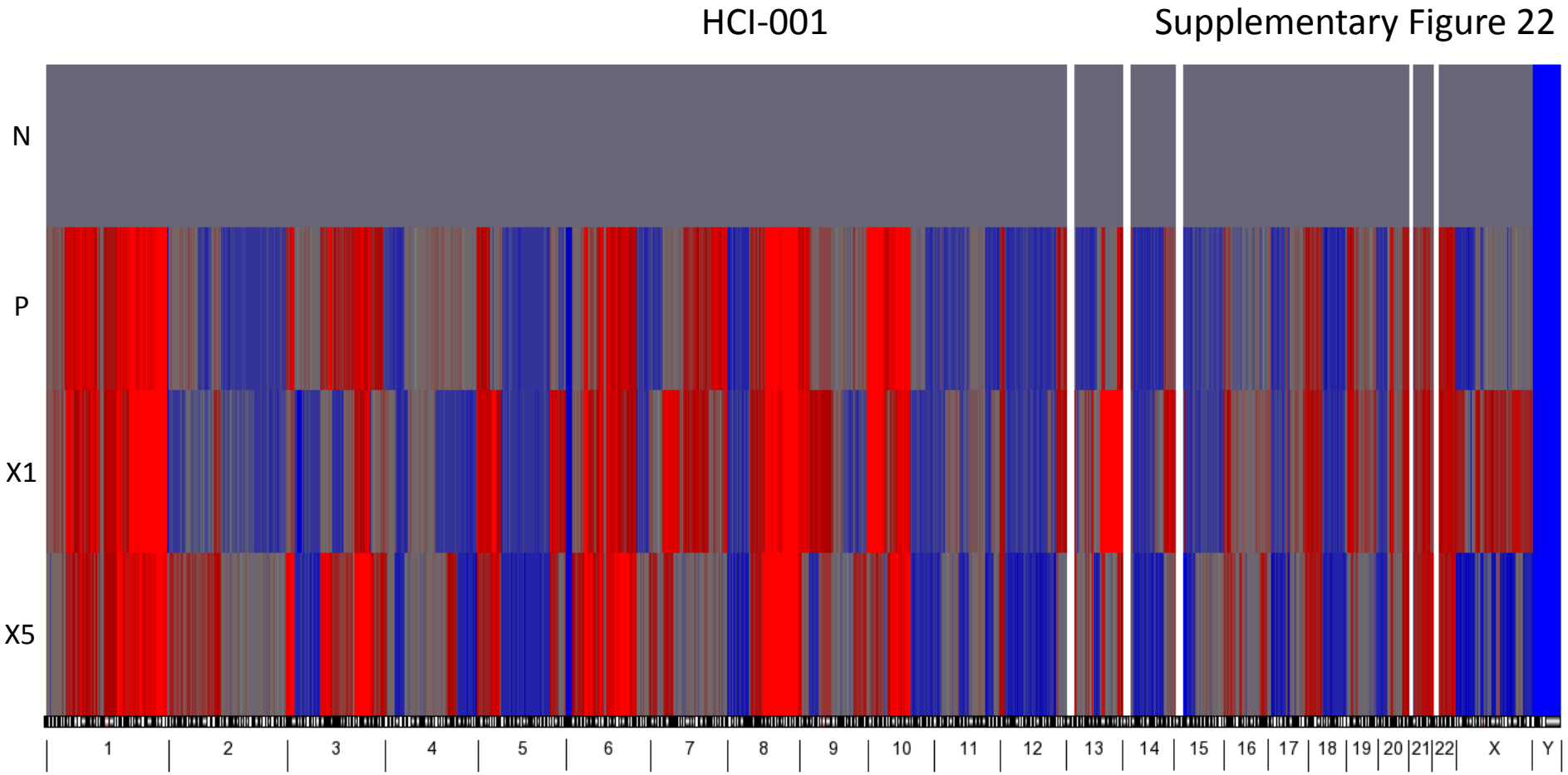
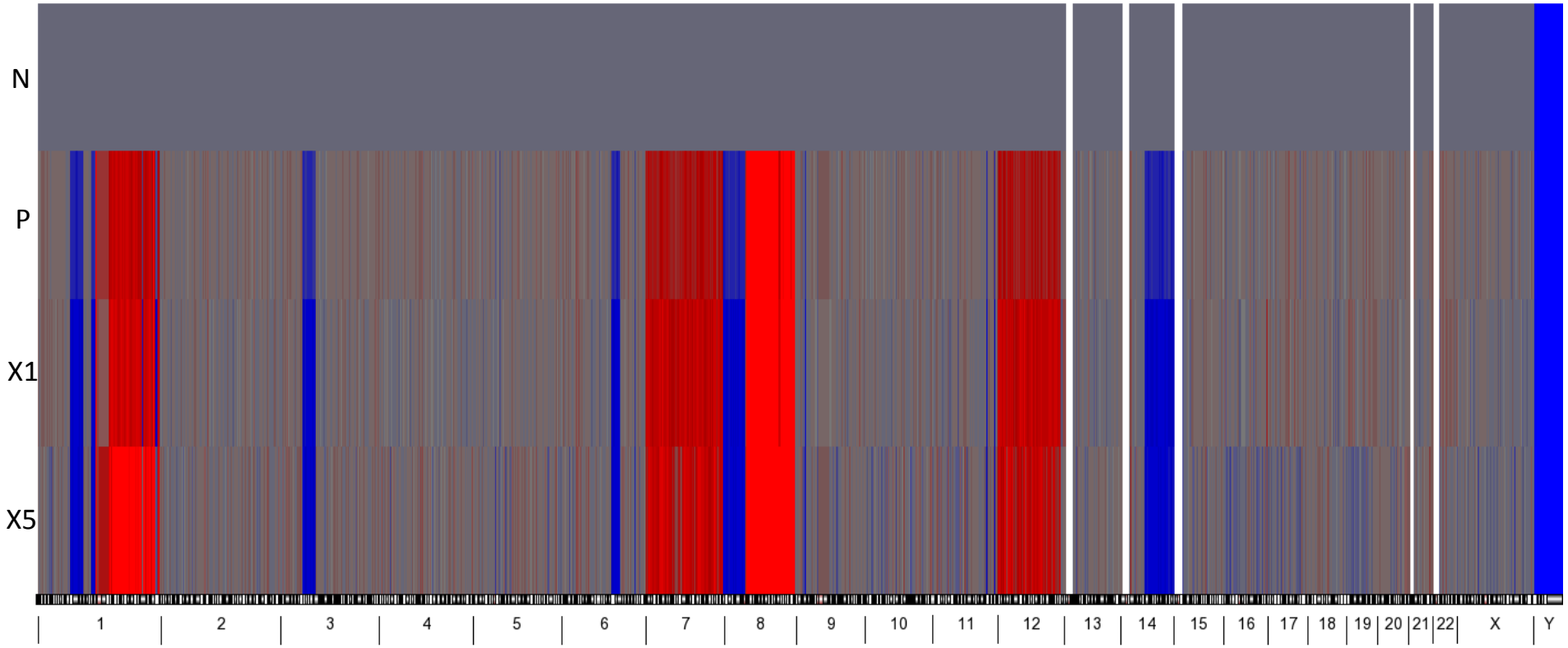
**Supplementary Figures 22-31.** SNP array data indicating genome-wide DNA copy number. Genome-wide single nucleotide polymorphism arrays were used to discern DNA copy number changes relative to normal DNA (isolated from normal blood donated by five individual, disease-free women and then pooled (N)). Each patient's tumor (P) and the corresponding tumorgraft (X) (and, in some cases tumor grafts that were serially passaged five times; X1 or X5, respectively) are indicated on the left. A copy number of 2 (normal) is indicated by gray; copy number greater than 2 (chromosomal gain or amplification) is shown in red; and copy number less than 2 (chromosomal loss or deletion) is shown in blue. The position of the copy number variants across the 22 autosomal chromosomes and 2 sex chromosomes is depicted at the bottom. Note the common low copy number of the Y chromosome (all patients and normal donors were females).



