

Supporting information to

***Bifidobacterium animalis* subsp. *lactis* Bbm-19 ameliorates insomnia by remodeling the gut microbiota and restoring γ -aminobutyric acid and serotonin signaling**

Supplementary Tables

Supplementary Table 1. Taxonomic classification of species-level genome bins (SGBs) identified in the mouse gut microbiota

SGB	Kingdom	Phylum	Class	Order	Family	Genus	Species
SGB 57	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>Lachnospiraceae bacterium</i>
SGB 190	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Lawsonibacter</i>	<i>Lawsonibacter sp. 949840775</i>
SGB 201	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Pumilibacteraceae</i>	<i>Anaerocaecibacter</i>	<i>Anaerocaecibacter muris</i>
SGB 107	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Acutalibacteraceae</i>	<i>Acutalibacter</i>	<i>Acutalibacter muris</i>
SGB 199	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Pelethomonas</i>	<i>Pelethomonas sp. 022797115</i>
SGB 120	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Ruminococcaceae</i>	<i>CAG-115</i>	<i>CAG-115 sp. 910587465</i>
SGB 155	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Petalouisia</i>	<i>Petalouisia sp. 947565885</i>
SGB 79	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Suilimivivens</i>	<i>Suilimivivens sp. 949878435</i>
SGB 24	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>UBA7173</i>	<i>UBA7173 sp. 001689485</i>
SGB 103	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Roseburia_B</i>	<i>Roseburia_B sp. 910586725</i>
SGB 179	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>UBA3700</i>	<i>RACS-045</i>	<i>RACS-045 sp. 910588015</i>
SGB 104	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Butyribacter</i>	<i>Butyribacter sp. 910586605</i>
SGB 19	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Suilimivivens</i>	<i>Suilimivivens sp. 009774465</i>
SGB 43	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>COE1</i>	<i>COE1 sp. 000403215</i>
SGB 111	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Dysosmobacter</i>	<i>Dysosmobacter sp. 949959305</i>
SGB 94	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Eubacterium_J</i>	<i>Eubacterium_J sp. 910584345</i>
SGB 186	Bacteria	Cyanobacteriota	Vampirovibrionia	Gastranaerophilales	<i>Gastranaerophilaceae</i>	<i>Zag111</i>	<i>Zag111 sp. 950022695</i>
SGB 206	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Ruminococcaceae</i>	<i>RGIG8773</i>	<i>RGIG8773 sp. 910584715</i>
SGB 191	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Marinifilaceae</i>	<i>Odoribacter</i>	<i>Odoribacter sp. 910578105</i>
SGB 37	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Petalouisia</i>	<i>Petalouisia sp. 910576385</i>
SGB 102	Bacteria	Bacillota_A	Clostridia	TANB77	<i>CAG-508</i>	<i>Scatovivens</i>	<i>Scatovivens sp. 948443845</i>
SGB 140	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>COE1</i>	<i>COE1 sp. 009774375</i>
SGB 71	Bacteria	Bacillota_I	Bacilli_A	Erysipelotrichales	<i>Erysipelotrichaceae</i>	<i>Faecalibaculum</i>	<i>Faecalibaculum rodentium</i>
SGB 6	Bacteria	Deferribacterota	Deferribacteres	Deferribacterales	<i>Mucispirillaceae</i>	<i>Mucisp. irillum</i>	<i>Mucispirillum schaedleri</i>

SGB 160	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	MD308	<i>MD308 sp. 910579335</i>
SGB 100	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	W0P33-017	<i>W0P33-017 sp. 910589045</i>
SGB 121	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	CAG-303	<i>CAG-303 sp. 910585215</i>
SGB 53	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Gallimonas</i>	<i>Gallimonas sp. 910586985</i>
SGB 218	Bacteria	Bacillota_A	Clostridia	TANB77	CAG-508	CAG-269	<i>CAG-269 sp. 947087745</i>
SGB 217	Bacteria	Bacillota_A	Clostridia	Christensenellales	UBA1242	<i>Caccovivens</i>	<i>Caccovivens sp. 910584295</i>
SGB 39	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma sp. 910586035</i>
SGB 195	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	COE1	<i>COE1 sp. 947175775</i>
SGB 7	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Acetatifactor</i>	<i>Acetatifactor sp. 910583845</i>
SGB 174	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	UBA3282	<i>UBA3282 sp. 910578475</i>
SGB 158	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Butyribacter</i>	<i>Butyribacter sp. 910588655</i>
SGB 214	Bacteria	Pseudomonadota	Gammaproteobacteria	Burkholderiales	<i>Burkholderiaceae</i>	<i>Parasutterella</i>	<i>Parasutterella excrementihominis</i>
SGB 146	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Sp. orofaciens</i>	<i>Sp. orofaciens sp. 009774295</i>
SGB 3	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Rikenellaceae</i>	<i>Alistipes</i>	<i>Alistipes sp. 003979135</i>
SGB 4	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	UBA3263	<i>UBA3263 sp. 001689615</i>
SGB 22	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Bacteroidaceae</i>	<i>Bacteroides</i>	<i>Bacteroides acidifaciens</i>
SGB 128	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Hominiventricola</i>	<i>Hominiventricola sp. 009774145</i>
SGB 145	Bacteria	Bacillota	Bacilli	MOL361	<i>Turicibacteraceae</i>	<i>Turicibacter</i>	<i>Turicibacter sp. 002311155</i>
SGB 62	Bacteria	Bacillota	Bacilli	Lactobacillales	<i>Lactobacillaceae</i>	<i>Limosilactobacillus</i>	<i>Limosilactobacillus reuteri_G</i>
SGB 17	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	CAG-873	<i>CAG-873 sp. 011959565</i>
SGB 115	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Petaloulisia</i>	<i>Petaloulisia sp. 000403315</i>
SGB 86	Bacteria	Pseudomonadota	Gammaproteobacteria	Burkholderiales	<i>Burkholderiaceae</i>	<i>Parasutterella</i>	<i>Parasutterella muris</i>
SGB 18	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Duncaniella</i>	<i>Duncaniella freteri</i>
SGB 161	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Pelethomonas</i>	<i>Pelethomonas sp. 022800665</i>
SGB 168	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma sp. 910586065</i>
SGB 12	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Rikenellaceae</i>	<i>Alistipes</i>	<i>Alistipes muris</i>

