CLAIMS

1. A method, comprising:

using at least one computer hardware processor to perform:

obtaining RNA expression data and/or whole exome sequencing (WES) data for a biological sample from a subject;

determining a molecular-functional (MF) profile for the subject at least in part by determining, using the RNA expression data, a gene group expression level for each gene group in a set of gene groups, the set of gene groups comprising gene groups associated with cancer malignancy and different gene groups associated with cancer microenvironment,

wherein the gene groups associated with cancer malignancy comprise at least one gene group comprising at least three genes selected from the tumour properties group: MKI67, ESCO2, CETN3, CDK2, CCND1, CCNE1, AURKA, AURKB, CDK4, CDK6, PRC1, E2F1, MYBL2, BUB1, PLK1, CCNB1, MCM2, MCM6, PIK3CA, PIK3CB, PIK3CG, PIK3CD, AKT1, MTOR, PTEN, PRKCA, AKT2, AKT3, BRAF, FNTA, FNTB, MAP2K1, MAP2K2, MKNK1, MKNK2, ALK, AXL, KIT, EGFR, ERBB2, FLT3, MET, NTRK1, FGFR1, FGFR2, FGFR3, ERBB4, ERBB3, BCR-ABL, PDGFRA, PDGFRB, NGF, CSF3, CSF2, FGF7, IGF1, IGF2, IL7, FGF2, TP53, SIK1, PTEN, DCN, MTAP, AIM2, RB1, ESRP1, CTSL, HOXA1, SMARCA4, SNAI2, TWIST1, NEDD9, PAPPA, HPSE, KISS1, ADGRG1, BRMS1, TCF21, CDH1, PCDH10, NCAM1, MITF, APC, ARID1A, ATM, ATRX, BAP1, BRAF, BRCA2, CDH1, CDKN2A, CTCF, CTNNB1, DNMT3A, EGFR, FBXW7, FLT3, GATA3, HRAS, IDH1, KRAS, MAP3K1, MTOR, NAV3, NCOR1, NF1, NOTCH1, NPM1, NRAS, PBRM1, PIK3CA, PIK3R1, PTEN, RB1, RUNX1, SETD2, STAG2, TAF1, TP53, and VHL; and

wherein the gene groups associated with cancer microenvironment comprise:

at least one gene group comprising at least three genes selected from the anti-tumour microenvironment group: HLA-A, HLA-B, HLA-C, B2M, TAP1, TAP2, HLA-DRA, HLA-DRB1, HLA-DOB, HLA-DPB2, HLA-DMA, HLA-DOA, HLA-DPA1, HLA-DPB1, HLA-DMB, HLA-DQB1, HLA-DQA1, HLA-DRB5, HLA-DQA2, HLA-DQB2, HLA-DRB6, CD80, CD86, CD40, CD83, TNFRSF4, ICOSLG, CD28, IFNG, GZMA, GZMB, PRF1, LCK, GZMK, ZAP70, GNLY, FASLG, TBX21, EOMES, CD8A,

CD8B, NKG7, CD160, CD244, NCR1, KLRC2, KLRK1, CD226, GZMH, GNLY, IFNG, KIR2DL4, KIR2DS1, KIR2DS2, KIR2DS3, KIR2DS4, KIR2DS5, CXCL9, CXCL10, CXCR3, CX3CL1, CCR7, CXCL11, CCL21, CCL2, CCL3, CCL4, CCL5, EOMES, TBX21, ITK, CD3D, CD3E, CD3G, TRAC, TRBC1, TRBC2, LCK, UBASH3A, TRAT1, CD19, MS4A1, TNFRSF13C, CD27, CD24, CR2, TNFRSF17, TNFRSF13B, CD22, CD79A, CD79B, BLK, NOS2, IL12A, IL12B, IL23A, TNF, IL1B, SOCS3, IFNG, IL2, CD40LG, IL15, CD27, TBX21, LTA, IL21, HMGB1, TNF, IFNB1, IFNA2, CCL3, TNFSF10, and FASLG,

