

Supplementary Material

Supplementary Figure 1. Phylogeny of NRY haplogroup Q1 sequences. Terminal branches are color-coded by linguistic affiliation as in Figure 1.

Supplementary Figure 2. Pairwise Φ_{ST} s for mtDNA in lower diagonal and NRY in upper diagonal. The stars indicate significance (p-value <0.05) after Benjamin-Hochberg correction for multiple tests.

Supplementary Figure 3. MDS plots for mtDNA and NRY. Stress values (within parentheses) are indicated in percentages.

Supplementary Figure 4. Mantel test depicted as histograms of the distribution of the correlation between distance matrices after 9999 random permutations for: A) mtDNA and NRY genetic distances, B) mtDNA and geographic distances, and C) NRY and geographic distances. The point indicates the observed correlation (r) between matrices.

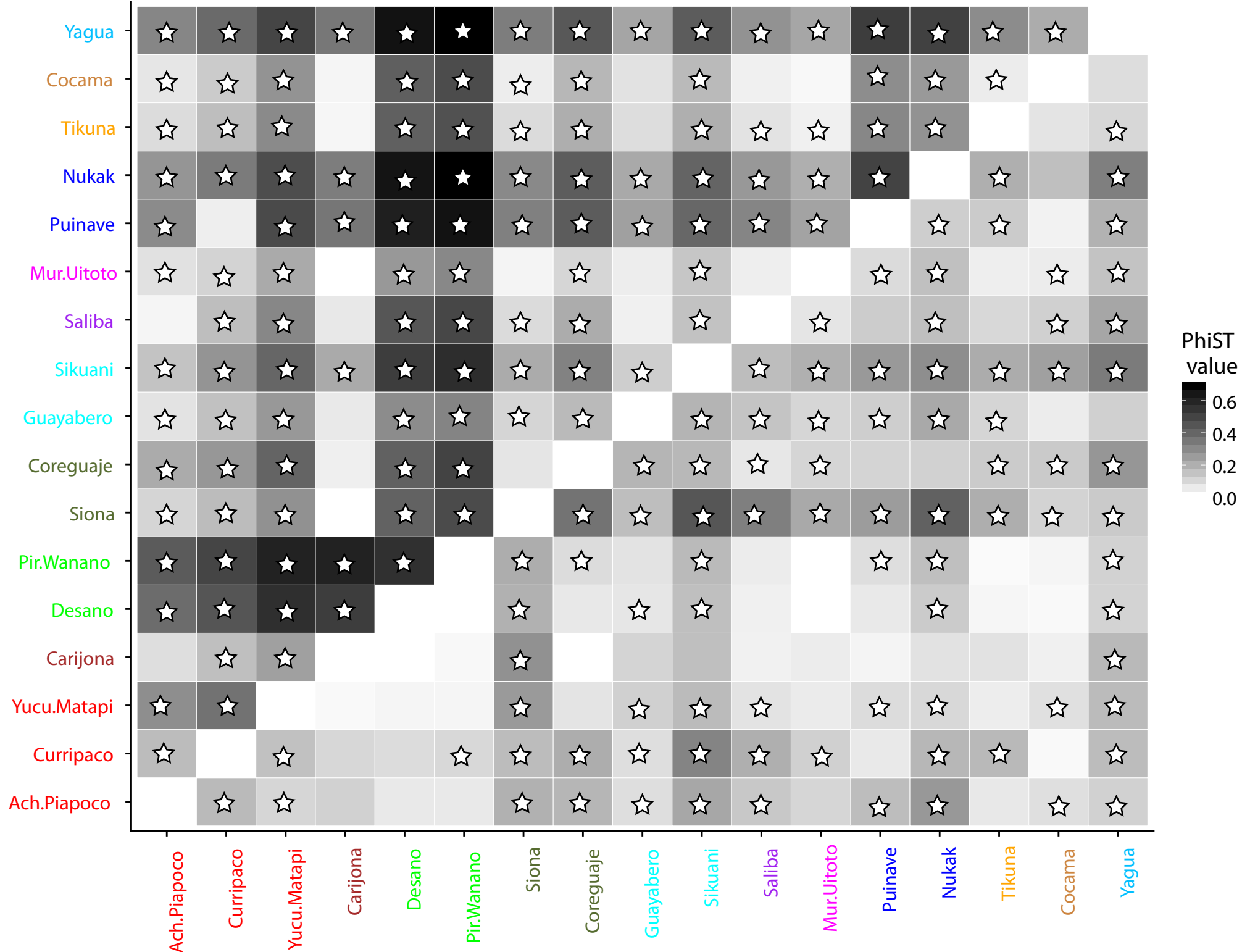
Supplementary Figure 5. Network of haplotypes from haplogroup Q1 color-coded by language family. Clades highlighted with circles contain related haplotypes discussed in the main text.

Supplementary Figure 6. Phylogeny of mtDNA sequences. Terminal branches are color-coded by linguistic affiliation as in Figure 1. Main Native American haplogroups are indicated.

Supplementary Figure 7. BSP plots from different sampling schemes of the NRY. A) Pooled. B) Scattered. C) By population. Dotted lines represent the 95% highest posterior density (HPD).

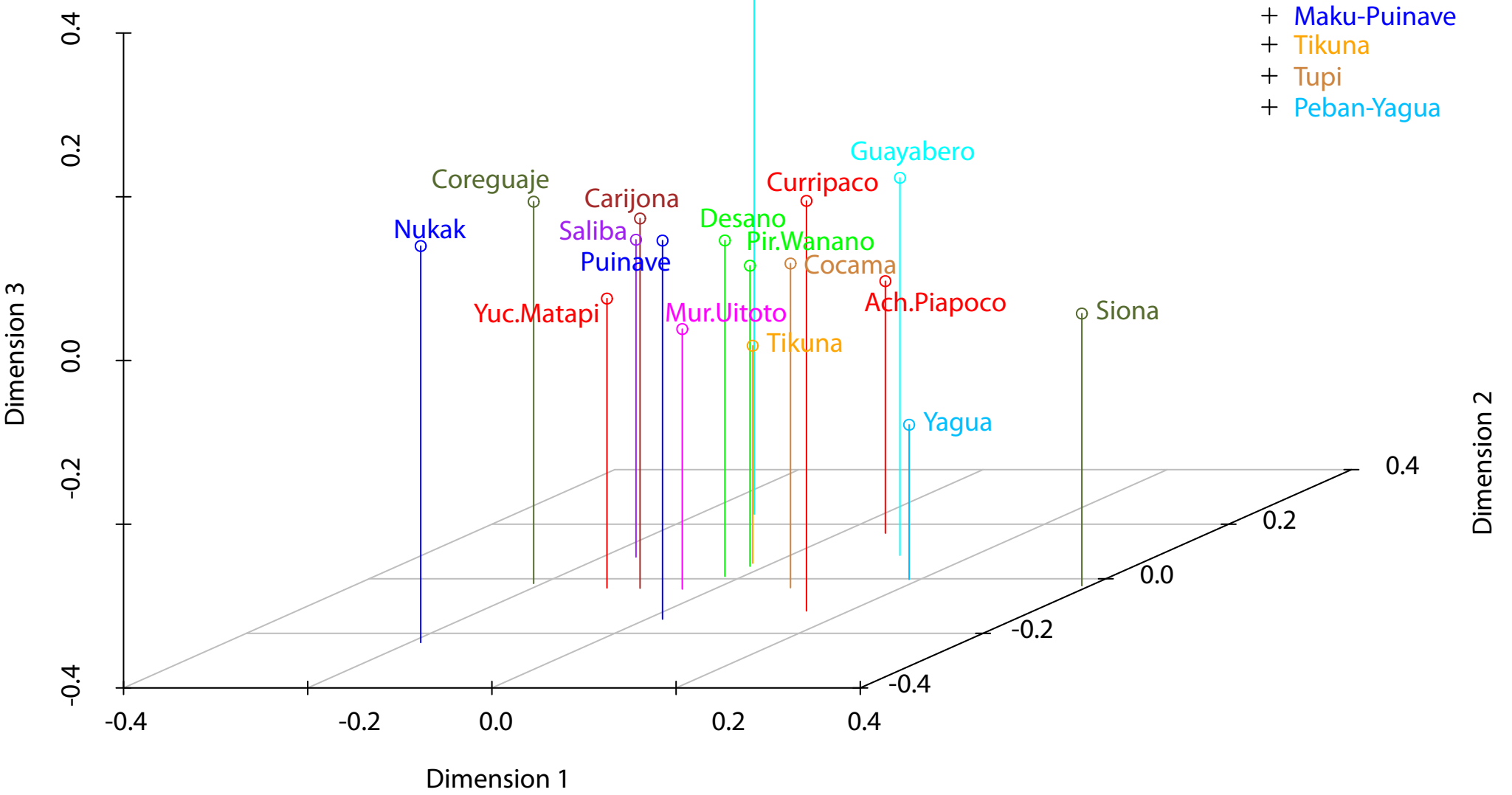
Supplementary Figure 8. BSP plots from different sampling schemes of the mtDNA. A) Pooled. B) Scattered. C) By population. Dotted lines represent the 95% highest posterior density (HPD).





