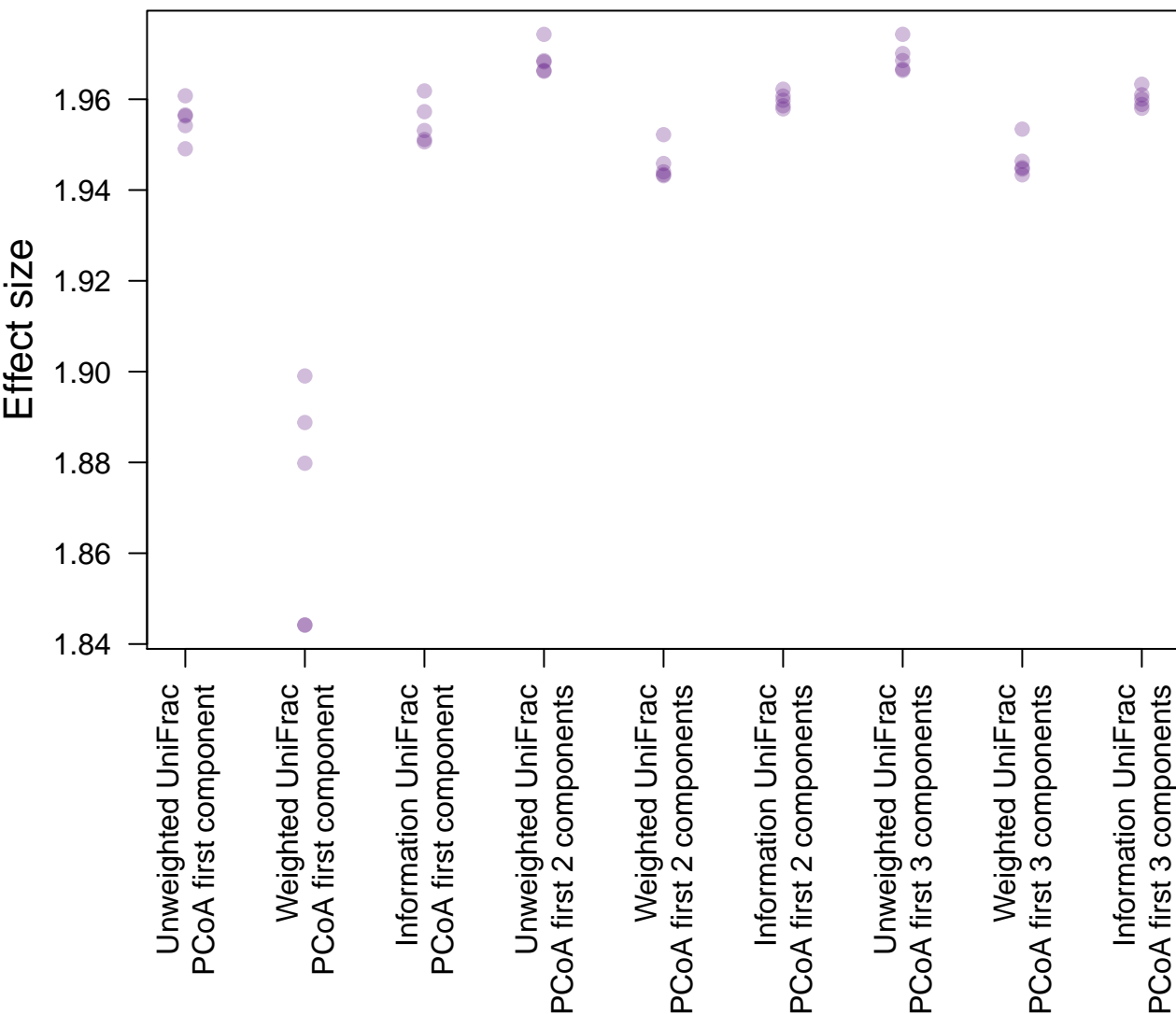
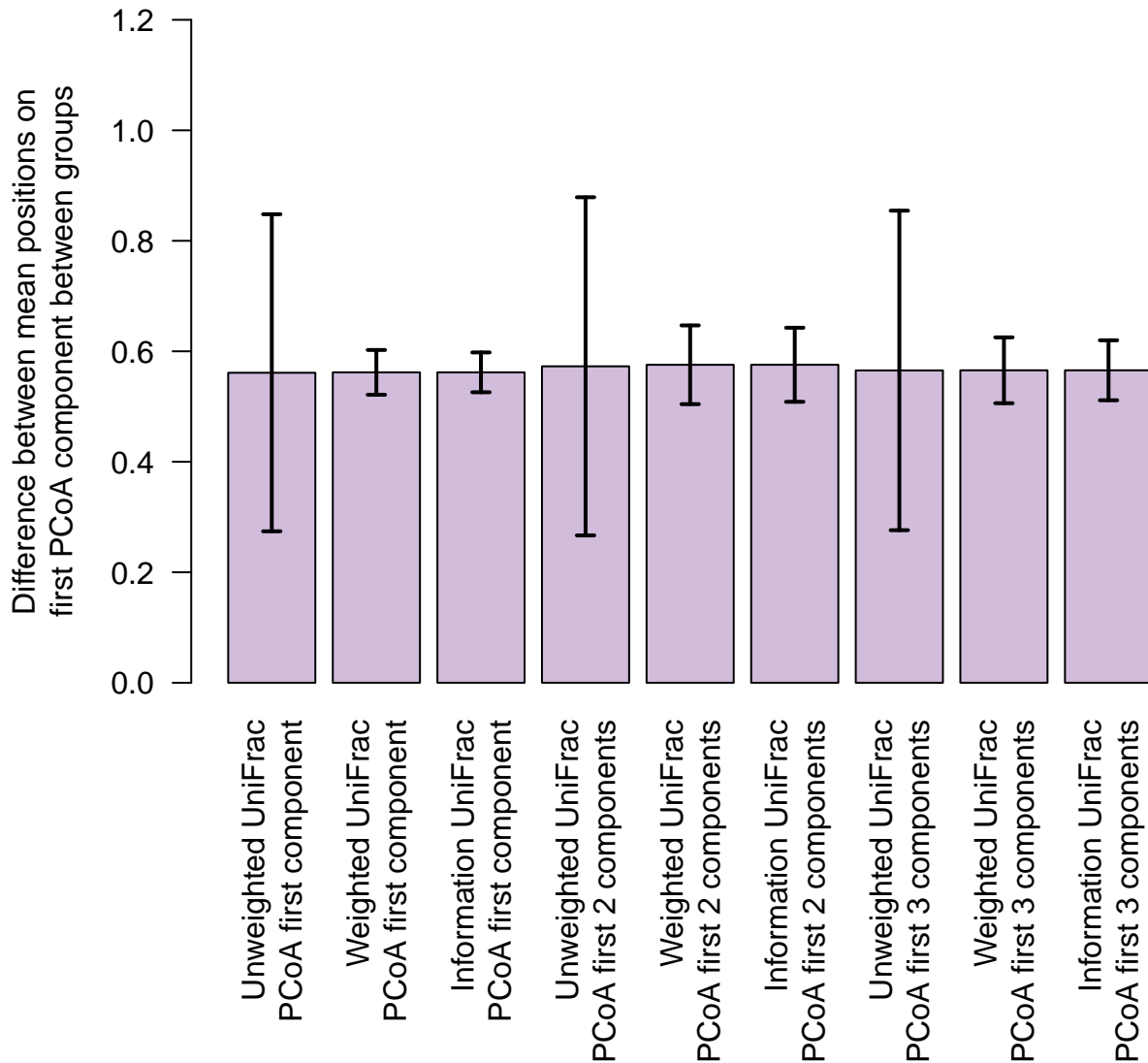


