

Of the inputted 229 genes, 171 genes exist in the brain cell type expression dataset, 58 genes do not, which are: DCAMKL1,KA21,ATP2B3,C10RF173,STS-1,PTD004,C20ORF100,PTHR2,RBM9,PFTK1,LOC387856,OR2L13,TOMM20,MAP4,NGFRAP1L1,A2BP1,TARBP1,FLJ37440,RPS4Y1,

Some genes either do not have clear homologues in mice, or were not on the array. Those are listed here.

Varying stringencies for enrichment (pSI): 0.01 = large lists, enriched and specific. 0.0001 = shorter lists, more specific to the cell type of interest

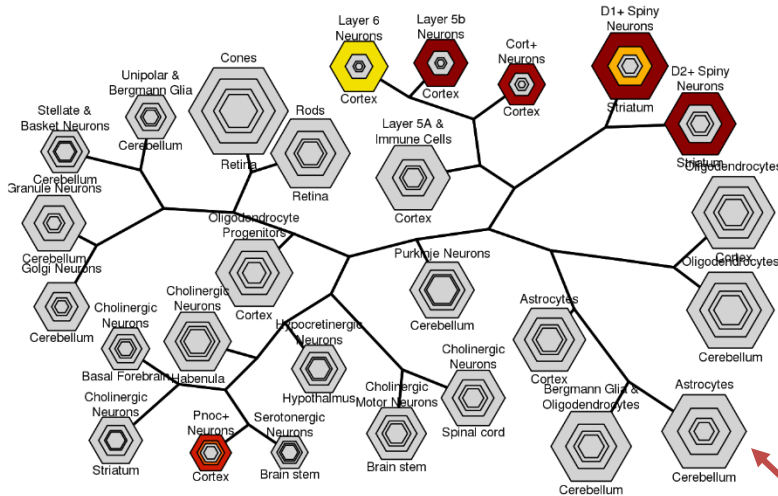
Interpretation of CSEA results table:

The first row lists the pSI thresholds, and the first column lists the brain cell types
 The values in the tables are the Fisher's Exact p-values, followed by the Benjamini-Hochberg (BH) corrected values in parentheses.
 Click the linked p-values to see the overlapped genes for the corresponding brain cell types and thresholds.
 The BH corrected p-values are also illustrated graphically in the figure at the end.

Brain Cell Types and P-Values	0.05	0.01	0.001	0.0001
RetC.Cones	0.944 (1.000)	0.959 (1.000)	0.846 (1.000)	1.000 (1.000)
RetR.Rods	0.889 (1.000)	1.000 (1.000)	1.000 (1.000)	1.000 (1.000)
Hyp	0.092 (0.190)	0.577 (1.000)	0.293 (1.000)	1.000 (1.000)
Hyp.Hcrt	0.014 (0.038)	0.062 (0.243)	0.192 (0.958)	0.112 (1.000)
BF	1.190e-04 (0.001)	0.002 (0.028)	1.000 (1.000)	1.000 (1.000)
BF.Chat	0.047 (0.104)	0.337 (0.694)	1.000 (1.000)	1.000 (1.000)
BS	0.549 (0.724)	1.000 (1.000)	1.000 (1.000)	1.000 (1.000)
BS.Chat	0.002 (0.012)	0.038 (0.175)	1.000 (1.000)	1.000 (1.000)
BS.Slc6a4	0.007 (0.026)	0.169 (0.422)	1.000 (1.000)	1.000 (1.000)
Cb	0.558 (0.724)	0.795 (1.000)	1.000 (1.000)	1.000 (1.000)
Cb.Septin4	0.978 (1.000)	1.000 (1.000)	1.000 (1.000)	1.000 (1.000)
Cb.Pcp2	0.297 (0.433)	0.091 (0.318)	0.754 (1.000)	0.665 (1.000)
Cb.Neurod1	0.288 (0.433)	0.818 (1.000)	1.000 (1.000)	1.000 (1.000)
Cb.Lypd6	0.001 (0.007)	0.040 (0.175)	0.138 (0.957)	0.370 (1.000)
Cb.Grp	0.285 (0.433)	1.000 (1.000)	1.000 (1.000)	1.000 (1.000)
Cb.Grm2	0.022 (0.056)	0.702 (1.000)	1.000 (1.000)	1.000 (1.000)
Cb.Aldh1L1	0.959 (1.000)	0.962 (1.000)	0.690 (1.000)	1.000 (1.000)
Cb.Cnp	1.000 (1.000)	1.000 (1.000)	1.000 (1.000)	1.000 (1.000)
Cpu	0.010 (0.033)	0.155 (0.422)	1.000 (1.000)	1.000 (1.000)
Cpu.D2	0.046 (0.104)	0.316 (0.692)	0.543 (1.000)	0.337 (1.000)
Cpu.D1	1.575e-04 (0.001)	0.004 (0.046)	0.164 (0.957)	1.000 (1.000)
Cpu.Chat	0.201 (0.350)	0.401 (0.780)	0.467 (1.000)	0.345 (1.000)
Ctx	0.003 (0.012)	0.022 (0.126)	1.000 (1.000)	1.000 (1.000)

P-value for Fisher's Exact Test for overlap of cell type and candidate gene list. Parenthesis is Benjamini Hochberg corrected p-value. Hyperlink will take you to list of genes that are overlapping.

Cell types



Varying stringencies for enrichment (pSI): are represented by the size of the hexagons going from least specific lists (outer hexagons) to most specific lists (center). Hexagons scaled to size of gene lists.

Cell types



Graphical Version of the table (Bullseye plot), with B-H P-values plotted by color

The overlapped genes for every cell type (pSI threshold 0.05) are:

RetC.Cones : CRYM, RTN4, STEAP2, CIRBP, PREPL, CACNA2D3
 RetR.Rods : CITED2, STAC2, TOX, RHBDL3
 Hyp : ZCCHC12, SLC17A6, DLX1, ADCYAP1, GPX3, SST
 Hyp.Hcrt : VGF, PCSK1, ZCCHC12, SLC17A6, ENTDP3, NCALD, GPX3, NELL1
 BF : CRH, KIF17, ZCCHC12, GAD2, CRYM, DLX1, PLCXD3, TAC1, SERTAD4, FAM81A, SST

The list of genes overlapping between each cell type, and the candidate gene list, for a given pSI threshold.