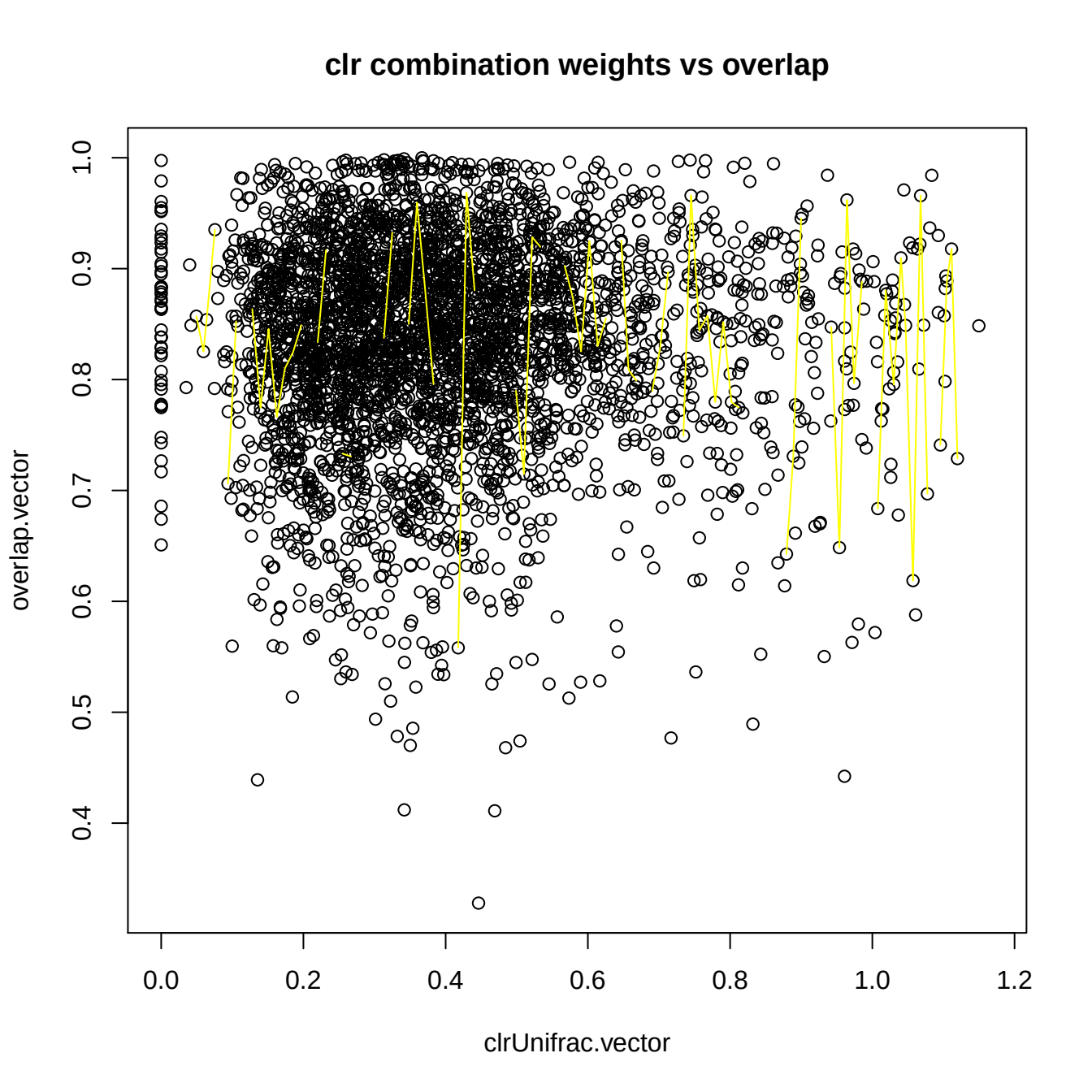
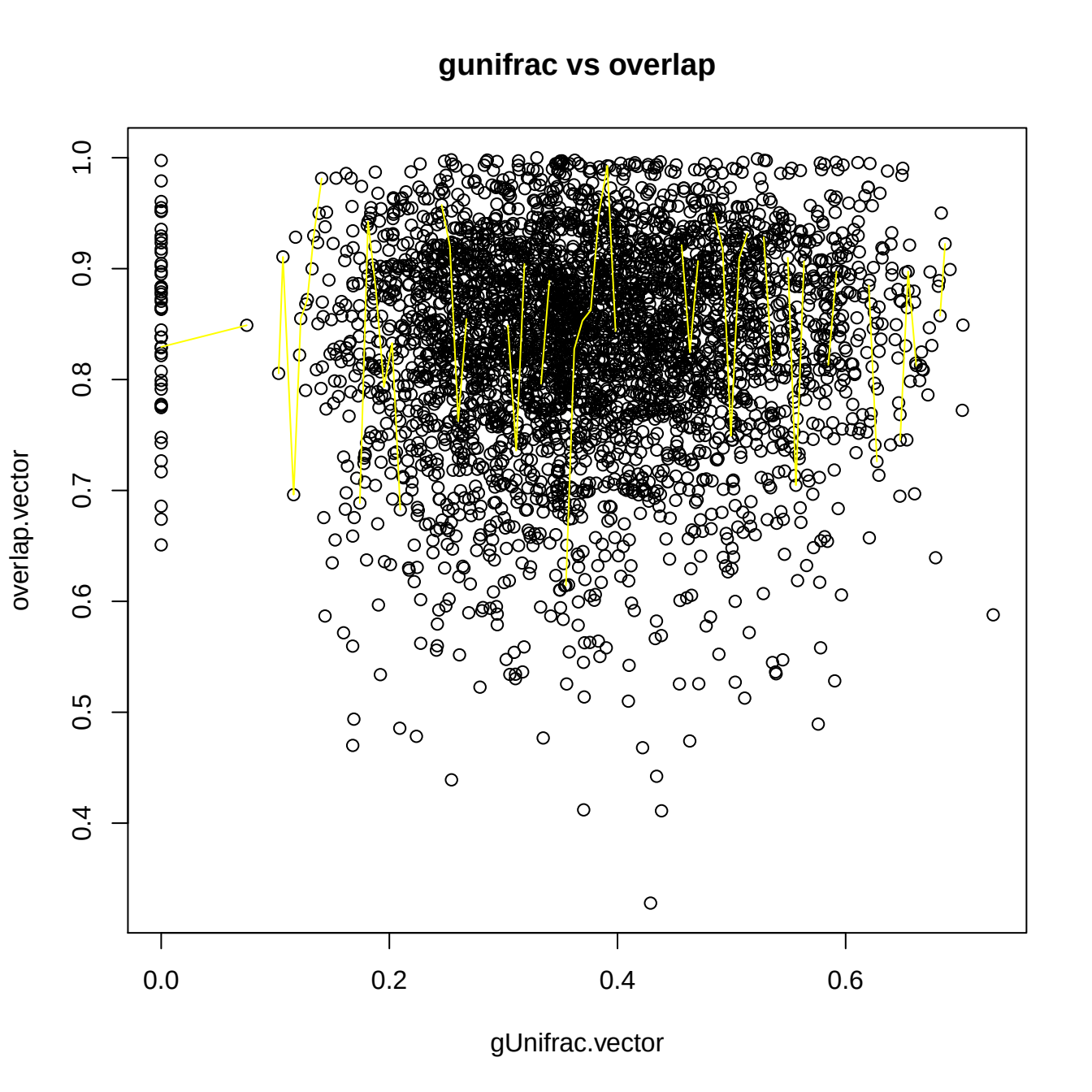
