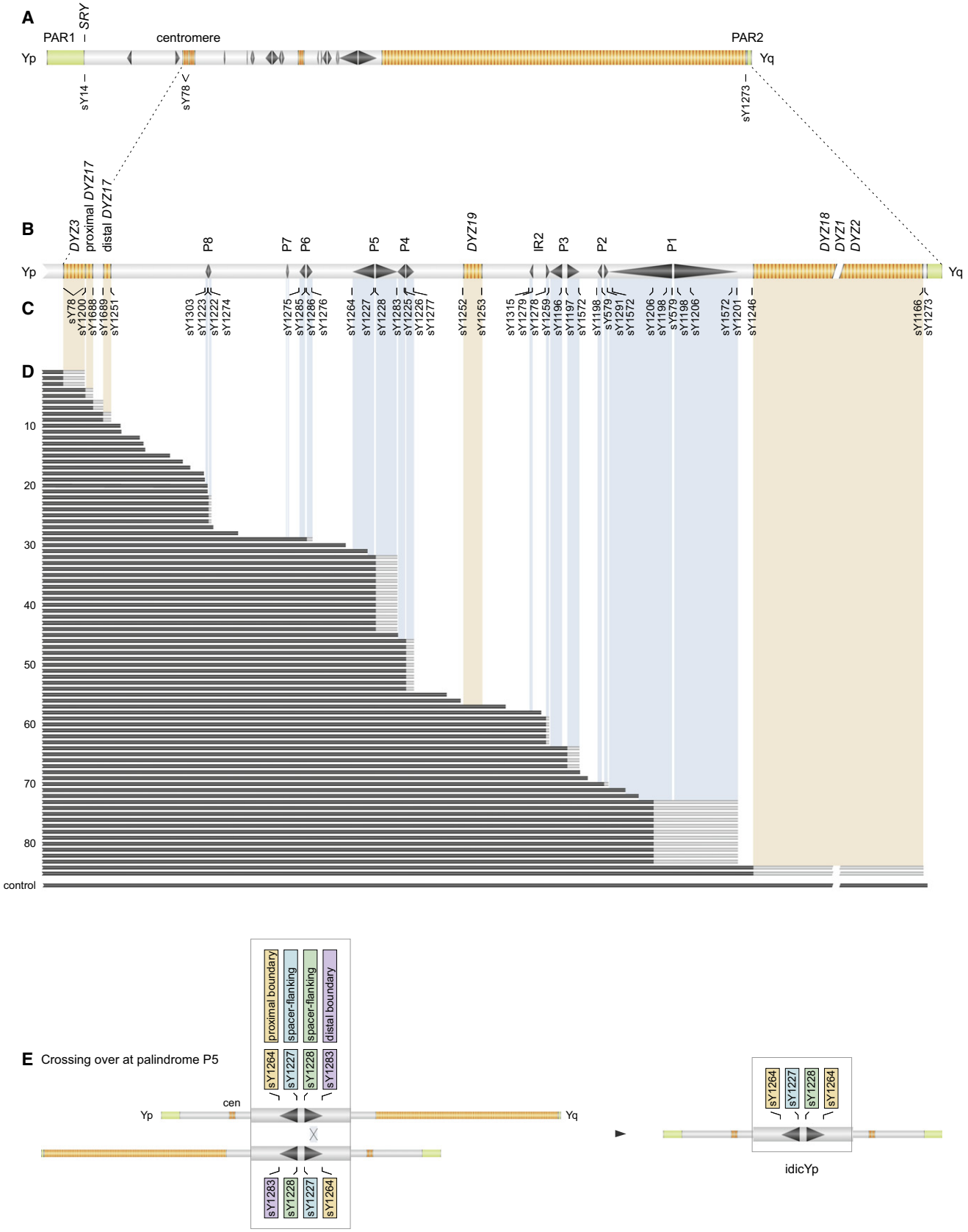
A
PAR1
SRY
centromere
PAR2
Yp
Yq
sY14
sY78
sY1273
B
DYZ3
proximal DYZ17
distal DYZ17
P8
P7
P6
P5
P4
DYZ19
IR2
P3
P2
P1
DYZ18
DYZ1
DYZ2
C
D
control
E Crossing over at palindrome P5
proximal boundary
spacer-flanking
spacer-flanking
distal boundary
cen
idicYp

Figure 2. STS Content of Structurally Anomalous Y Chromosomes in 85 Patients with Deletion Breakpoints in Yq or Centromere

(A) Locations of three STSs assayed in initial screen for Yq or centromeric breakpoints.

(B) Expanded view of centromere and Yq, with palindromes P1–P8, inverted repeat IR2, and heterochromatic blocks (orange).

(C) STSs employed in fine-mapping of breakpoints. These include boundary and spacer-flanking markers for each palindrome and inverted repeat, and markers around each heterochromatic block.

(D) Results of testing DNAs from 85 patients for presence or absence of STSs. Solid black bars encompass STSs found to be present. Gray bars indicate breakpoint intervals that could not be further narrowed because of cross-amplification at other loci. See Figure S2 for identifiers of patients tested.

(E) Predicted molecular signature of idicYp formed by homologous recombination between sister chromatids at palindrome P5. Thirteen individuals with this molecular signature are shown in (D).