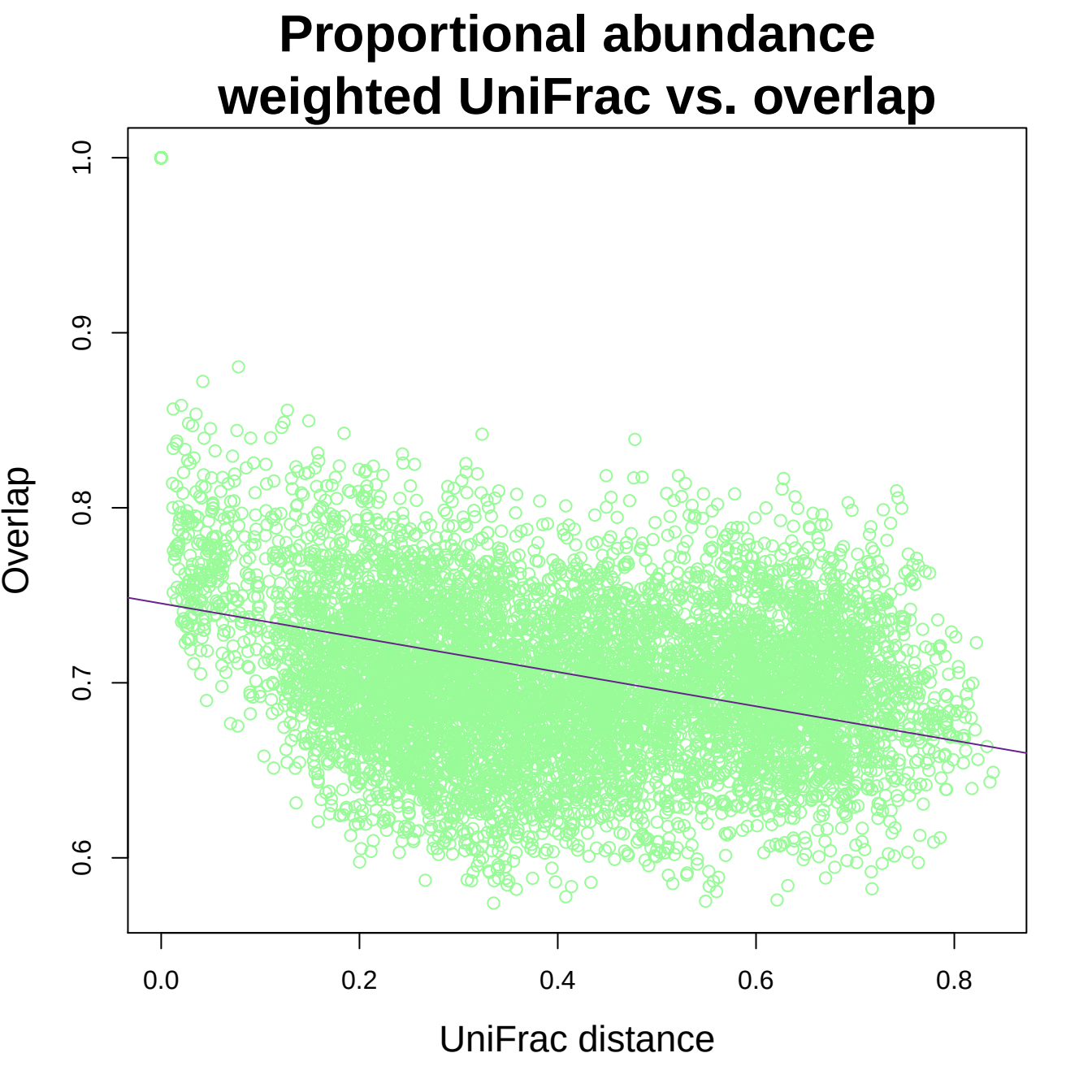
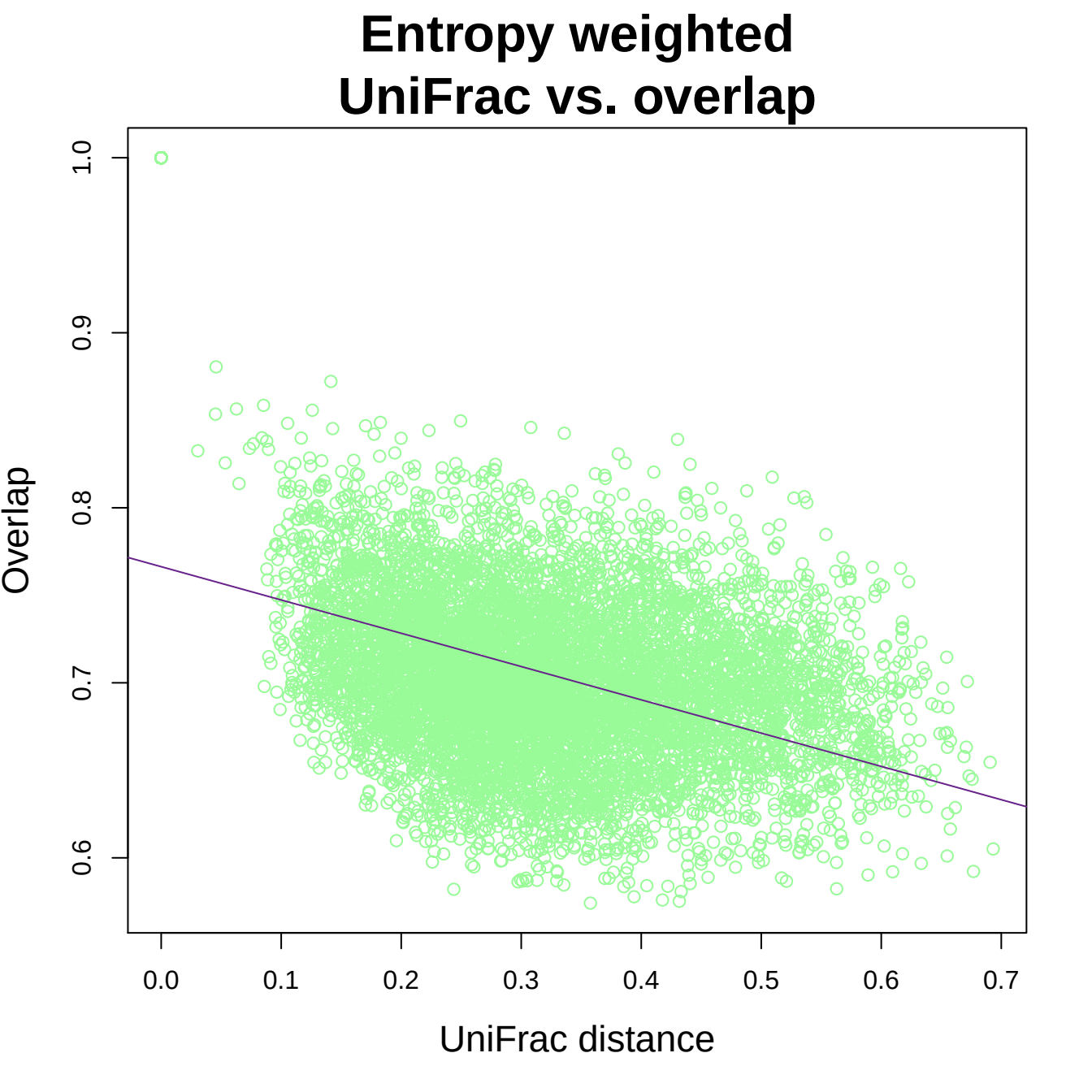
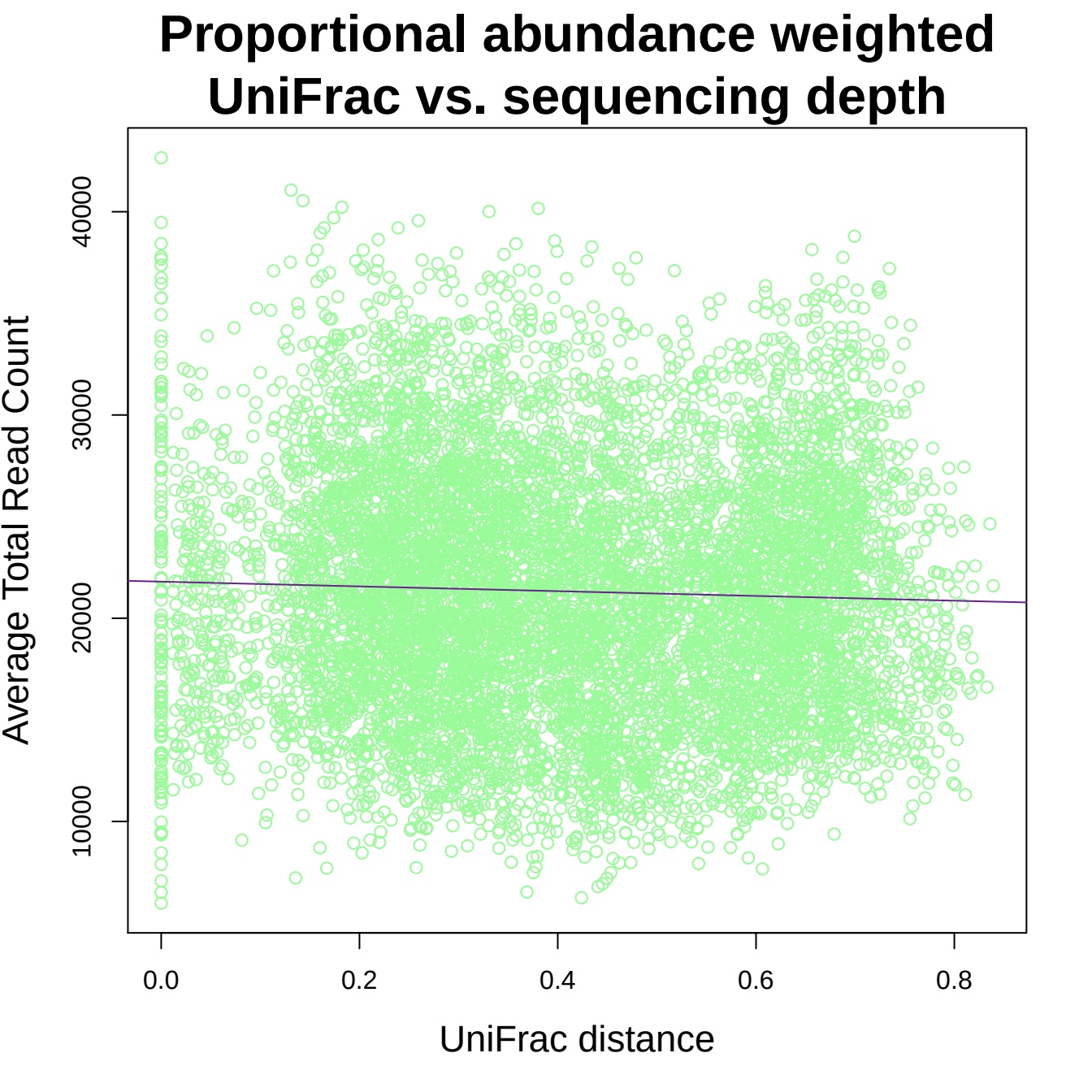
