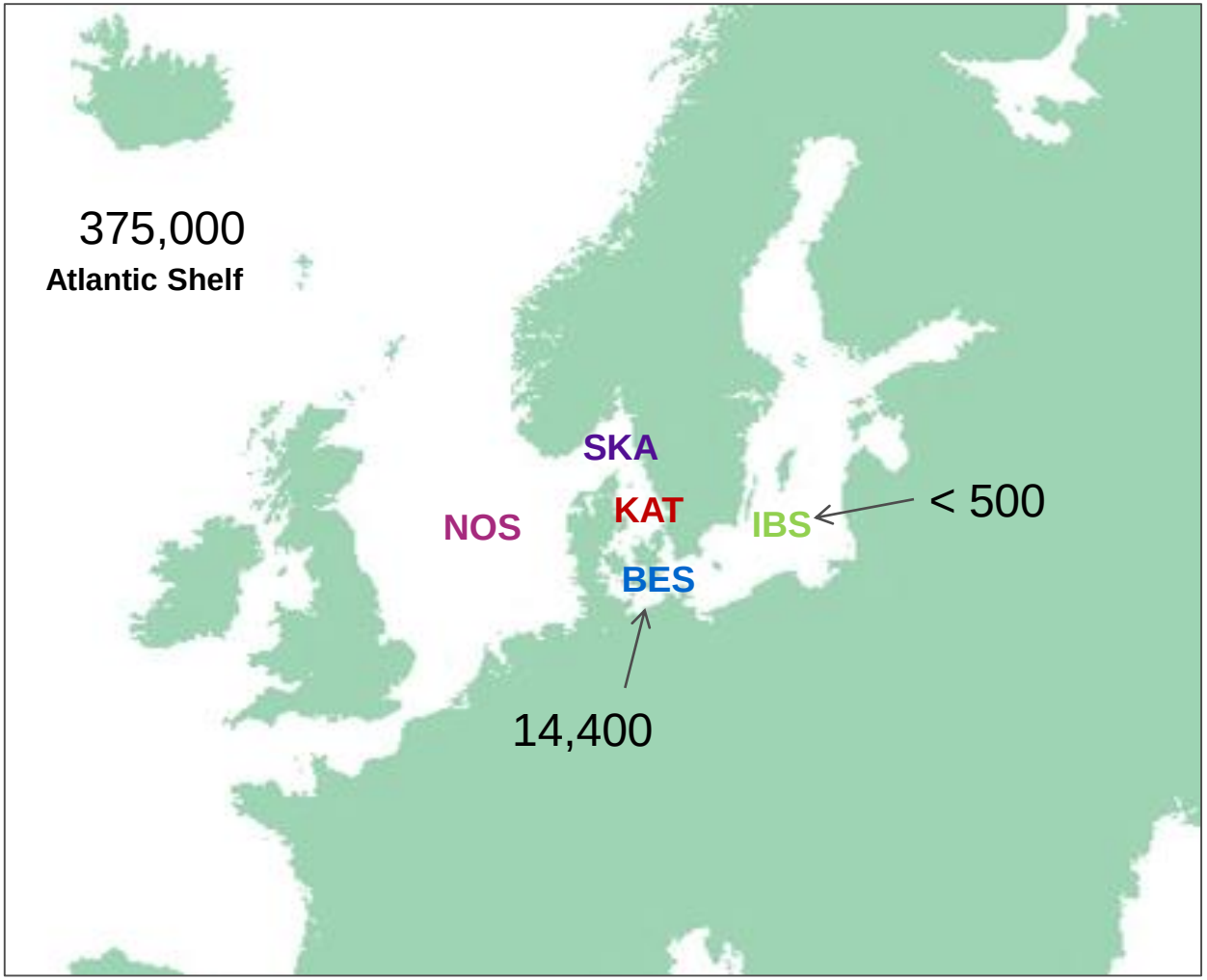


GENOMICS AND LOCAL ADAPTATION IN HARBOUR PORPOISES OF THE NORTH ATLANTIC AND ADJACENT WATERS

Tiedemann, R., **Tomowski, M., Celemín, E., Tiedemann, K.E., Havenstein, K.,** Autenrieth, M., Benke, H., Dähne, M., Denkinger, J., Dennis, A.B., Gunnlaugsson, Þ., Hartmann, S., Klemens, L., Lah, L., Pampoulie, C., Pawliczka, I., Roos, A., Sánchez, M.Q., Siebert, U., Sigurðsson, G.M., Víkingsson, G. (†), Westphal, L..

THE HARBOUR PORPOISE IN THE NORTH ATLANTIC AND ADJACENT WATERS





North Sea - **NOS**
Skagerrak - **SKA**
Kattegat - **KAT**
Belt Sea - **BES**
Inner Baltic Sea - **IBS**

