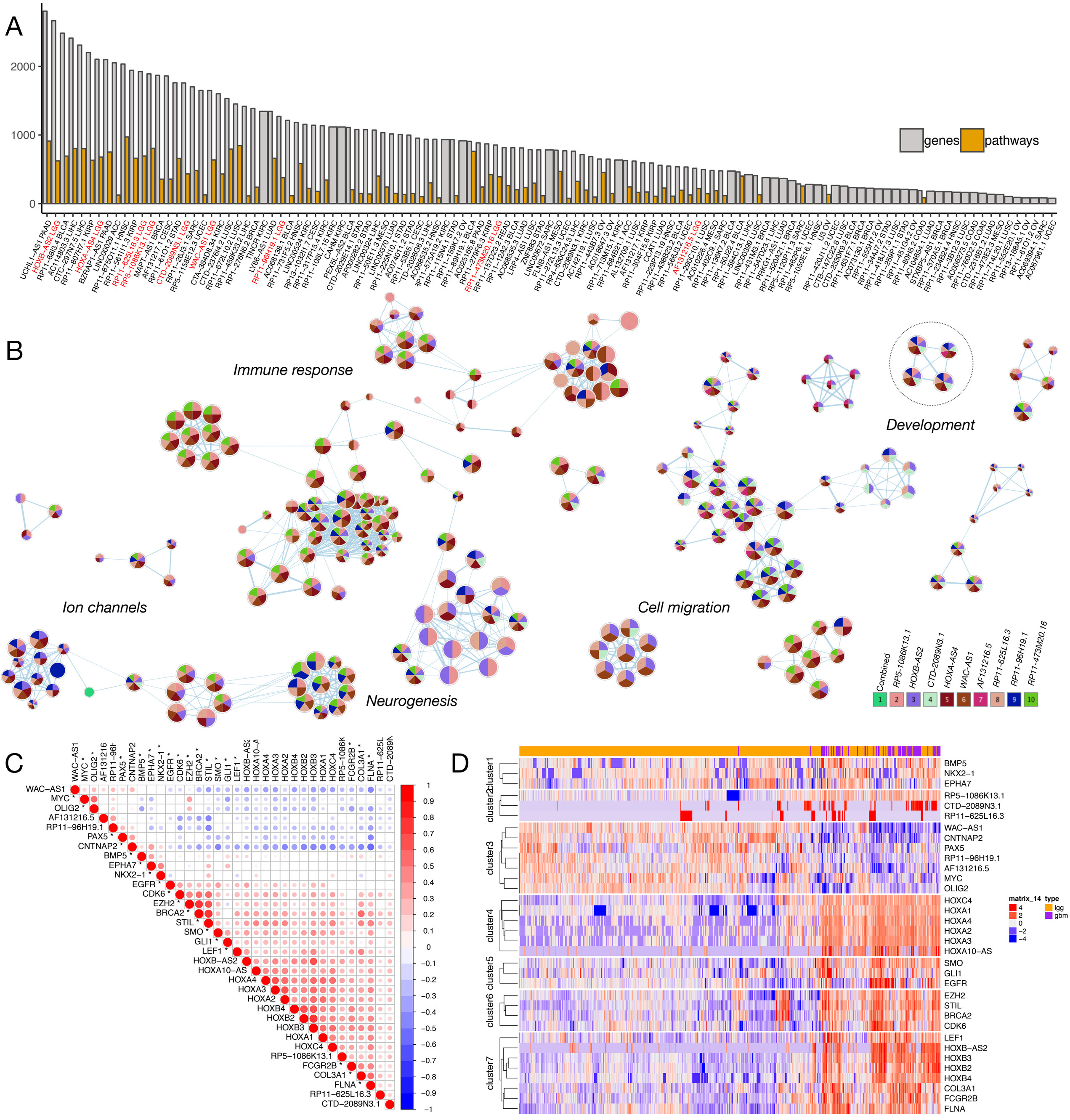