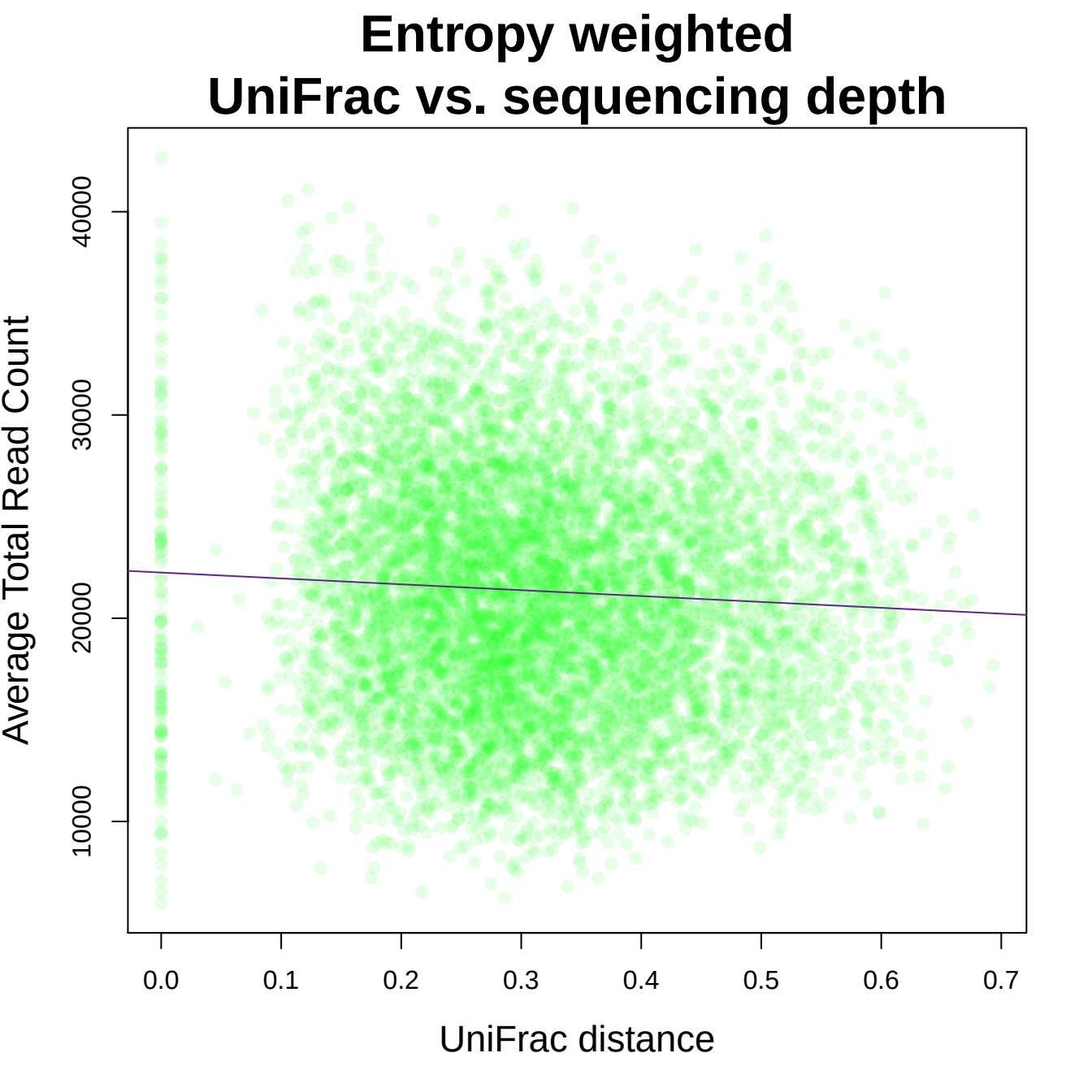
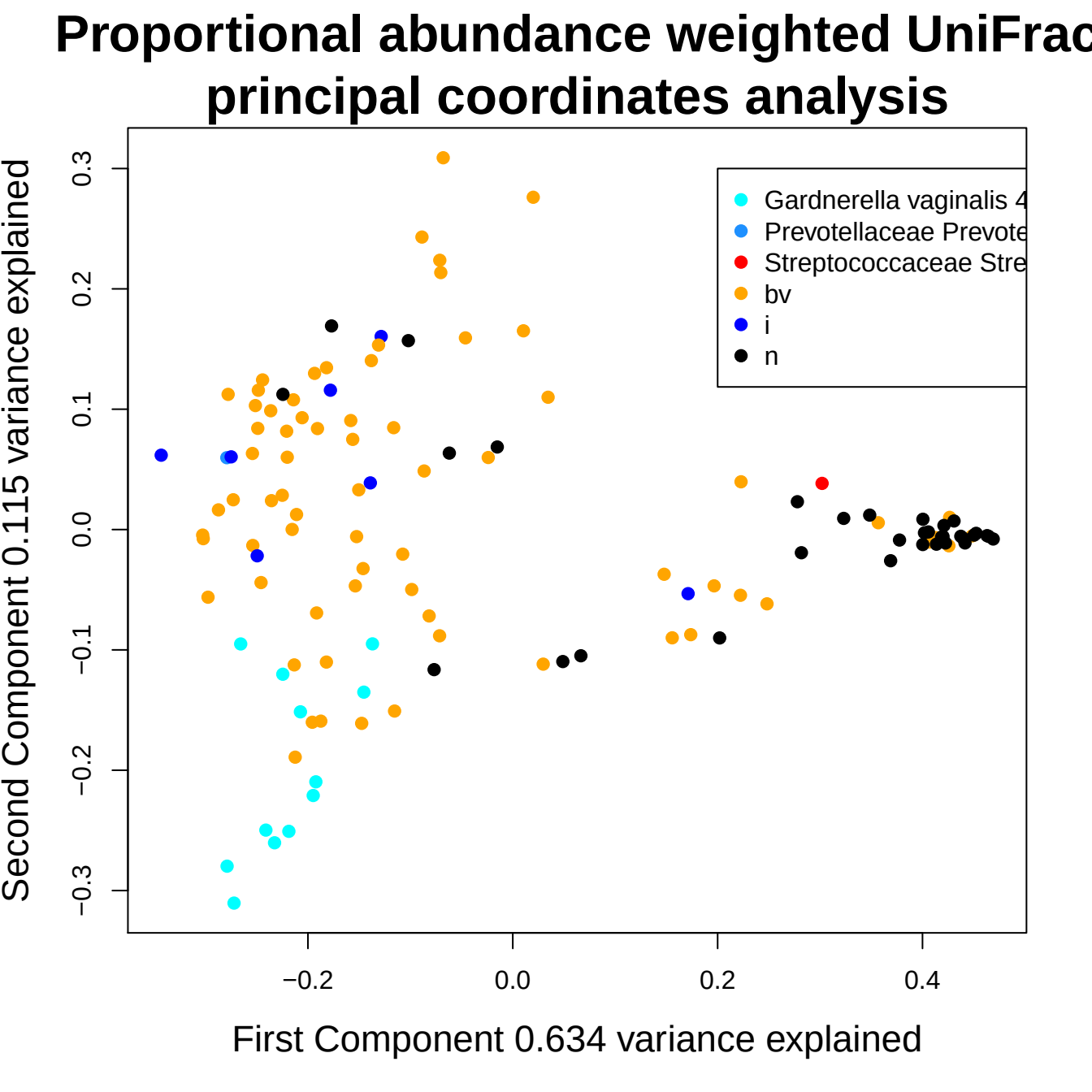
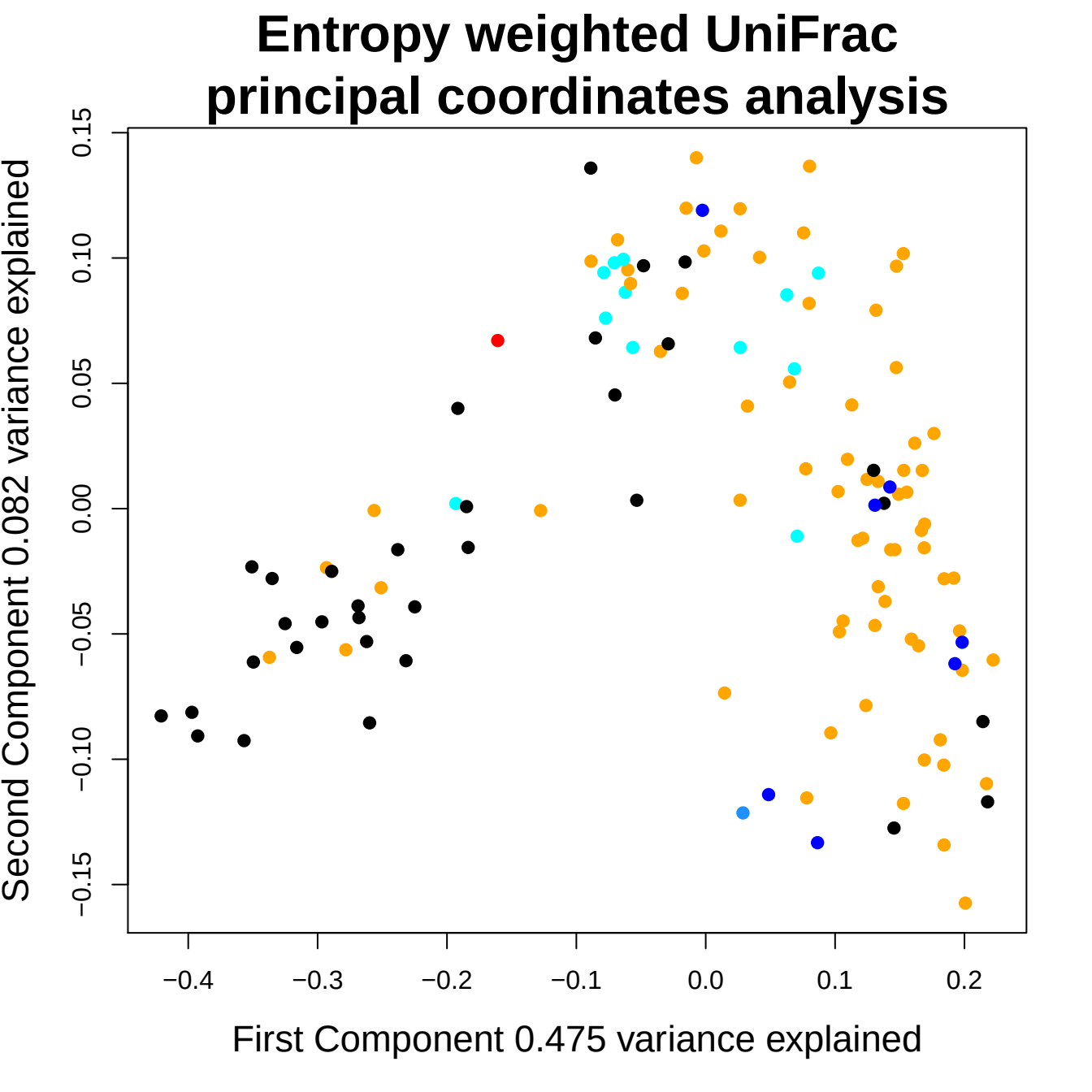

