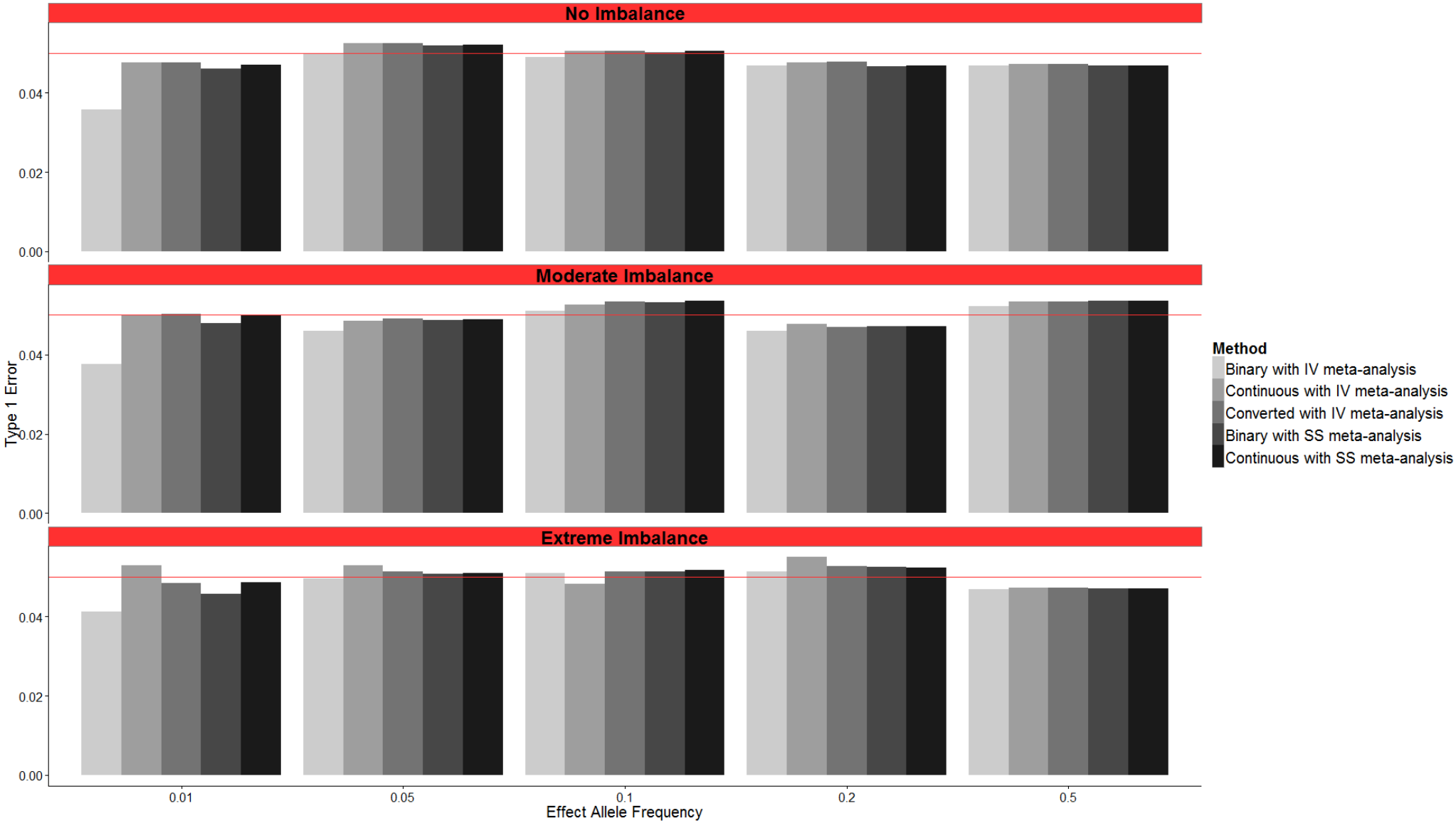
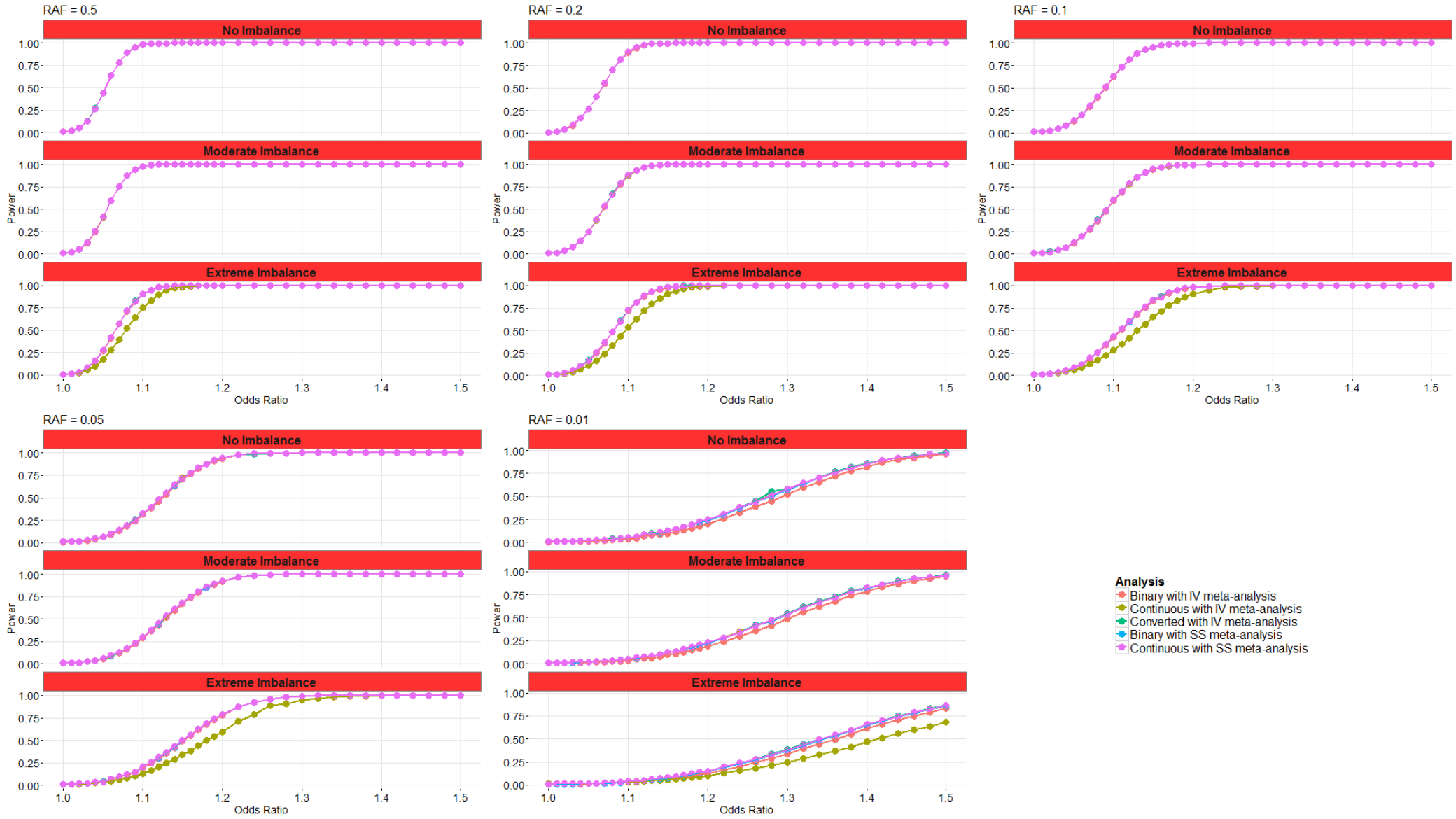
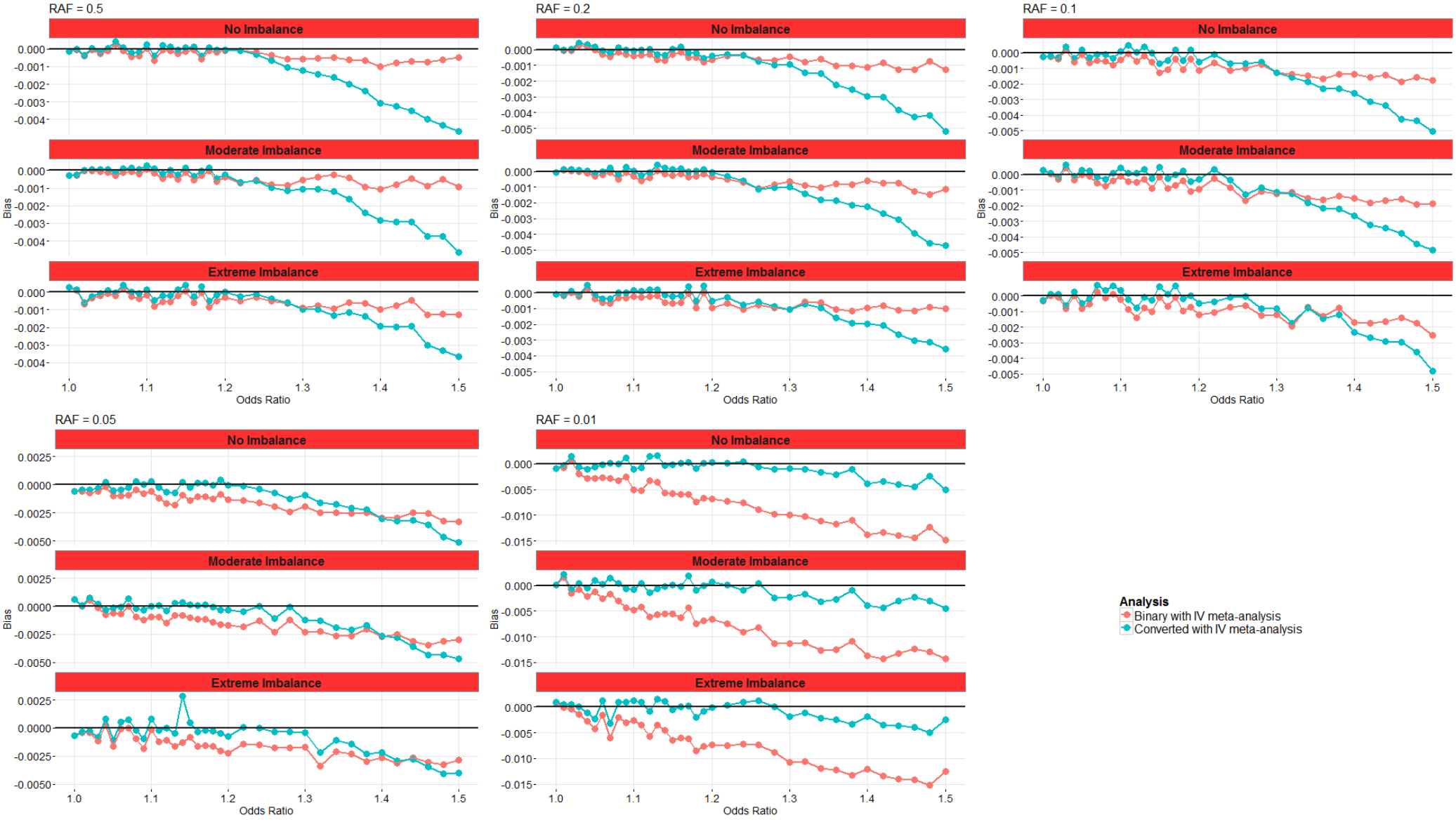



**Supplementary Figure S1.** Type I error rates to detect association ($p$<0.05) of a binary phenotype with a causal SNP, in the absence of population stratification or confounders, using alternative meta-analysis strategies for summary statistics obtained from linear and logistic regression models without random effects for the GRM (**Table 1**). Results are presented for a SNP with MAF in the range of 1-50%, and for variable extent of case-control imbalance (defined in **Table 2**).

