1   **Appendix**

2   The material presented in this appendix is meant to provide additional details on the

3   construction of both room similarity networks and co-occurrence networks. Both methods and

4   the justification for certain choices are presented here.

5   **Room Similarity Networks**

6   For constructing networks of room similarity we use the Brainerd-Robinson (B-R) coefficient to

7   define the scale of similarity among rooms where the similarity (*S*) between room *a* and room *b*

8   is defined as follows:

9
$$S_{ab} = \frac{200 - \sum_{k} | P_{ak} - P_{bk} |}{200}$$

10   where *k* is all artifact classes, P_{ak} is the percent of class *k* in room *a*, and P_{bk} is the percent of

11   class *k* in room *b* (Brainerd 1951; Robinson 1951). Specifically, we converted the counts of the

12   13 artifact classes from each room to percentages and then calculated the Brainerd-Robinson (B-

13   R) similarity coefficient (Brainerd 1951; Robinson 1951) among every possible pairwise

14   combination of rooms. The result is a symmetric matrix of B-R similarity scores among all

15   rooms, with the number of rows and columns equal to the number of rooms.

16

17   This matrix was then converted to a weighted network graph with the weight of ties

18   between nodes (rooms) equal to the B-R similarity of that room pair. The network was then

19   binarized by removing all ties with values below 75% similarity (a B-R score below 150). This

20   threshold of 75% is arbitrary, but was selected based on examination of histograms of overall

21   similarity scores across the entire dataset in order to capture the strongest (most similar)

22   relationships among rooms. While it is often important to use weighted ties (which indicate the

23   strength or value of the relationship between two nodes) in network analysis of archaeological

24 materials, rather than ties based on presence-absence data (see Peeples and Roberts 2013), the

25 current research is concerned primarily with the strongest associations among different artifact

26 classes. Weak ties are less useful in evaluating these relationships since they are more likely to

27 be driven by sampling error (especially when considering rare objects with low overall

28 frequencies) and associations among the most common objects. Consequently, use of binarized

29 data based on excluding weaker ties (below 75 percent similarity in this case) provides both

30 useful visuals and a powerful tool for reducing complexity in the overall dataset by highlighting

31 only the strongest similarities and associations (see also discussions in Hill et al. 2015 and

32 Weidele et al. 2016).

33   One consequence of examining only these strong ties (greater than 75% similarity) is that

34 the resulting network graphs tend to include many small clusters of rooms or individual rooms

35 isolated from the rest of the overall network. These clusters and individual rooms would

36 otherwise have been connected to the rest of the network through a number of weakly similar

37 relationships, but become disconnected when examining only strong ties. In this case, the use of

38 only strong ties helps us to identify the most internally cohesive groupings of rooms in the

39 network. Since the ties in this analysis are defined on the basis of a similarity measure (the B-R

40 coefficient), internal cohesion of a group indicates high similarity of all rooms in that group. This

41 exclusion of rooms connected to the network only by weak ties is therefore a desirable outcome

42 in evaluating strongly consistent patterning of archaeological material, rather than focusing on

43 outliers and weaker patterns. An examination of the rooms with no strong ties to other rooms

44 suggests that their isolation is largely driven by high proportions of the rarest artifact classes.

45 While these isolated rooms may offer interesting insights into the diversity of depositional

46 practices within the site, they do not help to characterize the primary depositional behaviors that

47   resulted in the site assemblage and which is the primary focus of the current research.

48   Clustering within the room similarity networks was evaluated by applying the Girvan-

49   Newman method to each network graph. This method calculates the centrality of each tie in the

50   network and breaks the network into clusters by removing the most central relationships. This

51   process effectively acts like traditional cluster analysis except working on a subtractive, rather

52   than additive, principle. The primary benefit of the Girvan-Newman analysis in comparison with

53   cluster analysis is that, as a subtractive analysis, it is more likely to accurately assign peripheral

54   members to a cluster. As an additive analysis, cluster analysis is more likely to miss-assign these

55   peripheral members of a cluster (Newman and Girvan 2004:2). The use of the Girvan-Newman

56   analysis follows the same justification as our use of a 75% threshold in constructing the network,

57   as a method for isolating the most internally cohesive clusters of rooms and strongest patterns of

58   relationships within the network.

