A
Total= 2816 variables
-Log10 P
Fold-change (log2)
SF3B1mut vs. SF3B1wt UM
ROMS
PRPF38A
RPS15A
CDK2
RPL4
ERGIC3
DRG2
DRG2
BRD9
SLC4A3
NOP58
PPP6R3
NACA
SNRPN
CC2D1A
ENOSF1
SH3D21
ATP8B2
FBXL19
DHX38
ERVK3-1
DNHD1
MYL6B
SH3D21
TCERG1
PUM3
GTSD1
NCLN
USP39
PLEKHA5
SUN1
ARRSD1
MICU3
PLXNC1
PLEKHA5
BRD9
ATXN2
BRD9
AP3D1
B
Total= 1843 variables
-Log10 P
Fold-change (log2)
SF3B1mut vs. SF3B1wt UM
TCGA-UVM
ERGIC3
VEGFB
CC2D1A
TESK1
FAR2
CC2D1A
PPP2R5A
NRSN2
POLR1E
NRSN2
RPL4
OAS1
BRD9
EIF4B
MPRIP
USP39
RABGAP1
ATP8B2
DDX27
USP39
SOAT1
PDCD4
DIP2A
PNKP
PNKP
PNKP
DDX42
ELP2
KTN1
DHX8
HDLBP
PNKP
ARMC9
TYW1
CTNNBL1
AC004475.1
PSMD1
AP1S3
BRD9
BRD9
Direction of gene expression
Down-regulated
Not significant
Up-regulated
Found significant DE in ROMS & TCGA-UVM
C
ROMS
Number of aberrations (log10)
1685
230
101
66
50
12
Other
Novel splicing aberration (Acceptor)
Novel splicing aberration (Donor)
SF3B1mut vs SF3B1wt
TCGA
2641
230
374
66
110
12
Differential in ROMS & TCGA
No
Yes