UK Biobank participants included in the primary analyses

```
          Total study size
             503,325
                |
                v
   With genetics data (May 2015 interim release)
        Identified as 'white British'
             120,286
                |
                v
          Aged 55-70
            76,339
          /        \
    (A)  /          \  (B)
```

A With father's age at death
(premature deaths <46 excluded)
63,775

B With mother's age at death
(premature deaths <57 excluded)
52,776

C With age at death of both parents
45,627

Top 1% of range
≥95 years (n=558)

Top 1% of range
≥98 years (n=367)

Number of participants with either mother
or father in top 1% range
907
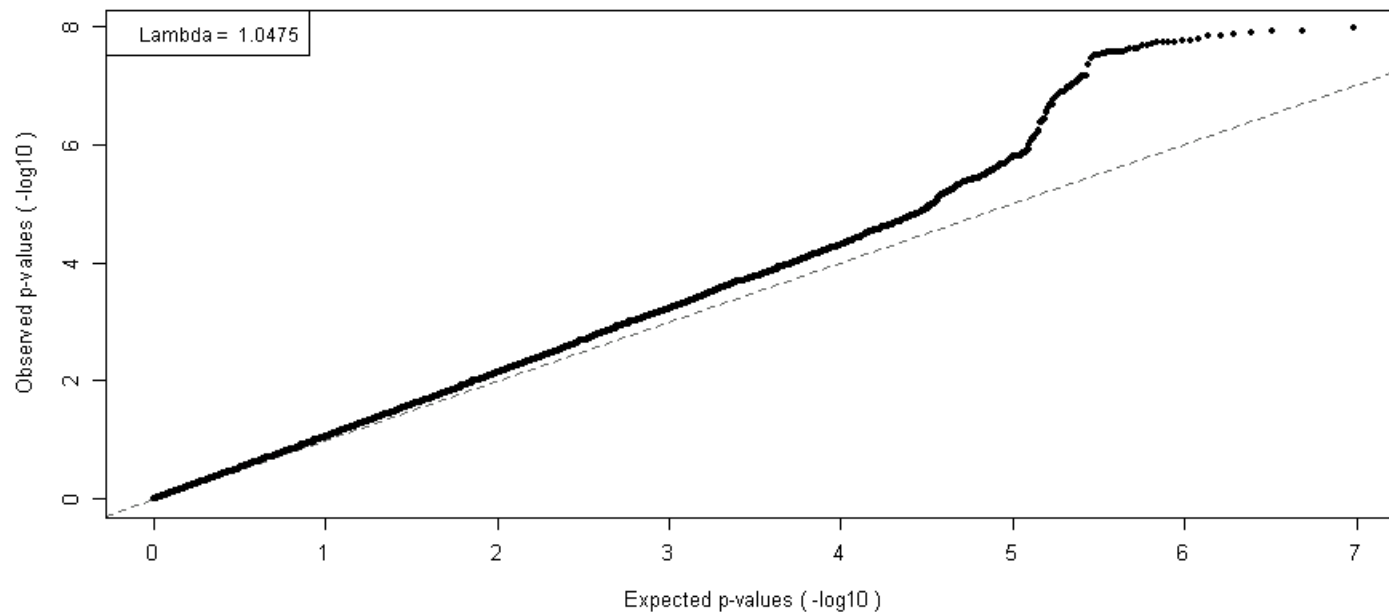(40,934 controls: excluded if "discordant" (one long, one short) or still alive)

D With alive parents reaching the cut-off
1,339 (40,934 controls)