59   Importantly, as in any cluster analysis, the number of clusters produced by the Girvan-

60   Newman technique is determined by the researcher through the selection of a modularity value,

61   producing anywhere from a minimum number of clusters (of one) up to as many clusters as there

62   are nodes in the network. However, a modularity score can be calculated to evaluate how much

63   variance is accounted for by the addition of each cluster. This modularity score is based on

64   eigenvalues calculated for each cluster added to the network (Newman 2006). For instance, the

65   NBNK dataset the maximum modularity score was achieved for a seven-cluster network (**Figure

66   2** in the main text), accounting for 67.90 percent of the variance in the data.

67   **Co-Occurrence Measurement**

68   The measure of co-occurrence used in constructing our co-occurrence networks was

69   calculated using a binomial model defined for artifact classes *a* and *b* as:

70
$$C_{ab} = \frac{o - Np_{ab}}{\sqrt{Np_{ab}(1 - p_{ab})}}$$

71   o = the observed number of co-occurrences between artifact classes a and b
72   N = the total number of assemblages
73   p = the expected proportion of co-occurrences for artifact classes a and b defined as the
74   expected proportion of occurrences for class a multiplied by the expected proportion of
75   occurrences for artifact class b
76
77   Observed values of co-occurrence can be obtained by multiplying the binary version of the data

78   matrix by its transpose. The expected proportion of occurrence for each artifact class is defined

79   simply as the total number of occurrences divided by the number of assemblages. Thus, Np_{ab}

80   represents the expected count of co-occurrences between class a and class b.

81   This measure, originally described by Kintigh (2006), provides an index of the number of

82   co-occurrences observed in relation to the number that would be expected by chance given the

83   overall frequency of each artifact class. This measure approximates a Z-score such that the

84   absolute values can be interpreted in standard deviation units above and below 0. Thus, we might

85   expect the distribution of values for a given table of occurrence data to have a mean of

86   approximately 0 with roughly equivalent numbers of positive and negative values. As **Table 2** in

87   the main text of this article illustrates, however, the range of values obtained from the NBNK

88   dataset was highly positively skewed (skewness = 1.36; see also **Figure S.1**). The values

89   obtained for the other datasets evaluated in this research were similarly skewed. In order to

90   assess the potential factors driving this skewed distribution, we conducted a simulation

91   experiment.

92   First, we created 10,000 randomized versions of the original n x m matrix of occurrences

93   (n = number of rooms and m = number of artifact classes) for the NBNK dataset by permuting

94   each column independently. Thus, this procedure resulted in randomized co-associations while

95   preserving the relative frequencies of artifact classes. Next, we calculated our measure of co-

96   occurrence C as described above for each random matrix, resulting in 10,000 m x m matrices of

97   co-occurrence scores. The distribution of values obtained for all of these random runs combined

98   is normally distributed (**Figure S.2**) with a mean of 0. In only 0.42% of all randomized matrices

99   did we obtain a skewness greater than or equal to the observed value of 1.36 in our original

100   matrix. Importantly, all random runs that resulted in highly positively skewed distributions (>1)

101   were characterized by multiple co-associations among the 5 rarest artifact classes including

102   spindle whorls, crystals, jet, copper, and cylinder jars whereas such co-associations were less

103   common in random runs with skewness values closer to 0. Indeed, **Figure S.3** shows the average

104   skewness value increases in relation to the number of co-occurrences of the rarest artifact

105   classes. If we return to our original dataset we find a total of 10 co-occurrences among the 5

106   rarest artifact classes (higher than almost all random runs). Overall, this suggests that the positive

107   skew of C values in our original observed table is driven by the tendency for rare objects to

108   cluster in the NBNK dataset and is not simply an artifact of the method of assessing co-

109   occurrence. The result of this procedure is a table with artifact classes as both rows and columns

110   and with each cell representing the co-occurrence index between two artifact classes. See **Table**

111   **2** for an example from the NBNK dataset.

