal consistency (i.e., fewer topologies) when only the backbone is analyzed but lower consistency when all internal nodes are compared (higher nRF values) relative to FastTree. The reasons for the different behavior of IQ-Tree between backbone and internal nodes are unknown and will be investigated in the future. Nonetheless, despite this, we did not find FastTree and IQ-Tree to be significantly different in the general trends produced, as has been suggested before (e.g., Lees, *et al.*, 2018; Parks, *et al.*, 2018).

2.2 MID sampling scenario: ancestry versus control

There were two scenarios considered under MID sampling. The first was a scenario driven by the ancestry of the species within a given phylum (MIDanc), the second acted as a control to this scenario where species were chosen randomly (MIDran) (details given in main text and supplemental methods section 1.3). Twenty random samples (MIDran) were created for each MIDanc permutation within Actinobacteria (ACT) and Deinococcus-Thermus (DT); Chloroflexi was not included for saturation concerns due to the low number of species (two or three) kept for each MIDanc permutation.

To analyze discord within internal nodes, we evaluated the average discord produced from two samples within the 20 randomly sampled trees for a given scenario and compared that to the discord produced from the same two scenarios within the ancestry driven sample. For example, within Deinococcus-Thermus there were only two MID scenarios: one where we kept 10 species belonging to the Deinococcus genus (DT10) and another where we kept 6 species belonging to the Thermus genus (DT6). Within MIDran, we assessed the nRF of the 20 trees for each DT10 and DT6 and compared the average of discord produced to the discord produced from the two MIDanc trees. Results from DT and ACT are opposite: in DT, MIDran trees had lower average discord (nRF=0.0033) than the discord produced between the MIDanc trees (nRF=0.0094); in ACT, the majority of the comparisons shows higher discord for MIDran (Supplementary Material, Fig.1). These opposite results are likely to represent a saturation effect within DT given the small number of species to select from for the MIDran scenario. Thus, results from ACT are likely to be more informative.

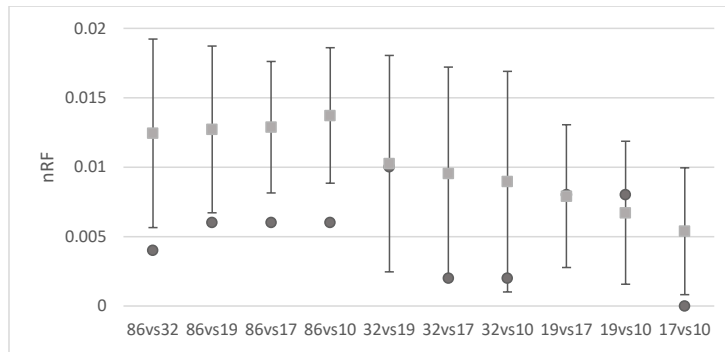


Figure S1 Normalized Robinson-Foulds (nRF) scores produced from MID level sampling in ACT. Ancestry driven nRF values (MIDanc: totals between two trees shown in dark grey circles) are compared to those from randomly sampled datasets (MIDran: averages from 40 trees shown in light grey squares with error bars showing standard deviation).

At the backbone level, we see that the selection of species based on ancestry is less likely to produce stable topologies (compare results from Fig. 7a in the main text and Fig. S2). This is especially true within DT permutations where not only did both ancestry trees, DT10 and DT6, differ from the reference tree (i.e., FULL: tree A) but they differed between each other. However, within the randomly sampled trees, not only are the majority of the trees produced in agreement with each other, they are also consistently recovering the reference tree (Fig. S2: red bars). Within Actinobacteria, although we see more disagreement among the topologies, the reference tree is recovered especially in samples that have higher number of species kept (Fig. S2: purple bars).

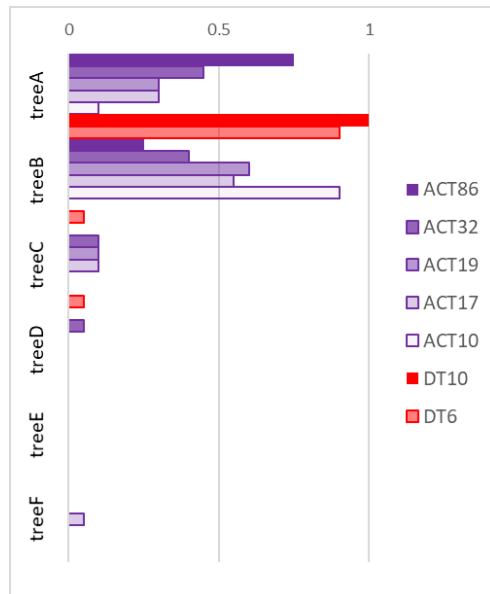


Figure S2 Backbone frequency results for MID random sampling scenario. Trees A-F as shown in figure 5 of main text.

2.4 CTP/TSN investigation

To test the influence of *Coprothermobacter proteolyticus* (CTP) and *Thermodesulfobium narugense* (TSN) independently, we repeated our reconstruction methods with both CTP and TSN removed, as well as removing one of them at a time. We then reran our pipeline for each phylum permutation in small groups (Deinococcus-Thermus and Chloroflexi) and for 5 permutations of each sampling scenario in the large group (Actinobacteria). We found that removing both CTP and TSN or excluding CTP only produced different backbone topologies. When we kept in CTP and excluded TSN we found all phyla and sampling scenarios resulted in the same backbone topology as our FULL dataset (tree A in Fig 3 in the main text). While the other two cases yielded different results depending on the phylum permuted, specifically, iterations within our sampling scenarios for Chloroflexi different then the results of backbone topologies produced from permutations within Deinococcus-Thermus and Actinobacteria.

When we removed CTP and TSN all scenarios resulted in the same backbone topology as tree A if the branch containing CTP/TSN was simply pruned (i.e., Tree D in Fig 6a and Tree X in Fig. 6b in the main text). While Chloroflexi also recovered that topology under HIGH sampling, all permutations in MID and LOW sampling recovered Tree Z. Similarly, when we removed CTP and kept TSN, all trees recovered the same topology as Tree B except for permutations of Chloroflexi under MID and LOW sampling. For the majority of these Chloroflexi permutations under LOW and MID sampling, Tree E was recovered (8/14 and 3/4, respectively). Tree B was recovered for the other permutation in MID sampling and for 3 more permutations in LOW sampling. Interestingly, in the remaining 3 of the 14 Chloroflexi permutations under LOW sampling, a new topology was recovered which places Firmicutes/Tenericutes basal to the other ingroup phyla and places Chloroflexi as a sister clade to Deinococcus-Thermus and Actinobacteria. Taken together these results show that these two species exert a strong influence on the overall backbone topology of the Terrabacteria, especially Chloroflexi species

when alternatively sampled, a result that is unexpected from species that have been classified as part of a well-sampled group.

2.5 Other sources of bias: amino acids and branch lengths

Following our results, we investigated some of the possible causes of the phylogenetic instability, specifically number of genes used in the alignment (see Supplemental section 1.4) and compositional bias. Previous literature has attempted to identify the proportional weight that these factors have on phylogenetic instability and found that the level of incongruence that is caused is highly dependent on the data used (e.g., Reddy *et al.*, 2017). For example, several studies that have attempted to resolve deep animal relationship have shown that, despite the implementation of the same approach, the number of genes required for congruence differs based on the dataset (Philippe *et al.*, 2011).

To evaluate possible differences seen within amino acid usage of species, we calculated averages and standard deviations of the amino acids in each lineage. Species with an average amino acid usage within one standard deviation of the average of the total dataset were considered unbiased. We repeated this analysis for each ortholog separately and found no gene-specific difference in this trend. In particular, species that produced different phylogenies did not show to have a significantly different compositional bias compared to the other species in the phylum and across the phylogeny (Supplementary Fig. S3). Additionally, we considered the effect that changes in branch lengths might have on the backbone phylogeny when different species are selected, we used an R script to extract branch length for 119 trees and make statistical comparisons (e.g., pairwise distances) (Table S9). Overall, we found one species, within *Deinococcus-Thermus*, *Marinithermus hydrothermalis*, that had much smaller branch lengths (0.197) compared to other species (average: 0.592). However, this species was not identified as problematic through our Robinson-Foulds analysis (Fig. 5).

Neither of the factors we individually analyzed seems to be directly correlated with the species that produce different phylogenetic signals, which suggests that other factors might be disproportionately affecting tree reconstruction when these species are used (Philippe *et al.*, 2011). Thus, these species should be further investigated to determine their effect on reconstructed phylogenies, especially if they are used in small clades.

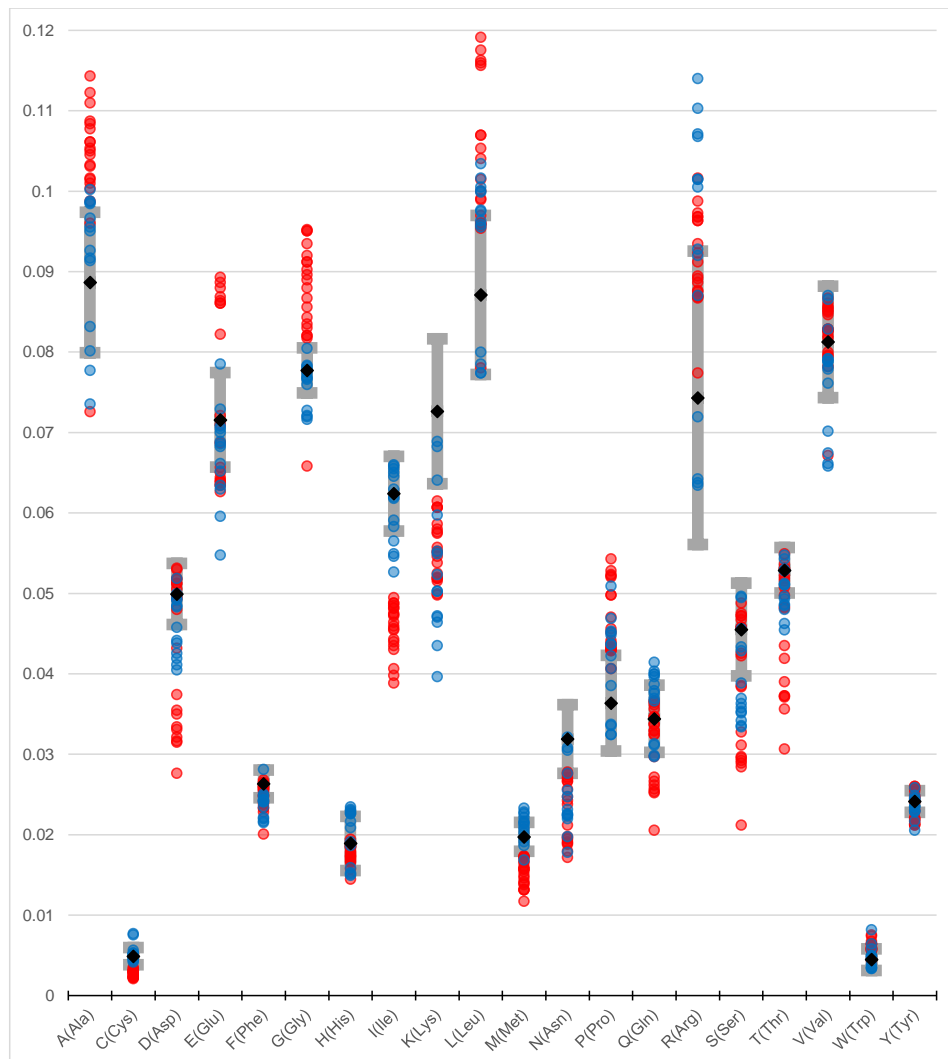


Figure S3 Average amino acid frequency for FULL (766 species) dataset (black dot) and plus/minus standard deviation (grey bars), as well as amino acid frequencies for species of *Deinococcus-Thermus* (red dots) and *Chloroflexi* (blue dots).

Commented [FUB1]: Add the y-axis

Table S9 Branch lengths in phylogenies for species of *Deinococcus-Thermus* (DT) and *Chloroflexi* (CHF) based on FULL (766 species) dataset and LOW sampling (i.e., where only species listed is included within corresponding phylum). Branch lengths were calculated from the stem node of the DT group to the tip of each lineage. Dcc.: *Deinococcus*, Th.: *Thermus*.

DT			CHF		
Species	FULL	LOW	Species	FULL	LOW
Dcc. actinosclerus	0.685	0.943	Anaerolinea thermophila	0.755	0.785
Dcc. deserti	0.635	0.993	Caldiilinea aerophila	0.66	0.683
Dcc. geothermalis	0.599	0.948	Chloroflexus aggregans	0.703	0.695
Dcc. gobiensis	0.65	0.966	Chloroflexus aurantiacus	0.702	0.689
Dcc. maricopensis	0.589	0.929	Chloroflexus sp. Y-400-II	0.7	0.69
Dcc. peraridilitoris	0.676	0.99	Dehalococcoides mccartyi	0.812	0.915
Dcc. proteolyticus	0.691	0.99	Dehalococcoides sp. UCH007	0.819	0.919
Dcc. radiodurans	0.687	0.395	Dehalogenimonas		
Dcc. soli	0.67	0.936	lykanthroporepellens	0.828	0.839
Dcc. swuensis	0.669	0.936	Dehalogenimonas sp. WBC-2	0.849	0.925
Marinith.			Herpetosiphon aurantiacus	0.707	0.727
hydrothermalis	0.197	0.805	Roseiflexus castenholzii	0.689	0.692
Meioth. silvanus	0.542	0.968	Roseiflexus sp. RS-1	0.678	0.686
Oceanith. profundus	0.558	0.83	Sphaerobacter thermophilus	0.606	0.629
Th. aquaticus	0.59	0.887	Thermomicrobium roseum	0.709	0.685
Th. oshimai	0.591	0.862			
Th. parvatiensis	0.563	0.903			
Th. scotoductus	0.608	0.876			
Th. sp. CCB	0.54	0.889			
Th. thermophilus	0.562	0.851			
Truepera radiovictrix	0.539	0.933			

