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Supplemental information

Inferring disease architecture and predictive ability with LDpred2-auto

Florian Privé, Clara Albiñana, Julyan Arbel, Bogdan Pasaniuc, and Bjarni J. Vilhjálmsson

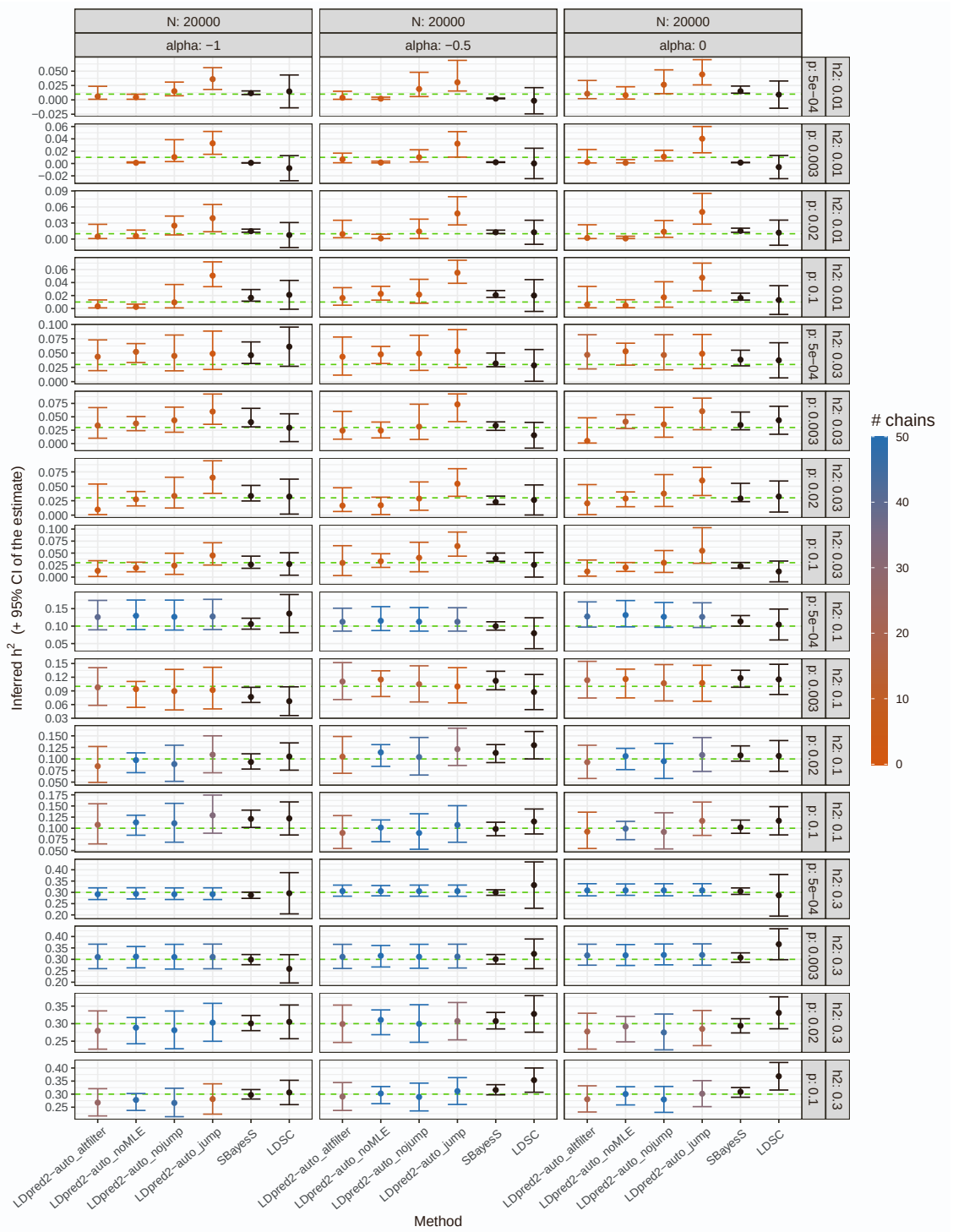


Figure S1: Inferred SNP heritability h^2 in simulations with continuous outcomes and N=20K. Horizontal dashed lines represent the true simulated values. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`), and "altfilter" is similar to "nojump" but uses a different post-filtering of chains (Methods). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the h^2 estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). The 95% confidence interval for the LD Score regression (LDSC) estimate is obtained as ± 1.96 of its standard error. Colors for LDpred2-auto models represent the number of chains kept (out of 50).

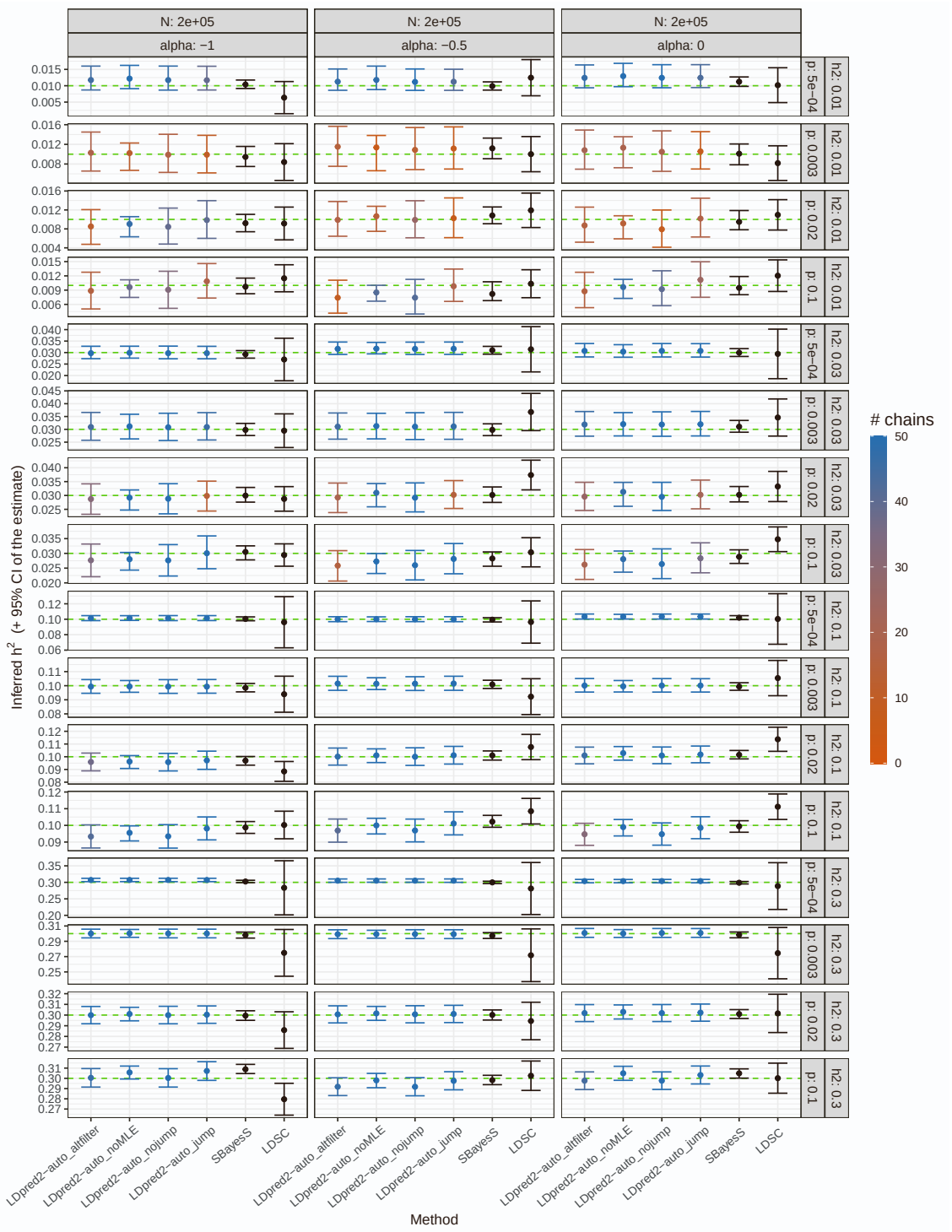


Figure S2: Inferred SNP heritability h^2 in simulations with continuous outcomes and N=200K. Horizontal dashed lines represent the true simulated values. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`), and "altfilter" is similar to "nojump" but uses a different post-filtering of chains (Methods). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the h^2 estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). The 95% confidence interval for the LD Score regression (LDSC) estimate is obtained as ± 1.96 of its standard error. Colors for LDpred2-auto models represent the number of chains kept (out of 50).

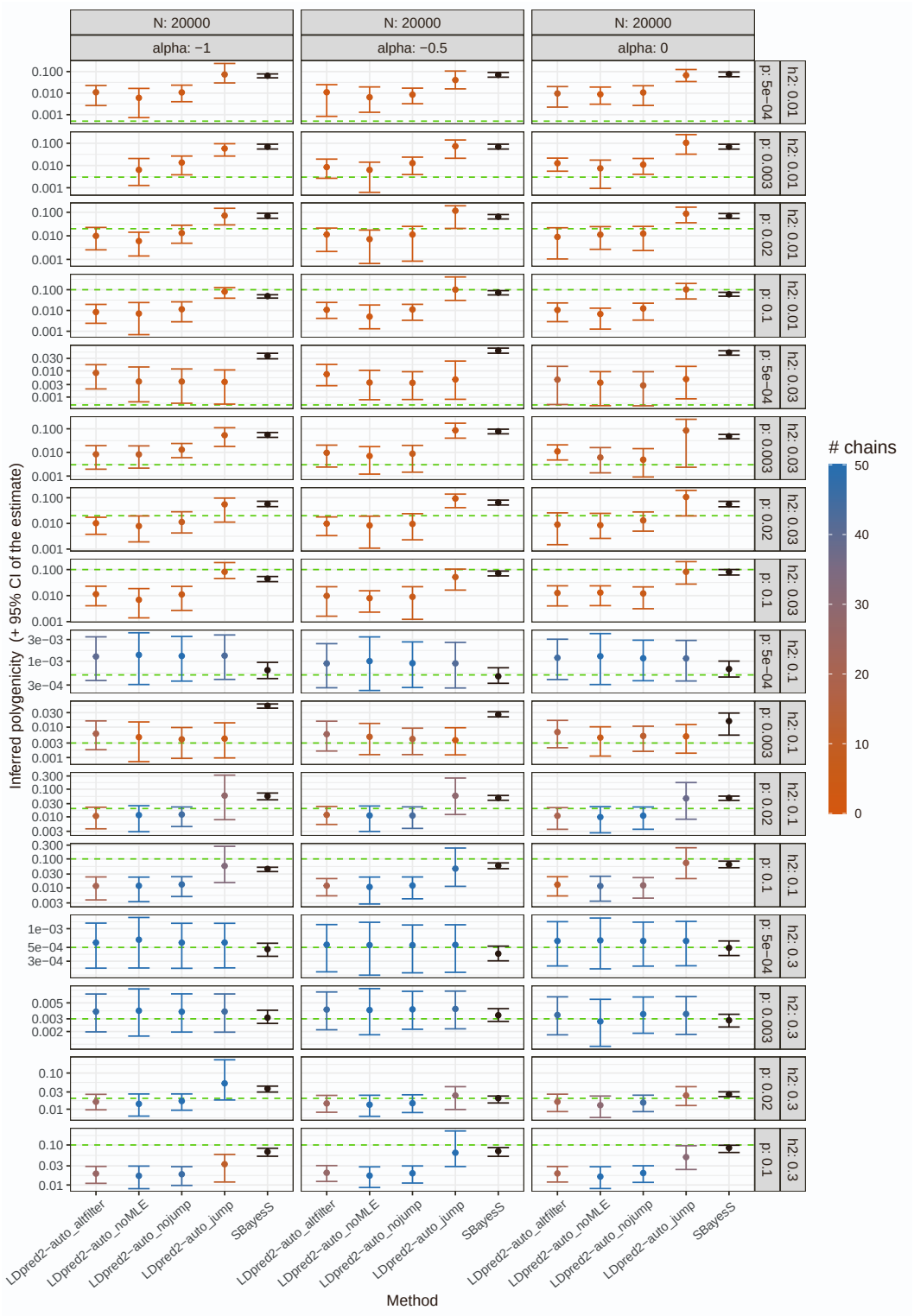


Figure S3: Inferred polygenicity p in simulations with continuous outcomes and N=20K. Horizontal dashed lines represent the true simulated values. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`), and "altfilter" is similar to "nojump" but uses a different post-filtering of chains (Methods). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the p estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). Colors for LDpred2-auto models represent the number of chains kept (out of 50).

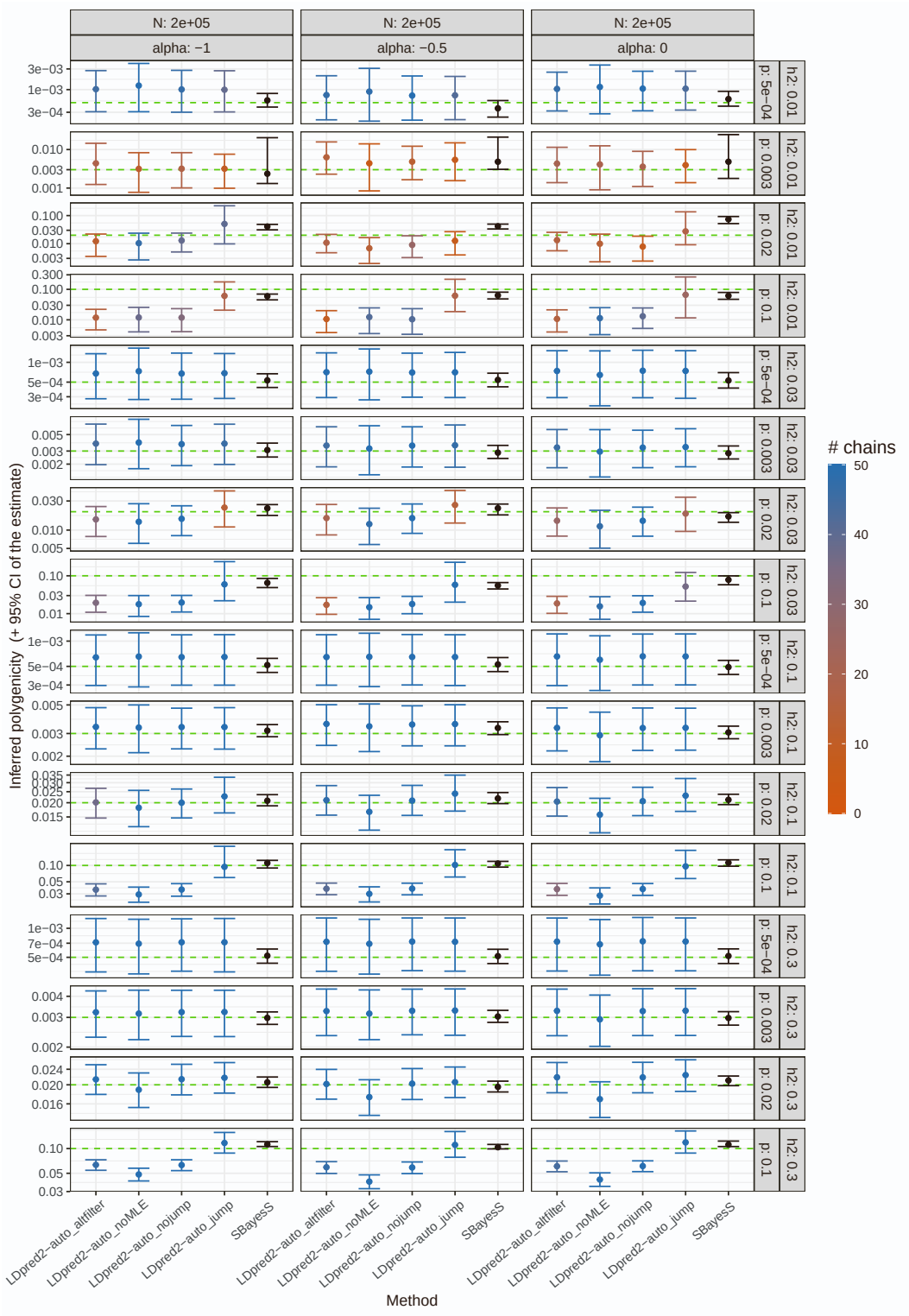


Figure S4: Inferred polygenicity p in simulations with continuous outcomes and N=200K. Horizontal dashed lines represent the true simulated values. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`), and "altfilter" is similar to "nojump" but uses a different post-filtering of chains (Methods). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the p estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). Colors for LDpred2-auto models represent the number of chains kept (out of 50).

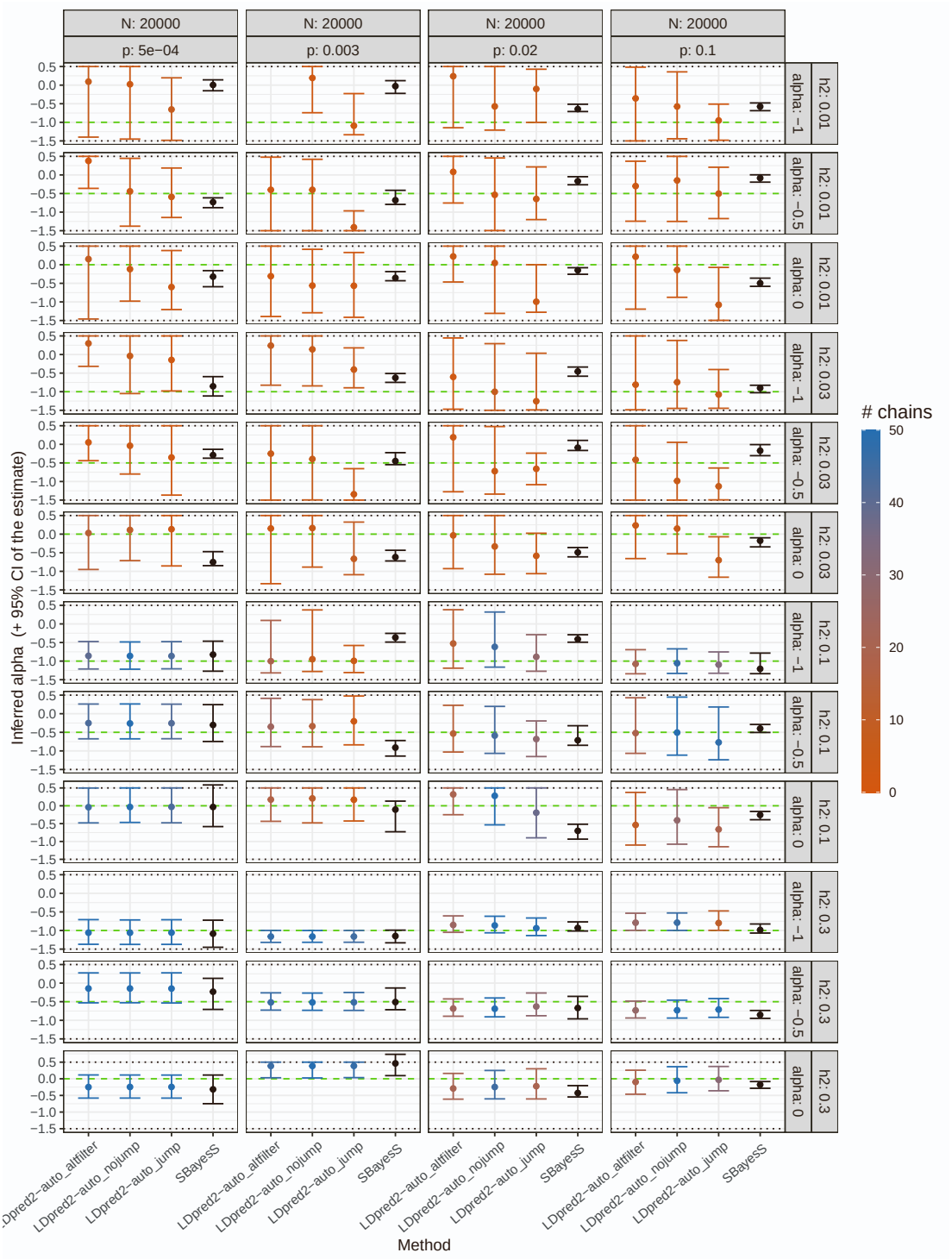


Figure S5: Inferred α in simulations with continuous outcomes and N=20K. Horizontal dashed lines represent the true simulated values. Horizontal dotted lines represent boundaries imposed on the LDpred2-auto estimates. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "altfilter" is similar to "nojump" but uses a different post-filtering of chains (Methods). Note that "LDpred2_noMLE" (`use_MLE = FALSE`) does not infer α. Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the α estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). Colors for LDpred2-auto models represent the number of chains kept (out of 50).

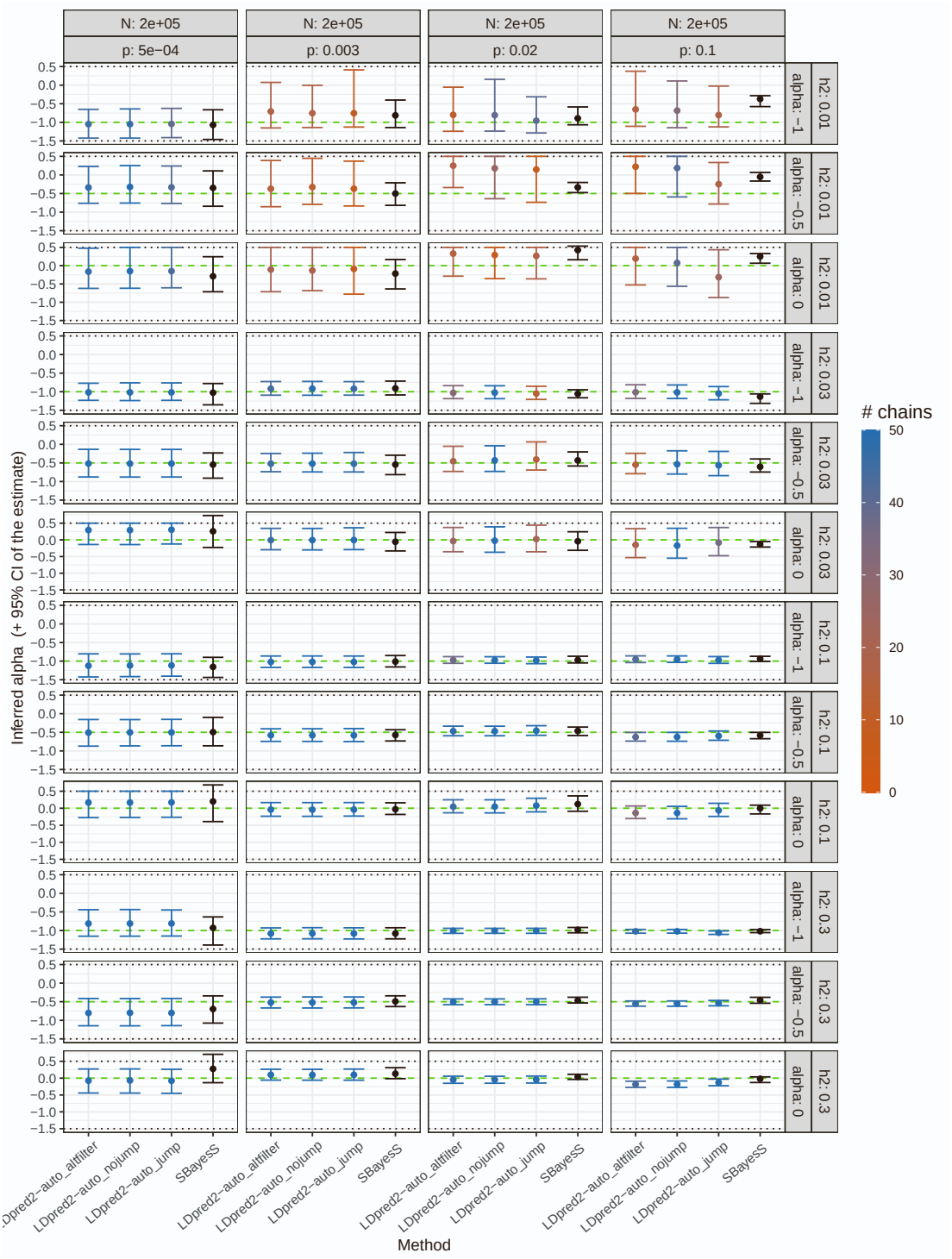


Figure S6: Inferred α in simulations with continuous outcomes and N=200K. Horizontal dashed lines represent the true simulated values. Horizontal dotted lines represent boundaries imposed on the LDpred2-auto estimates. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "altfilter" is similar to "nojump" but uses a different post-filtering of chains (Methods). Note that "LDpred2_noMLE" (`use_MLE = FALSE`) does not infer α. Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the α estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). Colors for LDpred2-auto models represent the number of chains kept (out of 50).

