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62/572,979 16 October 2017 (16.10.2017) US(71) Applicant (for all designated States except AL, AT, BA, BE, BG, CH, CN, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IN, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR): **GENEN-TECH, INC.** [US/US]; 1 DNA Way, South San Francisco, CA 94080-4990 (US).(71) Applicant (for AL, AT, BA, BE, BG, CH, CN, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IN, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR only): **F. HOFFMANN-LA ROCHE AG** [CH/CH]; Grenzacherstrasse 124, 4070 Basel (CH).(72) Inventors: **HEGDE, Priti**; 1 DNA Way, South San Francisco, CA 94080-4990 (US). **HUSENI, Mahrukh**; 1 DNA Way, South San Francisco, CA 94080-4990 (US).(74) Agent: **ELBING, Karen, L.**; Clark & Elbing LLP, 101 Federal Street, 15th Floor, Boston, MA 02110 (US).

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(54) Title: DIAGNOSTIC AND THERAPEUTIC METHODS FOR CANCER

(57) Abstract: The present invention provides diagnostic methods, therapeutic methods, and compositions for the treatment of cancer (e.g., kidney cancer (e.g., renal cell carcinoma (RCC)), lung cancer (e.g., non-small cell lung cancer (NSCLC)), bladder cancer (e.g., urothelial bladder cancer (UBC)), liver cancer (e.g., hepatocellular carcinoma (HCC)), ovarian cancer, or breast cancer (e.g., triple-negative breast cancer (TNBC))). The invention is based, at least in part, on the discovery that expression levels of one or more biomarkers described herein in a sample from an individual having cancer can be used in methods of predicting the therapeutic efficacy of treatment with a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., anti-PD-1 antibody)), or with an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))).

DIAGNOSTIC AND THERAPEUTIC METHODS FOR CANCER

SEQUENCE LISTING

5 The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on February 28, 2018, is named 50474-164WO4_Sequence_Listing_02.28.18_ST25 and is 235,647 bytes in size.

FIELD OF THE INVENTION

10 The present invention is directed to diagnostic and therapeutic methods for the treatment of cancer. Also provided are related kits and assays.

BACKGROUND OF THE INVENTION

15 Cancer remains one of the most deadly threats to human health. In the U.S., cancer affects nearly 1.3 million new patients each year and is the second leading cause of death after heart disease, accounting for approximately 1 in 4 deaths. It is also predicted that cancer may surpass cardiovascular diseases as the number one cause of death within 5 years. Solid tumors are responsible for most of those deaths. Although there have been significant advances in the medical treatment of certain cancers, the overall 5-year survival rate for all cancers has improved only by about 10% in the past 20 years. Malignant solid tumors, in particular, metastasize and grow rapidly in an uncontrolled manner, making
20 their timely detection and treatment extremely difficult.

Studies in humans with immune checkpoint inhibitors have demonstrated the promise of harnessing the immune system to control and eradicate tumor growth. The programmed death 1 (PD-1) receptor and its ligand programmed death-ligand 1 (PD-L1) are immune checkpoint proteins that have been implicated in the suppression of immune system responses during chronic infections, pregnancy,
25 tissue allografts, autoimmune diseases, and cancer. PD-L1 regulates the immune response by binding to the inhibitory receptor PD-1, which is expressed on the surface of T-cells, B-cells, and monocytes. PD-L1 negatively regulates T-cell function also through interaction with another receptor, B7-1. Formation of the PD-L1/PD-1 and PD-L1/B7-1 complexes negatively regulates T-cell receptor signaling, resulting in the subsequent downregulation of T-cell activation and suppression of anti-tumor immune activity.

30 Despite the significant advancement in the treatment of cancer, improved diagnostic methods and cancer therapies are still being sought.

SUMMARY OF THE INVENTION

35 The present invention provides diagnostic and therapeutic methods and compositions for treating an individual having a cancer (e.g., a kidney cancer (e.g., a renal cell carcinoma (RCC)), a lung cancer (e.g., a non-small cell lung cancer (NSCLC)), a bladder cancer (e.g., a urothelial bladder cancer (UBC)), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., a triple-negative breast cancer (TNBC))).

40 In one aspect, the invention features a method of identifying an individual having a kidney cancer who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1

axis binding antagonist, the method comprising determining the expression level of one or more of the following genes in a sample from the individual: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9; wherein (i) an expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample that is at or above a reference expression level of the one or more genes; or (ii) an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample that is below a reference expression level of the one or more genes identifies the individual as one who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist.

In another aspect, the invention features a method for selecting a therapy for an individual having a kidney cancer, the method comprising determining the expression level of one or more of the following genes in a sample from the individual: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9; wherein (i) an expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample that is at or above a reference expression level of the one or more genes; or (ii) an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample that is below a reference expression level of the one or more genes identifies the individual as one who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist.

In some embodiments of any of the preceding aspects, the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is at or above a reference expression level of the one or more genes, and the method further comprises administering to the individual an effective amount of the anti-cancer therapy. In some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 in the sample is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1. In some embodiments, the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2,

S100A8, or S100A9 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample is at or above a reference expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding aspects, the expression level of PD-L1 in the sample is at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 in the sample is at or above a reference expression level of the one or more additional genes.

In some embodiments of any of the preceding aspects, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes, and the method further comprises administering to the individual an effective amount of the anti-cancer therapy. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is below a reference level of the one or more genes, and the method further comprises administering to the individual an effective amount of the anti-cancer therapy.

In some embodiments of any of the preceding aspects, the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is below a reference level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample is below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding aspects, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is at or above a reference level of the one or more genes, and the method further comprises administering to the individual an effective amount of an anti-cancer therapy comprising a VEGF antagonist. In some embodiments, the anti-cancer therapy further comprises a PD-L1 axis binding antagonist. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 is at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1,

ANGPTL4, or CD34 in the sample is at or above a reference level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In another aspect, the invention features a method of treating an individual having a kidney cancer, the method comprising: (a) determining the expression level of one or more of the following genes in a sample from the individual: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9; wherein (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference expression level of the one or more genes; or (ii) the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be below a reference expression level of the one or more genes; and (b) administering an effective amount of an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist to the individual based on the expression level of the one or more genes determined in step (a).

In some embodiments of any of the preceding aspects, the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 in the sample is determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1. In some embodiments, the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample is determined to be at or above a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding aspects, the expression level of PD-L1 in the sample is determined to be at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference expression level of the one or more additional genes.

In some embodiments of any of the preceding aspects, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments of any of the preceding aspects, the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample is determined to be below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In another aspect, the invention provides a method of treating an individual having a kidney cancer, the method comprising administering to the individual an effective amount of an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist, wherein prior to treatment (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more genes; or (ii) the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be below a reference expression level of the one or more genes.

In some embodiments of any of the preceding aspects, the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least

sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 in the sample has been determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1. In some embodiments, the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 has been determined to be at or above a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments, the expression level of PD-L1 in the sample has been determined to be at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more additional genes.

In some embodiments of any of the preceding aspects, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be below a reference level of the one or more genes.

In some embodiments of any of the preceding aspects, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample has been determined to be below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In another aspect, the invention features a method of treating an individual having a kidney cancer, the method comprising: (a) determining the expression level of one or more of the following genes in a sample from the individual: VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be at or above a reference expression level of the one or more genes; and (b) administering an effective amount of an anti-cancer therapy comprising a VEGF antagonist to the individual based on the expression level of the one or more genes determined in step (a). In some embodiments, the anti-cancer therapy further comprises a PD-L1 axis binding antagonist. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is determined to be at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In another aspect, the invention features a method of treating an individual having a kidney cancer, the method comprising administering to the individual an effective amount of an anti-cancer therapy comprising VEGF antagonist, wherein prior to treatment the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the anti-cancer therapy further comprises a PD-L1 axis binding antagonist. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments of any of the preceding aspects, the reference level of the one or more genes is determined from a population of individuals having a kidney cancer. In some embodiments, the reference level of the one or more genes is a median expression level determined in a population of patients having a kidney cancer. In some embodiments, the reference level is a median of a Z-score of the normalized expression level of the one or more genes.

In some embodiments of any of the preceding aspects, the expression level is a nucleic acid expression level. In some embodiments, the nucleic acid expression level is an mRNA expression level. In some embodiments, the mRNA expression level is determined by RNA-seq, RT-qPCR, qPCR, multiplex qPCR or RT-qPCR, microarray analysis, SAGE, MassARRAY technique, ISH, or a combination thereof.

In other embodiments of any of the preceding aspects, the expression level is a protein expression level. In some embodiments, the protein expression level is determined by immunohistochemistry (IHC), Western blot, enzyme-linked immunosorbent assay (ELISA), immunoprecipitation, immunofluorescence, radioimmunoassay, or mass spectrometry.

In some embodiments of any of the preceding aspects, the sample is a tissue sample, a cell sample, a whole blood sample, a plasma sample, a serum sample, or a combination thereof. In some embodiments, the tissue sample is a tumor tissue sample. In some embodiments, the tumor tissue sample comprises tumor cells, tumor-infiltrating immune cells, stromal cells, or a combination thereof. In some embodiments, the tumor tissue sample is a formalin-fixed and paraffin-embedded (FFPE) sample, an archival sample, a fresh sample, or a frozen sample.

In some embodiments of any of the preceding aspects, the individual has not been previously treated for the kidney cancer. In some embodiments, the kidney cancer is renal cell carcinoma (RCC). In some embodiments, the RCC is metastatic RCC (mRCC).

In some embodiments of any of the preceding aspects, the VEGF antagonist is an anti-VEGF antibody or a VEGF receptor (VEGFR) inhibitor. In some embodiments, the VEGF antagonist is an anti-VEGF antibody. In some embodiments, the anti-VEGF antibody is bevacizumab. In some embodiments, the VEGF antagonist is a VEGFR inhibitor. In some embodiments, the VEGFR inhibitor is a multi-targeted tyrosine kinase inhibitor. In some embodiments, the multi-targeted tyrosine kinase inhibitor is sunitinib, axitinib, pazopanib, or cabozantinib. In some embodiments, the multi-targeted tyrosine kinase inhibitor is sunitinib.

In some embodiments of any of the preceding aspects, the PD-L1 axis binding antagonist is selected from the group consisting of a PD-L1 binding antagonist, a PD-1 binding antagonist, and a PD-L2 binding antagonist. In some embodiments, the PD-L1 axis binding antagonist is a PD-L1 binding antagonist. In some embodiments, the PD-L1 binding antagonist inhibits the binding of PD-L1 to one or more of its ligand binding partners. In some embodiments, the PD-L1 binding antagonist inhibits the binding of PD-L1 to PD-1. In some embodiments, the PD-L1 binding antagonist inhibits the binding of PD-L1 to B7-1. In some embodiments, the PD-L1 binding antagonist inhibits the binding of PD-L1 to both PD-1 and B7-1. In some embodiments, the PD-L1 binding antagonist is an anti-PD-L1 antibody. In some embodiments, the anti-PD-L1 antibody is selected from the group consisting of: MPDL3280A (atezolizumab), YW243.55.S70, MDX-1105, MEDI4736 (durvalumab), and MSB0010718C (avelumab). In some embodiments, the anti-PD-L1 antibody comprises the following hypervariable regions (HVRs): (a) an HVR-H1 sequence of GFTFSDSWIH (SEQ ID NO: 63); (b) an HVR-H2 sequence of AWISPYGGSTYYADSVKKG (SEQ ID NO: 64); (c) an HVR-H3 sequence of RHWPGGFDY (SEQ ID NO: 65); (d) an HVR-L1 sequence of RASQDVSTAVA (SEQ ID NO: 66); (e) an HVR-L2 sequence of SASFLYS (SEQ ID NO: 67); and (f) an HVR-L3 sequence of QQYLYHPAT (SEQ ID NO: 68). In some embodiments, the anti-PD-L1 antibody comprises: (a) a heavy chain variable (VH) domain comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of EVQLVESGGGLVQPGLSLRLSCAASGFTFSDSWIHWWRQAPGKGLEWVAWISPYGGSTYYADSVKGRF TISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGGQGLTVTVSS (SEQ ID NO: 69);

(b) a light chain variable (VL) domain comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of

DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTD
FTLTISLQPEDFATYYCQYLYHPATFGGQTKVEIKR (SEQ ID NO: 70); or (c) a VH domain as in (a)

and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 69; (b) a VL domain comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a) and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising an amino

acid sequence having at least 96% sequence identity to the amino acid sequence of SEQ ID NO: 69;

(b) a VL domain comprising an amino acid sequence having at least 96% sequence identity to the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a) and a VL domain as in (b). In some

embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising an amino acid sequence having at least 97% sequence identity to the amino acid sequence of SEQ ID NO: 69; (b) a VL domain

comprising an amino acid sequence having at least 97% sequence identity to the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a) and a VL domain as in (b). In some embodiments, the anti-

PD-L1 antibody comprises: (a) a VH domain comprising an amino acid sequence having at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 69; (b) a VL domain comprising an amino acid sequence having at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 70; or

(c) a VH domain as in (a) and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising an amino acid sequence having at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 69; (b) a VL domain comprising an amino acid sequence having at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a)

and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising the amino acid sequence of SEQ ID NO: 69; (b) a VL domain comprising the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a) and a VL domain as in (b). In some

embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising the amino acid sequence of SEQ ID NO: 69; and (b) a VL domain comprising the amino acid sequence of SEQ ID NO: 70. In some embodiments, the anti-PD-L1 antibody is atezolizumab.

In some embodiments of any of the preceding aspects, the method further comprises administering an additional therapeutic agent to the individual. In some embodiments, the additional therapeutic agent is selected from the group consisting of an immunotherapy agent, a cytotoxic agent, a growth inhibitory agent, a radiation therapy agent, an anti-angiogenic agent, and combinations thereof.

In some embodiments of any of the preceding aspects, the individual is a human.

In another aspect, the invention features a kit for identifying an individual having a kidney cancer who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist, the kit comprising: (a) reagents for determining the expression level of

determining the expression level of one or more of the following genes in a sample from the individual: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1,

CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1,

ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9; and, optionally, (b) instructions for using the reagents to identify an individual having a kidney cancer who may benefit from a treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist.

5 In some embodiments of the preceding aspect, the kit comprises reagents for determining the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2. In some embodiments, the kit comprises reagents for determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, 10 at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2. In some embodiments, the kit comprises reagents for determining the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1. In some embodiments, the kit comprises 15 reagents for determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1. In some embodiments, the kit comprises reagents for determining the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. In some embodiments, the kit comprises reagents for determining the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, 20 CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. In some embodiments, the kit comprises reagents for determining the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of the preceding aspect, the kit comprises reagents for determining the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. In some 25 embodiments, the kit comprises reagents for determining the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. In some embodiments, the kit comprises reagents for determining the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the kit comprises reagents for determining the expression level of VEGFA, KDR, ESM1, PECAM1, 30 ANGPTL4, and CD34.

In some embodiments of the preceding aspect, the kit comprises reagents for determining the expression level of PD-L1 and one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2.

35 In another aspect, the invention features a kit for identifying an individual having a kidney cancer who may benefit from treatment with a VEGF antagonist, the kit comprising: (a) reagents for determining the expression level of determining the expression level of one or more of the following genes in a sample from the individual: VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; and, optionally, (b) instructions for using the reagents to identify an individual having a kidney cancer who may benefit from a 40 treatment with an anti-cancer therapy comprising a VEGF antagonist. In some embodiments, the anti-

cancer therapy further comprises a PD-L1 axis binding antagonist. In some embodiments, the kit comprises reagents for determining the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. In some embodiments, the kit comprises reagents for determining the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the kit comprises reagents for determining the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In another aspect, the invention features an assay for identifying an individual having a kidney cancer who is a candidate for treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist, the assay comprising determining the expression level of one or more of the following genes in a sample from the individual: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9; wherein (i) an expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample that is above a reference expression level of the one or more genes; or (ii) an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample that is below a reference expression level of the one or more genes identifies the individual as one who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist.

In some embodiments of any of the preceding aspects, the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, or PD-L1. In some embodiments, the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8,

PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample is at or above a reference expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding aspects, the expression level of PD-L1 in the sample is at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is at or above a reference expression level of the one or more additional genes.

In some embodiments of any of the preceding aspects, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments of any of the preceding aspects, the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is below a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is below a reference level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample is below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In another aspect, the invention features an assay for identifying an individual having a kidney cancer who is a candidate for treatment comprising a VEGF antagonist, the assay comprising determining the expression level of one or more of the following genes in a sample from the individual: VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34, wherein an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample that is above a reference expression level of the one or more genes identifies the individual as one who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist. In some embodiments, the anti-cancer therapy further comprises a PD-L1 axis binding antagonist.

In some embodiments of the preceding aspect, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is above a reference level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In another aspect, the invention features an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use in a method of treating an individual suffering from a kidney cancer, wherein prior to treatment (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in a sample from the individual has been determined to be above a reference expression level of the one or more genes; or (ii) the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in a sample from the individual has been determined to be below a reference expression level of the one or more genes.

In another aspect, the invention provides for the use of an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist in the manufacture of a medicament for treating an individual suffering from a kidney cancer, wherein prior to treatment (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in a sample from the individual has been determined to be above a reference expression level of the one or more genes; or (ii) the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in a sample from the individual has been determined to be below a reference expression level of the one or more genes.

In some embodiments of any of the preceding aspects, the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1. In some embodiments, the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 has been determined to be at or above a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding aspects, the expression level of PD-L1 in the sample has been determined to be at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more additional genes.

In some embodiments of any of the preceding aspects, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments of any of the preceding aspects, the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample has been determined to be below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In another aspect, the invention features a VEGF antagonist for use in a method of treating an individual suffering from a kidney cancer, wherein prior to treatment the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in a sample from the individual has been determined to be above a reference expression level of the one or more genes. In some embodiments, the VEGF antagonist is formulated for use in combination with a PD-L1 axis binding antagonist.

In another aspect, the invention provides for the use of a VEGF antagonist in the manufacture of a medicament for treating an individual suffering from a kidney cancer, wherein prior to treatment the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in a sample from the individual has been determined to be above a reference expression level of the one or more genes. In some embodiments, the medicament is formulated for use in combination with a PD-L1 axis binding antagonist.

In some embodiments of any of the preceding aspects, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA,

KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments of any of the preceding aspects, the VEGF antagonist is an anti-VEGF antibody or a VEGF receptor (VEGFR) inhibitor. In some embodiments, the VEGF antagonist is an anti-VEGF antibody. In some embodiments, the anti-VEGF antibody is bevacizumab. In some embodiments, the VEGF antagonist is a VEGFR inhibitor. In some embodiments, the VEGFR inhibitor is a multi-targeted tyrosine kinase inhibitor. In some embodiments, the multi-targeted tyrosine kinase inhibitor is sunitinib, axitinib, pazopanib, or cabozantinib. In some embodiments, the multi-targeted tyrosine kinase inhibitor is sunitinib.

In some embodiments of any of the preceding aspects, the PD-L1 axis binding antagonist is selected from the group consisting of a PD-L1 binding antagonist, a PD-1 binding antagonist, and a PD-L2 binding antagonist. In some embodiments, the PD-L1 axis binding antagonist is a PD-L1 binding antagonist. In some embodiments, the PD-L1 binding antagonist inhibits the binding of PD-L1 to one or more of its ligand binding partners. In some embodiments, the PD-L1 binding antagonist inhibits the binding of PD-L1 to PD-1. In some embodiments, the PD-L1 binding antagonist inhibits the binding of PD-L1 to B7-1. In some embodiments, the PD-L1 binding antagonist inhibits the binding of PD-L1 to both PD-1 and B7-1. In some embodiments, the PD-L1 binding antagonist is an anti-PD-L1 antibody. In some embodiments, the anti-PD-L1 antibody is selected from the group consisting of: MPDL3280A (atezolizumab), YW243.55.S70, MDX-1105, MEDI4736 (durvalumab), and MSB0010718C (avelumab). In some embodiments, the anti-PD-L1 antibody comprises the following hypervariable regions (HVRs): (a) an HVR-H1 sequence of GFTFSDSWIH (SEQ ID NO: 63); (b) an HVR-H2 sequence of AWISPYGGSTYYADSVKVG (SEQ ID NO: 64); (c) an HVR-H3 sequence of RHWPGGFDY (SEQ ID NO: 65); (d) an HVR-L1 sequence of RASQDVSTAVA (SEQ ID NO: 66); (e) an HVR-L2 sequence of SASFLYS (SEQ ID NO: 67); and (f) an HVR-L3 sequence of QQYLYHPAT (SEQ ID NO: 68). In some embodiments, the anti-PD-L1 antibody comprises: (a) a heavy chain variable (VH) domain comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWWVRQAPGKGLEWVAWISPYGGSTYYADSVKGRF TISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSS (SEQ ID NO: 69); (b) a light chain variable (VL) domain comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYLYHPATFGQGTKVEIKR (SEQ ID NO: 70); or (c) a VH domain as in (a) and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 69; (b) a VL domain comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a) and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising an amino acid sequence having at least 96% sequence identity to the amino acid sequence of SEQ ID NO: 69;

(b) a VL domain comprising an amino acid sequence having at least 96% sequence identity to the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a) and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising an amino acid sequence having at least 97% sequence identity to the amino acid sequence of SEQ ID NO: 69; (b) a VL domain comprising an amino acid sequence having at least 97% sequence identity to the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a) and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising an amino acid sequence having at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 69; (b) a VL domain comprising an amino acid sequence having at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a) and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising an amino acid sequence having at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 69; (b) a VL domain comprising an amino acid sequence having at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a) and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising the amino acid sequence of SEQ ID NO: 69; (b) a VL domain comprising the amino acid sequence of SEQ ID NO: 70; or (c) a VH domain as in (a) and a VL domain as in (b). In some embodiments, the anti-PD-L1 antibody comprises: (a) a VH domain comprising the amino acid sequence of SEQ ID NO: 69; and (b) a VL domain comprising the amino acid sequence of SEQ ID NO: 70. In some embodiments, the anti-PD-L1 antibody is atezolizumab.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a graph showing the tumor burden over time among renal cell carcinoma (RCC) patients receiving atezolizumab and bevacizumab combination treatment. Points on the graph show the maximum reduction from baseline in the sum of the longest diameter (SLD) for target lesions. PR, partial response; PD, progressive disease; SD, stable disease.

FIG. 2 is a graph showing the duration of study treatment for each RCC patient. Time of first PR or CR is indicated with a circle; time of first PD is indicated with a triangle; treatment discontinuation is indicated with a black bar; and patients still on treatment as of the time of analysis are identified with an arrow.

FIG. 3 is a graph showing gene expression levels of tumor biomarkers following bevacizumab ("Bev") treatment. The expression levels of on-treatment tumor samples are shown relative to the baseline expression levels (pre-treatment). Vascular signature genes (ANGPT2, CD34, DLL4, EGFL7, and ESM1) are shown in black, CD8 T cell effector genes (CD8A, CD8B, EOMES, GZMA, IFNG, and PRF1) are shown in patterned gray, Th1 chemokines (CXCL10, CXCL11, CXCL13, and CXCL9) are shown in white, and natural killer (NK) cell genes (GZMB, KLRK1, and SLAMF7) are shown in solid gray.

FIG. 4 is a graph showing gene expression levels of tumor biomarkers following atezolizumab and bevacizumab combination ("Bev+Atezo") treatment. The expression levels of on-treatment tumor samples are shown relative to the baseline expression levels (pre-treatment). Vascular signature genes (ANGPT2, CD34, DLL4, EGFL7, and ESM1) are shown in black, CD8 T cell effector genes (CD8A, CD8B, EOMES, GZMA, IFNG, and PRF1) are shown in patterned gray, Th1 chemokines (CXCL10,

CXCL11, CXCL13, and CXCL9) are shown in white, and NK cell genes (GZMB, KLRK1, and SLAMF7) are shown in solid gray.

FIG. 5 is a series of representative images showing protein expression of immune and vasculature markers in tumor samples from patient 3, as assessed by immunohistochemistry (IHC).

CD31 is stained dark gray (first row), CD8 is stained dark gray (second row), MHC-I is stained dark gray (third row), and PD-L1 is stained dark gray (fourth row). Pre-treatment samples are shown in the left-hand column, post-bevacizumab samples are shown in the middle column, and post-bevacizumab+atezolizumab samples are shown in the right-hand column.

FIG. 6 is a series of graphs showing quantification of immune and vasculature markers at the indicated time points, as assessed by IHC. CD31 expression is shown in the top panel, CD8 expression is shown in the middle panel, and MHC-I expression is shown in the bottom panel. P values were determined by paired t-test. "VPOSVE" is a measure of vessel density.

FIG. 7 is a series of representative images showing protein expression of immune and vasculature markers from serial sections of tumor samples from Patient 3, as assessed by IHC. The first row shows expression of CD34, alpha smooth muscle actin (α SMA), and podoplanin. The second row shows expression of CD8 and Ki67. The third row shows expression of CD68 and CD163. Pre-treatment samples are shown in the left-hand column, post-bevacizumab samples are shown in the middle column, and post-bevacizumab+atezolizumab samples are shown in the right-hand column.

FIG. 8 is a series of representative images showing protein expression of CD34 and α SMA in tumor samples, as assessed by IHC. Pre-treatment samples are shown in the left-hand column, post-bevacizumab samples are shown in the middle column, and post-bevacizumab+atezolizumab samples are shown in the right-hand column. Sections of individual patients 1-6 are arranged on each row. The response of each patient is also indicated.

FIG. 9 is a series of representative images showing protein expression of immune and vasculature markers from serial sections of tumors, as assessed by IHC. The first row shows expression of CD34, α SMA, and podoplanin. The second row shows expression of CD8 and Ki67. The third row shows expression of CD68 and CD163. Post-bevacizumab samples are shown in the left-hand column, and post-bevacizumab+atezolizumab samples are shown in the right-hand column.

FIG. 10 is a series of representative images showing protein expression of immune and vasculature markers from serial sections of tumors post-bevacizumab+atezolizumab, as assessed by IHC. The top image shows expression of CD34, α SMA, and podoplanin. The middle image shows expression of CD8 and Ki67. The bottom image shows expression of CD68 and CD163.

FIG. 11 is a graph showing the upregulation of VEGF transcript expression in tumors in response to bevacizumab and bevacizumab+atezolizumab treatment. Expression is normalized to housekeeping (HK) gene expression. Each line represents an individual patient.

FIG. 12 is a series of representative images showing protein expression of CD8 (stained dark gray) from tumor sections, as assessed by IHC. Pre-treatment samples are shown in the left-hand column, post-bevacizumab samples are shown in the middle column, and post-bevacizumab+atezolizumab samples are shown in the right-hand column. Sections of individual patients 1-6 are arranged on each row. The response of each patient is also indicated.

FIG. 13 is a series of representative images showing protein expression of CD8 and Ki67 from tumor sections, as assessed by IHC. Pre-treatment samples are shown in the left-hand column, post-bevacizumab samples are shown in the middle column, and post-bevacizumab+atezolizumab samples are shown in the right-hand column. Sections of individual patients 1-6 are arranged on each row.

FIGS. 14A-14C are a series of graphs showing the number of cells expressing CD8 or both Ki67 and CD8 per square millimeter (mm²) tumor area for each patient at the pre-treatment time point. Fig. 14A shows data for patients 1 and 2. Fig. 14B shows data for patients 3 and 4. Fig. 14C shows data for patient 5. The response of each patient is also indicated.

FIGS. 15A-15C are a series of graphs showing the number of cells expressing CD8 or both Ki67 and CD8 per mm² tumor area for each patient at the post-bevacizumab time point. Fig. 15A shows data for patients 1 and 2. Fig. 15B shows data for patients 3 and 5. Fig. 15C shows data for patient 6. The response of each patient is also indicated.

FIGS. 16A-16C are a series of graphs showing the number of cells expressing CD8 or both Ki67 and CD8 per mm² tumor area for each patient at the post-bevacizumab+atezolizumab time point. Fig. 16A shows data for patients 1 and 2. Fig. 16B shows data for patients 3 and 4. Fig. 16C shows data for patients 5 and 6. The response of each patient is also indicated.

FIGS. 17A and 17B are a series of flow cytometry plots showing the percentage of CD8⁺ cells in tumor samples expressing CX3CR1. Pre-treatment samples are shown in the left-hand column, post-bevacizumab samples are shown in the middle column, and post-bevacizumab+atezolizumab samples are shown in the right-hand column. Each row shows the results from an individual patient. Fig. 17A shows data for patients 2 and 3. Fig. 17B shows data for patients 5 and 6.

FIG. 18 is a graph showing the expression of CX3CR1 as a percentage of total CD8⁺ cells (left) and as a percentage of tumor antigen-specific (Dex-APC⁺) T cells (right), based on flow cytometry analysis.

FIG. 19 is a series of flow cytometry plots showing representative frequencies of antigen-specific T cells in the blood. Representative data from two HLA-A2-positive patients with blood draws matched to tumor biopsy time points are shown.

FIG. 20 is a series of graphs showing the change in chemokine expression (CCL2, CCL5, CCR5, CX3CL1, CCR7, and CXCL10) in tumors at the indicated treatment time points. Expression was normalized to housekeeping (HK) gene expression.

FIGS. 21A-21C are a series of graphs showing the results of TCR β sequencing of infiltrating lymphocytes (TILs) before and after treatment in tumor samples from patient 6. The top clones (up to 25) for each group are shown. The prevalence of trending TCR β clone populations are shown in the darker lines in Figs. 21A (bottom panel), 21B, and 21C.

FIG. 22 is a graph showing the results of TCR β sequencing from Patient 3 TILs before and after bevacizumab+atezolizumab treatment.

FIGS. 23A and 23B are a series of graphs showing the results of TCR β sequencing of pre-treatment PBMCs, post-bevacizumab+atezolizumab peripheral blood mononuclear cells (PBMCs), and post-bevacizumab+atezolizumab TILs from patients 2, 3, and 6. Fig. 23A shows data for patients 2 and 3, and Fig. 23B shows data for patient 6. The top clones (up to 25) for each group are shown.

FIG. 24 is a heat map showing the number of viral antigen-specific clones in the PBMC pool versus the TIL pool at each treatment time point, for Patients 3 and 6.

FIG. 25 is a graph showing the overall response rate (ORR) correlated with progression-free survival (PFS) in the indicated gene expression subgroups. Atezo, atezolizumab; atezo+bev; atezolizumab and bevacizumab. Ang indicates VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34; Teff indicates CD8A, EOMES, PRF1, IFNG, and PD-L1.

FIG. 26 is a heatmap showing a transcriptome map of angiogenesis, immune associated, and myeloid associated genes in RCC tumors.

FIGS. 27A and 27B is a series of graphs showing that addition of bevacizumab to atezolizumab was associated with improved PFS benefit in the T-effector (Teff) high/myeloid inflammation (Myeloid) high subgroup (Fig. 27B), but not in the Teff high myeloid low subgroup (Fig. 27A). Teff indicates CD8A, EOMES, PRF1, IFNG, and PD-L1. Myeloid indicates IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2. High: $\geq$ median expression, Low: $<$ median expression.

FIG. 28 is a graph showing that the Myeloid genes (IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2), independently of the Teff genes, were associated with relatively worse PFS outcome when comparing Myeloid High versus Myeloid Low patients within the Atezo+Bev arm of the study described in Example 5. When compared to sunitinib (Sun), Atezo+Bev was not different from Sun in the Myeloid High population, but Atezo+Bev demonstrated improved PFS benefit in the Myeloid Low population. High: $\geq$ median expression, Low: $<$ median expression.

FIGS. 29A and 29B are a series of graphs showing that atezolizumab+bevacizumab demonstrated improved PFS compared to sunitinib in the Angiogenesis low subgroup (Fig. 29A), whereas sunitinib treatment demonstrated improved PFS in the Angiogenesis high subgroup (Fig. 29B). PFS for patients having high ($\geq$ median expression) or low ($<$ median expression) expression of Angiogenesis genes (VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34) is shown for the indicated treatment arms.

FIGS. 30A-30C are a series of graphs showing that sunitinib treatment demonstrated improved PFS in the Angiogenesis high subset compared to the Angiogenesis low subset. PFS for patients in the sunitinib (Fig. 30A), atezolizumab+bevacizumab (Fig. 30B), and atezolizumab (Fig. 30C) treatment arms was evaluated for the patient subgroups having high ($\geq$ median expression) or low ($<$ median expression) expression of Angiogenesis genes (VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34). The tables under the graph show hazard ratio (HR) and 95% confidence interval (95% CI).

FIGS. 31A and 31B are a series of graphs showing that atezolizumab+bevacizumab demonstrated improved PFS compared to sunitinib in the Teff high subset. PFS for patients having high ($\geq$ median expression) (Fig. 31A) or low ($<$ median expression) (Fig. 31B) expression of Teff genes (CD8A, EOMES, PRF1, IFNG, and PD-L1) is shown for the indicated treatment arms.

FIGS. 32A-32C are a series of graphs showing that atezolizumab+bevacizumab demonstrated improved PFS in the Teff high subgroup versus the Teff low subgroup. PFS for patients in the sunitinib (Fig. 32A), atezolizumab+bevacizumab (Fig. 32B), and atezolizumab (Fig. 32C) treatment arms was evaluated for the patient subgroups having high ($\geq$ median expression) or low ($<$ median expression) expression of Teff genes (CD8A, EOMES, PRF1, IFNG, and PD-L1). The tables under the graph show hazard ratio (HR) and 95% confidence interval (95% CI).

FIG. 33 is a schematic diagram showing a flow chart of patients randomized to one of three treatment arms in the IMmotion150 trial: sunitinib, atezolizumab monotherapy, or atezolizumab+bevacizumab in combination. One patient in the sunitinib arm did not receive study drug due to withdrawal of consent and was excluded from the safety analysis.

FIGS. 34A-34C are a series of graphs showing positive independent review facility (IRF)-assessed efficacy associated with atezolizumab+bevacizumab in mRCC patients with PD-L1+ IC. Kaplan-Meier curves depict IRF-assessed median PFS in the atezolizumab bevacizumab, atezolizumab monotherapy, and sunitinib treatment arms in the ITT population (Fig. 34A) and PD-L1+ ($\geq 1\%$ PD-L1 expression on IC by IHC) population (Fig. 34B) across 33 months. Censored data are indicated by vertical tick marks in Kaplan-Meier curves. Objective response rate (ORR) as depicted by partial response (PR) and complete response (CR) for the ITT and PD-L1+ populations for each treatment arm (Fig. 34C).

FIGS. 35A and 35B are a series of graphs showing investigator (INV)-assessed PFS associated with atezolizumab+bevacizumab in mRCC patients with PD-L1+ IC. Kaplan-Meier curves depict INV-assessed median PFS in the atezolizumab+bevacizumab, atezolizumab monotherapy, and sunitinib treatment arms in the ITT population (Fig. 35A) and PD-L1+ ($\geq 1\%$ PD-L1 expression on IC by IHC) population (Fig. 35B) across 33 months. Censored data are indicated by vertical tick marks in Kaplan-Meier curves.

FIGS. 36A and 36B are a series of Forest plots showing IRF-assessed PFS hazard ratios (HRs) in key subgroups. The Forest plots are shown depicting median PFS versus sunitinib HRs in specific patient subgroups for atezolizumab+bevacizumab (Fig. 36A) and atezolizumab monotherapy (Fig. 36B). The analyses were unstratified.

FIGS. 37A and 37B are a series of graphs showing adverse events (AEs) with $> 5\%$ difference in frequency between the atezolizumab+bevacizumab versus sunitinib arms (Fig. 37A) and a $\geq 20\%$ frequency within the atezolizumab versus sunitinib populations (Fig. 37B).

FIG. 38A is a heatmap showing expression of genes of interest (rows) in 263 pretreatment tumors (columns). Normalized counts of genes related to angiogenesis, immune and antigen presentation, and myeloid inflammation were Z-score transformed before visualization. Sample annotations include PD-L1 IHC status for tumor-infiltrating immune cells (IC), presence of sarcomatoid features, MSKCC score, and tumor stage.

FIG. 38B is a graph showing that mean CD31 IHC staining intensity is higher in the $\text{Angio}^{\text{High}}$ population than in $\text{Angio}^{\text{Low}}$ population (two-tailed t test, $P = 4.19 \times 10^{-21}$). Sample number per group is indicated above the graph.

FIGS. 38C and 38D are a series of graphs showing that Teff signature scores are associated with PD-L1 protein expression levels on IC by IHC (Fig. 38C; Wald test $P = 3.26 \times 10^{-20}$) and intra-tumoral CD8A protein expression by IHC (Fig. 38D; two-tailed t test $P = 1.26 \times 10^{-28}$). Sample number per group is indicated above each graph.

FIG. 38E is a graph showing ORR (PR + CR) in the $\text{Angio}^{\text{High}}$ and $\text{Angio}^{\text{Low}}$ populations for each treatment arm. Error bars represent 95% CI for ORR.

FIG. 38F is a graph showing Forest plots of PFS HRs and CIs for Angio^{High} versus Angio^{Low} populations within each treatment arm.

FIGS. 38G and 38H are a series of graphs showing Kaplan-Meier curves showing the probability of PFS across treatment arms in the Angio^{Low} (Fig. 38G) and Angio^{High} (Fig. 38H) subgroups; HR calculated versus sunitinib.

FIG. 38I is a graph showing ORR (PR + CR) in the Teff^{High} and Teff^{Low} populations for each treatment arm. Error bars represent 95% CIs for ORR.

FIG. 38J is a graph showing Forest plots of PFS HRs and CIs for Teff^{High} versus Teff^{Low} populations within each treatment arm.

FIGS. 38K and 38L are a series of graphs showing Kaplan-Meier curves showing probability of PFS across treatment arms in Teff^{Low} (Fig. 38K) and Teff^{High} (Fig. 38L) subgroups; HR is calculated versus sunitinib.

FIGS. 38M and 38N are a series of graphs showing Kaplan-Meier curves showing probability of PFS in Teff^{High}Myeloid^{Low} (Fig. 38M) and Teff^{High}Myeloid^{High} (Fig. 38N) subgroups; HR is calculated versus atezolizumab monotherapy. Censored data are indicated by vertical tick marks in Kaplan-Meier curves. All HR and CI values for PFS were extracted from Cox proportional hazard regression models; median survival time per group is indicated.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides diagnostic methods and assays, therapeutic methods and uses, and compositions for the treatment of cancer (e.g., a kidney cancer (e.g., a renal cell carcinoma (RCC)), a lung cancer (e.g., a non-small cell lung cancer (NSCLC)), a bladder cancer (e.g., a urothelial bladder cancer (UBC)), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., a triple-negative breast cancer (TNBC))). The invention is based, at least in part, on the discovery that the expression level of one or more genes (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9) in a sample obtained from an individual having a cancer e.g., a kidney cancer (e.g., a renal cell carcinoma (RCC)), a lung cancer (e.g., a non-small cell lung cancer (NSCLC)), a bladder cancer (e.g., a urothelial bladder cancer (UBC)), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., a triple-negative breast cancer (TNBC))) can be used as a biomarker (e.g., a predictive biomarker) in methods of identifying whether the individual is likely to respond to treatment including a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)); selecting a therapy for treating the individual; optimizing therapeutic efficacy of a treatment that includes a VEGF antagonist and a PD-L1 axis binding antagonist; and/or monitoring the response of the individual to a treatment that includes a VEGF antagonist and a PD-L1 axis binding antagonist. The invention also provides methods for treating an individual having a

cancer (e.g., a kidney cancer (e.g., a renal cell carcinoma (RCC)), a lung cancer (e.g., a non-small cell lung cancer (NSCLC)), a bladder cancer (e.g., a urothelial bladder cancer (UBC)), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., a triple-negative breast cancer (TNBC))) by administering an anti-cancer therapy that includes a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)).

In another aspect, the invention is based, at least in part, on the discovery that the expression level of one or more genes (e.g., VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, and/or CD34) in a sample obtained from an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)) can be used as a biomarker (e.g., a predictive biomarker) in methods of identifying whether the individual is likely to respond to treatment with an anti-cancer therapy including an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))); selecting a therapy for treating the individual; optimizing therapeutic efficacy of a treatment with an anti-cancer therapy that includes an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))); and/or monitoring the response of the individual to a treatment that includes an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))). The invention also provides methods for treating an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)) by administering an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))). In some instances, the VEGF antagonist is administered as a monotherapy.

I. Definitions

It is to be understood that aspects and embodiments of the invention described herein include “comprising,” “consisting,” and “consisting essentially of” aspects and embodiments. As used herein, the singular form “a,” “an,” and “the” includes plural references unless indicated otherwise.

The term “about” as used herein refers to the usual error range for the respective value readily known to the skilled person in this technical field. Reference to “about” a value or parameter herein includes (and describes) embodiments that are directed to that value or parameter *per se*.

As used herein, the terms “individual,” “patient,” or “subject” are used interchangeably and refer to any single animal, more preferably a mammal (including such non-human animals as, for example, cats, dogs, horses, rabbits, zoo animals, cows, pigs, sheep, and non-human primates) for which treatment is desired. In particular embodiments, the patient herein is a human. The patient may be a “cancer

patient," i.e., one who is suffering from cancer, or at risk for suffering from cancer, or suffering from one or more symptoms of cancer.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include, but are not limited to, kidney or renal cancer (e.g., renal cell carcinoma (RCC)); lung cancer, including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, and squamous carcinoma of the lung; bladder cancer (e.g., urothelial bladder cancer (UBC), muscle invasive bladder cancer (MIBC), and BCG-refractory non-muscle invasive bladder cancer (NMIBC)); cancer of the urinary tract; breast cancer (e.g., HER2+ breast cancer and triple-negative breast cancer (TNBC), which are estrogen receptors (ER-), progesterone receptors (PR-), and HER2 (HER2-) negative); prostate cancer, such as castration-resistant prostate cancer (CRPC); cancer of the peritoneum; hepatocellular cancer; gastric or stomach cancer, including gastrointestinal cancer and gastrointestinal stromal cancer; pancreatic cancer; glioblastoma; cervical cancer; ovarian cancer; liver cancer (e.g., hepatocellular carcinoma (HCC)); hepatoma; colon cancer; rectal cancer; colorectal cancer; endometrial or uterine carcinoma; salivary gland carcinoma; prostate cancer; vulval cancer; thyroid cancer; hepatic carcinoma; anal carcinoma; penile carcinoma; melanoma, including superficial spreading melanoma, lentigo maligna melanoma, acral lentiginous melanomas, and nodular melanomas; multiple myeloma and B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL); small lymphocytic (SL) NHL; intermediate grade/follicular NHL; intermediate grade diffuse NHL; high grade immunoblastic NHL; high grade lymphoblastic NHL; high grade small non-cleaved cell NHL; bulky disease NHL; mantle cell lymphoma; AIDS-related lymphoma; and Waldenstrom's Macroglobulinemia); chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); acute myelogenous leukemia (AML); hairy cell leukemia; chronic myeloblastic leukemia (CML); post-transplant lymphoproliferative disorder (PTLD); and myelodysplastic syndromes (MDS), as well as abnormal vascular proliferation associated with phakomatoses, edema (such as that associated with brain tumors), Meigs' syndrome, brain cancer, head and neck cancer, and associated metastases. In some embodiments, the cancer is kidney cancer. In particular embodiments, the kidney cancer is RCC (e.g., advanced RCC or metastatic RCC (mRCC), including previously untreated RCC).

By "early stage cancer" or "early stage tumor" is meant a cancer that is not invasive or metastatic or is classified as a Stage 0, I, or II cancer.

An "advanced" cancer is one which has spread outside the site or organ of origin, either by local invasion or metastasis.

A "refractory" cancer is one which progresses even though an anti-tumor agent, such as a chemotherapeutic agent, is being administered to the cancer patient. An example of a refractory cancer is one which is platinum refractory.

A "recurrent" cancer is one which has regrown, either at the initial site or at a distant site, after a response to initial therapy.

The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are associated with some degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder is cancer.

The term "tumor," as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

The terms "cancer," "cancerous," "cell proliferative disorder," "proliferative disorder," and "tumor" are not mutually exclusive as referred to herein.

A "disorder" is any condition that would benefit from treatment including, but not limited to, chronic and acute disorders or diseases including those pathological conditions which predispose the mammal to the disorder in question.

The term "detection" includes any means of detecting, including direct and indirect detection.

The term "sample," as used herein, refers to a composition that is obtained or derived from a patient and/or individual of interest that contains a cellular and/or other molecular entity that is to be characterized and/or identified, for example, based on physical, biochemical, chemical, and/or physiological characteristics. Samples include, but are not limited to, tissue samples, primary or cultured cells or cell lines, cell supernatants, cell lysates, platelets, serum, plasma, vitreous fluid, lymph fluid, synovial fluid, follicular fluid, seminal fluid, amniotic fluid, milk, whole blood, blood-derived cells, urine, cerebro-spinal fluid, saliva, sputum, tears, perspiration, mucus, tumor lysates, and tissue culture medium, tissue extracts such as homogenized tissue, tumor tissue, cellular extracts, and combinations thereof.

As used herein, the expressions "cell," "cell line," and "cell culture" are used interchangeably and all such designations include progeny. Thus, the words "transformants" and "transformed cells" include the primary subject cell and cultures derived therefrom without regard for the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Mutant progeny that have the same function or biological activity as screened for in the originally transformed cell are included. Where distinct designations are intended, it will be clear from the context.

The terms "biomarker" and "marker" are used interchangeably herein to refer to a DNA, RNA, protein, carbohydrate, glycolipid, or cell-based molecular marker, the expression or presence of which in a patient's sample can be detected by standard methods (or methods disclosed herein). Such biomarkers include, but are not limited to, CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9. Expression of such a biomarker may be determined to be higher or lower in a sample obtained from a patient sensitive or responsive to a treatment (e.g., treatment with an anti-cancer therapy that includes a VEGF antagonist and a PD-L1 axis binding antagonist, or treatment with a multi-targeted tyrosine kinase inhibitor) than a reference level (including, e.g., the median expression level of the biomarker in a sample from a group/population of patients, e.g., patients having cancer, and being tested for responsiveness to a treatment; the median expression level of the biomarker in a sample from a group/population of patients, e.g., patients having cancer, and identified as not responding to a treatment; the level in a sample previously obtained from the individual at a prior time; or

the level in a sample from a patient who received prior treatment (e.g., with an anti-cancer therapy that includes a VEGF antagonist and a PD-L1 axis binding antagonist, or treatment with a multi-targeted tyrosine kinase inhibitor) in a primary tumor setting, and who now may be experiencing metastasis).

The term "CD8A" as used herein, refers to any native CD8A from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CD8A as well as any form of CD8A that results from processing in the cell. The term also encompasses naturally occurring variants of CD8A, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CD8A is set forth in SEQ ID NO: 1. The amino acid sequence of an exemplary protein encoded by human CD8A is shown in SEQ ID NO: 2.

The term "EOMES" as used herein, refers to any native EOMES (Eomesodermin) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed EOMES as well as any form of EOMES that results from processing in the cell. The term also encompasses naturally occurring variants of EOMES e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human EOMES is set forth in SEQ ID NO: 3. The amino acid sequence of an exemplary protein encoded by human EOMES is shown in SEQ ID NO: 4.

The term "GZMA" as used herein, refers to any native GZMA (Granzyme A) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed GZMA as well as any form of GZMA that results from processing in the cell. The term also encompasses naturally occurring variants of GZMA, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human GZMA is set forth in SEQ ID NO: 51. The amino acid sequence of an exemplary protein encoded by human GZMA is shown in SEQ ID NO: 52.

The term "GZMB" as used herein, refers to any native GZMB (Granzyme B) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed GZMB as well as any form of GZMB that results from processing in the cell. The term also encompasses naturally occurring variants of GZMB, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human GZMB is set forth in SEQ ID NO: 53. The amino acid sequence of an exemplary protein encoded by human GZMB is shown in SEQ ID NO: 54.

The term "PRF1" as used herein, refers to any native PRF1 (Perforin 1; also known as Pore Forming Protein) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed PRF1 as well as any form of PRF1 that results from processing in the cell. The term also encompasses naturally occurring variants of PRF1, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human PRF1 is set forth in SEQ ID NO: 5. The amino acid sequence of an exemplary protein encoded by human PRF1 is shown in SEQ ID NO: 6.

The term "IFNG" as used herein, refers to any native IFNG (Interferon, Gamma) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats),

unless otherwise indicated. The term encompasses “full-length,” unprocessed IFNG as well as any form of IFNG that results from processing in the cell. The term also encompasses naturally occurring variants of IFNG, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human IFNG is set forth in SEQ ID NO: 7. The amino acid sequence of an exemplary protein encoded by human IFNG is shown in SEQ ID NO: 8.

The terms “Programmed Death Ligand 1” and “PD-L1” refer herein to a native sequence PD-L1 polypeptide, polypeptide variants, and fragments of a native sequence polypeptide and polypeptide variants (which are further defined herein). The PD-L1 polypeptide described herein may be that which is isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods.

A “native sequence PD-L1 polypeptide” comprises a polypeptide having the same amino acid sequence as the corresponding PD-L1 polypeptide derived from nature. The term encompasses “full-length,” unprocessed PD-L1 as well as any form of IFNG that results from processing in the cell. The term also encompasses naturally occurring variants of IFNG, e.g., splice variants or allelic variants.

A “PD-L1 polypeptide variant,” or variations thereof, means a PD-L1 polypeptide, generally an active PD-L1 polypeptide, as defined herein having at least about 80% amino acid sequence identity with any of the native sequence PD-L1 polypeptide sequences as disclosed herein. Such PD-L1 polypeptide variants include, for instance, PD-L1 polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of a native amino acid sequence. Ordinarily, a PD-L1 polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity, to a native sequence PD-L1 polypeptide sequence as disclosed herein. Ordinarily, PD-L1 variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 281, 282, 283, 284, 285, 286, 287, 288, or 289 amino acids in length, or more. Optionally, PD-L1 variant polypeptides will have no more than one conservative amino acid substitution as compared to a native PD-L1 polypeptide sequence, alternatively no more than 2, 3, 4, 5, 6, 7, 8, 9, or 10 conservative amino acid substitutions as compared to the native PD-L1 polypeptide sequence.

The term “vascular endothelial growth factor” or “VEGF” refers to vascular endothelial growth factor protein A (VEGFA), as exemplified by Swiss Prot Accession Number P15692, Gene ID (NCBI): 7422. The term “VEGF” encompasses the protein having the amino acid sequence of Swiss Prot Accession Number P15692, Gene ID (NCBI): 7422 as well as homologues and isoforms thereof. The term “VEGF” also encompasses the known isoforms, e.g., splice isoforms, of VEGF, e.g., VEGF₁₁₁, VEGF₁₂₁, VEGF₁₄₅, VEGF₁₆₅, VEGF₁₈₉, and VEGF₂₀₆, together with the naturally-occurring allelic and processed forms thereof, including the 110 amino acid human vascular endothelial cell growth factor generated by plasmin cleavage of VEGF₁₆₅ as described in Ferrara *Mol. Biol. Cell.* 21:687, 2010; Leung et al., *Science*, 246:1306, 1989; and Houck et al., *Mol. Endocrin.*, 5:1806, 1991. The term “VEGF” also refers to VEGFs from non-human species such as mouse, rat or primate. Sometimes the VEGF from a specific species are indicated by terms such as hVEGF for human VEGF, mVEGF for murine VEGF, and

the like. The term "VEGF" is also used to refer to truncated forms of the polypeptide comprising amino acids 8 to 109 or 1 to 109 of the 165-amino acid human vascular endothelial cell growth factor.

Reference to any such forms of VEGF may be identified in the present application, e.g., by "VEGF₁₀₉," "VEGF (8-109)," "VEGF (1-109)" or "VEGF₁₆₅." The amino acid positions for a "truncated" native VEGF

are numbered as indicated in the native VEGF sequence. For example, amino acid position 17 (methionine) in truncated native VEGF is also position 17 (methionine) in native VEGF. The truncated native VEGF has binding affinity for the KDR and Flt-1 receptors comparable to native VEGF. The term "VEGF variant" as used herein refers to a VEGF polypeptide which includes one or more amino acid mutations in the native VEGF sequence. Optionally, the one or more amino acid mutations include amino acid substitution(s). For purposes of shorthand designation of VEGF variants described herein, it is noted that numbers refer to the amino acid residue position along the amino acid sequence of the putative native VEGF (provided in Leung et al., *supra* and Houck et al., *supra*). Unless specified otherwise, the term "VEGF" as used herein indicates VEGF-A.

The term "Kinase Insert Domain Receptor" or "KDR" as used herein, refers to any native KDR (also known in the art as Fetal Liver Kinase 1 (FLK1) or Vascular Endothelial Growth Factor Receptor 2 (VEGFR2)) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed KDR as well as any form of KDR that results from processing in the cell. The term also encompasses naturally occurring variants of KDR, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human KDR is set forth in SEQ ID NO: 9. The amino acid sequence of an exemplary protein encoded by human KDR is shown in SEQ ID NO: 10.

The term "Endothelial Cell Specific Molecule 1" or "ESM1" as used herein, refers to any native ESM1 (also known in the art as endocan) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed ESM1 as well as any form of ESM1 that results from processing in the cell. The term also encompasses naturally occurring variants of ESM1, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human ESM1 is set forth in SEQ ID NO: 11. The amino acid sequence of an exemplary protein encoded by human ESM1 is shown in SEQ ID NO: 12.

The term "Platelet And Endothelial Cell Adhesion Molecule 1" or "PECAM1" as used herein, refers to any native PECAM1 (also known in the art as CD31, endoCAM, GPIIA, or PECA1) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed PECAM1 as well as any form of PECAM1 that results from processing in the cell. The term also encompasses naturally occurring variants of PECAM1, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human PECAM1 is set forth in SEQ ID NO: 13. The amino acid sequence of an exemplary protein encoded by human PECAM1 is shown in SEQ ID NO: 14.

The term "FLT1" as used herein, refers to any native FLT1 (also known in the art as Vascular Endothelial Growth Factor Receptor 1 (VEGFR1) or fms related tyrosine kinase 1) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed FLT1 as well as any form of FLT1

that results from processing in the cell. The term also encompasses naturally occurring variants of FLT1, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human FLT1 is set forth in SEQ ID NO: 55. The amino acid sequence of an exemplary protein encoded by human FLT1 is shown in SEQ ID NO: 56.

5 The term "Angiopoietin Like 4" or "ANGPTL4" as used herein, refers to any native ANGPTL4 (also known in the art as Hepatic Fibrinogen/Angiopoietin-Related Protein (HFARP), Peroxisome Proliferator-Activated Receptor (PPAR) Gamma, Hepatic Angiopoietin-Related Protein (HARP), Angiopoietin-Related Protein 4 (Arp4), or Fasting-Induced Adipose Factor (FIAF)) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless
10 otherwise indicated. The term encompasses "full-length," unprocessed ANGPTL4 as well as any form of ANGPTL4 that results from processing in the cell. The term also encompasses naturally occurring variants of ANGPTL4, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human ANGPTL4 is set forth in SEQ ID NO: 15. The amino acid sequence of an exemplary protein encoded by human ANGPTL4 is shown in SEQ ID NO: 16.

15 The term "CD34" as used herein, refers to any native CD34 (also known in the art as CD34 molecule or CD34 antigen) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CD34 as well as any form of CD34 that results from processing in the cell. The term also encompasses naturally occurring variants of CD34, e.g., splice variants or allelic variants. The
20 nucleic acid sequence of an exemplary human CD34 is set forth in SEQ ID NO: 17. The amino acid sequence of an exemplary protein encoded by human CD34 is shown in SEQ ID NO: 18.

 The term "interleukin 6" or "IL6" as used herein, refers to any native IL6 from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed IL6 as well as any form of IL6 that
25 results from processing in the cell. The term also encompasses naturally occurring variants of IL6, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human IL6 is set forth in SEQ ID NO: 19. The amino acid sequence of an exemplary protein encoded by human IL6 is shown in SEQ ID NO: 20.

 The term "CXCL1" as used herein, refers to any native CXCL1 (chemokine (C-X-C motif) ligand
30 1; also known as GRO1 or neutrophil-activating protein 3 (NAP-3)) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CXCL1 as well as any form of CXCL1 that results from processing in the cell. The term also encompasses naturally occurring variants of CXCL1, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CXCL1 is set forth in SEQ
35 ID NO: 21. The amino acid sequence of an exemplary protein encoded by human CXCL1 is shown in SEQ ID NO: 22.

 The term "CXCL2" as used herein, refers to any native CXCL2 (chemokine (C-X-C motif) ligand
40 2; also known as macrophage inflammatory protein 2-alpha (MIP2-alpha)) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CXCL2 as well as any form of CXCL2 that

results from processing in the cell. The term also encompasses naturally occurring variants of CXCL2, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CXCL2 is set forth in SEQ ID NO: 23. The amino acid sequence of an exemplary protein encoded by human CXCL2 is shown in SEQ ID NO: 24.

5 The term "CXCL3" as used herein, refers to any native CXCL3 (chemokine (C-X-C motif) ligand 3; also known as macrophage inflammatory protein 2-beta (MIP2-beta)) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CXCL3 as well as any form of CXCL3 that results from processing in the cell. The term also encompasses naturally occurring variants of CXCL3, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CXCL3 is set forth in SEQ ID NO: 25. The amino acid sequence of an exemplary protein encoded by human CXCL3 is shown in SEQ ID NO: 26.

15 The term "CXCL8" as used herein, refers to any native CXCL8 (chemokine (C-X-C motif) ligand 8; also known as interleukin 8 (IL8)) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CXCL8 as well as any form of CXCL8 that results from processing in the cell. The term also encompasses naturally occurring variants of CXCL8, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CXCL8 is set forth in SEQ ID NO: 27. The amino acid sequence of an exemplary protein encoded by human CXCL8 is shown in SEQ ID NO: 28.

20 The term "PTGS2" as used herein, refers to any native PTGS2 (prostaglandin-endoperoxide synthase 2; also known as cyclooxygenase-2 (COX-2)) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed PTGS2 as well as any form of PTGS2 that results from processing in the cell. The term also encompasses naturally occurring variants of PTGS2, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human PTGS2 is set forth in SEQ ID NO: 29. The amino acid sequence of an exemplary protein encoded by human PTGS2 is shown in SEQ ID NO: 30.

30 The term "CXCR1" as used herein, refers to any native CXCR1 (C-X-C motif chemokine receptor 1; also known as interleukin 8 receptor, alpha, IL8RA, and CD181) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CXCR1 as well as any form of CXCR1 that results from processing in the cell. The term also encompasses naturally occurring variants of CXCR1, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CXCR1 is set forth in SEQ ID NO: 75. The amino acid sequence of an exemplary protein encoded by human CXCR1 is shown in SEQ ID NO: 76.

35 The term "CXCR2" as used herein, refers to any native CXCR2 (C-X-C motif chemokine receptor 2; also known as interleukin 8 receptor, beta, IL8RB, and CD182) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CXCR2 as well as any form of CXCR2 that results from processing in the cell. The term also encompasses naturally occurring variants of CXCR2, e.g., splice

variants or allelic variants. The nucleic acid sequence of an exemplary human CXCR2 is set forth in SEQ ID NO: 77. The amino acid sequence of an exemplary protein encoded by human CXCR2 is shown in SEQ ID NO: 78.

The term "S100A8" as used herein, refers to any native S100A8 (S100 calcium-binding protein A8; also known as calgranulin A) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. S100A8 can form a heterodimer with S100A9 called calprotectin. The term encompasses "full-length," unprocessed S100A8 as well as any form of S100A8 that results from processing in the cell. The term also encompasses naturally occurring variants of S100A8, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human S100A8 is set forth in SEQ ID NO: 79. The amino acid sequence of an exemplary protein encoded by human S100A8 is shown in SEQ ID NO: 80.

The term "S100A9" as used herein, refers to any native S100A9 (S100 calcium-binding protein A9; also known as calgranulin B and migration inhibitory factor-related protein 14 (MRP14)) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed S100A9 as well as any form of S100A9 that results from processing in the cell. The term also encompasses naturally occurring variants of S100A9, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human S100A9 is set forth in SEQ ID NO: 81. The amino acid sequence of an exemplary protein encoded by human S100A9 is shown in SEQ ID NO: 82.

The term "CXCL9" as used herein, refers to any native CXCL9 (Chemokine (C-X-C Motif) Ligand 9) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CXCL9 as well as any form of CXCL9 that results from processing in the cell. The term also encompasses naturally occurring variants of CXCL9, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CXCL9 is set forth in SEQ ID NO: 57. The amino acid sequence of an exemplary protein encoded by human CXCL9 is shown in SEQ ID NO: 58.

The term "CXCL10" as used herein, refers to any native CXCL10 (Chemokine (C-X-C Motif) Ligand 10) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CXCL10 as well as any form of CXCL10 that results from processing in the cell. The term also encompasses naturally occurring variants of CXCL10, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CXCL10 is set forth in SEQ ID NO: 59. The amino acid sequence of an exemplary protein encoded by human CXCL10 is shown in SEQ ID NO: 60.

The term "CXCL11" as used herein, refers to any native CXCL11 (Chemokine (C-X-C Motif) Ligand 11) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CXCL11 as well as any form of CXCL11 that results from processing in the cell. The term also encompasses naturally occurring variants of CXCL11, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CXCL11 is set forth in SEQ ID NO: 61. The amino acid sequence of an exemplary protein encoded by human CXCL11 is shown in SEQ ID NO: 62.

The term "CD27" as used herein, refers to any native CD27 (also known in the art as CD27L receptor or TNFRSF7) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CD27 as well as any form of CD27 that results from processing in the cell. The term also encompasses naturally occurring variants of CD27, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CD27 is listed in SEQ ID NO: 31. The amino acid sequence of an exemplary protein encoded by human CD27 is shown in SEQ ID NO: 32.

The term "FOXP3" as used herein, refers to any native FOXP3 (Forkhead Box P3, also known in the art as scurfin) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed FOXP3 as well as any form of FOXP3 that results from processing in the cell. The term also encompasses naturally occurring variants of FOXP3, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human FOXP3 is listed in SEQ ID NO: 33. The amino acid sequence of an exemplary protein encoded by human FOXP3 is shown in SEQ ID NO: 34.

The term "PD-1" as used herein, refers to any native PD-1 (also known as PDCD1, programmed cell death protein 1, or CD279) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed PD-1 as well as any form of PD-1 that results from processing in the cell. The term also encompasses naturally occurring variants of PD-1, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human PD-1 is listed in SEQ ID NO: 35. The amino acid sequence of an exemplary protein encoded by human PD-1 is shown in SEQ ID NO: 36.

The term "CTLA4" as used herein, refers to any native CTLA4 (Cytotoxic T-lymphocyte-associated protein 4, also known in the art as CD152) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed CTLA4 as well as any form of CTLA4 that results from processing in the cell. The term also encompasses naturally occurring variants of CTLA4, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human CTLA4 is listed in SEQ ID NO: 37. The amino acid sequence of an exemplary protein encoded by human CTLA4 is shown in SEQ ID NO: 38.

The term "TIGIT" as used herein, refers to any native TIGIT (T cell immunoreceptor with Ig and ITIM domains) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed TIGIT as well as any form of TIGIT that results from processing in the cell. The term also encompasses naturally occurring variants of TIGIT, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human TIGIT is listed in SEQ ID NO: 39. The amino acid sequence of an exemplary protein encoded by human TIGIT is shown in SEQ ID NO: 40.

The term "IDO1" as used herein, refers to any native IDO1 (indoleamine 2,3-dioxygenase 1) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed IDO1 as well as any form of IDO1 that results from processing in the cell. The term also encompasses naturally occurring

variants of IDO1, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human IDO1 is listed in SEQ ID NO: 41. The amino acid sequence of an exemplary protein encoded by human IDO1 is shown in SEQ ID NO: 42.

The term "PSMB8" as used herein, refers to any native PSMB8 (Proteasome Subunit Beta Type-8) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed PSMB8 as well as any form of PSMB8 that results from processing in the cell. The term also encompasses naturally occurring variants of PSMB8, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human PSMB8 is listed in SEQ ID NO: 43. The amino acid sequence of an exemplary protein encoded by human PSMB8 is shown in SEQ ID NO: 44.

The term "PSMB9" as used herein, refers to any native PSMB9 (Proteasome Subunit Beta Type-9) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed PSMB9 as well as any form of PSMB9 that results from processing in the cell. The term also encompasses naturally occurring variants of PSMB9, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human PSMB9 is listed in SEQ ID NO: 45. The amino acid sequence of an exemplary protein encoded by human PSMB9 is shown in SEQ ID NO: 46.

The term "TAP1" as used herein, refers to any native TAP1 (Transporter Associated with Antigen Processing 1; also known in the art as antigen peptide transporter 1) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed TAP1 as well as any form of TAP1 that results from processing in the cell. The term also encompasses naturally occurring variants of TAP1, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human TAP1 is listed in SEQ ID NO: 47. The amino acid sequence of an exemplary protein encoded by human TAP1 is shown in SEQ ID NO: 48.

The term "TAP2" as used herein, refers to any native TAP2 (antigen peptide transporter 2) from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed TAP2 as well as any form of TAP2 that results from processing in the cell. The term also encompasses naturally occurring variants of TAP2, e.g., splice variants or allelic variants. The nucleic acid sequence of an exemplary human TAP2 is listed in SEQ ID NO: 49. The amino acid sequence of an exemplary protein encoded by human TAP2 is shown in SEQ ID NO: 50.

The terms "level of expression" or "expression level" in general are used interchangeably and generally refer to the amount of a biomarker in a biological sample. "Expression" generally refers to the process by which information (e.g., gene-encoded and/or epigenetic information) is converted into the structures present and operating in the cell. Therefore, as used herein, "expression" may refer to transcription into a polynucleotide, translation into a polypeptide, or even polynucleotide and/or polypeptide modifications (e.g., posttranslational modification of a polypeptide). Fragments of the transcribed polynucleotide, the translated polypeptide, or polynucleotide and/or polypeptide modifications (e.g., posttranslational modification of a polypeptide) shall also be regarded as expressed whether they

originate from a transcript generated by alternative splicing or a degraded transcript, or from a post-translational processing of the polypeptide, e.g., by proteolysis. "Expressed genes" include those that are transcribed into a polynucleotide as mRNA and then translated into a polypeptide, and also those that are transcribed into RNA but not translated into a polypeptide (for example, transfer and ribosomal RNAs).

5 An expression level for more than one gene of interest may be determined by aggregation methods known to one skilled in the art and also disclosed herein, including, for example, by calculating the median or mean of all the expression levels of the genes of interest. Before aggregation, the expression level of each gene of interest may be normalized by using statistical methods known to one skilled in the art and also disclosed herein, including, for example, normalized to the expression level of one or more
10 housekeeping genes, or normalized to a total library size, or normalized to the median or mean expression level value across all genes measured. In some instances, before aggregation across multiple genes of interest, the normalized expression level of each gene of interest may be standardized by using statistical methods known to one skilled in the art and also disclosed herein, including, for example, by calculating the Z-score of the normalized expression level of each gene of interest.

15 A sample or cell that "expresses" a protein of interest is one in which mRNA encoding the protein, or the protein, including fragments thereof, is determined to be present in the sample or cell.

As used herein, the term "reference expression level" refers to an expression level against which another expression level, e.g., the expression level of one or more genes described herein (e.g., any gene set forth in Table 1 or any combination thereof (e.g., any combination set forth in any one of Tables
20 2-12) in a sample from an individual is compared, e.g., to make a predictive, diagnostic, prognostic, and/or therapeutic determination. For example, the reference expression level may be derived from expression levels in a reference population (e.g., the median expression level in a reference population, e.g., a population of patients having a cancer), a reference sample, and/or a pre-assigned value (e.g., a cut-off value which was previously determined to significantly (e.g., statistically significantly) separate a
25 first subset of individuals who have been treated with an anti-cancer therapy (e.g., an anti-cancer therapy including a VEGF antagonist and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., anti-PD-1 antibody)), or an anti-cancer therapy including a multi-targeted tyrosine kinase inhibitor) in a reference population and a second subset of individuals who have been treated with a different anti-cancer therapy
30 (or who have not been treated with the anti-cancer therapy) in the same reference population based on a significant difference between an individual's responsiveness to treatment with the anti-cancer therapy and an individual's responsiveness to treatment with the different anti-cancer therapy above the cut-off value and/or below the cut-off value). In some embodiments, the cut-off value may be the median or mean expression level in the reference population. In other embodiments, the reference level may be the
35 top 40%, the top 30%, the top 20%, the top 10%, the top 5%, or the top 1% of the expression level in the reference population. In particular embodiments, the cut-off value may be the median expression level in the reference population. It will be appreciated by one skilled in the art that the numerical value for the reference expression level may vary depending on the indication (e.g., a cancer (e.g., a kidney cancer, a breast cancer, a lung cancer, or a bladder cancer), the methodology used to detect expression levels

(e.g., RNA-seq or RT-qPCR), and/or the specific combinations of genes examined (e.g., any combination of the genes set forth in Table 1; or any one of the combinations of genes listed in Tables 2-12).

Expression “above” a level (e.g., above a reference level), “increased expression,” “increased expression level,” “increased levels,” “elevated expression,” “elevated expression levels,” or “elevated levels” refers to an increased expression or increased levels of a biomarker in an individual relative to the expression level of the biomarker in a control (e.g., an individual or individuals who are not suffering from the disease or disorder (e.g., cancer), an internal control (e.g., a housekeeping biomarker), or the level of a biomarker in a sample obtained prior to administration of a therapy (e.g., an anti-cancer therapy that includes a VEGF antagonist and a PD-L1 antagonist)), or relative to a reference level (e.g., the median expression level of the biomarker in samples from a group/population of patients, e.g., patients having cancer who are being tested for responsiveness to a VEGF antagonist and a PD-L1 axis binding antagonist; the median expression level of the biomarker in samples from a group/population of patients, e.g., patients having cancer who have been identified as not responding to a VEGF antagonist and a PD-L1 axis binding antagonist; or the level in a sample previously obtained from the individual at a prior time).

Expression “below” a level (e.g., below a reference level), “decreased expression,” “decreased expression level,” “decreased levels,” “reduced expression,” “reduced expression levels,” or “reduced levels” refers to a decrease expression or decreased levels of a biomarker in an individual relative to the expression level of the biomarker in a control (e.g., an individual or individuals who are not suffering from the disease or disorder (e.g., cancer), an internal control (e.g., a housekeeping biomarker), or the level of a biomarker in a sample obtained prior to administration of a therapy (e.g., an anti-cancer therapy that includes a VEGF antagonist and a PD-L1 antagonist)), or relative to a reference level (e.g., the median expression level of the biomarker in samples from a group/population of patients, e.g., patients having cancer who are being tested for responsiveness to a VEGF antagonist and a PD-L1 axis binding antagonist; the median expression level of the biomarker in samples from a group/population of patients, e.g., patients having cancer who have been identified as not responding to a VEGF antagonist and a PD-L1 axis binding antagonist; or the level in a sample previously obtained from the individual at a prior time). In some embodiments, reduced expression is little or no expression.

A “reference sample,” “reference cell,” “reference tissue,” “control sample,” “control cell,” or “control tissue,” as used herein, refers to a sample, cell, tissue, or standard that is used for comparison purposes. In one embodiment, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is obtained from a healthy and/or non-diseased part of the body (e.g., tissue or cells) of the same patient or individual. For example, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue may be healthy and/or non-diseased cells or tissue adjacent to the diseased cells or tissue (e.g., cells or tissue adjacent to a tumor). In another embodiment, a reference sample is obtained from an untreated tissue and/or cell of the body of the same patient or individual. In yet another embodiment, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is obtained from a healthy and/or non-diseased part of the body (e.g., tissues or cells) of an individual who is not the patient or individual. In even another embodiment, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is obtained from an untreated tissue and/or cell of the body of an individual who is not the patient or

individual. In another embodiment, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is obtained from a patient prior to administration of a therapy (e.g., an anti-cancer therapy that includes a VEGF antagonist and/or a PD-L1 axis binding antagonist).

The phrase “based on” when used herein means that the information about one or more biomarkers is used to inform a treatment decision, information provided on a package insert, or marketing/promotional guidance, etc.

The term “housekeeping biomarker” refers to a biomarker or group of biomarkers (e.g., polynucleotides and/or polypeptides) which are typically similarly present in all cell types. In some embodiments, the housekeeping biomarker is a “housekeeping gene.” A “housekeeping gene” refers herein to a gene or group of genes which encode proteins whose activities are essential for the maintenance of cell function and which are typically similarly present in all cell types.

By “correlate” or “correlating” is meant comparing, in any way, the performance and/or results of a first analysis or protocol with the performance and/or results of a second analysis or protocol. For example, one may use the results of a first analysis or protocol in carrying out a second protocols and/or one may use the results of a first analysis or protocol to determine whether a second analysis or protocol should be performed. With respect to the embodiment of polypeptide analysis or protocol, one may use the results of the polypeptide expression analysis or protocol to determine whether a specific therapeutic regimen should be performed. With respect to the embodiment of polynucleotide analysis or protocol, one may use the results of the polynucleotide expression analysis or protocol to determine whether a specific therapeutic regimen should be performed.

As used herein, “treatment” (and grammatical variations thereof such as “treat” or “treating”) refers to clinical intervention in an attempt to alter the natural course of the individual being treated, and can be performed either for prophylaxis or during the course of clinical pathology. Desirable effects of treatment include, but are not limited to, preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis. In some embodiments, antibodies (e.g., anti-VEGF antibodies and anti-PD-L1 antibodies or anti-PD-1 antibodies) are used to delay development of a disease or to slow the progression of a disease or disorder.

“Amplification,” as used herein generally refers to the process of producing multiple copies of a desired sequence. “Multiple copies” mean at least two copies. A “copy” does not necessarily mean perfect sequence complementarity or identity to the template sequence. For example, copies can include nucleotide analogs such as deoxyinosine, intentional sequence alterations (such as sequence alterations introduced through a primer comprising a sequence that is hybridizable, but not complementary, to the template), and/or sequence errors that occur during amplification.

The term “multiplex-PCR” refers to a single PCR reaction carried out on nucleic acid obtained from a single source (e.g., an individual) using more than one primer set for the purpose of amplifying two or more DNA sequences in a single reaction.

The technique of “polymerase chain reaction” or “PCR” as used herein generally refers to a procedure wherein minute amounts of a specific piece of nucleic acid, RNA and/or DNA, are amplified as

described, for example, in U.S. Pat. No. 4,683,195. Generally, sequence information from the ends of the region of interest or beyond needs to be available, such that oligonucleotide primers can be designed; these primers will be identical or similar in sequence to opposite strands of the template to be amplified. The 5' terminal nucleotides of the two primers may coincide with the ends of the amplified material. PCR can be used to amplify specific RNA sequences, specific DNA sequences from total genomic DNA, and cDNA transcribed from total cellular RNA, bacteriophage, or plasmid sequences, etc. See generally Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.* 51:263 (1987) and Erlich, ed., *PCR Technology*, (Stockton Press, NY, 1989). As used herein, PCR is considered to be one, but not the only, example of a nucleic acid polymerase reaction method for amplifying a nucleic acid test sample, comprising the use of a known nucleic acid (DNA or RNA) as a primer and utilizes a nucleic acid polymerase to amplify or generate a specific piece of nucleic acid or to amplify or generate a specific piece of nucleic acid which is complementary to a particular nucleic acid.

"Quantitative real-time polymerase chain reaction" or "qRT-PCR" refers to a form of PCR wherein the amount of PCR product is measured at each step in a PCR reaction. This technique has been described in various publications including, for example, Cronin et al., *Am. J. Pathol.* 164(1):35-42 (2004) and Ma et al., *Cancer Cell* 5:607-616 (2004).

The term "microarray" refers to an ordered arrangement of hybridizable array elements, preferably polynucleotide probes, on a substrate.

The term "RNA-seq," also called "Whole Transcriptome Shotgun Sequencing (WTSS)," refers to the use of high-throughput sequencing technologies to sequence and/or quantify cDNA to obtain information about a sample's RNA content. Publications describing RNA-seq include: Wang et al. *Nature Reviews Genetics* 10(1):57-63, 2009; Ryan et al. *BioTechniques* 45(1):81-94, 2008; and Maher et al. *Nature* 458(7234):97-101, 2009.

The term "diagnosis" is used herein to refer to the identification or classification of a molecular or pathological state, disease or condition (e.g., cancer (e.g., kidney cancer)). For example, "diagnosis" may refer to identification of a particular type of cancer. "Diagnosis" may also refer to the classification of a particular subtype of cancer, for instance, by histopathological criteria, or by molecular features (e.g., a subtype characterized by expression of one or a combination of biomarkers (e.g., particular genes or proteins encoded by said genes)).

A "tumor-infiltrating immune cell," as used herein, refers to any immune cell present in a tumor or a sample thereof. Tumor-infiltrating immune cells include, but are not limited to, intratumoral immune cells, peritumoral immune cells, other tumor stroma cells (e.g., fibroblasts), or any combination thereof. Such tumor-infiltrating immune cells can be, for example, T lymphocytes (such as CD8⁺ T lymphocytes and/or CD4⁺ T lymphocytes), B lymphocytes, or other bone marrow-lineage cells, including granulocytes (e.g., neutrophils, eosinophils, and basophils), monocytes, macrophages (e.g., CD68⁺/CD163⁺ macrophages), dendritic cells (e.g., interdigitating dendritic cells), histiocytes, and natural killer (NK) cells.

A "tumor cell" as used herein, refers to any tumor cell present in a tumor or a sample thereof. Tumor cells may be distinguished from other cells that may be present in a tumor sample, for example, stromal cells and tumor-infiltrating immune cells, using methods known in the art and/or described herein.

As used herein, “administering” is meant a method of giving a dosage of a compound (e.g., a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))), a PD-L1 axis binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab), and/or an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))) or a composition (e.g., a pharmaceutical composition, e.g., a pharmaceutical composition including a VEGF antagonist, a PD-L1 axis binding antagonist, and/or an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))) to a patient. The compositions utilized in the methods described herein can be administered, for example, intramuscularly, intravenously, intradermally, percutaneously, intraarterially, intraperitoneally, intralesionally, intracranially, intraarticularly, intraprostatically, intrapleurally, intratracheally, intrathecally, intranasally, intravaginally, intrarectally, topically, intratumorally, peritoneally, subcutaneously, subconjunctivally, intravesicularly, mucosally, intrapericardially, intraumbilically, intraocularly, intraorbitally, intravitreally (e.g., by intravitreal injection), by eye drop, orally, topically, transdermally, parenterally, by inhalation, by injection, by implantation, by infusion, by continuous infusion, by localized perfusion bathing target cells directly, by catheter, by lavage, in cremes, or in lipid compositions. The compositions utilized in the methods described herein can also be administered systemically or locally. The method of administration can vary depending on various factors (e.g., the compound or composition being administered and the severity of the condition, disease, or disorder being treated).

A “therapeutically effective amount” refers to an amount of a therapeutic agent to treat or prevent a disease or disorder (e.g., a cancer, e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)) in a mammal. In the case of cancers, the therapeutically effective amount of the therapeutic agent may reduce the number of cancer cells; reduce the primary tumor size; inhibit (i.e., slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (i.e., slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the disorder. To the extent the drug may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. For cancer therapy, efficacy in vivo can, for example, be measured by assessing the duration of survival (e.g., overall survival or progression-free survival), time to disease progression (TTP), response rates (e.g., complete response (CR) and partial response (PR)), duration of response, and/or quality of life.

The term “concurrently” is used herein to refer to administration of two or more therapeutic agents, where at least part of the administration overlaps in time. Accordingly, concurrent administration includes a dosing regimen when the administration of one or more agent(s) continues after discontinuing the administration of one or more other agent(s). For example, in some embodiments, a VEGF antagonist and a PD-L1 axis binding antagonist may be administered concurrently.

By “reduce or inhibit” is meant the ability to cause an overall decrease of 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, or greater. Reduce or inhibit can refer, for example, to the

symptoms of the disorder being treated, the presence or size of metastases, or the size of the primary tumor.

A “loading” dose herein generally comprises an initial dose of a therapeutic agent administered to a patient, and is followed by one or more maintenance dose(s) thereof. Generally, a single loading dose is administered, but multiple loading doses are contemplated herein. Usually, the amount of loading dose(s) administered exceeds the amount of the maintenance dose(s) administered and/or the loading dose(s) are administered more frequently than the maintenance dose(s), so as to achieve the desired steady-state concentration of the therapeutic agent earlier than can be achieved with the maintenance dose(s).

A “maintenance” dose or “extended” dose herein refers to one or more doses of a therapeutic agent administered to the patient over a treatment period. Usually, the maintenance doses are administered at spaced treatment intervals, such as approximately every week, approximately every 2 weeks, approximately every 3 weeks, or approximately every 4 weeks.

“Response to a treatment,” “responsiveness to treatment,” or “benefit from a treatment” can be assessed using any endpoint indicating a benefit to the individual, including, without limitation, (1) inhibition, to some extent, of disease progression (e.g., cancer progression), including slowing down and complete arrest; (2) a reduction in tumor size; (3) inhibition (i.e., reduction, slowing down or complete stopping) of cancer cell infiltration into adjacent peripheral organs and/or tissues; (4) inhibition (i.e. reduction, slowing down or complete stopping) of metastasis; (5) relief, to some extent, of one or more symptoms associated with the disease or disorder (e.g., cancer); (6) increase or extend in the length of survival, including overall survival (OS HR < 1) and progression free survival (PFS HR<1); and/or (9) decreased mortality at a given point of time following treatment (e.g., treatment with an anti-cancer therapy that includes a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody), or treatment with an anti-cancer therapy that includes an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))))).

An “objective response” refers to a measurable response, including complete response (CR) or partial response (PR). In some embodiments, the “objective response rate (ORR)” refers to the sum of complete response (CR) rate and partial response (PR) rate.

By “complete response” or “CR” is intended the disappearance of all signs of cancer (e.g., disappearance of all target lesions) in response to treatment. This does not always mean the cancer has been cured.

As used herein, “partial response” or “PR” refers to a decrease in the size of one or more tumors or lesions, or in the extent of cancer in the body, in response to treatment. For example, in some embodiments, PR refers to at least a 30% decrease in the sum of the longest diameters (SLD) of target lesions, taking as reference the baseline SLD.

“Sustained response” refers to the sustained effect on reducing tumor growth after cessation of a treatment. For example, the tumor size may remain to be the same or smaller as compared to the size at the beginning of the administration phase. In some embodiments, the sustained response has a duration at least the same as the treatment duration, at least 1.5x, 2.0x, 2.5x, or 3.0x length of the treatment duration, or longer.

As used herein, “stable disease” or “SD” refers to neither sufficient shrinkage of target lesions to qualify for PR, nor sufficient increase to qualify for PD, taking as reference the smallest SLD since the treatment started.

As used herein, “progressive disease” or “PD” refers to at least a 20% increase in the SLD of target lesions, taking as reference the smallest SLD recorded since the treatment started or the presence of one or more new lesions.

The term “survival” refers to the patient remaining alive, and includes overall survival as well as progression-free survival.

As used herein, “progression-free survival” or “PFS” refers to the length of time during and after treatment during which the disease being treated (e.g., cancer, e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), or a breast cancer (e.g., TNBC)) does not progress or get worse. Progression-free survival may include the amount of time individuals have experienced a complete response or a partial response, as well as the amount of time individuals have experienced stable disease.

As used herein, “overall survival” or “OS” refers to the percentage of subjects in a group who are likely to be alive after a particular duration of time (e.g., 6 months, 1 year, 2 years, 3 years, 4 years, 5 years, 10 years, 15 years, 20 years, or more than 20 years from the time of diagnosis or treatment).

By “extending survival” is meant increasing overall or progression-free survival in a treated patient relative to an untreated patient (i.e. relative to a patient not treated with the medicament), or relative to a patient who does not express a biomarker at the designated level, and/or relative to a patient treated with an approved anti-tumor agent (e.g., an anti-VEGF antibody (e.g., bevacizumab), a PD-L1 axis binding antagonist (e.g., atezolizumab), and/or a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib)).

