Supplementary Figures

Adipose tissue in health and disease through the lens of its building blocks

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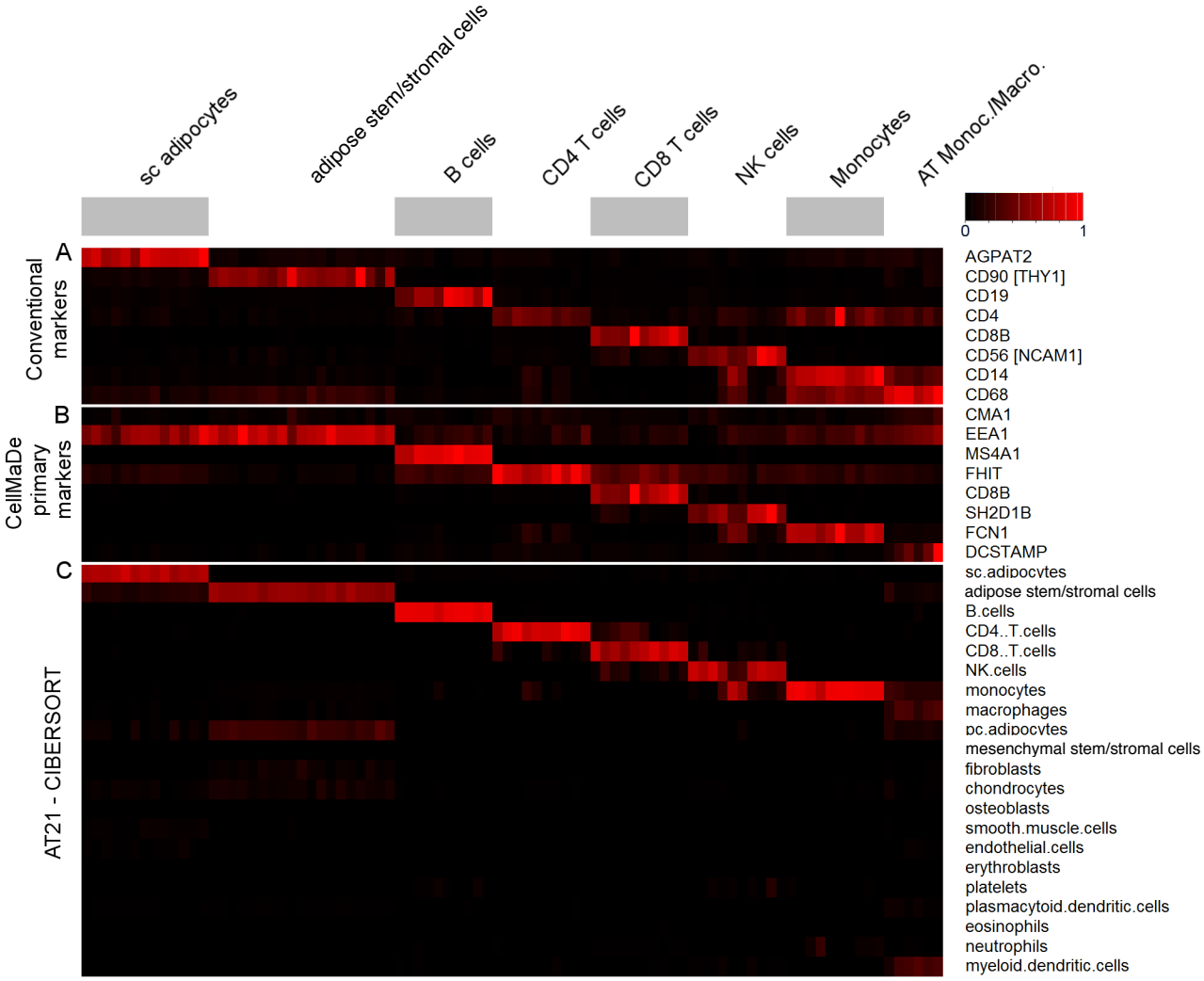
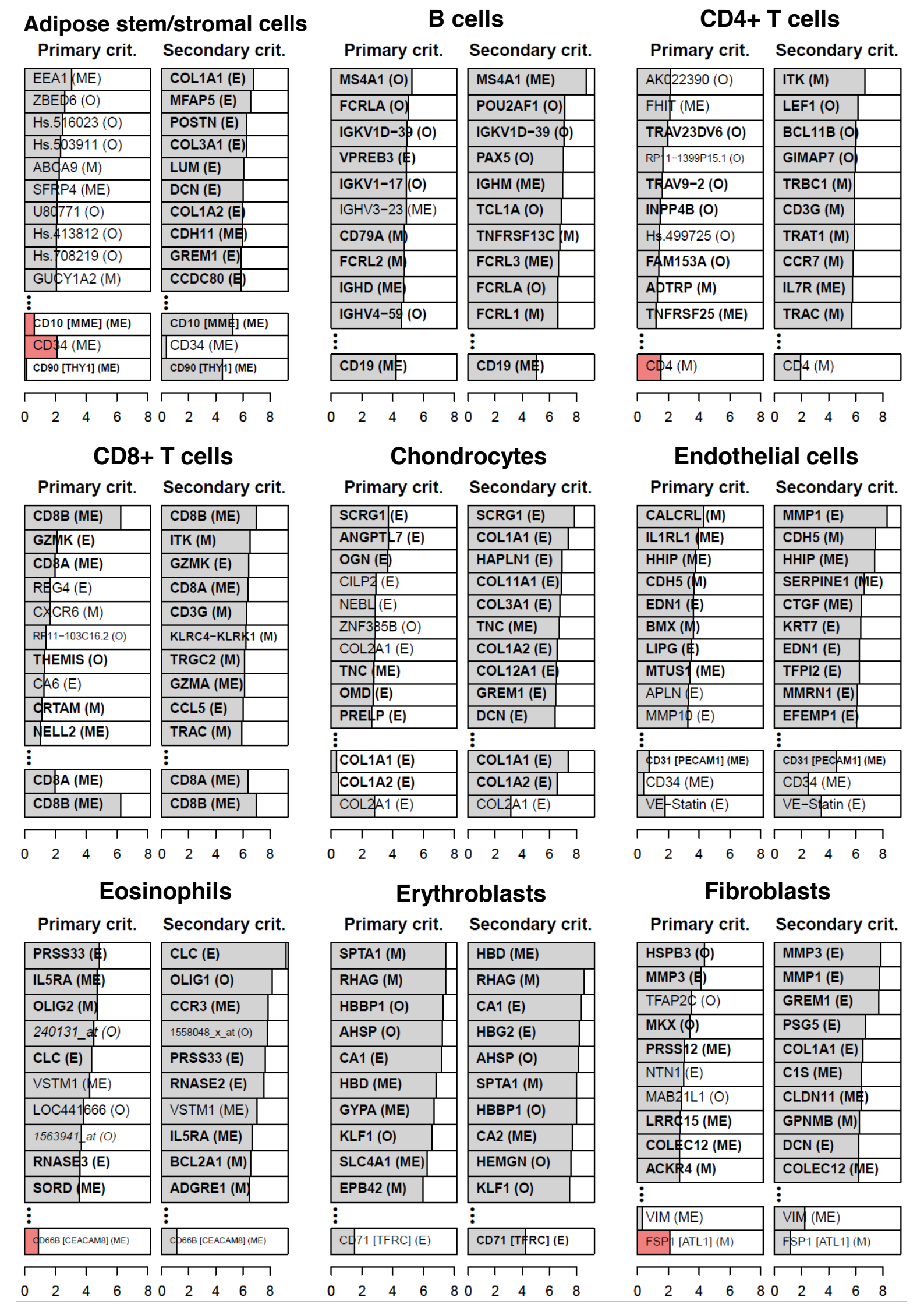
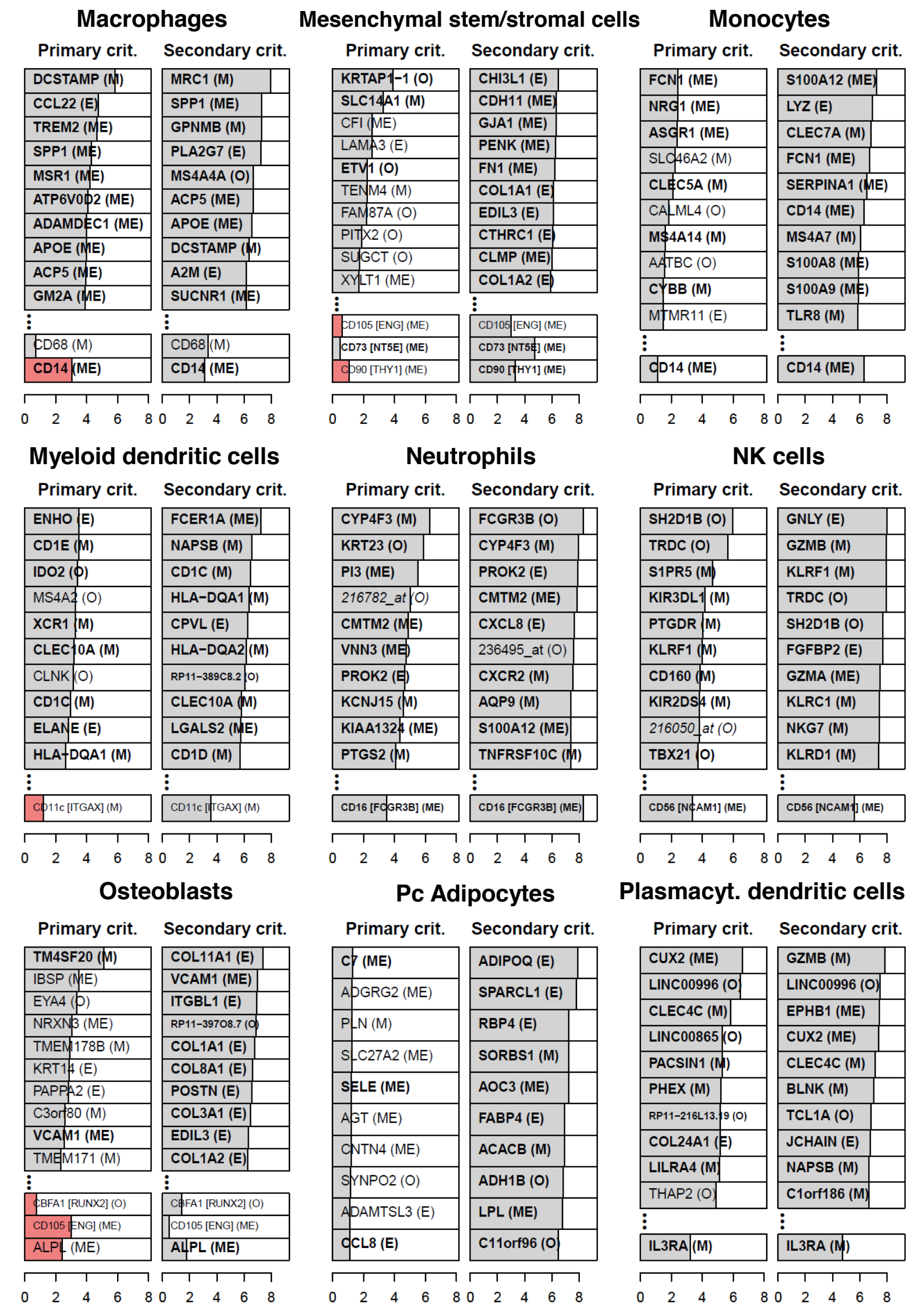
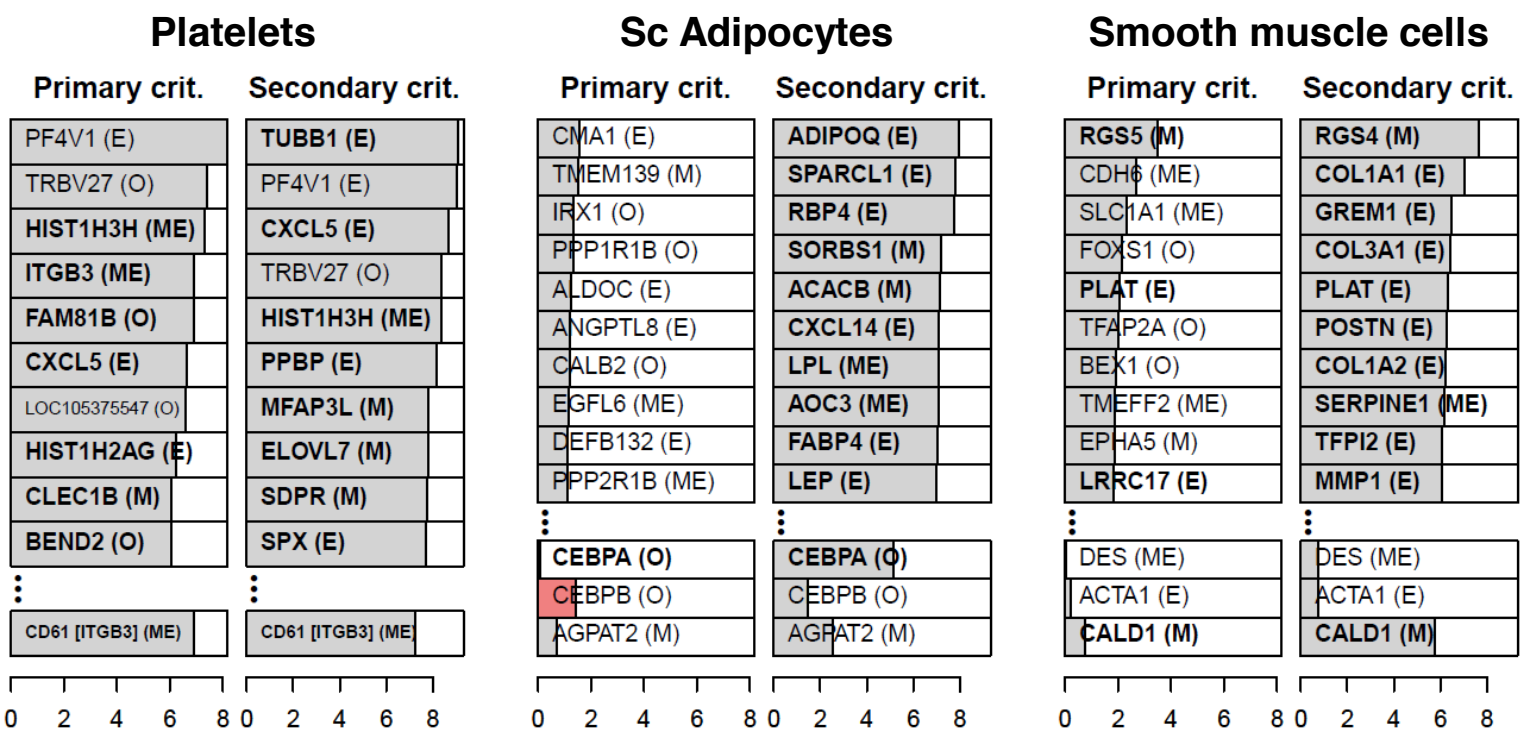


