# SUPPLEMENTARY MATERIAL

**Supplementary Figure 1. Immunohistochemical analysis of TAGLN, TAGLN2, and PPIA expression in pulmonary adenocarcinoma (patient LA11).** Photomicrographs of normal lung tissue (A) and lung adenocarcinoma (B) stained with hematoxylin-eosin. Protein expression of TAGLN (C, D), TAGLN2 (E, F), and PPIA (G, H) in lung tissue (left, normal; right, adenocarcinoma). Original magnifications: 640×.

**Supplementary Figure 2. Immunohistochemical analysis of TAGLN, TAGLN2, and PPIA expression in pulmonary adenocarcinoma (patient LA12).** Photomicrographs of normal lung tissue (A) and lung adenocarcinoma (B) stained with hematoxylin-eosin. Protein expression of TAGLN (C, D), TAGLN2 (E, F), and PPIA (G, H) in lung tissue (left, normal; right, adenocarcinoma). Original magnifications: 640×.

**Supplementary Figure 3. Immunohistochemical analysis of TAGLN, TAGLN2, and PPIA expression in pulmonary adenocarcinoma (patient LA10).** Protein expression of TAGLN (A, B), TAGLN2 (C, D), and PPIA (E, F) in lung tissue (left, normal; right, adenocarcinoma). Note the physiologic expression of TAGLN in smooth muscle cells of small blood vessels in normal lung (A, arrowheads). In this case, PPIA is expressed in few scattered cancer cells (F, arrowheads). Original magnifications: 400×.

**Supplementary Figure 4. Immunohistochemical analysis of TAGLN, TAGLN2, and PPIA expression in pulmonary adenocarcinoma (patient LA14).** Protein expression of TAGLN (A, B), TAGLN2 (C, D), and PPIA (E, F) in lung tissue (left, normal; right, adenocarcinoma). Original magnifications: 400×.

**Supplementary Figure 5. Expression of TAGLN in pulmonary squamous cell carcinomas.** (A, B) Representative immunohistochemical demonstration of TAGLN overexpression in myofibroblastic stroma surrounding invasive islands of squamous cell carcinoma (patient LS3). Arrowheads indicate examples of two smaller nests of carcinoma (A). Original magnifications: 100× (A), 400× (B). (C) Western blots of tissue protein extracts from four patients (LS1-4) with moderately differentiated pulmonary squamous cell carcinomas after heparin affinity enrichment.

