Table SI. Reverse transcription-quantitative PCR primer sequences.

| Gene  | Primer, forward (5’→3’) | Primer, reverse (5’→3’) |
|-------|-------------------------|-------------------------|
| Notch1 | GATGGCCTCAATGGGTACAAG   | TCGTTGTTGTTGATGTCACAGT  |
| Notch2 | GAGAAAAACCCGTCTCAGAATGG | GGTTGAGTTGAGCGAGTCCCT   |
| Notch3 | AGTCCATCTGGTACAACCTT    | CACTACGGGGTTCACACA      |
| Notch4 | GCGAGCGAGCTCCTCAACGAGT  | AGGAGGCGGATCGGAAATGT    |
| Jagged1| AACTGGTACGGGTGCAGA      | TGGATGCAAGATCTTCTCTAACA |
| Jagged2| TGGGGCGCAAATCCCTCTCT    | GCCTCCAGGATGAGGTAAAA    |
| DLL1  | TGCCACGGTACCTCCCTCT     | TCTTCTGTGGTTCTGTTG      |
| DLL3  | GTGACGGGTGCTGGATGGTAC   | AGCTCCACAGGAGTTCTCTTG   |
| Hey1  | GAAAAAGCGAGAGGGCATCA    | AGGCAATCTCTGCTCTCTCACA  |
| Hes1  | CGACACCGGAAACCAAA       | GAATGTCTGCTCTACAGTTA    |
| GAPDH | GCAAGAGAGAGGCCCTCAG     | TGGAAGGAGAGTGAAGTCTAGT  |
Table SII. Calculation of wound width.

|       | Control | 0.1 mM PA | 0.25 mM PA | 0.5 mM PA |
|-------|---------|-----------|------------|-----------|
|       | 0       | 12        | 24         | 36        | 48        | 72        | 0       | 12        | 24         | 36         | 48        | 72        | 0       | 12        | 24         | 36         | 48        | 72        |
| Time, h | 0 | 12 | 24 | 36 | 48 | 72 | 0 | 12 | 24 | 36 | 48 | 72 | 0 | 12 | 24 | 36 | 48 | 72 |
| LX2    | 1 | 0.78±0.04 | 0.79±0.01 | 0.73±0.04 | 0.64±0.05 | 0.54±0.06 | 1 | 0.83±0.02 | 0.83±0.01 | 0.70±0.05 | 0.69±0.05 | 0.67±0.08 | 1 | 0.79±0.03 | 0.77±0.05 | 0.71±0.03 | 0.70±0.03 | 0.67±0.02 | 1 |
| Huh7   | 1 | 0.82±0.01 | 0.67±0.04 | 0.65±0.03 | 0.55±0.05 | 0.53±0.03 | 1 | 0.84±0.02 | 0.73±0.01 | 0.62±0.07 | 0.60±0.08 | 0.45±0.08 | 1 | 0.76±0.03 | 0.71±0.01 | 0.65±0.01 | 0.56±0.02 | 0.51±0.03 | 1 |
| MIHA   | 1 | 0.92±0.02 | 0.92±0.03 | 0.90±0.03 | 0.89±0.04 | 0.86±0.03 | 1 | 1.07±0.06 | 0.99±0.02 | 0.94±0.02 | 0.94±0.02 | 0.90±0.04 | 1 | 1.0±0.07 | 0.97±0.13 | 0.99±0.12 | 0.99±0.09 | 0.95±0.14 | 1 |

PA, palmitic acid.