Supplementary Materials for

Interactions between human gut microbiome dynamics and sub-optimal health symptoms during seafaring expeditions

The additional tables include:

Table S1. Annotation for microbial species in the co-occurrence network

Table S2. The important score of the 28 microbial species and functions used in the Random Forest model

Table S3. Definitions of the 24 indicators in the questionnaire

Table S4. The questionnaire answers for all individuals before and after the voyage

The supplementary figures include:

Figure S1. Comparison of individual perturbations in the gut microbiome between ‘symptomless’ and ‘symptom’ crew members for 24 indicators (symptoms)

Figure S2. Co-occurrence networks of the SS and non-SS at beginning (day 1) and end (day 135) of the voyage

Reference

Table S1. Annotation for microbial species in the co-occurrence network.

Nodes ID	Species name (annotation in mOTUs2)	Nodes ID	Species name (annotation in mOTUs2)
S0004	Clostridiales species incertae sedis [meta_mOTU_v25_13280]	**S0716**	Coprobacter fastidiosus [ref_mOTU_v25_03667]
S0008	Faecalibacterium prausnitzii [ref_mOTU_v25_06109]	**S0720**	Ruminococcaceae species incertae sedis [meta_mOTU_v25_13151]
S0019	Bacteroides cellulosilyticus/fragilis [ref_mOTU_v25_01597]	**S0723**	Eubacterium sp. CAG:180 [ref_mOTU_v25_07675]
S0030	Bacteroides plebeius [ref_mOTU_v25_05069]	**S0727**	[Ruminococcus] torques [ref_mOTU_v25_03703]
S0032	Clostridiales species incertae sedis [meta_mOTU_v25_13006]	**S0735**	Dorea longicatena [ref_mOTU_v25_03692]
S0033	Clostridiales species incertae sedis [meta_mOTU_v25_12707]	**S0736**	Clostridiales species incertae sedis [meta_mOTU_v25_12434]
S0052	Ruminococcus bicirculans [ref_mOTU_v25_02792]	**S0749**	Bacteroides coprocola [ref_mOTU_v25_11279]
S0060	Coprococcus eutactus [ref_mOTU_v25_02378]	**S0752**	[Eubacterium] hallii [ref_mOTU_v25_03632]
S0082	Proteobacteria sp. [ref_mOTU_v25_00095]	**S0754**	Dorea longicatena [ref_mOTU_v25_03693]
S0085	Clostridiales species incertae sedis [meta_mOTU_v25_13168]	**S0756**	Bacteroides coprophilus [ref_mOTU_v25_04094]
S0093	Clostridiales species incertae sedis [meta_mOTU_v25_12253]	**S0761**	Faecalibacterium prausnitzii [ref_mOTU_v25_06108]
S0094	Firmicutes sp. [ref_mOTU_v25_03629]	**S0763**	Clostridium sp. CAG:127 [meta_mOTU_v25_12306]
S0100	Clostridiales species incertae sedis [meta_mOTU_v25_12356]	**S0766**	Bacteroides finegoldii [ref_mOTU_v25_03474]
S0103	Sutterella sp. CAG:351 [meta_mOTU_v25_13411]	**S0769**	Prevotella sp. CAG:279 [meta_mOTU_v25_12279]
S0114	Blautia obeum/wexlerae [ref_mOTU_v25_02154]	**S0770**	Roseburia inulinivorans [ref_mOTU_v25_00860]
S0115	Clostridium sp. AT4 [meta_mOTU_v25_12609]	**S0772**	Firmicutes sp. [ref_mOTU_v25_02374]
S0116	Paraprevotella xylaniphila [ref_mOTU_v25_03699]	**S0777**	Roseburia sp. CAG:303 [meta_mOTU_v25_12911]
S0117	Pasteurellaceae species incertae sedis [meta_mOTU_v25_13253]	**S0781**	Eubacterium sp. CAG:156 [ref_mOTU_v25_07673]
S0124	Clostridiales species incertae sedis [meta_mOTU_v25_12252]	**S0785**	Clostridiales species incertae sedis [meta_mOTU_v25_12265]
