>set.dir(input=M:\All\_data\_Run35\20180328IN\_Run35,output=M:\All\_data\_Run35\BaselinePaper\_20190315)

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| >make.contigs(file=stability.files, processors=4)  >summary.seqs(fasta=stability.trim.contigs.fasta)  >screen.seqs(fasta=stability.trim.contigs.fasta, group=stability.contigs.groups, maxambig=0, maxlength=275)  >unique.seqs(fasta=stability.trim.contigs.good.fasta)  >count.seqs(name=stability.trim.contigs.good.names, group=stability.contigs.good.groups)  >summary.seqs(count=stability.trim.contigs.good.count\_table)  >pcr.seqs(fasta= silva.nr\_v132.align, start=11894, end=25319, keepdots=F)  >summary.seqs(fasta=silva.nr\_v132.pcr.align)  >align.seqs(fasta=stability.trim.contigs.good.unique.fasta, reference=silva.nr\_v132.pcr.align)  >summary.seqs(fasta=stability.trim.contigs.good.unique.align, count=stability.trim.contigs.good.count\_table)  >screen.seqs(fasta=stability.trim.contigs.good.unique.align, count=stability.trim.contigs.good.count\_table, summary=stability.trim.contigs.good.unique.summary, start=1968, end=11550, maxhomop=8)  >filter.seqs(fasta=stability.trim.contigs.good.unique.good.align, vertical=T, trump=.)  >unique.seqs(fasta=stability.trim.contigs.good.unique.good.filter.fasta, count=stability.trim.contigs.good.good.count\_table)  >pre.cluster(fasta=stability.trim.contigs.good.unique.good.filter.unique.fasta, count=stability.trim.contigs.good.unique.good.filter.count\_table, diffs=2)  >chimera.vsearch(fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta,count=stability.trim.contigs.good.unique.good.filter.unique.precluster.count\_table, dereplicate=t)  >remove.seqs(fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta,accnos=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.accnos)  >classify.seqs(fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.fasta,count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.count\_table,reference=silva.nr\_v132.align,taxonomy=silva.nr\_v132.tax, cutoff=80)  >remove.lineage(fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.fasta,count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.count\_table,taxonomy=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.nr\_v132.wang.taxonomy,taxon=Chloroplast-Mitochondria-unknown-Archaea-Eukaryota)  #Test the sequence error rate  # Two mock microbial community DNA standards used: zymo.mock.V4.filter.fasta /HMP\_MOCK.v35.fasta  >get.groups(count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.count\_table,fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.fasta, groups= ZymoR353)  >seq.error(fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.fasta,count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.pick.count\_table,reference= zymo.mock.V4.filter.fasta, aligned=F)  >remove.groups(count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.count\_table,fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.fasta,taxonomy=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.nr\_v132.wang.pick.taxonomy, accnos=abrecovery.accnosgroups)  >cluster.split(fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.fasta,count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.pick.count\_table,taxonomy=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.nr\_v132.wang.pick.pick.taxonomy, splitmethod=classify, taxlevel=4, cutoff=0.03)  **>**classify.otu(list=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.list,count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.pick.count\_table,taxonomy=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.nr\_v132.wang.pick.pick.taxonomy, label=0.03)  >make.shared(list=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.list,count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.pick.count\_table, label=0.03)  >sub.sample(shared=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.shared, size=1066)  **>**get.relabund(shared=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.shared)  **>**summary.single(shared=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.shared,calc=nseqs-coverage-sobs-invsimpson-shannon-chao-simpsoneven, subsample=1066)  #AMOVA  >dist.shared(shared= Baseline5b.shared,calc=braycurtis)  >amova(phylip= Baseline5b.braycurtis.0.03.lt.dist,  design=Baseline\_5b\_Abx.design)  >dist.shared(shared= Subject2.shared,calc=braycurtis)  >amova(phylip= Subject2.braycurtis.0.03.lt.dist, design= Subject2.design) |