112   **Network Cliques**

113   After converting the matrix of co-occurrence values into a network graph, as described in

114   the main text, clustering within the network was evaluated using the network concept of a

115   "clique". A clique in network terms is a "maximal, complete subgraph of three or more nodes"

116   (Wasserman and Faust 1994:254). In this case, maximal means that no additional nodes can be

117   added to the clique that meet the criteria of the clique (having ties to every other clique member).

118   Due to their definition, two or more cliques can share members (though no clique can ever be

119   entirely contained within another, given the "maximal" definition of a clique). Since our analysis

120   is concerned with behavioral sets of things, overlap between cliques is a non-issue given that use

121   of objects from an artifact class in one context does not inherently preclude use of that same

122   artifact class in a different context. The clique concept is useful for an assemblage-oriented

123   approach because it moves beyond the evaluation of single artifact classes or pairings of artifact

124   classes to look at entire sets of co-occurrence within an assemblage.

125   In weighted networks the clique can be expanded to evaluate cliques hierarchically based

126   on the values of ties in a clique. In this case the clique definition is modified such that a 'clique

127   at level C' meets not only the basic definition of a clique, but also requires that all ties between

128   members of the clique 'at level C' are of value C or greater (Wasserman and Faust 1994: 278).

129   Applied to the network of co-occurrence indices, a clique in the network is a set of three-or-more

130   artifact classes which all co-occur with each-other more frequently than expected by chance at a

131   given threshold. The use of valued or weighted ties then helps identify the most cohesive cliques,

132   which for the co-occurrence network are only those cliques which have high values of co-

133   occurrence between all clique members.