S0127	Bifidobacterium pseudocatenulatum [ref_mOTU_v25_02700]	**S0792**	Prevotella stercorea [ref_mOTU_v25_00717]
S0129	[Ruminococcus] gnavus [ref_mOTU_v25_01594]	**S0794**	Clostridium sp. CAG:492 [meta_mOTU_v25_12462]
S0134	Ruminococcaceae species incertae sedis [meta_mOTU_v25_12664]	**S0804**	Oscillibacter sp. 57_20 [meta_mOTU_v25_12282]
S0144	Paraprevotella clara [ref_mOTU_v25_03698]	**S0812**	Roseburia sp. 40_7 [meta_mOTU_v25_12352]
S0146	Eubacterium species incertae sedis [meta_mOTU_v25_12474]	**S0814**	[Clostridium] clostridioforme/bolteae [ref_mOTU_v25_03442]
S0148	Bacteroides massiliensis [ref_mOTU_v25_02135]	**S0837**	Clostridiales species incertae sedis [meta_mOTU_v25_12301]
S0151	Clostridiales species incertae sedis [meta_mOTU_v25_12873]	**S0840**	Firmicutes bacterium CAG:227 [ref_mOTU_v25_07734]
S0155	Ruminococcaceae species incertae sedis [meta_mOTU_v25_12259]	**S0842**	Roseburia sp. [ref_mOTU_v25_03650]
S0156	Clostridiales species incertae sedis [meta_mOTU_v25_12452]	**S0850**	Clostridiales species incertae sedis [meta_mOTU_v25_12361]
S0164	uncultured Butyricicoccus sp. [ref_mOTU_v25_07314]	**S0853**	Ruminococcaceae species incertae sedis [meta_mOTU_v25_12239]
S0167	Clostridium sp. CAG:217 [meta_mOTU_v25_12270]	**S0867**	Clostridiales species incertae sedis [meta_mOTU_v25_12288]
S0191	[Ruminococcus] torques [ref_mOTU_v25_03659]	**S0868**	Clostridiales species incertae sedis [meta_mOTU_v25_12229]
S0197	Butyricicoccus species incertae sedis [meta_mOTU_v25_12336]	**S0874**	Veillonella parvula [ref_mOTU_v25_01938]
S0198	Streptococcus sp. [ref_mOTU_v25_00283]	**S0881**	Clostridiales species incertae sedis [meta_mOTU_v25_13200]
S0204	Oscillibacter sp. [ref_mOTU_v25_03341]	**S0883**	Odoribacter splanchnicus [ref_mOTU_v25_03697]
S0207	Prevotella species incertae sedis [meta_mOTU_v25_12332]	**S0890**	Holdemanella biformis [meta_mOTU_v25_12329]
S0211	Clostridiales species incertae sedis [meta_mOTU_v25_12522]	**S0899**	Bacteria sp. [ref_mOTU_v25_00077]
S0214	Bifidobacterium adolescentis [ref_mOTU_v25_02703]	**S0907**	Bacteroides stercoris [ref_mOTU_v25_01579]
S0229	Clostridiales species incertae sedis [meta_mOTU_v25_12251]	**S0916**	Clostridiales species incertae sedis [meta_mOTU_v25_12476]
S0236	Enterobacteriaceae sp. [ref_mOTU_v25_00096]	**S0924**	Alistipes putredinis [ref_mOTU_v25_03683]
S0240	Eubacterium sp. CAG:38 [ref_mOTU_v25_07679]	**S0932**	Clostridiales species incertae sedis [meta_mOTU_v25_13187]
S0247	Ruminococcus sp. CAG:177 [meta_mOTU_v25_12400]	**S0939**	Haemophilus influenzae/parainfluenzae [ref_mOTU_v25_01068]
S0253	Holdemanella biformis [ref_mOTU_v25_11382]	**S0952**	Roseburia species incertae sedis [meta_mOTU_v25_12366]
S0255	Bacteroides caccae [ref_mOTU_v25_03473]	**S0959**	Bifidobacterium ruminantium [ref_mOTU_v25_02702]
S0257	Eubacterium sp. CAG:274 [meta_mOTU_v25_12688]	**S0967**	Blautia massiliensis [ref_mOTU_v25_03342]
S0262	Eubacterium ramulus [ref_mOTU_v25_03570]	**S0970**	Clostridiales species incertae sedis [meta_mOTU_v25_14166]
S0264	Alistipes finegoldii [ref_mOTU_v25_03682]	**S0971**	Clostridium species incertae sedis [meta_mOTU_v25_12350]

