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* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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* Include model definition files including the full list of parameters used
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Both the mathematical model (R script) and the individual-based model (C-code) are available online on GitHub: <https://github.com/bramvandijk88/HGT_Genes_And_SGEs>. Also see “software used” on page 26 of the submitted PDF.