Kim et al., http://www.jem.org/cgi/content/full/jem.20070868/DC1

SUPPLEMENTAL MATERIALS AND METHODS

ClustalX analysis. TIR sequences were aligned and clustered using ClustalX (Thompson, J.D., T.J. Gibson, F. Plewniak, F. Jeanmougin, and D.G. Higgins. 1997. The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res.* 25:4876–4882.). The phylogenetic tree was drawn using HyperTree (Bingham, J., and S. Sudarsanam. 2000. Visualizing large hierarchical clusters in hyperbolic space. *Bioinformatics*. 16:660–661.).

FACS. FACSCalibur (BD Biosciences) was used for FACS analysis. PE-conjugated antibodies were used for CD11c (HL3), CD11b (M1/70) and CD4 (L3T4). Biotinylated antibodies were used for CD3 (145-2C11), CD4 (L3T4), CD8 (53–6.7) and B220 (RA3-6B2). Streptavidin-APC, streptavidin-PE or streptavidin-PECy5 was used to detect the biotinylated antibodies. The antibodies were purchased from BD PharMingen.

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