

1 **Skin Delivery of Modified Vaccinia Ankara Viral Vectors Generates Superior T**
2 **Cell Immunity Against a Respiratory Viral Challenge**

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14

15 **Abstract**

16 Modified Vaccinia Ankara (MVA) was recently approved as a Smallpox vaccine. Transmission
17 of Variola is by respiratory droplets, and MVA delivered by skin scarification (s.s.) protected
18 mice far more effectively against lethal respiratory challenge with VACV than any other route of
19 delivery, and at much lower doses. Comparisons of s.s. with intradermal, subcutaneous or
20 intramuscular routes showed that MVA_{OVA} s.s.-generated T cells were both more abundant and
21 transcriptionally distinct. MVA_{OVA} s.s. produced greater numbers of lung Ova-specific CD8⁺
22 T_{RM} and was superior in protecting mice against lethal VACV_{OVA} respiratory challenge. Nearly
23 as many lung T_{RM} were generated with MVA_{OVA} s.s. compared to direct pulmonary
24 immunization with MVA_{OVA}, and both routes vaccination protected mice against lethal
25 pulmonary challenge with VACV_{OVA}. Strikingly, MVA_{OVA} s.s.-generated effector T cells
26 exhibited overlapping gene transcriptional profiles to those generated via direct pulmonary
27 immunization. Overall, our data suggest that heterologous MVA vectors delivered via s.s. are
28 uniquely well-suited as vaccine vectors for respiratory pathogens like COVID-19. In addition,
29 MVA delivered via s.s. could represent a more effective dose-sparing smallpox vaccine.

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31 Vaccines against viral and bacterial pathogens have become a fundamental part of pediatric and
32 adult patient care¹⁻⁴. Once ubiquitous diseases like smallpox, polio, measles, tetanus, and
33 diphtheria have either been eliminated or substantially reduced in incidence by vaccination in
34 most of the industrialized world. Vaccination against seasonal influenza has been more
35 challenging, and vaccination against HIV has proven elusive⁵⁻⁷. Vaccines against emerging
36 diseases like Ebola, SARS, and MERS and most recently COVID-19 are the subject of intense
37 interest and widespread activity⁸⁻¹⁰. Most vaccines are administered by intramuscular or
38 subcutaneous injection. While readily accessible, skeletal muscle tissue is poorly adapted to
39 initiating immune responses, as is subcutaneous adipose tissue¹¹. In contrast, upper layers of the
40 skin are the site of continuous and multiple immune responses over a lifetime¹². Smallpox
41 vaccination through skin with Vaccinia virus (VACV) has been uniquely successful^{2,11}.

42 The eradication of smallpox by worldwide epicutaneous immunization with VACV was
43 the greatest public health achievement of the 20th century². Since that time, VACV has been
44 employed as a vaccine vector in many settings¹³. However, its use has been limited by
45 unacceptable morbidity, particularly in recipients who are immunocompromised¹⁴. More
46 recently, Modified Vaccinia Ankara (MVA), a replication-deficient variant of VACV, has come
47 into wider use¹⁵. Although it lacks ~10% of the parent genome¹⁶, it retains the immunogenicity
48 of the parent virus and has just been approved by the FDA as a modern alternative for smallpox
49 preventative vaccination¹⁷. Like VACV, it is also being widely used as heterologous vaccine
50 vector¹⁸. However, MVA and derivative vectors are almost invariably delivered intramuscularly
51 or subcutaneously¹⁹.

52 Several important features of smallpox vaccination deserve to be re-emphasized. In the 20th
53 century, delivery of VACV i.m. was ineffective at conferring protection against smallpox. In

54 contrast, development of a cutaneous “pox” lesions, achieved only after epicutaneous
55 immunization, was considered emblematic of successful protective vaccination, suggesting that
56 this mode of delivery was critically important¹⁴. In addition, smallpox vaccination was effective
57 in patients with agammaglobulinemia, while VACV immunization had disastrous complications
58 in patients with T cell deficiency²⁰. This suggested that T cells were critically important for
59 protective immunity^{21,22}. Finally, Variola virus is transmitted via respiratory droplets, suggesting
60 an oropharyngeal-pulmonary mode of transmission²³. It is notable that murine models of
61 epicutaneous skin immunization with VACV generate memory T cell populations in both skin
62 and lung, and these lung memory T cells protect against lethal pulmonary challenge with this
63 virus¹¹. Intramuscular immunization with VACV in these models did not yield comparable
64 protection. This suggests that protection against smallpox is at least in part mediated by T
65 cells^{22,24}, and that skin immunization is an effective means of generating protective memory T
66 cell populations in the lung¹¹.

67 In the present study, we asked whether immunization with MVA was more effective and
68 more effective if delivered epicutaneously (s.s.) as compared to intramuscularly (i.m.). We also
69 asked whether skin immunization with an MVA vector generated populations of antigen specific
70 CD8⁺ T cells in lung as well as skin. In addition, epicutaneous immunization was compared to
71 intradermal, subcutaneous, and intramuscular immunization in generated protective immunity
72 against a lethal pulmonary challenge. Finally, we asked if T cell imprinting by skin draining and
73 lung draining nodes was similar.

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77 **Results**

78 Doses from 10^4 pfu to 10^7 pfu of MVA were used for epicutaneous immunization (s.s.),
79 and after 7 days, lymph node and spleen T cells were harvested and stimulated *in vitro* with
80 VACV infected splenocytes, after which IFN- γ production was measured. All MVA doses led to
81 significant T cell IFN- γ production, with 10^6 and 10^7 pfu being equally potent (**Fig. 1a,b**). Other
82 groups of mice were immunized with these doses, and after 30 days these mice were challenged
83 on the skin with VACV. After 6 days, biopsies of the immunized sites were taken and VACV
84 DNA was measured by PCR. All immunization doses led to diminished VACV DNA at the
85 infected site (compared to unimmunized controls), but 10^6 and 10^7 pfu immunization showed
86 superior protection (**Fig. 1c**). Other groups of mice were immunized in an identical manner and
87 were subjected to lethal intranasal infection with VACV at day 30. All unimmunized mice
88 rapidly lost weight and succumbed to the infection. In contrast, 40% of 10^4 , 70% of 10^5 , and
89 100% of 10^6 and 10^7 pfu immunized mice survived the infection (**Fig. 1d,e**). Thus, 10^6 pfu is the
90 lowest MVA dose that provides both strong T cell cytokine production as well as optimal
91 protective immunity against skin and pulmonary infection.

92 To test whether delivery of MVA to scarified skin could induce poxvirus-specific
93 immune responses, we inoculated C57BL/6 mice with MVA or Vaccinia Virus (VACV) by
94 scarification. By 7 days after inoculation, a pustular lesion resembling a “pox” reaction had
95 formed at the inoculation site in all the immunized mice. The pox lesions induced by MVA and
96 VACV skin scarification followed similar patterns of evolution (although with different size and
97 kinetics), from macules to papules to vesicles and finally into pustules which ruptured and healed
98 over time with scars (**Extended data, Fig. 1**). MVA-induced pox reactions did heal more rapidly
99 than those induced by replication competent VACV (**Extended data, Fig. 1**). To determine the

100 safety of MVA in immunocompromised hosts, we next immunized immunodeficient Rag1^{-/-}
101 mice with VACV and MVA, respectively, and followed the mice for several weeks. While both
102 groups of mice lost some weight over the first two weeks, MVA immunized mice rapidly
103 regained the weight and flourished over the next several weeks (**Fig. 1g**). In contrast, 100% of
104 the VACV immunized mice developed progressive weight loss and expanding cutaneous lesions
105 of VACV infection, ultimately requiring euthanasia (**Fig. 1f-h**). Thus, MVA can be administered
106 safely to mice wholly deficient in adaptive immunity. In another set of experiments, we
107 immunized Wild-type (WT) mice as well as mice deficient in either Langerhans cells (Langerin
108 DTA) or both Langerhans cells and langerin positive dermal dendritic cells (Langerin DTR +
109 DT), respectively. Prior to infection, mice were loaded with OT-1 cells and the immunizing virus
110 was MVA_{OVA}. Spleen and lymph nodes were harvested at days 10 and 30, skin was harvested at
111 day 30, and OT-1 T cells were counted. At day 10, T_{eff} cells were somewhat diminished in
112 Langerin DTA mice and more markedly diminished in Langerin DTR + DT mice (**Fig. 1i**). At
113 day 30, skin T_{RM} were significantly diminished in Langerin DTA mice and even more
114 diminished in Langerin DTR+DT mice (**Fig. 1i**). This pattern was also true for T cells bearing
115 markers of T_{CM} and T_{EM}. These data suggest that both LC and langerin positive dermal DC play
116 an additive role in optimal antigen presentation of MVA-encoded antigens to T cells.