As used herein, “hazard ratio” or “HR” is a statistical definition for rates of events. For the purpose of the invention, hazard ratio is defined as representing the probability of an event (e.g., PFS or OS) in the experimental (e.g., treatment) group/arm divided by the probability of an event in the control group/arm at any specific point in time. An HR with a value of 1 indicates that the relative risk of an endpoint (e.g., death) is equal in both the “treatment” and “control” groups; a value greater than 1 indicates that the risk is greater in the treatment group relative to the control group; and a value less than 1 indicates that the risk is greater in the control group relative to the treatment group. “Hazard ratio” in progression-free survival analysis (i.e., PFS HR) is a summary of the difference between two progression-free survival curves, representing the reduction in the risk of death on treatment compared to control, over a period of follow-up. “Hazard ratio” in overall survival analysis (i.e., OS HR) is a summary of the difference between two overall survival curves, representing the reduction in the risk of death on treatment compared to control, over a period of follow-up.

The term “anti-cancer therapy” refers to a therapy useful in treating cancer. Examples of anti-cancer therapeutic agents include, but are limited to, cytotoxic agents, chemotherapeutic agents, growth inhibitory agents, agents used in radiation therapy, anti-angiogenesis agents, apoptotic agents, anti-tubulin agents, and other agents to treat cancer, for example, anti-CD20 antibodies, platelet derived growth factor inhibitors (e.g., GLEEVEC™ (imatinib mesylate)), a COX-2 inhibitor (e.g., celecoxib), interferons, cytokines, antagonists (e.g., neutralizing antibodies) that bind to one or more of the following targets: PDGFR- β , BlyS, APRIL, BCMA receptor(s), TRAIL/Apo2, other bioactive and organic chemical agents, and the like. Combinations thereof are also included in the invention.

A “VEGF antagonist” or “VEGF-specific antagonist” refers to a molecule capable of binding to VEGF, reducing VEGF expression levels, or neutralizing, blocking, inhibiting, abrogating, reducing, or interfering with VEGF biological activities, including, but not limited to, VEGF binding to one or more VEGF receptors, VEGF signaling, and VEGF mediated angiogenesis and endothelial cell survival or proliferation. For example, a molecule capable of neutralizing, blocking, inhibiting, abrogating, reducing, or interfering with VEGF biological activities can exert its effects by binding to one or more VEGF receptor (VEGFR) (e.g., VEGFR1, VEGFR2, VEGFR3, membrane-bound VEGF receptor (mbVEGFR), or soluble VEGF receptor (sVEGFR)). Such antagonists are also referred to herein as “VEGFR inhibitors.” Included as VEGF-specific antagonists useful in the methods of the invention are polypeptides that specifically bind to VEGF, anti-VEGF antibodies and antigen-binding fragments thereof, receptor molecules and derivatives which bind specifically to VEGF thereby sequestering its binding to one or more receptors, fusions proteins (e.g., VEGF-Trap (Regeneron)), and VEGF₁₂₁-gelonin (Peregrine). VEGF-specific antagonists also include antagonist variants of VEGF polypeptides, antisense nucleobase oligomers complementary to at least a fragment of a nucleic acid molecule encoding a VEGF polypeptide; small RNAs complementary to at least a fragment of a nucleic acid molecule encoding a VEGF polypeptide; ribozymes that target VEGF; peptibodies to VEGF; and VEGF aptamers. VEGF antagonists also include polypeptides that bind to VEGFR, anti-VEGFR antibodies, and antigen-binding fragments thereof, and derivatives which bind to VEGFR thereby blocking, inhibiting, abrogating, reducing, or interfering with VEGF biological activities (e.g., VEGF signaling), or fusions proteins. VEGF-specific antagonists also include nonpeptide small molecules that bind to VEGF or VEGFR and are capable of blocking, inhibiting, abrogating, reducing, or interfering with VEGF biological activities. Thus, the term “VEGF activities” specifically includes VEGF mediated biological activities of VEGF. In certain embodiments, the VEGF antagonist reduces or inhibits, by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more, the expression level or biological activity of VEGF. In some embodiments, the VEGF inhibited by the VEGF-specific antagonist is VEGF (8-109), VEGF (1-109), or VEGF₁₆₅.

As used herein VEGF antagonists can include, but are not limited to, anti-VEGFR2 antibodies and related molecules (e.g., ramucirumab, tanibirumab, aflibercept), anti-VEGFR1 antibodies and related molecules (e.g., icrucumab, aflibercept (VEGF Trap-Eye; EYLEA®), and ziv-aflibercept (VEGF Trap; ZALTRAP®)), bispecific VEGF antibodies (e.g., MP-0250, vanucizumab (VEGF-ANG2), and bispecific antibodies disclosed in US 2001/0236388), bispecific antibodies including combinations of two of anti-VEGF, anti-VEGFR1, and anti-VEGFR2 arms, anti-VEGFA antibodies (e.g., bevacizumab, sevacizumab), anti-VEGFB antibodies, anti-VEGFC antibodies (e.g., VGX-100), anti-VEGFD antibodies, and nonpeptide

small molecule VEGF antagonists (e.g., pazopanib, axitinib, vandetanib, stivarga, cabozantinib, lenvatinib, nintedanib, orantinib, telatinib, dovitinig, cediranib, motesanib, sulfatinib, apatinib, foretinib, famitinib, and tivozanib).

An “anti-VEGF antibody” is an antibody that binds to VEGF with sufficient affinity and specificity.

In certain embodiments, the antibody will have a sufficiently high binding affinity for VEGF, for example, the antibody may bind hVEGF with a K_d value of between 100 nM-1 pM. Antibody affinities may be determined, e.g., by a surface plasmon resonance based assay (such as the BIAcore® assay as described in PCT Application Publication No. WO2005/012359); enzyme-linked immunoabsorbent assay (ELISA); and competition assays (e.g. radioimmunoassays (RIAs)).

In certain embodiments, the anti-VEGF antibody can be used as a therapeutic agent in targeting and interfering with diseases or conditions wherein the VEGF activity is involved. Also, the antibody may be subjected to other biological activity assays, e.g., in order to evaluate its effectiveness as a therapeutic. Such assays are known in the art and depend on the target antigen and intended use for the antibody. Examples include the HUVEC inhibition assay; tumor cell growth inhibition assays (as described in WO 89/06692, for example); antibody-dependent cellular cytotoxicity (ADCC) and complement-mediated cytotoxicity (CDC) assays (U.S. Pat. No. 5,500,362); and agonistic activity or hematopoiesis assays (see WO 95/27062). An anti-VEGF antibody will usually not bind to other VEGF homologues such as VEGF-B or VEGF-C, nor other growth factors such as PlGF, PDGF, or bFGF. In one embodiment, anti-VEGF antibody is a monoclonal antibody that binds to the same epitope as the monoclonal anti-VEGF antibody A4.6.1 produced by hybridoma ATCC HB 10709. In another embodiment, the anti-VEGF antibody is a recombinant humanized anti-VEGF monoclonal antibody generated according to Presta et al. (*Cancer Res.* 57:4593-4599, 1997), including but not limited to the antibody known as bevacizumab (BV; AVASTIN®).

The anti-VEGF antibody “Bevacizumab (BV),” also known as “rhUMAb VEGF” or “AVASTIN®,” is a recombinant humanized anti-VEGF monoclonal antibody generated according to Presta et al. (*Cancer Res.* 57:4593-4599, 1997). It comprises mutated human IgG1 framework regions and antigen-binding complementarity-determining regions from the murine anti-hVEGF monoclonal antibody A.4.6.1 that blocks binding of human VEGF to its receptors. Approximately 93% of the amino acid sequence of bevacizumab, including most of the framework regions, is derived from human IgG1, and about 7% of the sequence is derived from the murine antibody A4.6.1. Bevacizumab has a molecular mass of about 149,000 daltons and is glycosylated. Bevacizumab and other humanized anti-VEGF antibodies are further described in U.S. Pat. No. 6,884,879 issued Feb. 26, 2005, the entire disclosure of which is expressly incorporated herein by reference. Additional preferred antibodies include the G6 or B20 series antibodies (e.g., G6-31, B20-4.1), as described in PCT Application Publication No. WO 2005/012359. For additional preferred antibodies see U.S. Pat. Nos. 7,060,269, 6,582,959, 6,703,020; 6,054,297; WO98/45332; WO 96/30046; WO94/10202; EP 0666868B1; U.S. Patent Application Publication Nos. 2006009360, 20050186208, 20030206899, 20030190317, 20030203409, and 20050112126; and Popkov et al., (*Journal of Immunological Methods* 288:149-164, 2004). Other preferred antibodies include those that bind to a functional epitope on human VEGF comprising of residues F17, M18, D19, Y21, Y25, Q89,

191, K101, E103, and C104 or, alternatively, comprising residues F17, Y21, Q22, Y25, D63, 183, and Q89.

The term “PD-L1 axis binding antagonist” refers to a molecule that inhibits the interaction of a PD-L1 axis binding partner with one or more of its binding partners, so as to remove T cell dysfunction resulting from signaling on the PD-1 signaling axis, with a result being restored or enhanced T cell function. As used herein, a PD-L1 axis binding antagonist includes a PD-L1 binding antagonist and a PD-1 binding antagonist as well as molecules that interfere with the interaction between PD-L1 and PD-1 (e.g., a PD-L2-Fc fusion).

The terms “anti-PD-L1 antibody” and “an antibody that binds to PD-L1” refer to an antibody that is capable of binding PD-L1 with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting PD-L1. In one embodiment, the extent of binding of an anti-PD-L1 antibody to an unrelated, non-PD-L1 protein is less than about 10% of the binding of the antibody to PD-L1 as measured, for example, by a RIA. In certain embodiments, an anti-PD-L1 antibody binds to an epitope of PD-L1 that is conserved among PD-L1 from different species.

The terms “anti-PD-1 antibody” and “an antibody that binds to PD-1” refer to an antibody that is capable of binding PD-1 with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting PD-1. In one embodiment, the extent of binding of an anti-PD-1 antibody to an unrelated, non-PD-1 protein is less than about 10% of the binding of the antibody to PD-1 as measured, for example, by a RIA. In certain embodiments, an anti-PD-1 antibody binds to an epitope of PD-1 that is conserved among PD-1 from different species.

The term “PD-L1 binding antagonist” refers to a molecule that decreases, blocks, inhibits, abrogates, or interferes with signal transduction resulting from the interaction of PD-L1 with either one or more of its binding partners, such as PD-1 or B7-1. In some embodiments, a PD-L1 binding antagonist is a molecule that inhibits the binding of PD-L1 to its binding partners. In a specific aspect, the PD-L1 binding antagonist inhibits binding of PD-L1 to PD-1 and/or B7-1. In some embodiments, the PD-L1 binding antagonists include anti-PD-L1 antibodies, antigen-binding fragments thereof, immunoadhesins, fusion proteins, oligopeptides, and other molecules that decrease, block, inhibit, abrogate, or interfere with signal transduction resulting from the interaction of PD-L1 with one or more of its binding partners, such as PD-1 or B7-1. In one embodiment, a PD-L1 binding antagonist reduces the negative co-stimulatory signal mediated by or through cell surface proteins expressed on T lymphocytes mediated signaling through PD-L1 so as to render a dysfunctional T-cell less dysfunctional (e.g., enhancing effector responses to antigen recognition). In some embodiments, a PD-L1 binding antagonist is an anti-PD-L1 antibody. In a specific embodiment, the anti-PD-L1 antibody is atezolizumab (CAS Registry Number: 1422185-06-5), also known as MPDL3280A, and described herein. In another specific embodiment, the anti-PD-L1 antibody is YW243.55.S70, described herein. In another specific embodiment, the anti-PD-L1 antibody is MDX-1105, described herein. In still another specific aspect, the anti-PD-L1 antibody is MEDI4736 (durvalumab), described herein. In still another specific aspect, the anti-PD-L1 antibody is MSB0010718C (avelumab), described herein.

As used herein, a “PD-1 binding antagonist” is a molecule that decreases, blocks, inhibits, abrogates or interferes with signal transduction resulting from the interaction of PD-1 with one or more of

its binding partners, such as PD-L1 and/or PD-L2. In some embodiments, the PD-1 binding antagonist is a molecule that inhibits the binding of PD-1 to its binding partners. In a specific aspect, the PD-1 binding antagonist inhibits the binding of PD-1 to PD-L1 and/or PD-L2. For example, PD-1 binding antagonists include anti PD-1 antibodies and antigen-binding fragments thereof, immunoadhesins, fusion proteins, oligopeptides, small molecule antagonists, polynucleotide antagonists, and other molecules that decrease, block, inhibit, abrogate or interfere with signal transduction resulting from the interaction of PD-1 with PD-L1 and/or PD-L2. In one embodiment, a PD-1 binding antagonist reduces the negative signal mediated by or through cell surface proteins expressed on T lymphocytes, and other cells, mediated signaling through PD-1 or PD-L1 so as to render a dysfunctional T cell less dysfunctional. In some embodiments, the PD-1 binding antagonist is an anti-PD-1 antibody. In a specific aspect, a PD-1 binding antagonist is MDX-1106 (nivolumab). In another specific aspect, a PD-1 binding antagonist is MK-3475 (pembrolizumab). In another specific aspect, a PD-1 binding antagonist is CT-011 (pidilizumab). In another specific aspect, a PD-1 binding antagonist is MEDI-0680 (AMP-514). In another specific aspect, a PD-1 binding antagonist is PDR001. In another specific aspect, a PD-1 binding antagonist is REGN2810. In another specific aspect, a PD-1 binding antagonist is BGB-108. In another specific aspect, a PD-1 binding antagonist is AMP-224.

An “angiogenesis inhibitor” or “anti-angiogenesis agent” refers to a small molecular weight substance, a polynucleotide, a polypeptide, an isolated protein, a recombinant protein, an antibody, or conjugates or fusion proteins thereof, that inhibits angiogenesis, vasculogenesis, or undesirable vascular permeability, either directly or indirectly. It should be understood that the anti-angiogenesis agent includes those agents that bind and block the angiogenic activity of the angiogenic factor or its receptor. For example, an anti-angiogenesis agent is an antibody or other antagonist to an angiogenic agent as defined above, e.g., antibodies to VEGF-A or the VEGF-A receptor (e.g., KDR receptor or Flt-1 receptor), anti-PDGFR inhibitors such as GLEEVEC™ (Imatinib Mesylate). Anti-angiogenesis agents also include native angiogenesis inhibitors, e.g., angiostatin, endostatin, etc. See, for example, Klagsbrun and D'Amore, *Annu. Rev. Physiol.*, 53:217-39 (1991); Streit and Detmar, *Oncogene*, 22:3172-3179 (2003) (e.g., Table 3 listing anti-angiogenic therapy in malignant melanoma); Ferrara & Alitalo, *Nature Medicine* 5(12):1359-1364 (1999); Tonini et al., *Oncogene*, 22:6549-6556 (2003) and, Sato *Int. J. Clin. Oncol.*, 8:200-206 (2003).

The term “cytotoxic agent” as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g., At²¹¹, I¹³¹, I¹²⁵, Y⁹⁰, Re¹⁸⁶, Re¹⁸⁸, Sm¹⁵³, Bi²¹², P³², and radioactive isotopes of Lu), chemotherapeutic agents, e.g., methotrexate, adriamycin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof such as nucleolytic enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof, and the various antitumor or anticancer agents disclosed below. A tumoricidal agent causes destruction of tumor cells.

A “chemotherapeutic agent” includes chemical compounds useful in the treatment of cancer. Examples of chemotherapeutic agents include erlotinib (TARCEVA®, Genentech/OSI Pharm.),

bortezomib (VELCADE®, Millennium Pharm.), disulfiram, epigallocatechin gallate, salinosporamide A, carfilzomib, 17-AAG (geldanamycin), radicicol, lactate dehydrogenase A (LDH-A), fulvestrant (FASLODEX®, AstraZeneca), sunitib (SUTENT®, Pfizer/Sugen), letrozole (FEMARA®, Novartis), imatinib mesylate (GLEEVEC®, Novartis), finasunate (VATALANIB®, Novartis), oxaliplatin (ELOXATIN®, Sanofi),
 5 5-FU (5-fluorouracil), leucovorin, Rapamycin (Sirolimus, RAPAMUNE®, Pfizer), Lapatinib (TYKERB®, GSK572016, Glaxo Smith Kline), Lonafamib (SCH 66336), sorafenib (NEXAVAR®, Bayer Labs), gefitinib (IRESSA®, AstraZeneca), AG1478, alkylating agents such as thiotepa and CYTOXAN® cyclophosphamide; alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including
 10 altretamine, triethylenemelamine, triethylenephosphoramidate, triethylenethiophosphoramidate and trimethylmelamine; acetogenins (especially bullatacin and bullatacinone); a camptothecin (including topotecan and irinotecan); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogs); cryptophycins (particularly cryptophycin 1 and cryptophycin 8); adrenocorticosteroids (including prednisone and prednisolone); cyproterone acetate; 5 α -reductases
 15 including finasteride and dutasteride; vorinostat, romidepsin, panobinostat, valproic acid, mocetinostat, dolastatin; aldesleukin, talc duocarmycin (including the synthetic analogs, KW-2189 and CB1-TM1); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlomaphazine, chlorophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard;
 20 nitrosoureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimustine; antibiotics such as the enediyne antibiotics (e.g., calicheamicin, especially calicheamicin γ 11 and calicheamicin ω 11 (*Angew. Chem. Intl. Ed. Engl.* 33:183-186, 1994); dynemicin, including dynemicin A; bisphosphonates, such as clodronate; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antibiotic chromophores), aclacinomysins, actinomycin, authramycin,
 25 azaserine, bleomycins, cactinomycin, carabycin, caminomycin, carzinophilin, chromomycinis, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, ADRIAMYCIN® (doxorubicin), morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins such as mitomycin C, mycophenolic acid, nogalamycin, olivomycins, peplomycin, porfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin,
 30 streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogs such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiothane,
 35 testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfomithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansinoids such as

maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidamrol; nitraerine; pentostatin; phenamet; pirarubicin; losoxantrone; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK® polysaccharide complex (JHS Natural Products, Eugene, Oreg.); razoxane; rhizoxin; sizofuran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, e.g., TAXOL (paclitaxel; Bristol-Myers Squibb Oncology, Princeton, N.J.), ABRAXANE® (Cremophor-free), albumin-engineered nanoparticle formulations of paclitaxel (American Pharmaceutical Partners, Schaumburg, Ill.), and TAXOTERE® (docetaxel, doxetaxel; Sanofi-Aventis); chloranmbucil; GEMZAR® (gemcitabine); 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; etoposide (VP-16); ifosfamide; mitoxantrone; vincristine; NAVELBINE® (vinorelbine); novantrone; teniposide; edatrexate; daunomycin; aminopterin; capecitabine (XELODA®); ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoids such as retinoic acid; and pharmaceutically acceptable salts, acids and derivatives of any of the above.

Chemotherapeutic agents also include anti-hormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens and selective estrogen receptor modulators (SERMs), including, for example, tamoxifen (including NOLVADEX®; tamoxifen citrate), raloxifene, droloxifene, iodoxyfene, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and FARESTON® (toremifine citrate); aromatase inhibitors that inhibit the enzyme aromatase, which regulates estrogen production in the adrenal glands, such as, for example, 4(5)-imidazoles, aminoglutethimide, MEGASE® (megestrol acetate), AROMASIN® (exemestane; Pfizer), formestane, fadrozole, RIVISOR® (vorozole), FEMARA® (letrozole; Novartis), and ARIMIDEX® (anastrozole; AstraZeneca); anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide and goserelin; buserelin, tripterelein, medroxyprogesterone acetate, diethylstilbestrol, premarin, fluoxymesterone, all transretinoic acid, fenretinide, as well as troxacitabine (a 1,3-dioxolane nucleoside cytosine analog); protein kinase inhibitors; lipid kinase inhibitors; antisense oligonucleotides, particularly those which inhibit expression of genes in signaling pathways implicated in aberrant cell proliferation, such as, for example, PKC-alpha, Ral and H-Ras; ribozymes such as VEGF expression inhibitors (e.g., ANGIOZYME®) and HER2 expression inhibitors; vaccines such as gene therapy vaccines, for example, ALLOVECTIN®, LEUVECTIN®, and VAXID®; PROLEUKIN®, rIL-2; a topoisomerase 1 inhibitor such as LURTOTECAN®; ABARELIX® mRH; and pharmaceutically acceptable salts, acids and derivatives of any of the above.

Chemotherapeutic agents also include antibodies such as alemtuzumab (Campath), bevacizumab (AVASTIN®, Genentech); cetuximab (ERBITUX®, Imclone); panitumumab (VECTIBIX®, Amgen), rituximab (RITUXAN®, Genentech/Biogen Idec), pertuzumab (OMNITARG®, 2C4, Genentech), trastuzumab (HERCEPTIN®, Genentech), tositumomab (Bexxar, Corixa), and the antibody drug conjugate, gemtuzumab ozogamicin (MYLOTARG®, Wyeth). Additional humanized monoclonal antibodies with therapeutic potential as agents in combination with the compounds of the invention

include: apolizumab, aselizumab, atlizumab, bapineuzumab, bivatuzumab mertansine, cantuzumab mertansine, cedelizumab, certolizumab pegol, cidfusituzumab, cidtuzumab, daclizumab, eculizumab, efalizumab, epratuzumab, erlizumab, felvizumab, fontolizumab, gemtuzumab ozogamicin, inotuzumab ozogamicin, ipilimumab, labetuzumab, lintuzumab, matuzumab, mepolizumab, motavizumab, 5 motovizumab, natalizumab, nimotuzumab, nolovizumab, numavizumab, ocrelizumab, omalizumab, palivizumab, pascolizumab, pecfusituzumab, pectuzumab, pexelizumab, ralivizumab, ranibizumab, reslivizumab, reslizumab, resyvizumab, rovelizumab, ruplizumab, sibrotuzumab, siplizumab, sontuzumab, tacatuzumab tetraxetan, tadocizumab, talizumab, tefibazumab, tocilizumab, toralizumab, tucotuzumab celmoleukin, tucusituzumab, umavizumab, urtoxazumab, ustekinumab, visilizumab, and the anti- 10 interleukin-12 (ABT-874/J695, Wyeth Research and Abbott Laboratories), which is a recombinant, exclusively human-sequence, full-length IgG1 λ antibody genetically modified to recognize interleukin-12 p40 protein.

Chemotherapeutic agents also include "EGFR inhibitors," which refers to compounds that bind to or otherwise interact directly with EGFR and prevent or reduce its signaling activity, and is alternatively 15 referred to as an "EGFR antagonist." Examples of such agents include antibodies and small molecules that bind to EGFR. Examples of antibodies which bind to EGFR include MAb 579 (ATCC CRL HB 8506), MAb 455 (ATCC CRL HB8507), MAb 225 (ATCC CRL 8508), MAb 528 (ATCC CRL 8509) (see, US Patent No. 4,943, 533, Mendelsohn et al.) and variants thereof, such as chimerized 225 (C225 or Cetuximab; ERBUTIX®) and reshaped human 225 (H225) (see, WO 96/40210, Imclone Systems Inc.); 20 IMC-11F8, a fully human, EGFR-targeted antibody (Imclone); antibodies that bind type II mutant EGFR (US Patent No. 5,212,290); humanized and chimeric antibodies that bind EGFR as described in US Patent No. 5,891,996; and human antibodies that bind EGFR, such as ABX-EGF or Panitumumab (see WO98/50433, Abgenix/Amgen); EMD 55900 (Stragliotto et al. *Eur. J. Cancer* 32A:636-640 (1996)); EMD7200 (matuzumab) a humanized EGFR antibody directed against EGFR that competes with both 25 EGF and TGF- α for EGFR binding (EMD/Merck); human EGFR antibody, HuMax-EGFR (GenMab); fully human antibodies known as E1.1, E2.4, E2.5, E6.2, E6.4, E2.11, E6.3 and E7.6.3 and described in US 6,235,883; MDX-447 (Medarex Inc); and mAb 806 or humanized mAb 806 (Johns et al., *J. Biol. Chem.* 279(29):30375-30384 (2004)). The anti-EGFR antibody may be conjugated with a cytotoxic agent, thus generating an immunoconjugate (see, e.g., EP659,439A2, Merck Patent GmbH). EGFR 30 antagonists include small molecules such as compounds described in US Patent Nos: 5,616,582, 5,457,105, 5,475,001, 5,654,307, 5,679,683, 6,084,095, 6,265,410, 6,455,534, 6,521,620, 6,596,726, 6,713,484, 5,770,599, 6,140,332, 5,866,572, 6,399,602, 6,344,459, 6,602,863, 6,391,874, 6,344,455, 5,760,041, 6,002,008, and 5,747,498, as well as the following PCT publications: WO98/14451, WO98/50038, WO99/09016, and WO99/24037. Particular small molecule EGFR antagonists include 35 OSI-774 (CP-358774, erlotinib, TARCEVA® Genentech/OSI Pharmaceuticals); PD 183805 (CI 1033, 2-propenamide, N-[4-[(3-chloro-4-fluorophenyl)amino]-7-[3-(4-morpholinyl)propoxy]-6-quinazolinyl]-, dihydrochloride, Pfizer Inc.); ZD1839, gefitinib (IRESSA®) 4-(3'-Chloro-4'-fluoroanilino)-7-methoxy-6-(3-morpholinopropoxy)quinazoline, AstraZeneca); ZM 105180 ((6-amino-4-(3-methylphenyl-amino)-

quinazoline, Zeneca); BIBX-1382 (N8-(3-chloro-4-fluoro-phenyl)-N2-(1-methyl-piperidin-4-yl)-pyrimido[5,4-d]pyrimidine-2,8-diamine, Boehringer Ingelheim); PKI-166 ((R)-4-[4-[(1-phenylethyl)amino]-1H-pyrrolo[2,3-d]pyrimidin-6-yl]-phenol); (R)-6-(4-hydroxyphenyl)-4-[(1-phenylethyl)amino]-7H-pyrrolo[2,3-d]pyrimidine); CL-387785 (N-[4-[(3-bromophenyl)amino]-6-quinazoliny]-2-butyramide); EKB-569 (N-[4-[(3-chloro-4-fluorophenyl)amino]-3-cyano-7-ethoxy-6-quinoliny]-4-(dimethylamino)-2-butenamide) (Wyeth); AG1478 (Pfizer); AG1571 (SU 5271; Pfizer); dual EGFR/HER2 tyrosine kinase inhibitors such as lapatinib (TYKERB®, GSK572016 or N-[3-chloro-4-[(3 fluorophenyl)methoxy]phenyl]-6[[[2methylsulfonyl)ethyl]amino]methyl]-2-furanyl]-4-quinazolinamine).

Chemotherapeutic agents also include "tyrosine kinase inhibitors" including the EGFR-targeted drugs noted in the preceding paragraph; small molecule HER2 tyrosine kinase inhibitor such as TAK165 available from Takeda; CP-724,714, an oral selective inhibitor of the ErbB2 receptor tyrosine kinase (Pfizer and OSI); dual-HER inhibitors such as EKB-569 (available from Wyeth) which preferentially binds EGFR but inhibits both HER2 and EGFR-overexpressing cells; lapatinib (GSK572016; available from Glaxo-SmithKline), an oral HER2 and EGFR tyrosine kinase inhibitor; PKI-166 (available from Novartis); pan-HER inhibitors such as canertinib (CI-1033; Pharmacia); Raf-1 inhibitors such as antisense agent ISIS-5132 available from ISIS Pharmaceuticals which inhibit Raf-1 signaling; non-HER targeted TK inhibitors such as imatinib mesylate (GLEEVEC®, available from Glaxo SmithKline); multi-targeted tyrosine kinase inhibitors such as sunitinib (SUTENT®, available from Pfizer); VEGF receptor tyrosine kinase inhibitors such as vatalanib (PTK787/ZK222584, available from Novartis/Schering AG); MAPK extracellular regulated kinase I inhibitor CI-1040 (available from Pharmacia); quinazolines, such as PD 153035, 4-(3-chloroanilino) quinazoline; pyridopyrimidines; pyrimidopyrimidines; pyrrolopyrimidines, such as CGP 59326, CGP 60261 and CGP 62706; pyrazolopyrimidines, 4-(phenylamino)-7H-pyrrolo[2,3-d]pyrimidines; curcumin (diferuloyl methane, 4,5-bis (4-fluoroanilino)phthalimide); tyrphostines containing nitrothiophene moieties; PD-0183805 (Warner-Lambert); antisense molecules (e.g. those that bind to HER-encoding nucleic acid); quinoxalines (US Patent No. 5,804,396); tryphostins (US Patent No. 5,804,396); ZD6474 (Astra Zeneca); PTK-787 (Novartis/Schering AG); pan-HER inhibitors such as CI-1033 (Pfizer); Affinitac (ISIS 3521; Isis/Lilly); imatinib mesylate (GLEEVEC®); PKI 166 (Novartis); GW2016 (Glaxo SmithKline); CI-1033 (Pfizer); EKB-569 (Wyeth); Semaxinib (Pfizer); ZD6474 (AstraZeneca); PTK-787 (Novartis/Schering AG); INC-1C11 (Imclone), rapamycin (sirolimus, RAPAMUNE®); or as described in any of the following patent publications: US Patent No. 5,804,396, WO 1999/09016, WO 1998/43960, WO 1997/38983, WO 1999/06378, WO 1999/06396, WO 1996/30347, WO 1996/33978, WO 1996/3397, and WO 1996/33980.

The term "multi-targeted tyrosine kinase inhibitor," as used herein, refers to a tyrosine kinase inhibitor that inhibits multiple (i.e., more than one) tyrosine kinase proteins. The tyrosine kinase proteins may be receptor tyrosine kinases and/or cellular tyrosine kinases. For example, the multi-targeted tyrosine kinase inhibitor may inhibit platelet-derived growth factor receptors (e.g., PDGFR- α , PDGFR- β , and/or PDGFR- $\alpha\beta$), VEGF receptors (e.g., VEGFR1 and/or VEGFR2), CD117 (c-Kit), RET, CD114, and/or CD135. Exemplary multi-targeted tyrosine kinase inhibitors include sunitinib (also known as N-[2-

(Diethylamino)ethyl]-5-[(Z)-(5-fluoro-2-oxo-1,2-dihydro-3H-indol-3-ylidene)methyl]-2,4-dimethyl-1H-pyrrole-3-carboxamide, SUTENT® or SU11248), SU6656, motesanib, sorafenib (e.g., NEXEVAR® or BAY439006), axitinib, afatinib, bosutinib, crizotinib, cabozantinib, dasatinib, entrectinib, pazopanib, lapatinib, and vandetanib (also known as ZACTIMA® or ZD6474). It is to be understood that a multi-targeted tyrosine kinase inhibitor that inhibits a VEGF receptor may also be considered a VEGFR inhibitor.

Chemotherapeutic agents also include dexamethasone, interferons, colchicine, metoprine, cyclosporine, amphotericin, metronidazole, alemtuzumab, alitretinoin, allopurinol, amifostine, arsenic trioxide, asparaginase, BCG live, bevacuzimab, bexarotene, cladribine, clofarabine, darbepoetin alfa, denileukin, dexrazoxane, epoetin alfa, elotinib, filgrastim, histrelin acetate, ibritumomab, interferon alfa-2a, interferon alfa-2b, lenalidomide, levamisole, mesna, methoxsalen, nandrolone, nelarabine, nofetumomab, oprelvekin, palifermin, pamidronate, pegademase, pegaspargase, pegfilgrastim, pemetrexed disodium, plicamycin, porfimer sodium, quinacrine, rasburicase, sargramostim, temozolomide, VM-26, 6-TG, toremifene, tretinoin, all-trans retinoic acid (ATRA), valrubicin, zoledronate, and zoledronic acid, and pharmaceutically acceptable salts thereof.

The term “prodrug” as used herein refers to a precursor or derivative form of a pharmaceutically active substance that is less cytotoxic to tumor cells compared to the parent drug and is capable of being enzymatically activated or converted into the more active parent form. See, for example, Wilman, “Prodrugs in Cancer Chemotherapy” *Biochemical Society Transactions*, 14, pp. 375-382, 615th Meeting Belfast (1986) and Stella et al., “Prodrugs: A Chemical Approach to Targeted Drug Delivery,” *Directed Drug Delivery*, Borchardt et al., (ed.), pp. 247-267, Humana Press (1985). The prodrugs of this invention include, but are not limited to, phosphate-containing prodrugs, thiophosphate-containing prodrugs, sulfate-containing prodrugs, peptide-containing prodrugs, D-amino acid-modified prodrugs, glycosylated prodrugs, β -lactam-containing prodrugs, optionally substituted phenoxyacetamide-containing prodrugs or optionally substituted phenylacetamide-containing prodrugs, 5-fluorocytosine and other 5-fluorouridine prodrugs which can be converted into the more active cytotoxic free drug. Examples of cytotoxic drugs that can be derivatized into a prodrug form for use in this invention include, but are not limited to, those chemotherapeutic agents described above.

A “growth inhibitory agent” when used herein refers to a compound or composition which inhibits growth and/or proliferation of a cell (e.g., a cell whose growth is dependent on PD-L1 expression) either *in vitro* or *in vivo*. Thus, the growth inhibitory agent may be one which significantly reduces the percentage of cells in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topoisomerase II inhibitors such as the anthracycline antibiotic doxorubicin ((8S-cis)-10-[(3-amino-2,3,6-trideoxy- α -L-lyxo-hexapyranosyl)oxy]-7,8,9,10-tetrahydro-6,8,11-trihydroxy-8-(hydroxyacetyl)-1-methoxy-5,12-naphthacenedione), epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in “*The Molecular Basis of Cancer*,” Mendelsohn and Israel, eds., Chapter 1, entitled “Cell cycle

regulation, oncogenes, and antineoplastic drugs” by Murakami et al. (WB Saunders: Philadelphia, 1995), especially p. 13. The taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (TAXOTERE®, Rhone-Poulenc Rorer), derived from the European yew, is a semisynthetic analogue of paclitaxel (TAXOL®, Bristol-Myers Squibb). Paclitaxel and docetaxel promote the assembly of microtubules from tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

By “radiation therapy” is meant the use of directed gamma rays or beta rays to induce sufficient damage to a cell so as to limit its ability to function normally or to destroy the cell altogether. It will be appreciated that there will be many ways known in the art to determine the dosage and duration of treatment. Typical treatments are given as a one-time administration and typical dosages range from 10 to 200 units (Grays) per day.

The term “pharmaceutical formulation” refers to a preparation which is in such form as to permit the biological activity of an active ingredient contained therein to be effective, and which contains no additional components which are unacceptably toxic to a patient to which the formulation would be administered.

A “pharmaceutically acceptable carrier” refers to an ingredient in a pharmaceutical formulation, other than an active ingredient, which is nontoxic to a patient. A pharmaceutically acceptable carrier includes, but is not limited to, a buffer, excipient, stabilizer, or preservative.

The term “package insert” is used to refer to instructions customarily included in commercial packages of therapeutic products, that contain information about the indications, usage, dosage, administration, combination therapy, contraindications, and/or warnings concerning the use of such therapeutic products.

A “sterile” formulation is aseptic or free from all living microorganisms and their spores.

An “article of manufacture” is any manufacture (e.g., a package or container) or kit comprising at least one reagent, e.g., a medicament for treatment of a disease or disorder (e.g., cancer), or a probe for specifically detecting a biomarker described herein. In certain embodiments, the manufacture or kit is promoted, distributed, or sold as a unit for performing the methods described herein.

The term “small molecule” refers to any molecule with a molecular weight of about 2000 daltons or less, preferably of about 500 daltons or less.

The word “label” when used herein refers to a compound or composition that is conjugated or fused directly or indirectly to a reagent such as a polynucleotide probe or an antibody and facilitates detection of the reagent to which it is conjugated or fused. The label may itself be detectable (e.g., radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable. The term is intended to encompass direct labeling of a probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin.

The term “antibody” is used in the broadest sense and specifically covers monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments so long as they exhibit the desired biological activity.

“Native antibodies” are usually heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies among the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (VH) followed by a number of constant domains. Each light chain has a variable domain at one end (VL) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains.

An “isolated” antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with research, diagnostic, and/or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In some embodiments, an antibody is purified (1) to greater than 95% by weight of antibody as determined by, for example, the Lowry method, and in some embodiments, to greater than 99% by weight; (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of, for example, a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using, for example, Coomassie blue or silver stain. An isolated antibody includes the antibody *in situ* within recombinant cells since at least one component of the antibody’s natural environment will not be present. Ordinarily, however, an isolated antibody will be prepared by at least one purification step.

A “blocking” antibody or an antibody “antagonist” is one which inhibits or reduces biological activity of the antigen it binds. For example, a VEGF-specific antagonist antibody binds VEGF and inhibits the ability of VEGF to induce vascular endothelial cell proliferation. Preferred blocking antibodies or antagonist antibodies completely inhibit the biological activity of the antigen.

Unless indicated otherwise, the expression “multivalent antibody” is used throughout this specification to denote an antibody comprising three or more antigen binding sites. The multivalent antibody is preferably engineered to have the three or more antigen binding sites and is generally not a native sequence IgM or IgA antibody.

The “light chains” of antibodies (immunoglobulins) from any mammalian species can be assigned to one of two clearly distinct types, called kappa (“κ”) and lambda (“λ”), based on the amino acid sequences of their constant domains.

The term “constant domain” refers to the portion of an immunoglobulin molecule having a more conserved amino acid sequence relative to the other portion of the immunoglobulin, the variable domain, which contains the antigen binding site. The constant domain contains the CH1, CH2, and CH3 domains (collectively, CH) of the heavy chain and the CHL (or CL) domain of the light chain.

The “variable region” or “variable domain” of an antibody refers to the amino-terminal domains of the heavy or light chain of the antibody. The variable domain of the heavy chain may be referred to as “VH.” The variable domain of the light chain may be referred to as “VL.” These domains are generally the most variable parts of an antibody and contain the antigen-binding sites.

5 The term “variable” refers to the fact that certain segments of the variable domains differ extensively in sequence among antibodies. The variable or “V” domain mediates antigen binding and defines specificity of a particular antibody for its particular antigen. However, the variability is not evenly distributed across the span of the variable domains. Instead, the V regions consist of relatively invariant stretches called framework regions (FRs) of 15-30 amino acids separated by shorter regions of extreme
10 variability called “hypervariable regions” that are each 9-12 amino acids long. The term “hypervariable region” or “HVR” when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from, for example, around about residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the VL, and around about residues 26-35 (H1), 49-65 (H2) and 95-102 (H3) in the VH (in one embodiment, H1 is around about
15 residues 31-35); Kabat et al., *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a “hypervariable loop” (e.g., residues 26-32 (L1), 50-52 (L2), and 91-96 (L3) in the VL, and 26-32 (H1), 53-55 (H2), and 96-101 (H3) in the VH; Chothia and Lesk, *J. Mol. Biol.* 196:901-917 (1987). The variable domains of native heavy and light chains each comprise four FRs, largely adopting a beta-sheet configuration,
20 connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the beta-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al., *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). Accordingly, the HVR
25 and FR sequences generally appear in the following sequence in VH (or VL): FR1-H1(L1)-FR2-H2(L2)-FR3-H3(L3)-FR4. The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

An “acceptor human framework” for the purposes herein is a framework comprising the amino
30 acid sequence of a light chain variable domain (VL) framework or a heavy chain variable domain (VH) framework derived from a human immunoglobulin framework or a human consensus framework, as defined below. An acceptor human framework “derived from” a human immunoglobulin framework or a human consensus framework may comprise the same amino acid sequence thereof, or it may contain amino acid sequence changes. In some embodiments, the number of amino acid changes are 10 or less,
35 9 or less, 8 or less, 7 or less, 6 or less, 5 or less, 4 or less, 3 or less, or 2 or less. In some embodiments, the VL acceptor human framework is identical in sequence to the VL human immunoglobulin framework sequence or human consensus framework sequence.

The term “hypervariable region,” “HVR,” or “HV,” as used herein, refers to the regions of an antibody variable domain which are hypervariable in sequence and/or form structurally defined loops.

40 Generally, antibodies comprise six HVRs; three in the VH (H1, H2, H3), and three in the VL (L1, L2, L3).

In native antibodies, H3 and L3 display the most diversity of the six HVRs, and H3 in particular is believed to play a unique role in conferring fine specificity to antibodies. See, for example, Xu et al., *Immunity* 13:37-45 (2000); Johnson and Wu, in *Methods in Molecular Biology* 248:1-25 (Lo, ed., Human Press, Totowa, N.J., 2003). Indeed, naturally occurring camelid antibodies consisting of a heavy chain only are functional and stable in the absence of light chain. See, for example, Hamers-Casterman et al., *Nature* 363:446-448 (1993); Sheriff et al., *Nature Struct. Biol.* 3:733-736 (1996).

A number of HVR delineations are in use and are encompassed herein. The Kabat Complementarity Determining Regions (CDRs) are based on sequence variability and are the most commonly used (Kabat et al., *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)). Chothia refers instead to the location of the structural loops (Chothia and Lesk *J. Mol. Biol.* 196:901-917 (1987)). The AbM HVRs represent a compromise between the Kabat HVRs and Chothia structural loops, and are used by Oxford Molecular's AbM antibody modeling software. The "contact" HVRs are based on an analysis of the available complex crystal structures. The residues from each of these HVRs are noted below.

Loop	Kabat	AbM	Chothia	Contact
L1	L24-L34	L24-L34	L26-L32	L30-L36
L2	L50-L56	L50-L56	L50-L52	L46-L55
L3	L89-L97	L89-L97	L91-L96	L89-L96
H1	H31-H35b	H26-H35b	H26-H32	H30-H35b (Kabat Numbering)
H1	H31-H35	H26-H35	H26-H32	H30-H35 (Chothia Numbering)
H2	H50-H65	H50-H58	H53-H55	H47-H58
H3	H95-H102	H95-H102	H96-H101	H93-H101

HVRs may comprise "extended HVRs" as follows: 24-36 or 24-34 (L1), 46-56 or 50-56 (L2) and 89-97 or 89-96 (L3) in the VL and 26-35 (H1), 50-65 or 49-65 (H2) and 93-102, 94-102, or 95-102 (H3) in the VH. The variable domain residues are numbered according to Kabat et al., *supra*, for each of these definitions.

"Framework" or "FR" residues are those variable domain residues other than the HVR residues as herein defined.

A "human consensus framework" is a framework which represents the most commonly occurring amino acid residues in a selection of human immunoglobulin VL or VH framework sequences. Generally, the selection of human immunoglobulin VL or VH sequences is from a subgroup of variable domain sequences. Generally, the subgroup of sequences is a subgroup as in Kabat et al., *Sequences of Proteins of Immunological Interest*, Fifth Edition, NIH Publication 91-3242, Bethesda MD (1991), vols. 1-3. In one embodiment, for the VL, the subgroup is subgroup kappa I as in Kabat et al., *supra*. In one embodiment, for the VH, the subgroup is subgroup III as in Kabat et al., *supra*.

The term "variable domain residue numbering as in Kabat" or "amino acid position numbering as in Kabat," and variations thereof, refers to the numbering system used for heavy chain variable domains or light chain variable domains of the compilation of antibodies in Kabat et al., *supra*. Using this

numbering system, the actual linear amino acid sequence may contain fewer or additional amino acids corresponding to a shortening of, or insertion into, a FR or HVR of the variable domain. For example, a heavy chain variable domain may include a single amino acid insert (residue 52a according to Kabat) after residue 52 of H2 and inserted residues (e.g., residues 82a, 82b, and 82c, etc. according to Kabat) after heavy chain FR residue 82. The Kabat numbering of residues may be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a "standard" Kabat numbered sequence.

The Kabat numbering system is generally used when referring to a residue in the variable domain (approximately residues 1-107 of the light chain and residues 1-113 of the heavy chain) (e.g., Kabat et al., *Sequences of Immunological Interest*. 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)). The "EU numbering system" or "EU index" is generally used when referring to a residue in an immunoglobulin heavy chain constant region (e.g., the EU index reported in Kabat et al., *supra*). The "EU index as in Kabat" refers to the residue numbering of the human IgG1 EU antibody. Unless stated otherwise herein, references to residue numbers in the variable domain of antibodies means residue numbering by the Kabat numbering system. Unless stated otherwise herein, references to residue numbers in the constant domain of antibodies means residue numbering by the EU numbering system (e.g., see United States Provisional Application No. 60/640,323, Figures for EU numbering).

Unless otherwise indicated, HVR residues and other residues in the variable domain (e.g., FR residues) are numbered herein according to Kabat et al., *supra*.

The terms "full-length antibody," "intact antibody," and "whole antibody" are used herein interchangeably to refer to an antibody in its substantially intact form, not antibody fragments as defined below. The terms particularly refer to an antibody with heavy chains that contain an Fc region.

"Antibody fragments" comprise a portion of an intact antibody, preferably comprising the antigen-binding region thereof. In some embodiments, the antibody fragment described herein is an antigen-binding fragment. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

The term "Fc region" herein is used to define a C-terminal region of an immunoglobulin heavy chain that contains at least a portion of the constant region. The term includes native sequence Fc regions and variant Fc regions. In one embodiment, a human IgG heavy chain Fc region extends from Cys226, or from Pro230, to the carboxyl-terminus of the heavy chain. However, the C-terminal lysine (Lys447) of the Fc region may or may not be present. Unless otherwise specified herein, numbering of amino acid residues in the Fc region or constant region is according to the EU numbering system, also called the EU index, as described in Kabat et al., *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991).

“Effector functions” refer to those biological activities attributable to the Fc region of an antibody, which vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity (CDC); Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down-regulation of cell surface receptors (e.g. B cell receptor); and B cell activation.

“Fv” is the minimum antibody fragment which contains a complete antigen-binding site. In one embodiment, a two-chain Fv species consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. In a single-chain Fv (scFv) species, one heavy- and one light-chain variable domain can be covalently linked by a flexible peptide linker such that the light and heavy chains can associate in a “dimeric” structure analogous to that in a two-chain Fv species. It is in this configuration that the three HVRs of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. Collectively, the six HVRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three HVRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment contains the heavy- and light-chain variable domains and also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab’ fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab’-SH is the designation herein for Fab’ in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab’)₂ antibody fragments originally were produced as pairs of Fab’ fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

“Single-chain Fv” or “scFv” antibody fragments comprise the VH and VL domains of antibody, wherein these domains are present in a single polypeptide chain. Generally, the scFv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables the scFv to form the desired structure for antigen binding. For a review of scFv, see, e.g., Pluckthün, in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds., (Springer-Verlag, New York, 1994), pp. 269-315.

The term “multispecific antibody” is used in the broadest sense and specifically covers an antibody comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), where the VH-VL unit has polyepitopic specificity (i.e., is capable of binding to two different epitopes on one biological molecule or each epitope on a different biological molecule). Such multispecific antibodies include, but are not limited to, full-length antibodies, antibodies having two or more VL and VH domains, antibody fragments such as Fab, Fv, dsFv, scFv, diabodies, bispecific diabodies and triabodies, antibody fragments that have been linked covalently or non-covalently. “Polyepitopic specificity” refers to the ability to specifically bind to two or more different epitopes on the same or different target(s). “Dual specificity” or “bispecificity” refers to the ability to specifically bind to two different epitopes on the same or different target(s). However, in contrast to bispecific antibodies, dual-specific antibodies have two antigen-binding arms that are identical in amino acid sequence and each Fab arm is capable of recognizing two antigens. Dual-specificity allows the antibodies to interact with high affinity with two

different antigens as a single Fab or IgG molecule. According to one embodiment, the multispecific antibody in an IgG1 form binds to each epitope with an affinity of 5 μ M to 0.001 pM, 3 μ M to 0.001 pM, 1 μ M to 0.001 pM, 0.5 μ M to 0.001 pM or 0.1 μ M to 0.001 pM. "Monospecific" refers to the ability to bind only one epitope.

5 The term "diabodies" refers to antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) in the same polypeptide chain (VH-VL). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies may be bivalent or bispecific. Diabodies are
10 described more fully in, for example, EP 404,097; WO 1993/01161; Hudson et al., *Nat. Med.* 9:129-134 (2003); and Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90: 6444-6448 (1993). Triabodies and tetrabodies are also described in Hudson et al., *Nat. Med.* 9:129-134 (2003).

The "class" of an antibody refers to the type of constant domain or constant region possessed by its heavy chain. There are five major classes of antibodies: IgA, IgD, IgE, IgG, and IgM, and several of
15 these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2. The heavy chain constant domains that correspond to the different classes of antibodies are called α , δ , ϵ , γ , and μ , respectively.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, e.g., the individual antibodies comprising the population are
20 identical except for possible mutations, e.g., naturally occurring mutations, that may be present in minor amounts. Thus, the modifier "monoclonal" indicates the character of the antibody as not being a mixture of discrete antibodies. In certain embodiments, such a monoclonal antibody typically includes an antibody comprising a polypeptide sequence that binds a target, wherein the target-binding polypeptide sequence was obtained by a process that includes the selection of a single target binding polypeptide
25 sequence from a plurality of polypeptide sequences. For example, the selection process can be the selection of a unique clone from a plurality of clones, such as a pool of hybridoma clones, phage clones, or recombinant DNA clones. It should be understood that a selected target binding sequence can be further altered, for example, to improve affinity for the target, to humanize the target binding sequence, to improve its production in cell culture, to reduce its immunogenicity *in vivo*, to create a multispecific
30 antibody, etc., and that an antibody comprising the altered target binding sequence is also a monoclonal antibody of this invention. In contrast to polyclonal antibody preparations, which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody of a monoclonal antibody preparation is directed against a single determinant on an antigen. In addition to their specificity, monoclonal antibody preparations are advantageous in that they are typically uncontaminated by other
35 immunoglobulins.

The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the invention may be made by a variety of techniques, including, for example, the hybridoma method
40 (e.g., Kohler and Milstein, *Nature* 256:495-97 (1975); Hongo et al., *Hybridoma* 14 (3): 253-260 (1995),

Harlow et al., *Antibodies: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling et al., in: *Monoclonal Antibodies and T cell Hybridomas* 563-681 (Elsevier, N.Y., 1981)), recombinant DNA methods (see, e.g., U.S. Pat. No. 4,816,567), phage-display technologies (see, e.g., Clackson et al., *Nature*, 352: 624-628, 1991; Marks et al., *J. Mol. Biol.* 222: 581-597, 1992; Sidhu et al., *J. Mol. Biol.* 338(2): 299-310, 2004; Lee et al., *J. Mol. Biol.* 340(5): 1073-1093, 2004; Fellouse, *Proc. Natl. Acad. Sci. USA* 101(34): 12467-12472, 2004; and Lee et al., *J. Immunol. Methods* 284(1-2): 119-132, 2004; and technologies for producing human or human-like antibodies in animals that have parts or all of the human immunoglobulin loci or genes encoding human immunoglobulin sequences (see, e.g., WO 1998/24893; WO 1996/34096; WO 1996/33735; WO 1991/10741; Jakobovits et al., *Proc. Natl. Acad. Sci. USA* 90: 2551, 1993; Jakobovits et al., *Nature* 362: 255-258, 1993; Bruggemann et al., *Year in Immunol.* 7:33, 1993; U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; and 5,661,016; Marks et al., *Bio/Technology* 10: 779-783 (1992); Lonberg et al., *Nature* 368: 856-859, 1994; Morrison, *Nature* 368: 812-813, 1994; Fishwild et al., *Nature Biotechnol.* 14: 845-851, 1996; Neuberger, *Nature Biotechnol.* 14: 826, 1996; and Lonberg et al., *Intern. Rev. Immunol.* 13: 65-93, 1995.

The monoclonal antibodies herein specifically include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (see, e.g., U.S. Pat. No. 4,816,567; and Morrison et al., *Proc. Natl. Acad. Sci. USA* 81:6851-6855 (1984)). Chimeric antibodies include PRIMATIZED® antibodies wherein the antigen-binding region of the antibody is derived from an antibody produced by, e.g., immunizing macaque monkeys with the antigen of interest.

A "human antibody" is one which possesses an amino acid sequence which corresponds to that of an antibody produced by a human or a human cell or derived from a non-human source that utilizes human antibody repertoires or other human antibody-encoding sequences. This definition of a human antibody specifically excludes a humanized antibody comprising non-human antigen-binding residues.

"Humanized" forms of non-human (e.g., rodent) antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or non-human primate having the desired antibody specificity, affinity, and capability. In some instances, FR residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies can comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see

Jones et al., *Nature* 321:522-525, 1986; Riechmann et al., *Nature* 332:323-329, 1988; and Presta, *Curr. Op. Struct. Biol.* 2:593-596, 1992.

A "wild-type (WT)" or "reference" sequence or the sequence of a "wild-type" or "reference" protein/polypeptide, such as an HVR or a variable domain of a reference antibody, may be the reference sequence from which variant polypeptides are derived through the introduction of mutations. In general, the "wild-type" sequence for a given protein is the sequence that is most common in nature. Similarly, a "wild-type" gene sequence is the sequence for that gene which is most commonly found in nature. Mutations may be introduced into a "wild-type" gene (and thus the protein it encodes) either through natural processes or through man-induced means. The products of such processes are "variant" or "mutant" forms of the original "wild-type" protein or gene.

A "variant" or "mutant" of a starting or reference polypeptide (e.g., a reference antibody or its variable domain(s)/HVR(s)), is a polypeptide that (1) has an amino acid sequence different from that of the starting or reference polypeptide and (2) was derived from the starting or reference polypeptide through either natural or artificial (man-made) mutagenesis. Such variants include, for example, deletions from, and/or insertions into and/or substitutions of, residues within the amino acid sequence of the polypeptide of interest, referred to herein as "amino acid residue alterations." Thus, a variant HVR refers to a HVR comprising a variant sequence with respect to a starting or reference polypeptide sequence (such as that of a source antibody or antigen binding fragment). An amino acid residue alteration, in this context, refers to an amino acid different from the amino acid at the corresponding position in a starting or reference polypeptide sequence (such as that of a reference antibody or fragment thereof). Any combination of deletion, insertion, and substitution may be made to arrive at the final variant or mutant construct, provided that the final construct possesses the desired functional characteristics. The amino acid changes also may alter post-translational processes of the polypeptide, such as changing the number or position of glycosylation sites.

"Affinity" refers to the strength of the sum total of noncovalent interactions between a single binding site of a molecule (e.g., an antibody) and its binding partner (e.g., an antigen). Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (e.g., antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_d). Affinity can be measured by common methods known in the art, including those described herein. Specific illustrative and exemplary embodiments for measuring binding affinity are described herein.

With regard to the binding of an antibody to a target molecule, the term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target means binding that is measurably different from a non-specific interaction. Specific binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule. For example, specific binding can be determined by competition with a control molecule that is similar to the target, for example, an excess of non-labeled target. In this case, specific binding is indicated if the binding of the labeled target to a probe is competitively inhibited by excess unlabeled target. The term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target as used herein can be exhibited, for example, by a molecule having a K_d for

the target of 10^{-4} M or lower, alternatively 10^{-5} M or lower, alternatively 10^{-6} M or lower, alternatively 10^{-7} M or lower, alternatively 10^{-8} M or lower, alternatively 10^{-9} M or lower, alternatively 10^{-10} M or lower, alternatively 10^{-11} M or lower, alternatively 10^{-12} M or lower or a K_d in the range of 10^{-4} M to 10^{-6} M or 10^{-6} M to 10^{-10} M or 10^{-7} M to 10^{-9} M. As will be appreciated by the skilled artisan, affinity and K_d values are inversely related. A high affinity for an antigen is measured by a low K_d value. In one embodiment, the term “specific binding” refers to binding where a molecule binds to a particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

An “affinity matured” antibody refers to an antibody with one or more alterations in one or more hypervariable regions (HVRs), compared to a parent antibody which does not possess such alterations, such alterations resulting in an improvement in the affinity of the antibody for antigen.

An “antibody that binds to the same epitope” as a reference antibody refers to an antibody that blocks binding of the reference antibody to its antigen in a competition assay by 50% or more, and conversely, the reference antibody blocks binding of the antibody to its antigen in a competition assay by 50% or more.

An “immunoconjugate” is an antibody conjugated to one or more heterologous molecule(s), including but not limited to a cytotoxic agent.

As used herein, the term “immunoadhesin” designates antibody-like molecules which combine the binding specificity of a heterologous protein (an “adhesin”) with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is “heterologous”), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG1, IgG2 (including IgG2A and IgG2B), IgG3, or IgG4 subtypes, IgA (including IgA1 and IgA2), IgE, IgD or IgM. The Ig fusions preferably include the substitution of a domain of a polypeptide or antibody described herein in the place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130. For example, useful immunoadhesins as medicaments useful for therapy herein include polypeptides that comprise the extracellular domain (ECD) or PD-1-binding portions of PD-L1 or PD-L2, or the extracellular or PD-L1- or PD-L2-binding portions of PD-1, fused to a constant domain of an immunoglobulin sequence, such as a PD-L1 ECD-Fc, a PD-L2 ECD-Fc, and a PD-1 ECD-Fc, respectively. Immunoadhesin combinations of Ig Fc and ECD of cell surface receptors are sometimes termed soluble receptors.

A “fusion protein” and a “fusion polypeptide” refer to a polypeptide having two portions covalently linked together, where each of the portions is a polypeptide having a different property. The property may be a biological property, such as activity in vitro or in vivo. The property may also be simple chemical or physical property, such as binding to a target molecule, catalysis of a reaction, and the like. The two portions may be linked directly by a single peptide bond or through a peptide linker but are in reading frame with each other.

“Percent (%) amino acid sequence identity” with respect to the polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the polypeptide being compared, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

“Polynucleotide,” or “nucleic acid,” as used interchangeably herein, refer to polymers of nucleotides of any length, and include DNA and RNA. The nucleotides can be deoxyribonucleotides, ribonucleotides, modified nucleotides or bases, and/or their analogs, or any substrate that can be incorporated into a polymer by DNA or RNA polymerase, or by a synthetic reaction. Thus, for instance, polynucleotides as defined herein include, without limitation, single- and double-stranded DNA, DNA including single- and double-stranded regions, single- and double-stranded RNA, and RNA including single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or include single- and double-stranded regions. In addition, the term “polynucleotide” as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules.

The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. The term "polynucleotide" specifically includes cDNAs.

A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and their
5 analogs. If present, modification to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after synthesis, such as by conjugation with a label. Other types of modifications include, for example, "caps," substitution of one or more of the naturally-occurring
10 nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, and the like) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, and the like), those containing pendant moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, and the like), those with intercalators (e.g., acridine, psoralen, and the like), those
15 containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, and the like), those containing alkylators, those with modified linkages (e.g., alpha anomeric nucleic acids), as well as unmodified forms of the polynucleotide(s). Further, any of the hydroxyl groups ordinarily present in the sugars may be replaced, for example, by phosphonate groups, phosphate groups, protected by standard protecting groups, or activated to prepare additional linkages to additional nucleotides, or may be
20 conjugated to solid or semi-solid supports. The 5' and 3' terminal OH can be phosphorylated or substituted with amines or organic capping group moieties of from 1 to 20 carbon atoms. Other hydroxyls may also be derivatized to standard protecting groups. Polynucleotides can also contain analogous forms of ribose or deoxyribose sugars that are generally known in the art, including, for example, 2'-O-methyl-, 2'-O-allyl-, 2'-fluoro-, or 2'-azido-ribose, carbocyclic sugar analogs, α -anomeric sugars, epimeric sugars such as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, sedoheptuloses,
25 acyclic analogs, and abasic nucleoside analogs such as methyl riboside. One or more phosphodiester linkages may be replaced by alternative linking groups. These alternative linking groups include, but are not limited to, embodiments wherein phosphate is replaced by P(O)S ("thioate"), P(S)S ("dithioate"), "(O)NR₂" ("amidate"), P(O)R, P(O)OR', CO or CH₂ ("formacetal"), in which each R or R' is independently H or substituted or unsubstituted alkyl (1-20 C) optionally containing an ether (-O-) linkage, aryl, alkenyl,
30 cycloalkyl, cycloalkenyl or araldyl. Not all linkages in a polynucleotide need be identical. The preceding description applies to all polynucleotides referred to herein, including RNA and DNA.

"Oligonucleotide," as used herein, generally refers to short, single stranded, polynucleotides that are, but not necessarily, less than about 250 nucleotides in length. Oligonucleotides may be synthetic. The terms "oligonucleotide" and "polynucleotide" are not mutually exclusive. The description above for
35 polynucleotides is equally and fully applicable to oligonucleotides.

The term "primer" refers to a single-stranded polynucleotide that is capable of hybridizing to a nucleic acid and allowing polymerization of a complementary nucleic acid, generally by providing a free 3'-OH group.

The terms "host cell," "host cell line," and "host cell culture" are used interchangeably and refer to
40 cells into which exogenous nucleic acid has been introduced, including the progeny of such cells. Host

cells include “transformants” and “transformed cells,” which include the primary transformed cell and progeny derived therefrom without regard to the number of passages. Progeny may not be completely identical in nucleic acid content to a parent cell, but may contain mutations. Mutant progeny that have the same function or biological activity as screened or selected for in the originally transformed cell are included herein.

The term “vector,” as used herein, refers to a nucleic acid molecule capable of propagating another nucleic acid to which it is linked. The term includes the vector as a self-replicating nucleic acid structure as well as the vector incorporated into the genome of a host cell into which it has been introduced. Certain vectors are capable of directing the expression of nucleic acids to which they are operatively linked. Such vectors are referred to herein as “expression vectors.”

An “isolated” nucleic acid molecule is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the nucleic acid. An isolated nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated nucleic acid molecules therefore are distinguished from the nucleic acid molecule as it exists in natural cells. However, an isolated nucleic acid molecule includes a nucleic acid molecule contained in cells that ordinarily express the antibody where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

II. DIAGNOSTIC METHODS AND ASSAYS

Provided herein are methods and assays for identifying an individual having a cancer (e.g., a kidney cancer (e.g., a renal cell carcinoma (RCC)), a lung cancer (e.g., a non-small cell lung cancer (NSCLC)), a bladder cancer (e.g., a urothelial bladder cancer (UBC)), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., a triple-negative breast cancer (TNBC))) who may benefit from a treatment with an anti-cancer therapy including a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)). Also provided herein are methods and assays for identifying an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)) who may benefit from a treatment with an anti-cancer therapy including an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))). In particular embodiments, the angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) therapy may be a monotherapy (e.g., a sunitinib monotherapy).

The methods and assays described herein are based on the finding that the expression level of one or more genes (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9) in a sample from the individual may be used to predict the therapeutic

efficacy of an anti-cancer therapy that includes a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)). In another aspect, methods and assays described herein are based on the finding that the expression level of one or more genes (e.g., VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, and/or CD34) in a sample from the individual may be used to predict the therapeutic efficacy of a treatment including an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))).

Further provided herein are methods and assays for selecting a therapy for an individual having a cancer (e.g., kidney cancer (e.g., RCC), lung cancer (e.g., NSCLC), bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or breast cancer (e.g., TNBC)); methods for determining whether an individual having a cancer is likely to respond to treatment including a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)); methods for determining whether an individual having a cancer is likely to respond to treatment including an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))); methods for predicting the responsiveness of an individual having a cancer to treatment comprising a VEGF antagonist and a PD-L1 axis binding antagonist; methods for predicting the responsiveness of an individual having a cancer to treatment comprising an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))); methods for monitoring the response of an individual having a cancer to treatment including a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)); and methods for monitoring the response of an individual having a cancer to treatment including an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))). Any of the methods provided herein may further include administering to the individual a VEGF antagonist and a PD-L1 axis binding antagonist (e.g., as described below in Section III) to the individual.

Provided herein is a method of identifying an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., TNBC)) who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding

antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) that involves determining the expression level of one or more of the genes set forth in Table 1 in a sample from the individual, wherein a change in the expression level of one or more of the genes set forth in Table 1 identifies the individual as one who may benefit from treatment with an anti-cancer therapy (e.g., an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist or a angiogenesis inhibitor). In some instances, the change is an increase. In other instances, the change is a decrease.

Table 1. Exemplary Biomarkers

Biomarkers
CD8A
EOMES
GZMA
GZMB
PRF1
IFNG
PD-L1
CXCL9
CXCL10
CXCL11
CD27
FOXP3
PD-1
CTLA4
TIGIT
IDO1
PSMB8
PSMB9
TAP1
TAP2
VEGFA
KDR
ESM1
PECAM1
FLT1
ANGPTL4
CD34
IL6
CXCL1
CXCL2
CXCL3
CXCL8
PTGS2
CXCR1
CXCR2

S100A8
S100A9

The invention also provides for selecting a therapy for an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., TNBC)) that includes
5 determining the expression level of one or more of the genes set forth in Table 1 in a sample from the individual, wherein a change in the expression level of one or more of the genes set forth in Table 1 identifies the individual as one who may benefit from treatment with an anti-cancer therapy (e.g., an anti-cancer therapy comprising a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody))), or an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))). In some instances, the change is an increase. In other instances, the change is a decrease.

15 In another embodiment, the invention provides a method of diagnosing or prognosing a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., TNBC)) that includes determining the expression level of one or more biomarkers in a sample from an individual and comparing the expression level of the one or more biomarkers in the sample with a reference level,
20 thereby diagnosing or prognosing the cancer. In some embodiments, a change in the expression level (e.g., an increase or a decrease) of the one or more biomarkers in the sample relative to the reference level diagnoses or prognoses the individual. In some embodiments, the biomarker is set forth in Table 1.

In yet another embodiment, the invention provides a method of determining whether a patient having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g.,
25 UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., TNBC)) is likely to respond to treatment with an anti-cancer therapy (e.g., an anti-cancer therapy comprising a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g.,
30 atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody))), or an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))). that includes determining the expression level of one or more biomarkers in a sample from the individual and comparing the expression level of the one or more biomarkers in the sample with a reference level, thereby identifying the individual
35 as one who is likely to respond to the anti-cancer therapy. In some embodiments, a change in the expression level (e.g., an increase or a decrease) of the one or more biomarkers in the biological sample

relative to the reference level identifies the patient as likely to respond to treatment with the anti-cancer therapy. In some embodiments, the biomarker is set forth in Table 1.

In other embodiments, the invention provides a method of optimizing therapeutic efficacy of an anti-cancer therapy (e.g., an anti-cancer therapy comprising a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)), or an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))) that includes determining the expression level of one or more biomarkers in a biological sample obtained from the patient and comparing the expression level of the one or more biomarkers in the sample with a reference level, wherein a change (e.g., an increase or decrease) in the expression level of the one or more biomarkers in the biological sample relative to the reference level identifies a patient who is likely to respond to the anti-cancer therapy. In some embodiments, the biomarker is set forth in Table 1.

In another embodiment, provided herein is a method of identifying an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., TNBC)) who may benefit from treatment with an anti-cancer therapy that includes a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) that includes determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, or 37) of the following genes in a sample from the individual: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9, wherein (i) an expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample that is at or above a reference expression level of the one or more genes; or (ii) an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample that is below a reference expression level of the one or more genes identifies the individual as one who may benefit from treatment with an anti-cancer therapy that includes a VEGF antagonist and a PD-L1 axis binding antagonist.

In yet another embodiment, provided herein is a method for selecting a therapy for an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., TNBC)) that includes determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,

12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, or 37) of the following genes in a sample from the individual: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9, wherein (i) an expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample that is at or above a reference expression level of the one or more genes; or (ii) an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample that is below a reference expression level of the one or more genes identifies the individual as one who may benefit from treatment with an anti-cancer therapy that includes a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody))).

In any of the preceding methods, the method may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2.

For example, any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1. In some embodiments, the method includes determining the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2. In some embodiments, the method includes determining the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3. In some embodiments, the method includes determining the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

Table 2: Two-Gene Combinations of CD8A, EOMES, PRF1, IFNG, and PD-L1

CD8A and EOMES
CD8A and PRF1
CD8A and IFNG
CD8A and PD-L1
EOMES and PRF1

EOMES and IFNG
EOMES and PD-L1
PRF1 and IFNG
PRF1 and PD-L1
IFNG and PD-L1

Table 3: Three-Gene Combinations of CD8A, EOMES, PRF1, IFNG, and PD-L1

CD8A, EOMES, and PRF1
CD8A, EOMES, and IFNG
CD8A, EOMES, and PD-L1
CD8A, PRF1, and IFNG
CD8A, PRF1, and PD-L1
CD8A, IFNG, and PD-L1
EOMES, PRF1, and IFNG
EOMES, PRF1, and PD-L1
EOMES, IFNG, and PD-L1
PRF1, IFNG, and PD-L1

Table 4: Four-Gene Combinations of CD8A, EOMES, PRF1, IFNG, and PD-L1

CD8A, EOMES, PRF1, and IFNG
CD8A, EOMES, PRF1, and PD-L1
CD8A, EOMES, IFNG, and PD-L1
CD8A, PRF1, IFNG, and PD-L1
EOMES, PRF1, IFNG, and PD-L1

5

In some embodiments, any of the preceding methods may include determining the expression level of PD-L1 and one or more additional genes, wherein the one or more additional genes is other than PD-L1. For example, in some embodiments, the method may include determining the expression level of PD-L1 and one or more additional genes (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 10 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36) selected from the group consisting of: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9. In some embodiments, the method includes determining the expression level of PD-L1 and one or more (e.g., 1, 2, 15 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19) additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2. In other embodiments, the method includes determining the expression level of PD-L1 and one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. In other embodiments, the method includes 20 determining the expression level of PD-L1 and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9.

Any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. In some embodiments, the method includes determining the expression level of at least two, at least three, at least 25 four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. For example, in some embodiments, the method includes determining the expression level of one or

more (e.g., 1, 2, 3, 4, 5, or 6) of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method includes determining the expression level of two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5. In some embodiments, the method includes determining the expression level of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6. In some embodiments, the method includes determining the expression level of four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 7. In some embodiments, the method includes determining the expression level of five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8. In some embodiments, the method includes determining the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

Table 5: Two-Gene Combinations of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34

VEGFA and KDR
VEGFA and ESM1
VEGFA and PECAM1
VEGFA and ANGPTL4
VEGFA and CD34
KDR and ESM1
KDR and PECAM1
KDR and ANGPTL4
KDR and CD34
ESM1 and PECAM1
ESM1 and ANGPTL4
ESM1 and CD34
PECAM1 and ANGPTL4
PECAM1 and CD34
ANGPTL4 and CD34

Table 6: Three-Gene Combinations of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34

VEGFA, KDR, and ESM1
VEGFA, KDR, and PECAM1
VEGFA, KDR, and ANGPTL4
VEGFA, KDR, and CD34
VEGFA, ESM1, and PECAM1
VEGFA, ESM1, and ANGPTL4
VEGFA, ESM1, and CD34
VEGFA, PECAM1, and ANGPTL4
VEGFA, PECAM1, and CD34
VEGFA, ANGPTL4, and CD34
KDR, ESM1, and PECAM1
KDR, ESM1, and ANGPTL4
KDR, ESM1, and CD34
KDR, PECAM1, and ANGPTL4
KDR, PECAM1, and CD34
KDR, ANGPTL4, and CD34
ESM1, PECAM1, and ANGPTL4
ESM1, PECAM1, and CD34

ESM1, ANGPTL4, and CD34
PECAM1, ANGPTL4, and CD34

Table 7: Four-Gene Combinations of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34

VEGFA, KDR, ESM1, and PECAM1
VEGFA, KDR, ESM1, and ANGPTL4
VEGFA, KDR, ESM1, and CD34
VEGFA, KDR, PECAM1, and ANGPTL4
VEGFA, KDR, PECAM1, and CD34
VEGFA, KDR, ANGPTL4, and CD34
VEGFA, ESM1, PECAM1, and ANGPTL4
VEGFA, ESM1, PECAM1, and CD34
VEGFA, ESM1, ANGPTL4, and CD34
VEGFA, PECAM1, ANGPTL4, and CD34
KDR, ESM1, PECAM1, and ANGPTL4
KDR, ESM1, PECAM1, and CD34
KDR, ESM1, ANGPTL4, and CD34
KDR, PECAM1, ANGPTL4, and CD34
ESM1, PECAM1, ANGPTL4, and CD34

Table 8: Five-Gene Combinations of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34

VEGFA, KDR, ESM1, PECAM1, and ANGPTL4
VEGFA, KDR, ESM1, PECAM1, and CD34
VEGFA, KDR, ESM1, ANGPTL4, and CD34
VEGFA, KDR, PECAM1, ANGPTL4, and CD34
VEGFA, ESM1, PECAM1, ANGPTL4, and CD34
KDR, ESM1, PECAM1, ANGPTL4, and CD34

5

Any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9. In some embodiments, the method includes determining the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9. In some embodiments, the method includes determining the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10. In some embodiments, the method includes determining the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11. In some embodiments, the method includes determining the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12. In some embodiments, the method includes determining the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13. In some embodiments, the method includes determining the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown

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in Table 14. In some embodiments, the method includes determining the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15. In some embodiments, the method includes determining the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16. In some embodiments, the method includes determining the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

Table 9: Two-Gene Combinations of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

IL6 and CXCL1
IL6 and CXCL2
IL6 and CXCL3
IL6 and CXCL8
IL6 and PTGS2
IL6 and CXCR1
IL6 and CXCR2
IL6 and S100A8
IL6 and S100A9
CXCL1 and CXCL2
CXCL1 and CXCL3
CXCL1 and CXCL8
CXCL1 and PTGS2
CXCL1 and CXCR1
CXCL1 and CXCR2
CXCL1 and S100A8
CXCL1 and S100A9
CXCL2 and CXCL3
CXCL2 and CXCL8
CXCL2 and PTGS2
CXCL2 and CXCR1
CXCL2 and CXCR2
CXCL2 and S100A8
CXCL2 and S100A9
CXCL3 and CXCL8
CXCL3 and PTGS2
CXCL3 and CXCR1
CXCL3 and CXCR2
CXCL3 and S100A8
CXCL3 and S100A9
CXCL8 and PTGS2
CXCL8 and CXCR1
CXCL8 and CXCR2
CXCL8 and S100A8
CXCL8 and S100A9
PTGS2 and CXCR1
PTGS2 and CXCR2
PTGS2 and S100A8
PTGS2 and S100A9

CXCR1 and CXCR2
CXCR1 and S100A8
CXCR1 and S100A9
CXCR2 and S100A8
CXCR2 and S100A9
S100A8 and S100A9

Table 10: Three-Gene Combinations of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

IL6, CXCL1, and CXCL2
IL6, CXCL1, and CXCL3
IL6, CXCL1, and CXCL8
IL6, CXCL1, and PTGS2
IL6, CXCL1, and CXCR1
IL6, CXCL1, and CXCR2
IL6, CXCL1, and S100A8
IL6, CXCL1, and S100A9
IL6, CXCL2, and CXCL3
IL6, CXCL2, and CXCL8
IL6, CXCL2, and PTGS2
IL6, CXCL2, and CXCR1
IL6, CXCL2, and CXCR2
IL6, CXCL2, and S100A8
IL6, CXCL2, and S100A9
IL6, CXCL3, and CXCL8
IL6, CXCL3, and PTGS2
IL6, CXCL3, and CXCR1
IL6, CXCL3, and CXCR2
IL6, CXCL3, and S100A8
IL6, CXCL3, and S100A9
IL6, CXCL8, and PTGS2
IL6, CXCL8, and CXCR1
IL6, CXCL8, and CXCR2
IL6, CXCL8, and S100A8
IL6, CXCL8, and S100A9
IL6, PTGS2, and CXCR1
IL6, PTGS2, and CXCR2
IL6, PTGS2, and S100A8
IL6, PTGS2, and S100A9
IL6, CXCR1, and CXCR2
IL6, CXCR1, and S100A8
IL6, CXCR1, and S100A9
IL6, CXCR2, and S100A8
IL6, CXCR2, and S100A9
IL6, S100A8, and S100A9
CXCL1, CXCL2, and CXCL3
CXCL1, CXCL2, and CXCL8
CXCL1, CXCL2, and PTGS2
CXCL1, CXCL2, and CXCR1
CXCL1, CXCL2, and CXCR2
CXCL1, CXCL2, and S100A8

CXCL1, CXCL2, and S100A9
CXCL1, CXCL3, and CXCL8
CXCL1, CXCL3, and PTGS2
CXCL1, CXCL3, and CXCR1
CXCL1, CXCL3, and CXCR2
CXCL1, CXCL3, and S100A8
CXCL1, CXCL3, and S100A9
CXCL1, CXCL8, and PTGS2
CXCL1, CXCL8, and CXCR1
CXCL1, CXCL8, and CXCR2
CXCL1, CXCL8, and S100A8
CXCL1, CXCL8, and S100A9
CXCL1, PTGS2, and CXCR1
CXCL1, PTGS2, and CXCR2
CXCL1, PTGS2, and S100A8
CXCL1, PTGS2, and S100A9
CXCL1, CXCR1, and CXCR2
CXCL1, CXCR1, and S100A8
CXCL1, CXCR1, and S100A9
CXCL1, CXCR2, and S100A8
CXCL1, CXCR2, and S100A9
CXCL1, S100A8, and S100A9
CXCL2, CXCL3, and CXCL8
CXCL2, CXCL3, and PTGS2
CXCL2, CXCL3, and CXCR1
CXCL2, CXCL3, and CXCR2
CXCL2, CXCL3, and S100A8
CXCL2, CXCL3, and S100A9
CXCL2, CXCL8, and PTGS2
CXCL2, CXCL8, and CXCR1
CXCL2, CXCL8, and CXCR2
CXCL2, CXCL8, and S100A8
CXCL2, CXCL8, and S100A9
CXCL2, PTGS2, and CXCR1
CXCL2, PTGS2, and CXCR2
CXCL2, PTGS2, and S100A8
CXCL2, PTGS2, and S100A9
CXCL2, CXCR1, and CXCR2
CXCL2, CXCR1, and S100A8
CXCL2, CXCR1, and S100A9
CXCL2, CXCR2, and S100A8
CXCL2, CXCR2, and S100A9
CXCL2, S100A8, and S100A9
CXCL3, CXCL8, and PTGS2
CXCL3, CXCL8, and CXCR1
CXCL3, CXCL8, and CXCR2
CXCL3, CXCL8, and S100A8
CXCL3, CXCL8, and S100A9
CXCL3, PTGS2, and CXCR1
CXCL3, PTGS2, and CXCR2
CXCL3, PTGS2, and S100A8
CXCL3, PTGS2, and S100A9

CXCL3, CXCR1, and CXCR2
CXCL3, CXCR1, and S100A8
CXCL3, CXCR1, and S100A9
CXCL3, CXCR2, and S100A8
CXCL3, CXCR2, and S100A9
CXCL3, S100A8, and S100A9
CXCL8, PTGS2, and CXCR1
CXCL8, PTGS2, and CXCR2
CXCL8, PTGS2, and S100A8
CXCL8, PTGS2, and S100A9
CXCL8, CXCR1, and CXCR2
CXCL8, CXCR1, and S100A8
CXCL8, CXCR1, and S100A9
CXCL8, CXCR2, and S100A8
CXCL8, CXCR2, and S100A9
CXCL8, S100A8, and S100A9
PTGS2, CXCR1, and CXCR2
PTGS2, CXCR1, and S100A8
PTGS2, CXCR1, and S100A9
PTGS2, CXCR2, and S100A8
PTGS2, CXCR2, and S100A9
PTGS2, S100A8, and S100A9
CXCR1, CXCR2, and S100A8
CXCR1, CXCR2, and S100A9
CXCR1, S100A8, and S100A9
CXCR2, S100A8, and S100A9

Table 11: Four-Gene Combinations of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

IL6, CXCL1, CXCL2, and CXCL3
IL6, CXCL1, CXCL2, and CXCL8
IL6, CXCL1, CXCL2, and PTGS2
IL6, CXCL1, CXCL2, and CXCR1
IL6, CXCL1, CXCL2, and CXCR2
IL6, CXCL1, CXCL2, and S100A8
IL6, CXCL1, CXCL2, and S100A9
IL6, CXCL1, CXCL3, and CXCL8
IL6, CXCL1, CXCL3, and PTGS2
IL6, CXCL1, CXCL3, and CXCR1
IL6, CXCL1, CXCL3, and CXCR2
IL6, CXCL1, CXCL3, and S100A8
IL6, CXCL1, CXCL3, and S100A9
IL6, CXCL1, CXCL8, and PTGS2
IL6, CXCL1, CXCL8, and CXCR1
IL6, CXCL1, CXCL8, and CXCR2
IL6, CXCL1, CXCL8, and S100A8
IL6, CXCL1, CXCL8, and S100A9
IL6, CXCL1, PTGS2, and CXCR1
IL6, CXCL1, PTGS2, and CXCR2
IL6, CXCL1, PTGS2, and S100A8
IL6, CXCL1, PTGS2, and S100A9

IL6, CXCL1, CXCR1, and CXCR2
IL6, CXCL1, CXCR1, and S100A8
IL6, CXCL1, CXCR1, and S100A9
IL6, CXCL1, CXCR2, and S100A8
IL6, CXCL1, CXCR2, and S100A9
IL6, CXCL1, S100A8, and S100A9
IL6, CXCL2, CXCL3, and CXCL8
IL6, CXCL2, CXCL3, and PTGS2
IL6, CXCL2, CXCL3, and CXCR1
IL6, CXCL2, CXCL3, and CXCR2
IL6, CXCL2, CXCL3, and S100A8
IL6, CXCL2, CXCL3, and S100A9
IL6, CXCL2, CXCL8, and PTGS2
IL6, CXCL2, CXCL8, and CXCR1
IL6, CXCL2, CXCL8, and CXCR2
IL6, CXCL2, CXCL8, and S100A8
IL6, CXCL2, CXCL8, and S100A9
IL6, CXCL2, PTGS2, and CXCR1
IL6, CXCL2, PTGS2, and CXCR2
IL6, CXCL2, PTGS2, and S100A8
IL6, CXCL2, PTGS2, and S100A9
IL6, CXCL2, CXCR1, and CXCR2
IL6, CXCL2, CXCR1, and S100A8
IL6, CXCL2, CXCR1, and S100A9
IL6, CXCL2, CXCR2, and S100A8
IL6, CXCL2, CXCR2, and S100A9
IL6, CXCL2, S100A8, and S100A9
IL6, CXCL3, CXCL8, and PTGS2
IL6, CXCL3, CXCL8, and CXCR1
IL6, CXCL3, CXCL8, and CXCR2
IL6, CXCL3, CXCL8, and S100A8
IL6, CXCL3, CXCL8, and S100A9
IL6, CXCL3, PTGS2, and CXCR1
IL6, CXCL3, PTGS2, and CXCR2
IL6, CXCL3, PTGS2, and S100A8
IL6, CXCL3, PTGS2, and S100A9
IL6, CXCL3, CXCR1, and CXCR2
IL6, CXCL3, CXCR1, and S100A8
IL6, CXCL3, CXCR1, and S100A9
IL6, CXCL3, CXCR2, and S100A8
IL6, CXCL3, CXCR2, and S100A9
IL6, CXCL3, S100A8, and S100A9
IL6, CXCL8, PTGS2, and CXCR1
IL6, CXCL8, PTGS2, and CXCR2
IL6, CXCL8, PTGS2, and S100A8
IL6, CXCL8, PTGS2, and S100A9
IL6, CXCL8, CXCR1, and CXCR2
IL6, CXCL8, CXCR1, and S100A8
IL6, CXCL8, CXCR1, and S100A9
IL6, CXCL8, CXCR2, and S100A8
IL6, CXCL8, CXCR2, and S100A9
IL6, CXCL8, S100A8, and S100A9