SGB 34	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>CAG-873</i>	<i>CAG-873 sp. 910587235</i>
SGB 183	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Lepagella</i>	<i>Lepagella sp. 002361215</i>
SGB 77	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>CAG-303</i>	<i>CAG-303 sp. 910584685</i>
SGB 137	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>CAG-873</i>	<i>CAG-873 sp. 009775265</i>
SGB 142	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Lepagella</i>	<i>Lepagella sp. 003979075</i>
SGB 46	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>UBA3282 sp. 003611805</i>
SGB 143	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma sp. 910577555</i>
SGB 194	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>UBA7173</i>	<i>UBA7173 sp. 002491305</i>
SGB 154	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Roseburia_B</i>	<i>Roseburia_B sp. 910585825</i>
SGB 8	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Muribaculum</i>	<i>Muribaculum gordoncarteri</i>
SGB 189	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>UBA3700</i>	<i>MGBC161649</i>	<i>MGBC161649 sp. 910587685</i>
SGB 63	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Suilimivivens</i>	<i>Suilimivivens sp. 000403495</i>
SGB 119	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Petalouisia</i>	<i>Petalouisia sp. 910588845</i>
SGB 40	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>UBA3282 sp. 009774575</i>
SGB 141	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>CAG-314</i>	<i>Fimimonas</i>	<i>Fimimonas sp. 910586905</i>
SGB 197	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Butyricicoccaceae</i>	<i>QXXE01</i>	<i>QXXE01 sp. 009911355</i>
SGB 164	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Dysosmobacter</i>	<i>Dysosmobacter sp. 947245315</i>
SGB 220	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>RGIG8607</i>	<i>RGIG8607 sp. 910588535</i>
SGB 5	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Duncaniella</i>	<i>Duncaniella sp. 910589485</i>
SGB 210	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Acutalibacteraceae</i>	<i>Acutalibacter</i>	<i>Acutalibacter sp. 910587995</i>
SGB 109	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma sp. 910587005</i>
SGB 25	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Amulumruptor</i>	<i>Amulumruptor sp. 900539915</i>
SGB 132	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Eubacterium_J</i>	<i>Eubacterium_J sp. 910574915</i>
SGB 147	Bacteria	Bacillota_A	Clostridia	TANB77	<i>CAG-508</i>	<i>UMGS1994</i>	<i>UMGS1994 sp. 948465565</i>
SGB 106	Bacteria	Desulfobacterota	Desulfovibrionia	Desulfovibrionales	<i>Desulfovibrionaceae</i>	<i>Bilophila</i>	<i>Bilophila sp. 910585945</i>
SGB 117	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Acetatifactor</i>	<i>Acetatifactor sp. 910579755</i>

SGB 130	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	UBA3402	<i>Lachnospiraceae</i> UBA3402 sp. 910588505
SGB 175	Bacteria	Bacillota_I	Bacilli_A	RF39	UBA660	<i>Scybalousia</i>	<i>Scybalousia</i> sp. 002493865
SGB 181	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	UBA3282	UBA3282 sp. 910587095
SGB 33	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma</i> sp. 910583855
SGB 176	Bacteria	Cyanobacteriota	Vampirovibrionia	Gastranaerophilales	<i>Gastranaerophilaceae</i>	Zag111	Zag111 sp. 947570135
SGB 112	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Eubacterium_F</i>	<i>Eubacterium_F</i> sp. 910585745
SGB 38	Bacteria	Patescibacteria	Saccharimonadia	Saccharimonadales	<i>Nanosyncoccaceae</i>	<i>Nanosyncoccus</i>	<i>Nanosyncoccus</i> sp. 947570505
SGB 50	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Eubacterium_F</i>	<i>Eubacterium_F</i> sp. 910584645
SGB 162	Bacteria	Bacillota_A	Clostridia	TANB77	CAG-508	CAG-269	CAG-269 sp. 947648905
SGB 69	Bacteria	Bacillota_A	Clostridia	Christensenellales	UBA3700	RACS-045	RACS-045 sp. 947246685
SGB 173	Bacteria	Actinomycetota	Coriobacteriia	Coriobacteriales	<i>Atopobiaceae</i>	<i>Granulimonas</i>	<i>Granulimonas faecalis</i>
SGB 184	Bacteria	Cyanobacteriota	Vampirovibrionia	Gastranaerophilales	<i>Gastranaerophilaceae</i>	<i>Stercorousia</i>	<i>Stercorousia</i> sp. 910588555
SGB 48	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	MGBC143606	MGBC143606 sp. 910587935
SGB 127	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	UBA3282	UBA3282 sp. 910588215
SGB 208	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Suilimivivens</i>	<i>Suilimivivens</i> sp. 910577275
SGB 177	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Rikenellaceae</i>	<i>Alistipes</i>	<i>Alistipes</i> sp. 948442615
SGB 87	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma</i> sp. 910583545
SGB 30	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Paramuribaculum</i>	<i>Paramuribaculum intestinale</i>
SGB 149	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	UBA3282	UBA3282 sp. 009774585
SGB 28	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Duncaniella</i>	<i>Duncaniella muris</i>
SGB 166	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	UBA3282	UBA3282 sp. 910586705
SGB 61	Bacteria	Bacillota_I	Bacilli_A	Erysipelotrichales	<i>Erysipelotrichaceae</i>	<i>Dubosiella</i>	<i>Dubosiella muris</i>
SGB 182	Bacteria	Pseudomonadota	Alphaproteobacteria	RF32	CAG-239	CAG-267	CAG-267 sp. 910580155
SGB 156	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	UBA3402	UBA3402 sp. 002358555
SGB 23	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	COE1	COE1 sp. 009774245
SGB 203	Bacteria	Bacillota_A	Clostridia	TANB77	CAG-508	<i>Scatovivens</i>	<i>Scatovivens</i> sp. 948517135

SGB 110	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>UBA3700</i>	<i>RACS-045</i>	<i>RACS-045 sp. 910584635</i>
SGB 171	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>CAG-303</i>	<i>CAG-303 sp. 910577835</i>
SGB 172	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Petalouisia</i>	<i>Petalouisia sp. 910586005</i>
SGB 205	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Acutalibacteraceae</i>	<i>Fimenecus</i>	<i>Fimenecus sp. 900540295</i>
SGB 105	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Eubacterium_F</i>	<i>Eubacterium_F sp. 910583555</i>
SGB 193	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>MGBC114844</i>	<i>MGBC114844 sp. 910585255</i>
SGB 116	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>COE1</i>	<i>COE1 sp. 910585765</i>
SGB 74	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma sp. 947053655</i>
SGB 204	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>UBA3282 sp. 910578645</i>
SGB 60	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Duncaniella</i>	<i>Duncaniella sp. 910576785</i>
SGB 139	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Acetatifactor</i>	<i>Acetatifactor sp. 910577235</i>
SGB 11	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Muribaculum</i>	<i>Muribaculum arabinoxylanisolvens</i>
SGB 76	Bacteria	Bacillota_I	Bacilli_A	Acholeplasmatales	<i>Anaeroplasmataceae</i>	<i>Pelethenecus</i>	<i>Pelethenecus sp. 910579215</i>
SGB 15	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>CAG-873</i>	<i>CAG-873 sp. 910586455</i>
SGB 65	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>COE1</i>	<i>COE1 sp. 003513705</i>
SGB 56	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Enterenecus</i>	<i>Enterenecus sp. 947564255</i>
SGB 211	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Roseburia_B</i>	<i>Roseburia_B sp. 947647505</i>
SGB 169	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Ruminococcaceae</i>	<i>Porcipelethomonas</i>	<i>Porcipelethomonas sp. 910588145</i>
SGB 135	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Eubacterium_F</i>	<i>Eubacterium_F sp. 910589595</i>
SGB 136	Bacteria	Actinomycetota	Actinomycetes	Actinomycetales	<i>Bifidobacteriaceae</i>	<i>Bifidobacterium</i>	<i>Bifidobacterium animalis</i>
SGB 82	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Eubacterium_J</i>	<i>Eubacterium_J sp. 910577225</i>
SGB 202	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>COE1</i>	<i>COE1 sp. 910588595</i>
SGB 91	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Lepagella</i>	<i>Lepagella muris_A</i>
SGB 207	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>CAG-632</i>	<i>CAG-632 sp. 910587045</i>
SGB 118	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Enterenecus</i>	<i>Enterenecus sp. 910585265</i>
SGB 64	Bacteria	Pseudomonadota	Alphaproteobacteria	Rs-D84	<i>Rs-D84</i>	<i>Enterousia</i>	<i>Enterousia sp. 013316395</i>

