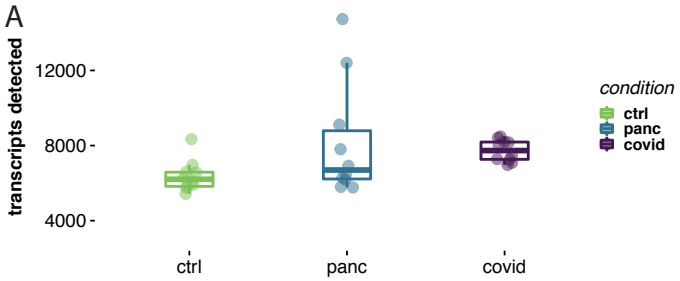
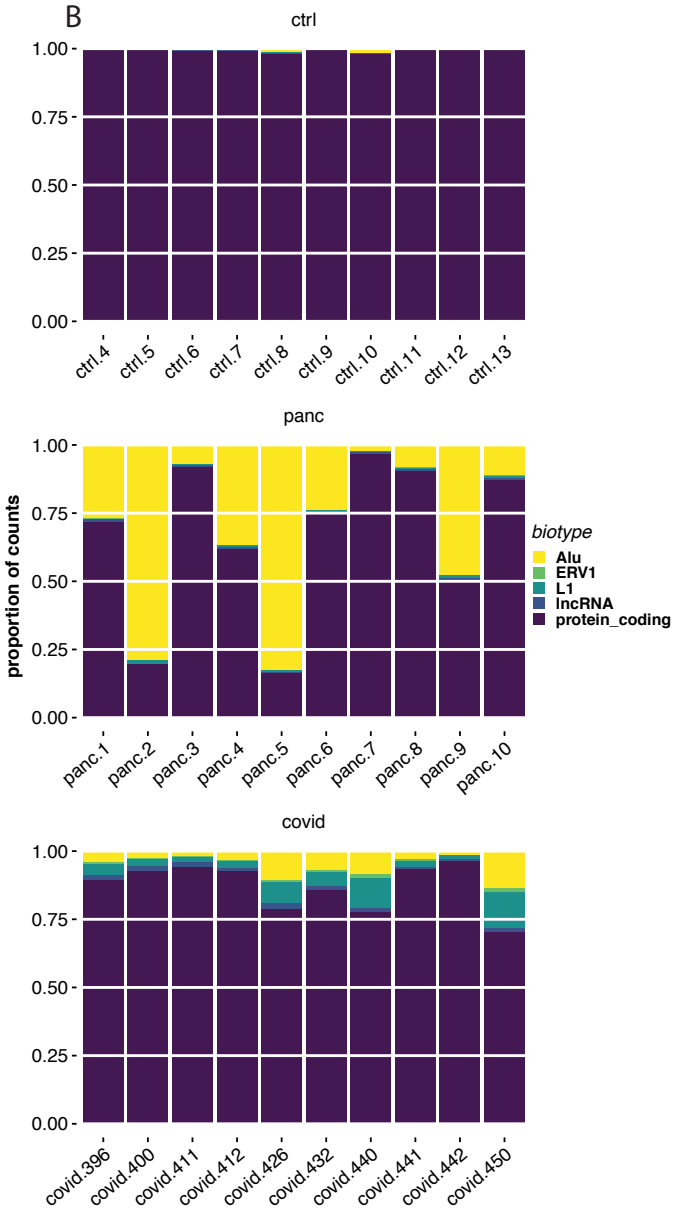
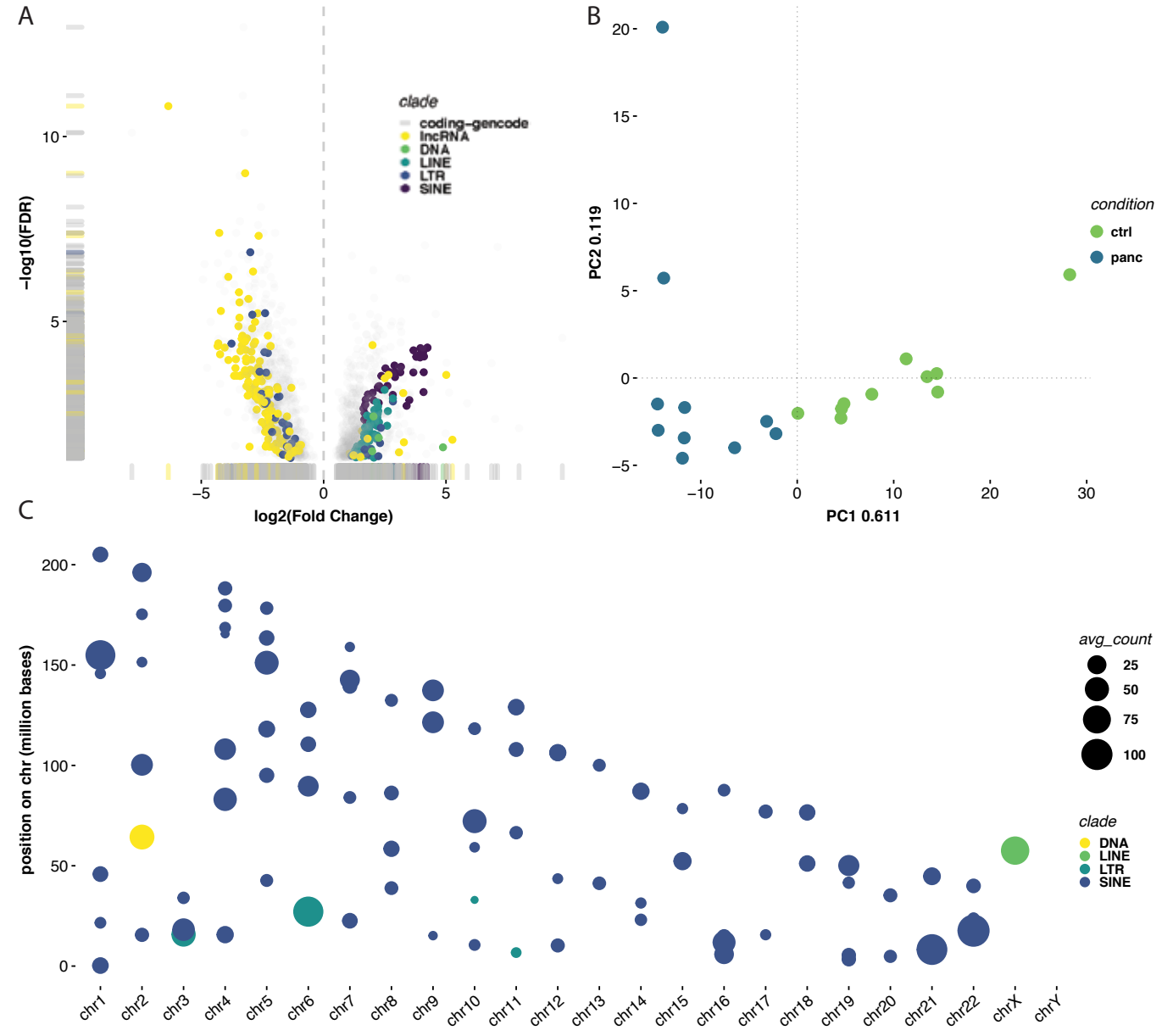
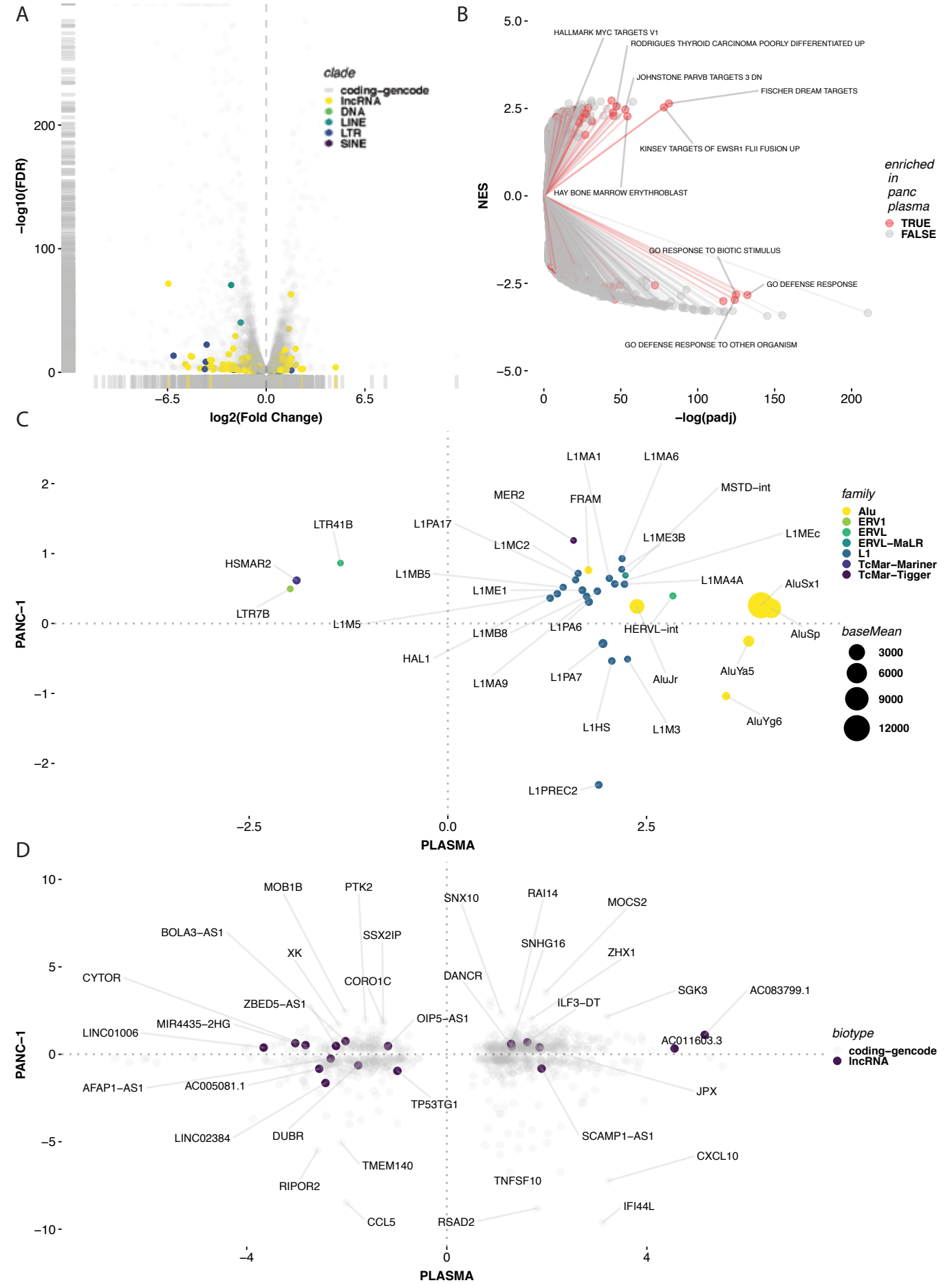
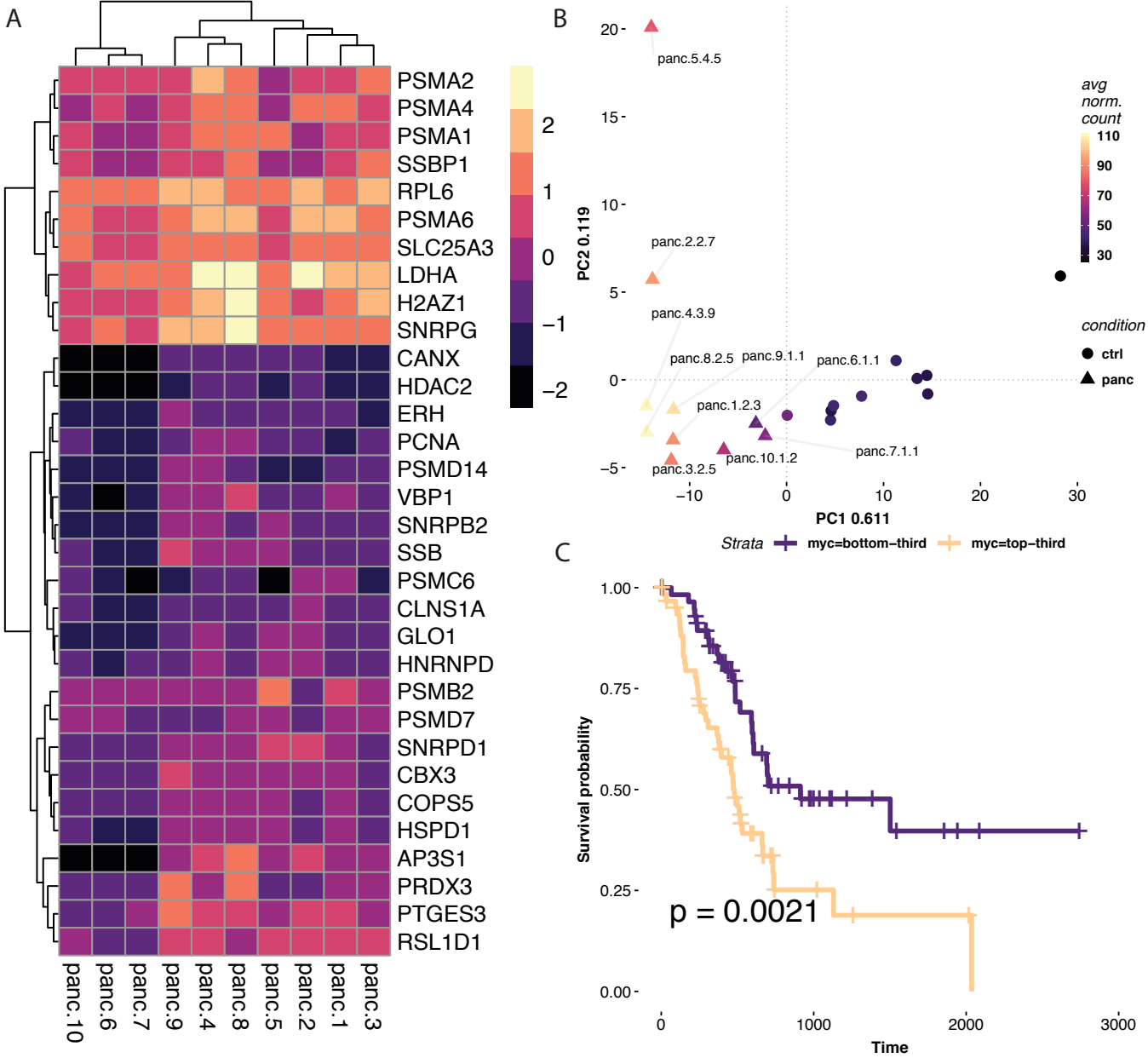

A
transcripts detected
12000
8000
4000
ctrl
panc
covid
condition
ctrl
panc
covid

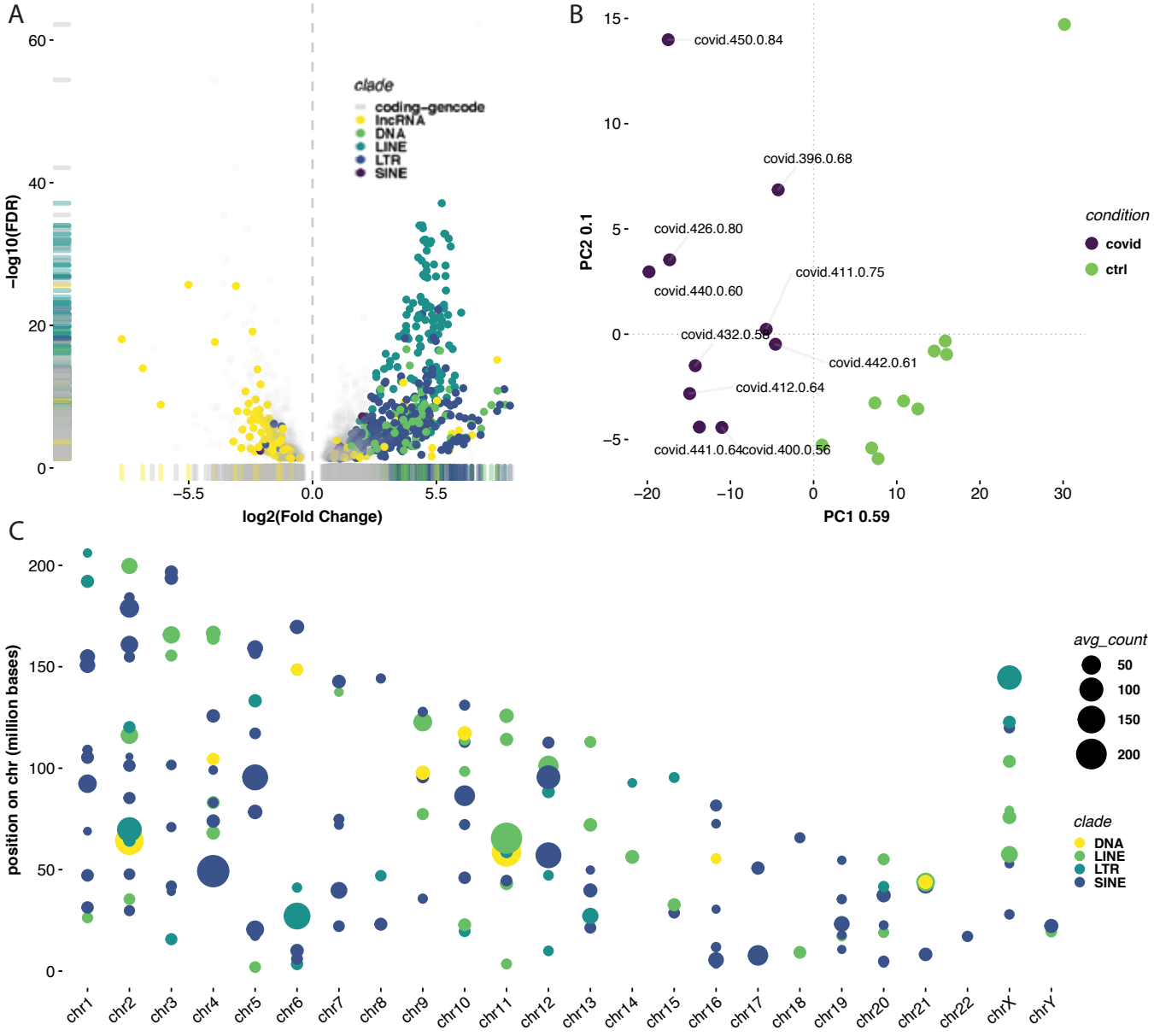

B
ctrl
1.00
0.75
0.50
0.25
0.00
ctrl.4
ctrl.5
ctrl.6
ctrl.7
ctrl.8
ctrl.9
ctrl.10
ctrl.11
ctrl.12
ctrl.13
panc
proportion of counts
panc.1
panc.2
panc.3
panc.4
panc.5
panc.6
panc.7
panc.8
panc.9
panc.10
biotype
