

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

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). In Supplementary II, Figure 1b of Zhong et al. (2010), we found that EHHST values of CHB+JPT and CEU samples are high while the EHHST values of YRI sample are low. In Figure 1a, we confirmed the results by xp-EHHST since the xp-EHHST values of CHB+JPT vs YRI and CEU vs YRI are significantly positive, while the xp-EHHST values of CEU vs CHB+JPT are around 0.

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 xp-EHHST in Figure 1b since the xp-EHHST values of CHB+JPT vs YRI are significantly positive and the xp-EHHST values of CEU vs CHB+JPT are significantly negative, while the xp-EHHST values of CEU vs YRI are around 0 in the region.

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 xp-EHHST in Figure 1c since the xp-EHHST values of CHB+JPT vs YRI are significantly positive and the xp-EHHST values of CEU vs CHB+JPT are significantly negative in the middle of *PCDH15* gene region, while the xp-EHHST values of CEU vs YRI are around 0.

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 xp-EHHST values in Figure 1d since the xp-EHHST values of CHB+JPT vs YRI and CEU vs YRI are significantly positive, while the xp-EHHST values of CEU vs CHB+JPT are low.

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 xp-EHHST values in Figure 1e, since the xp-EHHST values of CEU vs CHB+JPT and CEU vs YRI are significantly positive. In addition, the xp-EHHST values of CHB+JPT vs YRI are significantly positive and so the results are slightly confusing. However, combining with the results of EHHST in Zhong et al. (2010), Figure 1f of Supplementary II, we can clearly see the selection signals in CEU sample.

On chromosome 16, the CHB+JPT sample showed strong selection signal in a region around 64.3Mb. In Figure 1f, we showed that the xp-EHHST values of CHB+JPT vs YRI are significantly

positive and the xp-EHHST values of CEU vs CHB+JPT are significantly negative in the region of the two genes, while the xp-EHHST values of CEU vs YRI are around 0. Thus, we confirmed the result by xp-EHHST.

On chromosome 17, CHB+JPT sample had strong selection signal around 53.3Mb (Table 1, Sabeti et al. 2007). In Figure 2a, we found that the xp-EHHST values of CHB+JPT vs YRI are significantly positive and the xp-EHHST values of CEU vs CHB+JPT are significantly negative in the region, while the xp-EHHST values of CEU vs YRI are smaller.

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 xp-EHHST in Figure 2b since the xp-EHHST values of CHB+JPT vs YRI and CEU vs YRI are significantly negative, while the xp-EHHST values of CEU vs CHB+JPT are around 0.

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 xp-EHHST value in Figure 2c since the xp-EHHST values of CHB+JPT vs YRI and CEU vs YRI are significantly negative, while the xp-EHHST values of CEU vs CHB+JPT are around 0.

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 xp-EHHST values (Figure 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 (Figure 3b). 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 xp-EHHST values (Figure 3c).

