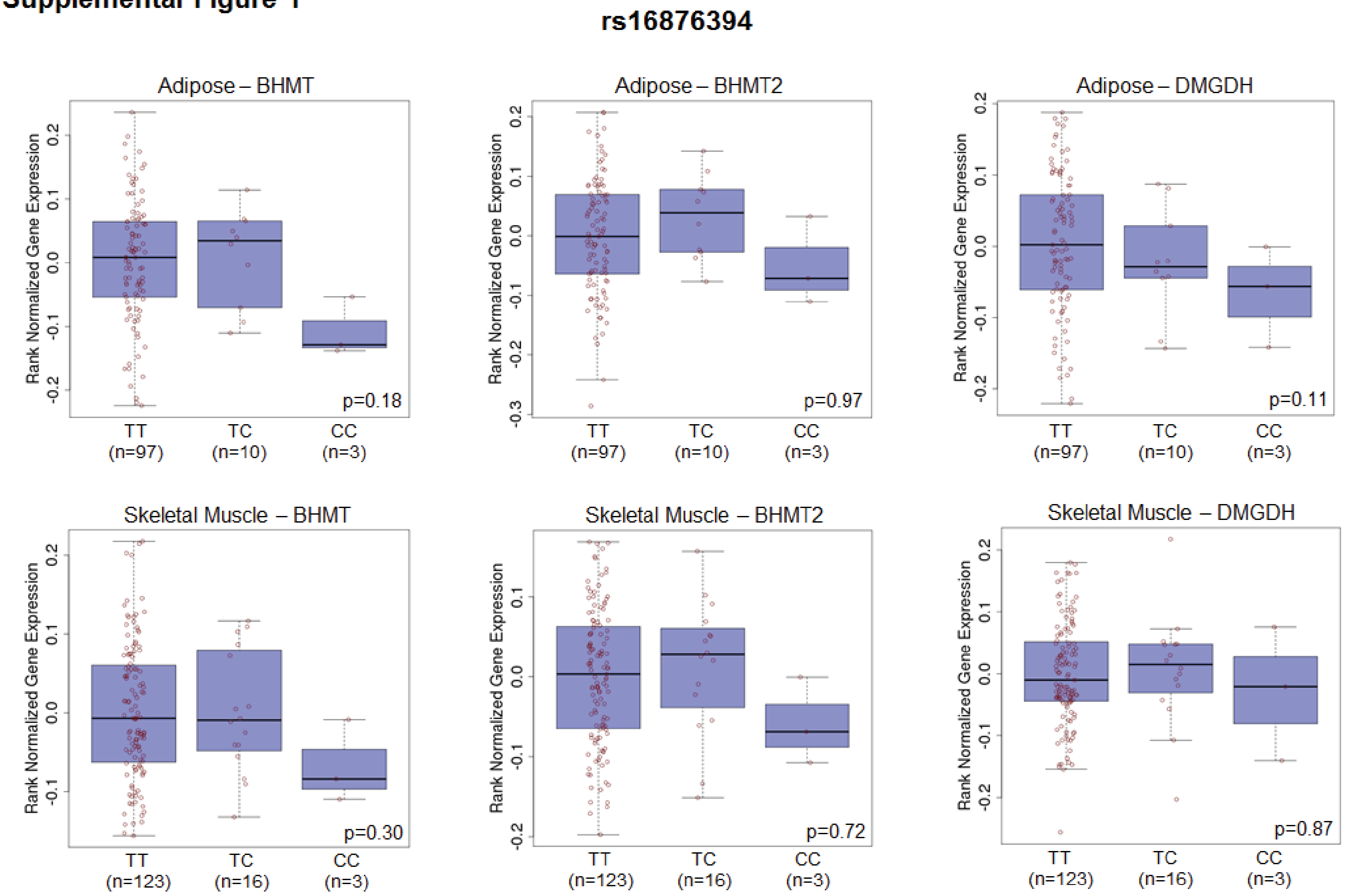
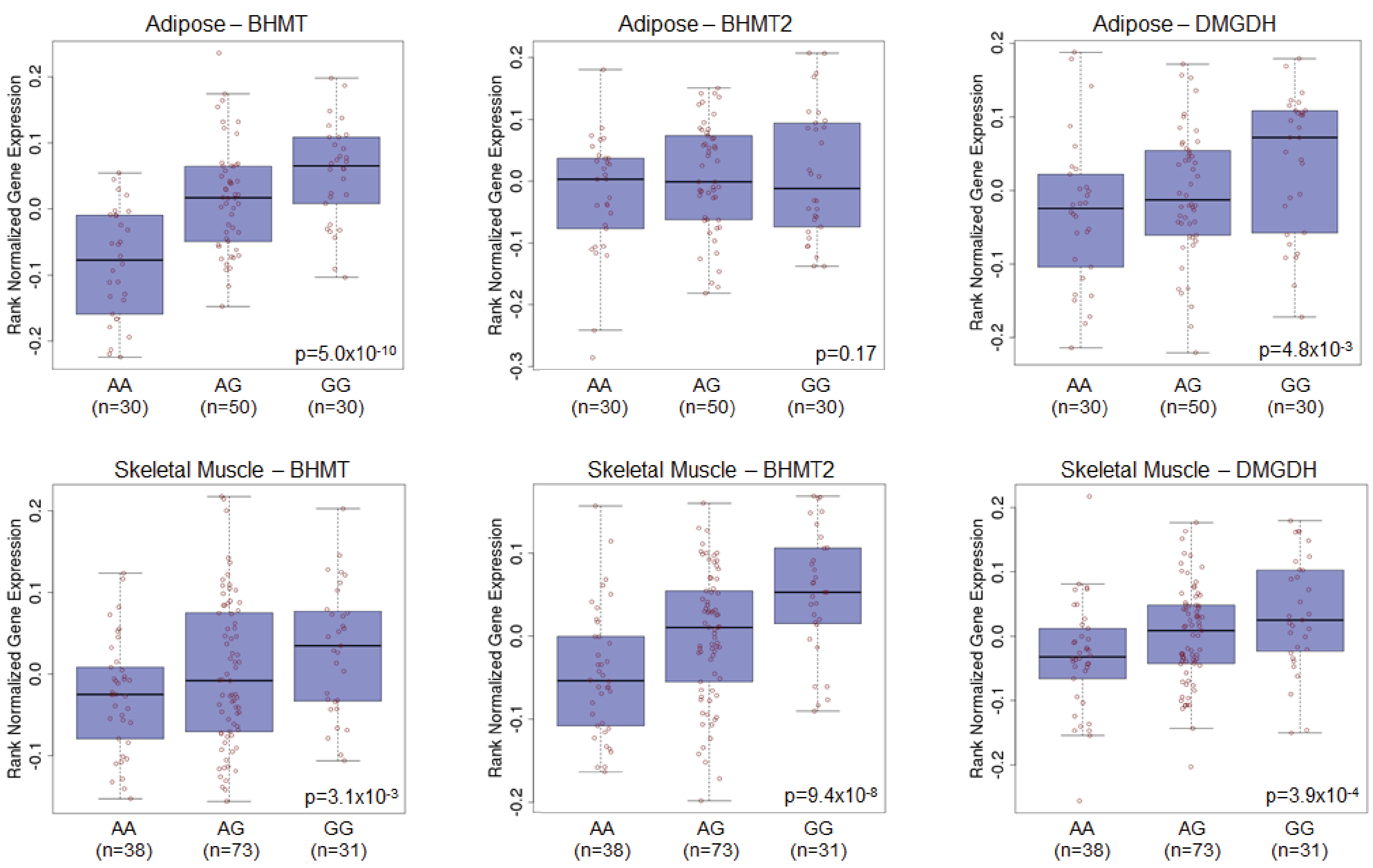
Supplemental Figure 1



