Supplemental materials

Title: Different agricultural practices specify bacterial community compositions in the soil rhizosphere and root zone

Running title: Agricultural practices specify bacterial community compositions

The supplemental materials include 2 supporting table and 5 supporting figures.

Table S1. Multiple factor analysis of relative abundance of microbial communities in phylum level under different treatments between rhizosphere and bulk soils

Variables	Proteobacteria		Acidobacteria		Actinobacteria		Bacteroidetes		Chloroflexi	
	F	*p*	F	*P*	F	*p*	F	*p*	F	*p*
(NT/RT)	0.09	0.77	1.08	0.31	0.00	0.99	0.86	0.37	0.07	0.80
(CC/CR)	0.00	0.98	1.74	0.21	1.42	0.25	0.15	0.70	1.80	0.20
(R/Z)	18.03	< 0.01	13.94	< 0.01	100.97	< 0.01	49.18	< 0.01	6.88	< 0.05
(NT/RT) * (CC/CR)	0.01	0.92	0.25	0.62	0.75	0.40	0.09	0.76	0.24	0.63
(NT/RT) * (R/Z)	1.32	0.27	0.76	0.40	0.01	0.92	0.67	0.43	0.01	0.92
(CC/CR) * (R/Z)	0.92	0.35	2.72	0.12	3.00	0.10	0.75	0.40	3.03	0.10
(NT/RT) * (CC/CR) * (R/Z)	0.06	0.81	0.68	0.42	1.01	0.33	0.00	1.00	0.04	0.85
	Planctomycetes		Firmicutes		Gemmatimonadetes		Verrucomicrobia		Others	
	F	*p*	F	*P*	F	*p*	F	*p*	F	*p*
(NT/RT)	0.00	0.99	3.83	0.07	0.08	0.79	0.27	0.61	0.67	0.42
(CC/CR)	4.06	0.06	0.35	0.56	0.17	0.68	0.43	0.52	4.19	0.06
(R/Z)	10.11	< 0.01	5.22	< 0.05	5.67	< 0.05	3.54	0.08	0.58	0.46
(NT/RT) * (CC/CR)	0.01	0.94	0.90	0.36	0.15	0.70	0.61	0.45	0.10	0.76
(NT/RT) * (R/Z)	0.10	0.75	0.90	0.36	1.24	0.28	0.14	0.71	0.11	0.74
(CC/CR) * (R/Z)	0.78	0.39	5.80	< 0.05	0.06	0.82	0.64	0.44	1.76	0.20
(NT/RT) * (CC/CR) * (R/Z)	0.08	0.78	0.01	0.91	0.06	0.81	0.72	0.41	1.07	0.32

Table S1. Alpha diversity indexes based on all sequence data and 500 sequence per sample