117 We next compared the anatomical route of vaccine delivery on the T cell response to
118 MVA vaccination. Using CFSE OT-1 loaded mice, MVA_{OVA} was delivered by epicutaneous
119 infection (s.s.), or injected intradermally (i.d.), subcutaneously (s.c.), or intramuscularly (i.m.).
120 Draining lymph nodes were harvested at 60 hours and 5 days, and OT-1 cells were analyzed by
121 FACS. LN from s.s. immunized mice showed roughly 90% of OT-1 proliferating, and 60%
122 making IFN- γ , at 60 hours, with comparable numbers at 5 days (**Fig. 2a,c**). Vaccination by i.d.

123 was less effective, with 71% of OT-1 cells proliferating and 33% making IFN- γ at 60 hours, with
124 modest improvement at 5 days post infection (**Fig. 2a,c**). Both s.c. and i.m. showed poor OT-1
125 activation at 60 hours with some improvement at 5 days (**Fig. 2a,c**). When lymph node or spleen
126 OT-1 cells were stimulated with antigen, significantly more IFN- γ was produced by OT-1 cells
127 from mice vaccinated via s.s. compared to other routes (**Extended data, Fig. 2**). Vaccination via
128 i.d. was intermediate with regard to IFN- γ production, while s.c. and i.m. led to nearly four-fold
129 lower IFN- γ levels (**Extended data, Fig. 2**). In terms of absolute numbers of OT-1 cells
130 generated, s.s. was superior to all modes of vaccination, with i.d. being second and both i.m. and
131 s.c. far less effective (**Fig. 2b,d**). We next took OT-1 cells from the 5-day post-immunization
132 time point and performed transcriptional profiling on OT-1 cells generated after s.s., i.d., s.c., or
133 i.m., respectively. While there was some overlap, there were surprisingly many differences
134 between T cells generated by different routes of immunization, even at the same day post
135 immunization (**Fig. 2e, Extended data, Fig. 3**). Principal component analysis revealed that T_{eff}
136 generated by s.s. and i.m. were transcriptionally quite distinct. T cells generated after s.s., i.d.,
137 and s.c., were more similar but still quite distinct from one another. T cells generated by s.s. and
138 i.d. clustered closely but were still clearly not overlapping. Moreover, s.s. generated most
139 abundant skin infiltrating cells at day 5 post immunization (**Fig. 2g**).

140 We next examined memory OT-1 T cells generated at 45 days by these four routes of
141 immunization. With regard to T_{CM}, s.s. generated the largest population of these cells, roughly
142 twice as many as i.m. (**Fig. 3a**). The difference was even more striking when T_{EM} were
143 examined; here, s.s. generated at least 3-fold more cells than did other modes of immunization,
144 with s.c. being least effective (**Fig. 3b**). T_{RM} were then examined, in both skin and lung.
145 Immunization via s.s. generated 3-fold more skin T_{RM}, and more than twice as many T_{EM}, with

146 i.d. being the second most effective route (**Fig. 3-f**). Because MVA is often delivered i.m., it is
147 important to note that the number of T_{RM} generated by this route was more than 4-fold lower
148 than by s.s. (**Fig. 3 c-f**). Transcriptional profiling showed that at 45 days, OT-1 T_{EM}'s still
149 showed non-overlapping PCA clusters from s.s, i.d., s.c., and i.m. immunized mice. In contrast,
150 T_{CM} from the same mice showed transcriptional profiles that were more tightly clustered,
151 indicating that differences between the groups were minimal (**Fig. 2e**). Skin T_{RM} could not be
152 compared because insufficient 45-day T_{RM} were generated by i.m. and s.c. immunization.

153 In subsequent experiments, we examined groups of mice vaccinated by these different
154 routes for their ability to respond to a lethal intranasal challenge of VACV_{OVA}. Groups of ten
155 mice assayed 45 days after initial vaccination were subjected to intranasal challenge, and mice
156 were weighed daily after vaccination. Mice that lost >20% of body weight were sacrificed.
157 **Figure 3g and h** show that naïve mice universally succumbed to the lethal infection, while mice
158 immunized epicutaneously (s.s.) showed minor transient weight loss but complete survival. In
159 contrast, mice vaccinated i.d., s.c., or i.m. lost substantial weight (**Fig. 3g**), and while 60% of i.d.
160 vaccinated mice survived, only 40% and 30% of mice vaccinated i.m. and s.c., respectively,
161 survived (**Fig. 3h**). These results are consistent with the superior production of different memory
162 T cell subsets after vaccination by s.s..

163 We were struck by the capacity of skin immunization via s.s. to generate both skin T_{RM}
164 and lung T_{RM}. While skin and gut T cell trafficking have been studied extensively, lung T cell
165 trafficking has been studied less comprehensively. We immunized CFSE OT-1 loaded mice with
166 MVA_{OVA} via three routes: s.s. to assess skin homing, intraperitoneally (i.p.) to assess gut
167 homing, and intra-tracheally (i.t.) to assess lung homing. At 60 hours, T cells were collected
168 from the respective draining lymph nodes (inguinal for skin, mesenteric for gut, and mediastinal

169 for lung) and were sorted based on CFSE expression into cells that had not divided (P0) or had
170 divided once through five times (P1-P5; **Fig. 4a**). Cells were subjected to transcriptional
171 profiling, and results were analyzed bioinformatically. By principal component analysis, P0 cells
172 from skin, gut, and lung homing nodes clustered near each other (**Fig. 4b**). However, as early as
173 P1 and clearly by P2, OT-1 cells activated in different nodes diverged significantly in
174 transcriptional profile. In particular, OT-1 cells from mesenteric nodes were quite distinct from
175 OT-1 cells from inguinal and mediastinal nodes (**Fig. 4b**). Interestingly, P1-P5 cells from
176 inguinal (skin draining) node clustered closely with P1-P5 cells from mediastinal (lung draining)
177 nodes, suggesting similar pathways involved in skin and lung homing imprinting (**Fig. 4b**).
178 Excluding genes upregulated in all T cell groups, lung and skin homing T cells shared
179 upregulation of 150 genes, compared to 73 and 90 upregulated in only skin or only lung,
180 respectively (**Fig. 4c, d**). In contrast, only 11 upregulated genes were shared between skin and
181 gut, and only 36 between lung and gut. Examination of chemokine receptors and integrin genes
182 showed homology between lung and skin, while gut immunization showed unique upregulation
183 of CCR9, $\alpha 4$ and $\beta 7$ integrins (**Fig. 4e**). These data suggest a very similar pattern of gene
184 expression of T cells activated in skin versus lung draining LN, and a pattern in gut draining LN
185 that is very different from lung and skin draining LN.

186 We next directly compared the capacity of skin (s.s.), lung (i.t.), and gut (i.p.)
187 immunization with MVA_{OVA} to generate lung T_{RM}. Mice were immunized by the above routes
188 and after 45 days, lung T_{RM} were analyzed. As expected, lung immunization resulted in the
189 highest number of lung T_{RM}, but skin immunization by s.s. generated more than half as many
190 T_{RM} in lung (**Fig. 4f**). In contrast, i.p. immunization resulted in less than 10% of the lung T_{RM}
191 compared to lung immunization (**Fig. 4f**). Like skin T_{RM}, lung T_{RM} were CD69⁺, CD103⁺,

192 CD62L⁻, KLRG1⁻, and expressed E and P selectin ligands (**Extended data, Fig. 4**). A
193 companion cohort of mice were subjected to lethal intranasal challenge with VACV_{OVA}. Mice
194 immunized i.t. or s.s. showed mild weight loss but 100% recovery and survival (**Fig. 4g,h**). Mice
195 immunized i.p. showed more severe weight loss, and only 60% survived the infectious challenge
196 (**Fig. 4g,h**). In another series of experiments, i.t. immunization was compared to s.s.
197 immunization with regard to generation of skin T_{RM}. While s.s. was most efficient at generating
198 skin T_{RM}, lung immunization via i.t. generated 50% of the skin T_{RM} compared to s.s.
199 immunization (**Extended data, Fig. 5**). These data confirm that lung immunization can generate
200 abundant skin T_{RM}, and skin immunization can generate abundant lung T_{RM}.
201

