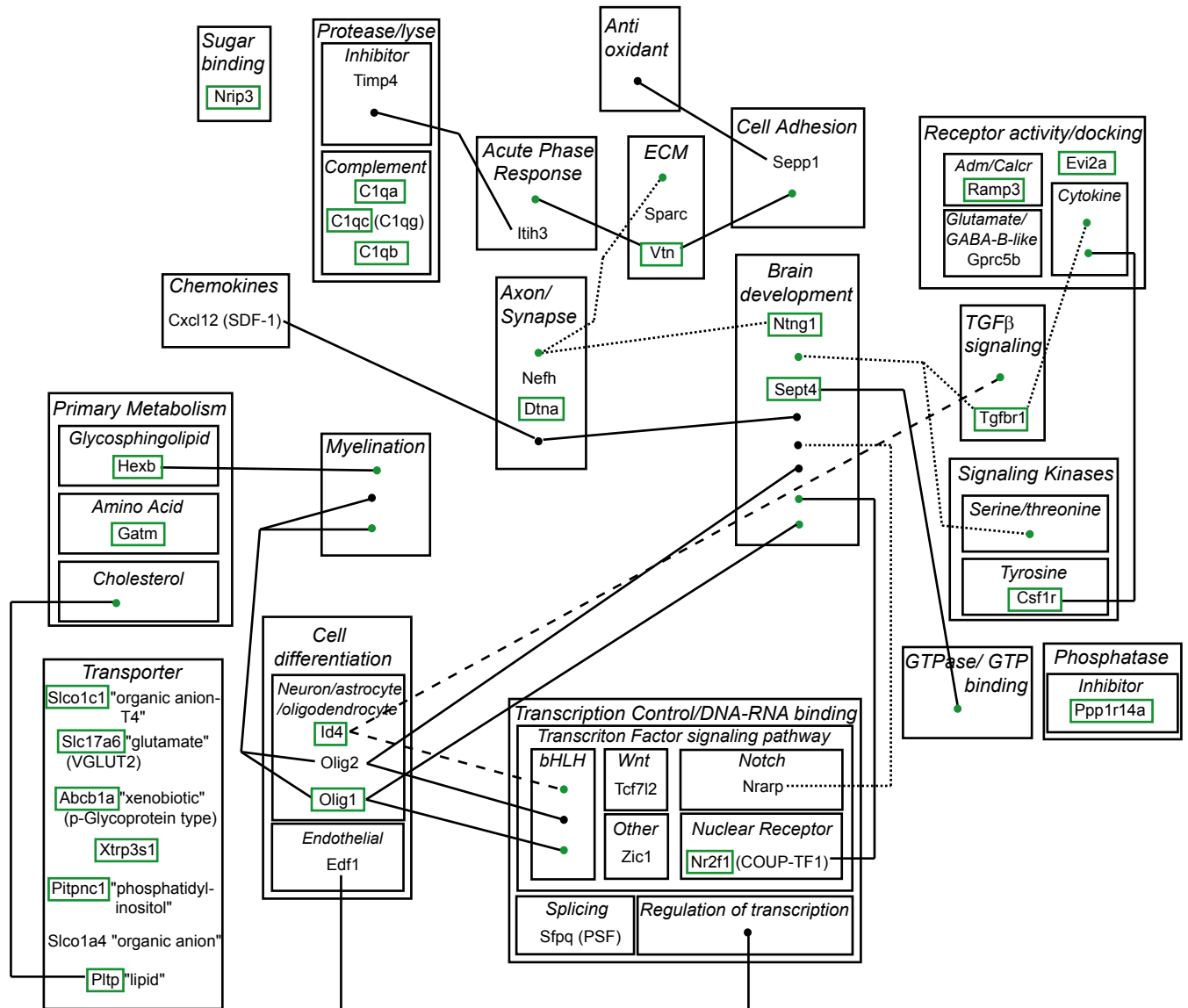
 LPS Downregulation
 attenuated by RU486

● Connector link: gene also present in other group(s)