**Supplementary Table 1.** Detailed information on the MS/MS sequencing of the three identified protein spots

## (1) Spot 1: TAGLN and TAGLN2

| Rank | Charge | Ions | dCn | XCorr | Reference | Redundancy | Peptide |
|---|---|---|---|---|---|---|---|
| 1 | 2 | 14/16 | 0.2503 | 2.3733 | UPSP:TAGL_HUMAN | 4 | K.AAEDYGVIK.T |
| 1 | 2 | 14/16 | 0.2615 | 3.0126 | UPSP:TAGL_HUMAN | 5 | K.KYDEELEER.L |
| 1 | 2 | 17/26 | 0.3433 | 3.9634 | UPSP:TAGL_HUMAN | 5 | K.LVNSLYPDGSKPVK.V |
| 1 | 3 | 28/96 | 0.2019 | 3.8116 | UPSP:TAGL_HUMAN | 5 | K.LVNSLYPDGSKPVKVPENPPSM*VFK.Q |
| 1 | 2 | 13/18 | 0.1365 | 2.7350 | UPSP:TAGL_HUMAN | 6 | K.QM*EQVAQFLK.A |
| 1 | 2 | 13/18 | 0.0112 | 2.4931 | UPSP:TAGL_HUMAN | 6 | K.QMEQVAQFLK.A |
| 1 | 2 | 18/24 | 0.3753 | 4.6052 | UPSP:TAGL_HUMAN | 6 | K.TDM*FQTVDLFEGK.D |
| 1 | 3 | 31/76 | 0.3029 | 4.0275 | UPSP:TAGL_HUMAN | 6 | K.TDM*FQTVDLFEGKDM*AAVQR.T |
| 1 | 2 | 13/20 | 0.1069 | 2.6708 | UPSP:TAGL_HUMAN | 6 | K.VPENPPSM*VFK.Q |
| 1 | 2 | 11/14 | 0.0086 | 2.0252 | UPSP:TAGL_HUMAN | 5 | K.YDEELEER.L |
| 1 | 2 | 17/20 | 0.2336 | 3.1748 | UPSP:TAGL_HUMAN | 5 | R.EFTESQLQEGK.H |
| 1 | 2 | 10/14 | 0.1633 | 1.8580 | UPSP:TAGL_HUMAN | 6 | R.GDPNWFM*K.K |
| 1 | 2 | 13/14 | 0.0631 | 2.8782 | UPSP:TAGL_HUMAN | 4 | R.LGFQVWLK.N |
| 1 | 2 | 17/34 | 0.1523 | 2.9128 | UPSP:TAGL_HUMAN | 4 | R.LVEWIIVQCGPDVGRPDR.G |
| 1 | 2 | 17/22 | 0.3242 | 3.7983 | UPSP:TAGL_HUMAN | 6 | R.TLM*ALGSLAVTK.N |
| 1 | 2 | 14/40 | 0.2070 | 2.1028 | UPSP:TAGL2_HUMAN | 5 | K.DGTVLCELINALYPEGQAPVK.K |
| 1 | 3 | 27/84 | 0.0695 | 3.0308 | UPSP:TAGL2_HUMAN | 5 | K.DGTVLCELINALYPEGQAPVKK.I |
| 1 | 2 | 12/16 | 0.0544 | 2.6770 | UPSP:TAGL2_HUMAN | 6 | K.IQASTM*AFK.Q |
| 1 | 2 | 15/20 | 0.1053 | 2.1763 | UPSP:TAGL2_HUMAN | 6 | K.NVIGLQM*GTNR.G |
| 1 | 2 | 21/26 | 0.3978 | 4.5299 | UPSP:TAGL2_HUMAN | 6 | K.QM*EQISQFLQAAER.Y |
| 1 | 2 | 19/26 | 0.2311 | 3.8568 | UPSP:TAGL2_HUMAN | 6 | K.QMEQISQFLQAAER.Y |
| 1 | 3 | 28/72 | 0.2739 | 4.7564 | UPSP:TAGL2_HUMAN | 6 | K.QYDADLEQILIQWITTQCR.K |
| 1 | 2 | 17/26 | 0.3401 | 3.9271 | UPSP:TAGL2_HUMAN | 6 | R.DDGLFSGDPNWFPK.K |
| 1 | 2 | 16/20 | 0.1198 | 3.0801 | UPSP:TAGL2_HUMAN | 6 | R.NFSDNQLQEGK.N |
| 1 | 2 | 19/22 | 0.3503 | 3.9924 | UPSP:TAGL2_HUMAN | 6 | R.TLM*NLGGLAVAR.D |
| 1 | 2 | 25/34 | 0.3975 | 5.8066 | UPSP:TAGL2_HUMAN | 6 | R.YGINTTDIFQTVDLWEGK.N |

| **UPSP:TAGL_HUMAN** (Q01995, homo sapiens): Transgelin (smooth muscle protein 22-alpha) [**MASS=22480**] |
|---|
| ANKGPSYGMS REVQSKIEK**K YDEELEERLV EWIIVQCGPD VGRPDR**GR**LG FQVWLK**NGVI LSK**LVNSLYP DGSKPVKVPE NPPSMVFKQM EQVAQFLKAA EDYGVIKTDM FQTVDLFEGK DMAAVQRTLM ALGSLAVTK**N DGHYR**GDPNW FMK**KAQEHKR **EFTESQLQEG K**HVIGLQMGS NRGASQAGMT GYGRPRQIIS |

| Position | MH+ | Sequence |
|---|---|---|
| 99-107 | 966.0789 | AAEDYGVIK |
| 49-56 | 991.2211 | LGFQVWLK |
| 146-153 | 995.1407 | GDPNWFMK |
| 21-28 | 1083.0967 | YDEELEER |
| 128-139 | 1205.4986 | TLMALGSLAVTK |
| 20-28 | 1211.2708 | KYDEELEER |
| 89-98 | 1222.4449 | QMEQVAQFLK |
| 78-88 | 1245.4793 | VPENPPSMVFK |
| 161-171 | 1296.3764 | EFTESQLQEGK |
| 64-77 | 1517.7655 | LVNSLYPDGSKPVK |
| 108-120 | 1531.7206 | TDMFQTVDLFEGK |
| 29-46 | 2053.3868 | LVEWIIVQCGPDVGRPDR |
| 108-127 | 2303.6102 | TDMFQTVDLFEGKDMAAVQR |
| 64-88 | 2744.2216 | LVNSLYPDGSKPVKVPENPPSMVFK |

