**Table S1**. **Gene expression data from microarray analysis (Affymetrix chips) of pancreatic samples. Genes with highest overexpression between PDAC and chronic pancreatitis/normal pancreas**

| **Affymetrix probe set ID** | **Gene description** | **Gene symbol** | **Gene ID** | **P value** |
| --- | --- | --- | --- | --- |
| 202381\_at | ADAM metallopeptidase domain 9 | ADAM9 | NM\_003816 | 0,04180 |
| 202207\_at | ADP-ribosylation factor-like 7 | ARL7 | BG435404 | 0,00423 |
| 206561\_s\_at | aldo-keto reductase family 1, member B10 | AKR1B10 | NM\_020299 | 0,05050 |
| 203559\_s\_at | amiloride binding protein 1  | ABP1 | NM\_001091 | 0,01560 |
| 209173\_at | anterior gradient 2 homolog | AGR2 | AF088867 | 0,00348 |
| 204416\_x\_at | apolipoprotein C-I | APOC1 | NM\_001645 | 0,01070 |
| 203382\_s\_at | apolipoprotein E | APOE | NM\_000041 | 0,00972 |
| 209281\_s\_at | ATPase, Ca++ transporting, plasma membrane 1 | ATP2B1 | L14561 | 0,30000 |
| 207173\_x\_at | cadherin 11, type 2, OB-cadherin (osteoblast) | CDH11 | D21254 | 0,00293 |
| 201884\_at | carcinoembryonic antigen cell adhesion molecule 5 | CEACAM5 | NM\_004363 | 0,00114 |
| 203757\_s\_at | carcinoembryonic antigen cell adhesion molecule 6 | CEACAM6 | BC005008 | 0,24500 |
| 205713\_s\_at | cartilage oligomeric matrix protein | COMP | NM\_000095 | 0,00241 |
| 200838\_at | cathepsin B | CTSB | NM\_001908 | 0,01240 |
| 205927\_s\_at | cathepsin E | CTSE | NM\_001910 | 0,00303 |
| 205173\_x\_at | CD58 antigen | CD58 | NM\_001779 | 0,02710 |
| 201005\_at | CD9 antigen (p24) | CD9 | NM\_001769 | 0,01850 |
| 204170\_s\_at | CDC28 protein kinase regulatory subunit 2 | CKS2 | NM\_001827 | 0,00307 |
| 210559\_s\_at | cell division cycle 2, G1 to S and G2 to M | CDC2 | D88357 | 0,00597 |
| 209201\_x\_at | chemokine (C-X-C motif) receptor 4 | CXCR4 | L01639 | 0,00003 |
| 204619\_s\_at | chondroitin sulfate proteoglycan 2 | CSPG2 | BF590263 | 0,00013 |
| 201310\_s\_at | chromosome 5 open reading frame 13 | C5orf13 | NM\_004772 | 0,00023 |
| 206284\_x\_at | clathrin, light polypeptide (Lcb) | CLTB | NM\_001834 | 0,02960 |
| 202404\_s\_at | collagen, type I, alpha 2 | COL1A2 | NM\_000089 | 0,01010 |
| 201852\_x\_at | collagen, type III, alpha 1 | COL3A1 | NM\_000090 | 0,02140 |
| 212489\_at | collagen, type V, alpha 1 | COL5A1 | AI983428 | 0,00004 |
| 217428\_s\_at | collagen, type X, alpha 1 | COL10A1 | X98568 | 0,00070 |
