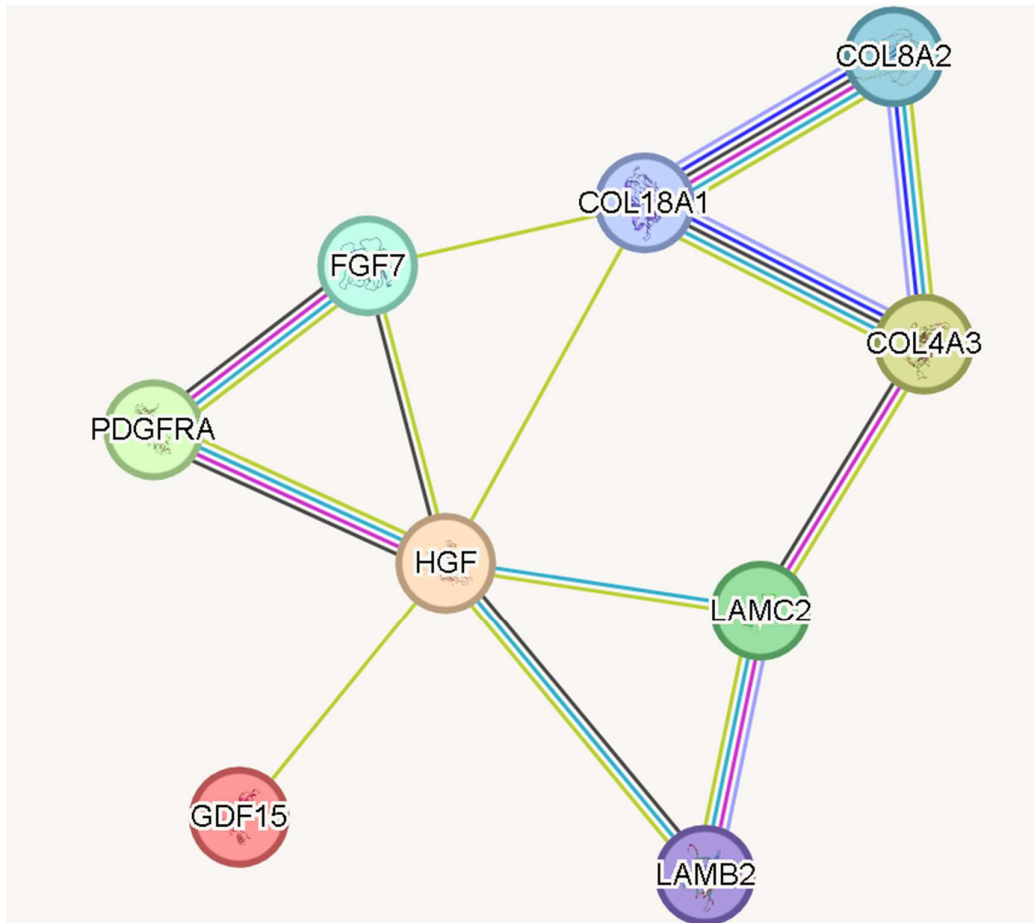


Figure S1. Raw images of bright-field microscopy in untreated and lidocaine-treated THP-1 cells. Cell morphology visualized using light microscope (20x magnification) at various lidocaine concentrations for 0, 6, 12 and 24 h. Representative images (cropped) were shown in Fig. 1B in the main figure.

Figure S2. Protein-protein interactions of identified genes. The STRING protein database was utilized to analyze the protein-protein interactions of GDF15, FGF7, HGF, COL4A3, COL8A2, LAMB2, LAMC2, PDGFRA, and VEGFA.

STRING parameters used to generate this figure.

- full STRING network



- evidence, line color indicates the type of interaction evidence
- medium confidence 0.400
- number of nodes: 9
- number of edges: 13
- average node degree: 2.89
- avg. local clustering coefficient: 0.652
- expected number of edges: 1
- PPI enrichment p-value: 1.93e-11

