Supplementary Figures

Figure S1. Testing of gut microbiota alpha-diversity across studies of MDD, BD and SZ. α -diversity metrics performed across comparison groups (N=39) by type of metric (i.e., composite index, richness, phylogenetic diversity, evenness) and disorder (MDD, BD, SZ). A purple square indicates lower α -diversity; orange indicates higher α -diversity; grey indicates no reported difference in α -diversity; and white indicates where a metric was not measured. MDD, major depressive disorder; BD, bipolar disorder; SZ, schizophrenia; ACE, abundance-based coverage estimator; TOS, total observed species; SOBS, number of observed species; ICE, incidence-based coverage estimator; MGS, whole-genome metagenomic sequencing; PD, phylogenetic diversity. ** Against the study name denotes MGS, all others used 16S.

Figure S2. Testing of gut microbiota beta-diversity across studies of MDD, BD and SZ. β -diversity metrics performed across comparison groups (N=34) by disorder (MDD, BD, SZ), indicated by a circle. A blue circle indicates a difference in β -diversity between groups, yellow indicates no difference in β -diversity between groups; and white reflects studies that only used β -diversity data to inform visual ordination plots rather than statistical analyses. MDD, major depressive disorder; BD, bipolar disorder; SZ, schizophrenia; ACE, abundance-based coverage estimator; TOS, total observed species; SOBS, number of observed species; ICE, incidence-based coverage estimator; MGS, whole-genome metagenomic sequencing; PD, phylogenetic diversity. ** Against the study name denotes MGS, all others used 16S.

Figure S3. Differentially abundant taxa at the phylum, class, order, and family level, in MDD, BD and SZ. Bacterial taxa that were differentially abundant in equal to or greater than 20% of the included studies at each taxonomic level were collated. A purple square indicates a lower abundance in cases, orange indicates higher abundance in cases, white indicates no difference reported, and grey indicates taxa were reported as both increased and decreased in the same study. MDD, major depressive disorder; BD, bipolar disorder; SZ, schizophrenia; 16S, 16S rRNA sequencing; MGS, whole-genome metagenomic sequencing; A-MDD, active major depressive disorder; R-MDD, remitted major depressive disorder; HCs, healthy controls; nBD, non-bipolar disorder relatives; FEP, first-episode; Treat, treated; rSZ, remitted schizophrenia. ** indicates studies that used MGS sequencing.

Figure S4. Differentially abundant taxa at the genus level in MDD, BD and SZ. Bacterial taxa that were differentially abundant in equal to or greater than 20% of the included studies at the genus level were collated. A purple square indicates a lower abundance in cases, orange indicates higher abundance in cases, white indicates no difference reported, and grey indicates taxa were reported as both increased and decreased in the same study. MDD, major depressive disorder; BD, bipolar disorder; SZ, schizophrenia; 16S, 16S rRNA sequencing; MGS, whole-genome metagenomic sequencing; A-MDD, active major depressive disorder; R-MDD, remitted major depressive disorder; HCs, healthy controls; nBD, non-bipolar disorder relatives; FEP, first-episode; Treat, treated; rSZ, remitted schizophrenia. ** indicates studies that used MGS sequencing.

Figure S5. Differentially abundant taxa at the species level in MDD, BD and SZ. Bacterial taxa that were differentially abundant in equal to or greater than 20% of the included studies at the species level were collated. A purple square indicates a lower abundance in cases, orange indicates higher abundance in cases, white indicates no difference reported, and grey indicates taxa were reported as both increased and decreased in the same study. MDD, major depressive disorder; BD, bipolar disorder; SZ, schizophrenia; 16S, 16S rRNA sequencing; MGS, whole-genome metagenomic sequencing; A-MDD, active major depressive disorder; R-MDD, remitted major depressive disorder; HCs, healthy controls; nBD, non-bipolar disorder relatives; FEP, first-episode; Treat, treated; rSZ, remitted schizophrenia.



Figure S1. Testing of gut microbiota alpha-diversity across studies of MDD, BD and SZ.

No difference
Higher α-diversity
Lower α-diversity
Not measured



Figure S2. Testing of gut microbiota beta-diversity across studies of MDD, BD and SZ.