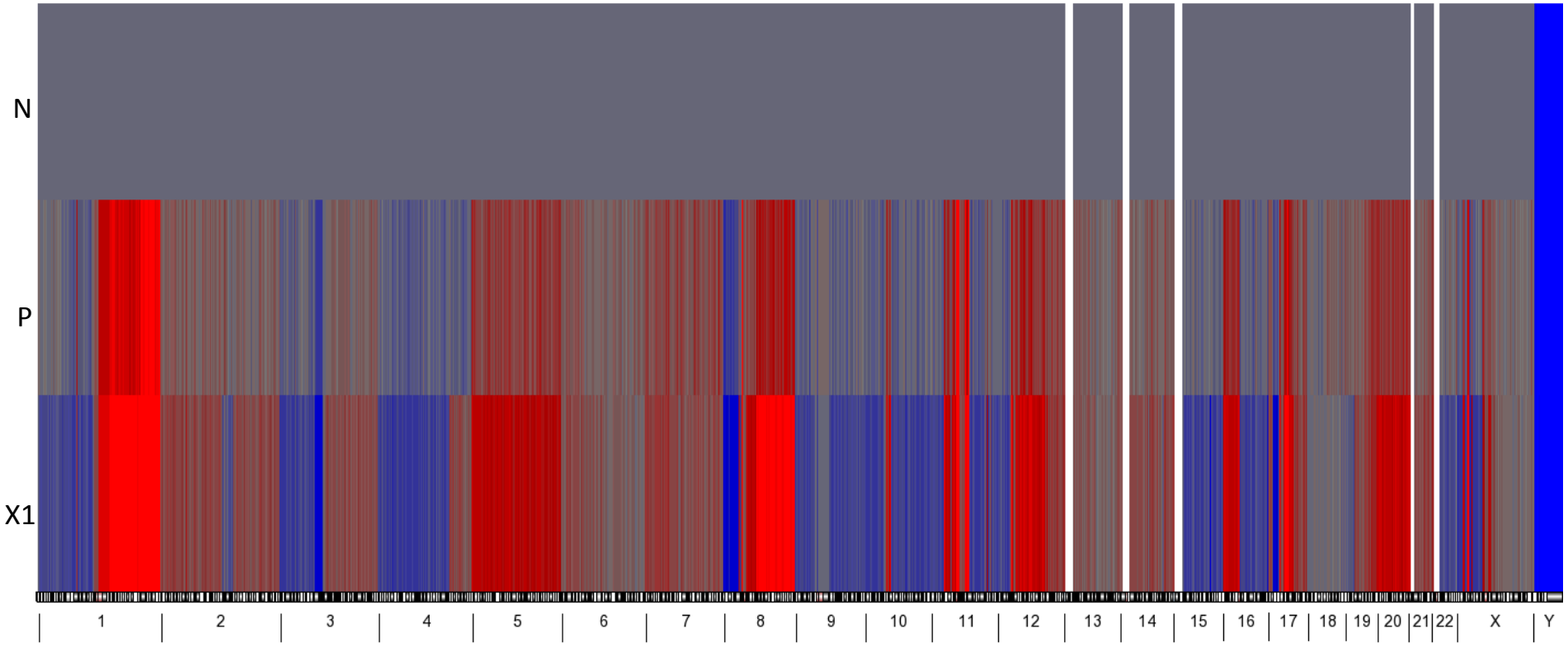
Supplementary Figure 23

HCI-002



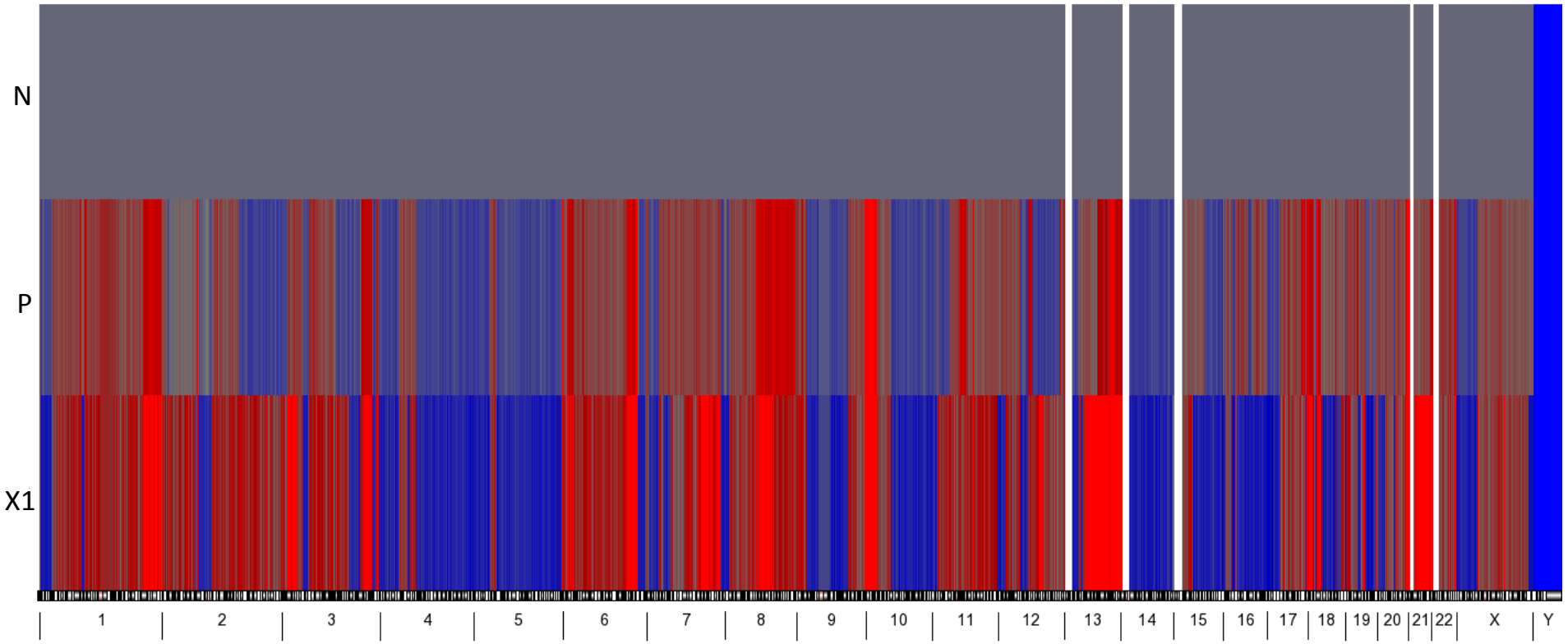
Supplementary Figure 24

HCI-003



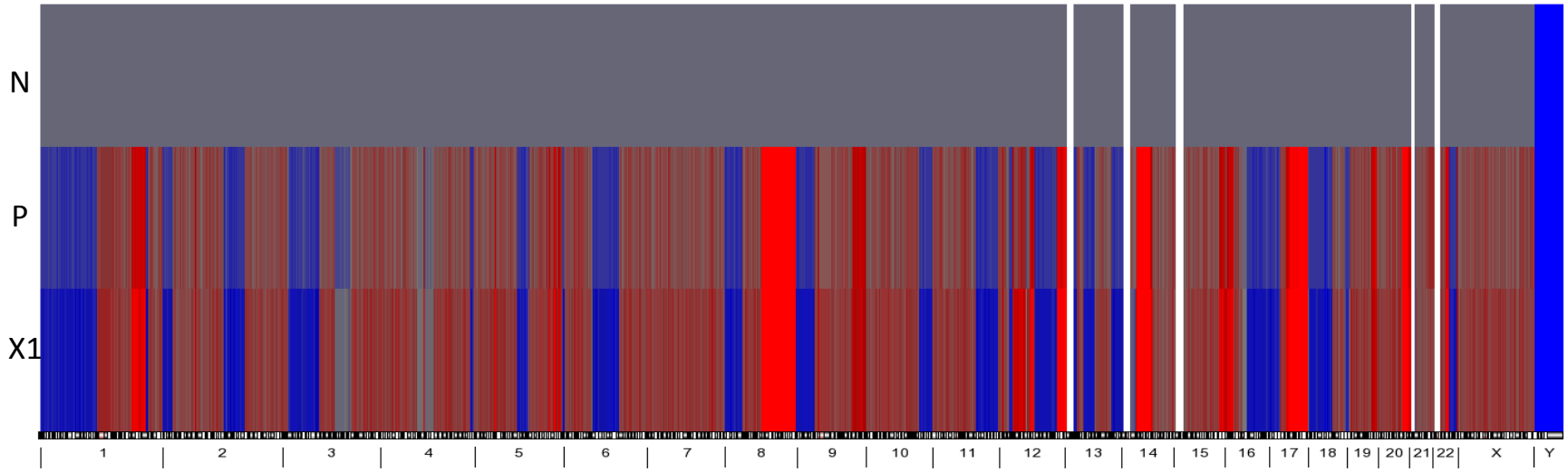
Supplementary Figure 25

