

Table S1. Detailed clinical characteristics of the TCGA pancreatic adenocarcinoma cohort.

Sample ID	Sample type	DNA methylation	Transcriptome profiling	OS (days)	Survival status	RFS (days)	Relapse status	Age (years)	Gender	Surgery type	TNM stage
TCGA-FZ-5919-11A	Normal	Yes	No	741	1	NA	NA	59	Female	Whipple	Stage II
TCGA-FZ-5920-11A	Normal	Yes	No	61	1	NA	NA	52	Male	Whipple	Stage II
TCGA-FZ-5922-11A	Normal	Yes	No	1,101	1	740	1	81	Male	Whipple	Stage II
TCGA-FZ-5923-11A	Normal	Yes	No	619	1	619	0	71	Male	Whipple	Stage IV
TCGA-FZ-5924-11A	Normal	Yes	No	480	1	480	0	83	Male	Other method	Stage II
TCGA-FZ-5926-11A	Normal	Yes	No	541	1	541	0	73	Female	Whipple	Stage III
TCGA-H6-8124-11A	Normal	Yes	Yes	392	0	259	1	56	Female	Whipple	Stage II
TCGA-H6-A45N-11A	Normal	Yes	Yes	421	1	363	1	88	Female	Distal pancreatectomy	Stage II
TCGA-HV-A5A3-11A	Normal	Yes	Yes	128	1	128	0	50	Male	Distal pancreatectomy	Stage II
TCGA-YB-A89D-11A	Normal	Yes	Yes	350	0	350	0	59	Male	Whipple	Stage II
TCGA-2J-AAAB1-01A	Tumor	Yes	Yes	66	1	66	0	65	Male	Whipple	Stage II
TCGA-2J-AAAB4-01A	Tumor	Yes	Yes	729	0	729	0	48	Male	Distal pancreatectomy	Stage II
TCGA-2J-AAAB6-01A	Tumor	Yes	Yes	293	1	NA	NA	75	Male	Distal pancreatectomy	Stage II
TCGA-2J-AAAB8-01A	Tumor	Yes	Yes	80	0	80	0	71	Male	Whipple	Stage II
TCGA-2J-AAAB9-01A	Tumor	Yes	Yes	627	1	NA	NA	70	Female	Whipple	Stage II
TCGA-2J-AABA-01A	Tumor	Yes	Yes	607	1	160	1	55	Male	Whipple	Stage II
TCGA-2J-AABE-01A	Tumor	Yes	Yes	676	0	676	0	73	Male	Distal pancreatectomy	Stage II
TCGA-2J-AABF-01A	Tumor	Yes	Yes	691	1	443	1	73	Male	Whipple	Stage II
TCGA-2J-AABH-01A	Tumor	Yes	Yes	1,287	0	1,287	1	61	Male	Distal pancreatectomy	Stage II
TCGA-2J-AABI-01A	Tumor	Yes	Yes	969	0	728	1	55	Female	Whipple	Stage II
TCGA-2J-AABK-01A	Tumor	Yes	Yes	484	0	484	0	71	Male	Whipple	Stage II
TCGA-2J-AABO-01A	Tumor	Yes	Yes	440	0	439	1	43	Male	Whipple	Stage II
TCGA-2J-AABP-01A	Tumor	Yes	Yes	463	0	463	0	58	Female	Distal pancreatectomy	Stage II
TCGA-2J-AABR-01A	Tumor	Yes	Yes	438	0	327	1	60	Female	Whipple	Stage II
TCGA-2J-AABT-01A	Tumor	Yes	Yes	319	0	NA	NA	72	Female	Whipple	Stage II
TCGA-2J-ABU-01A	Tumor	Yes	Yes	277	1	NA	NA	56	Male	Whipple	Stage II
TCGA-2J-ABV-01A	Tumor	Yes	Yes	652	1	126	1	74	Male	Whipple	Stage II
TCGA-2L-AAQA-01A	Tumor	Yes	Yes	143	1	143	0	76	Male	Whipple	Stage II
TCGA-2L-AAQE-01A	Tumor	Yes	Yes	684	1	684	0	56	Male	Whipple	Stage II
TCGA-2L-AAQI-01A	Tumor	Yes	Yes	103	1	103	0	66	Male	Whipple	Stage II
TCGA-2L-AAQJ-01A	Tumor	Yes	Yes	394	1	394	0	49	Female	Whipple	Stage III
TCGA-2L-AAQL-01A	Tumor	Yes	Yes	292	1	292	0	82	Male	Whipple	Stage II
TCGA-2L-AAQM-01A	Tumor	Yes	Yes	1,383	0	1,383	0	52	Male	Distal pancreatectomy	Stage II
TCGA-3A-A9I5-01A	Tumor	Yes	Yes	1,794	0	1,794	0	57	Male	Whipple	NA
TCGA-3A-A9I7-01A	Tumor	Yes	Yes	1,323	0	1,309	1	45	Male	Whipple	Stage II
TCGA-3A-A9I9-01A	Tumor	Yes	Yes	634	1	NA	NA	67	Male	Whipple	Stage II
TCGA-3A-A9IB-01A	Tumor	Yes	Yes	224	1	224	0	69	Female	Whipple	Stage II
TCGA-3A-A9IC-01A	Tumor	Yes	Yes	738	1	738	0	61	Female	Whipple	Stage II

Table S1. Continued.

