Question 14)   I would like to find a BAC containing the Drosophila melanogaster gene "GAF". How can I identify such a clone? The BACPAC website does not appear to have this information.

Indeed, we do not maintain copies or downloaded information from various public databases. Maintaining all the BAC-related information would far exceed our resources and funding.

With respect to the specific question: **how to find a Drosophila BAC for the GAF gene**. A search in the UCSC Genome Browser for the GAF gene had no success. The most likely reason: GAF is an abbreviation or synonym of the "official" locus name. A global Google search for "Drosophila GAF gene" came up with better names. From the FlyBase record: Trl as the official symbol, Trithorax-like for the full name. Other synonyms are: GAGA, GAF, Nc70F. Using Trl as the search term in the UCSC Browser, a genome map with annotated BAC names was found. Please note that the BACs are only displayed in the browser for the D. melanogaster Apr. 2006 (BDGP R5/dm3) Assembly. If the BACs are not displayed, then make sure to configure the browser to display the pull-down menu for "BAC End Pairs" to the "full" option.
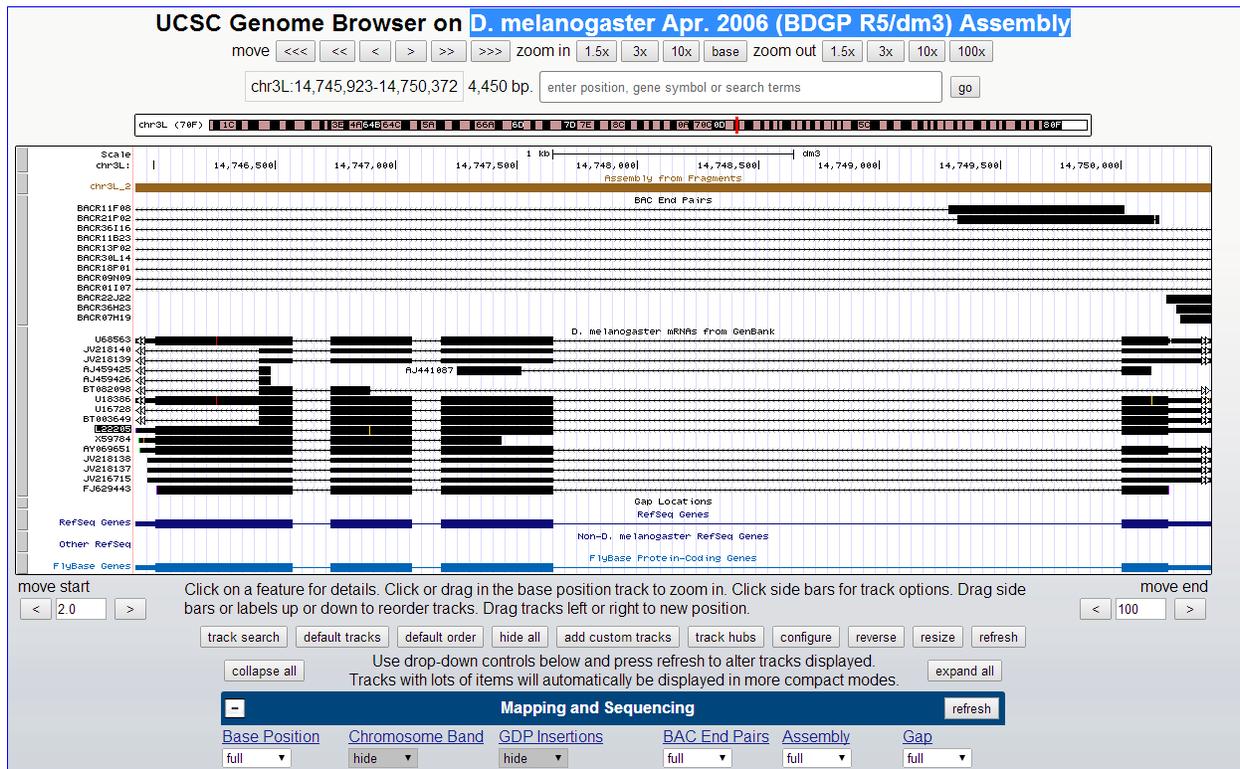
Figure 1: UCSC Genome Browser screenshot for the GAF gene (4.4 kb). Please note that only a small fraction of each BAC is displayed. Location: chr3L:14,745,923-14,750,372 [4,450 bp]