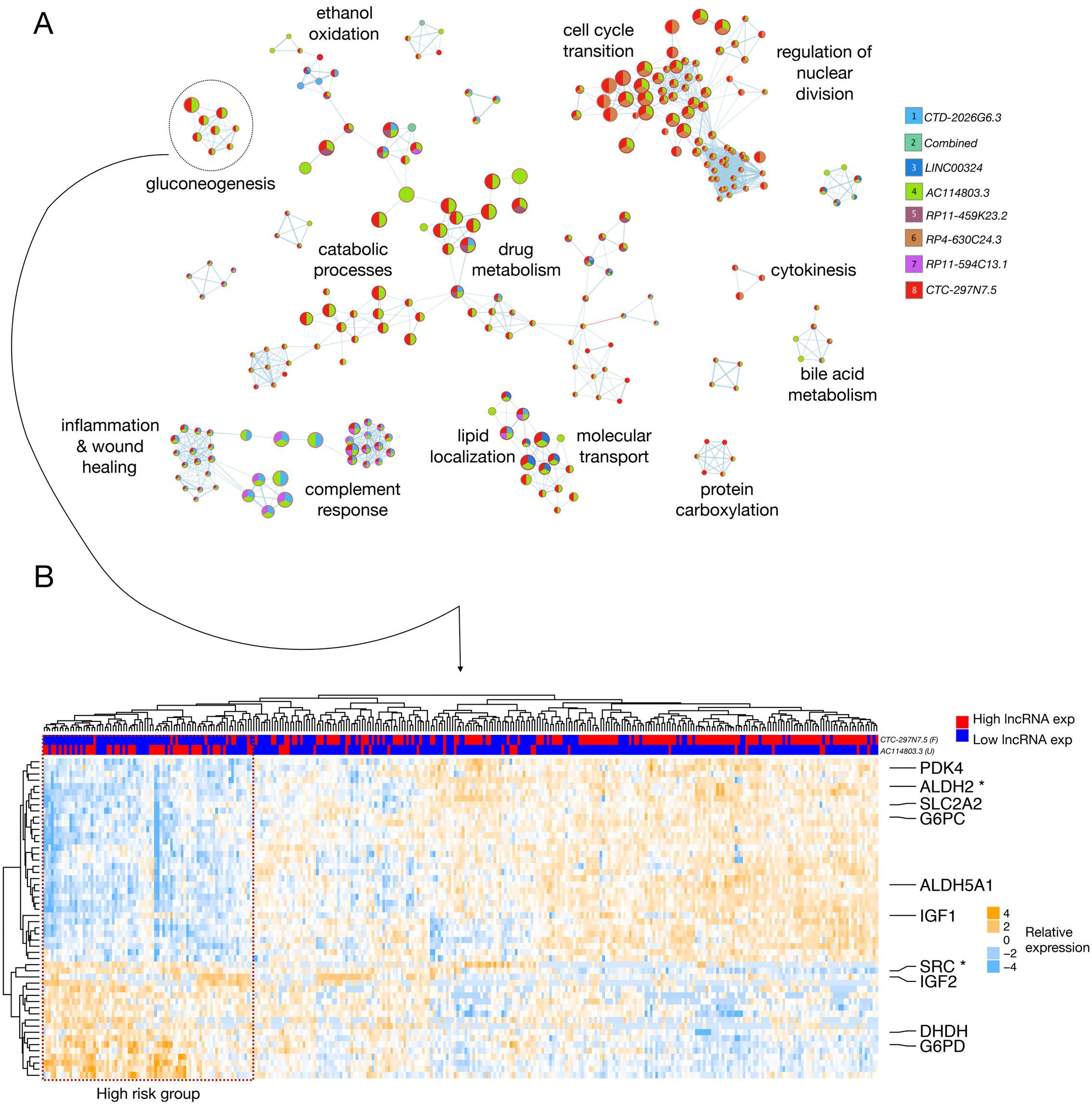
