



# POPULATION ASSIGNMENT OF HARBOUR PORPOISES IN NORTH AND BALTIC SEA USING WHOLE GENOME DATA

Tiedemann, R., Celemín Amaro, E., Havenstein, K., Autenrieth, M., Benke, H., Dähne, M., Dennis, A.B., Gunnlaugsson, P., Hartmann, S., Klemens, L., Lah, L., Pampoulie, C., Pawliczka, I., Roos, A., Sánchez, M.Q., Siebert, U., Sigurðsson, G.M., Víkingsson, G.<sup>(†)</sup>, Westphal, L.



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RESOURCE ARTICLE

WILEY MOLECULAR ECOLOGY  
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## High-quality whole-genome sequence of an abundant Holarctic odontocete, the harbour porpoise (*Phocoena phocoena*)

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RESOURCE ARTICLE

MOLECULAR ECOLOGY  
RESOURCES WILEY

## Evolutionary history and seascape genomics of Harbour porpoises (*Phocoena phocoena*) across environmental gradients in the North Atlantic and adjacent waters

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Christina Lockyer<sup>9</sup> | Per Berggren<sup>10</sup> | A. Amaha Öztürk<sup>11</sup> | Bayram Öztürk<sup>11</sup> |  
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Conservation Genetics  
<https://doi.org/10.1007/s10592-023-01589-0>

RESEARCH ARTICLE

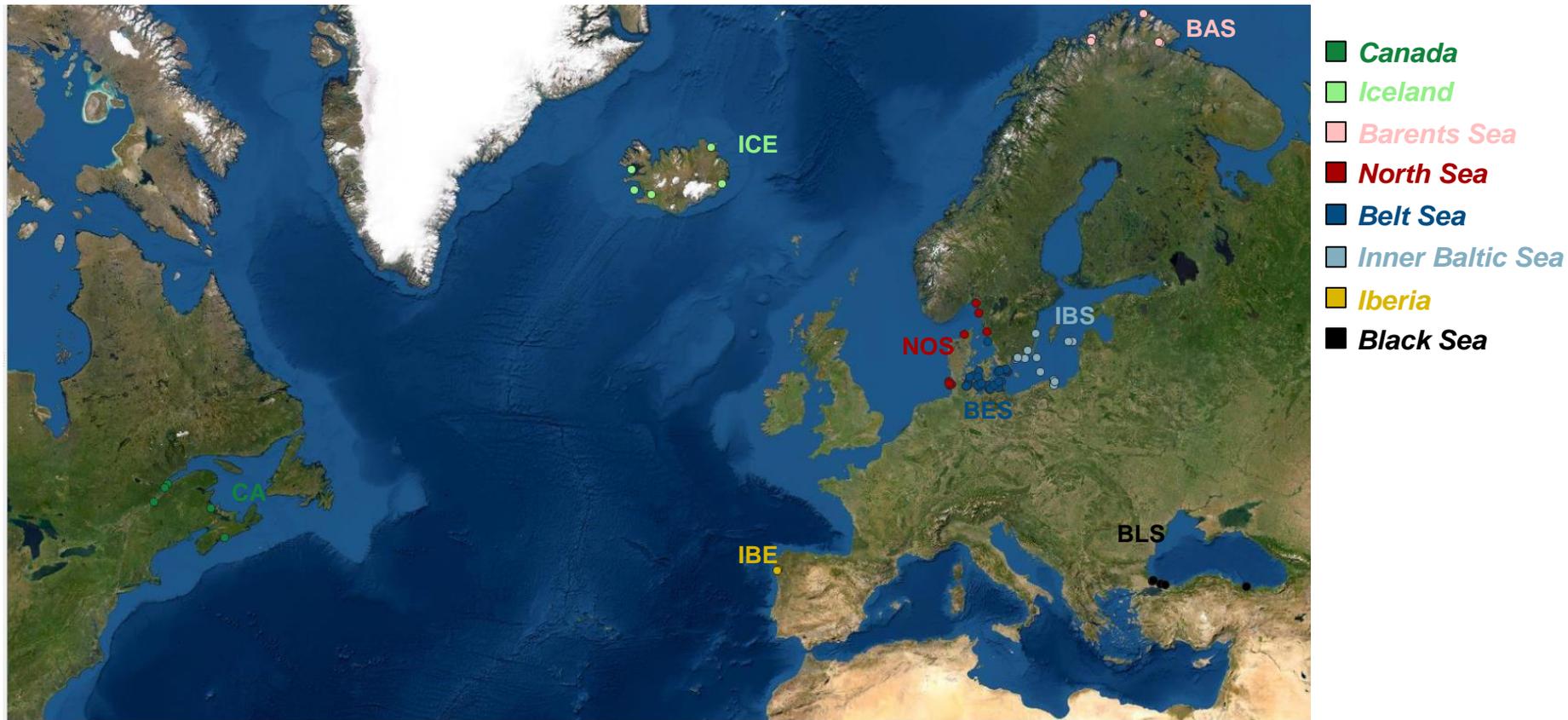


## Genome-wide analysis of the harbour porpoise (*Phocoena phocoena*) indicates isolation-by-distance across the North Atlantic and potential local adaptation in adjacent waters

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Christophe Pampoulie<sup>6</sup> · Guðjón Már Sigurðsson<sup>6</sup> · Ursula Siebert<sup>7</sup> · Morten Tange Olsen<sup>8</sup> · Vincent Biard<sup>8,9,10</sup> ·  
Mads Peter Heide-Jørgensen<sup>9</sup> · Ayaka Amaha Öztürk<sup>11</sup> · Bayram Öztürk<sup>11</sup> · John W. Lawson<sup>12</sup> · Ralph Tiedemann<sup>1</sup>