SGB 26	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>UBA7173</i>	<i>UBA7173 sp. 013316675</i>
SGB 96	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Pelethomonas</i>	<i>Pelethomonas sp. 910578505</i>
SGB 47	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Kineothrix</i>	<i>Kineothrix sp. 910587275</i>
SGB 9	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>CAG-873</i>	<i>CAG-873 sp. 009775535</i>
SGB 36	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Kineothrix</i>	<i>Kineothrix sp. 000403275</i>
SGB 133	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Sp. orofaciens</i>	<i>Sporofaciens sp. 910574715</i>
SGB 51	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Acetatifactor</i>	<i>Acetatifactor sp. 910578815</i>
SGB 81	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Enterenecus</i>	<i>Enterenecus sp. 910577525</i>
SGB 89	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>RGIG4057</i>	<i>RGIG4057 sp. 947053345</i>
SGB 125	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>UBA3282 sp. 910584965</i>
SGB 92	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma sp. 910587825</i>
SGB 209	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>CAG-510</i>	<i>CAG-510 sp. 910577015</i>
SGB 180	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Acetatifactor</i>	<i>Acetatifactor sp. 910577035</i>
SGB 90	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma sp. 910585705</i>
SGB 138	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>CAG-314</i>	<i>Fimimonas</i>	<i>Fimimonas sp. 910586625</i>
SGB 1	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Duncaniella</i>	<i>Duncaniella muricolitica</i>
SGB 35	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>UBA3282 sp. 009774215</i>
SGB 151	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Enterenecus</i>	<i>Enterenecus sp. 910579155</i>
SGB 73	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>CAG-510</i>	<i>CAG-510 sp. 003979355</i>
SGB 13	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Muribaculum</i>	<i>Muribaculum intestinale</i>
SGB 101	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>RGIG8607</i>	<i>RGIG8607 sp. 910577045</i>
SGB 200	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Hominiventricola</i>	<i>Hominiventricola sp. 910587765</i>
SGB 219	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>COE1</i>	<i>COE1 sp. 009774395</i>
SGB 122	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Sp. orofaciens</i>	<i>Sporofaciens sp. 910587575</i>
SGB 68	Bacteria	Pseudomonadota	Alphaproteobacteria	Rs-D84	<i>Rs-D84</i>	<i>Enterousia</i>	<i>Enterousia sp. 949082785</i>
SGB 20	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Lepagella</i>	<i>Lepagella muris</i>

SGB 29	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>CAG-873</i>	<i>CAG-873 sp. 001689665</i>
SGB 52	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Bacteroidaceae</i>	<i>Prevotella</i>	<i>Prevotella rodentium</i>
SGB 78	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>UBA3282 sp. 910585555</i>
SGB 150	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma sp. 013316055</i>
SGB 123	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	<i>Akkermansiaceae</i>	<i>Akkermansia</i>	<i>Akkermansia muciniphila</i>
SGB 54	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Ruminococcaceae</i>	<i>RGIG8773</i>	<i>RGIG8773 sp. 910584715</i>
SGB 163	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Petalouisia</i>	<i>Petalouisia sp. 910587895</i>
SGB 58	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Butyribacter</i>	<i>Butyribacter sp. 009774235</i>
SGB 159	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Acutalibacteraceae</i>	<i>Acutalibacter</i>	<i>Acutalibacter sp. 910584745</i>
SGB 129	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>VSOB01</i>	<i>VSOB01 sp. 910585345</i>
SGB 198	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Eubacterium_J</i>	<i>Eubacterium_J sp. 009774535</i>
SGB 42	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>RGIG4057</i>	<i>RGIG4057 sp. 910577675</i>
SGB 99	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>UBA3282 sp. 910579395</i>
SGB 213	Bacteria	Bacillota_A	Clostridia	TANB77	<i>CAG-508</i>	<i>Scatovivens</i>	<i>Scatovivens sp. 947385375</i>
SGB 187	Bacteria	Actinomycetota	Actinomycetes	Actinomycetales	<i>Bifidobacteriaceae</i>	<i>Bifidobacterium</i>	<i>Bifidobacterium globosum</i>
SGB 170	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Sp. orofaciens</i>	<i>Sporofaciens sp. 910585725</i>
SGB 44	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Bacteroidaceae</i>	<i>Bacteroides</i>	<i>Bacteroides muris</i>
SGB 72	Bacteria	Patescibacteria	Saccharimonadia	Saccharimonadales	<i>Nanosyncoccaceae</i>	<i>Nanosyncoccus</i>	<i>Nanosyncoccus sp. 013316435</i>
SGB 93	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Acetatifactor</i>	<i>Acetatifactor sp. 947385725</i>
SGB 10	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>bacterium</i>	<i>Muribaculaceae bacterium</i>
SGB 85	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Acetatifactor</i>	<i>Acetatifactor sp. 910585015</i>
SGB 27	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>CAG-873</i>	<i>CAG-873 sp. 002490635</i>
SGB 157	Bacteria	Patescibacteria	Saccharimonadia	Saccharimonadales	<i>Nanosyncoccaceae</i>	<i>Nanosyncoccus</i>	<i>Nanosyncoccus sp. 947364965</i>
SGB 16	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>CAG-873</i>	<i>CAG-873 sp. 009775195</i>
SGB 84	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Pelethomonas</i>	<i>Pelethomonas sp. 910584045</i>
SGB 114	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>MD308</i>	<i>MD308 sp. 010206225</i>

SGB 126	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>COE1</i>	<i>COE1</i> sp. 009774345
SGB 98	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>UBA3282</i> sp. 910575775
SGB 59	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Bacteroidaceae</i>	<i>Alloprevotella</i>	<i>Alloprevotella</i> sp. 002933955
SGB 196	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>COE1</i>	<i>COE1</i> sp. 949066965
SGB 88	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Eubacterium_G</i>	<i>Eubacterium_G</i> sp. 948560485
SGB 67	Bacteria	Pseudomonadota	Alphaproteobacteria	RF32	<i>CAG-239</i>	<i>Scatocola</i>	<i>Scatocola</i> sp. 910577205
SGB 95	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Butyribacter</i>	<i>Butyribacter</i> sp. 003611745
SGB 32	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Rikenellaceae</i>	<i>Alistipes</i>	<i>Alistipes</i> sp. 009774895
SGB 80	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Pelethomonas</i>	<i>Pelethomonas</i> sp. 014237695
SGB 41	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Muribaculum</i>	<i>Muribaculum faecis</i>
SGB 178	Bacteria	Bacillota_A	Clostridia	TANB77	<i>CAG-508</i>	<i>Scatovivens</i>	<i>Scatovivens</i> sp. 948678575
SGB 75	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Hominiventricola</i>	<i>Hominiventricola</i> sp. 009774155
SGB 192	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Bacteroidaceae</i>	<i>Bacteroides</i>	<i>Bacteroides caecimuris</i>
SGB 131	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3402</i>	<i>UBA3402</i> sp. 910579515
SGB 97	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Oscillospiraceae</i>	<i>Pelethomonas</i>	<i>Pelethomonas</i> sp. 022800525
SGB 108	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>UBA3282</i> sp. 009774175
SGB 212	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>MGBC114844</i>	<i>MGBC114844</i> sp. 910579865
SGB 167	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Ruminococcaceae</i>	<i>RGIG8773</i>	<i>RGIG8773</i> sp. 910586535
SGB 2	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Duncaniella</i>	<i>Duncaniella</i> sp. 021768245
SGB 31	Bacteria	Bacillota	Bacilli	Lactobacillales	<i>Lactobacillaceae</i>	<i>Ligilactobacillus</i>	<i>Ligilactobacillus murinus</i>
SGB 165	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>UBA3700</i>	<i>MGBC100798</i>	<i>MGBC100798</i> sp. 910584975
SGB 113	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Muribaculaceae</i>	<i>Lepagella</i>	<i>Lepagella</i> sp. 002361155
SGB 66	Bacteria	Bacillota_A	Clostridia	TANB77	<i>CAG-508</i>	<i>RGIG8482</i>	<i>RGIG8482</i> sp. 949948835
SGB 152	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Petaloulisia</i>	<i>Petaloulisia</i> sp. 910580195
SGB 45	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>UBA3282</i>	<i>UBA3282</i> sp. 937910785
SGB 14	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Rikenellaceae</i>	<i>Alistipes</i>	<i>Alistipes</i> sp. 002362235

