

This is a repository copy of Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility.

White Rose Research Online URL for this paper: http://eprints.whiterose.ac.uk/163759/

Version: Supplemental Material

Article:

Landi, MT, Bishop, DT orcid.org/0000-0002-8752-8785, MacGregor, S et al. (158 more authors) (2020) Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 52 (5). pp. 494-504. ISSN 1061-4036

https://doi.org/10.1038/s41588-020-0611-8

© 2020, Springer Nature. This is an author produced version of an article published in Nature Genetics. Uploaded in accordance with the publisher's self-archiving policy.

Reuse

Items deposited in White Rose Research Online are protected by copyright, with all rights reserved unless indicated otherwise. They may be downloaded and/or printed for private study, or other acts as permitted by national copyright laws. The publisher or other rights holders may allow further reproduction and re-use of the full text version. This is indicated by the licence information on the White Rose Research Online record for the item.

Takedown

If you consider content in White Rose Research Online to be in breach of UK law, please notify us by emailing eprints@whiterose.ac.uk including the URL of the record and the reason for the withdrawal request.



Figure 1. Manhattan plot for the total CM meta-analysis.