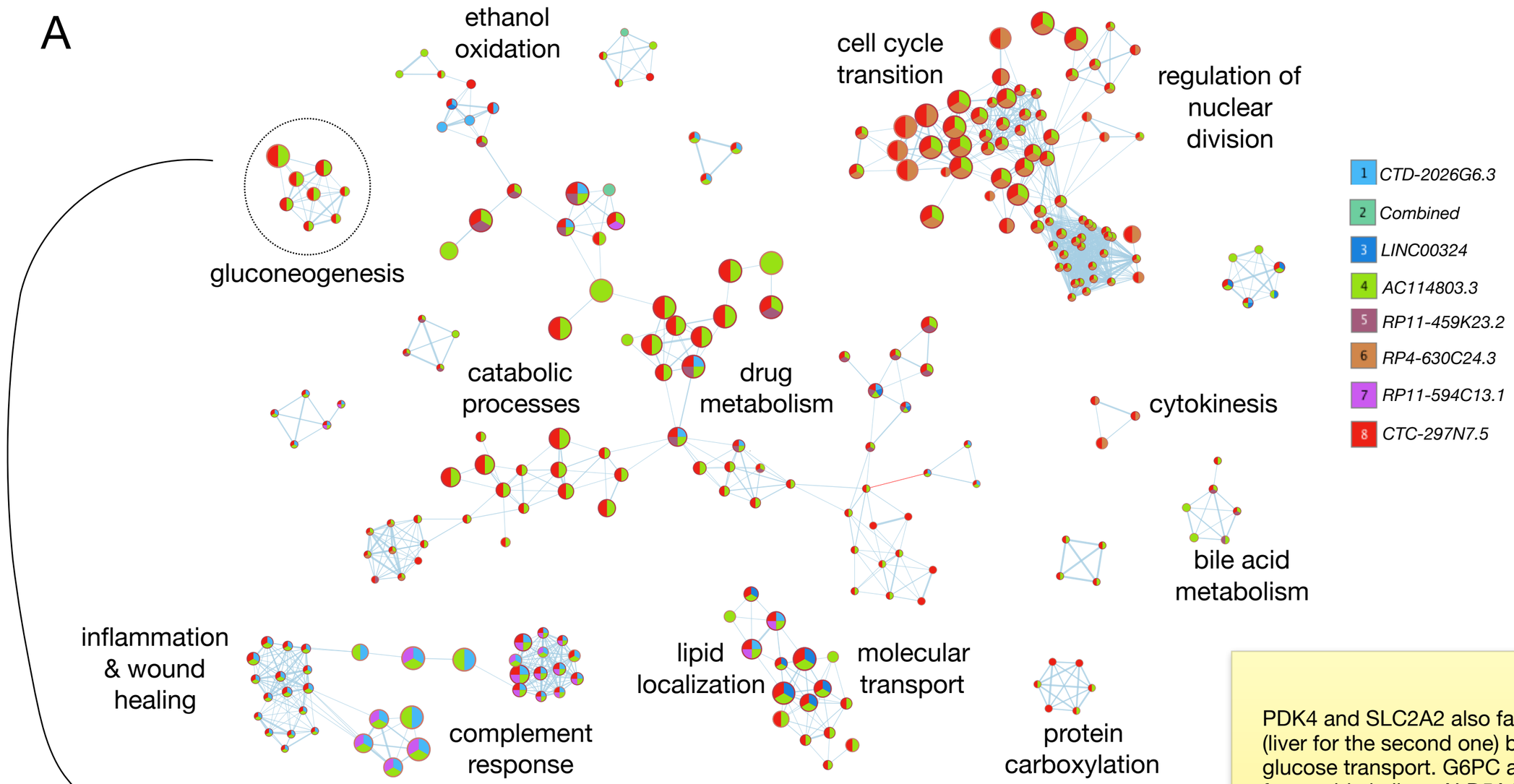
# Figure 6


