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(54) Title: CANCER BIOMARKERS AND CLASSIFIERS AND USES THEREOF

Predictor	Discovery	Validation
GC	0.88	0.75
Node Status	0.70	0.68
Lymphovascular Invasion	0.69	0.69
Tumor Stage	0.58	0.56
Age	0.53	0.50
Gender	0.47	0.46
IBCNC	0.73	0.74
G-IBCNC	0.89	0.82
CC	0.81	0.77
G-CC	0.93	0.85

(57) Abstract: The present invention relates to methods, systems and kits for the diagnosis, prognosis and the determination of cancer progression of cancer in a subject. The invention also provides methods, systems and kits for determining the treatment modality of a cancer in a subject. The methods, systems and kits comprise expression-based analysis of biomarkers. Further disclosed herein, in certain instances, are probe sets for use in assessing a cancer status in a subject. Further disclosed herein are classifiers for analyzing a cancer, such as, for example, bladder cancer.

CANCER BIOMARKERS AND CLASSIFIERS AND USES THEREOF

RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Patent Application Serial No. 61/899,648, filed on November 4, 2013, which is hereby incorporated by reference herein in its entirety.

FIELD OF THE INVENTION

[0002] The present invention relates to methods, systems and kits for the diagnosis, prognosis and the determination of cancer progression of cancer in a subject. The invention also provides methods, systems and kits for determining the treatment modality of a cancer in a subject. The methods, systems and kits comprise expression-based analysis of biomarkers. Further disclosed herein, in certain instances, are probe sets for use in assessing a cancer status in a subject. Further disclosed herein are classifiers for analyzing a cancer, such as, for example, bladder cancer.

BACKGROUND OF THE INVENTION

[0003] Cancer is the uncontrolled growth of abnormal cells anywhere in a body. The abnormal cells are termed cancer cells, malignant cells, or tumor cells. Many cancers and

[0004] the abnormal cells that compose the cancer tissue are further identified by the name of the tissue that the abnormal cells originated from (for example, bladder cancer, breast cancer, lung cancer, colon cancer, prostate cancer, pancreatic cancer, thyroid cancer). Cancer cells can proliferate uncontrollably and form a mass of cancer cells. Cancer cells can break away from this original mass of cells, travel through the blood and lymph systems, and lodge in other organs where they can again repeat the uncontrolled growth cycle. This process of cancer cells leaving an area and growing in another body area is often termed metastatic spread or metastatic disease. For example, if breast cancer cells spread to a bone (or anywhere else), it can mean that the individual has metastatic breast cancer.

[0005] Standard clinical parameters such as tumor size, grade, lymph node involvement and tumor–node–metastasis (TNM) staging (American Joint Committee on Cancer <http://www.cancerstaging.org>) may correlate with outcome and serve to stratify patients with respect to (neo)adjuvant chemotherapy, immunotherapy, antibody therapy and/or radiotherapy regimens. Incorporation of molecular markers in clinical practice may define tumor subtypes that are more likely to respond to targeted therapy. However, stage-matched tumors grouped by histological or molecular subtypes may respond differently to the same

treatment regimen. Additional key genetic and epigenetic alterations may exist with important etiological contributions. A more detailed understanding of the molecular mechanisms and regulatory pathways at work in cancer cells and the tumor microenvironment (TME) could dramatically improve the design of novel anti-tumor drugs and inform the selection of optimal therapeutic strategies. The development and implementation of diagnostic, prognostic and therapeutic biomarkers to characterize the biology of each tumor may assist clinicians in making important decisions with regard to individual patient care and treatment. Thus, provided herein are methods, compositions and systems for the analysis of coding and non-coding targets for the diagnosis, prognosis, and monitoring of a cancer.

[0006] This background information is provided for the purpose of making known information believed by the applicant to be of possible relevance to the present invention. No admission is necessarily intended, nor should be construed, that any of the preceding information constitutes prior art against the present invention.

SUMMARY OF THE INVENTION

[0007] The present invention relates to methods, systems and kits for the diagnosis, prognosis and determination of cancer progression of cancer in a subject. In some embodiments, the present invention provides a method of diagnosing, prognosing, determining the progression of cancer, predicting a therapeutic regimen or predicting benefit from therapy in a subject, comprising (a) assaying an expression level in a sample from the subject for a plurality of targets, wherein the plurality of targets comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; and (b) diagnosing, prognosing, determining the progression of cancer, predicting a therapeutic regimen or predicting benefit from therapy in the subject based on the expression levels of the plurality of targets. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a bladder cancer. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the plurality of targets comprises a coding target. In some embodiments, the coding target is an exonic sequence. In some embodiments, the plurality of targets comprises a non-coding target. In some embodiments, the non-coding target comprises an intronic sequence or partially overlaps an intronic sequence. In some

embodiments, the non-coding target comprises a sequence within the UTR or partially overlaps with a UTR sequence. In some embodiments, the target comprises a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs: 1-1440. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs: 1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 2B, Table 16 or SEQ ID NOs: 1-1440 or SEQ ID NOs: 1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs: 1-1440. In some embodiments, the plurality of targets comprises at least 30 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 35 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or

SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some embodiments, the diagnosing, prognosing, determining progression of cancer, predicting a therapeutic regimen or predicting benefit from therapy includes determining the malignancy of the cancer. In some embodiments, the diagnosing, prognosing, determining progression of cancer, predicting a therapeutic regimen or predicting benefit from therapy includes determining the stage of the cancer. In some embodiments, the diagnosing, prognosing, determining progression of cancer, predicting a therapeutic regimen or predicting benefit from therapy includes assessing the risk of cancer recurrence. In some embodiments, determining the treatment for the cancer includes determining the efficacy of treatment. In some embodiments, the method further comprises sequencing the plurality of targets. In some embodiments, the method further comprises hybridizing the plurality of targets to a solid support. In some embodiments, the solid support is a bead or array. In some embodiments, assaying the expression level of a plurality of targets may comprise the use of a probe set. In some embodiments, assaying the expression level may comprise the use of a classifier. The classifier may comprise a probe selection region (PSR). In some embodiments, the classifier may comprise the use of an algorithm. The algorithm may comprise a machine learning algorithm. In some embodiments, assaying the expression level may also comprise sequencing the plurality of targets.

[0008] Further disclosed herein in some embodiments is a probe set for assessing a cancer status of a subject comprising a plurality of probes, wherein the probes in the set are capable of detecting an expression level of one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440, wherein the expression level determines the cancer status of the subject with at least 40% specificity. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 30 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 35 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some

embodiments, the plurality of targets comprises at least 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer,

epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a bladder cancer. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the probe set further comprises a probe capable of detecting an expression level of at least one coding target. In some embodiments, the coding target is an exonic sequence. In some embodiments, the probe set further comprises a probe capable of detecting an expression level of at least one non-coding target. In some embodiments, the non-coding target is an intronic sequence or partially overlaps with an intronic sequence. In some embodiments, the non-coding target is a UTR sequence or partially overlaps with a UTR sequence. In some embodiments, assessing the cancer status includes assessing cancer recurrence risk. In some embodiments, assessing the cancer status includes determining a treatment modality. In some embodiments, assessing the cancer status includes determining the efficacy of treatment. In some embodiments, the target is a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In some embodiments, the probes are between about 15 nucleotides and about 500 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 450 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 400 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 350 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 300 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 250 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 200 nucleotides in length. In some embodiments, the probes are at least 15 nucleotides in length. In some embodiments, the probes are at least 25 nucleotides in length. In some embodiments, the expression level determines the cancer status of the subject with at least 50% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 60% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 65% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 70% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 75% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 80% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 85% specificity. In some embodiments, the non-coding target is a non-coding RNA transcript and the non-coding RNA transcript is non-polyadenylated.

[0009] Further disclosed herein in some embodiments is a system for analyzing a cancer, comprising: (a) a probe set comprising a plurality of target sequences, wherein (i) the plurality of target sequences hybridizes to one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; or (ii) the plurality of target sequences comprises one or more target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; and (b) a computer model or algorithm for analyzing an expression level and/or expression profile of the target hybridized to the probe in a sample from a subject suffering from a cancer. In some embodiments, the system further comprises an electronic memory for capturing and storing an expression profile. In some embodiments, the system further comprises a computer-processing device, optionally connected to a computer network. In some embodiments, the system further comprises a software module executed by the computer-processing device to analyze an expression profile. In some embodiments, the system further comprises a software module executed by the computer-processing device to compare the expression profile to a standard or control. In some embodiments, the system further comprises a software module executed by the computer-processing device to determine the expression level of the target. In some embodiments, the system further comprises a machine to isolate the target or the probe from the sample. In some embodiments, the system further comprises a machine to sequence the target or the probe. In some embodiments, the system further comprises a machine to amplify the target or the probe. In some embodiments, the system further comprises a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the system further comprises a software module executed by the computer-processing device to transmit an analysis of the expression profile to the individual or a medical professional treating the individual. In some embodiments, the system further comprises a software module executed by the computer-processing device to transmit a diagnosis or prognosis to the individual or a medical professional treating the individual. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 30 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 35 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some

embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a bladder cancer. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the system further comprises a sequence for sequencing the plurality of targets. In some

embodiments, the system further comprises an instrument for amplifying the plurality of targets. In some embodiments, the system further comprises a label for labeling the plurality of targets.

[0010] Further disclosed herein in some embodiments is a method of analyzing a cancer in an individual in need thereof, comprising: (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; and (b) comparing the expression profile from the sample to an expression profile of a control or standard. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 30 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 35 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or

SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the method further comprises providing diagnostic or prognostic information to the individual about the cardiovascular disorder based on the comparison. In some embodiments, the method further comprises diagnosing the individual with a cancer if the expression profile of the sample (a) deviates from the control or standard from a healthy individual or population of healthy individuals, or (b) matches the control or standard from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises predicting the susceptibility of the individual for developing a cancer based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises prescribing a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or

population of individuals who have or have had the cancer. In some embodiments, the method further comprises altering a treatment regimen prescribed or administered to the individual based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises predicting the individual's response to a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the deviation is the expression level of one or more targets from the sample is greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises quantifying the expression level of the plurality of targets. In some embodiments, the method further comprises labeling the plurality of targets. In some embodiments, assaying the expression level of a plurality of targets may comprise the use of a probe set. In some embodiments, obtaining the expression level may comprise the use of a classifier. The classifier may comprise a probe selection region (PSR). In some embodiments, the classifier may comprise the use of an algorithm. The algorithm may comprise a machine learning algorithm. In some embodiments, obtaining the expression level may also comprise sequencing the plurality of targets.

[0011] Disclosed herein in some embodiments is a method of diagnosing cancer in an individual in need thereof, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) diagnosing a cancer in the individual if the expression profile of the sample (i) deviates from the control or standard from a healthy individual or population of healthy individuals, or (ii) matches the control or standard from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 30 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 35 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets

comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of one or more targets from the sample is greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the

probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises quantifying the expression level of the plurality of targets. In some embodiments, the method further comprises labeling the plurality of targets. In some embodiments, obtaining the expression level may comprise the use of a classifier. The classifier may comprise a probe selection region (PSR). In some embodiments, the classifier may comprise the use of an algorithm. The algorithm may comprise a machine learning algorithm. In some embodiments, obtaining the expression level may also comprise sequencing the plurality of targets.

[0012] Further disclosed herein in some embodiments is a method of predicting whether an individual is susceptible to developing a cancer, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) predicting the susceptibility of the individual for developing a cancer based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 30 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 35 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some

embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation

is the expression level of one or more targets from the sample is greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, obtaining the expression level may comprise the use of a classifier. The classifier may comprise a probe selection region (PSR). In some embodiments, the classifier may comprise the use of an algorithm. The algorithm may comprise a machine learning algorithm. In some embodiments, obtaining the expression level may also comprise sequencing the plurality of targets. In some embodiments, obtaining the expression level may also comprise amplifying the plurality of targets. In some embodiments, obtaining the expression level may also comprise quantifying the plurality of targets.

[0013] Further disclosed herein in some embodiments is a method of predicting an individual's response to a treatment regimen for a cancer, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) predicting the individual's response to a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

[illegible]

selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of one or more targets from the sample is greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises quantifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises labeling the target, the probe, or any combination thereof. In some embodiments, obtaining the expression level may comprise the use of a classifier. The classifier may comprise a probe selection region (PSR). In some embodiments, the classifier may comprise the use of an algorithm. The algorithm may comprise a machine learning algorithm. In some embodiments, obtaining the expression level may

also comprise sequencing the plurality of targets. In some embodiments, obtaining the expression level may also comprise amplifying the plurality of targets. In some embodiments, obtaining the expression level may also comprise quantifying the plurality of targets.

[0014] Disclosed herein in some embodiments is a method of prescribing a treatment regimen for a cancer to an individual in need thereof, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) prescribing a treatment regimen based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 30 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 35 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some

embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of one or more targets from the sample is greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets

from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the method further comprises quantifying the expression level of the plurality of targets. In some embodiments, the method further comprises labeling the plurality of targets. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof. In some embodiments, obtaining the expression level may comprise the use of a classifier. The classifier may comprise a probe selection region (PSR). In some embodiments, the classifier may comprise the use of an algorithm. The algorithm may comprise a machine learning algorithm. In some embodiments, obtaining the expression level may also comprise sequencing the plurality of targets. In some embodiments, obtaining the expression level may also comprise amplifying the plurality of targets. In some embodiments, obtaining the expression level may also comprise quantifying the plurality of targets.

[0015] In other embodiments, the present invention provides a method of determining the risk of bladder cancer recurrence in a subject having bladder cancer, comprising: measuring the expression level, in a bladder tissue or cell sample isolated from a subject, for at least one marker selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; wherein an elevated or reduced expression level of the at least one marker, over a control expression level in a corresponding normal bladder cancer tissue or bladder cancer cell sample, is indicative of an increased risk of bladder cancer recurrence. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer.

[0016] Further disclosed herein is a classifier for analyzing a cancer, wherein the classifier has an AUC value of at least about 0.60. The AUC of the classifier may be at least about 0.60, 0.61, 0.62, 0.63, 0.64,

0.65, 0.66, 0.67, 0.68, 0.69, 0.70 or more. The AUC of the classifier may be at least about 0.71, 0.72, 0.73, 0.74, 0.75, 0.76, 0.77, 0.78, 0.79, 0.80 or more. The AUC of the classifier may be at least about 0.81, 0.82, 0.83, 0.84, 0.85, 0.86, 0.87, 0.88, 0.89, 0.90 or more. The AUC of the classifier may be at least about 0.91, 0.92, 0.93, 0.94, 0.95, 0.96, 0.97, 0.98, 0.99 or more. The 95% CI of a classifier or biomarker may be between about 1.10 to 1.70. In some instances, the difference in the range of the 95% CI for a biomarker or classifier is between about 0.25 to about 0.50, between about 0.27 to about 0.47, or between about 0.30 to about 0.45.

[0017] Further disclosed herein is a classifier for analyzing a cancer, wherein the classifier has an AUC value of at least about 0.60. The AUC of the classifier may be at least about 0.60, 0.61, 0.62, 0.63, 0.64, 0.65, 0.66, 0.67, 0.68, 0.69, 0.70 or more. The AUC of the classifier may be at least about 0.71, 0.72, 0.73, 0.74, 0.75, 0.76, 0.77, 0.78, 0.79, 0.80 or more. The AUC of the classifier may be at least about 0.81, 0.82, 0.83, 0.84, 0.85, 0.86, 0.87, 0.88, 0.89, 0.90 or more. The AUC of the classifier may be at least about 0.91, 0.92, 0.93, 0.94, 0.95, 0.96, 0.97, 0.98, 0.99 or more. The 95% CI of a classifier or biomarker may be between about 1.10 to 1.70. In some instances, the difference in the range of the 95% CI for a biomarker or classifier is between about 0.25 to about 0.50, between about 0.27 to about 0.47, or between about 0.30 to about 0.45.

[0018] Further disclosed herein is a method for analyzing a cancer, comprising use of one or more classifiers, wherein the significance of the one or more classifiers is based on one or more metrics selected from the group comprising T-test, P-value, KS (Kolmogorov Smirnov) P-value, accuracy, accuracy P-value, positive predictive value (PPV), negative predictive value (NPV), sensitivity, specificity, AUC, AUC P-value (Auc.pvalue), Wilcoxon Test P-value, Median Fold Difference (MFD), Kaplan Meier (KM) curves, survival AUC (survAUC), Kaplan Meier P-value (KM P-value), Univariable Analysis Odds Ratio P-value (uvaORPval), multivariable analysis Odds Ratio P-value (mvaORPval), Univariable Analysis Hazard Ratio P-value (uvaHRPval) and Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The significance of the one or more classifiers may be based on two or more metrics selected from the group comprising AUC, AUC P-value (Auc.pvalue), Wilcoxon Test P-value, Median Fold Difference (MFD), Kaplan Meier (KM) curves, survival AUC (survAUC), Univariable Analysis Odds Ratio P-value (uvaORPval), multivariable analysis Odds Ratio P-value (mvaORPval), Kaplan Meier P-value (KM P-value), Univariable Analysis Hazard Ratio P-value (uvaHRPval) and Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The significance of the one or more classifiers may be based on three or more metrics selected from the group comprising AUC, AUC P-value (Auc.pvalue), Wilcoxon Test P-value, Median Fold Difference (MFD), Kaplan Meier (KM) curves, survival AUC (survAUC), Kaplan Meier P-value (KM P-value), Univariable Analysis Odds Ratio P-value (uvaORPval),

multivariable analysis Odds Ratio P-value (mvaORPval), Univariable Analysis Hazard Ratio P-value (uvaHRPval) and Multivariable Analysis Hazard Ratio P-value (mvaHRPval).

[0019] The one or more metrics may comprise AUC. The one or more metrics may comprise AUC and AUC P-value. The one or more metrics may comprise AUC P-value and Wilcoxon Test P-value. The one or more metrics may comprise Wilcoxon Test P-value. The one or more metrics may comprise AUC and Univariable Analysis Odds Ratio P-value (uvaORPval). The one or more metrics may comprise multivariable analysis Odds Ratio P-value (mvaORPval) and Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The one or more metrics may comprise AUC and Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The one or more metrics may comprise Wilcoxon Test P-value and Multivariable Analysis Hazard Ratio P-value (mvaHRPval).

[0020] The clinical significance of the classifier may be based on the AUC value. The AUC of the classifier may be at least about 0.60, 0.61, 0.62, 0.63, 0.64, 0.65, 0.66, 0.67, 0.68, 0.69, 0.70 or more. The AUC of the classifier may be at least about 0.71, 0.72, 0.73, 0.74, 0.75, 0.76, 0.77, 0.78, 0.79, 0.80 or more. The AUC of the classifier may be at least about 0.81, 0.82, 0.83, 0.84, 0.85, 0.86, 0.87, 0.88, 0.89, 0.90 or more. The AUC of the classifier may be at least about 0.91, 0.92, 0.93, 0.94, 0.95, 0.96, 0.97, 0.98, 0.99 or more. The 95% CI of a classifier or biomarker may be between about 1.10 to 1.70. In some instances, the difference in the range of the 95% CI for a biomarker or classifier is between about 0.25 to about 0.50, between about 0.27 to about 0.47, or between about 0.30 to about 0.45.

[0021] The clinical significance of the classifier may be based on Univariable Analysis Odds Ratio P-value (uvaORPval). The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be between about 0-0.4. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be between about 0-0.3. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be between about 0-0.2. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be less than or equal to 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0022] The clinical significance of the classifier may be based on multivariable analysis Odds Ratio P-value (mvaORPval). The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be between about 0-1. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be between about 0-0.9. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be between about 0-0.8. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be less than or equal to 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The multivariable analysis Odds

Ratio P-value (mvaORPval) of the classifier may be less than or equal to 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0023] The clinical significance of the classifier may be based on the Kaplan Meier P-value (KM P-value). The Kaplan Meier P-value (KM P-value) of the classifier may be between about 0-0.8. The Kaplan Meier P-value (KM P-value) of the classifier may be between about 0-0.7. The Kaplan Meier P-value (KM P-value) of the classifier may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The Kaplan Meier P-value (KM P-value) of the classifier may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Kaplan Meier P-value (KM P-value) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Kaplan Meier P-value (KM P-value) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0024] The clinical significance of the classifier may be based on the survival AUC value (survAUC). The survival AUC value (survAUC) of the classifier may be between about 0-1. The survival AUC value (survAUC) of the classifier may be between about 0-0.9. The survival AUC value (survAUC) of the classifier may be less than or equal to 1, 0.98, 0.96, 0.94, 0.92, 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The survival AUC value (survAUC) of the classifier may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The survival AUC value (survAUC) of the classifier may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The survival AUC value (survAUC) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The survival AUC value (survAUC) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0025] The clinical significance of the classifier may be based on the Univariable Analysis Hazard Ratio P-value (uvaHRPval). The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be between about 0-0.4. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be between about 0-0.3. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be less than or equal to 0.40, 0.38, 0.36, 0.34, 0.32. The Univariable Analysis Hazard Ratio

P-value (uvaHRPval) of the classifier may be less than or equal to 0.30, 0.29, 0.28, 0.27, 0.26, 0.25, 0.24, 0.23, 0.22, 0.21, 0.20. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be less than or equal to 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0026] The clinical significance of the classifier may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be between about 0-1. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be between about 0-0.9. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 1, 0.98, 0.96, 0.94, 0.92, 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0027] The clinical significance of the classifier may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be between about 0 to about 0.60. significance of the classifier may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be between about 0 to about 0.50. significance of the classifier may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 0.50, 0.47, 0.45, 0.43, 0.40, 0.38, 0.35, 0.33, 0.30, 0.28, 0.25, 0.22, 0.20, 0.18, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11, 0.10. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 0.01, 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0028] The method may further comprise determining an expression profile based on the one or more classifiers. The method may further comprise providing a sample from a subject. The subject may be a healthy subject. The subject may be suffering from a cancer or suspected of suffering from a cancer. The

method may further comprise diagnosing a cancer in a subject based on the expression profile or classifier. The method may further comprise treating a cancer in a subject in need thereof based on the expression profile or classifier. The method may further comprise determining a treatment regimen for a cancer in a subject in need thereof based on the expression profile or classifier. The method may further comprise prognosing a cancer in a subject based on the expression profile or classifier.

[0029] Further disclosed herein is a kit for analyzing a cancer, comprising (a) a probe set comprising a plurality of target sequences, wherein the plurality of target sequences comprises at least one target sequence listed in Table 2B, Table 16 or SEQ ID NOs:1-1440; and (b) a computer model or algorithm for analyzing an expression level and/or expression profile of the target sequences in a sample. In some embodiments, the kit further comprises a computer model or algorithm for correlating the expression level or expression profile with disease state or outcome. In some embodiments, the kit further comprises a computer model or algorithm for designating a treatment modality for the individual. In some embodiments, the kit further comprises a computer model or algorithm for normalizing expression level or expression profile of the target sequences. In some embodiments, the kit further comprises a computer model or algorithm comprising a robust multichip average (RMA), frozen robust multichip average (fRMA), Single Channel Array Normalization (SCAN), ComBat (Combining Batches of gene expression), probe logarithmic intensity error estimation (PLIER), non-linear fit (NLFIT) quantile-based, nonlinear normalization, or a combination thereof. In some embodiments, the plurality of target sequences comprises at least 5 target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of target sequences comprises at least 10 target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of target sequences comprises at least 15 target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of target sequences comprises at least 20 target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of target sequences comprises at least 30 target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of target sequences comprises at least 35 target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 40 target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or

SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer.

[0030] Further disclosed herein is a kit for analyzing a cancer, comprising (a) a probe set comprising a plurality of target sequences, wherein the plurality of target sequences hybridizes to one or more targets

selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; and (b) a computer model or algorithm for analyzing an expression level and/or expression profile of the target sequences in a sample. In some embodiments, the kit further comprises a computer model or algorithm for correlating the expression level or expression profile with disease state or outcome. In some embodiments, the kit further comprises a computer model or algorithm for designating a treatment modality for the individual. In some embodiments, the kit further comprises a computer model or algorithm for normalizing expression level or expression profile of the target sequences. In some embodiments, the kit further comprises a computer model or algorithm comprising a robust multichip average (RMA), frozen robust multichip average (fRMA), Single Channel Array Normalization (SCAN), ComBat (Combining Batches of gene expression), probe logarithmic intensity error estimation (PLIER), non-linear fit (NLFIT) quantile-based, nonlinear normalization, or a combination thereof. In some embodiments, the targets comprise at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the targets comprise at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the targets comprise at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the targets comprise at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the targets comprise at least 30 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the targets comprise at least 35 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the targets comprise at least 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets

comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer.

[0031] In other embodiments, the present invention provides methods for analyzing a sample from a subject comprising (a) assaying an expression level in a sample from the subject for a plurality of targets, wherein the plurality of targets comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; and (b) comparing the expression level of the plurality of targets in the sample to a control level of the plurality of targets in a control sample. In other embodiments, the methods of the present invention further comprise a computer model or algorithm for analyzing the plurality of targets in the sample.

INCORPORATION BY REFERENCE

[0032] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference in their entireties to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0033] FIG. 1 shows AUC of receiver operating characteristics (ROC) of single clinical variables and classifiers in the discovery and validation set.

[0034] FIGS. 2A-C show survival ROC curves for various classifiers of the present invention. FIG. 2A shows survival ROC curves for GC and single clinical variables. FIG. 2B shows survival ROC curves for IBCNC compared to G-IBCNC. FIG. 2C shows survival ROC curves for CC compared to G-CC at 4 years in the validation set.

[0035] FIGS. 3A-B show decision curves of classifiers of the present invention. FIG. 3A shows IBCNC compared to G-IBCNC. FIG. 3B shows CC compared to G-CC in the validation set.

[0036] FIGS. 4A-E show discrimination plots in validation set. Classifier scores of cases and controls across IBCNC, CC, GC, G-IBCNC and G-CC models.

[0037] FIGS. 5A-B show survival AUC over time and Cumulative incidence plots of GC in LNI negative patients from the validation set.

[0038] FIG. 6 shows cumulative incidence plot comparing patients with high or low G-CC as determined by majority rule (cutoff = 0.5) in the validation set.

[0039] FIGS. 7A-B show reclassification by G-IBCNC and G-CC compared to IBCNC.

[0040] FIG. 8 shows genomic classifier and tumor stage relation.

[0041] FIGS. 9A-B show GC scores discrimination in LNI negative or positive subsets compared to CC.

[0042] FIGS. 10A-B show cumulative incidence plots of (A) CC and (B) GC in LNI negative patients from the validation set.

[0043] FIG. 11 shows survival AUC performance of external signatures in comparison to GC at predicting recurrence at 4 years.

[0044] FIG. 12 shows GO terms associated with the 15 features in GC.

DETAILED DESCRIPTION OF THE INVENTION

[0045] The present invention discloses systems and methods for diagnosing, predicting, and/or monitoring the status or outcome of a cancer in a subject using expression-based analysis of a plurality of targets. Generally, the method comprises (a) optionally providing a sample from a subject; (b) assaying the expression level for a plurality of targets in the sample; and (c) diagnosing, predicting and/or monitoring the status or outcome of a cancer based on the expression level of the plurality of targets.

[0046] Assaying the expression level for a plurality of targets in the sample may comprise applying the sample to a microarray. In some instances, assaying the expression level may comprise the use of an algorithm. The algorithm may be used to produce a classifier. Alternatively, the classifier may comprise a probe selection region. In some instances, assaying the expression level for a plurality of targets comprises detecting and/or quantifying the plurality of targets. In some embodiments, assaying the expression level for a plurality of targets comprises sequencing the plurality of targets. In some embodiments, assaying the expression level for a plurality of targets comprises amplifying the plurality of targets. In some embodiments, assaying the expression level for a plurality of targets comprises quantifying the plurality of targets. In some embodiments, assaying the expression level for a plurality of targets comprises conducting a multiplexed reaction on the plurality of targets.

[0047] In some instances, the plurality of targets comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, or at least about 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In other instances, the plurality of targets comprises at least about 12, at least about 15, at least about 17, at least about 20, at least about 22, at least about 25, at least about 27, at least about 30, at least about 32, at least about 35, at least about 37, or at least about 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or

SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some instances, the plurality of targets comprises a coding target, non-coding target, or any combination thereof. In some instances, the coding target comprises an exonic sequence. In other instances, the non-coding target comprises a non-exonic or exonic sequence. In some instances, the non-exonic sequence comprises an untranslated region (e.g., UTR), intronic region, intergenic region, antisense, or any combination thereof. Alternatively, the plurality of targets comprises an anti-sense sequence. In other instances, the plurality of targets comprises a non-coding RNA transcript.

[0048] Further disclosed herein, is a probe set for diagnosing, predicting, and/or monitoring a cancer in a subject. In some instances, the probe set comprises a plurality of probes capable of detecting an expression level of one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440, wherein the expression level determines the cancer status of the subject with at least about 45% specificity. In some instances, detecting an expression level comprise detecting gene expression, protein expression, or any combination thereof. In some instances, the plurality of targets comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, or at least about 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In other instances, the plurality of targets comprises at least about 12, at least about 15, at least about 17, at least about 20, at least about 22, at least about 25, at least about 27, at least about 30, at least about 32, at least about 35, at least about 37, or at least about 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B,

Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some instances, the plurality of targets comprises a coding target, non-coding target, or any combination thereof. In some instances, the coding target comprises an exonic sequence. In other instances, the non-coding target comprises a non-exonic or exonic sequence. In some instances, the non-exonic sequence comprises an untranslated region (e.g., UTR), intronic region, intergenic region, antisense or any combination thereof. Alternatively, the plurality of targets comprises an anti-sense sequence. In other instances, the plurality of targets comprises a non-coding RNA transcript.

[0049] Further disclosed herein are methods for characterizing a patient population. Generally, the method comprises: (a) providing a sample from a subject; (b) assaying the expression level for a plurality of targets in the sample; and (c) characterizing the subject based on the expression level of the plurality of

targets. In some instances, the plurality of targets comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, or at least about 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In other instances, the plurality of targets comprises at least about 12, at least about 15, at least about 17, at least about 20, at least about 22, at least about 25, at least about 27, at least about 30, at least about 32, at least about 35, at least about 37, or at least about 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 50 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 60 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 100 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 125 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 150 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 175 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 200 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 225 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 250 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 275 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 300 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 350 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 400 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 450 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 500 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 550 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 600 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 650 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 700 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 750 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets

comprises at least 800 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises SEQ ID NOs:1-15. In some instances, the plurality of targets comprises a coding target, non-coding target, or any combination thereof. In some instances, the coding target comprises an exonic sequence. In other instances, the non-coding target comprises a non-exonic or exonic sequence. In some instances, the non-exonic sequence comprises an untranslated region (e.g., UTR), intronic region, antisense, intergenic region, or any combination thereof. Alternatively, the plurality of targets comprises an anti-sense sequence. In other instances, the plurality of targets comprises a non-coding RNA transcript.

[0050] In some instances, characterizing the subject comprises determining whether the subject would respond to an anti-cancer therapy. Alternatively, characterizing the subject comprises identifying the subject as a non-responder to an anti-cancer therapy. Optionally, characterizing the subject comprises identifying the subject as a responder to an anti-cancer therapy.

[0051] Before the present invention is described in further detail, it is to be understood that this invention is not limited to the particular methodology, compositions, articles or machines described, as such methods, compositions, articles or machines can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention.

Definitions

[0052] Unless defined otherwise or the context clearly dictates otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. In describing the present invention, the following terms may be employed, and are intended to be defined as indicated below.

[0053] The term "polynucleotide" as used herein refers to a polymer of greater than one nucleotide in length of ribonucleic acid (RNA), deoxyribonucleic acid (DNA), hybrid RNA/DNA, modified RNA or DNA, or RNA or DNA mimetics, including peptide nucleic acids (PNAs). The polynucleotides may be single- or double-stranded. The term includes polynucleotides composed of naturally-occurring nucleobases, sugars and covalent internucleoside (backbone) linkages as well as polynucleotides having non-naturally-occurring portions which function similarly. Such modified or substituted polynucleotides are well known in the art and for the purposes of the present invention, are referred to as "analogues."

[0054] "Complementary" or "substantially complementary" refers to the ability to hybridize or base pair between nucleotides or nucleic acids, such as, for instance, between a sensor peptide nucleic acid or polynucleotide and a target polynucleotide. Complementary nucleotides are, generally, A and T (or A and U), or C and G. Two single-stranded polynucleotides or PNAs are said to be substantially complementary when the bases of one strand, optimally aligned and compared and with appropriate insertions or

deletions, pair with at least about 80% of the bases of the other strand, usually at least about 90% to 95%, and more preferably from about 98 to 100%.

[0055] Alternatively, substantial complementarity exists when a polynucleotide may hybridize under selective hybridization conditions to its complement. Typically, selective hybridization may occur when there is at least about 65% complementarity over a stretch of at least 14 to 25 bases, for example at least about 75%, or at least about 90% complementarity.

[0056] "Preferential binding" or "preferential hybridization" refers to the increased propensity of one polynucleotide to bind to its complement in a sample as compared to a noncomplementary polymer in the sample.

[0057] Hybridization conditions may typically include salt concentrations of less than about 1M, more usually less than about 500 mM, for example less than about 200 mM. In the case of hybridization between a peptide nucleic acid and a polynucleotide, the hybridization can be done in solutions containing little or no salt. Hybridization temperatures can be as low as 5° C, but are typically greater than 22° C, and more typically greater than about 30° C, for example in excess of about 37° C. Longer fragments may require higher hybridization temperatures for specific hybridization as is known in the art. Other factors may affect the stringency of hybridization, including base composition and length of the complementary strands, presence of organic solvents and extent of base mismatching, and the combination of parameters used is more important than the absolute measure of any one alone. Other hybridization conditions which may be controlled include buffer type and concentration, solution pH, presence and concentration of blocking reagents to decrease background binding such as repeat sequences or blocking protein solutions, detergent type(s) and concentrations, molecules such as polymers which increase the relative concentration of the polynucleotides, metal ion(s) and their concentration(s), chelator(s) and their concentrations, and other conditions known in the art.

[0058] "Multiplexing" herein refers to an assay or other analytical method in which multiple analytes are assayed. In some instances, the multiple analytes are from the same sample. In some instances, the multiple analytes are assayed simultaneously. Alternatively, the multiple analytes are assayed sequentially. In some instances, assaying the multiple analytes occurs in the same reaction volume. Alternatively, assaying the multiple analytes occurs in separate or multiple reaction volumes.

[0059] A "target sequence" as used herein (also occasionally referred to as a "PSR" or "probe selection region") refers to a region of the genome against which one or more probes can be designed. A "target sequence" may be a coding target or a non-coding target. A "target sequence" may comprise exonic and/or non-exonic sequences. Alternatively, a "target sequence" may comprise an ultraconserved region. An ultraconserved region is generally a sequence that is at least 200 base pairs and is conserved across multiple species. An ultraconserved region may be exonic or non-exonic. Exonic sequences may

comprise regions on a protein-coding gene, such as an exon, UTR, or a portion thereof. Non-exonic sequences may comprise regions on a protein-coding, non protein-coding gene, or a portion thereof. For example, non-exonic sequences may comprise intronic regions, promoter regions, intergenic regions, a non-coding transcript, an exon anti-sense region, an intronic anti-sense region, UTR anti-sense region, non-coding transcript anti-sense region, or a portion thereof. The term "target sequence" is used interchangeably with the terms "target", "marker", and "biomarker" throughout the specification.

