Height Meta-analysis for African ancestry

Meta-analysis data information

GWAS summary statistics

We use GWAS summary statistics for height from four sources: Uganda Genome Project (which is a meta-analysis of Uganda + 3 other populations from Africa); pan UKBB (AFR), this is a height GWAS done for each subpopulation in the UK Biobank separately; N'diaye et al. 2011, still the largest height GWAS performed in African ancestry individuals; PAGE, a large meta-analysis including 35% African Americans and the rest Hispanic/Latino and other minority ancestries.

Most were in hg19, except N'diaye, which we lift over to hg19 from hg18. Previous filtering was done in each of these studies, and there is often not enough information for us to perform our own filtering.

UGP: this is very recent. They filtered for imputation score > 0.3.

panUKBB: They filter for INFO scores > 0.8 and minimum allele count of 20 in each population. They also provide a True/False filter for "low_quality_AFR" which we use, retaining only those for which it is 'false'. GWAS included: Age, sex, Age*sex, Age2, age2*sex, the first 10 PCs. Inverse-normal transformation of height in cm.

N'diaye et al.: The genomic control inflation (GC) factor was calculated for each study and used for within-study correction, prior to the meta-analysis. THe overall lambda they report is 1.064 (which we confirm, see table below) suggesting no inflation in this meta-analysis. Imputation info score not available. Authors Filtered for >= 0.3. Betas and SE in units of z-score.
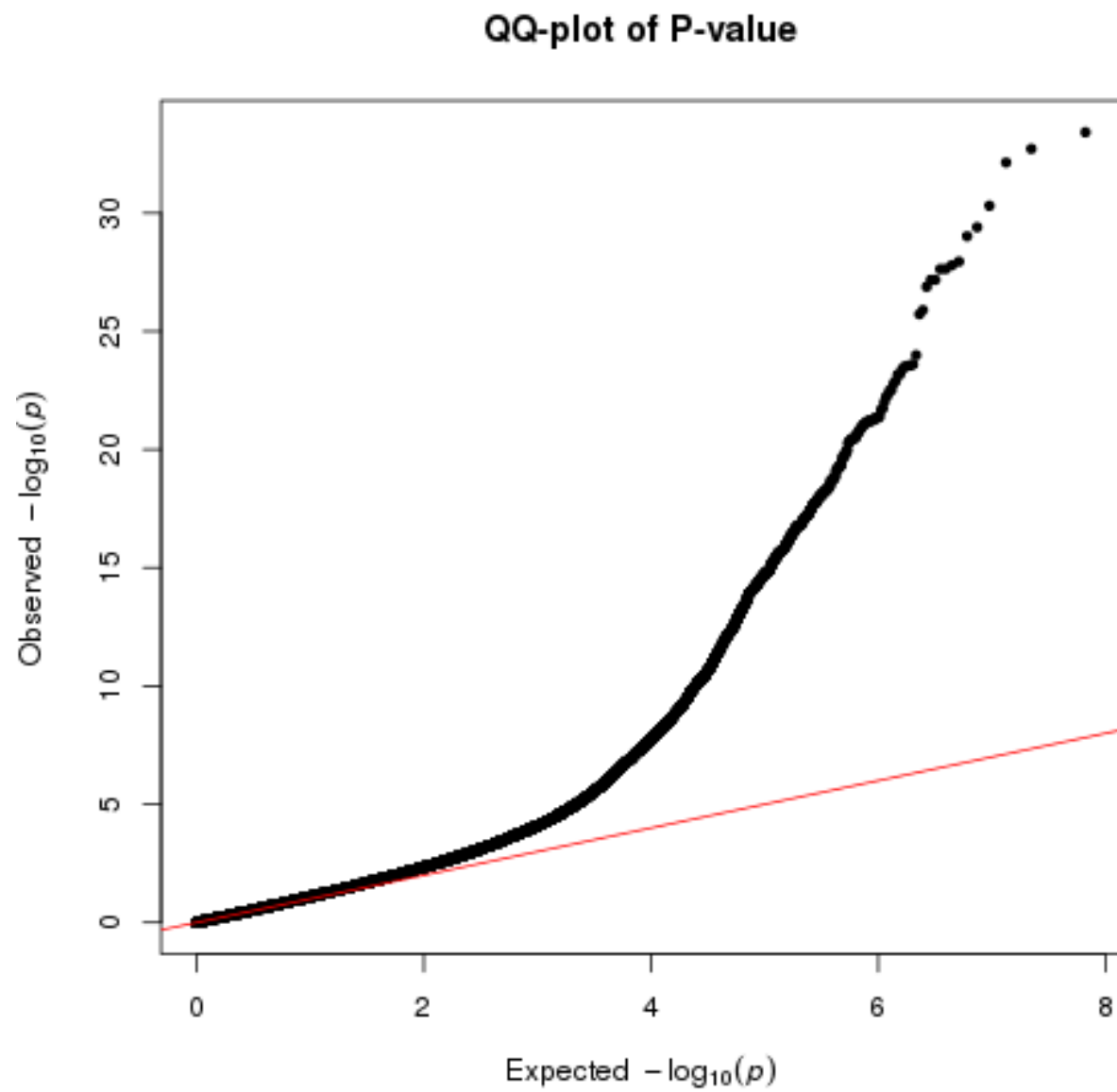
PAGE: inverse-normal-adjusted residuals for each trait outcome. Info score available. Filtered for > 0.4 by authors prior. We were more strict and filtered for > 0.8.

