Set up your genome in HealthOS

The optional deep-DNA analysis, step by step.

HealthOS reads the basics from your DNA the moment you drop in a genome file. This guide turns on the deep analysis: a pathogenic-variant screen across your whole genome, your drug-gene report, and how rare each of your variants is. It takes a Docker install, one big download, and a few hours of your Mac's time. Worth doing once.

WHAT YOU GET

- ClinVar pathogenic and likely-pathogenic variants, screened across your whole genome.
- Your pharmacogenomics: the medications your genes change the dose or risk for, using CPIC drug-gene guidance.
- How common or rare each flagged variant is, so a scary label on a variant that 40 percent of people carry gets the skepticism it deserves.
- If you have an aligned BAM, confirmation reads that recover gene calls a VCF alone misses.

BEFORE YOU START

- ✓ A Mac. Apple Silicon works; the analysis runs under emulation, so it is slower.
- ✓ Your whole-genome VCF, GRCh37 / b37, gzipped (`.vcf.gz`). A 23andMe or array chip will not work; it miscalls.
- ✓ About 30 GB of free disk for the reference data.
- ✓ Docker Desktop, which is free. The analysis runs inside it.
- ✓ A few hours, mostly unattended. The first pass returns results in minutes; the full pass grinds in the background.

THE STEPS

1 **Drop in your VCF.**

Put your `.vcf.gz` in the `genome` folder (`Settings` shows you where, or use the reveal button). HealthOS loads it and shows the basic findings right away.

2 **Open Settings, then Genome (advanced).**

This is the control panel for everything below. It shows what is ready and what is missing at each step.

3 **Turn on genome.**

One toggle. Nothing heavy happens yet; it tells HealthOS you want the deep analysis.

4 **Install Docker Desktop and start it.**

The panel links you to the download. Install it, open it, and wait until it says it is running. HealthOS then shows a green `Docker`.

5 **Install the tools.**

One button. It downloads the small command-line tools the pipeline needs and puts them where HealthOS can find them.

6 **Download the references.**

One button, then wait. This is the big one: about 27 GB of public reference data. It resumes if your connection drops, so you can close the lid and come back.

7 **Pull the Docker images.**

One button. It fetches the analysis containers.

8 **Run the analysis.**

When Docker, tools, and references all show green, the `Run` button lights up. The quick pass finishes in minutes (your MTHFR status and the first pathogenic hits). The full pass runs a few hours and fills in the rest. Progress shows live in the panel.

> **OPTIONAL: YOUR BAM**
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> If you have your aligned BAM file, usually 100 GB or more, drop it in the `genome/bam` folder. HealthOS uses it automatically to confirm low-confidence calls and recover drug-gene results a VCF cannot. No BAM, no problem; everything else still works.

> **IF SOMETHING STALLS**
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> **Run is greyed out.** One of Docker, tools, or references is not ready yet. The panel tells you which.
>
> **Docker shows red.** Docker Desktop is not running. Open it and wait for it to start.
>
> **The download will not finish.** Google Drive limits how often one file can be pulled. Wait a few hours and press `download` again, or ask for a mirror link.
>
> **Tools will not install.** Some tools need Homebrew. The panel says which; install them and press `recheck`.

PRIVACY Your DNA never leaves your Mac. The only thing that moves is the reference data coming in, which is public and the same for everyone. The analysis runs entirely on your machine.

HealthOS. Local-first. Your data stays yours.