Supplementary Information: Supplementary Figures

A comparison of computationally predicted functional metagenomes and microarray

analysis for microbial P cycle genes in a unique basalt-soil forest.

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Conflict of Interest Statement:

The authors declare no conflict of interest.

Supplementary Figures

Figure S1 Map of Gotjawal forest sample sites on Jeju Island, Korea. Originally published in Kim, J.-S. et al. Microbial Community Structure and Functional Potential of Lava-Formed Gotjawal Soils in Jeju, Korea. (In review)
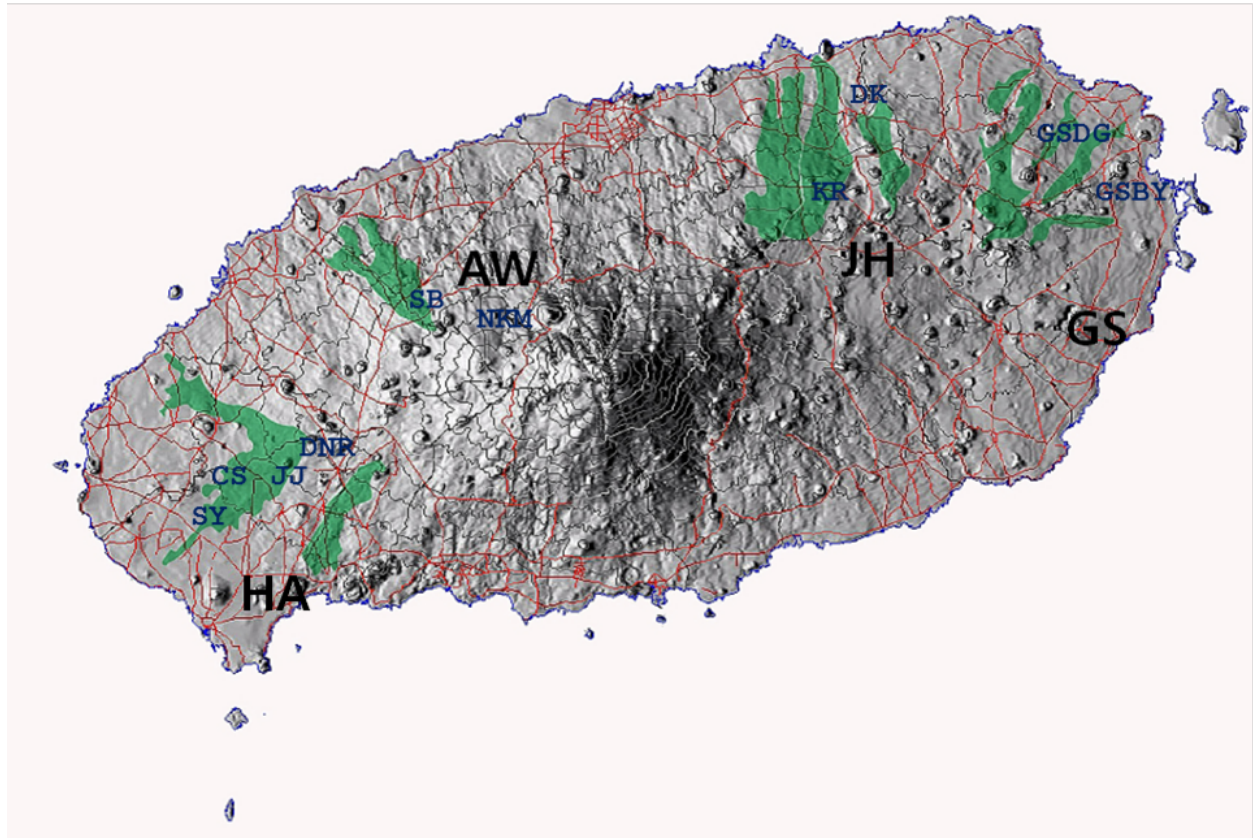
Figure S2 Bar plot of taxa at the phyla level in the system showing taxonomic homogeneity across sites. Rarefaction depth of 41,000 used.

