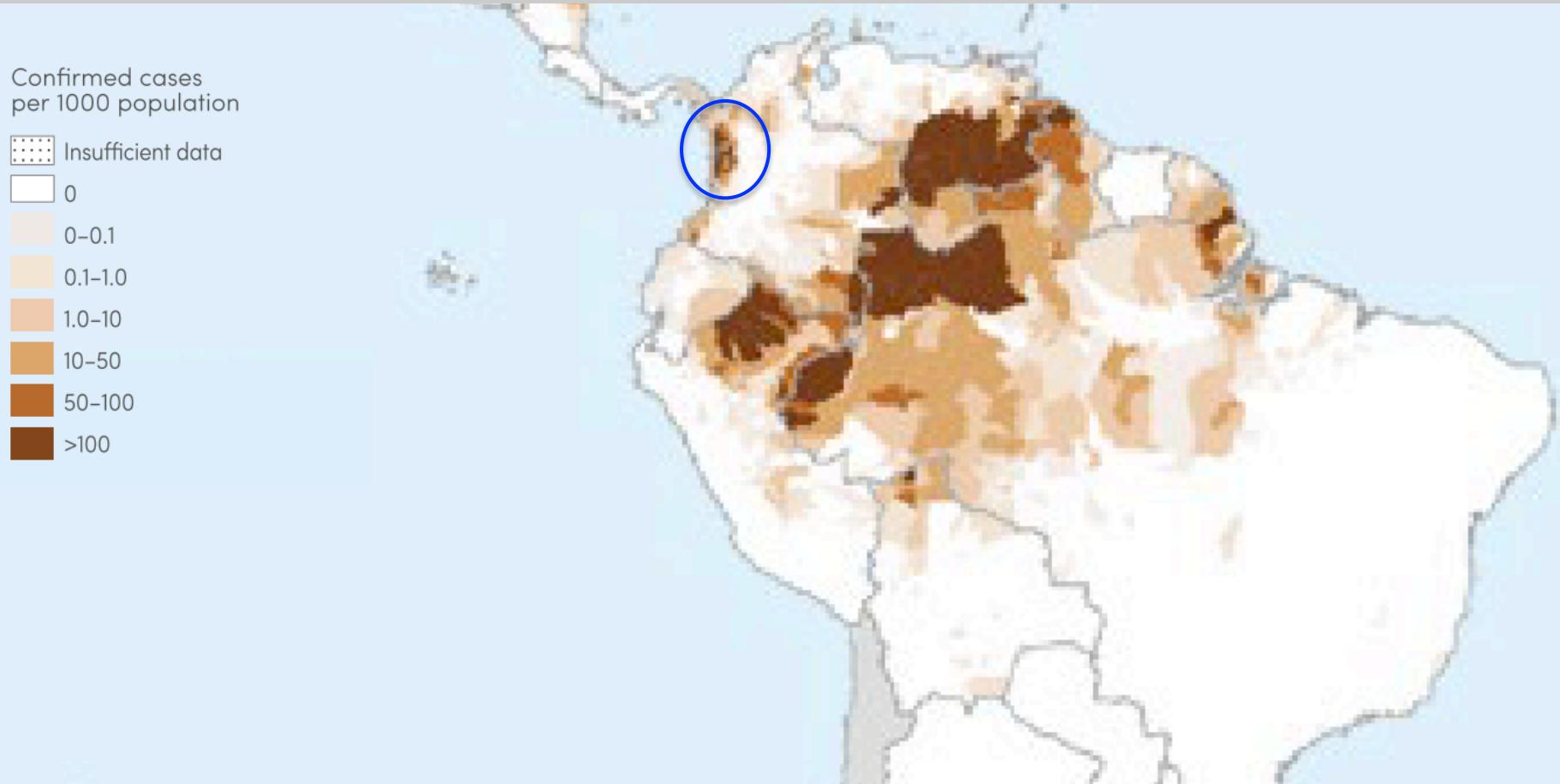


# Malaria and maritime traffic on the Colombian Pacific coast?

Aimee R. Taylor  
Diego F. Echevarry  
Timothy J. Anderson  
Daniel E. Neafsey  
Caroline O. Buckee

# Colombia

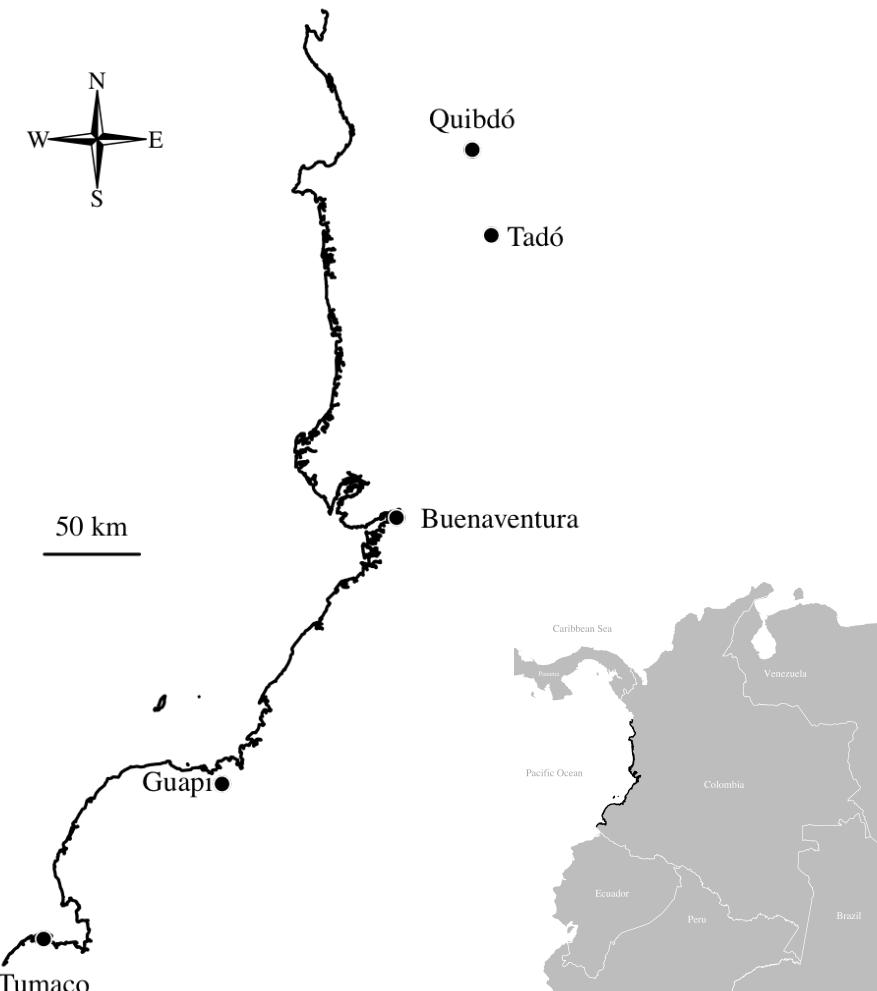


- Malaria incidence almost halved between 2010-2016
- However, cases doubled between 2015 and 2016
- More *P. falciparum* than *P. vivax* in 2016
- Hotspot of transmission: Choco

