**Figure S3**

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Power vs false-discovery rate for discovering genomic regions containing masked causal variants. Here power is defined as the expected proportion of causal variants (affecting either males or females) that are being tagged by at least one selected SNP *j* or window *j*\*. False discovery rate is defined as the proportion of selected SNPs or windows that are not tagging any causal variants. Each point is an estimate and error bars for both axes represent 95% confidence intervals. Point estimates and intervals were derived using 30 Monte Carlo replicates. Each facet corresponds to a different “target area”, a fixed width around each causal variant that defines the set of SNPs effectively tagging it. LBR (SNP): uses the $PP\_{SNP\_{j}}$ metric spanning 1-0. LBR (Window): uses the maximum between $PPM\_{σ\_{g\_{j^{\*}}}^{2}}$ and $PPF\_{σ\_{g\_{j^{\*}}}^{2}}$ spanning 1-0. SMR: uses the F-test-based *p-*value spanning (on the -log10 scale) 30-0.