



University of Dundee

The trans-ancestral genomic architecture of glyceic traits

LifeLines Cohort Study; Chen, Ji; Spracklen, Cassandra N.; Marenne, Gaëlle; Varshney, Arushi

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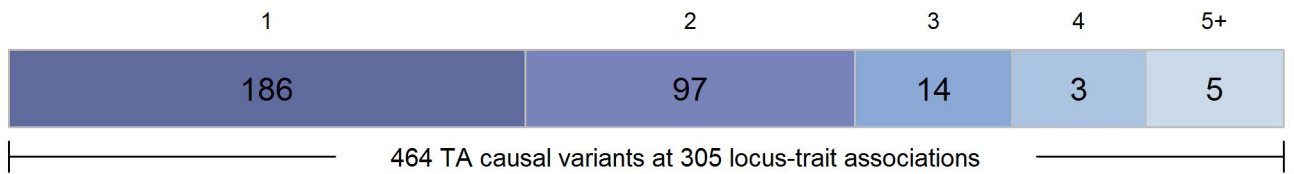
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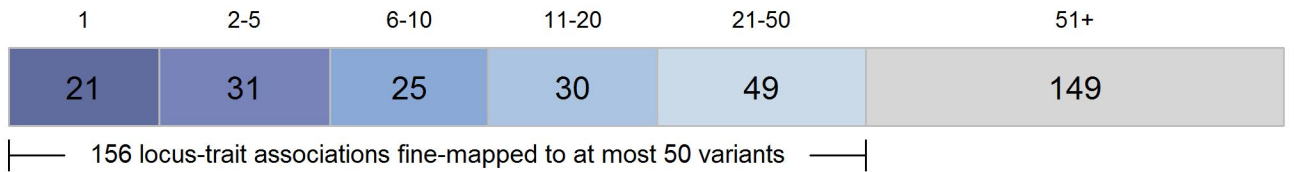
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A. Estimated number of causal variants at each locus-trait association



B. Number of variants at each 99% credible set



C. Fine-mapping resolution

