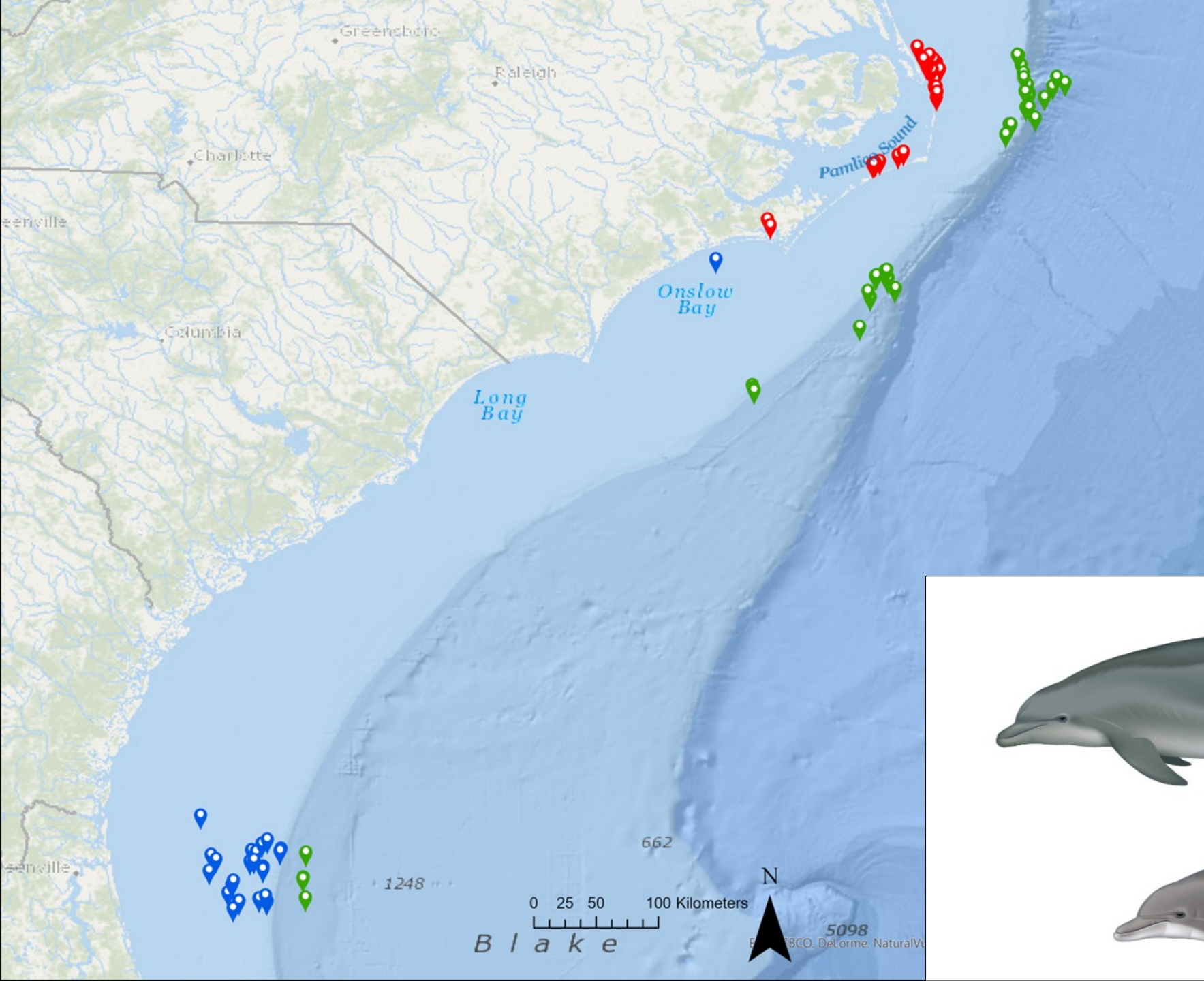


Population genetic structure of three distinct bottlenose dolphin (*Tursiops truncatus*) populations off North Carolina's coast

