1. Index the ENCODE reference genome using LongRanger version 2.1.2

$ longranger mkref GRCh38_no_alt_analysis_set_GCA_000001405.15.fasta

This create a directory of special indexed files which is described here:
http://support.10xgenomics.com/genome-exome/software/pipelines/latest/advanced/references

We used this version, but it turns out their software doesn't actually support using any alternate haplotypes.

2. For each sample, align reads, call and phase variants using LongRanger version 2.0.0

$ longranger-2.1.2/longranger-cs/2.1.2/bin/wgs --id=sge_Aug_encodev2_2_local --sex=$SEX --fastqs=$folder --sample=mysample --reference=$REF --maxjobs=10 --jobinterval=1000

SEX = male or female, as appropriate
FASTQ = directory to the FASTQ files
REF=ENCODE reference from step 1

This creates the phased_variants.vcf file, the phased_possorted_bam.bam file, and the loupe.loupe files that we posted on the website. I would refer to the LongRanger website for all the details: http://support.10xgenomics.com/genome-exome/software/pipelines/latest/what-is-long-ranger