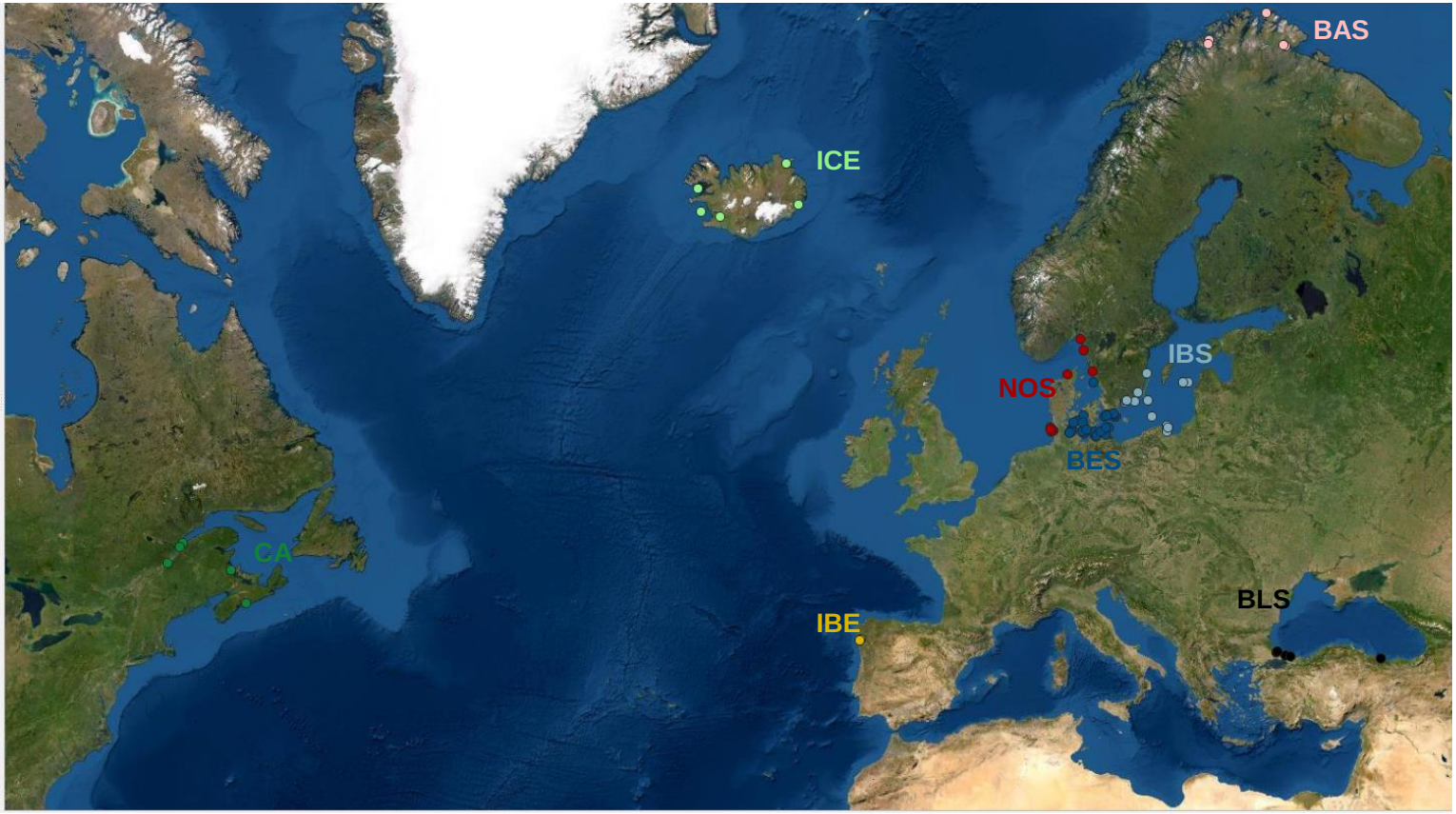
Baltic harbour porpoise

CR

(Phocoena phocoena)

74 Harbour porpoise whole genomes across the North Atlantic (mapped onto own reference genome)





- Canada
- Iceland
- Barents Sea
- North Sea
- Belt Sea
- Inner Baltic Sea
- Iberia
- Black Sea

BIOINFORMATIC PIPELINE – VARIANT CALLING



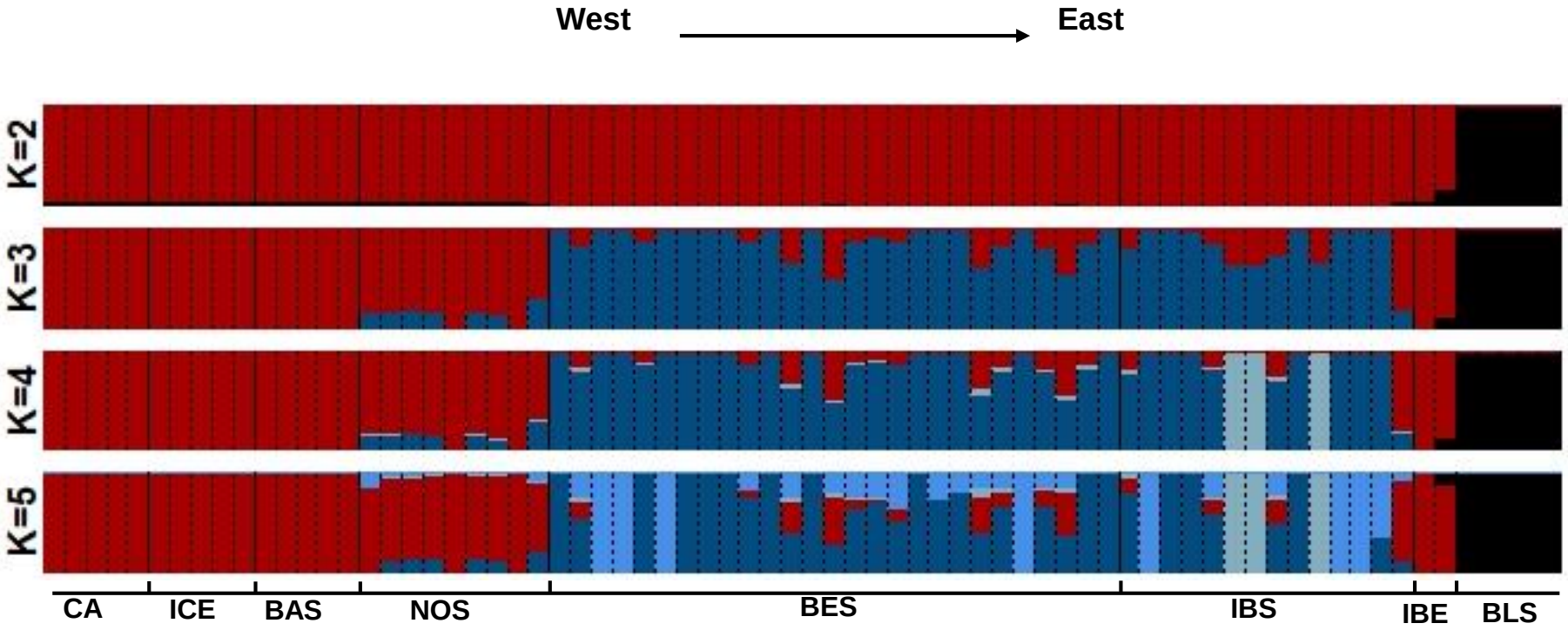
- Genotype likelihood estimation → *angsd*
- Linkage disequilibrium pruning → *ngsLD*
  - All 72 porpoises: *7,337,750 SNPs → 1,745,544 unlinked SNPs*
  - North Atlantic 67 porpoises: *7,404,321 SNPs → 1,741,332 unlinked SNPs*
  - Baltic 50 porpoises: ***7,674,541 SNPs → 1,506,953 unlinked SNPs***

