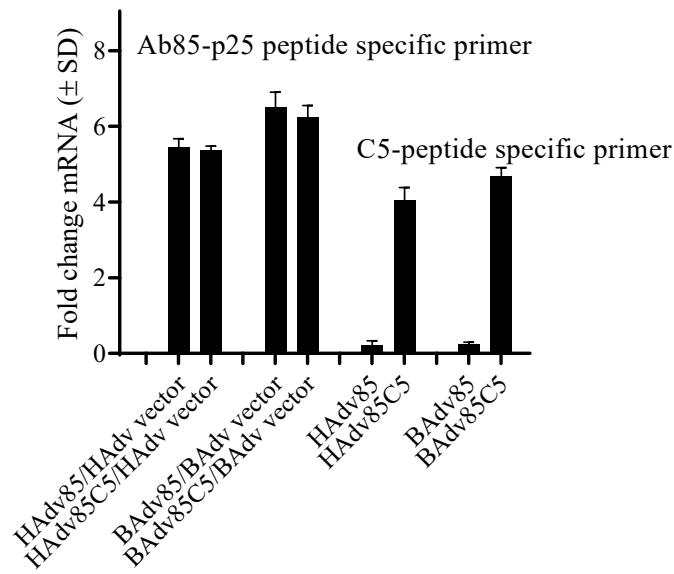


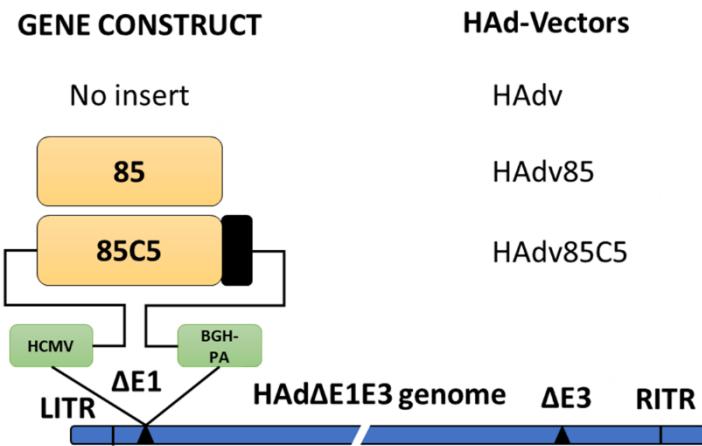
**Supplemental information**

**A recombinant bovine adenoviral mucosal vaccine  
expressing mycobacterial antigen-85B generates  
robust protection against tuberculosis in mice**

