

## Supplementary II: test scores in the autosome candidate regions of Table 1 of Sabeti et al. (2007)

In a 300kb region of the gene *SLC30A9* on chromosome 4, the CHB+JPT sample was reported to have strong signal of selection (Table 1, Sabeti et al. 2007). In Figure 1a, we confirmed the results by our EHHST values since the sharp peak of CHB+JPT sample located in the *SLC30A9* gene region, which was particular noteworthy. In the region around 33.9Mb on chromosome 4, all three samples of HapMap Phase II data were reported to have selection signal (Table 1, Sabeti et al. 2007). Our EHHST values confirm this for CHB+JPT and CEU samples in Figure 1b. Again in the region around 159Mb on chromosome 4, the CHB+JPT sample was reported to provide strong signal of selection. We confirmed the results by our EHHST values in Figure 1c.

On chromosome 10, the CHB+JPT sample was reported to show strong signal of selection in a 400kb region of the gene *PCDH15* (Table 1, Sabeti et al. 2007). We confirmed the result by our EHHST values in Figure 1d. Again on chromosome 10, the CEU and CHB+JPT samples showed strong signal of selection in a 300kb region around 22.7Mb (Table 1, Sabeti et al. 2007). We confirmed the results by our EHHST values in Figure 1e. Also on chromosome 10, the CEU sample was reported to show strong signal of selection in a 300kb region around 3Mb. We confirmed the results by the EHHST values in Figure 1f.

On chromosome 1, there was strong signal of selection in a 400kb region of the genes *BLZF1* and *SLC19A2* for CHB+JPT sample (Table 1, Sabeti et al., 2007). In Figure 2a, it was clear that the scores of the CHB+JPT sample were much higher than the scores of the CEU and YRI samples in the region of the two genes. A peak of EHHST occurred right between the two genes. Thus, our results confirmed the findings of Sabeti et al. (2007). On chromosome 16, the CHB+JPT sample showed strong selection signal in a region around 64.3Mb. We confirmed the result by high EHHST values in Figure 2b. On chromosome 17, CHB+JPT sample had strong selection signal around 53.3Mb. The EHHST values of both CHB+JPT and CEU samples are high in Figure 2c. On chromosome 19, YRI sample was reported to have strong signal of selection around a region 43.5Mb (Table 1, Sabeti et al. 2007). We confirmed the result by the EHHST values in Figure 2d. Again in the YRI sample, strong signal of selection was found in a 400kb region that lay entirely within the gene *LARGE* on

chromosome 22 (Table 1, Sabeti et al. 2007). We confirmed this evidence by the the EHHST value in Figure 2e.

On chromosome 12, the YRI sample showed strong signal of selection in a 800kb region around 78.3Mb (Table 1, Sabeti et al. 2007). We failed to confirm the results by the EHHST values (Fig. 3a). In Table 1 of Sabeti et al. (2007), *BCAS3* on chromosome 17 was found to have strong signal of selection for the CEU sample. We failed to confirm the results (Fig. 3b). Actually, the EHHST values of the CEU sample were lower than those of the CHB+JPT sample. In Table 1 of Sabeti et al. (2007), strong signal of selection was found in a 600kb region of *CHST5*, *ADAT1*, and *KARS* on chromosome 16 for CHB+JPT and YRI samples. We failed to confirm the results by the EHHST values (Fig. 3c).