at least one gene group comprising at least three genes selected from the tumor-promoting immune microenvironment group: PDCD1, CD274, CTLA4, LAG3, PDCD1LG2, BTLA, HAVCR2, VSIR, CXCL12, TGFB1, TGFB2, TGFB3, FOXP3, CTLA4, IL10, TNFRSF1B, CCL17, CXCR4, CCR4, CCL22, CCL1, CCL2, CCL5, CXCL13, CCL28, IDO1, ARG1, IL4R, IL10, TGFB1, TGFB2, TGFB3, NOS2, CYBB, CXCR4, CD33, CXCL1, CXCL5, CCL2, CCL4, CCL8, CCR2, CCL3, CCL5, CSF1, CXCL8, CXCL8, CXCL2, CXCL1, CCL11, CCL24, KITLG, CCL5, CXCL5, CCR3, CCL26, PRG2, EPX, RNASE2, RNASE3, IL5RA, GATA1, SIGLEC8, PRG3, CMA1, TPSAB1, MS4A2, CPA3, IL4, IL5, IL13, SIGLEC8, MPO, ELANE, PRTN3, CTSG, IL10, VEGFA, TGFB1, IDO1, PTGES, MRC1, CSF1, LRP1, ARG1, PTGS1, MSR1, CD163, CSF1R, IL4, IL5, IL13, IL10, IL25, GATA3, IL10, TGFB1, TGFB2, TGFB3, IL22, MIF, CFD, CFI, CD55, CD46, and CR1,

at least one gene group comprising at least three genes selected from the fibroblast group: LGALS1, COL1A1, COL1A2, COL4A1, COL5A1, TGFB1, TGFB2, TGFB3, ACTA2, FGF2, FAP, LRP1, CD248, COL6A1, COL6A2, and COL6A3, and

at least one gene group comprising at least three genes selected from an angiogenesis group: VEGFA, VEGFB, VEGFC, PDGFC, CXCL8, CXCR2, FLT1, PIGF, CXCL5, KDR, ANGPT1, ANGPT2, TEK, VWF, CDH5, NOS3, KDR, VCAM1, MMRN1, LDHA, HIF1A, EPAS1, CA9, SPP1, LOX, SLC2A1, and LAMP3;

identifying, from among multiple MF profile clusters, an MF profile cluster with which to associate the MF profile for the subject, the MF profile clusters comprising:

a first MF profile cluster associated with inflamed and vascularized biological samples and/or inflamed and fibroblast-enriched biological samples,

a second MF profile cluster associated with inflamed and non-vascularized biological samples and/or inflamed and non-fibroblast-enriched biological samples,

a third MF profile cluster associated with non-inflamed and vascularized biological samples and/or non-inflamed and fibroblast-enriched biological samples, and

a fourth MF profile cluster associated with non-inflamed and non-vascularized biological samples and/or non-inflamed and non-fibroblast-enriched biological samples, and

identifying at least one first therapy for the subject based on the identified MF profile cluster;

wherein the MF profile clusters were generated by:

determining a plurality of MF profiles for a respective plurality of subjects using RNA expression data obtained from biological samples from the plurality of subjects, each of the plurality of MF profiles containing a gene group expression level for each gene group in the set of gene groups; and

clustering the plurality of MF profiles to obtain the MF profile clusters.

2. The method of claim 1, wherein the gene groups associated with cancer malignancy are: the proliferation rate group, the PI3K/AKT/mTOR signaling group, the RAS/RAF/MEK signaling group, the receptor tyrosine kinases expression group, the tumor suppressors group, the metastasis signature group, the anti-metastatic factors group, and the mutation status group; and

wherein determining the MF profile for the subject comprises determining a gene group expression level for each of the proliferation rate group, the PI3K/AKT/mTOR signaling group, the RAS/RAF/MEK signaling group, the receptor tyrosine kinases expression group, the tumor suppressors group, the metastasis signature group, the anti-metastatic factors group, and the mutation status group.