Sample ID	Sample type	DNA methylation	Transcriptome profiling	OS (days)	Survival status	RFS (days)	Relapse status	Age (years)	Gender	Surgery type	TNM stage
TCGA-3A-A9IH-01A	Tumor	Yes	Yes	1,021	0	763	1	66	Female	Other method	Stage I
TCGA-3A-A9IJ-01A	Tumor	Yes	Yes	1,854	0	1,854	0	65	Male	Whipple	Stage I
TCGA-3A-A9IL-01A	Tumor	Yes	Yes	2,741	0	2,741	0	39	Female	Whipple	Stage I
TCGA-3A-A9IN-01A	Tumor	Yes	Yes	2,084	0	2,084	0	62	Female	Other method	Stage I
TCGA-3A-A9IO-01A	Tumor	Yes	Yes	1,942	0	1,942	0	55	Male	Distal pancreatectomy	NA
TCGA-3A-A9IR-01A	Tumor	Yes	Yes	1,542	0	1,542	0	64	Female	Distal pancreatectomy	Stage I
TCGA-3A-A9IS-01A	Tumor	Yes	Yes	998	0	998	0	67	Male	Distal pancreatectomy	Stage I
TCGA-3A-A9IU-01A	Tumor	Yes	Yes	458	1	NA	NA	65	Male	Whipple	Stage II
TCGA-3A-A9IV-01A	Tumor	Yes	Yes	1,103	0	1,103	0	59	Female	Other method	Stage I
TCGA-3A-A9IX-01A	Tumor	Yes	Yes	1,037	0	1,037	0	40	Male	Whipple	Stage I
TCGA-3A-A9IZ-01A	Tumor	Yes	Yes	308	1	NA	NA	47	Male	Whipple	Stage II
TCGA-3A-A9J0-01A	Tumor	Yes	Yes	743	0	363	1	75	Male	Whipple	Stage II
TCGA-3E-AAAY-01A	Tumor	Yes	Yes	2,285	0	2,285	0	67	Male	Other method	Stage II
TCGA-3E-AAAZ-01A	Tumor	Yes	Yes	2,182	1	NA	NA	71	Male	Other method	Stage II
TCGA-F2-6879-01A	Tumor	Yes	Yes	334	1	183	1	57	Male	Whipple	Stage II
TCGA-F2-6880-01A	Tumor	Yes	Yes	289	0	289	0	70	Male	Whipple	Stage II
TCGA-F2-7273-01A	Tumor	Yes	Yes	592	1	NA	NA	54	Male	Whipple	Stage II
TCGA-F2-7276-01A	Tumor	Yes	Yes	216	1	216	0	64	Male	Whipple	Stage II
TCGA-F2-A44G-01A	Tumor	Yes	Yes	233	1	214	1	79	Female	Whipple	Stage II
TCGA-F2-A44H-01A	Tumor	Yes	Yes	586	0	586	0	65	Male	Whipple	Stage II
TCGA-F2-A7TX-01A	Tumor	Yes	Yes	95	1	95	0	77	Male	Whipple	Stage II
TCGA-F2-A8YN-01A	Tumor	Yes	Yes	517	0	517	0	76	Male	Whipple	Stage II
TCGA-FB-A4P5-01A	Tumor	Yes	Yes	179	1	179	0	69	Female	Whipple	Stage II
TCGA-FB-A4P6-01A	Tumor	Yes	Yes	767	0	620	1	54	Male	Whipple	Stage II
TCGA-FB-A545-01A	Tumor	Yes	Yes	732	1	732	0	72	Female	Distal pancreatectomy	Stage II
TCGA-FB-A5VM-01A	Tumor	Yes	Yes	498	1	498	0	74	Male	Whipple	Stage I
TCGA-FB-A78T-01A	Tumor	Yes	Yes	375	1	375	0	71	Female	Whipple	Stage II
TCGA-FB-A7DR-01A	Tumor	Yes	Yes	353	1	353	0	48	Male	Total pancreatectomy	Stage II
TCGA-FB-AAPP-01A	Tumor	Yes	Yes	485	1	150	1	71	Male	Whipple	Stage II
TCGA-FB-AAPQ-01A	Tumor	Yes	Yes	1,130	1	NA	NA	65	Male	Whipple	Stage II
TCGA-FB-AAPS-01A	Tumor	Yes	Yes	228	0	NA	NA	62	Female	Whipple	Stage II
TCGA-FB-AAPU-01A	Tumor	Yes	Yes	381	1	381	0	41	Female	Whipple	Stage II
TCGA-FB-AAPY-01A	Tumor	Yes	Yes	1,059	1	1,059	0	71	Male	Whipple	Stage II
TCGA-FB-AAPZ-01A	Tumor	Yes	Yes	716	0	716	1	54	Male	Whipple	Stage II
TCGA-FB-AAQ0-01A	Tumor	Yes	Yes	473	1	473	0	68	Male	Whipple	Stage II
TCGA-FB-AAQ1-01A	Tumor	Yes	Yes	123	1	NA	NA	49	Male	Whipple	Stage II
TCGA-FB-AAQ2-01A	Tumor	Yes	Yes	153	1	92	1	81	Female	Whipple	Stage II
TCGA-FB-AAQ3-01A	Tumor	Yes	Yes	31	1	31	0	65	Female	Whipple	Stage II

Table S1. Continued.

