

Table 1. Genome-wide significant associations between *Leyella* and *Xylanibacter* abundance and host eQTL-linked SNPs in pigs.

Genus	Tissue	Microbiome	SNP	b	FDR
<i>Leyella</i>	Brain	Feces	6:67383248	−1.34	0.03
<i>Leyella</i>	Brain	Feces	6:42581428	−1.08	0.04
<i>Leyella</i>	Brain	Feces	6:46046487	−1.27	0.04
<i>Leyella</i>	Brain	Feces	15:78651704	−1.10	0.04
<i>Leyella</i>	Brain	Feces	3:111485873	−1.08	0.04
<i>Xylanibacter</i>	Brain	Cecum	9:3284896	−2.14	<0.01
<i>Xylanibacter</i>	Brain	Cecum	1:272835476	−1.64	0.02
<i>Xylanibacter</i>	Brain	Cecum	6:62442754	−1.99	0.02

Significant eQTL–microbiome associations for *Leyella* and *Xylanibacter* detected in brain tissue. Effect size (b) indicates the direction of allelic effects; q-values are FDR-corrected from λ -adjusted p-values.