Supporting Information

Kovach et al. 10.1073/pnas.0904077106

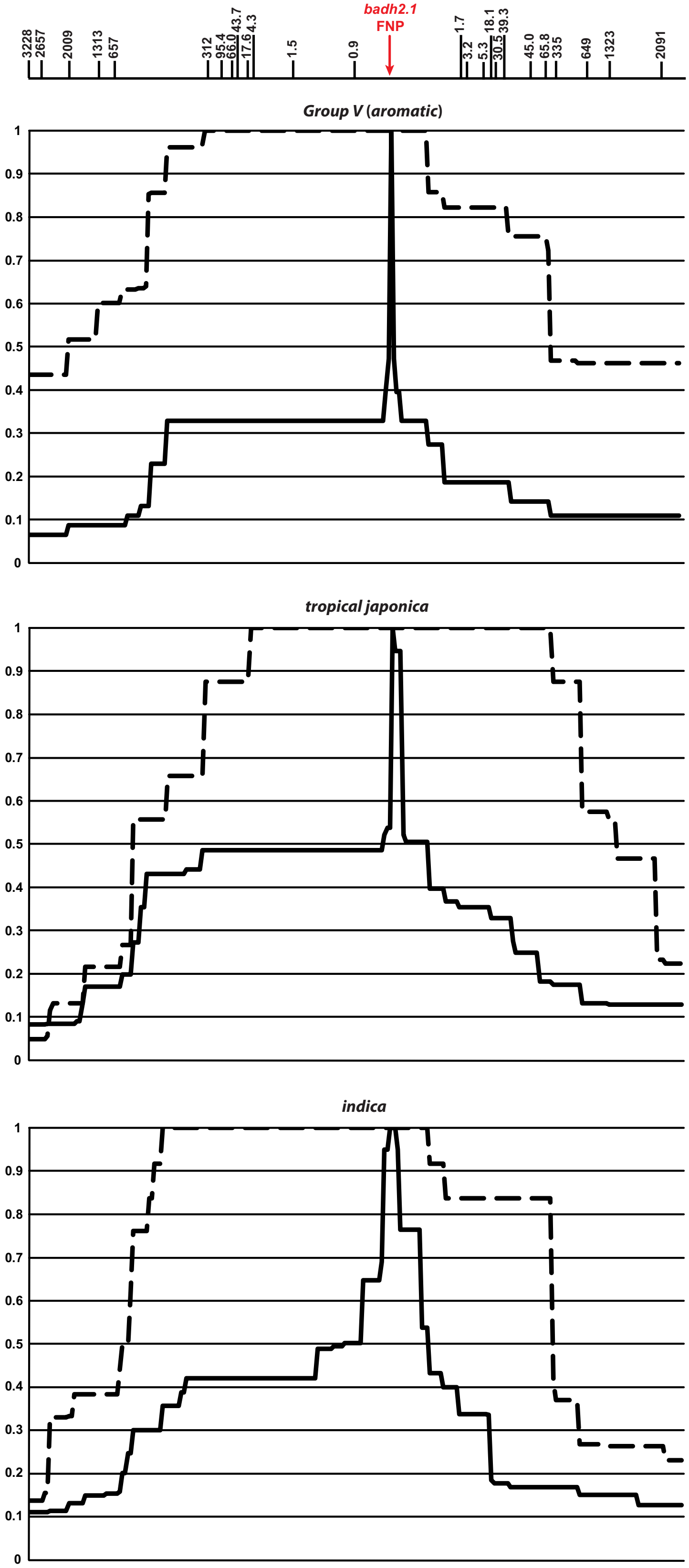

Fig. S1. EHH across the *BADH2* genomic region in individual subpopulations. EHH values were calculated for the *O. sativa* accessions examined in this study based on haplotype data across a 5.3-Mb genomic region surrounding the *BADH2* gene. In this figure, the EHH values were calculated for accessions within each subpopulation that possessed the *badh2.1* allele: *Group V* ($n = 67$), *tropical japonica* ($n = 54$), and *indica* ($n = 63$). Solid and dashed lines indicate the combined EHH values of accessions having the wild-type and *badh2.1* alleles, respectively. The position of the *badh2.1* FNP is indicated with an arrow. The locations of each amplicon used to obtain haplotype data are depicted across the top (Table S5) in terms of their physical distance from the *BADH2* gene (in kb). This figure demonstrates that the pattern of EHH decay around the *BADH2* gene for all of *O. sativa* (Fig. 3) is very similar to the pattern observed within each subpopulation individually.

Other Supporting Information Files

Table S1
Table S2
Table S3
Table S4
Table S5