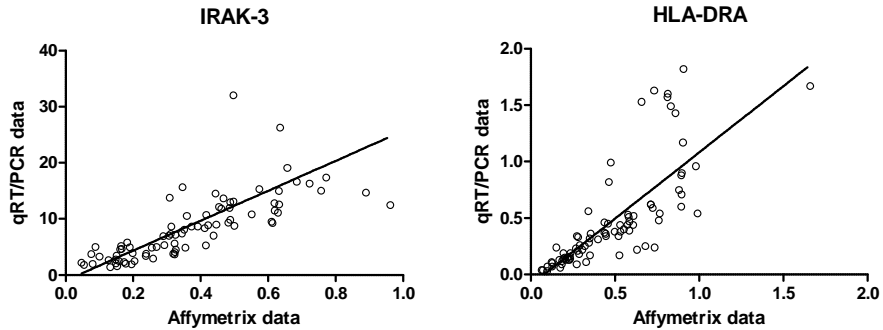


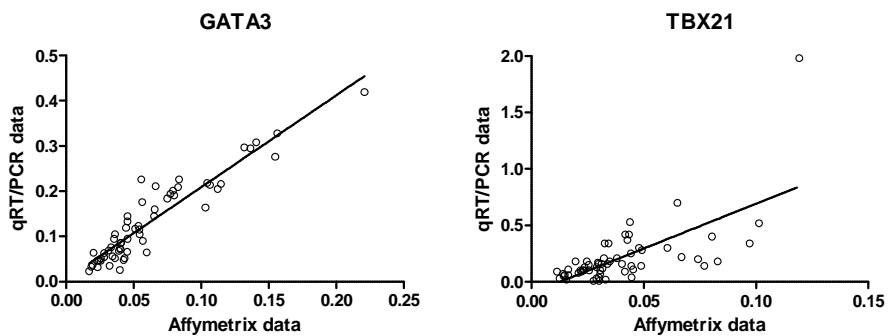
Figure S2. qRT-PCR correlation with affymetrix data.

- 1- Correlation for IRAK-3 identified in the list of up regulated genes from the most increased canonical pathways enriched at H0, and HLA-DRA identified from the top 10 gene families suppressed after septic shock.



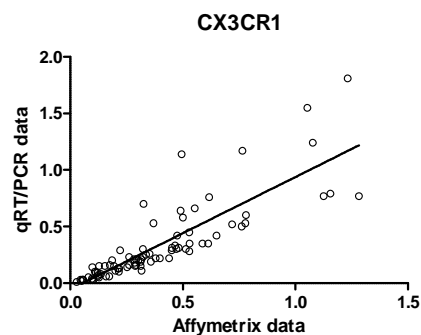
|                         |                |                         |                |
|-------------------------|----------------|-------------------------|----------------|
| Spearman r              | 0,8858         | Spearman r              | 0,8864         |
| 95% confidence interval | 0,826 to 0,926 | 95% confidence interval | 0,827 to 0,926 |
| P value (two-tailed)    | < 0,0001       | P value (two-tailed)    | < 0,0001       |
| Number of XY Pairs      | 82             | Number of XY Pairs      | 82             |

- 2- Correlation for the T cells transcription factor GATA3 and TBX21



|                         |                |                         |                |
|-------------------------|----------------|-------------------------|----------------|
| Spearman r              | 0,9148         | Spearman r              | 0,6718         |
| 95% confidence interval | 0,858 to 0,949 | 95% confidence interval | 0,496 to 0,795 |
| P value (two-tailed)    | < 0,0001       | P value (two-tailed)    | < 0,0001       |
| Number of XY Pairs      | 59             | Number of XY Pairs      | 59             |

- 3- Correlation for CX3CR1 differentially expressed between SAPSII-high and -low group of patients



|                         |                |
|-------------------------|----------------|
| Spearman r              | 0,94           |
| 95% confidence interval | 0,906 to 0,961 |
| P value (two-tailed)    | < 0,0001       |
| Number of XY Pairs      | 82             |