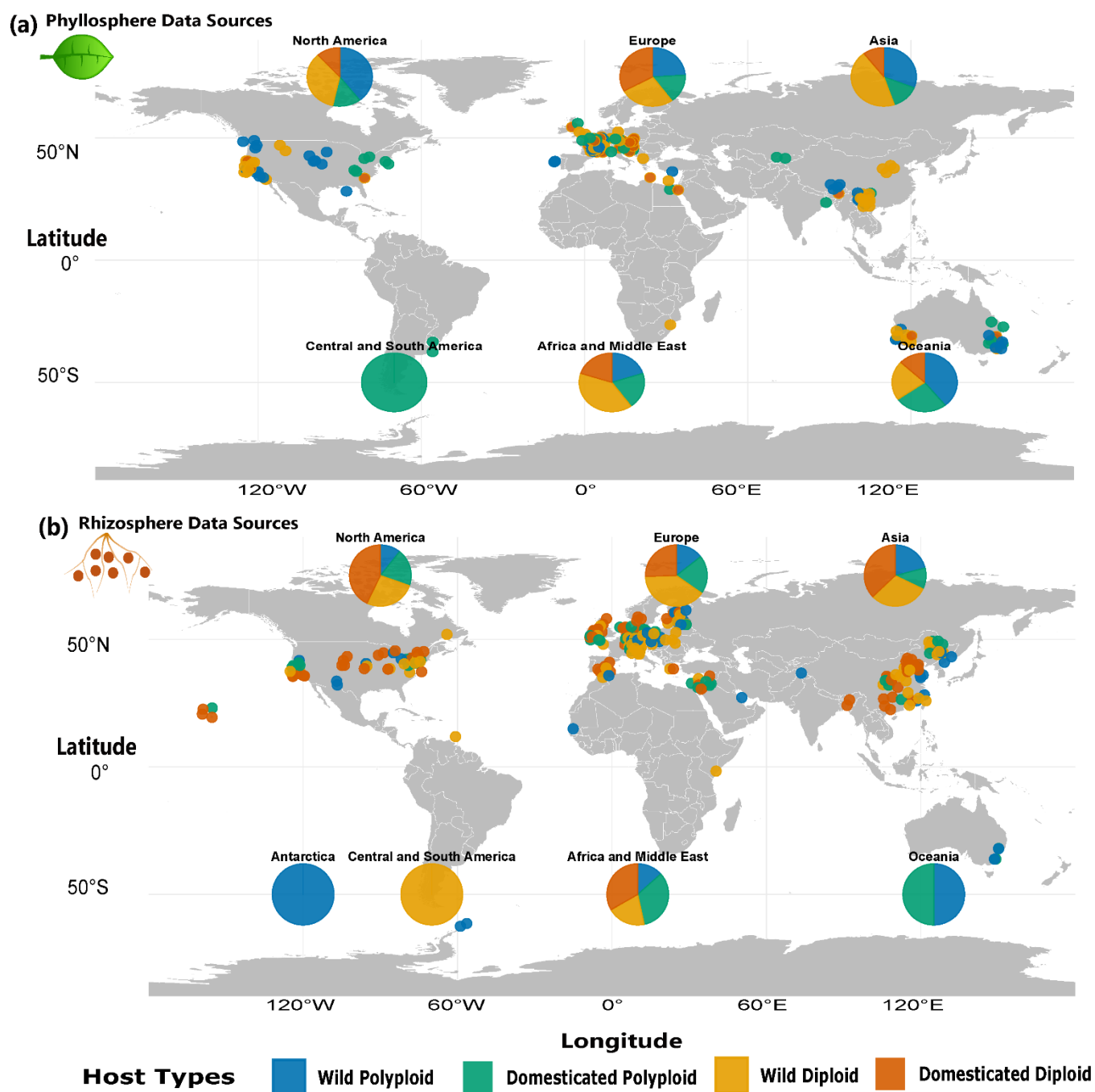
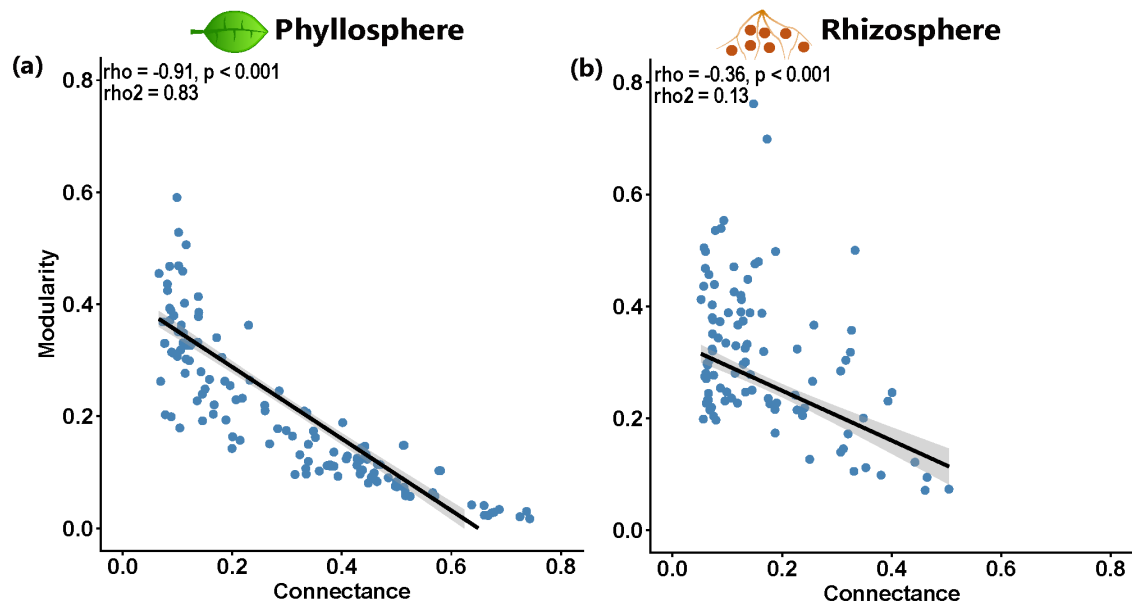
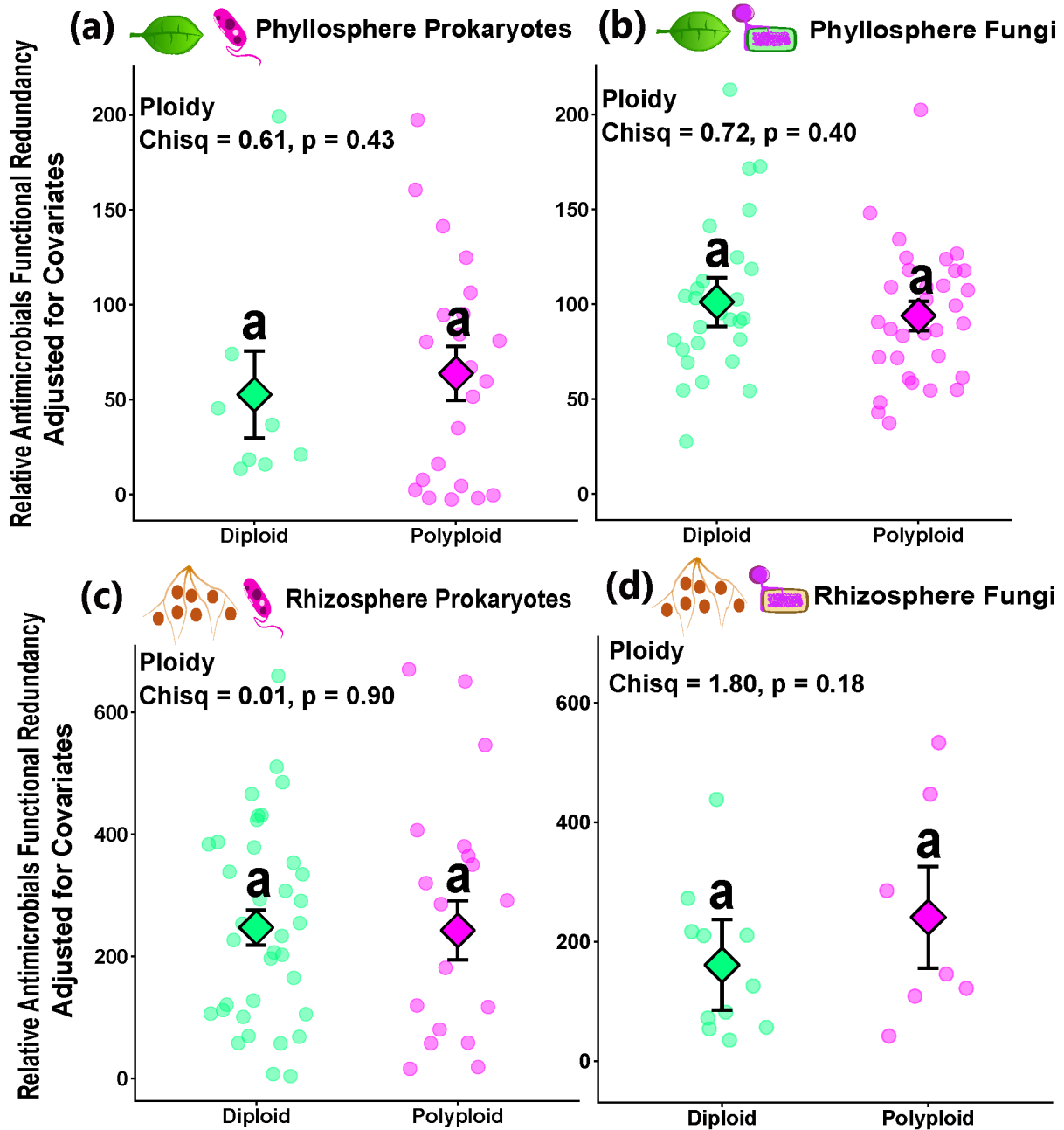




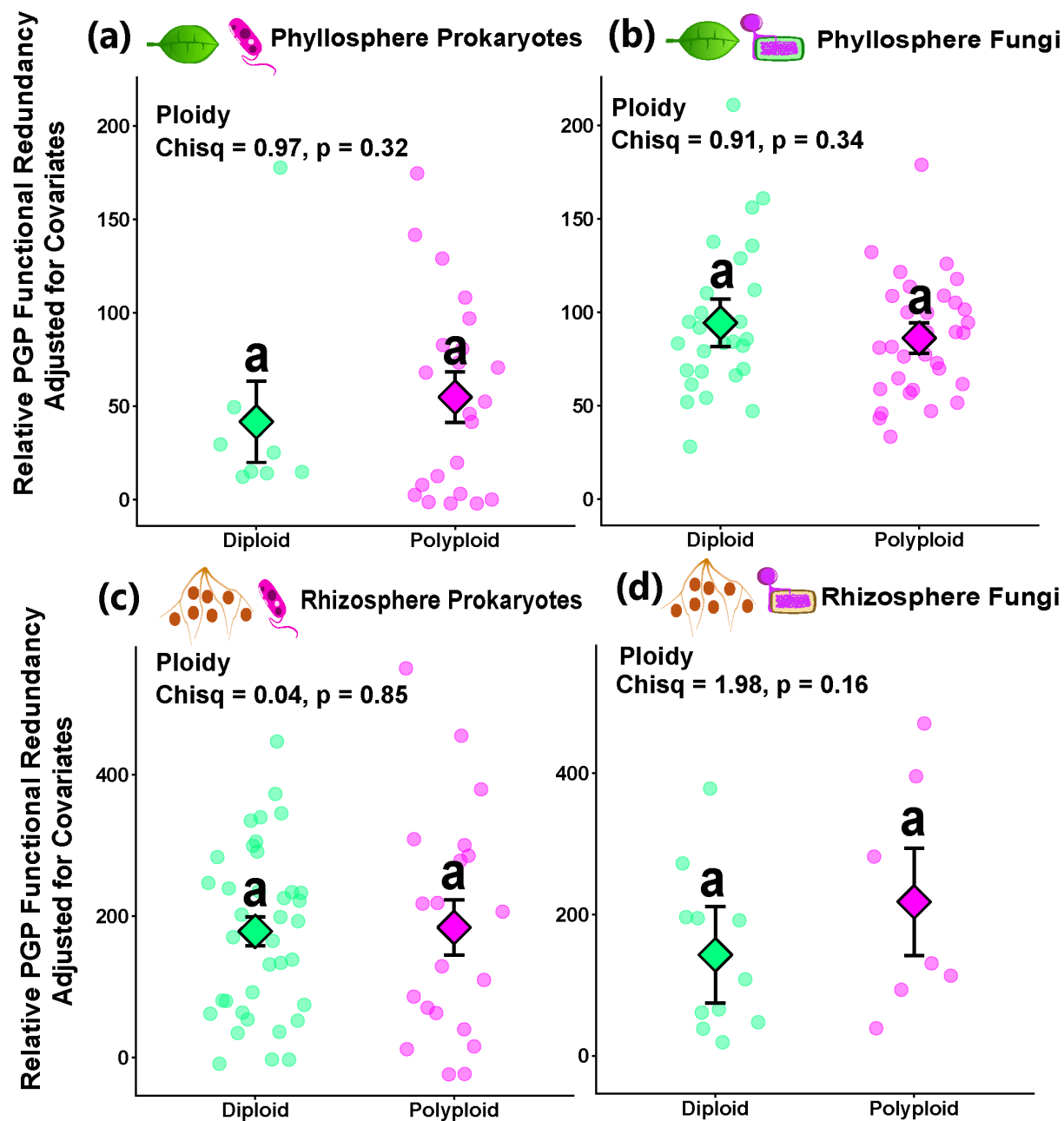
Extended Data Fig. 1. Locations of microbiome data sources. Each dot represents the location of a microbiome sampled from (a) phyllosphere ($n = 4131$ microbiomes) and (b) rhizosphere ($n = 3230$ microbiomes) obtained through publicly available data sources. The colors represent four host types: wild polyploids (blue), domesticated polyploids (green), wild diploids (yellow), and domesticated