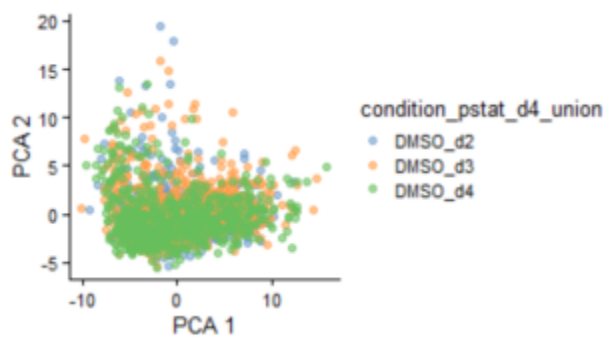


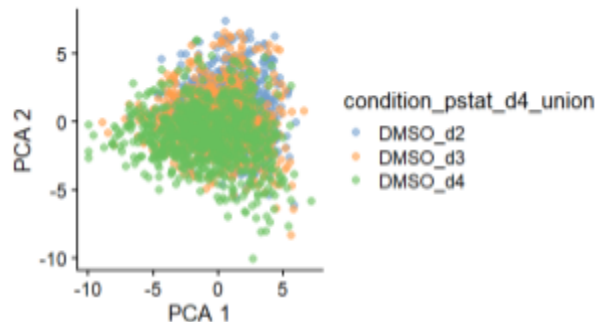
Glioblastoma Report

I used this [Bioconductor tutorial](#) and this [clustering tutorial](#) to learn more about analyzing RNA-seq data.

First, I subset the `sn503.data.scaled.4miner.zscore` and `sn520.data.scaled.4miner.zscore` data to only include the cells treated with DMSO. Because my RStudio wouldn't let me merge the two datasets together (I kept getting a memory allocation error), I analyzed the two datasets separately. I used the elbow method to find the optimal number of PCs, then ran PCA on both "DMSO only" datasets and labeled the cells based on day. I didn't see a large difference between the day 2, day 3, and day 4 cells.



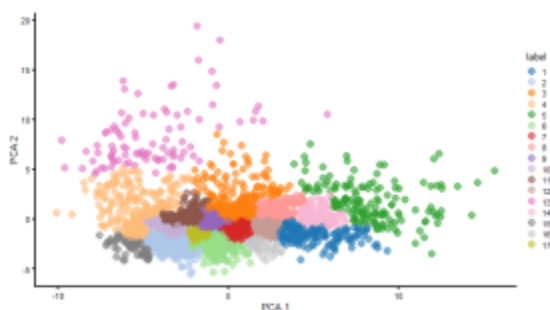
Results from PCA run on the sn503 "DMSO only" data.



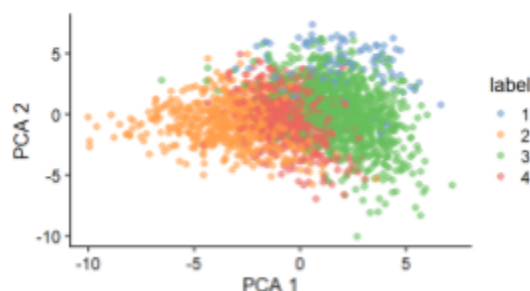
Results from PCA run on sn520 "DMSO only" data

For this reason, I focused on just looking at the sn503 and sn520 DMSO data across all time points rather than breaking up the datasets further into individual days. For future analysis, it might be interesting to look at clustering within each day to see whether the same genes/pathways are highly differentially expressed across all three days.

I then ran graph-based clustering on top of my PCA graph for both the sn503 and sn520 "DMSO only" datasets. I saw much more variation within the sn503 data (as defined by number of clusters) than within the sn520 data, which might speak to the heterogeneity of the non-responder cells.



Graph-based clustering on sn503 "DMSO only" data.



Graph-based clustering on sn520 "DMSO only" data.

I used a k of 10 for the sn503 data and a k of 20 for the sn520 data (a k of 10 for the sn520 data created 6 clusters, but not all of them were well-defined). These " k "s (the number of nearest neighbors) were

determined through an ad hoc, “what makes my clusters the most well-defined without overfitting the data” process, so a future step would be to use mathematical processes to find the optimal k for each dataset. I chose to focus on graph-based clustering, but it might be interesting to run k-means clustering and compare the results to my graph-based clusters, as well as run subclustering to detect subtle variations within major clusters.

I then looked within each cluster to determine the genes that were upregulated in that cluster compared to other clusters (essentially, genes that are highly differentially expressed across clusters). I measured differential expression based on the mean AUC, or area under the curve, which “represents the probability that a randomly chosen observation from our cluster of interest is greater than a randomly chosen observation from the other cluster” (as per the Bioconductor tutorial). A value closer to 1 means the gene is upregulated, and a value closer to 0 means the gene is downregulated. It is also possible to measure up/downregulation by looking at the minimum or median AUC—I chose the mean as it is a middle-of-the-road default for this analysis. I applied a log-fold threshold to reduce the likelihood of seeing genes with large effect sizes but low differential expression across clusters.

Within each cluster, I found the 6 genes that had the greatest mean AUC and plotted their expression against other clusters. In several of the clusters, the genes with the highest mean AUCs had a mean AUC value in the 0.6 - 0.7 range, which doesn’t seem very significant in comparison to mean AUC values from other clusters. A future step might be to analyze clusters with genes with lower mean AUCs to see if there is significant downregulation of genes instead of upregulation.

Finally, per cluster, I ran enrichment analysis on 100 genes with the highest mean AUC. I used Bioconductor’s genome-wide human annotation package to determine the 30 most active pathways within each cluster. sn503 had a diverse array of pathways (e.g. DNA/RNA regulation and repair, ion response, cell differentiation, nervous system regulation), while sn520’s pathways mostly related to the cell cycle/division.

sn503 Data - Summary of Pathways:

- Cluster #1: cardiovascular and ion-related
- Cluster #2: ribosomal activity, RNA transportation, chromatin/nucleosome assembly
- Cluster #3: O-glycan processing, glycosylation
- Cluster #4: neuron differentiation and nervous system development
- Cluster #5: membrane proteins, ion/cation response
- Cluster #6: ribosomal assembly, DNA and RNA regulation
- Cluster #7: myeloid dendritic cells, transmembrane transportation
- Cluster #8: intracellular transportation, metabolic process, muscle contractions
- Cluster #9: DNA repair and regulation, extracellular organization
- Cluster #10: protein localization regulation, regulation of protein catabolic processes
- Cluster #11: lipid biosynthetic processes, Schwann cells
- Cluster #12: cell growth and development, negative regulation of nervous system
- Cluster #13: axonogenesis, axon and nervous system development regulation
- Cluster #14: ion stress response/detoxification
- Cluster #15: ribosomal assembly, endothelial/epithelial cell fate commitment

Cluster #16: import across plasma membrane/blood-brain barrier, D-aspartate import

Cluster #17: myeloid cell differentiation, epithelial cell development

sn520 Data - Summary of Pathways:

Cluster #1: cell division

Cluster #2: neuron/axon regeneration and death, glial cell development, interleukin-1 beta production, ion transport/response

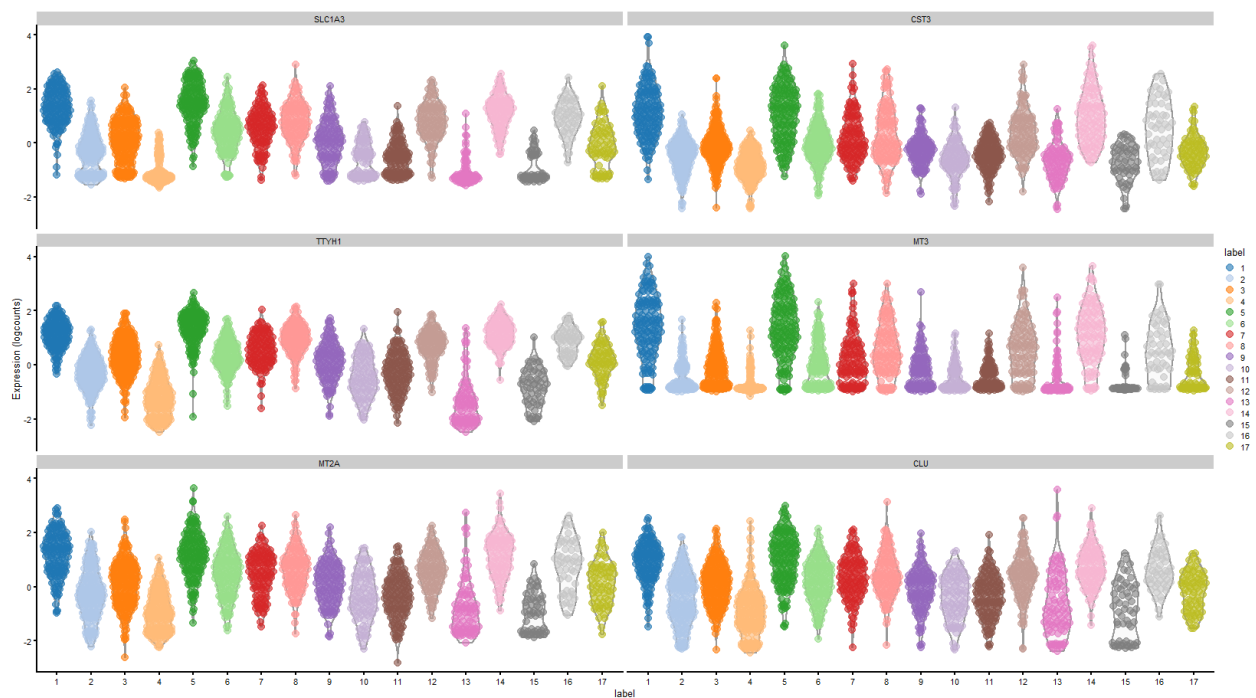
Cluster #3: protein catabolic and biosynthetic processes, telomere maintenance

Cluster #4: histone phosphorylation, cell division

As it doesn't make sense that, post-processing, sn520 would have so many pathways related to cell division, a future step would be to extract relevant genes from each pathway to cross-validate the results, as well as statistically analyze the significance of the pathways determined.

sn503 Data

Cluster #1:

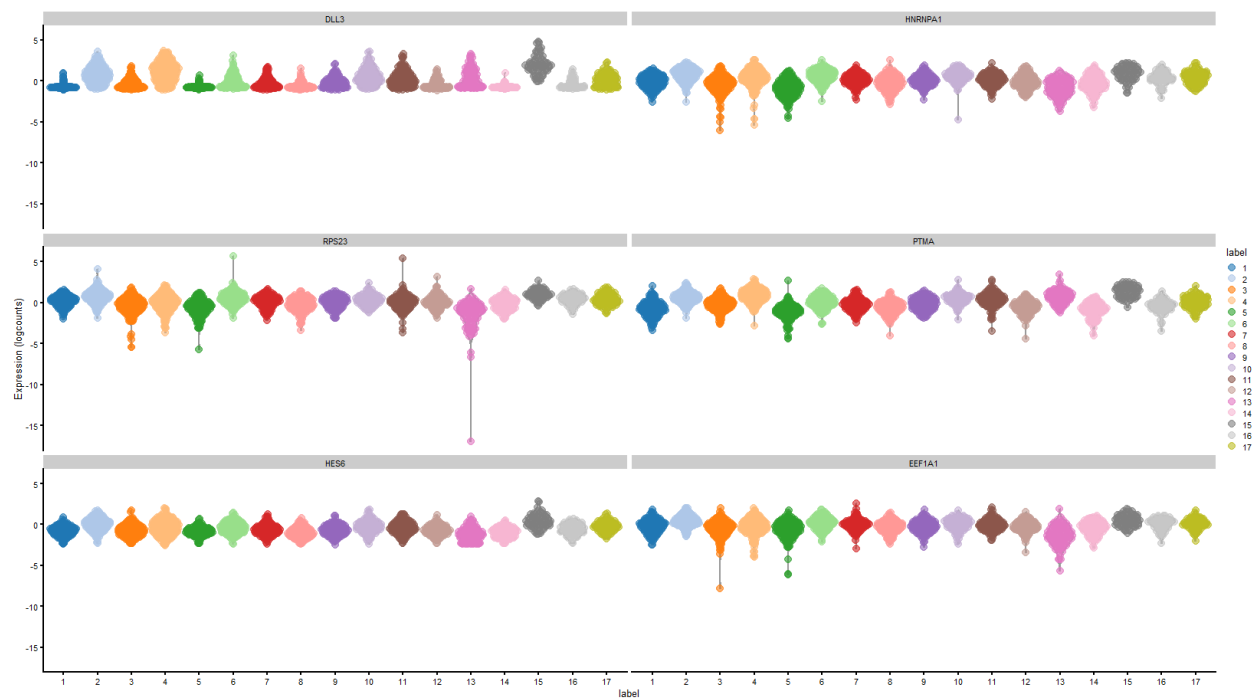


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
SLC1A3	0.830022	0.434640	0.888492	0.993676	1
CST3	0.825005	0.519290	0.886458	0.973316	1
TTYH1	0.803084	0.375579	0.859367	0.995644	1
MT3	0.800223	0.519290	0.842636	0.931111	2
MT2A	0.786176	0.516042	0.823148	0.971650	3

