

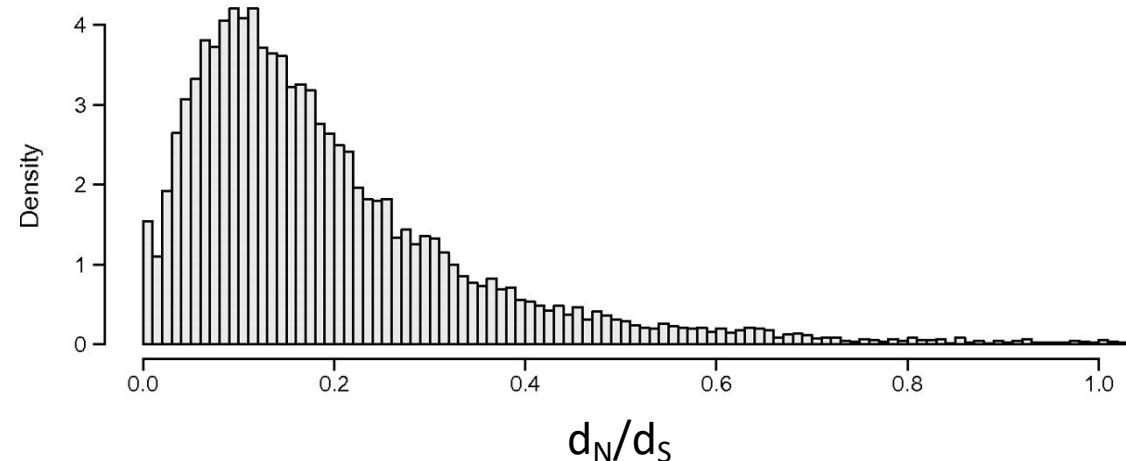
Week 6: detecting selection in genomic data

Detecting selection in genomic data

- Outlier scans
 - Basic fst based
 - More complex:
 - Bayscan, outflank, etc.
- Gene environment associations
- Cline analyses
- Experimental evolution
- Before and after studies
 - Think hurricanes, sea star wasting, etc.

d_N/d_S ratios

- Compare synonymous to non-synonymous changes
- Neutrality
 - The majority of NS mutations are selected against
- Positive selection
- Purifying selection

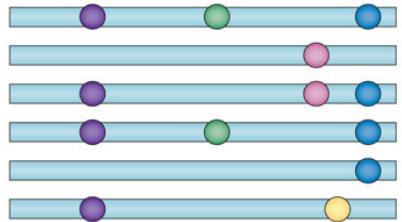


Can't tell you about a single site.
Only works in coding regions

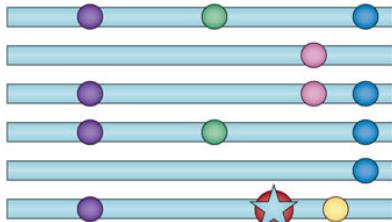
Types of selective sweeps

a Classic selective sweep

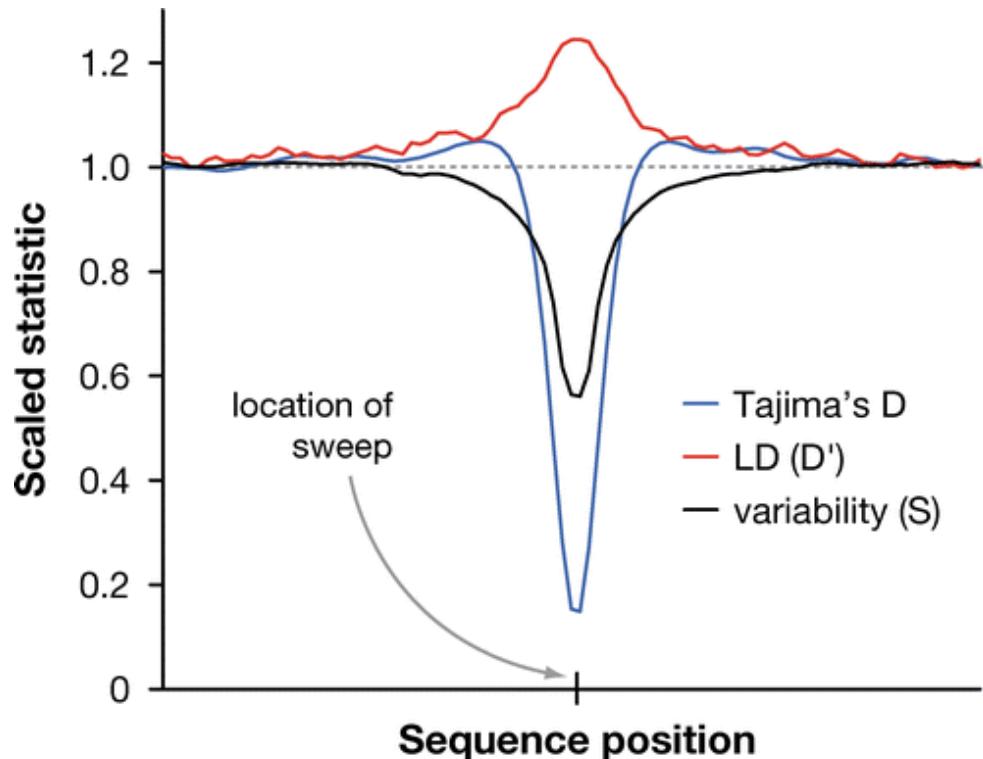
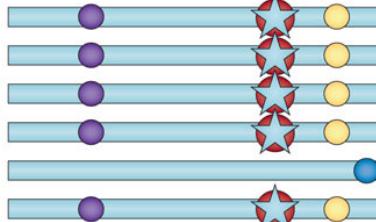
Neutral variation



An advantageous mutation arises

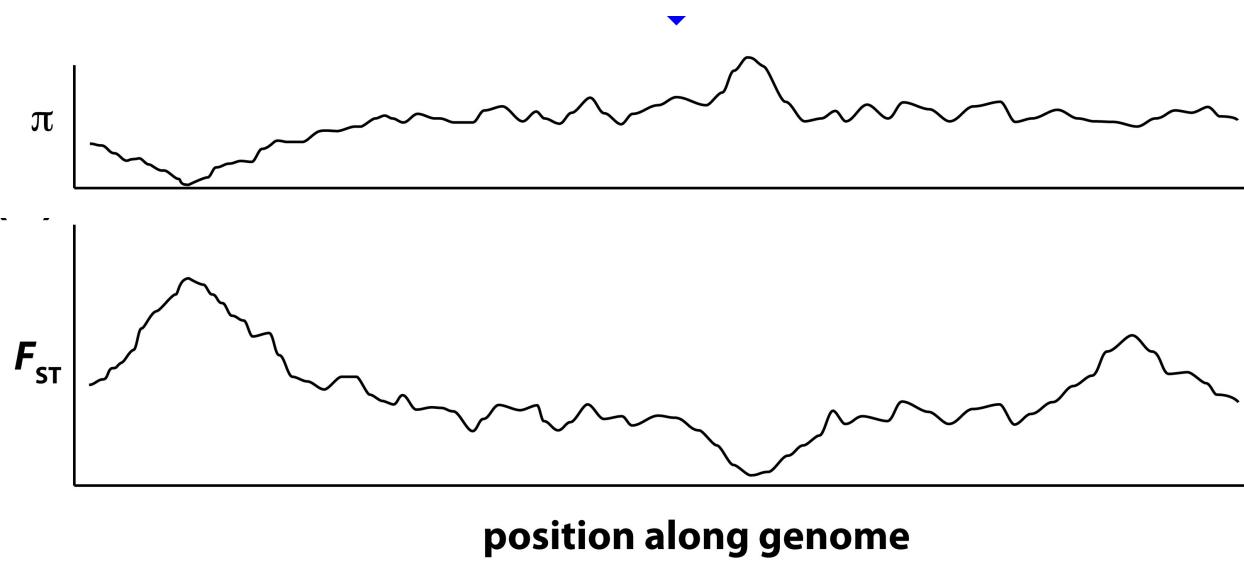


Over time, the advantageous mutation approaches fixation



Elevated: Fst, LD

Decreased: Tajima's D, genetic diversity



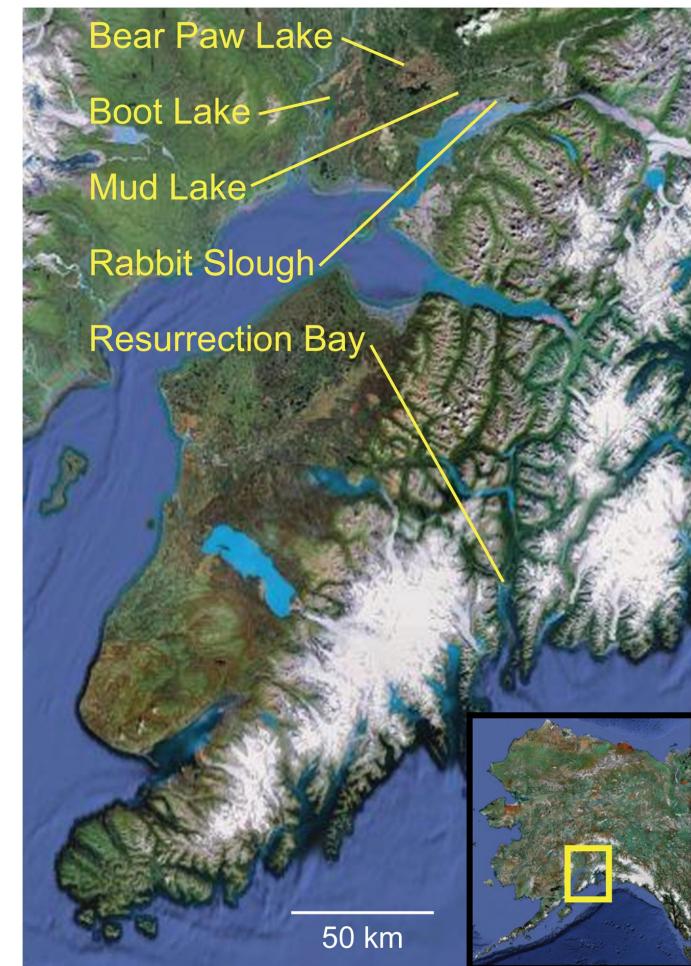
OPEN ACCESS Freely available online

PLOS GENETICS

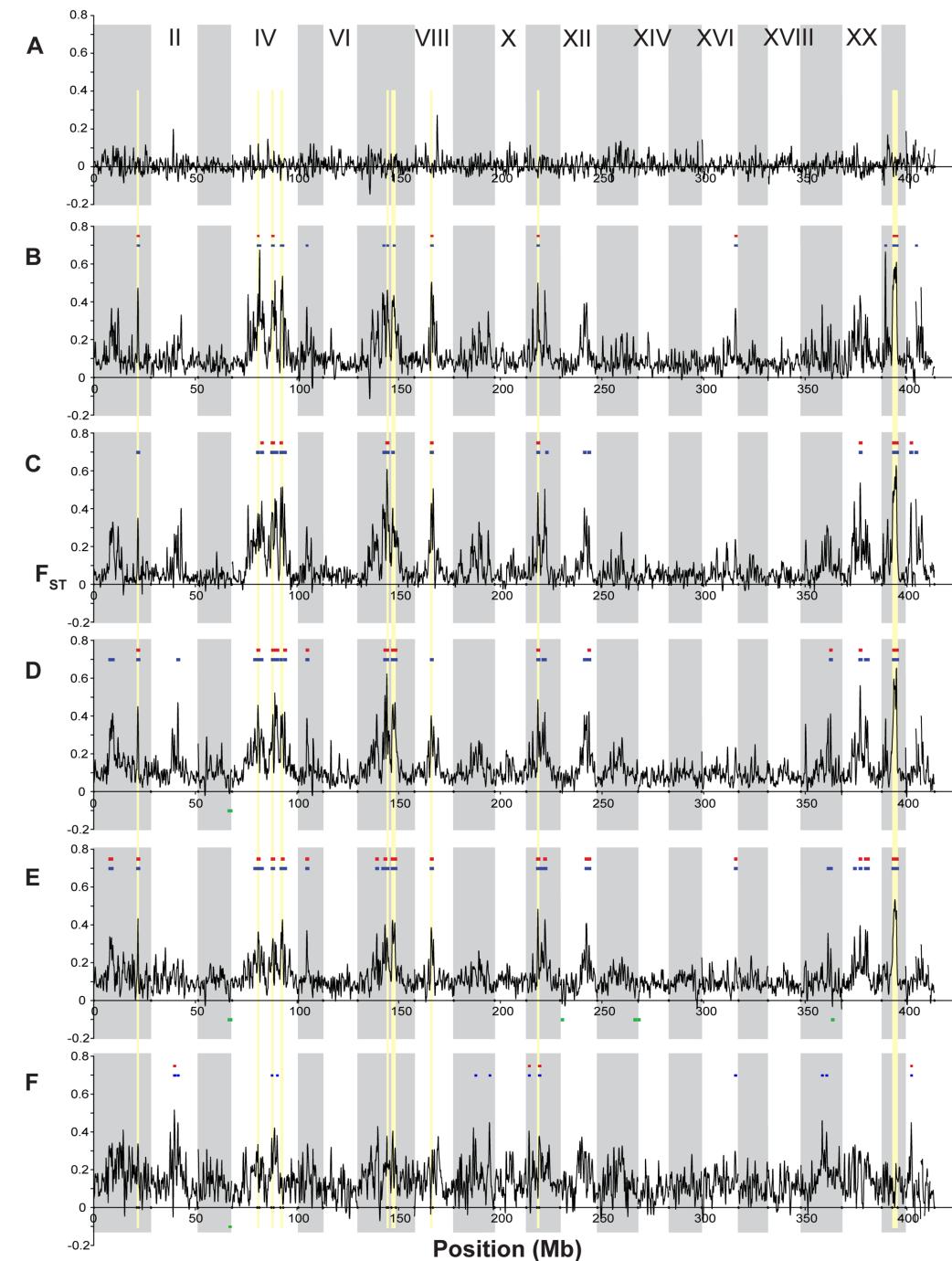
Population Genomics of Parallel Adaptation in Threespine Stickleback using Sequenced RAD Tags

