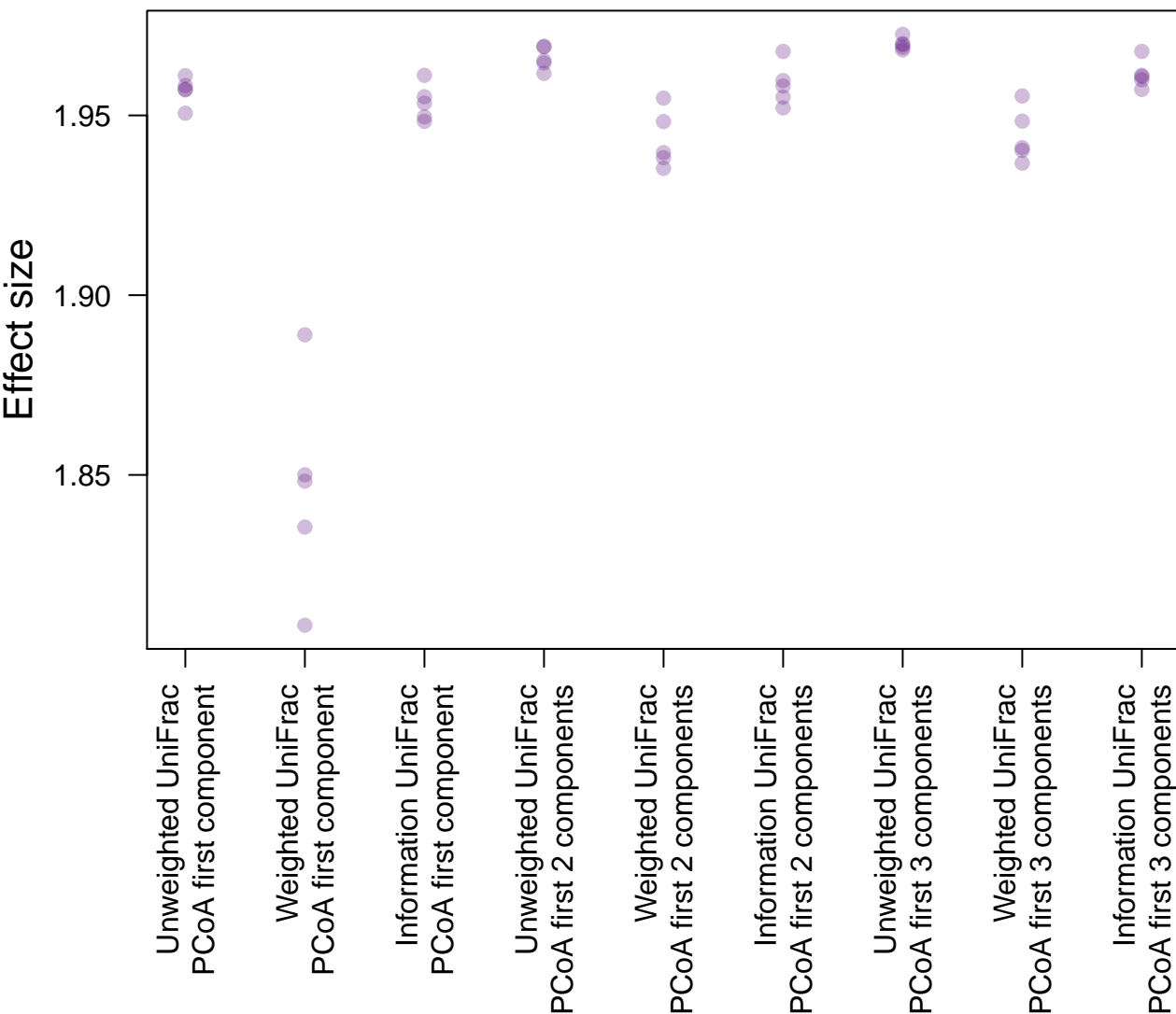
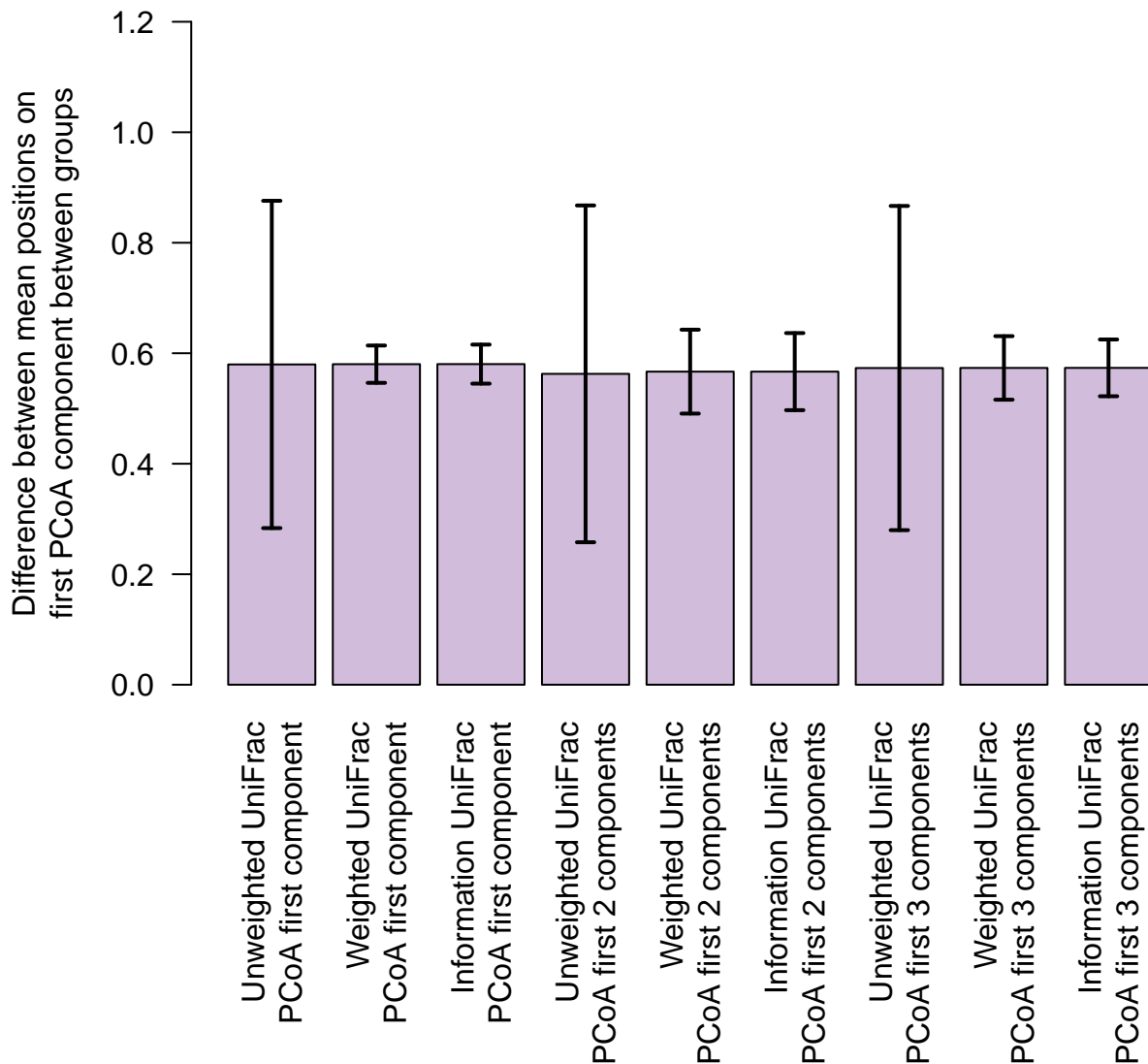