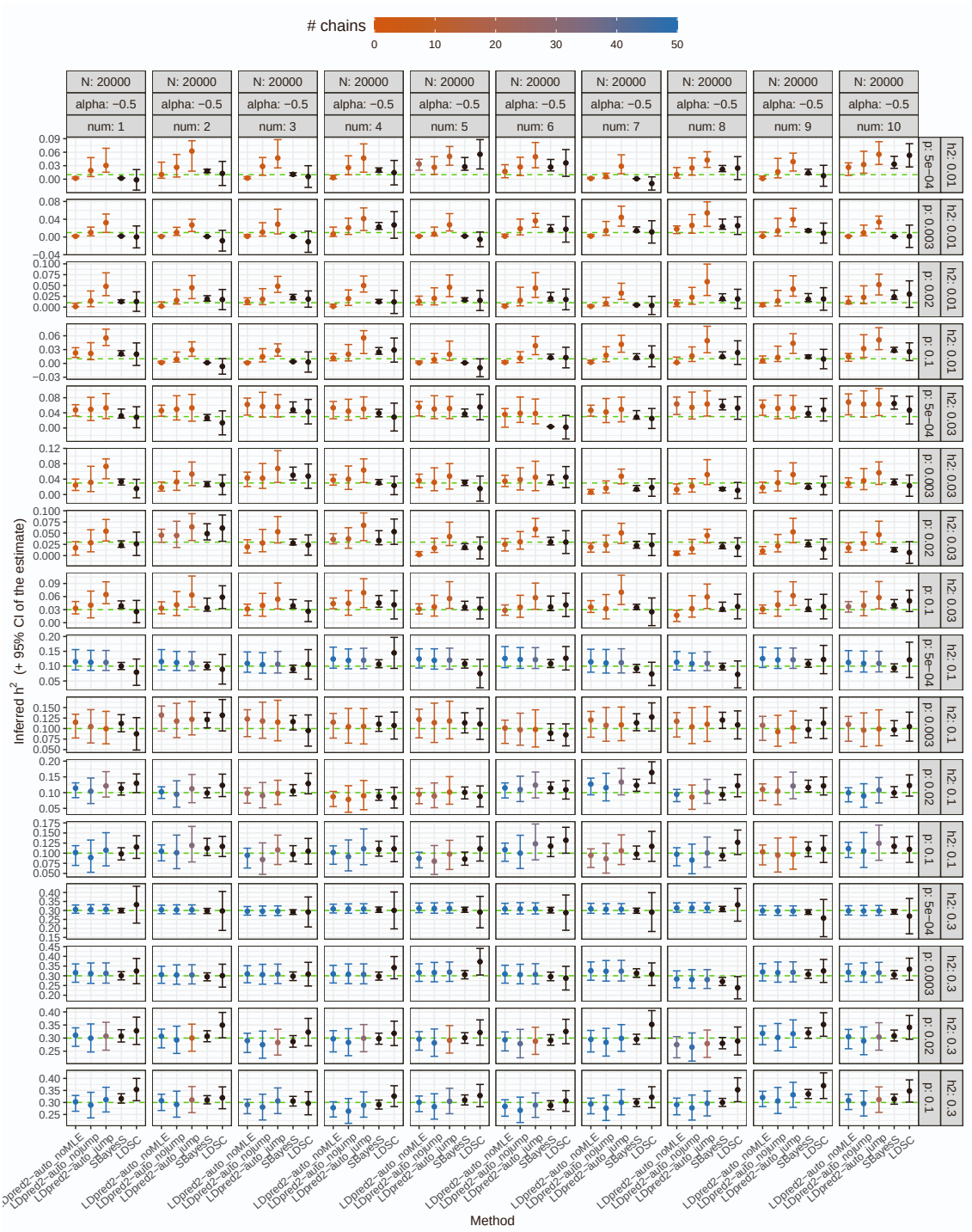


Figure S7: Inferred SNP heritability h^2 in simulations with continuous outcomes and N=20K, in 10 different runs ("num"). Horizontal dashed lines represent the true simulated values. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the h^2 estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). The 95% confidence interval for the LD Score regression (LDSC) estimate is obtained as ± 1.96 of its standard error. Colors for LDpred2-auto models represent the number of chains kept (out of 50).

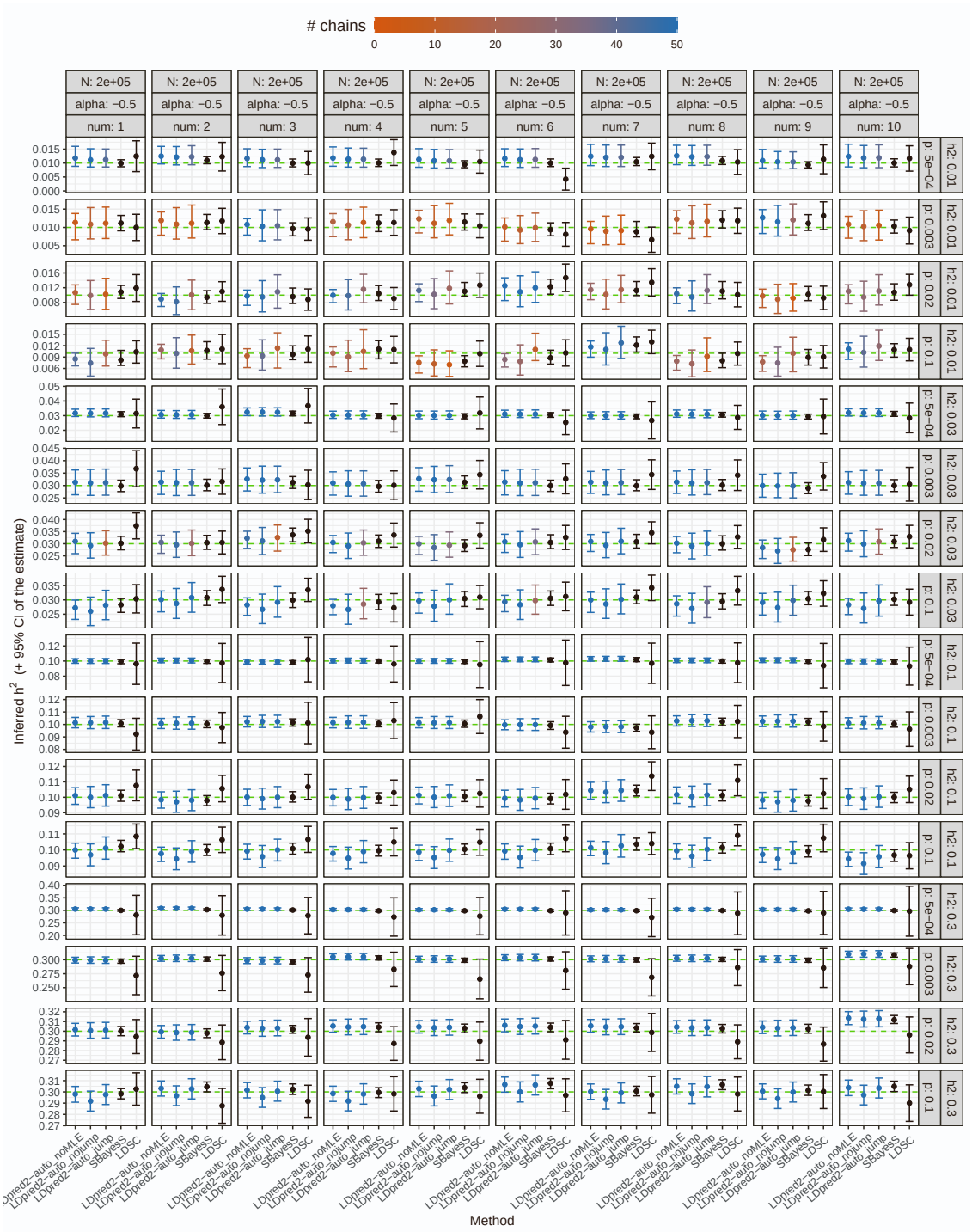


Figure S8: Inferred SNP heritability h^2 in simulations with continuous outcomes and N=200K, in 10 different runs ("num"). Horizontal dashed lines represent the true simulated values. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the h^2 estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). The 95% confidence interval for the LD Score regression (LDSC) estimate is obtained as ± 1.96 of its standard error. Colors for LDpred2-auto models represent the number of chains kept (out of 50).

Figure S9: Inferred polygenicity p in simulations with continuous outcomes and N=20K, in 10 different runs ("num"). Horizontal dashed lines represent the true simulated values. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the p estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). Colors for LDpred2-auto models represent the number of chains kept (out of 50).

Figure S10: Inferred polygenicity p in simulations with continuous outcomes and N=200K, in 10 different runs ("num"). Horizontal dashed lines represent the true simulated values. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the p estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). Colors for LDpred2-auto models represent the number of chains kept (out of 50).

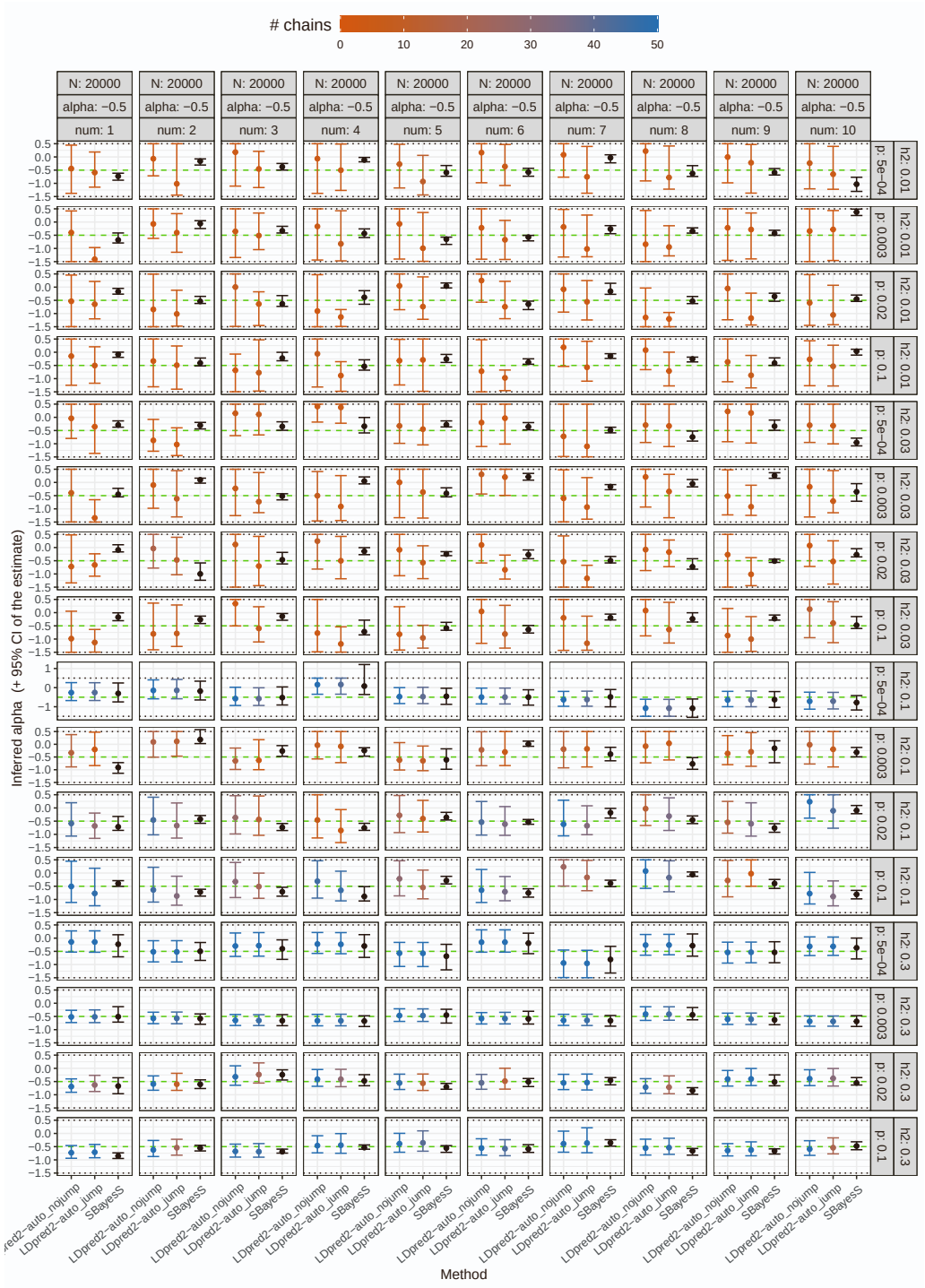


Figure S11: Inferred α in simulations with continuous outcomes and N=20K, in 10 different runs ("num"). Horizontal dashed lines represent the true simulated values. Horizontal dotted lines represent boundaries imposed on the LDpred2-auto estimates. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`). Note that "LDpred2_noMLE" (`use_MLE = FALSE`) does not infer α. Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the α estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). Colors for LDpred2-auto models represent the number of chains kept (out of 50).

Figure S12: Inferred α in simulations with continuous outcomes and N=200K, in 10 different runs ("num"). Horizontal dashed lines represent the true simulated values. Horizontal dotted lines represent boundaries imposed on the LDpred2-auto estimates. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`). Note that "LDpred2_noMLE" (`use_MLE = FALSE`) does not infer α. Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. The 95% confidence intervals for the LDpred2-auto and SBayesS estimates are obtained from the 2.5% and 97.5% quantiles of all the α estimates from the iterations (after burn-in) of the chains kept (note that only one chain is used and kept in SBayesS). Colors for LDpred2-auto models represent the number of chains kept (out of 50).

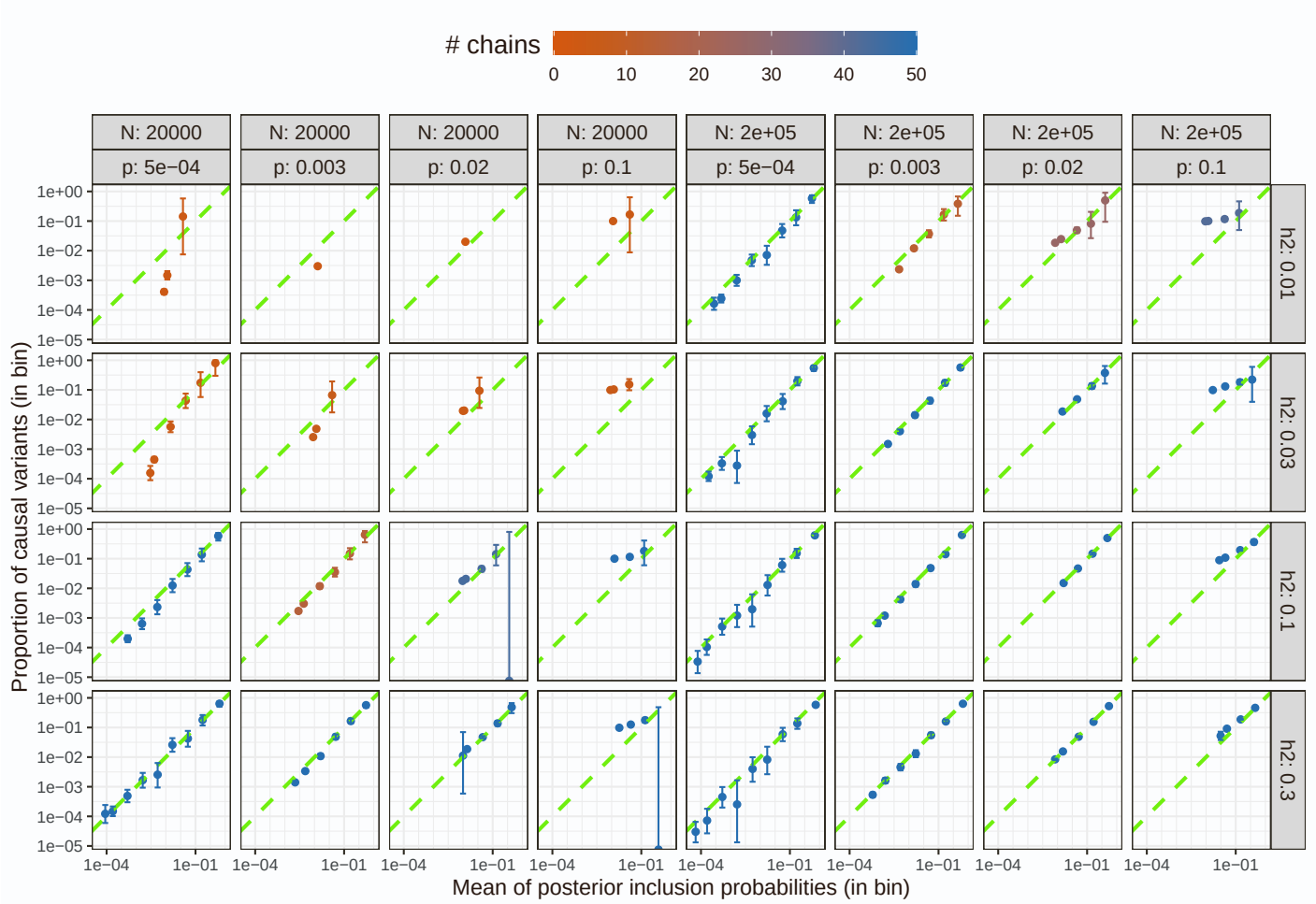


Figure S13: LDpred2-auto calibration of per-variant posterior probabilities of being causal (also known as posterior inclusion probabilities) in simulations with continuous outcomes. These probabilities are binned on a log-scale, and mean in each bin is compared to the proportion of simulated causal variants in the bin (with 95% CI). Green dashed lines represent the 1:1 line. Only results for $\alpha = -0.5$ and `allow_jump_sign = FALSE` are represented. Colors represent the number of chains kept (out of 50).

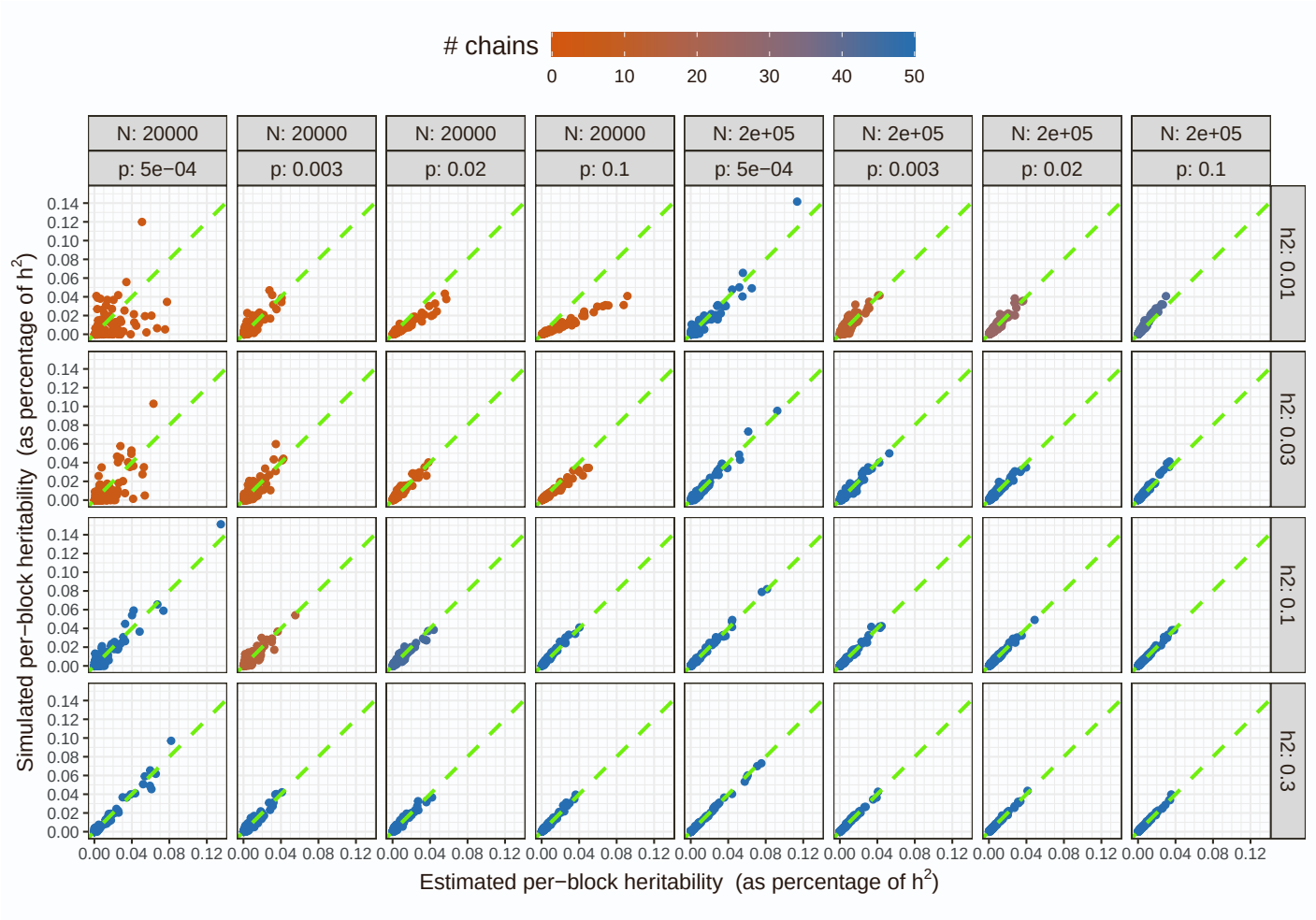
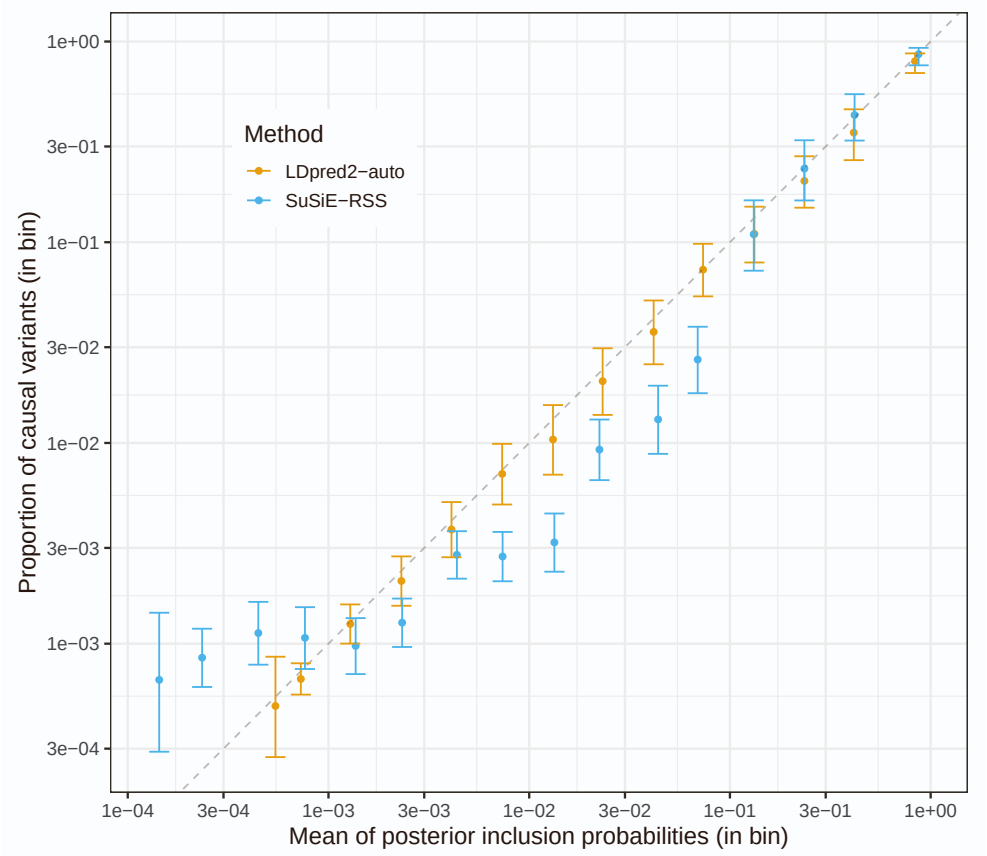
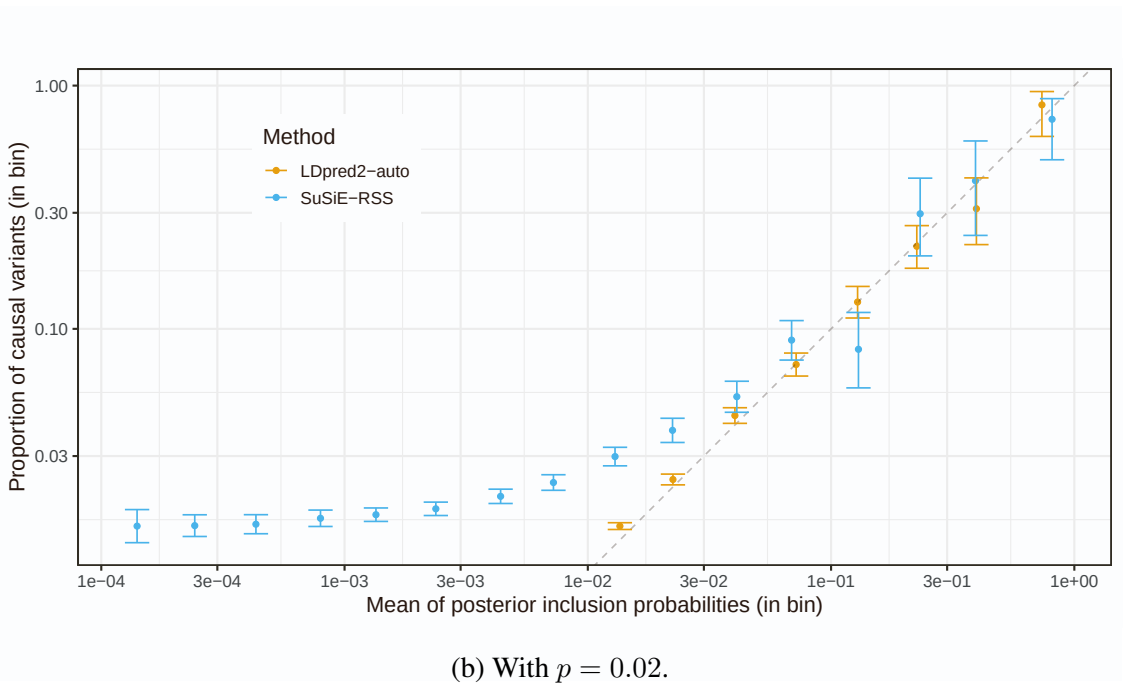