Sample ID	Sample type	DNA methylation	Transcriptome profiling	OS (days)	Survival status	RFS (days)	Relapse status	Age (years)	Gender	Surgery type	TNM stage
TCGA-FB-AAQ6-01A	Tumor	Yes	Yes	244	1	213	1	85	Male	Distal pancreatectomy	Stage I
TCGA-H6-8124-01A	Tumor	Yes	Yes	392	0	259	1	56	Female	Whipple	Stage II
TCGA-H6-A45N-01A	Tumor	Yes	Yes	421	1	363	1	88	Female	Distal pancreatectomy	Stage II
TCGA-H8-A6C1-01A	Tumor	Yes	Yes	671	0	455	1	53	Male	Whipple	Stage II
TCGA-HV-A5A3-01A	Tumor	Yes	Yes	128	1	128	0	50	Male	Distal pancreatectomy	Stage II
TCGA-HV-A5A4-01A	Tumor	Yes	Yes	232	0	232	0	72	Female	Distal pancreatectomy	Stage II
TCGA-HV-A5A5-01A	Tumor	Yes	Yes	289	0	289	0	61	Female	Other method	Stage II
TCGA-HV-A5A6-01A	Tumor	Yes	Yes	2,036	1	1,511	1	65	Female	NA	Stage II
TCGA-HV-A7OL-01A	Tumor	Yes	Yes	252	0	123	1	70	Male	Other method	Stage II
TCGA-HV-A7OP-01A	Tumor	Yes	Yes	978	0	346	1	72	Male	Whipple	Stage II
TCGA-HV-AA8V-01A	Tumor	Yes	Yes	920	0	526	1	50	Male	Other method	Stage II
TCGA-HV-AA8X-01A	Tumor	Yes	Yes	532	1	375	1	75	Female	Distal pancreatectomy	Stage II
TCGA-HZ-7289-01A	Tumor	Yes	Yes	661	1	228	1	77	Male	Whipple	Stage II
TCGA-HZ-7918-01A	Tumor	Yes	Yes	969	0	542	1	72	Male	Whipple	Stage II
TCGA-HZ-7919-01A	Tumor	Yes	Yes	593	1	593	0	52	Female	Whipple	Stage II
TCGA-HZ-7920-01A	Tumor	Yes	Yes	236	1	236	0	71	Male	Whipple	Stage I
TCGA-HZ-7922-01A	Tumor	Yes	Yes	4	0	4	0	61	Female	Whipple	Stage II
TCGA-HZ-7923-01A	Tumor	Yes	Yes	314	0	314	0	65	Male	Whipple	Stage II
TCGA-HZ-7924-01A	Tumor	Yes	Yes	840	0	831	1	60	Female	Whipple	Stage II
TCGA-HZ-7925-01A	Tumor	Yes	Yes	614	1	364	1	66	Male	Whipple	Stage II
TCGA-HZ-7926-01A	Tumor	Yes	Yes	518	1	340	1	57	Male	Whipple	Stage II
TCGA-HZ-8001-01A	Tumor	Yes	Yes	706	0	706	0	69	Male	Whipple	Stage III
TCGA-HZ-8002-01A	Tumor	Yes	Yes	366	1	366	0	61	Male	Whipple	Stage II
TCGA-HZ-8003-01A	Tumor	Yes	Yes	596	1	NA	NA	65	Female	Whipple	Stage II
TCGA-HZ-8005-01A	Tumor	Yes	Yes	120	1	120	0	81	Male	Whipple	Stage II
TCGA-HZ-8315-01A	Tumor	Yes	Yes	299	1	299	0	54	Female	Whipple	Stage II
TCGA-HZ-8317-01A	Tumor	Yes	Yes	378	1	378	0	69	Female	Whipple	Stage II
TCGA-HZ-8519-01A	Tumor	Yes	Yes	454	0	454	0	73	Male	Whipple	Stage II
TCGA-HZ-8636-01A	Tumor	Yes	Yes	545	1	545	0	58	Female	Other method	Stage I
TCGA-HZ-8637-01A	Tumor	Yes	Yes	517	1	517	0	76	Female	Whipple	Stage IV
TCGA-HZ-8638-01A	Tumor	Yes	Yes	151	1	151	0	84	Female	Whipple	Stage II
TCGA-HZ-A49G-01A	Tumor	Yes	Yes	660	0	660	0	58	Female	Whipple	Stage II
TCGA-HZ-A49H-01A	Tumor	Yes	Yes	491	0	491	0	68	Female	Whipple	Stage II
TCGA-HZ-A49I-01A	Tumor	Yes	Yes	308	1	308	0	77	Male	Whipple	Stage II
TCGA-HZ-A4BH-01A	Tumor	Yes	Yes	194	0	194	0	75	Male	Whipple	Stage II
TCGA-HZ-A4BK-01A	Tumor	Yes	Yes	657	0	657	0	72	Male	Whipple	Stage II
TCGA-HZ-A77O-01A	Tumor	Yes	Yes	160	1	98	1	77	Female	Whipple	Stage II
TCGA-HZ-A77P-01A	Tumor	Yes	Yes	330	0	330	0	77	Male	Whipple	Stage II

Table S1. Continued.

