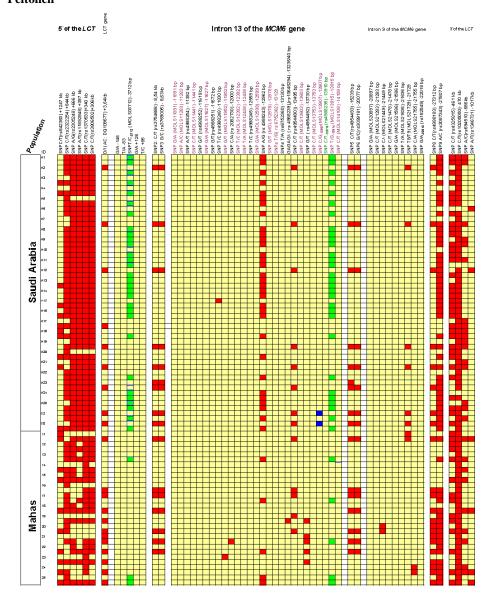
## **Supplemental Data**

## **Independent Introduction of Two Lactase-Persistence**

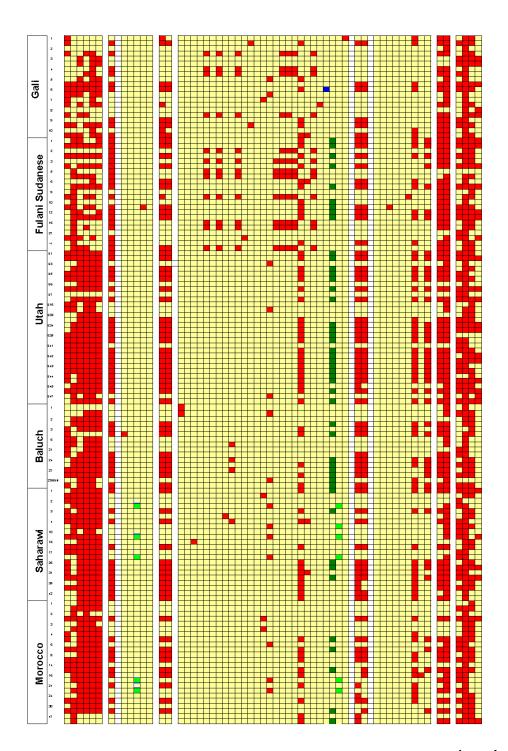
## **Alleles into Human Populations Reflects**

## **Different History of Adaptation to Milk Culture**

Nabil Sabri Enattah, Tine G.K. Jensen, Mette Nielsen, Rikke Lewinski, Mikko Kuokkanen, Heli Rasinpera, Hatem El-Shanti, Jeong Kee Seo, Michael Alifrangis, Insaf F. Khalil, Abdel-razak Natah, Ahmed Ali, Sirajedin Natah, David Comas, S. Qasim Mehdi, Leif Groop, Else Marie Vestergaard, Faiqa Imtiaz, Mohamed S. Rashed, Brian Meyer, Jesper Troelsen, and Leena Peltonen



(continued)



(continued)

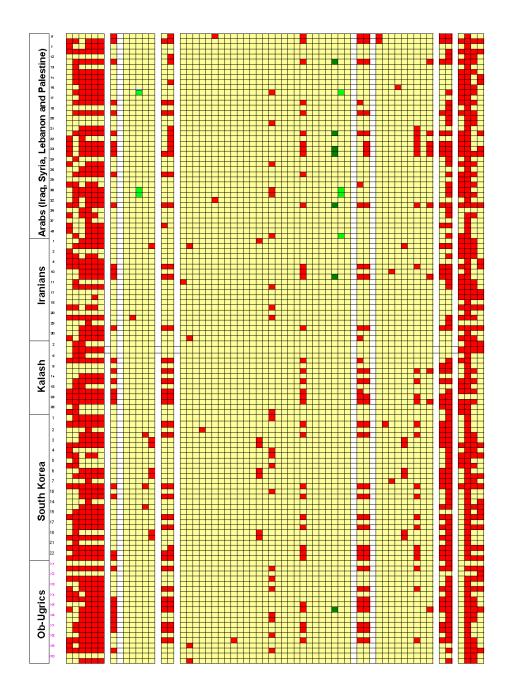


Figure S1. The Haplotypes of the Samples Analyzed for the 2 Mb Region of the *LCT* Region

The haplotype structure in 13 populations tested composed of 9 different contiguous regions (separated by empty columns) spanning more than 2 Mb, constructed manually for the regions where there is total homozygosity. Then, with PHASE version 2.1 program, we fitted every individual genotypes into haplotype. Every row represents the most probable haplotype and every individual represented by two haplotypes plotted in two consecutive rows. Yellow box represent ancestral allele, red box represent derived alleles. Light green, dark green, and blue boxed represent the derived alleles correlate with LP.