Genomic research on South Africa's sardine stocks

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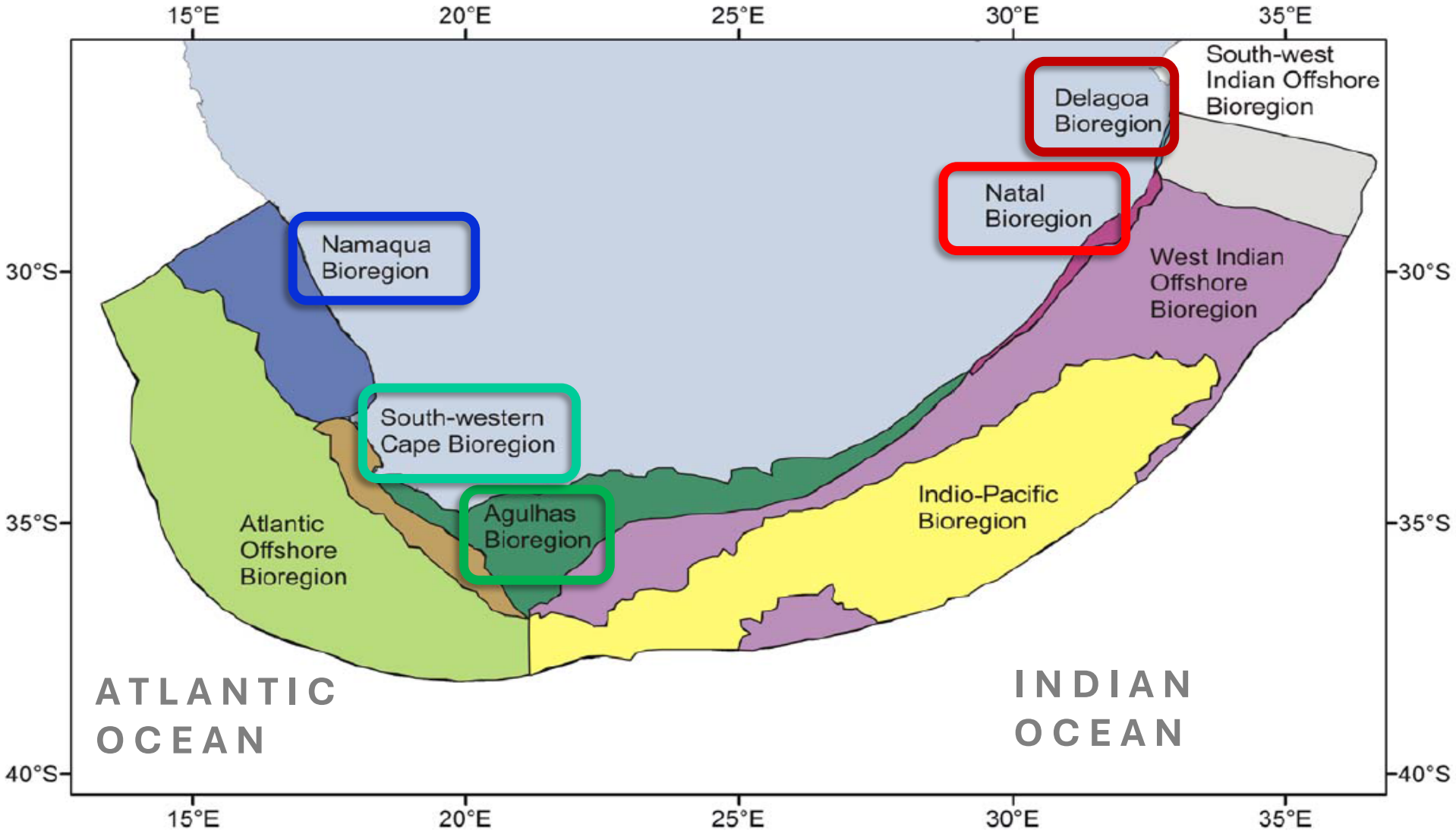
Ecological Genomics & Wildlife Conservation

South Africa's marine bioregions

Based on species assemblages, strongly linked to SST



Griffiths et al. (2010) PLoS ONE 5(8): e12008.

Genetic structure often mirrors biogeography

Many more examples, but not all as clearly defined

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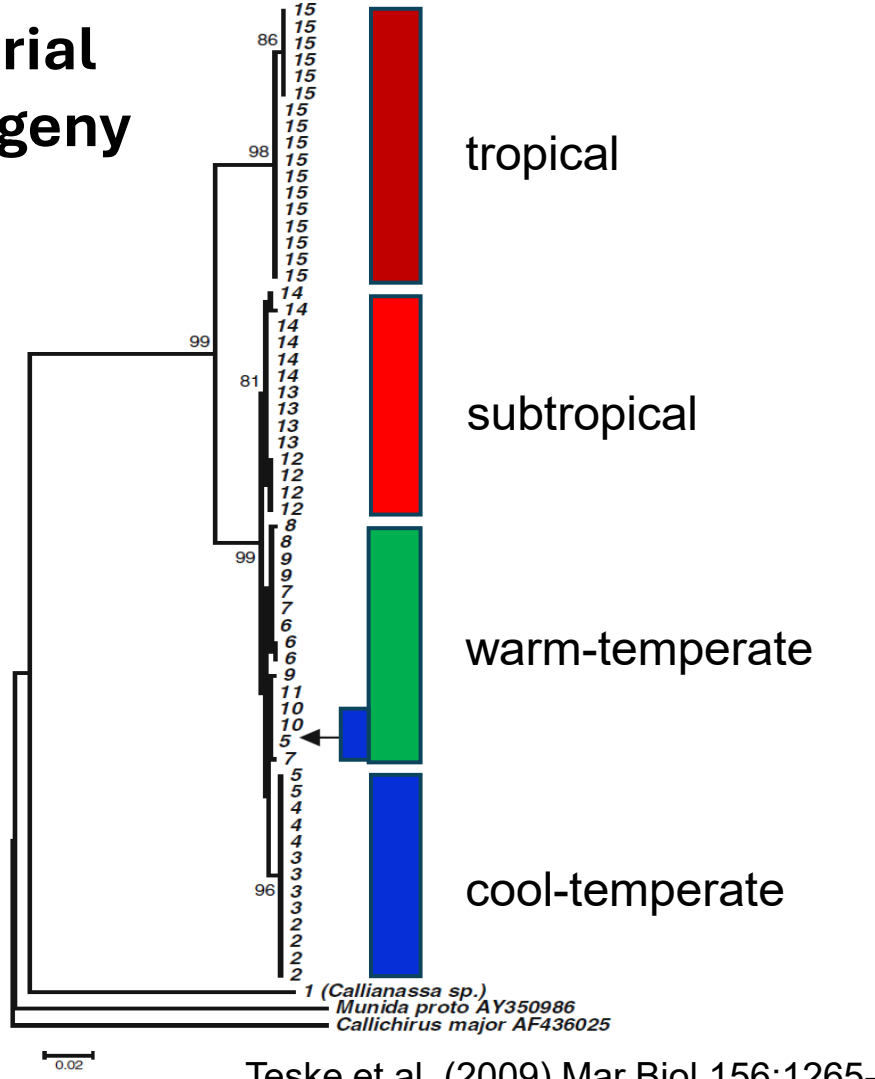
Kraussillichirus kraussi
(sandprawn)

