

1 **ALDH1A1 activity in tumor-initiating cells remodels myeloid-derived**
2 **suppressor cells to promote breast cancer progression**

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39 **Supplementary Materials and methods**

40 **Co-culture of Bone marrow cells and 4T1 cells**

41 Bone marrow cells (BMCs) were harvested from naive female Balb/c mice and contactless
42 co-cultured with 4T1 cells in six-well plates ($1-2 \times 10^5$ cells/well) for a total of 6 days. Bone
43 marrow cells were cultured in the bottom of a six-well dishes with 24 mm Transwell inserts
44 with a 0.4 μ m pore size on top (Corning Life Sciences, USA). In the Transwell insert, 1×10^4
45 4T1 cells were plated on day 0. Transwell inserts were discarded on day 3 and a fresh insert
46 with 1×10^4 corresponding 4T1 cells was added again. On day 7, bone marrow cells were
47 stained with CD45, Gr1 and CD11b, and percentage of Gr1⁺CD11b⁺MDSCs were analyzed
48 by flow cytometry. All experiments were repeated more than 3 times.

49 **MDSC depletion**

50 MDSCs were depleted with anti-Ly6G antibody (200ug/mouse, clone1A8; BioXCell, USA)
51 in vivo. Anti-Ly6G antibody and isotype control antibody (200 µg/mouse, IgG, Sigma-
52 Aldrich, USA) were administered intraperitoneally into tumor bearing mice every three days
53 starting from day 3 for a total of six times.

54 **ELISA and Western Blotting**

55 An enzyme linked immunosorbent assay (ELISA) was performed with cell culture
56 supernatants to determine GM-CSF levels, following manufacturer's recommendations
57 (ProteintechTM, USA), and GM-CSF levels were calculated according to the standard curve.
58 For Western Blots, total protein in cells was extracted and boiled in SDS loading buffer, then
59 protein lysates were separated by 10% SDS-PAGE, transferred onto a PVDF membrane and
60 probed with specific primary antibodies. The detailed information about antibodies were
61 shown in Table S1. HRP substrate (Millipore, USA) was used to detect HRP-conjugated
62 secondary with an Image Quant LAS 4000 mini-imaging system (GE, Fairfield, USA). All
63 experiments were repeated more than 3 times.

64 **Mammosphere formation assay**

65 Tumor cells were cultured with MammoCult Human Medium Kit (STEMCELL, USA)
66 supplemented with 4 µg/mL Heparin (STEMCELL), 1 µg/mL hydrocortisone (Sigma-
67 Aldrich), and 1% pen-strep antibiotic (Beyotime, China). 100 or 1000 tumor cells in 100ul
68 medium were plated in each well of 96-well ultra-low attachment plates (Corning Life
69 Sciences) and cultured for about 2 weeks. Fresh complete MammoCult medium was added
70 every 3 days. Sphere number were counted and photographed for further statistical analysis.
71 The same operation procedure was performed in 6-well ultralow attachment plates. After the
72 culture was completed, spheres were digested into single-cell suspensions with 0.25% trypsin
73 for subsequent experiments.

74 **HPLC-MS**

75 Samples were vortex mixed for 2 minutes, settled for several minutes, and then 1ml cold 70%
76 methanol solution was added and samples were vortexed for 3 minutes. Samples were soaked
77 in liquid nitrogen for 2 minutes, and then defrosted on ice for 5 minutes and vortexed for 2
78 minutes, repeat the above operation once again. Samples were added 300ul extracting reagent
79 containing internal standard 2-chlorophenylalanine (1 µg/ml), and splintered cells with
80 ultrasonic on ice for 5 minutes. Then, samples were centrifuged at 4 °C for 5 minutes at 12,000
81 rpm/min. Supernatants were placed in a new 1.5 ml tube. 100µL of supernatant was used for
82 UPLC-MS/MS. Ultraperformance liquid chromatography, UPLC (Shim-pack UFLC
83 SHIMADZU CBM30A, <https://www.shimadzu.com/>), tandem mass spectrometry, MS/MS
84 (QTRAP@6500+, <https://sciex.com/>).

85 **Intracellular pH detection in vitro**

86 BCECF (2',7'-bis-(2-carboxyethyl) -5-(and-6) -carboxyfluorescein) AM is the most widely
87 used fluorescent indicator for intracellular pH. Cancer cells were seeded in six-well plates and
88 incubated under normal conditions till approximately 70-80% confluency. Prepare viable cells
89 in suspension ($\sim 10^6$ cells/mL). Dilute an aliquot of 1 mM BCECF AM ester stock solution
90 100- to 500-fold into a physiological saline buffer such as PBS. Add one volume of aqueous
91 AM ester dispersion to one volume of cell suspension. Incubate for 15–60 minutes at 4 °C to
92 37 °C. Wash the cells twice with fresh culture medium and then detect the fluorescence at 488
93 nm by flow cytometry. All experiments were repeated more than 3 times.

