F42 F43 F44 F45 F46  $\mathsf{F47} \quad 0.0 \cdot 0$ F48 F49 

F2

F3

F5

F6

FQ

F13

F14

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0.0 0.0 0.2 0.1 0.0 0.3 proteomics crisprcas9 ngresponse metabolomics methylatior ranscriptomics

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

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

0.1 0.0 0.0 0.1 0.0 1.4

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

CopyNumberAttenuation GeneExpressionCorrelation CopyNumberInstability ploidy mutational burden growth  $0.0 \\ -0.2 \\ -0.3 \\ -0.1 \\ -0.1 \\ -0.1 \\ -0.1 \\ -0.1 \\ -0.0 \\ -0.2 \\ -0.2 \\ -0.0 \\ -0.1 \\ -0.1 \\ -0.1 \\ -0.1 \\ -0.1 \\ -0.1 \\ -0.1 \\ -0.1 \\ -0.2 \\ -0.2 \\ -0.1 \\ -0.2 \\ -0.2 \\ -0.1 \\ -0.2 \\ -0.2 \\ -0.2 \\ -0.2 \\ -0.2 \\ -0.1 \\$ size 02 02 0.1 0.4 0.2 0.3 0.0 0.3 0.4 0.3 0.0 0.2 0.1 0.2 0.0 0.2 0.1 0.2 0.0 0.1 0.4 0.4 0.2 0.1 0.1 0.1 0.3 0.0 0.2 0.3 0.0 0.2 0.3 0.0 0.2 0.0 0.4 0.3 0.1 0.2 0.1 0.1 0.2 0.2 0.0 0.3 0.1 0.4 0.3 0.0 0.2 0.1 0.1 0.1 0.1 0.1 RepsCorrelation 0 (44.77) 0 (43.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (10 (47.223.12) 20 (47.2233.12) 20 (47.2233.12) 20 (47.2233.12) 20 (47.2233.12) 20 (47.2 CDH1 prot VIM\_prot CDH1\_gexp VIM\_gexp D/F12 sanger\_Adherent sanger\_Semi-Adherent sanger\_Suspension 03-05-04-04-03-06 0.1 03-05-03-0.1 05-0.1 03-02-0.1 07-06-04-0.1-02-0.1-03-01-04-05-0.1-02-0.0 05-05-0.1-03-0.0 05-0.1-0.1-04-0.4-0.1-04-0.2 07705-0.0 -03-0.1-04-0.3-0.1-02-0.1-02-0.0 05-05-0.1-03-0.0 05-0.1-03-0.0 02-0.0 02-0.1-02-0.1-02-0.1-02-0.1-02-0.1-02-0.0 02-0.0 02-0.1-02-0 sanger\_Unknown broad\_Adherent 0204 03 03 02 04 0.1 03 05 03 0.0 04 0.1 03 05 03 0.0 04 0.1 02 0.1 0.1 06 05 03 0.0 02 0.1 02 0.0 03 04 0.0 02 0.0 05 05 0.0 0.2 0.1 04 0.2 0.0 05 05 0.0 02 0.1 04 0.2 0.0 broad Mixed broad Suspension broad Unknown Mean Proteomics MeanMethylation -0.2 0.5 0.4 0.4 0.3 0.5 -0.0 MeanDrugResponse 0.1 -0.4 -0.3 -0.3 -0.2 -0.4 0.0 0.4 -0.1 -0.1 -0.0 0.3 0.2 0.3 0.0 0.2 -0.3 0.1 0.3 -0.1 -0.3 -0.2 -0.4 0.4 0.2 -0.3 0.2 -0.3 0.4 -0.0 0.3 0.1 -0.2 -0.1 0.1 -0.1 0.3 0.3 0.3 -0.0 0.3 -0.0 -0.3 -0.0 -0.1 -0.2 -0.1 -0.1 0.2 0.1 drug responses

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

-0.0-0.00-0.0

0.1 + 0.0