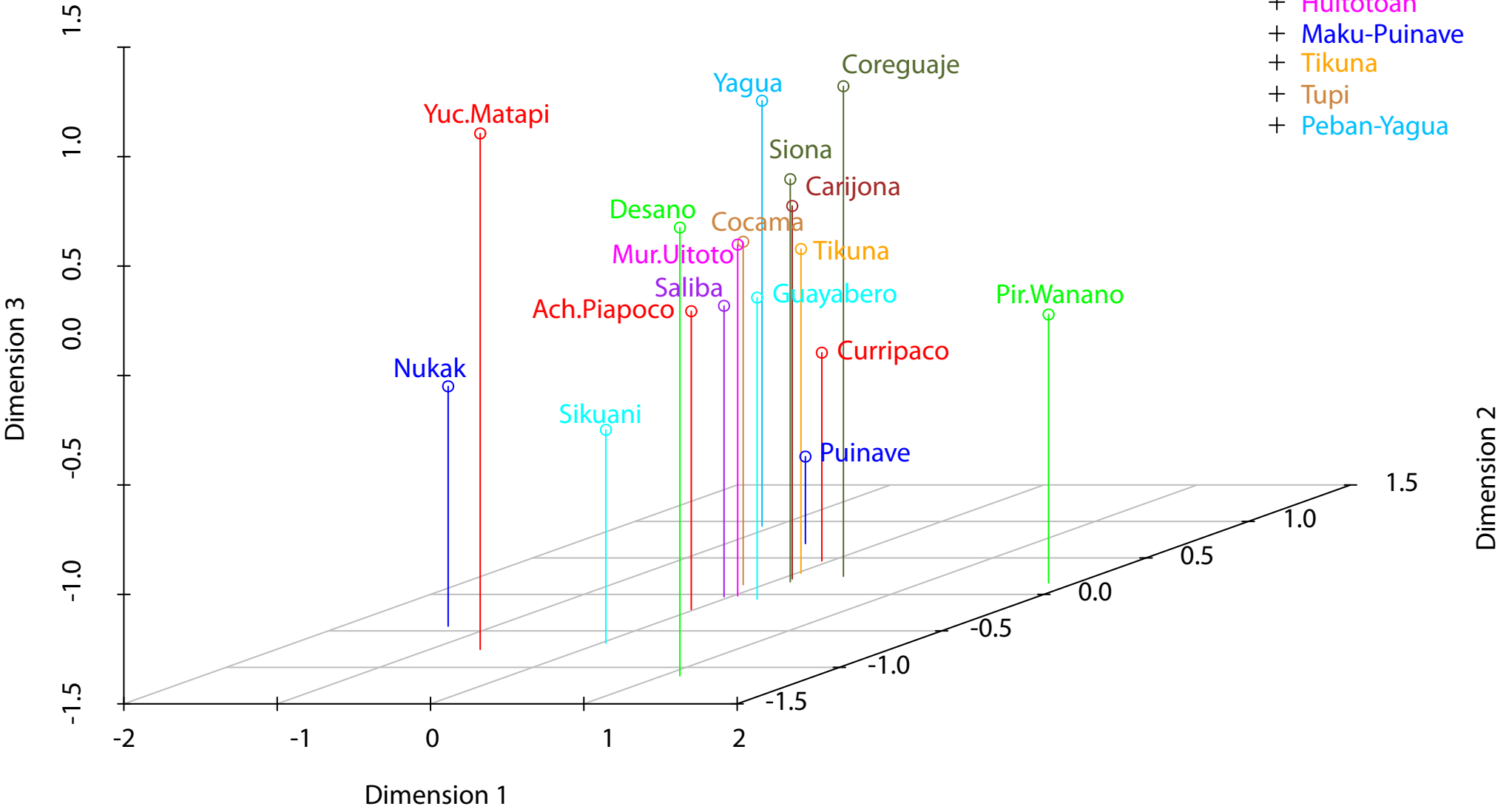
mtDNA (stress=6.4)

- + Arawakan
- + Carib
- + Eastern-Tukanoan
- + Western-Tukanoan
- + Guahiban
- + Piaroa-Saliba
- + Huitotoan
- + Maku-Puinave
- + Tikuna
- + Tupi
- + Peban-Yagua

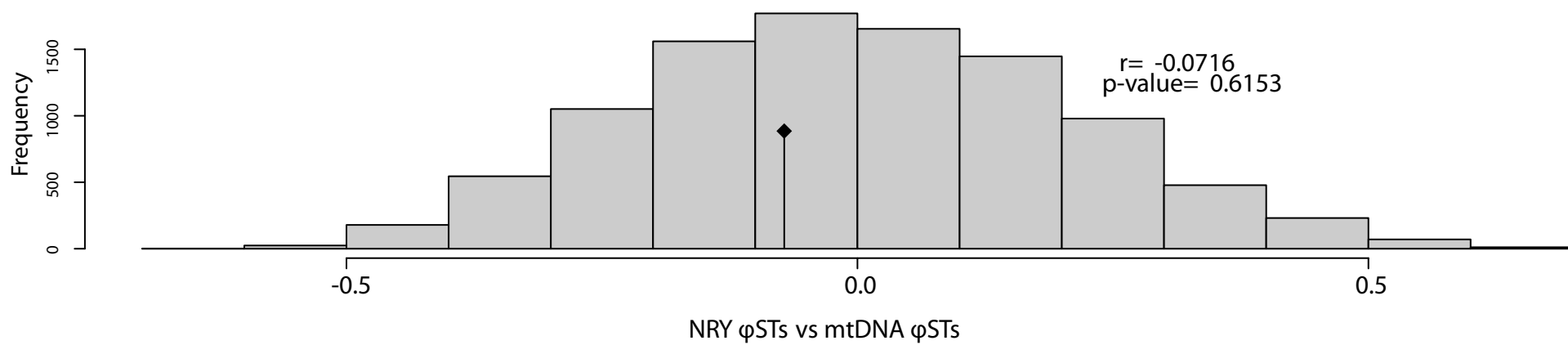


NRY (stress=10.41)

