Genetic diversity and natural selection footprints of the glycine amidinotransferase gene in various human populations

Running Title: Diversity and Natural selection on *GATM*

Keywords: *GATM, AGAT, Genetic diversity, Natural selection*

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Supplementary figures legends:

Figure S1: Estimation of pairwise F_{ST} values for the *GATM* gene among different human populations.

Figure S2: Distribution of F_{ST} differentiation ratios for the *GATM* gene and 68 statin response-associated genes. Black dots represent genes that contain no SNPs.

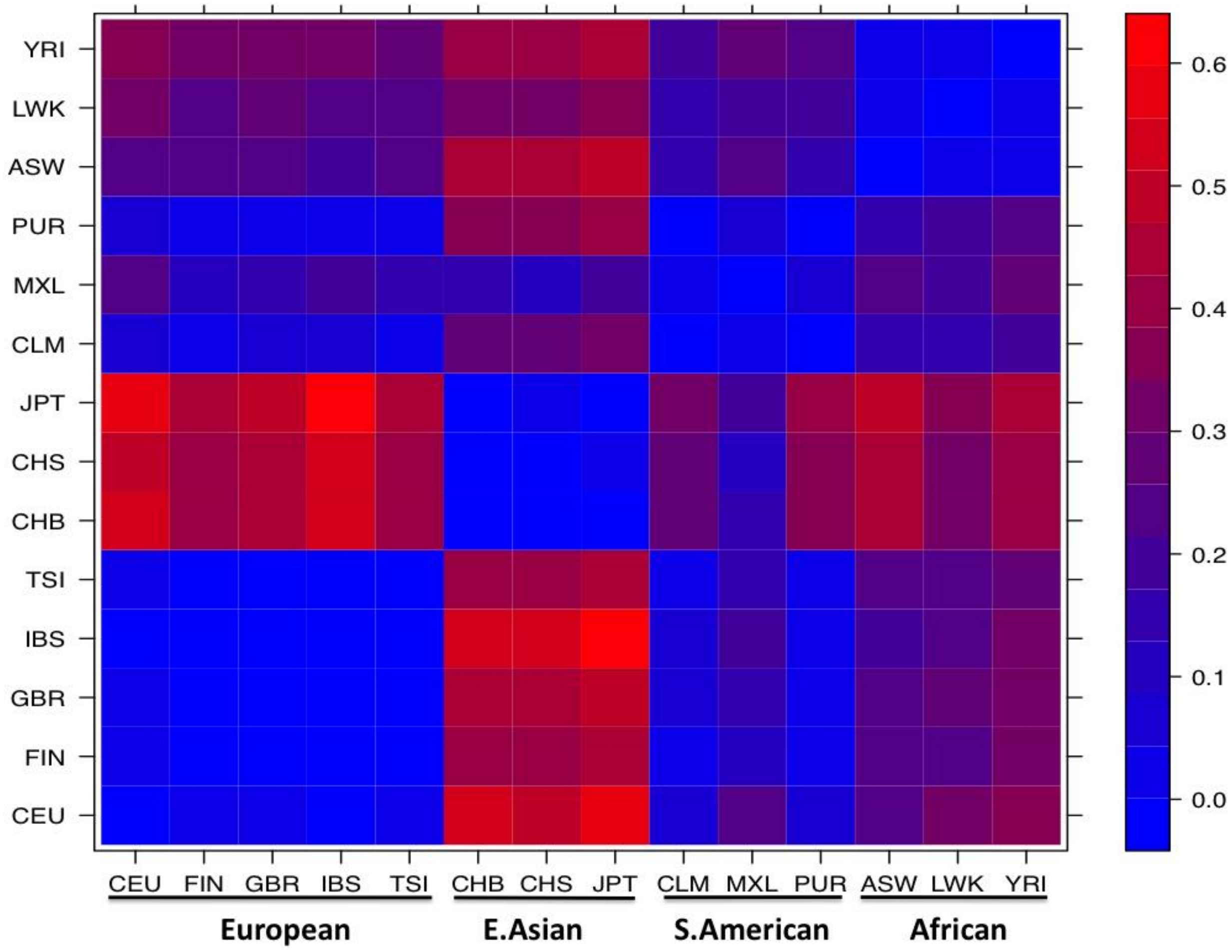
Figure S3: (A) Allele frequency plot of *GATM* eQTL experimentally proved to be associated with statin associated myopathy. (B) Population wide global *Fst* calculation for three eQTLs experimentally proved in association with statin response. Two of these eQTLs (i.e. rs1719247 and rs1346268) are showing allele frequency difference > 1 % whole genome *Fst* differentiation.