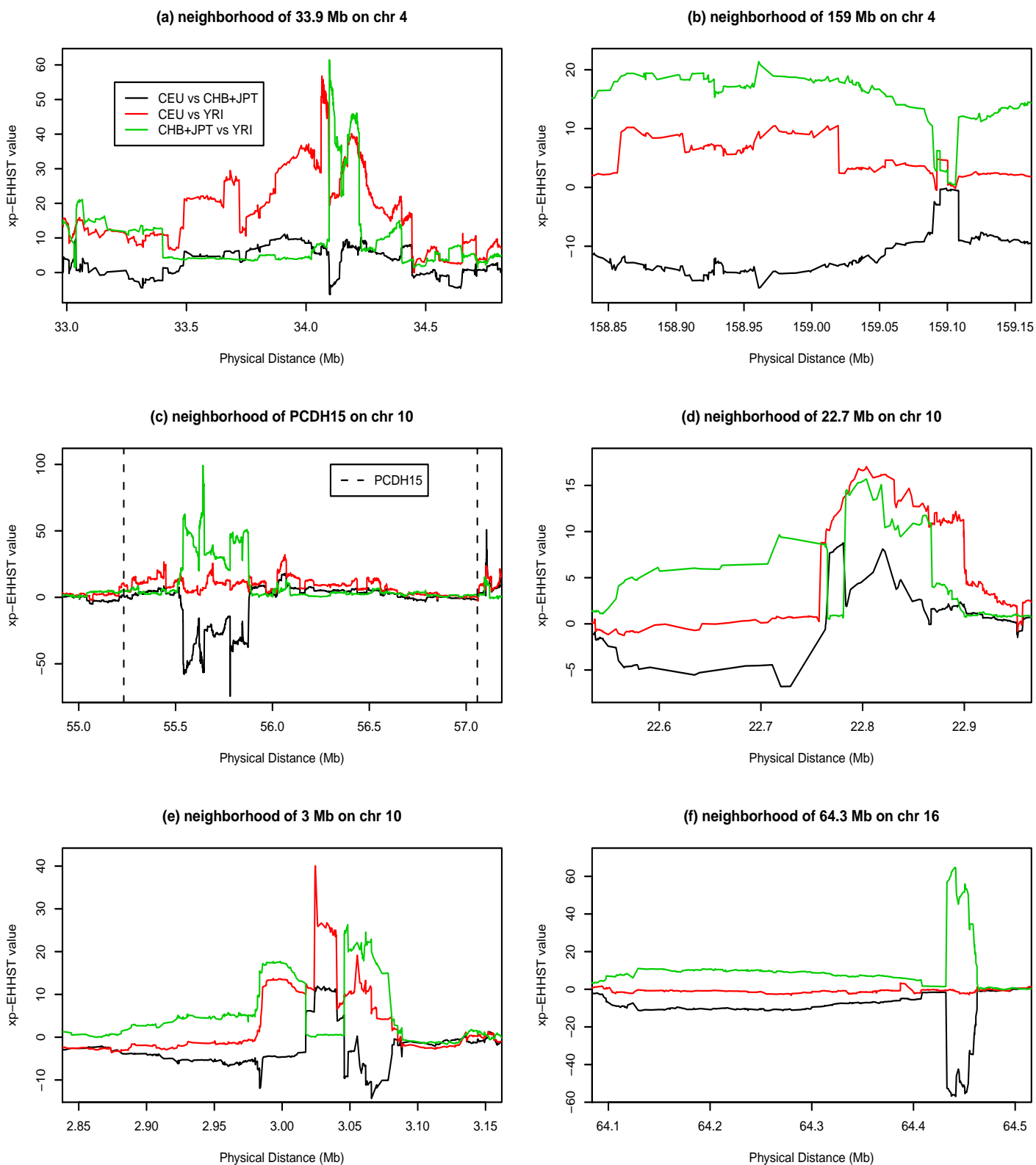


Figure 1: The xp-EHHST values of three population samples of HapMap Phase II data in the candidate regions on chromosome 4, 10 and 16. The dashed legend in Graph (d) indicated the location of gene *PCDH15*. **Abbreviation:** chr-chromosome.