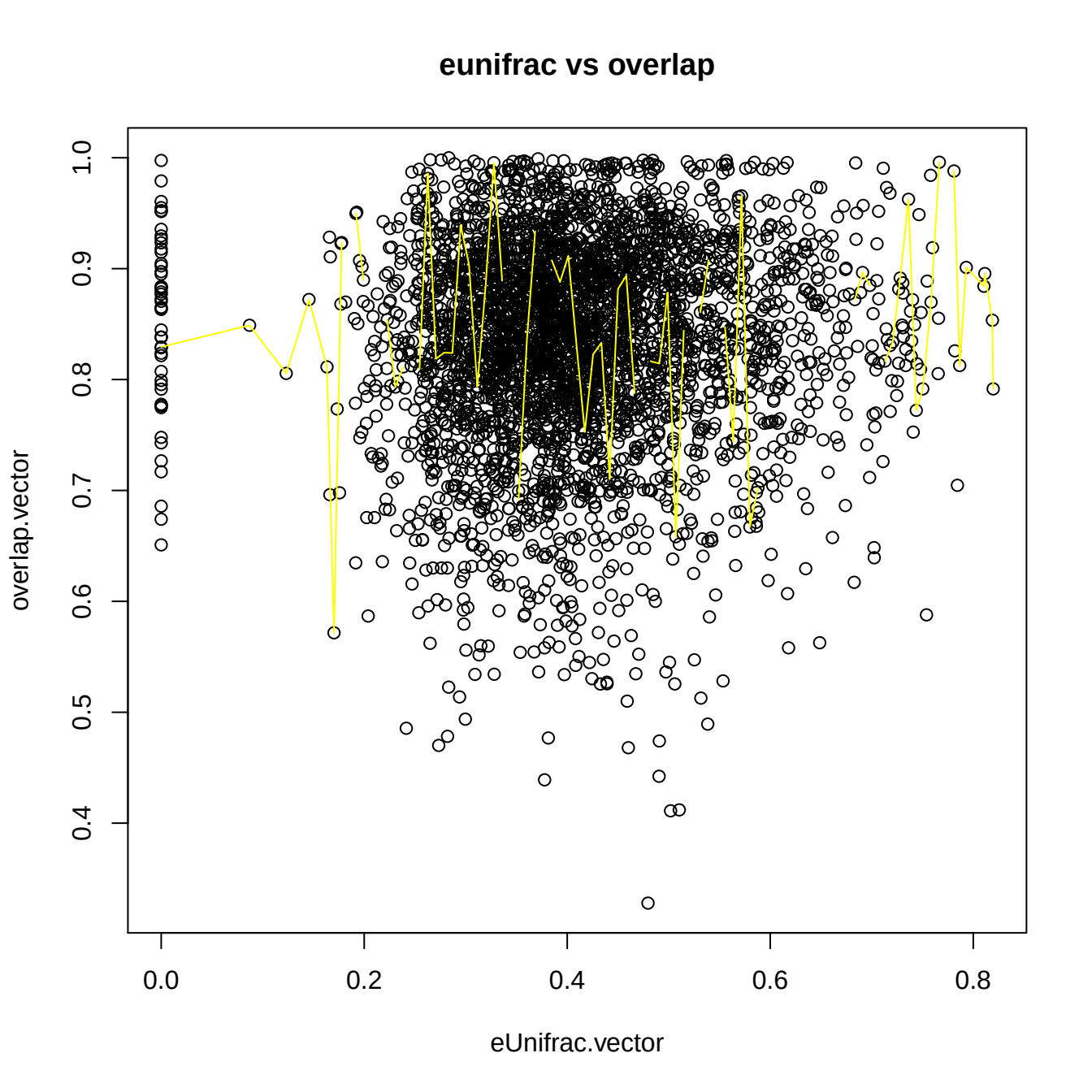
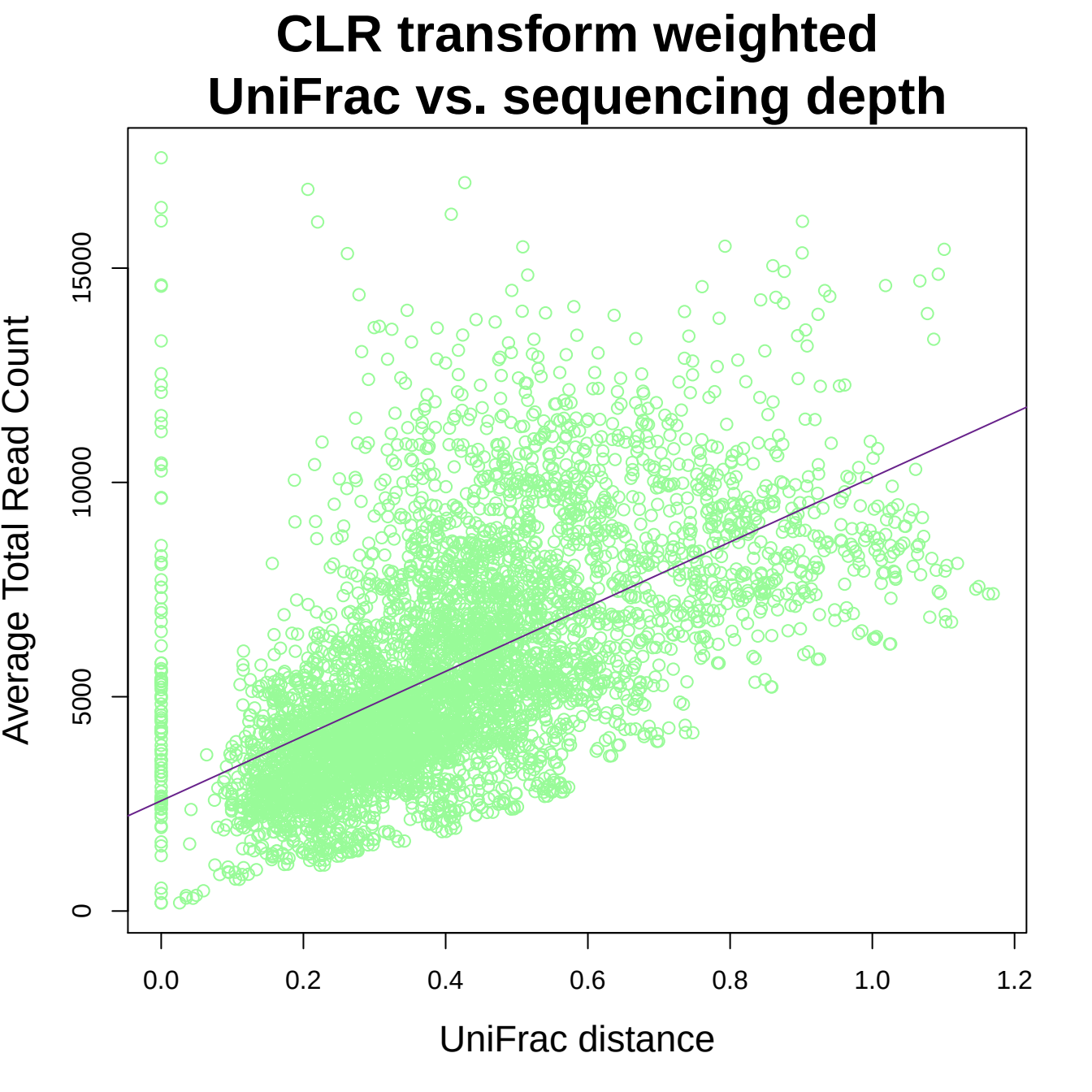