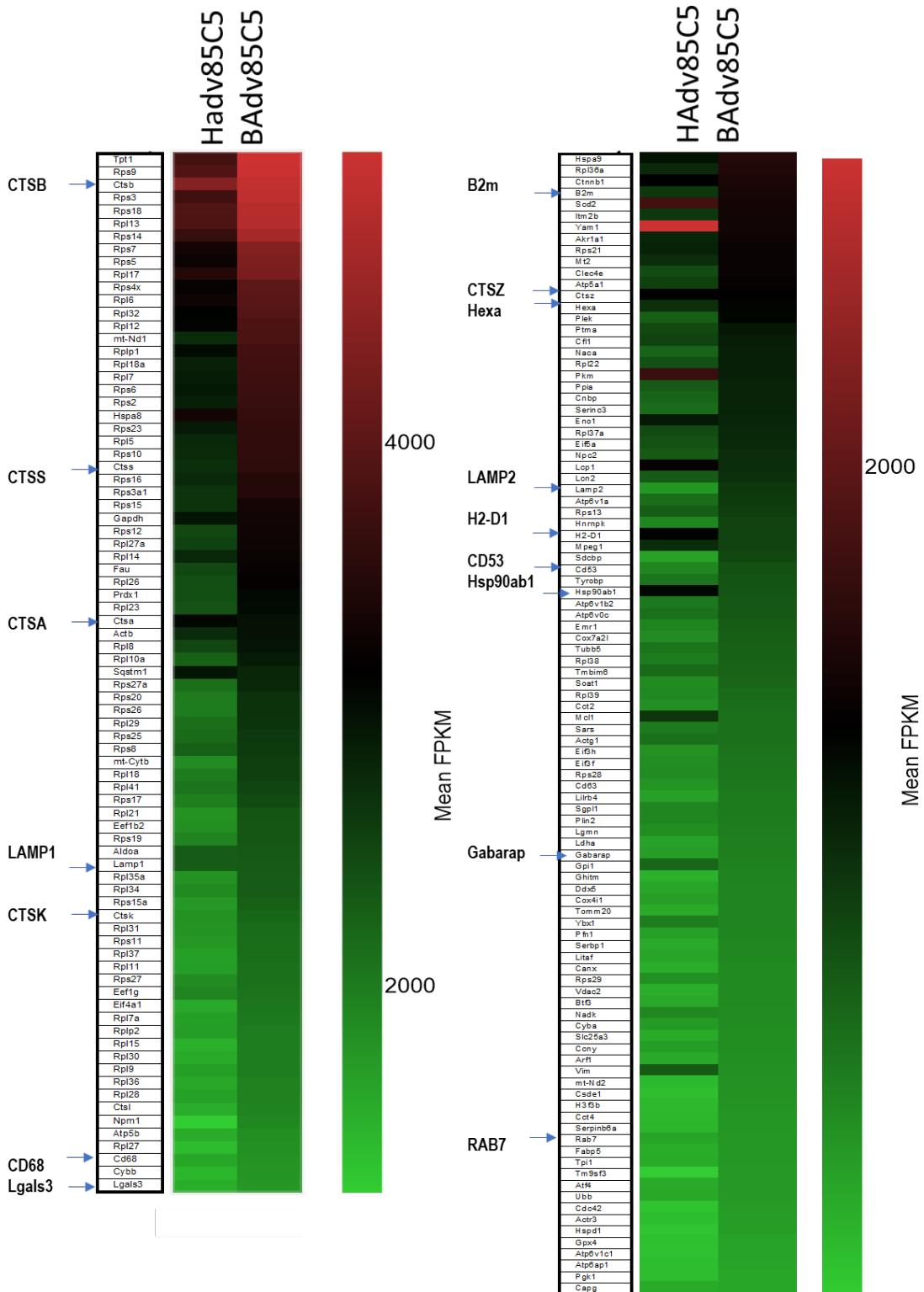
**Arshad Khan, Ekramy E. Sayedahmed, Vipul K. Singh, Abhishek Mishra, Stephanie Dorts-Estremera, Sita Nookala, David H. Canaday, Min Chen, Jin Wang, K. Jagannadha Sastry, Suresh K. Mittal, and Chinnaswamy Jagannath**

