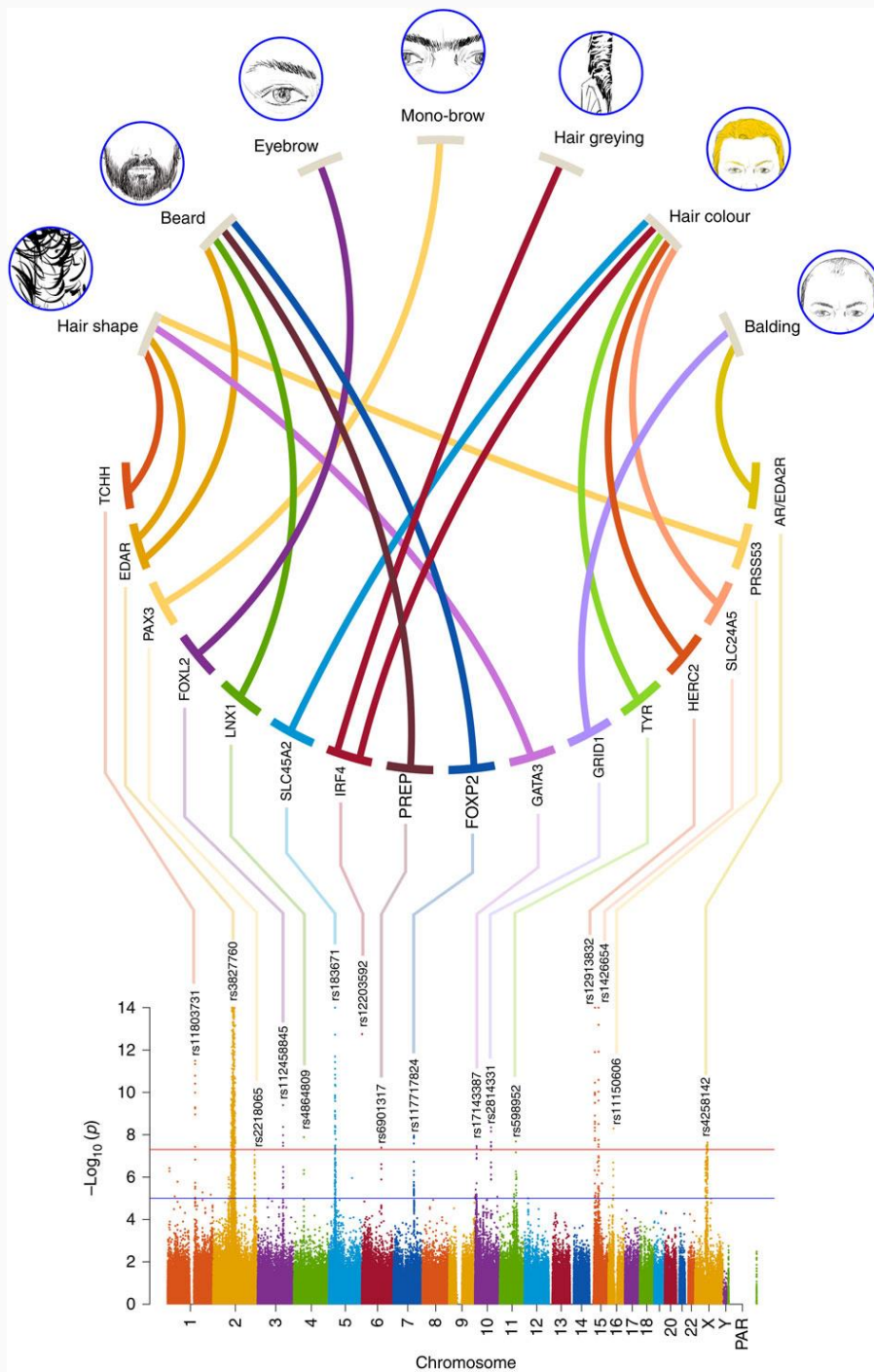


A genome-wide association scan in admixed Latin Americans identifies loci influencing facial and scalp hair features

We report a genome-wide association scan in over 6,000 Latin Americans for features of scalp hair (shape, colour, greying, balding) and facial hair (beard thickness, monobrow, eyebrow thickness). We found 18 signals of association reaching genome-wide significance (P values 5×10^{-8} to 3×10^{-119}), including 10 novel associations. These include novel loci for scalp hair shape and balding, and the first reported loci for hair greying, monobrow, eyebrow and beard thickness. A newly identified locus influencing hair shape includes a Q30R substitution in the Protease Serine S1 family member 53 (PRSS53). We demonstrate that this enzyme is highly expressed in the hair follicle, especially the inner root sheath, and that the Q30R substitution affects enzyme processing and secretion. The genome regions associated with hair features are enriched for signals of selection, consistent with proposals regarding the evolution of human hair.



At the top are shown drawings illustrating the seven hair features examined in the CANDELA study sample. Thick lines connect these features with the candidate genes identified in regions with SNPs reaching genome-wide significant association. At the bottom is shown a composite Manhattan plot displaying all significantly associated SNPs for the hair features examined. The rs number of the SNP with the smallest P value is shown at the top of each association peak.

<http://www.nature.com/ncomms/2016/160301/ncomms10815/full/ncomms10815.html#results>

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