

Technical information sheet

Data information is reported for the **256 newly genotyped French samples** included in the final **Dataset A** of the work “Reshaping the *Hexagone*: the genetic landscape of modern France” from *Biagini et al.*

Array: Axiom ® Genome-Wide Human Origins Arrays

File format: PLINK bed/bim/fam

Department_Full_Name	Department_Acronym	N° of Samples	average_LAT	average_LON
Bas-Rhin	BR	48	48.5734	7.7521
Ille-et-Vilaine	leV	44	48.1189	-1.6766
Puy-de-Dôme	PdD	33	45.7772	3.087
Nord	NO	45	50.6206	3.0653
Paris	PAR	22	48.8566	2.3522
Bouches-du-Rhône	BdR	21	43.2965	5.3698
Haute-Garonne	HG	43	43.6047	1.4442

Quality filters applied in PLINK

We filtered out all variants with missing call rates greater than 5%, those that failed Hardy-Weinberg test at $p < 10^{-5}$, and samples with more than 10% missing genotype data.

Final variants included: **520,564** SNPs

Please Note: In the manuscript, **Dataset A** also includes samples from other works and the final number of variants in that case is different. Here, we repeated the filters only using our newly genotyped samples. We made this to support the correct use of the data.