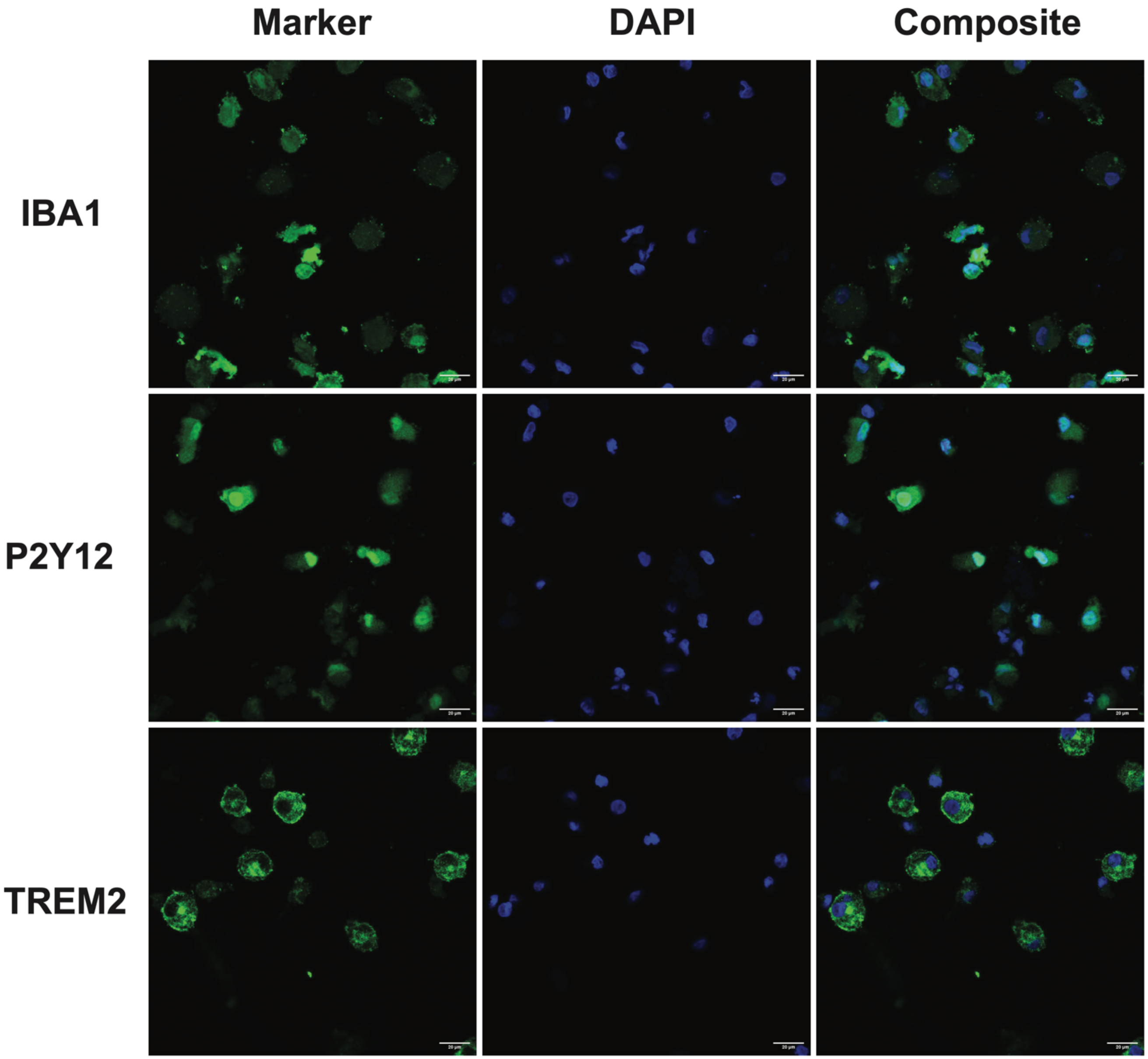
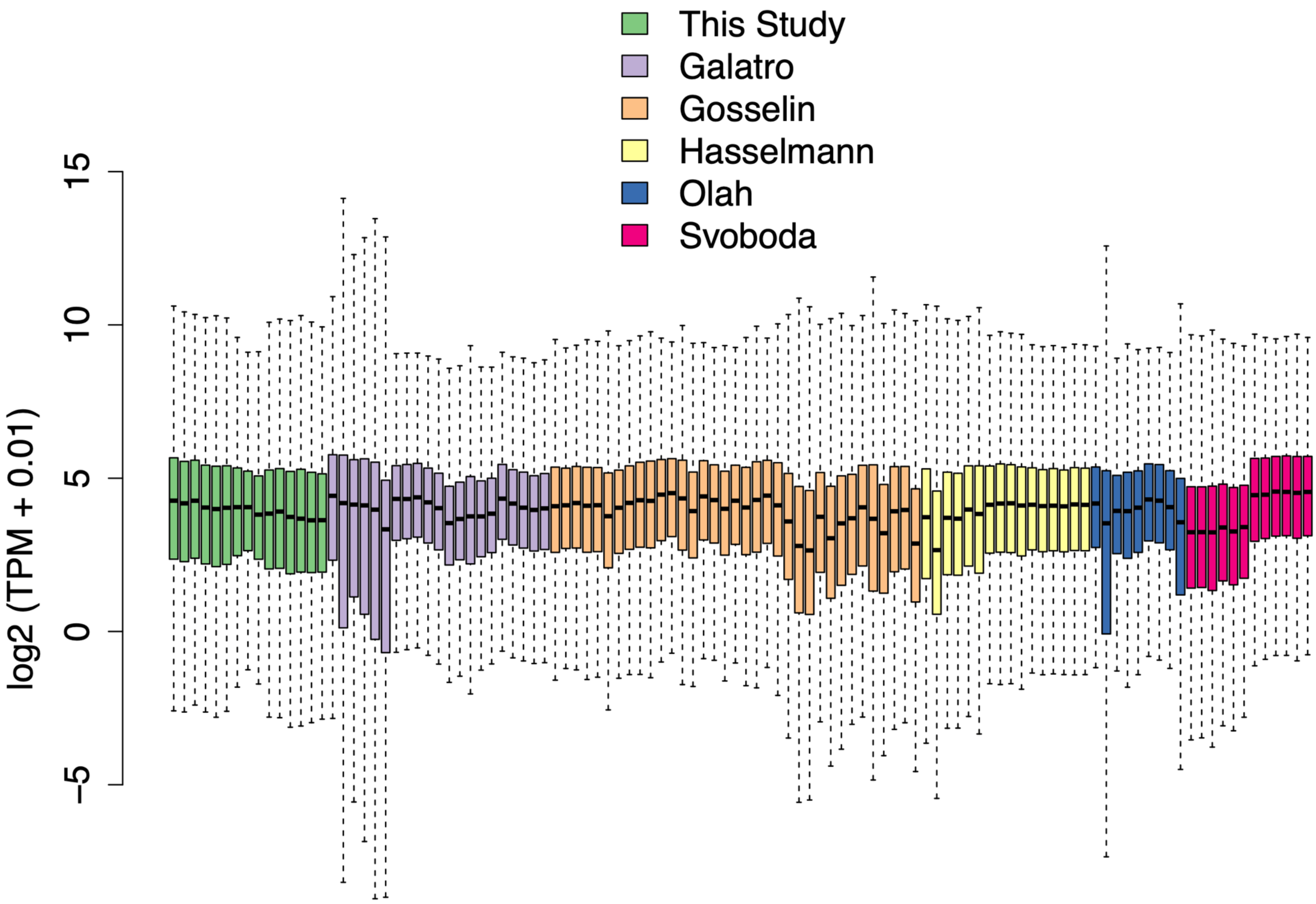
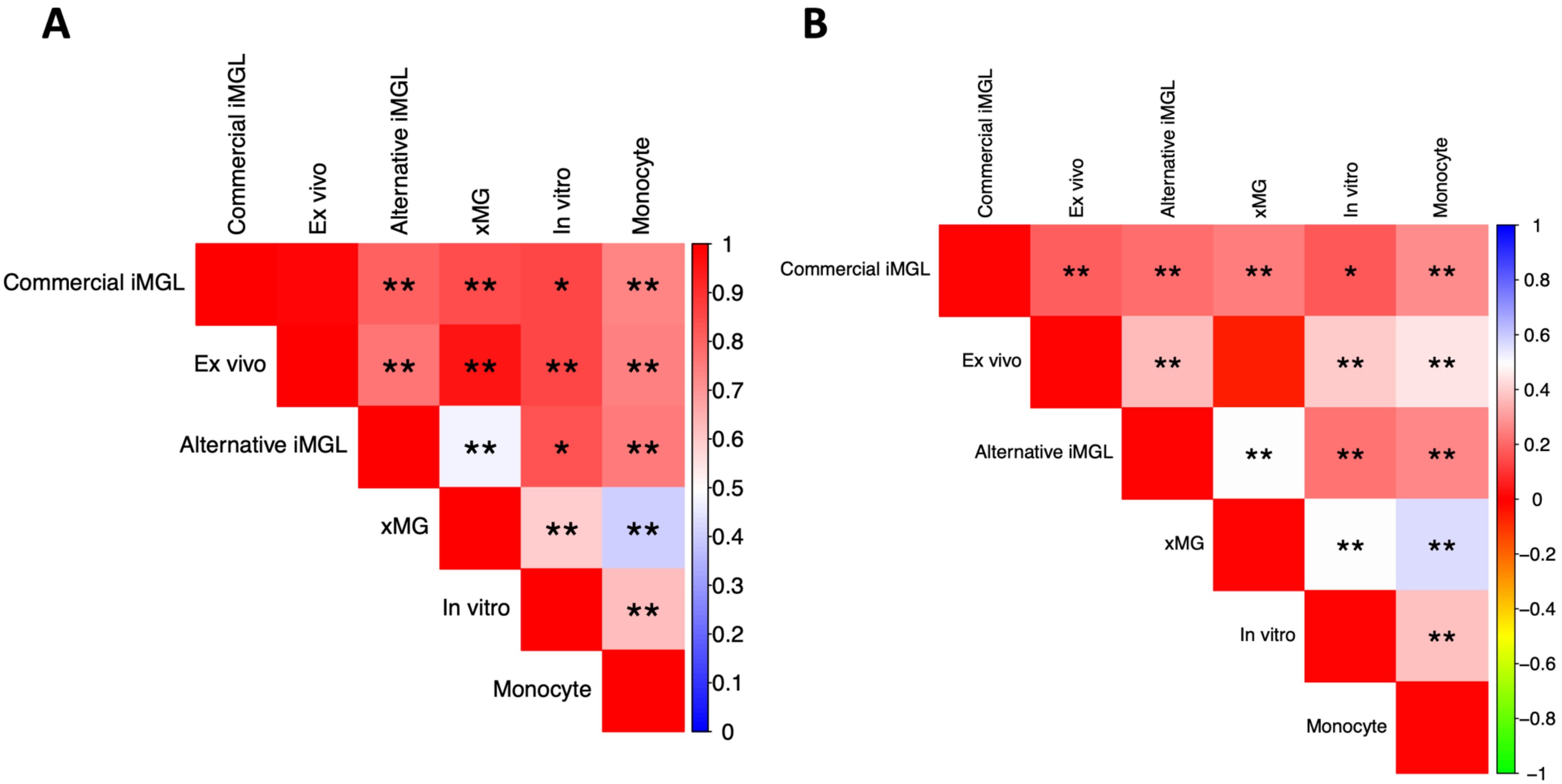

Marker
DAPI
Composite
IBA1
P2Y12
TREM2
20 μm

Supplementary Figure 1. Individual and composite immunofluorescence images of Commercial iMGL cells stained with *IBA1*, *P2Y12*, or *TREM2* (green) and DAPI (blue). The scale bar represents 20 μm.


This Study
Galatro
Gosselin
Hasselmann
Olah
Svoboda
log2 (TPM + 0.01)
−5
0
5
10
15

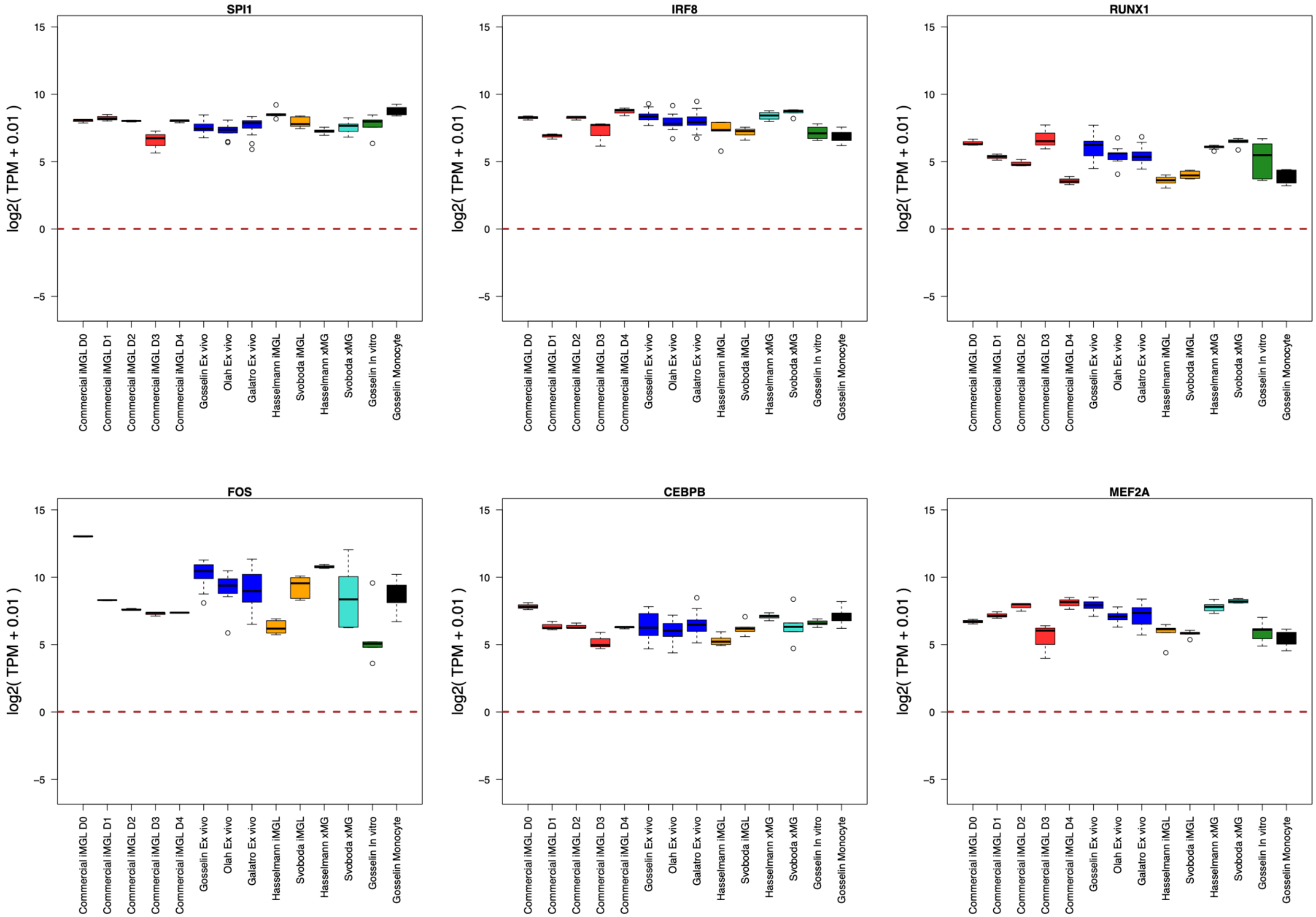
Supplementary Figure 2. Distribution of gene expression values for 12,392 expressed genes across the Commercial iMGL time course and external bulk RNA-seq datasets.

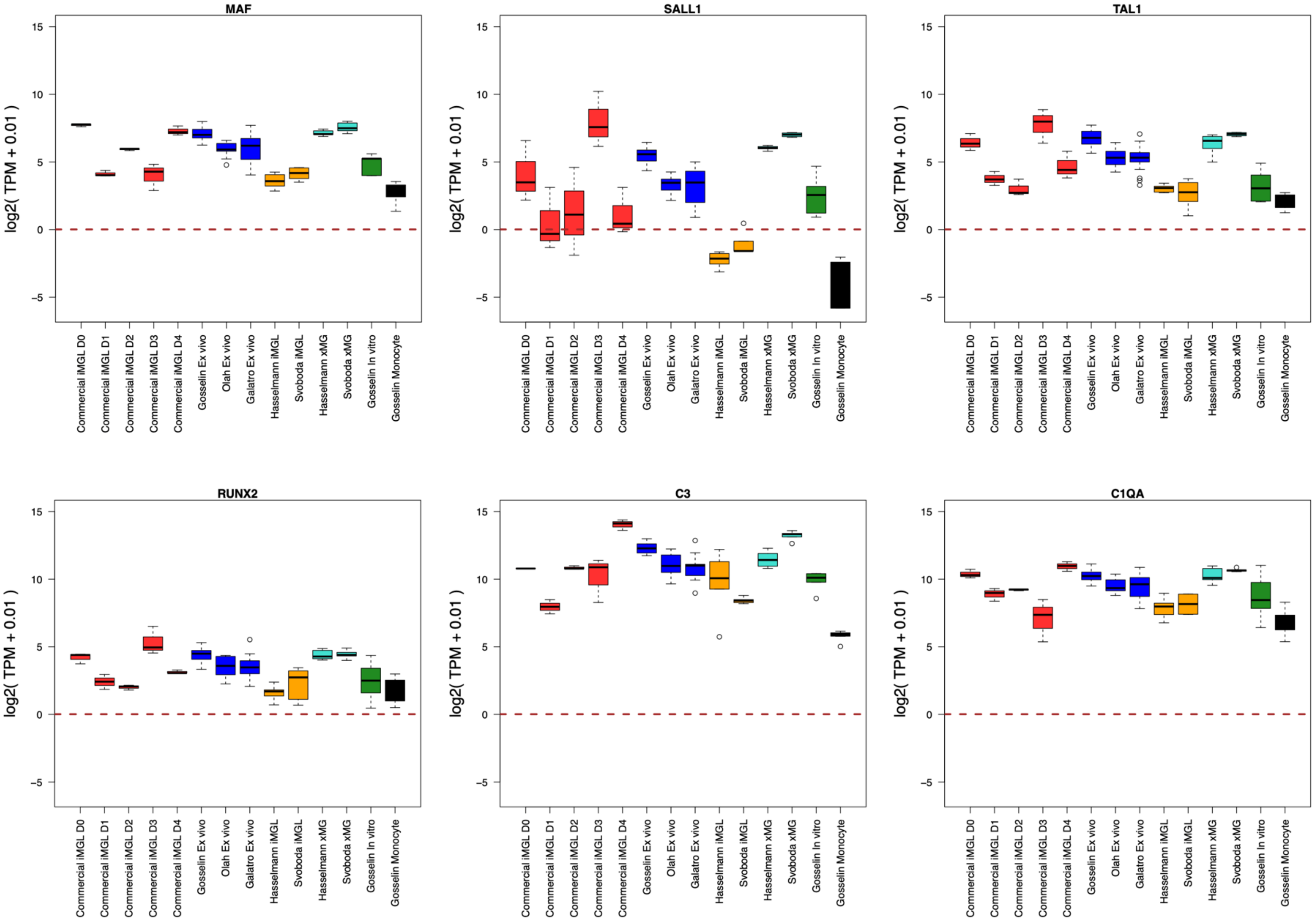

A
Commercial iMGL
Ex vivo
Alternative iMGL
xMG
In vitro
Monocyte
**
*
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
B
Commercial iMGL
Ex vivo
Alternative iMGL
xMG
In vitro
Monocyte
**
*
1
0.8
0.6
0.4
0.2
0
−0.2
−0.4
−0.6
−0.8
−1

