## This Supplementary Information file includes:

Supplementary Figure. 1 to 6

Caption for Supplementary Data.



Supplementary Fig. 1: The route of vaccination alters the magnitude of HPV-specific CD8<sup>+</sup>

**T cells. (a)** Flow cytometric analysis of single cells stained with E7 dextramer and CD44 antibody. The numbers indicate the percentage of cell population within the gate. Naive: unvaccinated; IV: intravenous; SC: subcutaneous.





- 0 Transitory effector memory
- 1 Naive
- 2 Effector memory
- 3 Naive
- 4 Naive
- 5 LAG3+ Tex
- 6 Effector 7 MKI67<sup>+</sup> Proliferating
- 8 ISG+
- 9 LAG3+ Tex
  - 10 ISG+
- 11 MCM<sup>+</sup> Proliferating
- 12 MKI67<sup>+</sup> Proliferating
- 13 Effector proliferating
- 14 TEMRA/ effector
- 15 IFITM⁺

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## Supplementary Fig. 2: Expression patterns of functional marker genes in different

subclusters. (a) The expression of genes encoding transcription factors, inhibitory receptors, memory, effector, proliferation and IFN-response markers across subclusters. The median is shown by the center line within the box of box plots, while the lower and upper box boundaries reflect the 25th and 75th percentiles, respectively, with whiskers drawn to the number that is closest to but still falls within the 1.5 interquartile range from top to bottom of the box borders.
(b) Heatmap of selected top differentially expressed (DE) genes in each cluster.



## **Supplementary Fig. 3: Distribution of TCR clonotypes in subclusters. (a)** Pie charts of TCR clonotype size for each cluster. **(b)** Distribution of TOP4 clonotypes projected onto t-SNE maps.



Supplementary Fig. 4: Application of PD-1 blockade in HPV+ OPSCC mouse model. (a) Representative images of tumors collected on day 25 following different treatment. The scale bar indicates 1 cm. (b-c) Tumor growth following treatment (n = 6). Statistics were assessed by the Mann–Whitney U test. \*P < 0.05, \*\*P < 0.01 and \*\*\*P < 0.001. Anti-PD1 (rat IgG2a, k, clone 29F.1A12, BioXcell) was administered intraperitoneally 200  $\mu$ g per treatment starting on day 5 with 5 additional times at 3-day intervals. Error bar = mean ± SEM.





Supplementary Fig. 5: HPV mRNA-LNP vaccination combined with immune checkpoint blockade generates HPV-specific CD8<sup>+</sup> T cells with superior antitumor capacity. (a) Representative images of tumors collected on day 25 following different treatment. The scale bar

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indicates 1 cm. (b) Distribution of CD8<sup>+</sup> T cells projected onto t-SNE maps using flowcytometry data and t-SNE heatmaps, for each marker applied on CD8<sup>+</sup> T cell events. Black circle indicates dextramer<sup>+</sup> population (c) Expression of different immune markers on CD8<sup>+</sup> T cells measured in spleen, blood, DLNs, and tumor (n = 4  $\sim$  8). DLNs: draining lymph nodes. Statistics were assessed by two-way ANOVA with Tukey's multiple comparison tests. \*P < 0.05, \*\*P < 0.01 and \*\*\*P < 0.001. Error bar = mean ± SEM.



**Supplementary Fig. 6: HPV mRNA-LNP vaccination combined with immune checkpoint blockade boosts HPV-specific CD8**<sup>+</sup> **T cells. (a)** Gating strategy for sorting HPV-specific CD8<sup>+</sup> T cells. (b) Flow cytometric analysis of single cells stained with E7 dextramer antibody. The numbers indicate the percentage of Dextramer<sup>+</sup> population within the gate. **Supplementary Data 1.** Differentially expressed genes of different cell clusters applied in scRNA-seq.

Supplementary Data 2. Cell percentages across treatments and tissues for each trajectory.

Supplementary Data 3. Frequencies and sequences of top expanded clonotypes (clone size  $\geq$ 

30).

**Supplementary Data 4.**TCR-wise cell counts of top clonotypes (clone size  $\geq$  30) across clusters in the spleens and tumors, respectively.