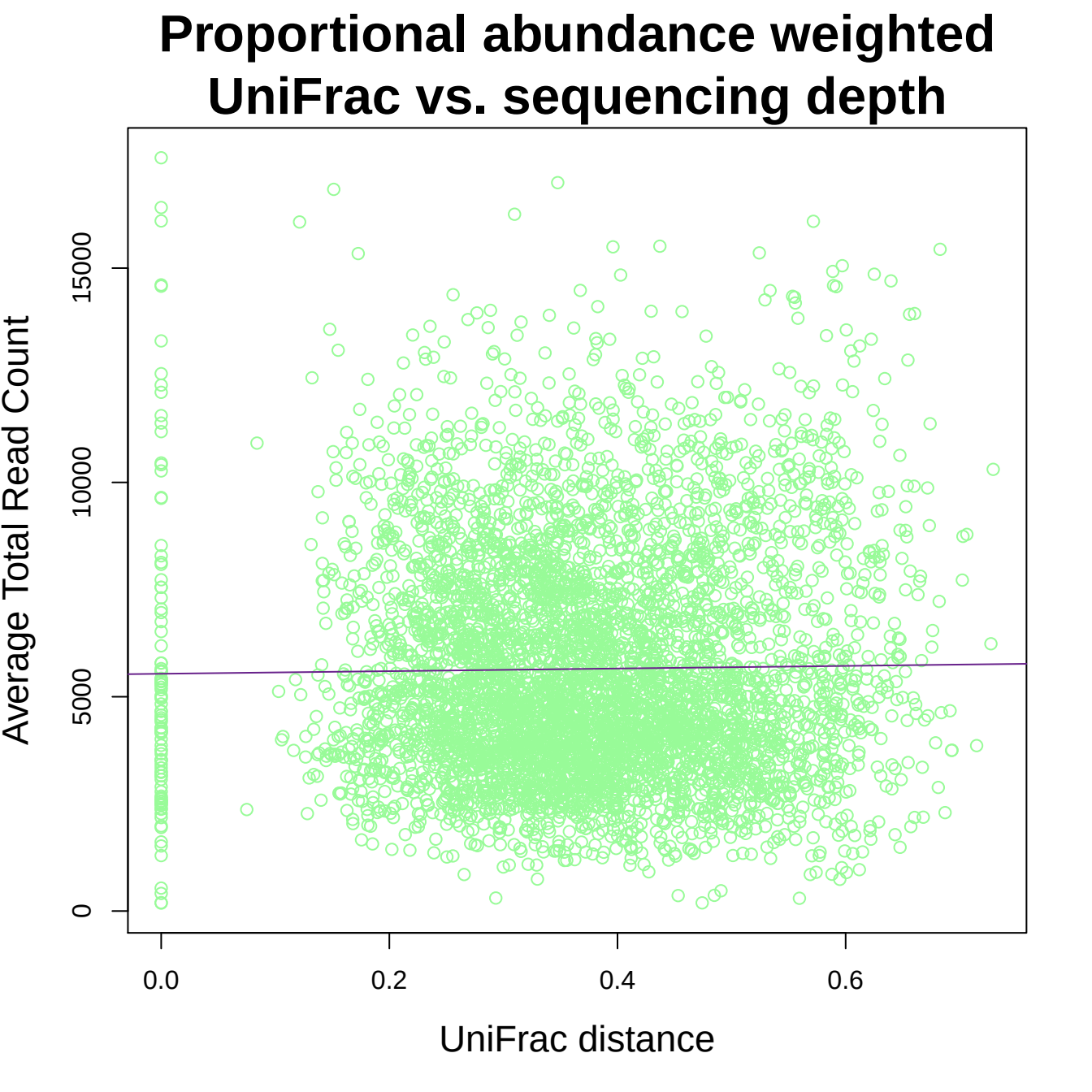
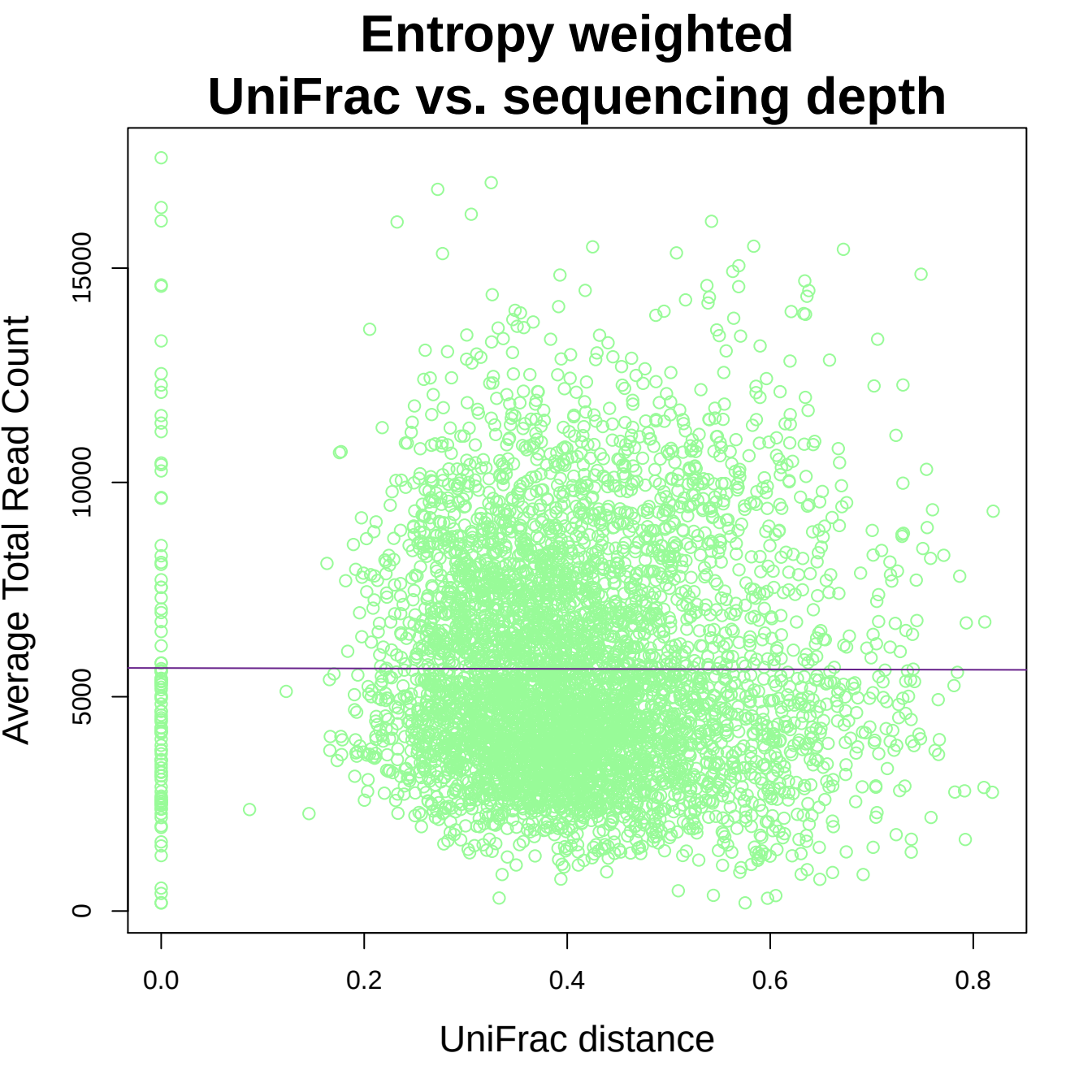