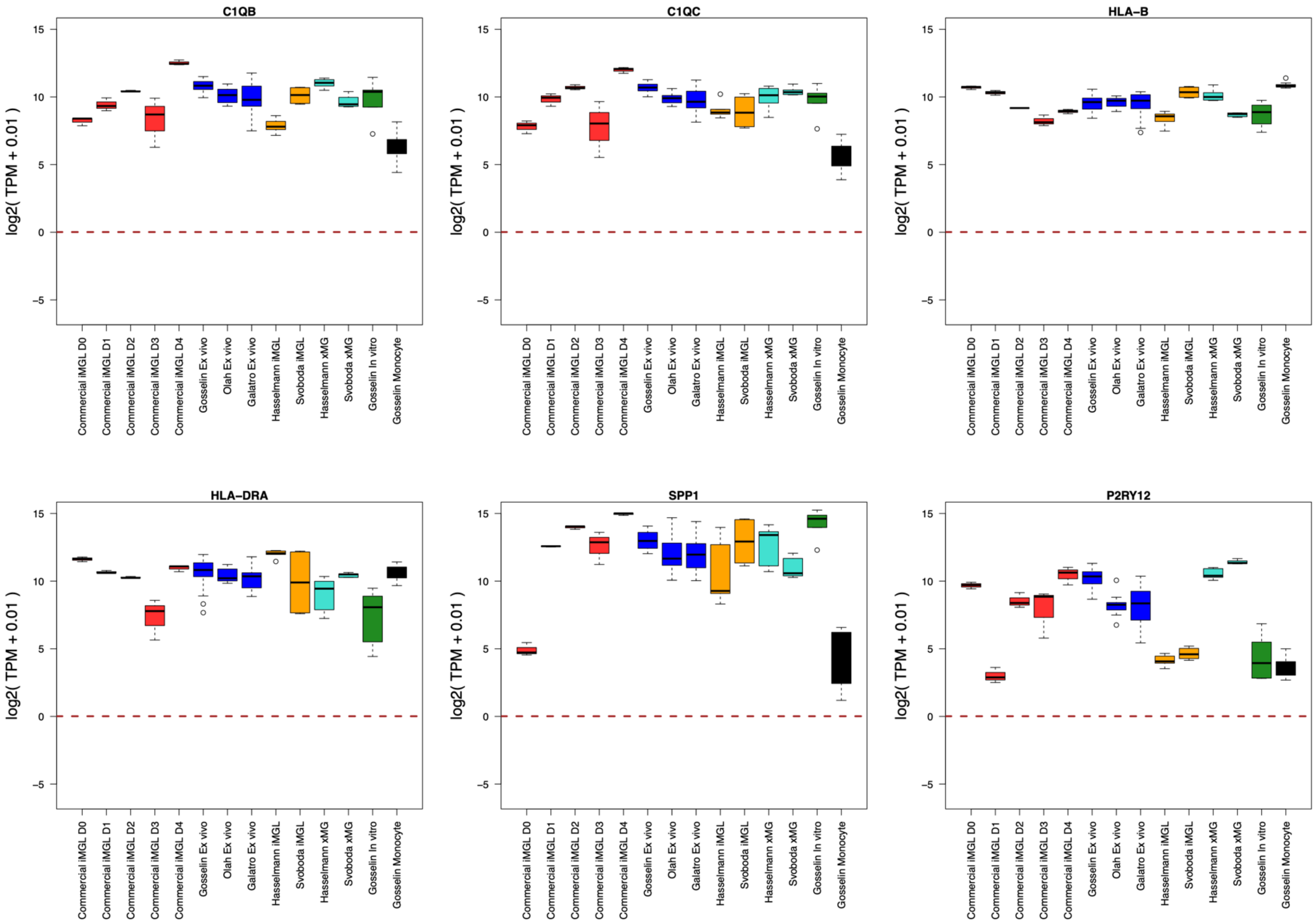
Supplementary Figure 3. Quantitative PCA comparisons

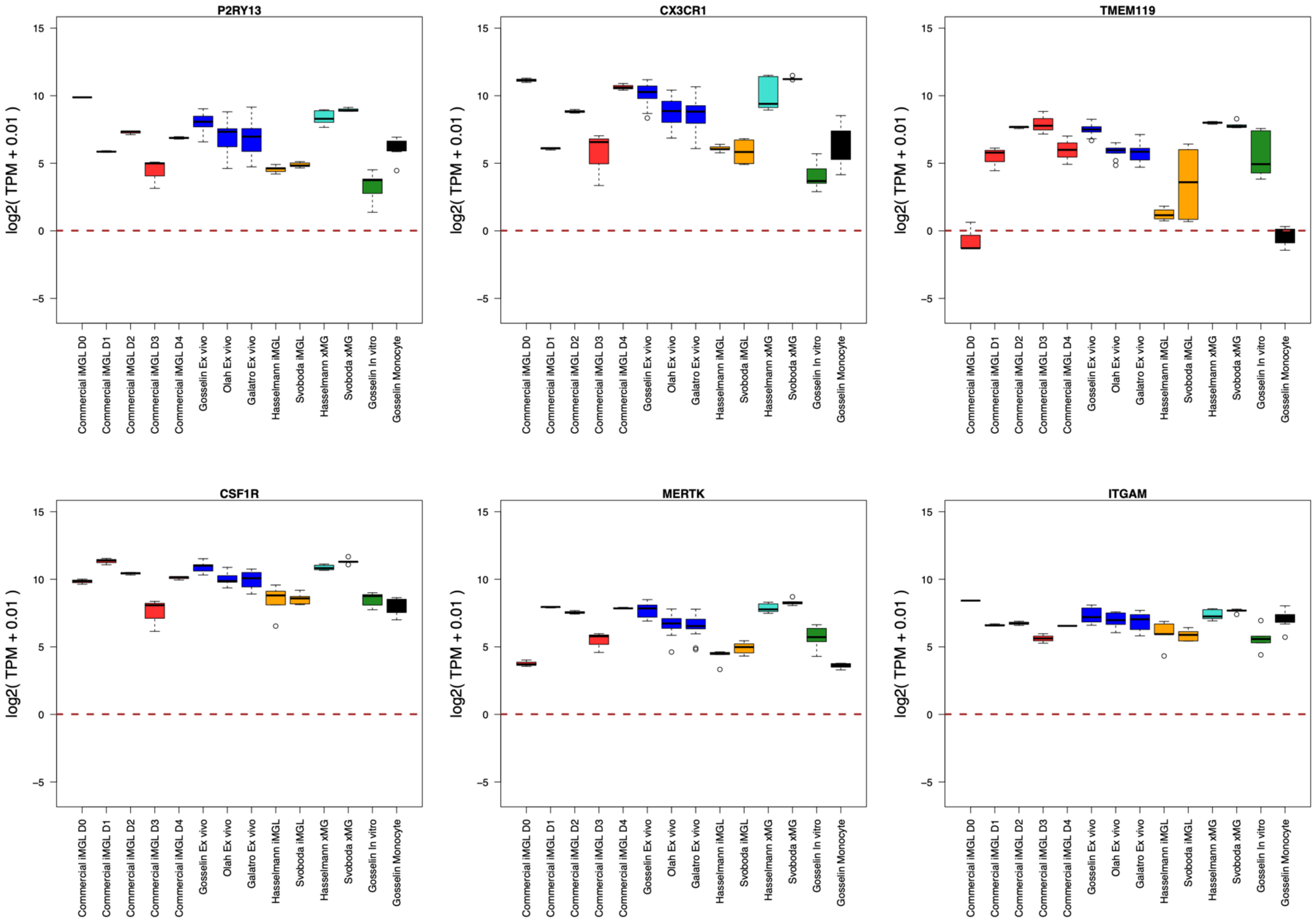
A) Pairwise Sigclust scores comparing Commercial iMGL samples and microglia comparator datasets using principal component analysis on all expressed genes. Each cell represents a comparison between two cell systems and is colored by the Sigclust score (0 to 1). * empirical p-value < 0.05, ** empirical p-value < 0.01

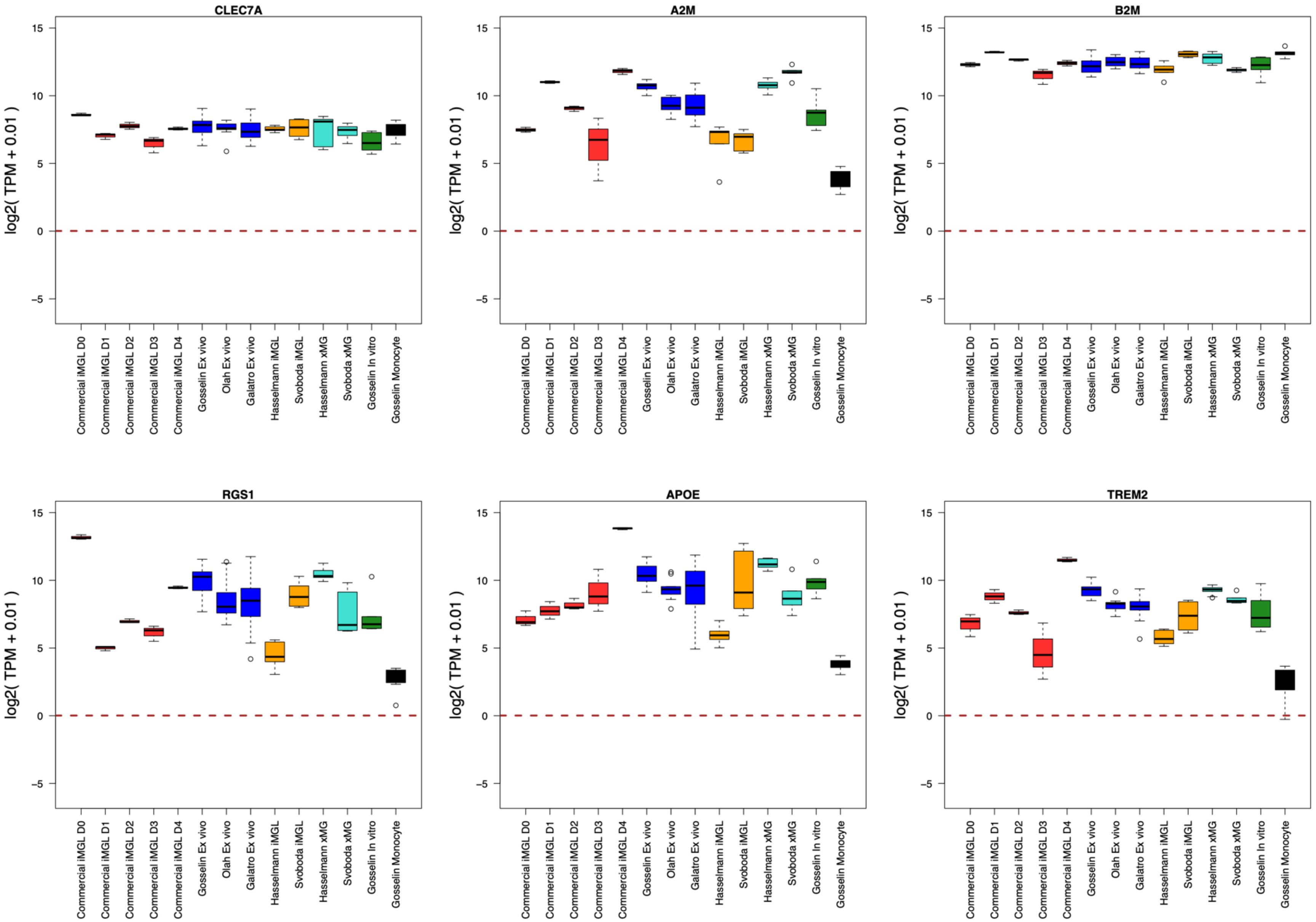
B) Pairwise average Silhouette scores comparing Commercial iMGL samples and microglia comparator datasets using principal component analysis on all expressed genes. Each cell represents a comparison between two cell systems and is colored by the average Silhouette score (-1 to 1). * empirical p-value < 0.05, ** empirical p-value < 0.01

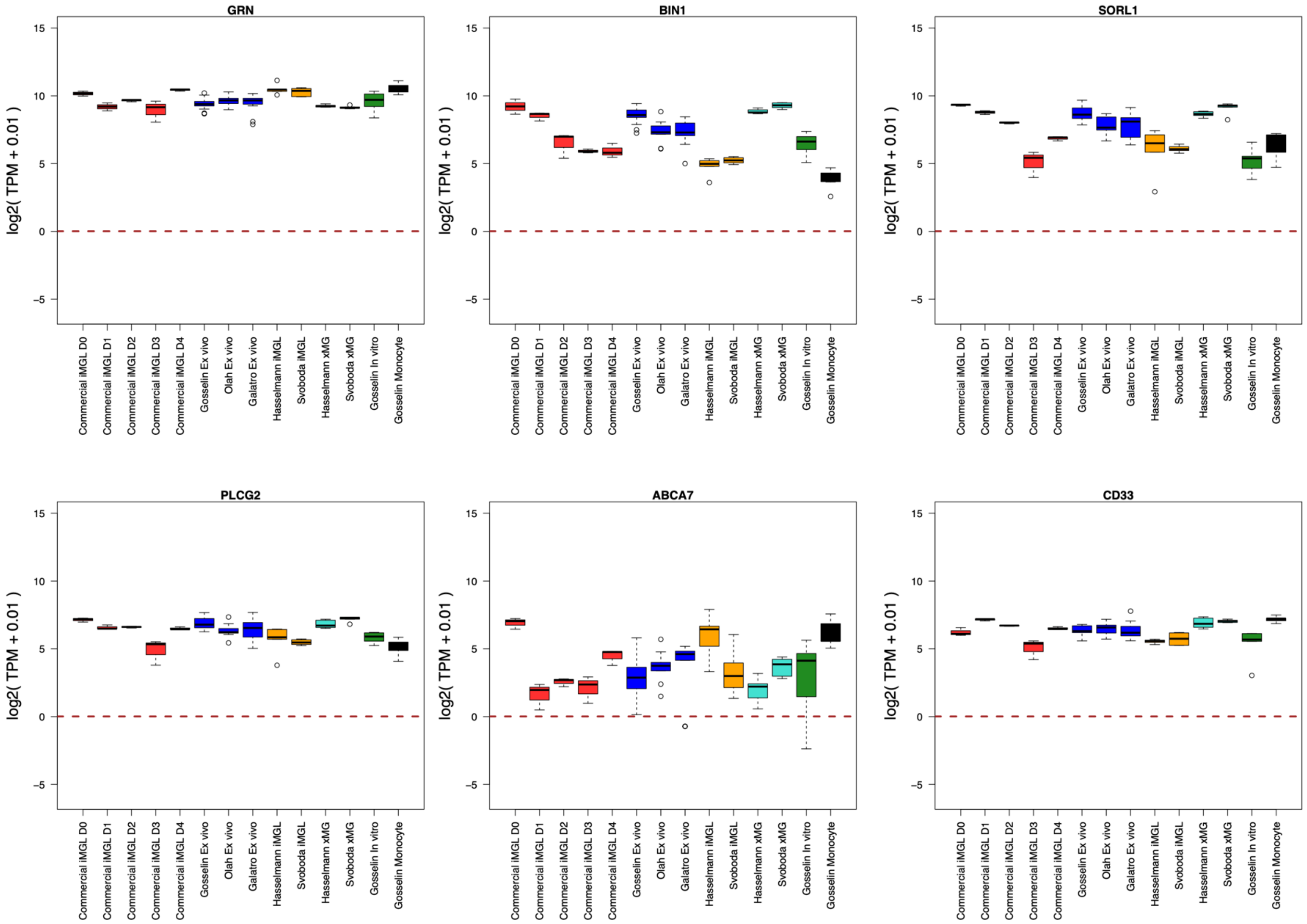

SPI1
IRF8
RUNX1
FOS
CEBPB
MEF2A
log2(TPM + 0.01)
15
10
5
0
−5
Commercial iMGL D0
Commercial iMGL D1
Commercial iMGL D2
Commercial iMGL D3
Commercial iMGL D4
Gosselin Ex vivo
Olah Ex vivo
Galatro Ex vivo
Hasselmann iMGL
Svoboda iMGL
Hasselmann xMG
Svoboda xMG
Gosselin In vitro
Gosselin Monocyte

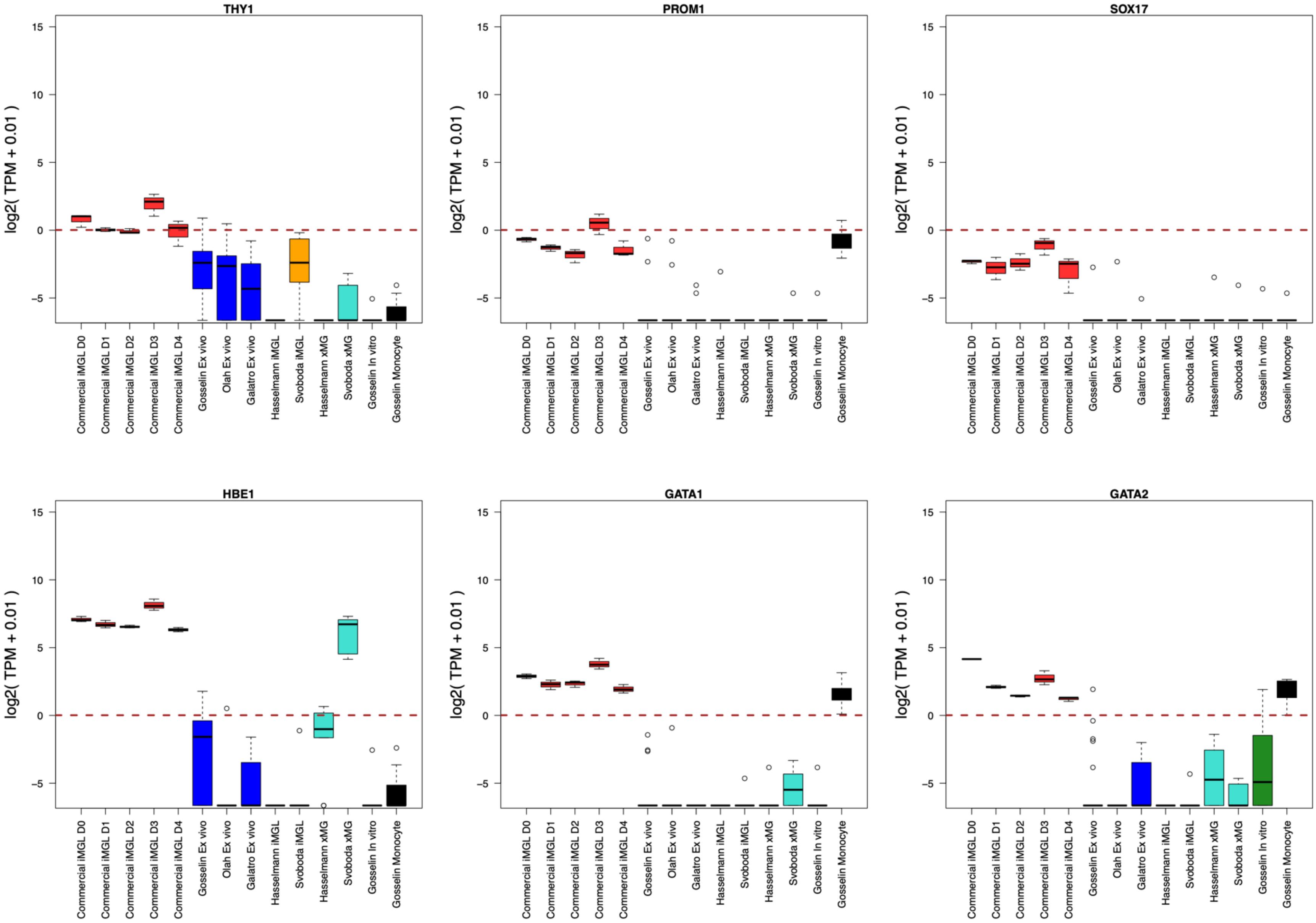

MAF
SALL1
TAL1
RUNX2
C3
C1QA
log2(TPM + 0.01)
15
10
5
0
−5
Commercial iMGL D0
Commercial iMGL D1
Commercial iMGL D2
Commercial iMGL D3
Commercial iMGL D4
Gosselin Ex vivo
Olah Ex vivo
Galatro Ex vivo
Hasselmann iMGL
Svoboda iMGL
Hasselmann xMG
Svoboda xMG
Gosselin In vitro
Gosselin Monocyte

