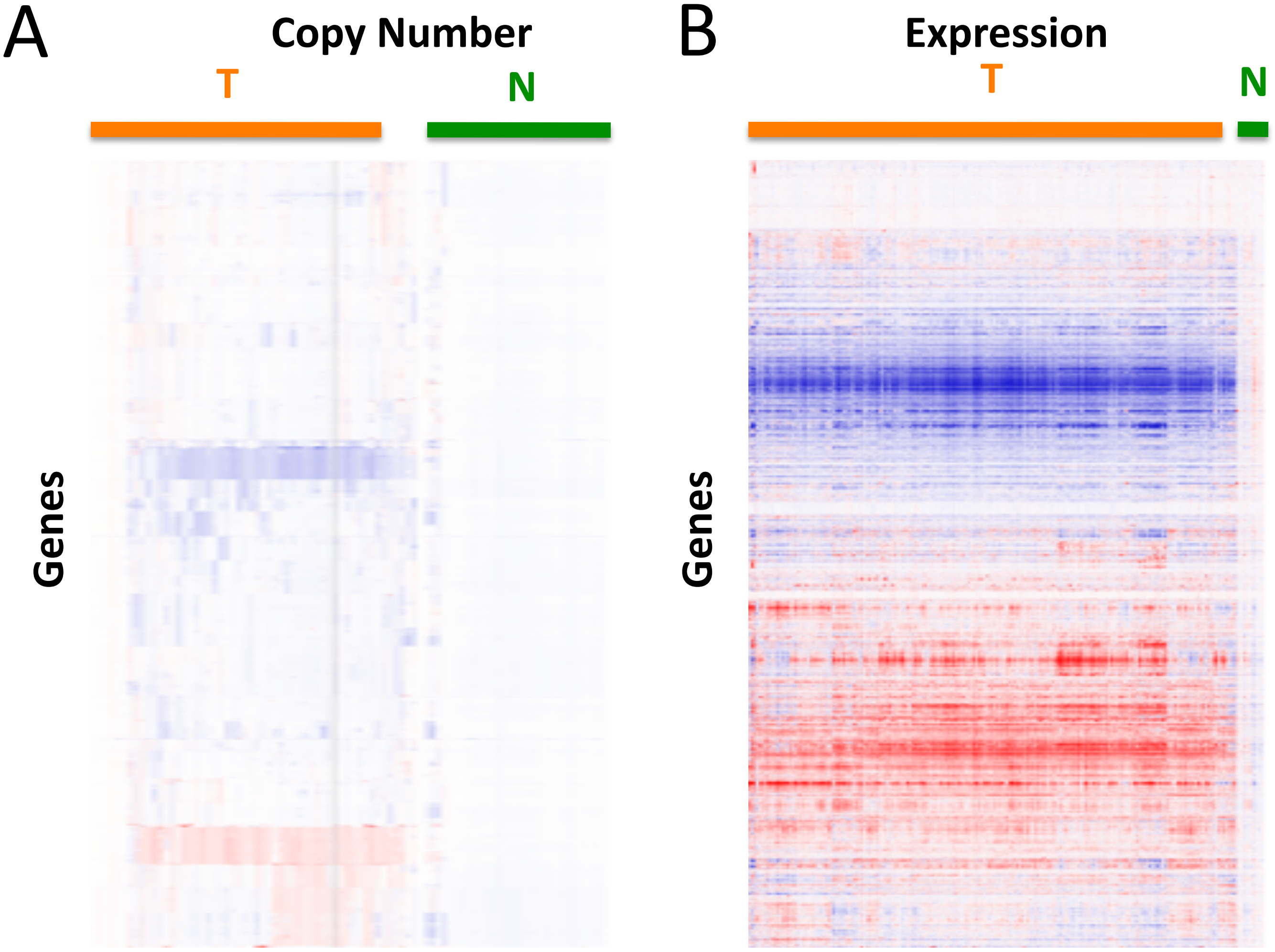

Supplementary Figure 1. Clustering glioblastoma multiform (GBM) datasets with HOPACH did not reveal any obvious patient sub-types when using either gene-level copy number or expression data. Patient samples (columns) were clustered according to gene-level copy number or expression (rows). Clustering may be dominated by the nearly patient-wide amplifications and deletions (and correlated high and low expression) for a subset of genes in the genome (large blue and red swaths in the heatmaps). **A.** Copy number estimates from competitive genome hybridization for 17,508 probes across 267 tomor (left) and 170 normal (right). **B.** Microarray gene expression data for 11,240 probes across 243 tumor (left) and 10 normal (right) samples.