**A screenshot of a graph

Description automatically generated**

**Suplemmentary Figure 1.** FACS quality control. А) Surface marker and gene matching. B) The expression levels of surface marker genes of innate immune cells derived from the spleen and bone marrow of BCG-vaccinated and control mice. The expression levels were extracted from the RNA-seq data and presented as mean TPM (transcripts per million) values with standard deviation bars (y axis) calculated from 3 independent samples. Gene abbreviations: Ptrpc – Protein Tyrosine Phosphatase Receptor Type C, Itgam – Integrin Subunit Alpha M, Ly6G – Lymphocyte antigen 6 complex locus G6D, Ly6c1/2 lymphocyte antigen 6 family member C1/2, Klrb1b/c – Killer cell lectin-like receptor subfamily B member 1b/c.

**A close-up of a diagram

Description automatically generated**

**Supplementary Figure 2.** The Network Analysis of enriched GO terms. The network is color-coded by cluster ID, a configuration where nodes sharing the same cluster ID tend to be closely positioned to one another. A. Metascape Network of enriched terms of 162 DEGs from splenic NK-cells from mice after BCG vaccination. B Metascape Network of enriched terms of 30 DEGs from Bone Marrow Monocytes from mice after BCG vaccination. C. Metascape Network of enriched terms of 184 DEGs from bulk Bone Marrow cells from mice after BCG vaccination.