Figure S14: LDpred2-auto calibration of per-block heritability estimates in simulations with continuous outcomes. Local h^2 estimate for each block is compared to the true simulated local heritability in the block. Green dashed lines represent the 1:1 line. Only results for $\alpha = -0.5$ and `allow_jump_sign = FALSE` are represented. Colors represent the number of chains kept (out of 50).



(a) With $p = 0.002$.



(b) With $p = 0.02$.

Figure S15: Calibration of per-variant posterior probabilities of being causal in two simulations with continuous outcomes, assuming $h^2 = 0.1$, $\alpha = -0.5$, and $N = 10^5$.

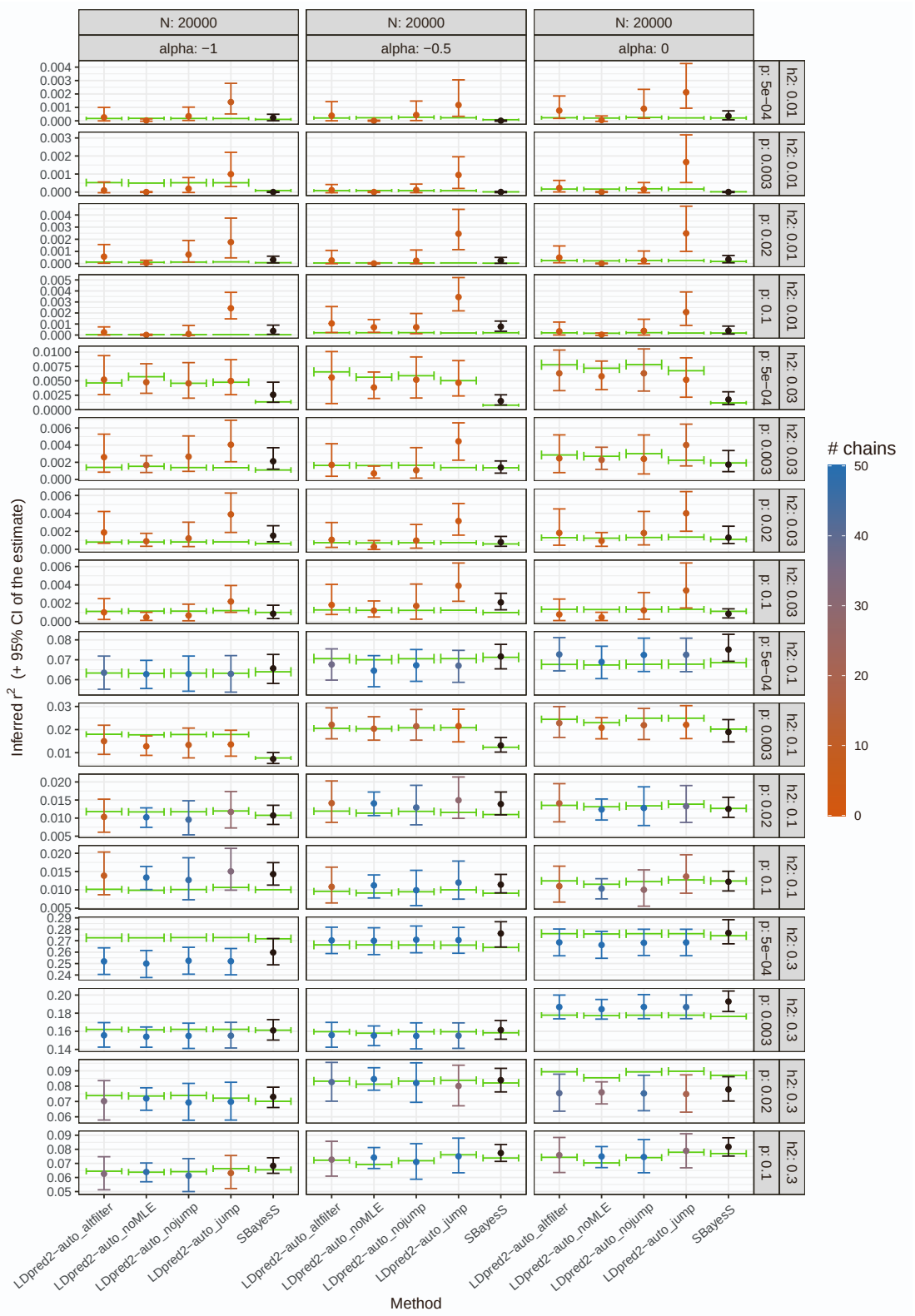


Figure S16: Inferred predictive performance r^2 in simulations with continuous outcomes and N=20K. Green segments represent r^2 in the test set. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`), and "altfilter" is similar to "nojump" but uses a different post-filtering of chains (Methods). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. Colors for LDpred2-auto models represent the number of chains kept (out of 50).

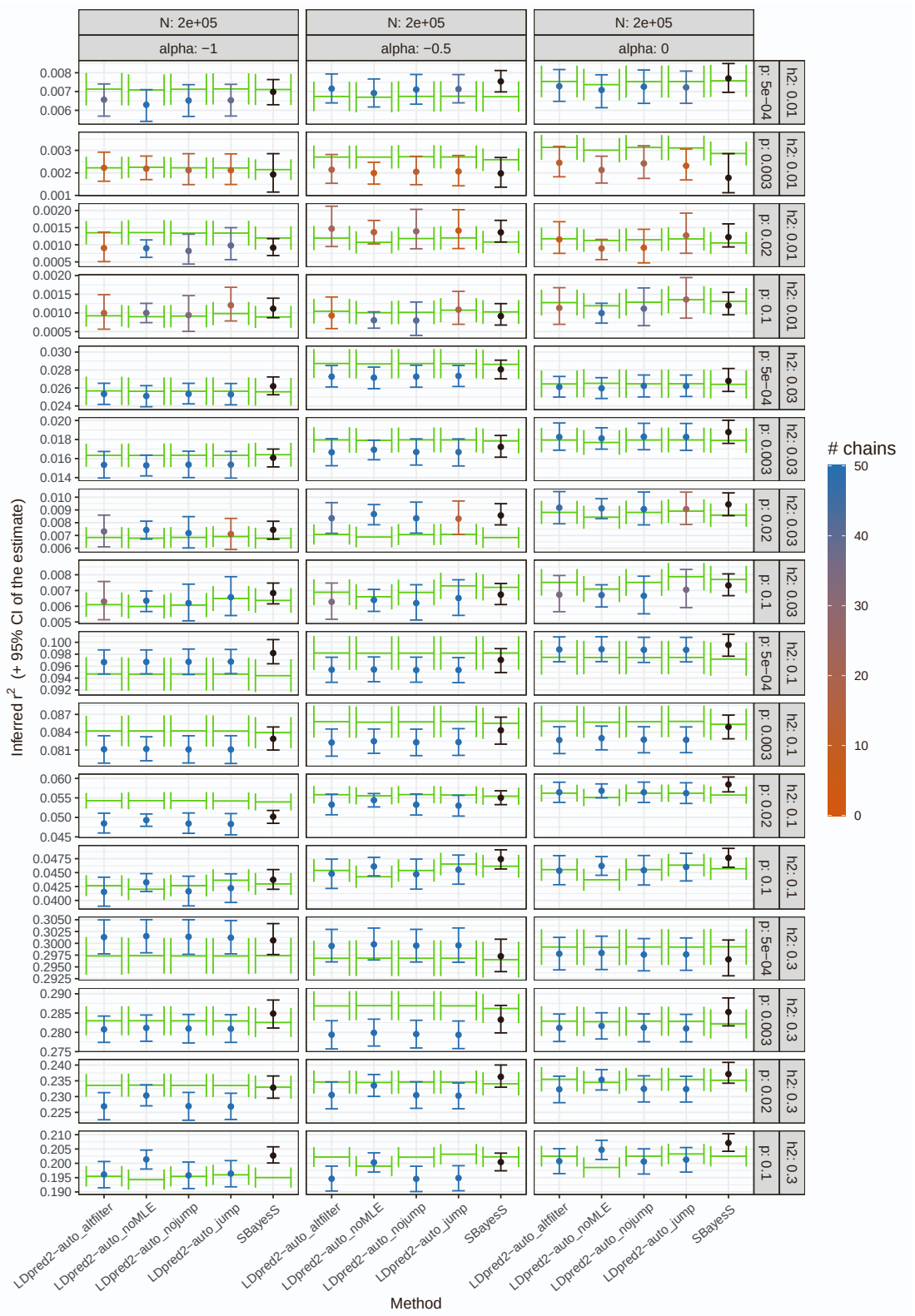


Figure S17: Inferred predictive performance r^2 in simulations with continuous outcomes and N=200K. Green segments represent r^2 in the test set. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`), and "altfilter" is similar to "nojump" but uses a different post-filtering of chains (Methods). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. Colors for LDpred2-auto models represent the number of chains kept (out of 50).

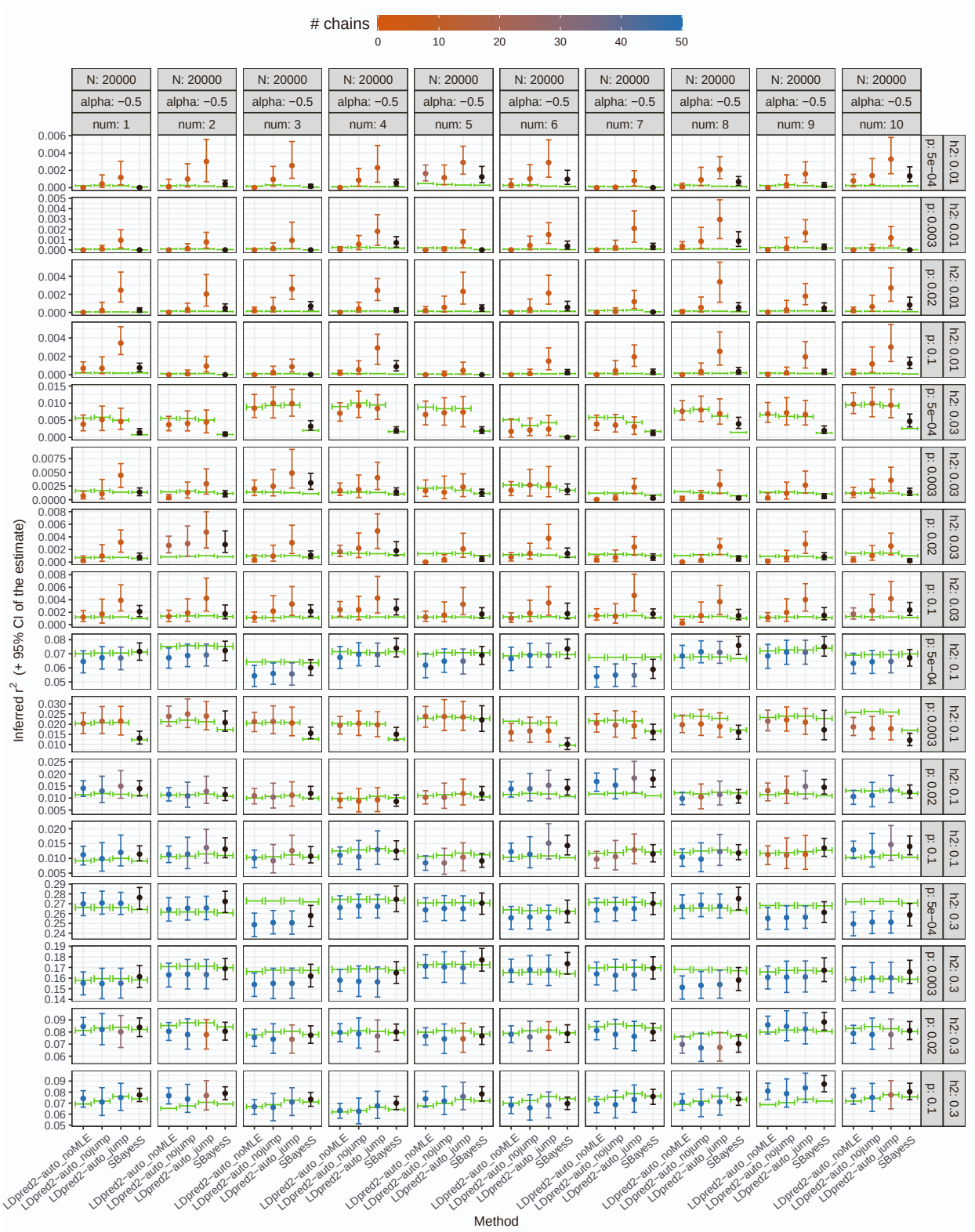


Figure S18: Inferred predictive performance r^2 in simulations with continuous outcomes and N=20K, in 10 different runs ("num"). Green segments represent r^2 in the test set. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. Colors for LDpred2-auto models represent the number of chains kept (out of 50).

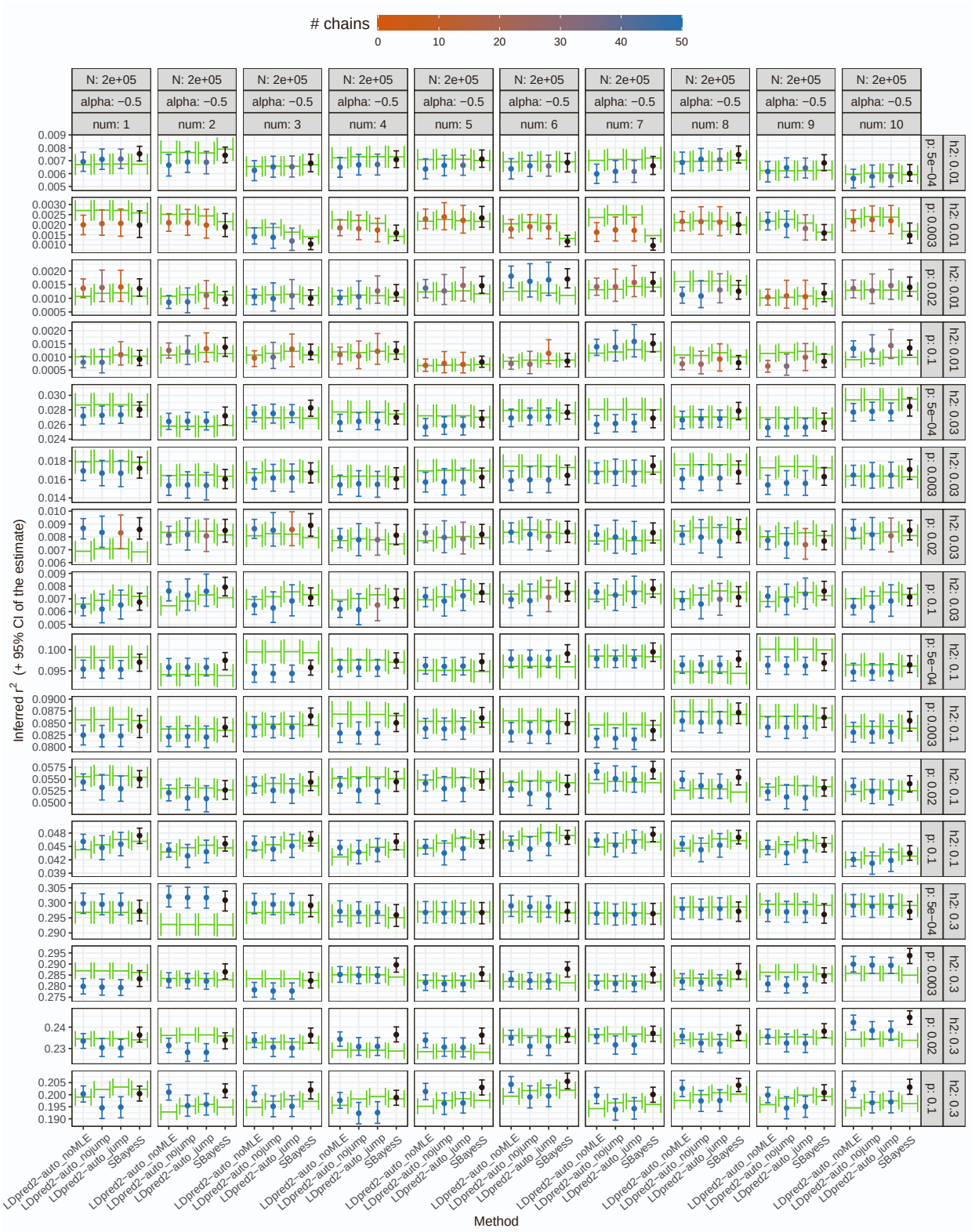


Figure S19: Inferred predictive performance r^2 in simulations with continuous outcomes and N=200K, in 10 different runs ("num"). Green segments represent r^2 in the test set. For LDpred2-auto, suffix "nojump"/"jump" refers to using `allow_jump_sign = FALSE/TRUE` (and `use_MLE = TRUE`), and "noMLE" refers to using `use_MLE = FALSE` (and `allow_jump_sign = FALSE`). Note that the recommended option is to use `allow_jump_sign = FALSE`[1]. Colors for LDpred2-auto models represent the number of chains kept (out of 50).

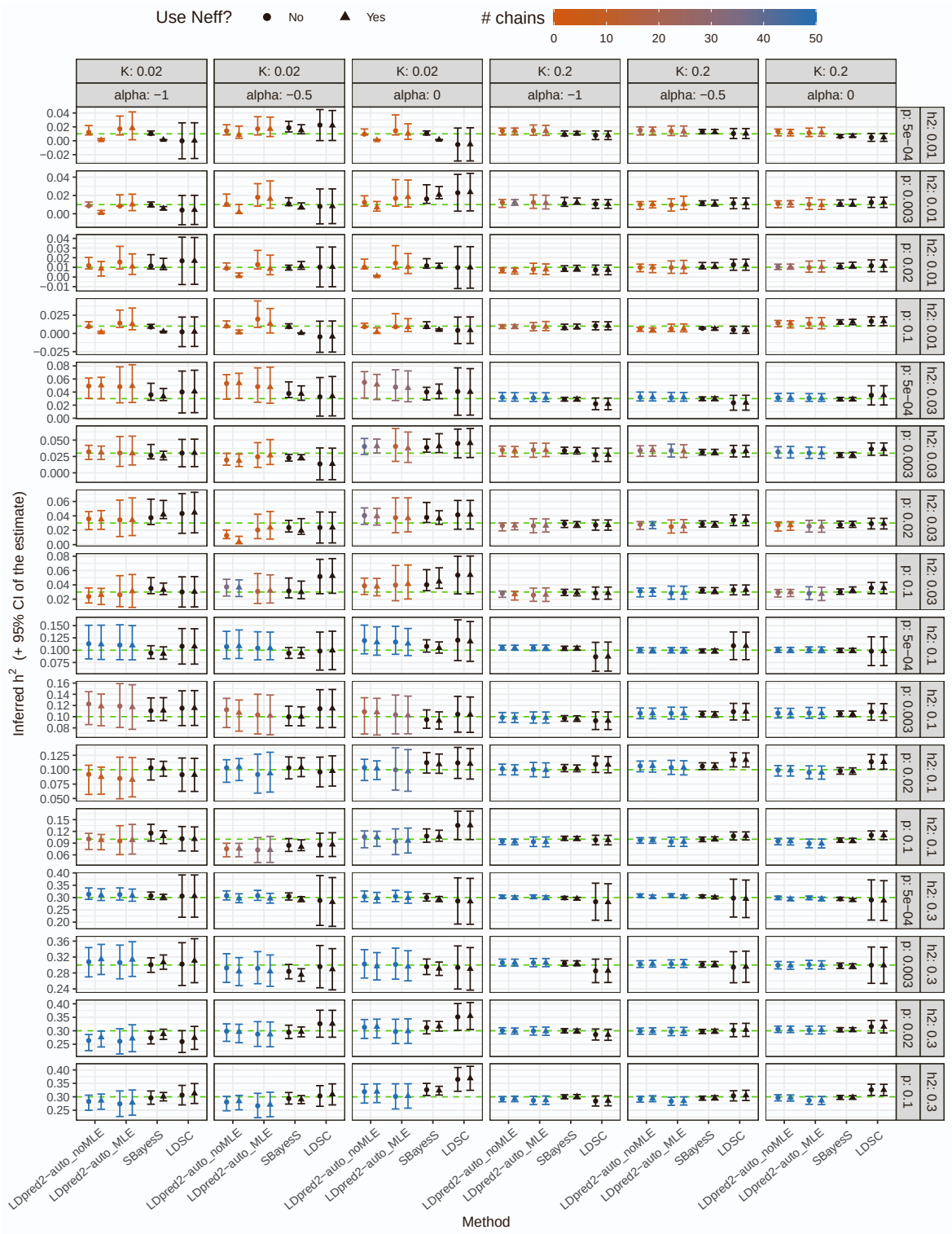


Figure S20: Inferred SNP heritability h^2 in simulations with binary outcomes. Horizontal dashed lines represent the true simulated values. The 95% confidence interval for the LDpred2-auto estimate is obtained from the 2.5% and 97.5% quantiles of all the h^2 estimates from the iterations (after burn-in) of the chains kept. The 95% confidence interval for the LD Score regression estimate is obtained from ± 1.96 times its standard error. Colors for LDpred2-auto models represent the number of chains kept (out of 50). Option `Neff` controls whether a logistic regression is used for the GWAS with the effective sample in LDpred2, or a linear regression and then the total sample size. All h^2 estimates are transformed to the liability scale with K_pop=K and K_GWAS either K (the simulated prevalence) or 0.5 (when using Neff) using function `coef_to_liab` from R package bigsnpr[2,3].