Figure	S3. Differ	entially	abundant	: taxa at t	he phyl	lum, class,	order, and	family	level, ir	n MDD, 1	BD and SZ.
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Hetero	genous		PHYLUM					ſ	Majo	r De	press	sive	Diso	rder						TOTAL		BIPO	LAR	TOTAL	1				:	Schiz	ophr	enia	1			Т	TOTAL
			Actinobacteria																	6↑3↓				2↑ 0↓	1											1	!↑ 0↓
Lower			Bacteroidetes																	9↑8↓				1↑ 3↓]											0)↑ 1↓
Higher			Firmicutes																	4↑ 9↓				2↑ 1↓												1	<u>↑</u> 2↓
			Fusobacteria																	3↑1↓				0↑ 0↓												1	!↑ 0↓
Not rep	ported		Proteobacteria																	5↑1↓				2↑ 0↓]											1	!↑ 1↓
		PHYLUM	CLASS					1	Majo	r Dej	press	sive	Diso	rder						TOTAL		BIPO	LAR	TOTAL						Schiz	ophr	enia	1				TOTAL
		Actinobacteria	Coriobacteriia																	1↑ 0↓				1↑ 0↓												1	↓ 0
		Bacteroidetes	Bacteroidia																	0↑1↓				0↑1↓												_ ()↑ 1↓
		Proteobacteria	Deltaproteobacteria																	0↑ 0↓	L			0↑ 0↓												3	i↓ 0↑
	PHYLUM	CLASS	ORDER					1	Majo	r Dej	press	sive	Diso	rder						TOTAL		BIPO	LAR	TOTAL						Schiz	ophr	enia	1				TOTAL
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	Negativicutes	Selenomonadales	Acidaminococcaceae																	4↑ 3↓	L			0↑ 0↓		\square			\square		\square			\square			•↑ •↓
	Bacilli	Lactobacillales	Enterococcaceae																	2↑1↓	L			1↑ 0↓										\square		1	!↑ 2↓
	bacim	Lactobacinaico	Lactobacillaceae																	2↑2↓				1↑ 0↓										\square		3	⊧≁ ∘↓
Firmicutes			Lachnospiraceae																	5↑ 11↓				1↑ 0↓	1	\square					\square			\square		1	!↑ 0↓
	Clostridia	Clostridiales	Peptostreptococcaceae																	1↑ 4↓				2↑ 0↓	1						\square			\square)↑ 2↓
	ciostinala	ciostitulues	Veillonellaceae																	2↑3↓				1↑ 0↓	1				\square		\square			\square)↑ 1↓
			Ruminococcaceae																	2↑9↓				0↑ 0↓	1						\square					1	!↑ 3↓
Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae																	4↑ 4↓	L			0↑1↓	1	\square					\square			\square)↑ 1↓
Bueter Bruetes	Butterorara	Bueter ordares	Rikenellaceaea																	6↑1↓				0↑ 0↓	1	\square			\square		\square			\square)↑ 1↓
Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae																	4↑ 0↓				2↑ 0↓	1									\square		1	!↑ 0↓
				Chen - Female (2018)	Chen - Male (2018) Chen - Middle aged (2020)	Chen - Young (2020)	Chen - 165 (2021) **Chen - MGS (2021)	Chung (2019)	Dong (2021) Hume (2018)	Jiang - Active MDD (2015)	Jiang - Remission MDD (2015)	**Lai (2019)	Liu (2016) Liu (2016)	Liu (2020)	Naseribafrouei (2014) **Rong (2019)	Ye (2021)	Zhang (2021)	Zheng (2016) Zheng (2020)	Zheng (2021)		Hu (2019)	**Lai (2021)	**Kong (2019) Zheng (2020)			Li (2020) Ma - Eirct anicoda (2020)	Ma - Treated (2020)	Manchia - Treat. resistant (2021	Miao (2021) Nguven (2019)	Nguyen (2021)	Pan - Remission (2020) Shen (2018)	Xu - Validation (2020)	Zhang (2019)	Zheng (2019) **Zhu (2020)	Zhu - Acute (2021)	(1777) - Kemission (2021)	

