

Figure S1

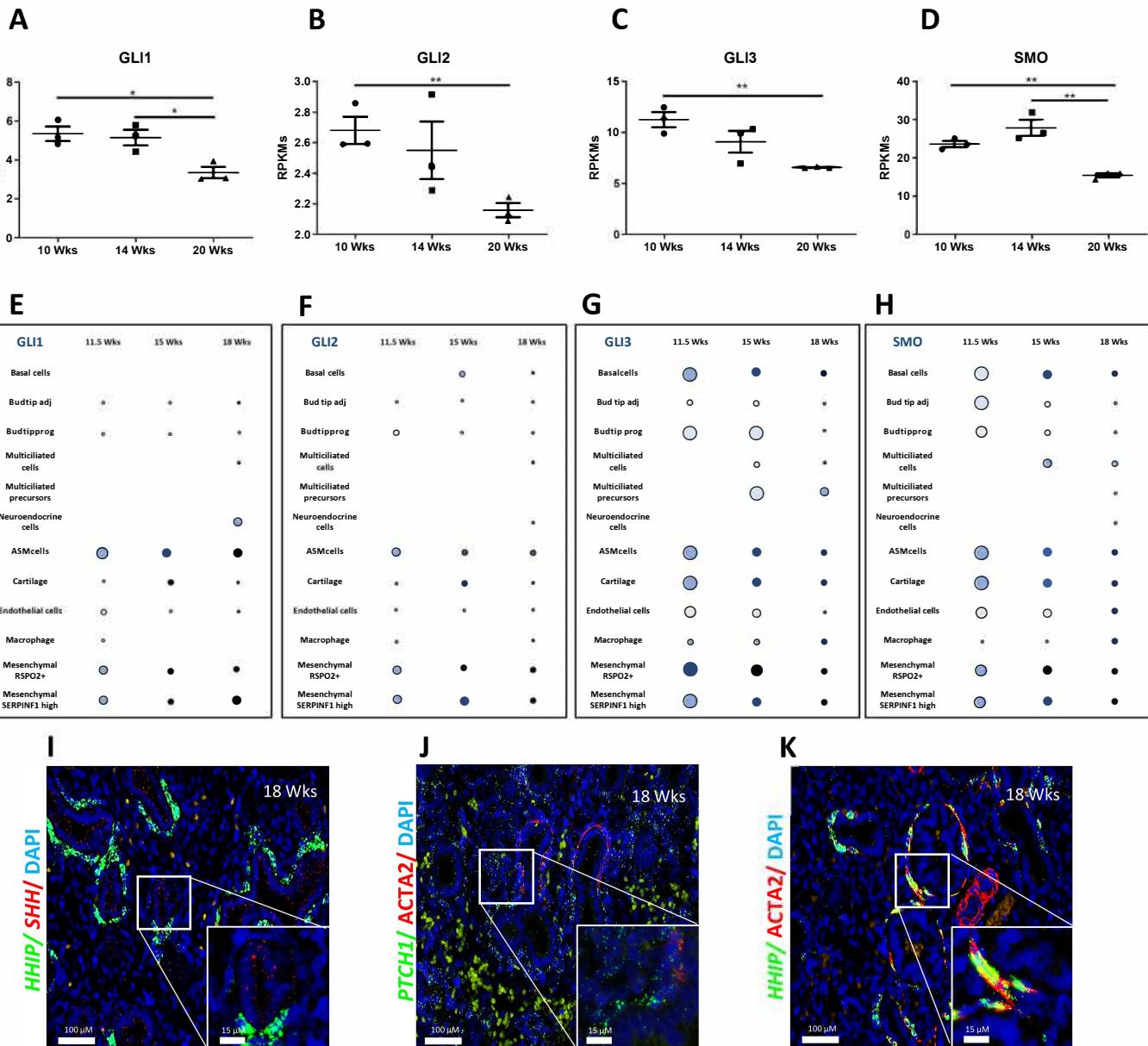
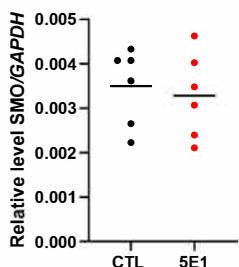


Figure S1: Complementary HH pathway actor expression during human lung development