3. Supplementary Data

FULL (766 species) tree in newick format:

```
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_odorifer.189426:0.00698,(Paenibacillus_sp._FSL_R5-0345.1536770:0.00165,Paenibacillus_sp._FSL_H7-0737.1536775:0.00266)0.999:0.00461)1.000:0.01946,((Paenibacillus_graminis.189425:0.00346,Paenibacillus_riograndensis_SBR5.1073571:0.00683)1.000:0.01372,((Paenibacillus_sp._FSL_R7-0273.1536772:0.00605,Paenibacillus_sp._FSL_R7-0331.1536773:0.00810)1.000:0.02248,(Paenibacillus_sp._FSL_H7-0357.1536774:0.01924,(Paenibacillus_borealis.160799:0.00252,(Paenibacillus_sp._FSL_P4-0081.1536769:0.00133,Paenibacillus_sp._FSL_R5-0912.1536771:0.00202)0.988:0.00221)1.000:0.01538)0.960:0.00611)0.136:0.00325)1.000:0.01092)1.000:0.02519,(Paenibacillus_stellifer.169760:0.03707,(Paenibacillus_durus.44251:0.01671,Paenibacillus_sabinae_T27.1268072:0.02047)0.988:0.01145)1.000:0.03428)1.000:0.05236,Paenibacillus_sp._IHB.10380.1566358:0.09564)0.437:0.01572)0.991:0.01959)0.986:0.02683)1.000:0.06993,(Thermobacillus_composti_KWC4.717605:0.15261,(Paenibacillus_sp._320-W.1695218:0.09556,(Paenibacillus_sp._JDR-2.324057:0.10228,Paenibacillus_beijingensis.1126833:0.10094)0.992:0.02699)0.721:0.02118)1.000:0.04574)1.000:0.03546)1.000:0.14689)1.000:0.10287)1.000:0.12074)0.089:0.03143)1.000:0.05228,(Thermosediminibacter_oceani_DSM_16646.555079:0.19951,Tepidanaerobacter_acetatoxydans_Re1.1209989:0.25862)1.000:0.23676)0.999:0.05148)0.927:0.03092,Mahella_australiensis_50-1_BON.697281:0.48583,((Caldicellulosiruptor_saccharolyticus_DSM_8903.351627:0.06859,((Caldicellulosiruptor_obsidiansis_OB4.7.608506:0.01156,Caldicellulosiruptor_owensensis_OL.632518:0.01628)1.000:0.00917,(Caldicellulosiruptor_hydrothermalis_108.63.2292:0.00900,((Caldicellulosiruptor_bescii_DSM_6725.521460:0.00907,Caldicellulosiruptor_kronotskyensis_2002.632348:0.00976)1.000:0.00999,(Caldicellulosiruptor_kristjanssonii_I77R1B.632335:0.00266,Caldicellulosiruptor_lactooaceticus_6A.632516:0.00281)1.000:0.00773)0.230:0.00310)1.000:0.01248)1.000:0.06983)1.000:0.43369,((Thermoanaerobacterium_thermosaccharolyticum_M07.95.698948:0.05411,(Thermoanaerobacterium_xylanolyticum_LX-11.858215:0.01231,Thermoanaerobacterium_saccharolyticum_JW_SL-YS485.1094508:0.01802)1.000:0.03954)1.000:0.18605,(Caldanaerobacter_subterraneus_subsp._tengcongensis_MB4.273068:0.10934,(Thermoanaerobacter_kivui.2325:0.07419,((Thermoanaerobacter_italicus_Ab9.580331:0.00486,Thermoanaerobacter_mathranii_i_subsp._mathranii_str._A3.583358:0.00539)1.000:0.03073,(Thermoanaerobacter_wiegeli_Rt8.B1.697303:0.01006,((Thermoanaerobacter_sp._X514.399726:0.00055,Thermoanaerobacter_sp._X513.573062:0.00074)0.992:0.00270,(Thermoanaerobacter_pseudetanolicus_ATCC_33223.340099:0.00055,Thermoanaerobacter_brockii_subsp._finnii_Ako-1.509193:0.00071)1.000:0.00466)1.000:0.00659)0.997:0.01005)0.939:0.02013)0.989:0.04667)1.000:0.11969)1.000:0.18714)0.884:0.03569);

Table S10 Full species list for 766 species used in the analysis with taxon id and internal species id.

Species	Taxon id	Species	Taxon id
Synechococcus elongatus	1140	Clostridium butyricum	1492
Synechocystis sp.	1147	Peptoclostridium difficile	1496
Synechocystis sp.	1148	Clostridium sp. orogenes	1509
Dermacoccus nishinomiyaensis	1274	Clostridium sticklandii	1511
Staphylococcus hyicus	1284	Clostridium beijerinckii	1520
Staphylococcus simulans	1286	Moorella thermoacetica	1525
Staphylococcus xylosus	1288	Clostridium scatologenes	1548
Staphylococcus schleiferi	1295	Lactobacillus paracasei	1597
Streptococcus gordonii	1302	Lactobacillus acetotolerans	1600
Enterococcus faecium	1352	Lactobacillus salivarius	1624
Enterococcus gallinarum	1353	Bifidobacterium adolescentis	1680
Planococcus kocurii	1374	Bifidobacterium bifidum	1681
Aerococcus viridans	1377	Bifidobacterium breve	1685
Bacillus coagulans	1398	Bifidobacterium coryneforme	1687
Bacillus pumilus	1408	Corynebacterium stationis	1705
Bacillus sp.	1409	Corynebacterium pseudotuberculosis	1719
Bacillus thuringiensis	1442	Mycobacterium fortuitum	1766
Bacillus smithii	1479		

Mycobacterium tuberculosis	1773	Aerococcus urinaeequi	51665
Mycobacterium microti	1806	Lactobacillus gallinarum	52242
Streptomyces albus	1888	Actinomyces meyeri	52773
Streptomyces glaucescens	1907	Enterococcus durans	53345
Streptomyces reticuli	1926	Streptomyces venezuelae	54571
Aeromicrobium erythreum	2041	Oscillatoria acuminata	56110
Pimelobacter simplex	2045	Actinotignum schaalii	59505
Mycoplasma arginini	2094	Paenibacillus peoriae	59893
Mycoplasma mycoides	2103	Prochlorococcus marinus	59922
Mycoplasma agalactiae	2110	Lactobacillus paraplantarum	60520
Mycoplasma californicum	2113	Acholeplasma brassicae	61635
Thermoanaerobacter kivui	2325	Nostoc punctiforme	63737
Dactylococcopsis salina	13035	Synechococcus sp.	64471
Lysinibacillus fusiformis	28031	Halotheca sp.	65093
Nostoc sp.	28072	Cyanothece sp.	65393
Clostridium cellulosi	29343	Kocuria palustris	71999
Synechococcus sp.	29410	Staphylococcus capitis	72758
Mycoplasma canadense	29554	Bacillus clausii	79880
Mycoplasma canis	29555	Pseudanabaena sp.	82654
Mycoplasma gallinaceum	29556	Clostridium acetium	84022
Clavibacter michiganensis	31964	Mycoplasma disp.ar	86660
Synechococcus sp.	32049	Bacillus weihenstephanensis	86662
Synechococcus sp.	32051	Aerococcus christensenii	87541
Mycobacterium bovis	33892	Brevibacterium flavum	92706
Mycobacterium africanum	33894	Bacillus sp.	98228
Acholeplasma oculi	35623	Calothrix sp.	99598
Corynebacterium kutscheri	35755	Rhodococcus jostii	101510
Nocardia farcinica	37329	Nostoc sp.	103690
Candidatus Phytoplasma	37692	Frankia sp.	106370
Streptomyces pristinaespiralis	38300	Synechococcus sp.	110662
Mycoplasma capricolum	40480	Actinomyces radidentis	111015
Cyanothece sp.	41431	Stanieria cyanosphaera	111780
Rubrobacter radiotolerans	42256	Leptolyngbya sp.	111781
Cyanothece sp.	43989	Pleurocapsa sp.	118163
Paenibacillus durus	44251	Aerococcus sanguinicola	119206
Anabaena sp.	46234	Arthrobacter sulfonivorans	121292

<i>Aerococcus urinaehominis</i>	128944	<i>Amycolatopsis japonica</i>	208439
<i>Mycobacterium goodii</i>	134601	<i>Carnobacterium</i> sp.	208596
<i>Actinoplanes</i> sp.	134676	<i>Streptococcus mutans</i>	210007
<i>Bacillus endophyticus</i>	135735	<i>Mycobacterium</i> sp.	212767
<i>Corynebacterium testudinis</i>	136857	<i>Mycobacterium marinum</i>	216594
<i>Weissella cibaria</i>	137591	<i>Spiroplasma litorale</i>	216942
<i>Desulfitobacterium hafniense</i>	138119	<i>Spiroplasma tunicum</i>	216946
<i>Rathayibacter toxicus</i>	145458	<i>Streptococcus uberis</i>	218495
<i>Lactobacillus kunkei</i>	148814	<i>Oceanobacillus iheyensis</i>	221109
<i>Corynebacterium imitans</i>	156978	<i>Enterococcus faecalis</i>	226185
<i>Paenibacillus borealis</i>	160799	<i>Streptomyces avermitilis</i>	227882
<i>Corynebacterium camporealensis</i>	161896	<i>Rhodococcus erythropolis</i>	234621
<i>Corynebacterium singulare</i>	161899	<i>Geobacillus kaustophilus</i>	235909
<i>Paenibacillus naphthalenovorans</i>	162209	<i>Anabaena variabilis</i>	240292
<i>Mycobacterium</i> sp.	164756	<i>Dehalococcoides mccartyi</i>	243164
<i>Mycobacterium</i> sp.	164757	<i>Deinococcus radiodurans</i>	243230
<i>Synechococcus</i> sp.	166314	<i>Mycobacterium avium</i>	243243
<i>Paenibacillus stellifer</i>	169760	<i>Mycoplasma arthritidis</i>	243272
<i>Staphylococcus epidermidis</i>	176279	<i>Carboxydotherrmus hydrogenoformans</i>	246194
<i>Oscillatoria nigro-viridis</i>	179408	<i>Staphylococcus equorum</i>	246432
<i>Streptococcus pneumoniae</i>	189423	<i>Gloeobacter violaceus</i>	251221
<i>Paenibacillus graminis</i>	189425	<i>Chroococcidiopsis thermalis</i>	251229
<i>Paenibacillus odorifer</i>	189426	<i>Arthrobacter arilaitensis</i>	256701
<i>Mycobacterium</i> sp.	189918	<i>Lactobacillus johnsonii</i>	257314
<i>Corynebacterium atypicum</i>	191610	<i>Exiguobacterium sibiricum</i>	262543
<i>Synechococcus</i> sp.	195253	<i>Mycoplasma hyopneumoniae</i>	262722
<i>Nocardioides</i> sp.	196162	<i>Onion yellows</i>	262768
<i>Corynebacterium efficiens</i>	196164	<i>Verrucospora maris</i>	263358
<i>Thermosynechococcus elongatus</i>	197221	<i>Rubrobacter xylanophilus</i>	266117
<i>Anoxybacillus gonensis</i>	198467	<i>Kineococcus radiotolerans</i>	266940
<i>Planococcus rifietoensis</i>	200991	<i>Mycoplasma mobile</i>	267748
<i>Ruminiclostridium thermocellum</i>	203119	<i>Thermobifida fusca</i>	269800
<i>Leuconostoc mesenteroides</i>	203120	<i>Anabaena cylindrica</i>	272123
<i>Oenococcus oeni</i>	203123	<i>Bacillus halodurans</i>	272558
<i>Trichodesmium erythraeum</i>	203124	<i>Mycoplasma penetrans</i>	272633
<i>Tropheryma whipplei</i>	203267		

Spiroplasma kunkelii	273035	Gordonia sp.	337191
Caldanaerobacter subterraneus	273068	Thermoanaerobacter pseudethanolicus	340099
Ureaplasma parvum	273119	Corynebacterium glutamicum	340322
Pediococcus pentosaceus	278197	Staphylococcus saprophyticus	342451
Streptomyces ambofaciens	278992	Desulfotomaculum reducens	349161
Staphylococcus haemolyticus	279808	Leuconostoc citreum	349519
Renibacterium salmoninarum	288705	Mycobacterium gilvum	350054
Arthrobacter aurescens	290340	Mycobacterium vanbaalenii	350058
Arthrobacter sp.	290399	Alkaliphilus oremlandii	350688
Symbiobacterium thermophilum	292459	Acidothermus cellulolyticus	351607
Cyanobacterium stanieri	292563	Caldicellulosiruptor saccharolyticus	351627
Cyanobium gracile	292564	Roseiflexus sp.	357808
Alkaliphilus metalliredigens	293826	Lachnoclostridium phytofermentans	357809
Lactococcus piscium	297352	Brevibacillus brevis	358681
Frankia sp.	298653	Exiguobacterium sp.	360911
Frankia sp.	298654	Mycobacterium ulcerans	362242
Corynebacterium jeikeium	306537	Streptomyces vietnamensis	362257
Coprothermobacter proteolyticus	309798	Spiroplasma cantharicola	362837
Thermomicrobium roseum	309801	Streptococcus mitis	365659
Lactobacillus sakei	314315	Microbacterium sp.	367477
Bacillus cytotoxicus	315749	Salinispora tropica	369723
Herpetosiphon aurantiacus	316274	Pelotomaculum thermopropionicum	370438
Synechococcus sp.	316278	Streptococcus pyogenes	370552
Synechococcus sp.	316279	Halothermothrix orenii	373903
Nostoc sp.	317936	Rivularia sp.	373994
Deinococcus geothermalis	319795	Synechococcus sp.	374982
Synechococcus sp.	321327	Kocuria rhizophila	378753
Synechococcus sp.	321332	Roseiflexus castenholzii	383372
Aster yellows	322098	Listeria welshimeri	386043
Paenibacillus sp.	324057	Clostridium novyi	386415
Chloroflexus aurantiacus	324602	Streptococcus sanguinis	388919
Frankia alni	326424	Salinispora arenicola	391037
Chloroflexus aggregans	326427	Bifidobacterium longum	391904
Acaryochloris marina	329726	Clostridium cellulolyticum	394503
Enterococcus silesiacus	332949		
Syntrophomonas wolfei	335541		

Cyanothece sp.	395961	Macrococcus caseolyticus	458233
Cyanothece sp.	395962	Mycobacterium liflandii	459424
Staphylococcus carnosus	396513	Micrococcus luteus	465515
Bacillus pseudofirmus	398511	Streptomyces sp.	465541
Thermoanaerobacter sp.	399726	Thermobisp.ora bisp.ora	469371
Corynebacterium ureicelerivorans	401472	Cryptobacterium curtum	469378
Virgibacillus sp.	403957	Conexibacter woesei	469383
Saccharopolysp.ora erythraea	405948	Geobacillus sp.	471223
Salinicoccus halodurans	407035	Thermomonosp.ora curvata	471852
Streptomyces xiamenensis	408015	Beutenbergia cavernae	471853
Microterricola viridarii	412690	Slackia heliotrinireducens	471855
Geobacillus thermodenitrificans	420246	Jonesia denitrificans	471856
Lactococcus garvieae	420890	Saccharomonosp.ora viridis	471857
Ammonifex degensii	429009	Devriesea agamarum	472569
Clostridium kluyveri	431943	Streptomyces cyaneogriseus	477245
Bacillus selenitireducens	439292	Modestobacter marinus	477641
Acholeplasma laidlawii	441768	Candidatus Desulforudis	477974
Amycolicoccus subflavus	443218	Kytococcus sedentarius	478801
Streptomyces sp.	444103	Nakamurella multipartita	479431
Lysinibacillus sp.haericus	444177	Streptosp.orangium roseum	479432
Pseudonocardia sp.	445576	Catenulisp.ora acidiphila	479433
Actinosynnema mirum	446462	Sphaerobacter thermophilus	479434
Brachybacterium faecium	446465	Kribbella flava	479435
Cellulomonas flavigena	446466	Eggerthella lenta	479437
Nocardiosis dassonvillei	446468	Chloroflexus sp.	480224
Sanguibacter keddiei	446469	Paenibacillus sp.	481743
Stackebrandtia nassauensis	446470	Desulfotomaculum acetoxidans	485916
Xylanimonas cellulosilytica	446471	Lactobacillus reuteri	491077
Kocuria flava	446860	Anoxybacillus flavithermus	491915
Microcystis aeruginosa	449447	Cyanothece sp.	497965
Bacillus cereus	451709	Heliobacterium modesticaldum	498761
Kitasatosp.ora setae	452652	Thermus aquaticus	498848
Arthrobacter chlorophenolicus	452863	Eggerthella sp.	502558
Streptomyces griseus	455632	Corynebacterium urealyticum	504474
Thermus parvatiensis	456163	Thermoanaerobacter brockii	509193
Natranaerobius thermophilus	457570	Lactobacillus buchneri	511437

<i>Mycoplasma crocodyli</i>	512564	<i>Bacillus anthracis</i>	568206
<i>Actinoplanes missouriensis</i>	512565	<i>Lactobacillus rhamnosus</i>	568704
<i>Agathobacter rectalis</i>	515619	<i>Luteipulveratus mongoliensis</i>	571913
<i>Eubacterium</i>	515620	<i>Corynebacterium mustelae</i>	571915
<i>Butyrivibrio proteoclasticus</i>	515622	<i>Halanaerobium praevalens</i>	572479
<i>Bifidobacterium angulatum</i>	518635	<i>Clostridium cellulovorans</i>	573061
<i>Atopobium parvulum</i>	521095	<i>Thermoanaerobacter sp.</i>	573062
<i>Tsukamurella paurometabola</i>	521096	<i>Acetohalobium arabaticum</i>	574087
<i>Caldicellulosiruptor bescii</i>	521460	<i>Thermoanaerobacter italicus</i>	580331
<i>Gardnerella vaginalis</i>	525284	<i>Geobacillus sp.</i>	581103
<i>Acidimicrobium ferrooxidans</i>	525909	<i>Thermoanaerobacter mathranii</i>	583358
<i>Geodermatophilus obscurus</i>	526225	<i>Roseburia hominis</i>	585394
<i>Gordonia bronchialis</i>	526226	<i>Synechococcus sp.</i>	585423
<i>Meiothermus silvanus</i>	526227	<i>Synechococcus sp.</i>	585425
<i>Rhodoluna laticola</i>	529884	<i>Terribacillus aidingensis</i>	586416
<i>Clostridium carboxidivorans</i>	536227	<i>Cellulomonas fimi</i>	590998
<i>Rhodococcus opacus</i>	543736	<i>Streptomyces pratensis</i>	591167
<i>Geobacillus sp.</i>	544556	<i>Cellulomonas gilvus</i>	593907
<i>Actinomyces oris</i>	544580	<i>Arthrobacter sp.</i>	595593
<i>Filifactor alocis</i>	546269	<i>Caldicellulosiruptor obsidiansis</i>	608506
<i>Deinococcus deserti</i>	546414	<i>Clostridium saccharolyticum</i>	610130
<i>Bifidobacterium pseudocatenulatum</i>	547043	<i>Caldicellulosiruptor hydrothermalis</i>	632292
<i>Corynebacterium aurimucosum</i>	548476	<i>Caldicellulosiruptor kristjanssonii</i>	632335
<i>Mobiluncus curtisii</i>	548479	<i>Caldicellulosiruptor kronotskyensis</i>	632348
<i>Geobacillus sp.</i>	550542	<i>Caldicellulosiruptor lactoaceticus</i>	632516
<i>Nostoc azollae</i>	551115	<i>Caldicellulosiruptor owensensis</i>	632518
<i>Dehalogenimonas lykanthroporepellens</i>	552811	<i>Olsenella uli</i>	633147
<i>Thermosediminibacter oceani</i>	555079	<i>Geobacillus thermoglucosidasius</i>	634956
<i>Mycobacterium kansasii</i>	557599	<i>Thermincola potens</i>	635013
<i>Corynebacterium doosanense</i>	558173	<i>Lactobacillus koreensis</i>	637971
<i>Mycobacterium leprae</i>	561304	<i>Segniliparus rotundus</i>	640132
<i>Kyrpidia tusciae</i>	562970	<i>Clostridium lentocellum</i>	642492
<i>Ureaplasma urealyticum</i>	565575	<i>Syntrophothermus lipocalidus</i>	643648
<i>Enterococcus casseliflavus</i>	565655	<i>Micromonospora aurantiaca</i>	644283
<i>Bifidobacterium catenulatum</i>	566552	<i>Arcanobacterium haemolyticum</i>	644284
		<i>Thermaerobacter marianensis</i>	644966

<i>Corynebacterium kroppenstedtii</i>	645127	<i>Pediococcus clausenii</i>	701521
<i>Syntrophobotulus glycolicus</i>	645991	<i>Deinococcus maricopensis</i>	709986
<i>Desulfosp. orosinus acidiphilus</i>	646529	<i>Mycobacterium chubuense</i>	710421
<i>Micromonospora</i> sp.	648999	<i>Mycobacterium rhodesiae</i>	710685
<i>Truepera radiovictrix</i>	649638	<i>Intraspora angium calvum</i>	710696
<i>Bacillus cellulosilyticus</i>	649639	<i>Actinomyces</i> sp.	712122
<i>Actinoplanes</i> sp.	649831	<i>Olsenella</i> sp.	712411
<i>Streptomyces violaceusniger</i>	653045	<i>Streptococcus</i> sp.	712633
<i>Frankia symbiont</i>	656024	<i>Amycolatopsis mediterranei</i>	713604
<i>Arthrobacter alpinus</i>	656366	<i>Lactobacillus sanfranciscensis</i>	714313
<i>Halanaerobium hydrogeniformans</i>	656519	<i>Thermobacillus composti</i>	717605
<i>Corynebacterium resistens</i>	662755	<i>Clostridium clariflavum</i>	720554
<i>Mycoplasma genitalium</i>	662945	<i>Bacillus atrophaeus</i>	720555
<i>Ethanoligenens harbinense</i>	663278	<i>Thermus scotoductus</i>	743525
<i>Staphylococcus aureus</i>	663951	<i>Spiroplasma eriocheiris</i>	743698
<i>Bacillus</i> sp.	666686	<i>Isoptericola variabilis</i>	743718
<i>Oceanithermus profundus</i>	670487	<i>Mycoplasma bovoculi</i>	743966
<i>Pseudonocardia dioxanivorans</i>	675635	<i>Mycoplasma yeatsii</i>	743967
<i>Streptomyces scabiei</i>	680198	<i>Mycoplasma flocculare</i>	743971
<i>Rothia mucilaginosa</i>	680646	<i>Deinococcus gobiensis</i>	745776
<i>Geobacillus</i> sp.	691437	<i>Thermodesulfobium narugense</i>	747365
<i>Oscillibacter valericigenes</i>	693746	<i>Halobacteroides halobius</i>	748449
<i>Deinococcus proteolyticus</i>	693977	<i>Clostridium ljungdahlii</i>	748727
<i>Desulfotomaculum ruminis</i>	696281	<i>Streptomyces bingchenggensis</i>	749414
<i>Mahella australiensis</i>	697281	<i>Thermus oshimai</i>	751945
<i>Paenibacillus larvae</i>	697284	<i>Propionibacterium freudenreichii</i>	754252
<i>Thermoanaerobacter wiegelsii</i>	697303	<i>Cyanobacterium aponinum</i>	755178
<i>Ruminococcus albus</i>	697329	<i>Clostridium</i> sp.	755731
<i>Staphylococcus lugdunensis</i>	698737	<i>Desulfotobacterium dehalogenans</i>	756499
<i>Amphibacillus xylanus</i>	698758	<i>Bacillus</i> sp.	756828
<i>Thermoanaerobacterium thermosaccharolyticum</i>	698948	<i>Weissella ceti</i>	759620
<i>Corynebacterium diphtheriae</i>	698962	<i>Desulfotomaculum kuznetsovii</i>	760568
<i>Mageeibacillus indolicus</i>	699246	<i>Streptococcus parasanguinis</i>	760570
<i>Coriobacterium glomerans</i>	700015	<i>Leuconostoc kimchii</i>	762051
<i>Mycobacterium neoaurum</i>	700508	<i>Rothia dentocariosa</i>	762948
		<i>Propionibacterium propionicum</i>	767029

Lactobacillus delbrueckii	767455
Desulfotomaculum gibsoniae	767817
Enterococcus hirae	768486
Mycoplasma suis	768700
Desulfofosp.orosinus meridiei	768704
Desulfofosp.orosinus orientis	768706
Bacillus methanolicus	796606
Thermus thermophilus	798128
Spiroplasma mirum	838561
Thermoanaerobacterium xylanolyticum	858215
Corynebacterium variabile	858619
Kibdelosp.orangium phytohabitans	860235
Streptomyces sp.	862751
Streptococcus intermedius	862967
Streptococcus constellatus	862969
Aerococcus urinae	866775
Halobacillus halophilus	866895
Paenibacillus sp.	867076
Desulfotomaculum nigrificans	868595
Marinithermus hydrothermalis	869210
Dehalobacter restrictus	871738
Desulfotobacterium dichloroeliminans	871963
Desulfotobacterium metallireducens	871968
Streptococcus parauberis	873447
Mycobacterium sinense	875328
Lactobacillus helveticus	880633
Paenibacillus polymyxa	886882
Eubacterium sulci	888727
Lactobacillus acidophilus	891391
Eubacterium limosum	903814
Caldiilinea aerophila	926550
Anaerolinea thermophila	926569
Streptococcus oralis	927666
Arthrobacter phenanthrenivorans	930171
Corynebacterium deserti	931089

Clostridium saccharoperbutylacetonicum	931276
Acetobacterium woodii	931626
Mycoplasma hyorhinis	936139
Deinococcus peraridilitoris	937777
Mycoplasma haemofelis	941640
Dehalogenimonas sp.	943347
Mycoplasma fermentans	943945
Tetragenococcus halophilus	945021
Mycoplasma bovis	956483
Microbacterium testaceum	979556
Leuconostoc sp.	979982
Strawberry lethal	980422
Streptococcus pasteurianus	981540
Staphylococcus argenteus	985002
Paenibacillus terrae	985665
Staphylococcus agnetis	985762
Streptococcus gallolyticus	990317
Clostridium	991789
Clostridium acetobutylicum	991791
Lactobacillus casei	998820
Solibacillus silvestris	1002809
Streptomyces cattleya	1003195
Mycoplasma gallisepticum	1006581
Lactobacillus ginsenosidimutans	1007676
Candidatus Arthromitus	1029718
Microlunatus phosp.hovorus	1032480
Lactobacillus kefiranoferiens	1033837
Paenibacillus mucilaginosus	1036673
Candidatus Arthromitus	1041504
Clostridium sp.	1042156
Brevibacillus laterosporus	1042163
Bifidobacterium animalis	1042403
Oenococcus oeni	1045004
Weissella koreensis	1045854
Streptococcus salivarius	1048332

Alicyclobacillus acidocaldarius	1048834	Dehalobacter sp.	1131462
Corynebacterium epidermidicanis	1050174	Nocardia brasiliensis	1133849
Streptococcus equi	1051072	Streptomyces hygroscopicus	1133850
Sulfobacillus acidophilus	1051632	Gordonia sp.	1136941
Streptococcus pseudopneumoniae	1054460	Mycobacterium intracellulare	1138383
Amycolatopsis methanolica	1068978	Mycobacterium yongonense	1138871
Streptococcus infantarius	1069533	Lysinibacillus varians	1145276
Lactobacillus ruminis	1069534	Blastococcus saxosidens	1146883
Corynebacterium uterequi	1072256	Bifidobacterium asteroides	1147128
Paenibacillus riograndensis	1073571	Dehalobacter sp.	1147129
Lactobacillus heilongjiangensis	1074467	Bifidobacterium dentium	1150423
Streptococcus lutetiensis	1076934	Bifidobacterium kashiwanohense	1150460
Leptolyngbya sp.	1080068	Bifidobacterium scardovii	1150461
Exiguobacterium antarcticum	1087448	Scardovia inopinata	1150468
Thermacetogenium phaeum	1089553	Streptococcus sp.	1156431
Thermoanaerobacterium saccharolyticum	1094508	Streptococcus sp.	1156433
Pseudonocardia sp.	1096856	Amycolatopsis orientalis	1156913
Pseudonocardia sp.	1096868	Ruminococcus bicirculans	1160721
Lactococcus lactis	1104322	Leuconostoc gelidum	1165892
Geobacillus thermoleovorans	1111068	Mycobacterium sp.	1168287
Thermus sp.	1111069	Propionibacterium avidum	1170318
Mycoplasma haemocanis	1111676	Calothrix sp.	1170562
Gordonia polyisoprenivorans	1112204	Propionibacterium acidipropionici	1171373
Spiroplasma atrichopogonis	1114980	Streptomyces globisporus	1172567
Streptococcus macedonicus	1116231	Crinalium epipsammum	1173022
Arthrobacter sp.	1118963	Geitlerinema sp.	1173025
Clostridium stercoarium	1121335	Gloeocapsa sp.	1173026
Corynebacterium callunae	1121353	Microcoleus sp.	1173027
Corynebacterium halotolerans	1121362	Synechococcus sp.	1173263
Bacillus amyloliquefaciens	1126211	Saccharothrix sp. anaensis	1179773
Paenibacillus beijingensis	1126833	Deinococcus swuensis	1182571
Nocardia cyriacigeorgica	1127134	Gloeobacter kilaeensis	1183438
Bacillus sp.	1127744	Staphylococcus warneri	1194526
Clostridium acidurici	1128398	Mycoplasma wenyonii	1197325
Lactobacillus mucosae	1130798	Corynebacterium terpenotabidum	1200352
		Mycobacterium haemophilum	1202450

Nocardiopsis alba	1205910	Staphylococcus pasteurii	1276282
Tepidanaerobacter acetatoxydans	1209989	Synechococcus sp.	1280380
Candidatus Mycoplasma	1212765	Lactobacillus plantarum	1284663
Streptomyces collinus	1214242	Corynebacterium casei	1285583
Clostridium bornimense	1216932	Eubacterium acidaminophilum	1286171
Corynebacterium humireducens	1223515	Lactobacillus hokkaidonensis	1291742
Corynebacterium marinum	1224162	Mycoplasma putrefaciens	1292033
Corynebacterium maris	1224163	Intestinimonas butyriciproducens	1297617
Corynebacterium vitaeruminis	1224164	Enterococcus mundtii	1300150
cyanobacterium endosymbiont	1228987	Streptococcus oligofermentans	1302863
Leuconostoc carnosum	1229758	Mycobacterium abscessus	1303024
Clostridium tetani	1231072	Streptomyces fulvissimus	1303692
Mycobacterium indicus	1232724	Deinococcus soli	1309411
Geobacillus sp.	1233873	Streptococcus agalactiae	1309807
Propionibacterium acnes	1234380	Ilumatobacter coccineus	1313172
Carnobacterium maltaromaticum	1234679	Acholeplasma palmae	1318466
Bacillus lehensis	1246626	Candidatus Mycoplasma	1318617
Mycoplasma cynos	1246955	Streptococcus iniae	1318633
Actinoplanes friuliensis	1246995	Bacillus bombysepticus	1330043
Streptococcus dysgalactiae	1247189	Calothrix sp.	1337936
Bifidobacterium thermophilum	1254439	Streptococcus suis	1340847
Streptomyces sp.	1262452	Clostridium autoethanogenum	1341692
Streptomyces sp.	1265601	Bifidobacterium indicum	1341694
Staphylococcus pseudintermedius	1266717	Clostridium saccharobutylicum	1345695
Carnobacterium inhibens	1266845	Geobacillus sp.	1345697
Mycoplasma hominis	1267000	Bacillus megaterium	1348623
Mycoplasma synoviae	1267001	Corynebacterium argenteratense	1348662
Paenibacillus sabiniae	1268072	Synechococcus sp.	1350461
Mycobacterium sp.	1273687	Streptococcus anginosus	1353243
Spiroplasma taiwanense	1276220	Bacillus infantis	1367477
Spiroplasma diminutum	1276221	Lactobacillus fermentum	1381124
Spiroplasma chrysopicola	1276227	Adlercreutzia equolifaciens	1384484
Spiroplasma syrphidicola	1276229	Leifsonia xyli	1389489
Spiroplasma culicicola	1276246	Exiguobacterium sp.	1399115
Spiroplasma sabaudiense	1276257	Lactobacillus gasseri	1403312
Spiroplasma apis	1276258	Mycoplasma parvum	1403316

Streptomyces lydicus	1403539	Dehalococcoides sp.	1522671
Corynebacterium glyciniphilum	1404245	Planococcus sp.	1526927
Mesoplasma florum	1406864	Corynebacteriales bacterium	1528099
Corynebacterium lactis	1408189	Coriobacteriaceae bacterium	1531429
Corynebacterium ulcerans	1408268	Paenibacillus sp.	1536769
Clostridium botulinum	1408283	Paenibacillus sp.	1536770
Nocardia nova	1415166	Paenibacillus sp.	1536771
Mycoplasma ovis	1415773	Paenibacillus sp.	1536772
Clostridium baratii	1415775	Paenibacillus sp.	1536773
Bacillus toyonensis	1415784	Paenibacillus sp.	1536774
Streptococcus sp.	1419814	Paenibacillus sp.	1536775
Bacillus methylotrophicus	1423138	Mollicutes bacterium	1541959
Candidatus Hepatoplasma	1427984	Lactobacillus sp.	1545702
Clostridium pasteurianum	1428454	Mycobacterium sp.	1545728
Streptomyces albulus	1434306	Corynebacteriales bacterium	1562462
Trueperella pyogenes	1435056	Rhodococcus sp.	1564114
Rhodococcus pyridinivorans	1435356	Carnobacterium sp.	1564681
Streptomyces leeuwenhoekii	1437453	Bacillus sp.	1565991
Bifidobacterium actinocoloniiforme	1437605	Paenibacillus sp.	1566358
Mycoplasma pneumoniae	1441379	Bacillus sp.	1570330
Bacillus sp.	1446792	Bacillus sp.	1574141
Bifidobacterium pseudolongum	1447715	Arthrobacter sp.	1588023
Kutzneria albida	1449976	Geminocystis sp.	1615909
Aneurinibacillus sp.	1450761	Paenibacillus bovis	1616788
Corynebacterium falsenii	1451189	Geminocystis sp.	1617448
Candidatus Atelocyanobacterium	1453429	Arthrobacter sp.	1618207
Amycolatopsis lurida	1460371	Bacillus sp.	1628753
Jeotgalicoccus sp.	1461582	Geobacillus sp.	1629723
Lentibacillus amyloliquefaciens	1472767	Microcystis panniformis	1638788
Corynebacterium sp.	1487956	Pseudonocardia sp.	1641402
Arthrobacter sp.	1494608	Anabaena sp.	1647413
Prochlorococcus sp.	1501268	Bacillus paralicheniformis	1648923
Prochlorococcus sp.	1501269	Streptomyces sp.	1649184
Jeotgalibacillus sp.	1508404	Actinobacteria bacterium	1650658
Candidatus Arthromitus	1508644	Arthrobacter sp.	1652545
Geobacillus sp.	1519377	Arsenicicoccus sp.	1658671

Herbinix sp.	1679721	Nostoc sp.	1751286
Pseudonocardia sp.	1688404	Streptomyces sp.	1751294
Arthrobacter sp.	1690248	Fischerella sp.	1752063
Paenibacillus sp.	1695218	Leptolyngbya sp.	1752064
Microbacterium sp.	1696072	Deinococcus actinosclerus	1768108
Arthrobacter sp.	1704044	Arthrobacter sp.	1771959
Microbacterium sp.	1714373	Bacillus sp.	1774743
Streptomyces sp.	1725411	Gemella sp.	1785995
Mycoplasma sp.	1749074	Microbacterium sp.	1795053
Kurthia sp.	1750719		

Table S11 List of *Deinococcus-Thermus* (DT) species kept during permutations under LOW sampling scenarios.

LOW1	<i>Deinococcus actinosclerus</i>	LOW11	<i>Marinithermus hydrothermalis</i> DSM 14884
LOW2	<i>Deinococcus deserti</i> VCD115	LOW12	<i>Meiothermus silvanus</i> DSM 9946
LOW3	<i>Deinococcus geothermalis</i> DSM 11300	LOW13	<i>Oceanithermus profundus</i> DSM 14977
LOW4	<i>Deinococcus gobiensis</i> I-0	LOW14	<i>Thermus aquaticus</i> Y51MC23
LOW5	<i>Deinococcus maricopensis</i> DSM 21211	LOW15	<i>Thermus oshimai</i> JL-2
LOW6	<i>Deinococcus peraridilitoris</i> DSM 19664	LOW16	<i>Thermus parvatiensis</i>
LOW7	<i>Deinococcus proteolyticus</i> MRP	LOW17	<i>Thermus scotoductus</i> SA-01
LOW8	<i>Deinococcus radiodurans</i> R1	LOW18	<i>Thermus</i> sp. CCB US3 UF1
