F26 -0.01 - 0.00 - 0.101 - 0.000 - 0.001 - 0.101 - 0.000 - 0.101 - 0.000 - 0.101 - 0.000 - 0.101F27 F28 F29 F30 F31 F32 F33 F34 F35 -0.0-0.000F36 

-0.0-0.100 0.0 -0.001 0.0 -0.000 0.0 -0.000 0.1 0.1 -0.000 0.0 -0.100 0.0 -0.000

0.0 - 0.0

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 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

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

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

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 broad Suspension broad Unknown Mean Proteomics MeanMethylation

F2

F3

F5

F6

F8

F13

F14

F15

F17

F18

F19

F21

F22

E41

F42

F43

F44

F45

F46

F47

F48

F49

