Supplementary material for: Using Multi-omic Cancer Data to Find Ways to Improve the Treatment of Bladder Cancer

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S1   Heatmaps

The heatmaps for GE, CNV and METH are presented in §2.4. The dendgrograms are generated using the BHC algorithm with the data of the relevant dataset.

Heatmaps for all three datasets with the superimposition of the patients dendrogram from a different dataset are presented in Figure S1. This has been done to check the existence of structure emerging from the data with a particular clustering of the patients.

S2   Enrichment Maps

The enrichment maps for the clusters of genes from each dataset that contribute to the different survival prognosis of the PCs are presented in Figures from S2 to S6. The node marker size signifies the number of genes in a pathway and the thickness of the edges denotes the Jaccard similarity between two pathways.

S3   Multiple Dataset Integration

The heatmaps have been constructed by superimposing the dendgrogram obtained with the MDI procedure from §3.7. The heatmap of CNV is presented in Figure S7 and the one of GE in Figure S8 whereas the heatmap for the METH dataset is presented in the report.
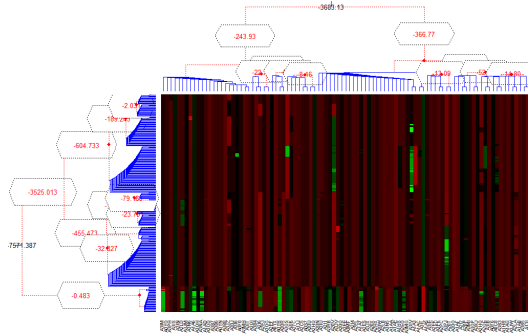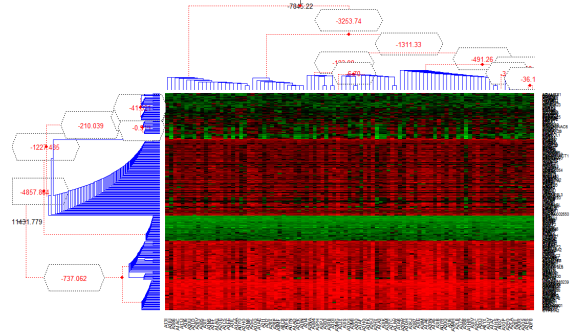
(a) Heatmap of CNV where the clustering of patients has been obtained from the GE dataset
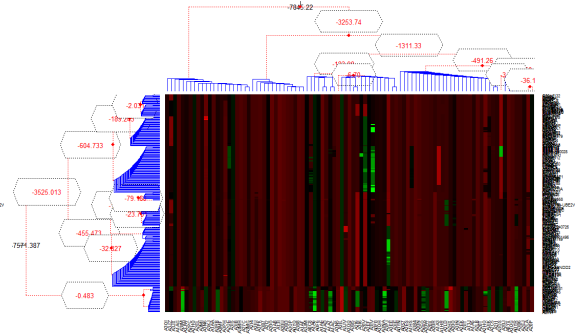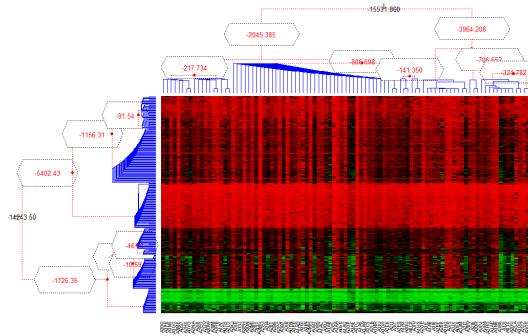
(b) Heatmap of CNV where the clustering of patients has been obtained from the METH dataset
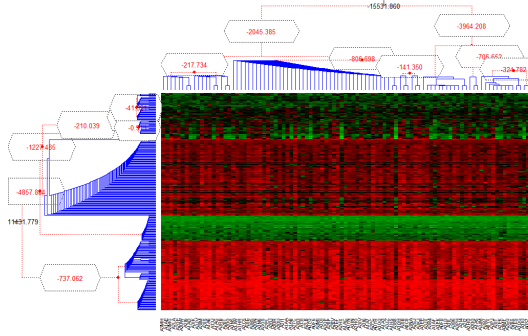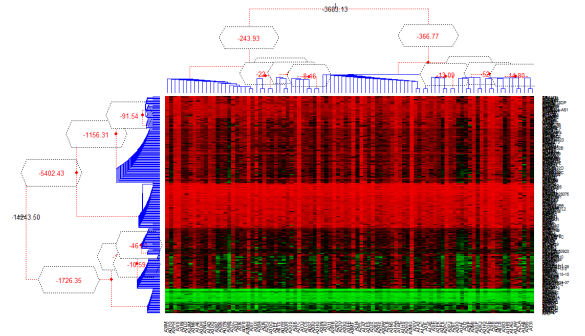
(c) Heatmap of GE where the clustering of patients has been obtained from the CNV dataset