LOW9	<i>Deinococcus soli</i> Cha et al	LOW19	<i>Thermus thermophilus</i> JL-18
LOW10	<i>Deinococcus swuensis</i>	LOW20	<i>Truepera radiovictrix</i> DSM 17093

Table S12 List of *Chloroflexi* (CHF) species kept during permutations under LOW sampling scenarios.

LOW1	<i>Anaerolinea thermophila</i> UNI-1	LOW5	<i>Chloroflexus</i> sp. Y-400-fl
LOW2	<i>Caldilinea aerophila</i> DSM 14535 NBRC 104270	LOW6	<i>Dehalococcoides mccartyi</i> 195
LOW3	<i>Chloroflexus aggregans</i> DSM 9485	LOW7	<i>Dehalococcoides</i> sp. UCH007
LOW4	<i>Chloroflexus aurantiacus</i> J-10-fl	LOW8	<i>Dehalogenimonas lykanthroporepellens</i> BL-DC-9

LOW9	Dehalogenimonas sp. WBC-2	LOW12	Roseiflexus sp. RS-1
LOW10	Herpetosiphon aurantiacus DSM 785	LOW13	Sphaerobacter thermophilus DSM 20745
LOW11	Roseiflexus castenholzii DSM 13941	LOW14	Thermomicrobium roseum DSM 5159

Table S13 List of Actinobacteria (ACT) species kept during permutations under LOW sampling scenarios.

LOW1	Amycolatopsis japonica.208439, Arthrobacter LS16.1690248, Corynebacterium argentoratense
LOW2	Bifidobacterium dentium, Corynebacterium jeikeium, Corynebacterium terpenotabidum
LOW3	Devriesea agamarum.472569, Micrococcus luteus, Rubrobacter xylanophilus
LOW4	Frankia Eul1c.298654, Frankia symbiont, Gardnerella vaginalis
LOW5	Corynebacteriales bacterium, Mycobacterium KMS.189918, Streptomyces griseus
LOW6	Corynebacterium terpenotabidum, Intraspangium calvum, Salinispora arenicola
LOW7	Corynebacterium halotolerans, Microlunatus phosphovorus, Mycobacterium VKM
LOW8	Rathayibacter toxicus.145458, Rhodococcus opacus, Rhodococcus B7740.1564114
LOW9	Arthrobacter phenanthrenivorans, Blastococcus saxosidens, Propionibacterium propionicum
LOW10	Corynebacterium diphtheriae, Eggerthella lenta, Thermomonospora curvata
LOW11	Corynebacterium argentoratense, Mycobacterium goodii.134601, Mycobacterium JLS.164757
LOW12	Corynebacterium diphtheriae, Corynebacterium ATCC, Propionibacterium acnes
LOW13	Kibdelosporangium phytohabitans.860235, Scardovia inopinata, Streptomyces leeuwenhoekii.1437453
LOW14	Actinoplanes SE50, Arthrobacter sulfonivorans.121292, Microterricola viridarii.412690
LOW15	Bifidobacterium longum, Corynebacterium ureicelerivorans.401472, Nocardiosis alba
LOW16	Bifidobacterium dentium, Corynebacterium imitans.156978, Corynebacterium ulcerans
LOW17	Clavibacter michiganensis, Corynebacterium urealyticum, Intraspangium calvum
LOW18	Bifidobacterium thermophilum, Mycobacterium KMS.189918, Tropheryma whipplei
LOW19	Micromonospora aurantiaca, Streptomyces pratensis, Streptomyces violaceusniger
LOW20	Actinotignum schaalii.59505, Corynebacterium argentoratense, Gordonia KTR9.337191

Table S14 List of Deinococcus-Thermus (DT) species kept during permutations under MID sampling scenarios.

MID1	Deinococcus actinosclerus, Deinococcus deserti VCD115, Deinococcus geothermalis DSM 11300, Deinococcus gobiensis I-0, Deinococcus maricopenensis DSM 21211, Deinococcus peraridilitoris DSM 19664, Deinococcus proteolyticus MRP, Deinococcus radiodurans R1, Deinococcus soli Cha et al, Deinococcus swuensis
MID2	Thermus aquaticus Y51MC23, Thermus oshimai JL-2, Thermus parvatiensis, Thermus scotoductus SA-01, Thermus sp. CCB US3 UF1, Thermus thermophilus JL-18

Table S15 List of Chloroflexi (CHF) species kept during permutations under MID sampling scenarios.

MID1	Chloroflexus aggregans, Chloroflexus aurantiacus, Chloroflexus sp. Y-400-fl
MID2	Dehalococcoides mccartyi, Dehalococcoides sp. UCH007,
MID3	Dehalogenimonas lykanthroporepellens, Dehalogenimonas sp. WBC-2.943347,
MID4	Roseiflexus sp. RS-1, Roseiflexus castenholzii,

Table S16 List of Actinobacteria (ACT) species kept during permutations under MID ancestry sampling scenarios.

MIDanc3 2	Streptomyces albus ZPM, Streptomyces albus, Streptomyces ambofaciens ATCC 23877, Streptomyces avermitilis MA-4680 = NBRC 14893, Streptomyces bingchenggensis BCW-1, Streptomyces cattleya NRRL 8057 = DSM 46488, Streptomyces collinus Tu 365, Streptomyces cyaneogriseus subsp. noncyanogenus, Streptomyces fulvissimus DSM 40593, Streptomyces glaucescens, Streptomyces globisporus C-1027, Streptomyces griseus subsp. griseus NBRC 13350, Streptomyces hygroscopicus subsp. jinggangensis 5008, Streptomyces leeuwenhoekii, Streptomyces lydicus A02, Streptomyces pratensis ATCC 33331, Streptomyces pristinaespiralis, Streptomyces reticuli, Streptomyces scabiei 87.22, Streptomyces sp. 4F, Streptomyces sp. 769, Streptomyces sp. CdTB01, Streptomyces sp. CFMR 7, Streptomyces sp. CNQ-509, Streptomyces sp. Mg1, Streptomyces sp. PAMC26508, Streptomyces sp. SirexAA-E, Streptomyces venezuelae, Streptomyces vietnamensis, Streptomyces violaceusniger Tu 4113, Streptomyces xiamenensis, Streptoporangium roseum DSM 43021, Thermobifida fusca YX
MIDanc1 7	Actinosynnema mirum DSM 43827, Amycolatopsis japonica, Amycolatopsis lurida NRRL 2430, Amycolatopsis mediterranei S699, Amycolatopsis methanolica 239, Amycolatopsis orientalis HCCB10007, Kibdelosporangium phytohabitans, Kutzneria albida DSM 43870, Pseudonocardia dioxanivorans CB1190, Pseudonocardia sp. AL041005-10, Pseudonocardia sp. EC080610-09, Pseudonocardia sp. EC080619-01, Pseudonocardia sp. EC080625-04, Pseudonocardia sp. HH130629-09, Saccharomonospora viridis DSM 43017, Saccharopolyspora erythraea NRRL 2338, Saccharothrix espanaensis DSM 44229
MIDanc1 0	Aeromicrobium erythreum, Kribbella flavida DSM 17836, Microlunatus phosphovorus NM-1, Nocardioides sp. JS614, Pimelobacter simplex, Propionibacterium acidipropionici ATCC 4875, Propionibacterium acnes C1, Propionibacterium avidum 44067, Propionibacterium freudenreichii subsp. shermanii CIRM-BIA1, Propionibacterium propionicum F0230a
MIDanc8 6	Atopobium parvulum DSM 20469, Coriobacteriaceae bacterium 68-1-3, Coriobacterium glomerans PW2, Olsenella sp. oral taxon 807, Olsenella uli DSM 7084, Amycolicococcus subflavus DQS3-9A1, [Brevibacterium] flavum, Corynebacteriales bacterium X1036, Corynebacteriales bacterium X1698, Corynebacterium argentoratense DSM 44202, Corynebacterium atypicum, Corynebacterium aurimucosum ATCC 700975, Corynebacterium callunae DSM 20147, Corynebacterium camporealensis, Corynebacterium casei LMG S-19264, Corynebacterium deserti GIMN1.010, Corynebacterium diphtheriae 31A, Corynebacterium doosanense CAU 212 = DSM 45436, Corynebacterium efficiens YS-314, Corynebacterium epidermidicanis, Corynebacterium falsenii DSM 44353, Corynebacterium glutamicum R, Corynebacterium glyciniphilum AJ 3170, Corynebacterium halotolerans YIM 70093 = DSM 44683, Corynebacterium humireducens NBRC 106098 = DSM 45392, Corynebacterium imitans, Corynebacterium jeikeium K411, Corynebacterium kroppenstedtii DSM 44385, Corynebacterium kutscheri, Corynebacterium lactis RW2-5, Corynebacterium marinum DSM 44953, Corynebacterium maris DSM 45190, Corynebacterium mustelae, Corynebacterium pseudotuberculosis, Corynebacterium resistens DSM 45100, Corynebacterium singulare, Corynebacterium sp. ATCC 6931, Corynebacterium stationis, Corynebacterium terpenotabidum Y-11, Corynebacterium testudinoris, Corynebacterium ulcerans FRC58, Corynebacterium urealyticum DSM 7109, Corynebacterium ureicelerivorans, Corynebacterium uterequi, Corynebacterium variabile DSM 44702, Corynebacterium vitaeruminis DSM 20294, Gordonia bronchialis DSM 43247, Gordonia polyisoprenivorans VH2, Gordonia sp. KTR9, Gordonia sp. QH-11, Mycobacterium abscessus subsp. bolletii 50594, Mycobacterium africanum, Mycobacterium avium 104, Mycobacterium bovis BCG, Mycobacterium chubuense NBB4, Mycobacterium fortuitum, Mycobacterium gilvum PYR-GCK, Mycobacterium goodii, Mycobacterium haemophilum DSM 44634, Mycobacterium indicus pranii MTCC 9506, Mycobacterium intracellulare MOTT-64, Mycobacterium kansasii ATCC 12478, Mycobacterium leprae Br4923, Mycobacterium liflandii 128FXT, Mycobacterium marinum M, Mycobacterium microti, Mycobacterium neoaurum VKM Ac-1815D, Mycobacterium rhodesiae NBB3, Mycobacterium sinense, Mycobacterium sp. EPa45, Mycobacterium sp. JLS, Mycobacterium sp. JS623, Mycobacterium sp. KMS, Mycobacterium sp. MCS, Mycobacterium sp. MOTT36Y, Mycobacterium sp. VKM Ac-1817D, Mycobacterium tuberculosis, Mycobacterium ulcerans AgY99, Mycobacterium vanbaalenii PYR-1, Mycobacterium yongonense 05-1390, Nocardia brasiliensis ATCC 700358, Nocardia cyriacigeorgica GUH-2, Nocardia farcinica, Nocardia nova SH22a, Rhodococcus erythropolis PR4, Rhodococcus jostii RHA1, Rhodococcus

opacus PD630, Rhodococcus pyridinivorans SB3094, Rhodococcus sp. B7740, Segniliparus rotundus DSM 44985, Tsukamurella paurometabola DSM 20162

MIDanc1
9 Bifidobacterium actinocoloniiforme DSM 22766, Bifidobacterium adolescentis, Bifidobacterium angulatum DSM 20098 = JCM 7096, Bifidobacterium animalis subsp. lactis CNCM I-2494, Bifidobacterium asteroides PRL2011, Bifidobacterium bifidum, Bifidobacterium breve, Bifidobacterium catenulatum DSM 16992 = JCM 1194 = LMG 11043, Bifidobacterium coryneforme, Bifidobacterium dentium JCM 1195 = DSM 20436, Bifidobacterium indicum LMG 11587 = DSM 20214, Bifidobacterium kashiwanohense JCM 15439 = DSM 21854, Bifidobacterium longum subsp. infantis ATCC 15697 = JCM 1222 = DSM 20088, Bifidobacterium pseudocatenulatum DSM 20438 = JCM 1200 = LMG 10505, Bifidobacterium pseudolongum PV8-2, Bifidobacterium scardovii JCM 12489 = DSM 13734, Bifidobacterium thermophilum RBL67, Gardnerella vaginalis ATCC 14019, Scardovia inopinata JCM 12537

Table S17 List of Deinococcus-Thermus (DT) species removed during permutations under HIGH sampling scenarios.

HIGH1	Deinococcus actinosclerus	HIGH11	Marinithermus hydrothermalis DSM 14884
HIGH2	Deinococcus deserti VCD115	HIGH12	Meiothermus silvanus DSM 9946
HIGH3	Deinococcus geothermalis DSM 11300	HIGH13	Oceanithermus profundus DSM 14977
HIGH4	Deinococcus gobiensis I-0	HIGH14	Thermus aquaticus Y51MC23
HIGH5	Deinococcus maricopensis DSM 21211	HIGH15	Thermus oshimai JL-2
HIGH6	Deinococcus peraridilitoris DSM 19664	HIGH16	Thermus parvatiensis
HIGH7	Deinococcus proteolyticus MRP	HIGH17	Thermus scotoductus SA-01
HIGH8	Deinococcus radiodurans R1	HIGH18	Thermus sp. CCB US3 UF1
HIGH9	Deinococcus soli Cha et al	HIGH19	Thermus thermophilus JL-18
HIGH10	Deinococcus swuensis	HIGH20	Truepera radiovictrix DSM 17093

Table S18 List of Chloroflexi (CHF) species removed during permutations under HIGH sampling scenarios.

HIGH1	Anaerolinea thermophila UNI-1
HIGH2	Caldiilinea aerophila DSM 14535 NBRC 104270
HIGH3	Chloroflexus aggregans DSM 9485
HIGH4	Chloroflexus aurantiacus J-10-fl
HIGH5	Chloroflexus sp. Y-400-fl
HIGH6	Dehalococcoides mccartyi 195
HIGH7	Dehalococcoides sp. UCH007
HIGH8	Dehalogenimonas lykanthroporepellens BL-DC-9
HIGH9	Dehalogenimonas sp. WBC-2
HIGH10	Herpetosiphon aurantiacus DSM 785
HIGH11	Roseiflexus castenholzii DSM 13941
HIGH12	Roseiflexus sp. RS-1
HIGH13	Sphaerobacter thermophilus DSM 20745
HIGH14	Thermomicrobium roseum DSM 5159

1 Table S19 List of Actinobacteria (ACT) species removed during permutations under HIGH sampling scenarios.

HIGH1	<i>Bifidobacterium coryneforme</i> .1687, <i>Conexibacter woesei</i> , <i>Corynebacteriales bacterium</i> , <i>Corynebacterium aurimucosum</i> , <i>Corynebacterium ulcerans</i> , <i>Geodermatophilus obscurus</i> , <i>Kocuria rhizophila</i> , <i>Kribbella flavida</i> , <i>Microbacterium</i> sp. CGR1.1696072, <i>Mobiluncus curtisii</i> , <i>Mycobacterium</i> sp. KMS.189918, <i>Nocardiopsis dassonvillei</i> , <i>Pseudonocardia</i> sp. EC080625-04.1096868, <i>Renibacterium salmoninarum</i> , <i>Rhodococcus pyridinivorans</i> , <i>Streptomyces albus</i> , <i>Streptomyces albus</i> .1888, <i>Streptomyces avermitilis</i> , <i>Streptomyces glaucescens</i> .1907, <i>Streptomyces hygroscopicus</i> , <i>Streptomyces leeuwenhoekii</i> .1437453, <i>Streptomyces lydicus</i> , <i>Streptomyces pratensis</i> , <i>Streptomyces scabiei</i> , <i>Streptomyces</i> sp. SirexAA-E.862751, <i>Verrucosipora maris</i>
HIGH2	<i>Acidimicrobium ferrooxidans</i> , <i>Actinomyces meyeri</i> .52773, <i>Arthrobacter aurescens</i> , <i>Bifidobacterium thermophilum</i> , <i>Blastococcus saxosidans</i> , <i>Clavibacter michiganensis</i> , <i>Corynebacterium casei</i> , <i>Corynebacterium epidermidicanis</i> .1050174, <i>Corynebacterium terpenotabidum</i> , <i>Corynebacterium uterequi</i> .1072256, <i>Frankia alni</i> , <i>Frankia</i> sp. Ccl3.106370, <i>Geodermatophilus obscurus</i> , <i>Gordonia</i> sp. QH-11.1136941, <i>Jonesia denitrificans</i> , <i>Mobiluncus curtisii</i> , <i>Mycobacterium indicus</i> , <i>Mycobacterium neoaurum</i> , <i>Mycobacterium sinense</i> .875328, <i>Nocardioideis</i> sp. JS614.196162, <i>Propionibacterium freudenreichii</i> , <i>Rhodoluna laticola</i> .529884, <i>Streptomyces cyaneogriseus</i> , <i>Streptomyces</i> sp. 4F.1751294, <i>Streptomyces venezuelae</i> .54571, <i>Verrucosipora maris</i>
HIGH3	<i>Acidothermus cellulolyticus</i> , <i>Actinotignum schaalii</i> .59505, <i>Arthrobacter</i> sp. A3.595593, <i>Arthrobacter</i> sp. IHBB, <i>Bifidobacterium pseudocatenulatum</i> , <i>Bifidobacterium pseudolongum</i> , <i>Corynebacterium argentoratense</i> , <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium humireducens</i> , <i>Corynebacterium terpenotabidum</i> , <i>Devriesea agamarum</i> .472569, <i>Gordonia</i> sp. QH-11.1136941, <i>Kribbella flavida</i> , <i>Luteipulveratus mongoliensis</i> .571913, <i>Microbacterium</i> sp. CGR1.1696072, <i>Mycobacterium goodii</i> .134601, <i>Nocardia brasiliensis</i> , <i>Nocardia nova</i> , <i>Pimelobacter simplex</i> .2045, <i>Pseudonocardia</i> sp. EC080610-09.1688404, <i>Renibacterium salmoninarum</i> , <i>Rhodococcus erythropolis</i> , <i>Saccharomonospora viridis</i> , <i>Scardovia inopinata</i> , <i>Streptomyces albus</i> , <i>Streptomyces vietnamensis</i> .362257
HIGH4	<i>Bifidobacterium breve</i> .1685, <i>Bifidobacterium dentium</i> , <i>Bifidobacterium kashiwanohense</i> , <i>Corynebacteriales bacterium</i> , <i>Corynebacterium aurimucosum</i> , <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium imitans</i> .156978, <i>Corynebacterium stationis</i> .1705, <i>Eggerthella lenta</i> , <i>Kocuria palustris</i> .71999, <i>Leifsonia xyli</i> , <i>Microbacterium</i> sp. XT11.367477, <i>Microbacterium testaceum</i> , <i>Micromonospora</i> sp. L5.648999, <i>Mycobacterium africanum</i> .33894, <i>Mycobacterium neoaurum</i> , <i>Mycobacterium</i> sp. MOTT36Y.1168287, <i>Nocardia cyriacigeorgica</i> , <i>Nocardia nova</i> , <i>Propionibacterium avidum</i> , <i>Rhodococcus erythropolis</i> , <i>Rothia mucilaginosa</i> , <i>Streptomyces ambofaciens</i> , <i>Streptomyces cyaneogriseus</i> , <i>Streptomyces</i> sp. PAMC26508.1265601, <i>Thermobifida fusca</i>
HIGH5	<i>Actinobacteria bacterium</i> , <i>Actinoplanes missouriensis</i> , <i>Actinoplanes</i> sp. N902-109.649831, <i>Aeromicrobium erythreum</i> .2041, <i>Arthrobacter</i> sp. A3.595593, <i>Beutenbergia cavernae</i> , <i>Bifidobacterium catenulatum</i> , <i>Bifidobacterium longum</i> , <i>Corynebacterium casei</i> , <i>Corynebacterium epidermidicanis</i> .1050174, <i>Corynebacterium falsenii</i> , <i>Corynebacterium glyciniphilum</i> , <i>Corynebacterium halotolerans</i> , <i>Leifsonia xyli</i> , <i>Micrococcus phosphovorus</i> , <i>Mycobacterium abscessus</i> , <i>Mycobacterium bovis</i> , <i>Mycobacterium marinum</i> , <i>Mycobacterium</i> sp. MCS.164756, <i>Nocardioideis</i> sp. JS614.196162, <i>Olsenella uli</i> , <i>Pseudonocardia</i> sp. EC080610-09.1688404, <i>Rathayibacter toxicus</i> .145458, <i>Renibacterium salmoninarum</i> , <i>Rhodococcus opacus</i> , <i>Streptomyces</i> sp. CdTB01.1725411, <i>Verrucosipora maris</i>
HIGH6	<i>Actinomyces meyeri</i> .52773, <i>Actinoplanes</i> sp. N902-109.649831, <i>Bifidobacterium breve</i> .1685, <i>Bifidobacterium dentium</i> , <i>Bifidobacterium kashiwanohense</i> , <i>Bifidobacterium thermophilum</i> , <i>Corynebacterium imitans</i> .156978, <i>Corynebacterium jeikeium</i> , <i>Corynebacterium kutscheri</i> .35755, <i>Corynebacterium maris</i> , <i>Corynebacterium stationis</i> .1705, <i>Corynebacterium uterequi</i> .1072256, <i>Frankia</i> sp. Eul1c.298654, <i>Micrococcus phosphovorus</i> , <i>Mycobacterium bovis</i> , <i>Mycobacterium chubuense</i> , <i>Mycobacterium marinum</i> , <i>Olsenella</i> sp. oral, <i>Propionibacterium propionicum</i> , <i>Pseudonocardia dioxanivorans</i> , <i>Pseudonocardia</i> sp. EC080625-04.1096868, <i>Rhodococcus opacus</i> , <i>Rubrobacter xylanophilus</i> , <i>Streptomyces cattleya</i> , <i>Streptomyces glaucescens</i> .1907, <i>Streptomyces vietnamensis</i> .362257
HIGH7	<i>Actinomyces radicitus</i> .111015, <i>Adlercreutzia equolifaciens</i> , <i>Amycolaticoccus subflavus</i> , <i>Arthrobacter</i> sp. A3.595593, <i>Bifidobacterium coryneforme</i> .1687, <i>Bifidobacterium pseudolongum</i> , <i>Cellulomonas gilvus</i> , <i>Corynebacteriales bacterium</i> , <i>Corynebacteriales bacterium</i> , <i>Corynebacterium camporealis</i> .161896, <i>Corynebacterium falsenii</i> , <i>Corynebacterium jeikeium</i> , <i>Corynebacterium</i> sp. ATCC, <i>Corynebacterium variabile</i> , <i>Ilumatobacter coccineus</i> , <i>Kocuria rhizophila</i> , <i>Kutzneria alba</i> , <i>Microbacterium testaceum</i> , <i>Mobiluncus curtisii</i> , <i>Mycobacterium africanum</i> .33894, <i>Propionibacterium propionicum</i> , <i>Saccharopolyspora erythraea</i> , <i>Salinispora arenicola</i> , <i>Scardovia inopinata</i> , <i>Segniliparus rotundus</i> , <i>Streptomyces bingchengensis</i>
HIGH8	<i>Actinomyces</i> sp. oral, <i>Adlercreutzia equolifaciens</i> , <i>Amycolatopsis methanolica</i> , <i>Arthrobacter aurescens</i> , <i>Arthrobacter</i> sp. LS16.1690248, <i>Bifidobacterium catenulatum</i> , <i>Bifidobacterium kashiwanohense</i> , <i>Bifidobacterium longum</i> , <i>Bifidobacterium pseudocatenulatum</i> , <i>Cellulomonas gilvus</i> , <i>Devriesea agamarum</i> .472569, <i>Frankia</i> sp. EAN1pec.298653, <i>Gordonia</i> sp. KTR9.337191, <i>Isophtericola variabilis</i> , <i>Microterricola viridarii</i> .412690, <i>Mycobacterium fortuitum</i> .1766, <i>Mycobacterium gilvus</i> , <i>Mycobacterium</i> sp. EPA45.1545728, <i>Nocardia cyriacigeorgica</i> , <i>Propionibacterium freudenreichii</i> , <i>Pseudonocardia</i> sp. HH130629-09.1641402, <i>Rhodoluna laticola</i> .529884,

Streptomyces collinus, *Streptomyces cyaneogriseus*, *Streptomyces* sp. Mg1.465541, *Streptomyces xiamenensis*.408015

- HIGH9 *Acidimicrobium ferrooxidans*, *Actinomyces oris*.544580, *Amycolatopsis mediterranei*, *Arthrobacter chlorophenolicus*, *Arthrobacter* sp. YC-RL1.1652545, *Bifidobacterium animalis*, *Bifidobacterium pseudolongum*, *Catenulispora acidiphila*, *Clavibacter michiganensis*, *Corynebacterium casei*, *Corynebacterium doosanense*, *Corynebacterium terpenotabidum*, *Frankia alni*, *Gardnerella vaginalis*, *Microbacterium* sp. PAMC, *Mycobacterium fortuitum*.1766, *Mycobacterium goodii*.134601, *Mycobacterium haemophilum*, *Mycobacterium leprae*, *Mycobacterium* sp. MCS.164756, *Olsenella* sp. oral, *Pimelobacter simplex*.2045, *Pseudonocardia* sp. EC080610-09.1688404, *Pseudonocardia* sp. HH130629-09.1641402, *Scardovia inopinata*, *Trueperella pyogenes*
- HIGH10 *Actinobacteria bacterium*, *Actinomyces radidentis*.111015, *Actinosynnema mirum*, *Arcanobacterium haemolyticum*, *Arthrobacter* sp. FB24.290399, *Beutenbergia cavernae*, *Bifidobacterium bifidum*.1681, *Coriobacteriaceae bacterium*, *Corynebacteriales bacterium*, *Corynebacterium camporealensis*.161896, *Corynebacterium marinum*, *Corynebacterium variabile*, *Ilumatobacter coccineus*, *Micromonospora* sp. L5.648999, *Mycobacterium indicus*, *Mycobacterium marinum*, *Mycobacterium vanbaalenii*, *Olsenella* sp. oral, *Renibacterium salmoninarum*, *Saccharothrix espanaensis*, *Sanguibacter keddiei*, *Streptomyces albus*.1888, *Streptomyces cyaneogriseus*, *Streptomyces pristinaespiralis*.38300, *Streptomyces violaceusniger*, *Xylanimonas cellulosilytica*
- HIGH11 *Actinomyces radidentis*.111015, *Actinoplanes friulensis*, *Actinoplanes missouriensis*, *Actinoplanes* sp. N902-109.649831, *Arthrobacter arilaitensis*.256701, *Arthrobacter phenanthrenivorans*, *Bifidobacterium coryneforme*.1687, *Catenulispora acidiphila*, *Corynebacterium diphtheriae*, *Kineococcus radiotolerans*, *Kytococcus sedentarius*, *Microbacterium* sp. No., *Microbacterium* sp. XT11.367477, *Micrococcus luteus*, *Micromonospora* sp. L5.648999, *Mycobacterium* sp. EPA45.1545728, *Mycobacterium* sp. JLS.164757, *Mycobacterium* sp. VKM, *Segniliparus rotundus*, *Slackia heliotrinireducens*, *Streptomyces cattleya*, *Streptomyces collinus*, *Streptomyces scabiei*, *Streptomyces* sp. 4F.1751294, *Streptomyces* sp. PAMC26508.1265601, *Tropheryma whipplei*
- HIGH12 *Arthrobacter alpinus*.656366, *Arthrobacter chlorophenolicus*, *Arthrobacter* sp. A3.595593, *Beutenbergia cavernae*, *Bifidobacterium dentium*, *Corynebacterium marinum*, *Corynebacterium pseudotuberculosis*.1719, *Corynebacterium stationis*.1705, *Cryptobacterium curtum*, *Isoptericola variabilis*, *Jonesia denitrificans*, *Kineococcus radiotolerans*, *Luteipulveratus mongoliensis*.571913, *Microbacterium* sp. No., *Mycobacterium chubuense*, *Mycobacterium fortuitum*.1766, *Mycobacterium sinense*.875328, *Mycobacterium* sp. EPA45.1545728, *Mycobacterium vanbaalenii*, *Olsenella uli*, *Rhodococcus* sp. B7740.1564114, *Rothia mucilaginosa*, *Rubrobacter xylanophilus*, *Sanguibacter keddiei*, *Stackebrandtia nassauensis*, *Streptomyces avermitilis*
- HIGH13 *Actinomyces oris*.544580, *Arthrobacter* sp. ATCC, *Arthrobacter* sp. Hiyo8.1588023, *Arthrobacter sulfonivorans*.121292, *Atopobium parvulum*, *Bifidobacterium coryneforme*.1687, *Cellulomonas flavigena*, *Clavibacter michiganensis*, *Corynebacterium epidermidicantis*.1050174, *Corynebacterium ulcerans*, *Corynebacterium variabile*, *Gordonia* sp. KTR9.337191, *Ilumatobacter coccineus*, *Kibdelosporangium phytohabitans*.860235, *Kribbella flavida*, *Microbacterium* sp. No., *Mycobacterium* sp. EPA45.1545728, *Mycobacterium* sp. MOTT36Y.1168287, *Mycobacterium yongonense*, *Nocardia nova*, *Saccharomonospora viridis*, *Saccharothrix espanaensis*, *Streptomyces pratensis*, *Streptomyces pristinaespiralis*.38300, *Streptomyces* sp. 769.1262452, *Thermobispora bispora*
- HIGH14 *Acidimicrobium ferrooxidans*, *Actinobacteria bacterium*, *Actinomyces meyeri*.52773, *Actinosynnema mirum*, *Adlercreutzia equolifaciens*, *Amycolatopsis methanolica*, *Amycolatopsis orientalis*, *Arcanobacterium haemolyticum*, *Arthrobacter arilaitensis*.256701, *Arthrobacter* sp. ERGS1, *Atopobium parvulum*, *Brachybacterium faecium*, *Corynebacterium urealyticum*, *Cryptobacterium curtum*, *Eggerthella* sp. YY7918.502558, *Frankia* sp. EAN1pec.298653, *Mycobacterium africanum*.33894, *Mycobacterium gilvum*, *Mycobacterium yongonense*, *Nocardioopsis dassonvillei*, *Propionibacterium acidipropionici*, *Rothia mucilaginosa*, *Salinispora tropica*, *Streptomyces reticuli*.1926, *Streptomyces* sp. CdTB01.1725411, *Tsukamurella paurometabola*
- HIGH15 *Actinobacteria bacterium*, *Actinoplanes missouriensis*, *Actinosynnema mirum*, *Amycolatopsis mediterranei*, *Arthrobacter alpinus*.656366, *Arthrobacter chlorophenolicus*, *Arthrobacter* sp. ATCC, *Catenulispora acidiphila*, *Corynebacterium glutamicum*, *Corynebacterium ulcerans*, *Eggerthella* sp. YY7918.502558, *Gordonia bronchialis*, *Kocuria flava*.446860, *Microbacterium testaceum*, *Mycobacterium rhodesiae*, *Mycobacterium* sp. MCS.164756, *Nocardia farcinica*.37329, *Olsenella* sp. oral, *Pseudonocardia* sp. EC080625-04.1096868, *Rhodococcus jostii*, *Salinispora arenicola*, *Salinispora tropica*, *Streptomyces ambofaciens*, *Streptomyces glaucescens*.1907, *Tropheryma whipplei*, *Verrucosipora maris*
- HIGH16 *Brevibacterium*, *Actinoplanes* sp. N902-109.649831, *Adlercreutzia equolifaciens*, *Amycolatopsis japonica*.208439, *Bifidobacterium actinocoloniiforme*, *Bifidobacterium breve*.1685, *Clavibacter michiganensis*, *Coriobacterium glomerans*, *Corynebacterium casei*, *Corynebacterium deserti*, *Corynebacterium glyciniphilum*, *Corynebacterium maris*, *Corynebacterium stationis*.1705, *Corynebacterium ulcerans*, *Kitasatospora setae*, *Luteipulveratus mongoliensis*.571913, *Mycobacterium gilvum*, *Mycobacterium goodii*.134601, *Mycobacterium liflandii*, *Mycobacterium ulcerans*, *Rothia dentocariosa*, *Salinispora arenicola*, *Streptomyces glaucescens*.1907, *Streptomyces lydicus*, *Streptomyces* sp. CNQ-509.444103, *Streptomyces xiamenensis*.408015

- HIGH1
7 Amycolatopsis methanolica, Bifidobacterium bifidum.1681, Cellulomonas gilvus, Coriobacteriaceae bacterium, Corynebacterium aurimucosum, Corynebacterium efficiens, Corynebacterium epidermidicanis.1050174, Corynebacterium kutscheri.35755, Corynebacterium stationis.1705, Gardnerella vaginalis, Kineococcus radiotolerans, Leifsonia xyli, Mycobacterium sp. KMS.189918, Mycobacterium sp. VKM, Nakamurella multipartita, Nocardia nova, Nocardioopsis dassonvillei, Olsenella uli, Propionibacterium freudenreichii, Saccharomonospora viridis, Streptomyces cyaneogriseus, Streptomyces hygroscopicus, Streptomyces sp. CNQ-509.444103, Streptomyces sp. Mg1.465541, Streptomyces vietnamensis.362257, Verrucosipora maris
- HIGH1
8 Actinoplanes missouriensis, Amycolatopsis orientalis, Arthrobacter sp. A3.595593, Arthrobacter sp. ATCC, Bifidobacterium animalis, Bifidobacterium indicum, Corynebacterium callunae, Corynebacterium humireducens, Corynebacterium ulcerans, Corynebacterium vitaeruminis, Frankia alni, Ilumatobacter coccineus, Mycobacterium bovis, Mycobacterium goodii.134601, Mycobacterium leprae, Propionibacterium acnes, Propionibacterium avidum, Pseudonocardia sp. EC080619-01.1096856, Rothia mucilaginosa, Saccharopolyspora erythraea, Salinispora tropica, Streptomyces sp. 4F.1751294, Streptomyces sp. CdTB01.1725411, Streptomyces sp. SirexAA-E.862751, Streptomyces violaceusniger, Streptosporangium roseum
- HIGH1
9 Actinoplanes missouriensis, Arthrobacter arilaitensis.256701, Bifidobacterium breve.1685, Brachybacterium faecium, Corynebacteriales bacterium, Corynebacterium glutamicum, Corynebacterium stationis.1705, Corynebacterium urealyticum, Frankia alni, Frankia sp. Eul1c.298654, Geodermatophilus obscurus, Kocuria flava.446860, Microbacterium testaceum, Mycobacterium haemophilum, Mycobacterium sp. JLS.164757, Mycobacterium sp. MOTT36Y.1168287, Nocardia brasiliensis, Nocardia farcinica.37329, Nocardia nova, Olsenella sp. oral, Renibacterium salmoninarum, Rubrobacter radiotolerans.42256, Stackebrandtia nassauensis, Streptomyces sp. CNQ-509.444103, Streptomyces sp. PAMC26508.1265601, Xylanimonas cellulosilytica
- HIGH2
0 Actinomyces meyeri.52773, Actinomyces oris.544580, Adlercreutzia equolifaciens, Amycolatopsis methanolica, Arcanobacterium haemolyticum, Beutenbergia cavernae, Clavibacter michiganensis, Corynebacterium atypicum.191610, Corynebacterium camporealensis.161896, Corynebacterium singulare.161899, Frankia sp. Eul1c.298654, Frankia symbiont, Leifsonia xyli, Luteipulveratus mongoliensis.571913, Microbacterium sp. No., Mycobacterium leprae, Propionibacterium freudenreichii, Pseudonocardia dioxanivorans, Saccharomonospora viridis, Streptomyces collinus, Streptomyces glaucescens.1907, Streptomyces griseus, Streptomyces pratensis, Streptomyces reticuli.1926, Streptomyces sp. CdTB01.1725411, Tsukamurella paurometabola

2

3 **Table S20** List of 6 Deinococcus-Thermus (DT) species kept for 20 permutations under MID6 random sampling scenarios (RSS).

RSS	species kept
0	Thermus_aquaticus_Y51MC23.498848,Deinococcus_radiodurans_R1.243230,Thermus_scotoductus_SA-01.743525,Truepera_radiovictrix_DSM_17093.649638,Deinococcus_actinosclerus.1768108,Thermus_sp._CCB_US3_UF1.1111069
1	Thermus_aquaticus_Y51MC23.498848,Deinococcus_actinosclerus.1768108,Deinococcus_peraridilitoris_DSM_19664.937777,Thermus_oshimai_JL-2.751945,Deinococcus_swuensis.1182571,Deinococcus_maricopensis_DSM_21211.709986
2	Thermus_scotoductus_SA-01.743525,Oceanithermus_profundus_DSM_14977.670487,Deinococcus_actinosclerus.1768108,Deinococcus_deserti_VCD115.546414,Deinococcus_swuensis.1182571,Thermus_oshimai_JL-2.751945