RNA expression of *GLI1*(A), *GLI2* (B), *GLI3* (C) and *SMO* (D) expressed in RPKMs \pm SEM within the developing lung at 10-, 14- and 20-week gestation ($n=3$ per time point, $*p<0.05$, $**p<0.01$). The dot plot shows the percentage of cells expressing the respective selected marker gene (*GLI1*, *GLI2*, *GLI3* and *SMO*) using dot size and the average expression level of that gene based on unique molecular identifier (UMI) counts (E-H). Representative pictures of *in situ* hybridization at 18 wks gestation on fetal human lung sections for *SHH* (I, red), *PTCH1* (J, green) and *HHIP* (K, green) with *ACTA2* (IF-red, J-K) and the respective dots quantification (L-N) (results show mean \pm SEM, $*p<0.05$, $n=3$ for each group).

Figure S2

A



B

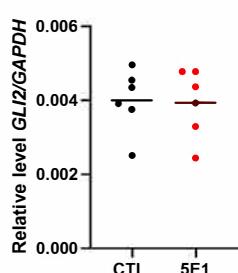


Figure S2: Extended HH pathway components expression after 5E1 treatment

RT-qPCR for *SMO* (A) and *GLI2* (B) in 5E1-treated explants compared to control (n=6 for each group).

Figure S3

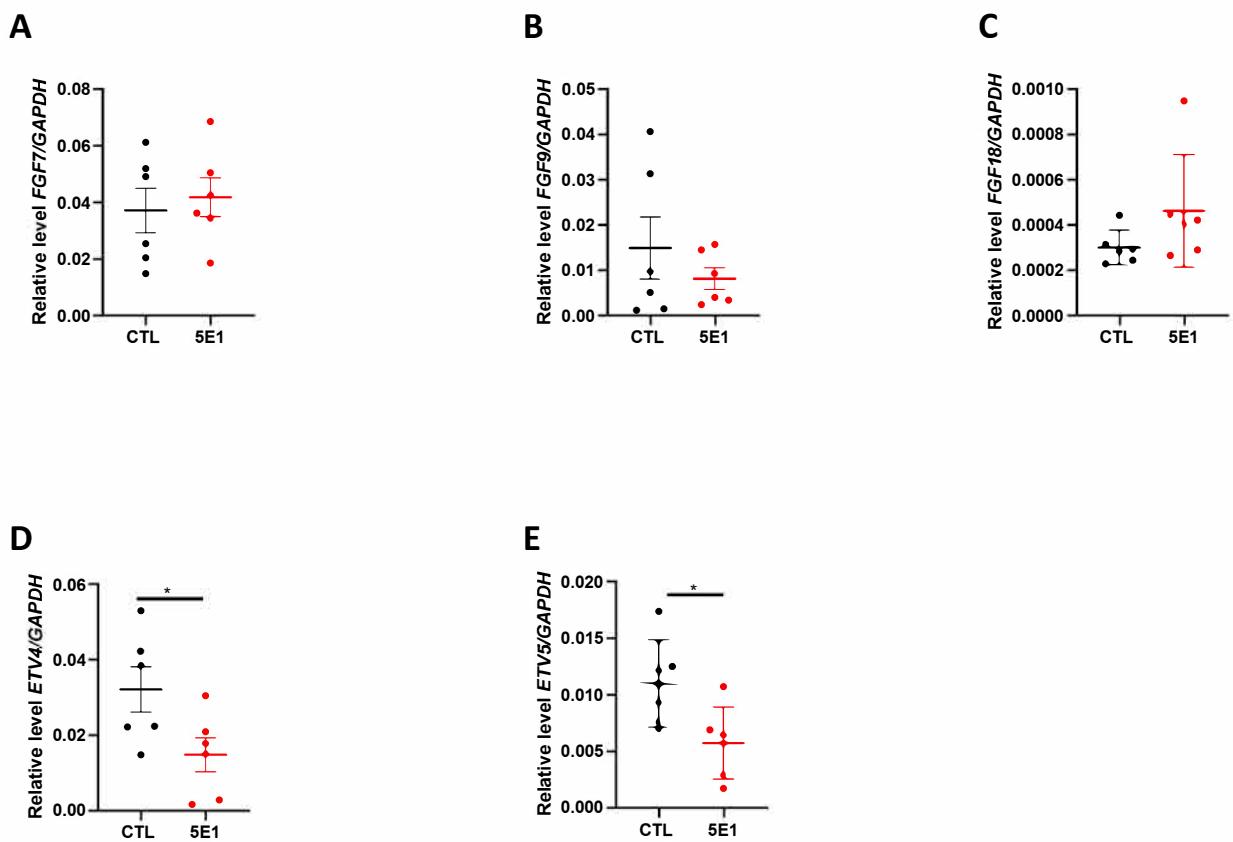


Figure S3: HH signaling effect on FGF and WNT pathway elements

RT-qPCR for $FGF7$ (A), $FGF9$ (B), $FGF18$ (C), $ETV4$ (D) and $ETV5$ (E) in control and 5E1-treated explants (results show mean \pm SEM, * $p < 0.05$, n=6 for each group).