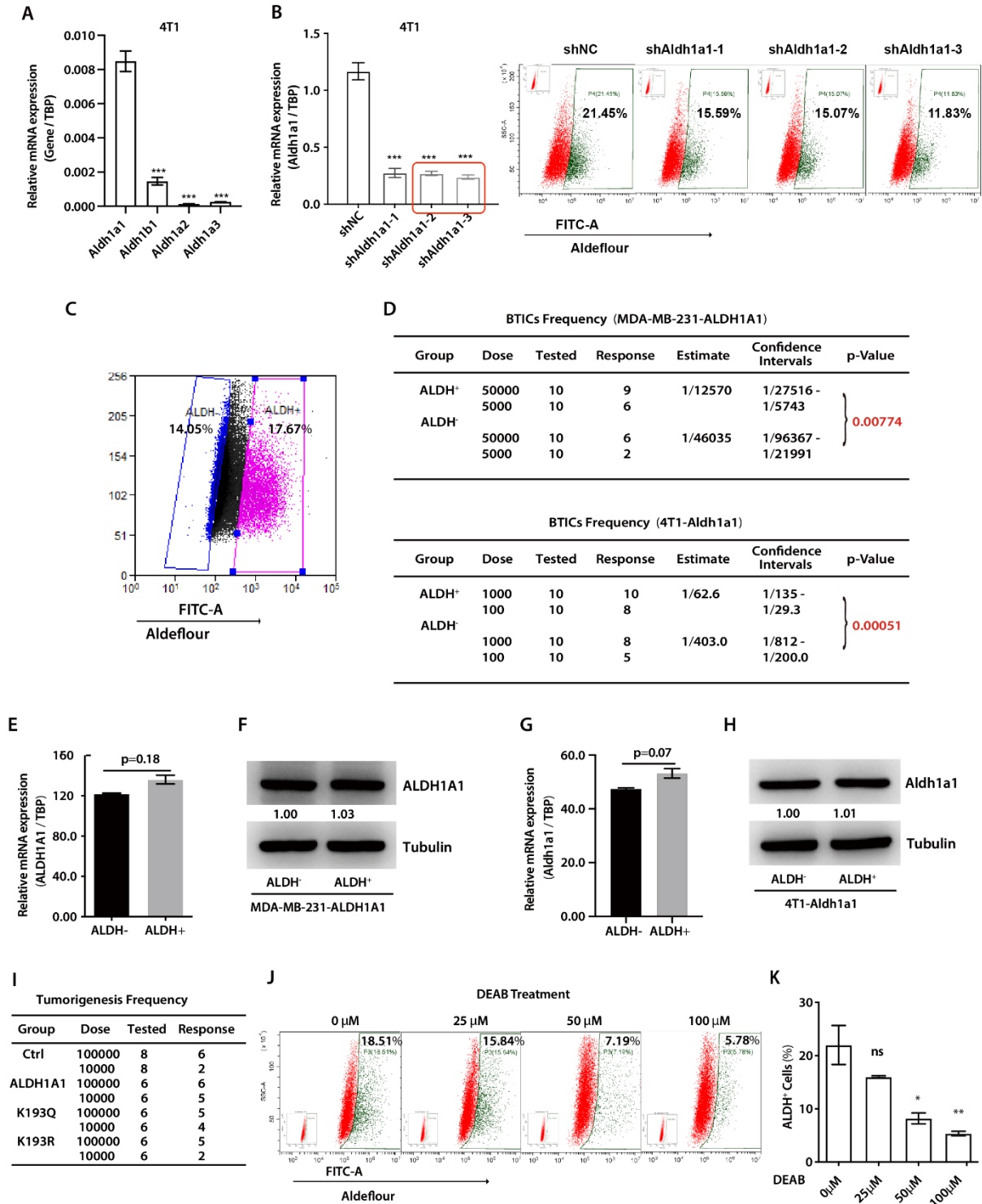
94 **pH_{enh} imaging with MRI in vivo**

95 Control, Aldh1a1 or K193Q/R mutant 4T1 (5×10^4) cells were transplanted orthotopically into
96 Balb/c mice respectively. After 18 days, tumors volumes were about 500 mm³, tumor-bearing
97 mice were imaged by Bruker BioSpec 11.7T horizontal MR scanner with a 75/40 mm
98 diameter quadrature volume coil. The mice were kept anesthetized by a gas mixture of

99 isoflurane/oxygen (2%/98%, volume ratio). Bite and ear bars were used to reduce
100 respiration-induced motion artifacts, and the respiration and rectal temperature were
101 monitored (SA Instruments, Inc., Stony Brook, NY, USA) during imaging. After a Localizer
102 scanning for animal positioning, respiration-gated T2-weighted imaging were achieved using
103 a rapid acquisition with relaxation enhancement sequence. For CEST-MRI, a continuous
104 wave (CW)-MT sequence with a saturation pulse power of $0.6\mu\text{T}$ and $1.1\mu\text{T}$ was used. Z-
105 spectra, presented as measured signals (S_{sat}) normalized by a reference signal (S_0), were
106 acquired with RF offsets from -2500 to 2500 Hz with a step width of 50 Hz (-5 to 5 ppm on
107 11.7 T). S_0 was obtained by setting the RF offset to 100000 Hz (20 ppm on 11.7 T) for signal
108 normalization. MRI data was processed using MATLAB R2018a software (MathWorks,
109 Natick, MA, USA). The enhancement of pH sensitivity was obtained by combining both
110 amide- and guanidyl-CEST images, and subtracting them.

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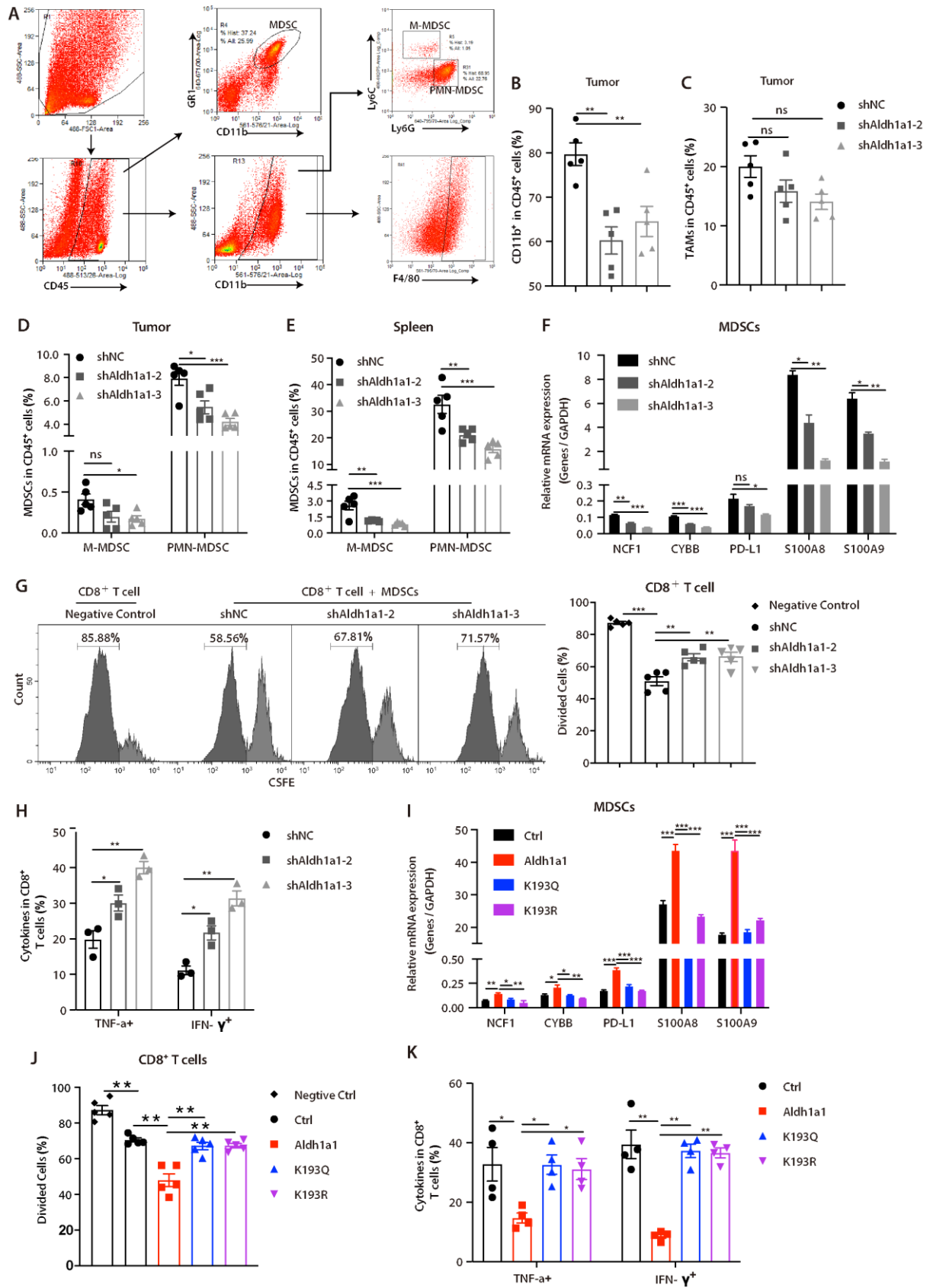
Supplementary Fig. S1