- Genotype calling: → *bcftools mpileup* (26,198,530SNPs)
- 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

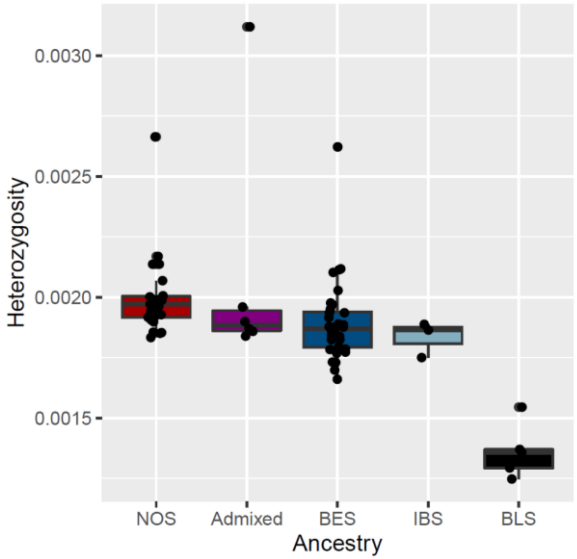
Population Structure – 72 unrelated porpoises





POPULATION GENOMICS – HETEROZYGOSITY





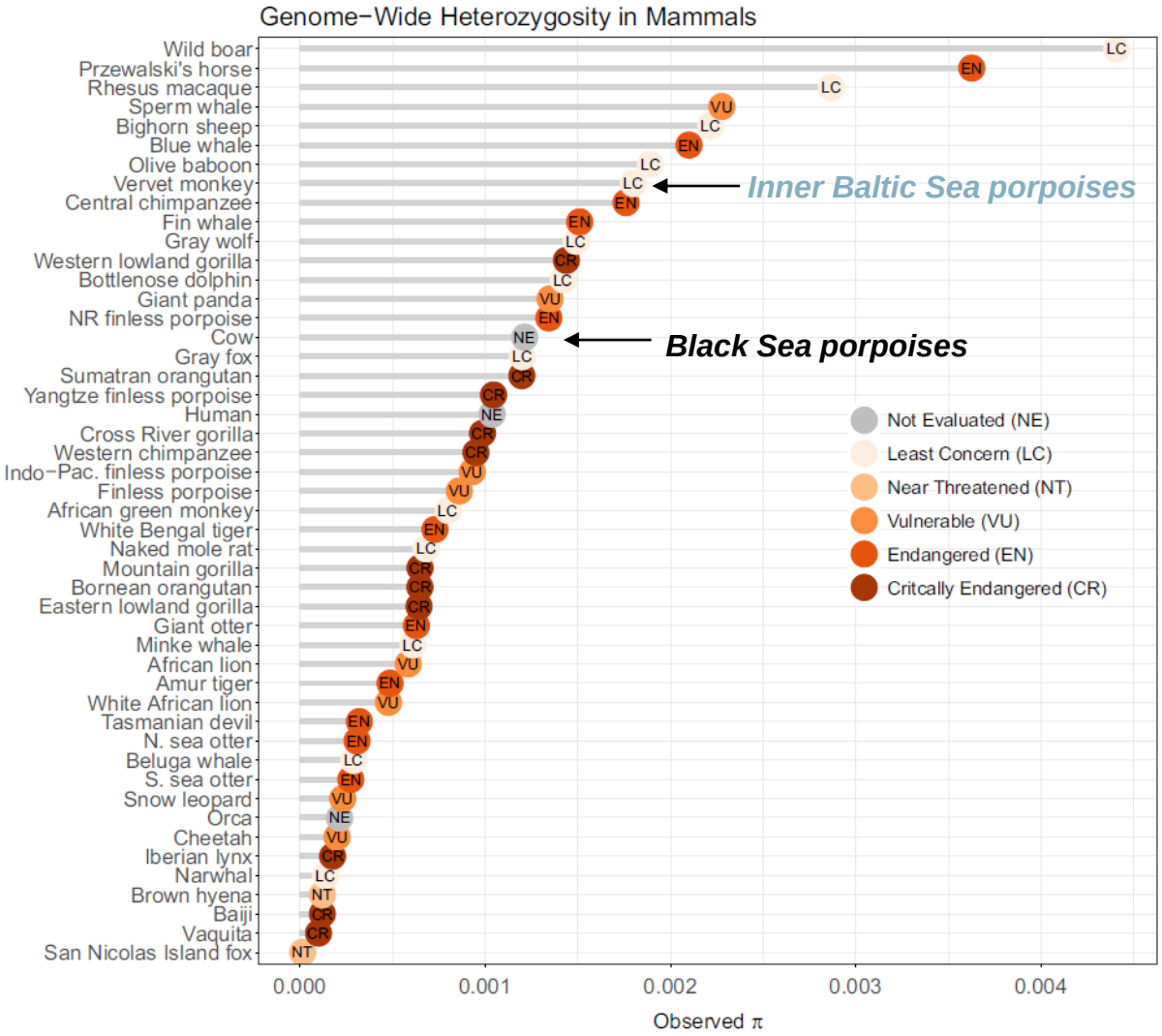
North Atlantic

Admixed