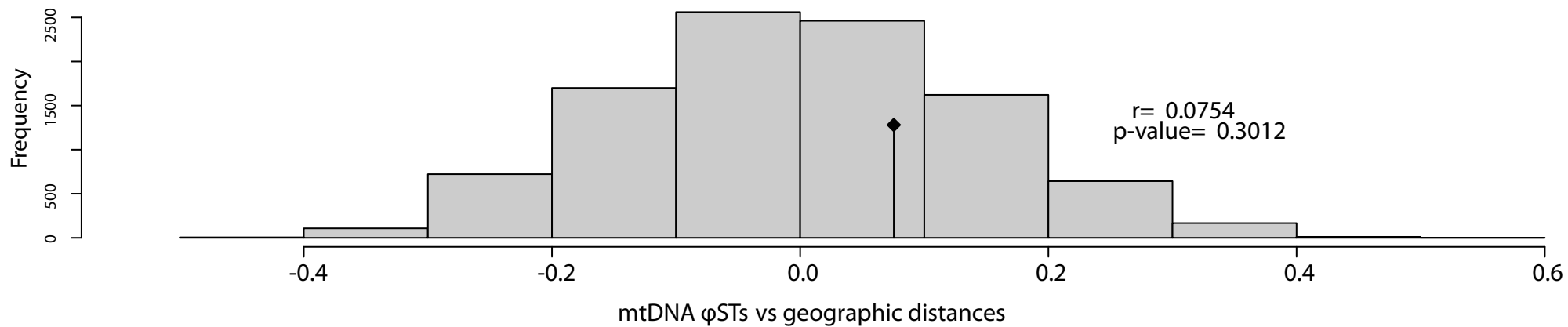
- + Arawakan
- + Carib
- + Eastern-Tukanoan
- + Western-Tukanoan
- + Guahiban
- + Piaroa-Saliba
- + Huitotoan
- + Maku-Puinave
- + Tikuna
- + Tupi
- + Peban-Yagua



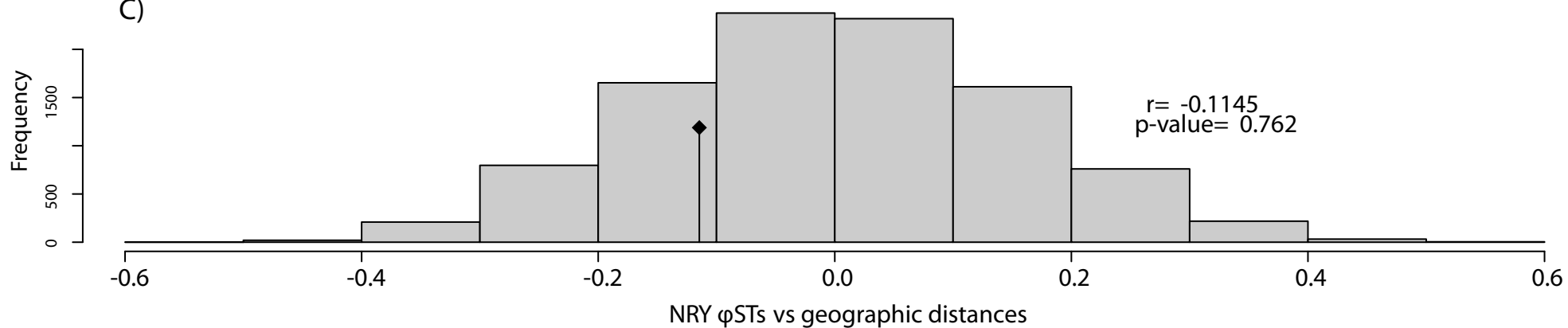
A)



B)