PHYLUM	FAMILY	GENUS	Major Depressive Disorder										TOTAL	Bipolar Disorder TOTAL						L Schizophrenia											TOTAL												
A shin shout suis	Bifidobacteriaceae	Bifidobacterium																		Γ	4↑ 3↓	Г					21	101	Г								Τ				Γ		1↑ 2↓
Actinobacteria	Eggerthellaceae	Eggerthella																			7↑ 0↓						31	101															2↑ 0↓
																													_														
	Rikenellaceae	Alistipes																			8↑ 2↓																						0↑ 1↓
Pactoroidatos	Bacteroidaceae	Bacteroides																			6↑ 5↓						21	∖ 3↓															1↑ 3↓
Bacterordetes	Tannerellaceae	Parabacteroides																			9↑ 1↓						11	r o↓															0↑ 1↓
	Prevotellaceae	Prevotella^																			3↑ 8↓						01	1 ↓															5个 0↓
		_																				_							_														
	Enterococcaceae	Enterococcus																			3↑ 0↓						21	101															2↑ 2↓
		Blautia																			5↑ 3↓																						3↑ 4↓
	Lachnospiraceae	Coprococcus^																			0↑ 5↓						01	► 2↓															1↑ 5↓
		Roseburia																			4↑ 5↓						01	► 2↓	L														0↑ 2↓
	Ruminococcaceae	Faecalibacterium																			1↑11↓						01	► 2↓															2↑ 4↓
	Nummococcuccuc	Ruminococcus^																			1↑6↓						01	► 2↓															2↑ 3↓
Firmcutes	Lactobacillaceae	Lactobacillus																			3↑1↓						31	101															5↑ 1↓
		Megasphaera																			2↑1↓						21	101															5↑1↓
	Veillonellaceae	Dialister																			2↑ 3↓						01	1 ↓															2↑ 1↓
		Veillonella																			4↑ 0↓								L														4↑ 0↓
	Oscillospiraceae	Flavonifractor																			6↑ 0↓						21	r o↓															1↑ 0↓
	Osemospiraceae	Oscillibacter																			5↑ 4↓						21	101															1↑ 0↓
	Streptococcaceae	Streptococcus																			6↑ 0↓						31	101															1↑ 3↓
		_																				_							_														
Proteobacteria	Enterobacteriaceae	Escherichia/Shigella																			2↑ 3↓						21	101															2↑ 0↓
Troteobacteria	Pasteurellaceae	Haemophilus																			1↑ 2↓	L					01	1 ↓	L														0↑ 5↓
Hi Lc Hi	eterogenous ower igher ot reported		Chen - Female (2018) Chen - Male (2018)	Chen - Middle aged (2020)	Chen - 16S (2021) **Chen - MGS (2021)	Chung (2019)	Dong (2021) Huang (2018)	Jiang - Active MDD (2015)	Jiang - Remission MDD (2015)	weny (2019) **Lai (2019)	Lin (2017)	Liu (2016)	Liu (2020) Naseribafrouei (2014)	**Rong (2019)	Shen - Baseline (2021)	Shen - Follow up (2021) ve (2021)	Te (2021) Zhang (2021)	Zheng (2016)	Zheng (2020)	Zheng (2021)		Coello - HCs (2019)	Coello - non-BD rels (2019)	Evans (2017) Hu (2019)	**Lai (2021)	**Rong (2019)			Li (2020)	Li (2021)	Ma - First episode (2020)	Ma - Treat. resistant (2021) Manchia - Treat. resistant (2021)	Manchia - All MDD (2021)	Miao (2021)	Nguyen (2019)	Pan - Kemission (2020) Shen (2018)	Xu - Validation (2020)	Yuan - Baseline (2021)	רבעטא Zheng (2019) Zheng (2019)	**Zhu (2020)	Zhu - Acute (2021)	Zhu - Remission (2021)	

Figure S4. Differentially abundant taxa at the genus level in MDD, BD and SZ.

SPECIES	М	DD	B	D	9	SZ		_	
Acidaminococcus fermentans									Heterogenous
Acidaminococcus intestini									Lower
Akkermansia muciniphila									Lower
Bacteroides helcogenes									Higher
Bifidobacterium adolescentis									Not reported
Bifidobacterium bifidum							I		
Bifidobacterium dentium									
Bifidobacterium longum									
Clostridium saccharolyticum									
Enterococcus faecium									
Escherichia coli									
Eubacterium rectale									
Haemophilus parainfluenzae									
Lactobacillus crispatus									
Megasphaera elsdenii									
Oscillibacter valericigenes									
Selenomonas ruminantium									

Lai (2019) Rong (2019) Yang (2020) Lai (2021) Rong (2019)

Xu (2020) Zhu (2020)

Figure S5. Differentially abundant taxa at the species level in MDD, BD and SZ.

Chen – MGS (2021)

Selenomonas sputigena