Pillay et al. 2017, Mar Ecol Prog Ser 347: 1–14

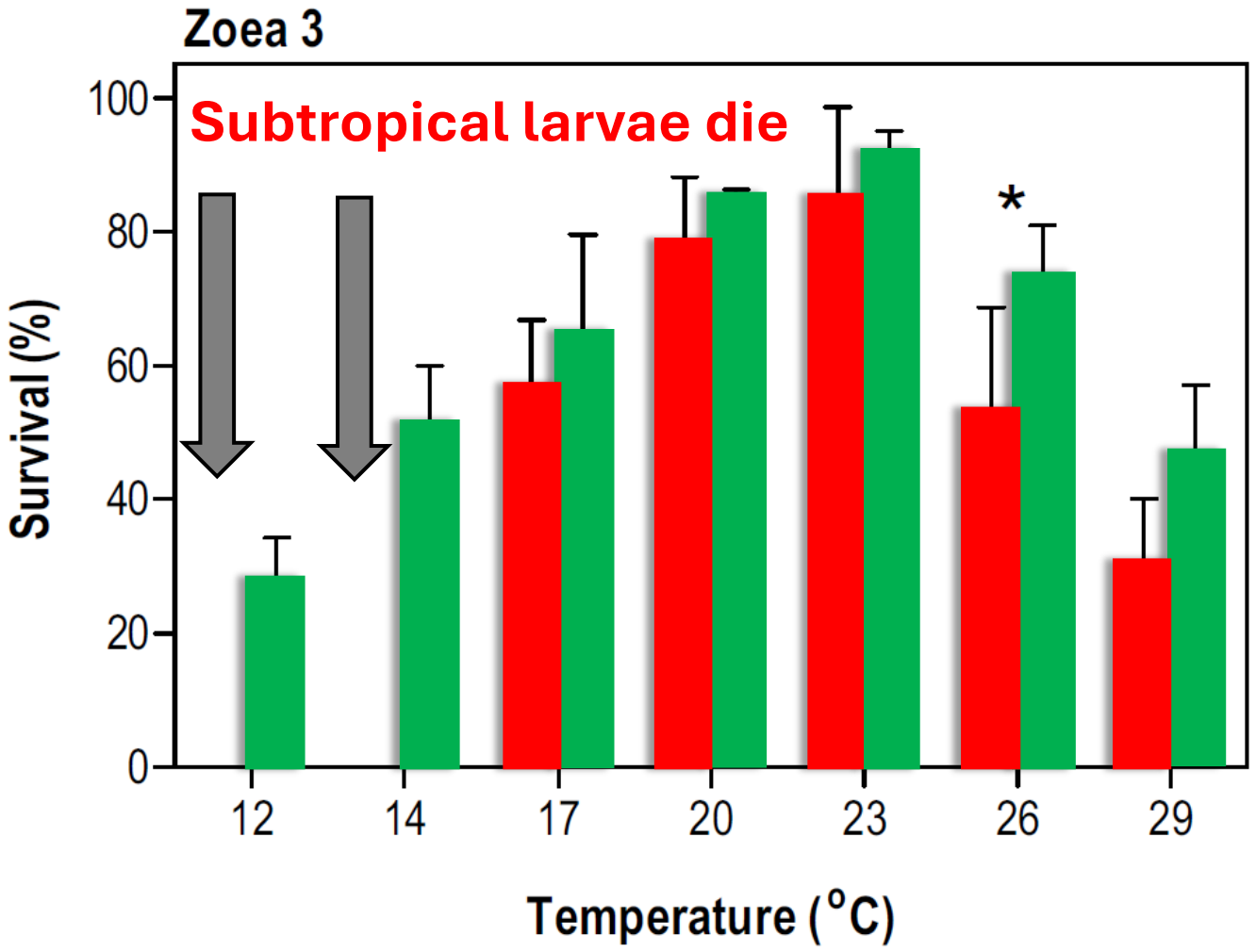
Mitochondrial DNA phylogeny

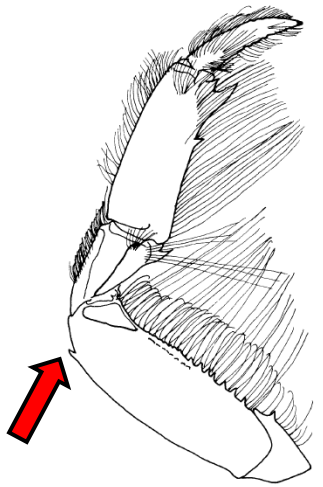


Teske et al. (2009) Mar Biol 156:1265-1275

Regional adaptation to temperature

Larval development in the prawn *Upogebia africana*





Warm-temperate

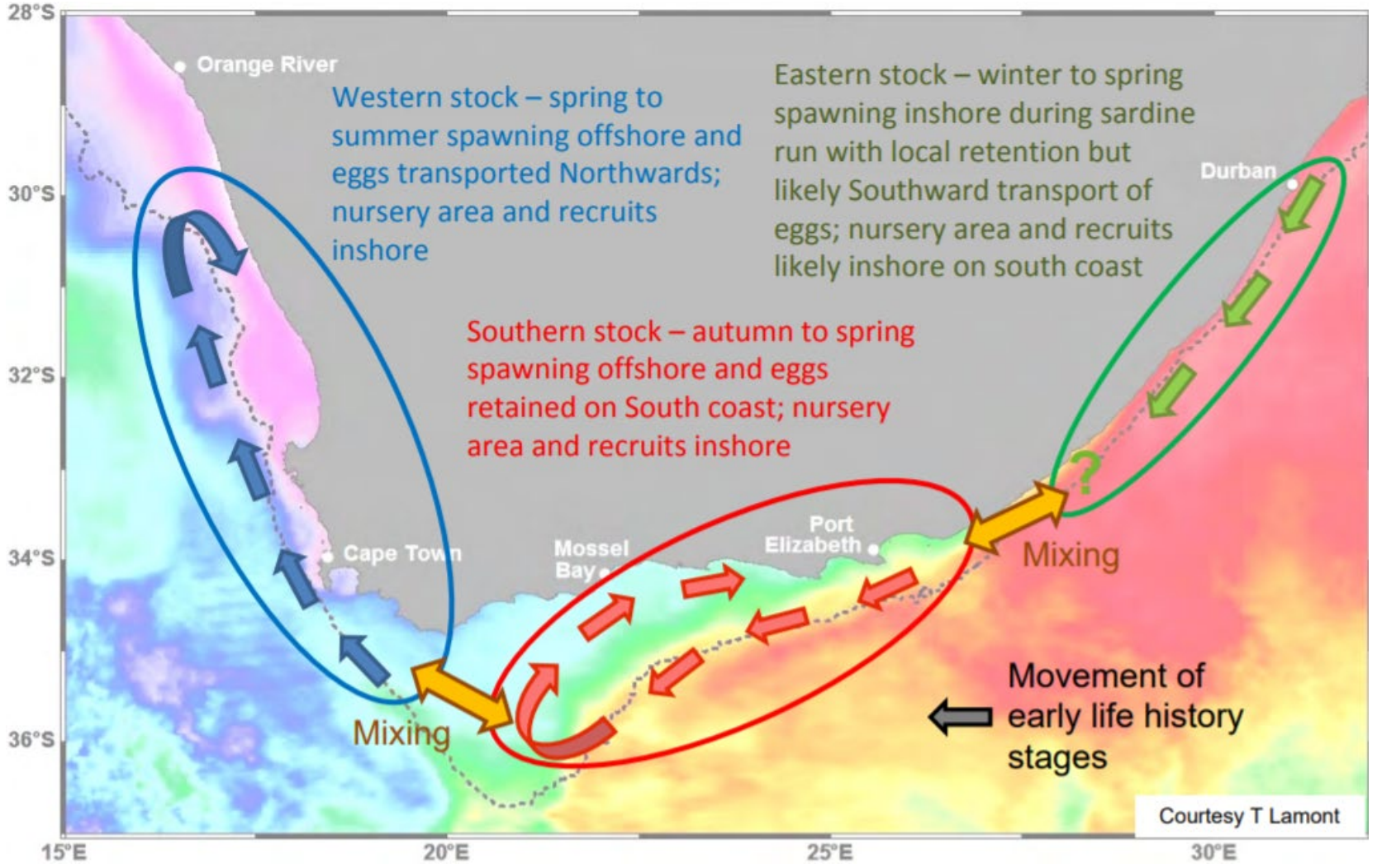
Subtropical

Teske et al. (2008) BMC Evol Biol 8:341

The KwaZulu-Natal Sardine Run

‘The Greatest Shoal on Earth’

Sardine: 3 stock hypothesis



van der Lingen C & Moloney C (unpublished)

Key contributors



South Africans:

Sampling and data interpretation

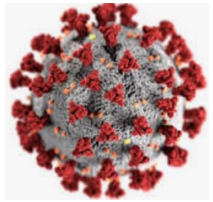


American Aussies and Iranian:

Molecular data generation and analysis

Indian PhD student:

Never published the work, but still graduated somehow




Virus ‘of unknown origin’ and Zero Booze Lockdown:

Motivated me to write the paper, or die of boredom

Genomic vs. exome datasets

Sardine/BG3

ddRADseq (genomics): 8 296 SNPs, 284 individuals, 40 sites

7 742 neutral

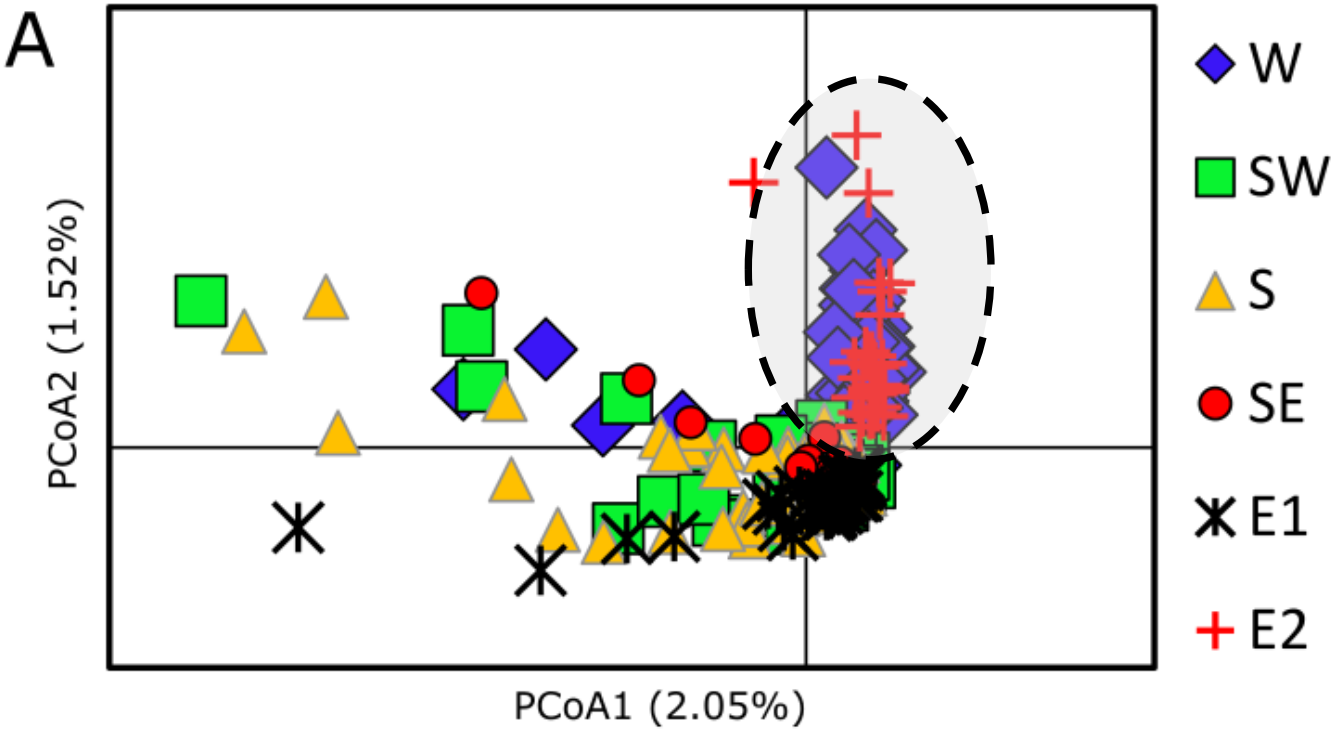
11 outliers

RNAseq (exome): 14 973 SNPs, 20 individuals, 9 sites

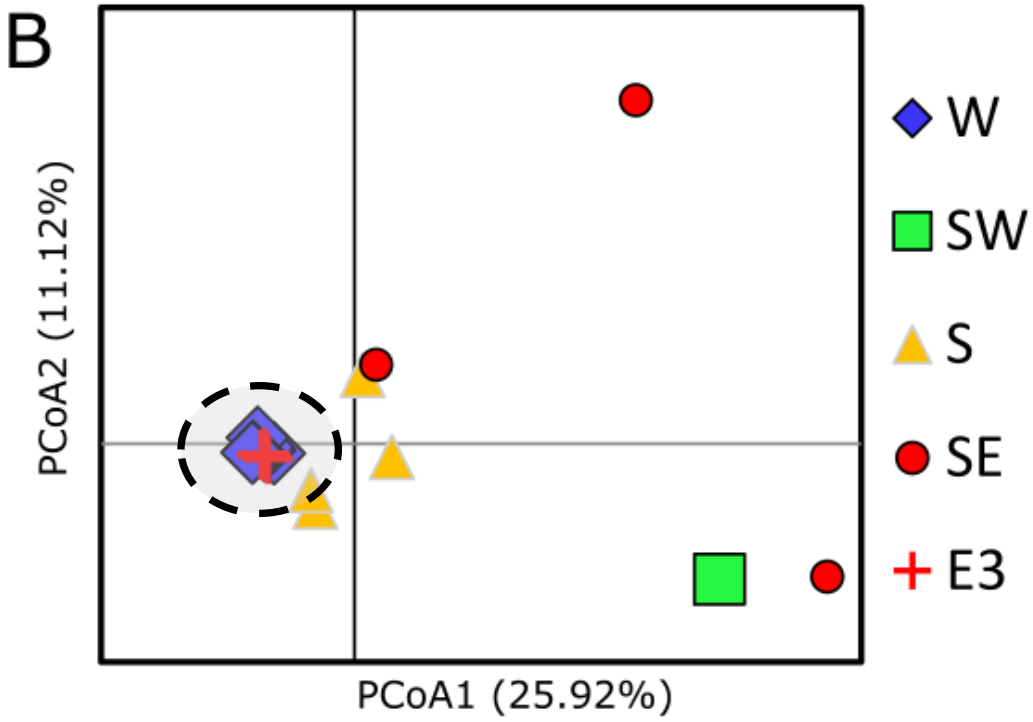
8 191 neutral

198 outliers

Selectively neutral SNPs

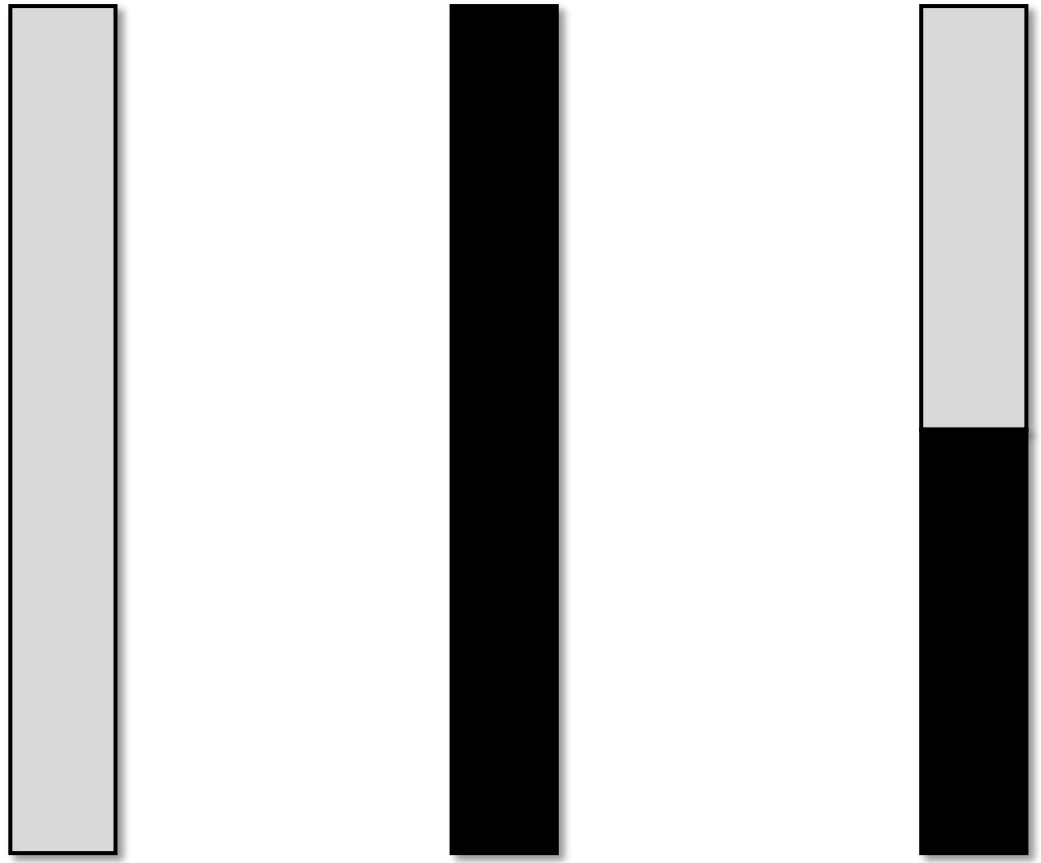


Genomic data



Exome data

Ancestry barplots (for outliers)