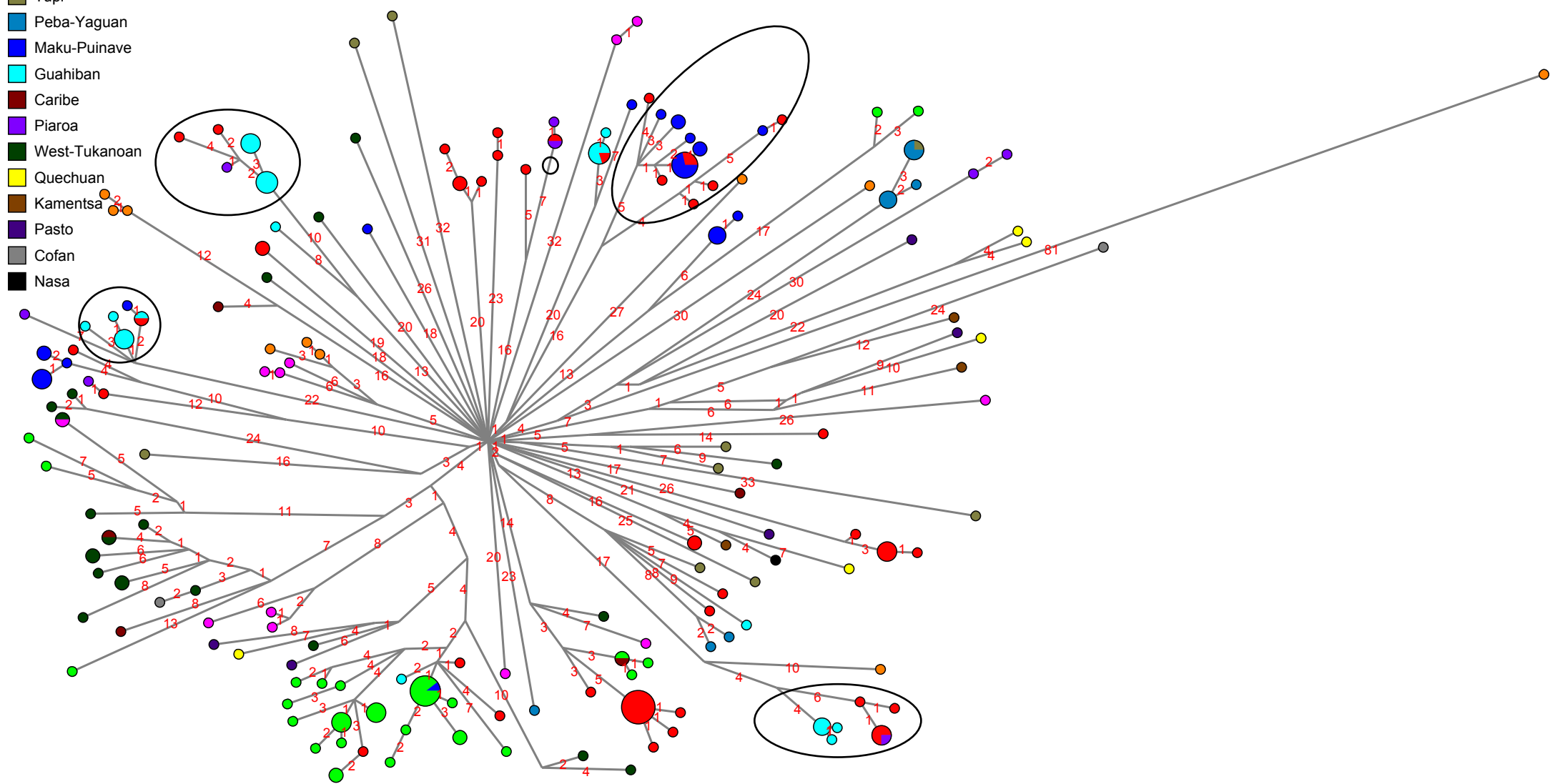


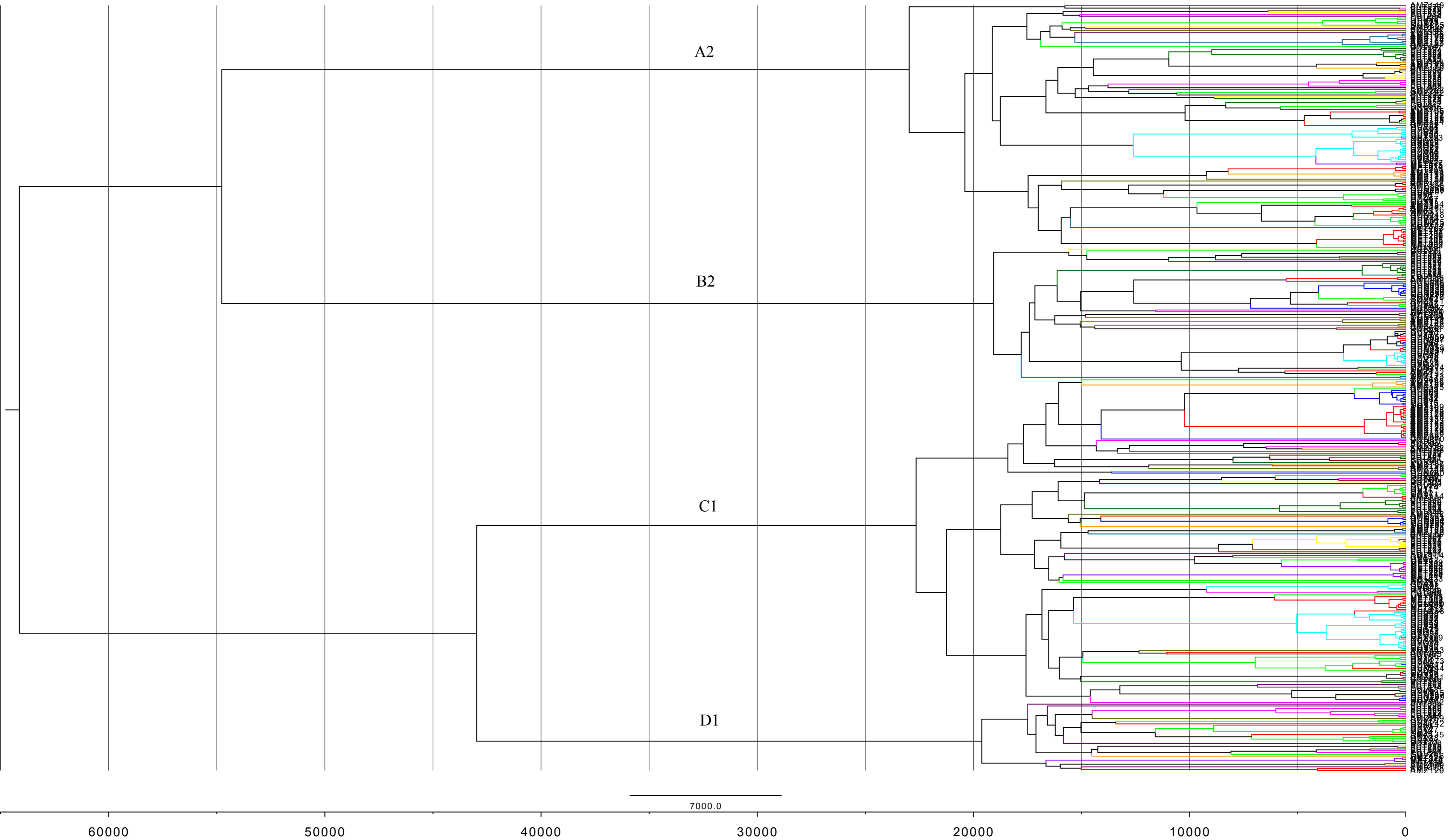
C)



Group1

- Arawakan
- East-Tukanoan
- Huitoto
- Tikunan
- Tupi
- Peba-Yaguan
- Maku-Puinave
- Guahiban
- Caribe
- Piaroa
- West-Tukanoan
- Quechuan
- Kamentsa
- Pasto
- Cofan
- Nasa