113 **Fig. S1. ALDH1A1 increased ALDH⁺ BTICs and promoted breast tumor progression**
 114 **relying on its enzyme activity.**
 115

116 (A) The mRNA expression of Aldh1a1, Aldh1a2, Aldh1a3 and Aldh1b1 in 4T1 cells were
117 quantified by qRT-PCR. (B) Aldh1a1 knockdown (shAldh1a1) in 4T1 significantly decreased
118 ALDH enzyme activity. The knockdown efficiency of Aldh1a1 in 4T1 was verified by qRT-
119 PCR. (C) ALDH⁻ and ALDH⁺ cells were sorted using the flow cytometry based on their
120 different ALDH enzyme activity in ALDH1A1-MDA-MB-231 and Aldh1a1-4T1 BC cells.
121 (D) ALDH⁺ cancer cells had more tumorigenic ability in comparison to the ALDH⁻ ones. The
122 grafted tumor assay was performed using serial dilutions with sorted ALDH⁻ and ALDH⁺
123 MDA-MB-231-ALDH1A1 cells (5×10^4 , 5×10^3 cells/fat pad) or sorted ALDH⁻ and ALDH⁺
124 4T1- Aldh1a1 cells (1000, 100 cells/fat pad) into female nude mice and Balb/c mice
125 respectively. Tumorigenesis was determined after 4 weeks for MDA-MB-231 cells and 4T1
126 cells. The BTIC frequency in tumors was calculated by the LDA. (E-H) The
127 ALDH1A1/Aldh1a1 protein and mRNA expression were equal between ALDH⁻ cells and
128 ALDH⁺ cells. ALDH1A1/Aldh1a1 mRNA expression was quantified by qRT-PCR and
129 ALDH1A1/Aldh1a1 protein was measured by Western Blots. (I) The xenografted tumor
130 assay was performed using serial dilutions (1×10^5 , 1×10^4 cells/fat pad) with ALDH1A1 or
131 K193Q/R mutant MDA-MB-231 cells. Tumorigenesis was determined after 4 weeks. (J, K)
132 4T1 cells were treated with the indicated concentrations of DEAB for 48 hours; the
133 percentage of ALDH⁺ BTIC population was subsequently decreased.
134 Data were presented as mean \pm SEM, unpaired t test was utilized for E and G, one or two-
135 way ANOVA test was utilized for other figures; ns, no significance, **p < 0.01, ***p < 0.001.

Supplementary Fig. S2

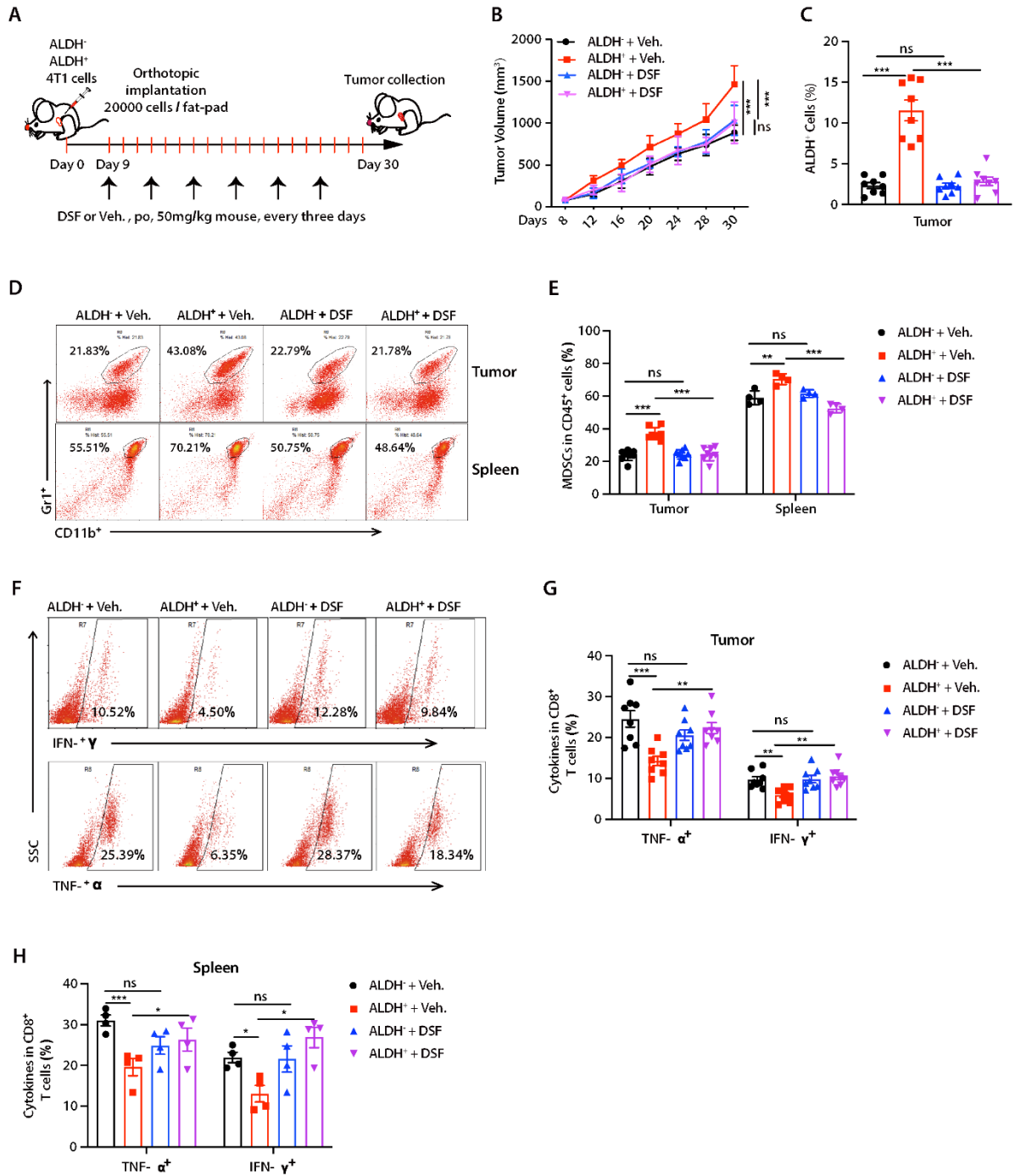


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137 **Fig. S2. Aldh1a1 increased MDSC enrichment as well as its immunosuppressive function.**