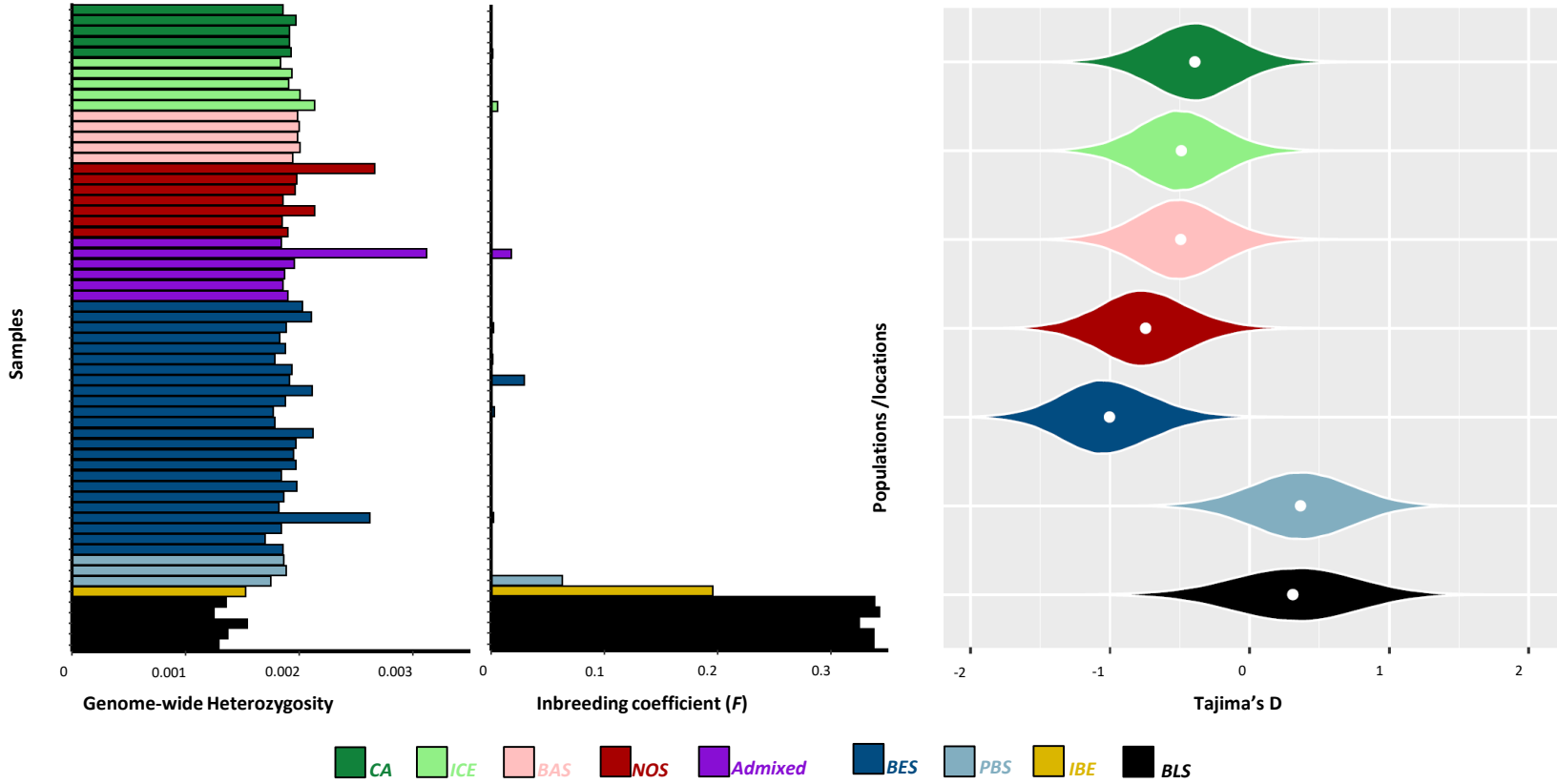
Belt Sea

Inner Baltic Sea

Black Sea



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

SALINITY MEAN IN THE NORTH ATLANTIC

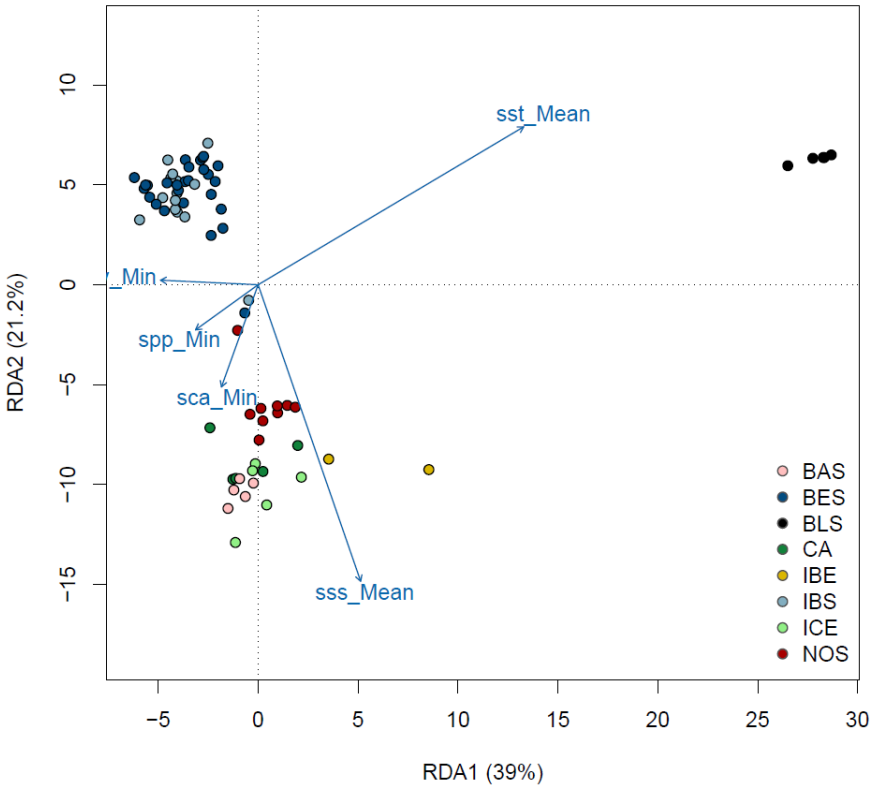




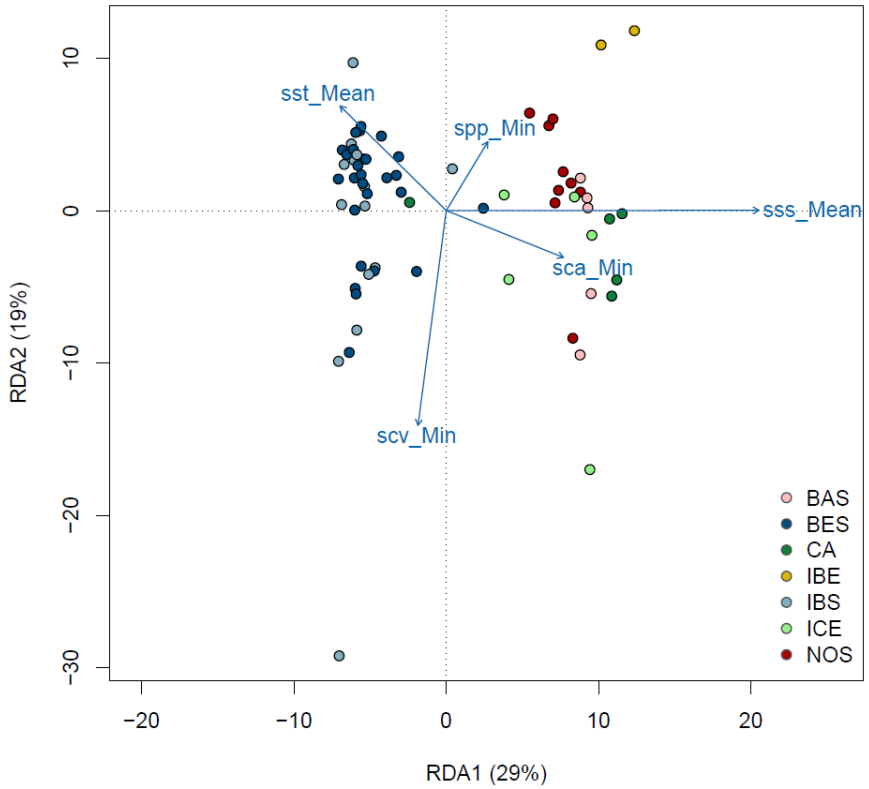
SEASCAPE GENOMICS – REDUNDANCY ANALYSIS



All