Figure S4

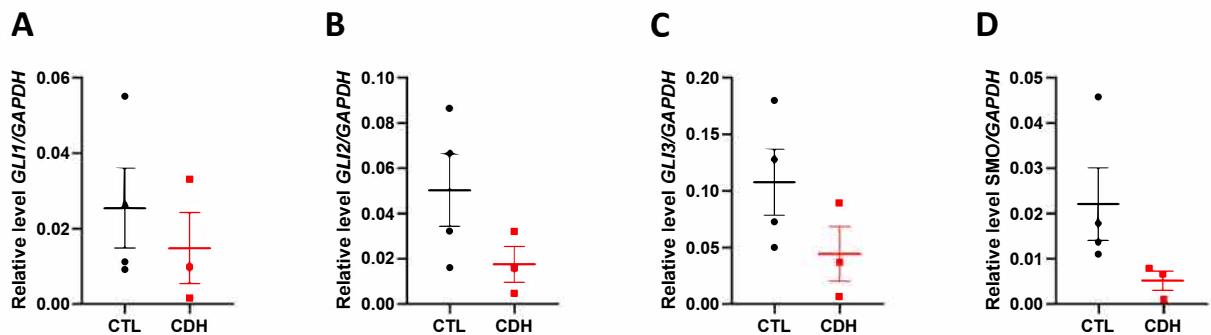


Figure S4: Additional HH pathway components expression in CDH

RT-qPCR for *GLI1* (A), *GLI2* (B), *GLI3* (C) and *SMO* (D) in 5E1-treated explants compared to controls.

Figure S5

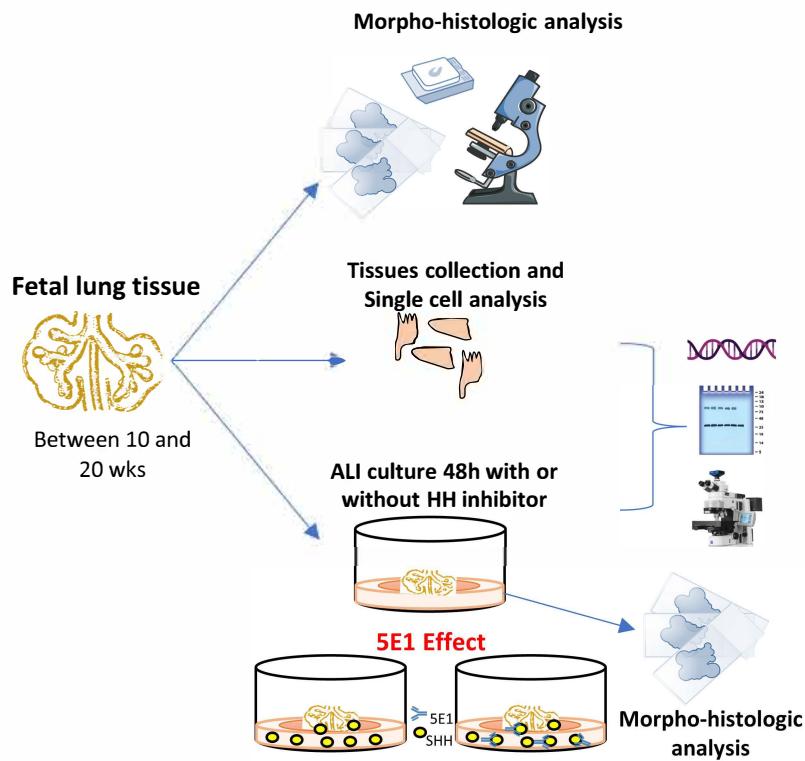


Figure S5: Schematic representation of methodology

Human fetal lung explant culture, from tissue to analyses.