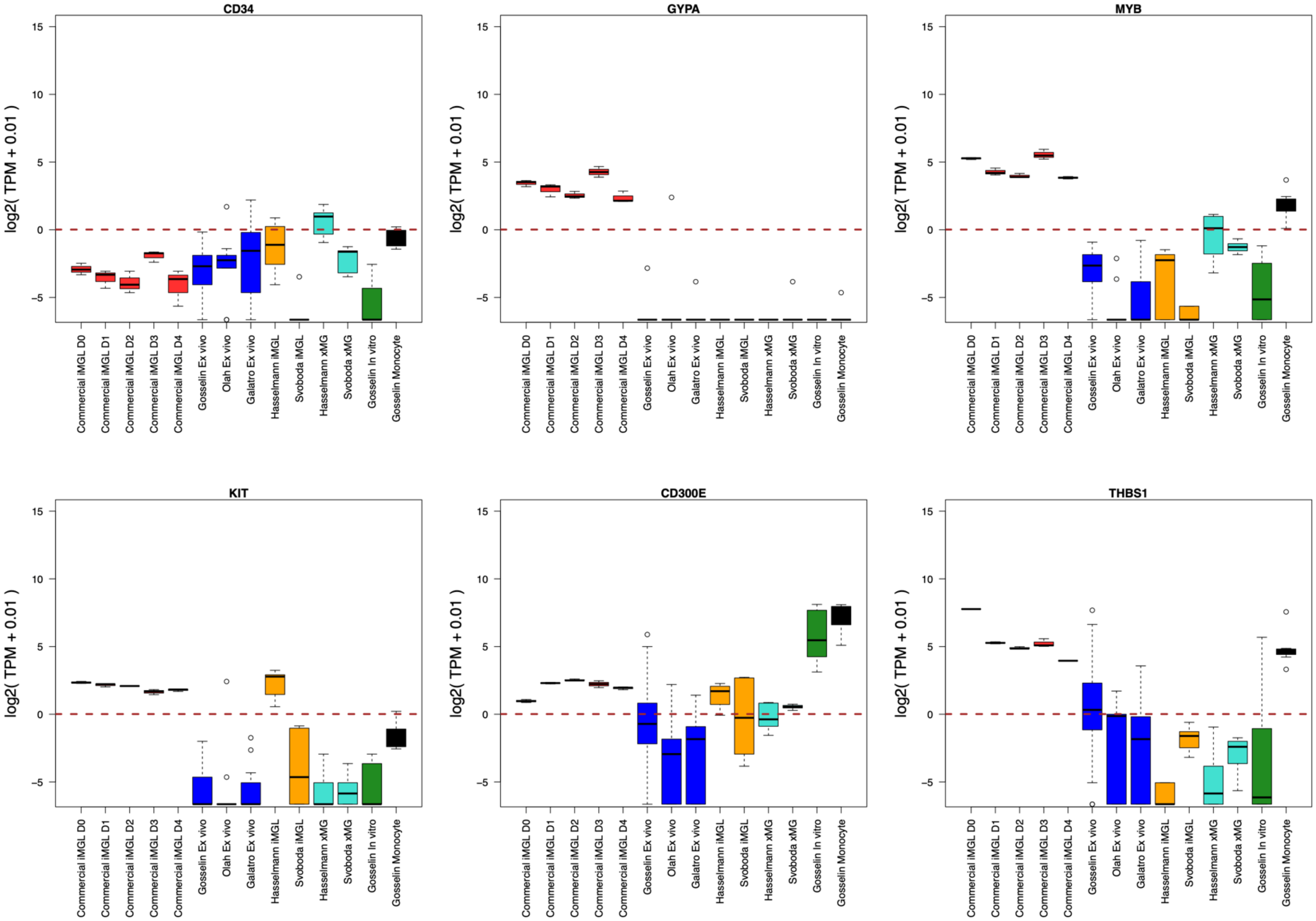

C1QB
C1QC
HLA−B
HLA−DRA
SPP1
P2RY12
log2(TPM + 0.01)
15
10
5
0
−5
Commercial iMGL D0
Commercial iMGL D1
Commercial iMGL D2
Commercial iMGL D3
Commercial iMGL D4
Gosselin Ex vivo
Olah Ex vivo
Galatro Ex vivo
Hasselmann iMGL
Svoboda iMGL
Hasselmann xMG
Svoboda xMG
Gosselin In vitro
Gosselin Monocyte

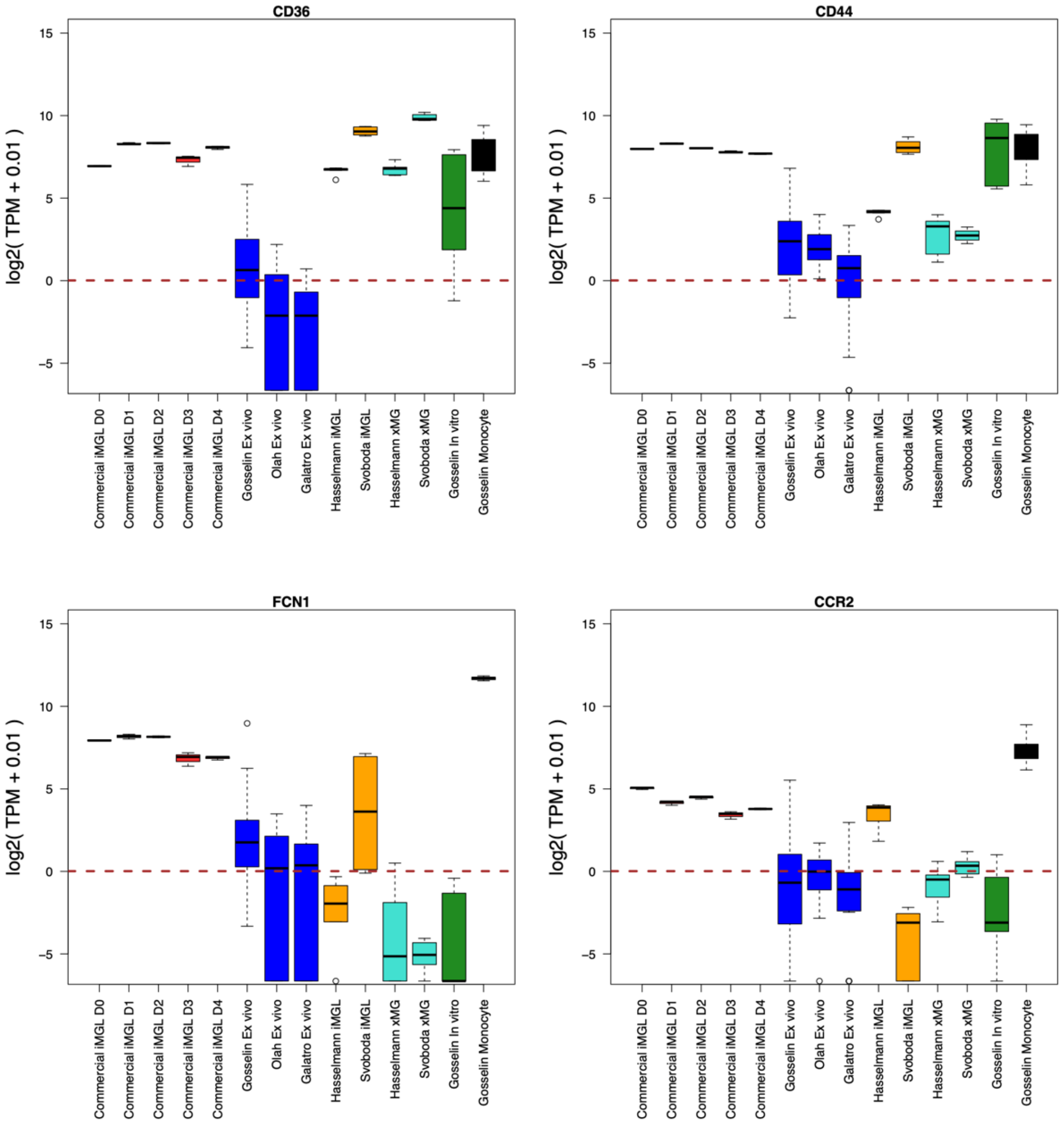

P2RY13
CX3CR1
TMEM119
CSF1R
MERTK
ITGAM
log2(TPM + 0.01)
15
10
5
0
−5
Commercial iMGL D0
Commercial iMGL D1
Commercial iMGL D2
Commercial iMGL D3
Commercial iMGL D4
Gosselin Ex vivo
Olah Ex vivo
Galatro Ex vivo
Hasselmann iMGL
Svoboda iMGL
Hasselmann xMG
Svoboda xMG
Gosselin In vitro
Gosselin Monocyte


CLEC7A
A2M
B2M
RGS1
APOE
TREM2
log2(TPM + 0.01)
15
10
5
0
−5
Commercial iMGL D0
Commercial iMGL D1
Commercial iMGL D2
Commercial iMGL D3
Commercial iMGL D4
Gosselin Ex vivo
Olah Ex vivo
Galatro Ex vivo
Hasselmann iMGL
Svoboda iMGL
Hasselmann xMG
Svoboda xMG
Gosselin In vitro
Gosselin Monocyte


GRN
BIN1
SORL1
PLCG2
ABCA7
CD33
log2(TPM + 0.01)
15
10
5
0
−5
Commercial iMGL D0
Commercial iMGL D1
Commercial iMGL D2
Commercial iMGL D3
Commercial iMGL D4
Gosselin Ex vivo
Olah Ex vivo
Galatro Ex vivo
Hasselmann iMGL
Svoboda iMGL
Hasselmann xMG
Svoboda xMG
Gosselin In vitro
Gosselin Monocyte


THY1
PROM1
SOX17
HBE1
GATA1
GATA2
log2(TPM + 0.01)
15
10
5
0
−5
Commercial iMGL D0
Commercial iMGL D1
Commercial iMGL D2
Commercial iMGL D3
Commercial iMGL D4
Gosselin Ex vivo
Olah Ex vivo
Galatro Ex vivo
Hasselmann iMGL
Svoboda iMGL
Hasselmann xMG
Svoboda xMG
Gosselin In vitro
Gosselin Monocyte


CD34
GYPA
MYB
KIT
CD300E
THBS1
log2(TPM + 0.01)
15
10
5
0
-5
Commercial iMGL D0
Commercial iMGL D1
Commercial iMGL D2
Commercial iMGL D3
Commercial iMGL D4
Gosselin Ex vivo
Olah Ex vivo
Galatro Ex vivo
Hasselmann iMGL
Svoboda iMGL
Hasselmann xMG
Svoboda xMG
Gosselin In vitro
Gosselin Monocyte


CD36
CD44
FCN1
CCR2
log2(TPM + 0.01)
15
10
5
0
−5
Commercial iMGL D0
Commercial iMGL D1
Commercial iMGL D2
Commercial iMGL D3
Commercial iMGL D4
Gosselin Ex vivo
Olah Ex vivo
Galatro Ex vivo
Hasselmann iMGL
Svoboda iMGL
Hasselmann xMG
Svoboda xMG
Gosselin In vitro
Gosselin Monocyte

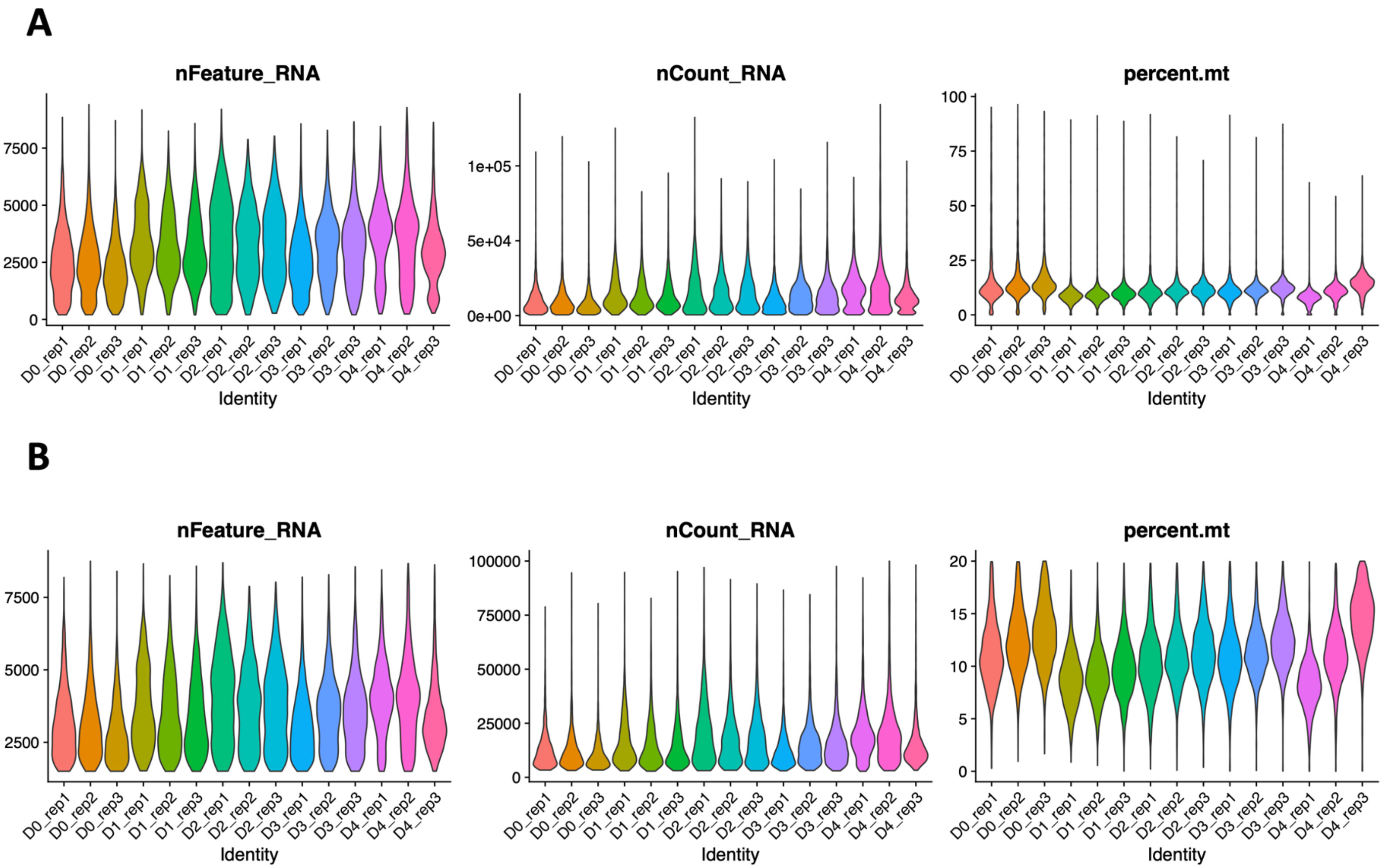
Supplementary Figure 4. Expression of key microglia related genes across the Commercial iMGL samples and microglia comparator datasets.

Microglia TFs: SPI1, IRF8, RUNX1, FOS, CEBPB, MEF2A, MAF, SALL1, TAL1, RUNX2

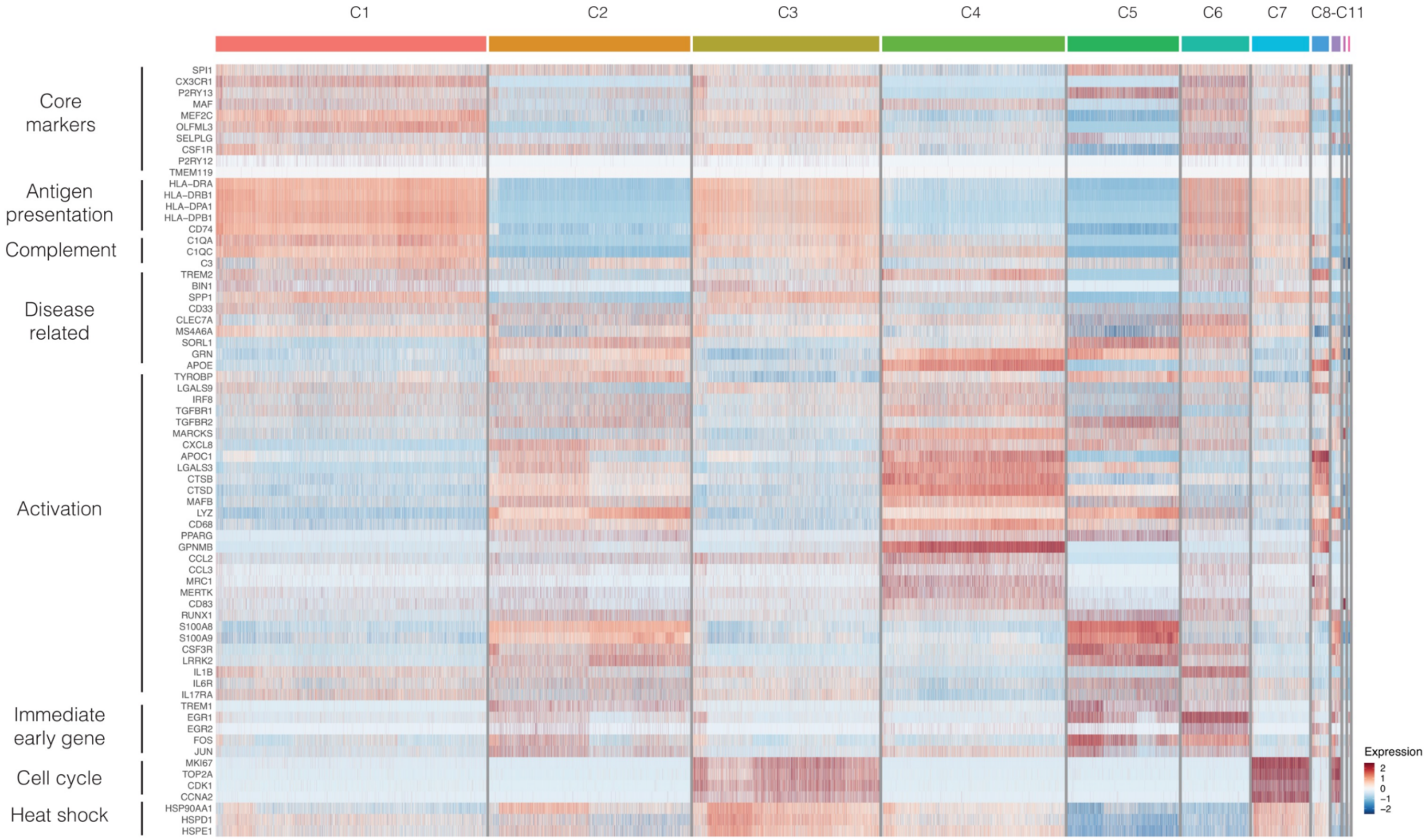
Microglia core marker genes: C3, C1QA, C1QB, C1QC, HLA-B. HLA-DRA, SPP1, P2RY12, P2RY13, CX3CR1, TMEM119, CSF1R, MERTK, ITGAM, CLEC7A, A2M, B2M, RGS1