Figure S4: Estimation of *lnRsb*, ΔDAF, and F_{ST} around the *GATM* gene. The red and green lines indicate the respective top 1% and top 5% thresholds of these abovementioned parameters at the whole-genome level.

Figure S5: Recombination hotspots observed within the vicinity of the *GATM* gene in the CEU population. The *GATM* gene is indicated in red. Data on the CHB and YRI populations are also shown for comparison.

Figure S6: Linkage disequilibrium (LD) plot across the *GATM* gene in the CEU, CHB, and YRI populations.

Figure S1



YRI
LWK
ASW
PUR
MXL
CLM
JPT
CHS
CHB
TSI
IBS
GBR
FIN
CEU
CEU
FIN
GBR
IBS
TSI
CHB
CHS
JPT
CLM
MXL
PUR
ASW
LWK
YRI
European
E.Asian
S.American
African
0.6
0.5
0.4
0.3
0.2
0.1
0.0

Figure S2

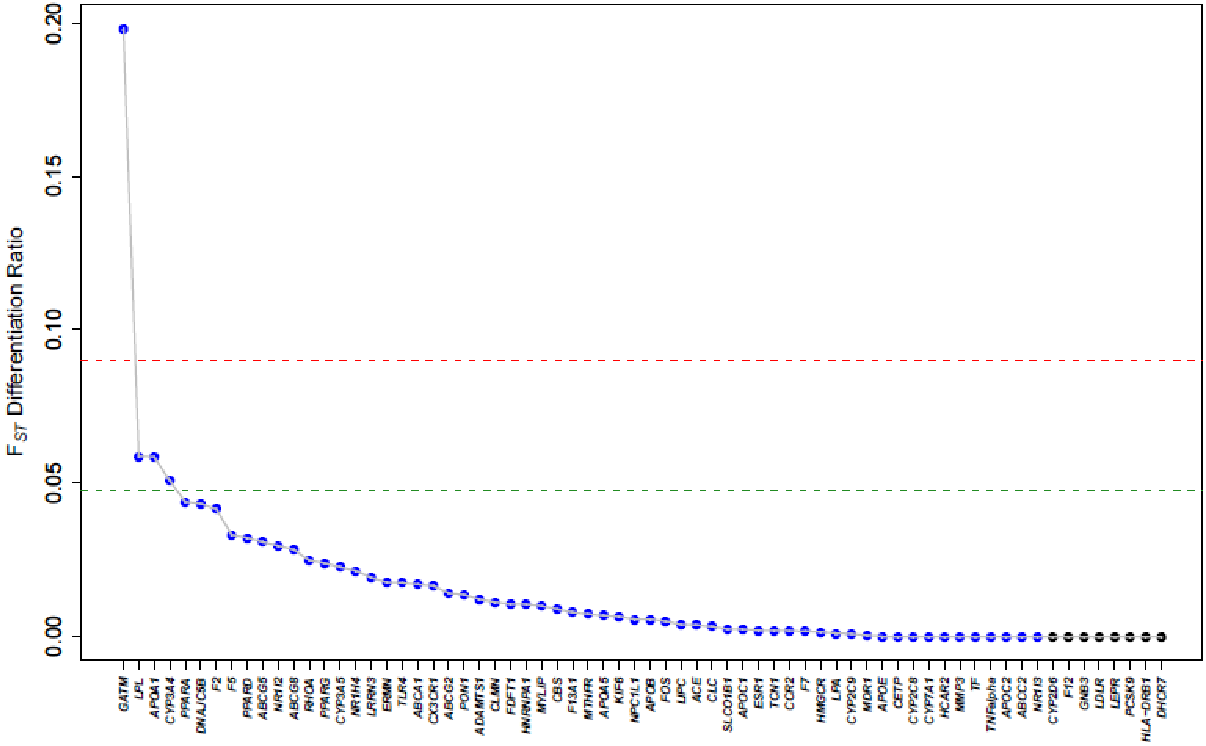
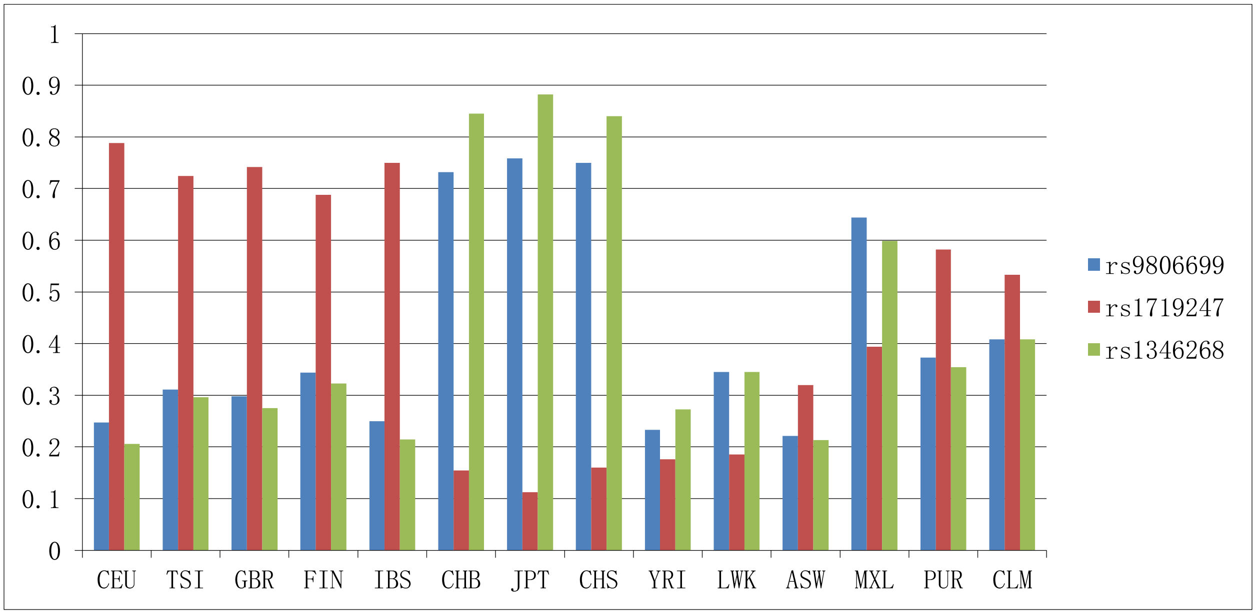