Paul A. Hohenlohe^{1,3}, Susan Bassham^{1,3}, Paul D. Etter², Nicholas Stiffler³, Eric A. Johnson², William A. Cresko^{1*}

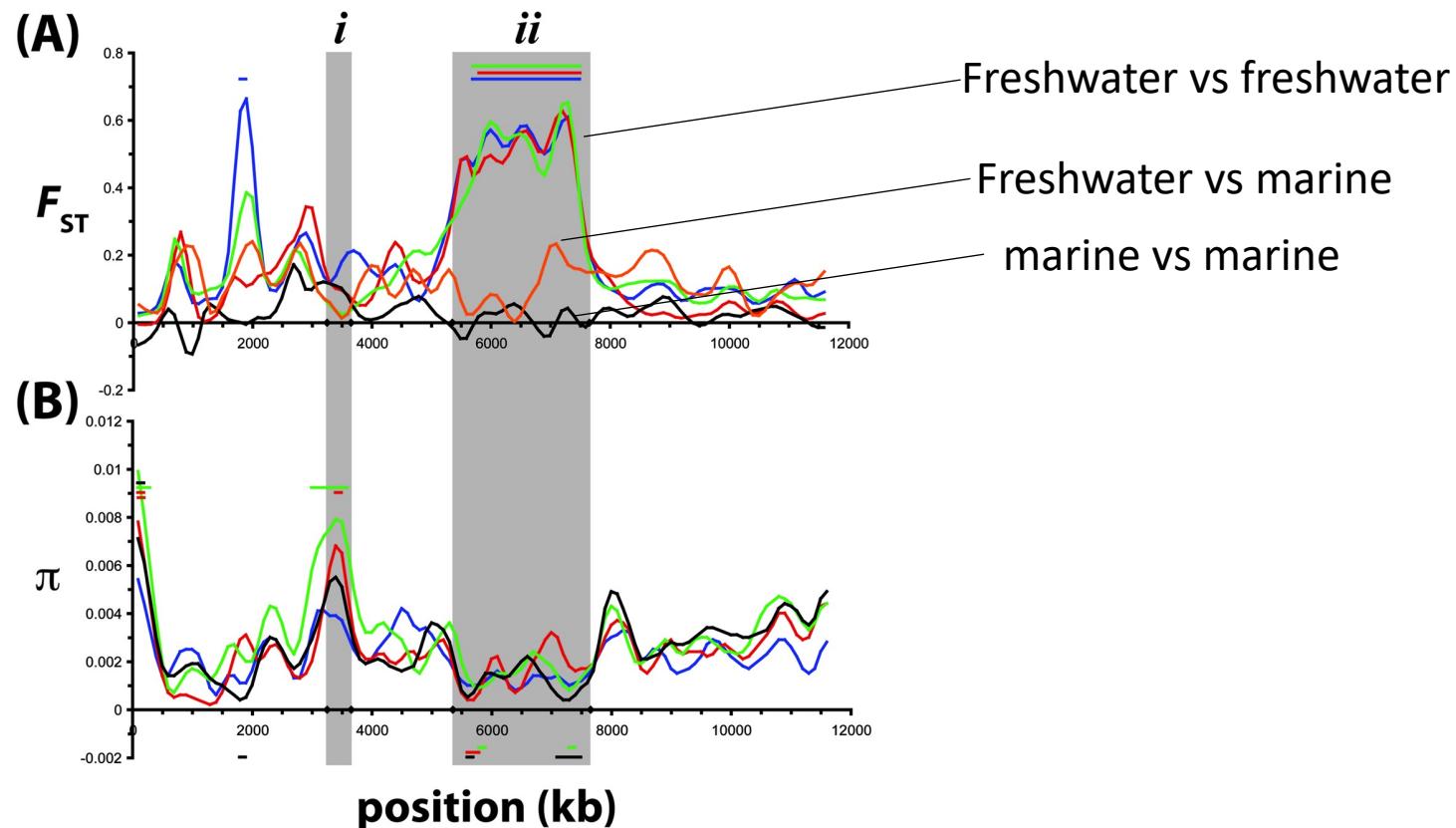
1 Center for Ecology and Evolutionary Biology, University of Oregon, Eugene, Oregon, United States of America, **2** Institute of Molecular Biology, University of Oregon, Eugene, Oregon, United States of America, **3** Genomics Core Facility, University of Oregon, Eugene, Oregon, United States of America



Hohenlohe, Phillip

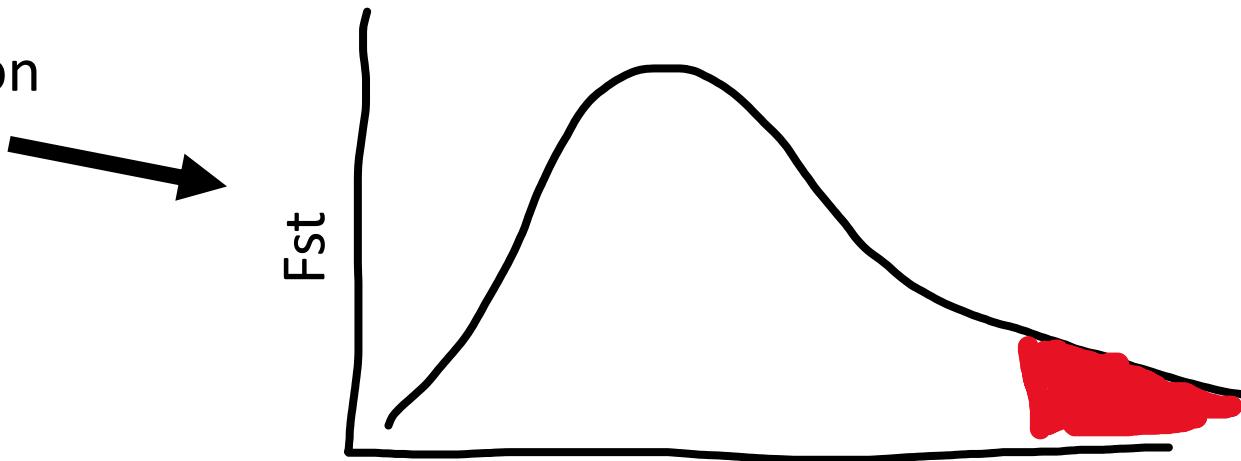
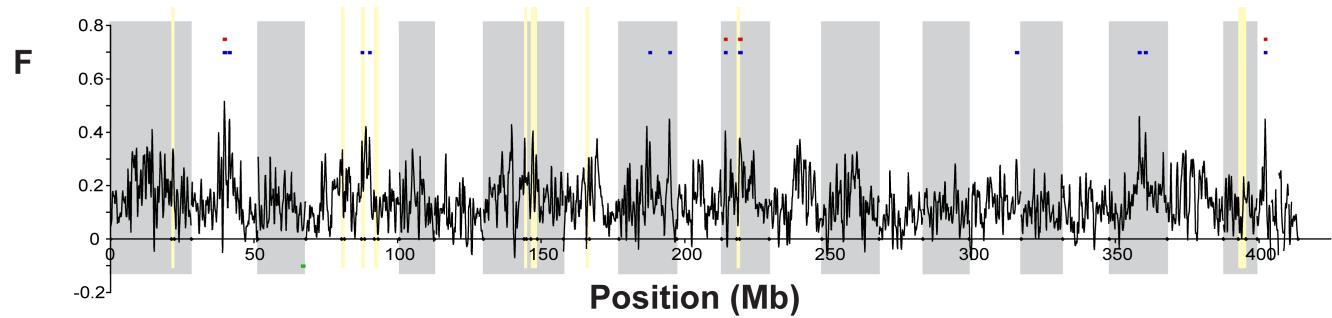


Hohenlohe, Phillips, and Cresko 2010



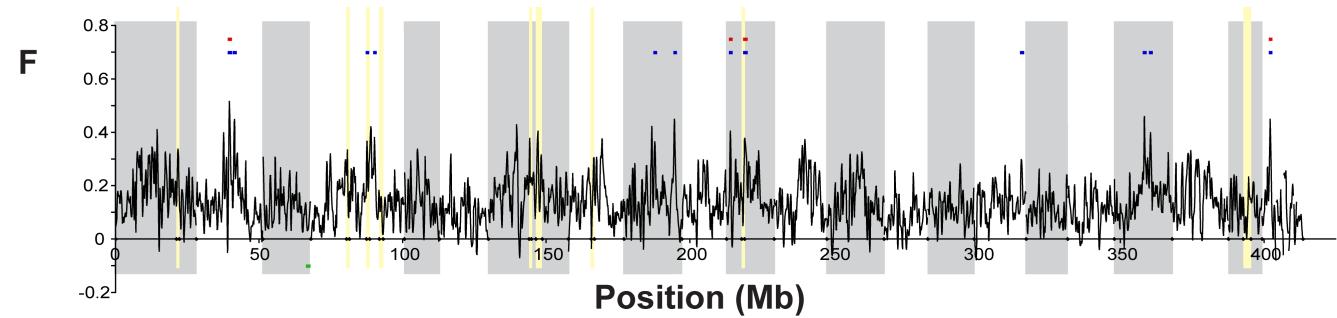
Detecting outlier regions

- What is the null distribution?
 - How to define “outliers”
 - Empirical: Tail of the distribution



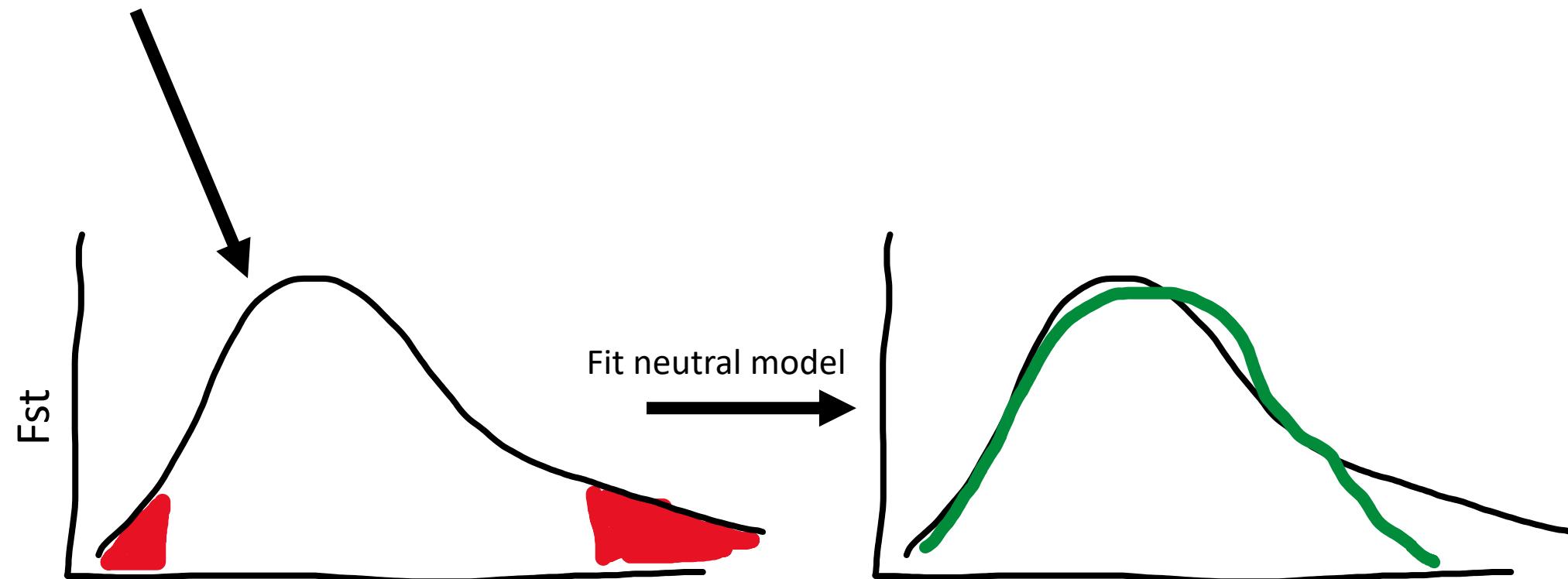
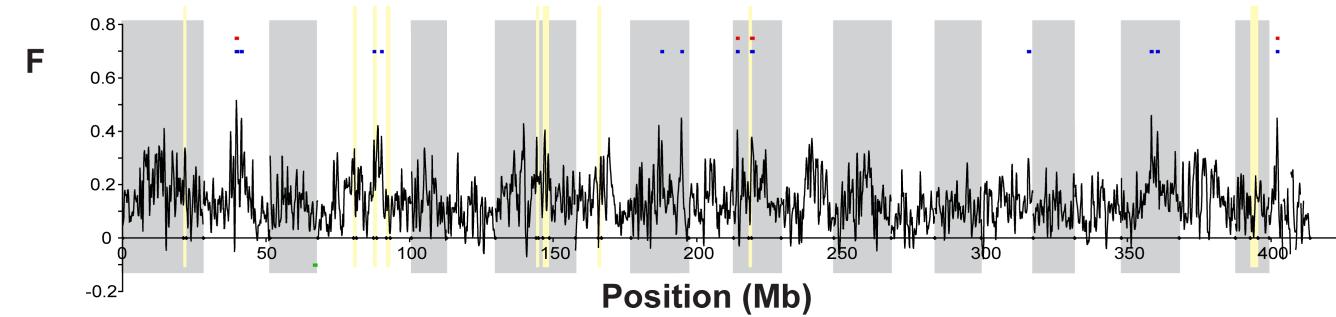
Detecting outlier regions

- What is the null distribution?
 - How to define “outliers”
- Demographic null
 - Bayescan
 - island model in which subpopulation allele frequencies are correlated through a common migrant gene pool from which they differ in varying degrees.
 - Which loci violate neutrality?