3	Oceanithermus_profundus_DSM_14977.670487,Deinococcus_peraridilitoris_DSM_19664.937777,Meiothermus_silvanus_DSM_9946.526227,Deinococcus_soli_Cha_et_al._2014.1309411,Thermus_parvatiensis.456163,Deinococcus_maricopensis_DSM_21211.709986
4	Deinococcus_maricopensis_DSM_21211.709986,Truepera_radiovictrix_DSM_17093.649638,Meiothermus_silvanus_DSM_9946.526227,Thermus_scotoductus_SA-01.743525,Deinococcus_radiodurans_R1.243230,Deinococcus_geothermalidis_DSM_11300.319795
5	Thermus_oshimai_JL-2.751945,Deinococcus_soli_Cha_et_al._2014.1309411,Deinococcus_proteolyticus_MRP.693977,Marinithermus_hydrothermalis_DSM_14884.869210,Deinococcus_radiodurans_R1.243230,Thermus_scotoductus_SA-01.743525
6	Deinococcus_peraridilitoris_DSM_19664.937777,Deinococcus_actinosclerus.1768108,Thermus_thermophilus_JL-18.798128,Deinococcus_deserti_VCD115.546414,Truepera_radiovictrix_DSM_17093.649638,Meiothermus_silvanus_DSM_9946.526227

- 7 Oceanithermus_profundus_DSM_14977.670487,Deinococcus_swuensis.1182571,Thermus_thermophilus_JL-18.798128,Deinococcus_deserti_VCD115.546414,Deinococcus_maricopensis_DSM_21211.709986,Deinococcus_gobien-
nsis_I-0.745776
- 8 Thermus_parvatiensis.456163,Oceanithermus_profundus_DSM_14977.670487,Marinithermus_hydrothermalis_DSM_14884.869210,Deinococcus_proteolyticus_MRP.693977,Thermus_thermophilus_JL-18.798128,Thermus_sp._CCB_US3_UF1.1111069
- 9 Thermus_aquaticus_Y51MC23.498848,Deinococcus_gobiensis_I-0.745776,Truepera_radiovictrix_DSM_17093.649638,Deinococcus_radiodurans_R1.243230,Deinococcus_proteolyticus_MRP.693977,Thermus_scotoductus_SA-01.743525
- 10 Truepera_radiovictrix_DSM_17093.649638,Meiothermus_silvanus_DSM_9946.526227,Thermus_parvatiensis.456163,Deinococcus_radiodurans_R1.243230,Deinococcus_proteolyticus_MRP.693977,Marinithermus_hydrothermalis_DSM_14884.869210
- 11 Thermus_sp._CCB_US3_UF1.1111069,Thermus_scotoductus_SA-01.743525,Deinococcus_proteolyticus_MRP.693977,Deinococcus_swuensis.1182571,Oceanithermus_profundus_DSM_14977.670487,Deinococcus_geothermalis_DSM_11300.319795
- 12 Truepera_radiovictrix_DSM_17093.649638,Deinococcus_gobiensis_I-0.745776,Thermus_oshimai_JL-2.751945,Deinococcus_proteolyticus_MRP.693977,Deinococcus_maricopensis_DSM_21211.709986,Deinococcus_radiodurans_R1.243230
- 13 Marinithermus_hydrothermalis_DSM_14884.869210,Thermus_thermophilus_JL-18.798128,Thermus_sp._CCB_US3_UF1.1111069,Deinococcus_radiodurans_R1.243230,Thermus_oshimai_JL-2.751945,Deinococcus_gobiensis_I-0.745776
- 14 Deinococcus_deserti_VCD115.546414,Thermus_oshimai_JL-2.751945,Deinococcus_proteolyticus_MRP.693977,Thermus_thermophilus_JL-18.798128,Deinococcus_actinosclerus.1768108,Thermus_aquaticus_Y51MC23.498848
- 15 Marinithermus_hydrothermalis_DSM_14884.869210,Deinococcus_proteolyticus_MRP.693977,Deinococcus_deserti_VCD115.546414,Deinococcus_radiodurans_R1.243230,Deinococcus_actinosclerus.1768108,Deinococcus_geothermalis_DSM_11300.319795
- 16 Deinococcus_peraridilitoris_DSM_19664.937777,Thermus_scotoductus_SA-01.743525,Marinithermus_hydrothermalis_DSM_14884.869210,Thermus_parvatiensis.456163,Truepera_radiovictrix_DSM_17093.649638,Deinococcus_actinosclerus.1768108
- 17 Deinococcus_swuensis.1182571,Deinococcus_gobiensis_I-0.745776,Thermus_scotoductus_SA-01.743525,Thermus_parvatiensis.456163,Deinococcus_deserti_VCD115.546414,Deinococcus_maricopensis_DSM_21211.709986
- 18 Thermus_oshimai_JL-2.751945,Deinococcus_maricopensis_DSM_21211.709986,Truepera_radiovictrix_DSM_17093.649638,Deinococcus_radiodurans_R1.243230,Thermus_aquaticus_Y51MC23.498848,Oceanithermus_profundus_DSM_14977.670487
- 19 Truepera_radiovictrix_DSM_17093.649638,Marinithermus_hydrothermalis_DSM_14884.869210,Thermus_scotoductus_SA-01.743525,Deinococcus_proteolyticus_MRP.693977,Thermus_oshimai_JL-2.751945,Thermus_thermophilus_JL-18.798128

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5

6 **Table S21** List of 10 *Deinococcus*-*Thermus* (DT) species kept for 20 permutations under MID10 random sampling scenarios (RSS).

RSS	species kept
0	<i>Thermus_scotoductus_SA</i> -01.743525, <i>Thermus_parvatiensis</i> .456163, <i>Thermus_sp._CCB_US3_UF1</i> .1111069, <i>Deinococcus_maricopensis_DSM_21211</i> .709986, <i>Deinococcus_actinosclerus</i> .1768108, <i>Deinococcus_gobiensis_I</i> -0.745776, <i>Deinococcus_peraridilitoris_DSM_19664</i> .937777, <i>Deinococcus_deserti_VCD115</i> .546414, <i>Thermus_thermophilus_JL</i> -18.798128, <i>Marinithermus_hydrothermalis_DSM_14884</i> .869210
1	<i>Deinococcus_gobiensis_I</i> -0.745776, <i>Meiothermus_silvanus_DSM_9946</i> .526227, <i>Deinococcus_soli_Cha_et_al.</i> .2014.1309411, <i>Deinococcus_peraridilitoris_DSM_19664</i> .937777, <i>Deinococcus_deserti_VCD115</i> .546414, <i>Thermus_sp._CCB_US3_UF1</i> .1111069, <i>Oceanithermus_profundus_DSM_14977</i> .670487, <i>Thermus_scotoductus_SA</i> -01.743525, <i>Marinithermus_hydrothermalis_DSM_14884</i> .869210, <i>Thermus_thermophilus_JL</i> -18.798128
2	<i>Truepera_radiovictrix_DSM_17093</i> .649638, <i>Oceanithermus_profundus_DSM_14977</i> .670487, <i>Deinococcus_maricopensis_DSM_21211</i> .709986, <i>Thermus_sp._CCB_US3_UF1</i> .1111069, <i>Deinococcus_geothermalis_DSM_11300</i> .319795, <i>Marinithermus_hydrothermalis_DSM_14884</i> .869210, <i>Thermus_thermophilus_JL</i> -18.798128, <i>Deinococcus_gobiensis_I</i> -0.745776, <i>Deinococcus_peraridilitoris_DSM_19664</i> .937777, <i>Thermus_oshimai_JL</i> -2.751945
3	<i>Thermus_parvatiensis</i> .456163, <i>Deinococcus_swuensis</i> .1182571, <i>Meiothermus_silvanus_DSM_9946</i> .526227, <i>Deinococcus_maricopensis_DSM_21211</i> .709986, <i>Thermus_sp._CCB_US3_UF1</i> .1111069, <i>Deinococcus_gobiensis_I</i> -0.745776, <i>Deinococcus_peraridilitoris_DSM_19664</i> .937777, <i>Thermus_oshimai_JL</i> -2.751945, <i>Truepera_radiovictrix_DSM_17093</i> .649638, <i>Deinococcus_radiodurans_R1</i> .243230
4	<i>Deinococcus_swuensis</i> .1182571, <i>Deinococcus_radiodurans_R1</i> .243230, <i>Deinococcus_actinosclerus</i> .1768108, <i>Thermus_aquaticus_Y51MC23</i> .498848, <i>Deinococcus_soli_Cha_et_al.</i> .2014.1309411, <i>Oceanithermus_profundus_DSM_14977</i> .670487, <i>Deinococcus_geothermalis_DSM_11300</i> .319795, <i>Thermus_oshimai_JL</i> -2.751945, <i>Deinococcus_proteolyticus_MRP</i> .693977, <i>Deinococcus_maricopensis_DSM_21211</i> .709986
5	<i>Meiothermus_silvanus_DSM_9946</i> .526227, <i>Oceanithermus_profundus_DSM_14977</i> .670487, <i>Deinococcus_actinosclerus</i> .1768108, <i>Thermus_scotoductus_SA</i> -01.743525, <i>Deinococcus_peraridilitoris_DSM_19664</i> .937777, <i>Deinococcus_deserti_VCD115</i> .546414, <i>Thermus_aquaticus_Y51MC23</i> .498848, <i>Thermus_oshimai_JL</i> -2.751945, <i>Deinococcus_proteolyticus_MRP</i> .693977, <i>Deinococcus_geothermalis_DSM_11300</i> .319795
6	<i>Deinococcus_deserti_VCD115</i> .546414, <i>Truepera_radiovictrix_DSM_17093</i> .649638, <i>Deinococcus_maricopensis_DSM_21211</i> .709986, <i>Thermus_parvatiensis</i> .456163, <i>Deinococcus_radiodurans_R1</i> .243230, <i>Deinococcus_geothermalis_DSM_11300</i> .319795, <i>Deinococcus_peraridilitoris_DSM_19664</i> .937777, <i>Thermus_thermophilus_JL</i> -18.798128, <i>Thermus_oshimai_JL</i> -2.751945, <i>Deinococcus_soli_Cha_et_al.</i> .2014.1309411
7	<i>Deinococcus_radiodurans_R1</i> .243230, <i>Marinithermus_hydrothermalis_DSM_14884</i> .869210, <i>Thermus_thermophilus_JL</i> -18.798128, <i>Truepera_radiovictrix_DSM_17093</i> .649638, <i>Deinococcus_proteolyticus_MRP</i> .693977, <i>Deinococcus_deserti_VCD115</i> .546414, <i>Deinococcus_geothermalis_DSM_11300</i> .319795, <i>Deinococcus_actinosclerus</i> .1768108, <i>Deinococcus_gobiensis_I</i> -0.745776, <i>Thermus_scotoductus_SA</i> -01.743525
8	<i>Deinococcus_proteolyticus_MRP</i> .693977, <i>Thermus_oshimai_JL</i> -2.751945, <i>Deinococcus_soli_Cha_et_al.</i> .2014.1309411, <i>Marinithermus_hydrothermalis_DSM_14884</i> .869210, <i>Deinococcus_gobiensis_I</i> -0.745776, <i>Deinococcus_deserti_VCD115</i> .546414, <i>Thermus_sp._CCB_US3_UF1</i> .1111069, <i>Truepera_radiovictrix_DSM_17093</i> .649638, <i>Deinococcus_peraridilitoris_DSM_19664</i> .937777, <i>Deinococcus_swuensis</i> .1182571
9	<i>Thermus_oshimai_JL</i> -2.751945, <i>Thermus_aquaticus_Y51MC23</i> .498848, <i>Thermus_sp._CCB_US3_UF1</i> .1111069, <i>Thermus_thermophilus_JL</i> -18.798128, <i>Deinococcus_soli_Cha_et_al.</i> .2014.1309411, <i>Deinococcus_actinosclerus</i> .1768108, <i>Meiothermus_silvanus_DSM_9946</i> .526227, <i>Oceanithermus_profundus_DSM_14977</i> .670487, <i>Deinococcus_gobiensis_I</i> -0.745776, <i>Deinococcus_swuensis</i> .1182571
10	<i>Thermus_aquaticus_Y51MC23</i> .498848, <i>Thermus_oshimai_JL</i> -2.751945, <i>Deinococcus_swuensis</i> .1182571, <i>Deinococcus_actinosclerus</i> .1768108, <i>Deinococcus_peraridilitoris_DSM_19664</i> .937777, <i>Thermus_parvatiensis</i> .456163, <i>Deinococcus_maricopensis_DSM_21211</i> .709986, <i>Deinococcus_soli_Cha_et_al.</i> .2014.1309411, <i>Deinococcus_gobiensis_I</i> -0.745776, <i>Deinococcus_geothermalis_DSM_11300</i> .319795
11	<i>Marinithermus_hydrothermalis_DSM_14884</i> .869210, <i>Deinococcus_deserti_VCD115</i> .546414, <i>Thermus_sp._CCB_US3_UF1</i> .1111069, <i>Deinococcus_maricopensis_DSM_21211</i> .709986, <i>Deinococcus_gobiensis_I</i> -0.745776, <i>Thermus_oshimai_JL</i> -

2.751945, *Thermus*_parvatiensis.456163, *Deinococcus*_geothermalis_DSM_11300.319795, *Oceanithermus*_profundus_DSM_14977.670487, *Deinococcus*_proteolyticus_MRP.693977

- 12 *Deinococcus*_maricopenis_DSM_21211.709986, *Deinococcus*_swuensis.1182571, *Truepera*_radiovictrix_DSM_17093.649638, *Marinithermus*_hydrothermalis_DSM_14884.869210, *Thermus*_scotoductus_SA-01.743525, *Deinococcus*_gobiensis_I-0.745776, *Deinococcus*_actinosclerus.1768108, *Thermus*_parvatiensis.456163, *Thermus*_thermophilus_JL-18.798128, *Thermus*_sp._CCB_US3_UF1.1111069
- 13 *Deinococcus*_swuensis.1182571, *Deinococcus*_geothermalis_DSM_11300.319795, *Deinococcus*_soli__Cha_et_al._2014.1309411, *Thermus*_sp._CCB_US3_UF1.1111069, *Marinithermus*_hydrothermalis_DSM_14884.869210, *Deinococcus*_proteolyticus_MRP.693977, *Thermus*_scotoductus_SA-01.743525, *Truepera*_radiovictrix_DSM_17093.649638, *Deinococcus*_maricopenis_DSM_21211.709986, *Deinococcus*_actinosclerus.1768108
- 14 *Deinococcus*_deserti_VCD115.546414, *Meiothermus*_silvanus_DSM_9946.526227, *Thermus*_scotoductus_SA-01.743525, *Marinithermus*_hydrothermalis_DSM_14884.869210, *Deinococcus*_peraridilitoris_DSM_19664.937777, *Oceanithermus*_profundus_DSM_14977.670487, *Deinococcus*_gobiensis_I-0.745776, *Deinococcus*_swuensis.1182571, *Truepera*_radiovictrix_DSM_17093.649638, *Thermus*_sp._CCB_US3_UF1.1111069
- 15 *Marinithermus*_hydrothermalis_DSM_14884.869210, *Deinococcus*_proteolyticus_MRP.693977, *Thermus*_scotoductus_SA-01.743525, *Deinococcus*_gobiensis_I-0.745776, *Thermus*_parvatiensis.456163, *Oceanithermus*_profundus_DSM_14977.670487, *Thermus*_thermophilus_JL-18.798128, *Thermus*_oshimai_JL-2.751945, *Deinococcus*_soli__Cha_et_al._2014.1309411, *Thermus*_aquaticus_Y51MC23.498848
- 16 *Oceanithermus*_profundus_DSM_14977.670487, *Thermus*_scotoductus_SA-01.743525, *Deinococcus*_soli__Cha_et_al._2014.1309411, *Deinococcus*_maricopenis_DSM_21211.709986, *Deinococcus*_geothermalis_DSM_11300.319795, *Truepera*_radiovictrix_DSM_17093.649638, *Deinococcus*_actinosclerus.1768108, *Deinococcus*_gobiensis_I-0.745776, *Thermus*_aquaticus_Y51MC23.498848, *Thermus*_thermophilus_JL-18.798128
- 17 *Meiothermus*_silvanus_DSM_9946.526227, *Thermus*_sp._CCB_US3_UF1.1111069, *Deinococcus*_gobiensis_I-0.745776, *Deinococcus*_geothermalis_DSM_11300.319795, *Thermus*_parvatiensis.456163, *Oceanithermus*_profundus_DSM_14977.670487, *Thermus*_aquaticus_Y51MC23.498848, *Deinococcus*_actinosclerus.1768108, *Thermus*_oshimai_JL-2.751945, *Deinococcus*_deserti_VCD115.546414
- 18 *Thermus*_sp._CCB_US3_UF1.1111069, *Marinithermus*_hydrothermalis_DSM_14884.869210, *Deinococcus*_radiodurans_R1.243230, *Thermus*_oshimai_JL-2.751945, *Meiothermus*_silvanus_DSM_9946.526227, *Oceanithermus*_profundus_DSM_14977.670487, *Thermus*_scotoductus_SA-01.743525, *Thermus*_parvatiensis.456163, *Deinococcus*_peraridilitoris_DSM_19664.937777, *Deinococcus*_deserti_VCD115.546414
- 19 *Deinococcus*_radiodurans_R1.243230, *Thermus*_aquaticus_Y51MC23.498848, *Truepera*_radiovictrix_DSM_17093.649638, *Thermus*_sp._CCB_US3_UF1.1111069, *Deinococcus*_gobiensis_I-0.745776, *Thermus*_thermophilus_JL-18.798128, *Oceanithermus*_profundus_DSM_14977.670487, *Deinococcus*_proteolyticus_MRP.693977, *Thermus*_parvatiensis.456163, *Deinococcus*_swuensis.1182571

9 **Table S22** List of 10 Actinobacteria (ACT) species kept for 20 permutations under MID10 random sampling scenarios (RSS).

RSS species kept

- 0 Streptomyces_globisporus_C-1027.1172567,Rhodoluna_lacicola.529884,Arthrobacter_sp._PAMC25486.1494608,Corynebacterium_ulcerans_FRC58.1408268,Tsukamurella_paurometabola_DSM_20162.521096,Arthrobacter_phenanthrenivorans_Sphe3.930171,Kocuria_rhizophila_DC2201.378753,Thermobifida_fusca_YX.269800,Frankia_sp._Eu11c.298654,Corynebacterium_aurimucosum_ATCC_700975.548476
- 1 Verrucosipora_maris_AB-18-032.263358,Salinispora_tropica_CNB-440.369723,Salinispora_arenicola_CNS-205.391037,Geodermatophilus_obscurus_DSM_43160.526225,Streptomyces_vietnamensis.362257,Arthrobacter_sp._Y C-RL1.1652545,Corynebacterium_stationis.1705,Actinomyces_meyeri.52773,Ilumatobacter_coccineus_YM16-304.1313172,Corynebacterium_terpenotabidum_Y-11.1200352
- 2 Arthrobacter_aurescens_TC1.290340,Corynebacterium_glyciniphilum_AJ_3170.1404245,Streptomyces_lydicus_A02.14 03539,Pseudonocardia_dioxanivorans_CB1190.675635,Streptomyces_scabiei_87.22.680198,Corynebacterium_singular e.161899,Corynebacterium_urealyticum_DSM_7109.504474,Streptomyces_collinus_Tu_365.1214242,Corynebacterium _lactis_RW2-5.1408189,Streptomyces_xiamenensis.408015
- 3 Adlercreutzia_equilifaciens_DSM_19450.1384484,Corynebacterium_atypicum.191610,Mycobacterium_yongonense_05-1390.1138871,Bifidobacterium_bifidum.1681,Cellulomonas_flavigena_DSM_20109.446466,Rhodococcus_jostii_RHA1.1 01510,Corynebacterium_kutscheri.35755,Microbacterium_sp._XT11.367477,Microbacterium_sp._PAMC_28756.179505 3,Mycobacterium_intracellulare_MOTT-64.1138383
- 4 Corynebacterium_aurimucosum_ATCC_700975.548476,Streptomyces_glaucescens.1907,Segniliparus_rotundus_DSM_44985.640132,Bifidobacterium_pseudolongum_PV8-2.1447715,Actinoplanes_sp._SE50_110.134676,Corynebacterium_argentoratense_DSM_44202.1348662,Corynebacteri um_pseudotuberculosis.1719,Mycobacterium_africanum.33894,Rhodococcus_erythropolis_PR4.234621,Corynebacteri um_camporealensis.161896
- 5 Mycobacterium_marinum_M.216594,Amycolicococcus_subflavus_DQS3-9A1.443218,Atopobium_parvulum_DSM_20469.521095,Pseudonocardia_sp._HH130629-09.1641402,Microbacterium_sp._PAMC_28756.1795053,Mycobacterium_sp._VKM_Ac-1817D.1273687,Mycobacterium_haemophilum_DSM_44634.1202450,Corynebacterium_humireducens_NBRC_106098_ _DSM_45392.1223515,Corynebacterium_maris_DSM_45190.1224163,Streptomyces_reticuli.1926
- 6 Corynebacterium_falsenii_DSM_44353.1451189,Frankia_sp._Eu11c.298654,Rhodococcus_erythropolis_PR4.234621,Str eptomyces_avermitilis_MA-4680_ _NBRC_14893.227882,Actinomyces_meyeri.52773,Nocardiopsis_alba_ATCC_BAA-2165.1205910,Mycobacterium_africanum.33894,Geodermatophilus_obscurus_DSM_43160.526225,Streptomyces_sp._7 69.1262452,Amycolatopsis_lurida_NRRL_2430.1460371
- 7 Streptomyces_ambofaciens_ATCC_23877.278992,Mycobacterium_haemophilum_DSM_44634.1202450,Coriobacteriac eae_bacterium_68-1-3.1531429,Corynebacterium_uterequi.1072256,Thermobispora_bispora_DSM_43833.469371,Rhodococcus_erythropolis _PR4.234621,Mycobacterium_goodii.134601,Frankia_sp._Eu11c.298654,Mycobacterium_chubuense_NBB4.710421,Sla ckia_heliotrinireducens_DSM_20476.471855
- 8 Corynebacterium_camporealensis.161896,Streptomyces_pratensis_ATCC_33331.591167,Streptomyces_venezuelae.54 571,Corynebacterium_maris_DSM_45190.1224163,Bifidobacterium_breve.1685,Bifidobacterium_kashiwanohense_JCM _15439_ _DSM_21854.1150460,Corynebacterium_urealyticum_DSM_7109.504474,Corynebacterium_efficiens_YS-314.196164,Thermobispora_bispora_DSM_43833.469371,Mycobacterium_sp._MOTT36Y.1168287

- 9 Arthrobacter_sulfonivorans.121292,Mycobacterium_fortuitum.1766,Kocuria_rhizophila_DC2201.378753,Propionibacterium_avidum_44067.1170318,Micromonospora_aurantiaca_ATCC_27029.644283,Pseudonocardia_sp._AL041005-10.445576,Arthrobacter_sp._ATCC_21022.1771959,Streptosporangium_roseum_DSM_43021.479432,Mycobacterium_rhodesiae_NBB3.710685,Bifidobacterium_breve.1685
- 10 Mycobacterium_sp._JLS.164757,Clavibacter_michiganensis_subsp._sepedonicus.31964,Amycolatopsis_japonica.208439,Kineococcus_radiotolerans_SRS30216____ATCC_BAA-149.266940,Actinomyces_meyeri.52773,Atopobium_parvulum_DSM_20469.521095,Mycobacterium_kansasii_ATCC_12478.557599,Arthrobacter_sp._Hiyo8.1588023,Streptomyces_sp._4F.1751294,Streptomyces_pristinaespiralis.38300
- 11 Amycolatopsis_lurida_NRRL_2430.1460371,Streptomyces_sp._Mg1.465541,Rothia_mucilaginoso_DY-18.680646,Rathayibacter_toxicus.145458,Mycobacterium_sp._KMS.189918,Streptomyces_cattlea_NRRL_8057____DSM_46488.1003195,Devriesea_agamarum.472569,Bifidobacterium_pseudocatenulatum_DSM_20438____JCM_1200____LMG_10505.547043,Trueperella_pyogenes_TP8.1435056,Corynebacterium_kroppenstedtii_DSM_44385.645127
- 12 Corynebacteriales_bacterium_X1036.1528099,Trueperella_pyogenes_TP8.1435056,Mycobacterium_sp._JLS.164757,Mycobacterium_bovis_BCG.33892,Bifidobacterium_breve.1685,Corynebacterium_glutamicum_R.340322,Coriobacteriaceae_bacterium_68-1-3.1531429,Micromonospora_sp._L5.648999,Corynebacterium_maris_DSM_45190.1224163,Arcanobacterium_haemolyticum_DSM_20595.644284
- 13 Corynebacterium_glutamicum_R.340322,Microbacterium_sp._XT11.367477,Aeromicrobium_erythreum.2041,Mycobacterium_tuberculosis.1773,Mycobacterium_indicus_pranii_MTCC_9506.1232724,Arthrobacter_arilaitensis.256701,Corynebacterium_maris_DSM_45190.1224163,Actinomyces_sp._oral_taxon_414.712122,Corynebacterium_sp._ATCC_6931.1487956,Mycobacterium_sp._EPa45.1545728
- 14 Arthrobacter_sp._FB24.290399,Mycobacterium_sp._KMS.189918,Arthrobacter_sp._IHBB_11108.1618207,Mycobacterium_bovis_BCG.33892,Cellulomonas_flavigena_DSM_20109.446466,Corynebacterium_halotolerans_YIM_70093____DSM_44683.1121362,Arthrobacter_alpinus.656366,Propionibacterium_freudenreichii_subsp._shermanii_CIRM-BIA1.754252,Corynebacterium_ureicelerivorans.401472,Actinomyces_oris.544580
- 15 Rathayibacter_toxicus.145458,Propionibacterium_acidipropionici_ATCC_4875.1171373,Saccharopolyspora_erythraea_NRRL_2338.405948,Geodermatophilus_obscurus_DSM_43160.526225,Streptomyces_ambofaciens_ATCC_23877.278992,Arthrobacter_phenanthrenivorans_Sphe3.930171,Corynebacteriales_bacterium_X1698.1562462,Mycobacterium_sp._MCS.164756,Bifidobacterium_indicum_LMG_11587____DSM_20214.1341694,Corynebacterium_glutamicum_R.340322
- 16 Corynebacteriales_bacterium_X1698.1562462,Nocardia_nova_SH22a.1415166,Streptomyces_pratensis_ATCC_33331.591167,Streptomyces_avermitilis_MA-4680____NBRC_14893.227882,Corynebacterium_resistens_DSM_45100.662755,Streptomyces_vietnamensis.362257,Streptomyces_glaucescens.1907,Leifsonia_xylii_subsp._cynodontis_DSM_46306.1389489,Bifidobacterium_longum_subsp._infantis_ATCC_15697____JCM_1222____DSM_20088.391904,Frankia_sp._CcI3.106370
- 17 Corynebacterium_camporealensis.161896,Kocuria_palustris.71999,Streptomyces_sp._769.1262452,Mycobacterium_ulcerans_Agy99.362242,Tropheryma_whipplei_str._Twist.203267,Streptomyces_sp._SirexAA-E.862751,Cellulomonas_flavigena_DSM_20109.446466,Propionibacterium_avidum_44067.1170318,Streptomyces_violaceusniger_Tu_4113.653045,Clavibacter_michiganensis_subsp._sepedonicus.31964
- 18 Mycobacterium_yongonense_05-1390.1138871,Corynebacterium_urealyticum_DSM_7109.504474,Aeromicrobium_erythreum.2041,Olsenella_sp._oral_taxon_807.712411,Bifidobacterium_breve.1685,Olsenella_uli_DSM_7084.633147,Actinomyces_meyeri.52773,Corynebacterium_kroppenstedtii_DSM_44385.645127,Corynebacterium_doosanense_CAU_212____DSM_45436.558173,Corynebacterium_testudinoris.136857
- 19 Gordonia_polyisoprenivorans_VH2.1112204,Stackebrandtia_nassauensis_DSM_44728.446470,Microbacterium_testaceum_STLB037.979556,Xylanimonas_cellulosilytica_DSM_15894.446471,Arthrobacter_sp._LS16.1690248,Corynebacterium_diphtheriae_31A.698962,Frankia_alni_ACN14a.326424,Rathayibacter_toxicus.145458,Bifidobacterium_breve.1685,Arthrobacter_sp._Rue61a.1118963

10 **Table S23** List of 17 Actinobacteria (ACT) species kept for 20 permutations under MID17 random sampling scenarios (RSS).

RSS species kept

- 0 Mycobacterium_sp._KMS.189918,Streptomyces_pristinaespiralis.38300,Streptomyces_violaceusniger_Tu_4113.653045,Arthrobacter_sp._Rue61a.1118963,Rothia_dentocariosa_ATCC_17931.762948,Conexibacter_woesei_DSM_14684.469383,Arcanobacterium_haemolyticum_DSM_20595.644284,Arthrobacter_phenanthrenivorans_Sphe3.930171,Propionibacterium_acidipropionici_ATCC_4875.1171373,Microbacterium_sp._PAMC_28756.1795053,Corynebacterium_singulare.161899,Streptomyces_albus.1888,Mycobacterium_kansasii_ATCC_12478.557599,Microbacterium_sp._No._7.1714373,Arthrobacter_sp._ATCC_21022.1771959,Bifidobacterium_catenuatum_DSM_16992____JCM_1194____LMG_11043.566552,Micromonospora_aurantiaca_ATCC_27029.644283
- 1 Amycolatopsis_lurida_NRRL_2430.1460371,Arthrobacter_phenanthrenivorans_Sphe3.930171,Leifsonia_xyli_subsp._cyodontis_DSM_46306.1389489,Frankia_alni_ACN14a.326424,Kibdelosporangium_phytohabitans.860235,Rhodococcus_jostii_RHA1.101510,Microbacterium_sp._PAMC_28756.1795053,Nocardia_brasiliensis_ATCC_700358.1133849,Gordonia_polyisoprenivorans_VH2.1112204,Arsenicococcus_sp._oral_taxon_190.1658671,Streptomyces_xiamenensis.408015,Corynebacterium_casei_LMG_S-19264.1285583,Brachybacterium_faecium_DSM_4810.446465,Saccharopolyspora_erythraea_NRRL_2338.405948,Streptomyces_cyaneogriseus_subsp._noncyanogenus.477245,Actinobacteria_bacterium_IMCC26256.1650658,Slackia_hellotrinireducens_DSM_20476.471855
- 2 Gordonia_sp._KTR9.337191,Arthrobacter_sp._IHBB_11108.1618207,Blastococcus_saxosidens_DD2.1146883,Arthrobacter_phenanthrenivorans_Sphe3.930171,Arthrobacter_sp._FB24.290399,Arthrobacter_sp._ERGS1_01.1704044,Mycobacterium_leprae_Br4923.561304,Kutzneria_albida_DSM_43870.1449976,Frankia_sp._Ccl3.106370,Corynebacteriales_bacterium_X1036.1528099,Corynebacterium_glutamicum_R.340322,Arthrobacter_arilaitensis.256701,Nocardia_nova_S_H22a.1415166,Corynebacterium_callunae_DSM_20147.1121353,Atopobium_parvulum_DSM_20469.521095,Saccharopolyspora_erythraea_NRRL_2338.405948,Pseudonocardia_sp._EC080625-04.1096868
- 3 Bifidobacterium_adolescentis.1680,Actinoplanes_missouriensis_431.512565,Corynebacterium_sp._ATCC_6931.1487956,Acidothermus_cellulolyticus_11B.351607,Actinoplanes_friuliensis_DSM_7358.1246995,Corynebacterium_glutamicum_R.340322,Mycobacterium_avium_104.243243,Mycobacterium_intracellulare_MOTT-64.1138383,Actinoplanes_sp._SE50_110.134676,Mycobacterium_vanbaalenii_PYR-1.350058,Streptomyces_pristinaespiralis.38300,Kutzneria_albida_DSM_43870.1449976,Arthrobacter_sp._FB24.290399,Arthrobacter_sp._LS16.1690248,Coriobacterium_glomerans_PW2.700015,Pimelobacter_simplex.2045,Mycobacterium_sp._MCS.164756
- 4 Corynebacterium_kroppenstedtii_DSM_44385.645127,Mycobacterium_leprae_Br4923.561304,Amycolatopsis_japonica.208439,Segniliparus_rotundus_DSM_44985.640132,Rubrobacter_radiotolerans.42256,Mycobacterium_kansasii_ATCC_12478.557599,Nocardia_brasiliensis_ATCC_700358.1133849,Mycobacterium_haemophilum_DSM_44634.1202450,Actinomyces_oris.544580,Actinotignum_schaalii.59505,Corynebacterium_ureicelerivorans.401472,Propionibacterium_freudenreichii_subsp._shermanii_CIRM-BIA1.754252,Brevibacterium_flavum.92706,Microlunatus_phosphovorax_NM-1.1032480,Mycobacterium_ulcerans_Agy99.362242,Arthrobacter_sp._PAMC25486.1494608,Corynebacterium_sp._ATCC_C_6931.1487956
- 5 Streptomyces_reticuli.1926,Propionibacterium_propionicum_F0230a.767029,Rothia_dentocariosa_ATCC_17931.762948,Propionibacterium_avidum_44067.1170318,Streptomyces_sp._SirexAA-E.862751,Nocardia_farcinica.37329,Corynebacterium_vitaeruminis_DSM_20294.1224164,Mycobacterium_indicus_pranii_MTCC_9506.1232724,Thermobifida_fusca_YX.269800,Mycobacterium_chubuense_NBB4.710421,Corynebacteriales_bacterium_X1698.1562462,Bifidobacterium_dentium_JCM_1195____DSM_20436.1150423,Gordonia_polyisoprenivorans_VH2.1112204,Arthrobacter_sulfonivorans.121292,Catenulispora_acidiphila_DSM_44928.479433,Coriobacterium_glomerans_PW2.700015,Mycobacterium_ulcerans_Agy99.362242
- 6 Intraporangium_calvum_DSM_43043.710696,Rothia_mucilaginos_a_DY-18.680646,Frankia_sp._Ccl3.106370,Pseudonocardia_sp._EC080625-04.1096868,Actinoplanes_missouriensis_431.512565,Bifidobacterium_angulatum_DSM_20098____JCM_7096.518635,Arthrobacter_sp._PAMC25486.1494608,Amycolatopsis_lurida_NRRL_2430.1460371,Corynebacterium_ureicelerivorans.401472,Nakamurella_multipartita_DSM_44233.479431,Mycobacterium_neoaurum_VKM_Ac-1815D.700508,Rubrobacter_radiotolerans.42256,Corynebacterium_diphtheriae_31A.698962,Arthrobacter_sp._IHBB_11108.1618207,Corynebacterium_aurimucosum_ATCC_700975.548476,Rathayibacter_toxicus.145458,Scardovia_inopinata_JCM_12537.1150468
- 7 Corynebacterium_mustelae.571915,Corynebacterium_efficiens_YS-314.196164,Arthrobacter_sp._ERGS1_01.1704044,Streptomyces_albus.1888,Arthrobacter_sp._Rue61a.1118963,Arthrobacter_sp._PAMC25486.1494608,Actinomyces_oris.544580,Adlercreutzia_equilifaciens_DSM_19450.1384484,Jonesia_denitrificans_DSM_20603.471856,Corynebacterium_humireducens_NBRC_106098____DSM_45392.1223515,Saccharomonospora_viridis_DSM_43017.471857,Mycobacterium_gilvum_PYR-GCK.350054,Actinoplanes_sp._SE50_110.134676,Coriobacterium_glomerans_PW2.700015,Nocardia_farcinica.37329,Corynebacterium_lactis_RW2-5.1408189,Corynebacterium_glutamicum_R.340322

- 8 Mycobacterium_sp._VKM_Ac-1817D.1273687,Corynebacterium_imitans.156978,Bifidobacterium_asteroides_PRL2011.1147128,Mycobacterium_sp._KMS.189918,Arthrobacter_sp._YC-RL1.1652545,Kribbella_flavida_DSM_17836.479435,Microterricola_viridarii.412690,Microlunatus_phosphovorus_NM-1.1032480,Streptomyces_sp._CdTB01.1725411,Rubrobacter_radiotolerans.42256,Coriobacteriaceae_bacterium_68-1-3.1531429,Pseudonocardia_sp._HH130629-09.1641402,Bifidobacterium_angulatum_DSM_20098____JCM_7096.518635,Arthrobacter_sp._Rue61a.1118963,Corynebacterium_argentoratense_DSM_44202.1348662,Microbacterium_sp._No._7.1714373,Streptomyces_glaucescens.1907
- 9 Mycobacterium_haemophilum_DSM_44634.1202450,Streptomyces_venezuelae.54571,Corynebacterium_urealyticum_DSM_7109.504474,Arthrobacter_sulfonivorans.121292,Kytococcus_sedentarius_DSM_20547.478801,Jonesia_denitrificans_DSM_20603.471856,Streptomyces_sp._4F.1751294,Gordonia_polyisoprenivorans_VH2.1112204,Arthrobacter_aurescens_TC1.290340,Gordonia_sp._QH-11.1136941,Streptomyces_xiamenensis.408015,Rathayibacter_toxicus.145458,Mycobacterium_sp._EPa45.1545728,Amycolatopsis_japonica.208439,Gordonia_sp._KTR9.337191,Kitasatospora_setae_KM-6054.452652,Mycobacterium_marinum_M.216594
- 10 Corynebacteriales_bacterium_X1036.1528099,Nakamurella_multipartita_DSM_44233.479431,Microlunatus_phosphovorus_NM-1.1032480,Mycobacterium_liflandii_128FXT.459424,Pseudonocardia_dioxanivorans_CB1190.675635,Streptomyces_ambofaciens_ATCC_23877.278992,Actinoplanes_sp._N902-109.649831,Kocuria_palustris.71999,Streptomyces_violaceusniger_Tu.4113.653045,Streptomyces_xiamenensis.408015,Kineococcus_radiotolerans_SRS30216____ATCC_BAA-149.266940,Propionibacterium_acidipropionici_ATCC_4875.1171373,Salinispora_tropica_CNB-440.369723,Rubrobacter_radiotolerans.42256,Corynebacterium_doosanense_CAU_212____DSM_45436.558173,Blastococcus_saxobidens_DD2.1146883,Rhodococcus_opacus_PD630.543736
- 11 Actinomyces_meyeri.52773,Corynebacterium_halotolerans_YIM_70093____DSM_44683.1121362,Mycobacterium_yongonense_05-1390.1138871,Frankia_sp._Ccl3.106370,Arthrobacter_sulfonivorans.121292,Bifidobacterium_dentium_JCM_1195____DSM_20436.1150423,Pseudonocardia_sp._EC080619-01.1096856,Mycobacterium_sp._MCS.164756,Micromonospora_aurantiaca_ATCC_27029.644283,Corynebacterium_testudinoris.136857,Xylanimonas_cellulosilytica_DSM_15894.446471,Cryptobacterium_curtum_DSM_15641.469378,Arthrobacter_sp._FB24.290399,Micrococcus_luteus_NCTC_2665.465515,Thermobifida_fusca_YX.269800,Streptomyces_sp._PAMC26508.1265601,Mycobacterium_marinum_M.216594
