

SUPPLEMENTAL MATERIAL

Sisirak et al., <http://www.jem.org/cgi/content/full/jem.20132522/DC1>

Dataset S1. Genome-wide expression analysis of splenocytes from B6.*Sle1.Sle3* mice with or without *Tcf4* haplodeficiency.

Probes used in the analysis included those used by the Immgen consortium that have definitive RefSeq annotations. Array results lists hybridization signals for all samples (each sample derived from a separate animal) and Log₁₀-transformed mean signals generated by the NIA Array software. PCA lists genes within each PCA-generated cluster (Fig. 5 B) with Log₁₀-transformed fold change between samples and correlation with the respective principal component. Indicated for cluster 1b are genes associated with the granulocyte signature and proliferation signature (modules 41 and 11 of the Immgen dataset, respectively). Indicated for cluster 2a are genes showing preferential expression in GC B cells in the Immgen dataset, and genes showing preferential expression in GC and/or plasma cells within the B cell lineage, as determined by the analysis of GEO dataset GDS1695. Dataset 1 is provided as an Excel file.