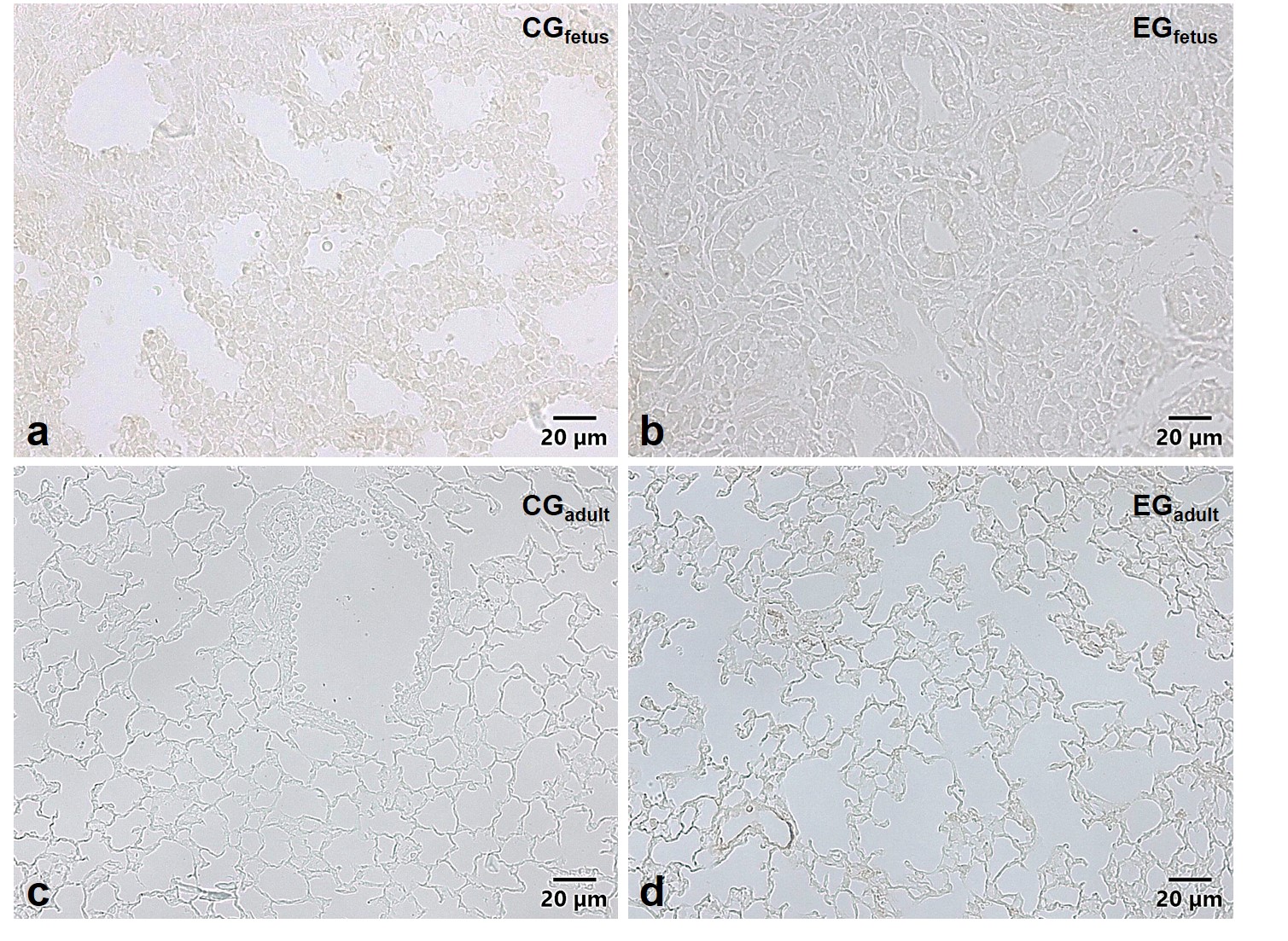
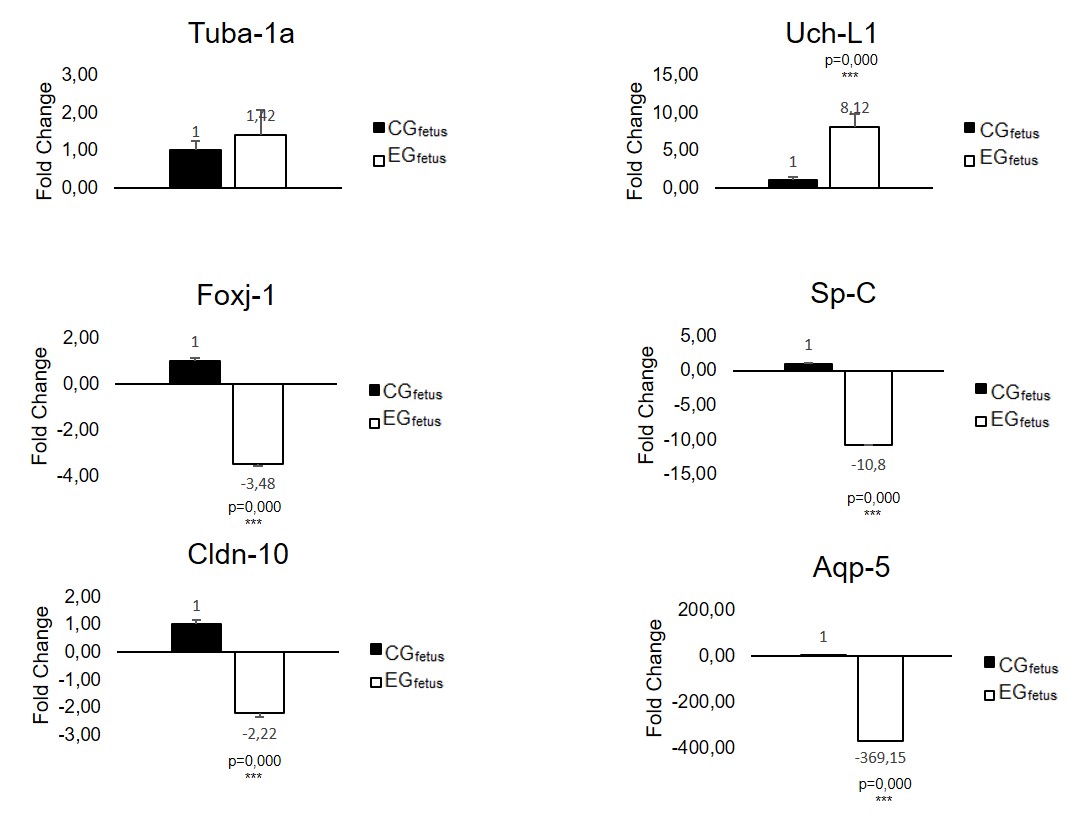


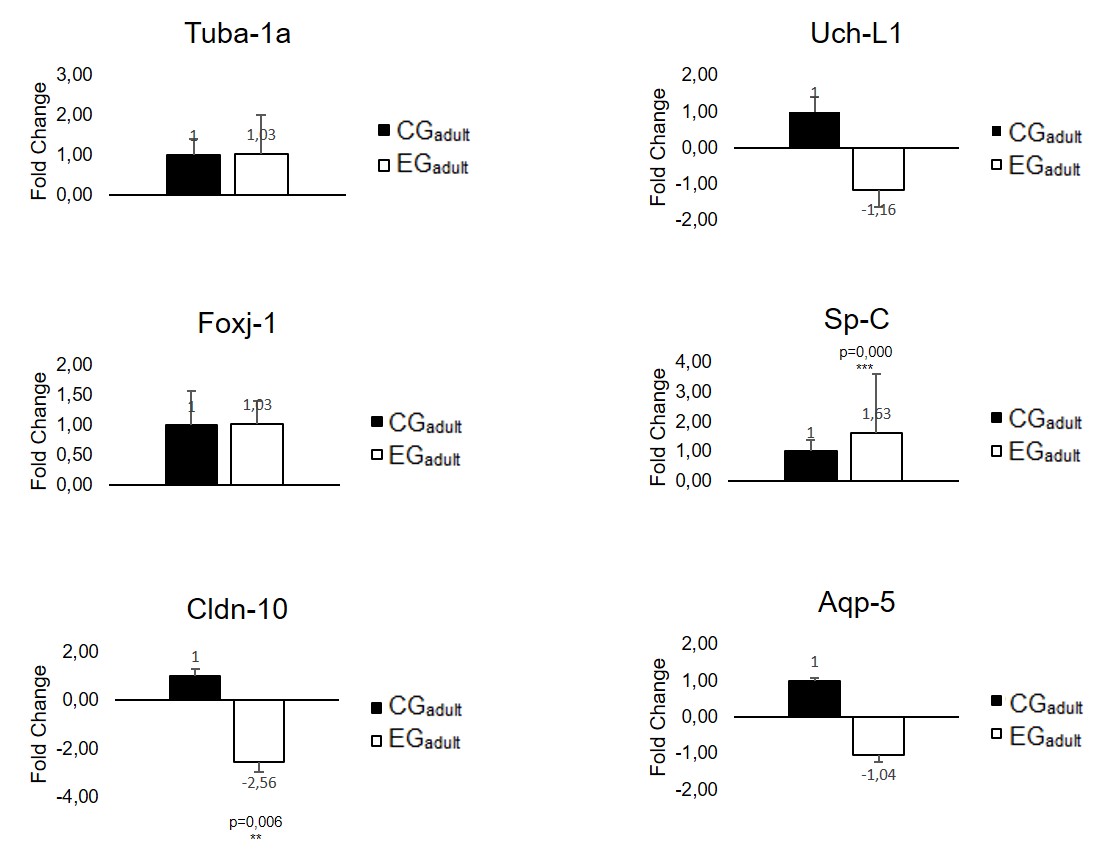
**Supplementary Figure 1.** Whole western blot images of Tuba, Cldn-10, Uch-L1, Sp-C and Aqp-5 in the fetal and adult lung tissue samples. Bands were visualized using peroxidase-labeled secondary antibodies. A specific band corresponding to Tuba, Cldn-10, UchL-1, Sp-C, and Aqp-5 could readily be detected in both fetal (**a**) and adult lung tissue samples (**b**), except for Aqp-5 in CGfetus and EGfetus (**a**). β-actin was used as an endogenous control. Pre-stained protein ladder V (Genaid, 10-180 kDa MW) was used as a protein marker. Sizes of bands for each protein are indicated. M: Markers; C1, C2, C3: Replications 1, 2, and 3 of the Control groups; E1, E2, E3: Replications 1, 2, and 3 of the Experimental groups.