- 12 Arthrobacter_sp._LS16.1690248,Intrasporangium_calvum_DSM_43043.710696,Streptomyces_griseus_subsp._griseus_NBRC_13350.455632,Pseudonocardia_sp._HH130629-09.1641402,Streptomyces_pratensis_ATCC_33331.591167,Bifidobacterium_catenuatum_DSM_16992____JCM_1194____LMG_11043.566552,Rhodococcus_opacus_PD630.543736,Mycobacterium_chubuense_NBB4.710421,Corynebacterium_argentoratense_DSM_44202.1348662,Rhodococcus_sp._B7740.1564114,Gordonia_bronchialis_DSM_43247.526226, Frankia_symbiont_of_Datisca_glomerata.656024, Brevibacterium_flavum.92706,Salinispora_tropica_CNB-440.369723,Actinotignum_schaalii.59505,Beutenbergia_cavernae_DSM_12333.471853,Jonesia_denitrificans_DSM_20603.471856
- 13 Corynebacterium_casei_LMG_S-19264.1285583,Streptomyces_fulvissimus_DSM_40593.1303692,Jonesia_denitrificans_DSM_20603.471856,Rhodococcus_opacus_PD630.543736,Corynebacterium_callunae_DSM_20147.1121353,Tropheryma_whipplei_str._Twist.203267,Mycobacterium_sinense.875328,Slackia_heliotrinireducens_DSM_20476.471855,Rhodococcus_jostii_RHA1.101510,Mycobacterium_gilvum_PYR-GCK.350054,Streptomyces_sp._CNQ-509.444103,Arthrobacter_sp._FB24.290399,Pseudonocardia_dioxanivorans_CB1190.675635,Corynebacterium_testudinoris.136857,Coriobacterium_glomerans_PW2.700015,Rubrobacter_radiotolerans.42256,Mycobacterium_chubuense_NBB4.710421
- 14 Mycobacterium_vanbaalenii_PYR-1.350058,Kitasatospora_setae_KM-6054.452652,Arthrobacter_sp._PAMC25486.1494608,Corynebacterium_mustelae.571915,Intrasporangium_calvum_DSM_43043.710696,Mycobacterium_indicus_pranii_MTCC_9506.1232724,Salinispora_arenicola_CNS-205.391037,Mycobacterium_kansasii_ATCC_12478.557599,Microbacterium_testaceum_StLB037.979556,Kibdelosporangium_phytohabitans.860235,Arthrobacter_sp._IHBB_11108.1618207,Corynebacterium_efficiens_YS-314.196164,Corynebacterium_pseudotuberculosis.1719,Catenulispora_acidiphila_DSM_44928.479433,Mycobacterium_ipeprae_Br4923.561304,Bifidobacterium_pseudocatenuatum_DSM_20438____JCM_1200____LMG_10505.547043,Actinomyces_radicidentis.111015
- 15 Actinoplanes_sp._SE50_110.134676,Arthrobacter_sp._YC-RL1.1652545,Bifidobacterium_animalis_subsp._lactis_CNMC-I-2494.1042403,Corynebacterium_kutscheri.35755,Adlercreutzia_equolifaciens_DSM_19450.1384484,Microbacterium_sp.

_PAMC_28756.1795053,Bifidobacterium_thermophilum_RBL67.1254439,Corynebacterium_lactis_RW2-5.1408189,Bifidobacterium_asteroides_PRL2011.1147128,Corynebacterium_kroppenstedtii_DSM_44385.645127,Mycobacterium_rhodesiae_NBB3.710685,Mycobacterium_sinense.875328,Mycobacterium_microti.1806,Actinomyces_oris.544580,Bifidobacterium_bifidum.1681,Arthrobacter_alpinus.656366,Bifidobacterium_adolescentis.1680

16 Streptomyces_violaceusniger_Tu_4113.653045,Microbacterium_testaceum_StLB037.979556,Nocardia_nova_SH22a.1415166,Corynebacterium_callunae_DSM_20147.1121353,Mycobacterium_rhodesiae_NBB3.710685,Acidothermus_cellulolyticus_11B.351607,Streptomyces_hygroscopicus_subsp._jinggangensis_5008.1133850,Pseudonocardia_sp._AL041005-10.445576,Geodermatophilus_obscurus_DSM_43160.526225,Micromonospora_aurantiaca_ATCC_27029.644283,Cellulomonas_fimi_ATCC_484.590998,Streptomyces_sp._Mg1.465541,Streptomyces_collinus_Tu_365.1214242,Kibdelosporangium_phytohabitans.860235,Bifidobacterium_indicum_LMG_11587____DSM_20214.1341694,Olsenella_sp._oral_taxon_807.712411,Slackia_heliotrinireducens_DSM_20476.471855

17 Thermobispora_bispora_DSM_43833.469371,Pseudonocardia_sp._HH130629-09.1641402,Amycolatopsis_japonica.208439,Amycolatopsis_lurida_NRRL_2430.1460371,Corynebacterium_kutscheri.35755,Corynebacterium_doosanense_CAU_212____DSM_45436.558173,Micromonospora_sp._L5.648999,Corynebacterium_falsenii_DSM_44353.1451189,Bifidobacterium_animalis_subsp._lactis_CNCM_I-2494.1042403,Mycobacterium_tuberculosis.1773,Arthrobacter_sp._ERGS1_01.1704044,Salinispora_tropica_CNB-440.369723,Corynebacterium_mustelae.571915,Streptomyces_globisporus_C-1027.1172567,Bifidobacterium_indicum_LMG_11587____DSM_20214.1341694,Corynebacterium_callunae_DSM_20147.1121353,Corynebacterium_efficiens_YS-314.196164

18 Actinoplanes_friuliensis_DSM_7358.1246995,Arthrobacter_sulfonivorans.121292,Corynebacterium_kroppenstedtii_DSM_44385.645127,Corynebacterium_glyciniphilum_AJ_3170.1404245,Propionibacterium_propionicum_F0230a.767029,Stactobacterium_nassauensis_DSM_44728.446470,Corynebacterium_vitaeruminis_DSM_20294.1224164,Microbacterium_sp._CGR1.1696072,Arthrobacter_alpinus.656366,Corynebacterium_callunae_DSM_20147.1121353,Micrococcus_luteus_NCTC_2665.465515,Coriobacteriaceae_bacterium_68-1-3.1531429,Actinoplanes_sp._N902-109.649831,Bifidobacterium_breve.1685,Arthrobacter_sp._A3.595593,Corynebacterium_aurimucosum_ATCC_700975.548476,Corynebacterium_resistens_DSM_45100.662755

19 Illuminibacter_coccineus_YM16-304.1313172,Arthrobacter_alpinus.656366,Rubrobacter_xylanophilus_DSM_9941.266117,Coriobacteriaceae_bacterium_68-1-3.1531429,Mycobacterium_africanum.33894,Rhodococcus_sp._B7740.1564114,Nocardiopsis_alba_ATCC_BAA-2165.1205910,Corynebacterium_singulare.161899,Corynebacterium_glyciniphilum_AJ_3170.1404245,Rhodococcus_erythropolis_PR4.234621,Olsenella_sp._oral_taxon_807.712411,Nocardia_nova_SH22a.1415166,Microbacterium_sp._CGR1.1696072,Mycobacterium_sp._JLS.164757,Catenulispora_acidiphila_DSM_44928.479433,Streptomyces_sp._Mg1.465541,Actinoplanes_friuliensis_DSM_7358.1246995

13 **Table S24** List of 19 Actinobacteria (ACT) species kept for 20 permutations under MID19 random sampling scenarios (RSS).

RSS	species kept
0	<i>Amycolatopsis_methanolica_239.1068978</i> , <i>Streptomyces_violaceusniger_Tu_4113.653045</i> , <i>Amycolatopsis_lurida_NRR L_2430.1460371</i> , <i>Mycobacterium_kansasii_ATCC_12478.557599</i> , <i>Corynebacterium_terpenotabidum_Y-11.1200352</i> , <i>Corynebacterium_variabile_DSM_44702.858619</i> , <i>Blastococcus_saxobsidens_DD2.1146883</i> , <i>Arthrobacter_s p_LS16.1690248</i> , <i>Mycobacterium_sp._EPa45.1545728</i> , <i>Propionibacterium_freudenreichii_subsp._shermanii_CIRM-BIA1.754252</i> , <i>Tropheryma_whipplei_str._Twist.203267</i> , <i>Streptomyces_venezuelae.54571</i> , <i>Modestobacter_marinus.4776 41</i> , <i>Mycobacterium_yongonense_05-1390.1138871</i> , <i>Corynebacterium_maris_DSM_45190.1224163</i> , <i>Bifidobacterium_pseudocatenulatum_DSM_20438_ JCM_1200_ LMG_10505.547043</i> , <i>Slackia_heliotrinireducens_DSM_20476.471855</i> , <i>Dermacoccus_nishinomiyaensis.1274</i> , <i>Isoptricola_variabilis_225.743718</i>
1	<i>Streptomyces_collinus_Tu_365.1214242</i> , <i>Propionibacterium_acnes_C1.1234380</i> , <i>Actinoplanes_missouriensis_431.5125 65</i> , <i>Streptomyces_sp._769.1262452</i> , <i>Arthrobacter_alpinus.656366</i> , <i>Rhodoluna_lacicola.529884</i> , <i>Frankia_sp._EAN1pec.29 8653</i> , <i>Pseudonocardia_sp._EC080610-09.1688404</i> , <i>Arthrobacter_aurescens_TC1.290340</i> , <i>Mycobacterium_sp._MOTT36Y.1168287</i> , <i>Bifidobacterium_kashiwano hense_JCM_15439_ DSM_21854.1150460</i> , <i>Corynebacterium_kroppenstedtii_DSM_44385.645127</i> , <i>Rhodococcus_sp._ B7740.1564114</i> , <i>Tsakumurella_paurometabola_DSM_20162.521096</i> , <i>Rathayibacter_toxicus.145458</i> , <i>Mycobacterium_gil vum_PYR-GCK.350054</i> , <i>Coriobacterium_glomerans_PW2.700015</i> , <i>Microbacterium_sp._CGR1.1696072</i> , <i>Frankia_sp._Eul1c.298654</i>
2	<i>Micrococcus_luteus_NCTC_2665.465515</i> , <i>Bifidobacterium_breve.1685</i> , <i>Geodermatophilus_obscurus_DSM_43160.5262 25</i> , <i>Eggerthella_lenta_DSM_2243.479437</i> , <i>Rhodococcus_opacus_PD630.543736</i> , <i>Mycobacterium_chubuense_NBB4.71 0421</i> , <i>Scardovia_inopinata_JCM_12537.1150468</i> , <i>Mycobacterium_gilvum_PYR-GCK.350054</i> , <i>Streptomyces_bingchenggensis_BCW-1.749414</i> , <i>Pseudonocardia_dioxanivorans_CB1190.675635</i> , <i>Kribbella_flavida_DSM_17836.479435</i> , <i>Amycolatopsis_orien talis_HCCB10007.1156913</i> , <i>Bifidobacterium_coryneforme.1687</i> , <i>Olsenella_uli_DSM_7084.633147</i> , <i>Actinoplanes_sp._N9 02-109.649831</i> , <i>Corynebacterium_halotolerans_YIM_70093_ DSM_44683.1121362</i> , <i>Corynebacterium_imitans.156978</i> , <i>Bifi dobacterium_thermophilum_RBL67.1254439</i> , <i>Rhodococcus_erythropolis_PR4.234621</i>
3	<i>Streptomyces_collinus_Tu_365.1214242</i> , <i>Frankia_symbiont_of_Datisca_glomerata.656024</i> , <i>Mycobacterium_gilvum_PY R-GCK.350054</i> , <i>Pseudonocardia_sp._AL041005-10.445576</i> , <i>Dermacoccus_nishinomiyaensis.1274</i> , <i>Nocardia_brasiliensis_ATCC_700358.1133849</i> , <i>Mycobacterium_kansa sii_ATCC_12478.557599</i> , <i>Corynebacterium_doosanense_CAU_212_ DSM_45436.558173</i> , <i>Corynebacteriales_bacteri um_X1698.1562462</i> , <i>Microbacterium_sp._XT11.367477</i> , <i>Mycobacterium_fortuitum.1766</i> , <i>Cellulomonas_flavigena_DSM_20109.446466</i> , <i>Actinosynnema_mirum_DSM_43827.446462</i> , <i>Corynebacterium_deserti_GIMN1.010.931089</i> , <i>Corynebact erium_glyciniphilum_AJ_3170.1404245</i> , <i>Bifidobacterium_pseudocatenulatum_DSM_20438_ JCM_1200_ LMG_1050 5.547043</i> , <i>Corynebacterium_ureicelerivorans.401472</i> , <i>Cryptobacterium_curtum_DSM_15641.469378</i> , <i>Gordonia_sp._KTR 9.337191</i>
4	<i>Mycobacterium_vanbaalenii_PYR-1.350058</i> , <i>Corynebacterium_mustelae.571915</i> , <i>Arthrobacter_sp._ERGS1_01.1704044</i> , <i>Brachybacterium_faecium_DSM_4810.446465</i> , <i>Streptomyces_cyaneogriseus_subsp._noncyanogenus.477245</i> , <i>Streptomyces_violaceusniger_Tu_4113.65 3045</i> , <i>Bifidobacterium_asteroides_PRL2011.1147128</i> , <i>Streptomyces_sp._769.1262452</i> , <i>Nocardia_farcinica.37329</i> , <i>Bifidob acterium_coryneforme.1687</i> , <i>Arthrobacter_aurescens_TC1.290340</i> , <i>Corynebacterium_singulare.161899</i> , <i>Mycobacterium_ sp._KMS.189918</i> , <i>Nocardia_nova_SH22a.1415166</i> , <i>Olsenella_uli_DSM_7084.633147</i> , <i>Amycolatopsis_orientalis_HCCB1 0007.1156913</i> , <i>Mycobacterium_sp._JLS.164757</i> , <i>Streptomyces_fulvissimus_DSM_40593.1303692</i> , <i>Bifidobacterium_ani malis_subsp._lactis_CNCM_I-2494.1042403</i>
5	<i>Corynebacterium_glyciniphilum_AJ_3170.1404245</i> , <i>Corynebacterium_maris_DSM_45190.1224163</i> , <i>Pseudonocardia_dio xanivorans_CB1190.675635</i> , <i>Pseudonocardia_sp._AL041005-10.445576</i> , <i>Mycobacterium_tuberculosis.1773</i> , <i>Bifidobacterium_asteroides_PRL2011.1147128</i> , <i>Conexibacter_woesei_DS M_14684.469383</i> , <i>Mycobacterium_sinense.875328</i> , <i>Streptomyces_vietnamensis.362257</i> , <i>Tsakumurella_paurometabola_ DSM_20162.521096</i> , <i>Arthrobacter_sp._ATCC_21022.1771959</i> , <i>Actinoplanes_missouriensis_431.512565</i> , <i>Actinomyces_o ris.544580</i> , <i>Microclunatus_phosphovorans_NM-1.1032480</i> , <i>Streptomyces_albus.1888</i> , <i>Mycobacterium_yongonense_05-1390.1138871</i> , <i>Bifidobacterium_adolescentis.1680</i> , <i>Atopobium_parvulum_DSM_20469.521095</i> , <i>Frankia_sp._Eul1c.2986 54</i>
6	<i>Frankia_sp._EAN1pec.298653</i> , <i>Propionibacterium_avidum_44067.1170318</i> , <i>Corynebacteriales_bacterium_X1698.15624 62</i> , <i>Bifidobacterium_scardovii_JCM_12489_ DSM_13734.1150461</i> , <i>Pimelobacter_simplex.2045</i> , <i>Nocardia_nova_SH22 a.1415166</i> , <i>Actinosynnema_mirum_DSM_43827.446462</i> , <i>Corynebacterium_glyciniphilum_AJ_3170.1404245</i> , <i>Mycobacter ium_marinum_M.216594</i> , <i>Mycobacterium_sp._MCS.164756</i> , <i>Arthrobacter_sp._YC-RL1.1652545</i> , <i>Frankia_sp._Eul1c.298654</i> , <i>Bifidobacterium_catenulatum_DSM_16992_ JCM_1194_ LMG_11043.566</i>

- 552, *Cellulomonas gilvus* ATCC_13127.593907, *Arcanobacterium haemolyticum* DSM_20595.644284, *Corynebacterium urealyticum* DSM_7109.504474, *Streptomyces lydicus* A02.1403539, *Rhodococcus jostii* RHA1.101510, *Thermomonospora curvata* DSM_43183.471852
- 7 Bifidobacterium_indicum_LMG_11587___DSM_20214.1341694, *Corynebacterium uterequi*.1072256, *Bifidobacterium_s cardovii*_JCM_12489___DSM_13734.1150461, *Mycobacterium microti*.1806, *Streptomyces*_sp_.769.1262452, *Mycobacterium abscessus*_subsp._bolletii_50594.1303024, *Actinosynnema mirum*_DSM_43827.446462, *Rothia mucilaginosa*_D Y-18.680646, *Corynebacteriales bacterium*_X1698.1562462, *Corynebacterium doosanense*_CAU_212___DSM_45436.558173, *Mycobacterium gilvum*_PYR-GCK.350054, *Actinotignum schaalii*.59505, *Kribbella flavida*_DSM_17836.479435, *Mycobacterium rhodesiae*_NBB3.710685, *Corynebacterium vitaeruminis*_DSM_20294.1224164, *Bifidobacterium kashiwanohense*_JCM_15439___DSM_21854.1150460, *Corynebacterium argentoratense*_DSM_44202.1348662, *Streptomyces ambofaciens*_ATCC_23877.278992, *Nocardioopsis dassonvillei*_subsp._dassonvillei_DSM_43111.446468
- 8 *Pseudonocardia*_sp._EC080610-09.1688404, *Streptomyces pratensis*_ATCC_33331.591167, *Streptomyces avermitilis*_MA-4680___NBRC_14893.227882, *Kibdelosporangium phytohabitans*.860235, *Devriesea agamarum*.472569, *Brevibacterium flavum*.92706, *Corynebacterium glutamicum*_R.340322, *Actinomyces meyeri*.52773, *Aeromicrobium erythreum*.2041, *Bifidobacterium animalis*_subsp._lactis_CNCM_I-2494.1042403, *Luteipulveratus mongoliensis*.571913, *Salinispora arenicola*_CNS-205.391037, *Arsenicicoccus*_sp._oral_taxon_190.1658671, *Micromonospora aurantiaca*_ATCC_27029.644283, *Mycobacterium microti*.1806, *Rhodococcus opacus*_PD630.543736, *Blastococcus saxobsidens*_DD2.1146883, *Microbacterium*_sp._XT11.367477, *Slackia heliotrinireducens*_DSM_20476.471855
- 9 *Beutenbergia cavernae*_DSM_12333.471853, *Olsenella*_sp._oral_taxon_807.712411, *Actinoplanes*_sp._N902-109.649831, *Streptomyces ambofaciens*_ATCC_23877.278992, *Arthrobacter arilaitensis*.256701, *Kytococcus sedentarius*_DSM_20547.478801, *Mycobacterium ulcerans*_Agy99.362242, *Catenulispora acidiphila*_DSM_44928.479433, *Streptomyces collinus*_Tu_365.1214242, *Kocuria palustris*.71999, *Corynebacterium glutamicum*_R.340322, *Cellulomonas flavigena*_DSM_20109.446466, *Microbacterium*_sp._XT11.367477, *Frankia*_sp._EAN1pec.298653, *Rhodococcus*_sp._B7740.1564114, *Propionibacterium avidum*.44067.1170318, *Saccharomonospora viridis*_DSM_43017.471857, *Microterricola viridarii*.412690, *Amycolatopsis japonica*.208439
- 10 *Pseudonocardia*_sp._HH130629-09.1641402, *Arthrobacter sulfonivorans*.121292, *Mycobacterium gilvum*_PYR-GCK.350054, *Bifidobacterium pseudocatenulatum*_DSM_20438___JCM_1200___LMG_10505.547043, *Propionibacterium freudenreichii*_subsp._shermanii_CIRM-BIA1.754252, *Salinispora tropica*_CNCB-440.369723, *Mycobacterium microti*.1806, *Bifidobacterium longum*_subsp._infantis_ATCC_15697___JCM_1222___DSM_20088.391904, *Kibdelosporangium phytohabitans*.860235, *Corynebacterium deserti*_GIMN1.010.931089, *Eggerthella*_sp._YY7918.502558, *Corynebacterium mustelae*.571915, *Arthrobacter*_sp._FB24.290399, *Actinoplanes missouriensis*.431.512565, *Geodermatophilus obscurus*_DSM_43160.526225, *Streptomyces pratensis*_ATCC_33331.591167, *Devriesea agamarum*.472569, *Actinomyces oris*.544580, *Saccharomonospora viridis*_DSM_43017.471857
- 11 *Amycolatopsis orientalis*_HCCB10007.1156913, *Rhodococcus pyridinivorans*_SB3094.1435356, *Microbacterium testaceum*_StLB037.979556, *Micromonospora*_sp._L5.648999, *Corynebacterium kroppenstedtii*_DSM_44385.645127, *Actinosynnema mirum*_DSM_43827.446462, *Mycobacterium rhodesiae*_NBB3.710685, *Mobiluncus curtisii*_ATCC_43063.548479, *Mycobacterium*_sp._JLS.164757, *Frankia alni*_ACN14a.326424, *Mycobacterium kansasii*_ATCC_12478.557599, *Arthrobacter alpinus*.656366, *Bifidobacterium catenulatum*_DSM_16992___JCM_1194___LMG_11043.566552, *Streptomyces pristinaespiralis*.38300, *Geodermatophilus obscurus*_DSM_43160.526225, *Streptomyces*_sp._Mg1.465541, *Stackebrandtia nassauensis*_DSM_44728.446470, *Corynebacterium variable*_DSM_44702.858619, *Bifidobacterium angulatum*_DSM_20098___JCM_7096.518635
- 12 *Eggerthella lenta*_DSM_2243.479437, *Arthrobacter*_sp._Hiyo8.1588023, *Propionibacterium freudenreichii*_subsp._shermanii_CIRM-BIA1.754252, *Sanguibacter keddieii*_DSM_10542.446469, *Streptomyces reticuli*.1926, *Gordonia*_sp._KTR9.337191, *Bifidobacterium adolescentis*.1680, *Dermacoccus nishinomiyaensis*.1274, *Arsenicicoccus*_sp._oral_taxon_190.1658671, *Streptomyces globisporus*_C-1027.1172567, *Bifidobacterium animalis*_subsp._lactis_CNCM_I-2494.1042403, *Cellulomonas flavigena*_DSM_20109.446466, *Streptomyces pristinaespiralis*.38300, *Corynebacterium lactis*_RW2-5.1408189, *Nakamurella multipartita*_DSM_44233.479431, *Frankia alni*_ACN14a.326424, *Kineococcus radiotolerans*_SRS30216___ATCC_BAA-149.266940, *Bifidobacterium bifidum*.1681, *Amycolatopsis japonica*.208439
- 13 *Rothia dentocariosa*_ATCC_17931.762948, *Cryptobacterium curtum*_DSM_15641.469378, *Amycolatopsis mediterranei*_S699.713604, *Frankia*_sp._EAN1pec.298653, *Corynebacterium resistens*_DSM_45100.662755, *Rhodococcus erythropolis*_PR4.234621, *Microbacterium*_sp._PAMC_28756.1795053, *Actinotignum schaalii*.59505, *Corynebacterium halotolerans*_YIM_70093___DSM_44683.1121362, *Brevibacterium flavum*.92706, *Amycolicoccus subflavus*_DQS3-9A1.443218, *Arthrobacter*_sp._ATCC_21022.1771959, *Streptomyces lydicus*_A02.1403539, *Corynebacterium jeikeium*_

K411.306537,*Nocardia_cyriaci*georgica_GUH-
2.1127134,*Acidothermus_cellulolyticus*_11B.351607,*Gordonia_polyisoprenivorans*_VH2.1112204,*Arthrobacter_phenanthrenivorans*_Sphe3.930171,*Bifidobacterium_adolescentis*.1680

- 14 *Bifidobacterium_actinocoloniiforme*_DSM_22766.1437605,*Actinoplanes_sp._N902*-109.649831,*Mycobacterium_kansasii*_ATCC_12478.557599,*Corynebacterium_aurimucosum*_ATCC_700975.548476,*Kibdelosporangium_phytohabitans*.860235,*Mycobacterium_yongonense*_05-1390.1138871,*Streptomyces_sp._Mg1*.465541,*Bifidobacterium_coryneforme*.1687,*Adlercreutzia_euquolifaciens*_DSM_19450.1384484,*Amycolatopsis_japonica*.208439,*Mycobacterium_africanum*.33894,*Streptomyces_sp._PAMC26508*.1265601,*Trueperella_pyogenes*_TP8.1435056,*Arthrobacter_sulfonivorans*.121292,*Aeromicrobium_erythreum*.2041,*Brevibacterium_flavum*.92706,*Coriobacteriaceae_bacterium*_68-1-3.1531429,*Corynebacterium_epidermidicantis*.1050174,*Mycobacterium_sp._JS623*.212767
- 15 *Micrococcus_luteus*_NCTC_2665.465515,*Mycobacterium_intracellulare*_MOTT-64.1138383,*Nocardia_farcinica*.37329,*Cellulomonas_fimi*_ATCC_484.590998,*Rhodococcus_erythropolis*_PR4.234621,*Kitasatospora_setae*_KM-6054.452652,*Gordonia_bronchialis*_DSM_43247.526226,*Corynebacterium_variabile*_DSM_44702.858619,*Actinosynnema_mirum*_DSM_43827.446462,*Arthrobacter_sulfonivorans*.121292,*Nocardiopsis_alba*_ATCC_BAA-2165.1205910,*Verrucosipora_maris_AB*-18-032.263358,*Corynebacteriales_bacterium_X*1698.1562462,*Nocardioides_sp._JS614*.196162,*Streptomyces_scabiei*_87.22.680198,*Mycobacterium_sp._JS623*.212767,*Streptomyces_collinus_Tu*_365.1214242,*Rhodococcus_pyridinivorans*_SB3094.1435356,*Actinoplanes_missouriensis*_431.512565
- 16 *Corynebacterium_callunae*_DSM_20147.1121353,*Mycobacterium_sp._MCS*.164756,*Streptomyces_albus*.1888,*Amycolaticoccus_subflavus*_DQS3-9A1.443218,*Tsukamurella_paurometabola*_DSM_20162.521096,*Tropheryma_whipplei_str._Twist*.203267,*Streptomyces_leeuwenhoekii*.1437453,*Mycobacterium_sinense*.875328,*Streptomyces_glaucescens*.1907,*Micrococcus_luteus*_NCTC_2665.465515,*Microbacterium_testaceum*_StLB037.979556,*Mycobacterium_chubuense*_NBB4.710421,*Actinomycetes_sp._oral_taxon_414*.712122,*Frankia_sp._EAN1pec*.298653,*Bifidobacterium_coryneforme*.1687,*Actinoplanes_missouriensis*_431.512565,*Kocuria_rhizophila*_DC2201.378753,*Mycobacterium_gilvum_PYR*-GCK.350054,*Rubrobacter_radiotolerans*.42256
- 17 *Cellulomonas_gilvus*_ATCC_13127.593907,*Mycobacterium_africanum*.33894,*Mycobacterium_gilvum_PYR*-GCK.350054,*Bifidobacterium_asteroides*_PRL2011.1147128,*Streptomyces_sp._Sirex*AA-E.862751,*Corynebacterium_marinum*_DSM_44953.1224162,*Nocardia_nova*_SH22a.1415166,*Corynebacterium_diphtheriae*_31A.698962,*Brachybacterium_faecium*_DSM_4810.446465,*Rothia_mucilaginosa_DY*-18.680646,*Streptomyces_cattleia_NRRL_8057*___DSM_46488.1003195,*Actinomycetes_radidentis*.111015,*Rhodococcus_sp._B7740*.1564114,*Jonesia_denitrificans*_DSM_20603.471856,*Streptomyces_cyaneogriseus_subsp._noncyanogenus*.477245,*Corynebacterium_mustelae*.571915,*Bifidobacterium_dentium*_JCM_1195___DSM_20436.1150423,*Bifidobacterium_actinocoloniiforme*_DSM_22766.1437605,*Kineococcus_radiotolerans*_SRS30216___ATCC_BAA-149.266940
- 18 *Kytococcus_sedentarius*_DSM_20547.478801,*Pseudonocardia_sp._EC080619*-01.1096856,*Nocardia_nova*_SH22a.1415166,*Mobiluncus_curtisii*_ATCC_43063.548479,*Coriobacterium_glomerans*_PW2.700015,*Nocardia_farcinica*.37329,*Bifidobacterium_catenulatum*_DSM_16992___JCM_1194___LMG_11043.566552,*Microbacterium_testaceum*_StLB037.979556,*Corynebacterium_imitans*.156978,*Amycolatopsis_methanolica*_239.1068978,*Thermomonospora_curvata*_DSM_43183.471852,*Tsukamurella_paurometabola*_DSM_20162.521096,*Propionibacterium_propionicum*_F0230a.767029,*Nocardiopsis_alba*_ATCC_BAA-2165.1205910,*Actinoplanes_sp._N902*-109.649831,*Cellulomonas_gilvus*_ATCC_13127.593907,*Streptomyces_glaucescens*.1907,*Arthrobacter_phenanthrenivorans*_Sphe3.930171,*Eggerthella_lenta*_DSM_2243.479437
- 19 *Mycobacterium_yongonense*_05-1390.1138871,*Nocardiopsis_dassonvillei_subsp._dassonvillei*_DSM_43111.446468,*Geodermatophilus_obscurus*_DSM_43160.526225,*Streptomyces_xiamenensis*.408015,*Amycolatopsis_methanolica*_239.1068978,*Pseudonocardia_sp._A*L04100_10.445576,*Gardnerella_vaginalis*_ATCC_14019.525284,*Microbacterium_sp._CGR1*.1696072,*Bifidobacterium_bifidum*.1681,*Rubrobacter_radiotolerans*.42256,*Streptomyces_glaucescens*.1907,*Arthrobacter_sp._IHBB*_11108.1618207,*Corynebacterium_doosanense*_CAU_212___DSM_45436.558173,*Mobiluncus_curtisii*_ATCC_43063.548479,*Leifsonia_xylii_subsp._cynodontis*_DSM_46306.1389489,*Nocardia_cyriaci*georgica_GUH-2.1127134,*Mycobacterium_gilvum_PYR*-GCK.350054,*Streptomyces_sp._PAMC26508*.1265601,*Renibacterium_salmoninarum*_ATCC_33209.288705

16 **Table S25** List of 32 Actinobacteria (ACT) species kept for 20 permutations under MID32 random sampling scenarios (RSS).

RSS	species kept
0	Microbacterium_sp._PAMC_28756.1795053,Kytococcus_sedentarius_DSM_20547.478801,Micromonospora_sp._L5.648999,Pseudonocardia_dioxanivorans_CB1190.675635,Streptomyces_sp._CdTB01.1725411,Kitasatospora_setae_KM-6054.452652,Propionibacterium_acnes_C1.1234380,Streptomyces_vietnamensis.362257,Actinoplanes_missouriensis_431.512565,Clavibacter_michiganensis_subsp._sepedonicus.31964,Mycobacterium_sp._KMS.189918,Nakamurella_multi- partita_DSM_44233.479431,Bifidobacterium_dentium_JCM_1195_DSM_20436.1150423,Cellulomonas_gilvus_ATCC_13127.593907,Olsenella_sp._oral_taxon_807.712411,Streptomyces_sp._769.1262452,Eggerthella_lenta_DSM_2243.479437,Actinomyces_radici- dentis.111015,Arthrobacter_sp._Rue61a.1118963,Thermomonospora_curvata_DSM_43183.471852,Cryptobacterium_curtum_DSM_15641.469378,Arthrobacter_sp._PAMC25486.1494608,Saccharopolyspora_eryth- raea_NRRL_2338.405948,Actinotignum_schaalii.59505,Gordonia_polyisoprenivorans_VH2.1112204,Mycobacterium_go- odii.134601,Mobiluncus_curtisii_ATCC_43063.548479,Mycobacterium_fortuitum.1766,Rubrobacter_radiotolerans.42256, Arthrobacter_chlorophenolicus_A6.452863,Amycolatopsis_orientalis_HCCB10007.1156913,Streptomyces_lydicus_A02- 1403539
1	Mycobacterium_sp._EPa45.1545728,Bifidobacterium_catenulatum_DSM_16992_JCM_1194_LMG_11043.566552, Bifidobacterium_pseudocatenulatum_DSM_20438_JCM_1200_LMG_10505.547043,Streptomyces_hygroscopicus_ subsp._jinggangensis_5008.1133850,Streptomyces_sp._CFMR_7.1649184,Streptomyces_glaucescens.1907,Corynebac- terium_jeikeium_K411.306537,Arthrobacter_sp._LS16.1690248,Mycobacterium_haemophilum_DSM_44634.1202450,Ce- llulomonas_fimi_ATCC_484.590998,Rhodococcus_erythropolis_PR4.234621,Mycobacterium_neoaurum_VKM_Ac- 1815D.700508,Mycobacterium_ulcerans_Agy99.362242,Actinotignum_schaalii.59505,Streptomyces_scabiei_87.22.6801 98,Coriobacterium_glomerans_PW2.700015,Arthrobacter_sp._ERGS1_01.1704044,Corynebacterium_halotolerans_YIM_70093_DSM_44683.1121362,Nocardiopsis_dassonvillei_subsp._dassonvillei_DSM_43111.446468,Streptomyces_sp_769.1262452,Corynebacterium_kroppenstedtii_DSM_44385.645127,Pseudonocardia_sp._HH130629- 09.1641402,Mycobacterium_intracellulare_MOTT-64.1138383,Thermobifida_fusca_YX.269800,Rothia_mucilaginoso_DY- 18.680646,Bifidobacterium_asteroides_PRL2011.1147128,Arthrobacter_sulfonivorans.121292,Kribbella_flavida_DSM_17836.479435,Intrasporangium_calvum_DSM_43043.710696,Bifidobacterium_pseudolongum_PV8- 2.1447715,Bifidobacterium_indicum_LMG_11587_DSM_20214.1341694,Rhodoluna_lacicola.529884
2	Rothia_mucilaginoso_DY-18.680646,Geodermatophilus_obscurus_DSM_43160.526225,Streptomyces_vietnamensis.362257,Arthrobacter_sp._YC-RL1.1652545,Pseudonocardia_sp._AL041005-10.445576,Arthrobacter_sp._Hiyo8.1588023,Streptomyces_sp._Mg1.465541,Mycobacterium_kansasii_ATCC_12478.557599,Rhodococcus_sp._B7740.1564114,Gardnerella_vaginalis_ATCC_14019.525284,Bifidobacterium_breve.1685,Myco- bacterium_indicus_pranii_MTCC_9506.1232724,Nocardiopsis_dassonvillei_subsp._dassonvillei_DSM_43111.446468,Th- ermobifida_fusca_YX.269800,Saccharopolyspora_erythraea_NRRL_2338.405948,Rhodococcus_pyridinivorans_SB3094 .1435356,Mycobacterium_tuberculosis.1773,Bifidobacterium_longum_subsp._infantis_ATCC_15697_JCM_1222_DSM_20088.391904,Streptomyces_sp._CFMR_7.1649184,Mycobacterium_vanbaalenii_PYR-1.350058,Corynebacterium_uterequi.1072256,Mycobacterium_haemophilum_DSM_44634.1202450,Mycobacterium_neo- aurum_VKM_Ac-1815D.700508,Streptomyces_sp._769.1262452,Kocuria_flava.446860,Kineococcus_radiotolerans_SRS30216_ATCC_BAA-149.266940,Olsenella_sp._oral_taxon_807.712411,Arthrobacter_sp._LS16.1690248,Streptomyces_leeuwenhoekii.1437453,Corynebacterium_glyciniphilum_AJ_3170.1404245,Kytococcus_sedentarius_DSM_20547.478801,Arthrobacter_aure- scens_TC1.290340
3	Corynebacteriales_bacterium_X1698.1562462,Streptomyces_albulus_ZPM.1434306,Isoptericola_variabilis_225.743718, Bifidobacterium_indicum_LMG_11587_DSM_20214.1341694,Bifidobacterium_adolescentis.1680,Intrasporangium_cal- vum_DSM_43043.710696,Arthrobacter_alpinus.656366,Arthrobacter_sp._IHBB_11108.1618207,Corynebacterium_arge- ntoratense_DSM_44202.1348662,Rathayibacter_toxicus.145458,Streptomyces_sp._SirexAA-E.862751,Mycobacterium_abscessus_subsp._bolletii_50594.1303024,Arthrobacter_arilaitensis.256701,Bifidobacterium_ka- shiwano_hense_JCM_15439_DSM_21854.1150460,Streptomyces_sp._769.1262452,Kribbella_flavida_DSM_17836.479435,Micrococcus_luteus_NCTC_2665.465515,Actinobacteria_bacterium_IMCC26256.1650658,Mycobacterium_afric- anum.33894,Frankia_sp._Ccl3.106370,Corynebacterium_sp._ATCC_6931.1487956,Actinosynnema_mirum_DSM_43827.446462,Actinoplanes_sp._N902-109.649831,Jonesia_denitrificans_DSM_20603.471856,Amycolatopsis_orientalis_HCCB10007.1156913,Corynebacteriu- m_atypicum.191610,Bifidobacterium_thermophilum_RBL67.1254439,Rhodococcus_jostii_RHA1.101510,Rothia_mucilagi- nosa_DY-18.680646,Actinomyces_meyeri.52773,Corynebacterium_camporealeensis.161896,Corynebacterium_variabile_DSM_44702.858619
4	Corynebacterium_humireducens_NBRC_106098_DSM_45392.1223515,Clavibacter_michiganensis_subsp._sepedoni- cus.31964,Mycobacterium_rhodesiae_NBB3.710685,Actinomyces_radici- dentis.111015,Mycobacterium_kansasii_ATCC_13127.593907

- 12478.557599,Pseudonocardia_sp._AL041005-10.445576,Mycobacterium_sp._VKM_Ac-1817D.1273687,Corynebacterium_imitans.156978,Gardnerella_vaginalis_ATCC_14019.525284,Kutzneria_albida_DSM_43870.1449976,Slackia_heliotrinireducens_DSM_20476.471855,Mycobacterium_fortuitum.1766,Conexibacter_woesei_DSM_14684.469383,Mycobacterium_sp._MCS.164756,Luteipulveratus_mongoliensis.571913,Eggerthella_sp._YY7918.502558,Frankia_sp._Ccl3.106370,Bifidobacterium_breve.1685,Corynebacterium_resistens_DSM_45100.662755,Rubrobacter_radiotolerans.42256,Arthrobacter_sp._FB24.290399,Streptomyces_globisporus_C-1027.1172567,Amycolatopsis_mediterranei_S699.713604,Rhodococcus_jostii_RHA1.101510,Corynebacterium_glyciniphilum_AJ_3170.1404245,Streptomyces_griseus_subsp._griseus_NBRC_13350.455632,Gordonia_bronchialis_DSM_43247.526226,Streptomyces_cyaneogriseus_subsp._noncyanogenus.477245,Streptomyces_leeuwenhoekii.1437453,Mycobacterium_indicus_pranii_MTCC_9506.1232724,Mycobacterium_liflandii_128FXT.459424,Arthrobacter_aurescens_TC1.290340