Sample ID	Sample type	DNA methylation	Transcriptome profiling	OS (days)	Survival status	RFS (days)	Relapse status	Age (years)	Gender	Surgery type	TNM stage
TCGA-HZ-A77Q-01A	Tumor	Yes	Yes	33	0	33	0	55	Female	Whipple	Stage II
TCGA-HZ-A8P0-01A	Tumor	Yes	Yes	NA	NA	NA	NA	76	Male	Whipple	Stage II
TCGA-HZ-A8P1-01A	Tumor	Yes	Yes	7	0	7	0	81	Male	Other method	Stage I
TCGA-HZ-A9TJ-01A	Tumor	Yes	Yes	603	0	555	1	70	Male	Total pancreatectomy	Stage IV
TCGA-HZ-A9TJ-06A	Tumor	Yes	Yes	603	0	555	1	70	Male	Total pancreatectomy	Stage IV
TCGA-IB-7644-01A	Tumor	Yes	Yes	394	1	394	0	65	Female	Whipple	Stage IV
TCGA-IB-7645-01A	Tumor	Yes	Yes	1,502	1	1,210	1	44	Female	Whipple	Stage II
TCGA-IB-7646-01A	Tumor	Yes	Yes	145	1	145	0	60	Male	Whipple	Stage II
TCGA-IB-7649-01A	Tumor	Yes	Yes	467	1	467	0	73	Female	Whipple	Stage II
TCGA-IB-7651-01A	Tumor	Yes	Yes	603	1	581	1	64	Female	Whipple	Stage II
TCGA-IB-7652-01A	Tumor	Yes	Yes	1,116	0	1,116	0	49	Female	Distal pancreatectomy	Stage II
TCGA-IB-7654-01A	Tumor	Yes	Yes	476	1	476	0	80	Male	Whipple	Stage II
TCGA-IB-7885-01A	Tumor	Yes	Yes	1,257	0	1,257	0	78	Female	Whipple	Stage II
TCGA-IB-7886-01A	Tumor	Yes	Yes	123	1	123	0	80	Male	Whipple	Stage II
TCGA-IB-7887-01A	Tumor	Yes	Yes	110	1	110	0	62	Female	Whipple	Stage II
TCGA-IB-7888-01A	Tumor	Yes	Yes	1,332	1	1,332	0	66	Female	Whipple	Stage II
TCGA-IB-7889-01A	Tumor	Yes	Yes	481	1	481	0	85	Female	Whipple	Stage II
TCGA-IB-7890-01A	Tumor	Yes	Yes	598	1	519	1	73	Male	Distal pancreatectomy	Stage I
TCGA-IB-7891-01A	Tumor	Yes	Yes	913	1	872	1	49	Female	Whipple	Stage II
TCGA-IB-7893-01A	Tumor	Yes	Yes	117	1	80	1	64	Male	Distal pancreatectomy	Stage II
TCGA-IB-7897-01A	Tumor	Yes	Yes	486	1	486	0	53	Female	Whipple	Stage II
TCGA-IB-8126-01A	Tumor	Yes	Yes	462	0	83	1	79	Female	Whipple	Stage III
TCGA-IB-8127-01A	Tumor	Yes	Yes	522	0	486	1	59	Male	Whipple	Stage II
TCGA-IB-A550-01A	Tumor	Yes	Yes	365	1	276	1	71	Male	Whipple	Stage II
TCGA-IB-A55P-01A	Tumor	Yes	Yes	482	0	482	0	77	Male	Whipple	Stage II
TCGA-IB-A55Q-01A	Tumor	Yes	Yes	219	1	NA	NA	56	Female	Whipple	Stage I
TCGA-IB-A55S-01A	Tumor	Yes	Yes	460	1	460	0	64	Female	Distal pancreatectomy	Stage II
TCGA-IB-A55T-01A	Tumor	Yes	Yes	635	0	635	0	64	Female	Whipple	Stage II
TCGA-IB-A6UF-01A	Tumor	Yes	Yes	666	0	593	1	63	Male	Whipple	Stage II
TCGA-IB-A6UG-01A	Tumor	Yes	Yes	41	1	41	0	65	Male	Whipple	Stage II
TCGA-IB-A7LX-01A	Tumor	Yes	Yes	250	1	230	1	57	Male	Whipple	Stage II
TCGA-IB-A7M4-01A	Tumor	Yes	Yes	483	0	483	0	81	Male	Distal pancreatectomy	Stage II
TCGA-IB-AAUM-01A	Tumor	Yes	Yes	8	0	8	0	76	Male	Whipple	Stage II
TCGA-IB-AAUN-01A	Tumor	Yes	Yes	144	1	144	0	74	Female	Whipple	Stage I
TCGA-IB-AAUO-01A	Tumor	Yes	Yes	239	1	211	1	64	Female	Whipple	Stage II
TCGA-IB-AAUP-01A	Tumor	Yes	Yes	431	0	431	0	68	Male	Other method	Stage II
TCGA-IB-AAUQ-01A	Tumor	Yes	Yes	183	1	183	0	50	Male	Distal pancreatectomy	Stage II
TCGA-IB-AAUR-01A	Tumor	Yes	Yes	338	0	330	1	67	Male	Whipple	Stage II

Table S1. Continued.