# Previously published *P. falciparum* data from the Colombian Pacific Coast

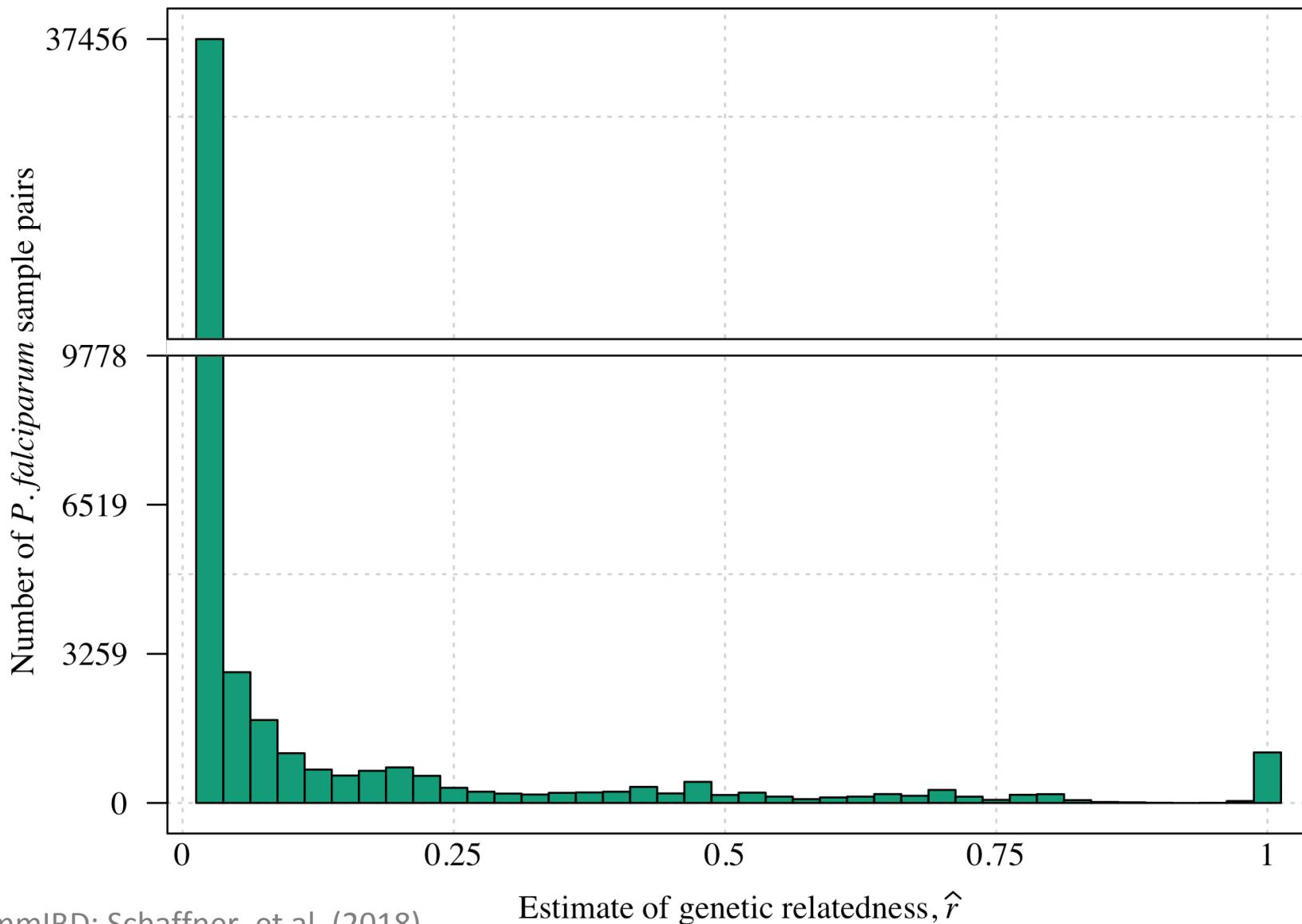
325 single-genotype parasite samples collected between 1993 and 2007 and genotyped at 250 single nucleotide polymorphisms (SNPs)

Echeverry,D.F. et al. (2013) BMC Genet.

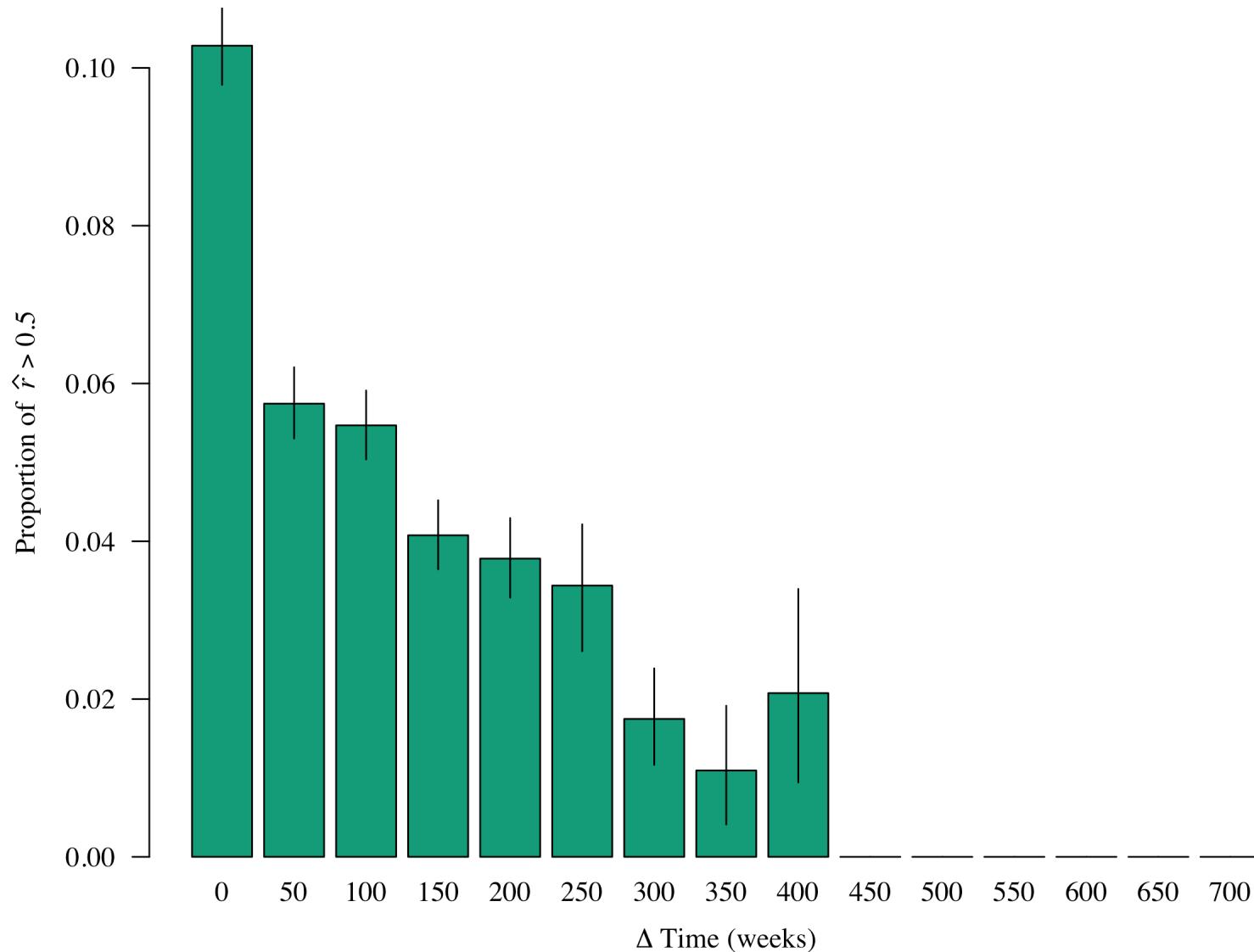


	1993	1994	1997	1999	2000	2001	2002	2003	2004	2005	2006	2007	Total
Tumaco	0	0	0	2	2	10	11	59	0	23	0	25	132
Guapi	0	0	0	1	1	0	0	66	0	0	0	0	68
Buenaventura	4	1	0	5	0	0	0	0	12	15	10	0	47
Quibdo	0	0	2	0	6	1	0	0	14	6	13	22	64
Tado	0	0	0	0	0	12	2	0	0	0	0	0	14
Total	4	1	2	8	9	23	13	125	26	44	23	47	325