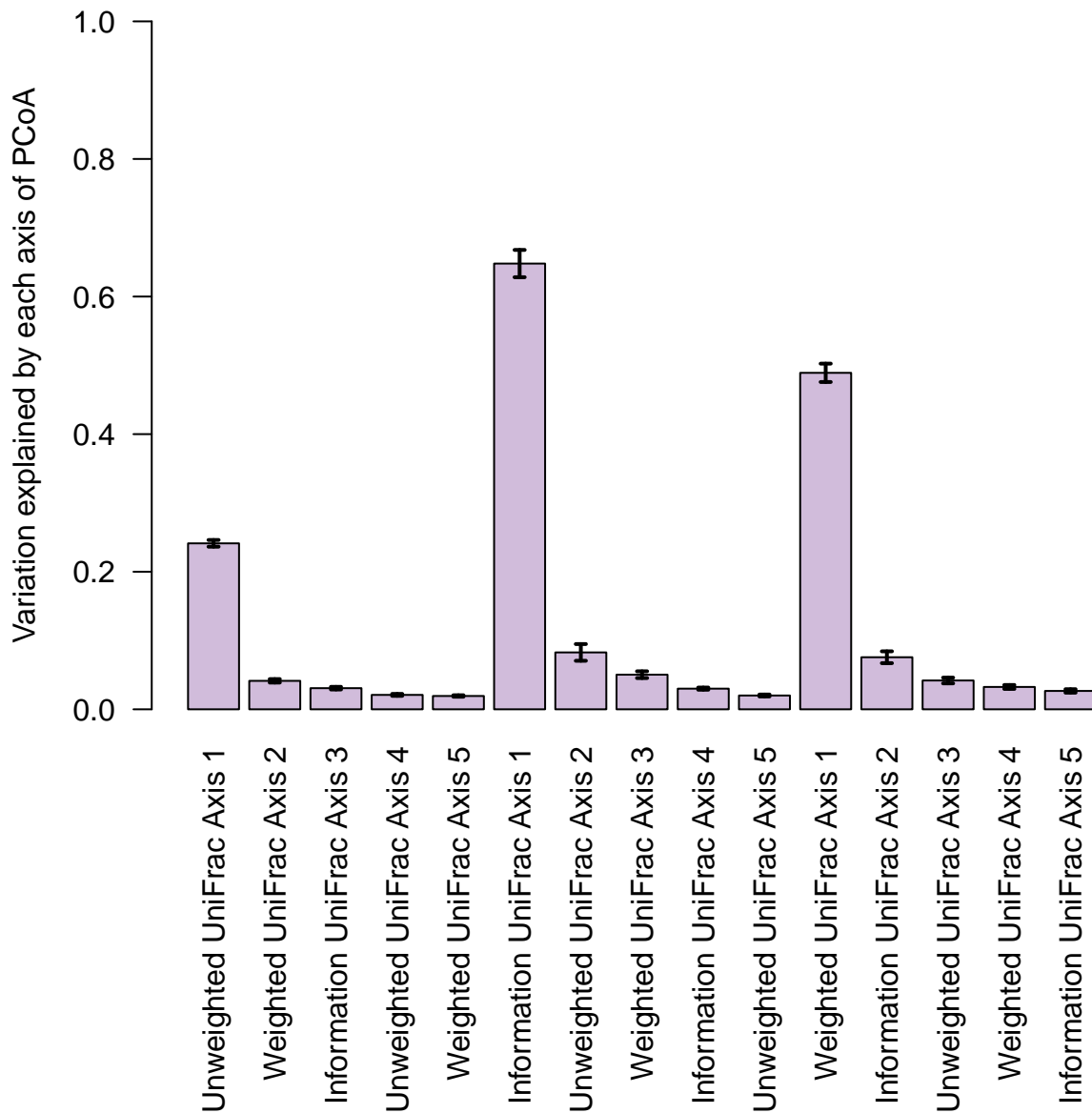
Sequencing depth < 3000 vs. 3000–6000 reads/sample



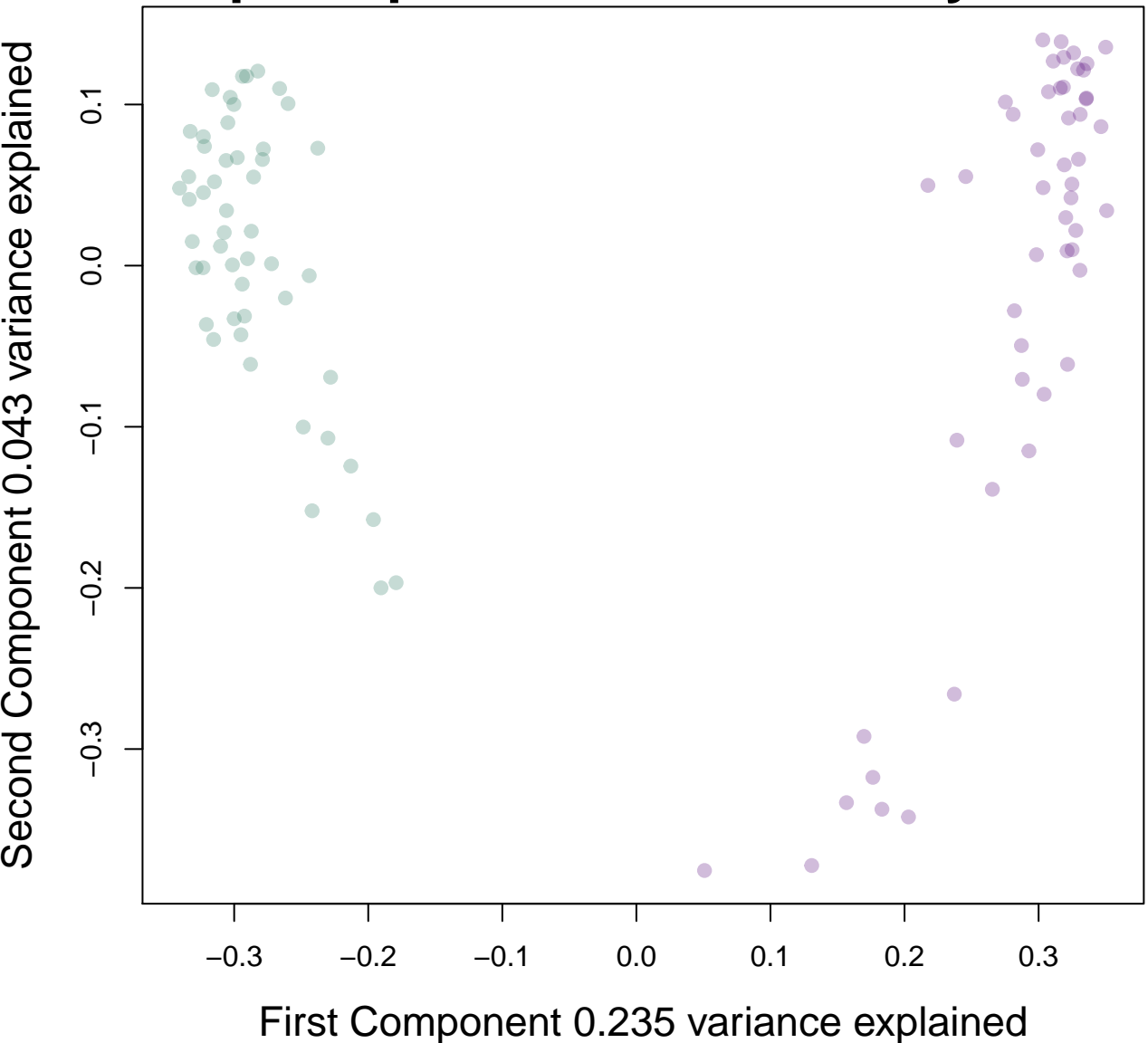
Sequencing depth < 3000 vs. 3000–6000 reads/sample