| Biological Process (Gene Ontology) | | | | |
|------------------------------------|---------------------------------------------------------------|------------------|----------|----------------------|
| GO-term | description | count in network | strength | false discovery rate |
| GO:0060665 | Regulation of branching involved in salivary gland morphog... | 2 of 3 | 3.16 | 0.0033 |
| GO:0051450 | Myoblast proliferation | 2 of 7 | 2.8 | 0.0075 |
| GO:0072224 | Metanephric glomerulus development | 2 of 11 | 2.6 | 0.0126 |
| GO:0032836 | Glomerular basement membrane development | 2 of 11 | 2.6 | 0.0126 |
| GO:0032835 | Glomerulus development | 3 of 56 | 2.07 | 0.0033 |
| GO:0030198 | Extracellular matrix organization | 5 of 278 | 1.6 | 0.0011 |
| GO:0050673 | Epithelial cell proliferation | 3 of 170 | 1.59 | 0.0312 |
| GO:0007169 | Transmembrane receptor protein tyrosine kinase signaling ... | 5 of 425 | 1.41 | 0.0022 |
| GO:0006935 | Chemotaxis | 5 of 516 | 1.33 | 0.0033 |
| GO:0071363 | Cellular response to growth factor stimulus | 4 of 473 | 1.27 | 0.0253 |
| GO:0030335 | Positive regulation of cell migration | 4 of 529 | 1.22 | 0.0335 |
| GO:0007155 | Cell adhesion | 6 of 965 | 1.13 | 0.0033 |
| GO:0009887 | Animal organ morphogenesis | 6 of 997 | 1.12 | 0.0033 |
| GO:0009888 | Tissue development | 6 of 1723 | 0.88 | 0.0214 |
| GO:0009653 | Anatomical structure morphogenesis | 7 of 2229 | 0.84 | 0.0075 |
| GO:0048513 | Animal organ development | 8 of 3246 | 0.73 | 0.0055 |
| GO:0048731 | System development | 8 of 3867 | 0.66 | 0.0129 |
| GO:0032501 | Multicellular organismal process | 9 of 6490 | 0.48 | 0.0288 |

| Molecular Function (Gene Ontology) | | | | |
|------------------------------------|---------------------------------------------|------------------|----------|----------------------|
| GO-term | description | count in network | strength | false discovery rate |
| GO:0005201 | Extracellular matrix structural constituent | 4 of 131 | 1.82 | 0.0013 |
| GO:0005102 | Signaling receptor binding | 7 of 1499 | 1.01 | 0.0013 |

| Cellular Component (Gene Ontology) | | | | |
|------------------------------------|-----------------------------|------------------|----------|----------------------|
| GO-term | description | count in network | strength | false discovery rate |
| GO:0043256 | Laminin complex | 2 of 12 | 2.56 | 0.0043 |
| GO:0005604 | Basement membrane | 5 of 98 | 2.05 | 8.97e-07 |
| GO:0005581 | Collagen trimer | 3 of 95 | 1.84 | 0.0029 |
| GO:0005788 | Endoplasmic reticulum lumen | 4 of 312 | 1.45 | 0.0026 |
| GO:0005615 | Extracellular space | 8 of 3247 | 0.73 | 0.0017 |
| GO:0012505 | Endomembrane system | 8 of 4721 | 0.57 | 0.0159 |

| Local network cluster (STRING) | | | | |
|--------------------------------|-----------------------------------------------------------------|------------------|----------|----------------------|
| cluster | description | count in network | strength | false discovery rate |
| CL:19651 | Laminin interactions | 2 of 21 | 2.32 | 0.0214 |
| CL:17332 | Activated point mutants of FGFR2, and Fibroblast growth fa... | 2 of 25 | 2.24 | 0.0269 |
| CL:17331 | Mixed, incl. FGFR2 ligand binding and activation, and PDGF/... | 3 of 45 | 2.16 | 0.0011 |
| CL:19458 | Collagen formation, and Protein complex involved in cell ad... | 4 of 119 | 1.87 | 0.00081 |
| CL:17327 | Mixed, incl. Constitutive Signaling by Aberrant PI3K in Canc... | 4 of 154 | 1.75 | 0.0011 |

| KEGG Pathways | | | | |
|---------------|-------------------------------------------|------------------|----------|----------------------|
| pathway | description | count in network | strength | false discovery rate |
| hsa05218 | Melanoma | 3 of 72 | 1.96 | 0.00037 |
| hsa04512 | ECM-receptor interaction | 3 of 88 | 1.87 | 0.00053 |
| hsa05222 | Small cell lung cancer | 3 of 92 | 1.85 | 0.00053 |
| hsa04974 | Protein digestion and absorption | 3 of 100 | 1.82 | 0.00055 |
| hsa05146 | Amoebiasis | 3 of 101 | 1.81 | 0.00055 |
| hsa04510 | Focal adhesion | 5 of 195 | 1.75 | 2.10e-06 |
| hsa01521 | EGFR tyrosine kinase inhibitor resistance | 2 of 77 | 1.75 | 0.0145 |
| hsa05145 | Toxoplasmosis | 2 of 103 | 1.63 | 0.0237 |
| hsa04151 | PI3K-Akt signaling pathway | 6 of 349 | 1.58 | 8.83e-07 |
| hsa04015 | Rap1 signaling pathway | 3 of 201 | 1.51 | 0.0033 |
| hsa05226 | Gastric cancer | 2 of 146 | 1.48 | 0.0436 |
| hsa04014 | Ras signaling pathway | 3 of 225 | 1.47 | 0.0041 |
| hsa05200 | Pathways in cancer | 6 of 515 | 1.41 | 2.92e-06 |
| hsa04010 | MAPK signaling pathway | 3 of 286 | 1.36 | 0.0075 |
| hsa05165 | Human papillomavirus infection | 3 of 324 | 1.31 | 0.0099 |