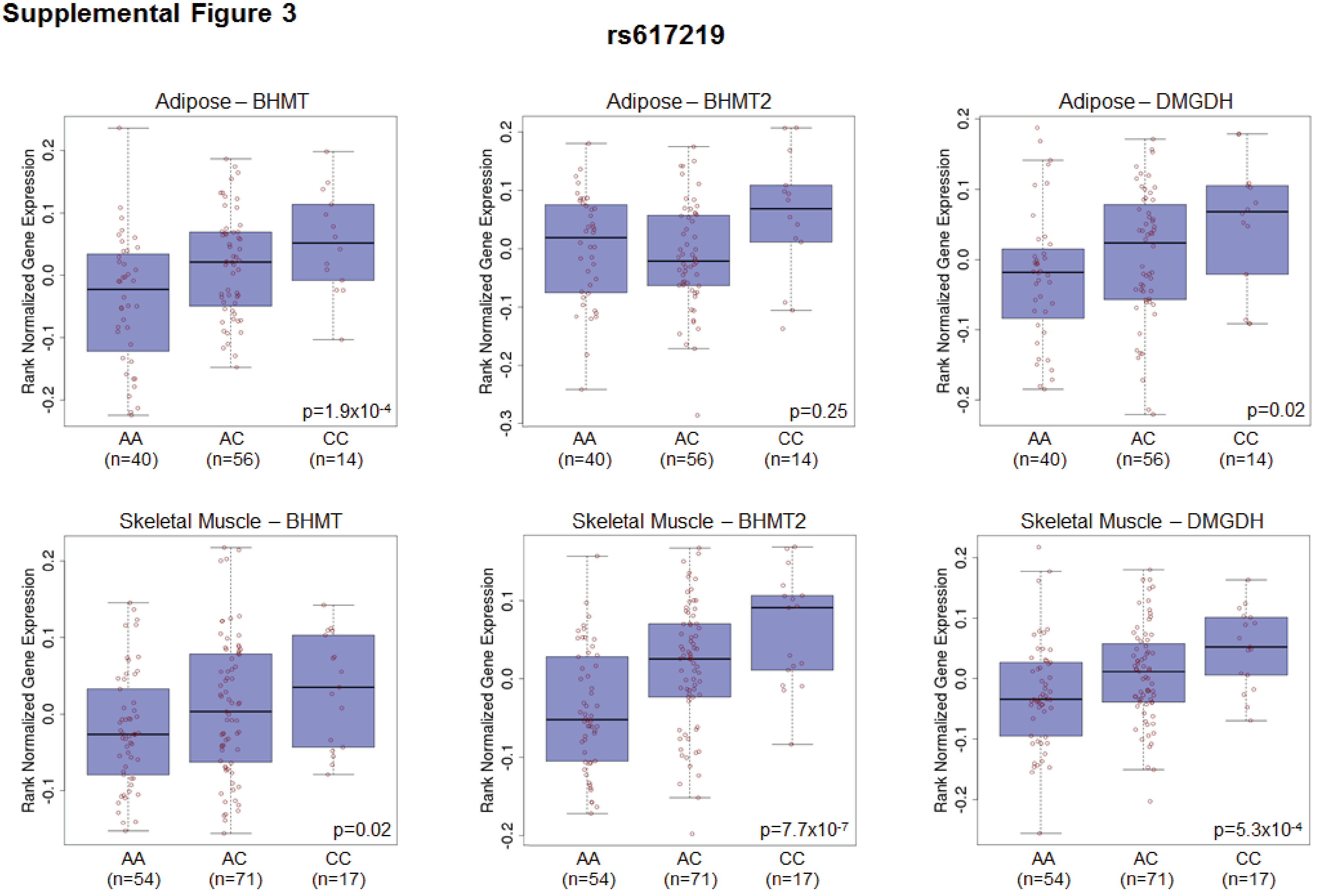
Supplemental Figure 1. ***Cis*** **eQTLs for** ***BHMT*****,** ***BHMT2*****, and** ***DMGDH*** **with rs16876394 at the Chromosome 5q14.1 Locus.** There were no significant eQTLs in either subcutaneous adipose tissue or skeletal muscle with rs16876394. Data were taken from the publicly available Genotype-Tissue Expression Project database (http://www.gtexportal.org/).

