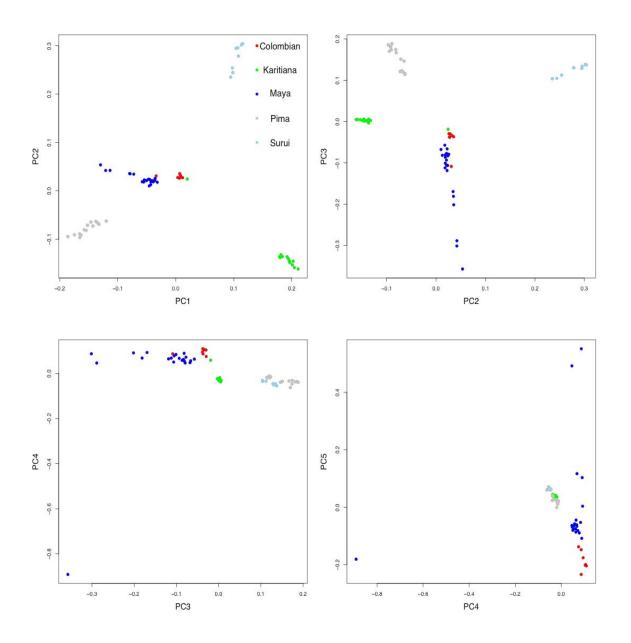
## **Supplemental Data**

## **Genome-wide Insights into the Patterns and Determinants**

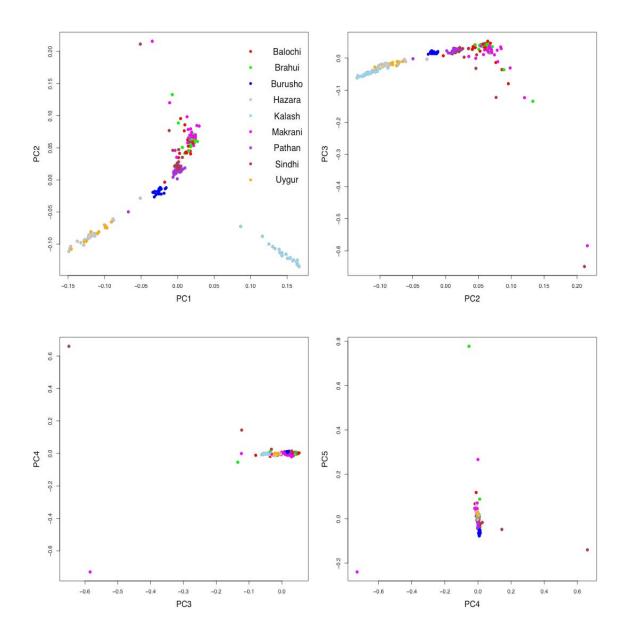
## of Fine-Scale Population Structure in Humans

Shameek Biswas, Laura B. Scheinfeldt, and Joshua M. Akey

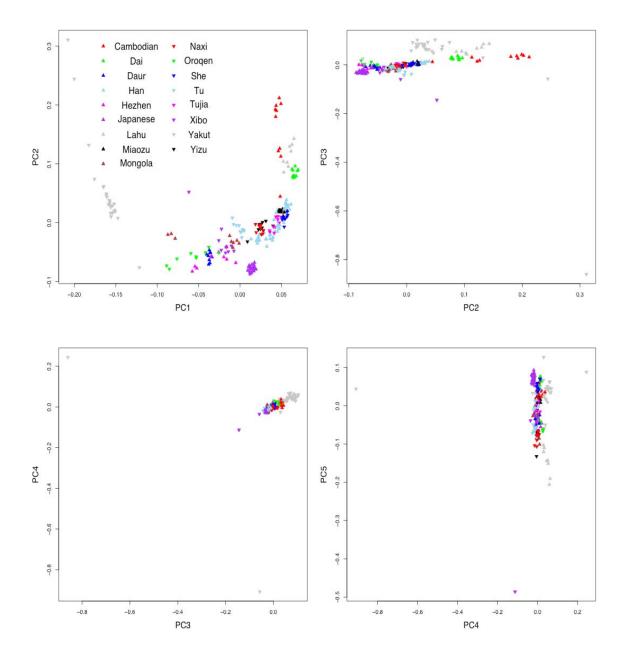
**Figure S1 Intra-continental differentiation within Americas.** The 64 samples are represented as filled circles. The top five PCs are plotted with each panel representing a biplot of consecutive PCs.