S0269	Flavonifractor plautii [ref_mOTU_v25_02971]	**S0972**	uncultured Flavonifractor sp. [ref_mOTU_v25_07315]
S0271	Acinetobacter sp. [ref_mOTU_v25_03673]	**S0973**	Flavonifractor plautii [ref_mOTU_v25_05238]
S0272	Firmicutes sp. [ref_mOTU_v25_03641]	**S0974**	Alistipes shahii [ref_mOTU_v25_01014]
S0274	Bacteroidales species incertae sedis [meta_mOTU_v25_13286]	**S0981**	Bacteroides faecis/thetaiotaomicron [ref_mOTU_v25_01657]
S0277	Butyricicoccus species incertae sedis [meta_mOTU_v25_12617]	**S0994**	Bacteroides salyersiae [ref_mOTU_v25_02140]
S0279	Bifidobacterium longum [ref_mOTU_v25_01099]	**S1006**	Bacteroides fragilis [ref_mOTU_v25_01598]
S0287	Ruminococcus lactaris [ref_mOTU_v25_01595]	**S1016**	Clostridiales species incertae sedis [meta_mOTU_v25_13390]
S0303	Clostridium sp. CAG:230 [ref_mOTU_v25_07616]	**S1018**	Clostridiales species incertae sedis [meta_mOTU_v25_12463]
S0305	Clostridiales species incertae sedis [meta_mOTU_v25_12631]	**S1019**	Clostridium sp. CAG:7 [ref_mOTU_v25_07647]
S0306	Blautia obeum [ref_mOTU_v25_05140]	**S1021**	Collinsella aerofaciens [ref_mOTU_v25_03626]
S0308	Clostridium sp. [ref_mOTU_v25_03622]	**S1023**	Sutterella wadsworthensis [ref_mOTU_v25_04772]
S0310	Burkholderiales species incertae sedis [meta_mOTU_v25_12785]	**S1034**	Eubacterium ventriosum [ref_mOTU_v25_11151]
S0321	Lachnospiraceae species incertae sedis [meta_mOTU_v25_12240]	**S1043**	Roseburia intestinalis [ref_mOTU_v25_03702]
S0327	Clostridium species incertae sedis [meta_mOTU_v25_12399]	**S1047**	Clostridium sp. CAG:138 [meta_mOTU_v25_12233]
S0344	Eubacterium sp. CAG:202 [meta_mOTU_v25_12308]	**S1052**	Prevotella sp. CAG:520 [ref_mOTU_v25_00718]
S0357	Roseburia hominis [ref_mOTU_v25_00861]	**S1053**	Alistipes ihumii [ref_mOTU_v25_07379]
S0363	Oscillibacter sp. [ref_mOTU_v25_04664]	**S1059**	Clostridiales species incertae sedis [meta_mOTU_v25_12411]
S0367	Clostridium sp. CAG:58 [ref_mOTU_v25_07640]	**S1065**	Clostridiales sp. [ref_mOTU_v25_03634]
S0389	Faecalibacterium species incertae sedis [meta_mOTU_v25_12303]	**S1066**	Clostridiales species incertae sedis [meta_mOTU_v25_12653]
S0400	Faecalibacterium species incertae sedis [meta_mOTU_v25_12325]	**S1067**	Bacteroides caecimuris [ref_mOTU_v25_03476]
S0401	Streptococcus parasanguinis [ref_mOTU_v25_00312]	**S1069**	Clostridiales species incertae sedis [meta_mOTU_v25_12554]
S0403	Clostridiales species incertae sedis [meta_mOTU_v25_12742]	**S1070**	Ruminococcaceae species incertae sedis [meta_mOTU_v25_12264]
S0406	Romboutsia timonensis [ref_mOTU_v25_09389]	**S1075**	Clostridiales species incertae sedis [meta_mOTU_v25_12635]
S0421	Ruminococcus callidus [ref_mOTU_v25_11153]	**S1078**	Bacteroidales species incertae sedis [meta_mOTU_v25_13098]
