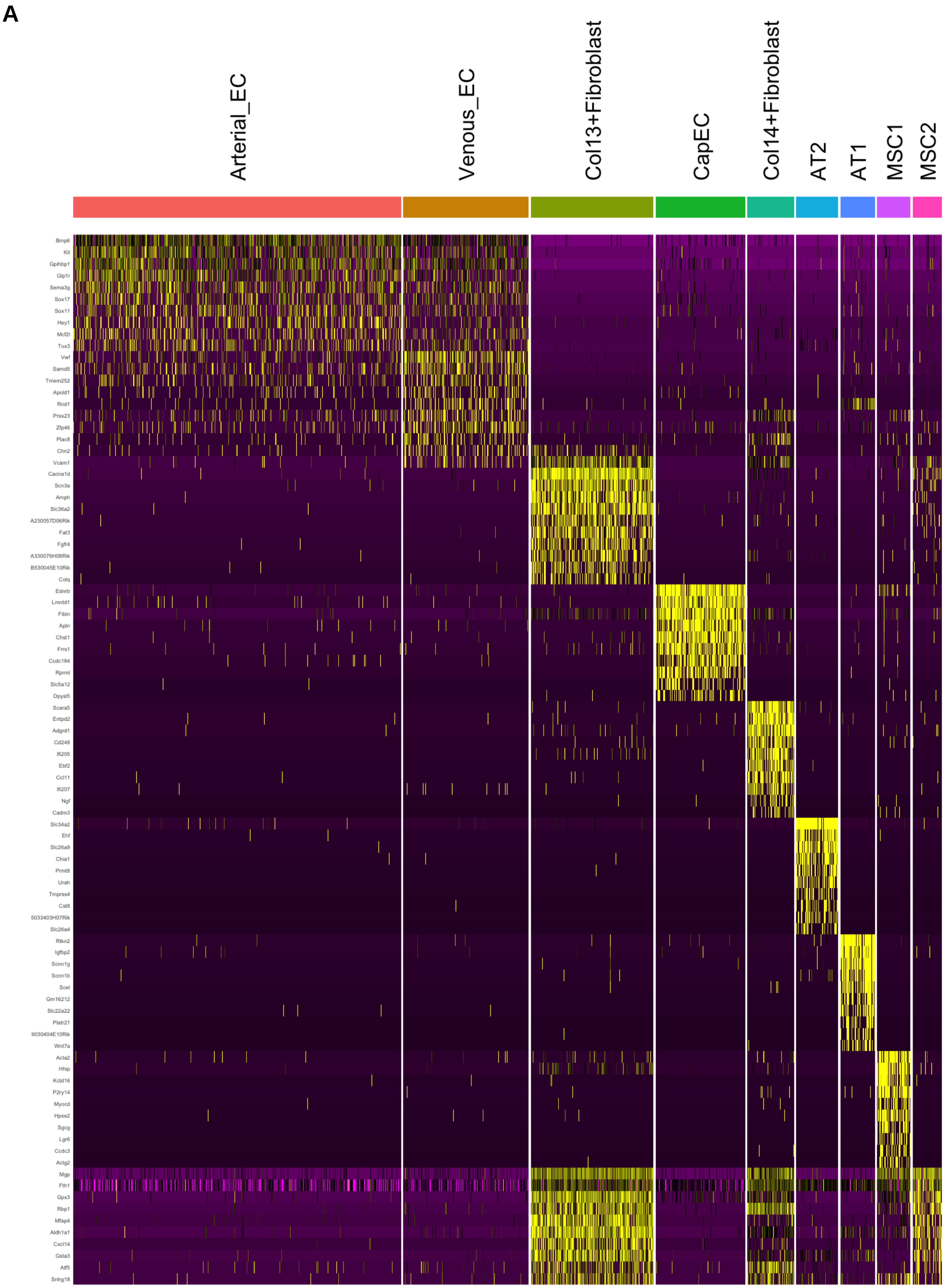
A
Arterial_EC
Venous_EC
Col13+Fibroblast
CapEC
Col14+Fibroblast
AT2
AT1
MSC1
MSC2
Bmp6
Kit
Gpihbp1
Glp1r
Sema3g
Sox17
Sox11
Hey1
Mcf2l
Tox3
Vwf
Samd5
Tmem252
Apold1
Rnd1
Prss23
Zfp46
Plac8
Chn2
Vcam1
Cacna1d
Scn3a
Amph
Slc36a2
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Fat3
Fgfr4
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B530045E10Rik
Colq
Ednrb
Lmntd1
Fibin
Apln
Chst1
Frrs1
Ccdc184
Rprml
Slc5a12
Dpysl5
Scara5
Entpd2
Adgrd1
Cd248
Ifi205
Ebf2
Ccl11
Ifi207
Ngf
Cadm3
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Ehf
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Chia1
Prmt8
Urah
Tmprss4
Cst8
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Slc26a4
Rtkn2
Igfbp2
Scnn1g
Scnn1b
Scel
Gm16212
Slc22a22
Platr21
9030404E10Rik
Wnt7a
Acta2
Hhip
Kctd16
P2ry14
Myocd
Hpse2
Sgcg
Lgr6
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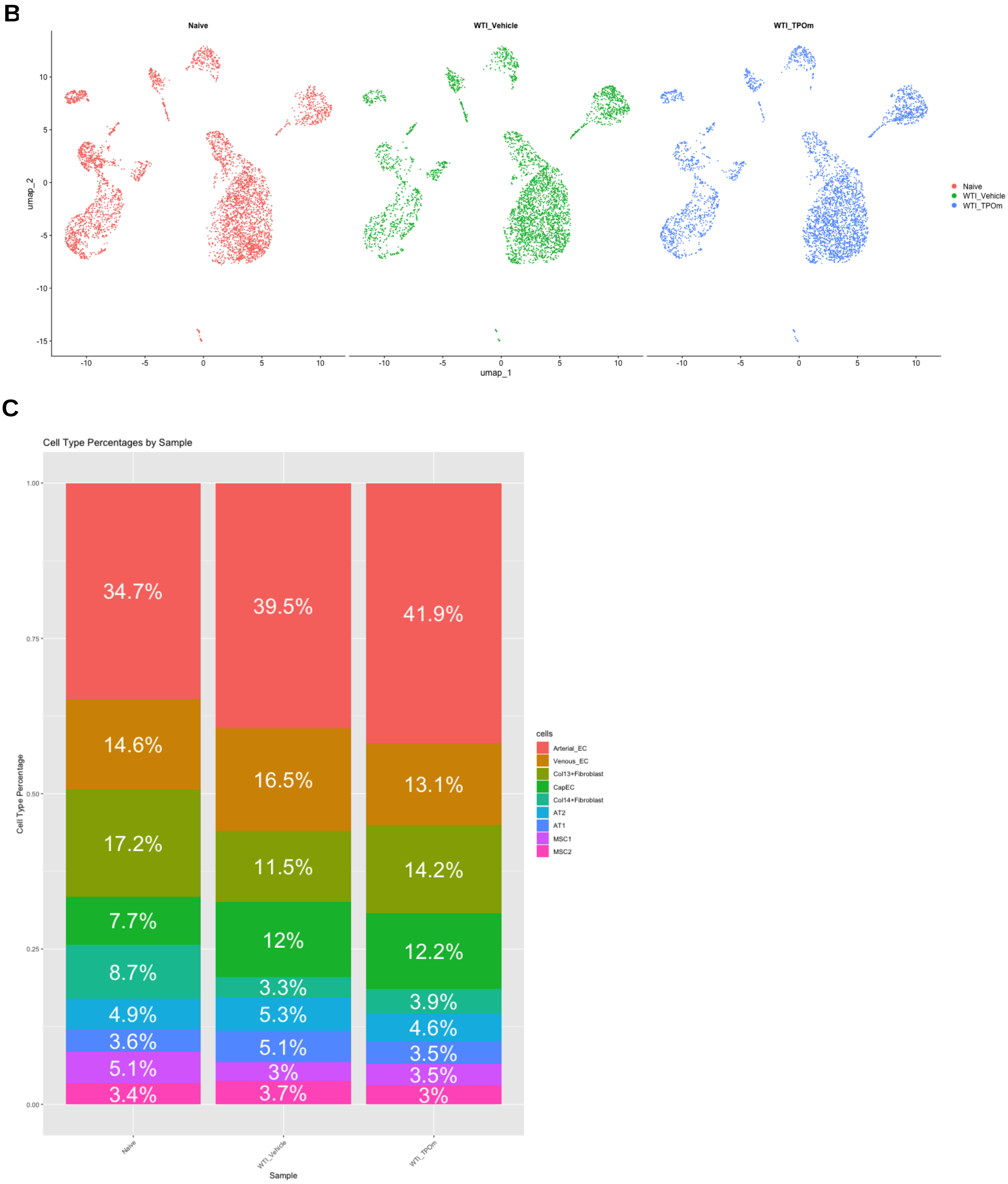
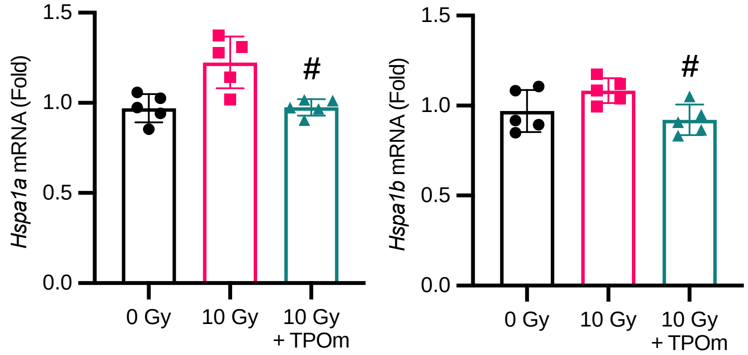