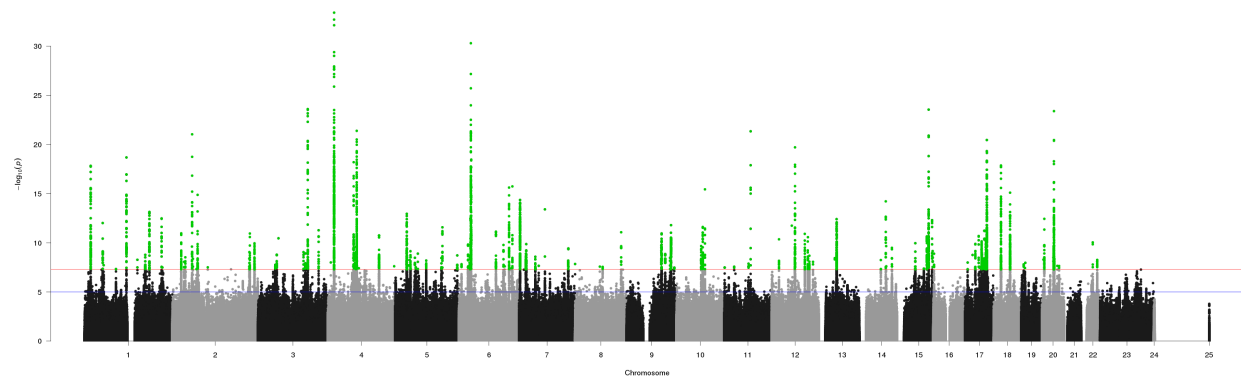| Datasets	Subsets	Total_AFR	Total_other	Grant_total	Lambda
pan_UKBB	AFR	6636	0	6636	1.037
Uganda Genome Project	All from meta-analysis (AFR)	14126	0	14126	0.823*
N'diaye et al.	All from meta-analysis (AFR)	20427	0	20427	1.065
PAGE	All ancestries	17299	32540	49839	1.183
ALL	ALL	58488	32540	91028	NA