A2

B2

C1

D1

7000.0

60000

50000

40000

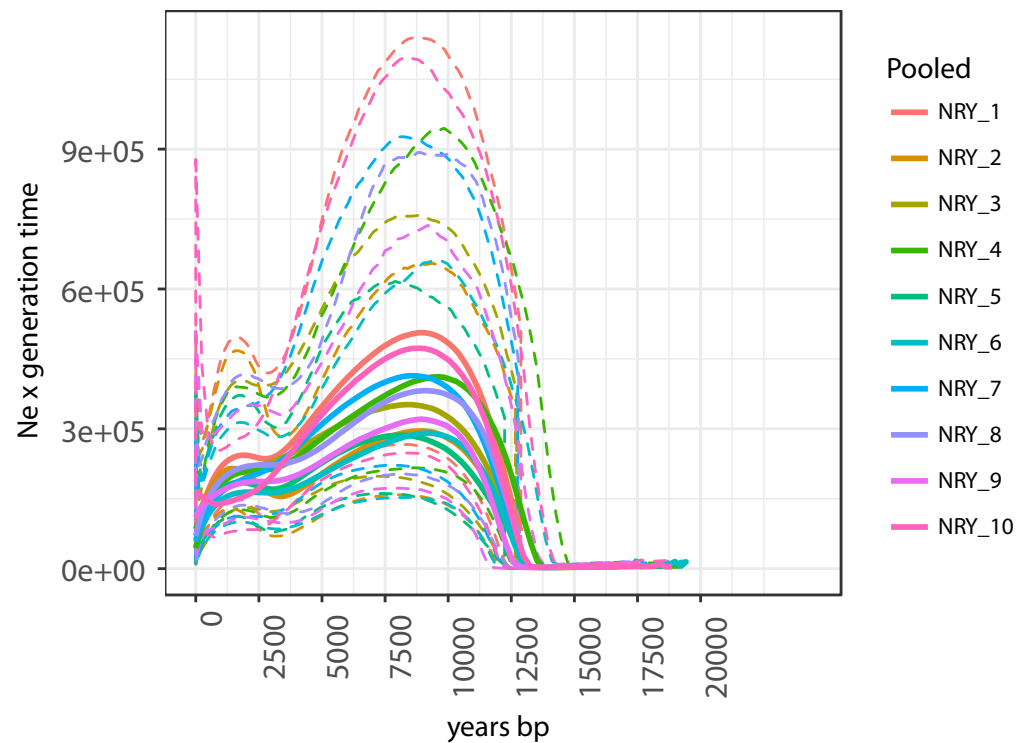
30000

20000

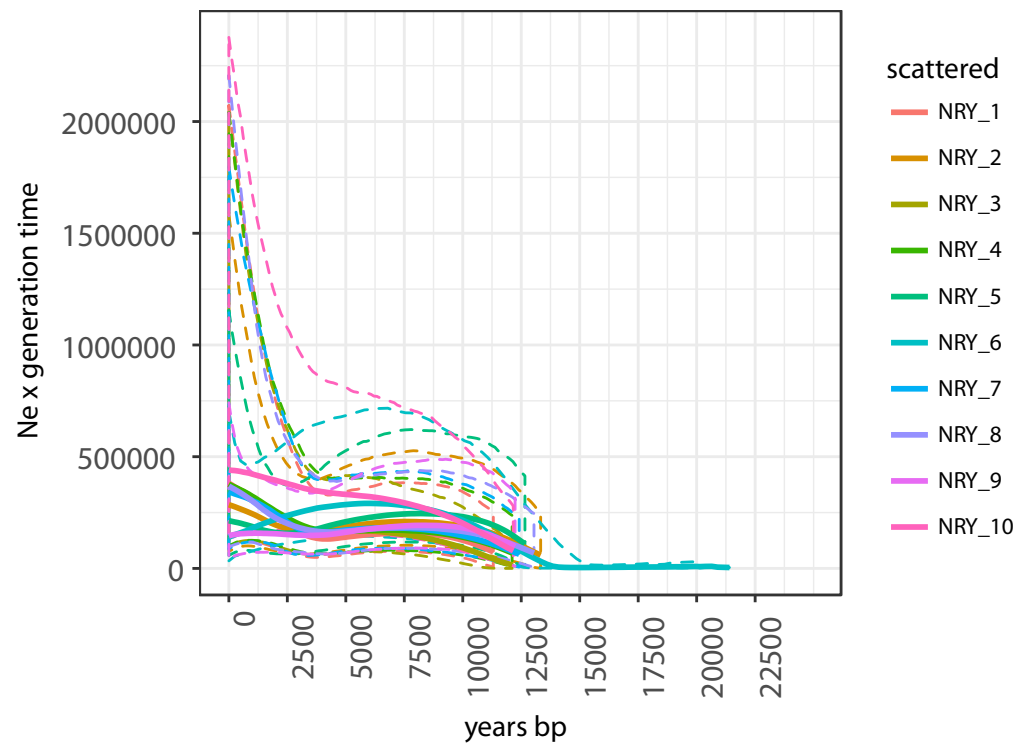
10000

0

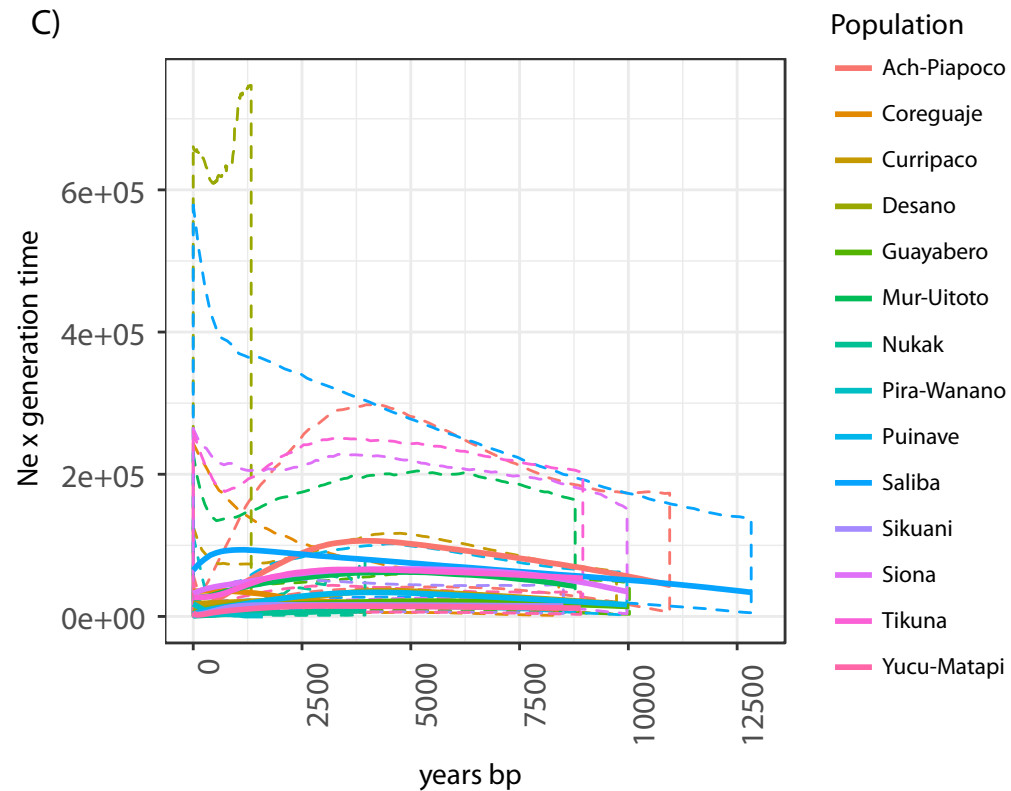
A)



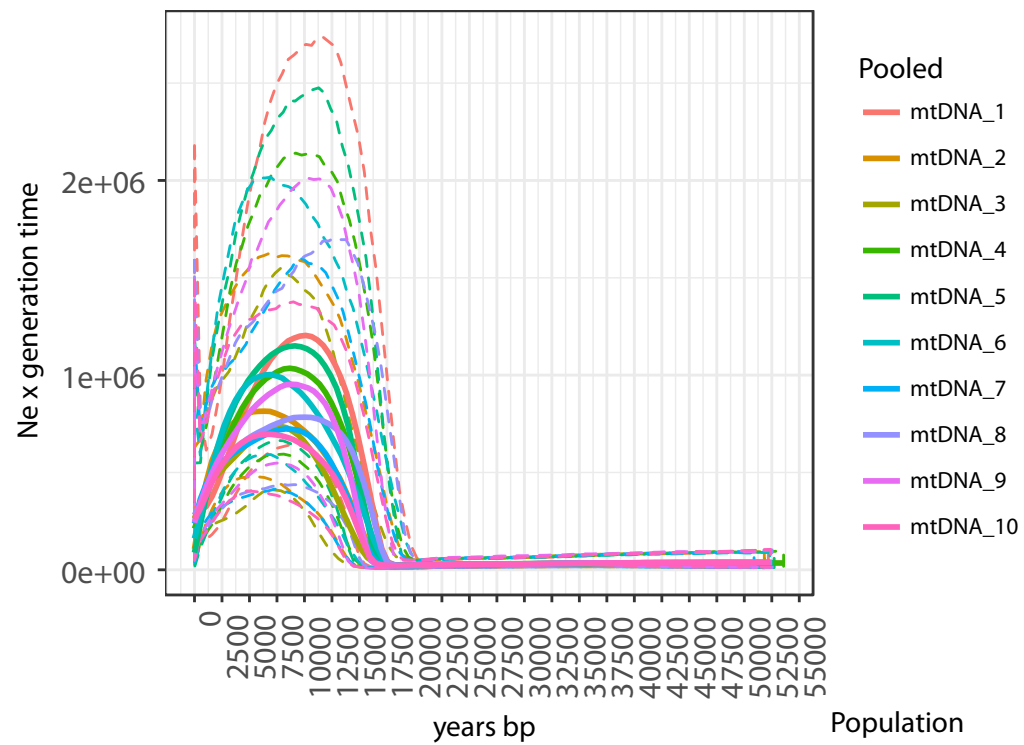
B)