(d) Heatmap of GE where the clustering of patients has been obtained from the METH dataset

(e) Heatmap of METH where the clustering of patients has been obtained from the CNV dataset

(f) Heatmap of METH where the clustering of patients has been obtained from the GE dataset

Figure S1: Heatmaps of all three datasets with the superimposition of the patients dendrogram obtained from a different dataset.
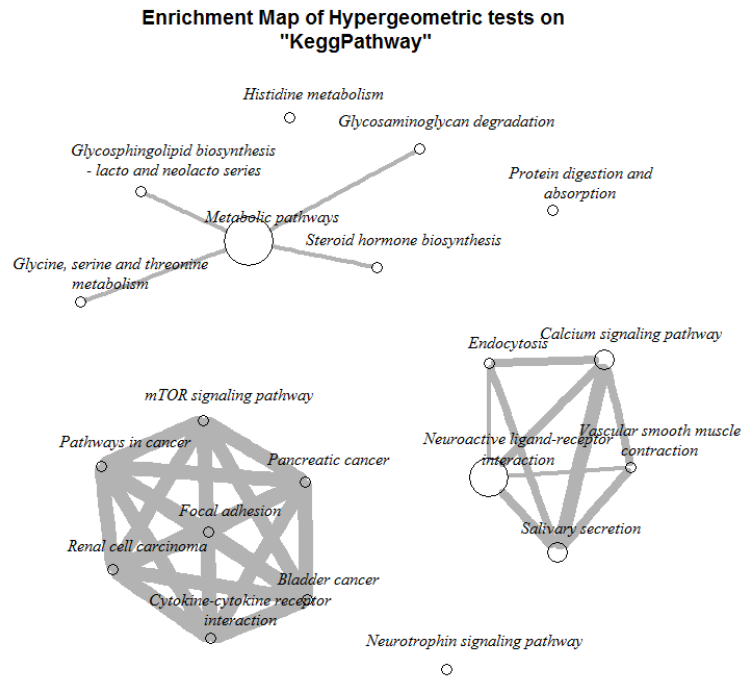
**Enrichment Map of Hypergeometric tests on
"KeggPathway"**

Figure S2: Gene set enrichment map of the 20 most enriched KEGG pathways in GC1 in GE

**Enrichment Map of Hypergeometric tests on
"KeggPathway"**
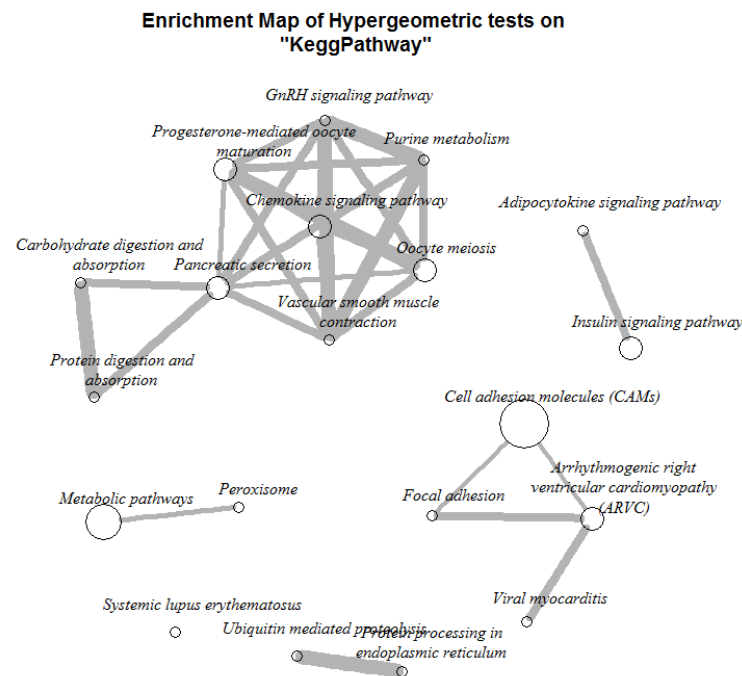
Figure S3: Gene set enrichment map of the 20 most enriched KEGG pathways in GC2 in GE

