

Supplementary Table 1 Training set consisted of 178 PAAD samples are from the TCGA Databases

sample_id	CCNA2	PLAU	CAPN2	Risk
				Score
TCGA-2J-AAB1-01A-11R-A41	3.5234741	5.7312973	7.4647352	2.1070958
B-07	37	06	38	65
TCGA-2J-AAB4-01A-12R-A41	4.0180109	7.8029298	7.8229716	2.6049170
B-07	6	89	39	1
TCGA-2J-AAB6-01A-11R-A41	4.3093872	10.886140	8.3021147	3.2042465
B-07	2	7	52	15
TCGA-2J-AAB8-01A-12R-A41	4.4327723	8.5224763	7.1782764	2.8495947
B-07	79	9	29	9
TCGA-2J-AAB9-01A-11R-A41	3.0284277	7.5419910	7.0906798	2.2429251
B-07	05	03	56	13
TCGA-2J-AABA-01A-21R-A4	3.4081140	6.6221719	7.1986336	2.2140617
1B-07	1	17	23	85
TCGA-2J-AABE-01A-12R-A41	2.5701228	7.7214054	7.9183570	2.1324898
B-07	62	72	13	08
TCGA-2J-AABF-01A-31R-A41	4.3394794	6.5562485	7.7227365	2.5027343
B-07	85	31	04	32
TCGA-2J-AABH-01A-21R-A4	3.5159647	6.7164861	8.0697880	2.2698216
1B-07	02	37	8	86
TCGA-2J-AABI-01A-12R-A41	4.9071214	8.6303202	7.3790793	3.0192447
B-07	08	81	99	74
TCGA-2J-AABK-01A-31R-A4	3.3513880	5.1879379	6.5979467	1.9576462
1B-07	48	41	61	41
TCGA-2J-AABO-01A-21R-A4	3.4837255	8.2314573	7.6544434	2.5040413
1B-07	05	7	18	65
TCGA-2J-AABP-01A-11R-A41	5.1003049	7.5568033	6.0134332	2.8957224

B-07	06	76	27	71
TCGA-2J-AABR-01A-11R-A4		6.4824191	7.1416248	2.2513711
1B-07	3.5987225	53	87	72
TCGA-2J-AABT-01A-11R-A41	3.1719113	5.6684538	6.7168057	1.9799470
B-07	47	84	46	04
TCGA-2J-AABU-01A-11R-A4	4.3623787	8.2496463	7.9553383	2.7881432
1B-07	09	33	8	36
TCGA-2J-AABV-01A-12R-A4	1.2486562	3.2092661	4.3116774	0.9507876
1B-07	7	93	84	83
TCGA-2L-AAQA-01A-21R-A	4.0390067	7.5479379	7.9877244	2.5711039
38C-07	55	15	64	03
TCGA-2L-AAQE-01A-11R-A3	3.7244210	8.4280070	7.3321081	2.6103078
9D-07	81	98	78	07
TCGA-2L-AAQI-01A-12R-A3	4.5533052	6.5019279	7.7305170	2.5618207
9D-07	03	23	09	18
TCGA-2L-AAQJ-01A-12R-A3	3.8388610	7.4808556	7.8751534	2.4958033
9D-07	29	21	16	52
TCGA-2L-AAQL-01A-11R-A3	2.7759354	7.1668961	7.6401784	2.1053525
8C-07	88	72	04	48
TCGA-2L-AAQM-01A-11R-A	2.8077670	2.2687338	4.8783280	1.2962926
39D-07	62	01	8	45
TCGA-3A-A9I5-01A-11R-A38	3.1571084	6.0059703	6.7321470	2.0304650
C-07	04	05	7	27
TCGA-3A-A9I7-01A-21R-A38	3.4076790	7.5873177	7.2747275	2.3720506
C-07	54	3	73	99
TCGA-3A-A9I9-01A-11R-A38	2.5437680	6.7271063	6.2053025	1.9497498
C-07	64	27	76	28
TCGA-3A-A9IB-01A-21R-A39	4.4947995	9.3711160	7.4454047	3.0097354
D-07	95	11	56	02

TCGA-3A-A9IC-01A-11R-A38	3.9377398	8.7370235	7.2313095	2.7277987
C-07	55	26	16	69
TCGA-3A-A9IH-01A-12R-A3	3.7769356	7.6138712	7.8136773	2.4974267
9D-07	67	18	13	22
TCGA-3A-A9IJ-01A-11R-A39	0.3917677	2.3979945	6.1372165	0.5590165
D-07	2	78	96	85
TCGA-3A-A9IL-01A-11R-A38	1.9401667	4.7051706	5.6942673	1.4243374
C-07	5	51	35	84
TCGA-3A-A9IN-01A-11R-A3	1.9451581	3.9381257	5.6171603	1.3001351
9D-07	95	97	43	91
TCGA-3A-A9IO-01A-11R-A3		3.0907518	6.3610822	0.9070039
8C-07	1.1264443	29	85	85
TCGA-3A-A9IR-01A-11R-A38	1.5527705	3.0931375	5.8895027	1.0394675
C-07	24	82	47	27
TCGA-3A-A9IS-01A-21R-A39	3.0983521	2.6916011	5.8903469	1.4647166
D-07	78	62	75	29
TCGA-3A-A9IU-01A-11R-A3	3.7573219	8.5235345	8.4373767	2.6441074
9D-07	99	13	36	48
TCGA-3A-A9IV-01A-11R-A41	4.0604970	5.1171838	6.2636973	2.1689297
B-07	75	59	67	91
TCGA-3A-A9IX-01A-11R-A41	2.5918230	6.2020513	6.7407427	1.8830328
B-07	09	2	61	62
TCGA-3A-A9IZ-01A-12R-A41	5.1740907	7.6426214	7.4098270	2.9429622
B-07	74	36	73	56
TCGA-3A-A9J0-01A-11R-A41	3.8621240	7.7241324	7.7050883	2.5417209
B-07	33	95	8	21
TCGA-3E-AAAY-01A-11R-A3	3.4558729	6.9055855	7.3122676	2.2763020
8C-07	57	69	37	77
TCGA-3E-AAAZ-01A-11R-A3	3.5410067	6.9591070	7.7981944	2.3154848