| **37892\_at** | **collagen, type XI, alpha 1** | **COL11A1** | **J04177** | **0,00008** |
| 204636\_at | collagen, type XVII, alpha 1 | COL17A1 | NM\_000494 | 0,17700 |
| 205081\_at | cysteine-rich protein 1 (intestinal) | CRIP1 | NM\_001311 | 0,00229 |
| 205765\_at | cytochrome P450, family 3, subfamily A, ppe 5 | CYP3A5 | NM\_000777 | 0,05110 |
| 206439\_at | dermatan sulfate proteoglycan 3 | DSPG3 | NM\_004950 | 0,01800 |
| 206414\_s\_at | development and differentiation enhancing factor 2 | DDEF2 | NM\_003887 | 0,00556 |
| 201430\_s\_at | dihydropyrimidinase-like 3 | DPYSL3 | W72516 | 0,00342 |
| 201697\_s\_at | DNA (cytosine-5-)-methyltransferase 1 | DNMT1 | NM\_001379 | 0,06830 |
| 31845\_at | E74-like factor 4 (ets domain transcription factor) | ELF4 | U32645 | 0,01130 |
| 209682\_at | ecotropic retroviral transforming sequence b | CBLB | U26710 | 0,00059 |
| 204858\_s\_at | endothelial cell growth factor 1 | ECGF1 | NM\_001953 | 0,04460 |
| 204464\_s\_at | endothelin receptor type A | EDNRA | NM\_001957 | 0,00072 |
| 201231\_s\_at | enolase 1, (alpha) | ENO1 | NM\_001428 | 0,00847 |
| 202668\_at | ephrin-B2 | EFNB2 | BF001670 | 0,00600 |
| 202609\_at | epidermal growth factor receptor, substrate 8 | EPS8 | NM\_004447 | 0,06910 |
| 219787\_s\_at | epithelial cell transforming sequence 2 oncogene | ECT2 | NM\_018098 | 0,01400 |
| 205419\_at | Epstein-Barr virus induced gene 2 | EBI2 | NM\_004951 | 0,00089 |
| 216836\_s\_at | erythroblastic leukemia viral oncogene homolog 2 | ERBB2 | X03363 | 0,08650 |
| 201798\_s\_at | fer-1-like 3, myoferlin (C. elegans) | FER1L3 | NM\_013451 | 0,01770 |
| 209955\_s\_at | fibroblast activation protein, alpha | FAP | U76833 | 0,00214 |
| 212464\_s\_at | fibronectin 1 | FN1 | X02761 | 0,00330 |
| 202949\_s\_at | four and a half LIM domains 2 | FHL2 | NM\_001450 | 0,14200 |
| 201141\_at | glycoprotein (transmembrane) nmb | GPNMB | NM\_002510 | 0,01960 |
| 217771\_at | golgi phosphoprotein 2 | GOLPH2 | NM\_016548 | 0,21700 |
| 218468\_s\_at | gremlin 1, cysteine knot superfamily | GREM1 | NM\_013372 | 0,07060 |
| 202581\_at | heat shock 70kDa protein 1B | HSPA1B | NM\_005346 | 0,03870 |
| 218280\_x\_at | histone 2, H2aa | HIST2H2 | BC001629 | 0,02070 |
| 213299\_at | HIV-1 inducer of short transcripts binding protein | FBI1 | NM\_015898 | 0,11200 |
| 211597\_s\_at | homeodomain-only protein | HOP | AB059408 | 0,00732 |