	Term
GO:0006813	potassium ion transport
GO:0001504	neurotransmitter uptake
GO:0010273	detoxification of copper ion
GO:1990169	stress response to copper ion
GO:0036376	sodium ion export across plasma membrane
GO:0071805	potassium ion transmembrane transport
GO:0014031	mesenchymal cell development
GO:0006875	cellular metal ion homeostasis
GO:0003018	vascular process in circulatory system
GO:0001755	neural crest cell migration
GO:0070839	metal ion export
GO:0008016	regulation of heart contraction
GO:0008015	blood circulation

GO:0010721 negative regulation of cell development
GO:0071276 cellular response to cadmium ion
GO:0097501 stress response to metal ion
GO:0061687 detoxification of inorganic compound
GO:0006814 sodium ion transport
GO:0051936 gamma-aminobutyric acid reuptake
GO:0031345 negative regulation of cell projection organization
GO:1903522 regulation of blood circulation
GO:0035725 sodium ion transmembrane transport
GO:0043090 amino acid import
GO:0050768 negative regulation of neurogenesis
GO:0051961 negative regulation of nervous system development
GO:0010977 negative regulation of neuron projection development
GO:0072503 cellular divalent inorganic cation homeostasis
GO:0140115 export across plasma membrane
GO:0060047 heart contraction
GO:0072507 divalent inorganic cation homeostasis

Cluster #2:

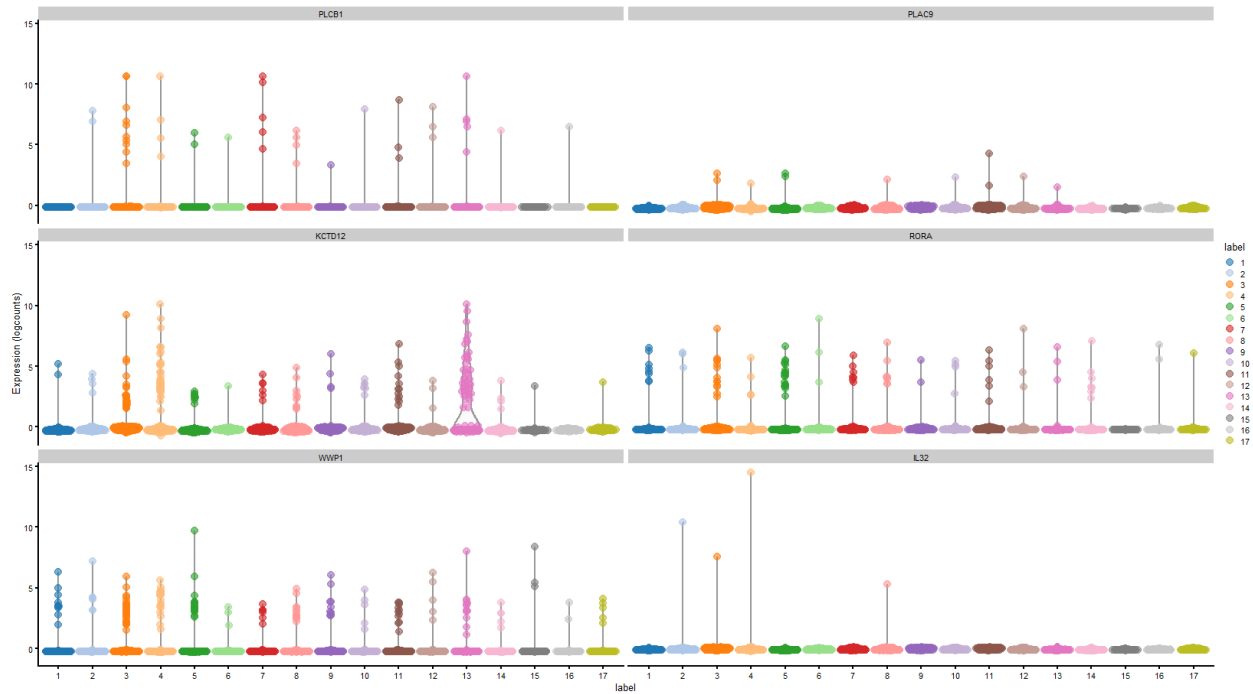


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
DLL3	0.731432	0.219046	0.789028	0.938559	1
HNRNPA1	0.721558	0.446132	0.748681	0.906803	1
RPS23	0.720244	0.392264	0.731637	0.936887	2
PTMA	0.717242	0.238610	0.785089	0.952632	1

HES6 0.714641 0.365642 0.754638 0.854316 4

GO:0002181	cytoplasmic translation
GO:0042273	ribosomal large subunit biogenesis
GO:0042255	ribosome assembly
GO:0000027	ribosomal large subunit assembly
GO:0044387	negative regulation of protein kinase activity by regulation of protein phosphorylation
GO:0022618	ribonucleoprotein complex assembly
GO:0071826	ribonucleoprotein complex subunit organization
GO:2000059	negative regulation of ubiquitin-dependent protein catabolic process
GO:0031497	chromatin assembly
GO:0034728	nucleosome organization
GO:0006334	nucleosome assembly
GO:1903051	negative regulation of proteolysis involved in cellular protein catabolic process
GO:1901796	regulation of signal transduction by p53 class mediator
GO:0006338	chromatin remodeling
GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process
GO:1903363	negative regulation of cellular protein catabolic process
GO:0072331	signal transduction by p53 class mediator
GO:0006403	RNA localization
GO:0050657	nucleic acid transport
GO:0050658	RNA transport
GO:1901799	negative regulation of proteasomal protein catabolic process
GO:0051236	establishment of RNA localization
GO:0045861	negative regulation of proteolysis
GO:0006405	RNA export from nucleus
GO:0045727	positive regulation of translation
GO:0048025	negative regulation of mRNA splicing, via spliceosome
GO:2000271	positive regulation of fibroblast apoptotic process
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage
GO:0035909	aorta morphogenesis
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process

Cluster #3:

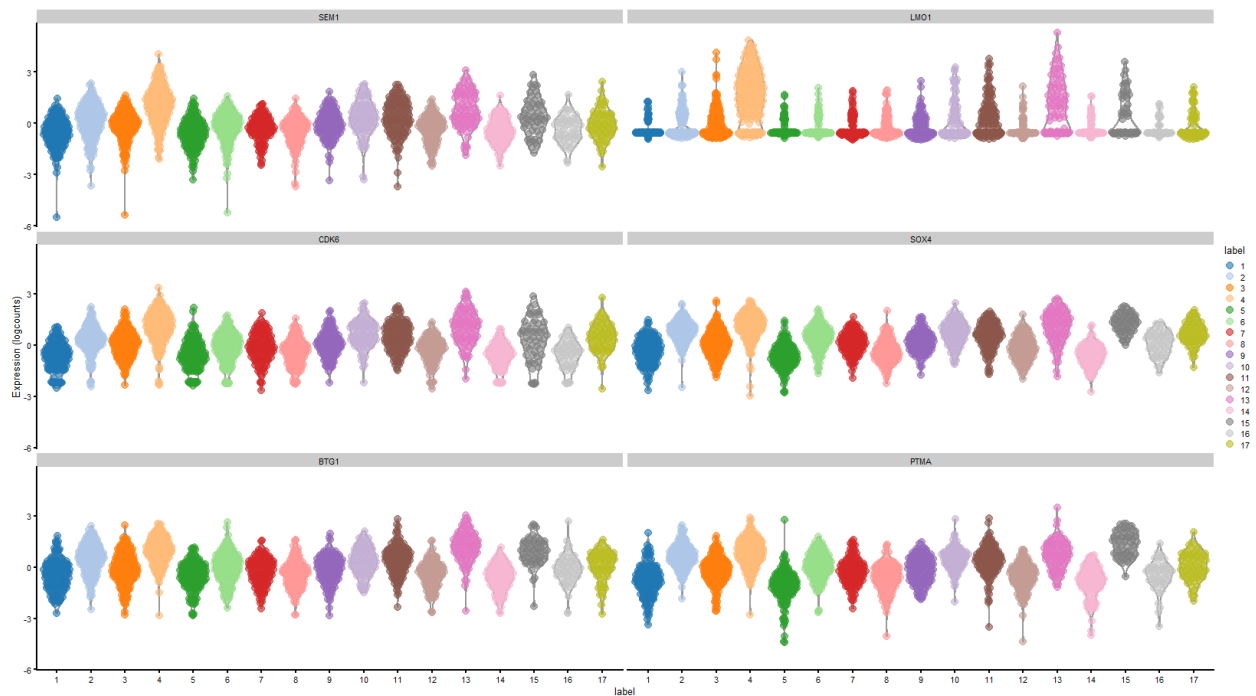


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
PLCB1	0.703992	0.522731	0.687311	0.856994	1
PLAC9	0.698638	0.517861	0.678214	0.844805	3
KCTD12	0.695392	0.484018	0.696032	0.834896	1
RORA	0.693652	0.540837	0.684418	0.858811	19
WWP1	0.692628	0.557161	0.681497	0.836485	9

GO:0016266	O-glycan processing
GO:0018243	protein O-linked glycosylation via threonine
GO:0006493	protein O-linked glycosylation
GO:0010927	cellular component assembly involved in morphogenesis
GO:0110053	regulation of actin filament organization
GO:0045214	sarcomere organization
GO:0046718	viral entry into host cell
GO:0030010	establishment of cell polarity
GO:0009101	glycoprotein biosynthetic process
GO:0044409	entry into host
GO:0010613	positive regulation of cardiac muscle hypertrophy
GO:0014742	positive regulation of muscle hypertrophy
GO:0018242	protein O-linked glycosylation via serine
GO:0031032	actomyosin structure organization
GO:0070252	actin-mediated cell contraction
GO:0032956	regulation of actin cytoskeleton organization
GO:0048675	axon extension

GO:0018210 peptidyl-threonine modification
GO:0030239 myofibril assembly
GO:0055002 striated muscle cell development
GO:0052126 movement in host environment
GO:0032231 regulation of actin filament bundle assembly
GO:0030048 actin filament-based movement
GO:0006486 protein glycosylation
GO:0043413 macromolecule glycosylation
GO:0050901 leukocyte tethering or rolling
GO:0030866 cortical actin cytoskeleton organization
GO:0051496 positive regulation of stress fiber assembly
GO:1903036 positive regulation of response to wounding
GO:0007163 establishment or maintenance of cell polarity

Cluster #4:

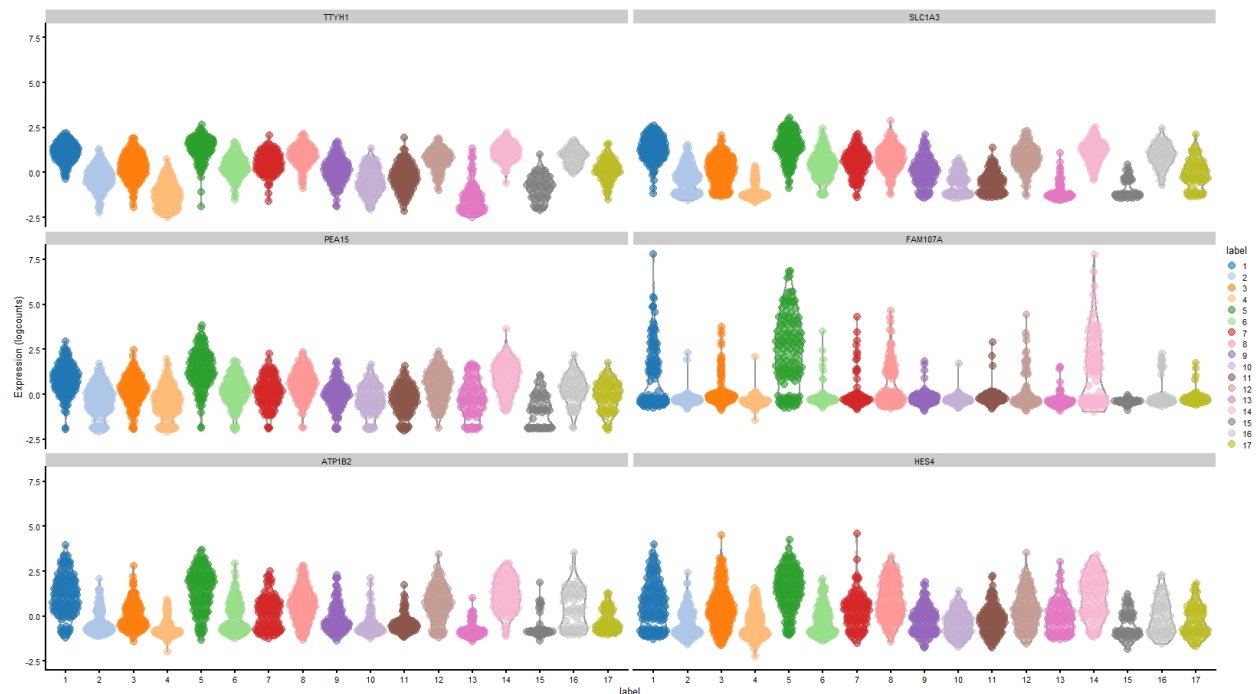


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
SEM1	0.797282	0.581015	0.823507	0.883871	2
LMO1	0.796316	0.586590	0.828544	0.850508	1
CDK6	0.795140	0.520049	0.822004	0.922081	1
SOX4	0.779019	0.452918	0.840591	0.951230	1
BTG1	0.773756	0.405329	0.822297	0.921648	1

