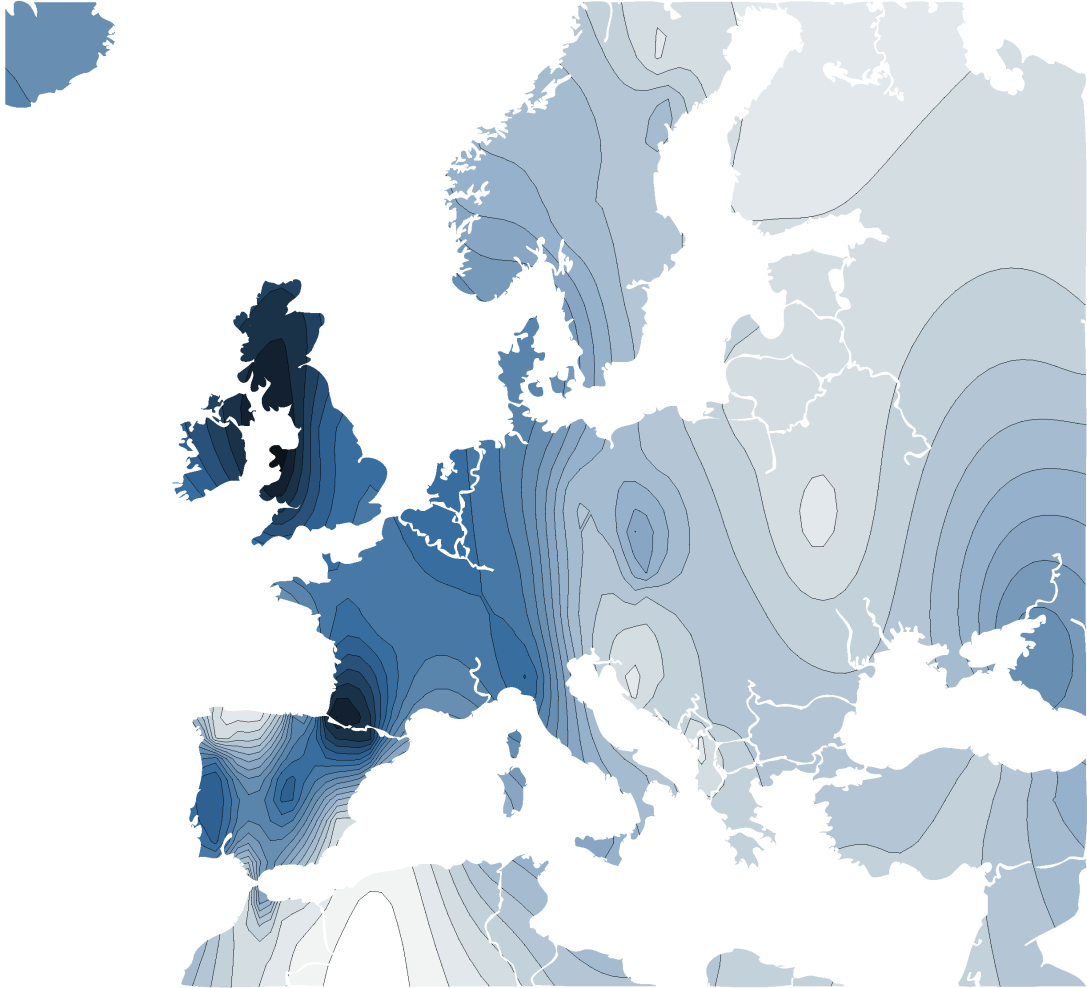


Distribution map for Y-chromosome
haplogroup R1b



**:: Marker Testing ::**

To determine which haplogroup you are in, your DNA was first extracted from the sample you provided. It then underwent a primary screen which looks at several SNP markers at the very top of the Y-chromosome tree. This primary panel, called Multiplex A-R, is listed below along with the secondary panels. Based upon the results of this primary screen, the secondary panel was chosen. The panels that you were tested upon are marked light blue and the markers that you were positive on shown light green.

Multiplex	A-R	AB	CD	E	FGHI	J
Region covered	All	African (for 168C samples)	Asian (for M168T/M89C/M96G samples)	African, Middle Eastern (for M96C samples)	Eurasian (for M89T/M9G/M304A samples)	Middle Eastern (for M304C samples)
Markers Tested	M9	M31	M15	DYS391	M26	M47
	M45	M32	M38	M2	M52	M67
	M89	M42	M48	M33	M170	M92
	M96	M150	M55	M35	M201	M172
	M122	M146	M125	M58	M253	M241
	M168	M182	M130	M75	P15	M267
	M175	P4	M131	M78	P16	
	M207		M145	M81	P37	
	M304		M151	M123		
	M343		M210			
	AmelXY		M217			

Multiplex	KLMN	O1	O2	PQ	R1	R2
Region covered	Eurasian (for M9C/M45G/M175+ samples)	SE-Asian (for M175-/M122T samples)	SE-Asian (for M175-/M122C samples)	Asian, Native American (for M45A/M207A samples)	Indo-European (for M207G/M343C samples)	Indo-European (for M343A samples)
Markers Tested	M5	M88	M7	M3	M17	M18
	M11	M95	M113	M19	M56	M37
	M70	M101	M117	M120	M87	M65
	M178	M103	M121	M143	M124	M126
	M214	M119	M134	M194	M157	M153
	M231	P31	M159	M199	M173	M269
	SRY9138	SRY465	M164	M242	SRY10831	P25
	Tat			M323		SRY-2627

