Supplemental Figure Legends

SFigure 1. Quantile-Quantile Plot. Distribution of observed versus predicted p values under the null hypothesis of no association, from Stage 1 meta-analysis of genome-wide association studies of age at menarche in 18,089 African-American women.

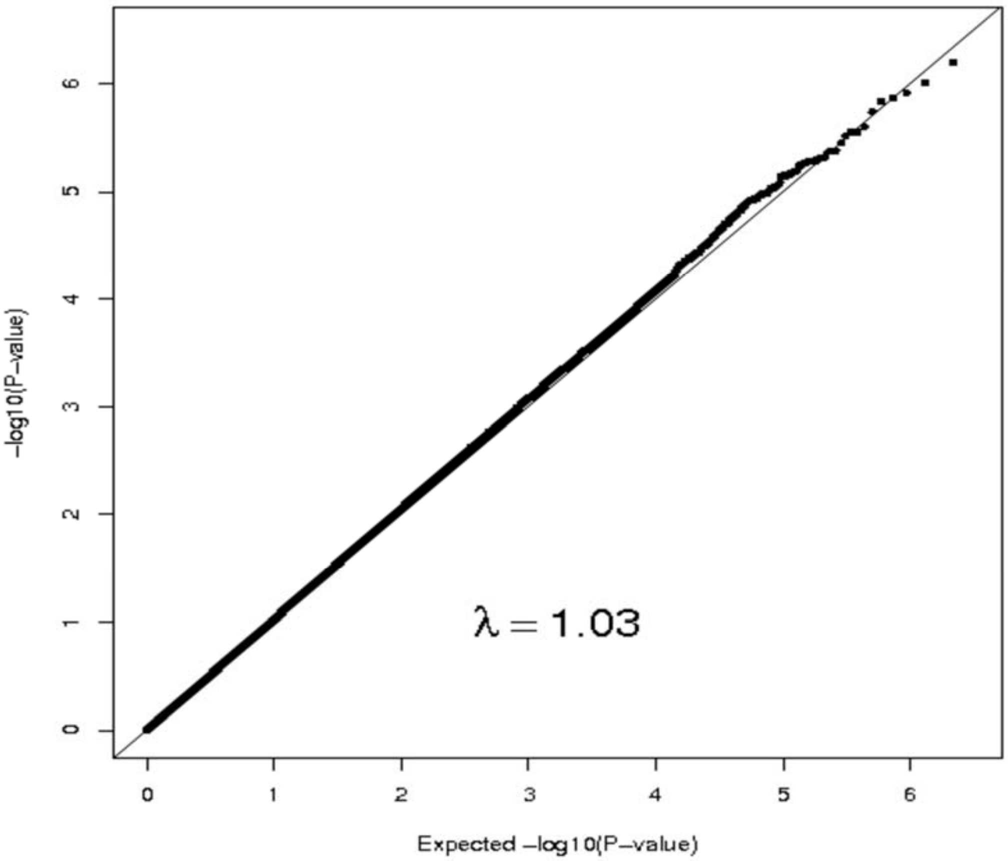
SFigure 2. Manhattan Plot. –log10 p values from meta-analysis of genome-wide association studies of age at menarche in 18,089 African-American women, by chromosome. Each point indicates the p value for the additive association of each of ~2.5 million imputed SNPs in the analysis.

SFigure 3. Regional association of meta-analysis results. Regional association plots of the 20 top SNPs from the Stage 1 meta-analysis of age at menarche genome-wide association studies are presented showing linkage disequilibrium with the top SNP (named and indicated by purple diamond) using the 1KGP AFR reference panel.