S0433	Coprococcus catus [ref_mOTU_v25_11851]	**S1082**	Clostridium sp. CAG:302 [meta_mOTU_v25_12499]
S0436	Clostridiales species incertae sedis [meta_mOTU_v25_13377]	**S1091**	Firmicutes species incertae sedis [meta_mOTU_v25_12231]
S0437	Eubacterium species incertae sedis [meta_mOTU_v25_12314]	**S1092**	Ruminococcus sp. CAG:254 [meta_mOTU_v25_12276]
S0440	Clostridiales species incertae sedis [meta_mOTU_v25_12473]	**S1102**	Clostridiales species incertae sedis [meta_mOTU_v25_14118]
S0448	Streptococcus sp. [ref_mOTU_v25_01350]	**S1114**	Fusobacterium mortiferum [ref_mOTU_v25_11278]
S0450	Clostridium sp. CAG:299 [ref_mOTU_v25_07619]	**S1122**	Firmicutes bacterium CAG:102 [ref_mOTU_v25_07726]
S0452	Faecalibacterium prausnitzii [ref_mOTU_v25_06110]	**S1123**	Parabacteroides merdae [ref_mOTU_v25_05401]
S0488	Parabacteroides distasonis [ref_mOTU_v25_03640]	**S1142**	Clostridiales species incertae sedis [meta_mOTU_v25_12309]
S0489	Alistipes obesi [ref_mOTU_v25_06695]	**S1145**	Firmicutes bacterium CAG:114 [ref_mOTU_v25_07728]
S0493	Clostridiales species incertae sedis [meta_mOTU_v25_12563]	**S1149**	Ruminococcus bromii [ref_mOTU_v25_00853]
S0512	[Clostridium] leptum [ref_mOTU_v25_03688]	**S1159**	Clostridiales sp. [ref_mOTU_v25_03658]
S0519	Anaerostipes hadrus [ref_mOTU_v25_00857]	**S1160**	Ruminococcus species incertae sedis [meta_mOTU_v25_12766]
S0520	Blautia obeum [ref_mOTU_v25_05139]	**S1161**	Bacteroides dorei/vulgatus [ref_mOTU_v25_02367]
S0526	Sutterella wadsworthensis [ref_mOTU_v25_03066]	**S1167**	Faecalibacterium species incertae sedis [meta_mOTU_v25_12403]
S0548	[Eubacterium] eligens [ref_mOTU_v25_02376]	**S1168**	Bacteroides intestinalis [ref_mOTU_v25_02809]
S0551	Allisonella histaminiformans [ref_mOTU_v25_10689]	**S1186**	Clostridium species incertae sedis [meta_mOTU_v25_12324]
S0562	Clostridiales species incertae sedis [meta_mOTU_v25_13227]	**S1187**	Clostridiales species incertae sedis [meta_mOTU_v25_12786]
S0572	Clostridium sp. [ref_mOTU_v25_03680]	**S1190**	Bacteroidales species incertae sedis [meta_mOTU_v25_12262]
S0578	Coprococcus sp. [ref_mOTU_v25_01683]	**S1191**	Clostridiales species incertae sedis [meta_mOTU_v25_12674]
S0585	Alistipes finegoldii/onderdonkii [ref_mOTU_v25_03069]	**S1193**	unclassified
S0588	Barnesiella intestinihominis [ref_mOTU_v25_03595]	**S1194**	Clostridiales sp. [ref_mOTU_v25_03605]
S0590	Dialister sp. CAG:357 [meta_mOTU_v25_12661]	**S1208**	Oscillibacter sp. 57_20 [meta_mOTU_v25_12610]
S0596	Eubacterium sp. [ref_mOTU_v25_03633]	**S1209**	Faecalibacterium sp. [ref_mOTU_v25_03636]
S0602	Blautia hansenii [ref_mOTU_v25_03670]	**S1215**	Coprococcus comes [ref_mOTU_v25_03690]
S0606	Clostridium species incertae sedis [meta_mOTU_v25_12762]	**S1225**	[Eubacterium] eligens [ref_mOTU_v25_02375]