Disease genes: APOE, TREM2, GRN, BIN1, SORL1, PLCG2, ABCA7, CD33

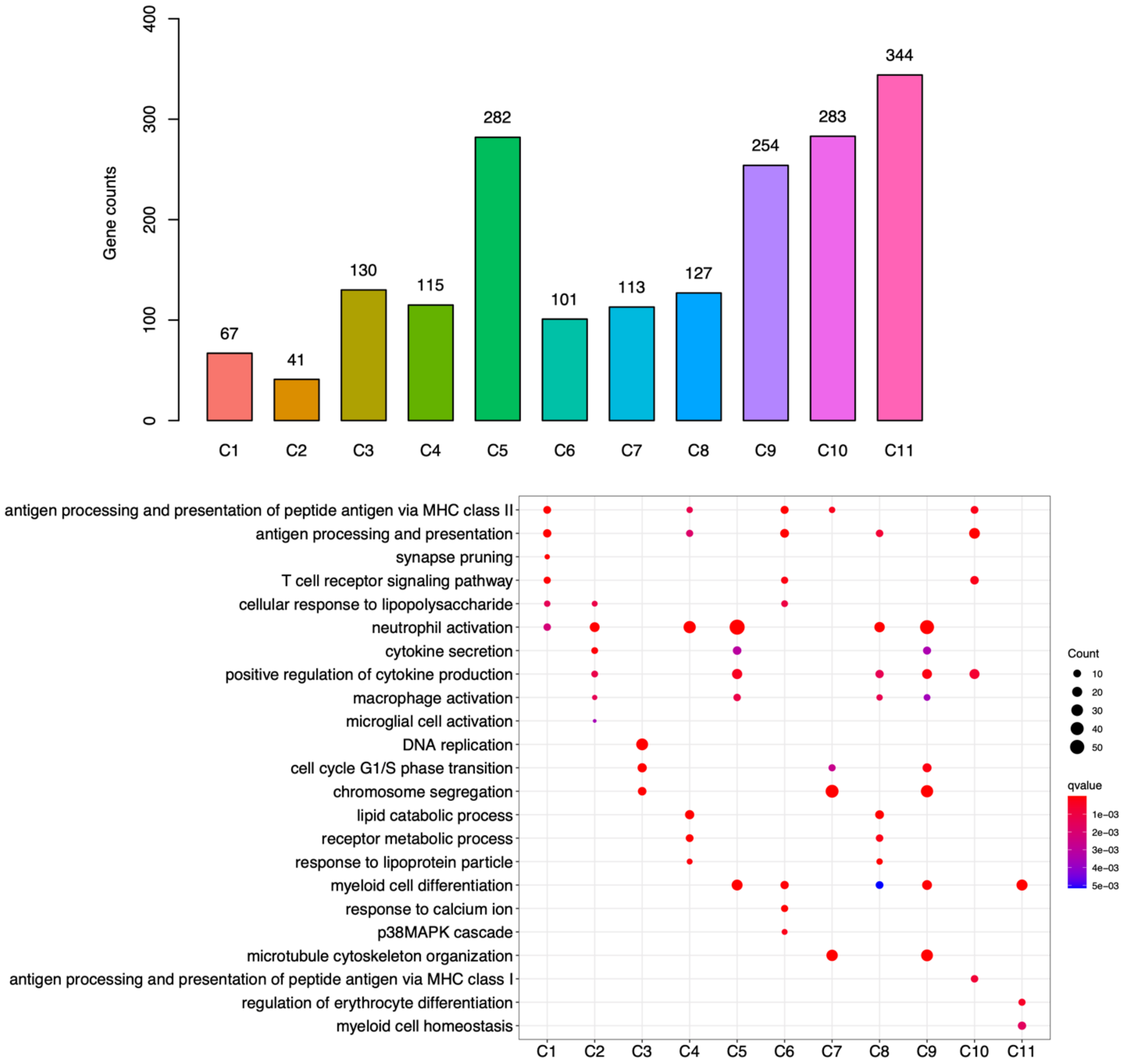
Myeloid progenitor and monocyte marker genes: THY1, PROM1, SOX17, HBE1, GATA1, GATA2, CD34, GYPA, MYB, KIT, CD300E, THBS1, CD36, CD44, FCN1, CCR2


A
nFeature_RNA
0
2500
5000
7500
nCount_RNA
0e+00
5e+04
1e+05
percent.mt
0
25
50
75
100
D0_rep1
D0_rep2
D0_rep3
D1_rep1
D1_rep2
D1_rep3
D2_rep1
D2_rep2
D2_rep3
D3_rep1
D3_rep2
D3_rep3
D4_rep1
D4_rep2
D4_rep3
Identity
B
nFeature_RNA
2500
5000
7500
nCount_RNA
0
25000
50000
75000
100000
percent.mt
0
5
10
15
20
D0_rep1
D0_rep2
D0_rep3
D1_rep1
D1_rep2
D1_rep3
D2_rep1
D2_rep2
D2_rep3
D3_rep1
D3_rep2
D3_rep3
D4_rep1
D4_rep2
D4_rep3
Identity

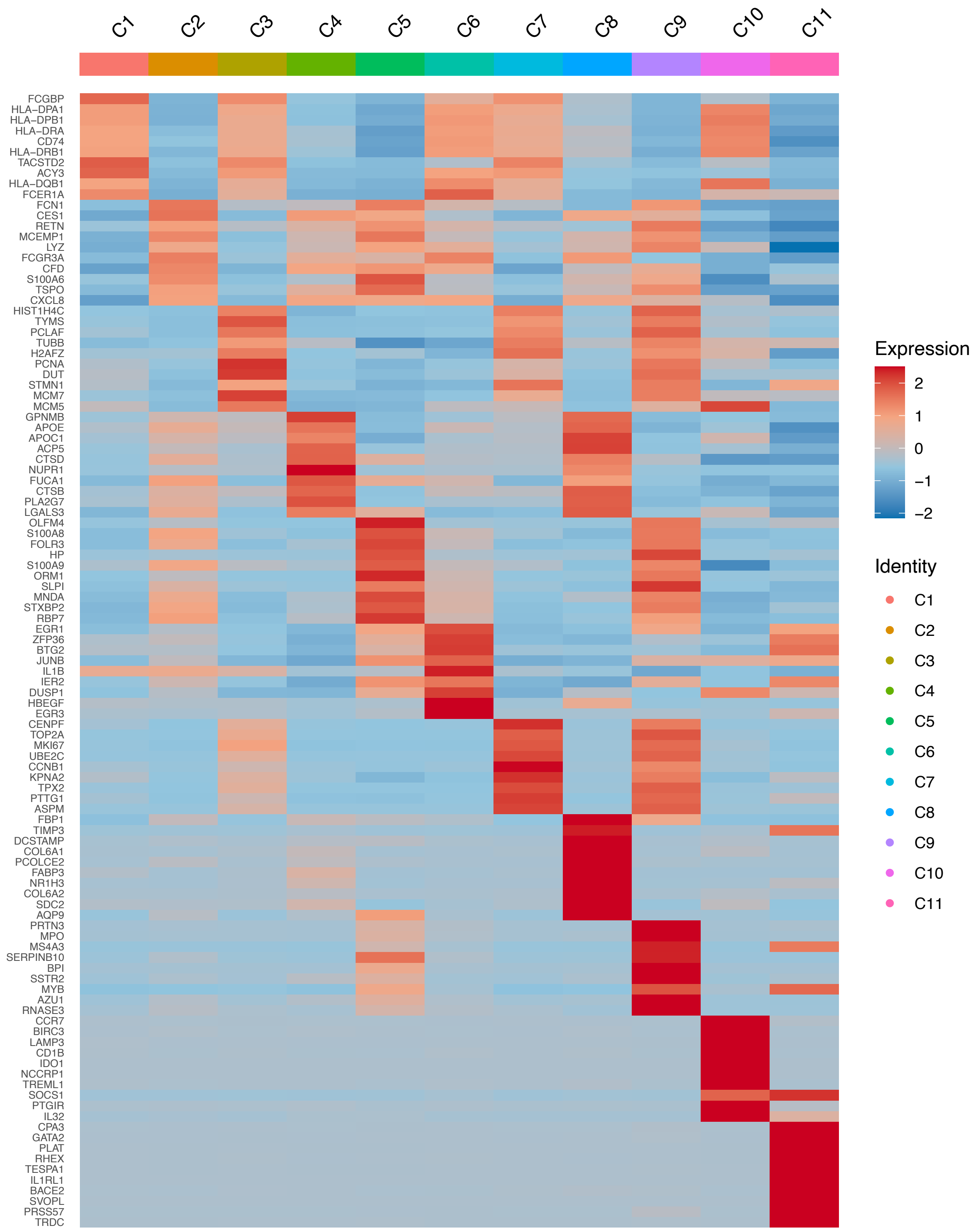
Supplementary Figure 5. Quality control (QC) metrics for Commercial iMGL time course single cell RNA-seq dataset. The number of genes (nFeature_RNA), reads (nCount_RNA), and percentage of mitochondrial reads (percent.mt) for cells in each sample **A**) before and **B**) after applying QC filters.


C1
C2
C3
C4
C5
C6
C7
C8-C11
Core markers
SPI1
CX3CR1
P2RY13
MAF
MEF2C
OLFML3
SELPLG
CSF1R
P2RY12
TMEM119
Antigen presentation
HLA−DRA
HLA−DRB1
HLA−DPA1
HLA−DPB1
CD74
Complement
C1QA
C1QC
C3
Disease related
TREM2
BIN1
SPP1
CD33
CLEC7A
MS4A6A
SORL1
GRN
APOE
Activation
TYROBP
LGALS9
IRF8
TGFBR1
TGFBR2
MARCKS
CXCL8
APOC1
LGALS3
CTSB
CTSD
MAFB
LYZ
CD68
PPARG
GPNMB
CCL2
CCL3
MRC1
MERTK
CD83
RUNX1
S100A8
S100A9
CSF3R
LRRK2
IL1B
IL6R
IL17RA
Immediate early gene
TREM1
EGR1
EGR2
FOS
JUN
Cell cycle
MKI67
TOP2A
CDK1
CCNA2
Heat shock
HSP90AA1
HSPD1
HSPE1
Expression
2
1
0
−1
−2

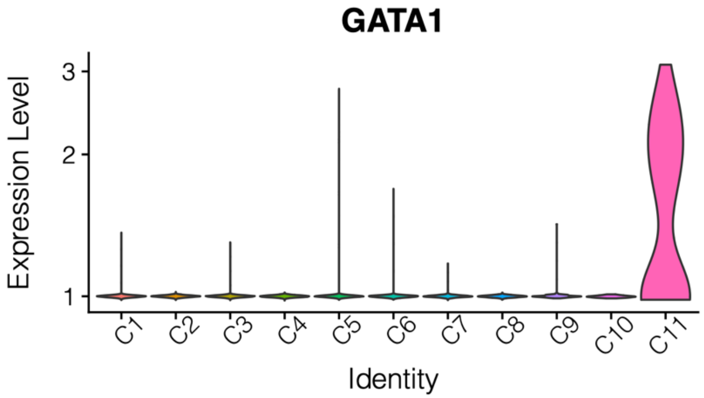
Supplementary Figure 6. Gene expression heatmap of microglia functional marker genes in the time course single cell RNA-seq dataset.

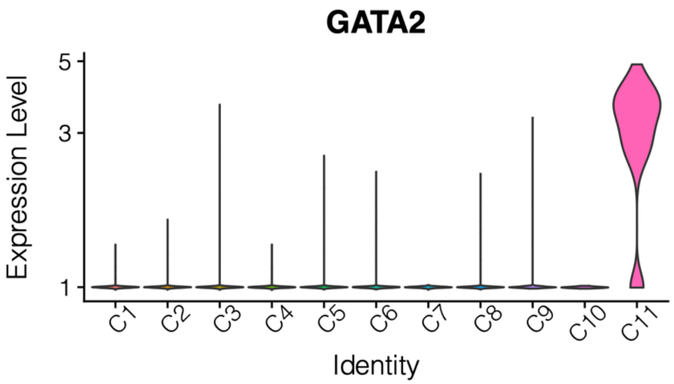

Gene counts
0
100
200
300
400
67
41
130
115
282
101
113
127
254
283
344
C1
C2
C3
C4
C5
C6
C7
C8
C9
C10
C11
antigen processing and presentation of peptide antigen via MHC class II
antigen processing and presentation
synapse pruning
T cell receptor signaling pathway
cellular response to lipopolysaccharide
neutrophil activation
cytokine secretion
positive regulation of cytokine production
macrophage activation
microglial cell activation
DNA replication
cell cycle G1/S phase transition
chromosome segregation
lipid catabolic process
receptor metabolic process
response to lipoprotein particle
myeloid cell differentiation
response to calcium ion
p38MAPK cascade
microtubule cytoskeleton organization
antigen processing and presentation of peptide antigen via MHC class I
regulation of erythrocyte differentiation
myeloid cell homeostasis
C1
C2
C3
C4
C5
C6
C7
C8
C9
C10
C11
Count
10
20
30
40
50
qvalue
1e−03
2e−03
3e−03
4e−03
5e−03

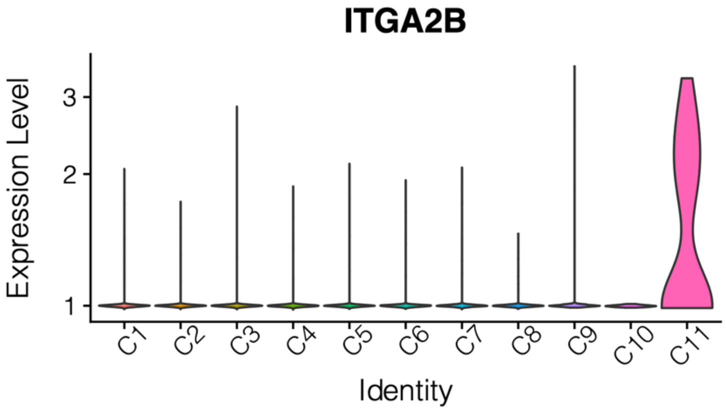
Supplementary Figure 7. Identification of preferentially expressed marker genes and their top gene ontology enrichments for each cellular cluster in the time course single cell RNA-seq dataset.

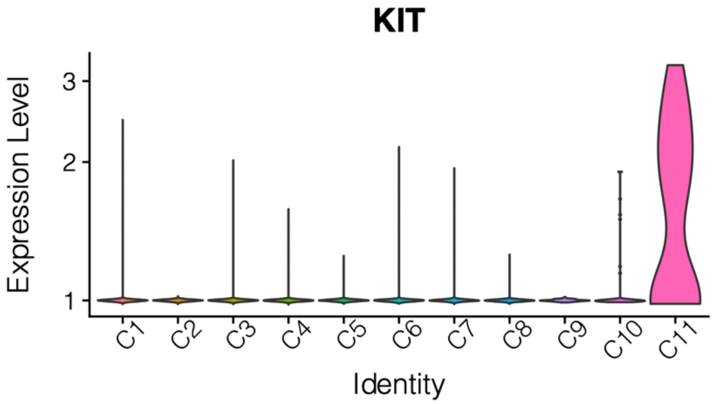

C1
C2
C3
C4
C5
C6
C7
C8
C9
C10
C11
FCGBP
HLA−DPA1
HLA−DPB1
HLA−DRA
CD74
HLA−DRB1
TACSTD2
ACY3
HLA−DQB1
FCER1A
FCN1
CES1
RETN
MCEMP1
LYZ
FCGR3A
CFD
S100A6
TSPO
CXCL8
HIST1H4C
TYMS
PCLAF
TUBB
H2AFZ
PCNA
DUT
STMN1
MCM7
MCM5
GPNMB
APOE
APOC1
ACP5
CTSD
NUPR1
FUCA1
CTSB
PLA2G7
LGALS3
OLFM4
S100A8
FOLR3
HP
S100A9
ORM1
SLPI
MNDA
STXBP2
RBP7
EGR1
ZFP36
BTG2
JUNB
IL1B
IER2
DUSP1
HBEGF
EGR3
CENPF
TOP2A
MKI67
UBE2C
CCNB1
KPNA2
TPX2
PTTG1
ASPM
FBP1
TIMP3
DCSTAMP
COL6A1
PCOLCE2
FABP3
NR1H3
COL6A2
SDC2
AQP9
PRTN3
MPO
MS4A3
SERPINB10
BPI
SSTR2
MYB
AZU1
RNASE3
CCR7
BIRC3
LAMP3
CD1B
IDO1
NCCRP1
TREML1
SOCS1
PTGIR
IL32
CPA3
GATA2
PLAT
RHEX
TESPA1
IL1RL1
BACE2
SVOPL
PRSS57
TRDC
Expression
2
1
0
−1
−2
Identity
C1
C2
C3
C4
C5
C6
C7
C8
C9
C10
C11

Supplementary Figure 8. Heatmap of average gene expression per cluster of the top 10 marker genes for each cluster in the time course single cell RNA-seq dataset.