A
2000
1000
0
genes
pathways
UCHL1–AS1 PAAD
HOXB–AS2 LGG
RP11–68I3.4 BLCA
AC114803.3 LIHC
CTC–297N7.5 LIHC
RP11–807H7.1 KIRP
HOXA–AS4 LGG
BZRAP1–AS1 PAAD
LINC00029 ACC
RP11–875O11.1 HNSC
RP11–561I11.3 KIRP
RP11–625L16.3 LGG
RP5–1086K13.1 LGG
MAPT–AS1 BRCA
AF131217.1 CESC
RP11–61O1.2 STAD
CTD–2089N3.1 LGG
RP11–26J3.1 SARC
RP5–1158E12.3 UCEC
WAC–AS1 LGG
CTA–384D8.34 KIRC
CTD–2276I4.2 LUSC
RP11–672L10.2 LUSC
RP11–459K23.2 LIHC
RP1–276N6.2 BRCA
TINCR KIRC
LY86–AS1 LUAD
RP11–96H19.1 LGG
AC068138.1 BLCA
RP11–731F5.2 HNSC
LINC00524 KIRC
RP13–1032I11.7 CESC
RP11–317P15.4 KIRC
RP11–108L7.15 KIRC
CAHM KIRC
PEX5L–AS2 BLCA
CTD–2029E14.1 STAD
AP000282.2 STAD
LINC00324 LIHC
RP11–50E11.3 MESO
LINC00370 LUAD
RP11–225N10.1 STAD
AC074011.2 STAD
RP11–53B5.1 CESC
AC068535.2 LIHC
RP11–575A19.2 HNSC
RP11–115N4.1 STAD
RP11–159K7.2 OV
RP11–89H19.1 BLCA
AC025165.8 PAAD
RP11–279F6.3 KIRP
RP1–473M20.16 LGG
RP11–157D23.2 READ
RP11–12A2.3 BLCA
AC068535.3 LUAD
LRP4–AS1 LUSC
ZNF883 STAD
LINC00672 SARC
FLNB–AS1 MESO
RP4–630C24.3 LIHC
CTD–2089N3.1 KIRC
AC142119.1 LUSC
RP11–443B7.3 OV
AC018647.3 OV
RP11–713M15.1 KIRC
RP11–684B21.1 ACC
AL132709.1 LUSC
AF131217.1 KIRP
RP11–304F15.6 KIRP
CCAT1 LUAD
RP11–229P13.19 HNSC
RP11–438B23.2 BLCA
RP11–566J3.2 UCEC
AF131216.5 LGG
RP11–290C10.1 LUSC
AC010226.4 MESO
RP11–402C9.1 SARC
RP1–136K7.2 BLCA
RP1–50J22.4 BLCA
RP11–594C13.1 LIHC
LINC00399 LUSC
RP11–431M8.1 BRCA
RP11–547D23.1 LHC
PRKG1–AS1 LUAD
RP5–1120P11.3 BRCA
RP11–462P6.1 UCEC
RP5–1050E16.1 HNSC
RP11–420J11.2 UCEC
CTB–147C22.8 LUSC
RP11–2330K9.2 BLCA
AC073130.1 BRCA
RP11–555H7.2 OV
RP11–344J7.2 STAD
RP11–418J17.3 LUSC
RP11–259P11.1 STAD
RP11–451G4.2 OV
RP11–80H5.2 COAD
AC104654.1 LUAD
STXBP5–AS1 BRCA
RP11–370A5.1 BRCA
RP11–234B24.4 HNSC
RP11–3B12.3 LUSC
AC006273.5 COAD
CTD–2316B1.2 LUAD
RP11–760D2.5 COAD
RP11–473E2.3 MESO
RP11–714L20.1 LUSC
RP11–552E20.1 OV
RP13–188A5.1 OV
RP11–61O1.2 OV
AC069394.1 SARC
AC067961.1 UCEC
B
Immune response
Development
Ion channels
Cell migration
Neurogenesis
Combined
RP5-1086K13.1
HOXB-AS2
CTD-2089N3.1
HOXA-AS4
WAC-AS1
AF131216.5
RP11-625L16.3
RP11-96H19.1
RP11-473M20.16
1
2
3
4
5
6
7
8
9
10
C
WAC–AS1
MYC *
OLIG2 *
AF131216
RP11–96H
PAX5 *
CNTNAP2
BMP5 *
EPHA7 *
NKX2–1 *
EGFR *
CDK6 *
EZH2 *
BRCA2 *
STIL *
SMO *
GLI1 *
LEF1 *
HOXB–AS2
HOXA10–A
HOXA4
HOXA3
HOXA2
HOXB4
HOXB2
HOXB3
HOXA1
HOXC4
RP5–1086K
FCGR2B *
COL3A1 *
FLNA *
RP11–625L
CTD–2089N
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
−0.1
−0.2
−0.3
−0.4
−0.5
−0.6
−0.7
−0.8
−0.9
−1
D
cluster1
cluster2
cluster3
cluster4
cluster5
cluster6
cluster7
BMP5
NKX2–1
EPHA7
RP5–1086K13.1
CTD–2089N3.1
RP11–625L16.3
WAC–AS1
CNTNAP2
PAX5
RP11–96H19.1
AF131216.5
MYC
OLIG2
HOXC4
HOXA1
HOXA4
HOXA2
HOXA3
HOXA10–AS
SMO
GLI1
EGFR
EZH2
STIL
BRCA2
CDK6
LEF1
HOXB–AS2
HOXB3
HOXB2
HOXB4
COL3A1
FCGR2B
FLNA
matrix_14
4
2
0
−2
−4
type
lgg
gbm