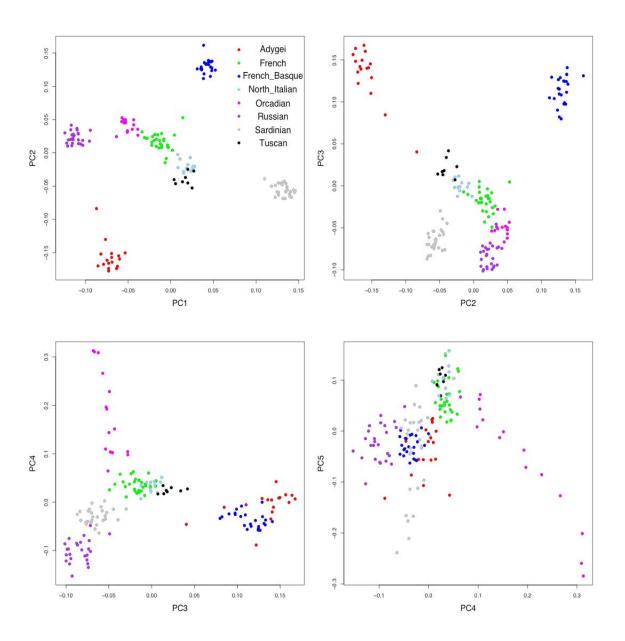
**Figure S2 Intra-continental differentiation within Central/South Asia.** The 201 samples are represented as filled circles. The top five PCs are plotted with each panel representing a biplot of consecutive PCs.



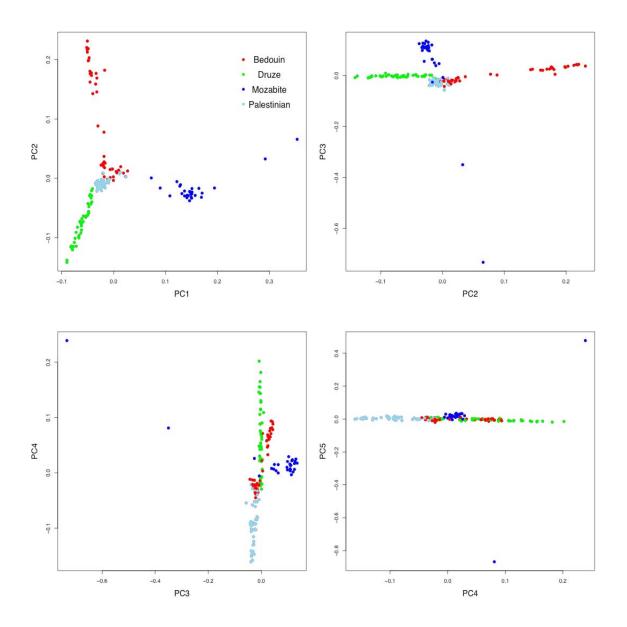
**Figure S3 Intra-continental differentiation within East Asia.** The 229 samples are represented as filled triangles. The top five PCs are plotted with each panel representing a biplot of consecutive PCs.



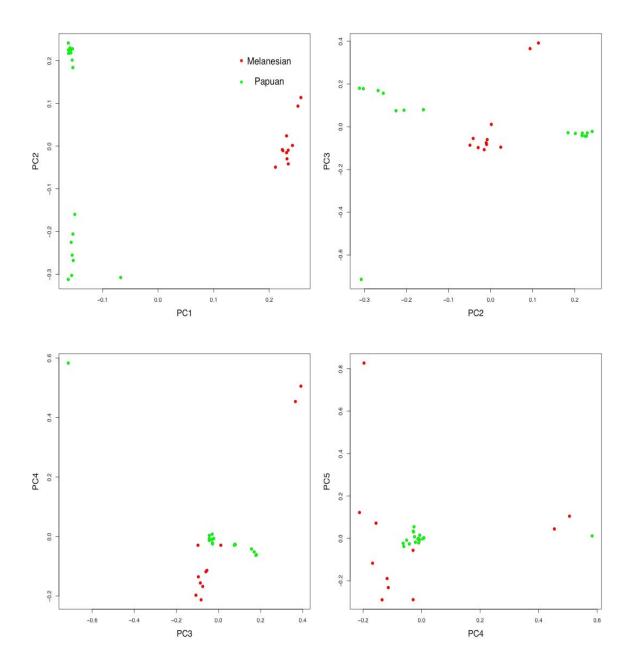
**Figure S4 Intra-continental differentiation within Europe.** The 158 samples are represented as filled circles. The top five PCs are plotted with each panel representing a biplot of consecutive PCs.