Taxonomy	BY1	BY2	CS1	CS2	DG1	DG2	DK1	DK2	DNR1	DNR2	JI1	JI2	KR1	KR2	NKM1	NKM2	SB1	SB2	SY1	SY2
Unassigned;Other	3.7%	4.4%	4.1%	3.5%	3.3%	4.6%	3.8%	3.7%	4.2%	3.3%	3.7%	3.5%	2.9%	4.0%	3.9%	3.6%	3.6%	3.5%	3.4%	4.3%
k__Archaea;p__Crenarchaeota	0.0%	0.0%	0.1%	0.1%	0.3%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Archaea;p__Euryarchaeota	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Archaea;p__[Parvarchaeota]	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;Other	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__AD3	0.2%	0.3%	0.2%	0.1%	0.8%	0.3%	0.2%	0.1%	0.5%	0.1%	0.0%	0.1%	0.1%	0.2%	0.0%	0.4%	0.0%	0.1%	0.0%	0.0%
k__Bacteria;p__Acidobacteria	12.8%	12.8%	12.7%	15.9%	20.2%	11.2%	11.5%	9.9%	14.4%	11.9%	10.1%	13.4%	14.9%	13.6%	11.4%	14.6%	11.5%	11.1%	11.3%	12.3%
k__Bacteria;p__Actinobacteria	13.8%	13.2%	11.4%	13.0%	13.3%	10.9%	14.2%	17.3%	11.5%	17.1%	17.6%	15.8%	17.6%	10.4%	9.8%	12.6%	12.4%	13.9%	15.2%	13.9%
k__Bacteria;p__Armatimonadetes	0.2%	0.3%	0.3%	0.2%	0.3%	0.2%	0.1%	0.1%	0.2%	0.1%	0.1%	0.2%	0.2%	0.3%	0.3%	0.3%	0.3%	0.3%	0.2%	0.1%
k__Bacteria;p__BHI80-139	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__BRC1	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__Bacteroidetes	9.2%	7.1%	7.5%	7.8%	4.2%	10.7%	8.8%	8.7%	7.7%	6.4%	9.6%	7.1%	8.3%	12.0%	13.1%	7.4%	13.1%	11.3%	9.2%	10.4%
k__Bacteria;p__Chlamydiae	0.8%	1.0%	1.1%	1.0%	0.9%	0.8%	0.7%	0.9%	0.8%	1.1%	0.6%	0.8%	0.9%	0.7%	0.9%	0.6%	0.6%	0.6%	0.9%	0.6%
k__Bacteria;p__Chlorobi	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.3%	0.3%	0.2%	0.1%	0.1%	0.1%	0.2%	0.2%	0.1%	0.2%	0.1%	0.3%
k__Bacteria;p__Chloroflexi	5.1%	7.2%	6.1%	3.9%	6.2%	6.0%	5.4%	6.2%	5.4%	4.7%	5.1%	6.2%	3.9%	4.5%	4.3%	6.0%	3.9%	5.1%	5.0%	3.8%
k__Bacteria;p__Cyanobacteria	0.3%	0.4%	0.3%	0.6%	0.3%	0.2%	0.2%	0.2%	0.4%	0.2%	0.2%	0.5%	0.3%	0.3%	0.2%	0.4%	0.4%	0.3%	0.2%	0.3%
k__Bacteria;p__Elusimicrobia	0.4%	0.3%	0.5%	0.7%	0.5%	0.5%	0.4%	0.1%	0.5%	0.2%	0.2%	0.4%	0.3%	0.3%	0.5%	0.3%	0.5%	0.5%	0.3%	0.5%
k__Bacteria;p__FBP	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__FCPU426	0.1%	0.1%	0.1%	0.1%	0.1%	0.2%	0.1%	0.0%	0.2%	0.0%	0.0%	0.1%	0.0%	0.1%	0.1%	0.0%	0.1%	0.1%	0.0%	0.1%
k__Bacteria;p__Fibrobacteres	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%
k__Bacteria;p__Firmicutes	0.6%	0.5%	0.5%	1.1%	1.3%	0.3%	0.2%	0.5%	0.2%	0.5%	0.3%	0.7%	0.7%	1.2%	0.5%	1.0%	0.7%	0.3%	0.6%	0.5%
k__Bacteria;p__Fusobacteria	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__GAL15	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__GN02	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__GN04	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__GOUTA4	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__Gemmatimonadetes	1.0%	0.9%	1.2%	0.9%	0.9%	1.3%	1.4%	0.7%	0.8%	1.2%	1.0%	0.9%	0.7%	1.3%	1.1%	1.3%	1.1%	1.0%	1.2%	0.9%
k__Bacteria;p__Kazan-3B-28	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__MVP-21	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__NKB19	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__Nitrospirae	1.1%	1.2%	1.0%	0.7%	0.2%	1.2%	1.4%	1.4%	0.8%	2.4%	1.4%	0.7%	0.7%	1.2%	1.4%	1.1%	0.5%	0.9%	1.4%	1.4%
k__Bacteria;p__OC31	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__OD1	1.3%	1.3%	1.4%	1.4%	0.9%	1.8%	1.2%	0.4%	1.4%	0.3%	0.7%	1.0%	0.5%	1.0%	2.1%	1.1%	1.8%	2.1%	1.1%	2.2%
k__Bacteria;p__OP11	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%
k__Bacteria;p__OP3	0.1%	0.1%	0.1%	0.1%	0.1%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%
k__Bacteria;p__Planctomycetes	13.5%	14.3%	15.3%	12.9%	10.1%	14.1%	14.0%	13.7%	13.4%	14.6%	14.6%	12.9%	13.6%	13.2%	13.9%	12.8%	12.1%	13.3%	14.2%	13.7%
k__Bacteria;p__Proteobacteria	24.7%	23.7%	25.9%	24.8%	23.2%	24.3%	25.1%	24.6%	25.6%	24.8%	23.1%	24.5%	23.2%	25.0%	25.1%	23.8%	27.1%	24.6%	26.0%	24.7%
k__Bacteria;p__SR1	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__Spirochaetes	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__TM6	0.1%	0.1%	0.1%	0.1%	0.2%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.2%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%
k__Bacteria;p__TM7	0.8%	0.6%	0.8%	0.9%	0.7%	0.8%	0.7%	0.4%	0.7%	0.4%	0.7%	0.9%	0.8%	0.7%	0.9%	1.1%	1.5%	1.3%	0.9%	0.8%
k__Bacteria;p__Tenericutes	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.2%	0.1%	0.0%	0.1%	0.0%
k__Bacteria;p__Verrucomicrobia	9.1%	9.2%	8.1%	9.5%	11.4%	8.7%	9.1%	10.4%	9.1%	9.4%	9.7%	9.8%	10.0%	8.6%	9.0%	9.5%	7.5%	8.5%	7.9%	7.8%
k__Bacteria;p__WPS-2	0.1%	0.1%	0.1%	0.3%	0.6%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.2%	0.1%	0.0%	0.0%	0.2%	0.3%	0.2%	0.0%	0.1%
k__Bacteria;p__WS2	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.1%	0.0%	0.0%
k__Bacteria;p__WS3	0.4%	0.4%	0.4%	0.2%	0.0%	0.8%	0.7%	0.4%	0.6%	0.8%	0.5%	0.1%	0.1%	0.6%	0.5%	0.5%	0.2%	0.2%	0.5%	0.6%
k__Bacteria;p__WS4	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__WS5	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__WS6	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k__Bacteria;p__[Caldithrix]	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%

