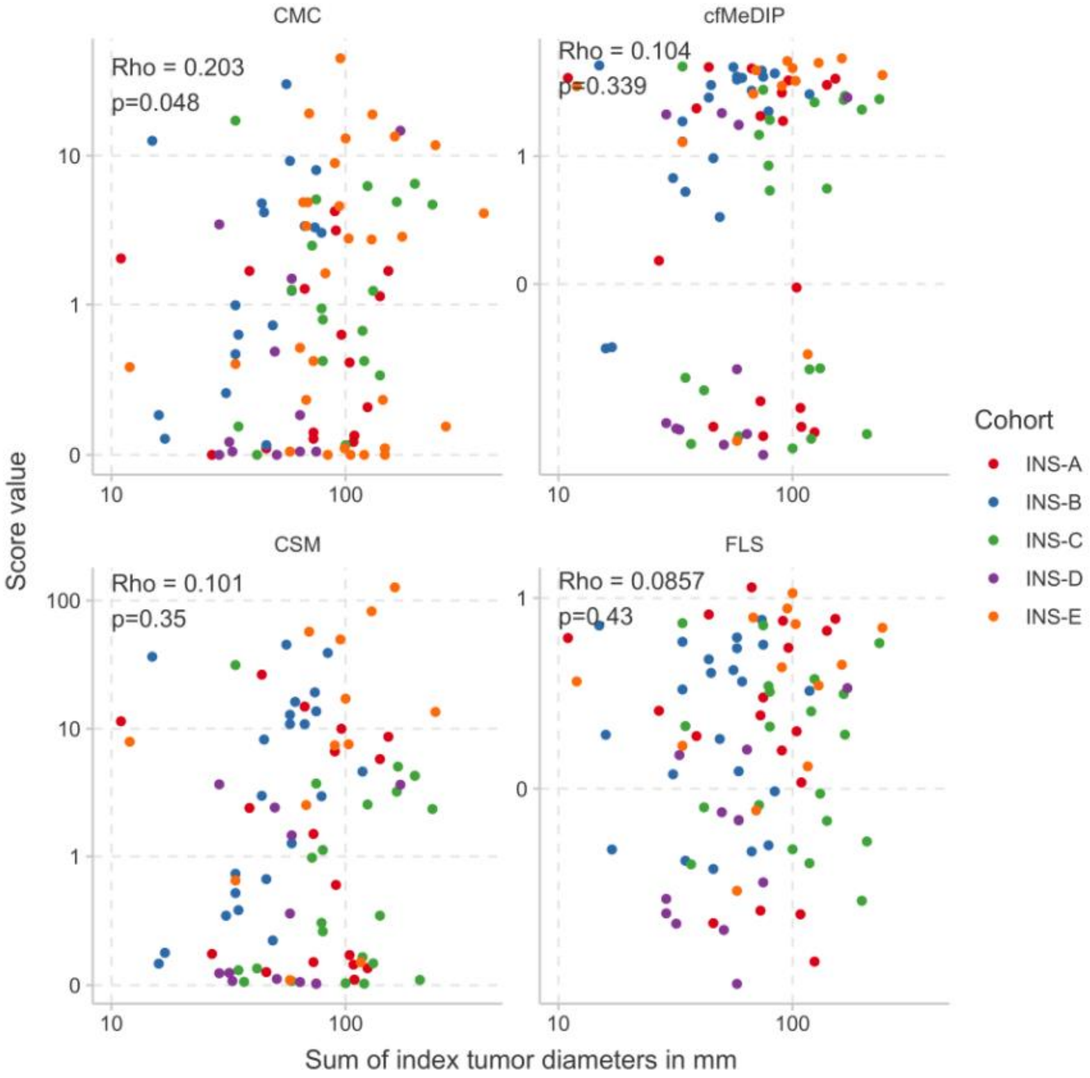
Supplementary Figure 7



Supplementary Figure 7. Association of tumor burden with cancer mutation concentration (CMC), as well as cancer-specific methylation (CSM) and fragment length score (FLS). We computed CMC from personalized tumor-informed mutation arrays. We also computed CSM and FLS from methylation and fragmentomic analysis respectively of data from cell-free methylated DNA immunoprecipitation and sequencing (cfMeDIP-seq) assays. Coefficients and p-values were computed using Spearman correlations.