| 211430\_s\_at | immunoglobulin heavy constant mu | IGHM | M87789 | 0,00001 |
| 214677\_x\_at | immunoglobulin lambda locus | IGLJ3 | X57812 | 0,00256 |
| 210511\_s\_at | inhibin, beta A | INHBA | M13436 | 0,00007 |
| 210095\_s\_at | insulin-like growth factor binding protein 3 | IGFBP3 | M31159 | 0,00004 |
| 206502\_s\_at | insulinoma-associated 1 | INSM1 | NM\_002196 | 0,21900 |
| 214660\_at | integrin, alpha subunit | ITGA1 | X68742 | 0,03400 |
| 202859\_x\_at | interleukin 8 | IL8 | NM\_000584 | 0,01600 |
| 205157\_s\_at | keratin 17 | KRT17 | NM\_000422 | 0,00585 |
| 201650\_at | keratin 19 | KRT19 | NM\_002276 | 0,12400 |
| 203726\_s\_at | laminin, alpha 3 | LAMA3 | NM\_000227 | 0,00513 |
| 209270\_at | laminin, beta 3 | LAMB3 | L25541 | 0,01490 |
| 201105\_at | lectin, galactoside-binding, soluble, 1 | LGALS1 | NM\_002305 | 0,04540 |
| 208949\_s\_at | lectin, galactoside-binding, soluble, 3 (galectin 3) | LGALS3 | BC001120 | 0,06000 |
| 221558\_s\_at | lymphoid enhancer-binding factor 1 | LEF1 | AF288571 | 0,00008 |
| 209480\_at | Major histocompatibility complex, class II | HLA | M16276 | 0,00345 |
| 209373\_at | mal, T-cell differentiation protein-like | MALL | BC003179 | 0,02550 |
| 204475\_at | matrix metallopeptidase 1 | MMP1 | NM\_002421 | 0,77600 |
| 204580\_at | matrix metallopeptidase 12 | MMP12 | NM\_002426 | 0,00147 |
| 204885\_s\_at | mesothelin | MSLN | NM\_005823 | 0,01830 |
| 209035\_at | midkine (neurite growth-promoting factor 2) | MDK | M69148 | 0,00223 |
| 202555\_s\_at | myosin, light polypeptide kinase | MLCK | NM\_005965 | 0,21000 |
| 201621\_at | neuroblastoma, suppression of tumorigenicity 1 | NBL1 | NM\_005380 | 0,00751 |
| 209627\_s\_at | oxysterol binding protein-like 3 | OSBPL3 | AY008372 | 0,03880 |
| 210809\_s\_at | periostin, osteoblast specific factor | POSTN | D13665 | 0,00280 |
| 201037\_at | phosphofructokinase, platelet | PFKP | NM\_002627 | 0,00026 |
| 203554\_x\_at | pituitary tumor-transforming 1 | PTTG1 | NM\_004219 | 0,00005 |
| 205190\_at | plastin 1 (I isoform) | PLS1 | NM\_002670 | 0,07220 |
| 218644\_at | pleckstrin 2 | PLEK2 | NM\_016445 | 0,00634 |
| 209803\_s\_at | pleckstrin homology-like domain, family A, m 2 | PHLDA2 | AF001294 | 0,19900 |
| 201251\_at | pyruvate kinase, muscle | PKM2 | NM\_002654 | 0,00813 |
| 217763\_s\_at | RAB31, member RAS oncogene family | RAB31 | AF183421 | 0,01540 |
