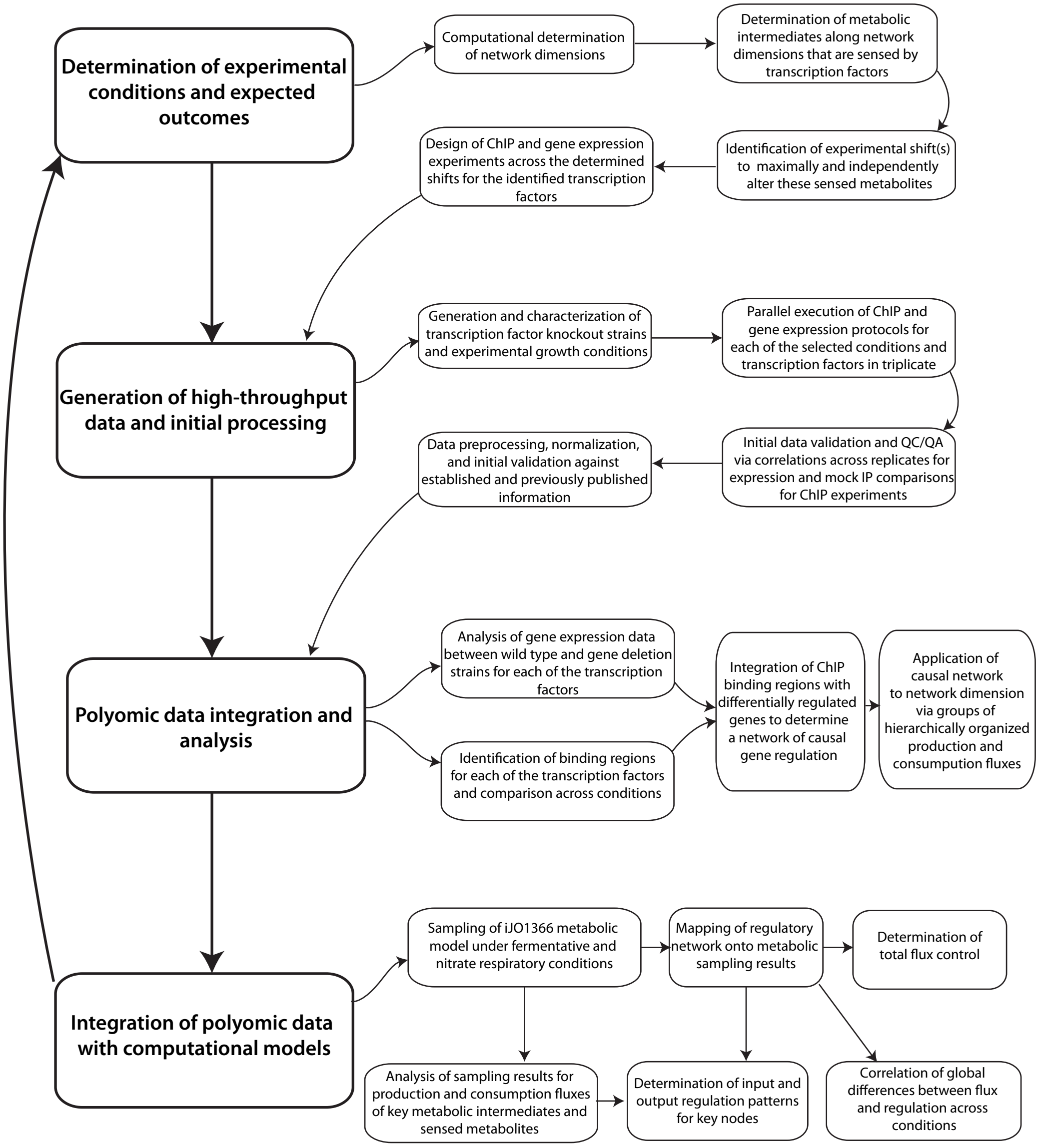
Determination of experimental conditions and expected outcomes
Computational determination of network dimensions
Determination of metabolic intermediates along network dimensions that are sensed by transcription factors
Identification of experimental shift(s) to maximally and independently alter these sensed metabolites
Design of ChIP and gene expression experiments across the determined shifts for the identified transcription factors
Generation of high-throughput data and initial processing
Generation and characterization of transcription factor knockout strains and experimental growth conditions
Parallel execution of ChIP and gene expression protocols for each of the selected conditions and transcription factors in triplicate
Initial data validation and QC/QA via correlations across replicates for expression and mock IP comparisons for ChIP experiments
Data preprocessing, normalization, and initial validation against established and previously published information
Polyomic data integration and analysis
Analysis of gene expression data between wild type and gene deletion strains for each of the transcription factors
Identification of binding regions for each of the transcription factors and comparison across conditions
Integration of ChIP binding regions with differentially regulated genes to determine a network of causal gene regulation
Application of causal network to network dimension via groups of hierarchically organized production and consumption fluxes
Integration of polyomic data with computational models
Sampling of iJO1366 metabolic model under fermentative and nitrate respiratory conditions
Mapping of regulatory network onto metabolic sampling results
Determination of total flux control
Analysis of sampling results for production and consumption fluxes of key metabolic intermediates and sensed metabolites
Determination of input and output regulation patterns for key nodes
Correlation of global differences between flux and regulation across conditions