3. The method of claim 2, wherein

(a) the gene groups associated with cancer malignancy comprise:

a gene group comprising at least three genes selected from the proliferation rate group: MKI67, ESCO2, CETN3, CDK2, CCND1, CCNE1, AURKA, AURKB, CDK4, CDK6, PRC1, E2F1, MYBL2, BUB1, PLK1, CCNB1, MCM2, and MCM6;
a gene group comprising at least three genes selected from the PI3K/AKT/mTOR signaling group: PIK3CA, PIK3CB, PIK3CG, PIK3CD, AKT1, MTOR, PTEN, PRKCA, AKT2, and AKT3;
a gene group comprising at least three genes selected from the RAS/RAF/MEK signaling group: BRAF, FNTA, FNTB, MAP2K1, MAP2K2, MKNK1, and MKNK2;
a gene group comprising at least three genes selected from the receptor tyrosine kinases expression group: ALK, AXL, KIT, EGFR, ERBB2, FLT3, MET, NTRK1, FGFR1, FGFR2, FGFR3, ERBB4, ERBB3, BCR-ABL, PDGFRA, and PDGFRB;
a gene group comprising at least three genes selected from the tumor suppressors group: TP53, SIK1, PTEN, DCN, MTAP, AIM2, and RB1;
a gene group comprising at least three genes selected from the metastasis signature group: ESRP1, CTSL, HOXA1, SMARCA4, SNAI2, TWIST1, NEDD9, PAPPA, and HPSE;
a gene group comprising at least three genes selected from the anti-metastatic factors group: KISS1, ADGRG1, BRMS1, TCF21, CDH1, PCDH10, NCAM1, and MITF; and
a gene group comprising at least three genes selected from the mutation status group: APC, ARID1A, ATM, ATRX, BAP1, BRAF, BRCA2, CDH1, CDKN2A, CTCF, CTNNB1, DNMT3A, EGFR, FBXW7, FLT3, GATA3, HRAS, IDH1, KRAS, MAP3K1, MTOR, NAV3, NCOR1, NF1, NOTCH1, NPM1, NRAS, PBRM1, PIK3CA, PIK3R1, PTEN, RB1, RUNX1, SETD2, STAG2, TAF1, TP53, and VHL, and/or

(b) determining the MF profile comprises determining the gene group expression level for the proliferation rate group, the PI3K/AKT/mTOR signaling group, the RAS/RAF/MEK signaling group, the receptor tyrosine kinases expression group, the tumor suppressors group, the metastasis signature group, the anti-metastatic factors group, and the mutation status group using the gene expression level obtained from the RNA sequence data for at least three genes in each of the respective groups.

4. The method of claim 1 or any other preceding claim, wherein the gene groups associated with cancer microenvironment are: the antigen presentation group, the cytotoxic T and NK cells group, the B cells group, the anti-tumor microenvironment group, the checkpoint inhibition group, the Treg group, the MDSC group, the granulocytes group, the cancer associated fibroblasts group, the angiogenesis group, and the tumor-promotive

immune group; and wherein determining the MF profile for the subject comprises determining a gene group expression level for each of the antigen presentation group, the cytotoxic T and NK cells group, the B cells group, the anti-tumor microenvironment group, the checkpoint inhibition group, the Treg group, the MDSC group, the granulocytes group, the cancer associated fibroblasts group, the angiogenesis group, and the tumor-promotive immune group.

5. The method of claim 4, wherein:

(a) the gene groups associated with cancer microenvironment comprise:

a gene group comprising at least three genes selected from the cancer associated fibroblasts group: LGALS1, COL1A1, COL1A2, COL4A1, COL5A1, TGFB1, TGFB2, TGFB3, ACTA2, FGF2, FAP, LRP1, CD248, COL6A1, COL6A2, and COL6A3;

a gene group comprising at least three genes selected from the angiogenesis group: VEGFA, VEGFB, VEGFC, PDGFC, CXCL8, CXCR2, FLT1, PIGF, CXCL5, KDR, ANGPT1, ANGPT2, TEK, VWF, CDH5, NOS3, KDR, VCAM1, MMRN1, LDHA, HIF1A, EPAS1, CA9, SPP1, LOX, SLC2A1, and LAMP3;

a gene group comprising at least three genes selected from the antigen presentation group: HLA-A, HLA-B, HLA-C, B2M, TAP1, TAP2, HLA-DRA, HLA-DRB1, HLA-DOB, HLA-DPB2, HLA-DMA, HLA-DOA, HLA-DPA1, HLA-DPB1, HLA-DMB, HLA-DQB1, HLA-DQA1, HLA-DRB5, HLA-DQA2, HLA-DQB2, HLA-DRB6, CD80, CD86, CD40, CD83, TNFRSF4, ICOSLG, and CD28;