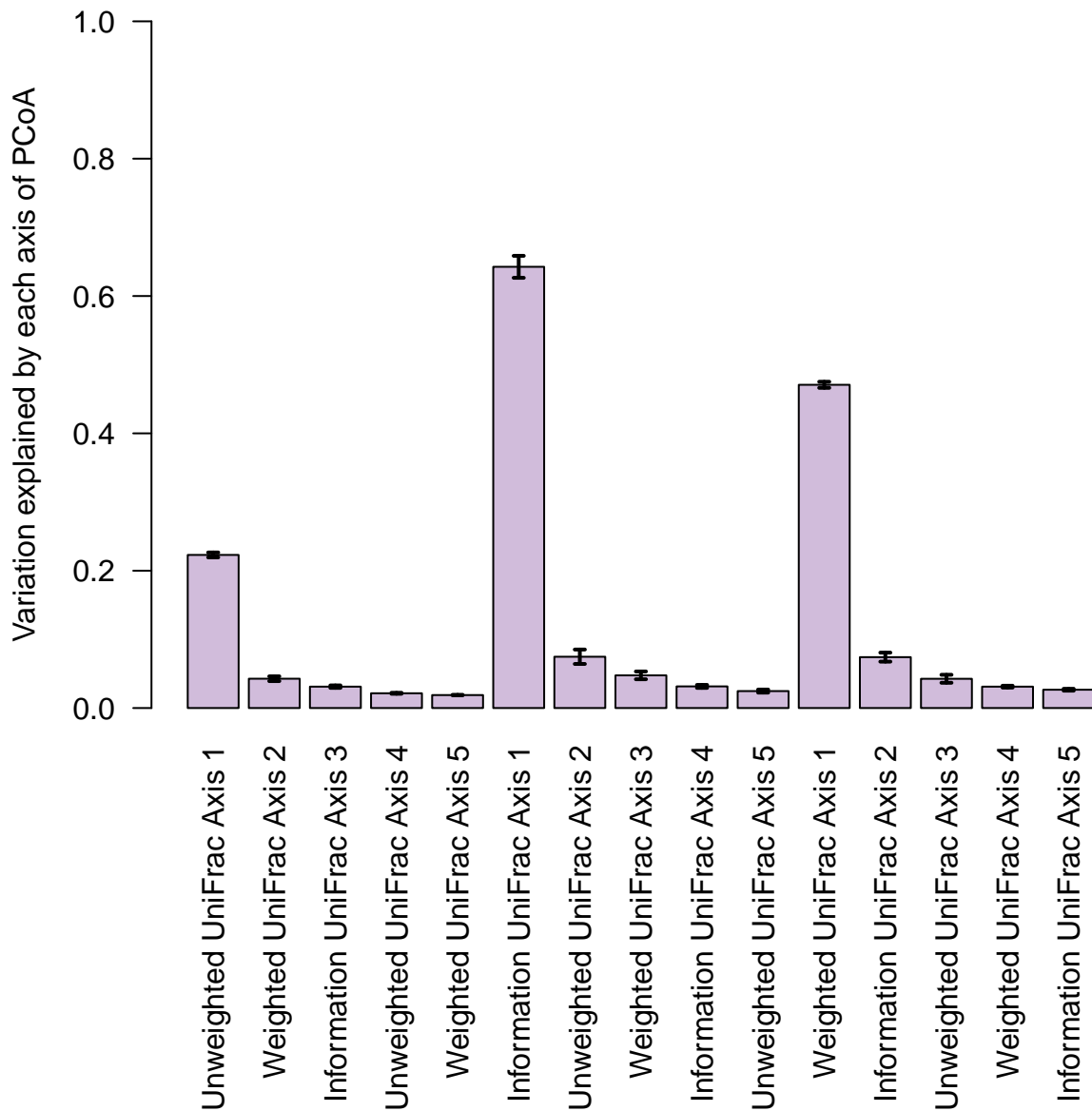
Sequencing depth < 3000 reads/sample



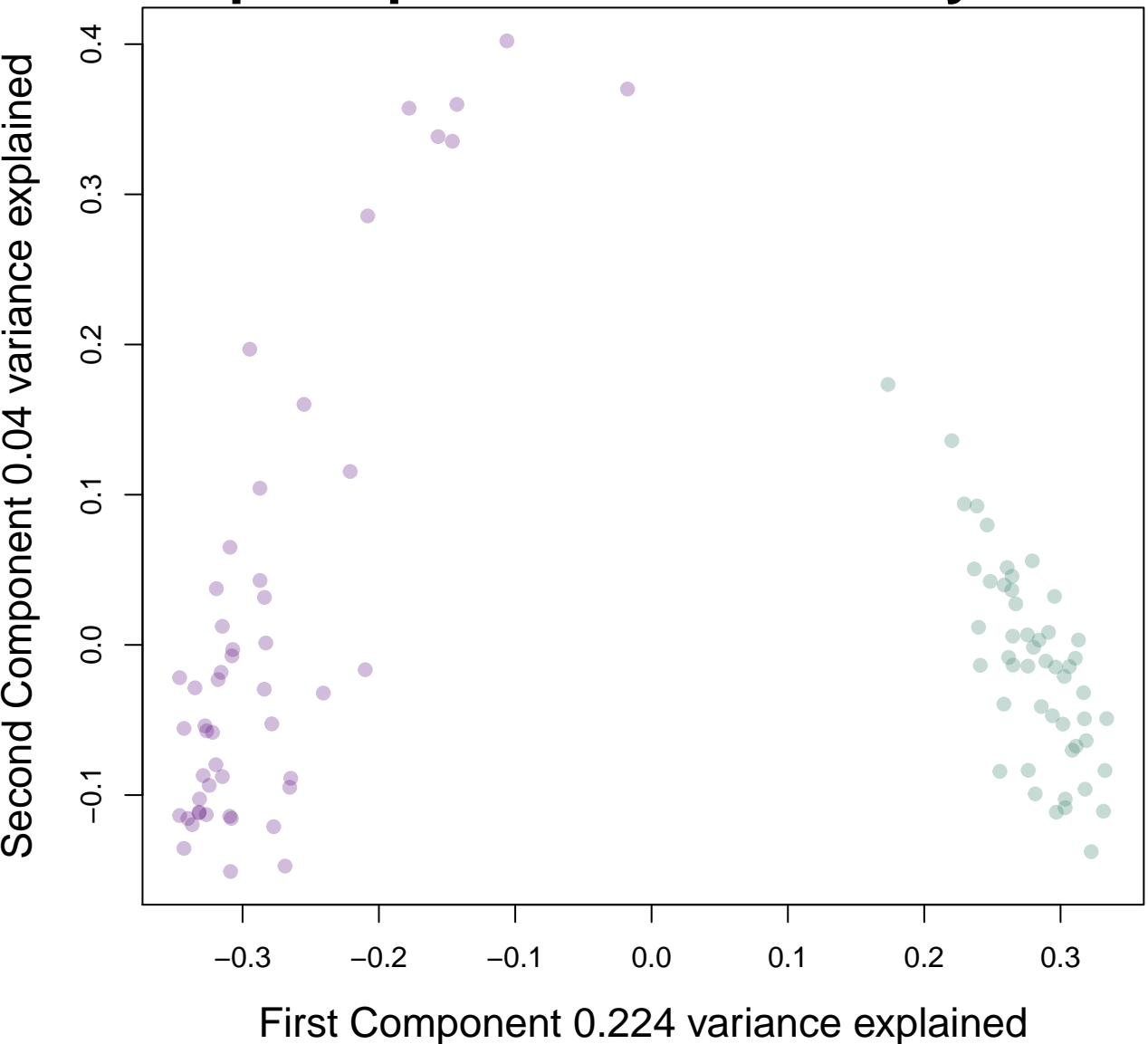
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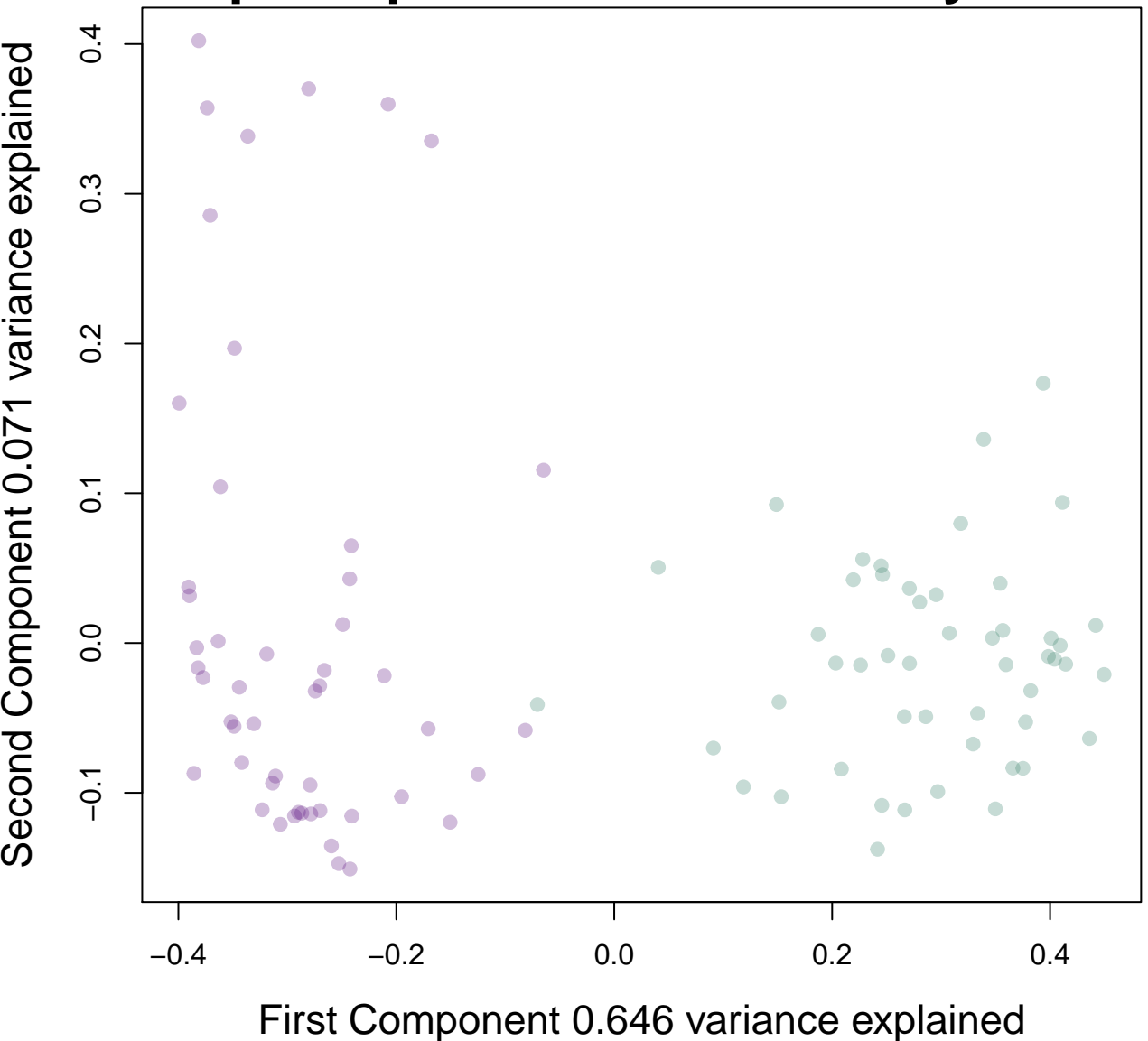
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Unweighted UniFrac principal coordinates analysis