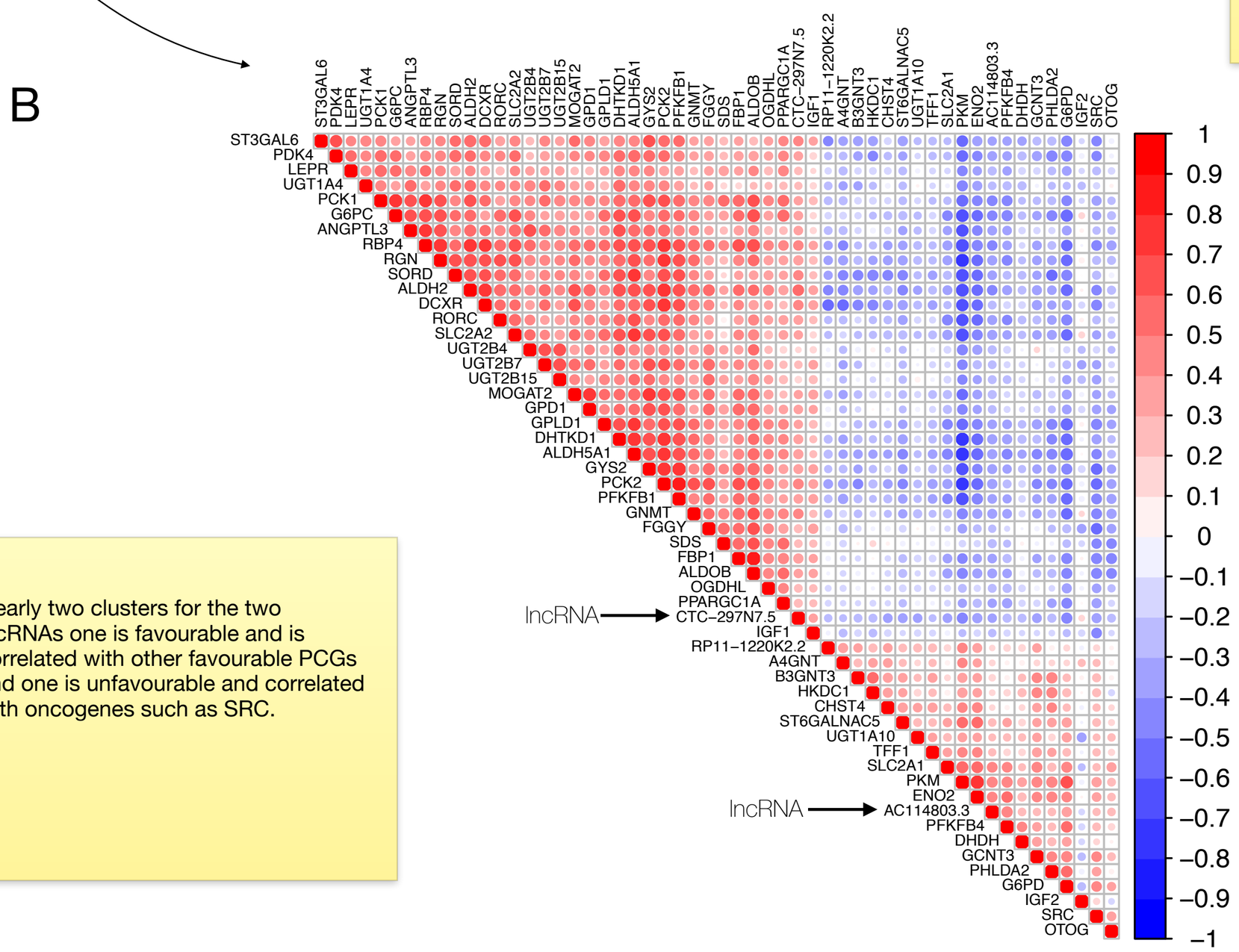
# Supplementary Figure 6



# Supplementary Figure 6 V2




PDK4 and SLC2A2 also favourable (liver for the second one) bidirectional glucose transport. G6PC also favourable in liver. ALD5A1 also. G6PD unfavourable in liver cancer.




clearly two clusters for the two lncRNAs one is favourable and is correlated with other favourable PCGs and one is unfavourable and correlated with oncogenes such as SRC.

most of these PCGs are not prognostic
HOXA1 - unfavourable in head and neck cancer
HOXA4 - unfavourable in endometrial cancer
HOXA3 - unfavourable in renal cancer

but these lncRNAs actually are associated with lots of pathways 1000s to hundreds of genes but we can see that they still falll on the same pathways

EPHA7 -> brain development nervous system (upregulated bad)

CNTNAP2 -> one of largest genes, regulated by FOXP2 related to speech and language development
PAX5 -> early regulator of development B cell lineage specific activator , developing CNAs and testis
OLIG2 -> essential regulator of ventral neuroectodermal progenitor cell fat
^ down regulated good genes

GLI1 - > The activity and nuclear localization of this protein is negatively regulated by p53 in an inhibitory loop. activated by sonic hedgehog.

maybe survival curve taking into account pathway
developmental active pathways vs inactive pathways

EZH2
are these genes also more expression in GBM compared to LGG
ie, low risk LGG, high risk LGG, GBM