Sample ID	Sample type	DNA methylation	Transcriptome profiling	OS (days)	Survival status	RFS (days)	Relapse status	Age (years)	Gender	Surgery type	TNM stage
TCGA-IB-AAUS-01A	Tumor	Yes	Yes	225	0	225	0	84	Female	Whipple	Stage II
TCGA-IB-AAUT-01A	Tumor	Yes	Yes	287	0	287	0	65	Male	Whipple	Stage II
TCGA-IB-AAUU-01A	Tumor	Yes	Yes	245	0	245	0	35	Male	Whipple	Stage II
TCGA-IB-AAUV-01A	Tumor	Yes	Yes	404	0	404	0	49	Male	Whipple	Stage II
TCGA-IB-AAUW-01A	Tumor	Yes	Yes	230	1	185	1	63	Female	Whipple	Stage II
TCGA-L1-A7W4-01A	Tumor	Yes	Yes	278	1	129	1	48	Female	Whipple	Stage II
TCGA-LB-A7SX-01A	Tumor	Yes	Yes	393	1	393	0	74	Female	Whipple	Stage II
TCGA-LB-A8F3-01A	Tumor	Yes	Yes	379	0	379	0	64	Female	Whipple	Stage II
TCGA-LB-A9Q5-01A	Tumor	Yes	Yes	313	1	290	1	63	Female	Whipple	Stage II
TCGA-M8-A5N4-01A	Tumor	Yes	Yes	584	0	NA	NA	48	Female	Whipple	Stage II
TCGA-OE-A75W-01A	Tumor	Yes	Yes	267	1	146	1	75	Male	Distal pancreatectomy	Stage II
TCGA-PZ-A5RE-01A	Tumor	Yes	Yes	470	1	393	1	44	Female	Whipple	Stage II
TCGA-Q3-A5QY-01A	Tumor	Yes	Yes	416	0	416	0	58	Male	Whipple	Stage II
TCGA-Q3-AA2A-01A	Tumor	Yes	Yes	95	0	95	0	64	Female	Whipple	Stage I
TCGA-RB-A7B8-01A	Tumor	Yes	Yes	466	1	449	1	81	Female	Whipple	Stage II
TCGA-RB-AA9M-01A	Tumor	Yes	Yes	286	0	258	1	43	Male	Distal pancreatectomy	Stage II
TCGA-RL-AAAS-01A	Tumor	Yes	Yes	9	0	9	0	60	Female	Whipple	Stage I
TCGA-S4-A8RM-01A	Tumor	Yes	Yes	737	0	737	0	67	Male	Total pancreatectomy	Stage II
TCGA-S4-A8RO-01A	Tumor	Yes	Yes	525	0	291	1	75	Female	Whipple	Stage II
TCGA-S4-A8RP-01A	Tumor	Yes	Yes	702	1	NA	NA	77	Female	Whipple	Stage II
TCGA-US-A774-01A	Tumor	Yes	Yes	695	1	NA	NA	76	Female	Whipple	Stage II
TCGA-US-A776-01A	Tumor	Yes	Yes	1,216	0	1,216	0	61	Male	Whipple	Stage II
TCGA-US-A779-01A	Tumor	Yes	Yes	511	1	NA	NA	54	Female	Whipple	Stage II
TCGA-US-A77E-01A	Tumor	Yes	Yes	430	1	NA	NA	73	Male	Whipple	Stage II
TCGA-US-A77G-01A	Tumor	Yes	Yes	12	1	NA	NA	64	Male	Whipple	Stage II
TCGA-US-A77J-01A	Tumor	Yes	Yes	568	1	NA	NA	81	Female	Whipple	Stage II
TCGA-XD-AAUG-01A	Tumor	Yes	Yes	420	0	420	0	66	Female	Other method	Stage IV
TCGA-XD-AAUH-01A	Tumor	Yes	Yes	395	0	87	1	57	Female	Whipple	Stage II
TCGA-XD-AAUI-01A	Tumor	Yes	Yes	366	1	184	1	50	Female	Whipple	Stage II
TCGA-XD-AAUL-01A	Tumor	Yes	Yes	498	0	498	0	56	Male	Whipple	Stage II
TCGA-XN-A8T3-01A	Tumor	Yes	Yes	951	0	461	1	67	Male	Whipple	Stage I
TCGA-XN-A8T5-01A	Tumor	Yes	Yes	720	0	242	1	53	Female	Whipple	Stage I
TCGA-YB-A89D-01A	Tumor	Yes	Yes	350	0	350	0	59	Male	Whipple	Stage II
TCGA-YH-A8SY-01A	Tumor	Yes	Yes	388	0	NA	NA	73	Female	Whipple	Stage III
TCGA-YY-A8LH-01A	Tumor	Yes	Yes	2,016	0	2,016	0	61	Female	Other method	Stage II
TCGA-Z5-AAPL-01A	Tumor	Yes	Yes	467	0	467	0	74	Female	NA	Stage II

OS, overall survival; RFS, recurrence-free survival; TCGA, The Cancer Genome Atlas; NA, not available.

Table SII. MethylMix models for the seven DNA methylation-driven genes.

Gene	Normal mean DNA methylation	Tumor mean DNA methylation	Log ₂ FC	P-value	Adjusted P-value	Pearson correlation	Pearson correlation P-value
ZNF208	0.229628198	0.37030526	0.689415	1.00x10 ⁻⁵	0.000191	-0.43427	1.39x10 ⁻⁹
EOMES	0.200380253	0.29929061	0.578807	3.43x10 ⁻⁴	0.006517	-0.4733	2.53x10 ⁻¹¹
PTGDR	0.246551618	0.361059454	0.550347	1.93x10 ⁻⁵	0.000366	-0.34637	2.18x10 ⁻⁶
C12orf42	0.226085619	0.328240513	0.537884	8.73x10 ⁻⁶	0.000166	-0.31677	1.65x10 ⁻⁵
ITGA4	0.332801183	0.46275722	0.475595	7.79x10 ⁻⁵	0.00148	-0.53869	8.75x10 ⁻¹⁵
DOCK8	0.67211299	0.80454679	0.259473	1.68x10 ⁻⁵	0.00032	-0.39213	6.19x10 ⁻⁸
PPP1R14D	0.547627109	0.444988357	-0.29943	4.58x10 ⁻⁵	0.00087	-0.55943	4.79x10 ⁻¹⁶

FC, fold change; ZNF208, zinc finger protein 208; EOMES, eomesodermin; PTGDR, prostaglandin D2 receptor; C12orf42, chromosome 12 open reading frame 42; ITGA4, integrin subunit α 4; DOCK8, dedicator of cytokinesis 8; PPP1R14D, protein phosphatase 1 regulatory inhibitor subunit 14D.

Table SIII. Out of seven DNA methylation-driven genes, six were associated with overall survival in pancreatic adenocarcinoma.

Gene/expression status	DNA methylation level	Number of patients	Mean survival time (years)	P-value
ITGA4				0.001
High	>0.470	77	2.077	
Low	≤0.470	99	3.759	
ZNF208				0.003
High	>0.348	101	2.256	
Low	≤0.348	75	3.861	
C12orf42				0.004
High	>0.237	155	2.414	
Low	≤0.237	21	5.512	
PPP1R14D				0.004
High	>0.541	18	4.914	
Low	≤0.541	158	2.659	
EOMES				0.006
High	>0.235	115	2.335	
Low	≤0.235	61	4.063	
PTGDR				0.034
High	>0.263	159	2.462	
Low	≤0.263	17	4.567	
DOCK8				0.138
High	>0.874	20	3.421	
Low	≤0.874	156	2.722	

ZNF208, zinc finger protein 208; EOMES, eomesodermin; PTGDR, prostaglandin D2 receptor; C12orf42, chromosome 12 open reading frame 42; ITGA4, integrin subunit α 4; DOCK8, dedicator of cytokinesis 8; PPP1R14D, protein phosphatase 1 regulatory inhibitor subunit 14D.