Protein coverage by amino acid count: 130/200 = **65.0%**
Protein coverage by mass: 14818/22480 = **65.9%**

| **UPSP:TAGL2_HUMAN** (P37802, homo sapiens): Transgelin-2 (sm22-alpha homolog) [**MASS=22260**] |
|---|
| ANRGPAYGLS REVQQKIEK**Q YDADLEQILI QWITTQCR**KD VGRPQPGREN FQNWLK**DGTV LCELINALYP EGQAPVKKIQ ASTMAFKQME QISQFLQAAE RYGINTTDIF QTVDLWEGK**N MACVQR**TLMN LGGLAVARDD GLFSGDPNWF PK**KSKENPR**N FSDNQLQEGK NVIGLQMGTN R**GASQAGMTG YGMPRQIL |

| Position | MH+ | Sequence |
|---|---|---|
| 79-87 | 997.1975 | IQASTMAFK |
| 171-181 | 1203.4019 | NVIGLQMGTNR |
| 127-138 | 1216.4844 | TLMNLGGLAVAR |
| 160-170 | 1280.3365 | NFSDNQLQEGK |
| 139-152 | 1595.7081 | DDGLFSGDPNWFPK |
| 88-101 | 1679.8883 | QMEQISQFLQAAER |
| 102-119 | 2101.3202 | YGINTTDIFQTVDLWEGK |
| 57-77 | 2231.5689 | DGTVLCELINALYPEGQAPVK |
| 20-38 | 2338.6402 | QYDADLEQILIQWITTQCR |
| 57-78 | 2359.7430 | DGTVLCELINALYPEGQAPVKK |

Protein coverage by amino acid count: 130/198 = **65.7%**
Protein coverage by mass: 14620/22260 = **65.7%**

## (2) Spot 3: PPIA

| Rank | Charge | Ions | dCn | XCorr | Reference | Redundancy | Peptide |
|---|---|---|---|---|---|---|---|
| 1 | 2 | 11/20 | 0.1456 | 2.1931 | UPTR:Q3KQW3_HUMAN | 6 | K.EGM*NIVEAM*ER.F |
| 1 | 2 | 14/16 | 0.0115 | 3.3212 | UPTR:Q3KQW3_HUMAN | 4 | K.FEDENFILK.H |
| 1 | 3 | 40/104 | 0.2938 | 6.3140 | UPTR:Q3KQW3_HUMAN | 5 | K.HTGPGILSM*ANAGPNTNGSQFFICTAK.T |
| 1 | 1 | 12/18 | 0.2374 | 2.0223 | UPTR:Q3KQW3_HUMAN | 4 | K.ITIADCGQLE.- |
| 1 | 2 | 14/20 | 0.0544 | 2.5882 | UPTR:Q3KQW3_HUMAN | 4 | K.KITIADCGQLE.- |
| 1 | 2 | 21/28 | 0.2476 | 5.5171 | UPTR:Q3KQW3_HUMAN | 4 | K.SIYGEKFEDENFILK.H |
| 1 | 2 | 9/12 | 0.0210 | 1.6488 | UPTR:Q3KQW3_HUMAN | 7 | K.TEWLDGK.H |
| 1 | 2 | 11/24 | 0.1353 | 1.8577 | UPTR:Q3KQW3_HUMAN | 6 | K.VKEGM*NIVEAM*ER.F |
| 1 | 2 | 19/26 | 0.3914 | 1.6097 | UPTR:Q3KQW3_HUMAN | 5 | R.IIPGFM*CQGGDFTR.H |
| 1 | 2 | 14/16 | 0.2000 | 3.3743 | UPTR:Q3KQW3_HUMAN | 4 | R.VSFELFADK.V |

| **UPTR:Q3KQW3_HUMAN** (Q3kqw3, homo sapiens): Peptidylprolyl isomerase a, isoform 1 [**MASS=18012**] |
|---|
| MVNPTVFFDI AVDGEPLGR**V SFELFADK**VP KTAENFRALS TGEKGFGYKG SCFHR**IIPGF MCQGGDFTR**H NGTGGK**SIYG**<br>**EKFEDENFIL KHTGPGILSM ANAGPNTNGS QFFICTAKTE WLDGK**HVVFG K**VKEGMNIVE AMER**FGSRNG KTSK**KITIAD CGQLE** |

| Position | MH+ | Sequence |
|---|---|---|
| 119-125 | 848.9310 | TEWLDGK |
| 20-28 | 1056.2036 | VSFELFADK |
| 156-165 | 1063.2108 | ITIADCGQLE |
| 83-91 | 1155.2927 | FEDENFILK |
| 155-165 | 1191.3849 | KITIADCGQLE |
| 134-144 | 1279.4689 | EGMNIVEAMER |
| 132-144 | 1506.7756 | VKEGMNIVEAMER |
| 56-69 | 1542.8109 | IIPGFMCQGGDFTR |
| 77-91 | 1833.0478 | SIYGEKFEDENFILK |
| 92-118 | 2736.0924 | HTGPGILSMANAGPNTNGSQFFICTAK |