GO:0060563 neuroepithelial cell differentiation
GO:0003357 noradrenergic neuron differentiation

GO:0000380	alternative mRNA splicing, via spliceosome
GO:0048485	sympathetic nervous system development
GO:0042421	norepinephrine biosynthetic process
GO:0002065	columnar/cuboidal epithelial cell differentiation
GO:0061351	neural precursor cell proliferation
GO:1902904	negative regulation of supramolecular fiber organization
GO:0048813	dendrite morphogenesis
GO:0010976	positive regulation of neuron projection development
GO:0060411	cardiac septum morphogenesis
GO:0031016	pancreas development
GO:0043392	negative regulation of DNA binding
GO:0042415	norepinephrine metabolic process
GO:1902177	positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway
GO:0002190	cap-independent translational initiation
GO:0060485	mesenchyme development
GO:0045664	regulation of neuron differentiation
GO:0016358	dendrite development
GO:0045666	positive regulation of neuron differentiation
GO:0048483	autonomic nervous system development
GO:0009713	catechol-containing compound biosynthetic process
GO:0042423	catecholamine biosynthetic process
GO:0003211	cardiac ventricle formation
GO:0006338	chromatin remodeling
GO:0000381	regulation of alternative mRNA splicing, via spliceosome
GO:0042063	gliogenesis
GO:0060174	limb bud formation
GO:0048012	hepatocyte growth factor receptor signaling pathway
GO:0003207	cardiac chamber formation

Cluster #5:

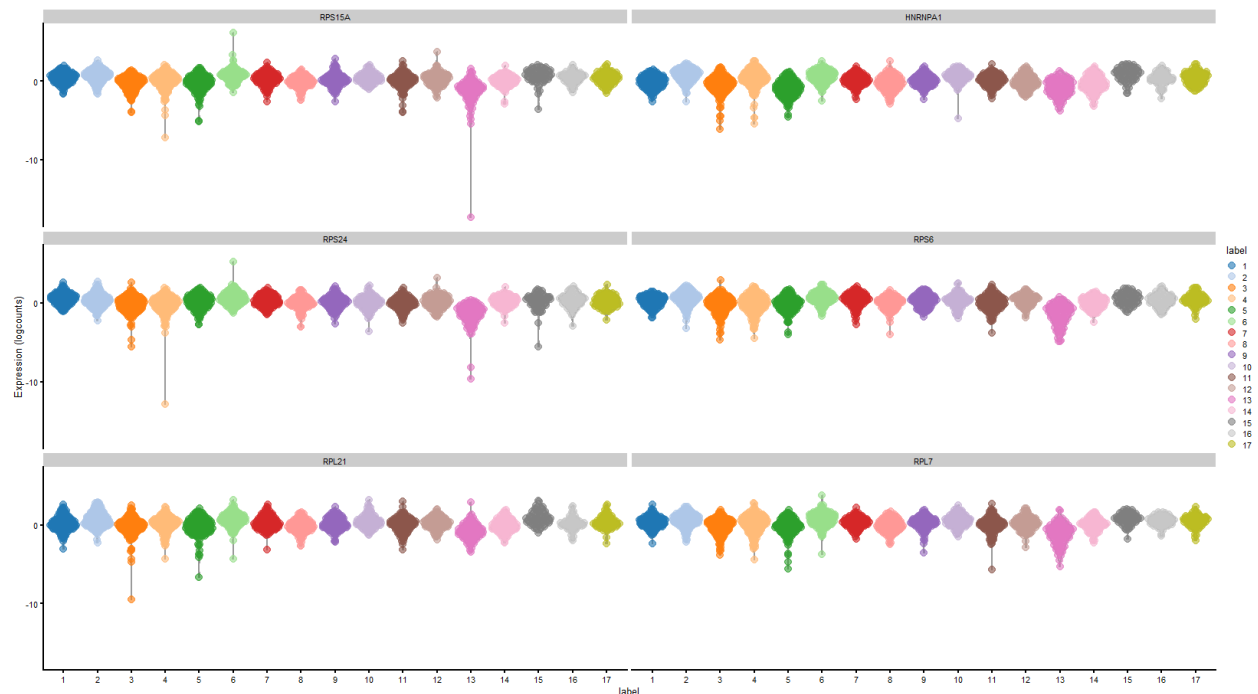


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
TTYH1	0.858133	0.624421	0.893662	0.989950	1
SLC1A3	0.851702	0.565360	0.894453	0.994138	1
PEA15	0.835463	0.629061	0.854252	0.956285	2
FAM107A	0.830300	0.654461	0.847770	0.905339	1
ATP1B2	0.818230	0.578378	0.845412	0.954770	3

GO:0051043	regulation of membrane protein ectodomain proteolysis
GO:0006509	membrane protein ectodomain proteolysis
GO:0006875	cellular metal ion homeostasis
GO:0033619	membrane protein proteolysis
GO:0010977	negative regulation of neuron projection development
GO:0045926	negative regulation of growth
GO:0010951	negative regulation of endopeptidase activity
GO:0010466	negative regulation of peptidase activity
GO:0003018	vascular process in circulatory system
GO:0010038	response to metal ion
GO:0001504	neurotransmitter uptake
GO:0014074	response to purine-containing compound
GO:0031345	negative regulation of cell projection organization
GO:0071248	cellular response to metal ion
GO:0021782	glial cell development
GO:0072503	cellular divalent inorganic cation homeostasis
GO:0072507	divalent inorganic cation homeostasis

GO:0051044	positive regulation of membrane protein ectodomain proteolysis
GO:0010273	detoxification of copper ion
GO:1990169	stress response to copper ion
GO:0051591	response to cAMP
GO:0071805	potassium ion transmembrane transport
GO:0010232	vascular transport
GO:0150104	transport across blood-brain barrier
GO:0003012	muscle system process
GO:0071276	cellular response to cadmium ion
GO:0051592	response to calcium ion
GO:1990000	amyloid fibril formation
GO:0009636	response to toxic substance
GO:0097501	stress response to metal ion

Cluster #6:

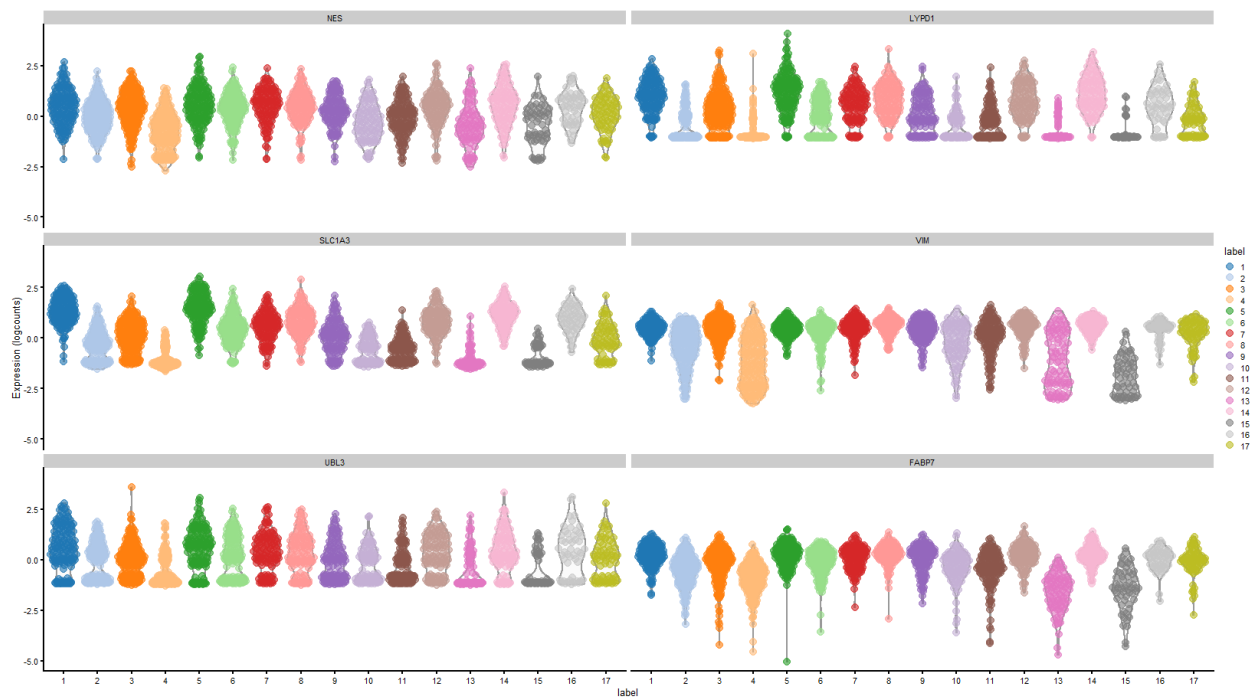


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
RPS15A	0.683957	0.473228	0.684520	0.919717	1
HNRNPA1	0.675387	0.397837	0.702911	0.885714	1
RPS24	0.673582	0.520947	0.652676	0.950575	4
RPS6	0.670931	0.508287	0.658622	0.945024	5
RPL21	0.670850	0.438638	0.670727	0.876503	2

GO:0002181	cytoplasmic translation
GO:0042273	ribosomal large subunit biogenesis
GO:0032071	regulation of endodeoxyribonuclease activity
GO:0032070	regulation of deoxyribonuclease activity
GO:0001570	vasculogenesis
GO:0000027	ribosomal large subunit assembly
GO:0036304	umbilical cord morphogenesis
GO:0061027	umbilical cord development
GO:0051145	smooth muscle cell differentiation
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0042255	ribosome assembly
GO:0036017	response to erythropoietin
GO:0036018	cellular response to erythropoietin
GO:2000820	negative regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation
GO:2000116	regulation of cysteine-type endopeptidase activity
GO:0032069	regulation of nuclease activity

GO:0002262 myeloid cell homeostasis
GO:0060347 heart trabecula formation
GO:0052548 regulation of endopeptidase activity
GO:0043280 positive regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0045664 regulation of neuron differentiation
GO:0035907 dorsal aorta development
GO:0035912 dorsal aorta morphogenesis
GO:0060633 negative regulation of transcription initiation from RNA polymerase II promoter
GO:2000143 negative regulation of DNA-templated transcription, initiation
GO:0052547 regulation of peptidase activity
GO:2001056 positive regulation of cysteine-type endopeptidase activity
GO:0006364 rRNA processing
GO:0060674 placenta blood vessel development
GO:0010043 response to zinc ion