Sardine 1
CTS

Sardine 2
WTS

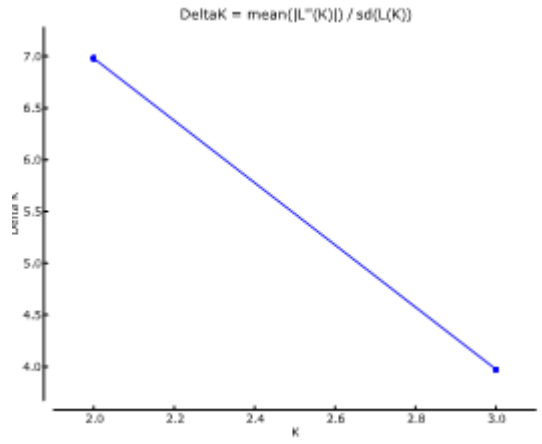
Sardine 3
Mixed ancestry

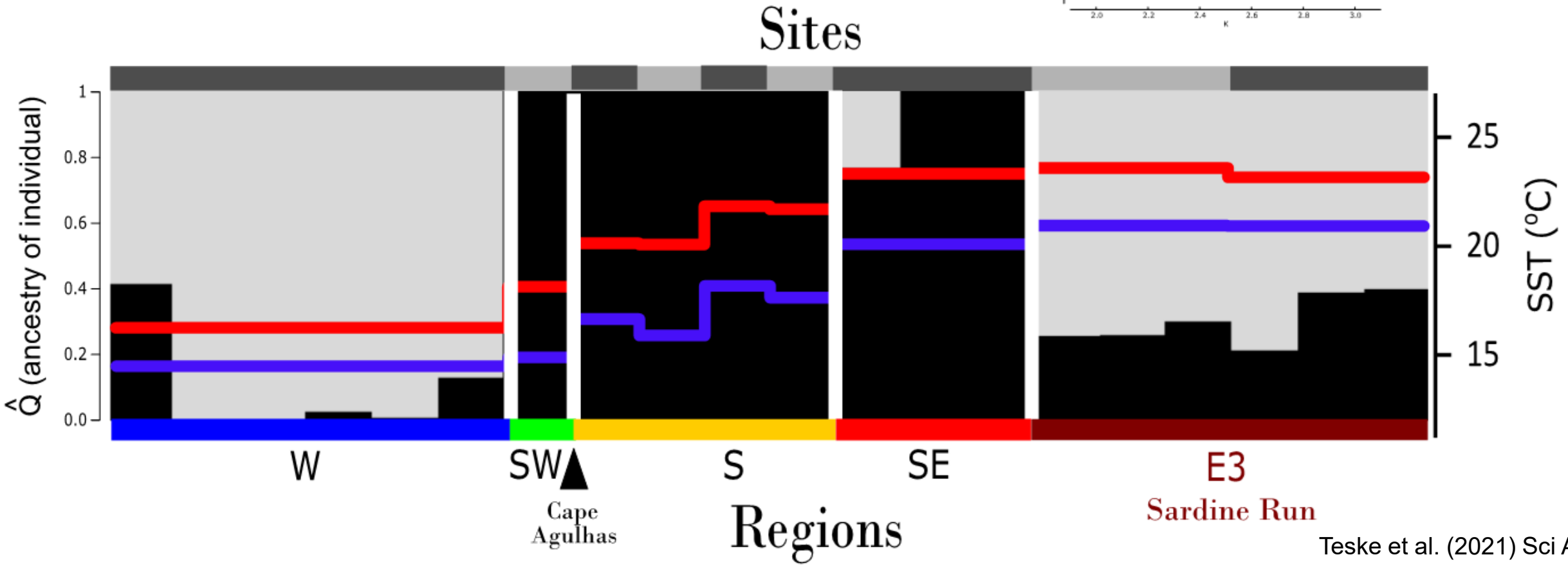
CTS
(Cool-temperate stock)

WTS
(Warm-temperate stock)