HCI-004

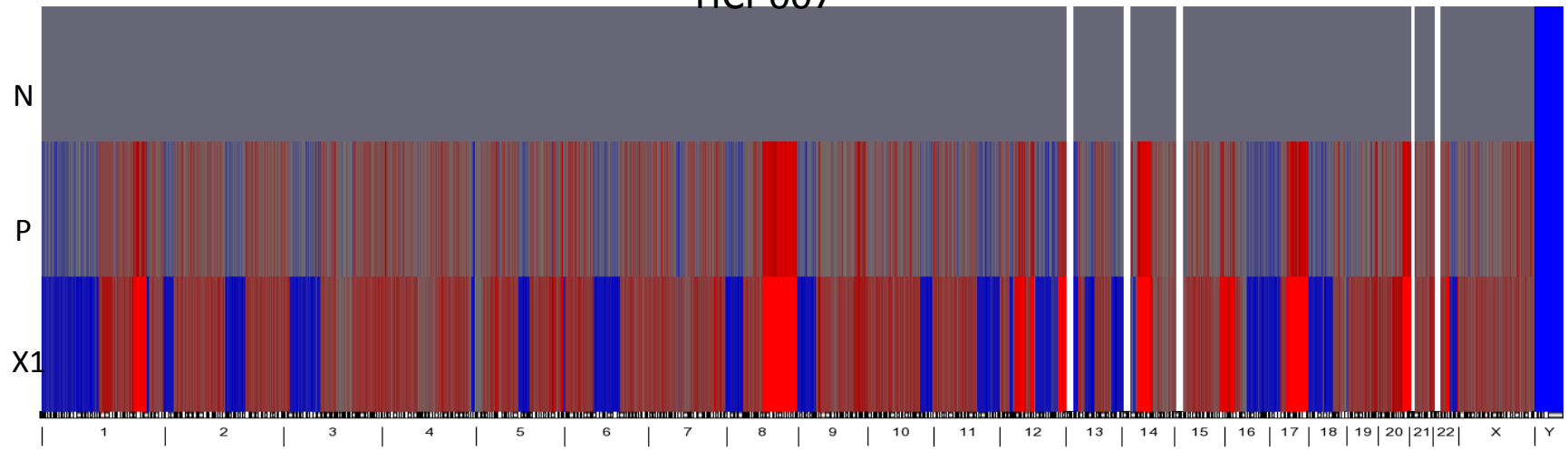


HCI-005

Supplementary Figure 26



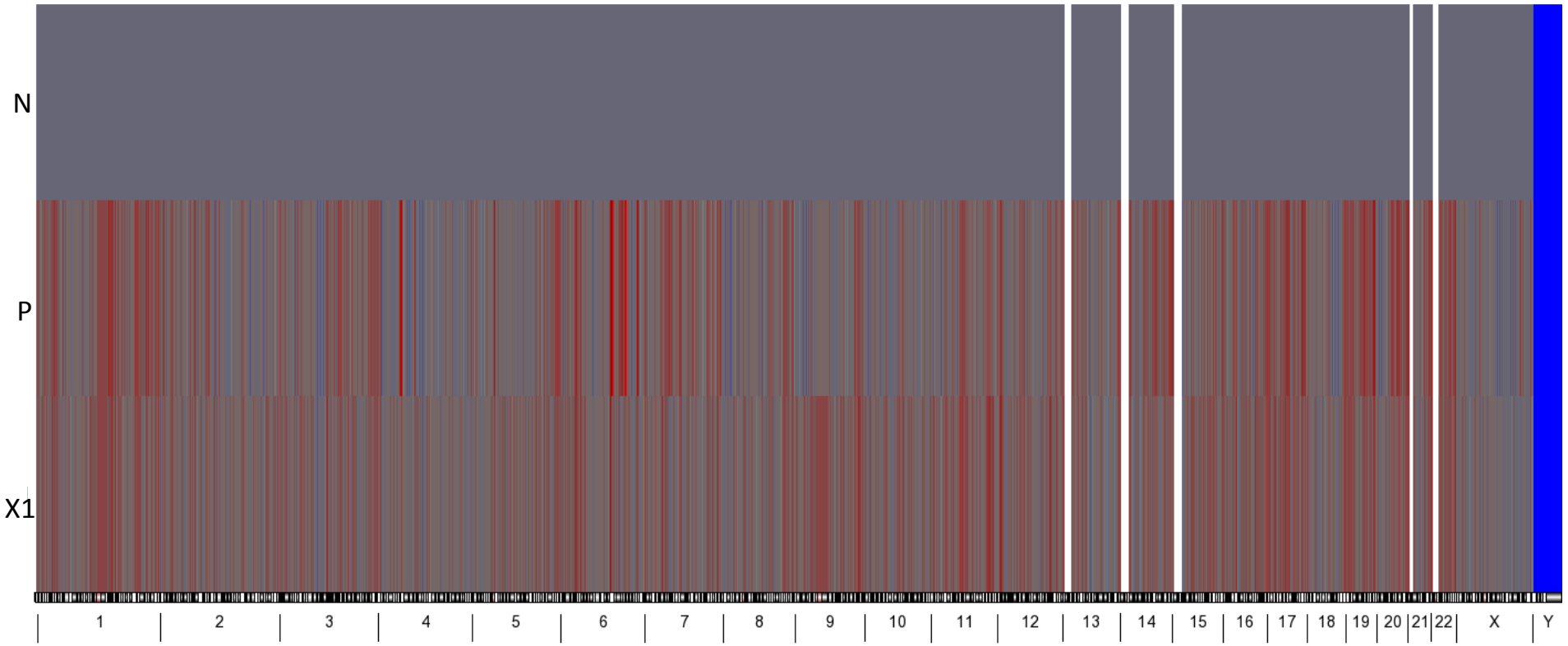

HCI-007




**Additional information for Supplementary Figure 26.** SNP array data indicating genome-wide DNA copy number points to the stability of tumor cells and subsequent tumor grafts from the same patient. Data are presented in the same manner as in Supplementary Figures 22-31, except that two samples and subsequent tumor grafts are shown from the same patient. HCI-005 was obtained first, and HCI-007 was obtained 8 months later, during a relapse (See Supplementary Table 1).