The displayed map (Fig. 1) spans the full gene (4.4 kb) which is only a small fraction of the size of typical BACs. Use the zoom out option to see a better display of the BAC and any nearby genes contained within the same BACs. The BACs displayed in the UCSC Browser have names like "BACR…" and BACN…", which correspond to the RPCI-98 and EDGP-DrosBAC libraries. The typical BAC sizes for these libraries range between 75 -180 kb. To see the full size of the BACs and additional gene content, please "zoom out" in the Browser. See Fig. 2 for a display of a 30X larger region. The two BAC libraries were created from the same fly stock used for creation of the reference genome assembly, sampled around the same date. Please note that for ordering into our electronic shopping cart, the BAC names displayed on the UCSC Browser need to be converted into standard NCBI names. This is explained on the web pages for the RPCI-98 and EDGP-DrosBAC libraries.
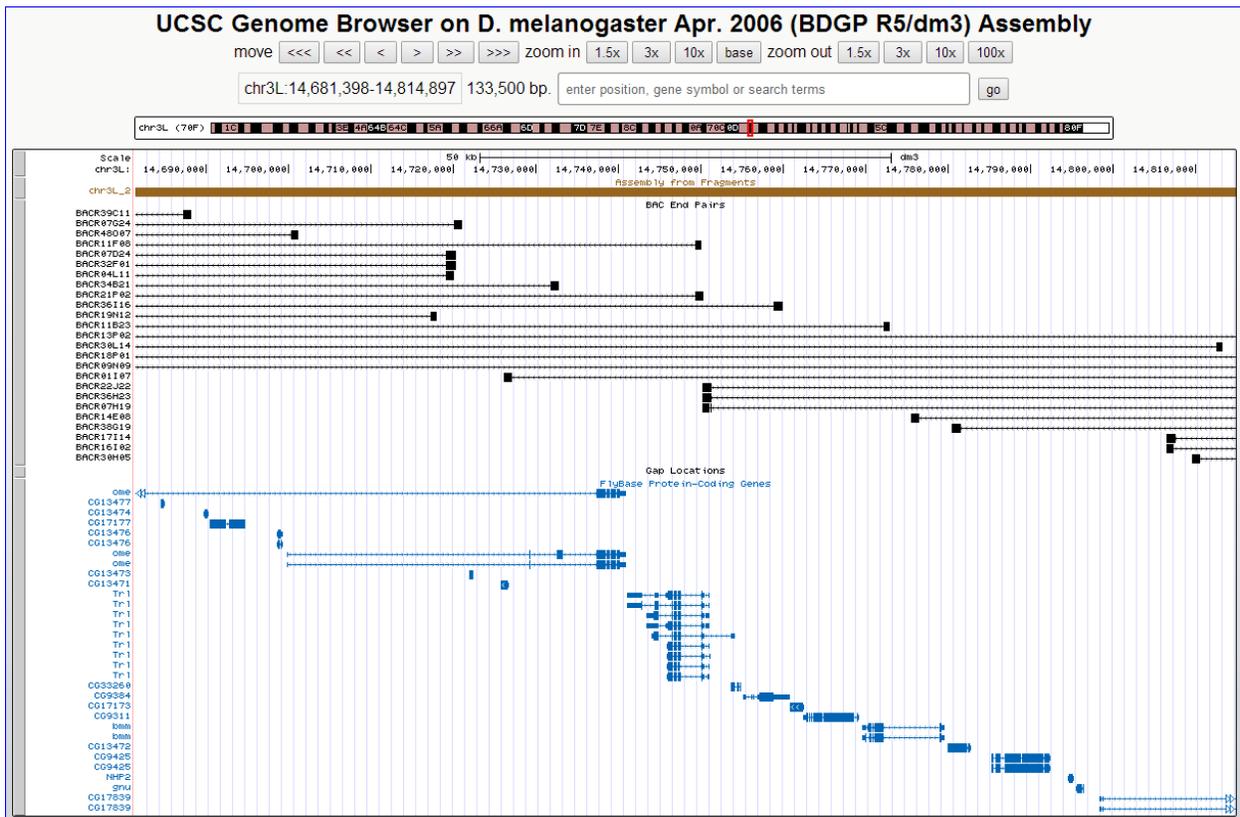
Figure 2: UCSC map at 30X zoom-out. chr3L:14,681,398-14,814,897 [133,500 bp]