SGB 134	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>C-53</i>	<i>C-53 sp. 003612525</i>
SGB 215	Bacteria	Bacillota_I	Bacilli_A	RF39	<i>UBA660</i>	<i>UMGS995</i>	<i>UMGS995 sp. 910586635</i>
SGB 144	Bacteria	Bacillota_A	Clostridia	Oscillospirales	<i>Acutalibacteraceae</i>	<i>Eubacterium_R</i>	<i>Eubacterium_R sp. 011958665</i>
SGB 185	Bacteria	Bacillota_A	Clostridia	TANB77	<i>CAG-508</i>	<i>UMGS1994</i>	<i>UMGS1994 sp. 947368535</i>
SGB 216	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Gallimonas</i>	<i>Gallimonas sp. 910585595</i>
SGB 49	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Suilimivivens</i>	<i>Suilimivivens sp. 910587295</i>
SGB 55	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>Lachnoclostridium_B</i>	<i>Lachnoclostridium_B sp. 910584265</i>
SGB 21	Bacteria	Bacillota	Bacilli	Lactobacillales	<i>Lactobacillaceae</i>	<i>Lactobacillus</i>	<i>Lactobacillus sp. 910589675</i>
SGB 153	Bacteria	Bacillota_A	Clostridia	Lachnospirales	<i>Lachnospiraceae</i>	<i>COE1</i>	<i>COE1 sp. 014239155</i>
SGB 124	Bacteria	Bacillota_A	Clostridia	Christensenellales	<i>Borkfalkiaceae</i>	<i>Coproplasma</i>	<i>Coproplasma sp. 910579585</i>
SGB 148	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	<i>Tannerellaceae</i>	<i>Parabacteroides</i>	<i>Parabacteroides sp. 902493135</i>

Supplementary Table 2. Differentially abundant species-level genome bins (SGBs) between the healthy control (HEL) and insomnia model (INS) groups at day 14

SGB	Mean relative abundance ± SD (%)		<i>P</i> -value, Wilcoxon rank-sum test	Species assignment
	HEL group	INS group		
SGB 11	9.29 ± 4.98	3.71 ± 3.06	0.00	<i>Muribaculum arabinosylans</i>
SGB 114	0.19 ± 0.09	0.68 ± 0.74	0.03	<i>MD308 sp. 010206225</i>
SGB 116	0.20 ± 0.16	1.48 ± 1.49	0.01	<i>COE1 sp. 910585765</i>
SGB 117	0.09 ± 0.05	0.37 ± 0.62	0.02	<i>Acetatifactor sp. 910579755</i>
SGB 120	0.13 ± 0.10	0.68 ± 0.45	0.00	<i>CAG-115 sp. 910587465</i>
SGB 124	0.17 ± 0.41	0.25 ± 0.19	0.01	<i>Copropasma sp. 910579585</i>
SGB 126	0.17 ± 0.17	0.54 ± 0.35	0.00	<i>COE1 sp. 009774345</i>
SGB 137	0.86 ± 0.27	1.18 ± 0.46	0.02	<i>CAG-873 sp. 009775265</i>
SGB 14	2.74 ± 0.98	3.80 ± 1.25	0.02	<i>Alistipes sp. 002362235</i>
SGB 140	0.17 ± 0.22	0.50 ± 0.65	0.02	<i>COE1 sp. 009774375</i>
SGB 142	1.34 ± 0.34	1.72 ± 0.49	0.05	<i>Lepagella sp. 003979075</i>
SGB 144	0.16 ± 0.24	0.25 ± 0.21	0.04	<i>Eubacterium_R sp. 011958665</i>
SGB 16	3.01 ± 2.18	1.27 ± 0.76	0.03	<i>CAG-873 sp. 009775195</i>
SGB 165	0.46 ± 0.37	0.78 ± 0.34	0.04	<i>MGB100798 sp. 910584975</i>
SGB 183	0.25 ± 0.03	0.20 ± 0.04	0.01	<i>Lepagella sp. 002361215</i>
SGB 196	0.10 ± 0.05	0.25 ± 0.25	0.03	<i>COE1 sp. 949066965</i>
SGB 201	0.16 ± 0.21	0.29 ± 0.22	0.02	<i>Anaerocacibacter muris</i>
SGB 202	0.12 ± 0.06	0.29 ± 0.21	0.02	<i>COE1 sp. 910588595</i>
SGB 208	0.55 ± 0.35	0.34 ± 0.41	0.01	<i>Suilmivivens sp. 910577275</i>
SGB 214	0.16 ± 0.09	0.09 ± 0.08	0.05	<i>Parasutterella excrementihominis</i>
SGB 26	7.47 ± 3.88	3.51 ± 2.16	0.01	<i>UBA7173 sp. 013316675</i>
SGB 38	1.73 ± 1.95	2.08 ± 0.87	0.04	<i>Nanosyncoccus sp. 947570505</i>
SGB 79	0.92 ± 0.82	0.32 ± 0.26	0.02	<i>Suilmivivens sp. 949878435</i>
SGB 8	31.7 ± 4.59	18.67 ± 9.56	0.00	<i>Muribaculum gordoncarteri</i>
SGB 88	0.41 ± 0.45	4.00 ± 4.32	0.01	<i>Eubacterium_G sp. 948560485</i>
SGB 91	1.81 ± 0.36	2.61 ± 0.75	0.01	<i>Lepagella muris_A</i>
SGB 93	0.28 ± 0.24	0.73 ± 0.84	0.05	<i>Acetatifactor sp. 947385725</i>
SGB 94	0.12 ± 0.06	0.60 ± 0.85	0.00	<i>Eubacterium_J sp. 910584345</i>

Supplementary Table 3. Differentially abundant species-level genome bins (SGBs) between the insomnia model (INS) and probiotic treatment (Bb) groups at day 14

SGB	Mean relative abundance ± SD (%)		<i>P</i> -value, Wilcoxon rank-sum test	Species assignment
	INS group	Bb group		
SGB 57	0.24 ± 0.18	1.65 ± 1.73	0.00	<i>UBA3282 sp. 947243845</i>
SGB 19	0.31 ± 0.22	2.10 ± 3.16	0.00	<i>Suilmivivens sp. 009774465</i>
SGB 37	0.76 ± 2.06	0.28 ± 0.13	0.04	<i>Petralousia sp. 910576385</i>
SGB 160	0.18 ± 0.15	0.70 ± 0.63	0.02	<i>MD308 sp. 910579335</i>
SGB 146	0.34 ± 0.32	1.18 ± 0.90	0.01	<i>Sp. orofaciens sp. 009774295</i>