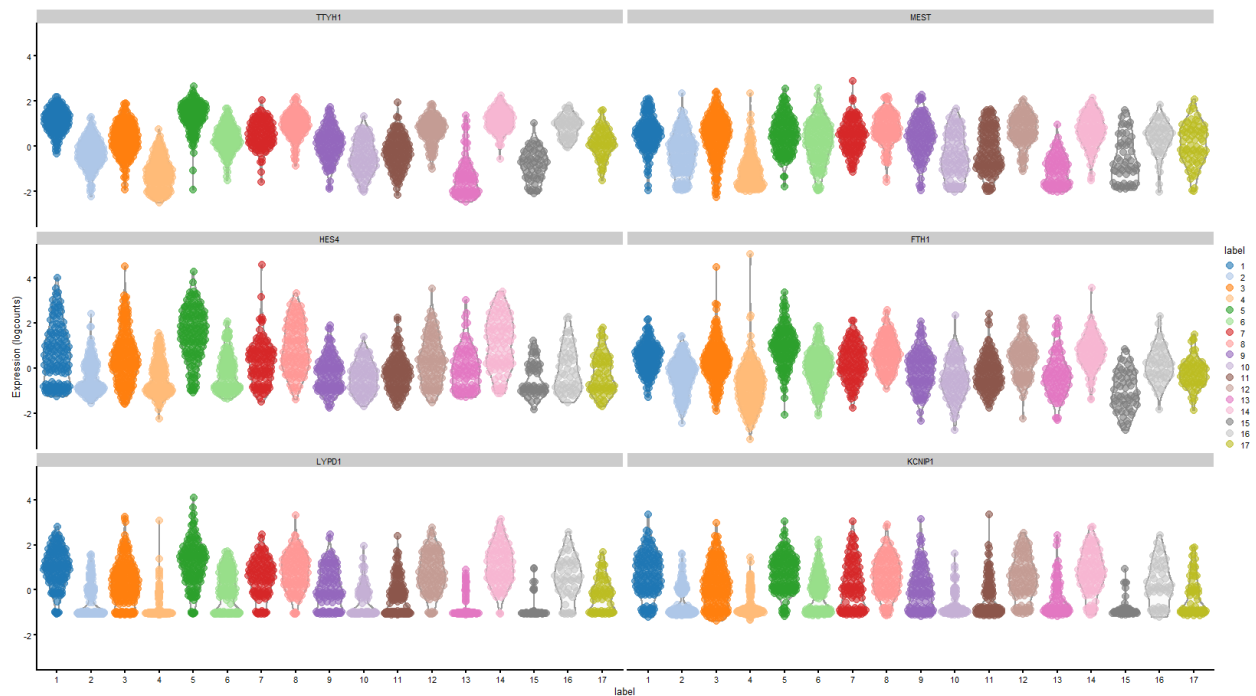
Cluster #7:



	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
NES	0.630178	0.494177	0.584467	0.850219	7
LYPD1	0.625056	0.305114	0.659294	0.893328	1
SLC1A3	0.620087	0.193496	0.682307	0.959311	1
VIM	0.613676	0.407310	0.549594	0.978553	1
UBL3	0.611749	0.461341	0.608127	0.798429	16

GO:0072089	stem cell proliferation
GO:0097089	methyl-branched fatty acid metabolic process
GO:0015871	choline transport
GO:0001768	establishment of T cell polarity
GO:0001767	establishment of lymphocyte polarity
GO:0038166	angiotensin-activated signaling pathway
GO:0043011	myeloid dendritic cell differentiation
GO:0006730	one-carbon metabolic process
GO:0001773	myeloid dendritic cell activation
GO:0051938	L-glutamate import
GO:0098712	L-glutamate import across plasma membrane
GO:1905039	carboxylic acid transmembrane transport
GO:1903825	organic acid transmembrane transport
GO:1902001	fatty acid transmembrane transport
GO:0022010	central nervous system myelination
GO:0032291	axon ensheathment in central nervous system
GO:0097028	dendritic cell differentiation
GO:0070633	transepithelial transport
GO:0055067	monovalent inorganic cation homeostasis
GO:0095500	acetylcholine receptor signaling pathway
GO:0006907	pinocytosis
GO:0048169	regulation of long-term neuronal synaptic plasticity
GO:0051495	positive regulation of cytoskeleton organization
GO:0031579	membrane raft organization
GO:1905144	response to acetylcholine
GO:1905145	cellular response to acetylcholine
GO:0018400	peptidyl-proline hydroxylation to 3-hydroxy-L-proline
GO:0002334	transitional two stage B cell differentiation
GO:0002343	peripheral B cell selection
GO:0002344	B cell affinity maturation

Cluster #8:

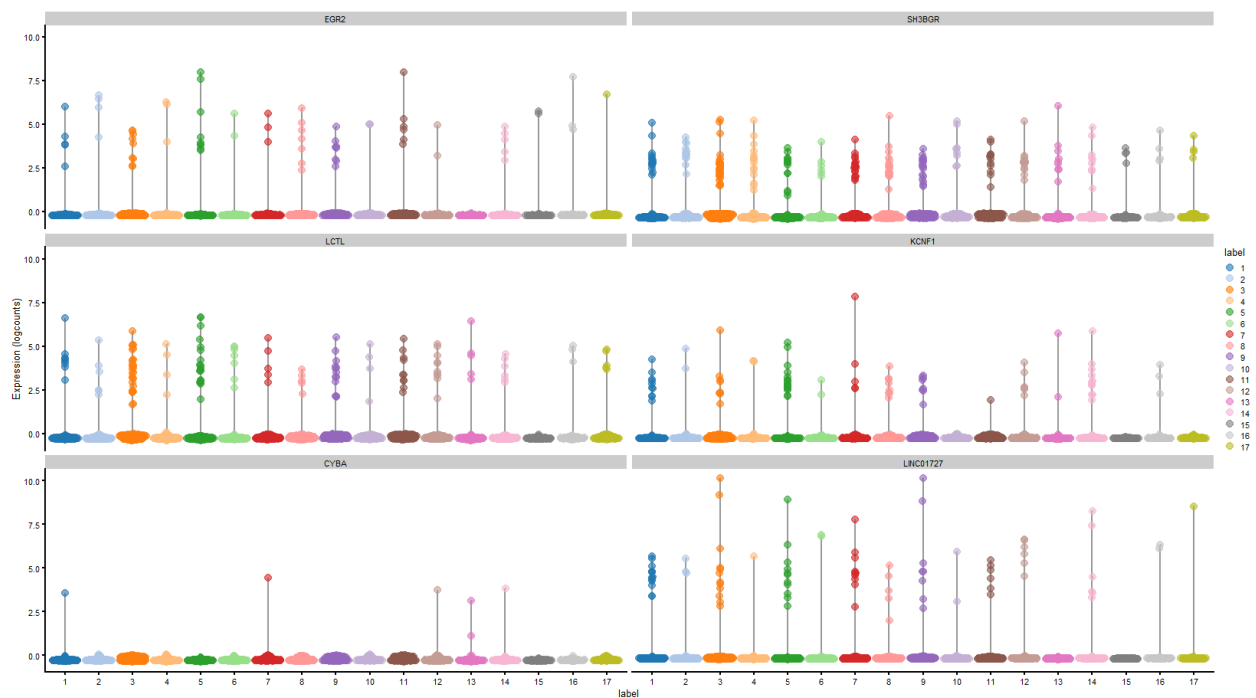


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
TTYH1	0.743074	0.298892	0.802916	0.987962	1
MEST	0.719858	0.526718	0.689184	0.965162	4
HES4	0.711404	0.355873	0.770680	0.850882	1
FTH1	0.707993	0.386210	0.730462	0.925770	3
LYPD1	0.707522	0.385176	0.745921	0.940436	2

GO:0070777	D-aspartate transport
GO:0070779	D-aspartate import across plasma membrane
GO:0042940	D-amino acid transport
GO:0003018	vascular process in circulatory system
GO:0008015	blood circulation
GO:0045785	positive regulation of cell adhesion
GO:0003012	muscle system process
GO:0033631	cell-cell adhesion mediated by integrin
GO:0034238	macrophage fusion
GO:0070633	transepithelial transport
GO:0014829	vascular associated smooth muscle contraction
GO:0008212	mineralocorticoid metabolic process
GO:0032341	aldosterone metabolic process
GO:0001504	neurotransmitter uptake
GO:0022409	positive regulation of cell-cell adhesion
GO:0048588	developmental cell growth

GO:0008016 regulation of heart contraction
GO:0007422 peripheral nervous system development
GO:0042060 wound healing
GO:0055078 sodium ion homeostasis
GO:0006939 smooth muscle contraction
GO:0071314 cellular response to cocaine
GO:0014908 myotube differentiation involved in skeletal muscle regeneration
GO:0015740 C4-dicarboxylate transport
GO:0043410 positive regulation of MAPK cascade
GO:1990138 neuron projection extension
GO:0044057 regulation of system process
GO:0040013 negative regulation of locomotion
GO:0001755 neural crest cell migration
GO:0089718 amino acid import across plasma membrane

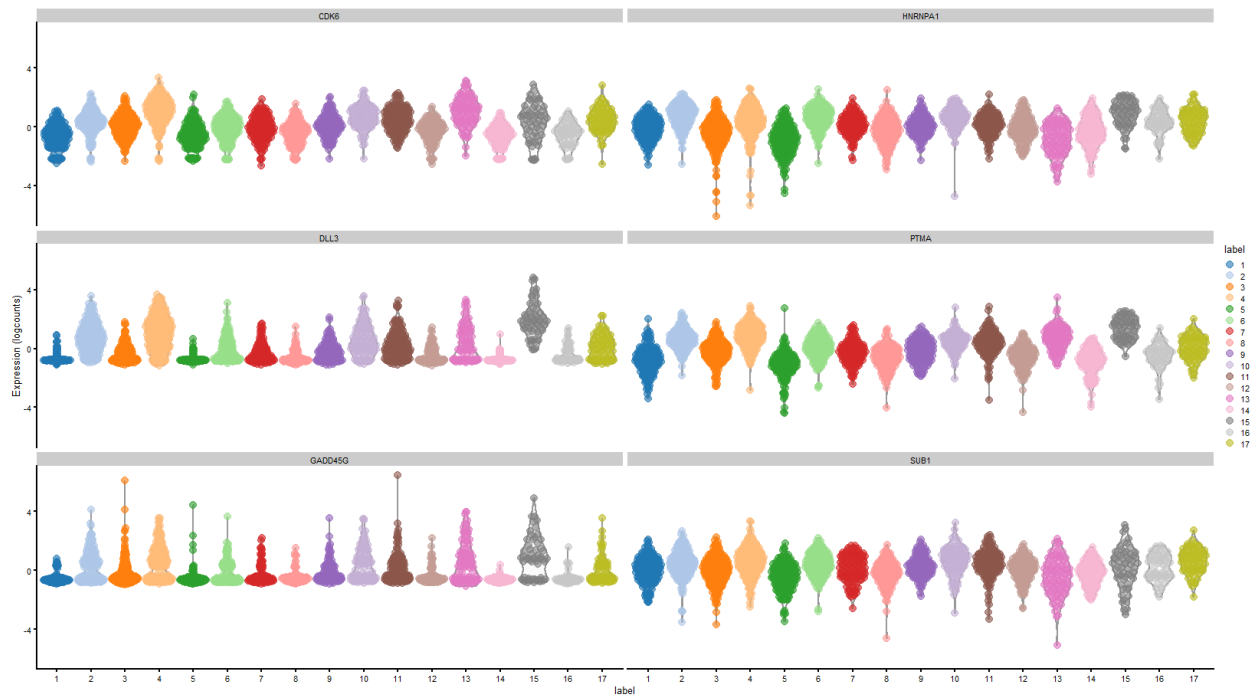
Cluster #9:



	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
EGR2	0.666933	0.493447	0.674670	0.809617	5
SH3BGR	0.665334	0.521759	0.680322	0.765379	3
LCTL	0.659183	0.508369	0.682440	0.778345	6
KCNF1	0.658900	0.537305	0.654360	0.807448	17
CYBA	0.657600	0.494809	0.657759	0.786426	18

GO:2001033	negative regulation of double-strand break repair via nonhomologous end joining
GO:1902510	regulation of apoptotic DNA fragmentation
GO:1903624	regulation of DNA catabolic process
GO:0030010	establishment of cell polarity
GO:0030198	extracellular matrix organization
GO:0043062	extracellular structure organization
GO:0045229	external encapsulating structure organization
GO:0030574	collagen catabolic process
GO:0006309	apoptotic DNA fragmentation
GO:0010667	negative regulation of cardiac muscle cell apoptotic process
GO:0007492	endoderm development
GO:0010664	negative regulation of striated muscle cell apoptotic process
GO:0009620	response to fungus
GO:0031589	cell-substrate adhesion
GO:0061847	response to cholecystokinin
GO:0032076	negative regulation of deoxyribonuclease activity
GO:1902511	negative regulation of apoptotic DNA fragmentation
GO:1903625	negative regulation of DNA catabolic process
GO:0003412	establishment of epithelial cell apical/basal polarity involved in camera-type eye morphogenesis
GO:0036255	response to methylamine
GO:1903442	response to lipoic acid
GO:0061408	positive regulation of transcription from RNA polymerase II promoter in response to heat stress
GO:1904842	response to nitroglycerin
GO:1904843	cellular response to nitroglycerin
GO:1990911	response to psychosocial stress
GO:0060346	bone trabecula formation
GO:0071660	positive regulation of IP-10 production
GO:1900130	regulation of lipid binding
GO:1900131	negative regulation of lipid binding
GO:0006530	asparagine catabolic process

Cluster #10:

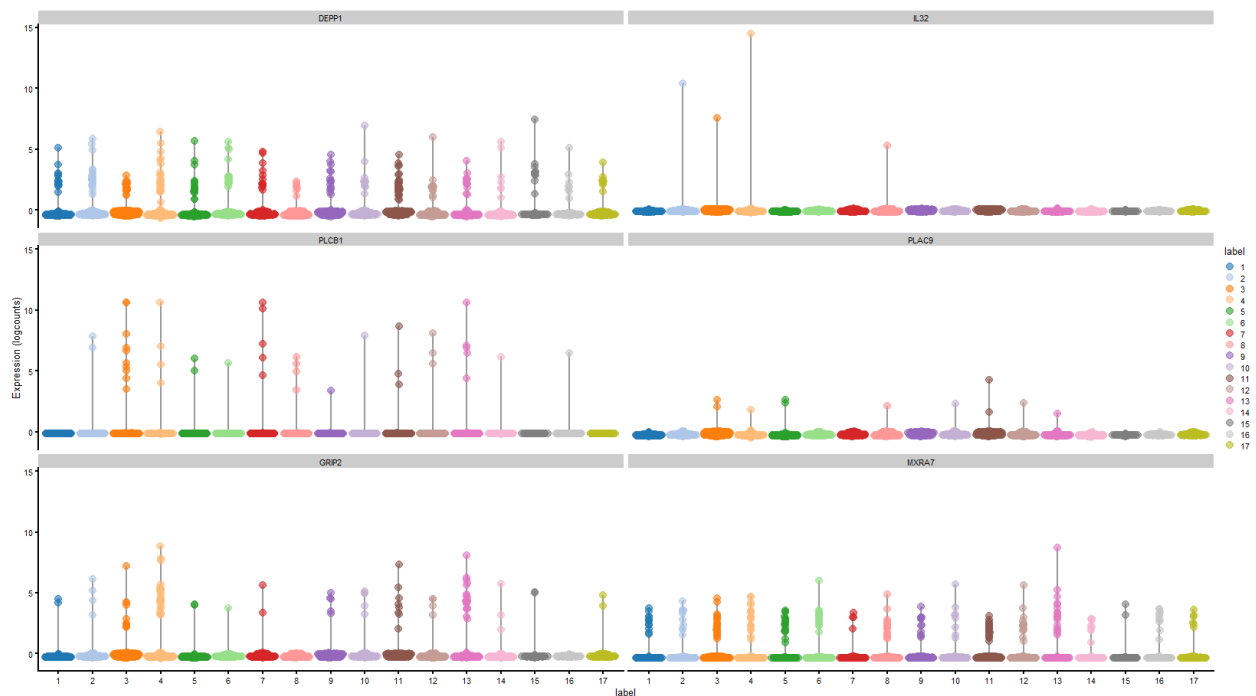


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
CDK6	0.695664	0.345571	0.732048	0.888798	1
HNRNPA1	0.675051	0.385754	0.705970	0.889084	1
DLL3	0.669140	0.179902	0.728440	0.889801	3
PTMA	0.668929	0.184605	0.738354	0.935875	1
GADD45G	0.655516	0.419192	0.665857	0.815538	3

GO:0045793	positive regulation of cell size
GO:1904816	positive regulation of protein localization to chromosome, telomeric region
GO:1904814	regulation of protein localization to chromosome, telomeric region
GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process
GO:2000573	positive regulation of DNA biosynthetic process
GO:1901799	negative regulation of proteasomal protein catabolic process
GO:2000059	negative regulation of ubiquitin-dependent protein catabolic process
GO:0000723	telomere maintenance
GO:2001252	positive regulation of chromosome organization
GO:0032200	telomere organization
GO:0032206	positive regulation of telomere maintenance
GO:1903051	negative regulation of proteolysis involved in cellular protein catabolic process
GO:0044387	negative regulation of protein kinase activity by regulation of protein phosphorylation
GO:0006403	RNA localization
GO:2000278	regulation of DNA biosynthetic process
GO:0007130	synaptonemal complex assembly

GO:0048368 lateral mesoderm development
GO:0003231 cardiac ventricle development
GO:0070198 protein localization to chromosome, telomeric region
GO:1903363 negative regulation of cellular protein catabolic process
GO:0003279 cardiac septum development
GO:0044417 translocation of molecules into host
GO:0006278 RNA-templated DNA biosynthetic process
GO:0007004 telomere maintenance via telomerase
GO:1900182 positive regulation of protein localization to nucleus
GO:0060485 mesenchyme development
GO:0070193 synaptonemal complex organization
GO:0035329 hippo signaling
GO:0032212 positive regulation of telomere maintenance via telomerase
GO:0010833 telomere maintenance via telomere lengthening

Cluster #11:

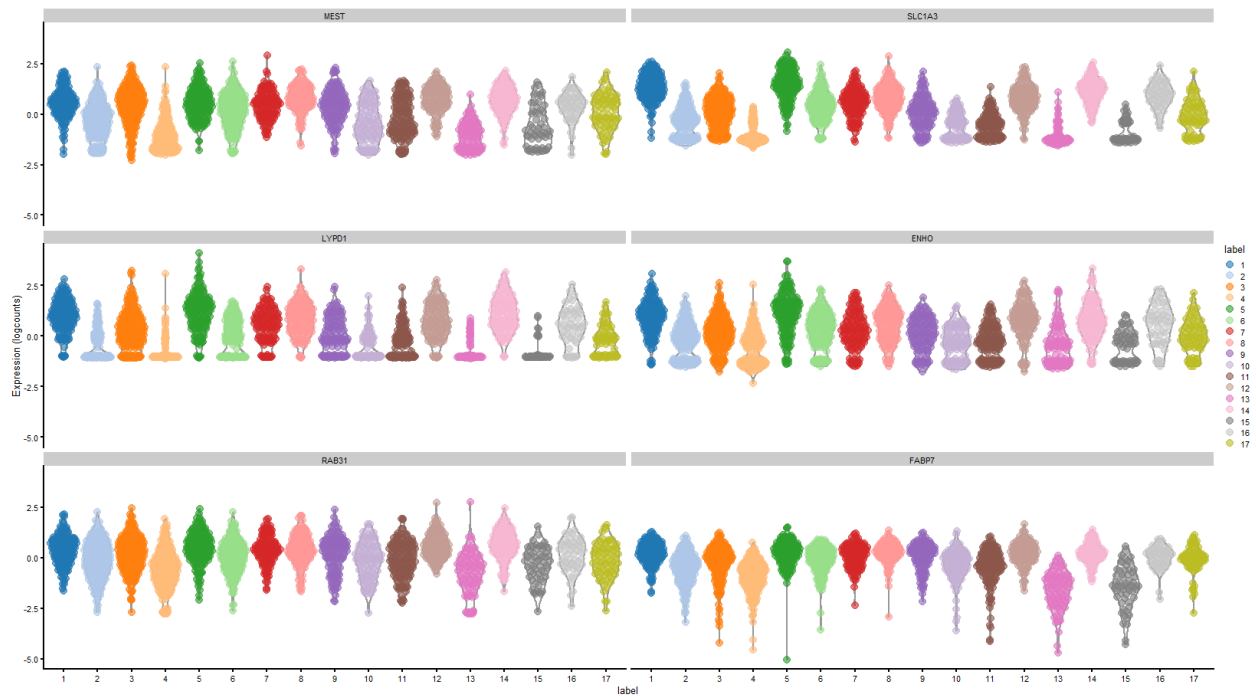


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
DEPP1	0.703190	0.575939	0.697128	0.823381	3
IL32	0.695060	0.493088	0.679630	0.863601	3
PLCB1	0.692397	0.477269	0.677723	0.853077	5
PLAC9	0.686723	0.482139	0.664709	0.840174	9
GRIP2	0.681336	0.496160	0.659115	0.863464	4

GO:0006688 glycosphingolipid biosynthetic process
GO:0009247 glycolipid biosynthetic process

GO:0046467	membrane lipid biosynthetic process
GO:0030148	sphingolipid biosynthetic process
GO:0097503	sialylation
GO:0035329	hippo signaling
GO:0006664	glycolipid metabolic process
GO:1903509	liposaccharide metabolic process
GO:0099515	actin filament-based transport
GO:0006687	glycosphingolipid metabolic process
GO:0046513	ceramide biosynthetic process
GO:0060487	lung epithelial cell differentiation
GO:0060479	lung cell differentiation
GO:0006643	membrane lipid metabolic process
GO:0045210	FasL biosynthetic process
GO:0014011	Schwann cell proliferation involved in axon regeneration
GO:0036135	Schwann cell migration
GO:1900147	regulation of Schwann cell migration
GO:1900148	negative regulation of Schwann cell migration
GO:1905044	regulation of Schwann cell proliferation involved in axon regeneration
GO:1905045	negative regulation of Schwann cell proliferation involved in axon regeneration
GO:0051582	positive regulation of neurotransmitter uptake
GO:0051943	positive regulation of amino acid uptake involved in synaptic transmission
GO:0051951	positive regulation of glutamate uptake involved in transmission of nerve impulse
GO:0150103	reactive gliosis
GO:1901979	regulation of inward rectifier potassium channel activity
GO:2000346	negative regulation of hepatocyte proliferation
GO:2001205	negative regulation of osteoclast development
GO:1904235	regulation of substrate-dependent cell migration, cell attachment to substrate
GO:1904237	positive regulation of substrate-dependent cell migration, cell attachment to substrate

Cluster #12:

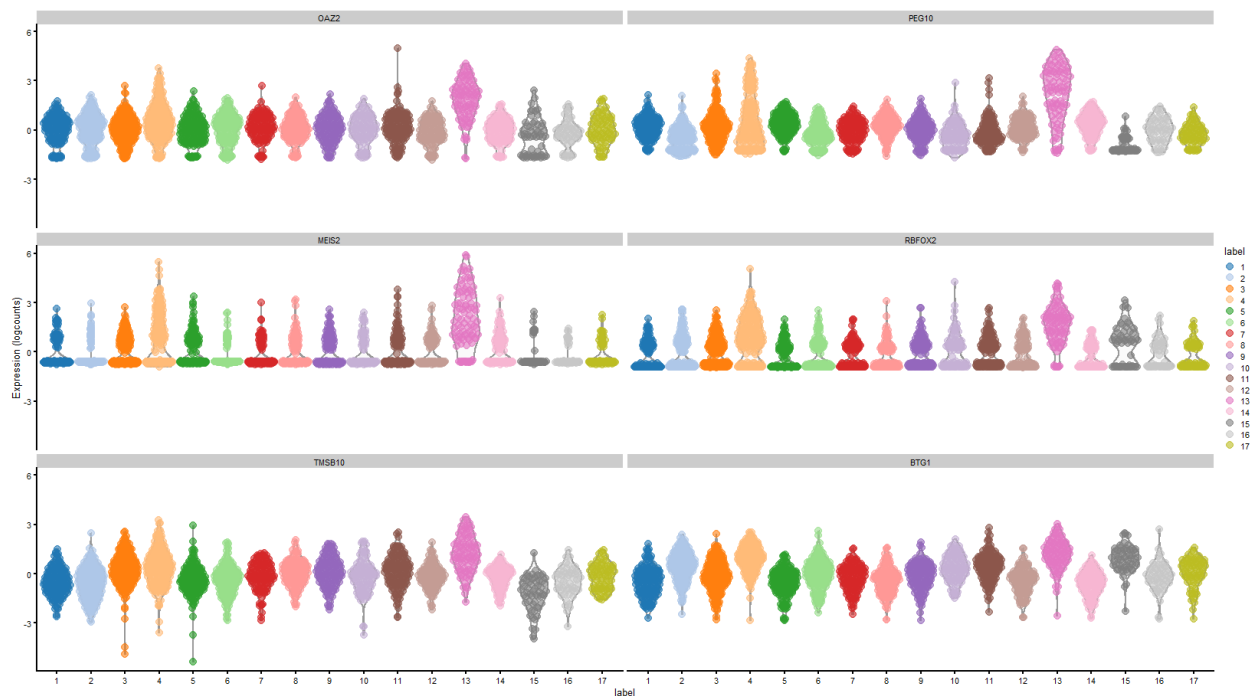


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
MEST	0.699712	0.473282	0.665145	0.960629	3
SLC1A3	0.693498	0.253763	0.763320	0.979167	1
LYPD1	0.686627	0.378219	0.721574	0.922913	2
ENHO	0.678008	0.394155	0.705667	0.848250	1
RAB31	0.671706	0.456764	0.667169	0.890344	8

GO:0001755	neural crest cell migration
GO:0033631	cell-cell adhesion mediated by integrin
GO:0048588	developmental cell growth
GO:0006821	chloride transport
GO:0008015	blood circulation
GO:0010721	negative regulation of cell development
GO:0071805	potassium ion transmembrane transport
GO:0014032	neural crest cell development
GO:0055078	sodium ion homeostasis
GO:0014031	mesenchymal cell development
GO:0048864	stem cell development
GO:1990138	neuron projection extension
GO:0006813	potassium ion transport
GO:0014033	neural crest cell differentiation
GO:0048675	axon extension
GO:0006875	cellular metal ion homeostasis

