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★ Moles (Falchi, 2009)

Mario Falchi, et al.
Nature Genetics

Skin Cancer

STUDY SUMMARY

Identification of 2 genomic regions associated with the number of moles on the body.

STUDY DESCRIPTION



Moles are pigmented skin lesions, usually developing during adulthood in sun-exposed areas of the skin. In most cases, moles are benign and don't require treatment. However, sometimes they turn into skin cancer. The count of moles on the body is the strongest known risk factor for melanoma, a type of cancer that develops from pigment-producing cells. This study examined genetic predisposition to developing moles by examining the genomes of over 1500 individuals of European descent. The study discovered 2 genomic regions that are significantly associated with the number of moles on the body. The genetic variants in these regions have also been directly linked to melanoma in previous studies.

DID YOU KNOW?

Most people have 10 to 40 moles. Moles may change in appearance or fade away over time. Hormonal changes of adolescence and pregnancy may cause moles to become darker and larger.

YOUR DETAILED RESULTS

The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to moles. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to moles. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to moles. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our [Nebula Library tutorial](#).

VARIANT [ⓘ]	YOUR GENOTYPE [ⓘ]	EFFECT SIZE [ⓘ]	VARIANT FREQUENCY [ⓘ]	SIGNIFICANCE [ⓘ]
rs4636294_A 	G / G	0.20 (-)	48%	3.40×10^{-45}
rs2284063_G 	A / A	-0.08 (-)	35%	3.40×10^{-8}