

## Supplementary Figure Legends

**Supplementary Figure 1.** Consensus clustering analysis from miR expression profiling data obtained using qRT-PCR in the whole 30 leukemic MCL series. (A) Consensus plot of empirical cumulative distribution function (CDF) showing that approximate maximum stability of partitioning is reached at  $k=3$ , indicating that the optimal number of robust clusters in this data set is three. (B) Consensus matrix plots showing the clusters generated from  $k=2$  to  $k=6$  showing the correlations in the consensus matrix for each partitioning. Best apparent partitioning appears at  $k=3$  although two cases seem to correlate with a similar frequency between two of the clusters (arrow). (C) Item consensus plots confirm that two samples show ambiguous cluster membership (the two central cases –arrows–) and therefore are not representative for the robust cluster definition obtained excluding these samples (as depicted in Figure 1).

**Supplementary Figure 2.** Venn diagram of overlapping significant differentially expressed miRs between subgroups with different *IGHV* status among the core clusters (as defined in Supplementary Table 3). Only 3 miRs (miR-455-5p/3p and miR-708) were found differentially expressed in all comparisons regarding *IGHV* status and, noticeably, these were the only miRs overexpressed in U-MCL vs M-MCL cases inside cluster C.

**Supplementary Figure 3.** Plots of the significant enrichment profiles showing the distribution of the top significant gene sets identified in the GSEA analysis for the inversely correlated predicted targets of the miRs differentially expressed regarding *IGHV* mutational status categories. Top enriched gene sets were determined on the basis

of statistical significance ( $P < 0.05$ ) and ranked on the basis of false discovery rate (FDR  $< 0.25$ ) and the normalized enriched score (NES  $> |1.3|$ ). See detailed results in Supplementary Table 7b.

**Supplementary Figure 4.** Correlation plots between the expression levels measured by qRT-PCR of miR-455-5p/miR-708 and their putative targets corresponding to histone methylation transferases, and that were previously found correlated in leukemic MCL with microarray gene expression data. MLL2 was found significantly inversely expressed to miR-455-5p.

**Supplementary Figure 5.** Overall survival of the 30 leukemic MCL patients according to *IGHV* status (A) and SOX11 expression level (B). U-MCL patients have a significant shorter overall survival (5-year overall survival: 40%) than patients showing M-MCL (5-year overall survival: 95%) ( $P = 0.008$ ). Similarly, patients with high SOX11 expression showed a significant shorter overall survival (5-year overall survival: 55%) than patients with low SOX11 expression levels (5-year overall survival: 95%) ( $P = 0.039$ ).

**Supplementary Figure 6.** Overall survival of the 30 leukemic MCL patients according to *IGHV* status (A) and SOX11 expression level (B) in combination with miR-34a expression level. Significant differences were found inside U-MCL ( $P = 0.037$ ) and SOX11 high expression ( $P = 0.008$ ) groups, respectively, showing a worse prognosis those patients with low levels of miR-34a inside each category.

**Supplementary Figure 7.** Overall survival of the validation series of 29 MCL patients according to miR-34a expression level. Patients with low levels of miR-34a showed worse prognosis (Median OS: 24.5 months) compared to patients with higher miR-34a levels (Median OS: 67) ( $P=0.041$ ).