Highlighted here with A-D
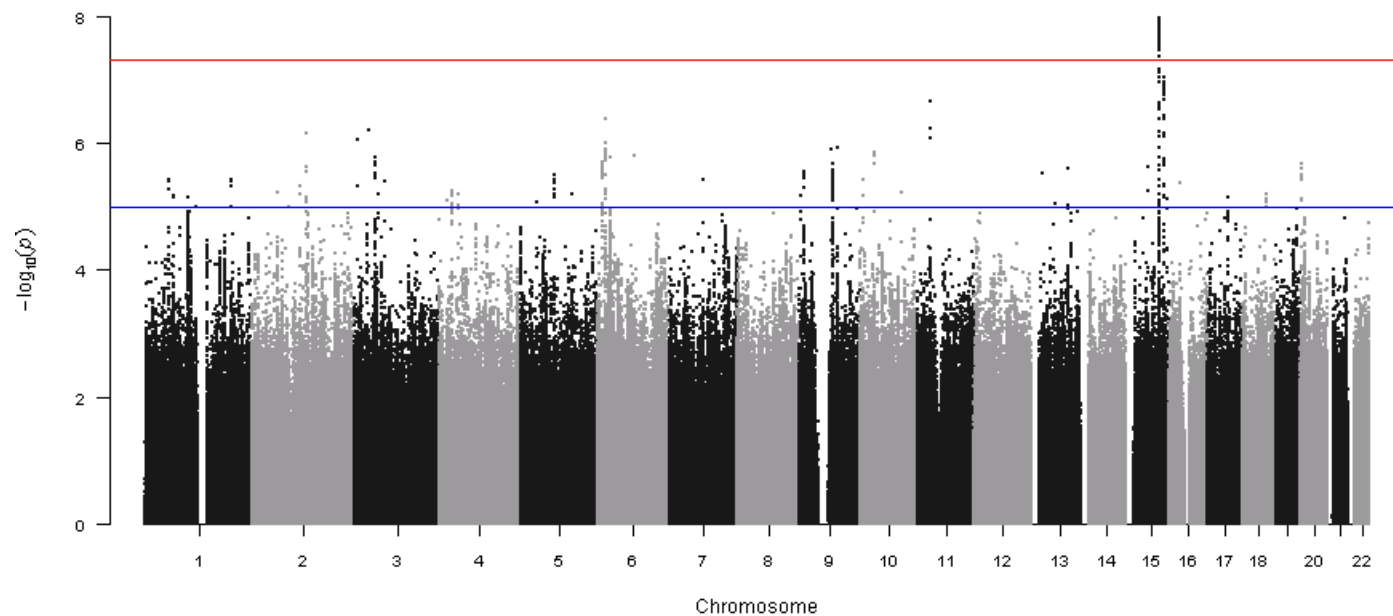
A) Father's age at death,
B) Mother's age at death,
C) Combined parental age at death (z-scored),
D) Binary phenotype: at least one parent attained the top 1% cut-off, derived from the mother's/father's ages at death

75,244 participants included in at least one analysis

QQ plot for GWAS of father's age at death in 63,775 UK Biobank participants (9million imputed variants)
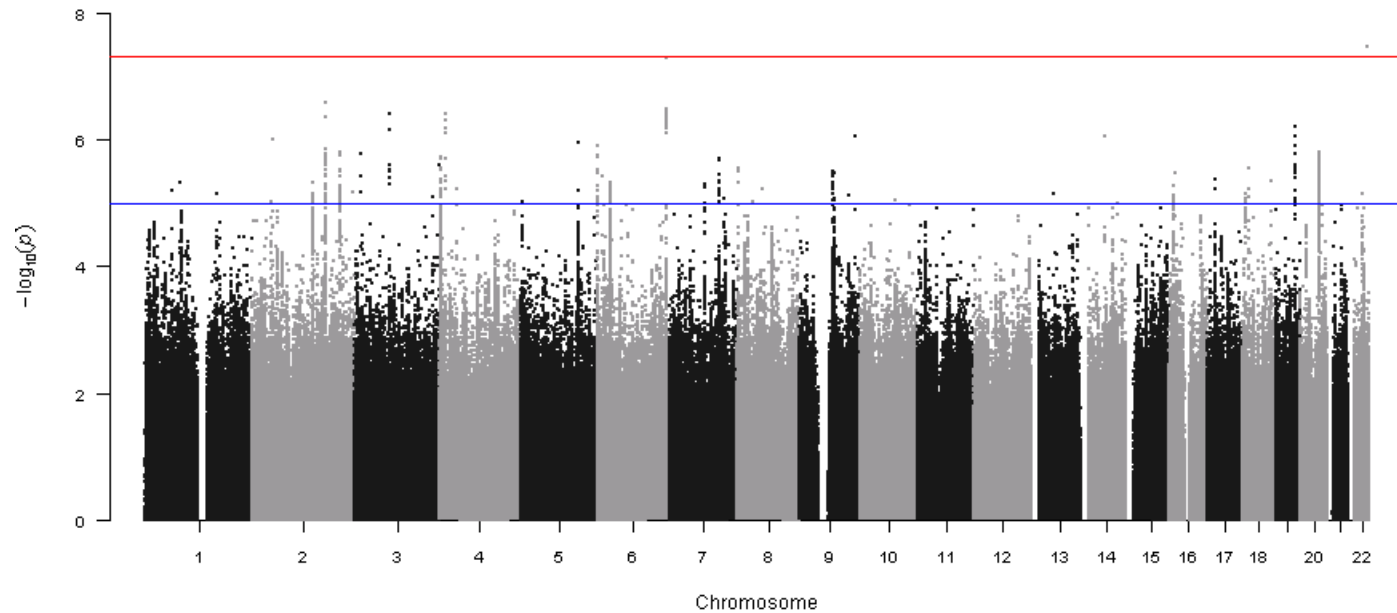

