Correlation (pearson's r)
Variance explained
F1 F2 F3 F4 F5 F6 F7 F8 F9 F10 F11 F12 F13 F14 F15 F16 F17 F18 F19 F20 F21 F22 F23 F24 F25 F26 F27 F28 F29 F30 F31 F32 F33 F34 F35 F36 F37 F38 F39 F40 F41 F42 F43 F44 F45 F46 F47 F48 F49
1.3 14.8 9.8 9.8 9.7 11.0
0.9 1.0 1.2 9.5 3.3 8.2
0.9 2.7 4.1 2.6 5.2 6.3
0.0 16.9 0.0 0.0 0.3 0.2
0.0 0.0 0.0 0.0 15.2 0.0
0.1 0.0 0.0 6.4 0.1 0.4
0.5 1.0 0.7 1.5 1.3 2.0
0.4 1.4 0.5 1.1 1.2 1.9
4.8 0.1 0.2 0.1 0.1 0.2
0.2 0.9 0.8 0.8 1.4 1.3
0.0 0.1 0.1 4.5 0.1 0.4
0.0 0.1 0.2 4.3 0.2 0.4
0.0 0.0 0.0 0.0 0.0 5.1
0.2 0.7 0.6 1.1 0.8 1.3
0.1 0.7 0.8 1.2 0.6 1.3
1.2 1.6 0.6 0.2 0.3 0.3
0.1 0.5 0.5 0.9 0.7 1.2
0.2 0.5 0.3 1.1 0.4 1.2
0.2 0.5 0.5 0.8 0.6 1.1
3.0 0.0 0.2 0.1 0.0 0.1
0.1 0.3 0.6 0.1 1.1 0.7
0.2 0.3 0.3 0.4 0.9 0.8
0.1 0.3 0.2 0.8 0.4 0.6
0.0 0.7 0.1 0.0 1.3 0.4
2.2 0.0 0.1 0.1 0.0 0.1
0.2 0.5 0.1 0.7 0.3 0.6
0.2 0.2 0.3 0.4 0.5 0.7
0.1 0.1 0.2 0.8 0.3 0.7
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
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
0.1 0.2 0.3 0.2 0.3 0.6
0.8 0.0 0.4 0.2 0.1 0.2
0.9 0.0 0.4 0.3 0.0 0.1
0.1 0.0 0.0 0.1 0.0 1.4
0.1 0.1 0.1 0.3 0.4 0.5
0.0 0.1 0.1 0.0 0.7 0.5
0.0 0.1 0.2 0.7 0.2 0.3
0.0 0.0 0.0 1.0 0.1 0.2
0.0 0.1 0.1 0.2 0.4 0.4
0.0 0.1 0.0 0.0 0.3 0.5
0.2 0.0 0.0 0.0 0.0 0.7
0.0 0.0 0.2 0.1 0.0 0.3
CopNumberAttenuation
GeneExpressionCorrelation
CopNumberInstability
ploidy
mutational_burden
growth
size
RepsCorrelation
CDH1_prot
VIM_prot
D/F12
R
sanger_Adherent
sanger_Semi-Adherent
sanger_Suspension
sanger_Unknown
broad_Adherent
broad_Mixed
broad_Suspension
broad_Unknown
MeanProteomics
MeanDrugResponse
drug_responses
crispcas9
drugresponse
metabolomics
methylation
proteomics
transcriptomics
L1 L2 L3 L4 L5 L6 L7 L8 L9 L10 L11 L12 L13 L14 L15 L16 L17 L18 L19 L20 L21 L22 L23 L24 L25 L26 L27 L28 L29 L30 L31 L32 L33 L34 L35 L36 L37 L38 L39 L40 L41 L42 L43 L44 L45 L46 L47 L48 L49 L50
Covariates correlation