S0610	Clostridium species incertae sedis [meta_mOTU_v25_12640]	**S1227**	Dorea formicigenerans [ref_mOTU_v25_03668]
S0615	Bacteroides eggerthii [ref_mOTU_v25_01577]	**S1232**	Clostridiales species incertae sedis [meta_mOTU_v25_12556]
S0622	Ruminococcaceae species incertae sedis [meta_mOTU_v25_12286]	**S1243**	Ruthenibacterium lactatiformans [ref_mOTU_v25_04716]
S0653	Enterobacterales sp. [ref_mOTU_v25_00085]	**S1248**	Clostridiales species incertae sedis [meta_mOTU_v25_12437]
S0657	[Eubacterium] rectale [ref_mOTU_v25_03657]	**S1257**	Clostridiales species incertae sedis [meta_mOTU_v25_12284]
S0663	Clostridiales species incertae sedis [meta_mOTU_v25_12776]	**S1259**	bacterium LF-3 [ref_mOTU_v25_03628]
S0677	Clostridiales species incertae sedis [meta_mOTU_v25_13012]	**S1264**	Anaerostipes hadrus [ref_mOTU_v25_00856]
S0679	Bacteroides sp. [ref_mOTU_v25_03475]	**S1265**	Phascolarctobacterium succinatutens [ref_mOTU_v25_03700]
S0681	Faecalibacterium prausnitzii [ref_mOTU_v25_06112]	**S1267**	Eubacterium species incertae sedis [meta_mOTU_v25_12260]
S0684	Bacteroides rodentium/uniformis [ref_mOTU_v25_00855]	**S1276**	Ruminococcus sp. [ref_mOTU_v25_03681]
S0698	Clostridiales species incertae sedis [meta_mOTU_v25_13863]	**S1277**	Oscillibacter species incertae sedis [meta_mOTU_v25_12353]
S0699	Prevotella copri [ref_mOTU_v25_03701]	**S1287**	Bacteroides sp. [ref_mOTU_v25_02810]
S0703	Bilophila wadsworthia [ref_mOTU_v25_04300]	**S1289**	[Ruminococcus] torques [ref_mOTU_v25_03660]
S0709	Bifidobacterium bifidum [ref_mOTU_v25_03116]	**S1293**	Firmicutes species incertae sedis [meta_mOTU_v25_12744]
S0710	Parasutterella excrementihominis [ref_mOTU_v25_03674]	**S1294**	Megamonas funiformis/rupellensis [ref_mOTU_v25_02318]
S0711	Clostridium species incertae sedis [meta_mOTU_v25_12234]		