			Alpha diversity of all sequence data				**Alpha diversity of 500 sequence per sample**			
Treatments	Sequence Count	Coverage (%)	observed Species	Chao1	Inverted Simpson	ACE	observed Species	Chao1	Inverted Simpson	ACE
NTCCR_a	5798	79.4	1581.59	3445.11	224.69	3723.53	360.13	1319.10	169.20	1468.97
NTCCR_b	7675	82.9	1553.43	3345.5	196.16	3727.03	349.73	1281.02	147.71	1444.40
NTCCR_c	13507	87.6	1618.2	3569.46	201.41	3922.79	355.9	1401.68	153.66	1559.12
NTCCZ_a	23640	95.6	1058.21	2031.11	168.89	2100.5	287.34	792.76	130.68	877.17
NTCCZ_b	14419	94.0	1086.46	1975.12	205.5	2038.25	299.76	814.18	150.87	912.48
NTCCZ_c	14914	95.4	970.15	1710.54	172.1	1755.17	282.59	724.34	135.31	802.01
NTCRR_a	8507	85.0	1441.3	3134.66	105.83	3364.54	331.24	1209.57	91.01	1407.63
NTCRR_b	16283	89.4	1542.37	3453.3	204.25	3724.31	351.73	1274.67	156.35	1413.70
NTCRR_c	4939	79.1	1430.07	3270.57	165.26	3505.33	333.33	1150.18	130.95	1320.51
NTCRZ_a	23377	95.6	1155.07	2206.48	235.77	2291.3	311.97	856.48	169.47	956.96
NTCRZ_b	14112	93.2	1111.44	2157.11	209.74	2258.89	298.87	829.54	152.31	912.68