Table SIV. Out of seven DNA methylation-driven genes, six were associated with relapse-free survival in pancreatic adenocarcinoma.

Gene/methylation status	DNA methylation level	Number of patients	Mean relapse-free survival (years)	P-value
ITGA4				0.001
High	>0.544	43	1.689	
Low	≤0.544	111	4.097	
EOMES				0.004
High	>0.193	137	2.778	
Low	≤0.193	17	7.072	
PTGDR				0.009
High	>0.266	139	2.542	
Low	≤0.266	15	6.498	
ZNF208				0.013
High	>0.242	138	2.744	
Low	≤0.242	16	6.457	
C12orf42				0.021
High	>0.232	138	2.713	
Low	≤0.232	16	5.908	
PPP1R14D				0.026
High	>0.411	100	4.520	
Low	≤0.411	54	2.097	
DOCK8				0.302
High	>0.819	74	3.471	
Low	≤0.819	80	3.231	

ZNF208, zinc finger protein 208; EOMES, eomesodermin; PTGDR, prostaglandin D2 receptor; C12orf42, chromosome 12 open reading frame 42; ITGA4, integrin subunit α 4; DOCK8, dedicator of cytokinesis 8; PPP1R14D, protein phosphatase 1 regulatory inhibitor subunit 14D.

Table SV. Gene enrichment in the DNA methylation-driven genes hypermethylation group of patients with pancreatic adenocarcinoma.

Pathway name	Size	ES	NES	NOM P-val	FDR q-val	FWER P-val	Rank at max	Leading edge
A, ZNF208								
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	252	0.594743	2.212443	0	0	0	3910	Tags=38%, List=14%, Signal=44%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	112	0.545371	1.839789	0	0.010674	0.039	5911	Tags=44%, List=22%, Signal=56%
KEGG_BASAL_CELL_CARCINOMA	55	0.571808	1.747291	0	0.027511	0.145	2107	Tags=27%, List=8%, Signal=29%
KEGG_CALCIIUM_SIGNALING_PATHWAY	168	0.461002	1.648131	0	0.073091	0.421	4069	Tags=29%, List=15%, Signal=33%
KEGG_MELANOGENESIS	101	0.462593	1.562708	0.003125	0.139896	0.717	3980	Tags=26%, List=15%, Signal=30%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	0.494607	1.505588	0.01855	0.190959	0.878	2107	Tags=23%, List=8%, Signal=25%
KEGG_TYPE_I_DIABETES_MELLITUS	39	0.514126	1.459959	0.039655	0.242273	0.957	5364	Tags=38%, List=20%, Signal=48%
KEGG_GAP_JUNCTION	86	0.43832	1.419934	0.023772	0.294666	0.988	3980	Tags=24%, List=15%, Signal=28%
KEGG_WNT_SIGNALING_PATHWAY	145	0.384857	1.341232	0.034935	0.382296	1	3288	Tags=17%, List=12%, Signal=19%
B, EOMES								
Pathway name	Size	ES	NES	NOM P-val	FDR q-val	FWER P-val	Rank at max	Leading edge
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	252	0.598928	2.184037	0	0	0	4251	Tags=39%, List=15%, Signal=46%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	112	0.550514	1.817459	0	0.013608	0.044	5473	Tags=43%, List=20%, Signal=53%
KEGG_BASAL_CELL_CARCINOMA	55	0.583623	1.755041	0.001553	0.024787	0.118	2562	Tags=29%, List=9%, Signal=32%
KEGG_CALCIIUM_SIGNALING_PATHWAY	168	0.489236	1.729817	0	0.025092	0.155	4861	Tags=33%, List=18%, Signal=40%
KEGG_MELANOGENESIS	101	0.515603	1.700824	0.001473	0.029737	0.228	3933	Tags=28%, List=14%, Signal=32%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	0.53189	1.603355	0.00625	0.082142	0.578	3789	Tags=30%, List=14%, Signal=35%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	0.640549	1.495475	0.034608	0.196121	0.914	2194	Tags=20%, List=8%, Signal=22%
KEGG_GAP_JUNCTION	86	0.461965	1.485445	0.007278	0.187108	0.923	4112	Tags=24%, List=15%, Signal=29%
KEGG_WNT_SIGNALING_PATHWAY	145	0.407871	1.409852	0.017045	0.256834	0.996	4966	Tags=25%, List=18%, Signal=30%
C, PTGDR								
Pathway name	Size	ES	NES	NOM P-val	FDR q-val	FWER P-val	Rank at max	Leading edge
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	252	0.622541	2.432184	0	0	0	3579	Tags=40%, List=13%, Signal=45%
KEGG_CALCIIUM_SIGNALING_PATHWAY	168	0.476982	1.762563	0	0.029698	0.135	4403	Tags=32%, List=16%, Signal=38%
KEGG_BASAL_CELL_CARCINOMA	55	0.544611	1.748362	0.001618	0.022748	0.155	3883	Tags=36%, List=14%, Signal=42%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	112	0.487984	1.740775	0	0.019216	0.176	5826	Tags=43%, List=21%, Signal=54%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	0.50923	1.617801	0.001686	0.06419	0.557	3883	Tags=34%, List=14%, Signal=39%

Table SV. Continued.