Figure S1B -Genes Downregulated by LPS



Genes Upregulated by LPS only in presence of RU486

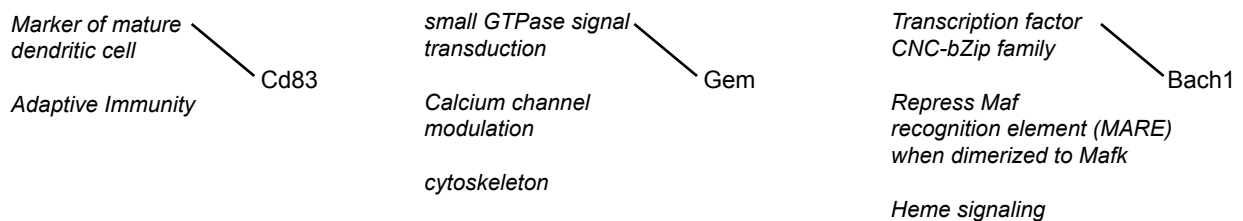


Figure S1C - RU486 main effect probe sets

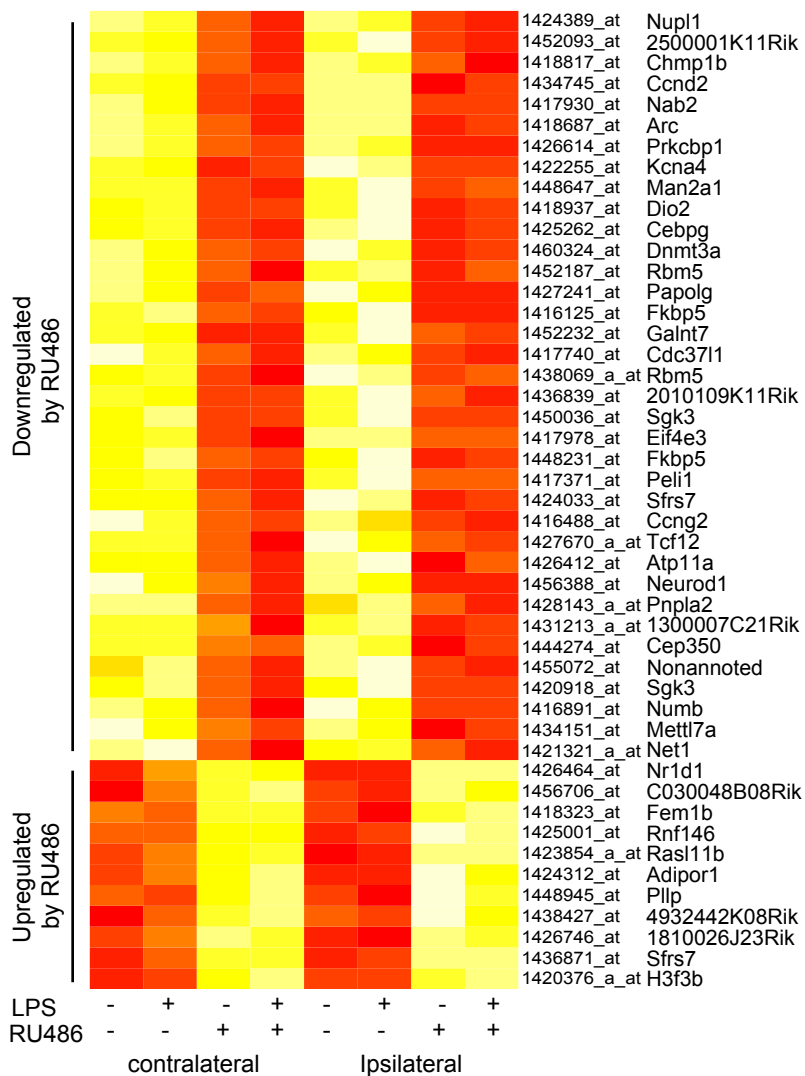


Figure S1D - RU486 Main effect 2-contrast plot

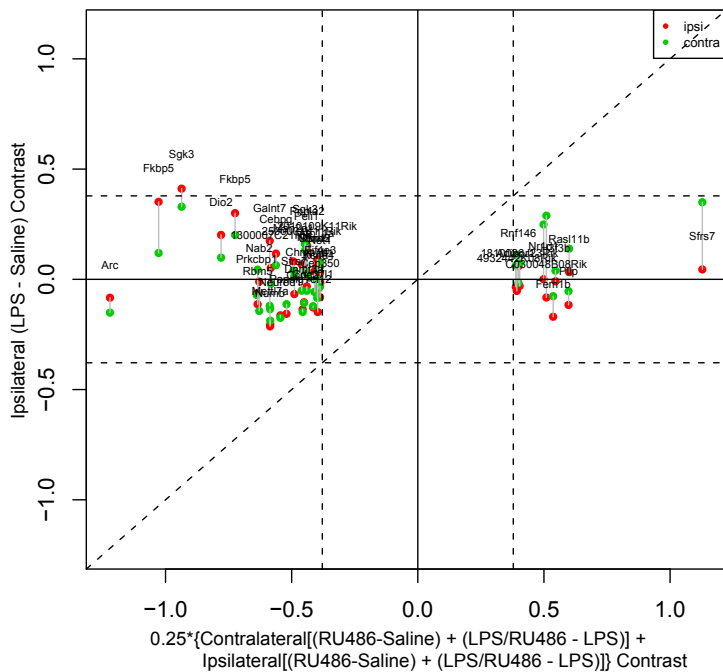


Figure S1E

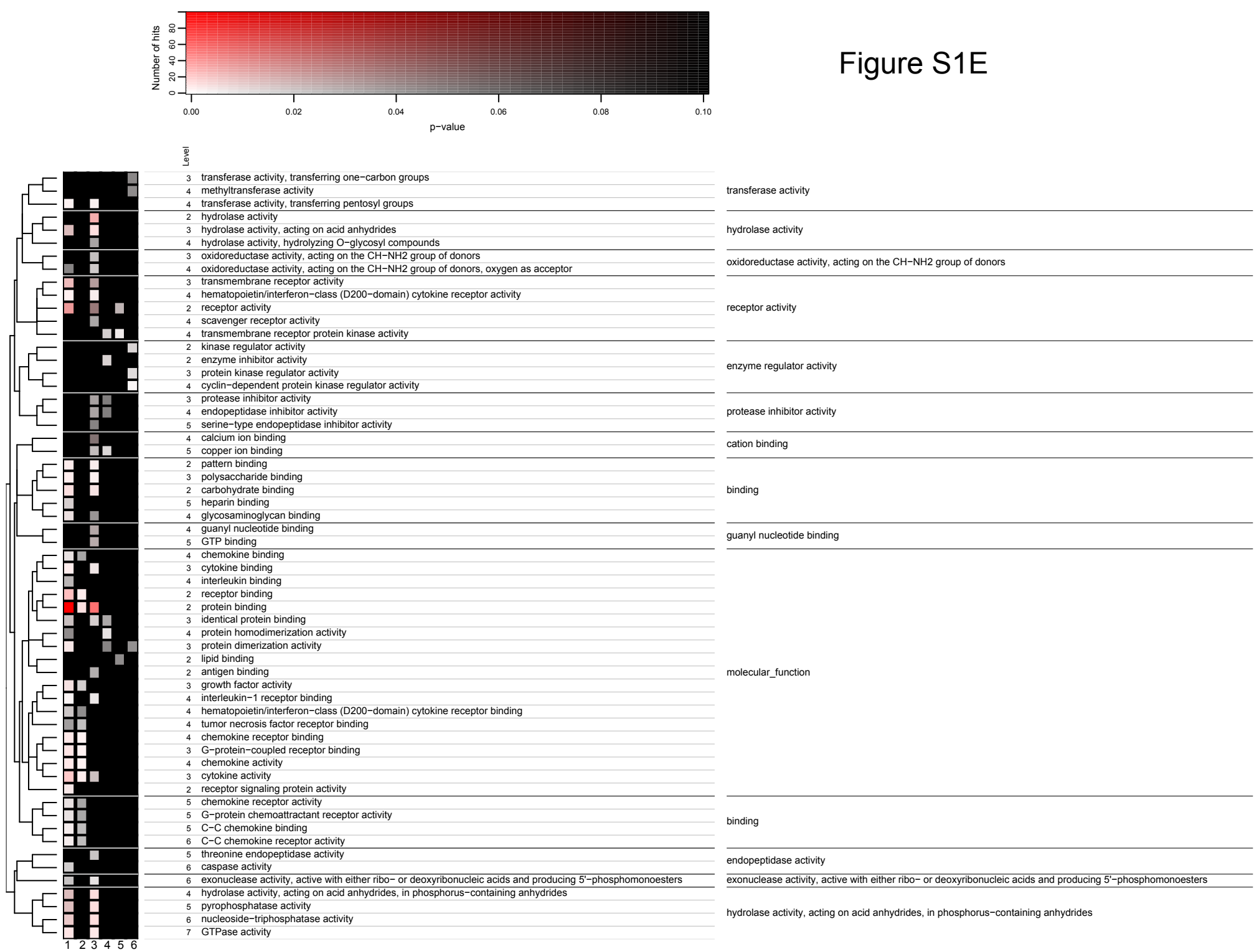


Figure S1F

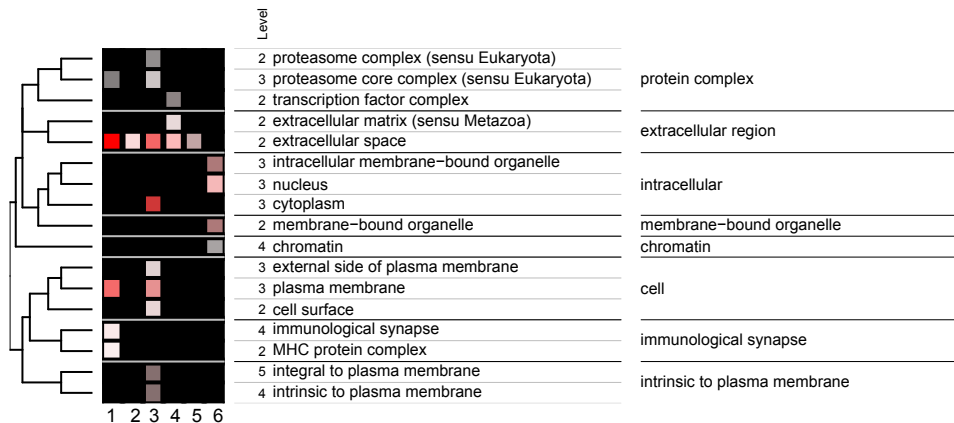
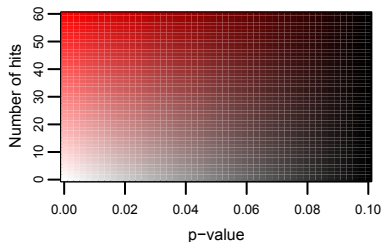


Figure S1A – Diagram representing relevant functional categories of genes upregulated by LPS. Genes selected by oligonucleotide array statistical analysis were grouped in each category box and vertically organized according to a fold change sorting (in each box). Such classification was organized according to authors' interpretation of the results. For non-biased statistical inference of gene function readers should refer to Figure 2 of the main manuscript. Gene symbols surrounded by green boxes indicate activated genes that had a significant lower expression when animals received RU486 pre-treatment before LPS challenge. Red boxes indicate genes that presented exacerbated expression by RU486 in combination to LPS.