Proportional abundance
weighted UniFrac vs. overlap
Overlap
1.0
0.9
0.8
0.7
0.6
0.0
0.2
0.4
0.6
0.8
UniFrac distance

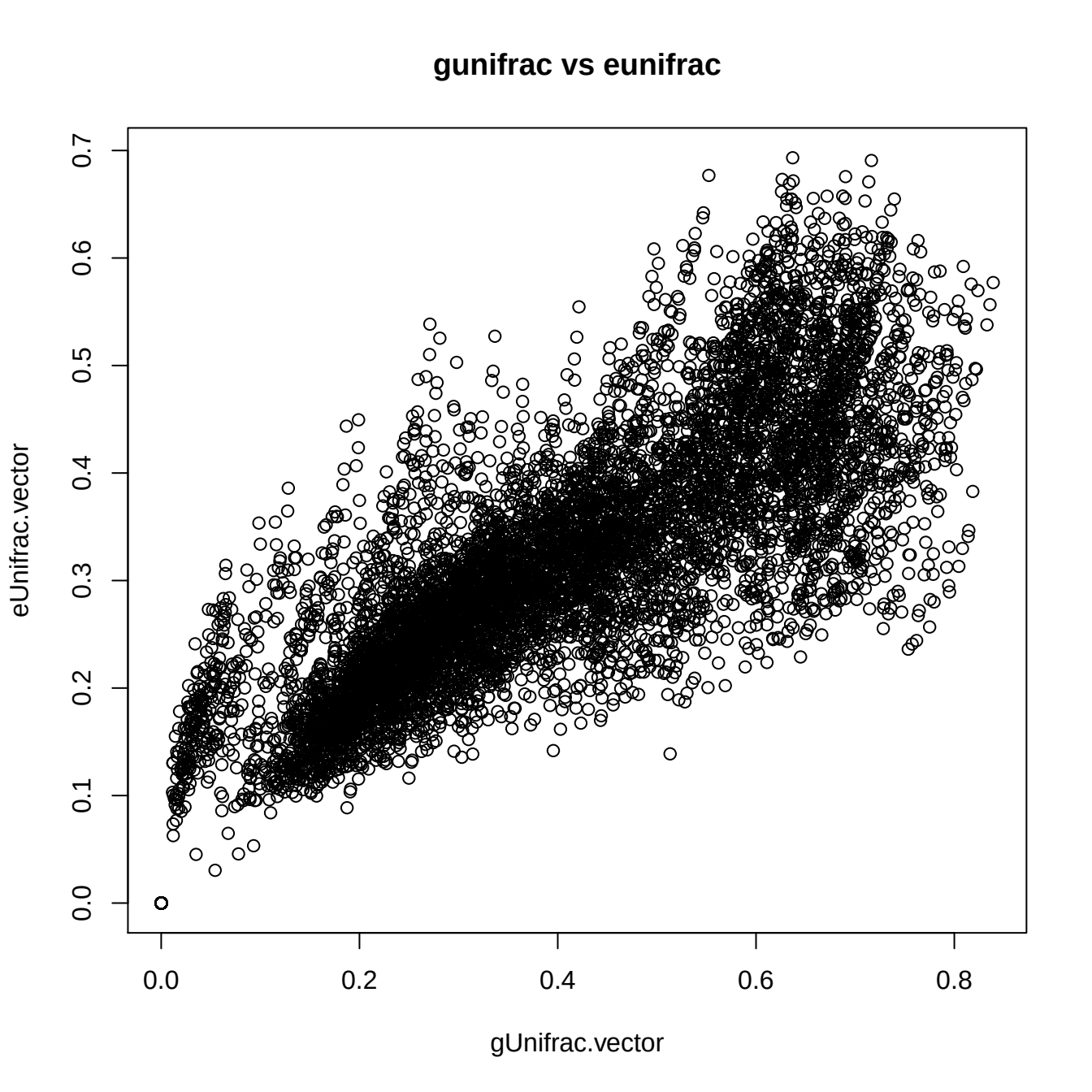

Entropy weighted
UniFrac vs. overlap
Overlap
1.0
0.9
0.8
0.7
0.6
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
UniFrac distance

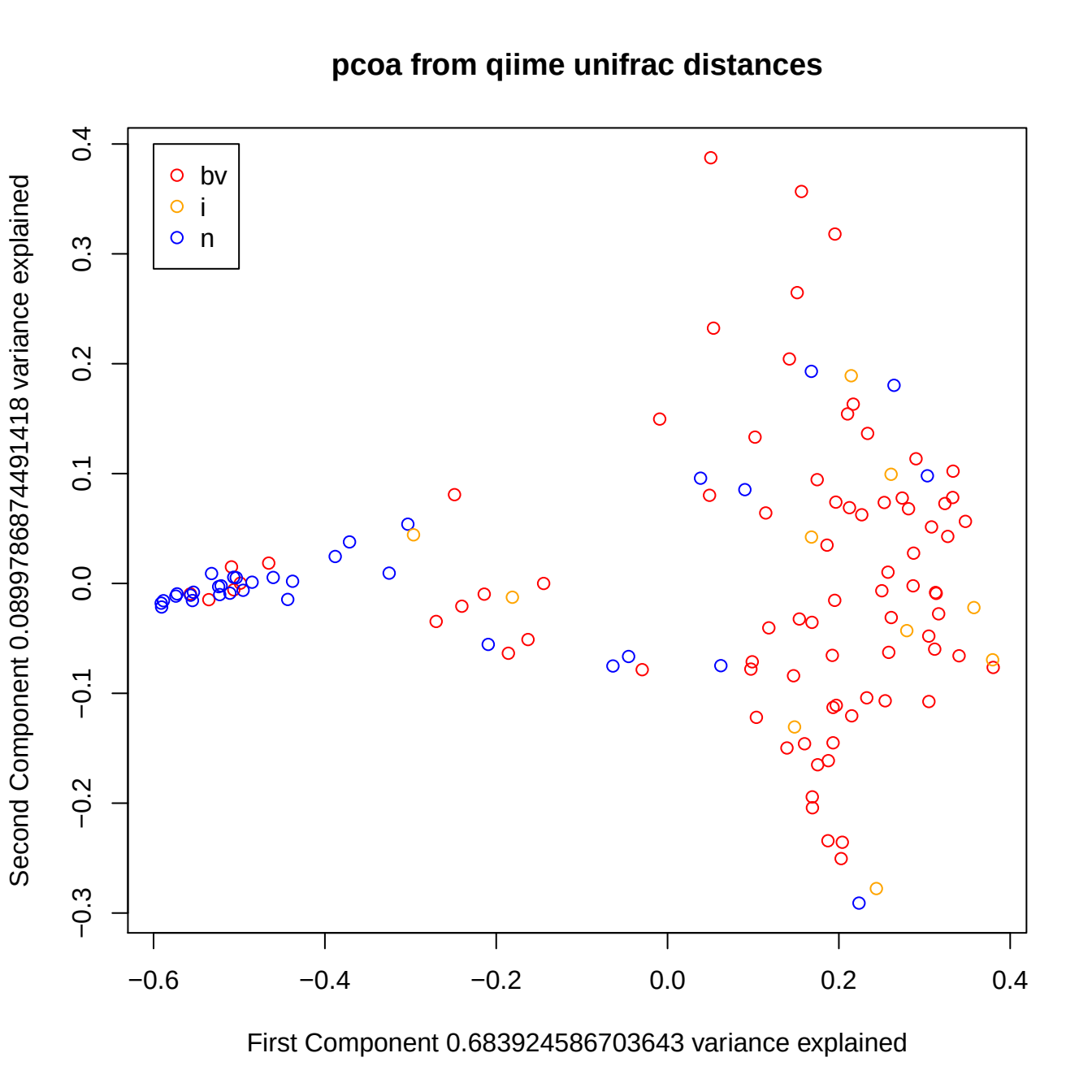

Proportional abundance weighted UniFrac vs. sequencing depth
Average Total Read Count
10000
20000
30000
40000
0.0
0.2
0.4
0.6
0.8
UniFrac distance

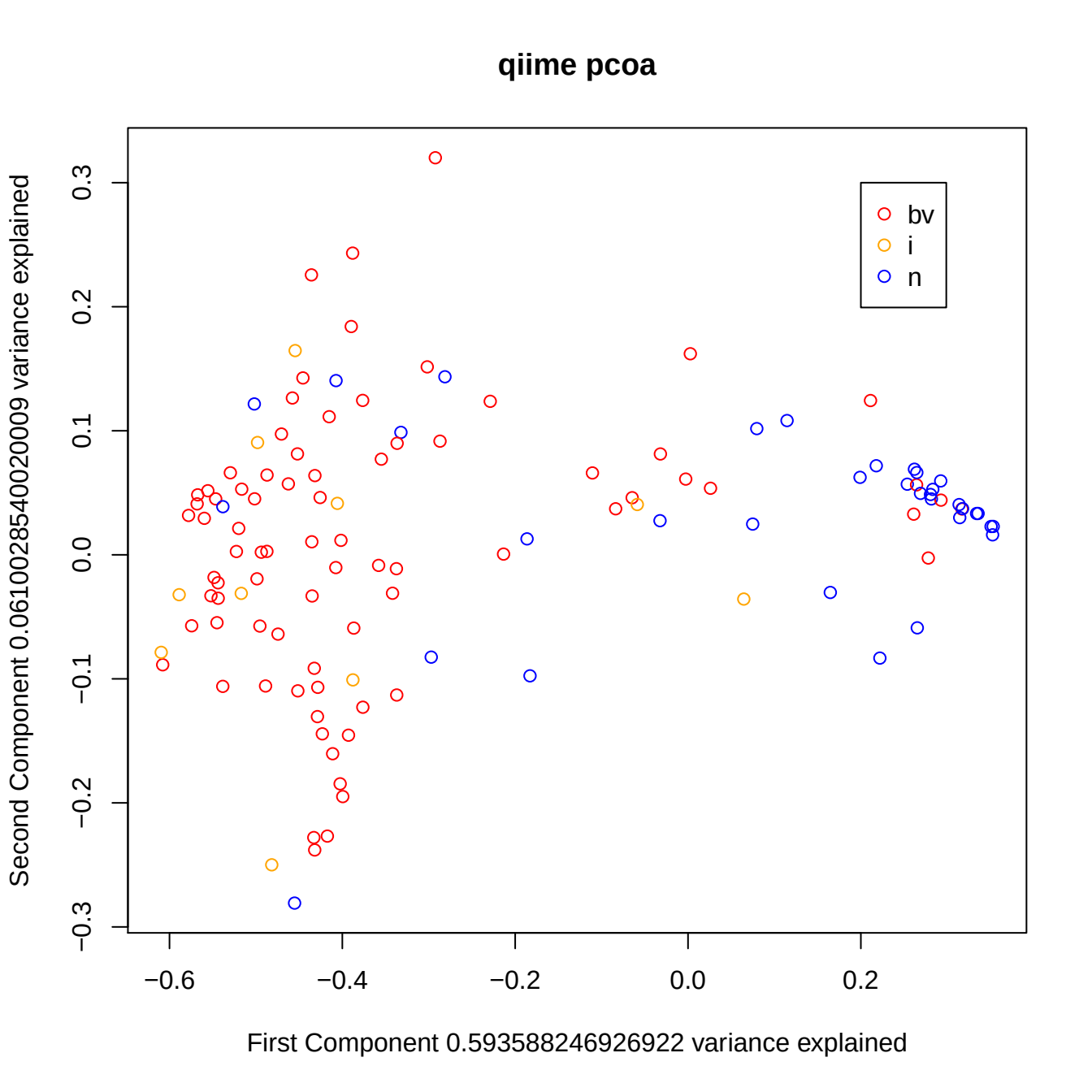

Entropy weighted
UniFrac vs. sequencing depth
Average Total Read Count
10000
20000
30000
40000
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
UniFrac distance

