

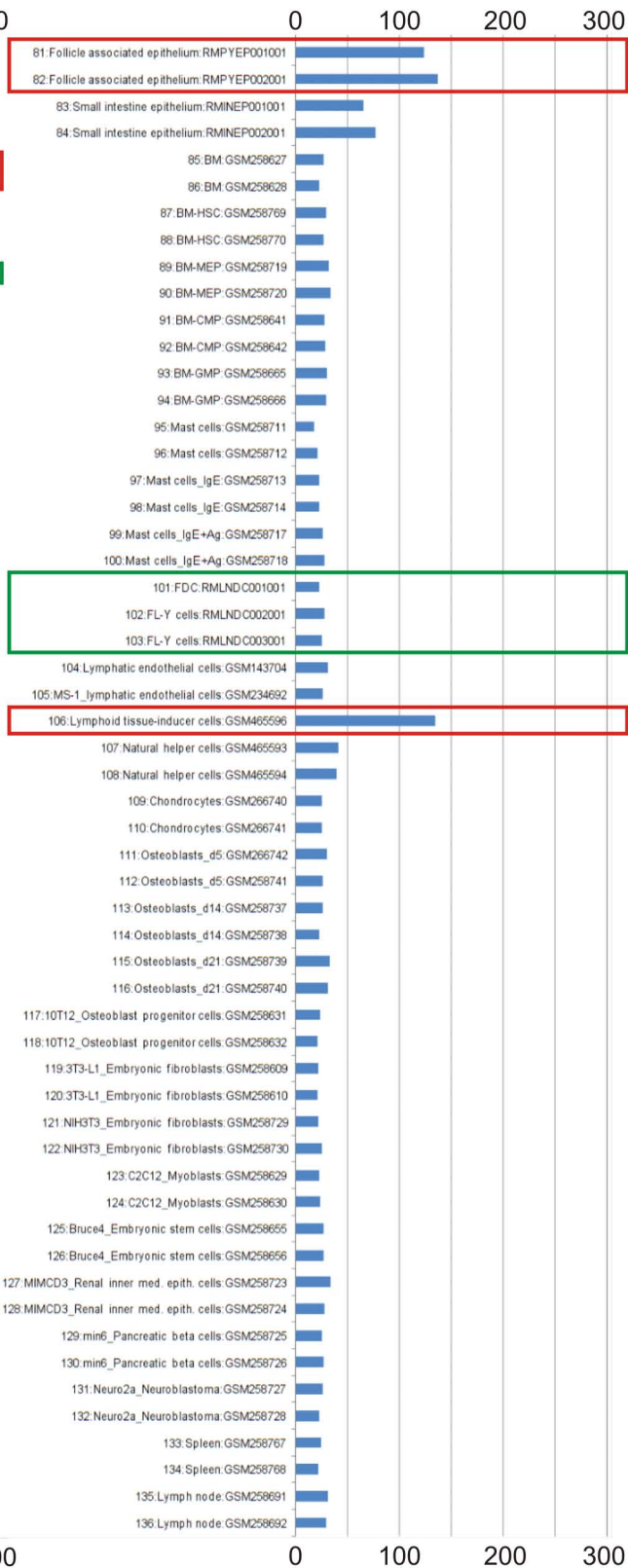
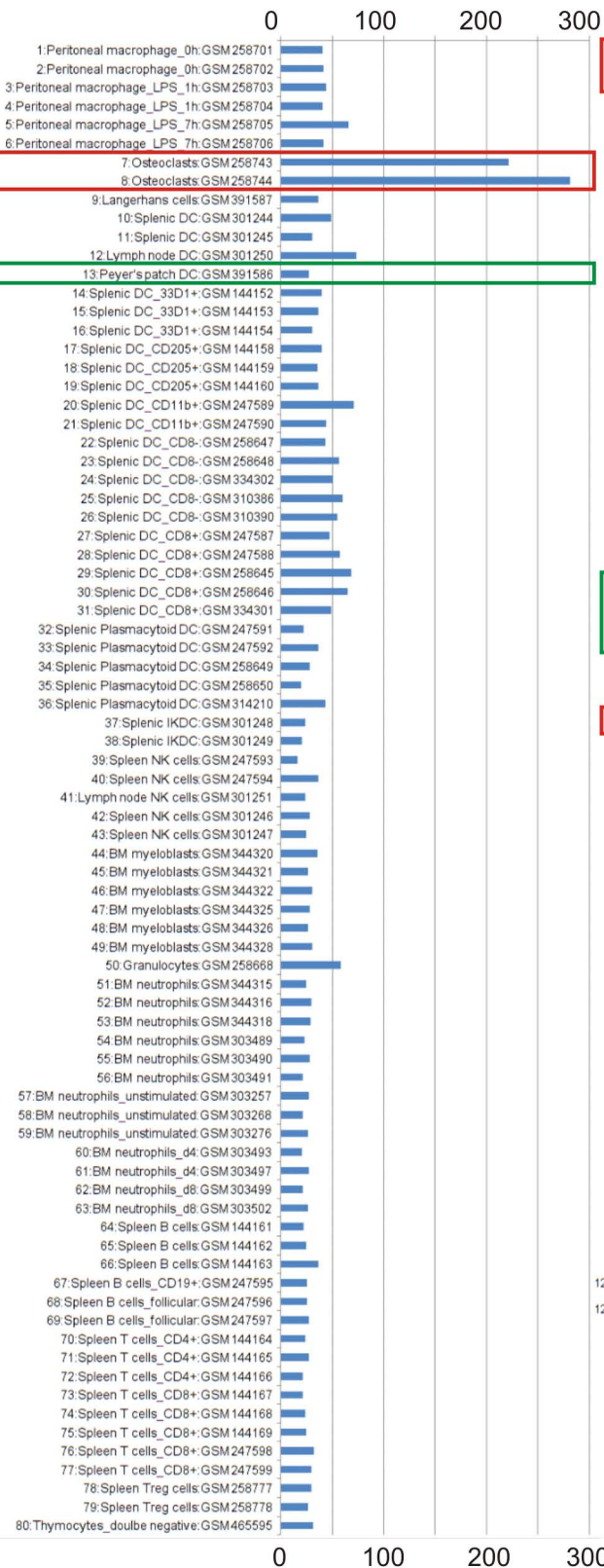
M cell depletion blocks oral prion disease pathogenesis

Running title: Role of M cells in prion pathogenesis

DS Donaldson, A Kobayashi, H Ohno, H Yagita, IR Williams & NA Mabbott

Supplementary Figure 1. Comparison of *Tnfrsf11a* mRNA expression in a large collection of murine cells and tissues

Meta-analysis of the expression profile of *Tnfrsf11a* (which encodes RANK; probe set ID 1430259_at) across 136 individual publicly-available microarray data sets representing a wide range of mouse cell-lineages and tissues. All sample analysis was performed on the Affymetrix MOE430 2.0 expression array. Prior to analysis raw data (.cel) files were downloaded, quality-checked and normalised using the robust multi-array average (RMA) expression measure by RMAExpress (rmaexpress.bmbolstad.com). Normalised probe set expression level data for each tissue and cell type are shown. These data show high expression of *Tnfrsf11a* by Peyer's patch FAE, osteoclasts and lymphoid tissue inducer cells (highlighted by red boxes), but negligible levels by FDC and classical DC from Peyer's patches (highlighted by green boxes). The chip identification accession numbers for each data set are indicated. Each sample is annotated as follows: Sample number:cell/tissue description:chip ID.

Tnfrsf11a : 1430259_at*Tnfrsf11a* : 1430259_at

Relative probe set expression level