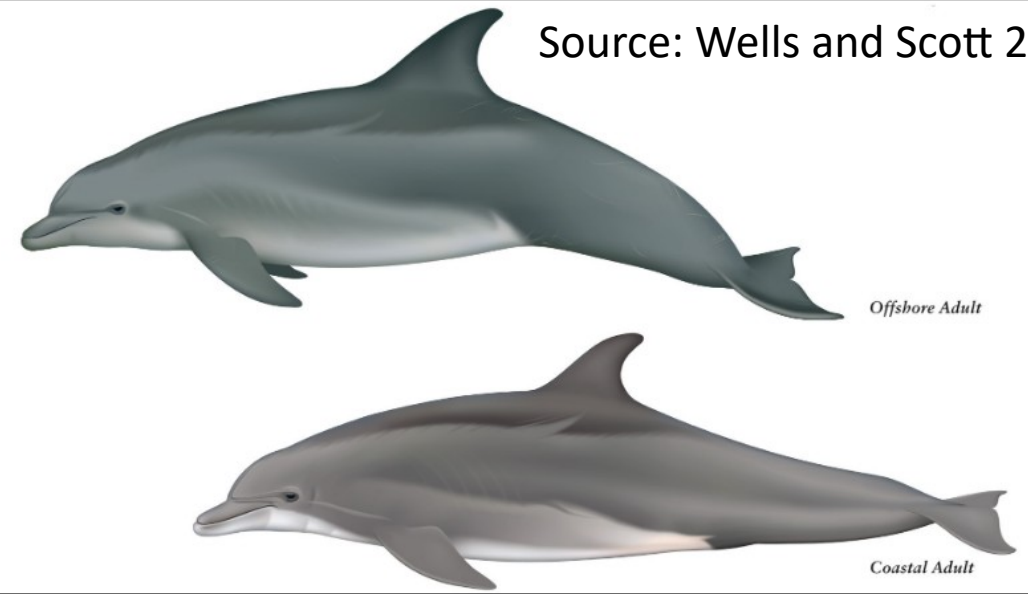
Christian Campbell, Tom Schultz

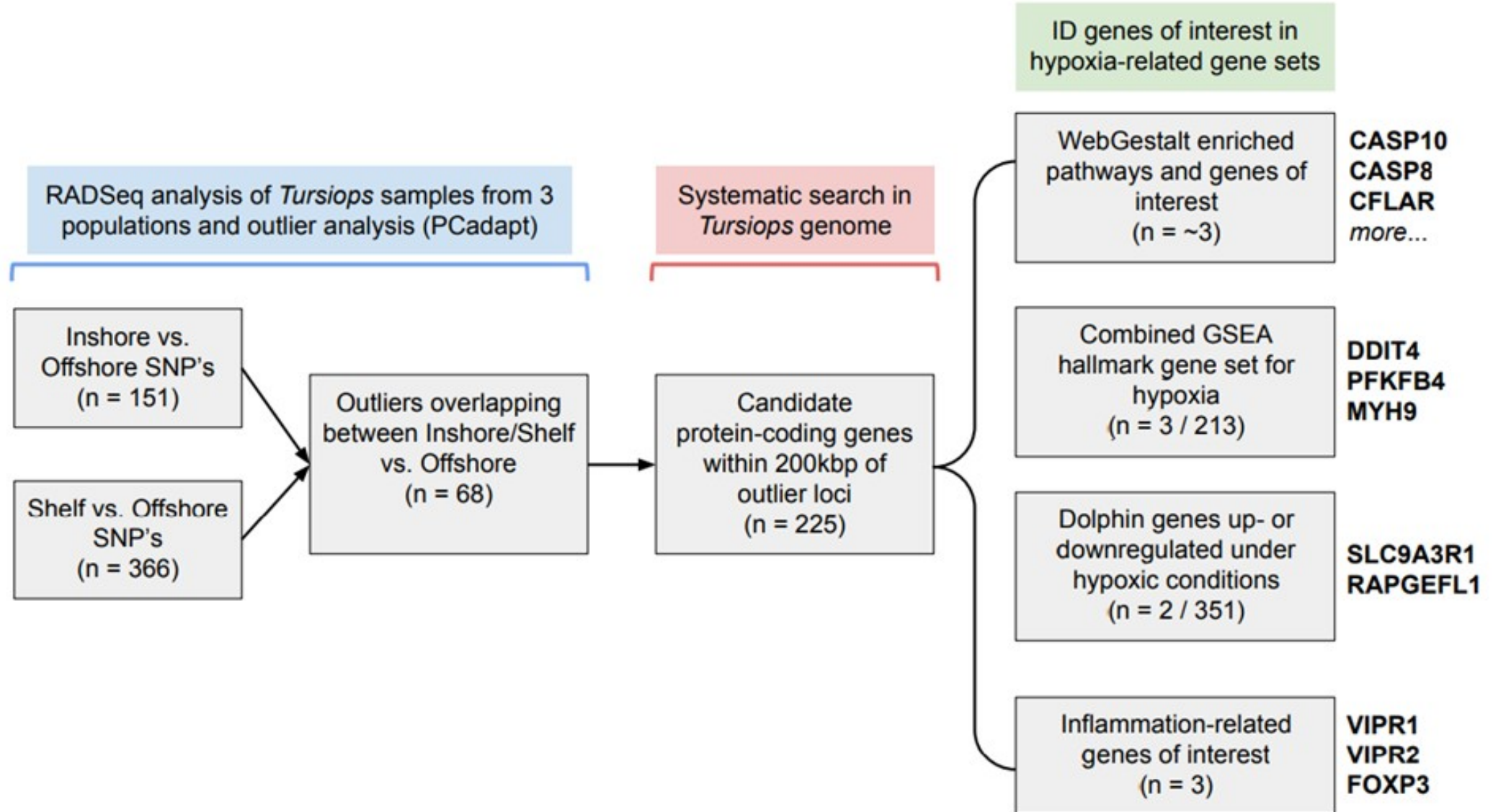


Population types

- Morphology driven by geography
- Independent life cycles

Source: Wells and Scott 2018





We want to identify regions under selection in bottlenose dolphins and assess the level of differentiation between each population

1 AGATCGCTGC

2 AGATCGCTTC

NUCLEOTIDE DIVERSITY IS AKA PI

4 AGATCGCTTC

5 AGATCGCTTC

AGATCGCTGCATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCG
AGATCGCTGCATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCG
AGATCGCTGCATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCG
AGATCGCTGCATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCG
AGATCGCTGCATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCG

[illegible][illegible][illegible]

5KB window

1 AGATCGCTGCATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGAGAA
2 AGATCGCTGCATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGAGAA
3 AGATCGCTGCATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGAGAA
4 AGATCGCTGCATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGAGAA
5 AGATCGCTGCATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGATCGCTGAGAA

The diagram illustrates five identical DNA sequences, each 60 nucleotides long. The sequences are listed vertically from 1 to 5. A vertical blue bar spans across all five sequences, highlighting the first 10 nucleotides: AGATCGCTGC.

5KB window

[illegible]

5KB window

[illegible]

5KB window

[illegible]

5KB window

[illegible]

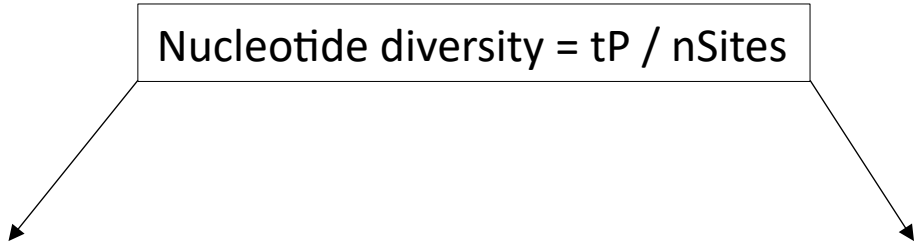
2.3 BILLION bp genome

ANGSD pipeline to calculate nucleotide diversity (π)