138 **(A)** Gating strategy for the analysis of MDSCs and TAMs by flow cytometry. Proportion (in
139 CD45⁺ cells) of MDSCs from tumors and host spleens were analyzed with surface markers
140 CD11b and Gr1. CD45⁺CD11b⁺Ly6C^{high}Ly6G⁻ for M-MDSCs, CD45⁺CD11b⁺Ly6C^{low}Ly6G⁺
141 for PMN-MDSCs and CD45⁺CD11b⁺F4/80⁺ for TAMs. **(B)** Percentage of CD11b⁺ myeloid
142 cells from shNC- and shAldh1a1-4T1 tumors (n=5 /group). **(C)** Proportion (in CD45⁺ cells) of
143 TAMs from shNC- and shAldh1a1-4T1 tumors (n=5 /group). **(D, E)** Proportion (in CD45⁺
144 cells) of M-MDSCs and PMN-MDSCs in the tumors and host spleens from shNC- and
145 shAldh1a1-4T1 mice (n=5 /group). **(F)** qRT-PCR analysis of the expression of NCF1, CYBB,
146 PD-L1, S100A8 and S100A9 in MDSCs derived from shNC- and shAldh1a1-4T1 tumors
147 (n=3 /group). **(G)** CD8⁺ T cells were isolated from wild-type Balb/c mice and stimulated with
148 cocktail. These CD8⁺ T cells were co-cultured in vitro with MDSCs derived from shNC- and
149 shAldh1a1-4T1 tumors, and the proliferation of T cells was analyzed with CFSE assay (n=5
150 /group). **(H)** The proportion IFN- γ ⁺ CD8⁺ T cells and TNF- α ⁺ CD8⁺ T cells in co-culture
151 between MDSCs and activated CD8⁺ T cells in vitro (n=3 /group). **(I)** qRT-PCR analysis of
152 the expression of NCF1, CYBB, PD-L1, S100A8 and S100A9 in MDSCs derived from Ctrl-,
153 Aldh1a1- and K193Q/R-4T1 tumors (n=3 /group). **(J)** The proliferation of CD8⁺ T cells of co-
154 culture with MDSCs derived from Ctrl-, Aldh1a1- and K193Q/R-4T1 tumors was analyzed
155 with CFSE assay (n=5 /group). **(K)** The activation of CD8⁺ T cells of co-culture with MDSCs
156 derived from Ctrl-, Aldh1a1- and K193Q/R-4T1 tumors was validated by the proportion of
157 IFN- γ ⁺ CD8⁺ T cells and TNF- α ⁺ CD8⁺ T cells (n=4 /group). Data were presented as mean \pm
158 SEM, one-way ANOVA test was utilized; ns, no significance, *p < 0.05, **p < 0.01, ***p <
159 0.001.

Supplementary Fig. S3



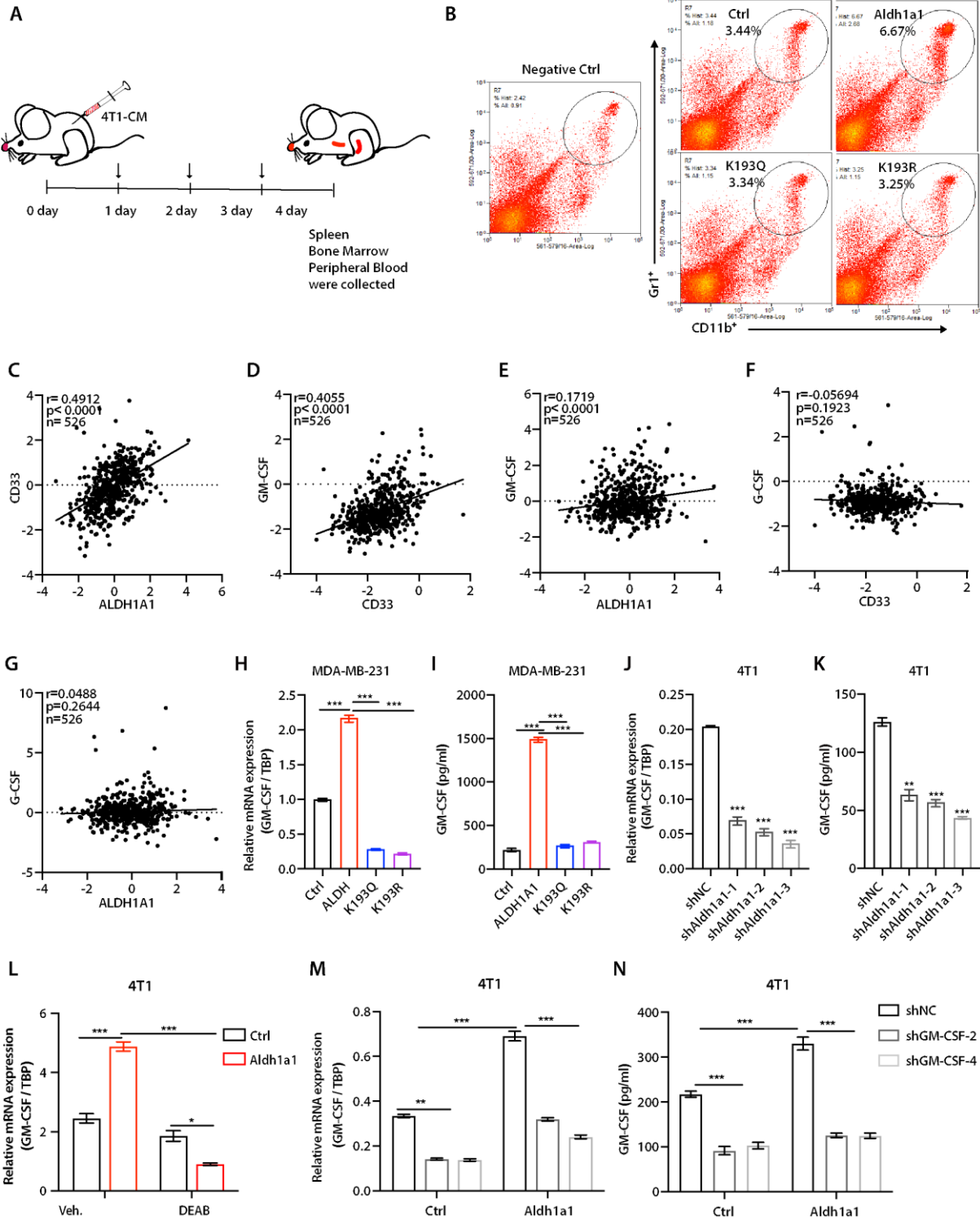
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161 **Fig. S3. Inhibition of ALDH1A1 enzyme activity reduced MDSC enrichment.**