NTCRZ_c	5145	88.3	1086.32	1913.07	211.57	2023.72	304.34	800.25	154.92	881.28
RTCCR_a	7281	82.6	1478.64	3355.63	124.68	3626.74	327.48	1307.40	104.39	1522.82
RTCCR_b	17140	89.5	1567.05	3573.86	157.1	3926.3	343.17	1354.73	125.26	1532.52
RTCCR_c	5370	79.0	1480.77	3489.7	210.99	3680.68	338.31	1189.38	153.93	1387.86
RTCCZ_a	8945	89.9	1282.69	2351.3	303.25	2467.02	335.01	967.20	198.31	1097.28
RTCCZ_b	16086	95.1	1075.71	1920.15	202	1983.55	300.81	795.73	151.48	888.38
RTCRR_a	19036	16449	1586.04	3658.03	166.32	3965.26	350.06	1358.11	132.71	1461.76
RTCRR_b	8015	7691	1036.5	2253.29	18.32	2321.67	251	819.41	17.934	889.05
RTCRR_c	6870	5876	1627.75	3816.9	211.84	4196.78	355.39	1359.57	158.46	1523.73
RTCRZ_a	13445	13060	1314.18	2475.39	314.38	2633.35	337.98	1005.68	202.86	1129.39
RTCRZ_b	14630	13919	1245.22	2486.13	207.75	2617.74	316.69	947.61	151.52	1100.35
RTCRZ_c	9901	9555	1164.42	2135.49	192.25	2211.45	310.33	878.86	145.54	990.36

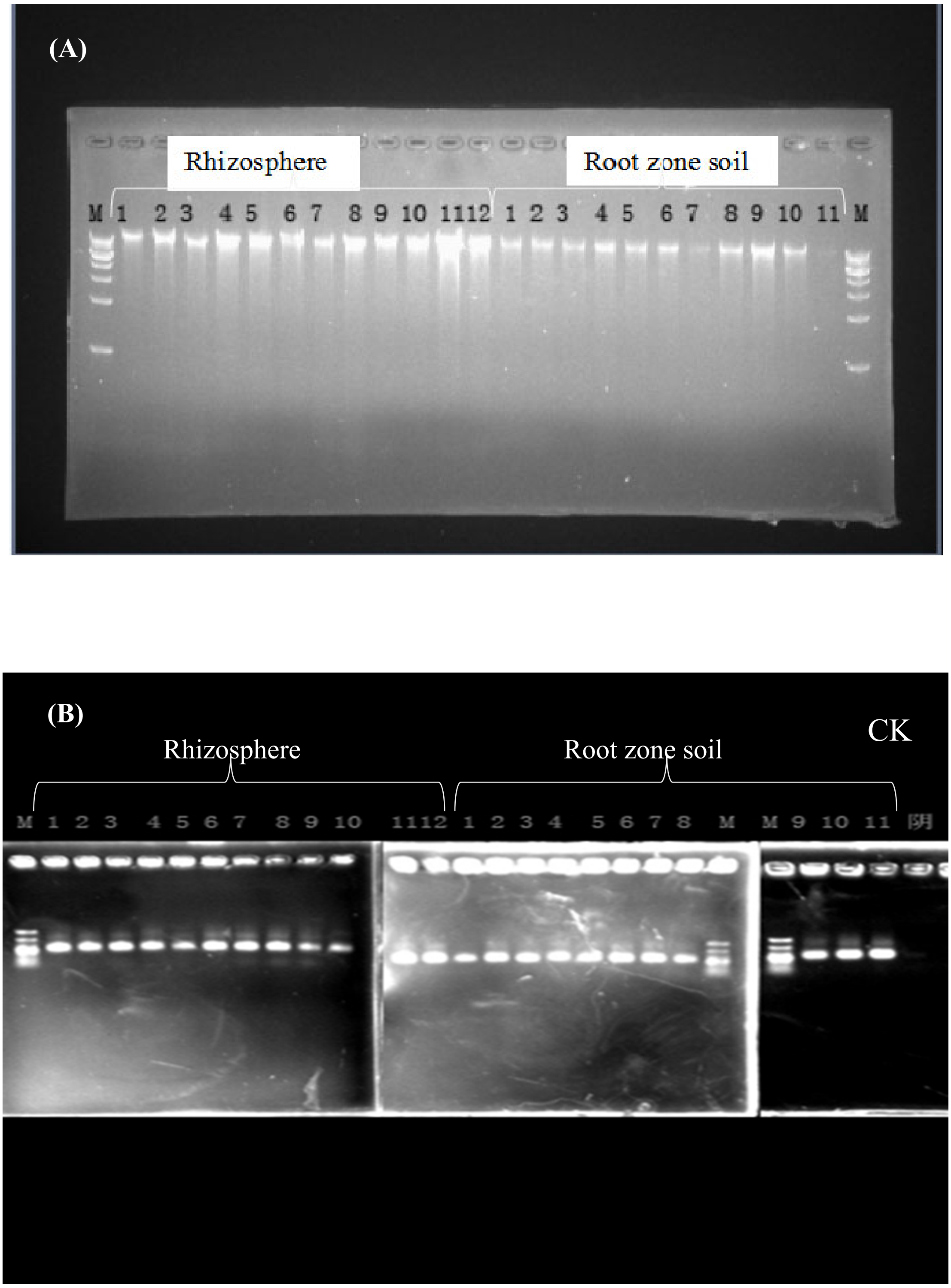
Fig. S1 Gel electrophoresis map of soil DNA (A) and PCR products (B)

