**S4 Table. Signal peptide prediction of wild-type and mutant COL4A3 amino acid sequences**

|  |  |  |  |
| --- | --- | --- | --- |
| *COL4A3* sequence | SignalP 4.11 | PrediSi2 | Signal-3L3 |
| **Score** | **Cleavage position** | **Signal Peptide** | **Score** | **Cleavage position** | **Signal Peptide** | **Secreted?** | **Cleavage position** | **Signal Peptide** |
| *Wild type* | 0.79 | 28 | Y | 1.00 | 28 | Y | Y | 26 | Y |
| *24bp-del* *(Family 3)* | 0.21 | n.c. | N | 0.45 | 22 | N | N | n.c. | N |
| *rs570469692**(12-bp del)* | 0.71 | 26 | Y | 1.00 | 26 | Y | Y | 26 | Y |
| *24bp-del**(Longo et al. 2002)* | 0.21 | n.c. | N | 0.45 | 22 | N | N | n.c. | N |

n.c. not calculated

1 SignalP 4.1, http://www.cbs.dtu.dk/services/SignalP/

2 PREDIction of SIgnal peptides, http://www.predisi.de/

3 Signal-3L 2.0, http://www.csbio.sjtu.edu.cn/bioinf/Signal-3L/