- 5 Corynebacterium_falsenii_DSM_44353.1451189,Bifidobacterium_kashiwanohense_JCM_15439_DSM_21854.1150460,Nakamurella_multipartita_DSM_44233.479431,Bifidobacterium_pseudocatenulatum_DSM_20438_JCM_1200_LMG_10505.547043,Salinispora_arenicola_CNS-205.391037,Microbacterium_sp._CGR1.1696072,Xylanimonas_cellulosilytica_DSM_15894.446471,Mycobacterium_sp._KMS.189918,Kocuria_rhizophila_DC2201.378753,Streptomyces_scabiei_87.22.680198,Arthrobacter_alpinus.656366,Streptomyces_leeuwenhoekii.1437453,Corynebacterium_efficiens_Ys-314.196164,Bifidobacterium_longum_subsp._infantis_ATCC_15697_JCM_1222_DSM_20088.391904,Frankia_alni_ACN14a.326424,Mycobacterium_bovis_BCG.33892,Pseudonocardia_sp._EC080619-01.1096856,Frankia_sp._Ccl3.106370,Actinobacteria_bacterium_IMCC26256.1650658,Gordonia_bronchialis_DSM_43247.526226,Arthrobacter_sp._LS16.1690248,Arthrobacter_sp._IHBB_11108.1618207,Bifidobacterium_actinocoloniiforme_DSM_22766.1437605,Gordonia_polyisoprenivorans_VH2.1112204,Rhodococcus_opacus_PD630.543736,Dermacoccus_nishinomiyaensis.1274,Corynebacterium_pseudotuberculosis.1719,Modestobacter_marinus.477641,Mycobacterium_tuberculosis.1773,Amycolatopsis_orientalis_HCCB10007.1156913,Rathayibacter_toxicus.145458,Arthrobacter_sp._ERG_S1_01.1704044
- 6 Kribbella_flavida_DSM_17836.479435,Corynebacterium_singulare.161899,Microbacterium_sp._XT11.367477,Mycobacterium_tuberculosis.1773,Bifidobacterium_adolescentis.1680,Adlercreutzia_equilifaciens_DSM_19450.1384484,Nocardia_cyriacigeorgica_GUH-2.1127134,Arthrobacter_sp._FB24.290399,Kocuria_flava.446860,Nocardioides_sp._JS614.196162,Mycobacterium_bovis_BCG.33892,Gordonia_sp._KTR9.337191,Rhodococcus_erythropolis_PR4.234621,Thermobifida_fusca_YX.269800,Eggerthella_lenta_DSM_2243.479437,Arthrobacter_phenanthrenivorans_Spe3.930171,Arthrobacter_sp._ATCC_21022.171959,Streptomyces_vietnamensis.362257,Arthrobacter_sp._Rue61a.1118963,Cellulomonas_fimi_ATCC_484.590998,Truerperella_pyogenes_TP8.1435056,Mycobacterium_microti.1806,Kitasatospora_setae_KM-6054.452652,Mycobacterium_kansasii_ATCC_12478.557599,Cryptobacterium_curtum_DSM_15641.469378,Arthrobacter_sp._Hiyo8.1588023,Corynebacterium_utequei.1072256,Mycobacterium_sp._MOTT36Y.1168287,Arthrobacter_arilaiteensis.256701,Bifidobacterium_catenulatum_DSM_16992_JCM_1194_LMG_11043.566552,Arthrobacter_alpinus.656366,Nocardia_farcinica.37329
- 7 Corynebacterium_imitans.156978,Pseudonocardia_sp._HH130629-09.1641402,Corynebacterium_ulcerans_FRC58.1408268,Amycolatopsis_orientalis_HCCB10007.1156913,Streptomyces_collinus_Tu_365.1214242,Slackia_heliotrinireducens_DSM_20476.471855,Eggerthella_lenta_DSM_2243.479437,Streptomyces_sp._CNQ-509.444103,Amycolatopsis_lurida_NRRL_2430.1460371,Streptomyces_sp._CdTB01.1725411,Bifidobacterium_thermophilum_RBL67.1254439,Mycobacterium_indicus_pranii_MTCC_9506.1232724,Mycobacterium_ulcerans_Agy99.362242,Arthrobacter_sulfonivorans.121292,Corynebacteriales_bacterium_X1698.1562462,Arthrobacter_sp._FB24.290399,Streptomyces_sp._Mg1.465541,Rhodococcus_erythropolis_PR4.234621,Frankia_sp._EAN1pec.298653,Corynebacterium_mariis_DSM_45190.1224163,Corynebacterium_mustelae.571915,Corynebacterium_aurimucosum_ATCC_700975.548476,Mycobacterium_microti.1806,Tropheryma_whipplei_str._Twist.203267,Streptomyces_leeuwenhoekii.1437453,Thermobifida_fusca_YX.269800,Intrasporangium_calvum_DSM_43043.710696,Salinispora_tropica_CNB-440.369723,Mycobacterium_fortuitum.1766,Amycolatopsis_mediterranei_S699.713604,Arthrobacter_sp._Rue61a.1118963,Bifidobacterium_scardovii_JCM_12489_DSM_13734.1150461
- 8 Mycobacterium_gilvum_PYR-GCK.350054,Bifidobacterium_indicum_LMG_11587_DSM_20214.1341694,Amycolaticoccus_subflavus_DQS3-9A1.443218,Arthrobacter_sp._Hiyo8.1588023,Arthrobacter_phenanthrenivorans_Spe3.930171,Nocardia_opsis_dassonvillei_subsp._dassonvillei_DSM_43111.446468,Actinomyces_sp._oral_taxon_414.712122,Sanguibacter_keddiei_DSM_10542.446469,Cellulomonas_gilvus_ATCC_13127.593907,Pseudonocardia_sp._AL041005-10.445576,Streptomyces_griseus_subsp._griseus_NBRC_13350.455632,Corynebacterium_imitans.156978,Corynebacterium_deserti_GIMN1.010.931089,Kocuria_rhizophila_DC2201.378753,Corynebacterium_ureicelivorans.401472,Arthrobacter_sp._YC-RL1.1652545,Arthrobacter_sp._LS16.1690248,Corynebacterium_variabile_DSM_44702.858619,Mycobacterium_abscessus_subsp._bolletii_50594.1303024,Mycobacterium_intracellulare_MOTT-64.1138383,Streptomyces_leeuwenhoekii.1437453,Bifidobacterium_bifidum.1681,Corynebacterium_aurimucosum_ATCC_700975.548476,Microbacterium_sp._XT11.367477,Luteipulveratus_mongoliensis.571913,Frankia_sp._Eul1c.298654,

Actinosynnema_mirum_DSM_43827.446462,Propionibacterium_propionicum_F0230a.767029,Saccharothrix_espanaensis_DSM_44229.1179773,Geodermatophilus_obscurus_DSM_43160.526225,Corynebacterium_vitaeruminis_DSM_20294.1224164,Cellulomonas_fimi_ATCC_484.590998

- 9 Leifsonia_xyli_subsp._cynodontis_DSM_46306.1389489,Cellulomonas_flavigena_DSM_20109.446466,Arthrobacter_sp._Hiyo8.1588023,Microlunatus_phosphovorus_NM-1.1032480,Streptomyces_reticuli.1926,Propionibacterium_avidum_44067.1170318,Kocuria_rhizophila_DC2201.378753,Amycolaticoccus_subflavus_DQS3-9A1.443218,Kibdelosporangium_phytohabitans.860235,Actinoplanes_friuliensis_DSM_7358.1246995,Atopobium_parvulum_DSM_20469.521095,Salinispora_tropica_CNB-440.369723,Kitasatospora_setae_KM-6054.452652,Corynebacterium_glyciniphilum_AJ_3170.1404245,Microbacterium_sp._CGR1.1696072,Amycolatopsis_mediterranei_S699.713604,Rubrobacter_radiotolerans.42256,Corynebacterium_kutscheri.35755,Dermaecoccus_nishinomiyaensis.1274,Streptomyces_griseus_subsp._griseus_NBRC_13350.455632,Mycobacterium_yongonense_05-1390.1138871,Bifidobacterium_longum_subsp._infantis_ATCC_15697___JCM_1222___DSM_20088.391904,Pseudonocardia_sp._EC080619-01.1096856,Streptomyces_collinus_Tu_365.1214242,Corynebacterium_halotolerans_YIM_70093___DSM_44683.1121362,Olsenella_uli_DSM_7084.633147,Corynebacterium_imitans.156978,Corynebacterium_kroppenstedtii_DSM_44385.645127,Frankia_alni_ACN14a.326424,Streptomyces_pristinaespiralis.38300,Nocardiopsis_alba_ATCC_BAA-2165.1205910,Actinomyces_radiciensis.111015
- 10 Propionibacterium_freudenreichii_subsp._shermanii_CIRM-BIA1.754252,Coriobacterium_glomerans_PW2.700015,Mycobacterium_yongonense_05-1390.1138871,Arthrobacter_sp._ATCC_21022.1771959,Corynebacteriales_bacterium_X1036.1528099,Corynebacterium_camporealensis.161896,Brevibacterium_flavum.92706,Ilumatobacter_coccineus_YM16-304.1313172,Mycobacterium_sp._JLS.164757,Bifidobacterium_coryneforme.1687,Catenulispora_acidiphila_DSM_44928.479433,Pseudonocardia_sp._EC080625-04.1096868,Streptomyces_vietnamensis.362257,Brachybacterium_faecium_DSM_4810.446465,Nocardiopsis_alba_ATCC_BAA-2165.1205910,Corynebacteriales_bacterium_X1698.1562462,Dermaecoccus_nishinomiyaensis.1274,Mycobacterium_aviu_104.243243,Mycobacterium_marinum_M.216594,Cellulomonas_gilvus_ATCC_13127.593907,Corynebacterium_statonis.1705,Rhodococcus_sp._B7740.1564114,Corynebacterium_lactis_RW2-5.1408189,Arthrobacter_chlorophenolicus_A6.452863,Mycobacterium_liflandii_128FXT.459424,Actinomyces_radiciensis.111015,Corynebacterium_variabile_DSM_44702.858619,Mycobacterium_indicus_pranii_MTCC_9506.1232724,Bifidobacterium_pseudolongum_PV8-2.1447715,Microbacterium_sp._PAMC_28756.1795053,Conexibacter_woesei_DSM_14684.469383,Corynebacterium_mustelae.571915
- 11 Corynebacterium_casei_LMG_S-19264.1285583,Corynebacterium_ureicelerivorans.401472,Mycobacterium_africanum.33894,Mycobacterium_kansasii_ATCC_12478.557599,Acidothermus_cellulolyticus_11B.351607,Brevibacterium_flavum.92706,Sanguibacter_keddiei_DSM_10542.446469,Corynebacterium_kutscheri.35755,Tsukamurella_paurometabola_DSM_20162.521096,Microbacterium_sp._No_7.1714373,Streptomyces_bingchenggensis_BCW-1.749414,Bifidobacterium_pseudocatenulatum_DSM_20438___JCM_1200___LMG_10505.547043,Amycolatopsis_orientalis_HCCB10007.1156913,Kibdelosporangium_phytohabitans.860235,Mycobacterium_haemophilum_DSM_44634.1202450,Microbacterium_sp._XT11.367477,Gordonia_sp._KTR9.337191,Conexibacter_woesei_DSM_14684.469383,Frankia_sp._Ccl3.106370,Aeromicrobium_erythreum.2041,Renibacterium_salmoninarum_ATCC_33209.288705,Actinosynnema_mirum_DSM_43827.446462,Streptomyces_reticuli.1926,Streptomyces_hygroscopicus_subsp._jinggangensis_5008.1133850,Mycobacterium_tuberculosis.1773,Bifidobacterium_dentium_JCM_1195___DSM_20436.1150423,Mycobacterium_sp._EPA45.1545728,Arthrobacter_sulfonivorans.121292,Segniliparus_rotundus_DSM_44985.640132,Corynebacterium_efficiens_YS-314.196164,Corynebacterium_argentoratense_DSM_44202.1348662,Stackebrandtia_nassauensis_DSM_44728.446470
- 12 Mycobacterium_indicus_pranii_MTCC_9506.1232724,Mycobacterium_africanum.33894,Corynebacterium_atypicum.191610,Streptomyces_cattlea_NRRL_8057___DSM_46488.1003195,Streptomyces_sp._CNQ-509.444103,Salinispora_arenicola_CNS-205.391037,Gordonia_bronchialis_DSM_43247.526226,Micrococcus_luteus_NCTC_2665.465515,Bifidobacterium_coryneforme.1687,Gordonia_polyisoprenivorans_VH2.1112204,Nocardia_farcinica.37329,Gordonia_sp._QH-11.1136941,Corynebacterium_glutamicum_R.340322,Streptomyces_venezuelae.54571,Amycolatopsis_lurida_NRRL_2430.1460371,Corynebacterium_stationis.1705,Rothia_mucilaginosa_DY-18.680646,Arthrobacter_sp._PAMC25486.1494608,Bifidobacterium_longum_subsp._infantis_ATCC_15697___JCM_1222___DSM_20088.391904,Pseudonocardia_sp._EC080625-04.1096868,Mycobacterium_liflandii_128FXT.459424,Mycobacterium_testaceum_StLB037.979556,Gardnerella_vaginalis_ATCC_14019.525284,Mycobacterium_sp._VKM_Ac-1817D.1273687,Streptomyces_reticuli.1926,Rhodococcus_sp._B7740.1564114,Renibacterium_salmoninarum_ATCC_3

3209.288705,Arthrobacter_sp._Hiyo8.1588023,Corynebacterium_kutscheri.35755,Scardovia_inopinata_JCM_12537.1150468,Corynebacterium_vitaeruminis_DSM_20294.1224164,Slackia_heliotrinireducens_DSM_20476.471855

- 13 Microbacterium_testaceum_StLB037.979556,Kocuria_rhizophila_DC2201.378753,Streptomyces_pratensis_ATCC_3333.1.591167,Pseudonocardia_dioxanivorans_CB1190.675635,Olsenella_uli_DSM_7084.633147,Streptomyces_vietnamensis.362257,Kibdelosporangium_phytohabitans.860235,Jonesia_denitrificans_DSM_20603.471856,Corynebacterium_epidermidicantis.1050174,Corynebacterium_aurimucosum_ATCC_700975.548476,Streptomyces_albulus_ZPM.1434306,Kocuria_flava.446860,Leifsonia_xyli_subsp._cynodontis_DSM_46306.1389489,Corynebacterium_uteriquei.1072256,Arthrobacter_sp._FB24.290399,Sanguibacter_keddiei_DSM_10542.446469,Mycobacterium_tuberculosis.1773,Segniliparus_rotundus_DSM_44985.640132,Streptomyces_violaceusniger_Tu_4113.653045,Bifidobacterium_asteroides_PRL2011.1147128,Streptomyces_cattleya_NRRL_8057_DSM_46488.1003195,Arthrobacter_sp._A3.595593,Streptomyces_sp._CNQ-509.444103,Olsenella_sp._oral_taxon_807.712411,Illumatobacter_coccineus_YM16-304.1313172,Stackebrandtia_nassauensis_DSM_44728.446470,Mycobacterium_chubuense_NBB4.710421,Streptomyces_glaucescens.1907,Isoptricicola_variabilis_225.743718,Mycobacterium_intracellulare_MOTT-64.1138383,Corynebacterium_atypicum.191610,Geodermatophilus_obscurus_DSM_43160.526225
- 14 Corynebacterium_marinum_DSM_44953.1224162,Mycobacterium_ulcerans_Agy99.362242,Corynebacterium_atypicum.191610,Arthrobacter_sp._Hiyo8.1588023,Streptomyces_sp._PAMC26508.1265601,Streptomyces_hygroscopicus_subsp._jinggangensis_5008.1133850,Nocardioides_sp._JS614.196162,Amycolatopsis_mediterranei_S699.713604,Sanguibacter_keddiei_DSM_10542.446469,Rhodoluna_lacicola.529884,Bifidobacterium_actinocoloniiforme_DSM_22766.1437605,Saccharopolyspora_erythraea_NRRL_2338.405948,Mycobacterium_abscessus_subsp._bolletii_50594.1303024,Mycobacterium_leprae_Br4923.561304,Mycobacterium_testaceum_StLB037.979556,Bifidobacterium_pseudocatenulatum_DSM_20438_JCM_1200_LMG_10505.547043,Leifsonia_xyli_subsp._cynodontis_DSM_46306.1389489,Brachybacterium_faecium_DSM_4810.446465,Thermobifida_fusca_YX.269800,Bifidobacterium_scardovii_JCM_12489_DSM_13734.1150461,Bifidobacterium_thermophilum_RBL67.1254439,Actinomyces_meyeri.52773,Propionibacterium_acnes_C1.1234380,Corynebacterium_argentoratense_DSM_44202.1348662,Beutenbergia_cavernae_DSM_12333.471853,Rhodococcus_sp._B7740.1564114,Arsenicicoccus_sp._oral_taxon_190.1658671,Salinispora_arenicola_CNS-205.391037,Modestobacter_marinus.477641,Frankia_sp._EAN1pec.298653,Arthrobacter_alpinus.656366,Bifidobacterium_dentium_JCM_1195_DSM_20436.1150423
- 15 Nakamurella_multipartita_DSM_44233.479431,Corynebacterium_marinum_DSM_44953.1224162,Rubrobacter_radiotolerans.42256,Streptomyces_sp._4F.1751294,Arthrobacter_sp._A3.595593,Cryptobacterium_curtum_DSM_15641.469378,Actinoplanes_sp._SE50_110.134676,Pseudonocardia_sp._HH130629-09.1641402,Mycobacterium_sp._JLS.164757,Mycobacterium_haemophilum_DSM_44634.1202450,Arthrobacter_arilaiteensis.256701,Kineococcus_radiotolerans_SRS30216_ATCC_BAA-149.266940,Corynebacterium_terpenetabidum_Y-11.1200352,Streptomyces_violaceusniger_Tu_4113.653045,Mycobacterium_gilvum_PYR-GCK.350054,Mycobacterium_goodii.134601,Bifidobacterium_scardovii_JCM_12489_DSM_13734.1150461,Streptomyces_orangium_roseum_DSM_43021.479432,Streptomyces_cattleya_NRRL_8057_DSM_46488.1003195,Cellulomonas_fla-vigena_DSM_20109.446466,Rhodococcus_pyridinivorans_SB3094.1435356,Arthrobacter_aurescens_TC1.290340,Tsukamurella_paurometabola_DSM_20162.521096,Coriobacterium_glomerans_PW2.700015,Streptomyces_ambotaciensis_ATCC_23877.278992,Mycobacterium_kansasii_ATCC_12478.557599,Streptomyces_sp._PAMC26508.1265601,Saccharothrix_espansensis_DSM_44229.1179773,Arthrobacter_sp._FB24.290399,Corynebacterium_pseudotuberculosis.1719,Jonesia_denitrificans_DSM_20603.471856,Arthrobacter_sp._ERGS1_01.1704044
- 16 Mycobacterium_marinum_M.216594,Mycobacterium_avium_104.243243,Mycobacterium_intracellulare_MOTT-64.1138383,Arthrobacter_aurescens_TC1.290340,Microlunatus_phosphovorus_NM-1.1032480,Mycobacterium_bovis_BCG.33892,Actinotignum_schaalii.59505,Amycolatopsis_methanolica_239.1068978,Rubrobacter_radiotolerans.42256,Mycobacterium_chubuense_NBB4.710421,Mycobacterium_sp._VKM_Ac-1817D.1273687,Microterricola_viridarii.412690,Rhodococcus_pyridinivorans_SB3094.1435356,Nocardia_nova_SH22a.1415166,Scardovia_inopinata_JCM_12537.1150468,Streptomyces_venezuelae.54571,Verrucosipora_maris_AB-18-032.263358,Cellulomonas_fimi_ATCC_484.590998,Corynebacterium_glyciniphilum_AJ_3170.1404245,Modestobacter_marinus.477641,Beutenbergia_cavernae_DSM_12333.471853,Corynebacterium_halotolerans_YIM_70093_DSM_44683.1121362,Nocardioides_sp._JS614.196162,Corynebacterium_ureicelerivorans.401472,Streptomyces_sp._4F.1751294,Pseudonocardia_sp._AL041005-10.445576,Streptomyces_glaucescens.1907,Micromonospora_sp._L5.648999,Actinobacteria_bacterium_IMCC26256.1650658,Intrasporangium_calvum_DSM_43043.710696,Pseudonocardia_sp._HH130629-09.1641402,Streptomyces_sp._Mg1.465541
- 17 Mycobacterium_rhodesiae_NBB3.710685,Bifidobacterium_kashiwanohense_JCM_15439_DSM_21854.1150460,Frankia_sp._Eu1c.298654,Mycobacterium_marinum_M.216594,Pseudonocardia_sp._AL041005-10.445576,Mycobacterium_sp._MCS.164756,Mycobacterium_avium_104.243243,Streptomyces_sp._Mg1.465541,Propionibacterium_freudenreichii_subsp._shermanii_CIRM-BIA1.754252,Corynebacterium_maris_DSM_45190.1224163,Arcanobacterium_haemolyticum_DSM_20595.644284,Thermobispora_bispora_DSM_43833.469371,Arthrobacter_arilaiteensis.256701,Nakamurella_multipartita_DSM_44233.479431,Mycobacterium_chubuense_NBB4.710421,Rhodoluna_lacicola.529884,Arthrobacter_sp._YC-RL1.1652545,Micromonospora_aurantiaca_ATCC_27029.644283,Corynebacterium_glyciniphilum_AJ_3170.1404245,Ki

neococcus_radiotolerans_SRS30216____ATCC_BAA-
 149.266940,Rubrobacter_xylanophilus_DSM_9941.266117,Atopobium_parvulum_DSM_20469.521095,Corynebacterium_atypicum.191610,Pseudonocardia_dioxanivorans_CB1190.675635,Gardnerella_vaginalis_ATCC_14019.525284,Mycobacterium_gilvum_PYR-
 GCK.350054,Adlercreutzia_equolifaciens_DSM_19450.1384484,Kutzneria_albida_DSM_43870.1449976,Micromonospora_sp._L5.648999,Streptomyces_sp._CdTB01.1725411,Mycobacterium_abscessus_subsp._bolletii_50594.1303024,Mycobacterium_sp._JS623.212767

- 18 Mycobacterium_gilvum_PYR-
 GCK.350054,Saccharothrix_espanaensis_DSM_44229.1179773,Nocardioides_sp._JS614.196162,Luteipulveratus_mon
 goliensis.571913,Propionibacterium_freudenreichii_subsp._shermanii_CIRM-
 BIA1.754252,Corynebacterium_lactis_RW2-5.1408189,Frankia_alni_ACN14a.326424,Verrucosispora_maris_AB-18-
 032.263358,Saccharomonospora_viridis_DSM_43017.471857,Corynebacterium_stationis.1705,Corynebacterium_testudi
 noris.136857,Micromonospora_aurantiaca_ATCC_27029.644283,Blastococcus_saxobsidens_DD2.1146883,Streptomyces_lydicus_A02.1403539,Kocuria_palustris.71999,Bifidobacterium_breve.1685,Arthrobacter_sp._LS16.1690248,Mycobacterium_leprae_Br4923.561304,Nocardia_cyriacigeorgica_GUH-2.1127134,Mycobacterium_yongonense_05-
 1390.1138871,Corynebacterium_mustelae.571915,Arthrobacter_alpinus.656366,Corynebacterium_kutscheri.35755,Micr
 obacterium_testaceum_StLB037.979556,Bifidobacterium_kashiwanohense_JCM_15439____DSM_21854.1150460,Xylani
 monas_cellulosilytica_DSM_15894.446471,Microterricola_viridarii.412690,Pimelobacter_simplex.2045,Kineococcus_radi
 otolerans_SRS30216____ATCC_BAA-
 149.266940,Mycobacterium_indicus_pranii_MTCC_9506.1232724,Arthrobacter_arilaitensis.256701,Amycolatopsis_meth
 anolica_239.1068978
- 19 Rhodoluna_lacicola.529884,Scardovia_inopinata_JCM_12537.1150468,Isopterocola_variabilis_225.743718,Sanguibacter_keddiei_DSM_10542.446469,Nocardia_nova_SH22a.1415166,Kutzneria_albida_DSM_43870.1449976,Nakamurella_multipartita_DSM_44233.479431,Corynebacterium_camporealensis.161896,Streptomyces_ambofaciens_ATCC_23877.278992,Rothia_mucilaginoso_DY-
 18.680646,Clavibacter_michiganensis_subsp._sepedonicus.31964,Microbacterium_sp._CGR1.1696072,Aeromicrobium_erythreum.2041,Corynebacteriales_bacterium_X1698.1562462,Actinoplanes_friuliensis_DSM_7358.1246995,Mycobacterium_sp._JS623.212767,Corynebacterium_glutamicum_R.340322,Jonesia_denitrificans_DSM_20603.471856,Rubrobacter_xylanophilus_DSM_9941.266117,Streptomyces_scabiei_87.22.680198,Streptosporangium_roseum_DSM_43021.479432,Atopobium_parvulum_DSM_20469.521095,Rhodococcus_pyridinivorans_SB3094.1435356,Corynebacterium_humireducens_NBRC_106098____DSM_45392.1223515,Streptomyces_collinus_Tu_365.1214242,Renibacterium_salmoninarum_ATCC_33209.288705,Salinispora_arenicola_CNS-
 205.391037,Nocardia_brasiliensis_ATCC_700358.1133849,Olsenella_sp._oral_taxon_807.712411,Corynebacterium_de
 serti_GIMN1.010.931089,Mycobacterium_kansasii_ATCC_12478.557599,Frankia_sp._EAN1pec.298653

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19 **Table S26** List of 86 Actinobacteria (ACT) species kept for 20 permutations under MID86 random sampling scenarios (RSS).

RSS species kept

- 0 Streptomyces_sp._CdTB01.1725411, Microbacterium_testaceum_StLB037.979556, Coriobacteriaceae_bacterium_68-1-3.1531429, Streptomyces_avermitilis_MA-4680__NBRC_14893.227882, Arcanobacterium_haemolyticum_DSM_20595.644284, Tropheryma_whipplei_str._Twist.203267, Bifidobacterium_longum_subsp._infantis_ATCC_15697__JCM_1222__DSM_20088.391904, Mycobacterium_marinum_M.216594, Mycobacterium_microti.1806, Microterricola_viridarii.412690, Actinosynnema_mirum_DSM_43827.446462, Bifidobacterium_scardovii_JCM_12489__DSM_13734.1150461, Mycobacterium_yongonense_05-1390.1138871, Acidimicrobium_ferroxidans_DSM_10331.525909, Streptomyces_cattleia_NRRL_8057__DSM_46488.1003195, Pseudonocardia_sp._AL041005-10.445576, Propionibacterium_freudenreichii_subsp._shermanii_CIRM-BIA1.754252, Thermobifida_fusca_YX.269800, Corynebacterium_urealyticum_DSM_7109.504474, Nakamurella_multipartita_DSM_44233.479431, Bifidobacterium_angulatum_DSM_20098__JCM_7096.518635, Amycolatopsis_methanolica_239.1068978, Corynebacterium_singulare.161899, Actinoplanes_sp._N902-109.649831, Streptomyces_globisporus_C-1027.1172567, Kocuria_palustris.71999, Pseudonocardia_dioxanivorans_CB1190.675635, Mycobacterium_indicus_pranii_MTCC_9506.1232724, Rhodococcus_opacus_PD630.543736, Amycolatopsis_japonica.208439, Corynebacterium_maris_DSM_45190.1224163, Mycobacterium_aviium_104.243243, Corynebacterium_kutscheri.35755, Kocuria_rhizophila_DC2201.378753, Mycobacterium_tuberculosis.1773, Kibdelosporangium_phytohabitans.860235, Streptomyces_sp._PAMC26508.1265601, Propionibacterium_propionicum_F0230a.767029, Mycobacterium_sinense.875328, Gordonia_sp._QH-11.1136941, Arthrobacter_sp._ATCC_21022.1771959, Microbacterium_sp._PAMC_28756.1795053, Arthrobacter_chlorophenolicus_A6.452863, Beutenbergia_cavernae_DSM_12333.471853, Xylanimonas_cellulosilytica_DSM_15894.446471, Streptomyces_violaceusniger_Tu_4113.653045, Acidothermus_cellulolyticus_11B.351607, Actinoplanes_sp._SE50_110.134676, Streptomyces_hygroscopicus_subsp._jinggangensis_5008.1133850, Actinoplanes_friuliensis_DSM_7358.1246995, Devriesea_agamarum.472569, Mycobacterium_africanum.33894, Bifidobacterium_catenulatum_DSM_16992__JCM_1194__LMG_11043.566552, Propionibacterium_acidipropionici_ATCC_4875.1171373, Microlunatus_phosphovorus_NM-1.1032480, Microbacterium_sp._CGR1.1696072, Nocardiopsis_dassonvillei_subsp._dassonvillei_DSM_43111.446468, Streptomyces_pratensis_ATCC_33331.591167, Streptomyces_pristinaespiralis.38300, Rhodoluna_lacicola.529884, Mobiluncus_curtisii_ATCC_43063.548479, Micrococcus_luteus_NCTC_2665.465515, Nocardioides_sp._JS614.196162, Arthrobacter_sulfonivorans.121292, Corynebacterium_pseudotuberculosis.1719, Actinoplanes_missouriensis_431.512565, Corynebacterium_kropfenstedtii_DSM_44385.645127, Rubrobacter_xylanophilus_DSM_9941.266117, Nocardiopsis_alba_ATCC_BAA-2165.1205910, Gordonia_sp._KTR9.337191, Luteipulveratus_mongoliensis.571913, Corynebacterium_testudinoris.136857, Mycobacterium_sp._MOTT36Y.1168287, Gordonia_polyisoprenivorans_VH2.1112204, Arthrobacter_phenanthrenivorans_Sph_e3.930171, Atopobium_parvulum_DSM_20469.521095, Mycobacterium_ulcerans_Agy99.362242, Streptomyces_sp._Mg1.465541, Thermomonospora_curvata_DSM_43183.471852, Corynebacterium_resistens_DSM_45100.662755, Arthrobacter_sp._FB24.290399, Arthrobacter_sp._Hiyo8.1588023, Mycobacterium_sp._MCS.164756, Bifidobacterium_animalis_subsp._lactis_CNCM_J-2494.1042403, Streptomyces_fulvissimus_DSM_40593.1303692, Bifidobacterium_asteroides_PRL2011.1147128
- 1 Streptomyces_albulus_ZPM.1434306, Corynebacterium_stationis.1705, Arthrobacter_sp._Hiyo8.1588023, Atopobium_parvulum_DSM_20469.521095, Mycobacterium_aviium_104.243243, Corynebacterium_camporealensis.161896, Pimelobacter_simplix.2045, Eggerthella_lenta_DSM_2243.479437, Bifidobacterium_actinocoloniiforme_DSM_22766.1437605, Amycolatopsis_japonica.208439, Mycobacterium_sp._JS623.212767, Arthrobacter_arilaitensis.256701, Mycobacterium_sinense.875328, Bifidobacterium_kashiwanohense_JCM_15439__DSM_21854.1150460, Corynebacterium_variabile_DSM_44702.858619, Corynebacterium_testudinoris.136857, Pseudonocardia_sp._EC080610-09.1688404, Thermobispora_bispora_DSM_43833.469371, Gordonia_bronchialis_DSM_43247.526226, Mobiluncus_curtisii_ATCC_43063.548479, Mycobacterium_sp._KMS.189918, Coriobacteriaceae_bacterium_68-1-3.1531429, Bifidobacterium_catenulatum_DSM_16992__JCM_1194__LMG_11043.566552, Actinoplanes_sp._N902-109.649831, Arthrobacter_alpinus.656366, Streptomyces_avermitilis_MA-4680__NBRC_14893.227882, Dermacoccus_nishinomiyaensis.1274, Corynebacterium_glutamicum_R.340322, Propionibacterium_acidipropionici_ATCC_4875.1171373, Corynebacterium_ureicelerivorans.401472, Isosporicola_variabilis_225.743718, Streptomyces_bingchenggensis_BCW-1.749414, Mycobacterium_neoaurum_VKM_Ac-1815D.700508, Streptomyces_pratensis_ATCC_33331.591167, Cellulomonas_gilvus_ATCC_13127.593907, Rubrobacter_xylanophilus_DSM_9941.266117, Tropheryma_whipplei_str._Twist.203267, Bifidobacterium_asteroides_PRL2011.1147128, Mycobacterium_microti.1806, Micromonospora_aurantiaca_ATCC_27029.644283, Tsukamurella_paurometabola_DSM_20162.521096, Propionibacterium_avidum_44067.1170318, Streptomyces_venezuelae.54571, Corynebacterium_glyciniphilum_AJ_3170.1404245, Microlunatus_phosphovorus_NM-1.1032480, Mycobacterium_bovis_BCG.33892, Pseudonocardia_sp._HH130629-09.1641402, Arthrobacter_sp._A3.595593, Cellulomonas_flavigena_DSM_20109.446466, Streptomyces_cattleia_NRRL_8057__DSM_46488.1003195, Propionibacterium_propionicum_F0230a.767029, Arthrobacter_aurescens_TC1.290340, Corynebacterium_imitans.156978, Streptomyces_leeuwenhoekii.1437453, Streptomyces_cyaneogriseus_subsp._noncyanogenus.477245, Cryptobacterium_curtum_DSM_15641.469378, Mycobacterium_sp._MOTT36Y.1168287, Actinomyces_sp._oral_taxon_414.712122, Corynebacterium_utequei.1072256, Streptomyces_glaucescens.1907, Frankia_sp._EAN1pec.298653, Frankia_symbiont_of_Datisca_glomerata.656024, Streptomyces_sp._CNQ-509.444103, Microbacterium_sp._CGR1.1696072, Arthrobacter_sp._ERGS1_01.1704044, Corynebacterium_argentoratense_DSM_44202.1348662, Micromonospora_sp._L5.648999, Streptomyces_scabiei_87.22.680198, Mycobacterium_rhodesiae_N

BB3.710685, *Corynebacterium*_sp._ATCC_6931.1487956, *Bifidobacterium_pseudolongum_PV8-*
 2.1447715, *Nocardiopsis_dassonvillei_subsp._dassonvillei_DSM_43111.446468*, *Mycobacterium_africanum.33894*, *Kutzneria*
_albida_DSM_43870.1449976, *Streptomyces_griseus_subsp._griseus_NBRC_13350.455632*, *Olsenella_uli_DSM_7084.633*
 147, *Saccharothrix_espanaensis_DSM_44229.1179773*, *Mycobacterium_gilvum_PYR-*
 GCK.350054, *Mycobacterium_leprae_Br4923.561304*, *Corynebacterium_deserti_GIMN1.010.931089*, *Intrasporangium_calvu*
m_DSM_43043.710696, *Scardovia_inopinata_JCM_12537.1150468*, *Corynebacterium_halotolerans_YIM_70093_DSM_44*
 683.1121362, *Beutenbergia_cavernae_DSM_12333.471853*, *Streptomyces_collinus_Tu_365.1214242*, *Streptomyces_ambofa*
ciens_ATCC_23877.278992

- 2 *Rhodoluna_lacicola.529884*, *Microbacterium_sp._XT11.367477*, *Olsenella_sp._oral_taxon_807.712411*, *Trueperella_pyogene*
s_TP8.1435056, *Mycobacterium_neoaurum_VKM_Ac-1815D.700508*, *Microlunatus_phosphovorans_NM-*
1.1032480, *Cellulomonas_gilvus_ATCC_13127.593907*, *Arthrobacter_sulfonivorans.121292*, *Bifidobacterium_angulatum_DS*
M_20098_JCM_7096.518635, *Streptomyces_leeuwenhoekii.1437453*, *Amycolatopsis_japonica.208439*, *Arthrobacter_sp._*
A3.595593, *Olsenella_uli_DSM_7084.633147*, *Streptomyces_venezuelae.54571*, *Streptomyces_pratensis_ATCC_33331.591*
167, *Mycobacterium_sinense.875328*, *Corynebacterium_callunae_DSM_20147.1121353*, *Bifidobacterium_breve.1685*, *Arthrob*
acter_sp._ERGS1_01.1704044, *Streptomyces_sp._CdTB01.1725411*, *Streptomyces_avermitilis_MA-*
4680_NBRC_14893.227882, *Bifidobacterium_bifidum.1681*, *Xylanimonas_cellulosilytica_DSM_15894.446471*, *Arsenicicocc*
us_sp._oral_taxon_190.1658671, *Mycobacterium_sp._JS623.212767*, *Mycobacterium_leprae_Br4923.561304*, *Geodermatop*
hilus_obscurus_DSM_43160.526225, *Mycobacterium_sp._KMS.189918*, *Scardovia_inopinata_JCM_12537.1150468*, *Actinopl*
anes_friuliensis_DSM_7358.1246995, *Corynebacterium_kroppenstedtii_DSM_44385.645127*, *Streptomyces_violaceusniger_Tu_4113.653045*, *Streptomyces_lydicus_A02.1403539*, *Corynebacterium_imitans.156978*, *Pseudonocardia_sp._AL041005-*
10.445576, *Streptomyces_sp._CNQ-*
509.444103, *Dermacoccus_nishinomiyaensis.1274*, *Corynebacterium_glyciniphilum_AJ_3170.1404245*, *Streptomyces_fulvis*
mus_DSM_40593.1303692, *Propionibacterium_acnes_C1.1234380*, *Microbacterium_testaceum_StLB037.979556*, *Arthrobact*
er_sp._PAMC25486.1494608, *Coriobacteriaceae_bacterium_68-1-*
3.1531429, *Corynebacterium_variabile_DSM_44702.858619*, *Mycobacterium_sp._VKM_Ac-*
1817D.1273687, *Arthrobacter_chlorophenolicus_A6.452863*, *Nakamurella_multipartita_DSM_44233.479431*, *Corynebacteriu*
m_sp._ATCC_6931.1487956, *Arthrobacter_sp._LS16.1690248*, *Gardnerella_vaginalis_ATCC_14019.525284*, *Corynebacteriu*
m_ulcerans_FRC58.1408268, *Micromonospora_sp._L5.648999*, *Corynebacterium_singulare.161899*, *Pseudonocardia_dioxan*
ivorans_CB1190.675635, *Kineococcus_radiotolerans_SRS30216_ATCC_BAA-*
149.266940, *Mycobacterium_goodii.134601*, *Rhodococcus_jostii_RHA1.101510*, *Actinomyces_oris.544580*, *Streptomyces_reti*
culi.1926, *Saccharothrix_espanaensis_DSM_44229.1179773*, *Jonesia_denitrificans_DSM_20603.471856*, *Kutzneria_albida_DSM_43870.1449976*, *Corynebacterium_efficiens_YS-*
314.196164, *Nocardioides_sp._JS614.196162*, *Streptomyces_collinus_Tu_365.1214242*, *Corynebacterium_mustelae.571915*,
Isoptricola_variabilis_225.743718, *Kocuria_palustris.71999*, *Stackebrandtia_nassauensis_DSM_44728.446470*, *Kocuria_rhiz*
ophila_DC2201.378753, *Segniliparus_rotundus_DSM_44985.640132*, *Nocardia_brasiliensis_ATCC_700358.1133849*, *Nocard*