GO:0050768 negative regulation of neurogenesis
 GO:0051961 negative regulation of nervous system development
 GO:0030517 negative regulation of axon extension
 GO:0033630 positive regulation of cell adhesion mediated by integrin
 GO:0010273 detoxification of copper ion
 GO:1990169 stress response to copper ion
 GO:0050770 regulation of axonogenesis
 GO:0008217 regulation of blood pressure
 GO:0003073 regulation of systemic arterial blood pressure
 GO:0015698 inorganic anion transport
 GO:0030516 regulation of axon extension
 GO:0033627 cell adhesion mediated by integrin
 GO:0060560 developmental growth involved in morphogenesis
 GO:0045446 endothelial cell differentiation

Cluster #13:

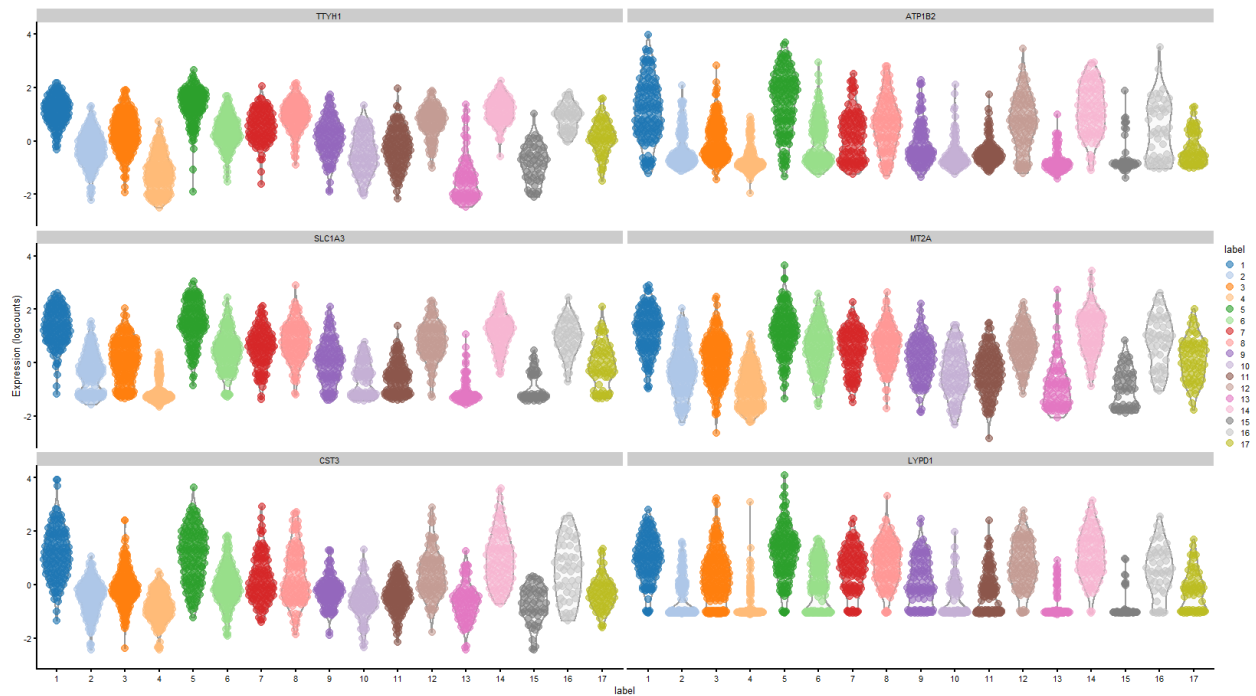


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
OAZ2	0.886092	0.789331	0.889748	0.913087	1
PEG10	0.859081	0.765804	0.861191	0.941306	1
MEIS2	0.856964	0.723865	0.867533	0.894420	1
RBFOX2	0.851449	0.682385	0.867050	0.905903	3
TMSB10	0.837386	0.710158	0.848198	0.952311	1

GO:0048675 axon extension
 GO:0050770 regulation of axonogenesis

GO:0050772	positive regulation of axonogenesis
GO:0060563	neuroepithelial cell differentiation
GO:1990138	neuron projection extension
GO:0051962	positive regulation of nervous system development
GO:0030516	regulation of axon extension
GO:0048483	autonomic nervous system development
GO:0061387	regulation of extent of cell growth
GO:0050769	positive regulation of neurogenesis
GO:0045666	positive regulation of neuron differentiation
GO:0030336	negative regulation of cell migration
GO:0048588	developmental cell growth
GO:0048485	sympathetic nervous system development
GO:2000146	negative regulation of cell motility
GO:0097118	neuroligin clustering involved in postsynaptic membrane assembly
GO:0060560	developmental growth involved in morphogenesis
GO:0002065	columnar/cuboidal epithelial cell differentiation
GO:0051271	negative regulation of cellular component movement
GO:0021602	cranial nerve morphogenesis
GO:0040013	negative regulation of locomotion
GO:0008038	neuron recognition
GO:0032271	regulation of protein polymerization
GO:0032535	regulation of cellular component size
GO:1902414	protein localization to cell junction
GO:0051017	actin filament bundle assembly
GO:0061572	actin filament bundle organization
GO:0110021	cardiac muscle myoblast proliferation
GO:0110022	regulation of cardiac muscle myoblast proliferation
GO:0110024	positive regulation of cardiac muscle myoblast proliferation

Cluster #14:

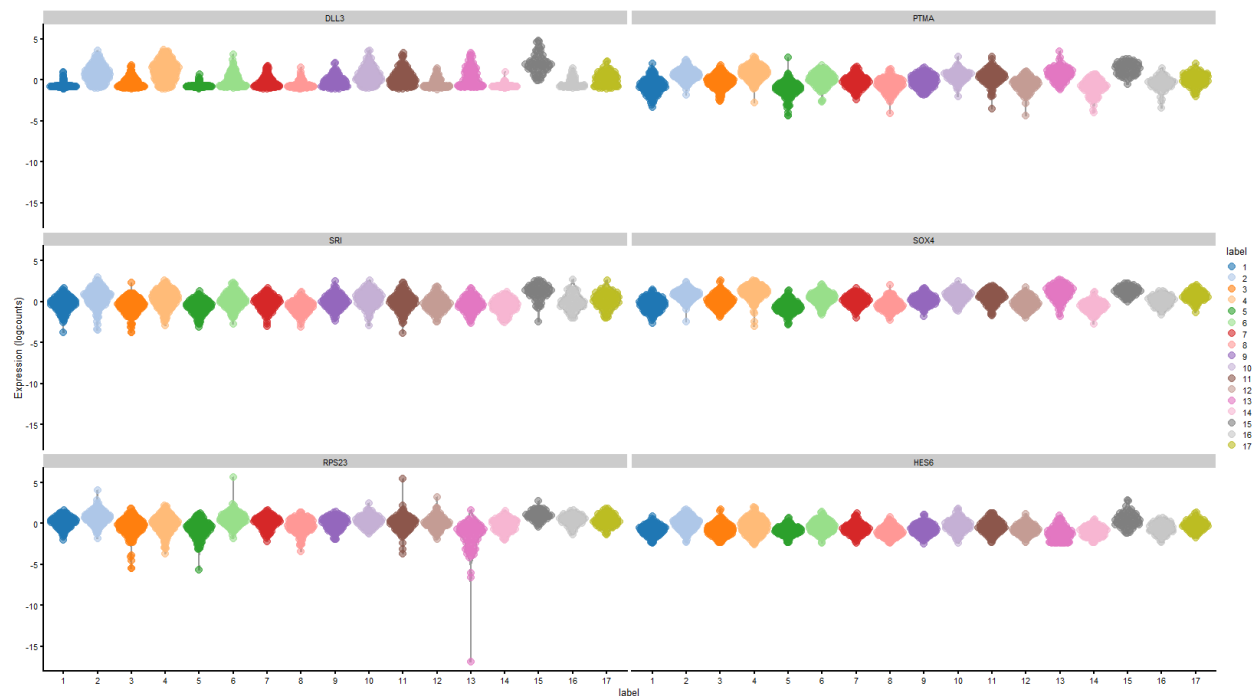


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
TTYH1	0.811293	0.374659	0.872300	0.995972	1
ATP1B2	0.795037	0.421622	0.842406	0.965018	2
SLC1A3	0.790241	0.361116	0.857580	0.994413	1
MT2A	0.778426	0.481649	0.820019	0.974216	1
CST3	0.777707	0.436363	0.837591	0.961755	2

GO:0010273	detoxification of copper ion
GO:1990169	stress response to copper ion
GO:0097501	stress response to metal ion
GO:0061687	detoxification of inorganic compound
GO:0071276	cellular response to cadmium ion
GO:0003018	vascular process in circulatory system
GO:0071294	cellular response to zinc ion
GO:0006875	cellular metal ion homeostasis
GO:0001504	neurotransmitter uptake
GO:0071280	cellular response to copper ion
GO:0010977	negative regulation of neuron projection development
GO:0071248	cellular response to metal ion
GO:0006882	cellular zinc ion homeostasis
GO:0055069	zinc ion homeostasis
GO:0046686	response to cadmium ion
GO:0034329	cell junction assembly

GO:0010232 vascular transport
 GO:0150104 transport across blood-brain barrier
 GO:0010038 response to metal ion
 GO:0033631 cell-cell adhesion mediated by integrin
 GO:0010043 response to zinc ion
 GO:0043403 skeletal muscle tissue regeneration
 GO:0046688 response to copper ion
 GO:0009636 response to toxic substance
 GO:0045926 negative regulation of growth
 GO:0051936 gamma-aminobutyric acid reuptake
 GO:0034238 macrophage fusion
 GO:0071241 cellular response to inorganic substance
 GO:0055076 transition metal ion homeostasis
 GO:0031345 negative regulation of cell projection organization

Cluster #15:

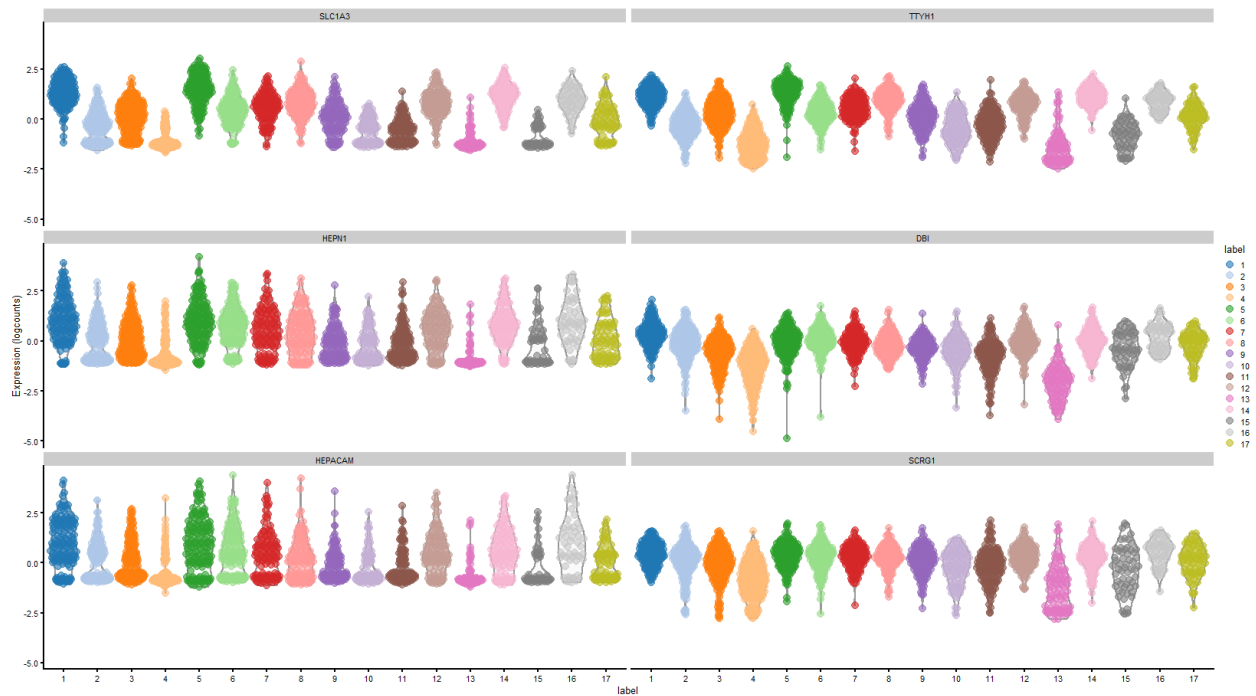


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
DLL3	0.916866	0.694297	0.957331	0.997981	1
PTMA	0.886515	0.673077	0.926073	0.984872	2
SRI	0.836788	0.681526	0.850922	0.927744	3
SOX4	0.834749	0.545304	0.898966	0.987574	2
RPS23	0.822828	0.607736	0.828652	0.974321	1