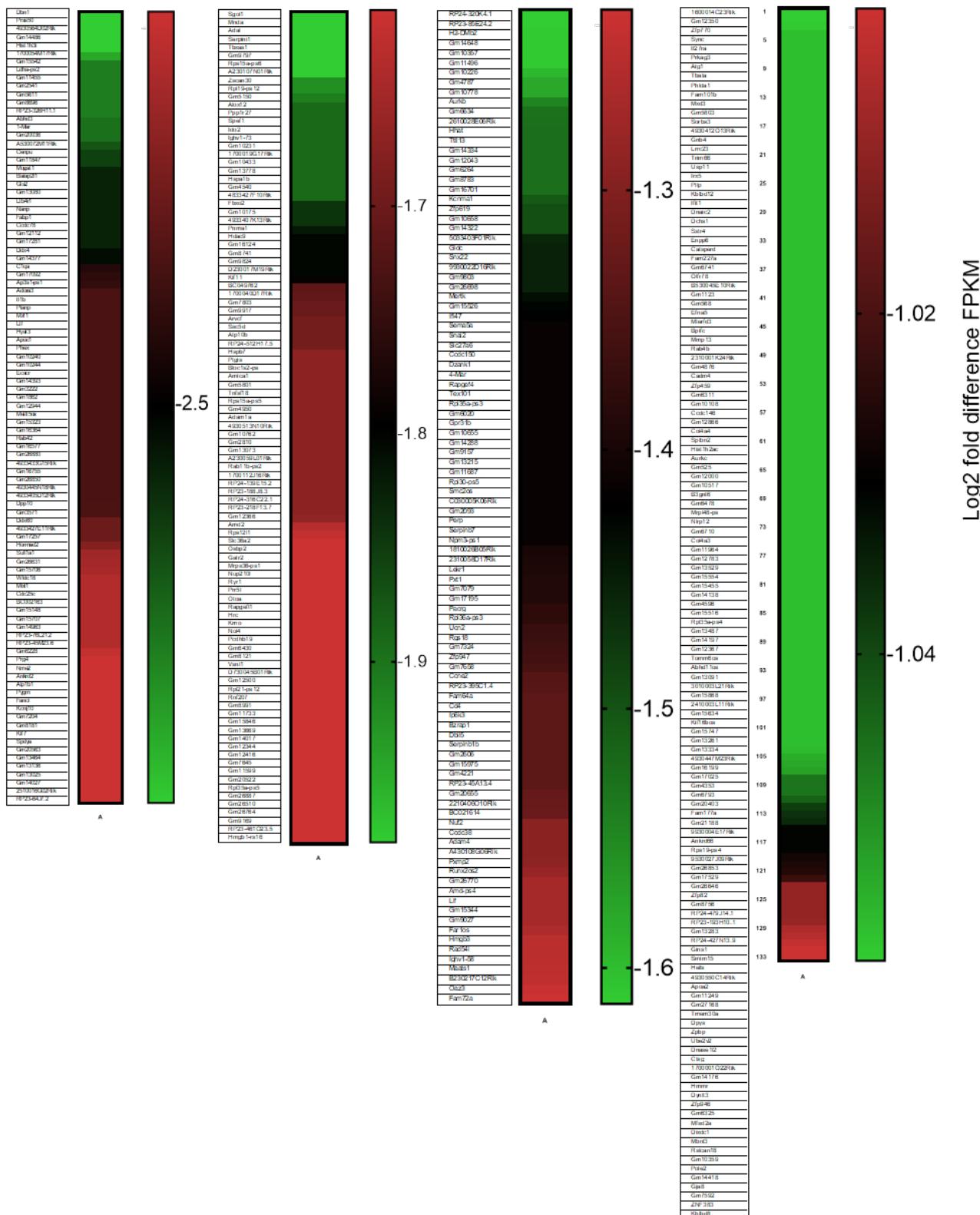


**Supplemental Figure- 1a:** qPCR validation of Antigen 85B derived p25 and CFP-10 derived C5 related to Fig.1. Primers shown in *Supplemental Fig.8*.