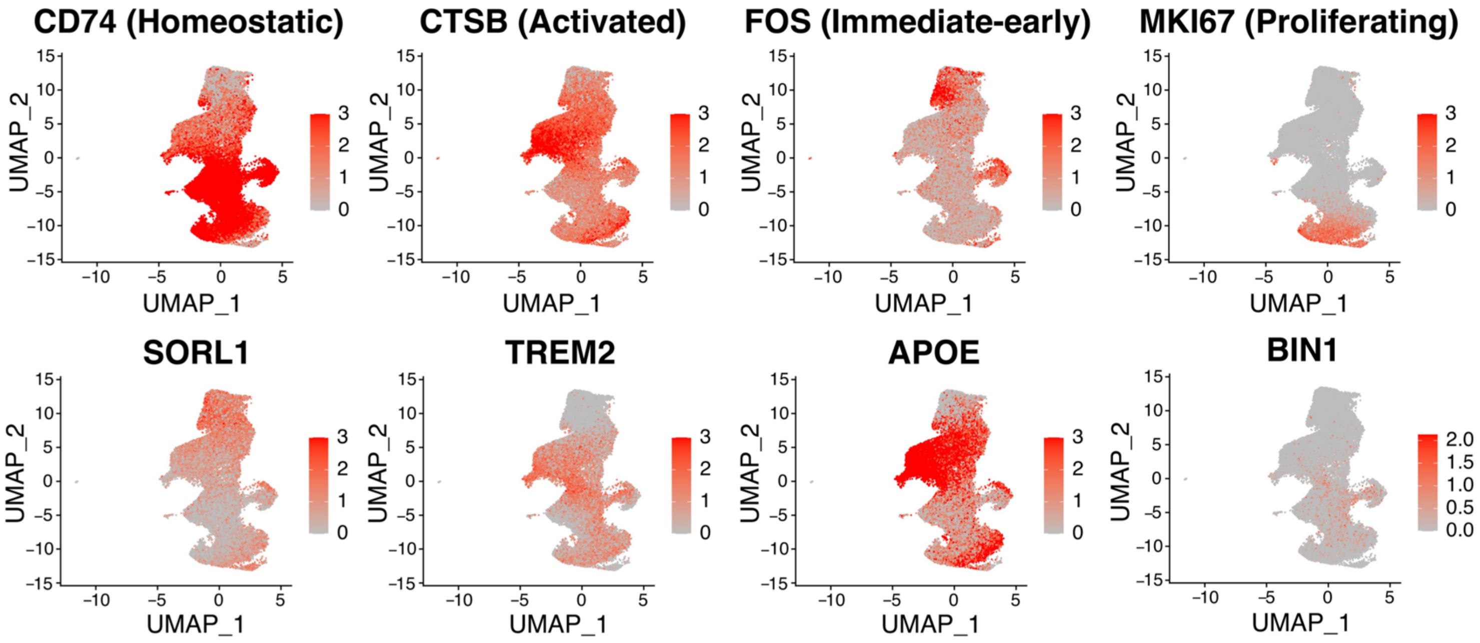

GATA1
Expression Level
3
2
1
C1
C2
C3
C4
C5
C6
C7
C8
C9
C10
C11
Identity


GATA2
Expression Level
5
3
1
C1
C2
C3
C4
C5
C6
C7
C8
C9
C10
C11
Identity


ITGA2B
Expression Level
3
2
1
C1
C2
C3
C4
C5
C6
C7
C8
C9
C10
C11
Identity


KIT
Expression Level
3
2
1
C1
C2
C3
C4
C5
C6
C7
C8
C9
C10
C11
Identity

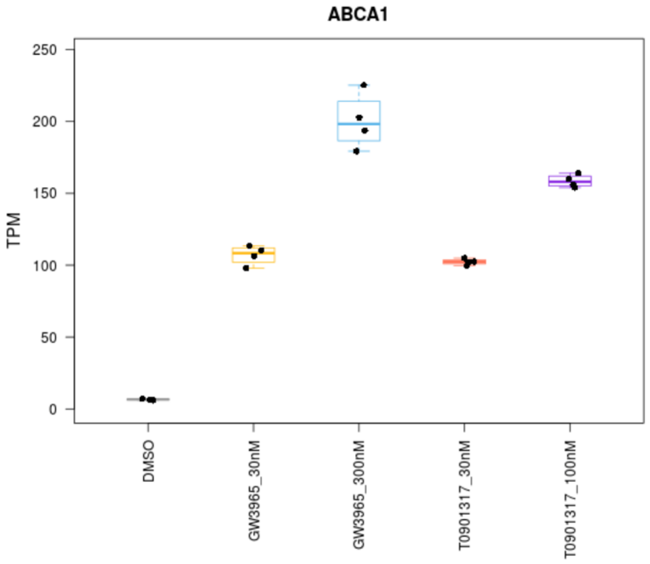
Supplementary Figure 9. Expression of progenitor (GATA1, GATA2, KIT) and monocyte (ITGA2B) marker genes across the 11 single cell clusters.

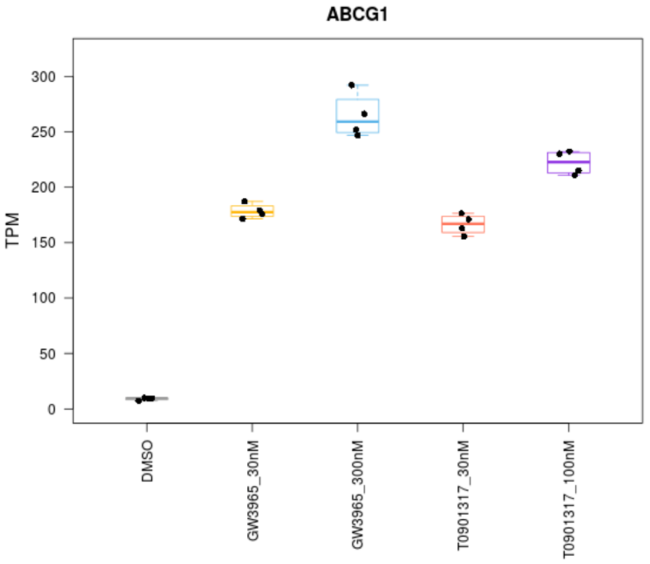

CD74 (Homeostatic)
CTSB (Activated)
FOS (Immediate-early)
MKI67 (Proliferating)
SORL1
TREM2
APOE
BIN1
UMAP_1
UMAP_2
15
10
5
0
−5
−10
−15
3
2
1
0
2.0
1.5
1.0
0.5
0.0

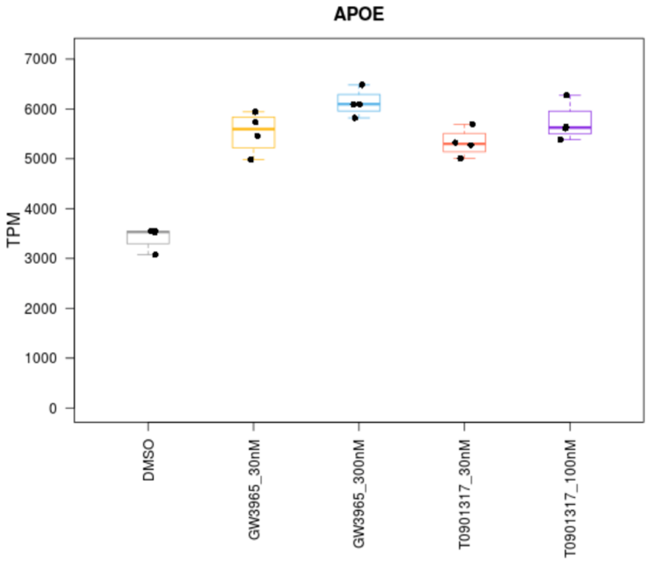
Supplementary Figure 10. Relative expression of key homeostatic (CD74), activated (CTSB), immediate-early (FOS), proliferating (MKI67), and AD-associated (SORL1, TREM2, APOE, BIN1) genes across the individual cells. Expression values were scaled using the FeaturePlot method in Seurat.

Ex vivo subcluster	Functional annotation
Olah 1	Homeostatic
Olah 2	Homeostatic
Olah 3	Activated, distressed
Olah 4	Activated, interferon response
Olah 5	Activated, anti-inflammatory
Olah 6	Activated, anti-inflammatory
Olah 7	Homeostatic, antigen presentation
Olah 8	Metabolic
Olah 9	Proliferative
Olah 10	Monocytes
Olah 11	T cells
Olah 12	B cells
Olah 13	GFAP+ cells
Olah 14	Red blood cells
Sankowski 1	Activated
Sankowski 2	Homeostatic, antigen presentation
Sankowski 3	Homeostatic
Sankowski 5	Activated
Sankowski 6	Metabolic
Sankowski 7	Metabolic
Sankowski 8	Activated
Sankowski 9	Activated

Supplementary Figure 11. Functional annotations of ex vivo cell clusters curated from their descriptions in the Olah and Sankowski publications.

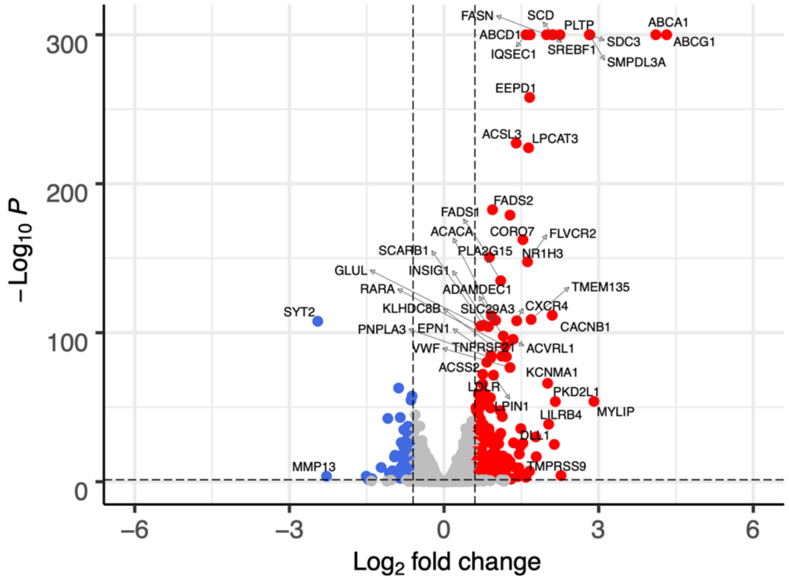

ABCA1


ABCG1

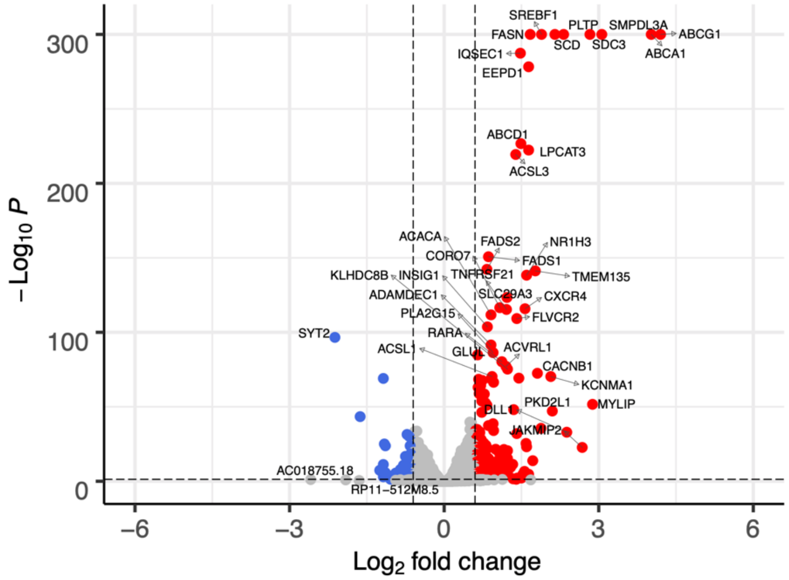

APOE

Supplementary Figure 12. Expression of known LXR pathway response genes (ABCA1, ABCG1, APOE) in the LXR pathway agonist treatment bulk RNA-seq dataset.

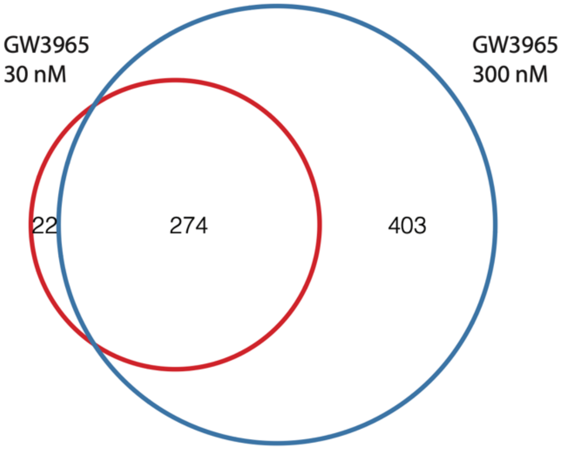
GW3965 30nM:

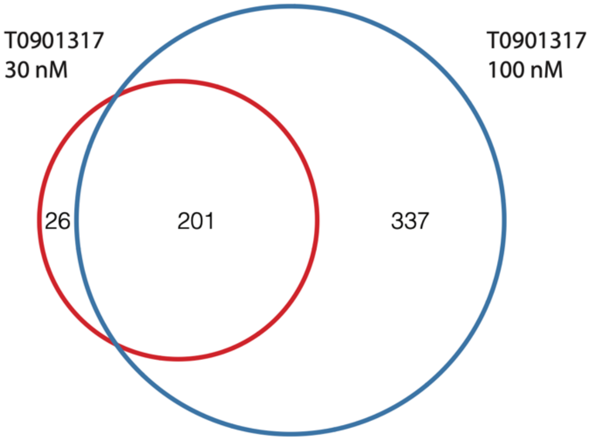


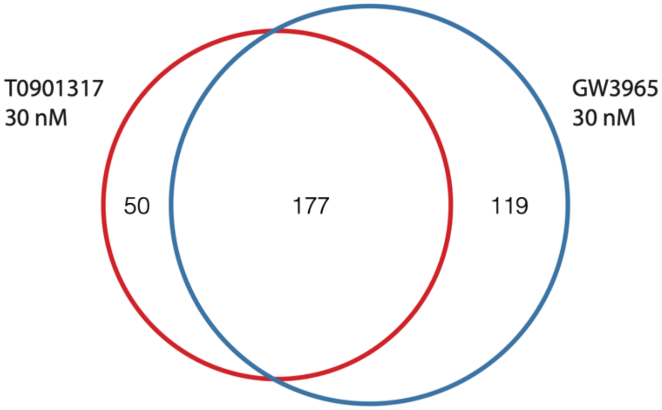
T0901317 30nM:



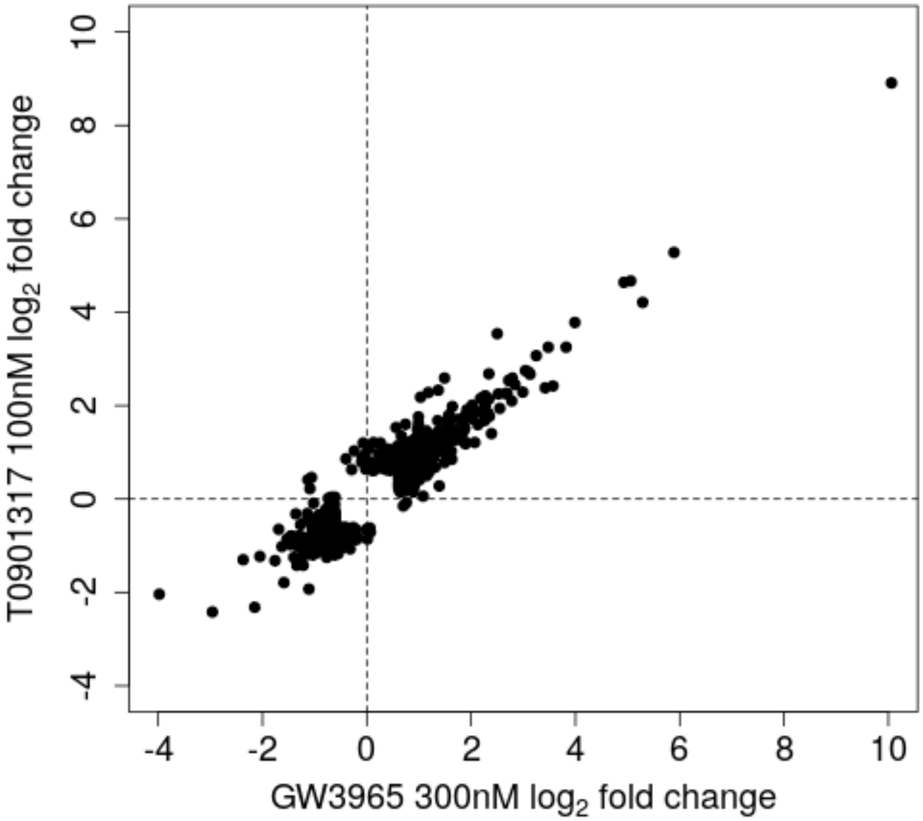
Supplementary Figure 13. Volcano plots showing relationship between expression fold change and significance for differential gene expression between GW3965 30nM and T0901317 30nM with DMSO treated cells. Genes with significant upregulation and downregulation are colored red and blue, respectively.