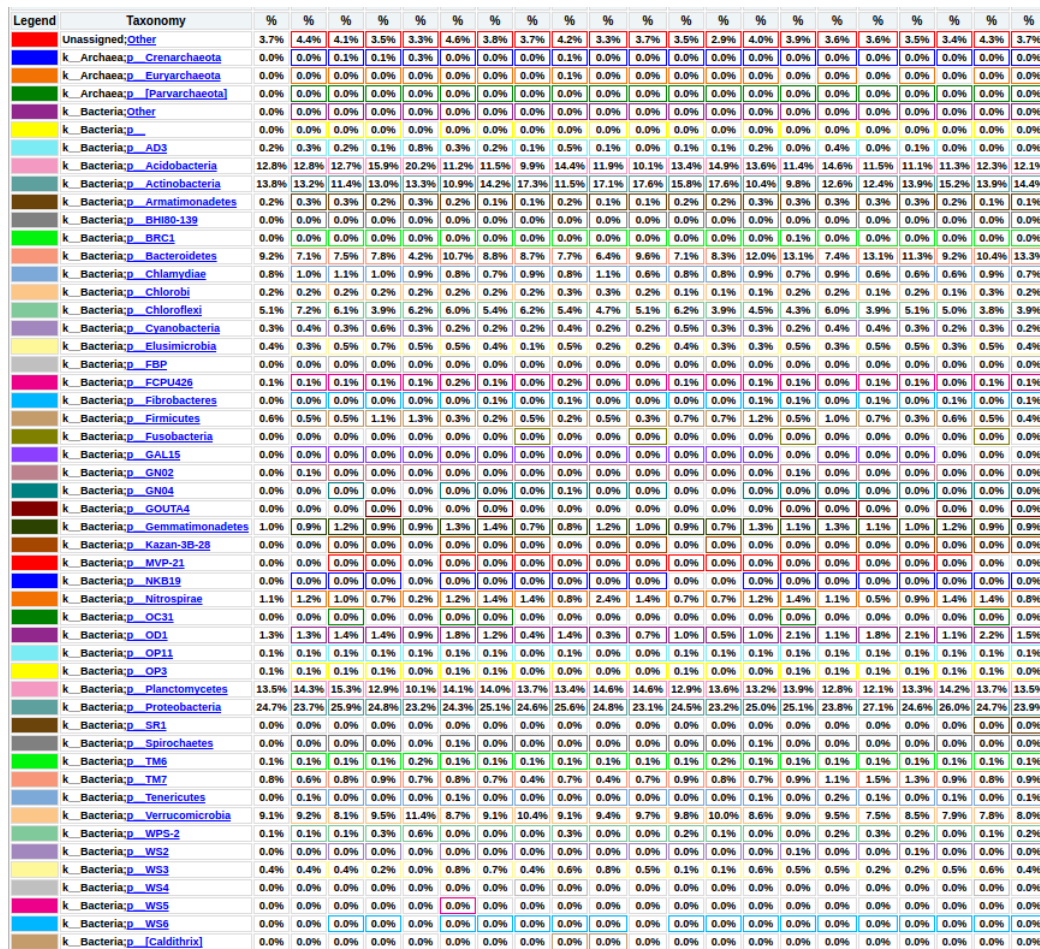**Figure S3** Counts of P genes by PICRUSt and GeoChip scaled independently.