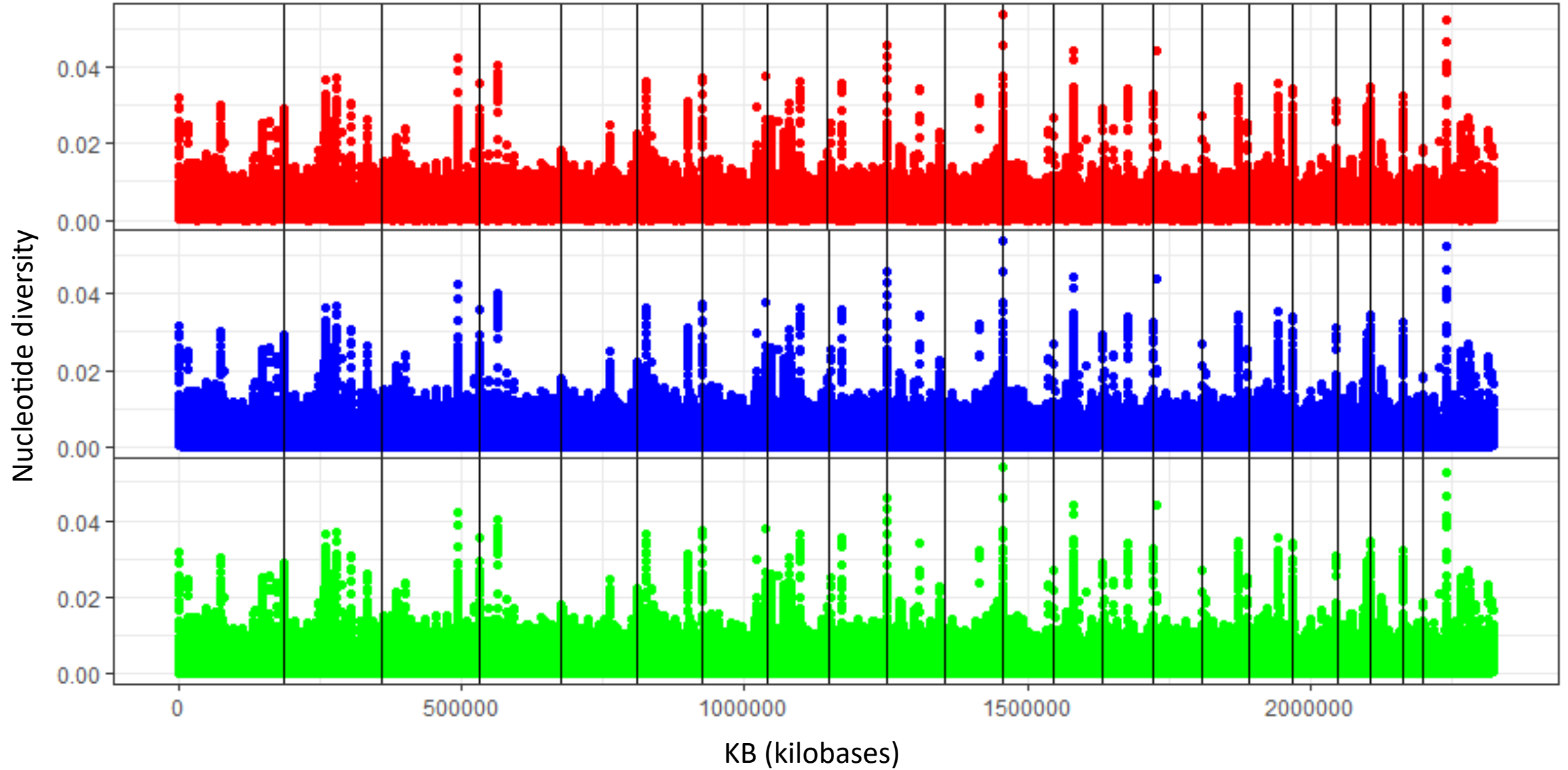


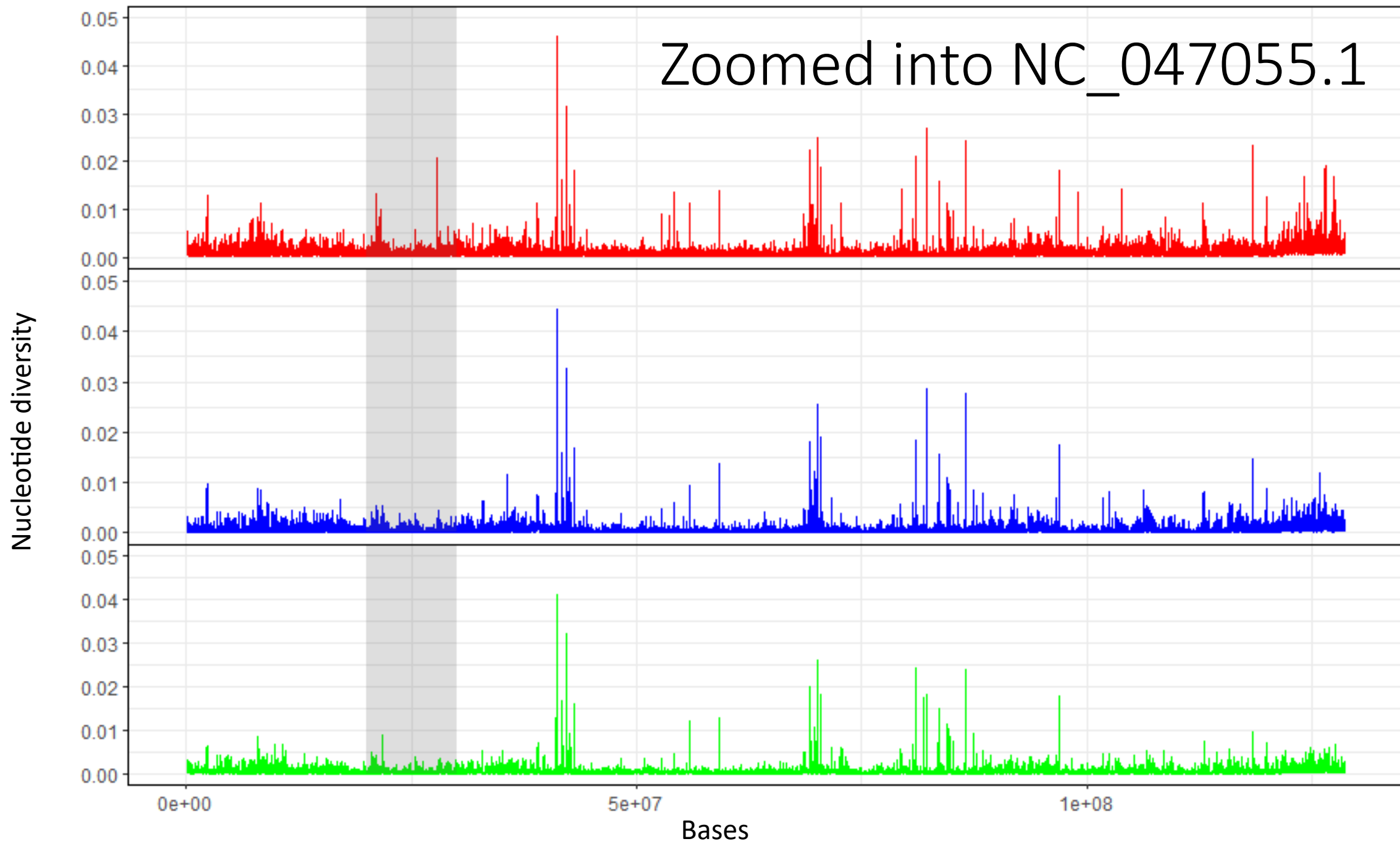
5kb sliding window results

Nucleotide diversity = $tP / nSites$

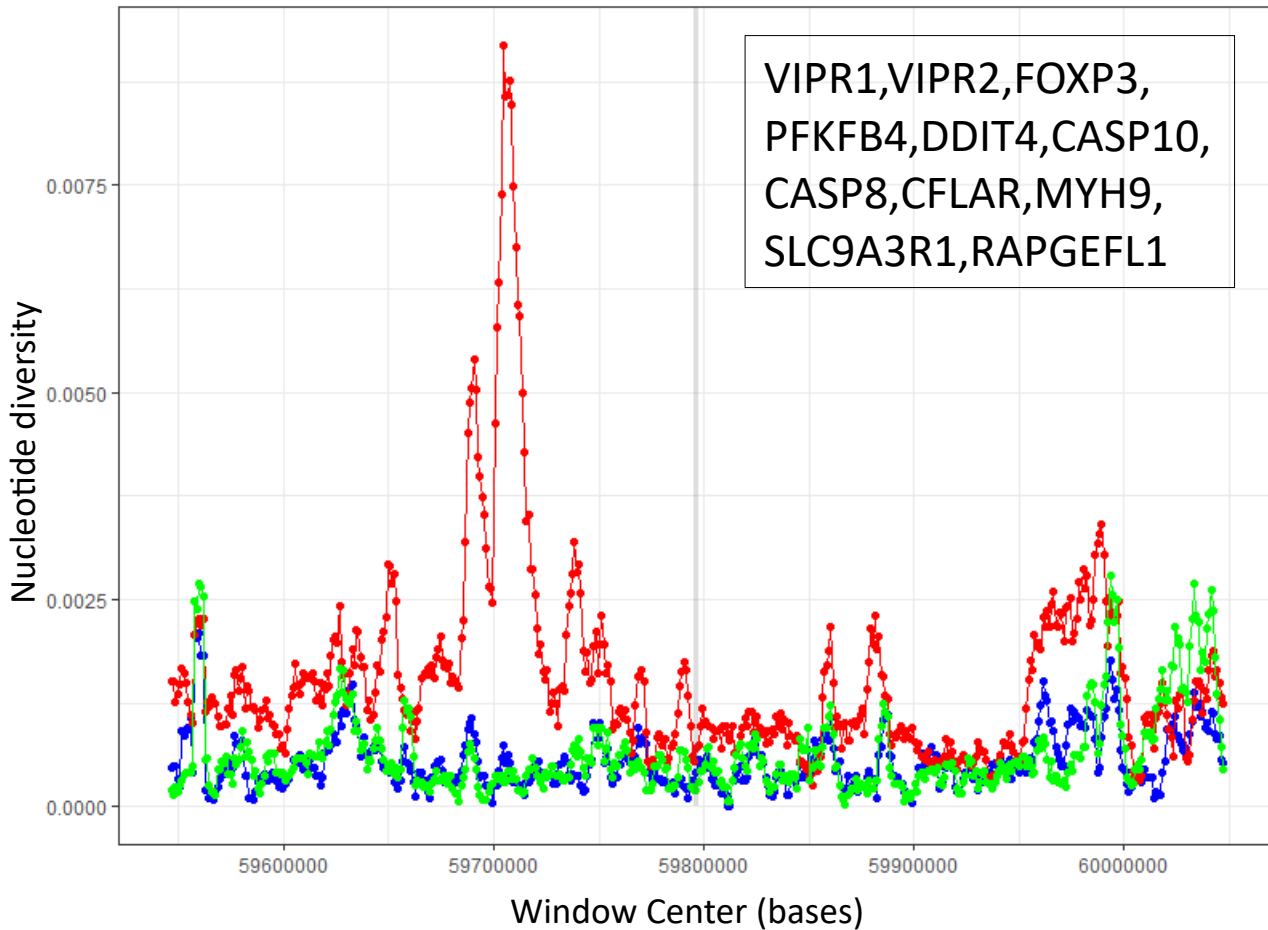


#(indexStart,indexStop)(firstPos_withData,lastPos_withData)(WinStart,WinStop)	Chr	WinCenter	tW	tP	tF	tH	tL	Tajima	fuf	fud	fayh	zeng	nSites
(999,5820)(1000,6000)(1000,6000)	NC_012059.1	3500	10.59177	11.5653	0	0	0	0.485574	1.896107	1.950938	1.636241	-1.759843	4821
(1999,6820)(2000,7000)(2000,7000)	NC_012059.1	4500	13.671764	14.989551	0	0	0	0.513831	1.943745	1.994389	1.657673	-1.788442	4821
(2999,7820)(3000,8000)(3000,8000)	NC_012059.1	5500	17.142838	18.846694	0	0	0	0.533243	1.978439	2.026419	1.672737	-1.8092	4821
(3999,8820)(4000,9000)(4000,9000)	NC_012059.1	6500	17.914188	19.703837	0	0	0	0.536562	1.984471	2.032005	1.675317	-1.812792	4821
(4820,9820)(5000,10000)(5000,10000)	NC_012059.1	7500	18.512379	20.214275	0	0	0	0.494153	1.973766	2.036046	1.66447	-1.815386	5000