GW3965
30 nM
GW3965
300 nM
22
274
403

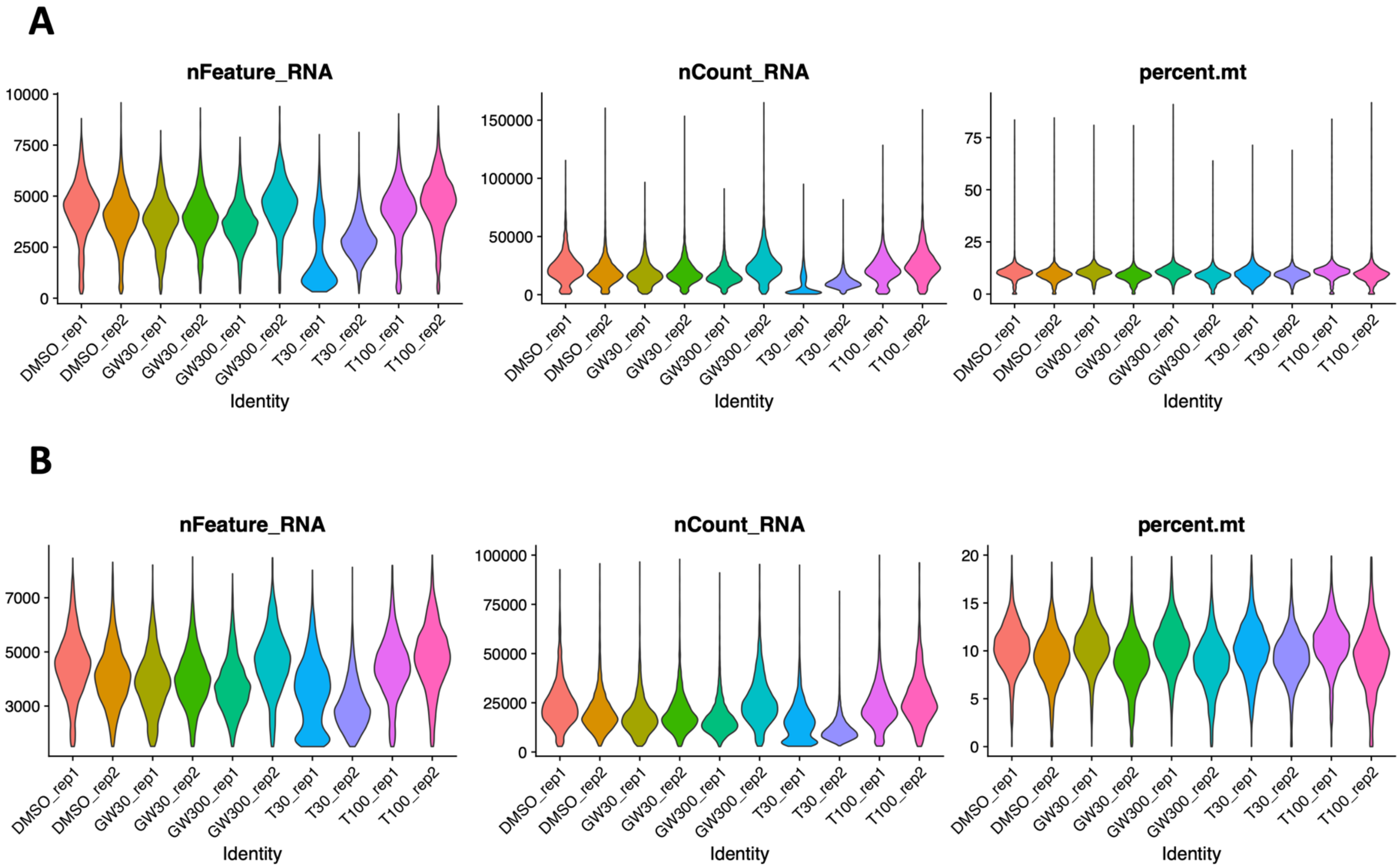

T0901317
30 nM
T0901317
100 nM
26
201
337


T0901317
30 nM
GW3965
30 nM
50
177
119

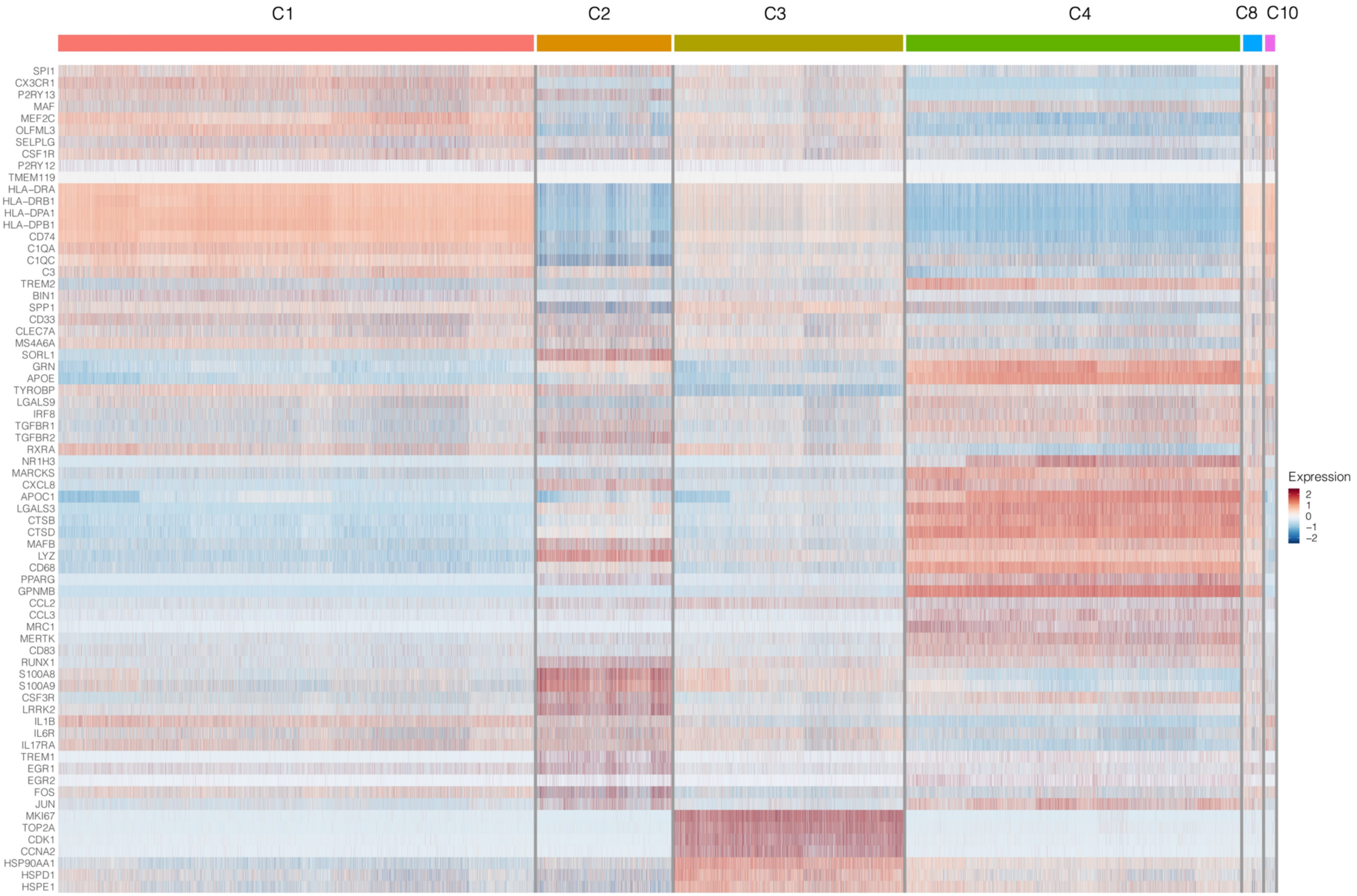
Supplementary Figure 14. Overlap in DEGs between GW3965 30nM and 300nM treatments. Overlap in DEGs between T0901317 30nM and 100nM treatments. Overlap in DEGs between GW3965 30nM and T0901317 30nM treatments.


10
8
6
4
2
0
-2
-4
T0901317 100nM $\log_2$ fold change
-4
-2
0
2
4
6
8
10
GW3965 300nM $\log_2$ fold change

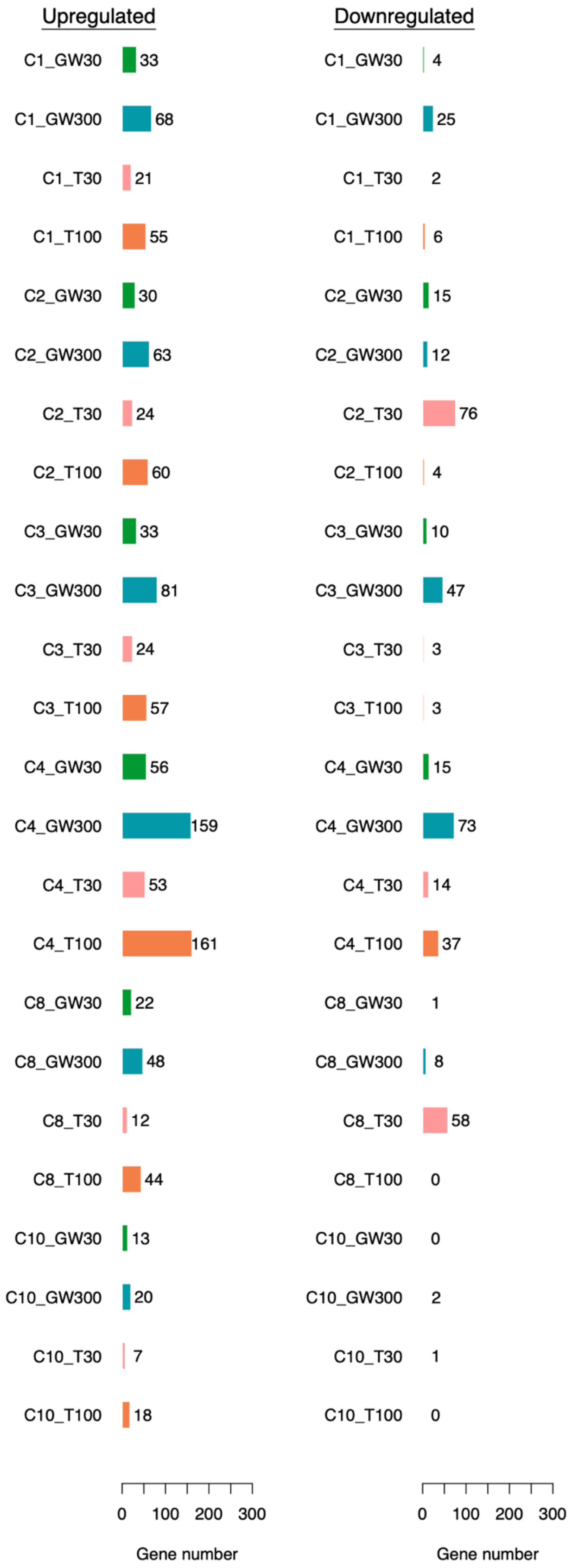
Supplementary Figure 15. Comparison of DEG fold changes between GW3965 300nM and T0901317 100nM treatments. The union of DEGs between the two treatments were used in this comparison.


A
nFeature_RNA
10000
7500
5000
2500
0
nCount_RNA
150000
100000
50000
0
percent.mt
75
50
25
0
DMSO_rep1
DMSO_rep2
GW30_rep1
GW30_rep2
GW300_rep1
GW300_rep2
T30_rep1
T30_rep2
T100_rep1
T100_rep2
Identity
B
nFeature_RNA
7000
5000
3000
nCount_RNA
100000
75000
50000
25000
0
percent.mt
20
15
10
5
0
DMSO_rep1
DMSO_rep2
GW30_rep1
GW30_rep2
GW300_rep1
GW300_rep2
T30_rep1
T30_rep2
T100_rep1
T100_rep2
Identity

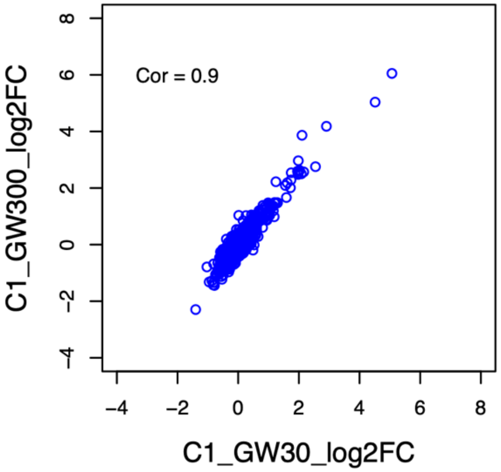
Supplementary Figure 16. QC metrics for LXR pathway agonist treatment single cell RNA-seq dataset. The number of genes (nFeature_RNA), reads (nCount_RNA), and percentage of mitochondrial reads (percent.mt) for cells for cells in each sample **A**) before and **B**) after applying QC filters.

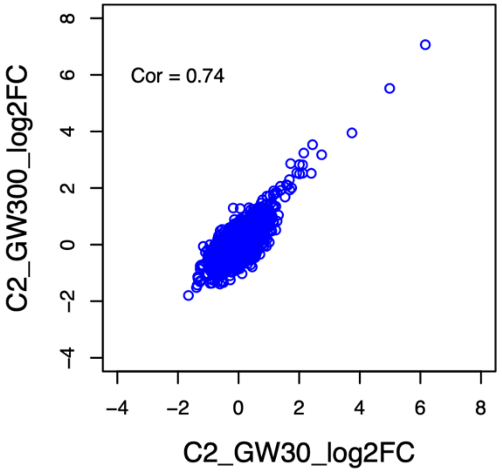

C1
C2
C3
C4
C8
C10
SPI1
CX3CR1
P2RY13
MAF
MEF2C
OLFML3
SELPLG
CSF1R
P2RY12
TMEM119
HLA-DRA
HLA-DRB1
HLA-DPA1
HLA-DPB1
CD74
C1QA
C1QC
C3
TREM2
BIN1
SPP1
CD33
CLEC7A
MS4A6A
SORL1
GRN
APOE
TYROBP
LGALS9
IRF8
TGFBR1
TGFBR2
RXRA
NR1H3
MARCKS
CXCL8
APOC1
LGALS3
CTSB
CTSD
MAFB
LYZ
CD68
PPARG
GPNMB
CCL2
CCL3
MRC1
MERTK
CD83
RUNX1
S100A8
S100A9
CSF3R
LRRK2
IL1B
IL6R
IL17RA
TREM1
EGR1
EGR2
FOS
JUN
MKI67
TOP2A
CDK1
CCNA2
HSP90AA1
HSPD1
HSPE1
Expression
2
1
0
−1
−2

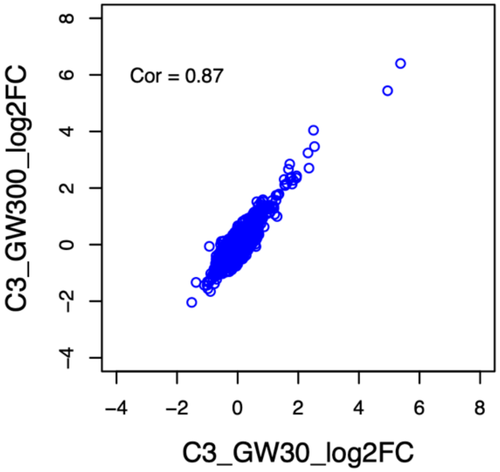
Supplementary Figure 17. Gene expression heatmap of microglia functional marker genes in the LXR pathway agonist treatment single cell RNA-seq dataset.

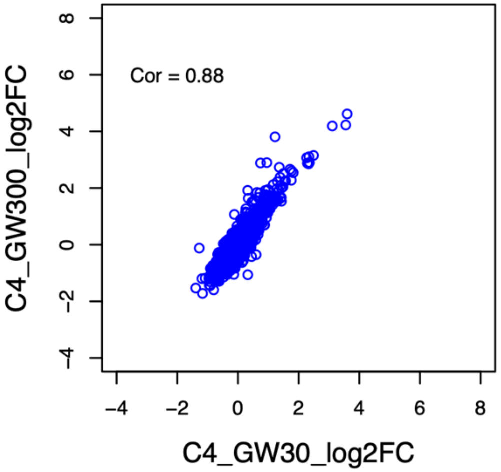

Upregulated
Downregulated
C1_GW30 33
C1_GW300 68
C1_T30 21
C1_T100 55
C2_GW30 30
C2_GW300 63
C2_T30 24
C2_T100 60
C3_GW30 33
C3_GW300 81
C3_T30 24
C3_T100 57
C4_GW30 56
C4_GW300 159
C4_T30 53
C4_T100 161
C8_GW30 22
C8_GW300 48
C8_T30 12
C8_T100 44
C10_GW30 13
C10_GW300 20
C10_T30 7
C10_T100 18
C1_GW30 4
C1_GW300 25
C1_T30 2
C1_T100 6
C2_GW30 15
C2_GW300 12
C2_T30 76
C2_T100 4
C3_GW30 10
C3_GW300 47
C3_T30 3
C3_T100 3
C4_GW30 15
C4_GW300 73
C4_T30 14
C4_T100 37
C8_GW30 1
C8_GW300 8
C8_T30 58
C8_T100 0
C10_GW30 0
C10_GW300 2
C10_T30 1
C10_T100 0
0
100
200
300
Gene number
0
100
200
300
Gene number

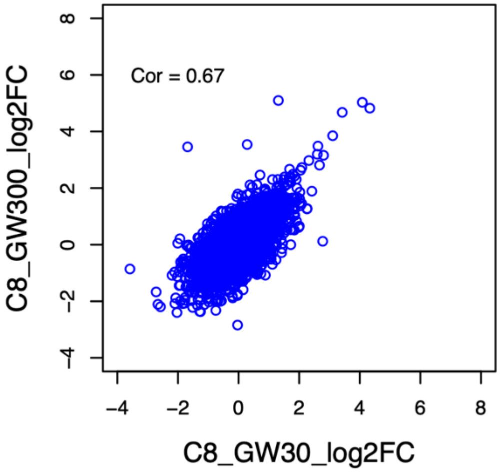
Supplementary Figure 18. Number of DEGs identified in each single cell cluster for each treatment condition against DMSO. GW30: GW3965 30 nM, GW300: GW3965 300 nM, T30: T0901317 30 nM, T100: T0901317 100 nM.