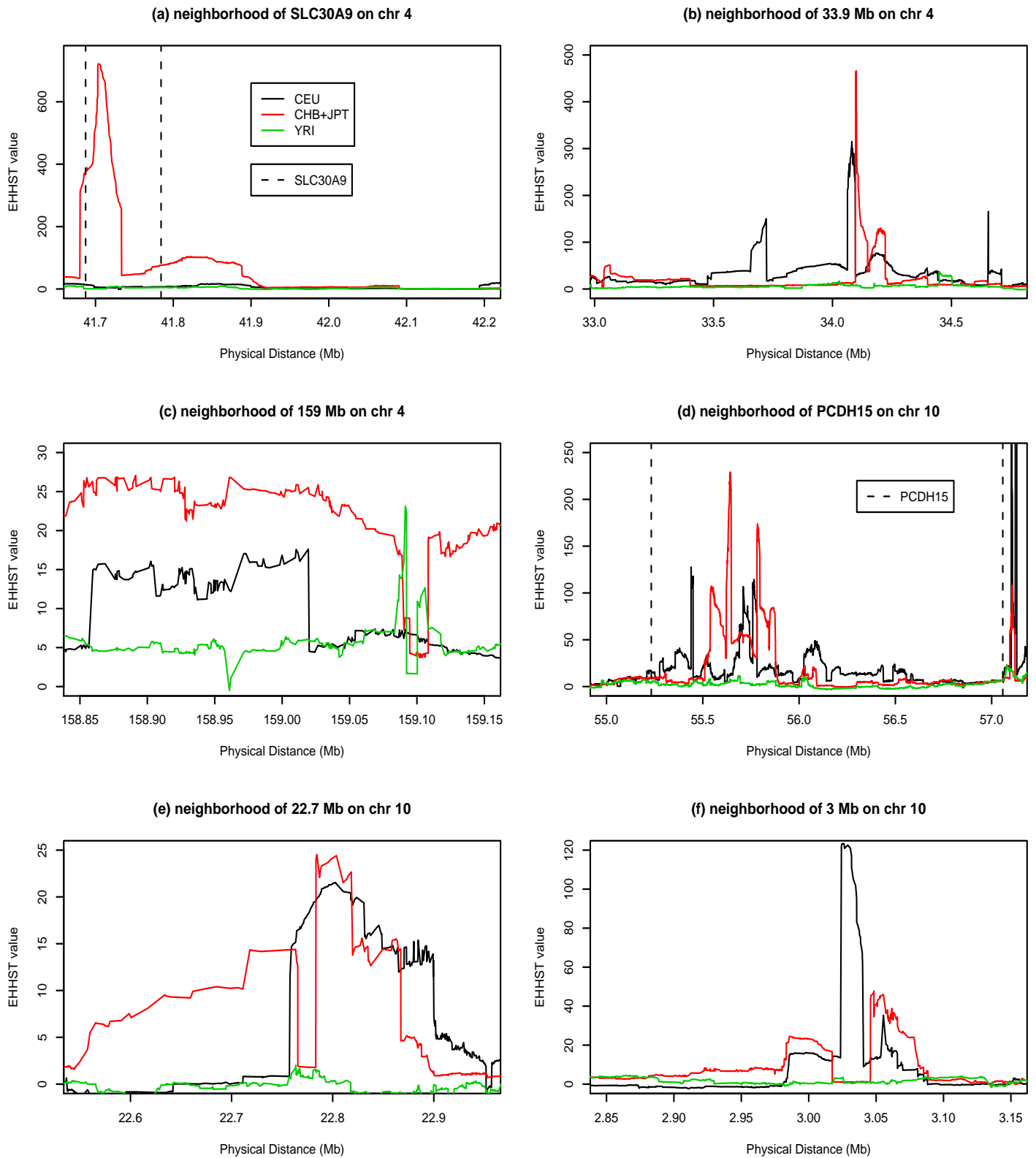


Figure 1: The EHHST values of three population samples of HapMap Phase II data in the candidate regions on chromosome 4 and 10. The dashed legend in Graph (a) indicated the location of gene *SLC30A9*, and similarly the location of *PCDH15* in Graph (d). **Abbreviation:** chr-chromosome.