202 **Discussion**

203 Smallpox vaccination via epidermal disruption using Vaccinia virus (VACV) provided
204 broad and effective protective immunity against Smallpox caused by Variola major, and led to
205 the eradication of this devastating infectious disease¹⁴. MVA is derived from VACV but has lost
206 10% of the parent genome, including several immune inhibitory genes that block CC
207 chemokines, IFN α/β , IFN γ , TNF α , and STING²⁵, and does not replicate in mammalian cells¹⁸.
208 In addition to its use as a smallpox vaccine, MVA has been used extensively as a heterologous
209 vaccine vector¹⁵, although we were unable to find any description of it being delivered through
210 skin scarification. Rather, intramuscular or subcutaneous injection appear to be the preferred
211 routes. There are no clear reasons that MVA has not been delivered via s.s., other than the
212 assumption that replication was required for this route of administration. Here, we show that
213 MVA delivered by s.s. can provoke a potent immune response at doses much lower than those
214 used for i.m. and s.c. injection. In a direct comparison of delivery via i.m., s.c., and i.d. routes,
215 s.s. administration of lower doses of MVA provide superior protective immunity against a lethal
216 VACV challenge. These data suggest that like VACV, MVA delivered by s.s. provides a potent
217 and durable immune response. We found that both Langerhans cells and CD207+ dermal
218 dendritic cells were both required for optimal immunization via this route. In contrast to VACV,
219 mice deficient in adaptive immunity could be safely immunized via s.s. with MVA, supporting
220 the safety of this vector in immunocompromised hosts. One other advantage of the s.s. mode of
221 delivery is dose sparing—doses of MVA too low to elicit immune response i.m. are quite
222 immunogenic when delivered by s.s.

223 When used as a heterologous vaccine vector encoding for a T cell antigen, MVA_{OVA}
224 delivered s.s. provided robust early activation of OVA-specific T cells (OT-1) in skin draining

225 lymph nodes. Interestingly, early CD8⁺ effector T cells in skin draining lymph nodes at day 5
226 showed different patterns of gene expression after immunization s.s., i.d., s.c., and i.m.,
227 respectively. T cells generated by i.m. immunization were most distinct transcriptionally from
228 those generated by s.s. immunization. When T cells were harvested from spleens at day 45 after
229 immunization, cells with T_{EM} markers retained distinct transcriptional profiles, with i.m.
230 generated T_{EM} cells being most distinct from s.s. generated T_{EM} cells. Day 45 memory T cells
231 expressing CD62L (T_{CM}) showed smaller transcriptional differences across immunization routes,
232 but s.s. generated T_{CM} cells were still readily distinguished from those generated by i.m.
233 immunization. These surprising data suggest that there are qualitative differences in T_{eff} and T_M
234 cells generated by immunization route that are evident by day 5 and persist at day 45.

235 There were also quantitative differences in T_M generation depending on route of
236 administration. Immunization via s.s. generated greater numbers of both T_{EM} and T_{CM} at 45 days
237 after immunization. When skin T_{RM} were measured, s.s. generated more T cells than other routes,
238 with i.m. being least efficient. Because lethal intranasal challenge with VACV results in death
239 from pulmonary inflammation, we also measured lung T_{RM}. Strikingly, s.s. generated higher
240 numbers of lung T_{RM} than other routes, consistent with previous reports^{11,26}, with i.m. generating
241 fewest lung T_{RM}. T_{RM} from skin and lung both expressed CD69 and CD103, with expression of
242 E- and P-selectin ligands detectable as well. When animals were challenged by lethal intranasal
243 infection with VACV_{OVA}, only mice immunized by s.s. showed minimal weight loss and 100%
244 survival. Mice immunized by all other routes showed greater morbidity and some mortality, with
245 i.m. immunization being least effective. Whether the ability of s.s. immunized mice to uniformly
246 survive the intranasal challenge of VACV_{OVA} was due to higher numbers of lung T_{RM},
247 circulating T_{EM} and T_{CM}, or qualitatively different T_{eff} and memory T cells cannot be determined

248 from these data. However, this suggests that the original method of smallpox vaccination— s.s.
249 administration—appears to be uniquely effective at generating robust protective immunity
250 against airway challenge.

251 Because s.s. immunization was so efficient at generating lung T cells and protective
252 immunity against a pulmonary infectious challenge, we compared skin infection with direct lung
253 infection, and assess T_{eff} in skin and lung draining LN, respectively, using i.p. injection and
254 mesenteric nodes as a control. Thus, three routes of immunization were compared— s.s.,
255 intratracheal (i.t.), and intraperitoneal (i.p.), and T_{eff} from draining lymph nodes—inguinal,
256 mediastinal, and mesenteric, respectively--- were compared by transcriptional profiling. While
257 proliferating T_{eff} from skin graining and gut draining nodes rapidly diverged, proliferating T_{eff}
258 from skin draining and lung draining nodes showed significant overlap over time. Both $\alpha 1\beta 1$
259 intergrin, CCR4, and CCR8 were preferentially elevated in T cells from skin and lung draining
260 nodes, and $\alpha 4\beta 7$ and CCR9 were preferentially upregulated in mesenteric lymph nodes,
261 consistent with previously reported data²⁷⁻²⁹. When lung T_{RM} were examined after 45 days, both
262 skin and lung infection generated abundant lung T_{RM}, while i.p. immunization was less efficient
263 at generating these cells. Protection against lethal intranasal challenge was complete in skin and
264 lung immunized mice, but incomplete after i.p. immunization. These data suggest that there is
265 substantial overlap in T cells imprinted by skin and lung draining lymph nodes and suggests that
266 skin immunization is well-suited at generating T cells with lung tropic properties.

267 Two important conclusions can be drawn from this study that are relevant to human
268 disease. First, immunization with MVA generates powerful immunity, but like VACV the most
269 potent local and systemic immunity generated occurs after superficial skin immunization (s.s.)
270 that involves epidermal disruption. The dose of MVA used in s.s. delivery can be much lower

271 than required in muscle/i.m. delivery. This suggests that doses of MVA being stockpiled in
272 anticipation of a dystopian future smallpox attack may protect orders of magnitude for more
273 people if delivered s.s. instead of MVA. The second conclusion is that MVA delivered by s.s. is
274 a very effective way of generating protective T_{RM} in lung, in addition to a more robust circulating
275 T cell response. MVA vaccines are being developed for respiratory pathogens, including
276 influenza A and respiratory syncytial virus^{30,31}, but these are being tested only by i.m. or s.c.
277 injection. Our data strongly suggests that delivering these vaccines via s.s. may generate even
278 more effective protective immunity to pathogens that infect lung. Whether MVA encoding for
279 Coronavirus genes and delivered s.s. could provide protective immunity against COVID-19 is an
280 intriguing question that we are pursuing presently.

281

282 **Methods**

283 Methods and associated references are available in the online version of the paper.

284 **Acknowledgements**

285 We thank Dr. Mike Seaman (Beth Israel Deaconess Medical Center, Boston, MA) for providing
286 the initial stock of MVA, Dr. Bernard Moss (NIH) for providing the initial stocks of VACV.

287 This work was supported by grants R01 AI127654 to Dr. T. S. Kupper from National Institutes
288 of Health/NIAID and R01 AR065807 from the National Institutes of Health/NIAMS.

289 **Supplementary Information**

290 Supplementary Information is linked to the online version of the paper.

291 **Competing interests statement**

292 The authors declare that they have no competing financial interests.

293 **Figure Legends**

294 **Figure 1. MVA immunization via skin scarification (s.s.) elicits dose-dependent anti-**
295 **vaccinia immune response. a-b.** IFN- γ secretion by vaccinia-specific T cells isolated from
296 draining lymph nodes (a) or spleens (b) at 7 days post MVA infection at indicated dose. **c.**
297 Quantitative real time PCR (qRT-PCR) analysis of skin viral load at 6 days post re-infection.
298 Mice were immunized with the indicated doses of MVA via s.s. 45 days later, mice were re-
299 challenged with 1.8×10^6 pfu vaccinia virus (VACV). Then 6 days later, skin tissues were
300 harvested and processed to qRT-PCR. **d-e.** Body weight (BW) (d) and survival measurements (e)
301 of WR-VACV re-challenged mice that were immunized previously with MVA at indicated dose
302 45 days earlier. **f.** Photographs of pox lesion in Rag1^{-/-} mice taken on day 4, 7, 14 and 28 post-
303 immunization with the same amount (1.8×10^6 pfu) of MVA or VACV. **g-h.** Immunized Rag1^{-/-}
304 mice were monitored for BW change (g) and survival (h) for up to 12 weeks after immunization
305 with the same amount (1.8×10^6 pfu) of MVA or VACV. **i.** Quantification of effector T cell (T_{eff},
306 day 5), central memory (T_{CM}, day 45), effector memory (T_{EM}, day 45) or tissue resident memory
307 (T_{RM}, day 45) T cells post MVA infection. Naïve OT-I Thy1.1⁺ cells were transferred into
308 Thy1.2⁺ recipient mice one day before mice were infected with 1.8×10^6 pfu MVA-Ova. Then at
309 different time points post infection, OT-I cells were isolated from lymph nodes (T_{eff}, T_{CM}, T_{EM})
310 or skin (T_{RM}) and analyzed by flow cytometry. a-c. Data is representative of three independent
311 experiments. Symbols represent individual mice (n = 5 mice/group). c-d. Unimmunized (UI)
312 mice were included as controls. Graphs show mean \pm s. d., ns = not significant, *p < 0.05, **p <
313 0.01.