Supplementary Figure S1 : Ex-vivo validation of the TissueDecoder framework with an independent dataset. A) Normalized expression of selected conventional markers from literature; B) normalized expression of CellMaDe predicted primary markers; and C) cell type composition prediction from CIBERSORT with the AT21 signature matrix. The common x-axis above the figure denotes the reported cell type of the samples from the validation dataset.


Adipose stem/stromal cells
Primary crit.
EEA1 (ME)
ZBED6 (O)
Hs.516023 (O)
Hs.503911 (O)
ABCA9 (M)
SFRP4 (ME)
U80771 (O)
Hs.413812 (O)
Hs.708219 (O)
GUCY1A2 (M)
CD10 [MME] (ME)
CD34 (ME)
CD90 [THY1] (ME)
Secondary crit.
COL1A1 (E)
MFAP5 (E)
POSTN (E)
COL3A1 (E)
LUM (E)
DCN (E)
COL1A2 (E)
CDH11 (ME)
GREM1 (E)
CCDC80 (E)
CD10 [MME] (ME)
CD34 (ME)
CD90 [THY1] (ME)
0 2 4 6 8
B cells
Primary crit.
MS4A1 (O)
FCRLA (O)
IGKV1D−39 (O)
VPREB3 (E)
IGKV1−17 (O)
IGHV3−23 (ME)
CD79A (M)
FCRL2 (M)
IGHD (ME)
IGHV4−59 (O)
CD19 (ME)
Secondary crit.
MS4A1 (ME)
POU2AF1 (O)
IGKV1D−39 (O)
PAX5 (O)
IGHM (ME)
TCL1A (O)
TNFRSF13C (M)
FCRL3 (ME)
FCRLA (O)
FCRL1 (M)
CD19 (ME)
0 2 4 6 8
CD4+ T cells
Primary crit.
AK022390 (O)
FHIT (ME)
TRAV23DV6 (O)
RP11−1399P15.1 (O)
TRAV9−2 (O)
INPP4B (O)
Hs.499725 (O)
FAM153A (O)
ADTRP (M)
TNFRSF25 (ME)
CD4 (M)
Secondary crit.
ITK (M)
LEF1 (O)
BCL11B (O)
GIMAP7 (O)
TRBC1 (M)
CD3G (M)
TRAT1 (M)
CCR7 (M)
IL7R (ME)
TRAC (M)
CD4 (M)
0 2 4 6 8
CD8+ T cells
Primary crit.
CD8B (ME)
GZMK (E)
CD8A (ME)
REG4 (E)
CXCR6 (M)
RP11−103C16.2 (O)
THEMIS (O)
CA6 (E)
CRTAM (M)
NELL2 (ME)
CD8A (ME)
CD8B (ME)
Secondary crit.
CD8B (ME)
ITK (M)
GZMK (E)
CD8A (ME)
CD3G (M)
KLRC4−KLRK1 (M)
TRGC2 (M)
GZMA (ME)
CCL5 (E)
TRAC (M)
CD8A (ME)
CD8B (ME)
0 2 4 6 8
Chondrocytes
Primary crit.
SCRG1 (E)
ANGPTL7 (E)
OGN (E)
CILP2 (E)
NEBL (E)
ZNF385B (O)
COL2A1 (E)
TNC (ME)
OMD (E)
PRELP (E)
COL1A1 (E)
COL1A2 (E)
COL2A1 (E)
Secondary crit.
SCRG1 (E)
COL1A1 (E)
HAPLN1 (E)
COL11A1 (E)
COL3A1 (E)
TNC (ME)
COL1A2 (E)
COL12A1 (E)
GREM1 (E)
DCN (E)
COL1A1 (E)
COL1A2 (E)
COL2A1 (E)
0 2 4 6 8
Endothelial cells
Primary crit.
CALCRL (M)
IL1RL1 (ME)
HHIP (ME)
CDH5 (M)
EDN1 (E)
BMX (M)
LIPG (E)
MTUS1 (ME)
APLN (E)
MMP10 (E)
CD31 [PECAM1] (ME)
CD34 (ME)
VE−Statin (E)
Secondary crit.
MMP1 (E)
CDH5 (M)
HHIP (ME)
SERPINE1 (ME)
CTGF (ME)
KRT7 (E)
EDN1 (E)
TFPI2 (E)
MMRN1 (E)
EFEMP1 (E)
CD31 [PECAM1] (ME)
CD34 (ME)
VE−Statin (E)
0 2 4 6 8
Eosinophils
Primary crit.
PRSS33 (E)
IL5RA (ME)
OLIG2 (M)
240131_at (O)
CLC (E)
VSTM1 (ME)
LOC441666 (O)
1563941_at (O)
RNASE3 (E)
SORD (ME)
CD66B [CEACAM8] (ME)
Secondary crit.
CLC (E)
OLIG1 (O)
CCR3 (ME)
1558048_x_at (O)
PRSS33 (E)
RNASE2 (E)
VSTM1 (ME)
IL5RA (ME)
BCL2A1 (M)
ADGRE1 (M)
CD66B [CEACAM8] (ME)
0 2 4 6 8
Erythroblasts
Primary crit.
SPTA1 (M)
RHAG (M)
HBBP1 (O)
AHSP (O)
CA1 (E)
HBD (ME)
GYPA (ME)
KLF1 (O)
SLC4A1 (ME)
EPB42 (M)
CD71 [TFRC] (E)
Secondary crit.
HBD (ME)
RHAG (M)
CA1 (E)
HBG2 (E)
AHSP (O)
SPTA1 (M)
HBBP1 (O)
CA2 (ME)
HEMGN (O)
KLF1 (O)
CD71 [TFRC] (E)
0 2 4 6 8
Fibroblasts
Primary crit.
HSPB3 (O)
MMP3 (E)
TFAP2C (O)
MKX (O)
PRSS12 (ME)
NTN1 (E)
MAB21L1 (O)
LRRC15 (ME)
COLEC12 (ME)
ACKR4 (M)
VIM (ME)
FSP1 [ATL1] (M)
Secondary crit.
MMP3 (E)
MMP1 (E)
GREM1 (E)
PSG5 (E)
COL1A1 (E)
C1S (ME)
CLDN11 (ME)
GPNMB (M)
DCN (E)
COLEC12 (ME)
VIM (ME)
FSP1 [ATL1] (M)
0 2 4 6 8

