

2021.7.16 Results

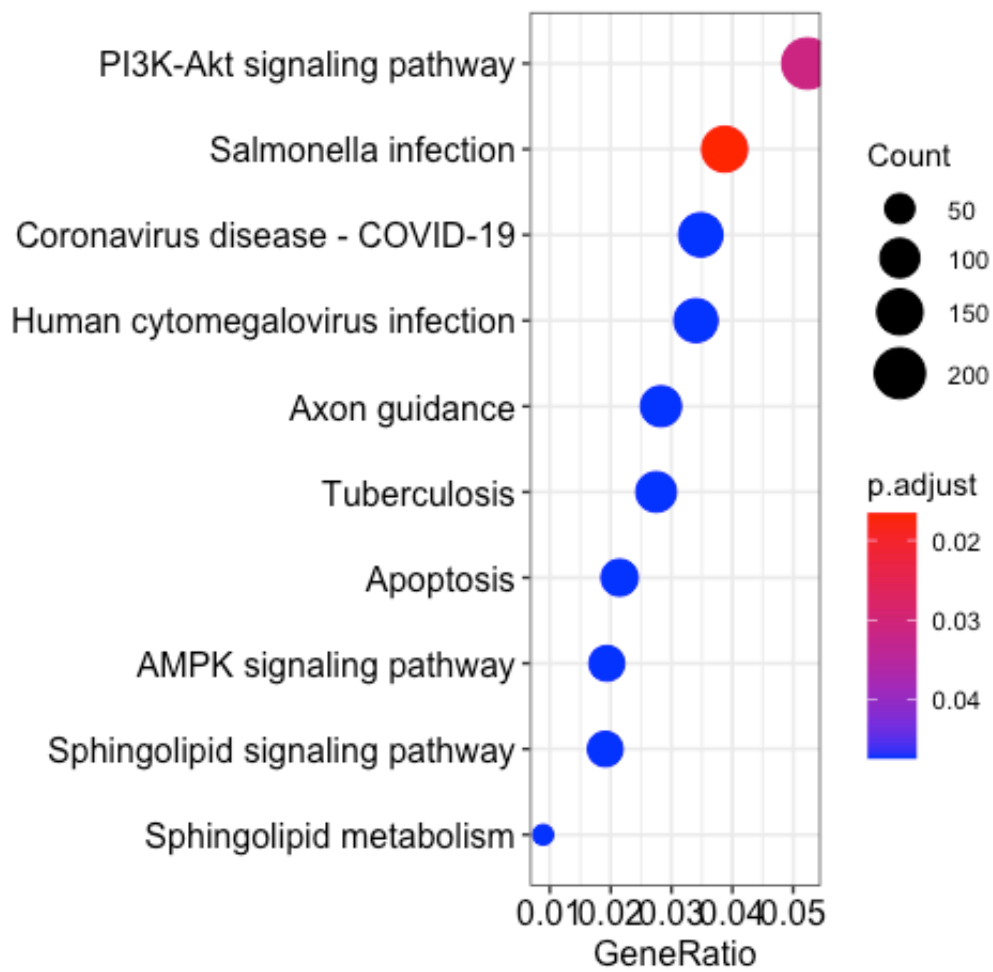
KEGG基因富集分析

```
all_genes <- read.table(file =  
  '/Users/keqinliu/Downloads/GSE42133.top.table.tsv', sep = '\t', header = TRUE)  
library(ggplot2)  
library(clusterProfiler)  
library(org.Hs.eg.db)  
s2e <- bitr(unique(all_genes$Gene.symbol), fromType = "SYMBOL",  
  toType = c("ENTREZID"),  
  OrgDb = 'org.Hs.eg.db')  
all_DEG <- merge(s2e, all_genes, by.y = "Gene.symbol", by.x = "SYMBOL")  
kegg_all <- enrichKEGG(gene = all_DEG$ENTREZID,  
  organism = 'hsa',  
  pvalueCutoff = 0.99,  
  qvalueCutoff = 0.99)
```

