CopyNumberAttenuation GeneExpressionCorrelation CopyNumberInstability ploidy mutational burden growth size RepsCorrelation CDH1 prot VIM_prot CDH1_gexp VIM_gexp D/F12 sanger_Adherent sanger_Semi-Adherent sanger_Suspension sanger_Unknown broad_Adherent broad Mixed

F2

F3

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-0.000 -

 $F37 \\ -0.000 \\ -0.000 \\ -0.1 \\ -0.000 \\ -0.000 \\ -0.1 \\ -0.000 \\ \phantom{+$

-0.000 -

-0.000.00 -0.000.00 -0.000.00 -0.100 -

 $0.0 - 0.0 \ 0.0 \ 0.0 - 0.0 - 0.0 \ 0.0 - 0.0 - 0.0 \ 0.0 - 0.0 \ 0.0 - 0.0 \ 0.0$

0.0 0.0 0.2 0.1 0.0 0.3 proteomics ngresponse

crisprcas9

0.1 0.1 0.7 0.9 0.1 0.2

0.1 0.2 0.2 0.4 0.4 0.6

1.1 0.1 0.0 0.3 0.1 0.2

0.1 0.0 0.0 0.0 0.2 1.5

0.0 0.0 1.3 0.2 0.2 0.1

0.2 0.1 0.2 0.6 0.2 0.4

01 02 03 02 03 06

08 00 04 02 01 02

0.9 0.0 0.4 0.3 0.0 0.1

01 00 00 01 00 14

01 01 01 03 04 05

00 01 01 00 07 05

0.0 0.1 0.2 0.7 0.2 0.3

0.0 0.0 0.0 1.0 0.1 0.2

00 01 01 02 04 04

00 01 00 00 03 05

0.2 0.0 0.0 0.0 0.0 0.7