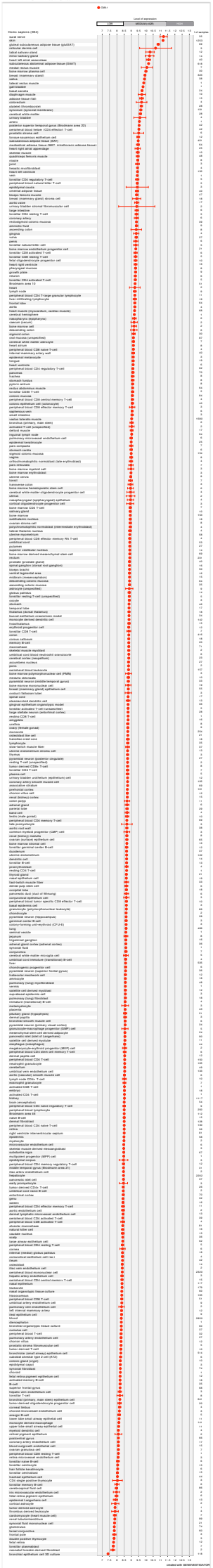

Macrophages
Primary crit.
DCSTAMP (M)
CCL22 (E)
TREM2 (ME)
SPP1 (ME)
MSR1 (ME)
ATP6V0D2 (ME)
ADAMDEC1 (ME)
APOE (ME)
ACP5 (ME)
GM2A (ME)
CD68 (M)
CD14 (ME)
Secondary crit.
MRC1 (M)
SPP1 (ME)
GPNMB (M)
PLA2G7 (E)
MS4A4A (O)
ACP5 (ME)
APOE (ME)
DCSTAMP (M)
A2M (E)
SUCNR1 (ME)
CD68 (M)
CD14 (ME)
0 2 4 6 8
Mesenchymal stem/stromal cells
Primary crit.
KRTAP1−1 (O)
SLC14A1 (M)
CFI (ME)
LAMA3 (E)
ETV1 (O)
TENM4 (M)
FAM87A (O)
PITX2 (O)
SUGCT (O)
XYLT1 (ME)
CD105 [ENG] (ME)
CD73 [NT5E] (ME)
CD90 [THY1] (ME)
Secondary crit.
CHI3L1 (E)
CDH11 (ME)
GJA1 (ME)
PENK (ME)
FN1 (ME)
COL1A1 (E)
EDIL3 (E)
CTHRC1 (E)
CLMP (ME)
COL1A2 (E)
CD105 [ENG] (ME)
CD73 [NT5E] (ME)
CD90 [THY1] (ME)
0 2 4 6 8
Monocytes
Primary crit.
FCN1 (ME)
NRG1 (ME)
ASGR1 (ME)
SLC46A2 (M)
CLEC5A (M)
CALML4 (O)
MS4A14 (M)
AATBC (O)
CYBB (M)
MTMR11 (E)
CD14 (ME)
Secondary crit.
S100A12 (ME)
LYZ (E)
CLEC7A (M)
FCN1 (ME)
SERPINA1 (ME)
CD14 (ME)
MS4A7 (M)
S100A8 (ME)
S100A9 (ME)
TLR8 (M)
CD14 (ME)
0 2 4 6 8
Myeloid dendritic cells
Primary crit.
ENHO (E)
CD1E (M)
IDO2 (O)
MS4A2 (O)
XCR1 (M)
CLEC10A (M)
CLNK (O)
CD1C (M)
ELANE (E)
HLA−DQA1 (M)
CD11c [ITGAX] (M)
Secondary crit.
FCER1A (ME)
NAPSB (M)
CD1C (M)
HLA−DQA1 (M)
CPVL (E)
HLA−DQA2 (M)
RP11−389C8.2 (O)
CLEC10A (M)
LGALS2 (ME)
CD1D (M)
CD11c [ITGAX] (M)
0 2 4 6 8
Neutrophils
Primary crit.
CYP4F3 (M)
KRT23 (O)
PI3 (ME)
216782_at (O)
CMTM2 (ME)
VNN3 (ME)
PROK2 (E)
KCNJ15 (M)
KIAA1324 (ME)
PTGS2 (M)
CD16 [FCGR3B] (ME)
Secondary crit.
FCGR3B (O)
CYP4F3 (M)
PROK2 (E)
CMTM2 (ME)
CXCL8 (E)
236495_at (O)
CXCR2 (M)
AQP9 (M)
S100A12 (ME)
TNFRSF10C (M)
CD16 [FCGR3B] (ME)
0 2 4 6 8
NK cells
Primary crit.
SH2D1B (O)
TRDC (O)
S1PR5 (M)
KIR3DL1 (M)
PTGDR (M)
KLRF1 (M)
CD160 (M)
KIR2DS4 (M)
216050_at (O)
TBX21 (O)
CD56 [NCAM1] (ME)
Secondary crit.
GNLY (E)
GZMB (M)
KLRF1 (M)
TRDC (O)
SH2D1B (O)
FGFBP2 (E)
GZMA (ME)
KLRC1 (M)
NKG7 (M)
KLRD1 (M)
CD56 [NCAM1] (ME)
0 2 4 6 8
Osteoblasts
Primary crit.
TM4SF20 (M)
IBSP (ME)
EYA4 (O)
NRXN3 (ME)
TMEM178B (M)
KRT14 (E)
PAPPA2 (E)
C3orf80 (M)
VCAM1 (ME)
TMEM171 (M)
CBFA1 [RUNX2] (O)
CD105 [ENG] (ME)
ALPL (ME)
Secondary crit.
COL11A1 (E)
VCAM1 (ME)
ITGBL1 (E)
RP11−397O8.7 (O)
COL1A1 (E)
COL8A1 (E)
POSTN (E)
COL3A1 (E)
EDIL3 (E)
COL1A2 (E)
CBFA1 [RUNX2] (O)
CD105 [ENG] (ME)
ALPL (ME)
0 2 4 6 8
Pc Adipocytes
Primary crit.
C7 (ME)
ADGRG2 (ME)
PLN (M)
SLC27A2 (ME)
SELE (ME)
AGT (ME)
CNTN4 (ME)
SYNPO2 (O)
ADAMTSL3 (E)
CCL8 (E)
Secondary crit.
ADIPOQ (E)
SPARCL1 (E)
RBP4 (E)
SORBS1 (M)
AOC3 (ME)
FABP4 (E)
ACACB (M)
ADH1B (O)
LPL (ME)
C11orf96 (O)
0 2 4 6 8
Plasmacyt. dendritic cells
Primary crit.
CUX2 (ME)
LINC00996 (O)
CLEC4C (M)
LINC00865 (O)
PACSIN1 (M)
PHEX (M)
RP11−216L13.19 (O)
COL24A1 (E)
LILRA4 (M)
THAP2 (O)
IL3RA (M)
Secondary crit.
GZMB (M)
LINC00996 (O)
EPHB1 (ME)
CUX2 (ME)
CLEC4C (M)
BLNK (M)
TCL1A (O)
JCHAIN (E)
NAPSB (M)
C1orf186 (M)
IL3RA (M)
0 2 4 6 8



Supplementary Figure S2: Primary and secondary markers for all 21 cell types. Bar plots show the top ten cell type markers identified by the primary criterion and the secondary criterion of CellMaDe. Below each column conventional markers are demonstrated with their associated score. **Bold** font indicates the presence of the gene in the AT21 signature matrix and red colored bars indicate the value of the (primary/secondary) criterion was negative. Letters in brackets (M: membrane, E: extracellular, ME: both membrane and extracellular, or O: other) specify the gene ontology cellular location of the corresponding protein.

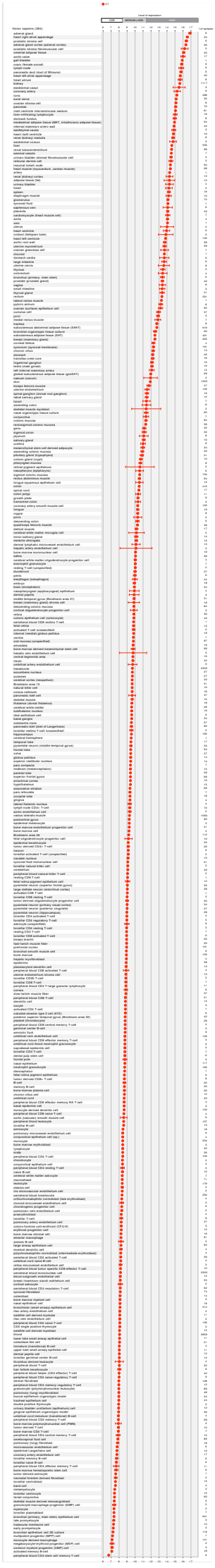
Supplementary Figure S3. Tissue expressions of the most significant Primary Marker per cell type identified by CellMaDe analyzed by Genevestigator from 394 human anatomically annotated tissue expression profiles.
The genes are predicted to be expressed in A) Subcutaneous Adipocytes, B)Pericardial Adipocytes, C) A. Stromal/ Stem Cells,D) Mesenchymal stromal/stem Cells, E) Fibroblasts, F) Chondrocytes, G) Osteoblasts, H) Smooth Muscle Cells, I) Endothelial Cells, J) Erytrhoblasts, K) Platelets, L) Natural Killer Cells, M) CD4+ T cells, N) CD8+ T cells, O) B Cells, P) Plasmacytoid Dendritic Cells, Q) Eosinophils, R) Neutrophils, S) Myeloid Dendritic Cells, U) Monocyes, V) Macrophages.

*The data is accessed on 12/08/2017.

