NOTE: Please save this file locally before filling in the table, DO NOT work on the file within your internet browser as changes will not be saved. Adobe Acrobat Reader (available free here) is recommended for completion.

The ARRIVE guidelines 2.0: author checklist

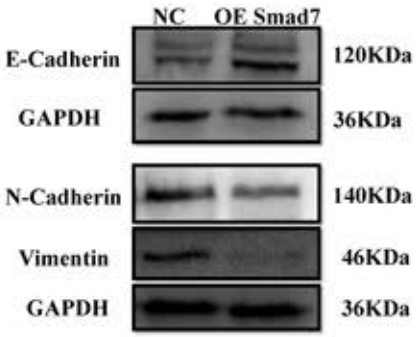
The ARRIVE Essential 10

These items are the basic minimum to include in a manuscript. Without this information, readers and reviewers cannot assess the reliability of the findings.

Item		Recommendation	Section/line number, or reason for not reporting
Study design	1	For each experiment, provide brief details of study design including: a. The groups being compared, including control groups. If no control group has been used, the rationale should be stated. b. The experimental unit (e.g. a single animal, litter, or cage of animals).	
Sample size	2	a. Specify the exact number of experimental units allocated to each group, and the total number in each experiment. Also indicate the total number of animals used. b. Explain how the sample size was decided. Provide details of any *a priori* sample size calculation, if done.	
Inclusion and exclusion criteria	3	a. Describe any criteria used for including and excluding animals (or experimental units) during the experiment, and data points during the analysis. Specify if these criteria were established *a priori.* If no criteria were set, state this explicitly. b. For each experimental group, report any animals, experimental units or data points not included in the analysis and explain why. If there were no exclusions, state so. c. For each analysis, report the exact value of *n* in each experimental group.	
Randomisation	4	a. State whether randomisation was used to allocate experimental units to control and treatment groups. If done, provide the method used to generate the randomisation sequence. b. Describe the strategy used to minimise potential confounders such as the order of treatments and measurements, or animal/cage location. If confounders were not controlled, state this explicitly.	
Blinding	5	Describe who was aware of the group allocation at the different stages of the experiment (during the allocation, the conduct of the experiment, the outcome assessment, and the data analysis).	
Outcome measures	6	a. Clearly define all outcome measures assessed (e.g. cell death, molecular markers, or behavioural changes). b. For hypothesis-testing studies, specify the primary outcome measure, i.e. the outcome measure that was used to determine the sample size.	
Statistical methods	7	a. Provide details of the statistical methods used for each analysis, including software used. b. Describe any methods used to assess whether the data met the assumptions of the statistical approach, and what was done if the assumptions were not met.	
Experimental animals	8	a. Provide species-appropriate details of the animals used, including species, strain and substrain, sex, age or developmental stage, and, if relevant, weight. b. Provide further relevant information on the provenance of animals, health/immune status, genetic modification status, genotype, and any previous procedures.	
Experimental procedures	9	For each experimental group, including controls, describe the procedures in enough detail to allow others to replicate them, including: a. What was done, how it was done and what was used. b. When and how often. c. Where (including detail of any acclimatisation periods). d. Why (provide rationale for procedures).	
Results	10	For each experiment conducted, including independent replications, report: a. Summary/descriptive statistics for each experimental group, with a measure of variability where applicable (e.g. mean and SD, or median and range). b. If applicable, the effect size with a confidence interval.	

Supplementary Figure 1. Smad7 modulates TGF-β1 induced EMT in bronchial epithelial cells

After BEAS-2B cells were transfected with Smad7 plasmid, higher E-Cadherin and lower N-Cadherin and Vimentin, were confirmed by Western blot (A-B). On the contrast, after being transfected with Smad7 siRNA, BEAS-2B cells exhibited higher E-Cadherin in mRNA level, lower N-Cadherin but no differences in Vimentin (C). Additionally, administration of TGF-β (20ng/ml) exhibited the same directional trend of each parameter (D). Further Western Blot indicated that over-expression of Smad7 could partly block the TGF-β induced EMT in BEAS-2B cells, However, siRNA of Smad7 had the opposite effect, completely reversing the observed changes (E-G). *: $p<0.05$. **: $p<0.01$. ***$p<0.005$. ****$p<0.001$.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GAPDH
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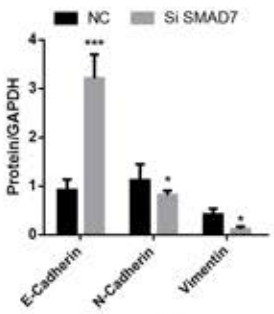
N-Cadherin
140KDa
Vimentin
46KDa
GAPDH
36KDa