F_{ST} Differentiation Ratio
0.00
0.05
0.10
0.15
0.20
GATM
LPL
APOA1
CYP3A4
PPARA
DNAJC5B
F2
F5
PPARD
ABCG5
NR1I2
ABCG8
RHOA
PPARG
CYP3A5
NR1H4
LRRN3
ERMN
TLR4
ABCA1
CX3CR1
ABCG2
PON1
ADAMTS1
CLMN
FDFT1
HNRNPA1
MYLIP
CBS
F13A1
MTHFR
APOA5
KIF6
NPC1L1
APOB
FOS
LIPC
ACE
CLC
SLCO1B1
APOC1
ESR1
TCN1
CCR2
F7
HMGCR
LPA
CYP2C9
MDR1
APOE
CETP
CYP2C8
CYP7A1
HCAR2
MMP3
TF
TNFalpha
APOC2
ABCC2
NR1I3
CYP2D6
F12
GNB3
LDLR
LEPR
PCSK9
HLA−DRB1
DHCR7

Figure S3

A.


1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
CEU
TSI
GBR
FIN
IBS
CHB
JPT
CHS
YRI
LWK
ASW
MXL
PUR
CLM
rs9806699
rs1719247
rs1346268

B.

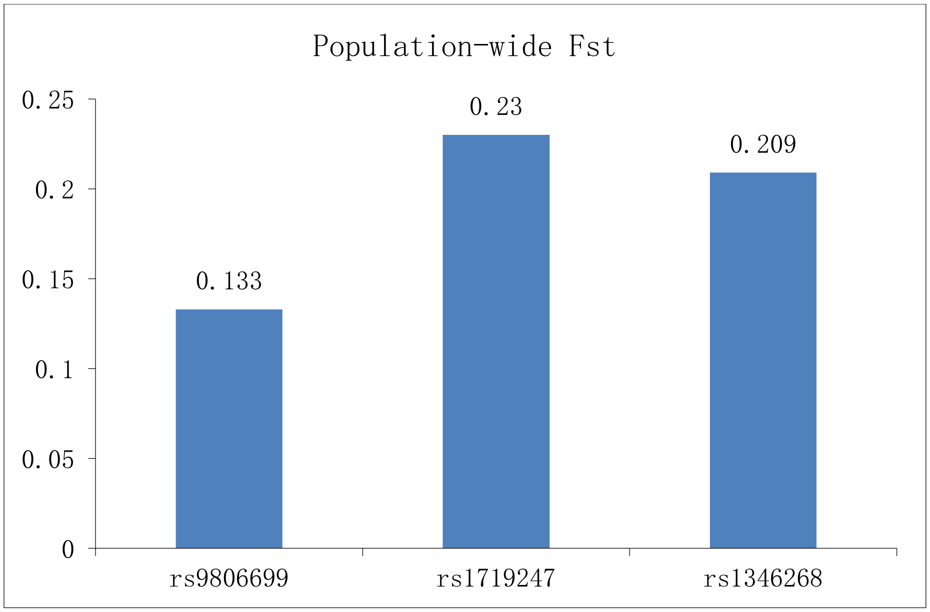
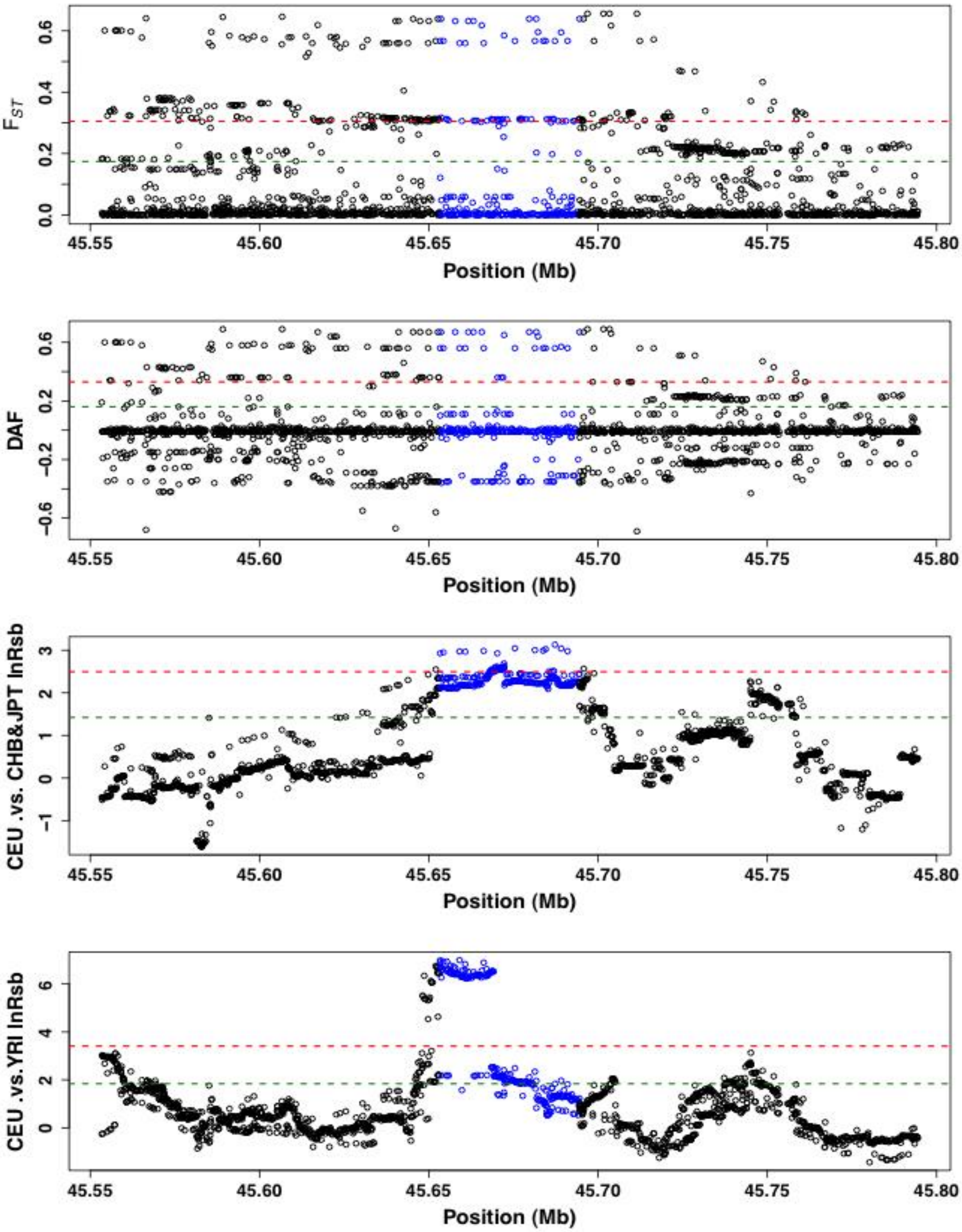

