

SUPPLEMENTARY DATA 1.1:

Mothur's commands used to process sequences before their classification:

```
summary.seqs(fasta=PruebaMcMahon.fasta)
```

```
screen.seqs(fasta=PruebaMcMahon.fasta, group=PruebaMcMahon.groups,  
summary=PruebaMcMahon.summary, maxambig=0, maxlength=150, processors=8)
```

```
unique.seqs(fasta=PruebaMcMahon.good.fasta)
```

```
count.seqs(name=PruebaMcMahon.good.names, group=PruebaMcMahon.good.groups)
```

```
summary.seqs(fasta=PruebaMcMahon.good.unique.fasta, count=PruebaMcMahon.good.count_table)
```

```
align.seqs(fasta=PruebaMcMahon.good.unique.fasta, reference=silva.bacteria.fasta)
```

```
screen.seqs(fasta=PruebaMcMahon.good.unique.align, count=PruebaMcMahon.good.count_table,  
summary=PruebaMcMahon.good.unique.summary, start=13862, end=21774, maxhomop=8,  
minlength=149, processors=8)
```

```
filter.seqs(fasta=PruebaMcMahon.good.unique.good.align, vertical=T, trump=.)
```

```
unique.seqs(fasta=PruebaMcMahon.good.unique.good.filter.fasta,  
count=PruebaMcMahon.good.good.count_table)
```

```
chimera.uchime(fasta=PruebaMcMahon.strain.fasta, count=PruebaMcMahon.strain.count_table,  
dereplicate=t, processors=8)
```

```
remove.seqs(fasta=PruebaMcMahon.strain.fasta, accnos=PruebaMcMahon.strain.denovo.uchime.accnos)
```

```
sub.sample(fasta=PruebaMcMahon.strain.pick.fasta,  
count=PruebaMcMahon.strain.denovo.uchime.pick.count_table, size=10000, persample=true)
```

SUPPLEMENTARY DATA 1.2

Mothur commands used to cluster the sequences for the species-level analysis

```
dist.seqs(fasta=PruebaMcMahon.strain.ready.fasta, cutoff=0.10)
```

```
cluster(column=PruebaMcMahon.strain.ready.reduced.dist,  
count=PruebaMcMahon.strain.ready.count_table)
```

```
make.shared(list=PruebaMcMahon.strain.ready.list,  
count=PruebaMcMahon.strain.ready.count_table, label=0.03)
```

rarefaction.single(shared=PruebaMcMahon.strain.ready.shared)
SUPPLEMENTARY DATA 1.3:

Oligotyping commands used to classify sequences into oligotypes:

entropy-analysis OTU_X

oligotype OTU_X OTU_X-ENTROPY -c 1 -M 10 -a 5

Being OTU_X the group of related sequences to be analysed.