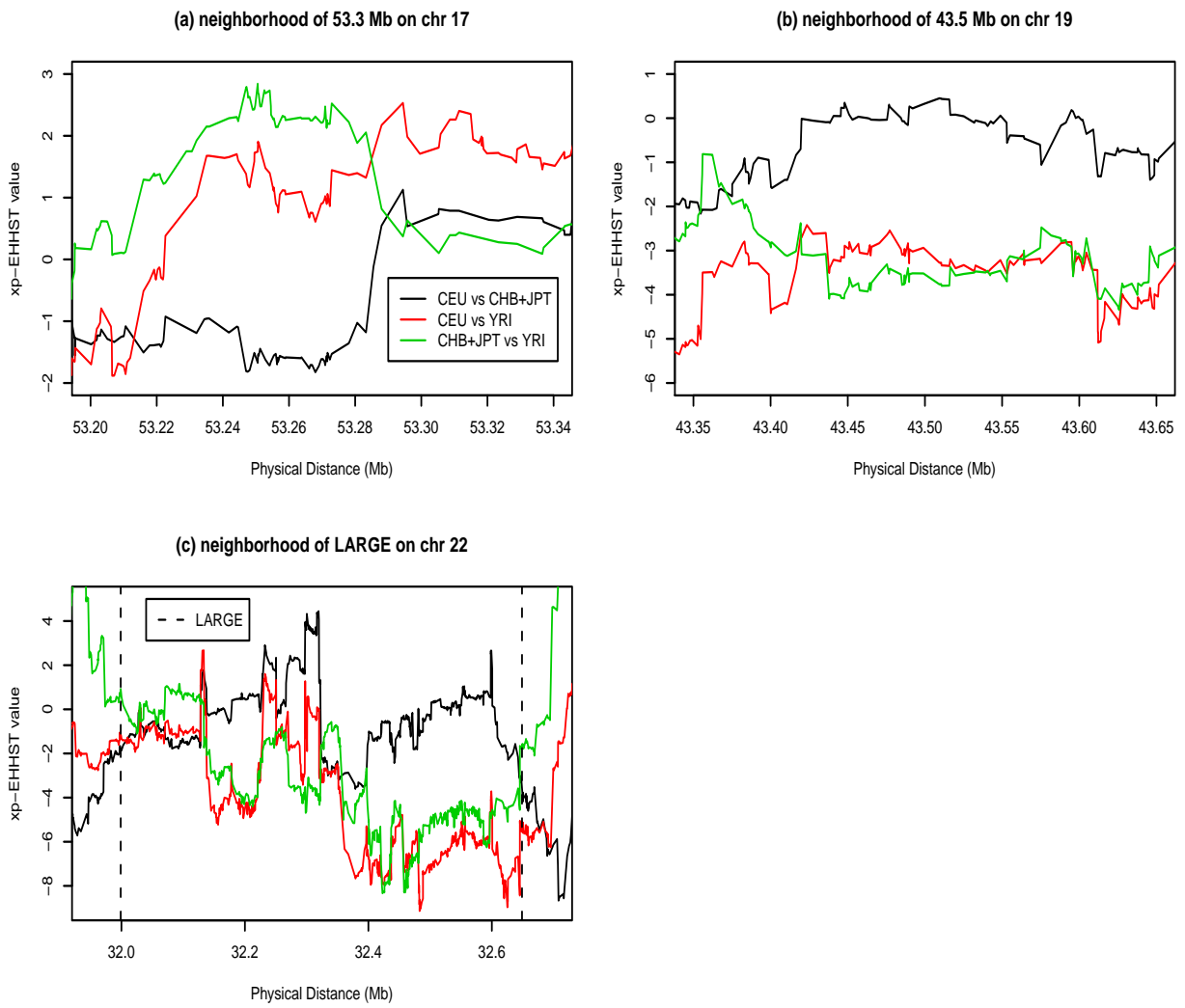


Figure 2: The xp-EHHST values of three population sample of HapMap Phase II data in the candidate regions on chromosomes 17, 19 and 22. The dashed legend indicated the location of gene *LARGE* in Graph (c).

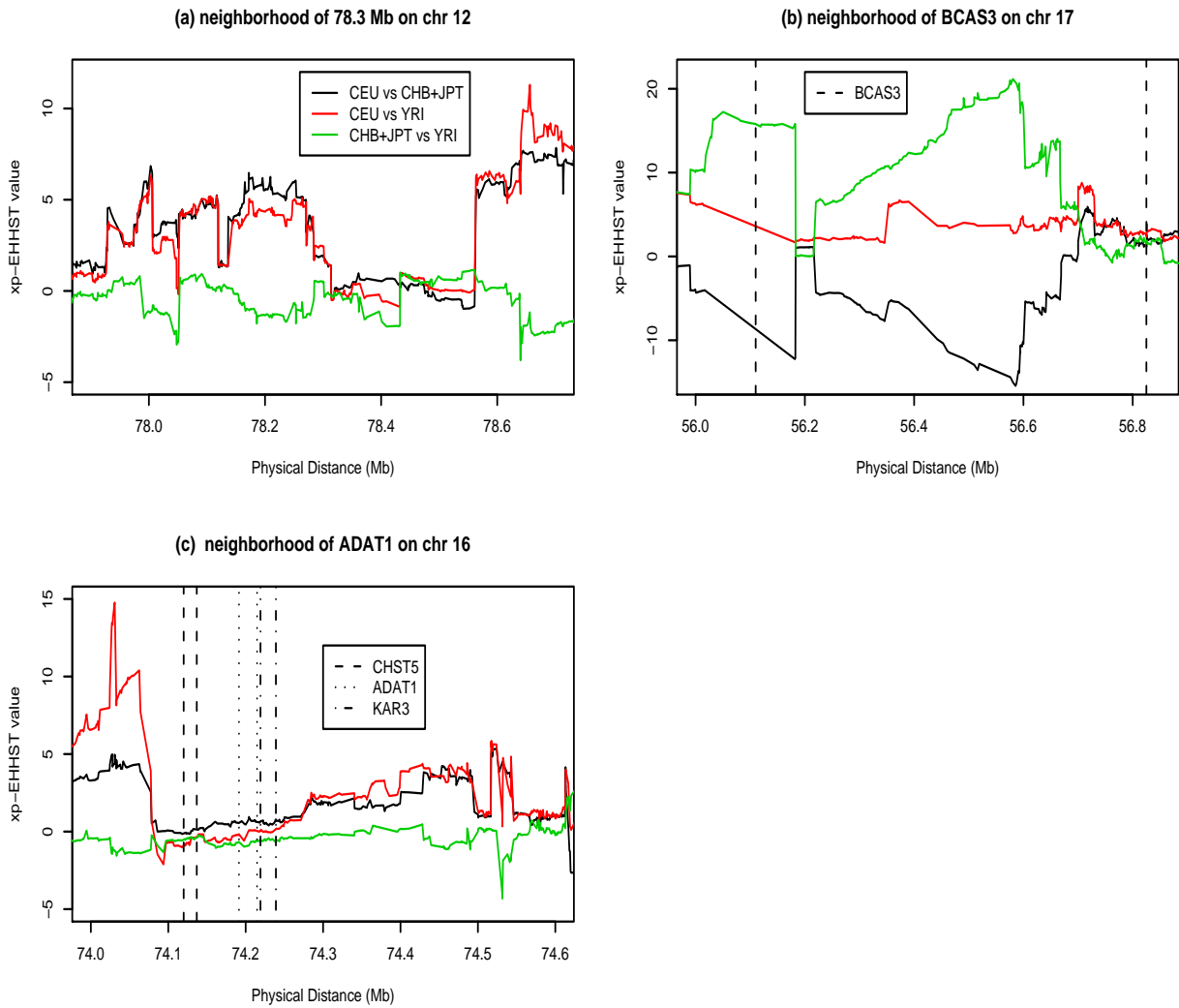


Figure 3: The xp-EHHST values of three population sample of HapMap Phase II data in the candidate regions on chromosome 12, 16 and 17. The dashed legend indicated the location of gene *BCAS3* in Graph (b). In Graph (c), the dashed, dotted and dashed-dotted legends indicated the locations of *CHST5*,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