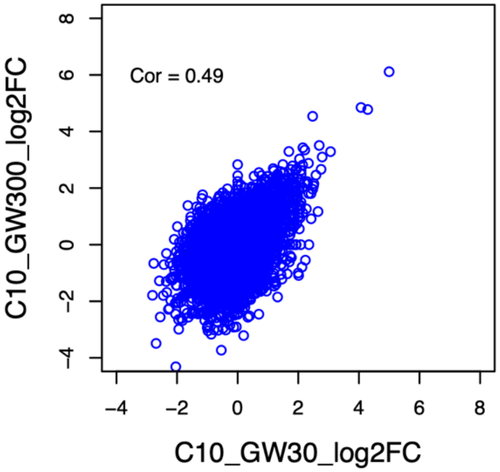

Cor = 0.9
C1_GW300_log2FC
C1_GW30_log2FC
8
6
4
2
0
−2
−4
−4
−2
0
2
4
6
8

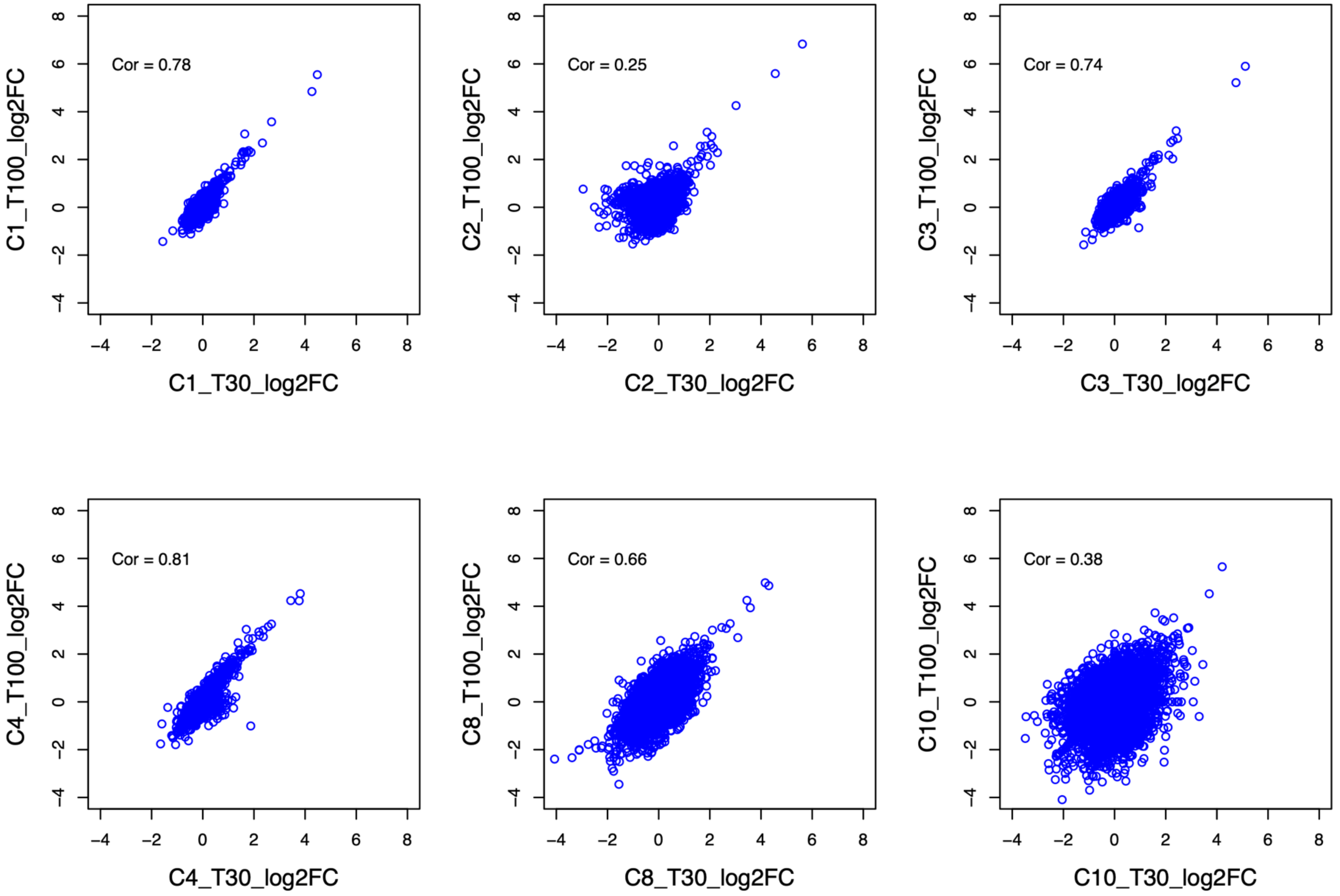

Cor = 0.74
C2_GW300_log2FC
C2_GW30_log2FC
8
6
4
2
0
−2
−4
−4
−2
0
2
4
6
8


Cor = 0.87
C3_GW300_log2FC
C3_GW30_log2FC
8
6
4
2
0
−2
−4
−4
−2
0
2
4
6
8

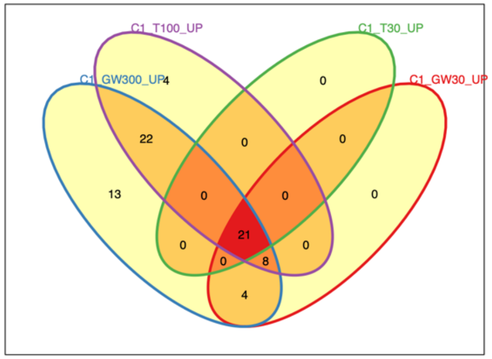

Cor = 0.88
C4_GW300_log2FC
C4_GW30_log2FC
8
6
4
2
0
−2
−4
−4
−2
0
2
4
6
8

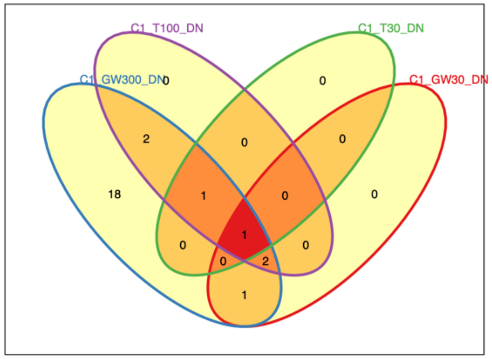

Cor = 0.67
C8_GW300_log2FC
C8_GW30_log2FC
8
6
4
2
0
−2
−4
−4
−2
0
2
4
6
8

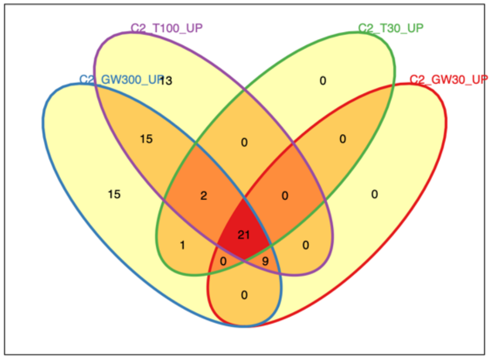

Cor = 0.49
C10_GW300_log2FC
C10_GW30_log2FC
8
6
4
2
0
−2
−4
−4
−2
0
2
4
6
8

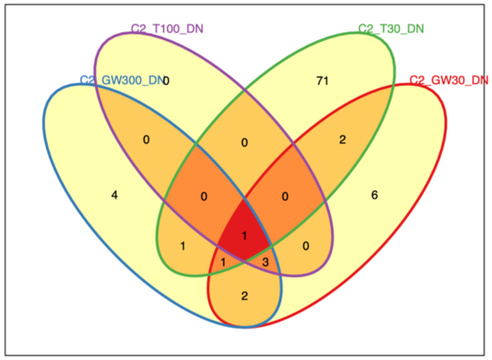

Cor = 0.78
C1_T30_log2FC
C1_T100_log2FC
Cor = 0.25
C2_T30_log2FC
C2_T100_log2FC
Cor = 0.74
C3_T30_log2FC
C3_T100_log2FC
Cor = 0.81
C4_T30_log2FC
C4_T100_log2FC
Cor = 0.66
C8_T30_log2FC
C8_T100_log2FC
Cor = 0.38
C10_T30_log2FC
C10_T100_log2FC
−4
−2
0
2
4
6
8

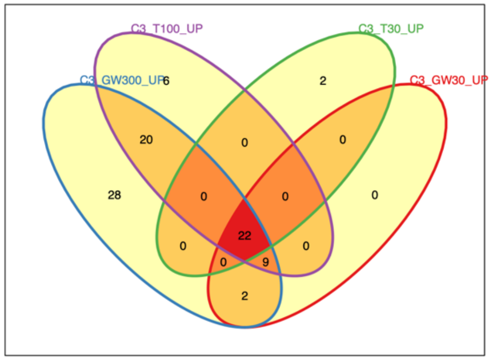
Supplementary Figure 19. Correlation of gene fold changes between the low and high dose of each treatment within the same single cell cluster. Pearson’s correlations are shown. GW30: GW3965 30 nM, GW300: GW3965 300 nM, T30: T0901317 30 nM, T100: T0901317 100 nM.

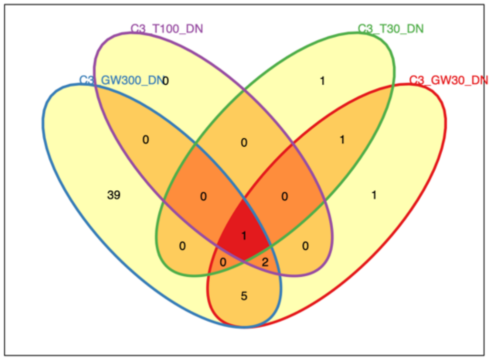

C1_T100_UP
C1_T30_UP
C1_GW300_UP
C1_GW30_UP
4
0
22
0
0
13
0
0
0
21
0
0
8
4

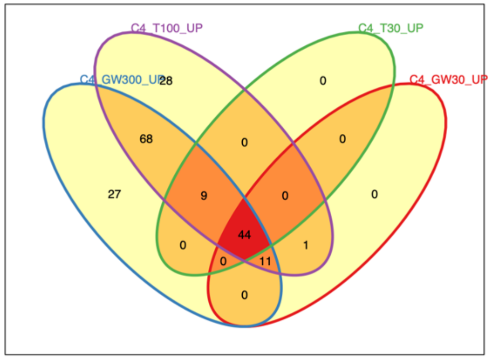

C1_T100_DN
C1_T30_DN
C1_GW300_DN
C1_GW30_DN
0
0
2
0
0
18
1
0
0
1
0
0
2
1

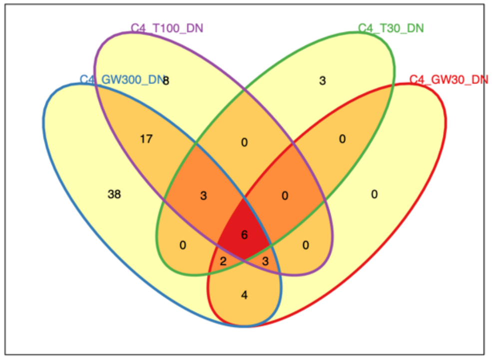

C2_T100_UP
C2_T30_UP
C2_GW300_UP
C2_GW30_UP
13
0
15
0
0
15
2
0
0
1
21
0
0
9
0

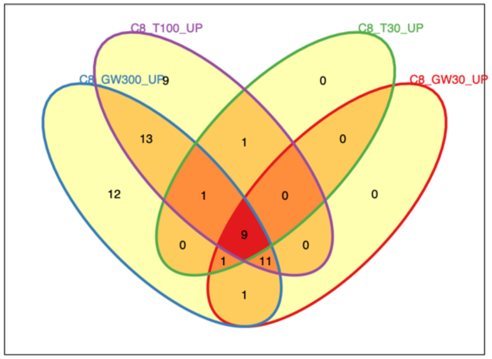

C2_T100_DN
C2_T30_DN
C2_GW300_DN
C2_GW30_DN
0
71
0
0
2
4
0
0
6
1
1
0
1
3
2

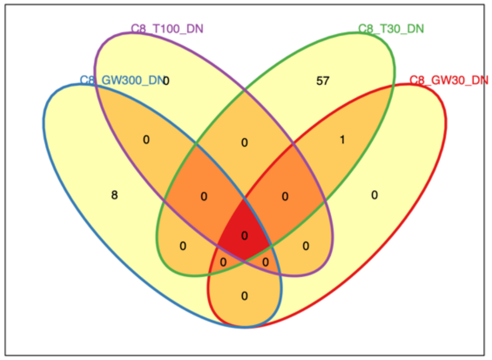

C3_T100_UP
C3_T30_UP
C3_GW300_UP
C3_GW30_UP
6
2
20
0
0
28
0
0
0
0
22
0
0
9
2

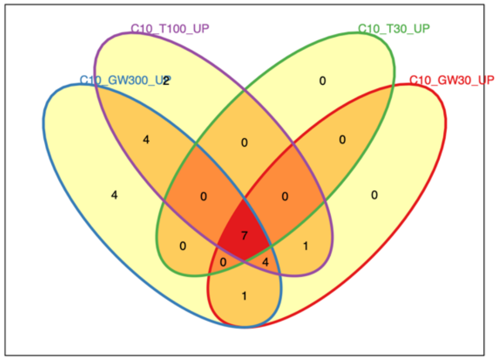

C3_T100_DN
C3_T30_DN
C3_GW300_DN
C3_GW30_DN
0
1
0
0
1
39
0
0
1
0
1
0
0
2
5

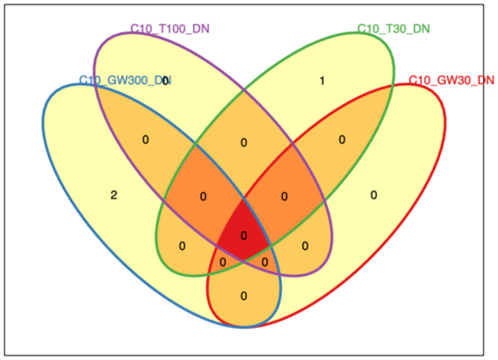

C4_T100_UP
C4_T30_UP
C4_GW300_UP
28
0
C4_GW30_UP
68
0
0
27
9
0
0
44
0
0
11
1
0


C4_T100_DN
C4_T30_DN
C4_GW300_DN
8
3
C4_GW30_DN
17
0
0
38
3
0
0
6
0
2
3
0
4

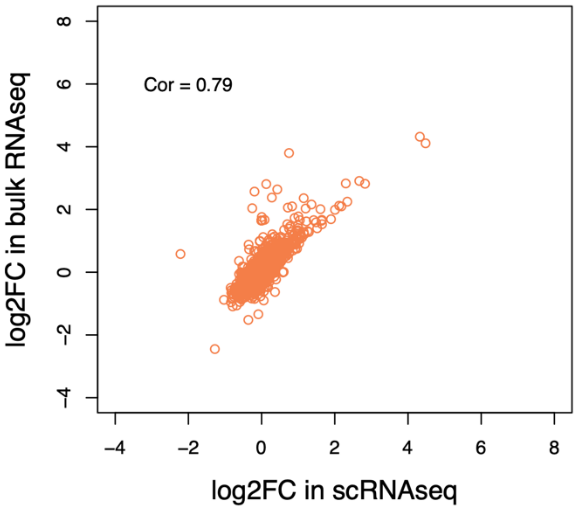

C8_T100_UP
C8_T30_UP
C8_GW300_UP
9
0
C8_GW30_UP
13
1
0
12
1
0
0
9
0
1
11
0
1

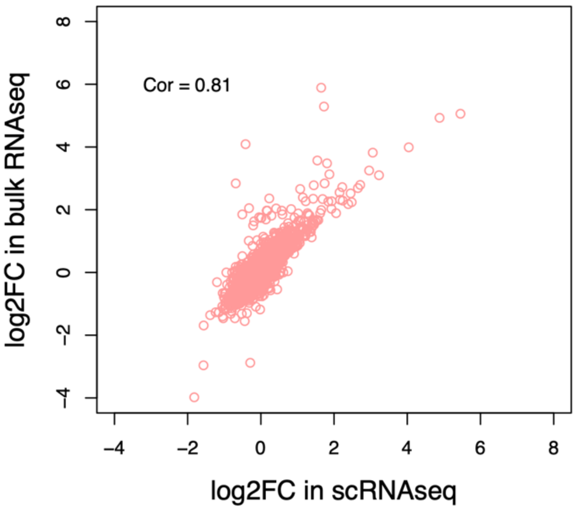

C8_T100_DN
C8_T30_DN
C8_GW300_DN
0
57
C8_GW30_DN
0
0
1
8
0
0
0
0
0
0
0
0
0

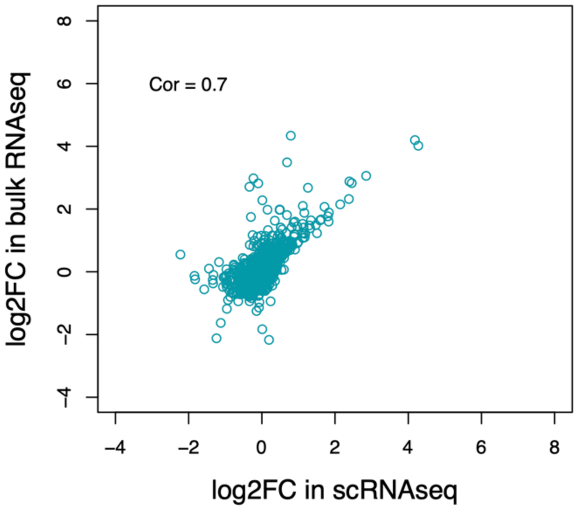

C10_T100_UP
C10_T30_UP
C10_GW300_UP
2
0
C10_GW30_UP
4
0
0
4
0
0
0
7
0
0
4
1
1

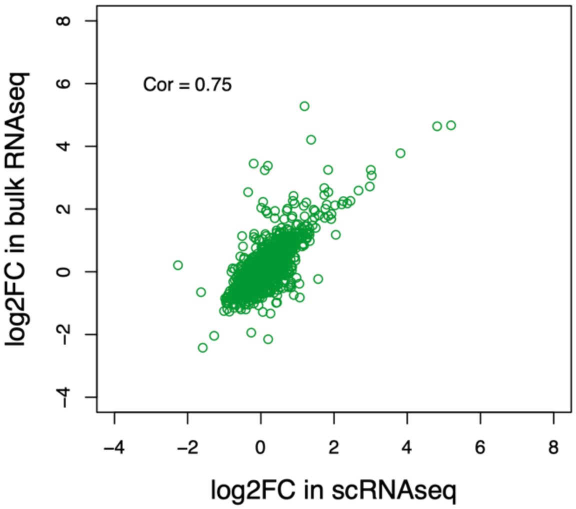

C10_T100_DN
C10_T30_DN
C10_GW300_DN
0
1
C10_GW30_DN
0
0
0
2
0
0
0
0
0
0
0
0
0

Supplementary Figure 20. Overlap in DEGs identified in each treatment within the same single cell cluster. UP: upregulated in the treatment compared to DMSO, DN: downregulated in the treatment compared to DMSO. GW30: GW3965 30 nM, GW300: GW3965 300 nM, T30: T0901317 30 nM, T100: T0901317 100 nM.

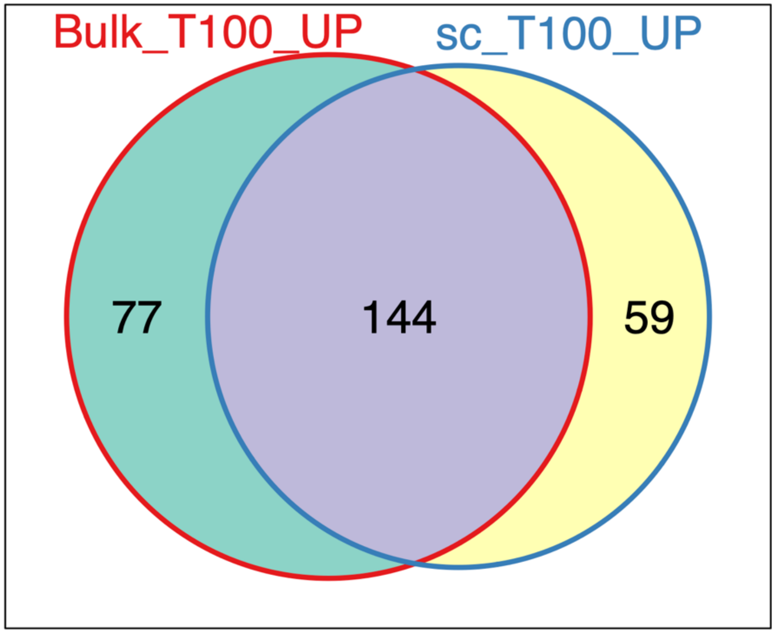

GW3965 30nM vs DMSO

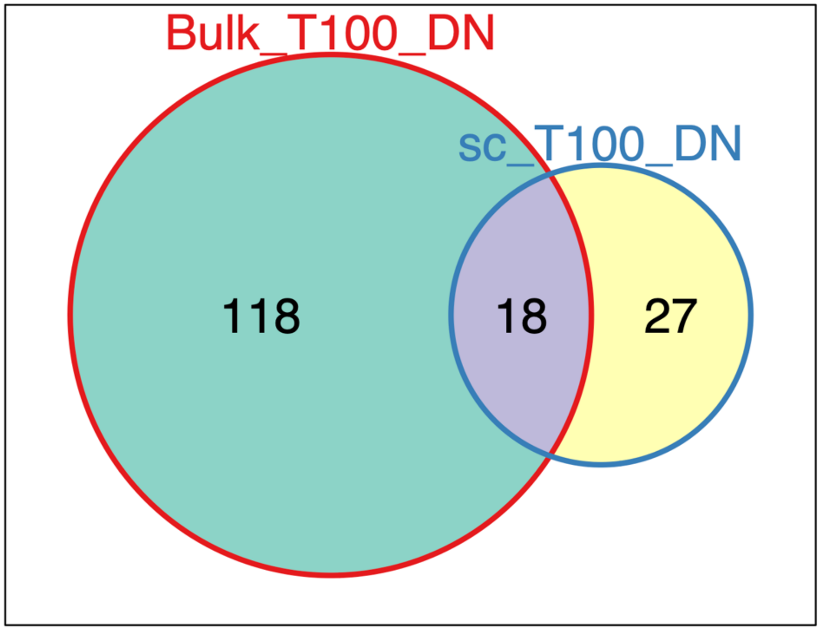

GW3965 300nM vs DMSO


T0901317 30nM vs DMSO

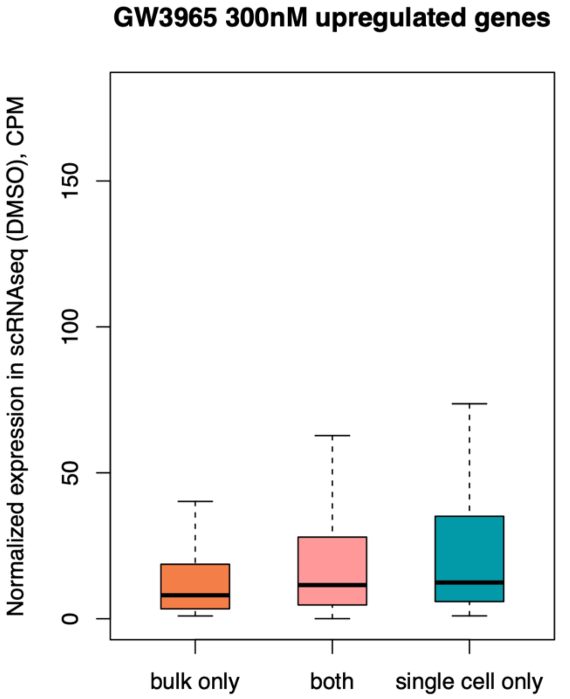

T0901317 100nM vs DMSO

Supplementary Figure 21. Correlation of gene fold changes between bulk and single cell RNA-seq for each treatment. Single cell fold changes were calculated using the mean expression across all single cells associated with a treatment compared to the mean expression across all single cells associated with DMSO. Pearson’s correlations are shown.