# 74 HARBOUR PORPOISE WHOLE GENOMES ACROSS THE NORTH ATLANTIC (MAPPED ONTO OWN REFERENCE GENOME)



# BIOINFORMATIC PIPELINE – VARIANT CALLING



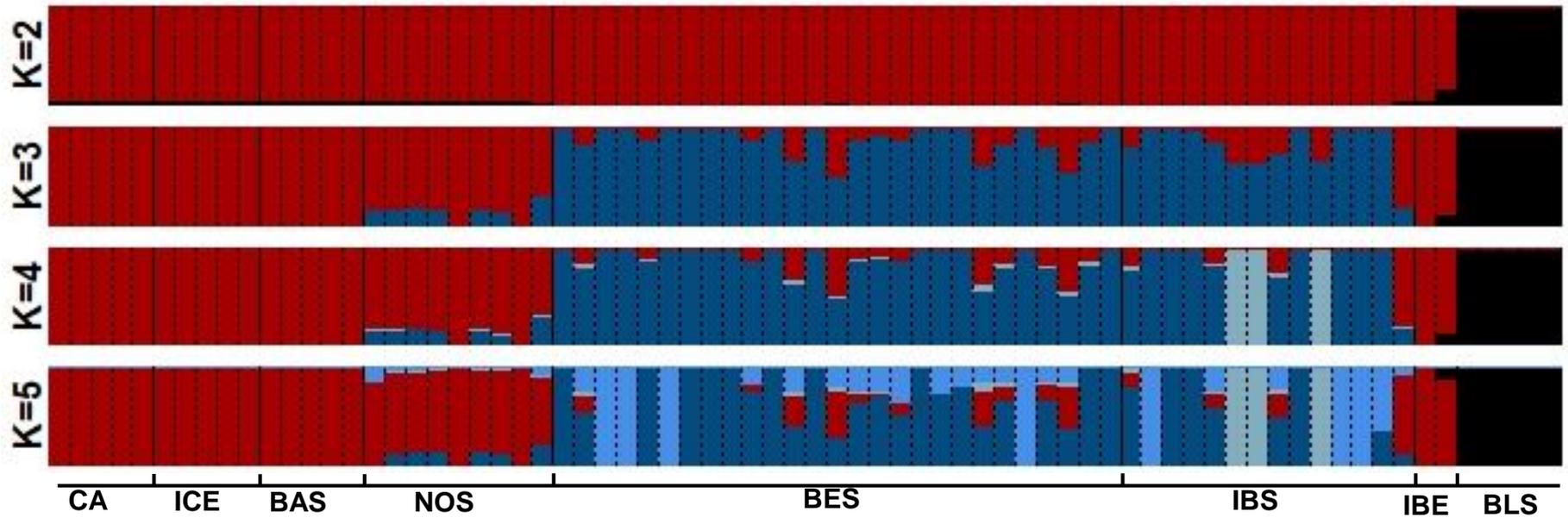
- Genotype likelihood estimation → *angsd*
- Linkage disequilibrium pruning → *ngsLD*
  - All 72 porpoises: 7,337,750 SNPs → 1,745,544 *unlinked SNPs*
  - North Atlantic 67 porpoises: 7,404,321 SNPs → 1,741,332 *unlinked SNPs*
  - Baltic 50 porpoises: **7,674,541 SNPs → 1,506,953 *unlinked SNPs***
- Genotype calling: → *bcftools mpileup* (26,198,530 SNPs)
- Genotype filtering: (nonbiallelic sites, indels, minimum MAF of 0.05, minimum mapping quality of 30, minimum genotype quality of 20, minimum phred score quality of 30, minimum genotype information in 75% of individuals → *bcftools view* (**6,186,462 *filtered SNPs***))