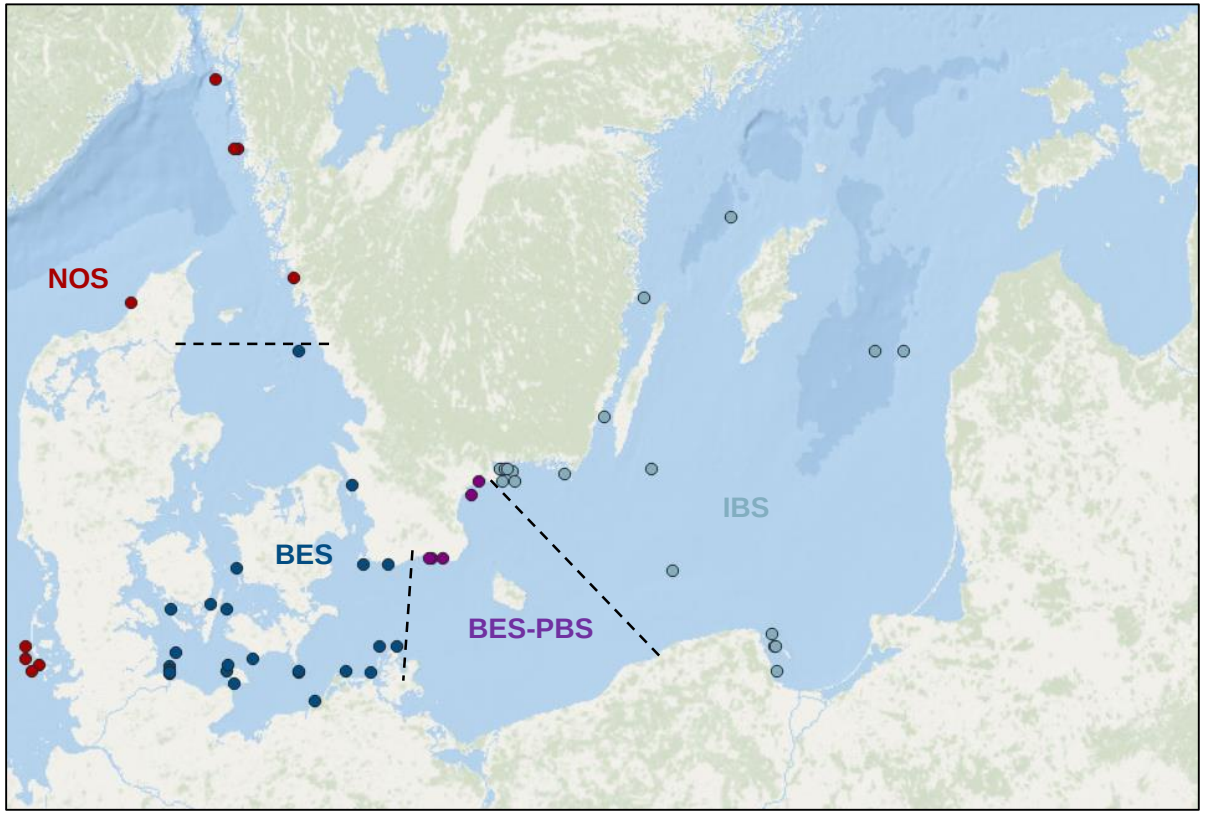
Without Black Sea



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





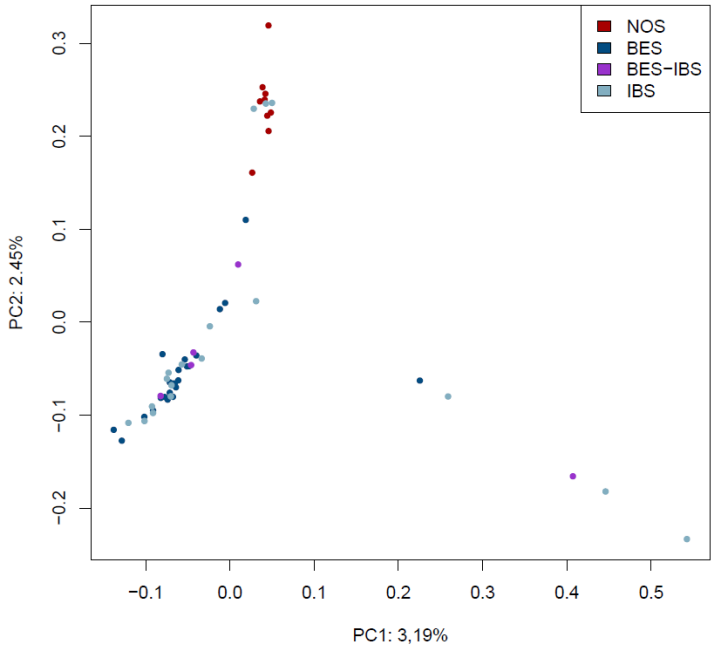
Colored by sampling location: *NOS* *BES* *BES-PBS* *PBS*

Objectives:

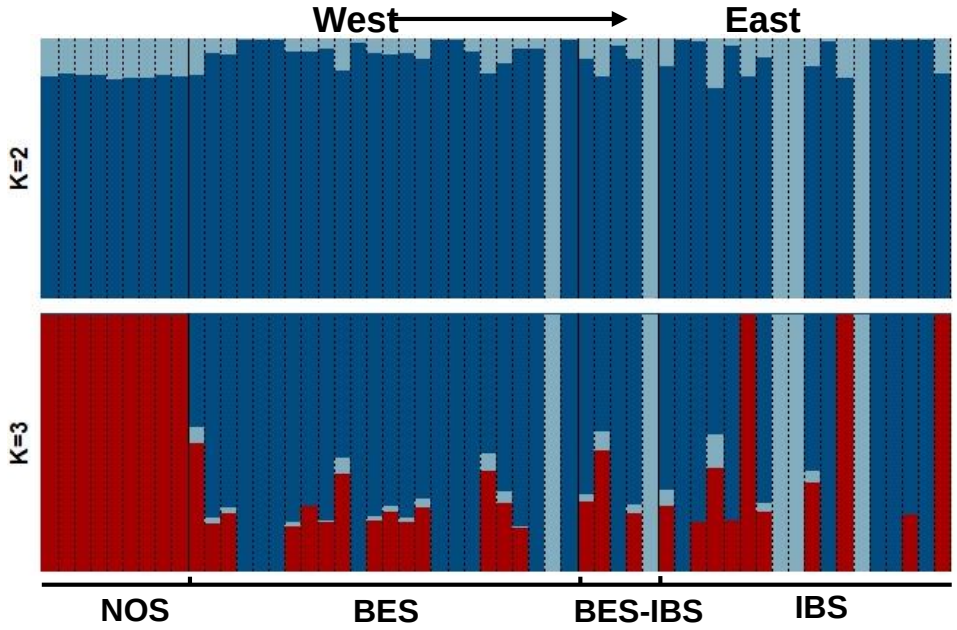
- Genomics:
  - Population structure in the Baltic
  - Role of selection and genetic drift on the origin and maintenance of the Baltic populations
  - Selective sweeps vs. outlier scan selection methods
- Genetics:
  - SNP panel for population assignment
  - Iterative SNP panel improvement
  - Genetic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