8C-07	59	68	14	57
TCGA-F2-6879-01A-11R-2156-07	4.9460711	5.4182709	7.5503089	2.5083372
	11	2	09	14
TCGA-F2-6880-01A-11R-2156-07	0.4029404	2.3415303	4.4791723	0.5417133
	2	87	45	59
TCGA-F2-7273-01A-11R-2156-07	2.6747544	5.8876617	7.4490429	1.8630021
	04	35	68	14
TCGA-F2-7276-01A-11R-2156-07	2.8428581	7.0730200	7.3785697	2.1094404
	83	61	11	81
TCGA-F2-A44G-01A-11R-A26-U-07	4.3500304	8.0872862	7.3509992	2.7534715
	17	06	74	59
TCGA-F2-A44H-01A-11R-A26U-07	2.9825281	7.7131342	6.8499404	2.2546056
	88	15	8	58
TCGA-F2-A7TX-01A-33R-A38C-07	5.2306180	8.9535454	7.4328132	3.1751274
	51	97	94	57
TCGA-F2-A8YN-01A-11R-A37L-07	3.8707986	7.6267056	7.5232608	2.5272917
	96	02	4	68
TCGA-FB-A4P5-01A-11R-A26-U-07	4.0852291	6.5002220	6.9467226	2.4074036
	79	55	74	6
TCGA-FB-A4P6-01A-12R-A26-U-07	3.1806252	5.7206423	7.9675012	2.0000095
	85	77	24	65
TCGA-FB-A545-01A-11R-A26-U-07	4.2300492	8.5260104	8.2284425	2.7931631
	65	98	79	26
TCGA-FB-A5VM-01A-11R-A32O-07	4.0949960	9.2120169	6.4742819	2.8499846
	72	88	01	62
TCGA-FB-A78T-01A-12R-A32O-07	3.6852337	6.4243191	7.6241104	2.2727411
	61	6	01	86
TCGA-FB-A7DR-01A-21R-A33R-07	3.8560295	8.7295476	7.5799328	2.7030761
	5	72	64	81

TCGA-FB-AAPP-01A-12R-A4	5.3964232	2.7866172	7.5651470	2.2217451
1B-07	56	7	25	56
TCGA-FB-AAPQ-01A-11R-A4	3.7718855	6.0149020	7.4238176	2.2320014
1B-07	79	03	48	3
TCGA-FB-AAPS-01A-12R-A3	2.7801000	8.9702192	6.9816003	2.3965094
9D-07	84	3	88	71
TCGA-FB-AAPU-01A-31R-A4	4.9064336	5.5876110	7.6752358	2.5242771
1B-07	7	2	58	05
TCGA-FB-AAPY-01A-11R-A4	2.5473264	6.7461689	6.6284688	1.9569610
1B-07	32	74	71	22
TCGA-FB-AAPZ-01A-11R-A4	3.8851838	6.9425930	7.4329585	2.4195214
1B-07	66	89	72	91
TCGA-FB-AAQ0-01A-31R-A4	4.2464232	6.4497792	7.4855226	2.4541349
1B-07	89	48	28	7
TCGA-FB-AAQ1-01A-12R-A4	4.5569382	7.9927293	7.1813769	2.8025466
1B-07	24	5	07	64
TCGA-FB-AAQ2-01A-31R-A4	5.0828303	8.0099864	7.8876897	2.9773192
1B-07	01	52	58	51
TCGA-FB-AAQ3-01A-11R-A4	3.8441747	7.0152399	6.4741780	2.4116349
1B-07	17	67	48	09
TCGA-FB-AAQ6-01A-11R-A4	3.7788078	6.2216064	7.7794646	2.2704461
1B-07	22	54	04	54
TCGA-H6-8124-01A-11R-2404	4.3374399	7.9229666	8.0238979	2.7273630
-07	37	92	23	72
TCGA-H6-A45N-01A-11R-A2	3.5890203	7.2015505	7.7474223	2.3699628
6U-07	8	51	12	98
TCGA-H8-A6C1-01A-11R-A3	3.8488382	6.1143732	7.2366829	2.2713674
2O-07	33	72	88	83
TCGA-HV-A5A3-01A-11R-A2	3.3298268	7.5583587	8.1000835	2.3483897