314 **Figure 2. Delivery of MVA via s.s. generates T cells that are both quantitatively more**
315 **abundant and qualitatively distinct from those generated from i.d., s.c., i.m.. a-d.** Flow

316 cytometric analysis (a, c) and quantification (b, d) of OT-I cell proliferation in draining lymph
317 nodes of recipient mice at 60 hours (a, b) and 5 days (c, d) post MVA infection via different
318 routes. CFSE-labeled naïve OT-I Thy1.1⁺ cells were transferred into Thy1.2⁺ recipient mice one
319 day before mice were infected with 1.8×10^6 pfu MVA-Ova via indicated infection routes. **e.**
320 Principal component analysis (PCA) of gene-expression for T cells generated by MVA infection
321 via different routes. Naïve T cells (T_N) were sorted from the peripheral lymph nodes of naïve
322 OT-I mice. Effector T cells (T_{eff}) were sorted from draining lymph nodes at 5 days post
323 infection. Central memory T cells (T_{CM}) and effector memory T cells (T_{EM}) were sorted from the
324 spleen of mice at 45 days post infection. Each dot represents an individual experiment wherein
325 mRNA was pooled from 15-20 mice from 3-4 independent biological groups (5 mice/group). **f.**
326 Heatmap of differentially expressed genes selected from a pair-wise comparison between s.s.
327 generated T_{eff} cells and naïve T cells. **g.** Quantification of skin infiltrating T cells at day 5 post
328 1.8×10^6 pfu MVA-Ova infection via indicated routes. a, c, Data are representative of three
329 independent experiments (n = 5 mice per group). Graphs show mean \pm s. d. of 5 mice per group.
330 *p < 0.05, **p < 0.01.

331 **Figure 3. Delivery of MVA via s.s. is superior in generating memory T cells and is superior**
332 **in protecting mice against lethal respiratory challenge. a-b.** Quantification of OT-I T_{CM} and
333 T_{EM} cells from spleen of mice at 45 days post MVA infection via indicated routes. **c-f.** Flow
334 cytometric analysis (c, e) and quantification (d, f) of OT-I T_{RM} cells isolated from skin (c, d) or
335 lung (e, f) tissue at 45 days post MVA infection via indicated routes. **g-h.** Body weight (BW) (g)
336 and survival measurements (h) of WR-VACV re-challenged mice that were previously
337 immunized with MVA via indicated routes 45 days earlier. OT-I WT cells were adoptively
338 transferred into μ MT mice before mice were infected with 1.8×10^6 pfu MVA via indicated

339 routes. 45 days later, mice were re-challenged with a lethal dose of WR-VACV by intranasal
340 infection. c, e, Data are representative of three independent experiments (n = 5 mice per group).
341 Graphs show the mean \pm s. d. of 5 mice per group. Un-immun. = un-immunized. **p < 0.01.

342 **Figure 4. MVA s.s. generates more than half number of lung T_{RM} compared to intra-**
343 **tracheal (i.t.) and is sufficient to protect mice against lethal respiratory challenge. a.** Flow
344 cytometric analysis of OT-I cell proliferation in draining lymph nodes at 60 hours post MVA
345 infection via s.s.. CFSE-labeled naïve OT-I Thy1.1⁺ cells were transferred into Thy1.2⁺ recipient
346 mice one day before mice were infected with 1.8×10^6 pfu MVA-Ova. **b.** PCA of gene-
347 expression data for nineteen CD8⁺ T cell populations based on CFSE signal and different
348 infection routes. Each dot represents an individual experiment wherein mRNA was pooled from
349 15-20 mice from 3-4 independent biological groups (5 mice/group). **c.** Heatmap of differentially
350 expressed genes selected from a pair-wise comparison between s.s. and intra-peritoneal (i.p.)
351 activated T cells. **d.** Venn diagram analysis of genes differentially expressed in pairwise
352 comparisons between s.s., i.t. and i.p. activated T cells relative to T_N (fold change cutoff, ≥ 2). **e.**
353 Quantitative real-time PCR (qRT-PCR) analysis of cell homing molecule gene expression in s.s.,
354 i.t. and i.p. activated T cells. **f.** Flow cytometric analysis (left) and quantification (right) of lung
355 T_{RM} cells at day 45 post MVA infection via indicated routes. **g-h.** Body weight (BW) (g) and
356 survival measurements (h) of WR-VACV re-challenged mice that were immunized previously
357 with MVA via indicated routes 45 days earlier. OT-I WT cells were adoptively transferred into
358 μ MT mice before mice were infected with 1.8×10^6 pfu MVA via indicated routes. 45 days later,
359 mice were re-challenged with a lethal dose of WR-VACV by intranasal infection. Graphs show
360 the mean \pm s. d. of 5 mice per group. Un-immun. = un-immunized. ns = not significant, *p <
361 0.05, **p < 0.01.

362 **Extended Data Figure Legends**

363 **Extended Data Figure 1. MVA skin scarification induced smaller pox lesions that healed**
364 **significantly faster compared to VACV skin scarification in immunocompetent mice.**

365 C57BL/6 mice were immunized with 1.8×10^6 pfu MVA or VACV by skin scarification.

366 Photographs of pox lesion were taken on day 4, 7, 14 and 28 post-immunization.

367 **Extended Data Figure 2. Delivery of MVA via s.s. generates stronger cellular responses**

368 **compared to i.d., s.c., and i.m. infection routes.** C57BL/6 mice were immunized with $1.8 \times$

369 10^6 pfu MVA via indicated routes. Activated T cells in draining lymph nodes (a) and spleen (b)

370 were isolated at 7 days post infection, and T cell response against VACV was measured based on

371 IFN- γ secretion. Symbols represent individual mice (n = 5 mice/group). *p < 0.05, **p < 0.01.

372 **Extended Data Figure 3. Delivery of MVA via s.s. generates T cells that are qualitatively**

373 **distinct from those generated from i.d., s.c., i.m.. a-b.** Venn diagram analysis of genes up-

374 regulated (a) or down-regulated (b) in pairwise comparisons between T cells activated via MVA

375 s.s., i.d., s.c., i.m. (day 5) relative to that of T_N. **c-d.** Fold change analysis of genes shared among

376 s.s., i.d., s.c. and i.m. activated T cells (day 5) relative to that of T_N. c, 146 shared up-regulated

377 genes, d, 41 shared down-regulated genes. **e.** Quantitative real-time PCR (qRT-PCR) analysis of

378 cell homing molecule gene expression in s.s., i.d., s.c. and i.m. activated T cells (day 5) relative

379 to that of T_N. ns = not significant, *p < 0.05, **p < 0.01.

380 **Extended Data Figure 4. Phenotyping of tissue-resident memory T cell surface marker on**

381 **lung CD8⁺ T_{RM} cells generated by MVA infection via skin scarification, intra-tracheal**

382 **administration or intra-peritoneal injection.** Flow cytometric analysis of T cell proliferation

383 and homing receptor expression on OT-I cells residing in lung at 45 days post MVA infection.

384 Naïve OT-I Thy1.1⁺ cells were transferred into Thy1.2⁺ recipient mice one day before mice were

385 infected with 1.8×10^6 pfu MVA-Ova by s.s., i.t. or i.p.. At 45 days after infection, proliferation
386 and tissue-homing receptor expression of OT-I T_{RM} cells isolated from lung tissue were analyzed
387 by flow cytometry. Data are representative of three independent experiments (n = 5 mice per
388 group). ESL, E-selectin ligand.

389 **Extended Data Figure 5. Skin T_{RM} cells generated by MVA infection via skin scarification,**
390 **intra-tracheal administration or intra-peritoneal injection.** Flow cytometric analysis and
391 quantification of skin T_{RM} cells at day 45 post 1.8×10^6 pfu MVA infection via indicated routes.
392 Data are representative of three independent experiments (n = 5 mice per group). **p < 0.01.