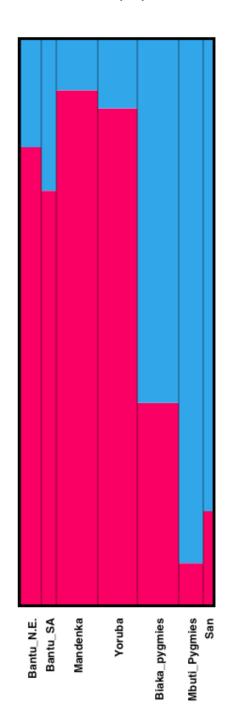
**Figure S5 Intra-continental differentiation within Middle East.** The 162 samples are represented as filled circles. The top five PCs are plotted with each panel representing a biplot of consecutive PCs.



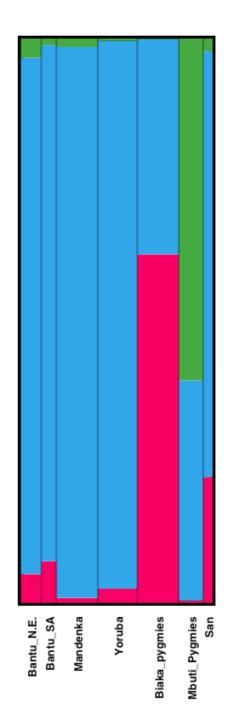
**Figure S6 Intra-continental differentiation within Oceania.** The 28 samples are represented as filled circles. The top five PCs are plotted with each panel representing a biplot of consecutive PCs.



**Figure S7 Cluster analysis of PC1 correlated markers in Africa.** Structure was used to cluster samples into two groups (K=2). 11, 811 correlated markers were used. Red and blue represent the two cluster proportions.



**Figure S8 Cluster analysis of PC2 correlated markers in Africa.** Structure was used to cluster samples into three groups (K=3). 1,446 correlated markers were used. Red, blue and green represent the three cluster proportions.



**Table S1. HGDP-CEPH Populations** Details about the sample sizes and population membership of individuals that were included in the analysis.

		#
Region	Population	Chr
	Bantu_N.E.	22
	Bantu_SA	16
	Biaka_pygmies	44
	Mandenka	44
	Mbuti_Pygmies	26
	San	10
Africa	Yoruba	42
	Bedouin	90
-	Druze	84
-	Mozabite	58
Middle East	Palestinian	92
	Adygei	34
	French	56
	French_Basque	48
-	North Italian	26
-	Orcadian	30
-	Russian	50
-	Sardinian	56
Europe	Tuscan	16
1	Balochi	48
-	Brahui	50
	Burusho	50
	Hazara	44
-	Kalash	46
	Makrani	50
	Pathan	46
Central/South	Sindhi	48
Asia	Uygur	20
East Asia	Cambodian	20
	Dai	20
	Daur	18
	Han	88
	Hezhen	18
	Japanese	56
	Japanese	
	Lahu	16

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	Naxi	16
	Oroqen	18
	She	20
	Tu	20
	Tujia	20
	Xibo	18
	Yakut	50
	Yizu	20
	Colombian	14
	Karitiana	28
	Maya	42
	Pima	28
America	Surui	16
	Melanesian	22
Oceania	Papuan	34

Continent	Populations	Method	
		Permutation	ANOVA
All	52	12	22
Africa	7	4	5
America	5	7	4
C/S Asia	9	5	4
East Asia	17	5	7
Europe	8	3	4
Middle East	4	5	4
Oceania	2	3	1

**Table S2. Significance Analysis of PCs** Number of significant PCs (p < 0.001) using two different methods