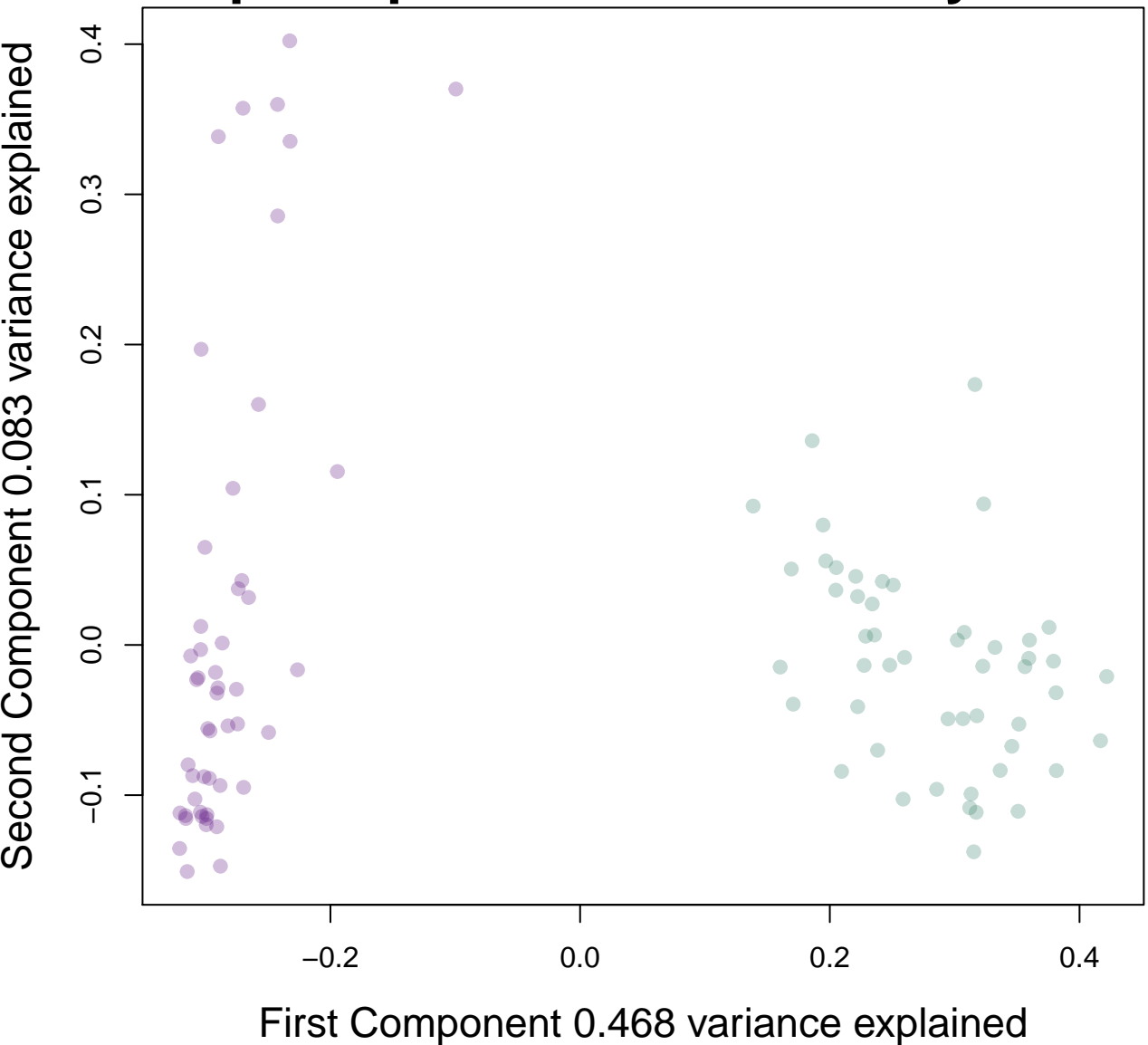


Weighted UniFrac principal coordinates analysis

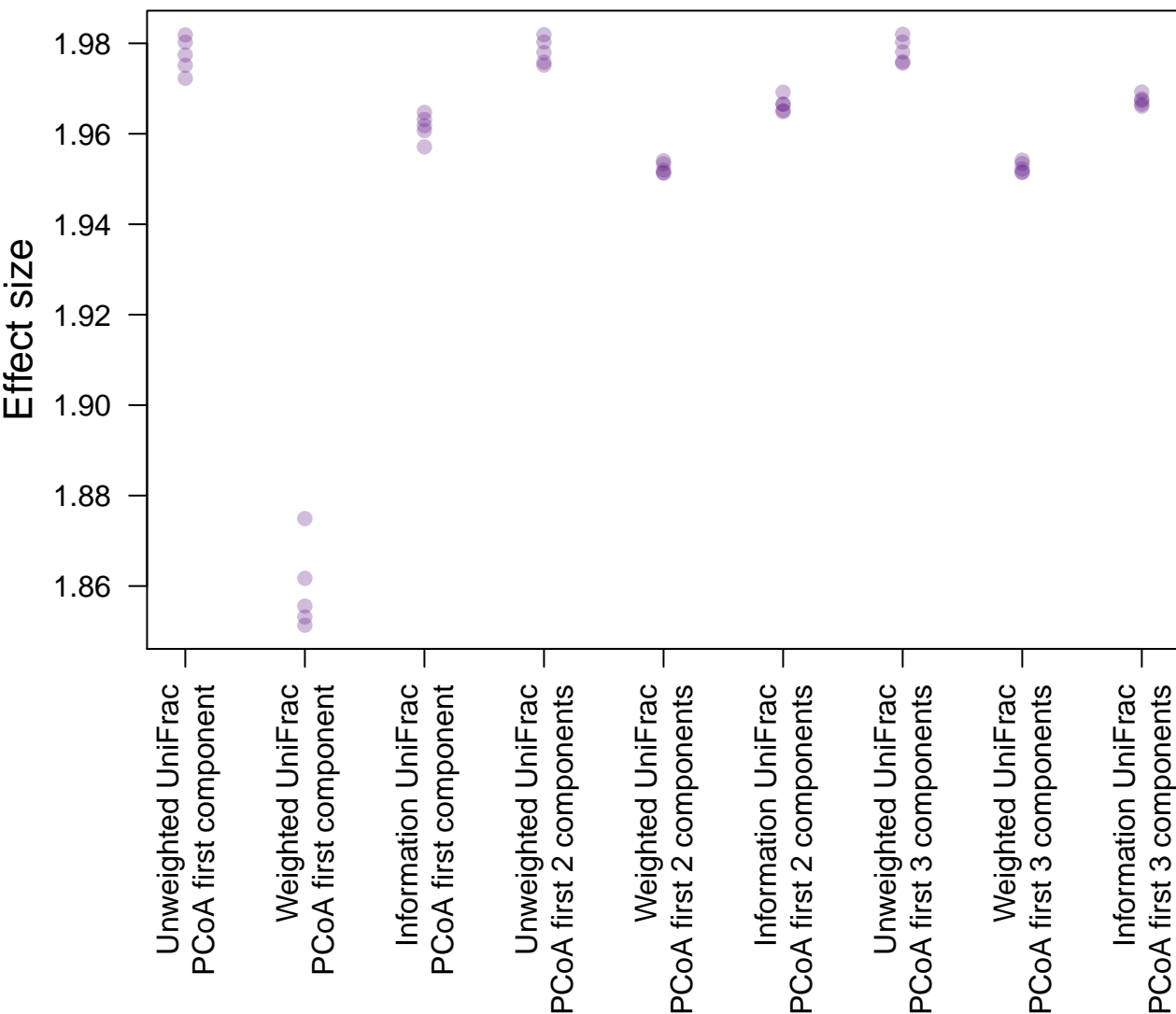


Information UniFrac

