

S3_Table: Comparison of ePAR haplotype structures with phase-known X chromosomes - summary data

	block A	block B	block C	block D	block E	block F	block G	block H	block I
no. SNPs:	6	47	11	29	19	29	41	7	
hg19 (chr X) start:	2699645	2702047	2724389	2732634	2748292	2767637	2778322	2792662	2800000
hg19 (chr X) end:	2700202	2718189	2729346	2741406	2759615	2775601	2786038	2798480	2806000
no. different haplotypes amongst:									
I2a ePAR (n=10)	2	7	2	3	1	4	4	2	
R1b ePAR (n=1)	1	1	1	1	1	1	1	1	
CEU (n=49)	5	20	5	9	4	13	11	6	
GBR (n=46)	6	17	5	6	4	11	9	5	
no. unique haplotypes amongst:									
I2a ePAR (n=10)	0	4	0	2	0	2	1	0	
R1b ePAR (n=1)	0	1	0	0	0	1	0	0	
CEU (n=49)	0	12	2	5	0	6	4	3	
GBR (n=46)	1	9	2	2	1	5	2	5	
% I2a ePAR shared with:									
CEU	100	54.5	100	81.8	100	72.7	90.9	100	90.9
GBR	100	54.5	100	81.8	100	72.7	90.9	100	90.9
% CEU haplotypes shared with:									
all ePARs	69.4	49.0	89.8	55.1	67.3	16.3	69.4	55.1	40.0
GBR	100	71.4	91.8	89.8	100	81.6	91.8	83.7	70.0
% GBR haplotypes shared with:									
all ePARs	73.9	45.7	89.1	45.7	60.9	17.4	50.0	80.4	60.0
CEU	97.8	76.1	91.3	93.5	97.8	84.8	84.8	91.3	80.0

Adjacent blocks of markers are separated by clusters of mapped meiotic DSBs as reported in Pratto *et al.* 2014 *Science* 346: 1256442.

NOTE: To lift over to hg38 add 81959 to hg19 co-ordinate