IL6, PTGS2, CXCR1, and CXCR2
IL6, PTGS2, CXCR1, and S100A8
IL6, PTGS2, CXCR1, and S100A9
IL6, PTGS2, CXCR2, and S100A8
IL6, PTGS2, CXCR2, and S100A9
IL6, PTGS2, S100A8, and S100A9
IL6, CXCR1, CXCR2, and S100A8
IL6, CXCR1, CXCR2, and S100A9
IL6, CXCR1, S100A8, and S100A9
IL6, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, and CXCL8
CXCL1, CXCL2, CXCL3, and PTGS2
CXCL1, CXCL2, CXCL3, and CXCR1
CXCL1, CXCL2, CXCL3, and CXCR2
CXCL1, CXCL2, CXCL3, and S100A8
CXCL1, CXCL2, CXCL3, and S100A9
CXCL1, CXCL2, CXCL8, and PTGS2
CXCL1, CXCL2, CXCL8, and CXCR1
CXCL1, CXCL2, CXCL8, and CXCR2
CXCL1, CXCL2, CXCL8, and S100A8
CXCL1, CXCL2, CXCL8, and S100A9
CXCL1, CXCL2, PTGS2, and CXCR1
CXCL1, CXCL2, PTGS2, and CXCR2
CXCL1, CXCL2, PTGS2, and S100A8
CXCL1, CXCL2, PTGS2, and S100A9
CXCL1, CXCL2, CXCR1, and CXCR2
CXCL1, CXCL2, CXCR1, and S100A8
CXCL1, CXCL2, CXCR1, and S100A9
CXCL1, CXCL2, CXCR2, and S100A8
CXCL1, CXCL2, CXCR2, and S100A9
CXCL1, CXCL2, S100A8, and S100A9
CXCL1, CXCL3, CXCL8, and PTGS2
CXCL1, CXCL3, CXCL8, and CXCR1
CXCL1, CXCL3, CXCL8, and CXCR2
CXCL1, CXCL3, CXCL8, and S100A8
CXCL1, CXCL3, CXCL8, and S100A9
CXCL1, CXCL3, PTGS2, and CXCR1
CXCL1, CXCL3, PTGS2, and CXCR2
CXCL1, CXCL3, PTGS2, and S100A8
CXCL1, CXCL3, PTGS2, and S100A9
CXCL1, CXCL3, CXCR1, and CXCR2
CXCL1, CXCL3, CXCR1, and S100A8
CXCL1, CXCL3, CXCR1, and S100A9
CXCL1, CXCL3, CXCR2, and S100A8
CXCL1, CXCL3, CXCR2, and S100A9
CXCL1, CXCL3, S100A8, and S100A9
CXCL1, CXCL8, PTGS2, and CXCR1
CXCL1, CXCL8, PTGS2, and CXCR2
CXCL1, CXCL8, PTGS2, and S100A8
CXCL1, CXCL8, PTGS2, and S100A9
CXCL1, CXCL8, CXCR1, and CXCR2
CXCL1, CXCL8, CXCR1, and S100A8

CXCL1, CXCL8, CXCR1, and S100A9
CXCL1, CXCL8, CXCR2, and S100A8
CXCL1, CXCL8, CXCR2, and S100A9
CXCL1, CXCL8, S100A8, and S100A9
CXCL1, PTGS2, CXCR1, and CXCR2
CXCL1, PTGS2, CXCR1, and S100A8
CXCL1, PTGS2, CXCR1, and S100A9
CXCL1, PTGS2, CXCR2, and S100A8
CXCL1, PTGS2, CXCR2, and S100A9
CXCL1, PTGS2, S100A8, and S100A9
CXCL1, CXCR1, CXCR2, and S100A8
CXCL1, CXCR1, CXCR2, and S100A9
CXCL1, CXCR1, S100A8, and S100A9
CXCL1, CXCR2, S100A8, and S100A9
CXCL2, CXCL3, CXCL8, and PTGS2
CXCL2, CXCL3, CXCL8, and CXCR1
CXCL2, CXCL3, CXCL8, and CXCR2
CXCL2, CXCL3, CXCL8, and S100A8
CXCL2, CXCL3, CXCL8, and S100A9
CXCL2, CXCL3, PTGS2, and CXCR1
CXCL2, CXCL3, PTGS2, and CXCR2
CXCL2, CXCL3, PTGS2, and S100A8
CXCL2, CXCL3, PTGS2, and S100A9
CXCL2, CXCL3, CXCR1, and CXCR2
CXCL2, CXCL3, CXCR1, and S100A8
CXCL2, CXCL3, CXCR1, and S100A9
CXCL2, CXCL3, CXCR2, and S100A8
CXCL2, CXCL3, CXCR2, and S100A9
CXCL2, CXCL3, S100A8, and S100A9
CXCL2, CXCL8, PTGS2, and CXCR1
CXCL2, CXCL8, PTGS2, and CXCR2
CXCL2, CXCL8, PTGS2, and S100A8
CXCL2, CXCL8, PTGS2, and S100A9
CXCL2, CXCL8, CXCR1, and CXCR2
CXCL2, CXCL8, CXCR1, and S100A8
CXCL2, CXCL8, CXCR1, and S100A9
CXCL2, CXCL8, CXCR2, and S100A8
CXCL2, CXCL8, CXCR2, and S100A9
CXCL2, CXCL8, S100A8, and S100A9
CXCL2, PTGS2, CXCR1, and CXCR2
CXCL2, PTGS2, CXCR1, and S100A8
CXCL2, PTGS2, CXCR1, and S100A9
CXCL2, PTGS2, CXCR2, and S100A8
CXCL2, PTGS2, CXCR2, and S100A9
CXCL2, PTGS2, S100A8, and S100A9
CXCL2, CXCR1, CXCR2, and S100A8
CXCL2, CXCR1, CXCR2, and S100A9
CXCL2, CXCR1, S100A8, and S100A9
CXCL2, CXCR2, S100A8, and S100A9
CXCL3, CXCL8, PTGS2, and CXCR1
CXCL3, CXCL8, PTGS2, and CXCR2
CXCL3, CXCL8, PTGS2, and S100A8

CXCL3, CXCL8, PTGS2, and S100A9
CXCL3, CXCL8, CXCR1, and CXCR2
CXCL3, CXCL8, CXCR1, and S100A8
CXCL3, CXCL8, CXCR1, and S100A9
CXCL3, CXCL8, CXCR2, and S100A8
CXCL3, CXCL8, CXCR2, and S100A9
CXCL3, CXCL8, S100A8, and S100A9
CXCL3, PTGS2, CXCR1, and CXCR2
CXCL3, PTGS2, CXCR1, and S100A8
CXCL3, PTGS2, CXCR1, and S100A9
CXCL3, PTGS2, CXCR2, and S100A8
CXCL3, PTGS2, CXCR2, and S100A9
CXCL3, PTGS2, S100A8, and S100A9
CXCL3, CXCR1, CXCR2, and S100A8
CXCL3, CXCR1, CXCR2, and S100A9
CXCL3, CXCR1, S100A8, and S100A9
CXCL3, CXCR2, S100A8, and S100A9
CXCL8, PTGS2, CXCR1, and CXCR2
CXCL8, PTGS2, CXCR1, and S100A8
CXCL8, PTGS2, CXCR1, and S100A9
CXCL8, PTGS2, CXCR2, and S100A8
CXCL8, PTGS2, CXCR2, and S100A9
CXCL8, PTGS2, S100A8, and S100A9
CXCL8, CXCR1, CXCR2, and S100A8
CXCL8, CXCR1, CXCR2, and S100A9
CXCL8, CXCR1, S100A8, and S100A9
CXCL8, CXCR2, S100A8, and S100A9
PTGS2, CXCR1, CXCR2, and S100A8
PTGS2, CXCR1, CXCR2, and S100A9
PTGS2, CXCR1, S100A8, and S100A9
PTGS2, CXCR2, S100A8, and S100A9
CXCR1, CXCR2, S100A8, and S100A9

Table 12: Five-Gene Combinations of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

IL6, CXCL1, CXCL2, CXCL3, and CXCL8
IL6, CXCL1, CXCL2, CXCL3, and PTGS2
IL6, CXCL1, CXCL2, CXCL3, and CXCR1
IL6, CXCL1, CXCL2, CXCL3, and CXCR2
IL6, CXCL1, CXCL2, CXCL3, and S100A8
IL6, CXCL1, CXCL2, CXCL3, and S100A9
IL6, CXCL1, CXCL2, CXCL8, and PTGS2
IL6, CXCL1, CXCL2, CXCL8, and CXCR1
IL6, CXCL1, CXCL2, CXCL8, and CXCR2
IL6, CXCL1, CXCL2, CXCL8, and S100A8
IL6, CXCL1, CXCL2, CXCL8, and S100A9
IL6, CXCL1, CXCL2, PTGS2, and CXCR1
IL6, CXCL1, CXCL2, PTGS2, and CXCR2
IL6, CXCL1, CXCL2, PTGS2, and S100A8
IL6, CXCL1, CXCL2, PTGS2, and S100A9
IL6, CXCL1, CXCL2, CXCR1, and CXCR2

IL6, CXCL1, CXCL2, CXCR1, and S100A8
IL6, CXCL1, CXCL2, CXCR1, and S100A9
IL6, CXCL1, CXCL2, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCR2, and S100A9
IL6, CXCL1, CXCL2, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCL8, and PTGS2
IL6, CXCL1, CXCL3, CXCL8, and CXCR1
IL6, CXCL1, CXCL3, CXCL8, and CXCR2
IL6, CXCL1, CXCL3, CXCL8, and S100A8
IL6, CXCL1, CXCL3, CXCL8, and S100A9
IL6, CXCL1, CXCL3, PTGS2, and CXCR1
IL6, CXCL1, CXCL3, PTGS2, and CXCR2
IL6, CXCL1, CXCL3, PTGS2, and S100A8
IL6, CXCL1, CXCL3, PTGS2, and S100A9
IL6, CXCL1, CXCL3, CXCR1, and CXCR2
IL6, CXCL1, CXCL3, CXCR1, and S100A8
IL6, CXCL1, CXCL3, CXCR1, and S100A9
IL6, CXCL1, CXCL3, CXCR2, and S100A8
IL6, CXCL1, CXCL3, CXCR2, and S100A9
IL6, CXCL1, CXCL3, S100A8, and S100A9
IL6, CXCL1, CXCL8, PTGS2, and CXCR1
IL6, CXCL1, CXCL8, PTGS2, and CXCR2
IL6, CXCL1, CXCL8, PTGS2, and S100A8
IL6, CXCL1, CXCL8, PTGS2, and S100A9
IL6, CXCL1, CXCL8, CXCR1, and CXCR2
IL6, CXCL1, CXCL8, CXCR1, and S100A8
IL6, CXCL1, CXCL8, CXCR1, and S100A9
IL6, CXCL1, CXCL8, CXCR2, and S100A8
IL6, CXCL1, CXCL8, CXCR2, and S100A9
IL6, CXCL1, CXCL8, S100A8, and S100A9
IL6, CXCL1, PTGS2, CXCR1, and CXCR2
IL6, CXCL1, PTGS2, CXCR1, and S100A8
IL6, CXCL1, PTGS2, CXCR1, and S100A9
IL6, CXCL1, PTGS2, CXCR2, and S100A8
IL6, CXCL1, PTGS2, CXCR2, and S100A9
IL6, CXCL1, PTGS2, S100A8, and S100A9
IL6, CXCL1, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCL8, and PTGS2
IL6, CXCL2, CXCL3, CXCL8, and CXCR1
IL6, CXCL2, CXCL3, CXCL8, and CXCR2
IL6, CXCL2, CXCL3, CXCL8, and S100A8
IL6, CXCL2, CXCL3, CXCL8, and S100A9
IL6, CXCL2, CXCL3, PTGS2, and CXCR1
IL6, CXCL2, CXCL3, PTGS2, and CXCR2
IL6, CXCL2, CXCL3, PTGS2, and S100A8
IL6, CXCL2, CXCL3, PTGS2, and S100A9
IL6, CXCL2, CXCL3, CXCR1, and CXCR2
IL6, CXCL2, CXCL3, CXCR1, and S100A8
IL6, CXCL2, CXCL3, CXCR1, and S100A9

IL6, CXCL2, CXCL3, CXCR2, and S100A8
IL6, CXCL2, CXCL3, CXCR2, and S100A9
IL6, CXCL2, CXCL3, S100A8, and S100A9
IL6, CXCL2, CXCL8, PTGS2, and CXCR1
IL6, CXCL2, CXCL8, PTGS2, and CXCR2
IL6, CXCL2, CXCL8, PTGS2, and S100A8
IL6, CXCL2, CXCL8, PTGS2, and S100A9
IL6, CXCL2, CXCL8, CXCR1, and CXCR2
IL6, CXCL2, CXCL8, CXCR1, and S100A8
IL6, CXCL2, CXCL8, CXCR1, and S100A9
IL6, CXCL2, CXCL8, CXCR2, and S100A8
IL6, CXCL2, CXCL8, CXCR2, and S100A9
IL6, CXCL2, CXCL8, S100A8, and S100A9
IL6, CXCL2, PTGS2, CXCR1, and CXCR2
IL6, CXCL2, PTGS2, CXCR1, and S100A8
IL6, CXCL2, PTGS2, CXCR1, and S100A9
IL6, CXCL2, PTGS2, CXCR2, and S100A8
IL6, CXCL2, PTGS2, CXCR2, and S100A9
IL6, CXCL2, PTGS2, S100A8, and S100A9
IL6, CXCL2, CXCR1, CXCR2, and S100A8
IL6, CXCL2, CXCR1, CXCR2, and S100A9
IL6, CXCL2, CXCR1, S100A8, and S100A9
IL6, CXCL2, CXCR2, S100A8, and S100A9
IL6, CXCL3, CXCL8, PTGS2, and CXCR1
IL6, CXCL3, CXCL8, PTGS2, and CXCR2
IL6, CXCL3, CXCL8, PTGS2, and S100A8
IL6, CXCL3, CXCL8, PTGS2, and S100A9
IL6, CXCL3, CXCL8, CXCR1, and CXCR2
IL6, CXCL3, CXCL8, CXCR1, and S100A8
IL6, CXCL3, CXCL8, CXCR1, and S100A9
IL6, CXCL3, CXCL8, CXCR2, and S100A8
IL6, CXCL3, CXCL8, CXCR2, and S100A9
IL6, CXCL3, CXCL8, S100A8, and S100A9
IL6, CXCL3, PTGS2, CXCR1, and CXCR2
IL6, CXCL3, PTGS2, CXCR1, and S100A8
IL6, CXCL3, PTGS2, CXCR1, and S100A9
IL6, CXCL3, PTGS2, CXCR2, and S100A8
IL6, CXCL3, PTGS2, CXCR2, and S100A9
IL6, CXCL3, PTGS2, S100A8, and S100A9
IL6, CXCL3, CXCR1, CXCR2, and S100A8
IL6, CXCL3, CXCR1, CXCR2, and S100A9
IL6, CXCL3, CXCR1, S100A8, and S100A9
IL6, CXCL3, CXCR2, S100A8, and S100A9
IL6, CXCL8, PTGS2, CXCR1, and CXCR2
IL6, CXCL8, PTGS2, CXCR1, and S100A8
IL6, CXCL8, PTGS2, CXCR1, and S100A9
IL6, CXCL8, PTGS2, CXCR2, and S100A8
IL6, CXCL8, PTGS2, CXCR2, and S100A9
IL6, CXCL8, PTGS2, S100A8, and S100A9
IL6, CXCL8, CXCR1, CXCR2, and S100A8
IL6, CXCL8, CXCR1, CXCR2, and S100A9
IL6, CXCL8, CXCR1, S100A8, and S100A9

IL6, CXCL8, CXCR2, S100A8, and S100A9
IL6, PTGS2, CXCR1, CXCR2, and S100A8
IL6, PTGS2, CXCR1, CXCR2, and S100A9
IL6, PTGS2, CXCR1, S100A8, and S100A9
IL6, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2
CXCL1, CXCL2, CXCL3, CXCL8, and CXCR1
CXCL1, CXCL2, CXCL3, CXCL8, and CXCR2
CXCL1, CXCL2, CXCL3, CXCL8, and S100A8
CXCL1, CXCL2, CXCL3, CXCL8, and S100A9
CXCL1, CXCL2, CXCL3, PTGS2, and CXCR1
CXCL1, CXCL2, CXCL3, PTGS2, and CXCR2
CXCL1, CXCL2, CXCL3, PTGS2, and S100A8
CXCL1, CXCL2, CXCL3, PTGS2, and S100A9
CXCL1, CXCL2, CXCL3, CXCR1, and CXCR2
CXCL1, CXCL2, CXCL3, CXCR1, and S100A8
CXCL1, CXCL2, CXCL3, CXCR1, and S100A9
CXCL1, CXCL2, CXCL3, CXCR2, and S100A8
CXCL1, CXCL2, CXCL3, CXCR2, and S100A9
CXCL1, CXCL2, CXCL3, S100A8, and S100A9
CXCL1, CXCL2, CXCL8, PTGS2, and CXCR1
CXCL1, CXCL2, CXCL8, PTGS2, and CXCR2
CXCL1, CXCL2, CXCL8, PTGS2, and S100A8
CXCL1, CXCL2, CXCL8, PTGS2, and S100A9
CXCL1, CXCL2, CXCL8, CXCR1, and CXCR2
CXCL1, CXCL2, CXCL8, CXCR1, and S100A8
CXCL1, CXCL2, CXCL8, CXCR1, and S100A9
CXCL1, CXCL2, CXCL8, CXCR2, and S100A8
CXCL1, CXCL2, CXCL8, CXCR2, and S100A9
CXCL1, CXCL2, CXCL8, S100A8, and S100A9
CXCL1, CXCL2, PTGS2, CXCR1, and CXCR2
CXCL1, CXCL2, PTGS2, CXCR1, and S100A8
CXCL1, CXCL2, PTGS2, CXCR1, and S100A9
CXCL1, CXCL2, PTGS2, CXCR2, and S100A8
CXCL1, CXCL2, PTGS2, CXCR2, and S100A9
CXCL1, CXCL2, PTGS2, S100A8, and S100A9
CXCL1, CXCL2, CXCR1, CXCR2, and S100A8
CXCL1, CXCL2, CXCR1, CXCR2, and S100A9
CXCL1, CXCL2, CXCR1, S100A8, and S100A9
CXCL1, CXCL2, CXCR2, S100A8, and S100A9
CXCL1, CXCL3, CXCL8, PTGS2, and CXCR1
CXCL1, CXCL3, CXCL8, PTGS2, and CXCR2
CXCL1, CXCL3, CXCL8, PTGS2, and S100A8
CXCL1, CXCL3, CXCL8, PTGS2, and S100A9
CXCL1, CXCL3, CXCL8, CXCR1, and CXCR2
CXCL1, CXCL3, CXCL8, CXCR1, and S100A8
CXCL1, CXCL3, CXCL8, CXCR1, and S100A9
CXCL1, CXCL3, CXCL8, CXCR2, and S100A8
CXCL1, CXCL3, CXCL8, CXCR2, and S100A9
CXCL1, CXCL3, CXCL8, S100A8, and S100A9
CXCL1, CXCL3, PTGS2, CXCR1, and CXCR2

CXCL1, CXCL3, PTGS2, CXCR1, and S100A8
CXCL1, CXCL3, PTGS2, CXCR1, and S100A9
CXCL1, CXCL3, PTGS2, CXCR2, and S100A8
CXCL1, CXCL3, PTGS2, CXCR2, and S100A9
CXCL1, CXCL3, PTGS2, S100A8, and S100A9
CXCL1, CXCL3, CXCR1, CXCR2, and S100A8
CXCL1, CXCL3, CXCR1, CXCR2, and S100A9
CXCL1, CXCL3, CXCR1, S100A8, and S100A9
CXCL1, CXCL3, CXCR2, S100A8, and S100A9
CXCL1, CXCL8, PTGS2, CXCR1, and CXCR2
CXCL1, CXCL8, PTGS2, CXCR1, and S100A8
CXCL1, CXCL8, PTGS2, CXCR1, and S100A9
CXCL1, CXCL8, PTGS2, CXCR2, and S100A8
CXCL1, CXCL8, PTGS2, CXCR2, and S100A9
CXCL1, CXCL8, PTGS2, S100A8, and S100A9
CXCL1, CXCL8, CXCR1, CXCR2, and S100A8
CXCL1, CXCL8, CXCR1, CXCR2, and S100A9
CXCL1, CXCL8, CXCR1, S100A8, and S100A9
CXCL1, CXCL8, CXCR2, S100A8, and S100A9
CXCL1, PTGS2, CXCR1, CXCR2, and S100A8
CXCL1, PTGS2, CXCR1, CXCR2, and S100A9
CXCL1, PTGS2, CXCR1, S100A8, and S100A9
CXCL1, PTGS2, CXCR2, S100A8, and S100A9
CXCL1, CXCR1, CXCR2, S100A8, and S100A9
CXCL2, CXCL3, CXCL8, PTGS2, and CXCR1
CXCL2, CXCL3, CXCL8, PTGS2, and CXCR2
CXCL2, CXCL3, CXCL8, PTGS2, and S100A8
CXCL2, CXCL3, CXCL8, PTGS2, and S100A9
CXCL2, CXCL3, CXCL8, CXCR1, and CXCR2
CXCL2, CXCL3, CXCL8, CXCR1, and S100A8
CXCL2, CXCL3, CXCL8, CXCR1, and S100A9
CXCL2, CXCL3, CXCL8, CXCR2, and S100A8
CXCL2, CXCL3, CXCL8, CXCR2, and S100A9
CXCL2, CXCL3, CXCL8, S100A8, and S100A9
CXCL2, CXCL3, PTGS2, CXCR1, and CXCR2
CXCL2, CXCL3, PTGS2, CXCR1, and S100A8
CXCL2, CXCL3, PTGS2, CXCR1, and S100A9
CXCL2, CXCL3, PTGS2, CXCR2, and S100A8
CXCL2, CXCL3, PTGS2, CXCR2, and S100A9
CXCL2, CXCL3, PTGS2, S100A8, and S100A9
CXCL2, CXCL3, CXCR1, CXCR2, and S100A8
CXCL2, CXCL3, CXCR1, CXCR2, and S100A9
CXCL2, CXCL3, CXCR1, S100A8, and S100A9
CXCL2, CXCL3, CXCR2, S100A8, and S100A9
CXCL2, CXCL8, PTGS2, CXCR1, and CXCR2
CXCL2, CXCL8, PTGS2, CXCR1, and S100A8
CXCL2, CXCL8, PTGS2, CXCR1, and S100A9
CXCL2, CXCL8, PTGS2, CXCR2, and S100A8
CXCL2, CXCL8, PTGS2, CXCR2, and S100A9
CXCL2, CXCL8, PTGS2, S100A8, and S100A9
CXCL2, CXCL8, CXCR1, CXCR2, and S100A8
CXCL2, CXCL8, CXCR1, CXCR2, and S100A9

CXCL2, CXCL8, CXCR1, S100A8, and S100A9
CXCL2, CXCL8, CXCR2, S100A8, and S100A9
CXCL2, PTGS2, CXCR1, CXCR2, and S100A8
CXCL2, PTGS2, CXCR1, CXCR2, and S100A9
CXCL2, PTGS2, CXCR1, S100A8, and S100A9
CXCL2, PTGS2, CXCR2, S100A8, and S100A9
CXCL2, CXCR1, CXCR2, S100A8, and S100A9
CXCL3, CXCL8, PTGS2, CXCR1, and CXCR2
CXCL3, CXCL8, PTGS2, CXCR1, and S100A8
CXCL3, CXCL8, PTGS2, CXCR1, and S100A9
CXCL3, CXCL8, PTGS2, CXCR2, and S100A8
CXCL3, CXCL8, PTGS2, CXCR2, and S100A9
CXCL3, CXCL8, PTGS2, S100A8, and S100A9
CXCL3, CXCL8, CXCR1, CXCR2, and S100A8
CXCL3, CXCL8, CXCR1, CXCR2, and S100A9
CXCL3, CXCL8, CXCR1, S100A8, and S100A9
CXCL3, CXCL8, CXCR2, S100A8, and S100A9
CXCL3, PTGS2, CXCR1, CXCR2, and S100A8
CXCL3, PTGS2, CXCR1, CXCR2, and S100A9
CXCL3, PTGS2, CXCR1, S100A8, and S100A9
CXCL3, PTGS2, CXCR2, S100A8, and S100A9
CXCL3, CXCR1, CXCR2, S100A8, and S100A9
CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
CXCL8, PTGS2, CXCR1, S100A8, and S100A9
CXCL8, PTGS2, CXCR2, S100A8, and S100A9
CXCL8, CXCR1, CXCR2, S100A8, and S100A9
PTGS2, CXCR1, CXCR2, S100A8, and S100A9

Table 13: Six-Gene Combinations of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2
IL6, CXCL1, CXCL2, CXCL3, CXCL8, and CXCR1
IL6, CXCL1, CXCL2, CXCL3, CXCL8, and CXCR2
IL6, CXCL1, CXCL2, CXCL3, CXCL8, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCL8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, PTGS2, and CXCR1
IL6, CXCL1, CXCL2, CXCL3, PTGS2, and CXCR2
IL6, CXCL1, CXCL2, CXCL3, PTGS2, and S100A8
IL6, CXCL1, CXCL2, CXCL3, PTGS2, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCR1, and CXCR2
IL6, CXCL1, CXCL2, CXCL3, CXCR1, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCR1, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL3, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL8, PTGS2, and CXCR1
IL6, CXCL1, CXCL2, CXCL8, PTGS2, and CXCR2
IL6, CXCL1, CXCL2, CXCL8, PTGS2, and S100A8
IL6, CXCL1, CXCL2, CXCL8, PTGS2, and S100A9
IL6, CXCL1, CXCL2, CXCL8, CXCR1, and CXCR2

IL6, CXCL1, CXCL2, CXCL8, CXCR1, and S100A8
IL6, CXCL1, CXCL2, CXCL8, CXCR1, and S100A9
IL6, CXCL1, CXCL2, CXCL8, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL8, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL8, S100A8, and S100A9
IL6, CXCL1, CXCL2, PTGS2, CXCR1, and CXCR2
IL6, CXCL1, CXCL2, PTGS2, CXCR1, and S100A8
IL6, CXCL1, CXCL2, PTGS2, CXCR1, and S100A9
IL6, CXCL1, CXCL2, PTGS2, CXCR2, and S100A8
IL6, CXCL1, CXCL2, PTGS2, CXCR2, and S100A9
IL6, CXCL1, CXCL2, PTGS2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCL8, PTGS2, and CXCR1
IL6, CXCL1, CXCL3, CXCL8, PTGS2, and CXCR2
IL6, CXCL1, CXCL3, CXCL8, PTGS2, and S100A8
IL6, CXCL1, CXCL3, CXCL8, PTGS2, and S100A9
IL6, CXCL1, CXCL3, CXCL8, CXCR1, and CXCR2
IL6, CXCL1, CXCL3, CXCL8, CXCR1, and S100A8
IL6, CXCL1, CXCL3, CXCL8, CXCR1, and S100A9
IL6, CXCL1, CXCL3, CXCL8, CXCR2, and S100A8
IL6, CXCL1, CXCL3, CXCL8, CXCR2, and S100A9
IL6, CXCL1, CXCL3, CXCL8, S100A8, and S100A9
IL6, CXCL1, CXCL3, PTGS2, CXCR1, and CXCR2
IL6, CXCL1, CXCL3, PTGS2, CXCR1, and S100A8
IL6, CXCL1, CXCL3, PTGS2, CXCR1, and S100A9
IL6, CXCL1, CXCL3, PTGS2, CXCR2, and S100A8
IL6, CXCL1, CXCL3, PTGS2, CXCR2, and S100A9
IL6, CXCL1, CXCL3, PTGS2, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL3, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL3, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL8, PTGS2, CXCR1, and CXCR2
IL6, CXCL1, CXCL8, PTGS2, CXCR1, and S100A8
IL6, CXCL1, CXCL8, PTGS2, CXCR1, and S100A9
IL6, CXCL1, CXCL8, PTGS2, CXCR2, and S100A8
IL6, CXCL1, CXCL8, PTGS2, CXCR2, and S100A9
IL6, CXCL1, CXCL8, PTGS2, S100A8, and S100A9
IL6, CXCL1, CXCL8, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL8, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL8, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL8, CXCR2, S100A8, and S100A9
IL6, CXCL1, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL1, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL1, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL1, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCL8, PTGS2, and CXCR1
IL6, CXCL2, CXCL3, CXCL8, PTGS2, and CXCR2

IL6, CXCL2, CXCL3, CXCL8, PTGS2, and S100A8
IL6, CXCL2, CXCL3, CXCL8, PTGS2, and S100A9
IL6, CXCL2, CXCL3, CXCL8, CXCR1, and CXCR2
IL6, CXCL2, CXCL3, CXCL8, CXCR1, and S100A8
IL6, CXCL2, CXCL3, CXCL8, CXCR1, and S100A9
IL6, CXCL2, CXCL3, CXCL8, CXCR2, and S100A8
IL6, CXCL2, CXCL3, CXCL8, CXCR2, and S100A9
IL6, CXCL2, CXCL3, CXCL8, S100A8, and S100A9
IL6, CXCL2, CXCL3, PTGS2, CXCR1, and CXCR2
IL6, CXCL2, CXCL3, PTGS2, CXCR1, and S100A8
IL6, CXCL2, CXCL3, PTGS2, CXCR1, and S100A9
IL6, CXCL2, CXCL3, PTGS2, CXCR2, and S100A8
IL6, CXCL2, CXCL3, PTGS2, CXCR2, and S100A9
IL6, CXCL2, CXCL3, PTGS2, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCR1, CXCR2, and S100A8
IL6, CXCL2, CXCL3, CXCR1, CXCR2, and S100A9
IL6, CXCL2, CXCL3, CXCR1, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL8, PTGS2, CXCR1, and CXCR2
IL6, CXCL2, CXCL8, PTGS2, CXCR1, and S100A8
IL6, CXCL2, CXCL8, PTGS2, CXCR1, and S100A9
IL6, CXCL2, CXCL8, PTGS2, CXCR2, and S100A8
IL6, CXCL2, CXCL8, PTGS2, CXCR2, and S100A9
IL6, CXCL2, CXCL8, PTGS2, S100A8, and S100A9
IL6, CXCL2, CXCL8, CXCR1, CXCR2, and S100A8
IL6, CXCL2, CXCL8, CXCR1, CXCR2, and S100A9
IL6, CXCL2, CXCL8, CXCR1, S100A8, and S100A9
IL6, CXCL2, CXCL8, CXCR2, S100A8, and S100A9
IL6, CXCL2, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL2, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL2, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL2, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL3, CXCL8, PTGS2, CXCR1, and CXCR2
IL6, CXCL3, CXCL8, PTGS2, CXCR1, and S100A8
IL6, CXCL3, CXCL8, PTGS2, CXCR1, and S100A9
IL6, CXCL3, CXCL8, PTGS2, CXCR2, and S100A8
IL6, CXCL3, CXCL8, PTGS2, CXCR2, and S100A9
IL6, CXCL3, CXCL8, PTGS2, S100A8, and S100A9
IL6, CXCL3, CXCL8, CXCR1, CXCR2, and S100A8
IL6, CXCL3, CXCL8, CXCR1, CXCR2, and S100A9
IL6, CXCL3, CXCL8, CXCR1, S100A8, and S100A9
IL6, CXCL3, CXCL8, CXCR2, S100A8, and S100A9
IL6, CXCL3, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL3, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL3, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL3, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL3, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL8, PTGS2, CXCR2, S100A8, and S100A9

IL6, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
IL6, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, and CXCR1
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, and CXCR2
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, and S100A8
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, and CXCR2
CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, and S100A8
CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, CXCR2, and S100A8
CXCL1, CXCL2, CXCL3, CXCL8, CXCR2, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, and CXCR2
CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, and S100A8
CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, and S100A9
CXCL1, CXCL2, CXCL3, PTGS2, CXCR2, and S100A8
CXCL1, CXCL2, CXCL3, PTGS2, CXCR2, and S100A9
CXCL1, CXCL2, CXCL3, PTGS2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCR1, CXCR2, and S100A8
CXCL1, CXCL2, CXCL3, CXCR1, CXCR2, and S100A9
CXCL1, CXCL2, CXCL3, CXCR1, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, and CXCR2
CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, and S100A8
CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, and S100A9
CXCL1, CXCL2, CXCL8, PTGS2, CXCR2, and S100A8
CXCL1, CXCL2, CXCL8, PTGS2, CXCR2, and S100A9
CXCL1, CXCL2, CXCL8, PTGS2, S100A8, and S100A9
CXCL1, CXCL2, CXCL8, CXCR1, CXCR2, and S100A8
CXCL1, CXCL2, CXCL8, CXCR1, CXCR2, and S100A9
CXCL1, CXCL2, CXCL8, CXCR1, S100A8, and S100A9
CXCL1, CXCL2, CXCL8, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, PTGS2, CXCR1, CXCR2, and S100A8
CXCL1, CXCL2, PTGS2, CXCR1, CXCR2, and S100A9
CXCL1, CXCL2, PTGS2, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, and CXCR2
CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, and S100A8
CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, and S100A9
CXCL1, CXCL3, CXCL8, PTGS2, CXCR2, and S100A8
CXCL1, CXCL3, CXCL8, PTGS2, CXCR2, and S100A9
CXCL1, CXCL3, CXCL8, PTGS2, S100A8, and S100A9
CXCL1, CXCL3, CXCL8, CXCR1, CXCR2, and S100A8
CXCL1, CXCL3, CXCL8, CXCR1, CXCR2, and S100A9
CXCL1, CXCL3, CXCL8, CXCR1, S100A8, and S100A9
CXCL1, CXCL3, CXCL8, CXCR2, S100A8, and S100A9
CXCL1, CXCL3, PTGS2, CXCR1, CXCR2, and S100A8
CXCL1, CXCL3, PTGS2, CXCR1, CXCR2, and S100A9
CXCL1, CXCL3, PTGS2, CXCR1, S100A8, and S100A9
CXCL1, CXCL3, PTGS2, CXCR2, S100A8, and S100A9
CXCL1, CXCL3, CXCR1, CXCR2, S100A8, and S100A9

CXCL1, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
CXCL1, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
CXCL1, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
CXCL1, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
CXCL1, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and CXCR2
CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and S100A8
CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and S100A9
CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, and S100A8
CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, and S100A9
CXCL2, CXCL3, CXCL8, PTGS2, S100A8, and S100A9
CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, and S100A8
CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, and S100A9
CXCL2, CXCL3, CXCL8, CXCR1, S100A8, and S100A9
CXCL2, CXCL3, CXCL8, CXCR2, S100A8, and S100A9
CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, and S100A8
CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, and S100A9
CXCL2, CXCL3, PTGS2, CXCR1, S100A8, and S100A9
CXCL2, CXCL3, PTGS2, CXCR2, S100A8, and S100A9
CXCL2, CXCL3, CXCR1, CXCR2, S100A8, and S100A9
CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
CXCL2, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
CXCL2, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
CXCL2, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
CXCL2, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
CXCL3, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
CXCL3, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
CXCL3, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
CXCL3, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

Table 14: Seven-Gene Combinations of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, and CXCR1
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, and CXCR2
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, and CXCR2
IL6, CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCL8, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, and CXCR2
IL6, CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, and S100A8
IL6, CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, and S100A9
IL6, CXCL1, CXCL2, CXCL3, PTGS2, CXCR2, and S100A8

IL6, CXCL1, CXCL2, CXCL3, PTGS2, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL3, PTGS2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, and CXCR2
IL6, CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, and S100A8
IL6, CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, and S100A9
IL6, CXCL1, CXCL2, CXCL8, PTGS2, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL8, PTGS2, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL8, PTGS2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL8, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL8, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL8, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL8, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL2, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL2, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL2, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, and CXCR2
IL6, CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, and S100A8
IL6, CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, and S100A9
IL6, CXCL1, CXCL3, CXCL8, PTGS2, CXCR2, and S100A8
IL6, CXCL1, CXCL3, CXCL8, PTGS2, CXCR2, and S100A9
IL6, CXCL1, CXCL3, CXCL8, PTGS2, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCL8, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL3, CXCL8, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL3, CXCL8, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCL8, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL3, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL3, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL3, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL3, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and CXCR2
IL6, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and S100A8
IL6, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and S100A9
IL6, CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, and S100A8
IL6, CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, and S100A9
IL6, CXCL2, CXCL3, CXCL8, PTGS2, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, and S100A8
IL6, CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, and S100A9
IL6, CXCL2, CXCL3, CXCL8, CXCR1, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCL8, CXCR2, S100A8, and S100A9

IL6, CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL2, CXCL3, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL2, CXCL3, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL2, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL2, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL2, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL3, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL3, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL3, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL3, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and CXCR2
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and S100A8
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, and S100A8
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, and S100A8
CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, and S100A8
CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, and S100A9
CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, PTGS2, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
CXCL1, CXCL2, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
CXCL1, CXCL3, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
CXCL1, CXCL3, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL3, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

Table 15: Eight-Gene Combinations of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and CXCR2
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL3, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

Table 16: Nine-Gene Combinations of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A8
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, CXCL8, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL3, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL2, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL1, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
IL6, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9
CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9

In any of the preceding methods, the method may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2, and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. For example, in some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2, and at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

For example, any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1, and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1, and at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9. In some embodiments, the method comprises determining the expression level of any one of the combinations set forth in Tables 2-4 and any one of the combinations set forth in Tables 9-16. For example, in some embodiments, the method includes determining the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, and two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9. In some embodiments, the method includes determining the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, and three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10. In some embodiments, the method includes determining the expression level of four of CD8A,

EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, and four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In other embodiments, in any of the preceding methods, the method may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2, and one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. For example, in some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2, and at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34.

For example, any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1, and one or more (e.g., 1, 2, 3, 4, 5, or 6) of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1, and at least one, at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method comprises determining the expression level of any one of the combinations set forth in Tables 2-4 and any one of the combinations set forth in Tables 5-8. For example, in some embodiments, the method includes determining the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for

example, any of the exemplary combinations shown in Table 2, and two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5. In some embodiments, the method includes determining the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, and three of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6. In some embodiments, the method includes determining the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, and four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 7. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In a further embodiment, in any of the preceding methods, the method may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9, and one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. For example, in some embodiments, the method includes determining the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, and at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34.

For example, any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9, and one or more (e.g., 1, 2, 3, 4, 5, or 6) of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, and at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method comprises determining the expression level of any one of the combinations set forth in Tables 9-16 and any one of the combinations set forth in Tables 5-8. For example, in some embodiments, the method includes determining the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9, and two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5. In some embodiments, the method includes determining the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10, and three of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6. In some embodiments, the method includes determining the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11, and

four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 7. In some embodiments, the method involves determining the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12, and five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8. In some embodiments, the method involves determining the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13, and VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method involves determining the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14, and VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method involves determining the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15, and VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method involves determining the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16, and VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method involves determining the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, S100A9, VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is at or above a reference expression level of the one or more genes, and the method further includes administering to the individual an effective amount of the anti-cancer therapy. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 is at or above a reference expression level of the one or more genes. In some instances, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 2-4 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 in the sample is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is at or above a reference expression level of the one or more genes. In some

embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 9-16 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample is at or above a reference expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 is at or above a reference expression level of the one or more genes, and the method further includes administering to the individual an effective amount of the anti-cancer therapy. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 is at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is at or above a reference expression level of the one or more genes. In some embodiments, an expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 at or above a reference expression level of the one or more genes identifies the presence of myeloid inflammation in a tumor.

For example, in some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 is at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of any one of the combinations set forth in Tables 2-4 is at or above a reference expression level of the one or more genes and the expression level of any one of the combinations set forth in Tables 9-16 is at or

above a reference expression level of the one or more genes. For example, in some embodiments, the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, is at or above a reference expression level of the one or more genes, and the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9, is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, is at or above a reference expression level of the one or more genes, and the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10, is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, is at or above a reference expression level of the one or more genes, and the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11, is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12, is at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13, is at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14, is at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15, is at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16, is at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9. In some embodiments, an expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7,

8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 at or above a reference expression level of the one or more genes identifies the presence of myeloid inflammation in a tumor. In some embodiments, an expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample at or above a reference expression level of the one or more genes, and an expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 at or above a reference expression level of the one or more genes indicates that the individual is less likely to benefit (e.g., is resistant to) a PD-L1 axis binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab) monotherapy.

In other embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 is below a reference expression level of the one or more genes, and the method further includes administering to the individual an effective amount of a PD-L1 axis binding antagonist (e.g., an anti-PD-L1 antibody (e.g., atezolizumab) or an anti-PD-1 antibody) monotherapy. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 is at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is below a reference expression level of the one or more genes.

For example, in some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 is at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 is below a reference expression level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is below a reference expression level of the one or more genes. In some embodiments, the expression level of any one of the combinations set forth in Tables 2-4 is at or above a reference expression level of the one or more genes and the expression level of any one of the combinations set forth in Tables 9-16 is below a reference expression level of the one or more genes. For example, in some embodiments, the expression level of

two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, is at or above a reference expression level of the one or more genes, and the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9, is below a reference expression level of the one or more genes. In some embodiments, the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, is at or above a reference expression level of the one or more genes, and the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10, is below a reference expression level of the one or more genes. In some embodiments, the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, is at or above a reference expression level of the one or more genes, and the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11, is below a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12, is below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13, is below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14, is below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15, is below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16, is below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is below a reference expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding methods, the expression level of PD-L1 in the sample is at or above a reference expression level of PD-L1, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19) additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is at or above a reference expression level of the one or more additional genes.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes, and the method further comprises administering to the individual an effective amount of the anti-cancer therapy. For example, in some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 5-8 in the sample is below a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes. For example, in some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In other embodiments, in any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 is at or above a reference level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 is below a reference level of the one or more genes, and the method further comprises administering to the individual an effective amount of the anti-cancer therapy. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 is at or above a reference level of the one or more genes, and the expression level of at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 is below a reference level of the one or more genes.

For example, in some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 is at or above a reference level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, or 6) of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 is below a reference level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34

is below a reference level for the one or more genes. In some embodiments, the expression level of any one of the combinations set forth in Tables 2-4 is at or above a reference level of the one or more genes, and the expression level of any one of the combinations set forth in Tables 5-8 is below a reference level of the one or more genes. For example, in some embodiments, the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, is at or above a reference level of the one or more genes, and the expression level of two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5, is below a reference level of the one or more genes. In some embodiments, the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, is at or above a reference level of the one or more genes, and the expression level of three of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6, is below a reference level of the one or more genes. In some embodiments, the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, is at or above a reference level of the one or more genes, and the expression level of four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 7, is below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8, is below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 is below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, or 6) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is below a reference level of the one or more genes, and the method further comprises administering to the individual an effective amount of the anti-cancer therapy. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is below a reference level of the one or more genes. For example, in some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 9-16 in the sample is below a reference expression level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample is below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In other embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is at or above a reference level of the one or more genes, and the method further includes administering to the individual an effective amount of an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR

inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))). In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 is at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, 5, or 6) of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 5-8 in the sample is at or above a reference expression level of the one or more genes. In some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In certain embodiments of any of the preceding methods, a reference level is the expression level of the one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, or 37) genes (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9) in a reference population, for example, a population of individuals having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., TNBC)). In particular embodiments, the cancer is a kidney cancer (e.g., RCC, e.g., mRCC). In certain embodiments, a reference level is the median expression level of the one or more genes in a reference population, for example, a population of individuals having a cancer. In other embodiments, the reference level may be the top 40%, the top 30%, the top 20%, the top 10%, the top 5%, or the top 1% of the expression level in the reference population. In certain embodiments, the reference level is a pre-assigned expression level for the one or more genes. In some embodiments, the reference level is the expression level of the one or more genes in a biological sample obtained from the patient at a previous time point, wherein the previous time point is following administration of the anti-cancer therapy. In some embodiments of any of the preceding methods, a reference level is the expression level of the one or more genes (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9) in a biological sample from the patient obtained prior to (e.g., minutes, hours, days, weeks (e.g., 1, 2, 3, 4, 5, 6, or 7 weeks), months, or years prior to) administration of the anti-cancer therapy. In other embodiments, the reference level is the expression level of the one or more genes in a biological sample obtained from the patient at a subsequent time point (e.g., minutes, hours, days, weeks, months, or years after administration of an anti-cancer therapy).

The presence and/or expression level of any of the biomarkers described above may be assessed qualitatively and/or quantitatively based on any suitable criterion known in the art, including but not limited to DNA, mRNA, cDNA, proteins, protein fragments, and/or gene copy number. Methodologies for measuring such biomarkers are known in the art and understood by the skilled artisan, including, but not limited to, immunohistochemistry ("IHC"), Western blot analysis, immunoprecipitation, molecular

binding assays, ELISA, ELIFA, fluorescence activated cell sorting ("FACS"), MassARRAY, proteomics, quantitative blood based assays (e.g., Serum ELISA), biochemical enzymatic activity assays, in situ hybridization (ISH), fluorescence in situ hybridization (FISH), Southern analysis, Northern analysis, whole genome sequencing, polymerase chain reaction (PCR) including quantitative real time PCR (qRT-PCR) and other amplification type detection methods, such as, for example, branched DNA, SISBA, TMA and the like, RNA-Seq, microarray analysis, gene expression profiling, whole-genome sequencing (WGS), and/or serial analysis of gene expression ("SAGE"), as well as any one of the wide variety of assays that can be performed by protein, gene, and/or tissue array analysis. Typical protocols for evaluating the status of genes and gene products are found, for example, in Ausubel et al. eds. (*Current Protocols In Molecular Biology*, 1995), Units 2 (Northern Blotting), 4 (Southern Blotting), 15 (Immunoblotting) and 18 (PCR Analysis). Multiplexed immunoassays such as those available from Rules Based Medicine or Meso Scale Discovery ("MSD") may also be used.

In some embodiments of any of the preceding methods, the expression level of a biomarker may be a nucleic acid expression level (e.g., a DNA expression level or an RNA expression level (e.g., an mRNA expression level)). Any suitable method of determining a nucleic acid expression level may be used. In some embodiments, the nucleic acid expression level is determined using RNA-seq, RT-qPCR, qPCR, multiplex qPCR or RT-qPCR, microarray analysis, SAGE, MassARRAY technique, ISH, or a combination thereof.

Methods for the evaluation of mRNAs in cells are well known and include, for example, serial analysis of gene expression (SAGE), whole genome sequencing (WGS), hybridization assays using complementary DNA probes (such as in situ hybridization using labeled riboprobes specific for the one or more genes, Northern blot and related techniques) and various nucleic acid amplification assays (such as RT-PCR (e.g., qRT-PCR) using complementary primers specific for one or more of the genes, and other amplification type detection methods, such as, for example, branched DNA, SISBA, TMA and the like). In addition, such methods can include one or more steps that allow one to determine the levels of target mRNA in a biological sample (e.g., by simultaneously examining the levels a comparative control mRNA sequence of a "housekeeping" gene such as an actin family member). Optionally, the sequence of the amplified target cDNA can be determined. Optional methods include protocols which examine or detect mRNAs, such as target mRNAs, in a tissue or cell sample by microarray technologies. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes whose expression correlates with increased or reduced clinical benefit of treatment comprising a VEGF antagonist and a PD-L1 axis binding antagonist may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene.

In other embodiments of any of the preceding methods, the expression level of a biomarker may be a protein expression level. In certain embodiments, the method comprises contacting the sample with antibodies that specifically bind to a biomarker described herein under conditions permissive for binding of the biomarker, and detecting whether a complex is formed between the antibodies and biomarker.

Such method may be an *in vitro* or *in vivo* method. In some instances, an antibody is used to select patients eligible for therapy with a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)), e.g., a biomarker for selection of individuals. In other instances, an antibody is used to select patients eligible for therapy with an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))), e.g., a biomarker for selection of individuals. Any method of measuring protein expression levels known in the art or provided herein may be used. For example, in some embodiments, a protein expression level of a biomarker is determined using a method selected from the group consisting of flow cytometry (e.g., fluorescence-activated cell sorting (FACS™)), Western blot, enzyme-linked immunosorbent assay (ELISA), immunoprecipitation, immunohistochemistry (IHC), immunofluorescence, radioimmunoassay, dot blotting, immunodetection methods, HPLC, surface plasmon resonance, optical spectroscopy, mass spectrometry, and HPLC. In some embodiments, the protein expression level of the biomarker is determined in tumor-infiltrating immune cells. In some embodiments, the protein expression level of the biomarker is determined in tumor cells. In some embodiments, the protein expression level of the biomarker is determined in tumor-infiltrating immune cells and/or in tumor cells. In some embodiments, the protein expression level of the biomarker is determined in peripheral blood mononuclear cells (PBMCs).

In certain embodiments, the presence and/or expression level/amount of a biomarker protein in a sample is examined using IHC and staining protocols. IHC staining of tissue sections has been shown to be a reliable method of determining or detecting the presence of proteins in a sample. In some embodiments of any of the methods, assays and/or kits, the biomarker is one or more of the protein expression products of the following genes: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9. In one embodiment, an expression level of biomarker is determined using a method comprising: (a) performing IHC analysis of a sample (such as a tumor sample obtained from a patient) with an antibody; and (b) determining expression level of a biomarker in the sample. In some embodiments, IHC staining intensity is determined relative to a reference. In some embodiments, the reference is a reference value. In some embodiments, the reference is a reference sample (e.g., a control cell line staining sample, a tissue sample from non-cancerous patient, or a tumor sample that is determined to be negative for the biomarker of interest).

IHC may be performed in combination with additional techniques such as morphological staining and/or *in situ* hybridization (e.g., ISH). Two general methods of IHC are available; direct and indirect assays. According to the first assay, binding of antibody to the target antigen is determined directly. This direct assay uses a labeled reagent, such as a fluorescent tag or an enzyme-labeled primary antibody, which can be visualized without further antibody interaction. In a typical indirect assay, unconjugated primary antibody binds to the antigen and then a labeled secondary antibody binds to the primary

antibody. Where the secondary antibody is conjugated to an enzymatic label, a chromogenic or fluorogenic substrate is added to provide visualization of the antigen. Signal amplification occurs because several secondary antibodies may react with different epitopes on the primary antibody.

The primary and/or secondary antibody used for IHC typically will be labeled with a detectable moiety. Numerous labels are available which can be generally grouped into the following categories: (a) radioisotopes, such as ^{35}S , ^{14}C , ^{125}I , ^3H , and ^{131}I ; (b) colloidal gold particles; (c) fluorescent labels including, but are not limited to, rare earth chelates (europium chelates), Texas Red, rhodamine, fluorescein, dansyl, lissamine, umbelliferone, phycocrytherin, phycocyanin, or commercially-available fluorophores such as SPECTRUM ORANGE7 and SPECTRUM GREEN7 and/or derivatives of any one or more of the above; (d) various enzyme-substrate labels are available and U.S. Patent No. 4,275,149 provides a review of some of these. Examples of enzymatic labels include luciferases (e.g., firefly luciferase and bacterial luciferase; see, e.g., U.S. Patent No. 4,737,456), luciferin, 2,3-dihydrophthalazinediones, malate dehydrogenase, urease, peroxidase such as horseradish peroxidase (HRPO), alkaline phosphatase, β -galactosidase, glucoamylase, lysozyme, saccharide oxidases (e.g., glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase), heterocyclic oxidases (such as uricase and xanthine oxidase), lactoperoxidase, microperoxidase, and the like.

Examples of enzyme-substrate combinations include, for example, horseradish peroxidase (HRPO) with hydrogen peroxide as a substrate; alkaline phosphatase (AP) with para-Nitrophenyl phosphate as chromogenic substrate; and β -D-galactosidase (β -D-Gal) with a chromogenic substrate (e.g., p-nitrophenyl- β -D-galactosidase) or fluorogenic substrate (e.g., 4-methylumbelliferyl- β -D-galactosidase). For a general review of these, see, for example, U.S. Patent Nos. 4,275,149 and 4,318,980.

Specimens may be prepared, for example, manually, or using an automated staining instrument (e.g., a Ventana BenchMark XT or Benchmark ULTRA instrument). Specimens thus prepared may be mounted and coverslipped. Slide evaluation is then determined, for example, using a microscope, and staining intensity criteria, routinely used in the art, may be employed. In one embodiment, it is to be understood that when cells and/or tissue from a tumor is examined using IHC, staining is generally determined or assessed in tumor cell(s) and/or tissue (as opposed to stromal or surrounding tissue that may be present in the sample). In some embodiments, it is understood that when cells and/or tissue from a tumor is examined using IHC, staining includes determining or assessing in tumor-infiltrating immune cells, including intratumoral or peritumoral immune cells. In some embodiments, the presence of a biomarker is detected by IHC in >0% of the sample, in at least 1% of the sample, in at least 5% of the sample, in at least 10% of the sample, in at least 15% of the sample, in at least 15% of the sample, in at least 20% of the sample, in at least 25% of the sample, in at least 30% of the sample, in at least 35% of the sample, in at least 40% of the sample, in at least 45% of the sample, in at least 50% of the sample, in at least 55% of the sample, in at least 60% of the sample, in at least 65% of the sample, in at least 70% of the sample, in at least 75% of the sample, in at least 80% of the sample, in at least 85% of the sample, in at least 90% of the sample, in at least 95% of the sample, or more. Samples may be scored using any method known in the art, for example, by a pathologist or automated image analysis.

In some embodiments of any of the methods, the biomarker is detected by immunohistochemistry using a diagnostic antibody (i.e., primary antibody). In some embodiments, the diagnostic antibody specifically binds human antigen. In some embodiments, the diagnostic antibody is a non-human antibody. In some embodiments, the diagnostic antibody is a rat, mouse, or rabbit antibody. In some
 5 embodiments, the diagnostic antibody is a rabbit antibody. In some embodiments, the diagnostic antibody is a monoclonal antibody. In some embodiments, the diagnostic antibody is directly labeled. In other embodiments, the diagnostic antibody is indirectly labeled.

In some embodiments of any of the preceding embodiments, the sample is obtained from the individual prior to (e.g., minutes, hours, days, weeks (e.g., 1, 2, 3, 4, 5, 6, or 7 weeks), months, or years
 10 prior to) administration of the anti-cancer therapy. In some embodiments of any of the preceding methods, the sample from the individual is obtained about 2 to about 10 weeks (e.g., 2, 3, 4, 5, 6, 7, 8, 9, or 10 weeks) following administration of the anti-cancer therapy. In some embodiments, the sample from the individual is obtained about 4 to about 6 weeks following administration of the anti-cancer therapy.

In some embodiments of any of the preceding methods, the expression level or number of a
 15 biomarker is detected in a tissue sample, a primary or cultured cells or cell line, a cell supernatant, a cell lysate, platelets, serum, plasma, vitreous fluid, lymph fluid, synovial fluid, follicular fluid, seminal fluid, amniotic fluid, milk, whole blood, blood-derived cells, urine, cerebro-spinal fluid, saliva, sputum, tears, perspiration, mucus, tumor lysates, and tissue culture medium, tissue extracts such as homogenized tissue, tumor tissue, cellular extracts, or any combination thereof. In some embodiments, the sample is a
 20 tissue sample (e.g., a tumor tissue sample), a cell sample, a whole blood sample, a plasma sample, a serum sample, or a combination thereof. In some embodiments, the tumor tissue sample wherein the tumor tissue sample includes tumor cells, tumor-infiltrating immune cells, stromal cells, or a combination thereof. In some embodiments, the tumor tissue sample is a formalin-fixed and paraffin-embedded (FFPE) sample, an archival sample, a fresh sample, or a frozen sample.

For example, in some embodiments of any of the preceding methods, the expression level of a
 25 biomarker is detected in tumor-infiltrating immune cells, tumor cells, PBMCs, or combinations thereof using known techniques (e.g., flow cytometry or IHC). Tumor-infiltrating immune cells include, but are not limited to, intratumoral immune cells, peritumoral immune cells or any combinations thereof, and other tumor stroma cells (e.g., fibroblasts). Such tumor infiltrating immune cells may be T lymphocytes (such
 30 as CD8⁺ T lymphocytes (e.g., CD8⁺ T effector (T_{eff}) cells) and/or CD4⁺ T lymphocytes (e.g., CD4⁺ T_{eff} cells), B lymphocytes, or other bone marrow-lineage cells including granulocytes (neutrophils, eosinophils, basophils), monocytes, macrophages, dendritic cells (e.g., interdigitating dendritic cells), histiocytes, and natural killer (NK) cells. In some embodiments, the staining for a biomarker is detected as membrane staining, cytoplasmic staining, or combinations thereof. In other embodiments, the
 35 absence of a biomarker is detected as absent or no staining in the sample, relative to a reference sample.

In particular embodiments of any of the preceding methods, the expression level of a biomarker is assessed in a sample that contains or is suspected to contain cancer cells. The sample may be, for example, a tissue biopsy or a metastatic lesion obtained from a patient suffering from, suspected to suffer from, or diagnosed with cancer (e.g., a kidney cancer, in particular renal cell carcinoma (RCC), such as
 40 advanced RCC or metastatic RCC (mRCC)). In some embodiments, the sample is a sample of kidney

tissue, a biopsy of an kidney tumor, a known or suspected metastatic kidney cancer lesion or section, or a blood sample, e.g., a peripheral blood sample, known or suspected to comprise circulating cancer cells, e.g., kidney cancer cells. The sample may comprise both cancer cells, i.e., tumor cells, and non-cancerous cells (e.g., lymphocytes, such as T cells or NK cells), and, in certain embodiments, comprises both cancerous and non-cancerous cells. Methods of obtaining biological samples including tissue resections, biopsies, and body fluids, e.g., blood samples comprising cancer/tumor cells, are well known in the art.

In some embodiments of any of the preceding methods, the patient has carcinoma, lymphoma, blastoma (including medulloblastoma and retinoblastoma), sarcoma (including liposarcoma and synovial cell sarcoma), neuroendocrine tumors (including carcinoid tumors, gastrinoma, and islet cell cancer), mesothelioma, schwannoma (including acoustic neuroma), meningioma, adenocarcinoma, melanoma, and leukemia or lymphoid malignancies. In some embodiments, the cancer is kidney cancer (e.g., renal cell carcinoma (RCC), e.g., advanced RCC or metastatic RCC (mRCC)), squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer (including small-cell lung cancer (SCLC), non-small cell lung cancer (NSCLC), adenocarcinoma of the lung, and squamous carcinoma of the lung), cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer (e.g., HCC), hepatoma, breast cancer (including metastatic breast cancer), bladder cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, Merkel cell cancer, mycoses fungoids, testicular cancer, esophageal cancer, tumors of the biliary tract, head and neck cancer, B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL); small lymphocytic (SL) NHL; intermediate grade/follicular NHL; intermediate grade diffuse NHL; high grade immunoblastic NHL; high grade lymphoblastic NHL; high grade small non-cleaved cell NHL; bulky disease NHL; mantle cell lymphoma; AIDS-related lymphoma; and Waldenstrom's Macroglobulinemia); chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); Hairy cell leukemia; chronic myeloblastic leukemia; and post-transplant lymphoproliferative disorder (PTLD), abnormal vascular proliferation associated with phakomatoses, edema (such as that associated with brain tumors), or Meigs' syndrome. In some embodiments, the cancer is a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC). In preferred embodiments, the patient has a kidney cancer (e.g., RCC, e.g., advanced RCC or mRCC, e.g., previously untreated advanced RCC or mRCC). The patient may optionally have an advanced, refractory, recurrent, chemotherapy-resistant, and/or platinum-resistant form of the cancer.

In certain embodiments, the presence and/or expression levels/amount of a biomarker in a first sample is increased or elevated as compared to presence/absence and/or expression levels/amount in a second sample. In certain embodiments, the presence/absence and/or expression levels/amount of a biomarker in a first sample is decreased or reduced as compared to presence and/or expression levels/amount in a second sample. In certain embodiments, the second sample is a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue.

In certain embodiments, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is a single sample or combined multiple samples from the same patient or individual that are obtained at one or more different time points than when the test sample is obtained. For example, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is obtained at an earlier time point from the same patient or individual than when the test sample is obtained. Such reference sample, reference cell, reference tissue, control sample, control cell, or control tissue may be useful if the reference sample is obtained during initial diagnosis of cancer and the test sample is later obtained when the cancer becomes metastatic.

In certain embodiments, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is a combined multiple samples from one or more healthy individuals who are not the patient. In certain embodiments, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is a combined multiple samples from one or more individuals with a disease or disorder (e.g., cancer) who are not the patient or individual. In certain embodiments, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is pooled RNA samples from normal tissues or pooled plasma or serum samples from one or more individuals who are not the patient. In certain embodiments, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is pooled RNA samples from tumor tissues or pooled plasma or serum samples from one or more individuals with a disease or disorder (e.g., cancer) who are not the patient.

In some embodiments of any of the preceding methods, an expression level above a reference level, or an elevated or increased expression or number, refers to an overall increase of about any of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater, in the level or number of a biomarker (e.g., protein, nucleic acid (e.g., gene or mRNA), or cell), detected by methods such as those described herein and/or known in the art, as compared to a reference level, reference sample, reference cell, reference tissue, control sample, control cell, or control tissue. In certain embodiments, the elevated expression or number refers to the increase in expression level/amount of a biomarker (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2 CXCR1, CXCR2, S100A8, and/or S100A9) in the sample wherein the increase is at least about any of 1.1x, 1.2x, 1.3x, 1.4x, 1.5x, 1.6x, 1.7x, 1.8x, 1.9x, 2x, 2.1x, 2.2x, 2.3x, 2.4x, 2.5x, 2.6x, 2.7x, 2.8x, 2.9x, 3x, 3.5x, 4x, 4.5x, 5x, 6x, 7x, 8x, 9x, 10x, 15x, 20x, 30x, 40x, 50x, 100x, 500x, or 1000x the expression level/amount of the respective biomarker in a reference level, reference sample, reference cell, reference tissue, control sample, control cell, or control tissue. In some embodiments, elevated expression or number refers to an overall increase in expression level/amount of a biomarker (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2 CXCR1, CXCR2, S100A8, and/or S100A9) of greater than about 1.1-fold, about 1.2-fold, about 1.3-fold, about 1.4-fold, about 1.5-fold, about 1.6-fold, about 1.7-fold, about 1.8-fold, about 1.9-fold, about 2-fold, about 2.1-fold, about 2.2-fold, about 2.3-fold, about 2.4-fold, about 2.5-fold, about 2.6-fold, about 2.7-fold,

about 2.8-fold, about 2.9-fold, about 3-fold, about 3.5-fold, about 4-fold, about 4.5-fold, about 5-fold, about 6-fold, about 7-fold, about 8-fold, about 9-fold, about 10-fold, about 15-fold, about 20-fold, about 30-fold, about 40-fold, about 50-fold, about 100-fold, about 500-fold, about 1,000-fold or greater as compared to a reference level, reference sample, reference cell, reference tissue, control sample, control cell, control tissue, or internal control (e.g., housekeeping gene).

In some embodiments of any of the preceding methods, an expression level below a reference level, or a reduced (decreased) expression or number, refers to an overall reduction of about any of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater, in the level of biomarker (e.g., protein, nucleic acid (e.g., gene or mRNA), or cell), detected by standard art known methods such as those described herein, as compared to a reference level, reference sample, reference cell, reference tissue, control sample, control cell, or control tissue. In certain embodiments, reduced expression or number refers to the decrease in expression level/amount of a biomarker (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9) in the sample wherein the decrease is at least about any of 0.9x, 0.8x, 0.7x, 0.6x, 0.5x, 0.4x, 0.3x, 0.2x, 0.1x, 0.05x, or 0.01x the expression level/amount of the respective biomarker in a reference level, reference sample, reference cell, reference tissue, control sample, control cell, or control tissue. In some embodiments, reduced (decreased) expression or number refers to an overall decrease in expression level/amount of a biomarker (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9) of greater than about 1.1-fold, about 1.2-fold, about 1.3-fold, about 1.4-fold, about 1.5-fold, about 1.6-fold, about 1.7-fold, about 1.8-fold, about 1.9-fold, about 2-fold, about 2.1-fold, about 2.2-fold, about 2.3-fold, about 2.4-fold, about 2.5-fold, about 2.6-fold, about 2.7-fold, about 2.8-fold, about 2.9-fold, about 3-fold, about 3.5-fold, about 4-fold, about 4.5-fold, about 5-fold, about 6-fold, about 7-fold, about 8-fold, about 9-fold, about 10-fold, about 15-fold, about 20-fold, about 30-fold, about 40-fold, about 50-fold, about 100-fold, about 500-fold, about 1,000-fold or greater as compared to a reference level, reference sample, reference cell, reference tissue, control sample, control cell, control tissue, or internal control (e.g., housekeeping gene).

III. THERAPEUTIC METHODS AND USES

Provided herein are methods for treating an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., a TNBC)). In particular embodiments, the cancer is a kidney cancer, such as RCC, e.g., advanced RCC or mRCC, e.g., previously untreated advanced RCC or mRCC. In some instances, the methods of the invention include administering to the individual an anti-cancer therapy that includes a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1

binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) based on the expression level of a biomarker of the invention. In other embodiments, the methods of the invention include administering to the individual an anti-cancer therapy that includes an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))). Any of the VEGF antagonists, PD-L1 axis binding antagonists, angiogenesis inhibitors (e.g., multi-targeted tyrosine kinase inhibitors), or other anti-cancer agents described herein (e.g., as described below in Section IV and/or the Examples) or known in the art may be used in the methods. The invention further relates to methods for improving progression-free survival (PFS) and/or overall survival (OS) of a patient suffering from a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., a TNBC)) by administration of an anti-cancer therapy that includes a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)). The invention further relates to methods for improving progression-free survival (PFS) and/or overall survival (OS) of a patient suffering from a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., a TNBC)) by administration of an anti-cancer therapy that includes an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))). The expression level or number of any of the biomarkers described herein may be determined using any method known in the art and/or described herein, for example, in Section II above and/or in the working Examples.

Provided herein is a method of treating an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., TNBC)) that includes (a) determining the expression level of one or more of the genes set forth in Table 1 in a sample from the individual, wherein the expression level of one or more of the genes set forth in Table 1 is determined to be changed relative to a reference level; and (b) administering an effective amount of an anti-cancer therapy (e.g., an anti-cancer therapy comprising a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)), or an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))) to the individual based on the expression level of the one or more genes determined in step (a). In some instances, the change is an increase. In other instances, the change is a decrease.

Also provided herein is a method of treating an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g.,

hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., TNBC)) that includes administering an effective amount of an anti-cancer therapy (e.g., an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)), or an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))) to the individual, wherein the expression level of one or more of the genes set forth in Table 1 in a sample from the individual has been determined to be changed relative to a reference level, wherein a change in the expression level of one or more of the genes set forth in Table 1 identifies the individual as one who may benefit from treatment with an anti-cancer therapy. In some instances, the change is an increase. In other instances, the change is a decrease.

In another aspect, provided herein is a method of treating an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., hepatocellular carcinoma (HCC)), an ovarian cancer, or a breast cancer (e.g., TNBC)) that includes (a) determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, or 37) of the following genes in a sample from the individual: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9, wherein (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference expression level of the one or more genes; or (ii) the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be below a reference expression level of the one or more genes; and (b) administering an effective amount of an anti-cancer therapy comprising a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) to the individual based on the expression level of the one or more genes determined in step (a).

Any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2.

For example, any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1. In some embodiments, the method includes determining the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2. In some embodiments, the method includes determining the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3. In some embodiments, the method includes determining the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

In some embodiments, any of the preceding methods may include determining the expression level of PD-L1 and one or more additional genes, wherein the one or more additional genes is other than PD-L1. For example, in some embodiments, the method may include determining the expression level of PD-L1 and one or more additional genes (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36) selected from the group consisting of: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9. In some embodiments, the method includes determining the expression level of PD-L1 and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19) additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2. In other embodiments, the method includes determining the expression level of PD-L1 and one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. In other embodiments, the method includes determining the expression level of PD-L1 and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9.

Any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. For example, in some embodiments, the method includes determining the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method includes determining the expression level of two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5. In some embodiments, the method includes determining the expression level of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6. In some embodiments, the method includes determining the expression level of four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4,

and CD34, for example, any of the exemplary combinations shown in Table 7. In some embodiments, the method includes determining the expression level of five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8. In some embodiments, the method includes determining the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

Any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9. In some embodiments, the method includes determining the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9. In some embodiments, the method includes determining the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10. In some embodiments, the method includes determining the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11. In some embodiments, the method includes determining the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12. In some embodiments, the method includes determining the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13. In some embodiments, the method includes determining the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14. In some embodiments, the method includes determining the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15. In some embodiments, the method includes determining the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16. In some embodiments, the method includes determining the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In any of the preceding methods, the method may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2, and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. For example, in some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1,

CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2, and at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

5 For example, any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1, and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1, and at least one, at least
10 two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9. In some embodiments, the method comprises determining the expression level of any one of the combinations set forth in Tables 2-4 and any one of the combinations set forth in Tables 9-16. For example, in some
15 embodiments, the method includes determining the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, and two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9. In some embodiments, the method includes determining the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the
20 exemplary combinations shown in Table 3, and three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10. In some embodiments, the method includes determining the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, and four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for
25 example, any of the exemplary combinations shown in Table 11. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary
30 combinations shown in Table 13. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15. In
35 some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, IL6,
40 CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In other embodiments, in any of the preceding methods, the method may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2, and one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. For example, in some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2, and at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34.

For example, any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1, and one or more (e.g., 1, 2, 3, 4, 5, or 6) of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1, and at least one, at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method comprises determining the expression level of any one of the combinations set forth in Tables 2-4 and any one of the combinations set forth in Tables 5-8. For example, in some embodiments, the method includes determining the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, and two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5. In some embodiments, the method includes determining the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, and three of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6. In some embodiments, the method includes determining the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, and four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 7. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In a further embodiment, in any of the preceding methods, the method may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9, and one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. For example, in some embodiments, the method includes determining the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2,

CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, and at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34.

For example, any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9, and one or more (e.g., 1, 2, 3, 4, 5, or 6) of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, and at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method comprises determining the expression level of any one of the combinations set forth in Tables 9-16 and any one of the combinations set forth in Tables 5-8. For example, in some embodiments, the method includes determining the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9, and two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5. In some embodiments, the method includes determining the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10, and three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6. In some embodiments, the method includes determining the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 for example, any of the exemplary combinations shown in Table 11, and four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 7. In some embodiments, the method involves determining the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12, and five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8. In some embodiments, the method involves determining the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13, and and at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method involves determining the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14, and and at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method involves determining the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15, and and at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method involves determining the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16, and and at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1,

ANGPTL4, and CD34. In some embodiments, the method involves determining the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, S100A9, VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference expression level of the one or more genes. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 is determined to be at or above a reference expression level of the one or more genes. In some instances, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 2-4 in the sample is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 in the sample is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 9-16 in the sample is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample is determined to be at or above a reference expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 is determined to be at or above a reference expression level of the one or more genes. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at

least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 is determined to be at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is determined to be at or above a reference expression level of the one or more genes.

For example, in some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 is determined to be at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of any one of the combinations set forth in Tables 2-4 is determined to be at or above a reference expression level of the one or more genes and the expression level of any one of the combinations set forth in Tables 9-16 is determined to be at or above a reference expression level of the one or more genes. For example, in some embodiments, the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, is determined to be at or above a reference expression level of the one or more genes, and the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9, is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, is determined to be at or above a reference expression level of the one or more genes, and the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10, is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, is determined to be at or above a reference expression level of the one or more genes, and the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11, is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for

example, any of the exemplary combinations shown in Table 12, is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13, is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14, is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15, is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16, is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding methods, the expression level of PD-L1 in the sample is determined to be at or above a reference expression level of PD-L1, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19) additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference expression level of the one or more additional genes.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be below a reference level of the one or more genes. For example, in some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 5-8 in the sample is determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is determined to be below a reference level of the one or more genes. For example, in some embodiments, the expression level of

VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In other embodiments, in any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 is determined to be at or above a reference level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 is determined to be below a reference level of the one or more genes. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 is determined to be at or above a reference level of the one or more genes, and the expression level of at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 is determined to be below a reference level of the one or more genes.

For example, in some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 is determined to be at or above a reference level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, or 6) of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of any one of the combinations set forth in Tables 2-4 is determined to be at or above a reference level of the one or more genes, and the expression level of any one of the combinations set forth in Tables 5-8 is determined to be below a reference level of the one or more genes. For example, in some embodiments, the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, is determined to be at or above a reference level of the one or more genes, and the expression level of two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5, is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, is determined to be at or above a reference level of the one or more genes, and the expression level of three of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6, is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, is determined to be at or above a reference level of the one or more genes, and the expression level of four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for

example, any of the exemplary combinations shown in Table 7, is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8, is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 is determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be below a reference level of the one or more genes. For example, in some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 9-16 in the sample is determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample is determined to be below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In another aspect, provided herein is a method of treating an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)) that includes (a) determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, or 37) of the following genes in a sample from the individual: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9, wherein (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference expression level of the one or more genes; and (ii) the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample is determined to be below a reference expression level of the one or more genes; and (b) administering an effective amount of a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) monotherapy to the individual based on the expression level of the one or more genes determined in step (a).

In any of the preceding methods, the method may include determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES,

GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2, and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. For example, in some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2, and at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

For example, any of the preceding methods may include determining the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1, and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1, and at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9. In some embodiments, the method comprises determining the expression level of any one of the combinations set forth in Tables 2-4 and any one of the combinations set forth in Tables 9-16. For example, in some embodiments, the method includes determining the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, and two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9. In some embodiments, the method includes determining the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, and three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10. In some embodiments, the method includes determining the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, and four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2, for example, any of the exemplary combinations shown in Table 12. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2, for example, any of the exemplary combinations shown in Table 13. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2, for example, any of the exemplary combinations shown in Table 14. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2, for

example, any of the exemplary combinations shown in Table 15. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2, for example, any of the exemplary combinations shown in Table 16. In some embodiments, the method involves determining the expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 is determined to be below a reference expression level of the one or more genes. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 is determined to be at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is determined to be below a reference expression level of the one or more genes.

For example, in some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 is determined to be at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 is determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of any one of the combinations set forth in Tables 2-4 is determined to be at or above a reference expression level of the one or more genes and the expression level of any one of the combinations set forth in Tables 9-16 is determined to be below a reference expression level of the one or more genes. For example, in some embodiments, the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, is determined to be at or above a reference expression level of the one or more genes, and the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9, is determined to be

below a reference expression level of the one or more genes. In some embodiments, the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, is determined to be at or above a reference expression level of the one or more genes, and the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10, is determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, is determined to be at or above a reference expression level of the one or more genes, and the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11, is determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12, is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13, is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14, is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15, is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16, is determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 is determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 is determined to be below a reference expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In another aspect, provided herein is a method of treating an individual having (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g.,

HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)), the method including administering to the individual an effective amount of an anti-cancer therapy comprising a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist, wherein (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more genes; or (ii) the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of the genes has been determined prior to treatment with the anti-cancer therapy. In other embodiments, the expression level of one or more of the genes has been determined after treatment with the anti-cancer therapy.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more genes. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 has been determined to be at or above a reference expression level of the one or more genes. In some instances, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 2-4 in the sample has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 in the sample has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 9-16 in the sample has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2,

CXCR1, CXCR2, S100A8, and S100A9 in the sample has been determined to be at or above a reference expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 has been determined to be at or above a reference expression level of the one or more genes. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 has been determined to be at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 has been determined to be at or above a reference expression level of the one or more genes.

For example, in some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 has been determined to be at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of any one of the combinations set forth in Tables 2-4 has been determined to be at or above a reference expression level of the one or more genes and the expression level of any one of the combinations set forth in Tables 9-16 has been determined to be at or above a reference expression level of the one or more genes. For example, in some embodiments, the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, has been determined to be at or above a reference expression level of the one or more genes, and the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9, has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of

three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, has been determined to be at or above a reference expression level of the one or more genes, and the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10, has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, has been determined to be at or above a reference expression level of the one or more genes, and the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11, has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12, has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13, has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14, has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15, has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16, has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, PD-L1, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding methods, the expression level of PD-L1 in the sample has been determined to be at or above a reference expression level of PD-L1, and the expression

level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19) additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more additional genes.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes. For example, in some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 5-8 in the sample has been determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes. For example, in some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In other embodiments, in any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 has been determined to be at or above a reference level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 has been determined to be below a reference level of the one or more genes. For example, in some embodiments, the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 has been determined to be at or above a reference level of the one or more genes, and the expression level of at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 has been determined to be below a reference level of the one or more genes.

For example, in some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 has been determined to be at or above a reference level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, or 6) of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference level of the one or more genes, and the expression level of at least one, at least two, at least three, at least

four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 has been determined to be below a reference level for the one or more genes. In some embodiments, the expression level of any one of the combinations set forth in Tables 2-4 has been determined to be at or above a reference level of the one or more genes, and the expression level of any one of the combinations set forth in

5 Tables 5-8 has been determined to be below a reference level of the one or more genes. For example, in some embodiments, the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, has been determined to be at or above a reference level of the one or more genes, and the expression level of two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5, has been

10 determined to be below a reference level of the one or more genes. In some embodiments, the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, has been determined to be at or above a reference level of the one or more genes, and the expression level of three of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6, has been determined to be

15 below a reference level of the one or more genes. In some embodiments, the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, has been determined to be at or above a reference level of the one or more genes, and the expression level of four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 7, has been determined to be below a reference level of the one

20 or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8, has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and

25 PD-L1 has been determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 has been determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be below a reference level of the one or more genes.

30 In some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be below a reference level of the one or more genes. For example, in some embodiments, the expression

35 level of one or more of the exemplary combinations set forth in Tables 9-16 in the sample has been determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 in the sample has been determined to be below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In another aspect, provided herein is a method of treating an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)) that includes (a) determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of the following genes in a sample from the individual: VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be at or above a reference expression level of the one or more genes; and (b) administering an effective amount of an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))) to the individual based on the expression level of the one or more genes determined in step (a).

In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. For example, in some embodiments, the method includes determining the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the method includes determining the expression level of at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the method includes determining the expression level of two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5. In some embodiments, the method includes determining the expression level of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6. In some embodiments, the method includes determining the expression level of four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 7. In some embodiments, the method includes determining the expression level of five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8. In some embodiments, the method includes determining the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be at or above a reference level of the one or more genes. For example, in some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 5-8 in the sample is determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is determined to be at or above a reference level of the one or more genes. For example, in some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is determined to be at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In another aspect, provided herein is a method of treating an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer

(e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)) that includes administering to the individual an effective amount of an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))))), wherein the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference expression level of the one or more genes.

In some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes. For example, in some embodiments, the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes. In some embodiments, the expression level of one or more of the exemplary combinations set forth in Tables 5-8 in the sample has been determined to be at or above a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes. For example, in some embodiments, the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In another aspect, provided herein is a method of treating an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)), the method including administering to the individual an effective amount of a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) monotherapy, wherein (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more genes; or (ii) the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 in the sample has been determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of one or more of the genes has been determined prior to treatment with the PD-L1 axis binding antagonist monotherapy. In other embodiments, the expression level of one or more of the genes has been determined after treatment with the PD-L1 axis binding antagonist monotherapy.

In some of any of the preceding methods, the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 has been determined to be below a reference expression level of the one or more genes. For example, in some embodiments, the

expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 has been determined to be at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 has been determined to be below a reference expression level of the one or more genes.

For example, in some embodiments, the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1 has been determined to be at or above a reference expression level of the one or more genes, and the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9 has been determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of the one or more genes, and the expression level of at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or all ten of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 has been determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of any one of the combinations set forth in Tables 2-4 has been determined to be at or above a reference expression level of the one or more genes and the expression level of any one of the combinations set forth in Tables 9-12 has been determined to be below a reference expression level of the one or more genes. For example, in some embodiments, the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2, has been determined to be at or above a reference expression level of the one or more genes, and the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9, has been determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3, has been determined to be at or above a reference expression level of the one or more genes, and the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10, has been determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 4, has been determined to be at or above a reference expression level of the one or more genes, and the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11, has been determined to be below a reference expression level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression

level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12, has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13, has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14, has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15, has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16, has been determined to be below a reference level of the one or more genes. In some embodiments, the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1, and the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9 has been determined to be below a reference expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In some embodiments of any of the preceding methods, therapy with a VEGF antagonist (e.g., an anti-VEGF antibody, such as bevacizumab) in combination with a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) preferably extends and/or improves survival, including progression free survival (PFS) and/or overall survival (OS). In one embodiment, therapy with the VEGF antagonist (e.g., an anti-VEGF antibody, such as bevacizumab) in combination with a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) extends survival by at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 200%, or more, relative to the survival achieved by administering an approved anti-tumor agent, or standard of care, for the cancer being treated.

In other embodiments of any of the preceding methods, therapy with the angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g.,

sunitinib, axitinib, pazopanib, or cabozantinib)))) preferably extends and/or improves survival, including progression free survival (PFS) and/or overall survival (OS). In one embodiment, therapy with the angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))) extends survival by at least about
 5 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 200%, or more, relative to the survival achieved by administering an approved anti-tumor agent, or standard of care, for the cancer being treated.

In certain embodiments of any of the preceding methods, a reference level is the expression level of the one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24,
 10 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, or 37) genes (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9) in a reference population, for example, a population of individuals having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC),
 15 a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)). In particular embodiments, the cancer is a kidney cancer (e.g., RCC, e.g., mRCC). In certain embodiments, a reference level is the median expression level of the one or more genes in a reference population, for example, a population of individuals having a cancer. In other embodiments, the reference level may be the top 40%, the top 30%, the top 20%, the top 10%, the top 5%, or the top 1% of the
 20 expression level in the reference population. In certain embodiments, the reference level is a pre-assigned expression level for the one or more genes. In some embodiments, the reference level is the expression level of the one or more genes in a biological sample obtained from the patient at a previous time point, wherein the previous time point is following administration of the anti-cancer therapy. In some embodiments of any of the preceding methods, a reference level is the expression level of the one or
 25 more genes (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9) in a biological sample from the patient obtained prior to (e.g., minutes, hours, days, weeks (e.g., 1, 2, 3, 4, 5, 6, or 7 weeks), months, or years prior to) administration of the anti-cancer
 30 therapy. In other embodiments, the reference level is the expression level of the one or more genes in a biological sample obtained from the patient at a subsequent time point (e.g., minutes, hours, days, weeks, months, or years after administration of an anti-cancer therapy).

In some embodiments of any of the preceding embodiments, the sample is obtained from the individual prior to (e.g., minutes, hours, days, weeks (e.g., 1, 2, 3, 4, 5, 6, or 7 weeks), months, or years
 35 prior to) administration of the anti-cancer therapy. In some embodiments of any of the preceding methods, the sample from the individual is obtained about 2 to about 10 weeks (e.g., 2, 3, 4, 5, 6, 7, 8, 9, or 10 weeks) following administration of the anti-cancer therapy. In some embodiments, the sample from the individual is obtained about 4 to about 6 weeks following administration of the anti-cancer therapy.

In some embodiments of any of the preceding methods, the expression level or number of a
 40 biomarker is detected in a tissue sample, a primary or cultured cells or cell line, a cell supernatant, a cell

lysate, platelets, serum, plasma, vitreous fluid, lymph fluid, synovial fluid, follicular fluid, seminal fluid, amniotic fluid, milk, whole blood, blood-derived cells, urine, cerebro-spinal fluid, saliva, sputum, tears, perspiration, mucus, tumor lysates, and tissue culture medium, tissue extracts such as homogenized tissue, tumor tissue, cellular extracts, or any combination thereof. In some embodiments, the sample is a
 5 tissue sample (e.g., a tumor tissue sample), a cell sample, a whole blood sample, a plasma sample, a serum sample, or a combination thereof. In some embodiments, the tumor tissue sample wherein the tumor tissue sample includes tumor cells, tumor-infiltrating immune cells, stromal cells, or a combination thereof. In some embodiments, the tumor tissue sample is a formalin-fixed and paraffin-embedded (FFPE) sample, an archival sample, a fresh sample, or a frozen sample.

