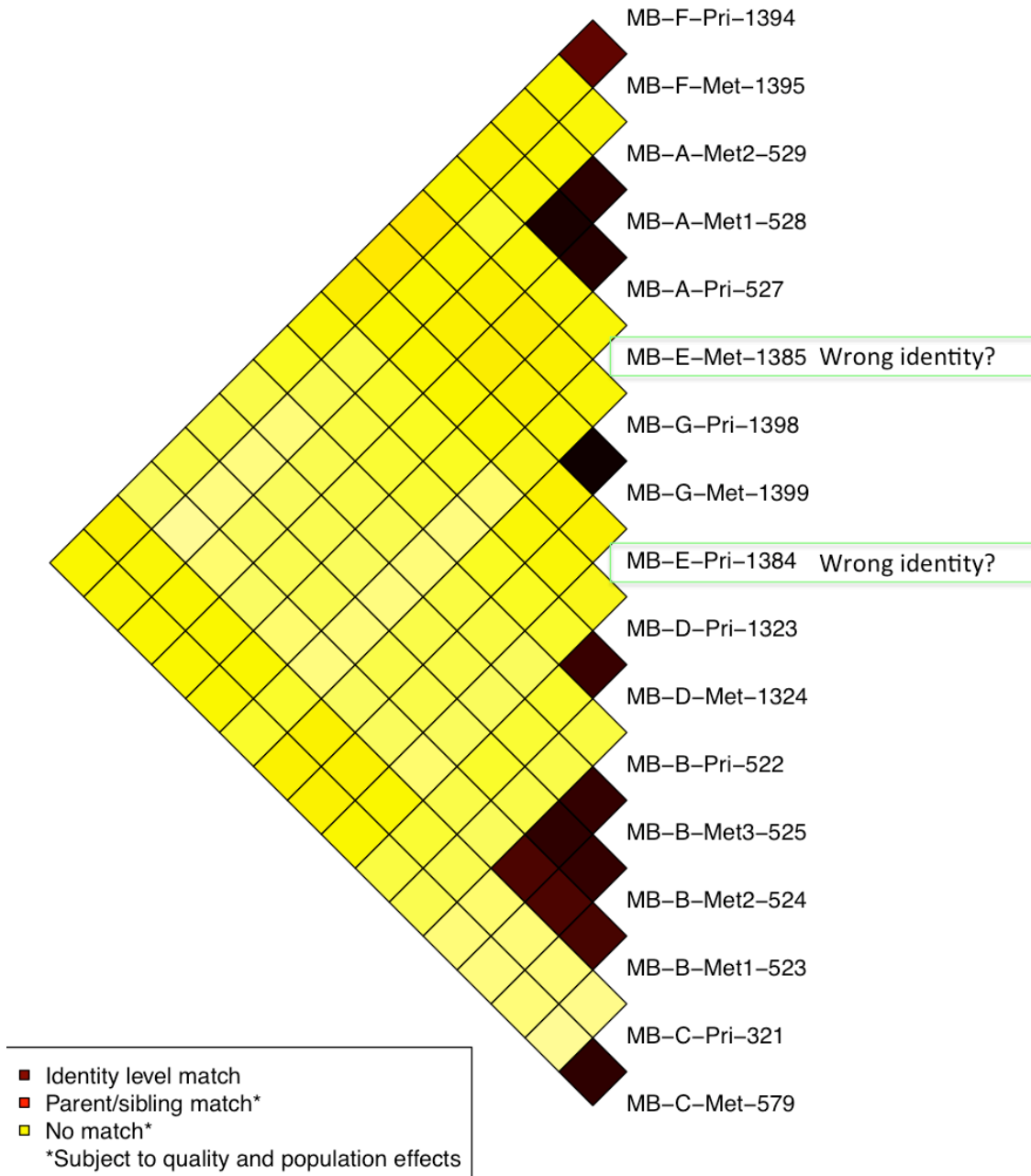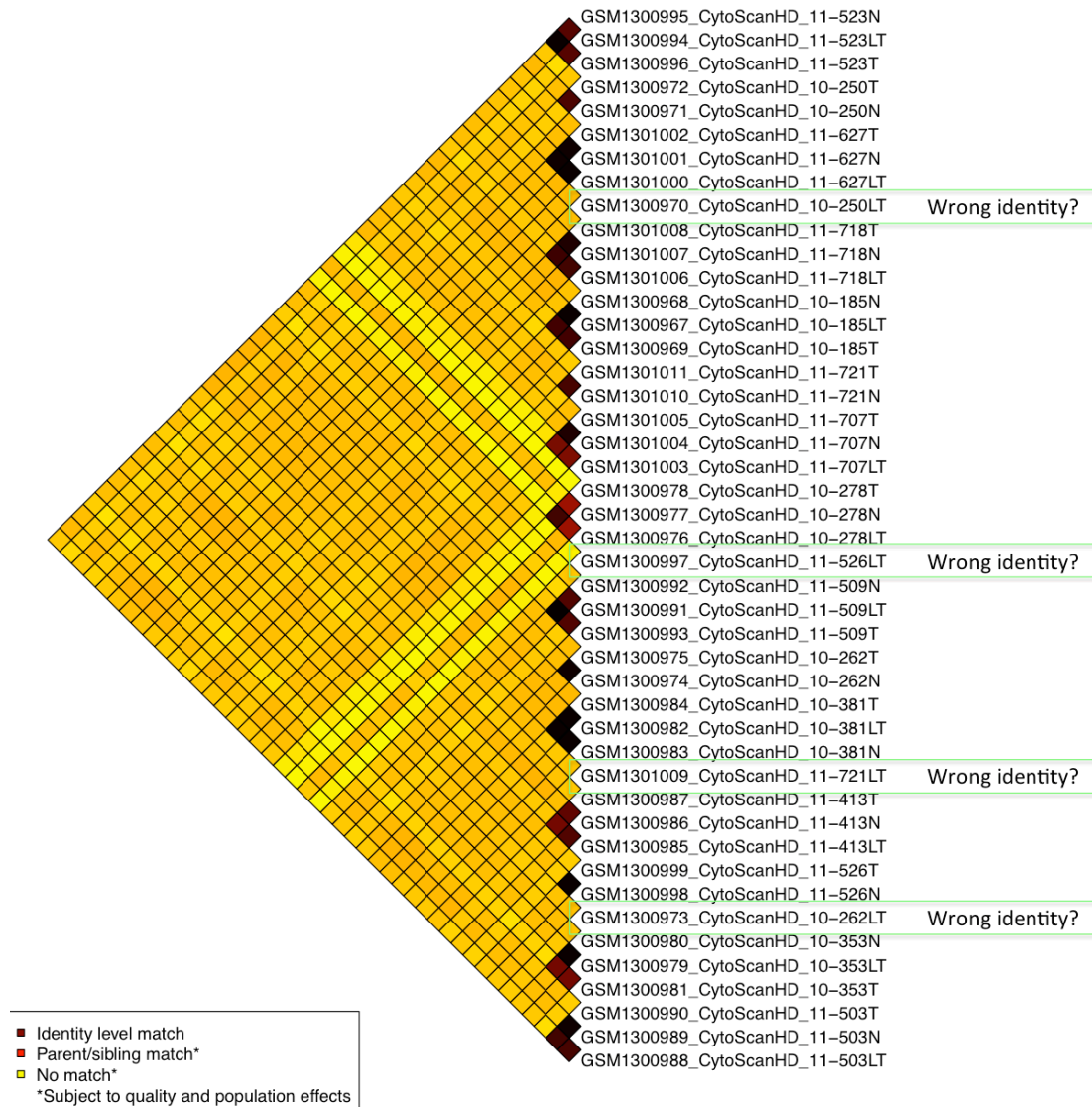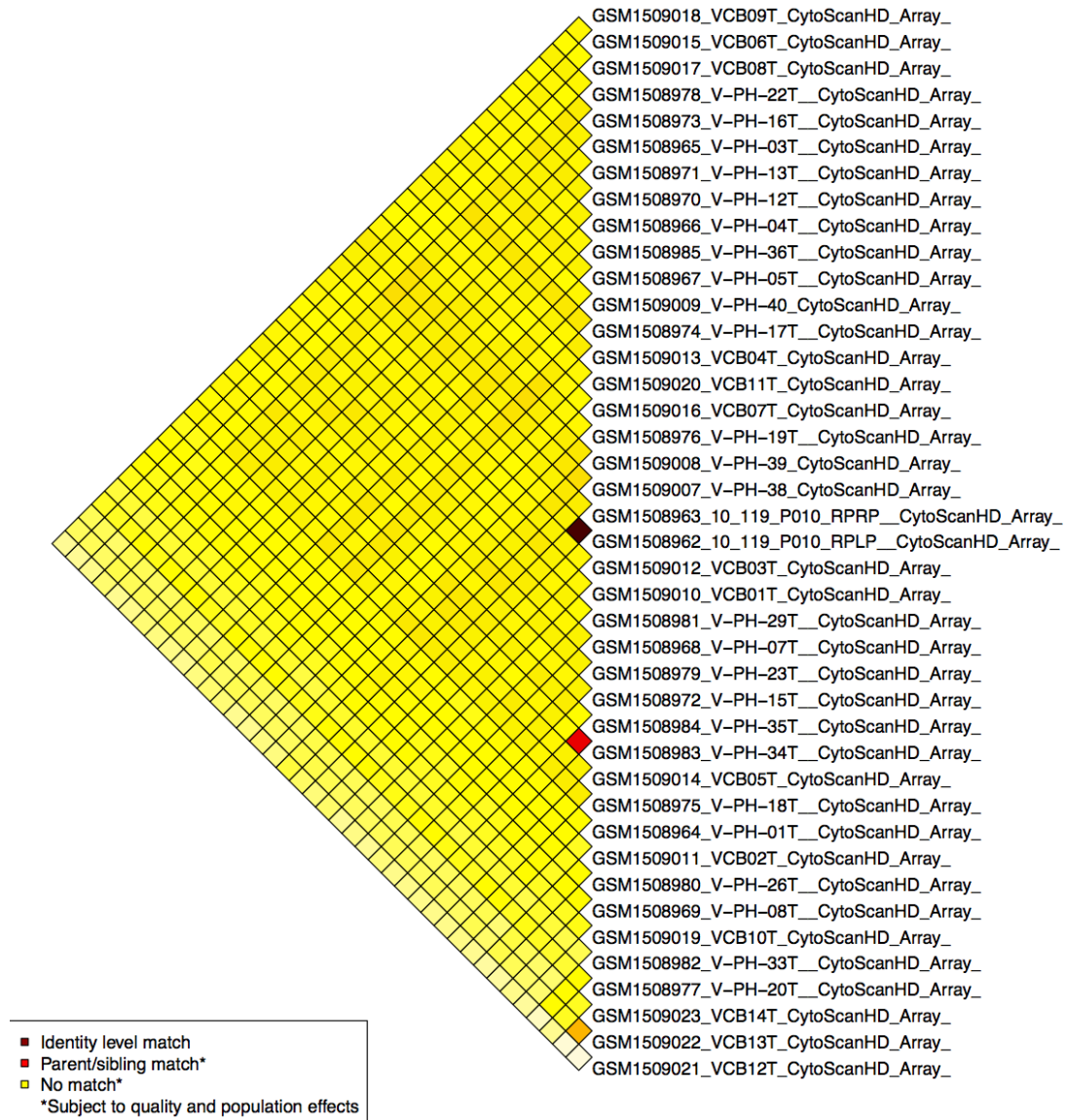# Examples of Rawcopy sample set distograms

Example 1. Medulloblastoma samples, with multiple samples per patient (GEO:GSE34280). Sample sets A, B, C, D and F all match properly, while sample set E appears unmatched with their genetic dissimilarity equal to that of any unmatched pair of samples in the study.

GSM1300995_CytoScanHD_11−523N
GSM1300994_CytoScanHD_11−523LT
GSM1300996_CytoScanHD_11−523T
GSM1300972_CytoScanHD_10−250T
GSM1300971_CytoScanHD_10−250N
GSM1301002_CytoScanHD_11−627T
GSM1301001_CytoScanHD_11−627N
GSM1301000_CytoScanHD_11−627LT
GSM1300970_CytoScanHD_10−250LT — Wrong identity?
GSM1301008_CytoScanHD_11−718T
GSM1301007_CytoScanHD_11−718N
GSM1301006_CytoScanHD_11−718LT
GSM1300968_CytoScanHD_10−185N
GSM1300967_CytoScanHD_10−185LT
GSM1300969_CytoScanHD_10−185T
GSM1301011_CytoScanHD_11−721T
GSM1301010_CytoScanHD_11−721N
GSM1301005_CytoScanHD_11−707T
GSM1301004_CytoScanHD_11−707N
GSM1301003_CytoScanHD_11−707LT
GSM1300978_CytoScanHD_10−278T
GSM1300977_CytoScanHD_10−278N
GSM1300976_CytoScanHD_10−278LT
GSM1300997_CytoScanHD_11−526LT — Wrong identity?
