Identify publicly gene expression studies curated in BSCE (e.g., search for 'coronavirus studies)

Categorize experimental design for logical aggregate analyses (e.g, infected vs control, animal studies, etc)

Perform QC and visualization : Cluster & PCA analyses

Run aggregate analyses using BSCE Meta-Analysis app for normalized, rank based prioritization of biomarkers

Generate Meta-Signatures: using bioset-specific normalized gene scores modified with fold change directionality, sum and take mean

Perform compound analysis with BSCE Pharmaco Atlas: Identify candidate compounds with potential to reverse dysregulated RNA expression patterns

Perform gene network analysis using String

Perform Functional Enrichment in BSCE, GSEA, or Reactome: functionally related gene set analysis to prioritize and distinguish biological activities

Perform gene perturbation analysis with BSCE Knockdown Atlas: identify candidate genes with potential to reverse dysregulated RNA expression patterns

Analyze/Validate with published nonRNA expression data ??

Generate novel *in silico* insights for further refinement and experimentation