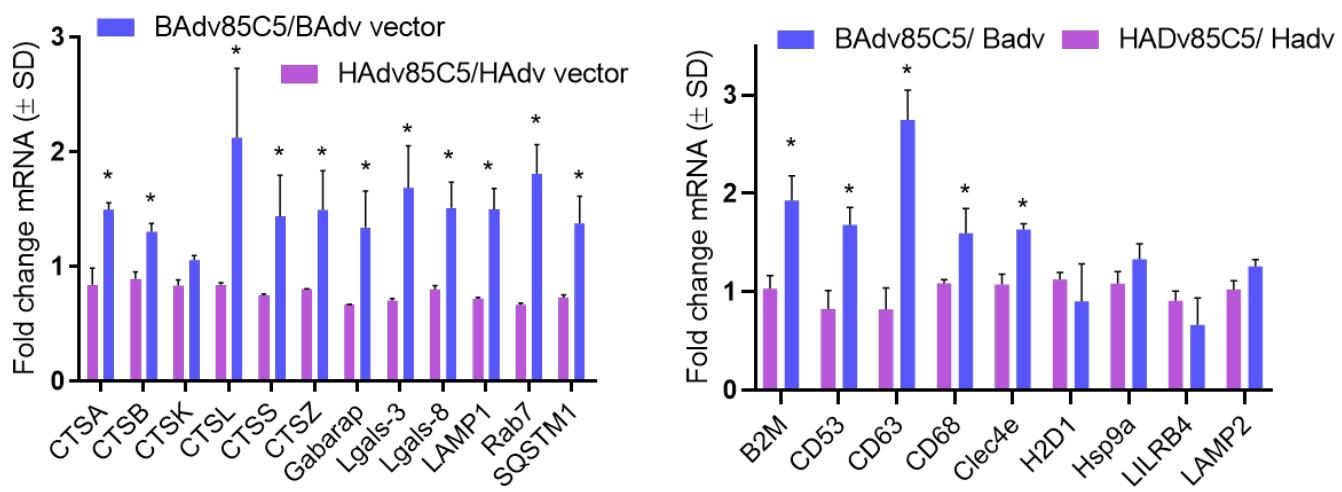


**Supplemental Figure- 1b:** Gene cassette of HAdv constructs related to Fig.1.

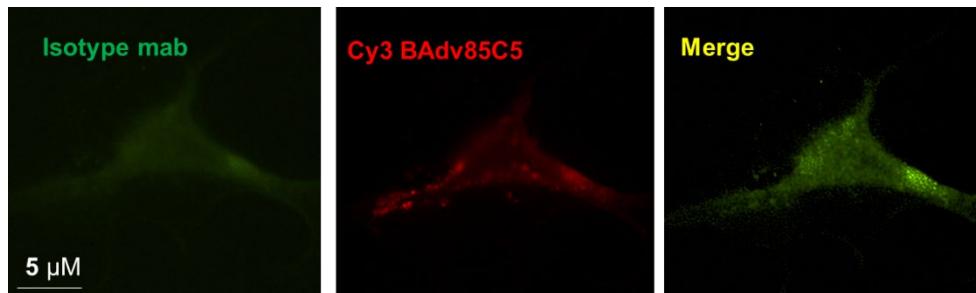




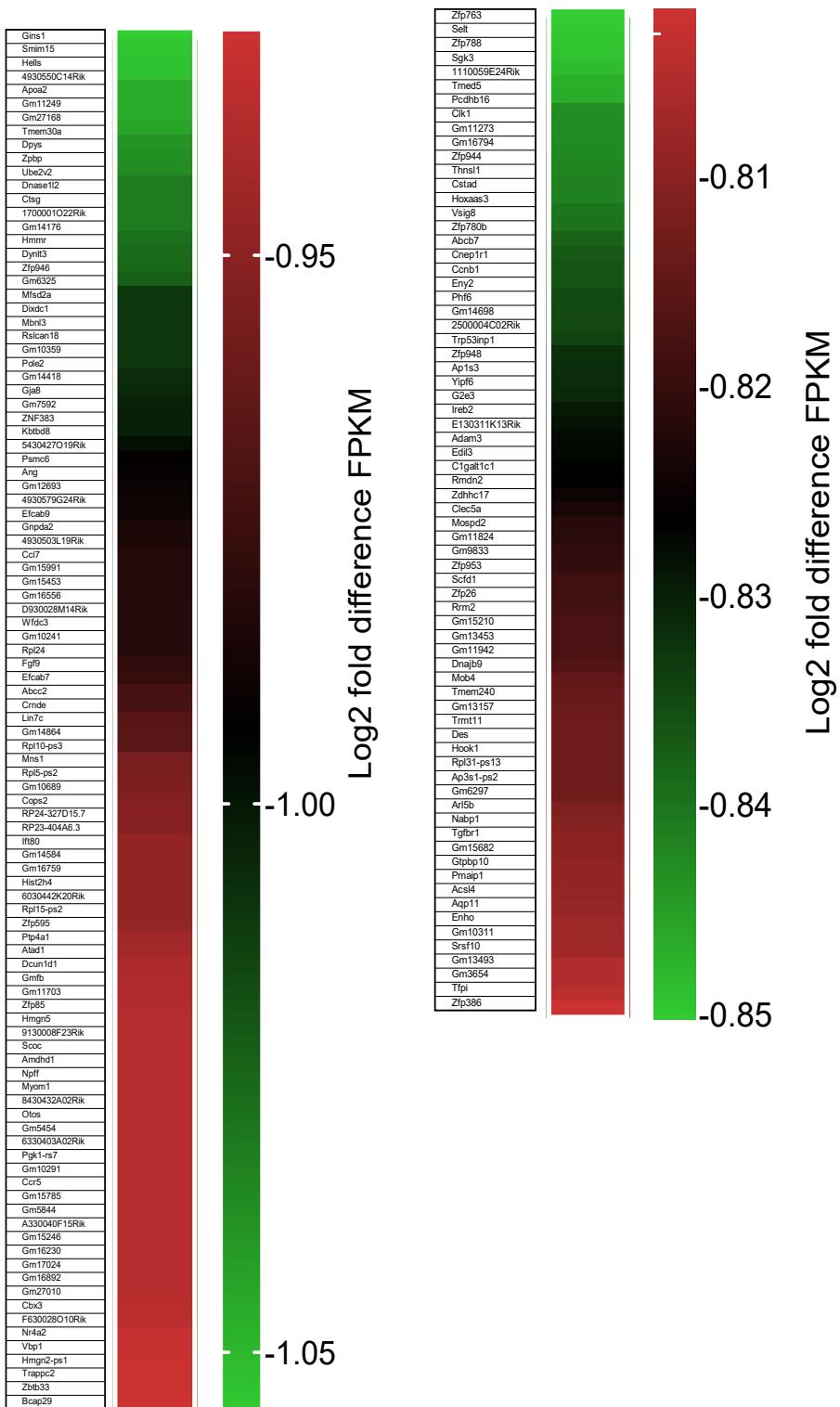
**Supplemental Figure- 3:** DEGs of BAdv<sup>85C5</sup> in wt-DCs vs. BAdv<sup>85C5</sup> in ATG7KODCs, related to Fig.2.



