

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)
```

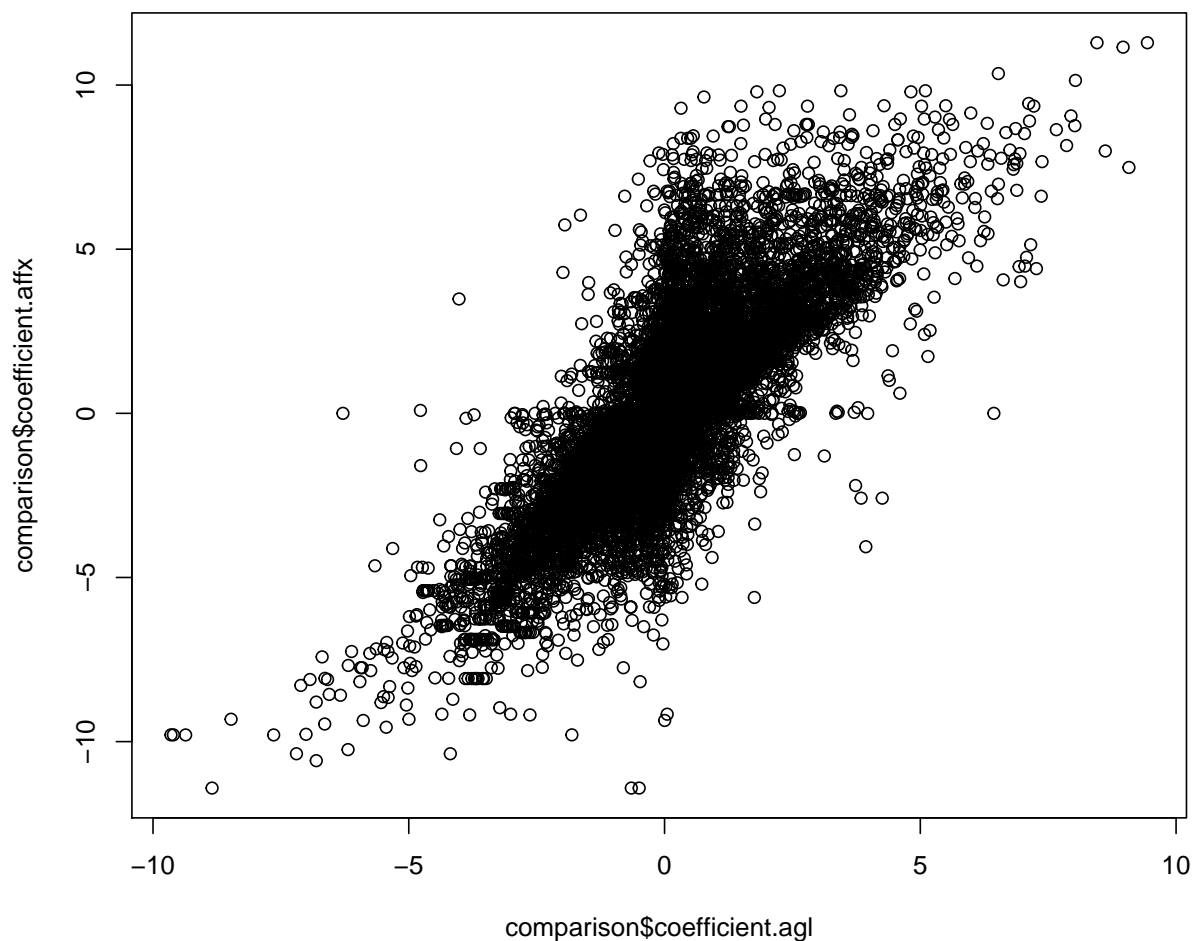
```
##      annotation coefficient.affx  pvalue.affx adj.pvalue.affx
## 278      STMN4      8.640565 5.827534e-15  9.324833e-13
## 267      AHSG     -9.797090 5.285278e-15  8.861847e-13
## 3431     HBG1     -9.794047 6.772382e-11  8.836666e-10
## 313     SPARCL1    11.154347 8.484570e-15  1.213538e-12
## 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.

```
comparaison <- 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(comparaison$coefficient.agl,comparaison$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
```