Pathway name	Size	ES	NES	NOM P-val	FDR q-val	FWER P-val	Rank at max	Leading edge
C, PTGDR								
KEGG_MELANOGENESIS	101	0.435495	1.54489	0.009274	0.110824	0.803	3883	Tags=26%, List=14%, Signal=30%
KEGG_TYPE_I_DIABETES_MELLITUS	39	0.490135	1.463671	0.042301	0.189482	0.964	5556	Tags=36%, List=20%, Signal=45%
KEGG_WNT_SIGNALING_PATHWAY	145	0.358233	1.325961	0.048706	0.324882	1	2244	Tags=14%, List=8%, Signal=16%
D, C12orf42								
Pathway name								
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	252	0.614826	2.271452	0	0	0	2968	Tags=35%, List=11%, Signal=38%
KEGG_BASAL_CELL_CARCINOMA	55	0.600736	1.824457	0	0.009605	0.041	2121	Tags=27%, List=8%, Signal=29%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	112	0.508716	1.722249	0	0.029748	0.173	4855	Tags=36%, List=18%, Signal=43%
KEGG_CALCIIUM_SIGNALING_PATHWAY	168	0.485002	1.718423	0	0.024018	0.185	4554	Tags=32%, List=17%, Signal=38%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	0.542191	1.623738	0.006441	0.064696	0.506	2180	Tags=23%, List=8%, Signal=25%
KEGG_MELANOGENESIS	101	0.467836	1.586882	0.002981	0.102111	0.729	4242	Tags=28%, List=15%, Signal=33%
KEGG_GLYCOPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	0.632486	1.505021	0.037523	0.142084	0.884	2364	Tags=20%, List=9%, Signal=22%
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	24	0.551631	1.46383	0.048696	0.179453	0.95	2484	Tags=38%, List=9%, Signal=41%
KEGG_GAP_JUNCTION	86	0.435387	1.421312	0.039454	0.225727	0.987	3571	Tags=23%, List=13%, Signal=27%
KEGG_WNT_SIGNALING_PATHWAY	145	0.396254	1.386129	0.021277	0.266954	0.997	2682	Tags=15%, List=10%, Signal=17%
E, ITGA4								
Pathway name								
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	252	0.608302	2.231988	0	0	0	3815	Tags=38%, List=14%, Signal=44%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	112	0.57615	1.963052	0	5.82E-04	0.002	4454	Tags=38%, List=16%, Signal=46%
KEGG_BASAL_CELL_CARCINOMA	55	0.60677	1.842558	0	0.006509	0.035	1831	Tags=27%, List=7%, Signal=29%
KEGG_CALCIIUM_SIGNALING_PATHWAY	168	0.492083	1.749327	0	0.018207	0.123	4594	Tags=33%, List=17%, Signal=39%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	0.56016	1.69473	0	0.032629	0.259	1691	Tags=23%, List=6%, Signal=25%
KEGG_MELANOGENESIS	101	0.487829	1.620455	0	0.064642	0.493	3828	Tags=27%, List=14%, Signal=31%
KEGG_GLYCOPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	0.654545	1.525112	0.043876	0.14724	0.84	2260	Tags=20%, List=8%, Signal=22%
KEGG_GAP_JUNCTION	86	0.454534	1.481882	0.007564	0.187334	0.926	3832	Tags=24%, List=14%, Signal=28%
KEGG_TYPE_I_DIABETES_MELLITUS	39	0.511236	1.458973	0.044481	0.180068	0.954	4698	Tags=31%, List=17%, Signal=37%
KEGG_WNT_SIGNALING_PATHWAY	145	0.40051	1.386438	0.017956	0.291819	0.999	3456	Tags=18%, List=13%, Signal=20%

Table SV. Continued.

Pathway name	Size	ES	NES	NOM P-val	FDR q-val	FWER P-val	Rank at max	Leading edge
KEGG_BASAL_CELL_CARCINOMA	55	0.562771	1.888317	0	0.026736	0.022	5210	Tags=38%, List=19%, Signal=47%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	112	0.496946	1.877308	0	0.015191	0.025	5617	Tags=40%, List=20%, Signal=50%
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	252	0.443688	1.848408	0	0.01376	0.034	6305	Tags=38%, List=23%, Signal=50%
KEGG_MELANOGENESIS	101	0.428658	1.601633	0	0.265451	0.568	7533	Tags=43%, List=27%, Signal=58%
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	24	0.557809	1.59008	0.016014	0.242118	0.62	3048	Tags=46%, List=11%, Signal=52%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	0.613481	1.56843	0.031414	0.253864	0.705	1726	Tags=20%, List=6%, Signal=21%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	0.466463	1.567015	0.005068	0.220739	0.71	3459	Tags=25%, List=13%, Signal=29%
KEGG_MAPK_SIGNALING_PATHWAY	257	0.366005	1.54441	0	0.23962	0.794	7877	Tags=39%, List=29%, Signal=55%
KEGG_PATHWAYS_IN_CANCER	314	0.355193	1.53594	0	0.230392	0.814	5290	Tags=27%, List=19%, Signal=33%
KEGG_APOPTOSIS	81	0.415191	1.517257	0.017771	0.243539	0.866	8105	Tags=47%, List=30%, Signal=66%
KEGG_CALCIIUM_SIGNALING_PATHWAY	168	0.365885	1.47827	0.005917	0.304015	0.939	6939	Tags=33%, List=25%, Signal=44%
KEGG_TYPE_I_DIABETES_MELLITUS	39	0.452133	1.447112	0.039655	0.359231	0.973	4086	Tags=31%, List=15%, Signal=36%
KEGG_AMYOTROPIC_LATERAL_SCLEROSIS_ALS	50	0.432979	1.43949	0.042208	0.354766	0.977	4192	Tags=28%, List=15%, Signal=33%
KEGG_WNT_SIGNALING_PATHWAY	145	0.365004	1.428769	0.009317	0.357635	0.987	7305	Tags=34%, List=27%, Signal=47%
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	84	0.379794	1.382112	0.031949	0.470754	1	8039	Tags=38%, List=29%, Signal=54%
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	109	0.366082	1.371295	0.028875	0.473952	1	7673	Tags=40%, List=28%, Signal=56%
KEGG_CELL_ADHESION_MOLECULES_CAMS	123	0.348806	1.338286	0.033333	0.527531	1	5912	Tags=34%, List=22%, Signal=43%
G_PPP1R14D								
Pathway name	Size	ES	NES	NOM P-val	FDR q-val	FWER P-val	Rank at max	Leading edge
KEGG_GLYCOLYSIS_GLUONEOGENESIS	58	0.553743	1.755887	0	0.136289	0.096	2969	Tags=28%, List=11%, Signal=31%
KEGG_TYROSINE_METABOLISM	40	0.57889	1.73958	0.001996	0.082935	0.114	2973	Tags=30%, List=11%, Signal=34%
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	56	0.540539	1.736085	0.004264	0.057989	0.118	4461	Tags=41%, List=16%, Signal=49%
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	31	0.608324	1.715271	0.003831	0.057883	0.154	7861	Tags=68%, List=29%, Signal=95%
KEGG_HISTIDINE_METABOLISM	28	0.626153	1.701934	0.002114	0.055349	0.183	2973	Tags=32%, List=11%, Signal=36%
KEGG_FATTY_ACID_METABOLISM	40	0.562469	1.69852	0.001996	0.048167	0.191	5235	Tags=43%, List=19%, Signal=52%

