

**Question 15) Can the map-confirmed human BAC clone set of ~32,000 BACs ("32k-set") be displayed in the UCSC Human Genome Browser? We would prefer ordering clones with minimal risk of being mismatched with mapping data? (posted May 12, 2016)**

The BC Genome Science Center (BCGSC) has previously generated a custom "[32k BAC track](#)" for an older version of the Human Genome Assembly, which is no longer being displayed at the UCSC Genome site. This track was published in our [Nucleic Acids Research manuscript](#). BACPAC Resources Center (BPRC) staff has recently used the [liftover tool](#) to convert the old track into versions compatible with the newer genome assemblies. You can upload these updated custom tracks by following the instructions in the next paragraph. The displayed data will very likely be correct, but we do not guarantee this. Hence, use at your own risk.

How can one find the 32k BAC clones displayed within the UCSC Browser? Click on the appropriate **UCSC Assembly Version** in the table (below) to open the correct upload window. Then, click on the corresponding **Custom Track URL** and Copy & Paste this URL into the upload UCSC upload window. For instance, the URL to be pasted into the hg38 assembly is:

<https://bacpacresources.org/download/humanbacHg18To38/humanbacs.hg38.track>

UCSC Assembly version	Custom Track URL to upload
<a href="#">Dec.2013 (GRCh38/hg38)</a>	<a href="#">humanbacs.hg38.track</a>
<a href="#">Feb.2009 (GRCh37/hg19)</a>	<a href="#">humanbacs.hg19.track</a>
<a href="#">Mar.2006 (NCBI36/hg18)</a>	<a href="#">humanbacs.hg18.track</a>
<a href="#">Mar.2004 (NCBI35/hg17)</a>	<a href="#">humanbacs.hg17.track</a>

Here's how the UCSC track window looks when uploading the hg38 track. You only will have to click on "Submit" to upload the track.

Genomes Genome Browser Tools Mirrors Downloads My Data

### Add Custom Tracks

clade  genome  assembly

Display your own data as custom annotation tracks in the browser. Data must be formatted in [bigBed](#), [bigGenePred](#), [bigWig](#), [BAM](#), [VCF](#), [BED](#), [BED detail](#), [bedGraph](#), [broadPeak](#), [GFF](#), [GTF](#), [MAF](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). Data in the bigBed, bigWig, bigGenePred, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Examples are [here](#).

Paste URLs or data: Or upload:  No file chosen

Below are 2 examples for arbitrary genome regions (X-chromosome, Hprt1 locus) with displayed 32k BACs (titled “**BCGSC Human Bac Rearray**”) for the hg38 and hg19 assemblies, respectively. Note that after uploading the Custom Track, one will need to configure the UCSC Browser display for the track appropriately, by selecting “**Full**” on the custom tracks **sub-menu**.