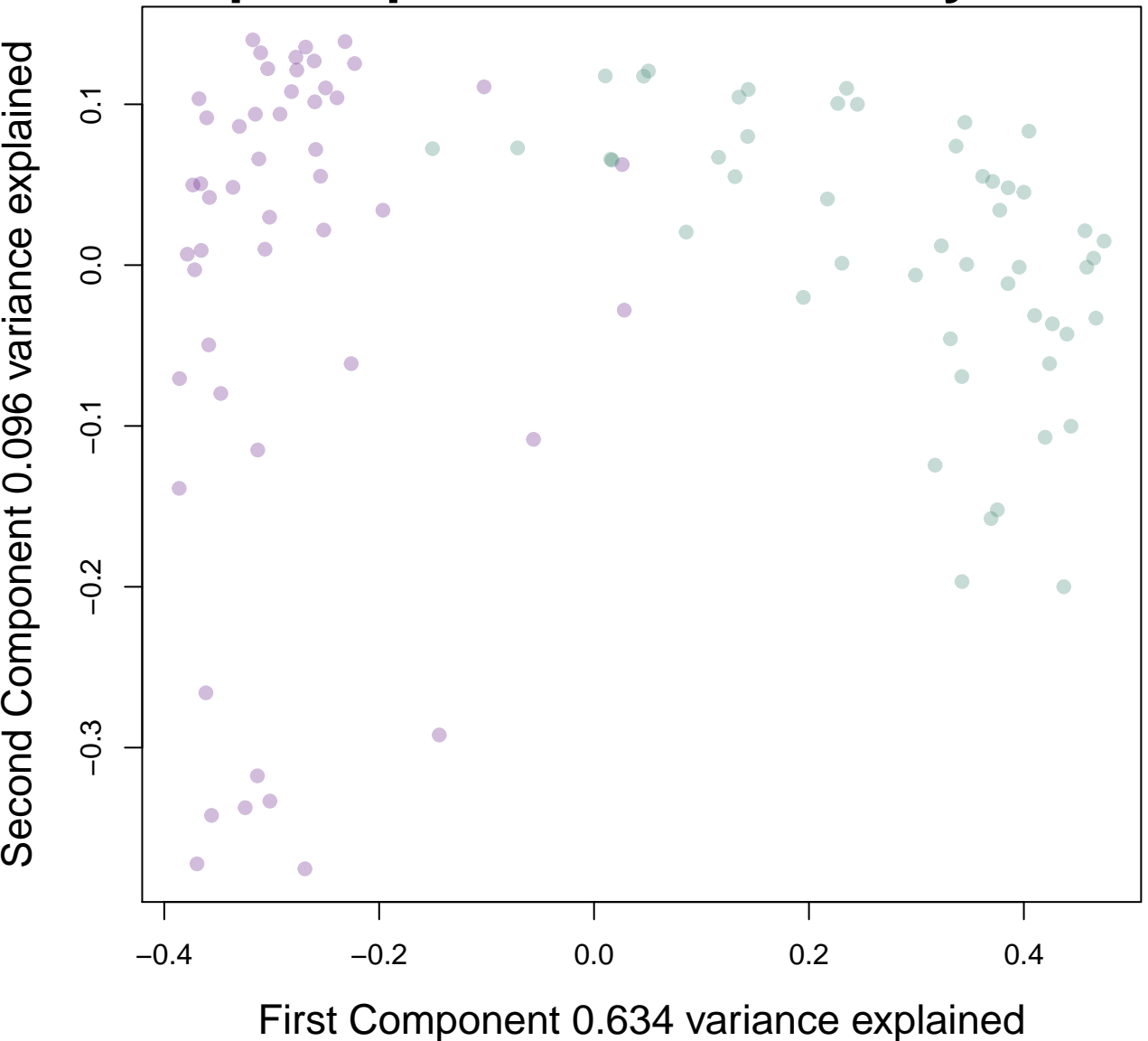
Sequencing depth < 3000 vs. 3000–6000 reads/sample