(5820,10820)(6000,11000)(6000,11000)	NC_012059.1	8500	21.212121	23.392857	0	0	0	0.554262	2.007748	2.05167	1.686041	-1.825373	5000
(6820,11820)(7000,12000)(7000,12000)	NC_012059.1	9500	24.683195	27.25	0	0	0	0.562282	2.02403	2.067082	1.692716	-1.835161	5000
(7820,12820)(8000,13000)(8000,13000)	NC_012059.1	10500	24.29752	26.821429	0	0	0	0.561502	2.022436	2.065572	1.692066	-1.834205	5000
(8820,13820)(9000,14000)(9000,14000)	NC_012059.1	11500	24.29752	26.821429	0	0	0	0.561502	2.022436	2.065572	1.692066	-1.834205	5000
(9820,14820)(10000,15000)(10000,15000)	NC_012059.1	12500	25.454545	28.285715	0	0	0	0.601726	2.03996	2.069975	1.70472	-1.836991	5000
(10820,15820)(11000,16000)(11000,16000)	NC_012059.1	13500	30.854053	34.491213	0	0	0	0.639692	2.0674	2.0864	1.720096	-1.847341	5000
(266,284)(1000,13687)(1000,6000)	NC_047034.1	3500	0.025036	0.024603	0	0	0	-0.015531	0.194387	0.215779	0.252016	-0.226367	18