[0060] As used herein, a probe is any polynucleotide capable of selectively hybridizing to a target sequence or its complement, or to an RNA version of either. A probe may comprise ribonucleotides, deoxyribonucleotides, peptide nucleic acids, and combinations thereof. A probe may optionally comprise one or more labels. In some embodiments, a probe may be used to amplify one or both strands of a target sequence or an RNA form thereof, acting as a sole primer in an amplification reaction or as a member of a set of primers.

[0061] As used herein, a non-coding target may comprise a nucleotide sequence. The nucleotide sequence is a DNA or RNA sequence. A non-coding target may include a UTR sequence, an intronic sequence, antisense, or a non-coding RNA transcript. A non-coding target also includes sequences which partially overlap with a UTR sequence or an intronic sequence. A non-coding target also includes non-exonic or exonic transcripts.

[0062] As used herein, a coding target includes nucleotide sequences that encode for a protein and peptide sequences. The nucleotide sequence is a DNA or RNA sequence. The coding target includes protein-coding sequence. Protein-coding sequences include exon-coding sequences (e.g., exonic sequences).

[0063] As used herein, diagnosis of cancer may include the identification of cancer in a subject, determining the malignancy of the cancer, or determining the stage of the cancer.

[0064] As used herein, prognosis of cancer may include predicting the clinical outcome of the patient, assessing the risk of cancer recurrence, determining treatment modality, or determining treatment efficacy.

[0065] "Having" is an open-ended phrase like "comprising" and "including," and includes circumstances where additional elements are included and circumstances where they are not.

[0066] "Optional" or "optionally" means that the subsequently described event or circumstance may or may not occur, and that the description includes instances where the event or circumstance occurs and instances in which it does not.

[0067] As used herein 'NED' describes a clinically distinct disease state in which patients show no evidence of disease (NED') at least 5 years after surgery, 'PSA' describes a clinically distinct disease state in which patients show biochemical relapse only (two successive increases in prostate-specific antigen

levels but no other symptoms of disease with at least 5 years follow up after surgery; 'PSA') and 'SYS' describes a clinically distinct disease state in which patients develop biochemical relapse and present with systemic cancer disease or metastases ('SYS') within five years after the initial treatment with radical prostatectomy.

[0068] The terms "METS", "SYS", "systemic event", "Systemic progression", "CR" or "Clinical Recurrence" may be used interchangeably and generally refer to patients that experience BCR (biochemical recurrence) and that develop metastases (confirmed by bone or CT scan). The patients may experience BCR within 5 years of RP (radical prostatectomy). The patients may develop metastases within 5 years of BCR. In some cases, patients regarded as METS may experience BCR after 5 years of RP. In other cases, patients may exhibit cancer recurrence after radical cystectomy (e.g., bladder cancer recurrence). A further preferred surgery is cystectomy, in particular radical or partial cystectomy. The term "cystectomy" refers to removal of all (radical cystectomy) or part (partial cystectomy) of the urinary bladder. This kind of surgery is usually carried out in invasive bladder cancer, and in particular, muscle invasive bladder cancer.

[0069] As used herein, the term "about" refers to approximately a +/-10% variation from a given value. It is to be understood that such a variation is always included in any given value provided herein, whether or not it is specifically referred to.

[0070] Use of the singular forms "a," "an," and "the" include plural references unless the context clearly dictates otherwise. Thus, for example, reference to "a polynucleotide" includes a plurality of polynucleotides, reference to "a target" includes a plurality of such targets, reference to "a normalization method" includes a plurality of such methods, and the like. Additionally, use of specific plural references, such as "two," "three," etc., read on larger numbers of the same subject, unless the context clearly dictates otherwise.

[0071] Terms such as "connected," "attached," "linked" and "conjugated" are used interchangeably herein and encompass direct as well as indirect connection, attachment, linkage or conjugation unless the context clearly dictates otherwise.

[0072] Where a range of values is recited, it is to be understood that each intervening integer value, and each fraction thereof, between the recited upper and lower limits of that range is also specifically disclosed, along with each subrange between such values. The upper and lower limits of any range can independently be included in or excluded from the range, and each range where either, neither or both limits are included is also encompassed within the invention. Where a value being discussed has inherent limits, for example where a component can be present at a concentration of from 0 to 100%, or where the pH of an aqueous solution can range from 1 to 14, those inherent limits are specifically disclosed. Where a value is explicitly recited, it is to be understood that values, which are about the same quantity or

amount as the recited value, are also within the scope of the invention, as are ranges based thereon. Where a combination is disclosed, each sub-combination of the elements of that combination is also specifically disclosed and is within the scope of the invention. Conversely, where different elements or groups of elements are disclosed, combinations thereof are also disclosed. Where any element of an invention is disclosed as having a plurality of alternatives, examples of that invention in which each alternative is excluded singly or in any combination with the other alternatives are also hereby disclosed; more than one element of an invention can have such exclusions, and all combinations of elements having such exclusions are hereby disclosed.

Coding and Non-coding Targets

[0073] The methods disclosed herein often comprise assaying the expression level of a plurality of targets. The plurality of targets may comprise coding targets and/or non-coding targets of a protein-coding gene or a non protein-coding gene. A protein-coding gene structure may comprise an exon and an intron. The exon may further comprise a coding sequence (CDS) and an untranslated region (UTR). The protein-coding gene may be transcribed to produce a pre-mRNA and the pre-mRNA may be processed to produce a mature mRNA. The mature mRNA may be translated to produce a protein.

[0074] A non protein-coding gene structure may comprise an exon and intron. Usually, the exon region of a non protein-coding gene primarily contains a UTR. The non protein-coding gene may be transcribed to produce a pre-mRNA and the pre-mRNA may be processed to produce a non-coding RNA (ncRNA).

[0075] A coding target may comprise a coding sequence of an exon. A non-coding target may comprise a UTR sequence of an exon, intron sequence, intergenic sequence, promoter sequence, non-coding transcript, CDS antisense, intronic antisense, UTR antisense, or non-coding transcript antisense. A non-coding transcript may comprise a non-coding RNA (ncRNA).

[0076] In some instances, the plurality of targets may be differentially expressed. In some instances, a plurality of probe selection regions (PSRs) is differentially expressed.

[0077] In some instances, the plurality of targets comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, or at least about 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In other instances, the plurality of targets comprises at least about 12, at least about 15, at least about 17, at least about 20, at least about 22, at least about 25, at least about 27, at least about 30, at least about 32, at least about 35, at least about 37, or at least about 40 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. The plurality of targets may comprise about 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. The plurality of targets

may comprise about 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500 or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. The plurality of targets may comprise about 500, 525, 550, 575, 600, 625, 650, 675, 700, 725, 750, 775, 800, 810, 820, 830, 840, 850 or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises a coding target, non-coding target, or any combination thereof. In some instances, the coding target comprises an exonic sequence. In other instances, the non-coding target comprises a non-exonic or exonic sequence. Alternatively, a non-coding target comprises a UTR sequence, an intronic sequence, antisense, or a non-coding RNA transcript. In some instances, a non-coding target comprises sequences which partially overlap with a UTR sequence or an intronic sequence. A non-coding target also includes non-exonic and/or exonic transcripts. Exonic sequences may comprise regions on a protein-coding gene, such as an exon, UTR, or a portion thereof. Non-exonic sequences may comprise regions on a protein-coding, non protein-coding gene, or a portion thereof. For example, non-exonic sequences may comprise intronic regions, promoter regions, intergenic regions, a non-coding transcript, an exon anti-sense region, an intronic anti-sense region, UTR anti-sense region, non-coding transcript anti-sense region, or a portion thereof. In other instances, the plurality of targets comprises a non-coding RNA transcript.

[0078] In some instances, the plurality of targets is at least about 70% identical to a sequence selected from SEQ ID NOs 1-1440. Alternatively, the plurality of targets is at least about 80% identical to a sequence selected from SEQ ID NOS 1-1440. In some instances, the plurality of targets is at least about 85% identical to a sequence selected from SEQ ID NOS 1-1440. In some instances, the plurality of targets is at least about 90% identical to a sequence selected from SEQ ID NOS 1-1440. Alternatively, the plurality of targets is at least about 95% identical to a sequence selected from SEQ ID NOS 1-1440.

[0079] The plurality of targets may comprise one or more targets selected from a classifier disclosed herein. The classifier may be generated from one or more models or algorithms. The one or more models or algorithms may be Naïve Bayes (NB), recursive Partitioning (Rpart), random forest (RF), support vector machine (SVM), k-nearest neighbor (KNN), high dimensional discriminate analysis (HDDA), or a combination thereof. The classifier may have an AUC of equal to or greater than 0.60. The classifier may have an AUC of equal to or greater than 0.61. The classifier may have an AUC of equal to or greater than 0.62. The classifier may have an AUC of equal to or greater than 0.63. The classifier may have an AUC of equal to or greater than 0.64. The classifier may have an AUC of equal to or greater than 0.65. The classifier may have an AUC of equal to or greater than 0.66. The classifier may have an AUC of equal to or greater than 0.67. The classifier may have an AUC of equal to or greater than 0.68. The classifier may have an AUC of equal to or greater than 0.69. The classifier may have an AUC of equal to or greater than 0.70. The classifier may have an AUC of equal to or greater than 0.75. The classifier may have an AUC

of equal to or greater than 0.77. The classifier may have an AUC of equal to or greater than 0.78. The classifier may have an AUC of equal to or greater than 0.79. The classifier may have an AUC of equal to or greater than 0.80. The AUC may be clinically significant based on its 95% confidence interval (CI). The accuracy of the classifier may be at least about 70%. The accuracy of the classifier may be at least about 73%. The accuracy of the classifier may be at least about 75%. The accuracy of the classifier may be at least about 77%. The accuracy of the classifier may be at least about 80%. The accuracy of the classifier may be at least about 83%. The accuracy of the classifier may be at least about 84%. The accuracy of the classifier may be at least about 86%. The accuracy of the classifier may be at least about 88%. The accuracy of the classifier may be at least about 90%. The p-value of the classifier may be less than or equal to 0.05. The p-value of the classifier may be less than or equal to 0.04. The p-value of the classifier may be less than or equal to 0.03. The p-value of the classifier may be less than or equal to 0.02. The p-value of the classifier may be less than or equal to 0.01. The p-value of the classifier may be less than or equal to 0.008. The p-value of the classifier may be less than or equal to 0.006. The p-value of the classifier may be less than or equal to 0.004. The p-value of the classifier may be less than or equal to 0.002. The p-value of the classifier may be less than or equal to 0.001.

[0080] The plurality of targets may comprise one or more targets selected from a Random Forest (RF) classifier. The plurality of targets may comprise two or more targets selected from a Random Forest (RF) classifier. The plurality of targets may comprise three or more targets selected from a Random Forest (RF) classifier. The plurality of targets may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more targets selected from a Random Forest (RF) classifier. The RF classifier may be an RF2, and RF3, or an RF4 classifier. The RF classifier may be an RF15 classifier (e.g., a Random Forest classifier with 15 targets).

[0081] In some instances, the plurality of targets is at least about 70% identical to a sequence selected from a target selected from a RF classifier. Alternatively, the plurality of targets is at least about 80% identical to a sequence selected from a target selected from a RF classifier. In some instances, the plurality of targets is at least about 85% identical to a sequence selected from a target selected from a RF classifier. In some instances, the plurality of targets is at least about 90% identical to a sequence selected from a target selected from a RF classifier. Alternatively, the plurality of targets is at least about 95% identical to a sequence selected from a target selected from a RF classifier. The RF classifier may be an RF2 classifier. The RF classifier may be an RF15 classifier.

[0082] The RF15 classifier may comprise SEQ ID NO. 1, SEQ ID NO. 2, SEQ ID NO. 3, SEQ ID NO. 4, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 11, SEQ ID NO. 12, SEQ ID NO. 13, SEQ ID NO. 14, SEQ ID NO. 15, or a combination thereof. In some instances, the RF2 classifier is selected from Table 11, Table 12, Table 13, Table 14, Table 15, or

Table 20. A RF classifier of the present invention may comprise two or more targets comprising two or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

[0083] The plurality of targets may comprise one or more targets selected from an SVM classifier. The plurality of targets may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10 or more targets selected from an SVM classifier. The plurality of targets may comprise 12, 13, 14, 15, 17, 20, 22, 25, 27, 30 or more targets selected from an SVM classifier. The plurality of targets may comprise 32, 35, 37, 40, 43, 45, 47, 50, 53, 55, 57, 60 or more targets selected from an SVM classifier. The SVM classifier may be an SVM2 classifier.

[0084] In some instances, the plurality of targets is at least about 70% identical to a sequence selected from a target selected from a SVM classifier. Alternatively, the plurality of targets is at least about 80% identical to a sequence selected from a target selected from a SVM classifier. In some instances, the plurality of targets is at least about 85% identical to a sequence selected from a target selected from a SVM classifier. In some instances, the plurality of targets is at least about 90% identical to a sequence selected from a target selected from a SVM classifier. Alternatively, the plurality of targets is at least about 95% identical to a sequence selected from a target selected from a SVM classifier. The SVM classifier may be an SVM2 classifier. In some instances, the SVM2 classifier is selected from Table 11, Table 12, Table 13, Table 14, Table 15, or Table 20. A SVM classifier of the present invention may comprise two or more targets comprising two or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

[0085] The plurality of targets may comprise one or more targets selected from a KNN classifier. The plurality of targets may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10 or more targets selected from a KNN classifier. The plurality of targets may comprise 12, 13, 14, 15, 17, 20, 22, 25, 27, 30 or more targets selected from a KNN classifier. The plurality of targets may comprise 32, 35, 37, 40, 43, 45, 47, 50, 53, 55, 57, 60 or more targets selected from a KNN classifier. The plurality of targets may comprise 65, 70, 75, 80, 85, 90, 95, 100 or more targets selected from a KNN classifier. The plurality of targets may comprise 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 390 or more targets selected from a KNN classifier. The KNN classifier may be a KNN2 classifier.

[0086] In some instances, the plurality of targets is at least about 70% identical to a sequence selected from a target selected from a KNN classifier. Alternatively, the plurality of targets is at least about 80% identical to a sequence selected from a target selected from a KNN classifier. In some instances, the plurality of targets is at least about 85% identical to a sequence selected from a target selected from a KNN classifier. In some instances, the plurality of targets is at least about 90% identical to a sequence selected from a target selected from a KNN classifier. Alternatively, the plurality of targets is at least about 95% identical to a sequence selected from a target selected from a KNN classifier. The KNN classifier may be a KNN2 classifier. In some instances, the KNN2 classifier is selected from Table 11,

Table 12, Table 13, Table 14, Table 15, or Table 20. A KNN classifier of the present invention may comprise two or more targets comprising two or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

[0087] The plurality of targets may comprise one or more targets selected from a Naïve Bayes (NB) classifier. The plurality of targets may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10 or more targets selected from an NB classifier. The plurality of targets may comprise 12, 13, 14, 15, 17, 20, 22, 25, 27, 30 or more targets selected from an NB classifier. The plurality of targets may comprise 32, 35, 37, 40, 43, 45, 47, 50, 53, 55, 57, 60 or more targets selected from a NB classifier. The plurality of targets may comprise 65, 70, 75, 80, 85, 90, 95, 100 or more targets selected from a NB classifier. The plurality of targets may comprise 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 390 or more targets selected from a NB classifier. The NB classifier may be a NB2 classifier.

[0088] In some instances, the plurality of targets is at least about 70% identical to a sequence selected from a target selected from a NB classifier. Alternatively, the plurality of targets is at least about 80% identical to a sequence selected from a target selected from a NB classifier. In some instances, the plurality of targets is at least about 85% identical to a sequence selected from a target selected from a NB classifier. In some instances, the plurality of targets is at least about 90% identical to a sequence selected from a target selected from a NB classifier. Alternatively, the plurality of targets is at least about 95% identical to a sequence selected from a target selected from a NB classifier. The NB classifier may be a NB2 classifier. In some instances, the NB2 classifier is selected from Table 11, Table 12, Table 13, Table 15, or Table 20. An NB classifier of the present invention may comprise two or more targets comprising two or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

[0089] The plurality of targets may comprise one or more targets selected from a recursive Partitioning (Rpart) classifier. The plurality of targets may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10 or more targets selected from an Rpart classifier. The plurality of targets may comprise 12, 13, 14, 15, 17, 20, 22, 25, 27, 30 or more targets selected from an Rpart classifier. The plurality of targets may comprise 32, 35, 37, 40, 43, 45, 47, 50, 53, 55, 57, 60 or more targets selected from an Rpart classifier. The plurality of targets may comprise 65, 70, 75, 80, 85, 90, 95, 100 or more targets selected from an Rpart classifier. The plurality of targets may comprise 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 390 or more targets selected from an Rpart classifier. The Rpart classifier may be an Rpart2 classifier.

[0090] In some instances, the plurality of targets is at least about 70% identical to a sequence selected from a target selected from an Rpart classifier. Alternatively, the plurality of targets is at least about 80% identical to a sequence selected from a target selected from an Rpart classifier. In some instances, the plurality of targets is at least about 85% identical to a sequence selected from a target selected from an Rpart classifier. In some instances, the plurality of targets is at least about 90% identical to a sequence

selected from a target selected from an Rpart classifier. Alternatively, the plurality of targets is at least about 95% identical to a sequence selected from a target selected from an Rpart classifier. The Rpart classifier may be an Rpart2 classifier. In some instances, the Rpart2 classifier is selected from Table 11, Table 12, Table 13, Table 14, Table 15, or Table 20. An Rpart classifier of the present invention may comprise two or more targets comprising two or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

[0091] The plurality of targets may comprise one or more targets selected from a high dimensional discriminate analysis (HDDA) classifier. The plurality of targets may comprise two or more targets selected from a high dimensional discriminate analysis (HDDA) classifier. The plurality of targets may comprise three or more targets selected from a high dimensional discriminate analysis (HDDA) classifier. The plurality of targets may comprise 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more targets selected from a high dimensional discriminate analysis (HDDA) classifier.

[0092] In some instances, the plurality of targets is at least about 70% identical to a sequence selected from a target selected from a HDDA classifier. Alternatively, the plurality of targets is at least about 80% identical to a sequence selected from a target selected from a HDDA classifier. In some instances, the plurality of targets is at least about 85% identical to a sequence selected from a target selected from a HDDA classifier. In some instances, the plurality of targets is at least about 90% identical to a sequence selected from a target selected from a HDDA classifier. Alternatively, the plurality of targets is at least about 95% identical to a sequence selected from a target selected from a HDDA classifier.

Probes/Primers

[0093] The present invention provides for a probe set for diagnosing, monitoring and/or predicting a status or outcome of a cancer in a subject comprising a plurality of probes, wherein (i) the probes in the set are capable of detecting an expression level of at least one non-coding target; and (ii) the expression level determines the cancer status of the subject with at least about 40% specificity.

[0094] The probe set may comprise one or more polynucleotide probes. Individual polynucleotide probes comprise a nucleotide sequence derived from the nucleotide sequence of the target sequences or complementary sequences thereof. The nucleotide sequence of the polynucleotide probe is designed such that it corresponds to, or is complementary to the target sequences. The polynucleotide probe can specifically hybridize under either stringent or lowered stringency hybridization conditions to a region of the target sequences, to the complement thereof, or to a nucleic acid sequence (such as a cDNA) derived therefrom.

[0095] The selection of the polynucleotide probe sequences and determination of their uniqueness may be carried out *in silico* using techniques known in the art, for example, based on a BLASTN search of the

polynucleotide sequence in question against gene sequence databases, such as the Human Genome Sequence, UniGene, dbEST or the non-redundant database at NCBI. In one embodiment of the invention, the polynucleotide probe is complementary to a region of a target mRNA derived from a target sequence in the probe set. Computer programs can also be employed to select probe sequences that may not cross hybridize or may not hybridize non-specifically.

[0096] In some instances, microarray hybridization of RNA, extracted from bladder cancer tissue samples and amplified, may yield a dataset that is then summarized and normalized by the fRMA technique. After removal (or filtration) of cross-hybridizing PSRs, and PSRs containing less than 4 probes, the remaining PSRs can be used in further analysis. Following fRMA and filtration, the data can be decomposed into its principal components and an analysis of variance model is used to determine the extent to which a batch effect remains present in the first 10 principal components.

[0097] These remaining PSRs can then be subjected to filtration by a T-test between CR (clinical recurrence) and non-CR samples. Using a p-value cut-off of 0.01, the remaining features (e.g., PSRs) can be further refined. Feature selection can be performed by regularized logistic regression using the elastic-net penalty. The regularized regression may be bootstrapped over 1000 times using all training data; with each iteration of bootstrapping, features that have non-zero co-efficient following 3-fold cross validation can be tabulated. In some instances, features that were selected in at least 25% of the total runs were used for model building.

[0098] One skilled in the art understands that the nucleotide sequence of the polynucleotide probe need not be identical to its target sequence in order to specifically hybridize thereto. The polynucleotide probes of the present invention, therefore, comprise a nucleotide sequence that is at least about 65% identical to a region of the coding target or non-coding target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In another embodiment, the nucleotide sequence of the polynucleotide probe is at least about 70% identical a region of the coding target or non-coding target from Table 2B, Table 16 or SEQ ID NOs:1-1440. In another embodiment, the nucleotide sequence of the polynucleotide probe is at least about 75% identical a region of the coding target or non-coding target from Table 2B, Table 16 or SEQ ID NOs:1-1440. In another embodiment, the nucleotide sequence of the polynucleotide probe is at least about 80% identical a region of the coding target or non-coding target from Table 2B, Table 16 or SEQ ID NOs:1-1440. In another embodiment, the nucleotide sequence of the polynucleotide probe is at least about 85% identical a region of the coding target or non-coding target from Table 2B, Table 16 or SEQ ID NOs:1-1440. In another embodiment, the nucleotide sequence of the polynucleotide probe is at least about 90% identical a region of the coding target or non-coding target from Table 2B, Table 16 or SEQ ID NOs:1-1440. In a further embodiment, the nucleotide sequence of the polynucleotide probe is at least about 95%

identical to a region of the coding target or non-coding target from Table 2B, Table 16 or SEQ ID NOs:1-1440.

[0099] Methods of determining sequence identity are known in the art and can be determined, for example, by using the BLASTN program of the University of Wisconsin Computer Group (GCG) software or provided on the NCBI website. The nucleotide sequence of the polynucleotide probes of the present invention may exhibit variability by differing (*e.g.* by nucleotide substitution, including transition or transversion) at one, two, three, four or more nucleotides from the sequence of the coding target or non-coding target.

[0100] Other criteria known in the art may be employed in the design of the polynucleotide probes of the present invention. For example, the probes can be designed to have <50% G content. The probes can be designed to have between about 25% and about 70% G+C content. Strategies to optimize probe hybridization to the target nucleic acid sequence can also be included in the process of probe selection.

[0101] Hybridization under particular pH, salt, and temperature conditions can be optimized by taking into account melting temperatures and by using empirical rules that correlate with desired hybridization behaviors. Computer models may be used for predicting the intensity and concentration-dependence of probe hybridization.

[0102] The polynucleotide probes of the present invention may range in length from about 15 nucleotides to the full length of the coding target or non-coding target. In one embodiment of the invention, the polynucleotide probes are at least about 15 nucleotides in length. In another embodiment, the polynucleotide probes are at least about 20 nucleotides in length. In a further embodiment, the polynucleotide probes are at least about 25 nucleotides in length. In another embodiment, the polynucleotide probes are between about 15 nucleotides and about 500 nucleotides in length. In other embodiments, the polynucleotide probes are between about 15 nucleotides and about 450 nucleotides, about 15 nucleotides and about 400 nucleotides, about 15 nucleotides and about 350 nucleotides, about 15 nucleotides and about 300 nucleotides, about 15 nucleotides and about 250 nucleotides, about 15 nucleotides and about 200 nucleotides in length. In some embodiments, the probes are at least 15 nucleotides in length. In some embodiments, the probes are at least 15 nucleotides in length. In some embodiments, the probes are at least 20 nucleotides, at least 25 nucleotides, at least 50 nucleotides, at least 75 nucleotides, at least 100 nucleotides, at least 125 nucleotides, at least 150 nucleotides, at least 200 nucleotides, at least 225 nucleotides, at least 250 nucleotides, at least 275 nucleotides, at least 300 nucleotides, at least 325 nucleotides, at least 350 nucleotides, at least 375 nucleotides in length.

[0103] The polynucleotide probes of a probe set can comprise RNA, DNA, RNA or DNA mimetics, or combinations thereof, and can be single-stranded or double-stranded. Thus the polynucleotide probes can be composed of naturally-occurring nucleobases, sugars and covalent internucleoside (backbone) linkages

as well as polynucleotide probes having non-naturally-occurring portions which function similarly. Such modified or substituted polynucleotide probes may provide desirable properties such as, for example, enhanced affinity for a target gene and increased stability. The probe set may comprise a coding target and/or a non-coding target. Preferably, the probe set comprises a combination of a coding target and non-coding target.

[00104] In some embodiments, the probe set comprise a plurality of target sequences that hybridize to at least about 5 coding targets and/or non-coding targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. Alternatively, the probe set comprise a plurality of target sequences that hybridize to at least about 10 coding targets and/or non-coding targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to at least about 15 coding targets and/or non-coding targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to at least about 20 coding targets and/or non-coding targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to at least about 30 coding targets and/or non-coding targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. The probe set can comprise a plurality of targets that hybridize to at least about 40, 50, 60, 70, 80, 90, 100 or more coding targets and/or non-coding targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. The probe set can comprise a plurality of targets that hybridize to at least about 100, 125, 150, 175, 200, 225, 250, 275, 300 or more coding targets and/or non-coding targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. The probe set can comprise a plurality of targets that hybridize to at least about 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600 or more coding targets and/or non-coding targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. The probe set can comprise a plurality of targets that hybridize to at least about 600, 625, 650, 675, 700, 725, 750, 775, 800, 825, 850 or more coding targets and/or non-coding targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

[00105] In some embodiments, the probe set comprises a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 20% of the plurality of targets are targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprises a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 25% of the plurality of targets are targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 30% of the plurality of targets are targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 35% of the plurality of targets are targets selected from

Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 40% of the plurality of targets are targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 45% of the plurality of targets are targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 50% of the plurality of targets are targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 60% of the plurality of targets are targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 70% of the plurality of targets are targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

[00106] The system of the present invention further provides for primers and primer pairs capable of amplifying target sequences defined by the probe set, or fragments or subsequences or complements thereof. The nucleotide sequences of the probe set may be provided in computer-readable media for *in silico* applications and as a basis for the design of appropriate primers for amplification of one or more target sequences of the probe set.

[00107] Primers based on the nucleotide sequences of target sequences can be designed for use in amplification of the target sequences. For use in amplification reactions such as PCR, a pair of primers can be used. The exact composition of the primer sequences is not critical to the invention, but for most applications the primers may hybridize to specific sequences of the probe set under stringent conditions, particularly under conditions of high stringency, as known in the art. The pairs of primers are usually chosen so as to generate an amplification product of at least about 50 nucleotides, more usually at least about 100 nucleotides. Algorithms for the selection of primer sequences are generally known, and are available in commercial software packages. These primers may be used in standard quantitative or qualitative PCR-based assays to assess transcript expression levels of RNAs defined by the probe set. Alternatively, these primers may be used in combination with probes, such as molecular beacons in amplifications using real-time PCR.

[00108] In one embodiment, the primers or primer pairs, when used in an amplification reaction, specifically amplify at least a portion of a nucleic acid sequence of a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440 (or subgroups thereof as set forth herein), an RNA form thereof, or a complement to either thereof.

[00109] As is known in the art, a nucleoside is a base-sugar combination and a nucleotide is a nucleoside that further includes a phosphate group covalently linked to the sugar portion of the nucleoside. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear polymeric compound, with the normal linkage or backbone of RNA and DNA being a 3' to 5' phosphodiester linkage. Specific examples of polynucleotide probes or primers useful in this invention include oligonucleotides containing modified backbones or non-natural internucleoside linkages. As defined in this specification, oligonucleotides having modified backbones include both those that retain a phosphorus atom in the backbone and those that lack a phosphorus atom in the backbone. For the purposes of the present invention, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleotides.

[00110] Exemplary polynucleotide probes or primers having modified oligonucleotide backbones include, for example, those with one or more modified internucleotide linkages that are phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included.

[00111] Exemplary modified oligonucleotide backbones that do not include a phosphorus atom are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. Such backbones include morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulphone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulphamate backbones; methyleneimino and methylenehydrazino backbones; sulphonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH₂ component parts.

[00112] The present invention also contemplates oligonucleotide mimetics in which both the sugar and the internucleoside linkage of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. An example of such an oligonucleotide mimetic, which has been shown to have excellent hybridization properties, is a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an

amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza-nitrogen atoms of the amide portion of the backbone.

[00113] The present invention also contemplates polynucleotide probes or primers comprising "locked nucleic acids" (LNAs), which may be novel conformationally restricted oligonucleotide analogues containing a methylene bridge that connects the 2'-O of ribose with the 4'-C. LNA and LNA analogues may display very high duplex thermal stabilities with complementary DNA and RNA, stability towards 3'-exonuclease degradation, and good solubility properties. Synthesis of the LNA analogues of adenine, cytosine, guanine, 5-methylcytosine, thymine and uracil, their oligomerization, and nucleic acid recognition properties have been described. Studies of mismatched sequences show that LNA obey the Watson-Crick base pairing rules with generally improved selectivity compared to the corresponding unmodified reference strands.

[00114] LNAs may form duplexes with complementary DNA or RNA or with complementary LNA, with high thermal affinities. The universality of LNA-mediated hybridization has been emphasized by the formation of exceedingly stable LNA:LNA duplexes. LNA:LNA hybridization was shown to be the most thermally stable nucleic acid type duplex system, and the RNA-mimicking character of LNA was established at the duplex level. Introduction of three LNA monomers (T or A) resulted in significantly increased melting points toward DNA complements.

[00115] Synthesis of 2'-amino-LNA and 2'-methylamino-LNA has been described and thermal stability of their duplexes with complementary RNA and DNA strands reported. Preparation of phosphorothioate-LNA and 2'-thio-LNA have also been described.

[00116] Modified polynucleotide probes or primers may also contain one or more substituted sugar moieties. For example, oligonucleotides may comprise sugars with one of the following substituents at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C₁ to C₁₀ alkyl or C₂ to C₁₀ alkenyl and alkynyl. Examples of such groups are: O[(CH₂)_n O]_mCH₃, O(CH₂)_n OCH₃, O(CH₂)_n NH₂, O(CH₂)_n CH₃ ONH₂, and O(CH₂)_n ON[[(CH₂)_n CH₃]]₂, where n and m are from 1 to about 10.

Alternatively, the oligonucleotides may comprise one of the following substituents at the 2' position: C₁ to C₁₀ lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH₃, OCN, Cl, Br, CN, CF₃, OCF₃, SOCH₃, SO₂ CH₃, ONO₂, NO₂, N₃, NH₂, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. Specific examples include 2'-methoxyethoxy (2'-O--CH₂ CH₂ OCH₃, also known as 2'-O-(2-

methoxyethyl) or 2'-MOE), 2'-dimethylaminooxyethoxy ($\text{O}(\text{CH}_2)_2 \text{ON}(\text{CH}_3)_2$ group, also known as 2'-DMAOE), 2'-methoxy (2'-O-- CH_3), 2'-aminopropoxy (2'- $\text{OCH}_2 \text{CH}_2 \text{CH}_2 \text{NH}_2$) and 2'-fluoro (2'-F).

[00117] Similar modifications may also be made at other positions on the polynucleotide probes or primers, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Polynucleotide probes or primers may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar.

[00118] Polynucleotide probes or primers may also include modifications or substitutions to the nucleobase. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U).

[00119] Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808; The Concise Encyclopedia Of Polymer Science And Engineering, (1990) pp 858-859, Kroschwitz, J. I., ed. John Wiley & Sons; Englisch *et al.*, *Angewandte Chemie, Int. Ed.*, 30:613 (1991); and Sanghvi, Y. S., (1993) *Antisense Research and Applications*, pp 289-302, Crooke, S. T. and Lebleu, B., ed., CRC Press. Certain of these nucleobases are particularly useful for increasing the binding affinity of the polynucleotide probes of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C.

[00120] One skilled in the art recognizes that it is not necessary for all positions in a given polynucleotide probe or primer to be uniformly modified. The present invention, therefore, contemplates the incorporation of more than one of the aforementioned modifications into a single polynucleotide probe or even at a single nucleoside within the probe or primer.

[00121] One skilled in the art also appreciates that the nucleotide sequence of the entire length of the polynucleotide probe or primer does not need to be derived from the target sequence. Thus, for example, the polynucleotide probe may comprise nucleotide sequences at the 5' and/or 3' termini that are not derived from the target sequences. Nucleotide sequences which are not derived from the nucleotide sequence of the target sequence may provide additional functionality to the polynucleotide probe. For

example, they may provide a restriction enzyme recognition sequence or a "tag" that facilitates detection, isolation, purification or immobilization onto a solid support. Alternatively, the additional nucleotides may provide a self-complementary sequence that allows the primer/probe to adopt a hairpin configuration. Such configurations are necessary for certain probes, for example, molecular beacon and Scorpion probes, which can be used in solution hybridization techniques.

[00122] The polynucleotide probes or primers can incorporate moieties useful in detection, isolation, purification, or immobilization, if desired. Such moieties are well-known in the art (see, for example, Ausubel *et al.*, (1997 & updates) *Current Protocols in Molecular Biology*, Wiley & Sons, New York) and are chosen such that the ability of the probe to hybridize with its target sequence is not affected.

[00123] Examples of suitable moieties are detectable labels, such as radioisotopes, fluorophores, chemiluminophores, enzymes, colloidal particles, and fluorescent microparticles, as well as antigens, antibodies, haptens, avidin/streptavidin, biotin, haptens, enzyme cofactors / substrates, enzymes, and the like.

[00124] A label can optionally be attached to or incorporated into a probe or primer polynucleotide to allow detection and/or quantitation of a target polynucleotide representing the target sequence of interest. The target polynucleotide may be the expressed target sequence RNA itself, a cDNA copy thereof, or an amplification product derived therefrom, and may be the positive or negative strand, so long as it can be specifically detected in the assay being used. Similarly, an antibody may be labeled.

[00125] In certain multiplex formats, labels used for detecting different targets may be distinguishable. The label can be attached directly (e.g., via covalent linkage) or indirectly, e.g., via a bridging molecule or series of molecules (e.g., a molecule or complex that can bind to an assay component, or via members of a binding pair that can be incorporated into assay components, e.g. biotin-avidin or streptavidin). Many labels are commercially available in activated forms which can readily be used for such conjugation (for example through amine acylation), or labels may be attached through known or determinable conjugation schemes, many of which are known in the art.

[00126] Labels useful in the invention described herein include any substance which can be detected when bound to or incorporated into the biomolecule of interest. Any effective detection method can be used, including optical, spectroscopic, electrical, piezoelectrical, magnetic, Raman scattering, surface plasmon resonance, colorimetric, calorimetric, etc. A label is typically selected from a chromophore, a lumiphore, a fluorophore, one member of a quenching system, a chromogen, a hapten, an antigen, a magnetic particle, a material exhibiting nonlinear optics, a semiconductor nanocrystal, a metal nanoparticle, an enzyme, an antibody or binding portion or equivalent thereof, an aptamer, and one member of a binding pair, and combinations thereof. Quenching schemes may be used, wherein a quencher and a fluorophore as members of a quenching pair may be used on a probe, such that a change in optical parameters occurs

upon binding to the target introduce or quench the signal from the fluorophore. One example of such a system is a molecular beacon. Suitable quencher/fluorophore systems are known in the art. The label may be bound through a variety of intermediate linkages. For example, a polynucleotide may comprise a biotin-binding species, and an optically detectable label may be conjugated to biotin and then bound to the labeled polynucleotide. Similarly, a polynucleotide sensor may comprise an immunological species such as an antibody or fragment, and a secondary antibody containing an optically detectable label may be added.