SGB 161	0.56 ± 0.63	0.78 ± 0.74	0.04	<i>Pelethomonas sp.</i> 022800665
SGB 46	0.54 ± 0.52	0.72 ± 0.58	0.05	<i>UBA3282 sp.</i> 003611805
SGB 194	0.38 ± 0.09	0.28 ± 0.06	0.01	<i>UBA7173 sp.</i> 002491305
SGB 164	0.64 ± 0.60	1.13 ± 0.72	0.00	<i>Dysosmobacter</i> sp. 947245315
SGB 210	0.28 ± 0.29	0.56 ± 0.48	0.01	<i>Acutalibacter sp.</i> 910587995
SGB 127	0.83 ± 1.15	1.57 ± 1.59	0.04	<i>UBA3282 sp.</i> 910588215
SGB 208	0.34 ± 0.41	0.48 ± 0.18	0.01	<i>Suilimivivens sp.</i> 910577275
SGB 149	0.16 ± 0.14	1.04 ± 2.87	0.02	<i>UBA3282 sp.</i> 009774585
SGB 166	0.22 ± 0.25	0.47 ± 0.60	0.04	<i>UBA3282 sp.</i> 910586705
SGB 23	0.69 ± 0.69	3.18 ± 2.97	0.02	<i>COE1 sp.</i> 009774245
SGB 205	0.13 ± 0.11	0.20 ± 0.20	0.04	<i>Fimenecus sp.</i> 900540295
SGB 204	0.29 ± 0.21	0.80 ± 0.59	0.00	<i>UBA3282 sp.</i> 910578645
SGB 211	0.12 ± 0.13	0.18 ± 0.18	0.04	<i>Roseburia_B sp.</i> 947647505
SGB 136	0.03 ± 0.03	7.11 ± 23.83	0.00	<i>Bifidobacterium animalis</i>
SGB 92	0.48 ± 0.55	1.03 ± 0.89	0.01	<i>Coproplasma sp.</i> 910587825
SGB 209	0.25 ± 0.18	0.29 ± 0.12	0.04	<i>CAG-510 sp.</i> 910577015
SGB 180	0.15 ± 0.16	0.19 ± 0.13	0.04	<i>Acetatifactor sp.</i> 910577035
SGB 138	0.07 ± 0.09	0.96 ± 1.87	0.01	<i>Fimimonas sp.</i> 910586625
SGB 1	5.68 ± 2.06	3.58 ± 2.11	0.03	<i>Duncaniella muricolitica</i>
SGB 35	0.79 ± 0.49	2.37 ± 1.72	0.04	<i>UBA3282 sp.</i> 009774215
SGB 73	0.13 ± 0.13	0.33 ± 0.33	0.01	<i>CAG-510 sp.</i> 003979355
SGB 20	39.20 ± 15.78	20.26 ± 12.13	0.01	<i>Lepagella muris</i>
SGB 129	0.30 ± 0.40	1.10 ± 2.15	0.03	<i>VSOB01 sp.</i> 910585345
SGB 42	0.58 ± 0.72	1.55 ± 2.36	0.04	<i>RGIG4057 sp.</i> 910577675
SGB 170	0.22 ± 0.17	0.38 ± 0.15	0.00	<i>Sporofaciens sp.</i> 910585725
SGB 32	7.79 ± 2.69	5.87 ± 2.40	0.05	<i>Alistipes sp.</i> 009774895
SGB 80	1.76 ± 1.63	2.40 ± 1.12	0.05	<i>Pelethomonas sp.</i> 014237695
SGB 131	0.25 ± 0.41	0.55 ± 0.86	0.05	<i>UBA3402 sp.</i> 910579515
SGB 108	0.49 ± 0.89	0.56 ± 0.44	0.03	<i>UBA3282 sp.</i> 009774175

Supplementary Table 4. Differentially abundant species-level genome bins (SGBs) between the healthy control (HEL) and insomnia model (INS) groups at day 42

SGB	Mean relative abundance ± SD (%)		<i>P</i> -value, Wilcoxon rank-sum test	Species assignment
	HEL group	INS group		
SGB 120	0.35 ± 0.49	0.68 ± 0.60	0.03	<i>CAG-115 sp.</i> 910587465
SGB 24	26.76 ± 8.96	11.54 ± 11.15	0.01	<i>UBA7173 sp.</i> 001689485
SGB 104	0.35 ± 0.15	0.80 ± 0.67	0.05	<i>Butyribacter sp.</i> 910586605
SGB 206	0.31 ± 0.45	0.07 ± 0.05	0.02	<i>RGIG8773 sp.</i> 910584715
SGB 191	0.10 ± 0.03	0.80 ± 0.97	0.00	<i>Odoribacter sp.</i> 910578105
SGB 17	13.11 ± 3.75	7.83 ± 3.73	0.01	<i>CAG-873 sp.</i> 011959565
SGB 86	0.85 ± 0.65	0.16 ± 0.10	0.00	<i>Parasutterella muris</i>
SGB 168	0.38 ± 0.45	1.37 ± 1.24	0.00	<i>Coproplasma sp.</i> 910586065

SGB 183	0.91 ± 1.28	1.98 ± 1.13	0.01	<i>Lepagella</i> sp. 002361215
SGB 184	0.83 ± 0.65	0.29 ± 0.21	0.04	<i>Stercorousia</i> sp. 910588555
SGB 60	4.02 ± 3.86	1.10 ± 2.32	0.01	<i>Duncaniella</i> sp. 910576785
SGB 11	12.74 ± 4.74	8.02 ± 9.73	0.02	<i>Muribaculum</i> <i>arabinoxylanisolvens</i>
SGB 76	2.76 ± 1.41	1.89 ± 3.40	0.04	<i>Pelethenecus</i> sp. 910579215
SGB 211	0.14 ± 0.12	0.34 ± 0.44	0.03	<i>Roseburia_B</i> sp. 947647505
SGB 207	0.55 ± 0.52	0.17 ± 0.20	0.01	<i>CAG-632</i> sp. 910587045
SGB 64	2.36 ± 2.63	0.60 ± 0.90	0.03	<i>Enterousia</i> sp. 013316395
SGB 13	6.29 ± 1.46	3.69 ± 2.02	0.00	<i>Muribaculum intestinale</i>
SGB 68	6.10 ± 4.04	3.37 ± 3.34	0.02	<i>Enterousia</i> sp. 949082785
SGB 29	2.62 ± 1.63	8.90 ± 7.12	0.01	<i>CAG-873</i> sp. 001689665
SGB 16	2.87 ± 1.79	1.24 ± 1.05	0.02	<i>CAG-873</i> sp. 009775195
SGB 196	0.15 ± 0.07	0.75 ± 1.62	0.01	<i>COE1</i> sp. 949066965
SGB 67	1.23 ± 0.89	0.58 ± 0.47	0.03	<i>Scatocola</i> sp. 910577205
SGB 113	2.06 ± 0.47	1.35 ± 0.55	0.01	<i>Lepagella</i> sp. 002361155
SGB 216	0.09 ± 0.04	0.15 ± 0.10	0.05	<i>Gallimonas</i> sp. 910585595
SGB 21	1.54 ± 2.03	0.43 ± 0.80	0.04	<i>Lactobacillus</i> sp. 910589675
SGB 124	0.12 ± 0.10	0.30 ± 0.28	0.03	<i>Coproplasma</i> sp. 910579585
SGB 110	1.15 ± 0.99	0.50 ± 0.01	0.04	<i>JAFLTL01</i> sp. 910578395
SGB 10	0.22 ± 0.2	0.08 ± 0.06	0.05	<i>Muribaculaceae bacterium</i>
SGB 44	2.66 ± 1.44	2.26 ± 1.09	0.05	<i>Bacteroides muris</i>

