S12 Table. Power to detect association, at genome-wide significance ($p<5\text{x}10^{-8}$), with a variant of MAF 1% in the current study.

Trait	Max *N*	Variant explaining 0.05% of the trait variance	Variant explaining 0.1% of the trait variance	Variant explaining 0.2% of the trait variance
BMI	87,084	0.880	0.999	0.999
$\text{WHR}_{\text{adjBMI}}$	54,572	0.421	0.975	0.999
FG	46,694	0.277	0.921	0.999
$\text{FI}_{\text{adjBMI}}$	24,245	0.026	0.309	0.939