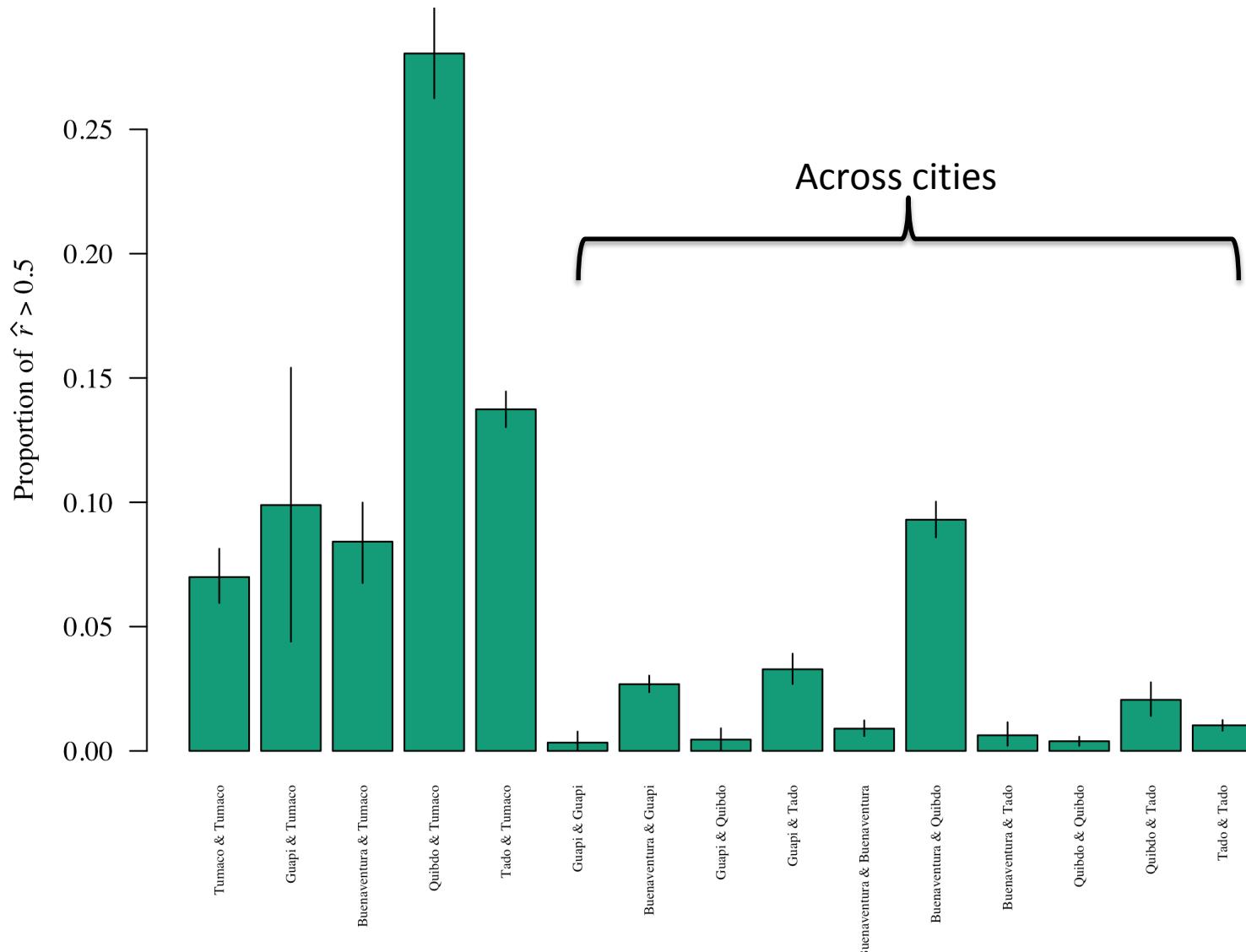
# Distribution of estimates genetic relatedness, $r$ for all pairwise comparisons of samples



*P. falciparum* sample pairs more highly related ( $> 0.5$ ) if collected closer together in time



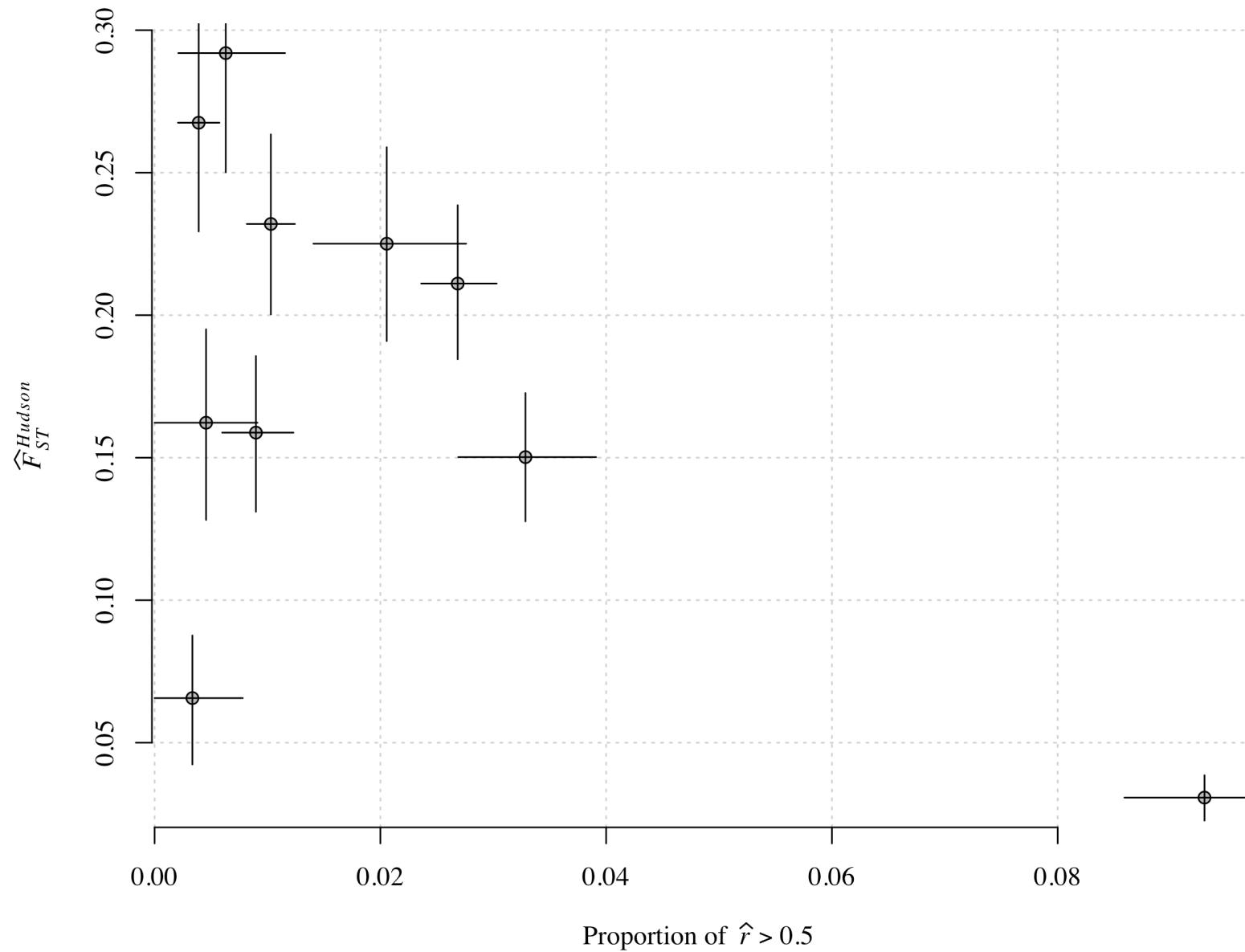
# *P. falciparum* sample pairs more highly related ( $> 0.5$ ) if collected closer together in space



