

S1 Table. Details of five highest associated locations of SNPs to *CMAH* that remained genome-wide significant after permutation testing.

Chromosome	SNP ID	6.2 assembly position	P_{raw}	P_{genome}
B2	chrB2.4545019	4487432	2.50e-10	0.00001
B2	chrB2.4625051	4449822	4.28e-5	0.004
B1	chrB1.122267584	99024960	8.10e-5	0.31
B1	chrB1.222834707	198985796	2.04e-5	0.56
C2	ChrC2.95368178	85312236	3.32e-5	0.71