**Supplementary Figure 2.** The negative control sections were treated in an identical manner except for the use of TBS (pH 7.6) instead of the primary antibody. After a final rinse and wash in TBS, immune positive cells were detected using 3, 3’ diaminobenzidine tetrahydrochloride (DAB) solution (3 mg/ml in Tris-HCl, pH 7,6 with 3 % H2O2). The sections were observed on an Olympus BX51 microscope and images were captured using Olympus DP70 camera with DP controller software (Ver. 3.1.1.267). No immune-positivity were detected in any of the negative control sections used for each antibody in CGfetus (**a**), EGfetus (**b**), CGadult (**c**) and EGadult (**d**).



**Supplementary Figure 3.** Real-time PCR analyses of Tuba-1a, Foxj-1, Cldn-10, Uch-L1, Sp-C and Aqp-5 using pooled fetal lung tissue samples. Transcript levels were quantified using SYBR® Green quantitative real-time PCR. β-actin was used as an endogenous reference gene for normalization of Ct values obtained for each gene. Fold changes in gene expression were calculated using 2−ΔΔCt method as described by Schmittgen and Livak (2008). \*\*\*p < .001.



**Supplementary Figure 4.** Real-time PCR analyses of Tuba-1a, Foxj-1, Cldn-10, Uch-L1, Sp-C and Aqp-5 using pooled adult lung tissue samples. Transcript levels were quantified using SYBR® Green quantitative real-time PCR. β-actin was used as an endogenous reference gene for normalization of Ct values obtained for each gene. Fold changes in gene expression were calculated using 2−ΔΔCt method as described by Schmittgen and Livak (2008). \*\*p < .01; \*\*\*p < .001.