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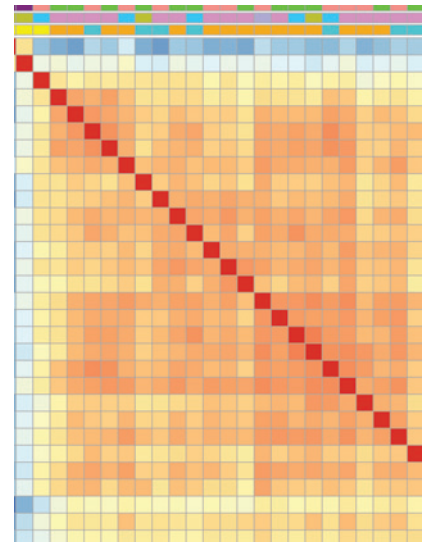
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ABOUT THE COVER

In this issue, Kaymaz and colleagues (beginning on page 563) investigate transcriptome expression and mutational profiles of patient-derived endemic Burkitt lymphoma (BL) tumors using RNA sequencing. The cover image shows the unsupervised hierarchical clustering heatmap of BL tumors based on their expression profiles of the most variant genes. While 2 sporadic BLs separate out from 28 endemic BLs, eBL tumor expression profiles demonstrate greater correlation within eBLs compared with sBLs. Transcriptome-wide gene expression correlations between eBLs did not reveal significant groupings suggesting that eBL tumors are relatively homogenous with no major underlying molecular phenotypes. Based on further analysis, the study reveals subtler differences in terms of gene expression as well as the pattern of somatic mutations that correlates EBV presence and EBV type in the tumor B cells.



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