Meta-analysis

We ran a meta-analysis using METAL using one file for each of the above datasets. We set genomic correction to "ON", meaning it is performed for each file (not the final values). We perform the meta-analysis using SCHEME STDERR, meaning betas and SE are used. We set AVERAGEFREQ and MINMAXFREQ to "ON" so that metal can track large allelic frequency differences accross datasets as suggestion of allelic mismatch. We only report results for variants that have a combined weight of at least 45000 individuals, resulting in about 32.5 million autosomal variants.
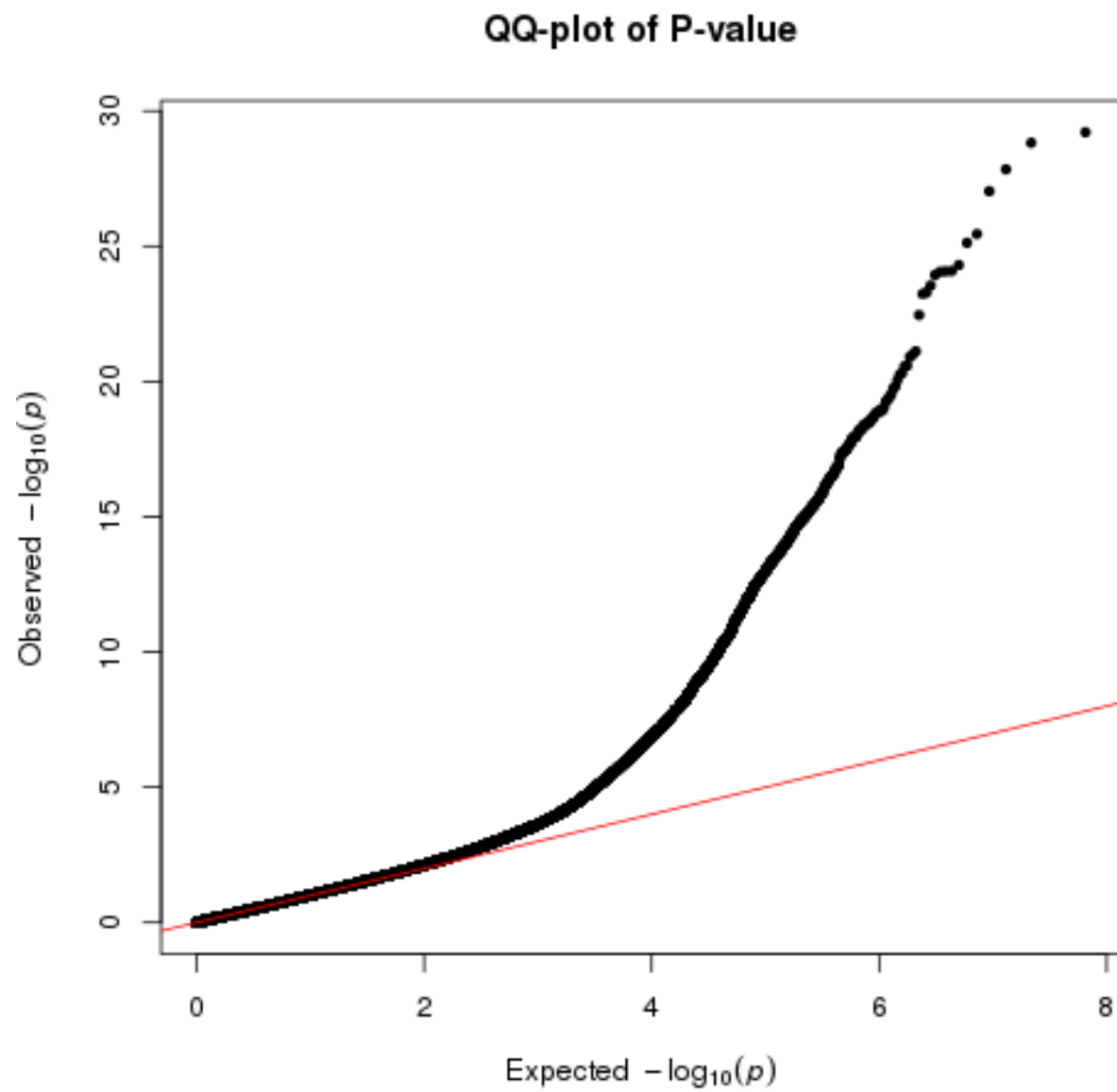
QQ plot from META-analysis (no correction)
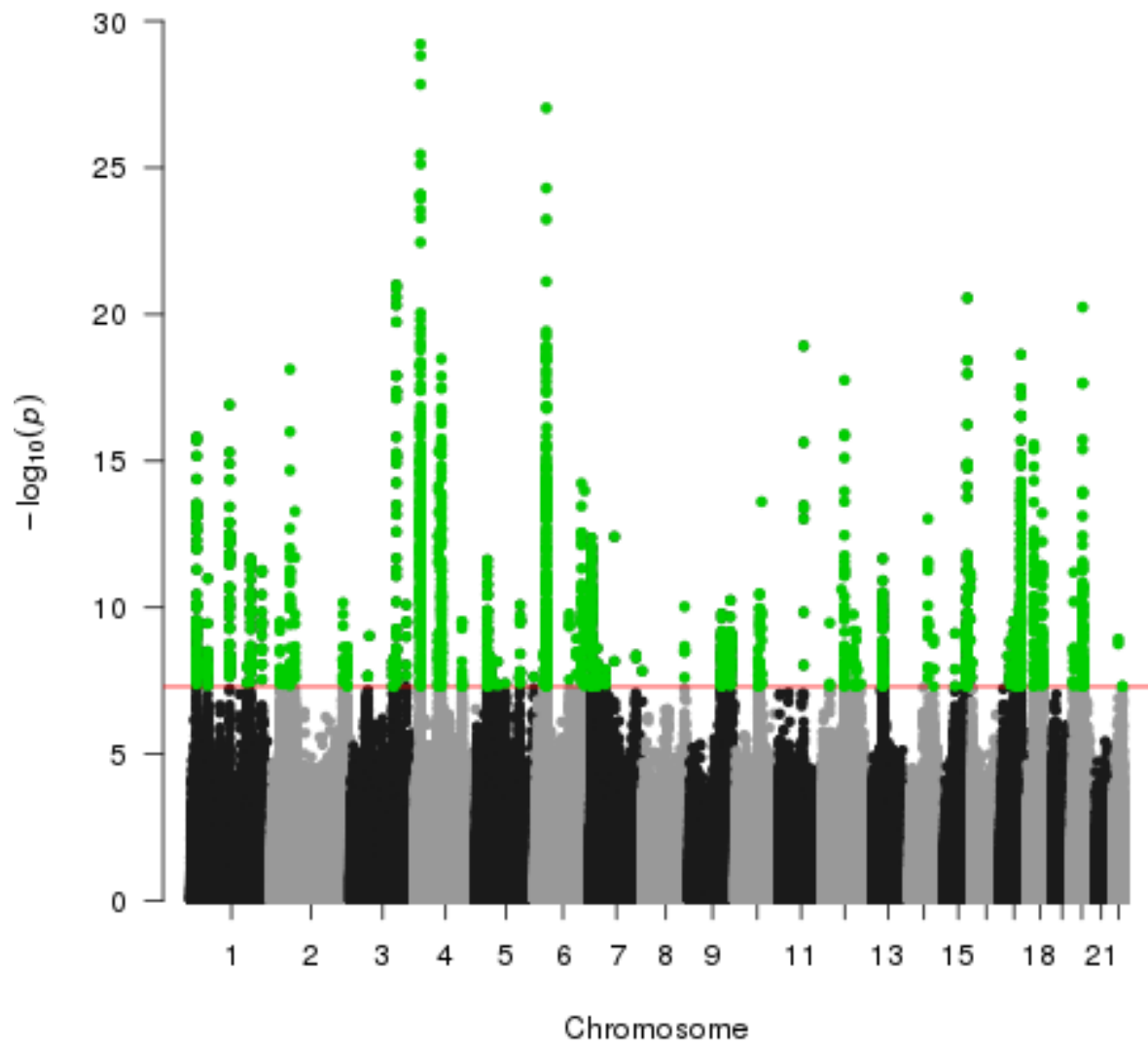