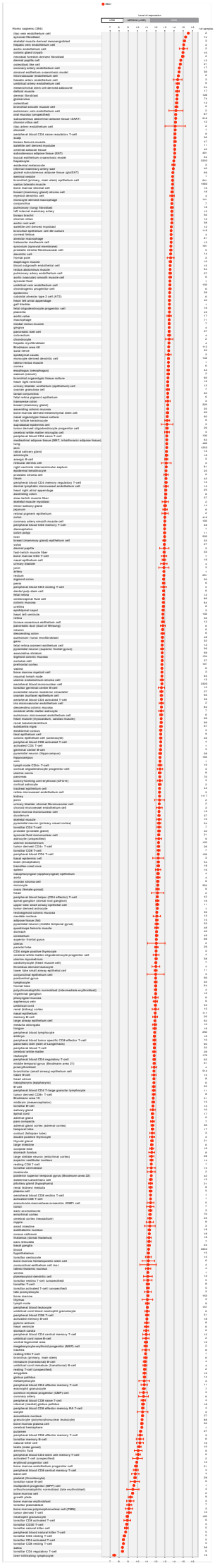


A) Subcutaneous Adipocytes

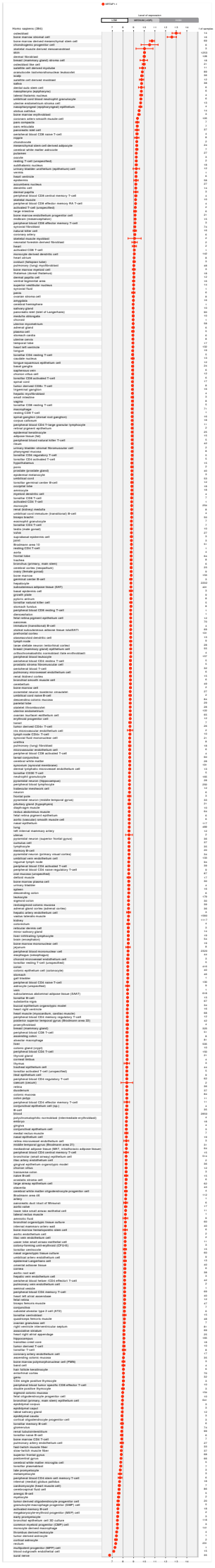
B) Pericardial Adipocytes



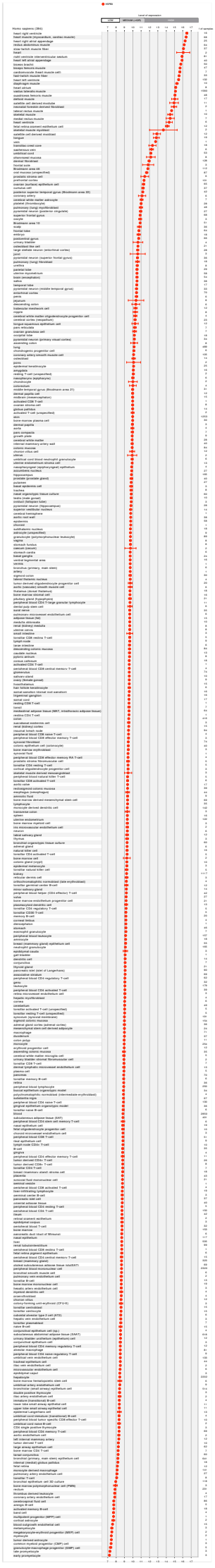
C) Adipose Stem/Stromal Cells



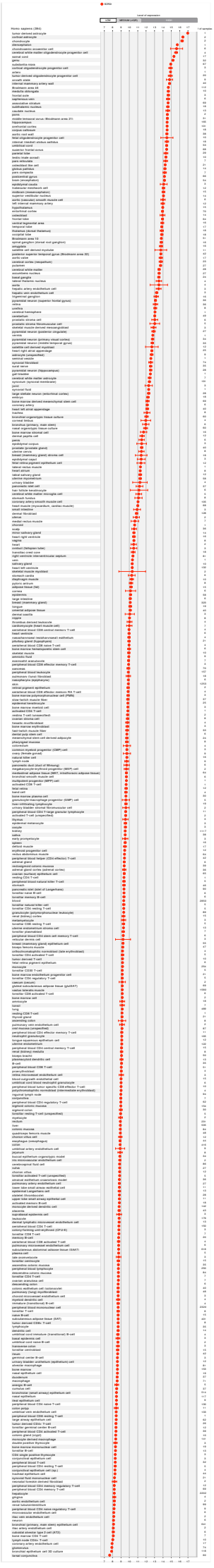
C) Mesenchymal Stem/Stromal Cells



E) Fibroblasts

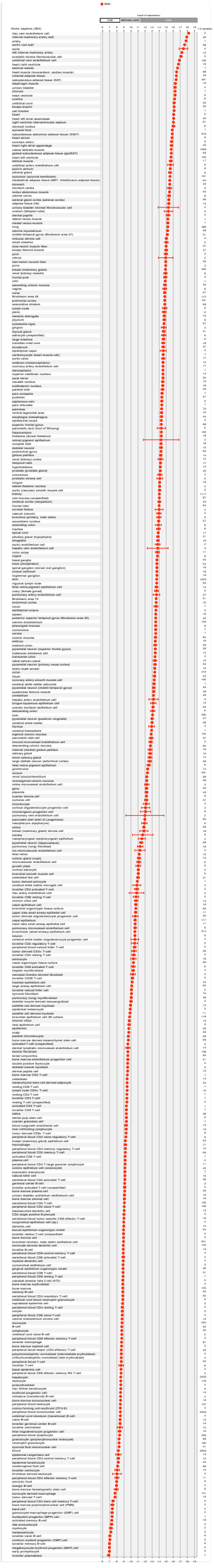


F) Chondrocytes

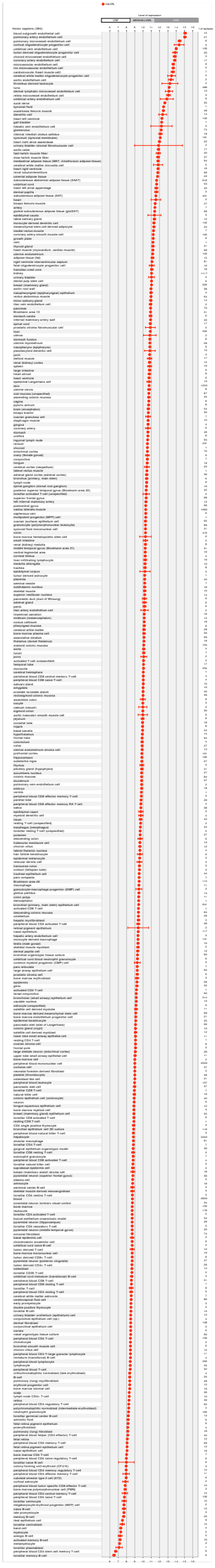


G) Osteoblasts

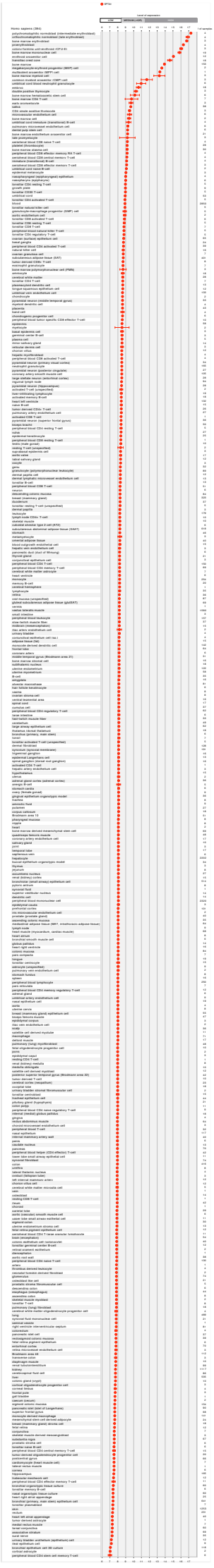
H) Smooth Muscle Cells



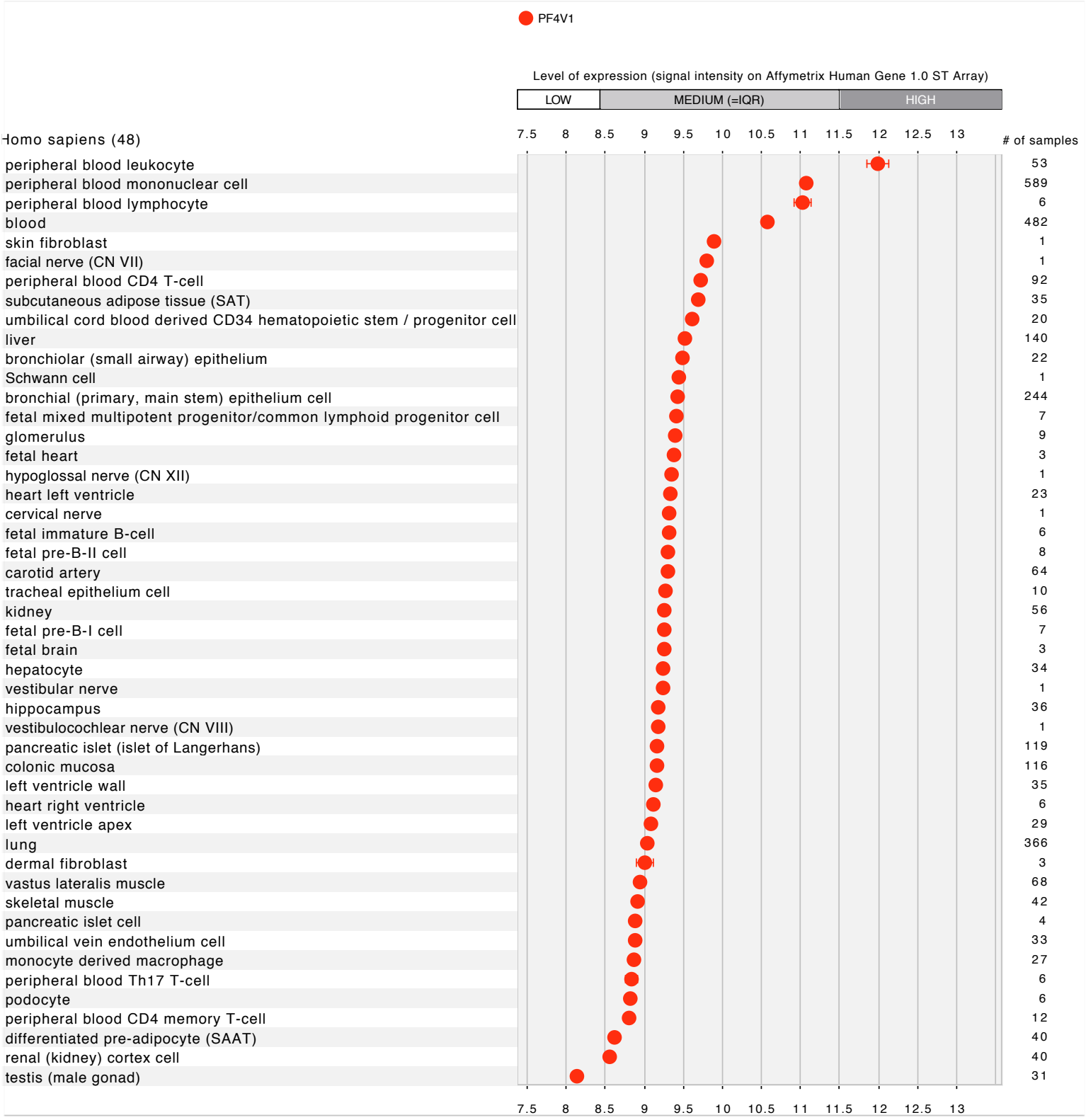
I) Endothelial Cells



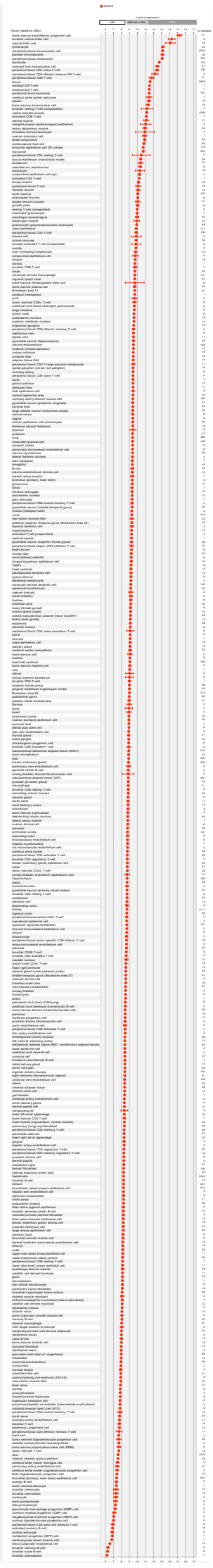
J) Erythroblasts



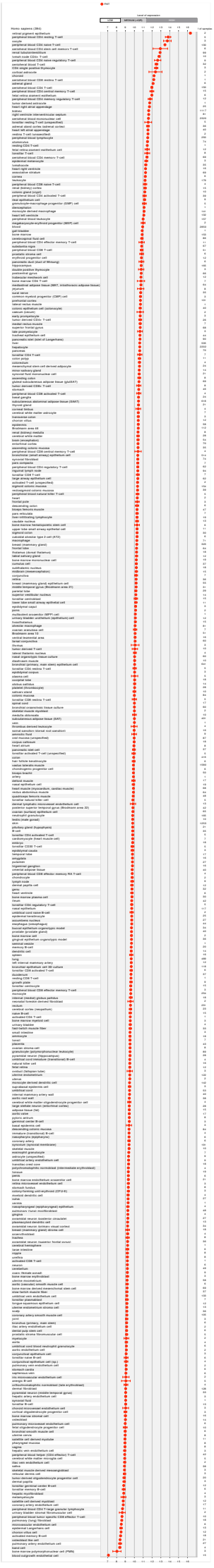
K) Platelets


PF4V1
Level of expression (signal intensity on Affymetrix Human Gene 1.0 ST Array)
LOW
MEDIUM (=IQR)
HIGH
7.5 8 8.5 9 9.5 10 10.5 11 11.5 12 12.5 13
Homo sapiens (48)
# of samples
peripheral blood leukocyte 53
peripheral blood mononuclear cell 589
peripheral blood lymphocyte 6
blood 482
skin fibroblast 1
facial nerve (CN VII) 1
peripheral blood CD4 T-cell 92
subcutaneous adipose tissue (SAT) 35
umbilical cord blood derived CD34 hematopoietic stem / progenitor cell 20
liver 140
bronchiolar (small airway) epithelium 22
Schwann cell 1
bronchial (primary, main stem) epithelium cell 244
fetal mixed multipotent progenitor/common lymphoid progenitor cell 7
glomerulus 9
fetal heart 3
hypoglossal nerve (CN XII) 1
heart left ventricle 23
cervical nerve 1
fetal immature B-cell 6
fetal pre-B-II cell 8
carotid artery 64
tracheal epithelium cell 10
kidney 56
fetal pre-B-I cell 7
fetal brain 3
hepatocyte 34
vestibular nerve 1
hippocampus 36
vestibulocochlear nerve (CN VIII) 1
pancreatic islet (islet of Langerhans) 119
colonic mucosa 116
left ventricle wall 35
heart right ventricle 6
left ventricle apex 29
lung 366
dermal fibroblast 3
vastus lateralis muscle 68
skeletal muscle 42
pancreatic islet cell 4
umbilical vein endothelium cell 33
monocyte derived macrophage 27
peripheral blood Th17 T-cell 6
podocyte 6
peripheral blood CD4 memory T-cell 12
differentiated pre-adipocyte (SAAT) 40
renal (kidney) cortex cell 40
testis (male gonad) 31
7.5 8 8.5 9 9.5 10 10.5 11 11.5 12 12.5 13