Fig. S2. Sequences information of taxa and length distribution

Fig. S3. LEfSe analysis show different taxa between rhizosphere and root zone. The circle radiating from the inside to the outside represents the classification level of the genus (or species). The diameter of the circle is proportional to the relative abundance. Coloring principles: Species with no significant difference were colored yellow, the red node was microorganisms that played an important role in the red group, and the green node was indicated to the green group.

Figure S5. R code and envfit result for RDA analysis

Figure S4. Rarefaction curves of the sequence data



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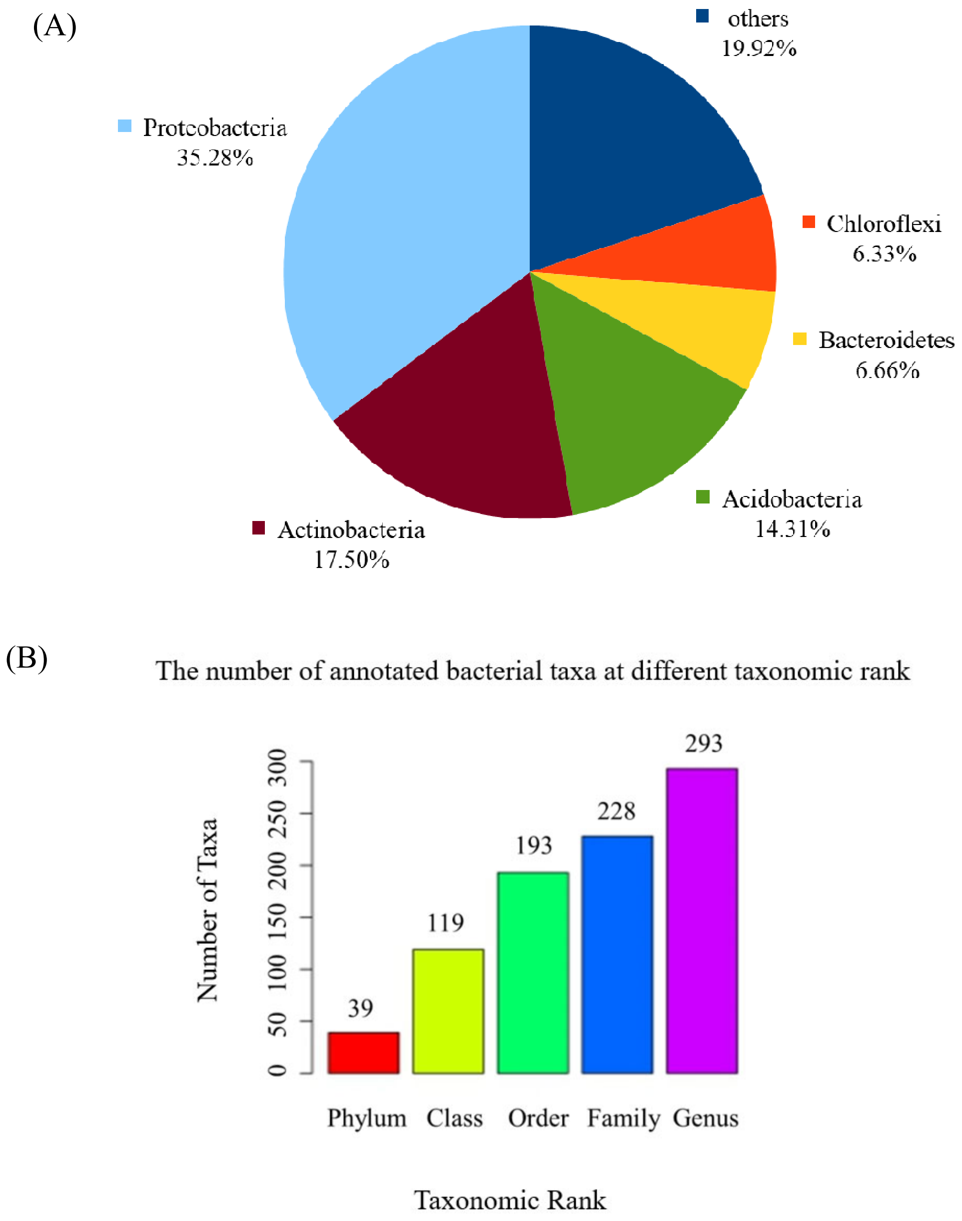


Fig. S2. Annotated information of bacterial taxa by *de novo* OTU picking protocol

