

## Supplementary data:

# Intraethnic variation in steroid-5-alpha-reductase polymorphisms in prostate cancer patients: a potential factor implicated in 5-alpha-reductase inhibitor treatment

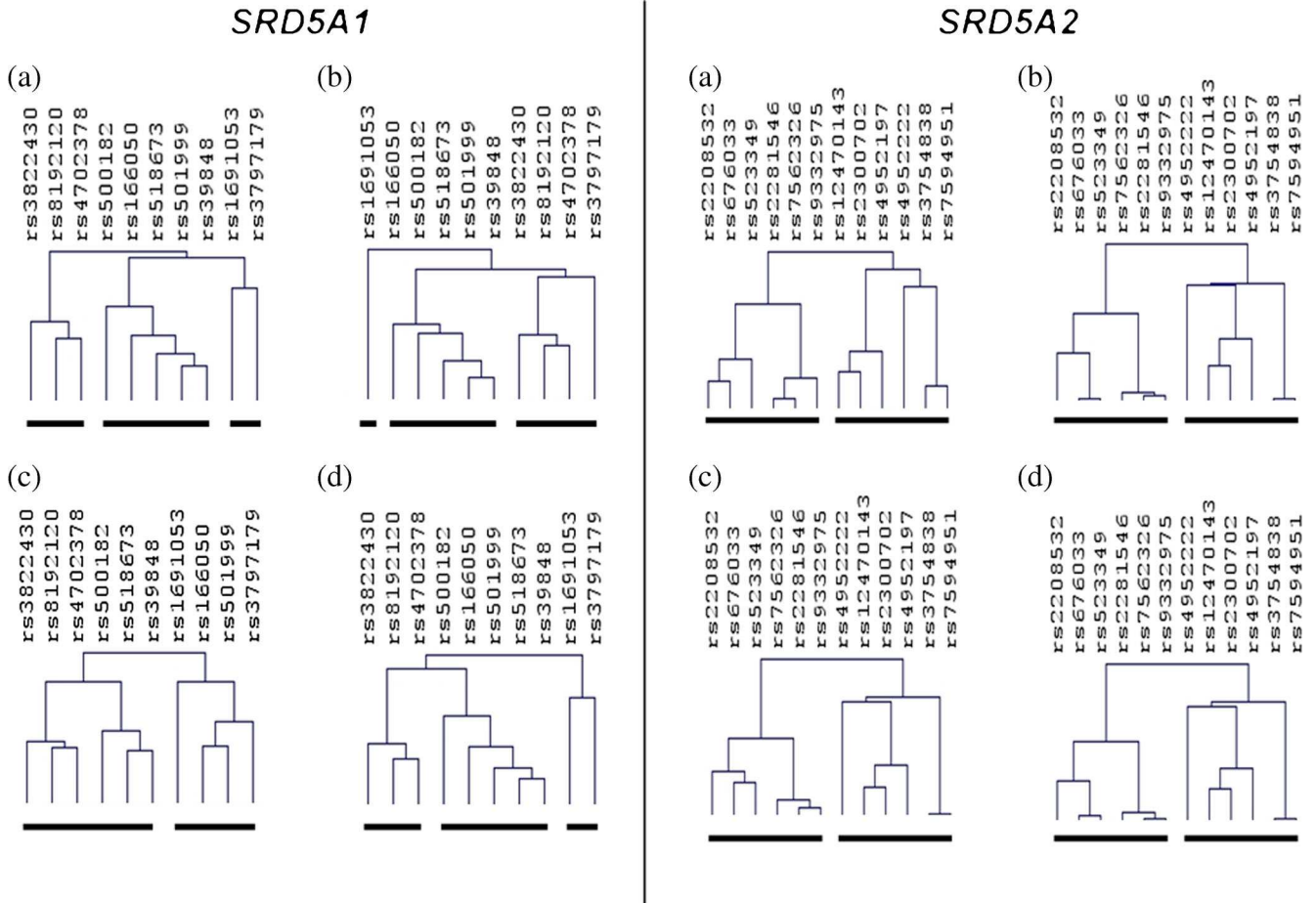
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**Table 1.** Description of SNPs included in the study and analysed by OpenArray.

Gene name	Symbol	Assay ID	SNP ID	Allele	Chr.	Position
Steroid-5-alpha-reductase, alpha polypeptide 1	SRD5A1	C–2935721_10	rs166050	A/G	5p13	6643847
	SRD5A1	C–7569675_10	rs501999	C/T	5p13	6635601
	SRD5A1	C–9766953_10	rs518673	A/G	5p13	6629930
	SRD5A1	C–2935715_10	rs3822430	A/G	5p13	6651970
	SRD5A1	C–820231_20	rs500182	G/T	5p13	6635799
	SRD5A1	C–1238034_20	rs8192120	A/C	5p13	6632320
	SRD5A1	C–27891058_10	rs4702378	C/T	5p13	6643874
	SRD5A1	AHS1EGH*	rs1691053	A/G	5p13	6677165
	SRD5A1	C–7569805_10	rs39848	C/T	5p13	6669762
	SRD5A1	C–29424231_10	rs3797179	A/G	5p13	6666922
	Steroid-5-alpha-reductase, alpha polypeptide 2	SRD5A2	C–2791128_10	rs2208532	A/G	2p13
SRD5A2		C–345976_10	rs12470143	C/T	2p13	31763558
SRD5A2		C–15876107_20	rs2281546	G/T	2p13	31757024
SRD5A2		C–2791143_10	rs3754838	T/C	2p13	31808300
SRD5A2		C–30116919_10	rs4952222	A/C	2p13	31799863
SRD5A2		C–2791134_10	rs7562326	C/T	2p13	31798765
SRD5A2		C–15755333_10	rs2300702	C/G	2p13	31788018
SRD5A2		AHUACMP*	rs4952197	A/G	2p13	31767131
SRD5A2		C–2362605_10	rs676033	C/T	2p13	31808970
SRD5A2		C–2362601_10	rs523349	C/G	2p13	31805706
SRD5A2		C–2486459_10	rs9332975	C/T	2p13	31750417
SRD5A2		C–11160708_10	rs7594951	C/T	2p13	31791793

Chr., chromosome; C, cytosine; T, thymine; A, adenine; G, guanine. All the assays are commercially available at Applied Biosystems, except \*Custom assays.



**Figure 1.** Nonsupervised hierarchical clustering of *SRD5A1* (left panel) and *SRD5A2* (right panel) SNPs in prostate cancer patients from (a) Andalusia, (b) Basque Country, (c) Canary and (d) Catalonia. Clustering was made using Euclidean distance correlation and average linkage, and was processed and displayed with MultiExperiment Viewer (<http://www.tigr.org>). The dendrogram shows clustering of SNPs. Lines below each panel show the main clusters generated.