CLAIMS:

1. A method for determining the likelihood that a patient has pancreatic ductal adenocarcinoma (PDAC), comprising:

(a) extracting a cell-free (cf)DNA sample from a blood sample obtained from the patient;

(b) sequencing the patient cfDNA in a manner that identifies 5-hydroxymethylcytosine (5hmC) containing sequences in the cfDNA;

(c) mapping the identified hydroxymethylated sequences to each of a plurality of reference loci comprising ADARB2-AS1, ANKRD36B, ASAH2B, ATG4B, ATP8B1, BOLA1, C11orf88, C17orf97, C1orf170, C3orf36, C8orf74, CAMSAP2, CCDC54, CCDC59, CKAP2, CLK2P, CRTC1, CSRP2, CYB5D1, DNAJC27, DYNAP, FAM166A, FAM188B, FAM196A, FAM86JP, FAT4, FBXO5, FGF2, FUT2, GAS2L2, GAS6, GGACT, GLRX5, GPX1, GPX5, HBD, HLA-A, HTR1F, IL36G, KANSL1, KCNH6, KCTD15, KLHL38, KLK2, KRT6B, LAMC1, LGALS14, LGALS8-AS1, LIFR, LINC00266-1, LINC00310, LOC100130452, LOC100130557, LOC100130894, LOC100288778, LOC100505633, LOC100505648, LOC100505738, LOC100652909, LOC389033, LOC90784, LRRC37A2, MED11, MRPL23-AS1, NAT8L, NEUROD1, NEUROG2, NME5, NOMO3, NPRL2, NXN, ODF3L1, ODF3L2, OSCP1, PARD6G, PGAM1, PLA2G2E, PLSCR4, PPAP2A, PPP1R15A, PPP1R3E, RASL10B, REXO1L1, RIMBP3, RNF126P1, RNU6-76, RPP25, RPS27, SH3PXD2B, SHISA4, SLC25A38, SLC4A1, SLCO5A1, SPDEF, SRSF6, STRA6, SYNM, TBCB, TDRD6, TEX26, TMEM253, TNFSF13B, TTC14, TUBA4A, UBB, VAMP8, VGLL2, WASH2P, WNT9B, XBP1, and ZNF789, wherein each reference locus:

(i) serves as a hydroxymethylation biomarker that exhibits at least a 1.5-fold differential 5hmC representation between PDAC samples and normal samples and a log2 [average 5hmC representation] of at least 4;

(ii) comprises a sequence contained within a gene feature selected from a 3'UTR, a TTS, an intron, and a promoter; and

(iii) is associated with a gene implicated in pancreatic development, with a gene related to cancer development, or with a gene established to exhibit increased or decreased hydroxymethylation density in PDAC;

(d) determining differences in extent of hydroxymethylation between the identified hydroxymethylated sequences in the patient cfDNA and the reference loci; and

(e) using the extent the differences in combination with at least one additional parameter correlated with a risk of developing PDAC, calculating a probability score representing the likelihood that the patient has or is at risk of developing PDAC.

2. The method of claim 1, wherein the at least one additional parameter is selected from lesion size; lesion location; presence or absence of pancreatic inflammation; jaundice; presence or absence of other symptoms; patient age; weight; gender; ethnicity; family history; genetic mutations; diabetes; physical activity; diet; pro-inflammatory cytokine levels; and smoking status of the patient.

3. The method of claim 1 or claim 2, further comprising one or more of the following loci:
GATA4, GATA6, PROX1, ONECUT2, YAP1, TEAD1, ONECUT2/ONECUT1-TCGA, IGF1, and *IGF2*.

4. The method of claim 1 or claim 2, wherein the patient has a germline mutation in a gene selected from *BRCA2, BRCA1, CDKN2A, ATM, STK11, PRSS1, MLH1, PALB2, KRAS, CDKN2A, TP53, SMAD4*, and combinations thereof.

5. The method of claim 1, wherein the patient has had an imaging scan in which a pancreatic lesion was identified and step (c) comprises generating an initial patient hydroxymethylation profile.

6. The method of claim 5, further including ascertaining a change in the pancreatic lesion by repeating steps (a) through (e) at a later time to generate a later patient hydroxymethylation profile and comparing the later hydroxymethylation profile with the initial patient hydroxymethylation profile to ascertain hydroxymethylation profile changes.

7. The method of claim 6, further including making a determination whether to implement a change in treatment of the patient based on the hydroxymethylation profile changes.

8. The method of any one of claims 1 to 7, wherein the probability score is calculated using a logistic regression analysis of the differences in hydroxymethylation level at each of the hydroxymethylation biomarkers.

9. The method of any one of claims 1 to 8, further including determining the likelihood that the individual has at least one additional type of cancer.

10. The method of claim 9, wherein the at least one additional type of cancer is selected from: bladder cancer; cancers of the blood and bone marrow; brain cancer; breast cancer; cervical cancer; colorectal cancer; esophageal cancer; liver cancer; lung cancer; ovarian cancer; prostate cancer; renal cancer; skin cancer; testicular cancer; thyroid cancer; and uterine cancer.