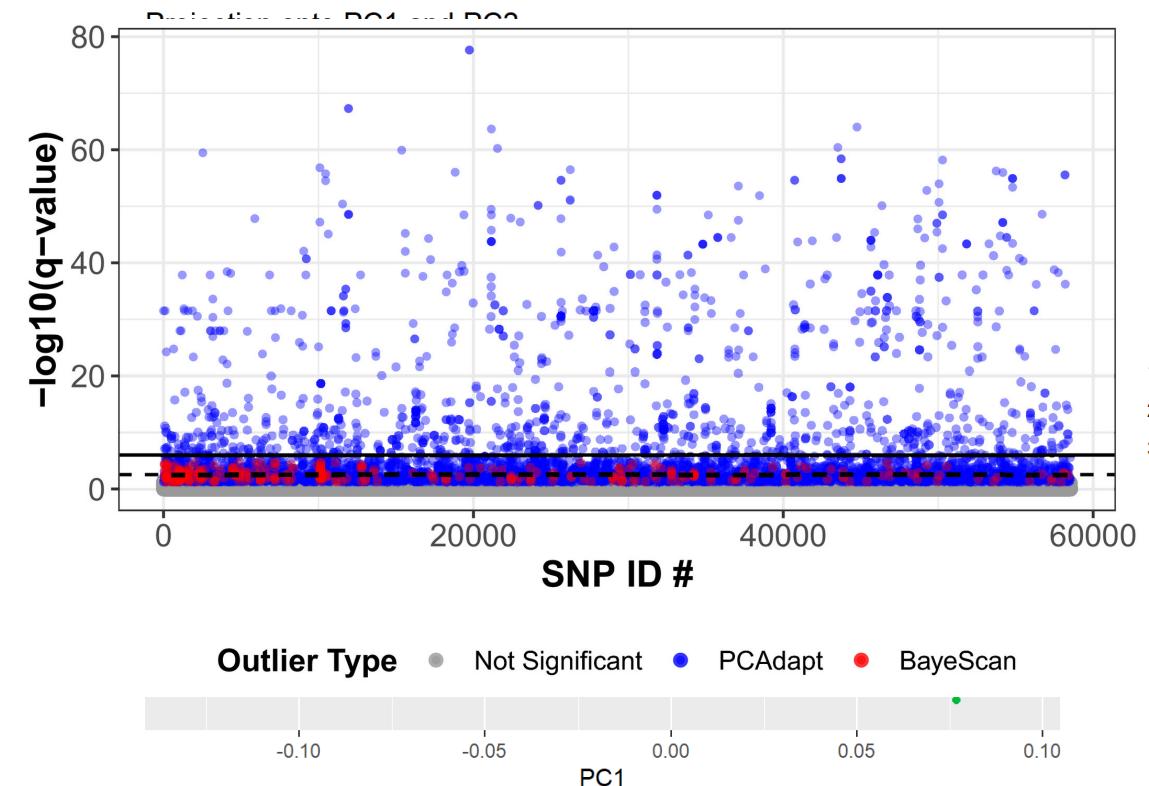
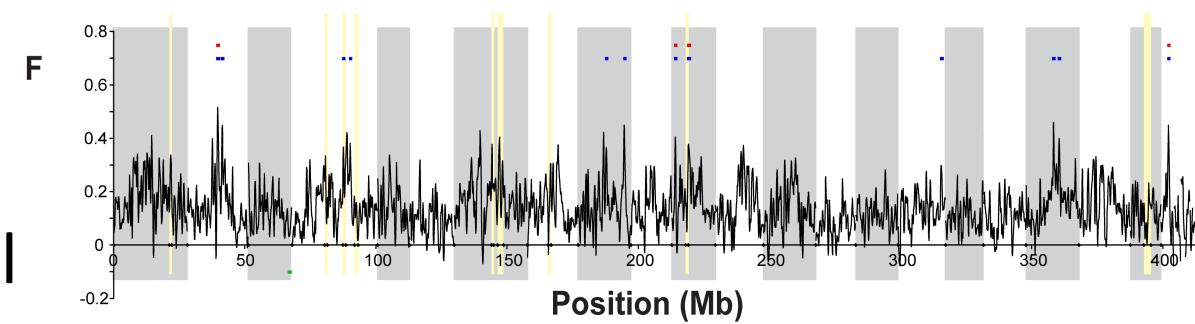
Detecting outlier regions

- What is the null distribution?
 - How to define “outliers”
 - Empirical: Tail of the distribution
 - OutFLANK

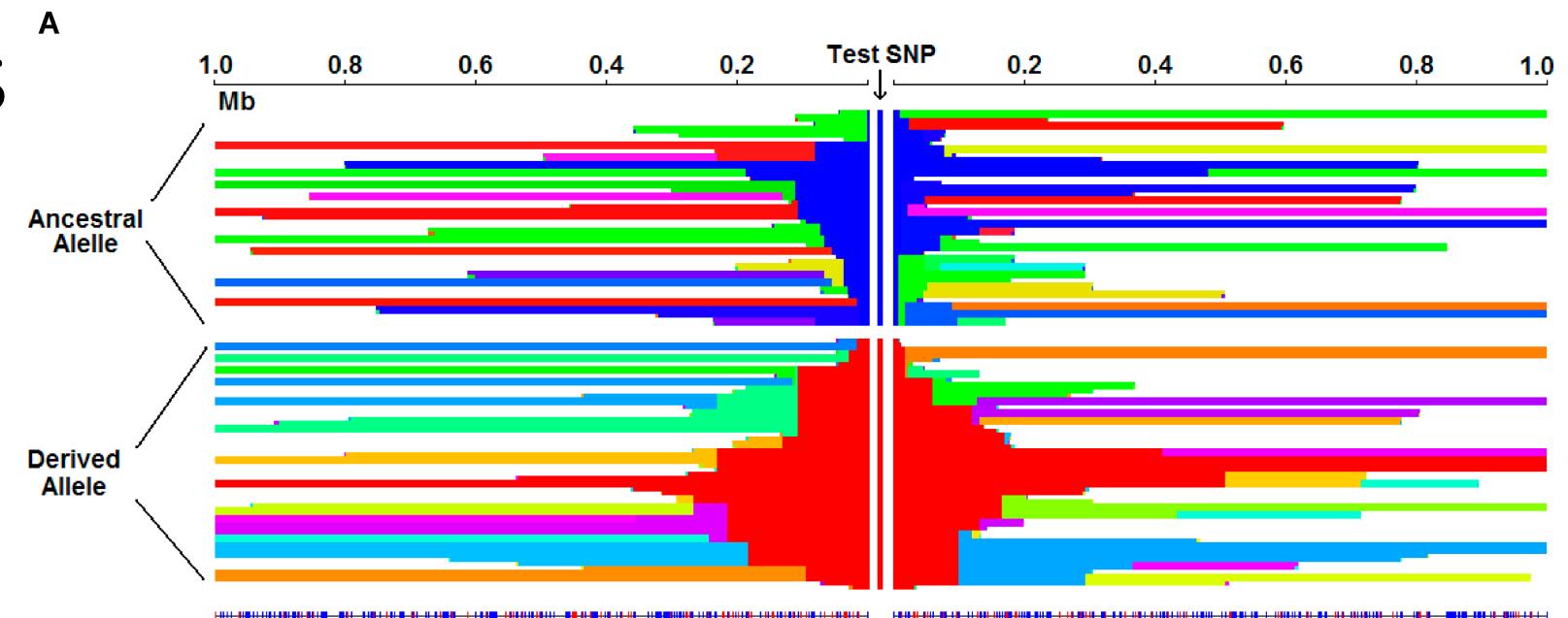


Detecting outlier regions

- Estimate covariance/structure among all populations, look for outliers after correction
- Baypass, bayenv2
- PCAdapt
 - PCA based
 - Don't need population assignments
 - markers excessively related to population structure are candidates for local adaptation

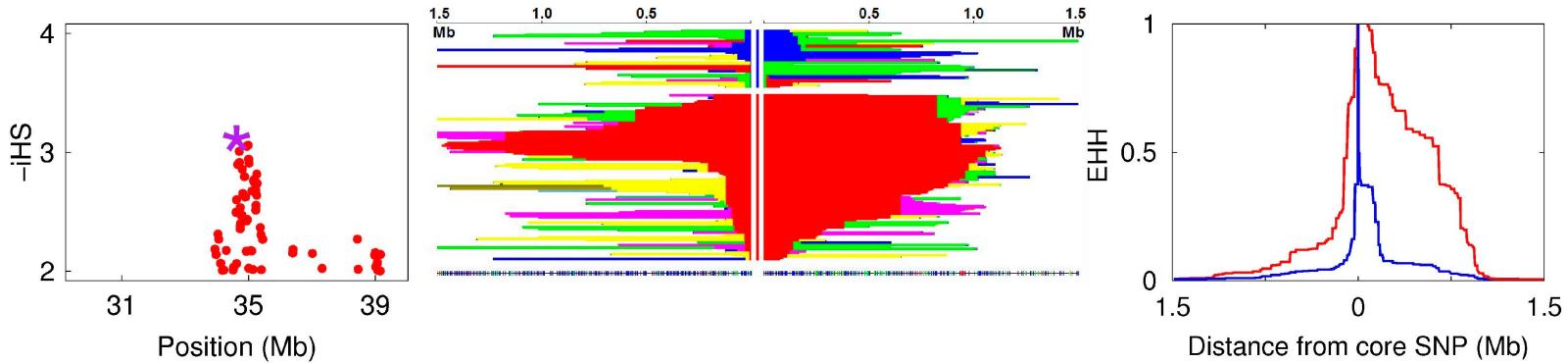


LD based methods

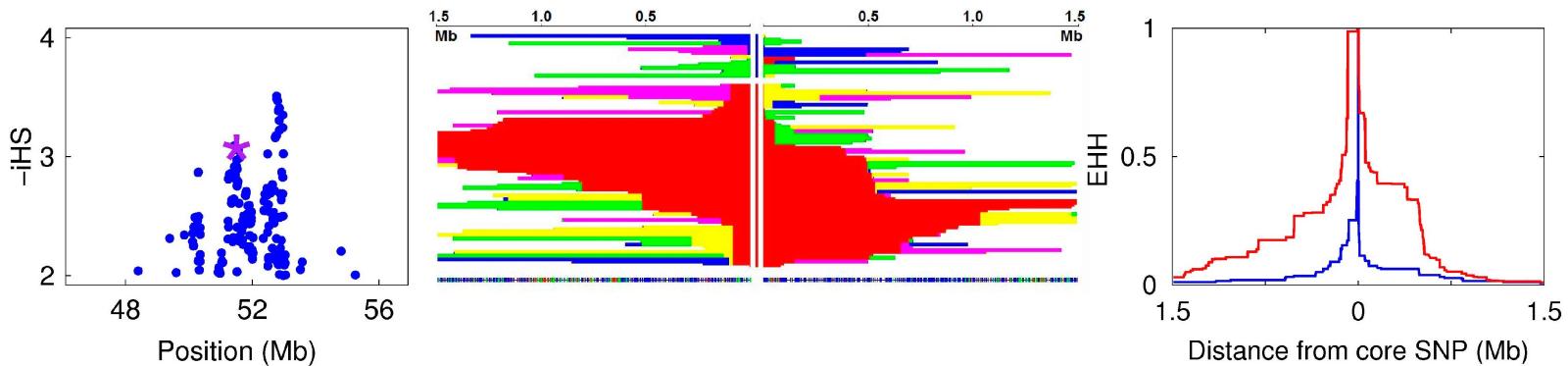


- Extended haplotype homozygosity: EHH
- integrated haplotype score (iHS)
 - A measure of EHH
 - Voight et al., 2006