clr combination weights vs overlap
overlap.vector
clrUnifrac.vector
0.4
0.5
0.6
0.7
0.8
0.9
1.0
0.0
0.2
0.4
0.6
0.8
1.0
1.2

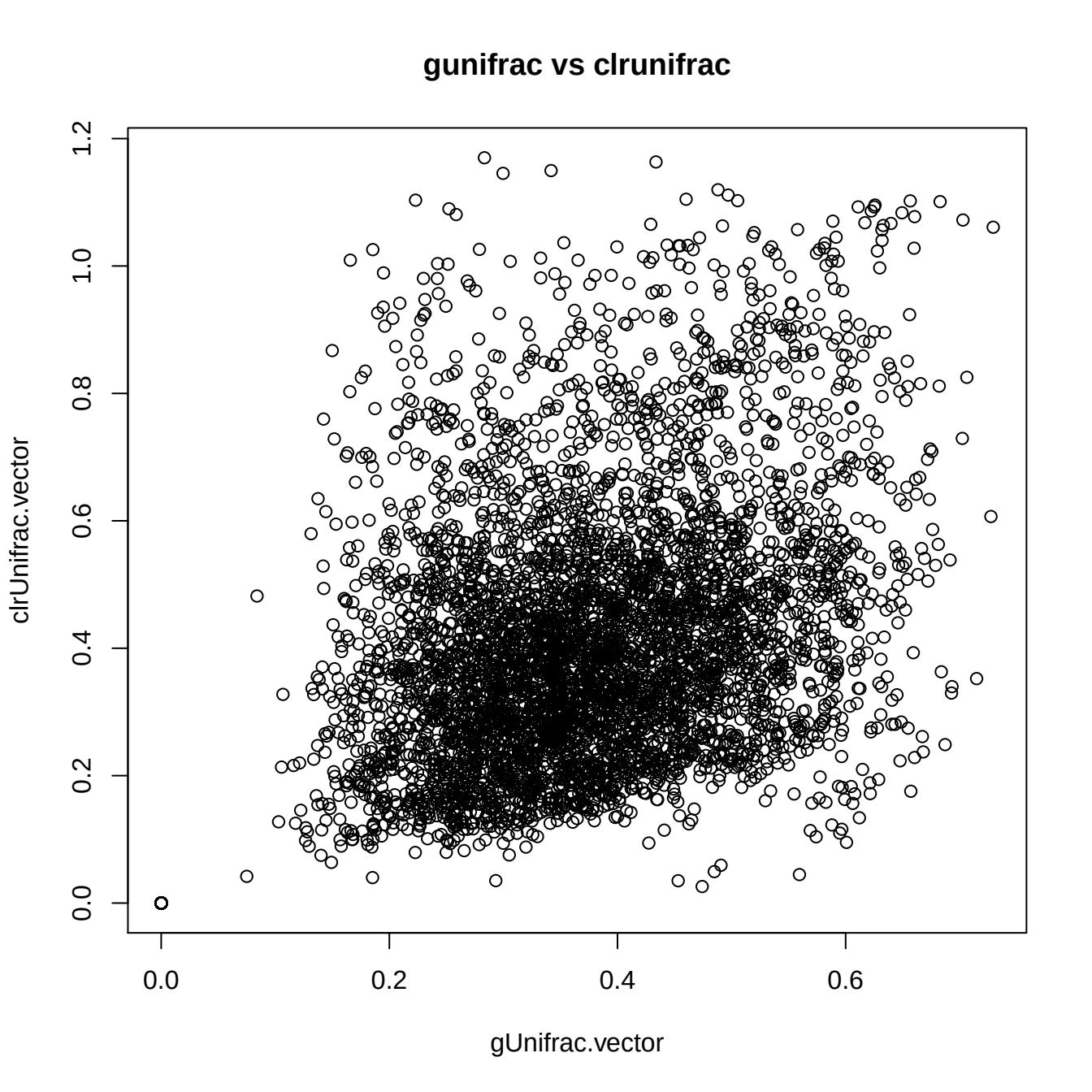

gunifrac vs overlap
overlap.vector
gUnifrac.vector
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.0
0.2
0.4
0.6