Table SV. Continued.

Pathway name	Size	ES	NES	NOM P-val	FDR q-val	FWER P-val	Rank at max	Leading edge
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	16	0.676063	1.679307	0.007692	0.055096	0.243	2826	Tags=31%, List=10%, Signal=35%
KEGG_RETINOL_METABOLISM	51	0.534012	1.671231	0.003738	0.052099	0.261	2401	Tags=27%, List=9%, Signal=30%
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	57	0.522528	1.651594	0	0.058147	0.32	4504	Tags=40%, List=16%, Signal=48%
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	38	0.551456	1.643069	0.008114	0.058145	0.354	6223	Tags=47%, List=23%, Signal=61%
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	68	0.492156	1.631483	0.003876	0.058786	0.383	6385	Tags=43%, List=23%, Signal=55%
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	15	0.681481	1.600807	0.018832	0.076631	0.489	5235	Tags=53%, List=19%, Signal=66%
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	43	0.520034	1.596392	0.017341	0.074374	0.507	5794	Tags=40%, List=21%, Signal=50%
KEGG_PYRIMIDINE_METABOLISM	91	0.462837	1.56622	0.007707	0.094078	0.613	6711	Tags=43%, List=24%, Signal=57%
KEGG_OLFACTORY_TRANSDUCTION	323	0.385125	1.542193	0	0.109462	0.686	7858	Tags=37%, List=29%, Signal=51%
KEGG_STARCH_AND_SUCROSE_METABOLISM	38	0.524011	1.541536	0.017375	0.103488	0.688	7861	Tags=47%, List=29%, Signal=66%
KEGG_PHENYLALANINE_METABOLISM	16	0.628765	1.52737	0.02214	0.110364	0.737	4884	Tags=56%, List=18%, Signal=68%
KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	18	0.594482	1.490558	0.038961	0.13935	0.843	4514	Tags=33%, List=16%, Signal=40%
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	72	0.452169	1.486665	0.011765	0.136974	0.857	4514	Tags=31%, List=16%, Signal=36%
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	17	0.600598	1.485368	0.045802	0.131372	0.86	4473	Tags=35%, List=16%, Signal=42%
KEGG_PPARG_SIGNALING_PATHWAY	65	0.461374	1.484232	0.01378	0.126468	0.861	4555	Tags=29%, List=17%, Signal=35%
KEGG_STEROID_HORMONE_BIOSYNTHESIS	44	0.490589	1.482796	0.025591	0.122487	0.864	4461	Tags=36%, List=16%, Signal=43%
KEGG_JAK_STAT_SIGNALING_PATHWAY	126	0.409776	1.472716	0.00409	0.127767	0.885	5057	Tags=30%, List=18%, Signal=37%
KEGG_PEROXISOME	72	0.434107	1.430692	0.013699	0.170264	0.949	6030	Tags=33%, List=22%, Signal=43%
KEGG_INSULIN_SIGNALING_PATHWAY	134	0.389931	1.423311	0.00996	0.174647	0.957	5653	Tags=28%, List=21%, Signal=35%
KEGG_CHRONIC_MYELOID_LEUKEMIA	70	0.416529	1.383552	0.035225	0.197437	0.986	7299	Tags=39%, List=27%, Signal=52%
KEGG_TIGHT_JUNCTION	127	0.374518	1.352319	0.011742	0.224666	0.996	3211	Tags=16%, List=12%, Signal=18%

KEGG, Kyoto Encyclopedia of Genes and Genomes; ES, enrichment score; NES, normalized enrichment score; NOM P-val, nominal P-value; FDR q-val, false discovery rate q value; FWER P-val, familywise-error rate P-value; ZNF208, zinc finger protein 208; EOMES, eomesodermin; PTGDR, prostaglandin D2 receptor; C12orf42, chromosome 12 open reading frame 42; ITGA4, integrin subunit α 4; DOCK8, dedicator of cytokinesis 8; PPP1R14D, protein phosphatase 1 regulatory inhibitor subunit 14D.