

Supplementary Table

Table S1. PERMANOVA test of the association between sample types and taxonomic composition of microbial metagenomes from phylum to species level.

	Stool, swab and tissue		Stool and swab	
	R ²	P	R ²	P
phylum	0.265	0.001	0.035	0.001
class	0.404	0.001	0.041	0.001
order	0.397	0.001	0.056	0.001
family	0.351	0.001	0.053	0.001
genus	0.316	0.001	0.050	0.001
species	0.256	0.001	0.040	0.001

Table S4. Correlation of the associations between taxonomic composition and host factors in stool, swab and tissue samples estimated with ALDEx2.

	stool vs swab		stool vs tissue		swab vs tissue	
	rho	P	rho	P	rho	P
age	0.193	0.025	-0.037	0.731	-0.083	0.430
BMI	-0.180	0.038	0.020	0.849	0.006	0.955
sex	0.427	3.55E-07	0.001	0.991	0.037	0.726
NSAIDS_use	0.206	0.017	0.022	0.840	0.045	0.668
antibiotics	0.326	1.70E-04	-0.070	0.515	-0.174	0.099

Table S5. Correlation of the associations between functional pathways and host factors in stool, swab and tissue samples estimated with ALDEx2.

	stool vs swab		stool vs tissue		swab vs tissue	
	rho	P	rho	P	rho	P
age	0.193	0.025	-0.037	0.731	-0.083	0.430
BMI	-0.180	0.038	0.020	0.849	0.006	0.955
sex	0.427	3.55E-07	0.001	0.991	0.037	0.726
NSAIDS_use	0.206	0.017	0.022	0.840	0.045	0.668
antibiotics	0.326	1.70E-04	-0.070	0.515	-0.174	0.099

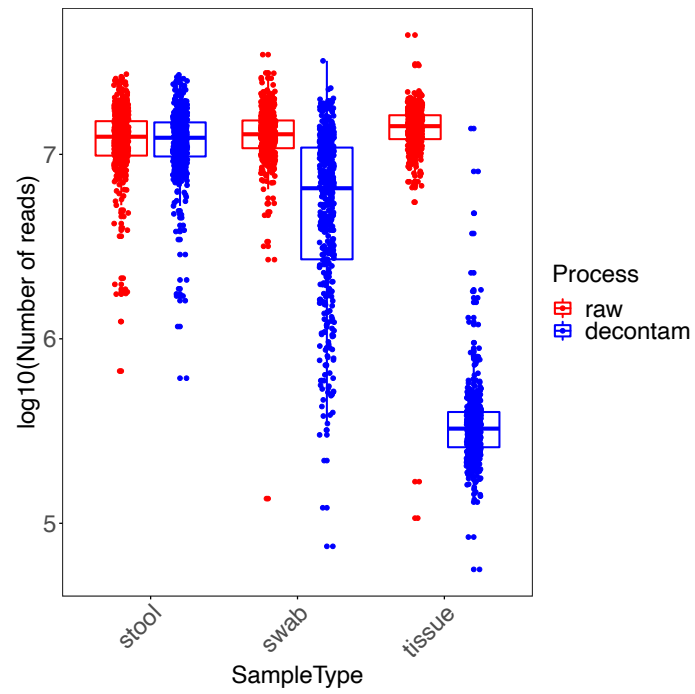
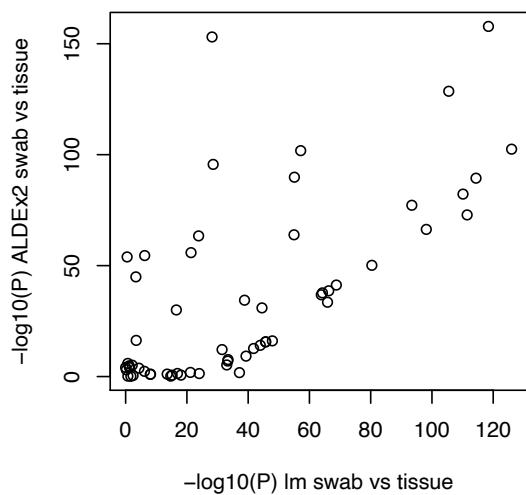
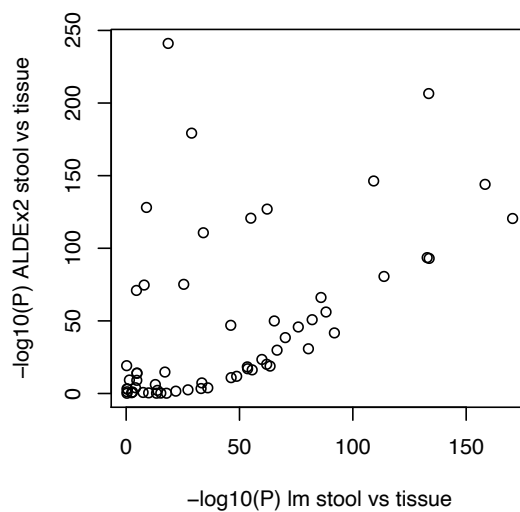
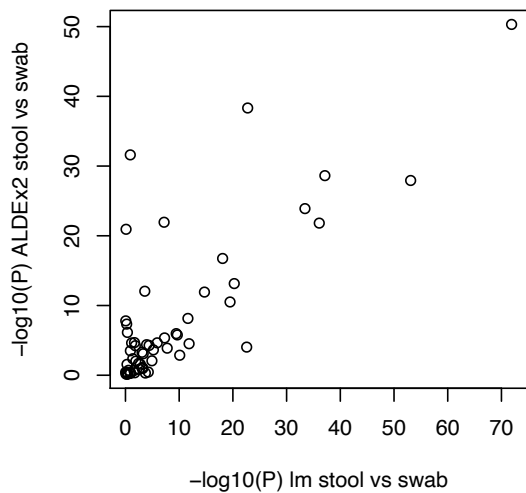