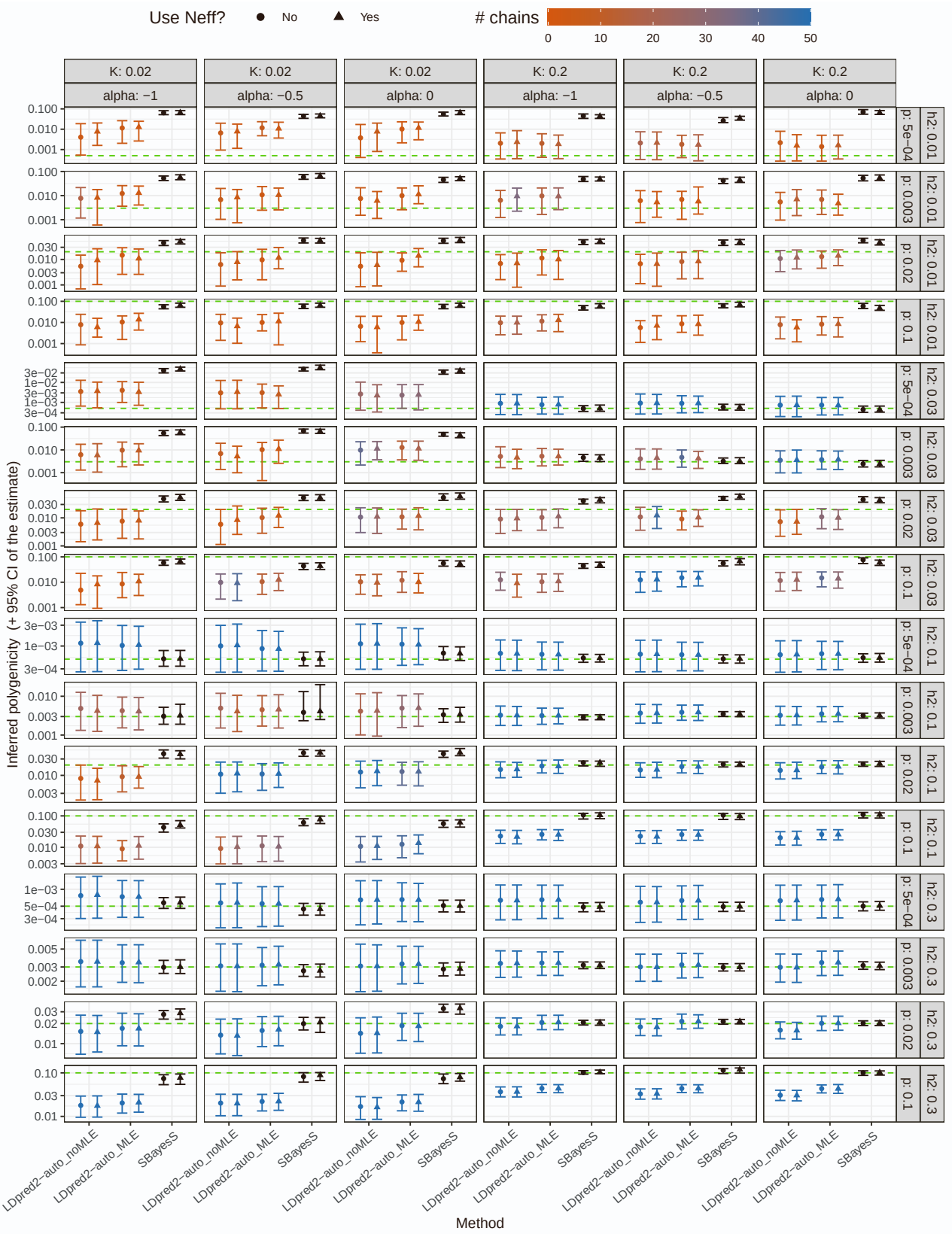


Figure S21: Inferred polygenicity p in simulations with binary outcomes. Horizontal dashed lines represent the true simulated values. Colors for LDpred2-auto models represent the number of chains kept (out of 50). Option `Neff` controls whether a logistic regression is used for the GWAS with the effective sample in LDpred2, or a linear regression and then the total sample size.

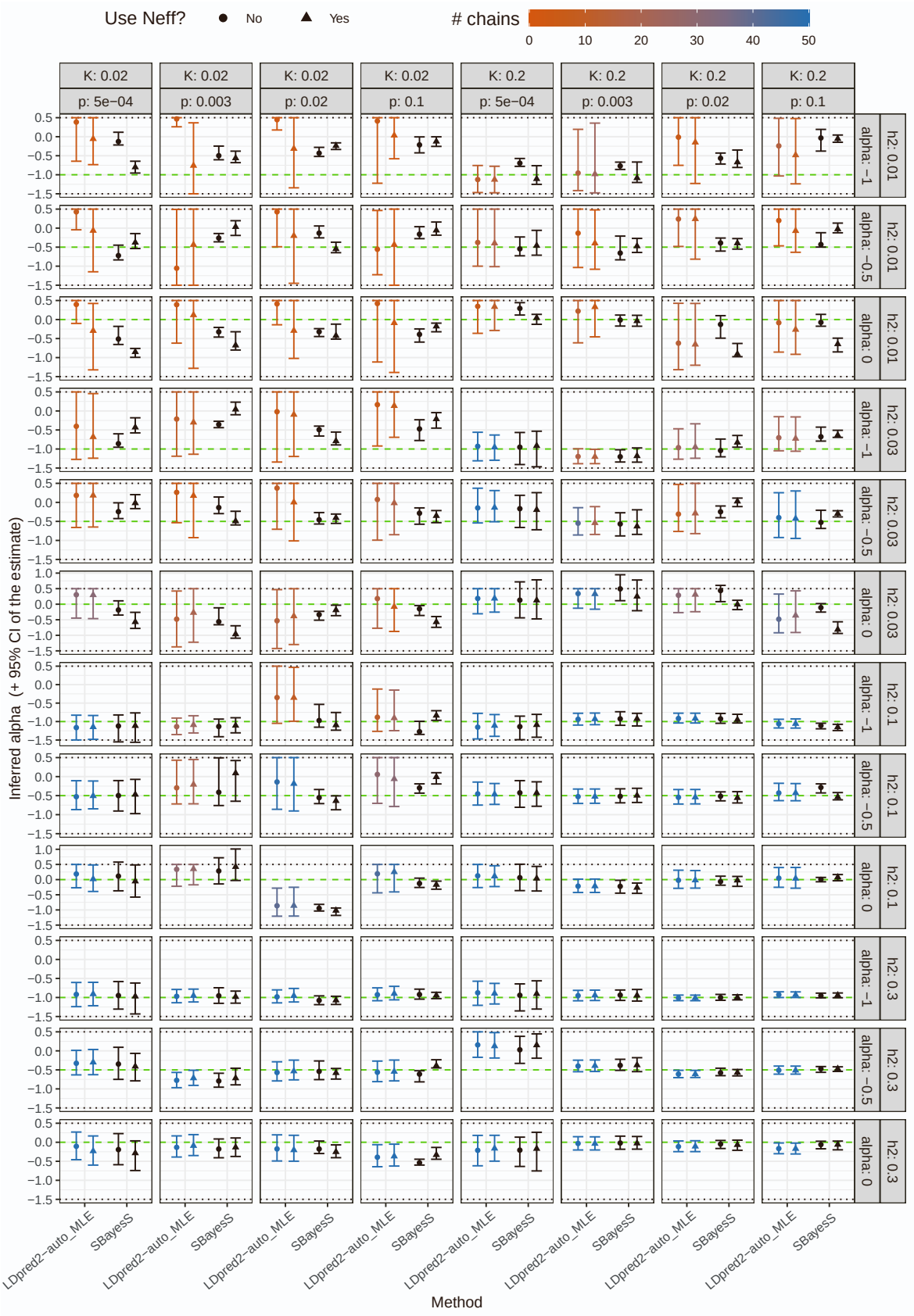


Figure S22: Inferred α in simulations with binary outcomes. Horizontal dashed lines represent the true simulated values. Horizontal dotted lines represent boundaries imposed on the estimates. Colors for LDpred2-auto models represent the number of chains kept (out of 50). Option `Neff` controls whether a logistic regression is used for the GWAS with the effective sample in LDpred2, or a linear regression and then the total sample size.

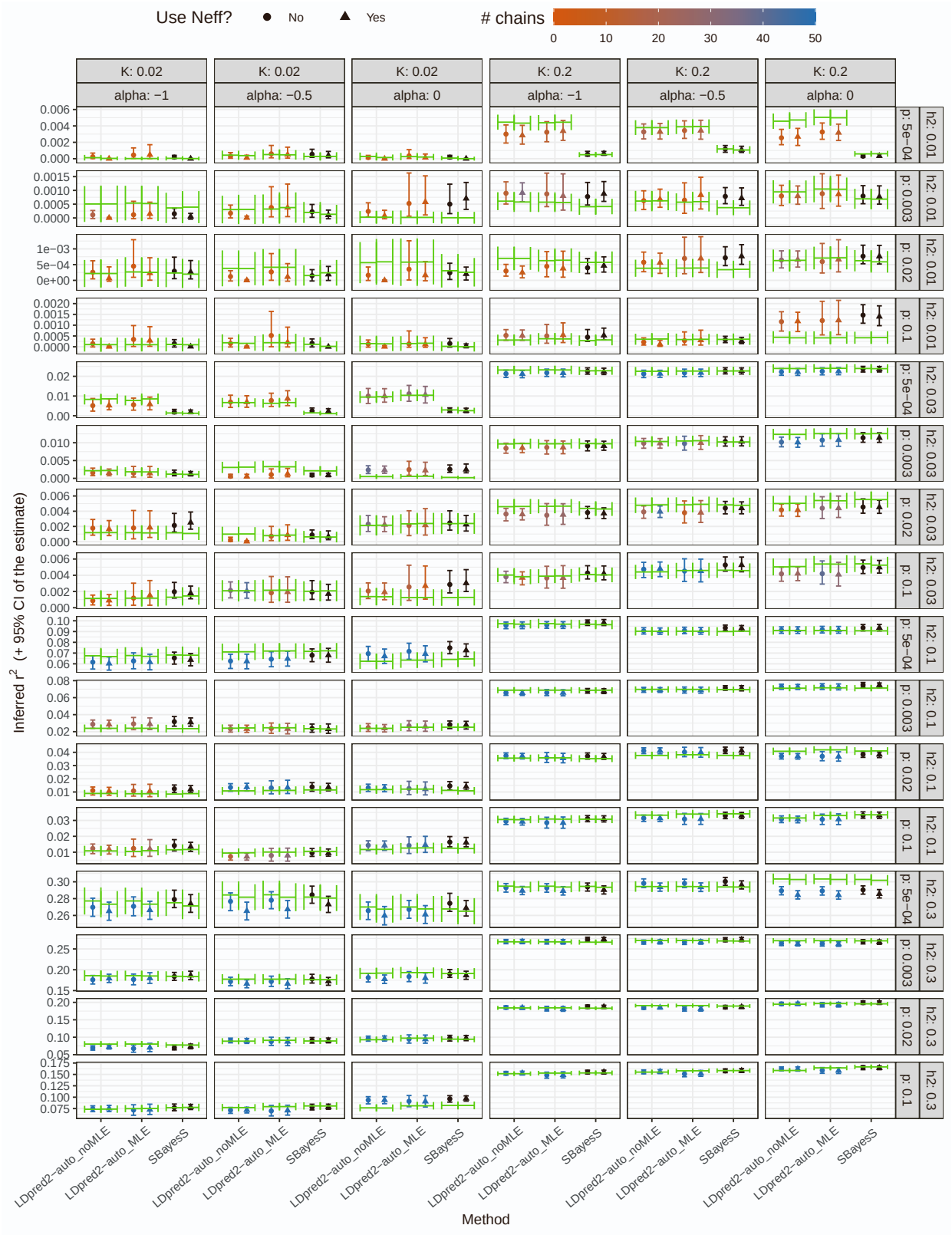


Figure S23: Inferred predictive performance r^2 in simulations with binary outcomes. Green segments represent r^2 in the test set. Colors for LDpred2-auto models represent the number of chains kept (out of 50). Option `Neff` controls whether a logistic regression is used for the GWAS with the effective sample in LDpred2, or a linear regression and then the total sample size. All r^2 estimates are transformed to the liability scale with K_pop=K and K_GWAS either K (the simulated prevalence) or 0.5 (when using Neff) using function `coef_to_liab` from R package bigsnpr[2,3]; the ones from the test set are transformed with K and K.

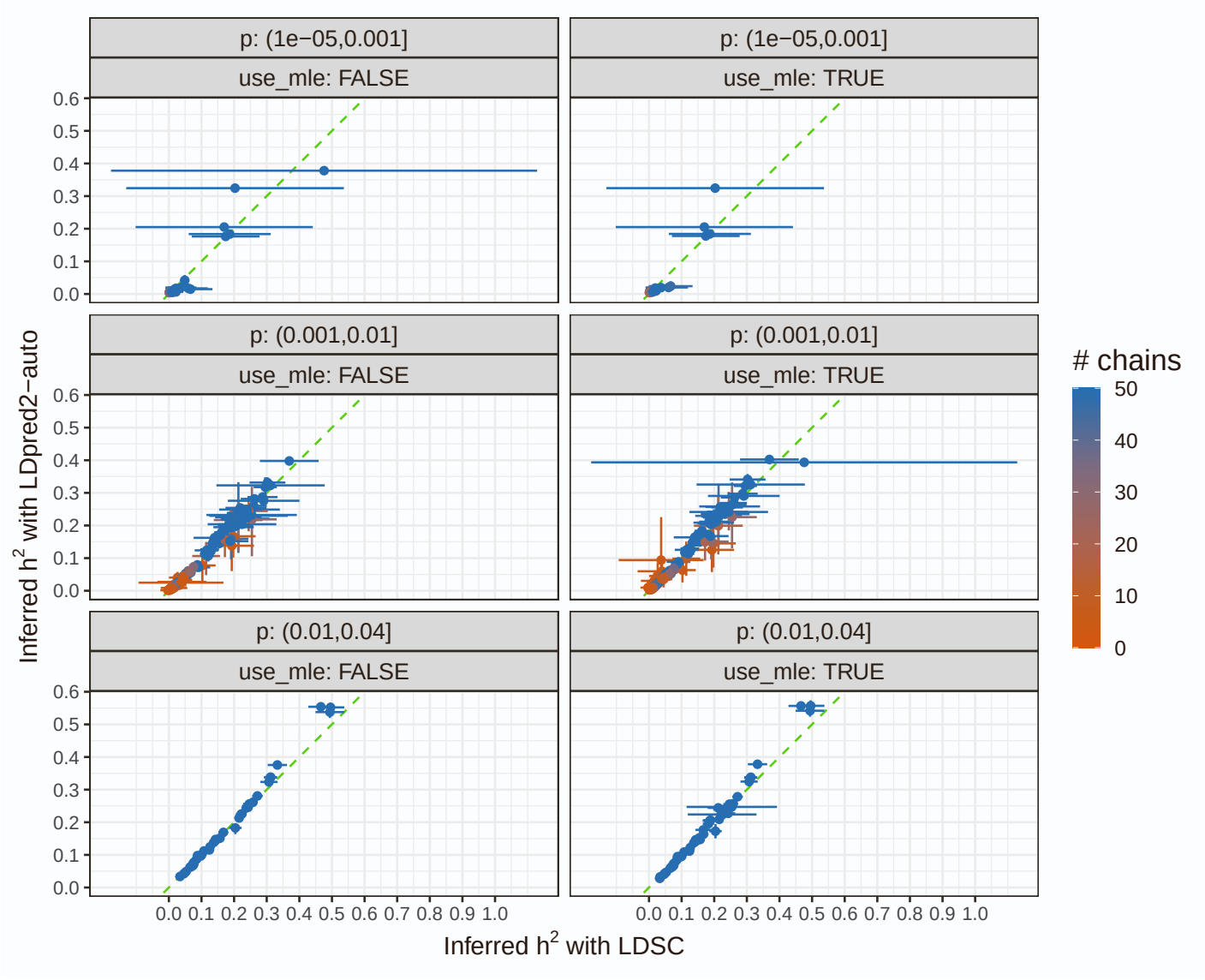


Figure S24: SNP heritability estimates from either LDpred2-auto or LD Score regression for all 248 phenotypes defined from the UK Biobank. These are stratified by the polygenicity estimated from LDpred2-auto. Green dashed lines represent the 1:1 line. The 95% confidence interval for the LDpred2-auto estimate is obtained from the 2.5% and 97.5% quantiles of all the h^2 estimates from the iterations (after burn-in) of the chains kept. The 95% confidence interval for the LD Score regression estimate is obtained from ± 1.96 times its standard error. "use_mle: TRUE" corresponds to using the extended 3-parameter model and sampling scheme (Methods). Colors represent the number of chains kept for LDpred2-auto (out of 50).

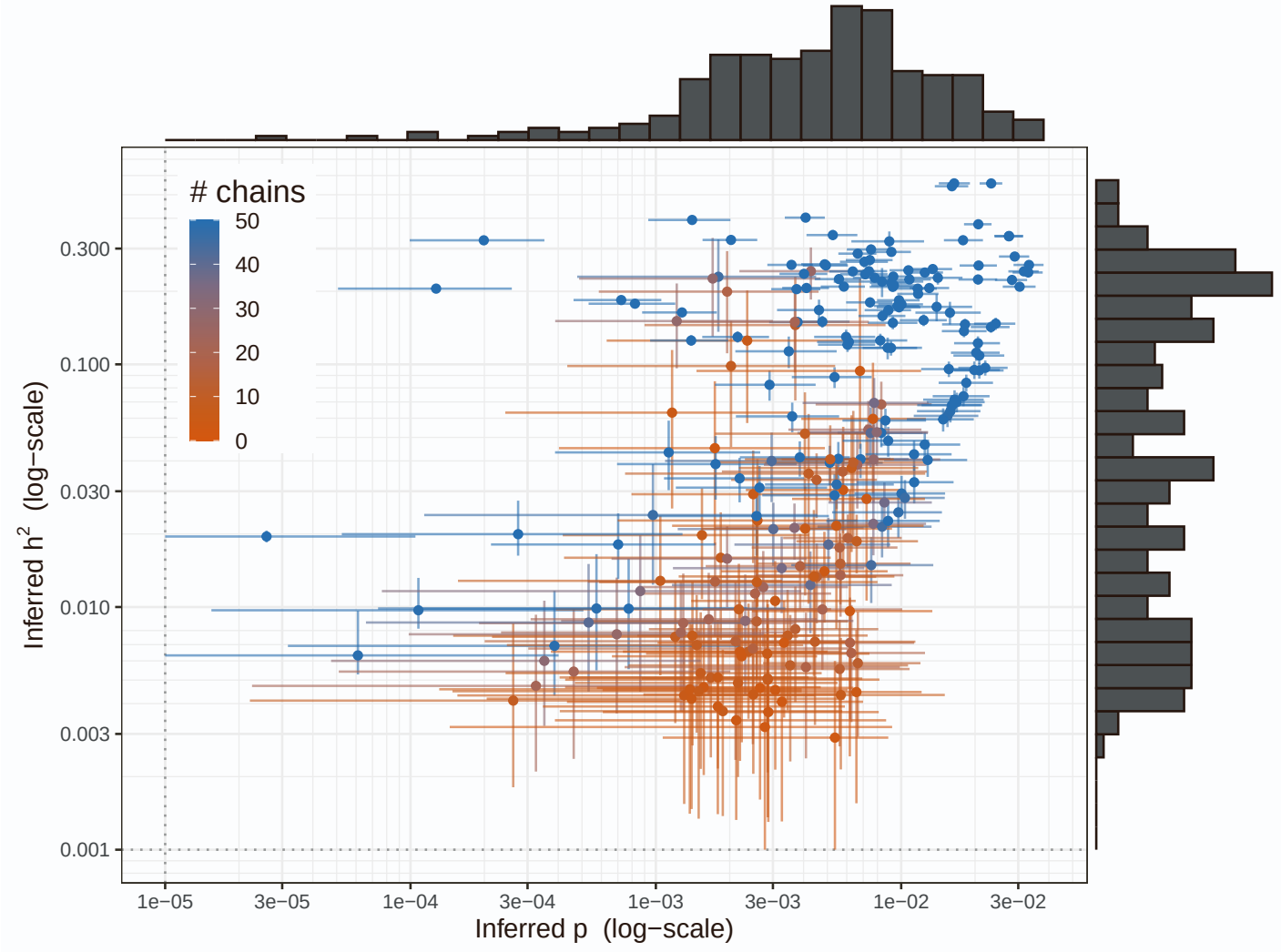


Figure S25: Estimates from LDpred2-auto for either the SNP heritability h^2 or the polygenicity p for all 248 phenotypes defined from the UK Biobank. Estimates of h^2 are constrained to be at least 0.001, and at least 10^{-5} for p. The 95% confidence interval for the LDpred2-auto estimate is obtained from the 2.5% and 97.5% quantiles of all the estimates from the iterations (after burn-in) of the chains kept. Colors represent the number of chains kept for LDpred2-auto (out of 50).

