Supplementary Materials

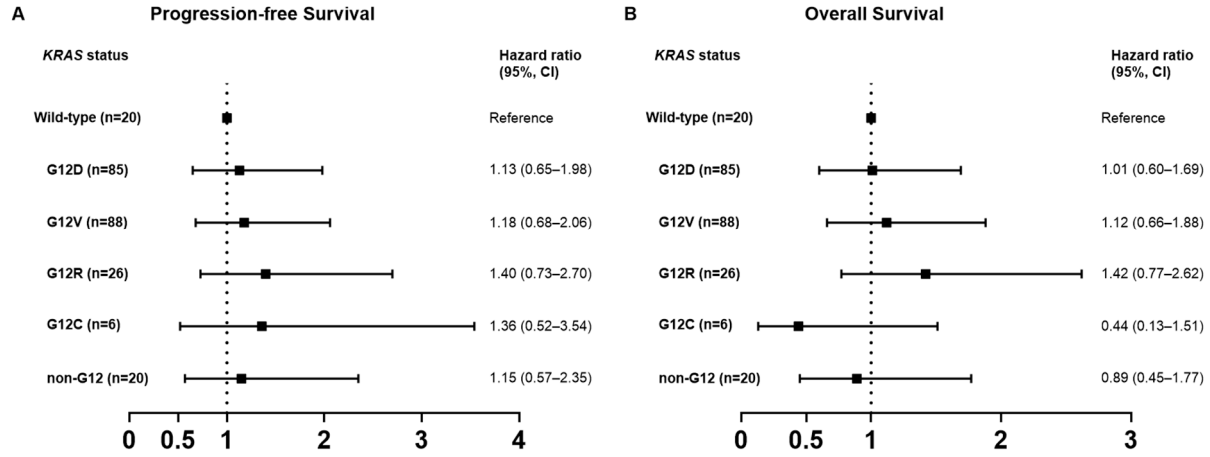


Figure S1. Comparison of median progression-free survival (A) and overall survival (B) between *KRAS* wild-type and *KRAS* codon-specific subtypes in the treated cohort.

Table S1. Actionable genomic alterations identified in *KRAS* wild-type pancreatic cancer patients

Wild type (n = 22)	**Gene alterations**	**Variant type**
Patient 1	*BRAF* Thr599dup, *TP53*, *ARID1A*	SNV
Patient 2	*AR*, *ARAF* amplification	CNV
Patient 3	*BRCA2*, *TP53*	SNV
Patient 4	*MDM2* amplification	CNV
Patient 5	*TP53*, *CDKN2A*	SNV
Patient 6	*EGFR* L858R, *PIK3CA* H1047R	SNV
Patient 7	*EGFR* exon 19 deletion, *ATM*	SNV
Patient 8	*AR*, *ARAF* amplification	CNV
Patient 9	Not detected	
Patient 10	*BRAF* V600E	SNV
Patient 11	*BRAF* V600E	SNV
Patient 12	*PTEN*, *RNF43*, *SND1-BRAF* fusion	SNV, Fusion
Patient 13	*PIK3CA* P539R, *SMAD4*	SNV
Patient 14	Not detected	
Patient 15	*ARID1A*	SNV
Patient 16	*BRAF V600E*, *TP53*	SNV
Patient 17	*BAP1*, *FGF3*, *PIK3R1*	SNV
Patient 18	*TP53*, *CDKN2A*, *NF1*	SNV
Patient 19	*TP53*, *PIK3CA* H1047R	SNV
Patient 20	Not detected	
Patient 21	*CDKN2A*	SNV
Patient 22	*TP53*	SNV
***BRAF* V600E**	3 (13.6%)	
***EGFR* mutation**	2 (9.1%)	
***PIK3CA* mutations**	3 (3.6%)	

SNV single nucleotide variant, *CNV* copy number variation.