**=> Both pipelines yield millions of SNPs shared by the majority of samples**

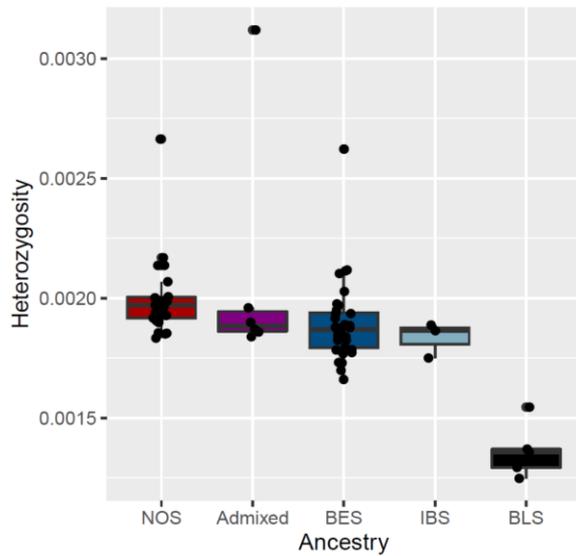


# POPULATION STRUCTURE – 72 UNRELATED PORPOISES

West  $\longrightarrow$  East



# POPULATION GENOMICS – HETEROZYGOSITY



■ **North Atlantic**

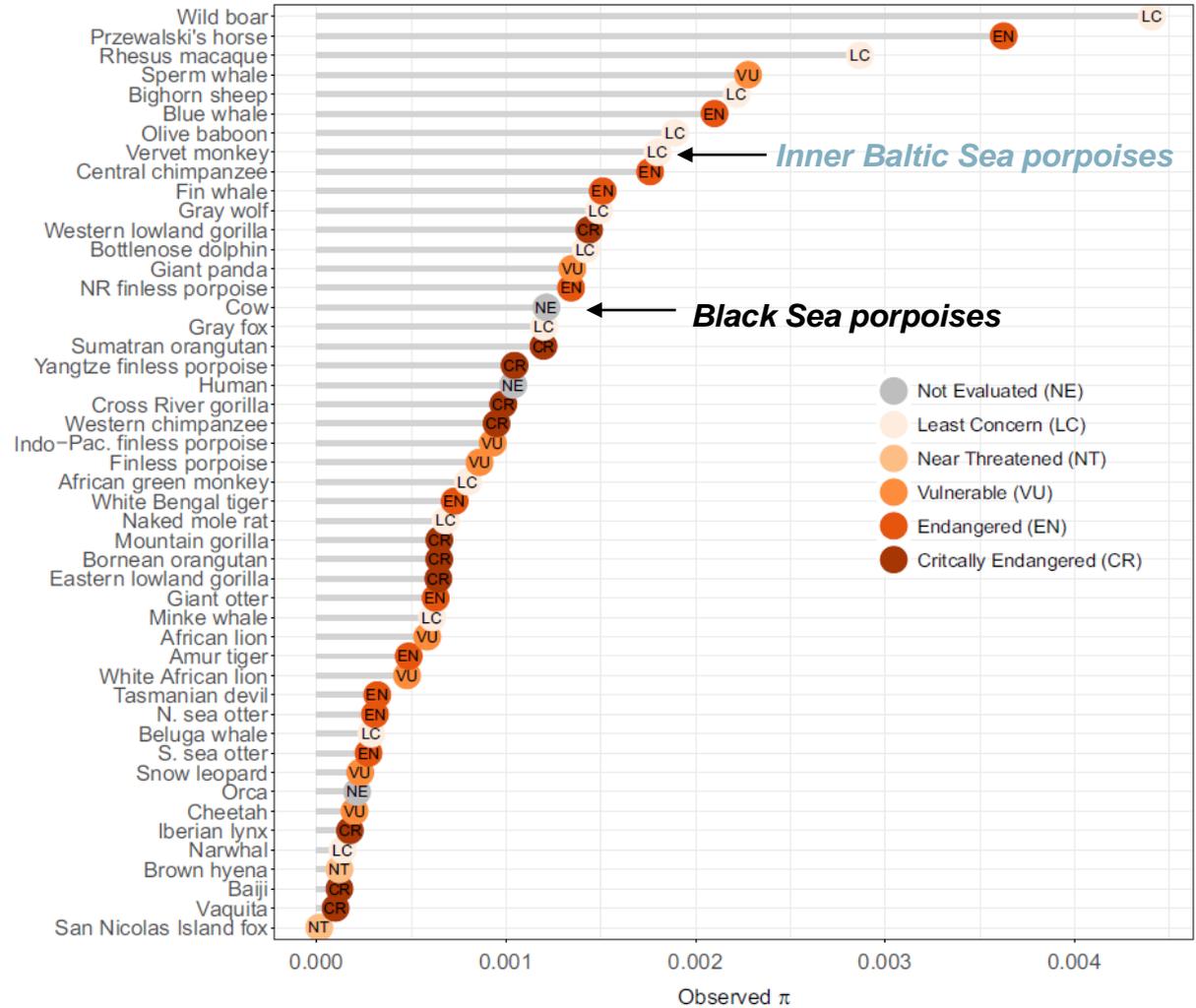
■ **Admixed**

■ **Belt Sea**

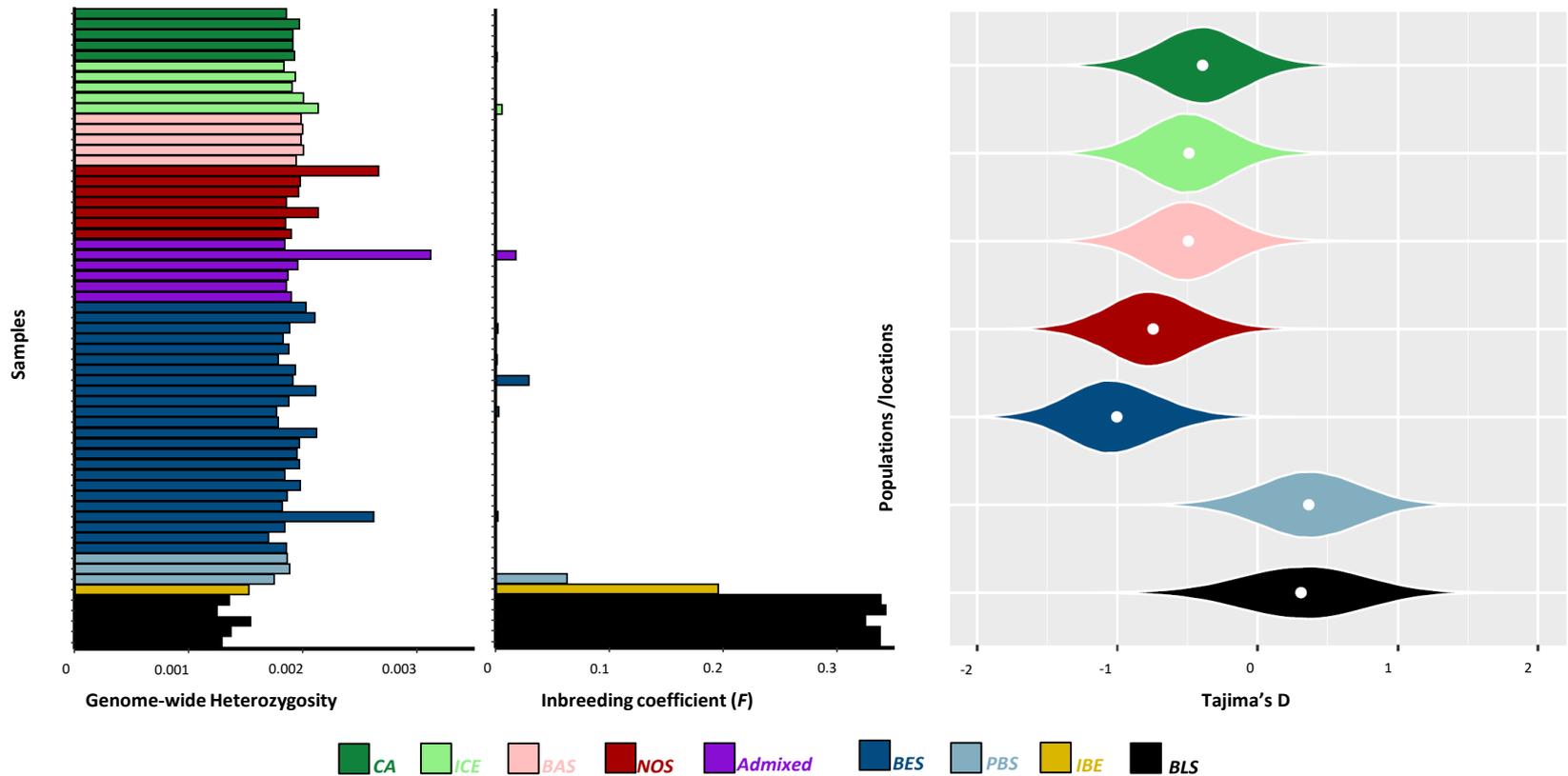
■ **Inner Baltic Sea**

■ **Black Sea**

Genome-Wide Heterozygosity in Mammals



# POPULATION GENOMICS – DIVERSITY, TAJIMA'S D

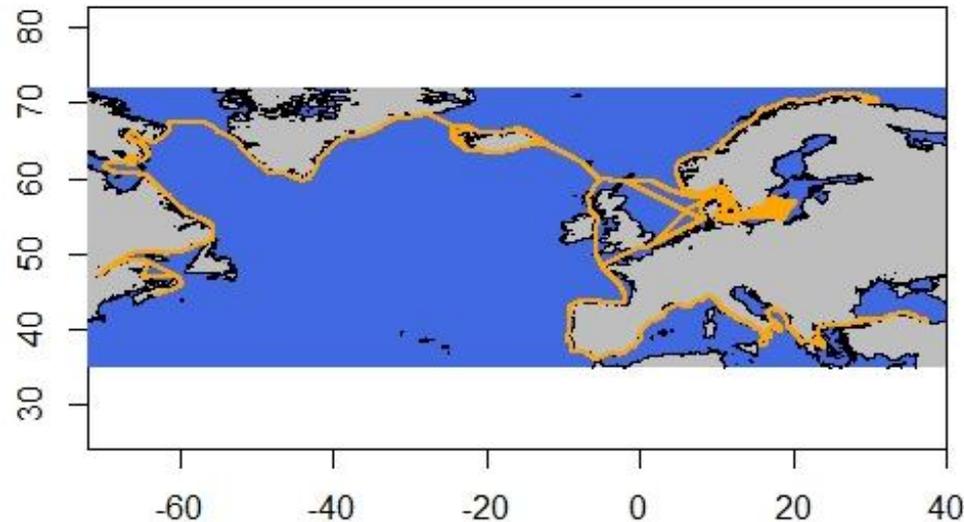


- ⇒ North Atlantic and Belt Sea populations are large and expanding
- ⇒ Inner Baltic Sea, Iberian and Black Sea populations are small and declining