Supplementary Table 5. Differentially abundant species-level genome bins (SGBs) between the insomnia model (INS) and probiotic treatment (Bb) groups at day 42

SGB	Mean relative abundance ± SD (%)		P-value, Wilcoxon rank-sum test	Species assignment
	INS group	Bb group		
SGB 57	0.99 ± 2.10	2.57 ± 2.40	0.05	<i>UBA3282</i> sp. 947243845
SGB 191	0.80 ± 0.97	0.12 ± 0.06	0.01	<i>Odoribacter</i> sp. 910578105
SGB 7	3.36 ± 5.67	0.99 ± 2.32	0.03	<i>Acetatifactor</i> sp. 910583845
SGB 86	0.16 ± 0.10	0.38 ± 0.28	0.01	<i>Parasutterella muris</i>
SGB 168	1.37 ± 1.24	0.77 ± 0.78	0.03	<i>Coproplasma</i> sp. 910586065
SGB 33	0.86 ± 0.62	1.99 ± 1.24	0.01	<i>Coproplasma</i> sp. 910583855
SGB 176	1.47 ± 1.76	0.48 ± 0.77	0.04	<i>Zag111</i> sp. 947570135
SGB 69	0.68 ± 1.15	1.78 ± 1.93	0.03	<i>RACS-045</i> sp. 947246685
SGB 184	0.29 ± 0.21	0.58 ± 0.35	0.01	<i>Stercorousia</i> sp. 910588555
SGB 87	1.53 ± 1.61	0.64 ± 0.44	0.04	<i>Coproplasma</i> sp. 910583545
SGB 30	10.71 ± 5.25	6.47 ± 4.20	0.02	<i>Paramuribaculum intestinale</i>
SGB 23	2.48 ± 2.95	0.88 ± 1.12	0.03	<i>COE1</i> sp. 009774245
SGB 136	0.09 ± 0.06	2.09 ± 2.48	0.00	<i>Bifidobacterium animalis</i>
SGB 207	0.17 ± 0.20	1.28 ± 1.83	0.01	<i>CAG-632</i> sp. 910587045
SGB 159	0.29 ± 0.20	0.17 ± 0.12	0.04	<i>Acutalibacter</i> sp. 910584745
SGB 129	1.19 ± 1.78	0.27 ± 0.26	0.02	<i>VSOB01</i> sp. 910585345

SGB 44	2.27 ± 1.10	4.07 ± 1.59	0.00	<i>Bacteroides muris</i>
SGB 124	0.30 ± 0.28	0.12 ± 0.09	0.02	<i>Coproplasma sp. 910579585</i>
SGB 10	0.08 ± 0.06	0.19 ± 0.17	0.03	<i>Muribaculaceae bacterium</i>

Supplementary Table 6. Differentially represented gut-brain modules (GBMs) across experimental groups at day 14

Comparison	GBM ID	Associated metabolic pathway	<i>P</i> -value, Wilcoxon rank-sum test
HEL vs INS	GBM005	Tryptophan synthesis	0.03
	GBM030	Polysaccharide A	0.04
	GBM031	17β-Estradiol degradation	0.01
	GBM038	Inositol degradation	0.01
	GBM047	Acetate degradation	0.01
INS vs Bb	GBM003	Melatonin synthesis	0.01
	GBM015	<i>p</i> -Cresol synthesis	0.08
	GBM019	GABA degradation	0.04
	GBM051	Glutamate degradation II	0.03
	GBM052	Butyrate synthesis I	0.04
	GBM058	Secondary bile acid biosynthesis I	0.13
HEL vs Bb	GBM003	Melatonin synthesis	0.00
	GBM019	GABA degradation	0.02
	GBM027	Nitric oxide degradation I (NO dioxygenase)	0.01
	GBM031	17β-Estradiol degradation	0.00
	GBM037	Inositol synthesis	0.04
	GBM051	Glutamate degradation II	0.02
	GBM052	Butyrate synthesis I	0.06
	GBM053	Butyrate synthesis II	0.02
	GBM058	Secondary bile acid biosynthesis I	0.00
INS vs LXP	GBM059	Secondary bile acid biosynthesis II	0.01
	GBM054	Propionate synthesis II	0.02
Bb vs Bb + LXP	GBM031	17β-Estradiol degradation	0.00
	GBM037	Inositol synthesis	0.02
	GBM058	Secondary bile acid biosynthesis I	0.02
Bb vs LXP	GBM031	17β-Estradiol degradation	0.01
	GBM052	Butyrate synthesis I	0.02
	GBM058	Secondary bile acid biosynthesis I	0.02
Bb + LXP vs LXP	GBM028	Nitric oxide degradation II (NO reductase)	0.00
	GBM049	Tryptophan degradation	0.01
	GBM051	Glutamate degradation II	0.02
	GBM052	Butyrate synthesis I	0.01
	GBM003	Melatonin synthesis	0.04

Remark: HEL, Healthy control group; INS, Insomnia model group; Bb, Probiotic treatment group; LXP, Lorazepam treatment group; Bb + LXP, Combination treatment group

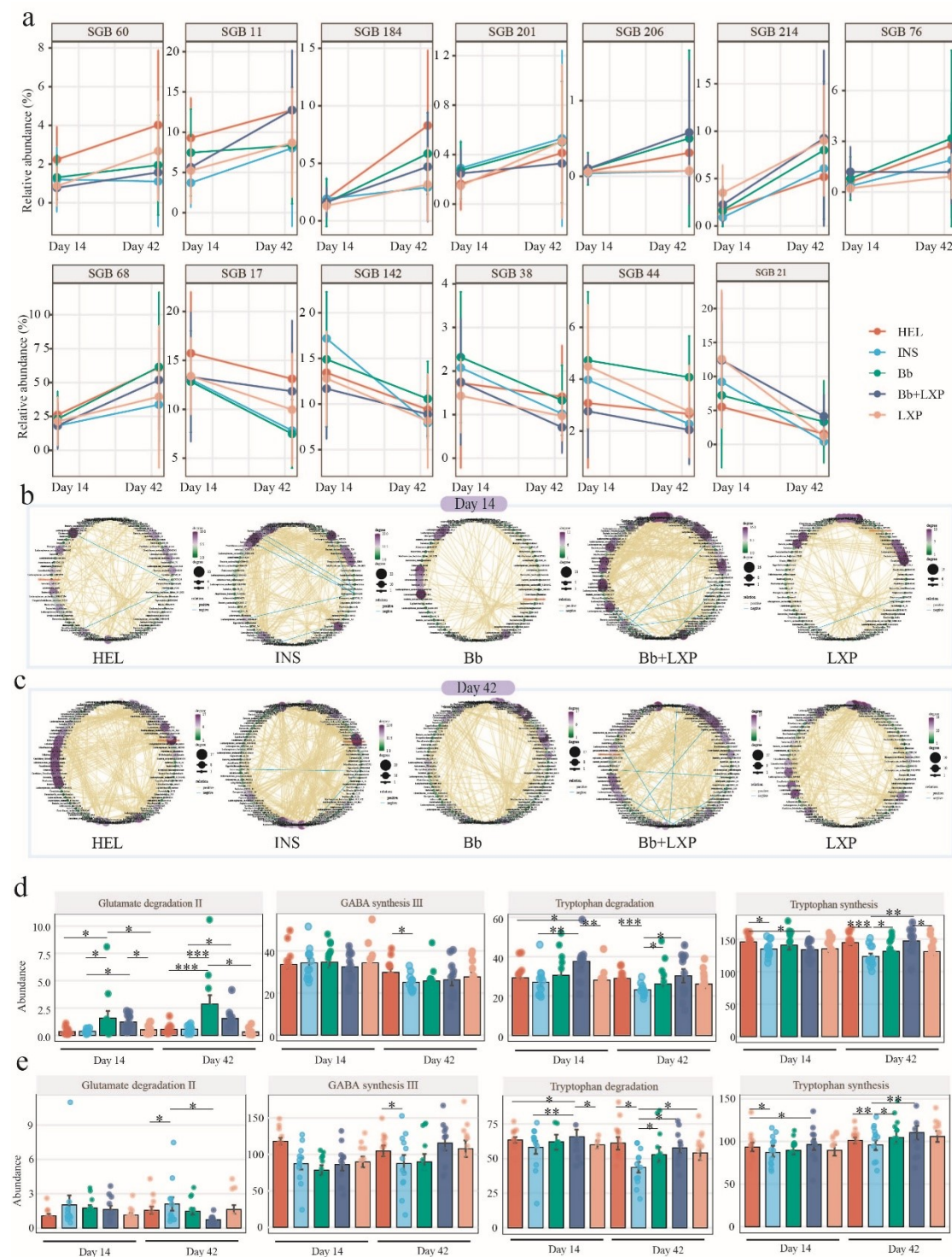
Supplementary Table 7. Differentially represented gut-brain modules (GBMs) across experimental groups at day 42

