

TABLE S5

Extended version of Table 1 from manuscript, including effective population estimators and demographic indicators.

Population	N	A	n(mt)	K(mt)	H(mt)	$\pi$	$\theta_\eta$	Fs	n(y)	K(y)	H(y)	$\theta_H$	GW
Aviles	154,627	555	26	25	0.997	0.008	0.014	-3.186***	15	15	0.48205	1.50258	0.8998
Caudal	67,820	837	44	44	1	0.008	0.016	-8.923***	13	13	0.59961	1.58265	0.94615
EoNavia	44,211	1,642	54	46	0.99	0.007	0.017	-6.628***	31	31	0.51944	1.50303	0.92051
Gijón	303,484	525	31	30	0.998	0.008	0.015	-5.049***	13	13	0.54931	1.51964	0.91111
Nalón	79,842	646	26	25	0.997	0.009	0.013	-1.676***	19	19	0.63518	1.65771	0.93718
Narcea	29,968	2,127	24	22	0.993	0.008	0.013	-2.628***	10	10	0.59487	1.57469	0.8011
Oriente	53,386	1,927	81	69	0.994	0.007	0.018	-13.708***	43	43	0.57833	1.55032	0.92885
Oviedo (Central)	262,372	1,265	48	38	0.981	0.006	0.015	-3.6592***	27	27	0.56125	1.53047	0.94829
Oviedo (South)	4,647	669	9	8	0.972	0.005	0.007	2.443	3	3	0.79487	2.56653	0.87821
Oviedo (East)	67,423	409	19	16	0.982	0.006	0.01	0.954	10	10	0.59658	1.57752	0.96795

N: Region census size.

A: Region area (in km<sup>2</sup>)

n (mt): Sample size of mtDNA sequences.

K (mt): Number of mitochondrial lineages.

H (mt): Haplotype diversity.

$\pi$ : Nucleotide diversity.

$\theta_\eta$ : Population-mutation rate parameter inferred from the minimum number of mutations.

Fs: Value of the Fu Fs statistic.

n (y): Sample size of NRY haplotypes.

K (y): Number of NRY haplotypes.

H (y): Nei unbiased diversity measure.

$\theta_H$ : Population-mutation rate parameter inferred from the expected heterozygosity.

GW: Value of the Garza-Williamson statistic.

Significance tests were based on 10,000 simulations. The original definition of the Fu Fs test notes that it should be considered as significant at the 5% level if the p-value is below 0.02, which is the initial cutoff value that we used.

\* =  $p < 0.02$       \*\* =  $p < 0.002$       \*\*\* =  $p < 0.0002$