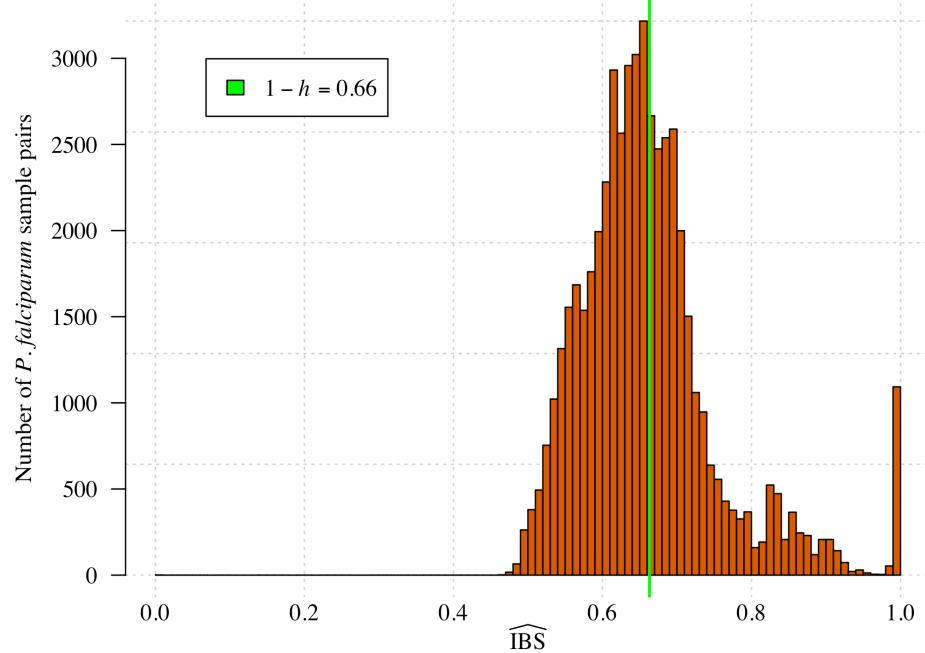
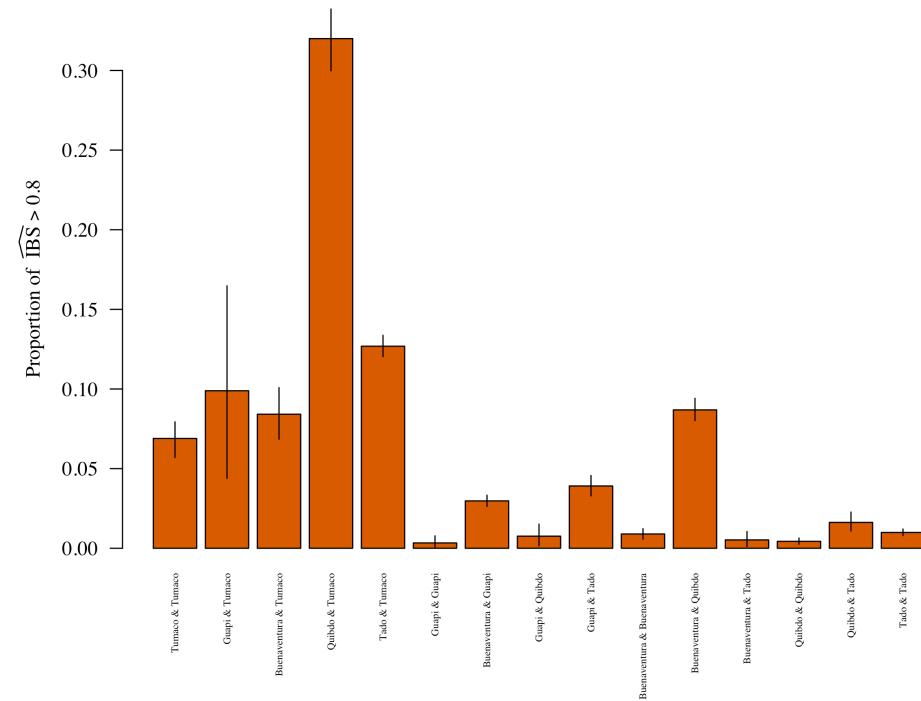
# Regression analyses support small but significant negative trends in relatedness with both space and time

	Fit to highly related versus not	Fit to $r$ estimates directly
	Generalised linear model	Ordinary linear model
(Intercept)	-2.86e+00 (0.00e+00)	8.58e-02 (4.21e-275)
geo_dist	-9.21e-04 (2.52e-05)	-8.42e-05 (2.64e-34)
time_dist	-3.29e-03 (8.85e-48)	-8.97e-05 (2.17e-35)
TumacoTRUE	1.37e+00 (1.37e-77)	9.15e-02 (1.03e-196)
GuapiTRUE	2.00e+00 (1.28e-130)	2.16e-01 (0.00e+00)
BuenaventuraTRUE	9.35e-01 (4.17e-13)	2.78e-02 (9.59e-06)
QuibdoTRUE	6.28e-01 (1.09e-08)	9.64e-02 (3.44e-88)
TadoTRUE	6.99e-01 (5.05e-02)	1.51e-01 (1.09e-13)

# Previously published $F_{ST}$ analyses agree



## Aside: Identity-by-state (IBS) estimates generate similar results vastly different distribution

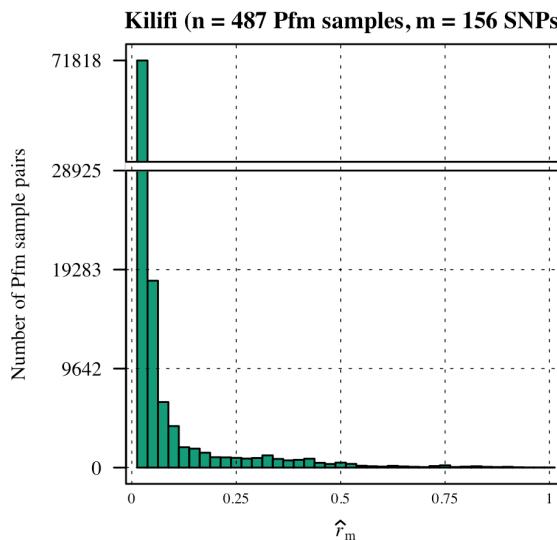
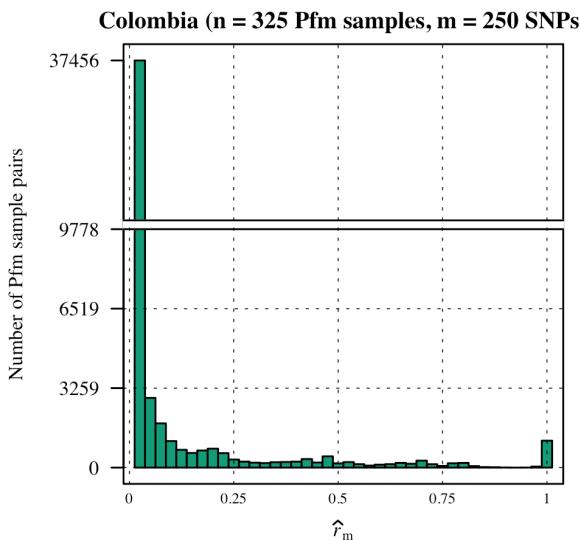
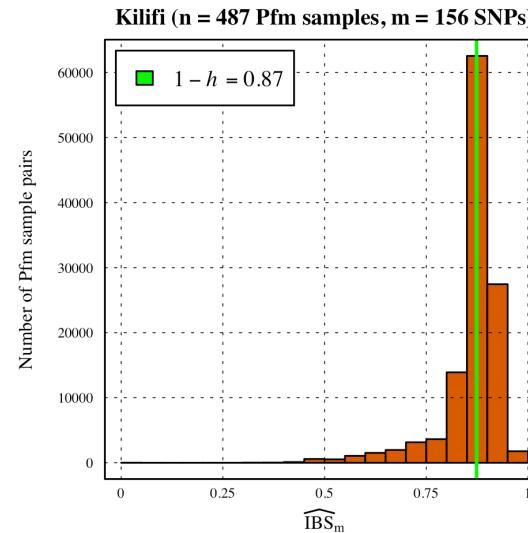
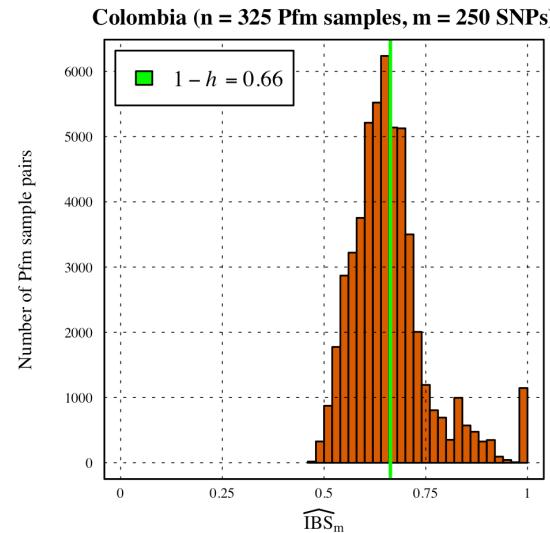


