Fosmidomycin-related community reorganization

% interaction prevalence (meta-community)

% taxon reduction

0 5 10 15 20 25 30 35 40

0.0 0.2 0.4 0.6 0.8 1.0

p(FP)

% microbial community affected (FP)

% metacommunity interaction prevalence

% affected microbiome (PF)