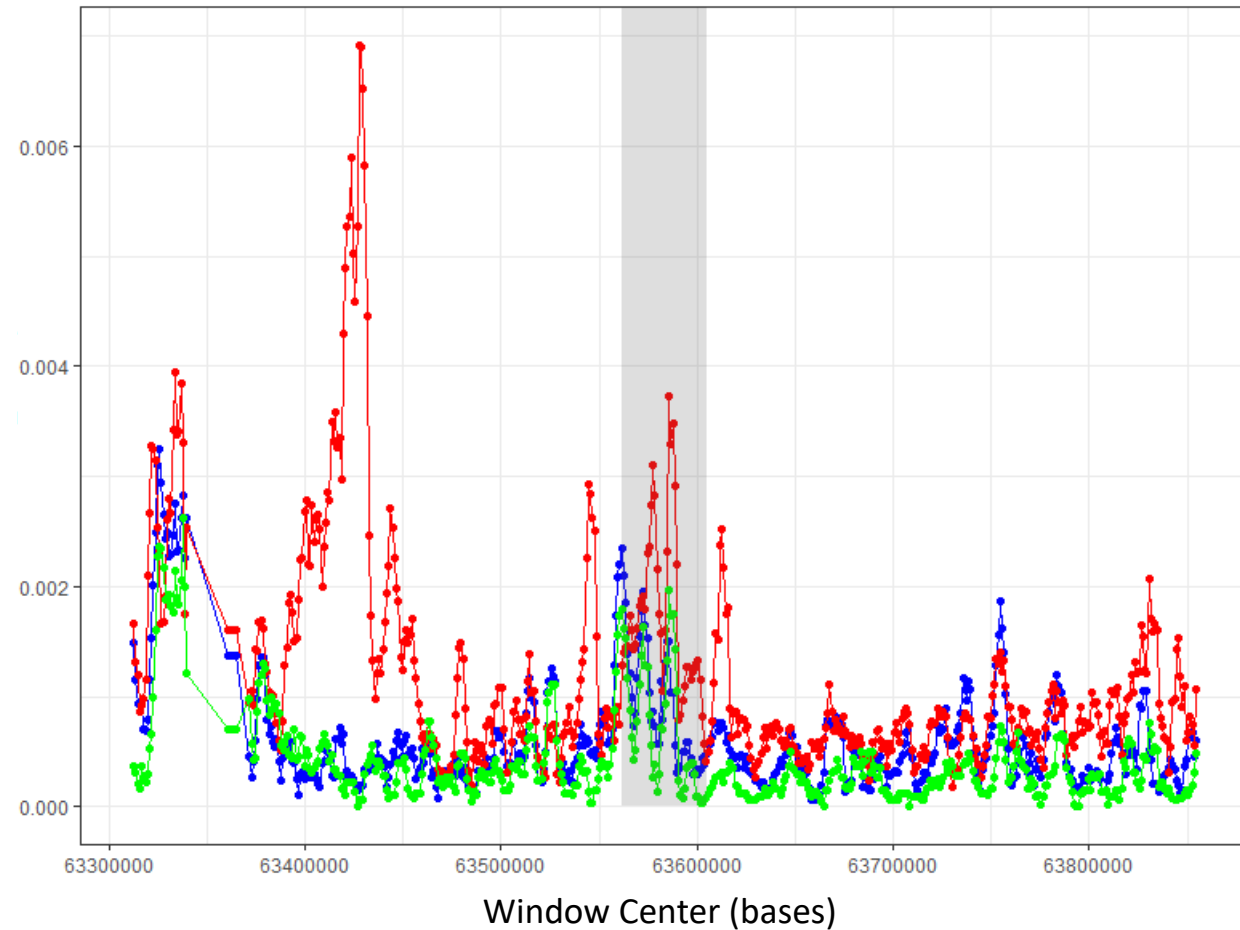




DDIT4 NC_047049.1 green=ins, red=off, blue=cstl



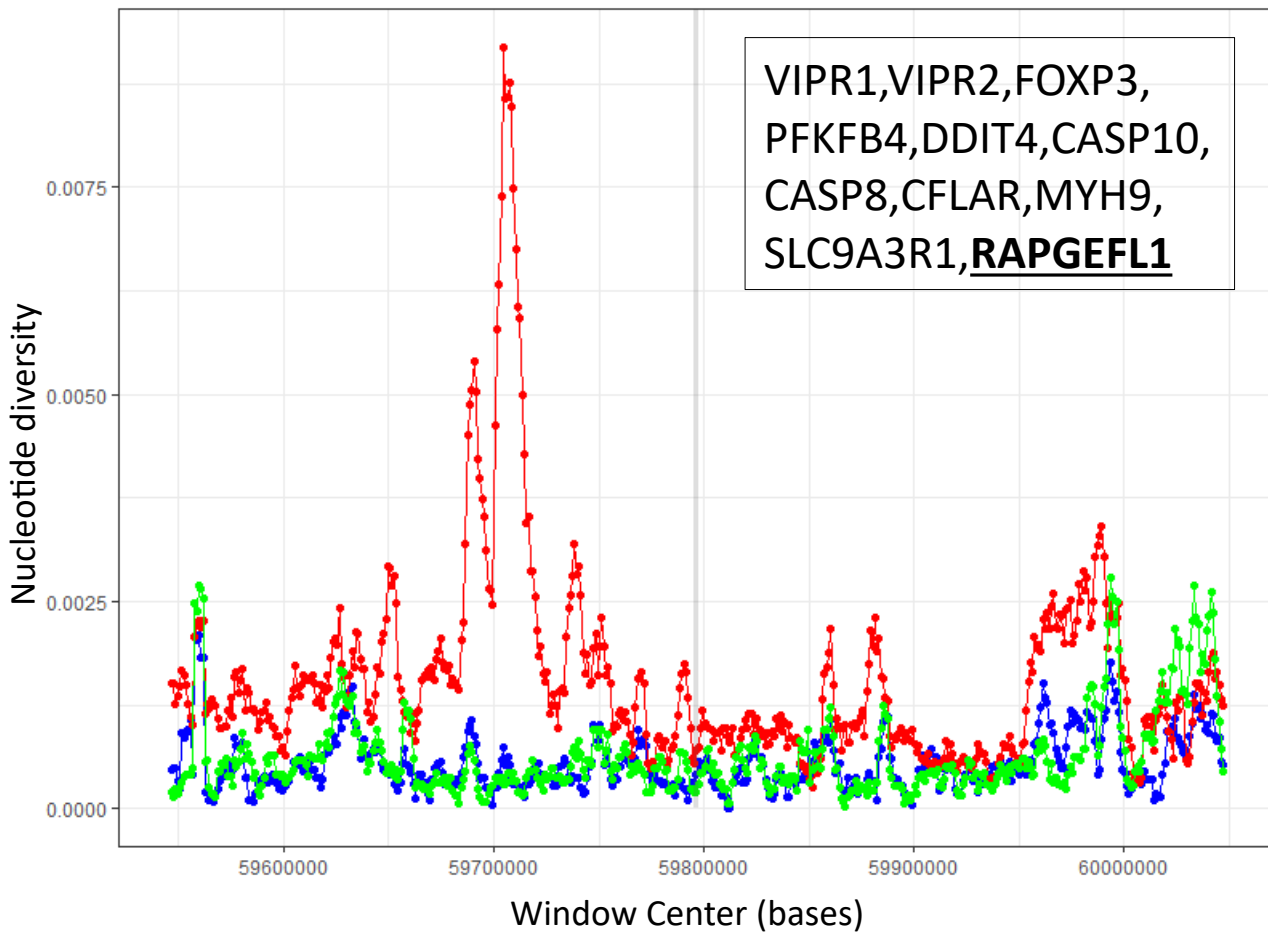
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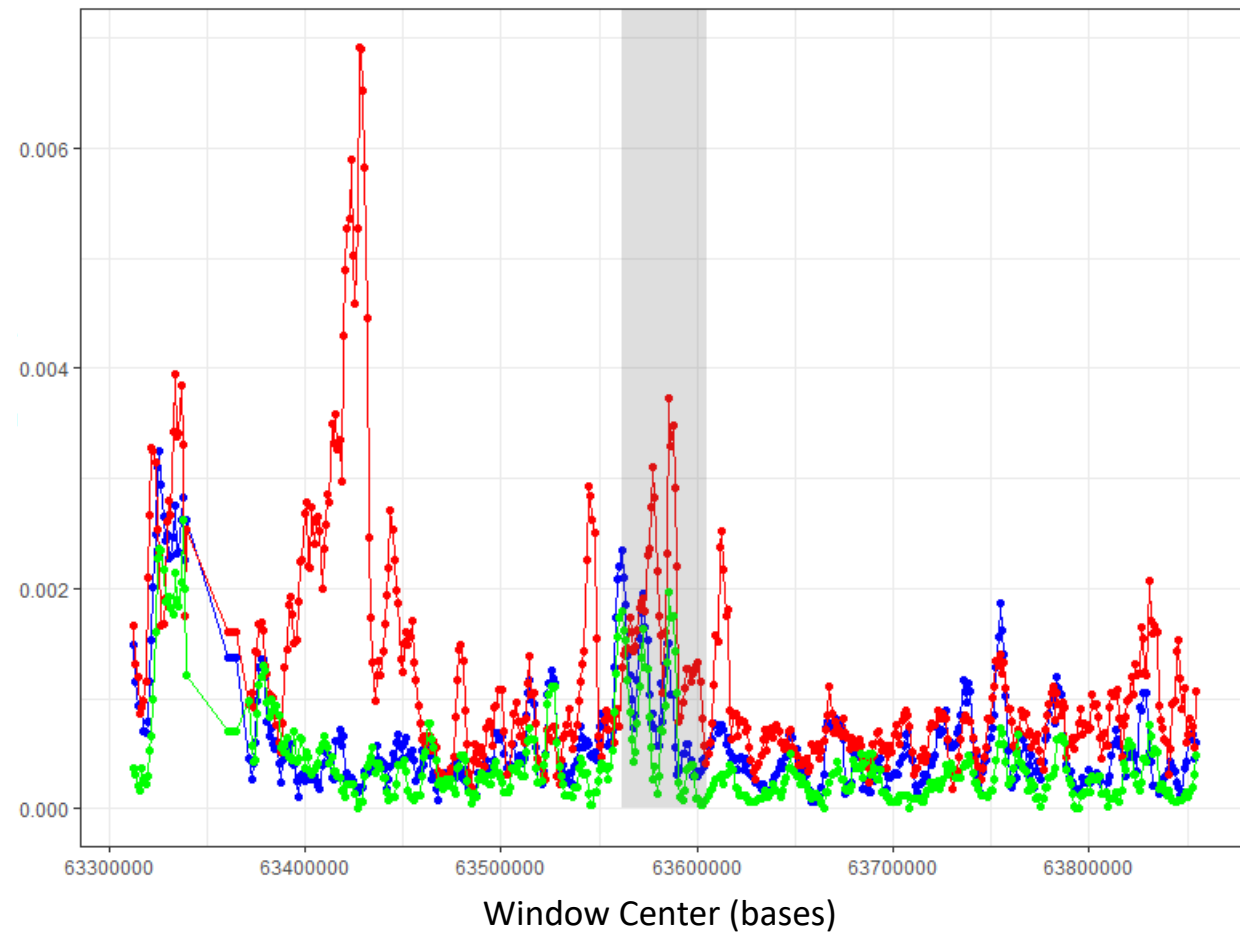
Pi per gene in a
500kb window