Protein coverage by amino acid count: 96/165 = **58.2%**
Protein coverage by mass: 10601/18012 = **58.9%**

## (3) Spot 5: TAGLN2

| Rank | Charge | Ions | dCn | XCorr | Reference | Redundancy | Peptide |
|---|---|---|---|---|---|---|---|
| 1 | 2 | 18/40 | 0.3948 | 3.2269 | UPSP:TAGL2_HUMAN | 5 | K.DGTVLCELINALYPEGQAPVK.K |
| 1 | 3 | 32/84 | 0.3908 | 3.9225 | UPSP:TAGL2_HUMAN | 5 | K.DGTVLCELINALYPEGQAPVKK.I |
| 1 | 2 | 11/16 | 0.0864 | 1.9669 | UPSP:TAGL2_HUMAN | 6 | K.IQASTM*AFK.Q |
| 1 | 2 | 18/20 | 0.2653 | 3.7665 | UPSP:TAGL2_HUMAN | 6 | K.NVIGLQM*GTNR.G |
| 1 | 2 | 21/26 | 0.3265 | 4.4890 | UPSP:TAGL2_HUMAN | 6 | K.QM*EQISQFLQAAER.Y |
| 1 | 2 | 20/26 | 0.2154 | 3.8847 | UPSP:TAGL2_HUMAN | 6 | K.QMEQISQFLQAAER.Y |
| 1 | 2 | 20/36 | 0.3535 | 4.6966 | UPSP:TAGL2_HUMAN | 6 | K.QYDADLEQILIQWITTQCR.K |
| 1 | 2 | 18/26 | 0.3376 | 4.5029 | UPSP:TAGL2_HUMAN | 6 | R.DDGLFSGDPNWFPK.K |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1 | 2 | 14/28 | 0.3001 | 3.7264 | UPSP:TAGL2_HUMAN | 6 | R.DDGLFSGDPNWFPKK.S |
| 1 | 2 | 14/20 | 0.2014 | 3.2672 | UPSP:TAGL2_HUMAN | 6 | R.NFSDNQLQEGK.N |
| 1 | 2 | 20/22 | 0.3892 | 4.0798 | UPSP:TAGL2_HUMAN | 6 | R.TLM*NLGGLAVAR.D |
| 1 | 2 | 20/22 | 0.2385 | 4.3082 | UPSP:TAGL2_HUMAN | 6 | R.TLMNLGGLAVAR.D |
| 1 | 3 | 34/68 | 0.3539 | 5.7351 | UPSP:TAGL2_HUMAN | 6 | R.YGINTTDIFQTVDLWEGK.N |

**UPSP:TAGL2_HUMAN** (P37802 homo sapiens): Transgelin-2 (sm22-alpha homolog) [**MASS=22260**]

ANRGPAYGLS REVQQKIEK**Q YDADLEQILI QWITTQCR**KD VGRPQPGREN FQNWLK**DGTV LCELINALYP EGQAPVKKIQ**
**ASTMAFKQME QISQFLQAAE RYGINTTDIF QTVDLWEGK**N MACVQR**TLMN LGGLAVARDD GLFSGDPNWF PKK**SKENPR**N**
**FSDNQLQEGK NVIGLQMGTN R**GASQAGMTG YGMPRQIL

| Position | MH+ | Sequence |
|---|---|---|
| 79-87 | 997.1975 | IQASTMAFK |
| 171-181 | 1203.4019 | NVIGLQMGTNR |
| 127-138 | 1216.4844 | TLMNLGGLAVAR |
| 160-170 | 1280.3365 | NFSDNQLQEGK |
| 139-152 | 1595.7081 | DDGLFSGDPNWFPK |
| 88-101 | 1679.8883 | QMEQISQFLQAAER |
| 139-153 | 1723.8822 | DDGLFSGDPNWFPKK |
| 102-119 | 2101.3202 | YGINTTDIFQTVDLWEGK |
| 57-77 | 2231.5689 | DGTVLCELINALYPEGQAPVK |
| 20-38 | 2338.6402 | QYDADLEQILIQWITTQCR |
| 57-78 | 2359.7430 | DGTVLCELINALYPEGQAPVKK |

Protein coverage by amino acid count: 131/198 = **66.2%**
Protein coverage by mass: 14748/22260 = **66.3%**