Appendix

Table S1. The underlying study characteristics for the 15 gut microbiome studies.

Country	Study design	# of samples	Sample type	Variable region	Seq. platform	Total reads per sample
USA	Cross-sectional	32 (14 HIV- & 18 HIV+)	Rectal swabs	V4	Illumina MiSeq	20,000
USA	Prospective cohort	36 (15 HIV- & 21 HIV+)	Stool samples	V3-V5	Roche 454	3,500
France	Case-control	56 (26 HIV- & 31 HIV+)	Stool samples	V3-V4	Illumina MiSeq	5,500
USA	Prospective cohort	37 (13 HIV- & 24 HIV+)	Rectal swabs	V4	Illumina MiSeq	18,000
Uganda	Prospective cohort	106 (37 HIV- & 69 HIV+)	Stool samples	V4	Illumina MiSeq	10,000
USA	Retrospective cohort	40 (21 HIV- & 19 HIV+)	Fecal samples from colon	V1-V3	Roche 454	1,000
Spain/Sweden	Cross-sectional	233 (34 HIV- & 199 HIV+)	Stool samples	V3-V4	Illumina MiSeq	10,000
Sweden	Prospective cohort	40 (9 HIV- & 31 HIV+)	Stool samples	V3-V4	Illumina MiSeq	10,000
Nigeria	Cross-sectional	119 (51 HIV- & 68 HIV+)	Rectal swabs	V3-V4	Illumina MiSeq	4,000
Mexico	Cross-sectional	43 (10 HIV- & 33 HIV+)	Stool samples	V3-V4	Illumina MiSeq	15,500
Spain	Prospective cohort	39 (9 HIV- & 30 HIV+)	Stool samples	V1-V3	Roche 454	1,000
Spain	Cross-sectional	24 (2 HIV- & 22 HIV+)	Stool samples	V3-V4	Illumina MiSeq	20,000
Sweden	Cross-sectional	62 (15 HIV- & 47 HIV+)	Stool samples	V3-V4	Illumina MiSeq	4,000
Spain	Cross-sectional	70 (21 HIV- & 49 HIV+)	Stool samples	V4	Illumina MiSeq	17,500
USA	Prospective cohort	58 (35 HIV- & 23 HIV+)	Rectal swabs	V3-V4	Illumina MiSeq	2,000

Study	Dilion et al. (2014)	Dinh et al. (2015)	Lozupone et al. (2013)	Dubourg et al. (2013)	Monaco et al. (2016)	Mutlu et al. (2014)	Noguera-Julian et al. (2016)	Nowak et al. (2015)	Nowak et al. (2017)	Pinto-Cardoso et al. (2017)	Serrano-Villar et al. (2017a)	Serrano-Villar et al. (2017b)	Vesterbacka et al. (2017)	Villanueva-Millan et al. (2017)	Yu et al. (2014)

Table S2. The p-values on the disparity in microbial α-diversity between HIV+ and HIV- persons using different methods of meta-analysis

Methods	Asymptotic method ($Het.\ under\ H_0$)		Permutation method ($Het.\ under\ H_0$)		Permutation method ($No\ het.\ under\ H_0$)	
	DL	SJ	DL	SJ	DL	SJ
Richness	<.001	<.001	<.001	<.001	<.001	<.001
Shannon	<.001	<.001	<.001	<.001	<.001	<.001
Simpson	<.001	<.001	<.001	<.001	<.001	<.001
PD	0.002	0.004	0.009	0.009	0.001	0.001
PE	0.016	0.030	0.036	0.035	0.016	0.015
PQE	0.205	0.249	0.232	0.232	0.182	0.176
mMeta	-	-	0.006	0.006	0.002	0.002
aMeta	-	-	0.001	0.001	<.001	<.001

** [Asymptotic method (Het. under* H_0*)] represents the p-value calculation method based on the asymptotic normality and for the traditional random effects meta-analysis for the existence of heterogeneity under* H_0*; [Permutation method (Het. under* H_0*)] represents the group permutation method and for the traditional random effects meta-analysis for the existence of heterogeneity under* H_0*; [Permutation method (No het. under* H_0*)] represents the group permutation method and for the Han and Eskin's modified random effects meta-analysis for the assumption of no heterogeneity under* H_0*. * DL and SJ represents the DerSimonian Laird (method of moments) estimator and the Sidik and Jonkman (robust variance or sandwich variance) estimator, respectively. * Richness, Shannon, Simpson, PD, PE and PQE represent the Species richness, Shannon, Simpson, PD, PE and PQE indices, respectively.*