[00127] Chromophores useful in the methods described herein include any substance which can absorb energy and emit light. For multiplexed assays, a plurality of different signaling chromophores can be used with detectably different emission spectra. The chromophore can be a lumophore or a fluorophore. Typical fluorophores include fluorescent dyes, semiconductor nanocrystals, lanthanide chelates, polynucleotide-specific dyes and green fluorescent protein.

[00128] Coding schemes may optionally be used, comprising encoded particles and/or encoded tags associated with different polynucleotides of the invention. A variety of different coding schemes are known in the art, including fluorophores, including SCNCs, deposited metals, and RF tags.

[00129] Polynucleotides from the described target sequences may be employed as probes for detecting target sequences expression, for ligation amplification schemes, or may be used as primers for amplification schemes of all or a portion of a target sequences. When amplified, either strand produced by amplification may be provided in purified and/or isolated form.

[00130] In one embodiment, polynucleotides of the invention include (a) a nucleic acid depicted in Table 1; (b) an RNA form of any one of the nucleic acids depicted in Table 1; (c) a peptide nucleic acid form of any of the nucleic acids depicted in Table 1; (d) a nucleic acid comprising at least 20 consecutive bases of any of (a-c); (e) a nucleic acid comprising at least 25 bases having at least 90% sequenced identity to any of (a-c); and (f) a complement to any of (a-e).

[00131] Complements may take any polymeric form capable of base pairing to the species recited in (a)-(e), including nucleic acid such as RNA or DNA, or may be a neutral polymer such as a peptide nucleic acid. Polynucleotides of the invention can be selected from the subsets of the recited nucleic acids described herein, as well as their complements.

[00132] In some embodiments, polynucleotides of the invention comprise at least 20 consecutive bases of the nucleic acid sequence of a target selected from Table 2B, Table 16 or SEQ ID NOs: 1-1440 or a complement thereto. The polynucleotides may comprise at least 21, 22, 23, 24, 25, 27, 30, 32, 35 or more consecutive bases of the nucleic acids sequence of a target selected from Table 1, as applicable.

[00133] The polynucleotides may be provided in a variety of formats, including as solids, in solution, or in an array. The polynucleotides may optionally comprise one or more labels, which may be chemically and/or enzymatically incorporated into the polynucleotide.

[00134] In one embodiment, solutions comprising polynucleotide and a solvent are also provided. In some embodiments, the solvent may be water or may be predominantly aqueous. In some embodiments, the solution may comprise at least two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, seventeen, twenty or more different polynucleotides, including primers and primer pairs, of the invention. Additional substances may be included in the solution, alone or in combination, including one or more labels, additional solvents, buffers, biomolecules, polynucleotides, and one or more enzymes useful for performing methods described herein, including polymerases and ligases. The solution may further comprise a primer or primer pair capable of amplifying a polynucleotide of the invention present in the solution.

[00135] In some embodiments, one or more polynucleotides provided herein can be provided on a substrate. The substrate can comprise a wide range of material, either biological, nonbiological, organic, inorganic, or a combination of any of these. For example, the substrate may be a polymerized Langmuir Blodgett film, functionalized glass, Si, Ge, GaAs, GaP, SiO₂, SiN₄, modified silicon, or any one of a wide variety of gels or polymers such as (poly)tetrafluoroethylene, (poly)vinylidenedifluoride, polystyrene, cross-linked polystyrene, polyacrylic, polylactic acid, polyglycolic acid, poly(lactide coglycolide), polyanhydrides, poly(methyl methacrylate), poly(ethylene-co-vinyl acetate), polysiloxanes, polymeric silica, latexes, dextran polymers, epoxies, polycarbonates, or combinations thereof. Conducting polymers and photoconductive materials can be used.

[00136] Substrates can be planar crystalline substrates such as silica based substrates (e.g. glass, quartz, or the like), or crystalline substrates used in, e.g., the semiconductor and microprocessor industries, such as silicon, gallium arsenide, indium doped GaN and the like, and include semiconductor nanocrystals.

[00137] The substrate can take the form of an array, a photodiode, an optoelectronic sensor such as an optoelectronic semiconductor chip or optoelectronic thin-film semiconductor, or a biochip. The location(s) of probe(s) on the substrate can be addressable; this can be done in highly dense formats, and the location(s) can be microaddressable or nanoaddressable.

[00138] Silica aerogels can also be used as substrates, and can be prepared by methods known in the art. Aerogel substrates may be used as free standing substrates or as a surface coating for another substrate material.

[00139] The substrate can take any form and typically is a plate, slide, bead, pellet, disk, particle, microparticle, nanoparticle, strand, precipitate, optionally porous gel, sheets, tube, sphere, container, capillary, pad, slice, film, chip, multiwell plate or dish, optical fiber, etc. The substrate can be any form

that is rigid or semi-rigid. The substrate may contain raised or depressed regions on which an assay component is located. The surface of the substrate can be etched using known techniques to provide for desired surface features, for example trenches, v-grooves, mesa structures, or the like.

[00140] Surfaces on the substrate can be composed of the same material as the substrate or can be made from a different material, and can be coupled to the substrate by chemical or physical means. Such coupled surfaces may be composed of any of a wide variety of materials, for example, polymers, plastics, resins, polysaccharides, silica or silica-based materials, carbon, metals, inorganic glasses, membranes, or any of the above-listed substrate materials. The surface can be optically transparent and can have surface Si-OH functionalities, such as those found on silica surfaces.

[00141] The substrate and/or its optional surface can be chosen to provide appropriate characteristics for the synthetic and/or detection methods used. The substrate and/or surface can be transparent to allow the exposure of the substrate by light applied from multiple directions. The substrate and/or surface may be provided with reflective "mirror" structures to increase the recovery of light.

[00142] The substrate and/or its surface is generally resistant to, or is treated to resist, the conditions to which it is to be exposed in use, and can be optionally treated to remove any resistant material after exposure to such conditions.

[00143] The substrate or a region thereof may be encoded so that the identity of the sensor located in the substrate or region being queried may be determined. Any suitable coding scheme can be used, for example optical codes, RFID tags, magnetic codes, physical codes, fluorescent codes, and combinations of codes.

Preparation of Probes and Primers

[00144] The polynucleotide probes or primers of the present invention can be prepared by conventional techniques well-known to those skilled in the art. For example, the polynucleotide probes can be prepared using solid-phase synthesis using commercially available equipment. As is well-known in the art, modified oligonucleotides can also be readily prepared by similar methods. The polynucleotide probes can also be synthesized directly on a solid support according to methods standard in the art. This method of synthesizing polynucleotides is particularly useful when the polynucleotide probes are part of a nucleic acid array.

[00145] Polynucleotide probes or primers can be fabricated on or attached to the substrate by any suitable method, for example the methods described in U.S. Pat. No. 5,143,854, PCT Publ. No. WO 92/10092, U.S. Patent Application Ser. No. 07/624,120, filed Dec. 6, 1990 (now abandoned), Fodor et al., Science, 251: 767-777 (1991), and PCT Publ. No. WO 90/15070). Techniques for the synthesis of these arrays using mechanical synthesis strategies are described in, e.g., PCT Publication No. WO 93/09668 and U.S.

Pat. No. 5,384,261. Still further techniques include bead based techniques such as those described in PCT Appl. No. PCT/US93/04145 and pin based methods such as those described in U.S. Pat. No. 5,288,514. Additional flow channel or spotting methods applicable to attachment of sensor polynucleotides to a substrate are described in U. S. Patent Application Ser. No. 07/980,523, filed Nov. 20, 1992, and U.S. Pat. No. 5,384,261.

[00146] Alternatively, the polynucleotide probes of the present invention can be prepared by enzymatic digestion of the naturally occurring target gene, or mRNA or cDNA derived therefrom, by methods known in the art.

Diagnostic Samples

[00147] Diagnostic samples for use with the systems and in the methods of the present invention comprise nucleic acids suitable for providing RNAs expression information. In principle, the biological sample from which the expressed RNA is obtained and analyzed for target sequence expression can be any material suspected of comprising cancer tissue or cells. The diagnostic sample can be a biological sample used directly in a method of the invention. Alternatively, the diagnostic sample can be a sample prepared from a biological sample.

[00148] In one embodiment, the sample or portion of the sample comprising or suspected of comprising cancer tissue or cells can be any source of biological material, including cells, tissue or fluid, including bodily fluids. Non-limiting examples of the source of the sample include an aspirate, a needle biopsy, a cytology pellet, a bulk tissue preparation or a section thereof obtained for example by surgery or autopsy, lymph fluid, blood, plasma, serum, tumors, and organs. In some embodiments, the sample is from urine. Alternatively, the sample is from blood, plasma or serum. In some embodiments, the sample is from saliva.

[00149] The samples may be archival samples, having a known and documented medical outcome, or may be samples from current patients whose ultimate medical outcome is not yet known.

[00150] In some embodiments, the sample may be dissected prior to molecular analysis. The sample may be prepared via macrodissection of a bulk tumor specimen or portion thereof, or may be treated via microdissection, for example via Laser Capture Microdissection (LCM).

[00151] The sample may initially be provided in a variety of states, as fresh tissue, fresh frozen tissue, fine needle aspirates, and may be fixed or unfixed. Frequently, medical laboratories routinely prepare medical samples in a fixed state, which facilitates tissue storage. A variety of fixatives can be used to fix tissue to stabilize the morphology of cells, and may be used alone or in combination with other agents. Exemplary fixatives include crosslinking agents, alcohols, acetone, Bouin's solution, Zenker solution, Hely solution, osmic acid solution and Carnoy solution.

[00152] Crosslinking fixatives can comprise any agent suitable for forming two or more covalent bonds, for example an aldehyde. Sources of aldehydes typically used for fixation include formaldehyde, paraformaldehyde, glutaraldehyde or formalin. Preferably, the crosslinking agent comprises formaldehyde, which may be included in its native form or in the form of paraformaldehyde or formalin. One of skill in the art would appreciate that for samples in which crosslinking fixatives have been used special preparatory steps may be necessary including for example heating steps and proteinase-k digestion; see methods.

[00153] One or more alcohols may be used to fix tissue, alone or in combination with other fixatives. Exemplary alcohols used for fixation include methanol, ethanol and isopropanol.

[00154] Formalin fixation is frequently used in medical laboratories. Formalin comprises both an alcohol, typically methanol, and formaldehyde, both of which can act to fix a biological sample.

[00155] Whether fixed or unfixed, the biological sample may optionally be embedded in an embedding medium. Exemplary embedding media used in histology including paraffin, Tissue-Tek® V.I.P.TM, Paramat, Paramat Extra, Paraplast, Paraplast X-tra, Paraplast Plus, Peel Away Paraffin Embedding Wax, Polyester Wax, Carbowax Polyethylene Glycol, PolyfinTM, Tissue Freezing Medium TFMFM, Cryo-GefTM, and OCT Compound (Electron Microscopy Sciences, Hatfield, PA). Prior to molecular analysis, the embedding material may be removed via any suitable techniques, as known in the art. For example, where the sample is embedded in wax, the embedding material may be removed by extraction with organic solvent(s), for example xylenes. Kits are commercially available for removing embedding media from tissues. Samples or sections thereof may be subjected to further processing steps as needed, for example serial hydration or dehydration steps.

[00156] In some embodiments, the sample is a fixed, wax-embedded biological sample. Frequently, samples from medical laboratories are provided as fixed, wax-embedded samples, most commonly as formalin-fixed, paraffin embedded (FFPE) tissues.

[00157] Whatever the source of the biological sample, the target polynucleotide that is ultimately assayed can be prepared synthetically (in the case of control sequences), but typically is purified from the biological source and subjected to one or more preparative steps. The RNA may be purified to remove or diminish one or more undesired components from the biological sample or to concentrate it. Conversely, where the RNA is too concentrated for the particular assay, it may be diluted.

RNA Extraction

[00158] RNA can be extracted and purified from biological samples using any suitable technique. A number of techniques are known in the art, and several are commercially available (e.g., FormaPure nucleic acid extraction kit, Agencourt Biosciences, Beverly MA, High Pure FFPE RNA Micro Kit, Roche

Applied Science, Indianapolis, IN). RNA can be extracted from frozen tissue sections using TRIzol (Invitrogen, Carlsbad, CA) and purified using RNeasy Protect kit (Qiagen, Valencia, CA). RNA can be further purified using DNase I treatment (Ambion, Austin, TX) to eliminate any contaminating DNA. RNA concentrations can be made using a Nanodrop ND-1000 spectrophotometer (Nanodrop Technologies, Rockland, DE). RNA can be further purified to eliminate contaminants that interfere with cDNA synthesis by cold sodium acetate precipitation. RNA integrity can be evaluated by running electropherograms, and RNA integrity number (RIN, a correlative measure that indicates intactness of mRNA) can be determined using the RNA 6000 PicoAssay for the Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA).

Kits

[00159] Kits for performing the desired method(s) are also provided, and comprise a container or housing for holding the components of the kit, one or more vessels containing one or more nucleic acid(s), and optionally one or more vessels containing one or more reagents. The reagents include those described in the composition of matter section above, and those reagents useful for performing the methods described, including amplification reagents, and may include one or more probes, primers or primer pairs, enzymes (including polymerases and ligases), intercalating dyes, labeled probes, and labels that can be incorporated into amplification products.

[00160] In some embodiments, the kit comprises primers or primer pairs specific for those subsets and combinations of target sequences described herein. The primers or pairs of primers suitable for selectively amplifying the target sequences. The kit may comprise at least two, three, four or five primers or pairs of primers suitable for selectively amplifying one or more targets. The kit may comprise at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100 or more primers or pairs of primers suitable for selectively amplifying one or more targets. The kit may comprise at least 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500 or more primers or pairs of primers suitable for selectively amplifying one or more targets. The kit may comprise at least 500, 550, 600, 650, 700, 750, 800, 850 or more primers or pairs of primers suitable for selectively amplifying one or more targets.

[00161] In some embodiments, the primers or primer pairs of the kit, when used in an amplification reaction, specifically amplify a non-coding target, coding target, exonic, or non-exonic target described herein, at least a portion of a nucleic acid sequence depicted in one of SEQ ID NOs: 1-1440, a nucleic acid sequence corresponding to a target selected from Table 1, an RNA form thereof, or a complement to either thereof. The kit may include a plurality of such primers or primer pairs which can specifically amplify a corresponding plurality of different amplify a non-coding target, coding target, exonic, or non-exonic transcript described herein, nucleic acids depicted in one of SEQ ID NOs: 1-1440, a nucleic acid

sequence corresponding to a target selected from Table 1, RNA forms thereof, or complements thereto. At least two, three, four or five primers or pairs of primers suitable for selectively amplifying the one or more targets can be provided in kit form. In some embodiments, the kit comprises from five to fifty primers or pairs of primers suitable for amplifying the one or more targets.

[00162] The reagents may independently be in liquid or solid form. The reagents may be provided in mixtures. Control samples and/or nucleic acids may optionally be provided in the kit. Control samples may include tissue and/or nucleic acids obtained from or representative of tumor samples from patients showing no evidence of disease, as well as tissue and/or nucleic acids obtained from or representative of tumor samples from patients that develop systemic cancer.

[00163] The nucleic acids may be provided in an array format, and thus an array or microarray may be included in the kit. The kit optionally may be certified by a government agency for use in prognosing the disease outcome of cancer patients and/or for designating a treatment modality.

[00164] Instructions for using the kit to perform one or more methods of the invention can be provided with the container, and can be provided in any fixed medium. The instructions may be located inside or outside the container or housing, and/or may be printed on the interior or exterior of any surface thereof. A kit may be in multiplex form for concurrently detecting and/or quantitating one or more different target polynucleotides representing the expressed target sequences.

Devices

[00165] Devices useful for performing methods of the invention are also provided. The devices can comprise means for characterizing the expression level of a target sequence of the invention, for example components for performing one or more methods of nucleic acid extraction, amplification, and/or detection. Such components may include one or more of an amplification chamber (for example a thermal cycler), a plate reader, a spectrophotometer, capillary electrophoresis apparatus, a chip reader, and/or robotic sample handling components. These components ultimately can obtain data that reflects the expression level of the target sequences used in the assay being employed.

[00166] The devices may include an excitation and/or a detection means. Any instrument that provides a wavelength that can excite a species of interest and is shorter than the emission wavelength(s) to be detected can be used for excitation. Commercially available devices can provide suitable excitation wavelengths as well as suitable detection component.

[00167] Exemplary excitation sources include a broadband UV light source such as a deuterium lamp with an appropriate filter, the output of a white light source such as a xenon lamp or a deuterium lamp after passing through a monochromator to extract out the desired wavelength(s), a continuous wave (cw) gas laser, a solid state diode laser, or any of the pulsed lasers. Emitted light can be detected through any

suitable device or technique; many suitable approaches are known in the art. For example, a fluorimeter or spectrophotometer may be used to detect whether the test sample emits light of a wavelength characteristic of a label used in an assay.

[00168] The devices typically comprise a means for identifying a given sample, and of linking the results obtained to that sample. Such means can include manual labels, barcodes, and other indicators which can be linked to a sample vessel, and/or may optionally be included in the sample itself, for example where an encoded particle is added to the sample. The results may be linked to the sample, for example in a computer memory that contains a sample designation and a record of expression levels obtained from the sample. Linkage of the results to the sample can also include a linkage to a particular sample receptacle in the device, which is also linked to the sample identity.

[00169] In some instances, the devices also comprise a means for correlating the expression levels of the target sequences being studied with a prognosis of disease outcome. In some instances, such means comprises one or more of a variety of correlative techniques, including lookup tables, algorithms, multivariate models, and linear or nonlinear combinations of expression models or algorithms. The expression levels may be converted to one or more likelihood scores, reflecting likelihood that the patient providing the sample may exhibit a particular disease outcome. The models and/or algorithms can be provided in machine readable format and can optionally further designate a treatment modality for a patient or class of patients.

[00170] The device also comprises output means for outputting the disease status, prognosis and/or a treatment modality. Such output means can take any form which transmits the results to a patient and/or a healthcare provider, and may include a monitor, a printed format, or both. The device may use a computer system for performing one or more of the steps provided.

[00171] In some embodiments, the method, systems, and kits disclosed herein further comprise the transmission of data/information. For example, data/information derived from the detection and/or quantification of the target may be transmitted to another device and/or instrument. In some instances, the information obtained from an algorithm is transmitted to another device and/or instrument. Transmission of the data/information may comprise the transfer of data/information from a first source to a second source. The first and second sources may be in the same approximate location (e.g., within the same room, building, block, campus). Alternatively, first and second sources may be in multiple locations (e.g., multiple cities, states, countries, continents, etc).

[00172] In some instances, transmission of the data/information comprises digital transmission or analog transmission. Digital transmission may comprise the physical transfer of data (a digital bit stream) over a point-to-point or point-to-multipoint communication channel. Examples of such channels are copper wires, optical fibers, wireless communication channels, and storage media. In some embodiments, the

data is represented as an electromagnetic signal, such as an electrical voltage, radiowave, microwave, or infrared signal.

[00173] Analog transmission may comprise the transfer of a continuously varying analog signal. The messages can either be represented by a sequence of pulses by means of a line code (baseband transmission), or by a limited set of continuously varying wave forms (passband transmission), using a digital modulation method. The passband modulation and corresponding demodulation (also known as detection) can be carried out by modem equipment. According to the most common definition of digital signal, both baseband and passband signals representing bit-streams are considered as digital transmission, while an alternative definition only considers the baseband signal as digital, and passband transmission of digital data as a form of digital-to-analog conversion.

Amplification and Hybridization

[00174] Following sample collection and nucleic acid extraction, the nucleic acid portion of the sample comprising RNA that is or can be used to prepare the target polynucleotide(s) of interest can be subjected to one or more preparative reactions. These preparative reactions can include *in vitro* transcription (IVT), labeling, fragmentation, amplification and other reactions. mRNA can first be treated with reverse transcriptase and a primer to create cDNA prior to detection, quantitation and/or amplification; this can be done *in vitro* with purified mRNA or *in situ*, e.g., in cells or tissues affixed to a slide.

[00175] By "amplification" is meant any process of producing at least one copy of a nucleic acid, in this case an expressed RNA, and in many cases produces multiple copies. An amplification product can be RNA or DNA, and may include a complementary strand to the expressed target sequence. DNA amplification products can be produced initially through reverse translation and then optionally from further amplification reactions. The amplification product may include all or a portion of a target sequence, and may optionally be labeled. A variety of amplification methods are suitable for use, including polymerase-based methods and ligation-based methods. Exemplary amplification techniques include the polymerase chain reaction method (PCR), the ligase chain reaction (LCR), ribozyme-based methods, self sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), the use of Q Beta replicase, reverse transcription, nick translation, and the like.

[00176] Asymmetric amplification reactions may be used to preferentially amplify one strand representing the target sequence that is used for detection as the target polynucleotide. In some cases, the presence and/or amount of the amplification product itself may be used to determine the expression level of a given target sequence. In other instances, the amplification product may be used to hybridize to an array or other substrate comprising sensor polynucleotides which are used to detect and/or quantitate target sequence expression.

[00177] The first cycle of amplification in polymerase-based methods typically forms a primer extension product complementary to the template strand. If the template is single-stranded RNA, a polymerase with reverse transcriptase activity is used in the first amplification to reverse transcribe the RNA to DNA, and additional amplification cycles can be performed to copy the primer extension products. The primers for a PCR must, of course, be designed to hybridize to regions in their corresponding template that can produce an amplifiable segment; thus, each primer must hybridize so that its 3' nucleotide is paired to a nucleotide in its complementary template strand that is located 3' from the 3' nucleotide of the primer used to replicate that complementary template strand in the PCR.

[00178] The target polynucleotide can be amplified by contacting one or more strands of the target polynucleotide with a primer and a polymerase having suitable activity to extend the primer and copy the target polynucleotide to produce a full-length complementary polynucleotide or a smaller portion thereof. Any enzyme having a polymerase activity that can copy the target polynucleotide can be used, including DNA polymerases, RNA polymerases, reverse transcriptases, enzymes having more than one type of polymerase or enzyme activity. The enzyme can be thermolabile or thermostable. Mixtures of enzymes can also be used. Exemplary enzymes include: DNA polymerases such as DNA Polymerase I ("Pol I"), the Klenow fragment of Pol I, T4, T7, Sequenase® T7, Sequenase® Version 2.0 T7, *Tub*, *Taq*, *Tth*, *Pfic*, *Pfu*, *Tsp*, *Tfl*, *Tli* and *Pyrococcus* sp. GB-D DNA polymerases; RNA polymerases such as *E. coli*, SP6, T3 and T7 RNA polymerases; and reverse transcriptases such as AMV, M-MuLV, MMLV, RNase H MMLV (SuperScript®), SuperScript® II, ThermoScript®, HIV-1, and RAV2 reverse transcriptases. All of these enzymes are commercially available. Exemplary polymerases with multiple specificities include RAV2 and *Tli* (exo-) polymerases. Exemplary thermostable polymerases include *Tub*, *Taq*, *Tth*, *Pfic*, *Pfu*, *Tsp*, *Tfl*, *Tli* and *Pyrococcus* sp. GB-D DNA polymerases.

[00179] Suitable reaction conditions are chosen to permit amplification of the target polynucleotide, including pH, buffer, ionic strength, presence and concentration of one or more salts, presence and concentration of reactants and cofactors such as nucleotides and magnesium and/or other metal ions (e.g., manganese), optional cosolvents, temperature, thermal cycling profile for amplification schemes comprising a polymerase chain reaction, and may depend in part on the polymerase being used as well as the nature of the sample. Cosolvents include formamide (typically at from about 2 to about 10 %), glycerol (typically at from about 5 to about 10 %), and DMSO (typically at from about 0.9 to about 10 %). Techniques may be used in the amplification scheme in order to minimize the production of false positives or artifacts produced during amplification. These include "touchdown" PCR, hot-start techniques, use of nested primers, or designing PCR primers so that they form stem-loop structures in the event of primer-dimer formation and thus are not amplified. Techniques to accelerate PCR can be used, for example centrifugal PCR, which allows for greater convection within the sample, and comprising

infrared heating steps for rapid heating and cooling of the sample. One or more cycles of amplification can be performed. An excess of one primer can be used to produce an excess of one primer extension product during PCR; preferably, the primer extension product produced in excess is the amplification product to be detected. A plurality of different primers may be used to amplify different target polynucleotides or different regions of a particular target polynucleotide within the sample.

[00180] An amplification reaction can be performed under conditions which allow an optionally labeled sensor polynucleotide to hybridize to the amplification product during at least part of an amplification cycle. When the assay is performed in this manner, real-time detection of this hybridization event can take place by monitoring for light emission or fluorescence during amplification, as known in the art.

[00181] Where the amplification product is to be used for hybridization to an array or microarray, a number of suitable commercially available amplification products are available. These include amplification kits available from NuGEN, Inc. (San Carlos, CA), including the WT-Ovation™ System, WT-Ovation™ System v2, WT-Ovation™ Pico System, WT-Ovation™ FFPE Exon Module, WT-Ovation™ FFPE Exon Module RiboAmp and RiboAmp^{Plus} RNA Amplification Kits (MDS Analytical Technologies (formerly Arcturus) (Mountain View, CA), Genisphere, Inc. (Hatfield, PA), including the RampUp Plus™ and SenseAmp™ RNA Amplification kits, alone or in combination. Amplified nucleic acids may be subjected to one or more purification reactions after amplification and labeling, for example using magnetic beads (e.g., RNAClean magnetic beads, Agencourt Biosciences).

[00182] Multiple RNA biomarkers can be analyzed using real-time quantitative multiplex RT-PCR platforms and other multiplexing technologies such as GenomeLab GeXP Genetic Analysis System (Beckman Coulter, Foster City, CA), SmartCycler® 9600 or GeneXpert(R) Systems (Cepheid, Sunnyvale, CA), ABI 7900 HT Fast Real Time PCR system (Applied Biosystems, Foster City, CA), LightCycler® 480 System (Roche Molecular Systems, Pleasanton, CA), xMAP 100 System (Luminex, Austin, TX) Solexa Genome Analysis System (Illumina, Hayward, CA), OpenArray Real Time qPCR (BioTrove, Woburn, MA) and BeadXpress System (Illumina, Hayward, CA).

Detection and/or Quantification of Target Sequences

[00183] Any method of detecting and/or quantitating the expression of the encoded target sequences can in principle be used in the invention. The expressed target sequences can be directly detected and/or quantitated, or may be copied and/or amplified to allow detection of amplified copies of the expressed target sequences or its complement.

[00184] Methods for detecting and/or quantifying a target can include Northern blotting, sequencing, array or microarray hybridization, by enzymatic cleavage of specific structures (e.g., an Invader® assay, Third Wave Technologies, e.g. as described in U.S. Pat. Nos. 5,846,717, 6,090,543; 6,001,567;

5,985,557; and 5,994,069) and amplification methods, e.g. RT-PCR, including in a TaqMan® assay (PE Biosystems, Foster City, Calif., e.g. as described in U.S. Pat. Nos. 5,962,233 and 5,538,848), and may be quantitative or semi-quantitative, and may vary depending on the origin, amount and condition of the available biological sample. Combinations of these methods may also be used. For example, nucleic acids may be amplified, labeled and subjected to microarray analysis.

[00185] In some instances, target sequences may be detected by sequencing. Sequencing methods may comprise whole genome sequencing or exome sequencing. Sequencing methods such as Maxam-Gilbert, chain-termination, or high-throughput systems may also be used. Additional, suitable sequencing techniques include classic dideoxy sequencing reactions (Sanger method) using labeled terminators or primers and gel separation in slab or capillary, sequencing by synthesis using reversibly terminated labeled nucleotides, pyrosequencing, 454 sequencing, allele specific hybridization to a library of labeled oligonucleotide probes, sequencing by synthesis using allele specific hybridization to a library of labeled clones that is followed by ligation, real time monitoring of the incorporation of labeled nucleotides during a polymerization step, and SOLiD sequencing.

[00186] Additional methods for detecting and/or quantifying a target include single-molecule sequencing (e.g., Helicos, PacBio), sequencing by synthesis (e.g., Illumina, Ion Torrent), sequencing by ligation (e.g., ABI SOLiD), sequencing by hybridization (e.g., Complete Genomics), in situ hybridization, bead-array technologies (e.g., Luminex xMAP, Illumina BeadChips), branched DNA technology (e.g., Panomics, Genisphere). Sequencing methods may use fluorescent (e.g., Illumina) or electronic (e.g., Ion Torrent, Oxford Nanopore) methods of detecting nucleotides.

Reverse Transcription for QRT-PCR Analysis

[00187] Reverse transcription can be performed by any method known in the art. For example, reverse transcription may be performed using the Omniscript kit (Qiagen, Valencia, CA), Superscript III kit (Invitrogen, Carlsbad, CA), for RT-PCR. Target-specific priming can be performed in order to increase the sensitivity of detection of target sequences and generate target-specific cDNA.

TaqMan® Gene Expression Analysis

[00188] TaqMan® RT-PCR can be performed using Applied Biosystems Prism (ABI) 7900 HT instruments in a 5 l.11 volume with target sequence-specific cDNA equivalent to 1 ng total RNA.

[00189] Primers and probes concentrations for TaqMan analysis are added to amplify fluorescent amplicons using PCR cycling conditions such as 95°C for 10 minutes for one cycle, 95°C for 20 seconds, and 60°C for 45 seconds for 40 cycles. A reference sample can be assayed to ensure reagent and process

stability. Negative controls (e.g., no template) should be assayed to monitor any exogenous nucleic acid contamination.

Classification Arrays

[00190] The present invention contemplates that a probe set or probes derived therefrom may be provided in an array format. In the context of the present invention, an "array" is a spatially or logically organized collection of polynucleotide probes. An array comprising probes specific for a coding target, non-coding target, or a combination thereof may be used. Alternatively, an array comprising probes specific for two or more of transcripts of a target selected from Table 2B, Table 16 or SEQ ID NOs: 1-1440 or a product derived thereof can be used. Desirably, an array may be specific for 5, 10, 15, 20, 25, 30, 50, 75, 100, 150, 200 or more of transcripts of a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. The array may be specific for 200, 225, 250, 275, 300, 325, 350, 375, 400 or more of the transcripts of a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. The array may be specific for 400, 425, 450, 475, 500, 525, 550, 575, 600 or more of the transcripts of a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. The array may be specific for 600, 625, 650, 675, 700, 725, 750, 775, 800, 825, 850 or more of the transcripts of a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

Expression of these sequences may be detected alone or in combination with other transcripts. In some embodiments, an array is used which comprises a wide range of sensor probes for bladder-specific expression products, along with appropriate control sequences. In some instances, the array may comprise the Human Exon 1.0 ST Array (HuEx 1.0 ST, Affymetrix, Inc., Santa Clara, CA.).

[00191] Typically the polynucleotide probes are attached to a solid substrate and are ordered so that the location (on the substrate) and the identity of each are known. The polynucleotide probes can be attached to one of a variety of solid substrates capable of withstanding the reagents and conditions necessary for use of the array. Examples include, but are not limited to, polymers, such as (poly)tetrafluoroethylene, (poly)vinylidenedifluoride, polystyrene, polycarbonate, polypropylene and polystyrene; ceramic; silicon; silicon dioxide; modified silicon; (fused) silica, quartz or glass; functionalized glass; paper, such as filter paper; diazotized cellulose; nitrocellulose filter; nylon membrane; and polyacrylamide gel pad. Substrates that are transparent to light are useful for arrays that may be used in an assay that involves optical detection.

[00192] Examples of array formats include membrane or filter arrays (for example, nitrocellulose, nylon arrays), plate arrays (for example, multiwell, such as a 24-, 96-, 256-, 384-, 864- or 1536-well, microtitre plate arrays), pin arrays, and bead arrays (for example, in a liquid "slurry"). Arrays on substrates such as glass or ceramic slides are often referred to as chip arrays or "chips." Such arrays are well known in the art. In one embodiment of the present invention, the Cancer Prognosticarray is a chip.

Data Analysis

[00193] In some embodiments, one or more pattern recognition methods can be used in analyzing the expression level of target sequences. The pattern recognition method can comprise a linear combination of expression levels, or a nonlinear combination of expression levels. In some embodiments, expression measurements for RNA transcripts or combinations of RNA transcript levels are formulated into linear or non-linear models or algorithms (e.g., an 'expression signature') and converted into a likelihood score. This likelihood score indicates the probability that a biological sample is from a patient who may exhibit no evidence of disease, who may exhibit systemic cancer, or who may exhibit biochemical recurrence. The likelihood score can be used to distinguish these disease states. The models and/or algorithms can be provided in machine readable format, and may be used to correlate expression levels or an expression profile with a disease state, and/or to designate a treatment modality for a patient or class of patients.

[00194] Assaying the expression level for a plurality of targets may comprise the use of an algorithm or classifier. Array data can be managed, classified, and analyzed using techniques known in the art. Assaying the expression level for a plurality of targets may comprise probe set modeling and data pre-processing. Probe set modeling and data pre-processing can be derived using the Robust Multi-Array (RMA) algorithm or variants GC-RMA, frozen robust multichip average (fRMA), Single Channel Array Normalization (SCAN), ComBat (Combining Batches of gene expression), Probe Logarithmic Intensity Error (PLIER) algorithm or variant iterPLIER. Variance or intensity filters can be applied to pre-process data using the RMA algorithm, for example by removing target sequences with a standard deviation of < 10 or a mean intensity of < 100 intensity units of a normalized data range, respectively.

[00195] Alternatively, assaying the expression level for a plurality of targets may comprise the use of a machine learning algorithm. The machine learning algorithm may comprise a supervised learning algorithm. Examples of supervised learning algorithms may include Average One-Dependence Estimators (AODE), Artificial neural network (e.g., Backpropagation), Bayesian statistics (e.g., Naive Bayes classifier, Bayesian network, Bayesian knowledge base), Case-based reasoning, Decision trees, Inductive logic programming, Gaussian process regression, Group method of data handling (GMDH), Learning Automata, Learning Vector Quantization, Minimum message length (decision trees, decision graphs, etc.), Lazy learning, Instance-based learning Nearest Neighbor Algorithm, Analogical modeling, Probably approximately correct learning (PAC) learning, Ripple down rules, a knowledge acquisition methodology, Symbolic machine learning algorithms, Subsymbolic machine learning algorithms, Support vector machines, Random Forests, Ensembles of classifiers, Bootstrap aggregating (bagging), and Boosting. Supervised learning may comprise ordinal classification such as regression analysis and Information fuzzy networks (IFN). Alternatively, supervised learning methods may comprise statistical classification,

such as AODE, Linear classifiers (e.g., Fisher's linear discriminant, Logistic regression, Naive Bayes classifier, Perceptron, and Support vector machine), quadratic classifiers, k-nearest neighbor, Boosting, Decision trees (e.g., C4.5, Random forests), Bayesian networks, and Hidden Markov models.

[00196] The machine learning algorithms may also comprise an unsupervised learning algorithm.

Examples of unsupervised learning algorithms may include artificial neural network, Data clustering, Expectation-maximization algorithm, Self-organizing map, Radial basis function network, Vector Quantization, Generative topographic map, Information bottleneck method, and IBSEAD. Unsupervised learning may also comprise association rule learning algorithms such as Apriori algorithm, Eclat algorithm and FP-growth algorithm. Hierarchical clustering, such as Single-linkage clustering and Conceptual clustering, may also be used. Alternatively, unsupervised learning may comprise partitional clustering such as K-means algorithm and Fuzzy clustering.