Lambda = 1.0475

Observed p-values (-log10)

Expected p-values (-log10)

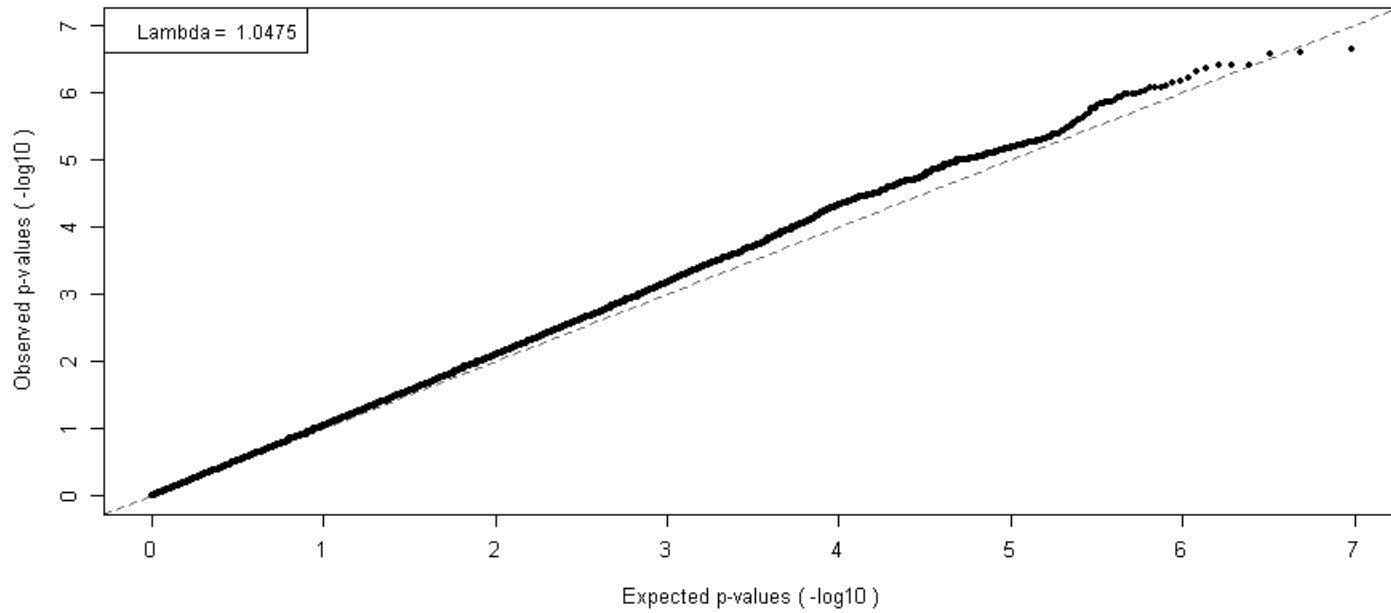## Manhattan plot of above data

−log₁₀(p)

