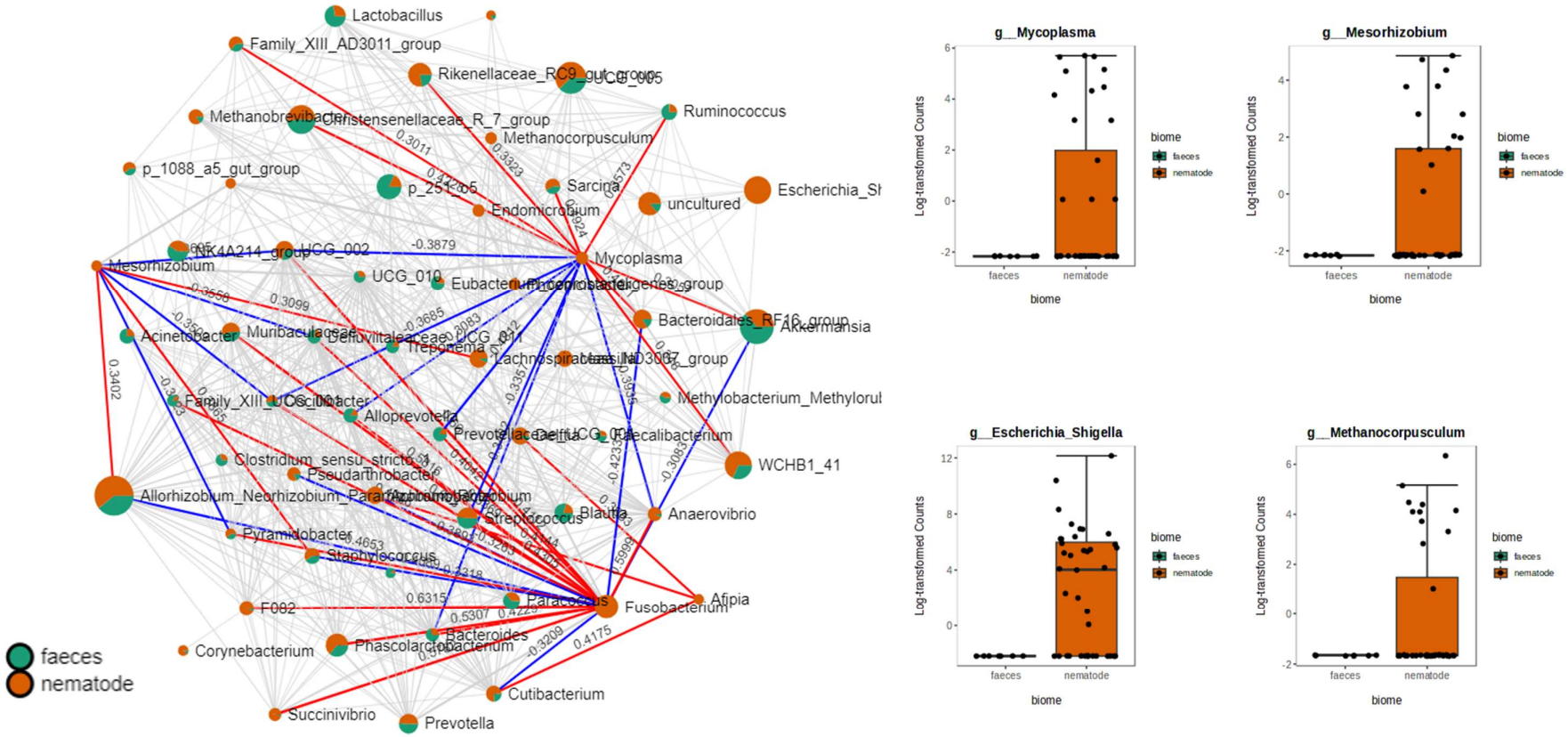

Lactobacillus
Family_XIII_AD3011_group
Rikenellaceae_RC9_gut_group
UCG_005
Ruminococcus
Methanobrevibacter
Christensenellaceae_R_7_group
Methanocorpusculum
p_1088_a5_gut_group
p_251_o5
Sarcina
Escherichia_Sh
Endomicrobium
uncultured
NK4A214_group
UCG_002
-0.3879
Mesorhizobium
Mycoplasma
UCG_010
Eubacterium_coprostanoligenes_group
Bacteroidales_RF16_group
Akkermansia
Muribaculaceae
Acinetobacter
Lachnospiraceae_NK3A20_group
Methylobacterium_Methylorul
Family_XIII_UCG_001
Alloprevotella
Prevotellaceae_Ga6A1_group
Faecalibacterium
WCHB1_41
Clostridium_sensu_stricto_1
Pseudarthrobacter
Allorhizobium_Neorhizobium_Pararhizobium_Rhizobium
Blautia
Anaerovibrio
Streptococcus
Pyramidobacter
Staphylococcus
Afipia
F082
Paracoccus
Fusobacterium
Bacteroides
Corynebacterium
Phascolarctobacterium
Cutibacterium
Succinivibrio
Prevotella
faeces
nematode

g__Mycoplasma
g__Mesorhizobium
g__Escherichia_Shigella
g__Methanocorpusculum
Log-transformed Counts
biome
faeces
nematode

S12 Fig