162 (A, B) ALDH⁺ cancer cells had accelerated tumor growth in comparison to the ALDH⁻ group,
 163 which was blocked by DSF. Sorted ALDH⁻ and ALDH⁺ 4T1 cells (2.5×10^4 /fat pad) were
 164 inoculated into female Balb/c mice. After cells inoculated for 3 days, the tumor-bearing mice
 165 were treated with DSF (50mg/kg) or vehicle (Veh.) every three days. Tumor growth was

166 monitored, and tumor volume were measured (n = 8/group). **(C)** DSF significantly reduced
167 ALDH⁺ BTICs by inhibiting the ALDH enzyme activity. **(D, E)** Gr1⁺CD11b⁺ MDSCs were
168 markedly increased in ALDH⁺ cell-derived tumors and spleens compared with the ALDH⁻
169 cell-derived ones, which was blocked by DSF. Representative flow cytometry dot plots **(D)**
170 showed Gr1⁺CD11b⁺ CD45⁺ cells in tumors and spleens of tumor-bearing mice. The
171 percentages (in CD45⁺ cells) of MDSCs were shown in tumors (n=8/group) and host spleens
172 (n=4/group) **(E)**. **(F-H)** Active CD8⁺ T cells were also markedly decreased in ALDH⁺ cell-
173 derived tumors and host spleens compared to the ALDH⁻ cell-derived ones, which was
174 recovered by DSF. Representative flow cytometry dot plots **(F)** and proportions of cytokines
175 IFN- γ and TNF- α in CD8⁺ T cells were shown in tumors (n =8/group) **(G)** and spleens **(H)** (n
176 = 4/group). Data were presented as mean \pm SEM, one or two-way ANOVA test was utilized;
177 ns, no significance, *p < 0.05, **p < 0.01, ***p < 0.001.

Supplementary Fig. S4



178

179 **Fig. S4. ALDH1A1 upregulated GM-CSF in BC cells to promote MDSC expansion.**

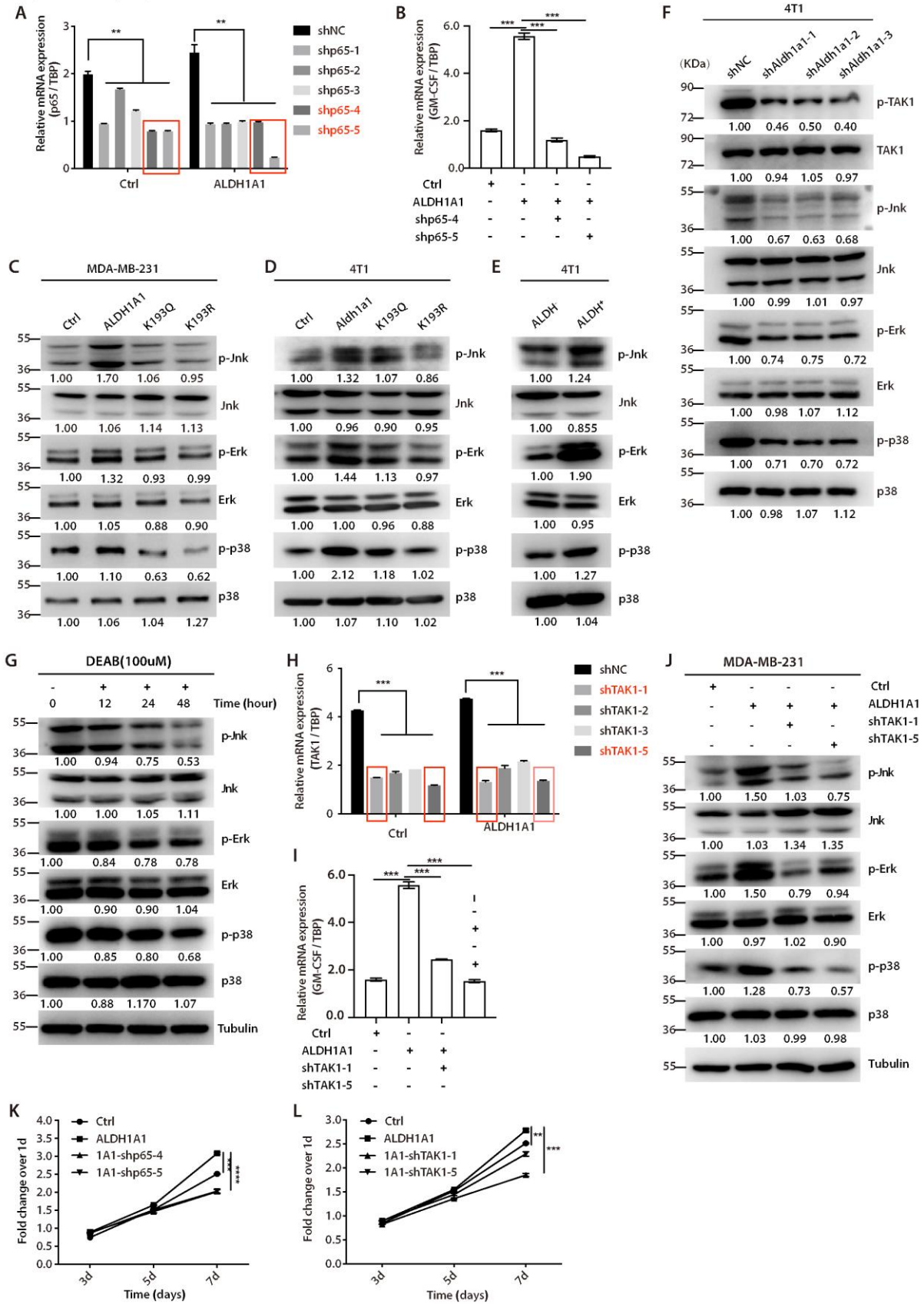
180 (A) The experimental diagram for MDSCs expansion in vivo induced by conditioned medium.