For example, in some embodiments of any of the preceding methods, the expression level of a
 10 biomarker is detected in tumor-infiltrating immune cells, tumor cells, PBMCs, or combinations thereof using known techniques (e.g., flow cytometry or IHC). Tumor-infiltrating immune cells include, but are not limited to, intratumoral immune cells, peritumoral immune cells or any combinations thereof, and other tumor stroma cells (e.g., fibroblasts). Such tumor infiltrating immune cells may be T lymphocytes (such
 15 as CD8⁺ T lymphocytes (e.g., CD8⁺ T effector (T_{eff}) cells) and/or CD4⁺ T lymphocytes (e.g., CD4⁺ T_{eff} cells), B lymphocytes, or other bone marrow-lineage cells including granulocytes (neutrophils, eosinophils, basophils), monocytes, macrophages, dendritic cells (e.g., interdigitating dendritic cells), histiocytes, and natural killer (NK) cells. In some embodiments, the staining for a biomarker is detected as membrane staining, cytoplasmic staining, or combinations thereof. In other embodiments, the
 20 absence of a biomarker is detected as absent or no staining in the sample, relative to a reference sample.

In particular embodiments of any of the preceding methods, the expression level of a biomarker is assessed in a sample that contains or is suspected to contain cancer cells. The sample may be, for example, a tissue biopsy or a metastatic lesion obtained from a patient suffering from, suspected to suffer from, or diagnosed with cancer (e.g., a kidney cancer, in particular renal cell carcinoma (RCC), such as
 25 advanced RCC or metastatic RCC (mRCC)). In some embodiments, the sample is a sample of kidney tissue, a biopsy of an kidney tumor, a known or suspected metastatic kidney cancer lesion or section, or a blood sample, e.g., a peripheral blood sample, known or suspected to comprise circulating cancer cells, e.g., kidney cancer cells. The sample may comprise both cancer cells, i.e., tumor cells, and non-cancerous cells (e.g., lymphocytes, such as T cells or NK cells), and, in certain embodiments, comprises
 30 both cancerous and non-cancerous cells. Methods of obtaining biological samples including tissue resections, biopsies, and body fluids, e.g., blood samples comprising cancer/tumor cells, are well known in the art.

In some embodiments of any of the preceding methods, the individual has carcinoma, lymphoma, blastoma (including medulloblastoma and retinoblastoma), sarcoma (including liposarcoma and synovial
 35 cell sarcoma), neuroendocrine tumors (including carcinoid tumors, gastrinoma, and islet cell cancer), mesothelioma, schwannoma (including acoustic neuroma), meningioma, adenocarcinoma, melanoma, and leukemia or lymphoid malignancies. In some embodiments, the cancer is kidney cancer (e.g., renal cell carcinoma (RCC), e.g., advanced RCC or metastatic RCC (mRCC)), squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer (including small-cell lung cancer (SCLC), non-small cell
 40 lung cancer (NSCLC), adenocarcinoma of the lung, and squamous carcinoma of the lung), cancer of the

peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer (e.g., HCC), hepatoma, breast cancer (including TNBC and metastatic breast cancer), bladder cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, Merkel cell cancer, mycoses fungoids, testicular cancer, esophageal cancer, tumors of the biliary tract, head and neck cancer, B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL); small lymphocytic (SL) NHL; intermediate grade/follicular NHL; intermediate grade diffuse NHL; high grade immunoblastic NHL; high grade lymphoblastic NHL; high grade small non-cleaved cell NHL; bulky disease NHL; mantle cell lymphoma; AIDS-related lymphoma; and Waldenstrom's Macroglobulinemia); chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); Hairy cell leukemia; chronic myeloblastic leukemia; and post-transplant lymphoproliferative disorder (PTLD), abnormal vascular proliferation associated with phakomatoses, edema (such as that associated with brain tumors), or Meigs' syndrome. In some embodiments, the cancer is a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC). In preferred embodiments, the patient has a kidney cancer (e.g., RCC, e.g., advanced RCC or mRCC, e.g., previously untreated advanced RCC or mRCC). The patient may optionally have an advanced, refractory, recurrent, chemotherapy-resistant, and/or platinum-resistant form of the cancer.

In certain embodiments, the presence and/or expression levels/amount of a biomarker in a first sample is increased or elevated as compared to presence/absence and/or expression levels/amount in a second sample. In certain embodiments, the presence/absence and/or expression levels/amount of a biomarker in a first sample is decreased or reduced as compared to presence and/or expression levels/amount in a second sample. In certain embodiments, the second sample is a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue.

In certain embodiments, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is a single sample or combined multiple samples from the same patient or individual that are obtained at one or more different time points than when the test sample is obtained. For example, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is obtained at an earlier time point from the same patient or individual than when the test sample is obtained. Such reference sample, reference cell, reference tissue, control sample, control cell, or control tissue may be useful if the reference sample is obtained during initial diagnosis of cancer and the test sample is later obtained when the cancer becomes metastatic.

In certain embodiments, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is a combined multiple samples from one or more healthy individuals who are not the patient. In certain embodiments, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is a combined multiple samples from one or more individuals with a disease or disorder (e.g., cancer) who are not the patient or individual. In certain embodiments, a reference sample, reference cell, reference tissue, control sample, control cell, or control tissue is pooled RNA samples from normal tissues or pooled plasma or serum samples from one or more individuals who are not the patient. In certain embodiments, a reference sample, reference cell, reference tissue, control

sample, control cell, or control tissue is pooled RNA samples from tumor tissues or pooled plasma or serum samples from one or more individuals with a disease or disorder (e.g., cancer) who are not the patient.

In some embodiments of any of the preceding methods, an expression level above a reference level, or an elevated or increased expression or number, refers to an overall increase of about any of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater, in the level or number of a biomarker (e.g., protein, nucleic acid (e.g., gene or mRNA), or cell), detected by methods such as those described herein and/or known in the art, as compared to a reference level, reference sample, reference cell, reference tissue, control sample, control cell, or control tissue. In certain embodiments, the elevated expression or number refers to the increase in expression level/amount of a biomarker (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9) in the sample wherein the increase is at least about any of 1.1x, 1.2x, 1.3x, 1.4x, 1.5x, 1.6x, 1.7x, 1.8x, 1.9x, 2x, 2.1x, 2.2x, 2.3x, 2.4x, 2.5x, 2.6x, 2.7x, 2.8x, 2.9x, 3x, 3.5x, 4x, 4.5x, 5x, 6x, 7x, 8x, 9x, 10x, 15x, 20x, 30x, 40x, 50x, 100x, 500x, or 1000x the expression level/amount of the respective biomarker in a reference level, reference sample, reference cell, reference tissue, control sample, control cell, or control tissue. In some embodiments, elevated expression or number refers to an overall increase in expression level/amount of a biomarker (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9) of greater than about 1.1-fold, about 1.2-fold, about 1.3-fold, about 1.4-fold, about 1.5-fold, about 1.6-fold, about 1.7-fold, about 1.8-fold, about 1.9-fold, about 2-fold, about 2.1-fold, about 2.2-fold, about 2.3-fold, about 2.4-fold, about 2.5-fold, about 2.6-fold, about 2.7-fold, about 2.8-fold, about 2.9-fold, about 3-fold, about 3.5-fold, about 4-fold, about 4.5-fold, about 5-fold, about 6-fold, about 7-fold, about 8-fold, about 9-fold, about 10-fold, about 15-fold, about 20-fold, about 30-fold, about 40-fold, about 50-fold, about 100-fold, about 500-fold, about 1,000-fold or greater as compared to a reference level, reference sample, reference cell, reference tissue, control sample, control cell, control tissue, or internal control (e.g., housekeeping gene).

In some embodiments of any of the preceding methods, an expression level below a reference level, or reduced (decreased) expression or number, refers to an overall reduction of about any of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater, in the level of biomarker (e.g., protein, nucleic acid (e.g., gene or mRNA), or cell), detected by standard art known methods such as those described herein, as compared to a reference level, reference sample, reference cell, reference tissue, control sample, control cell, or control tissue. In certain embodiments, reduced expression or number refers to the decrease in expression level/amount of a biomarker (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9) in the sample wherein the decrease is at least about any of 0.9x, 0.8x, 0.7x, 0.6x, 0.5x, 0.4x, 0.3x, 0.2x, 0.1x, 0.05x, or

0.01x the expression level/amount of the respective biomarker in a reference level, reference sample, reference cell, reference tissue, control sample, control cell, or control tissue. In some embodiments, reduced (decreased) expression or number refers to an overall decrease in expression level/amount of a biomarker (e.g., CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9) of greater than about 1.1-fold, about 1.2-fold, about 1.3-fold, about 1.4-fold, about 1.5-fold, about 1.6-fold, about 1.7-fold, about 1.8-fold, about 1.9-fold, about 2-fold, about 2.1-fold, about 2.2-fold, about 2.3-fold, about 2.4-fold, about 2.5-fold, about 2.6-fold, about 2.7-fold, about 2.8-fold, about 2.9-fold, about 3-fold, about 3.5-fold, about 4-fold, about 4.5-fold, about 5-fold, about 6-fold, about 7-fold, about 8-fold, about 9-fold, about 10-fold, about 15-fold, about 20-fold, about 30-fold, about 40-fold, about 50-fold, about 100-fold, about 500-fold, about 1,000-fold or greater as compared to a reference level, reference sample, reference cell, reference tissue, control sample, control cell, control tissue, or internal control (e.g., housekeeping gene).

For the prevention or treatment of cancer, the dose of an anti-cancer therapy (e.g., a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)), or an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))))) will depend on the type of cancer to be treated, as defined above, the severity and course of the cancer, whether the anti-cancer therapy is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the drug, and the discretion of the attending physician.

In some embodiments, the anti-cancer therapy (e.g., a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)), or an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))))) may be suitably administered to the patient at one time or over a series of treatments. One typical daily dosage might range from about 1 µg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment would generally be sustained until a desired suppression of disease symptoms occurs. Such doses may be administered intermittently, e.g., every week or every three weeks (e.g., such that the patient receives, for example, from about two to about twenty, or e.g., about six doses of the anti-cancer therapy). An initial higher loading dose, followed by one or more lower doses may be administered. However, other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays.

For example, as a general proposition, the therapeutically effective amount of a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and/or PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) administered to human will be in the range of about 0.01 to about 50 mg/kg of patient body weight, whether by one or more administrations. In some embodiments, the therapeutic agent (e.g., antibody) used is about 0.01 mg/kg to about 45 mg/kg, about 0.01 mg/kg to about 40 mg/kg, about 0.01 mg/kg to about 35 mg/kg, about 0.01 mg/kg to about 30 mg/kg, about 0.01 mg/kg to about 25 mg/kg, about 0.01 mg/kg to about 20 mg/kg, about 0.01 mg/kg to about 15 mg/kg, about 0.01 mg/kg to about 10 mg/kg, about 0.01 mg/kg to about 5 mg/kg, or about 0.01 mg/kg to about 1 mg/kg administered daily, weekly, every two weeks, every three weeks, or monthly, for example. In some embodiments, the antibody is administered at 15 mg/kg. However, other dosage regimens may be useful. In one embodiment, an VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and/or PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist, such as atezolizumab) is administered to a human at a dose of about 50 mg, about 100 mg, about 200 mg, about 300 mg, about 400 mg, about 420 mg, about 500 mg, about 525 mg, about 600 mg, about 700 mg, about 800 mg, about 840mg, about 900 mg, about 1000 mg, about 1050 mg, about 1100 mg, about 1200 mg, about 1300 mg, about 1400 mg, about 1500 mg, about 1600 mg, about 1700 mg, or about 1800 mg on day 1 of 21-day cycles (every three weeks, q3w).

In some embodiments, atezolizumab is administered at 1200 mg intravenously every three weeks (q3w). In some embodiments, bevacizumab is administered at a fixed dose at one time or over a series of treatments. Where a fixed dose is administered, preferably it is in the range from about 5 mg to about 2000 mg. For example, the fixed dose may be approximately 420 mg, approximately 525 mg, approximately 840 mg, or approximately 1050 mg. In some embodiments, bevacizumab is administered at 10 mg/kg intravenously every two weeks. In some embodiments, bevacizumab is administered at 15 mg/kg intravenously every three weeks. The dose of VEGF antagonist and/or PD-L1 axis binding antagonist may be administered as a single dose or as multiple doses (e.g., 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more doses). Where a series of doses are administered, these may, for example, be administered approximately every week, approximately every 2 weeks, approximately every 3 weeks, or approximately every 4 weeks. The dose of the antibody administered in a combination treatment may be reduced as compared to a single treatment. The progress of this therapy is easily monitored by conventional techniques.

Any suitable dose of a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) may be used in the methods described herein. Suitable dosages are well known in the art. For example, with respect to sunitinib, capsules of 12.5 mg, 25 mg, and 50 mg of sunitinib are commercially available. For example, for treatment of metastatic renal cell carcinoma or gastrointestinal stromal tumor, sunitinib may be administered at 50 mg by mouth (PO) once a day (qDay) for 4 weeks, followed by 2 weeks drug-free, with further repeats of the cycle. For treatment

of pancreatic neuroendocrine tumors, a standard dose is 37.5 mg PO qDay continuously without a scheduled off-treatment period.

VEGF antagonists (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and PD-L1 axis binding antagonists (e.g., an antibody (e.g., an anti-PD-L1 antibody, e.g., atezolizumab), binding polypeptide, and/or small molecule) described herein (any additional therapeutic agent) may be formulated, dosed, and administered in a fashion consistent with good medical practice. Likewise, angiogenesis inhibitors (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))) may be formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the particular disorder being treated, the particular mammal being treated, the clinical condition of the individual patient, the cause of the disorder, the site of delivery of the agent, the method of administration, the scheduling of administration, and other factors known to medical practitioners. The VEGF antagonist and PD-L1 antagonist, or the angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))))), need not be, but is optionally formulated with and/or administered concurrently with one or more agents currently used to prevent or treat the disorder in question. The effective amount of such other agents depends on the amount of the VEGF antagonist, PD-L1 antagonist, and/or angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))) present in the formulation, the type of disorder or treatment, and other factors discussed above. These are generally used in the same dosages and with administration routes as described herein, or about from 1 to 99% of the dosages described herein, or in any dosage and by any route that is empirically/clinically determined to be appropriate.

In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) is administered concurrently with a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)). In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) are administered as part of the same formulation. In other embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) is administered separately from a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)).

In some embodiments, any of the preceding methods may further include administering an additional therapeutic agent. In some embodiments, the additional therapeutic agent is selected from the group consisting of an immunotherapy agent, a cytotoxic agent, a growth inhibitory agent, a radiation therapy agent, an anti-angiogenic agent, and combinations thereof.

In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) is administered concurrently with an agonist directed against an activating co-stimulatory molecule. In some embodiments, an activating co-stimulatory molecule may include CD40, CD226, CD28, OX40, GITR, CD137, CD27, HVEM, or CD127. In some embodiments, the agonist directed against an activating co-stimulatory molecule is an agonist antibody that binds to CD40, CD226, CD28, OX40, GITR, CD137, CD27, HVEM, or CD127. In some embodiments, VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an antagonist directed against an inhibitory co-stimulatory molecule. In some embodiments, an inhibitory co-stimulatory molecule may include CTLA-4 (also known as CD152), TIM-3, BTLA, VISTA, LAG-3, B7-H3, B7-H4, IDO, TIGIT, MICA/B, or arginase. In some embodiments, the antagonist directed against an inhibitory co-stimulatory molecule is an antagonist antibody that binds to CTLA-4, TIM-3, BTLA, VISTA, LAG-3, B7-H3, B7-H4, IDO, TIGIT, MICA/B, or arginase.

In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an antagonist directed against CTLA-4 (also known as CD152), e.g., a blocking antibody. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with ipilimumab (also known as MDX-010, MDX-101, or YERVOY®). In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with tremelimumab (also known as ticilimumab or CP-675,206). In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an antagonist directed against B7-H3 (also known as CD276), e.g., a blocking antibody. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib,

pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with MGA271. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an antagonist directed against a TGF-beta, e.g., metelimumab (also known as CAT-192), fresolimumab (also known as GC1008), or LY2157299.

In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an agonist directed against CD137 (also known as TNFRSF9, 4-1BB, or ILA), e.g., an activating antibody. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with urelumab (also known as BMS-663513). In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an agonist directed against CD40, e.g., an activating antibody. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with CP-870893. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an agonist directed against OX40 (also known as CD134), e.g., an activating antibody. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an anti-OX40 antibody (e.g., AgonOX). In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase

inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an agonist directed against CD27, e.g., an activating antibody. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with CDX-1127. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an antagonist directed against TIGIT, for example, an anti-TIGIT antibody. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an antagonist directed against indoleamine-2,3-dioxygenase (IDO). In some embodiments, the IDO antagonist is 1-methyl-D-tryptophan (also known as 1-D-MT).

In some embodiments, VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with a cancer vaccine. In some embodiments, the cancer vaccine is a peptide cancer vaccine, which in some embodiments is a personalized peptide vaccine. In some embodiments the peptide cancer vaccine is a multivalent long peptide, a multi-peptide, a peptide cocktail, a hybrid peptide, or a peptide-pulsed dendritic cell vaccine (see, e.g., Yamada et al., *Cancer Sci.* 104:14-21, 2013). In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an adjuvant. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with a treatment comprising a TLR agonist, e.g., Poly-ICLC (also known as HILTONOL®), LPS, MPL, or CpG ODN. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-

L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with tumor necrosis factor (TNF) alpha. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with IL-1. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with HMGB1. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an IL-10 antagonist. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an IL-4 antagonist. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an IL-13 antagonist. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an HVEM antagonist. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with an ICOS agonist, e.g., by administration of ICOS-L, or an agonistic antibody directed against ICOS. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody)) may be administered in conjunction with a treatment targeting CX3CL1. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab)

or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody))) may be administered in conjunction with a treatment targeting CXCL9. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody))) may be administered in conjunction with a treatment targeting CXCL10. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody))) may be administered in conjunction with a treatment targeting CCL5. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody))) may be administered in conjunction with an LFA-1 or ICAM1 agonist. In some embodiments, a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody))) may be administered in conjunction with a Selectin agonist.

A chemotherapeutic agent, if administered, is usually administered at dosages known therefore, or optionally lowered due to combined action of the drugs or negative side effects attributable to administration of the chemotherapeutic agent. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Where the chemotherapeutic agent is paclitaxel, preferably, it is administered at a dose between about 130 mg/m² to 200 mg/m² (e.g., approximately 175 mg/m²), for instance, over 3 hours, once every 3 weeks. Where the chemotherapeutic agent is carboplatin, preferably it is administered by calculating the dose of carboplatin using the Calvert formula which is based on a patient's preexisting renal function or renal function and desired platelet nadir. Renal excretion is the major route of elimination for carboplatin. The use of this dosing formula, as compared to empirical dose calculation based on body surface area, allows compensation for patient variations in pretreatment renal function that might otherwise result in either underdosing (in patients with above average renal function) or overdosing (in patients with impaired renal function). The target AUC of 4-6 mg/mL/min using single agent carboplatin appears to provide the most appropriate dose range in previously treated patients.

In addition to the above therapeutic regimes, the patient may be subjected to surgical removal of tumors and/or cancer cells.

Such combination therapies noted above encompass combined administration (where two or more therapeutic agents are included in the same or separate formulations), and separate administration, in which case, administration of a VEGF antagonist and/or a PD-L1 axis binding antagonist, or an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))))), can occur prior to, simultaneously, and/or following, administration of the additional therapeutic agent or agents. In one embodiment, administration of VEGF antagonist and/or a PD-L1 axis binding antagonist, or a an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))))), and administration of an additional therapeutic agent occur within about one month, or within about one, two or three weeks, or within about one, two, three, four, five, or six days, of each other.

In embodiments where either the VEGF antagonist or the PD-L1 axis binding antagonist is an antibody (e.g., bevacizumab or atezolizumab), the administered antibody may be a naked antibody. The VEGF antagonist (e.g., an anti-VEGF antibody, such as bevacizumab) and/or the PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist, such as atezolizumab) administered may be conjugated with a cytotoxic agent. Preferably, the conjugated and/or antigen to which it is bound is/are internalized by the cell, resulting in increased therapeutic efficacy of the conjugate in killing the cancer cell to which it binds. In a preferred embodiment, the cytotoxic agent targets or interferes with nucleic acid in the cancer cell. Examples of such cytotoxic agents include maytansinoids, calicheamicins, ribonucleases, and DNA endonucleases.

The compositions utilized in the methods described herein can be administered by any suitable method, including, for example, intravenously, intramuscularly, subcutaneously, intradermally, percutaneously, intraarterially, intraperitoneally, intralesionally, intracranially, intraarticularly, intraprostatically, intrapleurally, intratracheally, intrathecally, intranasally, intravaginally, intrarectally, topically, intratumorally, peritoneally, subconjunctivally, intravesicularly, mucosally, intrapericardially, intraumbilically, intraocularly, intraorbitally, orally, topically, transdermally, intravitreally (e.g., by intravitreal injection), parenterally, by eye drop, by inhalation, by injection, by implantation, by infusion, by continuous infusion, by localized perfusion bathing target cells directly, by catheter, by lavage, in cremes, or in lipid compositions. The compositions utilized in the methods described herein can also be administered systemically or locally. The method of administration can vary depending on various factors (e.g., the compound or composition being administered and the severity of the condition, disease, or disorder being treated). In some embodiments, the PD-L1 axis binding antagonist is administered intravenously, intramuscularly, subcutaneously, topically, orally, transdermally, intraperitoneally, intraorbitally, by implantation, by inhalation, intrathecally, intraventricularly, or intranasally. In some embodiments, the multi-targeted tyrosine kinase inhibitor is administered orally. Dosing can be by any suitable route, e.g., by injections, such as intravenous or subcutaneous injections, depending in part on whether the administration is brief or chronic. Various dosing schedules including but not limited to single or multiple administrations over various time-points, bolus administration, and pulse infusion are contemplated herein.

IV. COMPOSITIONS AND PHARMACEUTICAL FORMULATIONS

In one aspect, the invention is based, in part, on the discovery that biomarkers of the invention can be used to identify individuals having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)) who may benefit from anti-cancer therapies that include VEGF antagonists and PD-L1 axis binding antagonists. In another aspect, the invention is based, in part, on the discovery that biomarkers of the invention can be used to identify individuals having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)) who may benefit from anti-cancer therapies that include an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))). These agents, and combinations thereof, are useful for the treatment of cancer, e.g., as part of any of the methods described herein, for example, in Sections II and III above. Any suitable VEGF antagonist, PD-L1 axis binding antagonist, and/or angiogenesis inhibitor can be used in the methods and assays described herein. Non-limiting examples suitable for use in the methods and assays of the invention are described further below.

A. Exemplary VEGF Antagonists

VEGF antagonists include any molecule capable of binding VEGF, reducing VEGF expression levels, or neutralizing, blocking, inhibiting, abrogating, reducing, or interfering with VEGF biological activities. An exemplary human VEGF is shown under UniProtKB/Swiss-Prot Accession No. P15692, Gene ID (NCBI): 7422.

In some instances, the VEGF antagonist is an anti-VEGF antibody. In some embodiments, the anti-VEGF antibody is bevacizumab, also known as “rhuMab VEGF” or “AVASTIN®.” Bevacizumab is a recombinant humanized anti-VEGF monoclonal antibody generated according to Presta et al. (*Cancer Res.* 57:4593-4599, 1997). It comprises mutated human IgG1 framework regions and antigen-binding complementarity-determining regions from the murine anti-hVEGF monoclonal antibody A.4.6.1 that blocks binding of human VEGF to its receptors. Approximately 93% of the amino acid sequence of bevacizumab, including most of the framework regions, is derived from human IgG1, and about 7% of the sequence is derived from the murine antibody A4.6.1. Bevacizumab has a molecular mass of about 149,000 daltons and is glycosylated. Bevacizumab and other humanized anti-VEGF antibodies are further described in U.S. Pat. No. 6,884,879 issued Feb. 26, 2005, the entire disclosure of which is expressly incorporated herein by reference. Additional preferred antibodies include the G6 or B20 series antibodies (e.g., G6-31, B20-4.1), as described in PCT Application Publication No. WO 2005/012359. For additional preferred antibodies see U.S. Pat. Nos. 7,060,269, 6,582,959, 6,703,020; 6,054,297; WO98/45332; WO 96/30046; WO94/10202; EP 0666868B1; U.S. Patent Application Publication Nos. 2006009360, 20050186208, 20030206899, 20030190317, 20030203409, and 20050112126; and Popkov et al. (*Journal of Immunological Methods* 288:149-164, 2004). Other preferred antibodies include those that bind to a functional epitope on human VEGF comprising of residues F17, M18, D19, Y21, Y25, Q89, 191, K101, E103, and C104 or, alternatively, comprising residues F17, Y21, Q22, Y25, D63, 183, and Q89.

In other instances, the VEGF antagonist is an anti-VEGFR2 antibody or related molecule (e.g., ramucirumab, tanibirumab, aflibercept); an anti-VEGFR1 antibody or related molecules (e.g., icrucumab, aflibercept (VEGF Trap-Eye; EYLEA®), or ziv-aflibercept (VEGF Trap; ZALTRAP®)); a bispecific VEGF antibody (e.g., MP-0250, vanucizumab (VEGF-ANG2), or bispecific antibodies disclosed in US 2001/0236388); a bispecific antibody including a combination of two of anti-VEGF, anti-VEGFR1, and anti-VEGFR2 arms; an anti-VEGFA antibody (e.g., bevacizumab, sevacizumab); an anti-VEGFB antibody; an anti-VEGFC antibody (e.g., VGX-100), an anti-VEGFD antibody; or a nonpeptide small molecule VEGF antagonist (e.g., pazopanib, axitinib, vandetanib, stivarga, cabozantinib, lenvatinib, nintedanib, orantinib, telatinib, dovitinib, cediranib, motesanib, sulfatinib, apatinib, foretinib, famitinib, or tivozanib).

It is expressly contemplated that such VEGF antagonist antibodies or other antibodies described herein (e.g., anti-VEGF antibodies for detection of VEGF expression levels) for use in any of the embodiments enumerated above may have any of the features, singly or in combination, described in Sections i-vii of Subsection C below.

B. Exemplary PD-L1 Axis Binding Antagonists

PD-L1 axis binding antagonists include PD-1 binding antagonists, PD-L1 binding antagonists, and PD-L2 binding antagonists. PD-1 (programmed death 1) is also referred to in the art as “programmed cell death 1,” “PDCD1,” “CD279,” and “SLEB2.” An exemplary human PD-1 is shown in UniProtKB/Swiss-Prot Accession No. Q15116. PD-L1 (programmed death ligand 1) is also referred to in the art as “programmed cell death 1 ligand 1,” “PDCD1LG1,” “CD274,” “B7-H,” and “PDL1.” An exemplary human PD-L1 is shown in UniProtKB/Swiss-Prot Accession No. Q9NZQ7.1. PD-L2 (programmed death ligand 2) is also referred to in the art as “programmed cell death 1 ligand 2,” “PDCD1LG2,” “CD273,” “B7-DC,” “Btdc,” and “PDL2.” An exemplary human PD-L2 is shown in UniProtKB/Swiss-Prot Accession No. Q9BQ51. In some embodiments, PD-1, PD-L1, and PD-L2 are human PD-1, PD-L1, and PD-L2. The PD-1 axis binding antagonist may, in some instances, be a PD-1 binding antagonist, a PD-L1 binding antagonist, or a PD-L2 binding antagonist.

(i) PD-L1 Binding Antagonists

In some instances, the PD-L1 binding antagonist inhibits the binding of PD-L1 to one or more of its ligand binding partners. In other instances, the PD-L1 binding antagonist inhibits the binding of PD-L1 to PD-1. In yet other instances, the PD-L1 binding antagonist inhibits the binding of PD-L1 to B7-1. In some instances, the PD-L1 binding antagonist inhibits the binding of PD-L1 to both PD-1 and B7-1. In some instances, the PD-L1 binding antagonist is an antibody. In some instances, the antibody is selected from the group consisting of: MPDL3280A (atezolizumab), YW243.55.S70, MDX-1105, MEDI4736 (durvalumab), and MSB0010718C (avelumab).

In some instances, the anti-PD-L1 antibody is a monoclonal antibody. In some instances, the anti-PD-L1 antibody is an antibody fragment selected from the group consisting of Fab, Fab'-SH, Fv, scFv, and (Fab')₂ fragments. In some instances, the anti-PD-L1 antibody is a humanized antibody. In some instances, the anti-PD-L1 antibody is a human antibody. In some instances, the anti-PD-L1

antibody described herein binds to human PD-L1. In some particular instances, the anti-PD-L1 antibody is atezolizumab (CAS Registry Number: 1422185-06-5). Atezolizumab (Genentech) is also known as MPDL3280A.

In some instances, the anti-PD-L1 antibody comprises a heavy chain variable region (HVR-H) comprising an HVR-H1, HVR-H2, and HVR-H3 sequence, wherein:

- (a) the HVR-H1 sequence is GFTFSDSWIH (SEQ ID NO: 62);
- (b) the HVR-H2 sequence is AWISPYGGSTYYADSVKG (SEQ ID NO: 63); and
- (c) the HVR-H3 sequence is RHWPGGFDY (SEQ ID NO: 64).

In some instances, the anti-PD-L1 antibody further comprises a light chain variable region (HVR-L) comprising an HVR-L1, HVR-L2, and HVR-L3 sequence, wherein:

- (a) the HVR-L1 sequence is RASQDVSTAVA (SEQ ID NO: 65);
- (b) the HVR-L2 sequence is SASFLYS (SEQ ID NO: 66); and
- (c) the HVR-L3 sequence is QQYLYHPAT (SEQ ID NO: 67).

In some instances, the anti-PD-L1 antibody comprises a heavy chain and a light chain sequence, wherein:

- (a) the heavy chain variable (VH) region sequence comprises the amino acid sequence:

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWRQAPGKGLEWVAWISPYGGSTYYADSVKGRF
TISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSS (SEQ ID NO: 69); and

- (b) the light chain variable (VL) region sequence comprises the amino acid sequence:

DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTD
FTLTISLQPEDFATYYCQQYLYHPATFGGQGTKVEIKR (SEQ ID NO: 70).

In some instances, the anti-PD-L1 antibody comprises a heavy chain and a light chain sequence, wherein:

- (a) the heavy chain comprises the amino acid sequence:

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWRQAPGKGLEWVAWISPYGGSTYYADSVKGRF
TISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP
SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 71); and

- (b) the light chain comprises the amino acid sequence:

DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTD
FTLTISLQPEDFATYYCQQYLYHPATFGGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC (SEQ ID NO: 72).

In some instances, the anti-PD-L1 antibody comprises (a) a VH domain comprising an amino acid sequence comprising having at least 95% sequence identity (e.g., at least 95%, 96%, 97%, 98%, or 99% sequence identity) to, or the sequence of (SEQ ID NO: 69); (b) a VL domain comprising an amino acid sequence comprising having at least 95% sequence identity (e.g., at least 95%, 96%, 97%, 98%, or 99%

sequence identity) to, or the sequence of (SEQ ID NO: 70); or (c) a VH domain as in (a) and a VL domain as in (b). In other instances, the anti-PD-L1 antibody is selected from the group consisting of YW243.55.S70, MDX-1105, MEDI4736 (durvalumab), and MSB0010718C (avelumab). Antibody YW243.55.S70 is an anti-PD-L1 described in PCT Pub. No. WO 2010/077634. MDX-1105, also known as BMS-936559, is an anti-PD-L1 antibody described in PCT Pub. No. WO 2007/005874. MEDI4736 (durvalumab) is an anti-PD-L1 monoclonal antibody described in PCT Pub. No. WO 2011/066389 and U.S. Pub. No. 2013/034559. Examples of anti-PD-L1 antibodies useful for the methods of this invention, and methods for making thereof are described in PCT Pub. Nos. WO 2010/077634, WO 2007/005874, and WO 2011/066389, and also in U.S. Pat. No. 8,217,149, and U.S. Pub. No. 2013/034559, which are incorporated herein by reference.

(ii) PD-1 Binding Antagonists

In some instances, the PD-L1 axis binding antagonist is a PD-1 binding antagonist. For example, in some instances, the PD-1 binding antagonist inhibits the binding of PD-1 to one or more of its ligand binding partners. In some instances, the PD-1 binding antagonist inhibits the binding of PD-1 to PD-L1. In other instances, the PD-1 binding antagonist inhibits the binding of PD-1 to PD-L2. In yet other instances, the PD-1 binding antagonist inhibits the binding of PD-1 to both PD-L1 and PD-L2. In some instances, the PD-1 binding antagonist is an antibody. In some instances, the antibody is selected from the group consisting of: MDX 1106 (nivolumab), MK-3475 (pembrolizumab), CT-011 (pidilizumab), MEDI-0680 (AMP-514), PDR001, REGN2810, and BGB-108. In some instances, the PD-1 binding antagonist is an Fc-fusion protein. For example, in some instances, the Fc-fusion protein is AMP-224.

In a further aspect, the invention provides for the use of a PD-L1 axis binding antagonist in the manufacture or preparation of a medicament. In one embodiment, the medicament is for treatment of a cancer. In a further embodiment, the medicament is for use in a method of treating a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), a liver cancer (e.g., HCC), an ovarian cancer, or a breast cancer (e.g., TNBC)) comprising administering to a patient suffering from cancer an effective amount of the medicament. In one such embodiment, the method further comprises administering to the individual an effective amount of at least one additional therapeutic agent, e.g., as described below.

In some embodiments, the PD-1 binding antagonist is a molecule that inhibits the binding of PD-1 to its ligand binding partners. In a specific aspect the PD-1 ligand binding partners are PD-L1 and/or PD-L2. In another embodiment, a PD-L1 binding antagonist is a molecule that inhibits the binding of PD-L1 to its binding ligands. In a specific aspect, PD-L1 binding partners are PD-1 and/or B7-1. In another embodiment, the PD-L2 binding antagonist is a molecule that inhibits the binding of PD-L2 to its ligand binding partners. In a specific aspect, the PD-L2 binding ligand partner is PD-1. The antagonist may be an antibody, an antigen binding fragment thereof, an immunoadhesin, a fusion protein, or oligopeptide.

In some embodiments, the PD-1 binding antagonist is an anti-PD-1 antibody (e.g., a human antibody, a humanized antibody, or a chimeric antibody), for example, as described below. In some embodiments, the anti-PD-1 antibody is selected from the group consisting of MDX-1106 (nivolumab), MK-3475 (pembrolizumab), CT-011 (pidilizumab), MEDI-0680 (AMP-514), PDR001, REGN2810, and

BGB-108. MDX-1106, also known as MDX-1106-04, ONO-4538, BMS-936558, or nivolumab, is an anti-PD-1 antibody described in WO2006/121168. MK-3475, also known as pembrolizumab or lambrolizumab, is an anti-PD-1 antibody described in WO 2009/114335. CT-011, also known as hBAT, hBAT-1 or pidilizumab, is an anti-PD-1 antibody described in WO 2009/101611. In some embodiments, the PD-1 binding antagonist is an immunoadhesin (e.g., an immunoadhesin comprising an extracellular or PD-1 binding portion of PD-L1 or PD-L2 fused to a constant region (e.g., an Fc region of an immunoglobulin sequence). In some embodiments, the PD-1 binding antagonist is AMP-224. AMP-224, also known as B7-DCIg, is a PD-L2-Fc fusion soluble receptor described in WO 2010/027827 and WO 2011/066342.

In some embodiments, the anti-PD-1 antibody is MDX-1106. Alternative names for "MDX-1106" include MDX-1106-04, ONO-4538, BMS-936558, and nivolumab. In some embodiments, the anti-PD-1 antibody is nivolumab (CAS Registry Number: 946414-94-4). In a still further embodiment, provided is an isolated anti-PD-1 antibody comprising a heavy chain variable region comprising the heavy chain variable region amino acid sequence from SEQ ID NO: 73 and/or a light chain variable region comprising the light chain variable region amino acid sequence from SEQ ID NO: 74.

In a still further embodiment, provided is an isolated anti-PD-1 antibody comprising a heavy chain and/or a light chain sequence, wherein:

(a) the heavy chain sequence has at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100%

sequence identity to the heavy chain sequence:

QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWDGSKRYYADSVKGR
FTISRDNSKNTLFLQMNSLRAEDTAVYYCATNDYWGQGTLLTVSSASTKGPSVFPLAPCSRSTSESTA
LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTCNVDHKPSNTKV
DKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVE
VHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPP
SQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGN
VFSCSVMEALHNHYTQKSLSLGLK (SEQ ID NO: 73), and

(b) the light chain sequences has at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100%

sequence identity to the light chain sequence:

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTD
FTLTISLEPEDFAVYYCQQSSNWPRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPY
REAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC (SEQ ID NO: 74).

It is expressly contemplated that such PD-L1 axis binding antagonist antibodies (e.g., anti-PD-L1 antibodies, anti-PD-1 antibodies, and anti-PD-L2 antibodies), or other antibodies described herein (e.g., anti-PD-L1 antibodies for detection of PD-L1 expression levels) for use in any of the embodiments enumerated above may have any of the features, singly or in combination, described in Sections i-vii of Subsection C below.

C. Antibodies

i. Antibody Affinity

In certain embodiments, an antibody provided herein (e.g., an anti-VEGF antibody, an anti-PD-L1 antibody or an anti-PD-1 antibody) has a dissociation constant (K_d) of $\leq 1 \mu\text{M}$, $\leq 100 \text{ nM}$, $\leq 10 \text{ nM}$, $\leq 1 \text{ nM}$, $\leq 0.1 \text{ nM}$, $\leq 0.01 \text{ nM}$, or $\leq 0.001 \text{ nM}$ (e.g., 10^{-8} M or less, e.g., from 10^{-8} M to 10^{-13} M , e.g., from 10^{-9} M to 10^{-13} M).

In one embodiment, K_d is measured by a radiolabeled antigen binding assay (RIA). In one embodiment, an RIA is performed with the Fab version of an antibody of interest and its antigen. For example, solution binding affinity of Fabs for antigen is measured by equilibrating Fab with a minimal concentration of (^{125}I)-labeled antigen in the presence of a titration series of unlabeled antigen, then capturing bound antigen with an anti-Fab antibody-coated plate (see, e.g., Chen et al., *J. Mol. Biol.* 293:865-881, 1999). To establish conditions for the assay, MICROTITER® multi-well plates (Thermo Scientific) are coated overnight with $5 \mu\text{g/ml}$ of a capturing anti-Fab antibody (Cappel Labs) in 50 mM sodium carbonate ($\text{pH } 9.6$), and subsequently blocked with 2% (w/v) bovine serum albumin in PBS for two to five hours at room temperature (approximately 23°C). In a non-adsorbent plate (Nunc #269620), 100 pM or 26 pM [^{125}I]-antigen are mixed with serial dilutions of a Fab of interest (e.g., consistent with assessment of the anti-VEGF antibody, Fab-12, in Presta et al., *Cancer Res.* 57:4593-4599, 1997). The Fab of interest is then incubated overnight; however, the incubation may continue for a longer period (e.g., about 65 hours) to ensure that equilibrium is reached. Thereafter, the mixtures are transferred to the capture plate for incubation at room temperature (e.g., for one hour). The solution is then removed and the plate washed eight times with 0.1% polysorbate 20 (TWEEN-20®) in PBS. When the plates have dried, $150 \mu\text{l/well}$ of scintillant (MICROSCINT-20™; Packard) is added, and the plates are counted on a TOPCOUNT™ gamma counter (Packard) for ten minutes. Concentrations of each Fab that give less than or equal to 20% of maximal binding are chosen for use in competitive binding assays.

According to another embodiment, K_d is measured using a BIACORE® surface plasmon resonance assay. For example, an assay using a BIACORE®-2000 or a BIACORE®-3000 (BIAcore, Inc., Piscataway, NJ) is performed at 25°C with immobilized antigen CM5 chips at ~ 10 response units (RU). In one embodiment, carboxymethylated dextran biosensor chips (CM5, BIACORE, Inc.) are activated with *N*-ethyl-*N'*-(3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and *N*-hydroxysuccinimide (NHS) according to the supplier's instructions. Antigen is diluted with 10 mM sodium acetate, $\text{pH } 4.8$, to $5 \mu\text{g/ml}$ ($\sim 0.2 \mu\text{M}$) before injection at a flow rate of $5 \mu\text{l/minute}$ to achieve approximately 10 response units (RU) of coupled protein. Following the injection of antigen, 1 M ethanolamine is injected to block unreacted groups. For kinetics measurements, two-fold serial dilutions of Fab (0.78 nM to 500 nM) are injected in PBS with 0.05% polysorbate 20 (TWEEN-20™) surfactant (PBST) at 25°C at a flow rate of approximately $25 \mu\text{l/min}$. Association rates (k_{on}) and dissociation rates (k_{off}) are calculated using a simple one-to-one Langmuir binding model (BIACORE® Evaluation Software version 3.2) by simultaneously fitting the association and dissociation sensorgrams. The equilibrium dissociation constant (K_d) is calculated as the ratio $k_{\text{off}}/k_{\text{on}}$. See, for example, Chen et al., (*J. Mol. Biol.* 293:865-881, 1999). If the on-rate exceeds $10^6 \text{ M}^{-1}\text{s}^{-1}$ by the surface plasmon resonance assay above, then the on-rate can be determined by using a fluorescent quenching technique that measures the increase or decrease in fluorescence emission

intensity (excitation = 295 nm; emission = 340 nm, 16 nm band-pass) at 25°C of a 20 nM anti-antigen antibody (Fab form) in PBS, pH 7.2, in the presence of increasing concentrations of antigen as measured in a spectrometer, such as a stop-flow equipped spectrophotometer (Aviv Instruments) or a 8000-series SLM-AMINCO™ spectrophotometer (ThermoSpectronic) with a stirred cuvette.

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ii. Antibody Fragments

In certain embodiments, an antibody (e.g., an anti-PD-L1 antibody or an anti-PD-1 antibody) provided herein is an antibody fragment. Antibody fragments include, but are not limited to, Fab, Fab', Fab'-SH, F(ab')₂, Fv, and scFv fragments, and other fragments described below. For a review of certain antibody fragments, see Hudson et al. (*Nat. Med.* 9:129-134, 2003). For a review of scFv fragments, see, e.g., Pluckthün, in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds., (Springer-Verlag, New York), pp. 269-315 (1994). See also WO 93/16185; and U.S. Patent Nos. 5,571,894 and 5,587,458. For discussion of Fab and F(ab')₂ fragments comprising salvage receptor binding epitope residues and having increased *in vivo* half-life, see U.S. Patent No. 5,869,046.

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Diabodies are antibody fragments with two antigen-binding sites that may be bivalent or bispecific. See, for example, EP 404,097, WO 1993/01161, Hudson et al. *Nat. Med.* 9:129-134, 2003, and Hollinger et al. *Proc. Natl. Acad. Sci. USA* 90: 6444-6448, 1993. Triabodies and tetrabodies are also described in Hudson et al. (*Nat. Med.* 9:129-134, 2003).

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Single-domain antibodies are antibody fragments comprising all or a portion of the heavy chain variable domain or all or a portion of the light chain variable domain of an antibody. In certain embodiments, a single-domain antibody is a human single-domain antibody (Domantis, Inc., Waltham, MA; see, e.g., U.S. Patent No. 6,248,516 B1).

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Antibody fragments can be made by various techniques, including but not limited to proteolytic digestion of an intact antibody as well as production by recombinant host cells (e.g., *E. coli* or phage), according to known methods.

iii. Chimeric and Humanized Antibodies

In certain embodiments, an antibody (e.g., an anti-VEGF antibody, an anti-PD-L1 antibody or an anti-PD-1 antibody) provided herein is a chimeric antibody. Certain chimeric antibodies are described, e.g., in U.S. Patent No. 4,816,567; and Morrison et al. (*Proc. Natl. Acad. Sci. USA*, 81:6851-6855, 1984). In one example, a chimeric antibody comprises a non-human variable region (e.g., a variable region derived from a mouse, rat, hamster, rabbit, or non-human primate, such as a monkey) and a human constant region. In a further example, a chimeric antibody is a "class switched" antibody in which the class or subclass has been changed from that of the parent antibody. Chimeric antibodies include antigen-binding fragments thereof.

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In certain embodiments, a chimeric antibody is a humanized antibody. Typically, a non-human antibody is humanized to reduce immunogenicity to humans, while retaining the specificity and affinity of the parental non-human antibody. Generally, a humanized antibody comprises one or more variable domains in which HVRs, e.g., CDRs, (or portions thereof) are derived from a non-human antibody, and FRs (or portions thereof) are derived from human antibody sequences. A humanized antibody optionally

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will also comprise at least a portion of a human constant region. In some embodiments, some FR residues in a humanized antibody are substituted with corresponding residues from a non-human antibody (e.g., the antibody from which the HVR residues are derived), e.g., to restore or improve antibody specificity or affinity.

Humanized antibodies and methods of making them are reviewed, e.g., in Almagro and Fransson, (*Front. Biosci.* 13:1619-1633, 2008), and are further described, e.g., in Riechmann et al. (*Nature* 332:323-329, 1988); Queen et al. (*Proc. Natl. Acad. Sci. USA* 86:10029-10033, 1989); US Patent Nos. 5, 821,337, 7,527,791, 6,982,321, and 7,087,409; Kashmiri et al. (*Methods* 36:25-34, 2005) (describing specificity determining region (SDR) grafting); Padlan, (*Mol. Immunol.* 28:489-498, 1991) (describing "resurfacing"); Dall'Acqua et al. (*Methods* 36:43-60, 2005) (describing "FR shuffling"); Osbourn et al. (*Methods* 36:61-68, 2005), and Klimka et al. (*Br. J. Cancer*, 83:252-260, 2000) (describing the "guided selection" approach to FR shuffling).

Human framework regions that may be used for humanization include but are not limited to: framework regions selected using the "best-fit" method (see, e.g., Sims et al. *J. Immunol.* 151:2296, 1993); framework regions derived from the consensus sequence of human antibodies of a particular subgroup of light or heavy chain variable regions (see, e.g., Carter et al. *Proc. Natl. Acad. Sci. USA*, 89:4285, 1992; and Presta et al. *J. Immunol.*, 151:2623, 1993); human mature (somatically mutated) framework regions or human germline framework regions (see, e.g., Almagro and Fransson, *Front. Biosci.* 13:1619-1633, 2008); and framework regions derived from screening FR libraries (see, e.g., Baca et al., *J. Biol. Chem.* 272:10678-10684, 1997; and Rosok et al. *J. Biol. Chem.* 271:22611-22618, 1996).

iv. Human Antibodies

In certain embodiments, an antibody (e.g., an anti-VEGF antibody, an anti-PD-L1 antibody or an anti-PD-1 antibody) provided herein is a human antibody. Human antibodies can be produced using various techniques known in the art. Human antibodies are described generally in van Dijk and van de Winkel, (*Curr. Opin. Pharmacol.* 5: 368-74, 2001) and Lonberg (*Curr. Opin. Immunol.* 20:450-459, 2008).

Human antibodies may be prepared by administering an immunogen to a transgenic animal that has been modified to produce intact human antibodies or intact antibodies with human variable regions in response to antigenic challenge. Such animals typically contain all or a portion of the human immunoglobulin loci, which replace the endogenous immunoglobulin loci, or which are present extrachromosomally or integrated randomly into the animal's chromosomes. In such transgenic mice, the endogenous immunoglobulin loci have generally been inactivated. For review of methods for obtaining human antibodies from transgenic animals, see Lonberg, (*Nat. Biotech.* 23:1117-1125, 2005). See also, e.g., U.S. Patent Nos. 6,075,181 and 6,150,584 describing XENOMOUSE™ technology; U.S. Patent No. 5,770,429 describing HUMAB® technology; U.S. Patent No. 7,041,870 describing K-M MOUSE® technology, and U.S. Patent Application Publication No. US 2007/0061900, describing VELOCIMOUSE® technology). Human variable regions from intact antibodies generated by such animals may be further modified, e.g., by combining with a different human constant region.

Human antibodies can also be made by hybridoma-based methods. Human myeloma and mouse-human heteromyeloma cell lines for the production of human monoclonal antibodies have been

described. See, e.g., Kozbor, (*J. Immunol.* 133: 3001, 1984); Brodeur et al. (*Monoclonal Antibody Production Techniques and Applications*, pp. 51-63, Marcel Dekker, Inc., New York, 1987); and Boerner et al. (*J. Immunol.*, 147: 86, 1991). Human antibodies generated via human B-cell hybridoma technology are also described in Li et al., *Proc. Natl. Acad. Sci. USA*, 103:3557-3562, 2006. Additional methods include those described, for example, in U.S. Patent No. 7,189,826 (describing production of monoclonal human IgM antibodies from hybridoma cell lines) and Ni, (*Xiandai Mianyixue*, 26(4):265-268, 2006) (describing human-human hybridomas). Human hybridoma technology (Trioma technology) is also described in Vollmers and Brandlein, (*Histology and Histopathology*, 20(3):927-937, 2005) and Vollmers and Brandlein, (*Methods and Findings in Experimental and Clinical Pharmacology*, 27(3):185-91, 2005).

Human antibodies may also be generated by isolating Fv clone variable domain sequences selected from human-derived phage display libraries. Such variable domain sequences may then be combined with a desired human constant domain. Techniques for selecting human antibodies from antibody libraries are described below.

v. Library-Derived Antibodies

Antibodies of the invention (e.g., anti-VEGF antibodies, anti-PD-L1 antibodies, or anti-PD-1 antibodies) may be isolated by screening combinatorial libraries for antibodies with the desired activity or activities. For example, a variety of methods are known in the art for generating phage display libraries and screening such libraries for antibodies possessing the desired binding characteristics. Such methods are reviewed, e.g., in Hoogenboom et al. (*Methods in Molecular Biology* 178:1-37, O'Brien et al., ed., Human Press, Totowa, NJ, 2001) and further described, e.g., in McCafferty et al. (*Nature* 348:552-554, 1990); Clackson et al. (*Nature* 352: 624-628, 1991); Marks et al. (*J. Mol. Biol.* 222: 581-597, 1992); Marks and Bradbury, (*Methods in Molecular Biology* 248:161-175, Lo, ed., Human Press, Totowa, NJ, 2003); Sidhu et al. (*J. Mol. Biol.* 338(2): 299-310, 2004); Lee et al. (*J. Mol. Biol.* 340(5): 1073-1093, 2004); Fellouse, (*Proc. Natl. Acad. Sci. USA* 101(34): 12467-12472, 2004); and Lee et al. (*J. Immunol. Methods* 284(1-2): 119-132, 2004).

In certain phage display methods, repertoires of VH and VL genes are separately cloned by polymerase chain reaction (PCR) and recombined randomly in phage libraries, which can then be screened for antigen-binding phage as described in Winter et al. (*Ann. Rev. Immunol.*, 12: 433-455, 1994). Phage typically display antibody fragments, either as single-chain Fv (scFv) fragments or as Fab fragments. Libraries from immunized sources provide high-affinity antibodies to the immunogen without the requirement of constructing hybridomas. Alternatively, the naive repertoire can be cloned (e.g., from human) to provide a single source of antibodies to a wide range of non-self and self antigens without any immunization as described by Griffiths et al. (*EMBO J*, 12: 725-734, 1993). Finally, naive libraries can also be made synthetically by cloning unrearranged V-gene segments from stem cells, and using PCR primers containing random sequence to encode the highly variable CDR3 regions and to accomplish rearrangement *in vitro*, as described by Hoogenboom and Winter, (*J. Mol. Biol.*, 227: 381-388, 1992). Patent publications describing human antibody phage libraries include, for example: US Patent No. 5,750,373, and US Patent Publication Nos. 2005/0079574, 2005/0119455, 2005/0266000, 2007/0117126, 2007/0160598, 2007/0237764, 2007/0292936, and 2009/0002360.

Antibodies or antibody fragments isolated from human antibody libraries are considered human antibodies or human antibody fragments herein.

vi. Multispecific Antibodies

5 In any one of the above aspects, an antibody (e.g., an anti-VEGF antibody, an anti-PD-L1 antibody, or an anti-PD-1 antibody) provided herein may be a multispecific antibody, for example, a bispecific antibody. Multispecific antibodies are monoclonal antibodies that have binding specificities for at least two different sites. In certain embodiments, an antibody provided herein is a multispecific antibody, e.g., a bispecific antibody. In certain embodiments, one of the binding specificities is for PD-L1
10 and the other is for any other antigen. In certain embodiments, one of the binding specificities is for VEGF and the other is for any other antigen. In certain embodiments, bispecific antibodies may bind to two different epitopes of PD-L1. In certain embodiments, bispecific antibodies may bind to two different epitopes of VEGF. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express PD-L1 or VEGF. Bispecific antibodies can be prepared as full length antibodies or antibody
15 fragments.

Techniques for making multispecific antibodies include, but are not limited to, recombinant co-expression of two immunoglobulin heavy chain-light chain pairs having different specificities (see Milstein and Cuello, *Nature* 305: 537, 1983), WO 93/08829 and Traunecker et al. *EMBO J.* 10: 3655, 1991) and “knob-in-hole” engineering (see, e.g., U.S. Patent No. 5,731,168). Multi-specific antibodies may also be
20 made by engineering electrostatic steering effects for making antibody Fc-heterodimeric molecules (see, e.g., WO 2009/089004A1); cross-linking two or more antibodies or fragments (see, e.g., US Patent No. 4,676,980, and Brennan et al. *Science* 229: 81, 1985); using leucine zippers to produce bi-specific antibodies (see, e.g., Kostelny et al. *J. Immunol.* 148(5): 1547-1553, 1992); using “diabody” technology for making bispecific antibody fragments (see, e.g., Hollinger et al. *Proc. Natl. Acad. Sci. USA* 90:6444-
25 6448, 1993); and using single-chain Fv (sFv) dimers (see, e.g., Gruber et al. *J. Immunol.* 152:5368, 1994); and preparing trispecific antibodies as described, e.g., in Tutt et al. *J. Immunol.* 147: 60, 1991).

Engineered antibodies with three or more functional antigen binding sites, including “Octopus antibodies,” are also included herein (see, e.g., US 2006/0025576A1).

The antibody or fragment herein includes a “Dual Acting FAb” or “DAF” comprising an antigen
30 binding site that binds to PD-L1 and another, different antigen. The antibody or fragment herein also includes a DAF comprising an antigen binding site that binds to VEGF and another, different antigen.

vii. Antibody Variants

In certain embodiments, amino acid sequence variants of the antibodies of the invention (e.g.,
35 anti-VEGF antibodies, anti-PD-L1 antibodies, and anti-PD-1 antibodies) are contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody. Amino acid sequence variants of an antibody may be prepared by introducing appropriate modifications into the nucleotide sequence encoding the antibody, or by peptide synthesis. Such modifications include, for example, deletions from, and/or insertions into and/or substitutions of residues within the amino acid
40 sequences of the antibody. Any combination of deletion, insertion, and substitution can be made to arrive

at the final construct, provided that the final construct possesses the desired characteristics, for example, antigen-binding.

a. Substitution, insertion, and deletion variants

5 In certain embodiments, antibody variants having one or more amino acid substitutions are provided. Sites of interest for substitutional mutagenesis include the HVRs and FRs. Conservative substitutions are shown in Table 17 under the heading of “preferred substitutions.” More substantial changes are provided in Table 17 under the heading of “exemplary substitutions,” and as further described below in reference to amino acid side chain classes. Amino acid substitutions may be
10 introduced into an antibody of interest and the products screened for a desired activity, for example, retained/improved antigen binding, decreased immunogenicity, or improved ADCC or CDC.

Table 17. Exemplary and Preferred Amino Acid Substitutions

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	Val; Leu; Ile	Val
Arg (R)	Lys; Gln; Asn	Lys
Asn (N)	Gln; His; Asp, Lys; Arg	Gln
Asp (D)	Glu; Asn	Glu
Cys (C)	Ser; Ala	Ser
Gln (Q)	Asn; Glu	Asn
Glu (E)	Asp; Gln	Asp
Gly (G)	Ala	Ala
His (H)	Asn; Gln; Lys; Arg	Arg
Ile (I)	Leu; Val; Met; Ala; Phe; Norleucine	Leu
Leu (L)	Norleucine; Ile; Val; Met; Ala; Phe	Ile
Lys (K)	Arg; Gln; Asn	Arg
Met (M)	Leu; Phe; Ile	Leu
Phe (F)	Trp; Leu; Val; Ile; Ala; Tyr	Tyr
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr
Thr (T)	Val; Ser	Ser
Trp (W)	Tyr; Phe	Tyr
Tyr (Y)	Trp; Phe; Thr; Ser	Phe
Val (V)	Ile; Leu; Met; Phe; Ala; Norleucine	Leu

15 Amino acids may be grouped according to common side-chain properties:

- (1) hydrophobic: Norleucine, Met, Ala, Val, Leu, Ile;
- (2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;
- (3) acidic: Asp, Glu;
- (4) basic: His, Lys, Arg;
- (5) residues that influence chain orientation: Gly, Pro;
- (6) aromatic: Trp, Tyr, Phe.

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Non-conservative substitutions will entail exchanging a member of one of these classes for another class.

One type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (e.g., a humanized or human antibody). Generally, the resulting variant(s) selected for further study will have modifications (e.g., improvements) in certain biological properties (e.g., increased affinity and/or reduced immunogenicity) relative to the parent antibody and/or will have substantially retained certain biological properties of the parent antibody. An exemplary substitutional variant is an affinity matured antibody, which may be conveniently generated, for example, using phage display-based affinity maturation techniques such as those described herein. Briefly, one or more HVR residues are mutated and the variant antibodies displayed on phage and screened for a particular biological activity (e.g., binding affinity).

Alterations (e.g., substitutions) may be made in HVRs, e.g., to improve antibody affinity. Such alterations may be made in HVR "hotspots," i.e., residues encoded by codons that undergo mutation at high frequency during the somatic maturation process (see, e.g., Chowdhury, *Methods Mol. Biol.* 207:179-196, 2008), and/or residues that contact antigen, with the resulting variant VH or VL being tested for binding affinity. Affinity maturation by constructing and reselecting from secondary libraries has been described, e.g., in Hoogenboom et al. (*Methods in Molecular Biology* 178:1-37, O'Brien et al., ed., Human Press, Totowa, NJ, 2001). In some embodiments of affinity maturation, diversity is introduced into the variable genes chosen for maturation by any of a variety of methods (e.g., error-prone PCR, chain shuffling, or oligonucleotide-directed mutagenesis). A secondary library is then created. The library is then screened to identify any antibody variants with the desired affinity. Another method to introduce diversity involves HVR-directed approaches, in which several HVR residues (e.g., 4-6 residues at a time) are randomized. HVR residues involved in antigen binding may be specifically identified, e.g., using alanine scanning mutagenesis or modeling. CDR-H3 and CDR-L3 in particular are often targeted.

In certain embodiments, substitutions, insertions, or deletions may occur within one or more HVRs so long as such alterations do not substantially reduce the ability of the antibody to bind antigen. For example, conservative alterations (e.g., conservative substitutions as provided herein) that do not substantially reduce binding affinity may be made in HVRs. Such alterations may, for example, be outside of antigen-contacting residues in the HVRs. In certain embodiments of the variant VH and VL sequences provided above, each HVR either is unaltered, or contains no more than one, two or three amino acid substitutions.

A useful method for identification of residues or regions of an antibody that may be targeted for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham and Wells (*Science*, 244:1081-1085, 1989). In this method, a residue or group of target residues (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) are identified and replaced by a neutral or negatively charged amino acid (e.g., alanine or polyalanine) to determine whether the interaction of the antibody with antigen is affected. Further substitutions may be introduced at the amino acid locations demonstrating functional sensitivity to the initial substitutions. Alternatively, or additionally, a crystal structure of an antigen-antibody complex to identify contact points between the antibody and antigen. Such contact residues and neighboring

residues may be targeted or eliminated as candidates for substitution. Variants may be screened to determine whether they contain the desired properties.

Amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from one residue to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Examples of terminal insertions include an antibody with an N-terminal methionyl residue. Other insertional variants of the antibody molecule include the fusion to the N- or C-terminus of the antibody to an enzyme (e.g., for ADEPT) or a polypeptide which increases the serum half-life of the antibody.

b. Glycosylation variants

In certain embodiments, antibodies of the invention can be altered to increase or decrease the extent to which the antibody is glycosylated. Addition or deletion of glycosylation sites to an antibody of the invention may be conveniently accomplished by altering the amino acid sequence such that one or more glycosylation sites is created or removed.

Where the antibody comprises an Fc region, the carbohydrate attached thereto may be altered. Native antibodies produced by mammalian cells typically comprise a branched, biantennary oligosaccharide that is generally attached by an N-linkage to Asn297 of the CH2 domain of the Fc region. See, e.g., Wright et al. *TIBTECH* 15:26-32, 1997. The oligosaccharide may include various carbohydrates, e.g., mannose, N-acetyl glucosamine (GlcNAc), galactose, and sialic acid, as well as a fucose attached to a GlcNAc in the "stem" of the biantennary oligosaccharide structure. In some embodiments, modifications of the oligosaccharide in an antibody of the invention may be made in order to create antibody variants with certain improved properties.

In one embodiment, antibody variants are provided having a carbohydrate structure that lacks fucose attached (directly or indirectly) to an Fc region. For example, the amount of fucose in such antibody may be from 1% to 80%, from 1% to 65%, from 5% to 65% or from 20% to 40%. The amount of fucose is determined by calculating the average amount of fucose within the sugar chain at Asn297, relative to the sum of all glycostructures attached to Asn 297 (e. g. complex, hybrid and high mannose structures) as measured by MALDI-TOF mass spectrometry, as described in WO 2008/077546, for example. Asn297 refers to the asparagine residue located at about position 297 in the Fc region (EU numbering of Fc region residues); however, Asn297 may also be located about ± 3 amino acids upstream or downstream of position 297, i.e., between positions 294 and 300, due to minor sequence variations in antibodies. Such fucosylation variants may have improved ADCC function. See, for example, U.S. Patent Publication Nos. US 2003/0157108; US 2004/0093621. Examples of publications related to "defucosylated" or "fucose-deficient" antibody variants include: US 2003/0157108; WO 2000/61739; WO 2001/29246; US 2003/0115614; US 2002/0164328; US 2004/0093621; US 2004/0132140; US 2004/0110704; US 2004/0110282; US 2004/0109865; WO 2003/085119; WO 2003/084570; WO 2005/035586; WO 2005/035778; WO2005/053742; WO2002/031140; Okazaki et al. (*J. Mol. Biol.* 336:1239-1249, 2004); and Yamane-Ohnuki et al. (*Biotech. Bioeng.* 87: 614, 2004). Examples of cell lines capable of producing defucosylated antibodies include Lec13 CHO cells deficient in protein fucosylation (Ripka et al. *Arch. Biochem. Biophys.* 249:533-545, 1986); U.S. Pat. Appl. No. US

2003/0157108 A1; and WO 2004/056312 A1, especially at Example 11), and knockout cell lines, such as alpha-1,6-fucosyltransferase gene, *FUT8*, knockout CHO cells (see, e.g., Yamane-Ohnuki et al. *Biotech. Bioeng.* 87: 614, 2004; Kanda, Y. et al. *Biotechnol. Bioeng.* 94(4):680-688, 2006; and WO 2003/085107).

Antibody variants are further provided with bisected oligosaccharides, for example, in which a biantennary oligosaccharide attached to the Fc region of the antibody is bisected by GlcNAc. Such antibody variants may have reduced fucosylation and/or improved ADCC function. Examples of such antibody variants are described, e.g., in WO 2003/011878; US Patent No. 6,602,684; and US 2005/0123546. Antibody variants with at least one galactose residue in the oligosaccharide attached to the Fc region are also provided. Such antibody variants may have improved CDC function. Such antibody variants are described, e.g., in WO 1997/30087; WO 1998/58964; and WO 1999/22764.

c. Fc region variants

In certain embodiments, one or more amino acid modifications may be introduced into the Fc region of an antibody of the invention, thereby generating an Fc region variant. The Fc region variant may comprise a human Fc region sequence (e.g., a human IgG1, IgG2, IgG3 or IgG4 Fc region) comprising an amino acid modification (e.g., a substitution) at one or more amino acid positions.

In certain embodiments, the invention contemplates an antibody variant that possesses some but not all effector functions, which make it a desirable candidate for applications in which the half-life of the antibody *in vivo* is important yet certain effector functions (such as complement and ADCC) are unnecessary or deleterious. *In vitro* and/or *in vivo* cytotoxicity assays can be conducted to confirm the reduction/depletion of CDC and/or ADCC activities. For example, Fc receptor (FcR) binding assays can be conducted to ensure that the antibody lacks FcγR binding (hence likely lacking ADCC activity), but retains FcRn binding ability. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, (*Annu. Rev. Immunol.* 9:457-492, 1991). Non-limiting examples of *in vitro* assays to assess ADCC activity of a molecule of interest is described in U.S. Patent No. 5,500,362 (see, e.g., Hellstrom, I. et al. *Proc. Natl. Acad. Sci. USA* 83:7059-7063, 1986) and Hellstrom, I et al. *Proc. Natl. Acad. Sci. USA* 82:1499-1502, 1985; U.S. Patent No. 5,821,337; Bruggemann et al. *J. Exp. Med.* 166:1351-1361, 1987). Alternatively, non-radioactive assays methods may be employed (see, for example, ACT1™ non-radioactive cytotoxicity assay for flow cytometry (CellTechnology, Inc. Mountain View, CA; and CYTOTOX 96® non-radioactive cytotoxicity assay (Promega, Madison, WI). Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed *in vivo*, e.g., in an animal model such as that disclosed in Clynes et al. (*Proc. Natl. Acad. Sci. USA* 95:652-656, 1998). C1q binding assays may also be carried out to confirm that the antibody is unable to bind C1q and hence lacks CDC activity. See, e.g., C1q and C3c binding ELISA in WO 2006/029879 and WO 2005/100402. To assess complement activation, a CDC assay may be performed (see, e.g., Gazzano-Santoro et al. *J. Immunol. Methods* 202:163, 1996; Cragg et al. *Blood.* 101:1045-1052, 2003; and Cragg et al. *Blood.* 103:2738-2743, 2004). FcRn binding and *in vivo*

clearance/half-life determinations can also be performed using methods known in the art (see, e.g., Petkova et al. *Int'l. Immunol.* 18(12):1759-1769, 2006).

Antibodies with reduced effector function include those with substitution of one or more of Fc region residues 238, 265, 269, 270, 297, 327 and 329 (U.S. Patent Nos. 6,737,056 and 8,219,149). Such Fc mutants include Fc mutants with substitutions at two or more of amino acid positions 265, 269, 270, 297 and 327, including the so-called "DANA" Fc mutant with substitution of residues 265 and 297 to alanine (US Patent No. 7,332,581 and 8,219,149).

Certain antibody variants with improved or diminished binding to FcRs are described (see, e.g., U.S. Patent No. 6,737,056; WO 2004/056312, and Shields et al., *J. Biol. Chem.* 9(2): 6591-6604, 2001).

In certain embodiments, an antibody variant comprises an Fc region with one or more amino acid substitutions which improve ADCC, e.g., substitutions at positions 298, 333, and/or 334 of the Fc region (EU numbering of residues).

In some embodiments, alterations are made in the Fc region that result in altered (i.e., either improved or diminished) C1q binding and/or Complement Dependent Cytotoxicity (CDC), e.g., as described in US Patent No. 6,194,551, WO 99/51642, and Idusogie et al. (*J. Immunol.* 164: 4178-4184, 2000).

Antibodies with increased half-lives and improved binding to the neonatal Fc receptor (FcRn), which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., *J. Immunol.* 117:587, 1976; and Kim et al. *J. Immunol.* 24:249, 1994), are described in U.S. Pub. No. 2005/0014934A1. Those antibodies comprise an Fc region with one or more substitutions therein which improve binding of the Fc region to FcRn. Such Fc variants include those with substitutions at one or more of Fc region residues: 238, 256, 265, 272, 286, 303, 305, 307, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 413, 424 or 434, e.g., substitution of Fc region residue 434 (U.S. Patent No. 7,371,826).

See also Duncan and Winter, (*Nature* 322:738-40, 1988); U.S. Patent No. 5,648,260; U.S. Patent No. 5,624,821; and WO 94/29351, concerning other examples of Fc region variants.

d. Cysteine engineered antibody variants

In certain embodiments, it may be desirable to create cysteine engineered antibodies, e.g., "thioMAbs," in which one or more residues of an antibody are substituted with cysteine residues. In particular embodiments, the substituted residues occur at accessible sites of the antibody. By substituting those residues with cysteine, reactive thiol groups are thereby positioned at accessible sites of the antibody and may be used to conjugate the antibody to other moieties, such as drug moieties or linker-drug moieties, to create an immunoconjugate, as described further herein. In certain embodiments, any one or more of the following residues may be substituted with cysteine: V205 (Kabat numbering) of the light chain; A118 (EU numbering) of the heavy chain; and S400 (EU numbering) of the heavy chain Fc region. Cysteine engineered antibodies may be generated as described, e.g., in U.S. Patent No. 7,521,541.

e. Antibody derivatives

In certain embodiments, an antibody provided herein may be further modified to contain additional nonproteinaceous moieties that are known in the art and readily available. The moieties suitable for derivatization of the antibody include but are not limited to water soluble polymers. Non-limiting examples of water soluble polymers include, but are not limited to, polyethylene glycol (PEG), copolymers of ethylene glycol/propylene glycol, carboxymethylcellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone, poly-1, 3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, polyaminoacids (either homopolymers or random copolymers), and dextran or poly(n-vinyl pyrrolidone) polyethylene glycol, propylene glycol homopolymers, polypropylene oxide/ethylene oxide copolymers, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, and mixtures thereof. Polyethylene glycol propionaldehyde may have advantages in manufacturing due to its stability in water. The polymer may be of any molecular weight, and may be branched or unbranched. The number of polymers attached to the antibody may vary, and if more than one polymer are attached, they can be the same or different molecules. In general, the number and/or type of polymers used for derivatization can be determined based on considerations including, but not limited to, the particular properties or functions of the antibody to be improved, whether the antibody derivative will be used in a therapy under defined conditions, etc.

In another embodiment, conjugates of an antibody and nonproteinaceous moiety that may be selectively heated by exposure to radiation are provided. In one embodiment, the nonproteinaceous moiety is a carbon nanotube (Kam et al. *Proc. Natl. Acad. Sci. USA* 102: 11600-11605, 2005). The radiation may be of any wavelength, and includes, but is not limited to, wavelengths that do not harm ordinary cells, but which heat the nonproteinaceous moiety to a temperature at which cells proximal to the antibody-nonproteinaceous moiety are killed.

f. Immunoconjugates

The invention also provides immunoconjugates comprising an antibody herein (e.g., an anti-VEGF antibody, an anti-PD-L1 antibody, or an anti-PD-1 antibody) conjugated to one or more cytotoxic agents, such as chemotherapeutic agents or drugs, growth inhibitory agents, toxins (e.g., protein toxins, enzymatically active toxins of bacterial, fungal, plant, or animal origin, or fragments thereof), or radioactive isotopes.

In one embodiment, an immunoconjugate is an antibody-drug conjugate (ADC) in which an antibody is conjugated to one or more drugs, including but not limited to a maytansinoid (see U.S. Patent Nos. 5,208,020 and 5,416,064 and European Patent EP 0 425 235 B1); an auristatin such as monomethylauristatin drug moieties DE and DF (MMAE and MMAF) (see U.S. Patent Nos. 5,635,483, 5,780,588, and 7,498,298); a dolastatin; a calicheamicin or derivative thereof (see U.S. Patent Nos. 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, and 5,877,296; Hinman et al. *Cancer Res.* 53:3336-3342, 1993; and Lode et al. *Cancer Res.* 58:2925-2928, 1998); an anthracycline such as daunomycin or doxorubicin (see Kratz et al. *Current Med. Chem.* 13:477-523, 2006; Jeffrey et al. *Bioorganic & Med. Chem. Letters* 16:358-362, 2006; Torgov et al., *Bioconj. Chem.* 16:717-721 (2005); Nagy et al., *Proc. Natl. Acad. Sci. USA* 97:829-834 (2000); Dubowchik et al., *Bioorg. & Med. Chem.*

Letters 12:1529-1532, 2002; King et al., *J. Med. Chem.* 45:4336-4343, 2002; and U.S. Patent No. 6,630,579); methotrexate; vindesine; a taxane such as docetaxel, paclitaxel, larotaxel, tesetaxel, and ortataxel; a trichothecene; and CC1065.

In another embodiment, an immunoconjugate comprises an antibody as described herein conjugated to an enzymatically active toxin or fragment thereof, including but not limited to diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolacca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes.

In another embodiment, an immunoconjugate comprises an antibody as described herein conjugated to a radioactive atom to form a radioconjugate. A variety of radioactive isotopes are available for the production of radioconjugates. Examples include At²¹¹, I¹³¹, I¹²⁵, Y⁹⁰, Re¹⁸⁶, Re¹⁸⁸, Sm¹⁵³, Bi²¹², P³², Pb²¹² and radioactive isotopes of Lu. When the radioconjugate is used for detection, it may comprise a radioactive atom for scintigraphic studies, for example tc99m or I123, or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance imaging, MRI), such as iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron. Conjugates of an antibody and cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al. (*Science* 238:1098, 1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026. The linker may be a "cleavable linker" facilitating release of a cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari et al. *Cancer Res.* 52:127-131, 1992; and U.S. Patent No. 5,208,020) may be used.

The immunoconjugates or ADCs herein expressly contemplate, but are not limited to such conjugates prepared with cross-linker reagents including, but not limited to, BMPS, EMCS, GMBS, HBVS, LC-SMCC, MBS, MPBH, SBAP, SIA, SIAB, SMCC, SMPB, SMPH, sulfo-EMCS, sulfo-GMBS, sulfo-KMUS, sulfo-MBS, sulfo-SIAB, sulfo-SMCC, and sulfo-SMPB, and SVSB (succinimidyl-(4-vinylsulfone)benzoate) which are commercially available (e.g., from Pierce Biotechnology, Inc., Rockford, IL., U.S.A.).

D. Multi-targeted Tyrosine Kinase Inhibitors

Any suitable multi-targeted tyrosine kinase inhibitor can be used in the methods described herein. For example, the multi-targeted tyrosine kinase inhibitor may inhibit platelet-derived growth factor receptors (e.g., PDGFR- $\alpha\alpha$, PDGFR- $\beta\beta$, and PDGFR- $\alpha\beta$), VEGF receptors (e.g., VEGFR1 and VEGFR2),
 5 CD117 (c-Kit), RET, CD114, and/or CD135. Exemplary multi-targeted tyrosine kinase inhibitors include sunitinib (also known as N-[2-(Diethylamino)ethyl]-5-[(Z)-(5-fluoro-2-oxo-1,2-dihydro-3H-indol-3-ylidene)methyl]-2,4-dimethyl-1H-pyrrole-3-carboxamide, SUTENT®, or SU11248), SU6656, motesanib, sorafenib (e.g., NEXEVAR® or BAY439006), axitinib, afatinib, bosutinib, crizotinib, cabozantinib, dasatinib, entrectinib, pazopanib, lapatinib, and vandetanib (also known as ZACTIMA® or ZD6474). In
 10 some embodiments, the multi-targeted tyrosine kinase inhibitor is a VEGFR inhibitor.

E. Pharmaceutical Formulations

Therapeutic formulations of the VEGF antagonists and the PD-L1 axis binding antagonists used in accordance with the present invention (e.g., an anti-VEGF antibody, such as bevacizumab, and an
 15 anti-PD-L1 antibody, such as atezolizumab) are prepared for storage by mixing the antagonist having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients, or stabilizers in the form of lyophilized formulations or aqueous solutions. Therapeutic formulations of the multi-targeted tyrosine kinase inhibitors used in accordance with the present invention (e.g., sunitinib) are also prepared for storage by mixing the antagonist having the desired degree of purity with optional pharmaceutically
 20 acceptable carriers, excipients, or stabilizers in the form of lyophilized formulations or aqueous solutions. For general information concerning formulations, see, e.g., Gilman et al. (eds.) *The Pharmacological Bases of Therapeutics*, 8th Ed., Pergamon Press, 1990; A. Gennaro (ed.), *Remington's Pharmaceutical Sciences*, 18th Edition, Mack Publishing Co., Pennsylvania, 1990; Avis et al. (eds.) *Pharmaceutical Dosage Forms: Parenteral Medications* Dekker, New York, 1993; Lieberman et al. (eds.) *Pharmaceutical Dosage Forms: Tablets* Dekker, New York, 1990; Lieberman et al. (eds.), *Pharmaceutical Dosage Forms: Disperse Systems* Dekker, New York, 1990; and Walters (ed.) *Dermatological and Transdermal Formulations* (Drugs and the Pharmaceutical Sciences), Vol 119, Marcel Dekker, 2002.

Acceptable carriers, excipients, or stabilizers are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids;
 30 antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine;
 35 monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™, or polyethylene glycol (PEG).

The formulation herein may also contain more than one active compound, preferably those with complementary activities that do not adversely affect each other. The type and effective amounts of such medicaments depend, for example, on the amount and type of antagonist present in the formulation, and clinical parameters of the patients.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nanoparticles and nanocapsules) or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed., 1980.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the antagonist, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Patent No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

V. ARTICLES OF MANUFACTURE AND KITS

In another aspect of the invention, a kit or an article of manufacture containing materials useful for the treatment, prevention, and/or diagnosis of individuals is provided.

In some instances, such kits or articles of manufacture can be used to identify an individual having a cancer (e.g., kidney cancer (e.g., RCC), lung cancer (e.g., NSCLC), bladder cancer (e.g., UBC), liver cancer (e.g., HCC), ovarian cancer, or breast cancer (e.g., TNBC)) who may benefit from an anti-cancer therapy that includes a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., anti-PD-1 antibody)). In other instances, such articles of manufacture or kits can be used to identify an individual having a cancer (e.g., kidney cancer (e.g., RCC), lung cancer (e.g., NSCLC), bladder cancer (e.g., UBC), or breast cancer (e.g., TNBC)) who may benefit from an anti-cancer therapy that includes an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))). Such articles of manufacture or kits may include (a) reagents for determining the expression level of one or more genes set forth in Table 1, or any combination thereof (e.g., any combination set forth in any one of Tables 2-12) in a sample from the individual and (b) instructions for using the reagents to identify an individual having a cancer (e.g., lung cancer (e.g., NSCLC), bladder cancer (e.g., UBC), kidney cancer (e.g., RCC), liver cancer (e.g., HCC),

ovarian cancer, or breast cancer (e.g., TNBC)) who may benefit from a treatment including a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., anti-PD-1 antibody)), or with an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))).

In one aspect, provided herein is a kit for identifying an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), liver cancer (e.g., HCC), ovarian cancer, or a breast cancer (e.g., TNBC)) who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) or a PD-1 binding antagonist (e.g., anti-PD-1 antibody)) that includes (a) reagents for determining the expression level of determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, or 37) of the following genes in a sample from the individual: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2; VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9; and, optionally, (b) instructions for using the reagents to identify an individual having a cancer who may benefit from a treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist.

Any of the preceding kits may include reagents for determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2. In some embodiments, the kit includes reagents for determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2.

For example, any of the preceding kits may include reagents for determining the expression level of one or more (e.g., 1, 2, 3, 4, or 5) of CD8A, EOMES, PRF1, IFNG, or PD-L1. In some embodiments, the kit includes determining the expression level of at least two, at least three, at least four, or all five of CD8A, EOMES, PRF1, IFNG, and PD-L1. In some embodiments, the kit includes reagents for determining the expression level of two of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 2. In some embodiments, the kit includes reagents for determining the expression level of three of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of the exemplary combinations shown in Table 3. In some embodiments, the kit includes reagents for determining the expression level of four of CD8A, EOMES, PRF1, IFNG, and PD-L1, for example, any of

the exemplary combinations shown in Table 4. In some embodiments, the kit includes reagents for determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

In some embodiments, any of the preceding kits may include reagents for determining the expression level of PD-L1 and one or more additional genes, wherein the one or more additional genes is other than PD-L1. For example, in some embodiments, the kit may include reagents for determining the expression level of PD-L1 and one or more additional genes (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36) selected from the group consisting of: CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, TAP2, VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, CD34, IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9. In some embodiments, the kit includes reagents for determining the expression level of PD-L1 and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19) additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2. In other embodiments, the kit includes reagents for determining the expression level of PD-L1 and one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. In other embodiments, the kit includes determining the expression level of PD-L1 and one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9.

Any of the preceding kits may include reagents for determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. In some embodiments, the kit includes reagents for determining the expression level of at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. For example, in some embodiments, the kit includes reagents for determining the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the kit includes reagents for determining the expression level of at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the kit includes reagents for determining the expression level of two of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5. In some embodiments, the kit includes reagents for determining the expression level of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6. In some embodiments, the kit includes reagents for determining the expression level of four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 7. In some embodiments, the kit includes reagents for determining the expression level of five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8. In some embodiments, the kit includes reagents for determining the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

Any of the preceding kits may include reagents for determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, or S100A9. In some embodiments, the kit includes reagents for determining the

expression level of at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9. In some embodiments, the kit includes reagents for determining the expression level of two of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 9. In some embodiments, the kit includes reagents for determining the expression level of three of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 10. In some embodiments, the kit includes reagents for determining the expression level of four of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 11. In some embodiments, the kit includes reagents for determining the expression level of five of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 12. In some embodiments, the kit includes reagents for determining the expression level of six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 13. In some embodiments, the kit includes reagents for determining the expression level of seven of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 14. In some embodiments, the kit includes reagents for determining the expression level of eight of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 15. In some embodiments, the kit includes reagents for determining the expression level of nine of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9, for example, any of the exemplary combinations shown in Table 16. In some embodiments, the kit includes reagents for determining the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, PTGS2, CXCR1, CXCR2, S100A8, and S100A9.

In one aspect, provided herein is a kit for identifying an individual having a cancer (e.g., a kidney cancer (e.g., RCC), a lung cancer (e.g., NSCLC), a bladder cancer (e.g., UBC), liver cancer (e.g., HCC), ovarian cancer, or a breast cancer (e.g., TNBC)) who may benefit from treatment with an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib)))) that includes (a) reagents for determining the expression level of determining the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of the following genes in a sample from the individual: VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; and, optionally, (b) instructions for using the reagents to identify an individual having a cancer who may benefit from a treatment with an anti-cancer therapy comprising an angiogenesis inhibitor.

In some embodiments, the kit includes reagents for determining the expression level of at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34. For example, in some embodiments, the kit includes reagents for determining the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34. In some embodiments, the kit includes reagents for determining the expression level of at least two, at least three, at least four, at least five, or all six of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34. In some embodiments, the kit includes reagents for determining the expression level of two of VEGFA, KDR,

ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 5. In some embodiments, the kit includes reagents for determining the expression level of three of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 6. In some embodiments, the kit includes reagents for determining the expression level of four of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 7. In some embodiments, the kit includes reagents for determining the expression level of five of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34, for example, any of the exemplary combinations shown in Table 8. In some embodiments, the kit includes reagents for determining the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

In some instances, such kits or articles of manufacture include a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist, e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) for treating an individual with a cancer (e.g., lung cancer (e.g., NSCLC), bladder cancer (e.g., UBC), kidney cancer (e.g., RCC), liver cancer (e.g., HCC), ovarian cancer, or breast cancer (e.g., TNBC)). In some instances, such articles of manufacture or kits further include a package insert including instructions for administration of an anti-cancer therapy comprising the VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and the PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist, e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A)) to an individual having a cancer (e.g., lung cancer (e.g., NSCLC), bladder cancer (e.g., UBC), kidney cancer (e.g., RCC), liver cancer (e.g., HCC), ovarian cancer, or breast cancer (e.g., TNBC)), wherein the patient is identified as one who may benefit from the anti-cancer therapy by any of the methods and/or kits described herein.