Exome outlier data

Assignment of sardines to 2 stocks





Teske et al. (2021) Sci Adv

Genomic outlier data

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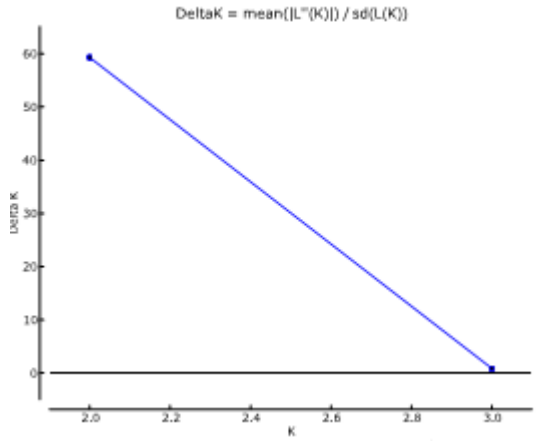
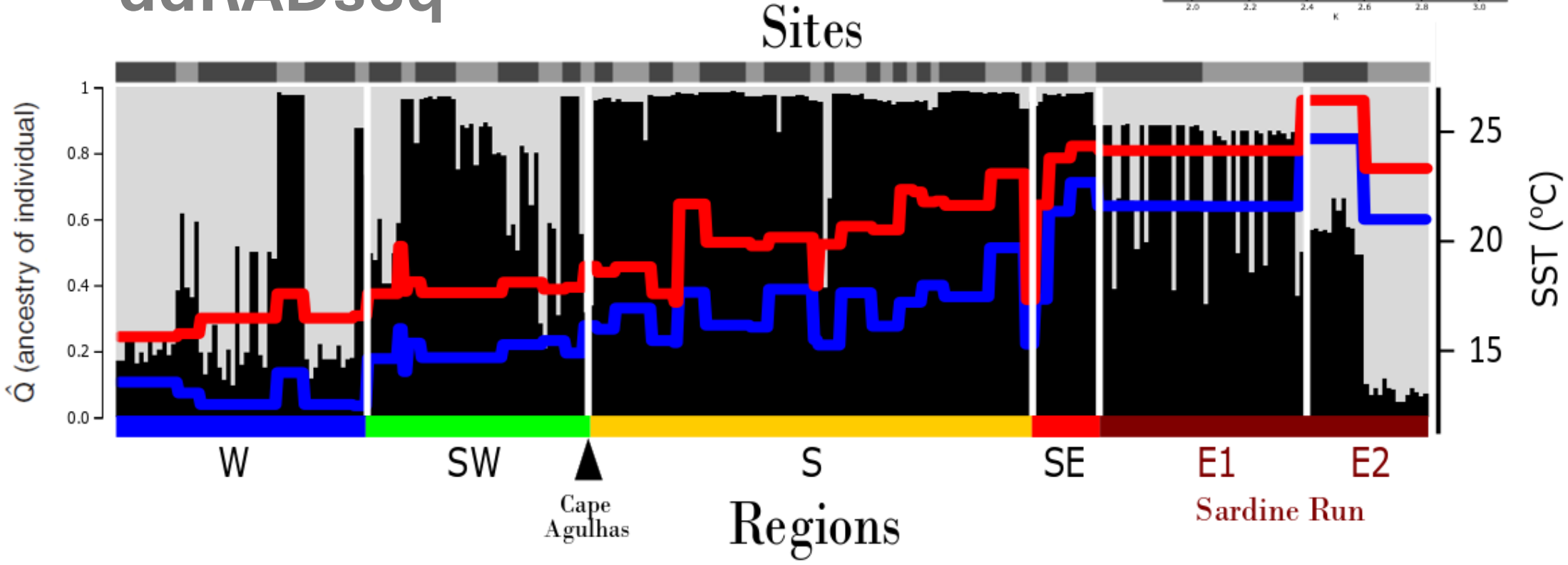


ddRADseq



Teske et al. (2021) Sci Adv

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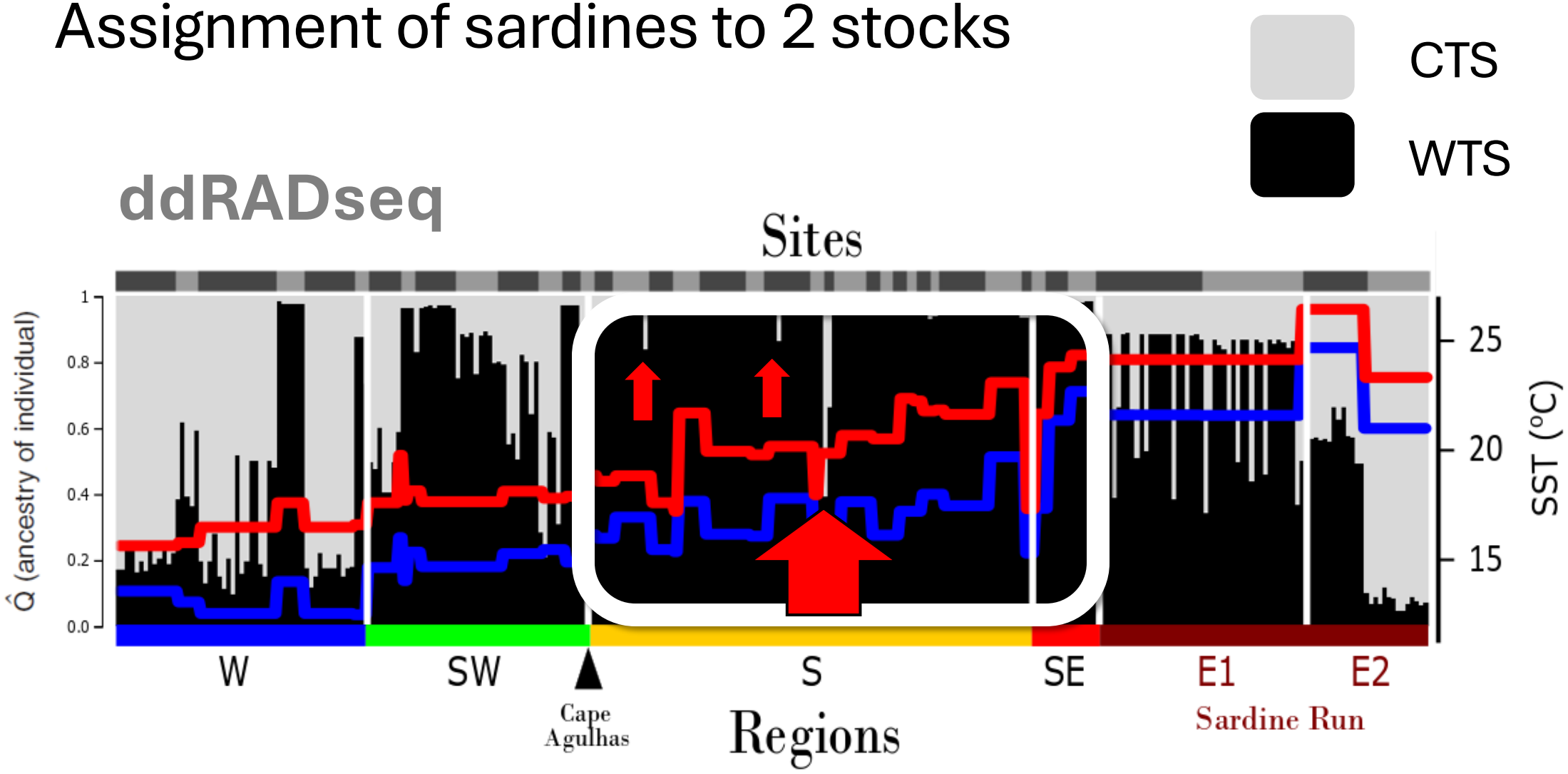