QQ-plot of P-value

Observed $-\log_{10}(p)$

Expected $-\log_{10}(p)$

Manhattan plot of META-analysis (no correction)

QQ plot from META-analysis (GC corrected)

QQ-plot of P-value

Manhattan plot of META-analysis (GC corrected)

PRS for Height

Discovery Cohort	Ancestry in Discovery Cohort	Phenotype	Co-variates	N_gwas	LD reference panel
UKBB	European (British)	Height	Sex+Age+Age2	360388	UKBB (EUR)
UKBB	European (British)	Height	Sex+Age+Age2	360388	UKBB (EUR)
UKBB	European (British)	Height	Sex+Age+Age2	360388	UKBB (EUR)
BBJ	East Asian (Japanese)	Height	Sex+Age+Age2	360388	UKBB (EUR)
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UKBB	European (British)	Height	Sex+Age+Age2+pEUR	360388	UKBB (EUR)
UKBB	European (British)	Height	Sex+Age+Age2+pEUR	360388	UKBB (EUR)
UKBB	European (British)	Height	Sex+Age+Age2+pEUR	360388	UKBB (EUR)
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BBJ	East Asian (Japanese)	Height	Sex+Age+Age2+pEUR	360388	UKBB (EUR)
BBJ	East Asian (Japanese)	Height	Sex+Age+Age2	159095	1000G (EAS)
BBJ	East Asian (Japanese)	Height	Sex+Age+Age2	159095	1000G (EAS)
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BBJ	East Asian (Japanese)	Height	Sex+Age+Age2	159095	1000G (EAS)
BBJ	East Asian (Japanese)	Height	Sex+Age+Age2	159095	1000G (EAS)

```r
dt2<-dt[Method=='LDpred-Inf'][Phenotype=='Height']
#dt2$Phenotype<-factor(dt2$Phenotype, levels=c('Height', 'BMI'))
my_plot2<-ggplot(dt2, aes(x=`Main Test Cohort Ancestry`,y=`Variance Explained (%)`, colour=`Discovery Co
#        facet_wrap(~Phenotype, dir='v') +
        geom_point(size=3) +
        scale_color_manual(values = wes_palette("Darjeeling2")) +
        theme_bw()+
        labs(title="Height")
print(my_plot2)
```

Height