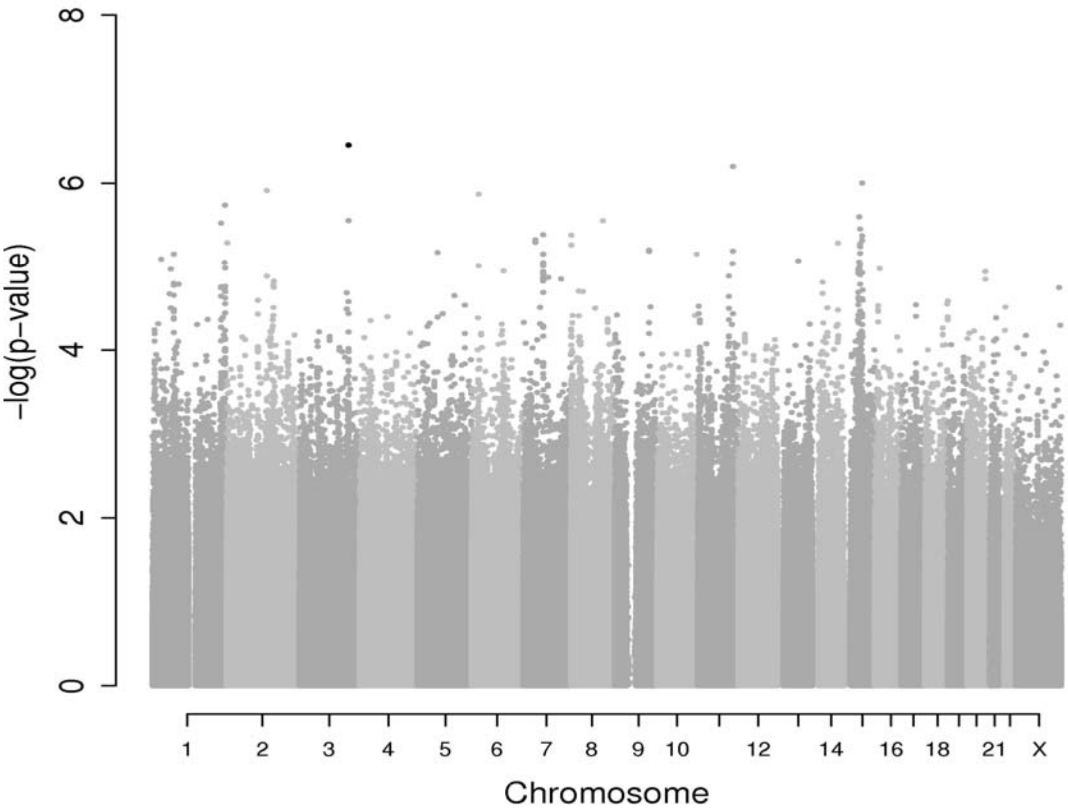
SFigure 4. Regional association in African American women of 42 previously reported menarche loci. Regional association plots of 42 previously reported menarche loci with age at menarche in African American (AA) women showing linkage disequilibrium with the index SNP (named and indicated by purple diamond) using the 1KGP EUR reference panel.

SFigure 5. Statistical Power of the Meta-Analysis (Stage 1). Power to detect an additive association between a SNP (varying in MAF from 0.05 to 0.50) and age at menarche (continuous), over a range of expected effect sizes (in weeks), in a sample of 18,089 unrelated individuals, assuming two-sided $p = 5 \times 10^{-8}$.

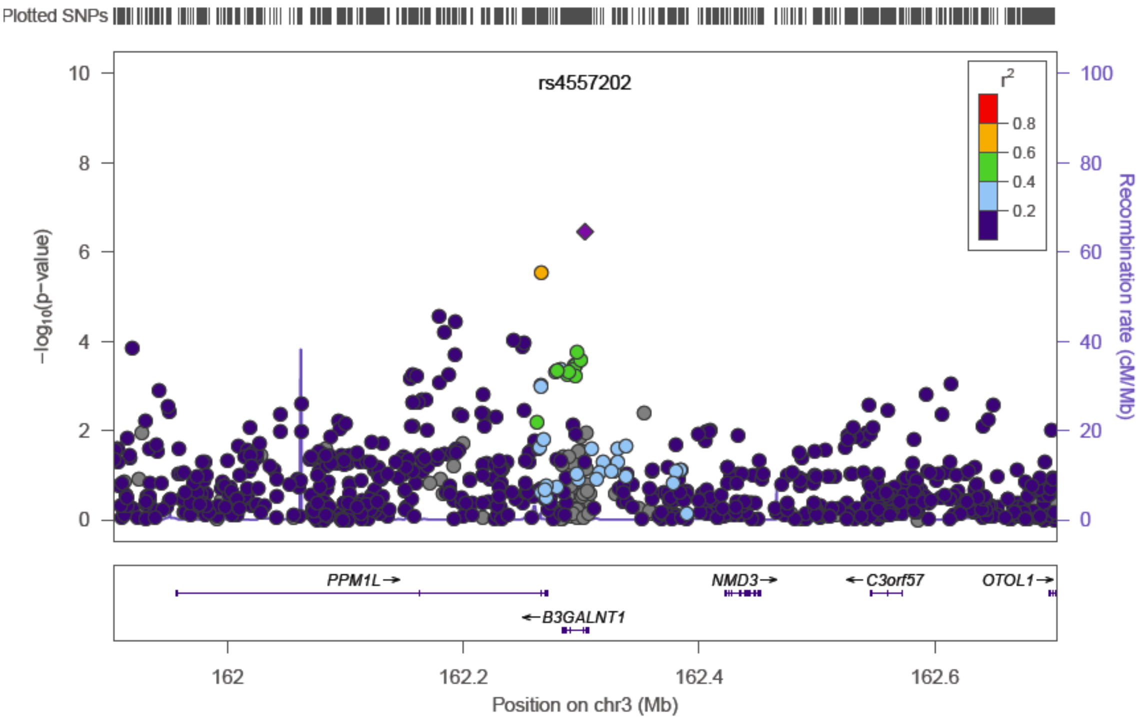
SFigure 6. Statistical Power of the Replication Study (Stage 2). Power to detect an additive association between a SNP (varying in MAF from 0.05 to 0.50) and age at menarche (continuous), over a range of expected effect sizes (in weeks), in a sample of 2,850 unrelated individuals, assuming two-sided $p = 0.05/20$.