Table S2. Comparison of clinical characteristics according to *KRAS* mutation subtypes in patients with pancreatic cancer

Variable	G12D (n = 93)	G12V (n = 97)	G12R (n = 28)	Non-G12 (n = 21)	Wild type (n = 22)	*p* value
Age, years						
< 65	43 (46.2)	37 (38.1)	9 (32.1)	7 (33.3)	7 (31.8)	0.501
≥ 65	50 (53.8)	60 (61.9)	19 (67.9)	14 (66.7)	15 (68.2)	
Gender						
Male	50 (53.8)	54 (55.7)	11 (39.3)	11 (52.4)	11 (50.0)	0.651
Female	43 (46.2)	43 (44.3)	17 (60.7)	10 (47.6)	11 (50.0)	
Tumor location						
Head	49 (52.7)	48 (49.5)	11 (39.3)	9 (42.9)	14 (63.6)	0.459
Body/Tail	44 (47.3)	49 (50.5)	17 (60.7)	12 (57.1)	8 (36.4)	
Differentiation						
Well to moderately	52 (70.3)	52 (70.3)	17 (73.9)	14 (82.4)	12 (80.0)	0.836
Poorly	22 (29.7)	18 (25.4)	6 (26.1)	3 (17.6)	3 (20.0)	
No. of organ metastasis						
0-1	62 (66.7)	68 (70.1)	17 (60.7)	15 (71.4)	15 (68.2)	0.900
≥ 2	31 (33.3)	29 (29.9)	11 (39.3)	6 (28.6)	7 (31.8)	
Site of metastasis						
Liver	55 (59.1)	48 (49.5)	15 (53.6)	12 (57.1)	10 (45.5)	0.644
Lung	12 (12.9)	19 (19.6)	8 (28.6)	4 (19.0)	2 (9.1)	0.268
Peritoneum	21 (22.6)	27 (27.8)	9 (32.1)	4 (19.0)	7 (31.8)	0.700
CA 19-9						
Normal	20 (22.2)	14 (14.6)	4 (14.8)	8 (42.1)	9 (40.9)	0.011
Elevated (≥ 34U/mL)	70 (77.8)	82 (85.4)	23 (85.2)	11 (57.9)	13 (59.1)	
CEA						
Normal	47 (52.8)	49 (52.1)	17 (63.0)	7 (36.8)	14 (63.6)	0.395
Elevated (≥ 5.0 μg/L)	42 (47.2)	45 (47.9)	10 (37.0)	12 (63.2)	8 (36.4)	
NLR						
< 3.0	60 (66.7)	56 (57.7)	16 (59.3)	8 (40.0)	11 (50.0)	0.201
≥ 3.0	30 (33.3)	41 (42.3)	11 (40.7)	12 (60.0)	11 (50.0)	

CA 19-9 carbohydrate antigen 19-9, *CEA* carcinoembryonic antigen, *NLR* neutrophil to lymphocyte ratio. Data are n (%).

Table S3. Treatment outcomes by first-line chemotherapy regimen in the treated cohort and *KRAS* G12D/G12V subgroups

	Total (n = 245)			**G12D (n =85)**			**G12V (n = 88)**		
Variable	**Gem-based (n = 138)**	**5-FU based (n = 107)**	***p* value**	**Gem-based (n = 138)**	**5-FU based (n = 107)**	***p* value**	**Gem-based (n = 138)**	**5-FU based (n = 107)**	***p* value**
Objective response rate	52 (37.7)	35 (32.7)	0.50	21 (42.9)	12 (33.3)	0.50	15 (30.6)	15 (38.5)	0.50
Disease control rate	117 (84.8)	92 (86.0)	0.86	44 (89.8)	31 (86.1)	0.74	39 (79.6)	36 (92.3)	0.13
mPFS, months [95% CI]	5.8 [5.3–7.2]	7.8 [5.7–9.6]	0.12	5.8 [5.4–7.5]	6.9 [4.8–11.8]	0.45	5.3 [3.7–7.6]	8.3 [6.9–12.8]	0.01
6-months PFS rate, %	48.4 [40.5–57.9]	56.0 [47.2–66.5]		48.3 [35.8–65.3	50.0 [36.1–69.3]		41.6 [29.4–58.8]	68.0 [54.6–84.8]	
mOS, months, [95% CI]	9.7 [8.0–12.6]	13.1 [10.8–16.0]	0.08	10.5 [8.3–17.2]	13.1 [8.8–19.6]	0.93	6.6 [4.9–13.0]	14.8 [13.0–19.3]	0.01
12-months OS rate, %	41.4 [33.8–50.8]	56.3 [47.5–66.8]		47.7 [35.5–64.3]	57.6 [43.4–76.5]		36.6 [25.0–53.4]	66.4 [53.0–83.1]	

Gem-based gemcitabine-based; *5-FU-based* fluorouracil-based; m*PFS* median progression-free survival; m*OS* median overall survival. Data are n (%). PFS and OS rates are expressed as percentages with 95% confidence intervals.