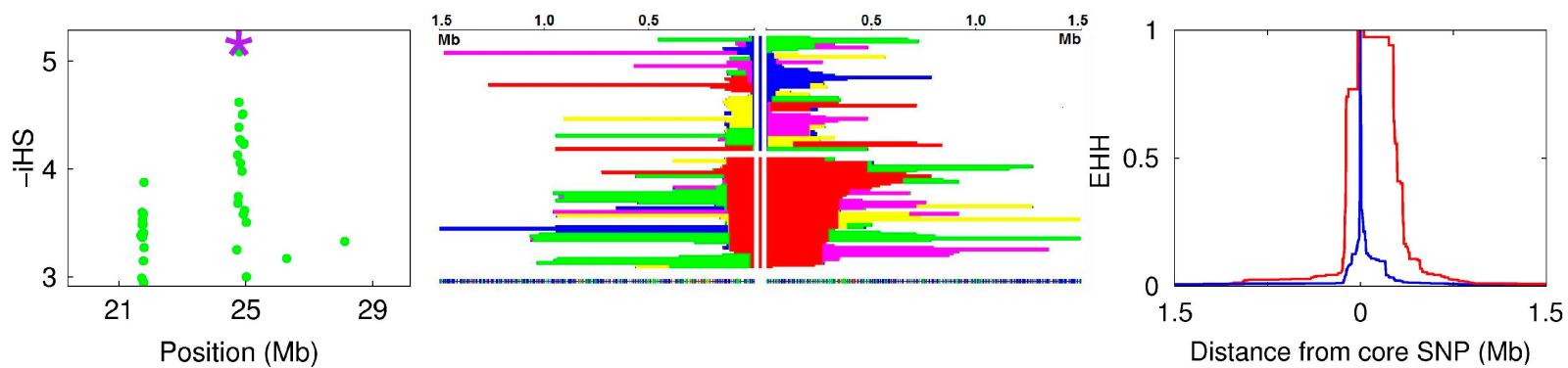
(a) East Asians, rs6060371 (in SPAG4), $p_d = 0.742$, 2.3 cM/Mb



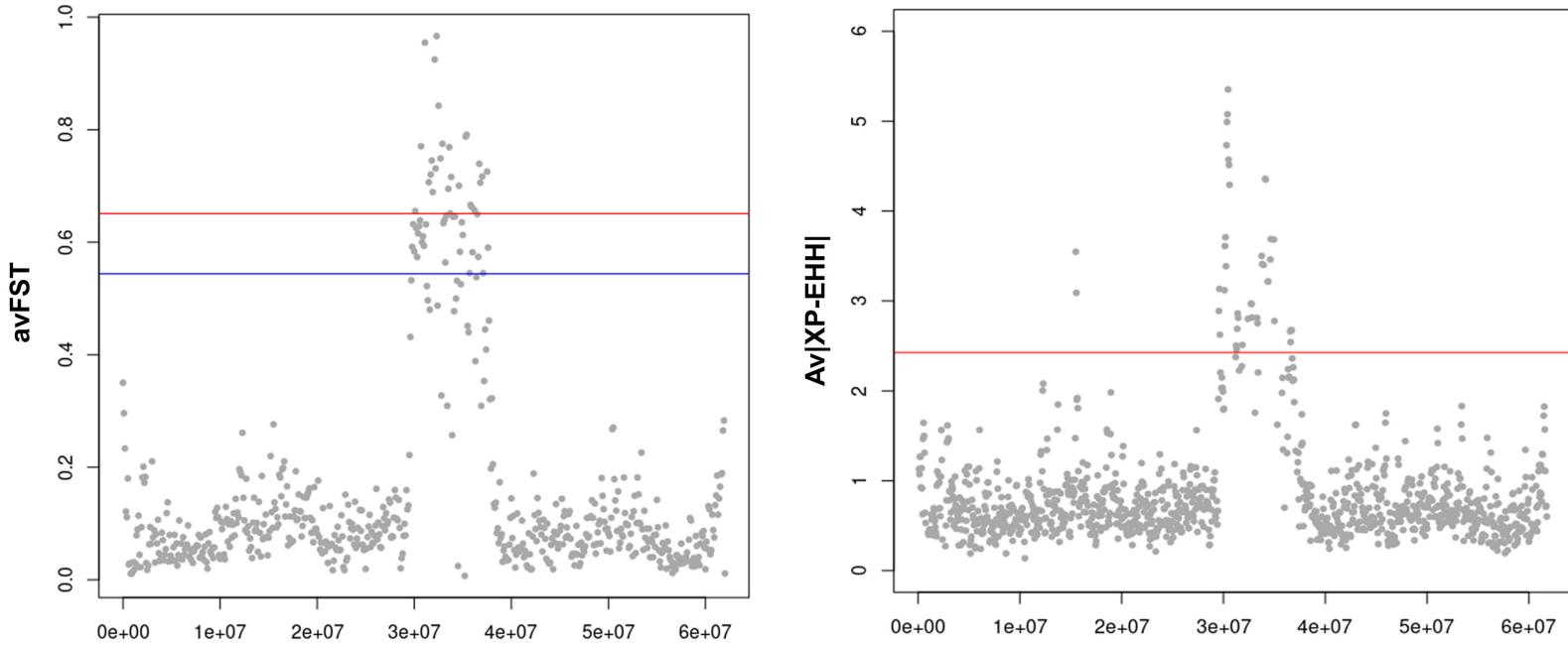
(b) CEPH, rs996521 (in SNTG1), $p_d = 0.808$, 0.28 cM/Mb



(c) Yoruba, rs995647 (in NCOA1), $p_d = 0.492$, 0.62 cM/Mb



Chr 6



Comparative genomics and signatures of selection in North Atlantic eels

Jose Martin Pujolar ^a, Magnus Wulff Jacobsen ^b, Francesca Bertolini ^{c,*}

^a Centre for Gelatinous Plankton Ecology and Evolution, National Institute of Aquatic Resources, Technical University of Denmark, Kongens Lyngby, Denmark

^b Section for Marine Living Resources, National Institute of Aquatic Resources, Technical University of Denmark, Silkeborg, Denmark

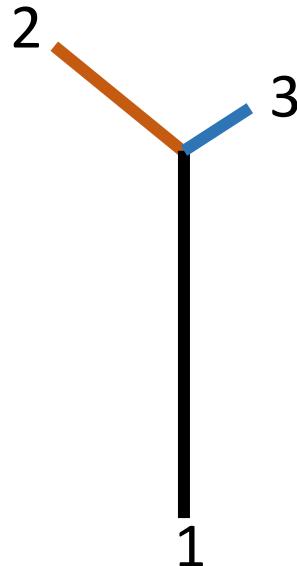
^c Section for Marine Living Resources, National Institute of Aquatic Resources, Technical University of Denmark, Kongens Lyngby, Denmark



Population branch statistics

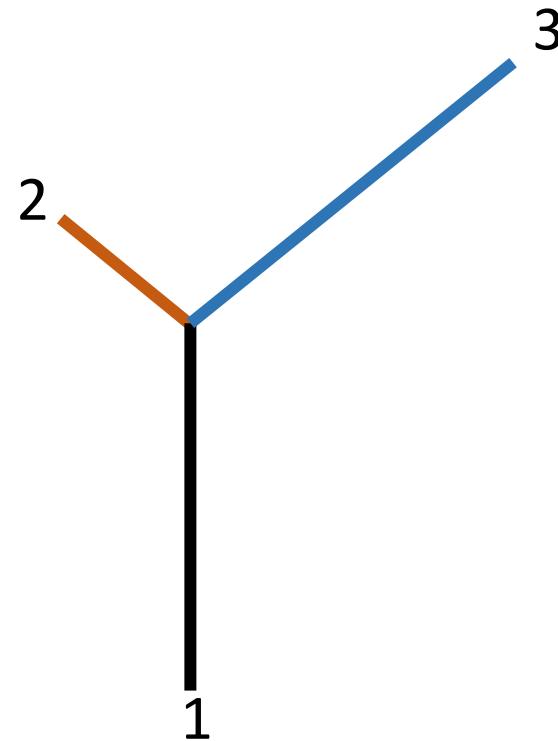
Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude

Xin Yi,^{1,2*} Yu Liang,^{1,2*} Emilia Huerta-Sanchez,^{3*} Xin Jin,^{1,4*} Zha Xi Ping Cuo,^{2,5*} John E. Pool,^{3,6*} Xun Xu,¹ Hui Jiang,¹ Nicolas Vinckenbosch,³ Thorfinn Sand Korneliussen,⁷ Hancheng Zheng,^{1,4} Tao Liu,¹ Weiming He,^{1,8} Kui Li,^{2,5} Ruibang Luo,^{4,4} Xifang Nie,¹ Honglong Wu,^{1,9} Meiru Zhao,¹ Hongzhi Cao,^{1,9} Jing Zou,¹ Ying Shan,^{1,4} Shuzheng Li,¹ Qi Yang,¹ Asan,^{1,2} Peixiang Ni,¹ Geng Tian,^{1,2} Junming Xu,¹ Xiao Liu,¹ Tao Jiang,^{1,9} Renhua Wu,¹ Guangyu Zhou,¹ Meifang Tang,¹ Junjie Qin,¹ Tong Wang,¹ Shuijian Feng,¹ Guohong Li,¹ Huasang,¹ Jiangbai Luosang,¹ Wei Wang,¹ Fang Chen,¹ Yading Wang,¹ Xiaoguang Zheng,^{1,2} Zhuo Li,¹ Zhuoma Bianba,¹⁰ Ge Yang,¹⁰ Xinping Wang,¹¹ Shuhui Tang,¹¹ Guoyi Gao,¹² Yong Chen,⁵ Zhen Luo,⁵ Lamu Gusang,⁵ Zheng Cao,¹ Qinghui Zhang,¹ Weihan Ouyang,¹ Xiaoli Ren,¹ Huiqing Liang,¹ Huisong Zheng,¹ Yebo Huang,¹ Jingxiang Li,^{1,7} Lars Bolund,¹ Karsten Kristiansen,^{1,7} Yingrui Li,¹ Yong Zhang,¹ Xiuqing Zhang,¹ Ruiqiang Li,^{1,7} Songgang Li,¹ Huanming Yang,¹ Rasmus Nielsen,^{1,3,7†} Jun Wang,^{1,7†} Jian Wang^{1†}