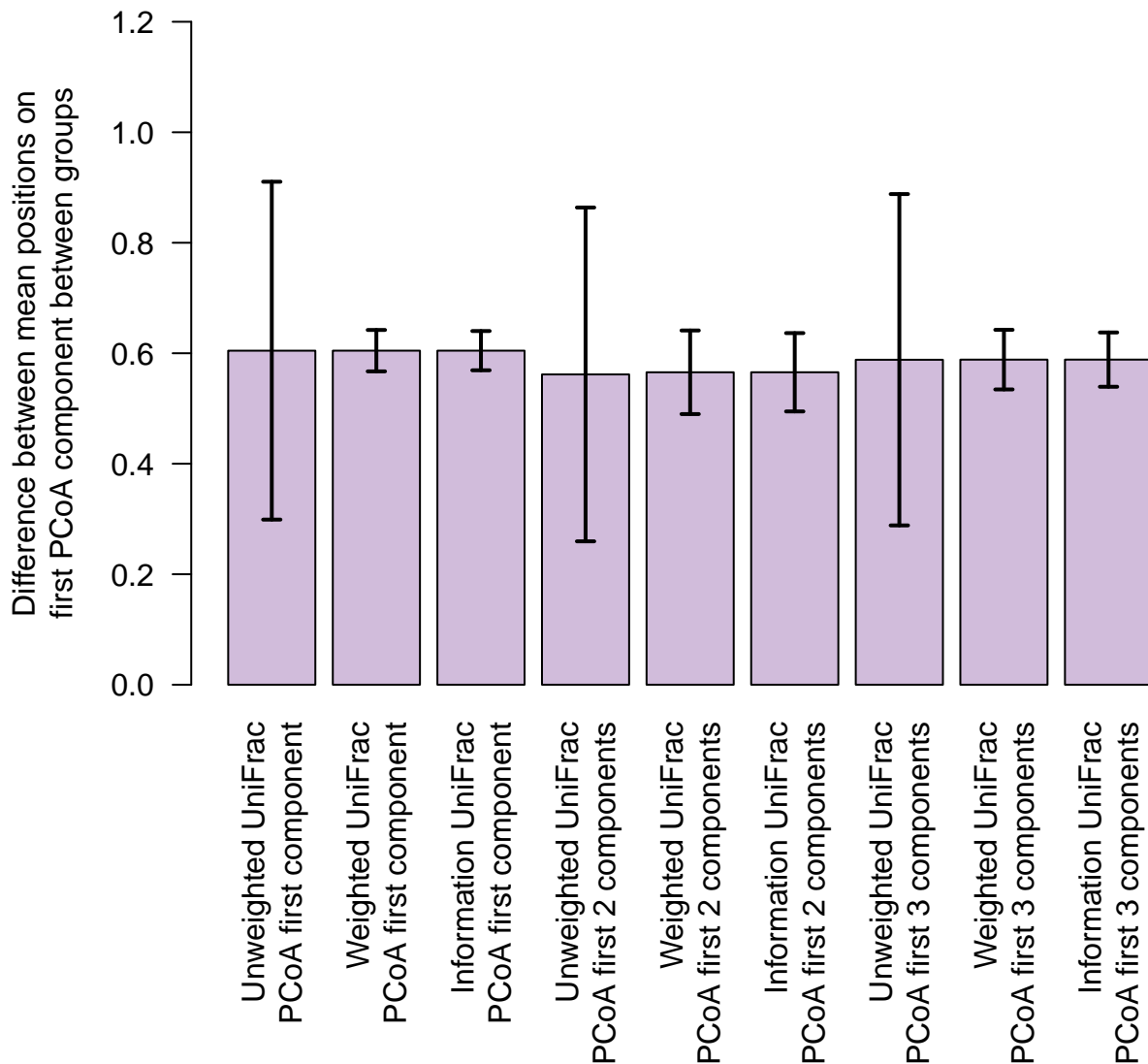
principal coordinates analysis



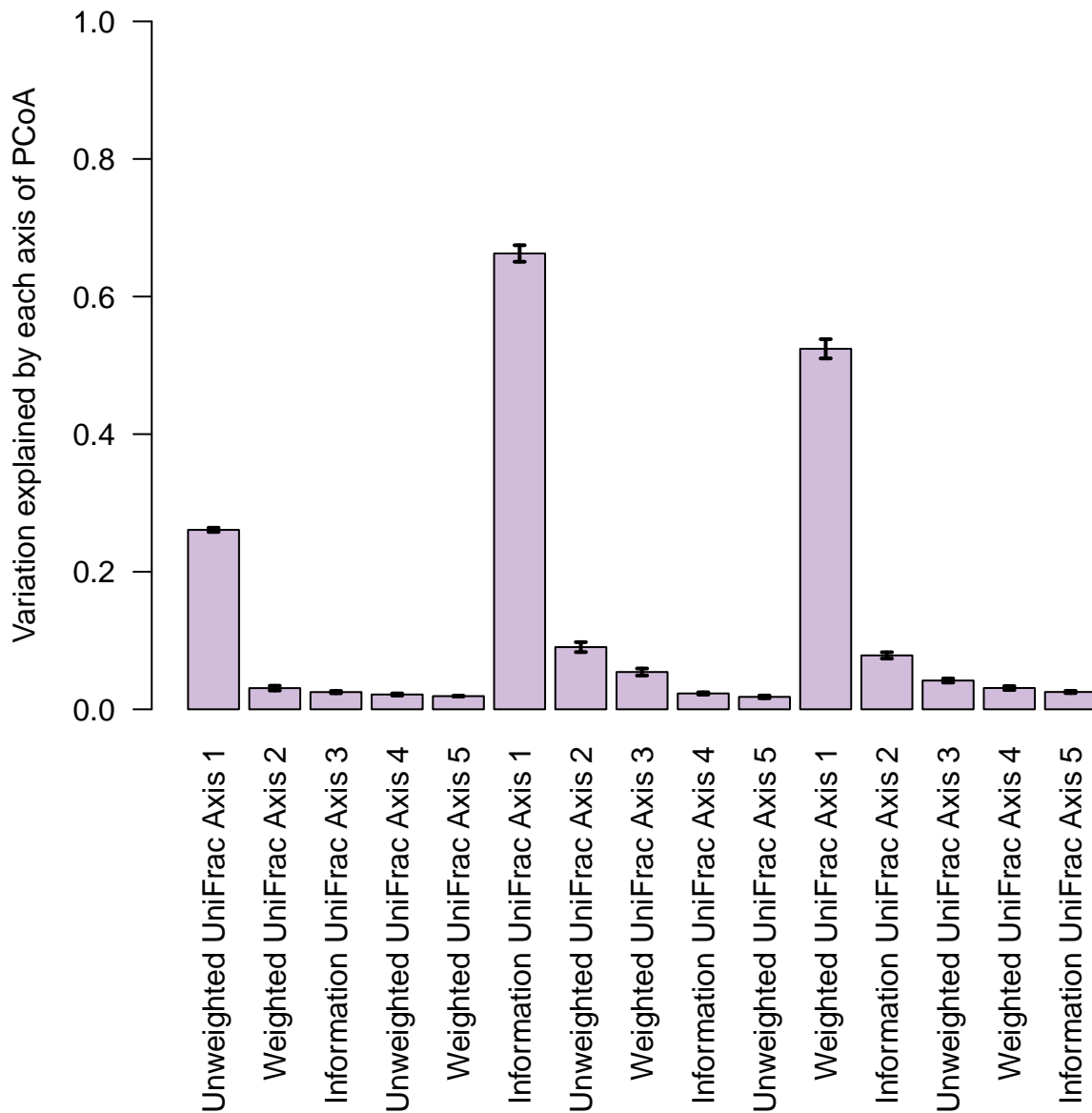
Sequencing depth 3000–6000 reads/sample