Chromosome

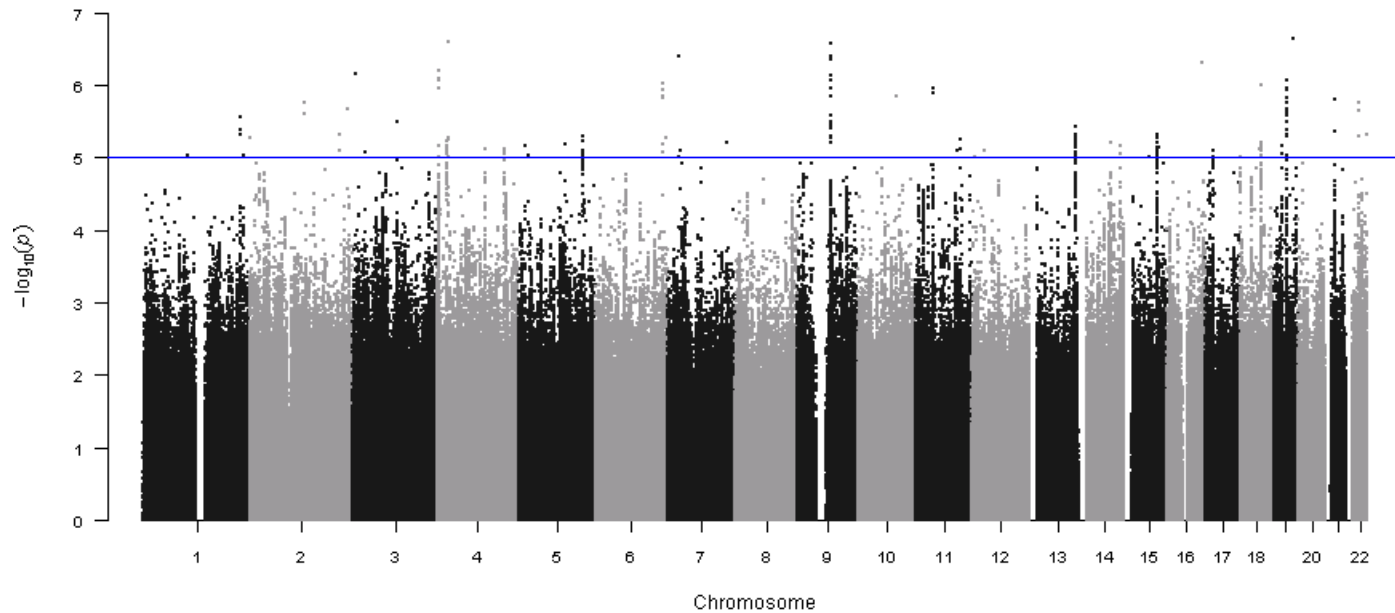# QQ plot for GWAS of mother's age at death in 52,776 UK Biobank participants (9million imputed variants)
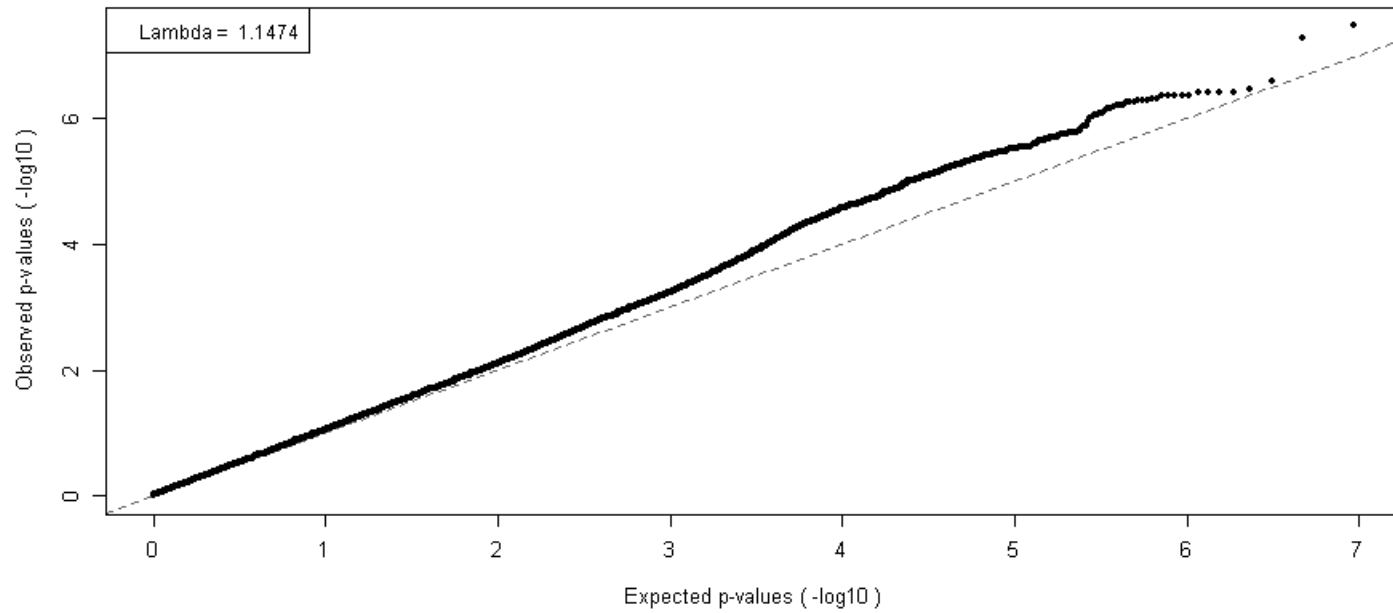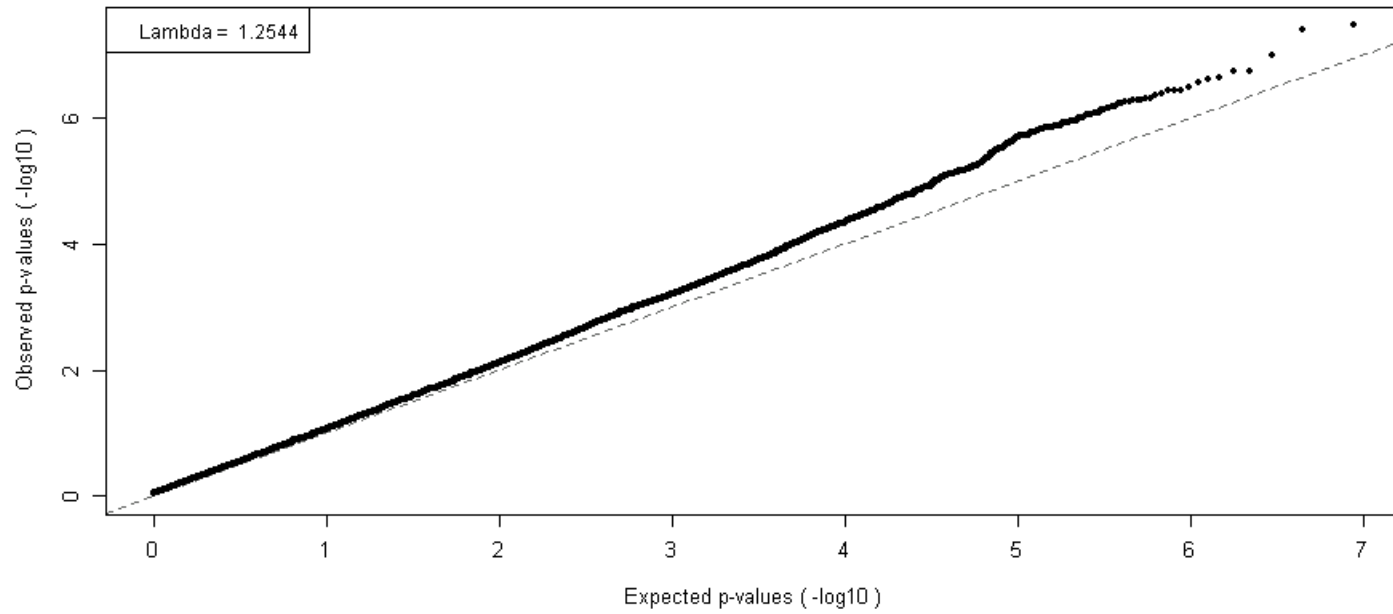