393

394 **Online Methods**

395 **Mice**

396 Wide-type (WT) C57BL/6, CD45.1⁺, Thy1.1⁺, Rag1^{-/-}, μ MT, Langerin-DTA, Langerin-DTR
397 mice were purchased from Jackson Laboratory. Thy1.1⁺ Rag1^{-/-} OT-I mice were maintained
398 through routine breeding in the animal facility of Harvard Institute of Medicine, Harvard
399 Medical School. Animal experiments were performed in accordance with the guidelines put forth
400 by the Center for Animal Resources and Comparative Medicine at Harvard Medical School.
401 Mice were randomly assigned to each group before start and experiments were performed
402 blinded with respect to treatment. For survival experiments, mice that had lost over 25% of
403 original BW were euthanized.

404 **Viruses**

405 An attenuated strain (VACV) of WR-VACV was used in some experiments as control vaccine
406 and was a kind gift from Dr. Bernald Moss (National Institutes of Health, Bethesda, MD). Wild-
407 type WR-VACV were purchased from American Tissue Culture Company (ATCC). The virus
408 stocks were expanded and tittered in Hela cells and CV-1 cells (ATCC) by standard procedures.
409 ACAM3000MVA (Acambis Modified Vaccinia Ankara) (MVA) and DF-1 Cells were gifted by
410 Dr. Michael Seaman (Beth Israel Deaconess Medical Center, Boston MA). MVA stocks were
411 expanded and titrated in DF-1 cells as previously described (39, 40).

412 **Virus Infection**

413 Mice were immunized with the MVA or VACV at the indicated doses by skin scarification as
414 previously described. Alternatively, mice were immunized by s.c., i.d., or i.m. injection at the
415 indicated dose. For secondary challenge, memory mice were challenged intranasally with a lethal

416 dose of WR-VACV (2×10^6 pfu in 20 μ l of PBS) at 6 to 20 weeks post immunization. The
417 change of BW and survival of mice were monitored daily following challenge for up to 12 days.

418 ***In vitro* restimulation assay**

419 Poxvirus-specific T cell response against poxvirus was assessed at day 7 post challenge. Single
420 cell suspension prepared from draining lymph nodes or spleens was re-suspended in T cell
421 medium (RPMI containing 10% FBS, 2mM 2- β mercaptoethanol, 1X nonessential amino acid,
422 1X sodium pyruvate), and were used as effector cells. For target cell preparation, naïve
423 splenocytes was infected at 37 °C for 5 h with WR-VACV at a MOI of 5 in RPMI medium
424 supplemented with 10% FCS. After infection, the cells were washed 3 times with PBS, and co-
425 cultured (5×10^5 cells/well) with effector cell at a 1:1 ratio in 96 well plate in T cell medium at
426 37 °C for 48 h. Uninfected naïve splenocytes co-cultured with target cells were used as negative
427 controls. IFN- γ concentration in the culture supernatants were measured by ELISA using anti-
428 IFN- γ mAb pairs (BD Pharmingen) according to manufacturer's protocol.

429 **Preparation of cell suspensions**

430 Lymph nodes and spleens were harvested and pressed through a 70- μ m nylon cell strainer to
431 prepare cell suspensions. Red blood cells (RBC) were lysed using RBC lysis buffer (00-4333-57;
432 eBioscience). Skin tissue was excised after hair removal, separated into dorsal and ventral
433 halves, minced, and then incubated in Hanks balanced salt solution (HBSS) supplemented with
434 1 mg/ml collagenase A (11088785103; Roche) and 40 μ g/ml DNase I (10104159001; Roche) at
435 37 °C for 30 min. After filtration through a 70- μ m nylon cell strainer, cells were collected and
436 washed three times with cold PBS before staining.

437 **Mouse adoptive transfer and treatment**

438 Lymph nodes were collected from naïve female donor mice at age of 6-8 weeks. T cells were
439 purified by magnetic cell sorting using a mouse CD8 α ⁺ T-cell isolation kit (130-104-075;
440 Miltenyi Biotec) or a mouse CD4⁺ T-cell isolation kit (130-104-454; Miltenyi Biotec), according
441 to the manufacturer's protocols. T cells were then transferred intravenously into female recipient
442 mice at a total number of 5×10^5 . T cells were labeled with carboxyfluorescein succinimidyl
443 ester (CFSE, 65-0850; eBioscience) before co-transfer, where indicated. In some experiments,
444 mice were treated daily with FTY720 (10006292; CAYMAN, 1 mg/kg) by intraperitoneal
445 injection.

446 **Microarray, data analysis and quantitative real-time PCR**

447 For each group of microarray dataset, OT-I cells from 15-20 mice were sorted with a FACS Aria
448 III (BD Biosciences) and pooled. RNA was extracted with a RNeasy Micro kit (74004; Qiagen).
449 RNA quality and quantity were assessed with a Bioanalyzer 2100 (Agilent). Then RNA was
450 amplified and converted into cDNA by a linear amplification method with WT-Ovation Pico
451 System (3302-60; Nugen). Subsequently cDNA was labeled with the Encore Biotin module
452 (4200-60; Nugen) and hybridized to GeneChip MouseGene 2.0 ST chips (Affymetrix) at the
453 Translational Genomics Core of Partners Healthcare, Harvard Medical School. GeneChips were
454 scanned using the Affymetrix GeneChip Scanner 3000 7G running Affymetrix Gene Command
455 Console version 3.2. The data were analyzed by using Affymetrix Expression Console version
456 1.3.0.187 using Analysis algorithm RMA. To evaluate overall performance of microarray data,
457 principal component analysis (PCA) and Pearson correlation coefficients among 12 diverse
458 samples were applied by using 26,662 transcripts (R Program). All microarray data was
459 submitted to the Gene Expression Omnibus.

460 For relative quantitative real-time PCR, RNA was prepared as described above. Bio-Rad iCycler
461 iQ Real-Time PCR Detection System (Bio-Rad) was used with the following settings: 45 cycles
462 of 15 s of denaturation at 95 °C, and 1 min of primer annealing and elongation at 60 °C. Real-
463 time PCR was performed with 1 µl cDNA plus 12.5 µl of 2× iQ SYBR Green Supermix (Bio-
464 Rad) and 0.5 µl (10 µM) specific primers. For absolute quantitative real-time PCR, each standard
465 curve was constructed using 10-fold serial dilutions of target gene template ranging from 10⁷ to
466 10² copies per mL and obtained by plotting values of the logarithm of their initial template copy
467 numbers versus the mean Ct values. The actual copy numbers of target genes were determined
468 by relating the Ct value to a standard curve.

469 **Determination of viral load**

470 Viral load in various tissues following MVA or VACV skin scarification was determined by
471 quantitative real-time PCR, as previously described (17). Briefly, DNA was purified using the
472 DNeasy Mini Kit (Qiagen, Valencia, CA). The primers and TagMan probe used in the
473 quantitative PCR assay are specific for the ribonucleotide reductase Vv14L of vaccinia virus. The
474 sequences are: (forward) 5'-GAC ACT CTG GCA GCC GAA AT-3'; (reverse) 5'-CTG GCG
475 GCT AGA ATG GCA TA-3'; (probe) 5'-AGC AGC CAC TTG TAC TAC ACA ACA TCC
476 GGA-3'. The probe was 5'-labeled with FAM and 3'-labeled with TAMRA (Applied Biosystems,
477 Foster City, CA). Real-time PCR was performed with the Bio-Rad iCycler iQTM Real-Time
478 PCR Detection System (Bio-Rad Laboratories). Thermal cycling conditions were 50°C for 2 min
479 and 95°C for 10 min for one cycle, followed by 45 cycles of amplification (94°C for 15 s and
480 60°C for 1 min). Standard curve was established from DNA of an MVA or VACV stock with
481 previously determined titer. Corresponding CT values obtained by the real time PCR reactions

482 were plotted on the standard curve to calculate viral load in the samples. The number of viral
483 DNA copies was normalized to that in the skin samples of uninfected naïve mice.

484 **Statistical analysis**

485 Comparisons for two groups were calculated using Student's t test (two tailed). Comparisons for
486 more than two groups were calculated with one-way analysis of variance (ANOVA) followed by
487 Bonferroni's multiple comparison tests. Two-way ANOVA with Holm–Bonferroni post hoc
488 analysis was used to compare weight loss between groups and Log-rank (Mantel-Cox) test was
489 used for survival curves. $p < 0.05$ was considered statistically significant.