Teske et al. (2021) Sci Adv

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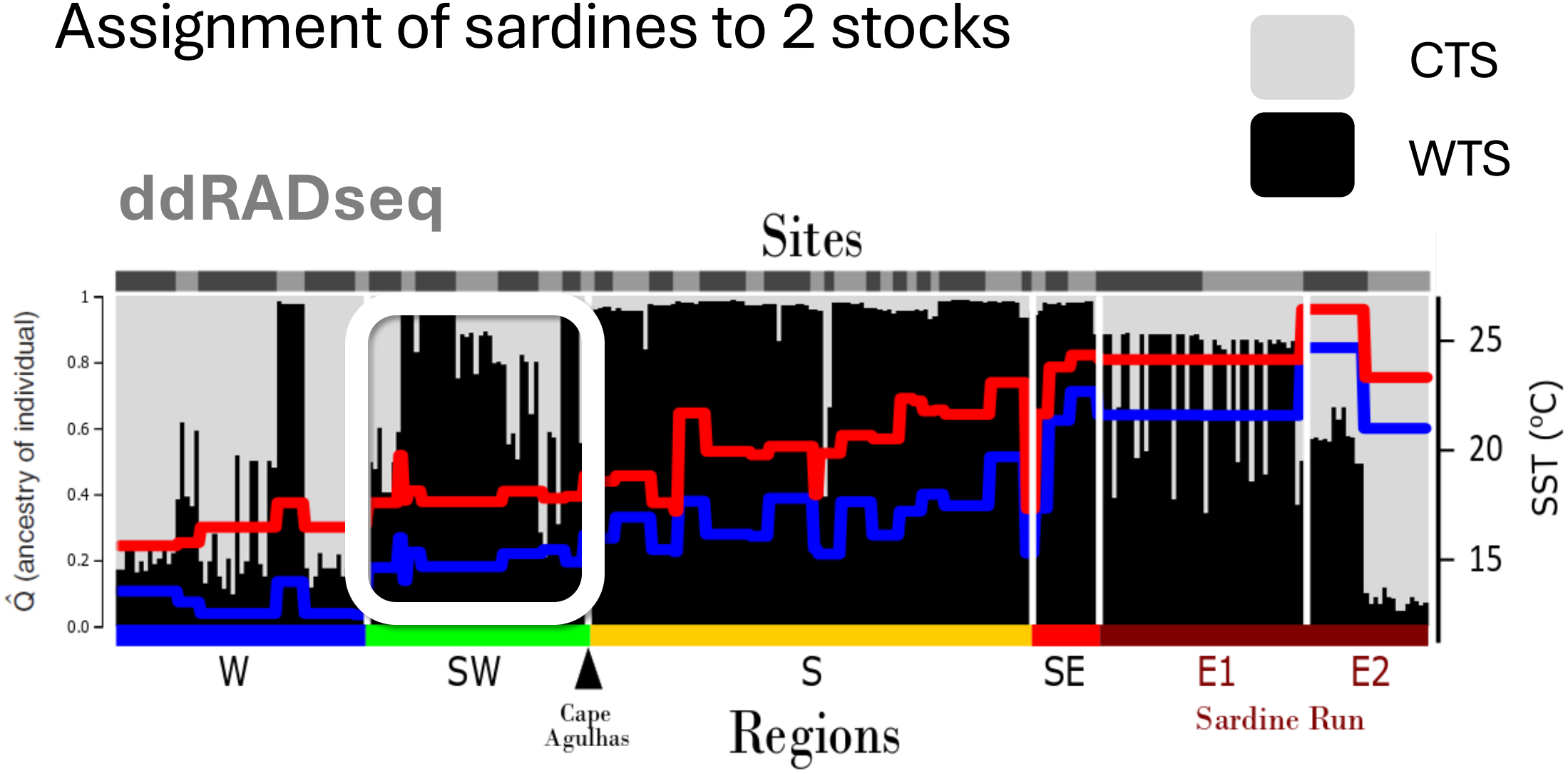

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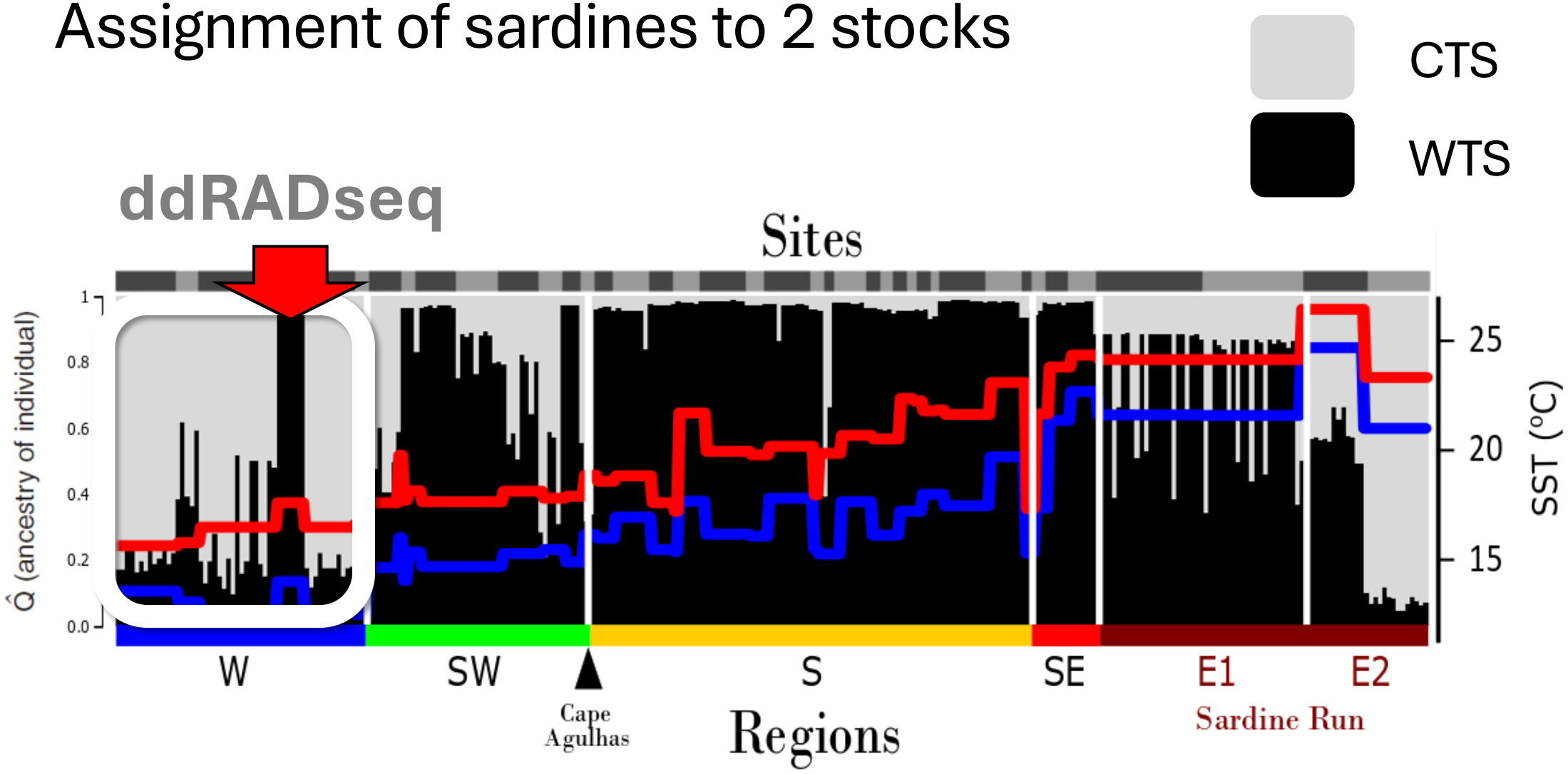