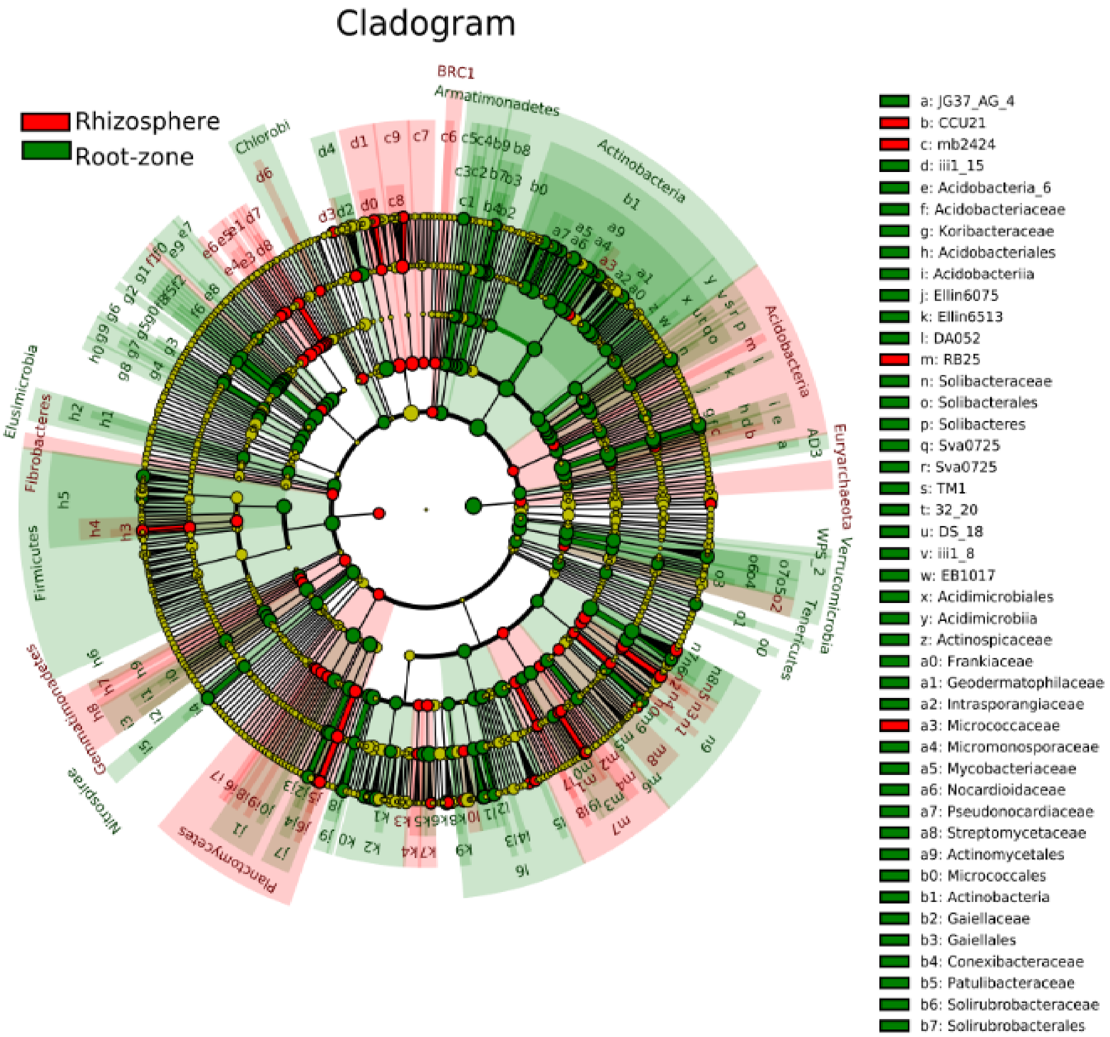


Fig. S3. LEfSe analysis show different taxa between rhizosphere and root zone. The circle radiating from the inside to the outside represents the classification level of the genus (or species). The diameter of the circle is proportional to the relative abundance. Coloring principles: Species with no significant difference were colored yellow, the red node was microorganisms that played an important role in the red group, and the green node was indicated to the green group.

