Correlation (pearson's r)   Variance explained

Rows: F1–F49

Bottom covariate rows:
CopyNumberAttenuation, GeneExpressionCorrelation, CopyNumberInstability, ploidy, mutational_burden, growth, size, RepsCorrelation, CDH1_prot, VIM_prot, CDH1_gexp, VIM_gexp, D/F12, R, sanger_Adherent, sanger_Semi-Adherent, sanger_Suspension, sanger_Unknown, broad_Adherent, broad_Mixed, broad_Suspension, broad_Unknown, MeanProteomics, MeanMethylation, MeanDrugResponse, drug_responses

Variance explained columns: crisprcas9, drugresponse, metabolomics, methylation, proteomics, transcriptomics

Covariates correlation (x-axis): L1–L50