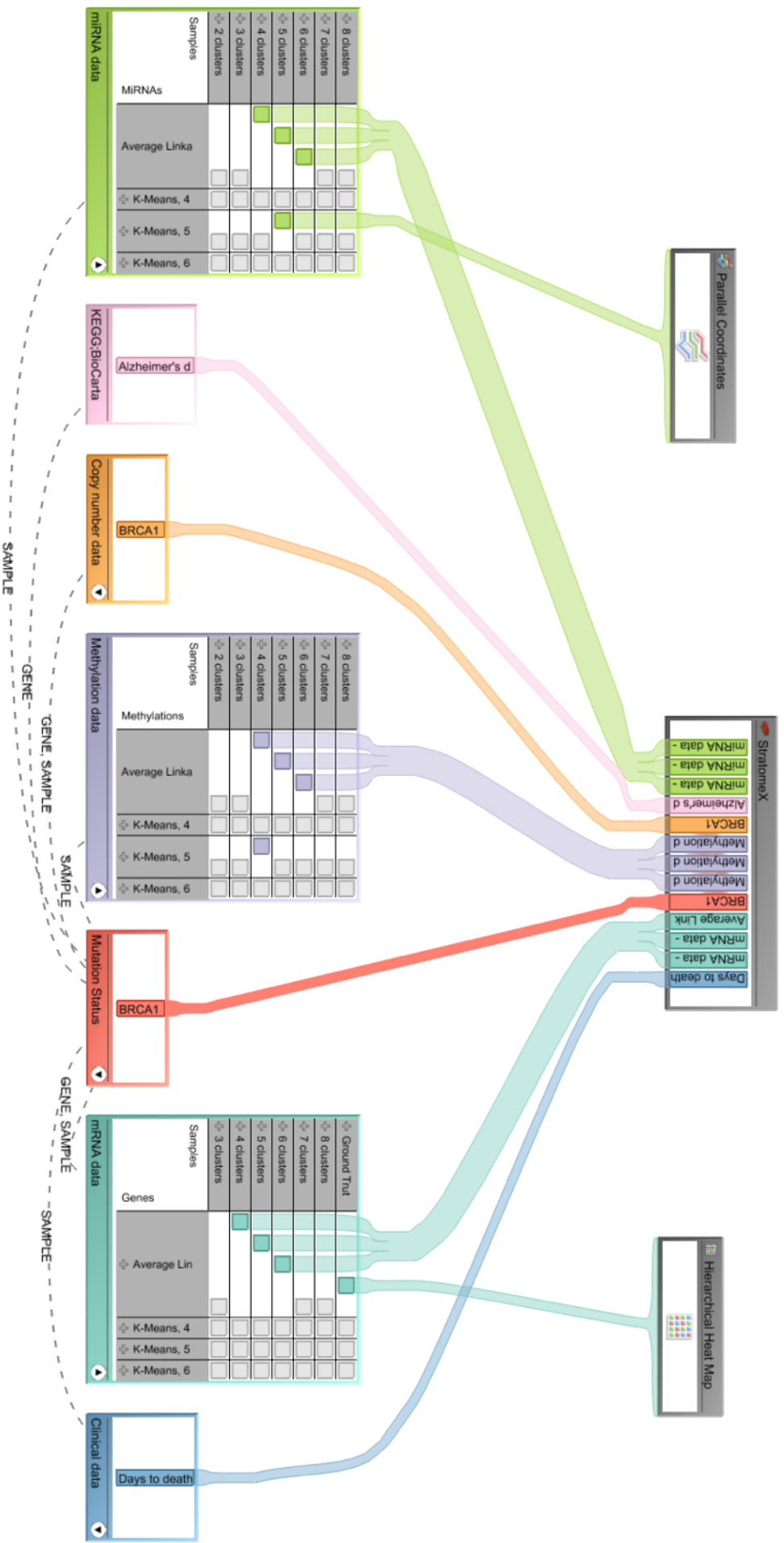
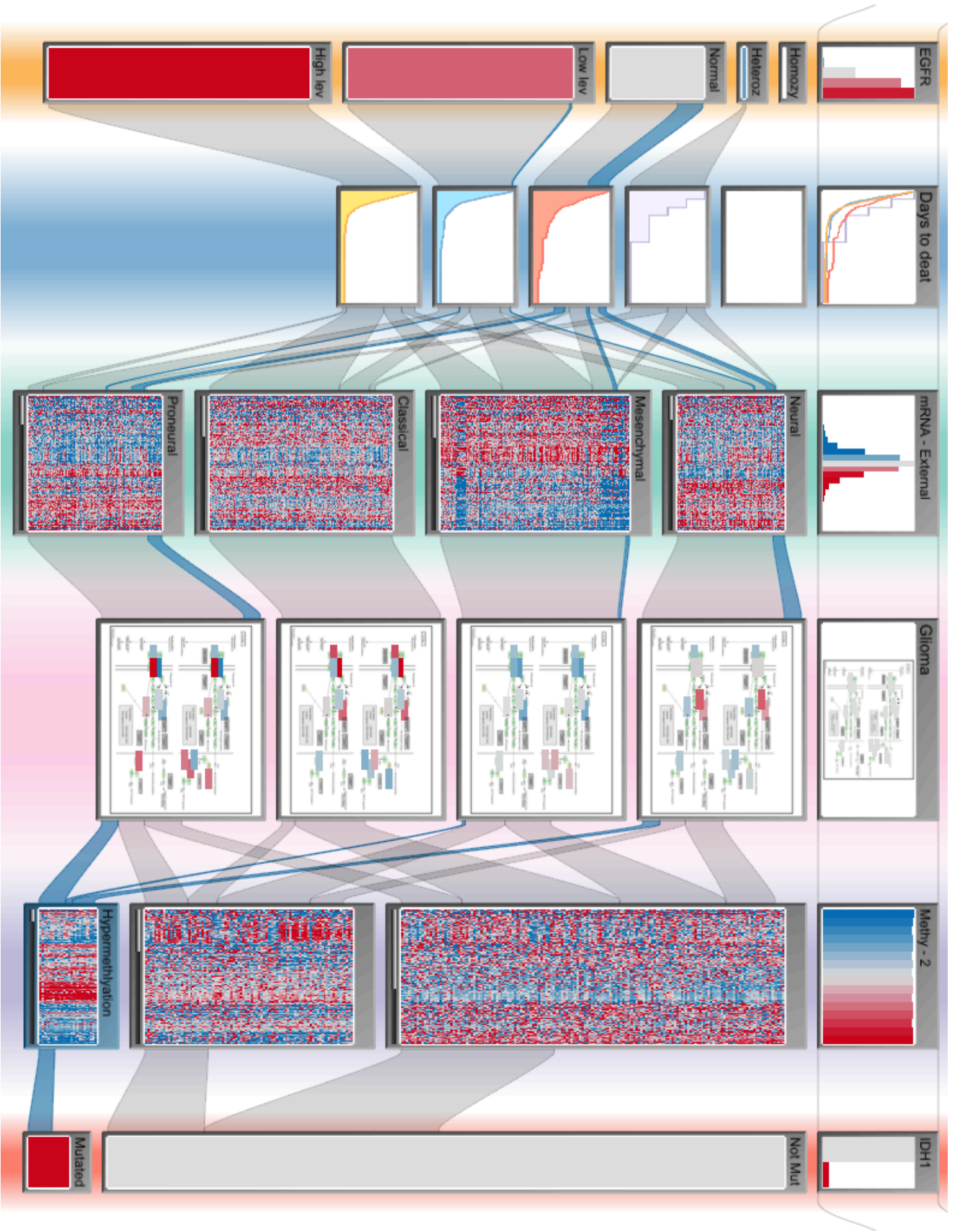


