IBS\_h\_C1\_metatranscriptomes\_family\_CORE: rank matrix & stability

	_			_	_	<i>-</i>			
uc_Bacteria	8	1	3	1	1	1	1	4	1
Lachnospiraceae	2	2	1	2	3	3	2	1	2
Ruminococcaceae	1	4	2	4	2	2	5	2	3
Bacteroidaceae	4	6	5	3	4	4	3	3	4
uc_Clostridiales	5	3	4	5	5	5	4	5	5
Prevotellaceae	3	5	6	6	6	6	6	8	6
uc_Firmicutes	9	7	8	8	8	8	7	7	7
Porphyromonadaceae	6	9	9	9	7	9	9	9	9
uc_Bacteroidales	7	13	7	10	10	10	11	6	10
uc_Clostridia	13	8	11	12	11	11	15	11	11
Puniceicoccaceae	10	14	25	15	9	14	10	10	8
uc_Alphaproteobacteria	18	15	36	7	23	7	8	17	23
uc_Proteobacteria	16	12	14	11	15	12	12	14	17
Rikenellaceae	11	21	16	18	12	21	21	13	18
Alcaligenaceae	12	11	12	17	17	16	18	15	14
uc_Bacteroidetes	14	20	15	14	13	15	16	12	13
Victivallaceae	34	18	13	22	19	13	17	23	16
Clostridiaceae	17	10	20	16	31	17	13	20	21
Peptostreptococcaceae	27	19	22	13	27	19	14	21	12
Erysipelotrichaceae	15	24	17	21	18	20	22	16	15
Veillonellaceae	20	17	19	19	14	22	20	25	19
Verrucomicrobiaceae	40	23	10	25	16	26	19	29	38
Peptococcaceae	24	16	24	20	26	18	27	18	20
uc_Burkholderiales	19	25	18	34	24	29	34	24	25
uc_Bacilli	31	27	26	23	30	24	24	19	27
uc_Opitutae	38	22	33	39	20	30	30	38	24
Desulfovibrionaceae	26	26	27	37	25	23	37	30	30
Clostridiales_incertae_sedis_XIV	23	30	38	26	29	27	25	27	28
uc_Verrucomicrobia	39	29	23	40	22	31	23	39	31
Coriobacteriaceae	25	37	35	27	21	32	36	36	22
Bifidobacteriaceae	21	33	30	31	32	34	28	26	26
uc_Betaproteobacteria	32	35	21	30	39	33	32	28	29
uc_Deltaproteobacteria	29	28	28	28	37	37	35	40	33
uc_Gammaproteobacteria	33	32	40	24	40	25	26	35	37
uc_Bacillales	36	34	29	29	33	28	33	32	35
uc_Lactobacillales	37	36	32	36	35	38	39	22	40
Synergistaceae	28	40	39	33	28	36	31	37	36
Clostridiales_incertae_sedis_XIII	22	39	34	38	34	40	29	31	34
uc_Desulfovibrionales	30	31	37	35	38	35	40	33	39
Eubacteriaceae	35	38	31	32	36	39	38	34	32
	~	Close	12021	7028	t,CZD3	\$	Cops	t,CZD5	<u>^</u>
	<sup>t,</sup> CZ <sub>D</sub> 2	Q	, ov	ÓV	27	Const.	Q <sup>x</sup>	27	^QZ <sub>Z</sub> ;
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Rank Stability Index (in %)