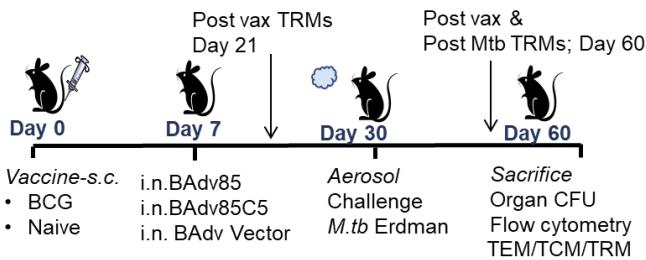
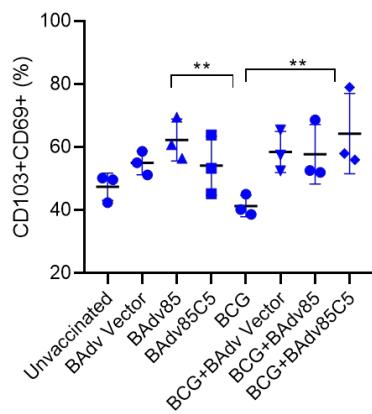
**Supplemental Figure- 4:** qPCR validation of genes in BAdv<sup>85C5</sup> infected DCs vs. HAdv<sup>85C5</sup> infected DCs, related to Figs. 2.



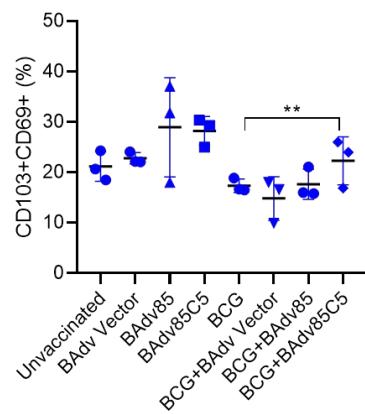
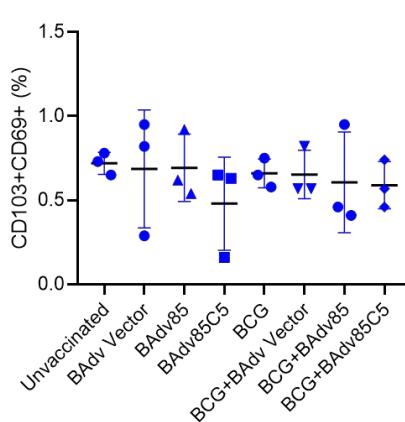
**Supplemental Figure- 5:** Isotype controls related to Fig.3.



