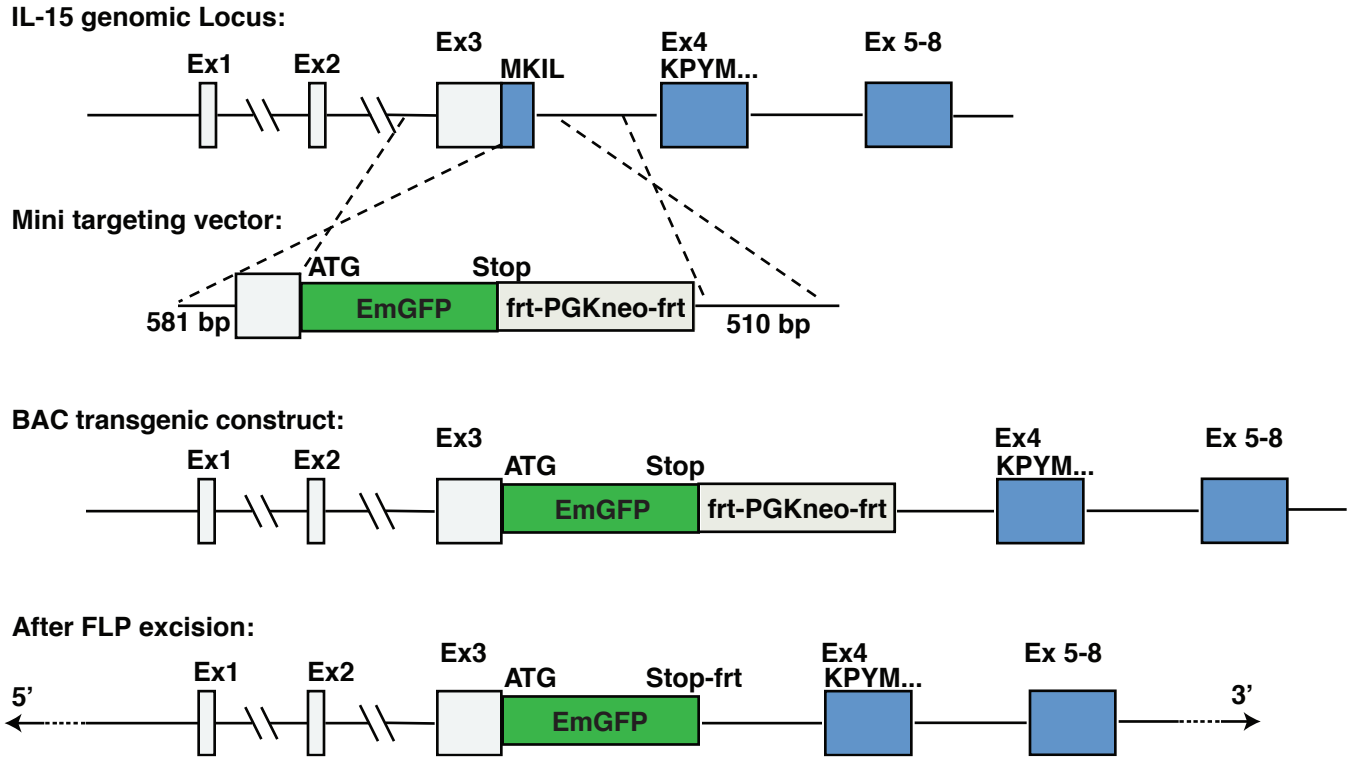
Supplemental Information

Supplemental Figure 1. Generation of EmGFP/IL-15 transgenic mice. A mini targeting vector consisting of DNA sequence homologous to 581 base pairs (bp) in intron 2 and exon 3 of the murine IL-15 genomic locus, EmGFP sequence, frt-PGKneo-frt sequence, and DNA homologous to 510 bp in intro 3 of the murine IL-15 locus was engineered by homologous recombination into BAC construct RP24-275P1 containing the murine IL-15 genomic locus. The transgenic construct was then randomly integrated into ES cells (129svev X C57BL6) by electroporation. The EmGFP/frt-PGKneo-frt sequence was situated do delete the first 4 codons of the IL-15 gene as well as a portion of intron 3, replacing a total of 56 bp of the endogenous sequence. The BAC IL-15 transgenic construct is approximately 180kb in length and contains the whole IL-15 gene and 42kb of the upstream sequence. The PGKneo sequence was removed by breeding the BAC-IL-15-EmGFP frt-PGKneo-frt line to the FLP recombinase transgenics. Presence of the BAC transgene was determined by PCR using primers specific for GFP (Primer 1: 5'-TCATCTGCACCACCGGCAAGC-3'; Primer 2: 5'-AGCAGGACCATGTGA TCGCGC-3'). All mice used for these experiments were backcrossed to C57BL/6 mice (Charles River-NCI) for at least three generations. After three generations, the process was accelerated using speed congenic technology (Speed Congenics Facility, Dartmouth Medical School, Hanover, NH). No differences in the levels of EmGFP/IL-15 expression were observed amongst subsequent generations throughout the back-crossing process.

Supplemental Figure 2. EmGFP expression correlates with endogenous IL-15 mRNA levels. Splenocytes were harvested from transgenic mice that were naïve or infected with VSV for 24

hrs. Prior to FACS sorting, cells were enriched by staining with CD11c-APC followed by anti-APC MACS beads. The cells were then sorted based on CD8 and EmGFP/IL-15 expression as shown by the gates. Histograms compare the levels of EmGFP/IL-15 on each of the corresponding three purified populations gated on in the dot plots. RNA was isolated from sorted cells with the RNeasy Mini Kit following cell disruption using QIAshredder (Qiagen). cDNA was made with SuperScript (Invitrogen). SYBR Green (Invitrogen) and the following primers (Integrated DNA Technologies) were used for quantitative PCR: IL-15 #1, 5'-GCTCTTACCTGGGCATTAAGTAATGAA-3'; IL-15 #2, 5'-TGACACAGCCCAAAATGAACAC-3'; β-actin #1, 5'-AGAGGGAAATCGTGCGTGAC-3'; β-actin #2, 5'-CAATAGTGATGACCTGGCCGT-3'. qPCR was performed on a Bio-Rad iCycler. IL-15 mRNA expression was normalized to β-actin expression ($2^{-\Delta CT}$). Graph depicts fold increase in IL-15 mRNA expression relative to the EmGFP/IL-15^{low} $CD8^-$ DC population (value of 1).

Supplemental Figure 1



Supplemental Figure 2