[00197] In some instances, the machine learning algorithms comprise a reinforcement learning algorithm. Examples of reinforcement learning algorithms include, but are not limited to, temporal difference learning, Q-learning and Learning Automata. Alternatively, the machine learning algorithm may comprise Data Pre-processing.

[00198] Preferably, the machine learning algorithms may include, but are not limited to, Average One-Dependence Estimators (AODE), Fisher's linear discriminant, Logistic regression, Perceptron, Multilayer Perceptron, Artificial Neural Networks, Support vector machines, Quadratic classifiers, Boosting, Decision trees, C4.5, Bayesian networks, Hidden Markov models, High-Dimensional Discriminant Analysis, and Gaussian Mixture Models. The machine learning algorithm may comprise support vector machines, Naïve Bayes classifier, k-nearest neighbor, high-dimensional discriminant analysis, or Gaussian mixture models. In some instances, the machine learning algorithm comprises Random Forests.

Additional Techniques and Tests

[00199] Factors known in the art for diagnosing and/or suggesting, selecting, designating, recommending or otherwise determining a course of treatment for a patient or class of patients suspected of having cancer can be employed in combination with measurements of the target sequence expression. The methods disclosed herein may include additional techniques such as cytology, histology, ultrasound analysis, MRI results, CT scan results, and measurements of PSA levels.

[00200] Certified tests for classifying disease status and/or designating treatment modalities may also be used in diagnosing, predicting, and/or monitoring the status or outcome of a cancer in a subject. A certified test may comprise a means for characterizing the expression levels of one or more of the target sequences of interest, and a certification from a government regulatory agency endorsing use of the test for classifying the disease status of a biological sample.

[00201] In some embodiments, the certified test may comprise reagents for amplification reactions used to detect and/or quantitate expression of the target sequences to be characterized in the test. An array of probe nucleic acids can be used, with or without prior target amplification, for use in measuring target sequence expression.

[00202] The test is submitted to an agency having authority to certify the test for use in distinguishing disease status and/or outcome. Results of detection of expression levels of the target sequences used in the test and correlation with disease status and/or outcome are submitted to the agency. A certification authorizing the diagnostic and/or prognostic use of the test is obtained.

[00203] Also provided are portfolios of expression levels comprising a plurality of normalized expression levels of the target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. Such portfolios may be provided by performing the methods described herein to obtain expression levels from an individual patient or from a group of patients. The expression levels can be normalized by any method known in the art; exemplary normalization methods that can be used in various embodiments include Robust Multichip Average (RMA), frozen robust multichip average (fRMA), Single Channel Array Normalization (SCAN), ComBat (Combining Batches of gene expression), probe logarithmic intensity error estimation (PLIER), non-linear fit (NLFIT) quantile-based and nonlinear normalization, and combinations thereof. Background correction can also be performed on the expression data; exemplary techniques useful for background correction include mode of intensities, normalized using median polish probe modeling and sketch-normalization.

[00204] In some embodiments, portfolios are established such that the combination of genes in the portfolio exhibit improved sensitivity and specificity relative to known methods. In considering a group of genes for inclusion in a portfolio, a small standard deviation in expression measurements correlates with greater specificity. Other measurements of variation such as correlation coefficients can also be used in this capacity. The invention also encompasses the above methods where the expression level determines the status or outcome of a cancer in the subject with at least about 45% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 50% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 55% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 60% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 65% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 70% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 75% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least

about 80% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 85% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 90% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 95% specificity.

[00205] The invention also encompasses the any of the methods disclosed herein where the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 45%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 50%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 55%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 60%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 65%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 70%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 75%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 80%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 85%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 90%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 95%.

[00206] The accuracy of a classifier or biomarker may be determined by the 95% confidence interval (CI). Generally, a classifier or biomarker is considered to have good accuracy if the 95% CI does not overlap 1. In some instances, the 95% CI of a classifier or biomarker is at least about 1.08, 1.10, 1.12, 1.14, 1.15, 1.16, 1.17, 1.18, 1.19, 1.20, 1.21, 1.22, 1.23, 1.24, 1.25, 1.26, 1.27, 1.28, 1.29, 1.30, 1.31, 1.32, 1.33, 1.34, or 1.35 or more. The 95% CI of a classifier or biomarker may be at least about 1.14, 1.15, 1.16, 1.20, 1.21, 1.26, or 1.28. The 95% CI of a classifier or biomarker may be less than about 1.75, 1.74, 1.73, 1.72, 1.71, 1.70, 1.69, 1.68, 1.67, 1.66, 1.65, 1.64, 1.63, 1.62, 1.61, 1.60, 1.59, 1.58, 1.57, 1.56, 1.55, 1.54, 1.53, 1.52, 1.51, 1.50 or less. The 95% CI of a classifier or biomarker may be less than about 1.61, 1.60, 1.59, 1.58, 1.56, 1.55, or 1.53. The 95% CI of a classifier or biomarker may be between about 1.10 to 1.70, between about 1.12 to about 1.68, between about 1.14 to about 1.62, between about 1.15 to about 1.61, between about 1.15 to about 1.59, between about 1.16 to about 1.60, between about 1.19 to about 1.55, between about 1.20 to about 1.54, between about 1.21 to about 1.53, between about 1.26 to about 1.63, between about 1.27 to about 1.61, or between about 1.28 to about 1.60.

[00207] In some instances, the accuracy of a biomarker or classifier is dependent on the difference in range of the 95% CI (e.g., difference in the high value and low value of the 95% CI interval). Generally, biomarkers or classifiers with large differences in the range of the 95% CI interval have greater variability and are considered less accurate than biomarkers or classifiers with small differences in the range of the 95% CI intervals. In some instances, a biomarker or classifier is considered more accurate if the difference in the range of the 95% CI is less than about 0.60, 0.55, 0.50, 0.49, 0.48, 0.47, 0.46, 0.45, 0.44, 0.43, 0.42, 0.41, 0.40, 0.39, 0.38, 0.37, 0.36, 0.35, 0.34, 0.33, 0.32, 0.31, 0.30, 0.29, 0.28, 0.27, 0.26, 0.25 or less. The difference in the range of the 95% CI of a biomarker or classifier may be less than about 0.48, 0.45, 0.44, 0.42, 0.40, 0.37, 0.35, 0.33, or 0.32. In some instances, the difference in the range of the 95% CI for a biomarker or classifier is between about 0.25 to about 0.50, between about 0.27 to about 0.47, or between about 0.30 to about 0.45.

[00208] The invention also encompasses the any of the methods disclosed herein where the sensitivity is at least about 45%. In some embodiments, the sensitivity is at least about 50%. In some embodiments, the sensitivity is at least about 55%. In some embodiments, the sensitivity is at least about 60%. In some embodiments, the sensitivity is at least about 65%. In some embodiments, the sensitivity is at least about 70%. In some embodiments, the sensitivity is at least about 75%. In some embodiments, the sensitivity is at least about 80%. In some embodiments, the sensitivity is at least about 85%. In some embodiments, the sensitivity is at least about 90%. In some embodiments, the sensitivity is at least about 95%.

[00209] In some instances, the classifiers or biomarkers disclosed herein are clinically significant. In some instances, the clinical significance of the classifiers or biomarkers is determined by the AUC value. In order to be clinically significant, the AUC value is at least about 0.5, 0.55, 0.6, 0.65, 0.7, 0.75, 0.8, 0.85, 0.9, or 0.95. The clinical significance of the classifiers or biomarkers can be determined by the percent accuracy. For example, a classifier or biomarker is determined to be clinically significant if the accuracy of the classifier or biomarker is at least about 50%, 55%, 60%, 65%, 70%, 72%, 75%, 77%, 80%, 82%, 84%, 86%, 88%, 90%, 92%, 94%, 96%, or 98%. In other instances, the clinical significance of the classifiers or biomarkers is determined by the median fold difference (MDF) value. In order to be clinically significant, the MDF value is at least about 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.9, or 2.0. In some instances, the MDF value is greater than or equal to 1.1. In other instances, the MDF value is greater than or equal to 1.2. Alternatively, or additionally, the clinical significance of the classifiers or biomarkers is determined by the t-test P-value. In some instances, in order to be clinically significant, the t-test P-value is less than about 0.070, 0.065, 0.060, 0.055, 0.050, 0.045, 0.040, 0.035, 0.030, 0.025, 0.020, 0.015, 0.010, 0.005, 0.004, or 0.003. The t-test P-value can be less than about 0.050. Alternatively, the t-test P-value is less than about 0.010. In some instances, the clinical significance of the classifiers or biomarkers is determined by the clinical outcome. For example, different clinical outcomes can have

different minimum or maximum thresholds for AUC values, MDF values, t-test P-values, and accuracy values that would determine whether the classifier or biomarker is clinically significant. In another example, a classifier or biomarker is considered clinically significant if the P-value of the t-test was less than about 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01, 0.005, 0.004, 0.003, 0.002, or 0.001. In some instances, the P-value may be based on any of the following comparisons: BCR vs non-BCR, CP vs non-CP, PCSM vs non-PCSM. For example, a classifier or biomarker is determined to be clinically significant if the P-values of the differences between the KM curves for BCR vs non-BCR, CP vs non-CP, PCSM vs non-PCSM is lower than about 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01, 0.005, 0.004, 0.003, 0.002, or 0.001.

[00210] In some instances, the performance of the classifier or biomarker is based on the odds ratio. A classifier or biomarker may be considered to have good performance if the odds ratio is at least about 1.30, 1.31, 1.32, 1.33, 1.34, 1.35, 1.36, 1.37, 1.38, 1.39, 1.40, 1.41, 1.42, 1.43, 1.44, 1.45, 1.46, 1.47, 1.48, 1.49, 1.50, 1.52, 1.55, 1.57, 1.60, 1.62, 1.65, 1.67, 1.70 or more. In some instances, the odds ratio of a classifier or biomarker is at least about 1.33.

[00211] The clinical significance of the classifiers and/or biomarkers may be based on Univariable Analysis Odds Ratio P-value (uvaORPval). The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be between about 0-0.4. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be between about 0-0.3. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be between about 0-0.2. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be less than or equal to 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[00212] The clinical significance of the classifiers and/or biomarkers may be based on multivariable analysis Odds Ratio P-value (mvaORPval). The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be between about 0-1. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be between about 0-0.9. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be between about 0-0.8. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be less than or equal to 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be less than or equal to 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The multivariable analysis Odds Ratio P-value

(mvaORPval) of the classifier and/or biomarker may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[00213] The clinical significance of the classifiers and/or biomarkers may be based on the Kaplan Meier P-value (KM P-value). The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be between about 0-0.8. The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be between about 0-0.7. The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[00214] The clinical significance of the classifiers and/or biomarkers may be based on the survival AUC value (survAUC). The survival AUC value (survAUC) of the classifier and/or biomarker may be between about 0-1. The survival AUC value (survAUC) of the classifier and/or biomarker may be between about 0-0.9. The survival AUC value (survAUC) of the classifier and/or biomarker may be less than or equal to 1, 0.98, 0.96, 0.94, 0.92, 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The survival AUC value (survAUC) of the classifier and/or biomarker may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The survival AUC value (survAUC) of the classifier and/or biomarker may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The survival AUC value (survAUC) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The survival AUC value (survAUC) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[00215] The clinical significance of the classifiers and/or biomarkers may be based on the Univariable Analysis Hazard Ratio P-value (uvaHRPval). The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be between about 0-0.4. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be between about 0-0.3. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be less

than or equal to 0.40, 0.38, 0.36, 0.34, 0.32. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.30, 0.29, 0.28, 0.27, 0.26, 0.25, 0.24, 0.23, 0.22, 0.21, 0.20. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[00216] The clinical significance of the classifiers and/or biomarkers may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be between about 0-1. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be between about 0-0.9. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 1, 0.98, 0.96, 0.94, 0.92, 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[00217] The clinical significance of the classifiers and/or biomarkers may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be between about 0 to about 0.60. significance of the classifier and/or biomarker may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be between about 0 to about 0.50. significance of the classifier and/or biomarker may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.50, 0.47, 0.45, 0.43, 0.40, 0.38, 0.35, 0.33, 0.30, 0.28, 0.25, 0.22, 0.20, 0.18, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11, 0.10. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Multivariable

Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.01, 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[00218] The classifiers and/or biomarkers disclosed herein may outperform current classifiers or clinical variables in providing clinically relevant analysis of a sample from a subject. In some instances, the classifiers or biomarkers may more accurately predict a clinical outcome or status as compared to current classifiers or clinical variables. For example, a classifier or biomarker may more accurately predict metastatic disease. Alternatively, a classifier or biomarker may more accurately predict no evidence of disease. In some instances, the classifier or biomarker may more accurately predict death from a disease. The performance of a classifier or biomarker disclosed herein may be based on the AUC value, odds ratio, 95% CI, difference in range of the 95% CI, p-value or any combination thereof.

[00219] The performance of the classifiers and/or biomarkers disclosed herein may be determined by AUC values and an improvement in performance may be determined by the difference in the AUC value of the classifier or biomarker disclosed herein and the AUC value of current classifiers or clinical variables. In some instances, a classifier and/or biomarker disclosed herein outperforms current classifiers or clinical variables when the AUC value of the classifier and/or or biomarker disclosed herein is greater than the AUC value of the current classifiers or clinical variables by at least about 0.05, 0.06, 0.07, 0.08, 0.09, 0.10, 0.11, 0.12, 0.13, 0.14, 0.15, 0.16, 0.17, 0.18, 0.19, 0.20, 0.22, 0.25, 0.27, 0.30, 0.32, 0.35, 0.37, 0.40, 0.42, 0.45, 0.47, 0.50 or more. In some instances, the AUC value of the classifier and/or or biomarker disclosed herein is greater than the AUC value of the current classifiers or clinical variables by at least about 0.10. In some instances, the AUC value of the classifier and/or or biomarker disclosed herein is greater than the AUC value of the current classifiers or clinical variables by at least about 0.13. In some instances, the AUC value of the classifier and/or or biomarker disclosed herein is greater than the AUC value of the current classifiers or clinical variables by at least about 0.18.

[00220] The performance of the classifiers and/or biomarkers disclosed herein may be determined by the odds ratios and an improvement in performance may be determined by comparing the odds ratio of the classifier or biomarker disclosed herein and the odds ratio of current classifiers or clinical variables. Comparison of the performance of two or more classifiers, biomarkers, and/or clinical variables can be generally be based on the comparison of the absolute value of (1-odds ratio) of a first classifier, biomarker or clinical variable to the absolute value of (1-odds ratio) of a second classifier, biomarker or clinical variable. Generally, the classifier, biomarker or clinical variable with the greater absolute value of (1-odds ratio) can be considered to have better performance as compared to the classifier, biomarker or clinical variable with a smaller absolute value of (1-odds ratio).

[00221] In some instances, the performance of a classifier, biomarker or clinical variable is based on the comparison of the odds ratio and the 95% confidence interval (CI). For example, a first classifier,

biomarker or clinical variable may have a greater absolute value of (1-odds ratio) than a second classifier, biomarker or clinical variable, however, the 95% CI of the first classifier, biomarker or clinical variable may overlap 1 (e.g., poor accuracy), whereas the 95% CI of the second classifier, biomarker or clinical variable does not overlap 1. In this instance, the second classifier, biomarker or clinical variable is considered to outperform the first classifier, biomarker or clinical variable because the accuracy of the first classifier, biomarker or clinical variable is less than the accuracy of the second classifier, biomarker or clinical variable. In another example, a first classifier, biomarker or clinical variable may outperform a second classifier, biomarker or clinical variable based on a comparison of the odds ratio; however, the difference in the 95% CI of the first classifier, biomarker or clinical variable is at least about 2 times greater than the 95% CI of the second classifier, biomarker or clinical variable. In this instance, the second classifier, biomarker or clinical variable is considered to outperform the first classifier.

[00222] In some instances, a classifier or biomarker disclosed herein more accurate than a current classifier or clinical variable. The classifier or biomarker disclosed herein is more accurate than a current classifier or clinical variable if the range of 95% CI of the classifier or biomarker disclosed herein does not span or overlap 1 and the range of the 95% CI of the current classifier or clinical variable spans or overlaps 1.

[00223] In some instances, a classifier or biomarker disclosed herein more accurate than a current classifier or clinical variable. The classifier or biomarker disclosed herein is more accurate than a current classifier or clinical variable when difference in range of the 95% CI of the classifier or biomarker disclosed herein is about 0.70, 0.60, 0.50, 0.40, 0.30, 0.20, 0.15, 0.14, 0.13, 0.12, 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02 times less than the difference in range of the 95% CI of the current classifier or clinical variable. The classifier or biomarker disclosed herein is more accurate than a current classifier or clinical variable when difference in range of the 95% CI of the classifier or biomarker disclosed herein between about 0.20 to about 0.04 times less than the difference in range of the 95% CI of the current classifier or clinical variable.

[00224] In some instances, the methods disclosed herein may comprise the use of a genomic classifier (GC) model. A general method for developing a GC model may comprise (a) providing a sample from a subject suffering from a cancer; (b) assaying the expression level for a plurality of targets; (c) generating a model by using a machine learning algorithm. In some instances, the machine learning algorithm comprises Random Forests. In another example, a GC model may developed by using a machine learning algorithm to analyze and rank genomic features. Analyzing the genomic features may comprise classifying one or more genomic features. The method may further comprise validating the classifier and/or refining the classifier by using a machine learning algorithm.

[00225] The methods disclosed herein may comprise generating one or more clinical classifiers (CC). The clinical classifier can be developed using one or more clinicopathologic variables. The clinicopathologic variables may be selected from the group comprising Lymph node invasion status (LNI); Surgical Margin Status (SMS); Seminal Vesicle Invasion (SVI); Extra Capsular Extension (ECE); Pathological Gleason Score; and the pre-operative PSA. The clinicopathologic variables may be selected from the group comprising Tumor Stage (e.g., CIS, Ta, T1, T2, T2a, T2b, T3, T3a, T4a, T4b), Nodal Status (e.g., N0, N1, N2, or N3), Lymphovascular invasion, age, or gender. The method may comprise using one or more of the clinicopathologic variables as binary variables. Alternatively, or additionally, the one or more clinicopathologic variables may be converted to a logarithmic value (e.g., log10). The method may further comprise assembling the variables in a logistic regression. In some instances, the CC is combined with the GC to produce a genomic clinical classifier (GCC).

[00226] In some instances, the methods disclosed herein may comprise the use of a genomic-clinical classifier (GCC) model. A general method for developing a GCC model may comprise (a) providing a sample from a subject suffering from a cancer; (b) assaying the expression level for a plurality of targets; (c) generating a model by using a machine learning algorithm. In some instances, the machine learning algorithm comprises Random Forests.

Cancer

[00227] The systems, compositions and methods disclosed herein may be used to diagnosis, monitor and/or predict the status or outcome of a cancer. Generally, a cancer is characterized by the uncontrolled growth of abnormal cells anywhere in a body. The abnormal cells may be termed cancer cells, malignant cells, or tumor cells. Many cancers and the abnormal cells that compose the cancer tissue are further identified by the name of the tissue that the abnormal cells originated from (for example, bladder cancer, lung cancer, colon cancer, prostate cancer, pancreatic cancer, thyroid cancer). Cancer is not confined to humans; animals and other living organisms can get cancer.

[00228] In some instances, the cancer may be malignant. Alternatively, the cancer may be benign. The cancer may be a recurrent and/or refractory cancer. Most cancers can be classified as a carcinoma, sarcoma, leukemia, lymphoma, myeloma, or a central nervous system cancer.

[00229] The cancer may be a sarcoma. Sarcomas are cancers of the bone, cartilage, fat, muscle, blood vessels, or other connective or supportive tissue. Sarcomas include, but are not limited to, bone cancer, fibrosarcoma, chondrosarcoma, Ewing's sarcoma, malignant hemangioendothelioma, malignant schwannoma, bilateral vestibular schwannoma, osteosarcoma, soft tissue sarcomas (e.g. alveolar soft part sarcoma, angiosarcoma, cystosarcoma phylloides, dermatofibrosarcoma, desmoid tumor, epithelioid sarcoma, extraskeletal osteosarcoma, fibrosarcoma, hemangiopericytoma, hemangiosarcoma, Kaposi's

sarcoma, leiomyosarcoma, liposarcoma, lymphangiosarcoma, lymphosarcoma, malignant fibrous histiocytoma, neurofibrosarcoma, rhabdomyosarcoma, and synovial sarcoma).

[00230] Alternatively, the cancer may be a carcinoma. Carcinomas are cancers that begin in the epithelial cells, which are cells that cover the surface of the body, produce hormones, and make up glands. By way of non-limiting example, carcinomas include breast cancer, pancreatic cancer, lung cancer, colon cancer, colorectal cancer, rectal cancer, kidney cancer, bladder cancer, stomach cancer, prostate cancer, liver cancer, ovarian cancer, brain cancer, vaginal cancer, vulvar cancer, uterine cancer, oral cancer, penic cancer, testicular cancer, esophageal cancer, skin cancer, cancer of the fallopian tubes, head and neck cancer, gastrointestinal stromal cancer, adenocarcinoma, cutaneous or intraocular melanoma, cancer of the anal region, cancer of the small intestine, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, cancer of the urethra, cancer of the renal pelvis, cancer of the ureter, cancer of the endometrium, cancer of the cervix, cancer of the pituitary gland, neoplasms of the central nervous system (CNS), primary CNS lymphoma, brain stem glioma, and spinal axis tumors. In some instances, the cancer is a skin cancer, such as a basal cell carcinoma, squamous, melanoma, nonmelanoma, or actinic (solar) keratosis. Preferably, the cancer is a bladder cancer.

Alternatively, the cancer may be a thyroid cancer, prostate cancer, or pancreatic cancer.

[00231] In some instances, the cancer is a lung cancer. Lung cancer can start in the airways that branch off the trachea to supply the lungs (bronchi) or the small air sacs of the lung (the alveoli). Lung cancers include non-small cell lung carcinoma (NSCLC), small cell lung carcinoma, and mesothelioma.

Examples of NSCLC include squamous cell carcinoma, adenocarcinoma, and large cell carcinoma. The mesothelioma may be a cancerous tumor of the lining of the lung and chest cavity (pleura) or lining of the abdomen (peritoneum). The mesothelioma may be due to asbestos exposure. The cancer may be a brain cancer, such as a glioblastoma.

[00232] In some instances, the cancer is a bladder cancer. Bladder cancer is the fourth most common type of cancer in men and the ninth most common cancer in women. Invasive bladder cancer has a high propensity for recurrence. In some instances, the bladder cancer can be non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer.

[00233] Alternatively, the cancer may be a central nervous system (CNS) tumor. CNS tumors may be classified as gliomas or nongliomas. The glioma may be malignant glioma, high grade glioma, diffuse intrinsic pontine glioma. Examples of gliomas include astrocytomas, oligodendrogliomas (or mixtures of oligodendroglioma and astrocytoma elements), and ependymomas. Astrocytomas include, but are not limited to, low-grade astrocytomas, anaplastic astrocytomas, glioblastoma multiforme, pilocytic astrocytoma, pleomorphic xanthoastrocytoma, and subependymal giant cell astrocytoma. Oligodendrogliomas include low-grade oligodendrogliomas (or oligoastrocytomas) and anaplastic

oligodendriogliomas. Nongliomas include meningiomas, pituitary adenomas, primary CNS lymphomas, and medulloblastomas. In some instances, the cancer is a meningioma.

[00234] The cancer may be a leukemia. The leukemia may be an acute lymphocytic leukemia, acute myelocytic leukemia, chronic lymphocytic leukemia, or chronic myelocytic leukemia. Additional types of leukemias include hairy cell leukemia, chronic myelomonocytic leukemia, and juvenile myelomonocytic-leukemia.

[00235] In some instances, the cancer is a lymphoma. Lymphomas are cancers of the lymphocytes and may develop from either B or T lymphocytes. The two major types of lymphoma are Hodgkin's lymphoma, previously known as Hodgkin's disease, and non-Hodgkin's lymphoma. Hodgkin's lymphoma is marked by the presence of the Reed-Sternberg cell. Non-Hodgkin's lymphomas are all lymphomas which are not Hodgkin's lymphoma. Non-Hodgkin lymphomas may be indolent lymphomas and aggressive lymphomas. Non-Hodgkin's lymphomas include, but are not limited to, diffuse large B cell lymphoma, follicular lymphoma, mucosa-associated lymphatic tissue lymphoma (MALT), small cell lymphocytic lymphoma, mantle cell lymphoma, Burkitt's lymphoma, mediastinal large B cell lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma (NMZL), splenic marginal zone lymphoma (SMZL), extranodal marginal zone B cell lymphoma, intravascular large B cell lymphoma, primary effusion lymphoma, and lymphomatoid granulomatosis.

Cancer Staging

[00236] Diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise determining the stage of the cancer. Generally, the stage of a cancer is a description (usually numbers I to IV with IV having more progression) of the extent the cancer has spread. The stage often takes into account the size of a tumor, how deeply it has penetrated, whether it has invaded adjacent organs, how many lymph nodes it has metastasized to (if any), and whether it has spread to distant organs. Staging of cancer can be used as a predictor of survival, and cancer treatment may be determined by staging.

Determining the stage of the cancer may occur before, during, or after treatment. The stage of the cancer may also be determined at the time of diagnosis.

[00237] Cancer staging can be divided into a clinical stage and a pathologic stage. Cancer staging may comprise the TNM classification. Generally, the TNM Classification of Malignant Tumours (TNM) is a cancer staging system that describes the extent of cancer in a patient's body. T may describe the size of the tumor and whether it has invaded nearby tissue, N may describe regional lymph nodes that are involved, and M may describe distant metastasis (spread of cancer from one body part to another). In the TNM (Tumor, Node, Metastasis) system, clinical stage and pathologic stage are denoted by a small "c" or "p" before the stage (e.g., cT3N1M0 or pT2N0).

[00238] Often, clinical stage and pathologic stage may differ. Clinical stage may be based on all of the available information obtained before a surgery to remove the tumor. Thus, it may include information about the tumor obtained by physical examination, radiologic examination, and endoscopy. Pathologic stage can add additional information gained by examination of the tumor microscopically by a pathologist. Pathologic staging can allow direct examination of the tumor and its spread, contrasted with clinical staging which may be limited by the fact that the information is obtained by making indirect observations at a tumor which is still in the body. The TNM staging system can be used for most forms of cancer.

[00239] Alternatively, staging may comprise Ann Arbor staging. Generally, Ann Arbor staging is the staging system for lymphomas, both in Hodgkin's lymphoma (previously called Hodgkin's disease) and Non-Hodgkin lymphoma (abbreviated NHL). The stage may depend on both the place where the malignant tissue is located (as located with biopsy, CT scanning and increasingly positron emission tomography) and on systemic symptoms due to the lymphoma ("B symptoms": night sweats, weight loss of >10% or fevers). The principal stage may be determined by location of the tumor. Stage I may indicate that the cancer is located in a single region, usually one lymph node and the surrounding area. Stage I often may not have outward symptoms. Stage II can indicate that the cancer is located in two separate regions, an affected lymph node or organ and a second affected area, and that both affected areas are confined to one side of the diaphragm - that is, both are above the diaphragm, or both are below the diaphragm. Stage III often indicates that the cancer has spread to both sides of the diaphragm, including one organ or area near the lymph nodes or the spleen. Stage IV may indicate diffuse or disseminated involvement of one or more extralymphatic organs, including any involvement of the liver, bone marrow, or nodular involvement of the lungs.

[00240] Modifiers may also be appended to some stages. For example, the letters A, B, E, X, or S can be appended to some stages. Generally, A or B may indicate the absence of constitutional (B-type) symptoms is denoted by adding an "A" to the stage; the presence is denoted by adding a "B" to the stage. E can be used if the disease is "extranodal" (not in the lymph nodes) or has spread from lymph nodes to adjacent tissue. X is often used if the largest deposit is >10 cm large ("bulky disease"), or whether the mediastinum is wider than 1/3 of the chest on a chest X-ray. S may be used if the disease has spread to the spleen.

[00241] The nature of the staging may be expressed with CS or PS. CS may denote that the clinical stage as obtained by doctor's examinations and tests. PS may denote that the pathological stage as obtained by exploratory laparotomy (surgery performed through an abdominal incision) with splenectomy (surgical removal of the spleen).

[00242] TNM classification may be used as the staging system for bladder tumors. In this aspect, the staging system takes into account how deep the tumor has grown into the bladder, whether there is cancer in the lymph nodes and whether the cancer has spread to any other part of the body. According to the TNM staging system, bladder cancer can be staged as follows: In bladder cancer stage 0, cancer cells are confined to the mucosa. In bladder cancer stage I the tumor invades the subepithelial connective tissue/lamina propria. In bladder cancer stage II cancer cells have invaded the muscularis propria but the tumor is still organ-confined. In bladder cancer stage III cancer cells have extended through the bladder wall to the perivesical tissue or to the Prostatic stroma, uterus or vagina. In bladder cancer stage IV cancer cells have proliferated to the lymph nodes, pelvic or abdominal wall, and/or other organs. The “bladder cancer” in the context of the present invention, may encompass any of the aforementioned stages.

Markers for Bladder Cancer

[00243] Several biomarkers for bladder cancer diagnosis have been described. The BTA-Stat test detects complement factor H (CFH) and related proteins (CFH-rp). The nuclear matrix protein 22 (NMP22) test (Matritech, Newton, MA) is a double monoclonal antibody test designed to measure quantitatively the nuclear mitotic apparatus (MUMA) protein. The ImmunoCyt test (Diagno-Cure Inc., Sainte-Foy, Quebec Canada) detects bladder cancer markers present on exfoliated cells using a cocktail of fluorescent antibodies (19A211, M344 and LDQ10). The UroVysion test (Vysis Chicago, IL) employs centromere probes specific to chromosomes 3, 7, 17 and 9 to detect aneuploidy associated with bladder cancer. Other markers for bladder cancer include survivin, cytokeratins, telomerase, BLCA-4, microsatellite detection, hyaluronic acid and hyaluronidase, urine fibronectin, and chorionic gonadotropin. Use of these markers in combination with the markers and genomic classifiers of the present invention are specifically contemplated herein.

Therapeutic regimens

[00244] Diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise treating a cancer or preventing a cancer progression. In addition, diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise identifying or predicting responders to an anti-cancer therapy. In some instances, diagnosing, predicting, or monitoring may comprise determining a therapeutic regimen. Determining a therapeutic regimen may comprise administering an anti-cancer therapy. Alternatively, determining a therapeutic regimen may comprise modifying, recommending, continuing or discontinuing an anti-cancer regimen. In some instances, if the sample expression patterns are consistent with the expression pattern for a known disease or disease outcome, the expression patterns can be used to designate one or more treatment modalities (e.g., therapeutic regimens, anti-cancer regimen). An anti-

cancer regimen may comprise one or more anti-cancer therapies. Examples of anti-cancer therapies include surgery, chemotherapy, radiation therapy, immunotherapy/biological therapy, photodynamic therapy.

[00245] Surgical oncology uses surgical methods to diagnose, stage, and treat cancer, and to relieve certain cancer-related symptoms. Surgery may be used to remove the tumor (e.g., excisions, resections, debulking surgery), reconstruct a part of the body (e.g., restorative surgery), and/or to relieve symptoms such as pain (e.g., palliative surgery). Surgery may also include cryosurgery. Cryosurgery (also called cryotherapy) may use extreme cold produced by liquid nitrogen (or argon gas) to destroy abnormal tissue. Cryosurgery can be used to treat external tumors, such as those on the skin. For external tumors, liquid nitrogen can be applied directly to the cancer cells with a cotton swab or spraying device. Cryosurgery may also be used to treat tumors inside the body (internal tumors and tumors in the bone). For internal tumors, liquid nitrogen or argon gas may be circulated through a hollow instrument called a cryoprobe, which is placed in contact with the tumor. An ultrasound or MRI may be used to guide the cryoprobe and monitor the freezing of the cells, thus limiting damage to nearby healthy tissue. A ball of ice crystals may form around the probe, freezing nearby cells. Sometimes more than one probe is used to deliver the liquid nitrogen to various parts of the tumor. The probes may be put into the tumor during surgery or through the skin (percutaneously). After cryosurgery, the frozen tissue thaws and may be naturally absorbed by the body (for internal tumors), or may dissolve and form a scab (for external tumors).

[00246] As used herein the term "tumor margin" refers to the tissue surrounding a discernible tumor. In the case of surgical removal of a solid tumor, the tumor margin is the tissue cut away with the discernible tumor that usually appears to be normal to the naked eye. More particularly, as used herein, "margin" refers to the edge, border or boundary of a tumor. The margin generally extends from about 1 mm to about 4 mm from the primary tumor but can be greater depending upon the size of the primary solid tumor. As used herein, the terms "surgical margin", "tumor free margin", "free margin", "normal skin margin", and "normal tissue margin" refer to the visible normal tissue or skin margin that is removed with the surgical excision of a tumor, growth, or malignancy. Surgical margin as read in a pathology report define the histological measurement of normal or unaffected tissue surrounding the visible tumor under a microscope on a glass mounted histology section. A "narrow" surgical margin implies that the tumor exists very close to the surgical margin, and a "wide" surgical margin implies the tumor exists far from the cut edge or the surgical margin.

[00247] Chemotherapeutic agents may also be used for the treatment of cancer. Examples of chemotherapeutic agents include alkylating agents, anti-metabolites, plant alkaloids and terpenoids, vinca alkaloids, podophyllotoxin, taxanes, topoisomerase inhibitors, and cytotoxic antibiotics. Cisplatin, carboplatin, and oxaliplatin are examples of alkylating agents. Other alkylating agents include

mechlorethamine, cyclophosphamide, chlorambucil, ifosfamide. Alkylating agents may impair cell function by forming covalent bonds with the amino, carboxyl, sulfhydryl, and phosphate groups in biologically important molecules. Alternatively, alkylating agents may chemically modify a cell's DNA.

[00248] Anti-metabolites are another example of chemotherapeutic agents. Anti-metabolites may masquerade as purines or pyrimidines and may prevent purines and pyrimidines from becoming incorporated into DNA during the "S" phase (of the cell cycle), thereby stopping normal development and division. Antimetabolites may also affect RNA synthesis. Examples of metabolites include azathioprine and mercaptopurine.

[00249] Alkaloids may be derived from plants and block cell division may also be used for the treatment of cancer. Alkaloids may prevent microtubule function. Examples of alkaloids are vinca alkaloids and taxanes. Vinca alkaloids may bind to specific sites on tubulin and inhibit the assembly of tubulin into microtubules (M phase of the cell cycle). The vinca alkaloids may be derived from the Madagascar periwinkle, *Catharanthus roseus* (formerly known as *Vinca rosea*). Examples of vinca alkaloids include, but are not limited to, vincristine, vinblastine, vinorelbine, or vindesine. Taxanes are diterpenes produced by the plants of the genus *Taxus* (yews). Taxanes may be derived from natural sources or synthesized artificially. Taxanes include paclitaxel (Taxol) and docetaxel (Taxotere). Taxanes may disrupt microtubule function. Microtubules are essential to cell division, and taxanes may stabilize GDP-bound tubulin in the microtubule, thereby inhibiting the process of cell division. Thus, in essence, taxanes may be mitotic inhibitors. Taxanes may also be radiosensitizing and often contain numerous chiral centers.

[00250] Alternative chemotherapeutic agents include podophyllotoxin. Podophyllotoxin is a plant-derived compound that may help with digestion and may be used to produce cytostatic drugs such as etoposide and teniposide. They may prevent the cell from entering the G1 phase (the start of DNA replication) and the replication of DNA (the S phase).

