

Supplementary Figure 1. A, Purity of *Listeria*-WT or *Listeria*-OVA tpCD4⁺ T cells after cell sorting. Size and complexity are shown by plotting side- (SSC) vs forward-scattered (FSC) light (left panels). **B.** Orthogonal views of *Listeria* $tpCD4^+$ T cells purified at 3 h of conjugate formation. Actin is shown in magenta, and *Listeria* in green. XY together with YZ and XZ views (from lines marked in XY) are shown. Bar = $10 \mu m$. C, OVA, bacteria-associated (BA) or in the concentrated supernatant (SN), detected by Western blotting. Bacteria tested were Listeria-WT (List-WT) or Listeria-OVA (List-OVA). Note that all original Western-blots together with the membranes stained for molecular size markers are provided at the end of the manuscript in Supplementary Fig. 5. D, Gating strategy for flow cytometry analysis to measure $CD8^+$ T cell proliferation induced by tpCD4⁺ T cells. Only viable cells (7-AAD-negative) were analyzed. CellTrace Violet staining was analyzed in the CD8⁺ population. E, Listeria-OVA tpCD4⁺ T were incubated with naïve OT-I CD8⁺ T cells (72 h). CellTrace Violet staining was analyzed in three CD8-positive populations: CD8^{+low} (1), CD8^{+high} (2) and CD4⁺CD8⁺ cell conjugates (3), which were also analyzed to detect blasts (activated T cells), which are larger than non-activated T cells (positive in FSC, forward scatter). F, Quantification of CD8⁺ T cells proliferation after 3 days activation with anti-CD3/CD28 antibodies (polyclonal activation; white), OVAp-I-loaded BM-DC (blue), BM-DC infected with Listeria-OVA (green) or with *Listeria*-OVA tpCD4⁺ T cells (red). The percentage of CD8⁺ T cells that divided at indicated times is shown. * $p \leq 0.05$; two-way ANOVA with the Bonferroni post-test. Data shown as mean \pm SD of four independent experiments. G, Listeria-WT (red line) or Listeria-OVA (blue line) tpCD4⁺ T cell activation measured by CD25 expression. CD25 levels of non-activated lymphocytes is shown in grey.



Supplementary Figure 2. A, Scheme, and B results of experiments to confirm the intracellular (bacteria) source of OVA. (A) Listeria-OVA-infected BM-DC were allowed to contact OT-II CD4⁺ T cells (condition 1). Alternatively, *Listeria*-OVA-infected BM-DC were cultured on a polycarbonate barrier (0.4 µm pore size transwell; TW) that allowed passage of soluble material including proteins or exosomes, but impeded cell contact with non-activated (condition 2) or activated (anti-CD3/CD28; condition 3) OT-II CD4⁺ T cells. After 16 h, CD4⁺ T cells were reisolated by cell sorting and used as APC to activate OT-I CD8⁺ T cells. (B) OT-I CD8⁺ T cell proliferation 4 days after contact with CD4⁺ T cells as APC. Condition 1, green line; condition 2, blue line; condition 3, magenta line. C, OVA-GFP architecture of Listeria-OVA2. P-HELP promoter, RBS from each gene, OVAp (I and II) as well as the restriction enzymes allowing the removal of the genes are indicated. **D**, OT-I naïve $CD8^+$ T cell proliferation measured by CellTrace Violet staining 3 days after contact with *Listeria*-OVA2 (black line) tpCD4⁺ T cells. Non-activated naïve CD8⁺ T cells are shown in grey. **E**, Scheme of the experiment in Figure 2A. BM-DC were infected with Listeria-WT or Listeria-OVA and loaded with OVAp-II (to allow bacterial transphagocytosis to OT-II CD4⁺ T cells) plus OVAp-I (the peptide that stimulates CD8⁺ T cells from OT-I mice). OT-II CD4⁺ T cells were incubated with these BM-DC to allow bacterial transphagocytosis; after 24 h, they were re-isolated by cell sorting and conjugated with naïve OT-I CD8⁺ T cells. During conjugation, tpCD4⁺ T cells might acquire MHC-I/OVAp-I from the DC membrane. If this was the main source of MHC-I/antigen that activates CD8⁺ T cells, similar activation would be detected in both groups; if tpCD4⁺ T cells process and present bacterial antigens via their own MHC-I, Listeria-OVA tpCD4⁺ T cells would induce more potent CD8⁺ T cell activation.