GSM1300992_CytoScanHD_11−509N
GSM1300991_CytoScanHD_11−509LT
GSM1300993_CytoScanHD_11−509T
GSM1300975_CytoScanHD_10−262T
GSM1300974_CytoScanHD_10−262N
GSM1300984_CytoScanHD_10−381T
GSM1300982_CytoScanHD_10−381LT
GSM1300983_CytoScanHD_10−381N
GSM1301009_CytoScanHD_11−721LT — Wrong identity?
GSM1300987_CytoScanHD_11−413T
GSM1300986_CytoScanHD_11−413N
GSM1300985_CytoScanHD_11−413LT
GSM1300999_CytoScanHD_11−526T
GSM1300998_CytoScanHD_11−526N
GSM1300973_CytoScanHD_10−262LT — Wrong identity?
GSM1300980_CytoScanHD_10−353N
GSM1300979_CytoScanHD_10−353LT
GSM1300981_CytoScanHD_10−353T
GSM1300990_CytoScanHD_11−503T
GSM1300989_CytoScanHD_11−503N
GSM1300988_CytoScanHD_11−503LT

■ Identity level match
■ Parent/sibling match*
□ No match*
*Subject to quality and population effects

Example 2. Colon cancer primary tumour and metastasis tissue samples and matched normals (GEO:GSE53799). The background dissimilarity between any two samples is slightly smaller than expected by Rawcopy as an effect of ethnicity. All samples group as expected in sets of three except for metastasis samples of patients 250, 262, 526 and 721, which appear unrelated to their respective primary tumour tissue and normal DNA.
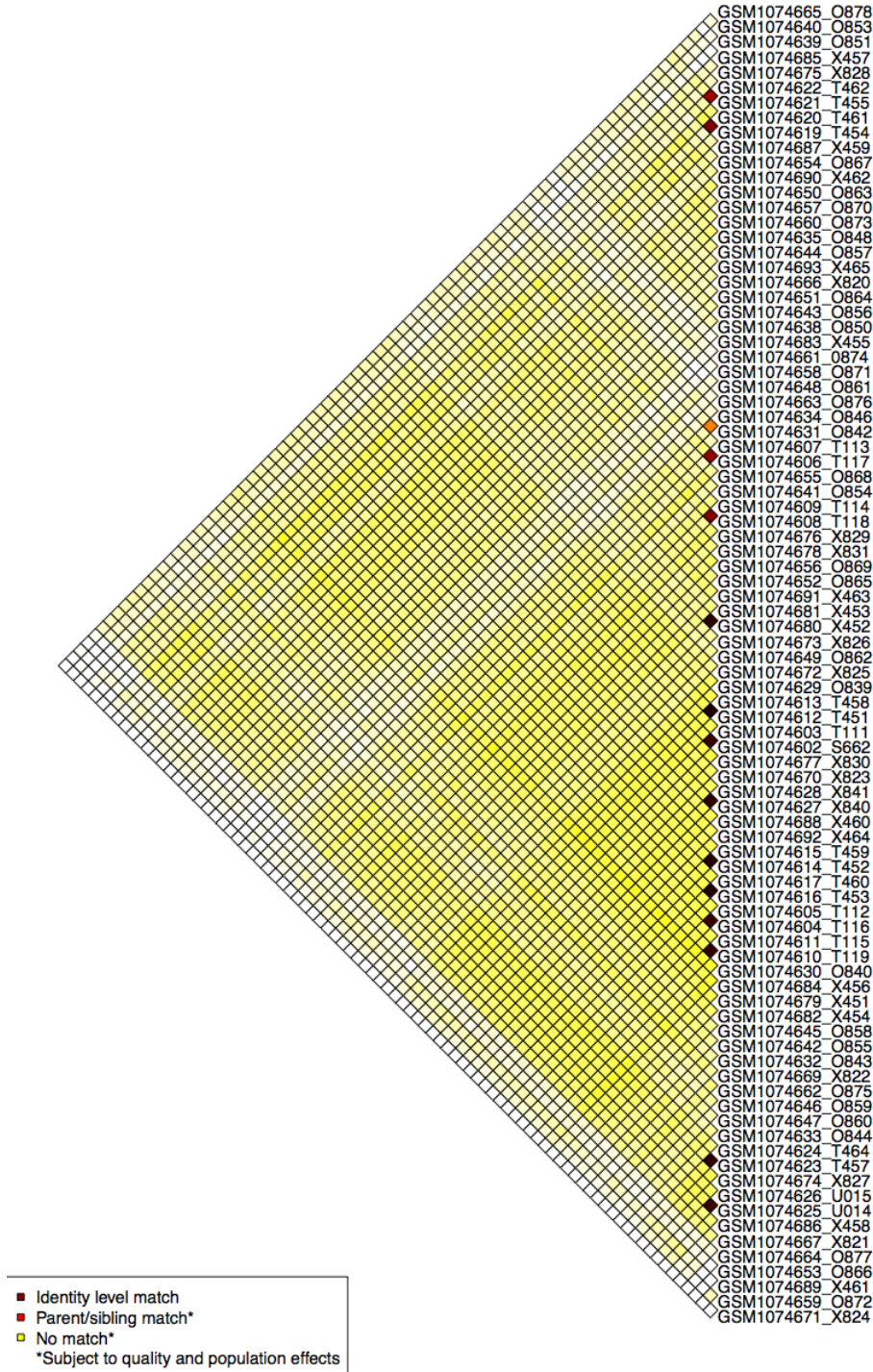
Example 3. Circulating tumour cells in metastatic melanoma (GEO:GSE43934). The dissimilarity between any two samples is somewhat lower than expected, likely due to variations in DNA quality. 14 pairs of samples are indicated as patient-matched (black or dark red). One pair is indicated as similar (O842-O846). A closer look at their copy number profiles indicated the same tumour but with some quality issues with O842 (not shown).

GSM1509018_VCB09T_CytoScanHD_Array_
GSM1509015_VCB06T_CytoScanHD_Array_
GSM1509017_VCB08T_CytoScanHD_Array_
GSM1508978_V–PH–22T__CytoScanHD_Array_
GSM1508973_V–PH–16T__CytoScanHD_Array_
