Title of project:	Origins and Spread of Stock Keeping
Name of database/ spreadsheet file:	ossk_db

Repeat the following section for each table within your database:

Name of table / worksheet 1:	t_site.csv	
Purpose of table/worksheet:	Records site name and location data	
Number of rows of data:	657	
Primary key (*database only*):	site_name	
Name of field	**Full description of field and codes or terminology used**	**Data type and field length (*database only*)**
site_name	Name of site	[VARCHAR 40]
country	Name of country	[VARCHAR 20]
coordinate_source	Data source for coordinate data	[MEMO]
latitude	Latitude in decimal degrees	[REAL]
longitude	Longitude in decimal degrees	[REAL]
references	Bibliographic reference	[MEMO]

Name of table / worksheet 2:	t_phase.csv	
Purpose of table/worksheet:	Descriptions of phases and archaeological recovery methods	
Number of rows of data:	971	
Primary key (*database only*):	phase_code	
Name of field	**Full description of field and codes or terminology used**	**Data type and field length (*database only*)**
site_name	Name of site	[VARCHAR 40]
phase_code	Phase code	[VARCHAR 10]
occupation_type	Description of type of occupation	[MEMO]
recovery_hand	Whether specimens were hand collected	[T/F]
recovery_drysieve	Whether specimens were collected using dry sieves	[T/F]
recovery_watersieve	Whether specimens were collected using water sieves	[T/F]
recovery_other	Whether other types of collection were used	[T/F]
total_assemblage_size	Total size of animal bone assemblage	[INT]
unidentifiable_specimens_incl	Whether total size of animal assemblage includes unidentifiable bones	[T/F]

Name of table / worksheet 3:	t_species.csv	
Purpose of table/worksheet:	Records bioarchaeological information on taxa from individual phases	
Number of rows of data:	13605	
Primary key (*database only*):	record_no	

Name of field	Full description of field and codes or terminology used	Data type and field length (*database only*)
record_no	Records entry ID	[INT]
phase_code	Phase code	[VARCHAR 10]
taxon_code	Code used to refer to taxon	[VARCHAR 10]
NISP	Numbers of Identified Specimens included in taxon record	[INT]
presence_only	Taxon recorded to presence only	[T/F]
age_trend	Age trend [0=not stated/recorded, 1=mainly neonatels/foetals, 2=mainly juveniles (1-12 months), 3=mainly subadults (1-2 years), 4=mainly subadults (2-3 years), 5=mainly adults 6=mainly young, 7=no trend]	[INT]
presence_of_foetals	Age evidence based on foetals/newborn	[T/F]
age_criteria_de	Age evidence based on dental eruption	[T/F]
age_criteria_da	Age evidence based on dental attrition	[T/F]
age_criteria_bf	Age evidence based on bone fusion	[T/F]
age_criteria_nr	Age evidence not recorded	[T/F]
age_note	Age evidence notes	[MEMO]
sex_trend	Sex trend [0=not stated/recorded, 1=majority male, 2=majority female, 3=equal ratios]	[INT]
sex_criteria_me	Sex trend evidence based on measurements	[T/F]
sex_criteria_mo	Sex trend evidence based on morphology	[T/F]
sex_criteria_nr	Sex trend evidence not recorded	[T/F]
sex_note	Sex trend evidence notes	[MEMO]
biometry_trend	Biometry trend [0=not stated/recorded, 1=size reduction 2=no change, 3=size increase, 4=increased upper range 5=increased lower range, 6=change in shape]	[INT]
biometry_trend_notes	Biometry trend evidence notes	[MEMO]
biometry_criteria_me	Biometry trend evidence based on measurements	[T/F]
biometry_criteria_in	Biometry trend evidence based on indexes	[T/F]
biometry_criteria_sg	Biometry trend evidence based on scattergrams	[T/F]
biometry_criteria_hs	Biometry trend evidence based on horn core size	[T/F]
biometry_criteria_nr	Biometry trend evidence not recorded	[T/F]
biometry_note	Biometry trend notes	[MEMO]
horncore_shape	Horn core [0=not stated/recorded, 1=little evident 2=moderate selection evident, 3=considerable selection evident, 4=no selection]	[INT]
horncore_note	Horncore shape evidence notes	[MEMO]
skeletal_element	Skeletal element (for all parts) [0=none, 1=few, 2=many, 3=present]	[INT]
skeletal_element_cr	Skeletal element representation of crania	[VARCHAR 20]
skeletal_element_tr	Skeletal element representation of trunk	[VARCHAR 20]
skeletal_element_ul	Skeletal element representation of upper limb	[VARCHAR 20]
skeletal_element_ll	Skeletal element representation of lower limb	[VARCHAR 20]
skeletal_element_fe	Skeletal element representation of feet	[VARCHAR 20]
skeletal_element_note	Skeletal element representation notes	[MEMO]
pathology	Evidence for pathology	[T/F]
pathology_note	Pathology evidence notes	[MEMO]
isotope_data	Isotope data available	[T/F]
isotope_data_note	Isotope data notes	[MEMO]
aDNA_data	Ancient DNA data available	[T/F]
aDNA_data_note	Ancient DNA data notes	[MEMO]

species_note	Additional notes on species	[MEMO]

Name of table / worksheet 4:	**t_taxa.csv**	
Purpose of table/worksheet:	**Records biological classification data for archaeofauna**	
Number of rows of data:	**583**	
Primary key (*database only*):	**taxon_code**	
Name of field	**Full description of field and codes or terminology used**	**Data type and field length (*database only*)**
taxon_code	Code used to refer to taxon	[VARCHAR 40]
full_name_of_taxon	Species taxonomic name to highest taxonomic level possible	[VARCHAR 40]
level_of_identification	Level of identification [1=species; 2=genus; 3=family; 4=order; 5=class]	[INT]
phylum	Phylum of specimen	[VARCHAR 12]
Class	Class of specimen	[VARCHAR 20]
order	Order of specimen	[VARCHAR 20]
family	Family of specimen	[VARCHAR 20]
genus	Genus of specimen	[VARCHAR 20]
species	Species of specimen	[VARCHAR 20]
wild_domestic_status	Notes on whether taxa is considered wild and/or domestic	[MEMO]

Relationships (*database only*)

Please include an entity relationship diagram to show the relationships between your database tables

t_site.csv	t_phase.csv	t_species	t_taxa
site_name*	site_name	record_no*	
	phase_code*	phase_code	
		taxon_code	taxon_code*