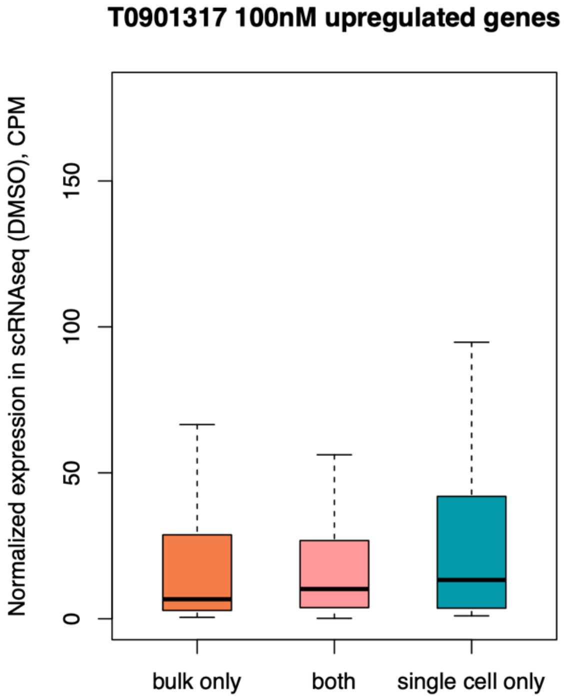

Bulk_T100_UP
sc_T100_UP
77
144
59


Bulk_T100_DN
sc_T100_DN
118
18
27

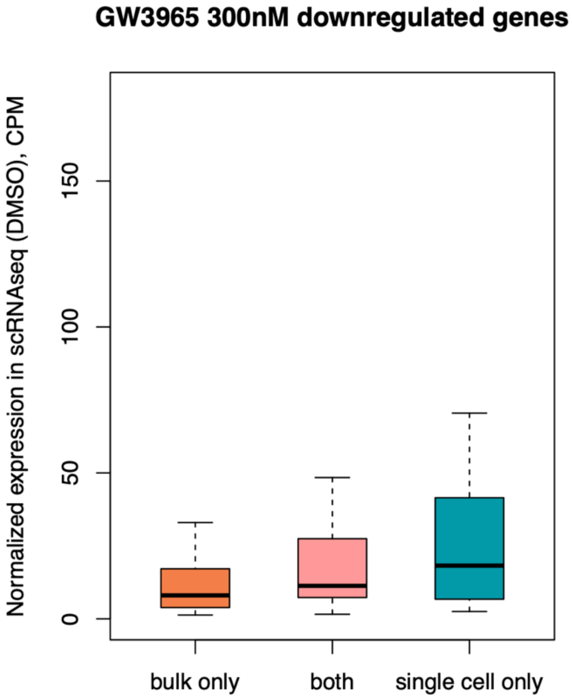
Supplementary Figure 22. Overlap in upregulated (UP) and downregulated (DN) DEGs between bulk RNA-seq and the union of single cell RNA-seq DEGs in clusters C1, C2, C3, C4, C8, and C10 with T0901317 100nM treatment. Bulk DEGs were filtered to genes tested in at least one single cell contrast.



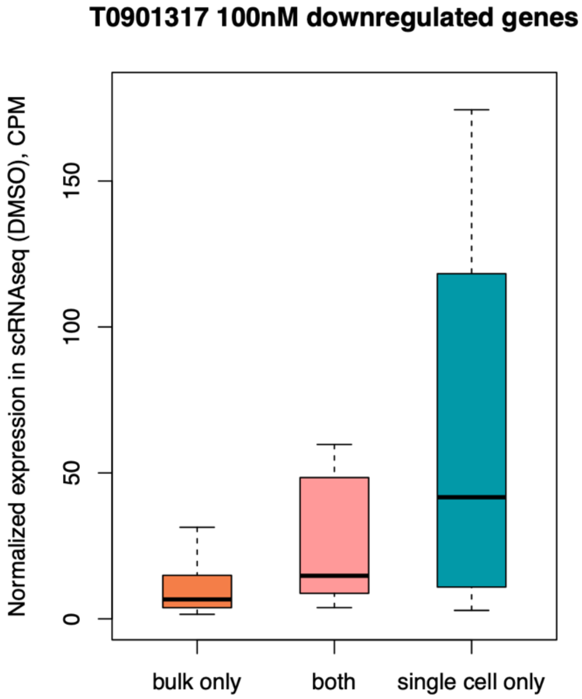
GW3965 300nM upregulated genes



T0901317 100nM upregulated genes

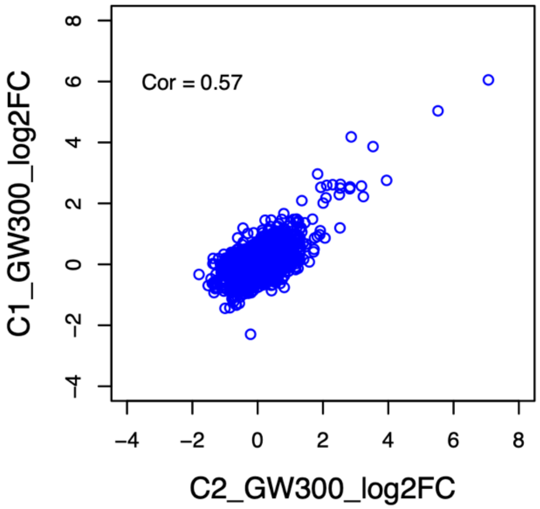


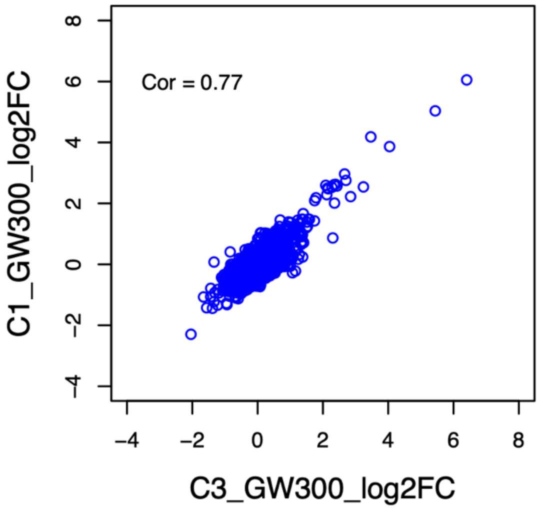
GW3965 300nM downregulated genes

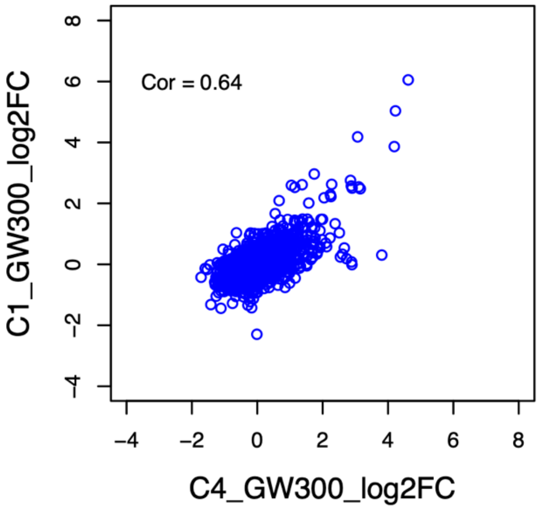


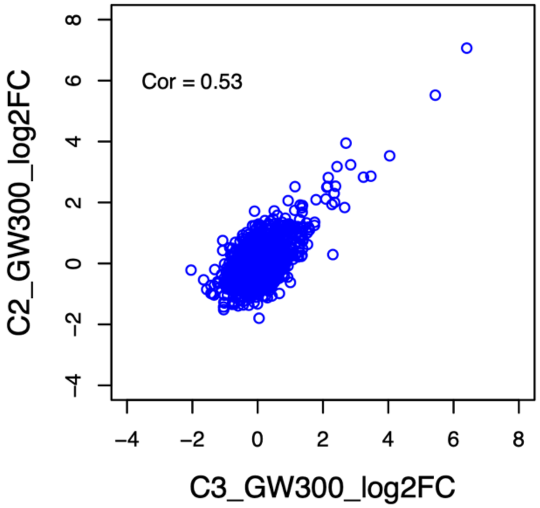
T0901317 100nM downregulated genes

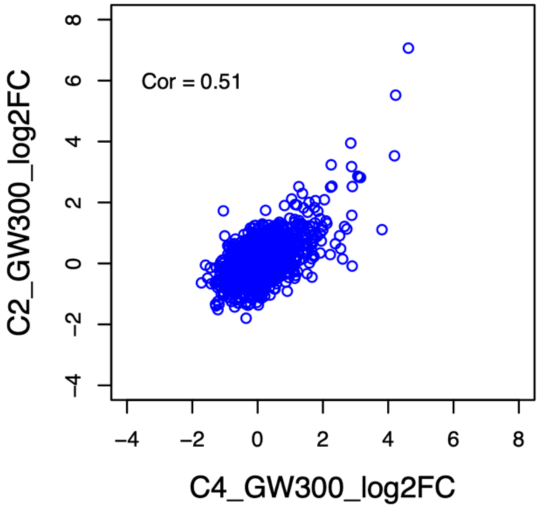
Supplementary Figure 23. Comparison of single cell expression levels in counts per million (CPM) for DEGs identified by bulk RNA-seq only, single cell RNA-seq only, or both methods for GW3965 300nM and T0901317 100nM treatments. Bulk DEGs were filtered to genes tested in at least one single cell contrast. For each gene, its single cell expression level was calculated as the mean expression across single cells in the DMSO samples.

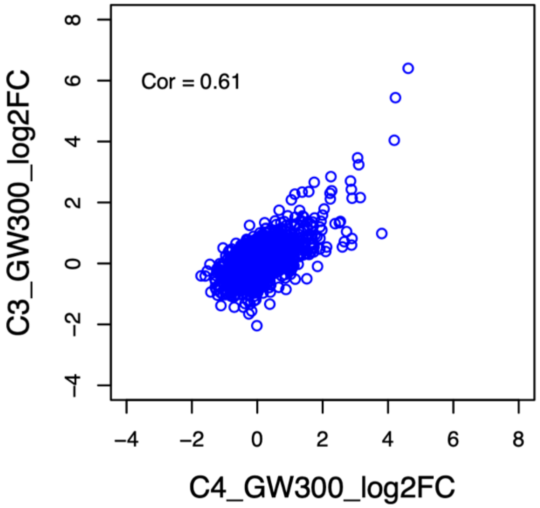

Cor = 0.57
C1_GW300_log2FC
C2_GW300_log2FC
−4
−2
0
2
4
6
8

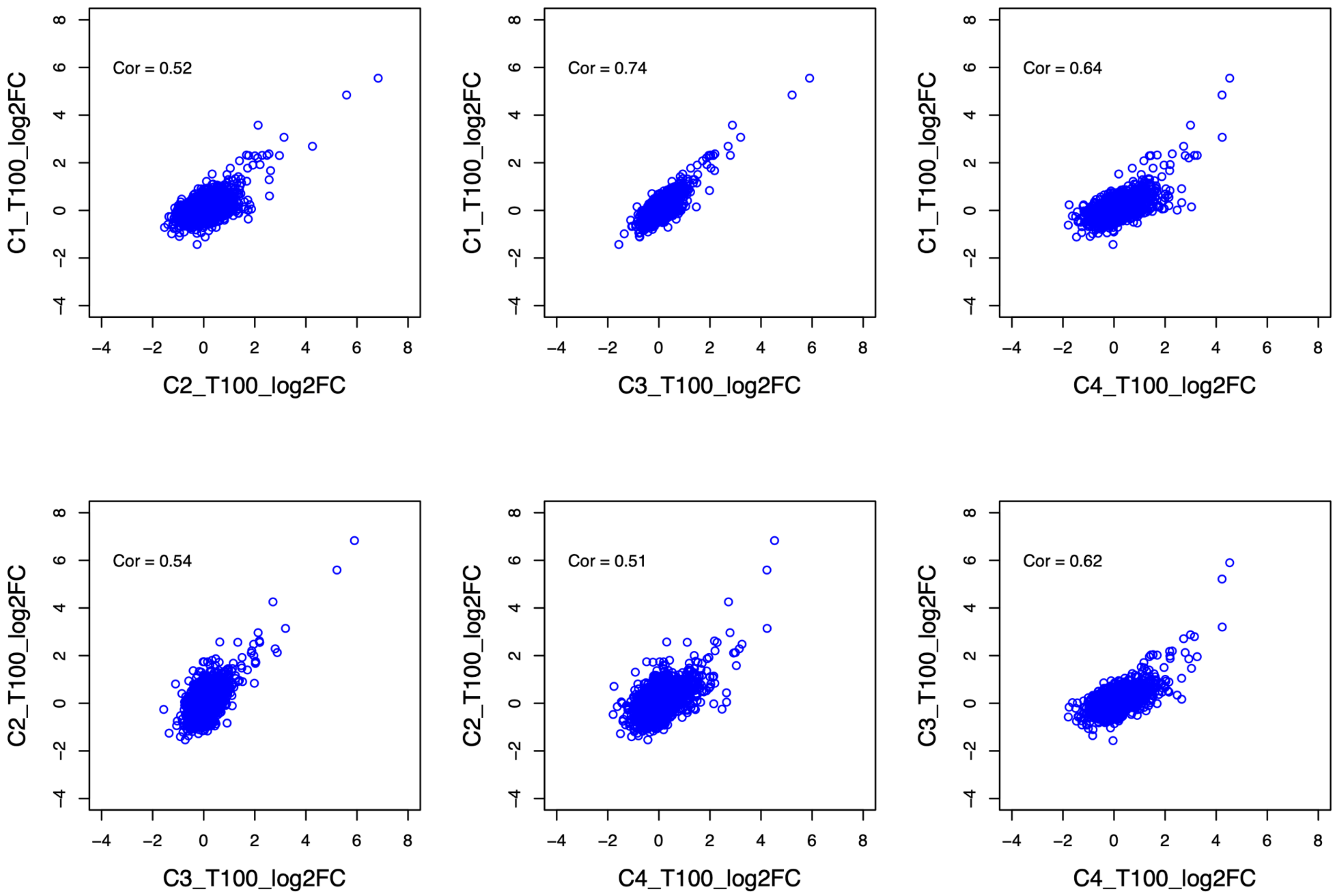

Cor = 0.77
C1_GW300_log2FC
C3_GW300_log2FC
−4
−2
0
2
4
6
8


Cor = 0.64
C1_GW300_log2FC
C4_GW300_log2FC
−4
−2
0
2
4
6
8

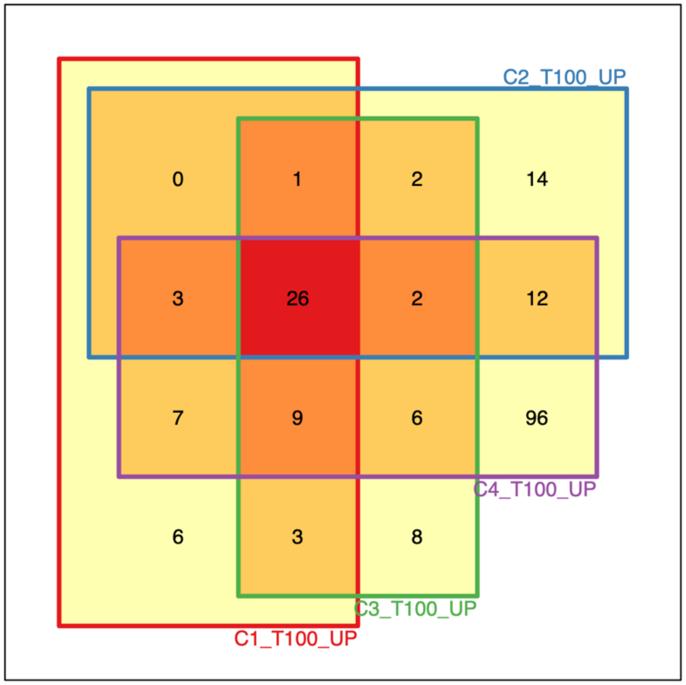

Cor = 0.53
C2_GW300_log2FC
C3_GW300_log2FC
−4
−2
0
2
4
6
8

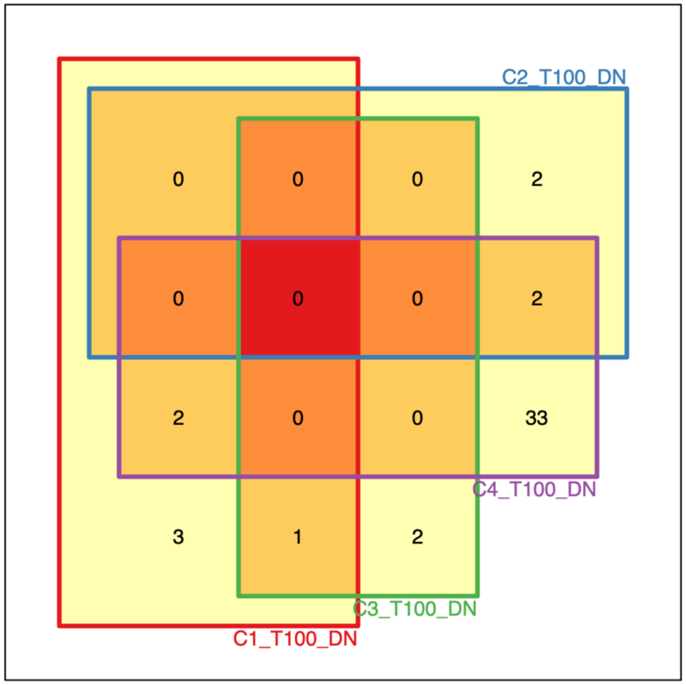

Cor = 0.51
C2_GW300_log2FC
C4_GW300_log2FC
−4
−2
0
2
4
6
8


Cor = 0.61
C3_GW300_log2FC
C4_GW300_log2FC
−4
−2
0
2
4
6
8


Cor = 0.52
C1_T100_log2FC
C2_T100_log2FC
Cor = 0.74
C1_T100_log2FC
C3_T100_log2FC
Cor = 0.64
C1_T100_log2FC
C4_T100_log2FC
Cor = 0.54
C2_T100_log2FC
C3_T100_log2FC
Cor = 0.51
C2_T100_log2FC
C4_T100_log2FC
Cor = 0.62
C3_T100_log2FC
C4_T100_log2FC
−4
−2
0
2
4
6
8

Supplementary Figure 24. Pairwise correlation of gene fold changes for the high doses of GW3965 and T0901317 across single cell clusters C1, C2, C3, and C4. Pearson's correlations are shown. GW300: GW3965 300 nM, T100: T0901317 100 nM.


C2_T100_UP
0
1
2
14
3
26
2
12
7
9
6
96
C4_T100_UP
6
3
8
C3_T100_UP
C1_T100_UP


C2_T100_DN
0
0
0
2
0
0
0
2
2
0
0
33
C4_T100_DN
3
1
2
C3_T100_DN
C1_T100_DN

Supplementary Figure 25. Overlap in upregulated (UP) and downregulated (DN) DEGs for single cell clusters C1, C2, C3, and C4 with T0901317 100nM treatment (T100).