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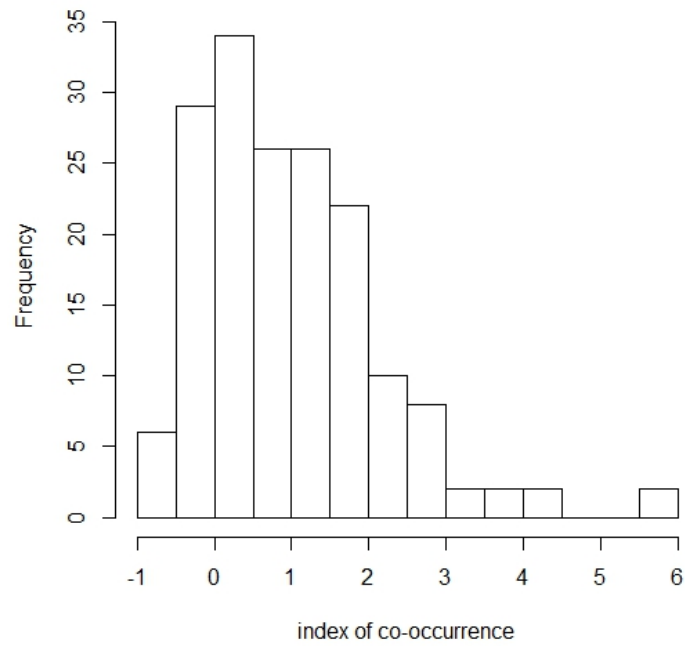
148
149 **Figure S.1.** Distribution of C co-occurrence values for original data table.
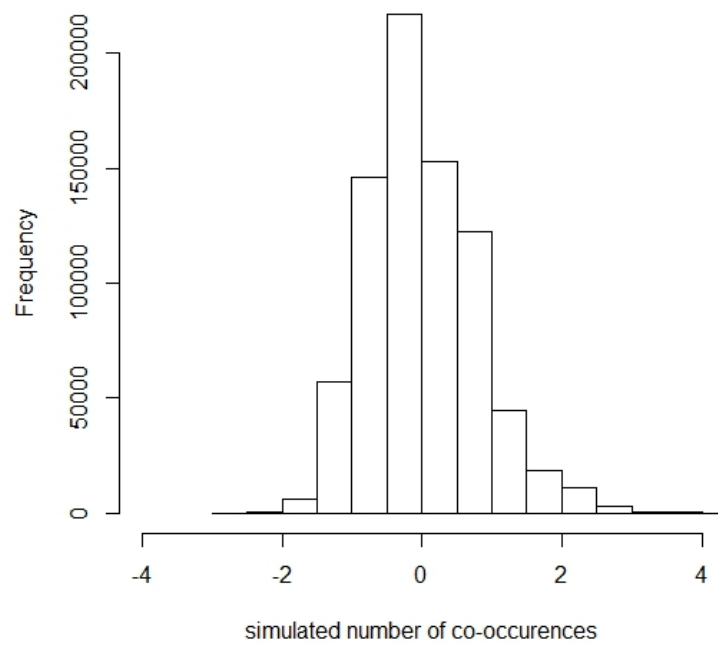
150
151 **Figure S.2.** Distribution of C co-occurrence values for the 10,000 randomized matrices.
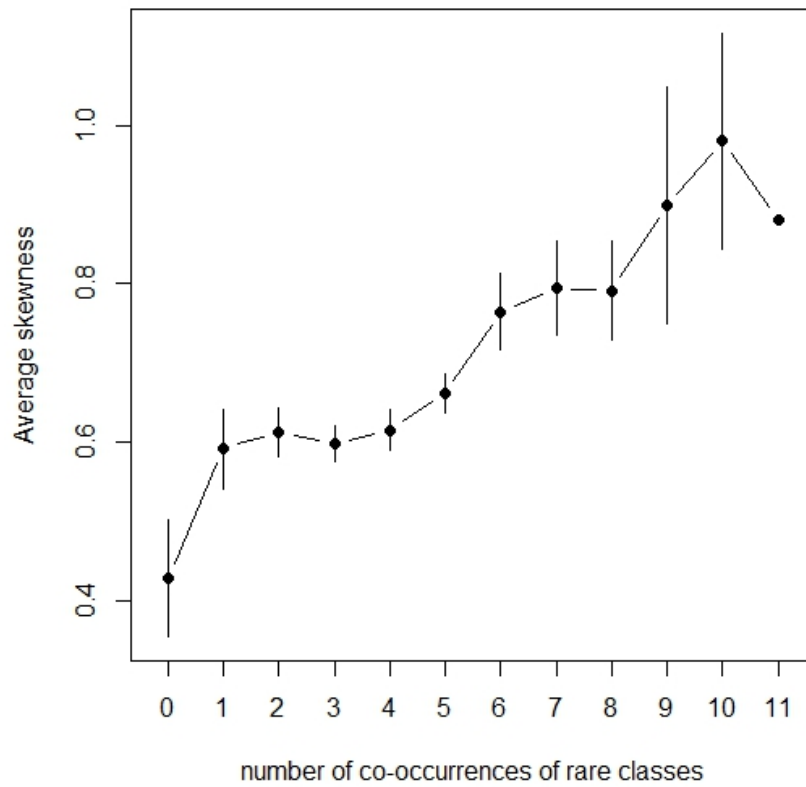152

Figure S.3. Plot showing the average skewness and confidence intervals for 10,000 randomized datasets in relation to the number of co-occurrences among the 5 rarest artifact classes.

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176
177   R function for calculating *C* index:
178   Input – Matrix *x* of *n* contexts/rooms as rows and *m* artifact classes as columns.
179   Data are assumed to be 0/1 presence/absence.
180
181
```
cooccur <- function(x) {

# calculate the proportional occurrence of each artifact class
nm.p <- colSums(x)/nrow(x)

# calculated observed co-occurrences through matrix multiplication
obs <- t(as.matrix(x)) %*% (as.matrix(x))
diag(obs) <- 0
# create matrix of expected values based on proportional occurrence
expect <- matrix(0,nrow(obs),ncol(obs))
for (i in 1:nrow(obs)) {
  for (j in 1:ncol(obs)) {
    expect[i,j] <- (nm.p[i]*nm.p[j])*nrow(x)}}

# convert expected count to expected proportion
p <- expect/nrow(x)

#calculate the denominator of the equation
denm <- sqrt(expect*(1-p))

# calculate final matrix of scores and output
out <- (obs-expect)/denm
diag(out) <- 0
return(out)}

## end code
```
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