Supplemental Figure 2



Supplemental Figure 2. ***Cis*** **eQTLs for** ***BHMT*****,** ***BHMT2*****, and** ***DMGDH*** **with rs557302 at the Chromosome 5q14.1 Locus.** Rs557302 yielded eQTLs for *BHMT*, *BHMT2*, or *DMGDH* at varying levels of significance in subcutaneous adipose tissue or skeletal muscle. Data were taken from the publicly available Genotype-Tissue Expression Project database (http://www.gtexportal.org/).

Supplemental Figure 3



Supplemental Figure 3. ***Cis*** **eQTLs for** ***BHMT*****,** ***BHMT2*****, and** ***DMGDH*** **with rs617219 at the Chromosome 5q14.1 Locus.** Rs617219 yielded eQTLs for *BHMT*, *BHMT2*, or *DMGDH* at varying levels of significance in subcutaneous adipose tissue or skeletal muscle. Data were taken from the publicly available Genotype-Tissue Expression Project database (http://www.gtexportal.org/).

Supplemental Table 1. Multivariate Analyses of Chromosomes 2q34 Locus (rs715) with Risk of CAD in the GeneBank Cohort Stratified by Sex.

	Females		Males	
Metabolite	**OR (95% CI)**	**p-value**	**OR (95% CI)**	**p-value**
None	0.63 (0.40-0.98)	0.04	0.88 (0.59-1.32)	0.54
Betaine	0.57 (0.33-0.94)	0.03	0.90 (0.55-1.46)	0.66
Glycine	0.69 (0.43-1.11)	0.12	0.96 (0.64-1.46)	0.86
Betaine and Glycine	0.64 (0.37-1.11)	0.11	0.94 (0.57-1.54)	0.81

Multivariate logistic regression analyses were carried out in in the subset of 400 age-, sex-, and CAD-matched GeneBank subjects for whom genetic, metabolomic, and clinical phenotype data were all available. Odds ratios (OR) with 95% confidence intervals (CI) were calculated for the C allele of rs715, with inclusion of the indicated metabolite in the multivariate model.

Supplemental Table 2. Association of Chromosome 5q14.1 SNPs with Prevalent CAD in the CARDIoGRAM Consortium.

SNP	n	Effect Allele	Frequency	OR (95% CI)	p–value
rs16876394	81,108	C	0.14	1.00 (0.96-1.04)	1.0
rs557302	84,211	G	0.51	1.01 (0.99-1.04)	0.29
[*]rs567754	67,852	C	0.65	1.00 (0.97-1.03)	0.96

Analyses were adjusted for age and sex.

[*] Used as proxy for rs617219 ($r^2 = 0.84$).

Supplementary Note 1

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