GSM1508965_V–PH–03T__CytoScanHD_Array_
GSM1508971_V–PH–13T__CytoScanHD_Array_
GSM1508970_V–PH–12T__CytoScanHD_Array_
GSM1508966_V–PH–04T__CytoScanHD_Array_
GSM1508985_V–PH–36T__CytoScanHD_Array_
GSM1508967_V–PH–05T__CytoScanHD_Array_
GSM1509009_V–PH–40_CytoScanHD_Array_
GSM1508974_V–PH–17T__CytoScanHD_Array_
GSM1509013_VCB04T_CytoScanHD_Array_
GSM1509020_VCB11T_CytoScanHD_Array_
GSM1509016_VCB07T_CytoScanHD_Array_
GSM1508976_V–PH–19T__CytoScanHD_Array_
GSM1509008_V–PH–39_CytoScanHD_Array_
GSM1509007_V–PH–38_CytoScanHD_Array_
GSM1508963_10_119_P010_RPRP__CytoScanHD_Array_
GSM1508962_10_119_P010_RPLP__CytoScanHD_Array_
GSM1509012_VCB03T_CytoScanHD_Array_
GSM1509010_VCB01T_CytoScanHD_Array_
GSM1508981_V–PH–29T__CytoScanHD_Array_
GSM1508968_V–PH–07T__CytoScanHD_Array_
GSM1508979_V–PH–23T__CytoScanHD_Array_
GSM1508972_V–PH–15T__CytoScanHD_Array_
GSM1508984_V–PH–35T__CytoScanHD_Array_
GSM1508983_V–PH–34T__CytoScanHD_Array_
GSM1509014_VCB05T_CytoScanHD_Array_
GSM1508975_V–PH–18T__CytoScanHD_Array_
GSM1508964_V–PH–01T__CytoScanHD_Array_
GSM1509011_VCB02T_CytoScanHD_Array_
GSM1508980_V–PH–26T__CytoScanHD_Array_
GSM1508969_V–PH–08T__CytoScanHD_Array_
GSM1509019_VCB10T_CytoScanHD_Array_
GSM1508982_V–PH–33T__CytoScanHD_Array_
GSM1508977_V–PH–20T__CytoScanHD_Array_
GSM1509023_VCB14T_CytoScanHD_Array_
GSM1509022_VCB13T_CytoScanHD_Array_
GSM1509021_VCB12T_CytoScanHD_Array_

- ■ Identity level match
- ■ Parent/sibling match*
- □ No match*
  *Subject to quality and population effects

Example 4. Phaeochromocytoma samples (GEO:GSE61594). The two patient-matched tumour samples are clearly indicated (black). Two other pairs are indicated as similar. Inspection of copy number profiles indicated separate copy number profiles and no DNA contamination. Patient data published with the study confirmed that two patients are siblings (red).