Unweighted UniFrac principal coordinates analysis

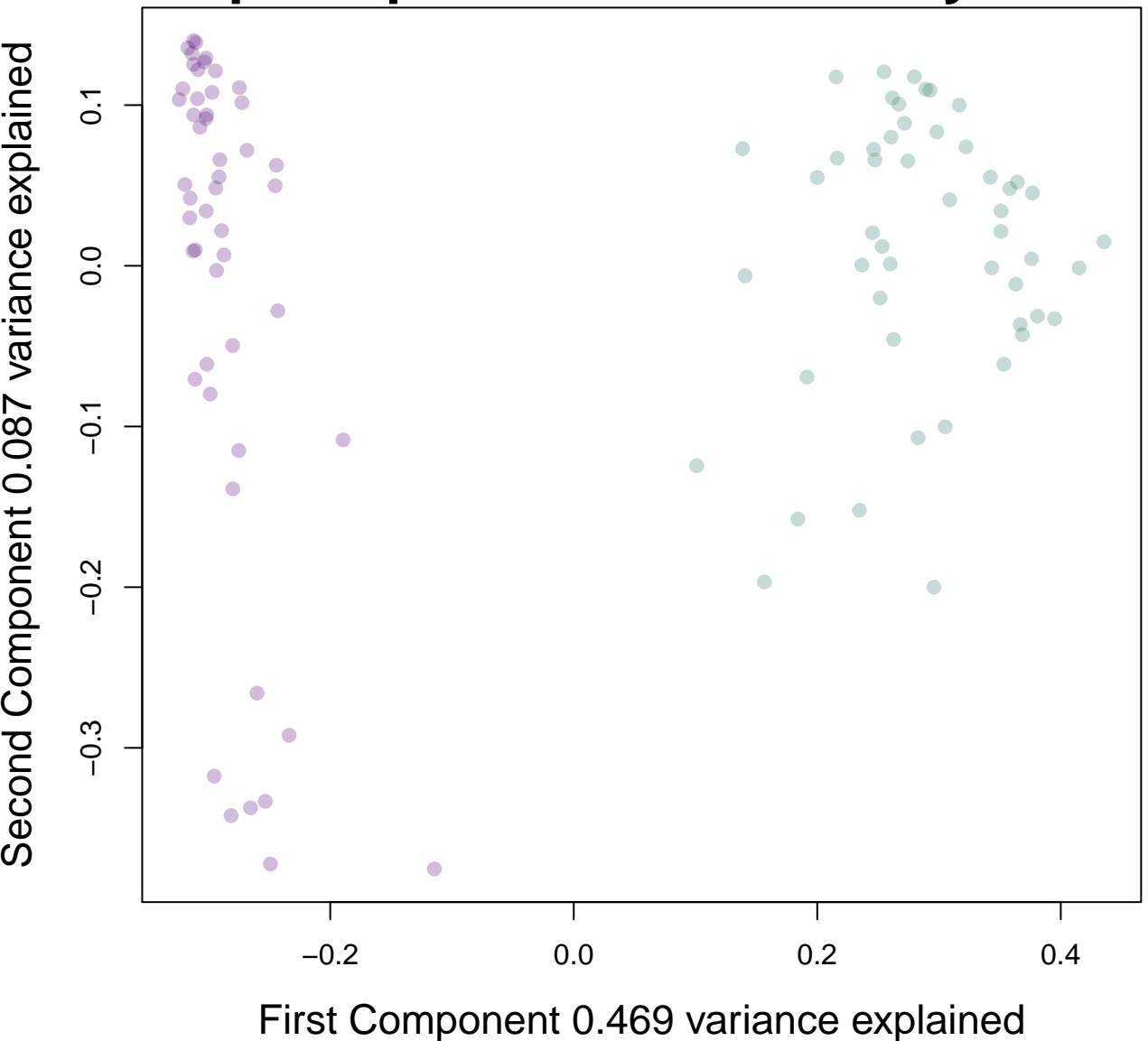


Weighted UniFrac principal coordinates analysis

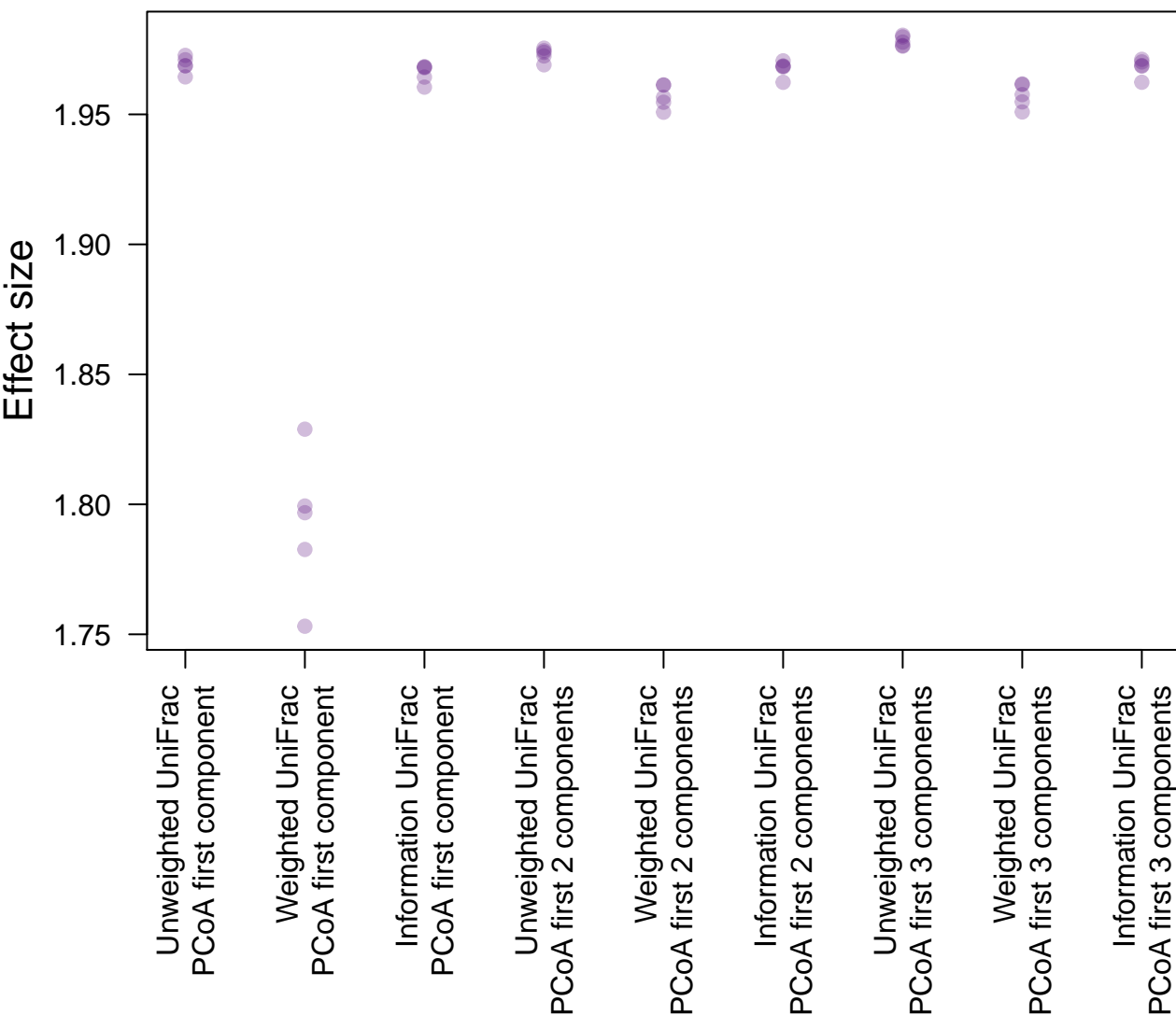