L) Natural Killer Cells

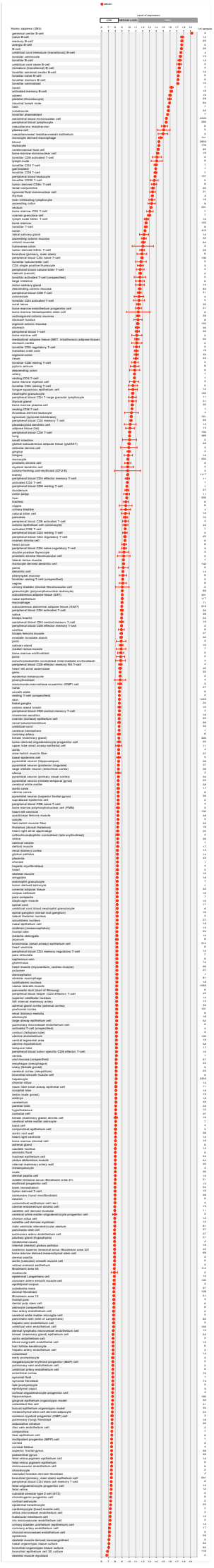


M) CD4+ T cells

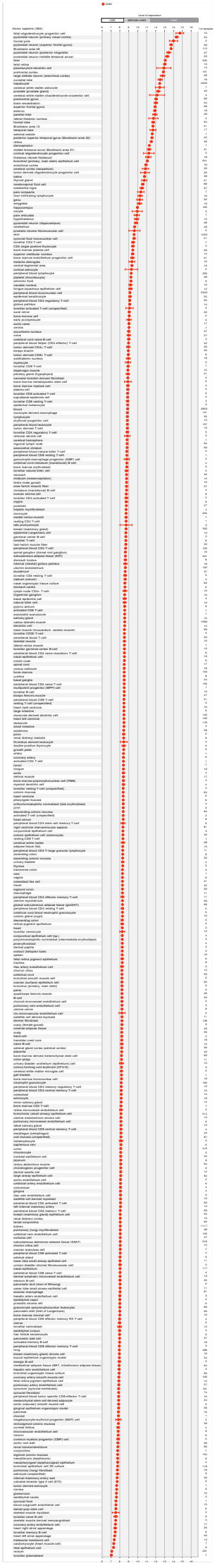

FANT
Level of expression
CAGE
Detected in pCAPs
FANTOM
Homo sapiens (3841)
1 ref samples
retinal pigment epithelium
peripheral blood CD4 resting T cell
T cell
peripheral blood CD4 naive T cell
peripheral blood CD4 stem cell memory T cell
renal tubule/interstitium
lymph node CD4+ T cell
peripheral blood CD4 regulatory regulatory T cell
peripheral blood T cell
CD8 single positive thymocyte
cortical astrocyte
choroid
peripheral blood CD8 restina T cell
adrenal gland
peripheral blood CD8 T cell
peripheral blood CD4 central memory T cell
fetal retina anamnii epithelium
peripheral blood CD4 effector memory regulatory T cell
tumor derived astrocyte
heart right atrial appendage
kidney
right ventricle interventricular septum
peripheral blood CD4 activated T cell
forebrain resting T cell (unspecified)
adrenal gland cortex (adrenal cortex)
heart left atrial appendage
restina T cell (unspecified)
peripheral blood lymphocyte
glutamatergic
resting CD4 T cell
peripheral blood vein endothelium cell
forebrain T cell
peripheral blood CD4 memory T cell
epidermal melanocyte
hymphocyte
left cardiac ventricle
associative striatum
cornea
leukocyte
peripheral blood CD8 naive T cell
lung microvascular
colonic gland (crypt)
peripheral blood CD4 activated T cell
ileal epithelium cell
granulocyte-macrophage progenitor (GMP) cell
monocyte
monocyte derived macrophage
heart left ventricle
peripheral blood leukocyte
megakaryocyte-erythroid progenitor (MEP) cell
lung
gall bladder
bone marrow
peripheral blood cell
peripheral blood CD4 effector memory T cell
substantia nigra
peripheral blood CD8 T cell
prostatic stroma cell
lung microvascular cell
pancreatic duct (duct of Wirsung)
hippocampus
double positive thymocyte
postcentral gyrus
peripheral blood monocyte cell
bone marrow CD8 T cell
mediastinal adipose tissue (MAT, intrathoracic adipose tissue)
thymus
aural nerve
common myeloid progenitor (CMP) cell
prefrontal cortex
lateral rectus muscle
colonic epithelium cell (colonocyte)
caecum (cecum)
bone marrow stromal
tumor derived CD8+ T cell
medial rectus muscle
superior frontal gyrus
late promyelocyte
pancreatic acinar cell
pancreatic islet (islet of Langerhans)
liver
melanocyte
placenta
forebrain CD4 T cell
colon proximal
colorectum
mesenchymal stem cell derived adipocyte
minor salivary gland
synovial fluid mononuclear cell
assembling colon
gluteal subcutaneous adipose tissue (gluSAT)
lung microvessel CD8+ T cell
stomach
peripheral blood CD8 activated T cell
basal ganglia
subcutaneous abdominal adipose tissue (SAAT)
lung adult
corneal limbus
cerebral white matter astrocyte
transverse colon
chorion villus
thyroid gland
Brodmann area 46
renal (kidney) medulla
cerebral white matter
brain (encephalon)
lung microvessel
ascending colonic mucosa
peripheral blood CD8 central memory T cell
bronchial epithelial (airway) epithelium cell
synovial fibroblast
pars compacta
peripheral blood CD4 regulatory T cell
inguinal lymph node
lung CD4+ T cell
large airway epithelium cell
activated T cell (unspecified)
sigmoid colonic mucosa
rectosigmoid colonic mucosa
peripheral blood natural killer T cell
hepatic
frontal pole
descending colon
biceps femoris muscle
lung epithelium
liver nonmalignant lymphocyte
caudate nucleus
bone marrow hematopoietic stem cell
upper lobe small airway epithelial cell
lung alveolus
subcostal alveolar type 2 cell (AT2)
macrophage
lung (pulmonary gland)
frontal lobe
thalamus (dorsal thalamus)
labial salivary gland
bone marrow mononuclear cell
lung lobe
subthalamic nucleus
midbrain (mesencephalon)
conjunctiva
retina
breast (mammary gland) epithelium cell
middle temporal gyrus (Brodmann area 21)
parietal lobe
superior vestibular nucleus
forebrain cerebellum
bronchial (primary) airway epithelial cell
epididymal caput
joints
multipotent enteroblor (MPP) cell
urinary bladder urothelium (epithelium) cell
lung macrophage
alveolar macrophage
ovarian granulosa cell
Brodmann area 10
ventral tegmental area
lung myofibrillas
fibroblast
luminal derived T cell
lung microvascular cell
neural organoid-cortex-tissue culture
diaphragm muscle
bronchial (primary, main stem) epithelium cell
forebrain CD4 restina T cell
hypothalamus
adenoid cell
occipital lobe
vastus lateralis
platelet (thrombocyte)
lung adventitia
colonic mucosa
forebrain CD8 restina T cell
spinal cord
bronchial organchoid tissue culture
bronchial epithelial cell
medulla oblongata
subcutaneous adipose tissue (SAT)
testis
fibroblast derived leukocyte
lung microvessel (dermal dust sensitizer)
amniotic fluid
oral mucosa (unspecified)
lung endothelium
heart atrium
pancreatic islet cell
forebrain activated T cell (unspecified)
saliva
lung alveolar keratinocyte
native tibialis muscle
chondrogenic progenitor cell
biceps brachii
artery
dermal muscle
nasal epithelium cell
head muscle (myocardium, cardiac muscle)
rectus abdominus muscle
quadriceps femoris muscle
lung microvessel cell
dermal lymphatic microvessel endothelium cell
posterior superior temporal gyrus (Brodmann area 22)
ovarian (surface) epithelium cell
neutrophil granulocyte
testis (male gonad)
skin
pituitary gland (hypophysis)
B cell
forebrain CD4 activated T cell
skeletal muscle (heart muscle cell)
embryo
forebrain CD30 T cell
temporal lobe
amygdala
puberem
trigeminal ganglion
peripheral blood tissue
peripheral blood CD8 effector memory RA T cell
chondrocyte
lymph node
dermal papilla cell
lung
heart ventricle
bone marrow plasma cell
cheek
forebrain CD8 regulatory T cell
lung epithelium
umbilical cord naive B cell
epidermal keratinocyte
oligodendrocyte nucleus
esophagus (oesophagus)
bone marrow hematopoietic model
prostate (prostate gland)
bone marrow cell
gingival epithelium organotypic model
seminal vesicle
lung alveolus
dendritic cell
sphenoid
spleen
left internal mammary artery
bronchial epithelium cell 3D culture
forebrain CD8 activated T cell
olecranon
forebrain CD8 T cell
growth plate
forebrain cerebellum
peripheral blood CD8 effector memory T cell
monocyte
nucleus (medial) globus pallidus
neonatal foreskin derived fibroblast
vesicum
cerebral cortex (neopallium)
naive B cell
forebrain CD4 T cell
bone marrow myeloid cell
urinary bladder
fast-twitch muscle fiber
small intestine
lung lobule
tunnel
placenta
lung adenoma cell
granulocyte (polymorphonuclear leukocyte)
pyramidal neuron (hippocampus)
umbilical cord vimentum (transitional) B cell
natural killer cell
lung lobe
conduct (fallopian tube)
uterine endometrium
uterus
monocyte derived dendritic cell
bone marrow stromal cell
umbilical cord
internal mammary artery wall
aortic root wall
cerebral white matter oligodendrocyte progenitor cell
forebrain cerebellum (cerebellar cortex)
adipose tissue (fat)
aortic valve
pyloric antrum
germinal center B cell
lung microvessel
descending colonic mucosa
vimentum (transitional) B cell
nasopharynx (nasopharynx)
coronary artery
meninx (cerebral membrane)
skeletal muscle
eosinophil granulocyte
lung microvessel
umbilical artery endothelium cell
transitional crest zone
polychromatophilic normoblast (intermediate erythroblast)
forearm
lung
bone marrow endothelium progenitor cell
retina microvessel endothelium cell
stomach fundus
colony-forming unit-erythroid (CFU-E)
dendritic cell
vulva
vermis
nasopharyngeal (epipharyngeal) epithelium
pulmonary (lung) myofibroblast
lung
endothelial neuron (posterior circulation)
plasmacytoid dendritic cell
endothelial neuron (primary visual cortex)
breast (mammary gland) stroma cell
lung alveolus
trachea
endothelial neuron (posterior frontal cortex)
cerebral hemisphere
large intestine
lung
urethra
activated CD8 T cell
cervix
endothelium
ovary (female gonad)
bone marrow erythroblast
uterine myometrium
bone marrow derived mesenchymal stem cell
bone marrow derived mesenchymal stem cell
slow-twitch muscle fiber
umbilical vein endothelium cell
forebrain plasmablast
peripheral blood CD4 T cell
uterine endometrium stroma cell
scalp
coronary artery smooth muscle cell
joints
forebrain (primary, main stem)
iliac artery endothelium cell
dental pulp stem cell
prostatic stroma fibromuscular cell
myelocyte
lung
umbilical cord blood neutrophil granulocyte
aortic endothelium cell
peripheral blood CD4 activated cell
forebrain naive B cell
conjunctival epithelium cell (sp.)
pulmonary vein endothelium cell
stomach cardia
lung epithelium
hiv microvascular endothelium cell
anergic B-cell
orthochromatophilic normoblast (late erythroblast)
dermal fibroblast
middle temporal gyrus (middle temporal gyrus)
hepatic artery endothelium cell
synovial fluid
forebrain B-cell
choroid microvessel endothelium cell
bone marrow mesenchymal progenitor cell
bone marrow stromal cell
osteoblast
pulmonary microvessel endothelium cell
fetal oligodendrocyte progenitor cell
skeletal muscle muscle cell
uterine cervix
satellite cell derived myotube
pharyngeal muscle
vagina
lung vein endothelium cell
peripheral blood helper (CD4 effector) T cell
cerebral white matter microglia cell
hepatic vein endothelium cell
colon
skeletal muscle derived mesenglobast
reticular dermis cell
tumor derived oligodendrocyte progenitor cell
lung adventitia
forebrain germinal center B-cell
forebrain memory B-cell
hepatic myofibroblast
metamyelocyte
peripheral blood myoblast
coronary artery endothelium cell
peripheral blood CD4 T helper granular lymphocyte
urinary bladder stromal fibromuscular cell
peripheral blood tumor specific CD8 effector T cell
lung microvessel cell
microvascular endothelium cell
epidermal Langerhans cell
chorion villus cell
activated memory B cell
lung alveolar cell
pulmonary artery endothelium cell
basal cell
bone marrow polymorphonuclear cell (PMN)
blood outgrowth endothelial cell