Comparison	GBM ID	Associated metabolic pathway	<i>P</i> value, Wilcoxon rank-sum test
HEL vs INS	GBM005	Tryptophan synthesis	0.00
	GBM007	Glutamate synthesis II	0.02
	GBM022	GABA synthesis III	0.04
	GBM027	Nitric oxide degradation I (NO dioxygenase)	0.00
	GBM029	ATP-dependent chaperone protein (ClpB)	0.00
	GBM032	Quinolinic acid synthesis	0.01
	GBM033	Quinolinic acid degradation	0.02
	GBM036	S-Adenosylmethionine synthesis	0.02
	GBM040	Menaquinone synthesis (vitamin K2) I	0.02
	GBM042	Polyunsaturated fatty acids synthesis (arachidonic acid, eicosapentaenoic acid, docosahexaenoic acid)	0.00
	GBM049	Tryptophan degradation	0.00
	GBM055	Propionate synthesis III	0.01
	GBM057	Corrinoid-dependent enzymes	0.03
	GBM058	Secondary bile acid biosynthesis I	0.01
	GBM003	Melatonin synthesis	0.03
	GBM017	Indole-3-propionic acid synthesis pathway	0.05
HEL vs Bb	GBM027	Nitric oxide degradation I (NO dioxygenase)	0.01
	GBM029	ATP-dependent chaperone protein (ClpB)	0.01
Bb	GBM032	Quinolinic acid synthesis	0.03
	GBM033	Quinolinic acid degradation	0.05
	GBM051	Glutamate degradation II	0.00
	GBM055	Propionate synthesis III	0.04
INS vs Bb	GBM051	Glutamate degradation II	0.00
INS vs Bb	GBM049	Tryptophan degradation	0.05
	GBM017	Indole-3-propionic acid synthesis pathway	0.04
INS vs LXP	GBM051	Glutamate degradation II	0.03
LXP	GBM036	S-Adenosylmethionine synthesis	0.02
	GBM054	Propionate synthesis II	0.03
Bb vs	GBM057	Corrinoid-dependent enzymes	0.04
	GBM011	Cortisol degradation	0.01
	GBM017	Indole-3-propionic acid synthesis pathway	0.00

Bb + LXP	GBM029	ATP-dependent chaperone protein (ClpB)	0.03
	GBM035	Isovaleric acid synthesis II (KADC pathway)	0.04
	GBM038	Inositol degradation	0.00
	GBM039	γ -Hydroxybutyric acid degradation	0.01
		Polyunsaturated fatty acids synthesis (arachidonic acid, eicosapentaenoic acid, docosahexaenoic acid)	
	GBM042		0.02
	GBM047	Acetate degradation	0.01
	GBM053	Butyrate synthesis II	0.00
	GBM054	Propionate synthesis II	0.04
Bb	GBM017	Indole-3-propionic acid synthesis pathway	0.00
vs	GBM051	Glutamate degradation II	0.00
LXP	GBM054	Propionate synthesis II	0.05
	GBM028	Nitric oxide degradation II (NO reductase)	0.04
	GBM035	Isovaleric acid synthesis II (KADC pathway)	0.05
	GBM038	Inositol degradation	0.00
Bb + LXP	GBM039	γ -Hydroxybutyric acid degradation	0.02
vs	GBM047	Acetate degradation	0.01
LXP	GBM051	Glutamate degradation II	0.00
	GBM053	Butyrate synthesis II	0.02
	GBM005	Tryptophan synthesis	0.05

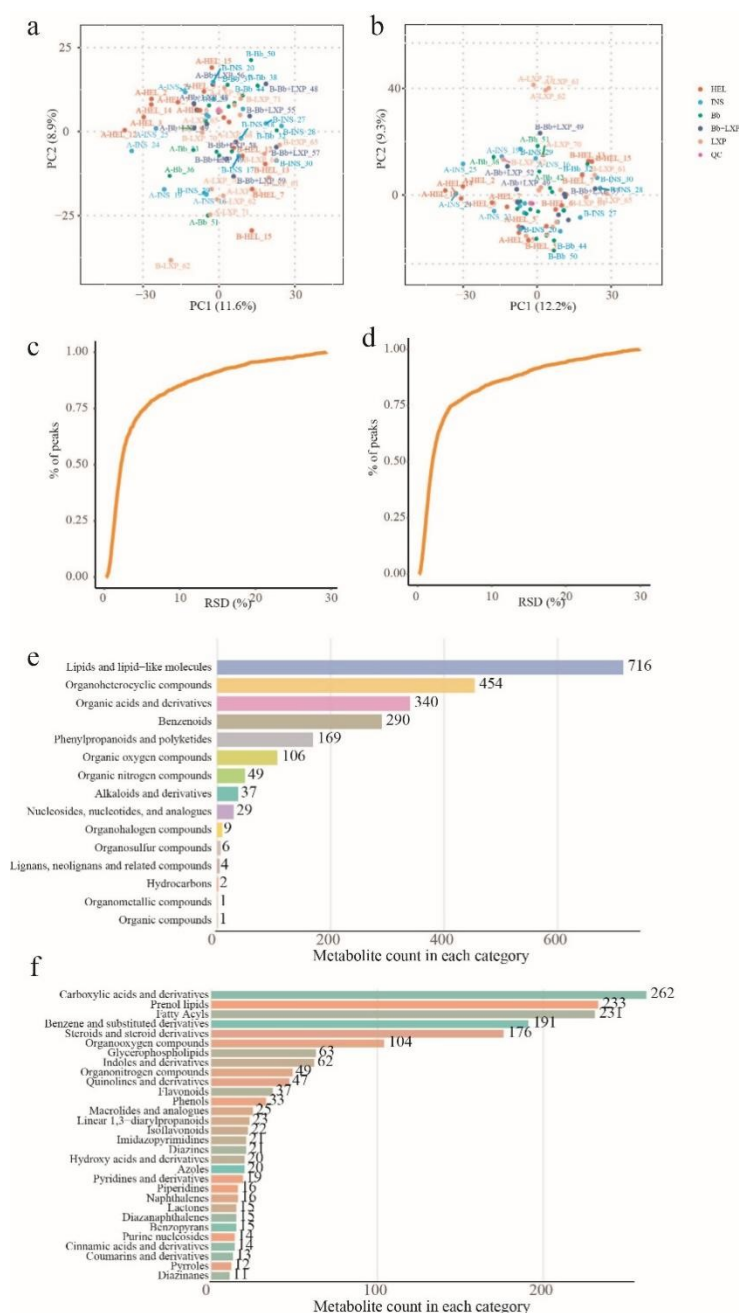
Remark: HEL, Healthy control group; INS, Insomnia model group; Bb, Probiotic treatment group; LXP, Lorazepam treatment group; Bb + LXP, Combination treatment group

