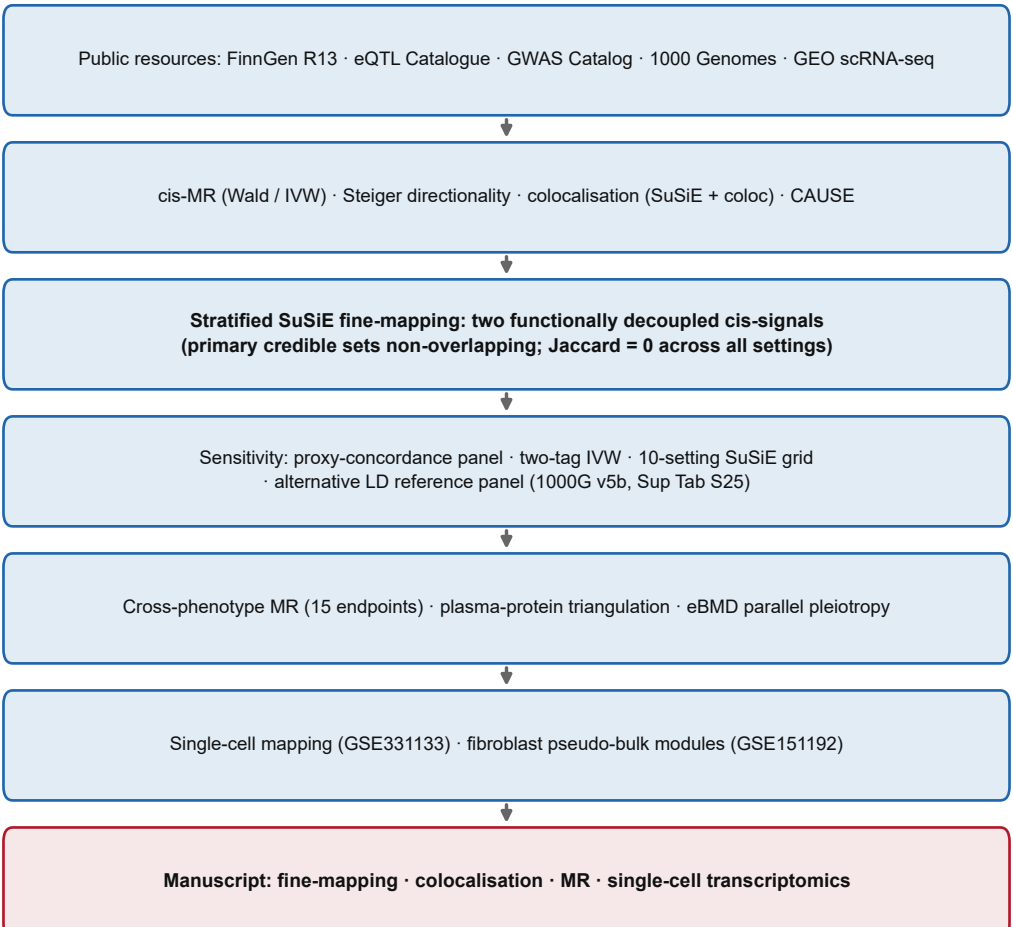
Primary analysis pipeline

— the statistical-inference chain reported in the manuscript



Reserve analyses (Hi-C chromatin looping, stratified LDSC, cross-tissue eQTL panel) were pre-computed for exploratory purposes only; none enters the main inference chain or any claim in the manuscript, and they are therefore not shown in this pipeline diagram.