GO:0002181 cytoplasmic translation

GO:0042255	ribosome assembly
GO:0042273	ribosomal large subunit biogenesis
GO:0000027	ribosomal large subunit assembly
GO:0060844	arterial endothelial cell fate commitment
GO:0060846	blood vessel endothelial cell fate commitment
GO:0060847	endothelial cell fate specification
GO:0097101	blood vessel endothelial cell fate specification
GO:0048663	neuron fate commitment
GO:0022618	ribonucleoprotein complex assembly
GO:0071826	ribonucleoprotein complex subunit organization
GO:0007517	muscle organ development
GO:0045793	positive regulation of cell size
GO:0060839	endothelial cell fate commitment
GO:0007386	compartment pattern specification
GO:0035909	aorta morphogenesis
GO:0021545	cranial nerve development
GO:0044387	negative regulation of protein kinase activity by regulation of protein phosphorylation
GO:0060842	arterial endothelial cell differentiation
GO:0036302	atrioventricular canal development
GO:0021953	central nervous system neuron differentiation
GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator
GO:0003208	cardiac ventricle morphogenesis
GO:0072148	epithelial cell fate commitment
GO:0003215	cardiac right ventricle morphogenesis
GO:0021554	optic nerve development
GO:0060837	blood vessel endothelial cell differentiation
GO:0001756	somitogenesis
GO:0090276	regulation of peptide hormone secretion
GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process

Cluster #16:

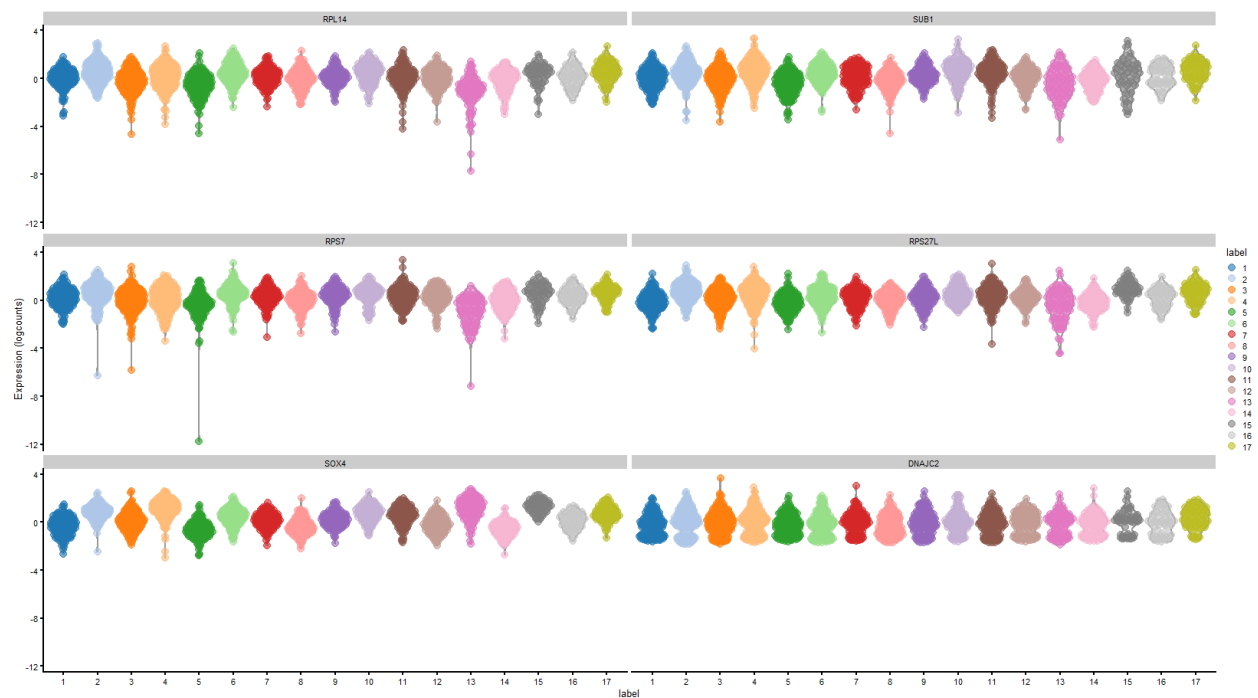


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
SLC1A3	0.732771	0.289957	0.805850	0.988389	1
TTYH1	0.716588	0.243579	0.784279	0.993832	1
HEPN1	0.692720	0.484741	0.712602	0.931754	4
DBI	0.686975	0.439534	0.664161	0.982336	1
HEPACAM	0.680811	0.498037	0.683493	0.876355	9

GO:0010232	vascular transport
GO:0150104	transport across blood-brain barrier
GO:0043090	amino acid import
GO:0098739	import across plasma membrane
GO:0003018	vascular process in circulatory system
GO:0089718	amino acid import across plasma membrane
GO:0051938	L-glutamate import
GO:0098712	L-glutamate import across plasma membrane
GO:0006814	sodium ion transport
GO:0098657	import into cell
GO:0035725	sodium ion transmembrane transport
GO:0070633	transepithelial transport
GO:1902475	L-alpha-amino acid transmembrane transport
GO:1903018	regulation of glycoprotein metabolic process
GO:0006821	chloride transport
GO:0015800	acidic amino acid transport

GO:0034756 regulation of iron ion transport
 GO:0070777 D-aspartate transport
 GO:0070779 D-aspartate import across plasma membrane
 GO:0015698 inorganic anion transport
 GO:0034764 positive regulation of transmembrane transport
 GO:1905039 carboxylic acid transmembrane transport
 GO:1903825 organic acid transmembrane transport
 GO:0006865 amino acid transport
 GO:0001504 neurotransmitter uptake
 GO:0006820 anion transport
 GO:0015813 L-glutamate transmembrane transport
 GO:0098656 anion transmembrane transport
 GO:0071314 cellular response to cocaine
 GO:0042940 D-amino acid transport

Cluster #17:



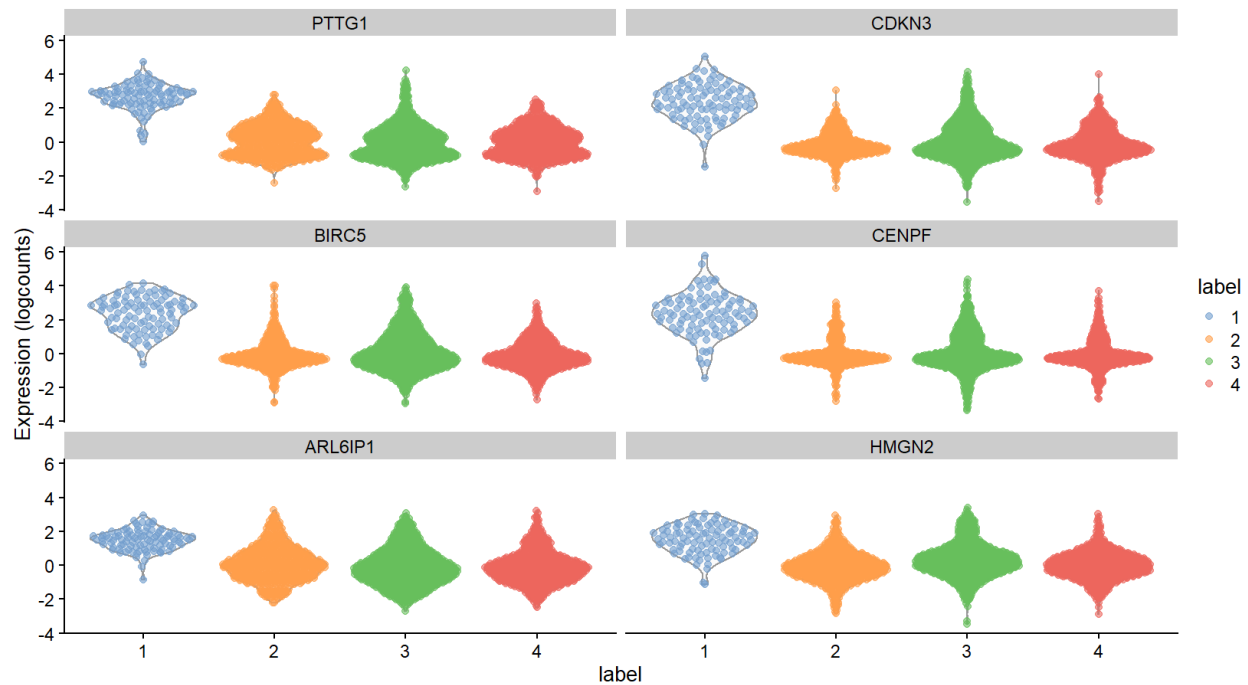
	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
RPL14	0.651902	0.504801	0.649684	0.870355	4
SUB1	0.640532	0.478653	0.650487	0.797075	4
RPS7	0.639753	0.493126	0.629243	0.888936	13
RPS27L	0.639632	0.380460	0.656937	0.779269	6
SOX4	0.636638	0.244138	0.718014	0.922523	1

GO:0045637 regulation of myeloid cell differentiation

GO:0061314	Notch signaling involved in heart development
GO:1903706	regulation of hemopoiesis
GO:0003184	pulmonary valve morphogenesis
GO:0045638	negative regulation of myeloid cell differentiation
GO:0045639	positive regulation of myeloid cell differentiation
GO:0003177	pulmonary valve development
GO:0030099	myeloid cell differentiation
GO:0061073	ciliary body morphogenesis
GO:0061311	cell surface receptor signaling pathway involved in heart development
GO:0002011	morphogenesis of an epithelial sheet
GO:0045165	cell fate commitment
GO:0007219	Notch signaling pathway
GO:1905314	semi-lunar valve development
GO:0072080	nephron tubule development
GO:0072716	response to actinomycin D
GO:0072014	proximal tubule development
GO:0061326	renal tubule development
GO:1901606	alpha-amino acid catabolic process
GO:0046950	cellular ketone body metabolic process
GO:1902224	ketone body metabolic process
GO:0072070	loop of Henle development
GO:0072009	nephron epithelium development
GO:0072015	glomerular visceral epithelial cell development
GO:0072310	glomerular epithelial cell development
GO:0010390	histone monoubiquitination
GO:0003179	heart valve morphogenesis
GO:0009063	cellular amino acid catabolic process
GO:0045646	regulation of erythrocyte differentiation
GO:0003170	heart valve development

sn520 Data

Cluster #1:

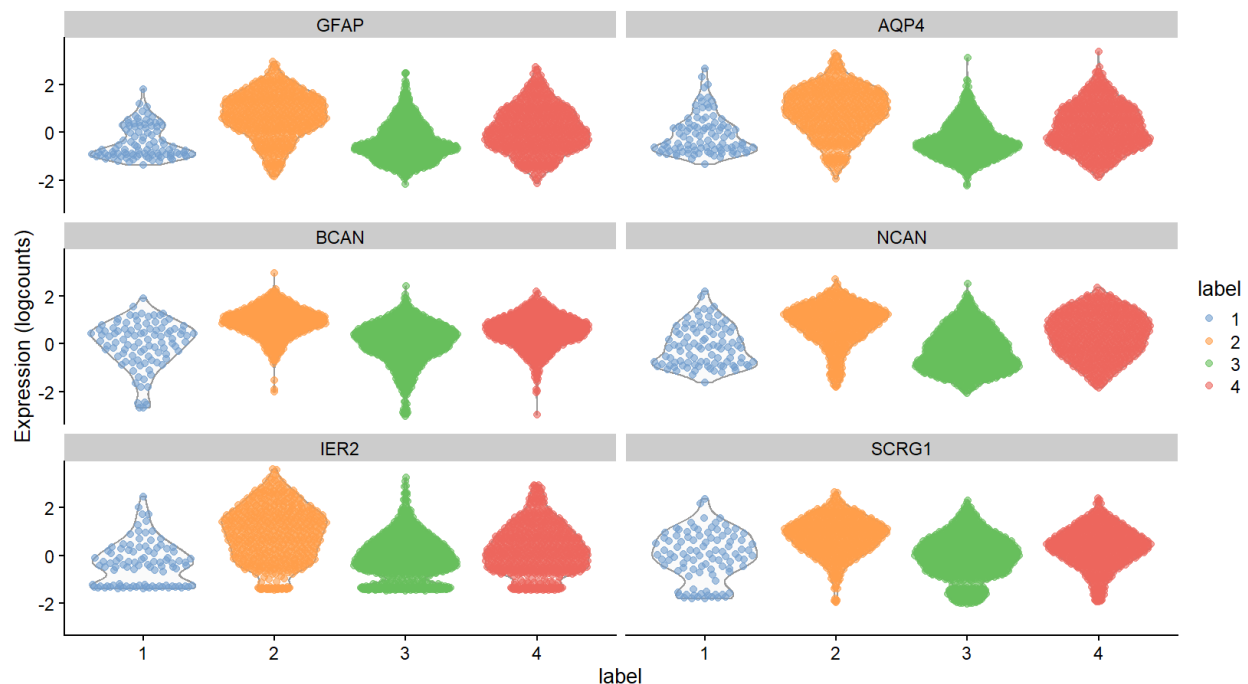


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
PTTG1	0.974373	0.965564	0.976048	0.981507	1
CDKN3	0.951782	0.926377	0.958661	0.970309	2
BIRC5	0.944146	0.913977	0.956684	0.961777	2
CENPF	0.925510	0.906686	0.933660	0.936186	4
ARL6IP1	0.890976	0.876443	0.886180	0.910303	5