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Cross-presentation of bacterial antigen by CD4⁺ T cells during bacterial infection in vivo



Analysis of CD45.1⁺ CD8⁺ T cells proliferation only possible by bacterial OVA cross-presentation in the context of $H-2K^b$



Supplementary Figure 3. A. Scheme of experimental approach used to determine whether $CD4^+$ T cells present bacterial antigens in the course of an *in vivo* bacterial infection, to activate naïve OT-I CD8⁺ T cells. C57BL/6 mice were lethally irradiated and transplanted i.v. with bone marrow cells from H-2K^k mice. One month later, H-2K^{k/k} CD4⁺ T cells (condition 1) or H-2K^{k/b} CD4⁺ T cells (condition 2) were adoptively transferred, together with CD8⁺CD45.1⁺ T cells from

OT-I mice and with MCC peptide. Recipient mice were also infected with *Listeria*-OVA (10^4 bacteria/mouse). At 5 days after infection, spleens were isolated from recipient mice and proliferation of CD8⁺ T cells from OT-I mice (prestained with CellTrace Violet) was measured by flow cytometry. **B**. To confirm bone marrow elimination in recipient mice, we tested for H-2K^b in spleen samples (CD45.1⁻CD4⁻). Red lines indicate secondary antibody background signal, blue lines indicate H-2K^b expression. **C**, Dot plots showing the OT-I CD8⁺ T cell (CD45.1⁺CD4⁻) population, analyzed 5 days after *Listeria*-OVA infection. **D**, Proliferation of the transferred OT-I CD8⁺ T cells, 5 days after infection. **E**, Size and complexity of transferred OT-I CD8⁺ T cells were analyzed in SSC-A and FSC-A to detect blasts (activated T cells). OT-I CD8⁺CD45.1⁺ cells were clearly activated in the mouse injected with H-2K^b CD4⁺ T cells (condition 2) and not in condition 1.



Supplementary Figure 4. A, Scheme of the experiment in Fig. 4. B, Gating strategy for flow cytometry analysis of memory $CD8^+$ T cells. All cells, excluding debris, were taken by size and

complexity (top left). From this selection, we gated for singlets (FSC-H vs FSC-W and SSC-H vs SSC-W) (top right, center left), then excluded dead cells (center right). Lymphocytes were analyzed by antibody staining for CD3⁺CD8⁺ (bottom). C, CD40L expression on polyclonal activated CD4⁺ T cells from WT (red line) and $Tap1^{-/-}$ (blue) mice. **D**, CCR-7 levels on CD3⁺CD8⁺CD44⁺CD62L^{high} population from a mouse injected with CD4⁺ WT cells (red line) or with $CD4^+$ Tap1^{-/-} cells (blue line) at 30 days after Listeria challenge. E-G, Phenotypic analysis of memory CD8⁺ T cell generation *in vivo*. Rag1^{-/-} mice were adoptively transferred i.v. with WT CD4⁺ T plus WT CD8⁺ T cells (group 1) or with $B2m^{-/-}$ CD4⁺ T plus WT CD8⁺ T cells (group 2). The following day, all mice were challenged with *Listeria*-OVA2 (10³ bacteria/mice; i.v.). 30 days after challenge, the $CD8^+$ T cell population from spleen was analyzed. (E), Representative dot plots showing CD62L and CD44 staining gated on the CD45.1⁺CD8⁺ T cell population. (F), Percentage of CD62L^{high} CD44⁺ gated on cells indicated in E (red outline). (G) Percentage of CD45.1⁺CD8⁺ T cells recognizing the H2-K^b/SIINFELK hexamer. Data shown as mean \pm SD for 3 mice/group (group 1, white; group 2, black). * p<0.05 analyzed by unparied t test.

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Original blots from Supp. figure 1C Independent exp List WT List OVA List WT List OVA kDa BA SN BA SN BA SN BA SN 75 50 Visible 37 Chemiluminiscence 75 50 Merged 37

Supplementary Figure 5. Original blots. A, Original blots corresponding to Figure 2 E,F were visualized using visible light to detect the molecular size staining markers (Precision Plus ProteinTM Dual Color Standards, #1610374; Bio Rad). The chemiluminiscence light emission from the HRP-conjugated secondary antibodies was detected on the same membranes. Arrows indicate the molecular size markers shown in Fig. 2E,F. **B**, Original blots corresponding to Supplementary Figure 1C. Molecular size staining markers (Precision Plus ProteinTM Dual Color Standards, #1610374; Bio Rad) are shown in the "visible" panel. "Chemiluminiscence" panel shows the light emission of the HRP-conjugated secondary antibodies of the same membranes. We included here, in addition, the results from another independent experiment analysed in the same membrane. These last images were acquired using an *Amersham Imager 600* from *GE Health Care Life Sciences*, that allowed us to mount a merged image fusing the visible and the chemiluminiscence images.