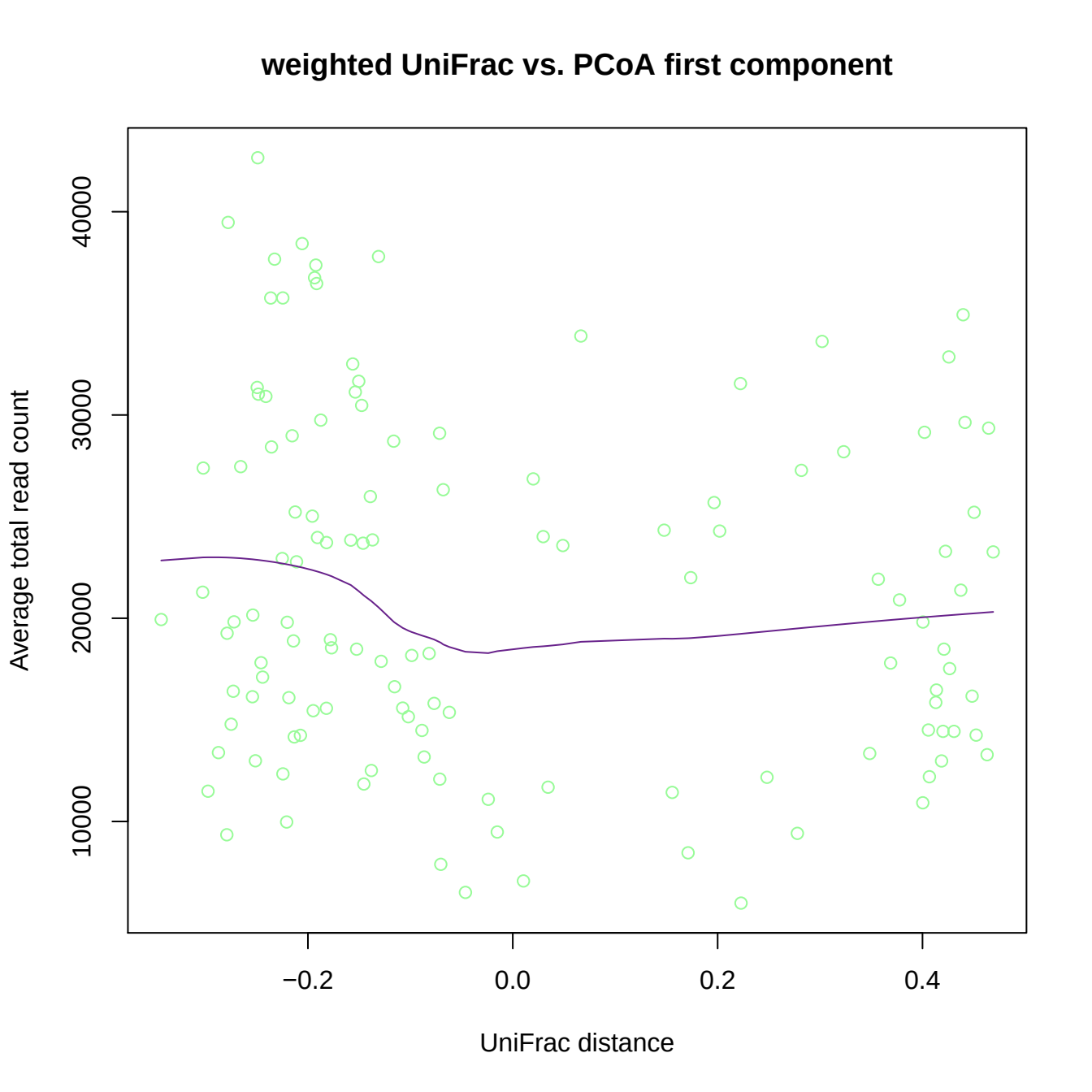

Proportional abundance weighted UniFrac
principal coordinates analysis
Gardnerella vaginalis 4
Prevotellaceae Prevote
Streptococcaceae Stre
bv
i
n
Second Component 0.115 variance explained
First Component 0.634 variance explained
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
−0.2
0.0
0.2
0.4

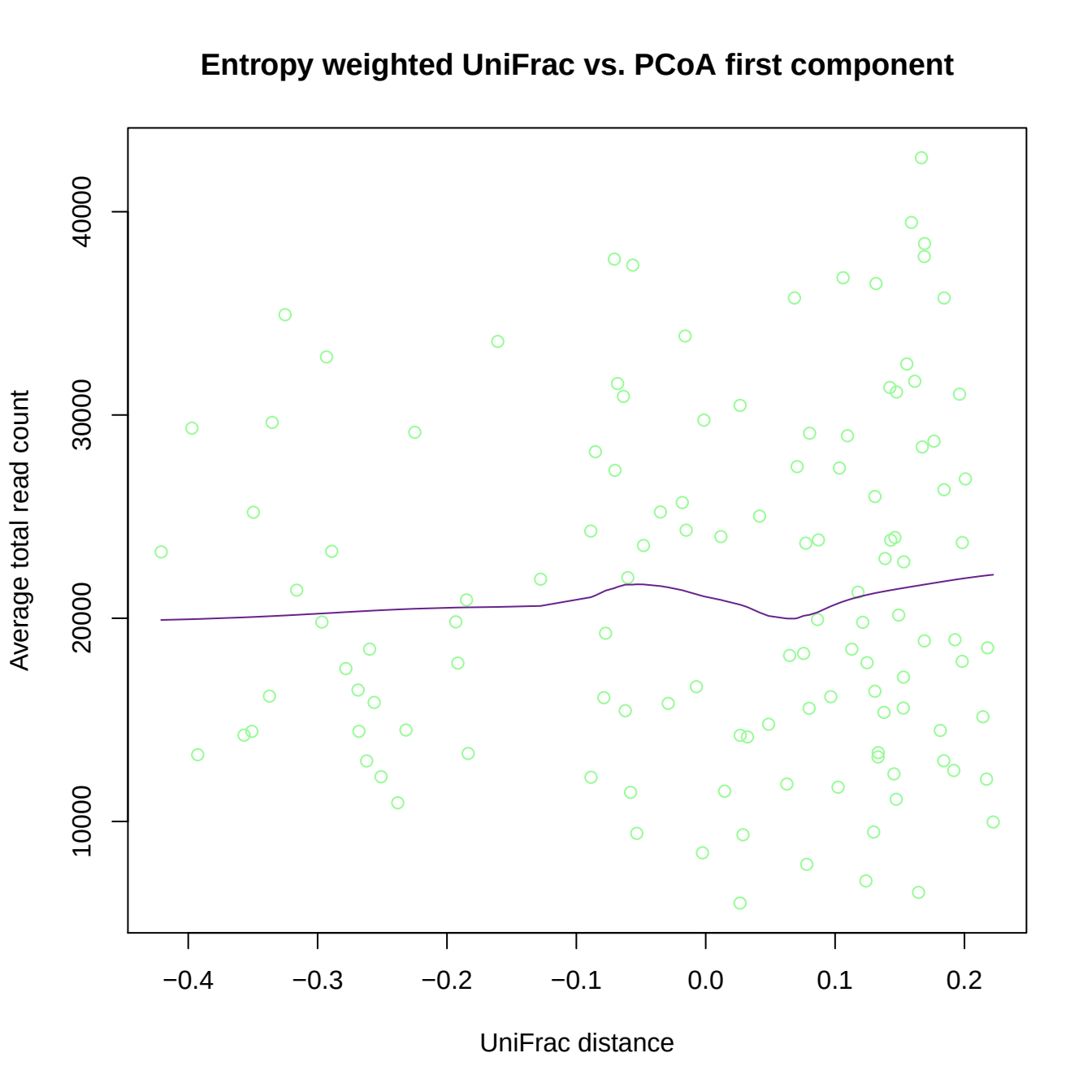

Entropy weighted UniFrac
principal coordinates analysis
Second Component 0.082 variance explained
First Component 0.475 variance explained
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.4
−0.3
−0.2
−0.1
0.0
0.1
0.2

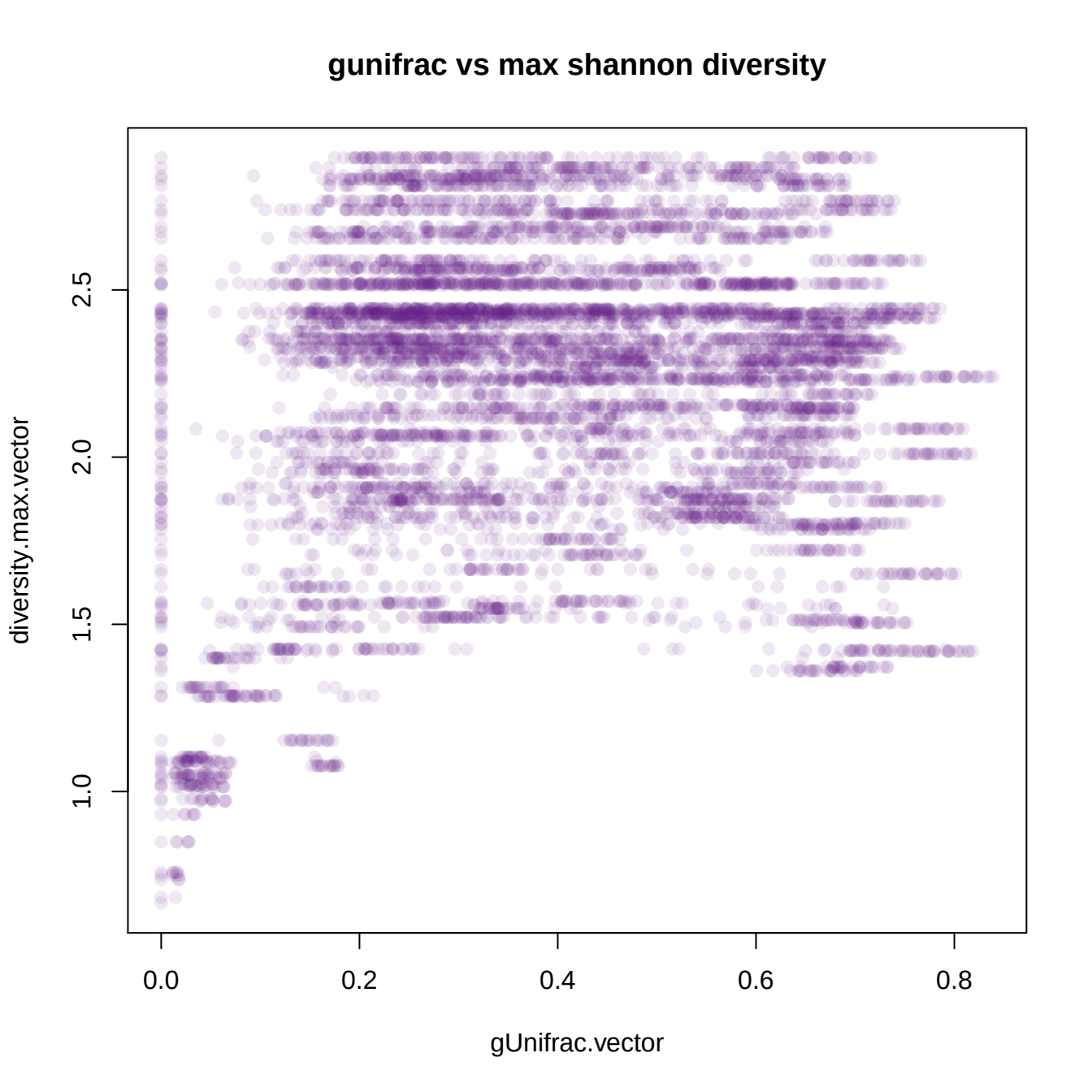

gunifrac vs eunifrac
eUnifrac.vector
gUnifrac.vector
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.0
0.2
0.4
0.6
0.8