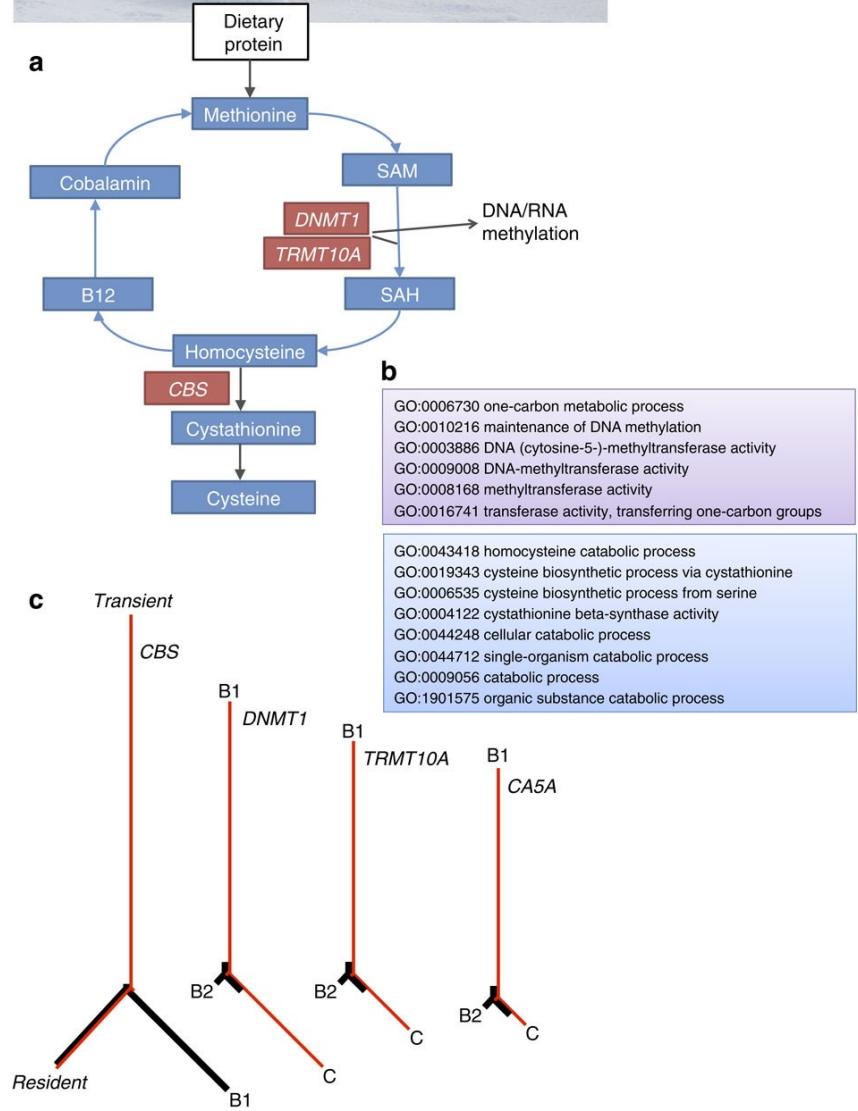


Genome-wide pattern

Longer branch = more divergent

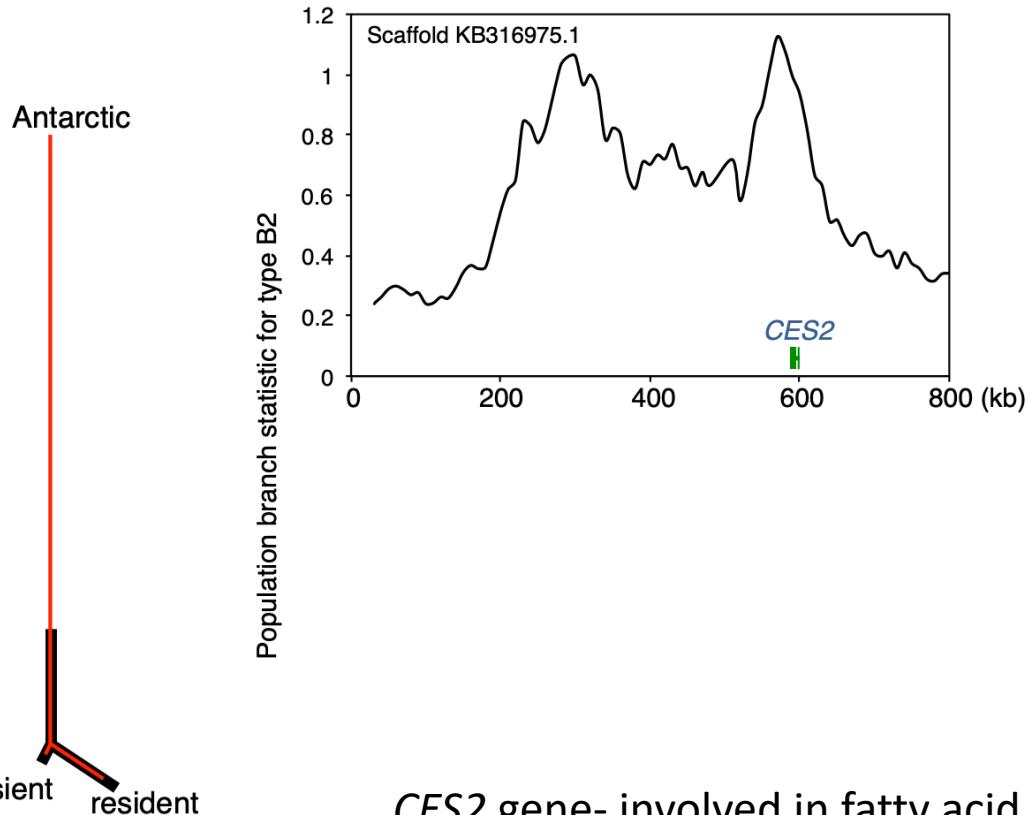


Where are there outlier branches?



Genome-culture coevolution promotes rapid divergence of killer whale ecotypes

Andrew D. Foote , Nagarjun Vijay, María C. Ávila-Arcos, Robin W. Baird, John W. Durban, Matteo Fumagalli, Richard A. Gibbs, M. Bradley Hanson, Thorfinn S. Korneliussen, Michael D. Martin, Kelly M. Robertson, Vitor C. Sousa, Filipe G. Vieira, Tomáš Vinař, Paul Wade, Kim C. Worley, Laurent Excoffier, Phillip A. Morin, M. Thomas P. Gilbert & Jochen B.W. Wolf

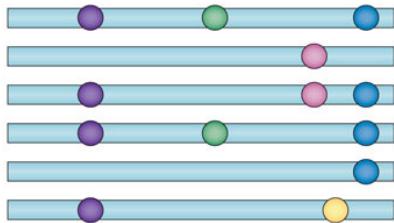


CES2 gene - involved in fatty acid metabolism

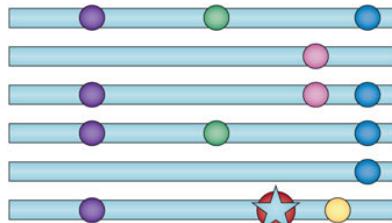
Types of selective sweeps

a Classic selective sweep

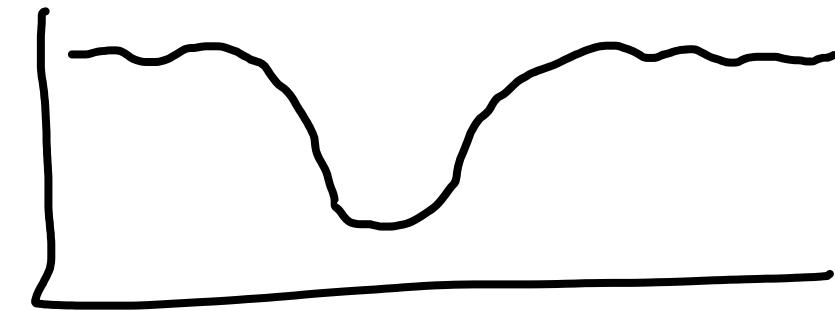
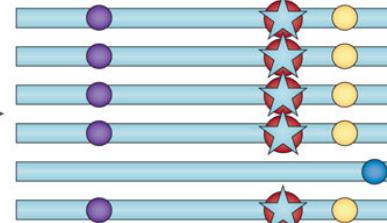
Neutral variation



An advantageous mutation arises



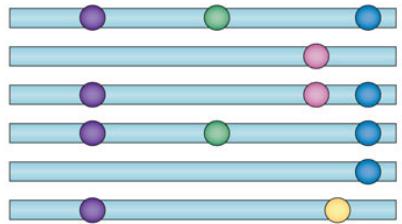
Over time, the advantageous mutation approaches fixation



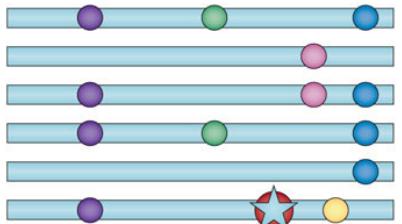
Types of selective sweeps

a Classic selective sweep

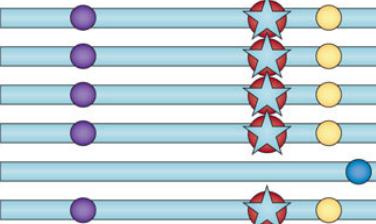
Neutral variation



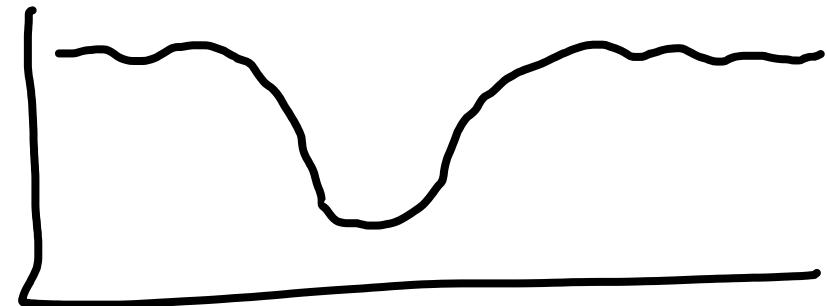
An advantageous mutation arises



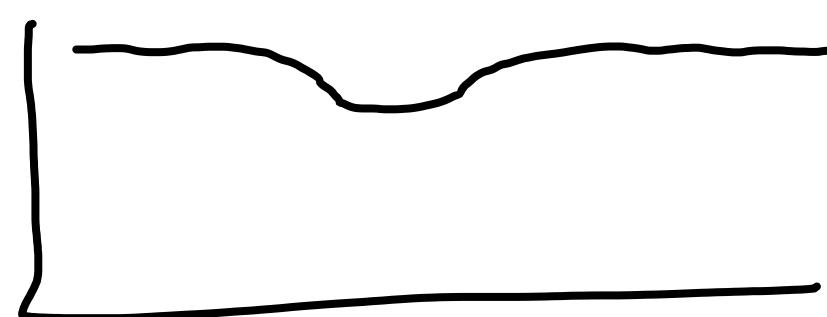
Over time, the advantageous mutation approaches fixation



Haplotype diversity



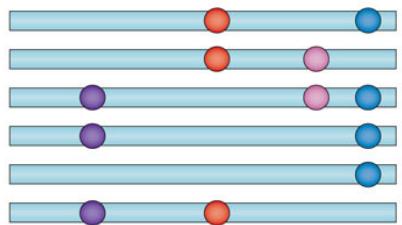
Haplotype diversity



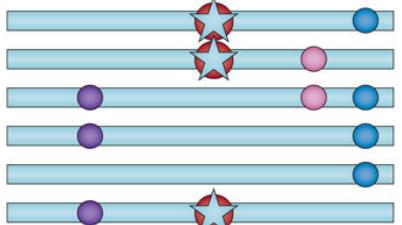
Haplotype diversity

b Selection from standing variation

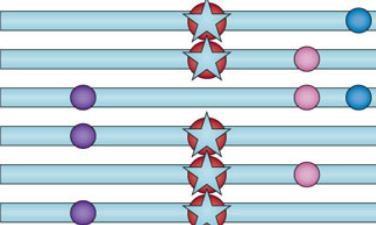
Neutral variation



A variant becomes adaptive in a new environment

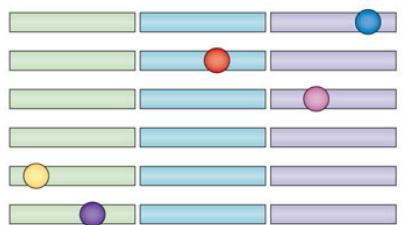


Over time, the advantageous mutation approaches fixation

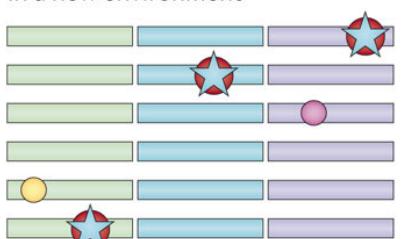


c Selection on a complex trait

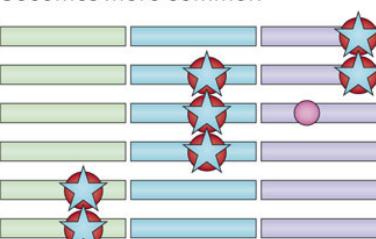
Neutral variation



A set of variants becomes adaptive in a new environment

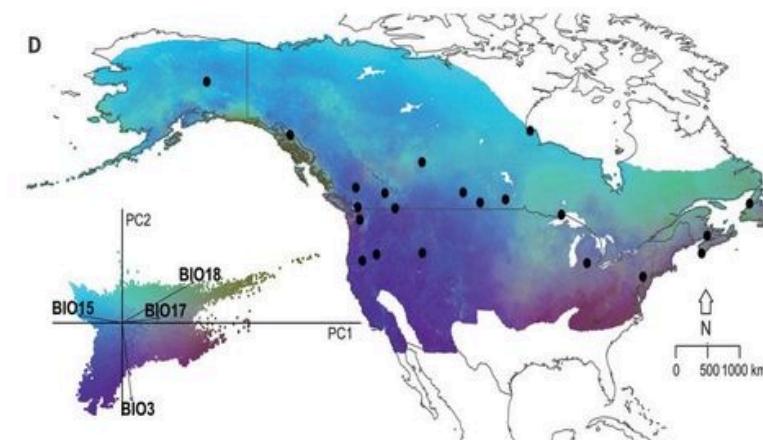


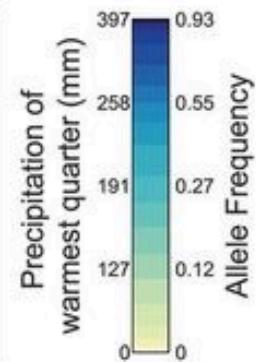
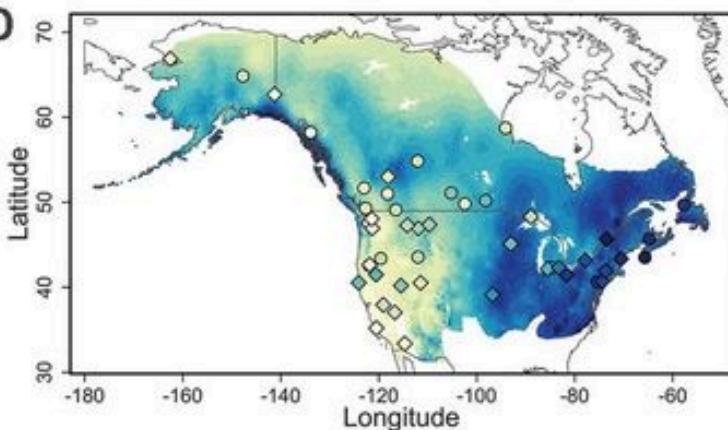
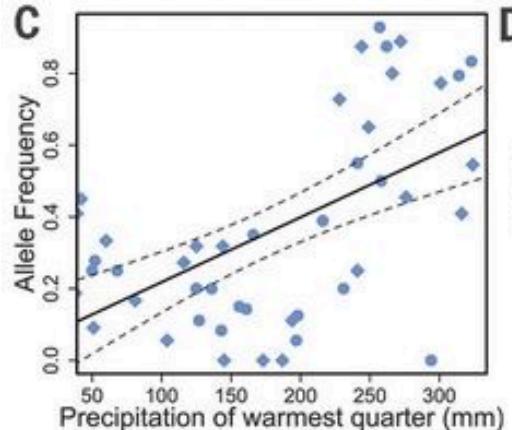
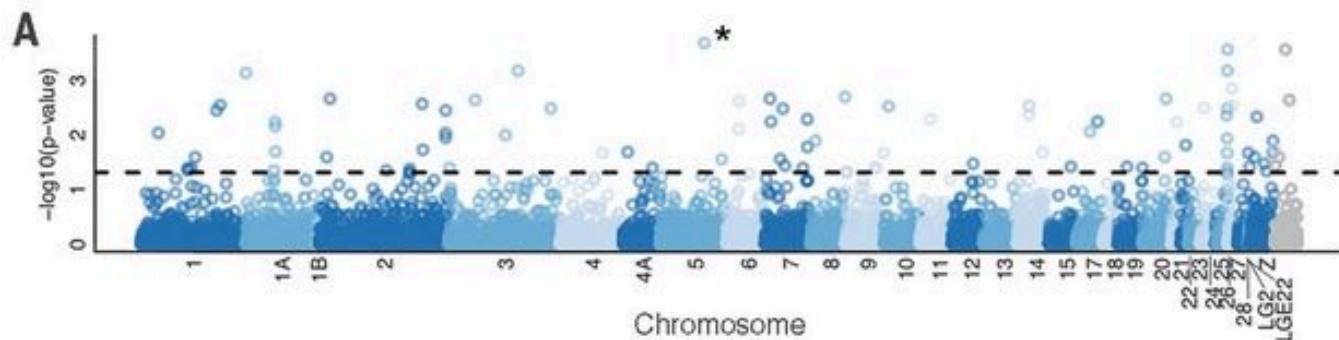
Over time, the set of variants becomes more common



