

NCBI Announcement: Changes coming to genomic clone data

Clone DB has been a valuable resource connecting users with information and reagents for genomic and cell-based clones. **Clone DB** was originally implemented as the Clone Registry during the human and mouse genome projects. In subsequent years, it expanded to represent clone-associated data for a broad range of organisms.

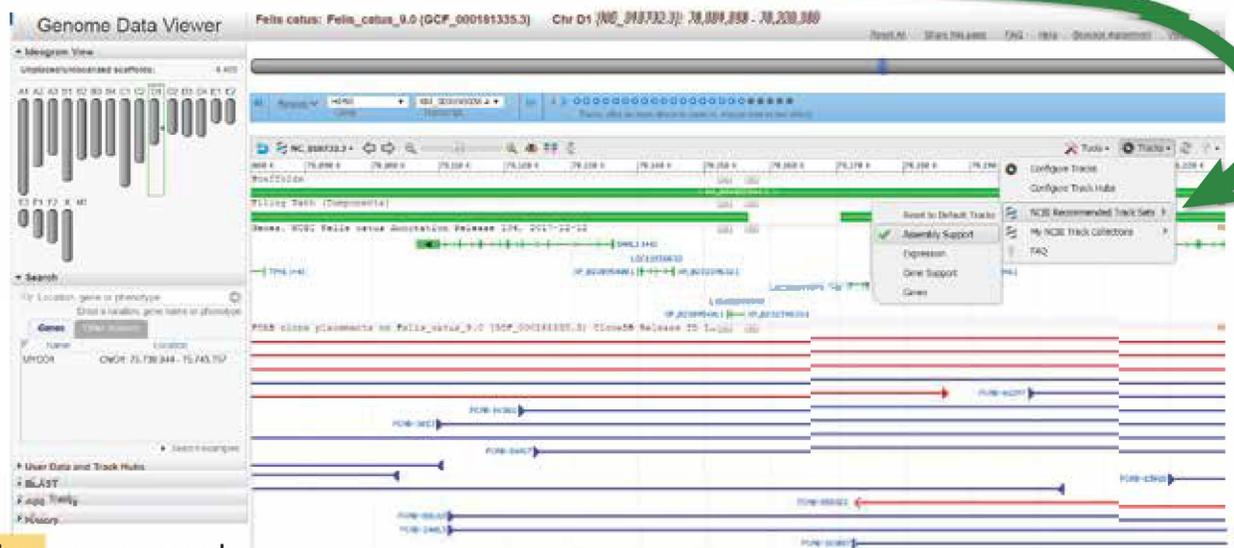
When: April 1st (expected)

Why: The need for a resource specifically dedicated to genomic clones has diminished- with the advent of short read sequencing, fewer and fewer genomic clone end and insert sequences are submitted to NCBI every year. Additionally, the highest value clone related data is available through other NCBI interfaces.

Looking for graphical views of clone placements?

1. Go to **Genome Data Viewer (GDV)**.
2. Select the **Assembly Support** from the **NCBI Recommended Track Sets** to display the clone placements.

ncbi.nlm.nih.gov/genome/gdv/



In the **search box**, you can search for a specific clone with Clone IDs (e.g. RP11-100A1).

To find clones whose placements overlap a gene or other feature of interest, search for that feature, and then scroll down to see the overlapping clones.

Looking for clone sequences, library statistics or placement files?

Go to the **Clone DB FTP site** and select organism you are interested in.

<ftp.ncbi.nlm.nih.gov/repository/clone/reports/>

Files **clone_acstate**, **endinfo** and **library files** provide metadata

Need more information?

000_README_REPORTS.txt

For the data on the placements shown in the graphical view, see the **.gff** files

000_README_GFF.txt

To **download** clone FASTA, see <ftp.ncbi.nlm.nih.gov/repository/clone/utility/>

README_UTILITIES.txt