Table S1 Expected proportion of A microbiome reads, assuming it is a mixture of two genomic DNA samples, as function of the genotypes of the two samples.

sample 1 genotype	sample 2 genotype	expected proportion of A allele
AA	AA	$1-\epsilon$
AA	AB	$(1-p)(1-\epsilon)+p/2$
AA	BB	$(1-p)(1-\epsilon) + p\epsilon$
AB	AA	$(1-p)/2 + p(1-\epsilon)$
AB	AB	1/2
AB	ВВ	$(1-p)/2 + p\epsilon$
BB	AA	$(1-p)\epsilon + p(1-\epsilon)$
BB	AB	$(1-p)\epsilon + p/2$
BB	BB	ϵ

p is the proportion of the microbiome sample coming from genomic DNA sample 2. ϵ is the rate of sequencing errors.