

Saving and Sharing Sessions on the UCSC Genome Browser

In this tutorial we will be discussing the ways to save a session and share the contents of your session with other users or to save it for future reference. An important aspect of this feature is that it saves an *active* session, not a static picture.

We will start by resetting the Browser here at the main page, genome.ucsc.edu. “Reset All User Settings” so that we start at the same page that an individual would who has never been to the Browser before. The default location on the gateway is the human genome assembly hg38.

[0:30 Set Browser to hg19 UCSC Genes and GTEx tracks.]

We'll switch to hg19 because it is still the best annotated of the human assemblies and with the [go] button navigate to our Genome Browser graphic. Many datasets are turned on by default so we will use the [hide all] button to turn all of them off, cleaning up the screen, and turn on just the UCSC Genes track to “pack.” And the GTEx track, which is a gene expression track, we'll set to “full.” Use the [refresh] button to turn them on.

[1:01 Set up interesting view on the hemoglobin gene cluster.]

Now let's navigate to a location that perhaps you've picked up from the literature: Hemoglobin gene, HBB, where you may read that the amino acid lysine 17 in a variant has changed to glutamate. We'll use HGVS nomenclature.

Using the [go] button now, we discover that we have in fact navigated to amino acid 17 but we're off by one. The lysine is at 18 and the Browser gives us a warning that this does not match the value. This is because some annotations in the literature for some genes do not count the methionine as one; they count it as zero if it's cleaved off and not present in the mature protein. You'll notice that the Browser highlights and takes us to amino acid 17 anyway.

You'll notice that the highest signal in the GTEx track is for whole blood, as you might expect for hemoglobin. Let's get a larger view of the genome in this region and see some of the other genes in the hemoglobin cluster. So let's zoom out by a factor of [100x] and then by another factor of [10x]. This puts two hemoglobin genes in the window: HBB and HBD.

Let's suppose this is the image that you want to save and share with your colleagues. You could try to describe all the steps you took to get here. Or, you could save it as a .pdf image, which is great for publication as it is vector graphics and therefore scalable to 300 dots per inch, but it is still a static image. Or you could save a session. Going to the top of the screen now, under “My Data, My Sessions,” a new user will have an opportunity to create an account, and existing users can login.

[2:33] Create and verify a user account.]

Let's "Create an account". We'll call it username: "videoDemol" and we'll use my email address, and the optional recovery email for now we'll leave blank. And we will create a password.

Now we have an account but it's necessary to go check our email and look for the message from the UCSC system. Here we see that it tells us that we have created an account. We can click the link to confirm we're not a robot and we're redirected to a page that tells us that the account has been activated.

We'll go back to the original Browser and "Login" using the username "videoDemol" and my new password and [Login]. This is the only place in the Genome Browser where a login is required, and that's so the system knows how to access your saved sessions and identify them as uniquely yours. You'll notice that we have a new section here called "My Sessions" which at the moment is empty and it's our opportunity now to create a session for the main Browser view. It's important to note that you can restore someone else's session without being logged in.

[3:43] Save an active session.]

So we can save the session as "hg19_hemoglobin" and [submit.] Now we have a session on our list and if we wish, we can use the right mouse button to keep the link that we can send to someone else or we can open up a mailer using this link here. Going back to the Genome Browser you'll find that we're at that same location.

Now to demonstrate how it works, let's navigate to some other gene in the genome such as "NF1" and [go.] If we go to "My Sessions," we can click on our session link and we're taken directly there. Or if we navigate to some other place on the Browser we can go once again to "My Data, My Sessions" and we can grab the link if we like, mail the link to someone else or copy it directly into the Browser and navigate to that page.

[4:35] Update a session.]

If we don't really want to have two gene sets turned on, we can turn off the RefSeq gene set, which came on when we used the HGVS nomenclature. We can go back to "My Data, My Sessions" and resave the session under the same name, "hg19_hemoglobin," and [submit.] We're prompted with an opportunity to not overwrite our existing session but we will overwrite here and the hit the "Browser" link.

It's important to note, if I go back here to the session, that the Browser prompts you with the name of the genome assembly in the section for saving. It's very useful to keep that, so you do not accidentally wind up on a genome assembly you did not expect to. If you simply name a session by a gene name and you save that session while you are looking at a mouse assembly, then come back a month later you may or may not

remember that the session was saved as the *mouse* hemoglobin gene and you might cause yourself a bit of confusion.

Anyone could restore this session using the link you provided, or simply using the username, videoDemo1, and the session name, hg19_hemoglobin, in the “Restore” section. You do not have to be logged in to restore someone else’s session.

[5:46 Share sessions privately and publicly.]

The last thing to notice about the interface is that you have the option to keep a session private so that only the person who has saved the session can view it. It's also possible to post in our public website where if you click this box, it makes the session public so everyone can see it. The person who creates the session is encouraged to document it so that anyone who views it will understand why it was saved. In a public session you might explain that “the genes hemoglobin B and hemoglobin D are both expressed in red blood cells but hemoglobin B is also expressed in many other tissues whereas hemoglobin D is expressed in red blood cells almost exclusively.” Then, [accept changes].

To view your public sessions go to “My Data, Public Sessions” and notice that there are a lot of sessions that have been made available for the public, and you can find it by typing in a keyword. Clicking on that link will activate the session.

That's a quick run-through of how to save a session and share a session with others.

Thank you for watching our video and thanks for being a Genome Browser user.