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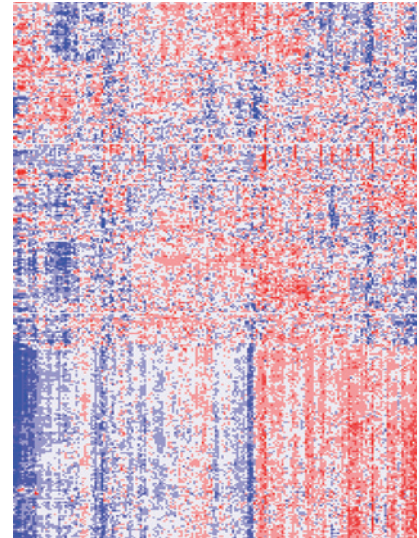
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The cover shows a heat map of oral squamous cell carcinoma (OSCC) tumor expression data from "The Cancer Genome Atlas (TCGA)" projected onto the YAP/TAZ-activated transcriptional signature identified from microarray studies performed by Hiemer and colleagues (beginning on page 957). Hierarchical clustering identified two tumor-associated sub-clusters which were enriched in either cell-cycle genes or genes responding to cancer-related signaling pathways.



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