Alu
ERV1
L1
lncRNA
protein_coding
covid
covid.396
covid.400
covid.411
covid.412
covid.426
covid.432
covid.440
covid.441
covid.442
covid.450

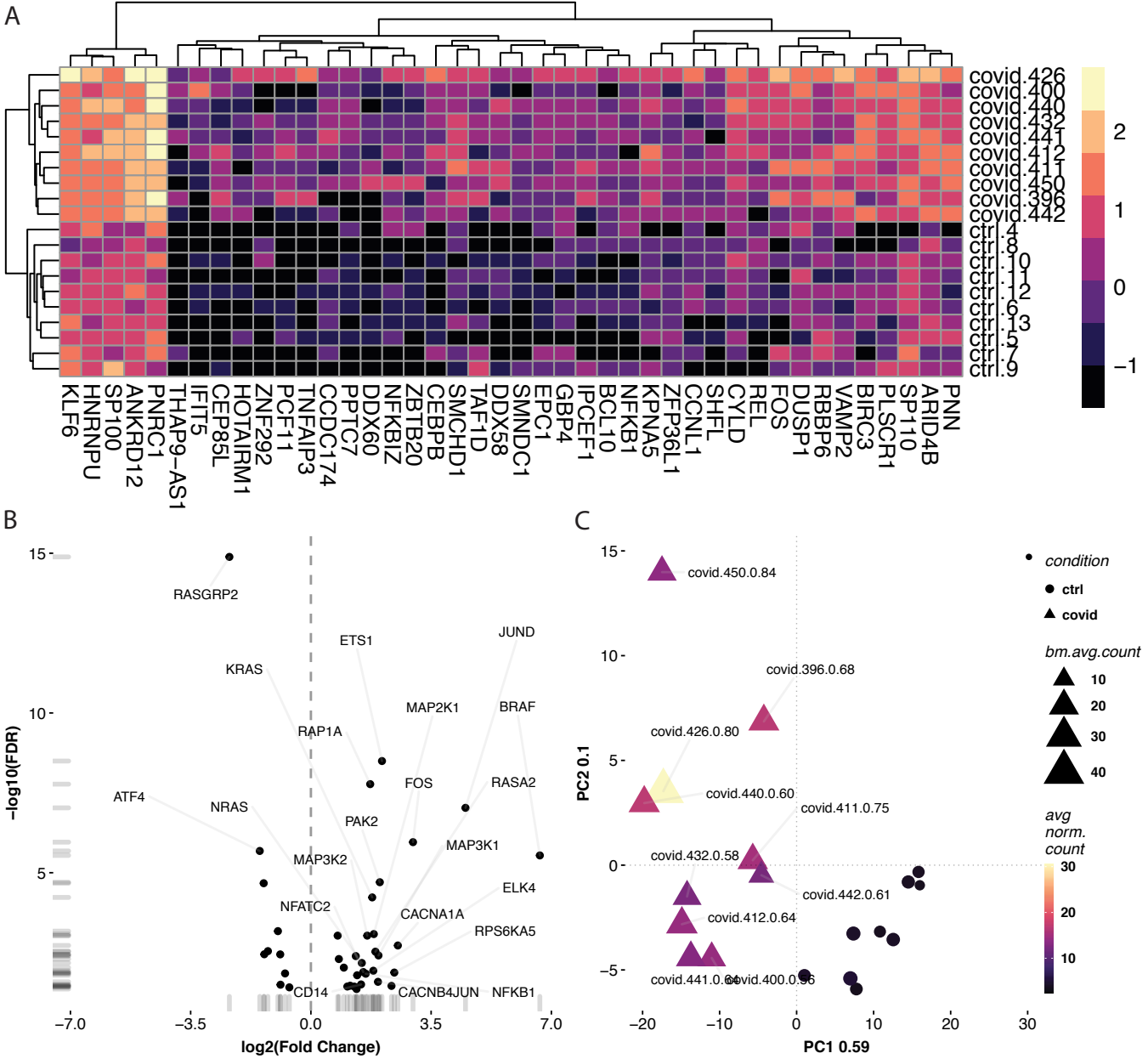
C


A
clade
coding-gencode
lncRNA
DNA
LINE
LTR
SINE
−log10(FDR)
log2(Fold Change)
B
condition
ctrl
panc
PC2 0.119
PC1 0.611
C
avg_count
25
50
75
100
clade
DNA
LINE
LTR
SINE
position on chr (million bases)
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY


A
clade
coding−gencode
lncRNA
DNA
LINE
LTR
SINE
−log10(FDR)
log2(Fold Change)
B
HALLMARK MYC TARGETS V1