ia_farcinica.37329, *Mycobacterium_gilvum_PYR-*
 GCK.350054, *Blastococcus_saxosidens_DD2.1146883*, *Corynebacterium_vitaeruminis_DSM_20294.1224164*, *Corynebacter*
iales_bacterium_X1698.1562462, *Microbacterium_sp._CGR1.1696072*, *Corynebacterium_atypicum.191610*, *Bifidobacterium_catenu*
latulum_DSM_16992_JCM_1194_LMG_11043.566552, *Corynebacteriales_bacterium_X1036.1528099*, *Arthrobact*
er_sp._Hiyo8.1588023, *Propionibacterium_avidum_44067.1170318*, *Corynebacterium_doosanense_CAU_212_DSM_4543*
6.558173, *Rhodococcus_opacus_PD630.543736*, *Clavibacter_michiganensis_subsp._sepedonicus.31964*
- 3 *Leifsonia_xyli_subsp._cynodontis_DSM_46306.1389489*, *Microbacterium_sp._PAMC_28756.1795053*, *Mycobacterium_indic*
us_pranii_MTCC_9506.1232724, *Corynebacterium_lactis_RW2-*
5.1408189, *Gordonia_bronchialis_DSM_43247.526226*, *Nakamurella_multipartita_DSM_44233.479431*, *Arthrobacter_penan*
threnivorans_Sphe3.930171, *Pseudonocardia_sp._EC080610-*
09.1688404, *Corynebacteriales_bacterium_X1036.1528099*, *Thermobifida_fusca_YX.269800*, *Streptomyces_xiamenensis.40*
8015, *Arthrobacter_chlorophenolicus_A6.452863*, *Mycobacterium_leprae_Br4923.561304*, *Mycobacterium_goodii.134601*, *Str*
eptomycies_albulus_ZPM.1434306, *Actinoplanes_missouriensis_431.512565*, *Pseudonocardia_sp._AL041005-*
10.445576, *Luteipulveratus_mongoliensis.571913*, *Pimelobacter_simplex.2045*, *Xylanimonas_cellulosilytica_DSM_15894.446*
471, *Corynebacterium_humireducens_NBRC_106098_DSM_45392.1223515*, *Bifidobacterium_bifidum.1681*, *Micromonosp*
ora_aurantiaca_ATCC_27029.644283, *Mycobacterium_vanbaalenii_PYR-*
1.350058, *Frankia_symbiont_of_Datisca_glomerata.656024*, *Blastococcus_saxosidens_DD2.1146883*, *Streptomyces_hygro*
scopicus_subsp._jinggagensis_5008.1133850, *Mycobacterium_liflandii_128FXT.459424*, *Streptomyces_reticuli.1926*, *Actino*
myces_oris.544580, *Slackia_heliotrinireducens_DSM_20476.471855*, *Mycobacterium_fortuitum.1766*, *Streptomyces_violaceu*
sniger_Tu_4113.653045, *Frankia_sp._EAN1pec.298653*, *Saccharothrix_espanaensis_DSM_44229.1179773*, *Actinomyces_sp*
_oral_taxon_414.712122, *Actinomyces_radicidentis.111015*, *Corynebacterium_argentoratense_DSM_44202.1348662*, *Bifido*
bacterium_scardovii_JCM_12489_DSM_13734.1150461, *Arthrobacter_sp._YC-*
RL1.1652545, *Streptomyces_sp._769.1262452*, *Mycobacterium_intracellulare_MOTT-*
64.1138383, *Corynebacterium_halotolerans_YIM_70093_DSM_44683.1121362*, *Rhodoluna_lacicola.529884*, *Corynebacter*
ium_callunae_DSM_20147.1121353, *Mycobacterium_rhodesiae_NBB3.710685*, *Bifidobacterium_thermophilum_RBL67.1254*
439, *Mycobacterium_yongonense_05-*
1390.1138871, *Corynebacterium_resistens_DSM_45100.662755*, *Actinobacteria_bacterium_IMCC26256.1650658*, *Micromon*
ospora_sp._L5.648999, *Nocardia_cyriaci-georgica_GUH-2.1127134*, *Kitasatospora_setae_KM-*

6054.452652, *Mycobacterium_kansasii*_ATCC_12478.557599, *Propionibacterium_propionicum*_F0230a.767029, *Bifidobacterium_catenumulatum*_DSM_16992___JCM_1194___LMG_11043.566552, *Corynebacterium_maris*_DSM_45190.1224163, *Salinispora_arenicola*_CNS-205.391037, *Bifidobacterium_coryneforme*.1687, *Arcanobacterium_haemolyticum*_DSM_20595.644284, *Nocardia_nova*_SH22a.1415166, *Streptomyces_glaucescens*.1907, *Corynebacterium_diphtheriae*_31A.698962, *Gordonia_sp._QH*-11.1136941, *Sanguibacter_keddiei*_DSM_10542.446469, *Ilumatobacter_coccineus*_YM16-304.1313172, *Arthrobacter_aureus*_TC1.290340, *Modestobacter_marinus*.477641, *Renibacterium_salmoninarum*_ATCC_33209.288705, *Arthrobacter_sp._ERGS1_01*.1704044, *Salinispora_tropica*_CNB-440.369723, *Kocuria_rhizophila*_DC2201.378753, *Microbacterium_testaceum*_StLB037.979556, *Microbacterium_sp._No._7*.1714373, *Streptomyces_sp._CdTB01*.1725411, *Isopetricola_variabilis*.225.743718, *Streptomyces_bingchenggensis*_BCW-1.749414, *Kribbella_flavida*_DSM_17836.479435, *Rothia_mucilaginosa*_DY-18.680646, *Streptomyces_pratensis*_ATCC_33331.591167, *Bifidobacterium_asteroides*_PRL2011.1147128, *Thermomonospora_curvata*_DSM_43183.471852, *Bifidobacterium_breve*.1685, *Propionibacterium_freudenreichii_subsp._shermanii*_CIRM-BIA1.754252, *Streptomyces_albus*.1888, *Mycobacterium_haemophilum*_DSM_44634.1202450

4 *Corynebacterium_jeikeium*_K411.306537, *Scardovia_inopinata*_JCM_12537.1150468, *Propionibacterium_acnes*_C1.1234380, *Actinomyces_sp._oral_taxon_414*.712122, *Streptomyces_sp._769*.1262452, *Streptomyces_sp._CFMR_7*.1649184, *Corynebacterium_halotolerans*_YIM_70093___DSM_44683.1121362, *Streptomyces_fulvisimus*_DSM_40593.1303692, *Amycolatopsis_japonica*.208439, *Streptomyces_vietnamensis*.362257, *Microterricola_viridarii*.412690, *Nocardia_cyriacigeorgica*_GUH-2.1127134, *Corynebacteriales_bacterium_X1036*.1528099, *Corynebacterium_humireducens*_NBRC_106098___DSM_45392.1223515, *Corynebacterium_glyciniphilum_AJ_3170*.1404245, *Blastococcus_saxobsidens*_DD2.1146883, *Corynebacterium_uterequi*.1072256, *Nocardiosis_dassonvillei_subsp._dassonvillei*_DSM_43111.446468, *Pseudonocardia_sp._AL041005*-10.445576, *Corynebacterium_marinum*_DSM_44953.1224162, *Arthrobacter_phenanthrenivorans*_Sphe3.930171, *Bifidobacterium_thermophilum_RBL67*.1254439, *Micromonospora_sp._L5*.648999, *Propionibacterium_acidipropionici*_ATCC_4875.1171373, *Mycobacterium_yongonense*_05-1390.1138871, *Slackia_heliotrinireducens*_DSM_20476.471855, *Streptomyces_xiamenensis*.408015, *Bifidobacterium_indicium_LMG_11587___DSM_20214*.1341694, *Frankia_symbiont_of_Datisca_glomerata*.656024, *Actinoplanes_sp._N902*-109.649831, *Mycobacterium_sp._KMS*.189918, *Bifidobacterium_pseudolongum_PV8*-2.1447715, *Streptomyces_glaucescens*.1907, *Mycobacterium_microti*.1806, *Geodermatophilus_obscurus*_DSM_43160.526225, *Microtholunatus_phosphovorus*_NM-1.1032480, *Coriobacteriaceae_bacterium_68*-1-3.1531429, *Bifidobacterium_angulatum*_DSM_20098___JCM_7096.518635, *Brachybacterium_faecium*_DSM_4810.446465, *Mycobacterium_rhodesiae*_NBB3.710685, *Eggerthella_lenta*_DSM_2243.479437, *Corynebacterium_kutscheri*.35755, *Actinoplanes_missouriensis*.431.512565, *Frankia_sp._EAN1pec*.298653, *Actinoplanes_friuliensis*_DSM_7358.1246995, *Saccharomonospora_viridis*_DSM_43017.471857, *Sanguibacter_keddiei*_DSM_10542.446469, *Arthrobacter_aureus*_TC1.290340, *Streptomyces_sp._CdTB01*.1725411, *Gordonia_sp._QH*-11.1136941, *Corynebacterium_kroppenstedtii*_DSM_44385.645127, *Cryptobacterium_curtum*_DSM_15641.469378, *Gordonia_sp._KTR9*.337191, *Corynebacterium_camporealis*.161896, *Arthrobacter_sp._PAMC25486*.1494608, *Actinosynnema_mirum*_DSM_43827.446462, *Bifidobacterium_asteroides*_PRL2011.1147128, *Corynebacterium_dooanense*_CAU_212___DSM_45436.558173, *Actinomyces_meyeri*.52773, *Rathayibacter_toxicus*.145458, *Rhodococcus_opacus_P*D630.543736, *Actinoplanes_sp._SE50*_110.134676, *Arthrobacter_sp._LS16*.1690248, *Verrucosipora_maris_AB*-18-032.263358, *Mycobacterium_sinense*.875328, *Intrasporangium_calvum*_DSM_43043.710696, *Jonesia_denitrificans*_DSM_20603.471856, *Corynebacterium_diphtheriae*_31A.698962, *Bifidobacterium_animalis_subsp._lactis*_CNCM_I-2494.1042403, *Kitasatospora_setae*_KM-6054.452652, *Mycobacterium_sp._MCS*.164756, *Corynebacterium_callunae*_DSM_20147.1121353, *Mycobacterium_gilvum_PYR*-GCK.350054, *Corynebacterium_deserti*_GIMN1.010.931089, *Mycobacterium_marinum_M*.216594, *Corynebacterium_casei*_LMG_S-19264.1285583, *Rothia_dentocariosa*_ATCC_17931.762948, *Amycolatopsis_mediterranei*_S699.713604, *Corynebacterium_maris*_DSM_45190.1224163, *Streptomyces_avermitilis*_MA-4680___NBRC_14893.227882, *Microbacterium_sp._PAMC_28756*.1795053, *Streptomyces_hygroscopicus_subsp._jinggangensis*_5008.1133850, *Amycolicococcus_subflavus*_DQS3-9A1.443218, *Bifidobacterium_longum_subsp._infantis*_ATCC_15697___JCM_1222___DSM_20088.391904, *Actinomyces_oris*.544580, *Nakamurella_multipartita*_DSM_44233.479431

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6 Streptomyces_vietnamensis.362257,Rhodoluna_lacicola.529884,Mycobacterium_rhodesiae_NBB3.710685,Frankia_alni_A
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- 7 Streptomyces_albulus_ZPM.1434306,Mycobacterium_sp._JS623.212767,Trueperella_pyogenes_TP8.1435056,Corynebacterium_lactis_RW2-5.1408189,Streptomyces_sp._CdTB01.1725411,Actinoplanes_sp._SE50_110.134676,Microbacterium_sp._No._7.1714373,Cellulomonas_gilvus_ATCC_13127.593907,Mycobacterium_microti.1806,Bifidobacterium_dentium_JCM_1195_DSM_20436.1150423,Rhodococcus_jostii_RHA1.101510,Intrasporangium_calvum_DSM_43043.710696,Stackebrandtia_nassauensis_DSM_44728.446470,Verrucosipora_maris_AB-18-032.263358,Nocardia_cyriacigeorgica_GUH-2.1127134,Corynebacterium_ureicelerivorans.401472,Bifidobacterium_bifidum.1681,Actinoplanes_friuliensis_DSM_7358.1246995,Kibdelosporangium_phytohabitans.860235,Streptomyces_violaceusniger_Tu_4113.653045,Luteipulveratus_mongolensis.571913,Pimelobacter_simplex.2045,Corynebacterium_kroppenstedtii_DSM_44385.645127,Amycolatopsis_mediterranei_S699.713604,Bifidobacterium_adolescentis.1680,Streptomyces_scabiei_87.22.680198,Bifidobacterium_scardovii_JCM_12489_DSM_13734.1150461,Mobiluncus_curtisii_ATCC_43063.548479,Arthrobacter_sp._FB24.290399,Mycobacterium_kansasii_ATCC_12478.557599,Mycobacterium_sp._MCS.164756,Mycobacterium_gilvum_PYR-GCK.350054,Propionibacterium_propionicum_F0230a.767029,Brevibacterium_flavum_92706,Microbacterium_sp._PAMC_28756.1795053,Conexibacter_woesei_DSM_14684.469383,Amycolatopsis_japonica.208439,Kitasatospora_setae_KM-6054.452652,Nocardia_farcinica.37329,Cryptobacterium_curtum_DSM_15641.469378,Amycolicicoccus_subflavus_DQS3-9A1.443218,Cellulomonas_flavigena_DSM_20109.446466,Thermobifida_fusca_YX.269800,Streptomyces_vietnamensis.362257,Rubrobacter_radiotolerans.42256,Mycobacterium_liflandii_128FXT.459424,Illumatobacter_coccineus_YM16-304.1313172,Corynebacterium_resistens_DSM_45100.662755,Streptomyces_sp._769.1262452,Nocardioopsis_dassonvillei_subsp._dassonvillei_DSM_43111.446468,Streptomyces_cattleya_NRRL_8057_DSM_46488.1003195,Arthrobacter_phenanthrenivorans_Sphe3.930171,Microterricola_viridarii.412690,Saccharothrix_espansensis_DSM_44229.1179773,Nakamuraella_multipartita_DSM_44233.479431,Gordonia_bronchialis_DSM_43247.526226,Nocardia_nova_SH22a.1415166,Arthrobacter_sp._A3.595593,Arthrobacter_sp._Rue61a.1118963,Actinobacteria_bacterium_IMCC26256.1650658,Arthrobacter_sp._ATCC_21022.1771959,Mycobacterium_neoaurum_VKM_Ac-1815D.700508,Segniliparus_rotundus_DSM_44985.640132,Jonesia_denitrificans_DSM_20603.471856,Streptomyces_albus.1888,Bifidobacterium_coryneforme.1687,Streptomyces_lydicus_A02.1403539,Micrococcus_luteus_NCTC_2665.465515,Coriobacteriaceae_bacterium_68-1-3.1531429,Mycobacterium_sp._JLS.164757,Acidothermus_cellulolyticus_11B.351607,Pseudonocardia_sp._EC080610-09.1688404,Leifsonia_xylii_subsp._cynodontis_DSM_46306.1389489,Arthrobacter_arilaitensis.256701,Actinotignum_schaalii.59505,Streptosporangium_roseum_DSM_43021.479432,Corynebacterium_camporealensis.161896,Dermaecoccus_nishino-miyaensis.1274,Rhodococcus_erythropolis_PR4.234621,Mycobacterium_leprae_Br4923.561304,Micromonospora_sp._L5.648999,Saccharomonospora_viridis_DSM_43017.471857,Mycobacterium_abscessus_subsp._bolletii_50594.1303024,Actinomyces_radicidentis.111015,Kocuria_palustris.71999,Microbacterium_sp._XT11.367477
- 8 Corynebacterium_vitaeruminis_DSM_20294.1224164,Streptomyces_sp._4F.1751294,Corynebacterium_diphtheriae_31A.698962,Micrococcus_luteus_NCTC_2665.465515,Pseudonocardia_sp._EC080610-09.1688404,Rathayibacter_toxicus.145458,Bifidobacterium_pseudocatenulatum_DSM_20438_JCM_1200_LMG_10505.547043,Bifidobacterium_longum_subsp._infantis_ATCC_15697_JCM_1222_DSM_20088.391904,Rhodococcus_opacus_PD630.543736,Brachybacterium_faecium_DSM_4810.446465,Bifidobacterium_indicum_LMG_11587_DSM_20214.1341694,Propionibacterium_propionicum_F0230a.767029,Illumatobacter_coccineus_YM16-304.1313172,Bifidobacterium_dentium_JCM_1195_DSM_20436.1150423,Frankia_sp._EAN1pec.298653,Corynebacterium_ureicelerivorans.401472,Nocardia_cyriacigeorgica_GUH-2.1127134,Modestobacter_marinus.477641,Mycobacterium_indicus_pranii_MTCC_9506.1232724,Actinomyces_oris.544580,Mycobacterium_chubuense_NBB4.710421,Arthrobacter_arilaitensis.256701,Bifidobacterium_bifidum.1681,Arthrobacter_sp._ATCC_21022.1771959,Rothia_mucilaginosa_DY-18.680646,Corynebacterium_stationis.1705,Verrucosipora_maris_AB-18-032.263358,Kocuria_palustris.71999,Acidimicrobium_ferroxidans_DSM_10331.525909,Mycobacterium_marinum_M.216594,Kitasatospora_setae_KM-6054.452652,Mycobacterium_sp._JS623.212767,Corynebacterium_atypicum.191610,Arcanobacterium_haemolyticum_DS_M_20595.644284,Mycobacterium_sp._EPa45.1545728,Kibdelosporangium_phytohabitans.860235,Intrasporangium_calvum_DSM_43043.710696,Arthrobacter_sp._LS16.1690248,Corynebacterium_pseudotuberculosis.1719,Arthrobacter_sp._ERGS1_01.1704044,Eggerthella_lenta_DSM_2243.479437,Corynebacterium_humireducens_NBRC_106098_DSM_45392.1223515,Actinosynnema_mirum_DSM_43827.446462,Coriobacterium_glomerans_PW2.700015,Renibacterium_salmoninarum_ATCC_33209.288705,Corynebacterium_deserti_GIMN1.010.931089,Bifidobacterium_scardovii_JCM_12489_DSM_13734.1150461,Rubrobacter_xylanophilus_DSM_9941.266117,Corynebacterium_ulcerans_FRC58.1408268,Rubrobacter_radiotolerans.42256,Dermaecoccus_nishinomiyaensis.1274,Mycobacterium_haemophilum_DSM_44634.1202450,Adlercreutzia_eq_uolificiens_DSM_19450.1384484,Nocardia_nova_SH22a.1415166,Streptomyces_pristinaespiralis.38300,Mycobacterium_kansasii_ATCC_12478.557599,Mycobacterium_leprae_Br4923.561304,Amycolatopsis_lurida_NRRL_2430.1460371,Cryptobacterium_curtum_DSM_15641.469378,Nocardioopsis_alba_ATCC_BAA-2165.1205910,Streptomyces_bingchenggensis_BCW-1.749414,Streptomyces_lydicus_A02.1403539,Tropheryma_whipplei_str._Twist.203267,Kutzneria_albida_DSM_43870.1449976,Isopterocola_variabilis_225.743718,Gordonia_polyisoprenivorans_VH2.1112204,Bifidobacterium_adolescentis.1680,Actinoplanes_missouriensis_431.512565,Streptomyces_sp._CNQ-509.444103,Corynebacterium_marinum_DSM_44953.1224162,Corynebacterium_jeikeium_K411.306537,Streptomyces_sp._Mg1.465541,Nocardioopsis_dassonvillei_subsp._dassonvillei_DSM_43111.446468,Rhodococcus_sp._B7740.1564114,Streptomyces_violaceusniger_Tu_4113.653045,Microbacterium_sp._PAMC_28756.1795053,Bifidobacterium_pseudolongum_P

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- 9 Mycobacterium_sp._JS623.212767,Streptomyces_vietnamensis.362257,Acidimicrobium_ferroxidans_DSM_10331.525909,Mycobacterium_avium_104.243243,Kribbella_flavida_DSM_17836.479435,Corynebacterium_uterequi.1072256,Kocuria_fla va.446860,Streptomyces_hygroscopicus_subsp._jinggangensis_5008.1133850,Nocardia_brasiliensis_ATCC_700358.11338 49,Mycobacterium_liflandii_128FXT.459424,Corynebacterium_ulcerans_FRC58.1408268,Cellulomonas_gilvus_ATCC_1312 7.593907,Corynebacterium_epidermidicanis.1050174,Atopobium_parvulum_DSM_20469.521095,Arthrobacter_sp._IHBB_1 1108.1618207,Streptomyces_collinus_Tu_365.1214242,Mycobacterium_tuberculosis.1773,Thermobispora_bispora_DSM_4 3833.469371,Saccharopolyspora_erythraea_NRRL_2338.405948,Bifidobacterium_angulatum_DSM_20098____JCM_7096.5 18635,Arthrobacter_sp._PAMC25486.1494608,Streptomyces_bingchenggensis_BCW-1.749414,Mycobacterium_sp._KMS.189918,Ilumatobacter_coccineus_YM16-304.1313172,Streptomyces_cattleya_NRRL_8057____DSM_46488.1003195,Corynebacterium_variabile_DSM_44702.85861 9,Corynebacterium_argentoratense_DSM_44202.1348662,Streptomyces_ambofaciens_ATCC_23877.278992,Arthrobacter_chlorophenolicus_A6.452863,Frankia_sp._Eul1c.298654,Corynebacterium_imitans.156978,Corynebacterium_glyciniphilum_AJ_3170.1404245,Intrasporangium_calvum_DSM_43043.710696,Mycobacterium_chubuense_NBB4.710421,Isopterocola_variabilis_225.743718,Gordonia_polyisoprenivorans_VH2.1112204,Mycobacterium_sp._Epa45.1545728,Actinomyces_mey eri.52773,Streptomyces_sp._PAMC26508.1265601,Corynebacterium_diphtheriae_31A.698962,Bifidobacterium_coryneform e.1687,Modestobacter_marinus.477641,Streptomyces_leeuwenhoekii.1437453,Corynebacterium_jeikeium_K411.306537,Bi fidobacterium_bifidum.1681,Corynebacterium_camporealis.161896,Xylanimonas_cellulosilytica_DSM_15894.446471,My cobacterium_indicus_pranii_MITCC_9506.1232724,Arthrobacter_sp._LS16.1690248,Mycobacterium_ulcerans_Agy99.36224 2,Bifidobacterium_pseudolongum_PV8-2.1447715,Corynebacterium_pseudotuberculosis.1719,Streptomyces_lydicus_A02.1403539,Actinomyces_sp._oral_taxon_4 14.712122,Arthrobacter_sp._ATCC_21022.1771959,Mycobacterium_marinum_M.216594,Blastococcus_saxobsidens_DD2. 1146883,Mycobacterium_sp._MOTT36Y.1168287,Streptomyces_sp._4F.1751294,Microbacterium_sp._CGR1.1696072,Stre ptomyces_xiamenensis.408015,Pseudonocardia_dioxanivorans_CB1190.675635,Corynebacterium_humireducens_NBRC_106098____DSM_45392.1223515,Propionibacterium_freudenreichii_subsp._shermanii_CIRM-BIA1.754252,Streptomyces_venezuelae.54571,Gordonia_bronchialis_DSM_43247.526226,Propionibacterium_acidipropioni ci_ATCC_4875.1171373,Bifidobacterium_longum_subsp._infantis_ATCC_15697____JCM_1222____DSM_20088.391904,Cor ynebacterium_casei_LMG_S-19264.1285583,Streptomyces_reticuli.1926,Rubrobacter_xylanophilus_DSM_9941.266117,Nakamurella_multipartita_DSM_44233.479431,Corynebacterium_mustelae.571915,Mycobacterium_gilvum_PYR-GCK.350054,Bifidobacterium_catenulatum_DSM_16992____JCM_1194____LMG_11043.566552,Trueperella_pyogenes_TP8 1.435056,Thermobifida_fusca_YX.269800,Corynebacterium_vitaeruminis_DSM_20294.1224164,Kitasatospora_setae_KM-6054.452652,Streptomyces_violaceusniger_Tu_4113.653045,Corynebacterium_kutscheri.35755,Conexibacter_woesei_DS M_14684.469383,Streptomyces_glaucescens.1907,Nocardiopsis_alba_ATCC_BAA-2165.1205910,Corynebacterium_urealyticum_DSM_7109.504474,Brachybacterium_faecium_DSM_4810.446465
- 10 Mycobacterium_sp._VKM_Ac-1817D.1273687,Actinobacteria_bacterium_IMCC26256.1650658,Arthrobacter_sp._LS16.1690248,Kocuria_rhizophila_DC22 01.378753,Streptomyces_cyaneogriseus_subsp._noncyanogenus.477245,Actinomyces_meyeri.52773,Gardnerella_vaginali s_ATCC_14019.525284,Kribbella_flavida_DSM_17836.479435,Microlunatus_phosphovorus_NM-1.1032480,Streptomyces_bingchenggensis_BCW-1.749414,Mycobacterium_ulcerans_Agy99.362242,Streptomyces_venezuelae.54571,Corynebacterium_pseudotuberculosis. 1719,Corynebacterium_glyciniphilum_AJ_3170.1404245,Arthrobacter_sp._PAMC25486.1494608,Geodermatophilus_obscur us_DSM_43160.526225,Streptomyces_scabiei_87.22.680198,Bifidobacterium_bifidum.1681,Streptomyces_collinus_Tu_36 5.1214242,Clavibacter_michiganensis_subsp._sepedonicus.31964,Corynebacterium_mustelae.571915,Cellulomonas_flavig ena_DSM_20109.446466,Cellulomonas_fimi_ATCC_484.590998,Corynebacterium_epidermidicanis.1050174,Streptomyces _albulus_ZPM.1434306,Streptomyces_ambofaciens_ATCC_23877.278992,Bifidobacterium_longum_subsp._infantis_ATCC _15697____JCM_1222____DSM_20088.391904,Microbacterium_sp._PAMC_28756.1795053,Amycolatopsis_orientalis_HCC B10007.1156913,Propionibacterium_propionicum_F0230a.767029,Frankia_symbiont_of_Datisca_glomerata.656024,Myco bacterium_chubuense_NBB4.710421,Corynebacterium_stationis.1705,Bifidobacterium_scardovii_JCM_12489____DSM_1373 4.1150461,Eggerthella_lenta_DSM_2243.479437,Streptomyces_glaucescens.1907,Streptomyces_sp._CNQ-509.444103,Pseudonocardia_dioxanivorans_CB1190.675635,Nocardioides_sp._JS614.196162,Brachybacterium_faecium_ DSM_4810.446465,Mycobacterium_sinense.875328,Microbacterium_sp._No_7.1714373,Actinoplanes_sp._N902-109.649831,Bifidobacterium_animalis_subsp._lactis_CNCM_I-2494.1042403,Frankia_alni_ACN14a.326424,Kytococcus_sedentarius_DSM_20547.478801,Saccharopolyspora_erythraea_ NRRL_2338.405948,Saccharothrix_espanaensis_DSM_44229.1179773,Luteipulveratus_mongoliensis.571913,Bifidobacteri um_angulatum_DSM_20098____JCM_7096.518635,Arthrobacter_sulfonivorans.121292,Intrasporangium_calvum_DSM_430 43.710696,Frankia_sp._Ccl3.106370,Gordonia_bronchialis_DSM_43247.526226,Microbacterium_sp._CGR1.1696072,Kine ococcus_radiotolerans_SRS30216____ATCC_BAA-149.266940,Micromonospora_sp._L5.648999,Propionibacterium_acnes_C1.1234380,Mycobacterium_sp._KMS.189918,Beu

- tenbergia_cavernae_DSM_12333.471853,Corynebacterium_sp._ATCC_6931.1487956,Mycobacterium_intracellulare_MOT T-
- 64.1138383,Corynebacterium_halotolerans_YIM_70093___DSM_44683.1121362,Corynebacterium_urealyticum_DSM_710 9.504474,Sanguibacter_keddiei_DSM_10542.446469,Streptomyces_griseus_subsp._griseus_NBRC_13350.455632,Actino myces_sp._oral_taxon_414.712122,Arthrobacter_sp._IHBB_11108.1618207,Saccharomonospora_viridis_DSM_43017.4718 57,Corynebacterium_deserti_GIMN1.010.931089,Nocardia_nova_SH22a.1415166,Corynebacterium_efficiens_YS- 314.196164,Salinispora_arenicola_CNS- 205.391037,Streptomyces_sp._Mg1.465541,Cellulomonas_gilvus_ATCC_13127.593907,Arthrobacter_sp._Hiyo8.1588023, Rhodococcus_opacus_PD630.543736,Mycobacterium_goodii.134601,Streptomyces_pristinaespiralis.38300,Mycobacterium _bovis_BCG.33892,Gordonia_sp._KTR9.337191,Jonesia_denitrificans_DSM_20603.471856,Kocuria_flava.446860,Microba cterium_testaceum_StLB037.979556,Corynebacterium_lactis_RW2-5.1408189,Corynebacterium_imitans.156978
- 11 Streptomyces_sp._Mg1.465541,Amycolatopsis_mediterranei_S699.713604,Corynebacterium_variabile_DSM_44702.85861 9,Frankia_sp._EAN1pec.298653,Amycolatopsis_japonica.208439,Actinoplanes_sp._N902- 109.649831,Geodermatophilus_obscurus_DSM_43160.526225,Corynebacterium_epidermidicantis.1050174,Gordonia_bronc hialis_DSM_43247.526226,Frankia_symbiont_of_Datisca_glomerata.656024,Mycobacterium_sp._KMS.189918,Frankia_sp. _Ccl3.106370,Propionibacterium_acidipropionici_ATCC_4875.1171373,Tropheryma_whipplei_str._Twist.203267,Arthrobact er_sp._LS16.1690248,Mycobacterium_indicus_pranii_MTCC_9506.1232724,Rhodococcus_pyridinivorans_SB3094.143535 6,Micromonospora_sp._L5.648999,Streptomyces_sp._SirexAA- E.862751,Olsenella_uli_DSM_7084.633147,Bifidobacterium_kashiwanohense_JCM_15439___DSM_21854.1150460,Strept omyces_albulus_ZPM.1434306,Streptomyces_sp._CNQ- 509.444103,Leifsonia_xyli_subsp._cynodontis_DSM_46306.1389489,Micrococcus_luteus_NCTC_2665.465515,Pseudonoc ardia_sp._EC080625- 04.1096868,Mycobacterium_chubuense_NBB4.710421,Gordonia_polyisoprenivorans_VH2.1112204,Corynebacterium_testu dinoris.136857,Bifidobacterium_angulatum_DSM_20098___JCM_7096.518635,Adlercreutzia_equolifaciens_DSM_19450.1 384484,Corynebacterium_aurimucosum_ATCC_700975.548476,Amycolatopsis_methanolica_239.1068978,Nocardioidea s_p._JS614.196162,Nocardiopsis_alba_ATCC_BAA- 2165.1205910,Propionibacterium_propionicum_F0230a.767029,Salinispora_tropica_CNB- 440.369723,Streptomyces_pratensis_ATCC_33331.591167,Nocardia_nova_SH22a.1415166,Corynebacterium_humireduce ns_NBRC_106098___DSM_45392.1223515,Corynebacterium_atypicum.191610,Arthrobacter_sp._Rue61a.1118963,Strept omyces_pristinaespiralis.38300,Arthrobacter_sp._YC- RL1.1652545,Intrasporangium_calvum_DSM_43043.710696,Coriobacteriaceae_bacterium_68-1- 3.1531429,Cellulomonas_gilvus_ATCC_13127.593907,Brachybacterium_faecium_DSM_4810.446465,Streptomyces_sp._C FMR_7.1649184,Corynebacterium_mustelae.571915,Corynebacterium_maris_DSM_45190.1224163,Modestobacter_marin us.477641,Mycobacterium_rhodesiae_NBB3.710685,Corynebacterium_terpenotabidum_Y- 11.1200352,Thermobifida_fusca_YX.269800,Actinoplanes_missouriensis_431.512565,Pseudonocardia_sp._EC080619- 01.1096856,Streptomyces_collinus_Tu_365.1214242,Isophtericola_variabilis_225.743718,Illumatobacter_coccineus_YM16- 304.1313172,Mycobacterium_tuberculosis.1773,Kibdelosporangium_phytohabitans.860235,Actinomyces_sp._oral_taxon_4 14.712122,Microbacterium_sp._XT11.367477,Streptomyces_sp._4F.1751294,Amycolatopsis_lurida_NRRL_2430.1460371, Corynebacteriales_bacterium_X1036.1528099,Bifidobacterium_asteroides_PRL2011.1147128,Streptomyces_hygroscopicu s_subsp._jinggangensis_5008.1133850,Arcanobacterium_haemolyticum_DSM_20595.644284,Corynebacterium_dooanense CAU_212___DSM_45436.558173,Aeromicrobium_erythreum.2041,Clavibacter_michiganensis_subsp._sepedonicus.319 64,Streptomyces_bingchengensis_BCW- 1.749414,Mycobacterium_liflandii_128FXT.459424,Mycobacterium_fortuitum.1766,Actinomyces_meyeri.52773,Corynebacte rium_kutscheri.35755,Streptomyces_leeuwenhoeckii.1437453,Propionibacterium_avidum_44067.1170318,Corynebacterium_ camporealensis.161896,Rothia_mucilaginosa_DY- 18.680646,Arthrobacter_sp._PAMC25486.1494608,Corynebacterium_jeikeium_K411.306537,Corynebacterium_imitans.156 978,Streptomyces_cyaneogriseus_subsp._noncyanogenus.477245
- 12 Mycobacterium_sp._EPa45.1545728,Microlunatus_phosphovorus_NM- 1.1032480,Blastococcus_saxosidens_DD2.1146883,Corynebacterium_variabile_DSM_44702.858619,Actinosynnema_mir um_DSM_43827.446462,Microbacterium_sp._XT11.367477,Mycobacterium_kansasii_ATCC_12478.557599,Corynebacteri um_dooanense_CAU_212___DSM_45436.558173,Arthrobacter_sp._IHBB_11108.1618207,Corynebacterium_ureiceleivor ans.401472,Propionibacterium_avidum_44067.1170318,Streptomyces_avermitilis_MA- 4680___NBRC_14893.227882,Amycolatopsis_mediterranei_S699.713604,Acidimicrobium_ferrooxidans_DSM_10331.5259 09,Trueperella_pyogenes_TP8.1435056,Luteipulveratus_mongoliensis.571913,Mycobacterium_gilvum_PYR- GCK.350054,Cellulomonas_fimi_ATCC_484.590998,Streptomyces_hygroscopicus_subsp._jinggangensis_5008.1133850,A mycolicococcus_subflavus_DQS3- 9A1.443218,Mycobacterium_aviium_104.243243,Coriobacterium_glomerans_PW2.700015,Eggerthella_lenta_DSM_2243.47 9437,Streptomyces_albus.1888,Mycobacterium_intracellulare_MOTT- 64.1138383,Tropheryma_whipplei_str._Twist.203267,Corynebacterium_marinum_DSM_44953.1224162,Bifidobacterium_in dicum_LMG_11587___DSM_20214.1341694,Mycobacterium_sp._VKM_Ac- 1817D.1273687,Corynebacterium_urealyticum_DSM_7109.504474,Bifidobacterium_breve.1685,Corynebacterium_stationis. 1705,Amycolatopsis_japonica.208439,Mycobacterium_sinense.875328,Amycolatopsis_lurida_NRRL_2430.1460371,Gordon ia_bronchialis_DSM_43247.526226,Mycobacterium_neoaurum_VKM_Ac-1815D.700508,Streptomyces_globisporus_C-

- 1027.1172567, *Streptomyces xiamenensis*.408015, *Mycobacterium rhodesiae*_NBB3.710685, *Propionibacterium acnes*_C1.1234380, *Jonesia denitrificans*_DSM_20603.471856, *Corynebacterium ulcerans*_FRC58.1408268, *Corynebacterium deserti*_GIMN1.010.931089, *Renibacterium salmoninarum*_ATCC_33209.288705, *Corynebacterium maris*_DSM_45190.1224163, *Eggerthella*_sp._YY7918.502558, *Bifidobacterium longum*_subsp._infantis_ATCC_15697____JCM_1222____DSM_20088.391904, *Pseudonocardia*_sp._EC080625-04.1096868, *Arthrobacter*_sp._YC-RL1.1652545, *Actinoplanes missouriensis*_431.512565, *Arthrobacter*_sp._Hiyo8.1588023, *Mycobacterium*_sp._MOTT36Y.1168287, *Corynebacterium halotolerans*_YIM_70093____DSM_44683.1121362, *Micromonospora aurantiaca*_ATCC_27029.644283, *Actinotignum schaalii*.59505, *Kitasatospora setae*_KM-6054.452652, *Propionibacterium freudenreichii*_subsp._shermanii_CIRM-BIA1.754252, *Arthrobacter chlorophenolicus*_A6.452863, *Sanguibacter keddiei*_DSM_10542.446469, *Nocardiopsis alba*_ATCC_BAA-2165.1205910, *Corynebacterium mustelae*.571915, *Acidothermus cellulolyticus*_11B.351607, *Scardovia inopinata*_JCM_12537.1150468, *Micrococcus luteus*_NCTC_2665.465515, *Corynebacterium atypicum*.191610, *Mycobacterium tuberculosis*.1773, *Corynebacterium diphtheriae*_31A.698962, *Corynebacterium uterequi*.1072256, *Corynebacteriales bacterium*_X1698.1562462, *Kocuria palustris*.71999, *Streptomyces*_sp._Mg1.465541, *Mycobacterium haemophilum*_DSM_44634.1202450, *Modestobacter marinus*.477641, *Kribbella flavida*_DSM_17836.479435, *Brachybacterium faecium*_DSM_4810.446465, *Rathayibacter toxicus*.145458, *Actinomyces radicidentis*.111015, *Corynebacterium terpenotabidum*_Y-11.1200352, *Arthrobacter*_sp._Rue61a.1118963, *Coriobacteriaceae bacterium*_68-1-3.1531429, *Rhodococcus jostii*_RHA1.101510, *Bifidobacterium coryneforme*.1687, *Cryptobacterium curtum*_DSM_15641.469378, *Corynebacterium kroppenstedtii*_DSM_44385.645127, *Gordonia*_sp._QH-11.1136941
