Supplemental Data

Inferring Human Demographic Histories

of Non-African Populations

from Patterns of Allele Sharing

Jeffrey D. Wall

Table S1. Proportion of sites supporting each topology (cf. Figure 2) for simulated sequence data. T_{AM} is the East Asian – Melanesian split time (in Kya), T_{EA} is the European – East Asian split time (in Kya), Ghost is the % ancestry in Melanesians inherited from an early Out of Africa 'ghost' population, EA Admix is the time (in Kya) of a one-way pulse migration event from East Asians into Melanesians, and Admix % is the % ancestry in Melanesians recently inherited from East Asian migrants. There are two sets of output values: the "No D" results use the site conditioning described in the text (which among other criteria excludes all sites not homozygous ancestral in the Denisovan genome). The "D" results remove the conditioning on the Denisovan genome (but retain the criteria of excluding sites that are not homozygous ancestral in 21 West/Central Africans and the Neanderthal). Blank entries for parameter values are identical to the value in the line above.

T_{AM}	T_{EA}	Ghost	EA Admix	Admix %	No D			D		
					P_{EA} (%)	P_{EM} (%)	P_{AM} (%)	P_{EA} (%)	P_{EM} (%)	P_{AM} (%)
40	30	2	20	20	36.7	31.1	32.3	36.6	31.1	32.3
				50	34.7	31	34.3	34.6	31	34.3
				80	33.1	31.5	35.4	33.1	31.6	35.3
				90	32.4	31.5	36.1	32.4	31.5	36.1

			10	80	31.2	30.3	38.5	31.3	30.3	38.4
				90	30.4	30	39.6	30.4	30	39.6
	60	0	---	0	29.9	28.8	41.4	29.8	28.9	41.3
		2			30	28.9	41	30	29.1	41
		5			30.7	29.1	40.2	30.5	29.3	40.2
	55	0			31.4	29.8	38.8	31.3	29.9	38.7
		2			31.1	30	38.8	31	30.1	38.8
		5			31.7	29.7	38.5	31.6	29.9	38.5
	50	0			32.6	30.8	36.6	32.4	30.9	36.7
		2			32.3	30.9	36.8	32.2	31	36.8
		5			32.7	30.9	36.4	32.6	30.9	36.4
45	50	2			33.4	31.7	34.9	33.3	31.8	34.9
	55				32.5	30.7	36.8	32.3	30.8	36.9
	60				31.1	30.1	38.8	30.9	30.2	38.9