Fig. S1. Number of sequencing reads before and after removing human genome contamination in each sample type.

a



b

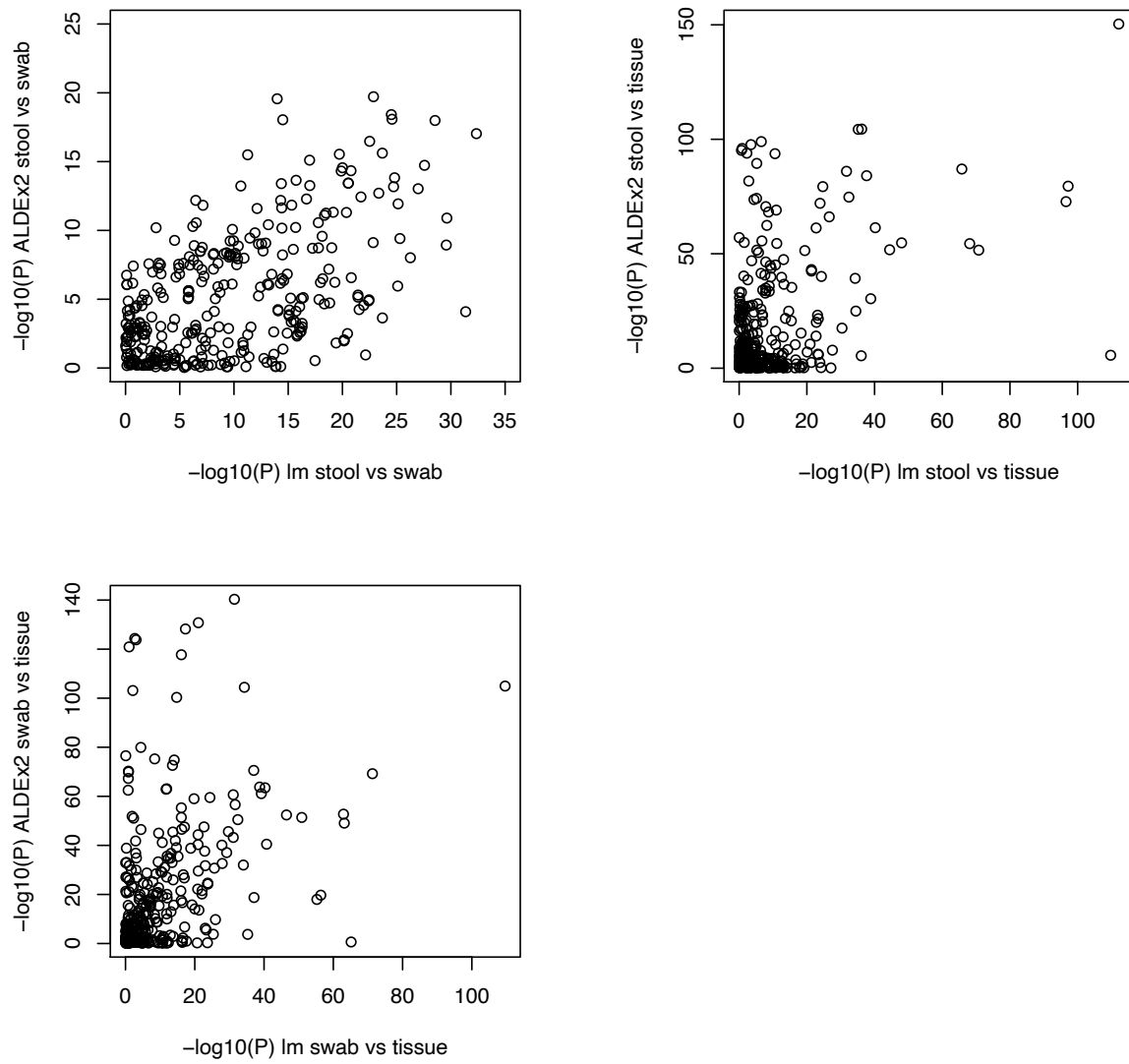


Fig. S3. Comparison of P values from ALDEx2 and mixed effects linear models for each pair of sample types for genus (a) and pathway abundance (b).