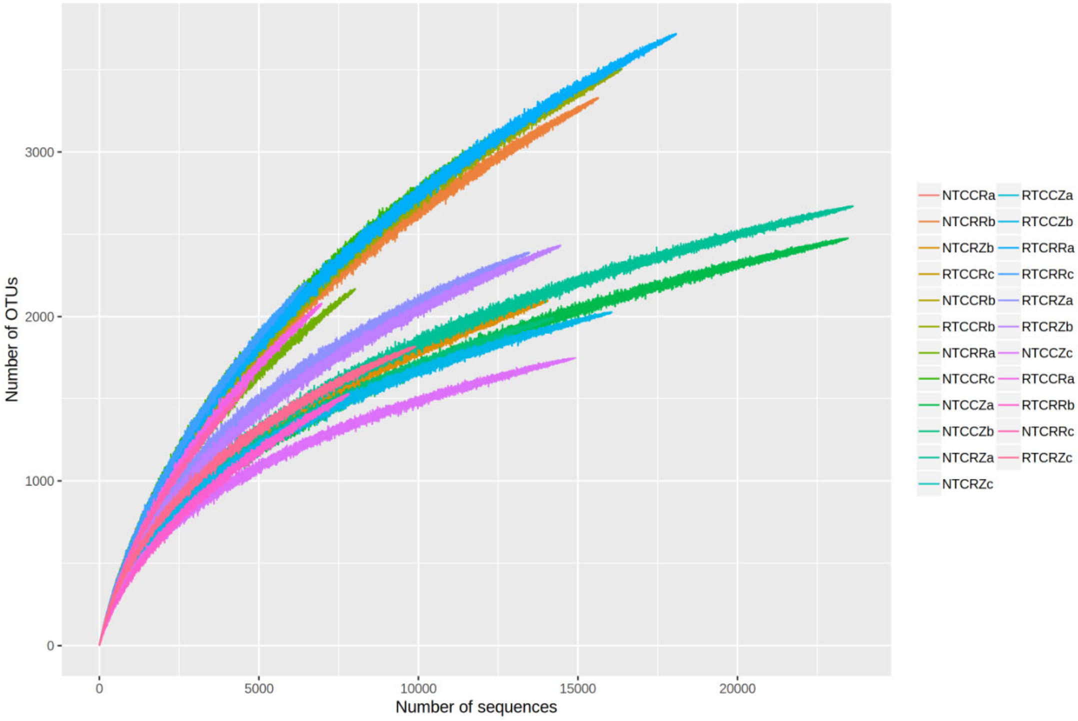
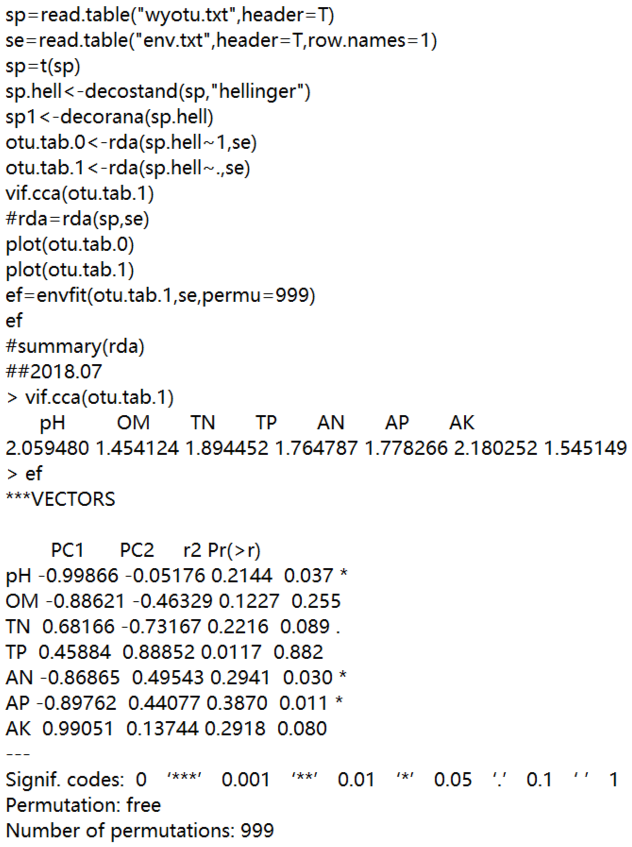


Figure S4. Rarefaction curves of the sequence data



```
sp=read.table("wyotu.txt",header=T)
se=read.table("env.txt",header=T,row.names=1)
sp=t(sp)
sp.hell<-decostand(sp,"hellinger")
sp1<-decorana(sp.hell)
otu.tab.0<-rda(sp.hell~1,se)
otu.tab.1<-rda(sp.hell~.,se)
vif.cca(otu.tab.1)
#rda=rda(sp,se)
plot(otu.tab.0)
plot(otu.tab.1)
ef=envfit(otu.tab.1,se,permu=999)
ef
#summary(rda)
##2018.07
> vif.cca(otu.tab.1)
      pH       OM       TN       TP       AN       AP       AK
2.059480 1.454124 1.894452 1.764787 1.778266 2.180252 1.545149
> ef
***VECTORS

        PC1      PC2     r2 Pr(>r)
pH -0.99866 -0.05176 0.2144  0.037 *
OM -0.88621 -0.46329 0.1227  0.255
TN  0.68166 -0.73167 0.2216  0.089 .
TP  0.45884  0.88852 0.0117  0.882
AN -0.86865  0.49543 0.2941  0.030 *
AP -0.89762  0.44077 0.3870  0.011 *
AK  0.99051  0.13744 0.2918  0.080
---
Signif. codes:  0  '***'  0.001  '**'  0.01  '*'  0.05  '.'  0.1  ' '  1
Permutation: free
Number of permutations: 999
```

Figure S5. R code and envfit result for RDA analysis