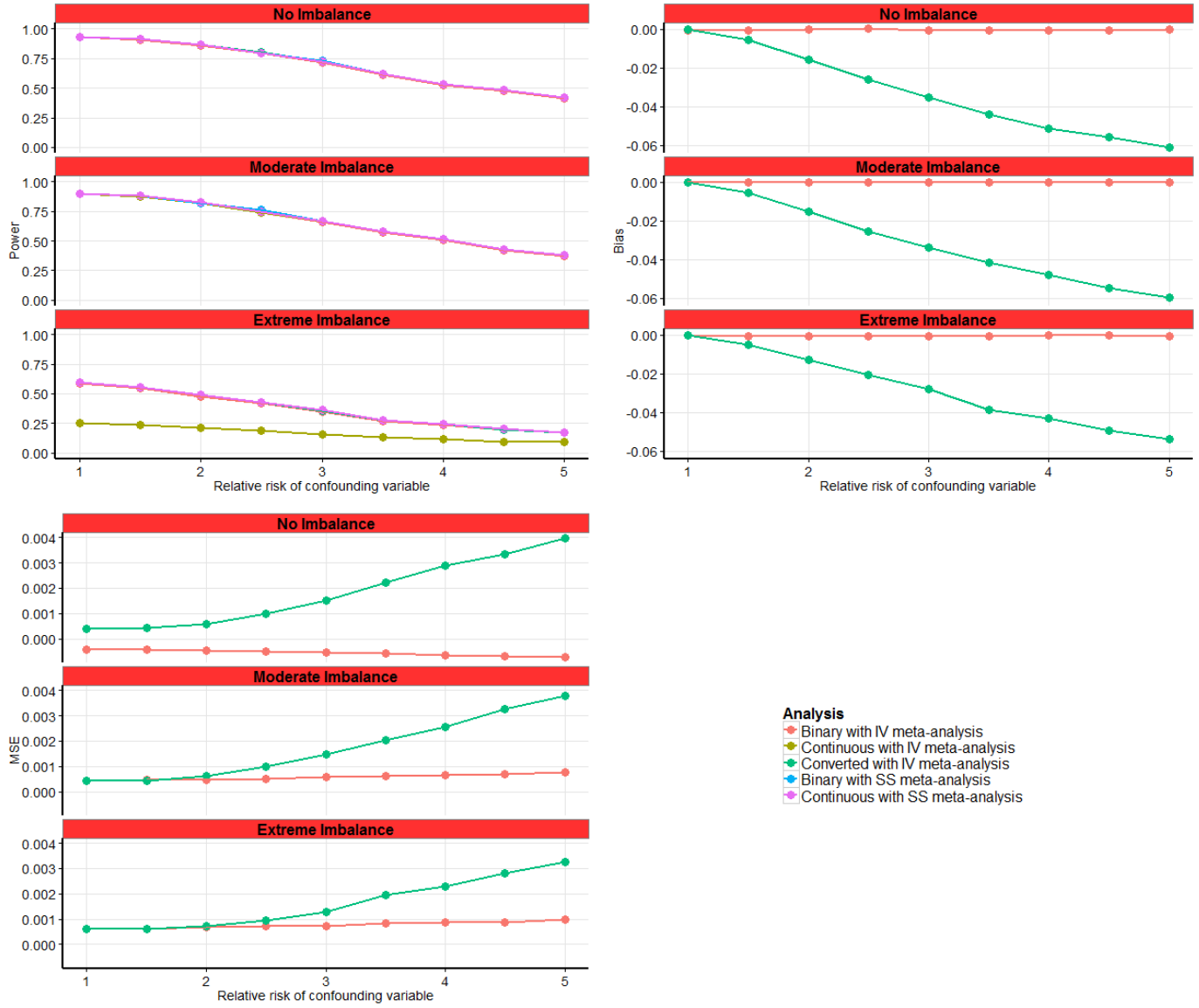



**Supplementary Figure S2.** Power to detect association ($p$<0.01) of a binary phenotype with a causal SNP, in the absence of population stratification or confounders, using alternative meta-analysis strategies for summary statistics obtained from linear and logistic regression models without random effects for the GRM (**Table 1**). Results are presented as a function of the allelic OR, for a causal SNP with RAF in the range of 1-50%, and for variable extent of case-control imbalance (defined in **Table 2**).