Population-wide Fst
0.25
0.2
0.15
0.1
0.05
0
0.133
0.23
0.209
rs9806699
rs1719247
rs1346268

Figure S4



F$_{ST}$
0.0
0.2
0.4
0.6
45.55
45.60
45.65
45.70
45.75
45.80
Position (Mb)
DAF
−0.6
−0.2
0.2
0.6
45.55
45.60
45.65
45.70
45.75
45.80
Position (Mb)
CEU .vs. CHB&JPT lnRsb
−1
0
1
2
3
45.55
45.60
45.65
45.70
45.75
45.80
Position (Mb)
CEU .vs.YRI lnRsb
0
2
4
6
45.55
45.60
45.65
45.70
45.75
45.80
Position (Mb)

Figure S5

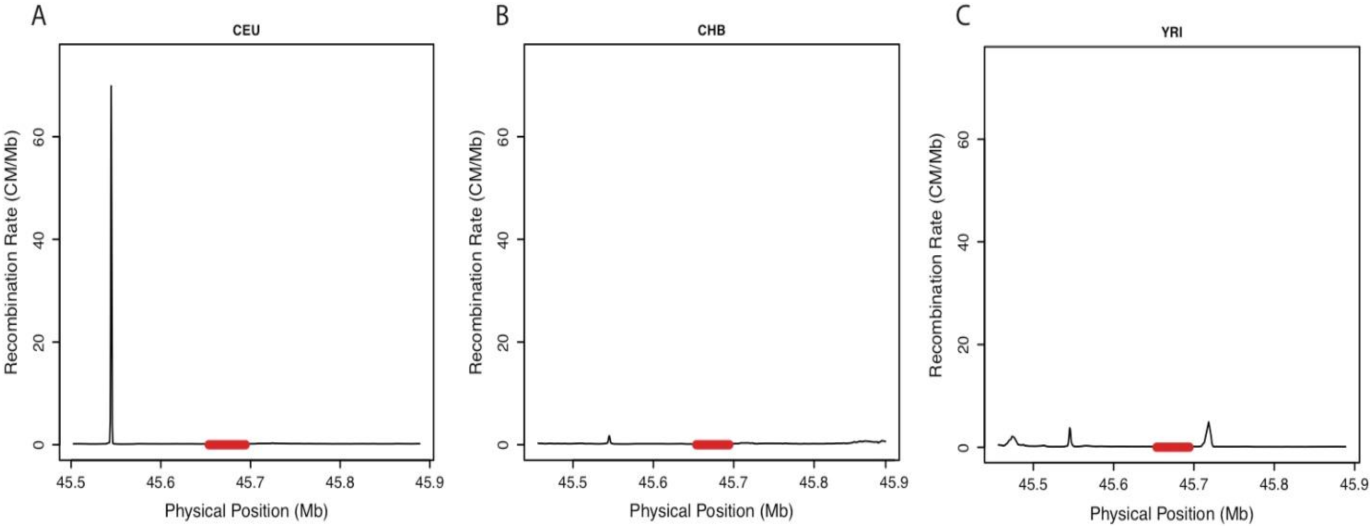

A
CEU
B
CHB
C
YRI
Recombination Rate (CM/Mb)
0
20
40
60
45.5
45.6
45.7
45.8
45.9
Physical Position (Mb)

Figure S6