Table S2. The important score of the 28 microbial species and functions used in the Random Forest model.

ID	Name	Importance	Mean for those with ocean-going syndrome	mean for the 'symptomless' group
K17076	Environmental Information Processing; Membrane transport; ABC transporters; lysY; putative lysine transport system ATP-binding protein	0.0102	7.71E-05	1.43E-04
K17074	Environmental Information Processing; Membrane transport; ABC transporters; lysX2; putative lysine transport system permease protein	0.0100	8.06E-05	1.48E-04
K17073	Environmental Information Processing; Membrane transport; ABC transporters; lysX1; putative lysine transport system substrate-binding protein	0.0117	7.16E-05	1.35E-04
K11928	Brite Hierarchies; Protein families: signaling and cellular processes; Transporters; putP; sodium/proline symporter	0.0104	3.50E-04	4.39E-04
K10118	Environmental Information Processing; Membrane transport; ABC transporters; msmF; raffinose/stachyose/melibiose transport system permease protein	0.0095	8.21E-04	1.11E-03
K09815	Environmental Information Processing; Membrane transport; ABC transporters; znuA; zinc transport system substrate-binding protein	0.0104	2.02E-04	2.65E-04
K07727	Brite Hierarchies; Protein families: genetic information processing; Transcription factors; putative transcriptional regulator	0.0044	4.69E-04	5.05E-04
K07080	Not Included in Pathway or Brite; Poorly characterized; Function unknown; uncharacterized protein	0.0192	1.40E-04	2.09E-04
K06379	Not Included in Pathway or Brite; Unclassified: metabolism; Enzymes with EC numbers; spoIIAB; stage II sporulation protein AB (anti-sigma F factor)	0.0157	4.52E-04	5.42E-04
K06188	Brite Hierarchies; Protein families: signaling and cellular processes; Transporters; aqpZ; aquaporin Z	0.0027	7.33E-05	5.51E-05
K04023	Not Included in Pathway or Brite; Unclassified: metabolism; Amino acid metabolism; eutH; ethanolamine transporter	0.0057	4.73E-05	1.87E-05
K03496	Brite Hierarchies; Protein families: genetic information processing; Chromosome and associated proteins; parA, soj; chromosome partitioning protein	0.0060	2.76E-03	3.11E-03
K03466	Brite Hierarchies; Protein families: genetic information processing; Chromosome and associated proteins; ftsK, spoIIIE; DNA segregation ATPase FtsK/SpoIIIE, S-DNA-T family	0.0149	2.39E-04	3.63E-04
K03458	Not Included in Pathway or Brite; Unclassified: signaling and cellular processes; Transport; TC.NCS2; nucleobase:cation symporter-2, NCS2 family	0.0061	1.30E-04	1.85E-04
K02662	Brite Hierarchies; Protein families: signaling and cellular processes; Secretion system; pilM; type IV pilus assembly protein PilM	0.0061	8.92E-05	1.29E-04
K02408	Cellular Processes; Cell motility; Flagellar assembly; fliE; flagellar hook-basal body complex protein FliE	0.0046	1.96E-04	2.42E-04
K01787	Metabolism; Carbohydrate metabolism; Amino sugar and nucleotide sugar metabolism; RENBP; N-acylglucosamine 2-epimerase	0.0023	1.43E-04	1.93E-04
K01775	Metabolism; Metabolism of other amino acids; D-Alanine metabolism; alr; alanine racemase	0.0062	4.99E-04	5.50E-04
K01278	Organismal Systems; Digestive system; Protein digestion and absorption; DPP4, CD26; dipeptidyl-peptidase 4	0.0006	1.61E-05	2.35E-05
K01182	Metabolism; Carbohydrate metabolism; Galactose metabolism; IMA, malL; oligo-1,6-glucosidase	0.0060	3.74E-04	3.84E-04
K00865	Metabolism; Carbohydrate metabolism; Glyoxylate and dicarboxylate metabolism; glxK, garK; glycerate 2-kinase	0.0037	5.23E-04	4.79E-04
K00806	Metabolism; Glycan biosynthesis and metabolism; Peptidoglycan biosynthesis; uppS; undecaprenyl diphosphate synthase	0.0152	6.21E-04	7.59E-04
K00171	Metabolism; Carbohydrate metabolism; Glycolysis / Gluconeogenesis; porD; pyruvate ferredoxin oxidoreductase delta subunit	0.0047	3.15E-05	2.72E-05
Eubacterium sp. CAG 192	*Eubacterium sp. CAG 192*	0.0016	0.00E+00	5.33E-06
uncultured Blautia sp.	*uncultured Blautia sp.*	0.0025	3.96E-05	1.74E-05
Eubacterium ventriosum	*Eubacterium ventriosum*	0.0059	1.35E-03	7.88E-04
Actinomyces viscosus oris	*Actinomyces viscosus oris*	0.0050	2.64E-06	1.53E-05

Table S3. Definitions of the 24 indicators in the questionnaire.