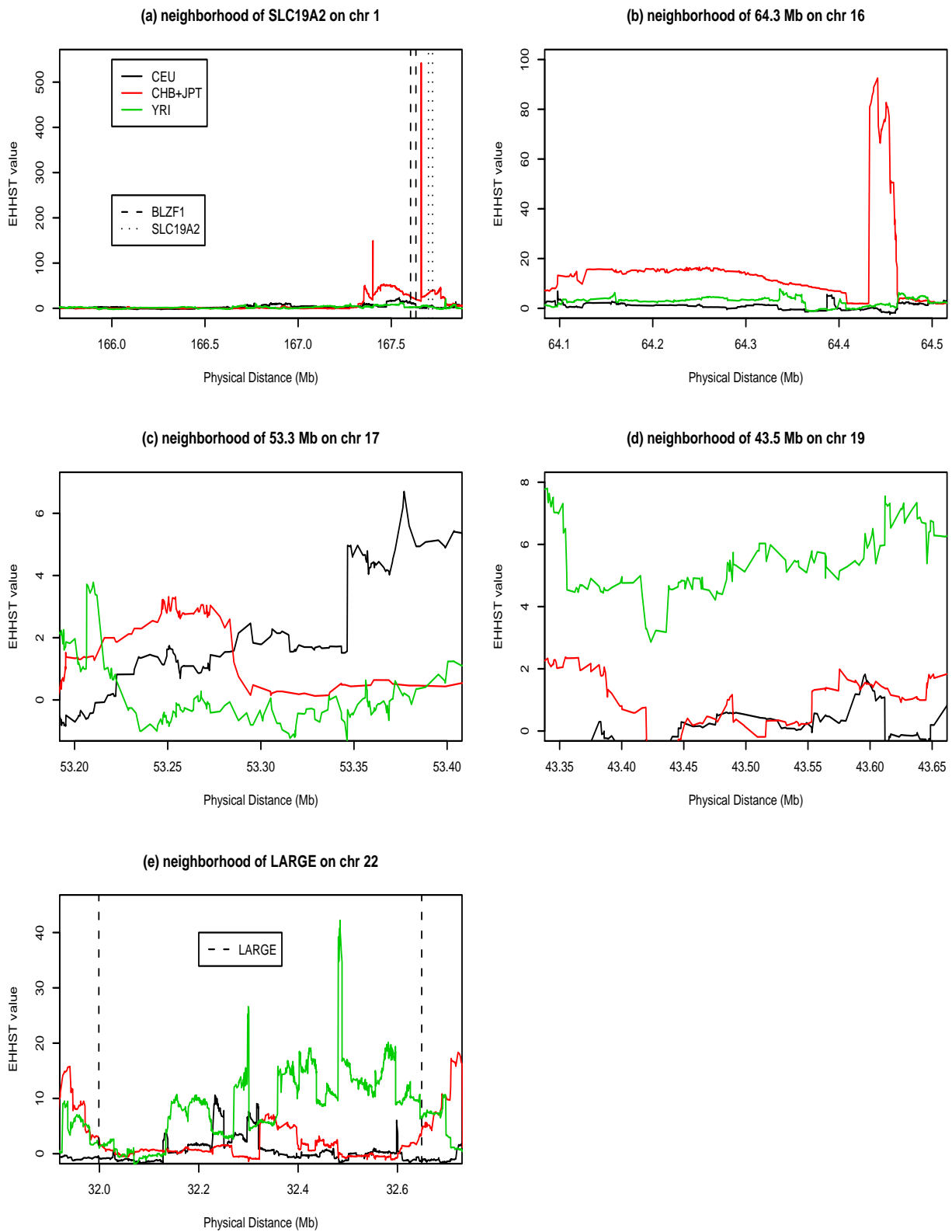


Figure 2: The EHHST values of three population sample of HapMap Phase II data in the candidate regions on chromosome 1, 16, 17, 19 and 22. In Graph (a), the dashed legend indicated the location of gene *BLZF1*, and the dotted legend indicated the location of gene *SLC19A2*. The dashed legend indicated the location of gene *LARGE* in Graph (e).