# STRATOOMEX

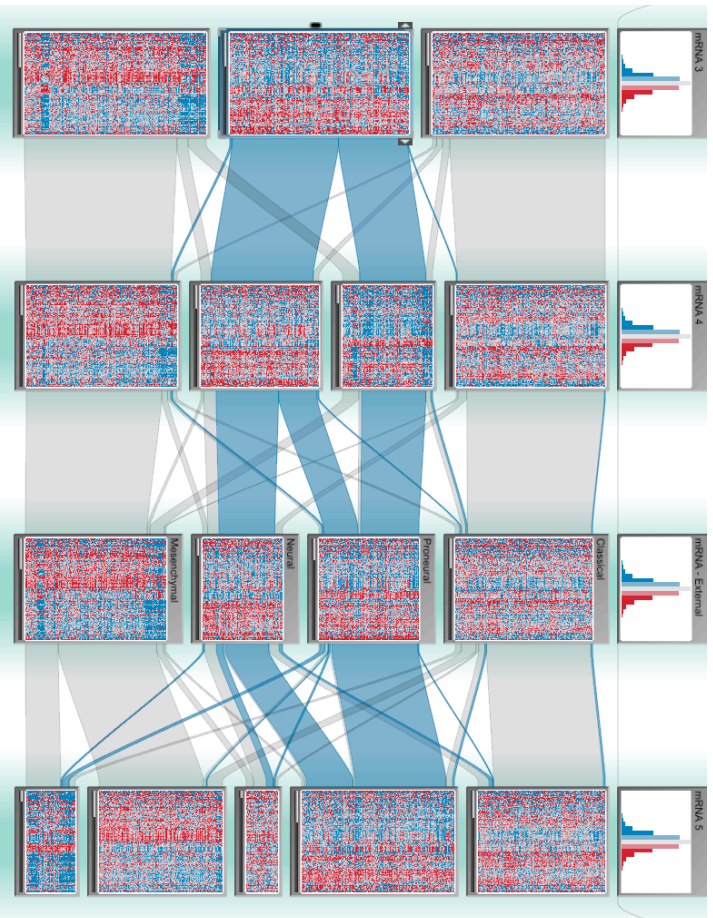




# INTEGRATIVE VISUALIZATION OF TUMOR SUBTYPES IN CANCER GENOMICS DATA SETS

Identification and characterization of cancer subtypes is an important area of research that is based on the integrated analysis of multiple heterogeneous genomics data sets. Since there are no tools supporting this process, much of this work is done using ad-hoc scripts and static plots, which is inefficient and limits visual exploration of the data. To address this, we have developed *StratomeX*, an integrative visualization tool that allows investigators to explore the relationships of candidate subtypes across multiple genomic data types such as gene expression, DNA methylation, or copy number data. *StratomeX* represents data sets as columns and subtypes as blocks in these columns. Ribbons between the columns connect blocks to show subtype relationships across data sets. Drill-down features enable detailed

exploration. *StratomeX* provides insights into the functional and clinical implications of candidate subtypes by employing small multiples, which allow investigators to assess the effect of subtypes on molecular pathways or outcomes such as patient survival. As the configuration of viewing parameters in such a multi-data set, multi-view scenario is complex, we propose a meta visualization and configuration interface for data set dependencies and data-view relations. *StratomeX* is developed in close collaboration with domain experts. We describe case studies that illustrate how investigators used the tool to explore subtypes in large data sets and demonstrate how they efficiently replicated findings from the literature and gained new insights into the data.



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