$$\widehat{\text{IBS}} \xrightarrow[m \rightarrow \infty]{\text{Probability}} 1 - h + hr$$

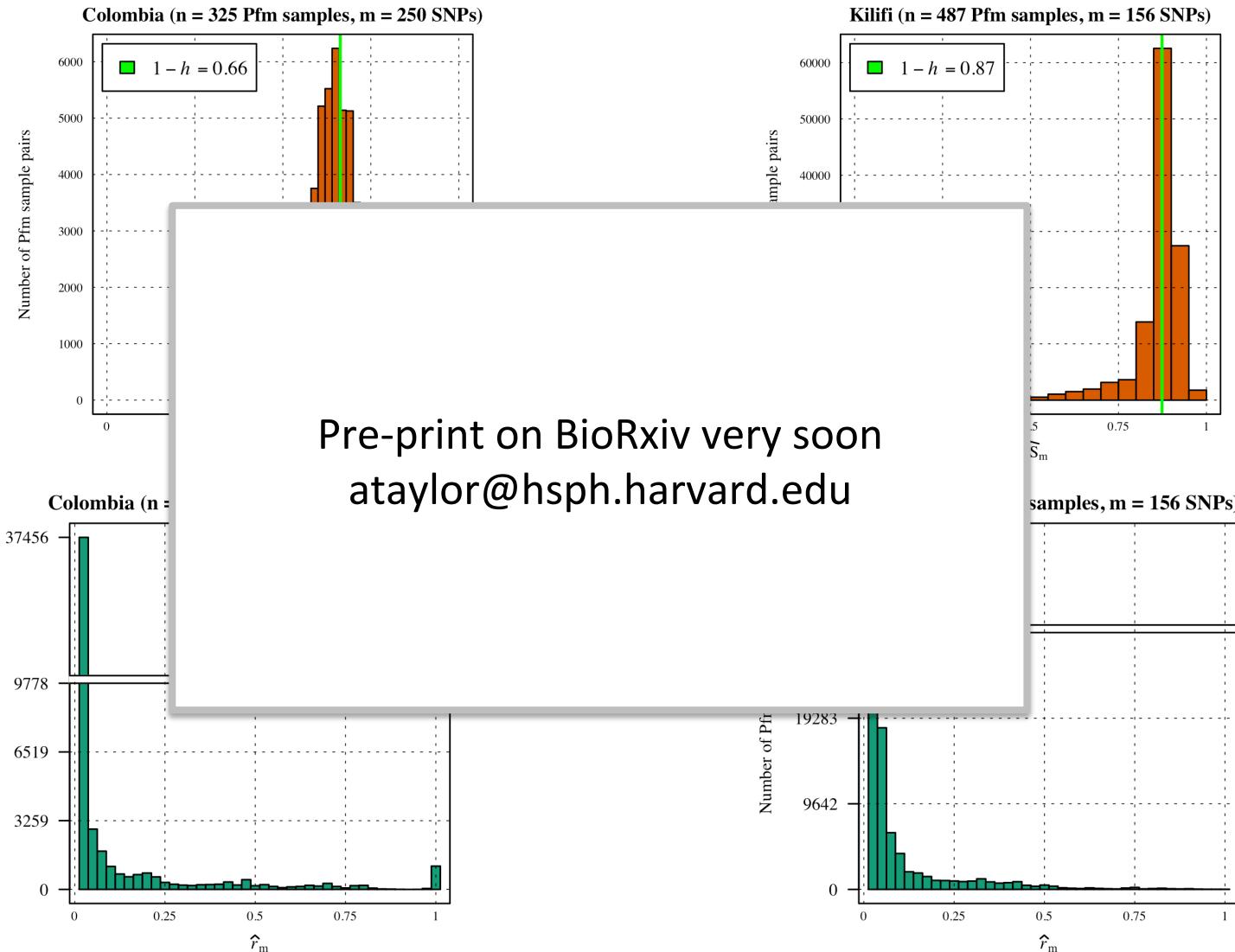
where  $m$  is the number of SNPs,  $r$  is relatedness and  $h = 1/m \sum_{t=1}^m 2f_t(1 - f_t)$

$f_t$  is the allele frequency at the  $t^{\text{th}}$  SNP

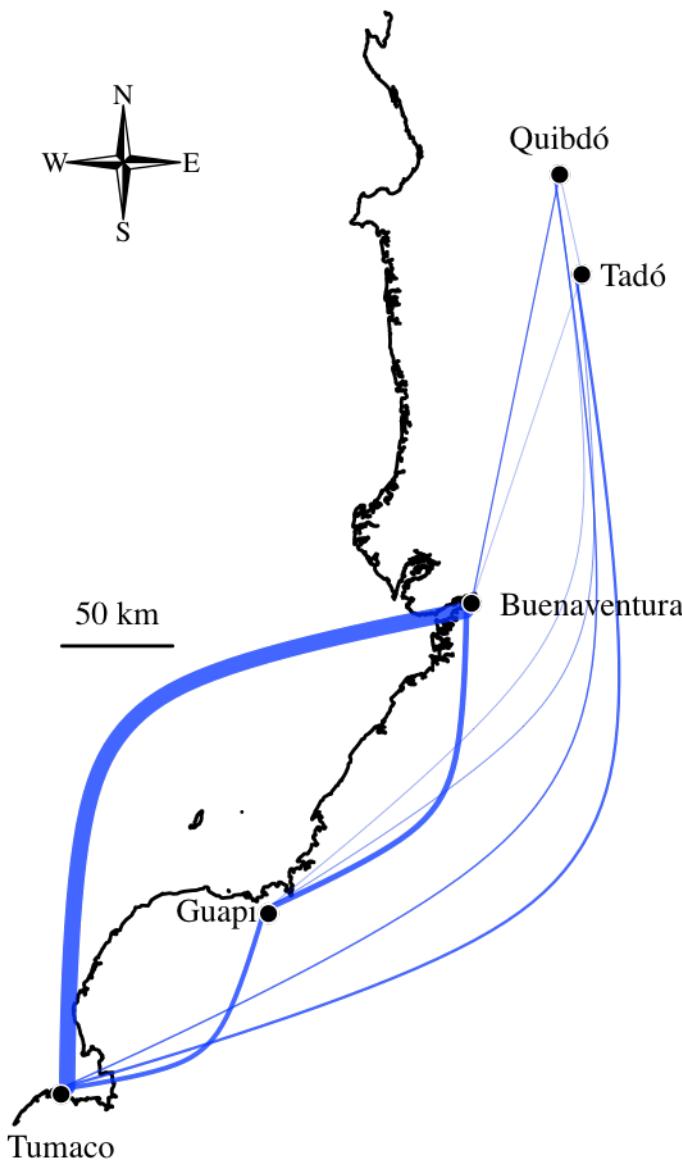
Aside: highly recommend estimating  $r$  versus IBS for comparability, SNP requirement and confidence interval calculation