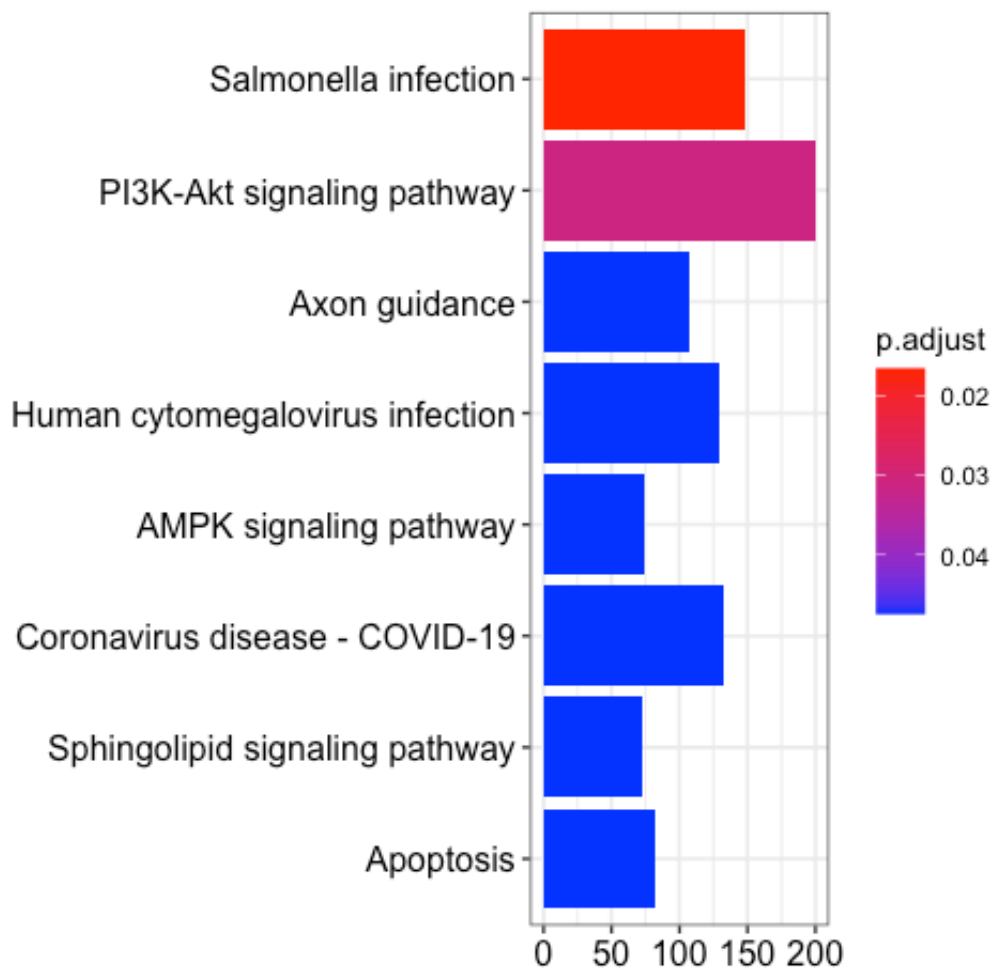
```
head(kegg_all)[,1:6]
```

##		ID	Description	GeneRatio	BgRatio
pvalue	p.adjust				
##	hsa05132	hsa05132	Salmonella infection	148/3821	249/8108
0.0000502238	0.01657385				
##	hsa04151	hsa04151	PI3K-Akt signaling pathway	200/3821	354/8108
0.0001888384	0.03115833				
##	hsa04360	hsa04360	Axon guidance	108/3821	182/8108
0.0005488339	0.04742483				
##	hsa05163	hsa05163	Human cytomegalovirus infection	130/3821	225/8108
0.0007431181	0.04742483				
##	hsa04152	hsa04152	AMPK signaling pathway	74/3821	120/8108
0.0008854247	0.04742483				
##	hsa05171	hsa05171	Coronavirus disease - COVID-19	133/3821	232/8108
0.0010000147	0.04742483				

```
dotplot(kegg_all)
```