181 The female Balb/c mice (n=3/group) were injected intradermally with CM derived from

182 control-, Aldh1a1- or K193Q/R-4T1 cells for 3 consecutive days, and the mice were

183 sacrificed on the fourth day. Aldh1a1-derived CM increased MDSCs in tumor-free Balb/c
184 mice. **(B)** Representative flow cytometry dot plots for Gr1⁺CD11b⁺CD45⁺ cells in spleen
185 were shown. **(C-E)** The mRNA expressions of ALDH1A1, CD33 and GM-CSF were
186 positively correlated with each other. Pearson's correlation was calculated. **(F, G)** G-CSF
187 showed no significantly correlation with either CD33 or ALDH1A1 in mRNA levels. **(H, I)**
188 ALDH1A1 upregulated GM-CSF expression. ALDH1A1 and K193Q/R mutant MDA-MB-
189 231 cells were cultured for 24 and 48 hours, respectively. GM-CSF mRNA expression was
190 quantified by qRT-PCR (H) and GM-CSF protein was measured in culture supernatant with
191 ELISA (I). **(J, K)** GM-CSF expression at both mRNA and protein levels were decreased after
192 Aldh1a1-knockdown in 4T1 cells. **(L)** GM-CSF mRNA upregulation induced by active
193 Aldh1a1 was blockaded by DEAB treatment in 4T1 cells. **(M, N)** GM-CSF knockdown
194 (shGM-CSF) efficiency was verified in control and Aldh1a1 4T1 cells. Data were presented
195 as mean \pm SEM, one-way ANOVA test was utilized; **p < 0.01, ***p < 0.001.

Supplementary Fig. S5

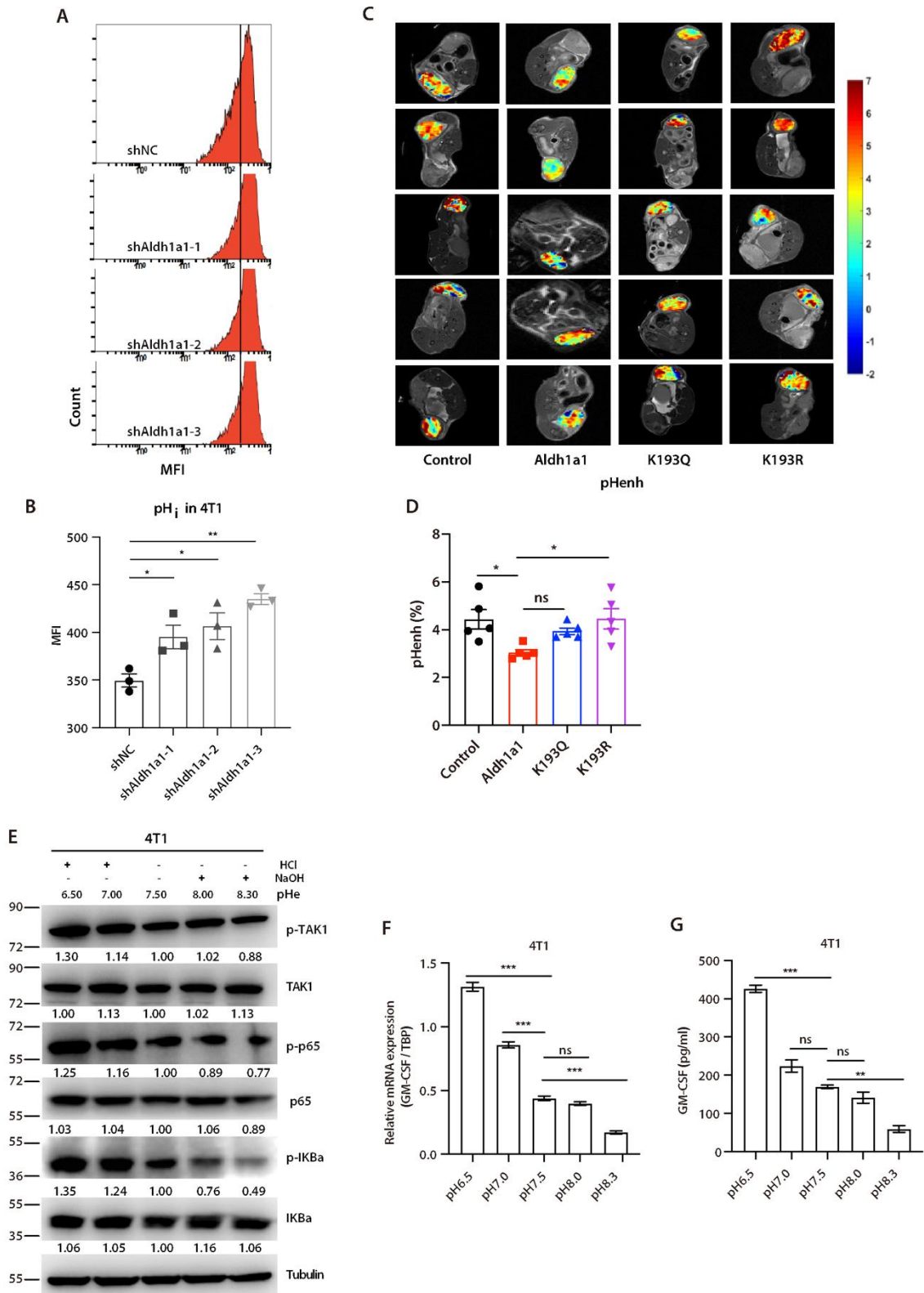


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197 **Fig. S5. ALDH1A1, relying on enzyme activity, increased TAK1 phosphorylation to**
 198 **activate MAPK signaling to regulate NFkB pathway.**

