SUPPLEMENTAL MATERIAL

Rossi et al., http://www.jem.org/cgi/content/full/jem.20120904/DC1

Table S1, which is presented as an Excel file, shows the features of the 8 SMZL discovery cases analyzed by whole-exome sequencing.

Table S2, which is presented as an Excel file, reports the results of Illumina sequencing after whole-exome capture.

Table S3, which is presented as an Excel file, reports the validated somatic mutations identified by whole-exome sequencing in the SMZL discovery panel.

Table S4, which is presented as an Excel file, illustrates the segments (regions) of tumor-acquired copy number alterations identified in the SMZL discovery panel.

Table S5, which is presented as an Excel file, and Table S6 list the patient's features in the screening and extension panel, respectively.

Table S7, which is presented as an Excel file, shows the mutations identified in the screening and extension panels by targeted resequencing of candidate genes.

Table S8, which is presented as an Excel file, reports the copy number aberrations encompassing any of the 61 genes that were subjected to targeted resequencing.

Table S9, which is presented as an Excel file, relates the genetic, immunogenetic, and biological features of SMZL and the mutations of MZ development genes.