6U-07	28	18	68	6
TCGA-HV-A5A4-01A-11R-A2	3.6725045	7.9560676	7.8377433	2.5203082
6U-07	47	91	44	18
TCGA-HV-A5A5-01A-11R-A2	3.2694521	7.0882889	6.8940295	2.2440017
6U-07	26	72	21	35
TCGA-HV-A5A6-01A-11R-A2	3.9001229	7.8380296	7.4430065	2.5705467
6U-07	34	24	09	5
TCGA-HV-A7OL-01A-11R-A	3.8890451	7.4164445	6.4540919	2.4912532
33R-07	48	68	75	89
TCGA-HV-A7OP-01A-11R-A	1.8963493	2.9367227	6.0142972	1.1239081
33R-07	59	32	63	96
TCGA-HV-AA8V-01A-11R-A	3.0821064	8.8164477	7.1302863	2.4683477
41B-07	52	11	72	95
TCGA-HV-AA8X-01A-11R-A	4.4179537	6.0516396	7.9233815	2.4466670
39D-07	53	46	67	74
TCGA-HZ-7289-01A-11R-215	4.5316434	4.6656770	7.0360153	2.2502387
6-07	61	07	2	98
TCGA-HZ-7918-01A-11R-215	4.1719993	6.3843503	6.8614095	2.4154394
6-07	87	37	37	82
TCGA-HZ-7919-01A-11R-215	4.6937880	7.7089114	8.4818704	2.8087842
6-07	1	37	55	03
TCGA-HZ-7920-01A-11R-220	3.0480617	6.4764173	7.0685977	2.0750135
4-07	68	33	28	83
TCGA-HZ-7922-01A-11R-215	4.0510065	8.0204644	8.1056890	2.6528982
6-07	96	2	77	51
TCGA-HZ-7923-01A-12R-215	3.0622080	6.8778828	6.7345375	2.1427153
6-07	78	7	7	78
TCGA-HZ-7924-01A-11R-215	4.8165945	4.2842772	7.7761941	2.2836424
6-07	87	18	54	21

TCGA-HZ-7925-01A-11R-215	3.1590963	8.0825823	7.7628085	2.3774048
6-07	11	17	55	41
TCGA-HZ-7926-01A-11R-215	4.0936953	8.3055556	8.5991626	2.7164670
6-07	8	32	69	43
TCGA-HZ-8001-01A-11R-220	3.5487202	7.7121892	7.3042527	2.4374357
4-07	04	43	43	68
TCGA-HZ-8002-01A-11R-220	3.4008930	7.2205176	7.6893194	2.3129114
4-07	95	32	31	9
TCGA-HZ-8003-01A-21R-220	3.2285878	6.5458309	5.8759667	2.1353082
4-07	41	48	76	65
TCGA-HZ-8005-01A-11R-220	4.9500670	9.1065802	7.7763053	3.1134348
4-07	91	13	72	16
TCGA-HZ-8315-01A-11R-240	3.1102295	8.6463707	7.2395536	2.4502740
4-07	92	79	61	74
TCGA-HZ-8317-01A-11R-240	3.6908640	6.8332012	6.8737885	2.3360295
4-07	27	99	96	37
TCGA-HZ-8519-01A-11R-240	2.7912097	5.2114211	6.8917934	1.7856544
4-07	84	07	22	26
TCGA-HZ-8636-01A-21R-240		8.0201765	8.3564370	2.7883238
4-07	4.4720783	83	04	84
TCGA-HZ-8637-01A-11R-240	3.9921520	6.2247676	6.6649336	2.3308923
4-07	73	91	12	33
TCGA-HZ-8638-01A-11R-240	4.6713046	5.0068455	7.8222081	2.3558117
4-07	97	52	6	42
TCGA-HZ-A49G-01A-11R-A2	3.1161318	7.6940423	7.0747708	2.2954920
6U-07	3	23	65	32
TCGA-HZ-A49H-01A-11R-A2	2.3828055	5.4452201	6.3757345	1.6905189
6U-07	68	62	39	54
TCGA-HZ-A49I-01A-12R-A26	2.8456907	7.4672656	7.9672129	2.1788435

U-07	6	21	99	49
TCGA-HZ-A4BH-01A-11R-A	3.8631455	7.6770148	7.9176632	2.5358429
26U-07	43	57	75	82
TCGA-HZ-A4BK-01A-11R-A2	3.7283232	7.6535867	7.5343628	2.4865150
6U-07	64	4	07	77
TCGA-HZ-A77O-01A-11R-A3	4.7104923	7.2406644	7.2922894	2.7292862
3R-07	81	65	19	46
TCGA-HZ-A77P-01A-11R-A3	3.4638709	5.6866573	6.8465146	2.0765426
3R-07	05	94	28	16
TCGA-HZ-A77Q-01A-11R-A3	3.2228354	8.7720212	7.2939957	2.5069313
6G-07	67	21	52	51
TCGA-HZ-A8P1-01A-11R-A3	4.0946414	5.7178080	8.0167631	2.2901431
7L-07	54	07	68	07
TCGA-HZ-A9TJ-01A-11R-A4	2.9628636	6.0791455	7.4299908	1.9856254
1I-07	24	37	15	1
TCGA-HZ-A9TJ-06A-11R-A4	3.1609201	5.7727856	7.4810155	1.9988535
1B-07	88	62	23	1
TCGA-IB-7644-01A-11R-2156-	4.7206177	6.1207728	7.4866612	2.5510043
07	54	59	84	7
TCGA-IB-7645-01A-22R-2204-	3.3653985	7.7460184	8.1103282	2.3903995
07	94	46	66	35
TCGA-IB-7646-01A-11R-2156-	5.1258618	8.2561261	8.0820761	3.0325385
07	37	12	06	59
TCGA-IB-7647-01A-11R-2156-	5.0763324	7.6578743	8.0839988	2.9191385
07	8	38	7	7
TCGA-IB-7649-01A-11R-2156-	2.7323343	6.4088833	6.6726799	1.9609479
07	31	58	13	58
TCGA-IB-7651-01A-11R-2156-	3.9313237	6.3179570	7.0798612	2.3297031
07	57	27	75	21