Manhattan plot of above data

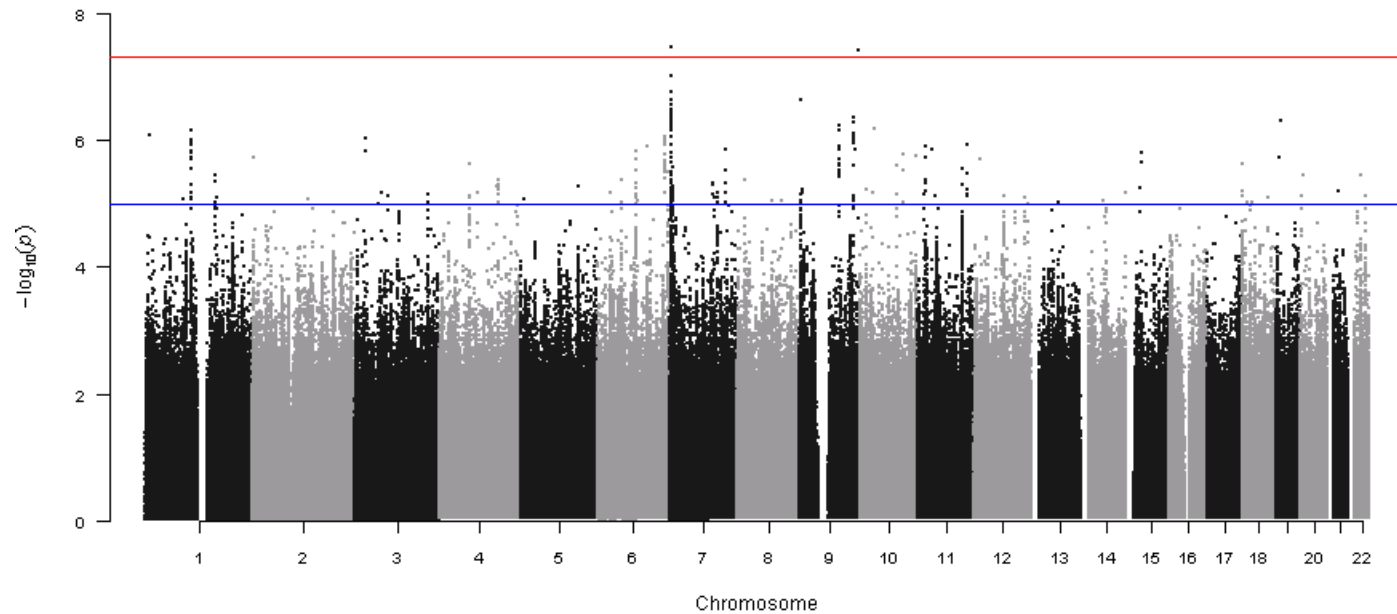QQ plot for GWAS of combined parent's age at death in 45,627 UK Biobank participants (9million imputed variants)