Indicator	**Definition**
Body mass index (BMI)	The BMI is defined as the body mass divided by the square of the body height (1).
Backache	Back pain, also known as backache, is pain felt in the back (2).
Headache	It is usually confined to the upper part of the head, including the upper edge of the eyebrow arch, the helix and the pain above the line connecting the external occipital protuberance (3).
Stomachache	Stomach pain refers to the pain in the epigastric part of the upper abdomen, above the connection line between the lower edges of ribs on both sides and near the heart socket under the xiphoid process (4).
Pectoralgia	Pectoralgia is a subjective feeling, feeling chest pain, severe pain, dull pain, stuffy pain or oppressive feeling (5).
Muscular soreness	Pain or tenderness in one or more muscles which can involve any area of the body.
Dyspnea	Dyspnea is a combination of subjective feeling and objective signs. Subjectively, breathing is laborious, objectively, the number of breaths increases, the movement is fast and the range increases (6).
Palpitation	Palpitation includes palpitation and palpitation, which is a kind of uncomfortable feeling or palpitation of conscious heart beating (7).
Insomnia	Insomnia is medically defined as being unable to fall asleep or remain asleep, resulting in insufficient sleep (8).
Shallow sleep	Difficulty in falling asleep, decreased sleep quality and sleep time.
Over-eating	Overeating means taking a huge amount of food in a very short time (9).
Nausea	Nausea is a kind of gastric discomfort that can cause vomiting impulse (10).
Inactivity	People's mental and physical abilities are not as good as before, and will feel tired when they engage in daily activities (11).
Poor appetite	Lack of appetite or lack the desire to eat (12).
Feelings of loneliness	Loneliness is an unpleasant emotional response to perceived isolation (13).
Depression	Depression (mood), a state of low mood and aversion to activity (14).
Self-accusation	Self-accusation is a cognitive process in which an individual attributes the occurrence of a stressful event to oneself (15).
Mistrustfulness	Mistrustfulness is an individual's distrust of other people's words, promises and statements (16).
Stool type	Type 1: Separate hard lumps (like nuts), or sausage-shaped (but lumpy); Type 2: Like a sausage but with cracks on its surface (can be black);Type 3: Like a sausage or snake, smooth and soft (average stool) Type 4: Soft blobs with clear cut edges; Type 5: A mushy stool or watery (diarrhoea) (17).
Bloody stools	The color of the stool is bright red, dark red or tar like (black stool) (18).
Incomplete defecation	This term is a feeling of incomplete defecation. When defecating, even if the intestinal contents have been emptied, they still want to be discharged.
Bowel difficulties	The defecation was laborious, painful and prolonged.
Bowel movement	Want to defecate but can't row out, or squat down for a long time to row out (19).
Defecation frequency (weekly)	Frequency of defecation per week. The normal frequency of bowel movements in adults is between three per day and three per week (20).