Figure S1B – Diagram representing relevant functional categories of genes downregulated by LPS or exclusively induced in response to LPS/RU486 treatment. Genes selected by oligonucleotide array statistical analysis were grouped in each category box and vertically organized according to a fold change sorting (in each box). Such classification was organized according to authors' interpretation of the results. Please see the Figure 2 (main manuscript) for non-biased statistical inference of gene function. Genes highlighted by green boxes are those locally repressed by LPS treatment, but their repressive effect is significantly attenuated by RU486 pre-treatment.

Figure S1C – List of RU486 main effect probe sets. The list is organized following a heat map. Lower expression values coded in red and higher values coded in white/yellow.

Figure S1D – A 2-contrast plot of genes selected as differently expressed according to RU486 main effect. The abscissa axis represents the difference (contrast) between all samples treated with RU486 treatment and those treated with DMSO (vehicle) in RMA expression levels;

ordinate axis represents the LPS *vs.* Saline contrast. Red dots represent ipsilateral contrast value; green dots, represent contralateral contrast values.

Figure S1E – Plot showing significant molecular function (hypergeometric distribution) associated with six different lists of differently expressed genes (1 - LPS upregulated, 2 - LPS upregulation exacerbated by RU486, 3 - LPS upregulation prevented by RU486, 4 - LPS downregulated, 5 - LPS downregulation prevented by RU486 and 6 - RU486 main effect). Hierarchical clustering of the Gene Ontology nodes was performed as described in experimental procedures supplementary file. A color/intensity code assigns number of genes and p-value for each molecular function associated with the lists' heat map.

Figure S1F –The plot depicts significant cellular components (hypergeometric distribution) associated with six different lists of differently expressed genes (1 - LPS upregulated, 2 - LPS upregulation exacerbated by RU486, 3 - LPS upregulation prevented by RU486, 4 - LPS downregulated, 5 - LPS downregulation prevented by RU486 and 6 - RU486 main effect). Hierarchical clustering of the Gene Ontology nodes was performed as described in experimental procedures supplementary file. A color/intensity code assigns number of genes and p-value for each cellular component associated with the lists' heat map.