Additional BACs in a different size range can be identified from the P[acman] BAC libraries. These BACs have additional benefits, which include the Drosophila White gene as a detection marker and the PhiC31 att site as a recombination site for site-specific integration in fly strains with corresponding PhiC31 att sites randomly integrated in by P-element transposition. BACs corresponding to the CHORI-321 and CHORI-322 libraries can be identified using the P[acman] Genome Browser.

Figure 3: Region of 4.4 kb defined by the GAF gene in the P[acman] browser, with BACs from the CHORI-321 and CHORI-322 libraries. See: http://bicoid.lbl.gov/cgi-bin/gbrowse/getbac/
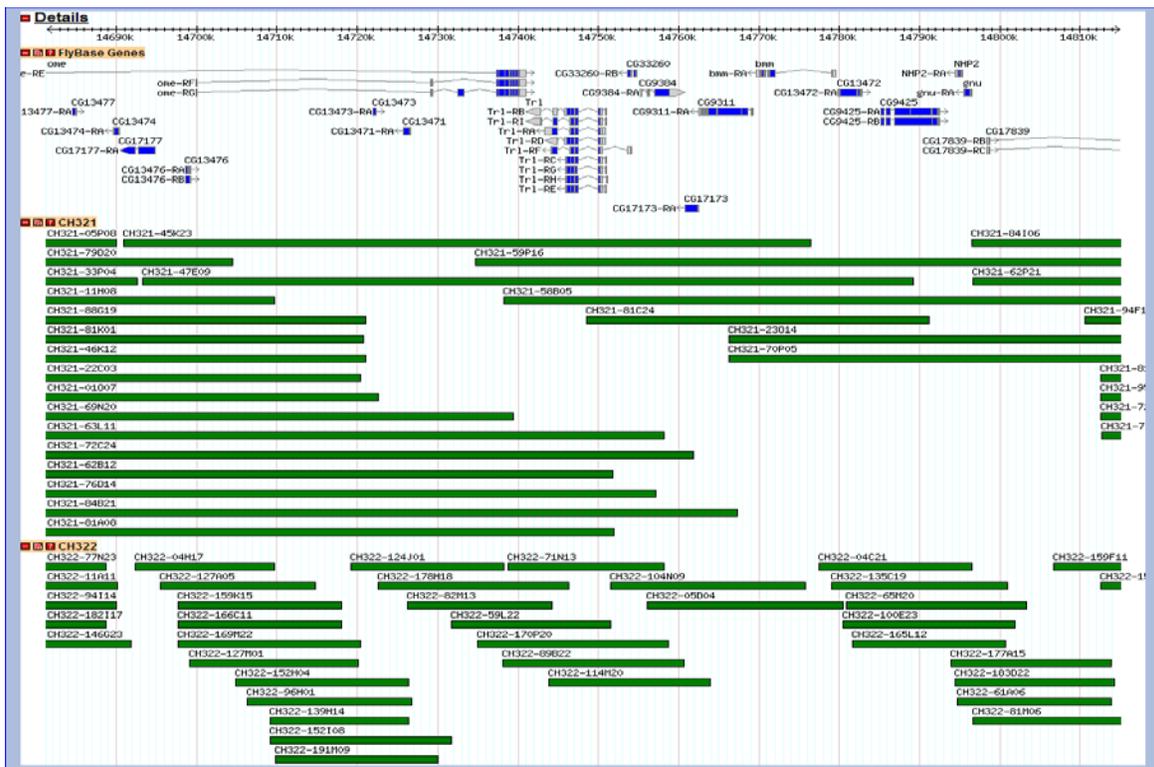
Figure 4: P[acman] browser display for the region centered on the GAF gene. Display of 133 kb region.