[00251] Topoisomerases are essential enzymes that maintain the topology of DNA. Inhibition of type I or type II topoisomerases may interfere with both transcription and replication of DNA by upsetting proper DNA supercoiling. Some chemotherapeutic agents may inhibit topoisomerases. For example, some type I topoisomerase inhibitors include *camptothecins*: irinotecan and topotecan. Examples of type II inhibitors include amsacrine, etoposide, etoposide phosphate, and teniposide.

[00252] Another example of chemotherapeutic agents is cytotoxic antibiotics. Cytotoxic antibiotics are a group of antibiotics that are used for the treatment of cancer because they may interfere with DNA replication and/or protein synthesis. Cytotoxic antibiotics include, but are not limited to, actinomycin, anthracyclines, doxorubicin, daunorubicin, valrubicin, idarubicin, epirubicin, bleomycin, plicamycin, and mitomycin.

[00253] Chemotherapeutic agents may be used alone or in combination. Examples of therapeutic combinations used to treat bladder cancer include: Gemcitabine and cisplatin; Methotrexate, vinblastine, doxorubicin (Adriamycin), and cisplatin (called M-VAC); Carboplatin and either paclitaxel or docetaxel (for patients with poor kidney function).

[00254] In some instances, the anti-cancer treatment may comprise radiation therapy. Radiation can come from a machine outside the body (external-beam radiation therapy) or from radioactive material placed in the body near cancer cells (internal radiation therapy, more commonly called brachytherapy). Systemic radiation therapy uses a radioactive substance, given by mouth or into a vein that travels in the blood to tissues throughout the body.

[00255] External-beam radiation therapy may be delivered in the form of photon beams (either x-rays or gamma rays). A photon is the basic unit of light and other forms of electromagnetic radiation. An example of external-beam radiation therapy is called 3-dimensional conformal radiation therapy (3D-CRT). 3D-CRT may use computer software and advanced treatment machines to deliver radiation to very precisely shaped target areas. Many other methods of external-beam radiation therapy are currently being tested and used in cancer treatment. These methods include, but are not limited to, intensity-modulated radiation therapy (IMRT), image-guided radiation therapy (IGRT), Stereotactic radiosurgery (SRS), Stereotactic body radiation therapy (SBRT), and proton therapy.

[00256] Intensity-modulated radiation therapy (IMRT) is an example of external-beam radiation and may use hundreds of tiny radiation beam-shaping devices, called collimators, to deliver a single dose of radiation. The collimators can be stationary or can move during treatment, allowing the intensity of the radiation beams to change during treatment sessions. This kind of dose modulation allows different areas of a tumor or nearby tissues to receive different doses of radiation. IMRT is planned in reverse (called inverse treatment planning). In inverse treatment planning, the radiation doses to different areas of the tumor and surrounding tissue are planned in advance, and then a high-powered computer program calculates the required number of beams and angles of the radiation treatment. In contrast, during traditional (forward) treatment planning, the number and angles of the radiation beams are chosen in advance and computers calculate how much dose may be delivered from each of the planned beams. The goal of IMRT is to increase the radiation dose to the areas that need it and reduce radiation exposure to specific sensitive areas of surrounding normal tissue.

[00257] Another example of external-beam radiation is image-guided radiation therapy (IGRT). In IGRT, repeated imaging scans (CT, MRI, or PET) may be performed during treatment. These imaging scans may be processed by computers to identify changes in a tumor's size and location due to treatment and to allow the position of the patient or the planned radiation dose to be adjusted during treatment as

needed. Repeated imaging can increase the accuracy of radiation treatment and may allow reductions in the planned volume of tissue to be treated, thereby decreasing the total radiation dose to normal tissue.

[00258] Tomotherapy is a type of image-guided IMRT. A tomotherapy machine is a hybrid between a CT imaging scanner and an external-beam radiation therapy machine. The part of the tomotherapy machine that delivers radiation for both imaging and treatment can rotate completely around the patient in the same manner as a normal CT scanner. Tomotherapy machines can capture CT images of the patient's tumor immediately before treatment sessions, to allow for very precise tumor targeting and sparing of normal tissue.

[00259] Stereotactic radiosurgery (SRS) can deliver one or more high doses of radiation to a small tumor. SRS uses extremely accurate image-guided tumor targeting and patient positioning. Therefore, a high dose of radiation can be given without excess damage to normal tissue. SRS can be used to treat small tumors with well-defined edges. It is most commonly used in the treatment of brain or spinal tumors and brain metastases from other cancer types. For the treatment of some brain metastases, patients may receive radiation therapy to the entire brain (called whole-brain radiation therapy) in addition to SRS. SRS requires the use of a head frame or other device to immobilize the patient during treatment to ensure that the high dose of radiation is delivered accurately.

[00260] Stereotactic body radiation therapy (SBRT) delivers radiation therapy in fewer sessions, using smaller radiation fields and higher doses than 3D-CRT in most cases. SBRT may treat tumors that lie outside the brain and spinal cord. Because these tumors are more likely to move with the normal motion of the body, and therefore cannot be targeted as accurately as tumors within the brain or spine, SBRT is usually given in more than one dose. SBRT can be used to treat small, isolated tumors, including cancers in the lung and liver. SBRT systems may be known by their brand names, such as the CyberKnife®.

[00261] In proton therapy, external-beam radiation therapy may be delivered by proton. Protons are a type of charged particle. Proton beams differ from photon beams mainly in the way they deposit energy in living tissue. Whereas photons deposit energy in small packets all along their path through tissue, protons deposit much of their energy at the end of their path (called the Bragg peak) and deposit less energy along the way. Use of protons may reduce the exposure of normal tissue to radiation, possibly allowing the delivery of higher doses of radiation to a tumor.

[00262] Other charged particle beams such as electron beams may be used to irradiate superficial tumors, such as skin cancer or tumors near the surface of the body, but they cannot travel very far through tissue.

[00263] Internal radiation therapy (brachytherapy) is radiation delivered from radiation sources (radioactive materials) placed inside or on the body. Several brachytherapy techniques are used in cancer treatment. Interstitial brachytherapy may use a radiation source placed within tumor tissue, such as within

a bladder tumor. Intracavitary brachytherapy may use a source placed within a surgical cavity or a body cavity, such as the chest cavity, near a tumor. Episcleral brachytherapy, which may be used to treat melanoma inside the eye, may use a source that is attached to the eye. In brachytherapy, radioactive isotopes can be sealed in tiny pellets or “seeds.” These seeds may be placed in patients using delivery devices, such as needles, catheters, or some other type of carrier. As the isotopes decay naturally, they give off radiation that may damage nearby cancer cells. Brachytherapy may be able to deliver higher doses of radiation to some cancers than external-beam radiation therapy while causing less damage to normal tissue.

[00264] Brachytherapy can be given as a low-dose-rate or a high-dose-rate treatment. In low-dose-rate treatment, cancer cells receive continuous low-dose radiation from the source over a period of several days. In high-dose-rate treatment, a robotic machine attached to delivery tubes placed inside the body may guide one or more radioactive sources into or near a tumor, and then removes the sources at the end of each treatment session. High-dose-rate treatment can be given in one or more treatment sessions. An example of a high-dose-rate treatment is the MammoSite® system. Brachytherapy may be used to treat patients with breast cancer who have undergone breast-conserving surgery.

[00265] The placement of brachytherapy sources can be temporary or permanent. For permanent brachytherapy, the sources may be surgically sealed within the body and left there, even after all of the radiation has been given off. In some instances, the remaining material (in which the radioactive isotopes were sealed) does not cause any discomfort or harm to the patient. Permanent brachytherapy is a type of low-dose-rate brachytherapy. For temporary brachytherapy, tubes (catheters) or other carriers are used to deliver the radiation sources, and both the carriers and the radiation sources are removed after treatment. Temporary brachytherapy can be either low-dose-rate or high-dose-rate treatment. Brachytherapy may be used alone or in addition to external-beam radiation therapy to provide a “boost” of radiation to a tumor while sparing surrounding normal tissue.

[00266] In systemic radiation therapy, a patient may swallow or receive an injection of a radioactive substance, such as radioactive iodine or a radioactive substance bound to a monoclonal antibody. Radioactive iodine (131I) is a type of systemic radiation therapy commonly used to help treat cancer, such as thyroid cancer. Thyroid cells naturally take up radioactive iodine. For systemic radiation therapy for some other types of cancer, a monoclonal antibody may help target the radioactive substance to the right place. The antibody joined to the radioactive substance travels through the blood, locating and killing tumor cells. For example, the drug ibritumomab tiuxetan (Zevalin®) may be used for the treatment of certain types of B-cell non-Hodgkin lymphoma (NHL). The antibody part of this drug recognizes and binds to a protein found on the surface of B lymphocytes. The combination drug regimen of tositumomab and iodine I 131 tositumomab (Bexxar®) may be used for the treatment of certain types of cancer, such as

NHL. In this regimen, nonradioactive tositumomab antibodies may be given to patients first, followed by treatment with tositumomab antibodies that have ¹³¹I attached. Tositumomab may recognize and bind to the same protein on B lymphocytes as ibritumomab. The nonradioactive form of the antibody may help protect normal B lymphocytes from being damaged by radiation from ¹³¹I.

[00267] Some systemic radiation therapy drugs relieve pain from cancer that has spread to the bone (bone metastases). This is a type of palliative radiation therapy. The radioactive drugs samarium-153-lexidronam (Quadramet®) and strontium-89 chloride (Metastron®) are examples of radiopharmaceuticals may be used to treat pain from bone metastases.

[00268] In certain cases, radiation therapy is combined with a chemotherapeutic agent. Examples of chemotherapeutic agents which are used in combination with radiation to treat bladder cancer include Cisplatin; Cisplatin plus fluorouracil (5-FU); and Mitomycin with 5-FU.

[00269] Biological therapy (sometimes called immunotherapy, biotherapy, or biological response modifier (BRM) therapy) uses the body's immune system, either directly or indirectly, to fight cancer or to lessen the side effects that may be caused by some cancer treatments. Biological therapies include interferons, interleukins, colony-stimulating factors, monoclonal antibodies, vaccines, gene therapy, and nonspecific immunomodulating agents.

[00270] Interferons (IFNs) are types of cytokines that occur naturally in the body. Interferon alpha, interferon beta, and interferon gamma are examples of interferons that may be used in cancer treatment.

[00271] Like interferons, interleukins (ILs) are cytokines that occur naturally in the body and can be made in the laboratory. Many interleukins have been identified for the treatment of cancer. For example, interleukin-2 (IL-2 or aldesleukin), interleukin 7, and interleukin 12 have may be used as an anti-cancer treatment. IL-2 may stimulate the growth and activity of many immune cells, such as lymphocytes, that can destroy cancer cells. Interleukins may be used to treat a number of cancers, including leukemia, lymphoma, and brain, colorectal, ovarian, breast, kidney and bladder cancers.

[00272] Colony-stimulating factors (CSFs) (sometimes called hematopoietic growth factors) may also be used for the treatment of cancer. Some examples of CSFs include, but are not limited to, G-CSF (filgrastim) and GM-CSF (sargramostim). CSFs may promote the division of bone marrow stem cells and their development into white blood cells, platelets, and red blood cells. Bone marrow is critical to the body's immune system because it is the source of all blood cells. Because anticancer drugs can damage the body's ability to make white blood cells, red blood cells, and platelets, stimulation of the immune system by CSFs may benefit patients undergoing other anti-cancer treatment, thus CSFs may be combined with other anti-cancer therapies, such as chemotherapy. CSFs may be used to treat a large variety of cancers, including lymphoma, leukemia, multiple myeloma, melanoma, and cancers of the brain, lung, bladder, esophagus, breast, uterus, ovary, prostate, kidney, colon, and rectum.

[00273] Another type of biological therapy includes monoclonal antibodies (MOABs or MoABs). These antibodies may be produced by a single type of cell and may be specific for a particular antigen. To create MOABs, a human cancer cells may be injected into mice. In response, the mouse immune system can make antibodies against these cancer cells. The mouse plasma cells that produce antibodies may be isolated and fused with laboratory-grown cells to create “hybrid” cells called hybridomas. Hybridomas can indefinitely produce large quantities of these pure antibodies, or MOABs. MOABs may be used in cancer treatment in a number of ways. For instance, MOABs that react with specific types of cancer may enhance a patient's immune response to the cancer. MOABs can be programmed to act against cell growth factors, thus interfering with the growth of cancer cells.

[00274] MOABs may be linked to other anti-cancer therapies such as chemotherapeutics, radioisotopes (radioactive substances), other biological therapies, or other toxins. When the antibodies latch onto cancer cells, they deliver these anti-cancer therapies directly to the tumor, helping to destroy it. MOABs carrying radioisotopes may also prove useful in diagnosing certain cancers, such as bladder, colorectal, ovarian, and prostate.

[00275] Rituxan® (rituximab) and Herceptin® (trastuzumab) are examples of MOABs that may be used as a biological therapy. Rituxan may be used for the treatment of non-Hodgkin lymphoma. Herceptin can be used to treat metastatic breast cancer in patients with tumors that produce excess amounts of a protein called HER2. Alternatively, MOABs may be used to treat lymphoma, leukemia, melanoma, and cancers of the brain, breast, lung, kidney, colon, bladder, rectum, ovary, prostate, and other areas.

[00276] Cancer vaccines are another form of biological therapy. Cancer vaccines may be designed to encourage the patient's immune system to recognize cancer cells. Cancer vaccines may be designed to treat existing cancers (therapeutic vaccines) or to prevent the development of cancer (prophylactic vaccines). Therapeutic vaccines may be injected in a person after cancer is diagnosed. These vaccines may stop the growth of existing tumors, prevent cancer from recurring, or eliminate cancer cells not killed by prior treatments. Cancer vaccines given when the tumor is small may be able to eradicate the cancer. On the other hand, prophylactic vaccines are given to healthy individuals before cancer develops. These vaccines are designed to stimulate the immune system to attack viruses that can cause cancer. By targeting these cancer-causing viruses, development of certain cancers may be prevented. For example, cervarix and gardasil are vaccines to treat human papilloma virus and may prevent cervical cancer. Therapeutic vaccines may be used to treat melanoma, lymphoma, leukemia, and cancers of the brain, breast, lung, kidney, ovary, prostate, pancreas, bladder, colon, and rectum. Cancer vaccines can be used in combination with other anti-cancer therapies.

[00277] Gene therapy is another example of a biological therapy. Gene therapy may involve introducing genetic material into a person's cells to fight disease. Gene therapy methods may improve a patient's

immune response to cancer. For example, a gene may be inserted into an immune cell to enhance its ability to recognize and attack cancer cells. In another approach, cancer cells may be injected with genes that cause the cancer cells to produce cytokines and stimulate the immune system.

[00278] In some instances, biological therapy includes nonspecific immunomodulating agents.

Nonspecific immunomodulating agents are substances that stimulate or indirectly augment the immune system. Often, these agents target key immune system cells and may cause secondary responses such as increased production of cytokines and immunoglobulins. Two nonspecific immunomodulating agents used in cancer treatment are bacillus Calmette-Guerin (BCG) and levamisole. BCG may be used in the treatment of superficial bladder cancer following surgery. BCG may work by stimulating an inflammatory, and possibly an immune, response. A solution of BCG may be instilled in the bladder. Levamisole is sometimes used along with fluorouracil (5-FU) chemotherapy in the treatment of stage III (Dukes' C) colon cancer following surgery. Levamisole may act to restore depressed immune function.

[00279] Photodynamic therapy (PDT) is an anti-cancer treatment that may use a drug, called a photosensitizer or photosensitizing agent, and a particular type of light. When photosensitizers are exposed to a specific wavelength of light, they may produce a form of oxygen that kills nearby cells. A photosensitizer may be activated by light of a specific wavelength. This wavelength determines how far the light can travel into the body. Thus, photosensitizers and wavelengths of light may be used to treat different areas of the body with PDT.

[00280] In the first step of PDT for cancer treatment, a photosensitizing agent may be injected into the bloodstream. The agent may be absorbed by cells all over the body but may stay in cancer cells longer than it does in normal cells. Approximately 24 to 72 hours after injection, when most of the agent has left normal cells but remains in cancer cells, the tumor can be exposed to light. The photosensitizer in the tumor can absorb the light and produces an active form of oxygen that destroys nearby cancer cells. In addition to directly killing cancer cells, PDT may shrink or destroy tumors in two other ways. The photosensitizer can damage blood vessels in the tumor, thereby preventing the cancer from receiving necessary nutrients. PDT may also activate the immune system to attack the tumor cells.

[00281] The light used for PDT can come from a laser or other sources. Laser light can be directed through fiber optic cables (thin fibers that transmit light) to deliver light to areas inside the body. For example, a fiber optic cable can be inserted through an endoscope (a thin, lighted tube used to look at tissues inside the body) into the lungs or esophagus to treat cancer in these organs. Other light sources include light-emitting diodes (LEDs), which may be used for surface tumors, such as skin cancer. PDT is usually performed as an outpatient procedure. PDT may also be repeated and may be used with other therapies, such as surgery, radiation, or chemotherapy.

[00282] Extracorporeal photopheresis (ECP) is a type of PDT in which a machine may be used to collect the patient's blood cells. The patient's blood cells may be treated outside the body with a photosensitizing agent, exposed to light, and then returned to the patient. ECP may be used to help lessen the severity of skin symptoms of cutaneous T-cell lymphoma that has not responded to other therapies. ECP may be used to treat other blood cancers, and may also help reduce rejection after transplants.

[00283] Additionally, photosensitizing agent, such as porfimer sodium or Photofrin®, may be used in PDT to treat or relieve the symptoms of esophageal cancer and non-small cell lung cancer. Porfimer sodium may relieve symptoms of esophageal cancer when the cancer obstructs the esophagus or when the cancer cannot be satisfactorily treated with laser therapy alone. Porfimer sodium may be used to treat non-small cell lung cancer in patients for whom the usual treatments are not appropriate, and to relieve symptoms in patients with non-small cell lung cancer that obstructs the airways. Porfimer sodium may also be used for the treatment of precancerous lesions in patients with Barrett esophagus, a condition that can lead to esophageal cancer.

[00284] Laser therapy may use high-intensity light to treat cancer and other illnesses. Lasers can be used to shrink or destroy tumors or precancerous growths. Lasers are most commonly used to treat superficial cancers (cancers on the surface of the body or the lining of internal organs) such as basal cell skin cancer and the very early stages of some cancers, such as cervical, penile, vaginal, vulvar, and non-small cell lung cancer.

[00285] Lasers may also be used to relieve certain symptoms of cancer, such as bleeding or obstruction. For example, lasers can be used to shrink or destroy a tumor that is blocking a patient's trachea (windpipe) or esophagus. Lasers also can be used to remove colon polyps or tumors that are blocking the colon or stomach.

[00286] Laser therapy is often given through a flexible endoscope (a thin, lighted tube used to look at tissues inside the body). The endoscope is fitted with optical fibers (thin fibers that transmit light). It is inserted through an opening in the body, such as the mouth, nose, anus, or vagina. Laser light is then precisely aimed to cut or destroy a tumor.

[00287] Laser-induced interstitial thermotherapy (LITT), or interstitial laser photocoagulation, also uses lasers to treat some cancers. LITT is similar to a cancer treatment called hyperthermia, which uses heat to shrink tumors by damaging or killing cancer cells. During LITT, an optical fiber is inserted into a tumor. Laser light at the tip of the fiber raises the temperature of the tumor cells and damages or destroys them. LITT is sometimes used to shrink tumors in the liver.

[00288] Laser therapy can be used alone, but most often it is combined with other treatments, such as surgery, chemotherapy, or radiation therapy. In addition, lasers can seal nerve endings to reduce pain after surgery and seal lymph vessels to reduce swelling and limit the spread of tumor cells.

[00289] Lasers used to treat cancer may include carbon dioxide (CO₂) lasers, argon lasers, and neodymium:yttrium-aluminum-garnet (Nd:YAG) lasers. Each of these can shrink or destroy tumors and can be used with endoscopes. CO₂ and argon lasers can cut the skin's surface without going into deeper layers. Thus, they can be used to remove superficial cancers, such as skin cancer. In contrast, the Nd:YAG laser is more commonly applied through an endoscope to treat internal organs, such as the uterus, esophagus, and colon. Nd:YAG laser light can also travel through optical fibers into specific areas of the body during LITT. Argon lasers are often used to activate the drugs used in PDT.

[00290] Target sequences can be grouped so that information obtained about the set of target sequences in the group can be used to make or assist in making a clinically relevant judgment such as a diagnosis, prognosis, or treatment choice.

[00291] A patient report is also provided comprising a representation of measured expression levels of a plurality of target sequences in a biological sample from the patient, wherein the representation comprises expression levels of target sequences corresponding to any one, two, three, four, five, six, eight, ten, twenty, thirty, fifty or more of the target sequences corresponding to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440, the subsets described herein, or a combination thereof. A patient report is also provided comprising a representation of measured expression levels of a plurality of target sequences in a biological sample from the patient, wherein the representation comprises expression levels of target sequences corresponding to 40, 50, 60, 70, 80, 90, 100 or more of the target sequences corresponding to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440, the subsets described herein, or a combination thereof. or more coding targets and/or non-coding targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. A patient report is also provided comprising a representation of measured expression levels of a plurality of target sequences in a biological sample from the patient, wherein the representation comprises expression levels of target sequences corresponding to 100, 125, 150, 175, 200, 225, 250, 275, 300 or more of the target sequences corresponding to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440, the subsets described herein, or a combination thereof. A patient report is also provided comprising a representation of measured expression levels of a plurality of target sequences in a biological sample from the patient, wherein the representation comprises expression levels of target sequences corresponding to 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600 or more of the target sequences corresponding to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440, the subsets described herein, or a combination thereof. A patient report is also provided comprising a representation of measured expression levels of a plurality of target sequences in a biological sample from the patient, wherein the representation comprises expression levels of target sequences corresponding to 600, 625, 650, 675, 700, 725, 750, 775, 800, 825, 850 or more of the target sequences corresponding to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440, the subsets

described herein, or a combination thereof. In some embodiments, the representation of the measured expression level(s) may take the form of a linear or nonlinear combination of expression levels of the target sequences of interest. The patient report may be provided in a machine (e.g., a computer) readable format and/or in a hard (paper) copy. The report can also include standard measurements of expression levels of said plurality of target sequences from one or more sets of patients with known disease status and/or outcome. The report can be used to inform the patient and/or treating physician of the expression levels of the expressed target sequences, the likely medical diagnosis and/or implications, and optionally may recommend a treatment modality for the patient.

[00292] Also provided are representations of the gene expression profiles useful for treating, diagnosing, prognosticating, and otherwise assessing disease. In some embodiments, these profile representations are reduced to a medium that can be automatically read by a machine such as computer readable media (magnetic, optical, and the like). The articles can also include instructions for assessing the gene expression profiles in such media. For example, the articles may comprise a readable storage form having computer instructions for comparing gene expression profiles of the portfolios of genes described above. The articles may also have gene expression profiles digitally recorded therein so that they may be compared with gene expression data from patient samples. Alternatively, the profiles can be recorded in different representational format. A graphical recordation is one such format. Clustering algorithms can assist in the visualization of such data.

Exemplary embodiments

[00293] Disclosed herein, in some embodiments, is a method for diagnosing, predicting, and/or monitoring a status or outcome of a cancer a subject, comprising: (a) assaying an expression level of a plurality of targets in a sample from the subject, wherein at least one target of the plurality of targets is selected from the group consisting of targets identified in Table 1; and (b) for diagnosing, predicting, and/or monitoring a status or outcome of a cancer based on the expression levels of the plurality of targets. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a bladder cancer. In some embodiments, the cancer is a lung

cancer. In some embodiments, the method further comprises assaying an expression level of a coding target. In some instances, the coding target is selected from the group consisting of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the coding target is an exon-coding transcript. In some embodiments, the exon-coding transcript is an exonic sequence. In some embodiments, the method further comprises assaying an expression level of a non-coding target. In some instances, the non-coding target is selected from the group consisting of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the non-coding target is a non-coding transcript. In other instances, the non-coding target is an intronic sequence. In other instances, the non-coding target is an intergenic sequence. In some instances, the non-coding target is a UTR sequence. In other instances, the non-coding target is a non-coding RNA transcript. In some embodiments, the target comprises a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In other instances, the target comprises a polypeptide sequence. In some instances, the plurality of targets comprises 2 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 5 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 10 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 15 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 20 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 25 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 30 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 35 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 40 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, assaying the expression level comprises detecting and/or quantifying a nucleotide sequence of the plurality of targets. Alternatively, assaying the expression level comprises detecting and/or quantifying a polypeptide sequence of the plurality of targets. In some embodiments, assaying the expression level comprises detecting and/or quantifying the DNA levels of the plurality of targets. In some embodiments, assaying the expression level comprises detecting and/or quantifying the RNA or mRNA levels of the plurality of targets. In some embodiments, assaying the expression level comprises detecting and/or quantifying the protein level of the plurality of targets. In some embodiments, the diagnosing, predicting, and/or monitoring the status or outcome of a cancer

comprises determining the malignancy of the cancer. In some embodiments, the diagnosing, predicting, and/or monitoring the status or outcome of a cancer includes determining the stage of the cancer. In some embodiments, the diagnosing, predicting, and/or monitoring the status or outcome of a cancer includes assessing the risk of cancer recurrence. In some embodiments, diagnosing, predicting, and/or monitoring the status or outcome of a cancer may comprise determining the efficacy of treatment. In some embodiments, diagnosing, predicting, and/or monitoring the status or outcome of a cancer may comprise determining a therapeutic regimen. Determining a therapeutic regimen may comprise administering an anti-cancer therapeutic. Alternatively, determining the treatment for the cancer may comprise modifying a therapeutic regimen. Modifying a therapeutic regimen may comprise increasing, decreasing, or terminating a therapeutic regimen.

[00294] Further disclosed, is method for determining a treatment for a cancer in a subject, comprising: a) assaying an expression level of a plurality of targets in a sample from the subject, wherein at least one target of the plurality of targets is selected from the group consisting of targets identified in Table 1; and b) determining the treatment for a cancer based on the expression levels of the plurality of targets. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a bladder cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the coding target is selected from a sequence listed in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the method further comprises assaying an expression level of a coding target. In some instances, the coding target is selected from the group consisting of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the coding target is an exon-coding transcript. In some embodiments, the exon-coding transcript is an exonic sequence. In some embodiments, the method further comprises assaying an expression level of a non-coding target. In some instances, the non-coding target is selected from the group consisting of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the non-coding target is a non-coding transcript. In other instances, the non-coding target is an intronic sequence. In other instances, the non-coding target is an intergenic sequence. In some instances, the non-coding target is a UTR sequence. In other instances, the non-coding target is a non-coding RNA

transcript. In some embodiments, the target comprises a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In other instances, the target comprises a polypeptide sequence. In some instances, the plurality of targets comprises 2 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 5 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 10 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 15 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 20 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 25 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 30 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 35 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 40 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, assaying the expression level comprises detecting and/or quantifying a nucleotide sequence of the plurality of targets. In some embodiments, determining the treatment for the cancer includes determining the efficacy of treatment. Determining the treatment for the cancer may comprise administering an anti-cancer therapeutic. Alternatively, determining the treatment for the cancer may comprise modifying a therapeutic regimen. Modifying a therapeutic regimen may comprise increasing, decreasing, or terminating a therapeutic regimen.

[00295] The methods use the probe sets, probes and primers described herein to provide expression signatures or profiles from a test sample derived from a subject having or suspected of having cancer. In some embodiments, such methods involve contacting a test sample with a probe set comprising a plurality of probes under conditions that permit hybridization of the probe(s) to any target nucleic acid(s) present in the test sample and then detecting any probe:target duplexes formed as an indication of the presence of the target nucleic acid in the sample. Expression patterns thus determined are then compared to one or more reference profiles or signatures. Optionally, the expression pattern can be normalized. The methods use the probe sets, probes and primers described herein to provide expression signatures or profiles from a test sample derived from a subject to classify the cancer as recurrent or non-recurrent.

[00296] In some embodiments, such methods involve the specific amplification of target sequences nucleic acid(s) present in the test sample using methods known in the art to generate an expression profile or signature which is then compared to a reference profile or signature.

[00297] In some embodiments, the invention further provides for prognosing patient outcome, predicting likelihood of recurrence after cystectomy and/or for designating treatment modalities.

[00298] In one embodiment, the methods generate expression profiles or signatures detailing the expression of the target sequences having altered relative expression with different cancer outcomes. In some embodiments, the methods detect combinations of expression levels of sequences exhibiting positive and negative correlation with a disease status. In one embodiment, the methods detect a minimal expression signature.

[00299] The gene expression profiles of each of the target sequences comprising the portfolio can be fixed in a medium such as a computer readable medium. This can take a number of forms. For example, a table can be established into which the range of signals (e.g., intensity measurements) indicative of disease or outcome is input. Actual patient data can then be compared to the values in the table to determine the patient samples diagnosis or prognosis. In a more sophisticated embodiment, patterns of the expression signals (e.g., fluorescent intensity) are recorded digitally or graphically.

[00300] The expression profiles of the samples can be compared to a control portfolio. The expression profiles can be used to diagnose, predict, or monitor a status or outcome of a cancer. For example, diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise diagnosing or detecting a cancer, cancer metastasis, or stage of a cancer. In other instances, diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise predicting the risk of cancer recurrence. Alternatively, diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise predicting mortality or morbidity.

[00301] Further disclosed herein are methods for characterizing a patient population. Generally, the method comprises: (a) providing a sample from a subject; (b) assaying the expression level for a plurality of targets in the sample; and (c) characterizing the subject based on the expression level of the plurality of targets. In some embodiments, the method further comprises assaying an expression level of a coding target. In some instances, the coding target is selected from the group consisting of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the coding target is an exon-coding transcript. In some embodiments, the exon-coding transcript is an exonic sequence. In some embodiments, the method further comprises assaying an expression level of a non-coding target. In some instances, the non-coding target is selected from the group consisting of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the non-coding target is a non-coding transcript. In other instances, the non-coding target is an intronic sequence. In other instances, the non-coding target is

an intergenic sequence. In some instances, the non-coding target is a UTR sequence. In other instances, the non-coding target is a non-coding RNA transcript. In some embodiments, the target comprises a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In other instances, the target comprises a polypeptide sequence. In some instances, the plurality of targets comprises 2 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 5 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 10 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 15 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 20 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 25 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 30 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 35 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 40 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, assaying the expression level comprises detecting and/or quantifying a nucleotide sequence of the plurality of targets. In some instances, the method may further comprise diagnosing a cancer in the subject. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a bladder cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some instances, characterizing the subject comprises determining whether the subject would respond to an anti-cancer therapy. Alternatively, characterizing the subject comprises identifying the subject as a non-responder to an anti-cancer therapy. Optionally, characterizing the subject comprises identifying the subject as a responder to an anti-cancer therapy.

[00302] Further disclosed herein are methods for selecting a subject suffering from a cancer for enrollment into a clinical trial. Generally, the method comprises: (a) providing a sample from a subject; (b) assaying the expression level for a plurality of targets in the sample; and (c) characterizing the subject based on the expression level of the plurality of targets. In some embodiments, the method further comprises assaying an expression level of a coding target. In some instances, the coding target is selected from the group consisting of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the coding target is an exon-coding transcript. In some embodiments, the exon-coding transcript is an exonic sequence. In some embodiments, the method further comprises assaying an expression level of a non-coding target. In some instances, the non-coding target is selected from the group consisting of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the non-coding target is a non-coding transcript. In other instances, the non-coding target is an intronic sequence. In other instances, the non-coding target is an intergenic sequence. In some instances, the non-coding target is a UTR sequence. In other instances, the non-coding target is a non-coding RNA transcript. In some embodiments, the target comprises a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In other instances, the target comprises a polypeptide sequence. In some instances, the plurality of targets comprises 2 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 5 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 10 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 15 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 20 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 25 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 30 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 35 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some instances, the plurality of targets comprises 40 or more targets selected from the group of targets identified in Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, assaying the expression level comprises detecting and/or quantifying a nucleotide sequence of the plurality of targets. In some instances, the method may further comprise diagnosing a cancer in the subject. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the

group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the bladder cancer is non-invasive bladder cancer, muscle-invasive bladder cancer, or advanced bladder cancer. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a bladder cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some instances, characterizing the subject comprises determining whether the subject would respond to an anti-cancer therapy. Alternatively, characterizing the subject comprises identifying the subject as a non-responder to an anti-cancer therapy. Optionally, characterizing the subject comprises identifying the subject as a responder to an anti-cancer therapy.

[00303] Further disclosed herein is a method of analyzing a cancer in an individual in need thereof, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; and (b) comparing the expression profile from the sample to an expression profile of a control or standard. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, wherein the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the method further comprises providing diagnostic or prognostic information to the individual about the cardiovascular disorder based on the comparison. In some embodiments, the method further comprises diagnosing the individual with a cancer if the expression profile of the sample (a) deviates from the control or standard from a healthy individual or population of healthy individuals, or (b) matches the control or standard from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises predicting the susceptibility of the individual for developing a cancer based on (a) the deviation of the expression profile of the sample from a control or

standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises prescribing a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises altering a treatment regimen prescribed or administered to the individual based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises predicting the individual's response to a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the deviation is the expression level of one or more targets from the sample is greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Table 2B, Table 16 or SEQ ID NOs: 1-1440 or a combination thereof. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score

that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

[00304] Also disclosed herein is a method of diagnosing cancer in an individual in need thereof, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) diagnosing a cancer in the individual if the expression profile of the sample (i) deviates from the control or standard from a healthy individual or population of healthy individuals, or (ii) matches the control or standard from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, wherein the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises

contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

[00305] In some embodiments is a method of predicting whether an individual is susceptible to developing a cancer, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 1; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) predicting the susceptibility of the individual for developing a cancer based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, wherein the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or

population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

[00306] In some embodiments is a method of predicting an individual's response to a treatment regimen for a cancer, comprising: (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) predicting the individual's response to a treatment regimen based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, wherein the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some

embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

[00307] A method of prescribing a treatment regimen for a cancer to an individual in need thereof, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) prescribing a treatment regimen based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived

from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of one or more targets from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

[00308] Further disclosed herein is a kit for analyzing a cancer, comprising (a) a probe set comprising a plurality of target sequences, wherein the plurality of target sequences comprises at least one target sequence listed in Table 2B, Table 16 or SEQ ID NOs:1-1440; and (b) a computer model or algorithm for analyzing an expression level and/or expression profile of the target sequences in a sample. In some embodiments, the kit further comprises a computer model or algorithm for correlating the expression level or expression profile with disease state or outcome. In some embodiments, the kit further comprises a computer model or algorithm for designating a treatment modality for the individual. In some embodiments, the kit further comprises a computer model or algorithm for normalizing expression level or expression profile of the target sequences. In some embodiments, the kit further comprises a computer model or algorithm comprising a robust multichip average (RMA), frozen robust multichip average (fRMA), Single Channel Array Normalization (SCAN), ComBat (Combining Batches of gene expression), probe logarithmic intensity error estimation (PLIER), non-linear fit (NLFIT) quantile-based, nonlinear normalization, or a combination thereof. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.

[00309] Further disclosed herein is a system for analyzing a cancer, comprising (a) one or more probe sets comprising a plurality of target sequences, wherein (i) the plurality of target sequences hybridizes to one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; or (ii) the plurality of target sequences comprises one or more target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; and (b) a computer model or algorithm for analyzing an expression level and/or expression profile of the target hybridized to the probe in a sample from a subject suffering from a cancer. In some embodiments, the system further comprises electronic memory for capturing and storing an expression profile. In some embodiments, the system further comprises a computer-processing device, optionally connected to a computer network. In some embodiments, the system further comprises a software module executed by the computer-processing device to analyze an expression profile. In some embodiments, the system further comprises a software module executed by the computer-processing device to compare the expression profile to a standard or control. In some embodiments, the system further comprises a software

module executed by the computer-processing device to determine the expression level of the target. In some embodiments, the system further comprises a machine to isolate the target or the probe from the sample. In some embodiments, the system further comprises a machine to sequence the target or the probe. In some embodiments, the system further comprises a machine to amplify the target or the probe. In some embodiments, the system further comprises a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the system further comprises a software module executed by the computer-processing device to transmit an analysis of the expression profile to the individual or a medical professional treating the individual. In some embodiments, the system further comprises a software module executed by the computer-processing device to transmit a diagnosis or prognosis to the individual or a medical professional treating the individual. In some embodiments, the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the plurality of targets comprises at least 20 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.