RODRIGUES THYROID CARCINOMA POORLY DIFFERENTIATED UP
JOHNSTONE PARVB TARGETS 3 DN
FISCHER DREAM TARGETS
KINSEY TARGETS OF EWSR1 FLII FUSION UP
HAY BONE MARROW ERYTHROBLAST
GO RESPONSE TO BIOTIC STIMULUS
GO DEFENSE RESPONSE
GO DEFENSE RESPONSE TO OTHER ORGANISM
NES
−log(padj)
enriched in panc plasma
TRUE
FALSE
C
L1MA1
L1MA6
MSTD−int
MER2
FRAM
LTR41B
L1PA17
L1MC2
L1ME3B
L1MEc
HSMAR2
L1MB5
L1ME1
L1MA4A
AluSx1
LTR7B
L1M5
L1MB8
L1PA6
HERVL−int
AluSp
HAL1
L1MA9
L1PA7
AluJr
AluYa5
L1HS
L1M3
AluYg6
L1PREC2
PANC−1
PLASMA
family
Alu
ERV1
ERVL
ERVL−MaLR
L1
TcMar−Mariner
TcMar−Tigger
baseMean
3000
6000
9000
12000
D
MOB1B
PTK2
SNX10
RAI14
MOCS2
BOLA3−AS1
SSX2IP
XK
SNHG16
ZHX1
CYTOR
CORO1C
DANCR
SGK3
AC083799.1
ZBED5−AS1
ILF3−DT
MIR4435−2HG
OIP5−AS1
LINC01006
AC011603.3
AFAP1−AS1
AC005081.1
JPX
TP53TG1
LINC02384
DUBR
SCAMP1−AS1
CXCL10
TMEM140
RIPOR2
TNFSF10
IFI44L
CCL5
RSAD2
PANC−1
PLASMA
biotype
coding−gencode
lncRNA


A
PSMA2
PSMA4
PSMA1
SSBP1
RPL6
PSMA6
SLC25A3
LDHA
H2AZ1
SNRPG
CANX
HDAC2
ERH
PCNA
PSMD14
VBP1
SNRPB2
SSB
PSMC6
CLNS1A
GLO1
HNRNPD
PSMB2
PSMD7
SNRPD1
CBX3
COPS5
