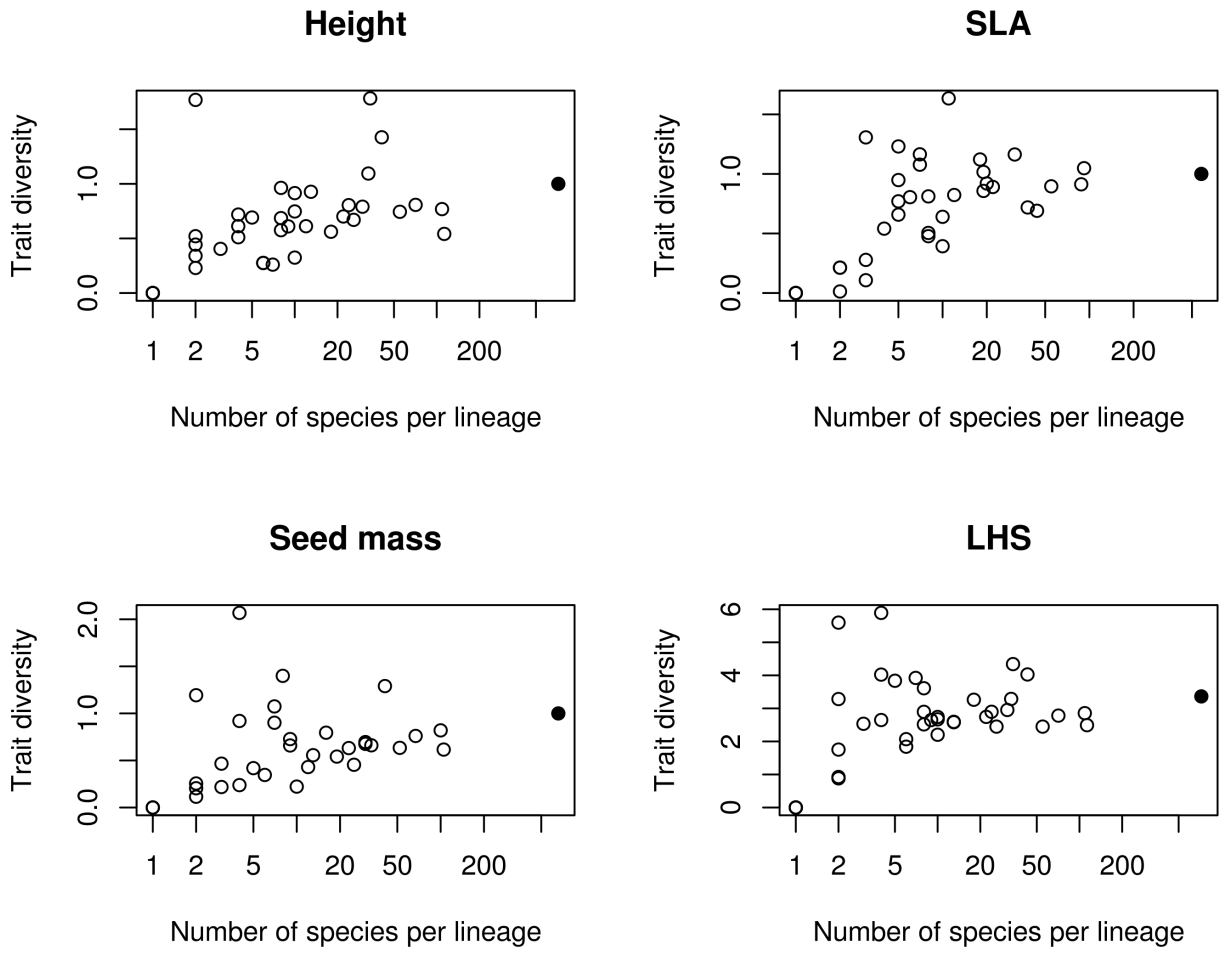Figure S6. Relationship between trait diversity and number of species per lineage (from the extended species pool at an intermediate evolutionary scale), used to generate Figure S2. All trait values were log-transformed and standardized. Trait diversity was evaluated as the standard deviation of the trait values within each lineage. The trait diversity values are compared to the number of species per lineage with a non-missing trait value. «LHS» (Leaf-Height-Seed) refers to the multi-trait diversity index calculated as the mean Euclidean trait distance between species of a lineage. The black dot represents the diversity of the traits among all species of all lineages.