EXAMPLES

Example 1: A 15 Marker Genomic Classifier Predicts Risk for Recurrence After Cystectomy in Muscle Invasive Bladder Cancer Patients.

[00310] A 15-marker genomic classifier containing biologically relevant RNA sequences using FFPE tumor tissue specimens obtained from a large cohort of patients who underwent radical cystectomy for muscle invasive bladder cancer was developed as follows. Bladder cancer patients who underwent radical cystectomy with curative intent formed the primary source of study material. From this population, a representative set of 225 patients with organ-confined, muscle-invasive (pT2N0M0), extravesical (pT3-4aN0M0), and node-positive (pTanyN1-3M0) UCB was identified. Each patient had a minimum post-cystectomy follow-up of two years unless they died of UCB prior to that date. Two-thirds of the cohort of 225 patients were assigned to a discovery set and the balance one-third to a validation set. The clinical end-point used to select discover biomarkers was recurrence-free survival (RFS) duration.

Specimen processing and initial microarray analysis

[00311] Archival formalin-fixed paraffin-embedded (FFPE) primary tumor specimens of the 225 study patients were obtained for histopathological re-review. Hematoxylin/eosin-stained sections were used to guide tumor specimen selection using a 1 mm diameter core tissue microarray punch tool (Beecher Instruments, Sun Prairie, WI). Total RNA was extracted and purified using RNeasy FFPE kit (Qiagen, Valencia, CA). RNA was amplified and labeled using the Ovation WTA FFPE system (NuGen, San Carlos, CA) and hybridized to Human Exon 1.0 ST microarrays (Affymetrix, Santa Clara, CA) according to the manufacturer's recommendations. Human Exon GeneChips profile coding and non-coding regions of the entire human transcriptome using probe selection regions (PSRs), hereinafter referred to as features.

Patient cohorts, classifier development and application

[00312] Samples from 199 (88.4%) patient specimens passed microarray quality control. To identify features most clinically relevant to RFS, area under the receiver-operating characteristic (ROC) curve, t-test statistics and median fold difference (MFD) were calculated in the discovery cohort. Based on these metrics, features were filtered by area under ROC curve (AUC) >0.6, unadjusted t-test $P < 0.050$ and MFD >1.5. Selected features were combined to produce a genomic classifier (GC) score using a random forest algorithm with 50,000 trees based on the discovery set. Each tree generated by the random forest algorithm was based on a bootstrapped subset of the discovery set. In each bootstrapping iteration, an "out-of-bag" subset of patients was excluded from the creation of the decision tree. The out-of-bag error rate was estimated based on the misclassification rate of this group. The selection of random forest mtry and nodesize parameters was based on minimizing the out-of-bag error rate. The GC outputs a continuous score between 0 and 1, with higher scores indicating higher probability of recurrence.

[00313] The prognostic ability of GC was benchmarked against two clinical nomograms: the International Bladder Cancer Nomogram Consortium (IBCNC) (Bochner et al. 2006) and an in-house "clinical-only" classifier (CC). The latter was developed on the discovery set and incorporated age, gender, pathological stage, and lymphovascular invasion status modeled using logistic regression. Additionally, to evaluate the joint prognostic value of genomic information and clinicopathologic variables, GC was combined with IBCNC and CC by logistic regression in the discovery set into integrated G-IBCNC and G-CC, respectively. Analogous to GC, patients were scored using the above classifiers between 0 and 1. For CC and G-CC, interactions between different clinicopathologic factors were explored in the discovery cohort and applied to the model when significant. The locked genomic, clinical and genomic-clinical models were then applied to patients in the validation cohort in a blinded fashion.

Statistical analyses

[00314] Univariable prognostic abilities of classifiers were compared using discrimination boxplots, Wilcoxon rank-sum test and logistic regression. Cumulative incidence curves for RFS were constructed

using Fine-Gray competing risks analysis.(Fine and Gray 1999) Deaths were considered a competing risk. Concordance summary index, an extension of AUC for censored data, was also used to compare performance of genomic classifiers, external signatures and clinical nomograms with respect to RFS. For the analyses where GC was categorized, majority rule criterion with classifier scores of >0.5 and ≤ 0.5 grouped as high-risk and low-risk, respectively was used. Analyses were performed using R v2.15.2. All tests were two-sided with type I error probability of 5%.

[00315] Time-dependent survival ROC curves were evaluated for prediction of recurrence within four years post-cystectomy.(Heagerty et al. 2000) For survival ROC, the nearest-neighbor estimator with $\lambda=0.002$ was used to approximate survival function density. The 95% confidence intervals (CIs) for survival-ROC AUCs were approximated through bootstrapping. Decision curve analyses were used to assess the net clinical benefit of genomic versus clinical models across different threshold probabilities. (Vickers and Elkin 2006). Reassignment of patients to risk strata based on addition of genomic information was assessed using reclassification plots. (Pepe 2011).

[00316] Importance of genomic-based classifiers relative to individual and combined clinical information, and their independent prognostic abilities were evaluated by multivariable Cox regression models. Proportional hazards assumptions of the Cox model were confirmed by evaluating the scaled Schoenfeld residuals. (Grambsch and Therneau 1994). For univariable and multivariable analyses, classifier scores were assessed as continuous variables (step size=0.1) unless dichotomization was required. For the analyses where GC was categorized, majority rule criterion with classifier scores of >0.5 and ≤ 0.5 grouped as high-risk and low-risk, respectively was used. Estimates of censoring distribution were used to calculate follow-up duration. (Korn 1986).

Analysis of biological interactions between prognostic markers

[00317] To understand the biological interactions of constituent markers within GC, first-degree partners of their respective genes were extracted using the Human Signaling Network v5, a curated database with nearly 63,000 directed and undirected interactions between approximately 6,300 proteins.(Cui et al. 2007) Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.7 was used to assess biological processes, molecular functions and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways of the gene network.(Kanehisa et al. 2004; Huang et al. 2009b; Huang et al. 2009a) Enriched processes, molecular functions or KEGG pathways with Benjamini-Hochberg-corrected $P<0.05$ were selected.(Benjamini and Hochberg 1995) Enrichment Map, a network-based gene set enrichment visualization method implemented as a Cytoscape plugin, was used to visualize the highly enriched biological concepts and group similar terms together.(Merico et al. 2010) Nodes in the Enrichment Map represent individual Gene Ontology (GO) terms or KEGG pathways and lines represent the amount of overlap between the terms..

Discovery and initial performance of genomic-based classifiers

[00318] To test the hypothesis that risk prediction models incorporating genomic expression signatures which may better characterize the biology that determines the propensity of tumor recurrence post-cystectomy than clinical variables alone, a genomic classifier (GC) was developed and tested on the discovery set. Clinical characteristics of the cohort of patients analyzed are listed in Table 1. Median patient age was 68.5 (IQR: 63.6-75.6) years. Median follow-up was 9.2 years; 68 (51.1%) patients recurred and 77 (57.9%) patients were dead at last follow-up.

[00319] Expressions of nearly 1.4 million RNA features in tumors of patients who recurred were compared to those who remained recurrence-free at last follow-up. Following normalization and feature selection, 15 markers were identified corresponding to RNAs from protein-coding and non-coding regions of the genome that were differentially expressed based on recurrence (Table 2A, Table 2B). A random forest machine-learning algorithm assembled these markers into a GC that assigned a score to each patient. GC performance was compared to that of individual clinicopathologic variables, the IBCNC postoperative nomogram, (Bochner et al. 2006) and a clinical-only classifier (CC) that represented an optimized clinicopathologic prognostic model developed on the discovery set.

[00320] GC had an AUC of 0.88 (95% CI: 0.81-0.93) in the discovery set, with *ENAH* being the most prognostic individual marker within the signature (AUC=0.66). The performance of GC was higher than any individual clinicopathologic variable such as tumor and nodal stages, and lymphovascular invasion status (Figure 1). The IBCNC and CC clinical risk prediction models had AUCs of 0.73 and 0.81, respectively. To examine whether the combination of clinical and genomic risk prediction models could boost model performance for prediction of recurrence GC was combined with IBCNC (G-IBCNC) and CC (G-CC). AUCs of these combined models in the discovery cohort were 0.89 (95% CI: 0.84-0.95) and 0.93 (95% CI: 0.88-0.97), respectively.

Independent validation of genomic-based classifiers

[00321] The prognostic performance of the locked classifiers was then assessed (with bioinformaticians blinded to clinical variables) on an independent validation set of 66 UCB patients. Clinical characteristics of patients in the validation and discovery sets were comparable (Table 1). Median patient age was 69.8 (IQR: 63.1-74.3) years. Median follow-up was 10.8 years; 33 (50%) patients recurred and 45 (68.2%) patients were dead by end of follow-up. By univariate analysis, GC ($P=0.003$), nodal status ($P=0.006$) and LVI ($P=0.005$) were prognostic for RFS, with GC having the highest hazard ratio (1.23 per every 10% increase in GC score; Table 3). GC performance as measured by standard ROC analysis was superior to single clinicopathologic variables (Figure 1). This was confirmed by survival ROC analysis where AUC for GC (0.77; 95% CI: 0.65-0.90) was higher than any individual clinicopathologic variable (Figure 2A).

TABLE 1

	Discovery Cohort			Not recurred vs. Recurred P	Validation Cohort			Not recurred vs. Recurred P	Discovery vs. Validation P
	Total	Not recurred	Recurred		Total	Not recurred	Recurred		
	n (cohort %)	n (column %)*	n (column %)*		n (cohort %)	n (column %)*	n (column %)*		
Cohort (row %)	133 (100)	65 (48.9)	68 (51.1)		66 (100)	33 (50.0)	33 (50.0)		
Age				0.49				1.00	0.55
<70 years	73 (54.9)	38 (58.5)	35 (51.5)		33 (50.0)	17 (51.5)	16 (48.5)		
≥70 years	60 (45.1)	27 (41.5)	33 (48.5)		33 (50.0)	16 (48.5)	17 (51.5)		
Gender				0.82				0.73	1.00
Male	111 (83.5)	55 (84.6)	56 (82.4)		56 (84.8)	29 (87.9)	27 (81.8)		
Female	22 (16.5)	10 (15.4)	12 (17.6)		10 (15.2)	4 (12.1)	6 (18.2)		
Race				0.32				0.43	0.65
Caucasian	115 (86.5)	54 (83.1)	61 (89.7)		59 (89.4)	31 (93.9)	28 (84.8)		
Non-Caucasian	18 (13.5)	11 (16.9)	7 (10.3)		7 (10.6)	2 (6.1)	5 (15.2)		
Tumor Stage				0.033				0.013	0.76
pT1	3 (2.3)	1 (1.5)	2 (3.0)		3 (4.5)	2 (6.1)	1 (3.0)		
pT2	44 (33.1)	28 (43.1)	16 (23.5)		20 (30.3)	13 (39.4)	7 (21.2)		
pT3	58 (43.6)	28 (43.1)	30 (44.1)		31 (47.0)	17 (51.5)	14 (42.4)		
pT4a	28 (21.0)	8 (12.3)	20 (29.4)		12 (18.2)	1 (3.0)	11 (33.3)		
Nodal Status				<0.001				0.011	0.64
N0	68 (66.2)	56 (86.2)	32 (47.1)		41 (62.1)	26 (78.8)	15 (45.5)		
N1-3	45 (33.8)	9 (13.8)	36 (52.9)		25 (37.9)	7 (21.2)	18 (54.5)		
Lymphovascular Invasion				<0.001				0.005	1.00
Absent	58 (43.6)	39 (60.6)	19 (31.7)		30 (45.5)	20 (60.6)	10 (31.3)		
Present	58 (43.6)	17 (30.4)	41 (68.3)		41 (47.0)	9 (31.0)	22 (68.7)		
Adjuvant Chemotherapy				0.022				0.22	0.17
Not administered	78 (58.6)	45 (69.2)	33 (49.4)		52 (48.5)	19 (57.6)	13 (39.4)		
Administered	54 (40.8)	20 (30.8)	34 (50.7)		34 (51.5)	14 (42.4)	20 (60.6)		
Status at Last Follow-up				<0.001				<0.001	0.17
Alive	56 (42.1)	50 (76.9)	6 (8.8)		21 (31.8)	21 (63.6)	0 (0.0)		
Dead	77 (57.9)	15 (23.1)	62 (91.2)		45 (68.2)	12 (36.4)	33 (100)		

P values based on Fisher's exact test

* Except where noted

Clinicopathologic characteristics of patients in the discovery and validation cohorts.

TABLE 2A

Feature and Type	Associated Gene	Chromosomal Location	Recurrence-specific Feature Metrics in Discovery Cohort			Important Biological Process(es)				
			AUC	t-test P	MFD	Cell proliferation/Cell cycle regulation/Apoptosis	Cell differentiation	Regulation of transcription	Signaling pathways/Signal transduction	Other
1 ^a	FOXO6	1p34.2	0.6251	0.0065	1.6514	✓		✓	✓	Angiogenesis regulation
2 ^b	HSD17B7	1q23	0.6234	0.0138	1.5401					Cholesterol metabolism
3 ^b	ARID4B	1q42.1-q43	0.6223	0.0310	1.5427			✓		Histone methylation
4 ^a	ENAH	1q42.12	0.6617	0.0028	1.6644	✓			✓	
5 ^b	MAP4K3	2p22.1	0.6067	0.0327	1.5895	✓	✓		✓	Protein ubiquitination
6 ^a	MARCKS	2q24.2	0.6020	0.0275	1.5425			✓		
7 ^c	MECOM	3q26.2	0.6434	0.0045	1.5113	✓	✓	✓	✓	
8 ^a	IRBA	4q31.3	0.6261	0.0081	1.5432	✓	✓		✓	
9 ^a	MYT	6p12.3	0.6206	0.0232	1.5150			✓	✓	Lipid metabolism
10 ^b	CRCP	7q11.21	0.6135	0.0259	1.5144	✓	✓	✓	✓	
11 ^a	SYPL1	7q22.3	0.6064	0.0485	1.5378				✓	
12 ^b	AREGEF1	8q13	0.6322	0.0354	1.5580				✓	
13 ^b	EHF	11p12	0.6437	0.0022	1.7470	✓		✓		
14 ^a	MEITL2A	12q13.12	0.6128	0.0201	1.6586			✓	✓	Methyltransferase activity
15 ^b	PPP1R12A	12q15-q21	0.6104	0.0406	1.5429	✓		✓	✓	Cell adhesion

^a Exonic feature^b Exonic antisense feature^c Intronic antisense feature

Biological processes summarized using Gene Ontology Annotation database [Dimmer EC, Huntley BP, Alam-Faruque Y, et al. The UniProt-GO Annotation database in 2011. Nucleic Acids Res 40:D565-D570, 2012].

Abbreviations: AUC, area under receiver operating characteristic curve; MFD, median fold difference.

Summary description of markers comprising the genomic classifier for predicting post-cystectomy bladder cancer recurrence.

TABLE 2B

SEQ ID NO	Affymetrix Probeset ID	Gene	Category	Chromosome	Start	End	Strand
SEQ ID NO. 1	3326487	EHF	Coding	chr11	34673110	34673157	+
SEQ ID NO. 2	2458376	ENAH	Coding	chr1	225692693	225692726	-
SEQ ID NO. 3	3414753	METTL7A	Non coding (3' UTR)	chr12	51326219	51326283	+
SEQ ID NO. 4	2332285	FOXO6	Non coding (3' UTR)	chr1	41849216	41849252	+
SEQ ID NO. 5	2478155	MAP4K3	Non coding (3' UTR Antisense)	chr2	39476662	39476964	+
SEQ ID NO. 6	3139092	ARFGEF1	Coding	chr8	68151048	68151077	-
SEQ ID NO. 7	2789391	LRBA	Coding	chr4	151791678	151791746	-
SEQ ID NO. 8	3463598	PPP1R12A	Coding	chr12	80190589	80190729	-
SEQ ID NO. 9	2461837	ARID4B	Coding	chr1	235392607	235392699	-
SEQ ID NO. 10	2512364	MARCH7	Coding	chr2	160621140	160621185	+
SEQ ID NO. 11	2364325	HSD17B7	Non coding (3' UTR)	chr1	162782497	162782521	+
SEQ ID NO. 12	3066770	SYPL1	Non coding (3' UTR)	chr7	105731011	105731149	-
SEQ ID NO. 13	2956442	MUT	Non coding (3' UTR)	chr6	49399033	49399073	-
SEQ ID NO. 14	3005357	CRCP	Non coding (3' UTR)	chr7	65619506	65619539	+
SEQ ID NO. 15	2651515	MECOM	Non coding (Intronic Antisense)	chr3	169003654	169003734	+

Genomic characteristics of markers comprising the genomic classifier for predicting post-cystectomy bladder cancer recurrence.

TABLE 3

	Relative Risk of Recurrence	
	Hazard ratio (95% CI)	P
GC	1.23 (1.07 - 1.42)	0.003
Age <70 years	1.00 (0.99 - 1.01)	0.72
Male Gender	0.97 (0.89 - 1.06)	0.46
Caucasian Race	0.95 (0.85 - 1.05)	0.29
Tumor Stage [reference: pT2]		
pT1	1.02 (0.83 - 1.26)	0.87
pT3	1.23 (0.50 - 3.05)	0.66
pT4a	3.37 (1.27 - 8.93)	0.015
Nodal Status N1-3	1.10 (1.03 - 1.19)	0.006
Lymphovascular Invasion present	1.12 (1.03 - 1.20)	0.005
Adjuvant Chemotherapy administered	1.03 (0.96 - 1.11)	0.35

Abbreviations: CI, confidence interval; GC, genomic classifier.

Univariable associations of genomic and clinicopathologic features with risk of post-cystectomy bladder cancer recurrence in the validation cohort.

[00322] Prognostic performance of IBCNC and CC were comparable (standard-ROC AUC of 0.74 and 0.77, respectively) with the genomic model in the validation set. Again, the combined genomic-clinical models measured the highest performance of models tested (Figure 1). Furthermore in survival ROC analysis (which factors in time to recurrence) the boost in performance with the combined models was more marked in terms of AUC (IBCNC versus G-IBCNC, 0.73 versus 0.82; CC versus G-CC, 0.78 versus 0.86). Figures 2B and C show that the combined genomic-clinical classifiers had the highest specificity and sensitivity across the widest range of cut-offs.

[00323] Multivariable analyses (Based on Cox proportional hazards analysis with ridge regression) showed that the independent prognostic significance of the combined genomic-clinical classifiers for predicting recurrence compared to clinical models alone (Table 4). Decision curve analysis showed a higher overall net benefit for genomic-based classifiers compared to clinical-only risk models (Figure 3). Discrimination plots confirmed that while GC identified patients who recurred better than clinical models alone, the combined G-IBCNC and G-CC models were superior at this discrimination with G-CC performing the best ($P=5.55 \times 10^{-7}$; Figure 4). G-CC was therefore considered the benchmark genomic-clinicopathologic classifier for further evaluation.

TABLE 4

	Relative Risk of Recurrence	
	Hazard ratio (95% CI)	<i>P</i>
Model 1		
G-IBCNC	1.18 (1.03 - 1.36)	0.016
IBCNC	1.04 (0.90 - 1.20)	0.62
Model 2		
G-CC	1.18 (1.04 - 1.33)	0.008
CC	1.10 (0.92 - 1.31)	0.30

Multivariable analysis comparing genomic-clinicopathologic versus clinical-only models in the validation cohort. Based on Cox proportional hazards analysis with ridge regression.

[00324] When survival-ROC AUCs were measured across a range of post-cystectomy intervals, G-CC showed consistently superior performance compared to CC and GC alone, indicating that the combined genomic-clinicopathologic classifier was the most prognostic indicator for RFS at any point in time after cystectomy (Figure 5A). Validation set patients were then categorized by G-CC score and grouped as high-risk (G-CC score > 0.5) or low-risk (G-CC score ≤ 0.5). By competing risk analysis, high-risk patients had significantly elevated recurrence probabilities compared to low-risk patients (4-year probability: 81.5% versus 20.6%, respectively; $P < 0.001$; Figure 6). Patients were similarly risk-stratified based on IBCNC and G-IBCNC scores, and categorization by the “clinical-only” IBCNC nomogram was compared with genomic-clinical classifiers (Figure 7). In Figure 7, qQuadrants in grey represent situations where the combined genomic-clinical classifier reclassifies patients compared to the clinical classifier. Patients are colored by recurrence event and size of dots represent pathological tumor stage. Patients with no recurrence in the top left quadrant are reclassified correctly while patients with recurrence in the bottom right quadrant are reclassified correctly by the genomic-clinical classifier. Of the patients that are reclassified, the majority result in correct classification. Addition of genomic features to the IBCNC

nomogram (as G-IBCNC) reclassified a total of 18 validation set patients into lower and higher predicted risk categories than those classified by IBCNC, of which 12 (66.7%) were reclassified correctly by outcome. Similarly, G-CC reclassified 12 patients that were originally risk stratified by IBCNC, of which 10 (83.3%) were reclassified correctly.

TABLE 5

	Relative Risk of Recurrence	
	Hazard ratio (95% CI)	P
GC	1.42 (1.11 - 1.81)	0.005
Age <70 years	0.90 (0.78 - 1.03)	0.12
Male Gender	0.00 (0.00 - 3.03)	0.084
Caucasian Race	0.36 (0.11 - 1.20)	0.097
Tumor Stage [reference: pT2]		
pT1	2.06 (0.15 - 27.73)	0.59
pT3	1.82 (0.61 - 5.42)	0.29
pT4a	1.83 (0.50 - 6.69)	0.36
Nodal Status N1-3	9.80 (1.50 - 64.04)	0.017
Lymphovascular Invasion present	2.74 (1.02 - 7.33)	0.045
Adjuvant Chemotherapy administered	0.94 (0.41 - 2.13)	0.88
GC × Nodal Status *	0.03 (0.00 - 0.72)	0.030
Gender × Age *	1.12 (0.98 - 1.29)	0.098

* Interaction term

Abbreviations: CI, confidence interval; GC, genomic classifier.

Multivariable associations of genomic and clinicopathologic features with risk of post-cystectomy bladder cancer recurrence in the validation cohort

Nodal status and performance of genomic-based classifier

[00325] When validation cohort patients were categorized based on pathological stage, median GC scores were consistently higher in patients who recurred compared to those who did not (Figure 8). By multivariable analysis, after adjusting for demographic, clinicopathologic and treatment covariates, GC remained prognostic for recurrence ($P=0.005$; Table 5). In this analysis, a significant interaction was noted between GC and nodal status ($P=0.030$) that prompted further exploration of GC score distribution based on nodal stage. When categorized by nodal status, GC scores were able to better discriminate validation cohort patients compared to CC (Figure 9). As shown in Figure 9, GC separates cases from controls in both LNI positive and LNI negative patients, as indicated by the non-overlapping 95% CI. In comparison, CC does not separate cases from controls as well. 95% CI calculated based on McGill et al. GC Wilcoxon rank-sum p-value for comparing case with control is 0.0078 compared CC with a p-value of 0.069 in the LNI negative patients. While in LNI positive patients, GC and CC has p-values of 0.16 and 0.41 respectively.

[00326] A subset analysis was then conducted on node-negative patients. These patients represent subjects who do not routinely receive adjuvant therapy. Assuming that higher risk patients have more to gain from therapeutic intensification in comparison to low risk, better identification of the subset of men most at risk by a more accurate risk prediction model could be beneficial. CC showed a trend towards significance in separating node-negative patients into risk groups ($P=0.051$). However, GC significantly stratified these patients based on recurrence (4-year probabilities: high 56.2% versus low 13%; $P=0.004$; Figure 10). When measured across time, AUCs for genomic-based classifiers were consistently higher compared to CC alone in node-negative patients (Figure 5B).

Analysis of prior signatures and biological processes

[00327] As the microarrays used to profile the study cohorts offer transcriptome-wide coverage including ability to interrogate entire lengths of protein-coding genes and non-coding RNAs, it was feasible to evaluate the performance of previously reported prognostic signatures for invasive UCB derived using early-generation microarrays. The performances of seven published post-cystectomy prognostic genomic signatures for muscle-invasive UCB were compared with the GC developed in this study (Table 6). (Blaveri et al. 2005; Sanchez-Carbajo et al. 2006; Kim et al. 2010; Kim et al. 2011; Riester et al. 2012) Genomic markers that comprised the individual signatures were mapped back to the respective Human Exon GeneChip features, and the performance of each signature was optimized in the discovery set as done originally for GC. Therefore, as expected, nearly all published signatures demonstrated high survival-ROC AUCs in the discovery set as that observed with GC. However, when these locked signatures were applied to the validation set (again, with bioinformaticians blinded to clinical variables) the AUC for each model decreased leaving the GC having the best validated performance (Figure 11). Of the AUCs of published signatures that were modeled, lower bounds of the 95% CIs of 5/7 signatures were >0.50 , suggesting a statistically significant ability to predict recurrence greater than random chance. The AUC of GC was 0.05 points higher than the best performing published signature, a 61-feature signature for post-cystectomy survival in patients with muscle-invasive and node-positive UCB reported by Kim et al. (Kim et al. 2010) which had an AUC of 0.72 (95% CI: 0.60-0.87).

TABLE 6

Predictor Label ^a	Discovery Cohort n [†]	Discovery Profiling Array Platform	Signature Size (no. of mappable transcripts)	Prognostic Endpoint	Survival-ROC AUC (95% CI)	
					Discovery cohort	Validation cohort
GC ⁴	133 ³	Human Exon 1.0 ST GeneChip (Affymetrix)	15	Recurrence-free survival	0.83 (0.75 - 0.91)	0.77 (0.65 - 0.91)
Kim 2010 - OS ²	62 ⁵	Human 6 v2.0 Expression BeadChip (Illumina)	61	Overall survival	0.85 (0.78 - 0.92)	0.72 (0.60 - 0.87)
Kim 2010 - CSS ²	62 ⁵	Human 6 v2.0 Expression BeadChip (Illumina)	49	Cancer-specific survival	0.82 (0.75 - 0.91)	0.72 (0.60 - 0.85)
Kim 2010 - Prog ²	62 ⁵	Human 6 v2.0 Expression BeadChip (Illumina)	44	Progression	0.82 (0.75 - 0.90)	0.71 (0.59 - 0.85)
Riester 2012 ³	78 ⁶	Human Genome U133 Plus 2.0 GeneChip (Affymetrix)	20	Overall survival	0.79 (0.71 - 0.89)	0.71 (0.58 - 0.84)
Sanchez-Carbajo 2006 ⁴	74 ⁶	Human Genome U133A GeneChip (Affymetrix)	85	Overall survival	0.86 (0.80 - 0.93)	0.67 (0.54 - 0.83)
Blaveri 2005 ⁷	40 ⁹	Custom cDNA array	24	Overall survival	0.83 (0.76 - 0.90)	0.63 (0.50 - 0.77)
Kim 2011 ⁸	38 ⁸	Human 6 v2.0 Expression BeadChip (Illumina)	3	Progression	0.82 (0.75 - 0.90)	0.51 (0.37 - 0.66)

Summary and performance metrics of prior prognostic signatures for high-risk bladder cancer in comparison with the genomic classifier.

†Patients with muscle-invasive or node-positive bladder cancer

a Paraffin-embedded primary tumor specimens

b Frozen primary tumor specimens

TABLE 7

Pathway	Percentage of GC Genes Directly Associated with Pathway*
Positive regulation of kinase activity	
Receptor signaling pathways	
Intracellular signaling cascade	
Regulation of protein transport/localization	
Regulation of cell proliferation	
Positive regulation of cell differentiation	
Response to organic/hormone stimulus	
Homeostatic process	
ERBB signaling pathway	
Regulation of muscle differentiation	
Chronic myeloid leukemia	
MAPK cascade	
Mitosis and cell cycle	
Regulation of translation initiation in response to stress	

Associations of markers comprising the genomic classifier with major Gene Ontology clusters

Biological interactions based on Human Signaling Network v5

*Nine genes within GC directly associated with one or more pathways

[00328] To analyze the biological relevance of markers included in GC, an interactome network-based gene set enrichment analysis of their 257 first-degree partners was performed (Figure 12). Of these, 248 unique genes were identified to biologically interact with at least one of the 15 markers within GC. Biological processes and KEGG pathways were analyzed using the DAVID functional annotation tool, which indicated enrichment of GO terms associated with regulation of kinase activity and protein transport/localization. Additionally, GC signature genes were also well represented within GO terms associated with receptor and intracellular signaling pathways, and regulation of cell proliferation and differentiation (Table 7).

[00329] These results showed that whole transcriptome expression profiling could be utilized to stratify risk of disease recurrence in patients who have undergone radical cystectomy for muscle invasive bladder cancer. These results further showed that a 15-marker genomic classifier (GC) of the present invention surpasses the predictive power of previously reported clinical and genomic prognostic markers in bladder cancer. The results demonstrated that methods and markers of the present invention are useful for predicting risk for cancer recurrence. These results suggested that the methods and markers of the present invention would be useful for diagnosing, prognosing, determining the progression of cancer, or predicting benefit from therapy in a subject having cancer.

Example 2: Prognostic Value of Univariable and Combinations of Markers From a 15 Biomarker Panel for Muscle Invasive Bladder Cancer.

[00330] The 15 markers identified in the genomic classifier in Example 1 (Table 2A, Table 2B) were assessed for their performance across a range of different metrics for the prediction of cancer recurrence within different subsets of clinical relevancy.

[00331] As shown in Table 8, these 15 markers, as univariable classifiers, were statistically significant in a pooled discovery and validation set (n=199; see Example 1) based on the Wilcoxon test (p-value ≤ 0.05) for the Area under the ROC curve (AUC). The probeset ID number of the corresponding markers (Table 2B) as provided by Affymetrix (<http://www.affymetrix.com/analysis/index.affx>) was used to represent each marker.

[00332] Significance of the selected features was evidenced by multiple additional metrics (either in their raw values or as their associated P-value for assessment of statistical significance) including:

- Sensitivity: proportion of the actual number of patients with the event that are correctly identified as such. Higher values indicate better performance.
- Specificity: proportion of the actual number of patients without the event that are correctly identified as such. Higher values indicate better performance.
- Area under the ROC curve (AUC): Corresponds to the area under the receiver operating characteristic curve, which plots the performance of a feature or classifier for all thresholds of sensitivity and specificity. Higher values indicate better performance. For survival AUC, performance was calculated for 4 years.
- Accuracy: Proportion of patients correctly predicted. Higher values indicate better performance.
- Positive Predictive Value (PPV): proportion of predicted events that are true events. Higher values indicate better performance.
- Negative Predictive Value (NPV): proportion of predicted non-events that are true non-events. Higher values indicate better performance.

- Median Fold Difference (MFD): the ratio of the median expression value for each group. Values away from 1 indicate better performance.
- Univariable Analysis (UVA) odds ratio (OR): measures the effect size of the feature or classifier when partitioning the scores into low and high risk groups. For this metric, these groups are obtained by partitioning the set of samples into low and high risk expression values using the PAM clustering method. Values away from 1 indicate better performance.
- Multivariable Analysis (MVA) odds ratio (OR): measures the independent prognostic ability of the feature or classifier when partitioning the values into low and high risk groups. For this metric, these groups are obtained by partitioning the set of samples into low and high risk expression values using the PAM clustering method. Values away from 1 indicate better performance.
- UVA hazard ratio (HR): measures the ratio of the hazard rates when partitioning the expression values into low and high risk groups and incorporates the time to event through Cox proportionate hazard modeling. For this metric, these groups are obtained by partitioning the expression values into low and high risk using the PAM clustering method. Values away from 1 indicate better performance.
- MVA hazard ratio (HR): measures the independent prognostic ability relative to other variables when partitioning the values into low and high risk groups and incorporates the time to event through Cox proportionate hazard modeling. For this metric, these groups are obtained by partitioning the expression values into low and high risk using the PAM clustering method. Values away from 1 indicate better performance.

[00333] Multivariable analyses included the following clinical data: age, gender, tumor stage, lymphovascular invasion, node status, race and adjuvant chemotherapy status (see Table 1).

[00334] The associated p-value provided for the metrics gives a measure of the statistical significance of the corresponding metric. The threshold of P-value ≤ 0.05 is used as a way of defining those features that are statistically significant for the given metric and endpoint. The cut-off used for each marker is indicated. When dichotomization is necessary for a performance metric, the marker expression values are dichotomized using unsupervised clustering in the pamr package.

[00335] The superior performance provided by the 15 markers of the present invention is observed not only within the entire cohort used, but also when excluding the group of patients with pT2 (organ-confined) disease (Table 9) and within patients with negative lymph node involvement (Table 10). The former group represents patients that are prime candidates for therapy. The assessment of their likelihood of recurrence based on these 15 markers of the present invention can provide additional insight into the need for treatment. In contrast, patients with Lymph Node negative status represent a group that would be

a candidate for observation; indications of aggressive disease based on these 15 markers of the present invention may be used to suggest treatment for these patients.

The 15 markers of the present invention are useful as univariable predictors; additionally, the combination of subsets of these 15 markers through a machine learning algorithm results in enhanced performance. As shown in Table 11, pairwise classifiers can result in an improved performance for the recurrence endpoint compared to their univariable counterparts, with all the classifiers listed presenting statistical significance based on, at least, Wilcoxon P-value. In Table 11, each classifier is described by the machine learning algorithm that combines the markers (column 'classifier') as well as the probeset ID number of the corresponding markers as provided by Affymetrix (<http://www.affymetrix.com/analysis/index.affx>).

[00336] These classifiers were trained and tuned in the discovery cohort (n = 133) and the performance shown in Table 11 corresponds to that obtained for different metrics in the validation set (n = 66). When dichotomization is necessary for a performance metric, the classifier scores are dichotomized using unsupervised clustering in the pamr package. The machine learning algorithms used are Naïve Bayes (NB), recursive Partitioning (Rpart), Support Vector Machines (SVMs), Random Forest (RF) and K Nearest Neighbors (KNN). These machine learning algorithms were executed with default parameters using packages rpart 4.1-0, HDclassif 1.2.2, randomForest 4.6-7, caret 5.15-61, cluster 1.14.3, e1071 1.6-1, class 7.3-5 in R. Each classifier generates a score between 0 and 1, except for SVM which generates a score from $-\infty$ to $+\infty$; in all cases, higher score values indicate higher probability of recurrence.

[00337] The improved performance of the classifiers built from combinations of subsets of the 15 markers is also observed within patients with negative lymph node involvement (Table 12), pT2 (organ-confined disease) patients (Table 13), patients with positive lymph node involvement (Table 14) as well as within the subset of patients that excludes the group with pT2 (organ-confined) disease (see Table 15). Patients with clinical low risk such as the first two groups (LNI- and pT2) can be candidates for treatment if aggressive disease based on the likelihood of recurrence obtained from the 15 markers is detected. In contrast, patients at a higher risk such as the second two groups may be spared unnecessary treatment if a low likelihood of recurrence is observed from the 15 markers of the present invention.