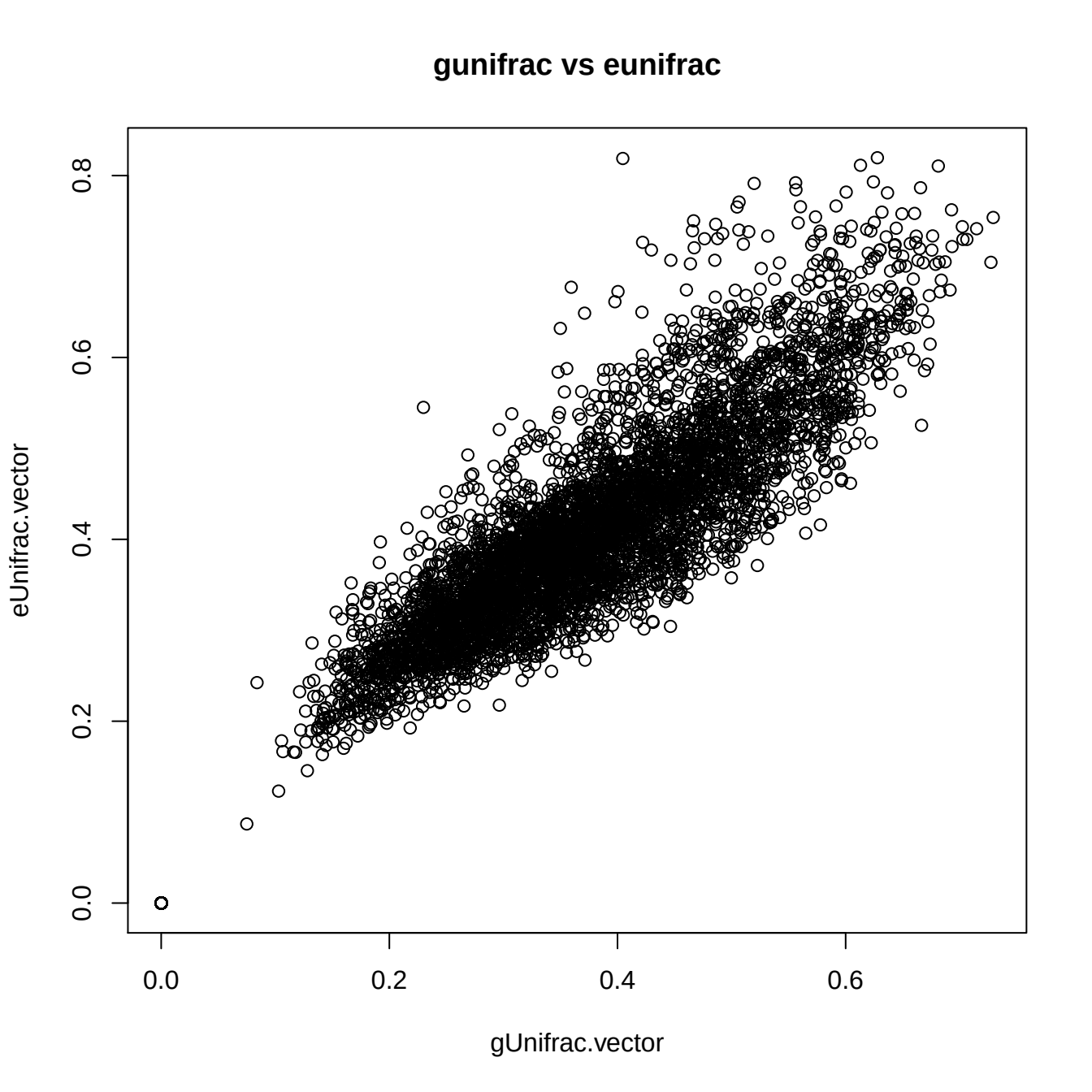

eunifrac vs overlap
overlap.vector
eUnifrac.vector
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.0
0.2
0.4
0.6
0.8

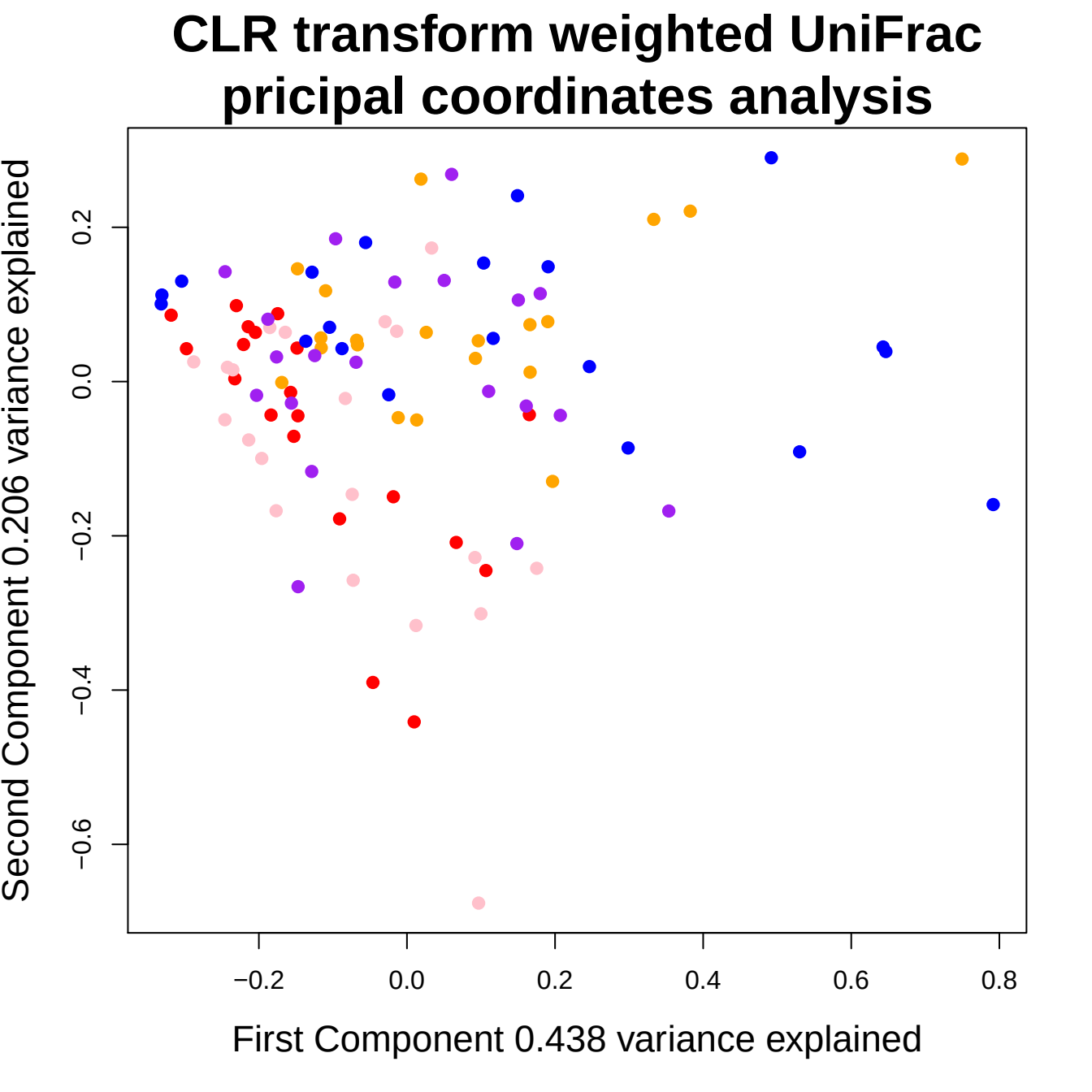

CLR transform weighted
UniFrac vs. sequencing depth
Average Total Read Count
0
5000
10000
15000
0.0
0.2
0.4
0.6
0.8
1.0
1.2
UniFrac distance