Enrichment Map of Hypergeometric tests on "KeggPathway"
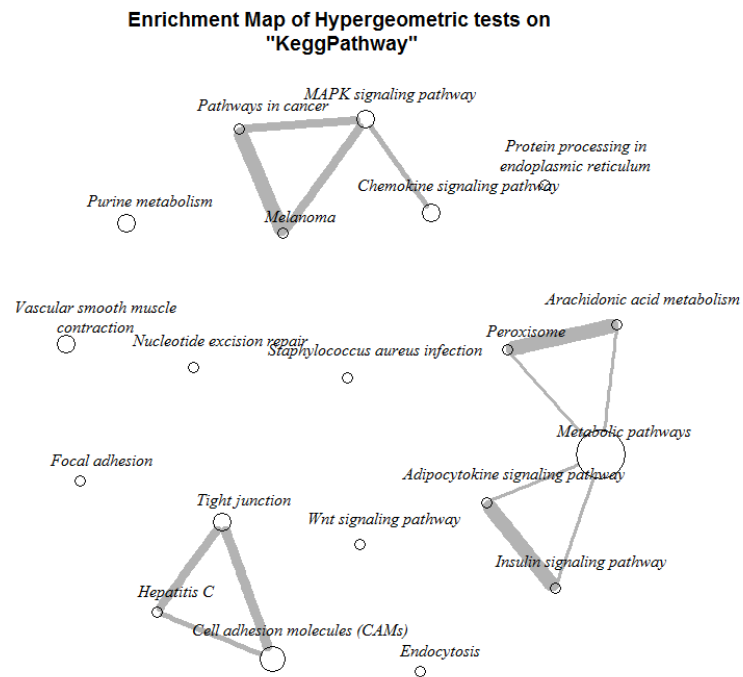
Figure S4: Gene set enrichment map of the 20 most enriched KEGG pathways in GC4 in GE

Enrichment Map of Hypergeometric tests on "KeggPathway"
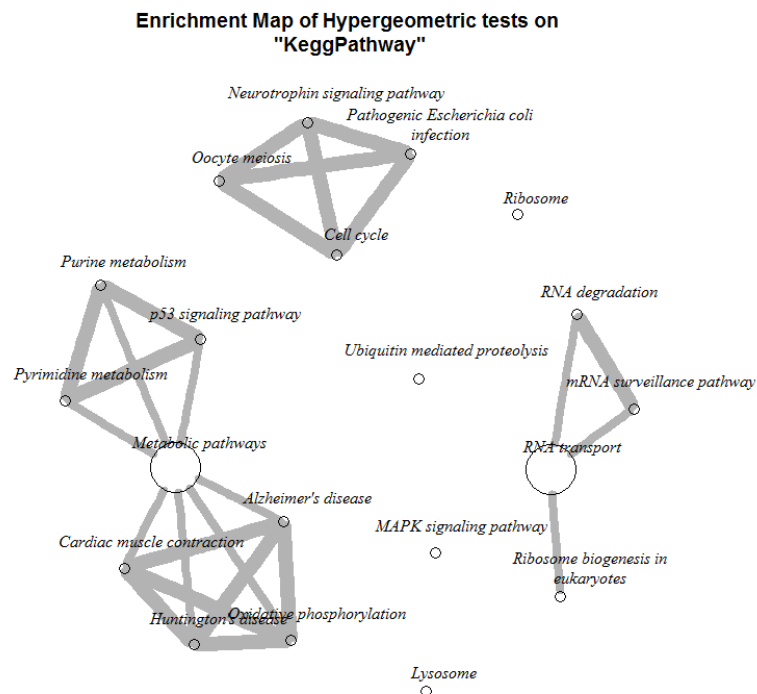
Figure S5: Gene set enrichment map of the 20 most enriched KEGG pathways in GC1 in CNV