Supplementary Figures



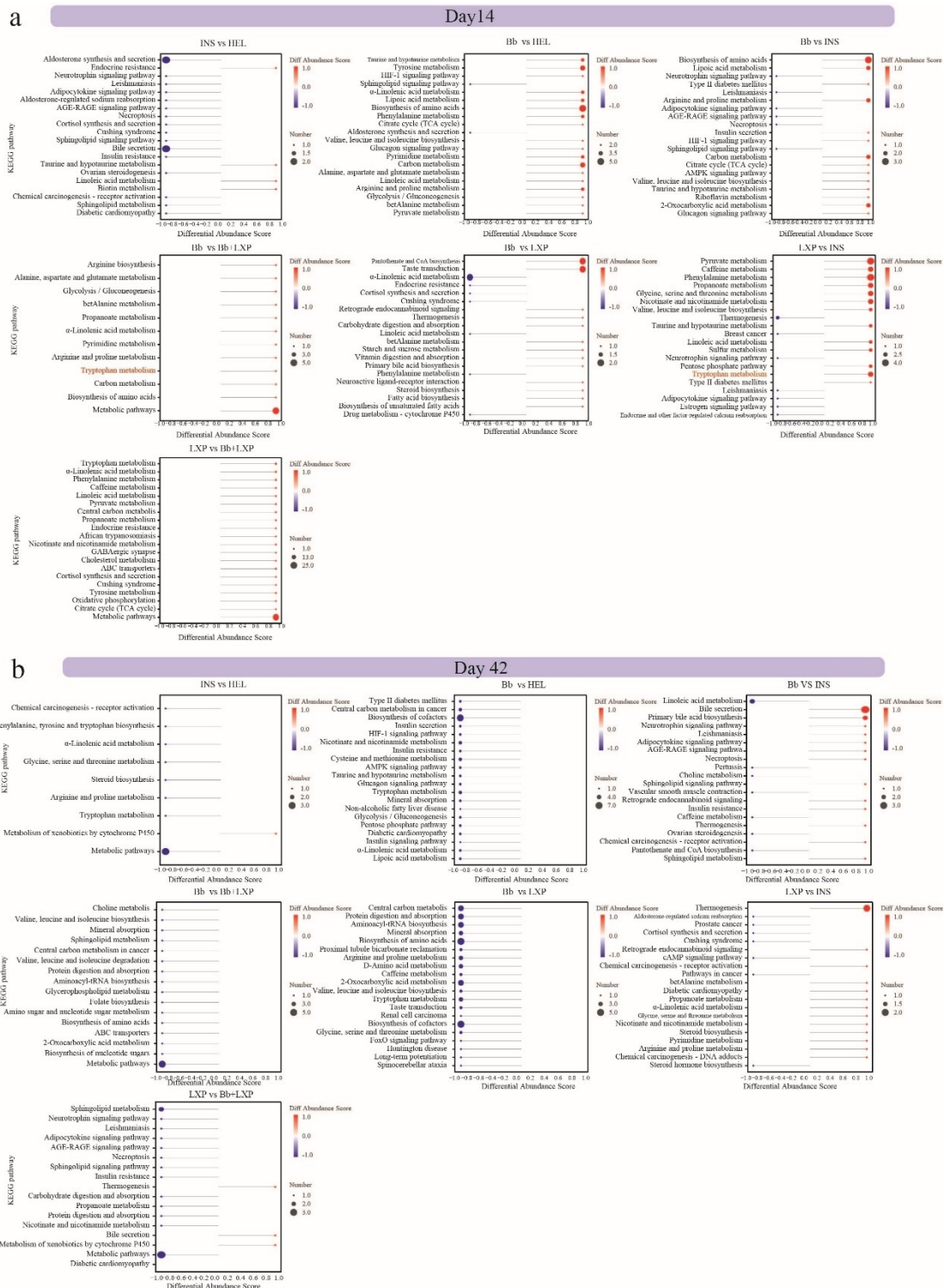
Supplementary Figure 1. Dynamics of species-level genome bin (SGB) abundance, microbial co-occurrence networks, and gut-brain modules over time. Mice were assigned to five experimental groups: healthy control (HEL), insomnia model (INS), probiotic treatment (Bb), lorazepam treatment (LXP), and combination treatment (Bb + LXP). (a) Temporal changes in the relative abundance of selected SGBs across experimental groups from day 14 to day 42. (b, c) Microbial co-occurrence network

plots based on Spearman correlation ($|r| > 0.8$, $P < 0.01$) within each group at (b) day 14 and (c) day 42. Nodes represent SGBs; edges represent significant correlations. Node size reflects number of edges. Beige lines denote positive correlations; blue lines denote negative correlations. (d, e) Abundances of (d) gut-brain modules associated with key neuroactive pathways: glutamate degradation II, GABA synthesis III, tryptophan degradation, and tryptophan synthesis and (e) SGBs encoding enzymes in these pathways. Their abundances are expressed in reads per kilobase per million mapped reads (RPKM). Error bars represent SD. Statistical significance was determined by Wilcoxon rank-sum test. * $P < 0.05$, ** $P < 0.01$.



Supplementary Figure 2. Quality control and classification of fecal metabolomics data. Mice were assigned to five experimental groups: healthy control (HEL), insomnia

model (INS), probiotic treatment (Bb), lorazepam treatment (LXP), and combination treatment (Bb + LXP). (a, b) Principal component analysis score plots showing the distribution of fecal metabolite samples of day 42 in (a) positive and (b) negative ionization modes. QC represents quality control samples. (c, d) Reproducibility assessment of metabolite peak intensities in (c) positive and (d) negative modes, with curves depicting the percentage of metabolite features meeting defined relative standard deviation (RSD) thresholds. (e, f) Classification of detected metabolites by (e) chemical superclass and (f) class, based on annotations from the Human Metabolome Database (HMDB; <http://www.hmdb.ca>), METLIN (<http://metlin.scripps.edu>), Massbank (<http://www.massbank.jp/>), and mzCloud (<https://www.mzcloud.org>).



Supplementary Figure 3. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of differentially abundant fecal metabolites. Mice were assigned to five experimental groups: healthy control (HEL), insomnia model (INS), probiotic treatment (Bb), lorazepam treatment (LXP), and combination treatment (Bb + LXP). Pathway enrichment was performed for pairwise comparisons at (a) day 14 and (b) day 42. Comparison pairs include: INS vs. HEL, Bb vs. HEL, Bb vs. INS, LXP vs. INS, Bb vs. LXP, Bb vs. Bb+LXP, and LXP vs. Bb+LXP.