After your study has been released, and you would like to submit new data or update existing data (correcting, removing, or adding rows or columns of data), dbGaP will create a new version of your study. This means that the study accession of your study will be updated (e.g. phs000999.v1.p1 to phs000999.v2.p?, where the version number (v#) will increment by one and the participant set number (p#) will increment by one if subjects have been retired or have moved from one consent group to another. If only new subjects have been added, then the p# will not be incremented. For new versions of a study, we ask users to continue to follow the instructions in the dbGaP Submission Package and to go through the following checklist:

1. Submitters should continue to submit data using the dbGaP Submission Portal. Please email Lora Ziyabari ([ziyabarl@ncbi.nlm.nih.gov](mailto:ziyabarl@ncbi.nlm.nih.gov)) for more information.

2. \*\*\*\*\*Only new or updated files should be submitted. Please do not submit files that have been submitted previously and are unchanged. The Subject Consent file, Subject Sample Mapping file, Pedigree file, and Sample Attributes file should always be cumulative, i.e. all subjects and samples used in version 1 should be included in the version 2 subject consent and subject sample mapping files and so forth. If a subject or sample is not included, dbGaP will mark the subject or sample as retired and the data will no longer be available in the new version. Those retired samples will also be removed from SRA. If the study config file is updated, it should also be cumulative and describe all versions of the study. All other phenotype files, may either be cumulative or be marked as a brand new dataset. Prior to submission, please check that the files you submit contain the expected number of subjects and samples and the appropriate consent information.

3. Please retain the format and corrections that were made in the previous version following the Submission Guide. Much effort has been given to make these changes.

1. Please check that variable names in the Dataset and the matching Data Dictionary are identical in spelling, i.e. have the same number of spaces, same case, etc.
2. Please check that every variable has a variable description. Please check that coded values in the Dataset have code meanings listed in the Data Dictionary.
3. Please check that the gender of a subject remains consistent throughout a single study. If the gender has been changed as a result of a correction, please let dbGaP know via email.
4. Please check that the case-control status of a subject remains consistent throughout a single study.
5. Please check that all subjects have been assigned a consent group.
6. Please check that the existing subject and sample ID mappings remain the same between versions, unless there is an error and an ID needs to be re-mapped. In case of ID re-mapping, please let dbGaP know which IDs need to be remapped.
7. Please check that all samples are mapped to a subject and therefore to a consent group.
8. Please check that the data files contain the values you expect. Check for truncated values. Compare new files to the final files submitted for the previous version to check for differences and to make sure all changes are intended. If you need more information regarding which files were incorporated into the final release of the previous version, please make a request to dbGaP.

4. To help us better understand the new version, please let your phenotype curator know:

1. Have new subjects been added? How many?
2. Have any subjects been deleted or changed consent groups? How many?
3. Have new samples been added? How many?
4. Have any samples been deleted? How many?
5. Have any samples been remapped to new subjects? How many?
6. Have new datasets been added? What are their filenames?
7. Have new variables been added or deleted in existing datasets? How many?
8. Have variables been renamed between versions? What are they?
9. Have molecular data been added?