a gene group comprising at least three genes selected from the cytotoxic T and NK cells group: IFNG, GZMA, GZMB, PRF1, LCK, GZMK, ZAP70, GNLY, FASLG, TBX21, EOMES, CD8A, CD8B, NKG7, CD160, CD244, NCR1, KLRC2, KLRK1, CD226, GZMH, GNLY, IFNG, KIR2DL4, KIR2DS1, KIR2DS2, KIR2DS3, KIR2DS4, KIR2DS5, CXCL9, CXCL10, CXCR3, CX3CL1, CCR7, CXCL11, CCL21, CCL2, CCL3, CCL4, CCL5, EOMES, TBX21, ITK, CD3D, CD3E, CD3G, TRAC, TRBC1, TRBC2, LCK, UBASH3A, and TRAT1;

a gene group comprising at least three genes selected from the B cells group: CD19, MS4A1, TNFRSF13C, CD27, CD24, CR2, TNFRSF17, TNFRSF13B, CD22, CD79A, CD79B, and BLK;

a gene group comprising at least three genes selected from the anti-tumor microenvironment group: NOS2, IL12A, IL12B, IL23A, TNF, IL1B, SOCS3, IFNG, IL2, CD40LG, IL15, CD27, TBX21, LTA, IL21, HMGB1, TNF, IFNB1, IFNA2, CCL3, TNFSF10, and FASLG;

a gene group comprising at least three genes selected from the checkpoint inhibition group: PDCD1, CD274, CTLA4, LAG3, PDCD1LG2, BTLA, HAVCR2, and VSIR;
a gene group comprising at least three genes selected from the Treg group: CXCL12, TGFB1, TGFB2, TGFB3, FOXP3, CTLA4, IL10, TNFRSF1B, CCL17, CXCR4, CCR4, CCL22, CCL1, CCL2, CCL5, CXCL13, and CCL28;
the MDSC group: IDO1, ARG1, IL4R, IL10, TGFB1, TGFB2, TGFB3, NOS2, CYBB, CXCR4, CD33, CXCL1, CXCL5, CCL2, CCL4, CCL8, CCR2, CCL3, CCL5, CSF1, and CXCL8;
a gene group comprising at least three genes selected from the granulocytes group: CXCL8, CXCL2, CXCL1, CCL11, CCL24, KITLG, CCL5, CXCL5, CCR3, CCL26, PRG2, EPX, RNASE2, RNASE3, IL5RA, GATA1, SIGLEC8, PRG3, CMA1, TPSAB1, MS4A2, CPA3, IL4, IL5, IL13, SIGLEC8, MPO, ELANE, PRTN3, and CTSG;
a gene group comprising at least three genes selected from the tumor-promotive immune group: IL10, VEGFA, TGFB1, IDO1, PTGES, MRC1, CSF1, LRP1, ARG1, PTGS1, MSR1, CD163, CSF1R, IL4, IL5, IL13, IL10, IL25, GATA3, IL10, TGFB1, TGFB2, TGFB3, IL22, MIF, CFD, CFI, CD55, CD46, and CR1; and/or

(b) determining the MF profile comprises determining the gene group expression level for the cancer associated fibroblasts group, the angiogenesis group, the antigen presentation group, the cytotoxic T and NK cells group, the B cells group, the anti-tumor microenvironment group, the checkpoint inhibition group, the Treg group, the MDSC group, the granulocytes group, and the tumor-promotive immune group using the gene expression level obtained from the RNA sequence data for at least three genes in each of the respective groups.

6. The method of claim 1 or any other preceding claim,

(a) wherein the gene groups associated with cancer malignancy are: the proliferation rate group, the PI3K/AKT/mTOR signaling group, the RAS/RAF/MEK signaling group, the receptor tyrosine kinases expression group, the growth factors group, the tumor suppressors group, the metastasis signature group, the anti-metastatic factors group, and the mutation status group; and wherein determining the MF profile for the subject comprises determining a gene group expression level for each of the proliferation rate group, the PI3K/AKT/mTOR signaling group, the RAS/RAF/MEK signaling group, the receptor tyrosine kinases expression group, the growth factors group, the tumor suppressors group, the metastasis signature group, the anti-metastatic factors group, and the mutation status group; and/or

