1.1. Methods M4

BRB Array Tools analysis methods: Fluorescence intensities from the three replicates of each sample condition were $\log_2$ transformed and normalized to an average TCPS reference array (average of three 14 d TCPS samples). Intensities for multiple probes corresponding to one gene were averaged. Genes were also excluded if less than 10 % of arrays showed a 1.5-fold change from the median.

Hierarchical cluster analysis, with centered correlation and average linkage, was performed using all arrays (except the TCPS controls) based on the subset of 199 genes not excluded by the above criteria. A dendrogram along with a heat map for each gene is shown in [Figure 7a].

For SAM analysis, a target proportion of false discoveries of 0.05 with 100 permutations and percentile set to 90 % was used as a threshold for each SAM comparison.

Within the DAVID database, GO terms for biological process (BP), cellular component (CC), and molecular function (MF) were queried along with Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways and processed by functional annotation clustering for enriched terms [33]. An annotation cluster was considered significant if its enrichment score exceed 1.3 and individual KEGG Pathways and GO terms were considered significant if their p-values exceeded 0.05 [32]. For simplicity, only BP GO terms and the first three GO terms in each annotation cluster are presented if more than one annotation cluster was found to be significantly enriched.