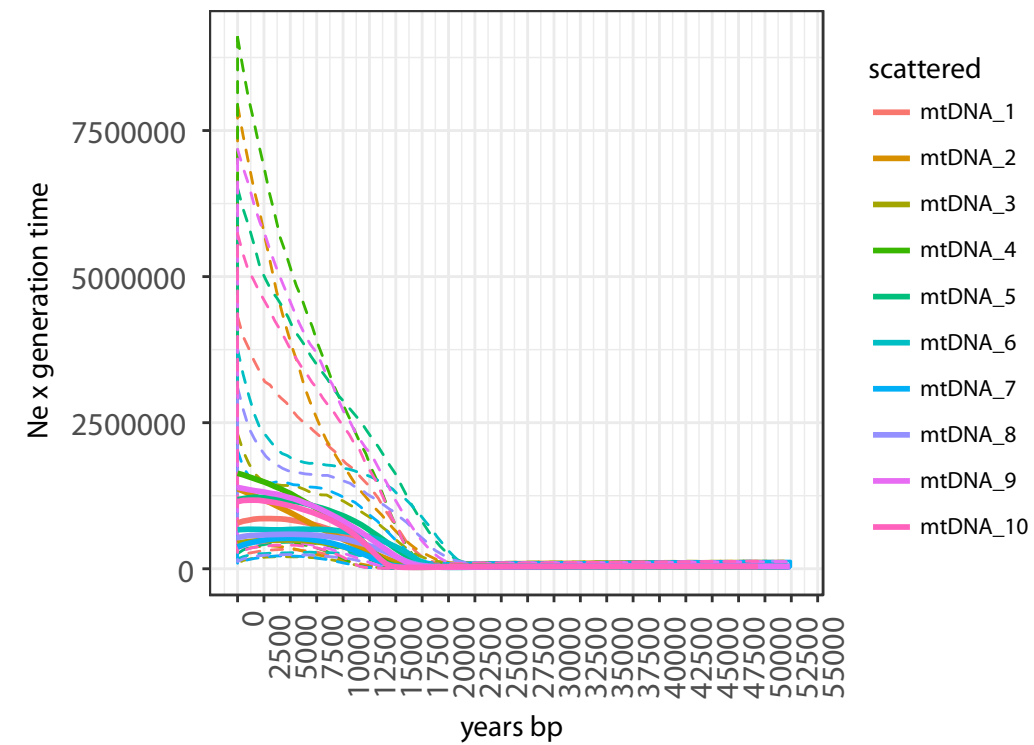
C)



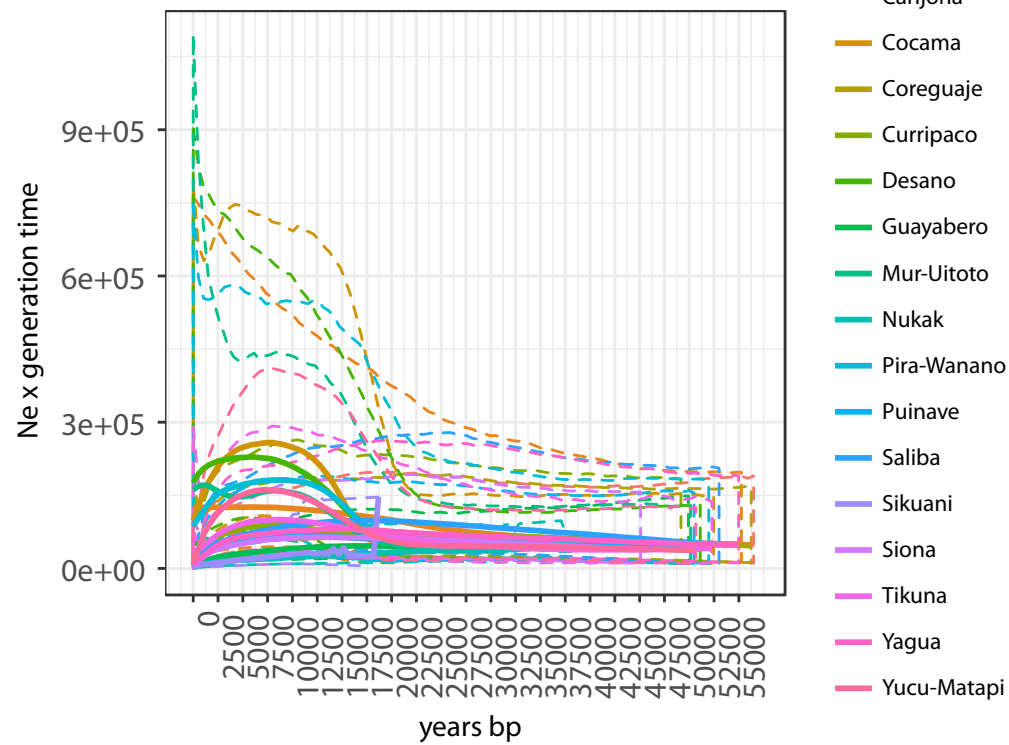
A)



B)



C)



Supplementary Table 1. Sequencing coverage per sample

ID	mean coverage	No. of non-genotyped sites
AMZ100	31.86	1
AMZ103	30.49	3
AMZ104	15.18	10
AMZ107	52.2	0
AMZ109	25.58	2
AMZ113	29.1	0
AMZ116	54.98	0
AMZ117	40.98	1
AMZ118	27.81	5
AMZ119	29.2	3
AMZ120	18.57	6
AMZ125	44.8	0
AMZ126	24.22	1
AMZ127	73.21	0
AMZ128	97.5	0
AMZ133	28.41	1
AMZ134	37.82	4
AMZ135	30.7	0
AMZ136	48.26	0
AMZ138	26.77	2
AMZ139	64.53	0
AMZ140	87.44	4
AMZ142	47.33	0
AMZ144	75.03	0
AMZ146	21.2	6
AMZ147	27.84	6
AMZ151	36.44	0
AMZ153	48.01	0
AMZ155	42.89	0
AMZ156	31.88	1
AMZ157	26.32	4
AMZ159	39.15	4
AMZ160	36.97	3
AMZ161	46.73	0
AMZ162	39.57	0
AMZ164	51.41	0
AMZ165	27.21	1
AMZ169	63.62	0
AMZ171	40.73	3
AMZ172	38.7	1
AMZ173	30.05	2
AMZ174	40	0
AMZ175	67.88	0
AMZ177	84.15	0
AMZ179	54.81	0
AMZ180	97.1	0
AMZ182	74.71	1
AMZ183	41.09	0