(b) wherein the gene groups associated with cancer microenvironment are: the cancer associated fibroblasts group, the angiogenesis group, the MHCI group, the MHCII group, the coactivation molecules group, the effector cells group, the NK cells group, the T cell traffic group, the T cells group, the B cells group, the M1 signatures group, the Th1 signature group, the antitumor cytokines group, the checkpoint inhibition group, the Treg group, the MDSC group, the granulocytes group, the M2 signature group, the Th2 signature group, the protumor cytokines group, and the complement inhibition group; and wherein determining the MF profile for the subject comprises determining a gene group expression level for each of the cancer associated fibroblasts group, the angiogenesis group, the MHCI group, the MHCII group, the coactivation molecules group, the effector cells group, the NK cells group, the T cell traffic group, the T cells group, the B cells group, the M1 signatures group, the Th1 signature group, the antitumor cytokines group, the checkpoint inhibition group, the Treg group, the MDSC group, the granulocytes group, the M2 signature group, the Th2 signature group, the protumor cytokines group, and the complement inhibition group.

7. The method of claim 6 or any other preceding claim, wherein:

(a) the gene groups associated with cancer malignancy comprise:

a gene group comprising at least three genes selected from the proliferation rate group: MKI67, ESCO2, CETN3, CDK2, CCND1, CCNE1, AURKA, AURKB, CDK4, CDK6, PRC1, E2F1, MYBL2, BUB1, PLK1, CCNB1, MCM2, and MCM6;

a gene group comprising at least three genes selected from the PI3K/AKT/mTOR signaling group: PIK3CA, PIK3CB, PIK3CG, PIK3CD, AKT1, MTOR, PTEN, PRKCA, AKT2, and AKT3;

a gene group comprising at least three genes selected from the RAS/RAF/MEK signaling group: BRAF, FNTA, FNTB, MAP2K1, MAP2K2, MKNK1, and MKNK2;

a gene group comprising at least three genes selected from the receptor tyrosine kinases expression group: ALK, AXL, KIT, EGFR, ERBB2, FLT3, MET, NTRK1, FGFR1, FGFR2, FGFR3, ERBB4, ERBB3, BCR-ABL, PDGFRA, and PDGFRB;

a gene group comprising at least three genes selected from the growth factors group: NGF, CSF3, CSF2, FGF7, IGF1, IGF2, IL7, and FGF2;

a gene group comprising at least three genes selected from the tumor suppressors group: TP53, SIK1, PTEN, DCN, MTAP, AIM2, and RB1;

a gene group comprising at least three genes selected from the metastasis signature group: ESRP1, CTSL, HOXA1, SMARCA4, SNAI2, TWIST1, NEDD9, PAPPA, and HPSE;

a gene group comprising at least three genes selected from the anti-metastatic factors group: KISS1, ADGRG1, BRMS1, TCF21, CDH1, PCDH10, NCAM1, and MITF; and

a gene group comprising at least three genes selected from the mutation status group: APC, ARID1A, ATM, ATRX, BAP1, BRAF, BRCA2, CDH1, CDKN2A, CTCF, CTNNB1, DNMT3A, EGFR, FBXW7, FLT3, GATA3, HRAS, IDH1, KRAS, MAP3K1, MTOR, NAV3, NCOR1, NF1, NOTCH1, NPM1, NRAS, PBRM1, PIK3CA, PIK3R1, PTEN, RB1, RUNX1, SETD2, STAG2, TAF1, TP53, and VHL; and/or

(b) the gene groups associated with cancer microenvironment comprise:

a gene group comprising at least three genes selected from the cancer associated fibroblasts group: LGALS1, COL1A1, COL1A2, COL4A1, COL5A1, TGFB1, TGFB2, TGFB3, ACTA2, FGF2, FAP, LRP1, CD248, COL6A1, COL6A2, and COL6A3;

a gene group comprising at least three genes selected from the angiogenesis group: VEGFA, VEGFB, VEGFC, PDGFC, CXCL8, CXCR2, FLT1, PIGF, CXCL5, KDR, ANGPT1, ANGPT2, TEK, VWF, CDH5, NOS3, KDR, VCAM1, MMRN1, LDHA, HIF1A, EPAS1, CA9, SPP1, LOX, SLC2A1, and LAMP3;