Teske et al. (2021) Sci Adv

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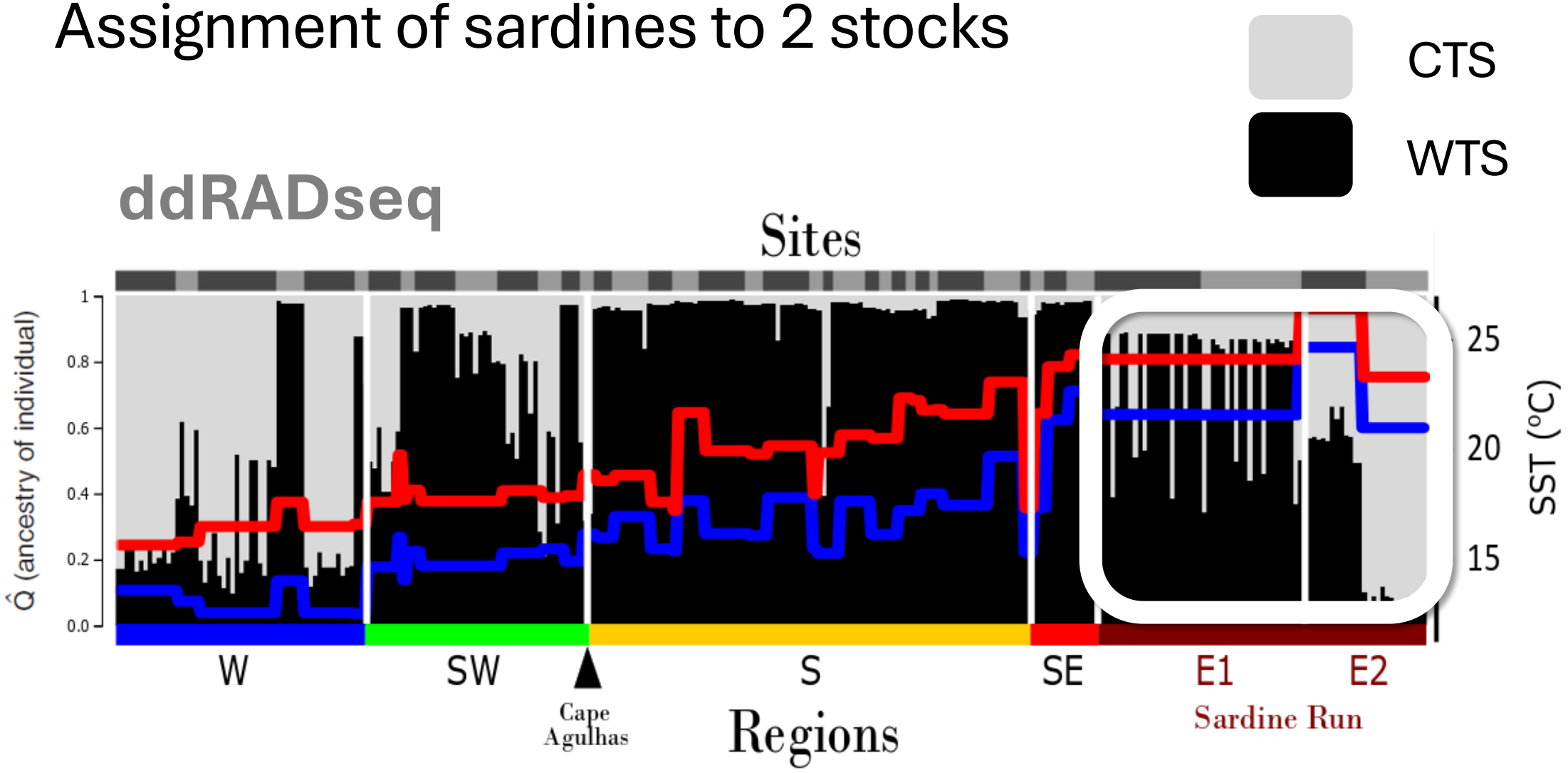

Teske et al. (2021) Sci Adv

2023 panel: key suggestions

P-values vs. magnitude of correlation coefficient

Extract more information from the genomic dataset by using more environmental variables (not only SST)

Explore selection

Finding genetic structure in such a high-dispersal species means there is strong selection (low genetic drift means fewer adaptive loci are stochastically lost)

Exome data vs. Genomic data

Generate more data using the more informative approach