Structure-PCA WGS data



Colored by sampling location

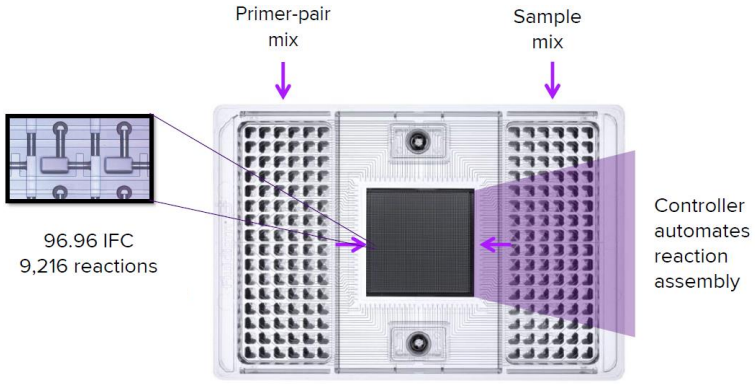


Colored by genomic ancestry

ERECTION OF SNP PANEL- FLUIDIGM PLATFORM

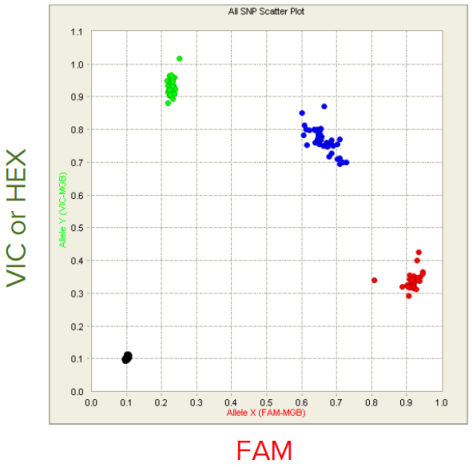


- Fluidigm Integrated fluidic circuit (IFC)