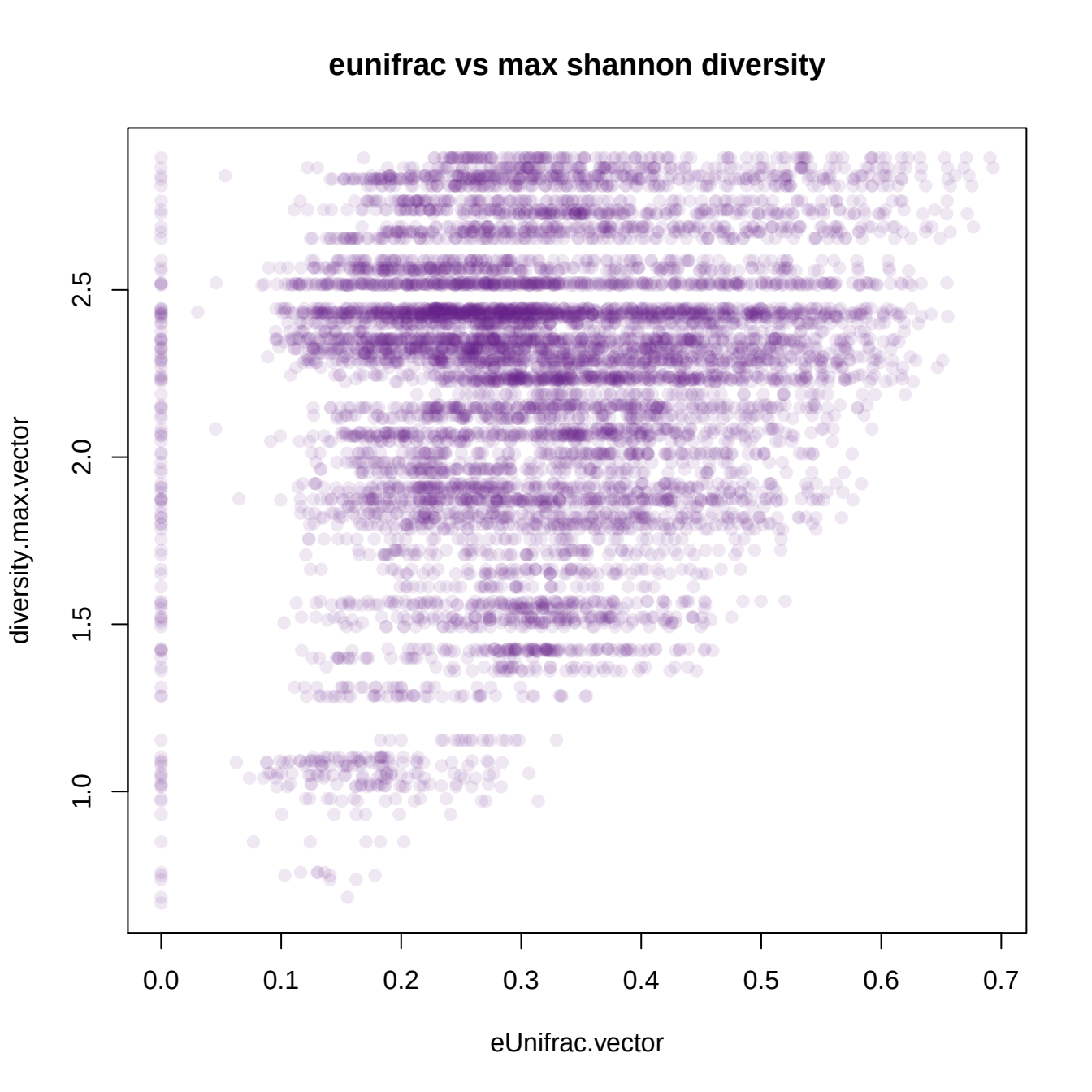

pcoa from qiime unifrac distances
bv
i
n
Second Component 0.0899786874491418 variance explained
First Component 0.683924586703643 variance explained
0.4
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
−0.6
−0.4
−0.2
0.0
0.2
0.4

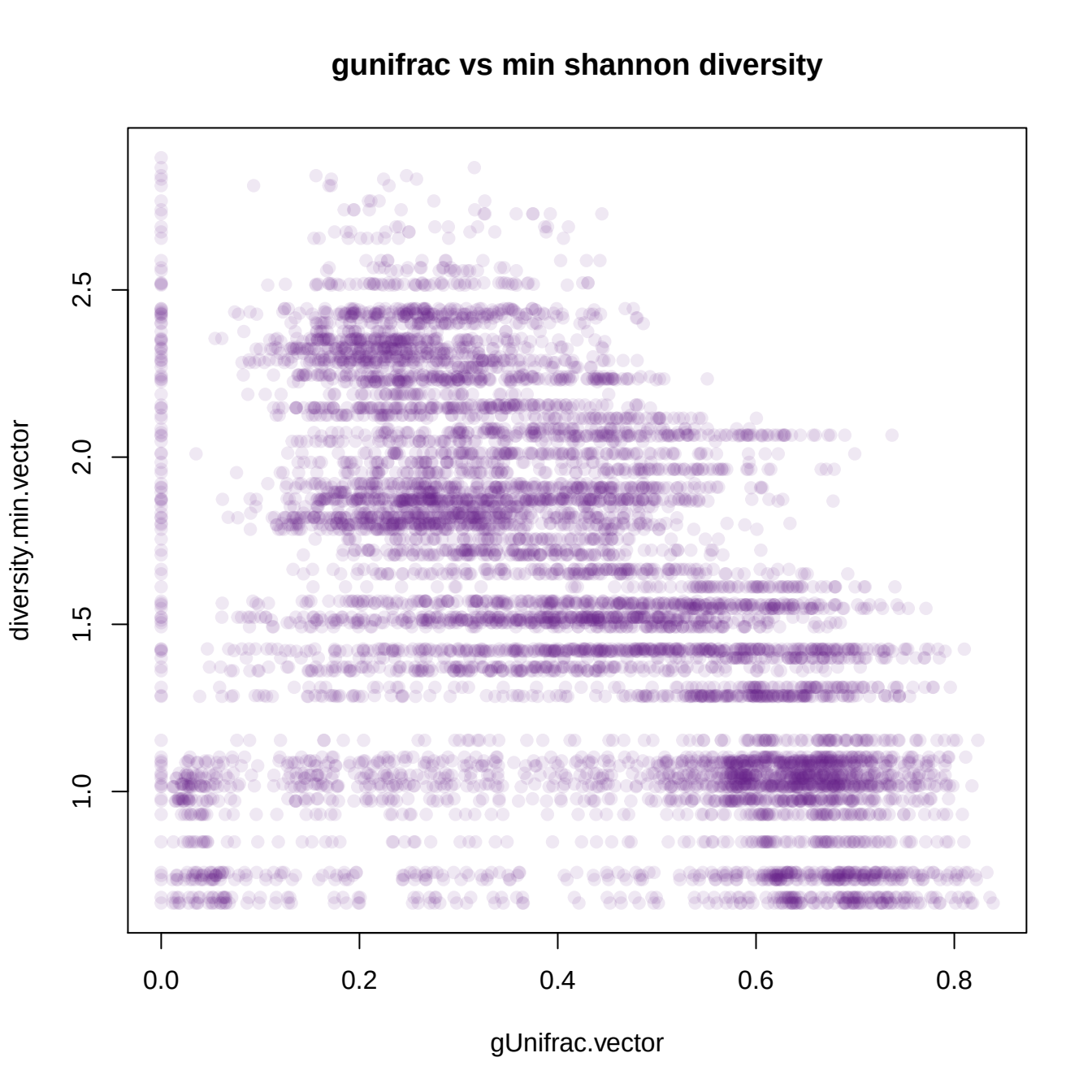

qiime pcoa
bv
i
n
Second Component 0.061002854002009 variance explained
First Component 0.593588246926922 variance explained
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
−0.6
−0.4
−0.2
0.0
0.2

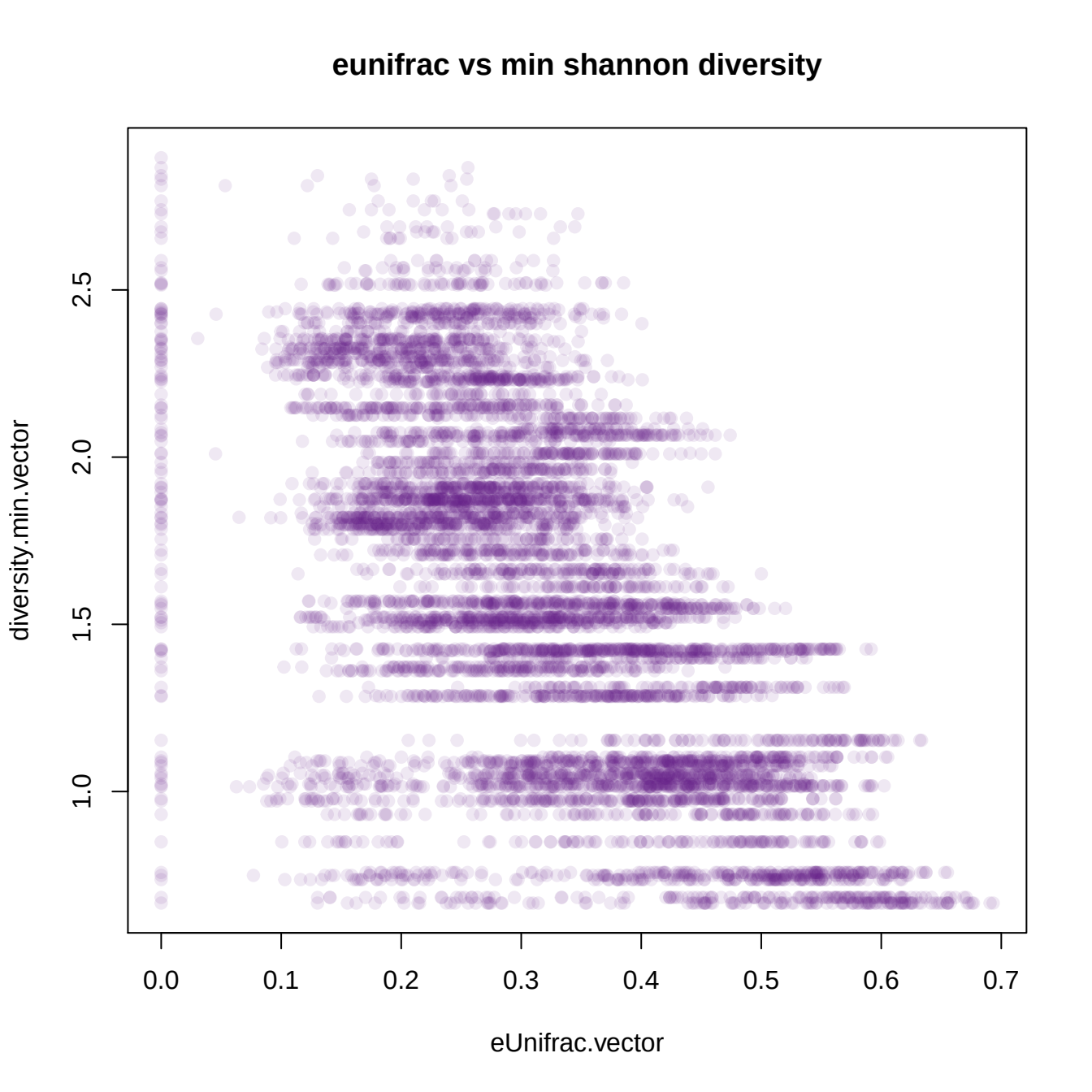

weighted UniFrac vs. PCoA first component
Average total read count
10000
20000
30000
40000
−0.2
0.0
0.2
0.4
UniFrac distance

