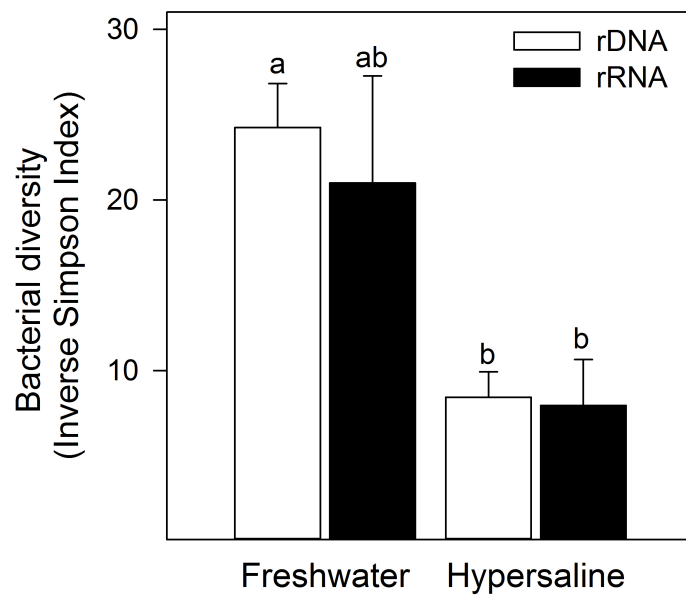


SUPPLEMENTAL FIGURE 1 | Hypersaline lakes support lower levels of bacterial diversity. Diversity was calculated as the inverse Simpson index. Data are means \pm SEM ($n = 5$) based on 97% similarity cutoffs from 16S rRNA gene (rDNA) and 16S rRNA (rRNA) community libraries with different letters indicating significant differences ($P < 0.05$) based on a two-way ANOVA and Tukey's HSD test.



SUPPLEMENTAL FIGURE 2 | As the cutoff classifying dormancy increased or became more stringent the number of bacterial OTUs exhibiting dormancy decreased. Indicator linear regression analysis ($R^2 = 0.68$, $F_{86,8} = 186$, $P < 0.001$, $n = 10$) was calculated from the number of dormant OTUs across a range of cutoffs (0.1 – 0.9) from the equation $1 - (\text{rRNA recovery} / \text{rDNA recovery})$ for each OTU based on rDNA and rRNA community libraries.