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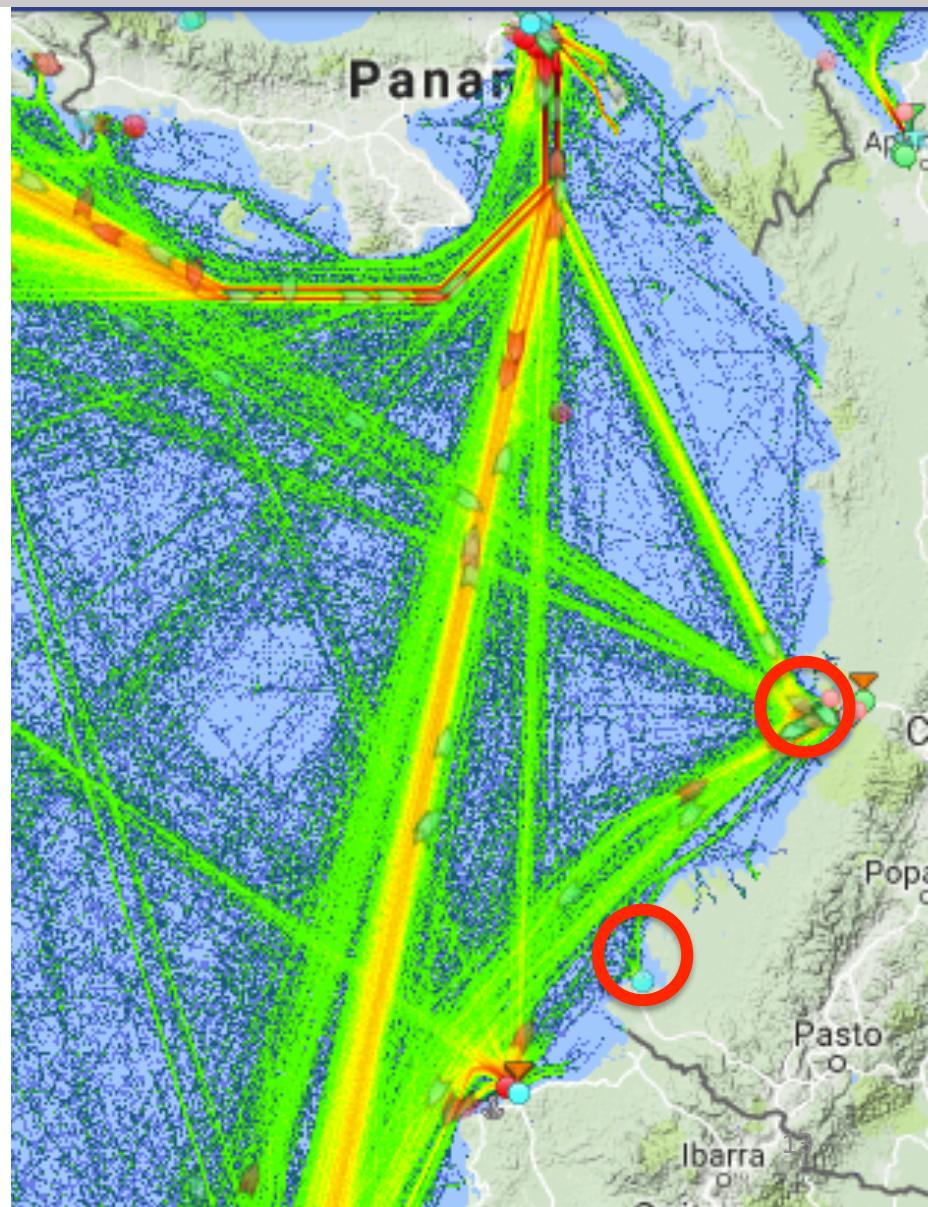
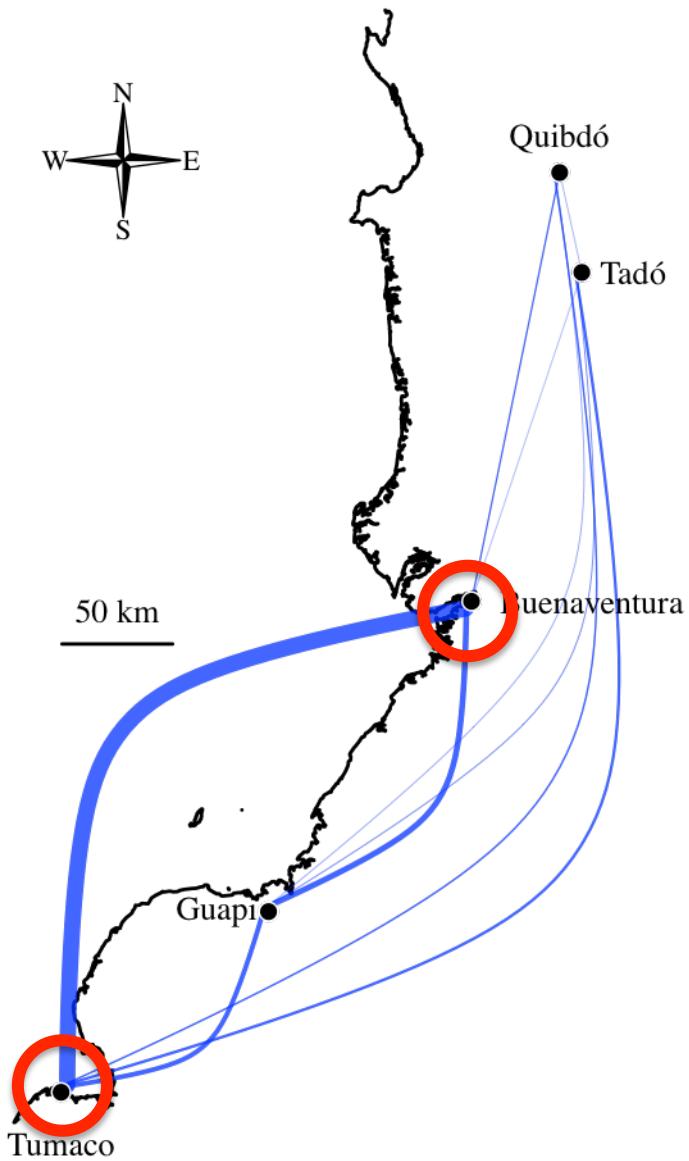


