

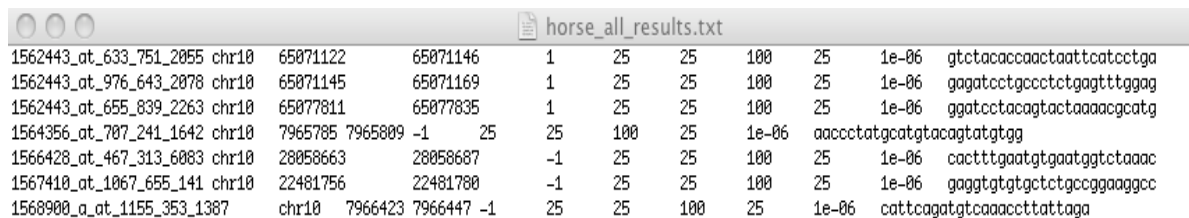
## Using deblast and maskit Xspecies script

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: probe-ID\_x-position\_y-position\_mismatch and saved as a .txt file.



```
horse_all_results.txt
1562443_at_633_751_2055 chr10 65071122 65071146 1 25 25 100 25 1e-06 gtctacaccaactaattcatcctga
1562443_at_976_643_2078 chr10 65071145 65071169 1 25 25 100 25 1e-06 gagatcctgccctctgagtttgag
1562443_at_655_839_2263 chr10 65077811 65077835 1 25 25 100 25 1e-06 ggatcctacagtactaaaacgcatg
1564356_at_707_241_1642 chr10 7965785 7965809 -1 25 25 100 25 1e-06 aacctatgcatgtacagtatgtg
1566428_at_467_313_6083 chr10 28058663 28058687 -1 25 25 100 25 1e-06 cactttgaatgtgaatggtaaac
1567410_at_1067_655_141 chr10 22481756 22481780 -1 25 25 100 25 1e-06 gaggtgtgtgctctgccggaaggcc
1568900_a_at_1155_353_1387 chr10 7966423 7966447 -1 25 25 100 25 1e-06 cattcagatgtcaaaccttattaga
```

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.



```
gspots.ufo
g spots
13 449 62
557 101 345
698 539 513
626 661 66
331 355 184
35 41 260
113 237 135
---
```

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`