Adam and Eve never met 😞

The same is true for ancestral rRNAs, EF, ATPases!
Humans as Hybrids

Genetic analysis of ancient bones, including a girl’s finger bone found in a Siberian cave, suggests that modern humans encountered and bred with Neanderthals and Denisovans, two of the other human groups still living some 30,000 years ago.

From: http://www.nytimes.com/2012/01/31/science/gains-in-dna-are-speeding-research-into-human-origins.html?_r=1
The multiregional hypothesis

From http://en.wikipedia.org/wiki/Multiregional_Evolution
Archaic human admixture with modern Homo sapiens

An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia

Morten Rasmussen, Xiaosen Guo, Yong Wang, Kirk E. Lohmueller, Simon Rasmussen.
Ancient migrations. The proportions of Denisovan DNA in modern human populations are shown as red in pie charts, relative to New Guinea and Australian Aborigines (3). Wallace's Line (8) is formed by the powerful Indonesian flow-through current (blue arrows) and marks the limit of the Sunda shelf and Eurasian placental mammals.
For more discussion on archaic and early humans see:
http://en.wikipedia.org/wiki/Denisova_hominin


http://www.abc.net.au/science/articles/2012/08/31/3580500.htm

http://www.sciencemag.org/content/334/6052/94.full
http://www.sciencemag.org/content/334/6052/94/F2.expansion.html

Other ways to detect positive selection

Selective sweeps ->
A) fewer alleles present in population
(allele shows little within allele divergence - see contributions from archaic Humans for example),
B) SNP and neighboring SNPs have not yet been broken up by recombination.

Repeated episodes of positive selection -> high dN
(work well for repeated positive – aka diversifying – selection;
e.g. virus interaction with the immune system)
Fig. 1 Current world-wide frequency distribution of CCR5-Δ32 allele frequencies. Only the frequencies of Native populations have been evidenced in Americas, Asia, Africa and Oceania. Map redrawn and modified principally from <ce:cross-ref refid="bib5"> B...

Eric Faure, Manuela Royer-Carenzi

Is the European spatial distribution of the HIV-1-resistant CCR5-Δ32 allele formed by a breakdown of the pathocenosis due to the historical Roman expansion?

Infection, Genetics and Evolution, Volume 8, Issue 6, 2008, 864 - 874

http://dx.doi.org/10.1016/j.meegid.2008.08.007
Geographic origin of the three populations studied.

196,524 SNPs -> PCA

Hafid Laayouni et al. PNAS 2014;111:2668-2673
Manhattan plot of results of selection tests in Rroma, Romanians, and Indians using TreeSelect statistic (A) and XP-CLR statistic (B). 

Laayouni H et al. PNAS 2014;111:2668-2673

Convergent evolution in European and Rroma populations reveals pressure exerted by plague on Toll-like receptors.
Each population's geographic origin, number of individuals, and frequency of haplogroup D chromosomes are given in parentheses as follows:

1, Southeastern and Southwestern Bantu (South Africa, 8, 0%); 2, San (Namibia, 7, 0%); 3, Mbuti Pygmy (Democratic Republic of Congo, 14, 7.1%); 4, Masai (Tanzania, 26, 11.5%); 5, Sandawe (Tanzania, 33, 22.7%); 6, Burunge (Tanzania, 28, 12.5%); 7, Turu (Tanzania, 27, 7.4%); 8, Northeastern Bantu (Kenya, 12, 4.2%); 9, Bika Pygmy (Central African Republic, 32, 6.3%); 10, Zime (Cameroon, 25, 2%); 11, Bakola Pygmy (Cameroon, 27, 0%); 12, Bamoun (Cameroon, 29, 5.2%); 13, Yoruba (Nigeria, 24, 2.1%); 14, Mandinka (Senegal, 24, 4.2%); 15, Mozabite (Algeria (Mzab region), 29, 31%); 16, Druze [Israel (Carmel region), 45, 52.2%]; 17, Palestinian [Israel (Central), 43, 46.5%]; 18, Bedouin [Israel (Negev region), 46, 37%]; 19, Hazara (Pakistan, 19, 15.8%); 20, Balochi (Pakistan, 23, 13%); 21, Pathan (Pakistan, 21, 40.5%); 22, Burusho (Pakistan, 23, 28.3%); 23, Makrani (Pakistan, 25, 32%); 24, Brahui (Pakistan, 24, 33.3%); 25, Kalash (Pakistan, 25, 60%); 26, Sindhi (Pakistan, 25, 44%); 27, Hezhen (China, 9, 5.6%); 28, Mongola (China, 9, 11.1%); 29, Daur (China, 8, 6.3%); 30, Orogen (China, 10, 5%); 31, Miao (China, 10, 10%); 32, Yizu (China, 10, 25%); 33, Tuja (China, 10, 20%); 34, Han (China, 42, 17.9%); 35, Xibo (China, 9, 0%); 36, Uyghur (China, 10, 30%); 37, Dai (China, 10, 25%); 38, Lahu (China, 10, 10%); 39, She (China, 7, 21.4%); 40, Naxi (China, 9, 11.1%); 41, Tu (China, 9, 16.7%); 42, Cambodian (Cambodia, 10, 0%); 43, Japanese (Japan, 28, 10.7%); 44, Yakut (Russia (Siberia region), 24, 12.5%); 45, Papuan (New Guinea, 16, 59.4%); 46, NAG Melanesian (Bougainville, 18, 11.1%); 47, French Basque (France, 15, 40%); 48, French (France, 29, 50%); 49, Sardinian (Italy, 27, 46.3%); 50, North Italian (Italy (Bergamo region), 12, 45.8%); 51, Tuscan (Italy, 8, 37.5%); 52, Orcadian (Orkney Islands, 16, 40.6%); 53, Russian (Russia, 25, 38%); 54, Adygei (Russia (Caucasus region), 15, 40%); 55, Karitiana (Brazil, 24, 0%); 56, Surui (Brazil, 21, 0%); 57, Colombian (Colombia, 13, 3.8%); 58, Pima (Mexico, 25, 2%); 59, Maya (Mexico, 24, 12.5%).
The age of haplogroup D was found to be ~37,000 years

Evidence that the adaptive allele of the brain size gene *microcephalin* introgressed into *Homo sapiens* from an archaic *Homo* lineage

Patrick D. Evans, **†‡** Mikel-Bobrov, **†‡** Eric J. Vallender, **†‡** Richard R. Hudson, § and Bruce T. Lahn **†‡**

A

Non-D chromosomes (~30% worldwide frequency)  D chromosomes (~70% worldwide frequency)

B

Chromosomes not under positive selection  Chromosomes under positive selection

~1,700,000 years

~990,000 years

~37,000 years
Adam and Eve never met 😞

The same is true for ancestral rRNAs, EF, ATPases!
“Genotyping of a DNA sample that was submitted to a commercial genetic-testing facility demonstrated that the Y chromosome of this African American individual carried the ancestral state of all known Y chromosome SNPs. To further characterize this lineage, which we dubbed A00 ...”