| 218657\_at | Rap guanine nucleotide exchange factor -like 1 | RGEFL1 | NM\_016339 | 0,01760 |
| 202988\_s\_at | regulator of G-protein signalling 1 | RGS1 | NM\_002922 | 0,00658 |
| 212724\_at | Rho family GTPase 3 | RND3 | BG054844 | 0,05240 |
| 201288\_at | Rho GDP dissociation inhibitor (GDI) beta | ARHGDIB | NM\_001175 | 0,01750 |
| 201890\_at | ribonucleotide reductase M2 polypeptide | RRM2 | BE966236 | 0,00575 |
| 209360\_s\_at | runt-related transcription factor 1 | RUNX1 | BF432501 | 0,01530 |
| 200872\_at | S100 calcium binding protein A10 | S100A10 | NM\_002966 | 0,00402 |
| 200660\_at | S100 calcium binding protein A11 | S100A11 | NM\_005620 | 0,06420 |
| 204351\_at | S100 calcium binding protein P | S100P | NM\_005980 | 0,00220 |
| 200665\_s\_at | secreted protein, acidic, cysteine-rich | SPARC | NM\_003118 | 0,00421 |
| 203789\_s\_at | sema domain, immunoglobulin domain | SEMA3C | NM\_006379 | 0,00528 |
| 204855\_at | serpin peptidase inhibitor, clade B, member 5 | SERPINB5 | NM\_002639 | 0,00434 |
| 202628\_s\_at | serpin peptidase inhibitor, clade E | SERPINE1 | NM\_000602 | 0,00689 |
| 209016\_s\_at | Similar to keratin 7 | KRT7 | BC002700 | 0,00230 |
| 204401\_at | small conductance calcium-activated channel | KCNN4 | NM\_002250 | 0,05010 |
| 202856\_s\_at | solute carrier family 16 | SLC16A3 | NM\_004207 | 0,00245 |
| 204588\_s\_at | solute carrier family 7 | SLC7A7 | NM\_003982 | 0,00019 |
| 33322\_i\_at | stratifin | SFN | X57348 | 0,05650 |
| 203083\_at | thrombospondin 2 | THBS2 | NM\_003247 | 0,00002 |
| 201666\_at | TIMP metallopeptidase inhibitor 1 | TIMP1 | NM\_003254 | 0,03270 |
| 201291\_s\_at | topoisomerase (DNA) II alpha 170kDa | TOP2A | AU159942 | 0,20900 |
| 201506\_at | transforming growth factor, beta-induced | TGFBI | NM\_000358 | 0,00719 |
| 201042\_at | transglutaminase 2 | TGM2 | AL031651 | 0,12600 |
| 218960\_at | transmembrane protease, serine 4 | TMPRSS4 | NM\_016425 | 0,00544 |
| 214476\_at | trefoil factor 2 (spasmolytic protein 1) | TFF2 | NM\_005423 | 0,26200 |
| 202504\_at | tripartite motif-containing 29 | TRIM29 | NM\_012101 | 0,00968 |
| 204083\_s\_at | tropomyosin 2 (beta) | TPM2 | NM\_003289 | 0,31500 |
| 215111\_s\_at | TSC22 domain family, member 1 | TSC22D1 | AK027071 | 0,03870 |
| 208623\_s\_at | villin 2 (ezrin) | VIL2 | J05021 | 0,18800 |
| 209950\_s\_at | villin-like | VILL | BC004300 | 0,06840 |