Black = PICRUSt. Red = Geochip. Separated for scale.

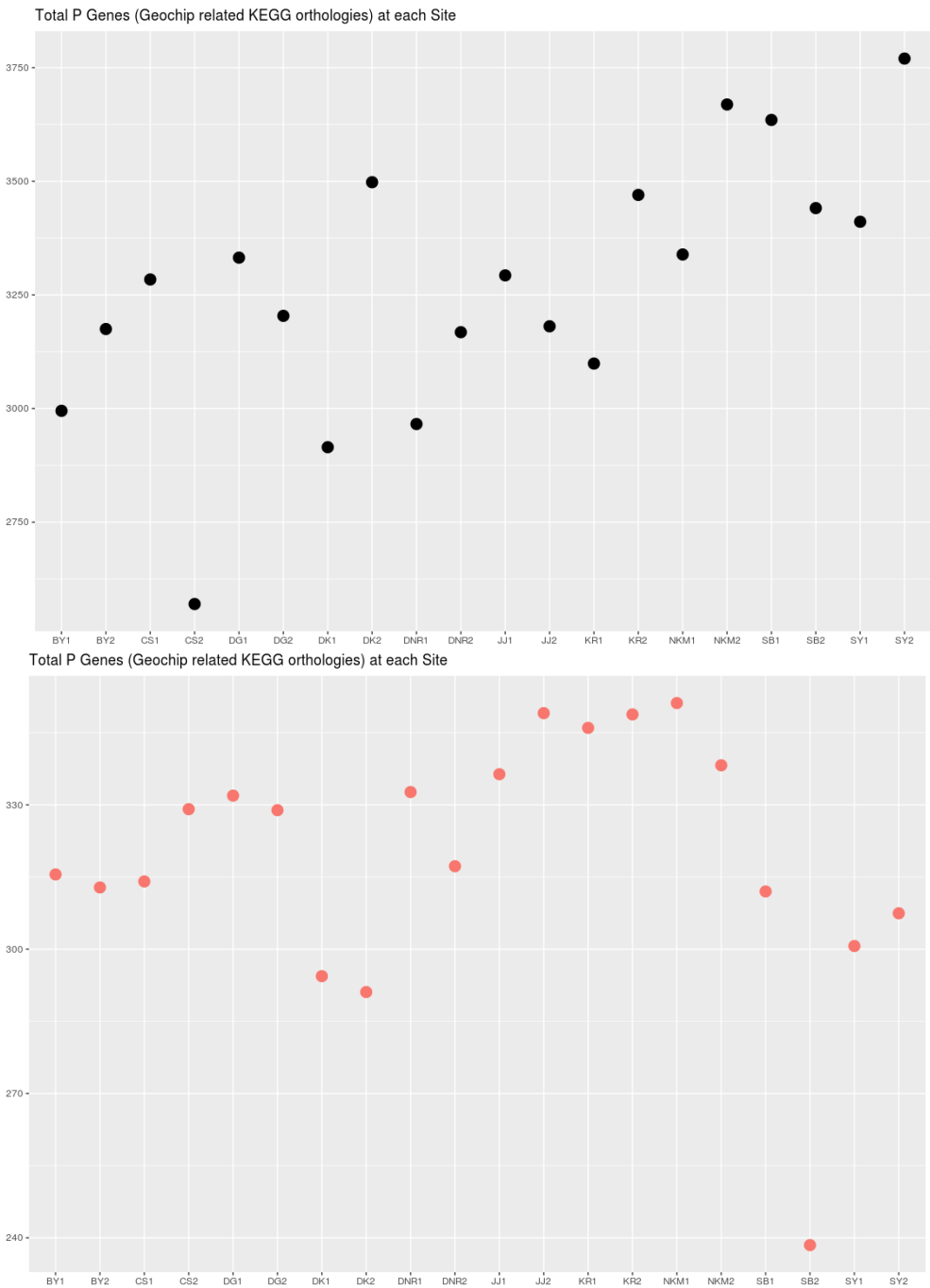Total P Genes (Geochip related KEGG orthologies) at each Site