N) CD8+ T cells

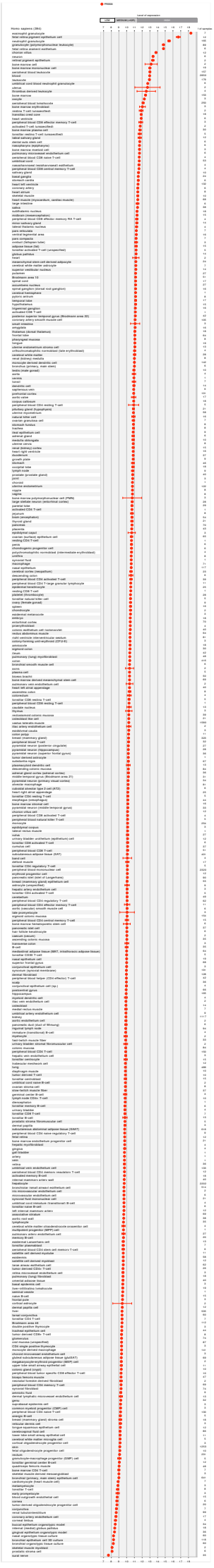
O) B Cells



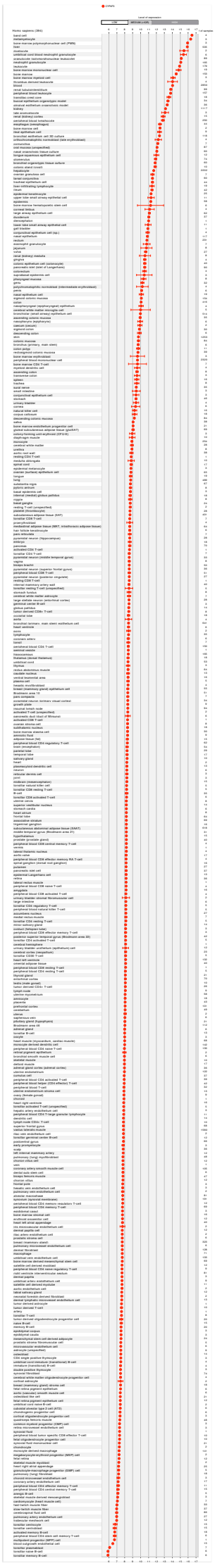
P) Plasmacytoid Dendritic Cells



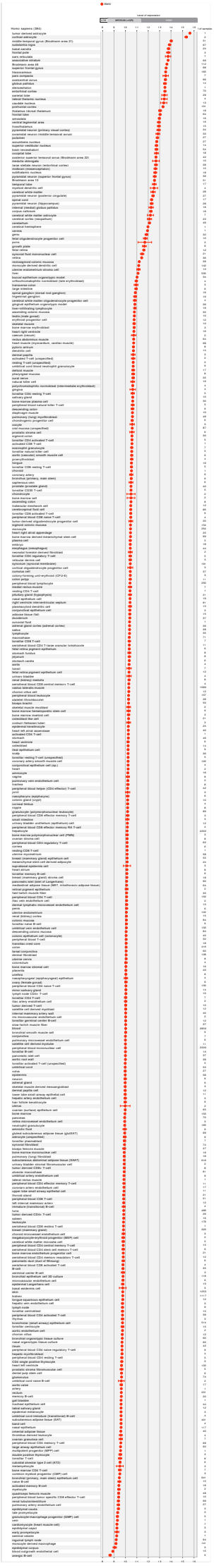
Q) Eosinophils



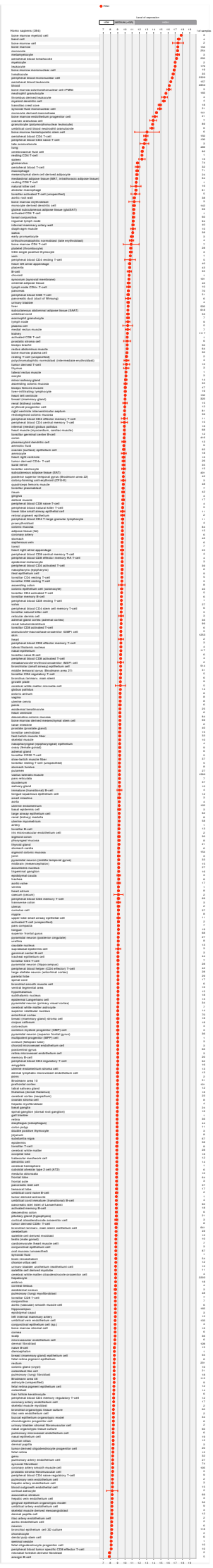
R) Neutrophils



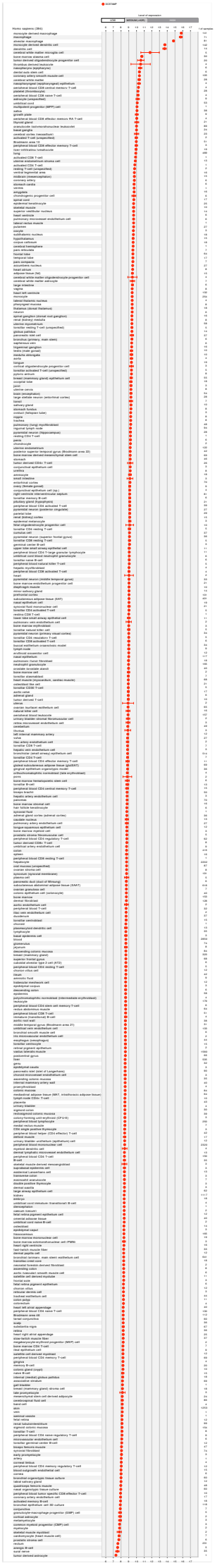
S) Myeloid Dendritic Cells

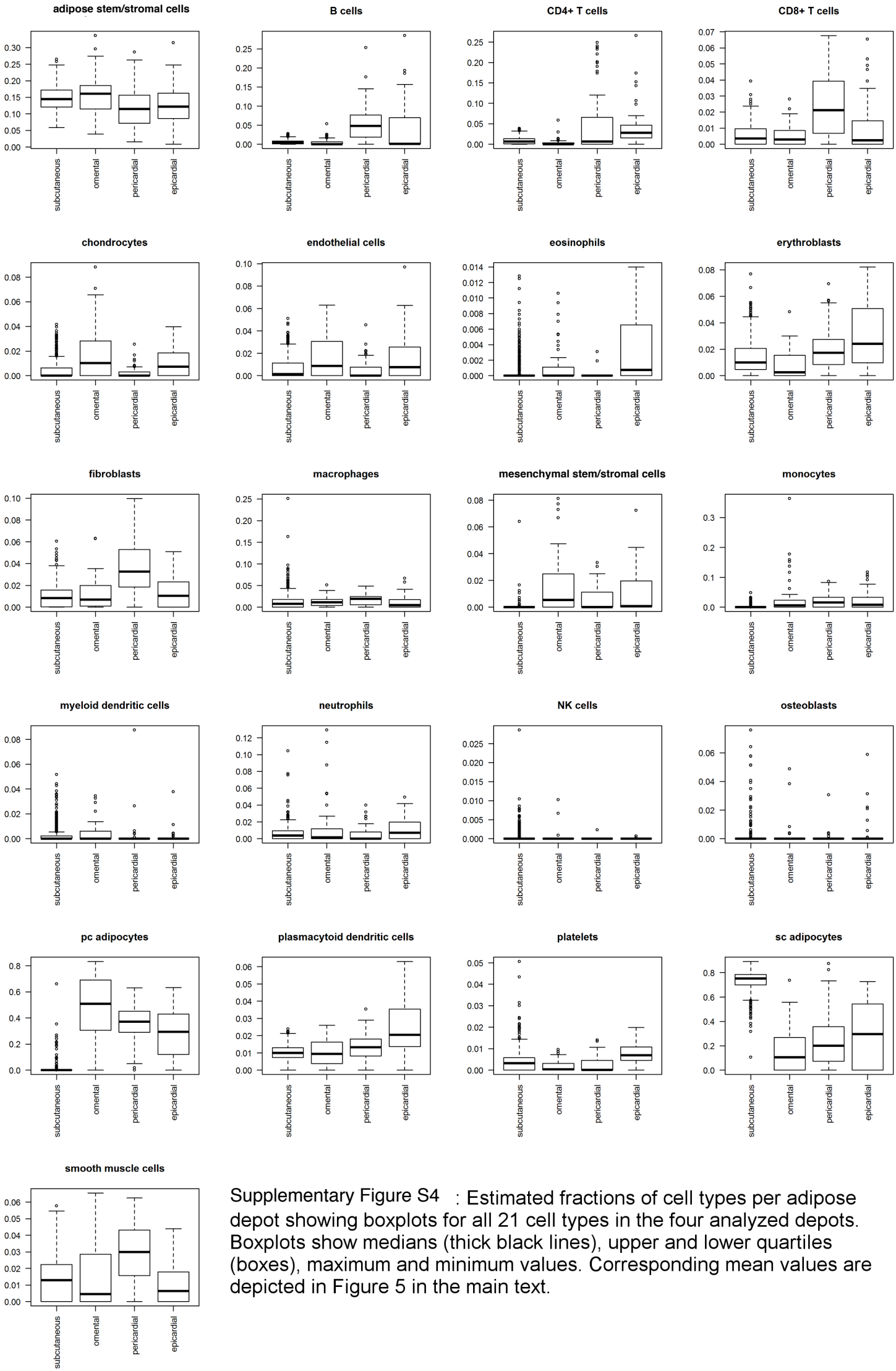


U) Monocytes

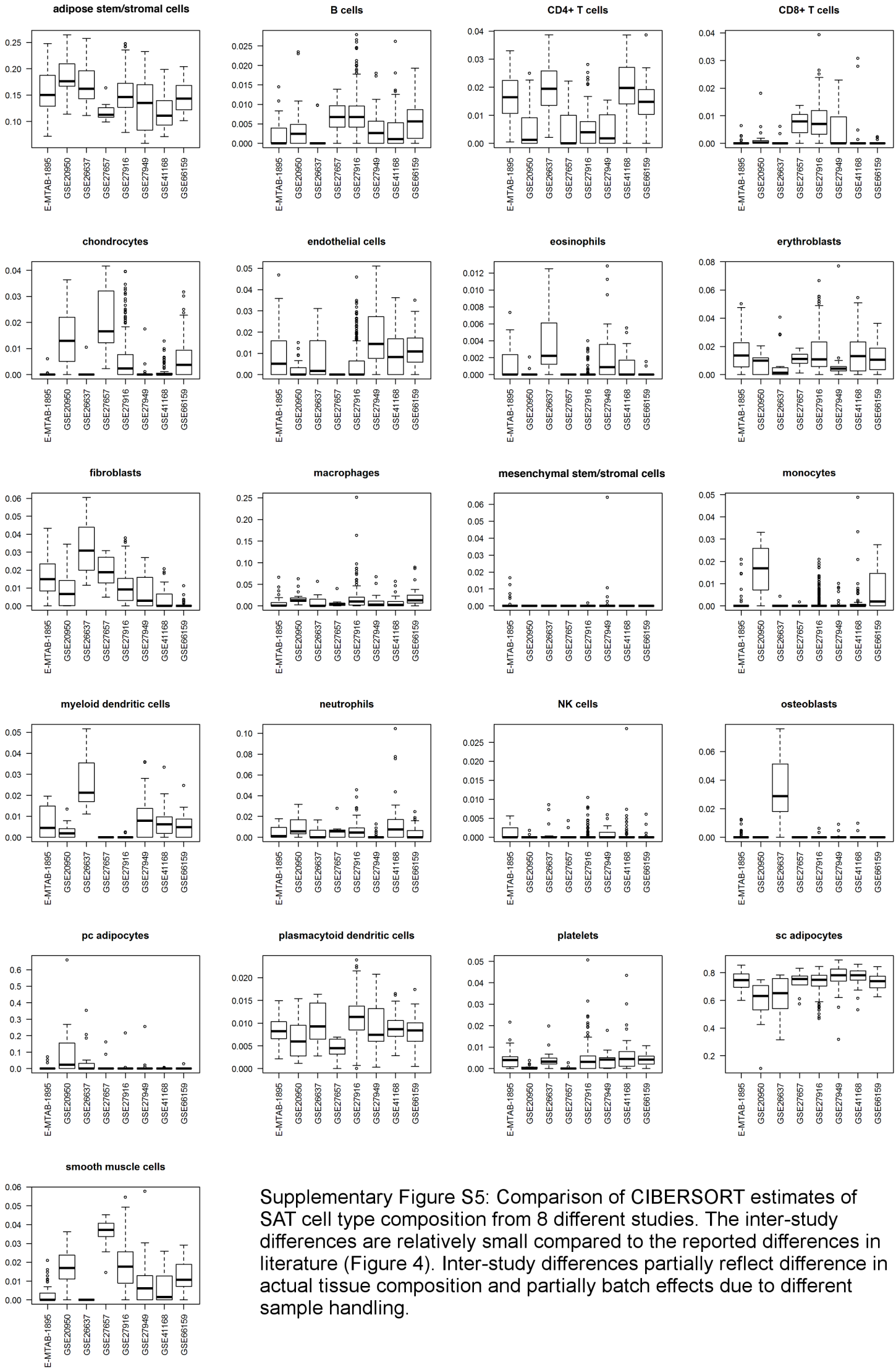

FDA1
Level of expression
Low
Medium
High
Homo sapiens (364)
bone marrow myeloid cell
basal cell
bone marrow cell
bone marrow
monocyte
metamyelocyte
peripheral blood lymphocyte
peripheral blood leukocyte
blood
bone marrow mononuclear cell (FMN)
metamyelocyte
thrombus derived leukocyte
bone marrow cell
interstitial cell
synovial fluid mononuclear cell
monocyte derived macrophage
bone marrow endothelium progenitor cell
basophil
granulocyte (polymorphonuclear leukocyte)
umbilical cord blood neutrophil granulocyte
bone marrow hematopoietic stem cell
peripheral blood CD4 T-cell
peripheral blood CD4 naive T-cell
late erythroblast
lung
bronchoalveolar fluid cell
resting CD4 T-cell
spleen
glomerulus
peripheral blood T-cell
fibroblast
mesenchymal stem cell derived adipocyte
mediastinal adipose tissue (MAT, intrathoracic adipose tissue)
resting CD8 T-cell
natural killer cell
bone marrow macrophage
bonefair activated T-cell (unspecified)
aortic root wall
bone marrow erythroblast
monocyte derived dendritic cell
subcutaneous abdominal adipose tissue (gluSCAT)
activated CD4 T-cell
lateral conjunctiva
inguinal lymph node
internal mammary artery wall
skeletal muscle
saliva
early promyelocyte
bone marrow basophilic normoblast (late erythroblast)
bone marrow CD4 T-cell
platelet (thrombocyte)
CD4 single positive thymocyte
vein
peripheral blood CD4 resting T-cell
heart left atrial appendage
placenta
B-cell
choroid
omental (synovial membrane)
visceral adipose tissue
lymph node CD3+ T-cell
pancreas
peripheral blood CD8 T-cell
Peyer's patch (sum of Wilsung)
urinary bladder
liver
subcutaneous abdominal adipose tissue (SAAT)
umbilical cord
mesenchymal stem cell
lymph node
plasma cell
medial rectus muscle
kidney
effector CD8 T-cell
prostatic stroma cell
triceps brachii
bone marrow plasma cell
resting T-cell (unspecified)
polychromatophilic normoblast (intermediate erythroblast)
tumor derived T-cell
T-cell
lateral rectus muscle
oocyte
minor salivary gland
ascending colonic mucosa
bone marrow stromal cell
liver-infiltrating lymphocyte
heart left ventricle
breast (mammary gland)
renal (kidney) cortex
peripheral blood T-cell
right ventricle interventricular septum
rectosigmoid colonic mucosa
peripheral blood CD4 effector memory T-cell
peripheral blood CD4 central memory T-cell
peripheral blood CD8 T-cell
heart muscle (myocardium, cardiac muscle)
bonefair germinal center B-cell
colon
plasmacytoid dendritic cell
cervix uteri
ovarian (surface) epithelium cell
eosinophil
heart left ventricle
tumor derived CD4+ T-cell
sural nerve
bonefair ventricle
subcutaneous adipose tissue (SAT)
primary visual cortex (striate cortex) (Brodmann area 22)
colony-forming unit-erythroid (CFU-E)
quadriceps femoris muscle
bonefair preendosteal
cecum
thymus
dermal muscle
peripheral blood CD8 naive T-cell
peripheral blood natural killer T-cell
lower lobe small airway epithelial cell
peripheral blood B-cell
peripheral blood CD3-/CD16+ natural killer lymphocyte
proerythroblast
colonic mucosa
adipose tissue (fat)
salivary gland
stomach
saphenous vein
uterus
heart right atrial appendage
peripheral blood CD8 central memory T-cell
peripheral blood CD8 effector memory RA T-cell
epidermal melanocyte
peripheral blood CD4 activated T-cell
nasopharynx (nasopharynx)
ileal epithelium cell
bonefair CD4 resting T-cell
bonefair CD8 resting T-cell
colon mucosa
colonic epithelium cell (sebreplyte)
bonefair CD4 activated T-cell
bonefair memory B-cell
peripheral blood CD8 resting T-cell
T-cell
peripheral blood CD4 stem cell memory T-cell
bonefair natural killer cell
reticular dermis cell
adrenal gland cortex (adrenal cortex)
bonefair CD8 T-cell
bonefair CD8 activated T-cell
exocrine/ductal-mucoadhesive exocervical (CSEF) cell
testis
heart
peripheral blood CD8 effector memory T-cell
lateral thalamic nucleus
nasal epithelium
peripheral blood T-cell
peripheral blood CD8 activated T-cell
mesoadrenocyte-erythroid exocervical (MEEP) cell
bronchiolar (small airway) epithelium cell
middle temporal gyrus (Brodmann area 21)
bonefair CD4 T-cell
bronchus, lobular, main stem)
growth plate
cerebral white matter microglia cell
globus pallidus
duodenum
vagina
uterine cervix
penis
epidermal keratinocyte
cervical canal
mesenchyme colonic mucosa
bone marrow derived mesenchymal stem cell
ileum intestine
prostate (prostate gland)
fast-twitch muscle fiber
skeletal muscle
nasopharynx (oropharyngeal) epithelium
nasal (fossa) gland
adrenal gland
bonefair CD3+ T-cell
slow-twitch muscle fiber
peripheral resting T-cell (unspecified)