# SEASCAPE GENOMICS – DATA PREPARATION

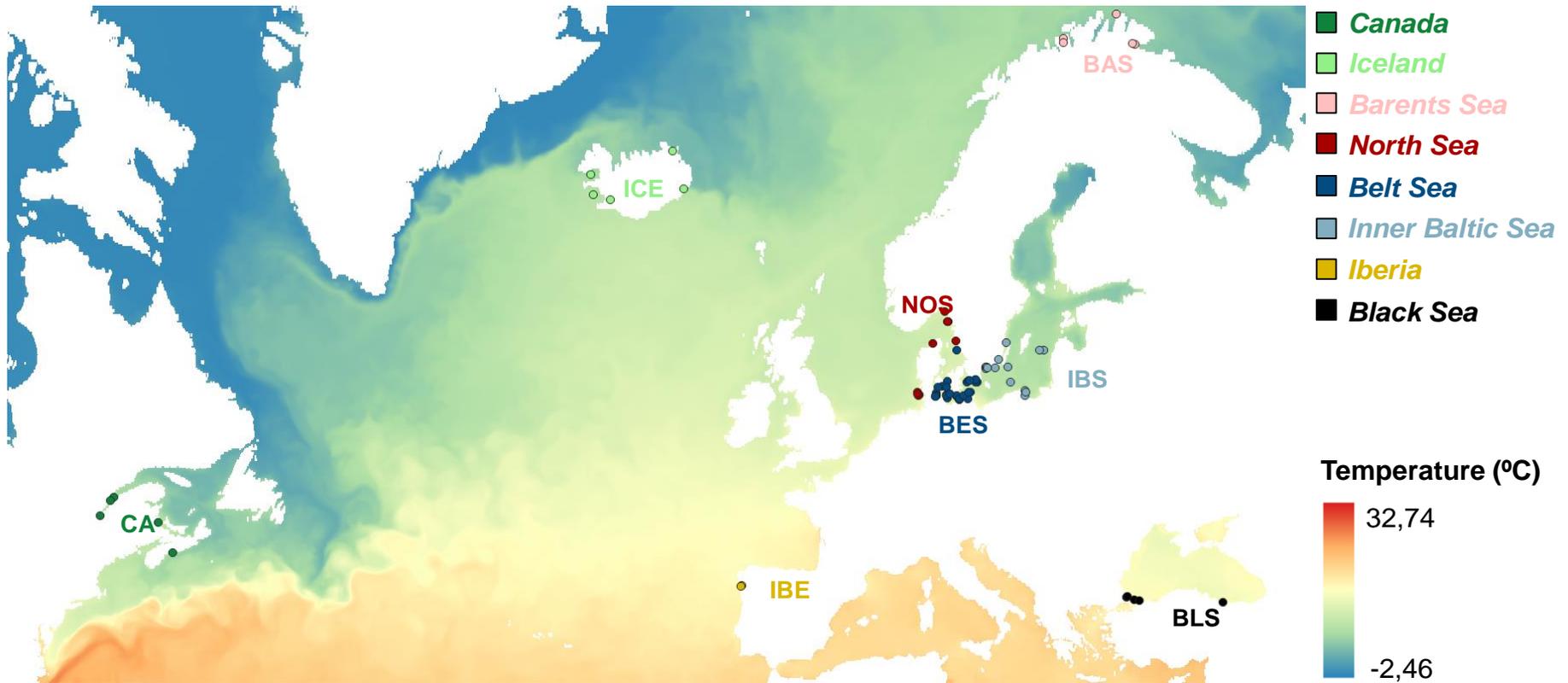


- Environmental data (from Bio-ORACLE): Temperature, Salinity, Current velocity, Primary productivity and Chlorophyll A (max, min, mean and range)
- Spatial data:
  - Compute least-cost paths between samples
  - Compute distance-based Moran's eigenvector maps (dbMEMs)



- Genetic data: 5,892,125 SNPs genotyped in 72 samples

# TEMPERATURE MEAN IN THE NORTH ATLANTIC



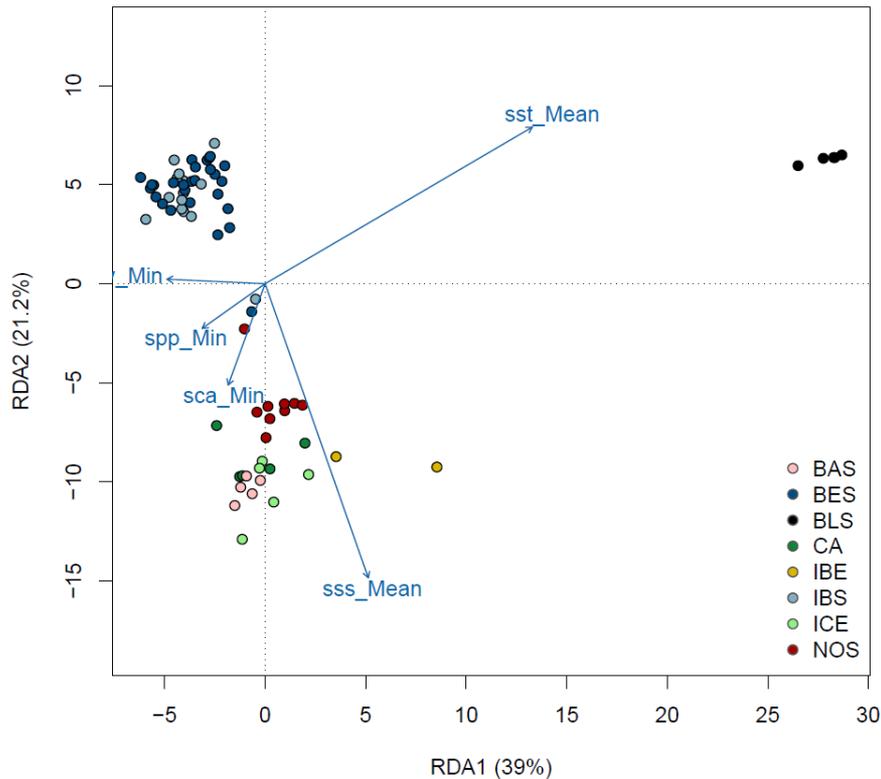
# SALINITY MEAN IN THE NORTH ATLANTIC



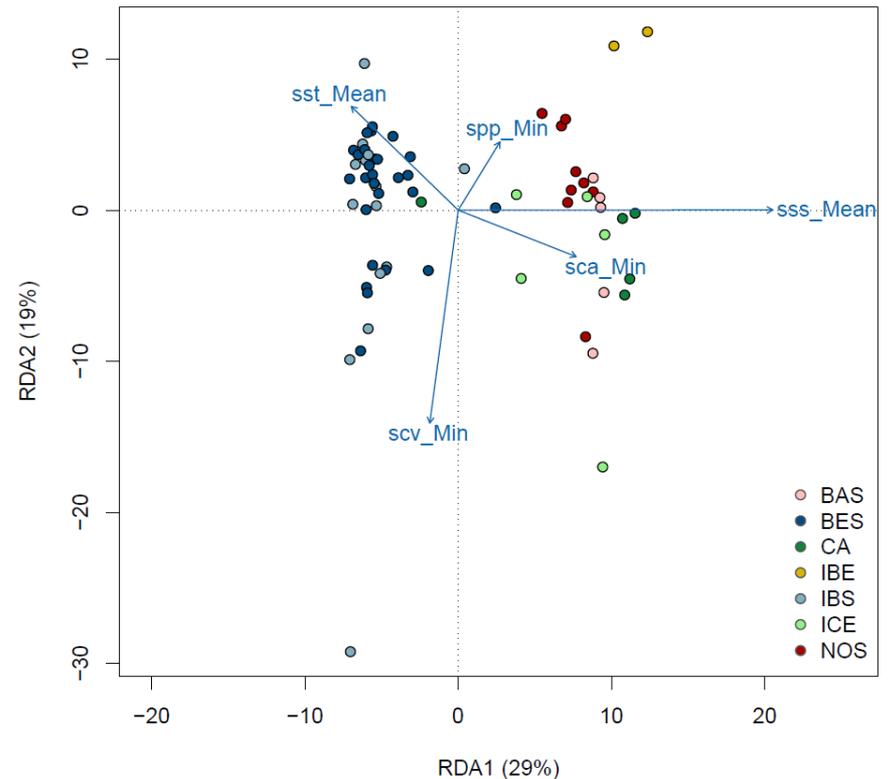
# SEASCAPE GENOMICS – REDUNDANCY ANALYSIS



### All



### Without Black Sea



sst: sea surface temperature; sss: sea surface salinity; scv: sea current velocity;  
spp: sea primary production; sca: sea chlorophyll a

# 60 Harbour porpoise genomes in the Baltic region



Colored by sampling location:

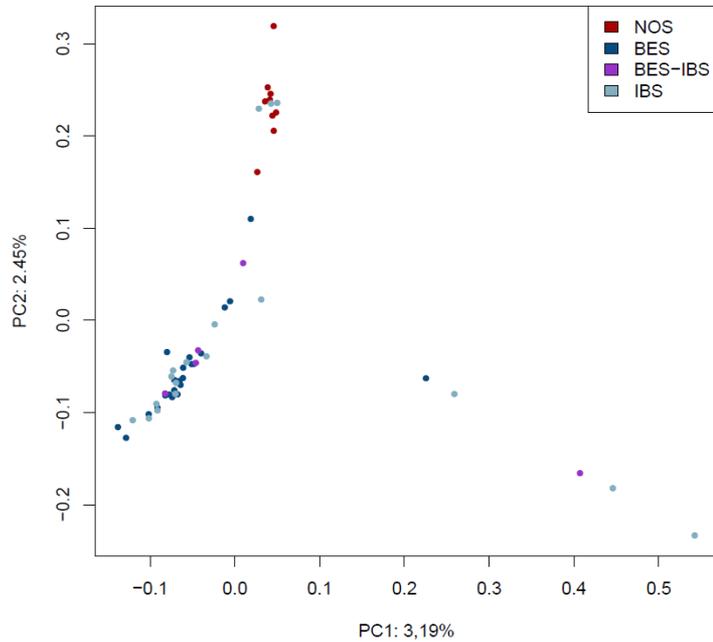
■ **NOS** ■ **BES** ■ **BES-PBS** ■ **PBS**