[00338] These results showed that the methods and markers of the present invention are useful for prognosing muscle invasive bladder cancer recurrence. These results further showed that the methods and markers of the present invention are useful for diagnosing, prognosing, determining the progression of cancer, or predicting benefit from therapy in a subject having cancer.

TABLE 8

Affymetrix Probeset ID	AUC	WILCOX P-VALUE	KS P- VALUE	MF D	T- TEST P- VAL	ACCURACY	ACCURACY P- VALUE	SENSITIVITY	SPECIFICITY	PPV	NPV

UE											
3326487	0.64	0.0008	0.001 6	1.4 1	0.000 4	0.59	0.0138	0.48	0.70	0.62	0.57
2458376	0.68	0.0000	0.000 1	1.6 5	0.000 0	0.63	0.0004	0.49	0.78	0.69	0.59
3414753	0.65	0.0003	0.000 2	1.6 8	0.000 3	0.64	0.0001	0.57	0.70	0.67	0.62
2332285	0.67	0.0000	0.000 0	1.8 0	0.000 0	0.63	0.0004	0.56	0.69	0.66	0.61
2478155	0.65	0.0002	0.000 1	1.5 8	0.000 3	0.60	0.0042	0.53	0.67	0.63	0.58
3139092	0.65	0.0003	0.000 2	1.5 8	0.001 3	0.59	0.0138	0.47	0.71	0.63	0.56
2789391	0.63	0.0012	0.000 4	1.4 4	0.000 7	0.63	0.0004	0.58	0.67	0.65	0.61
3463598	0.63	0.0016	0.000 0	1.4 6	0.001 6	0.64	0.0001	0.50	0.79	0.71	0.61
2461837	0.64	0.0007	0.000 0	1.4 4	0.001 7	0.59	0.0138	0.54	0.63	0.60	0.57
2512364	0.65	0.0004	0.000 0	1.5 6	0.000 3	0.63	0.0002	0.62	0.64	0.64	0.62
2364325	0.66	0.0001	0.000 1	1.3 9	0.000 2	0.60	0.0042	0.50	0.70	0.64	0.58
3066770	0.63	0.0016	0.000 3	1.4 9	0.002 4	0.62	0.0007	0.51	0.73	0.67	0.60
2956442	0.62	0.0039	0.002 1	1.4 2	0.004 9	0.62	0.0007	0.60	0.64	0.64	0.61
3005357	0.65	0.0002	0.000 1	1.7 3	0.000 4	0.61	0.0028	0.58	0.63	0.62	0.60
2651515	0.64	0.0006	0.000 0	1.4 3	0.000 4	0.65	0.0000	0.51	0.79	0.71	0.61
Affymetrix Probeset ID	CU TO FF	KMP- VALU E	SUR V- AUC	UV A HR	UVA HR P- VAL UE	UVA OR	UVA OR P-VALUE	MVA HR	MVA HR P-VALUE	MV A OR	MVA OR P- VAL UE
3326487	4.78	0.0136	0.64	1.1 6	0.000 4	1.27	0.0006	1.10	0.05	1.21	0.024
2458376	4.09	0.0001	0.67	1.2 1	0.000 1	1.40	0.0001	1.11	0.08	1.29	0.012
3414753	4.44	0.0002	0.66	1.1 4	0.001 1	1.26	0.0004	1.12	0.02	1.33	0.001
2332285	4.81	0.0004	0.66	1.1 7	0.000 1	1.30	0.0001	1.11	0.03	1.28	0.003
2478155	4.75	0.0035	0.64	1.1 7	0.000 7	1.30	0.0004	1.13	0.03	1.33	0.003
3139092	4.35	0.0077	0.67	1.1 5	0.002 7	1.26	0.0018	1.12	0.03	1.29	0.006
2789391	5.54	0.0002	0.64	1.1 5	0.000 8	1.23	0.0010	1.13	0.01	1.24	0.006
3463598	4.89	0.0000	0.64	1.1 6	0.003 2	1.28	0.0021	1.08	0.23	1.22	0.047
2461837	4.27	0.0214	0.64	1.1 6	0.003 1	1.27	0.0022	1.12	0.06	1.26	0.019
2512364	5.60	0.0001	0.65	1.1 6	0.000 4	1.26	0.0004	1.14	0.01	1.31	0.001
2364325	5.87	0.0022	0.67	1.1 5	0.000 5	1.27	0.0003	1.12	0.02	1.28	0.002
3066770	5.02	0.0012	0.64	1.1 3	0.004 8	1.23	0.0030	1.08	0.15	1.20	0.032

2956442	4.75	0.0003	0.62	1.13	0.0071	1.21	0.0057	1.12	0.04	1.21	0.025
3005357	4.34	0.0018	0.66	1.15	0.0009	1.26	0.0006	1.13	0.01	1.30	0.003
2651515	4.21	0.0000	0.63	1.19	0.0006	1.35	0.0007	1.14	0.03	1.42	0.002

Performance of the 15 markers across different metrics for the Recurrence endpoint

TABLE 9

Affymetrix Probeset ID	AUC	WILCO X P- VALUE	KS P- VALUE	MFD	T-TEST P-VALUE	ACCURA CY	ACCURAC Y P-VALUE	SENSITIVI TY	SPECIFICI TY
3326487	0.62	0.0166	0.0284	1.47	0.0074	0.58	0.5365	0.50	0.68
2458376	0.67	0.0006	0.0002	1.71	0.0021	0.61	0.2720	0.53	0.72
3414753	0.67	0.0010	0.0006	1.74	0.0004	0.64	0.0684	0.59	0.72
2332285	0.69	0.0002	0.0010	1.89	0.0001	0.64	0.0950	0.59	0.70
2478155	0.64	0.0058	0.0057	1.40	0.0061	0.61	0.2720	0.56	0.67
3139092	0.65	0.0030	0.0066	1.57	0.0075	0.57	0.6047	0.49	0.68
2789391	0.63	0.0089	0.0044	1.53	0.0039	0.63	0.1284	0.56	0.72
3463598	0.60	0.0467	0.0019	1.50	0.0307	0.63	0.1284	0.55	0.74
2461837	0.62	0.0207	0.0039	1.46	0.0440	0.56	0.6697	0.49	0.67
2512364	0.64	0.0075	0.0005	1.53	0.0038	0.61	0.2170	0.59	0.65
2364325	0.66	0.0014	0.0016	1.41	0.0015	0.60	0.3330	0.53	0.70
3066770	0.61	0.0330	0.0077	1.59	0.0320	0.61	0.2720	0.53	0.72
2956442	0.62	0.0149	0.0185	1.44	0.0172	0.63	0.1284	0.63	0.63
3005357	0.65	0.0025	0.0029	1.73	0.0032	0.59	0.3986	0.59	0.60
2651515	0.64	0.0073	0.0003	1.43	0.0069	0.64	0.0684	0.55	0.77
Affymetrix Probeset ID	PPV	NPV	CUTOFF	KM P- VAL UE	SURV- AUC	UVA HR	UVA HR P- VALUE	UVA OR	UVA OR P-VALUE
3326487	0.68	0.50	4.84	0.0639	0.63	1.13	0.0128	1.24	0.0088
2458376	0.72	0.53	4.10	0.0087	0.66	1.14	0.0110	1.33	0.0030
3414753	0.74	0.56	4.51	0.0011	0.67	1.15	0.0030	1.33	0.0008
2332285	0.73	0.56	4.95	0.0040	0.67	1.15	0.0013	1.33	0.0003
2478155	0.70	0.53	4.88	0.0116	0.62	1.14	0.0213	1.29	0.0074
3139092	0.68	0.49	4.40	0.0574	0.67	1.13	0.0159	1.27	0.0090
2789391	0.73	0.55	5.83	0.0018	0.62	1.14	0.0056	1.24	0.0049
3463598	0.74	0.55	4.89	0.0027	0.61	1.11	0.0672	1.22	0.0327
2461837	0.67	0.49	4.75	0.0934	0.61	1.11	0.0647	1.20	0.0458
2512364	0.70	0.54	5.93	0.0098	0.64	1.14	0.0066	1.24	0.0047
2364325	0.71	0.52	5.87	0.009	0.67	1.13	0.0067	1.27	0.0022

				0					
3066770	0.72	0.53	5.03	0.014 7	0.62	1.09	0.0760	1.19	0.0340
2956442	0.70	0.55	4.89	0.002 0	0.62	1.12	0.0342	1.22	0.0189
3005357	0.67	0.52	4.50	0.032 7	0.65	1.13	0.0099	1.27	0.0041
2651515	0.77	0.56	4.36	0.000 2	0.65	1.15	0.0151	1.31	0.0085

Performance of the 15 markers across different metrics for the Recurrence endpoint in the subset of patients excluding pT2 (organ-confined) disease.

TABLE 10

Affymetrix Probeset ID	AUC	WILC OX P- VALUE	KS P- VALUE	MFD	T-TEST P-VALUE	ACCURA CY	ACCURA CY P- VALUE	SENSITIVI TY	SPECIFIC ITY
3326487	0.62	0.022	0.005	1.40	0.0027	0.67	0.26	0.49	0.77
2458376	0.68	0.001	0.006	1.47	0.0007	0.66	0.33	0.43	0.79
3414753	0.64	0.009	0.001	1.78	0.0072	0.67	0.26	0.57	0.72
2332285	0.67	0.001	0.001	1.63	0.0007	0.64	0.54	0.49	0.72
2478155	0.71	0.000	0.000	1.77	0.0001	0.65	0.39	0.60	0.68
3139092	0.67	0.001	0.002	1.59	0.0054	0.62	0.68	0.40	0.74
2789391	0.66	0.003	0.000	1.51	0.0020	0.67	0.21	0.60	0.72
3463598	0.62	0.020	0.001	1.50	0.0191	0.70	0.08	0.51	0.80
2461837	0.65	0.006	0.002	1.46	0.0119	0.60	0.80	0.60	0.61
2512364	0.69	0.000	0.000	1.65	0.0003	0.66	0.33	0.68	0.65
2364325	0.68	0.001	0.001	1.41	0.0009	0.65	0.39	0.51	0.73
3066770	0.64	0.010	0.002	1.52	0.0124	0.69	0.12	0.57	0.76
2956442	0.60	0.052	0.044	1.41	0.0442	0.62	0.68	0.57	0.65
3005357	0.66	0.003	0.006	1.82	0.0026	0.63	0.61	0.62	0.63
2651515	0.67	0.001	0.001	1.43	0.0019	0.61	0.74	0.55	0.65
Affymetrix Probeset ID	PPV	NPV	CUTOFF	KM P- VAL UE	SURV- AUC	UVA HR	UVA HR P-VALUE	UVA OR	UVA OR P-VALUE
3326487	0.55	0.72	4.72	0.002	0.60	1.13	0.0027	1.28	0.004
2458376	0.54	0.71	4.06	0.006	0.67	1.13	0.0009	1.40	0.001
3414753	0.54	0.75	4.40	0.001	0.61	1.12	0.0119	1.24	0.009
2332285	0.50	0.71	4.82	0.021	0.63	1.13	0.0014	1.31	0.001
2478155	0.52	0.75	4.71	0.001	0.68	1.14	0.0002	1.40	0.000
3139092	0.48	0.69	4.40	0.056	0.69	1.13	0.0059	1.28	0.007
2789391	0.55	0.76	5.79	0.000	0.65	1.13	0.0026	1.28	0.003
3463598	0.60	0.74	4.90	0.000	0.61	1.12	0.0232	1.25	0.022
2461837	0.47	0.72	4.02	0.030	0.65	1.13	0.0120	1.27	0.014
2512364	0.52	0.78	5.61	0.000	0.69	1.13	0.0005	1.33	0.001
2364325	0.52	0.72	5.89	0.004	0.68	1.13	0.0016	1.30	0.001

3066770	0.57	0.76	4.83	0.000	0.64	1.12	0.0107	1.23	0.015
2956442	0.48	0.73	4.74	0.010	0.61	1.12	0.0518	1.18	0.046
3005357	0.49	0.74	4.37	0.005	0.66	1.13	0.0030	1.28	0.003
2651515	0.47	0.72	3.82	0.012	0.67	1.14	0.0010	1.39	0.003

Performance of the 15 markers across different metrics for the Recurrence endpoint in the subset of patients with negative lymph node involvement.

TABLE 11

CLASSIFIER	AUC	WILCOX P-VALUE	KS P-VALUE	T-TEST P-VALUE	ACCURACY	ACCURACY P-VALUE	SENSITIVITY	SPECIFICITY	PPV	NPV	CUTOFF	KM P-VALUE	SURV-AUC	UV AHR P-VALUE	UV AHR P-VALUE	MVAHR P-VALUE	MVAOR P-VALUE
nb:24781552364325	0.77	0.0001	0.0007	0.0001	0.73	0.0001	0.70	0.76	0.74	0.71	0.47	0.0002	0.77	0.0002	0.0007	0.0001	0.002
knn:24583762364325	0.78	0.0001	0.0053	0.0001	0.70	0.0009	0.64	0.76	0.72	0.68	0.50	0.0019	0.75	0.0003	0.0004	0.010	0.003
nb:23322853005357	0.77	0.0001	0.0007	0.0006	0.70	0.0009	0.61	0.79	0.74	0.67	0.49	0.0015	0.78	0.0008	0.0018	0.0006	0.003
rf:24781552364325	0.77	0.0001	0.0000	0.0000	0.76	0.0000	0.70	0.82	0.79	0.73	0.62	0.0000	0.77	0.0004	0.0004	0.0008	0.001
nb:24583763005357	0.77	0.0001	0.0019	0.0002	0.68	0.0021	0.48	0.88	0.80	0.63	0.50	0.0018	0.77	0.0005	0.0011	0.021	0.004
svm:24781553005357	0.77	0.0001	0.0019	0.0001	0.71	0.0004	0.73	0.70	0.71	0.72	-0.07	0.0006	0.79	0.0003	0.0004	0.0001	0.001
rf:24583762364325	0.77	0.0001	0.0001	0.0001	0.68	0.0021	0.55	0.82	0.75	0.64	0.65	0.0027	0.77	0.0005	0.0005	0.0007	0.001
svm:23322853066770	0.77	0.0001	0.0001	0.0004	0.67	0.0046	0.58	0.76	0.70	0.64	-0.08	0.0075	0.76	0.0011	0.0013	0.023	0.008
knn:34147533005357	0.77	0.0001	0.0022	0.0004	0.67	0.0046	0.64	0.70	0.68	0.66	0.50	0.0072	0.74	0.0008	0.0011	0.0007	0.002
svm:23322852364325	0.76	0.0002	0.0019	0.0002	0.73	0.0001	0.64	0.82	0.78	0.69	0.00	0.0002	0.77	0.0005	0.0007	0.0007	0.003
nb:2332	0.76	0.0000	0.0000	0.0001	0.68	0.0000	0.61	0.70	0.71	0.66	0.49	0.0000	0.76	0.0000	0.0000	0.010	0.005

285 313909 2 nb:2458 376 341475 3 knn:245 8376 300535 7 nb:3414 753 233228 5 nb:2478 155 313909 2 svm:34 14753 247815 5 knn:247 8155 300535 7 nb:2478 155 251236 4 nb:3414 753 300535 7 svm:23 32285 313909 2 nb:2458 376 251236 4 rf:2332 285 300535 7 nb:3414 753 236432 5 nb:2332 285 236432 5 svm:23 32285 295644 2 svm:24 58376 300535	2 01 2 21 6 33 20 29 0																	
0.76	0.000 2	0.00 07	0.000 2	0.65	0.00 93	0.42	0.8 8	0.78	0.60	0.53	0.01 22	0.76	0.00 06	0.00 13	0.08 4	0.011		
0.77	0.000 2	0.00 53	0.000 1	0.68	0.00 21	0.70	0.6 7	0.68	0.69	0.48	0.00 39	0.75	0.00 09	0.00 05	0.01 1	0.001		
0.76	0.000 2	0.00 07	0.001 3	0.64	0.01 78	0.48	0.7 9	0.70	0.60	0.52	0.01 57	0.74	0.00 20	0.00 32	0.04 8	0.011		
0.76	0.000 2	0.00 19	0.000 3	0.68	0.00 21	0.67	0.7 0	0.69	0.68	0.47	0.00 37	0.73	0.00 03	0.00 13	0.00 1	0.002		
0.76	0.000 2	0.00 02	0.000 2	0.65	0.00 93	0.64	0.6 7	0.66	0.65	- 0.18	0.02 01	0.76	0.00 03	0.00 09	0.01 1	0.002		
0.76	0.000 3	0.01 19	0.000 3	0.67	0.00 46	0.82	0.5 2	0.63	0.74	0.41	0.00 59	0.76	0.00 07	0.00 11	0.00 2	0.001		
0.75	0.000 3	0.00 02	0.000 2	0.70	0.00 09	0.73	0.6 7	0.69	0.71	0.47	0.00 14	0.73	0.00 03	0.00 07	0.00 4	0.002		
0.75	0.000 3	0.00 07	0.000 4	0.67	0.00 46	0.64	0.7 0	0.68	0.66	0.47	0.00 72	0.77	0.00 04	0.00 13	0.00 4	0.001		
0.75	0.000 3	0.00 02	0.000 2	0.71	0.00 04	0.76	0.6 7	0.69	0.73	0.01	0.00 06	0.77	0.00 11	0.00 08	0.00 3	0.001		
0.75	0.000 3	0.00 07	0.000 2	0.68	0.00 21	0.48	0.8 8	0.80	0.63	0.51	0.00 18	0.72	0.00 08	0.00 11	0.06 3	0.007		
0.76	0.000 4	0.00 03	0.000 2	0.70	0.00 09	0.79	0.6 1	0.67	0.74	0.39	0.00 15	0.78	0.00 05	0.00 08	0.00 1	0.001		
0.75	0.000 4	0.00 07	0.000 4	0.73	0.00 01	0.76	0.7 0	0.71	0.74	0.45	0.00 02	0.77	0.00 05	0.00 14	0.01 1	0.004		
0.75	0.000 4	0.00 07	0.000 7	0.70	0.00 09	0.55	0.8 5	0.78	0.65	0.53	0.00 07	0.76	0.00 11	0.00 20	0.01 5	0.006		
0.75	0.000 4	0.00 19	0.001 2	0.70	0.00 09	0.61	0.7 9	0.74	0.67	- 0.08	0.00 17	0.75	0.00 26	0.00 27	0.02 4	0.008		
0.75	0.000 4	0.00 48	0.000 2	0.70	0.00 09	0.52	0.8 8	0.81	0.64	0.11	0.00 10	0.74	0.00 15	0.00 09	0.04 8	0.003		

7																		
rf:2332																		
285																		
247815	0.75	0.000	0.00	0.000	0.67	0.00	0.85	0.4	0.62	0.76	0.42	0.00	0.74	0.00	0.00	0.08	0.005	
5		4	22	3		46		8				93		20	11	9		
rf:2458																		
376																		
300535	0.75	0.000	0.00	0.000	0.67	0.00	0.64	0.7	0.68	0.66	0.57	0.00	0.77	0.00	0.00	0.00	0.000	
7		4	53	2		46		0				78		13	08	2		
nb:2332																		
285																		
265151	0.75	0.000	0.00	0.001	0.70	0.00	0.55	0.8	0.78	0.65	0.47	0.00	0.73	0.00	0.00	0.08	0.011	
5		4	19	0		09		5				07		17	30	3		
nb:2458																		
376																		
313909	0.75	0.000	0.00	0.000	0.68	0.00	0.48	0.8	0.80	0.63	0.50	0.00	0.75	0.00	0.00	0.03	0.009	
2		4	48	4		21		8				39		13	20	1		
nb:2478																		
155																		
306677	0.75	0.000	0.00	0.000	0.68	0.00	0.55	0.8	0.75	0.64	0.49	0.00	0.71	0.00	0.00	0.00	0.004	
0		4	48	4		21		2				08		03	15	4		
nb:3005																		
357																		
265151	0.75	0.000	0.00	0.000	0.67	0.00	0.76	0.5	0.64	0.70	0.39	0.00	0.77	0.00	0.00	0.01	0.002	
5		4	19	4		46		8				63		03	17	3		
nb:2364																		
325																		
300535	0.75	0.000	0.00	0.000	0.74	0.00	0.73	0.7	0.75	0.74	0.46	0.00	0.76	0.00	0.00	0.00	0.001	
7		4	07	4		01		6				01		05	12	1		
nb:2512																		
364																		
236432	0.75	0.000	0.00	0.000	0.73	0.00	0.73	0.7	0.73	0.73	0.48	0.00	0.73	0.00	0.00	0.00	0.002	
5		5	01	3		01		3				02		05	10	5		
nb:3139																		
092																		
236432	0.74	0.000	0.00	0.000	0.68	0.00	0.70	0.6	0.68	0.69	0.45	0.00	0.76	0.00	0.00	0.00	0.004	
5		5	48	8		21		7				31		11	22	2		
nb:3139																		
092																		
300535	0.74	0.000	0.00	0.000	0.67	0.00	0.58	0.7	0.70	0.64	0.49	0.00	0.77	0.00	0.00	0.00	0.001	
7		5	02	7		46		6				13		10	20	1		
rf:2478																		
155																		
346359	0.75	0.000	0.00	0.000	0.70	0.00	0.55	0.8	0.78	0.65	0.64	0.00	0.72	0.00	0.00	0.08	0.003	
8		5	22	3		09		5				06		22	12	5		
knn:341																		
4753																		
251236	0.75	0.000	0.00	0.000	0.71	0.00	0.61	0.8	0.77	0.68	0.55	0.00	0.75	0.00	0.00	0.02	0.003	
4		6	22	3		04		2				05		08	09	6		
nb:3414																		
753																		
313909	0.74	0.000	0.00	0.001	0.64	0.01	0.48	0.7	0.70	0.60	0.51	0.01	0.76	0.00	0.00	0.00	0.004	
2		6	48	1		78		9				77		12	29	8		
svm:31																		
39092																		
236432	0.74	0.000	0.00	0.000	0.70	0.00	0.76	0.6	0.68	0.72	-	0.00	0.76	0.00	0.00	0.00	0.003	
5		6	48	5		09		4			0.15	13		12	14	1		
knn:245																		
8376																		
265151	0.74	0.000	0.00	0.000	0.71	0.00	0.58	0.8	0.79	0.67	0.50	0.00	0.73	0.00	0.00	0.02	0.005	
5		6	03	5		04		5				01		07	19	5		

rf:2458 376 233228 5	0.75	0.000 6	0.00 09	0.000 6	0.70	0.00 09	0.79	0.6 1	0.67	0.74	0.42	0.00 36	0.75	0.00 28	0.00 17	0.04 4	0.005
nb:3414 753 251236 4	0.74	0.000 6	0.00 07	0.000 4	0.73	0.00 01	0.73	0.7 3	0.73	0.73	0.48	0.00 02	0.74	0.00 06	0.00 12	0.01 8	0.003
svm:34 14753 251236 4	0.74	0.000 6	0.00 07	0.000 3	0.73	0.00 01	0.70	0.7 6	0.74	0.71	- 0.05	0.00 02	0.74	0.00 04	0.00 11	0.00 8	0.003
rpart:24 78155 295644 2	0.70	0.000 7	0.01 19	0.000 4	0.70	0.00 09	0.88	0.5 2	0.64	0.81	0.47	0.00 19	0.67	0.00 47	0.00 14	0.05 8	0.007
rpart:24 78155 306677 0	0.70	0.000 7	0.01 19	0.000 4	0.70	0.00 09	0.88	0.5 2	0.64	0.81	0.47	0.00 19	0.67	0.00 47	0.00 14	0.05 8	0.007
nb:3066 770 300535 7	0.74	0.000 7	0.00 48	0.000 8	0.65	0.00 93	0.52	0.7 9	0.71	0.62	0.48	0.00 54	0.76	0.00 07	0.00 21	0.00 3	0.003
rf:2332 285 265151 5	0.74	0.000 7	0.00 53	0.000 5	0.70	0.00 09	0.58	0.8 2	0.76	0.66	0.38	0.00 05	0.72	0.00 08	0.00 18	0.06 4	0.014
knn:346 3598 306677 0	0.73	0.000 8	0.00 53	0.000 4	0.71	0.00 04	0.55	0.8 8	0.82	0.66	0.54	0.00 01	0.74	0.00 10	0.00 16	0.02 9	0.007
svm:23 64325 300535 7	0.74	0.000 8	0.00 07	0.000 3	0.73	0.00 01	0.73	0.7 3	0.73	0.73	0.03	0.00 02	0.78	0.00 07	0.00 09	0.00 1	0.001
rf:3414 753 247815 5	0.74	0.000 8	0.00 22	0.000 8	0.65	0.00 93	0.64	0.6 7	0.66	0.65	0.53	0.02 01	0.75	0.00 33	0.00 17	0.03 5	0.003
knn:306 6770 300535 7	0.74	0.000 8	0.00 53	0.001 4	0.65	0.00 93	0.52	0.7 9	0.71	0.62	0.50	0.00 54	0.74	0.00 16	0.00 28	0.00 6	0.003
nb:2512 364 300535 7	0.74	0.000 8	0.00 48	0.000 4	0.70	0.00 09	0.67	0.7 3	0.71	0.69	0.50	0.00 07	0.74	0.00 06	0.00 11	0.00 2	0.001
nb:2512 364 306677 0	0.74	0.000 8	0.00 48	0.000 8	0.70	0.00 09	0.64	0.7 6	0.72	0.68	0.49	0.00 07	0.72	0.00 11	0.00 20	0.01 6	0.005
svm:24 58376 306677 0	0.74	0.000 8	0.00 48	0.001 4	0.65	0.00 93	0.52	0.7 9	0.71	0.62	0.31	0.02 19	0.70	0.00 75	0.00 30	0.12 4	0.007
knn:247 8155 251236 4	0.74	0.000 8	0.00 22	0.000 3	0.71	0.00 04	0.73	0.7 0	0.71	0.72	0.50	0.00 05	0.74	0.00 11	0.00 09	0.02 2	0.002
nb:2478 155	0.73	0.000 9	0.01 13	0.000 5	0.67	0.00 46	0.45	0.8 8	0.79	0.62	0.48	0.00 23	0.72	0.00 04	0.00 22	0.02 9	0.002

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knn:236 4325 300535 7	0.74	0.000 9	0.00 09	0.000 4	0.74	0.00 01	0.76	0.7 3	0.74	0.75	0.50	0.00 01	0.74	0.00 10	0.00 12	0.00 1	0.001
nb:2458 376 306677 0	0.73	0.000 9	0.00 48	0.000 6	0.71	0.00 04	0.52	0.9 1	0.85	0.65	0.47	0.00 02	0.71	0.00 11	0.00 27	0.10 8	0.027
nb:2461 837 236432 5	0.73	0.000 9	0.00 19	0.001 8	0.67	0.00 46	0.58	0.7 6	0.70	0.64	0.49	0.00 51	0.73	0.00 21	0.00 35	0.00 7	0.005
nb:3414 753 265151 5	0.73	0.000 9	0.01 13	0.001 0	0.64	0.01 78	0.39	0.8 8	0.76	0.59	0.50	0.00 43	0.75	0.00 10	0.00 39	0.10 2	0.010
nb:3463 598 300535 7	0.73	0.001 0	0.00 48	0.001 0	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.50	0.00 77	0.74	0.00 12	0.00 24	0.00 5	0.003
nb:2332 285 306677 0	0.73	0.001 0	0.00 07	0.001 5	0.68	0.00 21	0.61	0.7 6	0.71	0.66	0.46	0.00 59	0.74	0.00 20	0.00 36	0.03 3	0.018
nb:2478 155 246183 7	0.73	0.001 0	0.00 07	0.001 0	0.70	0.00 09	0.70	0.7 0	0.70	0.70	0.46	0.00 31	0.70	0.00 09	0.00 24	0.00 6	0.005
nb:2364 325 306677 0	0.73	0.001 1	0.00 19	0.000 8	0.70	0.00 09	0.52	0.8 8	0.81	0.64	0.50	0.00 01	0.75	0.00 08	0.00 23	0.00 9	0.007
svm:23 32285 246183 7	0.73	0.001 1	0.00 48	0.000 8	0.65	0.00 93	0.70	0.6 1	0.64	0.67	- 0.20	0.02 39	0.72	0.00 38	0.00 19	0.25 4	0.029
rpart:23 32285 247815 5	0.72	0.001 1	0.01 19	0.000 9	0.64	0.01 78	0.70	0.5 8	0.62	0.66	0.55	0.03 76	0.71	0.00 26	0.00 20	0.07 3	0.016
knn:251 2364 306677 0	0.73	0.001 1	0.02 55	0.000 6	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.56	0.00 57	0.71	0.00 14	0.00 16	0.03 9	0.004
knn:245 8376 346359 8	0.73	0.001 2	0.00 09	0.000 1	0.73	0.00 01	0.55	0.9 1	0.86	0.67	0.53	0.00 02	0.73	0.00 04	0.00 05	0.12 7	0.007
rf:3463 598 300535 7	0.73	0.001 2	0.00 53	0.000 6	0.65	0.00 93	0.55	0.7 6	0.69	0.63	0.57	0.01 72	0.74	0.00 18	0.00 15	0.00 4	0.001
svm:30 66770 300535 7	0.73	0.001 2	0.00 19	0.000 7	0.67	0.00 46	0.58	0.7 6	0.70	0.64	0.12	0.00 58	0.77	0.00 14	0.00 16	0.00 3	0.002
nb:3139 092 251236 4	0.73	0.001 3	0.00 19	0.000 7	0.68	0.00 21	0.64	0.7 3	0.70	0.67	0.48	0.00 21	0.75	0.00 12	0.00 19	0.00 4	0.002
knn:236 4325	0.73	0.001 3	0.00 22	0.000 4	0.70	0.00 09	0.48	0.9 1	0.84	0.64	0.55	0.00 01	0.73	0.00 03	0.00 16	0.00 4	0.002

306677 0 rf:2478 155 278939 1 svm:34 14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.73	0.001 3	0.00 53	0.000 9	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.44	0.01 06	0.71	0.00 26	0.00 21	0.01 5	0.002
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.73	0.001 3	0.00 48	0.001 0	0.71	0.00 04	0.64	0.7 9	0.75	0.68	- 0.01	0.00 04	0.73	0.00 28	0.00 20	0.03 0	0.006
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.73	0.001 4	0.00 19	0.001 3	0.68	0.00 21	0.58	0.7 9	0.73	0.65	0.40	0.00 42	0.73	0.00 30	0.00 53	0.19 5	0.024
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.70	0.001 4	0.01 19	0.001 0	0.70	0.00 09	0.76	0.6 4	0.68	0.72	0.48	0.00 25	0.69	0.00 41	0.00 18	0.05 7	0.006
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.72	0.001 5	0.00 48	0.002 0	0.71	0.00 04	0.67	0.7 6	0.73	0.69	0.18	0.00 04	0.73	0.00 39	0.00 37	0.03 4	0.004
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.73	0.001 5	0.00 22	0.000 6	0.71	0.00 04	0.64	0.7 9	0.75	0.68	0.50	0.00 03	0.74	0.00 12	0.00 15	0.01 6	0.004
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.73	0.001 5	0.02 55	0.004 3	0.65	0.00 93	0.52	0.7 9	0.71	0.62	0.50	0.00 81	0.68	0.00 57	0.00 67	0.00 7	0.003
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.70	0.001 5	0.01 19	0.001 0	0.70	0.00 09	0.73	0.6 7	0.69	0.71	0.51	0.00 10	0.72	0.00 19	0.00 19	0.00 2	0.002
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.70	0.001 5	0.01 19	0.001 0	0.70	0.00 09	0.73	0.6 7	0.69	0.71	0.51	0.00 10	0.72	0.00 19	0.00 19	0.00 2	0.002
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.70	0.001 5	0.01 19	0.001 0	0.70	0.00 09	0.73	0.6 7	0.69	0.71	0.51	0.00 10	0.72	0.00 19	0.00 19	0.00 2	0.002
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.72	0.001 5	0.00 48	0.000 6	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.51	0.00 65	0.71	0.00 07	0.00 18	0.00 9	0.006
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.72	0.001 5	0.00 19	0.007 3	0.64	0.01 78	0.73	0.5 5	0.62	0.67	- 0.03	0.02 38	0.77	0.00 78	0.01 06	0.00 1	0.001
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.73	0.001 5	0.02 55	0.001 2	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.58	0.00 92	0.75	0.00 44	0.00 25	0.05 1	0.004
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.72	0.001 6	0.01 19	0.003 4	0.67	0.00 46	0.42	0.9 1	0.82	0.61	0.64	0.00 14	0.75	0.00 47	0.00 66	0.07 4	0.010
14753 233228 5 nb:2458 376 265151 5 rpart:25 12364 236432 5 svm:25 12364 306677 0 rf:2332 285 236432 5 knn:278 9391 236432 5 rpart:23 32285 236432 5 rpart:23 64325 295644 2 rpart:23 64325 306677 0 nb:2478 155 346359 8 svm:31 39092 295644 2 rf:2458 376 341475 3 knn:233 2285 346359 8 knn:346 3598 251236 4	0.72	0.001 6	0.00 53	0.001 4	0.65	0.00 93	0.42	0.8 8	0.78	0.60	0.59	0.02 01	0.73	0.00 41	0.00 35	0.17 4	0.011

knn:346 3598 236432 5	0.73	0.001 6	0.00 22	0.000 6	0.68	0.00 21	0.55	0.8 2	0.75	0.64	0.53	0.00 27	0.76	0.00 17	0.00 16	0.01 2	0.002
nb:3326 487 300535 7	0.72	0.001 6	0.00 48	0.005 6	0.56	0.19 45	0.30	0.8 2	0.63	0.54	0.50	0.28 16	0.74	0.00 23	0.01 05	0.01 8	0.019
svm:24 58376 251236 4	0.72	0.001 6	0.00 02	0.002 5	0.71	0.00 04	0.61	0.8 2	0.77	0.68	0.10	0.00 07	0.70	0.00 36	0.00 51	0.12 7	0.004
svm:24 58376 265151 5	0.72	0.001 6	0.00 48	0.000 9	0.70	0.00 09	0.64	0.7 6	0.72	0.68	- 0.18	0.00 43	0.73	0.00 28	0.00 22	0.09 5	0.009
rf:2458 376 346359 8	0.73	0.001 7	0.00 09	0.000 3	0.74	0.00 01	0.55	0.9 4	0.90	0.67	0.63	0.00 00	0.74	0.00 11	0.00 11	0.05 2	0.005
nb:2332 285 346359 8	0.72	0.001 7	0.00 07	0.001 6	0.74	0.00 01	0.67	0.8 2	0.79	0.71	0.47	0.00 01	0.73	0.00 28	0.00 38	0.05 6	0.014
nb:2364 325 265151 5	0.72	0.001 8	0.01 13	0.001 2	0.64	0.01 78	0.45	0.8 2	0.71	0.60	0.48	0.01 52	0.75	0.00 12	0.00 37	0.03 6	0.006
nb:3463 598 251236 4	0.72	0.001 8	0.00 02	0.001 1	0.73	0.00 01	0.64	0.8 2	0.78	0.69	0.52	0.00 02	0.72	0.00 18	0.00 26	0.03 1	0.006
svm:31 39092 300535 7	0.72	0.001 8	0.00 48	0.000 9	0.70	0.00 09	0.73	0.6 7	0.69	0.71	0.19	0.00 08	0.77	0.00 15	0.00 23	0.00 0	0.001
knn:245 8376 251236 4	0.72	0.001 8	0.00 53	0.000 3	0.68	0.00 21	0.48	0.8 8	0.80	0.63	0.55	0.00 18	0.72	0.00 17	0.00 11	0.12 5	0.006
rf:2478 155 300535 7	0.72	0.001 9	0.00 22	0.000 1	0.71	0.00 04	0.70	0.7 3	0.72	0.71	0.66	0.00 03	0.76	0.00 05	0.00 04	0.00 1	0.001
knn:247 8155 313909 2	0.72	0.001 9	0.02 55	0.001 2	0.65	0.00 93	0.70	0.6 1	0.64	0.67	0.50	0.01 76	0.71	0.00 43	0.00 30	0.00 3	0.001
knn:341 4753 278939 1	0.72	0.001 9	0.01 19	0.000 8	0.70	0.00 09	0.58	0.8 2	0.76	0.66	0.50	0.00 07	0.72	0.00 11	0.00 20	0.01 5	0.005
nb:2461 837 300535 7	0.72	0.001 9	0.00 19	0.003 7	0.65	0.00 93	0.58	0.7 3	0.68	0.63	0.46	0.00 88	0.72	0.00 42	0.00 57	0.00 8	0.005
nb:3139 092 306677 0	0.72	0.001 9	0.00 19	0.003 2	0.64	0.01 78	0.48	0.7 9	0.70	0.60	0.49	0.01 17	0.74	0.00 30	0.00 59	0.00 8	0.008
svm:34 14753	0.72	0.001 9	0.01 13	0.001 6	0.68	0.00 21	0.76	0.6 1	0.66	0.71	- 0.01	0.00 45	0.78	0.00 43	0.00 29	0.00 6	0.002