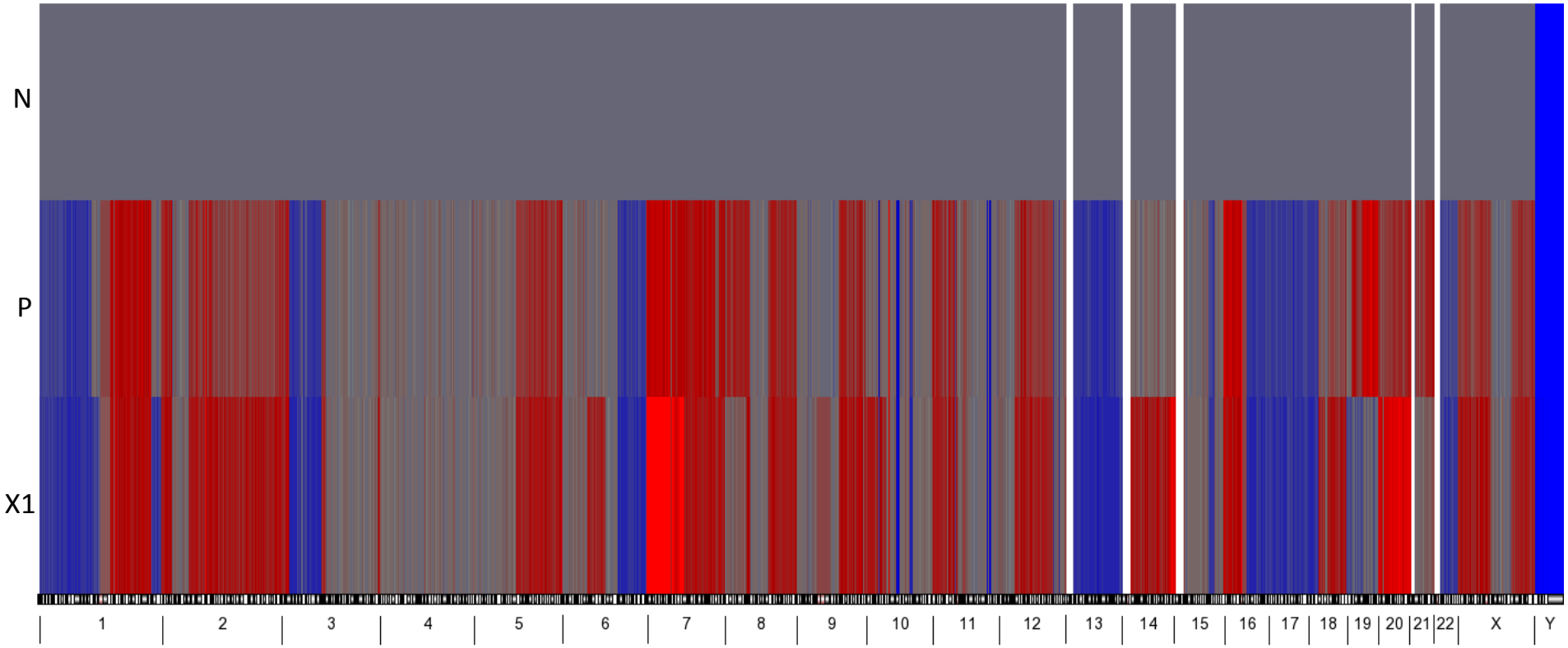
Supplementary Figure 27

HCI-008



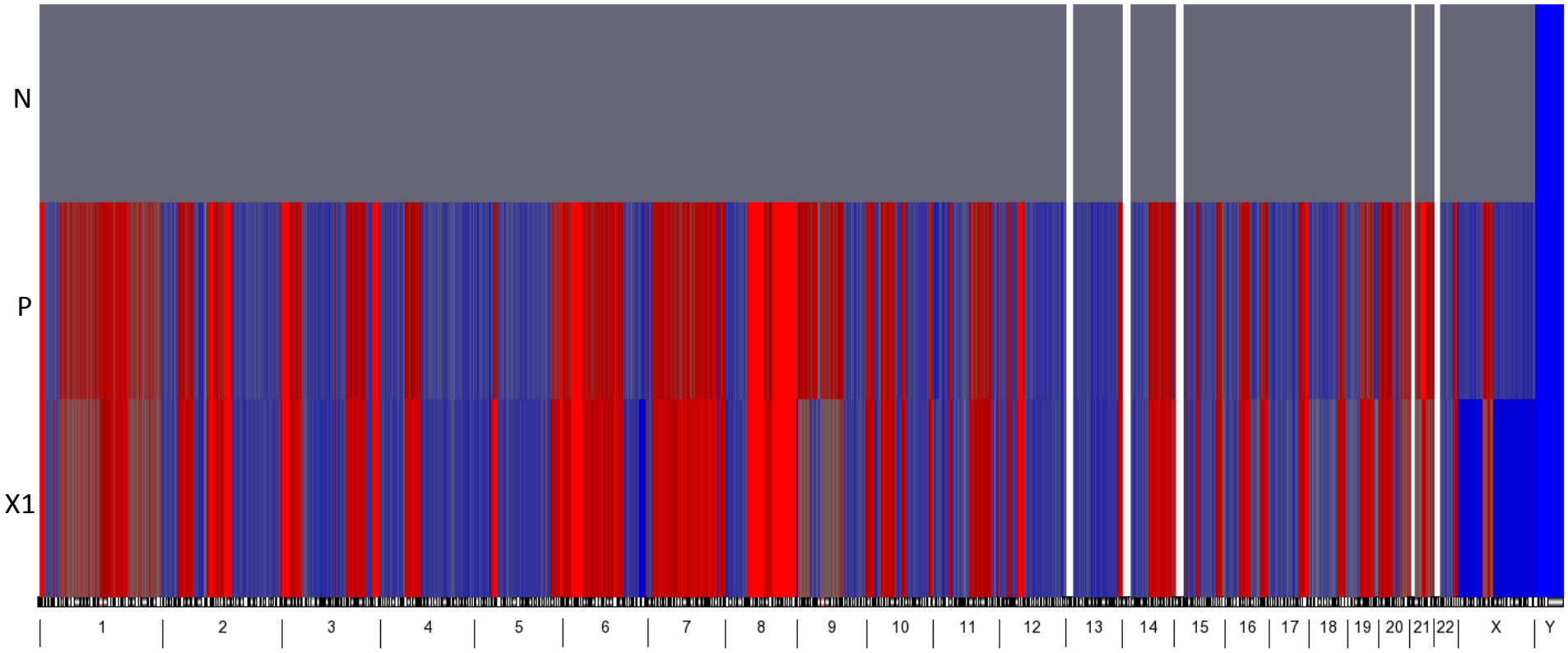
Supplementary Figure 28

HCI-009



