		1											ata 16311 Murrosoftin				16783 16783 161641	Rie
Josef L		J			-						þ					loc	018310 168710	
				10550			1137		1564 <sup>10</sup> × 32/17 /				A TRUTTIENT AVENUE INState	U5b2		2 2 122 100 100 100 100 100 100 100 100		9804 <b>100 100 100</b>
		152 9850		199 197 197		14484	(15) UBb	(15) U8b				8		ſ.	2 A		S.	
			cic.			USa			II		16219	6		L	199	3507 8743 8743		
			CTIN				16309									1		
					tin the second				- 				-10			16311	16129 16129	
				1408			U9a		<b>R</b>				,-					
		499	-				083							3			197 197 19 10	<b>1</b>
			4	14620	5		2(UA)							16181		11		16335
	1811			1			<u>361</u> 3237 35+3C 16	T Constant	•	3197 3197 1000							309+C	28
					<u>152</u> 3546		6119 <u>96</u> 6343 <u>9</u> 6								2.2	1	25 25	
		150 309+C	3 S	4640A	888	1910	9								9	-	5441 11778	(24)
			1545		0 5	90 19 19	. 6 5										723 5964	- <mark>(33</mark>
				226 667 928	16306	<u>4</u> 16	9 <del>1</del> 5		(re)							l	70+T	
			152	3720 5390 5426 6045	6152 13020 13734 13734 15007	16362	217 309+0	117 11	16519		3					5339		K
			L	14935 15061 16234	044 708 708	8023 8676	11890	da ta ta				793 256	1 60	5a1		-	1388	
			<u>146</u> 2706	12106 13194 15049	234 234 906	9094 9614	15930	16244 1636	<b>N</b>			41	163 163	ö		1 1	6023 6023 7569 8251	R
		16051											195 279 -	3531 3531 8395	11	157 115 16111 163	Ulb B	i.
			16206	5262 8572 11150	1562 1631 1631					285	15148	15954C 16249		2100	1	25		
73	pre-HV	14766	H	- <b>I</b>	4769 4769	<u>750</u>	263 3154C	15326	rcRS				224 499 6026 7581	16181 16181	0 <sup>1</sup>	385 d6216	53594 55594 5774 5894 10034	127 1342 16122

Reports

**Fig**<sup>-1</sup> Tree of 39 mtDNA sequences belonging to haplogroup U. The tree, rooted using the reference sequence (rCRS) (Andrews et al. 1999) as an outgroup, illustrates subhaplogroup affiliations. The sequencing procedure and phylogeny construction were performed as described elsewhere (Torroni et al. 2001 ; Achilli et al. 2004). For phylogeny construction, the highly variable site 16519 and the length variation in the poly-C stretch at nts 309–315 were not used, and half the weight was assigned to the control-region mutations, relative to that assigned to coding-region mutations. Mutations are shown on the branches; they are transitions unless a base change is explicitly indicated. Insertions are suffixed with a plus sign (+

## Elec ronic-Da aba e Informa ion

Accession numbers and URLs for data presented herein are as follows:

- Author's Web site, http://ipvgen.unipv.it/docs/projects/torroni \_data/torroni\_sequences.html (for the complete mtDNA sequences)
- GenBank, http://www.ncbi.nlm.nih.gov/Genbank/ (for the complete mtDNA sequences [accession numbers AY882379– AY882417])

## Reference

- Achilli A, Rengo C, Magri C, Battaglia V, Olivieri A, Scozzari R, Cruciani F, Zeviani M, Briem E, Carelli V, Moral P, Dugoujon JM, Roostalu U, Loogväli EL, Kivisild T, Bandelt HJ, Richards M, Villems R, Santachiara-Benerecetti AS, Semino O, Torroni A (2004) The molecular dissection of mtDNA haplogroup H confirms that the Franco-Cantabrian glacial refuge was a major source for the European gene pool. Am J Hum Genet 75:910–918
- Andrews RM, Kubacka I, Chinnery PF, Lightowlers RN, Turnbull DM, Howell N (1999) Reanalysis and revision of the Cambridge reference sequence for human mitochondrial DNA. Nat Genet 23:147
- Cann RL, Stoneking M, Wilson AC (1987) Mitochondrial DNA and human evolution. Nature 325:31–36
- Cavalli-Sforza LL, Menozzi P, Piazza A (1994) The history and geography of human genes. Princeton University Press, Princeton, NJ
- Forster P, Harding R, Torroni A, Bandelt H-J (1996) Origin and evolution of Native American mtDNA variation: a reappraisal. Am J Hum Genet 59:935–945
- Forster P, Torroni A, Renfrew C, Rohl A (2001) Phylogenetic star contraction applied to Asian and Papuan mtDNA evolution. Mol Biol Evol 18:1864–1881
- Kivisild T, Rootsi S, Metspalu M, Mastana S, Kaldma K, Parik J, Metspalu E, Adojaan M, Tolk HV, Stepanov V, Golge M, Usanga E, Papiha SS, Cinnioglu C, King R, Cavalli-Sforza L, Underhill PA, Villems R (2003) The genetic heritage of the earliest settlers persists both in Indian tribal and caste populations. Am J Hum Genet 72:313–332
- Mishmar D, Ruiz-Pesini E, Golik P, Macaulay V, Clark AG, Hosseini S, Brandon M, Easley K, Chen E, Brown MD, Sukers.aNBrown

tion shaped regional mtDNA variation in humans. Proc Natl Acad6Gown-176

Quintana-Murci6Go55.6(L,)-355.6(Chaix)-355.6(R)0(,)-355.6(W)72.3(ells)-355.6(RS3-3667.8(Behar)-30(rDM,)-367.8(Sayar)-355.6(H,)]TJ29.33