Manhattan plot of above data

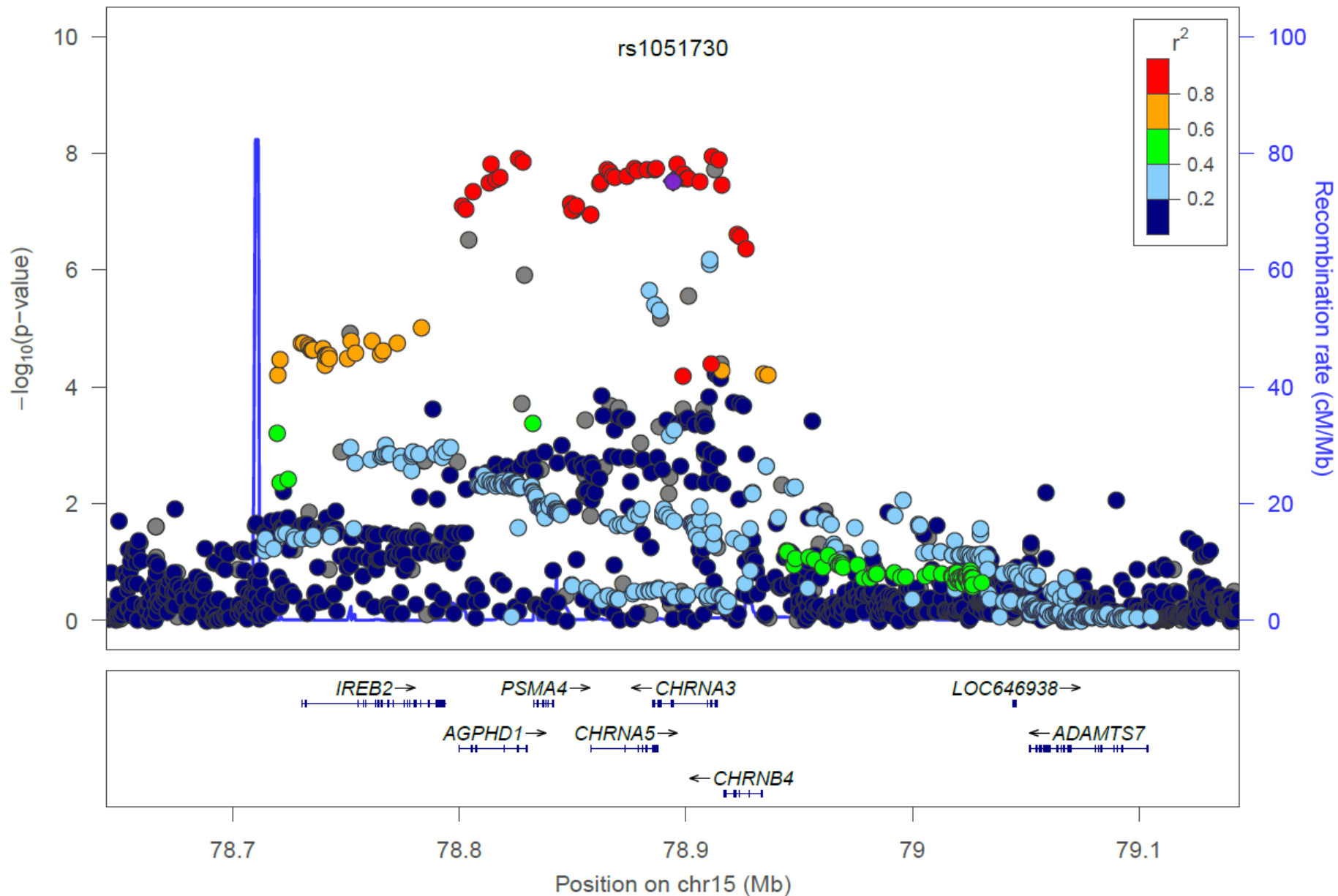QQ plot for GWAS of "top 1% of age at death range" in 42,273 UK Biobank participants (9million imputed variants)