stomach fundus
putamen
caudus lateralis muscle
pars reticulata
thyroid gland
salivary gland
immature (transitional) B-cell
tongue squamous epithelium cell
small intestine
ileum
uterine endometrium
basal epidermis cell
large airway epithelium cell
renal (kidney) medulla
lung microvasculature
artery
bonefair B-cell
iris microvascular endothelium cell
sigmoid colon
colon epithelium
thyroid gland
stomach cardia
sigmoid colonic mucosa
ileum
pyramidal neuron (middle temporal gyrus)
midbrain (mesencephalon)
ascusterna nucleus
accessory ganglion
epididymal cauda
trachea
aortic valve
vernix
cervix mucus
caecum (cecum)
peripheral blood CD4 memory T-cell
transverse colon
uterus
prostate cell
nipple
upper lobe small airway epithelial cell
activated T-cell (unspecified)
pars compacta
cerebellum
superior frontal gyrus
pyramidal neuron (posterior cingulate)
urethra
caudate nucleus
bronchial submucosa cell
germinal center B-cell
tracheal epithelium cell
cervix epithelium
pyramidal neuron (hippocampus)
peripheral blood helper (CD4 effector) T-cell
large vestibule neuron (vestibular cortex)
parietal lobe
lung lobe
bronchial smooth muscle cell
ventral tegmental area
hypothalamus
subthalamic nucleus
pyramidal neuron cell
pyramidal neuron (primary visual cortex)
cerebral white matter astrocyte
superior vestibular nucleus
endothelial cortex
exocrine (exocrine gland) stroma cell
corpus callosum
corioretum
common myeloid progenitor (CMP) cell
pyramidal neuron (superior frontal gyrus)
granulocyte-monocyte progenitor (GMP) cell
oviduct (fallopian tube)
choroid microvessel endothelium cell
lung microvasculature
retina microvessel endothelium cell
memory B-cell
peripheral blood CD4 regulatory T-cell
aorta
uterus endometrium stroma cell
dermal lymphatic microvessel endothelium cell
pons
Brodmann area 10
prefrontal cortex
Brodmann area 9
Thalamus (dorsal thalamus)
cerebral cortex (neopallium)
ovarian stroma cell
hepatic myofibroblast
cerebral cortex
spinal ganglion (dorsal root ganglion)
gall bladder
retina
esophagus (oesophagus)
cervix ectocervix
double positive thymocyte
jejunum
substantia nigra
epidermis
bonefair T-cell
cerebral white matter
occipital lobe
cerebellum vermis cell
interstitial cell
cerebral hemisphere
cuboidal alveolar type 2 cell (AT2)
medulla oblongata
lung alveolus
frontal lobe
pancreatic islet cell
temporal lobe
umbilical cord naive B-cell
cerebellum cortex
umbilical cord interstitial (transitional) B-cell
pancreatic islet (islet of Langerhans)
activated memory B-cell
descending colon
T-cell (sum of 4 subplots)
cutical (caudal)ectocuticle exosenticle cell
tumor derived CD8+ T-cell
bronchial (primary, main stem) epithelium cell
cerebellum
bonefair cell derived myoblast
testis (male gonad)
cardiomyocyte (heart muscle cell)
conjunctival epithelium cell
oral mucosa (unspecified)
lung epithelium
brain hemisphere
choroid plexus cell
urothelial (bladder, epithelium (epithelium) cell
epithelial cell derived myoblast
cerebral white matter cell
cerebral white matter cell
hepatocyte
embryo
embryonic bolbus
endothelial cortex
pulmonary (lung) myofibroblast
bonefair CD8 T-cell
conjunctiva
smooth (muscular) smooth muscle cell
hippocampus
epididymal caput
left internal mammary artery
umbilical vein endothelium cell
bonefair CD4 activated T-cell (Th0)
bone marrow stromal cell
cornea
scalp
microvascular endothelium cell
bonefair B-cell
naive B-cell
olfactophalion
bronchial (primary, main stem) epithelium cell
fetal retina pigment epithelium
residuum
colonic gland (crypt)
osteoblast like cell
Brodmann area 39 (fusiform)
Brodmann area 42
astrocyte (unspecified)
fetal retina pigment epithelium cell
osteoblast
peripheral blood basophilocyte
peripheral blood CD4 memory regulatory T-cell
coronary artery endothelium cell
skeletal muscle myotube
bronchial organoid/gen tissue culture
basal epithelium cell
basal epithelium organoid/gen model
chondrogenic progenitor cell
urinary bladder stromal fibromuscular cell
nasal organoid/gen tissue culture
bronchial (primary, main stem) endothelium cell
nasal epithelium cell
choroid villus
dermal papilla
tumor derived oligodendrocyte progenitor cell
basal cell
gland
pulmonary artery endothelium cell
bronchial smooth muscle cell
coronary artery smooth muscle cell
prostatic stroma fibromuscular cell
peripheral blood CD4 naive regulatory T-cell
pulmonary vein endothelium cell
bronchial vein endothelium cell
blood outgrowth endothelial cell
cortical astrocyte
endocervical villiation
hepatic vein endothelium cell
bronchial (primary, main stem) epithelium model
umbilical artery endothelium cell
skeletal muscle derived mesoangioblast
dermal papilla cell
iliac artery endothelium cell
lung epithelium cell
neuron
bronchial epithelium cell 3D culture
chondrocyte
dental pulp stem cell
fibroblast cell
fetal oligodendrocyte progenitor cell
peripheral blood tumor specific CD8 effector T-cell
neonatal foreskin derived fibroblast
anergic B-cell