## Objectives:

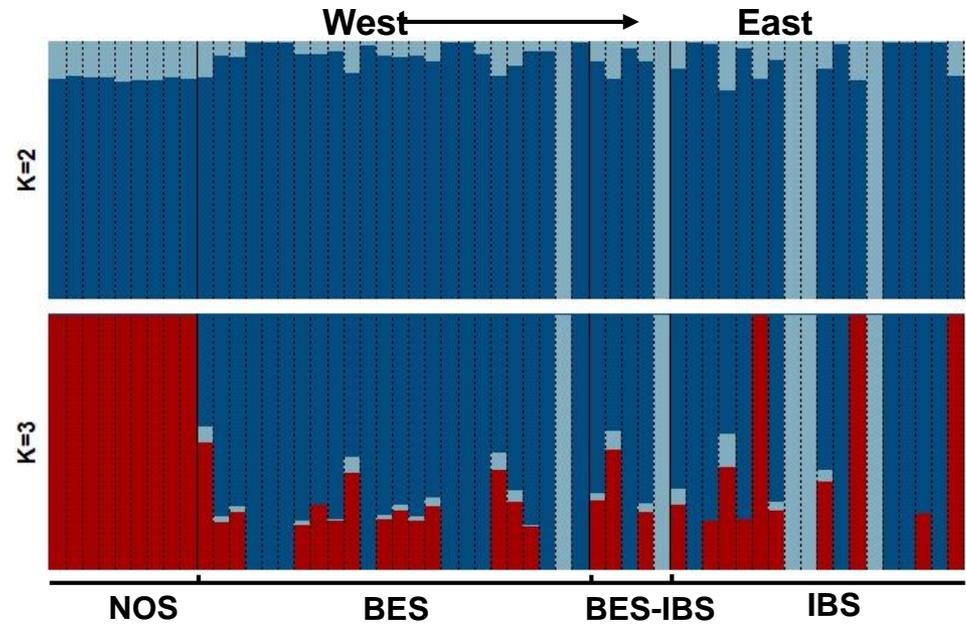
- Genomics:
  - Population structure in the Baltic
  - Role of selection and genetic drift on the origin and maintenance of the Baltic populations
  - Selective sweeps vs. outlier scan selection methods
- Genetics:
  - SNP panel for population assignment
  - Iterative SNP panel improvement
  - Genetic cline analyses



# Structure-PCA WGS data



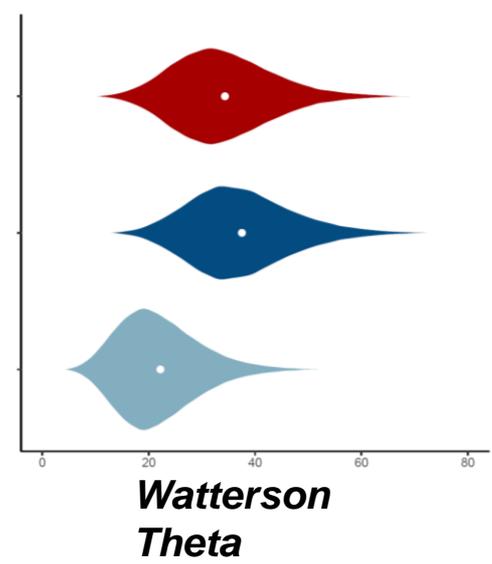
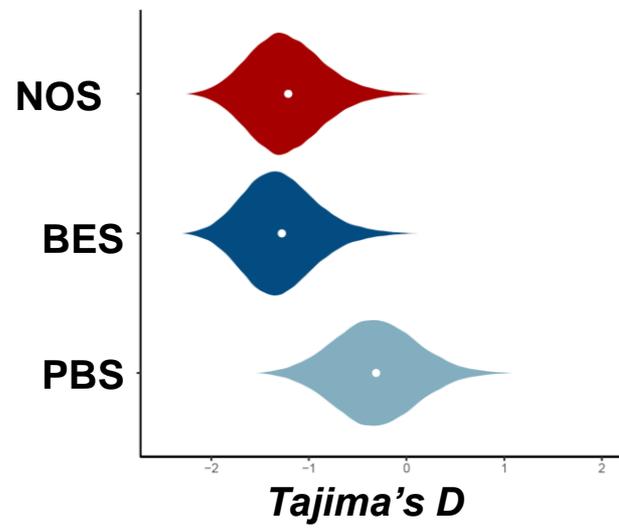
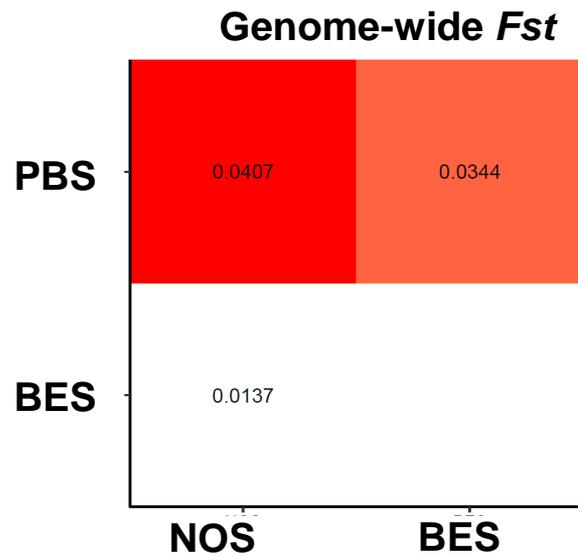
Colored by sampling location