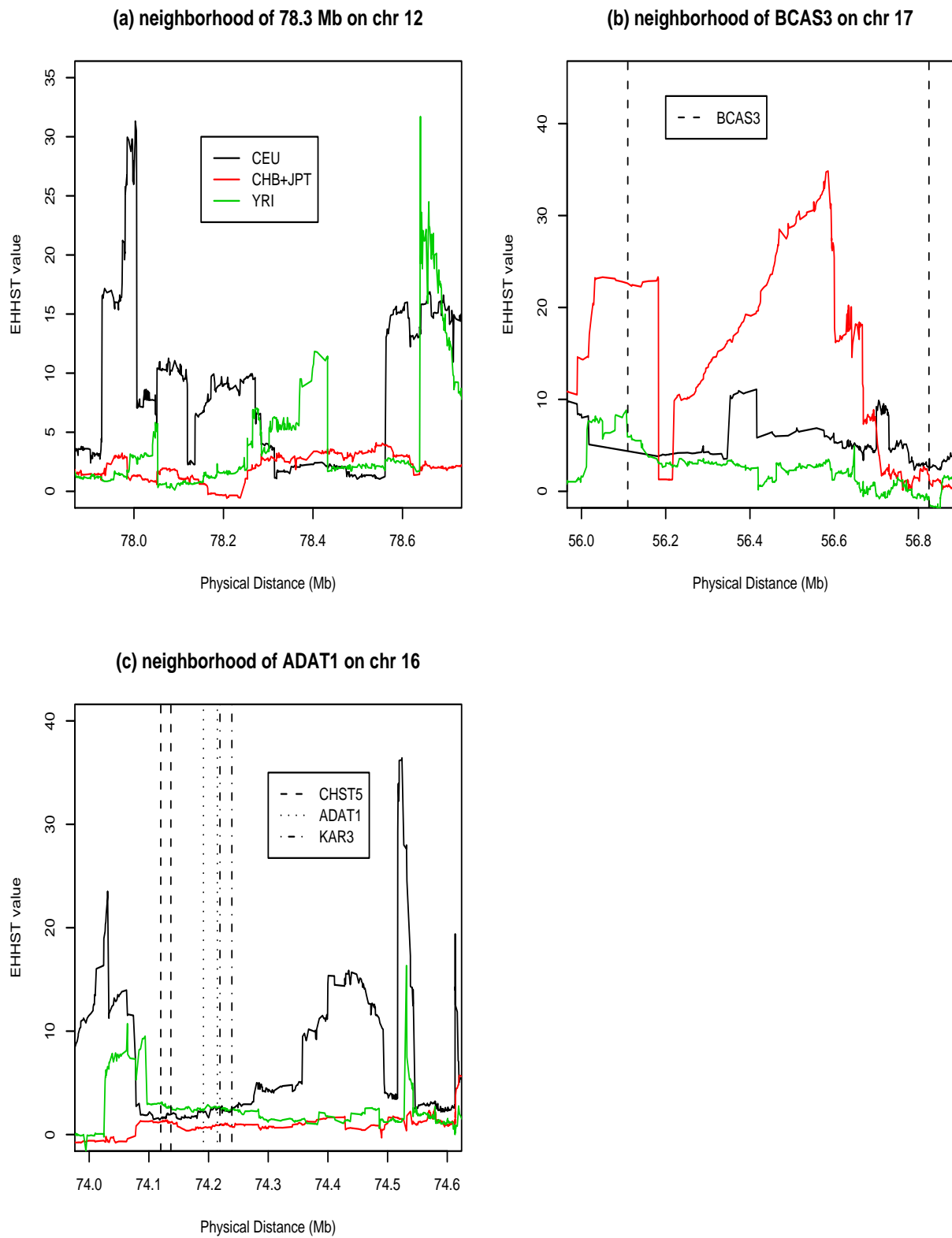


Figure 3: The EHHST values of three population sample of HapMap Phase II data in the candidate regions on chromosome 12, 16 and 17. The dashed legend indicated the location of gene *BCAS3* in Graph (b). In Graph (c), the dashed, dotted and dashed-dotted legends indicated the locations of *CHST5*, *ADAT1*, and *KARS* genes.