HSPD1
AP3S1
PRDX3
PTGES3
RSL1D1
panc.10
panc.6
panc.7
panc.9
panc.4
panc.8
panc.5
panc.2
panc.1
panc.3
2
1
0
−1
−2
B
PC2 0.119
PC1 0.611
avg norm. count
110
90
70
50
30
condition
ctrl
panc
panc.5.4.5
panc.2.2.7
panc.4.3.9
panc.8.2.5
panc.9.1.1
panc.6.1.1
panc.1.2.3
panc.10.1.2
panc.7.1.1
panc.3.2.5
Strata
myc=bottom−third
myc=top−third
C
Survival probability
Time
p = 0.0021


A
clade
coding_gencode
lncRNA
DNA
LINE
LTR
SINE
−log10(FDR)
log2(Fold Change)
B
covid.450.0.84
covid.396.0.68
covid.426.0.80
covid.411.0.75
covid.440.0.60
covid.432.0.58
covid.442.0.61
covid.412.0.64
covid.441.0.64
covid.400.0.56
condition
covid
ctrl
PC2 0.1
PC1 0.59
C
position on chr (million bases)
avg_count
50
100
150
200
clade
DNA
LINE
LTR
SINE
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY


A
covid.426
covid.400
covid.440
covid.432
covid.441
covid.412
covid.411
covid.450
covid.396
covid.442
ctr.4
ctr.8
ctr.10
ctr.11
ctr.12
ctr.6
ctr.13
ctr.5
ctr.7
ctr.9
KLF6
HNRNPU
SP100
ANKRD12
PNRC1
THAP9−AS1
IFIT5
CEP85L
HOTAIRM1
ZNF292
PCF11
TNFAIP3
CCDC174
PPTC7
DDX60
NFKBIZ
ZBTB20
CEBPB
SMCHD1
TAF1D
DDX58
SMNDC1
EPC1
GBP4
IPCEF1
BCL10
NFKB1
KPNA5
ZFP36L1
CCNL1
SHFL
CYLD
REL
FOS
DUSP1
RBBP6
VAMP2
BIRC3
PLSCR1
SP110
ARID4B
PNN
2
1
0
−1
B
−log10(FDR)
log2(Fold Change)
RASGRP2
ETS1
JUND
KRAS
MAP2K1
BRAF
RAP1A
FOS
RASA2
ATF4
NRAS
PAK2
MAP3K1
MAP3K2
ELK4
NFATC2
CACNA1A
RPS6KA5
CD14
CACNB4JUN
NFKB1
C
PC2 0.1
PC1 0.59
covid.450.0.84
covid.396.0.68
covid.426.0.80
covid.440.0.60
covid.411.0.75
covid.432.0.58
covid.442.0.61
covid.412.0.64
covid.441.0.64
covid.400.0.96
condition
ctrl
covid
bm.avg.count
10
20
30
40
avg norm. count
30
20
10