A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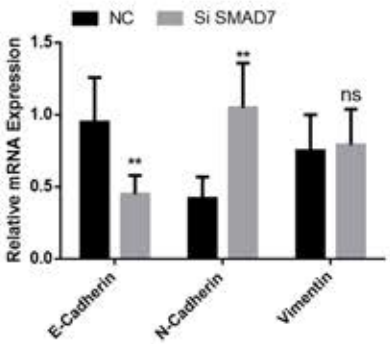
Protein/GAPDH
E-Cadherin
N-Cadherin
Vimentin

B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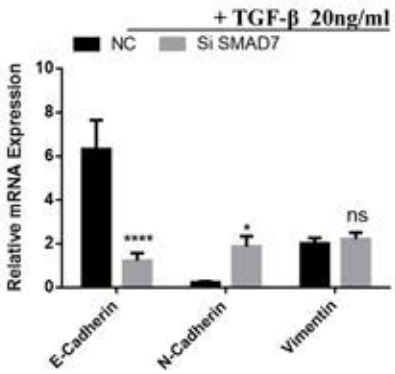
N-Cadherin
Vimentin
ns

C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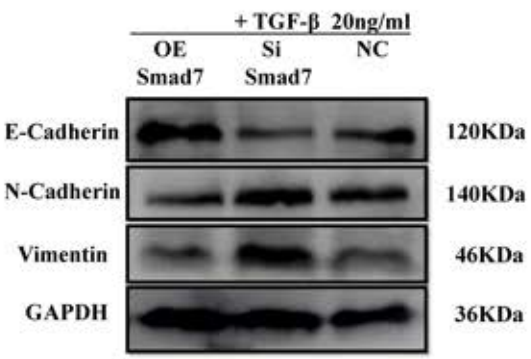
NC
Si SMAD7
Relative mRNA Expression
E-Cadherin
N-Cadherin
Vimentin
ns

D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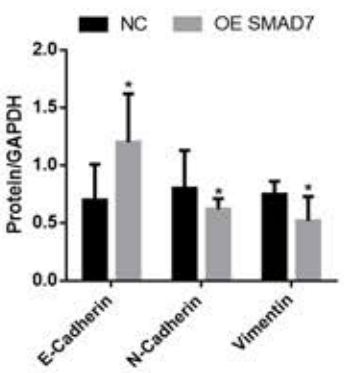
E-Cadherin
120KDa
N-Cadherin
140KDa
Vimentin
46KDa
GAPDH
36KDa

