tRNA-derived small RNA expression in normal and TGCT samples.
A Heatmap showing the expression data of the most highly expressed tRFs (variance stabilization transformed data). The dendrogram (bottom) indicates clustering according to expression profiles.
B Heatmap showing the expression data of the most highly expressed tRNA halves (variance stabilization transformed data). The dendrogram (bottom) indicates clustering according to expression profiles. **C** Volcano plot indicating the relationship between the Log2 fold change and p-values (Benjamini-Hochberg adjusted) for tRFs when comparing TGCT with normal samples. The CIS samples are included in the TGCT group. Color coding indicates the expression level as a function of normalized counts (BaseMean). **D** Volcano plot indicating the relationship between the Log2 fold change and p-values (Benjamini-Hochberg adjusted) for tRNA halves when comparing TGCT with normal samples. The CIS samples are included in the TGCT group. Color coding indicates the expression level as a function of normalized counts (BaseMean).