

Table S4. Significantly enriched Gene Ontology (GO) terms in the top empirical 1% and 5% of windows in each population.

Population	Statistic	GO term	Name of GO term	p value	Windows	Genes
Biaka Pygmy	XP-EHH CEU (0.05)	GO:0016571	histone methylation	0	6	<i>MEN1, EED, PRMT8, SUV420H2, NSD1, EHMT1</i>
	XP-EHH CEU (0.05)	GO:0007089	traversing start control point of mitotic cell cycle	5×10^{-5}	5	<i>CDK2, MDM2, CDC6, CDC25C, MTBP</i>
Namibian San	XP-EHH CEU (0.01)	GO:0006898 (P)	receptor-mediated endocytosis	0.00045	5	<i>PICALM, ASGR1, LRP1B, DAB2, IGF2R</i>
≠Khomani Bushmen	XP-EHH CEU (0.05)	GO:0006355	regulation of transcription, DNA-dependent	0.0	180	
Bantu SA	XP-EHH YRI (0.01)	GO:0006977	DNA damage response, signal transduction by p53 class mediator, cell cycle arrest	5×10^{-5}	3	<i>PML, GTSE1, GML</i>
Bantu Kenya	XP-EHH CEU (0.05)	GO:0030178	negative regulation of Wnt signaling pathway	5×10^{-5}	7	<i>DKK1, LRP1, GSC, TAX1BP3, FRZB, TLE1, BARX1</i>
Mandenka	iHS (0.01)	GO:002504 (also P)	antigen processing and presentation of peptide or polysaccharide via MHC Class II	0	3	<i>HLA-DRB5, HLA-DQB2, HLA-DPA1</i>
	iHS (0.01)	GO:0019882 (also P)	antigen processing	5×10^{-5}	5	<i>CD1A, HFE, HLA-DRB5, HLA-DQB2, HLA-DPA1</i>
	iHS (0.01)	GO:0015031 (P)	protein transport	0.00145	17	
	XP-EHH CEU (0.01)	GO:0006807 (P)	nitrogen compound metabolic process	0.00015	4	<i>NIT1, GLUL, NIT2, VNN1, VNN3</i>
	XP-EHH CEU (0.01)	GO:0006366 (P)	transcription from RNA polymerase II promoter	0.0009	8	<i>USF1, TRIM29, YBX2, HLF, SNAPC2, BAPX1, CREB5, POU6F2</i>
Yoruba	XP-EHH CEU (0.01)	GO:0007417	central nervous system development	5×10^{-5}	9	<i>ACCN1, NPTX1, NPAS1, ADAM23, DNER, CHRDL, PARK2, POU6F2, GLI3</i>
HapMap YRI	XP-EHH CEU (0.01)	GO:0045786	negative regulation of cell cycle	0.0186	2	<i>HRASLS3, MOV10L1</i>
	XP-EHH CEU (0.01)	GO:0006366 (P)	transcription from RNA polymerase II promoter	0.00015	9	<i>PRDM4, MAF, MN1, YBX2, NFIX, BAPX1, CREB5, POU6F2, GATA4</i>
	XP-EHH MKK (0.01)	GO:0055088	lipid homeostasis	5×10^{-5}	3	<i>USF1, USF2, PPARG</i>
	XP-EHH MKK (0.01)	GO:0000432	positive regulation of transcription from RNA polymerase II promoter by glucose	0.0001	2	<i>USF1, USF2</i>
	XP-EHH MKK (0.01)	GO:0009991	response to extracellular stimulus	0.00025	2	<i>RASGRP4, RPS19</i>
	XP-EHH KHB (0.01)	GO:0009991	response to extracellular stimulus	0.0	2	<i>RASGRP4, RPS19</i>

Significance determined as described in Methods, using an FDR cutoff of 0.05, within each population. The "Statistic" column indicates the statistic resulting in significance; the numbers in parentheses after the statistic indicate the empirical tail for which an enrichment was tested (top 0.001 are shown in the main text). Significant GO terms are indicated in the "GO Term" column. Next to a GO term, "(P)" indicates that the term is only significant when examining the PANTHER subset of terms; "(also P)" indicates that the term is significant both when examining PANTHER terms and when examining all GO terms; if nothing is next to the term, it indicates significance only when all GO terms are examined. We count the number of windows in the indicated empirical tail to which each term was associated ("Windows" column); rather than reporting those windows, we report the genes within those windows that were associated with the given GO term (in the "Genes" column).