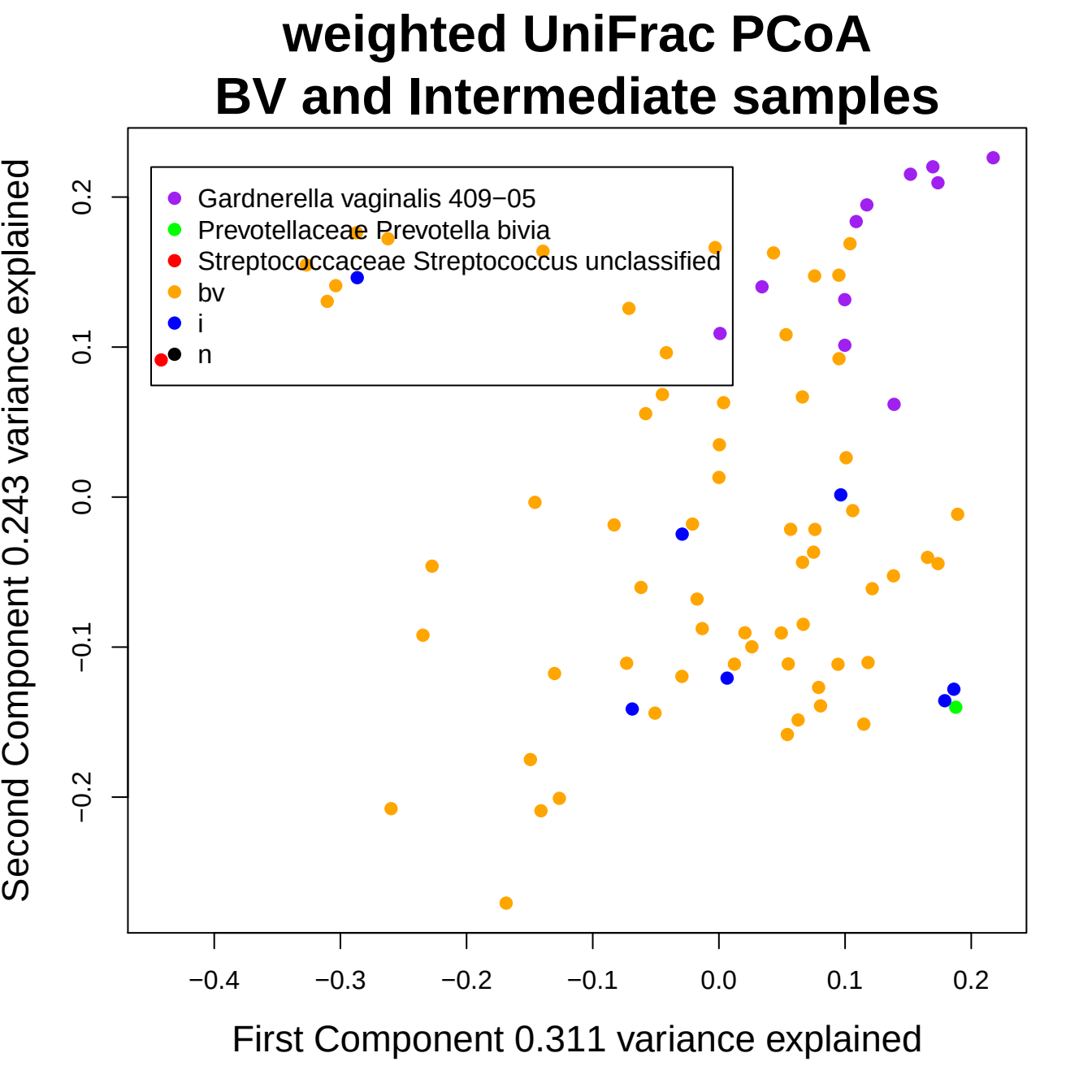

Entropy weighted UniFrac vs. PCoA first component
Average total read count
10000
20000
30000
40000
−0.4
−0.3
−0.2
−0.1
0.0
0.1
0.2
UniFrac distance

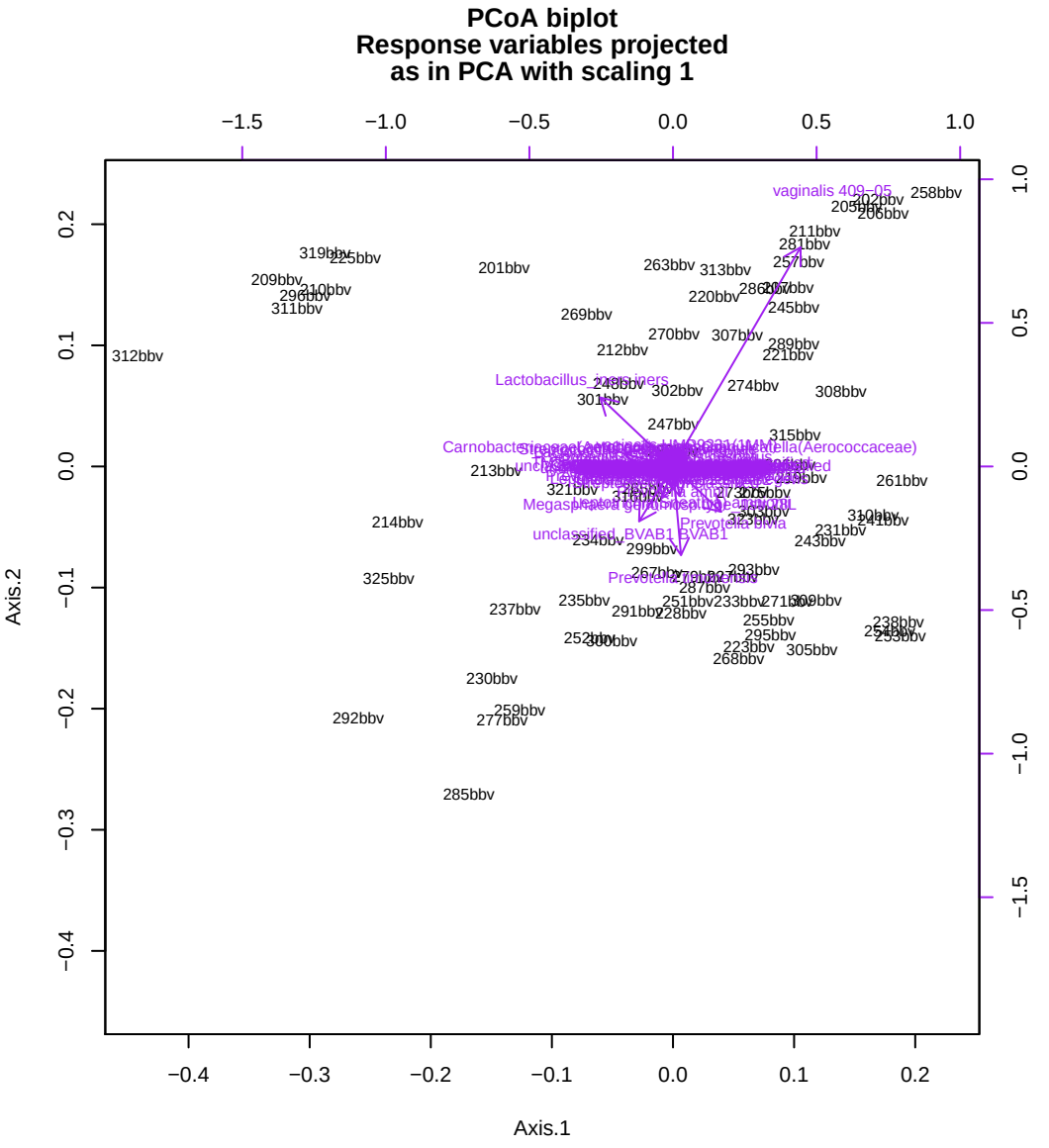

gunifrac vs max shannon diversity
diversity.max.vector
gUnifrac.vector
1.0
1.5
2.0
2.5
0.0
0.2
0.4
0.6
0.8

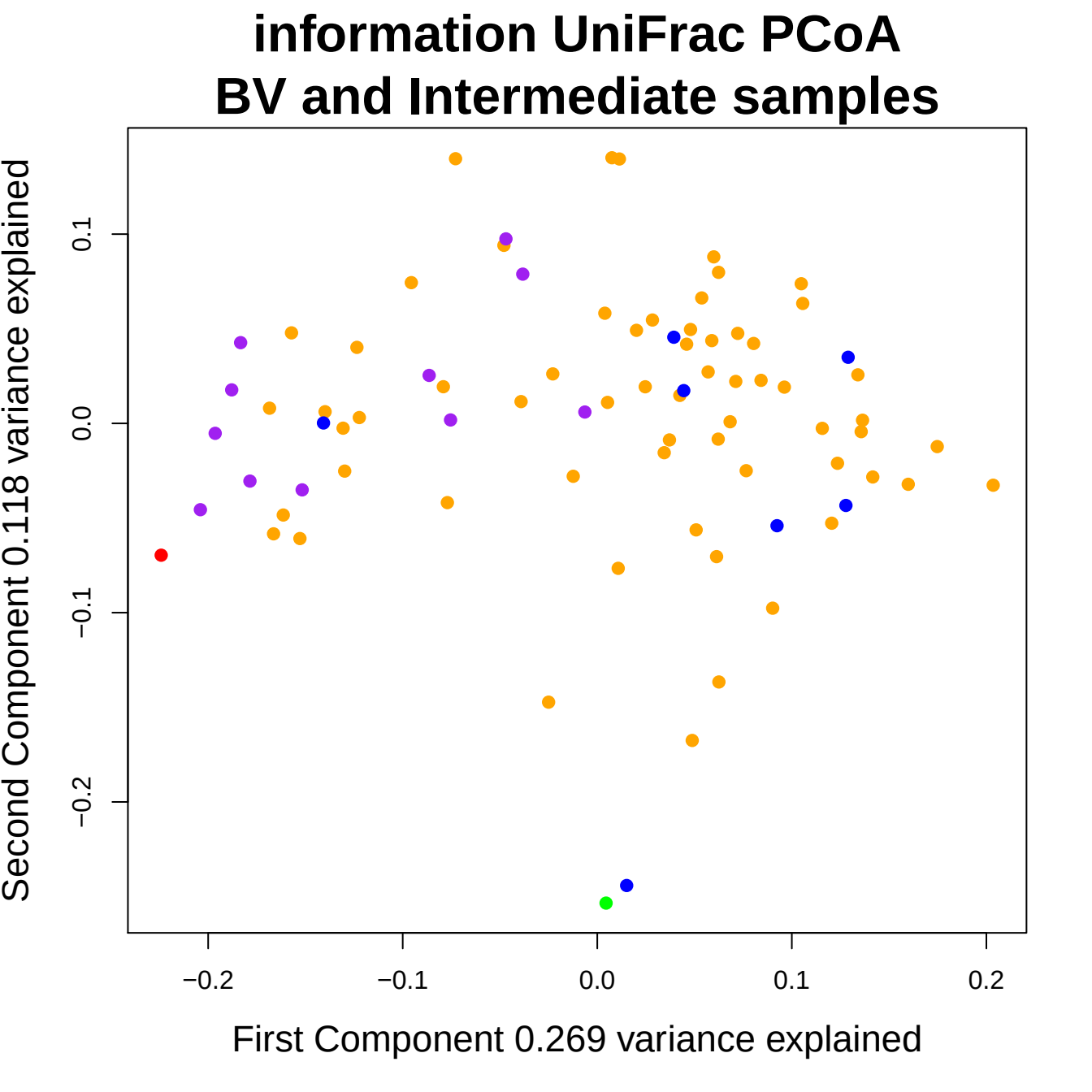

eunifrac vs max shannon diversity
diversity.max.vector
eUnifrac.vector
1.0
1.5
2.0
2.5
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7

