Table S4. Enrichment analysis of NM-R immune cell gene signatures.

Pathway	Gene ranks	NES	pval	padj
Erythroid–cell.2		2.29	1.9e–04	7.5e–04
Erythroid–cell.1		2.04	1.9e–04	7.5e–04
B–cell		−1.98	2.1e–04	7.5e–04
CD8–T–cell		−1.98	2.1e–04	7.5e–04
Macrophage.1		1.71	1.9e–03	5.3e–03
Neutrophil.2		1.74	2.8e–03	6.6e–03
Plasma–cell		−1.76	3.8e–03	7.5e–03
Ltf–high–neutrophil		1.65	8.1e–03	1.4e–02
Red–pulp–macrophage		1.50	2.4e–02	3.7e–02
Timeless–high–dendritic–cell		1.14	2.1e–01	2.8e–01
Macrophage.2		1.13	2.2e–01	2.8e–01
Naive–T–cell		−1.14	2.8e–01	3.3e–01
Mast–cell		0.91	6.6e–01	7.1e–01
Neutrophil.3		0.68	8.8e–01	8.8e–01

Gene rank axis: 0, 2500, 5000, 7500, 10000, 12500

ssNM-R   MM

Table S4: Enrichment analysis of NM-R immune cell gene signatures
GSEA results with custom pathway signature defined by the immune cell signatures from single cell transcriptomic data as described in [2]. Transcriptome data from spleens of ssNM-R versus MM were compared. NES, normalised enrichment score; pval, p value; padj, adjusted p value. For more details, see methods section.