TCGA-IB-7652-01A-11R-2156-07	3.5083525	6.8451914	7.6440610	2.2854334
	86	45	38	36
TCGA-IB-7654-01A-11R-2156-07	2.6559928	6.7883986	7.4898206	2.0044066
	84	05	71	05
TCGA-IB-7885-01A-11R-2156-07	4.1832006	8.7953990	7.9050367	2.8200042
	47	98	44	96
TCGA-IB-7886-01A-11R-2156-07	3.6322333	8.3569316	8.0437283	2.5744197
	11	88	59	14
TCGA-IB-7887-01A-11R-2156-07	3.8364392	8.2637306	7.4418162	2.6198256
	3	95	61	27
TCGA-IB-7888-01A-11R-2156-07	3.3693827	6.1529804	7.2058636	2.1252015
	25	14	11	37
TCGA-IB-7889-01A-11R-2156-07	2.8539357	7.3197470	7.7816908	2.1560728
	83	76	4	6
TCGA-IB-7890-01A-12R-2204-07	3.9257810	8.4560529	7.8988347	2.6828058
	99	07	39	92
TCGA-IB-7891-01A-11R-2204-07	3.0894303	7.2281702	7.0952081	2.2110865
	53	94	68	84
TCGA-IB-7893-01A-11R-2204-07	4.9243374	9.8175521	8.0184811	3.2230537
	64	12	78	36
TCGA-IB-7897-01A-21R-2204-07	3.7990769	6.8311881	7.3359691	2.3733066
	42	49	03	9
TCGA-IB-8126-01A-11R-2404-07	1.5259185	5.4295121	5.2808412	1.4081641
	23	94	8	21
TCGA-IB-8127-01A-11R-2404-07	4.1750774	7.7172905	7.9833077	2.6419355
	32	11	4	29
TCGA-IB-A5SO-01A-11R-A32-O-07	3.1471438	7.6114992	7.4368597	2.2944021
	57	22	59	84
TCGA-IB-A5SP-01A-11R-A32	3.0776873	5.0776489	7.4421580	1.8586449

O-07	63	13	91	2
TCGA-IB-A5SQ-01A-11R-A32	4.0879210	9.2419750	7.4614409	2.8595547
O-07	36	49	75	15
TCGA-IB-A5SS-01A-11R-A32	4.9520865	9.2925726	8.2006848	3.1474228
O-07	72	45	2	63
TCGA-IB-A5ST-01A-11R-A32	3.1043702	7.0510044	7.0254895	2.1864133
O-07	1	2	33	11
TCGA-IB-A6UF-01A-23R-A33	3.8804896	6.6738913	8.7550351	2.3834306
R-07	27	37	04	02
TCGA-IB-A6UG-01A-32R-A3	3.0297708	7.1029908	7.1938505	2.1723935
3R-07	97	45	77	48
TCGA-IB-A7LX-01A-12R-A36	4.8063704	8.6455946	8.2683319	2.9959830
G-07	62	71	26	91
TCGA-IB-A7M4-01A-11R-A3	4.4050597	7.6416948	6.8364935	2.6945789
6G-07	51	57	13	75
TCGA-IB-AAUM-01A-11R-A	1.7095112	4.7092575	6.1307764	1.3548210
37L-07	14	46	64	83
TCGA-IB-AAUN-01A-12R-A3	4.9092498	8.0596332	7.9866231	2.9309984
8C-07	76	41	14	28
TCGA-IB-AAUO-01A-12R-A3	3.6226844	9.1186499	6.7934823	2.6869934
8C-07	16	1	62	05
TCGA-IB-AAUP-01A-11R-A3	4.3947404	7.1040818	6.7108959	2.6026371
7L-07	88	59	54	5
TCGA-IB-AAUQ-01A-22R-A4	2.7929802	8.0188789	6.8301196	2.2441979
1I-07	56	34	59	76
TCGA-IB-AAUR-01A-21R-A3	3.2049232	7.8420605	6.9887857	2.3472540
8C-07	17	18	85	74
TCGA-IB-AAUS-01A-12R-A3	3.4389581	8.1990588	6.9808878	2.4798099
8C-07	48	24	71	68