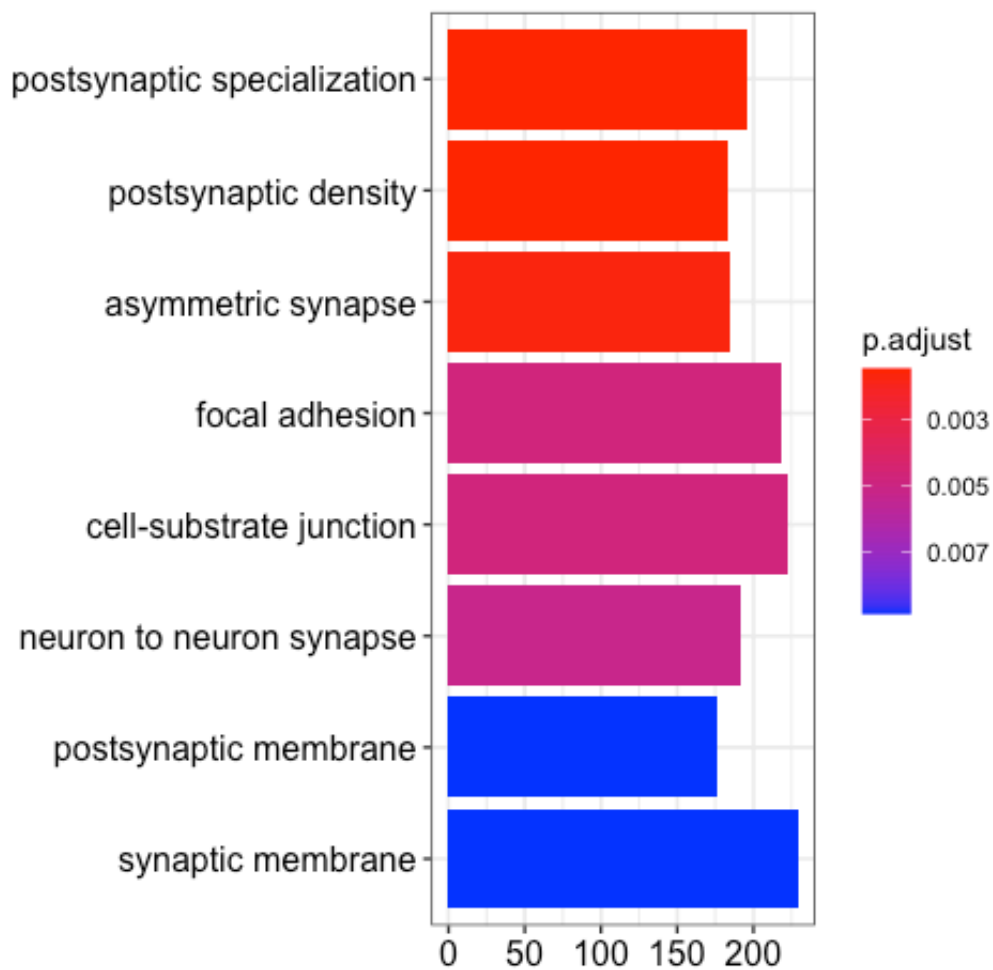
```
barplot(kegg_all)
```



GO富集分析

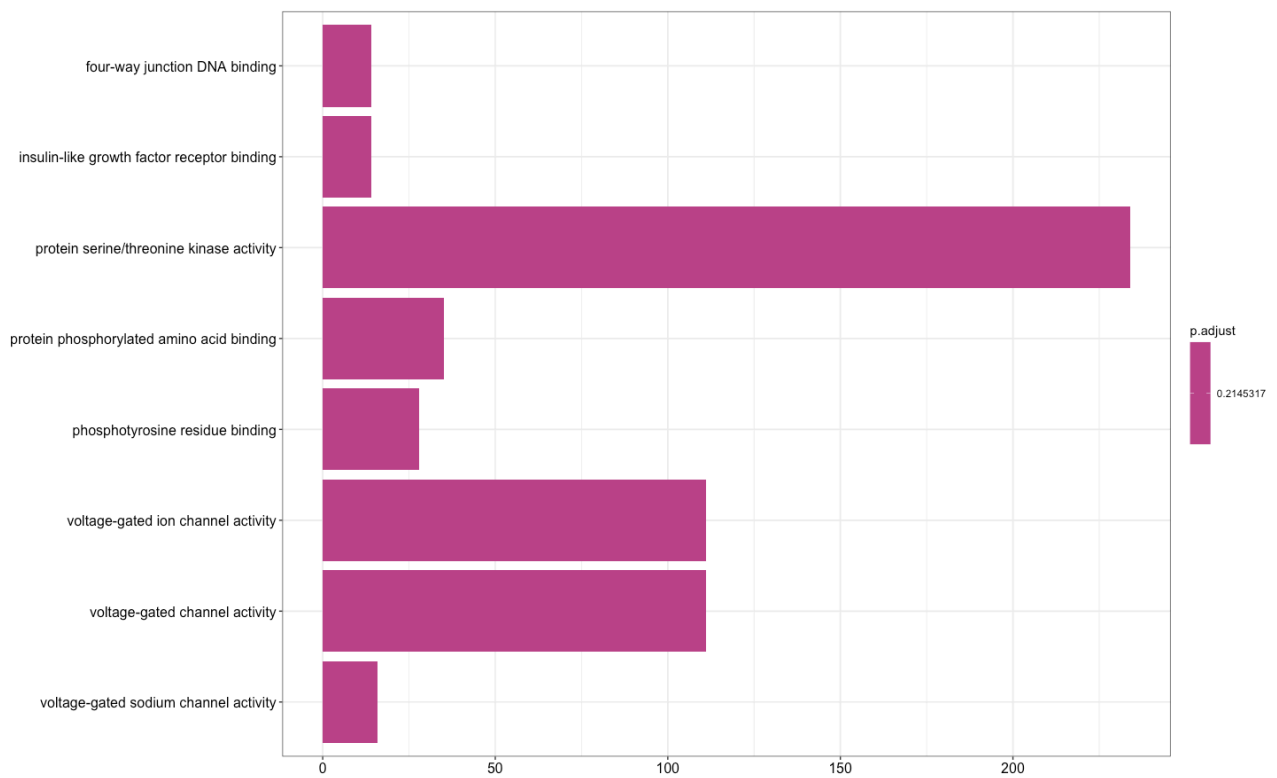
#细胞组分

```
erich.go.CC = enrichGO(gene = all_DEG$ENTREZID,  
                        OrgDb = org.Hs.eg.db,  
                        keyType = "ENTREZID",  
                        pAdjustMethod = "BH",  
                        ont = "CC",  
                        pvalueCutoff = 0.5,  
                        qvalueCutoff = 0.5,  
                        readable=T)  
  
barplot(erich.go.CC)
```



