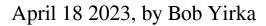
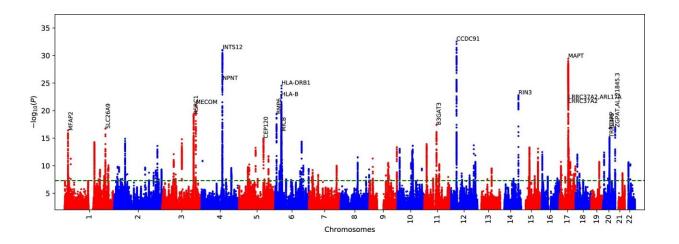


## Using machine learning applications to predict patients' risk of developing COPD





ML-based COPD GWAS Manhattan plot via DeepNull. We performed MLbased COPD GWAS where we used the same set of covariates as the Fig. 4 with one additional covariate provided by DeepNull. DeepNull model predicts the MLbased COPD using age, sex, genotype-array, and FEV<sub>1</sub>/FVC as inputs. The additional DeepNull-covariate is the DeepNull model prediction of ML-based COPD. DeepNull learns a function (that is, linear or non-linear) that predicts MLbased COPD via age, sex, genotype-array, and FEV<sub>1</sub>/FVC as inputs. Thus, this analysis is similar to the ML-based COPD GWAS conditional on FEV<sub>1</sub>/FVC where instead of assuming that FEV<sub>1</sub>/FVC has linear relationship with ML-based COPD, DeepNull handles cases where age, sex, and FEV<sub>1</sub>/FVC can have nonlinear relationship with ML-based COPD. We obtained p-values from BOLT-LMM using a two-sided test. The green dashed line is the genome-wide significant level (P

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