TCGA-IB-AAUT-01A-11R-A3	2.1004731	7.2342732	6.8999030	1.8966643
7L-07	21	95	8	02
TCGA-IB-AAUU-01A-11R-A3	4.1884088	7.5076479	7.8841027	2.6112417
7L-07	38	85	34	02
TCGA-IB-AAUV-01A-11R-A3	2.4381863	8.2016637	7.2912066	2.1646117
8C-07	76	54	22	7
TCGA-IB-AAUW-01A-12R-A	2.8152065	5.1289037	7.3107063	1.7827396
38C-07	11	44	83	65
TCGA-L1-A7W4-01A-12R-A3	5.7940622	9.5324418	7.9238765	3.4520218
6G-07	98	42	26	35
TCGA-LB-A7SX-01A-11R-A3	4.0485762	5.7392945	7.1444675	2.2729039
3R-07	39	67	7	7
TCGA-LB-A8F3-01A-11R-A36	2.9413317	5.8788356	7.2057228	1.9445070
G-07	14	73	84	89
TCGA-LB-A9Q5-01A-11R-A3	2.3849891	6.4269154	6.9163357	1.8553002
9D-07	87	98	12	85
TCGA-M8-A5N4-01A-11R-A2	3.7477096	8.2106922	8.2236421	2.5884733
6U-07	34	84	62	6
TCGA-OE-A75W-01A-12R-A	3.0614997	7.0708626	6.8840398	
32O-07	27	35	31	2.1750498
TCGA-PZ-A5RE-01A-11R-A3	3.4640147	7.4836062	7.5818679	2.3751605
2O-07	25	09	09	66
TCGA-Q3-A5QY-01A-12R-A3	3.0918182	6.7576353	5.8780828	2.1264755
2O-07	91	55	02	49
TCGA-Q3-AA2A-01A-11R-A3	3.0950804	7.6760353	7.0964126	2.2860186
7L-07	92	38	18	27
TCGA-RB-A7B8-01A-12R-A3	2.7863036	7.3080176	7.3660555	2.1297649
3R-07	11	88	1	21
TCGA-RB-AA9M-01A-11R-A	3.7830794	7.2954723	8.1815364	2.4499687

39D-07	3	31	27	39
TCGA-RL-AAAS-01A-32R-A	3.1902987	6.3297156	7.0177337	2.0958708
39D-07	92	26	67	03
TCGA-S4-A8RM-01A-11R-A3	3.4686875	5.2588090	8.6950479	2.0211790
7L-07	73	93	87	05
TCGA-S4-A8RO-01A-12R-A3	5.1040178	8.8992439	7.1778251	3.1242695
7L-07	9	2	3	09
TCGA-S4-A8RP-01A-11R-A36	3.6243231	7.1060949	7.7074288	2.3653065
G-07	91	21	49	23
TCGA-US-A774-01A-21R-A32	3.6968618	7.8371624	7.3053695	2.5048929
O-07	41	12	77	44
TCGA-US-A776-01A-13R-A33	4.7211101	3.3686286	6.8841045	2.0975515
R-07	29	82	66	65
TCGA-US-A779-01A-11R-A32	3.0833665	5.3951039	7.0785297	1.9097329
O-07	67	4	82	12
TCGA-US-A77E-01A-11R-A3	3.6694350	7.6631125	7.2660771	2.4674881
2O-07	18	97	97	52
TCGA-US-A77G-01A-11R-A3	4.1518020	4.0475034	8.1128163	2.0362339
2O-07	04	9	57	59
TCGA-US-A77J-01A-11R-A32	3.4829902	6.7590705	6.7997569	2.2573943
O-07	23	91	36	58
TCGA-XD-AAUG-01A-61R-A	2.0018742	7.8428292	7.1320318	1.9663498
41B-07	86	76	22	1
TCGA-XD-AAUH-01A-42R-A	2.1795110	6.9410264	6.9428886	1.8741821
41B-07	5	72	19	51
TCGA-XD-AAUI-01A-42R-A4	3.7051042	7.1469769	7.2509577	2.3944321
1B-07	82	25	85	67
TCGA-XD-AAUL-01A-21R-A	3.9262461	7.6339767	8.2837102	2.5514213
39D-07	74	68	22	61

TCGA-XN-A8T3-01A-11R-A3	4.6753530	8.4823731	7.5673492	2.9228087
6G-07	2	67	18	64
TCGA-XN-A8T5-01A-12R-A3	2.5627186	6.5785568	7.2599936	1.9389107
6G-07	64	61	54	22
TCGA-YB-A89D-01A-12R-A3	3.4575023	7.8983885	7.1713609	2.4379402
6G-07	64	57	7	3
TCGA-YH-A8SY-01A-11R-A3		8.8440745		2.7800038
7L-07	4.045242	75	7.315049	65
TCGA-YY-A8LH-01A-11R-A3	3.6678921	5.3782376	7.6691805	2.0967416
6G-07	25	24	82	68
TCGA-Z5-AAPL-01A-12R-A4	5.0955784	6.1664302	6.5758024	2.6711404
1B-07	69	52	25	81