V) Macrophages

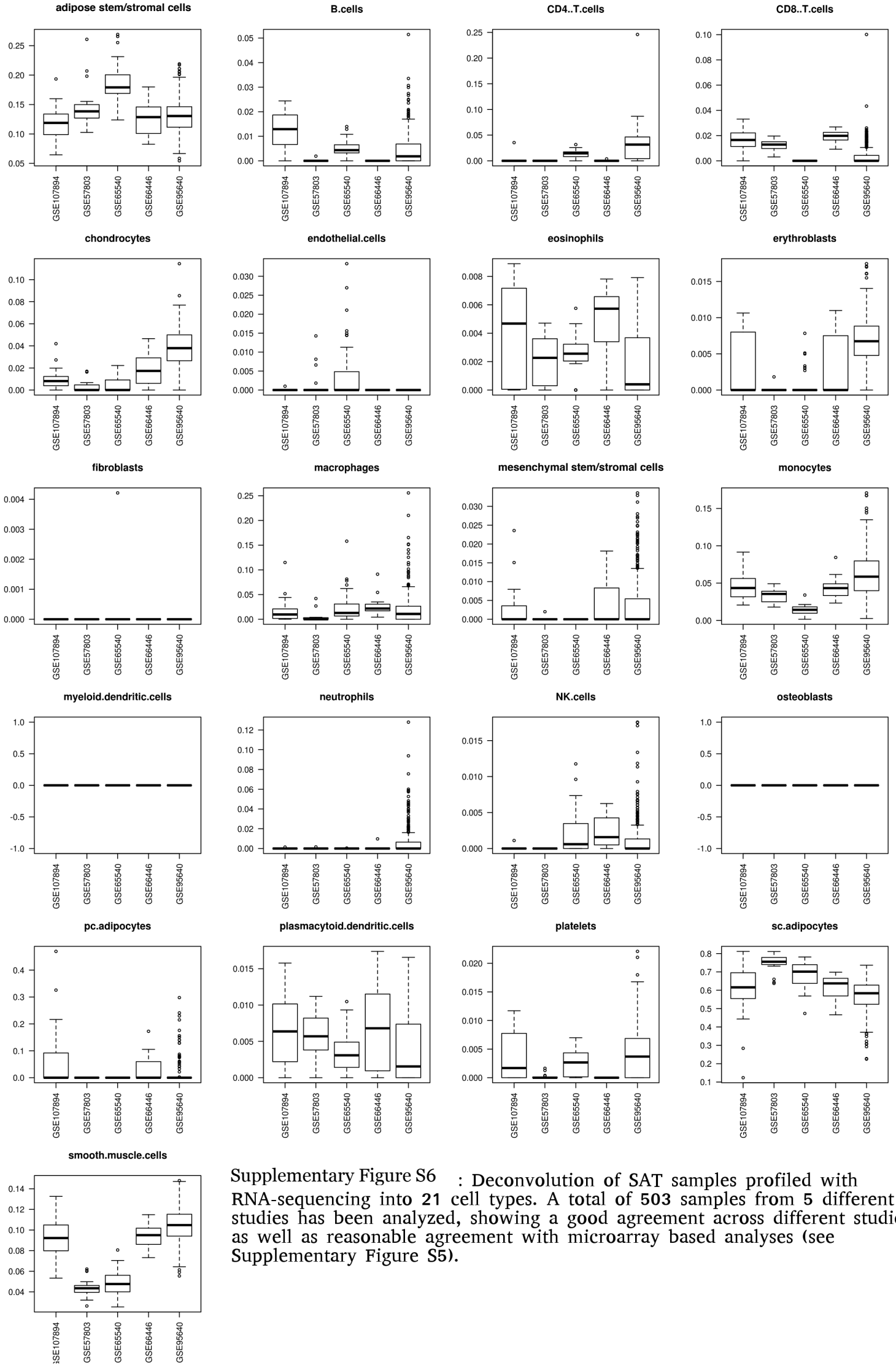




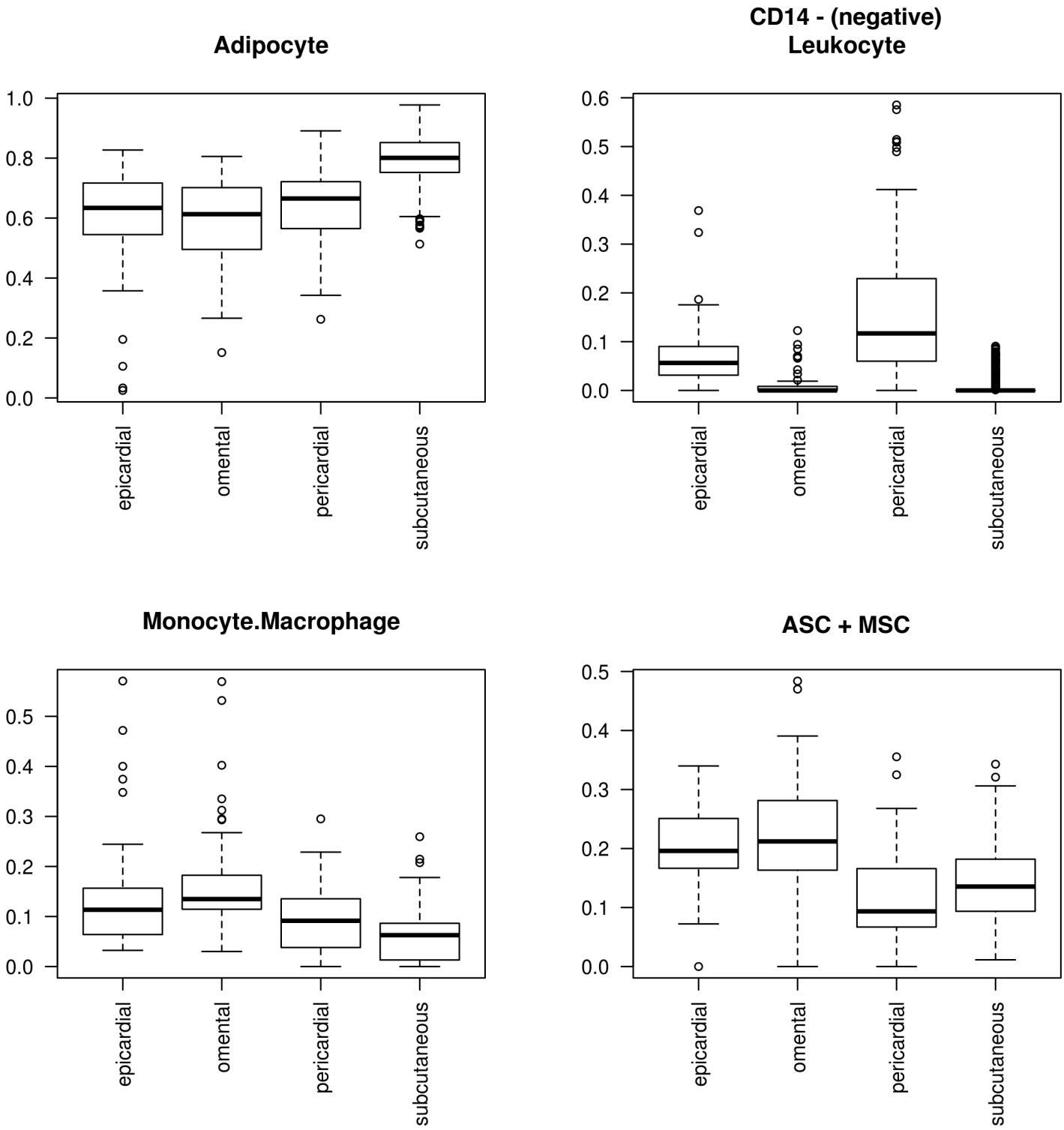
Supplementary Figure S4 : Estimated fractions of cell types per adipose depot showing boxplots for all 21 cell types in the four analyzed depots. Boxplots show medians (thick black lines), upper and lower quartiles (boxes), maximum and minimum values. Corresponding mean values are depicted in Figure 5 in the main text.



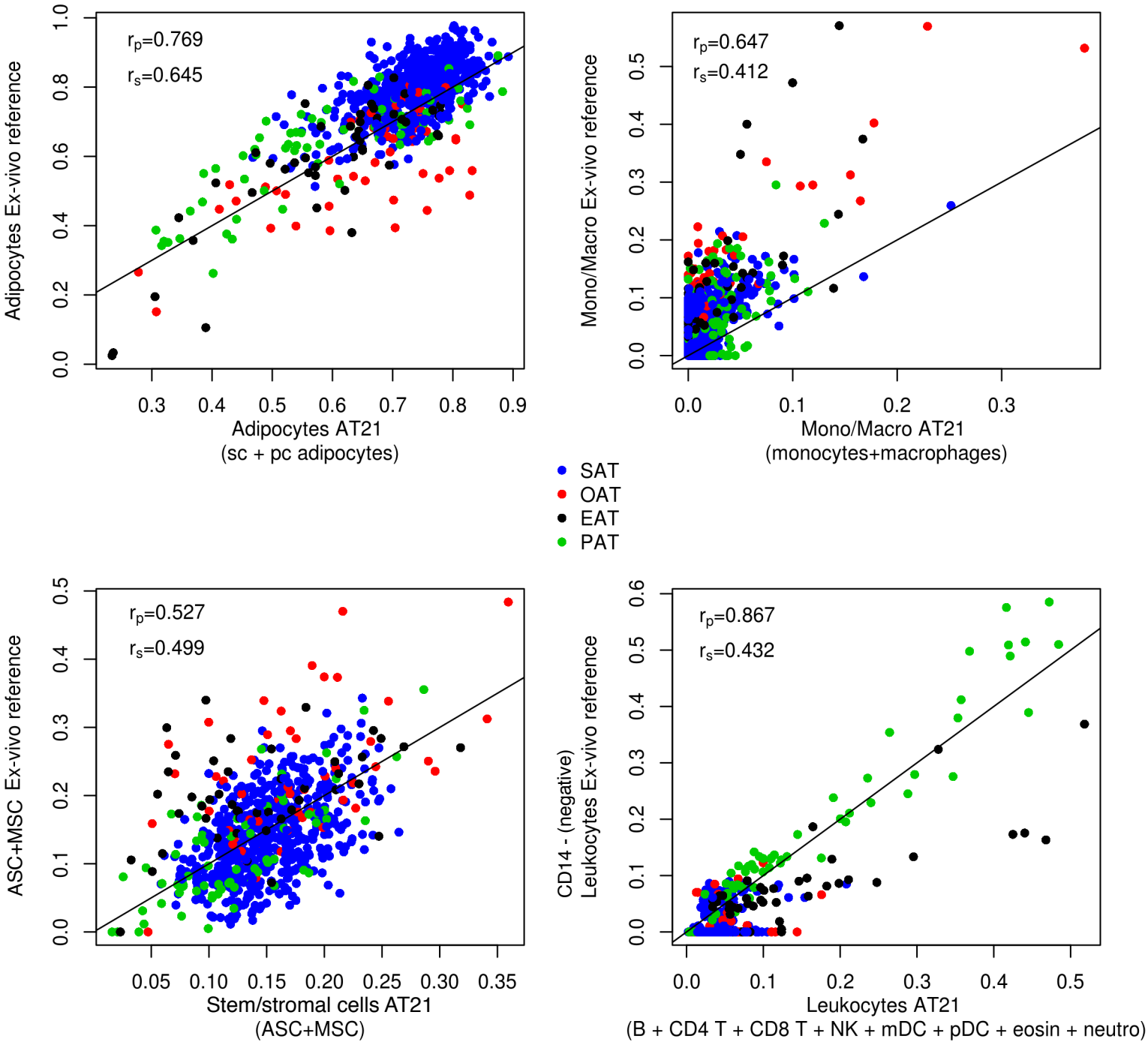
Supplementary Figure S5: Comparison of CIBERSORT estimates of SAT cell type composition from 8 different studies. The inter-study differences are relatively small compared to the reported differences in literature (Figure 4). Inter-study differences partially reflect difference in actual tissue composition and partially batch effects due to different sample handling.



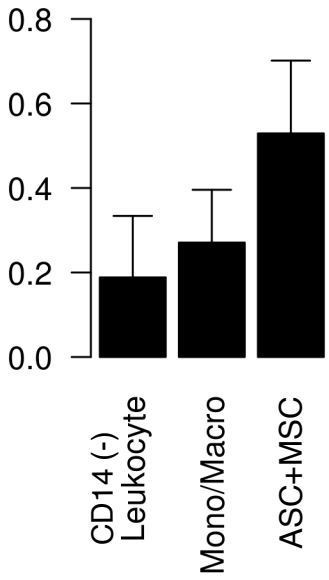
Supplementary Figure S6 : Deconvolution of SAT samples profiled with RNA-sequencing into 21 cell types. A total of 503 samples from 5 different studies has been analyzed, showing a good agreement across different studies as well as reasonable agreement with microarray based analyses (see Supplementary Figure S5).



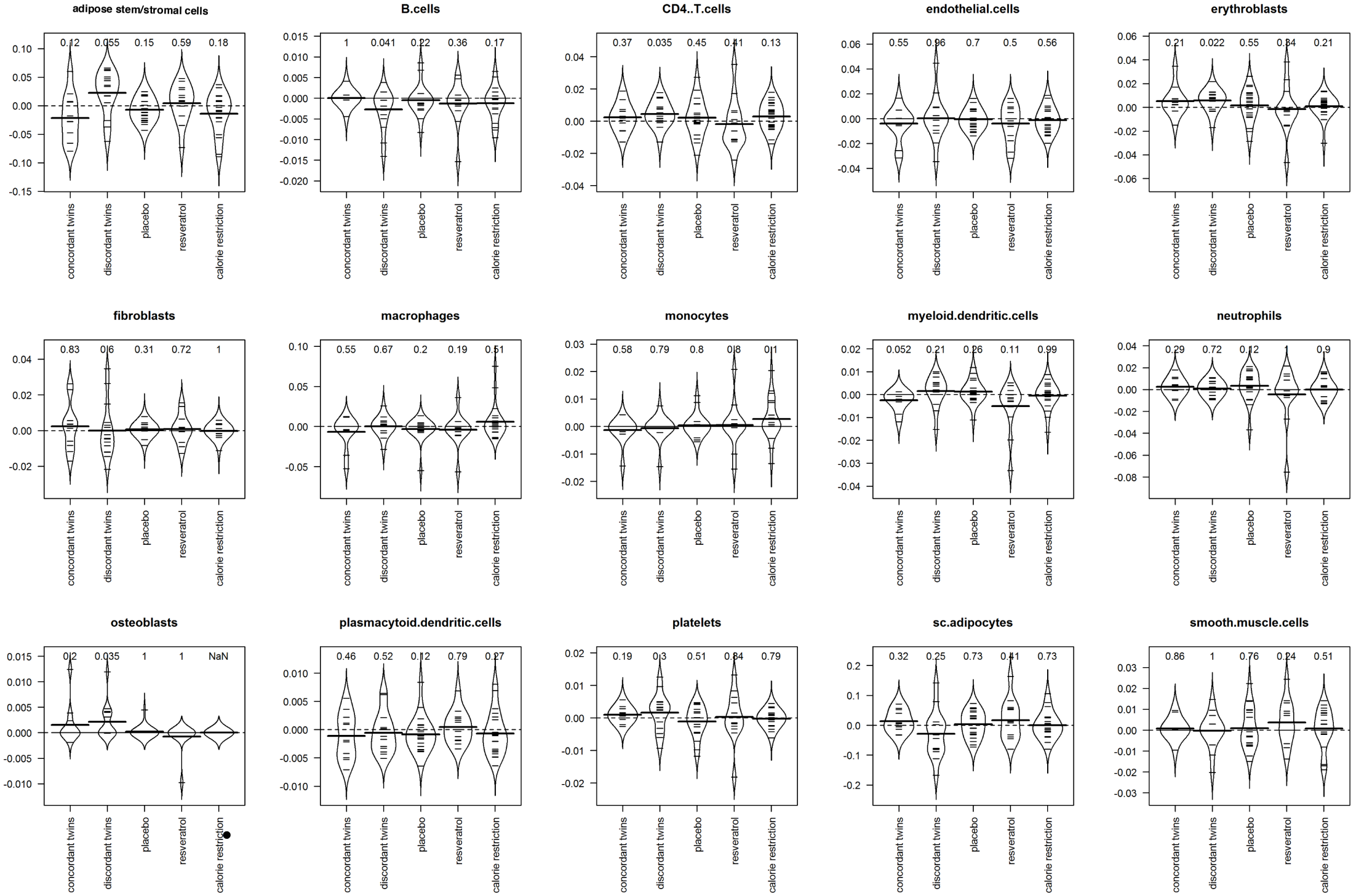
Supplementary Figure S7 : Estimated cell type fractions per adipose depot showing boxplots for the four cell fractions from the ex-vivo reference dataset.



Supplementary Figure S8 : Scatterplot comparing the cell type estimates based on the AT21 signature matrix to the estimates based on the ex-vivo reference dataset for 779 microarray adipose tissue samples from four different adipose tissue depots. For the AT21 estimates, cell fractions have been added up to resemble the less detailed cell fractions represented in the ex-vivo reference dataset.



Supplementary Figure S9 : Barplot of estimated cell fractions (mean and standard deviation) from adipose tissue stromal vascular fraction (SVF) deconvoluted using the ex-vivo reference dataset.



Supplementary Figure S10 : Bean plots showing the population distribution of the cell type percentages for the heavier vs leaner twin, discordant study. The y axis describes differences in estimated cell fractions between the heavier and leaner twin within a pair. P-values are provided above each bean.