

Downloading your 23andMe Raw Data File

1. Log onto 23andme.com
 2. Sign in with your email and password.
 3. On the homepage go to the far right where your name is and click on that.
 4. Select “browse raw data” from the dropdown menu.
 5. On the “Browse Your Raw Data” web page select the download button. Scrole down to ‘Request your raw data download’ and click on ‘Sumbit Request’ button.
- You will see a message that says ‘Your download request is in progress’. Once you recieve an email from 23andMe you can continue these intruction.

Your Raw Data

Search for specific genes and markers (SNPs) of interest.* You can view or download your data in its raw, uninterpreted format (your A’s, T’s, G’s, and C’s).

Once your raw data is ready you will see ‘Your raw data download is ready!’ Click on Download raw data.

6. Save the file.
7. Your raw data file will appear as a zip file and/or text file.

When you open the file it will appear like this.

```
# This data file generated by 23andMe on: Fri Sep 9 10:46:49 2011
#
# This file contains raw genotype data, including data that is not used in 23andMe reports.
# This data has undergone a general quality review however only a subset of markers have been
# individually validated for accuracy. As such, this data is suitable only for research,
# educational, and informational use and not for medical or other use.
#
# Below is a text version of your data. Fields are TAB-separated
# Each line corresponds to a single SNP. For each SNP, we provide its identifier
# (on chr, id, or an internal ID), its location on the reference human genome, and the
# genotype call oriented with respect to the plus strand on the human reference sequence.
# We are using reference human assembly build 37 (also known as Decimation Release 104).
# Note that it is possible that data downloaded at different times may be different due to ongoing
# improvements in our ability to call genotypes. More information about these changes can be found at:
# http://www.23andme.com/genotype/downloads/updates/
#
# More information on reference human assembly build 37 (see Annotation Release 104):
# http://www.ncbi.nlm.nih.gov/ncbiinfo/map_search.cgi?build=37
#
# File: chrpospos    position    genotype
rs12284882    1    724982    AA
rs1121872    2    782721    AC
rs10882894    3    748098    AC
rs12124818    5    778548    AA
rs11889198    5    787173    GC
rs11248777    7    748098    GC
rs2538349    7    824368    AA
rs4878353    7    838551    AC
rs4775651    7    848368    CT
rs1117716    7    854258    AC
rs11322182    7    865368    GC
rs25278186    7    864498    CT
rs4815295    7    873267    CT
```

8. Save the file to an area that you can easily locate. You will need this file to download your methylation, detox and MTHFR profiles.

9. Next go to mthfrsupport.com

10. Go to 'My Account' and create an account, you can use the same email and password.

11. Now you will click on 'Sterling's App' and scroll down to 'Order Reports'.

From here you will take the zip file from 23andme and put it in 'Upload My Genome File' and follow instructions. When you order reports, you will pick the 'Variant Report'.

Once downloaded, send the file to one of these three options.

- Email to info@dryoungberg.com
- Fax to 951•271•4455
- Or by this secure link [Click here for a HIPAA compliant secure link where you can easily drag and drop all appropriate files and forms from your computer onto the secure email and send them to us.](#)