In other instances, such kits or articles of manufacture include an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) for treating an individual with a cancer (e.g., lung cancer (e.g., NSCLC), bladder cancer (e.g., UBC), kidney cancer (e.g., RCC), liver cancer (e.g., HCC), ovarian cancer, or breast cancer (e.g., TNBC)) for treating an individual with a cancer (e.g., lung cancer (e.g., NSCLC), bladder cancer (e.g., UBC), kidney cancer (e.g., RCC), liver cancer (e.g., HCC), ovarian cancer, or breast cancer (e.g., TNBC)). In some instances, such articles of manufacture or kits further include a package insert including instructions for administration of an anti-cancer therapy comprising the an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))), wherein the patient is identified as one who may benefit from the anti-cancer therapy by any of the methods and/or kits described herein.

In other instances, such kits or articles of manufacture include a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist, e.g., an anti-PD-L1 antibody, e.g., atezolizumab (MPDL3280A), or a PD-1 binding antagonist, e.g., an anti-PD-1 antibody) monotherapy for treating an individual with a cancer (e.g., lung cancer (e.g., NSCLC), bladder cancer (e.g., UBC), kidney cancer (e.g., RCC), liver cancer (e.g., HCC), ovarian cancer, or breast cancer (e.g., TNBC)) for treating an individual with a cancer (e.g., lung cancer (e.g., NSCLC), bladder cancer (e.g., UBC), kidney cancer (e.g., RCC), liver cancer (e.g.,

HCC), ovarian cancer, or breast cancer (e.g., TNBC)). In some instances, such articles of manufacture or kits further include a package insert including instructions for administration of the PD-L1 axis binding antagonist monotherapy, wherein the patient is identified as one who may benefit from the anti-cancer therapy by any of the methods and/or kits described herein.

5 Any of the kits or articles of manufacture described may include a carrier means being compartmentalized to receive in close confinement one or more container means such as vials, tubes, and the like, each of the container means comprising one of the separate elements to be used in the method. Where the article of manufacture or kit utilizes nucleic acid hybridization to detect the target nucleic acid, the kit may also have containers containing nucleotide(s) for amplification of the target
10 nucleic acid sequence and/or a container comprising a reporter-means, such as an enzymatic, florescent, or radioisotope label.

In some instances, the article of manufacture or kit includes the container described above and one or more other containers including materials desirable from a commercial and user standpoint, including buffers, diluents, filters, needles, syringes, and package inserts with instructions for use. A label
15 may be present on the container to indicate that the composition is used for a specific application, and may also indicate directions for either in vivo or in vitro use, such as those described above. For example, the article of manufacture or kit may further include a container including a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution, and dextrose solution.

20 The kits or articles of manufacture described herein may have a number of embodiments. In one instance, the kits or articles of manufacture includes a container, a label on said container, and a composition contained within said container, wherein the composition includes one or more polynucleotides that hybridize to a complement of a gene listed herein (e.g., a gene set forth in Table 1, or any combination of genes set forth in Tables 2-12) under stringent conditions, and the label on said
25 container indicates that the composition can be used to evaluate the presence of a gene listed herein (e.g., a gene set forth in Table 1, or any combination of genes set forth in Tables 2-12) in a sample, and wherein the kit includes instructions for using the polynucleotide(s) for evaluating the presence of the gene RNA or DNA in a particular sample type.

For oligonucleotide-based articles of manufacture or kits, the article of manufacture or kit can
30 include, for example: (1) an oligonucleotide, e.g., a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a protein or (2) a pair of primers useful for amplifying a nucleic acid molecule. The article of manufacture or kit can also include, e.g., a buffering agent, a preservative, or a protein stabilizing agent. The article of manufacture or kit can further include components necessary for detecting the detectable label (e.g., an enzyme or a substrate). The article of manufacture or kit can also
35 contain a control sample or a series of control samples that can be assayed and compared to the test sample. Each component of the article of manufacture or kit can be enclosed within an individual container and all of the various containers can be within a single package, along with instructions for interpreting the results of the assays performed using the kit.

VI. EXAMPLES

The following is an example of the methods of the invention. It is understood that various other embodiments may be practiced, given the general description provided above.

5 Example 1: Materials and Experimental Methods

A. Study Design

The goal of the phase Ib study described in Examples 1-4 was to evaluate the safety and tolerability of the anti-PD-L1 antibody atezolizumab, in combination with bevacizumab, a human, monoclonal, engineered anti-VEGF antibody concurrently administered by intravenous infusion every 3
10 weeks (q3w) to patients with previously untreated advanced metastatic renal cell carcinoma (mRCC). Treatment was continued as long as patients were experiencing clinical benefit in the opinion of the investigator (i.e. in the absence of unacceptable toxicity or symptomatic deterioration attributed to disease progression). Patients were allowed to continue to receive study treatment at the discretion of the investigator if pseudoprogression was suspected or if there was evidence of a mixed response. Study
15 objectives included an evaluation of tumor and circulating pharmacodynamic markers associated with the administration of bevacizumab and atezolizumab and preliminary assessment of the antitumor activity of the treatment combination.

Safety evaluations (clinical and laboratory) were performed at screening and throughout the trial. A final evaluation occurred by 30 days after the last dose. The incidence, nature and severity of adverse
20 events (AEs) were graded according to National Cancer Institute Common Terminology Criteria for Adverse Events (CTCAE), version 4.0.

Any evaluable or measurable disease was documented at screening and reassessed at each tumor evaluation. Tumor evaluations were performed at the ends of cycles 2, 4, 6, 8, 12 and 16 or as clinically indicated. Assessments were performed during the last week of the drug administration cycle
25 and before the start of treatment in the next cycle. Patients who discontinued study treatment for reasons other than disease progression continued to have tumor assessments every 12 weeks until the patient experienced disease progression, initiated further systemic cancer therapy, or died.

Protocol-defined dose-limiting toxicity (DLT) criteria included standard Grade ≥ 3 or 4 hematologic and non-hematologic toxicities. Dosing commenced with the recommended Phase 2 dose of
30 atezolizumab administered in combination with the labeled q3w dose of bevacizumab, and no DLTs were reported.

B. Patients

Patients were eligible to participate in this cohort of the phase Ib study if they had advanced or
35 metastatic RCC for which they had not received prior systemic therapy. Patients were required to be at least 18 years old; have adequate hematological and end-organ function; and have an Eastern Cooperative Oncology Group performance status of 0 or 1. Disease had to be measurable per Response Evaluation Criteria in Solid Tumors (RECIST). Patients with known primary central nervous system (CNS) malignancy or symptomatic CNS metastases, history or risk of autoimmune disease, or history of
40 human immunodeficiency virus, hepatitis B, or hepatitis C infection were excluded. Also excluded were

patients who received prior treatment with anti-CTLA-4, anti-PD-1, or anti-PD-L1 therapeutic antibodies or pathway-targeting agents as well as patients who were treated with systemic immunostimulatory agents or systemic immunosuppressive medications within a specified period before study start.

Of the ten patients on study, six yielded biopsies with sufficient viable tumor cells at both post treatment time points. Of the six pairs (i.e., biopsies from the same patient at both on-treatment time points), seven were derived from kidney lesions, four from the abdominal/chest wall, one from a lung lesion, one from lymph node, and five were from undisclosed lesions.

C. Immunohistochemical Analysis for PD-L1, CD8, and MHC-I

Formalin-fixed, paraffin-embedded (FFPE) tissue sections of 4 µm thickness were stained for PD-L1 with an anti-human PD-L1 rabbit monoclonal antibody (clone SP142; Ventana, Tucson, AZ) on an automated staining platform (BenchMark; Ventana) using a concentration of 4.3 mg/ml, with signal visualization by diaminobenzidine; sections were counter-stained with haematoxylin. PD-L1 expression was evaluated on tumor cells and tumor-infiltrating immune cells. For tumor cells, the proportion of PD-L1-positive tumor cells was estimated as a percentage of the total number of tumor cells; tumor cells typically showed membranous staining with a variably strong component of cytoplasmic staining. The distribution of PD-L1-positive tumor cells within a given tumor sample was typically very focal; in tumors growing as solid aggregates, PD-L1-positive tumor cells were more commonly observed at the interface between malignant cells and stroma containing tumor-infiltrating immune cells. For tumor-infiltrating immune cells, the percentage of PD-L1-positive tumor-infiltrating immune cells occupying the tumor was determined. Tumor-infiltrating immune cells with clearly discernible cytoplasm, such as macrophages and dendritic cells, showed a membranous staining pattern for PD-L1. This was more difficult to determine for cells of small lymphoid morphology with scant amounts of cytoplasm. PD-L1-positive tumor-infiltrating immune cells were typically seen as variably-sized aggregates towards the periphery of the tumor mass, in stromal bands dissecting the tumor mass, as single cells scattered in stroma, or within tumor-infiltrating immune cell aggregates. Specimens were scored as IHC 0, 1, 2, or 3 if < 1%, ≥ 1% but < 5%, ≥ 5% but < 10%, or ≥ 10% of cells per area were PD-L1 positive, respectively. PD-L1 IHC scores in patients with multiple specimens were based on the highest score. CD8 (clone SP16 (Epitomics)) IHC was performed on a Discovery XT autostainer (Ventana) using CC1 antigen retrieval and OMNIMAP™ (Ventana) detection technology.

All MHC-I IHC steps were carried out on the Ventana Discovery XT automated platform (Ventana Medical Systems; Tucson, AZ). Sections were treated with Cell Conditioner 1, standard time, and then incubated in primary antibody, MHC Class I (EP1395Y, Novus, cat. # NB110-57201) at a 1:5000 dilution for 60 min at 37°C. Bound primary antibody was detected by the OMNIMAP™ anti-rabbit HRP detection kit, followed by DAB (Ventana Medical Systems; Tucson, AZ). Sections were counterstained with Hematoxylin II (Ventana Medical Systems; Tucson, AZ) for 4 min, bluing solution for 4 min, then dehydrated and cover-slipped. Human cell pellets endogenously expressing low, medium, and high MHC-I were used in parallel as positive controls. Negative controls were performed using rabbit monoclonal (Clone DA1E, Cell Signaling Technology, Cat#3900S) isotype antibody. MHC-I staining in tumor cells was scored using an H-score system. Briefly, staining intensity of tumor cell membranes was

assigned a numerical value of 0, 1, 2, or 3 corresponding to no, low, medium, or high 3,3'-diaminobenzidine (DAB) signal intensity, respectively. Relative to the overall tumor area, the percentage of cells at different staining intensities was determined by visual assessment. A final score was calculated by multiplying the membrane intensity score by the area percentage for each population present in a given tumor sample as follows: $1 \times (\% \text{ of } 1 + \text{cells}) + 2 \times (\% \text{ of } 2 + \text{cells}) + 3 \times (\% \text{ of } 3 + \text{cells}) = \text{H score}$. Cases were scored by two independent pathologists. Scoring brackets were defined as scores of ≤ 100 , 101-200, and 201-300, and concordance was defined as independent scores falling within the same bracket. Any discordance was resolved upon mutual review of the cases.

10 *D. Dual- and Triple-Color Immunohistochemistry and a Whole Slide Digital Analysis*

Consecutive 4 μm thickness sections of FFPE tumor tissues were stained with the following in-house developed IHC assays using Ventana Benchmark XT or Benchmark Ultra automated platforms (Ventana Medical Systems; Tucson, AZ): Ki67/CD8, PDPN/CD34/ASMA, and CD163/CD68.

For the Ki67/CD8 assay, sections were treated with Cell Conditioner 1 for 64 min. Sections were then incubated in primary antibody, Ki67 (30-9, RTU, Ventana) for 4 min at 37°C. Bound primary antibody was detected by the OptiView DAB IHC detection kit (Ventana Medical Systems; Tucson, AZ). Subsequently, slides were incubated in primary antibody anti-CD8 (SP239, Spring Biosciences) at a 1:100 dilution for 60 min at 37°C. Bound primary antibody was detected by the UltraView Universal AP Red detection kit (Ventana Medical Systems; Tucson, AZ). Sections were counterstained with Hematoxylin II (Ventana Medical Systems; Tucson, AZ) for 4 min, bluing solution for 4 min, then dehydrated and cover-slipped.

For the PDPN/CD34/ASMA assay, sections were treated with Cell Conditioner 1 for 32 min. Sections were then incubated in the primary antibody anti-Podoplanin (D2-40, RTU, Ventana) for 16 min at 37°C. Bound primary antibody was detected by the OptiView DAB IHC detection kit (Ventana Medical Systems; Tucson, AZ). Subsequently, slides were incubated in primary antibody anti-CD34 (QBEnd/10; RTU, Ventana) for 16 min at 37°C. Bound primary antibody was detected by the iView Blue Plus detection kit (Ventana Medical Systems; Tucson, AZ). Finally, slides were incubated in primary antibody anti-smooth muscle actin ("SMAActin") (1A4; RTU, Ventana) for 16 min at 37°C. Bound primary antibody was detected by the UltraView Universal AP Red detection kit (Ventana Medical Systems; Tucson, AZ). Sections were counterstained with Hematoxylin II (Ventana Medical Systems; Tucson, AZ) for 4 min, bluing solution for 4 min, then dehydrated and cover-slipped.

For the CD163/CD68 assay, sections were treated with Cell Conditioner 1 for 32 min and incubated in primary antibody anti-CD163 (MRQ-26, RTU, Ventana), for 8 min at 37°C. Bound primary antibody was detected by the OptiView DAB IHC detection kit (Ventana Medical Systems; Tucson, AZ). Subsequently, slides were incubated in primary antibody anti-CD68 (KP-1, RTU, Ventana) for 8 min at 37°C. Bound primary antibody was detected by the UltraView Universal AP Red detection kit (Ventana Medical Systems; Tucson, AZ). Sections were counterstained with Hematoxylin II (Ventana Medical Systems; Tucson, AZ) for 4 min, bluing solution for 4 min, then dehydrated and cover-slipped. Appropriate negative and positive controls were performed according to known methods.

Algorithms for the detection and classification of IHC-stained objects on a whole slide basis were written in Matlab. Following brightfield stain unmixing, IHC-stained objects were detected as cell candidates. For all cell candidates, quantitative features were extracted. Candidates were then classified into the various cell classes (e.g. CD8⁺/Ki67⁻ cells) using supervised machine learning. The classification method was trained using a ground truth gallery of true and false stained objects (provided by a pathologist). Finally, classified cells and tumor areas (provided by a pathologist through digital slide annotation) were reported and quality control (QC) images were generated for pathology review. The results of automated digital slide analysis were reported for tumor areas as follows: Ki67⁻/CD8⁺ and Ki67⁺/CD8⁺ cell densities (number of cell counts per mm²), CD68⁺/CD163⁺ and CD68⁺/CD163⁻ percent of area coverage (area coverage in relation to the whole tumor area), CD34⁺/αSMA⁻ and CD34⁺/αSMA⁺ vessel densities (vessel count per mm²).

E. RNA Isolation from FFPE Tumor Tissue

RNA isolation was performed as described by Schleifman et al. (*PLoS One* 8:e74231, 2014). Briefly, tumor FFPE sections were macro dissected to enrich for neoplastic tissue, and tissue was lysed using tumor lysis buffer and Proteinase K to allow for complete digestion and release of nucleic acids. RNA was isolated using the High Pure FFPE RNA Micro Kit (Roche Applied Sciences, Indianapolis, IN) according to the manufacturer's protocol. DNA was isolated using the QIAAMP® DNA FFPE Tissue Kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol. RNA and DNA were stored at 280 uC until the analyses were performed.

F. Fluidigm and Nanostring Expression Analysis

Gene-expression analysis was performed using the BioMark HD™ real-time PCR Platform (Fluidigm) as described by Schleifman et al. (*PLoS One* 8:e74231, 2014). All TAQMAN® assays in the expression panel used FAM™ dye-labeled TAQMAN® minor groove binder (MGB) probes and ordered through Life Technologies either made-to-order or custom-designed, including four reference genes: SP2, GUSB, TMEM55B and VPS33B. A geometric median of the Ct values for the four reference genes (SP2, GUSB, TMEM55B and VPS33B) was calculated for each sample, and expression levels were determined using the delta Ct (ΔCt) method as follows: Ct (target Gene) - 2GeoMedian Ct (reference genes). Median mRNA expression levels (as measured by immunochip (iChip)) across patients on study were used as cutoffs to derive high- versus low-expression categorization. P values were determined by t test.

NanoString gene expression data were processed using the R/Bioconductor package "NanoStringQCPro." Raw counts were adjusted by positive control counts before probe- and lane-specific background was calculated based on both negative controls and blank measurements. After background correction, counts were log₂ transformed and normalized by housekeeping gene expression (TMEM55B, VPS33B, TBP, and TUBB).

G. TCR Sequencing

The amplification and sequencing of TCR β repertoire were performed at Adaptive Biotechnologies as described by Klinger et al. (*PLoS One* 8:e74231, 2013).

H. Flow Cytometry

Whole blood flow cytometry for CD3, CD8, HLA-DR, and Ki-67 expression was performed at LabCorp central laboratory according to established protocols. Peripheral blood mononuclear cells (PBMCs) were isolated at Precision Bioservices and cryopreserved samples were shipped to Genentech for analysis of fractalkine receptor expression and detection of tumor-specific T cells. PBMCs were thawed and rested overnight, and a small aliquot of cells were stained with anti-HLA-A2-FITC (BB7.2, BD) and anti-CD45-APC-H7 (2D1, BD) to determine HLA-A2 status. The remaining cells were stained with a mixture of HLA-A*0201/peptide dextramers and pentamers (Immudex and Proimmune, see Table 18) for 10 min at room temperature followed by staining with anti-CD3-BV510 (UCHL1, Biolegend), anti-CD8-A700 (RPA-T8, BD), anti-CD4-PE-Cy7 (RPA-T4, eBioscience), anti-CD45RA-eVolve605 (HI100, eBioscience), anti-CCR7-BV421 (G043H7, Biolegend), anti-CX3CR1-PerCP-eFluor710 (2A9-1, eBioscience), and Fixable Viability Dye eFluor780 (eBioscience) for 30 minutes on ice. Samples were washed twice prior to data acquisition and sorting on a BD FACSARIA™ running FACSDIVA™ v8 software. A minimum of 10 dextramer-positive events out of 50,000 CD8⁺ T cells is considered a tumor-specific response. Table 18 shows a list of dextramers used for flow cytometry.

Table 18. Dextramers for flow cytometry

RCC-specific/associated antigens		
Dex-FITC	Dex-PE	Dex-APC
APOL1	MAGE-A1	G250 217-225
APOL1	PRAME-1	NY-ESO-1
MUC-1 12-20	PRAME-2	PRAME-4
MUC-1 13-21	PRAME-3	PRAME-5
SSX-2	Survivin	PRAME-6
SSX-2	CCND1	Survivin
DLK1	Hsp70-2	MET
EphA2	IDO	PLIN
NRP1	FLT1	PRUNE2
TEM1	KDR	

I. Statistical Analysis

Data from all ten patients with RCC who received more than one dose of atezolizumab and bevacizumab intravenously every 21 days were used to determine baseline characteristics and rates of adverse events. Efficacy was assessed according to RECIST v1.1. The best confirmed overall objective response rate was derived from investigator-reported assessments. Objective response rate (ORR) was defined as the number of patients with a best overall objective response of complete or partial response divided by the total number of patients with a baseline tumor assessment.

Patients who were alive and did not experience disease progression at the cutoff date were

censored at the time of last tumor assessment. Duration of response was obtained by Kaplan Meier method. Summaries of all AEs, AEs related to treatment, and grade 3-4 AEs are provided from all ten patients.

5 **Example 2: Gene Expression Analysis Identifies Biomarkers Associated with Bevacizumab Monotherapy and Bevacizumab and Atezolizumab Combination Therapy**

A phase 1b clinical study was performed in which 10 patients with previously untreated mRCC received a single dose of bevacizumab on C1D1, followed by combined administration of atezolizumab and bevacizumab every three weeks beginning on C2D1. Baseline demographics of the patient cohort are shown in Table 19. Partial responses (PR) were observed in four out of ten patients using RECIST v1.1, while an additional five patients had prolonged stable disease (SD) (Figs. 1 and 2). The clinical activity observed in this small cohort was higher than previously obtained with either monotherapy. The duration of response has not been reached and the median time to response was 4.2 months.

15 **Table 19. Baseline Demographics**

Characteristics	N = 10
Median age (range), y	62 (42-74)
Male, n (%)	7 (70%)
Patients with metastatic disease, n (%)	8 (80%)
Liver or lung	5 (50%)
Other than liver	6 (60%)

In addition to safety, tolerability, and clinical activity, one key objective of the phase 1b study described above was to evaluate the mechanism of combination activity. The trial design included a run-in period with bevacizumab to specifically interrogate the effects of bevacizumab on the local tumor immune microenvironment, followed by combination therapy with immune checkpoint blockade using atezolizumab. Tumor biopsies and blood were collected prior to treatment, 15-18 days following bevacizumab, and 4-6 weeks after the atezolizumab and bevacizumab combination treatment had been initiated.

To identify tumor markers associated with bevacizumab monotherapy or combination therapy, gene expression analysis was performed using both a 90 gene PCR-based Fluidigm panel and an 800 gene custom NanoString panel. Genes associated with the neo-vasculature, which reflect VEGF downstream signaling activity, were significantly decreased at both on-treatment time points in all patients (Fig. 3), confirming anti-angiogenic activity of bevacizumab. Surprisingly, comparison of the pre-treatment time point and the bevacizumab treatment alone time point revealed that there was increased gene expression of Th1 chemokines (CXCL9, CXCL10, CXCL11, and CXCL13) (ranging from about 0.7-fold to 6.9-fold relative to pre-treatment levels), CD8 T-effector markers (CD8A, CD8B, EOMES, GZMA, GZMB, IFNG, and PRF1) (ranging from about 0.4-fold to 6.2-fold relative to pre-treatment levels), as well as NK cell markers (GZMB, KLRK1, and SLAMF7) (ranging from about 0.7-fold to 8.2-fold relative to pre-treatment levels) (Fig. 3). Bevacizumab treatment resulted in four of the six patients showing a significant increase in gene signatures related to Th1 signaling. Importantly, at the individual patient level, these

signatures were delinked from the degree of reduction of the VEGF dependent signature. FasL expression by IHC has been described as a potential barrier to immune cells in several cancers including RCC (Motz et al. *Nat. Med.* 20:607-615, 2014). In this study, consistent changes in FasL gene expression with bevacizumab or combination treatment were not observed. Overall, these differences indicate that bevacizumab treatment alone results in modulation of tumor immune microenvironment with Th1-related signatures reflecting the most significant treatment-induced alterations in the tumor microenvironment.

The increased expression of Th1 chemokines (CXCL9, CXCL10, CXCL11, and CXCL13), CD8 T-effector markers (CD8A, CD8B, EOMES, GZMA, GZMB, IFNG, and PRF1), and NK cell markers (GZMB, KLRK1, and SLAMF7) were enhanced upon administration of atezolizumab in combination with bevacizumab (Fig. 4). The expression level of the Th1 chemokine signature was increased 2.9- to 250.4-fold at the bevacizumab+atezolizumab time point relative to pre-treatment, and increased 0.9- to 81.8-fold compared to the bevacizumab alone time point. The expression level of the CD8 T_{eff} signature was increased 0.8- to 51.8-fold at the bevacizumab+atezolizumab time point relative to pre-treatment, and increased 0.3- to 17.6-fold compared to the bevacizumab alone time point. The expression level of the NK cell signature was increased 0.7- to 7.8-fold at the bevacizumab+atezolizumab time point relative to pre-treatment, and increased 0.4- to 13.1-fold compared to the bevacizumab alone time point.

Example 3: Characterization of Biomarkers of Vascular and Immune Responses Following Bevacizumab Monotherapy or Combination Therapy in Both On-Treatment Time Points

To confirm the immune and vascular gene expression changes observed in the tumor, immune and vascular protein expression changes in pre-treatment and on-treatment tissue were evaluated by immunohistochemistry. A decrease in CD31, a marker of vessel-lining endothelial cells, was observed (Figs. 5 and 6). Dual staining of CD34, another marker of endothelial cells, with alpha-smooth muscle actin (α SMA) showed that immature or unstable vessels (CD34⁺/ α SMA⁻) were primarily affected with bevacizumab treatment (Figs. 7 and 8), consistent with other published reports (see, e.g., Gasparini et al. *Nat. Clin. Pract. Oncol.* 2:562-577, 2005). Morphological changes in endothelial cells were also evident for the combination treatment, consistent with findings in metastatic melanoma following ipilumimab and bevacizumab treatment (see, e.g., Hodi et al. *Cancer Immunol. Res.* 2:632-642, 2014). In addition, contextual localization of CD68⁺/CD163⁺ but not CD68⁺/CD163⁻ macrophages was observed in four patients on-treatment adjacent to the immature vessels but not the mature vessels, which were largely unaffected by bevacizumab therapy (Figs. 7, 9, and 10). Without wishing to be bound by theory, one potential explanation is that the macrophages localized to unstable vessels could be responding to the inflammation and vascular-induced changes caused by bevacizumab. Macrophages have been shown to promote vascularization by secreting VEGF (Lamagna et al. *J. Leukoc. Biol.* 80:705-713, 2006), and VEGF transcript expression was upregulated in the tumors on-treatment (Fig. 11).

Intratumoral CD8⁺ T cell increases were pronounced following combination treatment in all but one of the patients (Figs. 5, 6, and 12). However, upregulation of PD-L1, which is an IFN- γ response gene, was only detected by immunohistochemistry in one patient, who demonstrated a PR (Fig. 5). Conversely and unexpectedly, a concomitant increase in MHC-I staining was observed following both

bevacizumab and combination treatment (Figs. 5 and 6). The modulation of MHC-I by anti-VEGF antibody therapy has not been previously described and was not consistently associated with an increase in CD8⁺ T cells. Previous studies have found that hypoxia is linked to increased MHC-I expression through HIF-1 α (Ghosh et al. *Mol. Cell. Biol.* 33: 2718-2731, 2013).

To address if the increase in CD8⁺ T cell densities upon combination therapy were attributed to enhanced intratumoral proliferation or increased trafficking, dual immunohistochemistry staining of CD8 with the proliferation marker Ki67 was employed. The ratio of Ki67⁺/CD8⁺ cells to Ki67⁻/CD8⁺ cells remained unchanged on-treatment (Figs. 7, 13, 14A-14C, 15A-15C, and 16A-16C), suggesting that the CD8⁺ T cell increase was not due to enhanced intratumoral proliferation but rather due to increased trafficking and infiltration of proliferating CD8⁺ T cells.

Example 4: Characterization of Antigen-Specific T cell Response Following Combination Therapy

To confirm whether the elevation in intratumoral CD8⁺ T cells was due to increased trafficking, cell populations in the periphery were phenotyped by flow cytometry. HLA-A2 dextramers containing previously described RCC tumor antigen peptides (Table 18) were used to determine if antigen-specific T cells were present in patient blood and if these cell populations changed with treatment. Of the 10 patients, in only two HLA-A2 positive patients were positive for cells in the Dex-APC channel at the pre-treatment timepoint (Fig. 19). Of these two patients, only patient 6 demonstrated an increase in intratumoral CD8⁺ T cells. Interestingly, Dex-APC-positive staining decreased at least 3-fold by the post combination treatment timepoint for patient 6 but not for patient 2, who did not show an increase in intratumoral CD8⁺ T cells. These changes may suggest that RCC antigen-specific T cells traffic from the periphery into tumors.

Gene expression data also indicated that several other chemokines and chemokine receptors increased in patient tumors on-treatment (Fig. 20). The most significant change occurred with fractalkine (CX3CL1), which is known to be expressed on the membrane of activated endothelial cells in inflammatory or hypoxic environments (Szukiewicz et al. *Mediators Inflamm.* 2013:437576, 2013; Umehara et al. *Arterioscler. Thromb. Vasc. Biol.* 24:34-40, 2004).

The receptor for fractalkine, CX3CR1, has been shown to be expressed on armed CD8⁺ T cells (perforin⁺/granzyme B⁺) (Nishimura et al. *J. Immunol.* 168:6173-6180, 2002). In the present study, CX3CR1 was upregulated on peripheral CD8⁺ T cells following combination treatment (Fig. 13). Furthermore, the majority of dextramer-positive cells (Fig. 19) also expressed CX3CR1 (84% and 100% for patients 2 and 6, respectively; Fig. 16). The concordant upregulation of fractalkine and other chemokines in the tumor and CX3CR1 on CD8⁺ T cells on-treatment suggest a mechanism for the increased tumor infiltration of CD8⁺ T cells.

T cell receptor (TCR) sequencing was performed on tumors and CD8⁺ T cells were sorted from matched PBMCs to investigate treatment-induced changes in T cell repertoire and trafficking of T cells into the tumor. Comparison of the top clones from pre-treatment and on-treatment TILs for patients 3 and 6 showed that some clones were retained on-treatment (Figs. 21A-23C and 22). There were clones that appeared following bevacizumab alone while other clones emerged only after the combination therapy. There were also clones detected in pre-treatment but not on-treatment tumors. Altogether, these

dynamic changes in intratumoral T cell composition suggest that the anti-tumor T cell response is evolving on-treatment.

Evaluation of TCR sequences from sorted peripheral CD8⁺ T cells showed that many of the top clones were maintained between pre-treatment and on-treatment samples, but there was also some overlap between clones found in PBMCs versus on-treatment TILs (Figs. 23A and 23B). In particular, there were no shared clones between PBMCs and TILs of patient 2, the patient in which intratumoral CD8⁺ T cells did not increase on-treatment. For patients 3 and 6, there were some clones present at similar frequencies between PBMCs and TILs. A blast of the Adaptive Public Clone Database revealed that some of the top PBMC clones likely recognize viral antigens, but only some of these clones were detected in TILs, further suggesting that tumor antigen-specific T cells may be migrating into the tumor (Fig. 24). The majority of top clones in on-treatment TILs were present at much lower levels in the blood while the most dominant clones in the blood are not detected in the tumor. Because the relative proportions of top clones are not maintained in PBMCs compared to TILs, this may suggest that the increase in CD8⁺ T cells in the tumor induced by combination treatment occurs through a selective trafficking mechanism. It is also possible that the infiltration is non-biased and there is retention of antigen-specific T cells in the tumor.

Example 5: Molecular Correlates of Differential Response to Atezolizumab Monotherapy and Bevacizumab and Atezolizumab Combination Therapy Compared to Sunitinib Monotherapy

A phase II clinical study, IMmotion150 (NCT01984242), was performed to evaluate the safety and tolerability of atezolizumab, alone or in combination with bevacizumab, as compared to sunitinib in patients with previously untreated metastatic renal cell carcinoma (mRCC). Integrated tumor genomic analyses were also performed to correlate molecular biomarkers with observed clinical outcomes in the phase II study.

PD-L1 status on tumor-infiltrating immune cells (IC) was assessed in the phase II IMmotion150 study by immunohistochemistry (IHC) using the anti-human PD-L1 rabbit monoclonal antibody, SP142, and scored using an identical IHC scoring criteria (IC1/2/3 = $\geq 1\%$ of tumor-infiltrating lymphocytes are PD-L1-positive; IC2/3 = $\geq 5\%$ of tumor-infiltrating lymphocytes are PD-L1-positive) (n=297). PD-L1 status can be assessed as described in International Patent Application Publication Nos. WO 2016/183326 and WO 2016/196298. Mutation evaluations by whole exome sequencing (WES) and gene expression analyses by RNA-Seq (n=263) were also performed. For the gene expression analyses, gene expression levels were evaluated for T effector and IFN γ response (Teff) genes (CD8A, IFNG, PRF1, EOMES, and PD-L1), as well as for angiogenesis-related (Ang) genes (VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34), and myeloid inflammation-related (Myeloid) genes (IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2). The Teff genes at low expression levels (i.e., below the median expression levels of the evaluated Teff genes; "Teff low") and high expression levels (i.e., at or above the median expression levels of the evaluated Teff genes; "Teff high") were evaluated in relation to progress-free survival (PFS) per RECIST v.1.1 via Independent Review Facility (IRF) assessment. The Ang genes at low expression levels (i.e., below the median expression levels of the evaluated Ang genes; "Ang low") and high expression levels (i.e., at or above the median expression levels of the evaluated Ang genes; "Ang high")

were also evaluated in relation to PFS per RECIST v.1.1 via IRF assessment. The Myeloid genes at low expression levels (i.e., below the median expression levels of the evaluated Myeloid genes; "Myeloid low") and high expression levels (i.e., at or above the median expression levels of the evaluated Myeloid genes; "Myeloid high") were also evaluated in relation to PFS per RECIST v.1.1 via IRF assessment. To determine the median expression levels, first a Z-score was calculated for the normalized expression of all of the genes in a group. The median level of all the Z-scores across the dataset was used as a reference level to identify biomarker high versus biomarker low subgroups.

PFS was determined to be longer for PD-L1 IC2/3 and PD-L1 IC1/2/3 patients in the atezolizumab+bevacizumab treatment arm relative to PFS for patients in the sunitinib monotherapy arm. PFS was also determined to be longer for PD-L1 IC2/3 patients in the atezolizumab monotherapy arm relative to PFS for patients in the sunitinib monotherapy arm. When considering the evaluated gene expression levels, Teff high expression levels were found to be associated with PD-L1 IHC and longer PFS for patients in the atezolizumab+bevacizumab treatment arm compared to PFS for patients in the sunitinib monotherapy arm (Figs. 31A, 31B, and 32A-32C). Ang low expression levels were also found to be associated with improved PFS for patients in the atezolizumab+bevacizumab treatment arm compared to PFS for patients in the sunitinib monotherapy arm (Fig. 29A). Ang high expression levels, on the other hand, were associated with improved clinical activity in the sunitinib monotherapy arm, but not the atezolizumab+bevacizumab treatment arm (Figs. 29B and 30A-30C). PFS hazard ratios (HR) with 95% confidence intervals (95% CI) for both the atezolizumab+bevacizumab and atezolizumab treatment arms relative to the sunitinib treatment arm are provided in Table 20 for patients binned according to PD-L1 status, Teff gene expression levels, and Ang gene expression levels. The data in Table 20 with respect to PD-L1 IHC are unstratified HRs. The overall response rate (ORR) correlated with PFS in the gene expression subgroups (Fig. 25). Table 21 shows stratified PFS HRs with 95% CI for both the atezolizumab+bevacizumab and atezolizumab treatment arms relative to the sunitinib treatment arm for patients binned according to PD-L1 status and in the intent-to-treat (ITT) population.

Table 20. Molecular Correlates of PFS Responses to Atezolizumab+Bevacizumab Combination Therapy or Atezolizumab Monotherapy Compared to Sunitinib Monotherapy

PFS HR (95% CI)	Atezo + Bev vs Sun	Atezo vs Sun
	PFS HR (95% CI)	
PD-L1 IHC IC1/2/3	0.66 (0.41-1.07)	0.97 (0.61-1.55)
PD-L1 IHC IC2/3	0.36 (0.14-0.88)	0.54 (0.23-1.28)
Teff high	0.55 (0.32-0.95)	0.85 (0.50-1.43)
Teff low	1.41 (0.84-2.03)	1.33 (0.76-2.33)
Ang high	1.36 (0.78-2.36)	1.46 (0.81-2.60)
Ang low	0.58 (0.35-0.98)	0.75 (0.45-1.25)

Table 21: Molecular Correlates of PFS Responses to Atezolizumab+Bevacizumab Combination Therapy or Atezolizumab Monotherapy Compared to Sunitinib Monotherapy

PFS HR (95% CI)	Atezo + Bev vs Sun	Atezo vs Sun
	Stratified PFS HR (95% CI)	
ITT	1.00 (0.69-1.45)	1.19 (0.82-1.71)
PD-L1 IHC IC1/2/3	0.64 (0.38-1.08)	1.03 (0.63-1.67)
PD-L1 IHC IC2/3	0.34 (0.13-0.91)	0.64 (0.27-1.54)

Fig. 26 shows a transcriptome map of angiogenesis and immune-associated genes in RCC tumors. Expression levels of the genes shown in Fig. 26 can be used as predictive biomarkers for response to an anti-cancer therapy that includes a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody), or an anti-cancer therapy that includes an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))). In particular, genes associated with angiogenesis (e.g., VEGFA, KDR, ESM1, PECAM1, FLT1, ANGLT4, and/or CD34), immune/antigen presentation (e.g., CD8A, CD27, INFG, PD-L1 (CD274), FOXP3, EOMES, GZMA, PFR1, PD-1 (PDCD1), CLTA4, TIGIT, GZMB, IDO1, CXCL9, CXCL10, CXCL11, PSMB8, PSMB9, TAP1, and/or TAP2), and myeloid inflammation (e.g., CXCL1, CXCL2, CXCL3, CXCL8, IL6, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9) can be used to predict response to an anti-cancer therapy that includes a VEGF antagonist (e.g., an anti-VEGF antibody, (e.g., bevacizumab) or a VEGFR inhibitor (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))) and a PD-L1 axis binding antagonist (e.g., a PD-L1 binding antagonist (e.g., an anti-PD-L1 antibody, e.g., atezolizumab) or a PD-1 binding antagonist (e.g., an anti-PD-1 antibody), or an anti-cancer therapy that includes an angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., sunitinib, axitinib, pazopanib, or cabozantinib))). For example, an expression level of one or more of CD8A, CD27, INFG, PD-L1 (CD274), FOXP3, EOMES, GZMA, PFR1, PD-1 (PDCD1), CLTA4, TIGIT, GZMB, IDO1, CXCL9, CXCL10, CXCL11, PSMB8, PSMB9, TAP1, and/or TAP2 at or above a reference level of the one or more genes can indicate the patient may benefit from treatment with atezolizumab and bevacizumab (or other VEGF antagonists and PD-L1 axis binding antagonists). In some instances, such patients may have an expression level of one or more of CXCL1, CXCL2, CXCL3, CXCL8, IL6, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9 that is at or above a reference level of the one or more genes. In another example, an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGLT4, and/or CD34 below a reference level of the one or more genes can indicate the patient may benefit from treatment with atezolizumab and bevacizumab (or other VEGF antagonists and PD-L1 axis binding antagonists). In a further example, an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGLT4, and/or CD34 above a reference level can indicate the patient may benefit from treatment

with sunitinib (or another angiogenesis inhibitor (e.g., a VEGF antagonist (e.g., a VEGFR inhibitor, (e.g., a multi-targeted tyrosine kinase inhibitor (e.g., axitinib, pazopanib, or cabozantinib))))). In another example, an expression level of one or more of CXCL1, CXCL2, CXCL3, CXCL8, IL6, PTGS2, CXCR1, CXCR2, S100A8, and/or S100A9 that is below a reference level of the one or more genes can indicate that the patient may benefit from treatment with atezolizumab and bevacizumab (or other VEGF antagonists and PD-L1 axis binding antagonists).

Addition of bevacizumab to atezolizumab (Atezo+Bev) was associated with improved PFS in the Teff high/Myeloid high subgroup (Fig. 27). Reduced atezolizumab monotherapy 1L activity in Teff high/Myeloid high patients suggests a potential mechanism of immune escape, which may be rescued by the addition bevacizumab. The Myeloid genes, independently of the Teff-related genes, were associated with relatively worse PFS outcome when comparing Myeloid high expression levels to Myeloid low expression levels within the atezolizumab+bevacizumab treatment arm (Fig. 28). Treatment benefit in terms of PFS from atezolizumab+bevacizumab was not different from sunitinib monotherapy in the Myeloid high population, but was improved in the Myeloid low population compared to sunitinib monotherapy (Fig. 28).

After progression on atezolizumab or sunitinib, crossover to atezolizumab+bevacizumab was allowed in the IMmotion150 trial design (except that crossover following atezolizumab monotherapy was not allowed in Europe). 77% and 75% of patients crossed over after 1L sunitinib or atezolizumab, respectively, among patients who progressed and were eligible based on geographic location. The crossover patients were also analyzed by baseline tumor microenvironment (TME) gene expression status. A trend of a similar result with respect to improved PFS in the Teff high/Myeloid high subgroup for addition of bevacizumab to atezolizumab (Atezo+Bev) was observed (n=8).

In summary, these studies demonstrate that biomarkers described herein can be used to predict patient response to anti-cancer therapies (e.g., anti-cancer therapy that includes a VEGF antagonist and a PD-L1 axis binding antagonist, or a multi-targeted tyrosine kinase), and to select patients for an anti-cancer therapy that is optimized for their cancer.

Example 6: Atezolizumab Alone or in Combination with Bevacizumab versus Sunitinib: Efficacy, Safety and Molecular Correlates of Differential Response in a Randomized Phase 2 Trial in Renal Cell Carcinoma

In this example, additional primary clinical results of the phase 2 IMmotion150 study are described along with the results of molecular analyses conducted to evaluate the predictive value of biomarkers described herein.

A. Results

Study Design and Efficacy

The primary objective of this phase 2 trial was to evaluate the efficacy of atezolizumab+bevacizumab and atezolizumab monotherapy compared with sunitinib. The sample size of 100 patients per arm and 70% events rate was deemed adequate for estimation of effect size (including median PFS and hazard ratio [HR]) in the intention-to-treat (ITT) as well as the PD-L1+ subgroup.

Tumor specimens from patients acquired <12 months prior to study treatment were required for enrollment in the study. Tissue was prospectively tested for PD-L1 expression on IC by a central laboratory using the SP142 IHC assay (VENTANA, Tucson, AZ). IC staining was defined as follows: any discernible PD-L1 staining of any intensity in IC covering < 1% or absent, between $\geq 1\%$ and < 5%,
 5 between $\geq 5\%$ and <10%, or $\geq 10\%$ of tumor area.

Patients were enrolled in the study from January 8, 2014 to March 16, 2015. This report reflects the results of data with a clinical cutoff date of October 17, 2016 and a median survival follow-up of 20.7 months. All randomized patients were included in the ITT population (N = 305) for all efficacy analyses. Patients in the safety analysis population (n = 304) received more than one dose of study drug. One
 10 patient in the sunitinib arm was excluded from the safety analysis due to withdrawal of consent before receiving study drug (Fig. 33). Discontinuation of treatment was higher with atezolizumab (77.7%) and sunitinib (82.2%) than with atezolizumab+bevacizumab (68.3%), and disease progression was the most common reason for discontinuation among all treatment arms.

Patient demographics were comparable across treatment arms for the safety and ITT
 15 populations. (Table 22).

Table 22: Baseline demographics/patient characteristics

	Sunitinib n = 101	Atezolizumab + Bevacizumab n = 101	Atezolizumab n = 103
Age, median (range), y	61 (25-85)	62 (32-88)	61 (27-81)
Male, n (%)	79 (78%)	74 (73%)	77 (75%)
Karnofsky performance status (KPS) ≥ 80 , n (%)	94 (93%)	99 (99%)	101 (99%)
Predominant clear cell histology, n (%)	96 (96%)	97 (96%)	95 (92%)
Sarcomatoid component, n (%)	14 (14%)	15 (15%)	16 (15%)
Prior nephrectomy, n (%)	88 (87%)	88 (87%)	89 (86%)
Memorial Sloan Kettering Cancer Center (MSKCC) risk category, n (%)			
Favorable (0)	21 (21%)	30 (30%)	26 (25%)
Intermediate (1 or 2)	70 (69%)	62 (61%)	69 (67%)
Poor (≥ 3)	10 (10%)	9 (9%)	8 (8%)
$\geq 1\%$ PD-L1 expression on IC (PD-L1+), n (%)	60 (59%)	50 (50%)	54 (52%)

Independent review facility (IRF)–assessed efficacy endpoints are summarized as follows.

20 Stratified analysis in the ITT population showed a median progression-free survival (PFS) of 11.7 months (95% CI, 8.4-17.3) with atezolizumab+bevacizumab versus 8.4 months (95% CI, 7.0-14.0) with sunitinib (HR 1.00; 95% CI, 0.69-1.45) and 6.1 months (95% CI, 5.4-13.6) with atezolizumab monotherapy (HR 1.19; 95% CI, 0.82-1.71 versus sunitinib; Fig. 34A). In the PD-L1+ population, the median PFS was 14.7
 25 months (95% CI, 8.2-25.1) with atezolizumab+bevacizumab versus 7.8 months (95% CI, 3.8-10.8) with sunitinib (HR 0.64; 95% CI, 0.38-1.08) and 5.5 months (95% CI, 3.0-13.9) with atezolizumab monotherapy (HR 1.03; 95% CI, 0.63-1.67 versus sunitinib; Fig. 34B). The objective response rates (ORRs) were 32% (7% complete response [CR], 25% partial response [PR]), 25% (11% CR, 14% PR) and 29% (5% CR, 24% PR) with atezolizumab+bevacizumab, atezolizumab monotherapy, and sunitinib,

respectively (Fig. 34C). In PD-L1+ patients, the ORRs were 46% (12% CR, 34% PR), 28% (15% CR, 13% PR), and 27% (7% CR, 20% PR) with atezolizumab+bevacizumab, atezolizumab monotherapy, and sunitinib, respectively (Fig. 34C). The concordance between investigator-assessed PFS (Figs. 35A and 35B), and IRF-assessed PFS was 77% for all patients and was similar between study arms. PFS in key subgroups with atezolizumab+bevacizumab and atezolizumab monotherapy versus sunitinib is shown in Figs. 36A and 36B. Of note, we observed a trend for improved efficacy (PFS) with higher expression of PD-L1 with atezolizumab+bevacizumab and for atezolizumab monotherapy versus sunitinib at a PD-L1 cutoff of $\geq 5\%$ (unstratified analysis; Figs. 36A and 36B).

Safety

Treatment-related adverse events (AEs) leading to discontinuation occurred in 9% of patients in the atezolizumab+bevacizumab arm, 3% in the atezolizumab monotherapy arm, and 9% in the sunitinib arm (Table 23).

Table 23: Toxicity profile/safety summary

	Sunitinib n = 100	Atezolizumab + Bevacizumab n = 101	Atezolizumab n = 103
Treatment duration, median (range), mo	6.7 (0.1-33.1)	Atezolizumab: 11.8 (0.7-32.7) Bevacizumab: 10.3 (0.0-29.8)	7.6 (0.0-33.1)
All-grade AEs, any cause, n (%)	99 (99%)	101 (100%)	101 (98%)
Treatment-related AE	96 (96%)	91 (90%)	86 (83%)
Grade 3/4 AEs, any cause, n (%)	69 (69%)	64 (63%)	41 (40%)
Treatment-related grade 3/4 AEs	57 (57%)	40 (40%)	17 (17%)
AEs leading to death, n (%) ^a	2 (2%)	3 (3%)	2 (2%)
Treatment-related AEs leading to death ^a	2 (2%)	1 (1%)	0
AEs leading to withdrawal from treatment, n (%)	10 (10%)	15 (15%)	7 (7%)
Treatment-related AEs leading to withdrawal from treatment	9 (9%)	9 (9%)	3 (3%)
AEs leading to dose modification or interruption, n (%)	70 (70%)	61 (60%)	28 (27%)
^a Sunitinib arm: sudden death (related), intestinal hemorrhage (related). Atezolizumab arm: hematophagic hitiocytosis, lower respiratory tract infection. Atezolizumab+Bevacizumab arm: intracranial hemorrhage (related), hemorrhage, pneumonia.			

In the atezolizumab+bevacizumab group, proteinuria was the most common related AE leading to treatment discontinuation (5%). With sunitinib, the most common related AEs leading to treatment discontinuation were increased blood creatinine and palmar-plantar erythrodysesthesia syndrome (2% each). With atezolizumab monotherapy, nephritis, pancreatitis, and demyelination (1% each) were the treatment-related AEs leading to discontinuation of treatment. Figs. 38A and 38B show all-cause AEs occurring at frequency of $\geq 20\%$ in the atezolizumab+bevacizumab and sunitinib arms, or the

atezolizumab monotherapy and sunitinib arms, with a difference in incidence between the two arms of $\geq 5\%$. Select AEs of special interest are shown below in Table 24, and all AEs occurring in $\geq 20\%$ of patients in any of the three arms are shown in Table 25.

5 **Table 24: Selected AEs of special interest**

n (%)	Sunitinib n = 100	Atezo + Bev n = 101	Atezo n = 103	Sunitinib n = 100	Atezo + Bev n = 101	Atezo n = 103
	All Grade			Grade 3/4		
Pneumonitis	0	0	1 (1%)	0	0	0
Colitis	1 (1%)	1 (1%)	0	0	0	0
Elevated liver enzymes/ hepatitis	20 (20%)	16 (16%)	9 (9%)	4 (4%)	4 (4%)	3 (3%)
TSH decreased/ hypothyroidism	20 (20%)	23 (23%)	15 (15%)	0	0	0
TSH increased/ hyperthyroidism	6 (6%)	7 (7%)	5 (5%)	0	0	0
Decreased blood cortisol/ adrenal insufficiency	0	3 (3%)	0	0	1 (1%)	0

Table 25: All AEs occurring in $\geq 20\%$ of patients in any arm

Preferred Term	Sunitinib (n = 100)	Atezo (n = 103)	Atezo + Bev (n = 101)
Any AE	99 (99.0%)	101 (98.1%)	101 (100.0%)
Fatigue	70 (70.0%)	49 (47.6%)	60 (59.4%)
Arthralgia	18 (18.0%)	15 (14.6%)	38 (37.6%)
Hypertension	35 (35.0%)	6 (5.8%)	37 (36.6%)
Proteinuria	9 (9.0%)	8 (7.8%)	36 (35.6%)
Diarrhea	59 (59.0%)	17 (16.5%)	34 (33.7%)
Nausea	45 (45.0%)	19 (18.4%)	36 (35.6%)
Headache	23 (23.0%)	15 (14.6%)	33 (32.7%)
Constipation	30 (30.0%)	14 (13.6%)	28 (27.7%)
Epistaxis	12 (12.0%)	2 (1.9%)	28 (27.7%)
Rash	13 (13.0%)	21 (20.4%)	22 (21.8%)
Pruritus	10 (10.0%)	16 (15.5%)	22 (21.8%)
Decreased appetite	29 (29.0%)	10 (9.7%)	22 (21.8%)
Pyrexia	12 (12.0%)	25 (24.3%)	21 (20.8%)
Vomiting	20 (20.0%)	9 (8.7%)	19 (18.8%)
Cough	25 (25.0%)	23 (22.3%)	19 (18.8%)

Mucosal inflammation	33 (33.0%)	4 (3.9%)	15 (14.9%)
Stomatitis	25 (25.0%)	3 (2.9%)	13 (12.9%)
Dysgeusia	30 (30.0%)	3 (2.9%)	12 (11.9%)
Palmar-plantar erythrodysesthesia syndrome	40 (40.0%)	-	3 (3.0%)
Infections and infestations	32 (32.0%)	42 (40.8%)	63 (62.4%)

Molecular Correlates of Clinical Outcome

We conducted studies to evaluate molecular biomarkers relevant to the disease and tumor immune biology in RCC and their association with clinical outcomes within each treatment group and across treatment groups. Demographic and baseline characteristics in biomarker subgroups were generally consistent with those in the ITT population (Table 26).

Table 26: Demographic and baseline characteristics in ITT and biomarker evaluable populations

Covariate		ITT (%)	RNAseq (%)	WES (%)
Male sex		230 (75)	201 (76)	154 (74)
Prior nephrectomy		265 (87)	233 (89)	189 (91)
Has liver metastasis		73 (24)	66 (25)	47 (23)
PD-L1+		172 (56)	157 (60)	128 (62)
MSKCC	Favorable	77 (25)	59 (22)	47 (23)
	Intermediate	201 (66)	181 (69)	148 (71)
	Poor	27 (9)	23 (9)	13 (6)
Fuhrman grade	Grade 1	5 (2)	5 (2)	4 (2)
	Grade 2	38 (12)	32 (12)	30 (14)
	Grade 3	80 (26)	72 (27)	54 (26)
	Grade 4	73 (24)	63 (24)	51 (25)
	N/A	109 (36)	91 (35)	69 (33)

A heatmap of genes relevant to RCC and immune biology in 263 evaluable pretreatment tumors (Fig. 38A) shows distinct biological subgroups based on relative expression levels of angiogenesis (Angio), immune (including T-effector presence and function, IFN- γ response, checkpoint inhibitors, and antigen presentation), and myeloid inflammation-associated genes. The subgroup with high expression of the Angio gene signature (Angio^{High}) was characterized by relatively higher vascular density as evaluated by CD31 IHC (Fig. 38B), whereas the subgroup with high expression of the Teffector (Teff) gene signature (Teff^{High}) was positively associated with protein expression of PD-L1 on IC by IHC (Fig. 38C) and CD8 T-cell infiltration (Fig. 38D), indicative of pre-existing adaptive anti-tumor immunity. Additionally, differential expression of genes associated with myeloid inflammation within the Teff^{High} and Teff^{Low} subgroups was observed, suggesting further functional subcategories of these tumors (Fig. 38A). The association of clinical outcome in these biological subgroups within each treatment arm and across

treatment arms is shown in Table 27. The following comparisons represent a subset of the larger analysis. Biomarker associations with clinical outcome are discussed if the 95% CI for HR did not cross 1 for PFS evaluation and if the 95% CI were non-overlapping for ORR comparisons.

5 **Table 27: PFS HRs in biomarker subpopulations**

PFS, HR (95% CI)	Across Arm Analysis			Within Arm Analysis		
	Atezo + Bev vs Sunitinib	Atezo vs Sunitinib	Atezo + Bev vs Atezo	Atezo + Bev	Sunitinib	Atezo
Subpopulation						
Angio ^{High}	1.36 (0.78-2.36)	1.46 (0.81-2.60)	0.93 (0.54-1.60)	Angio ^{High} vs Angio ^{Low}		
Angio ^{Low}	0.59 (0.35-0.98)	0.75 (0.45-1.25)	0.78 (0.46-1.33)	0.90 (0.54-1.51)	0.31 (0.18-0.55)	0.74 (0.42-1.28)
Teff ^{High}	0.55 (0.32-0.95)	0.85 (0.50-1.43)	0.65 (0.37-1.14)	Teff ^{High} vs Teff ^{Low}		
Teff ^{Low}	1.41 (0.85-2.36)	1.33 (0.76-2.33)	1.06 (0.63-1.79)	0.50 (0.30-0.86)	1.31 (0.77-2.23)	0.83 (0.48-1.45)
Myeloid ^{High}	1.31 (0.79-2.17)	2.03 (1.21-3.40)	0.64 (0.39-1.06)	Myeloid ^{High} vs Myeloid ^{Low}		
Myeloid ^{Low}	0.57 (0.33-0.99)	0.53 (0.30-0.96)	1.07 (0.59-1.93)	1.71 (1.01-2.88)	0.82 (0.48-1.39)	2.98 (1.68-5.29)
Teff ^{High} Myeloid ^{High}	0.45 (0.20-1.05)	1.81 (0.92-3.58)	0.25 (0.10-0.60)	Teff ^{High} Myeloid ^{High} vs Teff ^{High} Myeloid ^{Low}		
Teff ^{High} Myeloid ^{Low}	0.6 (0.28-1.31)	0.47 (0.20-1.09)	1.29 (0.57-2.90)	0.80 (0.34-1.87)	1.10 (0.53-2.29)	3.82 (1.70-8.60)

To determine if highly angiogenic tumors were more responsive to anti-angiogenic therapy, we investigated the association of the Angio gene signature with clinical outcome in each treatment arm. High expression of the Angio gene signature, based on median signature score, was associated with improved ORR (45% in Angio^{High} versus 10% in Angio^{Low}, Fig. 38E) and PFS (HR 0.31; 95% CI, 0.18-0.55; Fig. 38E) within the sunitinib treatment arm. When evaluated across treatment arms, no apparent difference in PFS was observed in the Angio^{High} subgroup between the atezolizumab+bevacizumab and sunitinib arms or between the atezolizumab monotherapy and sunitinib arms (Fig. 38H). In the Angio^{Low} subgroup, atezolizumab+bevacizumab demonstrated improved PFS versus sunitinib (HR 0.59; 95% CI, 0.35-0.98; Fig. 38G).

We next asked if the presence of a pre-existing immune response, as identified by expression of the Teff gene signature, was associated with clinical benefit to immunotherapy containing regimens. High Teff gene signature expression, based on median signature score, was associated with improved ORR (50% in Teff^{High} versus 16% in Teff^{Low}; Fig. 38I) and PFS (HR 0.50; 95% CI, 0.30-0.86; Fig. 38J) versus low Teff gene signature expression within the atezolizumab+bevacizumab arm (Fig. 38J). When compared across treatment arms, high Teff gene signature expression was associated with improved PFS with atezolizumab+bevacizumab versus sunitinib (HR 0.55; 95% CI: 0.32-0.95, Fig. 38L).

Because myeloid inflammation has been associated with suppression of the anti-tumor adaptive T cell response, we next investigated the contribution of the myeloid inflammation signature to clinical outcome. High myeloid inflammation gene signature expression (Myeloid^{High}), based on median signature score, was associated with reduced PFS in the atezolizumab monotherapy arm (HR 2.98; 95% CI, 1.68-5.29) and, to a lesser extent, in the atezolizumab + bevacizumab arm (HR 1.71; 95% CI, 1.01-2.88) but not in the sunitinib arm (Table 27). When compared across treatment arms, Myeloid^{High} was associated with worse PFS with atezolizumab monotherapy versus sunitinib (HR 2.03; 95% CI, 1.21-3.40); however, this was not observed between atezolizumab+bevacizumab versus sunitinib (Table 27).

In addition to evaluation of gene expression signatures that distinguish between the clinical activity of atezolizumab+bevacizumab versus sunitinib, we investigated gene expression profiles that may differentiate the activity of atezolizumab+bevacizumab versus atezolizumab monotherapy. Teff, Angio, or Myeloid Inflammation (Myeloid) gene expression signatures did not differentiate activity of atezolizumab+bevacizumab versus atezolizumab monotherapy when evaluated across the respective dichotomized expression subgroups (Table 27). The heat map of the three gene signatures (Fig. 38A) showed a distinct population of Myeloid^{High} tumors within the inflamed (Teff^{High}) category of mRCC tumors. We asked if the presence of myeloid inflammation within this subgroup of Teff^{High} tumors impacted clinical outcome with the three therapies. Atezolizumab monotherapy had worse activity in the Teff^{High}Myeloid^{High} tumors compared with the Teff^{High}Myeloid^{Low} tumors (HR 3.82; 95% CI, 1.70-8.60; Table 27). When compared across treatment arms, atezolizumab+bevacizumab showed improved PFS compared with atezolizumab monotherapy (HR 0.25; 95% CI, 0.10-0.60; Fig. 38N). No apparent difference in PFS was observed between atezolizumab+bevacizumab and atezolizumab monotherapy in the Teff^{High}Myeloid^{Low} subgroup (Fig. 38M).

B. Discussion

To our knowledge, IMmotion150 is the first randomized study to evaluate the clinical activity of the combination of an anti-angiogenesis agent and an immune checkpoint inhibitor in treatment-naïve patients with mRCC. It is distinguished from other ongoing randomized trials investigating checkpoint inhibition in untreated mRCC by the inclusion of a PD-L1/PD-1 inhibitor monotherapy arm. The combination of atezolizumab+bevacizumab produced encouraging efficacy compared to the most commonly applied kidney cancer therapy, sunitinib, in the subgroup of patients with tumors expressing PD-L1 on ≥ 1% of IC (54% of enrolled patients). This finding will be further evaluated in a randomized phase 3 study (IMmotion151, NCT02420821). Atezolizumab also demonstrated anti-tumor activity when administered as a single agent and was well tolerated. Of note, the high response rate observed with atezolizumab monotherapy, including complete responses, supports its clinical efficacy, including in the adjuvant setting for patients with resected high-risk RCC (IMmotion010, NCT03024996). Safety in the atezolizumab+bevacizumab arm and the atezolizumab monotherapy arm was consistent with previous data for each drug alone, and AEs leading to treatment discontinuation were low.

A consistent trend of increasing efficacy with increasing levels of PD-L1 IC expression across both atezolizumab containing arms underscores the relevance of pre-existing immunity for differentiating the activity of atezolizumab and atezolizumab+bevacizumab from sunitinib in mRCC. This is particularly

true in the atezolizumab+bevacizumab arm, in which bevacizumab appears to enhance anti-tumor activity in immunogenic tumors (Fig. 38N). The predictive relevance of PD-L1 expression on IC is further supported by the strong correlation of PD-L1 IC determined by IHC with the Teff immune gene signature (Fig. 38C). These data support a PD-L1 IHC and/or an immune gene expression signature-based diagnostic or enrichment strategy in treatment naïve patients with mRCC.

To further identify determinants of differential activity across the three treatment groups, we interrogated three biological axes that we hypothesized play a role in the response to the treatment regimens studied: tumor angiogenesis, pre-existing immunity, and immunosuppressive myeloid inflammation. Sunitinib efficacy was enriched in highly angiogenic tumors (Angio^{High}) (Fig. 38F). The combination of atezolizumab+bevacizumab improved clinical benefit compared with sunitinib in Teff^{High} tumors (Fig. 38L). Atezolizumab monotherapy was effective in tumors with pre-existing immunity and a relatively lower expression of myeloid inflammation-associated genes (Teff^{High}Myeloid^{Low}), but less so in immunogenic tumors with concomitantly high myeloid inflammation (Teff^{High}Myeloid^{High}). Myeloid inflammation associated with high expression of IL-6, prostaglandins, and the CXCL8 family of chemokines has been implicated in accumulation of myeloid-derived suppressor cells (MDSCs) in tumors and suppression of anti-tumor immunity, and VEGF/VEGF receptor blockade has been shown to reduce MDSCs in tumors and blood in preclinical tumor models and human cancers. The improved clinical outcome associated with atezolizumab+bevacizumab compared with atezolizumab monotherapy in the immune-suppressed Teff^{High}Myeloid^{High} subgroup (Fig. 38N, Table 27) suggests that the addition of bevacizumab to atezolizumab may overcome innate inflammation-mediated resistance in these tumors. The molecular subgroups identified in this study are expected to have discriminatory characteristics with potential broad relevance for application of anti-angiogenesis and checkpoint inhibitor based therapies across a spectrum of cancers, for which VEGF expression may contribute to tumor immunosuppression. Notably, a recent study investigating chemotherapy in combination with atezolizumab+bevacizumab in NSCLC reported improved efficacy versus chemotherapy and bevacizumab alone. The combination of atezolizumab+bevacizumab is also under evaluation in hepatocellular carcinoma, gastric, and ovarian cancer (NCT02715531, NCT02715531, and NCT03038100, respectively).

Overall, data from IMmotion150 indicate that atezolizumab+bevacizumab may particularly enhance PFS benefit in patients with pre-existing anti-tumor immunity (as determined by a high Teff score and PD-L1 IC expression) compared with sunitinib. In addition, comprehensive biomarker analyses that expand our understanding of the biology of kidney cancer and identify patient populations that derive benefit from sunitinib, atezolizumab, or the combination of atezolizumab+bevacizumab may enable personalized therapy in patients with mRCC. Furthermore, our findings identify myeloid inflammation as a potential mechanism of innate resistance to atezolizumab monotherapy in mRCC that may be overcome by the addition of bevacizumab.

C. Methods

Study Design and Outcomes

IMmotion150 is a phase 2, multicenter, randomized, open-label study conducted in 96 institutions that was designed to evaluate the safety and to provide preliminary evidence of activity of

atezolizumab+bevacizumab versus sunitinib, and atezolizumab monotherapy versus sunitinib, as well as to inform the study design of the phase 3 trial (IMmotion151; NCT02420821). The sample size was approximately 100 patients per arm, and 70% events rate was deemed adequate for estimation of effect size (including median PFS and HR) in the ITT and PDL1+ subgroups. This trial, however, will not have sufficient power to detect clinically meaningful differences between treatment arms at a statistically significant α (type I) error level of 5%. For example, with 140 events in two comparator arms, there is only 56% power to detect HR = 0.7 at 5% significance level.

The original primary endpoint was PFS per Response Evaluation Criteria In Solid Tumors version 1.1 (RECIST v1.1) via IRF in the ITT population. Although patients were stratified by $\geq 5\%$ PD-L1 expression on IC, the definition of PD-L1 positivity was revised from $\geq 5\%$ to $\geq 1\%$ PD-L1 expression on IC, based on phase 1a data, and the study protocol was amended to create PD-L1 expression on IC as a coprimary endpoint of IRF-assessed PFS. This amendment likely contributed to the slight imbalance in the numbers of PD-L1+ patients between treatment arms (sunitinib, 59%; atezolizumab, 52%; atezolizumab+bevacizumab, 50%; Table 22). Secondary endpoints included investigator (INV)-assessed PFS, ORR, and duration of response (DOR) per RECIST v1.1, overall survival (OS), patient-reported outcomes, and safety. Key exploratory objectives included evaluation of the relationship between the expression of predictive and prognostic exploratory biomarkers and their association with disease status and efficacy as defined by ORR and PFS. All data are reported per IRF assessment, unless otherwise stated.

Participants

Eligible patients were ≥ 18 years of age, had a Karnofsky performance score ≥ 70 , and had unresectable advanced or mRCC with a component of clear cell histology and/or sarcomatoid histology not previously treated with any systemic agents for RCC. Patients were required to have adequate hematologic and end-organ function. Patients were excluded if they had known active brain or spinal cord metastases, uncontrolled pleural/pericardial effusion or ascites, or uncontrolled hypercalcemia.

Randomization and Masking

After written informed consent was obtained and eligibility determined, the study site obtained each patient's identification number and treatment assignment from the interactive voice/Web response system (IxRS). Stratification factors at the time of randomization included Memorial Sloan Kettering Cancer Center (MSKCC) risk category (low, intermediate, or high risk) (Motzer et al. *J. Clin. Oncol.* 17:2530-2540, 1999), prior nephrectomy (yes or no), and PD-L1 status ($\geq$ or $< 5\%$ PD-L1 expression on IC) as determined by IHC staining using the SP142 assay. Stratified permuted block randomization was used to assign patients in a 1:1:1 ratio to one of three treatment arms: atezolizumab+bevacizumab, atezolizumab, or sunitinib. The study was open-label and allocation was unmasked.

Procedures

Study treatment consisted of atezolizumab 1200 mg fixed intravenous dose + bevacizumab 15 mg/kg every three weeks, atezolizumab 1200 mg fixed intravenous dose every three weeks, or sunitinib

50 mg/day orally for four weeks followed by two weeks of rest. On disease progression (as assessed by the investigator per RECIST v1.1), patients randomized to atezolizumab monotherapy or sunitinib had the option to cross over and receive the atezolizumab+bevacizumab combination in some regions (option was not available in Europe). In the absence of unacceptable toxicity, treatment with the combination continued until evidence of progressive disease. Where permitted, patients in the atezolizumab-containing arms could continue to be treated beyond disease progression per RECIST v1.1 until lack of clinical benefit; those in non-European nations could cross over to atezolizumab+bevacizumab therapy at any time after disease progression per RECIST v1.1, provided all eligibility criteria were met.

During the study, each cycle was six weeks (42 days) in duration, and data on tumor measurement and survival status were collected for evaluation of PFS, milestone PFS (at 24, 52, and 76 weeks), OS, and ORR per RECIST v1.1. Tumor assessments occurred at baseline and every 12 weeks $\pm$ five business days after Cycle 1, Day 1, or more frequently if clinically indicated. Patients who discontinued first-line treatment or crossover treatment were followed up for survival approximately every three months until death, withdrawal of consent, loss to follow-up, or study termination. Patients who discontinued study treatment for reasons other than disease progression (e.g., toxicity) continued to undergo scheduled tumor assessments (every 12 weeks) until death, disease progression per RECIST v1.1, withdrawal of consent, or study termination, whichever occurred first.

Statistical Analysis

Kaplan-Meier methodology was used to estimate the median PFS for each treatment arm, and Kaplan-Meier curves were produced. The primary analysis was triggered when 140 INV-PFS events occurred among patients treated with atezolizumab+bevacizumab and with sunitinib or among patients treated with atezolizumab alone and with sunitinib, whichever occurred later. The HR estimates and their 95% CIs were determined by using the stratified Cox proportional hazards model. The stratification factors included prior nephrectomy, tumor PD-L1 status, and MSKCC score and were determined based on data from the electronic case report form; if such data were missing, data collected by the IxRS at the time of randomization were used. Tumor specimens were prospectively tested for PD-L1 expression on ICs by a central laboratory using the SP142 IHC assay (VENTANA, Tucson, AZ). IC staining was defined as follows: any discernible PD-L1 staining of any intensity in IC covering $< 1\%$ or absent (IC0), between $\geq 1\%$ and $< 5\%$ (IC1), between $\geq 5\%$ and $< 10\%$ (IC2), or $\geq 10\%$ (IC3) of tumor area occupied by tumor cells, associated intratumoral, and contiguous peri-tumoral desmoplastic stroma.

Gene Expression Analyses

Whole transcriptome profiles were generated for 263 patients using TRUSEQ® RNA Access technology (ILLUMINA®). RNAseq reads were first aligned to ribosomal RNA sequences to remove ribosomal reads. The remaining reads were aligned to the human reference genome (NCBI Build 38) using GSNAP version 2013-10-10 (Wu et al. *Bioinformatics* 26:873-881, 2010; Wu et al. *Methods Mol. Biol.* 1418:283-334, 2016), allowing a maximum of two mismatches per 75 base sequence (parameters: '-M 2 -n 10 -B 2 -i 1 -N 1 -w 200000 -E 1 --pairmax-rna=200000 --clip-overlap'). To quantify gene expression levels, the number of reads mapped to the exons of each RefSeq gene was calculated using

the functionality provided by the R/Bioconductor package GenomicAlignments (Lawrence et al. *PLoS Comput. Biol.* 9:e1003118, 2013).

Gene signatures were defined as follows: Angio: *VEGFA*, *KDR*, *ESM1*, *PECAM1*, *ANGPTL4*, and *CD34*; Teff: *CD8A*, *EOMES*, *PRF1*, *IFNG*, and *CD274*; Myeloid inflammation (Myeloid): *IL-6*, *CXCL1*, *CXCL2*, *CXCL3*, *CXCL8*, and *PTGS2*.

To calculate scores for each of these signatures, counts were first normalized using edgeR's normalization factors, followed by filtering out genes with low coverage (i.e., not reaching 0.25 CPM (counts per million) in at least one-tenth of available samples) and log₂ transformation using limma's voom (Ritchie et al. *Nucleic Acids Res.* 43:e47, 2015). For each sample, the average expression of all genes in a given signature was then computed, which is reported as the sample's signature score. For each gene signature, patients were divided into two groups based on the median gene signature score of all tumors: high gene signature expression was defined as expression at or above median levels, and low gene signature expression was defined as expression below the median.

For the heatmap (Fig. 38A), each patient was placed into high or low groups for all three gene expression signatures: Angio, Teff and Myeloid (based on median expression, as described above). Subsequently, patients were sorted by the combination of these three groups: first Teff^{High}, Angio^{Low} patients are shown, sorted by Myeloid low/high; then Teff^{High}, Angio^{High} patients are shown, sorted by Myeloid high/low; then Teff^{Low}, Angio^{High} patients are shown, sorted by Myeloid low/high; finally, Teff^{Low}, Angio^{Low} patients are shown, sorted by Myeloid high/low. Also, the ordering of the genes was predetermined, based on biological function. Z-score transformed normalized counts are shown.

Biomarker Association Analyses

For testing associations between a continuous variable and a binary trait (e.g., Figs. 38B and 38D), two-tailed t tests were used. Otherwise, for testing associations between a continuous variable and a categorical variable with more than two levels (e.g., Fig. 38C), likelihood ratio test *P* values were calculated using ANOVA. For testing association between two continuous variables, Pearson correlation coefficient was calculated.

All *P* values reported were for descriptive propose only and not adjusted for multiple testing. Biomarker associations with clinical outcome were further discussed above if the 95% CIs for HR did not cross 1 for PFS evaluation and if the 95% CIs were non-overlapping for ORR comparisons.

VII. OTHER EMBODIMENTS

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, the descriptions and examples should not be construed as limiting the scope of the invention. The disclosures of all patent and scientific literature cited herein are expressly incorporated in their entirety by reference.

CLAIMS

What is claimed is:

1. A method of identifying an individual having a kidney cancer who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist, the method comprising determining the expression level of one or more of the following genes in a sample from the individual:

CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2;
VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or
IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2;

wherein

(i) an expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample that is at or above a reference expression level of the one or more genes; or

(ii) an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample that is below a reference expression level of the one or more genes

identifies the individual as one who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist.

2. A method for selecting a therapy for an individual having a kidney cancer, the method comprising determining the expression level of one or more of the following genes in a sample from the individual:

CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2;
VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or
IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2;

wherein

(i) an expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample that is at or above a reference expression level of the one or more genes; or

(ii) an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample that is below a reference expression level of the one or more genes

identifies the individual as one who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist.

3. The method of claim 1 or 2, wherein the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is at or above a reference expression level of the one or

more genes, and the method further comprises administering to the individual an effective amount of the anti-cancer therapy.

4. The method of claim 3, wherein the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 is at or above a reference expression level of the one or more genes.

5. The method of claim 3 or 4, wherein the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample is at or above a reference expression level of the one or more genes.

6. The method of claim 5, wherein the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 in the sample is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

7. The method of any one of claims 3-6, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is at or above a reference expression level of the one or more genes.

8. The method of claim 7, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is at or above a reference expression level of the one or more genes.

9. The method of claim 7 or 8, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 in the sample is at or above a reference expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

10. The method of any one of claims 1-9, wherein the expression level of PD-L1 in the sample is at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, and TAP2 in the sample is at or above a reference expression level of the one or more additional genes.

11. The method of claim 1 or 2, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes, and the method further comprises administering to the individual an effective amount of the anti-cancer therapy.

12. The method of claim 11, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes.

13. The method of claim 11 or 12, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes.

14. The method of claim 13, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

15. The method of claim 1 or 2, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is below a reference level of the one or more genes, and the method further comprises administering to the individual an effective amount of the anti-cancer therapy.

16. The method of claim 15, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is below a reference level of the one or more genes.

17. The method of claim 15 or 16, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 in the sample is below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

18. The method of claim 1 or 2, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is at or above a reference level of the one or more genes, and the method further comprises administering to the individual an effective amount of an anti-cancer therapy comprising a VEGF antagonist.

19. The method of claim 18, wherein the anti-cancer therapy further comprises a PD-L1 axis binding antagonist.

20. The method of claim 18 or 19, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 is at or above a reference level of the one or more genes.

21. The method of any one of claims 18-20, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is at or above a reference level of the one or more genes.

22. The method of claim 21, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

23. A method of treating an individual having a kidney cancer, the method comprising:

(a) determining the expression level of one or more of the following genes in a sample from the individual:

CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2;
VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or
IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2;

wherein

(i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference expression level of the one or more genes; or
(ii) the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is determined to be below a reference expression level of the one or more genes; and

(b) administering an effective amount of an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist to the individual based on the expression level of the one or more genes determined in step (a).

24. The method of claim 23, wherein the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference level of the one or more genes.

25. The method of claim 24, wherein the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference level of the one or more genes.

26. The method of claim 24 or 25, wherein the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample is determined to be at or above a reference level of the one or more genes.

27. The method of claim 26, wherein the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 in the sample is determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

28. The method of any one of claims 24-27, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is determined to be at or above a reference level of the one or more genes.

29. The method of claim 28, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is determined to be at or above a reference level of the one or more genes.

30. The method of claim 28 or 29, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 in the sample is determined to be at or above a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

31. The method of any one of claims 23-30, wherein the expression level of PD-L1 in the sample is determined to be at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is determined to be at or above a reference expression level of the one or more additional genes.

32. The method of claim 23, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be below a reference level of the one or more genes.

33. The method of claim 32, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be below a reference level of the one or more genes.

34. The method of claim 32 or 33, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is determined to be below a reference level of the one or more genes.

35. The method of claim 34, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

36. The method of claim 23, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is determined to be below a reference level of the one or more genes.

37. The method of claim 36, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is determined to be below a reference level of the one or more genes.

38. The method of claim 36 or 37, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 in the sample is determined to be below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

39. A method of treating an individual having a kidney cancer, the method comprising administering to the individual an effective amount of an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist, wherein prior to treatment (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more genes; or (ii) the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be below a reference expression level of the one or more genes.

40. The method of claim 39, wherein the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference level of the one or more genes.

41. The method of claim 40, wherein the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference level of the one or more genes.

42. The method of claim 40 or 41, wherein the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample has been determined to be at or above a reference level of the one or more genes.

43. The method of claim 42, wherein the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 in the sample has been determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

44. The method of any one of claims 40-43, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be at or above a reference level of the one or more genes.

45. The method of claim 44, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be at or above a reference level of the one or more genes.

46. The method of claim 44 or 45, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 has been determined to be at or above a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

47. The method of any one of claims 39-46, wherein the expression level of PD-L1 in the sample has been determined to be at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more additional genes.

48. The method of claim 47, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes.

49. The method of claim 48, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes.

50. The method of claim 48 or 49, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes.

51. The method of claim 50, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

52. The method of claim 39, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be below a reference level of the one or more genes.

53. The method of claim 52, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be below a reference level of the one or more genes.

54. The method of claim 52 or 53, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 in the sample has been determined to be below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

55. A method of treating an individual having a kidney cancer, the method comprising:

(a) determining the expression level of one or more of the following genes in a sample from the individual: VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be at or above a reference expression level of the one or more genes; and

(b) administering an effective amount of an anti-cancer therapy comprising a VEGF antagonist to the individual based on the expression level of the one or more genes determined in step (a).

56. The method of claim 55, wherein the anti-cancer therapy further comprises a PD-L1 axis binding antagonist.

57. The method of claim 55 or 56, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is determined to be at or above a reference level of the one or more genes.

58. The method of any one of claims 55-57, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is determined to be at or above a reference level of the one or more genes.

59. The method of claim 58, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is determined to be at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

60. A method of treating an individual having a kidney cancer, the method comprising administering to the individual an effective amount of an anti-cancer therapy comprising VEGF antagonist, wherein prior to treatment the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or

CD34 in the sample has been determined to be at or above a reference expression level of the one or more genes.

61. The method of claim 60, the anti-cancer therapy further comprises a PD-L1 axis binding antagonist.

62. The method of claim 60 or 61, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes.

63. The method of any one of claims 60-62, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes.

64. The method of claim 63, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

65. The method of any one of claims 1-64, wherein the reference level of the one or more genes is determined from a population of individuals having a kidney cancer.

66. The method of claim 65, wherein the reference level of the one or more genes is a median expression level determined in a population of patients having a kidney cancer.

67. The method of claim 66, wherein the reference level is a median of a Z-score of the normalized expression level of the one or more genes.

68. The method of any one of claims 1-67, wherein the expression level is a nucleic acid expression level.

69. The method of claim 68, wherein the nucleic acid expression level is an mRNA expression level.

70. The method of claim 69, wherein the mRNA expression level is determined by RNA-seq, RT-qPCR, qPCR, multiplex qPCR or RT-qPCR, microarray analysis, SAGE, MassARRAY technique, ISH, or a combination thereof.

71. The method of any one of claims 1-67, wherein the expression level is a protein expression level.

72. The method of claim 71, wherein the protein expression level is determined by immunohistochemistry (IHC), Western blot, enzyme-linked immunosorbent assay (ELISA), immunoprecipitation, immunofluorescence, radioimmunoassay, or mass spectrometry.

73. The method of any one of claims 1-72, wherein the sample is a tissue sample, a cell sample, a whole blood sample, a plasma sample, a serum sample, or a combination thereof.

74. The method of claim 73, wherein the tissue sample is a tumor tissue sample.

75. The method of claim 74, wherein the tumor tissue sample comprises tumor cells, tumor-infiltrating immune cells, stromal cells, or a combination thereof.

76. The method of claim 74 or 75, wherein the tumor tissue sample is a formalin-fixed and paraffin-embedded (FFPE) sample, an archival sample, a fresh sample, or a frozen sample.

77. The method of any one of claims 1-76, wherein the individual has not been previously treated for the kidney cancer.

78. The method of any one of claims 1-77, wherein the kidney cancer is renal cell carcinoma (RCC).

79. The method of claim 78, wherein the RCC is metastatic RCC (mRCC).

80. The method of any one of claims 1-79, wherein the VEGF antagonist is an anti-VEGF antibody or a VEGF receptor (VEGFR) inhibitor.

81. The method of claim 80, wherein the VEGF antagonist is an anti-VEGF antibody.

82. The method of claim 81, wherein the anti-VEGF antibody is bevacizumab.

83. The method of claim 80, wherein the VEGF antagonist is a VEGFR inhibitor.

84. The method of claim 83, wherein the VEGFR inhibitor is a multi-targeted tyrosine kinase inhibitor.

85. The method of claim 84, wherein the multi-targeted tyrosine kinase inhibitor is sunitinib, axitinib, pazopanib, or cabozantinib.

86. The method of claim 85, wherein the multi-targeted tyrosine kinase inhibitor is sunitinib.

87. The method of any one of claims 1-54, 56-59, and 61-86, wherein the PD-L1 axis binding antagonist is selected from the group consisting of a PD-L1 binding antagonist, a PD-1 binding antagonist, and a PD-L2 binding antagonist.

88. The method of claim 87, wherein the PD-L1 axis binding antagonist is a PD-L1 binding antagonist.

89. The method of claim 88, wherein the PD-L1 binding antagonist inhibits the binding of PD-L1 to one or more of its ligand binding partners.

90. The method of claim 89, wherein the PD-L1 binding antagonist inhibits the binding of PD-L1 to PD-1.

91. The method of claim 89, wherein the PD-L1 binding antagonist inhibits the binding of PD-L1 to B7-1.

92. The method of any one of claims 88-91, wherein the PD-L1 binding antagonist inhibits the binding of PD-L1 to both PD-1 and B7-1.

93. The method of any one of claims 88-92, wherein the PD-L1 binding antagonist is an anti-PD-L1 antibody.

94. The method of claim 93, wherein the anti-PD-L1 antibody is selected from the group consisting of: MPDL3280A (atezolizumab), YW243.55.S70, MDX-1105, MEDI4736 (durvalumab), and MSB0010718C (avelumab).

95. The method of claim 93 or 94, wherein the anti-PD-L1 antibody comprises the following hypervariable regions (HVRs):

- (a) an HVR-H1 sequence of GFTFSDSWIH (SEQ ID NO: 63);
- (b) an HVR-H2 sequence of AWISPYGGSTYYADSVKG (SEQ ID NO: 64);
- (c) an HVR-H3 sequence of RHWPGGFDY (SEQ ID NO: 65);
- (d) an HVR-L1 sequence of RASQDVSTAVA (SEQ ID NO: 66);
- (e) an HVR-L2 sequence of SASFLYS (SEQ ID NO: 67); and
- (f) an HVR-L3 sequence of QQYLYHPAT (SEQ ID NO: 68).

96. The method of any one of claims 93-95, wherein the anti-PD-L1 antibody comprises:

(a) a heavy chain variable (VH) domain comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of
EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWRQAPGKGLEWVAWISPYGGSTYYADSVKGGRF
TISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSS (SEQ ID NO: 69);

(b) a light chain variable (VL) domain comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of

DIQMTQSPSSLSASVGDRVITTCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTD
FTLTISLQPEDFATYYCQQYLYHPATFGGGTKVEIKR (SEQ ID NO: 70); or

(c) a VH domain as in (a) and a VL domain as in (b).

97. The method of claim 96, wherein the anti-PD-L1 antibody comprises:

(a) a VH domain comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 69;

(b) a VL domain comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 70; or

(c) a VH domain as in (a) and a VL domain as in (b).

98. The method of claim 97, wherein the anti-PD-L1 antibody comprises:

(a) a VH domain comprising an amino acid sequence having at least 96% sequence identity to the amino acid sequence of SEQ ID NO: 69;

(b) a VL domain comprising an amino acid sequence having at least 96% sequence identity to the amino acid sequence of SEQ ID NO: 70; or

(c) a VH domain as in (a) and a VL domain as in (b).