diploids (orange). Pie charts summarize the proportion of each host type sampled in the corresponding geographic region.



Extended Data Fig. 2. Connectance is significantly negatively correlated with modularity. Each point represents the network properties of a plant species' microbiome network sampled from (a) phyllosphere and (b) rhizosphere. The accompanying statistics provided are Spearman's correlation tests.



Extended Data Fig. 3. Functional redundancy for antimicrobial functions is the same across ploidies. Each point indicates the functional redundancy of antimicrobial functions of a plant species' microbiome for (a) phyllosphere prokaryotes, (b) phyllosphere fungi, (c) rhizosphere prokaryotes, (d) rhizosphere fungi. Diamonds are the estimated marginal means (means adjusted for covariates), and the error bars are 95% CIs calculated from each respective PGLS model with accompanying statistics. The letters signify pairwise comparisons among estimated marginal means with Benjamini-Hochberg false discovery rate correction.



Extended Data Fig. 4. Functional redundancy for plant growth promoting functions is the same across ploidies. Each point indicates the functional redundancy of plant growth promoting functions of a plant species' microbiome for (a) phyllosphere prokaryotes, (b) phyllosphere fungi, (c) rhizosphere prokaryotes, (d) rhizosphere fungi. Diamonds are the estimated marginal means (means adjusted for covariates), and the error bars are 95% CIs calculated from each respective PGLS model with accompanying statistics. The letters signify pairwise comparisons among estimated marginal means with Benjamini-Hochberg false discovery rate correction.