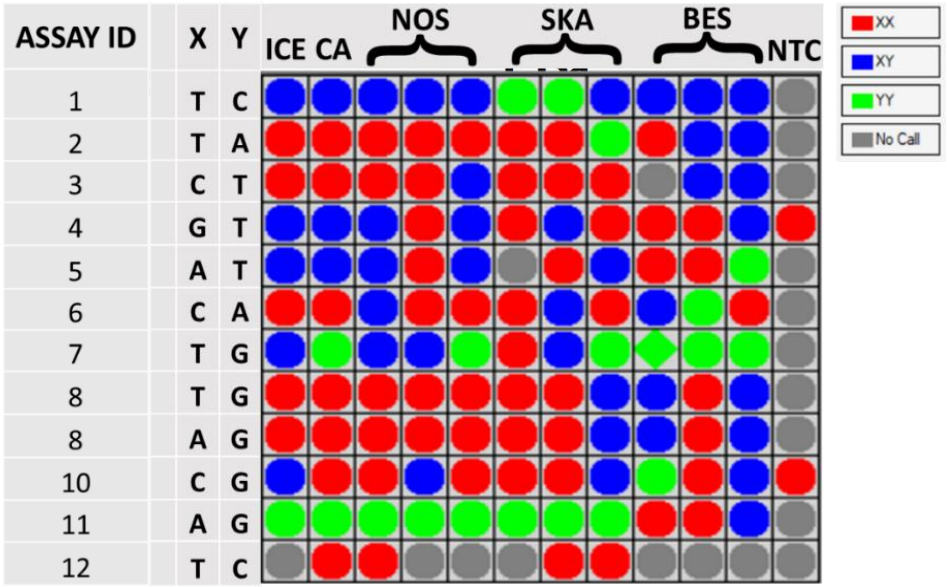






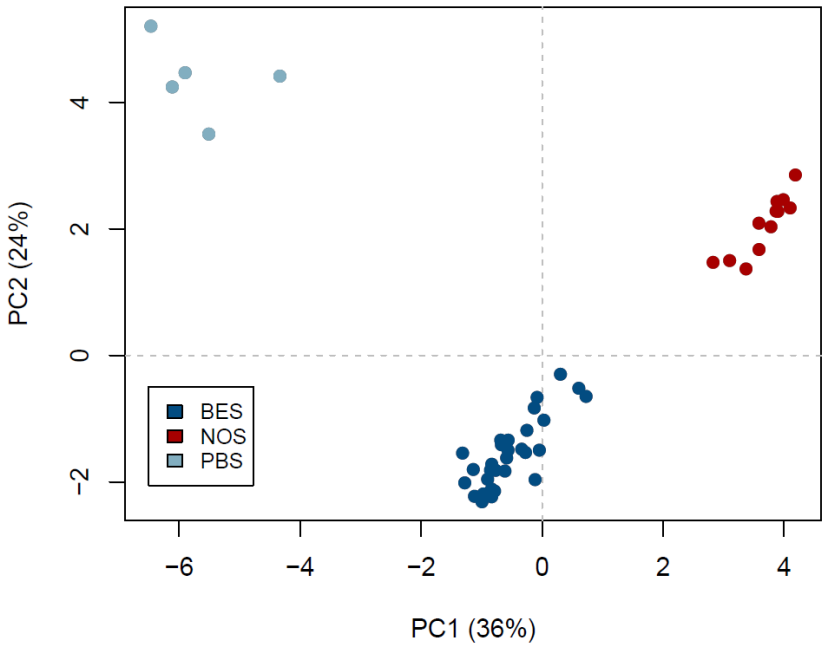


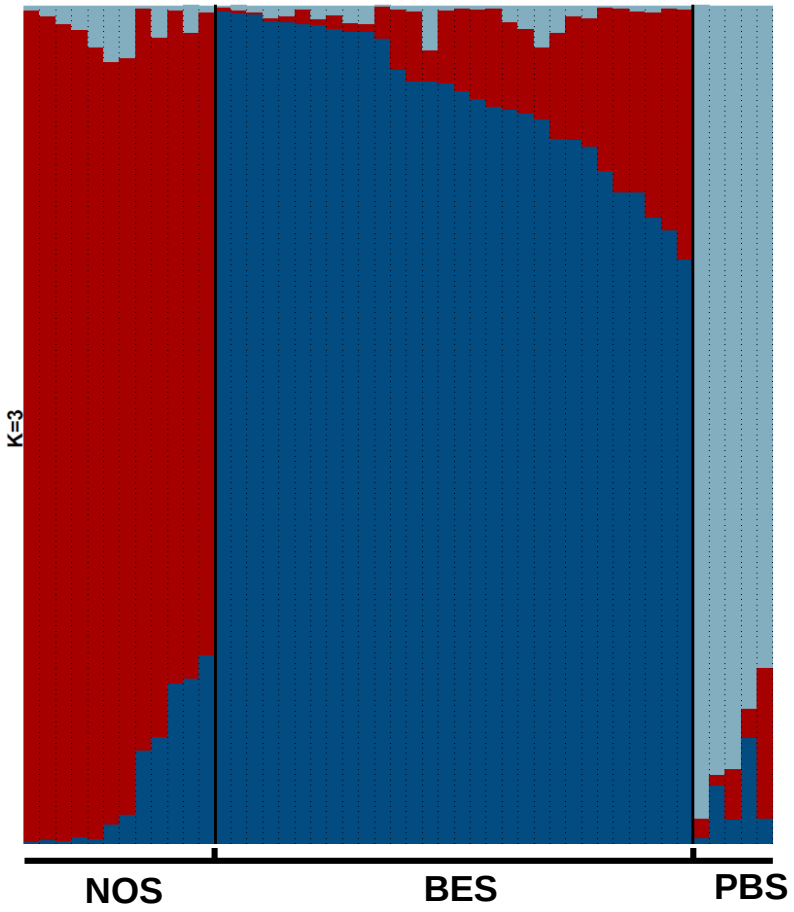
- **XX** (homozygote)
  High – FAM
  Low – VIC or HEX
- XY (heterozygote)
  Intermediate – FAM
  Intermediate – VIC or HEX
- YY (homozygote)
  High – VIC or HEX
  Low – FAM



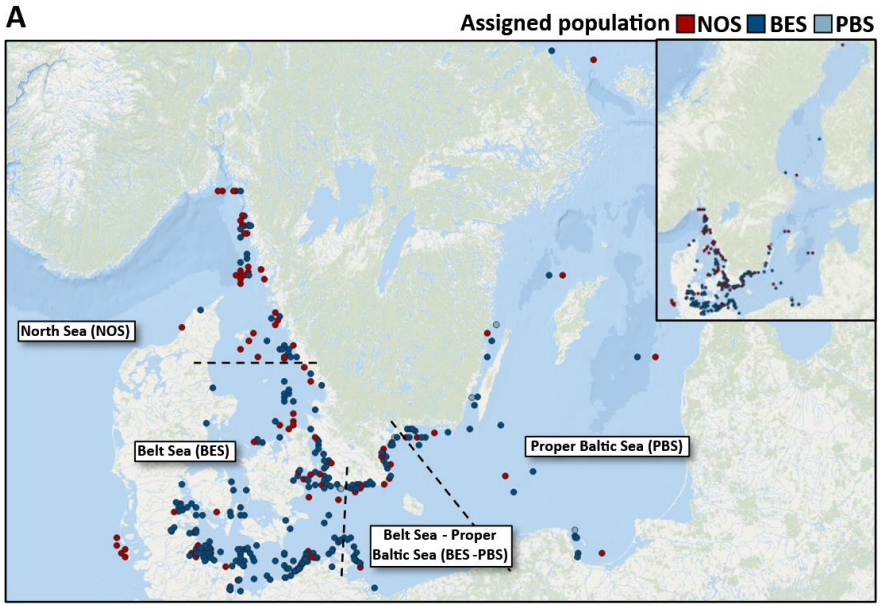
SNP 11 is informative regarding North vs. Belt sea

SNP Panel Evaluation - *PCA and Structure*





SNP Panel Results



	Assigned NOS	Assigned BES	Assigned PBS	
NOS region	37	25	0	**62**
BES region	30	199	3	**232**
BES-PBS region	8	34	1	**43**
PBS region	10	26	3	**39**
	85	**284**	**7**	

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
  - Salinity has most impact on genotype (local adaptation)

- **What next?**
  - Looking at candidate genes underlying local adaptation
  - Mass typing to clarify pop admixture/seasonal movements
  - Over 4000 samples spanning 4 decades yet untyped
  - Happy to type additional samples, if you want to join !!!