Supplementary S1: Kermavnar J., Marinšek A., Eler K., Kutnar L.
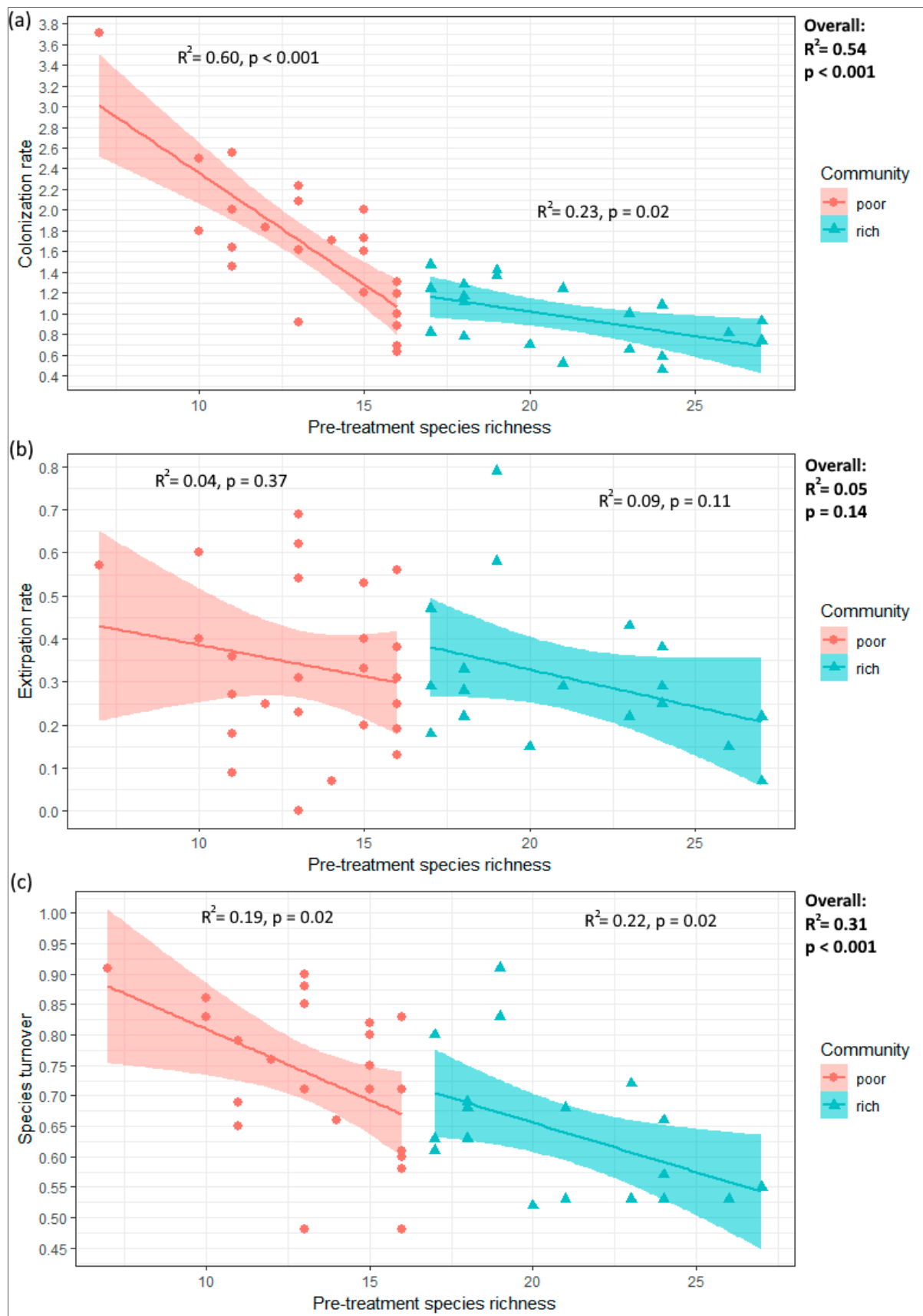
Figure S1. Linear regressions between pre-treatment species richness and (**a**) colonization rate, (**b**) extirpation rate, and (**c**) species turnover. Analysis is based on 45 plots from canopy gaps, i.e., 100% cutting treatment. Species richness is the total number of understory species in each sampling plot. For each plot, colonization rate was calculated as the ratio between the number of colonizing species (species not present before (2012), but recorded after the cutting (2014)) and pre-treatment species richness. Extirpation rate was calculated as the ratio between the number of lost species (species present before the disturbance, but not recorded in the same plot in the post-treatment sampling) and pre-treatment species richness. Plot-level species turnover was calculated as follows: Turnover = (C + E) / Tot, where C = number of colonized species, E = number of lost species, and Tot = total number of species recorded in both sampling years (2012 and 2014). Classification of plots into two groups (i.e., species-poor vs. species-rich communities) was based on pre-treatment species richness. First, we log-transformed the species richness data to improve its distribution, non-significantly different from normal (Shapiro–Wilks test: W = 0.975, p = 0.437). Then, based on the overall mean value of pre-treatment species richness (which was 16.7), plots with richness lower than the mean were classified as species-poor (n = 25) and plots with higher richness than the overall mean were considered as species-rich (n = 20). Coefficients of determination (R^2) and corresponding p-values are reported for each community type (poor, rich) as well as for the overall relationship, i.e., regardless of community type. Bands around the regression lines represent 95% confidence intervals.