199 **(A)** The knockdown efficiency of p65 (shp65) in control and ALDH1A1 MDA-MB-231 was
200 verified by qRT-PCR. **(B)** GM-CSF mRNA upregulation induced by ALDH1A1 was reversed
201 by p65 knockdown in MDA-MB-231 cells. **(C, D)** p-JNK, p-ERK and p-p38 were increased
202 in ALDH1A1/Aldh1a1 cells, but not K193Q/R mutant cells compared with control in MDA-
203 MB-231 and 4T1 cells analyzed by Western Blot. **(E)** p-JNK, p-ERK and p-p38 were
204 increased in ALDH⁺ cells analyzed by Western Blot. ALDH⁻ and ALDH⁺ cells were sorted
205 from 4T1 cells. **(F)** The expression of p-TAK1, p-JNK, p-ERK and p-p38 were inhibited after
206 Aldh1a1-knockdown in 4T1 cells analyzed by Western Blot. **(G)** DEAB treatment suppressed
207 p-JNK, p-ERK and p-p38 in ALDH1A1 MDA-MB-231 cells analyzed by Western Blot.
208 DEAB treatment (100uM) was applied for different time (0h, 12h, 24h, 48h). **(H)** The
209 knockdown efficiency of TAK1 (shTAK1) in control and ALDH1A1 MDA-MB-231 was
210 verified by qRT-PCR. **(I)** GM-CSF mRNA upregulation induced by ALDH1A1 was reversed
211 by TAK1 knockdown in MDA-MB-231 cells. **(J)** TAK1 knockdown decreased p-JNK, p-
212 ERK and p-p38 upregulated by active ALDH1A1 in MDA-MB-231 cells. **(K, L)** Promoting
213 effect of ALDH1A1 on cell proliferation was reversed by p65 or TAK1 knockdown in MDA-
214 MB-231 ALDH1A1 cells. Data were presented as mean \pm SEM, one/two-way ANOVA test
215 was utilized; **p < 0.01, ***p < 0.001.

Supplementary Fig. S6

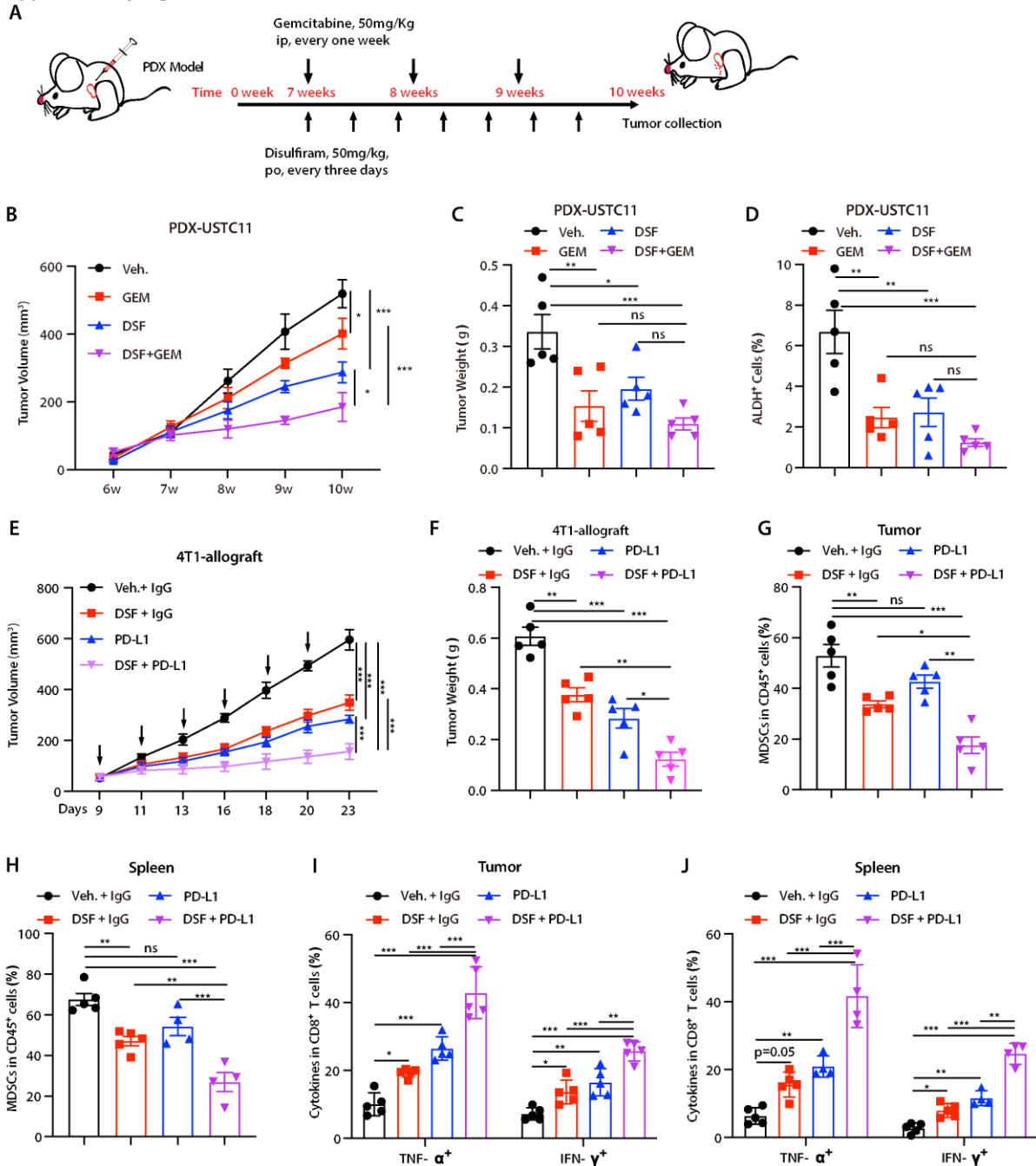


216

217 **Fig. S6. Aldh1a1 decreased the pH in BC cells to activate TAK1-NFκB pathway and**
 218 **upregulated GM-CSF expression.**

219 **(A, B)** The results of BCECF-AM fluorescent probe analysis showed that Aldh1a1-
220 knockdown induced the increase of pHi in 4T1 cells. **(C, D)** Control, Aldh1a1 or K193Q/R
221 mutant 4T1 (5×10^4) cells were transplanted orthotopically into Balb/c mice respectively. After
222 18 days, when the average tumor volume in Aldh1a1 group was about 500 mm^3 , tumor-
223 bearing mice were anesthetized and imaged **(C)** by Bruker Biospec 11.7T animal MR scanner,
224 and the pH_{enh} was calculated and graphed **(D)**. **(E)** p-TAK1, p-p65 and p-IKBa were increased
225 in 4T1 cells under acidic conditions as shown by Western Blots. 4T1 cells were treated with
226 HCl or NaOH to make pHe in a proper pH range ($\text{pHe} = 6.50 \sim 8.30$) for 12 hours. **(F, G)** The
227 GM-CSF expression was upregulated in 4T1 cells under acidic conditions. 4T1 cells were
228 treated with HCl or NaOH to make pHe in a proper pH range ($\text{pHe} = 6.50 \sim 8.30$) for 12 hours.
229 GM-CSF mRNA expression was quantified by qRT PCR **(B)** and GM-CSF protein was
230 measured in culture supernatant with ELISA **(C)**. Data were presented as mean \pm SEM, one-
231 way ANOVA test was utilized; ns, no significance, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Supplementary Fig. S7