List of genes overexpressed in PDAC compared to controls (normal pancreas and chronic pancreatitis) based on Affymetrix GCOS 1.2 software. **Bold**: COL11A1 gene Additionally, the p-value of the overexpression based on a parametric Welch t-test is also indicated (GeneSpring; Silicon Genetics, Redwood City, CA).

**Table S2. Quantitative analysis of cell distribution in peritumoral pancreatic cancer tissue.**

|  |  |
| --- | --- |
| proCOL11A1/CK7 (DI) | proCOL11A1/Desmin (DI) |
| proCOL11A1+ only 123 (60%)  | proCOL11A1+ only 140 (63%)  |
| CK7+ only 28 (15%)  | Desmin+ only 45 (20%)  |
| **proCOL11A1+/CK7+ 28 (15%)**  | **proCOL11A1+/Desmin+ 37 (17%)** |
| Total 119 (100%) | Total 222 (100%) |

One patient sample, valuation on four fields for each double immunostaining (DI) experiment. Cells stained with both Ab in **bold**

**Table S3. Patient characteristics and immunohistochemistry score with anti-proCOL11A1 pAb and mAb.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| PATIENT | SEX | AGE | pAb-Score | mAb-Score | TNM | STAGE | GRADE | PATHOLOGY |
| 1 | F | 74 | 12 | 4 | T3N0M0 | IIA | G2 | PDAC |
| 2 | F | 71 | 12 | 4 | T1N0M0 | IA | G1 | PDAC  |
| 3 | M | 54 | 4 | 2 | T2NOM0 | IB | G2 | PDAC |
| 4 | F | 46 | 8 | 8 | T2N1M1 | IV | G2-3 | PDAC |
| 5 | M | 72 | 12 | 2 | T2N0M0 | IB | G2 | PDAC |
| 6 | M | 36 | 0 | 1 |  |  |  | CP |
| 7 | M | 69 | 8 | 4 | T3N0M0 | IIA | G2 | PDAC |
| 8 | M | 71 | 0 | 8 | T1N0M0 | IA | G2 | PDAC |
| 9 | F | 77 | 12 | 12 | T3N0M0 | IIA | G2 | PDAC |
| 10 | M | 73 | 12 | 12 | T3N0M0 | IIA | G2 | PDAC |
| 11 | M | 65 | 0 |  |  |  |  | CP |
| 12 | F | 63 | 12 | 8 | T3N1M0 | IIB | G3 | PDAC |
| 13 | F | 81 | 8 | 8 | T2N0M0 | IB | G2 | PDAC |
| 14 | M | 52 | 0 | 2 |  |  |  | CP |
| ***15*** | ***M*** | ***63*** | ***0*** | ***4*** |  |  |  | ***CP*** |
| 16 | M | 51 | 8 | 3 | T3N1M0 | IIB | G2 | PDAC |
| 17 | F | 52 | 0 | 0 |  |  |  | CP |
| 18 | M | 48 | 0 |  |  |  |  | CP |
| 19 | M | 73 | 0 |  |  |  |  | CP |
| 20 | M | 52 | 0 | 0 |  |  |  | CP |
| 21 | M | 59 | 0 | 0 |  |  |  | CP |
| 22 | M | 74 | 12 |  | T1N0M0 | IA | G2 | PDAC |
| 23 | F | 64 | 12 | 8 | T3N0M0 | IIA | G2 | PDAC |
| 24 | M | 56 | 0 | 0 |  |  |  | CP |
| 25 | M | 44 | 0 | 0 |  |  |  | CP |
| 26 | M | 55 | 12 | 12 | T2NOMO | IA | G1 | PDAC |
| 27 | F | 57 | 4 | 2 | T2N1M0 | IIB | G2 | PDAC |
| 28 | M | 61 | 0 | 0 |  |  |  | CP |
| 29 | M | 61 | 0 | 0 |  |  |  | CP biliar |
| 30 | M | 60 | 8 | 8 | T4N1M0 | III | G1-2 | PDAC |
| ***31*** | ***M*** | ***73*** | ***8*** | ***4*** |  |  |  | ***autoimmune pancreatitis***  |
| 32 | F | 55 | 12 | 12 | T3N1M0 | IIB | G2 | PDAC |
| 33 | M | 56 | 8 | 0 |  |  |  | CP |
| 34 | M | 70 | 12 | 4 | T3N1M0 | IIB | G2 | PDAC |
| 35 | F | 49 | 4 | 6 | T3N0M1 | IV | G1 | PDAC |
| 36\* | F | 71 | 12 | 12 | TXNXM1 | IV |  | PDAC |
| 37 | F | 69 | 8 | 12 | T3N1M0 | IIB |  | PDAC |
| 38 | M | 65 | 8 | 4 | T3N1M0 | IIB | G1 | PDAC |
| 39 | M | 49 | 0 |  |  |  |  | CP |
| 40\* | M | 60 | 3 |  | T4N1M0 | IIB |  | PDAC |