99. The method of claim 98, wherein the anti-PD-L1 antibody comprises:

(a) a VH domain comprising an amino acid sequence having at least 97% sequence identity to the amino acid sequence of SEQ ID NO: 69;

(b) a VL domain comprising an amino acid sequence having at least 97% sequence identity to the amino acid sequence of SEQ ID NO: 70; or

(c) a VH domain as in (a) and a VL domain as in (b).

100. The method of claim 99, wherein the anti-PD-L1 antibody comprises:

(a) a VH domain comprising an amino acid sequence having at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 69;

(b) a VL domain comprising an amino acid sequence having at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 70; or

(c) a VH domain as in (a) and a VL domain as in (b).

101. The method of claim 100, wherein the anti-PD-L1 antibody comprises:

(a) a VH domain comprising an amino acid sequence having at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 69;

(b) a VL domain comprising an amino acid sequence having at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 70; or

(c) a VH domain as in (a) and a VL domain as in (b).

102. The method of claim 101, wherein the anti-PD-L1 antibody comprises:

- (a) a VH domain comprising the amino acid sequence of SEQ ID NO: 69;
- (b) a VL domain comprising the amino acid sequence of SEQ ID NO: 70; or
- (c) a VH domain as in (a) and a VL domain as in (b).

103. The method of claim 102, wherein the anti-PD-L1 antibody comprises:

- (a) a VH domain comprising the amino acid sequence of SEQ ID NO: 69; and
- (b) a VL domain comprising the amino acid sequence of SEQ ID NO: 70.

104. The method of claim 103, wherein the anti-PD-L1 antibody is atezolizumab.

105. The method of any one of claims 1-104, further comprising administering an additional therapeutic agent to the individual.

106. The method of claim 105, wherein the additional therapeutic agent is selected from the group consisting of an immunotherapy agent, a cytotoxic agent, a growth inhibitory agent, a radiation therapy agent, an anti-angiogenic agent, and combinations thereof.

107. The method of any one of claims 1-106, wherein the individual is a human.

108. A kit for identifying an individual having a kidney cancer who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist, the kit comprising:

- (a) reagents for determining the expression level of determining the expression level of one or more of the following genes in a sample from the individual:

CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2;
VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or
IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2; and, optionally,

(b) instructions for using the reagents to identify an individual having a kidney cancer who may benefit from a treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist.

109. The kit of claim 108, wherein the kit comprises reagents for determining the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2.

110. The kit of claim 109, wherein the kit comprises reagents for determining the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES,

GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2.

111. The kit of claim 109 or 110, wherein the kit comprises reagents for determining the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1.

112. The kit of claim 111, wherein the kit comprises reagents for determining the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

113. The kit of any one of claims 108-112, wherein the kit comprises reagents for determining the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2.

114. The kit of claim 113, wherein the kit comprises reagents for determining the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2.

115. The kit of claim 113 or 114, wherein the kit comprises reagents for determining the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

116. The kit of any one of claims 108-115, wherein the kit comprises reagents for determining the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34.

117. The kit of claim 116, wherein the kit comprises reagents for determining the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34.

118. The kit of claim 116 or 117, wherein the kit comprises reagents for determining the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34.

119. The kit of claim 118, wherein the kit comprises reagents for determining the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

120. The kit of any one of claims 108-119, wherein the kit comprises reagents for determining the expression level of PD-L1 and one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2.

121. A kit for identifying an individual having a kidney cancer who may benefit from treatment with a VEGF antagonist, the kit comprising:

(a) reagents for determining the expression level of determining the expression level of one or more of the following genes in a sample from the individual:

VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; and, optionally,

(b) instructions for using the reagents to identify an individual having a kidney cancer who may benefit from a treatment with an anti-cancer therapy comprising a VEGF antagonist.

122. The kit of claim 121, wherein the anti-cancer therapy further comprises a PD-L1 axis binding antagonist.

123. The kit of claim 121 or 122, wherein the kit comprises reagents for determining the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34.

124. The kit of any one of claims 121-123, wherein the kit comprises reagents for determining the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34.

125. The kit of claim 124, wherein the kit comprises reagents for determining the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

126. An assay for identifying an individual having a kidney cancer who is a candidate for treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist, the assay comprising determining the expression level of one or more of the following genes in a sample from the individual:

CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2;
VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or
IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2;

wherein

(i) an expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample that is above a reference expression level of the one or more genes; or

(ii) an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample that is below a reference expression level of the one or more genes

identifies the individual as one who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist.

127. The assay of claim 126, wherein the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1,

PSMB8, PSMB9, TAP1, or TAP2 in the sample is at or above a reference expression level of the one or more genes.

128. The assay of claim 127, wherein the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 is at or above a reference expression level of the one or more genes.

129. The assay of claim 127 or 128, wherein the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample is at or above a reference expression level of the one or more genes.

130. The assay of claim 129, wherein the expression level of CD8A, EOMES, PRF1, IFNG, or PD-L1 in the sample is at or above a reference expression level of CD8A, EOMES, PRF1, IFNG, or PD-L1.

131. The assay of any one of claims 127-130, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is at or above a reference expression level of the one or more genes.

132. The assay of claim 131, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is at or above a reference expression level of the one or more genes.

133. The assay of claim 131 or 132, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 in the sample is at or above a reference expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

134. The assay of any one of claims 126-133, wherein the expression level of PD-L1 in the sample is at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample is at or above a reference expression level of the one or more additional genes.

135. The assay of any one of claims 126-134, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes.

136. The assay of claim 135, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes.

137. The assay of claim 135 or 136, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is below a reference level of the one or more genes.

138. The assay of claim 137, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

139. The assay of any one of claims 126-138, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is below a reference level of the one or more genes.

140. The assay of claim 139, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample is below a reference level of the one or more genes.

141. The assay of claim 139 or 140, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 in the sample is below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

142. An assay for identifying an individual having a kidney cancer who is a candidate for treatment comprising a VEGF antagonist, the assay comprising determining the expression level of one or more of the following genes in a sample from the individual:

VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34,

wherein an expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample that is above a reference expression level of the one or more genes identifies the individual as one who may benefit from treatment with an anti-cancer therapy comprising a VEGF antagonist.

143. The assay of claim 142, wherein the anti-cancer therapy further comprises a PD-L1 axis binding antagonist.

144. The assay of claim 142 or 143, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is at or above a reference level of the one or more genes.

145. The assay of any one of claims 142-144, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample is above a reference level of the one or more genes.

146. The assay of claim 145, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample is above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

147. An anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use in a method of treating an individual suffering from a kidney cancer, wherein prior to treatment (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in a sample from the individual has been determined to be above a reference expression level of the one or more genes; or (ii) the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in a sample from the individual has been determined to be below a reference expression level of the one or more genes.

148. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 147, wherein the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 has been determined to be at or above a reference level of the one or more genes.

149. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 148, wherein the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference level of the one or more genes.

150. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 148 or 149, wherein the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 has been determined to be at or above a reference level of the one or more genes.

151. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 150, wherein the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

152. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of any one of claims 148-151, wherein the expression level of one or more of IL6, CXCL1, CXCL2,

CXCL3, CXCL8, or PTGS2 has been determined to be at or above a reference level of the one or more genes.

153. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 152, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be at or above a reference level of the one or more genes.

154. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 152 or 153, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 has been determined to be at or above a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

155. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of any one of claims 148-154, wherein the expression level of PD-L1 in the sample has been determined to be at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more additional genes.

156. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 147, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes.

157. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 156, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes.

158. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 156 or 157, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes.

159. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 158, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

160. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 147, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be below a reference level of the one or more genes.

161. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 160, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be below a reference level of the one or more genes.

162. The anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist for use of claim 160 or 161, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 in the sample has been determined to be below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

163. Use of an anti-cancer therapy comprising a VEGF antagonist and a PD-L1 axis binding antagonist in the manufacture of a medicament for treating an individual suffering from a kidney cancer, wherein prior to treatment (i) the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in a sample from the individual has been determined to be above a reference expression level of the one or more genes; or (ii) the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34; or IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in a sample from the individual has been determined to be below a reference expression level of the one or more genes.

164. The use of claim 163, wherein the expression level of one or more of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 has been determined to be at or above a reference level of the one or more genes.

165. The use of claim 164, wherein the expression level of at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or all twenty of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, PD-L1, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference level of the one or more genes.

166. The use of claim 163 or 165, wherein the expression level of one or more of CD8A, EOMES, PRF1, IFNG, or PD-L1 has been determined to be at or above a reference level of the one or more genes.

167. The use of claim 166, wherein the expression level of CD8A, EOMES, PRF1, IFNG, and PD-L1 has been determined to be at or above a reference level of CD8A, EOMES, PRF1, IFNG, and PD-L1.

168. The use of any one of claims 164-167, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 has been determined to be at or above a reference level of the one or more genes.

169. The use of claim 168, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be at or above a reference level of the one or more genes.

170. The use of claim 168 or 169, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 has been determined to be at or above a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

171. The use of any one of claims 163-170, wherein the expression level of PD-L1 in the sample has been determined to be at or above a reference expression level of PD-L1, and the expression level of one or more additional genes selected from the group consisting of CD8A, EOMES, GZMA, GZMB, PRF1, IFNG, CXCL9, CXCL10, CXCL11, CD27, FOXP3, PD-1, CTLA4, TIGIT, IDO1, PSMB8, PSMB9, TAP1, or TAP2 in the sample has been determined to be at or above a reference expression level of the one or more additional genes.

172. The use of claim 171, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes.

173. The use of claim 172, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes.

174. The use of claim 172 or 173, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be below a reference level of the one or more genes.

175. The use of claim 174, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be below a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

176. The use of claim 163, wherein the expression level of one or more of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be below a reference level of the one or more genes.

177. The use of claim 176, wherein the expression level of at least one, at least two, at least three, at least four, at least five, or all six of IL6, CXCL1, CXCL2, CXCL3, CXCL8, or PTGS2 in the sample has been determined to be below a reference level of the one or more genes.

178. The use of claim 176 or 177, wherein the expression level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2 in the sample has been determined to be below a reference level of IL6, CXCL1, CXCL2, CXCL3, CXCL8, and PTGS2.

179. A VEGF antagonist for use in a method of treating an individual suffering from a kidney cancer, wherein prior to treatment the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in a sample from the individual has been determined to be above a reference expression level of the one or more genes.

180. The VEGF antagonist for use of claim 179, wherein the VEGF antagonist is formulated for use in combination with a PD-L1 axis binding antagonist.

181. The VEGF antagonist for use of claim 179 or 180, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes.

182. The VEGF antagonist for use of any one of claims 179-181, wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes.

183. The VEGF antagonist for use of claim 182, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

184. Use of a VEGF antagonist in the manufacture of a medicament for treating an individual suffering from a kidney cancer, wherein prior to treatment the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in a sample from the individual has been determined to be above a reference expression level of the one or more genes.

185. The use of claim 184, wherein the medicament is formulated for use in combination with a PD-L1 axis binding antagonist.

186. The use of claim 184 or 185, wherein the expression level of at least one, at least two, at least three, at least four, at least five, at least six, or all seven of VEGFA, KDR, ESM1, PECAM1, FLT1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes.

187. The use of any one of claims 184-186 wherein the expression level of one or more of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, or CD34 in the sample has been determined to be at or above a reference level of the one or more genes.

188. The use of claim 187, wherein the expression level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34 in the sample has been determined to be at or above a reference level of VEGFA, KDR, ESM1, PECAM1, ANGPTL4, and CD34.

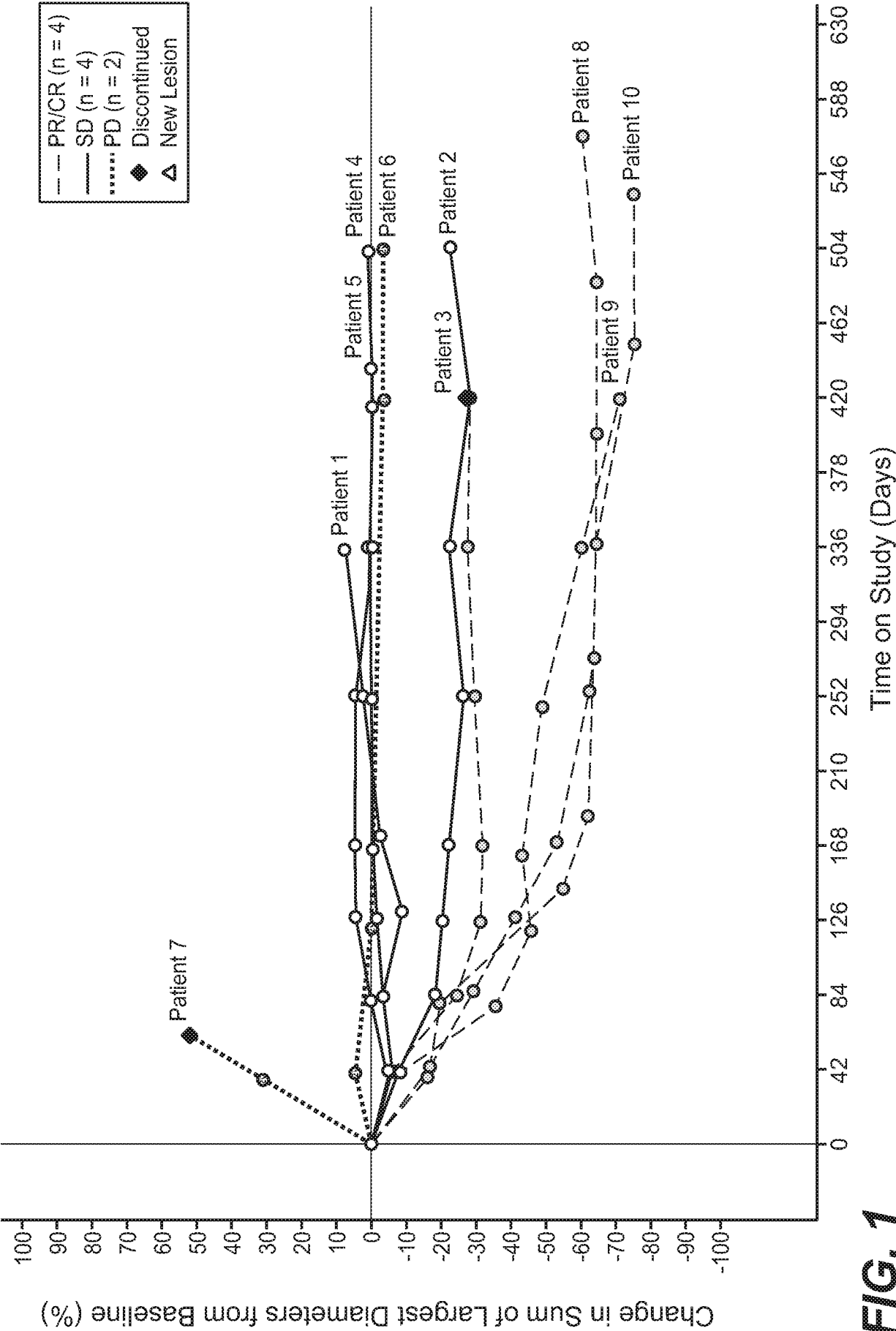


FIG. 1

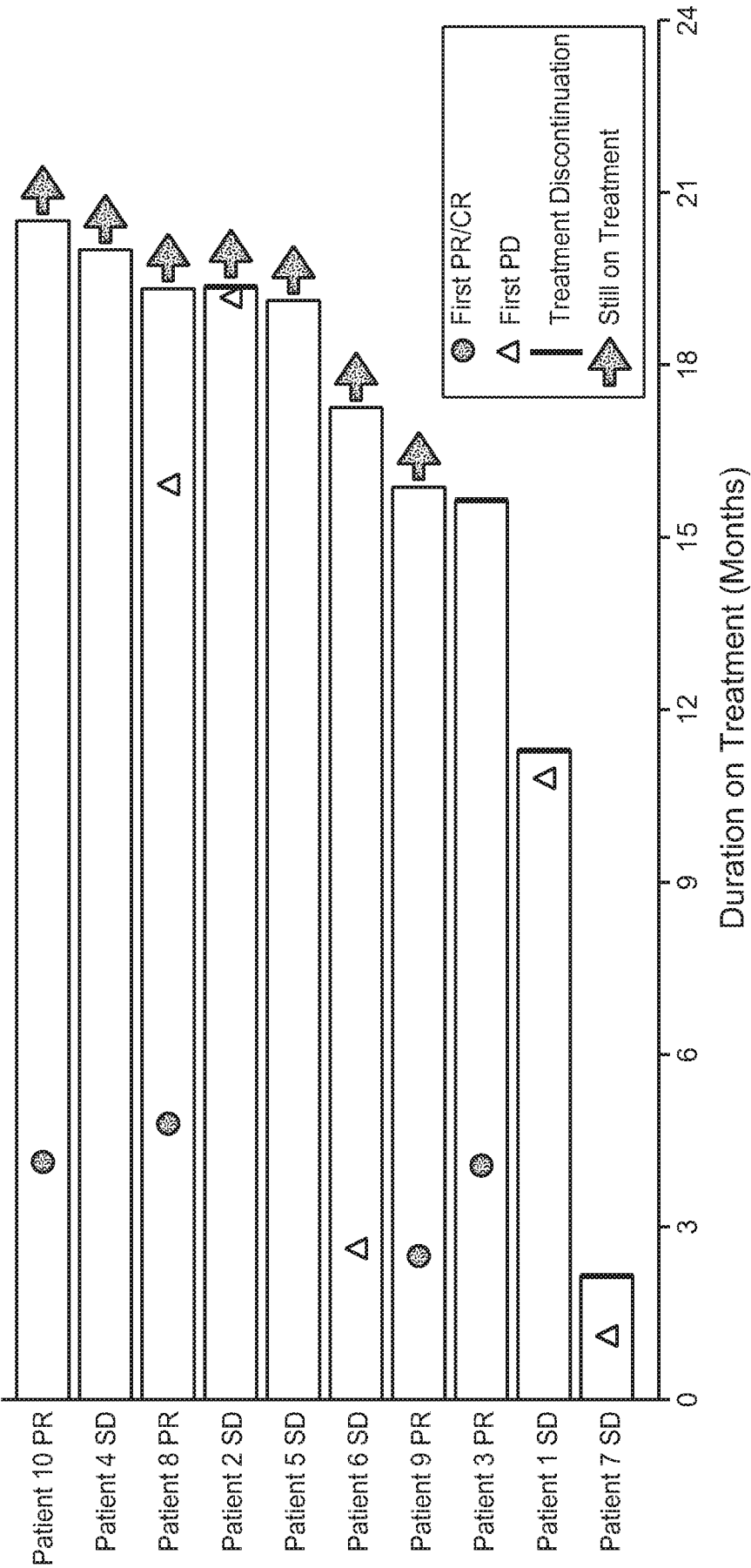
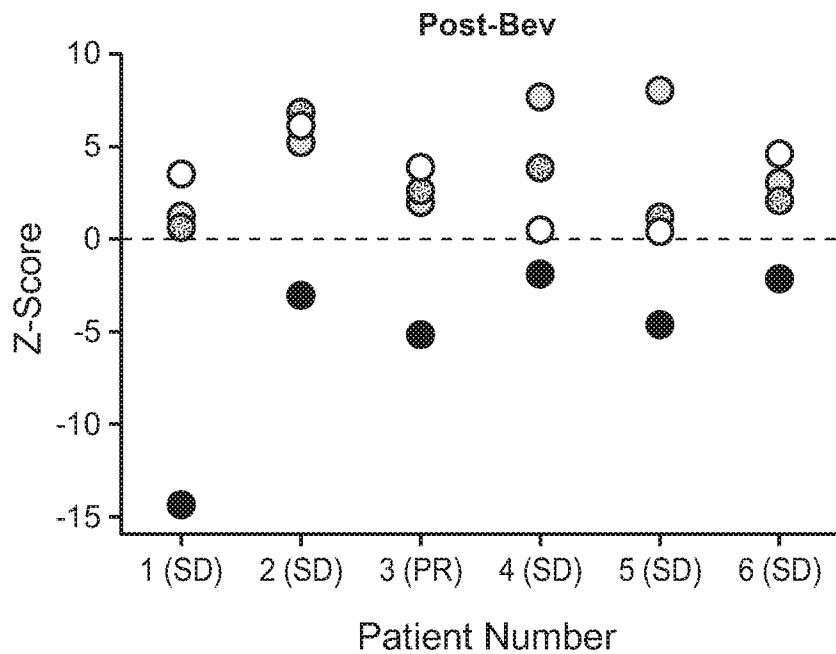
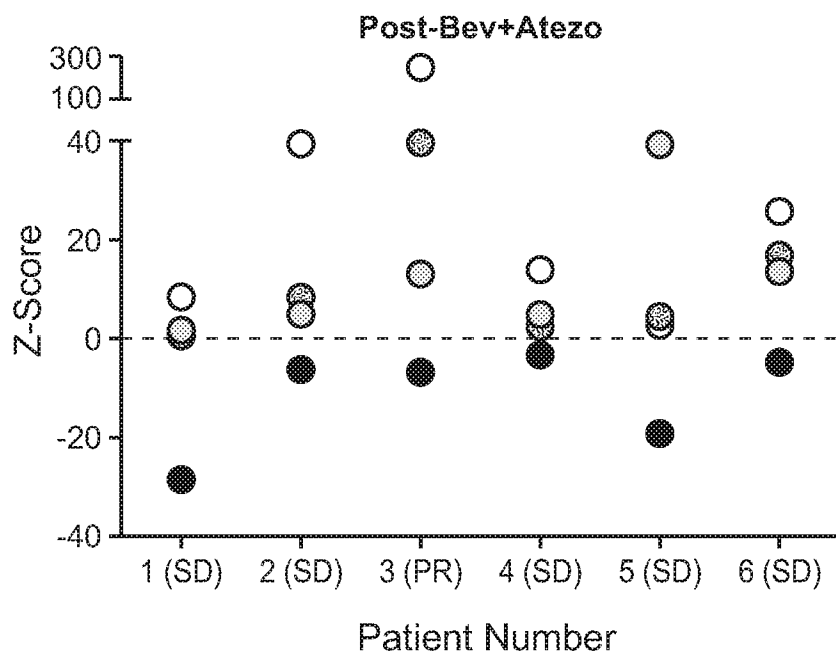
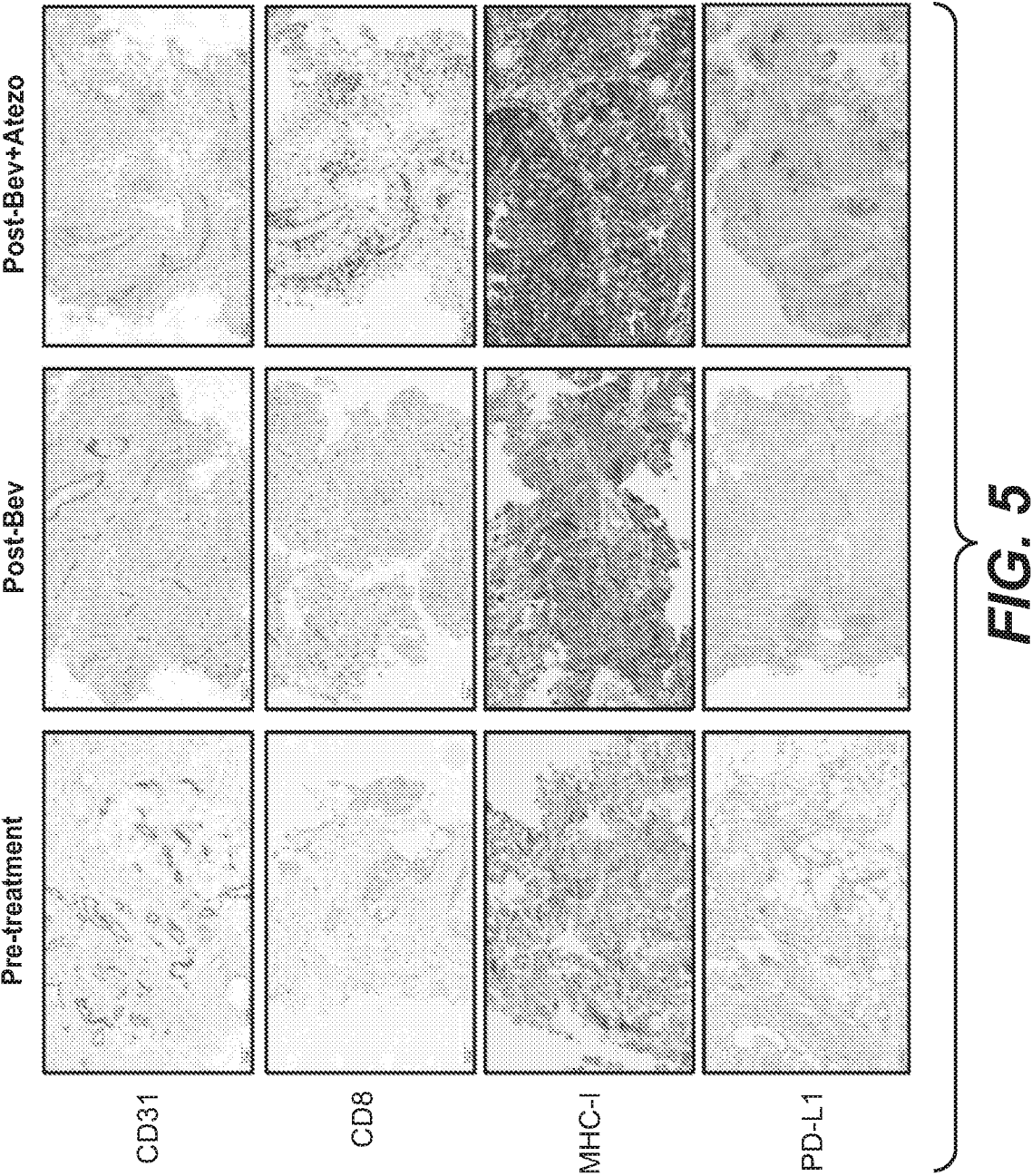


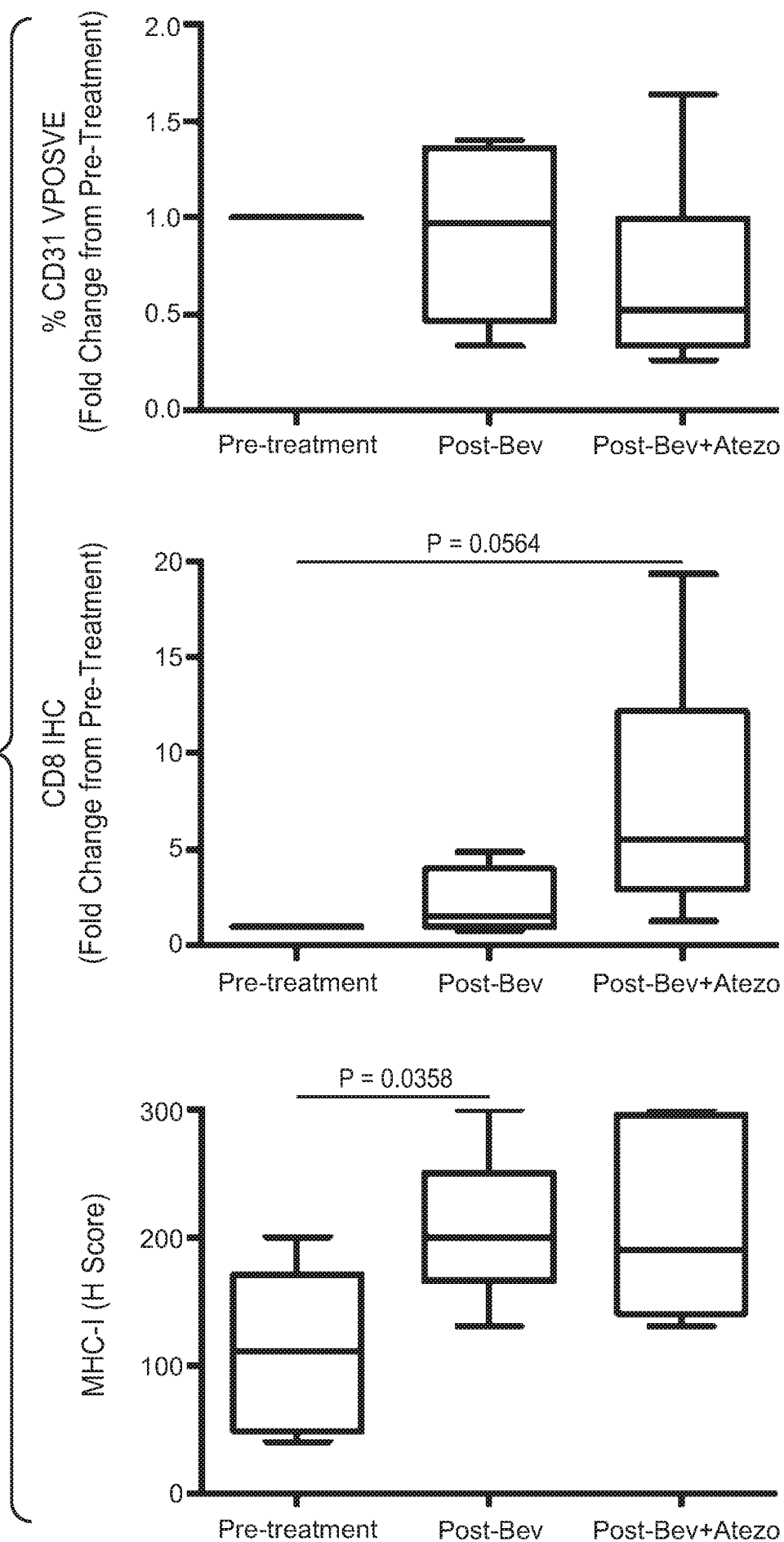
FIG. 2

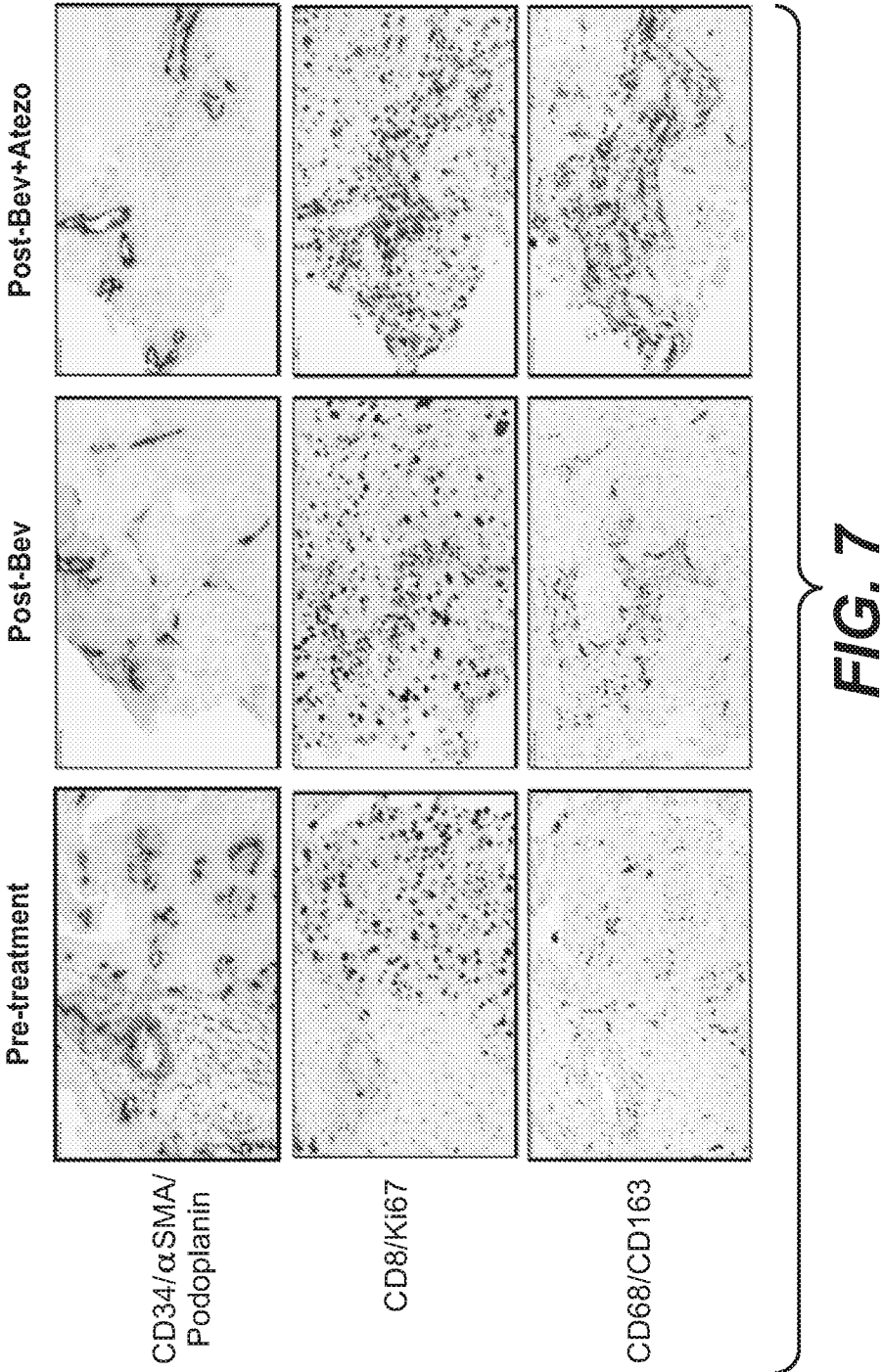
3 / 63

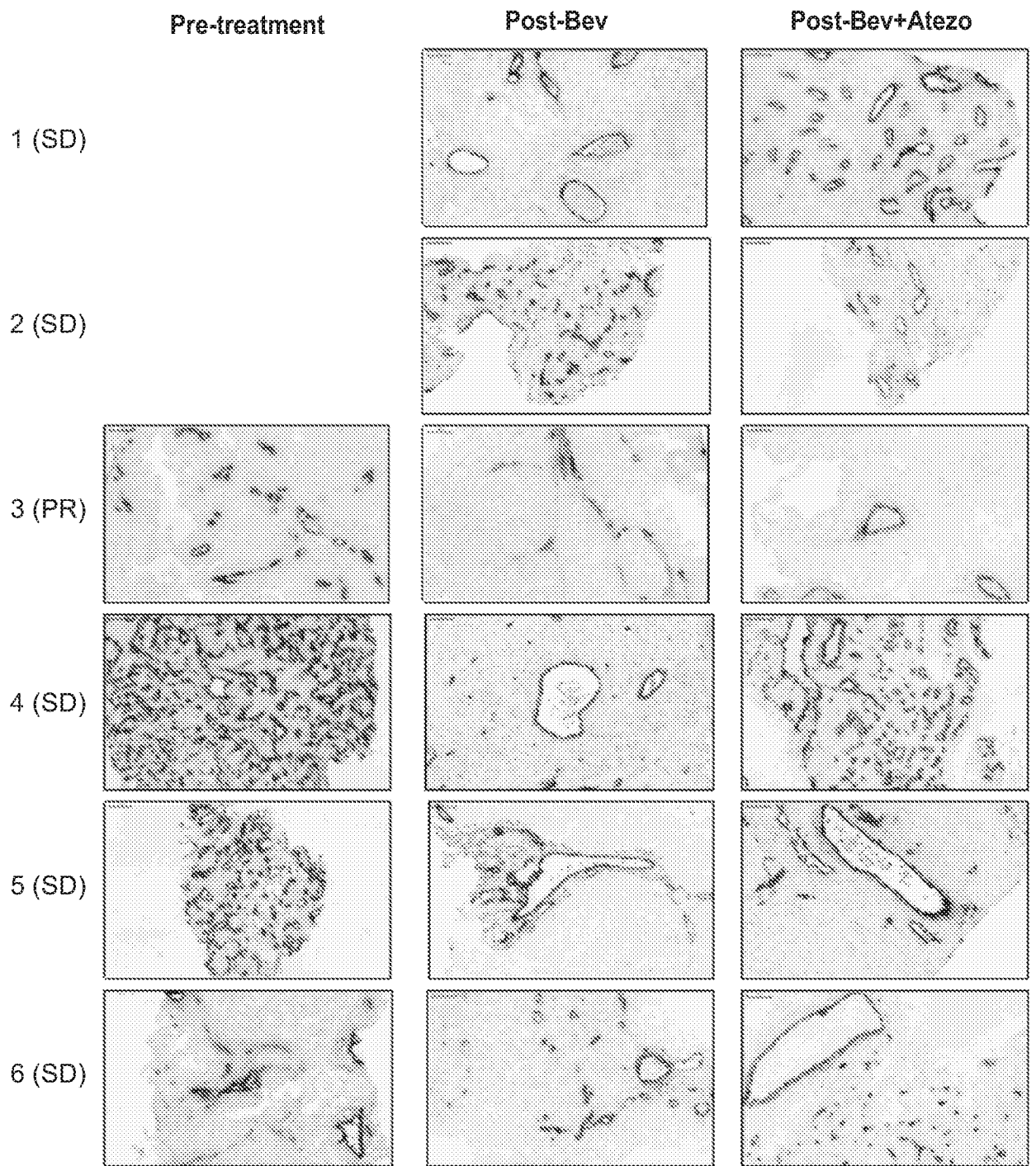
**FIG. 3****FIG. 4**

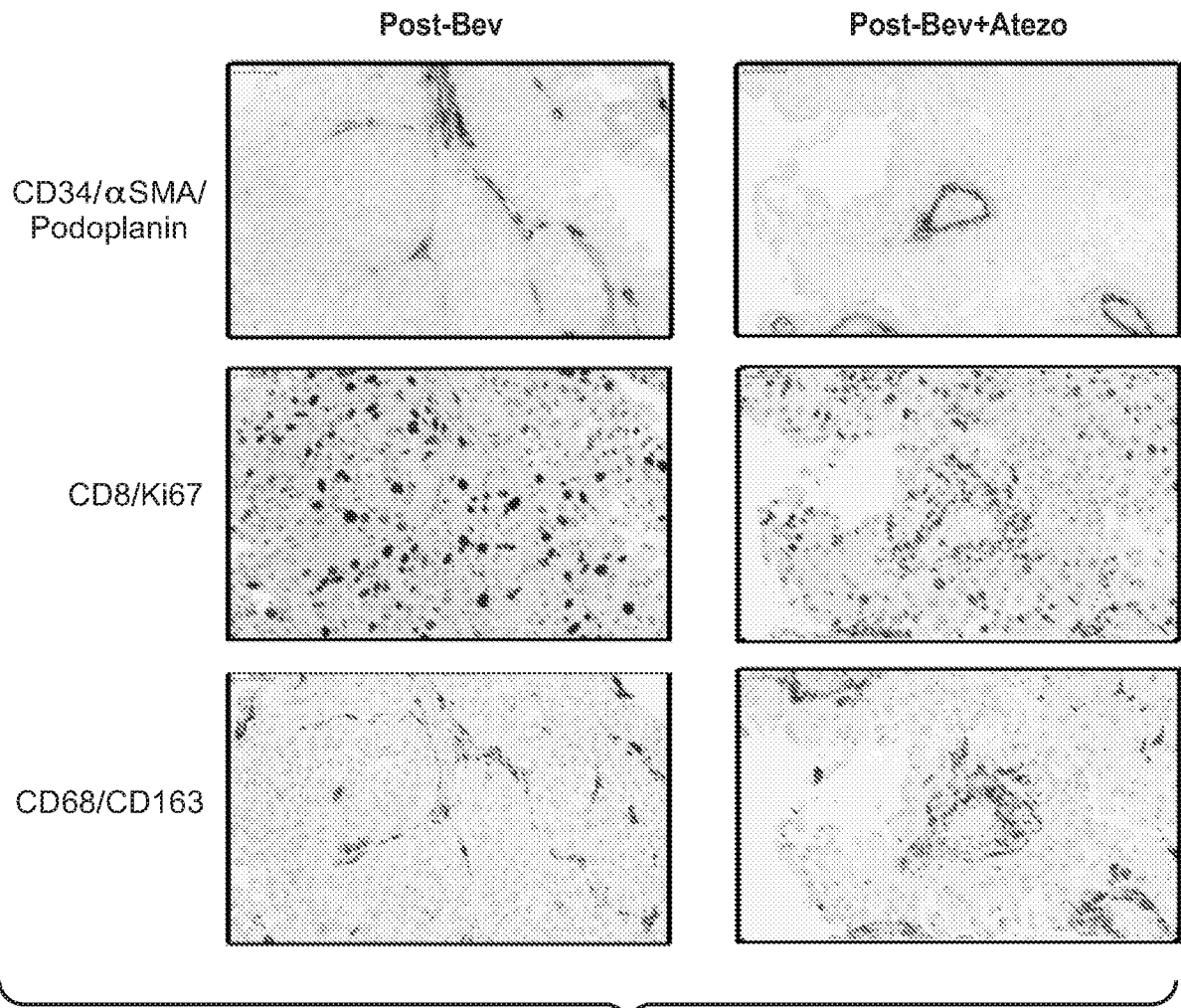


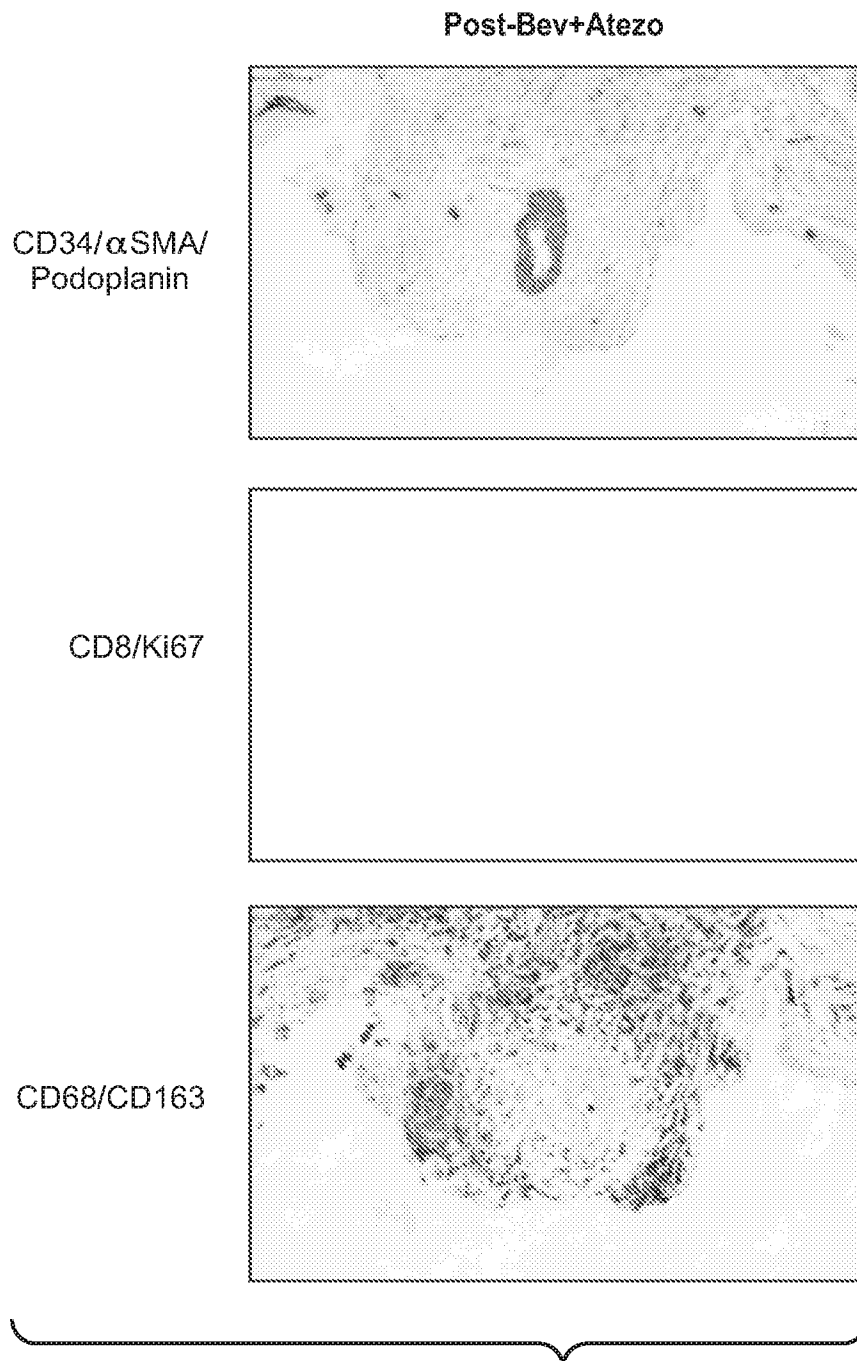
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FIG. 6

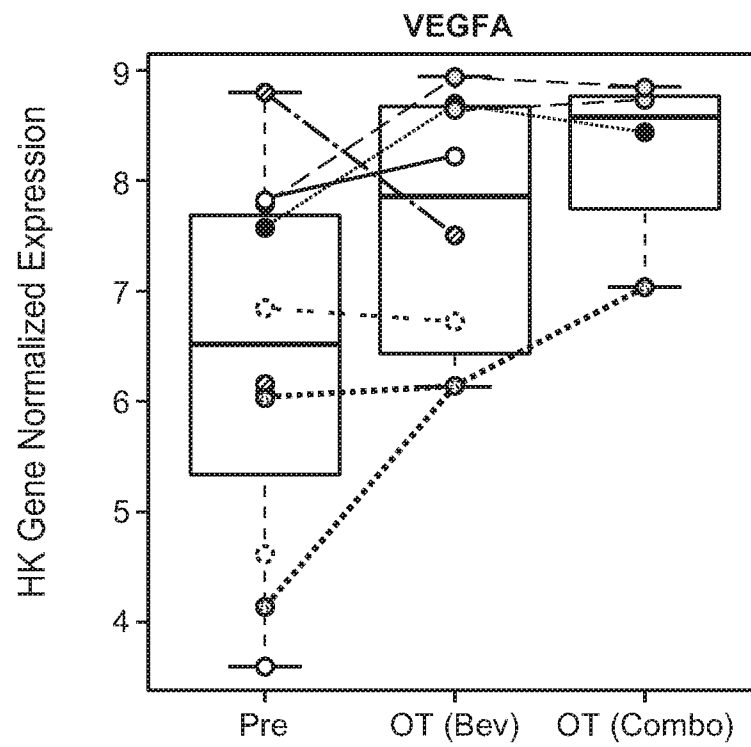


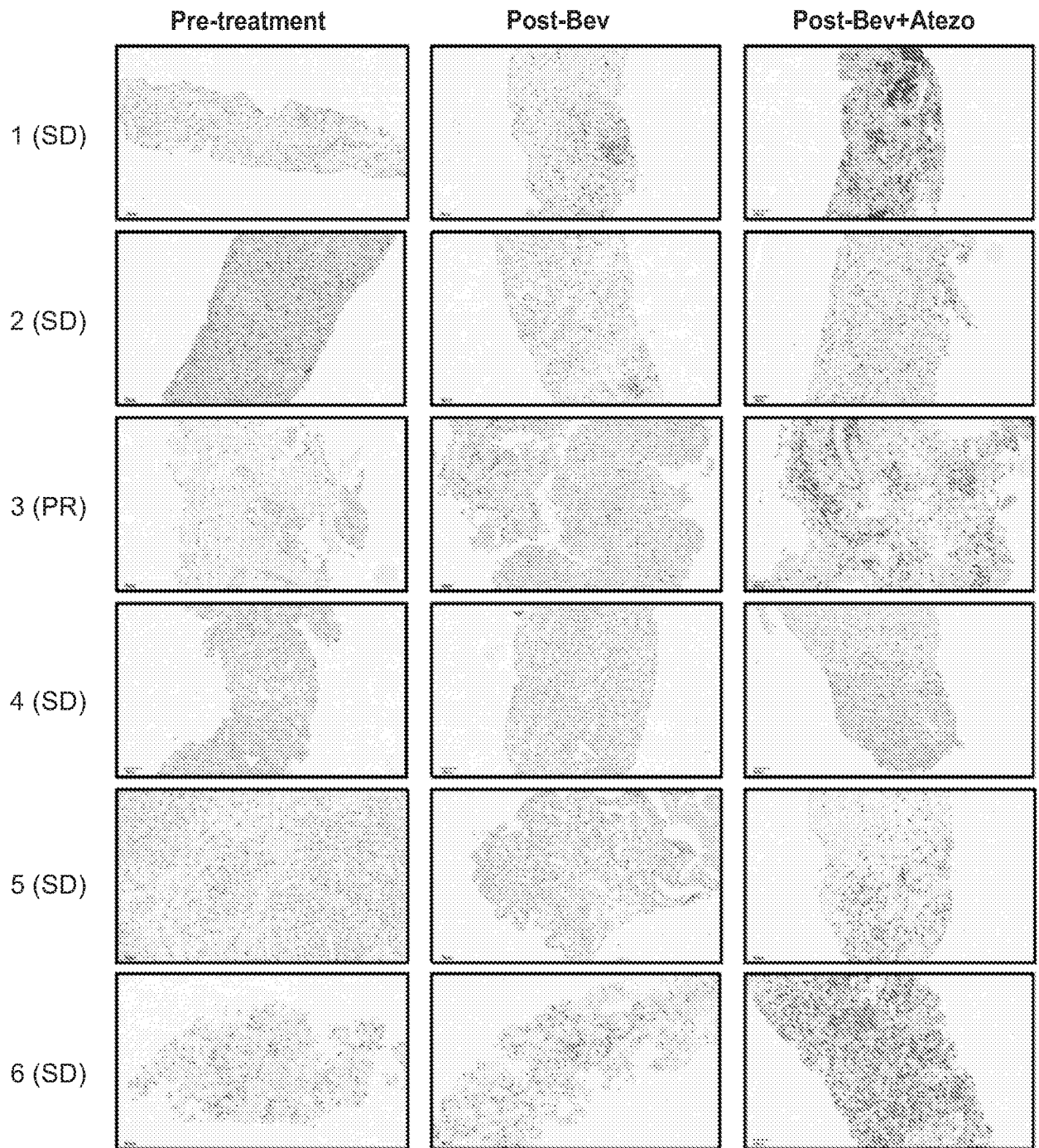
**FIG. 8**

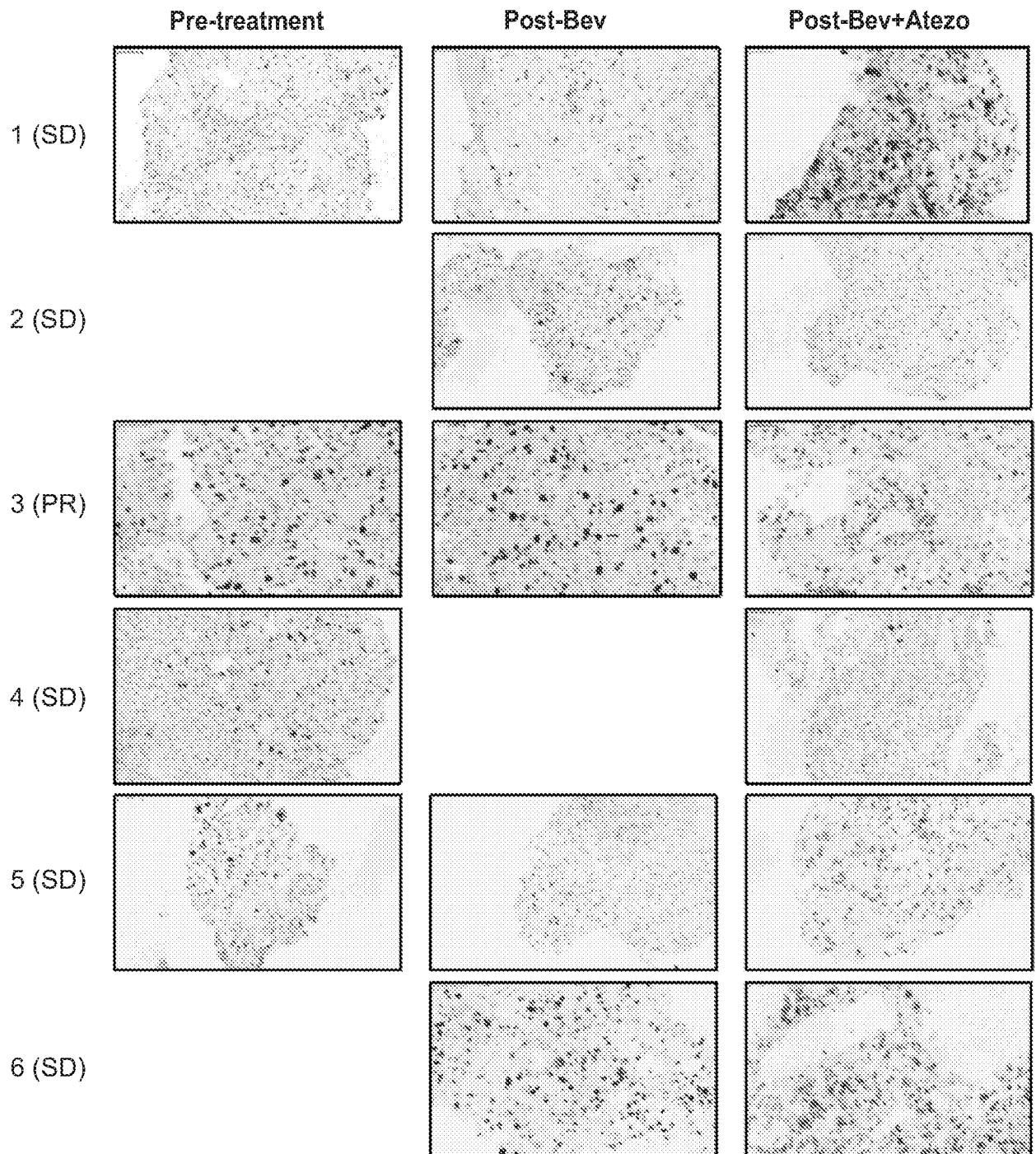
**FIG. 9**

**FIG. 10**

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**FIG. 11**

**FIG. 12**

**FIG. 13**

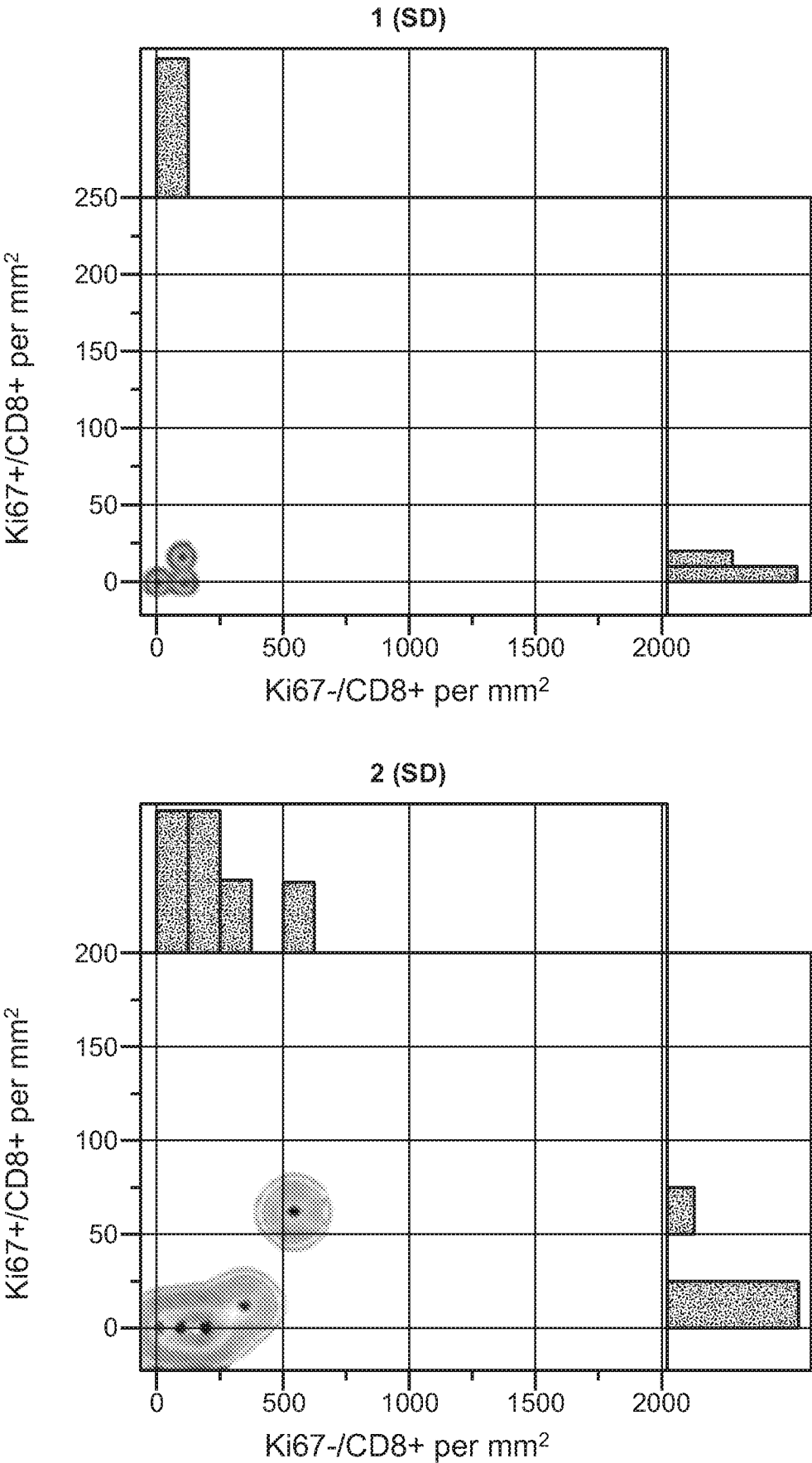
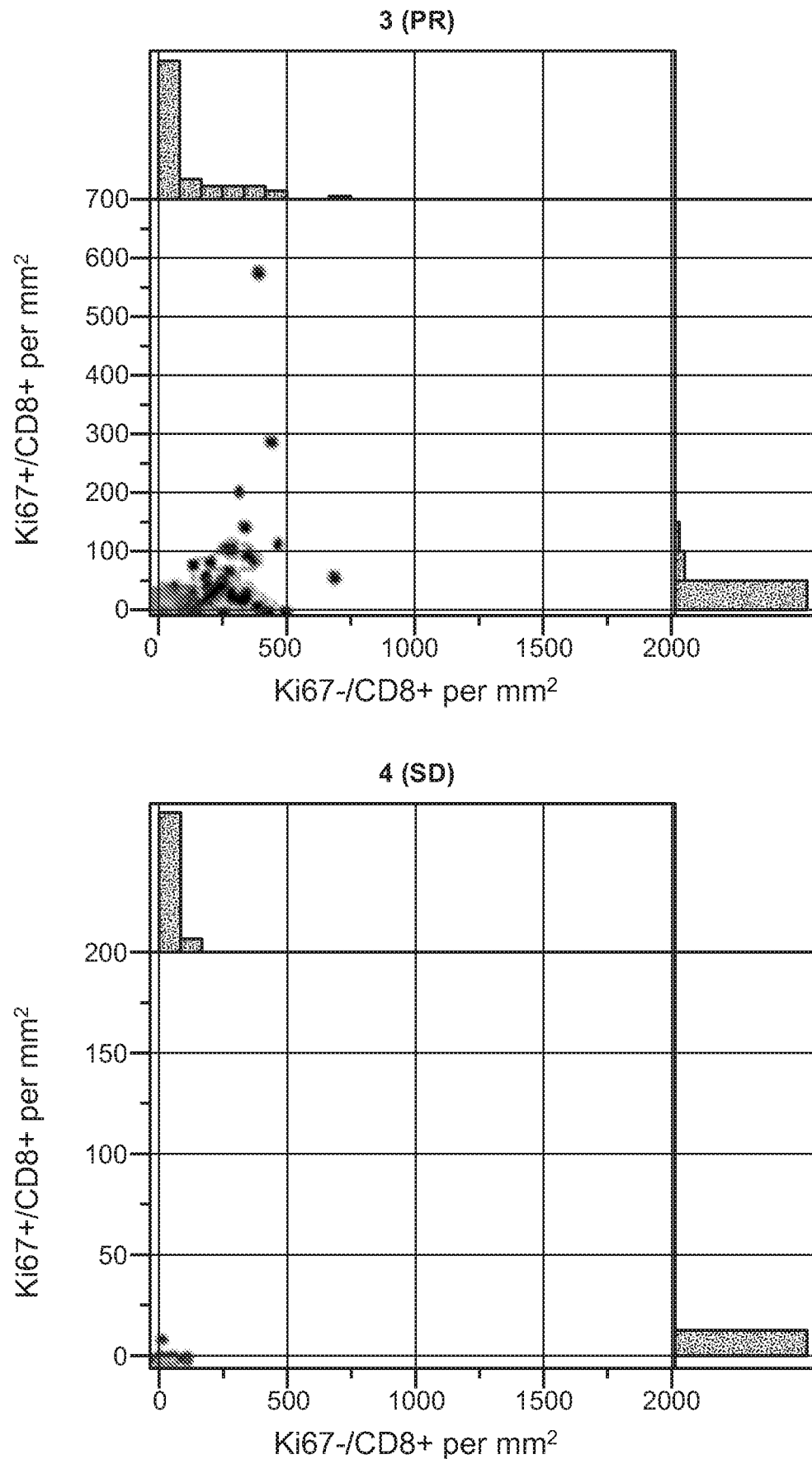


FIG. 14A

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**FIG. 14B**

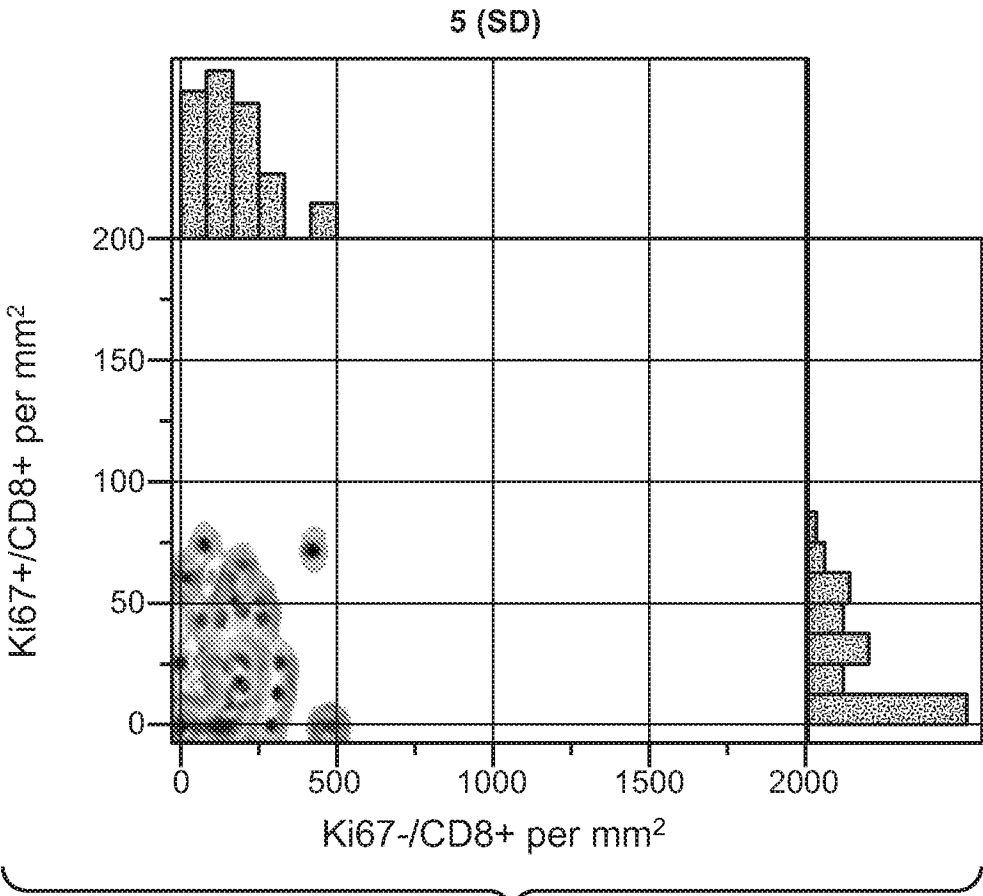
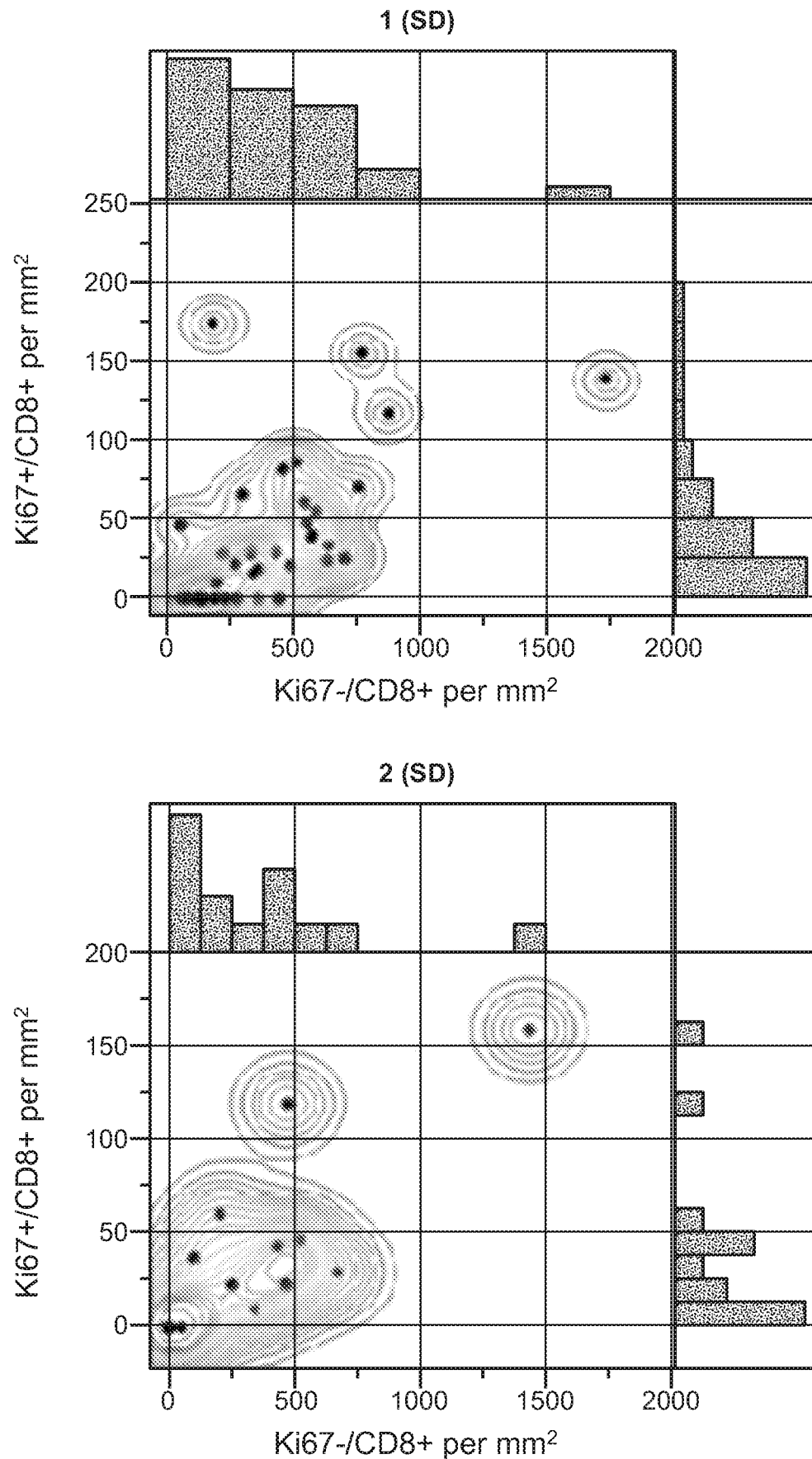


FIG. 14C

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**FIG. 15A**

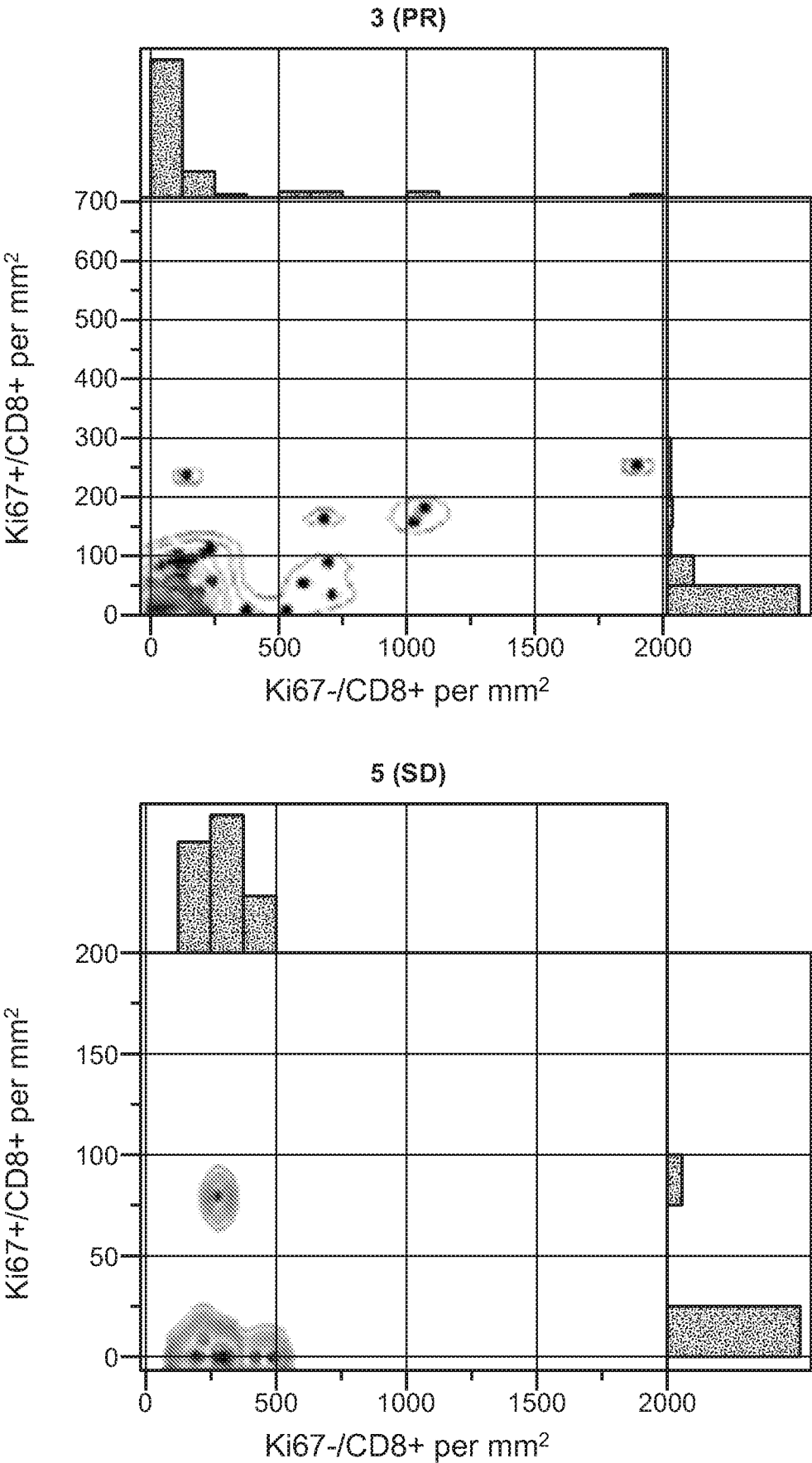


FIG. 15B

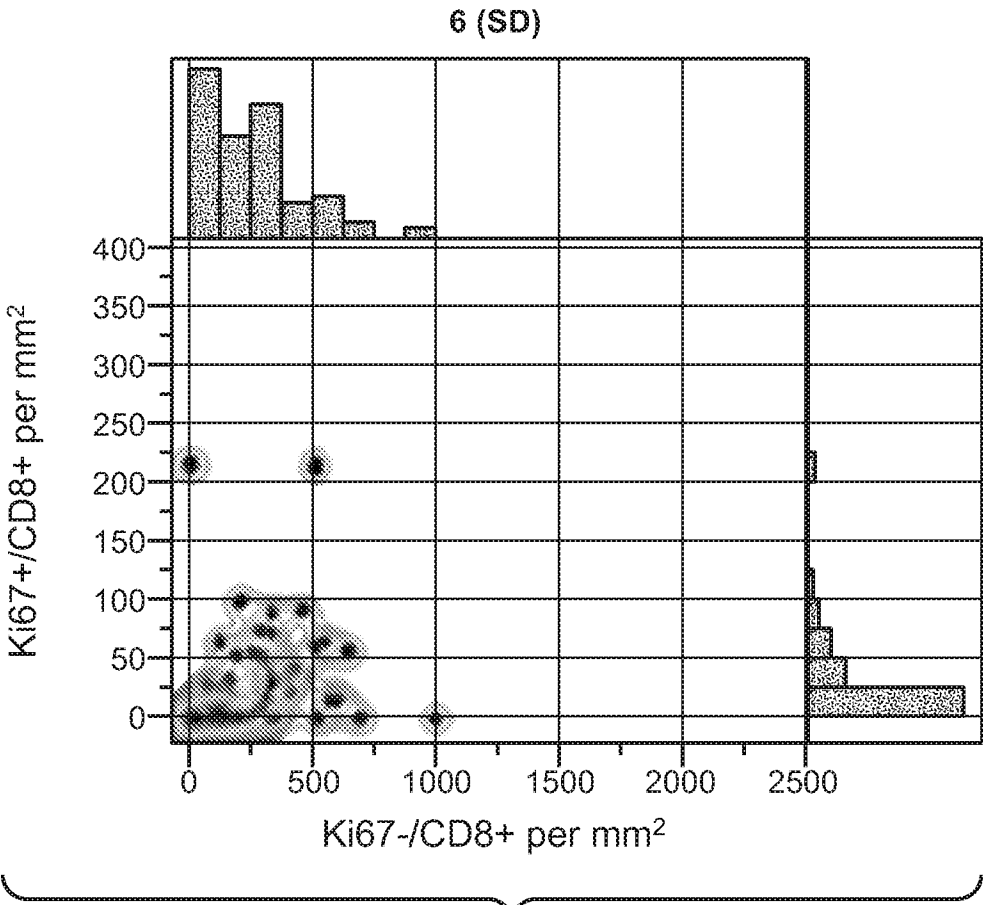
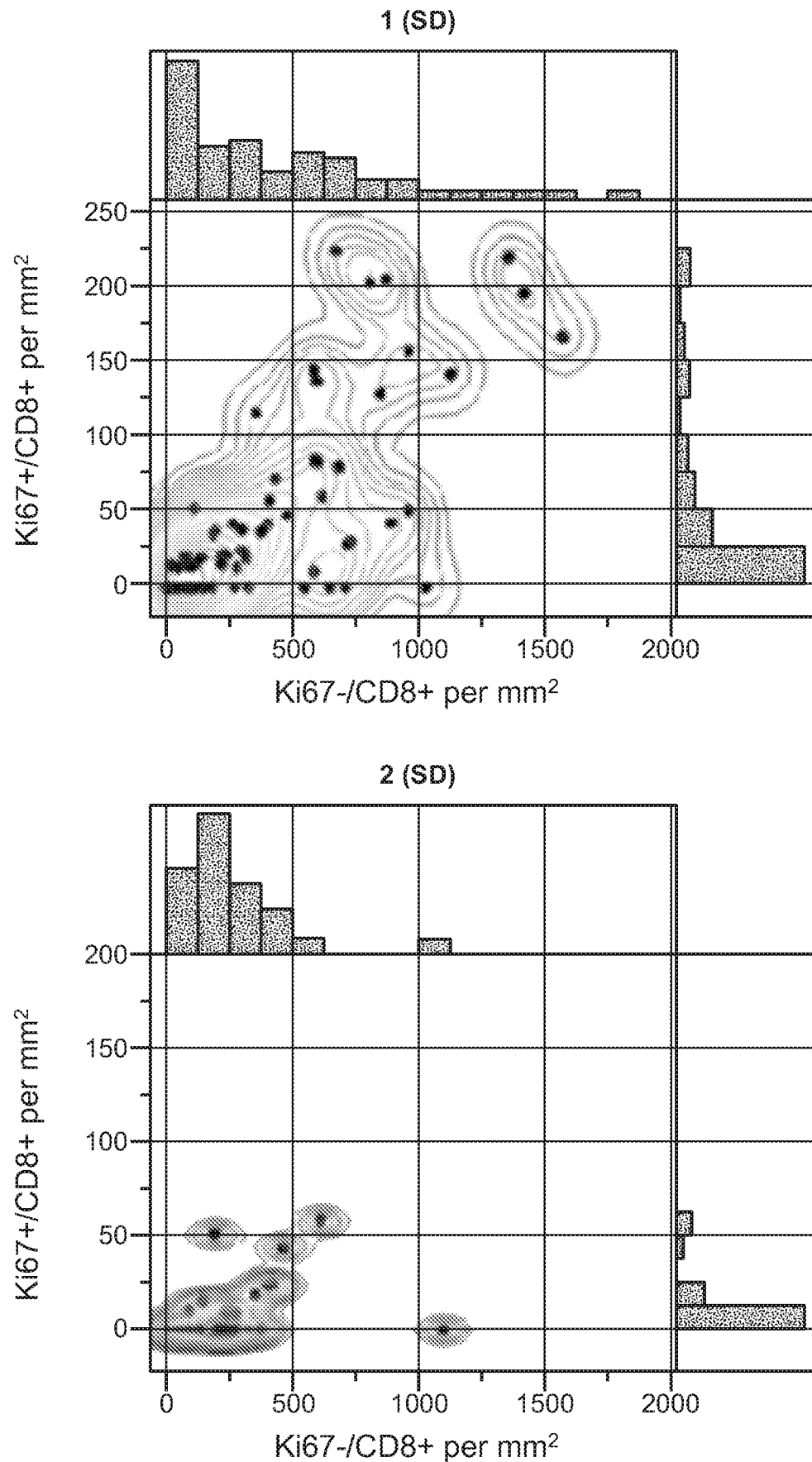
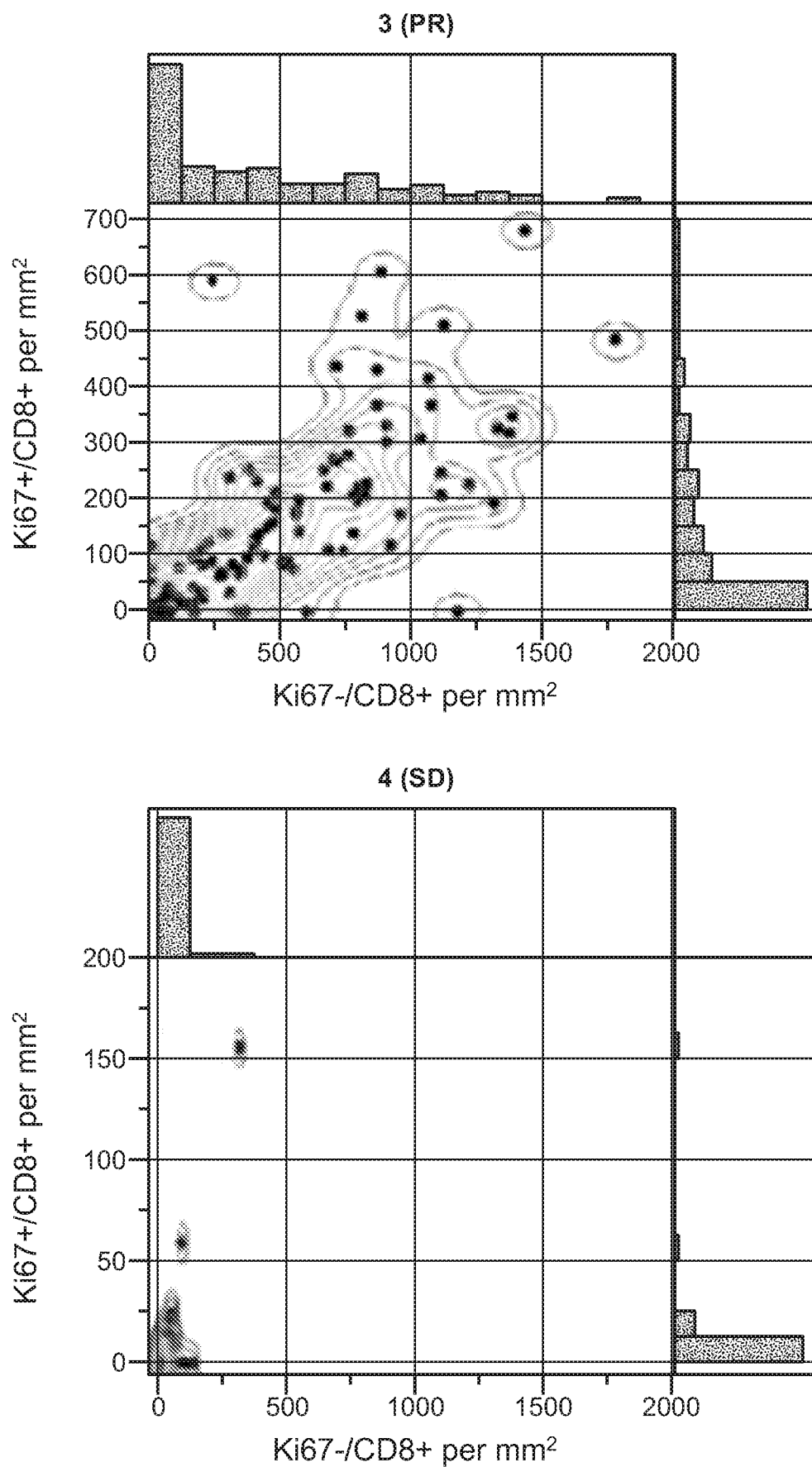