Supplementary Table 2 Verification set from GSE62452 and GSE28735

Sample ID	PLA U	CCN A2	CAP N2	Riskscore
<hr/> GSE62452 <hr/>				
human pancreatic tumor tissue 1	5.990 97	4.1468 3	8.0415 3	2.3514874 79
human pancreatic tumor tissue 100	8.039 16	5.7386 8	7.8483	3.1900685 53
human pancreatic tumor tissue 101	6.510 4	4.0705 8	7.3630 4	2.4073289 11
human pancreatic tumor tissue 103	7.169 97	4.4566 7	8.1341 3	2.6430401 45
human pancreatic tumor tissue 105	7.778 89	4.7017 3	7.9131 6	2.8187369 62
human pancreatic tumor tissue 106	6.415 96	5.4673 4	8.4032 2	2.8427533 55
human pancreatic tumor tissue 108	7.471 33	4.2501 9	7.9615 7	2.6254681 47
human pancreatic tumor tissue 109	6.503 06	4.7829 8	8.3620 2	2.6393644 33
human pancreatic tumor tissue 11	6.913 27	5.3141 4	7.5783 7	2.8695203 72
human pancreatic tumor tissue 111	6.792 61	3.7776 7	7.2344 9	2.3594924 75
human pancreatic tumor tissue 112	6.587 81	4.0510 6	6.9596 5	2.4109402 71
human pancreatic tumor tissue 114	7.912 49	5.7998 3	8.0779 5	3.1904148 52
human pancreatic tumor tissue 115	7.340	4.5193	7.6562	2.6873540

	09		4	91
human pancreatic tumor tissue 116	7.796	4.8026	8.6496	2.8588198
	46	5	3	5
human pancreatic tumor tissue 119	6.647	4.2822	7.6173	2.4986994
	34	8	6	7
human pancreatic tumor tissue 121	7.471	4.1618	8.2257	2.5992165
	01	5	9	9
human pancreatic tumor tissue 123	5.127	4.1238		2.1899650
	66	4	6.1517	22
human pancreatic tumor tissue 124	6.789	4.4819	7.0067	2.5810655
	63	8	6	25
human pancreatic tumor tissue 126	7.296	3.9549	7.5252	2.5001088
	58	2	2	08
human pancreatic tumor tissue 128	6.537	3.8035	7.8142	2.3300518
	01	8	3	11
human pancreatic tumor tissue 13	7.760	4.2490	8.2148	2.6741614
	8	9	6	85
human pancreatic tumor tissue 130	5.763	3.6118	7.0821	2.1376546
	02	6	8	53
human pancreatic tumor tissue 19	7.590	4.5065	8.0787	2.7271669
	5	8	9	26
human pancreatic tumor tissue 21	7.628	4.6016	7.7647	2.7614062
	87	1	3	54
human pancreatic tumor tissue 23	5.597	4.4269	7.5275	2.3725542
	35	2	8	52
human pancreatic tumor tissue 25	7.085	4.3063		2.5802085
	72	5	7.9431	25
human pancreatic tumor tissue 27	8.708		7.8775	2.7179882
	22	3.9074	3	74

human pancreatic tumor tissue 29	6.640 06	5.2918 7	7.4285 5	2.8167866 13
human pancreatic tumor tissue 3	8.062 4	5.2497 5	8.5631 5	3.0436157 8
human pancreatic tumor tissue 31	7.244 17	4.7760 2	7.8488	2.7545654 17
human pancreatic tumor tissue 33	5.814 33	3.9939	6.6534 9	2.2643442 07
human pancreatic tumor tissue 35	4.725 85	3.6233 7	6.6030 1	1.9685950 67
human pancreatic tumor tissue 37	7.688 82	4.8758	7.6864 9	2.8577166 81
human pancreatic tumor tissue 39	6.679 35	5.2451 3	8.2913	2.8144117 12
human pancreatic tumor tissue 42	6.730 22	4.6837	7.2383 9	2.6370469 02
human pancreatic tumor tissue 44	7.163 18	3.8154 8	7.6564 5	2.4349674 31
human pancreatic tumor tissue 46	6.991 33	4.1620 7	7.7193 1	2.5174094 26
human pancreatic tumor tissue 48	6.843 29	4.1098 1	7.9721 3	2.4784149 71
human pancreatic tumor tissue 5	6.685 56	5.5936 3	8.4028 1	2.9268758 66
human pancreatic tumor tissue 51	7.327 25	4.6434	7.4904 4	2.7235030 13
human pancreatic tumor tissue 53	6.950 77	4.3607 2	8.3207 4	2.5780879 59
human pancreatic tumor tissue 55	7.047	5.6377	7.6455	2.9946944

	63	5	5	51
human pancreatic tumor tissue 57	7.642	4.0417	8.1130	2.5882776
	41	6	8	27
human pancreatic tumor tissue 59	7.872	5.6438	8.3808	3.1364907
	5	9	9	22
human pancreatic tumor tissue 61	7.716	4.8291	7.9362	2.8491759
	47	7	5	61
human pancreatic tumor tissue 63	8.282	5.0248	7.9072	3.0035569
	69	2	7	68
human pancreatic tumor tissue 65	7.287	5.0922	7.3283	2.8584285
	69	1	8	06
human pancreatic tumor tissue 67	6.872	4.8943	7.2872	2.7275194
	59	2		81
human pancreatic tumor tissue 69	8.443	5.4050	8.3243	3.1535515
	89	6	9	59
human pancreatic tumor tissue 7	7.336	3.6053	7.4648	2.3951947
	53	3	9	36
human pancreatic tumor tissue 71	7.957	4.9154	7.7706	2.9147808
	59	4	6	55
human pancreatic tumor tissue 73	6.723	4.3363	7.8477	2.5298937
	31	6	5	16
human pancreatic tumor tissue 75	7.100	4.0452	7.4484	2.4963180
	91	9	6	01
human pancreatic tumor tissue 77	6.722	4.4150	7.8627	2.5548321
	3	8	8	64
human pancreatic tumor tissue 79	8.121	5.2382	7.8329	3.0445205
	64	7	1	59
human pancreatic tumor tissue 81	5.324	3.4186	6.7421	2.0022835
	35	4	5	73