- Selective sweeps
- 11 genes
- Some selective pressure only in offshore

DDIT4 NC_047049.1 green=ins, red=off, blue=cstl

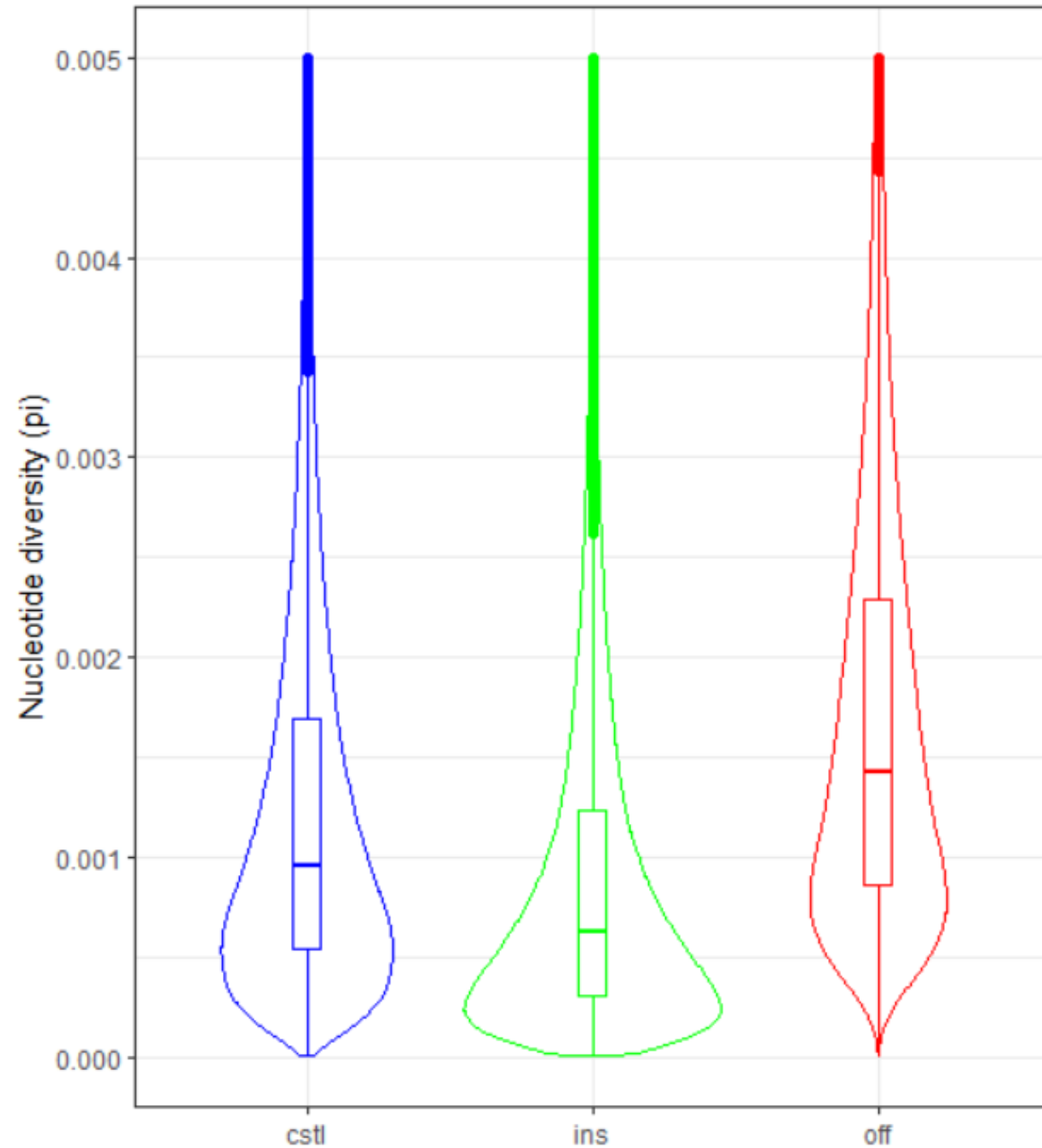


PFKFB4 NC_047043.1 green=ins, red=off, blue=cstl



Pi per gene in a
500kb window

- Selective sweeps
- 11 genes
- Some selective pressure only in offshore



Distribution of π (whole genome)