Supplemental Figure 1. Overview of clusters in lung cells analyzed by scRNA-Seq and their distributions in each treatment group. (**A**) Heatmap of the most differentially expressed genes of lung cells in the 9 different clusters. The color bars indicate gene expression level in log2 scale. (**B**) Two-dimensional UMAP projection split by treatment group. 4451 cells in naïve. 3925 cells in vehicle. 3862 cells in TPOm. (**C**) Each cluster's distribution by percentage iterated by treatment condition.



Supplemental Figure 2. The mRNA expression of *Hspa1a* and *Hspa1b* in mouse PMVECs. Mouse primary PMVECs were isolated from C57B/6J mouse and cultured. PMVECs from 0 Gy control and irradiated at 10 Gy 4 days after IR. The irradiated MPVECs were pretreated with PBS and TPOm 2 hours before IR. The mRNA expression of *Hspa1a* and *Hspa1b* was determined by qPCR. The results of qPCR analysis are normalized with *Hprt1* as an internal control and are expressed as fold change compared with the naive group. Data are shown as means ± SD (n=5/group). $^{*}P < 0.05$ *vs.* 0 Gy and $^{\#}P < 0.05$ *vs.* 10 Gy. Data were analyzed using non-parametric methods, using a one-way ANOVA with Tukey test as post-hoc comparison.