490

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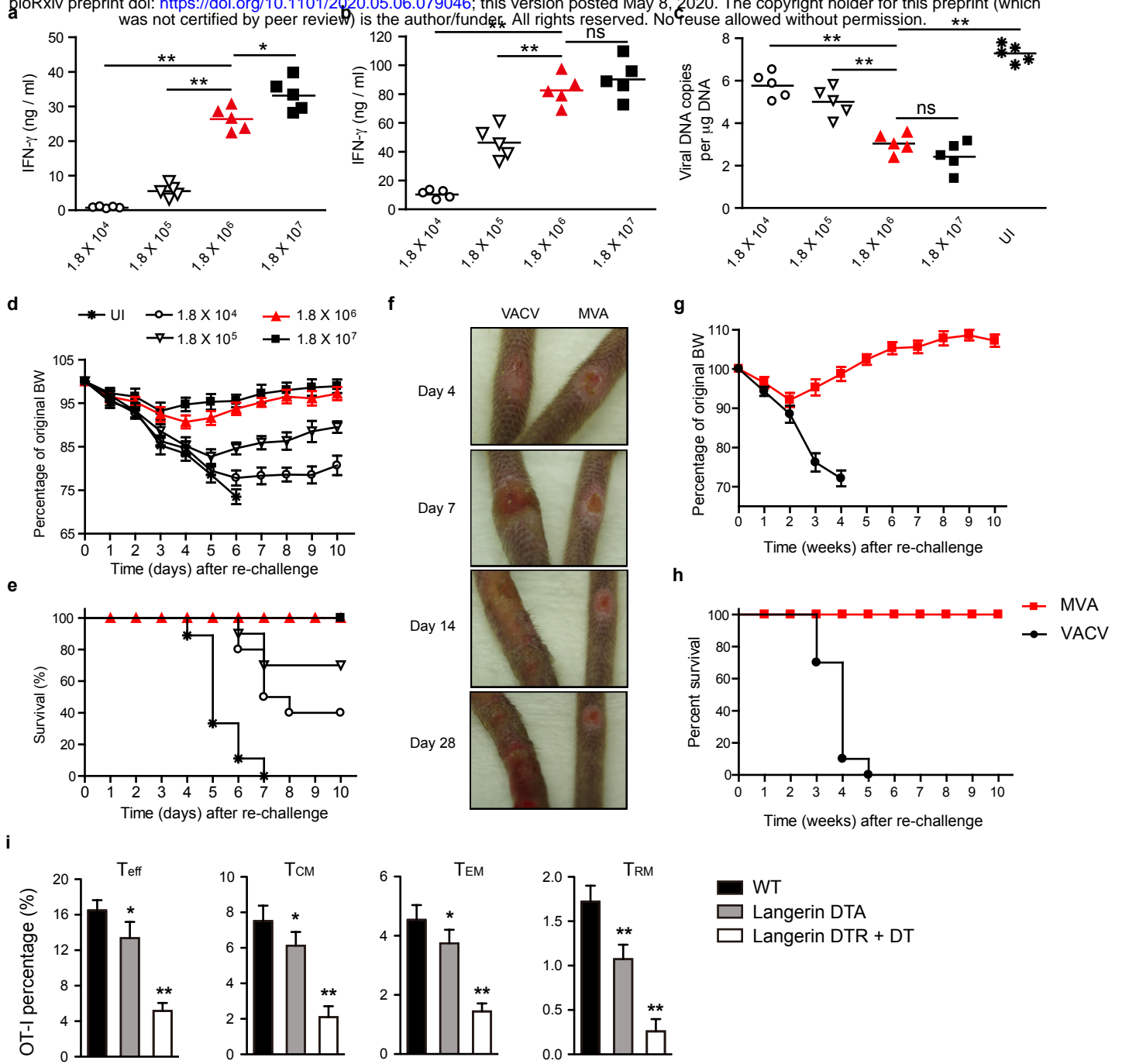