a gene group comprising at least three genes selected from the MHCI group: HLA-A, HLA-B, HLA-C, B2M, TAP1, and TAP2;

a gene group comprising at least three genes selected from the MHCII group: HLA-DRA, HLA-DRB1, HLA-DOB, HLA-DPB2, HLA-DMA, HLA-DOA, HLA-DPA1, HLA-DPB1, HLA-DMB, HLA-DQB1, HLA-DQA1, HLA-DRB5, HLA-DQA2, HLA-DQB2, and HLA-DRB6;

a gene group comprising at least three genes selected from the coactivation molecules group: CD80, CD86, CD40, CD83, TNFRSF4, ICOSLG, and CD28;

a gene group comprising at least three genes selected from the effector cells group: IFNG, GZMA, GZMB, PRF1, LCK, GZMK, ZAP70, GNLY, FASLG, TBX21, EOMES, CD8A, and CD8B;

a gene group comprising at least three genes selected from the NK cells group: NKG7, CD160, CD244, NCR1, KLRC2, KLRK1, CD226, GZMH, GNLY, IFNG, KIR2DL4, KIR2DS1, KIR2DS2, KIR2DS3, KIR2DS4, and KIR2DS5;

a gene group comprising at least three genes selected from the T cell traffic group: CXCL9, CXCL10, CXCR3, CX3CL1, CCR7, CXCL11, CCL21, CCL2, CCL3, CCL4, and CCL5;

a gene group comprising at least three genes selected from the T cells group: EOMES, TBX21, ITK, CD3D, CD3E, CD3G, TRAC, TRBC1, TRBC2, LCK, UBASH3A, and TRAT1;

a gene group comprising at least three genes selected from the B cells group: CD19, MS4A1, TNFRSF13C, CD27, CD24, CR2, TNFRSF17, TNFRSF13B, CD22, CD79A, CD79B, and BLK;

a gene group comprising at least three genes selected from the M1 signatures group: NOS2, IL12A, IL12B, IL23A, TNF, IL1B, and SOCS3;

a gene group comprising at least three genes selected from the Th1 signature group: IFNG, IL2, CD40LG, IL15, CD27, TBX21, LTA, and IL21;

a gene group comprising at least three genes selected from the antitumor cytokines group: HMGB1, TNF, IFNB1, IFNA2, CCL3, TNFSF10, and FASLG;

a gene group comprising at least three genes selected from the checkpoint inhibition group: PDCD1, CD274, CTLA4, LAG3, PDCD1LG2, BTLA, HAVCR2, and VSIR;

a gene group comprising at least three genes selected from the Treg group: CXCL12, TGFB1, TGFB2, TGFB3, FOXP3, CTLA4, IL10, TNFRSF1B, CCL17, CXCR4, CCR4, CCL22, CCL1, CCL2, CCL5, CXCL13, and CCL28;

a gene group comprising at least three genes selected from the MDSC group: IDO1, ARG1, IL4R, IL10, TGFB1, TGFB2, TGFB3, NOS2, CYBB, CXCR4, CD33, CXCL1, CXCL5, CCL2, CCL4, CCL8, CCR2, CCL3, CCL5, CSF1, and CXCL8;

a gene group comprising at least three genes selected from the granulocytes group: CXCL8, CXCL2, CXCL1, CCL11, CCL24, KITLG, CCL5, CXCL5, CCR3, CCL26, PRG2, EPX, RNASE2, RNASE3, IL5RA, GATA1, SIGLEC8, PRG3, CMA1, TPSAB1, MS4A2, CPA3, IL4, IL5, IL13, SIGLEC8, MPO, ELANE, PRTN3, and CTSG;

a gene group comprising at least three genes selected from the M2 signature group: IL10, VEGFA, TGFB1, IDO1, PTGES, MRC1, CSF1, LRP1, ARG1, PTGS1, MSR1, CD163, and CSF1R;

a gene group comprising at least three genes selected from the Th2 signature group: IL4, IL5, IL13, IL10, IL25, and GATA3;

a gene group comprising at least three genes selected from the protumor cytokines group: IL10, TGFB1, TGFB2, TGFB3, IL22, and MIF; and

a gene group comprising at least three genes selected from the complement inhibition group: CFD, CFI, CD55, CD46, and CR1.