# Connectivity across sites only

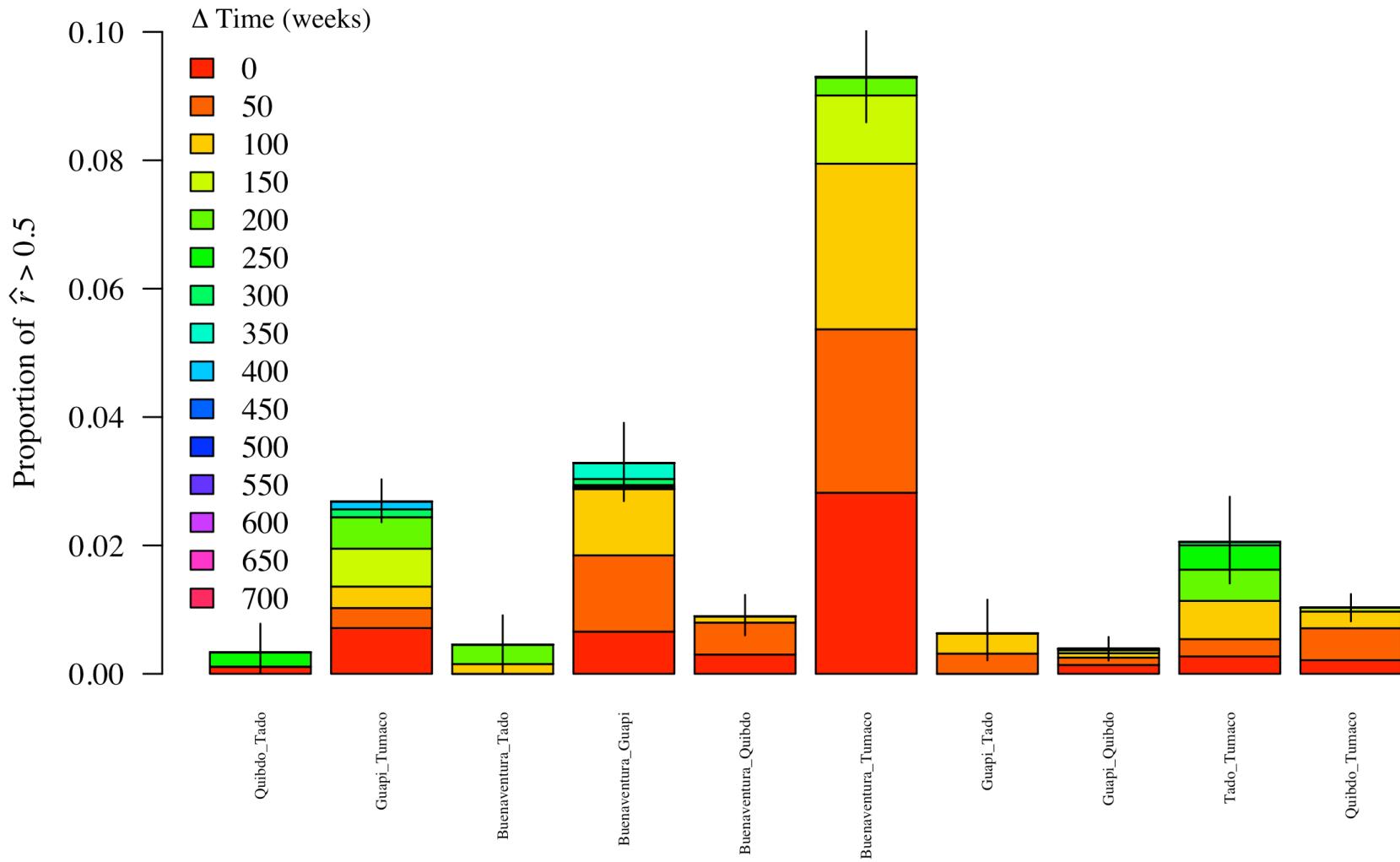


- Blue edges proportional to the proportion highly related between sites
- Tumaco and Buenaventura are disproportionately connected

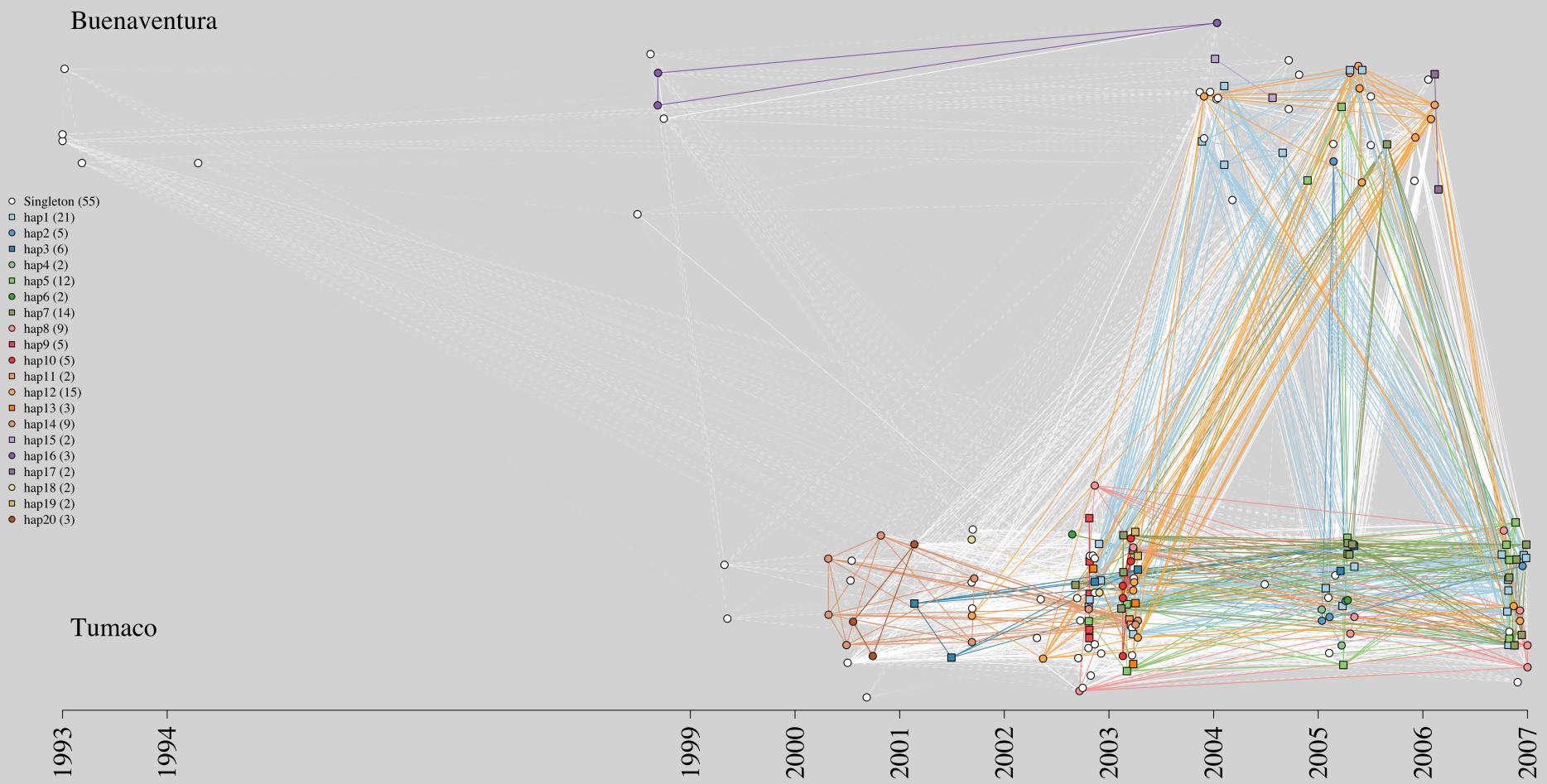
# Genetic connectively correlates with maritime traffic