#分子功能:

```
ego_MF <- enrichGO(gene = all_DEG$ENTREZID,  
                    OrgDb= org.Hs.eg.db,  
                    keyType = "ENTREZID",  
                    ont = "MF",  
                    pvalueCutoff = 0.5,  
                    qvalueCutoff = 0.5)  
  
barplot(ego_MF)
```



#生物过程

```
erich.go.BP = enrichGO(gene = all_DEG$ENTREZID,  
                        OrgDb = org.Hs.eg.db,  
                        keyType = "ENTREZID",  
                        ont = "BP",  
                        pvalueCutoff = 0.5,  
                        qvalueCutoff = 0.5,  
                        readable=T)  
  
barplot(erich.go.BP)
```


top DEGs between autistic&normal (adj.p.value < 0.05)

GENE SYMBOL	ENTREZID	ID	ADJ.P.VALUE	P.VALUE	LOG FC	GENE TITLE
MID2	11043	ILMN_1915188	0.00895	1.89e-07	-0.1790	midline 2
NR3C2	4306	ILMN_2210934	0.01225	6.03e-07	-0.2870	nuclear receptor subfamily 3 group C member 2
DCUN1D4	23142	ILMN_1801403	0.01597	2.36e-06	-0.1570	defective in cullin neddylation 1 domain containing 4
IFFO2	126917	ILMN_3236367	0.01597	2.09e-06	-0.1780	intermediate filament family orphan 2
ZNF609	23060	ILMN_1799082	0.01597	2.25e-06	-0.2040	zinc finger protein 609
PRKCA	5578	ILMN_1771800	0.01691	2.86e-06	-0.2400	protein kinase C alpha
PURB	5814	ILMN_1750079	0.01716	3.26e-06	-0.1340	purine rich element binding protein B
YTHDF1	54915	ILMN_1753885	0.02000	4.65e-06	-0.1210	YTH N6-methyladenosine RNA binding protein 1
PIK3R1	5295	ILMN_1760303	0.02358	6.51e-06	-0.2090	phosphoinositide-3-kinase regulatory subunit 1
PIP4K2A	5305	ILMN_3236637	0.02358	6.98e-06	-0.1950	phosphatidylinositol-5-phosphate 4-kinase type 2 alpha
PTPN11	5781	ILMN_1778236	0.02358	6.55e-06	-0.1300	protein tyrosine phosphatase, non-receptor type 11
KCNG1	3755	ILMN_1673769	0.03436	1.29e-05	-0.3410	potassium voltage-gated channel modifier subfamily G member 1
NANOS2	339345	ILMN_1694414	0.03436	1.29e-05	0.1040	nanos C2HC-type zinc finger 2
PTOV1	53635	ILMN_1700109	0.03480	1.40e-05	-0.1970	prostate tumor overexpressed 1
C14orf28	122525	ILMN_1807031	0.03516	1.63e-05	-0.1520	chromosome 14 open reading frame 28
SPOCK2	9806	ILMN_1656287	0.03516	1.71e-05	-0.2880	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2
TMEM245	23731	ILMN_1788384	0.03516	1.71e-05	-0.2160	transmembrane protein 245
CNNM3	26505	ILMN_1662328	0.03918	1.99e-05	-0.1900	cyclin and CBS domain divalent metal cation transport mediator 3
AK3	50808	ILMN_1778173	0.04054	3.29e-05	-0.1800	adenylate kinase 3
ELMSAN1	91748	ILMN_1763091	0.04054	3.14e-05	-0.2560	ELM2 and Myb/SANT domain containing 1
GPR68	8111	ILMN_1671142	0.04054	3.20e-05	-0.2240	G protein-coupled receptor 68
IGF2BP3	10643	ILMN_1807423	0.04054	2.71e-05	0.3200	insulin like growth factor 2 mRNA binding protein 3
LAMB2P1	22973	ILMN_3242152	0.04054	2.35e-05	-0.1210	laminin subunit beta 2 pseudogene 1
LINC00294	283267	ILMN_3244521	0.04054	2.81e-05	-0.1850	long intergenic non-protein coding RNA 294
MRRF	92399	ILMN_2298958	0.04054	2.66e-05	0.1270	mitochondrial ribosome recycling factor
NDRG3	57446	ILMN_1738229	0.04054	3.34e-05	-0.1710	NDRG family member 3
RUNX1	861	ILMN_1801504	0.04054	2.98e-05	-0.1560	runt related transcription factor 1
SMPD1	6609	ILMN_1757370	0.04054	3.20e-05	-0.1760	sphingomyelin phosphodiesterase 1
ZFPM1	161882	ILMN_1651438	0.04054	3.29e-05	-0.1380	zinc finger protein, FOG family member 1
CLOCK	9575	ILMN_1869087	0.04122	3.57e-05	-0.1410	clock circadian regulator
TM2D2	83877	ILMN_1741171	0.04269	3.79e-05	-0.1340	TM2 domain containing 2
YY1	7528	ILMN_1770892	0.04320	3.93e-05	-0.2170	YY1 transcription factor
CALM1	801	ILMN_1778242	0.04329	4.19e-05	-0.1610	calmodulin 1