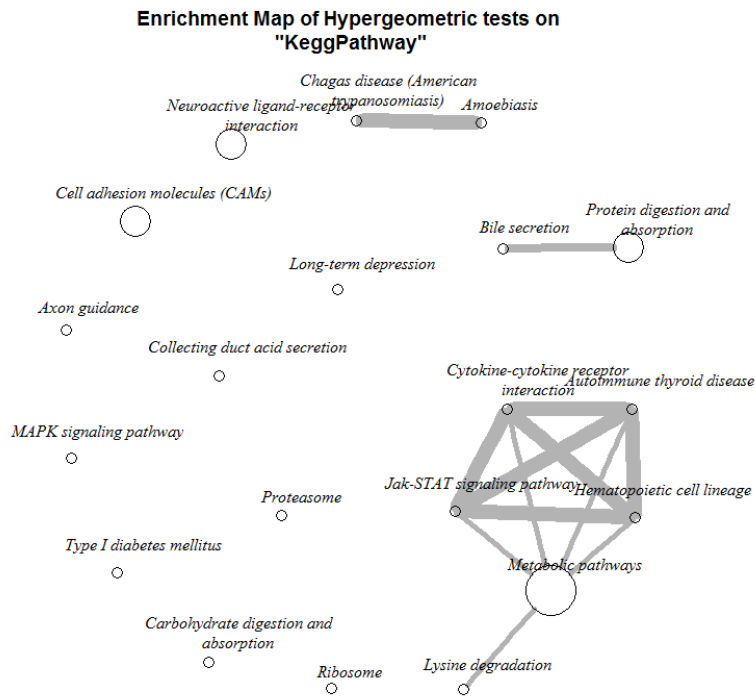**Enrichment Map of Hypergeometric tests on "KeggPathway"**

Figure S6: Gene set enrichment map of the 20 most enriched KEGG pathways in GC 2,3,4 and 5 in METH. The four clusters used have been considered as a single big cluster.
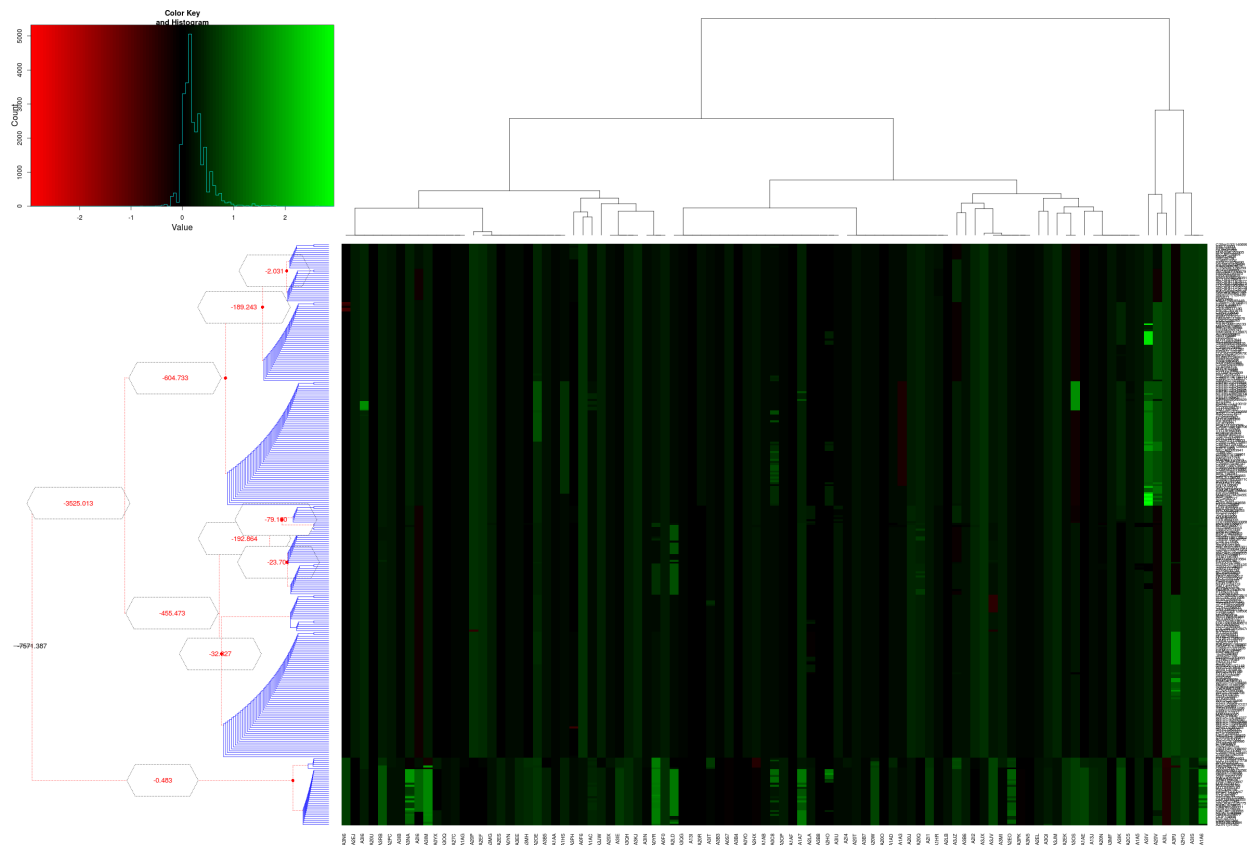