AMZ184	37.07	2
AMZ185	73.64	2
AMZ186	44.98	0
AMZ188	56.83	0
AMZ189	18.57	14
AMZ86	35.13	1
AMZ87	31.94	0
AMZ88	39.13	1
AMZ89	31.33	2
AMZ91	25.14	3
AMZ94	50.69	1
AMZ96	50.37	0
AMZ97	45.63	0
AMZ98	74.9	0
GUN234	32.63	3
GUN235	71.04	0
GUN236	23.33	7
GUN238	69.28	0
GUN239	46.83	1
GUN240	35.32	1
GUN241	29.52	2
GUN242	66.15	0
GUN243	63.94	0
GUN244	39.05	1
GUN245	55.53	0
GUN246	68.76	0
GUN248	45.44	1
GUN249	19.55	9
GUN250	11.5	24
GUN251	43.06	0
GUN252	30.09	5
GUN253	53.61	0
GUN254	38.15	2
GUN257	44.74	0
GUN258	45.4	2
GUN259	29.67	1
GUN260	31.3	4
GUN261	37.44	1
GUN262	18.28	17
GUN263	50.6	4
GUN264	33.79	4
GUN265	38.68	1
GUN266	36.9	0
GUN267	25.51	3
GUN268	30.17	0
GUN269	20.19	7
GUN270	35.01	0
GUN271	30.43	5
GUN272	35.54	3
GUN273	38.9	0

GUV01	17.24	11
GUV03	29.29	7
GUV06	17.64	6
GUV07	28.09	2
GUV08	25.02	6
GUV09	21.75	4
GUV10	22.27	3
GUV11	27.6	2
GUV12	65.39	0
GUV14	23.38	3
GUV15	27.49	8
GUV19	20.05	5
GUV20	38.06	0
GUV24	25.49	3
GUV28	17.52	5
GUV29	35.51	0
GUV30	43.68	0
GUV31	23.45	2
GUV32	26.91	5
GUV33	58.41	0
GUV34	28.17	0
GUV35	5.05	113
GUV36	9.79	29
GUV38	24.96	1
GUV41	25.6	2
GUV42	34.73	38
GUV43	22.85	6
GUV44	23.07	5
GUV45	29.41	1
GUV46	33.05	1
GUV47	39.73	1
GUV48	30.22	0
GUV49	26.76	3
GUV50	48.45	0
GUV51	46.4	0
GUV52	39.29	0
GUV53	14.44	7
GUV54	35.12	0
GUV55	28.01	1
GUV56	35.14	1
GUV57	41.67	1
GUV59	29.77	1
GUV60	41.38	1
GUV62	45.54	0
GUV64	66.06	0
GUV65	39.39	0
GUV66	34.96	2
GUV67	39.57	5
GUV69	29.36	2
GUV77	24.95	3

GUV80	39.86	2
GUV82	37.76	0
GUV85	45.8	0
GV1	36.78	4
GV10	32.66	3
GV15	45.83	3
GV19	50.75	2
GV2	27.3	3
GV21	30.12	5
GV22	21.01	2
GV23	32.67	7
GV24	23.62	9
GV26	26.65	10
GV28	34.53	2
GV29	27.52	119
GV3	16.66	22
GV30	32.52	3
GV34	42.66	4
GV6	36.59	12
GV9	58.16	2
GVG1	26.15	8
GVG10	21.34	16
GVG12	18.06	17
GVG19	32.37	3
GVG26	25.37	9
GVG28	39.75	9
GVG29	41.61	7
GVG3	44.81	1
GVG30	40.52	4
GVG5	33.99	8
GVG6	34.76	7
GVG7	33.4	9
GVG8	32.99	5
GVG9	51.74	2
MET191	73.91	0
MET192	42.3	0
MET193	29.76	3
MET194	31.63	1
MET195	50.43	0
MET196	70.02	0
MET197	80.85	1
MET199	37.46	1
MET201	37.33	0
MET202	29.83	0
MET204	53.44	0
MET205	30.15	4
MET206	24.39	7
MET207	24.02	2
MET208	47.81	0
MET209	47.82	4

MET210	40.42	1
MET211	56.67	0
MET212	40.05	3
MET213	62.07	0
MET214	37.12	1
MET215	27.86	7
MET216	21.29	4
MET217	38.13	7
MET218	47.66	3
MET219	53.71	0
MET220	45.89	1
MET222	62.94	0
MET224	44.39	3
MET225	21.99	12
MET226	32.32	1
MET229	13.39	17
MET230	85.09	0
MET231	102.69	0
PUT274	41.01	0
PUT279	29.47	1
PUT280	36.43	0
PUT281	31.51	3
PUT282	26.85	4
PUT283	34.73	2
PUT288	34.19	3
PUT289	33.5	3
PUT294	37.65	2
PUT295	45.19	3
PUT296	42.79	8
PUT297	35.25	1
PUT298	27.26	5
PUT300	41.09	0
PUT305	31.95	4
PUT306	32.27	2
PUT307	39.2	1
PUT308	31.21	1
PUT309	35.67	5
PUT310	22.26	0
PUT317	34.05	4
PUT319	24.12	7
PUT321	35.42	3
PUT324	28.97	2
PUT325	31.78	0
PUT327	34.1	3
PUT329	29.32	2
PUT330	34.95	1
PUT331	44.84	4
PUT332	28.3	1
PUT334	31.6	0
PUT336	36.37	2

PUT337	34.09	4
PUT338	21.92	4
PUT339	41.07	0
PUT342	30.37	2
PUT346	35.31	2
PUT347	26.72	4
PUT348	22.6	6
PUT349	39.08	2
PUT350	35.51	1
PUT351	25.12	2
PUT353	35.33	2
PUT355	26.29	6
PUT357	15.6	11
PUT360	17.61	9
PUT362	26.51	0
PUT366	14.92	13
PUT369	15.82	10
PUT370	33.88	1
PUT371	36.01	0
PUT372	26.76	2
PUT374	20.9	5
PUT375	33.07	38
PUT376	51.06	2
PUT377	25.58	2
PUT378	37.44	3
PUT382	30.47	3
PUT384	27.99	0
PUT385	32.76	0
PUT386	23.82	3
PUT387	32.03	0
PUT388	26.92	3
PUT389	25.04	0
PUT390	33.82	1
PUT392	32.12	1
PUT394	26.46	4
PUT395	30.27	2

Supplementary Table 2. Molecular diversity indices in the NRY (upper half) and the mtDNA (lower half)