Colored by genomic ancestry

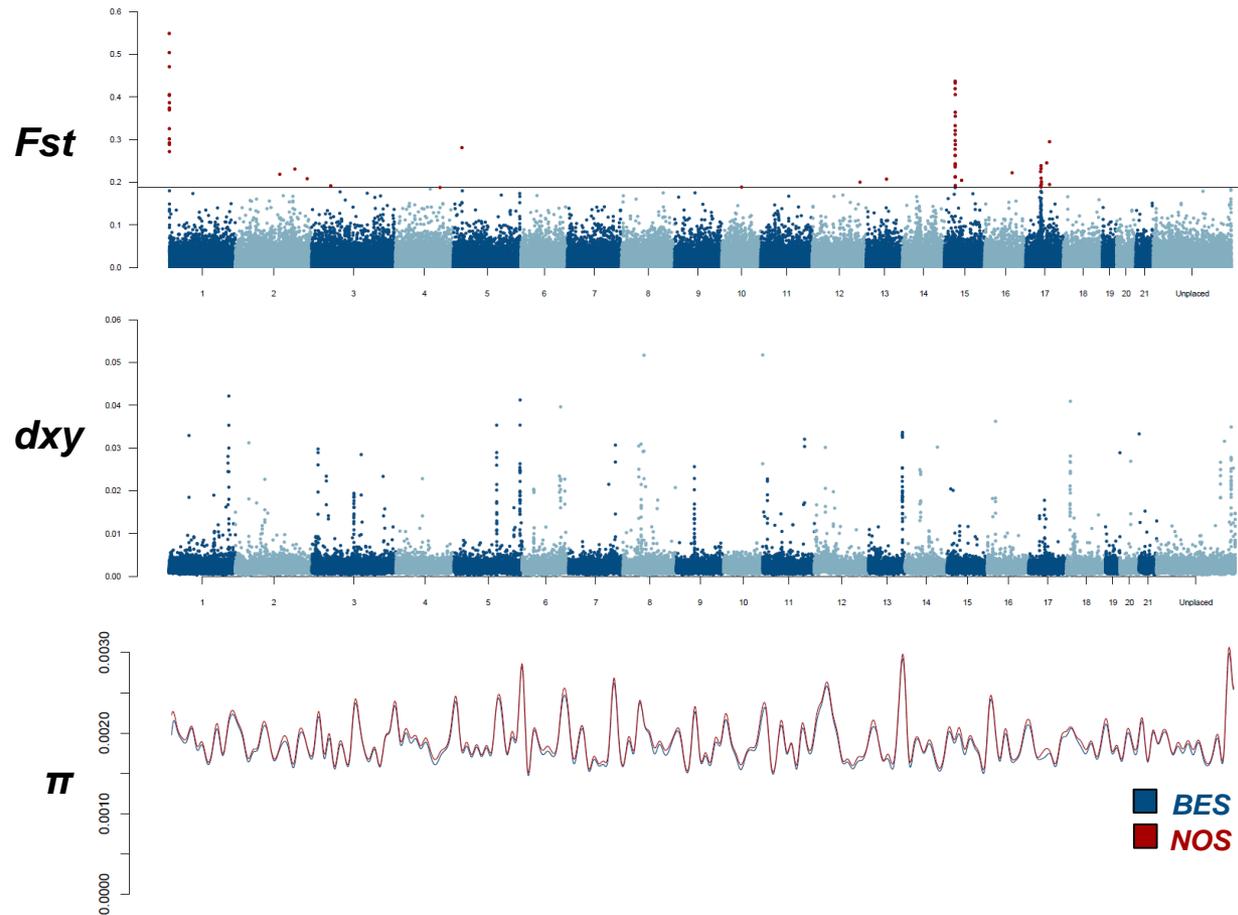


# Inferred population structure & demography



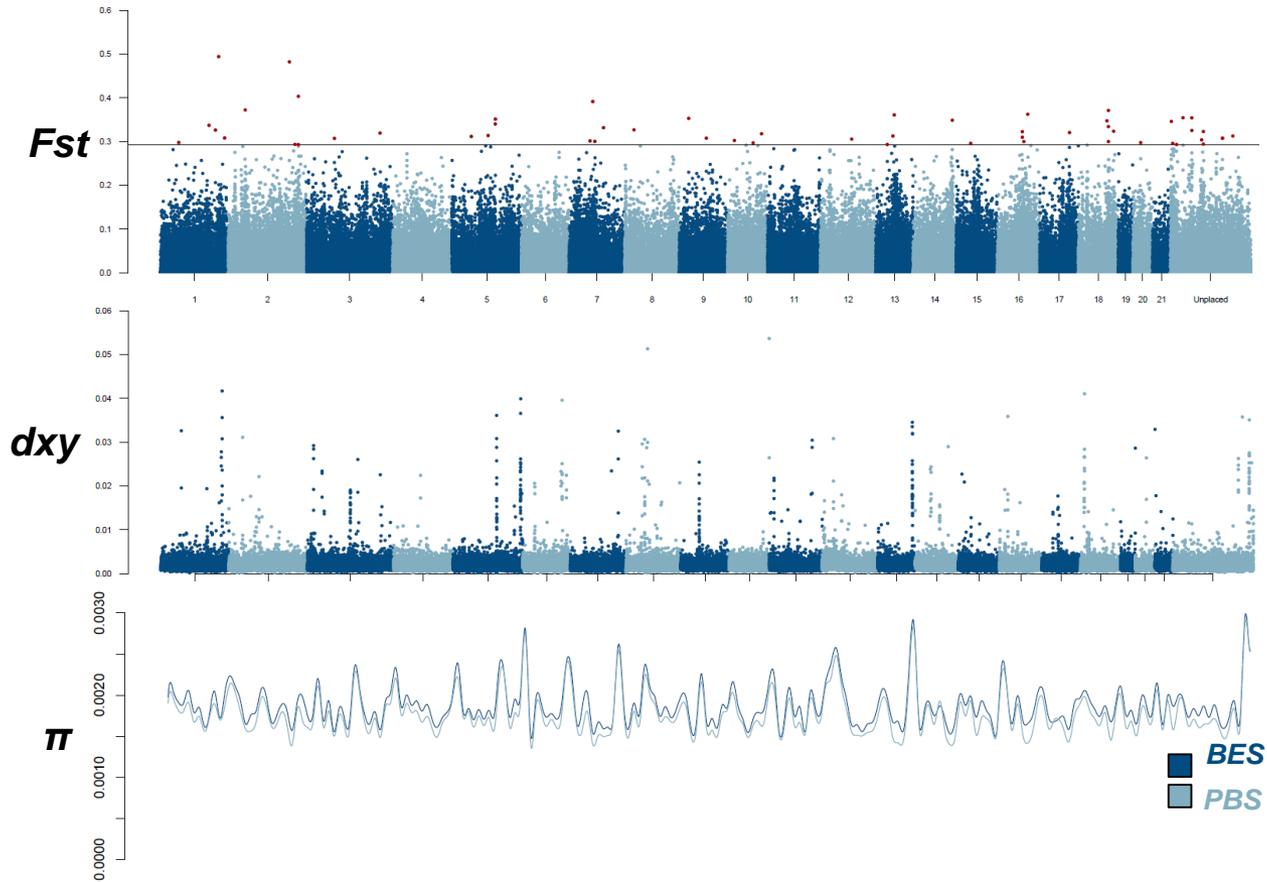


# Genomic landscape of NOS – BES





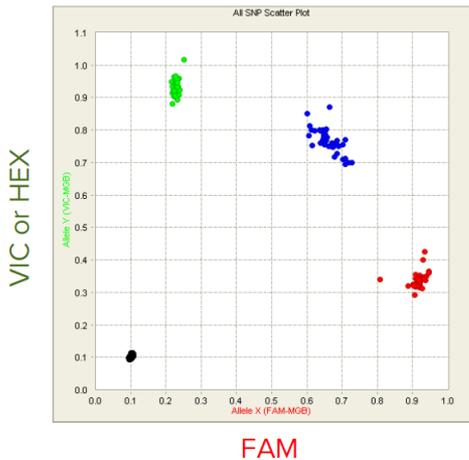
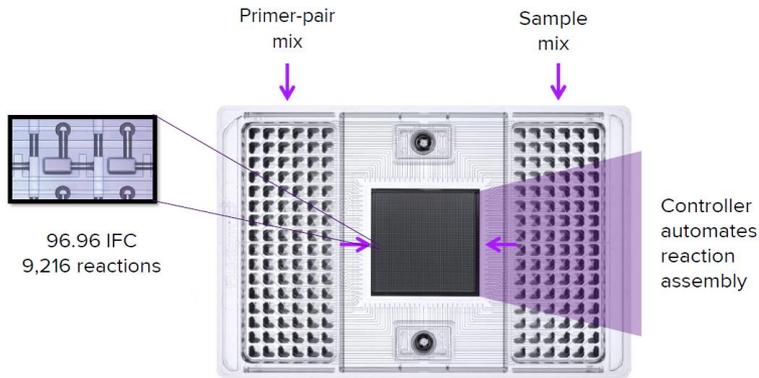
# Genomic landscape of BES – PBS