:: Haplogroup Result ::

The testing of your sample shows that you were positive on the above highlighted markers. Additionally, you were negative on the other markers within the panels tested. Knowing this we can determine your haplogroup. An asterisk after the haplogroup would designate that branch-defining markers below the haplogroup have been tested but proved negative - e.g. I* or R1b3*

We determine you to be in Y-chromosome haplogroup **R1b3***

R1b haplogroup is characterized by P25 mutation. Almost all R1b types fall within one of the sub-categories of R1b, defined by marker M269. 2003 version of the YCC (Y Chromosome Consortium) nomenclature (YCC 2003) named the group defined by M269 as R1b3. However, this group is still often referred to as R1b to avoid confusion between the 2002 and 2003 nomenclatures. In many studies published so far, the resolution level is lower and for that reason in some cases M173(x SRY 1532) individuals are deduced to belong to R1b clade according to Cruciani et al. (2002), where all studied western Europeans from this clade have been shown to share the additional mutation M269. R1b haplogroup was referred as haplogroup 1 (overlaps R1b only partly) or Eu 18 in earlier literature (Jobling et al. 1997; Rosser et al. 2000; Semino et al. 2000).

About 50% of present European Y chromosomes share the M173 marker that defines R1 clade and consists of two separate branches (R1a and R1b3) harboring contrasting geographic distributions. R1b-M173 lineages are considered to trace an Upper Paleolithic migration from West Asia to European regions then occupied by Aurignacian culture (Semino et al. 2000, Underhill et al. 2001, Wells et al. 2001). Therefore, the members of R1b3 are believed to be the descendants of the first modern humans who entered Europe about 35,000-40,000 years ago.

The distribution of hg R1b3 covers actually an area wider than Europe, but the centre of its cline in Europe lies in western Europe, revealing post-Last Glacial Maximum (post-LGM) spread from the Iberian refuge area as was supposed by Semino et al. (2000) and is associated with specific 49a,f TaqI haplotype 15 (Semino et al. 1996). After LGM, when the ice finally retreated, these people, who acquired the mutation that defines them as R1b3, moved from the refugee area in Iberian Peninsula and South-Western France up the Atlantic coast, continental Europe and also to the direction of Italy.

R1b3 is highly dominant lineage in Western Europe, covering about 40-70% of paternal gene pool of continental Western European populations (Spanish, Catalans Portuguese, French, Danes etc.) and reaching up to 82% in Irish population. Western European R1b3 is characterized by Atlantic Modal STR haplotype (AMH) defined by 6 STRs (DYS 19, 388, 390, 391, 392 393)- 14-12-24-11-13-13, which with its one step derivatives covers about 56% of Western European R1b individuals (Wilson et al. 2001). This haplotype is possibly the ancestral haplotype for haplogroup R1b in Europe, as it has modal values for each of the alleles and is well connected to all of the other haplotypes in the haplogroup. This common subtype of R1b is present primarily along the Atlantic coast in Europe and the British Isles. Because of the high prevalence of AMH among the Irish and Welsh, some researchers consider this haplotype to be representative of the early Celtic migrations and a distinguishing characteristic among the Celts and the Anglo-Saxons (Wilson et al. 2001).

There exists a minor sub-clade of R1b3, characterized by additional downstream mutation SRY2627 or M167 and named R1b3f (YCC 2003). This clade shows a specific focal distribution area, being spread only in limited geographic region in Iberia and France, mostly among Spanish and French Basques (20%), Catalans (20%) and with lower frequency in other Iberian populations and French (Rosser et al. 2000; Hurles et al. 1999). In other European regions this clade has practically not been detected. R1b3f haplogroup was referred as haplogroup 22 in earlier literature (Hurles et al. 1999; Rosser et al. 2000). There is also another minor sub-clade of R1b, namely R1b3d - defined by downstream mutation M153 and showing focal distribution (16-3%) in some Iberian

populations like Basques and Andalusians (Bosh et al. 2001).

Differentially from Western Europe, R1b3 individuals in the Balkans, the Caucasus and in Anatolia, mostly possess 49a,f TaqI haplotype 35 (Semino et al. 1996; Cinnioglu et al. 2004). The overall spatial distribution of R1b lineages shows a frequency peak (40% to 80%) in Western Europe and a decrease in Eastern (with the exception of 43% in the Ossetians) and Southern Europe, whereas R1b variance shows multiple peaks in West Europe and Asia Minor. While R1b variance displays a clear-cut northwestern-southeastern decline in South East Europe, R1b frequency decline continues from Western towards Southeastern and Southern Europe. These spatial patterns might be due to the fact that R1b lineages contain associated 49a,f haplotype 15 and 35 sub-lineages with opposite distributions possibly reflecting re-peopling of Europe from Iberia and Asia Minor during the Late Upper Paleolithic and Holocene (Cinnioglu et al. 2004). The overall R1b frequency distribution in the Balkan Peninsula suggests its possible arrival from two different source populations during re-colonization of Europe after the LGM.

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