

3: rapport d'analyse de la comparaison des résultats AGL et AFFYMETRIX

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1: Importation des données

```
resultat.agl <- read.table('2-result/1-fold-change-agl.txt',sep='\t',header=T)
resultat.affx <- read.table('2-result/2-fold-change-affx.txt',sep='\t',header=T)

head(resultat.agl)

##   annotation coefficient.agl    pvalue.agl adj.pvalue.agl
## 1      STMN4        7.659475 2.339391e-21  1.027718e-16
## 2      AHSG       -9.362454 5.764477e-21  1.266196e-16
## 3      HBG1       -9.648858 1.514123e-20  2.217232e-16
## 4     SPARCL1        8.964683 3.257294e-20  2.601207e-16
## 5      STMN2        9.439867 4.136058e-20  2.601207e-16
## 6      SCN2B        6.885920 4.433064e-20  2.601207e-16

head(resultat.affx)

##   annotation coefficient.affx    pvalue.affx adj.pvalue.affx
## 1      HBZ        -9.778036 1.552200e-20  3.507633e-16
## 2      RRM2       -9.187942 1.567027e-20  3.507633e-16
## 3      ALB        -11.415371 8.131817e-20  1.016181e-15
## 4     CADM2         7.181440 1.209417e-19  1.016181e-15
## 5     IGLC1       -9.037074 1.385960e-19  1.016181e-15
## 6      SYN2        8.780131 1.465968e-19  1.016181e-15
```

On constate que les résultats n'apparaissent pas dans le même ordre.

2: Alignement des tableaux de résultats

```
idx <- match(resultat.agl$annotation,resultat.affx$annotation)
resultat.affx <- resultat.affx[idx,]

head(resultat.agl)

##   annotation coefficient.agl    pvalue.agl adj.pvalue.agl
## 1      STMN4        7.659475 2.339391e-21  1.027718e-16
## 2      AHSG       -9.362454 5.764477e-21  1.266196e-16
## 3      HBG1       -9.648858 1.514123e-20  2.217232e-16
## 4     SPARCL1        8.964683 3.257294e-20  2.601207e-16
## 5      STMN2        9.439867 4.136058e-20  2.601207e-16
## 6      SCN2B        6.885920 4.433064e-20  2.601207e-16
```

```
head(resultat.affx)

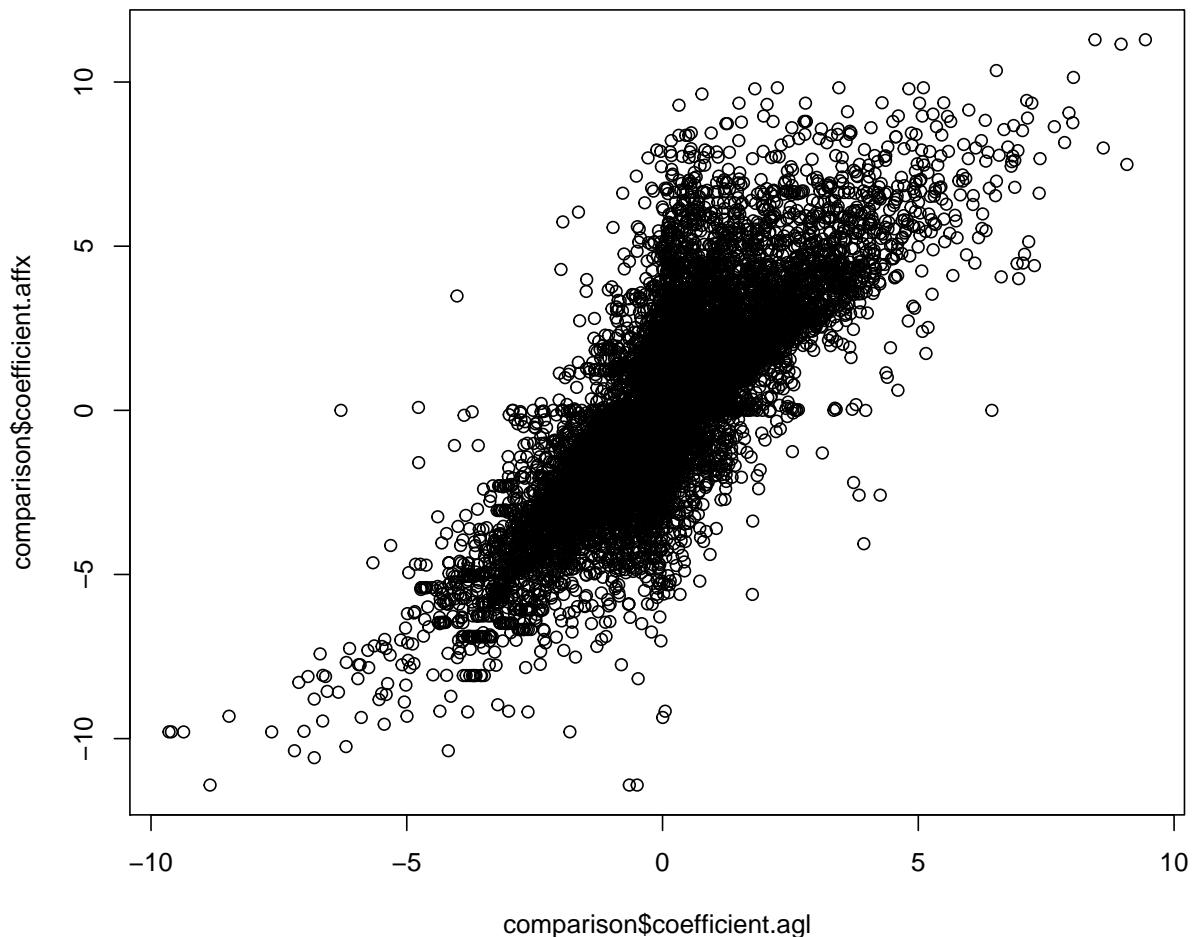
##      annotation coefficient.affx  pvalue.affx adj.pvalue.affx
## 278      STMN4          8.640565 5.827534e-15   9.324833e-13
## 267      AHSG         -9.797090 5.285278e-15   8.861847e-13
## 3431     HBG1         -9.794047 6.772382e-11   8.836666e-10
## 313      SPARCL1        11.154347 8.484570e-15   1.213538e-12
## 177      STMN2         11.289324 1.198833e-15   3.016249e-13
## 52       SCN2B          7.614857 4.083252e-17   3.515366e-14
```

On peut désormais créer un tableau avec les résultats des 2 plateformes.

```
comparison <- data.frame(resultat.agl,resultat.affx)
```

A partir de ce tableau, on crée facilement des graphiques de comparaison des log2 fold-changes et on calcule facilement des coefficients de corrélations entre les résultats des 2 plateformes (Affymetrix versus Agilent)

```
plot(comparison$coefficient.agl,comparison$coefficient.affx)
```



```
cor(comparison$coefficient.agl,comparison$coefficient.affx,use='complete.obs')

## [1] 0.8034789

cor(comparison$coefficient.agl,comparison$coefficient.affx,use='complete.obs',method='spearman')

## [1] 0.8042548
```