Information UniFrac

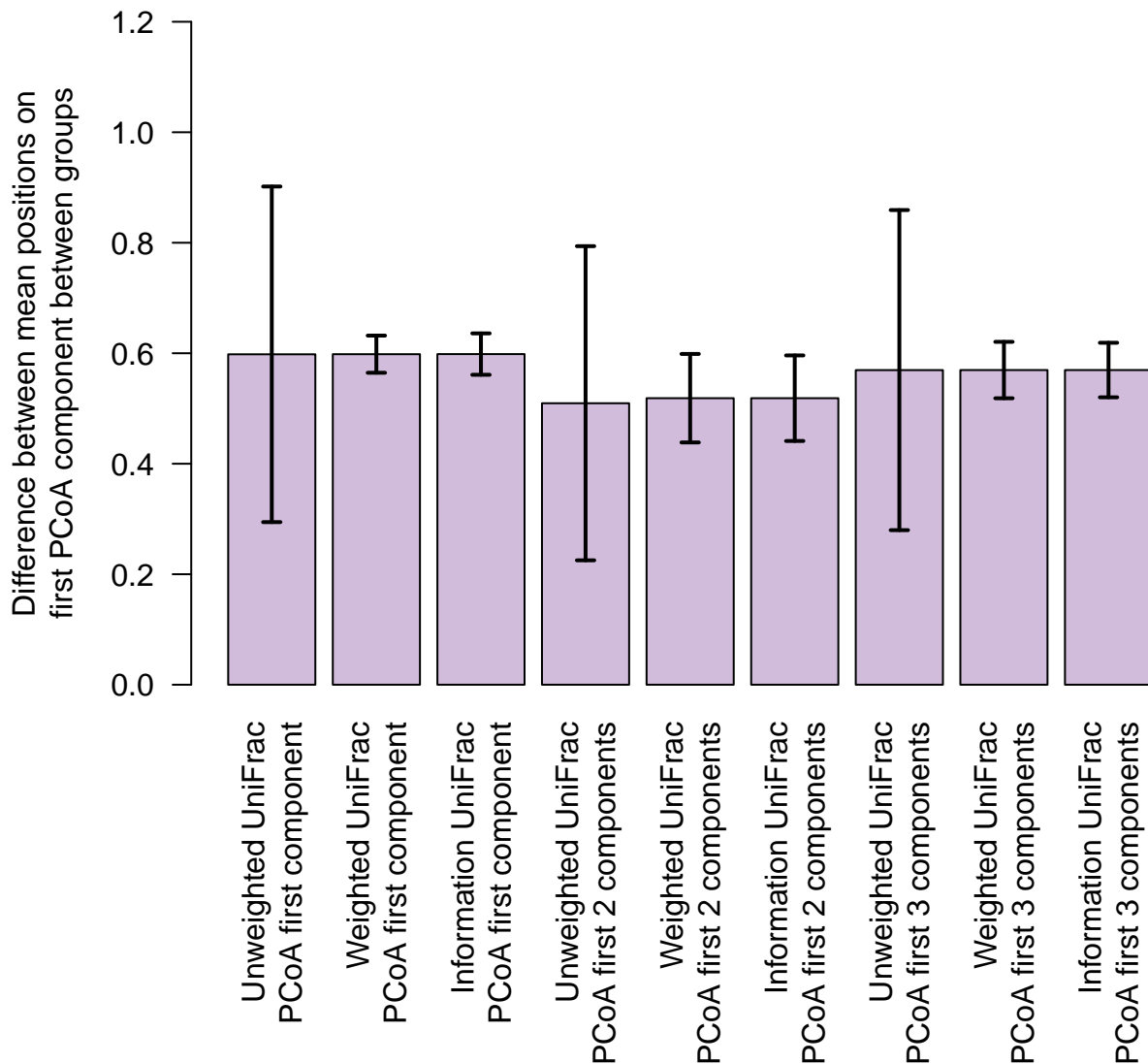
principal coordinates analysis



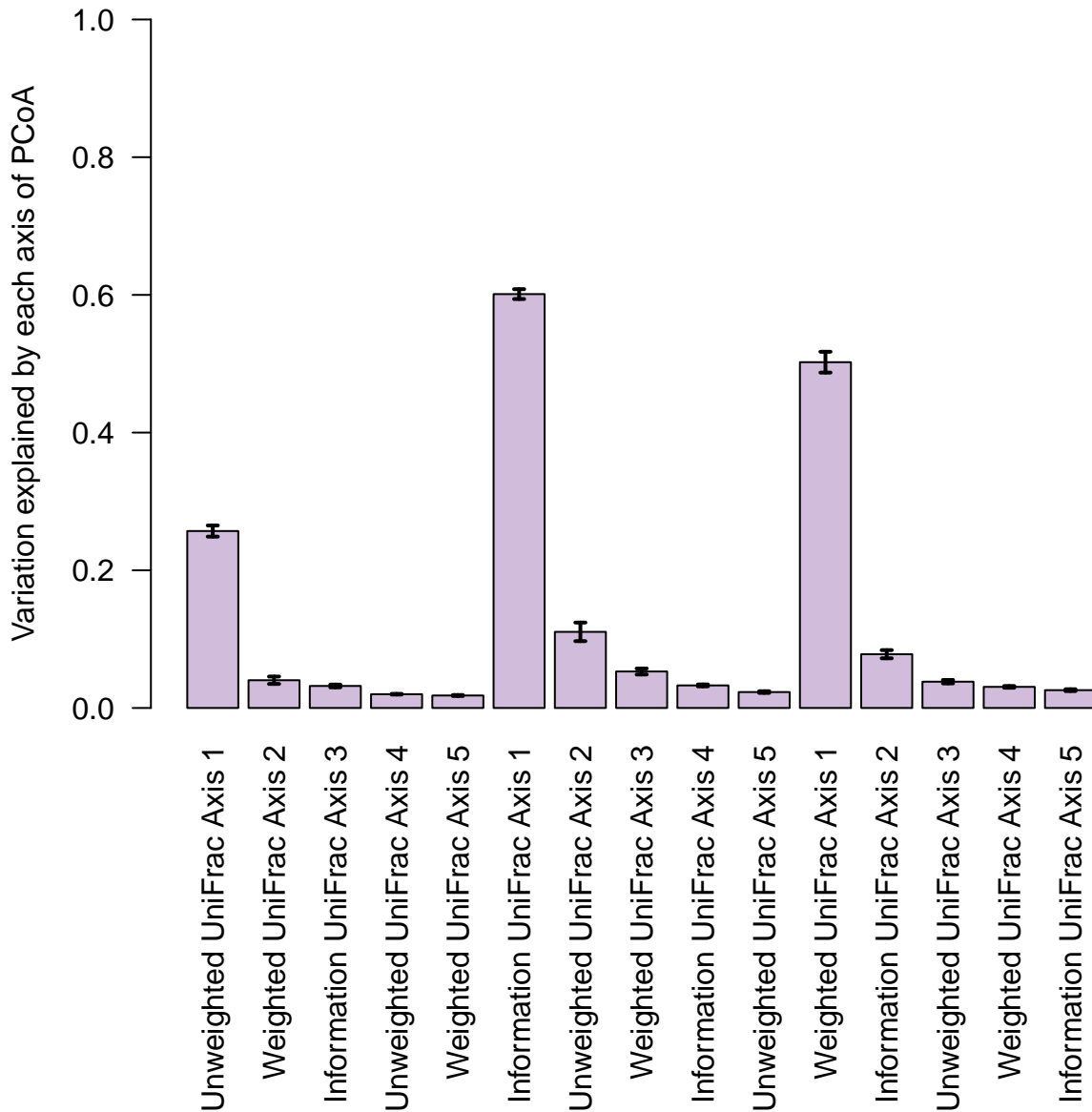
Sequencing depth 3000–6000 vs. > 6000 reads/sample