Manhattan plot of above data

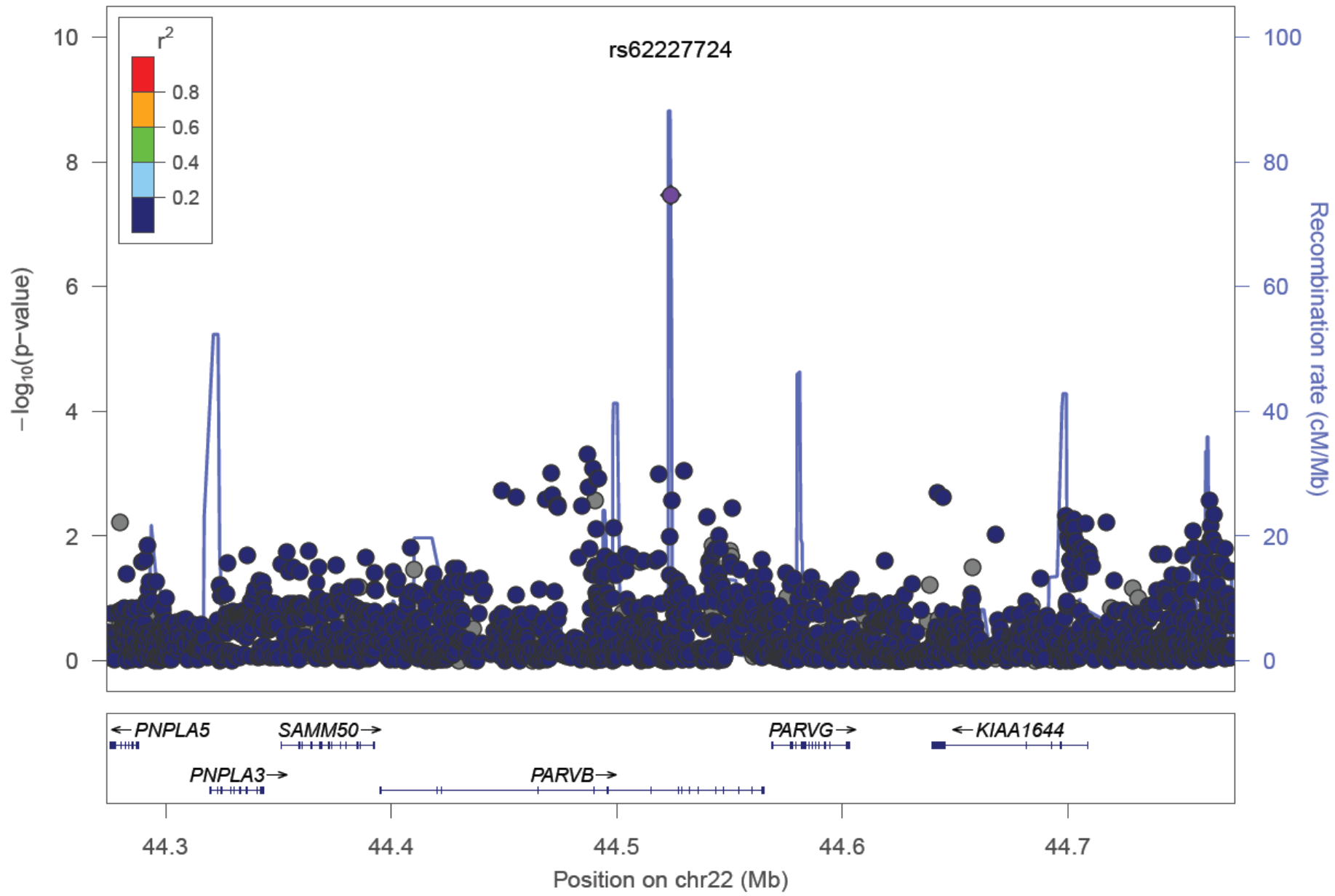Locus Zoom plot displaying variants +/- 250kbp around variant rs1051830
P-values are the association with Father's age at death

Locus Zoom plot displaying variants +/- 250kbp around variant rs62227724
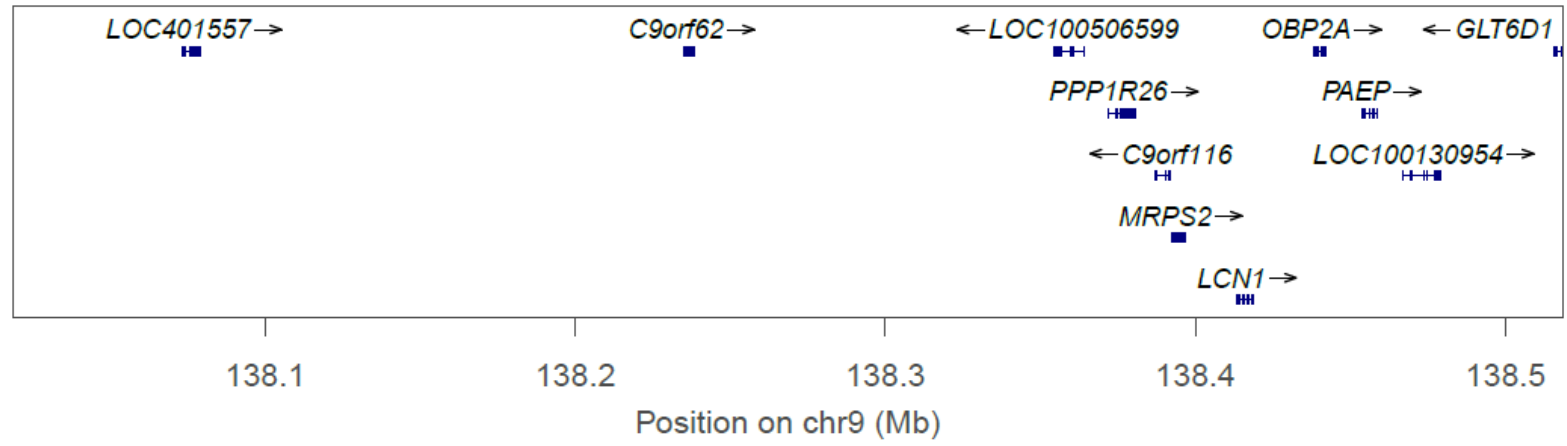P-values are the association with Mother's age at death