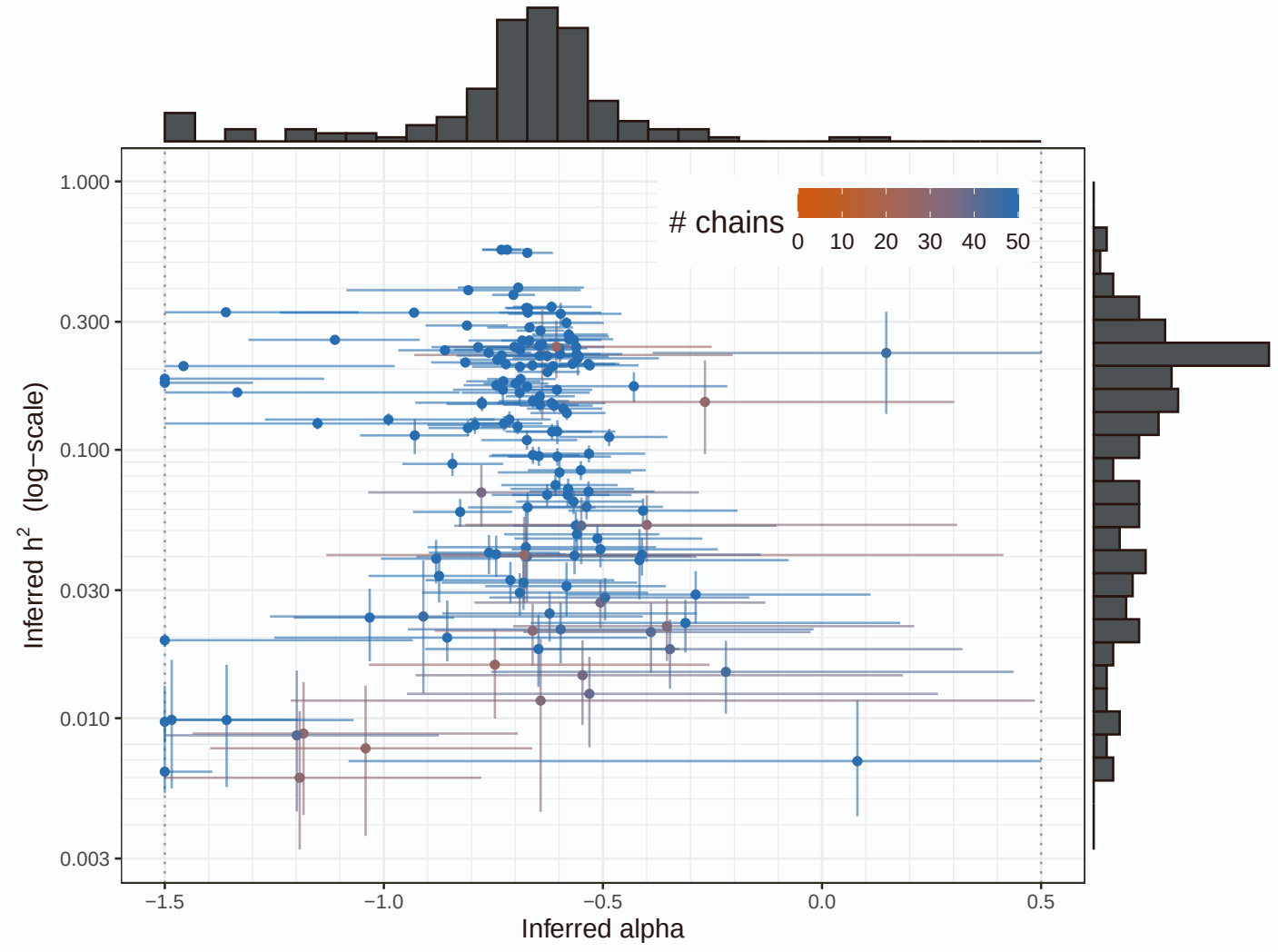


Figure S26: Estimates from LDpred2-auto for either the SNP heritability h^2 or α for all 248 phenotypes defined from the UK Biobank. The 95% confidence interval for the LDpred2-auto estimate is obtained from the 2.5% and 97.5% quantiles of all the estimates from the iterations (after burn-in) of the chains kept. Colors represent the number of chains kept for LDpred2-auto (out of 50). We only show phenotypes for which there are more than 25 chains kept, because simulations have shown that α estimates are unreliable when a small number of chains is kept (Figure S5).

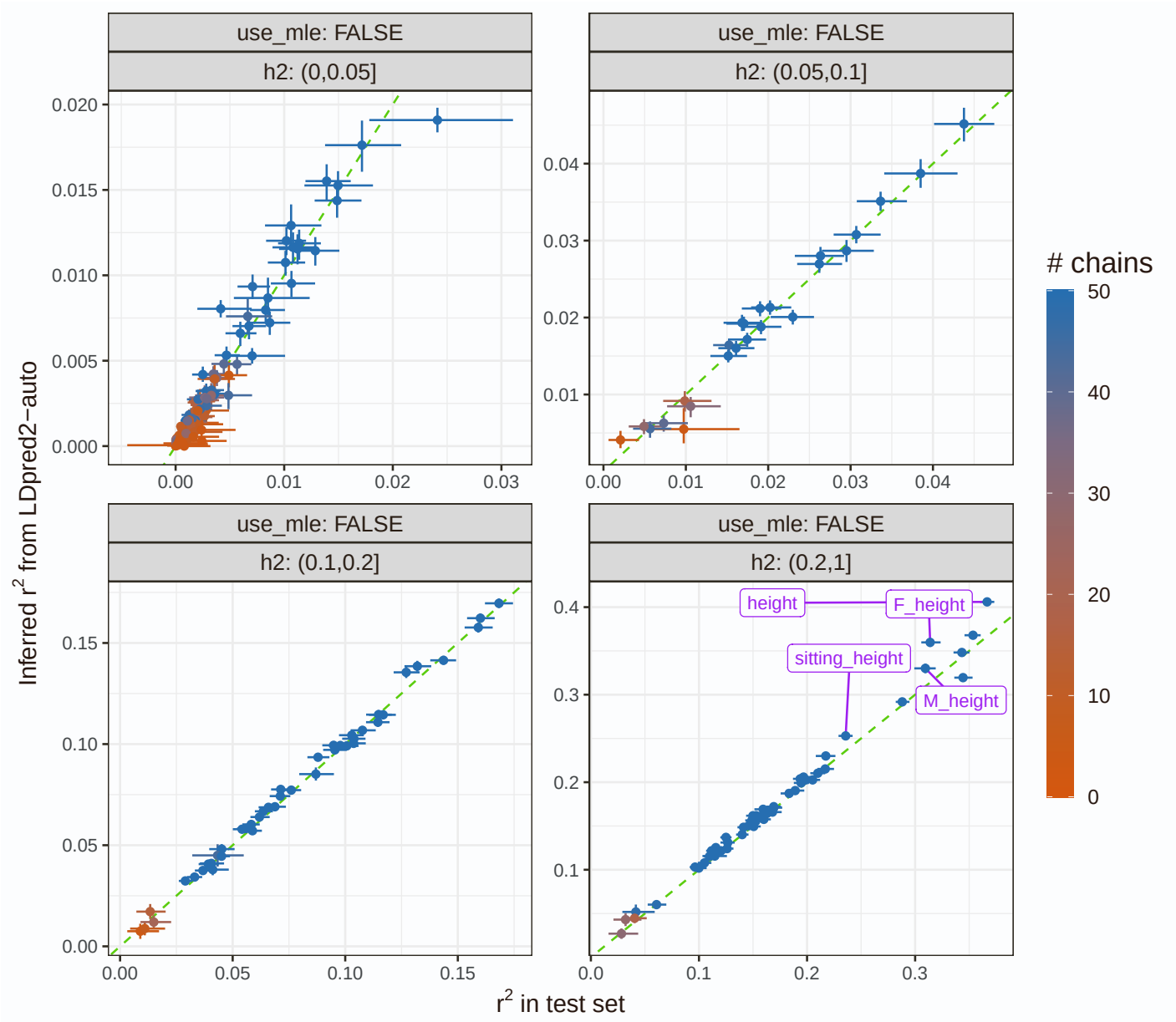


Figure S27: Inferred predictive performance r^2 from the Gibbs sampler of LDpred2-auto versus the ones obtained in the test set, for all 248 phenotypes defined from the UK Biobank. These are stratified by the polygenicity estimated from LDpred2-auto. Green dashed lines represent the 1:1 line. The 95% confidence interval for the LDpred2-auto estimate is obtained from the 2.5% and 97.5% quantiles of all the r^2 estimates from the iterations (after burn-in) of the chains kept. The 95% confidence interval for r^2 in the test set is obtained from bootstrap. Colors represent the number of chains kept (out of 50). "F_height" and "M_height" use females and males only, respectively (in both GWAS and test sets).

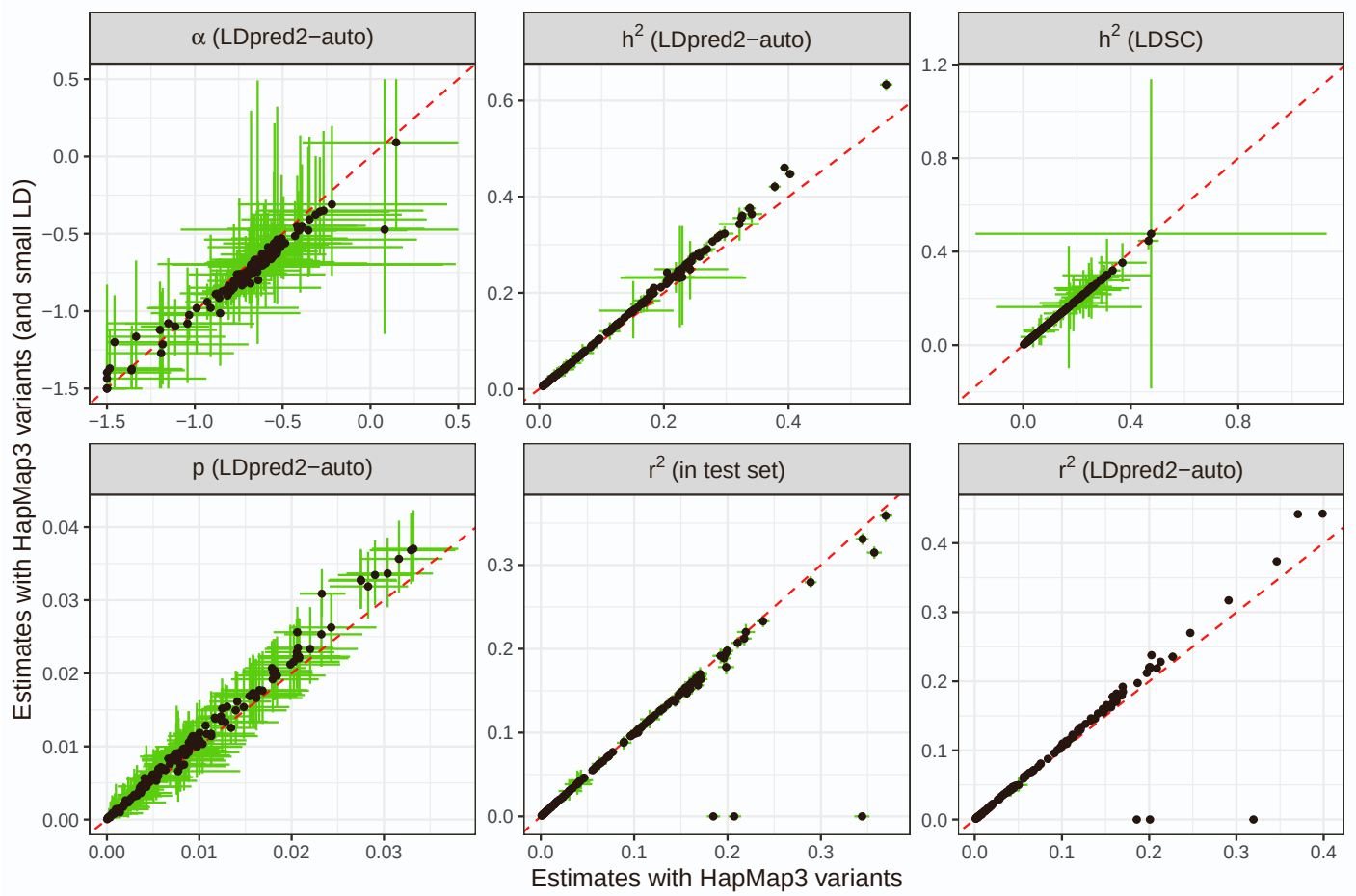


Figure S28: LDpred2-auto estimates for UKBB phenotypes with either a small or a large LD reference. Only 154 phenotypes with more than 25 chains kept when using the large LD reference are represented here. Red dashed lines represent the 1:1 line. The 95% confidence interval for the LDpred2-auto estimate (in green) is obtained from the 2.5% and 97.5% quantiles of all the estimates from the iterations (after burn-in) of the chains kept. The 95% confidence interval for r^2 in the test set is obtained from bootstrap.

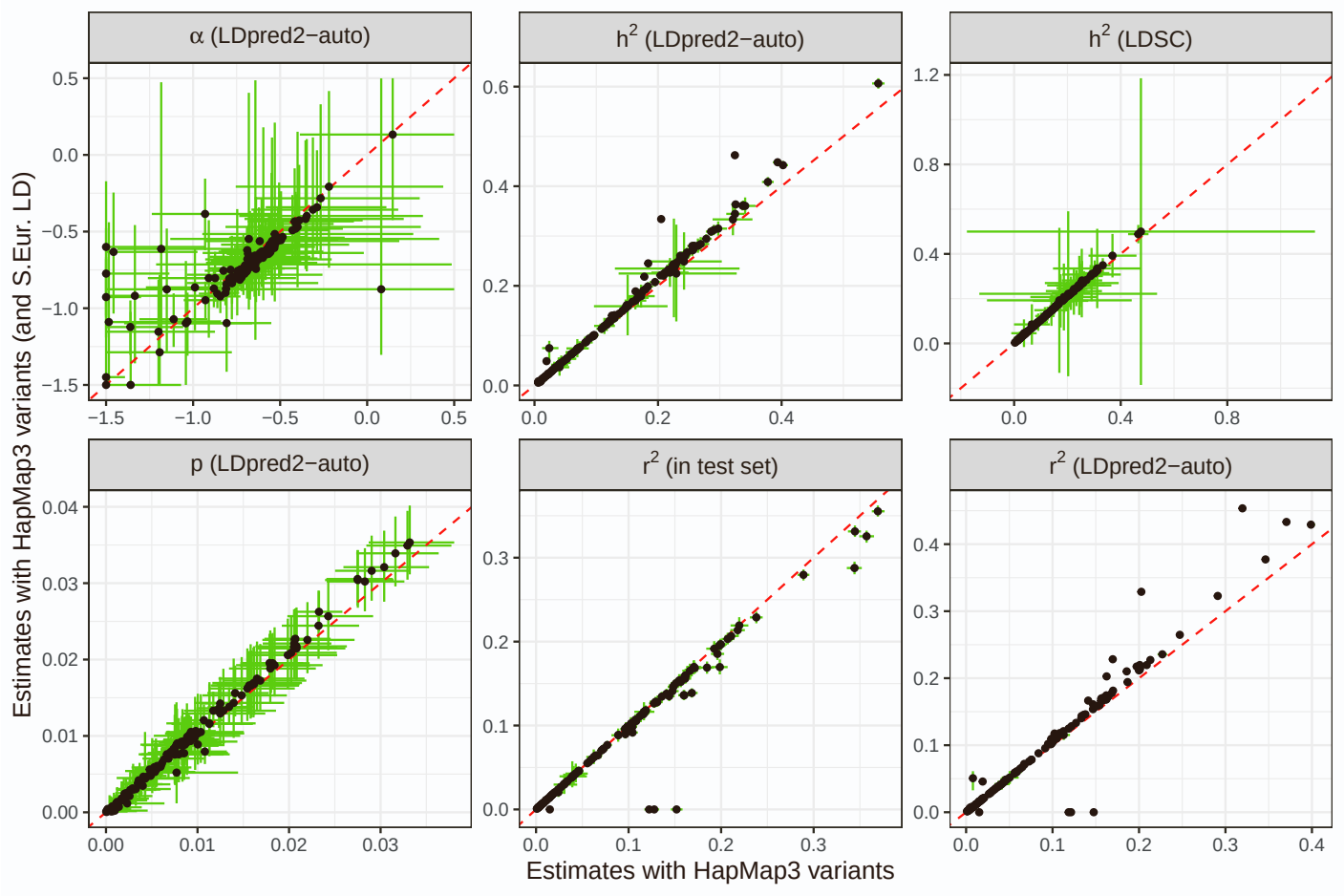


Figure S29: LDpred2-auto estimates for UKBB phenotypes with either a N.W. European or a S. European ("altpop") LD reference. Only 154 phenotypes with more than 25 chains kept when using the N.W. European LD reference are represented here. Red dashed lines represent the 1:1 line. The 95% confidence interval for the LDpred2-auto estimate (in green) is obtained from the 2.5% and 97.5% quantiles of all the estimates from the iterations (after burn-in) of the chains kept. The 95% confidence interval for r^2 in the test set is obtained from bootstrap.

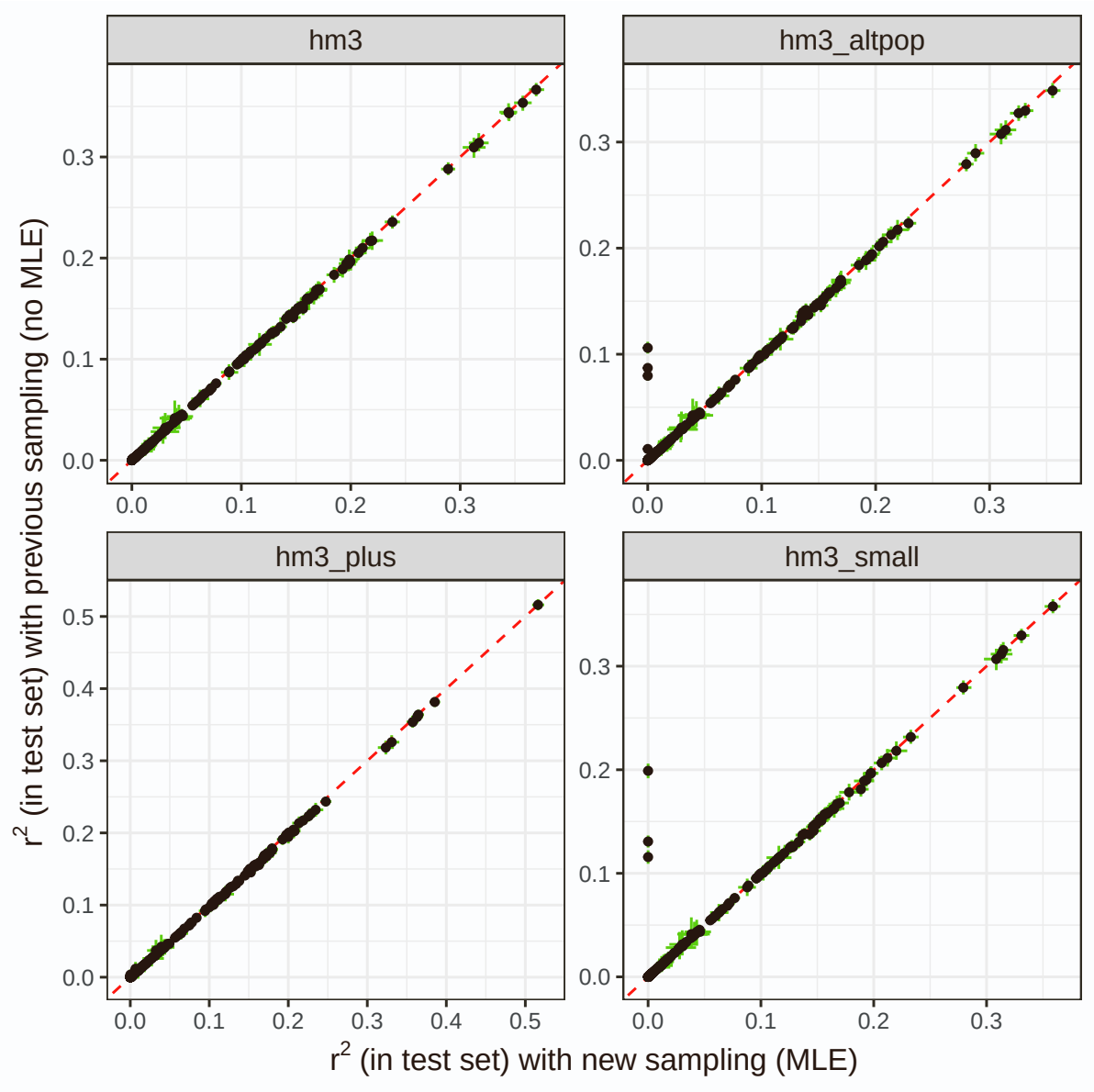


Figure S30: r^2 estimates (in the test set) for UKBB phenotypes, using LDpred2-auto with either the extended model and sampling (MLE, 3-parameter model) or the previous one (2-parameter model). Red dashed lines represent the 1:1 line. The 95% confidence interval for r^2 in the test set is obtained from bootstrap.

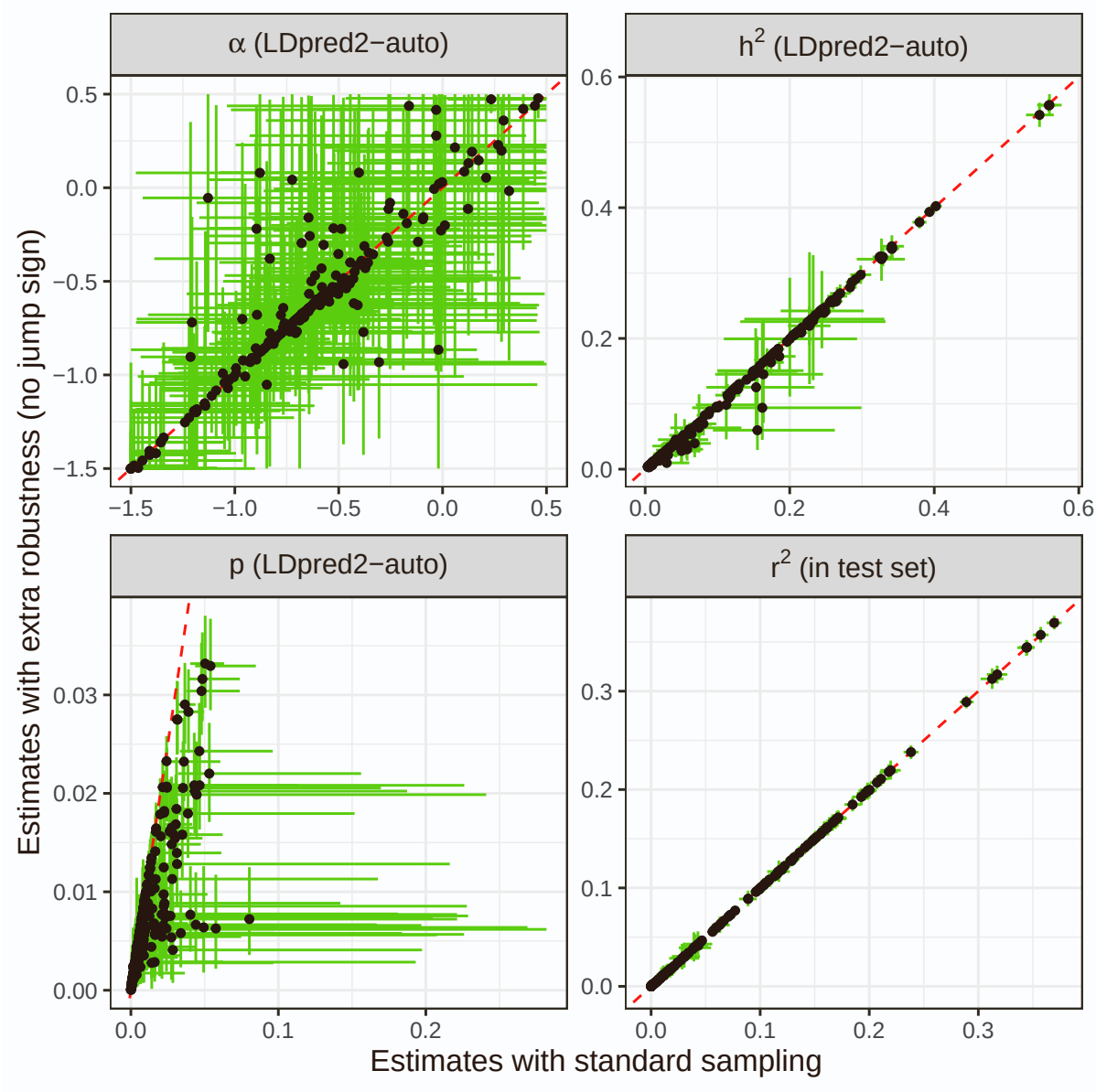


Figure S31: LDpred2-auto estimates for 248 UKBB phenotypes, with or without option 'allow_jump_sign' enabled. Red dashed lines represent the 1:1 line. The 95% confidence interval for the LDpred2-auto estimate (in green) is obtained from the 2.5% and 97.5% quantiles of all the estimates from the iterations (after burn-in) of the chains kept. The 95% confidence interval for r^2 in the test set is obtained from bootstrap.

