**Supplemental Text 1: Residue Methods**

*Sample preparation*

Sample preparation and CSIA extraction was performed at UC Davis by ST using methods based on those developed in similar studies (Eerkens, 2001; Evershed et al., 2002; Tushingham et al., 2013). Strict protocols were followed throughout sample preparation to avoid contamination. Prior to analysis, all artifacts were inspected for visible residue. A small (~1cm diameter) fragment of each potsherd was broken off and ~1mm of all exposed surfaces was removed with an abrasive silicon carbide/ steel dremel drill bit. Fragments were crushed into a powder using a small agate mortar and pestle and divided for CSIA and GC/MS analysis.

# Compound specific δ 13C analysis

For each sample, 200mg of crushed material was submersed in 2ml of a chloroform-methanol solvent (2:1, v/v), vortexed, sonicated for 20 minutes, and then centrifuged to separate the solvent mixture, now containing lipids, from the fine clay particles. The lipid extract was transferred to a second tube and evaporated under a gentle stream of nitrogen. Lipid extracts were derivatized by adding 100μl of methanolic HCl to the dried lipids, and heating at 60°C for 1 hour. Derivatized lipids were extracted with hexane and transferred into 2ml GC vials for compound-specific 13C isotope analysis (CSIA) of individual fatty acids using GC combustion isotope ratio mass spectrometry (GC-C-IRMS).

Compound specific stable isotope analysis was performed at the UC Davis Stable Isotope Facility (<http://stableisotopefacility.ucdavis.edu/>). Compounds were analyzed on a Trace GC Ultra gas chromatograph coupled to a Delta V Advantage isotope ratio mass spectrometer through a GC-C-III interface. Samples were injected, splitless, on a VF-5ms column (30m x 0.25mm ID, 0.25 μm film thickness). Once separated, FAMES were quantitatively converted to CO2 in a in a CuO/NiO/Pt oxidation reactor at 950°C, dried, and introduced to the IRMS. Corrections to provisional IRMS values were made based on working standards composed of FAMEs calibrated against NIST standard reference materials. The UC Davis Stable Isotope Facility reports that their long-term estimate of measurement error for CSIA of FAMES is generally better than ±0.5‰.

The δ13C values for FAME samples are expressed in permil as ratios of 13C to 12C relative to the ratio for the standard reference, V-PDB. The δ13C values were calculated as follows: (‰) = (R sample - R standard /R standard) × 1000, where R is equal to the ratio of the heavy to the light isotope (13C/ 12C) in the sample compared with that of the standard. Final δ13C values for sample FAMES were corrected for the isotopic contribution of methanol, incorporated during fatty acid derivatization, using a mass balance equation (Regert 2011:196).

*GC/TOF-MS*

GC/TOF-MS analysis was conducted by the Laboratory for Cellular Metabolism and Engineering Analytics facility at Washington State University. Lipids were extracted using a modified Bligh and Dyer technique similar to that employed in Buonasera et al. (2015). Crushed sherd samples (~1g) were extracted by sonication in 10ml of chloroform-methanol-water at a ratio of 1:2:0.8 (v/v/v) for 15min. After a 10min rest, the sonication was repeated. After a brief centrifugation, the solvent was removed, and the crushed pottery was washed with 2ml of the above solvent mixture, and the washing fraction combined with the extracts. For phase separation, 3ml chloroform and 3ml water were added. The chloroform phase was transferred to a new tube. The remaining aqueous phase was re-extracted with additional 3ml of chloroform. The combined chloroform extracts were dried under a gentle stream of nitrogen. The extracted lipids were derivatized with 3ml 1.25M HCl for 60 min at 60°C. After cooling, the solution was neutralized with saturated sodium bicarbonate solution and the derivatized fatty acids extracted with hexane. The hexane phase was dried under a stream of nitrogen, and the dry residue dissolved in chloroform and analyzed as below.

Derivatized lipid extracts were analyzed on an Agilent 7890A gas chromatograph coupled with a Pegasus 4D time-of-flight mass spectrometer (LECO), and signals were integrated using ChromaTOF software (LECO) and NIST library. The GC was fitted with an Rxi-5Sil® column (Restek), 30m x 0.25mm, 0.25μm df column, the carrier gas was He at a constant flow of 1ml min-1, and the inlet temperature was set to 250°C. Samples (1μl) were injected by a Gerstel MPS2 autosampler and split 1:15. After a 1 minute isothermal hold at 50°C, the temperature was ramped to 330°C at 20°C per minute, with a 5 minute final isothermal hold at 330°C. Mass spectra were collected at 17 spectra s-1.

Total ion count data for all samples were analyzed as .cdf files by TB with AMDIS 32, version 2.71. Lipid compounds were identified by comparing mass spectra for the samples to those in the NIST Standard Reference Database and to standard reference compounds (Supelco SP-37 FAME mixture) run the same instrument. Detection of ω-(*o*-alkylyphenyl)alkanoic acids 18, 20, and 22 carbons long was accomplished by analyzing mass spectra for selected ions. The compounds were identified by the presence of a dominant ion at m/z 105 along with M+ ions for C18 (290), C20 (318) and C22 (346) ω-(*o*-alkylyphenyl)alkanoic acids (Evershed et al., 2008; Hansel et al., 2004; Heron et al., 2010). The dominant ion at m/z 105 represents a dialkyl benzene fragment, C8H9+, common to all ω-(o-alkylyphenyl)alkanoic acids (Michael, 1966).

Fatty acid concentrations were calculated from internal standard (C12:0) and fatty acid peak areas reported in the δ 13C compound specific stable isotope analysis. Fatty acid concentrations could not be calculated from GC-TOF/MS data because internal standards were not added to these samples.