human pancreatic tumor tissue 83	7.722	4.9913	8.2568	2.9039678
	87	4	4	11
human pancreatic tumor tissue 85	7.398	4.3673	7.8931	2.6502389
	12	5	6	73
human pancreatic tumor tissue 87	7.061		7.4407	2.3834662
	98	3.7101	9	9
human pancreatic tumor tissue 89	7.367	4.1006		2.5586337
	56	1	7.6208	88
human pancreatic tumor tissue 92	7.453	4.4256	7.8593	2.6774796
	04	4	5	34
human pancreatic tumor tissue 94	8.633	5.4916		3.2103222
	04	6	8.0942	08
human pancreatic tumor tissue 95	7.831	4.5329	7.3437	2.7696932
	16	9	6	45
human pancreatic tumor tissue 96	6.363	4.0820	7.1851	2.3857112
	38	3	9	84
human pancreatic tumor tissue 98	8.816	4.8888	8.3433	3.0505794
	37	5	4	51
GSE28735				
human pancreatic tumor tissue, patient	6.382	4.2258	8.2918	2.4422690
sample 1	53	4	6	48
human pancreatic tumor tissue, patient	8.022	4.5377	8.3142	2.8092768
sample 10	59	7	8	12
human pancreatic tumor tissue, patient	8.069	4.6603	7.9975	2.8536799
sample 11	74	5	9	64
human pancreatic tumor tissue, patient	5.978	4.5261	7.7555	2.4679097
sample 12	52	7	5	57
human pancreatic tumor tissue, patient	7.508	4.3404	8.1746	2.6616213
sample 13	03	6	8	26

human pancreatic tumor tissue, patient	9.165	4.0142	8.1179	2.8282397
sample 14	36	2	6	64
human pancreatic tumor tissue, patient	7.046	5.3820	7.6414	2.9133621
sample 15	95	7	4	24
human pancreatic tumor tissue, patient	7.664	4.8406	8.0772	2.8452804
sample 16	17	8	6	51
human pancreatic tumor tissue, patient	6.207	4.0833	6.8685	2.3585146
sample 17	8	8		79
human pancreatic tumor tissue, patient	5.082	3.6713	6.8173	2.0435033
sample 18	17	1	1	23
human pancreatic tumor tissue, patient	8.118	4.9704	7.9202	2.9596189
sample 19	88		2	17
human pancreatic tumor tissue, patient	8.504	5.3508	8.8129	3.1496101
sample 2	21	4	4	96
human pancreatic tumor tissue, patient	7.099	5.3618	8.5330	2.9218172
sample 20	79	3	3	41
human pancreatic tumor tissue, patient	7.149	4.7194	7.4545	2.7184589
sample 21	96	7	4	63
human pancreatic tumor tissue, patient	7.592	3.9160	7.8992	2.5386540
sample 22	15	6	2	82
human pancreatic tumor tissue, patient	7.424	4.1530	7.9429	2.5869110
sample 23	97	2	7	02
human pancreatic tumor tissue, patient	7.267	4.1699	8.2048	2.5683852
sample 24	28	8	1	89
human pancreatic tumor tissue, patient	7.916	4.6020	8.2225	2.8117329
sample 25	58	4	6	19
human pancreatic tumor tissue, patient	7.750	4.7429	7.7114	2.8257389
sample 26	37		7	87
human pancreatic tumor tissue, patient	7.378	4.4052	8.5586	2.6637058

sample 27	24	8		1
human pancreatic tumor tissue, patient	7.469	5.7302	7.8736	3.0945230
sample 28	26	8	1	89
human pancreatic tumor tissue, patient	8.082	4.0863	8.3661	2.6760866
sample 29	53	8	3	31
human pancreatic tumor tissue, patient	7.105	5.6967	8.6557	3.0300071
sample 3	83	1	5	76
human pancreatic tumor tissue, patient	8.309	5.7006	8.6212	3.2276264
sample 30	89	7	6	8
human pancreatic tumor tissue, patient	8.159	4.9201	8.1661	2.9520048
sample 31	35	8	9	88
human pancreatic tumor tissue, patient	8.724		8.1427	3.1004303
sample 32	7	5.0974	8	74
human pancreatic tumor tissue, patient	7.726	5.1507		2.9502641
sample 33	96	3	7.546	92
human pancreatic tumor tissue, patient	7.288	4.9643	7.5167	2.8193121
sample 34	74	3	1	56
human pancreatic tumor tissue, patient	8.882	5.4367	8.5636	3.2368184
sample 35	01	1	4	99
human pancreatic tumor tissue, patient	8.406	4.9297	8.0069	2.9942557
sample 36	28	8	1	85
human pancreatic tumor tissue, patient	7.135	4.4167	8.0764	2.6243512
sample 37	57	8	5	82
human pancreatic tumor tissue, patient	7.534	4.2013	7.6769	2.6182492
sample 38	31	6	9	34
human pancreatic tumor tissue, patient	7.829	4.4312	8.1216	2.7425805
sample 39	56	5	1	63
human pancreatic tumor tissue, patient	7.765	3.6565	7.6971	2.4830939
sample 4	24	6	6	36