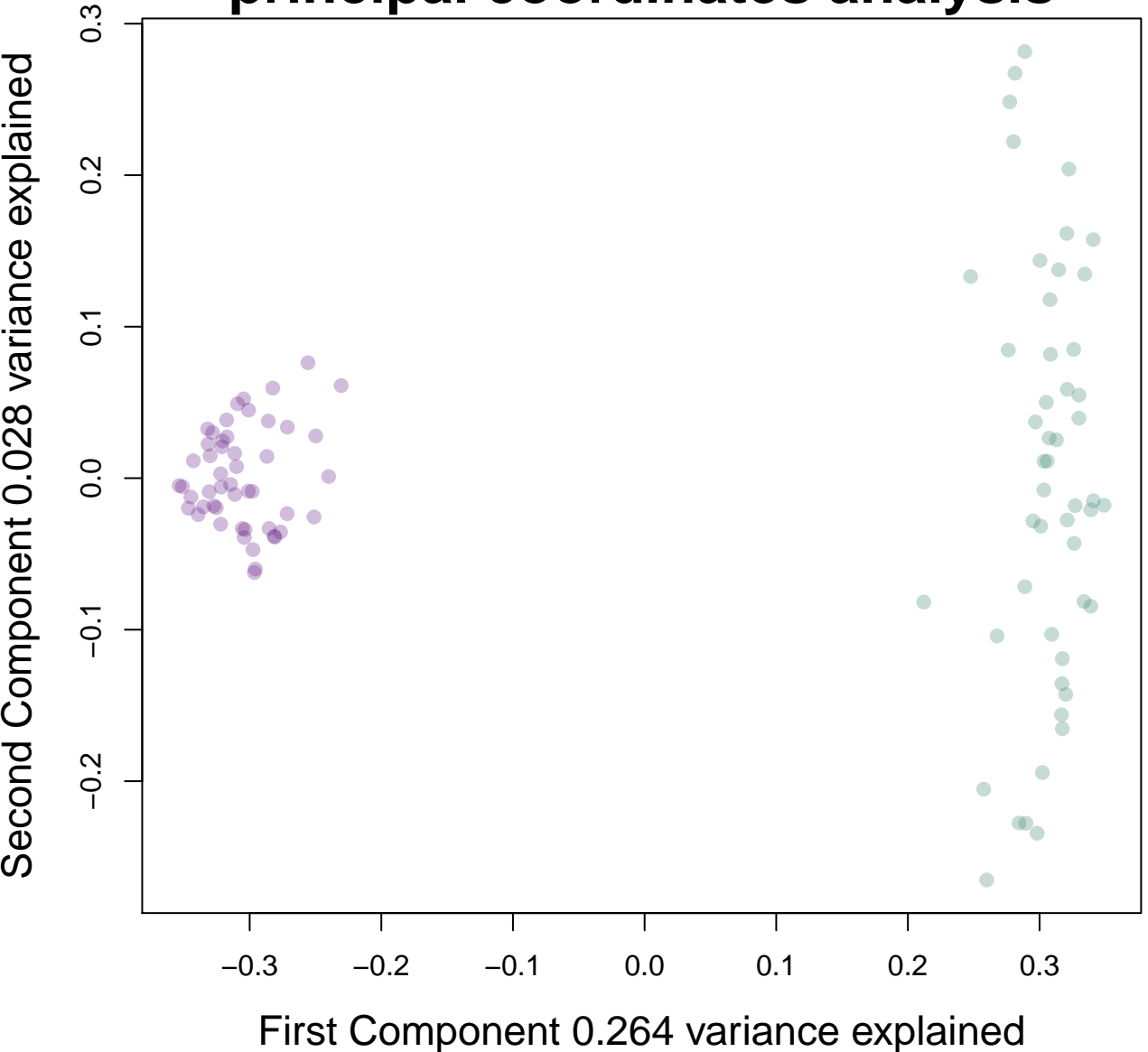
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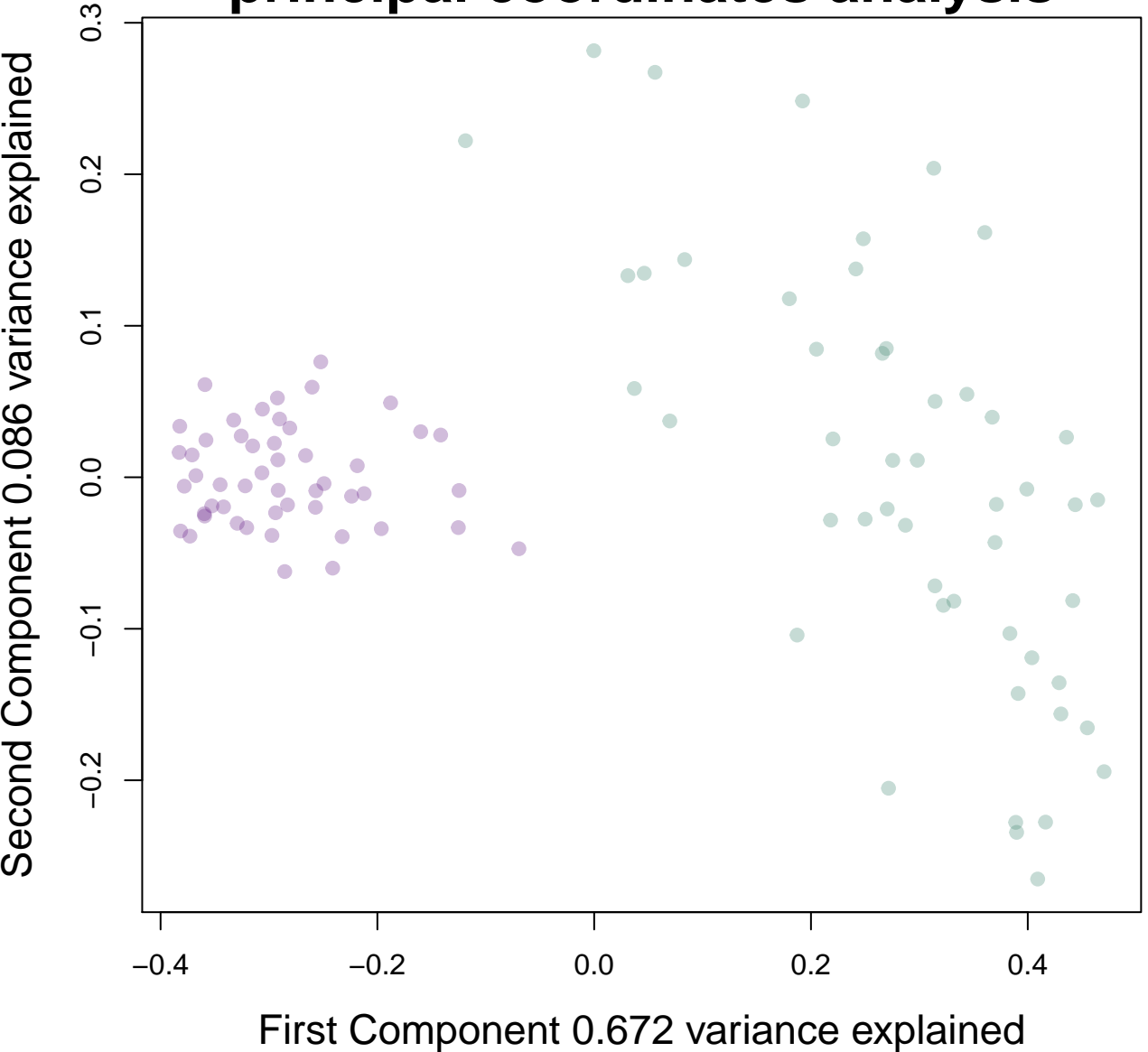
Sequencing depth 3000–6000 reads/sample



