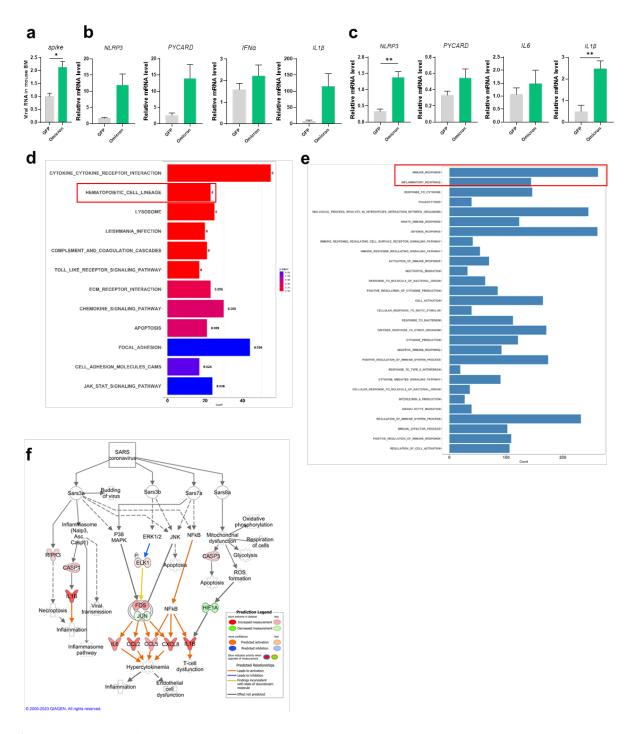
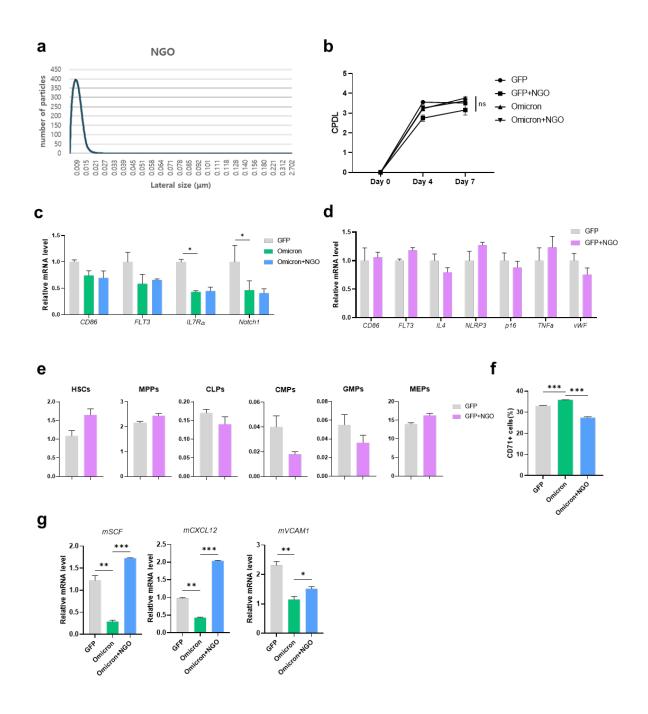


Supplementary Fig. 1. (a) A volcano plot highlighting DEGs in Omicron PsV-infected HSPCs compared to GFP-infected HSPCs. (b) IPA of inflammation/NLRP3-related signals in Omicron PsV-infected HSPCs compared to GFP-infected HSPCs is shown. (c) Transcriptional levels of ROS-related factor in Omicron PsV-infected HSPCs were determined by qRT-PCR. mRNA levels were normalized to *GAPDH*. *, p<0.05; **, p<0.01; ***, p<0.001. Results are represented as the means ± SEM.



Supplementary Fig. 2. (a-c) Transcription levels of viral RNA (a), pro-inflammatory genes and BM niche related factors (b) in bone marrow and pro-inflammatory genes in spleen (c) were determined by qRT-PCR. mRNA levels were normalized to *GAPDH*. (d, e) RNA sequencing was performed to evaluate the phenotype of BM human cells in NSG mice transplanted with Omicron PsV-infected HSPCs. (d) KEGG pathway analysis and (e) GO

enrichment analysis of the DEGs. (f) IPA analysis of BM human cells in NSG mice transplanted with Omicron PsV-infected HSPCs. *, p<0.05; **, p<0.01; ***, p<0.001. Results are shown as mean \pm SEM.



Supplementary Fig. 3. (a) Particle size distribution of NGOs. (b) CPDL of Omicron PsV-

infected HSPCs and NGO-treated HSPCs. (c) Transcriptional levels of lymphoid lineage-related genes in Omicron PsV-infected HSPCs were determined by qRT-PCR (d) Transcriptional levels of inflammaging-related genes in GFP- and NGO-treated HSPCs were determined by qRT-PCR. mRNA levels were normalized to *GAPDH*. (e) Hematopoietic lineage differentiation was investigated using lineage-specific markers and flow cytometry. Percentage HSPC lineage differentiation fractions in GFP- and NGO-treated group are shown. (f) Percentage of CD71+ RBC progenitor cells was determined by using flow cytometry (g) Transcriptional levels of BM-niche related genes in bone marrow were quantified using qRT-PCR. mRNA levels were normalized to *mGAPDH**, p<0.05; **, p<0.01; ***, p<0.001. Results are shown as mean ± SEM.