FIG. 15C

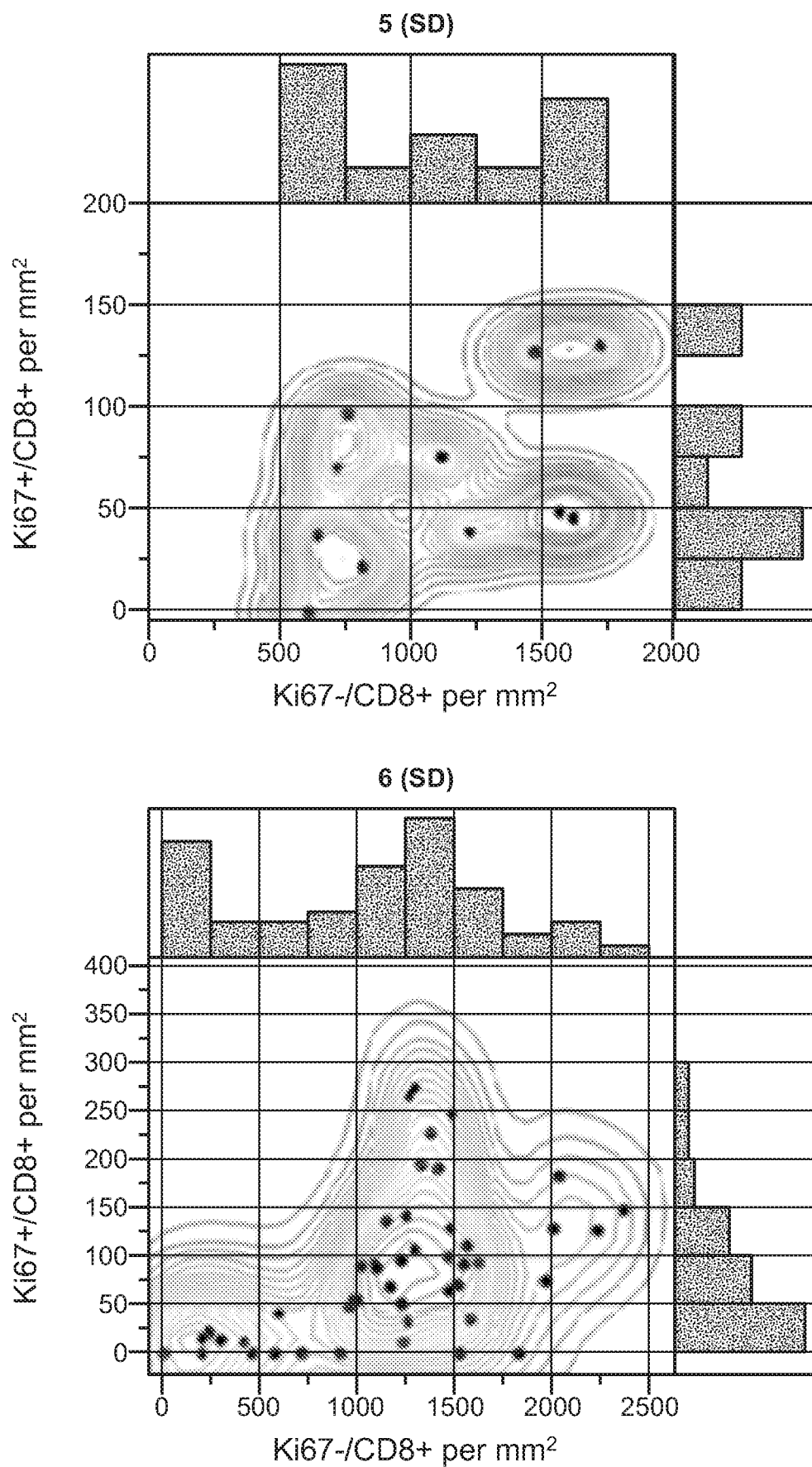
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**FIG. 16A**

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**FIG. 16B**

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**FIG. 16C**

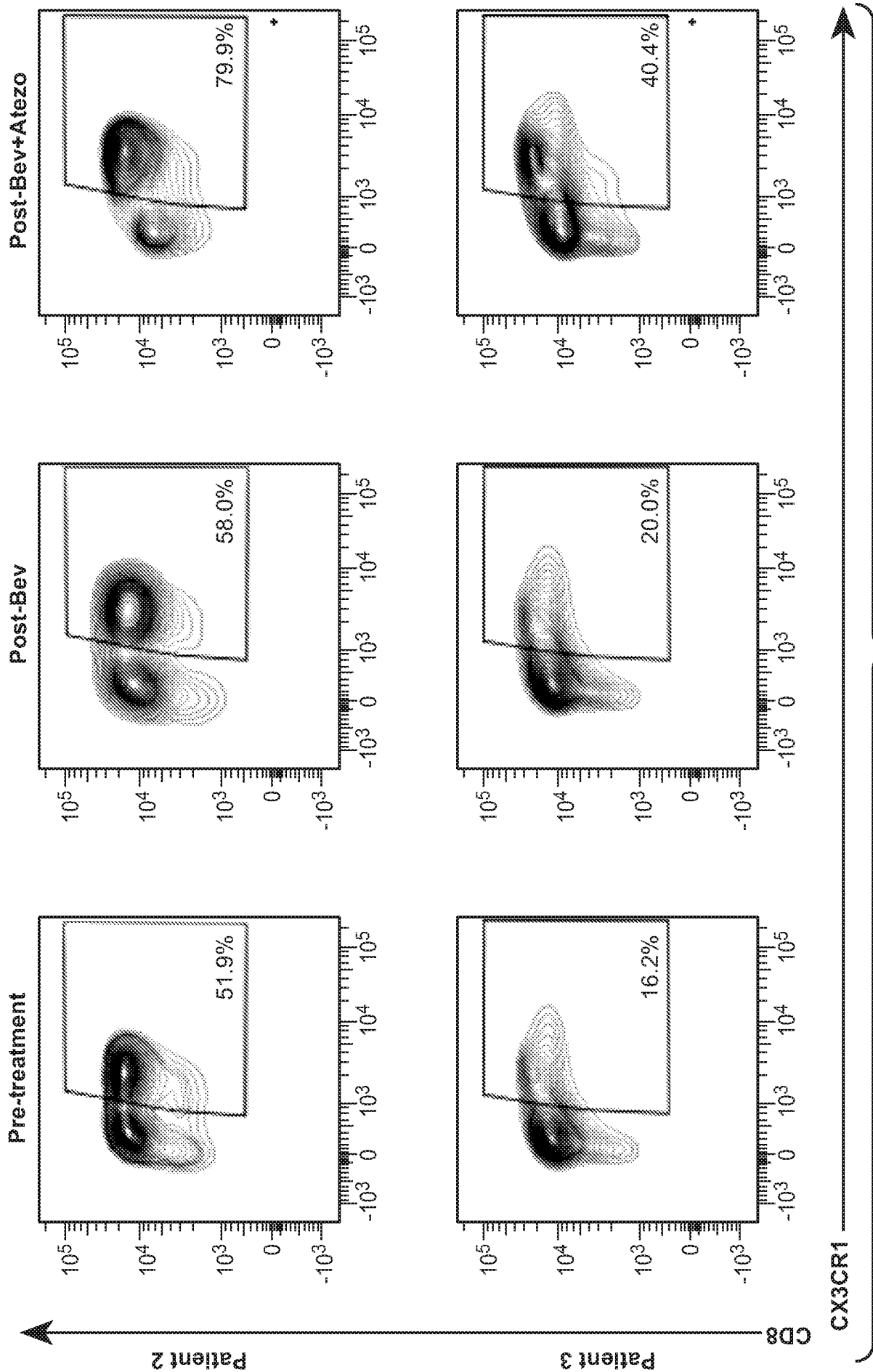


FIG. 17A

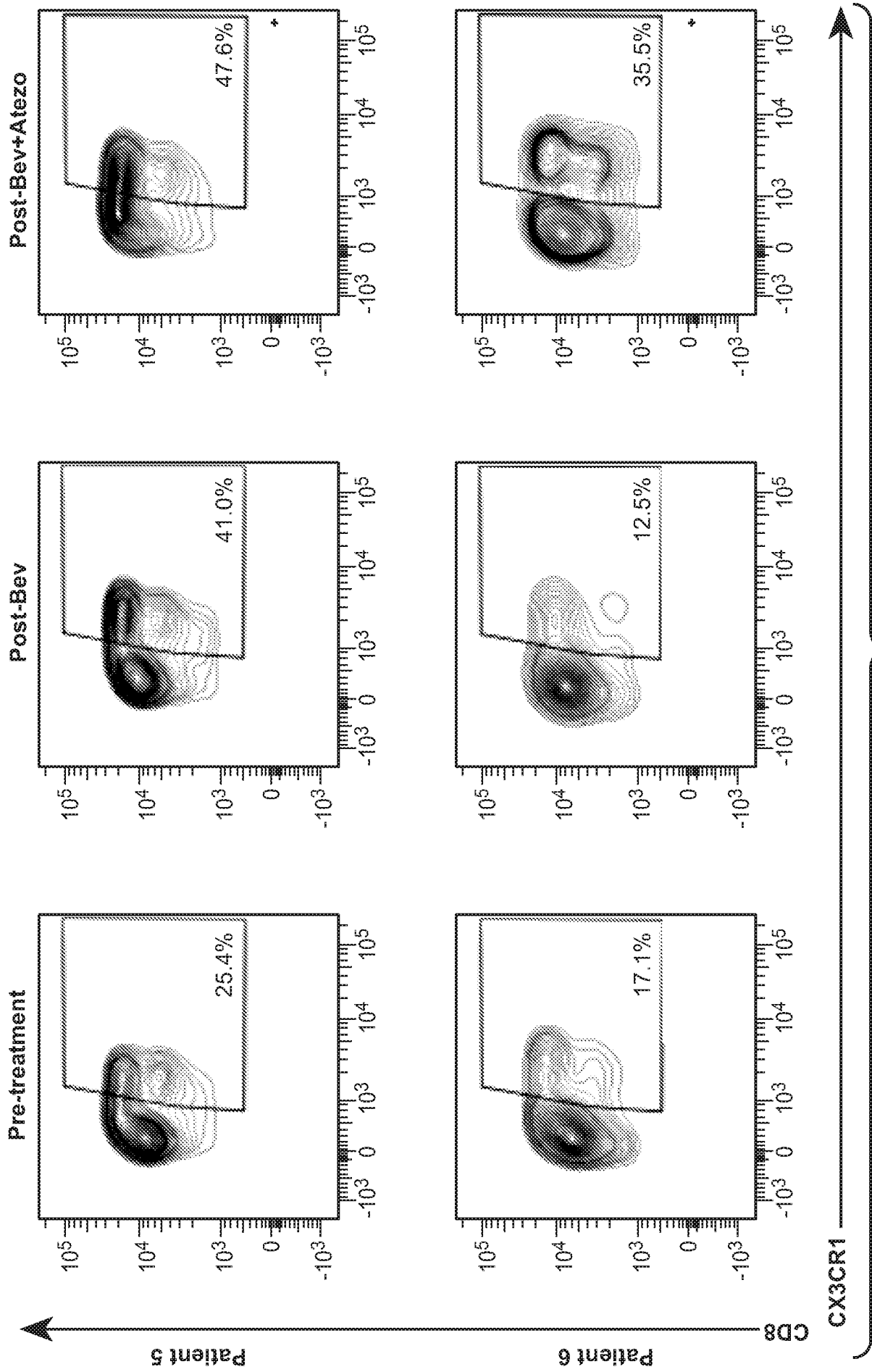
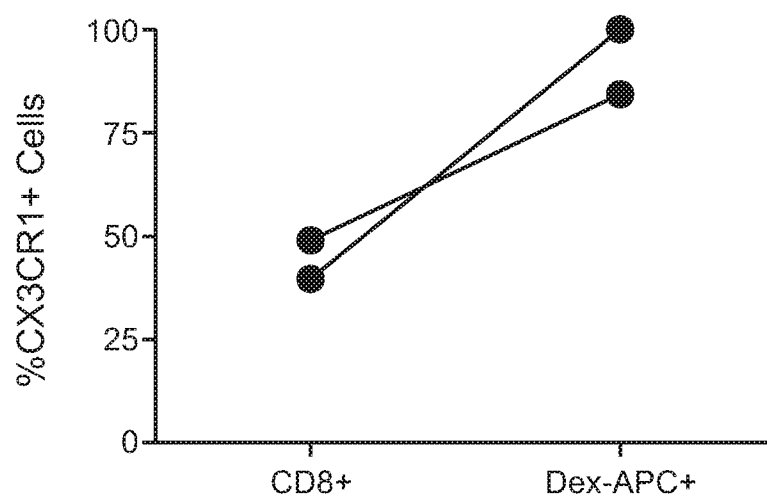


FIG. 17B

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**FIG. 18**

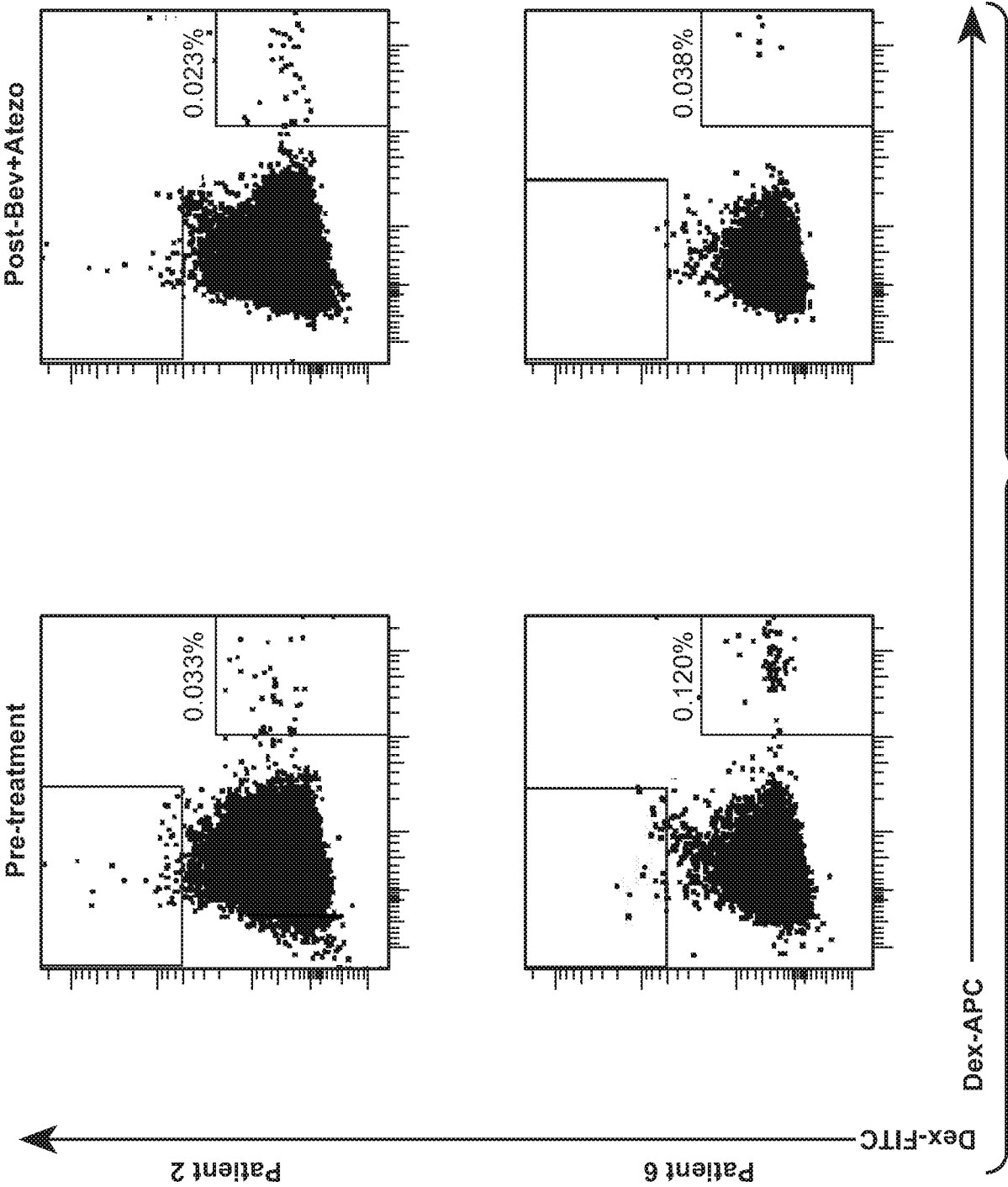


FIG. 19

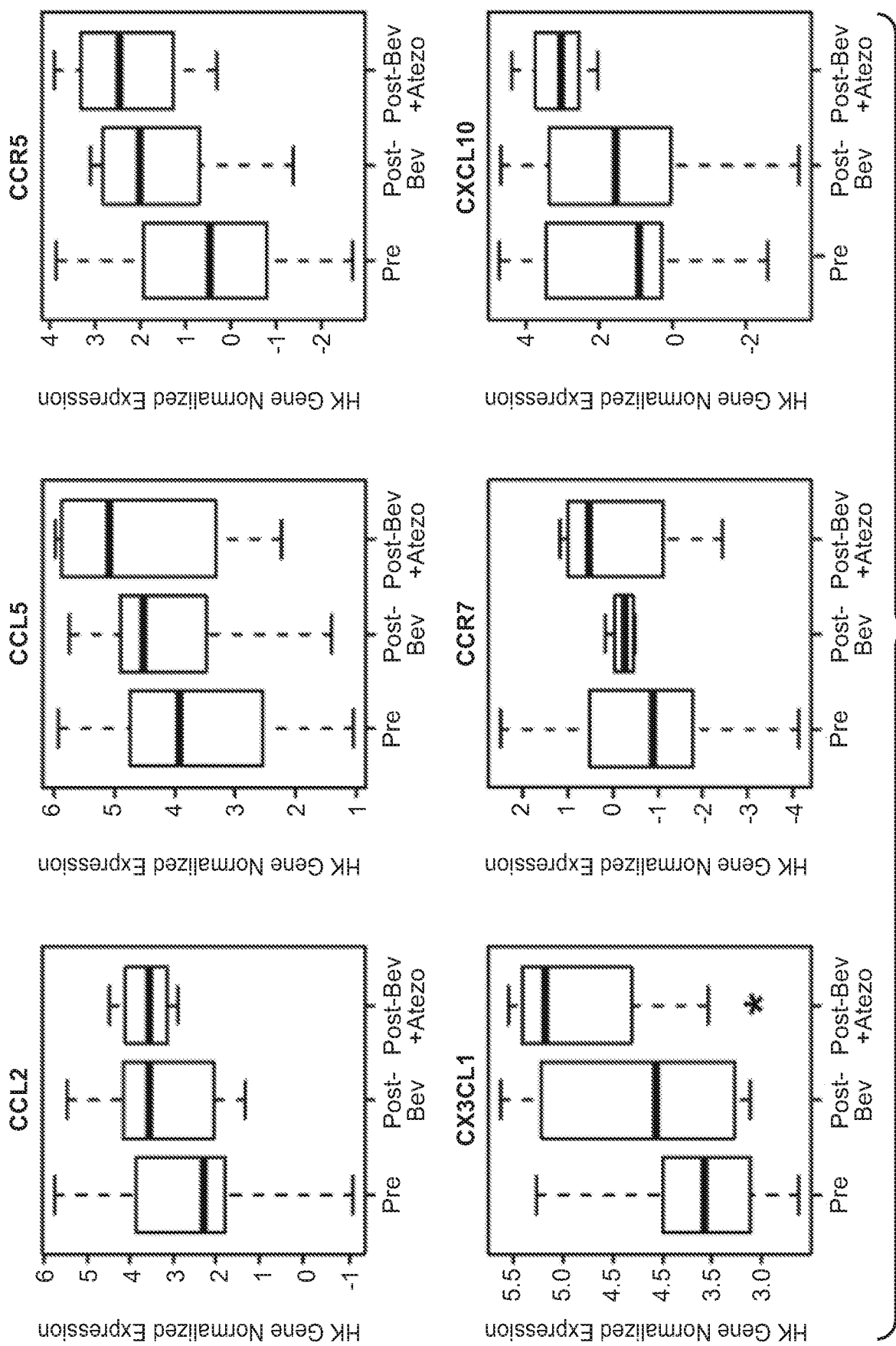
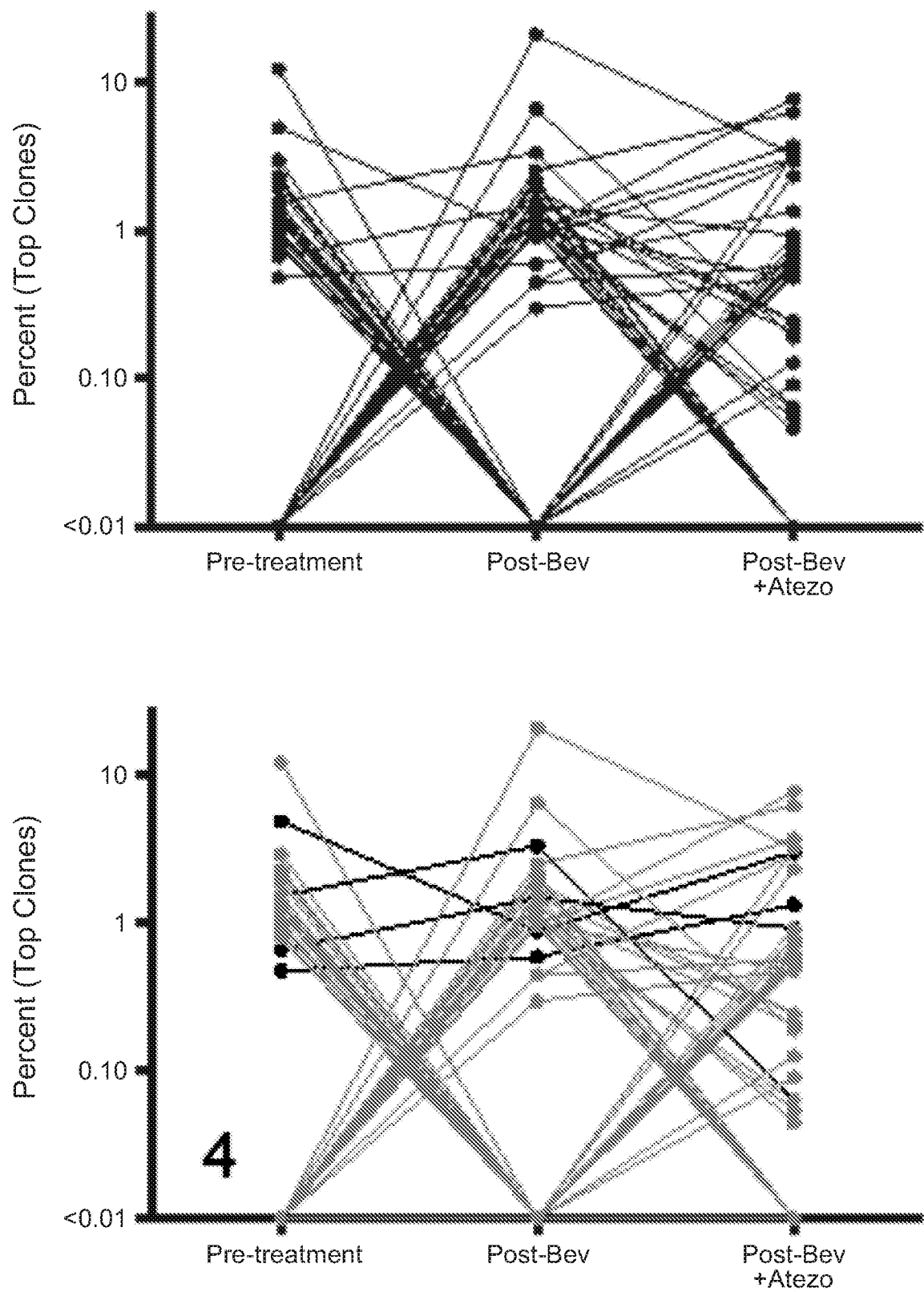
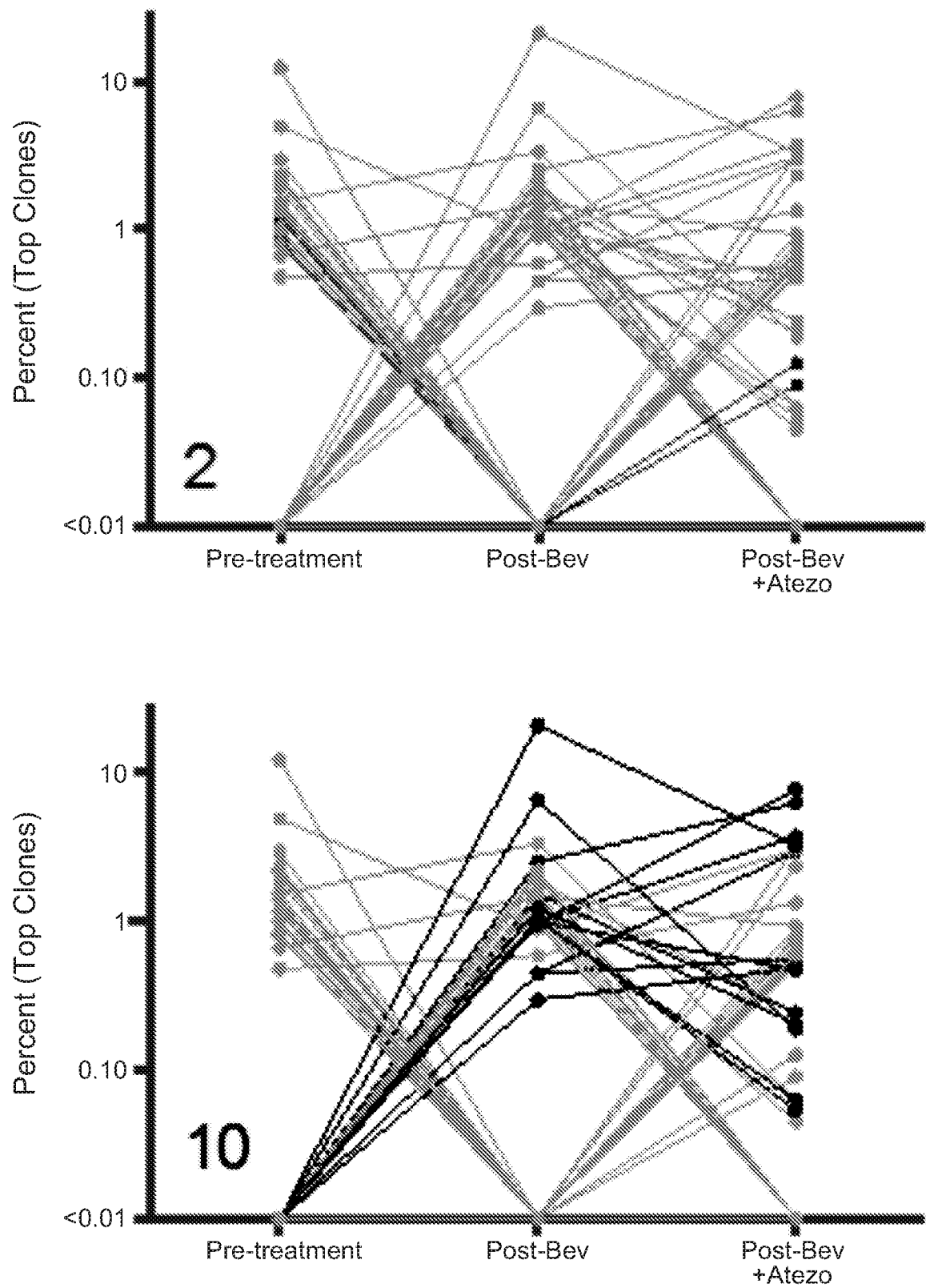
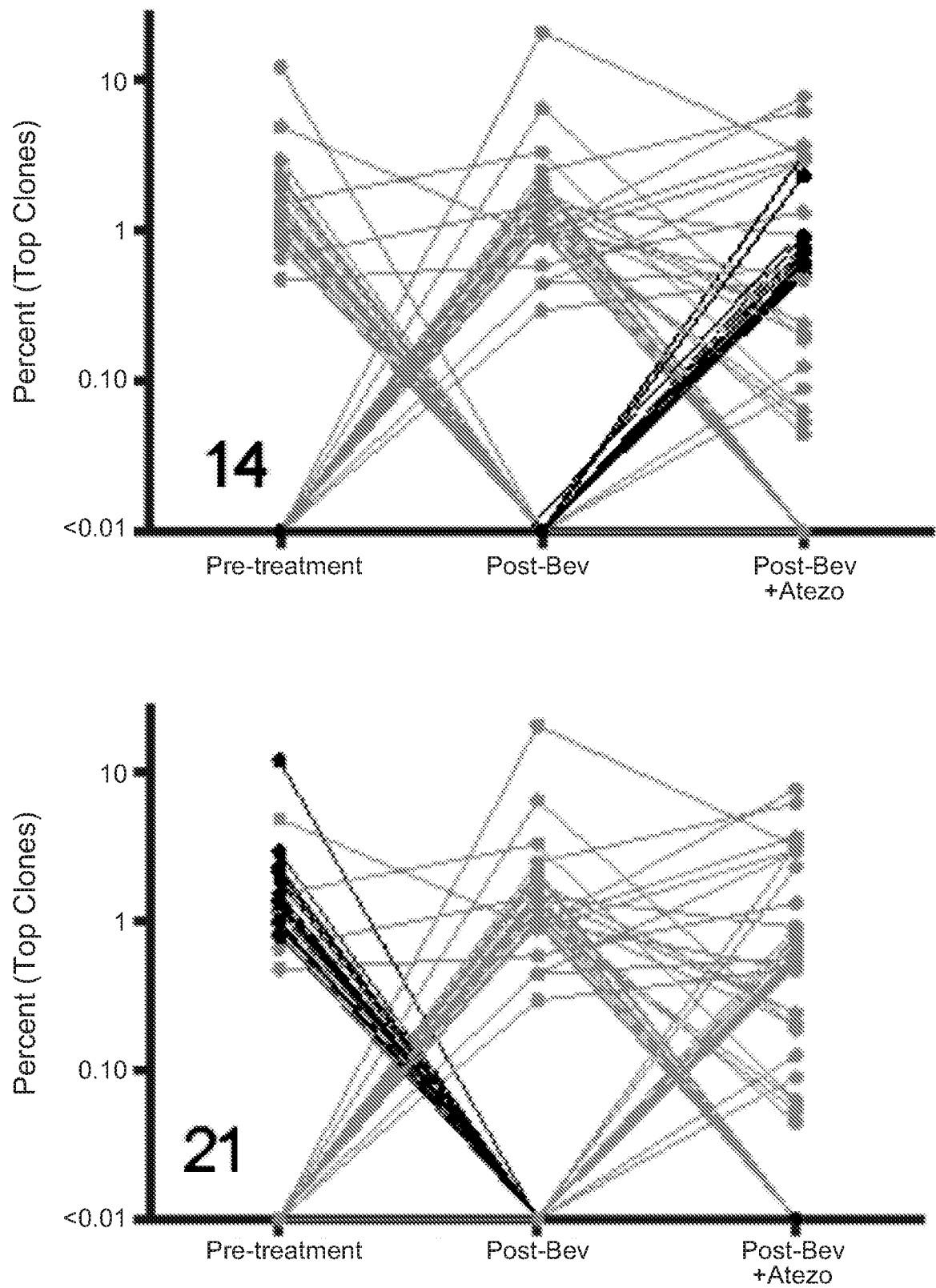


FIG. 20

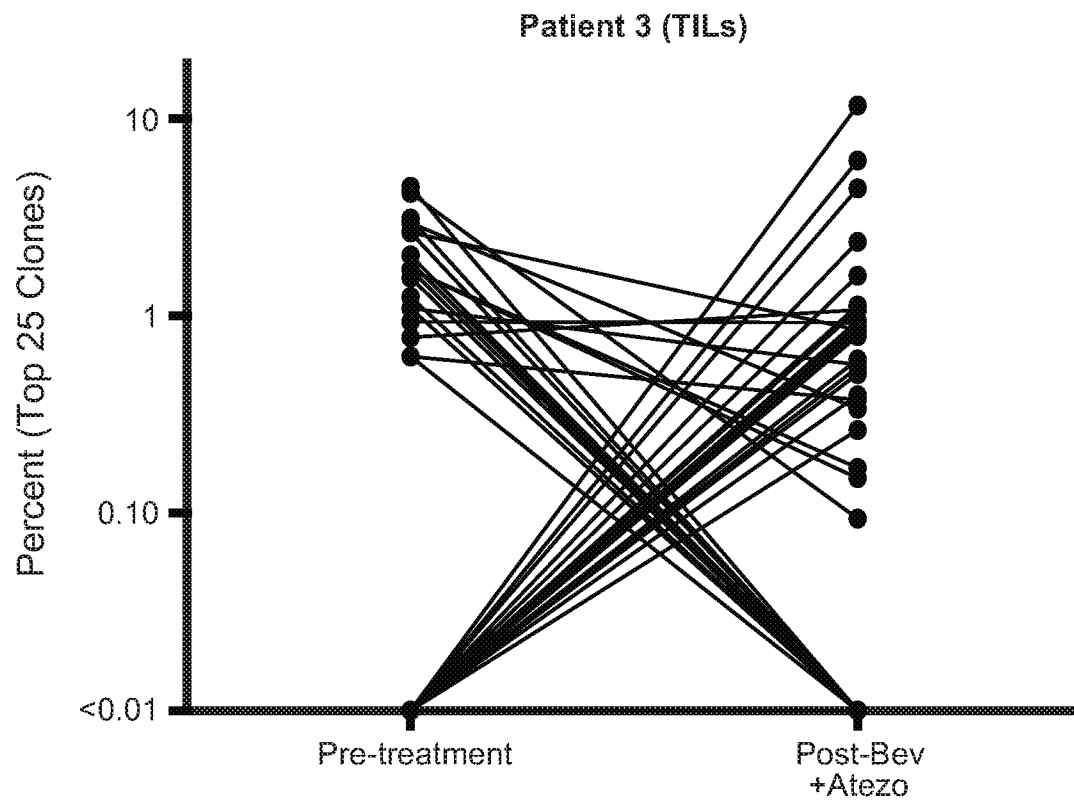
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**FIG. 21A**

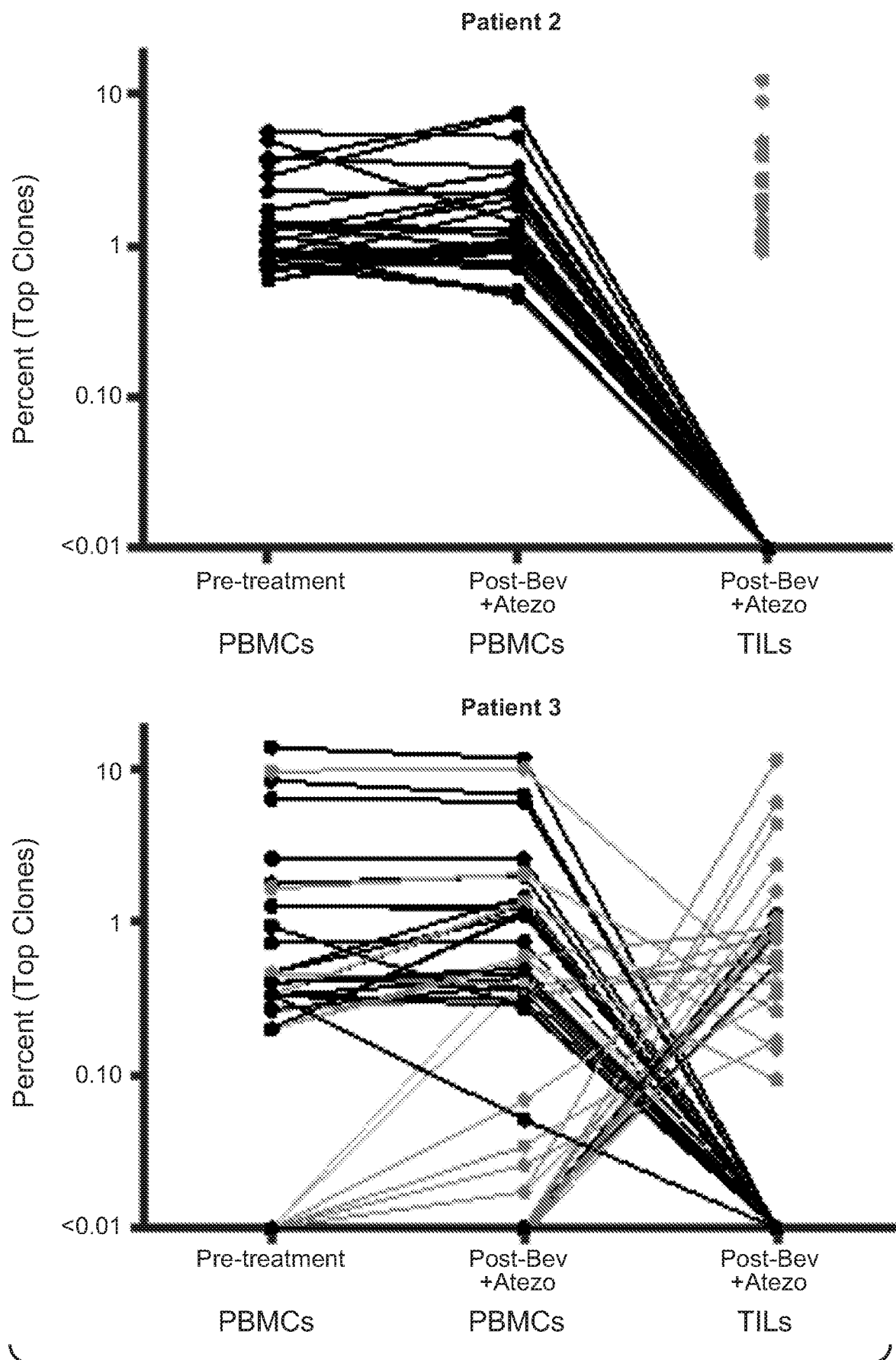
**FIG. 21B**

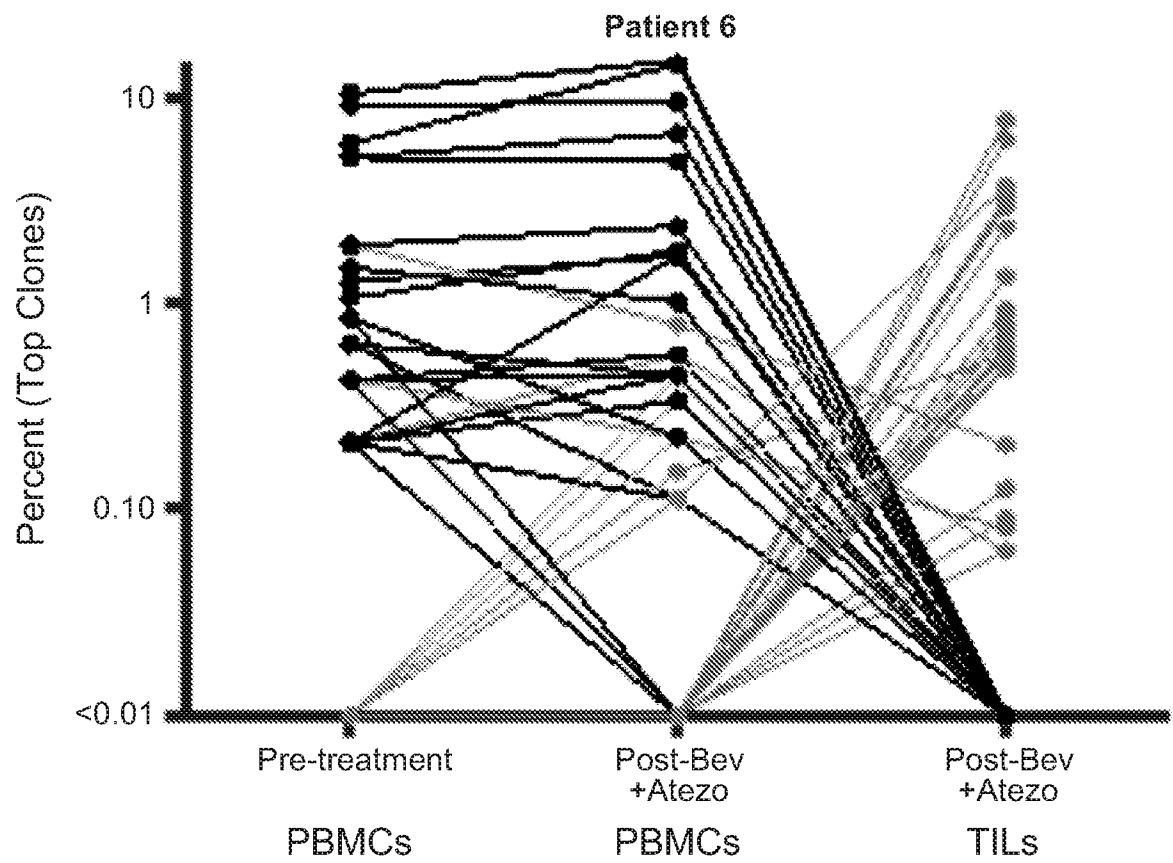
**FIG. 21C**

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**FIG. 22**

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**FIG. 23A**

**FIG. 23B**

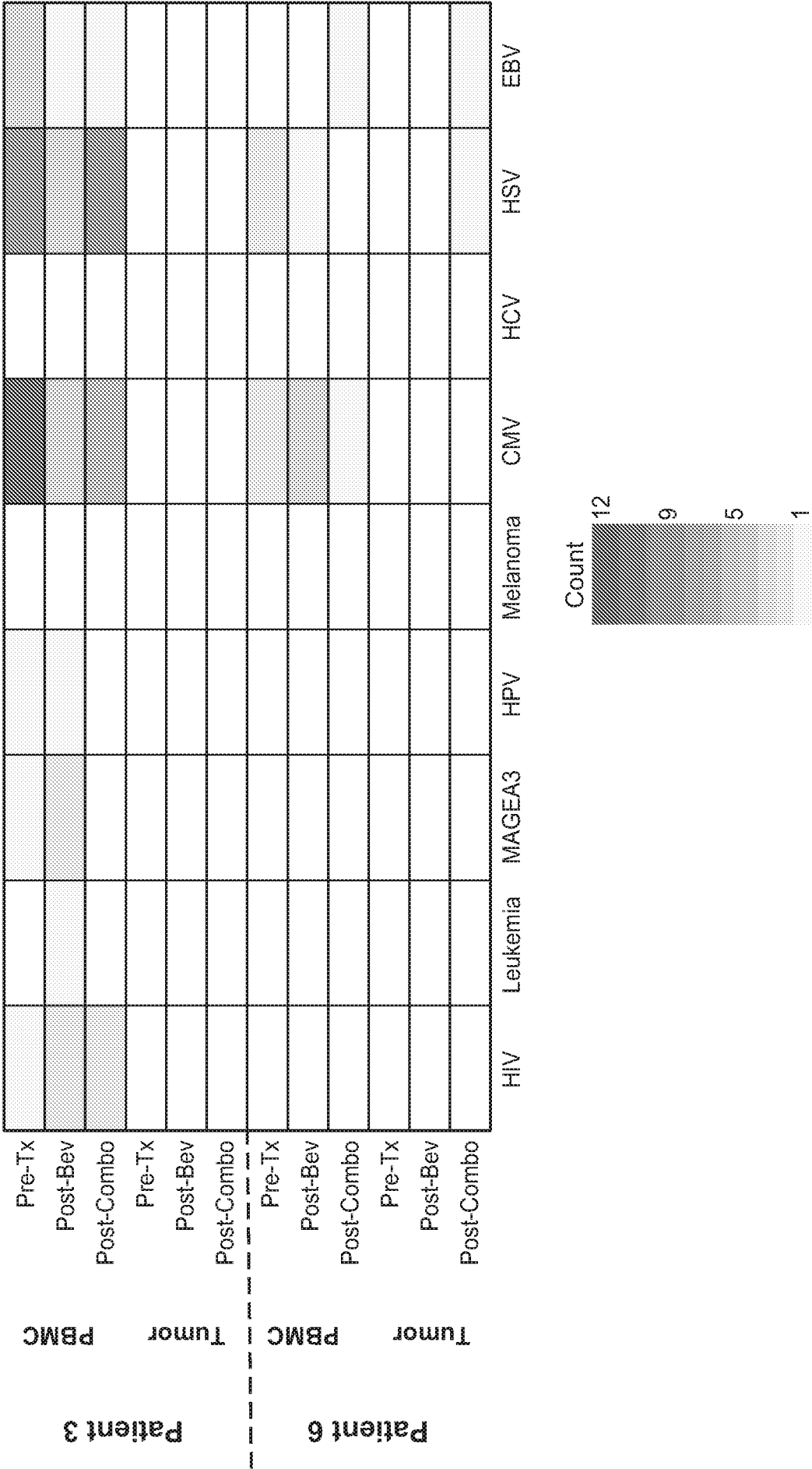


FIG. 24

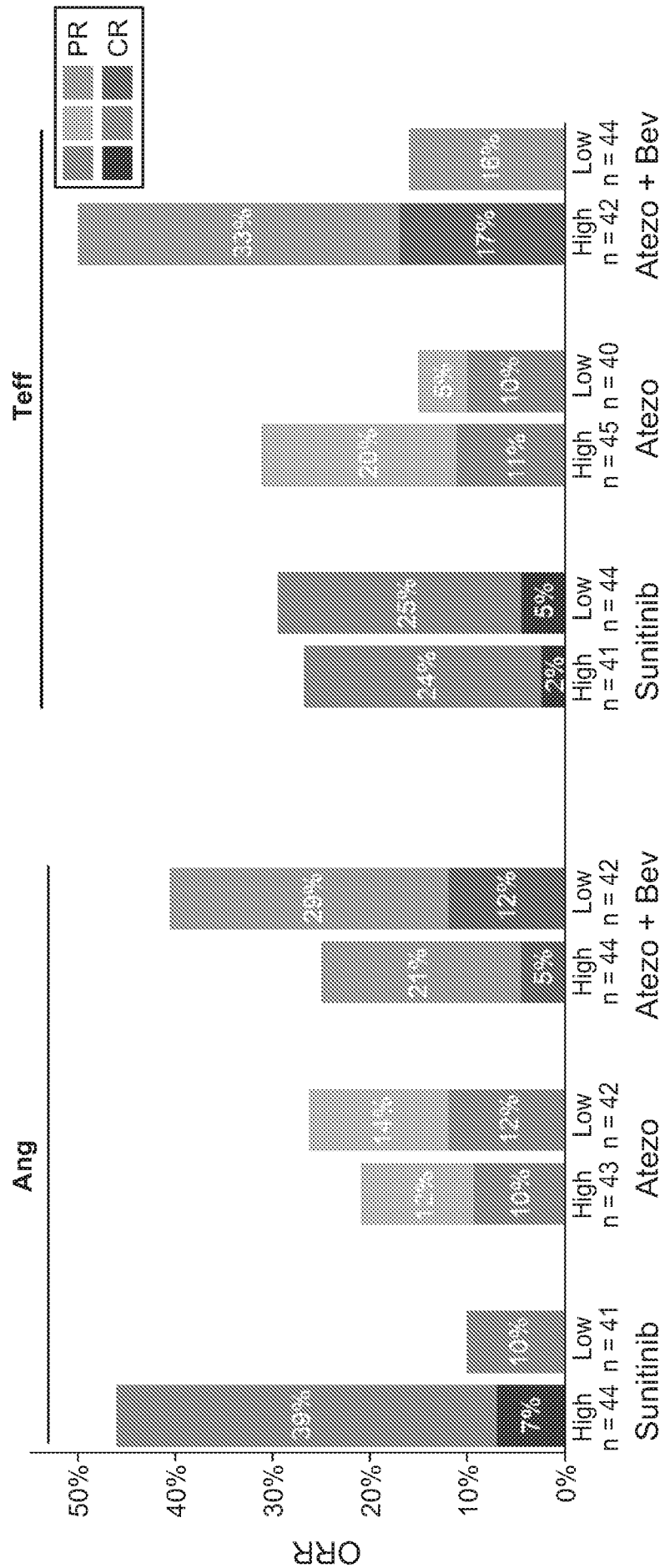
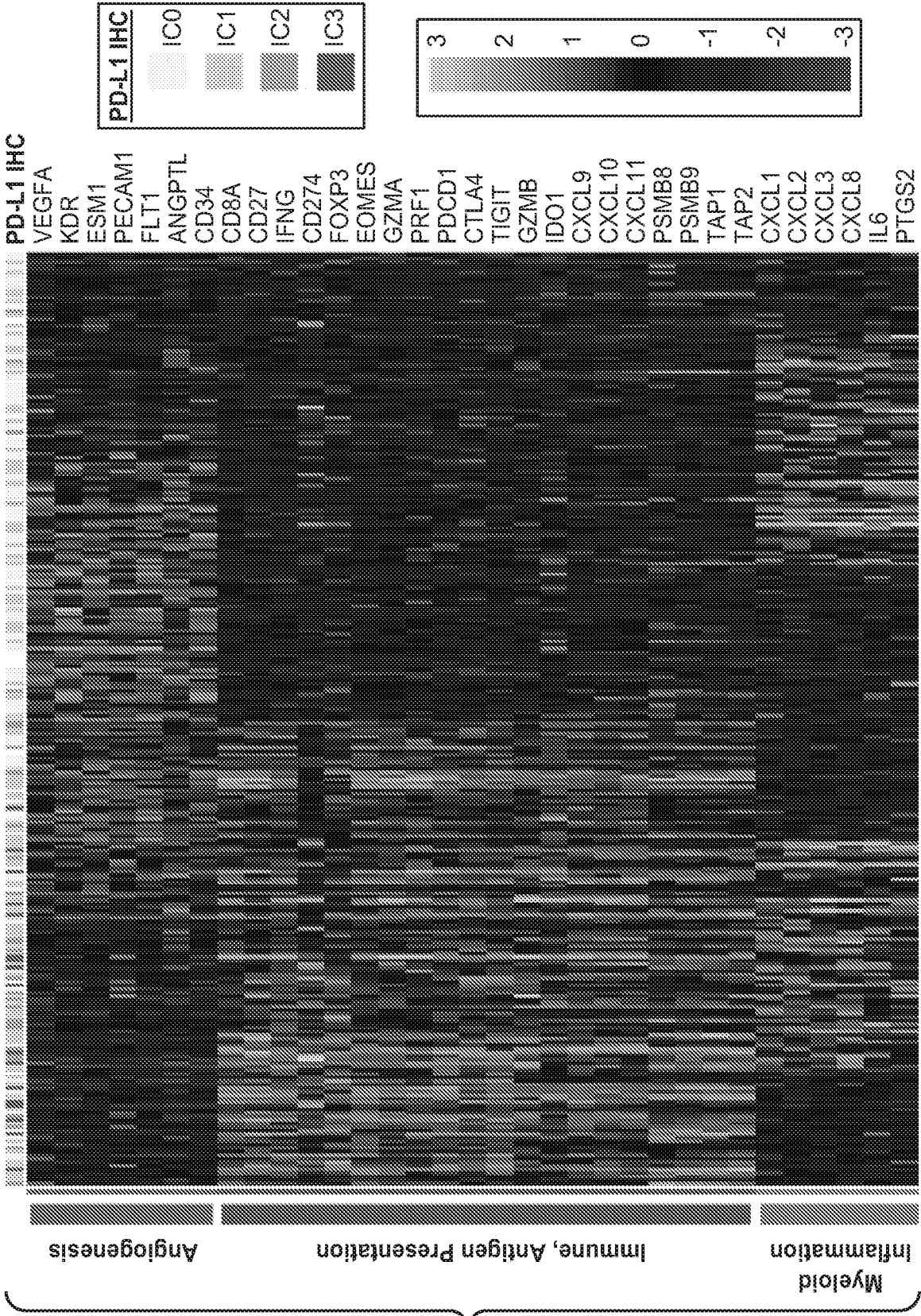
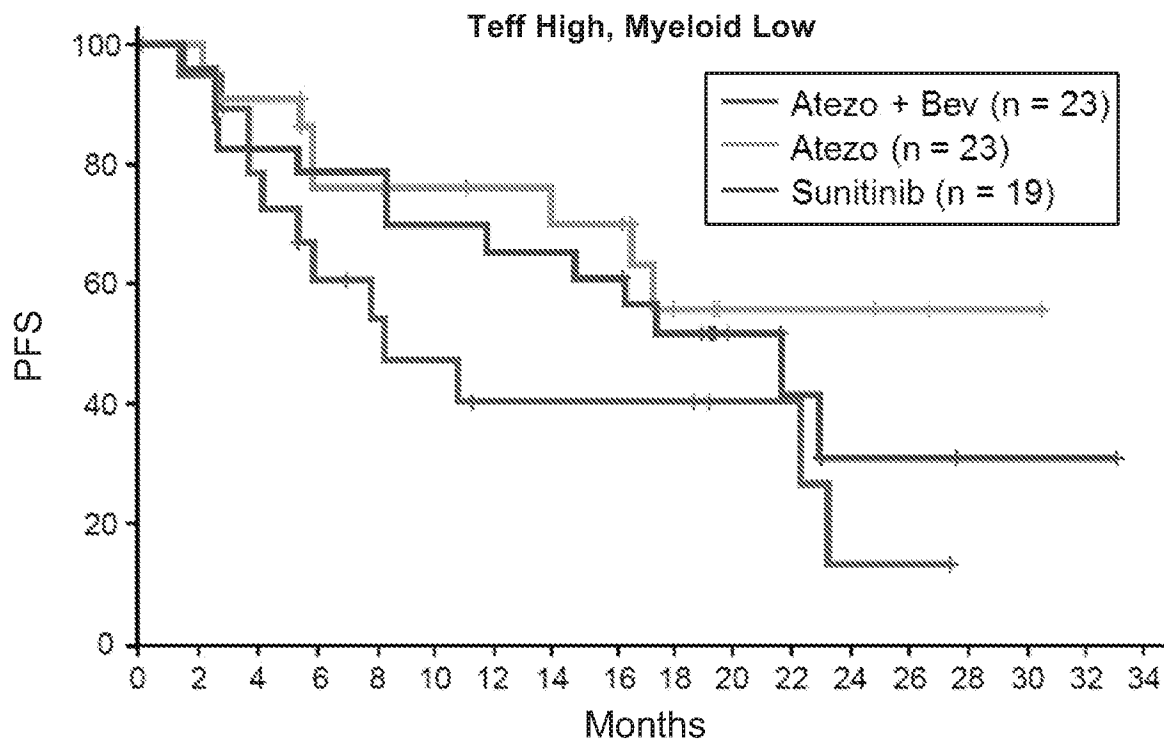
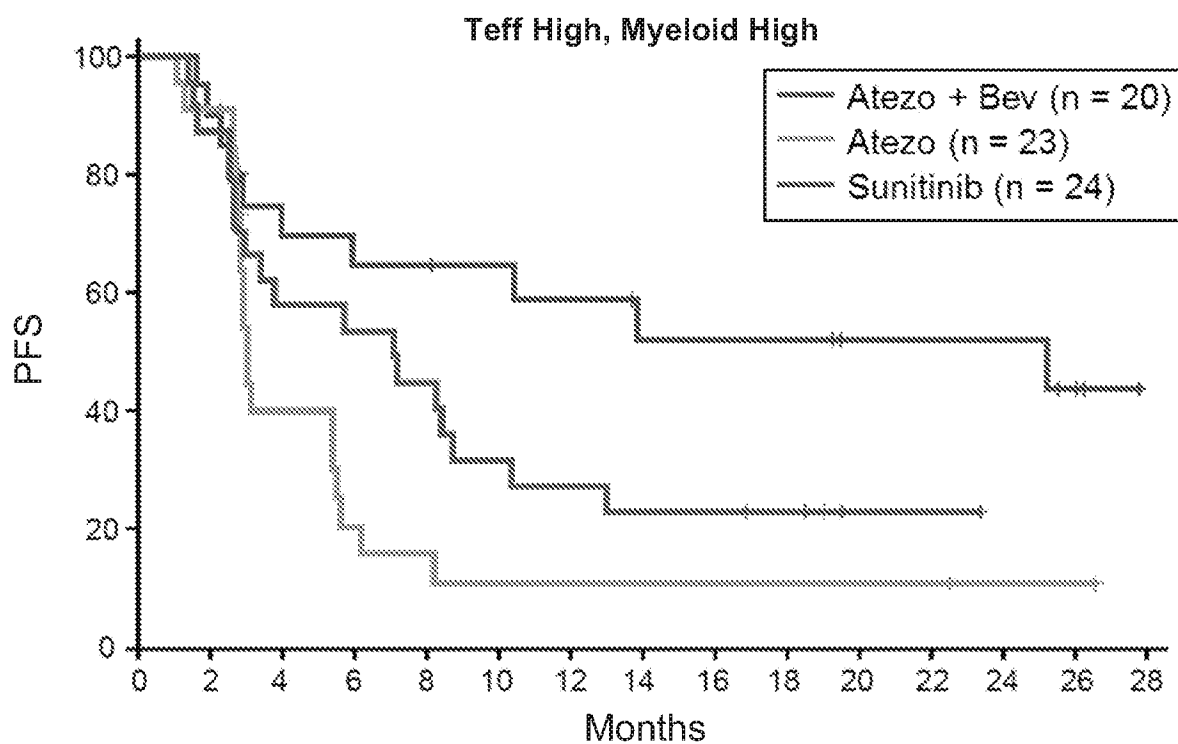


FIG. 25

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**FIG. 27A****FIG. 27B**

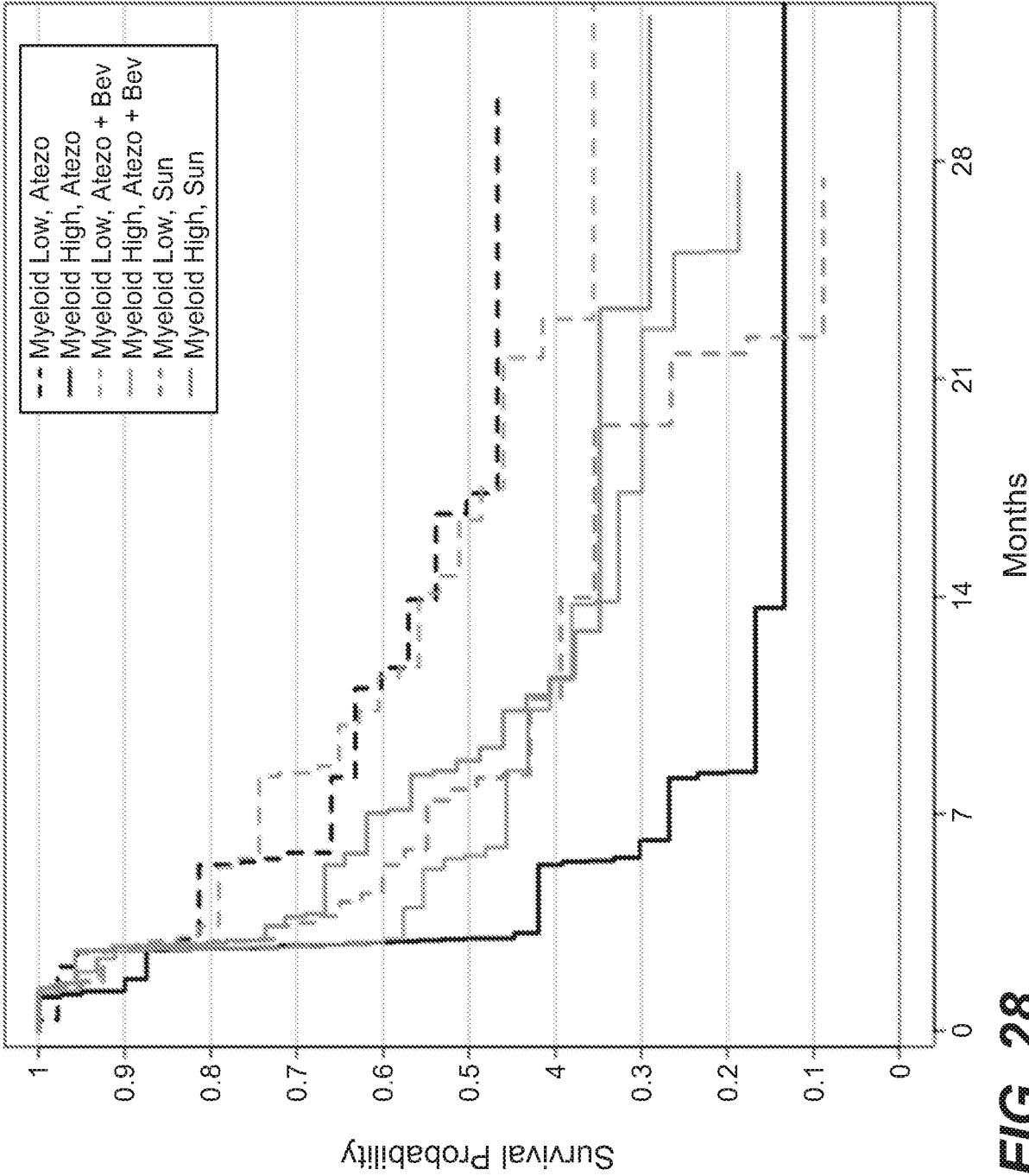
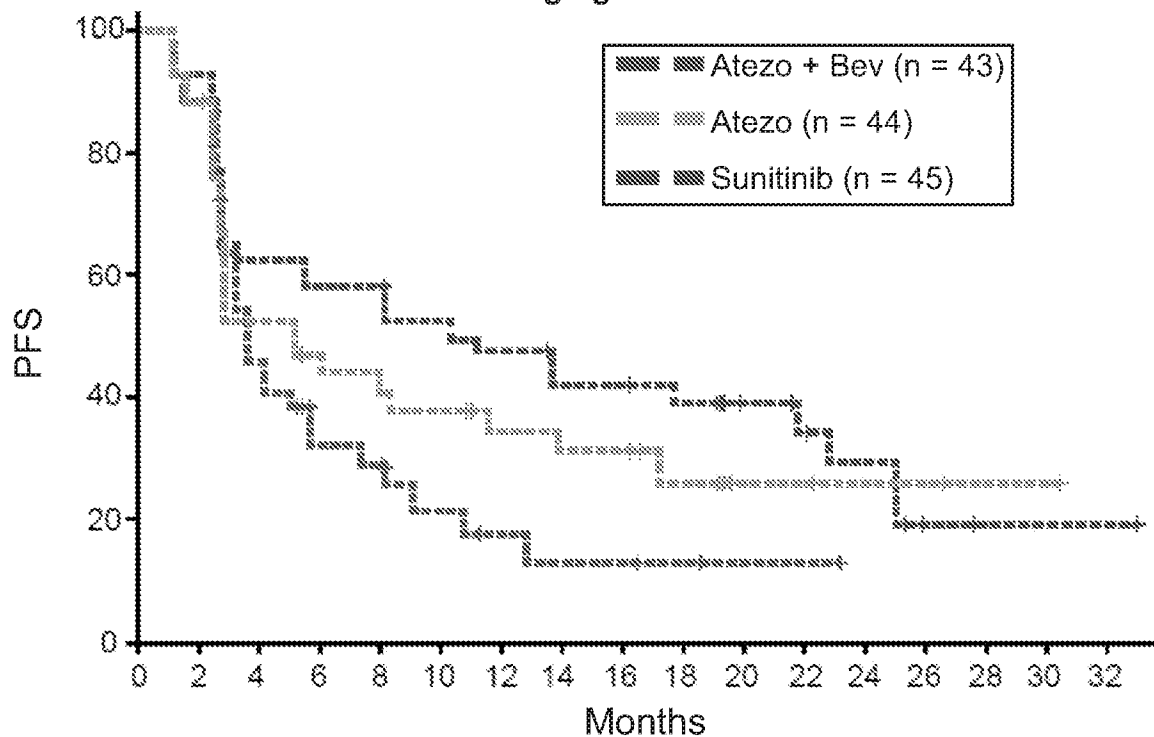


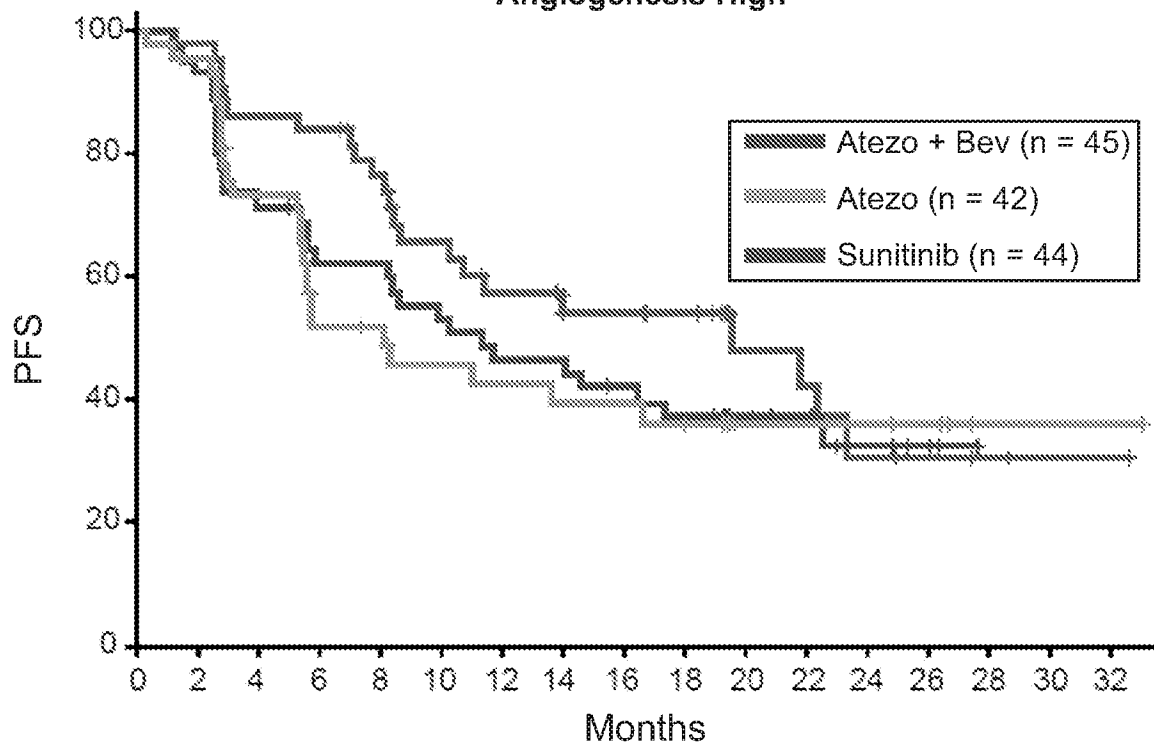
FIG. 28

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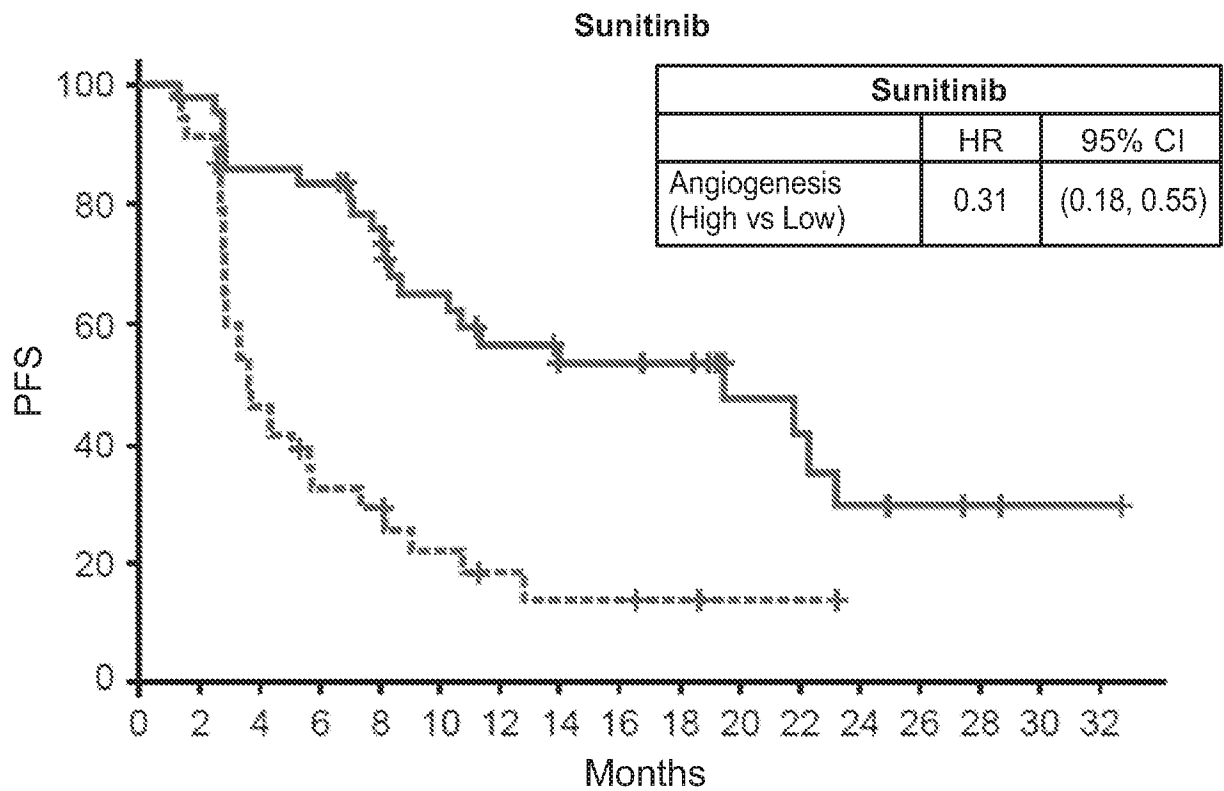
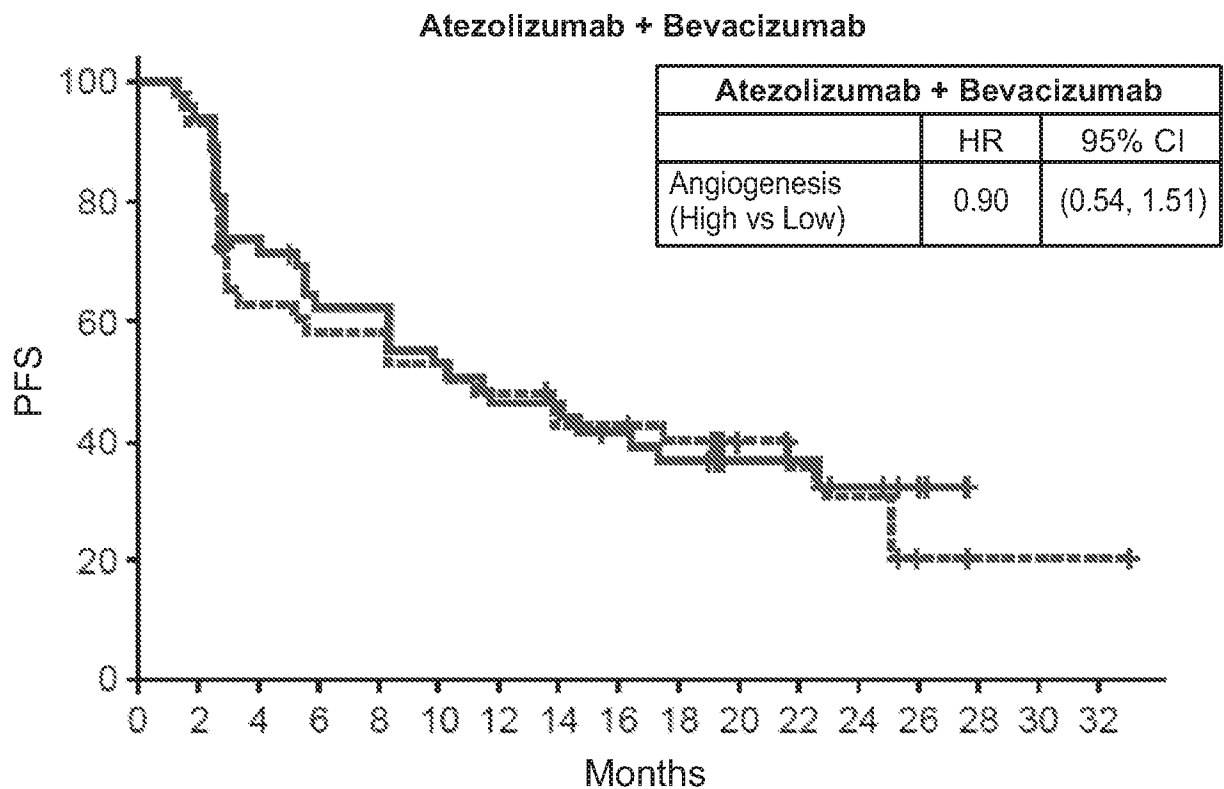
Angiogenesis Low

**FIG. 29A**

Angiogenesis High

**FIG. 29B**

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**FIG. 30A****FIG. 30B**

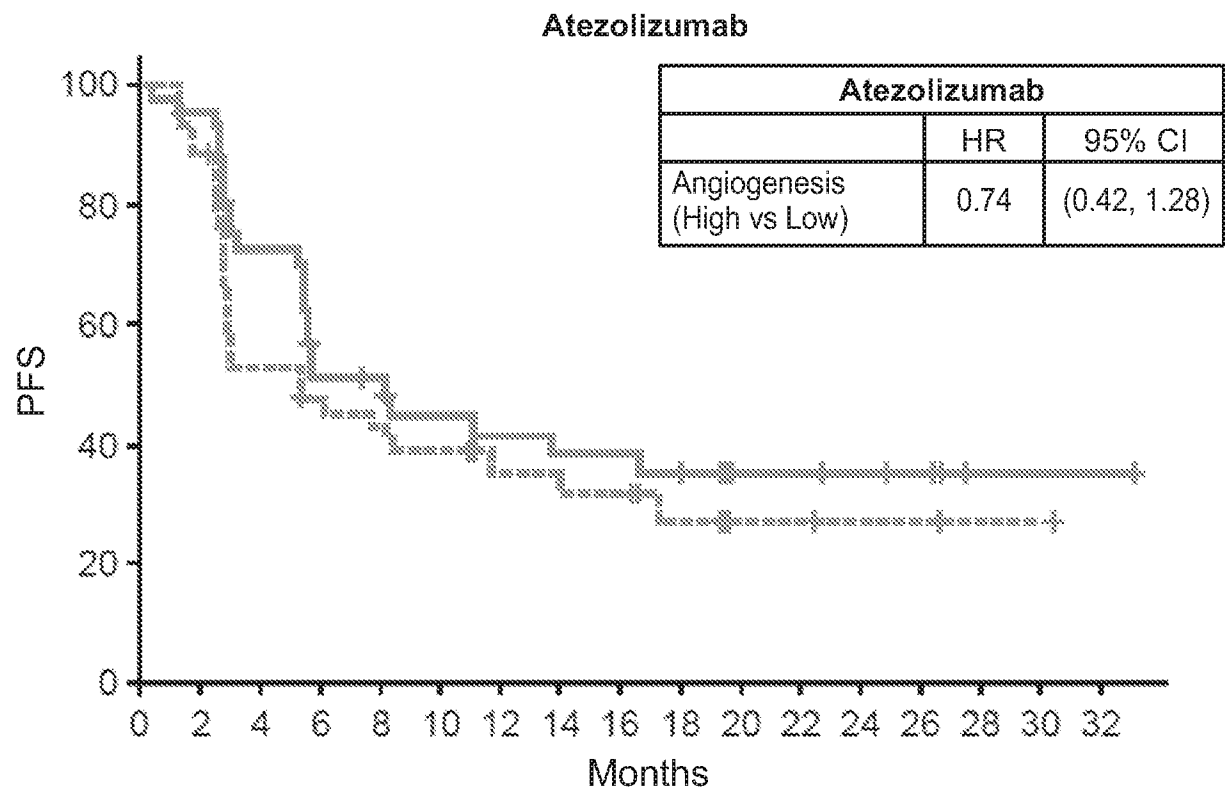
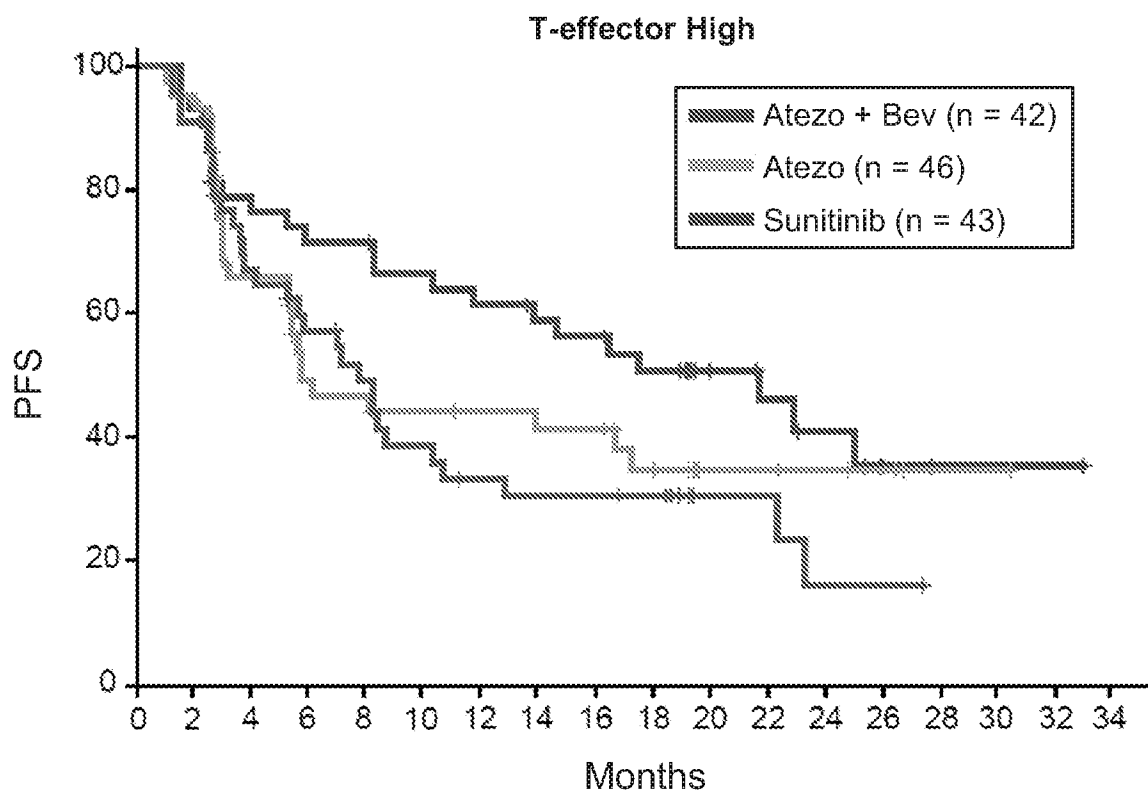
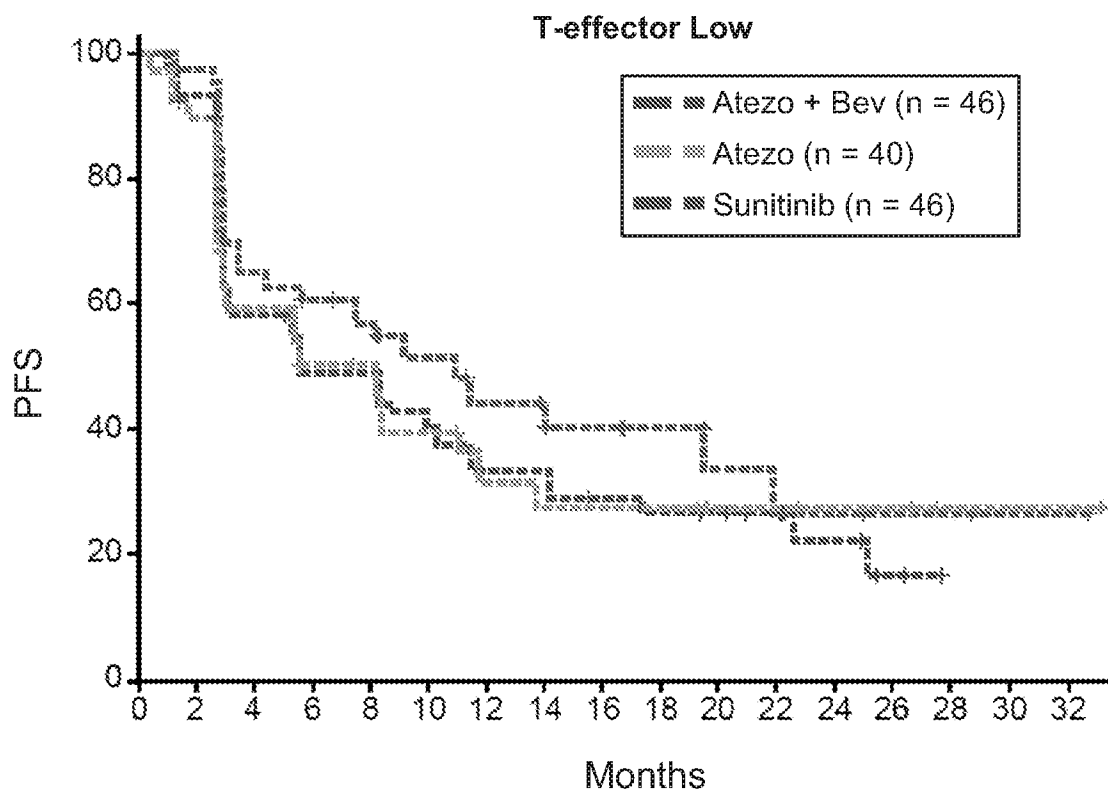
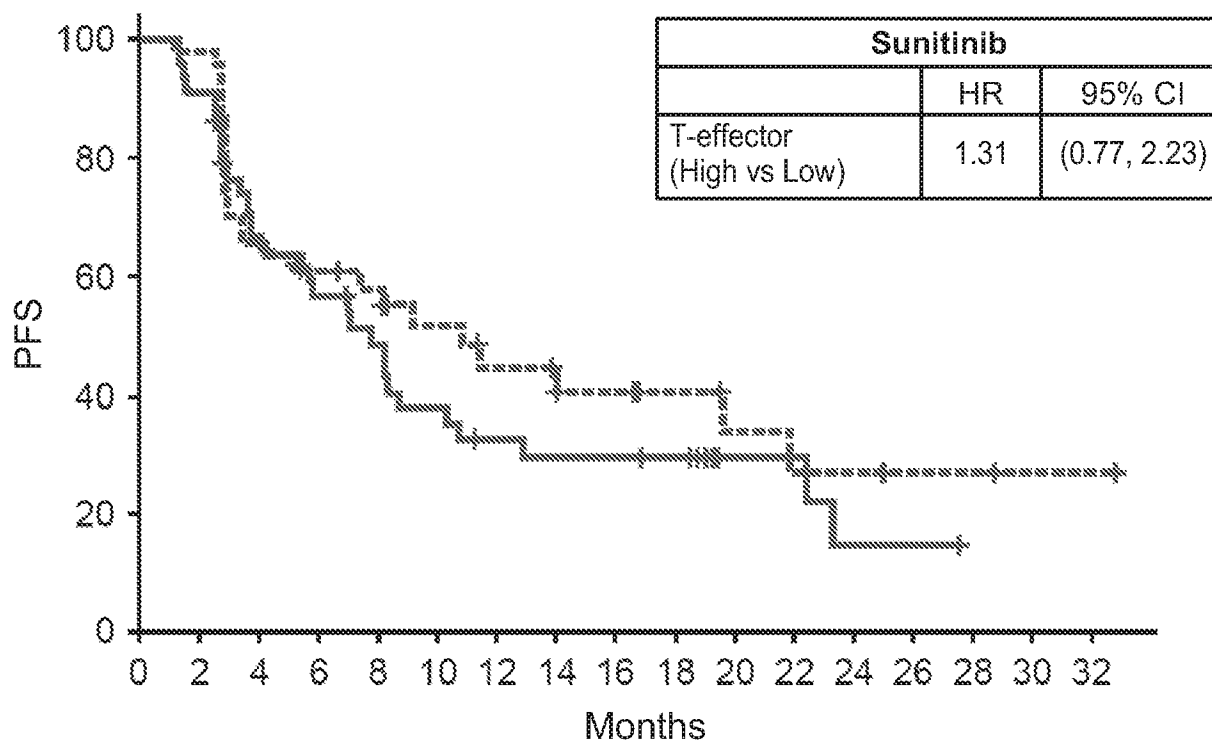
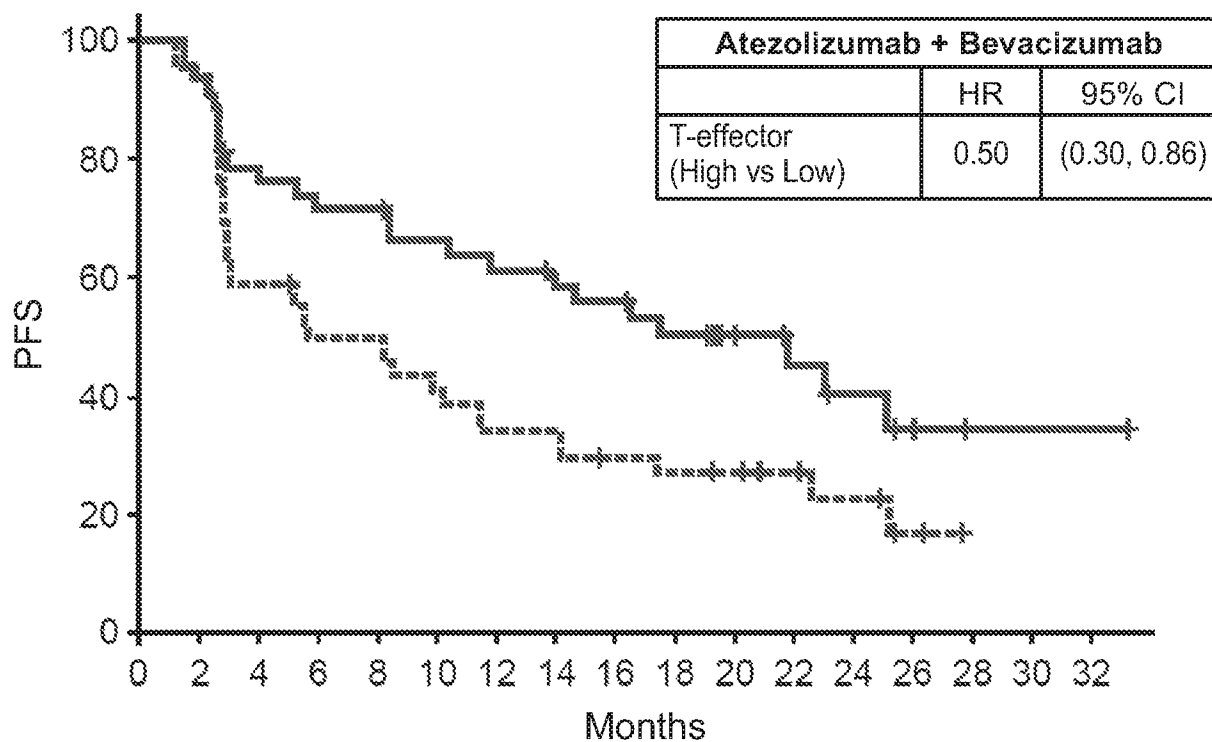