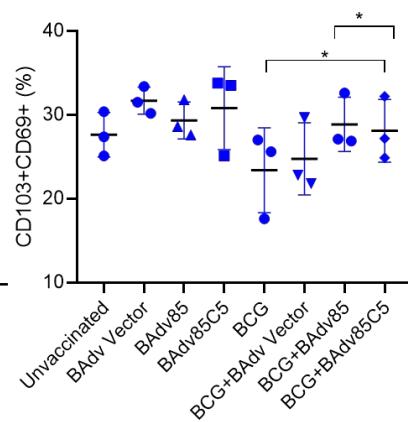
**Supplemental Figure- 6:** DEGs of BAdv<sup>85C5</sup> in C57Bl/6 derived wt-macrophages compared to HAdv<sup>85C5</sup>, related to Fig.2.

**A****B** TRMs Lungs post vax

TRMs Lungs post Mtb challenge

**C** TRMs Spleens post vax

TRMs Spleens post Mtb challenge

**Supplemental Figure- 7:**  $T_{RMs}$  ( $CD4^+CD103^+CD69^+$ ) on day 21 for post vaccination and day 60post Mtb challenge, related to *Fig. 7*.

<u>GENE</u>	<u>Forward primer 5'-&gt;3'</u>	<u>Reverse primer 5'-&gt;3'</u>
Ag85b	GATATCGGATCCGCCACC	GCGGCCGCCGATATC
Ag85bC5	GATATCGGATCCGCCACC	GCGGCCGCCGATATC
β-Actin	CATTGCTGACAGGGATGCAGAAGG	TGCTGGAAGGTGGACAGTGAGG
CTSA	TGTCGGAAGGCTCTCACATC	CACATCTCCGTTGAGAGCAGG
CTSB	AGTCAACGTGGAGGTGCTGCT	GTAGACTCCACCTGAAACCAGG
CTSK	AGCAGAACGGAGGCATTGACTC	CCCTCTGCATTTAGCTGCCTTG
CTSL	GGAAAATGGAGGTCTGGACTCG	GTGTCATTAGCCACAGCGAACTC
CTSS	GCATAGAGGCAGACGCTTCCTA	CCACTGCTTCTTCAGGGCATC
CTSZ	GTGTCAGAACGATGGCATCGA	CCTTGTAGGTGCTGGTCACGAT
GABARAP	CAAAGAGGAGCATCCGTTGAG	TTGTCCAGGTCTCCTATCCGAG
GAPDH	CATCACTGCCACCCAGAACAGTG	ATGCCAGTGAGCTTCCCAGTCAG
LGALS3	AACACGAAGCAGGACAATAACTGG	GCAGTAGGTGAGCATCGTTGAC
LGALS8	GAGGAGATCACCTACGACATGC	CGTACAGCAGAACATGCCTTCC
RAB7	GAGCGGACTTTCTGACCAAGGA	CAATCTGCACCTCTGTAGAAGGC
LAMP1	CCAGGCTTCAAGGTGGACAGT	GGTAGGCAATGAGGACGATGAG
Sqstm1	GCTCTCGGAAGTCAGCAAACC	GCAGTTCCGACTCCATCTGT

Fold change is calculated by using  $2^{-\Delta\Delta Ct}$  method

Briefly,

$$\Delta Ct = Ct \text{ (gene of interest)} - Ct \text{ (housekeeping gene)}$$

$$\Delta\Delta Ct = \Delta Ct \text{ (treated sample)} - \Delta Ct \text{ (untreated sample)}$$

$$\text{Fold change} = 2^{-\Delta\Delta Ct}$$

**Supplemental Figure- 8:** qPCR primers used in this study; related to *Figs.5 and 6.*