Fig. 1

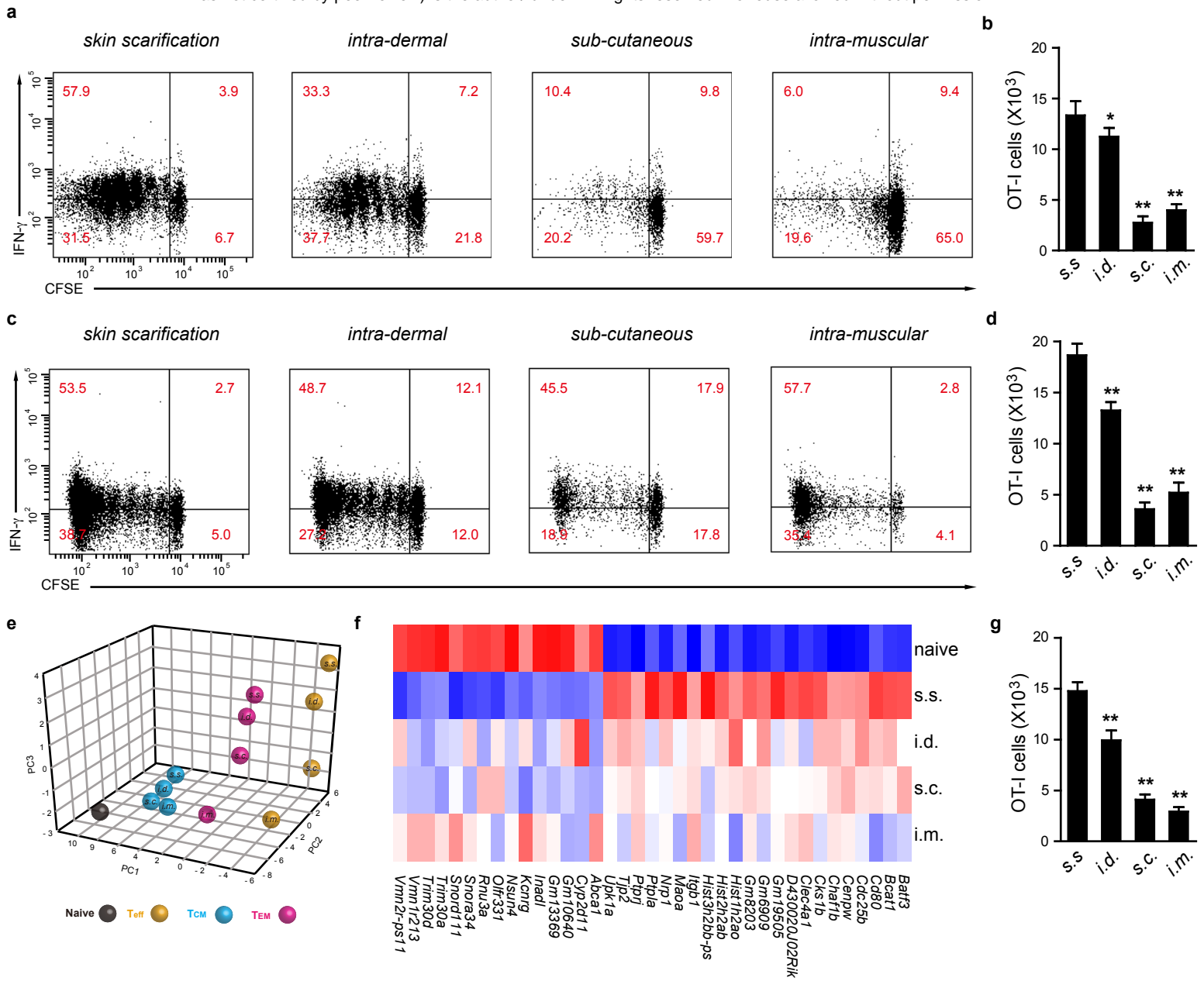


Fig. 2

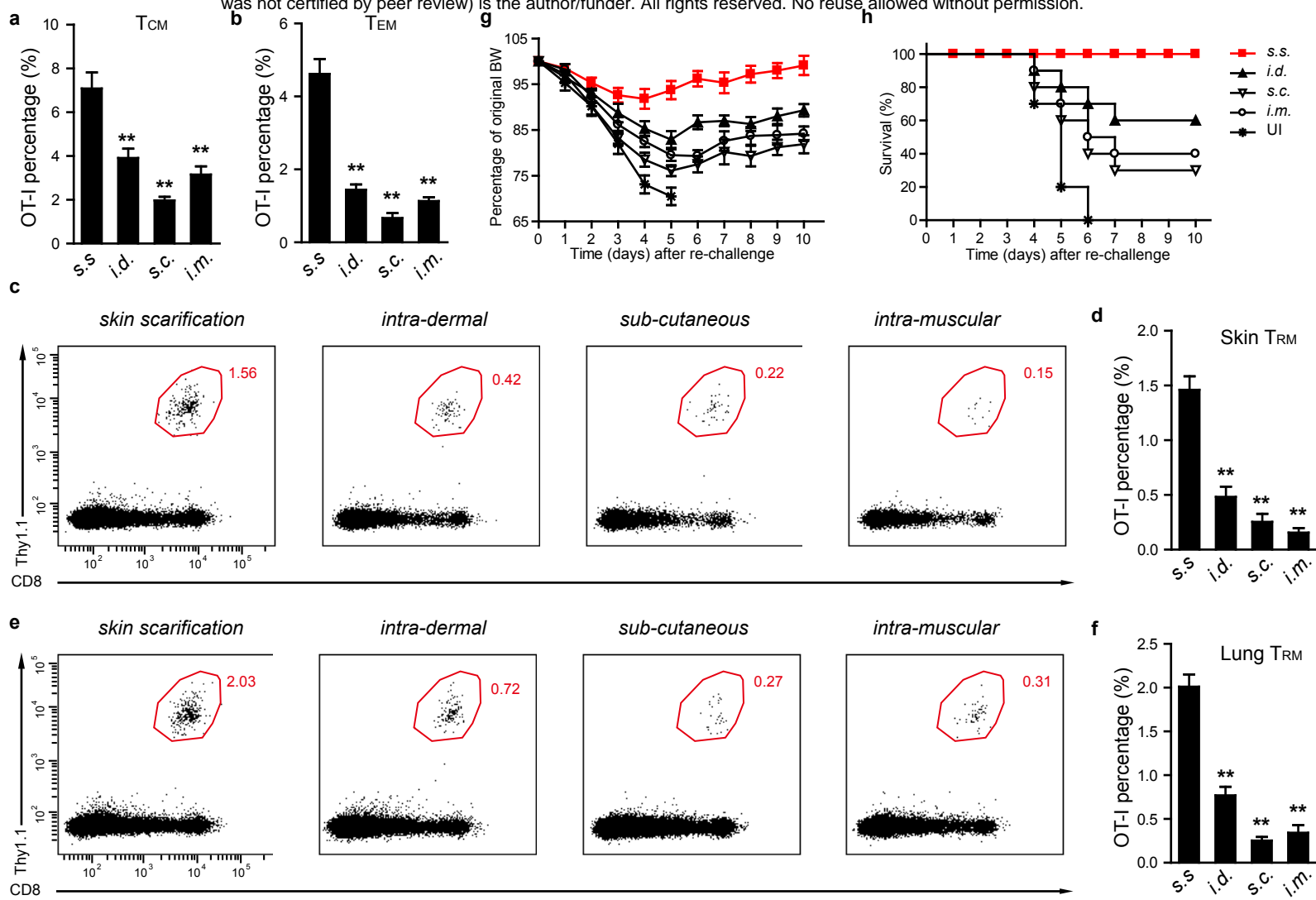
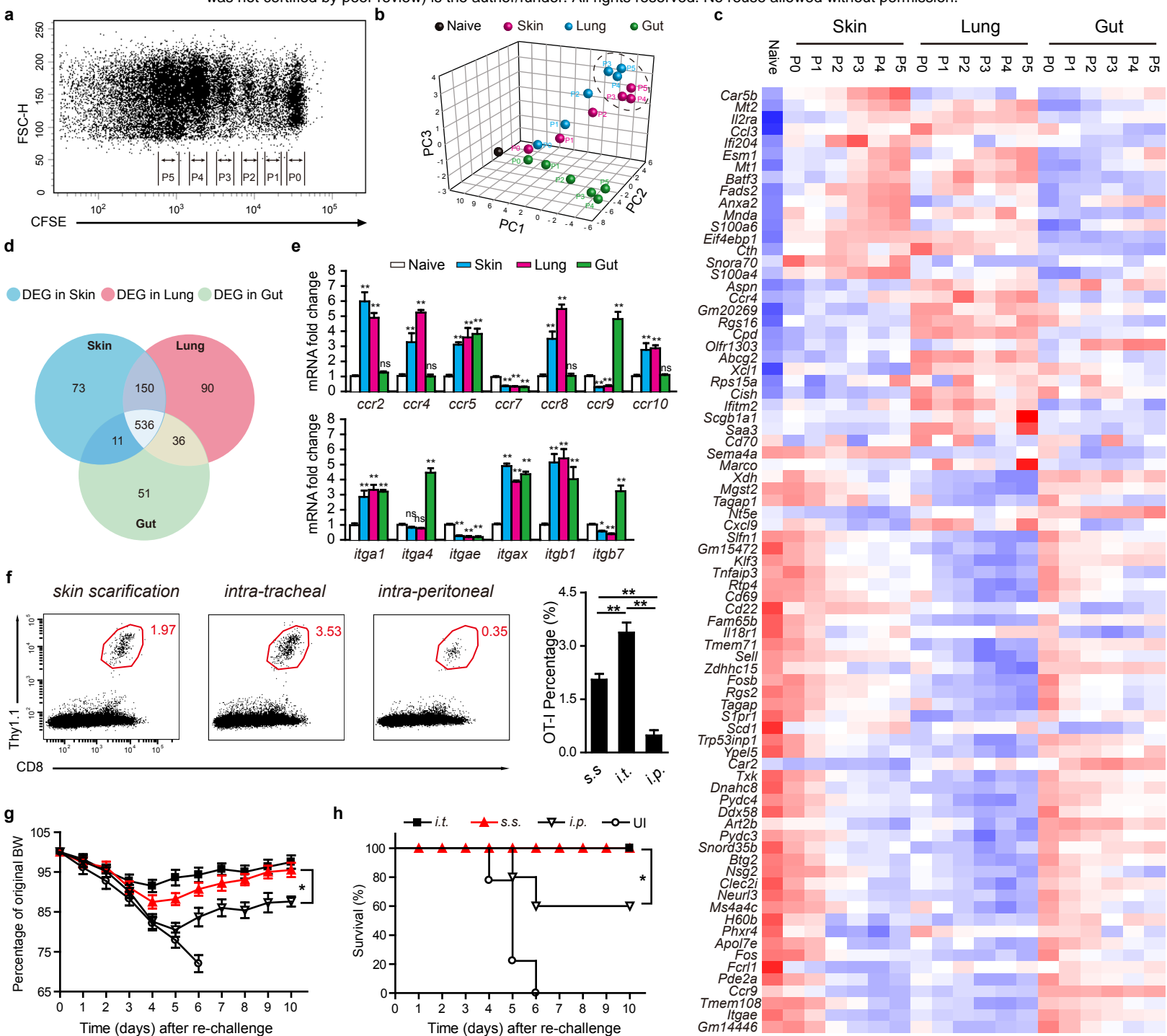
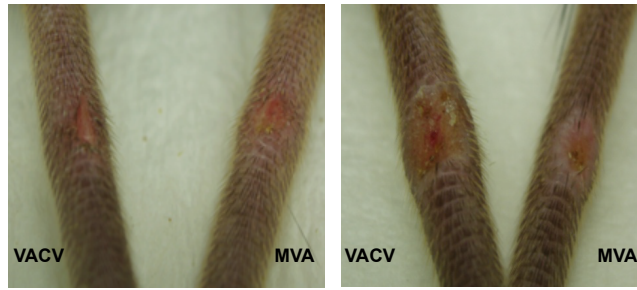


Fig. 3



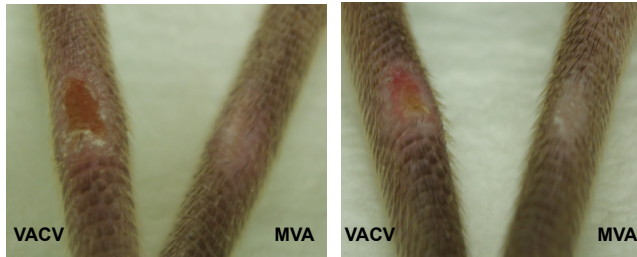
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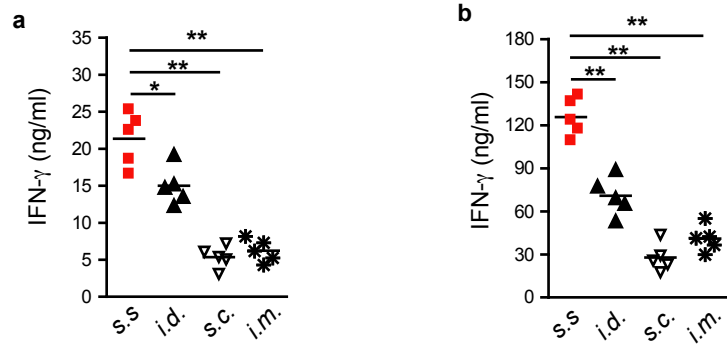


