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> library(HIV.db)
> library(Pviz)
> alignObj <- readAlign()
> refScale <- alignObj[[1]]
> refSeq <- alignObj[[2]]
> HIV_db <- loadFeatures(ref = "env")
> envBase <- getFeature(HIV_db)
> envStart = getHXB2Coordinates(envBase)[1, ][1]
> envEnd = getHXB2Coordinates(envBase)[1, ][2]
> proteins <- getFeature(HIV_db, category = "protein", start = envStart,
+   end = envEnd, frame = getFrame(envBase))
> antis <- getEpitope(envBase, name = c("VRC01"))
> helix <- getChildren(envBase, category = c("helix"))

> rpext <- ProteinAxisTrack(littleTicks = TRUE)
> rpref <- ProteinAxisTrack(refScale = refScale, adNC = TRUE)

> sTrack <- SequenceTrack(refSeq)

> data(pepMicroarrayEx)
> p1Track <- ProbeTrack(pepMicroarrayEx$probeSeq, pepMicroarrayEx$probeFreq,
+   pepMicroarrayEx$probePos, protein = "gp120", name = "sequence(B)")

> a2Track <- ATrack(id = proteins@values@unlistData@listData[["name"]],
+   start = start(proteins), end = end(proteins), genome = "hxb2",
+   name = "Protein", protein = "gp120", fill = "navyblue", size = 1)
> a3Track <- ATrack(id = helix@values@unlistData@listData[["name"]],
+   start = start(helix), end = end(helix), genome = "hxb2",
+   name = "Helix", fill = "orange", protein = "gp120")
> a6Track <- ATrack(id = antis@values@unlistData@listData[["name"]],
+   start = start(antis), end = end(antis), genome = "hxb2",
+   name = "Epitopes", fill = "gray", protein = "gp120")

> data(pepExprEx)
> library(IRanges)
> d6Track <- DTrack(range = IRanges(start = pepExprEx$dPos, width = 1),
+   groups = rownames(pepExprEx$dExpr), data = pepExprEx$dExpr,
+   genome = "hxb2", protein = "gp120", col = c("orange", "gray"),
+   cex = 1)

> plotTracks(trackList = c(rpext, rpref, sTrack, a2Track, a3Track,
+   a6Track, p1Track, d6Track), from = 1, to = 150, type = c("p",
+   "smooth"), stacking = "dense", legend = TRUE, showFeatureId = TRUE)

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