Table S1 *(Cont.)*

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| PATIENT | SEX | AGE | pAb-Score | mAb-Score | TNM | STAGE | GRADE | PATHOLOGY |
| **41** | **F** | **64** | **0** | **0** | **T1N0MO** | **IA** | **G2** | **PDAC** |
| 42 | F | 53 | 12 | 12 | T3N0M0 | IIA | G3 | PDAC |
| 43 | M | 69 | 0 | 0 |  |  |  | CP |
| **44** | **M** | **73** | **2** | **0** | **T2N0M0** | **IB** | **G2** | **PDAC** |
| 45 | M | 53 | 0 |  |  |  |  | CP |
| 46 | F | 66 | 4 | 4 | T3N1M0 | IIB | G1 | PDAC |
| 47 | M | 62 | 12 | 8 | T3N1M0 | IIB | G1 | PDAC |
| 48 | F | 78 | 12 | 12 | T2N0M0 | IB | G2 | PDAC |
| 49 | M | 77 | 12 | 3 | T3N0M0 | IIA | G2 | PDAC |
| 50 | M | 62 | 4 | 12 | T2N0M0 | IB | G1 | PDAC |
| 51 | M | 41 | 0 | 0 |  |  |  | CP |
| 52 | M | 54 | 8 | 8 | T3N1M0 | IIB | G3-4 | PDAC |
| 53 | F | 74 | 12 | 4 | T3N1M0 | IIB | G2 | PDAC |
| **54** | **M** | **67** | **1** | **0** | **T2N1M0** | **IIB** | **G2** | **PDAC** |
| 55 | M | 70 | 8 | 8 | T2N0M0 | IB | G1 | PDAC |
| 56 | M | 77 | 12 | 8 | T3N1M0 | IIB | G1 | PDAC |
| 57 | M | 68 | 12 | 8 | T3N0M0 | IIA | G2 | PDAC |
| 58 | M | 60 | 8 | 12 | T2N0M0 | IB | G3 | PDAC |
| 59 | M | 70 | 4 | 2 | T3N1M0 | IIB | G2 | PDAC |
| 60 | M | 62 | 0 | 0 |  |  |  | CP |
| 61 | M | 68 | 8 | 12 | T1N0M0 | IA | G2 | PDAC |
| 62 | M | 79 | 8 |  | T1N0M0 | IA | G2 | PDAC |
| 63 | M | 61 | 2 | 4 | T3N1M0 | IIB | G2 | PDAC |
| 64 | M | 69 | 12 | 4 | T3N1M1 | IV | G2 | PDAC |
| 65 | M | 51 | 12 | 8 | T3N1M0 | IIB | G2 | PDAC |
| 66 | M | 72 | 8 | 0 |  |  |  | CP |
| 67 | M | 64 | 12 | 8 | T3N1M0 | IIB | G1 | PDAC |
| 68\* | M | 51 | 6 | 12 | T4NXM0 | III |  | PDAC |
| 69 | M | 53 | 3 | 12 | T3N1M0 | IIB | G2 | PDAC |
| 70 | M | 68 | 8 | 12 | T2N1M0 | IIB | G1-2 | PDAC |
| 71\* | M | 61 | 12 | 12 | T4N1M0 | III | GX | PDAC |
| 72 | M | 25 | 8 | 0 |  |  |  | autoimmune pancreatitis  |
| 73 | M | 65 | 0 | 0 |  |  |  | CP |
| 74 | M | 70 | 8 | 8 | T3N1M0 | IIB | G2-3 | PDAC |
| 75 | M | 77 | 12 | 8 | T3N0M0 | IIA | G1 | PDAC |
| 76 | M | 61 | 12 | 12 | T2N1M0 | IIB | G2 | PDAC |
| 77 | M | 66 | 8 | 1 | T1N0M0 | IA | G2 | PDAC |

PDAC: Pancreatic ductal adenocarcinoma. CP: Chronic pancreatitis. **Bold** (41, 44, 54): PDAC cases with 0 points (false negatives). ***Bold cursive*** (15, 31): CP cases with high score (false positives). \* Cases with no Whipple/pancreatectomy procedure (36, 40, 68 and 71): Diagnosis through biopsy of pancreatic mass.

**Table S4. Discrimination between PDAC (pancreatic ductal adenocarcinoma) and CP (chronic pancreatitis) using pathologist score.**

|  |  |  |
| --- | --- | --- |
| **Parameters** | **pAb proCOL11A1 77 cases (54 *vs*. 23) Cut-off > 0**  | **mAb proCOL11A1 69 cases (51 *vs*. 18) Cut-off > 1** |
| Sensitivity | 98 % (90.1 - 100.0) | 92% (81.1 - 97.8) |
| Specificity | 83 % (61.2 - 95.0) | 83% (58.6 - 96.4) |
| False Positives | 17%  | 17%  |
| False Negatives | 2 %  | 8%  |
| + Predictive Value | 93 % | 94 % |
|  - Predictive Value | 95 % | 79 % |
| Accuracy | 94 % | 90 % |