NRY												
Population	N	No.hap	S	GD	GD.SD	ND	ND.SD	MPD	MPD.SD	TajD	Pval	Family
Yucu-Matapi	24	10	98	0.74	0.09	1.1E-05	4.9E-06	25.45	11.57	-0.119	0.511	Arawakan
Curripaco	13	12	133	0.99	0.04	1.5E-05	6.8E-06	34.62	16.14	-0.879	0.170	Arawakan
Ach-Piapoco	20	15	221	0.97	0.03	1.8E-05	8.2E-06	42.61	19.30	-1.313	0.070	Arawakan
Carijona	5	5	88	1.00	0.13	1.6E-05	8.5E-06	38.00	20.03	-0.762	0.318	Carib
Desano	14	5	42	0.59	0.14	2.8E-06	1.4E-06	6.60	3.32	-2.179	0.004	Tukanoan
Pira-Wanano	11	5	14	0.78	0.09	1.4E-06	7.6E-07	3.24	1.81	-1.423	0.082	Tukanoan
Siona	10	9	155	0.98	0.05	1.7E-05	8.3E-06	41.22	19.59	-1.233	0.118	Tukanoan
Coreguaje	11	10	112	0.98	0.05	1.2E-05	5.9E-06	29.42	13.95	-1.107	0.146	Tukanoan
Sikuani	13	6	93	0.79	0.09	1.3E-05	6.3E-06	31.77	14.84	0.273	0.634	Guahiban
Guayabero	17	9	348	0.90	0.04	3.8E-05	1.7E-05	88.78	40.19	-0.593	0.296	Guahiban
Guay_noC2	15	8	99	0.89	0.05	1.6E-05	7.2E-06	36.70	16.93	0.901	0.842	Guahiban
Saliba	8	8	172	1.00	0.06	2.3E-05	1.1E-05	53.71	26.07	-1.041	0.164	Piaroa-Saliban
Mur-Uitoto	13	13	412	1.00	0.03	3.1E-05	1.4E-05	72.97	33.66	-2.077	0.004	Huitotoan
Mur-Ui_noC2	12	12	166	1.00	0.03	1.6E-05	7.5E-06	37.79	17.70	-1.466	0.058	Huitotoan
Puinave	16	10	126	0.90	0.06	9.8E-06	4.6E-06	23.26	10.81	-1.678	0.035	Maku-Puinave
Nukak	11	5	48	0.82	0.08	1.0E-05	4.8E-06	23.75	11.33	2.118	0.998	Maku-Puinave
Tikuna	10	10	215	1.00	0.04	2.2E-05	1.1E-05	52.76	24.98	-1.527	0.050	Tikuna
Cocama	9	9	211	1.00	0.05	2.0E-05	9.7E-06	48.00	23.01	-1.984	0.001	Tupi
Yagua	10	6	81	0.87	0.09	1.2E-05	5.7E-06	28.07	13.45	-0.098	0.509	Peba-Yaguan

N: number of individuals

No.hap: number of haplotypes

S: number of segregating sites

GD, GD.SD: gene diversity and standard deviation

ND, ND.SD: nucleotide diversity and standard deviation

MPD, MPD.SD: mean number of pairwise differences and standard deviation

TajD: Tajima's D value

Pval: P values of Tajima's D

mtDNA

Population	N	No.hap	S	GD	GD.SD	ND	ND.SD	MPD	MPD.SD	TajD	Pval	Family
Yucu-Matapi	39	19	150	0.88	0.05	2.3E-03	1.1E-03	37.38	16.61	-0.211	0.440	Arawakan
Curripaco	17	11	111	0.88	0.07	2.3E-03	1.2E-03	38.54	17.64	-0.141	0.456	Arawakan
Ach-Piapoco	24	8	105	0.77	0.07	2.1E-03	1.1E-03	34.60	15.62	0.363	0.719	Arawakan
Carijona	8	6	97	0.89	0.11	2.6E-03	1.4E-03	42.71	20.80	-0.257	0.405	Carib
Desano	17	14	139	0.98	0.03	2.4E-03	1.2E-03	40.40	18.47	-0.546	0.322	Tukanoan
Pira-Wanano	13	11	119	0.96	0.05	2.4E-03	1.2E-03	39.08	18.18	-0.389	0.368	Tukanoan
Siona	17	8	87	0.82	0.07	2.0E-03	1.0E-03	32.31	14.84	0.194	0.613	Tukanoan
Coreguaje	19	12	104	0.92	0.05	2.0E-03	1.0E-03	33.70	15.37	-0.147	0.508	Tukanoan
Sikuani	16	7	55	0.87	0.05	1.5E-03	7.6E-04	24.08	11.18	1.310	0.941	Guahiban
Guayabero	35	11	80	0.88	0.03	2.3E-03	1.1E-03	37.31	16.62	2.318	0.992	Guahiban
Saliba	16	7	108	0.86	0.06	2.3E-03	1.2E-03	37.49	17.22	0.046	0.577	Piaroa-Saliban
Mur-Uitoto	26	23	159	0.99	0.01	2.3E-03	1.1E-03	37.46	16.84	-0.841	0.207	Huitotoan
Puinave	19	9	93	0.85	0.06	2.3E-03	1.2E-03	37.89	17.25	0.630	0.788	Maku-Puinave
Nukak	16	4	56	0.64	0.10	1.9E-03	9.7E-04	31.07	14.33	1.925	0.989	Maku-Puinave
Tikuna	18	13	109	0.94	0.04	2.2E-03	1.1E-03	37.02	16.90	0.399	0.722	Tikuna
Cocama	17	14	143	0.98	0.03	2.7E-03	1.4E-03	44.64	20.37	-0.580	0.274	Tupi
Yagua	13	8	98	0.92	0.05	2.3E-03	1.2E-03	37.26	17.35	0.205	0.646	Peba-Yaguan

N: number of individuals

No.hap: number of haplotypes

S: number of segregating sites

GD, GD.SD: gene diversity and standard deviation

ND, ND.SD: nucleotide diversity and standard deviation

MPD, MPD.SD: mean number of pairwise differences and standard deviation

TajD: Tajima's D value

Pval: P values of Tajima's D

Supplementary table 3A. AMOVA results of five replica datasets for the mtDA and NRY

	mtDNA % of variation							NRY % of variation						
	d.f	replica 1	replica 2	replica 3	replica 4	replica 5	mean	d.f.	replica 1	replica 2	replica 3	replica 4	replica 5	mean
Among populations	3	9.36	6.14	4.51	7.41	11.53	7.79	3	17.62	16.66	16.98	16.62	16.42	16.86
Within populations	73	90.84	93.86	95.45	91.59	88.47	92.042	73	82.38	83.34	83.02	83.38	83.58	83.14
Total	76	100.2	100	100	100	100	100.04	76	100	100	100	100	100	100
F_{ST}		0.094	0.061	0.05	0.08	0.12	0.081		0.18	0.17	0.17	0.17	0.17	0.172

Supplementary table 3B. Nucleotide diversity and standard deviations for each replica dataset

		mtDNA		NRY	
		nuc.div	S.D	nuc.div	S.D
Replica 1	nuc.div	2.3E-03	1.9E-05		
	S.D	1.1E-03	8.2E-06		
Replica 2	nuc.div	2.3E-03	2.0E-05		
	S.D	1.1E-03	8.7E-06		
Replica 3	nuc.div	2.2E-03	1.9E-05		
	S.D	1.1E-03	8.5E-06		
Replica 4	nuc.div	2.3E-03	2.0E-05		
	S.D	1.1E-03	8.6E-06		
Replica 5	nuc.div	2.3E-03	1.9E-05		
	S.D	1.1E-03	8.5E-06		