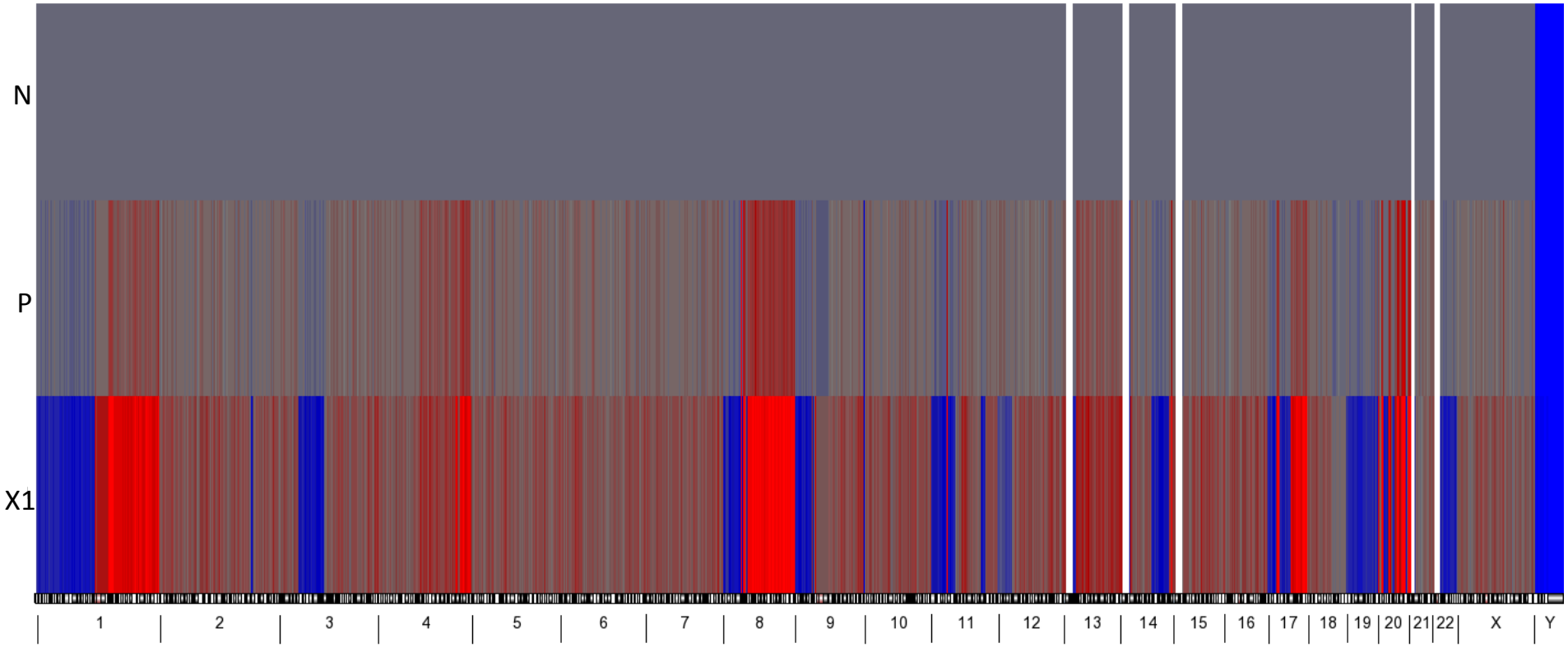
Supplementary Figure 29

HCI-010



Supplementary Figure 30

HCI-011



Supplementary Figure 31

HCI-012