8. The method of claim 7 or any other preceding claim, wherein determining the MF profile comprises:

(a) determining the gene group expression level for the proliferation rate group, the PI3K/AKT/mTOR signaling group, the RAS/RAF/MEK signaling group, the receptor tyrosine kinases expression group, the growth factors group, the tumor suppressors group, the metastasis signature group, the anti-metastatic factors group and the mutation status group using the gene expression level obtained from the RNA sequence data for at least three genes in each of the respective groups; and/or

(b) determining the gene group expression level for the cancer associated fibroblasts group, the angiogenesis group, the MHCI group, the MHCII group, the coactivation molecules group, the effector cells group, the NK cells group, the T cell traffic group, the T cells group, the B cells group, the M1 signatures group, the Th1 signature group, the antitumor cytokines group, the checkpoint inhibition group, the Treg group, the MDSC group, the granulocytes group, the M2 signature group, the Th2 signature group, the protumor cytokines group and the complement inhibition group using the gene expression level obtained from the RNA sequence data for at least three genes in each of the respective groups.

9. The method of claim 1 or any other preceding claim, wherein identifying the at least one therapy comprises identifying at least one therapy selected:

(a) from the group consisting of: chemotherapy, antibody drug conjugates, hormonal therapy, viral therapy, genetic therapy, non-immune protein therapy, antiangiogenic agents, anti-cancer vaccines, radiotherapy, soluble receptor therapy, cell based therapies, immunotherapy, and targeted therapy; and/or

(b) from the group consisting of: HGFR inhibitors, EGFR inhibitors, VEGF inhibitors, PDGF inhibitors, CXR2 inhibitors, CXCR4 inhibitors, DPP-4 inhibitors, galectin inhibitors, antifibrotic agents, LPR1 inhibitors, TGF-beta inhibitors, IL5 inhibitors, IL4 inhibitors, IL13 inhibitors, IL22 inhibitors, CSF1R inhibitors, IDO inhibitors, LPR1 inhibitors, CD25 inhibitors, GITR inhibitors, PD1 inhibitors, CTLA1 inhibitors, PDL1 inhibitors, LAG3 inhibitors, TIM3 inhibitors, vaccines, PRIMA-1 analogues, CD40 agonists, ICOS agonists, OX40 agonists, Bcl-2 inhibitors, AKT inhibitors, MYC-targeting siRNA, pan-tyrosine kinase inhibitors, CDK4/6 inhibitors, Aurora A inhibitors, vaccines, LAG3 inhibitors, and any antibody-drug conjugate; and/or

(c) from the group consisting of: HGFR inhibitors, EGFR inhibitors, VEGF inhibitors, PDGF inhibitors, CXR2 inhibitors, galectin inhibitors, antifibrotic agents, LPR1 inhibitors, TGF-beta inhibitors, IL5 inhibitors, IL4 inhibitors, IL13 inhibitors, IL22 inhibitors, CSF1R inhibitors, IDO inhibitors, CXCR4 inhibitors, CD25 inhibitors, GITR inhibitors, PD1 inhibitors, CTLA1 inhibitors, PDL1 inhibitors, LAG3 inhibitors, TIM3 inhibitors, and vaccines; and/or

(d) from the group consisting of: HGFR inhibitors, EGFR inhibitors, PRIMA-1 analogues, TGF-beta inhibitors, IL22 inhibitors, CSF1R inhibitors, IDO inhibitors, LPR1 inhibitors, CXCR4 inhibitors, CD25 inhibitors, GITR inhibitors, CD40 agonists, ICOS agonists, OX40 agonists, and vaccines; and/or

(e) from the group consisting of: Bcl-2 inhibitors, AKT inhibitors, MYC-targeting siRNA, PRIMA-1 analogues, VEGF inhibitors, PDGF inhibitors, CXR2 inhibitors, galectin inhibitors, antifibrotic agents, LPR1 inhibitors, TGF-beta inhibitors, IL5 inhibitors, IL4 inhibitors, IL13 inhibitors, CSF1R inhibitors, IDO inhibitors, CXCR4 inhibitors, and vaccines; and/or

(f) from the group consisting of: antibody-drug conjugates, HGFR inhibitors, EGFR inhibitors, VEGF inhibitors, PDGF inhibitors, CXCR2 inhibitors, galectin inhibitors, antifibrotic agents, LPR1 inhibitors, TGF-beta inhibitors, IL22 inhibitors, and CXCL10 disrupting inhibitors; and/or

(g) from the group consisting of: Bcl-2 inhibitors, AKT inhibitors, MYC-targeting siRNA, chemotherapy, pan-tyrosine kinase inhibitors, CDK4/6 inhibitors, Aurora A inhibitors, and DPP-4 inhibitors.

