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**Supplemental Information**

**Competition, Not Cooperation,  
Dominates Interactions  
among Culturable Microbial Species**

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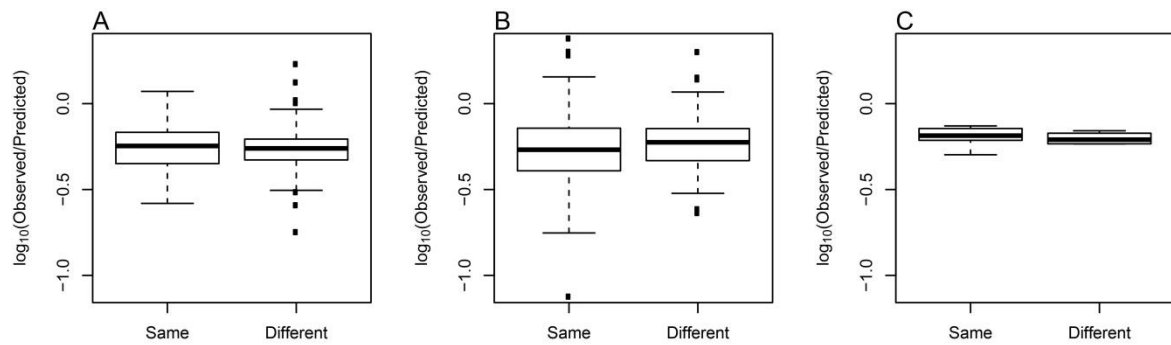
**Supplemental Inventory**

**Supplemental Figures and Tables**

Figure S1

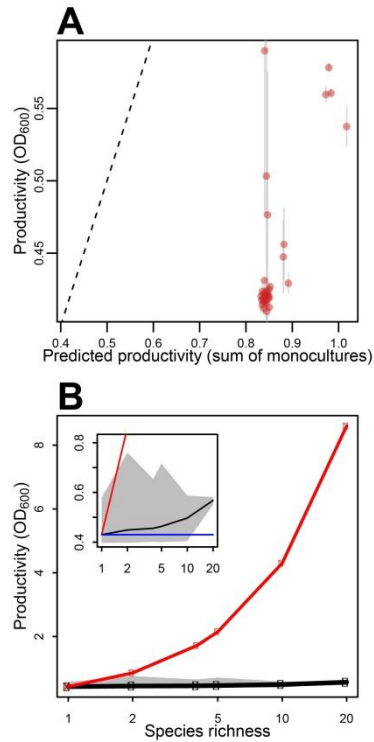
Figure S2

Table S1



**Figure S1. There Is No Significant Effect of Phylogeny on Species Interaction at the Level of Division**

For the pairwise assays (Fig. 1A-C), we calculated the observed respiration (“observed”) and the corresponding predicted respiration based on the sum of the constituent monocultures (“predicted”) for all of the pairwise assays. The  $\log_{10}(\text{observed}/\text{predicted})$  gives an estimate of the degree to which the observed differs from the predicted. Negative values indicate negative interactions (observed < additive prediction) while positive values indicate positive interactions (observed > additive prediction). These results were then divided into whether the two species were from the Same or Different phylogenetic divisions. None of the same vs. different comparisons differed significantly (analysis of variance, all  $p > 0.3$ ). Fig S2 A, B, C corresponds to the same panels of Fig. 1.



**Figure S2. Interactions among Marine Bacterial Isolates**

(A) Pairwise interactions between 20 bacterial strains collected from marine environments. The observed data were collected by measuring total productivity (total respiration measured as change in optical density (OD) of an CO<sub>2</sub> indicator) in randomly-chosen pairwise mixtures. Predicted values (y-axis) are the sum of the monoculture productivity. The dashed line is where predicted values equal observed value. Grey vertical lines are standard errors (SE). These data are extended across multiple levels of species richness up to 20-species. The black line is mean observed values with the full data range (min to max) shown in grey, which is only just visible in the main figures. The red line is mean sum of the monoculture productivities, which will occur if there is no interaction among species (Fig 1B). The blue line is the average of the monoculture productivities of the constituent species. The same data are plotted in the inset figure but different y-axis values are used to see all data at the lower end of the data range. Methods for this experiment are presented in [21] and data presented here are for the “Ancestral strains”.

**Table S1. List of Taxa used in Each Experiment**

Division	Genus	72-species	32-species
Actinobacteria	<i>Amycolatopsis</i>	1	
	<i>Arthrobacter</i>	1	
	<i>Cellulomonas</i>	10	
	<i>Clavibacter</i>	1	
	<i>Corynebacterium</i>	1	
	<i>Curtobacterium</i>	1	
	<i>Gordona</i>	1	
	<i>Kocuria</i>	4	
	<i>Kytococcus</i>	1	
	<i>Microbacterium</i>	4	1
	<i>Micrococcus</i>	2	
	<i>Nesterenkonia</i>	1	
	<i>Rhodococcus</i>	4	
	<i>Stenotrophomonas</i>		1
	<i>Streptoverticillium</i>	2	
Bacteroidetes	<i>Flavobacterium</i>	4	6
	<i>Pedobacter</i>	1	1
Firmicutes	<i>Aerococcus</i>	1	
	<i>Lysinibacillus</i>		1
	<i>Paenibacillus</i>	1	
Proteobacteria	<i>Staphylococcus</i>	1	
	<i>Acidovorax</i>	1	
	<i>Acinetobacter</i>	2	
	<i>Agrobacterium</i>		2
	<i>Bacillus</i>	6	7
	<i>Bosea</i>		1
	<i>Brevundimonas</i>	4	
	<i>Caulobacter</i>		2
	<i>Comamonas</i>	1	
	<i>Erwinia</i>		1
	<i>Hafnia</i>	1	
	<i>Hydrogenophaga</i>	3	
	<i>Moraxella</i>	1	
	<i>Neisseria</i>	1	
	<i>Pseudomonas</i>	7	6
	<i>Serratia</i>		1
	<i>Sphingomonas</i>	2	1
<i>Variovorax</i>	1	1	
	TOTAL	72	32