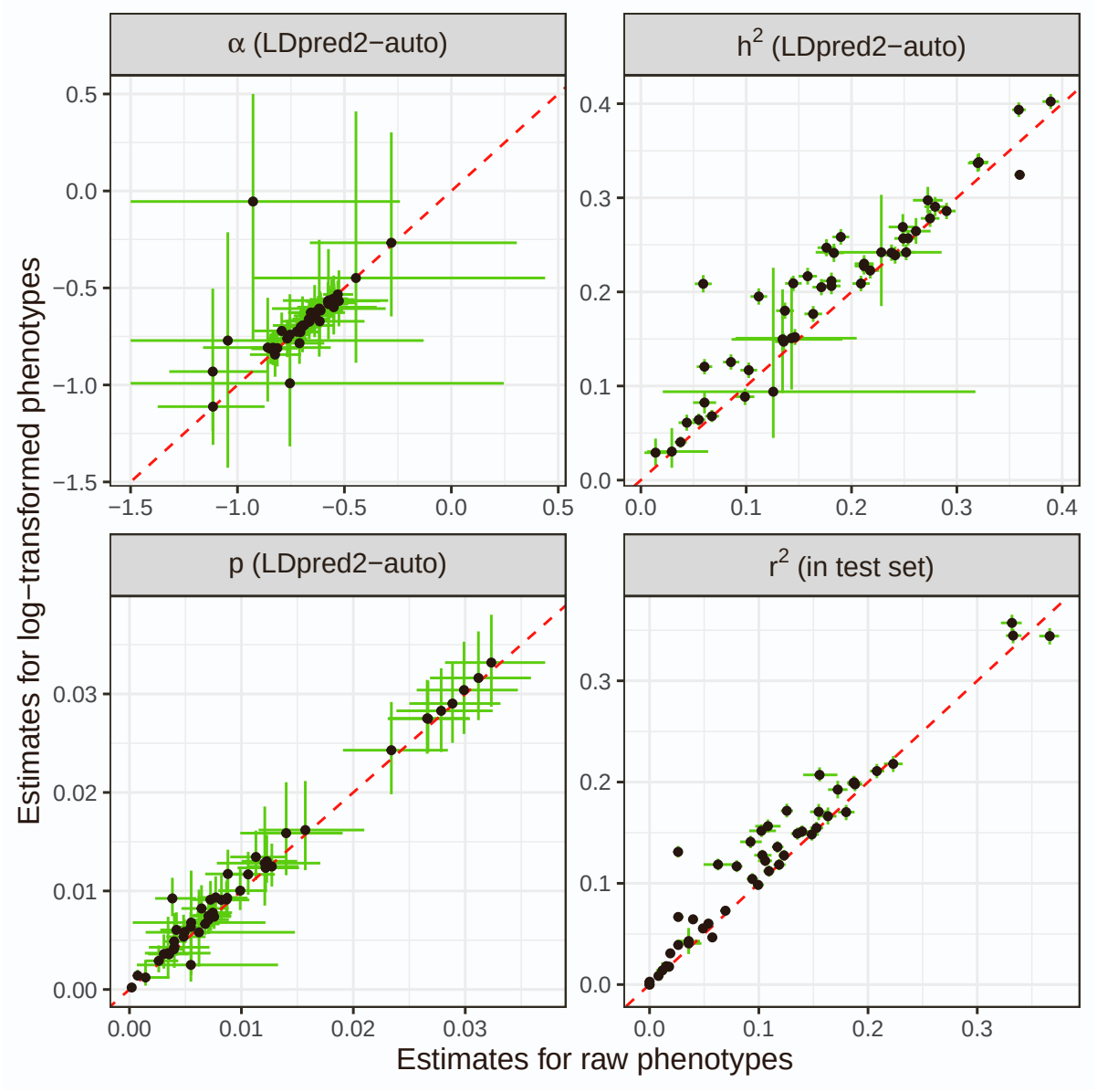


Figure S32: LDpred2-auto estimates for 49 log-transformed UKBB phenotypes, versus for their raw versions. Red dashed lines represent the 1:1 line. The 95% confidence interval for the LDpred2-auto estimate (in green) is obtained from the 2.5% and 97.5% quantiles of all the estimates from the iterations (after burn-in) of the chains kept. The 95% confidence interval for r^2 in the test set is obtained from bootstrap.

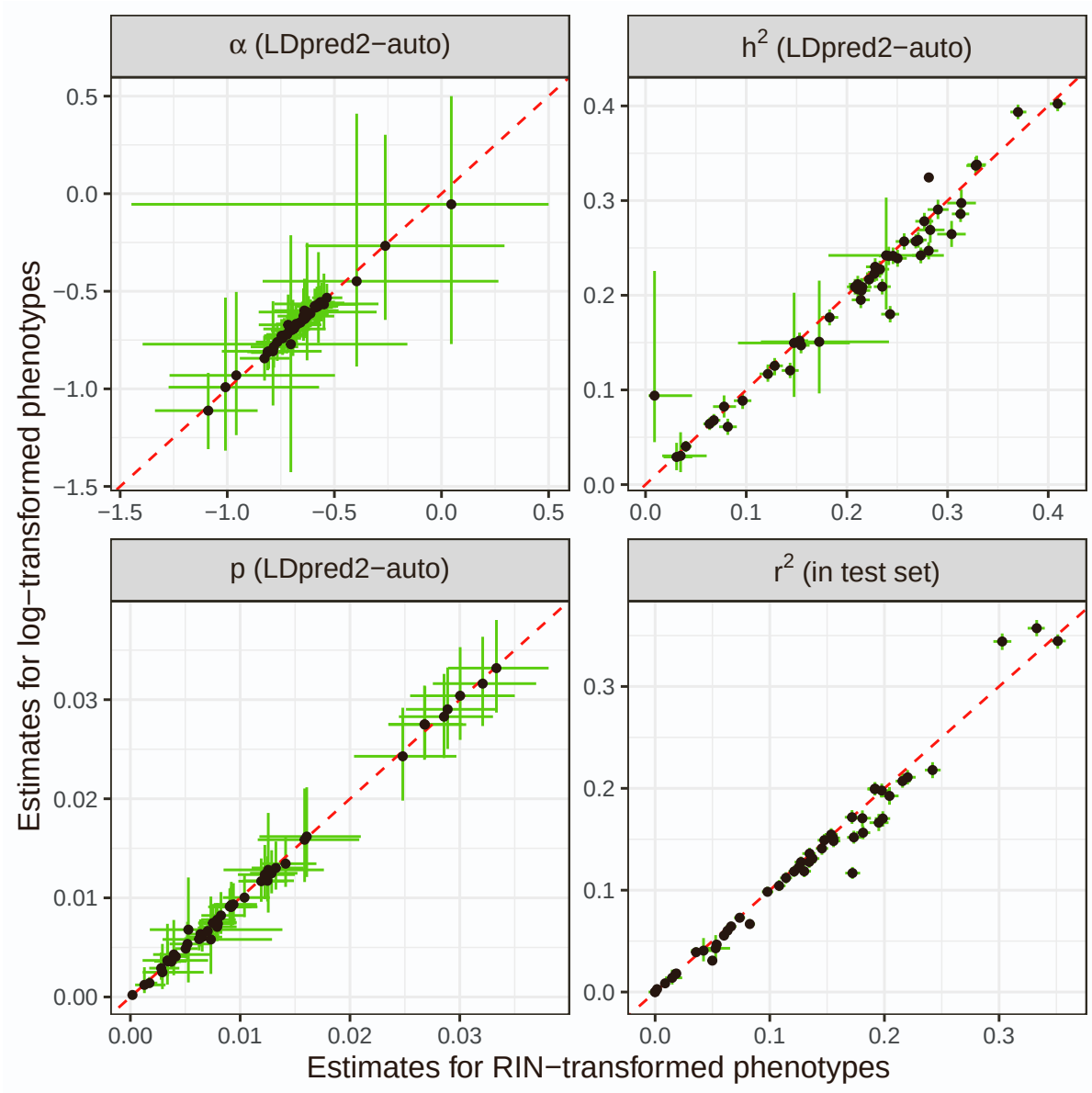


Figure S33: LDpred2-auto estimates for 49 log-transformed UKBB phenotypes, versus for their rank-based inverse normal (RIN) transformed versions. Red dashed lines represent the 1:1 line. The 95% confidence interval for the LDpred2-auto estimate (in green) is obtained from the 2.5% and 97.5% quantiles of all the estimates from the iterations (after burn-in) of the chains kept. The 95% confidence interval for r^2 in the test set is obtained from bootstrap.

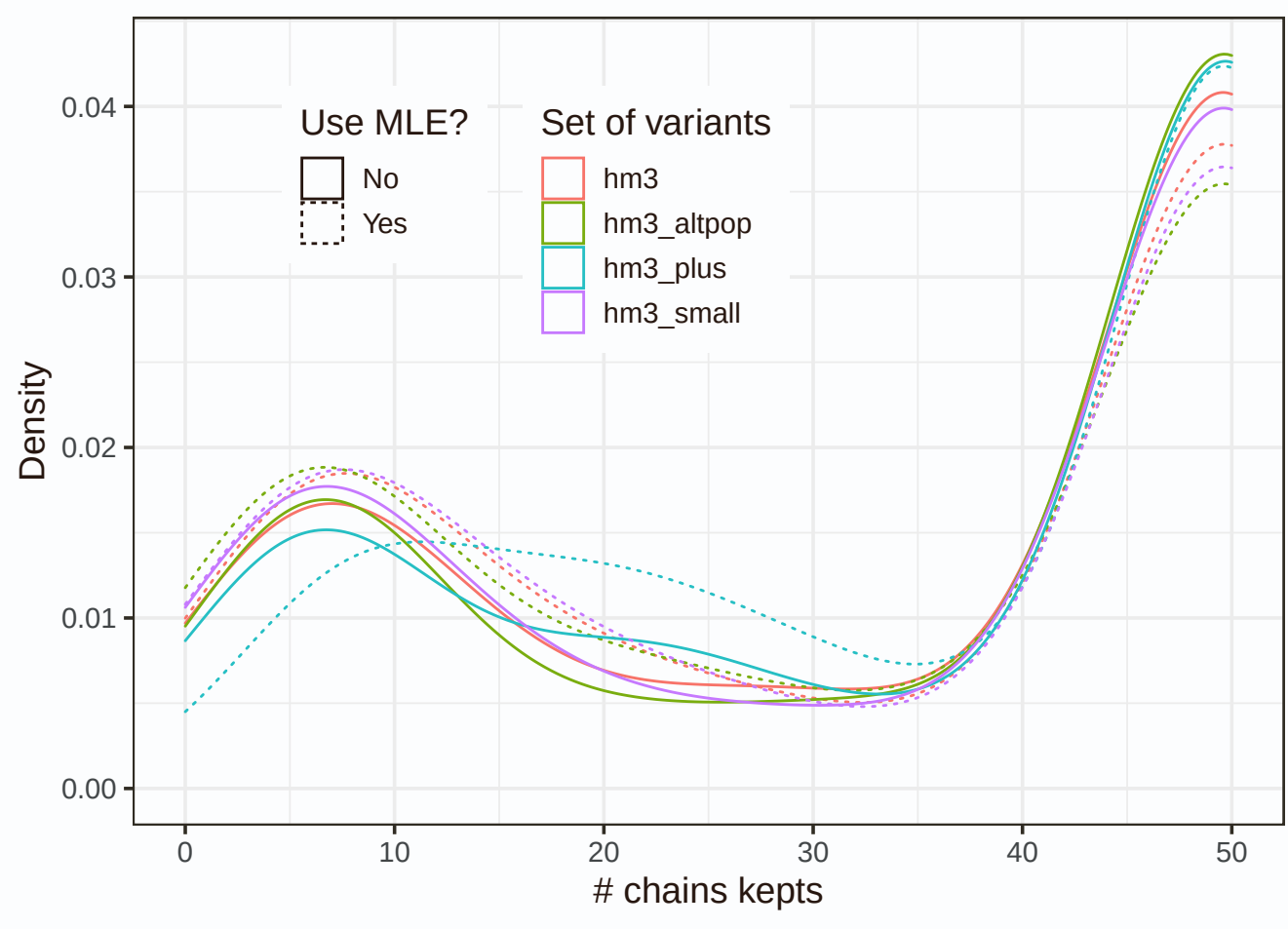


Figure S34: Distribution of the number of LDpred2-auto chains kept across 248 UKBB phenotypes. "Use MLE" corresponds to using the extended 3-parameter model and sampling scheme (Methods).

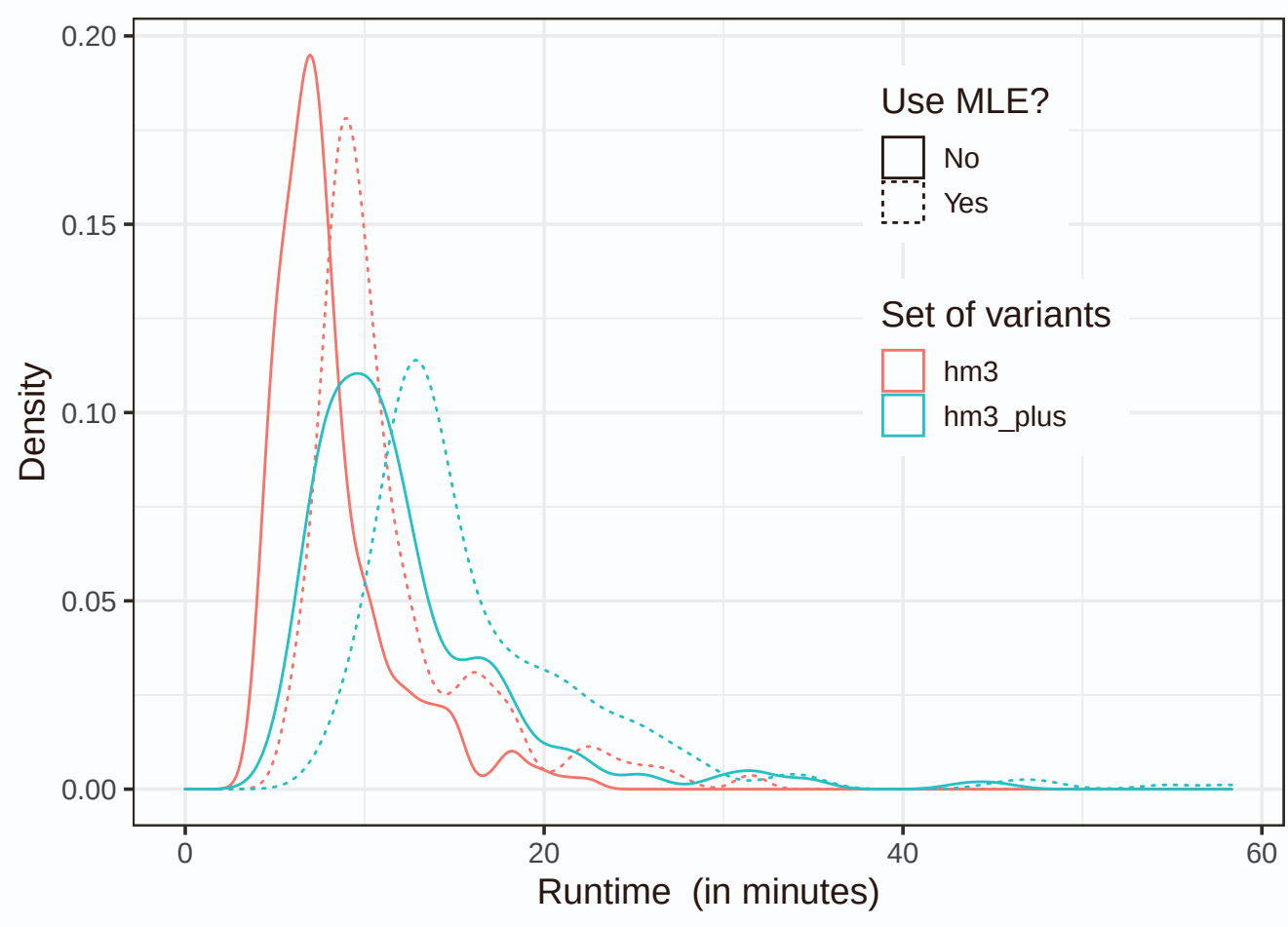


Figure S35: Distribution of LDpred2-auto runtimes across 248 UKBB phenotypes. "Use MLE" corresponds to using the extended 3-parameter model and sampling scheme (Methods). For each phenotype, 50 chains are used, parallelized over 13 cores.

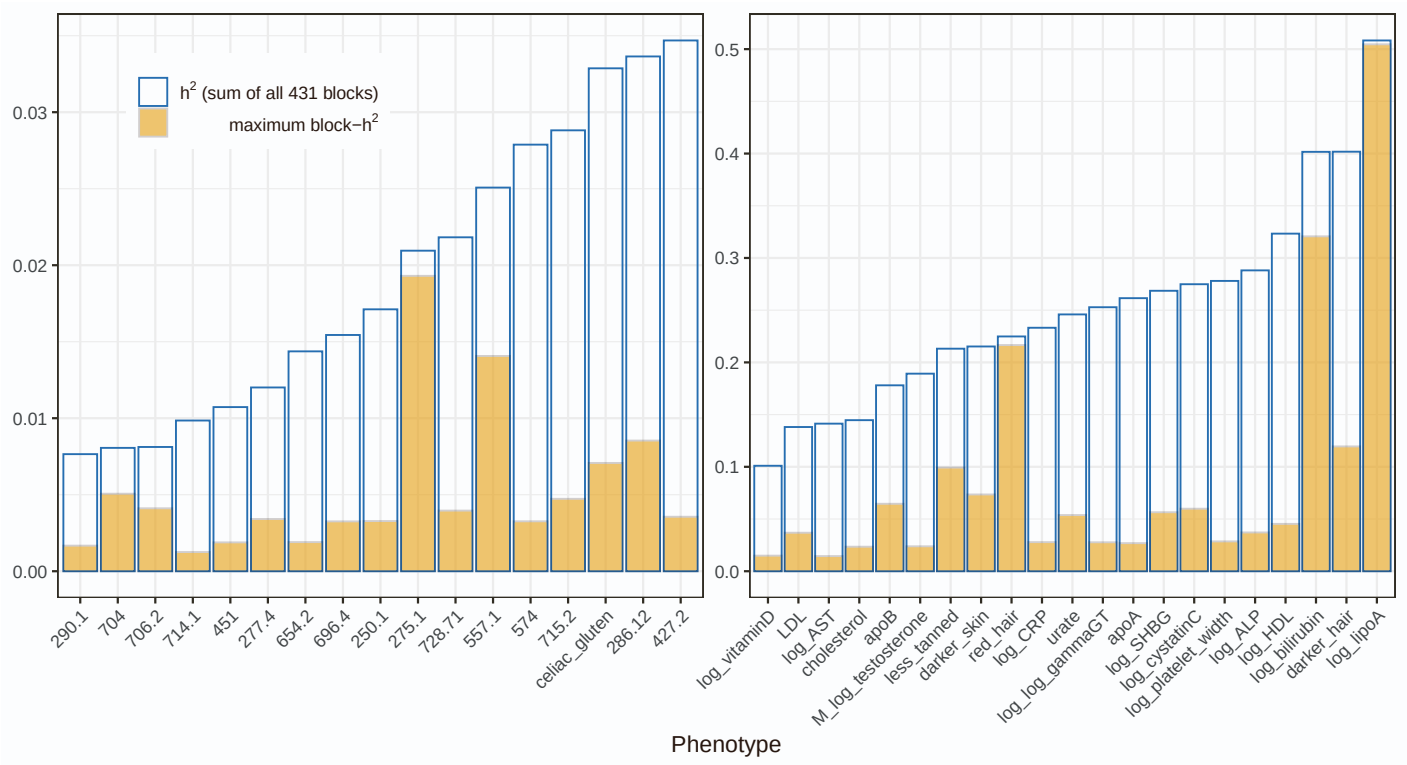


Figure S36: Genome-wide and per-block heritability estimates from LDpred2-auto for UKBB phenotypes. The HapMap3+ variants are used here. The maximum local h^2 is the maximum heritability estimate across all 431 independent LD blocks defined for this set of variants. Only phenotypes for which this represents at least 10% of the total heritability are represented.

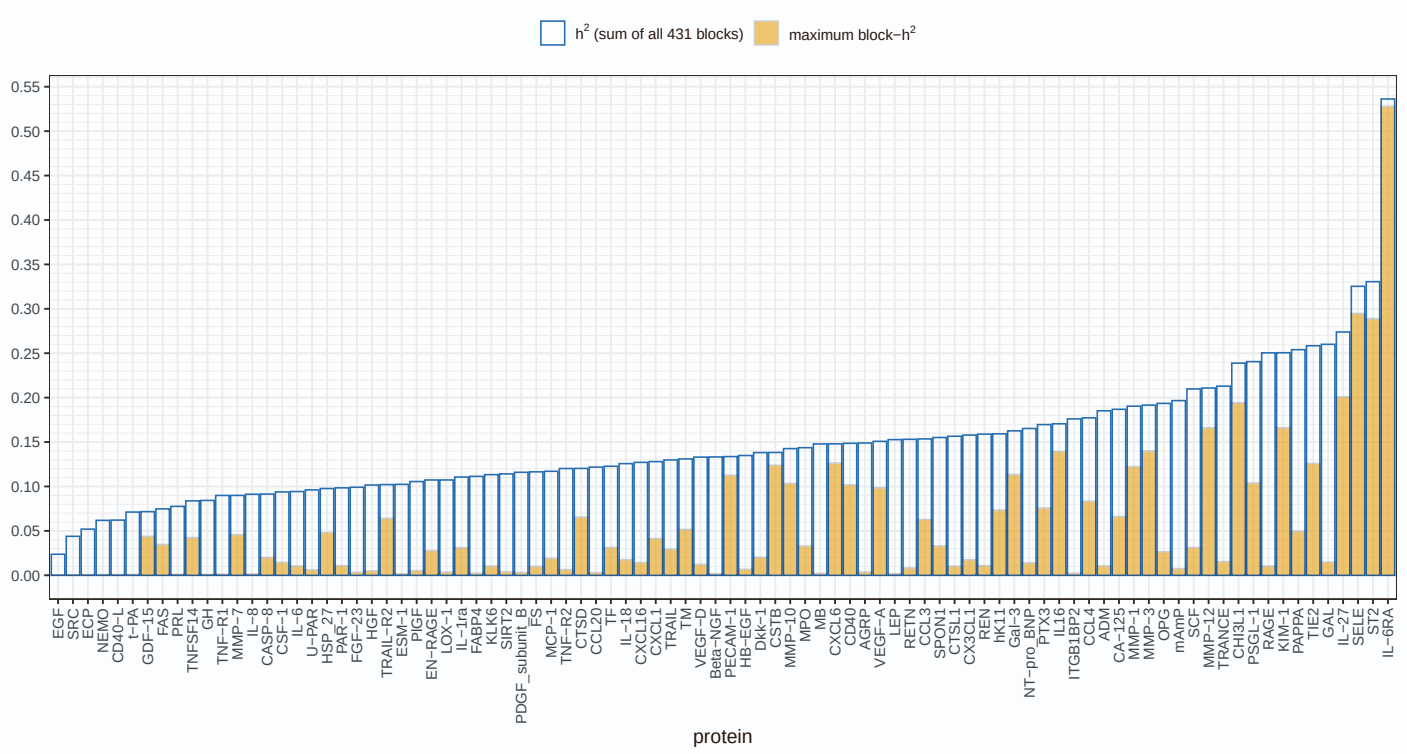


Figure S37: Genome-wide and per-block heritability estimates from LDpred2-auto for 90 protein concentrations[4]. The HapMap3+ variants are used here. The maximum local h^2 is the maximum heritability estimate across all 431 independent LD blocks defined for this set of variants.

