SAS instructions for merging the supplement file to an ATUS-X extract.

"suppfile" should be replaced with the name you have given the supplement file. "atusxfile" should be replaced with the name you have given your extract from the ATUS-X website. The first step in merging the two files is to sort each of them using CASEID and PERNUM. proc sort data = suppfile; by caseid pernum; run: proc sort data = atusxfile; by caseid pernum; run; Once the files have been sorted in this order, they can be merged using the same variables. data mergefile; merge suppfile atusxfile; by caseid pernum;

run;

The result of this merge will be a file that includes observations for all individuals with records on the supplement file *or* on the ATUS-X extract file you created. Each individual's record will include all of the variables on the linked supplement file and all of the variables on the ATUS-X extract you created. A person who does not have a record on the supplement file will have missing values for the supplement file variables and a person who does not have a record on the variables are cord on the ATUS-X extract you created will have missing values for those variables.

Some users may wish to restrict the merged dataset to keep only respondents with valid linked file weights. The following code uses the variable PER_STAT to drop other observations from the merged dataset.

data mergefile; set mergefile; if per_stat < 1 or per_stat > 3 then delete; run;