- 13 *Streptomyces cattleya*_NRRL_8057____DSM_46488.1003195, *Propionibacterium propionicum*_F0230a.767029, *Arthrobacter aureus*_TC1.290340, *Corynebacterium urealyticum*_DSM_7109.504474, *Kibdelosporangium phytohabitans*.860235, *Mycobacterium marinum*_M.216594, *Arthrobacter*_sp._A3.595593, *Brevibacterium flavum*.92706, *Propionibacterium acnes*_C1.1234380, *Eggerthella lenta*_DSM_2243.479437, *Nocardia farcinica*.37329, *Nocardia cyriacigeorgica*_GUH-2.1127134, *Beutenbergia cavernae*_DSM_12333.471853, *Corynebacterium glutamicum*_R.340322, *Micromonospora aurantiaca*_ATCC_27029.644283, *Rhodococcus jostii*_RHA1.101510, *Rhodococcus pyridinivorans*_SB3094.1435356, *Scardovia inopinata*_JCM_12537.1150468, *Saccharomonospora viridis*_DSM_43017.471857, *Streptosporangium roseum*_DSM_43021.479432, *Corynebacterium halotolerans*_YIM_70093____DSM_44683.1121362, *Corynebacterium ulcerans*_FRC58.1408268, *Verrucospora maris*_AB-18-032.263358, *Frankia*_sp._Ccl3.106370, *Pseudonocardia*_sp._EC080625-04.1096868, *Mycobacterium*_sp._KMS.189918, *Nocardiopsis alba*_ATCC_BAA-2165.1205910, *Microbacterium*_sp._PAMC_28756.1795053, *Arthrobacter*_sp._ERGS1_01.1704044, *Bifidobacterium adolescentis*.1680, *Catenulispora acidiphila*_DSM_44928.479433, *Trueperella pyogenes*_TP8.1435056, *Corynebacterium callunae*_DSM_20147.1121353, *Devriesea agamarum*.472569, *Leifsonia xyli*_subsp._cynodontis_DSM_46306.1389489, *Microbacterium testaceum*_STLB037.979556, *Rubrobacter radiotolerans*.42256, *Coriobacteriaceae bacterium*_68-1-3.1531429, *Streptomyces*_sp._PAMC26508.1265601, *Mycobacterium kansasii*_ATCC_12478.557599, *Actinobacteria bacterium*_IMCC26256.1650658, *Renibacterium salmoninarum*_ATCC_33209.288705, *Olsenella*_sp._oral_taxon_807.712411, *Streptomyces glaucus*.1907, *Mycobacterium fortuitum*.1766, *Rhodoluna lacticola*.529884, *Microbacterium*_sp._CGR1.1696072, *Bifidobacterium dentium*_JCM_1195____DSM_20436.1150423, *Corynebacterium singulare*.161899, *Adlercreutzia equolifaciens*_DSM_19450.1384484, *Mycobacterium intracellulare*_MOTT-64.1138383, *Streptomyces pristinaespiralis*.38300, *Actinoplanes*_sp._SE50_110.134676, *Streptomyces*_sp._4F.1751294, *Streptomyces leeuwenhoekii*.1437453, *Mycobacterium*_sp._VKM_Ac-1817D.1273687, *Actinomyces meyeri*.52773, *Streptomyces reticuli*.1926, *Isophtericola variabilis*.225.743718, *Mycobacterium*_sp._JLS.164757, *Salinispora arenicola*_CNS-205.391037, *Pseudonocardia*_sp._AL041005-10.445576, *Corynebacterium mustelae*.571915, *Mycobacterium haemophilum*_DSM_44634.1202450, *Corynebacterium imitans*.156978, *Streptomyces*_sp._SirexAA-E.862751, *Mycobacterium africanum*.33894, *Mycobacterium*_sp._EPa45.1545728, *Actinoplanes friuliensis*_DSM_7358.1246995, *Streptomyces pratensis*_ATCC_33331.591167, *Kocuria flava*.446860, *Corynebacterium aurimucosum*_ATCC_700975.548476, *Geodermatophilus obscurus*_DSM_43160.526225, *Bifidobacterium actinocoloniiforme*_DSM_22766.1437605, *Streptomyces*_sp._Mg1.465541, *Streptomyces griseus*_subsp._griseus_NBRC_13350.455632, *Arthrobacter sulfonivorans*.121292, *Salinispora tropica*_CNB-440.369723, *Segniliparus rotundus*_DSM_44985.640132, *Streptomyces bingchenggensis*_BCW-1.749414, *Rhodococcus erythropolis*_PR4.234621, *Corynebacterium uterequi*.1072256, *Amycolicococcus subflavus*_DQS3-9A1.443218, *Streptomyces*_sp._CFMR_7.1649184, *Aeromicrobium erythreum*.2041, *Streptomyces fulvissimus*_DSM_40593.1303692
- 14 *Bifidobacterium coryneforme*.1687, *Nocardioides*_sp._JS614.196162, *Bifidobacterium thermophilum*_RBL67.1254439, *Streptomyces fulvissimus*_DSM_40593.1303692, *Streptomyces vietnamensis*.362257, *Arthrobacter*_sp._Hiyo8.1588023, *Propionibacterium propionicum*_F0230a.767029, *Propionibacterium avidum*_44067.1170318, *Microbacterium*_sp._No_7.1714373, *Mycobacterium*_sp._MCS.164756, *Clavibacter michiganensis*_subsp._sepedonicus.31964, *Corynebacterium efficiens*_YS-314.196164, *Mycobacterium goodii*.134601, *Corynebacterium casei*_LMG_S-19264.1285583, *Coriobacteriaceae bacterium*_68-1-3.1531429, *Corynebacterium kroppenstedtii*_DSM_44385.645127, *Conexibacter woesei*_DSM_14684.469383, *Microbacterium*_sp._PAMC_28756.1795053, *Corynebacterium stationis*.1705, *Acidimicrobium ferrooxidans*_DSM_10331.525909, *Trueperella pyogenes*_TP8.1435056, *Actinoplanes friuliensis*_DSM_7358.1246995, *Mycobacterium neoaurum*_VKM_Ac-1815D.700508, *Arthrobacter chlorophenolicus*_A6.452863, *Nocardiopsis dassonvillei*_subsp._dassonvillei_DSM_43111.446

- 468, *Arthrobacter aureus* TC1.290340, *Ilumatobacter coccineus* YM16-304.1313172, *Arcanobacterium haemolyticum* DSM_20595.644284, *Corynebacterium* sp. ATCC_6931.1487956, *Scardovia inopinata* JCM_12537.1150468, *Luteipulveratus mongoliensis*.571913, *Streptomyces bingchengensis* BCW-1.749414, *Slackia heliotrinireducens* DSM_20476.471855, *Leifsonia xyli* subsp. *cynodontis* DSM_46306.1389489, *Microbacterium testaceum* StLB037.979556, *Mycobacterium haemophilum* DSM_44634.1202450, *Brevibacterium flavum*.92706, *Mycobacterium* sp. JLS.164757, *Corynebacterium aurimucosum* ATCC_700975.548476, *Renibacterium salmoninarum* ATCC_33209.288705, *Corynebacterium terpenotabidum* Y-11.1200352, *Rhodoluna laticola*.529884, *Streptomyces pristinaespiralis*.38300, *Streptomyces pratensis* ATCC_33331.591167, *Corynebacterium marinum* DSM_44953.1224162, *Microbacterium* sp. CGR1.1696072, *Streptomyces cattleya* NRRL_8057 DSM_46488.1003195, *Streptomyces avermitilis* MA-4680 NBRC_14893.227882, *Streptomyces ambofaciens* ATCC_23877.278992, *Rhodococcus jostii* RHA1.101510, *Nocardia brasiliensis* ATCC_700358.1133849, *Xylanimonas cellulositica* DSM_15894.446471, *Nocardiosis alba* ATCC_BAA-2165.1205910, *Corynebacterium imitans*.156978, *Microbacterium* sp. XT11.367477, *Pseudonocardia* sp. AL041005-10.445576, *Corynebacterium camporeale*.161896, *Propionibacterium acidipropionici* ATCC_4875.1171373, *Actinomyces oris*.544580, *Kutzneria alba* DSM_43870.1449976, *Mycobacterium* sp. VKM_Ac-1817D.1273687, *Microlunatus phosphovorus* NM-1.1032480, *Streptosporangium roseum* DSM_43021.479432, *Frankia* sp. EAN1pec.298653, *Streptomyces lydicus* A02.1403539, *Arthrobacter alpinus*.656366, *Corynebacterium atypicum*.191610, *Frankia* sp. Eu1c.298654, *Arthrobacter* sp. ERG S1_01.1704044, *Mycobacterium* sp. MOTT36Y.1168287, *Amycolatopsis methanolica*.239.1068978, *Rhodococcus erythropolis* PR4.234621, *Eggerthella lenta* DSM_2243.479437, *Micrococcus luteus* NCTC_2665.465515, *Corynebacterium pseudotuberculosis*.1719, *Mycobacterium vanbaalenii* PYR-1.350058, *Streptomyces* sp. CdTB01.1725411, *Mycobacterium abscessus* subsp. *bolletii*.50594.1303024, *Streptomyces reticuli*.1926, *Micromonospora* sp. L5.648999, *Corynebacterium humireducens* NBRC_106098 DSM_45392.1223515, *Thermomonospora curvata* DSM_43183.471852, *Mycobacterium liflandii* 128FXT.459424, *Saccharomonospora viridis* DSM_43017.471857, *Streptomyces albulus* ZPM.1434306, *Amycolatopsis orientalis* HCCB10007.1156913
- 15 *Streptomyces* sp. Mg1.465541, *Bifidobacterium indicum* LMG_11587 DSM_20214.1341694, *Mycobacterium marinum* M.216594, *Corynebacterium deserti* GIMN1.010.931089, *Microterricola viridarii*.412690, *Eggerthella lenta* DSM_2243.479437, *Bifidobacterium coryneforme*.1687, *Mycobacterium* sp. MCS.164756, *Luteipulveratus mongoliensis*.571913, *Adlercreutzia equolifaciens* DSM_19450.1384484, *Mycobacterium leprae* Br4923.561304, *Arthrobacter* sp. YC-RL1.1652545, *Bifidobacterium dentium* JCM_1195 DSM_20436.1150423, *Bifidobacterium animalis* subsp. *lactis* CNC M-1-2494.1042403, *Frankia* sp. Ccl3.106370, *Mycobacterium sinense*.875328, *Corynebacterium epidermidicantis*.1050174, *Mycobacterium ulcerans* Ag99.362242, *Bifidobacterium breve*.1685, *Corynebacterium argenteorotense* DSM_44202.1348662, *Corynebacterium urealyticum* DSM_7109.504474, *Arthrobacter* sp. PAMC25486.1494608, *Bifidobacterium pseudocatenulatum* DSM_20438 JCM_1200 LMG_10505.547043, *Eggerthella* sp. YY7918.502558, *Corynebacterium casei* LMG_S-19264.1285583, *Arthrobacter* sp. ERGS1_01.1704044, *Propionibacterium acidipropionici* ATCC_4875.1171373, *Mycobacterium intracellulare* MOTT-64.1138383, *Kitasatospora setae* KM-6054.452652, *Thermobispora bispora* DSM_43833.469371, *Cellulomonas fimi* ATCC_484.590998, *Mycobacterium goodii*.134601, *Bifidobacterium catenulatum* DSM_16992 JCM_1194 LMG_11043.566552, *Streptomyces* sp. CFMR_7.1649184, *Ilumatobacter coccineus* YM16-304.1313172, *Frankia alni* ACN14a.326424, *Pseudonocardia* sp. EC080619-01.1096856, *Mycobacterium* sp. Epa45.1545728, *Streptomyces collinus* Tu_365.1214242, *Arthrobacter* sp. IHBB_11108.1618207, *Micrococcus luteus* NCTC_2665.465515, *Pseudonocardia dioxanivorans* CB1190.675635, *Rathayibacter toxicus*.145458, *Bifidobacterium adolescentis*.1680, *Thermobifida fusca* YX.269800, *Kibdelosporangium phytohabitans*.860235, *Mycobacterium* sp. JS623.212767, *Trueperella pyogenes* TP8.1435056, *Streptomyces* sp. PAMC26508.1265601, *Bifidobacterium asteroides* PRL2011.1147128, *Arthrobacter* sp. Rue61a.1118963, *Arthrobacter alpinus*.656366, *Bifidobacterium angulatum* DSM_20098 JCM_7096.518635, *Mycobacterium fortuitum*.1766, *Streptomyces albulus* ZPM.1434306, *Corynebacterium uterequi*.1072256, *Verrucospora maris* AB-18-032.263358, *Mycobacterium abscessus* subsp. *bolletii*.50594.1303024, *Arthrobacter arilaitensis*.256701, *Corynebacterium ureicelerivorans*.401472, *Bifidobacterium bifidum*.1681, *Corynebacterium vitaeruminis* DSM_20294.1224164, *Streptomyces fulvissimus* DSM_40593.1303692, *Streptomyces cyaneogriseus* subsp. *noncyanogenus*.477245, *Streptomyces hygroscopicus* subsp. *jinggangensis*.5008.1133850, *Streptomyces vietnamensis*.362257, *Mycobacterium kansasii* ATCC_12478.557599, *Nocardia nova* SH22a.1415166, *Mycobacterium tuberculosis*.1773, *Mycobacterium neoaurum* VKM_Ac-1815D.700508, *Streptomyces avermitilis* MA-4680 NBRC_14893.227882, *Corynebacterium glyciniphilum* AJ_3170.1404245, *Tropheryma whipplei* str. Twist.203267, *Corynebacterium callunae* DSM_20147.1121353, *Actinobacteria bacterium* IMCC26256.1650658, *Pseudonocardia* sp. H1130629-09.1641402, *Microbacterium* sp. No_7.1714373, *Corynebacterium doosanense* CAU_212 DSM_45436.558173, *Microbacterium* sp. CGR1.1696072, *Rubrobacter xylanophilus* DSM_9941.266117, *Mycobacterium haemophilum* DSM_44634.1202450, *Streptomyces* sp. 769.1262452, *Streptomyces reticuli*.1926, *Streptosporangium roseum* DSM_43021.479432, *Streptomyces globisporus* C-1027.1172567, *Mycobacterium indicus pranii* MTCC_9506.1232724
- 16 *Corynebacterium ulcerans* FRC58.1408268, *Mycobacterium bovis* BCG.33892, *Microbacterium testaceum* StLB037.979556, *Brevibacterium flavum*.92706, *Arthrobacter* sp. IHBB_11108.1618207, *Actinoplanes friuliensis* DSM_7358.1246995, *Mycobacterium microti*.1806, *Sanguibacter keddiei* DSM_10542.446469, *Mycobacterium ulcerans* Ag99.362242, *Arthrobacter*

cter_sp._Rue61a.1118963,Streptomyces_venezuelae.54571,Thermobifida_fusca_YX.269800,Propionibacterium_acidipropionici_ATCC_4875.1171373,Salinispora_tropica_CNB-440.369723,Rhodococcus_pyridinivorans_SB3094.1435356,Streptomyces_ambofaciens_ATCC_23877.278992,Amicycolatopsis_japonica.208439,Corynebacterium_stationis.1705,Mycobacterium_haemophilum_DSM_44634.1202450,Dermacoccus_nishinomiyaensis.1274,Corynebacterium_argentoratense_DSM_44202.1348662,Leifsonia_xyli_subsp._cynodontis_DSM_46306.1389489,Mycobacterium_intracellulare_MOTT-64.1138383,Brachybacterium_faecium_DSM_4810.446465,Actinomyces_sp._oral_taxon_414.712122,Mycobacterium_sp._EPA45.1545728,Streptomyces_globisporus_C-1027.1172567,Jonesia_dentrificans_DSM_20603.471856,Bifidobacterium_asteroides_PRL2011.1147128,Gordonia_polyisoprenivorans_VH2.1112204,Saccharopolyspora_erythraea_NRRL_2338.405948,Bifidobacterium_coryneforme.1687,Streptomyces_pratensis_ATCC_33331.591167,Micromonospora_aurantiaca_ATCC_27029.644283,Thermobispora_bispora_DSM_43833.469371,Corynebacterium_casei_LMG_S-19264.1285583,Arthrobacter_sp._Hiyo8.1588023,Corynebacterium_efficiens_YS-314.196164,Pseudonocardia_sp._HH130629-09.1641402,Olsenella_sp._oral_taxon_807.712411,Microbacterium_sp._PAMC_28756.1795053,Mycobacterium_leprae_Br4923.561304,Amicycolatopsis_methanolica_239.1068978,Blastococcus_saxobsidens_DD2.1146883,Gardnerella_vaginalis_ATCC_14019.525284,Atopobium_parvulum_DSM_20469.521095,Bifidobacterium_scandovii_JCM_12489_DSM_13734.1150461,Rothia_dentocariosa_ATCC_17931.762948,Mycobacterium_africanum.33894,Mycobacterium_rhodesiae_NBB3.710685,Mycobacterium_sp._MOTT36Y.1168287,Kibdelosporangium_phytohabitans.860235,Corynebacterium_kroppenstedtii_DSM_44385.645127,Tropheryma_whipplei_str._Twist.203267,Mycobacterium_vanbaalenii_PYR-1.350058,Bifidobacterium_pseudolongum_PV8-2.1447715,Kutzneria_albida_DSM_43870.1449976,Amicycolatopsis_orientalis_HCCB10007.1156913,Cellulomonas_flavigena_DSM_20109.446466,Rhodococcus_sp._B7740.1564114,Corynebacterium_marinum_DSM_44953.1224162,Corynebacterium_pseudotuberculosis.1719,Mycobacterium_sp._KMS.189918,Corynebacterium_callunae_DSM_20147.1121353,Corynebacterium_maris_DSM_45190.1224163,Streptosporangium_roseum_DSM_43021.479432,Corynebacteriales_bacterium_X1698.1562462,Stackebrandtia_nassauensis_DSM_44728.446470,Propionibacterium_freudenreichii_subsp._shermanii_CIRM-BIA1.754252,Corynebacterium_kutscheri.35755,Microbacterium_sp._XT11.367477,Microbacterium_sp._CGR1.1696072,Streptomyces_pristinaespiralis.38300,Mycobacterium_chubuense_NBB4.710421,Rubrobacter_radiotolerans.42256,Arsenicoccus_sp._oral_taxon_190.1658671,Streptomyces_albus.1888,Pimelobacter_simplex.2045,Gordonia_sp._QH-11.1136941,Tsakumurella_paurometabola_DSM_20162.521096,Frankia_symbiont_of_Datisca_glomerata.656024,Corynebacterium_mustelae.571915,Kytococcus_sedentarius_DSM_20547.478801,Streptomyces_glaucescens.1907,Microbacterium_sp._No._7.1714373,Corynebacterium_jeikeium_K411.306537

- 17 Ilumatobacter_coccineus_YM16-304.1313172,Kocuria_flava.446860,Propionibacterium_propionicum_F0230a.767029,Coriobacteriaceae_bacterium_68-1-3.1531429,Kocuria_palustris.71999,Corynebacterium_urealyticum_DSM_7109.504474,Actinomyces_oris.544580,Corynebacterium_aurimucosum_ATCC_700975.548476,Pimelobacter_simplex.2045,Cellulomonas_fimi_ATCC_484.590998,Streptomyces_globisporus_C-1027.1172567,Frankia_alni_ACN14a.326424,Frankia_sp._EAN1pec.298653,Segniliparus_rotundus_DSM_44985.640132,Corynebacterium_pseudotuberculosis.1719,Streptomyces_ambofaciens_ATCC_23877.278992,Streptomyces_sp._CFMR_7.1649184,Mycobacterium_rhodesiae_NBB3.710685,Streptosporangium_roseum_DSM_43021.479432,Corynebacterium_epidemicum.1050174,Mycobacterium_aviium_104.243243,Microterricola_viridarii.412690,Mycobacterium_intracellulare_MOTT-64.1138383,Stackebrandtia_nassauensis_DSM_44728.446470,Mycobacterium_sp._KMS.189918,Mycobacterium_sp._VKM_Ac-1817D.1273687,Leifsonia_xyli_subsp._cynodontis_DSM_46306.1389489,Sanguibacter_keddiei_DSM_10542.446469,Bifidobacterium_pseudolongum_PV8-2.1447715,Mycobacterium_sinense.875328,Rubrobacter_radiotolerans.42256,Bifidobacterium_bifidum.1681,Arthrobacter_sp._ERGS1_01.1704044,Actinoplanes_sp._SE50_110.134676,Streptomyces_griseus_subsp._griseus_NBRC_13350.455632,Atopobium_parvulum_DSM_20469.521095,Mycobacterium_sp._JLS.164757,Cryptobacterium_curtum_DSM_15641.469378,Corynebacterium_humireducens_NBRC_106098_DSM_45392.1223515,Streptomyces_sp._769.1262452,Arthrobacter_sp._IHBB_11108.1618207,Aeromicrobium_erythreum.2041,Corynebacterium_glutamicum_R.340322,Microbacterium_testaceum_StLB037.979556,Brachybacterium_faecium_DSM_4810.446465,Gordonia_sp._KTR9.337191,Corynebacterium_ulcerans_FRC58.1408268,Actinomyces_sp._oral_taxon_414.712122,Corynebacteriales_bacterium_X1698.1562462,Mycobacterium_bovis_BCG.33892,Nakamurella_multipartita_DSM_44233.479431,Microbacterium_sp._CGR1.1696072,Kibdelosporangium_phytohabitans.860235,Clavibacter_michiganensis_subsp._sepedonicus.31964,Arthrobacter_alpinus.656366,Streptomyces_lydicus_A02.1403539,Corynebacterium_ureicelerivorans.401472,Streptomyces_sp._PAMC26508.1265601,Intrasporangium_calvum_DSM_43043.710696,Micromonospora_aurantiaca_ATCC_27029.644283,Amicycolatopsis_mediterranei_S699.713604,Corynebacterium_mustelae.571915,Mycobacterium_microti.1806,Mycobacterium_fortuitum.1766,Bifidobacterium_thermophilum_RBL67.1254439,Streptomyces_leeuwenhoekii.1437453,Streptomyces_sp._CdTB01.1725411,Kitasatospora_setae_KM-6054.452652,Mycobacterium_leprae_Br4923.561304,Coriobacterium_glomerans_PW2.700015,Mycobacterium_kansasii_ATCC_12478.557599,Salinispora_arenicola_CNS-205.391037,Mobiluncus_curtisii_ATCC_43063.548479,Propionibacterium_freudenreichii_subsp._shermanii_CIRM-BIA1.754252,Actinomyces_meyeri.52773,Thermobispora_bispora_DSM_43833.469371,Streptomyces_pratensis_ATCC_33

- 331.591167, *Arthrobacter_chlorophenolicus*_A6.452863, *Mycobacterium_yongonense*_05-1390.1138871, *Micrococcus_phosphovorus*_NM-1.1032480, *Olsenella_uli*_DSM_7084.633147, *Streptomyces_scabiei*_87.22.680198, *Pseudonocardia_dioxanivorans*_CB1190.675635, *Streptomyces_sp._CNQ-509.444103*, *Bifidobacterium_breve*.1685, *Cellulomonas_gilvus*_ATCC_13127.593907
- 18 *Slackia_heliotrinireducens*_DSM_20476.471855, *Corynebacterium_variabile*_DSM_44702.858619, *Mycobacterium_sp._JS62* 3.212767, *Blastococcus_saxosidens*_DD2.1146883, *Nocardia_nova*_SH22a.1415166, *Geodermatophilus_obscurus*_DSM_43160.526225, *Corynebacterium_terpenotabidum_Y-11*.1200352, *Streptomyces_sp._Sirex*AA-E.862751, *Corynebacterium_atypicum*.191610, *Actinobacteria_bacterium_IMCC26256*.1650658, *Eggerthella_lenta*_DSM_2243.479437, *Dermacoccus_nishinomiyaensis*.1274, *Corynebacterium_pseudotuberculosis*.1719, *Corynebacterium_kroppenstedtii*_DSM_44385.645127, *Arthrobacter_aurescens*_TC1.290340, *Corynebacterium_maris*_DSM_45190.1224163, *Corynebacterium_uterequi*.1072256, *Streptomyces_globisporus_C-1027*.1172567, *Frankia_sp._Ccl3*.106370, *Nocardiosis_alba*_ATCC_BAA-2165.1205910, *Streptomyces_sp._CNQ-509.444103*, *Streptomyces_venezuelae*.54571, *Pseudonocardia_dioxanivorans*_CB1190.675635, *Mycobacterium_leprae*_Br4923.561304, *Aeromicrobium_erythreum*.2041, *Streptomyces_collinus_Tu*.365.1214242, *Corynebacterium_marinum*_DSM_44953.1224162, *Arthrobacter_sp._Hiyo8*.1588023, *Rothia_dentocariosa*_ATCC_17931.762948, *Kytococcus_sedentarius*_DSM_20547.478801, *Streptomyces_scabiei*_87.22.680198, *Mycobacterium_bovis*_BCG.33892, *Pseudonocardia_sp._EC080610-09*.1688404, *Saccharopolyspora_erythraea_NRR1*.2338.405948, *Actinoplanes_sp._N902-109*.649831, *Saccharomonospora_viridis*_DSM_43017.471857, *Micrococcus_phosphovorus*_NM-1.1032480, *Nocardia_farcinica*.37329, *Arthrobacter_chlorophenolicus*_A6.452863, *Corynebacterium_glyciniphilum_AJ*.3170.1404245, *Arthrobacter_sp._LS16*.1690248, *Micromonospora_aurantiaca*_ATCC_27029.644283, *Thermobispora_bispora*_DSM_43833.469371, *Renibacterium_salmoninarum*_ATCC_33209.288705, *Kitasatospora_setae_KM-6054*.452652, *Olsenella_uli*_DSM_7084.633147, *Mycobacterium_haemophilum*_DSM_44634.1202450, *Streptomyces_sp._Mg1*.465541, *Mycobacterium_kansasii*_ATCC_12478.557599, *Intrasporangium_calvum*_DSM_43043.710696, *Arthrobacter_sp._FB24*.290399, *Mycobacterium_africanum*.33894, *Arthrobacter_arilaitensis*.256701, *Luteipulveratus_mongoliensis*.571913, *Catenulipora_acidiphila*_DSM_44928.479433, *Actinoplanes_missouriensis*.431.512565, *Leifsonia_xyli_subsp._cynodontis_DS*M_46306.1389489, *Propionibacterium_avidum*.44067.1170318, *Arthrobacter_phenanthrenivorans*_Sphe3.930171, *Mycobacterium_chubuense*_NBB4.710421, *Streptomyces_pratensis*_ATCC_33331.591167, *Frankia_sp._Eul1c*.298654, *Corynebacterium_resistens*_DSM_45100.662755, *Mycobacterium_vanbaalenii*_Pyr-1.350058, *Mycobacterium_sp._EPA45*.1545728, *Bifidobacterium_thermophilum_RBL67*.1254439, *Eggerthella_sp._YY7918*.502558, *Gordonia_sp._QH-11*.1136941, *Propionibacterium_acnes_C1*.1234380, *Actinoplanes_friuliensis*_DSM_7358.1246995, *Propionibacterium_freudei*_nreichii_subsp._shermanii_CIRM-BIA1.754252, *Arthrobacter_sp._YC-R1*.1652545, *Gardnerella_vaginalis*_ATCC_14019.525284, *Bifidobacterium_pseudolongum_PV8-2*.1447715, *Olsenella_sp._oral_taxon_807*.712411, *Rhodoluna_lacicola*.529884, *Streptomyces_cattleia_NRR1*.8057___DSM_46488.1003195, *Streptomyces_avermitilis_MA-4680*__NBRC_14893.227882, *Nakamurella_multipartita*_DSM_44233.479431, *Arthrobacter_sp._Rue61a*.1118963, *Corynebacterium_sp._ATCC_6931*.1487956, *Corynebacterium_stationis*.1705, *Mycobacterium_rhodesiae*_NBB3.710685, *Microtheriicola_viridarii*.412690, *Brachybacterium_faecium*_DSM_4810.446465, *Arthrobacter_sp._ERGS1_01*.1704044
- 19 *Nocardia_farcinica*.37329, *Streptomyces_sp._Mg1*.465541, *Mycobacterium_chubuense*_NBB4.710421, *Corynebacterium_pseudotuberculosis*.1719, *Mycobacterium_aviium*.104.243243, *Corynebacterium_stationis*.1705, *Streptomyces_scabiei*_87.22.680198, *Streptomyces_pratensis*_ATCC_33331.591167, *Bifidobacterium_thermophilum_RBL67*.1254439, *Arcanobacterium_haemolyticum*_DSM_20595.644284, *Thermomonospora_curvata*_DSM_43183.471852, *Amycolatopsis_japonica*.208439, *Corynebacterium_efficiens*_YS-314.196164, *Nocardiosis_dassonvillei_subsp._dassonvillei*_DSM_43111.446468, *Frankia_sp._Ccl3*.106370, *Gardnerella_vaginalis*_ATCC_14019.525284, *Corynebacterium_variabile*_DSM_44702.858619, *Verrucospora_maris_AB-18*.032.263358, *Bifidobacterium_kashiwanohense*_JCM_15439___DSM_21854.1150460, *Mycobacterium_indicus_pranii*_MTCC_9506.1232724, *Arthrobacter_sp._Rue61a*.1118963, *Amycolatopsis_mediterranei*_S699.713604, *Amycolatopsis_orientalis_H*_CCB10007.1156913, *Kitasatospora_setae_KM-6054*.452652, *Corynebacterium_uterequi*.1072256, *Streptomyces_xiamenensis*.408015, *Actinomyces_sp._oral_taxon_414*.712122, *Bifidobacterium_scardovii*_JCM_12489___DSM_13734.1150461, *Streptomyces_fulvissimus*_DSM_40593.1303692, *Rhodococcus_opacus_PD630*.543736, *Saccharomonospora_viridis*_DSM_43017.471857, *Mycobacterium_abscessus_subsp._boletii*_50594.1303024, *Bifidobacterium_actinocoloniiforme*_DSM_22766.1437605, *Kocuria_rhizophila_DC2201*.378753, *Corynebacterium_diphtheriae*_31A.698962, *Streptomyces_leeuwenhoekii*.1437453, *Corynebacterium_marinum*_DSM_44953.1224162, *Corynebacterium_atypicum*.191610, *Streptomyces_bingchenggensis*_BCW-1.749414, *Streptomyces_violaceusniger_Tu*.4113.653045, *Corynebacterium_sp._ATCC_6931*.1487956, *Saccharopolyspora_erythraea_NRR1*.2338.405948, *Mycobacterium_sp._CGR1*.1696072, *Micromonospora_aurantiaca*_ATCC_27029.644283, *Rhodococcus_pyridinivorans*_SB3094.1435356, *Catenulipora_acidiphila*_DSM_44928.479433, *Streptomyces_reticulosus*.1926, *Streptomyces_sp._4F*.1751294, *Thermobifida_fusca_YX*.269800, *Mycobacterium_tuberculosis*.1773, *Corynebacterium_lactis*_RW2-5.1408189, *Bifidobacterium_bifidum*.1681, *Rhodococcus_erythropolis*_PR4.234621, *Dermacoccus_nishinomiyaensis*.1274, *Bifidobacterium_animalis_subsp._lactis_CNCM*_I-2494.1042403, *Streptomyces_sp._CNQ-509*.444103, *Corynebacterium_argentoratense*_DSM_44202.1348662, *Mycobacterium_goodii*.134601, *Frankia_alni*_ACN14a.326424, *Leifsonia_xyli_subsp._cynodontis*_DSM_46306.1389489, *Slackia_heliotrinireducens*_DSM_20476.471855, *Corynebacterium*

cterium_maris_DSM_45190.1224163,Corynebacterium_testudinoris.136857,Corynebacterium_mustelae.571915,Nocardia_brasiliensis_ATCC_700358.1133849,Aeromicrobium_erythreum.2041,Rothia_dentocariosa_ATCC_17931.762948,Mycobacterium_kansasii_ATCC_12478.557599,Corynebacteriales_bacterium_X1036.1528099,Blastococcus_saxobsidens_DD2.1146883,Bifidobacterium_asteroides_PRL2011.1147128,Corynebacterium_terpenotabidum_Y-11.1200352,Actinomyces_meyeri.52773,Atopobium_parvulum_DSM_20469.521095,Brachybacterium_faecium_DSM_4810.446465,Nocardia_cyriacigeorgica_GUH-2.1127134,Bifidobacterium_breve.1685,Arsenicicoccus_sp._oral_taxon_190.1658671,Rubrobacter_xylanophilus_DSM_9941.266117,Micromonospora_sp._L5.648999,Rhodococcus_sp._B7740.1564114,Nocardia_nova_SH22a.1415166,Bifidobacterium_dentium_JCM_1195_DSM_20436.1150423,Streptomyces_vietnamensis.362257,Mycobacterium_sp._MOTT36Y.1168287,Gordonia_bronchialis_DSM_43247.526226

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21 **Table S27** Normalized Robinson-Foulds (nRF) matrix for Deinococcus-Thermus (DT) permutations on Hug *et al.* (2016) dataset.
22 Normalizing constant shown top left. Dcc.: Deinococcus, Th.: Thermus.

6150		FULL	HIGH1	HIGH2	HIGH3	HIGH4	HIGH5	HIGH6	MD1	MD2	LOW1	LOW2	LOW3	LOW4	LOW5	LOW6
FULL	all	0	0.02732	0.0452	0.04293	0.03317	0.03415	0.02959	0.03642	0.04098	0.02504	0.0348	0.02959	0.03154	0.02699	0.03447
HIGH1	Dcc. Geothermalls	0.02732	0	0.04	0.03154	0.01008	0.04	0.0374	0.04	0.03902	0.02407	0.04195	0.02211	0.03837	0.01659	0.02472
HIGH2	Truepera	0.0452	0.04	0	0.03024	0.03837	0.03707	0.0348	0.04618	0.02732	0.04553	0.05073	0.0439	0.04033	0.04	0.0413
HIGH3	Marinithermus hydrothermalis	0.04293	0.03154	0.03024	0	0.03089	0.02602	0.02407	0.0348	0.02537	0.03545	0.05659	0.02374	0.04976	0.02732	0.03935
HIGH4	Meiothermus ruber	0.03317	0.01008	0.03837	0.03089	0	0.0439	0.0413	0.03707	0.03642	0.02699	0.0439	0.01919	0.03935	0.01756	0.02732
HIGH5	Oceanithermus profundus	0.03415	0.04	0.03707	0.02602	0.0439	0	0.0065	0.03252	0.03317	0.03447	0.05431	0.03935	0.04846	0.03707	0.04553
HIGH6	Th. Oshimai	0.02959	0.0374	0.0348	0.02407	0.0413	0.0065	0	0.03089	0.03057	0.0322	0.05333	0.03707	0.04748	0.03447	0.04293
MD1	Dcc.	0.03642	0.04	0.04618	0.0348	0.03707	0.03252	0.03089	0	0.0413	0.03122	0.04878	0.0335	0.04325	0.03545	0.03935
MD2	Th.	0.04098	0.03902	0.02732	0.02537	0.03642	0.03317	0.03057	0.0413	0	0.04033	0.05431	0.0374	0.04911	0.03707	0.0478
LOW1	Dcc. Geothermalls	0.02504	0.02407	0.04553	0.03545	0.02699	0.03447	0.0322	0.03122	0.04033	0	0.03967	0.02439	0.03057	0.02244	0.02959
LOW2	Truepera	0.0348	0.04195	0.05073	0.05659	0.0439	0.05431	0.05333	0.04878	0.05431	0.03967	0	0.04195	0.02829	0.04325	0.03642
LOW3	Marinithermus hydrothermalis	0.02959	0.02211	0.0439	0.02374	0.01919	0.03935	0.03707	0.0335	0.0374	0.02439	0.04195	0	0.03772	0.01691	0.02504
LOW4	Meiothermus ruber	0.03154	0.03837	0.04033	0.04976	0.03935	0.04846	0.04748	0.04325	0.04911	0.03057	0.02829	0.03772	0	0.0387	0.02602
LOW5	Oceanithermus profundus	0.02699	0.01659	0.04	0.02732	0.01756	0.03707	0.03447	0.03545	0.03707	0.02244	0.04325	0.01691	0.0387	0	0.02634
LOW6	Th. Oshimai	0.03447	0.02472	0.0413	0.03935	0.02732	0.04553	0.04293	0.03935	0.0478	0.02959	0.03642	0.02504	0.02602	0.02634	0

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24 **Table S28** Normalized Robinson-Foulds (nRF) matrix for Deinococcus-Thermus (DT) permutations using 6 species from Hug *et al.*
25 (2016) dataset. Normalizing constant shown top left. Dcc.: Deinococcus, Th.: Thermus.

1488		FULL	HIGH1	HIGH2	HIGH3	HIGH4	HIGH5	HIGH6	MD1	MD2	LOW1	LOW2	LOW3	LOW4	LOW5	LOW6
FULL	all	0	0.0121	0.00269	0.00134	0	0.00269	0.00134	0.00403	0.00403	0.00403	0.00403	0.00269	0.00403	0.00269	0.00269
HIGH1	Dcc. Geothermalls	0.0121	0	0.0121	0.01344	0.0121	0.0121	0.01344	0.01478	0.01075	0.01478	0.01478	0.0121	0.01075	0.0121	0.0121
HIGH2	Truepera	0.00269	0.0121	0	0.00134	0.00269	0	0.00134	0.00269	0.00134	0.00269	0.00269	0	0.00134	0	0
HIGH3	Marinithermus hydrothermalis	0.00134	0.01344	0.00134	0	0.00134	0	0.00269	0.00269	0.00269	0.00269	0.00269	0.00134	0.00269	0.00134	0.00134
HIGH4	Meiothermus ruber	0	0.0121	0.00269	0.00134	0	0.00269	0.00134	0.00403	0.00403	0.00403	0.00403	0.00269	0.00403	0.00269	0.00269
HIGH5	Oceanithermus profundus	0.00269	0.0121	0	0.00134	0.00269	0	0.00134	0.00269	0.00134	0.00269	0.00269	0	0.00134	0	0
HIGH6	Th. Oshimai	0.00134	0.01344	0.00134	0	0.00134	0.00134	0	0.00269	0.00269	0.00269	0.00269	0.00134	0.00269	0.00134	0.00134
MD1	Dcc.	0.00403	0.01478	0.00269	0.00269	0.00403	0.00269	0.00269	0	0.00403	0	0	0.00269	0.00403	0.00269	0.00269
MD2	Th.	0.00403	0.01075	0.00134	0.00269	0.00403	0.00134	0.00269	0.00403	0	0.00403	0.00403	0.00134	0	0.00134	0.00134
LOW1	Dcc. Geothermalls	0.00403	0.01478	0.00269	0.00269	0.00403	0.00269	0.00269	0	0.00403	0	0	0.00269	0.00403	0.00269	0.00269
LOW2	Truepera	0.00403	0.01478	0.00269	0.00269	0.00403	0.00269	0.00269	0	0.00403	0	0	0.00269	0.00403	0.00269	0.00269
LOW3	Marinithermus hydrothermalis	0.00269	0.0121	0	0.00134	0.00269	0	0.00134	0.00269	0.00134	0.00269	0.00269	0	0.00134	0	0
LOW4	Meiothermus ruber	0.00403	0.01075	0.00134	0.00269	0.00403	0.00134	0.00269	0.00403	0	0.00403	0.00403	0.00134	0	0.00134	0.00134
LOW5	Oceanithermus profundus	0.00269	0.0121	0	0.00134	0.00269	0	0.00134	0.00269	0.00134	0.00269	0.00269	0	0.00134	0	0
LOW6	Th. Oshimai	0.00269	0.0121	0	0.00134	0.00269	0	0.00134	0.00269	0.00134	0.00269	0.00269	0	0.00134	0	0

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