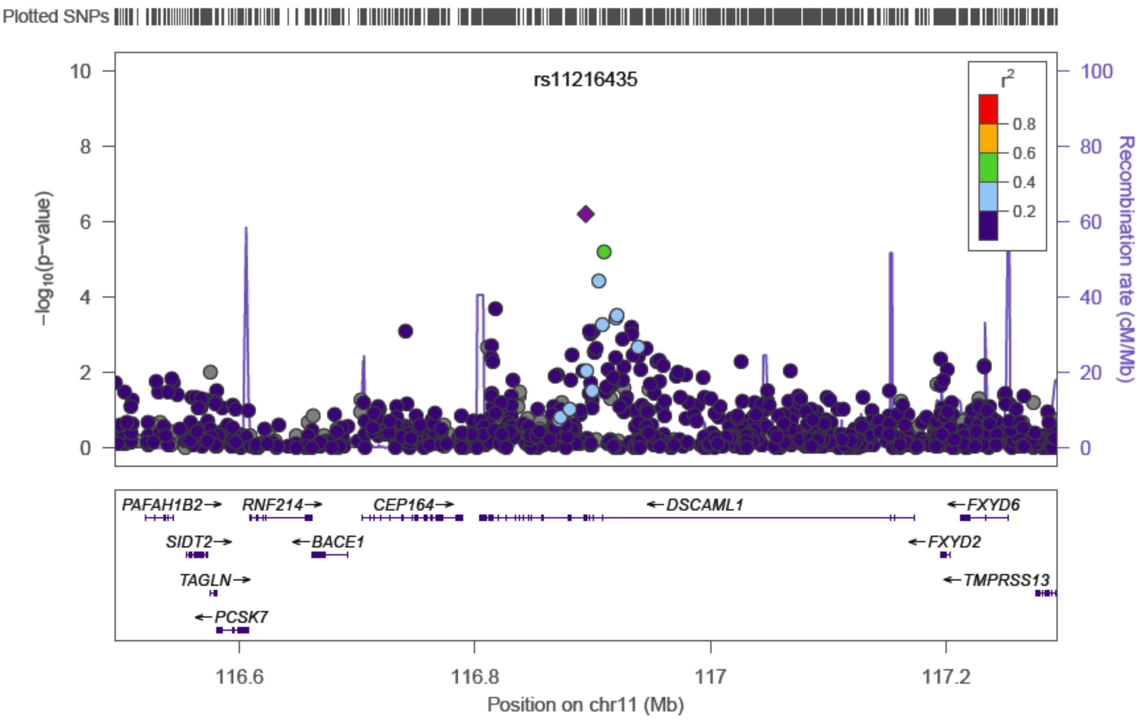
λ = 1.03
-log10(P-value)
Expected -log10(P-value)
0
1
2
3
4
5
6
0
1
2
3
4
5
6