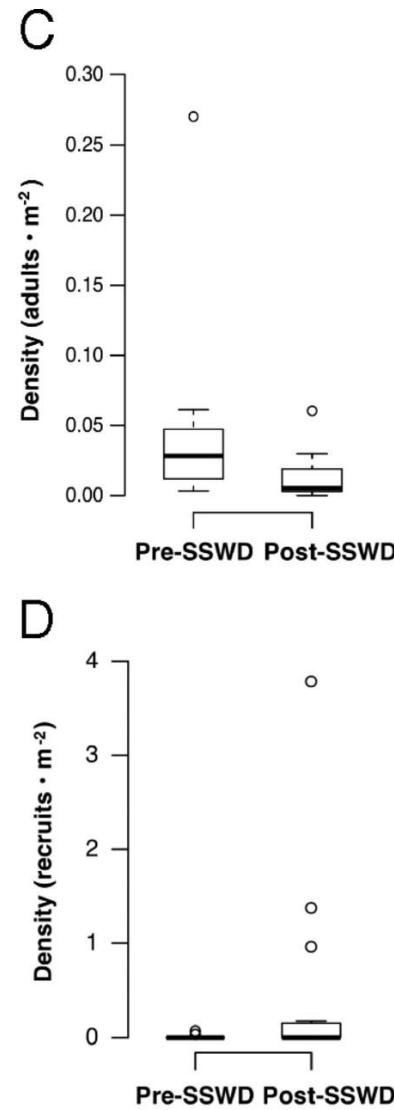
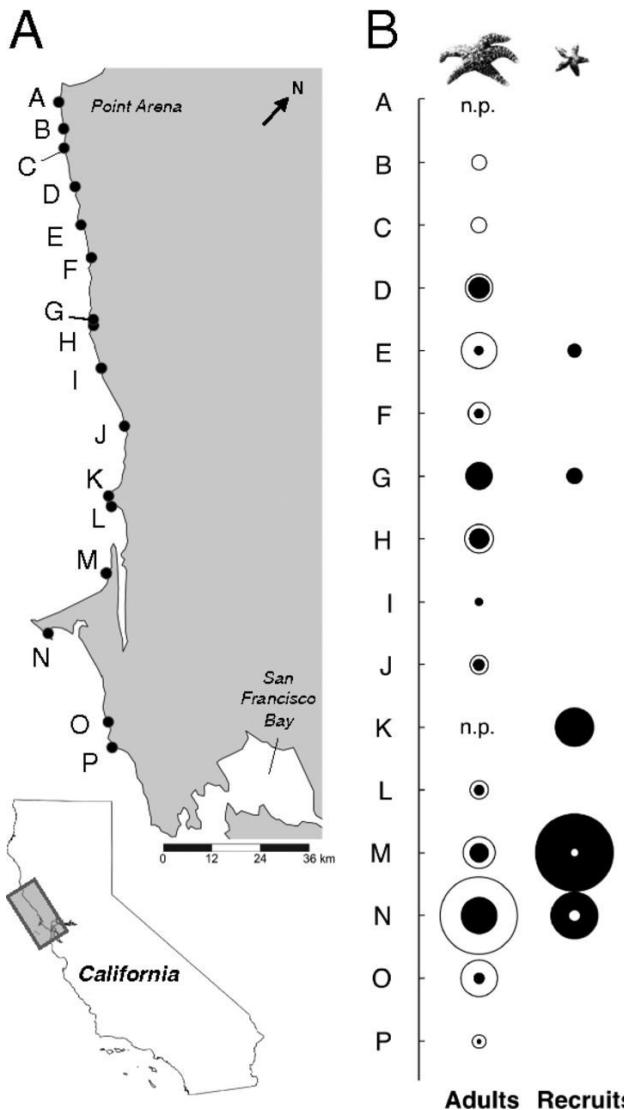
Gene environment associations

- Where is there a correlation between the environment and genetics?
- Important!
 - Must control for population structure!
- Methods:
 - Bayenv2
 - latent factor mixed models: LFMM2
 - Machine learning
 - Gradient Forests, random forests





Before and after sampling

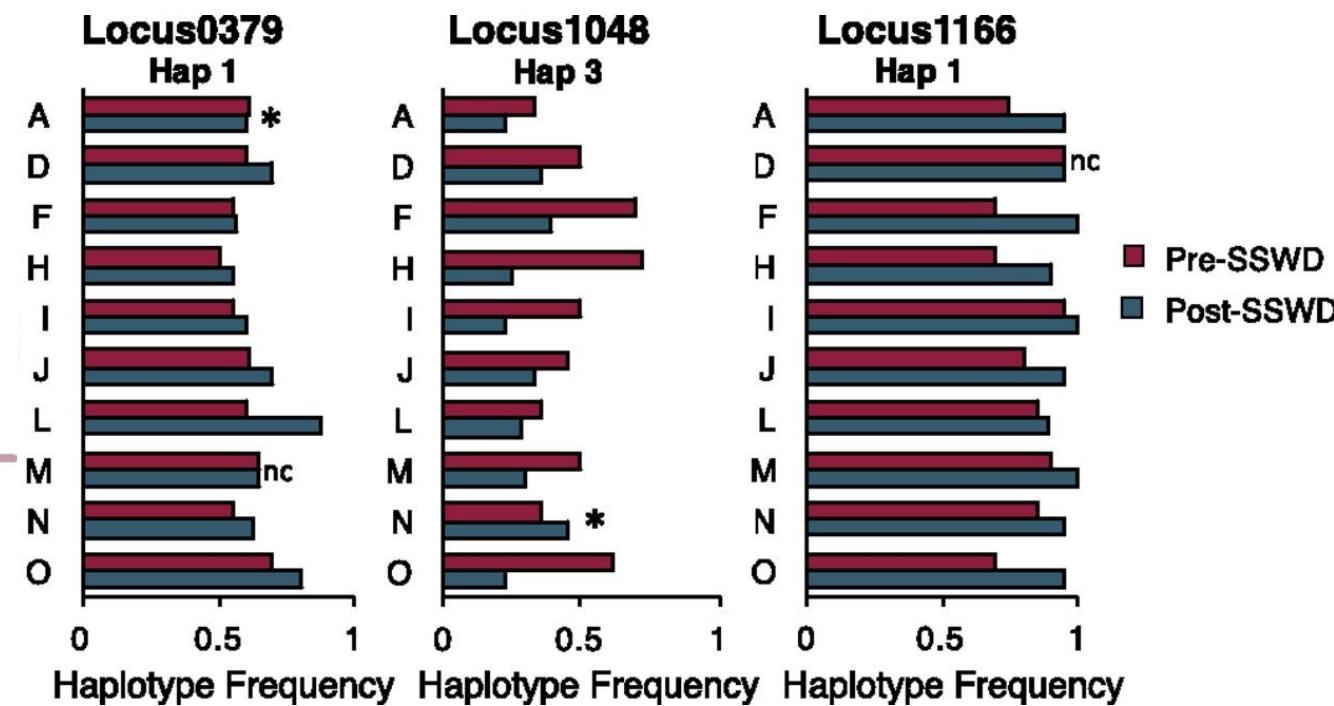
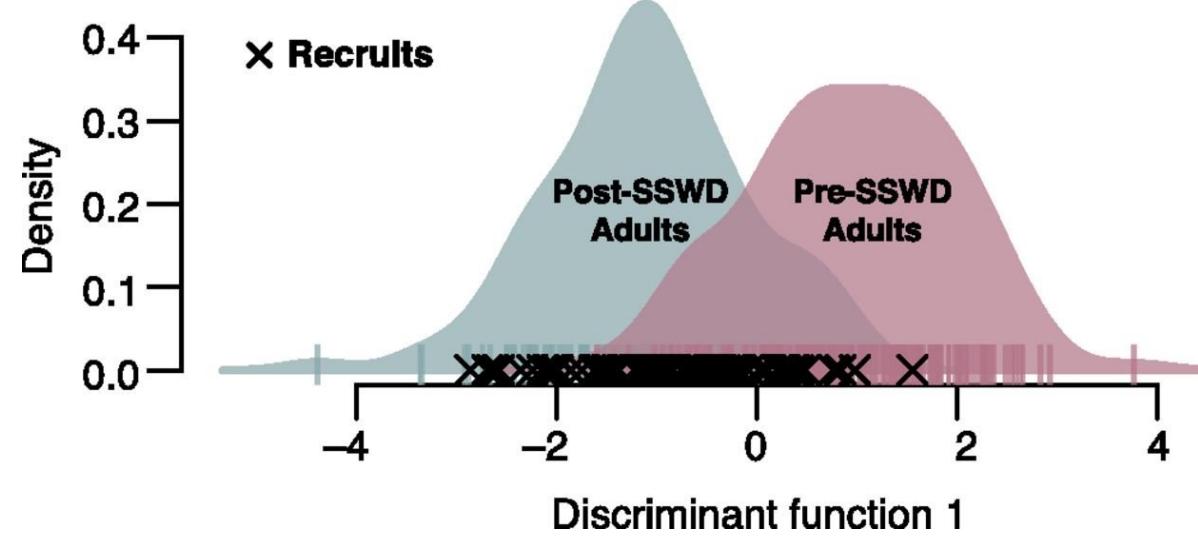


RESEARCH ARTICLE | BIOLOGICAL SCIENCES | FREE ACCESS

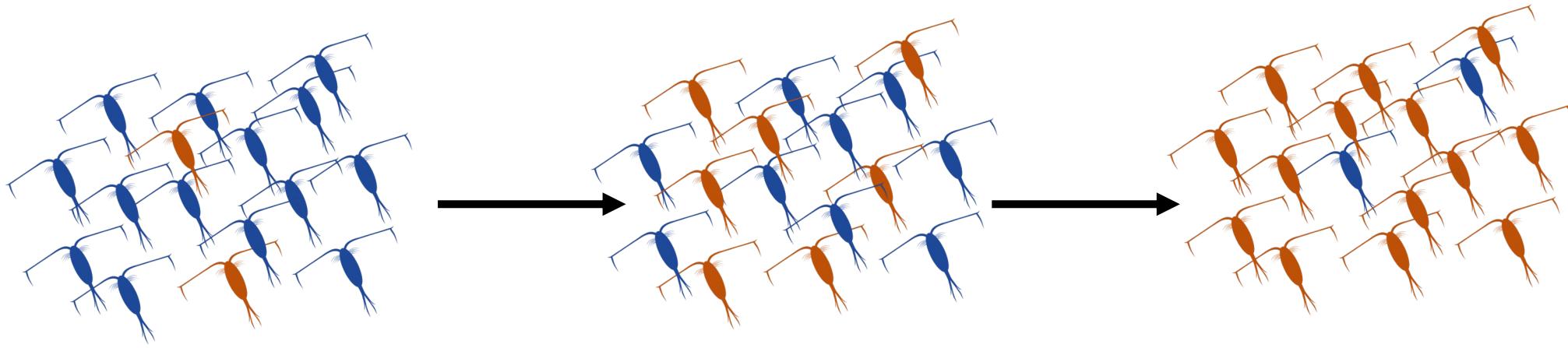
Decimation by sea star wasting disease and rapid genetic change in a keystone species, *Pisaster ochraceus*

Lauren M. Schiebelhut , Jonathan B. Puritz, and Michael N. Dawson [Authors Info & Affiliations](#)





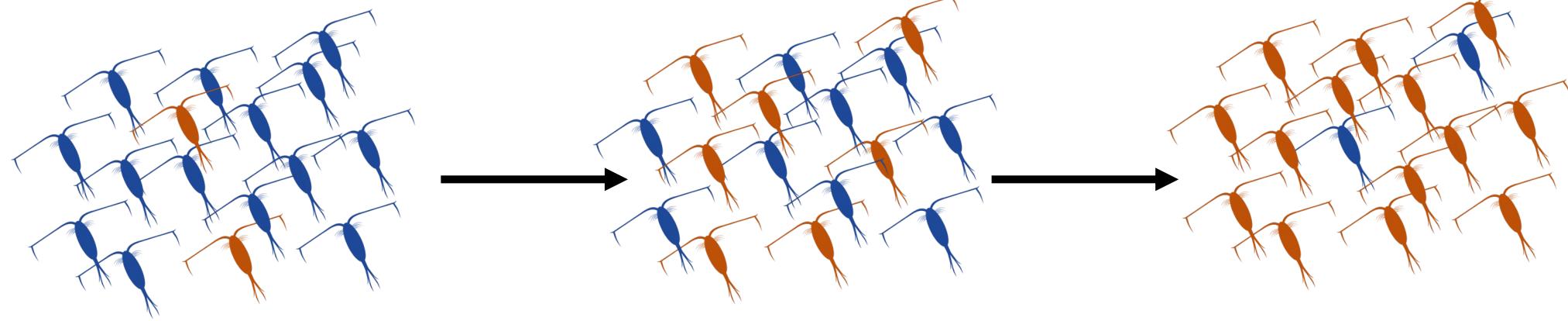
Experimental evolution/Evolve and resequence



