

seismic align

Sequencing Reads (FASTQ)

RNA Chemical Probing
DMS-MaPseq
SHAPE-MaP
ETC-MaP

Other Library Types
RNA editing
Bisulfite-seq
SNP quantification

→ Reads

Alignment Map (BAM)

AGTCTTATGGGTTTAC
AGTCTT~~T~~GGCTTCCTCA
AGTCTT-TGGGTTATCCACT
TCTCTGGCTT-TCCTCTGG
TTATGGCTTCTC-ACTGGAC
ATGGATTGTCCAGTGGAC
GGCTTATCCCTCTGGAC
AGTCTTATGGCTTATCCACTGGAC
Reference Sequence

seismic relate

Types of Relationships

- Match ■ Deletion
- Ambig. ■ Insertion
- Substitution to ...
- A ■ C ■ G ■ T

Matrix of Relationships



seismic pool

Sample 1

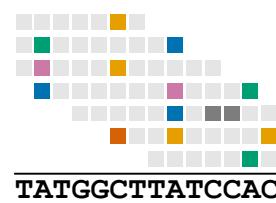


Pooled Sample

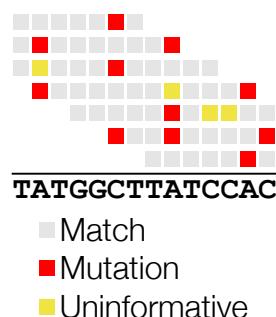


seismic mask

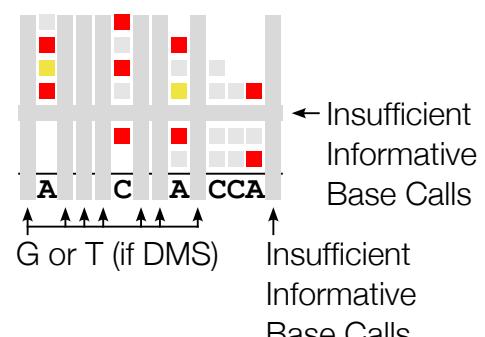
Select Region



Specify Mutation Types



Filter Reads and Positions

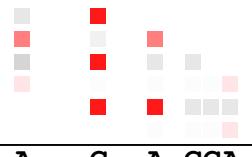


seismic cluster

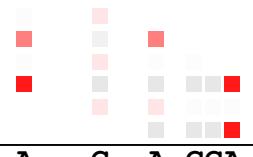
Probability of Cluster Membership

0.0 1.0

Cluster 1 (57%)

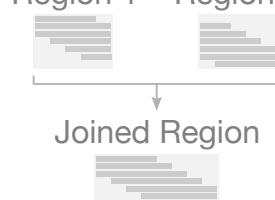


Cluster 2 (43%)



seismic join

Region 1



Region 2

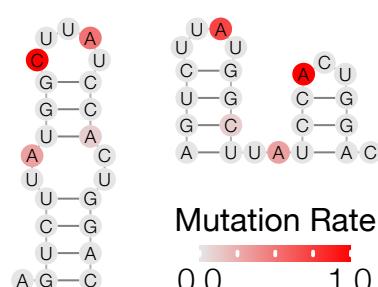


Joined Region

seismic fold

Cluster 1

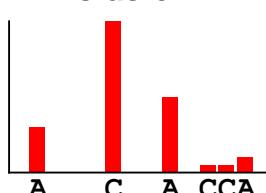
Cluster 2



seismic graph

Mutation Rate

Cluster 1



Cluster 2

