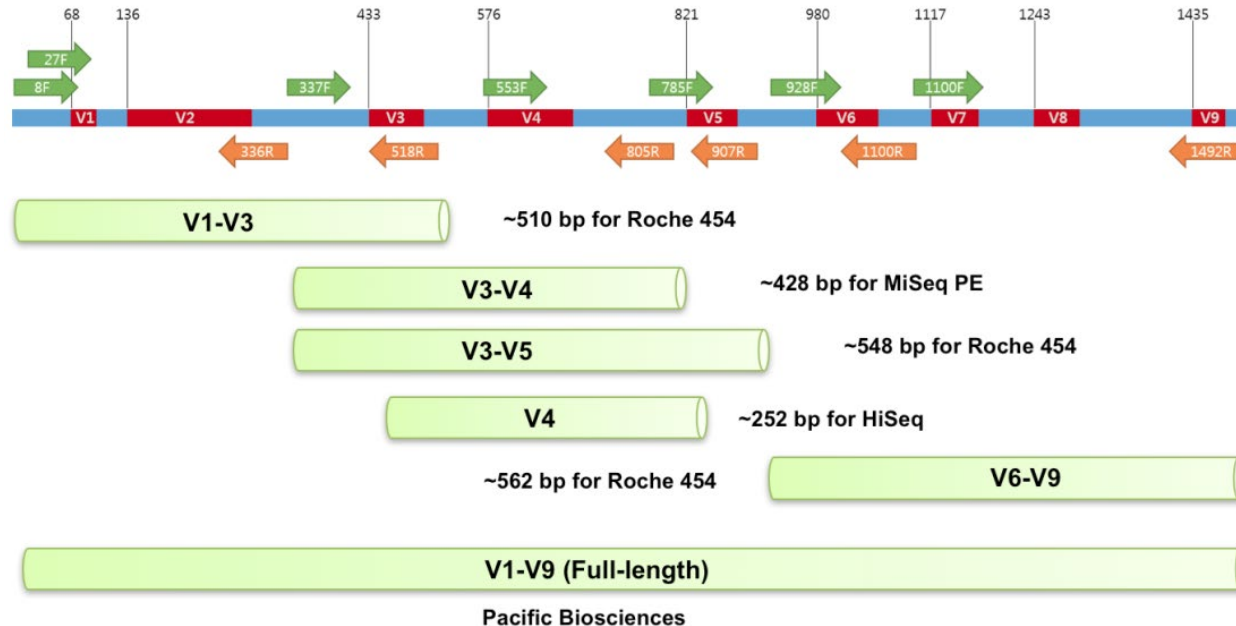


# 16S gene and primers used for metabarcoding





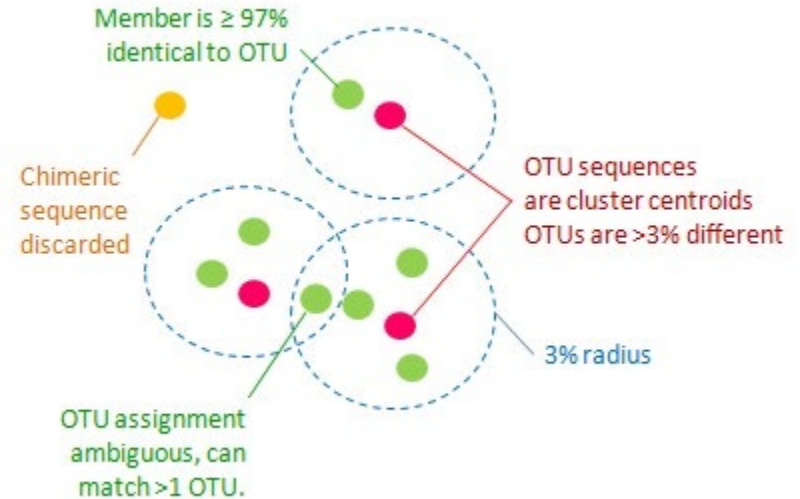
## Other genes used for metabarcoding

- COI
- 18S (eukaryotes)

# Metabarcoding sequence cl

Take into account:

- intraspecific variability
- sequencing errors
- 97% similarity: species threshold
- two types: *de novo* and reference-based





# From OTUs to ASVs

- Amplicon sequences variants (today's tutorial)  
The “true” biological sequences are inferred from reads

“Biological sequences are discriminated from errors on the basis of, in part, the expectation that biological sequences are more likely to be repeatedly observed than are error-containing sequences”.



## Further reading

<https://www.nature.com/articles/ismej2017119>