Unweighted UniFrac principal coordinates analysis

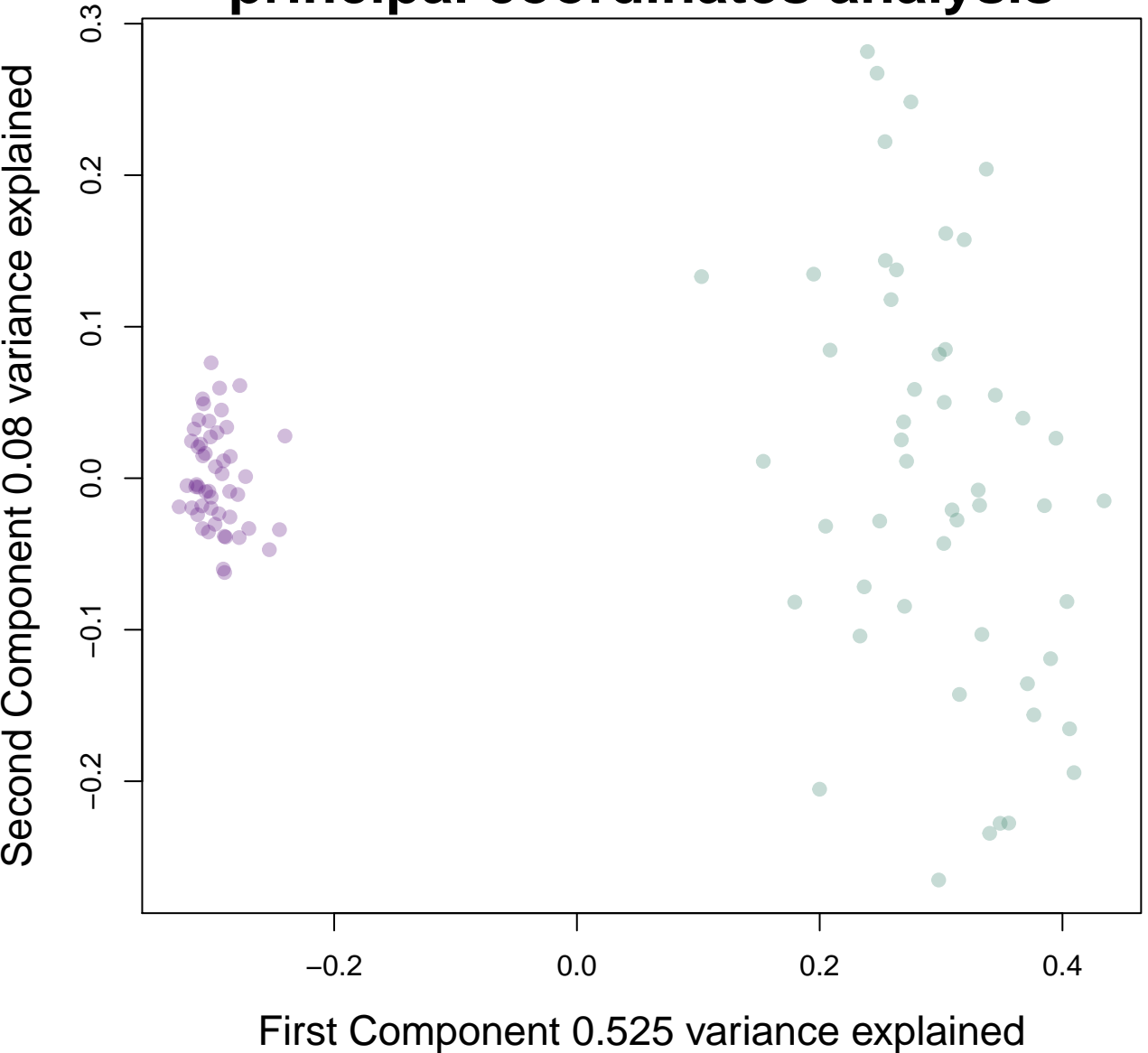


Weighted UniFrac principal coordinates analysis

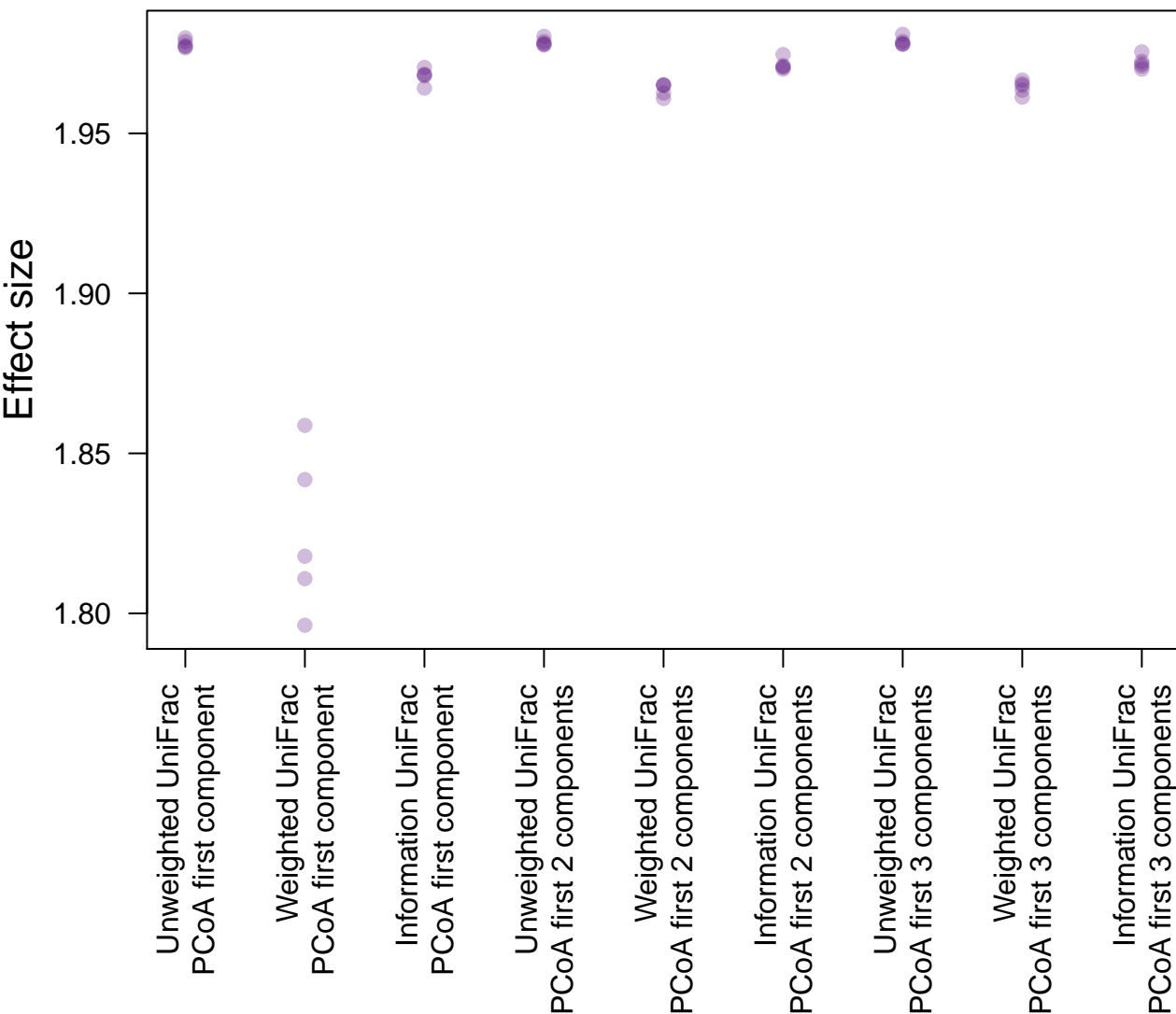


Information UniFrac

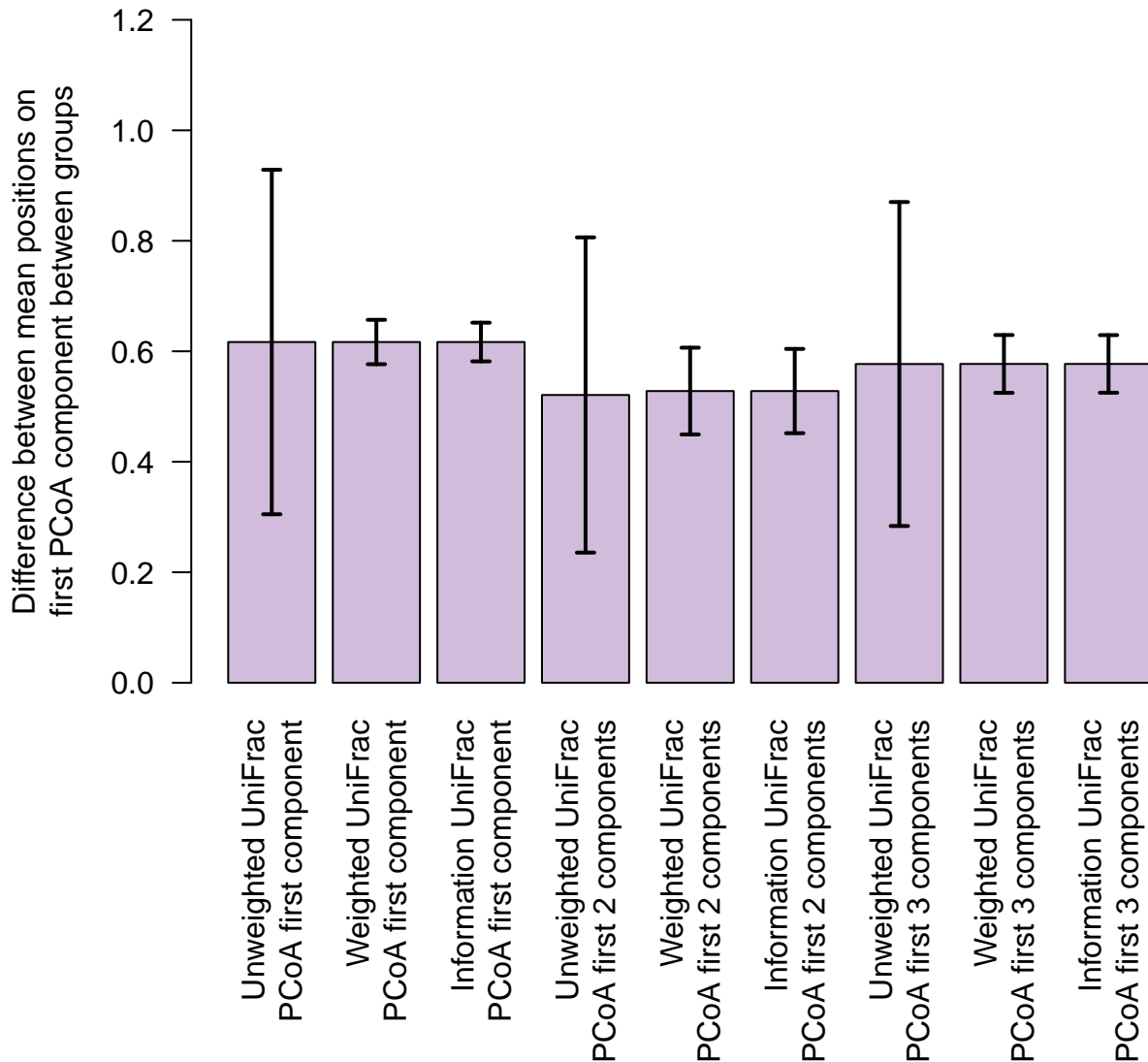
