



**Figure S2:** Mean genomic proportion contained in IBD segments versus mean genomic proportion contained in ROH segments. **(A)** Autosomes. **(B)** X chromosome. Thirteen populations are color-coded by regional group as in Kang *et al.* (2016) and Severson *et al.* (2019): Ethiopian, orange; European, blue; Middle Eastern, brown; North African, yellow; Yemenite, green. Population labels: Al, Algerian; As, Ashkenazi; Az, Azerbaijani; E, Ethiopian; Iq, Iraqi; Ir, Iranian; It, Italian; K, Kurdish; Mo, Moroccan; Se, Sephardi; T, Tunisian; U, Uzbekistani; Y, Yemenite. The regression equation is  $y = 0.074x - 0.002$  ( $R^2 = 0.27$ ,  $P = 0.07$ ) for autosomes and  $y = 0.068x - 0.005$  ( $R^2 = 0.49$ ,  $P = 0.008$ ) for the X chromosome. Both plots use the 13 Jewish populations with ROH data available for the X chromosome.