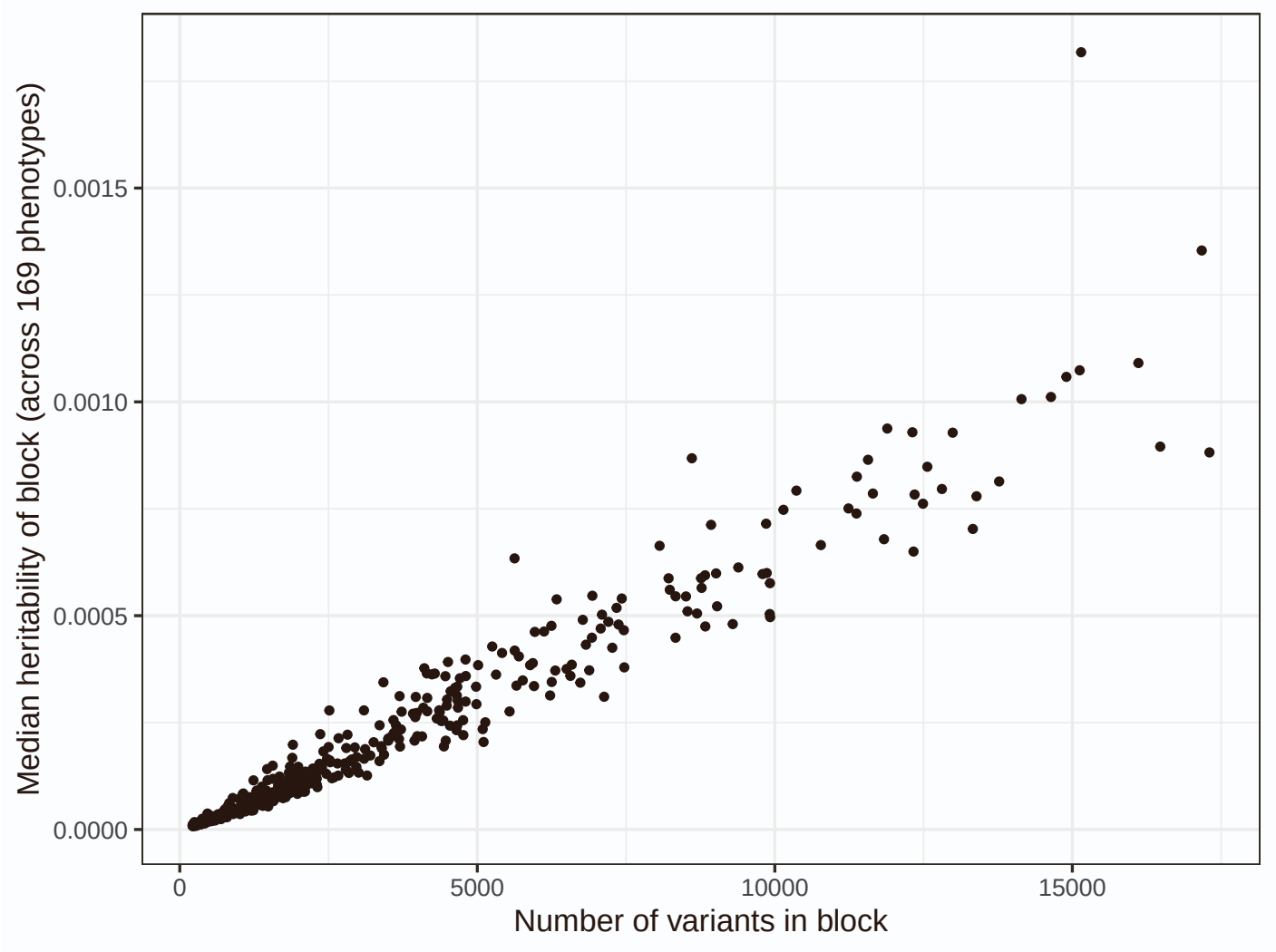


Figure S38: Per-block median heritability across 169 UKBB phenotypes. The HapMap3+ set of variants is used, with 431 independent LD blocks. Only phenotypes with more than 25 chains kept are used here. The top block is on chromosome 6 [22.1-41.4 Mb], which contains the HLA region.

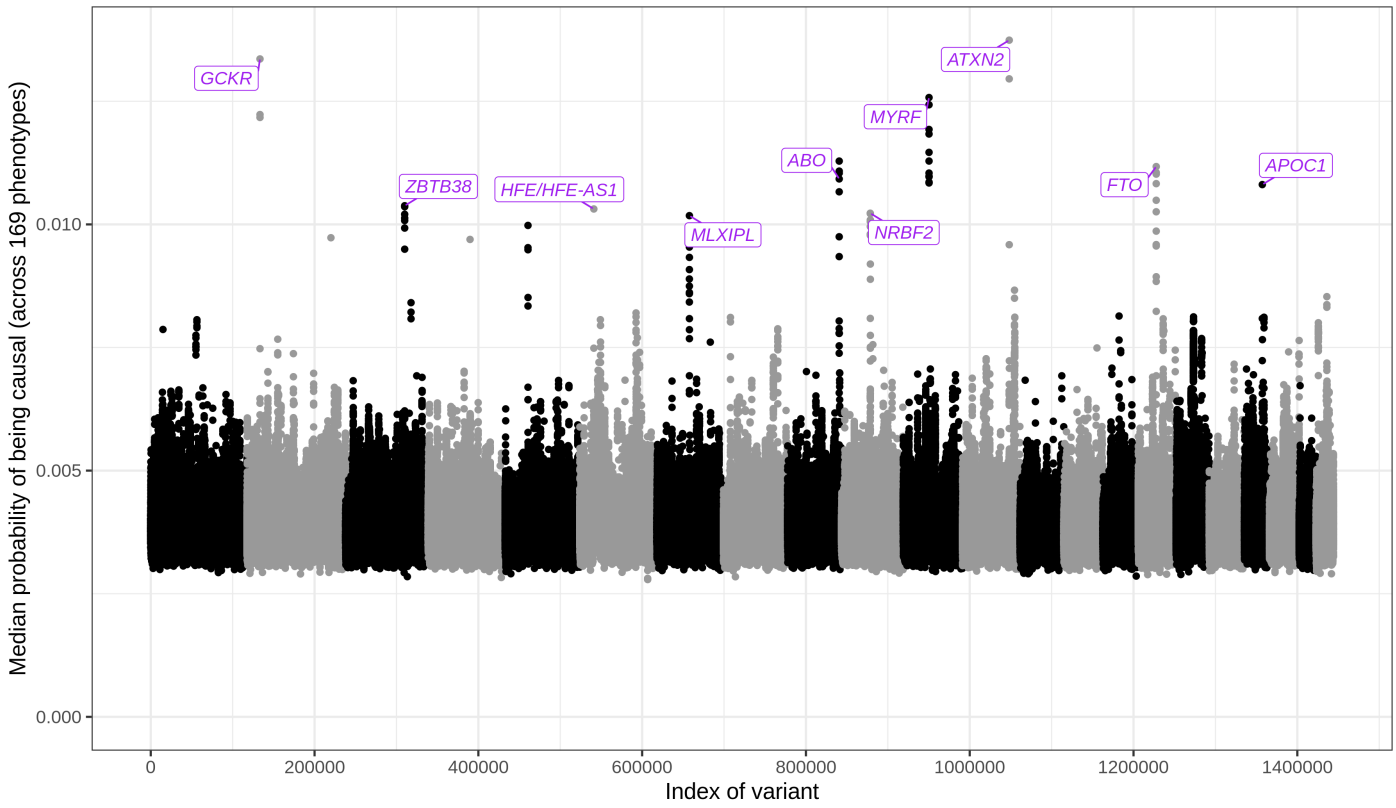


Figure S39: Per-variant median probabilities of being causal across 169 UKBB phenotypes. Variants with a median probability larger than 0.01 were mapped to genes using R package rsnps (only the largest per peak). The HapMap3+ set of variants is used. Only phenotypes with more than 25 chains kept are used here.

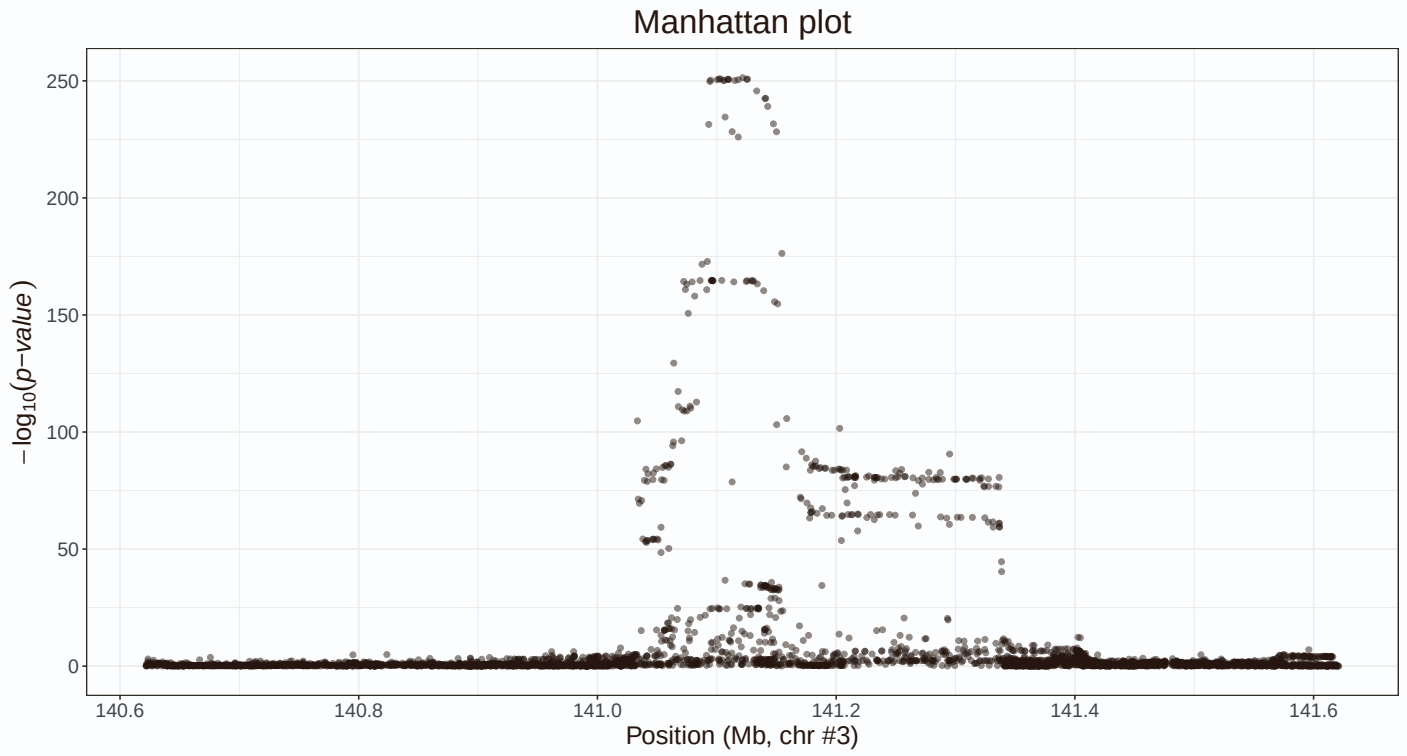
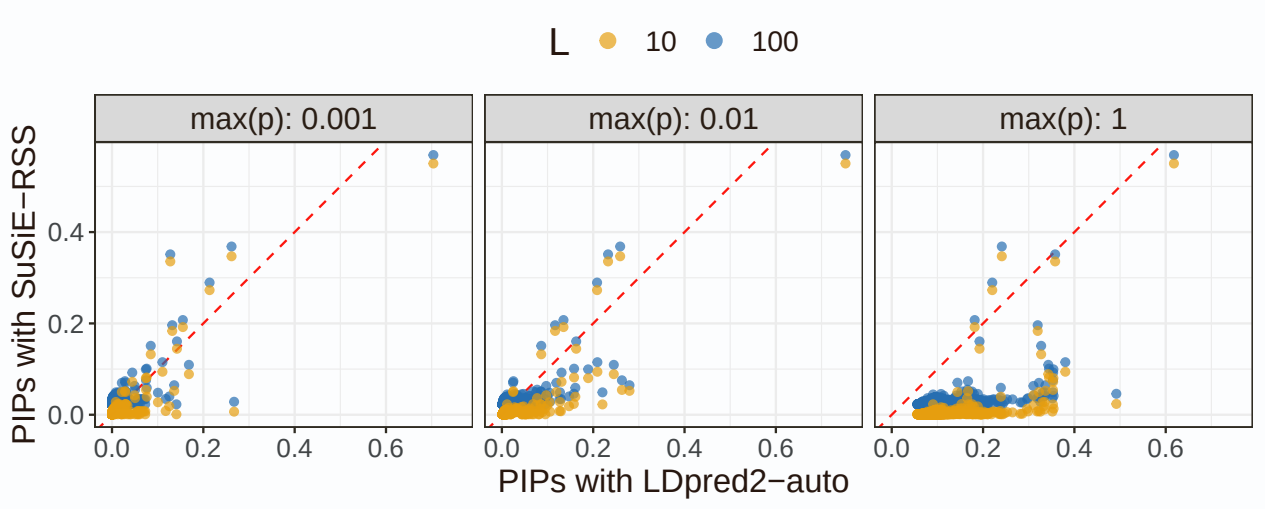


Figure S40: GWAS of height in a restricted region containing the most significant HapMap3+ variant for height.

A



B

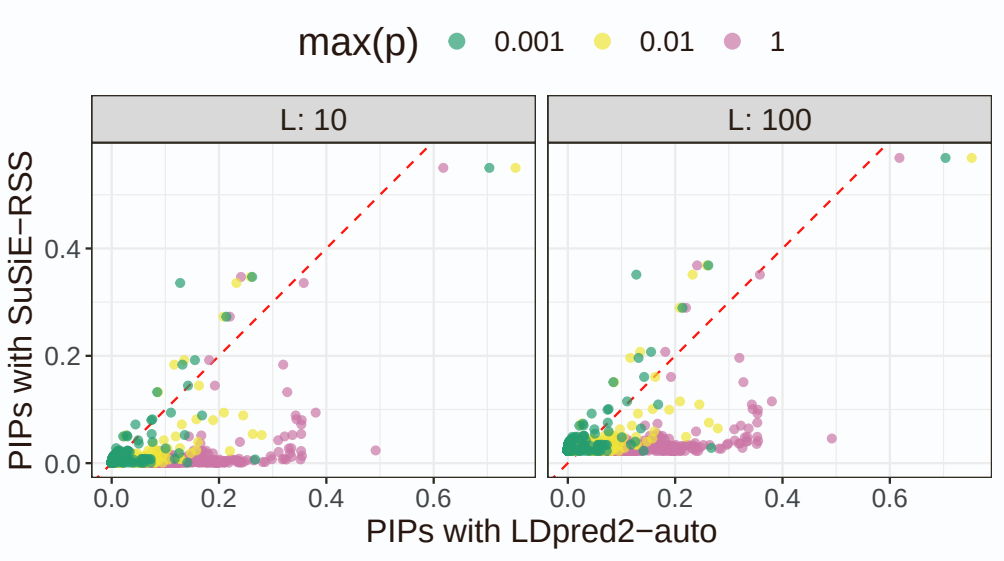


Figure S41: Posterior inclusion probabilities (PIPs) for the variants in Figure S40. L is the maximum number of causal variants in SuSiE-RSS, and max(p) is the maximum value of the estimated p in LDpred2-auto. Both panels A and B represent the same data, but colors and facets are changed.

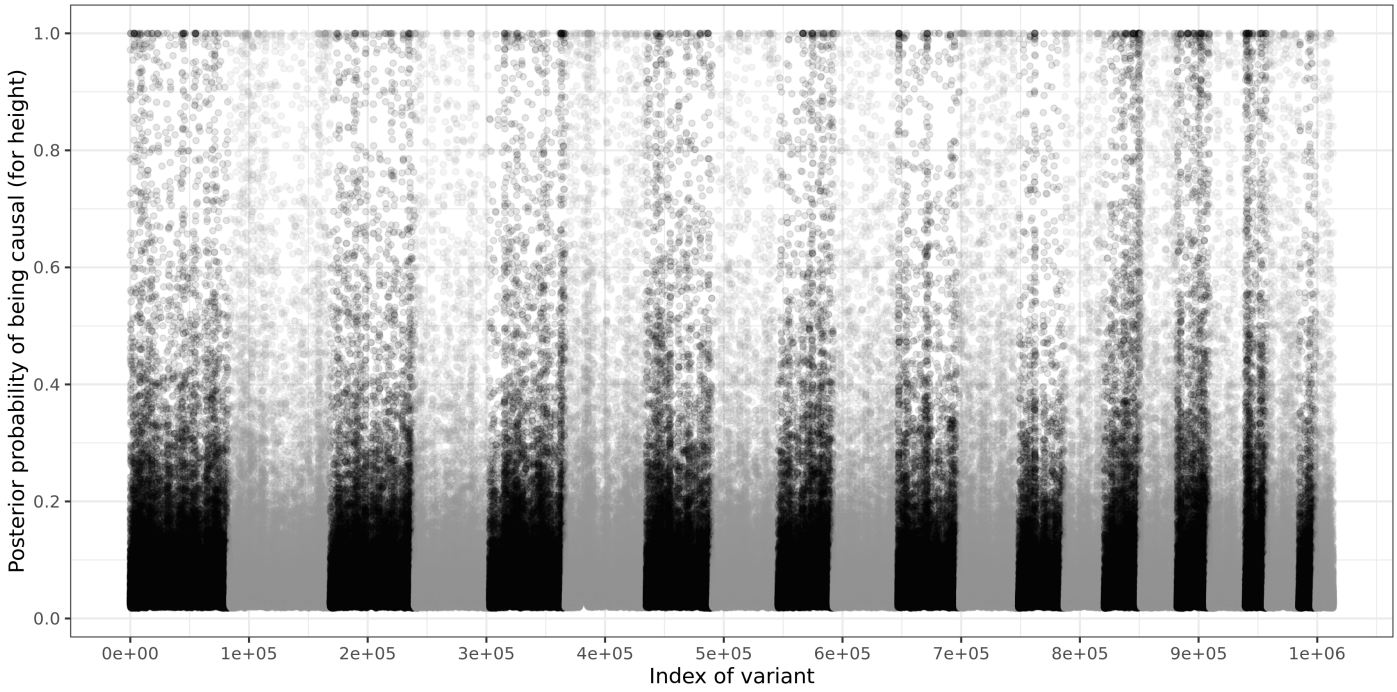
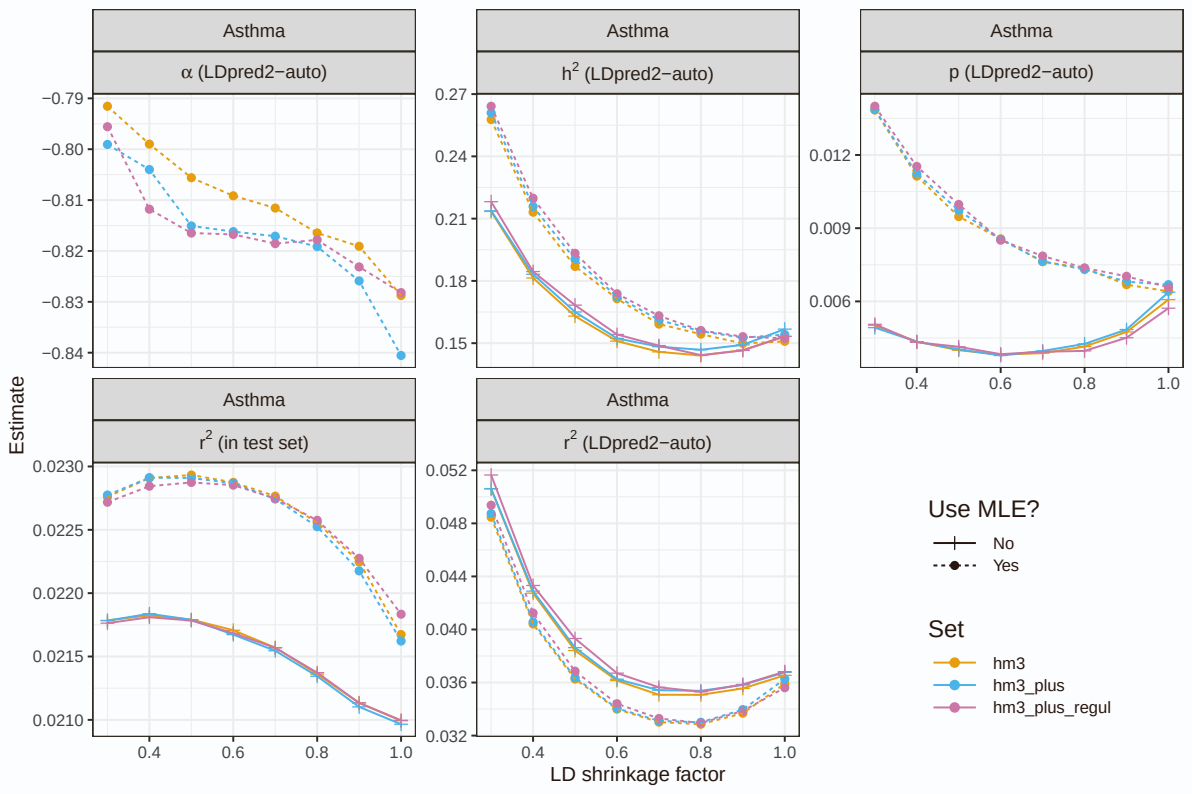
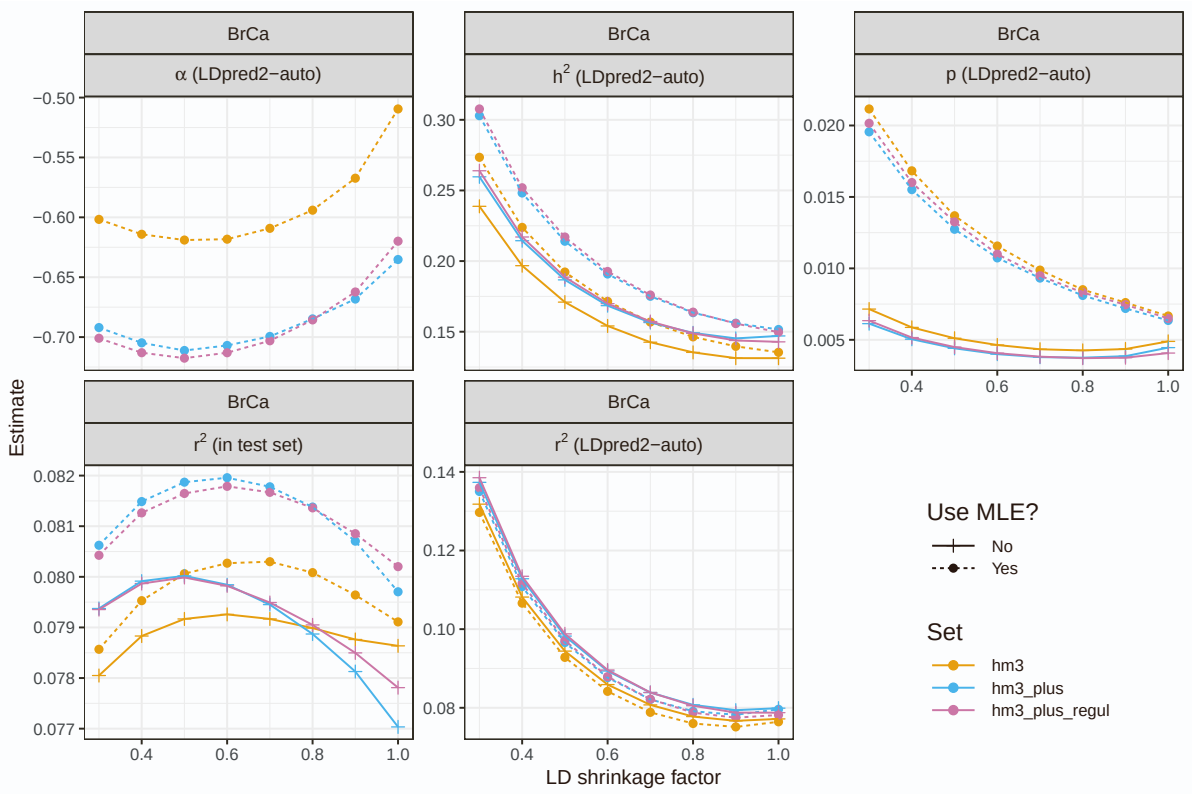


Figure S42: Per-variant probabilities of being causal for height. These are provided by LDpred2-auto when using the external GWAS summary statistics of 1.6M European individuals from[5].

