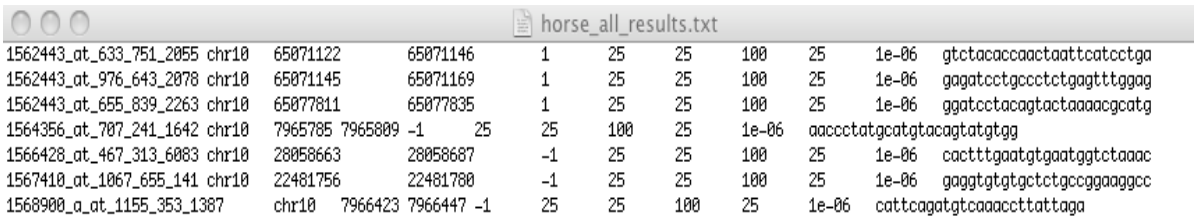
## Using deblast and maskit Xspecies script

Both deblast and maskit scripts can be downloaded as CDF_writer from the Xspecies web page at: http://affy.arabidopsis.info/xspecies/

You will need perl installed e.g. activeperl for windows – native for other OS

### deblast

1. Obtain a BLAST result file, where the format is: probest-ID_x-postion_y-position_mismatch and saved as a .txt file.




2. Put BLAST file and original CDF for the array in the CDF writer folder
3. Run the deblast.pl script and follow the instructions.

### maskit script

1. Create a probe list file (which can be used to create a CDF with just the probes in the list, where the probes in the list are excluded). The format of the file is: x-position<tab>y-position<tab>probe-interrogation-position and saved as a .ufo file.


2. Put the .ufo file and the original CDF (or modified CDF) file in the CDF_writer folder
3. Run the maskit script and follow the instructions using the command: >perl maskit.pl –v CDF_file_name ufo_file_name