

SUPPLEMENTARY TABLE S1. IDENTIFICATION OF GENES DIFFERENTIALLY EXPRESSED IN EPICAM^{POS} INTEGRIN $\alpha 6^{\text{HIGH}}$ CELLS ISOLATED FROM DIFFERENT REGIONS OF MOUSE LUNG

<i>gene</i>	<i>Trachea</i>	<i>Airways</i>	<i>Parenchyme</i>	<i>across regions</i>
c-kit	0.628022524	0.000292886	2.60E-05	0.004553657
CCSP	4.94E-06	1.08E-06	0.000738092	0.003451995
E-cadherin	0.033187301	0.187918181	0.001569322	0.789071605
FoxM1	0.038991481	0.0427384	0.023387348	0.619734395
ID2	0.000738092	0.001327769	4.05E-05	0.000723791
ITGA6	0.001516789	0.002581345	0.001187443	1.08E-06
ITGB4	0.000206162	4.05E-05	4.05E-05	0.010655546
K5	0.000646117	9.79E-05	0.000103477	0.038577116
KDR	0.772696877	0.000127727	4.94E-06	0.002052011
LGR6	0.023387348	4.94E-06	0.102956721	0.586094823
Muc5AC	0.002581345	0.002491248	N/D	0.640113813
NGFR	0.000456237	6.28E-06	0.007023855	0.032124023
p63	0.061072871	0.057000844	0.04705498	0.047139031
SPC	4.05E-05	0.000563423	0.000495272	0.010050114
Sca-1	0.001652257	1.08E-06	6.15E-05	0.096941599

To identify genes that are differentially expressed between integrin $\alpha 6^{\text{high}}$ and $\alpha 6^{\text{low}}$ epithelial cells, expression of each gene was compared by T-test within and across the studied regions. The *P* values were adjusted using Benjamini and Hochberg correction for multiple hypothesis testing [31]. The table represents the adjusted *P* values within and across the specified regions. Genes that are differentially expressed at 10% FDR are highlighted in bold.