F32 F33 F34 F36 F37 F38 F40 F42 F43 F44 F45

F46

F47

F48

F49

ploidy

growth

size

CopyNumberAttenuation

CopyNumberInstability

mutational burden

RepsCorrelation

sanger Adherent

sanger\_Unknown broad Adherent

broad\_Suspension

broad Unknown

MeanProteomics

MeanMethylation

broad Mixed

sanger\_Semi-Adherent sanger Suspension

CDH1 prot

VIM prot CDH1 gexp VIM\_gexp D/F12

GeneExpressionCorrelation

E3

F5

F6

F13

F14

F15

F17

F18

F19

F21

F22

F25

F26

F27

F28

F29

F30

-0.001 0.1 -0.0 0.1 0.0 -0.2 0.1 -0.1 0.1 -0.0 0.1 0.0 -0.2 0.1 -0.1 0.1 -0.0 0.1 0.0 -0.0 -0.1 0.0 -0 -0.0-0.000-0.0-0.0000-0.001 - 0.000 - 0.1 - 0.0 - 0.1 - 0.0 - 0.1 - 0.0 - 0.1 - 0.0 - 0.1 - 0.0 - 0.1 - 0.0 - 0.1 - 0.1 - 0.1 - 0.1 - 0.1 - 0.0 - 0.0 - 0.1 - 0.2 - 0.0 - 0.0 - 0.1 - 0.1 - 0.1 - 0.1 - 0.1 - 0.1 - 0.1 - 0.0 - 0.0 - 0.1 -

-0.000 - 0.000 = 0.000 - 0.100 = 0.100 = 0.100 = 0.100 = 0.000 - 0.000 = 0.0

-0.1-0.1 0.1 0.1 -0.0 -0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.0 -0.0 0.0 -0.1 0.0 0.1 0

0.1 -0.0 0.0 -0.1 -0.1 0.0 0.1 0.0 0.1 0.0 0.0 0.2 0.0 -0.0 -0.0 0.0 1.0 3 -0.0 0.0 0.0 0.1 0.0 -0.1 0.0 0.0 -0.0 1.0 0.0 -0.0 1.0 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 0.2 0.0 -0.0 0.1 0.2 0.0 -0.0 0.1 0.0 -0.0 0.1

proteomics ngresponse ranscriptomics

0.1 0.3 0.1 0.7 0.4 0.7

1.7 0.0 0.0 0.0 0.3 0.0

1.2 0.0 0.0 0.0 0.6 0.1

0.1 0.1 0.7 0.9 0.1 0.2

0.1 0.2 0.2 0.4 0.4 0.6

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

0.0 0.0 0.2 0.1 0.0 0.3

crisprcas9

MeanDrugResponse 0.1 0.3 0.0 0.2 0.3 -0.1 0.2 0.0 -0.1 0.3 0.4 -0.1 0.1 0.1 0.1 0.4 0.1 0.1 0.1 0.1 0.2 0.1 0.1 0.2 0.2 0.2 0.2 0.4 -0.4 0.6 0.0 0.1 0.2 0.3 -0.3 0.3 0.2 0.0 0.3 0.6 -0.1 0.1 0.0 0.2 0.2 -0.1 0.1 -0.0 0.0 1 0.0