FIG. 30C

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**FIG. 31A****FIG. 31B**

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Sunitinib**FIG. 32A****Atezolizumab + Bevacizumab****FIG. 32B**

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Atezolizumab

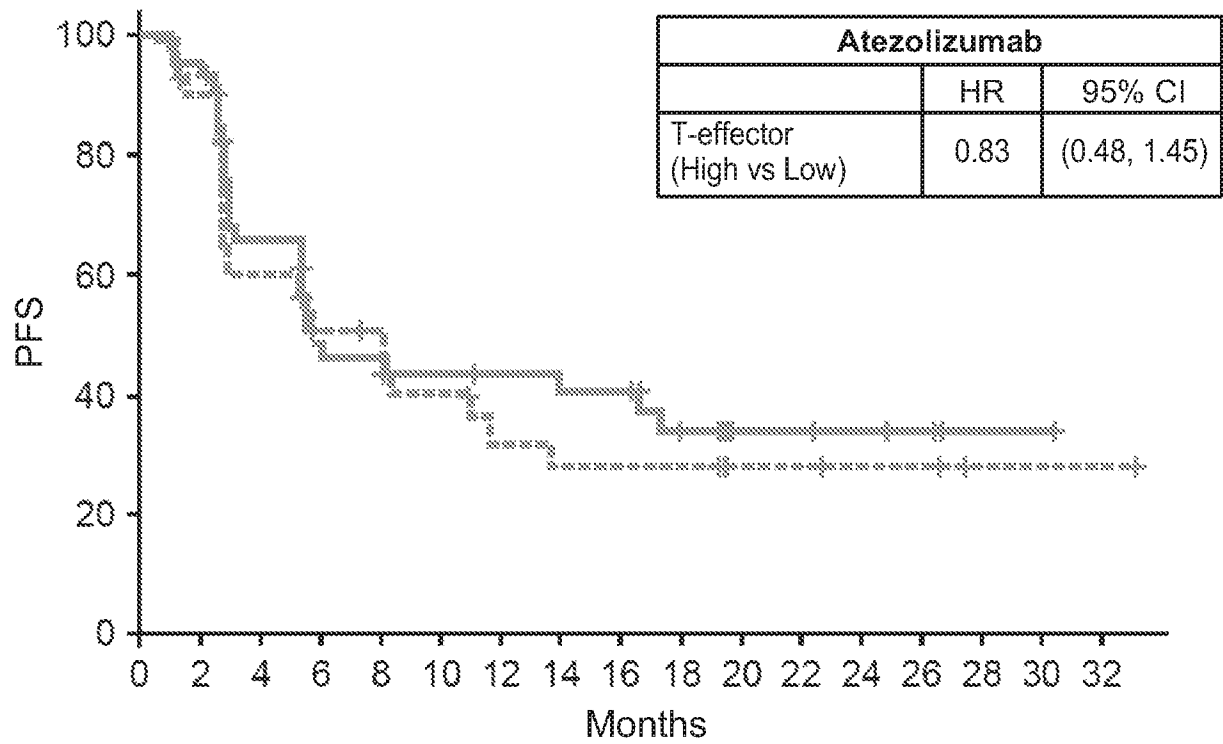


FIG. 32C

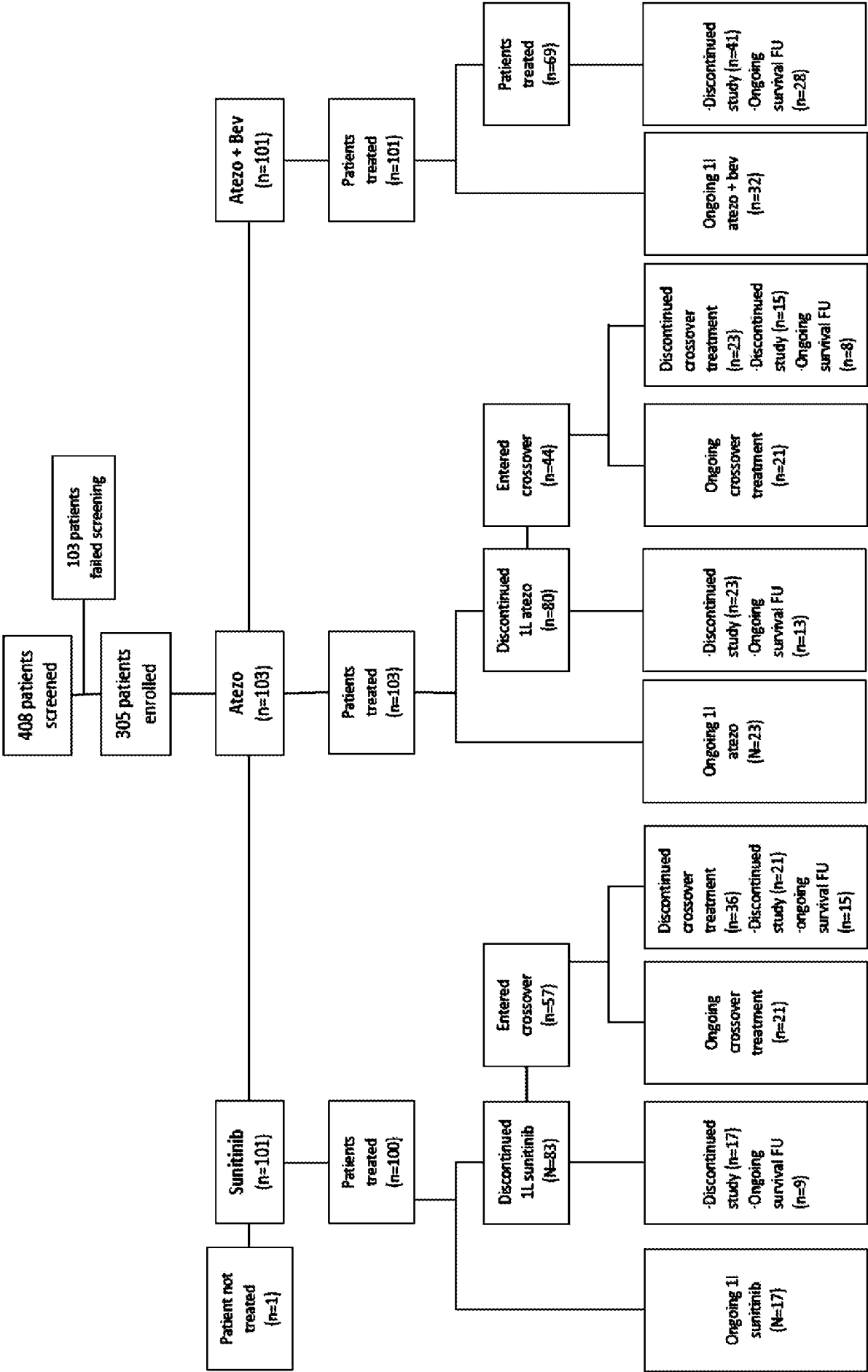
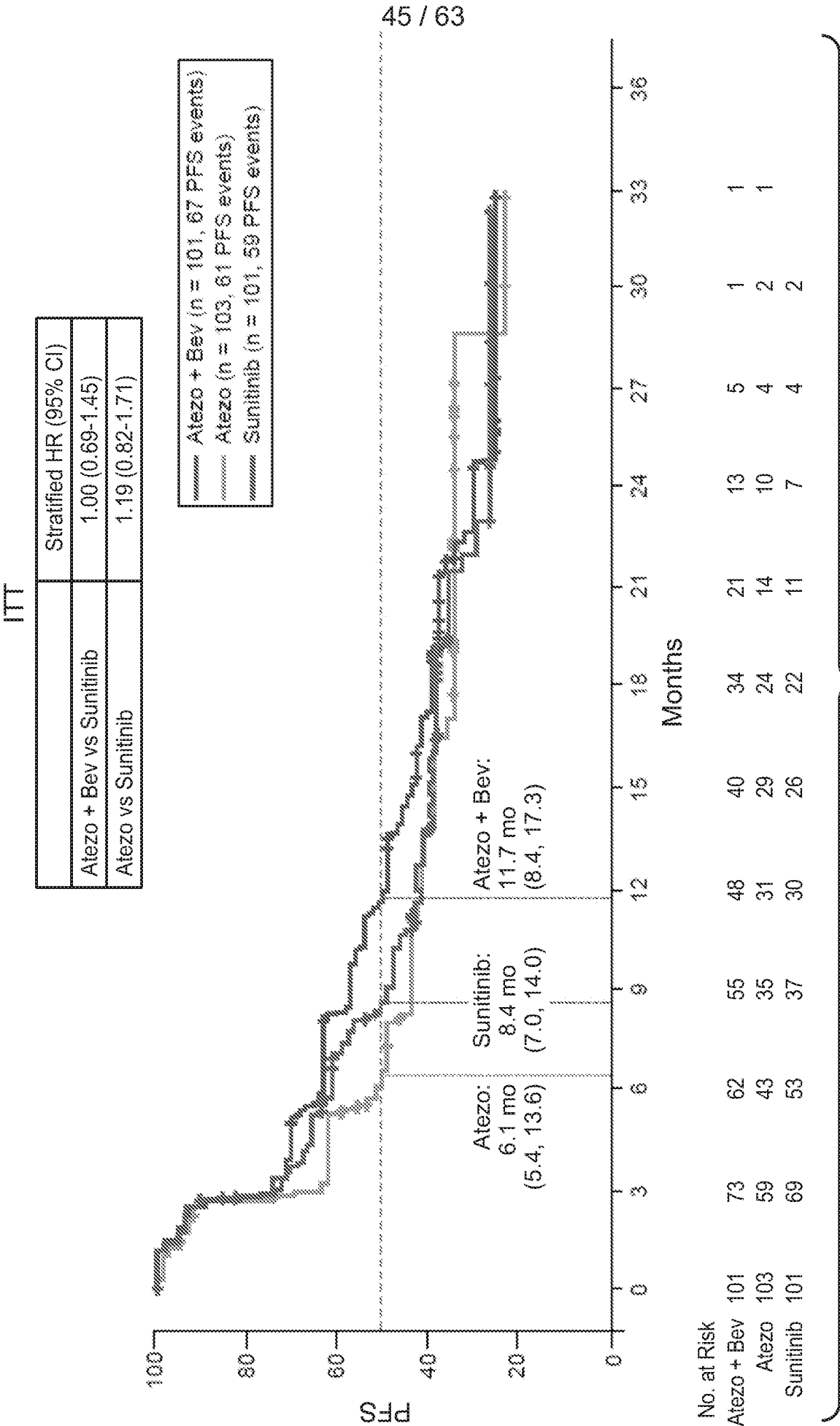
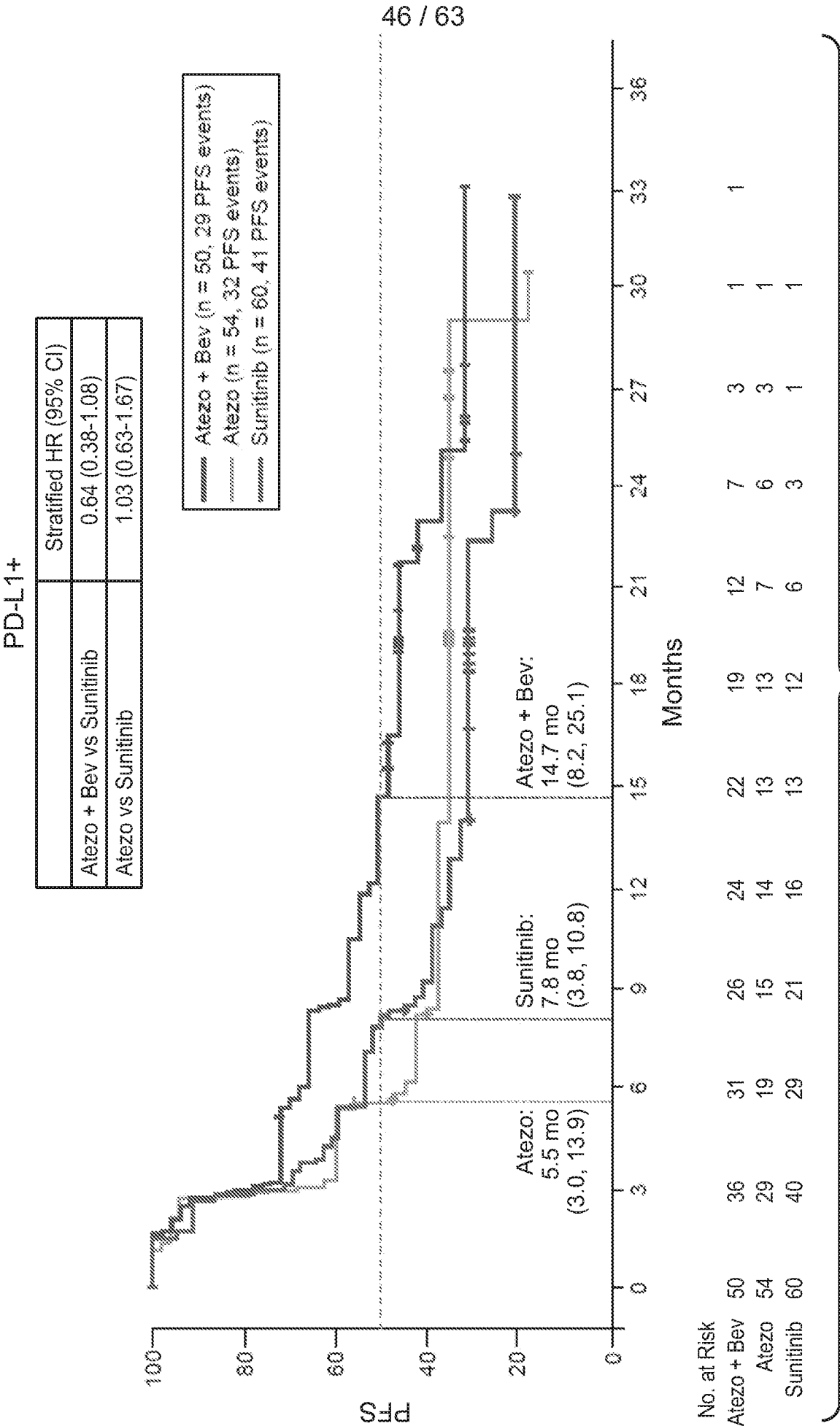


FIG. 33





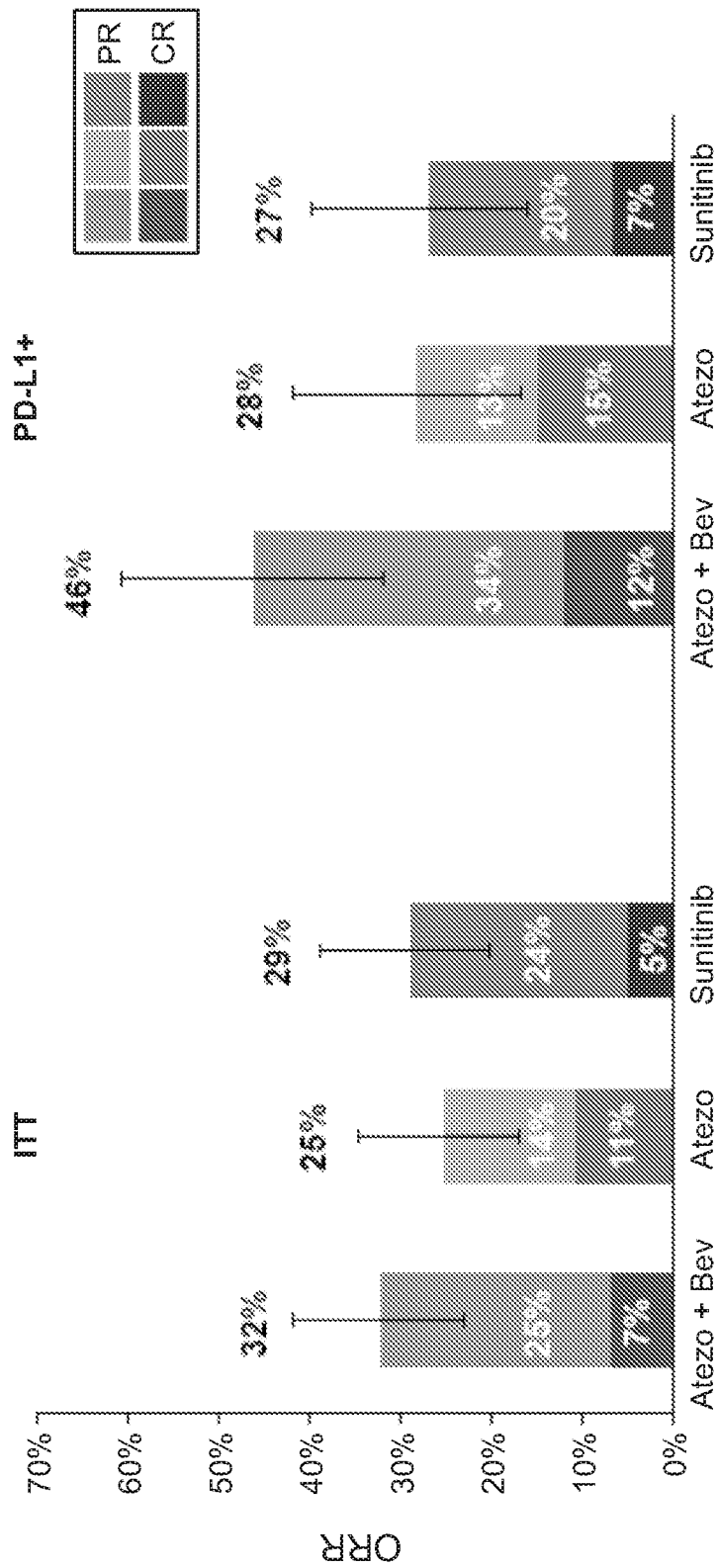
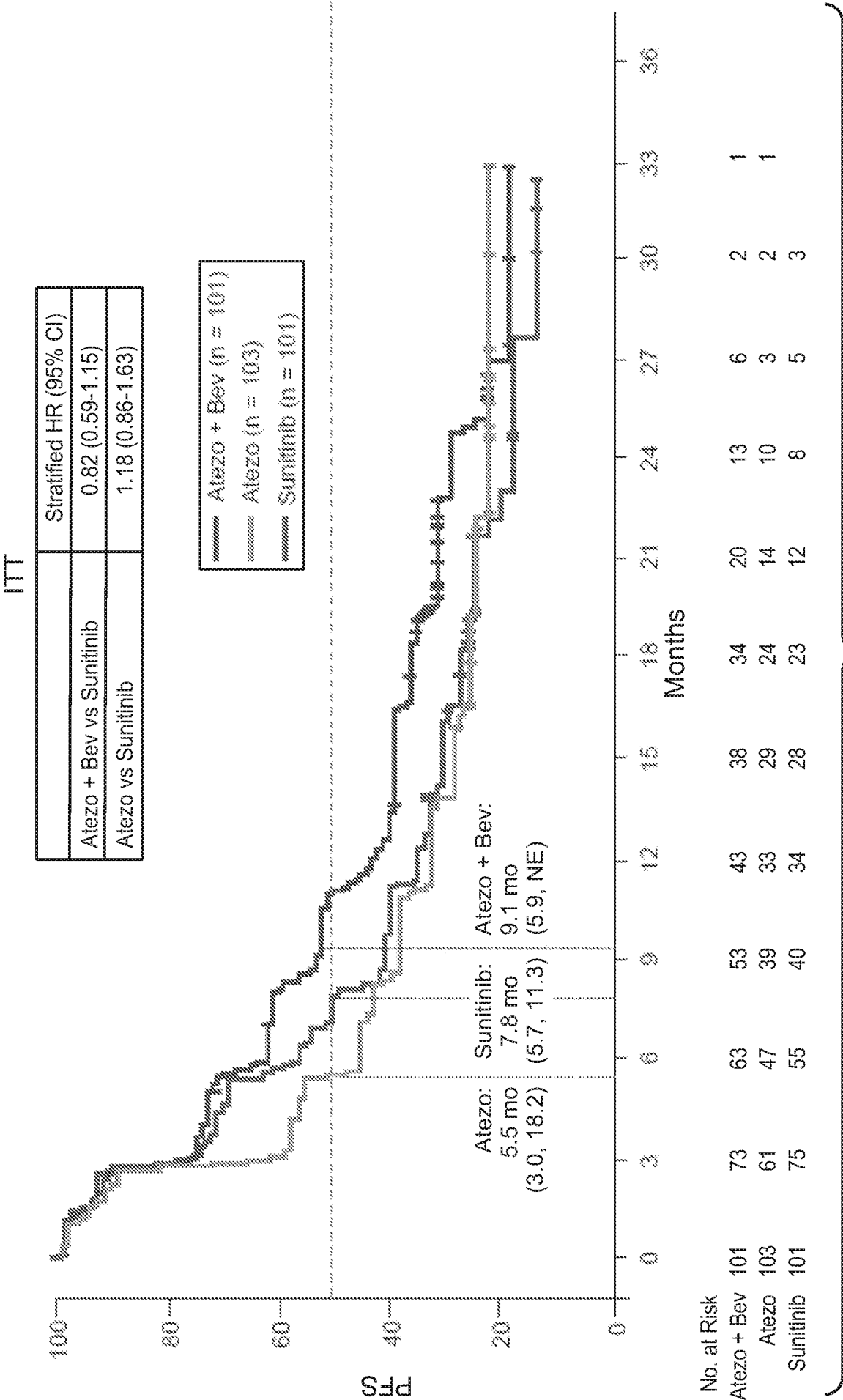
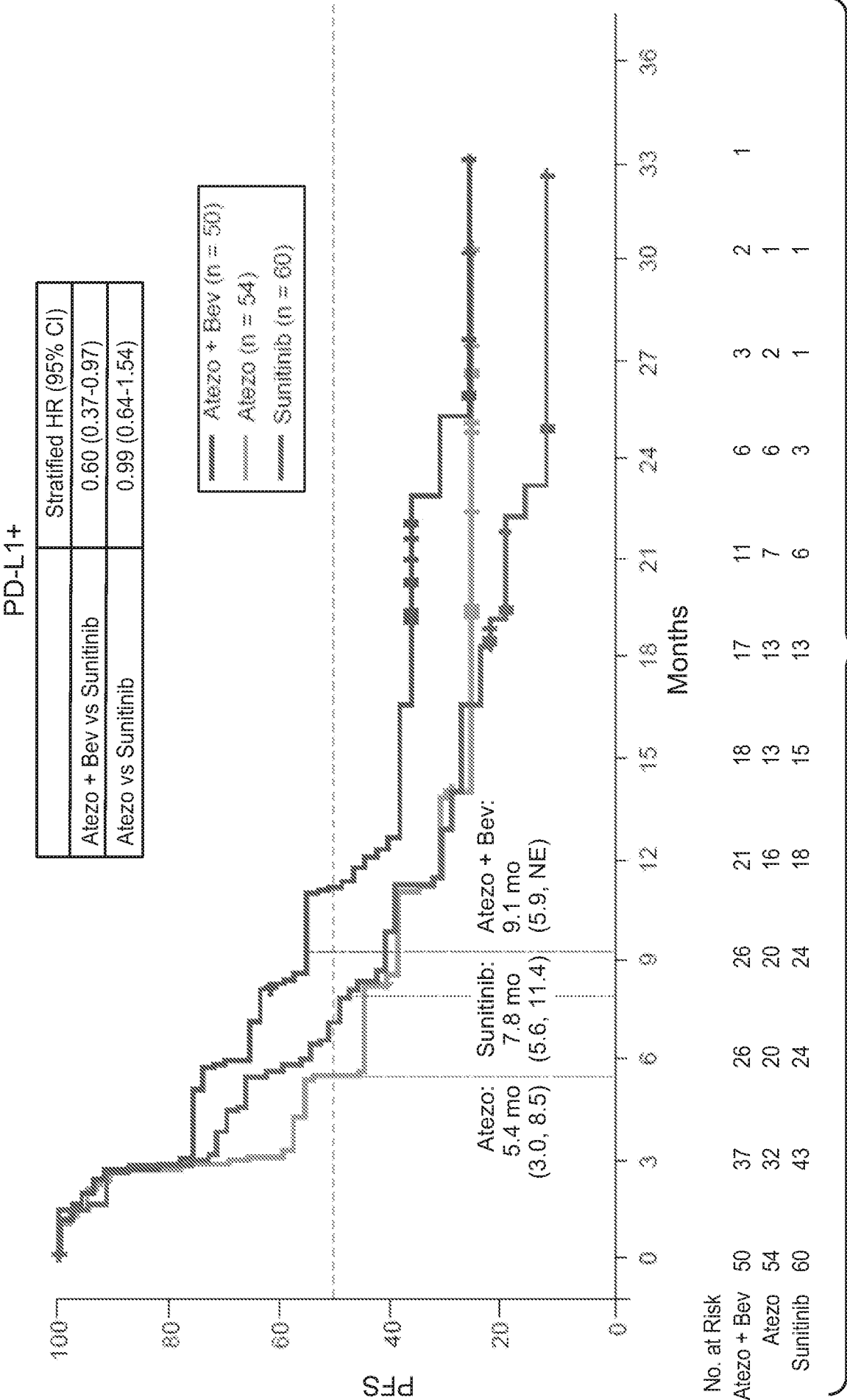


FIG. 34C





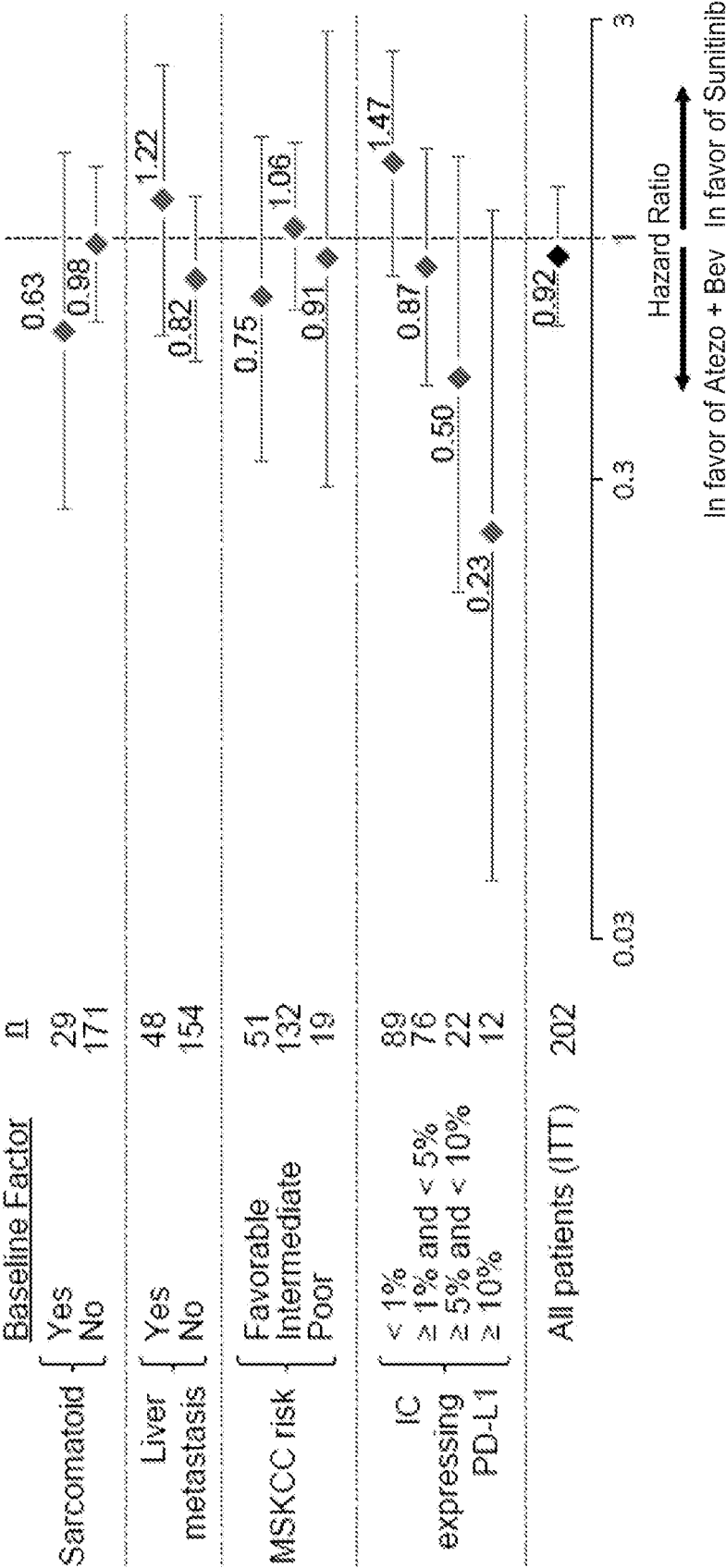


FIG. 36A

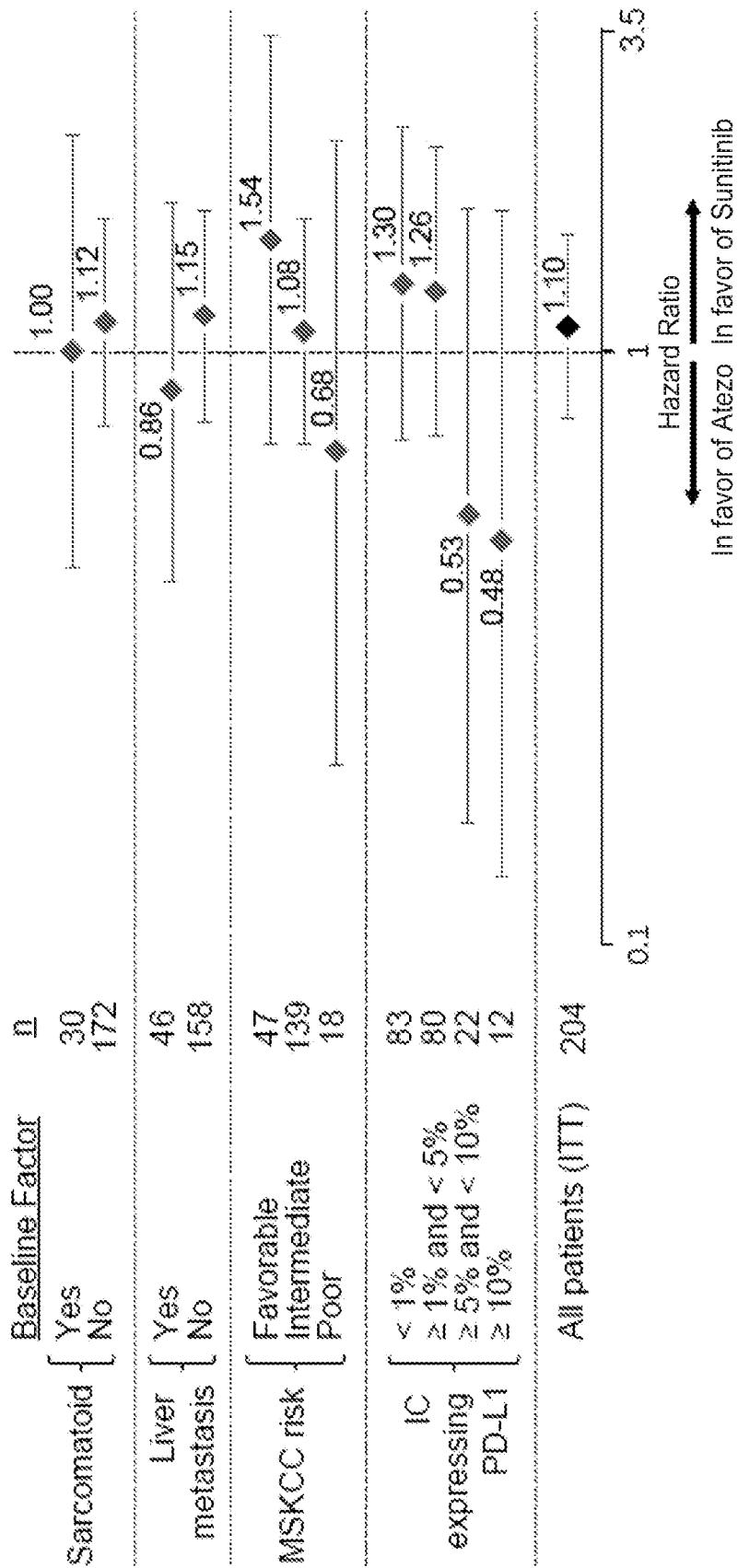


FIG. 36B

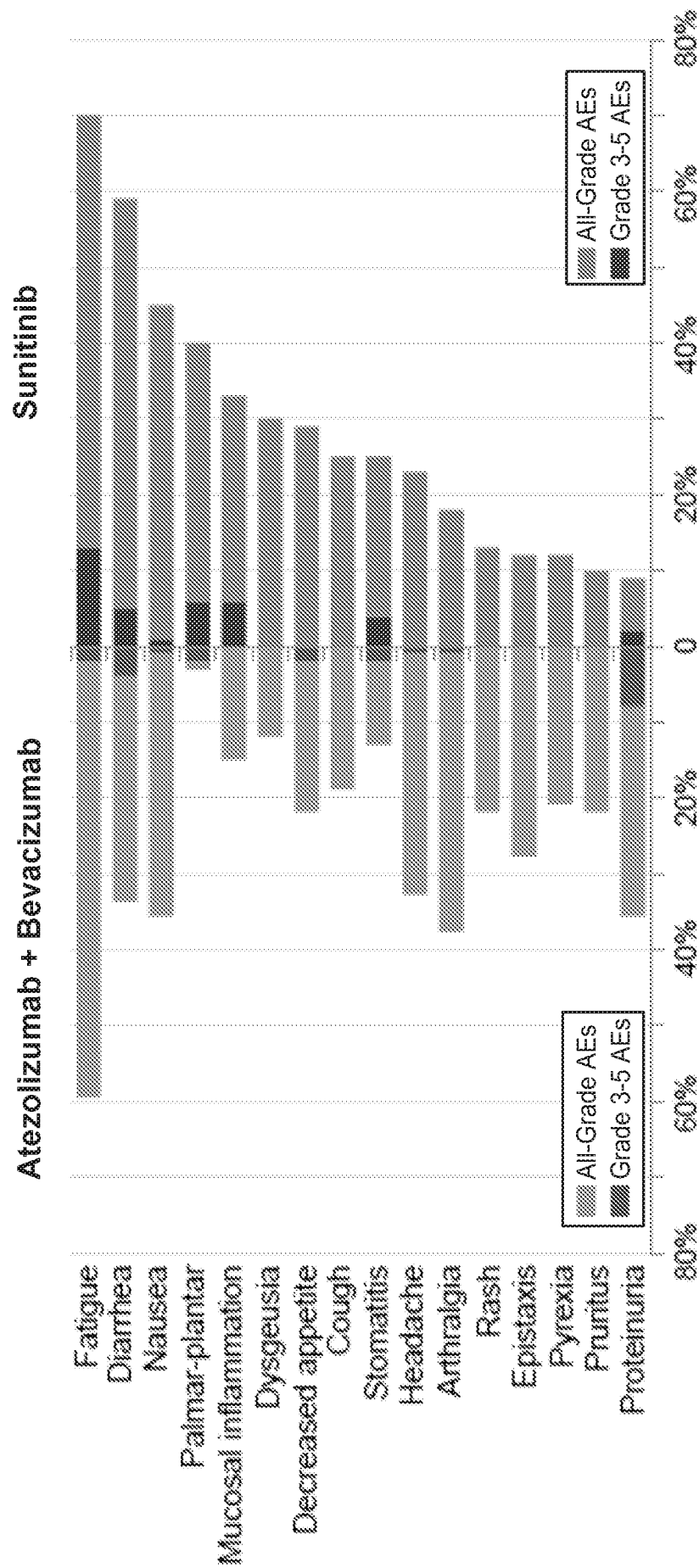


FIG. 37A

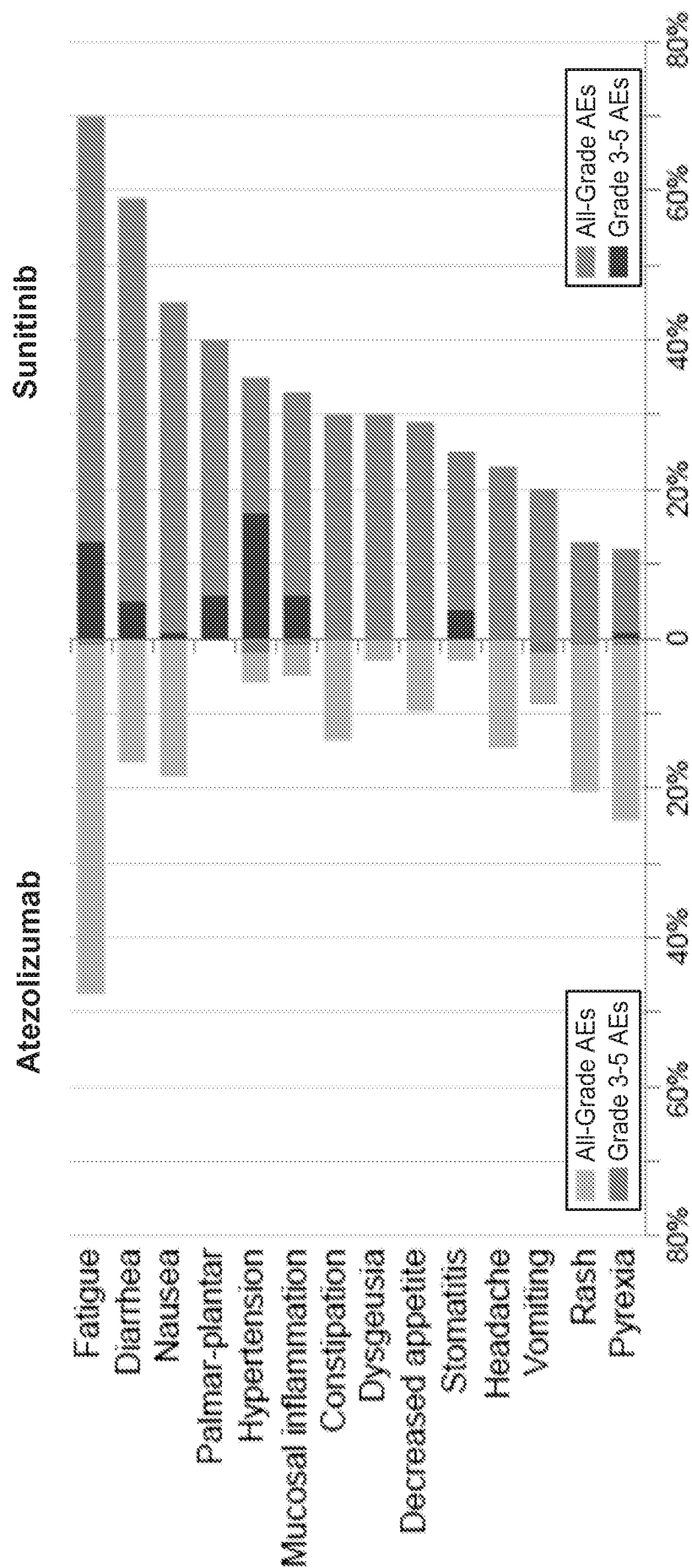


FIG. 37B

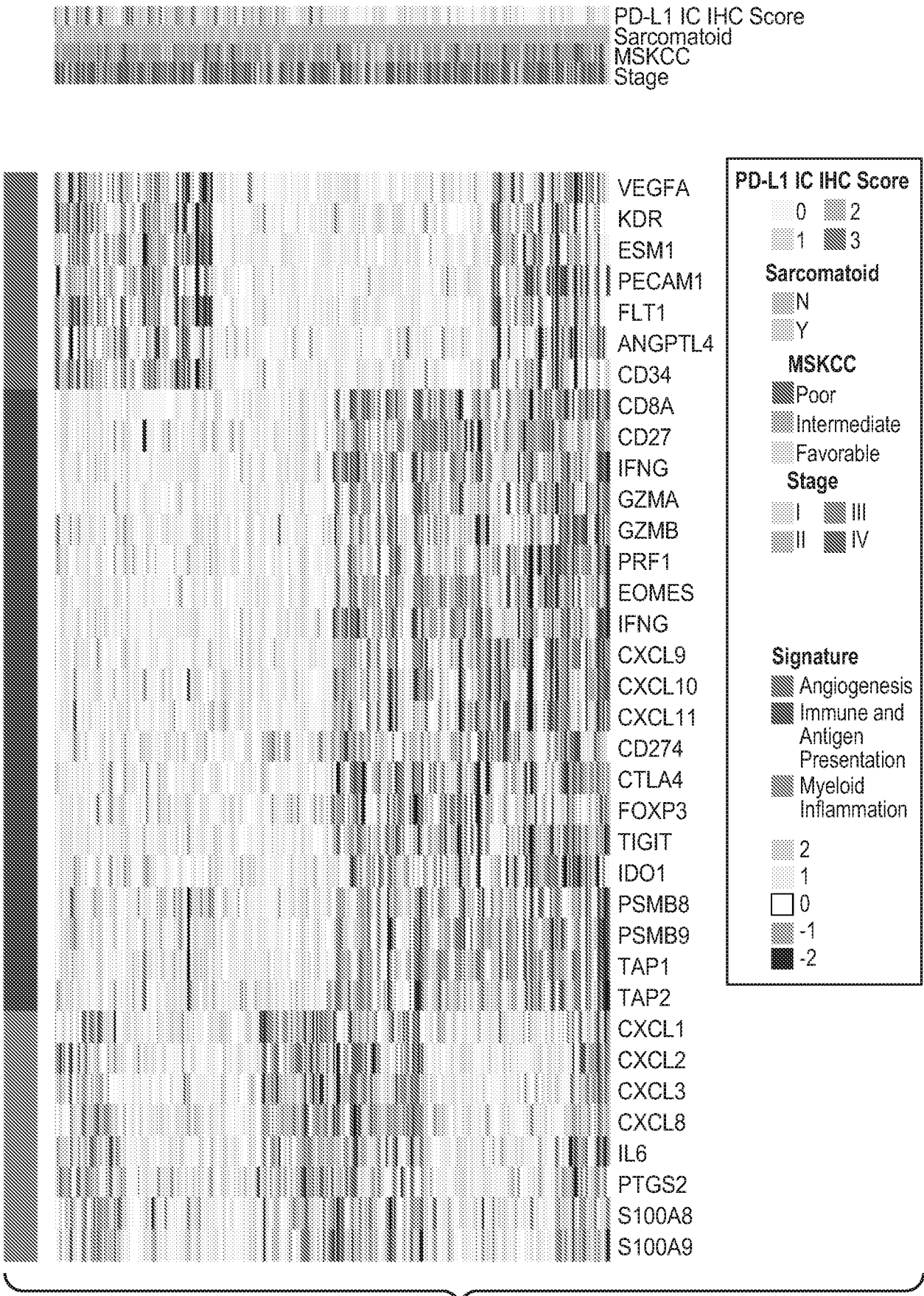


FIG. 38A

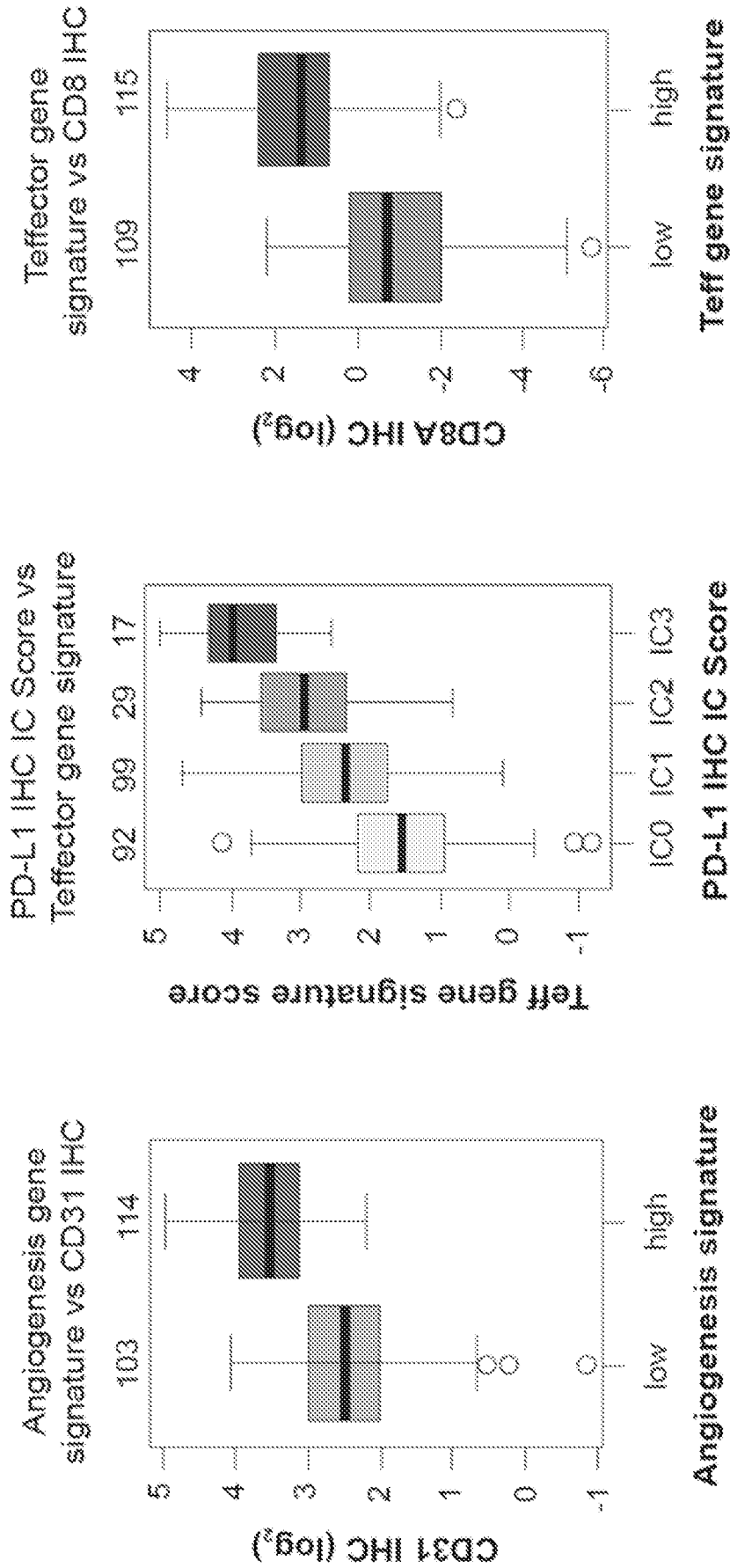
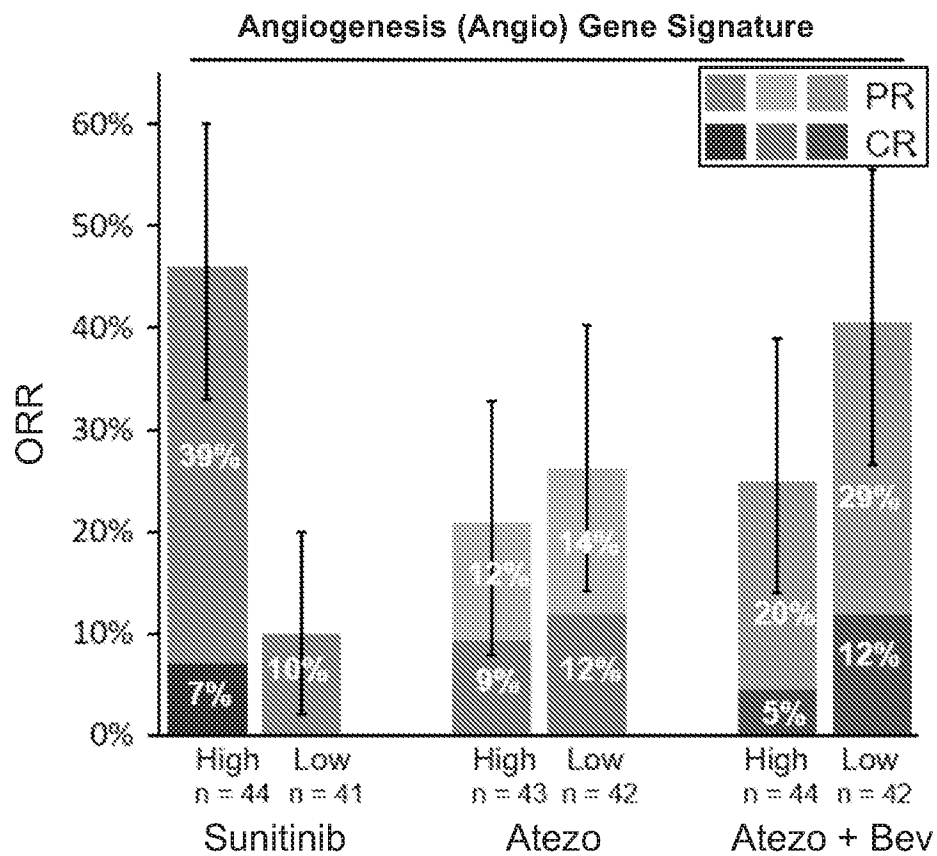
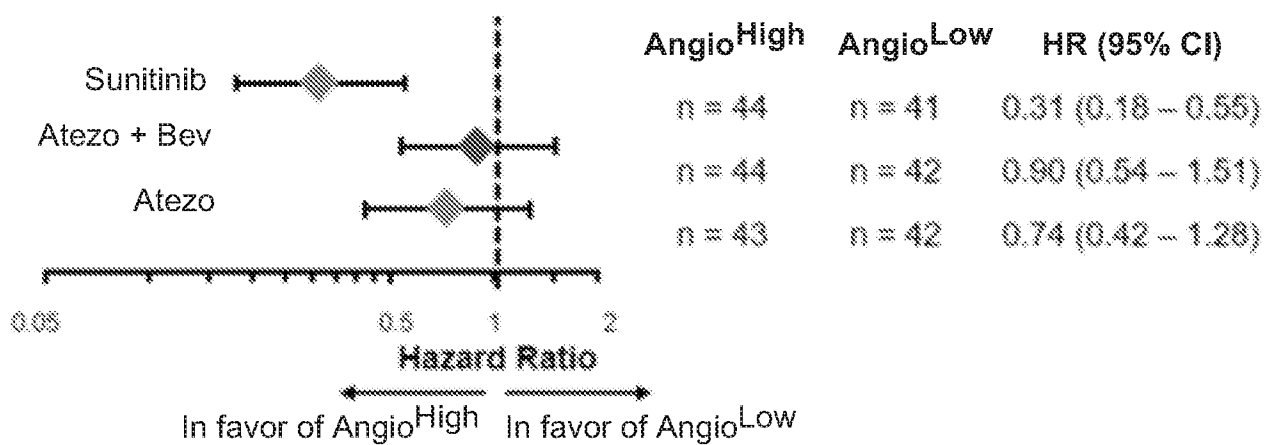


FIG. 38B

FIG. 38C

FIG. 38D

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**FIG. 38E****FIG. 38F**

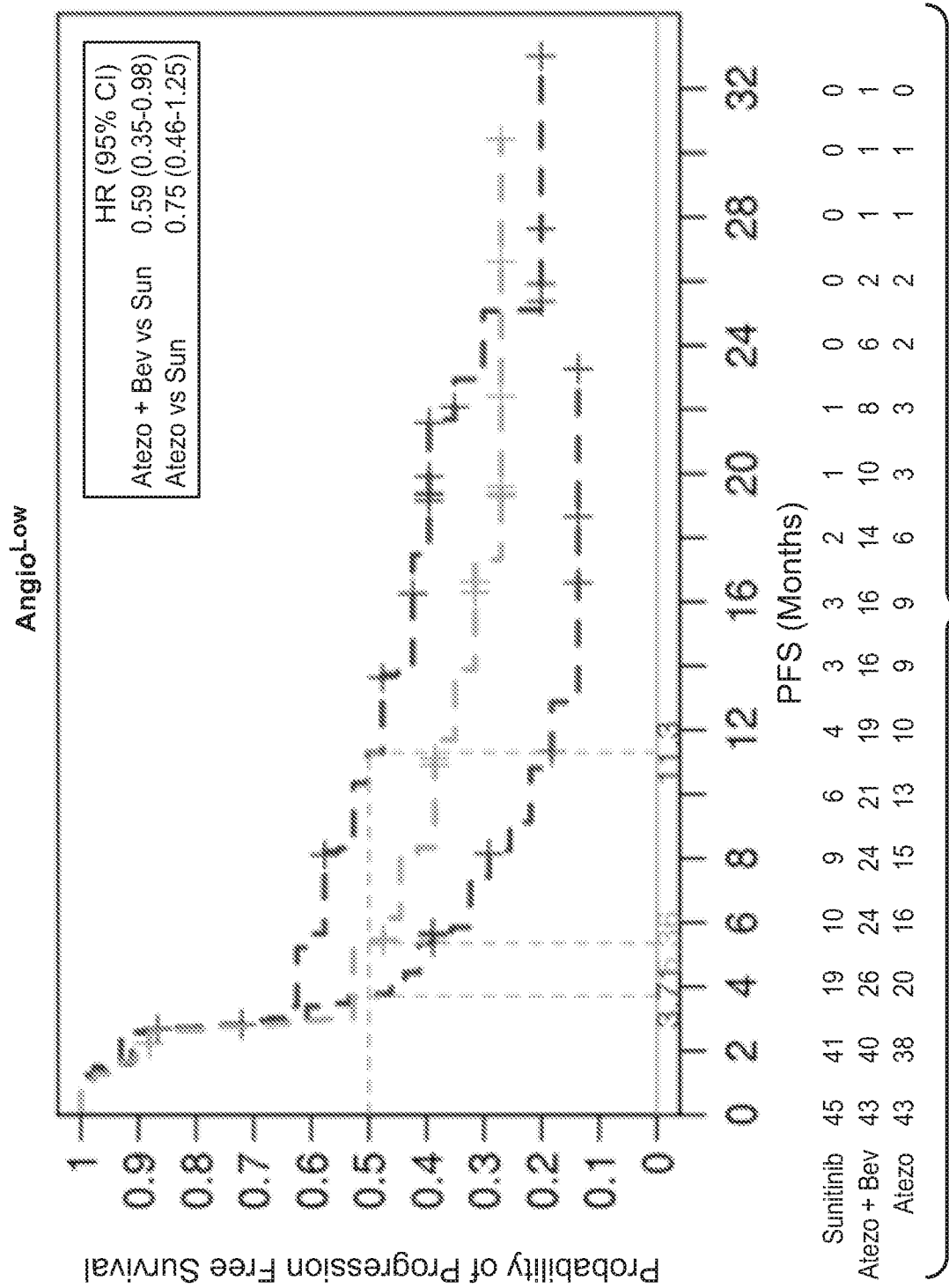


FIG. 38G

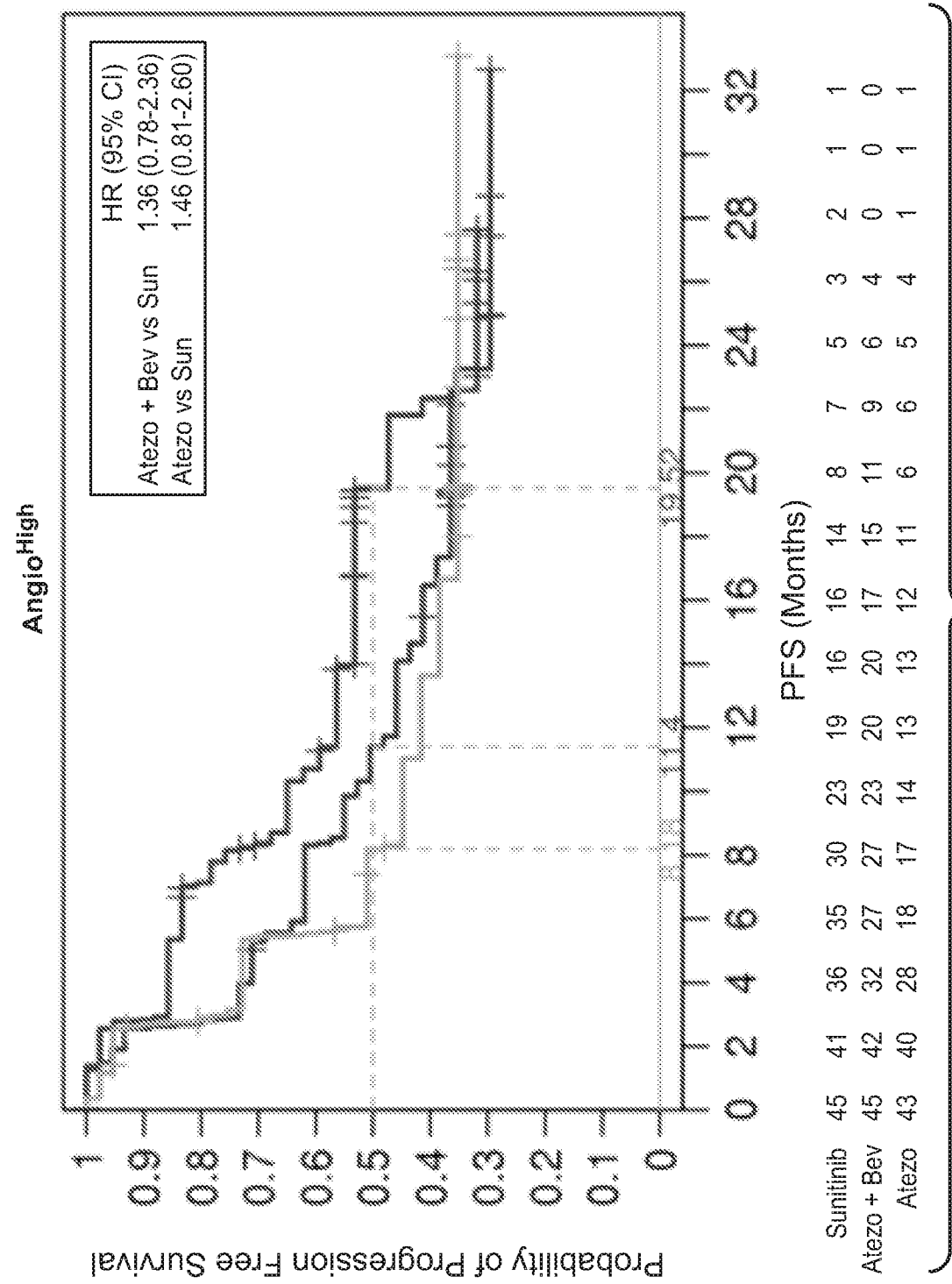
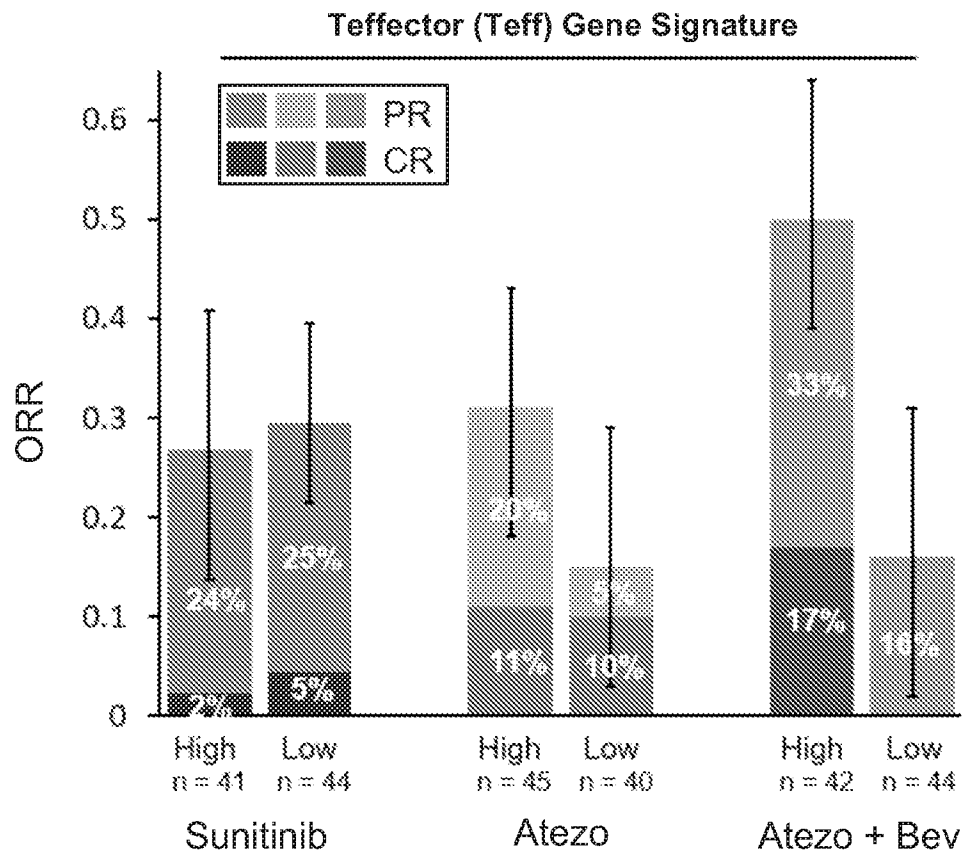
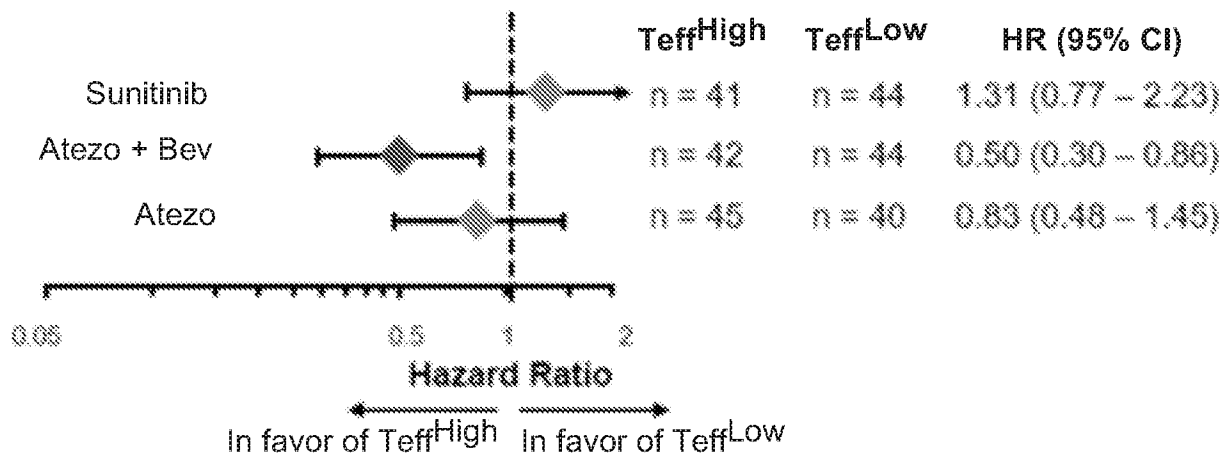


FIG. 38H

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**FIG. 38I****FIG. 38J**

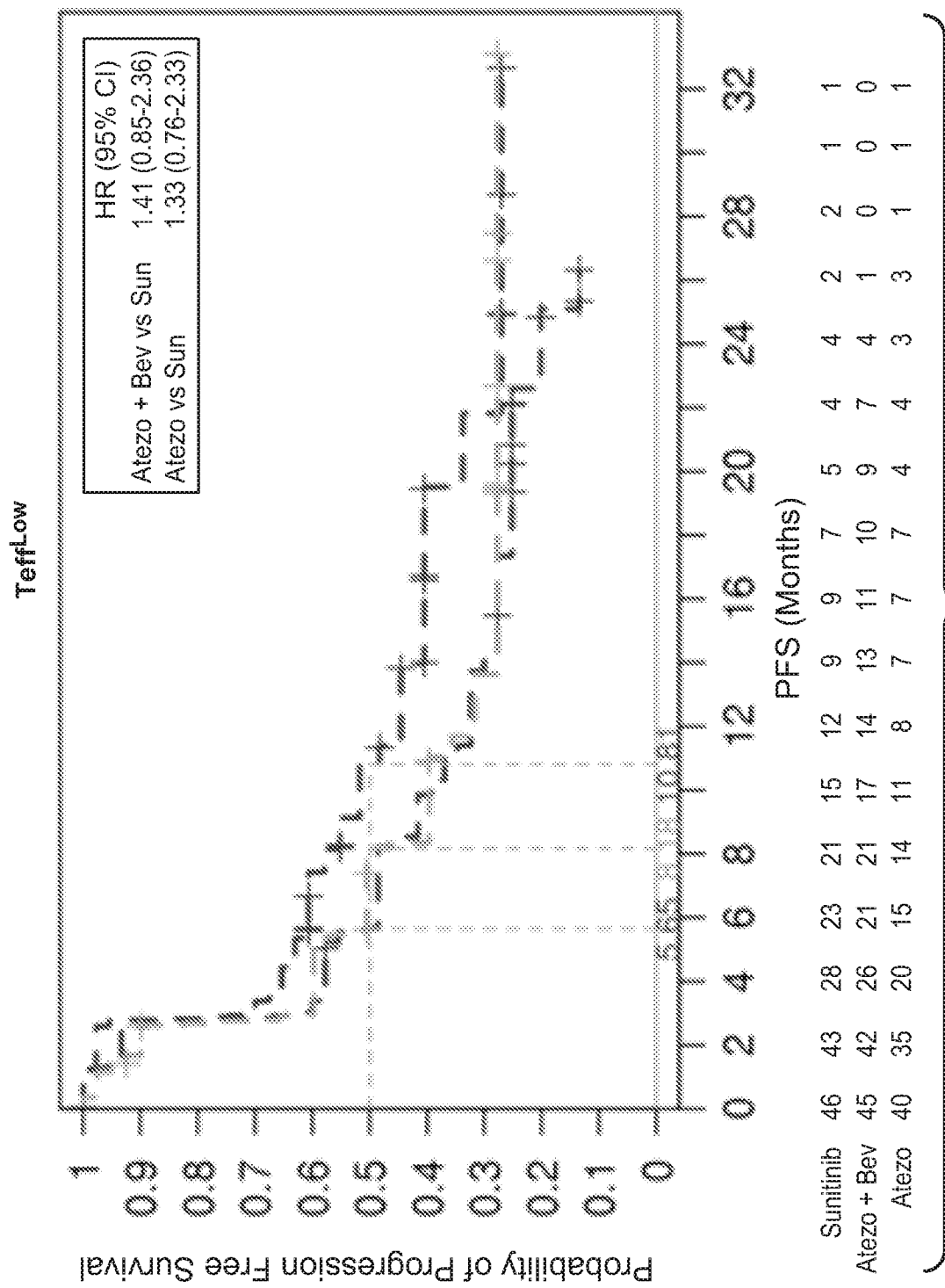


FIG. 38K

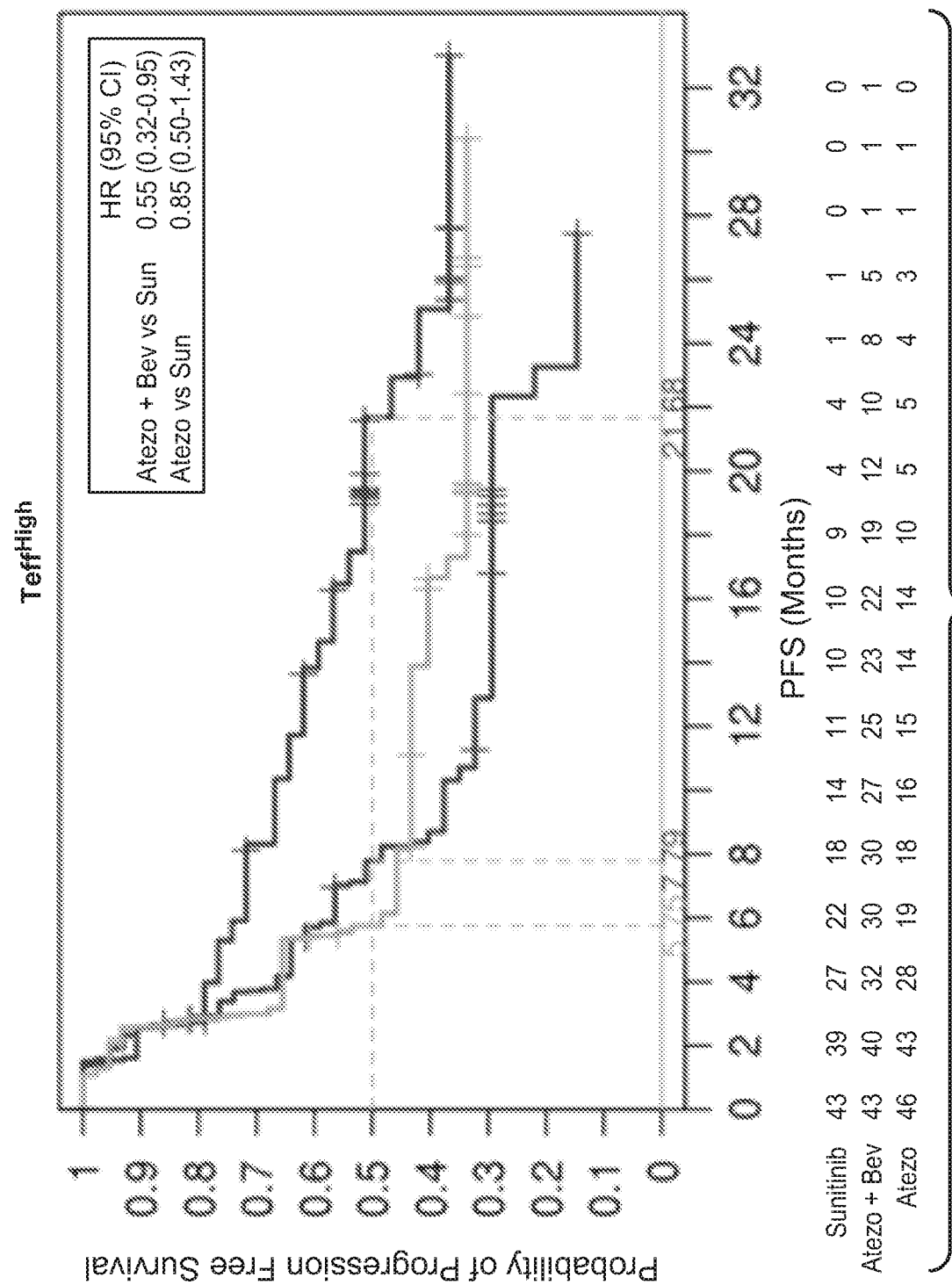


FIG. 38L

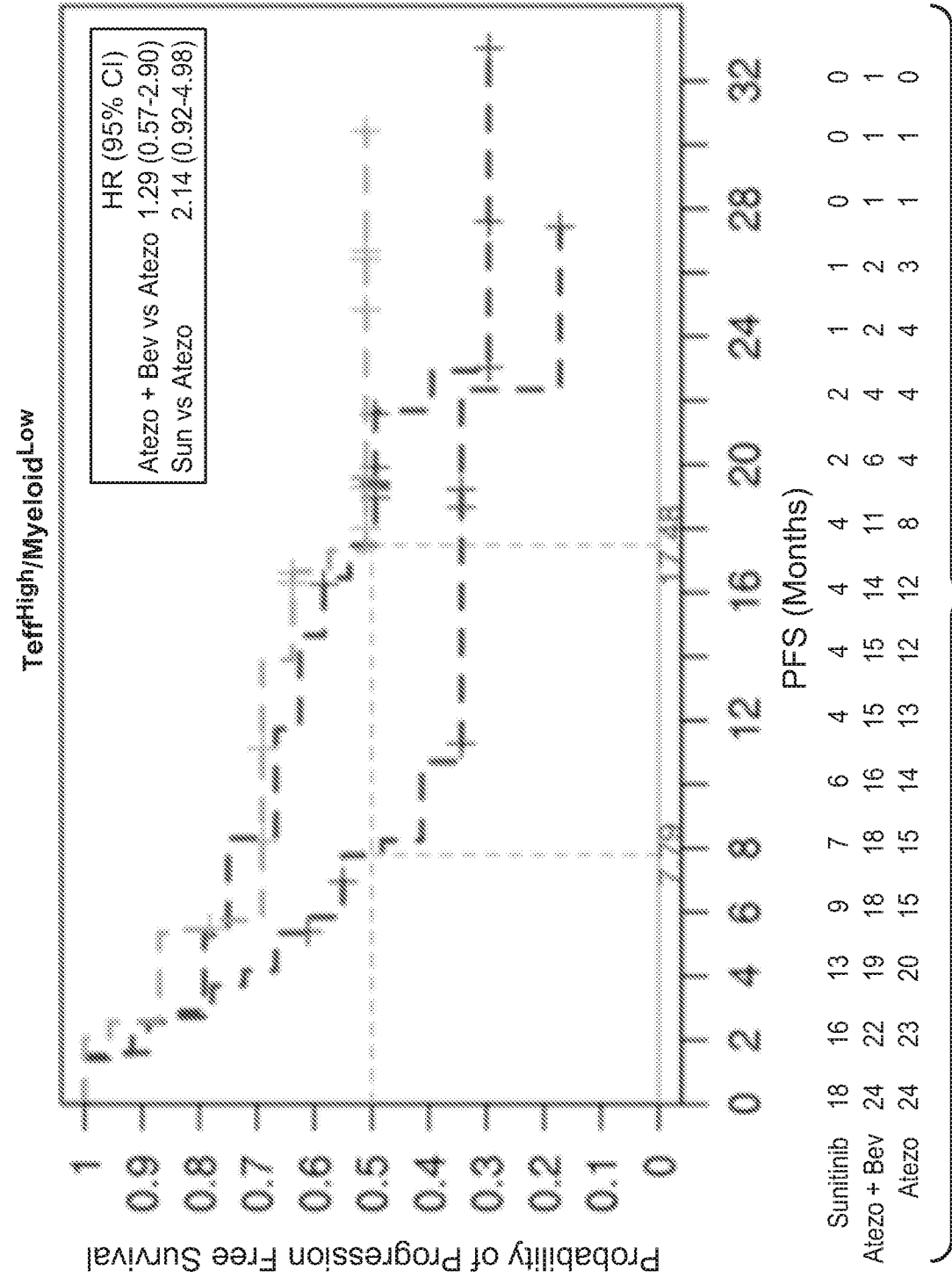


FIG. 38M

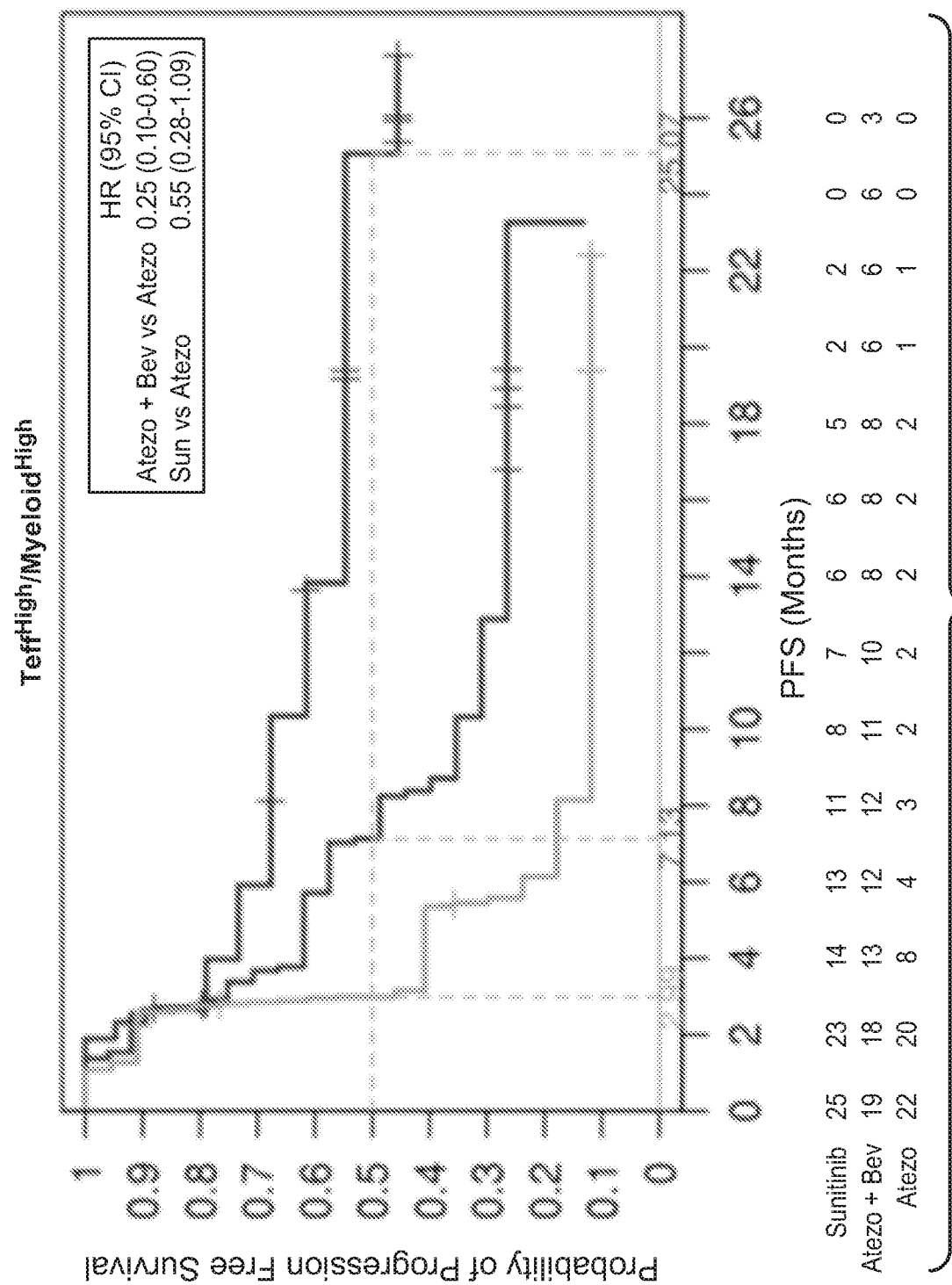


FIG. 38N

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2018/020460

A. CLASSIFICATION OF SUBJECT MATTER
 INV. C12Q1/6886
 ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, WPI Data, BIOSIS, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2015/119930 A1 (PFIZER [US]; MERCK SHARP & DOHME [US]) 13 August 2015 (2015-08-13) page 33, lines 14-20, paragraph 148 paragraph [0128]; claims 9,14	1-188
Y	WO 2016/200835 A1 (GENENTECH INC [US]) 15 December 2016 (2016-12-15) paragraph [0050] paragraphs [615(b)], [616(d)(e)]; example 3	1-188



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

25 April 2018

Date of mailing of the international search report

10/07/2018

Name and mailing address of the ISA/

European Patent Office, P.B. 5818 Patentlaan 2
 NL - 2280 HV Rijswijk
 Tel. (+31-70) 340-2040,
 Fax: (+31-70) 340-3016

Authorized officer

Aguilera, Miguel

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2018/020460

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	JEFFREY J. WALLIN ET AL: "Atezolizumab in combination with bevacizumab enhances antigen-specific T-cell migration in metastatic renal cell carcinoma", NATURE COMMUNICATIONS, vol. 7, 30 August 2016 (2016-08-30), page 12624, XP055396190, DOI: 10.1038/ncomms12624 the whole document -----	1-188
X	US 2015/071910 A1 (KOWANETZ MARCIN [US] ET AL) 12 March 2015 (2015-03-12)	108-125
Y	paragraphs [0138], [0433]; claim 14 -----	1-188
X	ALEJO RODRIGUEZ-VIDA ET AL: "Predictive and prognostic biomarkers of targeted agents and modern immunotherapy in renal cell carcinoma: Table 1", ESMO OPEN, vol. 1, no. 3, 1 May 2016 (2016-05-01), page e000013, XP055470188, DOI: 10.1136/esmoopen-2015-000013 page 9, column 1, paragraph 2 -----	108-125
X	X.-D. LIU ET AL: "Resistance to Antiangiogenic Therapy Is Associated with an Immunosuppressive Tumor Microenvironment in Metastatic Renal Cell Carcinoma", CANCER IMMUNOLOGY RESEARCH, vol. 3, no. 9, 26 May 2015 (2015-05-26), pages 1017-1029, XP055470192, US ISSN: 2326-6066, DOI: 10.1158/2326-6066.CIR-14-0244 page 3 -----	108-125

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2018/020460

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-188(partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-188(partially)

Methods to identify individuals for treatment or selecting therapy for kidney cancer comprising determining the expression level of CD8A. Therapeutic uses comprising said methods. Kits comprising reagents and instructions to carry out said methods.

2-33. claims: 1-188(partially)

Methods to identify individuals for treatment or selecting therapy for kidney cancer comprising determining the expression level of EOMES. Therapeutic uses comprising said methods. Kits comprising reagents and instructions to carry out said methods.

[idem for each one of the genes listed in claim 1]

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2018/020460

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2015119930 A1	13-08-2015	AU 2015214390 A1 BR 112016017256 A2 CA 2937521 A1 CN 105960415 A EA 201691376 A1 EP 3102605 A1 JP 2017506227 A KR 20160108566 A SG 11201605824X A TW 201615212 A US 2017166641 A1 WO 2015119930 A1	04-08-2016 17-10-2017 13-08-2015 21-09-2016 30-01-2017 14-12-2016 02-03-2017 19-09-2016 30-08-2016 01-05-2016 15-06-2017 13-08-2015
WO 2016200835 A1	15-12-2016	AU 2016274584 A1 CA 2988420 A1 CN 107750164 A EP 3303397 A1 KR 20180025888 A US 2017000885 A1 WO 2016200835 A1	04-01-2018 15-12-2016 02-03-2018 11-04-2018 09-03-2018 05-01-2017 15-12-2016
US 2015071910 A1	12-03-2015	AR 095363 A1 US 2015071910 A1 US 2017052188 A1	14-10-2015 12-03-2015 23-02-2017