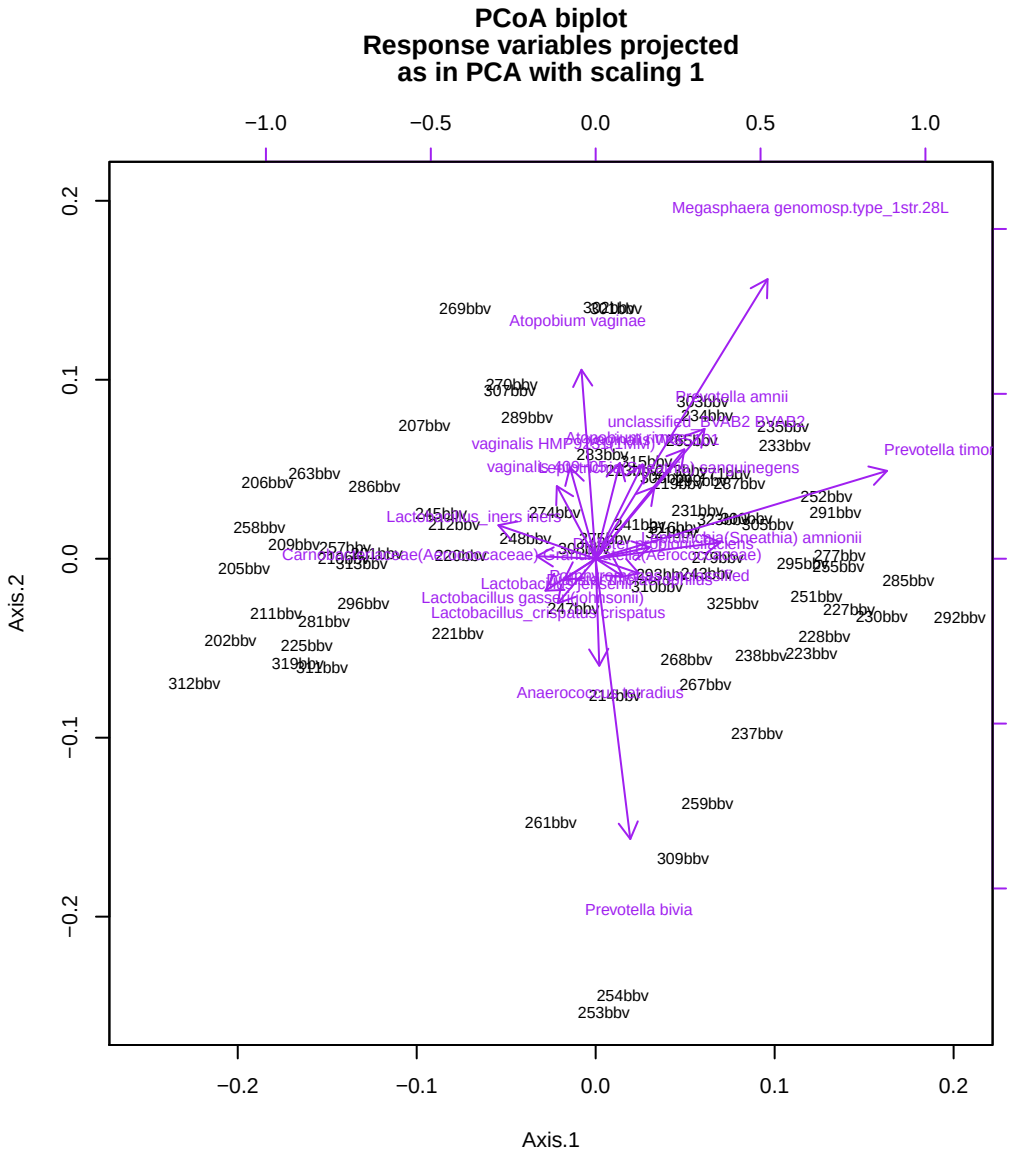

gunifrac vs min shannon diversity
diversity.min.vector
gUnifrac.vector
1.0
1.5
2.0
2.5
0.0
0.2
0.4
0.6
0.8

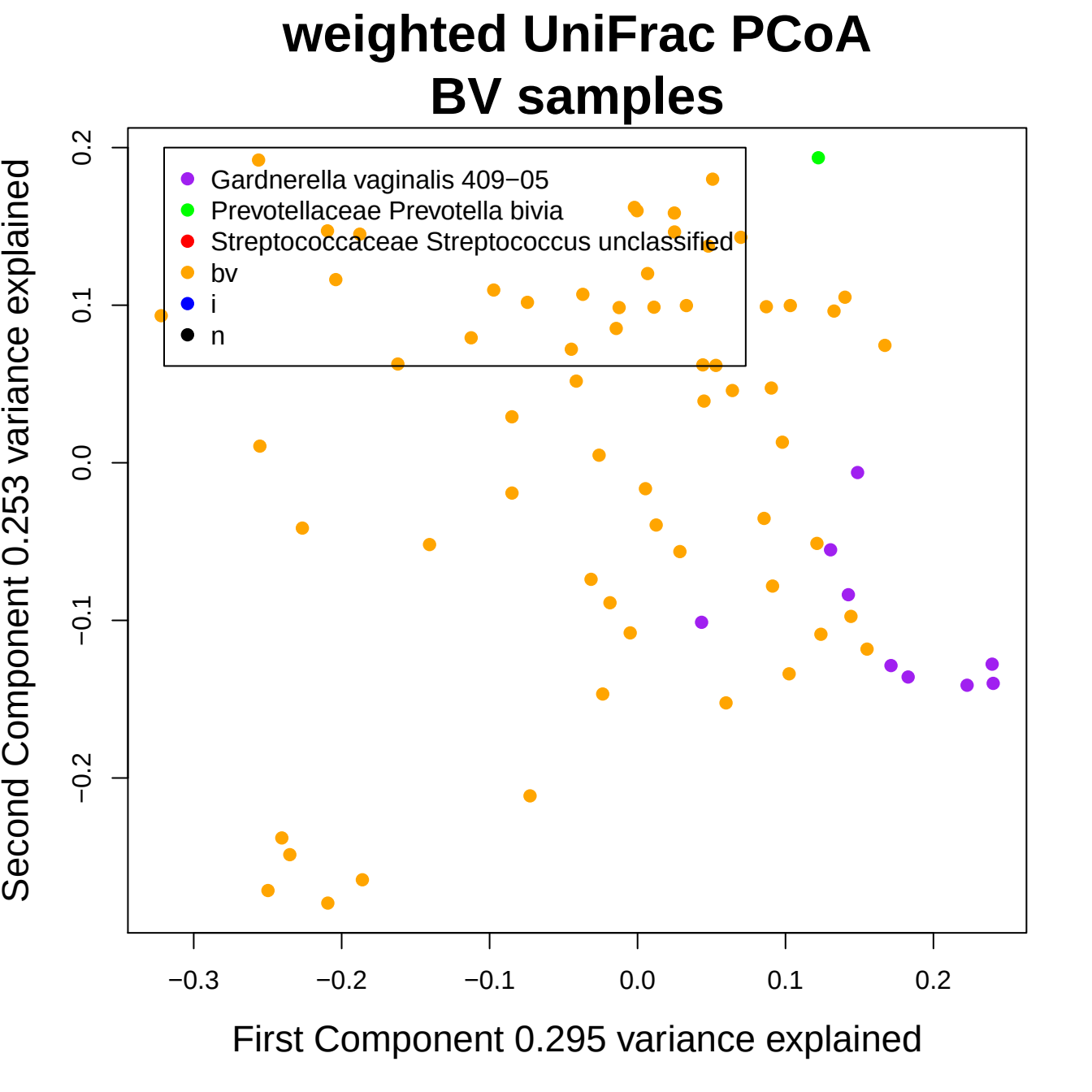

eunifrac vs min shannon diversity
diversity.min.vector
eUnifrac.vector
1.0
1.5
2.0
2.5
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7

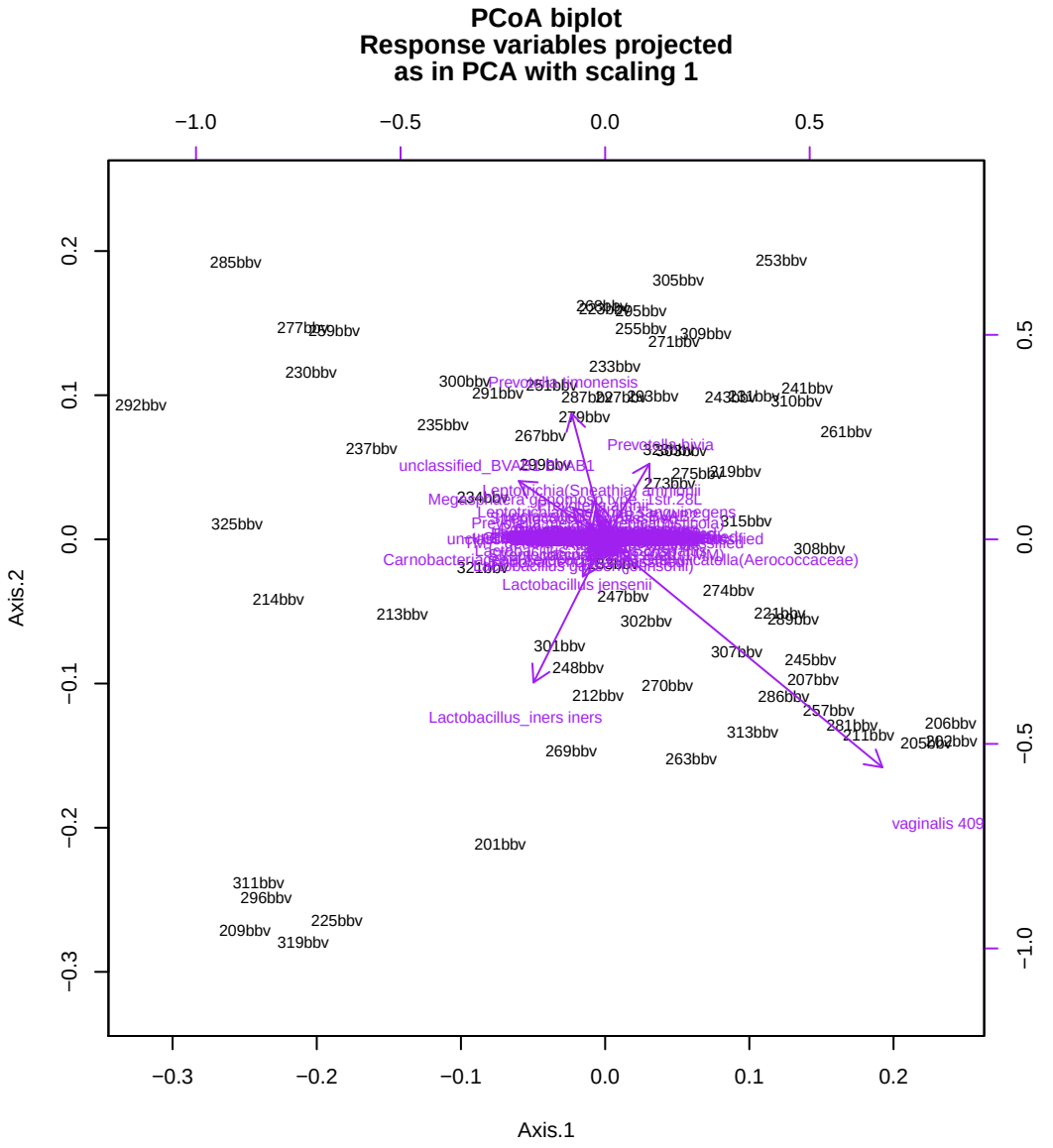

weighted UniFrac PCoA
BV and Intermediate samples
Gardnerella vaginalis 409−05
Prevotellaceae Prevotella bivia
Streptococcaceae Streptococcus unclassified
bv
i
n
Second Component 0.243 variance explained
First Component 0.311 variance explained
−0.4
−0.3
−0.2
−0.1
0.0
0.1
0.2