232

233 **Fig. S7. DSF enhanced the sensibility of the 4T1 tumors to GEM or PD-L1 antibody.**

234 (A) The experimental diagram for the combinational treatment. Tumor cells (1×10^6) digested

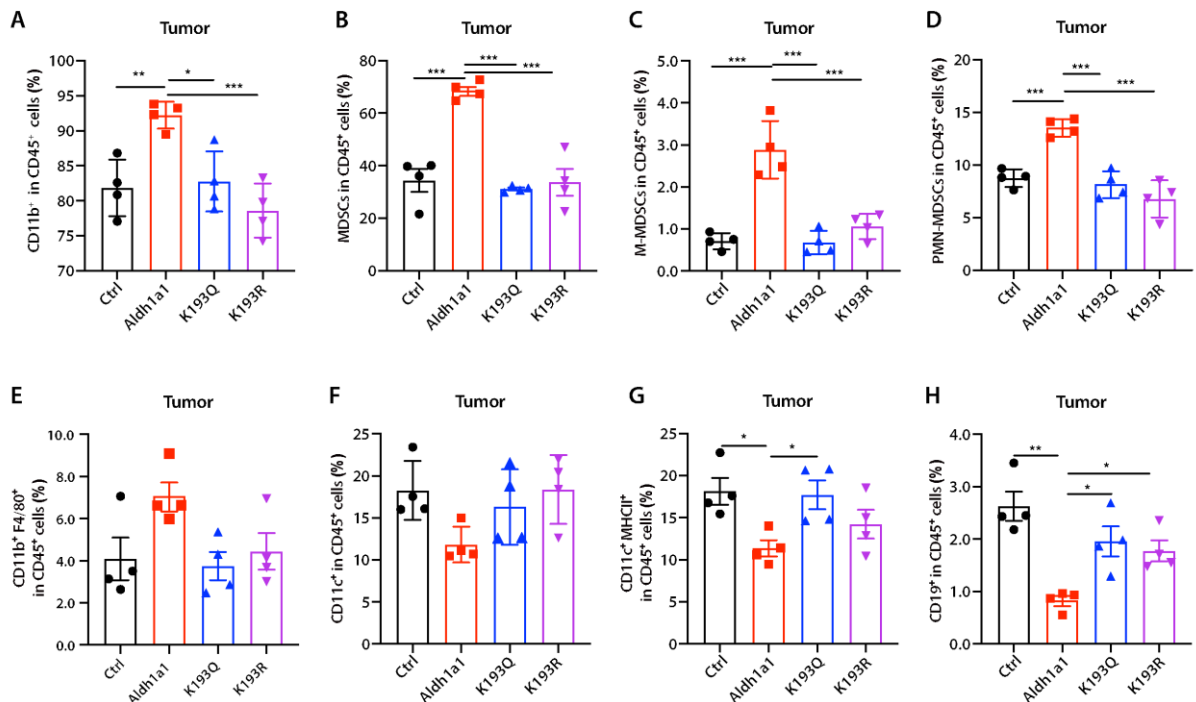
235 from PDX of TNBC (USTC11 established by our laboratory) were injected orthotopically

236 into NOD-SCID mice. When the average diameter of tumors reached to about 5mm, mice

237 were randomly divided into four groups and treated with Vehicle control, DSF (50mg/kg, po,

238 once every three days) and GEM (50mg/kg, ip, once a week) alone or in combination. **(B, C)**
239 The PDX tumor growth was significantly inhibited by the treatment of DSF and GEM alone
240 or in combination (n = 5/group). Tumor volume was monitored once a week, and tumors were
241 weighted after mice were euthanized. **(D)** ALDH⁺ BTICs were obviously decreased by the
242 treatment of DSF and GEM alone or in combination (n=5/group). **(E, F)** The growth of 4T1
243 allografts was significantly inhibited by the treatment of DSF alone and PD-L1 antibody alone
244 or in combination (n=5/group). 4T1 cells (5x10⁴) were injected orthotopically into female
245 Balb/c mice. After 9 days, mice bearing palpable tumors were randomly divided into four
246 groups and treated with Vehicle control, DSF (50mg/kg, po, every 2-3 days as the arrow
247 indicated) and PD-L1 antibody (200 ug/mice, ip, every 2-3 days as the arrow indicated) alone
248 or in combination. **(G, H)** The proportion of CD11b⁺Gr1⁺ MDSCs in the tumors and spleens
249 of control-, DSF-, PD-L1- and combination-treated mice were analyzed using flow cytometry
250 (n=5/group). **(I, J)** The proportion of IFN- γ ⁺CD8⁺ T cells and TNF- α ⁺ CD8⁺ T cells were
251 analyzed in tumors and host spleens after the treatment of DSF and PD-L1 antibody alone or
252 in combination (n=5/group). Data were presented as mean \pm SEM, one/two-way ANOVA test
253 was utilized; ns, no significance, *p < 0.05, **p < 0.01, ***p < 0.001.

Supplementary Fig. S8



254

255

Fig. S8 Aldh1a1 altered the infiltration of TAMs, DCs and B cells in tumor microenvironment.

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(A) Percentage (in CD45⁺ cells) of CD11b⁺ myeloid cells from control-, Aldh1a1⁻, K193Q-

258

and K193R-4T1 tumors (n=4 /group). (B) Proportion (in CD45⁺ cells) of CD11b⁺Gr1⁺

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MDSCs from control-, Aldh1a1⁻, K193Q- and K193R-4T1 tumors (n=4 /group). (C, D)

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Proportion (in CD45⁺ cells) of M-MDSCs and PMN-MDSCs in the tumors from control-,

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Aldh1a1⁻, K193Q- and K193R-4T1 tumors (n=4 /group). (E) Proportion (in CD45⁺ cells) of

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CD11b⁺F4/80⁺ TAMs in the tumors of control-, Aldh1a1⁻, K193Q- and K193R-mice were

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analyzed using flow cytometry (n=4 /group). (F) Percentage (in CD45⁺ cells) of CD11c⁺ cells

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from control-, Aldh1a1⁻, K193Q- and K193R-4T1 tumors (n=4 /group). (G) Percentage (in

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CD45⁺ cells) of CD11c⁺MHCII⁺ DC cells from control-, Aldh1a1⁻, K193Q- and K193R-4T1

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tumors (n=4 /group). (H) Percentage (in CD45⁺ cells) of CD19⁺ B cells from control-,

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Aldh1a1⁻, K193Q- and K193R-4T1 tumors (n=4 /group). Data were presented as mean ±

268

SEM, one-way ANOVA test was utilized; ns, no significance, *p < 0.05, **p < 0.01, ***p <

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0.001.