Were port samples all collected at the same time? No



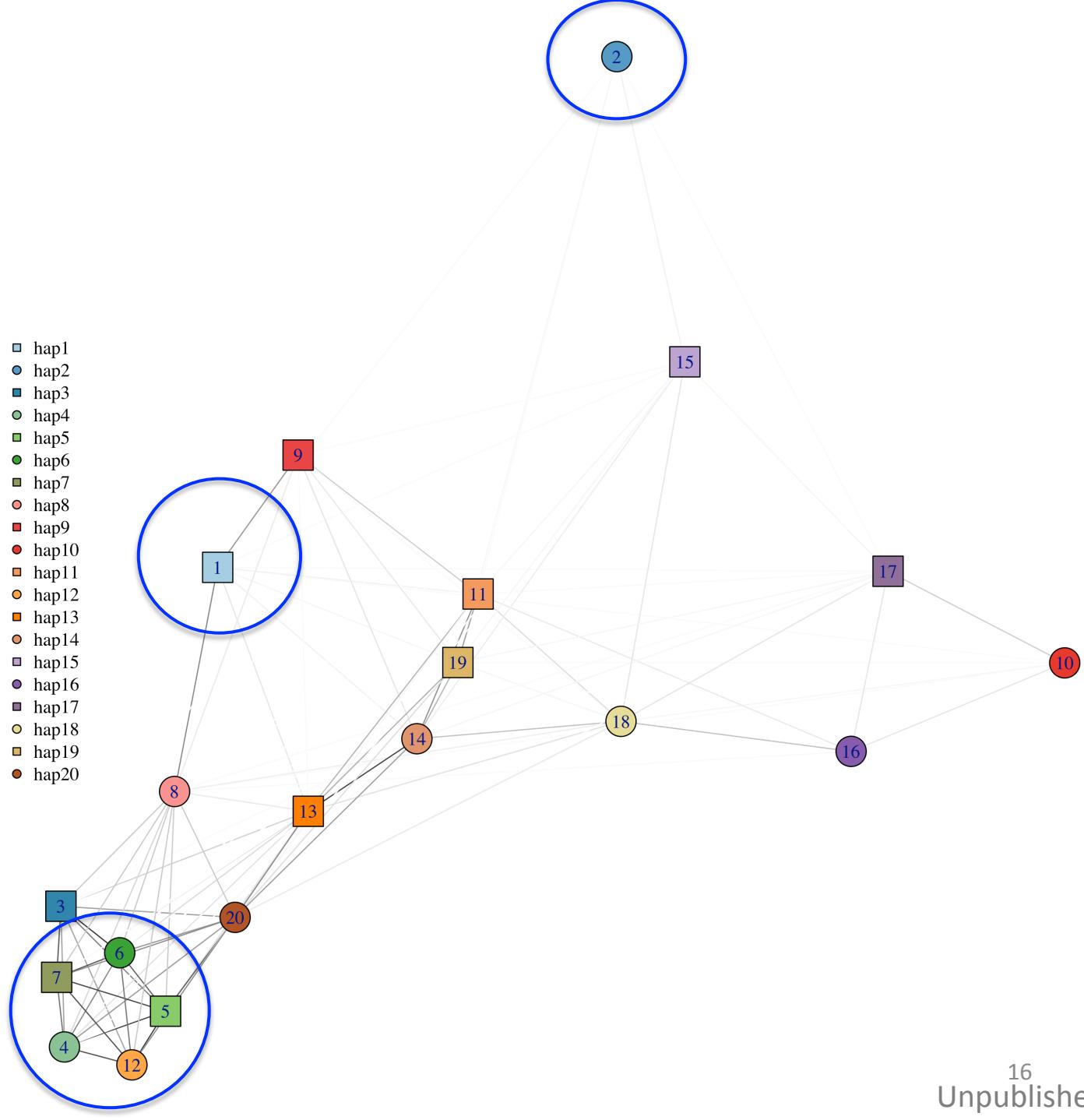
# Is a single clone driving the signal? No



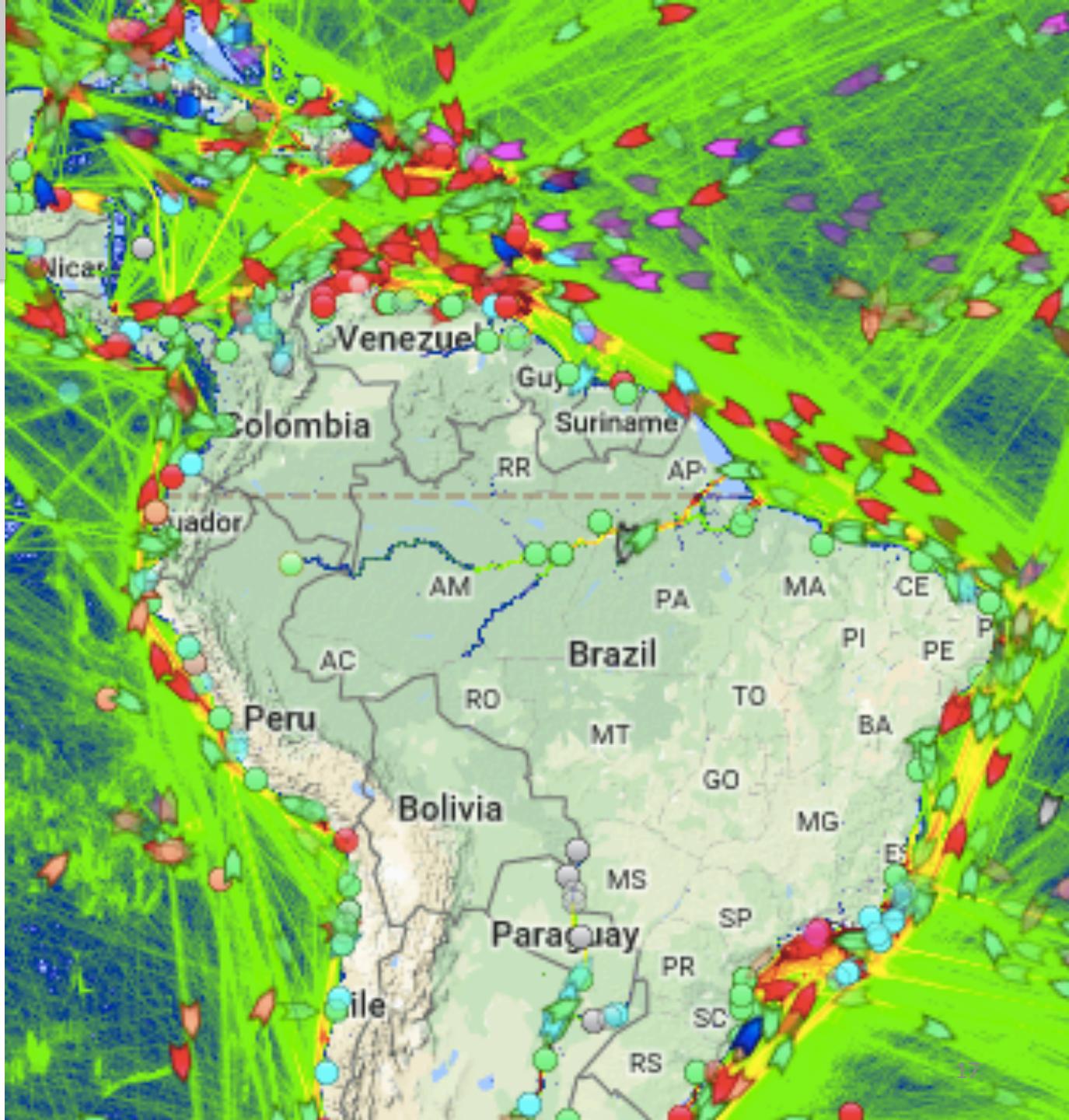
Pairwise comparisons between ports plotted by sample collection date and colored by haplotype where repeat haplotypes were observed. Solid:  $IBD > 0.5$ ; dashed:  $IBD \leq 0.5$

Are the repeat  
haplotypes highly  
related to one-  
another?  
Some, not all

Edges = r estimates



Does marine traffic  
impact malaria  
transmission more  
generally?



# A model framework that allows integration of different data layers

1. What are dominant processes that drive spatial structure?
2. How do they differ in different epidemiological settings?
3. What data are required in different settings?

Extract valuable information from complementary data types while preventing cross-contamination and multiple testing



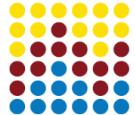
# Thank you

- Aimee R. Taylor
- Diego F. Echevarry
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