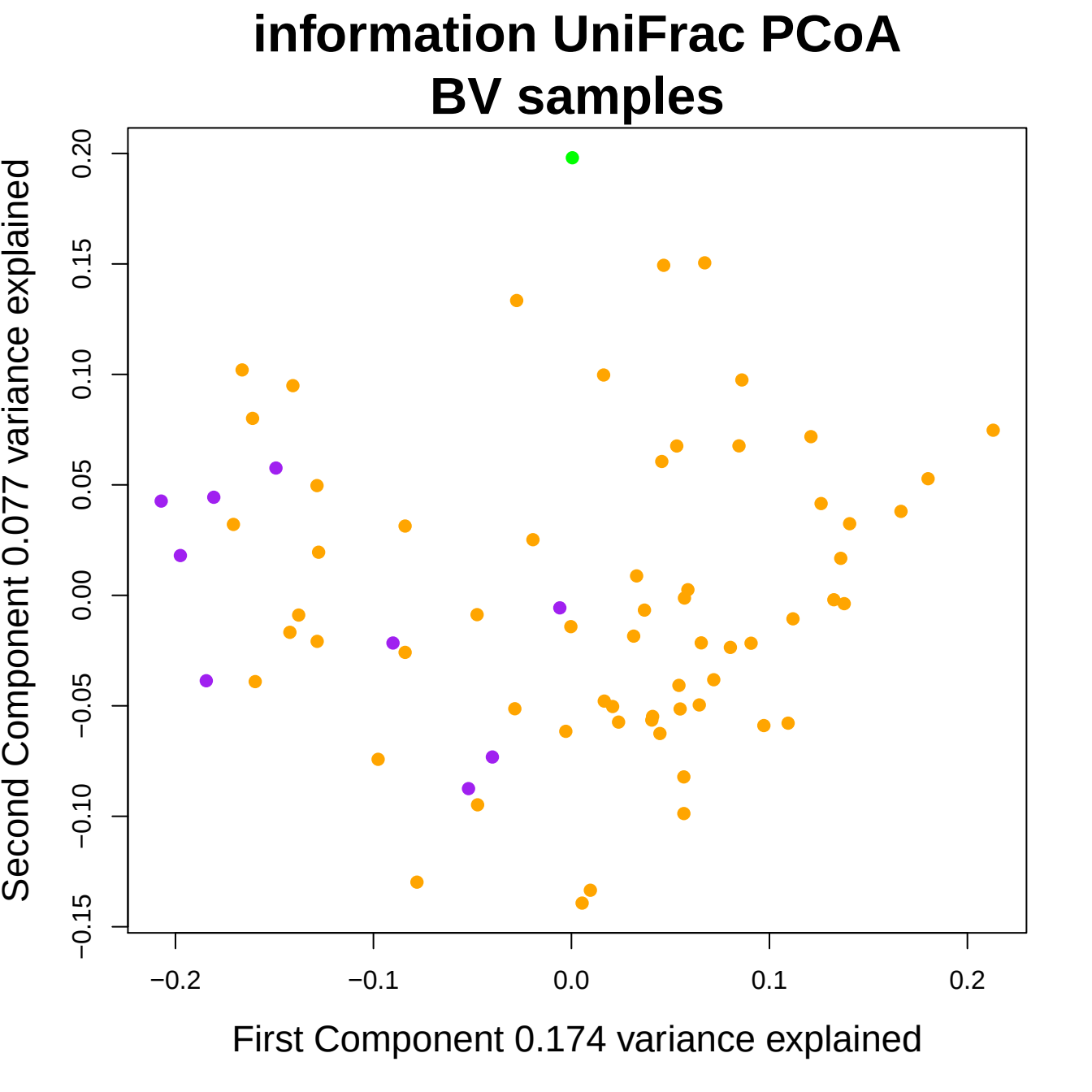

PCoA biplot
Response variables projected
as in PCA with scaling 1
Axis.1
Axis.2
vaginalis 409−05
Lactobacillus_iners
Carnobacteriaceae
Megasphaera genus
Prevotella bivia
unclassified_BVAB1 BVAB1
Prevotella
258bbv
211bbv
281bbv
257bbv
263bbv
313bbv
201bbv
209bbv
311bbv
269bbv
220bbv
245bbv
270bbv
307bbv
289bbv
221bbv
312bbv
212bbv
302bbv
274bbv
308bbv
247bbv
315bbv
213bbv
261bbv
214bbv
231bbv
243bbv
299bbv
325bbv
293bbv
287bbv
235bbv
237bbv
255bbv
295bbv
305bbv
268bbv
230bbv
292bbv
259bbv
277bbv
285bbv

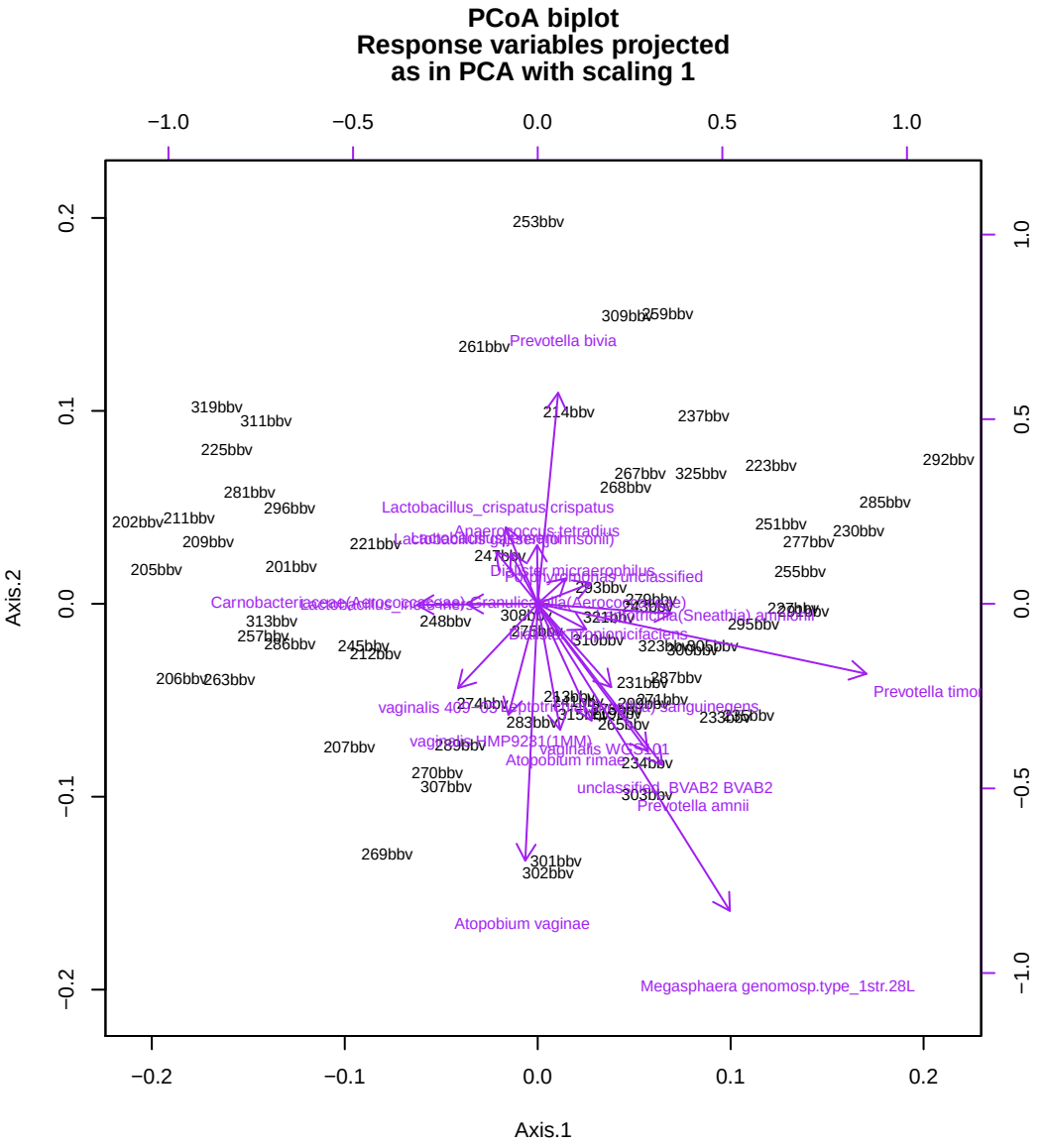

information UniFrac PCoA
BV and Intermediate samples
Second Component 0.118 variance explained
First Component 0.269 variance explained
0.1
0.0
−0.1
−0.2
−0.2
−0.1
0.0
0.1
0.2


PCoA biplot
Response variables projected
as in PCA with scaling 1
Axis.1
Axis.2
Megasphaera genomosp.type_1str.28L
Atopobium vaginae
Prevotella amnii
unclassified BVAB2 BVAB2
Prevotella timor
Lactobacillus_iners iners
Lactobacillus gasseri(johnsonii)
Lactobacillus_crispatus crispatus
Anaerococcus tetradius
Prevotella bivia
269bbv
289bbv
207bbv
263bbv
206bbv
286bbv
258bbv
205bbv
296bbv
211bbv
281bbv
202bbv
225bbv
312bbv
221bbv
268bbv
267bbv
237bbv
259bbv
261bbv
309bbv
254bbv
253bbv
285bbv
292bbv
228bbv
223bbv
238bbv
325bbv
251bbv
227bbv
230bbv
252bbv
291bbv
233bbv
235bbv
303bbv
234bbv
287bbv
231bbv
305bbv
277bbv
295bbv
255bbv
279bbv
310bbv
243bbv
248bbv
274bbv
212bbv
245bbv
283bbv
315bbv
219bbv
241bbv
220bbv
313bbv
209bbv
257bbv
279bbv
293bbv
247bbv
214bbv


weighted UniFrac PCoA
BV samples
Gardnerella vaginalis 409−05
Prevotellaceae Prevotella bivia
Streptococcaceae Streptococcus unclassified
bv
i
n
Second Component 0.253 variance explained
First Component 0.295 variance explained
0.2
0.1
0.0
−0.1
−0.2
−0.3
−0.2
−0.1
0.0
0.1
0.2


PCoA biplot
Response variables projected
as in PCA with scaling 1
Axis.1
Axis.2
−1.0
−0.5
0.0
0.5
−0.3
−0.2
−0.1
0.0
0.1
0.2
285bbv
253bbv
305bbv
277bbv
255bbv
309bbv
271bbv
233bbv
230bbv
300bbv
291bbv
241bbv
310bbv
292bbv
235bbv
279bbv
261bbv
267bbv
237bbv
275bbv
319bbv
273bbv
325bbv
315bbv
308bbv
214bbv
247bbv
274bbv
213bbv
302bbv
301bbv
307bbv
245bbv
248bbv
207bbv
270bbv
212bbv
286bbv
257bbv
206bbv
313bbv
211bbv
269bbv
263bbv
201bbv
311bbv
296bbv
225bbv
209bbv
319bbv
Lactobacillus_iners iners
vaginalis 409


information UniFrac PCoA
BV samples
Second Component 0.077 variance explained
First Component 0.174 variance explained
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.2
−0.1
0.0
0.1
0.2


PCoA biplot
Response variables projected
as in PCA with scaling 1
Axis.1
Axis.2
−1.0
−0.5
0.0
0.5
1.0
−0.2
−0.1
0.0
0.1
0.2
253bbv
309bbv
259bbv
261bbv
Prevotella bivia
319bbv
311bbv
214bbv
237bbv
225bbv
267bbv
325bbv
223bbv
292bbv
268bbv
281bbv
296bbv
Lactobacillus_crispatus crispatus
285bbv
202bbv
211bbv
Anaerococcus tetradius
251bbv
230bbv
209bbv
221bbv
277bbv
247bbv
205bbv
201bbv
255bbv
293bbv
279bbv
313bbv
248bbv
295bbv
257bbv
286bbv
245bbv
212bbv
206bbv
263bbv
287bbv
231bbv
Prevotella timo
274bbv
283bbv
265bbv
207bbv
289bbv
vaginalis WGS-101
Atopobium rimae
234bbv
270bbv
307bbv
unclassified_BVAB2 BVAB2
303bbv
Prevotella amnii
269bbv
301bbv
302bbv
Atopobium vaginae
Megasphaera genomosp.type_1str.28L