**Table S5. Summary statistics of immunohistochemical analyses**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Parameter** | **Mean** | **SD** | **Median** | **Range** | **P** |
| Nº + cells *PDAC*   | 310.21  | 219.46  | 251.50  | 42-832  | <0.001 |
| *CP* | 61.44 | 46.64 | 53.50 | 4 - 147 |  |
| StSurface *PDAC*  | 4,633.02  | 4,217.05  | 3,276.75  | 301.16 -20,648.04  | <0.001 |
| *CP* | 465.42 | 519.63 | 266.29 | 4.688 - 1,756.67 |  |
| RefArea *PDAC*  | 31,188.46  | 46,570.50  | 8,939.00  | 1,444 - 128,540  | <0.001 |
| *CP* | 112,554.56 | 43,680.71 | 128,540 | 315 - 128,540 |  |
| Nº + cells/mm2 *PDAC*  | 50,669.26  | 47,685.25  | 40,751.34  | 334.54 - 180,690  | 0.056 |
| *CP* | 19,209.98 | 52,035.75 | 443.46 | 31.12 - 174,840 |  |
| Nº + cells/RefArea *PDAC*  | 0.0507  | 0.0477  | 0.0408  | 0.0003 - 0.181  | 0.056 |
| *CP* | 0.0192 | 0.0520 | 0.0004 | 0.000 - 0.175 |  |
| StSurface/RefArea *PDAC*  | 0.632  | 0.4507  | 1.0000  | 0.0045 - 1.0000  | 0.001 |
| *CP* | 0.128 | 0.3404 | 0.0020 | 0.0000 - 1.0000 |  |
| Saturation *PDAC*  | 110.91  | 11.50  | 112.03  | 87.50 - 128.01  | 0.970 |
| *CP* | 110.77 | 11.21 | 109.36 | 92.95 - 125.45 |  |

PDAC (pancreatic ductal adenocarcinoma), 24 cases; CP (chronic pancreatitis), 16 cases. The saturation index, an indicator of the quality of imaging processing, is similar in both diseases. ANOVA test was applied for significances.

**Table S6. Area under the ROC curve (AUC) of image analysis parameters (pancreatic ductal adenocarcinoma) PDAC vs. CP (chronic pancreatitis)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Parameter** | **AUC** | **Standard error** | **P (Area=0.5)** |
| Area | 0.802 | 0.0753 | 0.0001 |
| **Nº + cells** | **0.901** | 0.0486 | 0.0001 |
| **Staining surface** | **0.964** | 0.029 | 0.0001 |
| Nº + cells/Area | 0.852 | 0.0598 | 0.0001 |
| Staining surface/Area | 0.893 | 0.0506 | 0.0001 |
| Nº + cells/mm2 | 0.857 | 0.0588 | 0.0001 |

The best AUCs are highlighted in **bold**

**Table S7. Discrimination between PDAC (pancreatic ductal adenocarcinoma) and CP (chronic pancreatitis) using various diagnostic markers in tissues.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Immunostaining** | **Sample size PDAC/CP** | AUC | **Sensitivity%** | **Specificity%** |
| Mesothelin1 | 18/17  |  | 100 | 94 |
| MUC12 | 24/11  |  | 96 | 94 |
| MUC43 | 74/19  |  | 77 | 78 |
| p533 | 74/19  |  | 60 | 88 |
| Smad43 | 74/19  |  | 63 | 88 |
| Maspin3 | 74/19  |  | 90 | 67 |
| RCAS14 | 20/5  |  | 100 | 60 |
| c-erbB-25 | 36/13  |  | 42 | 92 |
| EGFR5 | 36/13  |  | 50 | 92 |
| TGF-β15 | 36/13  |  | 44 | 92 |
| KOC6 | 26/38  |  | 96 | 89 |
| G6PDH activity7 | 28/11  |  | 100 | 100 |
| COL11A1(current study) | 51/18  |  0.936 | 92 | 83 |

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**Table S8. Discrimination PDAC (pancreatic ductal adenocarcinoma) vs. CP (chronic pancreatitis) with anti-proCOL11A1 mAb by components of score and by total score.**

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Field score (F) 0-4 points** | **Staining Intensity(SI) 0-3 points** | **Total score (F x SI) 0-12 points** |
| CP, 18 cases (mean±SD) | 0.611 ± 1.335 | 0.222 ± 0.428 | 0.611 ± 1.335 |
| PDAC, 52 cases (mean±SD) | 3.389 ± 1.464 | 1.942 ± 0.938 | 7.327 ± 4.038 |
| P (PDAC vs. CP) | <0.0001 | <0.0001 | <0.0001 |
| AUC | 0.895 | 0.933 | 0.936 |
| Criterion (discriminant cut-off) | >1 | >0 | >1 |