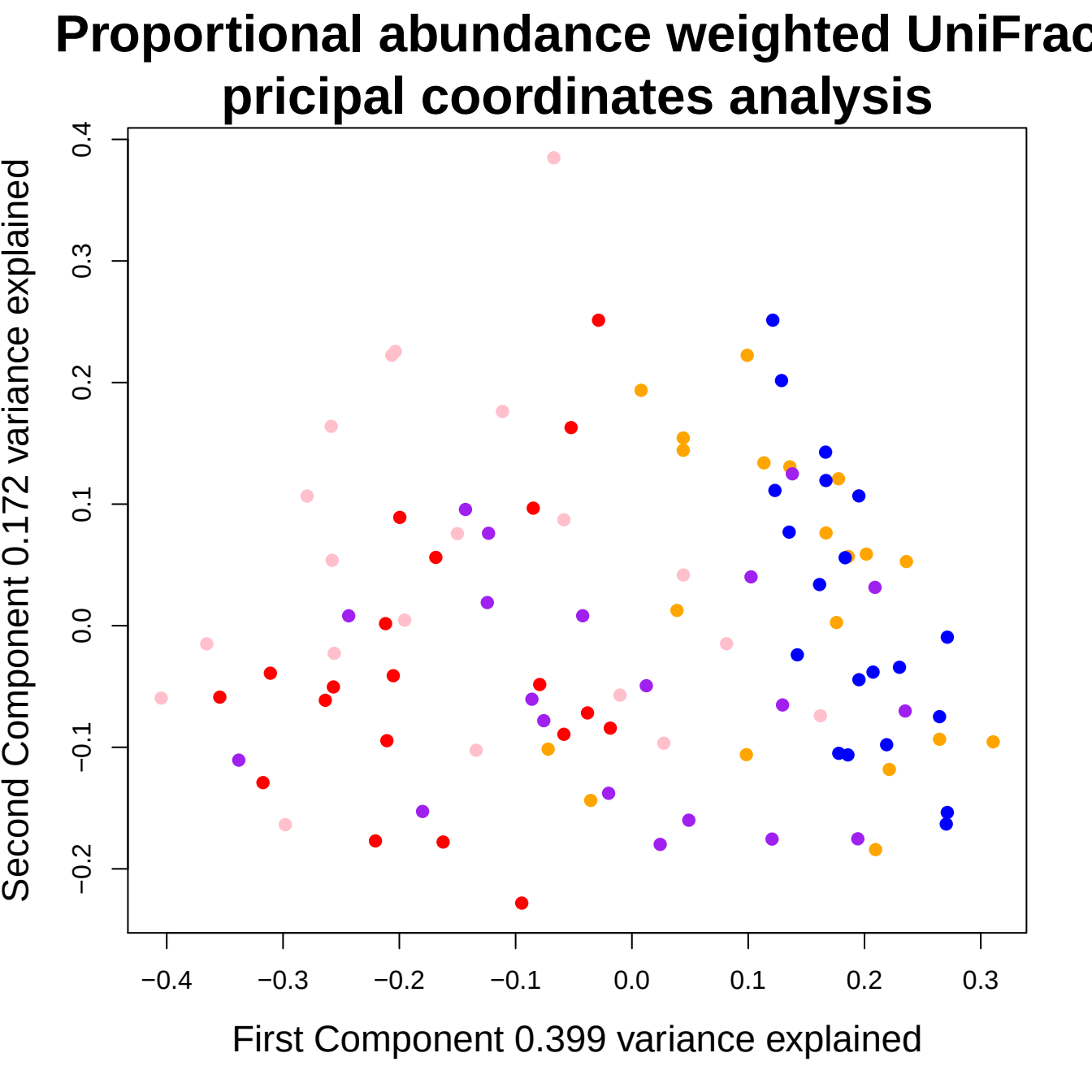

Proportional abundance weighted UniFrac vs. sequencing depth
Average Total Read Count
0
5000
10000
15000
0.0
0.2
0.4
0.6
UniFrac distance

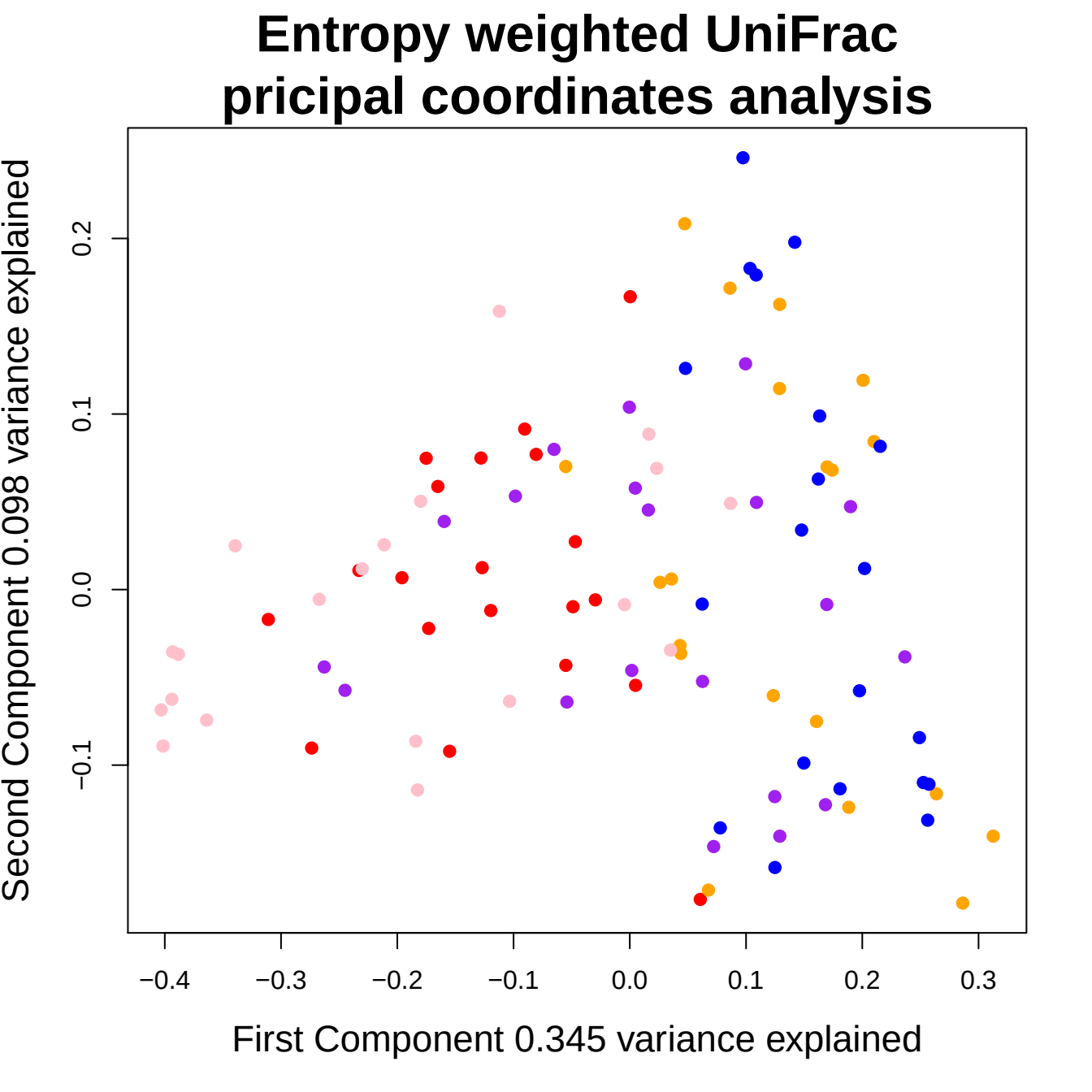

Entropy weighted
UniFrac vs. sequencing depth
Average Total Read Count
0
5000
10000
15000
0.0
0.2
0.4
0.6
0.8
UniFrac distance