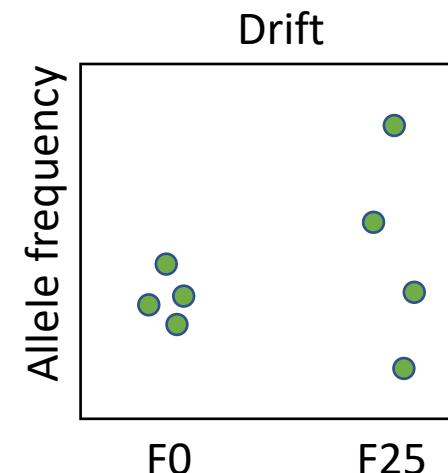
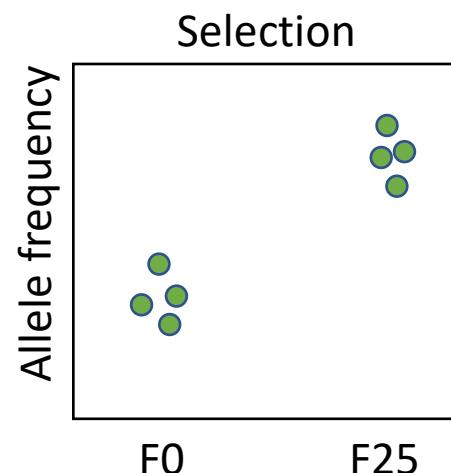
Observe evolution as it happens

Look for consistent changes in allele frequencies

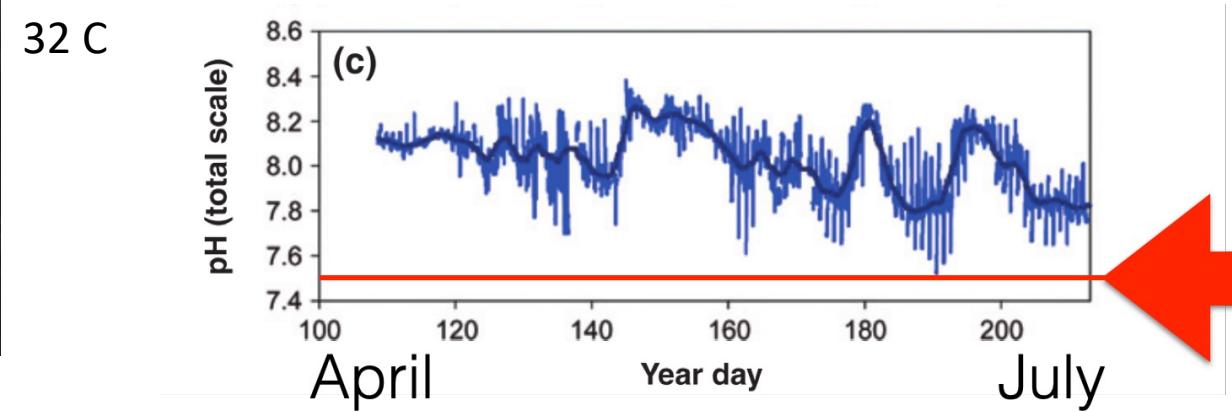
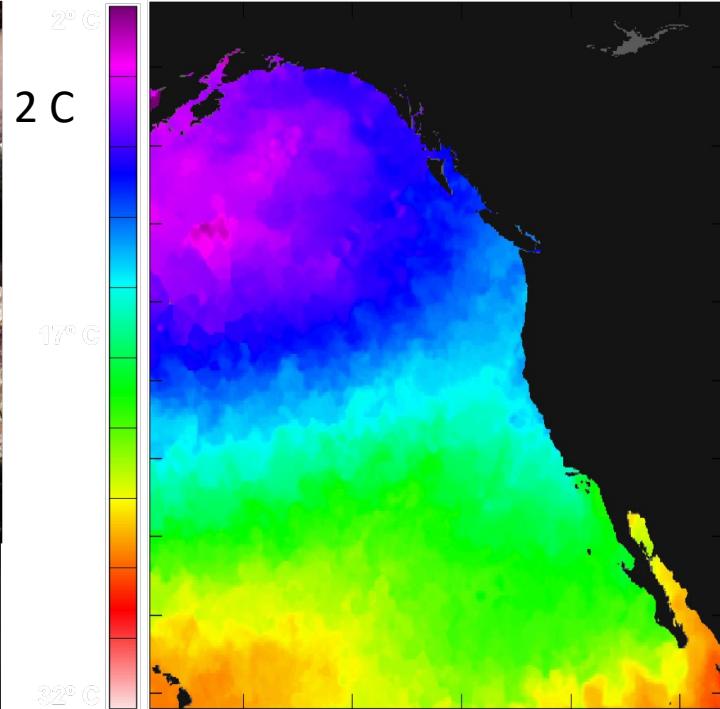
Experimental evolution/Evolve and resequence



Selection across generations



Purple sea urchin: single generation selection



Rare genetic variation and balanced polymorphisms are important for survival in global change conditions

Reid S. Brennan[†], April D. Garrett[†], Kaitlin E. Huber, Heidi Hargarten and Melissa H. Pespeni

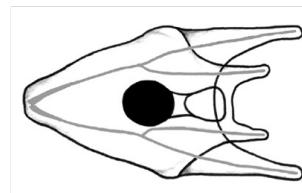
Blastula



Major skeletal growth

24 hours post fert.

4-arm pluteus

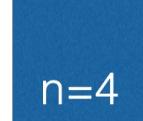


7 days post fert.

Genomic samples:



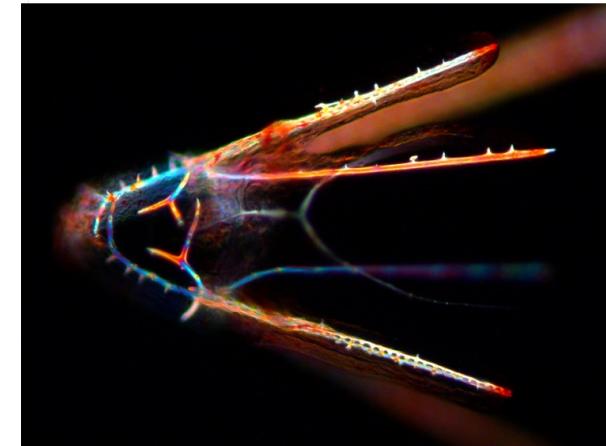
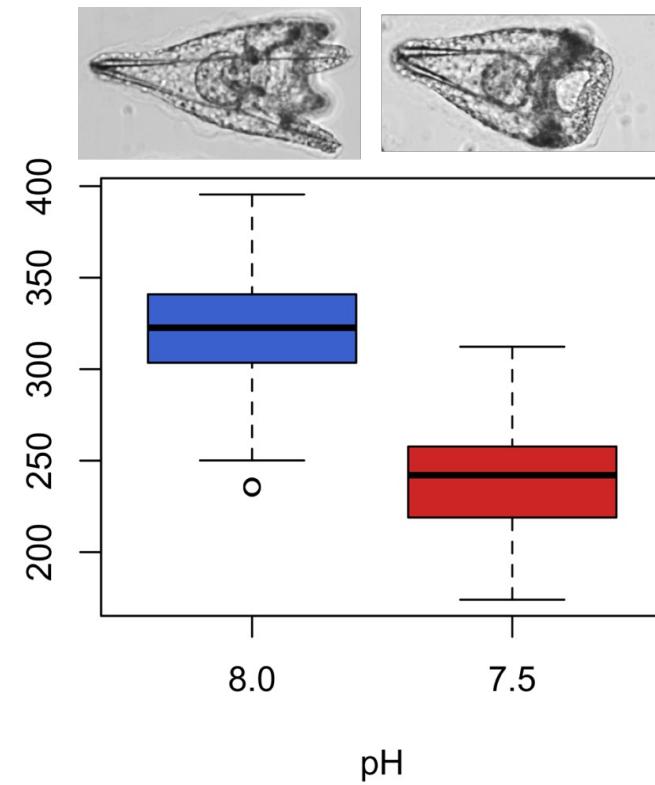
Mild: pH 8.0

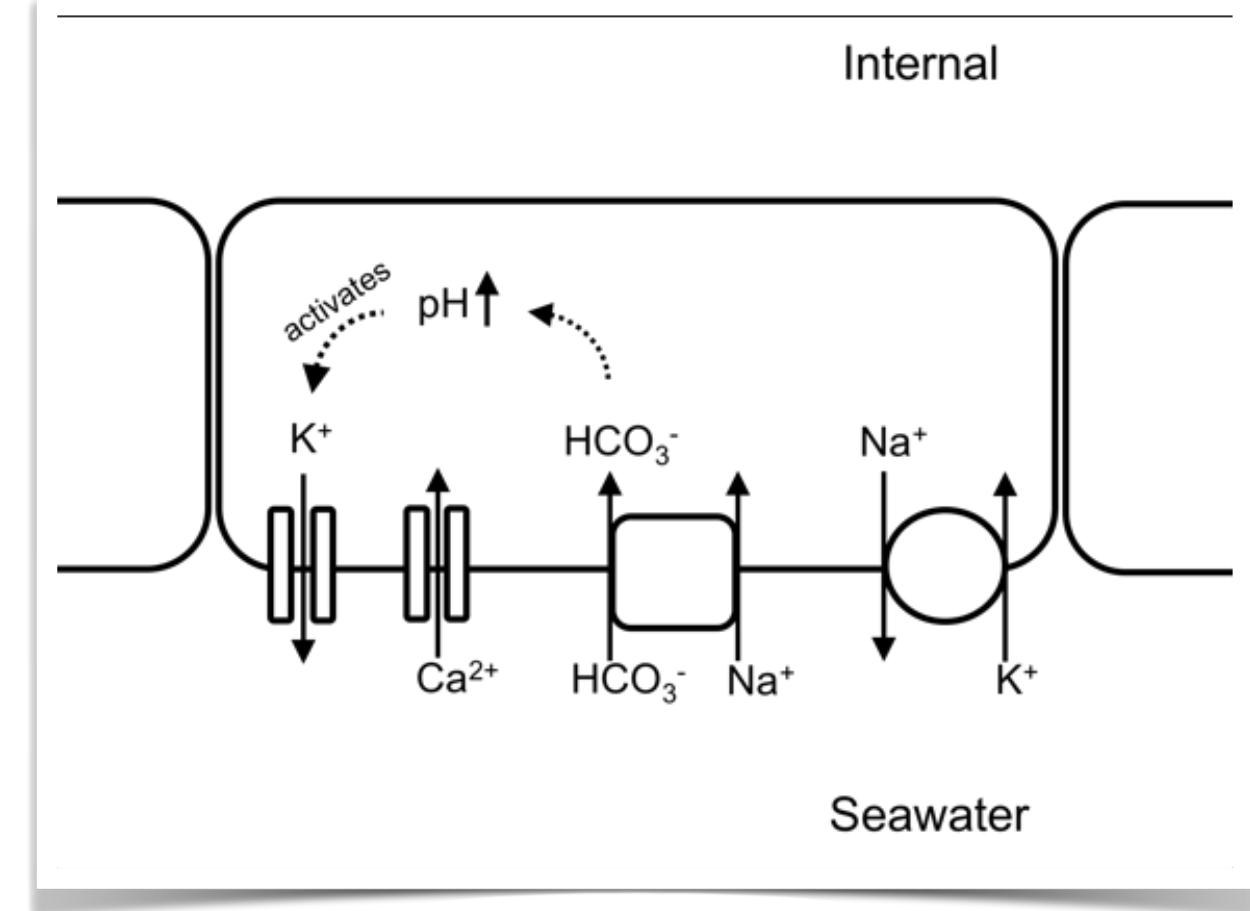
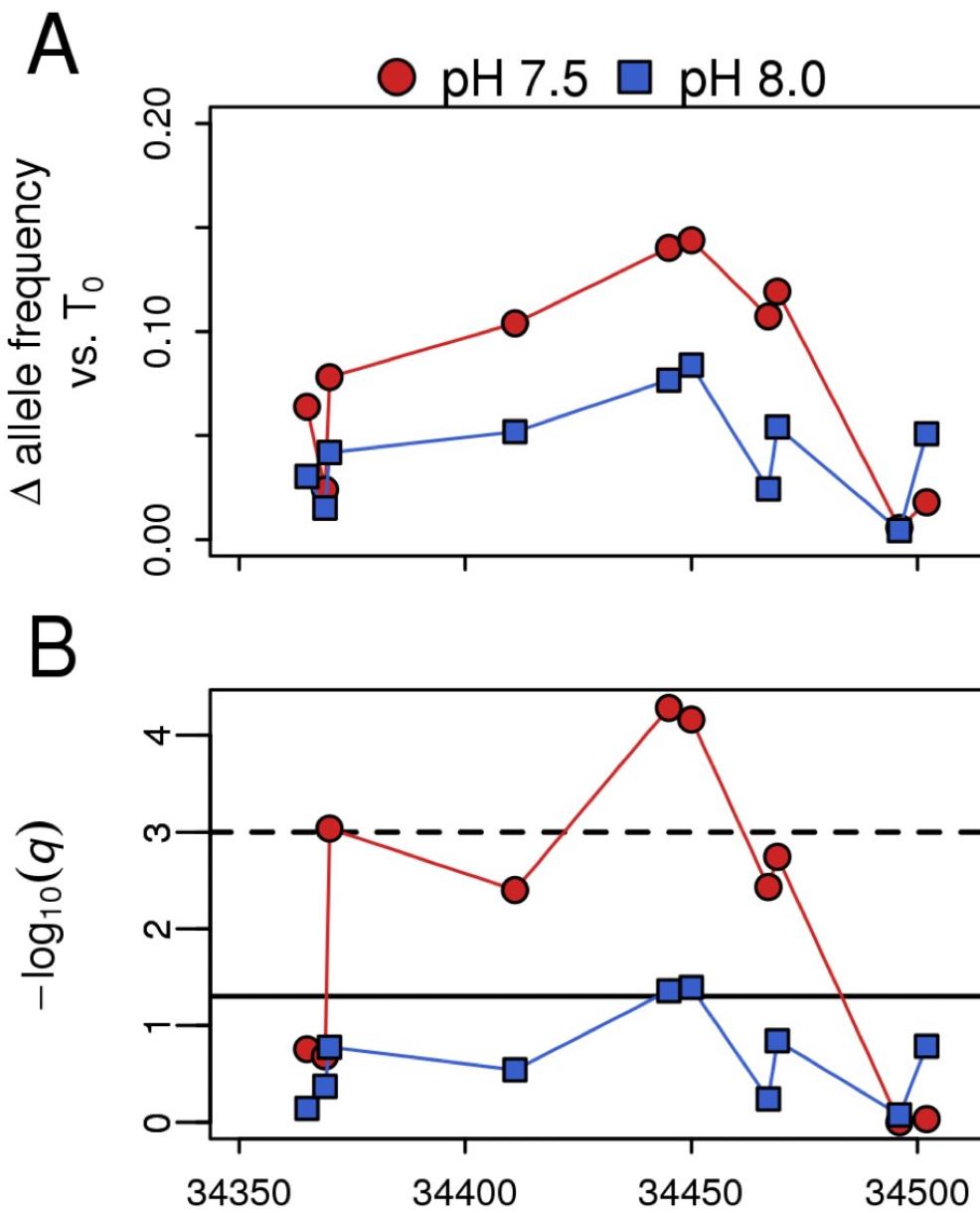


