F49 CopyNumberAttenuation GeneExpressionCorrelation CopyNumberInstability ploidy mutational burden growth size RepsCorrelation CDH1 prot VIM prot CDH1 gexp VIM\_gexp D/F12

F2

F3

F5

F6

E7

F8

FQ

E11

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F14

F15

F17

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-0.000 - 0.102 - 0.3 - 0.1 - 0.103 - 0.0 - 0.000 - 0.0 - 0.000 - 0.0 -sanger Adherent sanger\_Semi-Adherent sanger Suspension sanger\_Unknown broad Adherent broad Mixed broad\_Suspension broad Unknown MeanProteomics MeanMethylation 0.000 MeanDrugResponse 

 $-0.0-0.0 \times 0.0 \times$ 

 $\frac{1}{2}$ 

0.1 -0.0 -0.2 -0.1 -0.1 0.0 0.0 0.0 -0.1 -0.0 0.1 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.2 -0.0 0.0 -0.1 -0.1 0.0 0.0 0.1 -0.1 0.0 0.0 0.1 -0.0 0.0 0.0 -0.1 -0.0 0.0 0.0 -0.1 -0.0 0.0 0.0 -0.1 -0.0 -0.1 -0.0 -0.1 -0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.0 0.1 -0.0 0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.1 -0.0 0.0 0.0 0.1 -0.0 0.0

 $-0.000 \cdot 0.1 \cdot 0.0 \cdot 0.0 \cdot 0.1 \cdot 0.1 \cdot 0.0 \cdot 0$ 

0.0 0.0 0.2 0.1 0.0 0.3 proteomics enodsaubn. ranscriptomics

crisprcas9

11 01 00 03 01 02

0.1 0.0 0.0 0.0 0.2 1.5

0.0 0.0 1.3 0.2 0.2 0.1

02 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