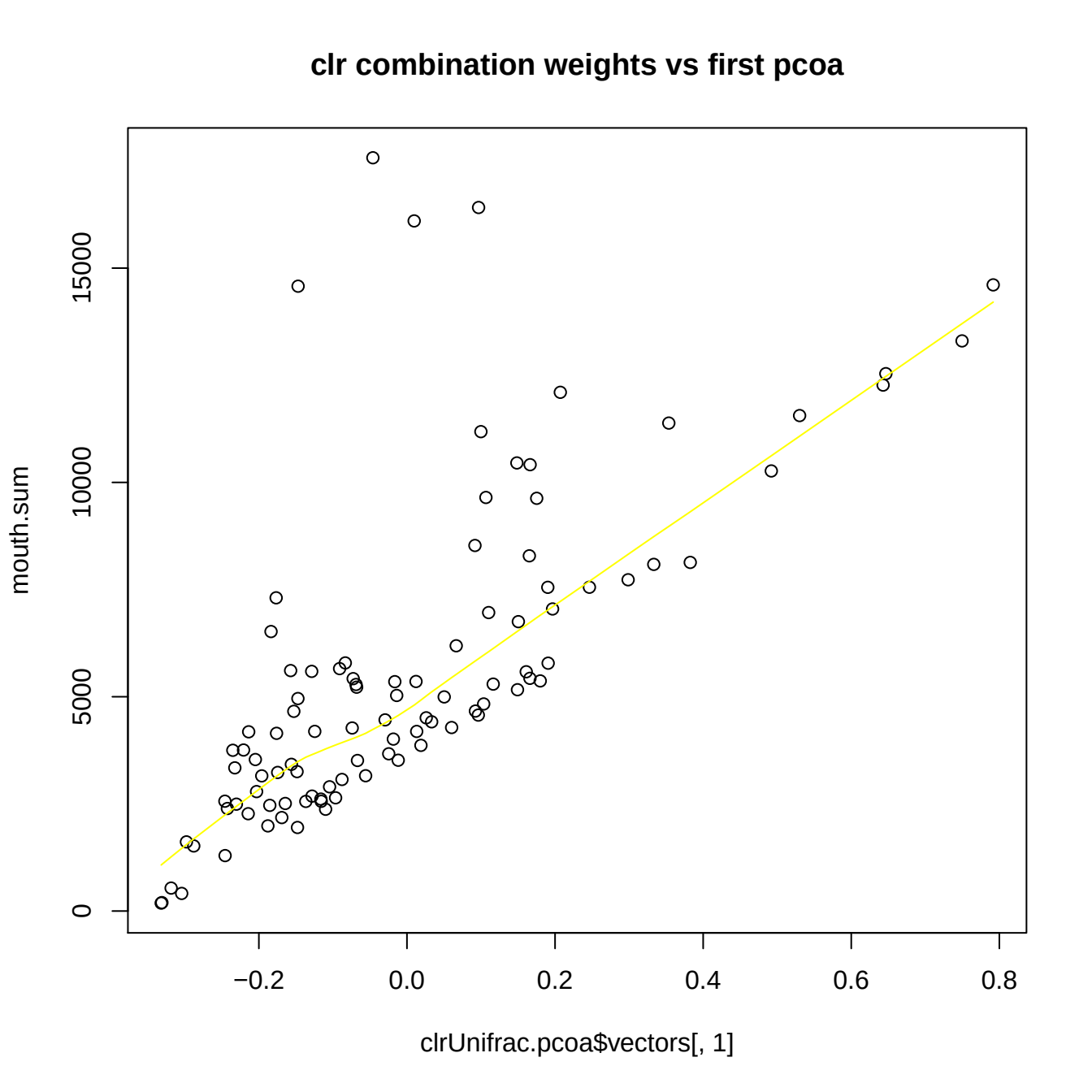

gunifrac vs clrunifrac
clrUnifrac.vector
gUnifrac.vector
0.0
0.2
0.4
0.6
0.8
1.0
1.2
0.0
0.2
0.4
0.6