ERI1	90459	ILMN_1652716	0.04329	4.16e-05	0.1730	exoribonuclease 1
MKLN1	4289	ILMN_1742578	0.04382	4.44e-05	-0.1410	muskelin 1
CAMK2N1	55450	ILMN_1794863	0.04509	5.81e-05	-0.1240	calcium/calmodulin dependent protein kinase II inhibitor 1
EFNB3	1949	ILMN_1695606	0.04509	5.36e-05	0.0957	ephrin B3
EPHA1	2041	ILMN_1664265	0.04509	5.80e-05	-0.2050	EPH receptor A1
FEZ1	9638	ILMN_1779071	0.04509	5.63e-05	-0.2500	fasciculation and elongation protein zeta 1
GPM6A	2823	ILMN_1711312	0.04509	5.77e-05	0.0896	glycoprotein M6A
IGIP	492311	ILMN_1685854	0.04509	4.97e-05	-0.1850	IgA inducing protein
LRFN3	79414	ILMN_2103919	0.04509	5.83e-05	-0.1620	leucine rich repeat and fibronectin type III domain containing 3
MMGT1	93380	ILMN_1776216	0.04509	5.91e-05	-0.1530	membrane magnesium transporter 1
RAB3GAP2	25782	ILMN_3236423	0.04509	4.86e-05	-0.1150	RAB3 GTPase activating non-catalytic protein subunit 2
SNORD62B	692093	ILMN_3248270	0.04509	5.32e-05	-0.3060	small nucleolar RNA, C/D box 62B
SRRM1	10250	ILMN_1697670	0.04509	5.35e-05	-0.1280	serine and arginine repetitive matrix 1
TSHZ2	128553	ILMN_1655611	0.04509	5.41e-05	-0.1200	teashirt zinc finger homeobox 2
ZNF571	51276	ILMN_2093864	0.04509	5.48e-05	-0.1310	zinc finger protein 571
ICK	22858	ILMN_1709882	0.04598	6.19e-05	-0.1440	intestinal cell (MAK-like) kinase
PITPNC1	26207	ILMN_1670638	0.04598	6.41e-05	-0.1580	phosphatidylinositol transfer protein, cytoplasmic 1
USP13	8975	ILMN_3251526	0.04598	6.51e-05	-0.1240	ubiquitin specific peptidase 13 (isopeptidase T-3)
WBP11	51729	ILMN_1766435	0.04996	7.39e-05	-0.1480	WW domain binding protein 11
ZNF524	147807	ILMN_1810147	0.04996	7.29e-05	-0.1240	zinc finger protein 524