E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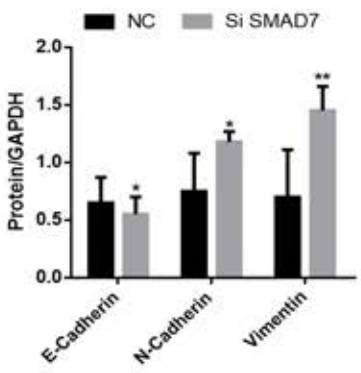
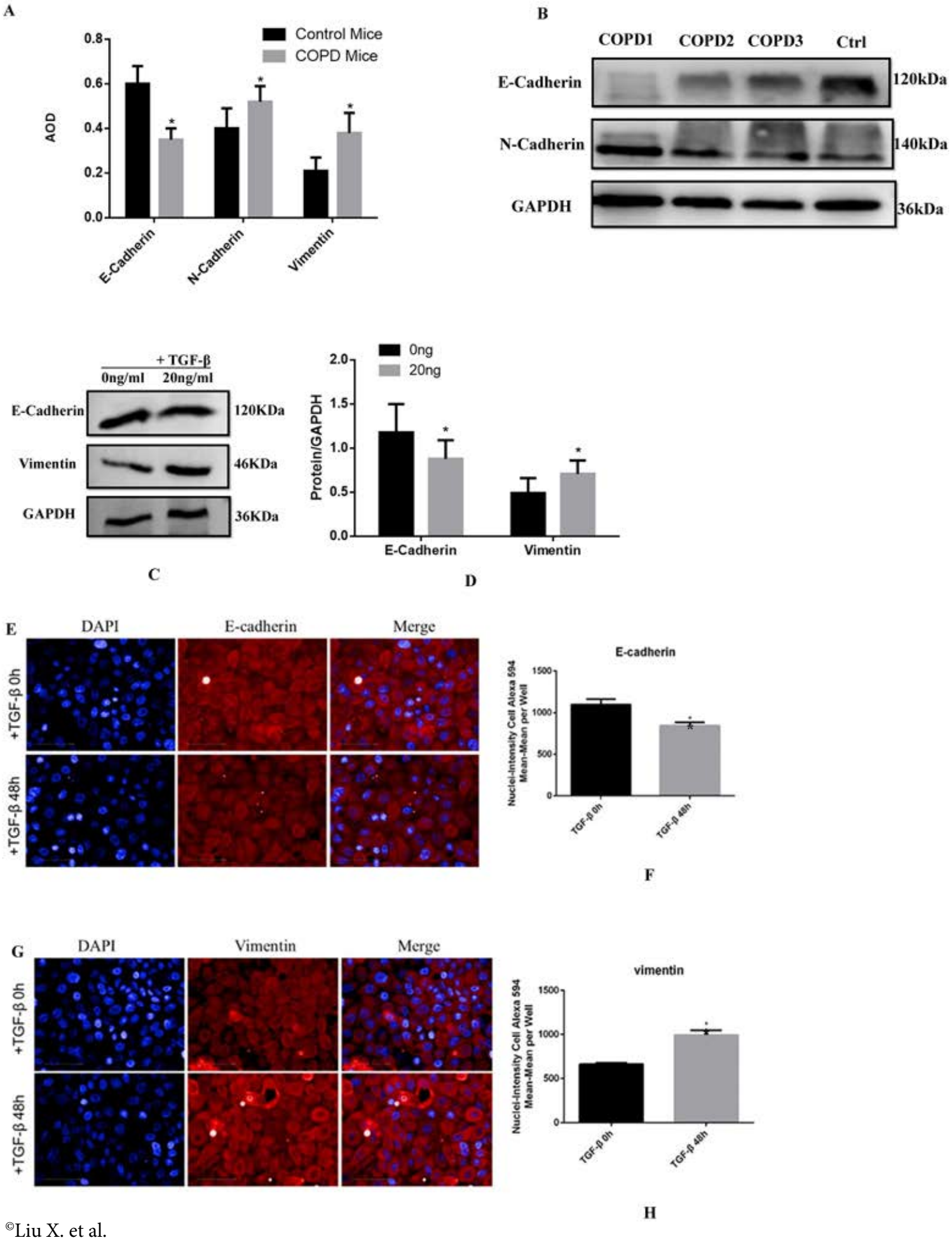
Protein/GAPDH
E-Cadherin
N-Cadherin
Vimentin
+ TGF-β 20ng/ml

F


NC
Si SMAD7
Protein/GAPDH
E-Cadherin
N-Cadherin
Vimentin
+ TGF-β 20ng/ml

G

Supplementary Figure 2. Airway remodeling and EMT in lungs of COPD patients and mice models and CSE enhance EMT process of bronchial epithelial cells through TGF-β1
Statistical analysis of the immunohistochemistry images in Figure 1A revealed that, in the COPD mouse model group, pulmonary E-cadherin expression was decreased, whereas N-cadherin and vimentin expression were increased(A). Further Western Blot of lungs from COPD patients and health people reconfirmed the Immunohistochemical staining results (B). Further Western Blot (C-D) and immunofluorescent staining (E-H) reconfirmed the rt-qPCR results in Figure 2C-2E. Bar: 20μm; *: $p<0.05$; **: $p<0.01$; ***: $p<0.005$; ****: $p<0.001$. Scale bar: 40μm. Data are presented as mean ± SEM. Pairwise comparisons were performed using independent-sample t-tests / Mann–Whitney U tests with Bonferroni correction for multiple comparisons.


A
Control Mice
COPD Mice
AOD
0.8
0.6
0.4
0.2
0.0
E-Cadherin
N-Cadherin
Vimentin
B
COPD1
COPD2
COPD3
Ctrl
E-Cadherin
120kDa
N-Cadherin
140kDa
GAPDH
36kDa
+ TGF-β
0ng/ml
20ng/ml
E-Cadherin
120KDa
Vimentin
46KDa
GAPDH
36KDa
C
0ng
20ng
Protein/GAPDH
2.0
1.5
1.0
0.5
0.0
E-Cadherin
Vimentin
D
E
DAPI
E-cadherin
Merge
+TGF-β 0h
+TGF-β 48h
E-cadherin
Nuclei-Intensity Cell Alexa 594
Mean-Mean per Well
1500
1000
500
0
TGF-β 0h
TGF-β 48h
F
G
DAPI
Vimentin
Merge
+TGF-β 0h
+TGF-β 48h
vimentin
Nuclei-Intensity Cell Alexa 594
Mean-Mean per Well
1500
1000
500
0
TGF-β 0h
TGF-β 48h
H