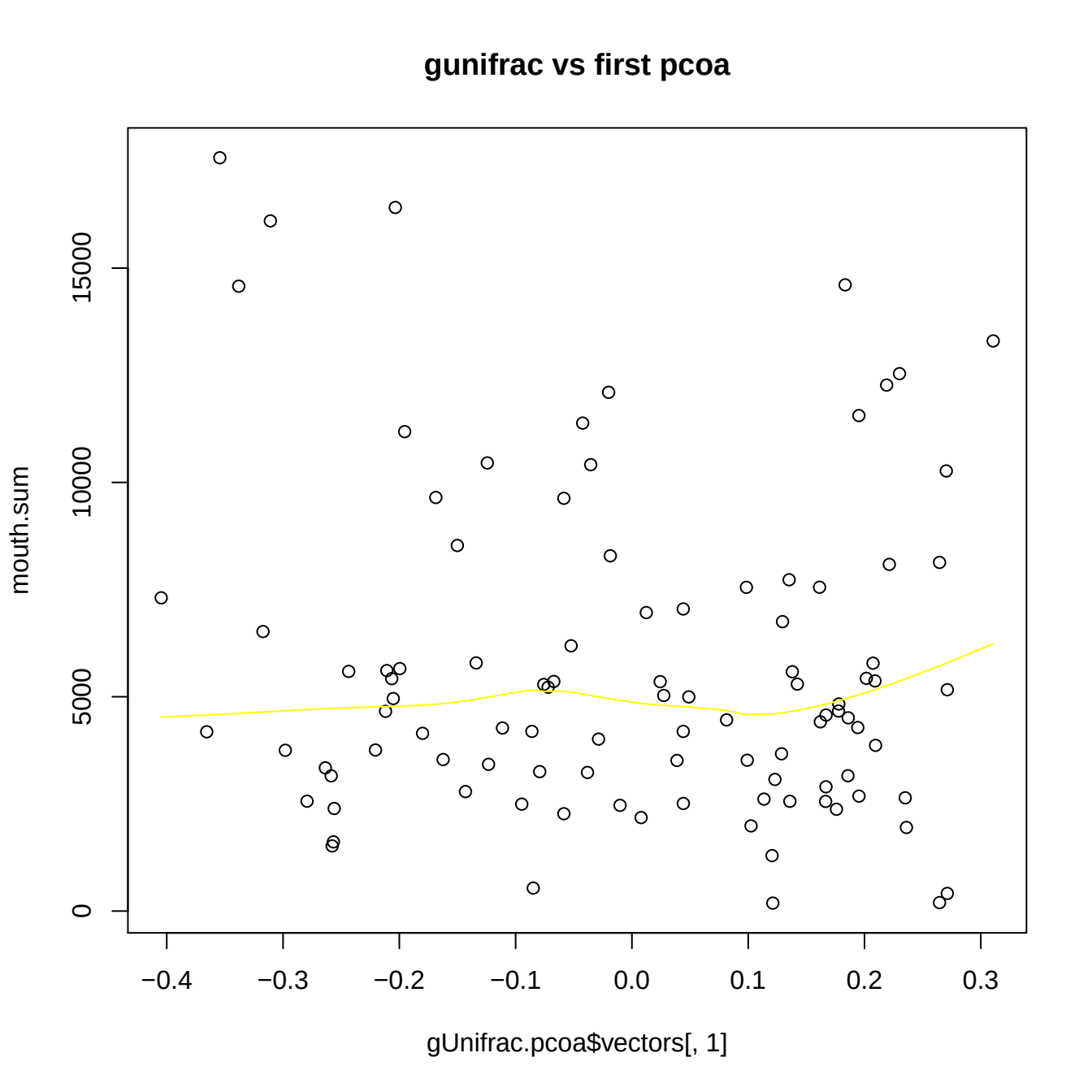

gunifrac vs eunifrac
eUnifrac.vector
gUnifrac.vector
0.0
0.2
0.4
0.6
0.8
0.0
0.2
0.4
0.6

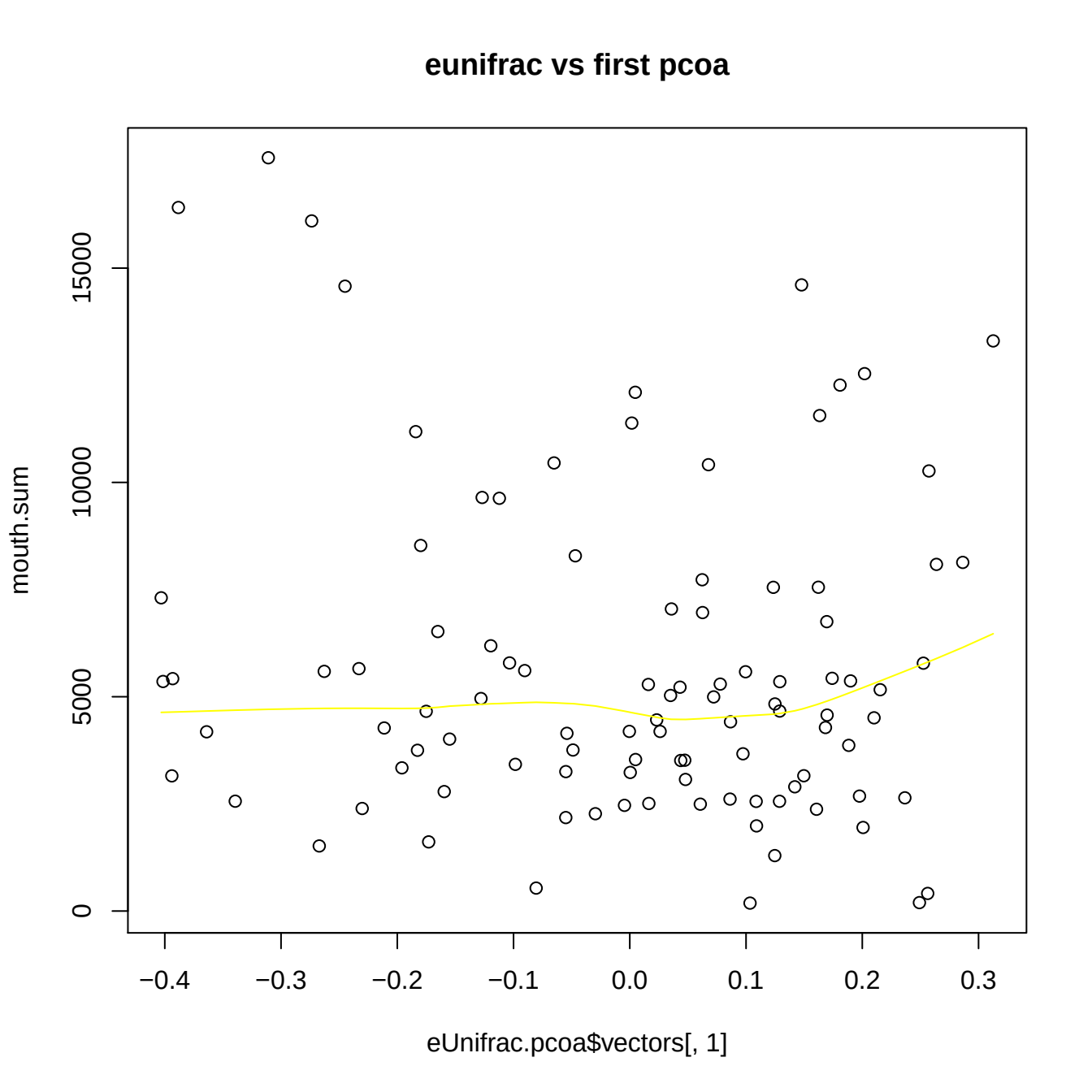

CLR transform weighted UniFrac
pricipal coordinates analysis
Second Component 0.206 variance explained
0.2
0.0
−0.2
−0.4
−0.6
−0.2
0.0
0.2
0.4
0.6
0.8
First Component 0.438 variance explained


Proportional abundance weighted UniFrac
pricipal coordinates analysis
Second Component 0.172 variance explained
First Component 0.399 variance explained
0.4
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.4
−0.3
−0.2
−0.1
0.0
0.1
0.2
0.3


Entropy weighted UniFrac
pricipal coordinates analysis
Second Component 0.098 variance explained
First Component 0.345 variance explained
0.2
0.1
0.0
−0.1
−0.4
−0.3
−0.2
−0.1
0.0
0.1
0.2
0.3


clr combination weights vs first pcoa
mouth.sum
0
5000
10000
15000
−0.2
0.0
0.2
0.4
0.6
0.8
clrUnifrac.pcoa$vectors[, 1]


gunifrac vs first pcoa
mouth.sum
0
5000
10000
15000
−0.4
−0.3
−0.2
−0.1
0.0
0.1
0.2
0.3
gUnifrac.pcoa$vectors[, 1]


eunifrac vs first pcoa
mouth.sum
0
5000
10000
15000
−0.4
−0.3
−0.2
−0.1
0.0
0.1
0.2
0.3
eUnifrac.pcoa$vectors[, 1]