GO:1905323	telomerase holoenzyme complex assembly
GO:1902850	microtubule cytoskeleton organization involved in mitosis
GO:0051383	kinetochore organization
GO:0000070	mitotic sister chromatid segregation
GO:0034508	centromere complex assembly
GO:0000819	sister chromatid segregation
GO:0010833	telomere maintenance via telomere lengthening
GO:0043486	histone exchange
GO:0071824	protein-DNA complex subunit organization
GO:0051972	regulation of telomerase activity
GO:0051131	chaperone-mediated protein complex assembly
GO:0051382	kinetochore assembly
GO:0007052	mitotic spindle organization
GO:0065004	protein-DNA complex assembly

GO:0051054 positive regulation of DNA metabolic process
GO:1902949 positive regulation of tau-protein kinase activity
GO:0007051 spindle organization
GO:0090128 regulation of synapse maturation
GO:0006403 RNA localization
GO:2000278 regulation of DNA biosynthetic process
GO:0034080 CENP-A containing chromatin assembly
GO:0061641 CENP-A containing chromatin organization
GO:1902947 regulation of tau-protein kinase activity
GO:0051783 regulation of nuclear division
GO:0050657 nucleic acid transport
GO:0050658 RNA transport
GO:0071897 DNA biosynthetic process
GO:0006278 RNA-templated DNA biosynthetic process
GO:0007004 telomere maintenance via telomerase
GO:2000573 positive regulation of DNA biosynthetic process

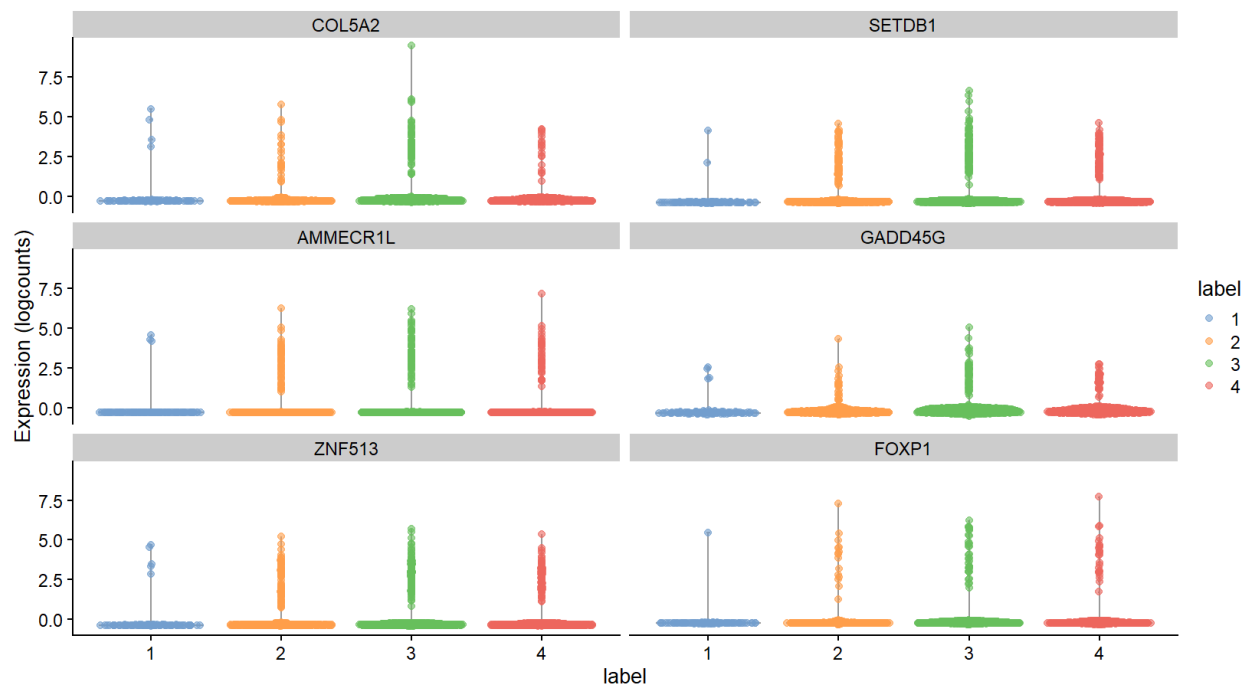
Cluster #2:



	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
GFAP	0.779015	0.683865	0.820877	0.832302	2
AQP4	0.765522	0.689936	0.776048	0.830580	1
BCAN	0.764342	0.675751	0.804828	0.812448	4
NCAN	0.751880	0.653058	0.783522	0.819060	3
IER2	0.731813	0.663677	0.746368	0.785395	7

GO:0031102	neuron projection regeneration
GO:0031099	regeneration
GO:0043409	negative regulation of MAPK cascade
GO:0051592	response to calcium ion
GO:0048708	astrocyte differentiation
GO:0043270	positive regulation of ion transport
GO:0007565	female pregnancy
GO:0044703	multi-organism reproductive process
GO:0006509	membrane protein ectodomain proteolysis
GO:0044706	multi-multicellular organism process
GO:0046683	response to organophosphorus
GO:0021537	telencephalon development
GO:0006816	calcium ion transport
GO:0014074	response to purine-containing compound
GO:0140115	export across plasma membrane
GO:0032611	interleukin-1 beta production
GO:0032651	regulation of interleukin-1 beta production
GO:0032102	negative regulation of response to external stimulus
GO:1901216	positive regulation of neuron death
GO:0010001	glial cell differentiation
GO:0021782	glial cell development
GO:0042063	gliogenesis
GO:0086064	cell communication by electrical coupling involved in cardiac conduction
GO:0051957	positive regulation of amino acid transport
GO:0051043	regulation of membrane protein ectodomain proteolysis
GO:0070471	uterine smooth muscle contraction
GO:0003012	muscle system process
GO:0061337	cardiac conduction
GO:0031103	axon regeneration
GO:0010038	response to metal ion

Cluster #3:

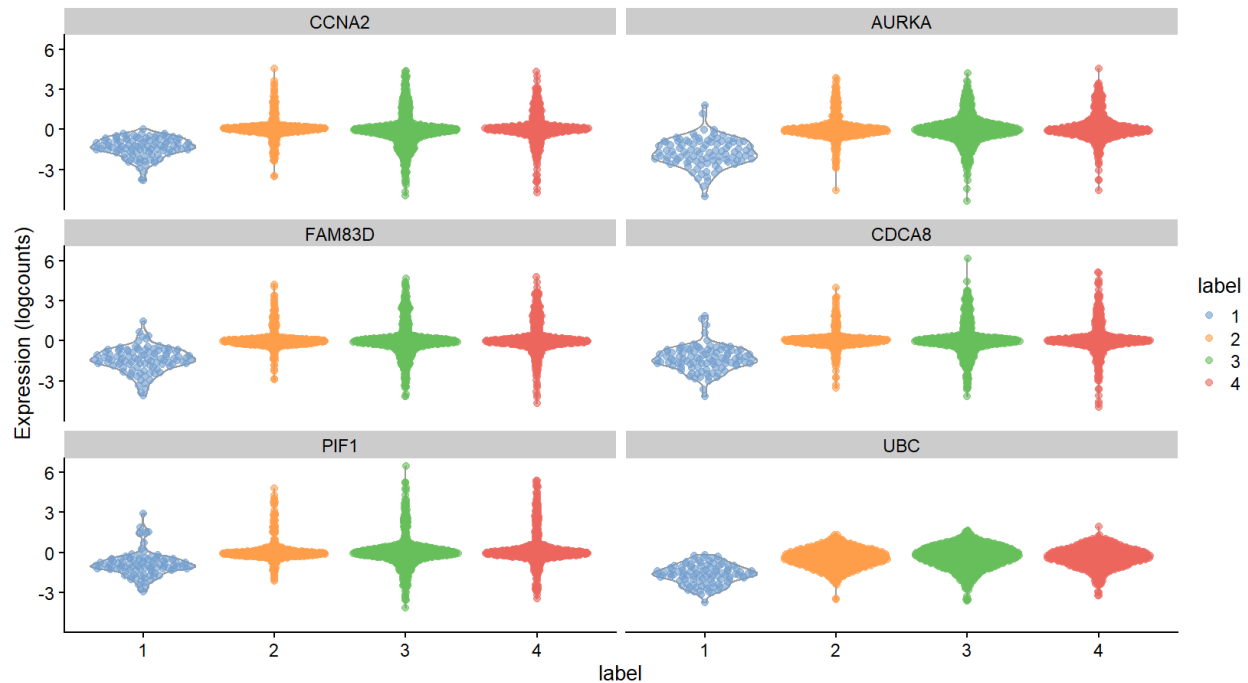


	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
COL5A2	0.657883	0.554846	0.666634	0.752169	57
SETDB1	0.656554	0.520644	0.586157	0.862859	6
AMMECR1L	0.654841	0.545789	0.596907	0.821826	82
GADD45G	0.652709	0.527873	0.623755	0.806500	153
ZNF513	0.651280	0.524250	0.607082	0.822509	78

GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process
GO:2000573	positive regulation of DNA biosynthetic process
GO:1901799	negative regulation of proteasomal protein catabolic process
GO:2000059	negative regulation of ubiquitin-dependent protein catabolic process
GO:0000723	telomere maintenance
GO:2001252	positive regulation of chromosome organization
GO:0032200	telomere organization
GO:0032206	positive regulation of telomere maintenance
GO:1903051	negative regulation of proteolysis involved in cellular protein catabolic process
GO:0044387	negative regulation of protein kinase activity by regulation of protein phosphorylation
GO:0006403	RNA localization
GO:2000278	regulation of DNA biosynthetic process
GO:0007130	synaptonemal complex assembly
GO:0048368	lateral mesoderm development
GO:0003231	cardiac ventricle development

GO:0070198 protein localization to chromosome, telomeric region
GO:1903363 negative regulation of cellular protein catabolic process
GO:0003279 cardiac septum development
GO:0044417 translocation of molecules into host
GO:0006278 RNA-templated DNA biosynthetic process
GO:0007004 telomere maintenance via telomerase
GO:1900182 positive regulation of protein localization to nucleus
GO:0060485 mesenchyme development
GO:0070193 synaptonemal complex organization
GO:0035329 hippo signaling
GO:0032212 positive regulation of telomere maintenance via telomerase
GO:0010833 telomere maintenance via telomere lengthening

Cluster #4:



	mean.AUC	min.AUC	median.AUC	max.AUC	rank.AUC
	<numeric>	<numeric>	<numeric>	<numeric>	<integer>
CCNA2	0.668200	0.502227	0.583843	0.918530	2
AURKA	0.667390	0.528686	0.536069	0.937416	1
FAM83D	0.656221	0.519411	0.551413	0.897839	4
CDCA8	0.645015	0.512608	0.528195	0.894243	5
PIF1	0.641451	0.536543	0.541561	0.846249	21

GO:0016572 histone phosphorylation
GO:0035404 histone-serine phosphorylation
GO:0000086 G2/M transition of mitotic cell cycle
GO:0010389 regulation of G2/M transition of mitotic cell cycle

GO:0045144	meiotic sister chromatid segregation
GO:0051177	meiotic sister chromatid cohesion
GO:0044839	cell cycle G2/M phase transition
GO:1902749	regulation of cell cycle G2/M phase transition
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle
GO:1902750	negative regulation of cell cycle G2/M phase transition
GO:0007135	meiosis II
GO:0061983	meiosis II cell cycle process
GO:0045143	homologous chromosome segregation
GO:0031100	animal organ regeneration
GO:1904668	positive regulation of ubiquitin protein ligase activity
GO:0007127	meiosis I
GO:0007095	mitotic G2 DNA damage checkpoint signaling
GO:0070601	centromeric sister chromatid cohesion
GO:0061982	meiosis I cell cycle process
GO:0000070	mitotic sister chromatid segregation
GO:0007098	centrosome cycle
GO:0090068	positive regulation of cell cycle process
GO:0031023	microtubule organizing center organization
GO:0007088	regulation of mitotic nuclear division
GO:0000819	sister chromatid segregation
GO:0044818	mitotic G2/M transition checkpoint
GO:0035504	regulation of myosin light chain kinase activity
GO:0035505	positive regulation of myosin light chain kinase activity
GO:0010124	phenylacetate catabolic process
GO:0006168	adenine salvage