10. The method of claim 1 or any other preceding claim, wherein:

(i) obtaining the RNA expression data is performed using whole transcriptome sequencing or mRNA sequencing, and/or

(ii) the WES data is used to quantify tumor burden (purity), identify specific mutations, and/or to calculate the number of neoantigens, and/or

(iii) each of the biological samples is from a tumor or tissue known or suspected of having cancerous cells.

11. The method of claim 1 or any other preceding claim, further comprising using the at least one computer hardware processor to perform:
generating the MF profile clusters, the generating comprising:

(a) obtaining RNA expression data from biological samples obtained from a plurality of subjects;

determining a respective plurality of MF profiles for the plurality of subjects, each of the plurality of MF profiles containing a gene group expression level for each gene group in the set of gene groups; and

clustering the plurality of MF profiles to obtain the MF profile clusters; or

(b) obtaining RNA expression data and/or whole exome sequencing (WES) data from biological samples from a plurality of subjects, at least some of the subjects having a cancer of a particular type;

determining a respective plurality of molecular-functional (MF) profiles for the plurality of subjects at least in part by, for each of the plurality of subjects, determining, using the RNA expression data, a respective gene group expression level for each group in the set of gene groups;

clustering the plurality of MF profiles to obtain the MF profile clusters; and

storing the plurality of MF profiles in association with information identifying the particular cancer type.

12. The method of claim 11, wherein clustering the plurality of MF profiles is performed by using a k-means clustering technique.

13. The method of any of claims 1 to 10, further comprising using the at least one computer hardware processor to perform: accessing information stored in one or more databases, the information comprising the MF profile clusters.

14. The method of claim 1 or any other preceding claim, further comprises using the at least one computer hardware processor to perform:

determining at least one visual characteristic of a first graphical user interface (GUI) element using a first gene group expression level for at least one gene group associated with cancer malignancy and at least one visual characteristic of a second GUI element using a second gene group expression level for at least one gene group associated with cancer microenvironment;

generating a personalized GUI personalized to the subject, the GUI comprising:

a first portion associated with cancer malignancy and containing the first GUI element; and

a second portion associated with cancer microenvironment and containing the second GUI element, wherein the second portion is different from the first portion; and

presenting the generated personalized GUI to a user.

15. The method of claim 14, wherein determining the at least one visual characteristic of the first GUI element comprises determining size and/or color of the first GUI element using the first gene group expression level; and/or

wherein the first portion comprises a first plurality of GUI elements representing a respective plurality of gene groups associated with cancer malignancy; and/or

wherein the second portion comprises a second plurality of GUI elements representing a respective plurality of gene groups associated with cancer microenvironment.

16. The method of claim 1 or any other preceding claim, wherein determining the MF profile for the subject comprises:

determining a first gene group expression level for a first gene group of the gene groups associated with cancer malignancy and for a second gene group of the gene groups associated with cancer microenvironment using a gene set enrichment analysis (GSEA) technique.

17. The method of claim 1 or any other preceding claim, wherein determining the MF profile for the subject comprises:

determining a first gene group expression level for a first gene group of the gene groups associated with cancer malignancy and for a second gene group of the gene groups associated with cancer microenvironment using a mutation count technique.

18. A system, comprising:

at least one computer hardware processor; and

at least one non-transitory computer-readable storage medium storing processor-executable instructions that, when executed by the at least one computer hardware processor, cause the at least one computer hardware processor to perform the method of any of claims 1 to 17.

19. At least one non-transitory computer-readable storage medium storing processor-executable instructions that, when executed by the at least one computer hardware processor, cause the at least one computer hardware processor to perform the method of any of claims 1 to 17.