Extreme: pH 7.5



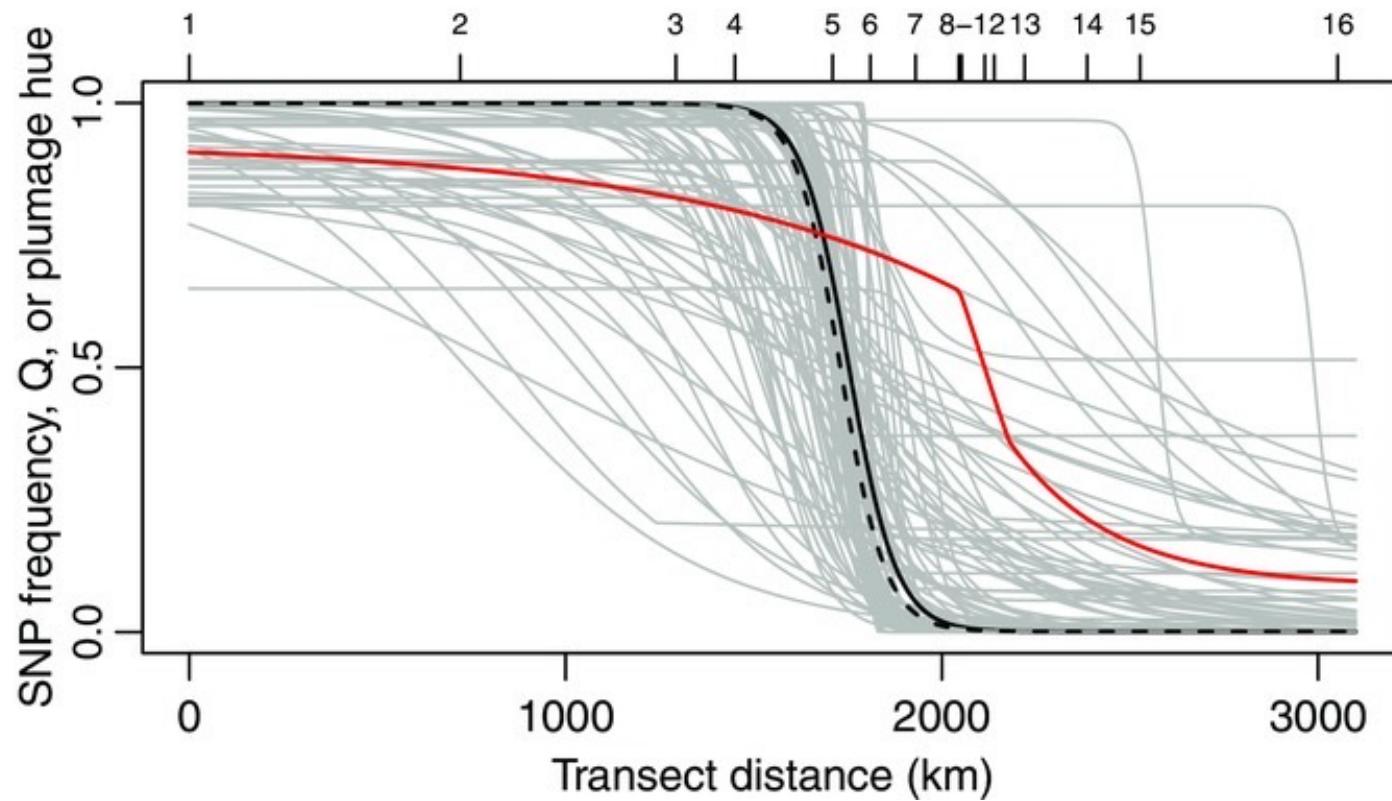
Total Body Length (micrometers)



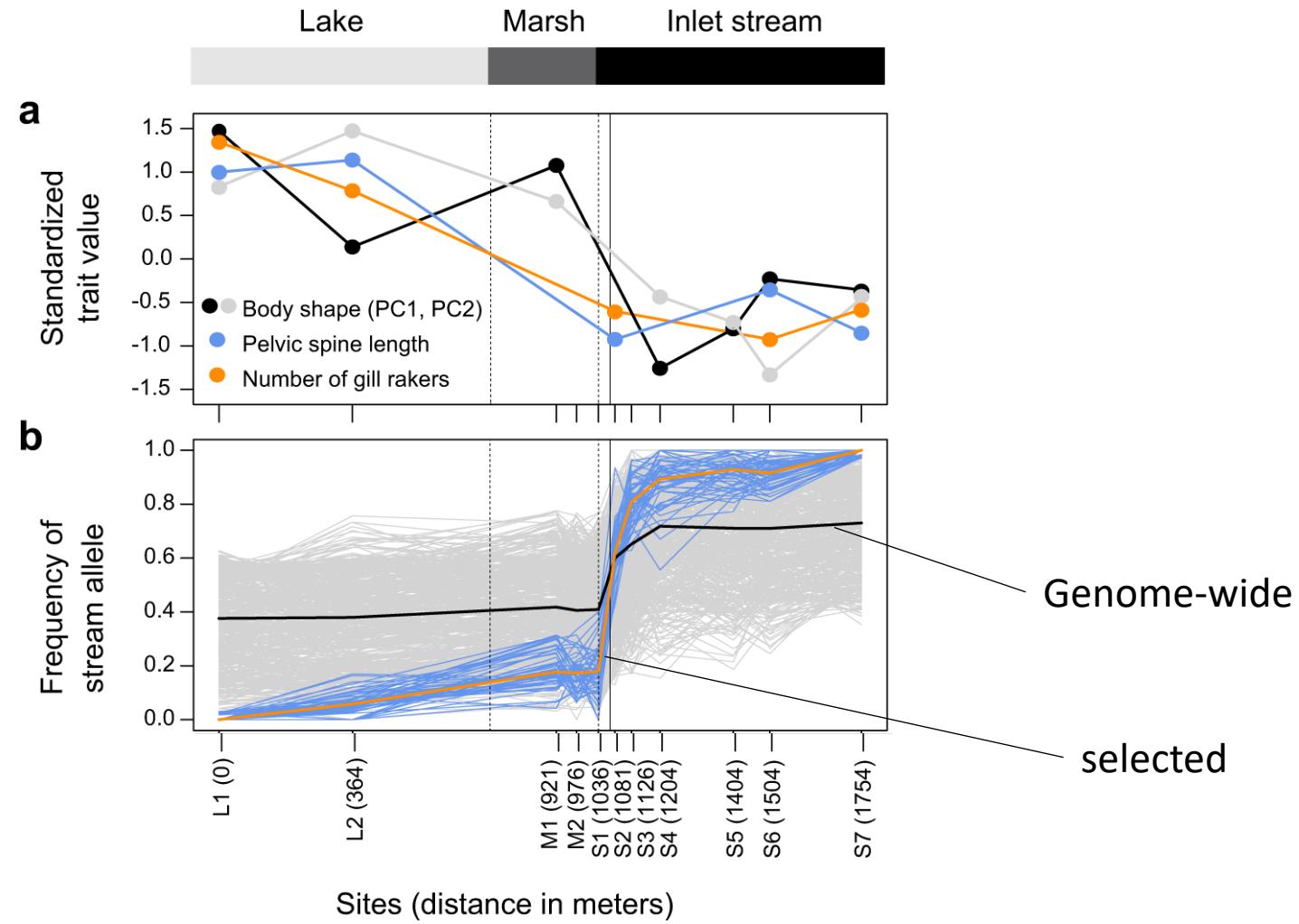
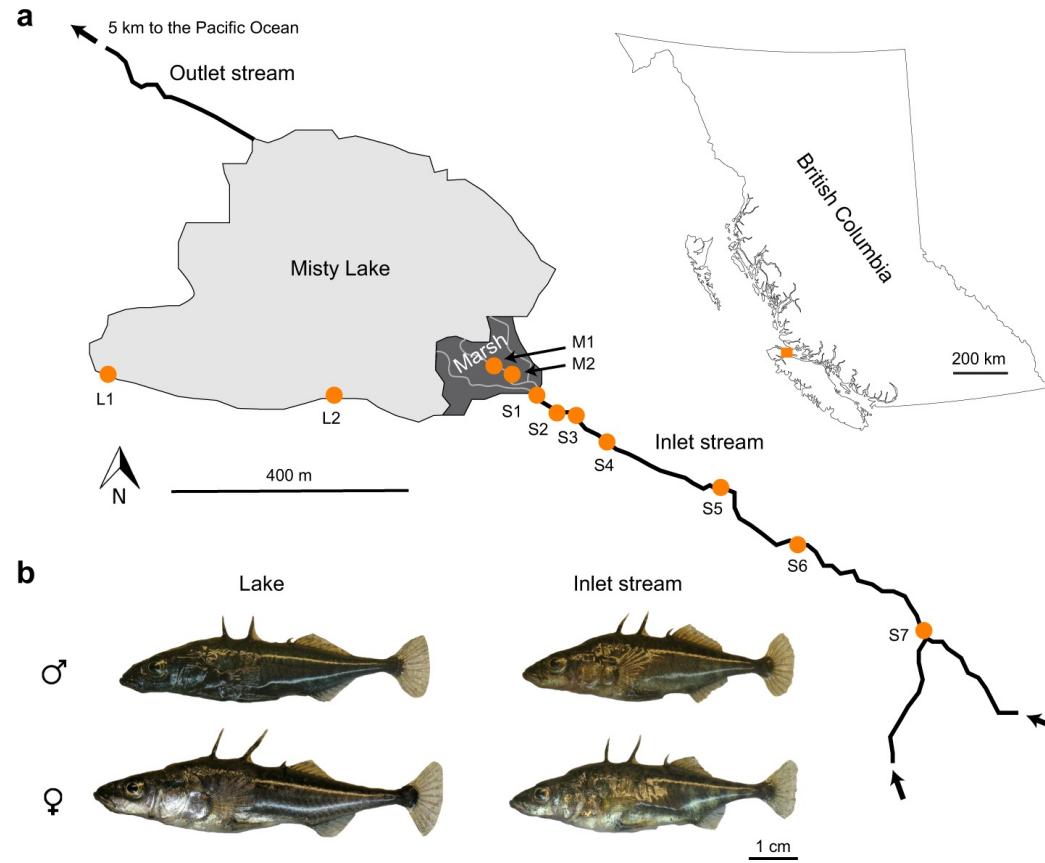


Cline analyses

- Hybrid zone:
 - Where genetically distinct populations meet, mate, and produce offspring
 - Expect neutral allele frequency transition
 - Where do you see violations of neutrality?



Cline analyses



ECOLOGICAL GENOMICS

The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish

Noah M. Reid,¹ Dina A. Proestou,² Bryan W. Clark,³ Wesley C. Warren,⁴
John K. Colbourne,⁵ Joseph R. Shaw,^{5,6} Sibel I. Karchner,^{7,8} Mark E. Hahn,^{7,8}
Diane Nacci,⁹ Marjorie F. Oleksiak,¹⁰ Douglas L. Crawford,¹⁰ Andrew Whitehead^{1*}