Using the GenoDive output in the functions:
dlr and *plot_assignment_dlr*

number.individuals = 394

number.pop = 9

l.skip = 33

we want to read this part of the file

pop.id.start = 5   **pop.id.end = 7**

My individual's id:
EST-GRA-ADU-2013-015

↑ ↑
5 7

note: No pop id constant in your individual's name?
use the strata argument

arguments: pop.levels and pop.labels

Ion the example of the GenoDive assignment analysis output file, I had combined sampling sites into populations.
Sites: JEN, LAN, GRA, BUR, GUL, ANG, LLI, WEI, FOX, GOD, HAY, CHU
Pop: JEN, LAN, GRA, BUR, GUL, LNR, LNR, LNR, FOX, HAY, HAY, CHU

ANG+LLI+WEI are regrouped into LNR
GOD + HAY are regrouped into HAY

How to handle this ?
option 1: With the pop.id.start, pop.id.end argument and levels and labels.
pop.levels = c("JEN", "LAN", "GRA", "BUR", "GUL", "ANG", "LLI", "WEI", "FOX", "GOD", "HAY", "CHU")
pop.labels = c("JEN", "LAN", "GRA", "BUR", "GUL", "LNR", "LNR", "LNR", "FOX", "HAY", "HAY", "CHU")

option 2: use the strata argument in the functions