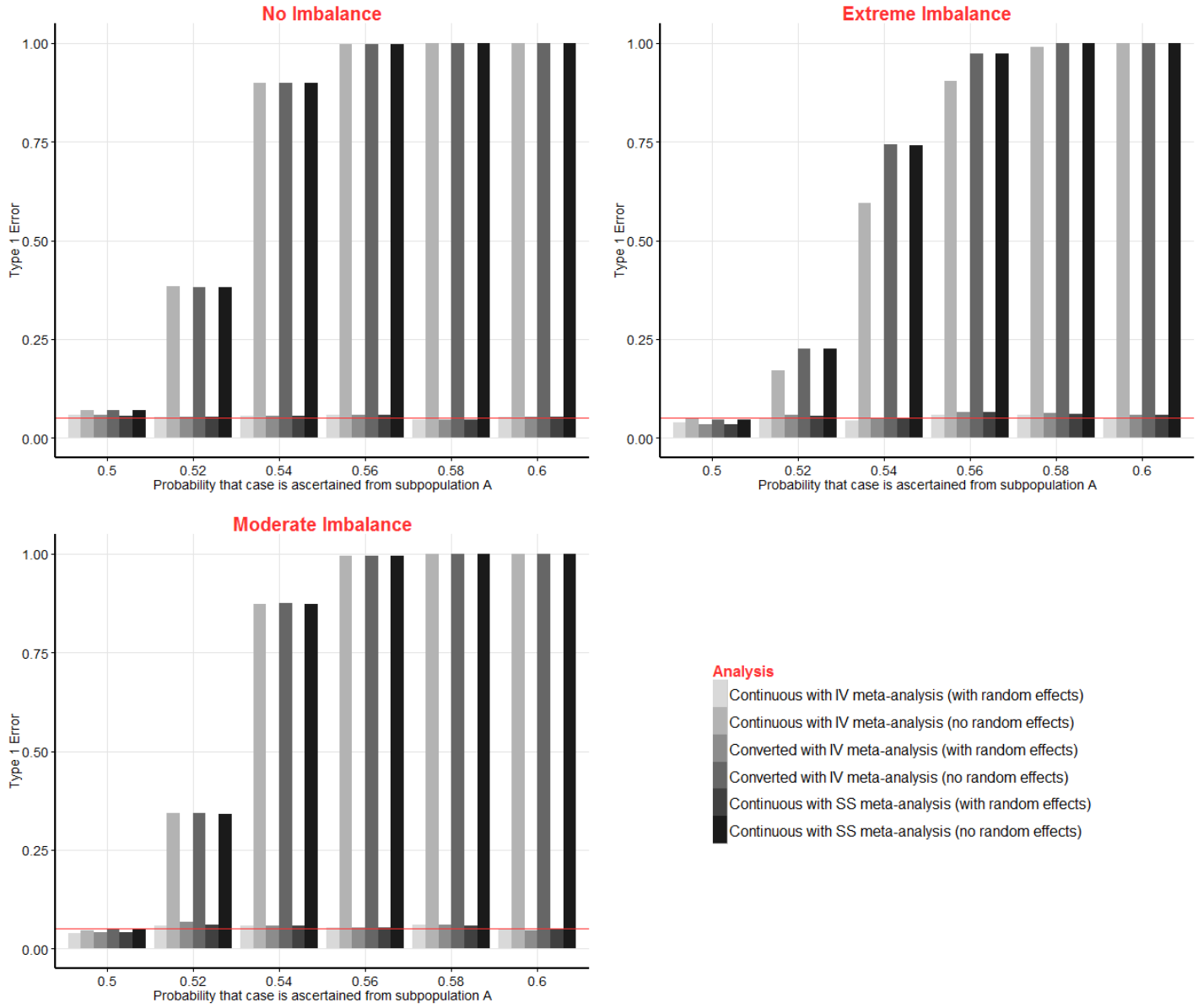



**Supplementary Figure S3.** Bias of the estimated allelic OR after meta-analysis under the inverse-variance weighting of effect sizes from the logistic regression model and the linear regression model after conversion to the log-odds scale. Results are presented as a function of the allelic OR, for a causal SNP with RAF in the range of 1-50%, and for variable extent of case-control imbalance (defined in **Table 2**).


**Supplementary Figure S4.** MSE of the estimated allelic OR after meta-analysis under the inverse-variance weighting of effect sizes from the logistic regression model and the linear regression model after conversion to the log-odds scale. Results are presented as a function of the allelic OR, for a causal SNP with RAF in the range of 1-50%, and for variable extent of case-control imbalance (defined in **Table 2**).




**Supplementary Figure S5.** Power to detect association (at genome-wide significance, $p<5x10^{-8}$) of a binary phenotype with a causal SNP, in the absence of population stratification, but with a confounding variable, using alternative meta-analysis strategies for summary statistics obtained from linear and logistic regression models without random effects for the GRM (**Table 1**). Bias of the estimated allelic OR after meta-analysis under the inverse-variance weighting of effect sizes from the logistic regression model and the linear regression model after conversion to the log-odds scale. Results are presented as a function of the relative risk of the confounding variable, for a causal SNP with RAF 50% and allelic OR of 1.15, for variable extent of case-control imbalance (defined in **Table 2**).




**Supplementary Figure S6.** Type I error rates to detect association ($p$<0.05) of a binary phenotype with a causal SNP, in the presence of population stratification, using alternative meta-analysis strategies for summary statistics obtained from linear regression models, with and without random effects for the GRM (**Table 1**), as a function of the probability that cases are ascertained from subpopulation A. Results are presented for a SNP with frequency of 40% in subpopulation A and 60% in subpopulation B, and for variable extent of case-control imbalance (defined in **Table 2**).