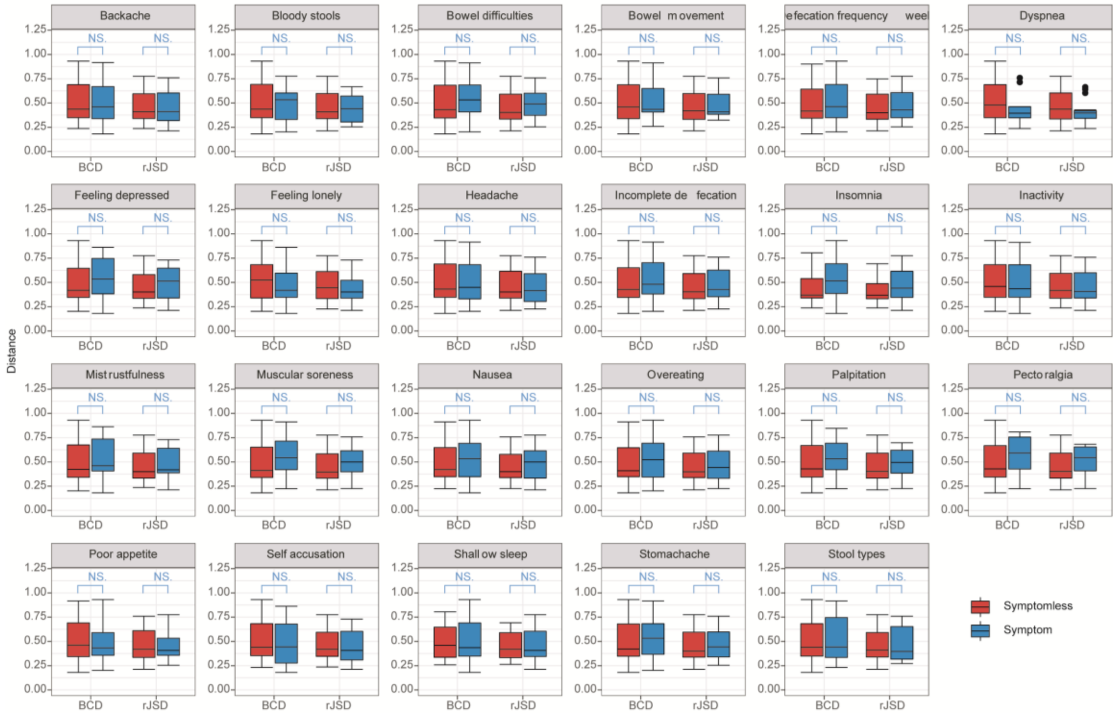
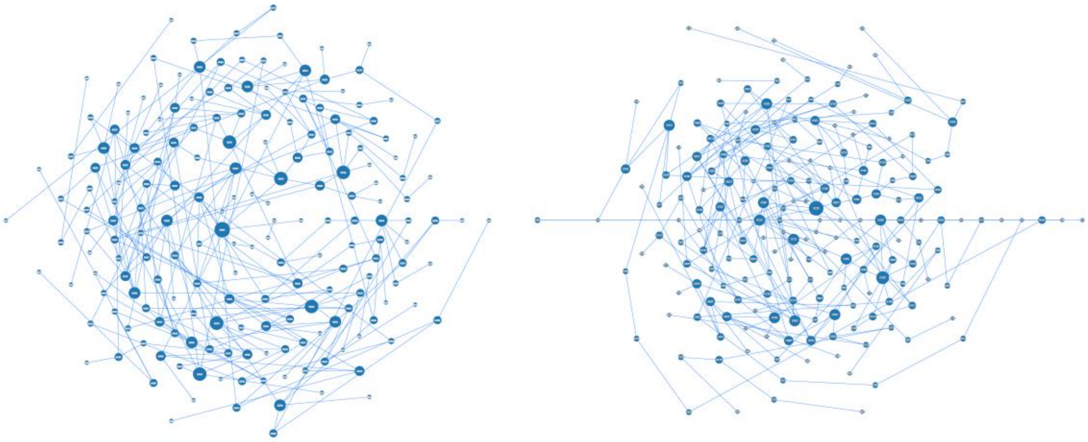
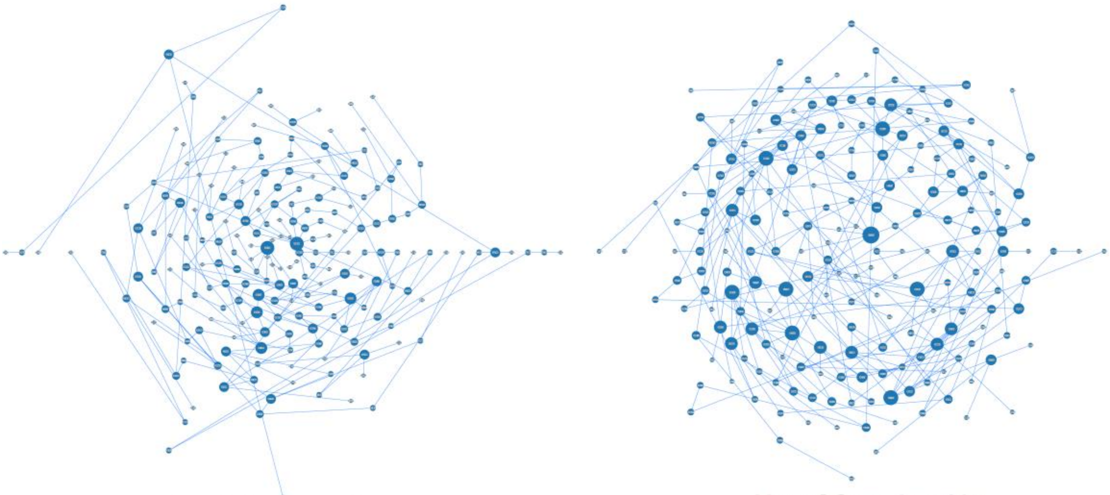


Figure S1. Comparison of individual perturbations in the gut microbiome between 'symptomless' and 'symptom' crew members for 24 indicators (symptoms). Individual perturbations (n=77) in the gut microbiome measured by BCD and rJSD were first grouped according to whether they were 'symptomless' or 'symptom' for each individual health indicator (symptom), and then compared with each other using Wilcoxon rank-sum Test.



SS at day 1

SS at day 135



Non-SS at day 1

Non-SS at day 135

Figure S2. Co-occurrence networks of SS and non-SS at beginning (day 1) and end (day 135) of the voyage. Four co-occurrence networks of SS and non-SS at the beginning (day 1) and end (day 135) of the voyage are separately illustrated, which are based on SparCC correlation inference algorithms. The nodes in the network refer to the identified species with the size of the nodes indicating their relative abundance; The edges between nodes represent correlations between the nodes they connect.

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