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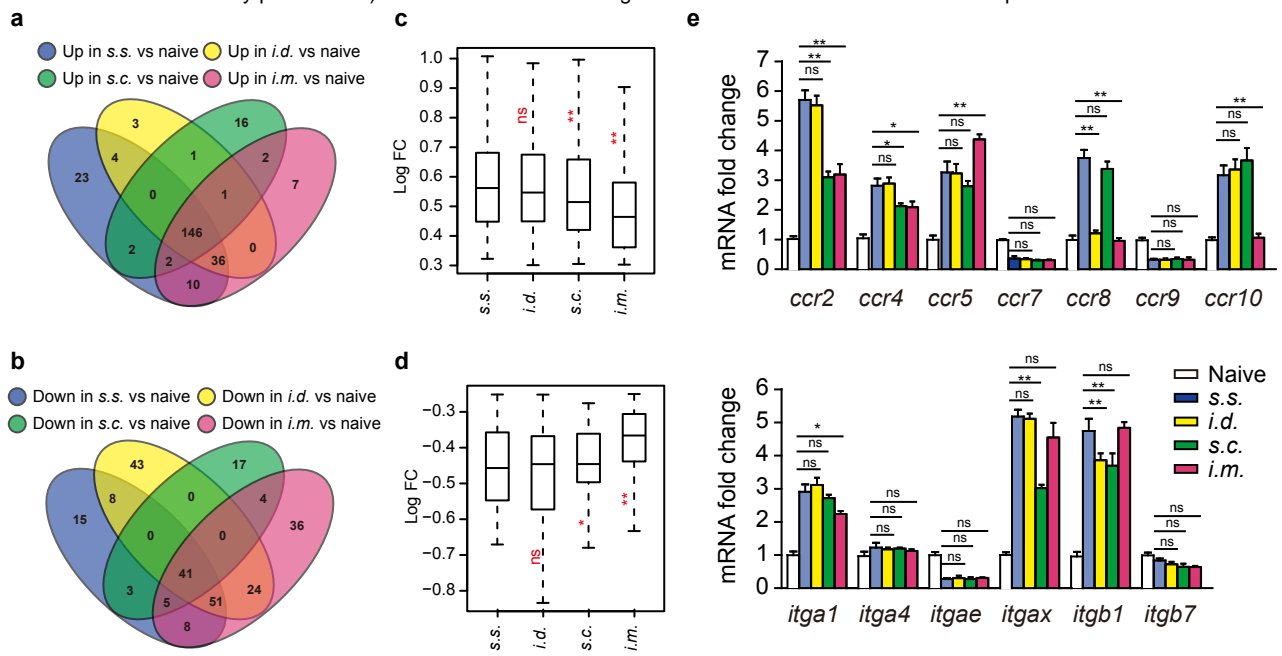
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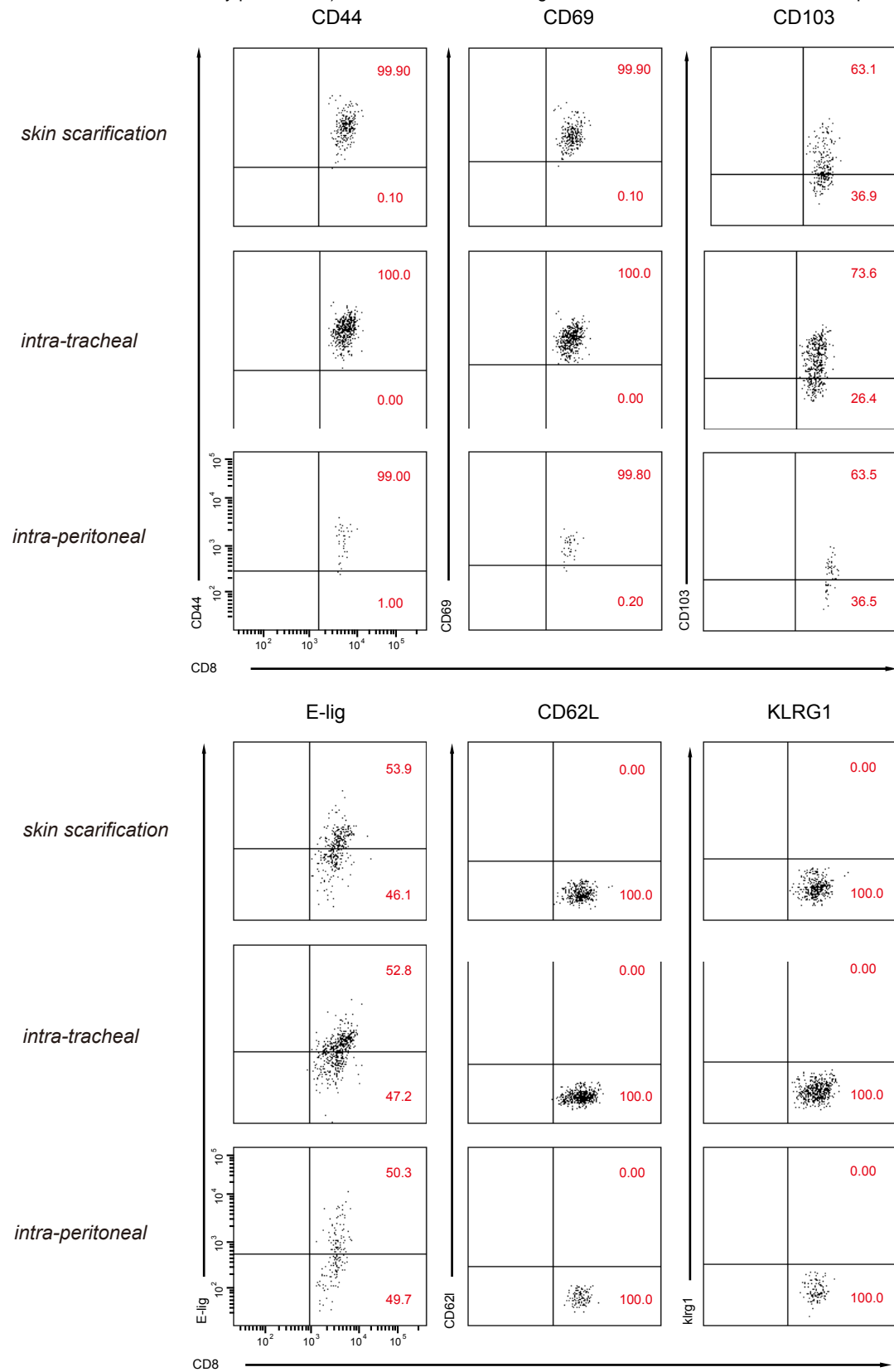
Extended data, Fig. 1



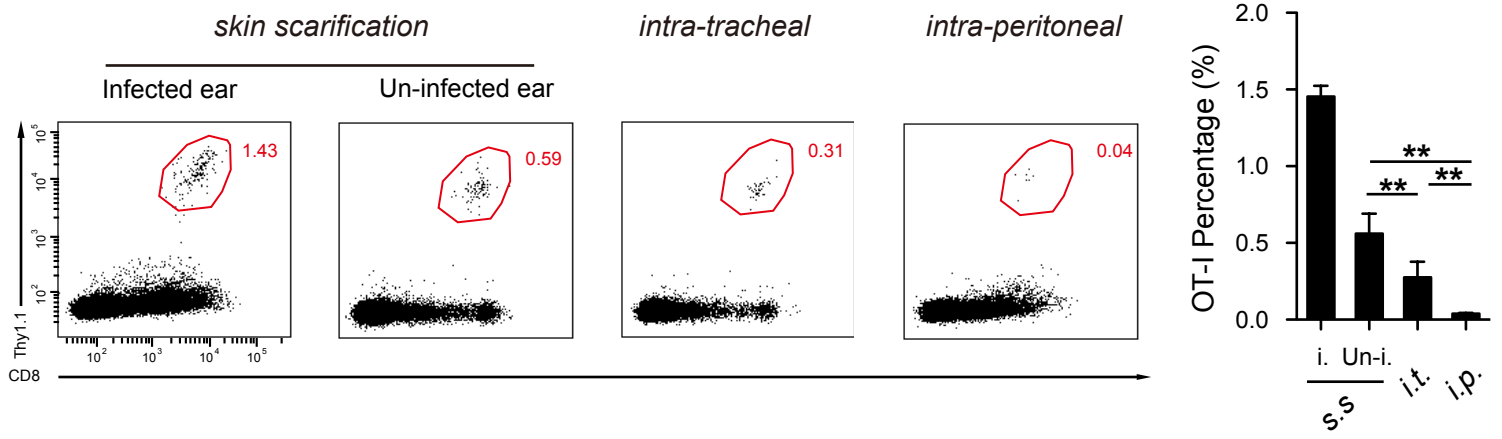
Extended data, Fig. 2



Extended data, Fig. 3



Extended data, Fig. 4



Extended data, Fig. 5