

Table 8. Detailed results of association of three SNPs in the *HBSIL - MYB* intergenic region and FC trait using Measured Haplotype Analysis in the combined European twin panels. Seven haplotype-specific effects [log (FC%)] are fitted in the unrestricted (general) model [haplotype TCA is very rare (frequency < 0.1%) so a specific effect was not modeled]. The estimated trait mean for a haplotype combination is the sum of the two additive haplotype mean estimates, plus a dominance effect when rs9399137 is heterozygous (-0.12 ± 0.03). Dominance terms are not significant at other sites and therefore are not included. Means for each haplotype fitted under the restricted additive allele substitution model are shown for comparison. Allele-specific substitution effects are tabulated in SI Table 9. The haplotypes are ordered to highlight allele substitution at rs9399137 with different allele backgrounds at the other sites. Under the allele substitution model, the T to C substitution at rs9399137 results in a change of 0.53 ± 0.03 (SI Table 9) in the haplotype mean irrespective of the background. The comparison of the haplotype estimates under the general and allele substitution models shows that the latter provides a good fit to the data for this site. Similar observations hold for the other sites, and overall the allele substitution model is not rejected when tested against the unrestricted measured haplotype model ($\chi^2_3 = 5.8$; $P = 0.12$).

| rs6904897 | rs9399137 | rs6929404 | Frequency | Unrestricted model | Allele substitution model |
|-----------|-----------|-----------|-----------|--------------------|---------------------------|
| T | T | C | 47.1% | 0.57 ± 0.01 | 0.56 |
| T | C | C | 3.4% | 1.17 ± 0.06 | 1.10 |
| G | T | C | 5.0% | 0.46 ± 0.05 | 0.46 |
| G | C | C | 20.4% | 0.97 ± 0.03 | 0.99 |
| G | T | A | 11.4% | 0.38 ± 0.03 | 0.37 |
| G | C | A | 3.5% | 0.96 ± 0.06 | 0.90 |
| T | T | A | 9.1% | 0.46 ± 0.03 | 0.48 |