# ERECTION OF SNP PANEL- FLUIDIGM PLATFORM



- Fluidigm Integrated fluidic circuit (IFC)



- **XX** (homozygote)  
High – FAM  
Low – VIC or HEX
- **XY** (heterozygote)  
Intermediate – FAM  
Intermediate – VIC or HEX
- **YY** (homozygote)  
High – VIC or HEX  
Low – FAM

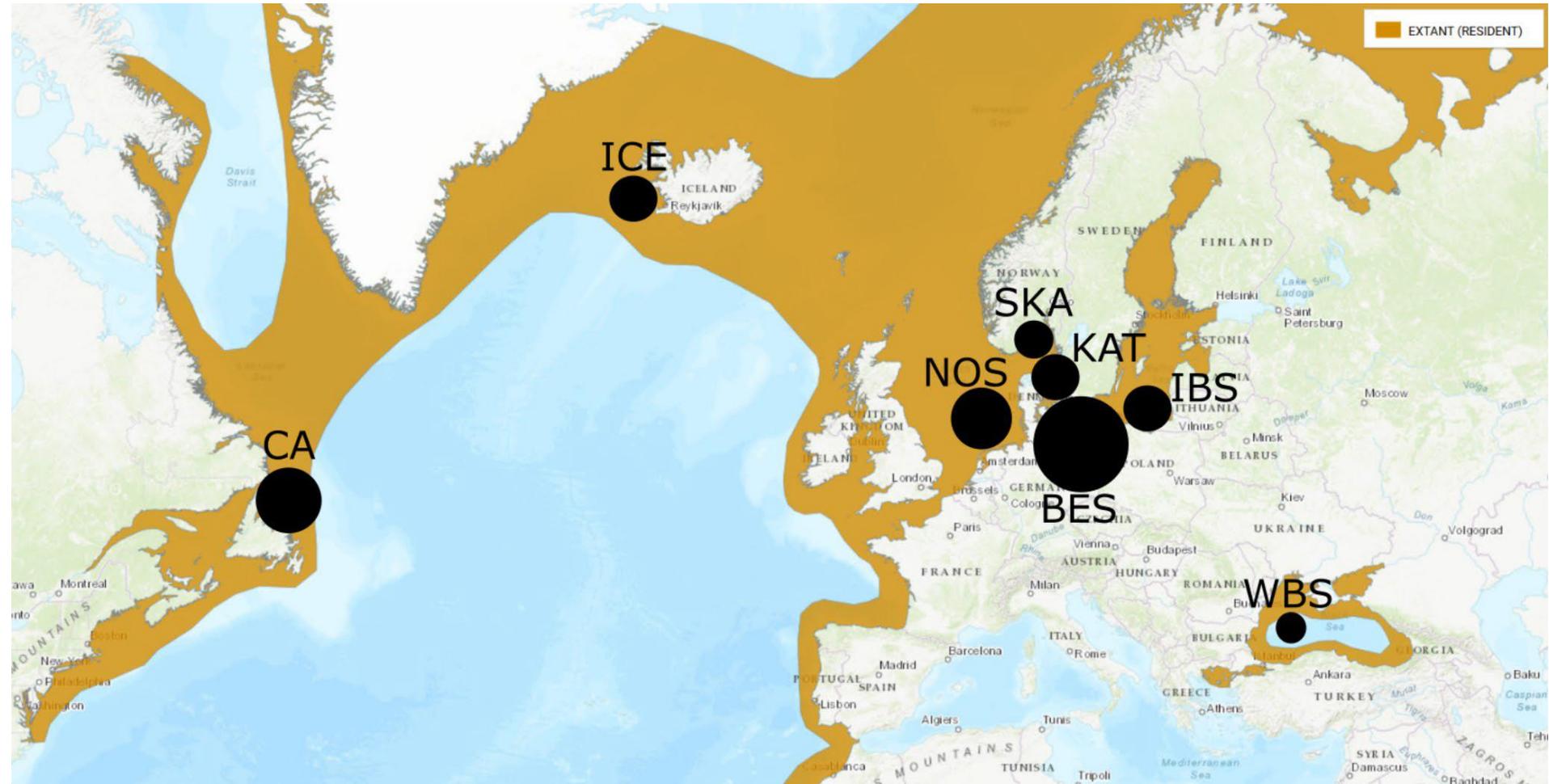
ASSAY ID	X	Y	ICE CA		NOS		SKA		BES		NTC		
			ICE	CA									
1	T	C	Blue	Blue	Blue	Blue	Green	Green	Blue	Blue	Blue	Grey	
2	T	A	Red	Red	Red	Red	Red	Green	Red	Blue	Blue	Grey	
3	C	T	Red	Red	Red	Blue	Red	Red	Grey	Blue	Blue	Grey	
4	G	T	Blue	Blue	Red	Blue	Red	Red	Red	Blue	Blue	Red	
5	A	T	Blue	Blue	Blue	Red	Grey	Red	Blue	Red	Red	Green	Grey
6	C	A	Red	Red	Blue	Red	Red	Blue	Red	Blue	Green	Red	Grey
7	T	G	Blue	Green	Blue	Blue	Green	Red	Green	Green	Green	Grey	
8	T	G	Red	Red	Red	Red	Red	Red	Blue	Blue	Red	Blue	Grey
8	A	G	Red	Red	Red	Red	Red	Red	Blue	Blue	Red	Blue	Grey
10	C	G	Blue	Red	Blue	Red	Red	Red	Blue	Green	Red	Blue	Red
11	A	G	Green	Green	Green	Green	Green	Green	Green	Red	Red	Blue	Grey
12	T	C	Grey	Red	Red	Grey	Grey	Red	Red	Grey	Grey	Grey	Grey