Total P Genes (Geochip related KEGG orthologies) at each Site

Figure S4 Procrustes Error Plot for Procrustes analysis between PICRUSt and

GeoChip datasets.

Procrustes Error Plot
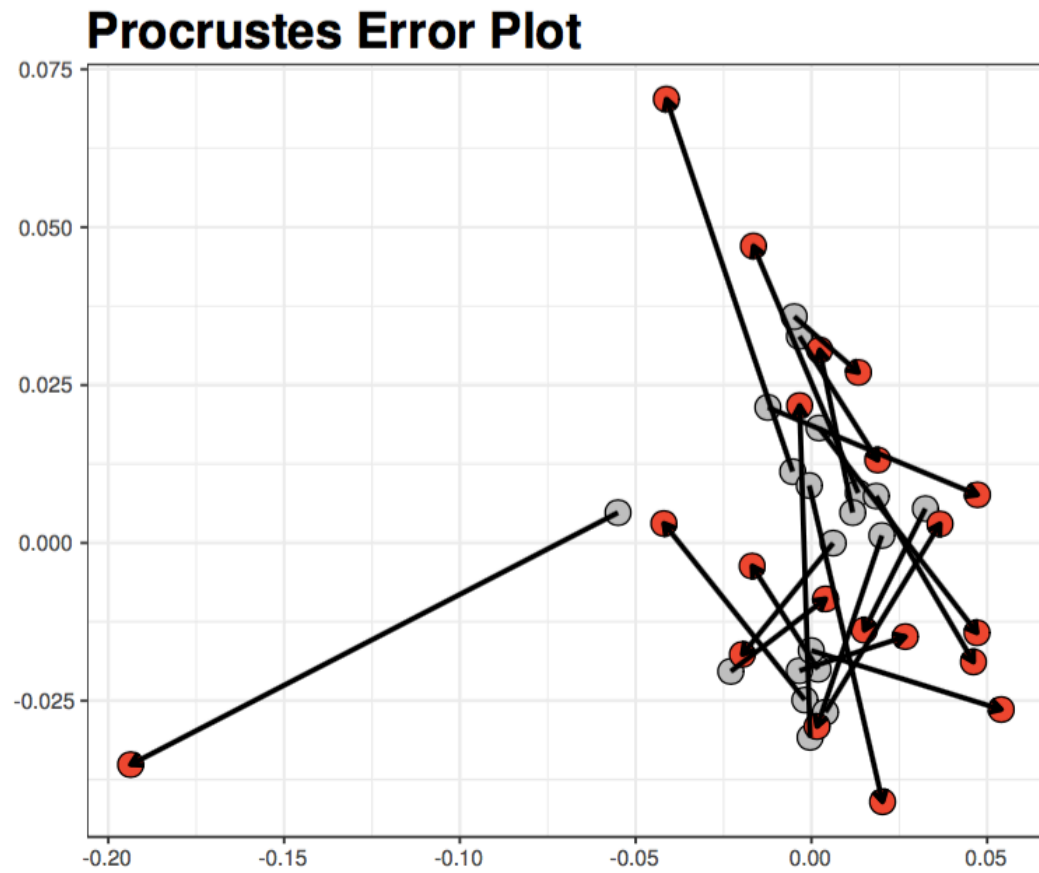
Figure 5 A) Bubble plot of taxa identified by new assay at each site. B) Total counts identified in new assay at each site by PICRUSt.

A)

B)