- Offshore π is greater on average
- Lower diversity on the X chromosome

GCF_011762595.1_mTurTru1.mat.Y_genomic

1.12Mbp

NC_047050.1

M

29.4M

29.6M

29.8M

30M

30.2M

Annotations

17

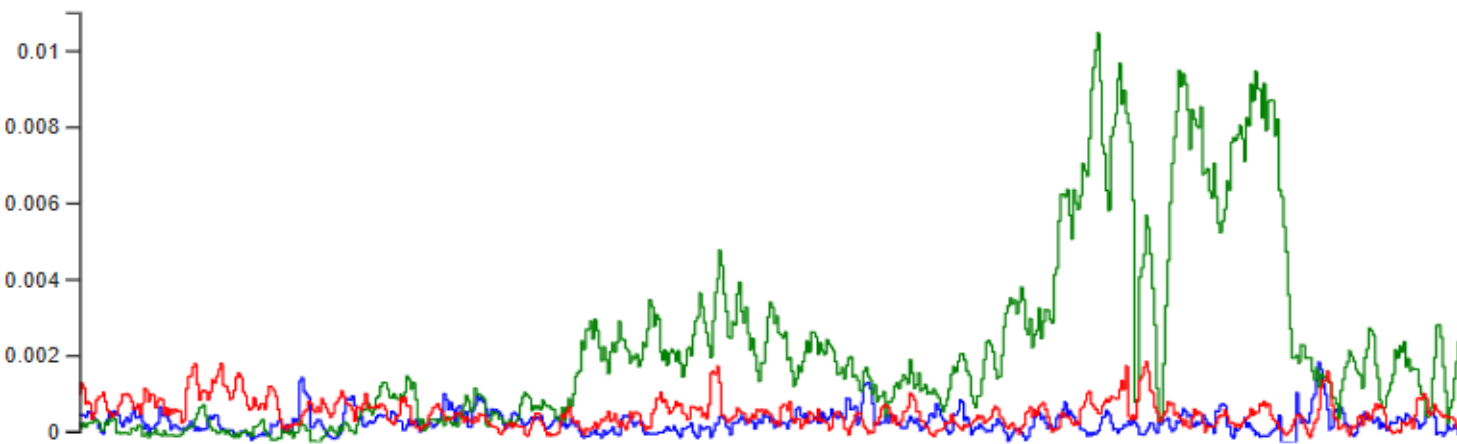
CNGB3

CNBD1

LOC101336337

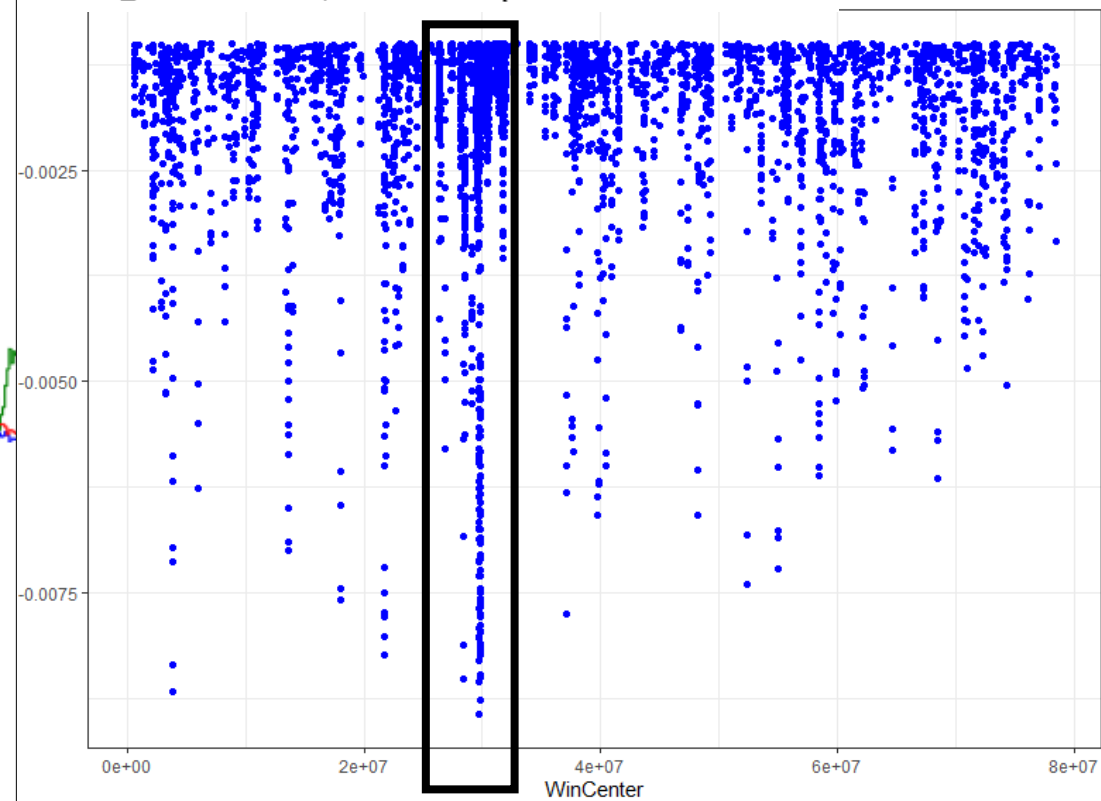
LOC101340084

Nucleotide diversity



$$\Delta pi = (pi \text{ offshore}) - (pi \text{ inshore})$$

NC_047050.1 3557 points where $\Delta pi < -0.001$



GCF_011762595.1_mTurTru1.mat.Y_genomic

1.12Mbp

NC_047050.1

M 29.4M 29.6M 29.8M 30M 30.2M

Annotations

17

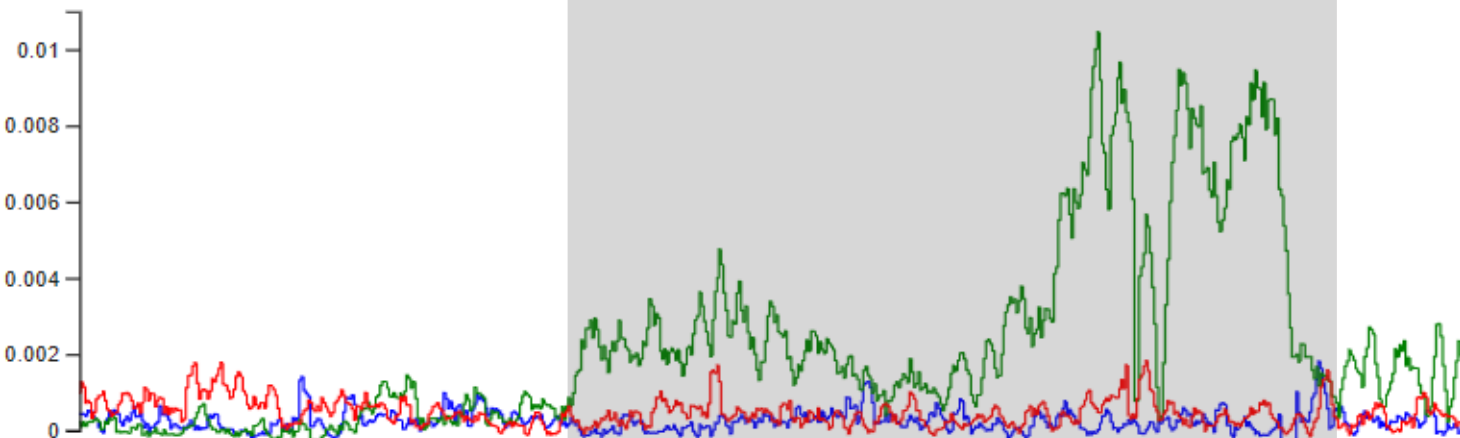
CNGB3

CNBD1

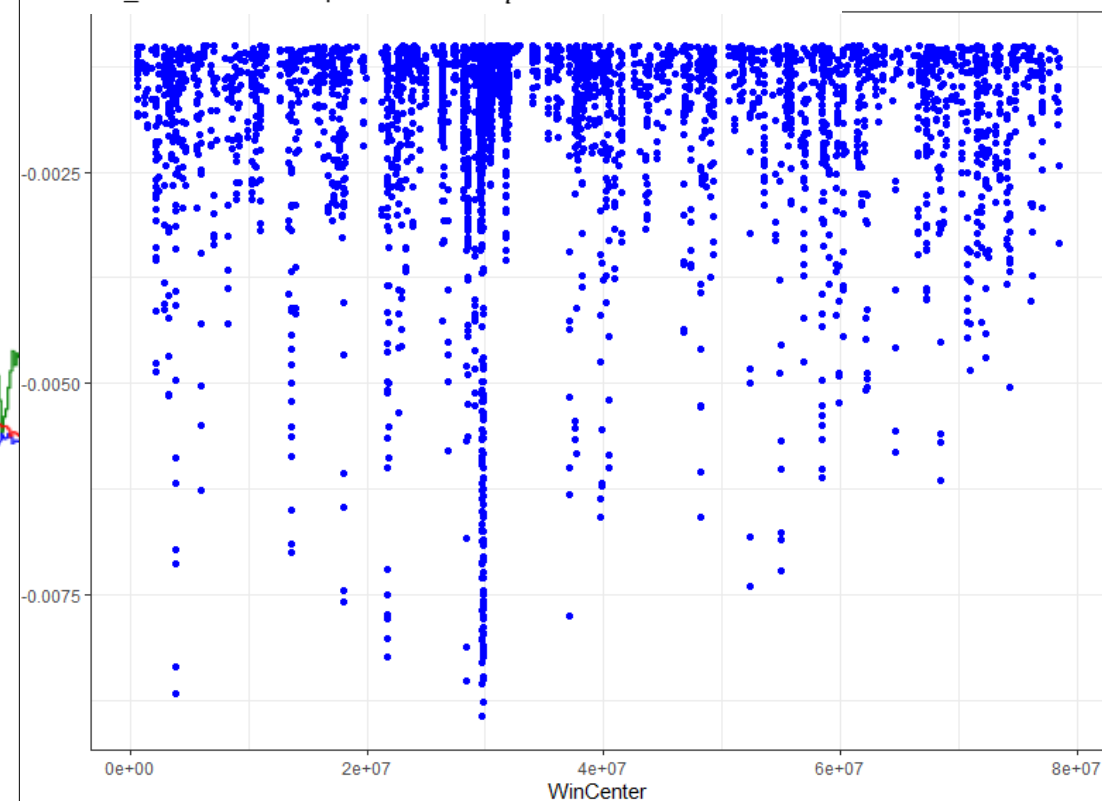
LOC101336337

LOC101340084

Nucleotide diversity



NC_047050.1 3557 points where $\Delta p_i < -0.001$



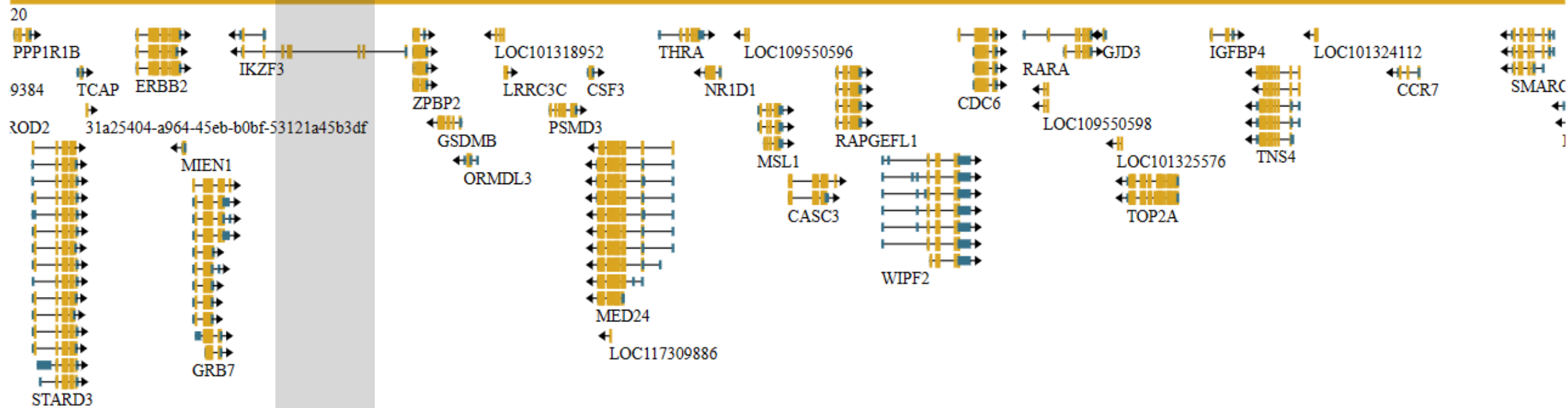