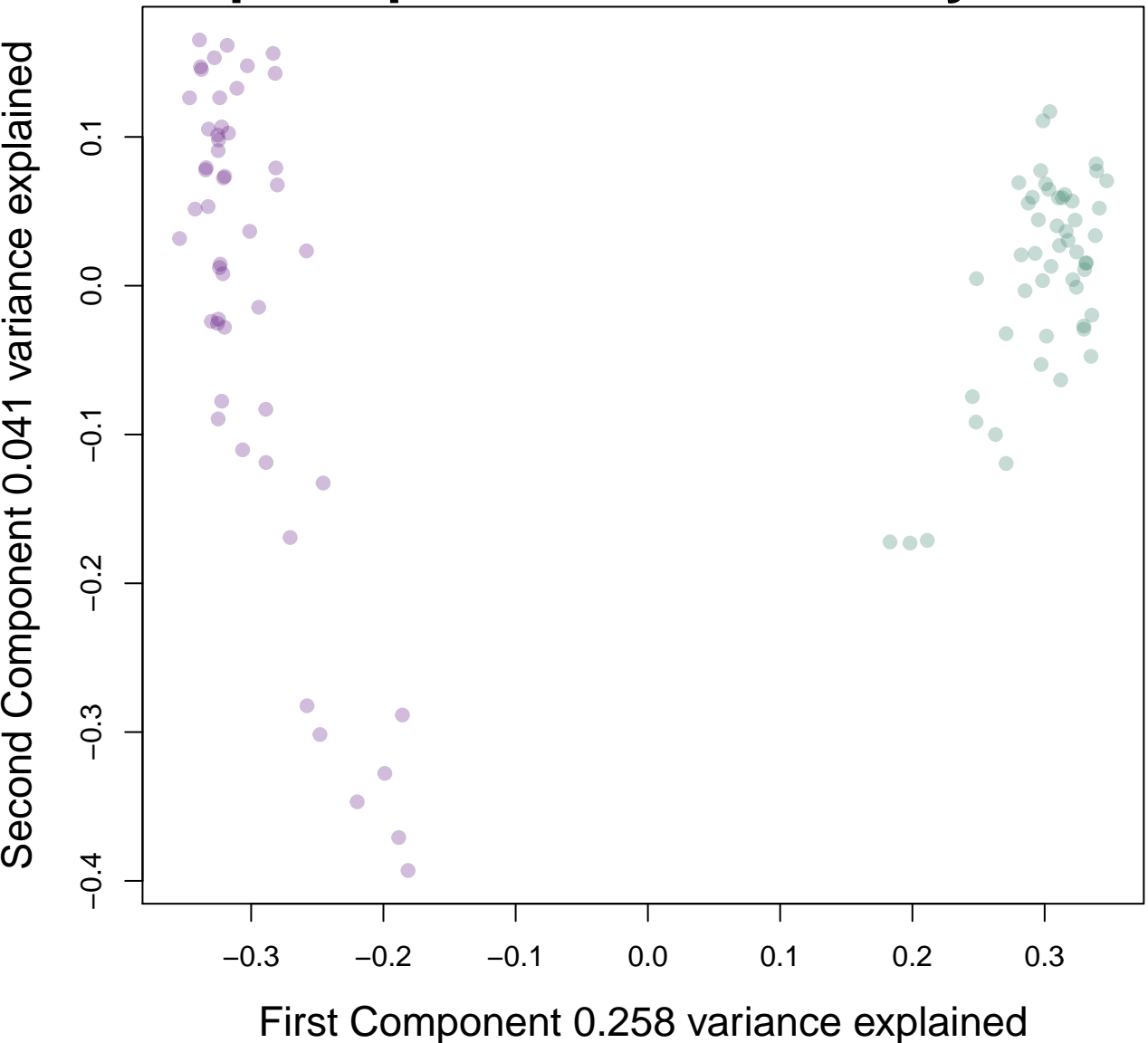
Sequencing depth 3000–6000 vs. > 6000 reads/sample



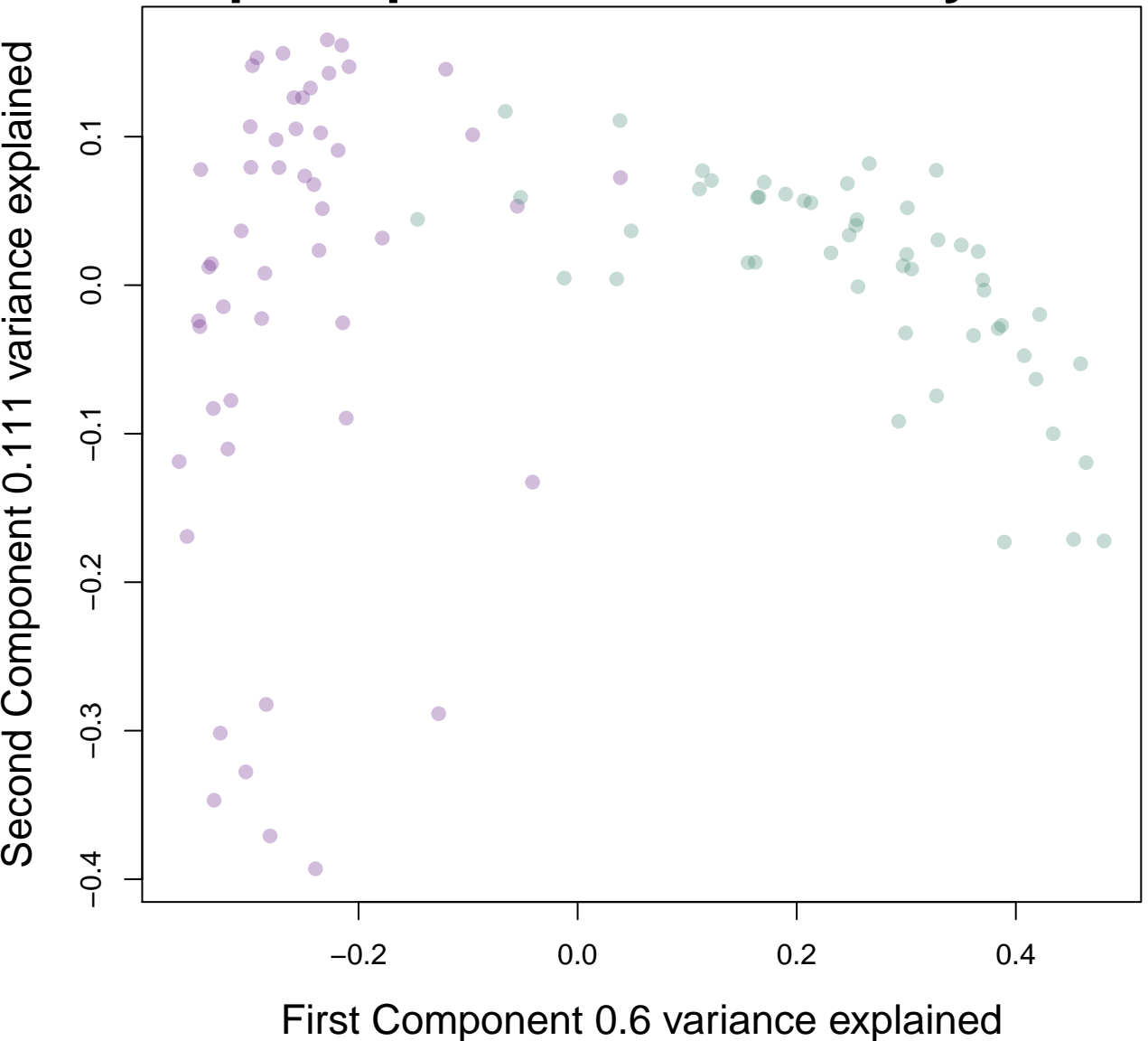
Sequencing depth 3000–6000 vs. > 6000 reads/sample