human pancreatic tumor tissue, patient	7.492	3.7820	7.6712	2.4782772
sample 40	78	6	9	52
human pancreatic tumor tissue, patient	7.801	4.1938	7.8574	2.6607275
sample 41	39	1	5	11
human pancreatic tumor tissue, patient	7.134	4.4749	8.0982	2.6427740
sample 42	41	1	2	61
human pancreatic tumor tissue, patient	8.555	5.3488	8.0635	3.1521273
sample 43	73	3	5	31
human pancreatic tumor tissue, patient	5.677	3.4740	6.9602	2.0791421
sample 44	98	2	9	42
human pancreatic tumor tissue, patient	8.171	5.0998	8.4994	3.0133439
sample 45	29	4	1	69
human pancreatic tumor tissue, patient	7.341	5.3848	7.8046	2.9634921
sample 6	6	2	8	6
human pancreatic tumor tissue, patient	8.200	4.3548	8.4594	2.7812629
sample 7	51	6	9	64

Supplementary Table 3 Gene and its primer sequence

Primer ID	Primer sequence(5'to3')
PLAU Forward	GGGAATGGTCACTTTTACCGAG
PLAU Reverse	GGGCATGGTACGTTTGCTG
CAPN2 Forward	CGCTGGCGGTACTGAAGTC
CAPN2 Reverse	GAGGAACGGTGACATGCTCAT
CCNA2 Forward	GGATGGTAGTTTTGAGTCACCAC
CCNA2 Reverse	CACGAGGATAGCTCTCATACTGT

Supplementary Table 4 Univariate COX regression of hypoxia-related genes

Characteristics	Total (N)	HR (95%CI) Univariate analysis	P value Univariate analysis
PGF	179		
Low	89	Reference	
High	90	0.969 (0.645 - 1.456)	0.879
PTGS2	179		
Low	89	Reference	
High	90	1.403 (0.931 - 2.114)	0.105
MMP2	179		
Low	89	Reference	
High	90	1.198 (0.795 - 1.804)	0.387
TGFB1	179		
Low	89	Reference	
High	90	0.928 (0.613 - 1.405)	0.725
CCNB1	179		
Low	89	Reference	
High	90	1.807 (1.194 - 2.734)	0.005
THBS1	179		
Low	89	Reference	
High	90	1.222 (0.811 - 1.842)	0.338

NOX4	179		
Low	89	Reference	
		1.269 (0.842 -	
High	90	1.913)	0.255
CCNA2	179		
Low	89	Reference	
		1.912 (1.252 -	
High	90	2.920)	0.003
VCAM1	179		
Low	89	Reference	
		1.016 (0.675 -	
High	90	1.529)	0.939
CXCR4	179		
Low	89	Reference	
		0.867 (0.575 -	
High	90	1.309)	0.498
LMNA	179		
Low	89	Reference	
		1.230 (0.817 -	
High	90	1.852)	0.321
CYBB	179		
Low	89	Reference	
		1.103 (0.731 -	
High	90	1.664)	0.642
ACTN4	179		
Low	89	Reference	
		1.476 (0.973 -	
High	90	2.239)	0.067
HIF1A	179		

Low	89	Reference	
		1.391 (0.921 -	
High	90	2.100)	0.116
ICAM1	179		
Low	89	Reference	
		1.404 (0.930 -	
High	90	2.121)	0.106
RHOA	179		
Low	89	Reference	
		1.413 (0.936 -	
High	90	2.132)	0.100
MMP14	179		
Low	89	Reference	
		1.690 (1.116 -	
High	90	2.557)	0.013
TGFB2	179		
Low	89	Reference	
		1.579 (1.037 -	
High	90	2.402)	0.033
HK2	179		
Low	89	Reference	
		1.421 (0.940 -	
High	90	2.147)	0.095
PLAU	179		
Low	89	Reference	
		1.735 (1.144 -	
High	90	2.632)	0.010
PGK1	179		
Low	89	Reference	

			1.413 (0.936 -	
High	90	2.134)		0.100
VEGFC	179			
Low	89	Reference		
			0.976 (0.648 -	
High	90	1.470)		0.908
UBC	179			
Low	89	Reference		
			1.357 (0.894 -	
High	90	2.059)		0.152
CASP3	179			
Low	89	Reference		
			1.741 (1.145 -	
High	90	2.646)		0.010
CAV1	179			
Low	89	Reference		
			1.416 (0.940 -	
High	90	2.133)		0.096
TWIST1	179			
Low	89	Reference		
			1.604 (1.062 -	
High	90	2.422)		0.025
BNIP3L	179			
Low	89	Reference		
			1.250 (0.827 -	
High	90	1.889)		0.291
GNB1	179			
Low	89	Reference		
High	90	1.492 (0.986 -		0.058

			2.257)	
CAPN2	179			
Low	89	Reference		
			1.905 (1.251 -	
High	90	2.901)		0.003
HMOX1	179			
Low	89	Reference		
			1.070 (0.710 -	
High	90	1.611)		0.747