Continuous points of negative differences show us where the inshore population is evolving at a faster rate than the offshore

790Kbp

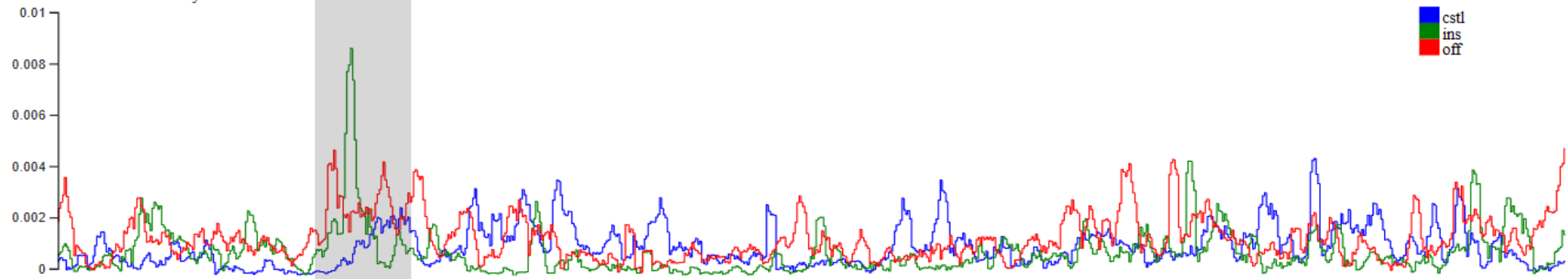
NC_047053.1

0 37,600,000 37,700,000 37,800,000 37,900,000 38,000,000 38,100,000 38,200,000 38,300,000

Annotations



Nucleotide diversity

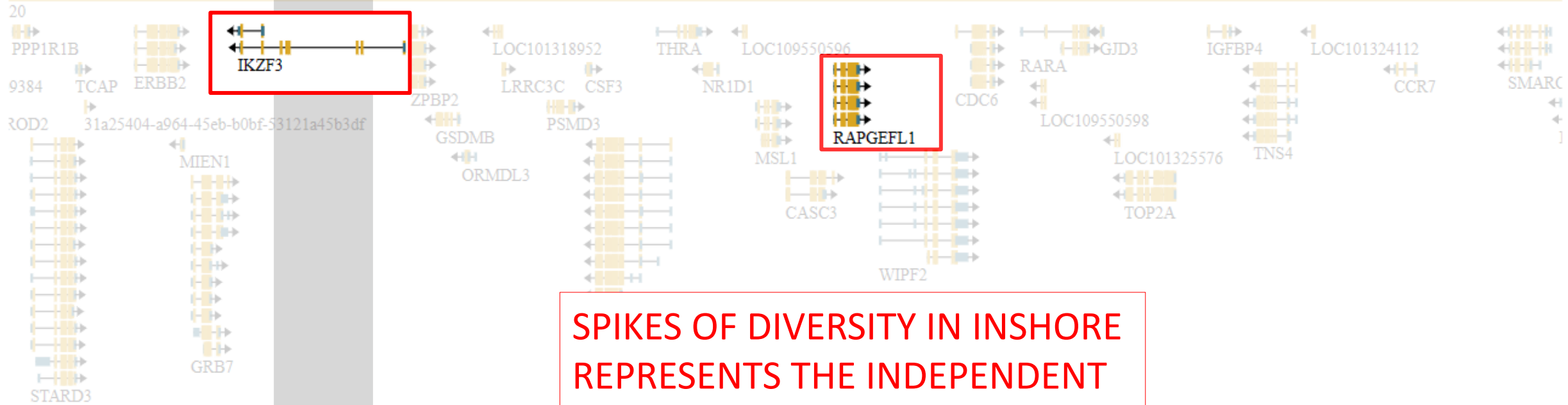


790Kbp

NC_047053.1

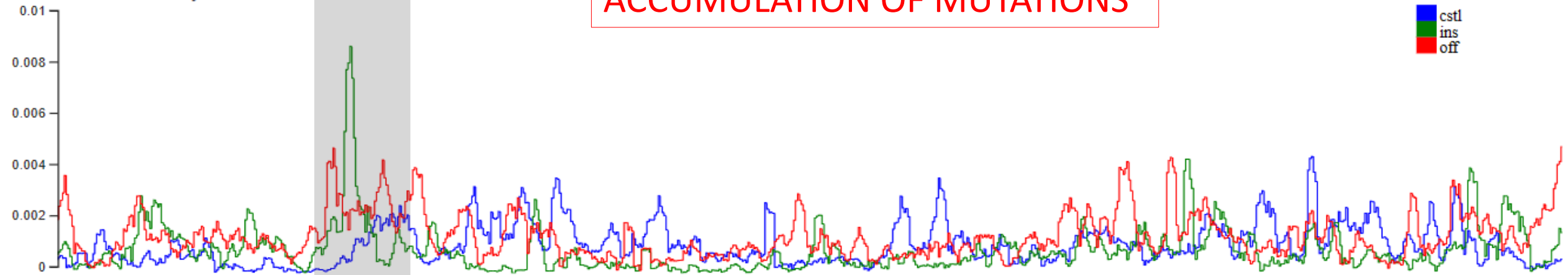
0 37,600,000 37,700,000 37,800,000 37,900,000 38,000,000 38,100,000 38,200,000 38,300,000

Annotations



SPIKES OF DIVERSITY IN INSHORE
REPRESENTS THE INDEPENDENT
ACCUMULATION OF MUTATIONS

Nucleotide diversity



Conclusions

- Offshore populations are the most diverse
- Inshore is evolving at a faster rate in select regions
- Inshore is independently accumulating mutations (sweeps)
- Recent founder events contribute to speciation (offshore > coastal > inshore)