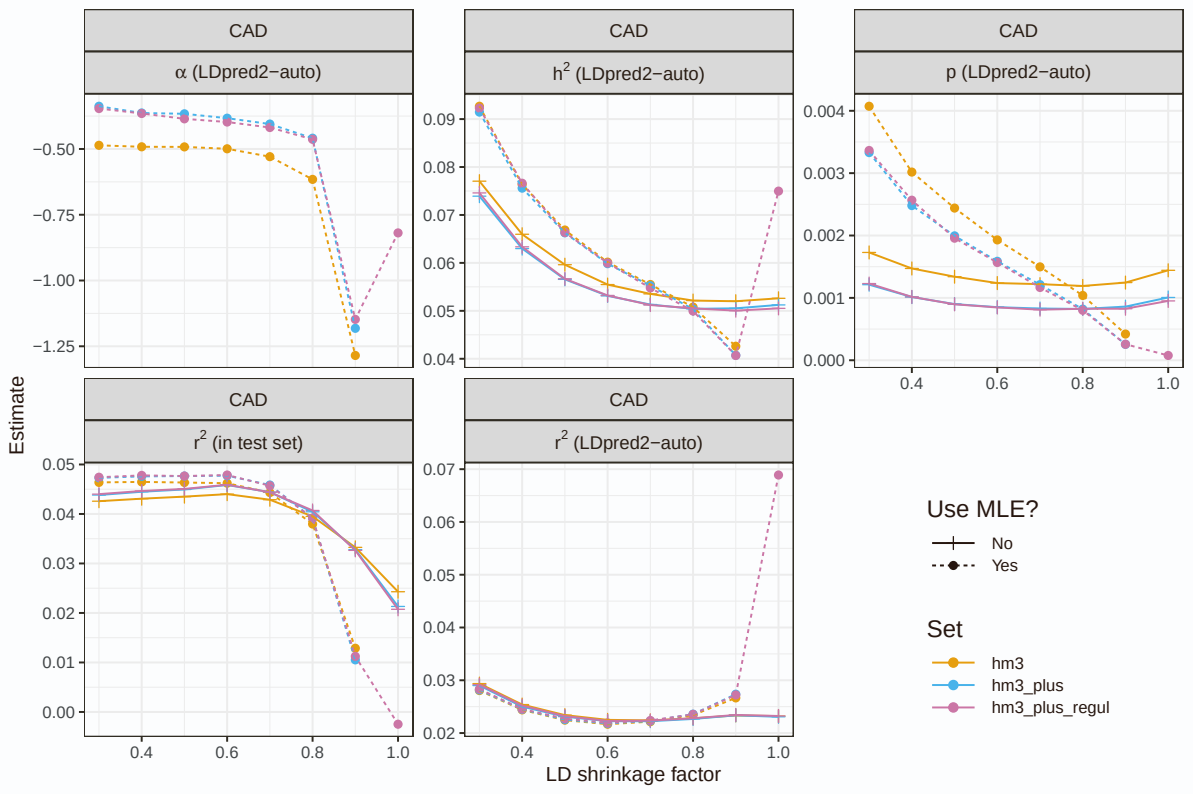
Figure S43: Heritability enrichment from LDpred2-auto for height across 50 functional annotations. The 95% confidence interval for the LDpred2-auto estimate is obtained from the 2.5% and 97.5% quantiles of all the estimates from the iterations (after burn-in) of the chains kept.



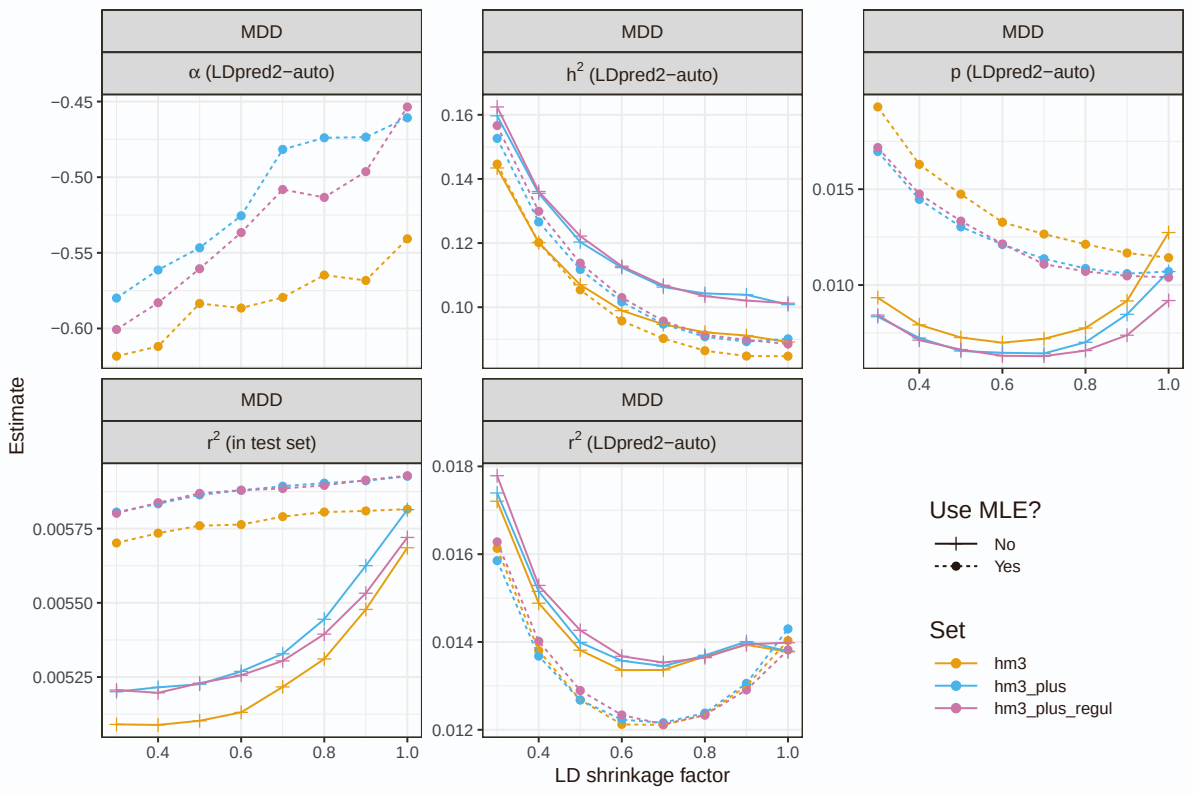
(a) Asthma



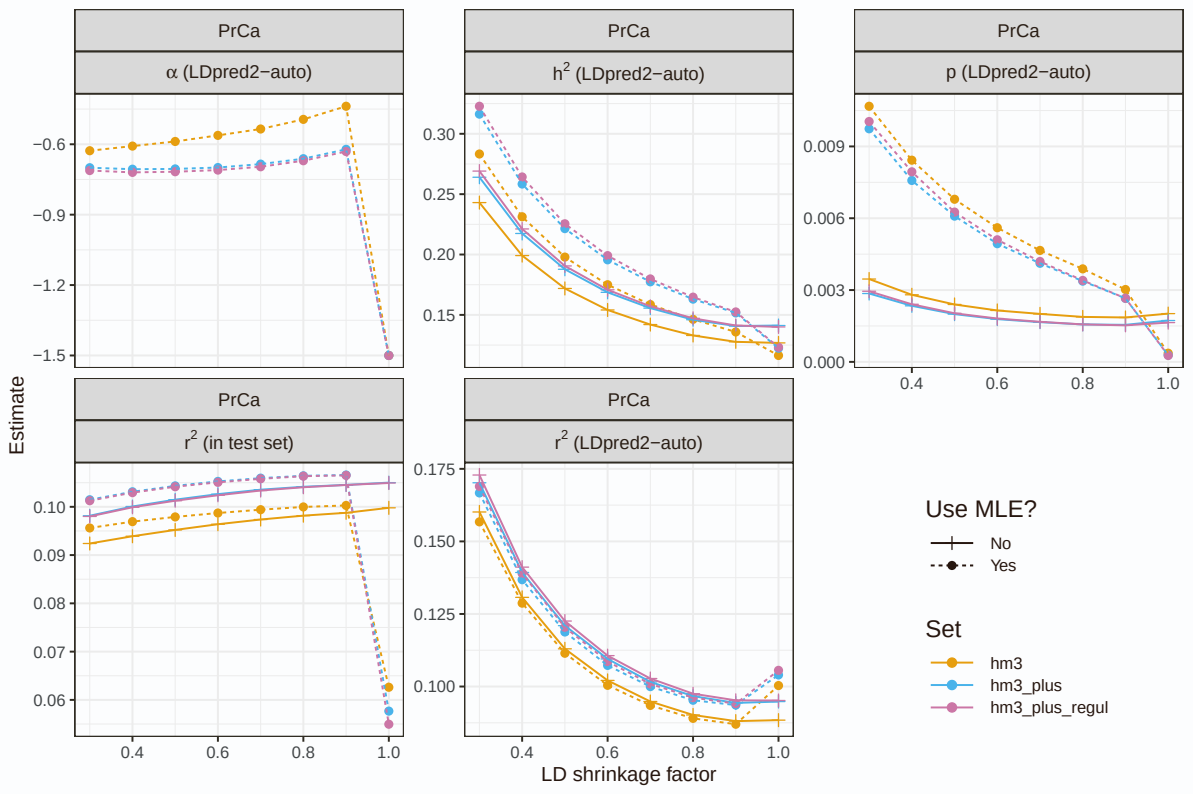
(b) Breast cancer



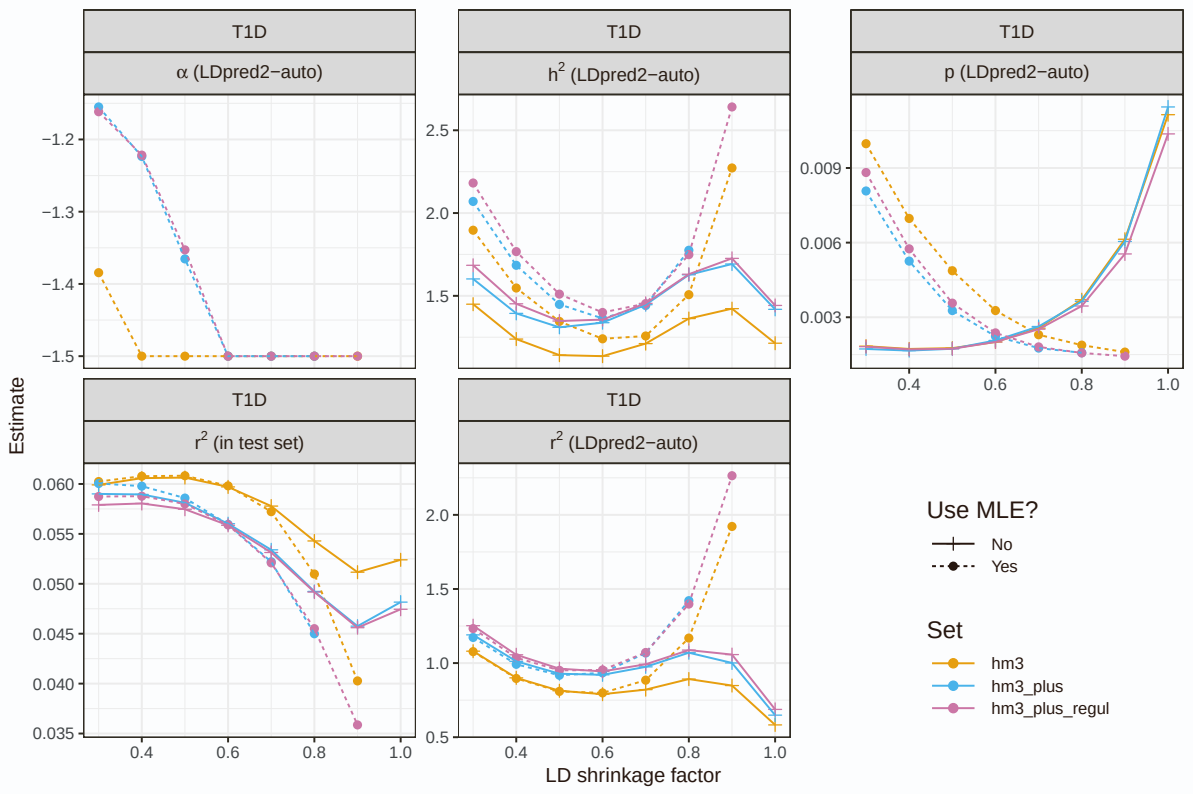
(c) Coronary artery disease



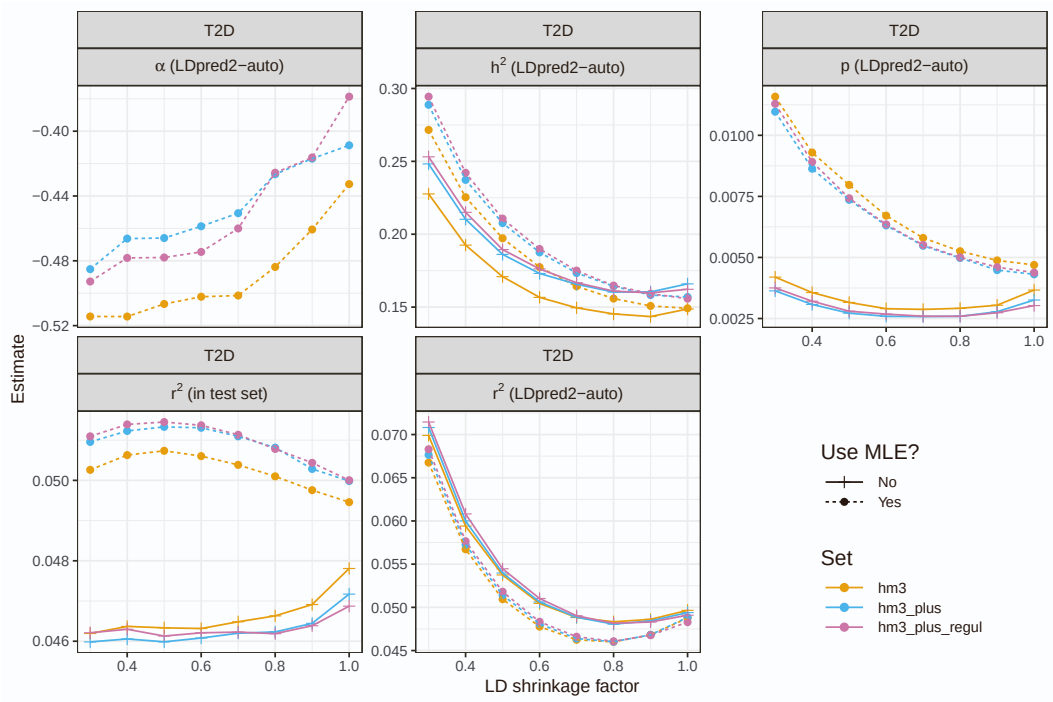
(d) Depression



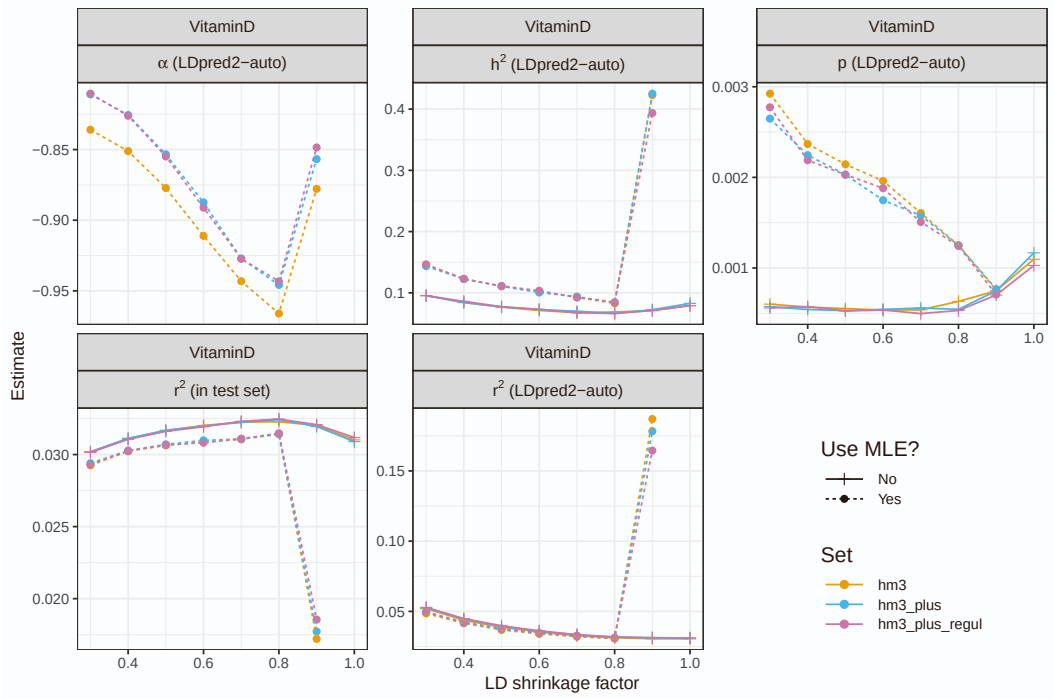
(e) Prostate cancer



(f) Type 1 diabetes



(g) Type 2 diabetes



(h) Vitamin D

Figure S44: LDpred2-auto results with external GWAS summary statistics. We run LDpred2-auto using either the HapMap3 or HapMap3+ variants, with either the extended or previous model and sampling (via parameter `use_MLE`, where setting to `TRUE` uses the extended model), and explore multiple values for parameter `coef_shrink` (multiplicative coefficient for shrinking/regularizing off-diagonal elements of the LD matrix). The UK Biobank is used as test set to compute r^2.

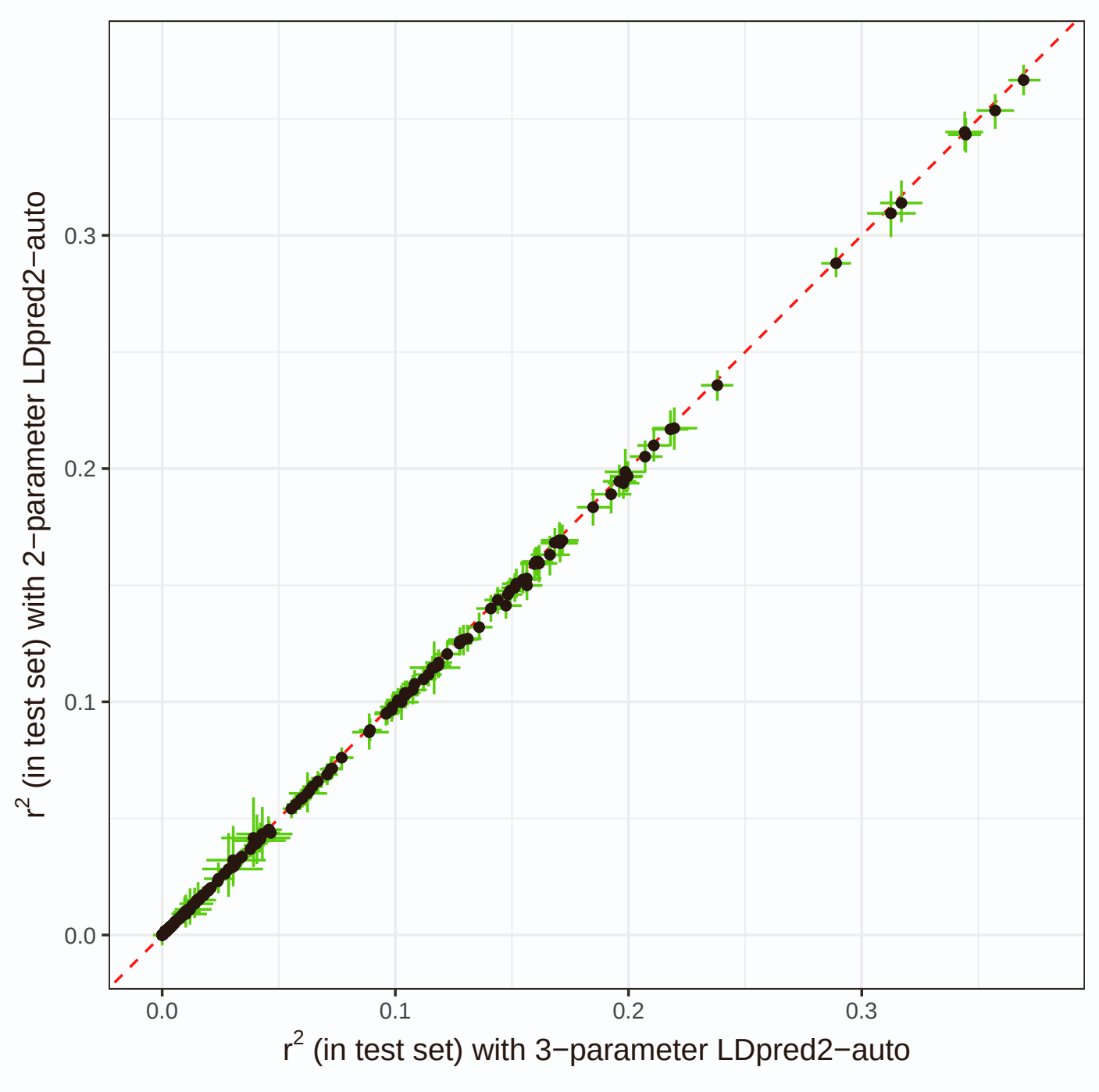


Figure S45: Predictive performance r^2 obtained in the test set, for all 248 phenotypes defined from the UK Biobank. The red dashed line represent the 1:1 line. The 95% confidence interval for r^2 in the test set is obtained from bootstrap.

References

[1] Privé, F., Arbel, J., Aschard, H., and Vilhjálmsson, B. J. (2022). Identifying and correcting for misspecifications in GWAS summary statistics and polygenic scores. Human Genetics and Genomics Advances *3*, 100136.

[2] Lee, S. H., Goddard, M. E., Wray, N. R., and Visscher, P. M. (2012). A better coefficient of determination for genetic profile analysis. Genetic Epidemiology *36*, 214–224.

[3] Privé, F., Aschard, H., Ziyatdinov, A., and Blum, M. G. B. (2018). Efficient analysis of large-scale genome-wide data with two R packages: bigstatsr and bigsnpr. Bioinformatics *34*, 2781–2787.

[4] Folkersen, L., Gustafsson, S., Wang, Q., Hansen, D. H., Hedman, Å. K., Schork, A., Page, K., Zhernakova, D. V., Wu, Y., Peters, J., et al. (2020). Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism *2*, 1135–1148.

[5] Yengo, L., Vedantam, S., Marouli, E., Sidorenko, J., Bartell, E., Sakaue, S., Graff, M., Eliasen, A. U., Jiang, Y., Raghavan, S., et al. (2022). A saturated map of common genetic variants associated with human height. Nature *610*, 704–712.