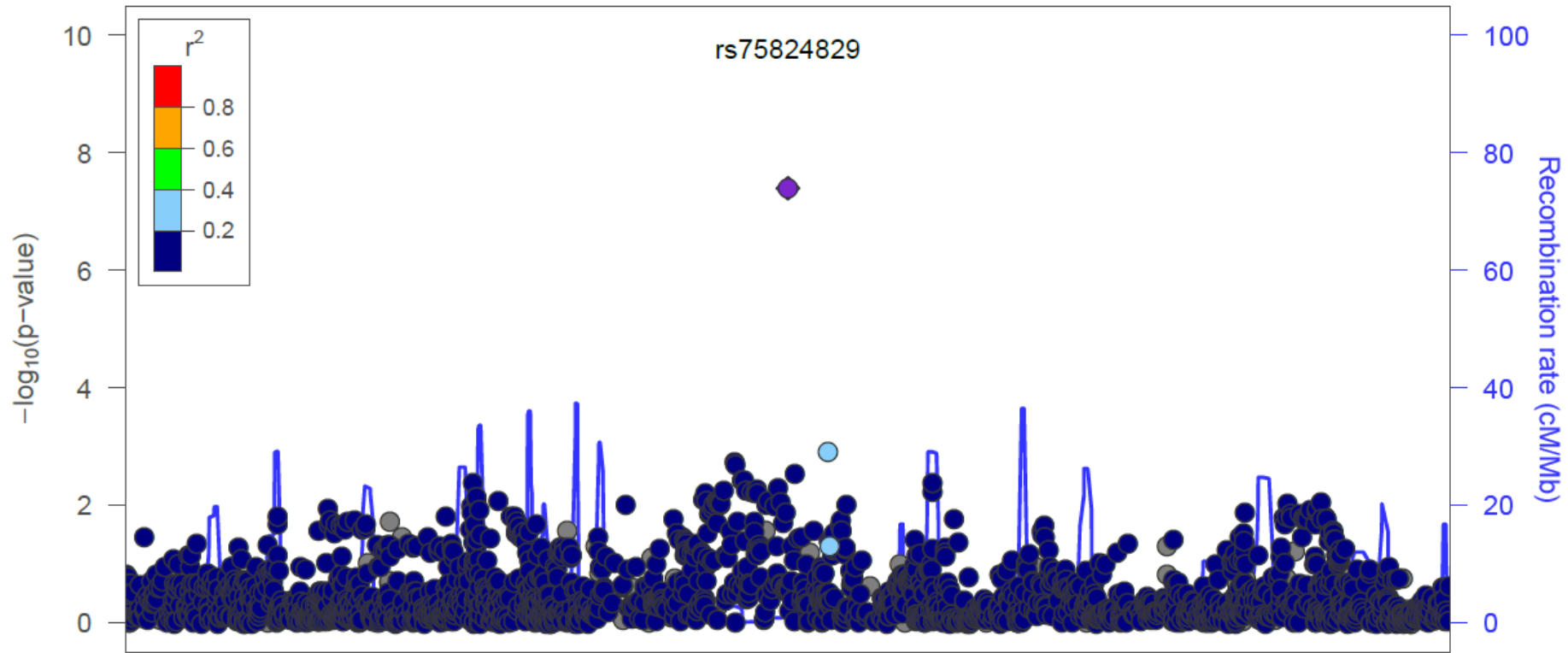# Locus Zoom plot displaying variants +/- 250kbp around variant rs75824829
P-values are the association with "top 1% of age at death range"

Locus Zoom plot displaying variants +/- 250kbp around variant rs528161076
P-values are the association with "top 1% of age at death range"