Supporting Information

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SI Text

A simple version of the MiDReG program is available at the following web site: [http://genepyramid.stanford.edu/microarray/](http://genepyramid.stanford.edu/microarray/MiDReG/) [MiDReG/.](http://genepyramid.stanford.edu/microarray/MiDReG/)

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Fig. S1. Purification of B-cell precursors. Precursor populations on B-cell development pathway were purified by fluorescent-activated cell sorting from either the marrow (A–G) or the spleen (H–I) of naive mice or the spleen from immunized mice (J). Definition of cell surface markers for populations are as follows: (A) HSC, CD34−Flk2−cKit⁺Sca-1⁺Lin(Mac-1, Gr-1, B220, CD4, CD8, IL-7Ra, and Ter119)⁻; MPP^{FL-}, CD34⁺Flk2⁺cKit+⁵ca-1+Lin⁻; MPP^{FL+}, CD34+Flk2⁺cKit⁺ Sca-1⁺Lin−; (B) CLP, Ly6c−NK1.1−CD11c−CD27+CD19−B220−Flk2+IL-7Rα+BP-1−; (C) fraction A, Ly6c−NK1.1−CD11c−CD27+CD19−B220+Flk2+IL-7Rα+BP-1−; (D) fraction B, Ly6c[−]NK1.1[−]CD11c[−]CD19⁺B220⁺IL-7Ra⁺BP-1⁻; (E) fraction C, IgD[−]NK1.1⁻IgM^{-B220+}CD43+CD19+IL-7Ra+BP-1+; (F) fraction D, IgD[−]NK1.1⁻ IgM−B220+CD43−CD19+IL-7Ra−; (G) fraction E, IgD−NK1.1−IgM+B220+CD43−CD19+IL-7Ra−; (H) T1, B220+AA4.1+IgM+CD23−Mac-1−Gr-1−CD3−CD4− CD8⁻Ter119⁻, T2, B220⁺AA4.1⁺IgM⁺CD23⁺Mac-1⁻Gr-1⁻CD3⁻CD4⁻CD8⁻Ter119⁻; (I) mature B, B220⁺AA4.1⁻IgM^{low}CD23⁺IgD^{high}Mac-1⁻Gr-1⁻CD3⁻ CD4−CD8−Ter119−; (J) germinal center (GC) B cells, B220+CD38−GL7+NP+Mac-1−Gr-1−CD3−CD4−CD8−Ter119−.

This table lists all 62 predicted B-cell precursor genes using MiDReG with their Affymetrix ID in human U133 Plus 2.0 and mouse 430 2.0 platform.

Table S2. Knockout phenotypes show defects in B-cell function and differentiation

41 genes were knocked out in mice out of the total 62 predicted B-cell precursor genes. Comprehensive review of the literatures identified 26 genes whose knockout phenotype show defects in B-cell function and differentiation. A short summary of this phenotype is listed here for each of the 26 genes.

Table S3. Detailed classification of predicted B-cell genes

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This table describes the detailed association of predicted B-cell genes to B-cell function and differentiation. Out of 62 predicted genes, 41 mouse knockouts were published in the literature. Out of 41 knockouts, 26 genes have a B-cell phenotype. Out of 62 genes, 9 other genes have B-cell functions according to other experiments, and 5 genes have indirect connections to B-cell functions.

Table S4. Predicted role of GLUT4 pathway in B cell

The most interesting genes identified by MiDReG were those with unexpected connections to B-cell development and function. For example, three genes (TBC1D1, RAB8B, and LNPEP) identified by MiDReG to be up-regulated in B-cell development are known components of a pathway seemingly unrelated to B-cell function, the GLUT4 glucose uptake pathway. GLUT4 is a glucose transporter normally sequestered in vesicles in muscle and adipose tissue. Upon insulin signaling, these vesicles are quickly fused to the plasma membrane leading to GLUT4 surface expression and rapid glucose uptake (93). GLUT4 surface levels are regulated by endocytic recycling (94). This endocytic recycling pathway bears some similarity to internalization of the BCR complex upon antigen encounter. When the BCR of a naïve B cell first encounters antigen, it is internalized through receptor-mediated endocytosis, and the antigen is processed and presented by MHC class II molecules on the cell surface for activation by Th2 helper T cells. Both BCR and GLUT4 endocytosis have clathrin-mediated pathways. In addition, both insulin and BCR signaling involve tyrosine kinases, PI-3 kinase, Protein Kinase C, Akt, Rho, and Rab GTPases, and Ca²⁺ flux (93, 95). The prediction of genes specific to the GLUT4 exocytic pathway in B cells leads to the surprising but testable hypothesis that genetic components important for GLUT4 endocytosis are also functionally important for BCR endocytosis. The identification of these genes and the prediction of similarities between GLUT4 and BCR endocytosis would not have been possible without MiDReG.

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Table S5. Antibodies used

House: conjugates made within the Weissman lab.

Cells were sorted into TRIzol (Invitrogen Life Technologies), and RNA was isolated according to manufacturer's instruction. cDNA was synthesized by using the Superscript III kit (Invitrogen Life Technologies) using random hexamers. Amplifications were performed by using SYBR Green PCR core reagents (Applied Biosystems), and transcript levels were quantified by using an ABI 7900 Sequence Detection Systems (Applied Biosystems). The mean ct value of triplicate reactions was normalized against the mean ct value of β-actin. Primers were used at 400 nM.