Unweighted UniFrac principal coordinates analysis

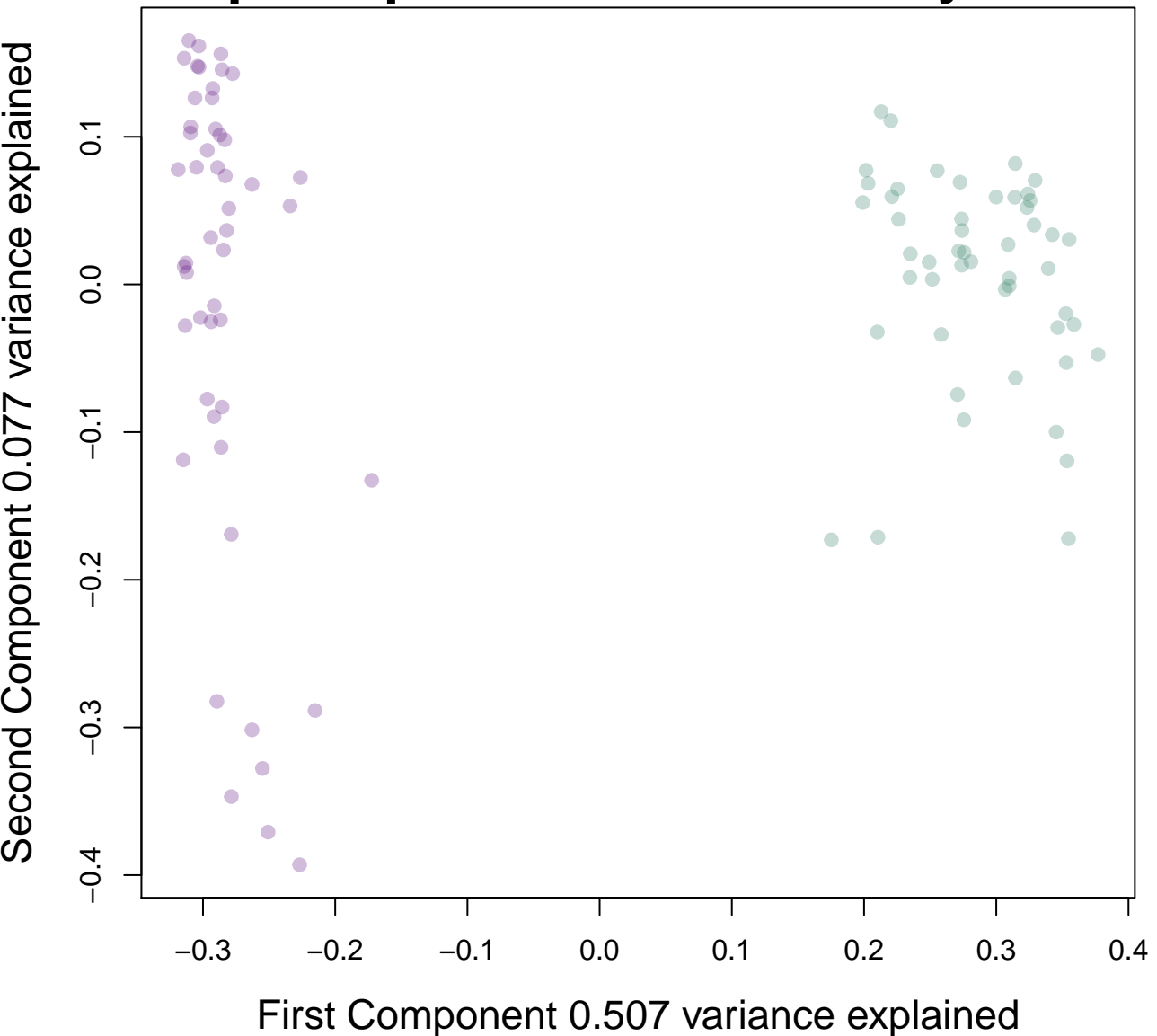


Weighted UniFrac principal coordinates analysis

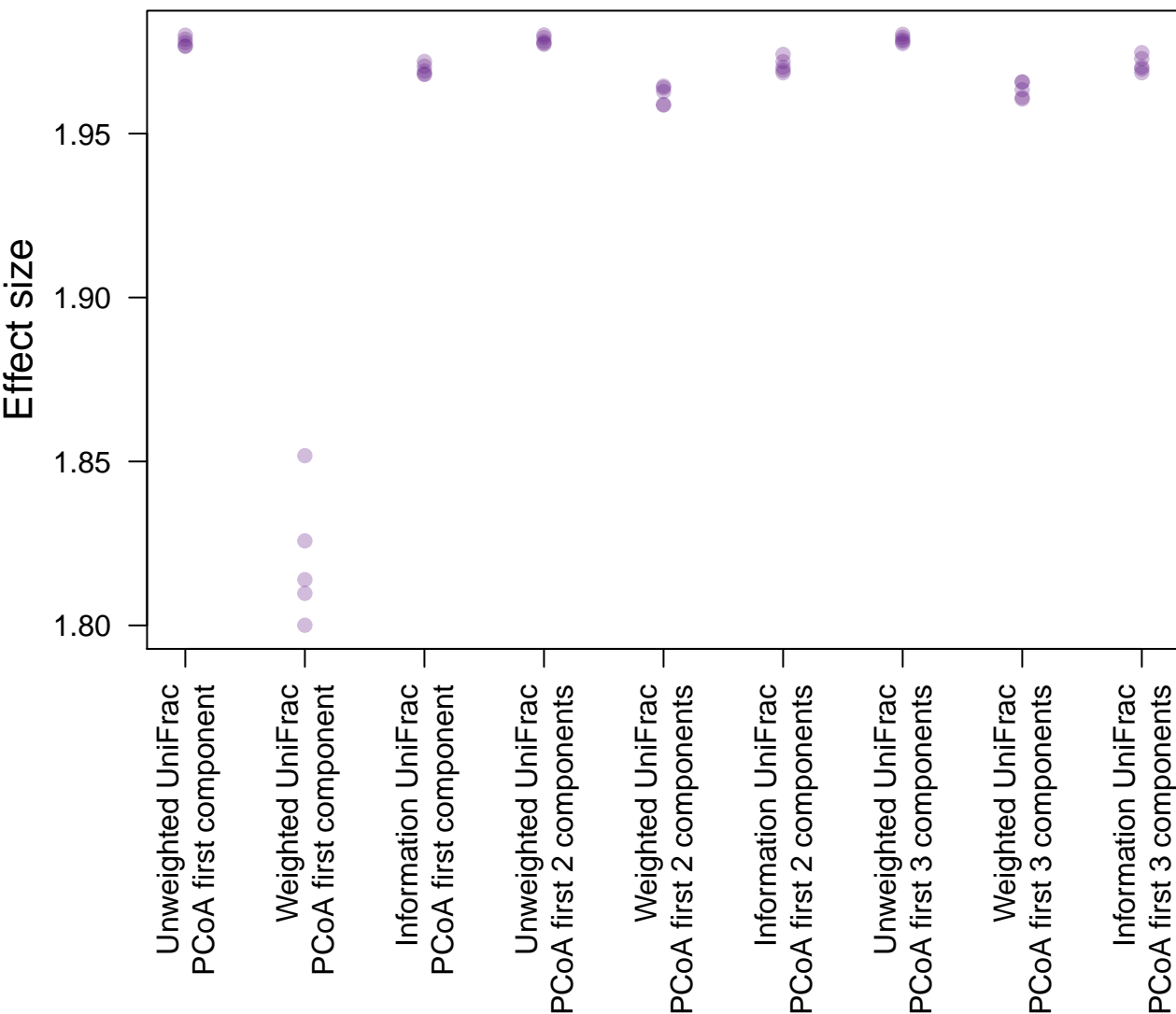


Information UniFrac

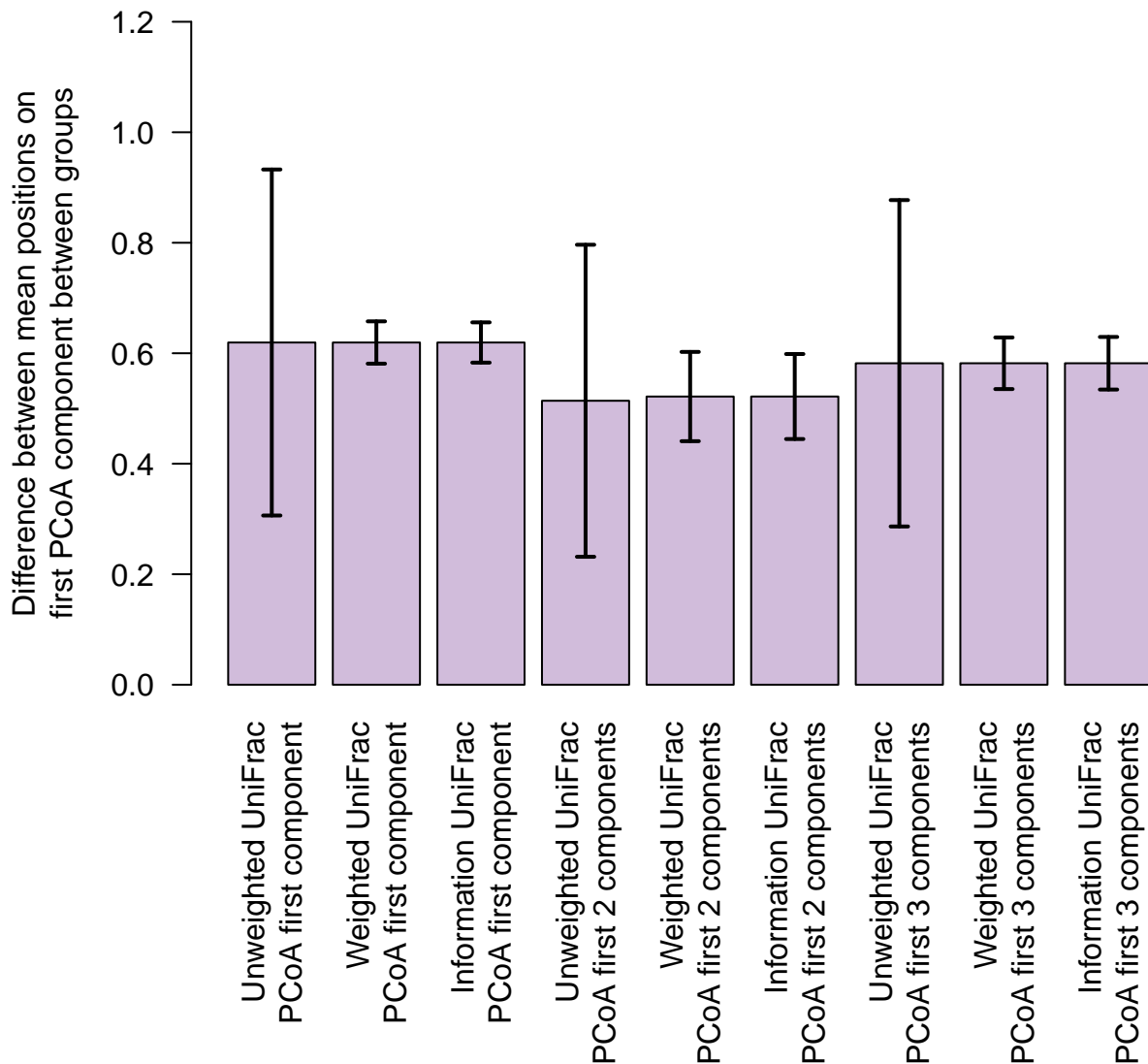
principal coordinates analysis



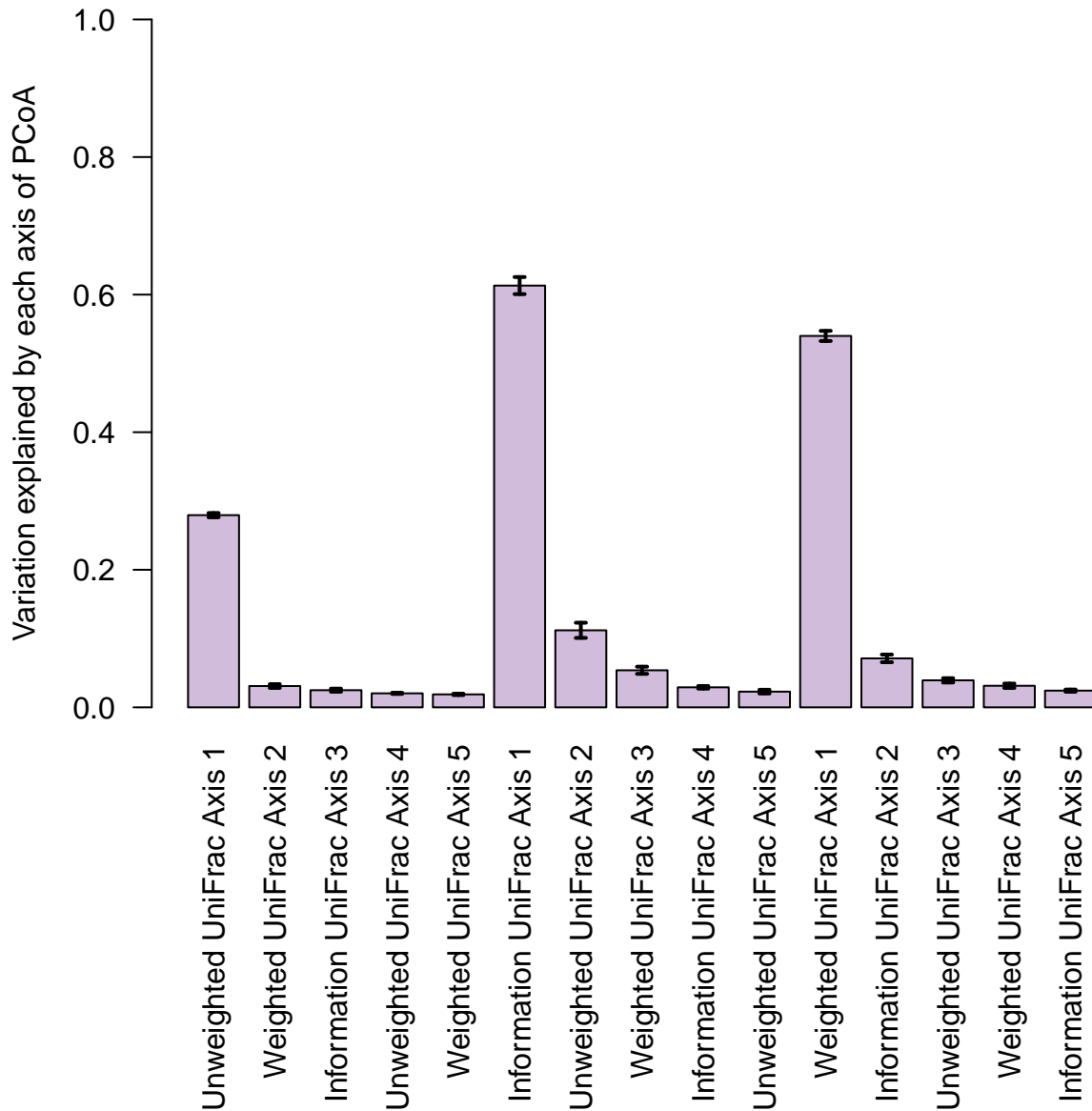
Sequencing depth 3000–6000 vs. > 6000 reads/sample