8
6
4
2
0
−log(p−value)
1
2
3
4
5
6
7
8
9
10
12
14
16
18
21
X
Chromosome

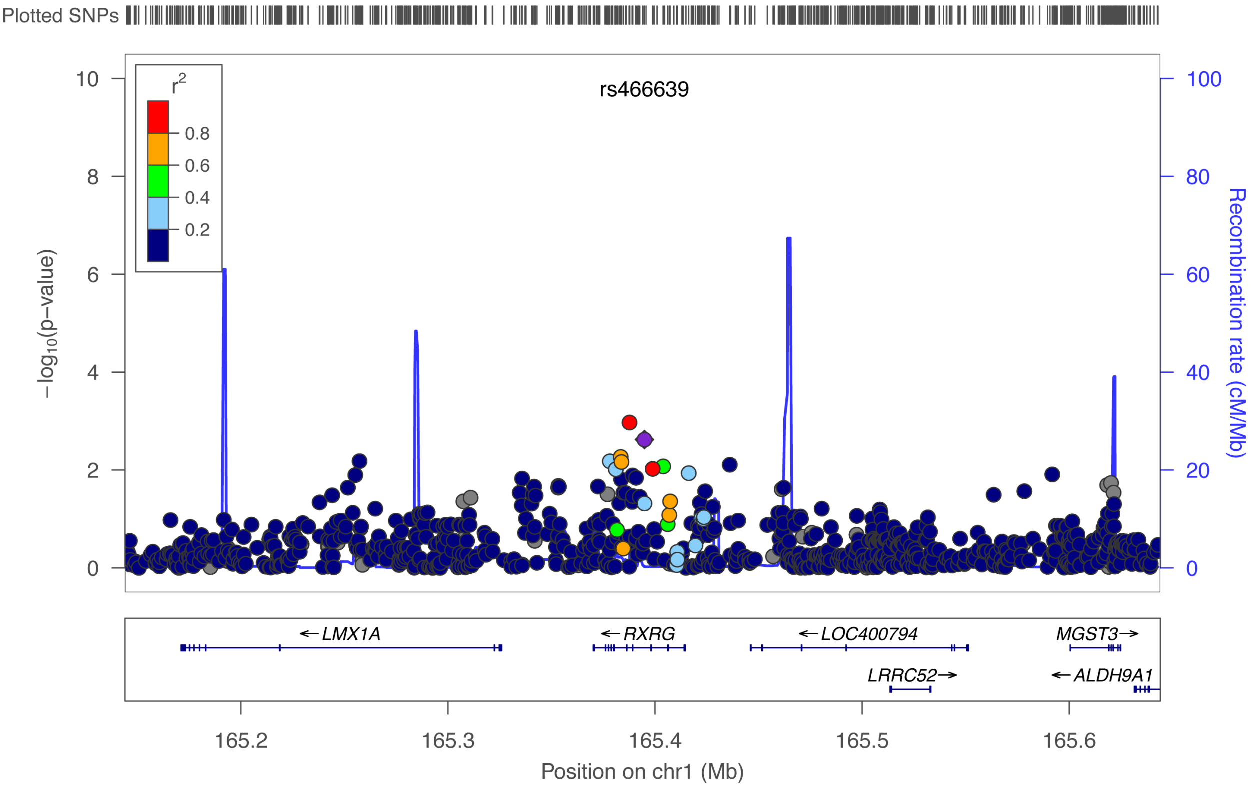
B3GALNT1



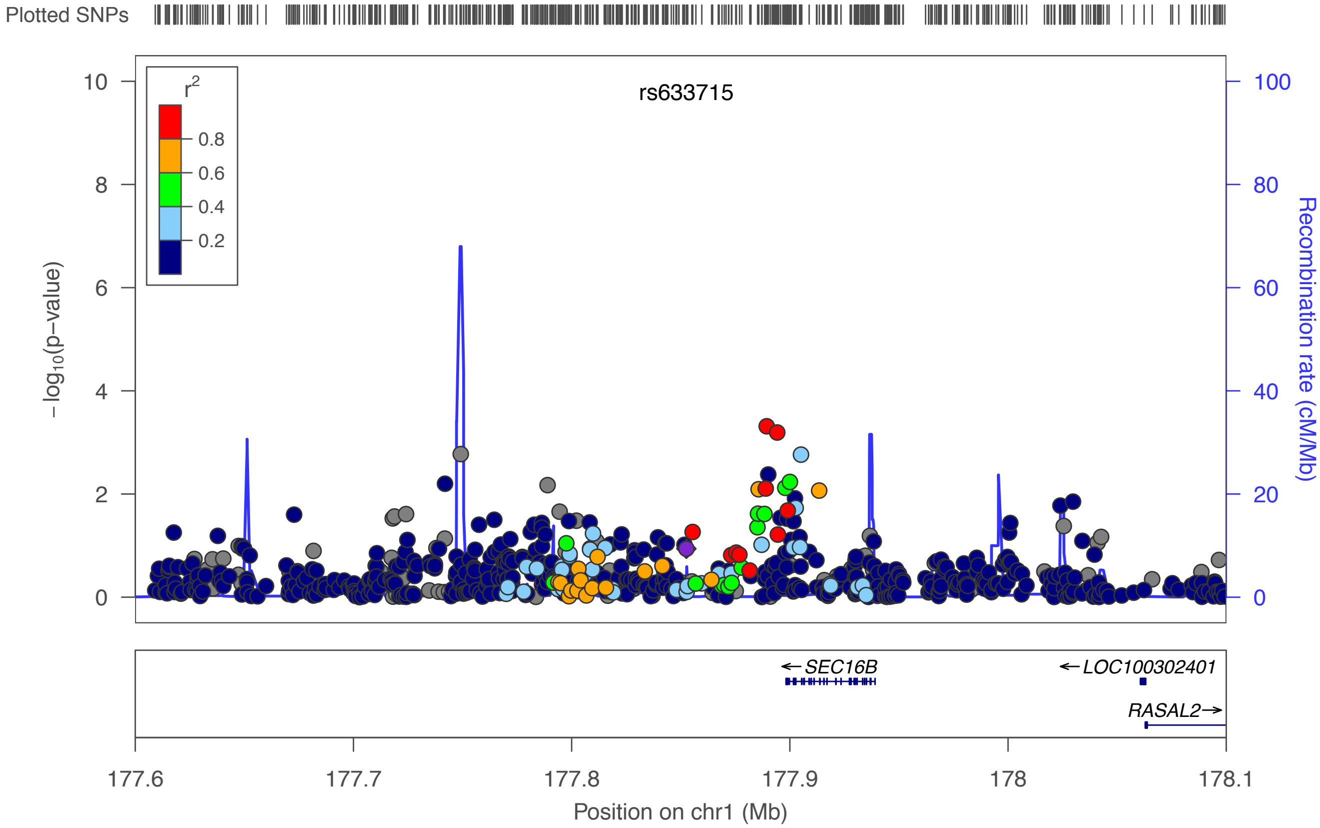
DSCAML1

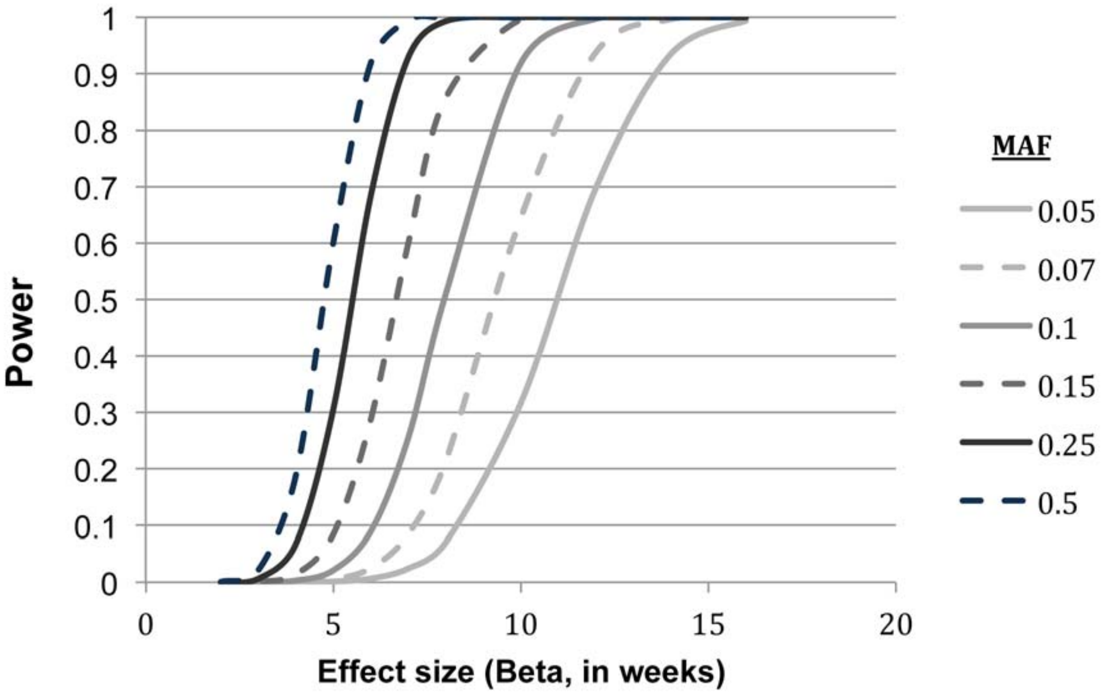


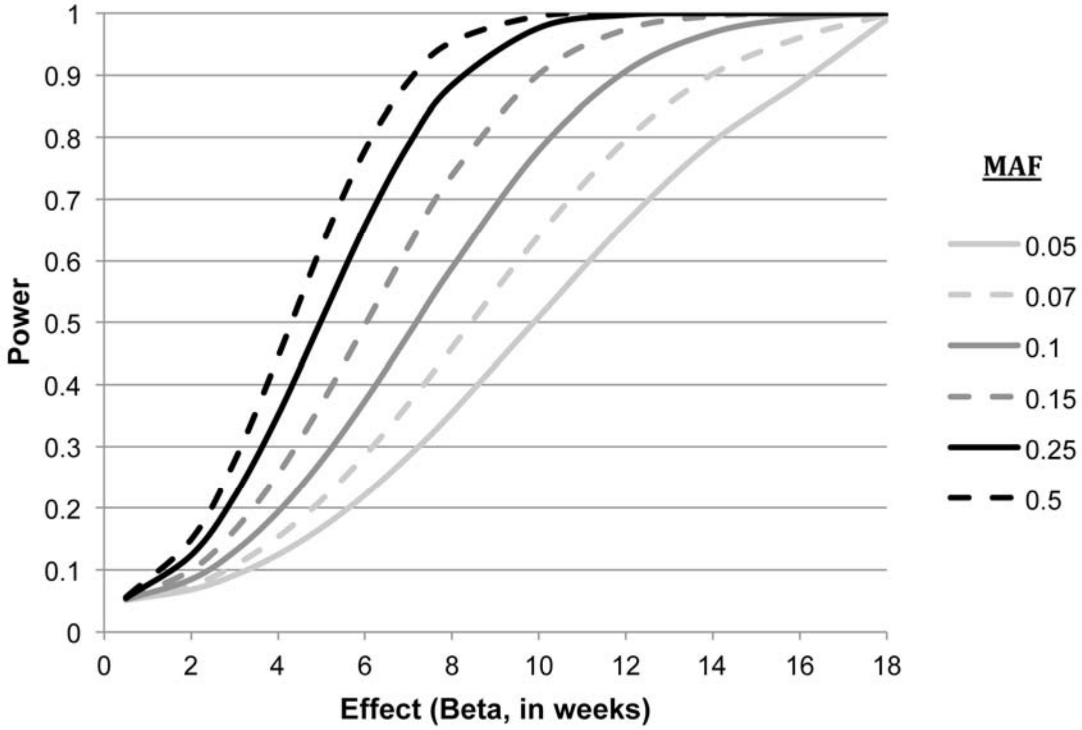
RXRG


Plotted SNPs
rs466639
r2
0.8
0.6
0.4
0.2
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
←LMX1A
←RXRG
←LOC400794
MGST3→
LRRC52→
←ALDH9A1
165.2
165.3
165.4
165.5
165.6
Position on chr1 (Mb)

SEC16B


Plotted SNPs
rs633715
r2
0.8
0.6
0.4
0.2
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
←SEC16B
←LOC100302401
RASAL2→
177.6
177.7
177.8
177.9
178
178.1
Position on chr1 (Mb)


Power
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
5
10
15
20
Effect size (Beta, in weeks)
MAF
0.05
0.07
0.1
0.15
0.25
0.5


Power
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
2
4
6
8
10
12
14
16
18
Effect (Beta, in weeks)
MAF
0.05
0.07
0.1
0.15
0.25
0.5