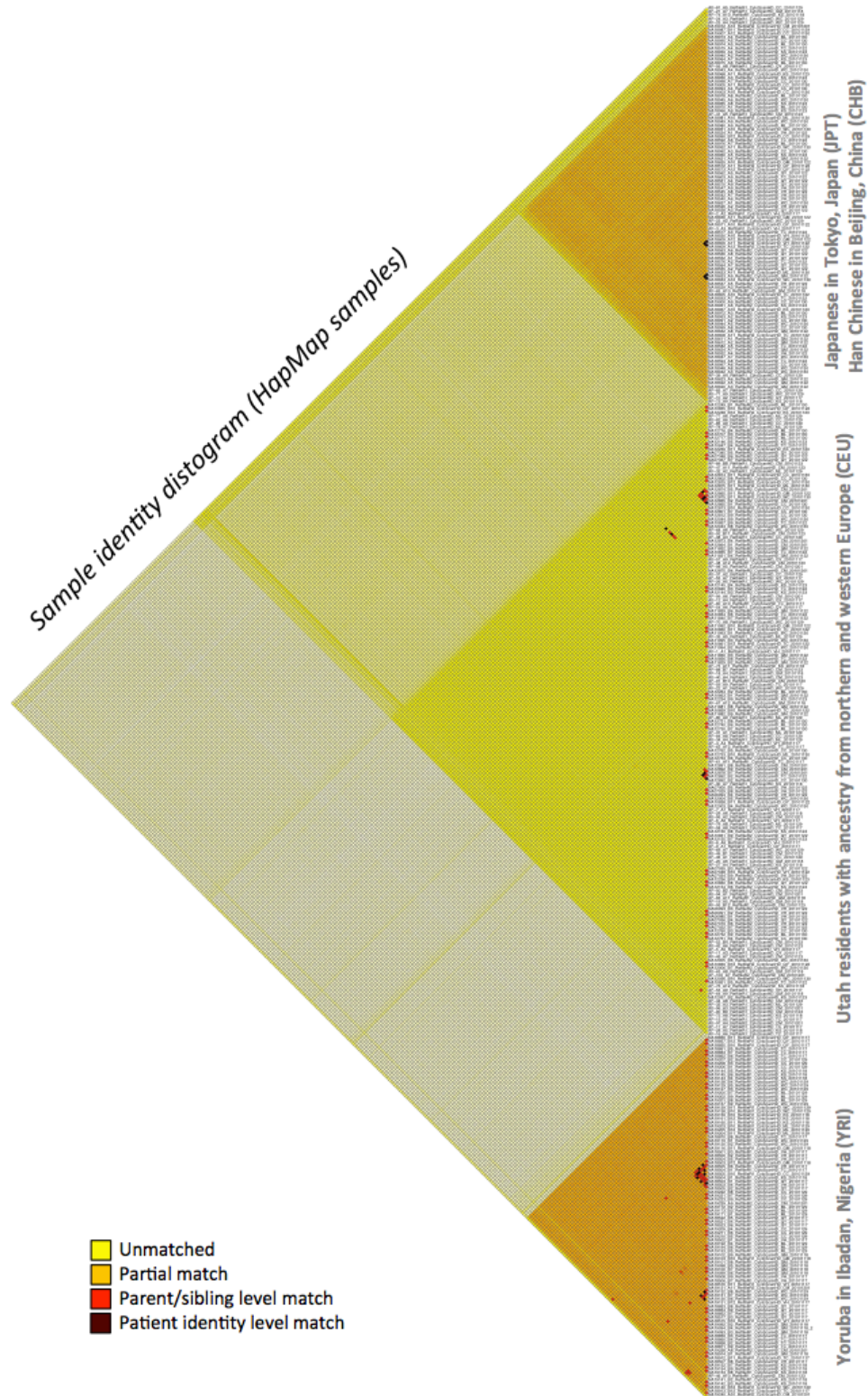
Example 5. Sample identity distogram with HapMap samples analyzed on the CytoScan HD array. The genetic dissimilarities are affected by both genetic background and familial relationship.