SNP 11 is informative regarding North vs. Belt sea



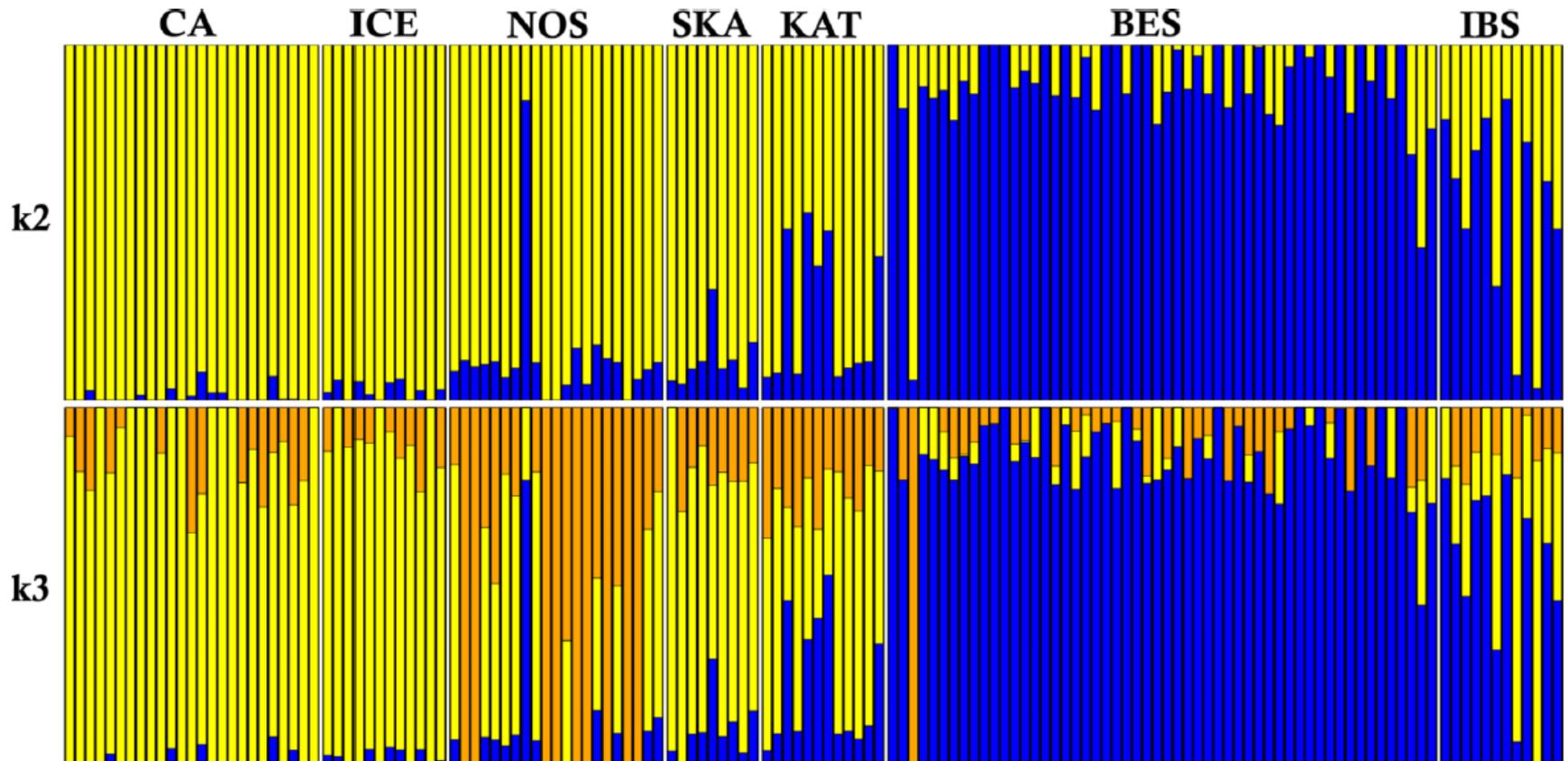


# ddRAD data: 11,978 SNPs from 150 individuals



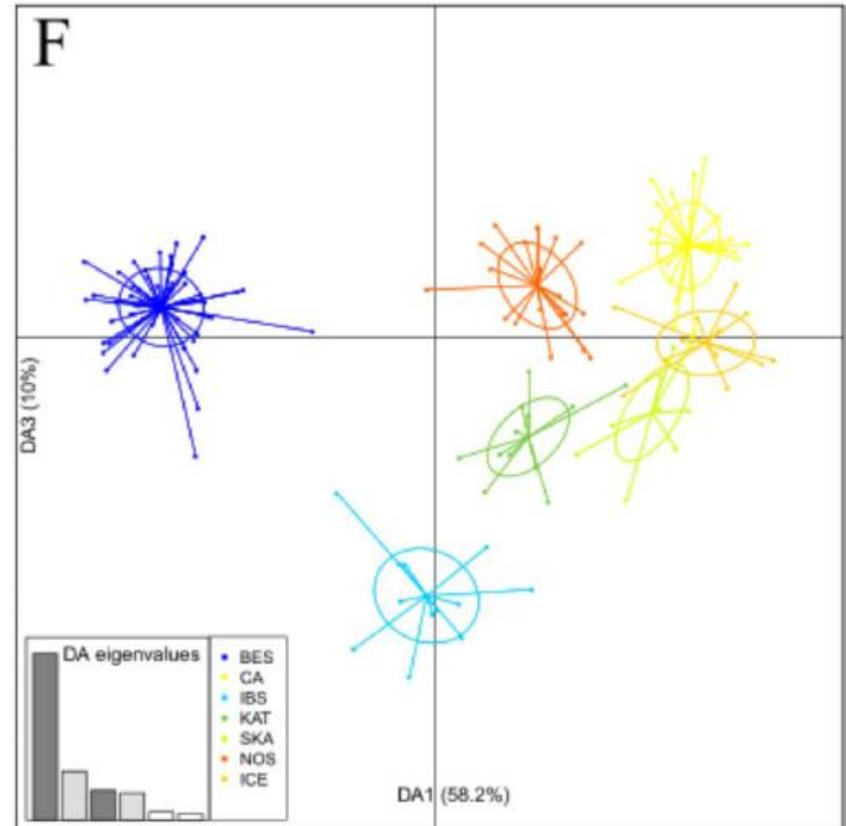
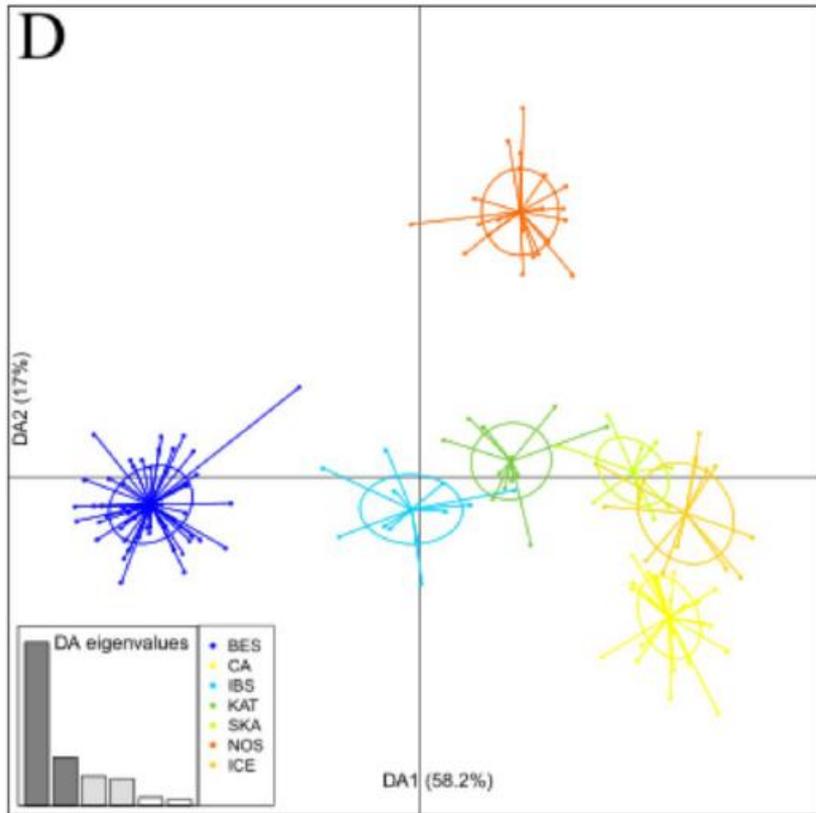


# Population assignment based on 11,978 SNPs





# Population assignment based on 11,978 SNPs



# GENOMICS AND LOCAL ADAPTATION IN HARBOUR PORPOISES OF THE NORTH ATLANTIC AND ADJACENT WATERS



- **Where are we?**

- Whole genome resequencing (n=72) provides highly resolved pop structure
- Porpoises similar across the entire North Atlantic, but highly differentiated in the Black Sea and the Baltic Sea
- Some differentiation within the North Sea
- Salinity has most impact on genotype (local adaptation)

- **What next?**

- Looking for candidate genes underlying local adaptation
- Mass typing to clarify pop admixture/seasonal movements
- Over 4000 samples spanning 4 decades yet untyped