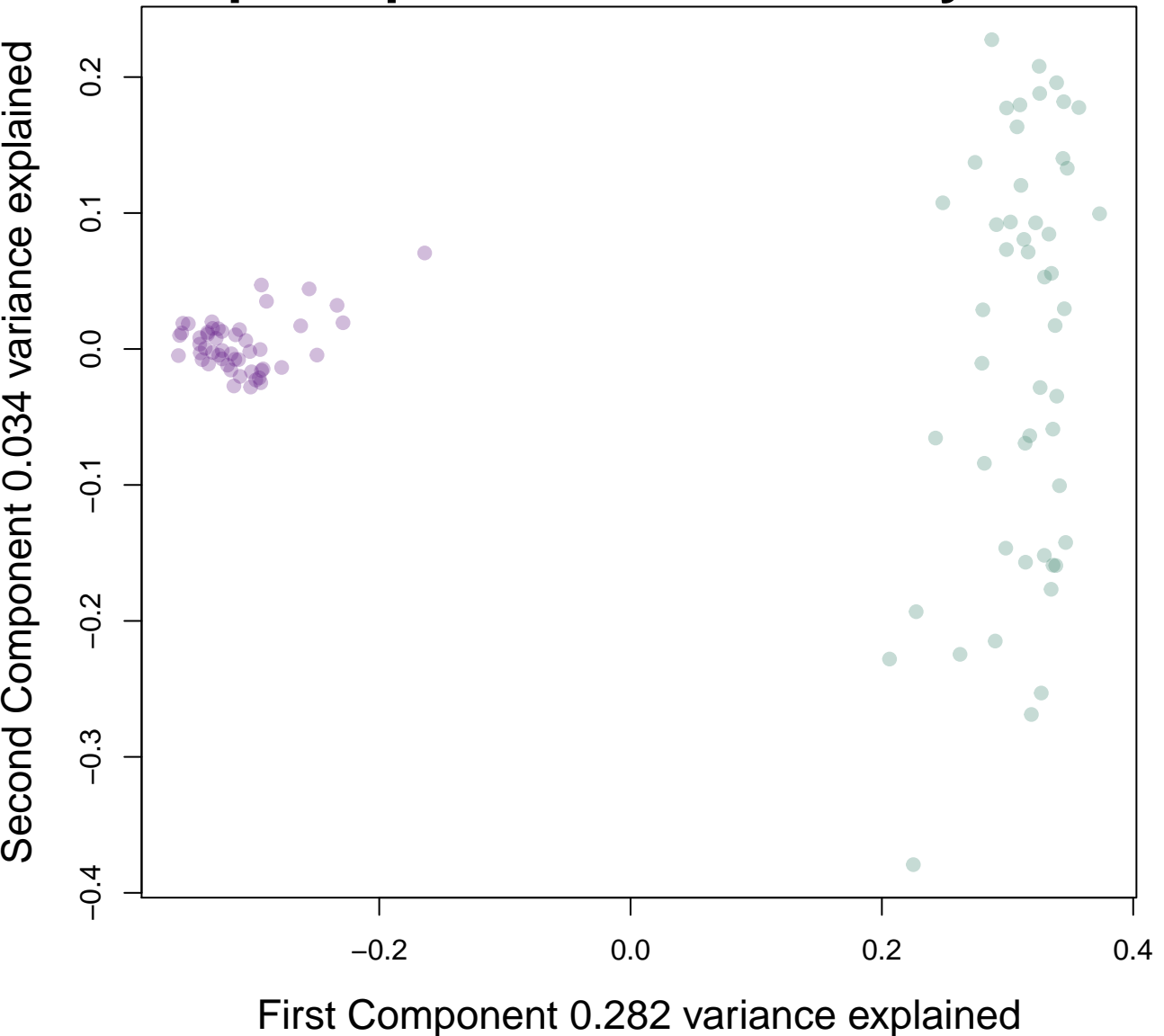
Sequencing depth 3000–6000 vs. > 6000 reads/sample



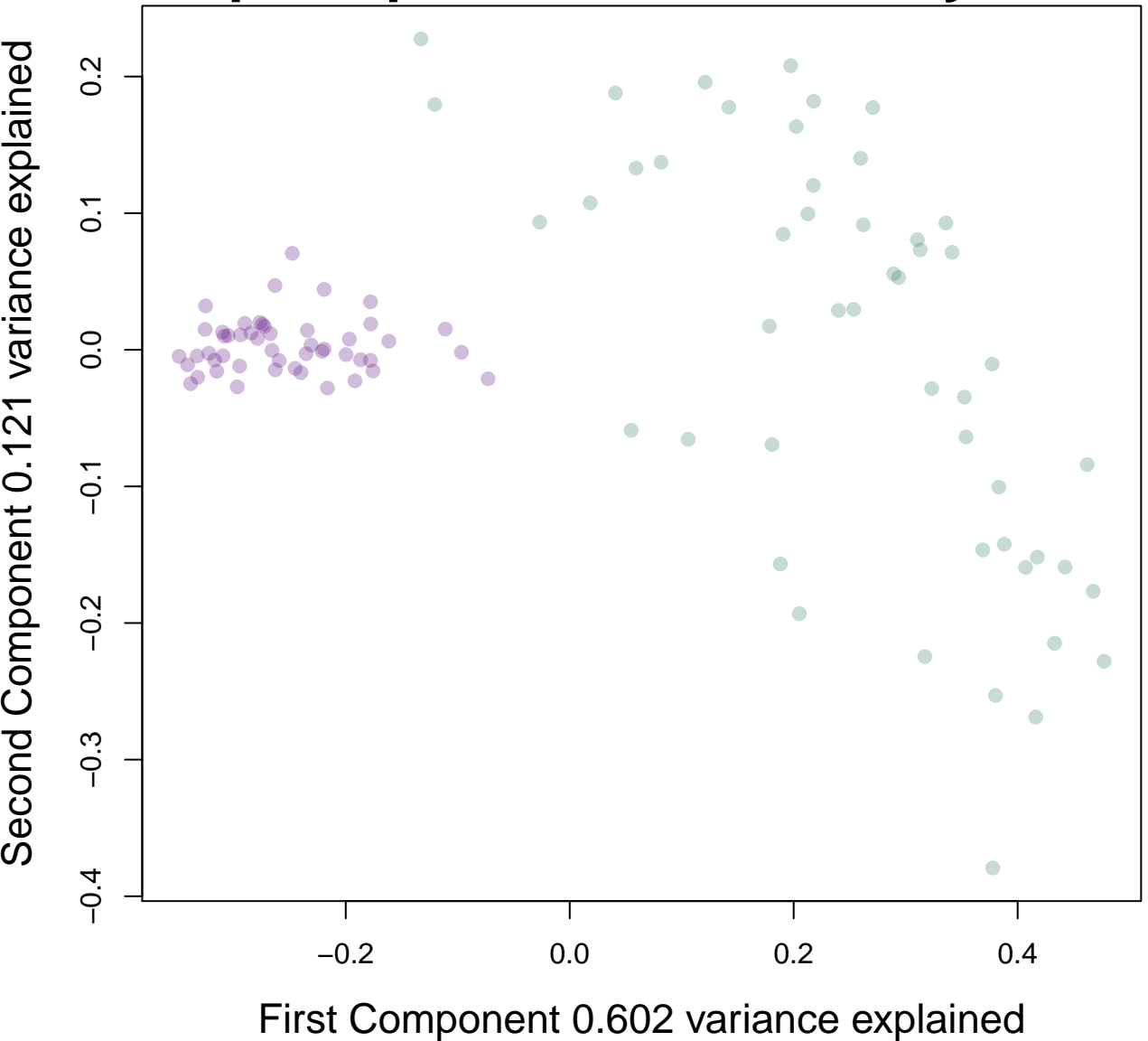
Sequencing depth 3000–6000 vs. > 6000 reads/sample



Unweighted UniFrac principal coordinates analysis



Weighted UniFrac principal coordinates analysis



Information UniFrac

principal coordinates analysis