principal coordinates analysis



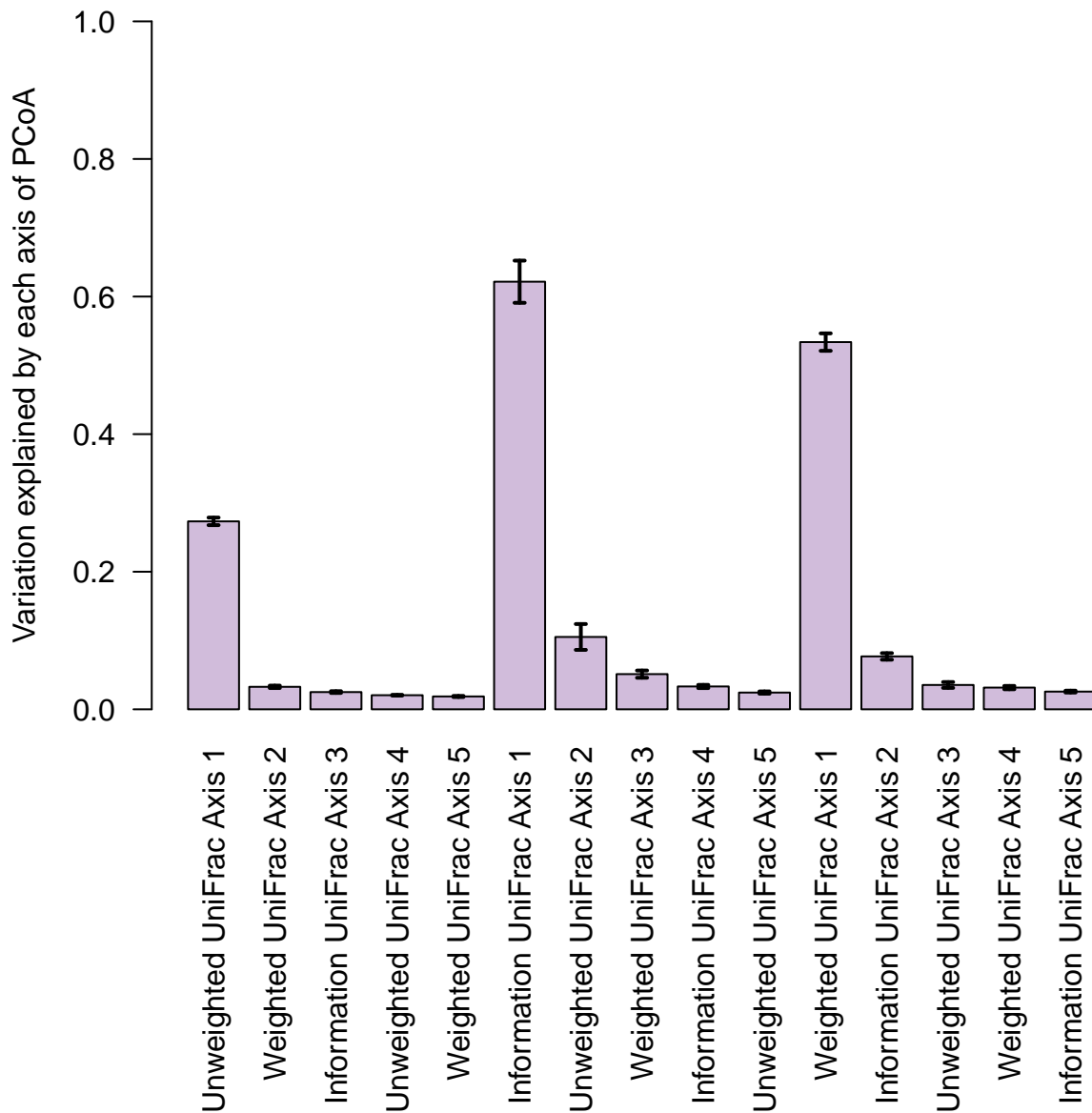
Sequencing depth > 6000 reads/sample



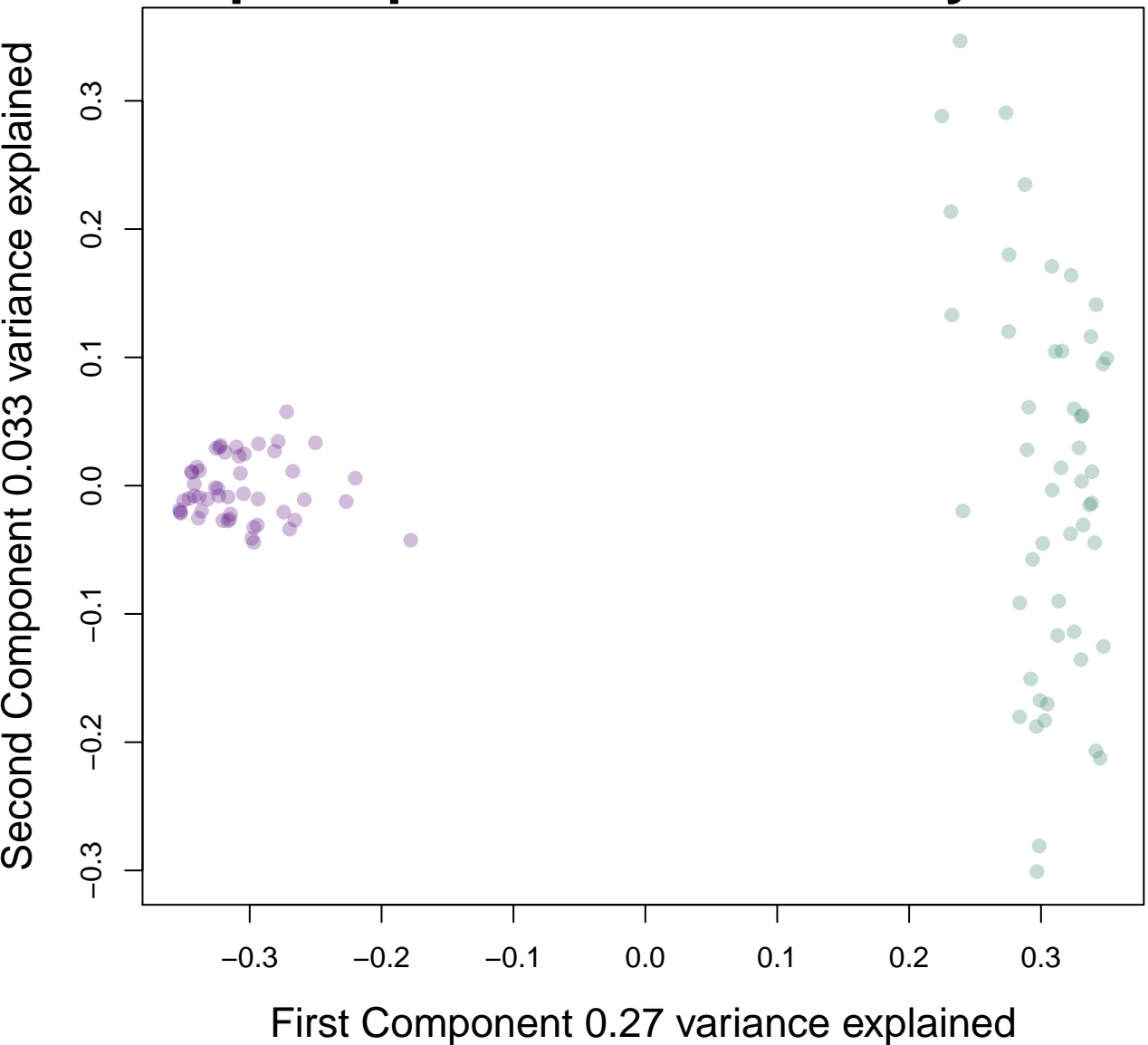
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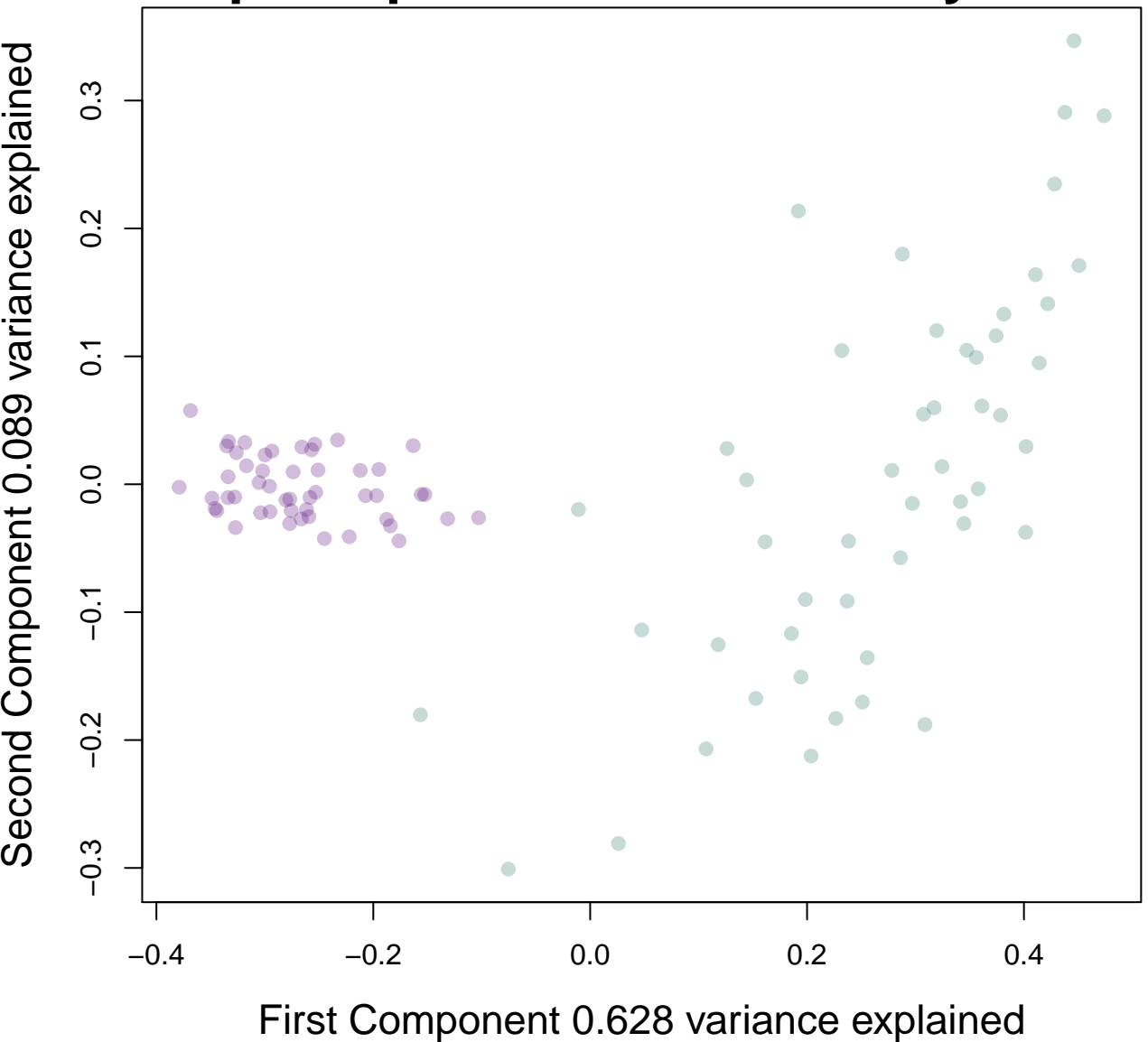
Sequencing depth > 6000 reads/sample



Unweighted UniFrac principal coordinates analysis



Weighted UniFrac principal coordinates analysis



Information UniFrac

principal coordinates analysis