Figure S7: Heatmap of Copy Number Variation where the clustering of patients has been obtained from MDI
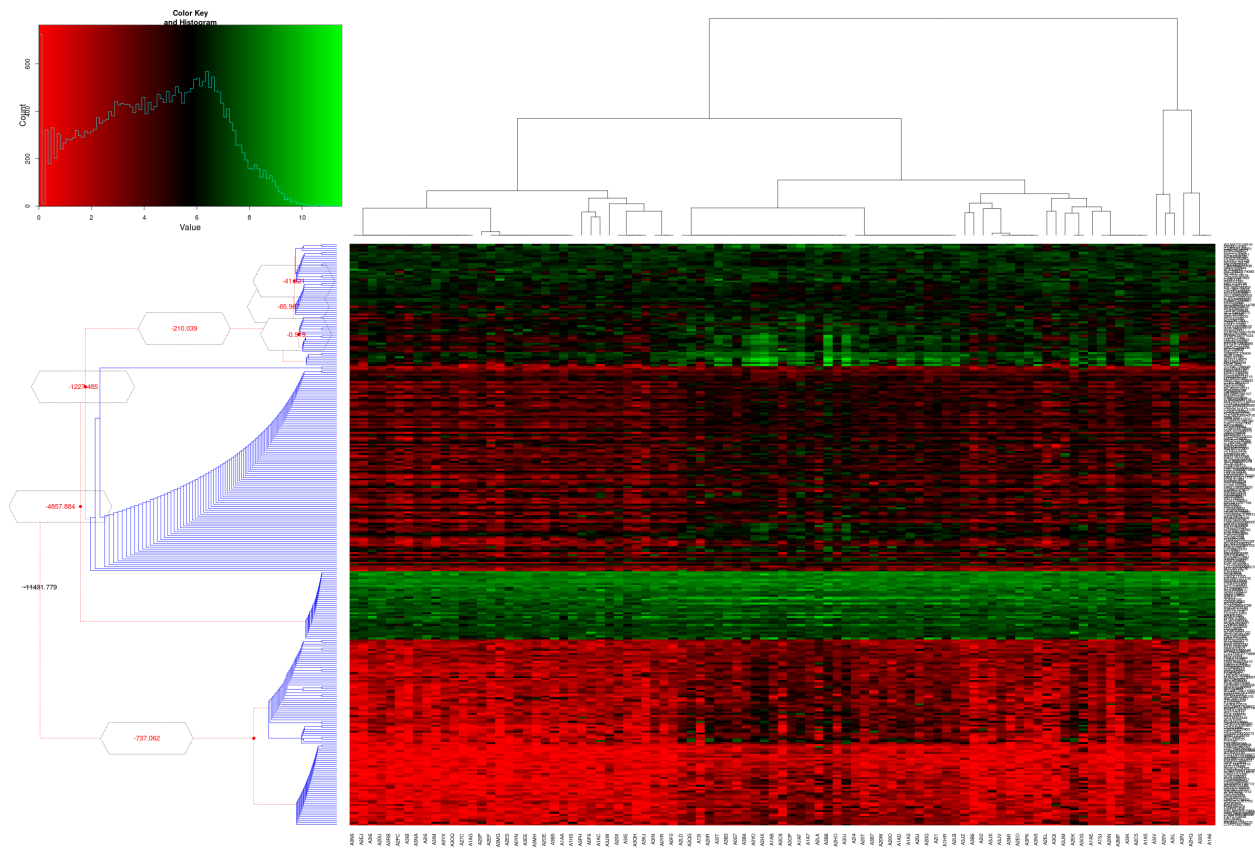
Figure S8: Heatmap of Gene Expression where the clustering of patients has been obtained from MDI