313909 2																	
knn:246 1837 300535 7	0.72	0.002 0	0.00 22	0.000 5	0.73	0.00 01	0.76	0.7 0	0.71	0.74	0.44	0.00 05	0.69	0.00 14	0.00 12	0.00 2	0.001
rf:3463 598 236432 5	0.72	0.002 0	0.00 22	0.000 5	0.70	0.00 09	0.58	0.8 2	0.76	0.66	0.57	0.00 13	0.75	0.00 15	0.00 14	0.03 2	0.003
svm:23 64325 306677 0	0.72	0.002 1	0.00 19	0.000 8	0.70	0.00 09	0.52	0.8 8	0.81	0.64	0.17	0.00 01	0.73	0.00 13	0.00 19	0.01 5	0.005
rpart:24 58376 265151 5	0.71	0.002 1	0.05 11	0.001 4	0.67	0.00 46	0.73	0.6 1	0.65	0.69	0.39	0.01 44	0.72	0.00 18	0.00 29	0.04 8	0.007
knn:245 8376 306677 0	0.72	0.002 2	0.02 55	0.001 3	0.68	0.00 21	0.64	0.7 3	0.70	0.67	0.50	0.00 35	0.70	0.00 47	0.00 33	0.30 2	0.019
nb:2478 155 278939 1	0.72	0.002 2	0.01 13	0.002 3	0.64	0.01 78	0.45	0.8 2	0.71	0.60	0.49	0.00 97	0.69	0.00 15	0.00 47	0.00 8	0.004
rpart:24 58376 295644 2	0.71	0.002 3	0.01 19	0.009 3	0.64	0.01 78	0.55	0.7 3	0.67	0.62	0.57	0.02 22	0.70	0.01 15	0.01 18	0.01 7	0.003
rf:3066 770 300535 7	0.72	0.002 3	0.00 22	0.001 0	0.67	0.00 46	0.64	0.7 0	0.68	0.66	0.53	0.00 51	0.75	0.00 13	0.00 21	0.00 2	0.002
knn:295 6442 265151 5	0.72	0.002 3	0.02 55	0.007 3	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.47	0.04 07	0.68	0.01 01	0.01 08	0.02 9	0.005
knn:247 8155 265151 5	0.72	0.002 3	0.00 53	0.000 4	0.71	0.00 04	0.55	0.8 8	0.82	0.66	0.52	0.00 01	0.71	0.00 07	0.00 14	0.03 3	0.002
nb:3326 487 247815 5	0.71	0.002 4	0.05 05	0.003 0	0.59	0.08 76	0.36	0.8 2	0.67	0.56	0.48	0.10 71	0.70	0.00 09	0.00 76	0.02 4	0.026
svm:23 32285 346359 8	0.71	0.002 4	0.00 02	0.000 2	0.74	0.00 01	0.67	0.8 2	0.79	0.71	- 0.19	0.00 01	0.71	0.00 09	0.00 06	0.02 2	0.003
rf:2789 391 265151 5	0.72	0.002 5	0.05 11	0.003 8	0.65	0.00 93	0.39	0.9 1	0.81	0.60	0.56	0.00 17	0.70	0.00 33	0.00 74	0.09 4	0.026
knn:341 4753 306677 0	0.71	0.002 6	0.02 55	0.003 2	0.65	0.00 93	0.48	0.8 2	0.73	0.61	0.55	0.00 48	0.71	0.00 32	0.00 55	0.01 8	0.010
knn:278 9391 306677 0	0.71	0.002 6	0.00 53	0.001 8	0.67	0.00 46	0.48	0.8 5	0.76	0.62	0.51	0.00 20	0.72	0.00 12	0.00 41	0.00 5	0.004

rpart:24 78155 300535 7	0.68	0.002 8	0.02 55	0.002 1	0.68	0.00 21	0.79	0.5 8	0.65	0.73	0.44	0.00 20	0.71	0.00 37	0.00 34	0.00 0	0.001
rpart:29 56442 300535 7	0.68	0.002 8	0.02 55	0.002 1	0.68	0.00 21	0.79	0.5 8	0.65	0.73	0.44	0.00 20	0.71	0.00 37	0.00 34	0.00 0	0.001
rpart:31 39092 300535 7	0.68	0.002 8	0.02 55	0.002 1	0.68	0.00 21	0.79	0.5 8	0.65	0.73	0.44	0.00 20	0.71	0.00 37	0.00 34	0.00 0	0.001
nb:3414 753 306677 0	0.71	0.002 8	0.00 48	0.001 2	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.47	0.00 54	0.74	0.00 09	0.00 31	0.03 4	0.013
nb:2789 391 300535 7	0.71	0.002 9	0.00 48	0.003 1	0.67	0.00 46	0.64	0.7 0	0.68	0.66	0.45	0.00 55	0.73	0.00 22	0.00 54	0.00 4	0.003
knn:313 9092 346359 8	0.71	0.003 0	0.01 19	0.002 9	0.67	0.00 46	0.73	0.6 1	0.65	0.69	0.47	0.00 90	0.73	0.00 59	0.00 48	0.01 2	0.004
nb:2332 285 278939 1	0.71	0.003 2	0.00 19	0.003 5	0.68	0.00 21	0.58	0.7 9	0.73	0.65	0.48	0.00 36	0.71	0.00 38	0.00 64	0.03 4	0.014
nb:3326 487 341475 3	0.71	0.003 2	0.00 48	0.007 6	0.58	0.13 39	0.42	0.7 3	0.61	0.56	0.44	0.24 32	0.71	0.00 32	0.01 46	0.09 4	0.068
svm:31 39092 306677 0	0.71	0.003 2	0.00 48	0.003 3	0.67	0.00 46	0.67	0.6 7	0.67	0.67	- 0.02	0.00 76	0.72	0.00 64	0.00 56	0.00 5	0.003
knn:233 2285 278939 1	0.71	0.003 2	0.00 53	0.002 1	0.65	0.00 93	0.52	0.7 9	0.71	0.62	0.53	0.01 15	0.70	0.00 31	0.00 38	0.02 1	0.006
rf:2789 391 236432 5	0.71	0.003 2	0.00 53	0.006 2	0.61	0.05 44	0.55	0.6 7	0.62	0.59	0.45	0.05 82	0.71	0.01 07	0.00 88	0.01 8	0.004
nb:2461 837 265151 5	0.71	0.003 3	0.01 13	0.002 7	0.65	0.00 93	0.67	0.6 4	0.65	0.66	0.41	0.01 20	0.72	0.00 28	0.00 59	0.08 0	0.013
nb:3463 598 236432 5	0.71	0.003 3	0.00 48	0.001 3	0.70	0.00 09	0.61	0.7 9	0.74	0.67	0.50	0.00 11	0.72	0.00 18	0.00 29	0.01 1	0.006
rf:2461 837 236432 5	0.71	0.003 5	0.01 19	0.001 8	0.68	0.00 21	0.61	0.7 6	0.71	0.66	0.54	0.00 31	0.70	0.00 39	0.00 31	0.00 8	0.002
rf:2789 391 300535 7	0.71	0.003 5	0.00 53	0.002 4	0.70	0.00 09	0.82	0.5 8	0.66	0.76	0.34	0.00 12	0.73	0.00 40	0.00 43	0.00 2	0.001
nb:3326 487	0.71	0.003 6	0.02 47	0.003 6	0.59	0.08 76	0.27	0.9 1	0.75	0.56	0.55	0.05 18	0.72	0.00 15	0.00 81	0.02 3	0.029

rf:2458 376																	
2478155	0.71	0.0037	0.0119	0.0027	0.64	0.0178	0.79	0.48	0.60	0.70	0.48	0.0533	0.70	0.0113	0.0051	0.091	0.010
rf:3463 598																	
2461837	0.71	0.0037	0.0053	0.0034	0.70	0.0009	0.76	0.64	0.68	0.72	0.47	0.0027	0.69	0.0095	0.0054	0.125	0.015
nb:2458 376																	
2789391	0.71	0.0038	0.0007	0.0013	0.67	0.0046	0.48	0.85	0.76	0.62	0.49	0.0038	0.71	0.0026	0.0038	0.081	0.017
rf:2458 376																	
2789391	0.71	0.0038	0.0053	0.0010	0.70	0.0009	0.55	0.85	0.78	0.65	0.53	0.0013	0.70	0.0028	0.0024	0.024	0.003
rf:3463 598																	
2956442	0.71	0.0038	0.0053	0.0022	0.65	0.0093	0.70	0.61	0.64	0.67	0.43	0.0229	0.71	0.0071	0.0038	0.119	0.014
knn:313 9092																	
2364325	0.71	0.0038	0.0053	0.0031	0.67	0.0046	0.64	0.70	0.68	0.66	0.54	0.0056	0.72	0.0060	0.0048	0.002	0.002
knn:300 5357																	
2651515	0.70	0.0039	0.0119	0.0047	0.58	0.1339	0.42	0.73	0.61	0.56	0.50	0.1856	0.74	0.0055	0.0078	0.023	0.006
rf:2478 155																	
3139092	0.71	0.0039	0.0053	0.0013	0.67	0.0046	0.79	0.55	0.63	0.72	0.55	0.0091	0.70	0.0044	0.0030	0.012	0.002
nb:2332 285																	
2461837	0.70	0.0039	0.0007	0.0019	0.70	0.0009	0.67	0.73	0.71	0.69	0.46	0.0035	0.73	0.0022	0.0039	0.023	0.012
rf:2332 285																	
2461837	0.71	0.0040	0.0022	0.0095	0.61	0.0544	0.70	0.52	0.59	0.63	0.37	0.1214	0.67	0.0182	0.0122	0.126	0.027
rf:2332 285																	
3139092	0.71	0.0040	0.0022	0.0032	0.70	0.0009	0.82	0.58	0.66	0.76	0.39	0.0019	0.73	0.0060	0.0054	0.011	0.003
rpart:23 32285																	
3005357	0.70	0.0042	0.0255	0.0129	0.64	0.0178	0.58	0.70	0.66	0.62	0.44	0.0060	0.72	0.0043	0.0154	0.002	0.003
knn:247 8155																	
2461837	0.70	0.0042	0.0119	0.0009	0.68	0.0021	0.91	0.45	0.63	0.83	0.45	0.0041	0.70	0.0055	0.0028	0.039	0.006
nb:3066 770																	
2651515	0.70	0.0043	0.0113	0.0023	0.64	0.0178	0.30	0.97	0.91	0.58	0.54	0.0004	0.70	0.0018	0.0073	0.106	0.018
svm:30 05357																	
2651515	0.70	0.0043	0.0505	0.0095	0.65	0.0093	0.55	0.76	0.69	0.63	-0.36	0.0078	0.72	0.0056	0.0147	0.045	0.008

svm:33 26487 233228 5	0.70	0.004 3	0.01 13	0.009 4	0.56	0.19 45	0.39	0.7 3	0.59	0.55	- 0.21	0.34 68	0.70	0.00 53	0.01 49	0.07 5	0.110
rf:3463 598 251236 4	0.70	0.004 3	0.02 55	0.001 0	0.68	0.00 21	0.45	0.9 1	0.83	0.63	0.61	0.00 14	0.71	0.00 28	0.00 30	0.25 2	0.015
rpart:34 14753 246183 7	0.69	0.004 5	0.02 55	0.001 8	0.68	0.00 21	0.55	0.8 2	0.75	0.64	0.57	0.00 19	0.67	0.00 40	0.00 32	0.05 5	0.015
nb:2461 837 251236 4	0.70	0.004 5	0.00 48	0.002 2	0.71	0.00 04	0.70	0.7 3	0.72	0.71	0.46	0.00 09	0.67	0.00 33	0.00 38	0.02 1	0.005
nb:3326 487 251236 4	0.70	0.004 5	0.02 47	0.004 3	0.56	0.19 45	0.33	0.7 9	0.61	0.54	0.50	0.33 90	0.69	0.00 24	0.00 81	0.04 7	0.028
nb:3414 753 246183 7	0.70	0.004 5	0.00 48	0.002 0	0.70	0.00 09	0.67	0.7 3	0.71	0.69	0.45	0.00 22	0.72	0.00 18	0.00 40	0.03 0	0.010
knn:247 8155 306677 0	0.70	0.004 5	0.02 55	0.002 8	0.61	0.05 44	0.61	0.6 1	0.61	0.61	0.50	0.06 87	0.69	0.00 83	0.00 55	0.01 6	0.002
knn:313 9092 306677 0	0.70	0.004 5	0.01 19	0.003 9	0.65	0.00 93	0.58	0.7 3	0.68	0.63	0.50	0.01 37	0.72	0.00 66	0.00 60	0.00 4	0.004
knn:341 4753 236432 5	0.70	0.004 6	0.01 19	0.001 5	0.68	0.00 21	0.61	0.7 6	0.71	0.66	0.48	0.00 22	0.76	0.00 24	0.00 30	0.01 0	0.003
nb:2789 391 236432 5	0.70	0.004 7	0.02 47	0.003 3	0.67	0.00 46	0.64	0.7 0	0.68	0.66	0.44	0.00 45	0.73	0.00 32	0.00 59	0.00 9	0.006
nb:3414 753 346359 8	0.70	0.004 7	0.00 48	0.001 3	0.70	0.00 09	0.61	0.7 9	0.74	0.67	0.49	0.00 26	0.72	0.00 14	0.00 32	0.05 0	0.014
knn:247 8155 295644 2	0.70	0.004 8	0.09 66	0.004 6	0.64	0.01 78	0.52	0.7 6	0.68	0.61	0.52	0.02 48	0.70	0.01 02	0.00 68	0.03 4	0.005
knn:313 9092 300535 7	0.70	0.004 8	0.00 22	0.001 3	0.71	0.00 04	0.88	0.5 5	0.66	0.82	0.41	0.00 05	0.73	0.00 15	0.00 30	0.00 0	0.002
svm:34 14753 346359 8	0.70	0.004 9	0.00 48	0.001 8	0.71	0.00 04	0.67	0.7 6	0.73	0.69	- 0.07	0.00 10	0.72	0.00 48	0.00 31	0.06 1	0.006
knn:246 1837 236432 5	0.70	0.004 9	0.02 55	0.004 3	0.68	0.00 21	0.55	0.8 2	0.75	0.64	0.59	0.00 06	0.69	0.00 51	0.00 68	0.00 5	0.004
rpart:33 26487	0.68	0.005 1	0.09 66	0.003 8	0.65	0.00 93	0.76	0.5 5	0.63	0.69	0.41	0.02 59	0.69	0.00 44	0.00 63	0.05 4	0.009

245837 6 nb:2458 376 246183 7 rf:3414 753 300535 7 knn:251 2364 236432 5 knn:245 8376 295644 2 rf:2789 391 346359 8 nb:2458 376 346359 8 nb:2789 391 251236 4 svm:23 64325 295644 2 svm:27 89391 251236 4 knn:251 2364 265151 5 svm:31 39092 346359 8 rf:2478 155 306677 0 rf:2364 325 295644 2 nb:3139 092 246183 7 svm:23 32285 265151 5	0.70	0.005 1	0.00 02	0.001 3	0.70	0.00 09	0.61	0.7 9	0.74	0.67	0.45	0.00 43	0.69	0.00 23	0.00 33	0.09 3	0.021
	0.70	0.005 2	0.02 55	0.003 4	0.65	0.00 93	0.55	0.7 6	0.69	0.63	0.53	0.01 46	0.75	0.00 55	0.00 54	0.00 9	0.003
	0.70	0.005 2	0.05 11	0.007 0	0.64	0.01 78	0.42	0.8 5	0.74	0.60	0.70	0.01 17	0.69	0.01 49	0.01 01	0.11 1	0.016
	0.70	0.005 3	0.01 19	0.002 0	0.65	0.00 93	0.55	0.7 6	0.69	0.63	0.53	0.02 10	0.69	0.00 58	0.00 38	0.04 6	0.008
	0.70	0.005 4	0.01 19	0.002 4	0.65	0.00 93	0.52	0.7 9	0.71	0.62	0.50	0.00 81	0.69	0.00 39	0.00 41	0.02 4	0.007
	0.70	0.005 5	0.00 19	0.000 8	0.70	0.00 09	0.42	0.9 7	0.93	0.63	0.54	0.00 03	0.71	0.00 18	0.00 31	0.13 8	0.026
	0.70	0.005 5	0.00 19	0.003 0	0.70	0.00 09	0.70	0.7 0	0.70	0.70	0.45	0.00 20	0.69	0.00 34	0.00 52	0.01 7	0.004
	0.70	0.005 5	0.00 48	0.005 5	0.64	0.01 78	0.48	0.7 9	0.70	0.60	0.04	0.02 39	0.72	0.00 90	0.00 80	0.01 8	0.005
	0.70	0.005 5	0.00 48	0.009 7	0.67	0.00 46	0.58	0.7 6	0.70	0.64	- 0.31	0.00 72	0.66	0.01 65	0.01 38	0.15 0	0.034
	0.69	0.005 6	0.01 19	0.003 9	0.68	0.00 21	0.61	0.7 6	0.71	0.66	0.50	0.00 34	0.73	0.00 41	0.00 63	0.12 2	0.027
	0.70	0.005 8	0.02 47	0.033 8	0.67	0.00 46	0.82	0.5 2	0.63	0.74	0.01	0.00 75	0.72	0.03 77	0.04 03	0.12 7	0.024
	0.70	0.005 8	0.02 55	0.002 6	0.65	0.00 93	0.79	0.5 2	0.62	0.71	0.38	0.01 02	0.69	0.00 73	0.00 45	0.11 5	0.009
	0.70	0.005 9	0.00 53	0.004 6	0.68	0.00 21	0.58	0.7 9	0.73	0.65	0.54	0.00 17	0.73	0.00 56	0.00 69	0.01 3	0.005
	0.70	0.006 0	0.00 07	0.005 5	0.67	0.00 46	0.61	0.7 3	0.69	0.65	0.46	0.00 60	0.71	0.00 69	0.00 82	0.01 0	0.007
	0.70	0.006 0	0.02 47	0.002 3	0.67	0.00 46	0.58	0.7 6	0.70	0.64	- 0.30	0.00 25	0.71	0.00 18	0.00 43	0.04 5	0.014

svm:27 89391 236432 5	0.70	0.006 0	0.02 47	0.004 6	0.65	0.00 93	0.64	0.6 7	0.66	0.65	- 0.23	0.01 04	0.70	0.00 39	0.00 77	0.01 2	0.007
knn:278 9391 265151 5	0.70	0.006 2	0.09 66	0.012 4	0.64	0.01 78	0.45	0.8 2	0.71	0.60	0.51	0.01 31	0.64	0.01 65	0.01 63	0.06 9	0.010
rf:2478 155 295644 2	0.70	0.006 2	0.01 19	0.002 9	0.68	0.00 21	0.79	0.5 8	0.65	0.73	0.44	0.00 48	0.71	0.00 78	0.00 51	0.05 7	0.005
rf:2332 285 278939 1	0.70	0.006 3	0.00 53	0.003 9	0.65	0.00 93	0.48	0.8 2	0.73	0.61	0.54	0.00 54	0.68	0.00 62	0.00 63	0.03 5	0.007
rpart:24 58376 233228 5	0.67	0.006 4	0.05 11	0.005 4	0.67	0.00 46	0.76	0.5 8	0.64	0.70	0.48	0.01 51	0.66	0.01 93	0.00 72	0.04 2	0.004
rpart:24 58376 236432 5	0.67	0.006 4	0.05 11	0.005 4	0.67	0.00 46	0.76	0.5 8	0.64	0.70	0.48	0.01 51	0.66	0.01 93	0.00 72	0.04 2	0.004
rpart:24 58376 247815 5	0.67	0.006 4	0.05 11	0.005 4	0.67	0.00 46	0.76	0.5 8	0.64	0.70	0.48	0.01 51	0.66	0.01 93	0.00 72	0.04 2	0.004
rpart:24 58376 278939 1	0.67	0.006 4	0.05 11	0.005 4	0.67	0.00 46	0.76	0.5 8	0.64	0.70	0.48	0.01 51	0.66	0.01 93	0.00 72	0.04 2	0.004
rpart:24 58376 300535 7	0.67	0.006 4	0.05 11	0.005 4	0.67	0.00 46	0.76	0.5 8	0.64	0.70	0.48	0.01 51	0.66	0.01 93	0.00 72	0.04 2	0.004
rpart:24 58376 306677 0	0.67	0.006 4	0.05 11	0.005 4	0.67	0.00 46	0.76	0.5 8	0.64	0.70	0.48	0.01 51	0.66	0.01 93	0.00 72	0.04 2	0.004
rpart:24 58376 313909 2	0.67	0.006 4	0.05 11	0.005 4	0.67	0.00 46	0.76	0.5 8	0.64	0.70	0.48	0.01 51	0.66	0.01 93	0.00 72	0.04 2	0.004
nb:2332 285 295644 2	0.69	0.006 5	0.02 47	0.009 4	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.49	0.01 07	0.72	0.01 21	0.01 30	0.05 4	0.019
rf:3139 092 346359 8	0.69	0.006 7	0.01 19	0.008 1	0.65	0.00 93	0.73	0.5 8	0.63	0.68	0.54	0.01 73	0.72	0.01 54	0.01 13	0.04 9	0.007
knn:245 8376 246183 7	0.69	0.006 8	0.02 55	0.006 6	0.62	0.03 20	0.70	0.5 5	0.61	0.64	0.45	0.06 93	0.68	0.01 51	0.00 90	0.07 5	0.014
nb:3139 092 278939 1	0.69	0.006 8	0.02 47	0.006 6	0.68	0.00 21	0.55	0.8 2	0.75	0.64	0.49	0.00 22	0.69	0.00 54	0.01 04	0.00 8	0.005
nb:3326 487	0.69	0.006 8	0.01 13	0.015 5	0.56	0.19 45	0.30	0.8 2	0.63	0.54	0.47	0.25 95	0.69	0.00 67	0.02 39	0.10 7	0.144

306677 0 svm:24 78155 346359 8	0.69	0.006 8	0.02 47	0.004 5	0.65	0.00 93	0.73	0.5 8	0.63	0.68	0.12	0.02 53	0.63	0.01 32	0.00 69	0.07 7	0.013
svm:33 26487 300535 7	0.69	0.006 8	0.00 48	0.014 5	0.55	0.26 93	0.36	0.7 3	0.57	0.53	0.02	0.42 87	0.71	0.01 62	0.01 87	0.06 7	0.063
knn:246 1837 251236 4	0.69	0.006 9	0.00 22	0.005 2	0.73	0.00 01	0.73	0.7 3	0.73	0.73	0.50	0.00 02	0.67	0.00 98	0.00 75	0.05 5	0.005
knn:251 2364 300535 7	0.69	0.007 0	0.09 66	0.006 5	0.62	0.03 20	0.61	0.6 4	0.63	0.62	0.50	0.04 40	0.70	0.00 52	0.00 92	0.00 9	0.004
nb:3414 753 278939 1	0.69	0.007 1	0.00 48	0.003 4	0.67	0.00 46	0.64	0.7 0	0.68	0.66	0.44	0.00 83	0.70	0.00 26	0.00 65	0.03 2	0.009
nb:3139 092 346359 8	0.69	0.007 3	0.00 48	0.003 9	0.68	0.00 21	0.64	0.7 3	0.70	0.67	0.47	0.00 49	0.72	0.00 39	0.00 66	0.00 7	0.008
rf:2364 325 300535 7	0.69	0.007 3	0.01 19	0.001 4	0.68	0.00 21	0.76	0.6 1	0.66	0.71	0.47	0.00 25	0.73	0.00 25	0.00 27	0.00 0	0.001
rpart:24 58376 246183 7	0.67	0.007 4	0.05 11	0.006 2	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.47	0.00 97	0.65	0.01 25	0.00 79	0.03 8	0.012
rpart:24 61837 236432 5	0.67	0.007 4	0.05 11	0.006 2	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.47	0.00 97	0.65	0.01 25	0.00 79	0.03 8	0.012
rpart:24 61837 295644 2	0.67	0.007 4	0.05 11	0.006 2	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.47	0.00 97	0.65	0.01 25	0.00 79	0.03 8	0.012
rpart:24 61837 300535 7	0.67	0.007 4	0.05 11	0.006 2	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.47	0.00 97	0.65	0.01 25	0.00 79	0.03 8	0.012
rpart:24 78155 246183 7	0.67	0.007 4	0.05 11	0.006 2	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.47	0.00 97	0.65	0.01 25	0.00 79	0.03 8	0.012
rpart:27 89391 246183 7	0.67	0.007 4	0.05 11	0.006 2	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.47	0.00 97	0.65	0.01 25	0.00 79	0.03 8	0.012
rpart:31 39092 246183 7	0.67	0.007 4	0.05 11	0.006 2	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.47	0.00 97	0.65	0.01 25	0.00 79	0.03 8	0.012
rpart:33 26487 246183 7	0.67	0.007 4	0.05 11	0.006 2	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.47	0.00 97	0.65	0.01 25	0.00 79	0.03 8	0.012

rf:34 63598 246183 7	0.67	0.007 4	0.05 11	0.006 2	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.47	0.00 97	0.65	0.01 25	0.00 79	0.03 8	0.012
knn:233 2285 300535 7	0.69	0.007 4	0.02 55	0.009 3	0.68	0.00 21	0.64	0.7 3	0.70	0.67	0.50	0.00 34	0.69	0.01 31	0.01 31	0.06 7	0.007
rf:3005 357 265151 5	0.69	0.007 5	0.00 22	0.007 5	0.65	0.00 93	0.61	0.7 0	0.67	0.64	0.45	0.01 03	0.73	0.00 88	0.01 01	0.06 4	0.045
svm:24 58376 247815 5	0.69	0.007 6	0.02 47	0.006 6	0.62	0.03 20	0.58	0.6 7	0.63	0.61	0.06	0.08 42	0.67	0.01 36	0.00 96	0.03 7	0.008
knn:247 8155 346359 8	0.69	0.007 7	0.02 55	0.007 0	0.65	0.00 93	0.79	0.5 2	0.62	0.71	0.44	0.02 07	0.66	0.02 18	0.01 05	0.37 1	0.031
knn:245 8376 233228 5	0.69	0.007 7	0.05 11	0.008 1	0.67	0.00 46	0.64	0.7 0	0.68	0.66	0.50	0.01 74	0.70	0.01 49	0.01 12	0.20 9	0.047
rf:2458 376 265151 5	0.69	0.007 8	0.00 53	0.004 4	0.65	0.00 93	0.39	0.9 1	0.81	0.60	0.55	0.00 17	0.70	0.00 39	0.00 83	0.12 7	0.031
rf:2789 391 251236 4	0.69	0.007 9	0.00 53	0.003 1	0.70	0.00 09	0.67	0.7 3	0.71	0.69	0.45	0.00 19	0.68	0.00 56	0.00 49	0.02 7	0.004
rf:3326 487 236432 5	0.69	0.007 9	0.02 55	0.004 2	0.58	0.13 39	0.27	0.8 8	0.69	0.55	0.60	0.12 99	0.73	0.00 28	0.00 79	0.03 0	0.021
svm:34 14753 295644 2	0.69	0.008 0	0.02 47	0.007 8	0.65	0.00 93	0.55	0.7 6	0.69	0.63	- 0.17	0.01 08	0.72	0.00 85	0.01 15	0.04 7	0.009
knn:233 2285 236432 5	0.69	0.008 0	0.00 53	0.002 7	0.70	0.00 09	0.67	0.7 3	0.71	0.69	0.50	0.00 21	0.72	0.00 33	0.00 45	0.02 7	0.007
knn:233 2285 251236 4	0.69	0.008 2	0.00 03	0.002 1	0.73	0.00 01	0.64	0.8 2	0.78	0.69	0.55	0.00 02	0.72	0.00 51	0.00 39	0.13 5	0.015
rf:2956 442 300535 7	0.69	0.008 2	0.00 53	0.009 8	0.64	0.01 78	0.64	0.6 4	0.64	0.64	0.46	0.02 33	0.71	0.01 35	0.01 24	0.00 4	0.002
svm:33 26487 236432 5	0.69	0.008 3	0.05 05	0.018 4	0.58	0.13 39	0.39	0.7 6	0.62	0.56	- 0.18	0.21 83	0.70	0.01 41	0.02 41	0.12 1	0.127
knn:341 4753 247815 5	0.69	0.008 4	0.05 11	0.009 2	0.61	0.05 44	0.67	0.5 5	0.59	0.62	0.45	0.11 23	0.70	0.01 56	0.01 24	0.19 8	0.020
rf:30 66770	0.67	0.008 4	0.02 55	0.006 7	0.64	0.01 78	0.67	0.6 1	0.63	0.65	0.56	0.02 38	0.69	0.00 93	0.00 87	0.00 1	0.002

300535 7 rf:2458 376 295644 2 nb:2364 325 295644 2 svm:34 14753 278939 1 rf:2461 837 300535 7 rpart:23 32285 265151 5 rpart:23 64325 265151 5 rpart:24 78155 265151 5 rpart:25 12364 265151 5 rpart:27 89391 265151 5 rpart:29 56442 265151 5 rpart:30 05357 265151 5 rpart:30 66770 265151 5 rpart:33 26487 265151 5 rpart:34 14753 265151 5 rpart:34 63598 265151 5	0.69

rf:2478 155 251236 4	0.69	0.009 1	0.00 53	0.015 9	0.59	0.08 76	0.70	0.4 8	0.58	0.62	0.43	0.21 17	0.66	0.02 53	0.01 93	0.37 9	0.044
knn:341 4753 346359 8	0.69	0.009 1	0.00 53	0.001 3	0.70	0.00 09	0.61	0.7 9	0.74	0.67	0.50	0.00 26	0.73	0.00 56	0.00 27	0.12 8	0.009
knn:233 2285 313909 2	0.69	0.009 1	0.00 09	0.001 3	0.71	0.00 04	0.67	0.7 6	0.73	0.69	0.50	0.00 05	0.75	0.00 30	0.00 24	0.00 7	0.003
rf:2956 442 265151 5	0.69	0.009 2	0.02 55	0.004 7	0.62	0.03 20	0.30	0.9 4	0.83	0.57	0.58	0.00 85	0.70	0.00 36	0.00 91	0.12 7	0.040
rf:2478 155 246183 7	0.69	0.009 2	0.02 55	0.003 8	0.67	0.00 46	0.61	0.7 3	0.69	0.65	0.64	0.00 98	0.64	0.01 14	0.00 62	0.07 5	0.009
rf:2458 376 306677 0	0.69	0.009 2	0.02 55	0.012 5	0.61	0.05 44	0.48	0.7 3	0.64	0.59	0.55	0.08 25	0.67	0.02 91	0.01 66	0.29 7	0.021
svm:34 63598 306677 0	0.69	0.009 3	0.00 48	0.002 5	0.71	0.00 04	0.58	0.8 5	0.79	0.67	- 0.29	0.00 04	0.69	0.00 13	0.00 57	0.02 7	0.026
knn:236 4325 265151 5	0.68	0.009 5	0.17 17	0.013 6	0.64	0.01 78	0.33	0.9 4	0.85	0.58	0.61	0.00 04	0.70	0.00 64	0.02 03	0.02 3	0.035
nb:2461 837 306677 0	0.68	0.009 7	0.00 48	0.006 7	0.64	0.01 78	0.52	0.7 6	0.68	0.61	0.48	0.00 92	0.68	0.00 57	0.00 97	0.04 5	0.026
rf:3414 753 236432 5	0.69	0.009 8	0.00 22	0.001 8	0.68	0.00 21	0.64	0.7 3	0.70	0.67	0.52	0.00 43	0.75	0.00 37	0.00 32	0.01 8	0.004
knn:236 4325 295644 2	0.68	0.010 0	0.02 55	0.007 2	0.65	0.00 93	0.55	0.7 6	0.69	0.63	0.54	0.01 28	0.73	0.01 24	0.00 98	0.01 0	0.004
knn:313 9092 295644 2	0.68	0.010 2	0.05 11	0.012 6	0.64	0.01 78	0.79	0.4 8	0.60	0.70	0.44	0.02 43	0.73	0.01 42	0.01 69	0.00 2	0.002
knn:313 9092 278939 1	0.68	0.010 4	0.02 55	0.004 5	0.68	0.00 21	0.61	0.7 6	0.71	0.66	0.48	0.00 20	0.71	0.00 57	0.00 66	0.00 9	0.004
knn:278 9391 246183 7	0.68	0.010 4	0.05 11	0.008 1	0.65	0.00 93	0.55	0.7 6	0.69	0.63	0.50	0.00 97	0.69	0.00 91	0.01 09	0.03 7	0.009
nb:3326 487 245837 6	0.68	0.010 9	0.02 47	0.004 2	0.68	0.00 21	0.42	0.9 4	0.88	0.62	0.49	0.00 09	0.65	0.00 33	0.00 99	0.16 9	0.098
nb:2789 391	0.68	0.011 3	0.01 13	0.006 2	0.64	0.01 78	0.52	0.7 6	0.68	0.61	0.44	0.01 36	0.69	0.00 50	0.01 18	0.08 4	0.012

265151																		
5																		
nb:3326																		
487																		
313909	0.68	0.011	0.02	0.013	0.59	0.08	0.45	0.7	0.63	0.57	0.43	0.14	0.71	0.00	0.02	0.03	0.041	
2		3	47	7		76		3				52		60	02	0		
svm:33																		
26487	0.68	0.011	0.02	0.006	0.61	0.05	0.48	0.7	0.64	0.59	-	0.15	0.66	0.01	0.00	0.22	0.081	
245837		3	47	1		44		3			0.08	75		34	92	4		
6																		
rpart:33																		
26487	0.66	0.011	0.17	0.008	0.64	0.01	0.70	0.5	0.62	0.66	0.41	0.02	0.69	0.00	0.01	0.02	0.007	
313909		5	17	3		78		8				63		38	21	1		
2																		
rf:2789																		
391	0.68	0.011	0.01	0.009	0.65	0.00	0.58	0.7	0.68	0.63	0.51	0.01	0.65	0.01	0.01	0.04	0.019	
306677		5	19	8		93		3				16		05	28	8		
0																		
nb:3414																		
753	0.68	0.011	0.02	0.010	0.65	0.00	0.64	0.6	0.66	0.65	0.45	0.02	0.72	0.01	0.01	0.05	0.012	
295644		7	47	0		93		7				40		14	35	7		
2																		
svm:27																		
89391	0.68	0.011	0.01	0.007	0.68	0.00	0.58	0.7	0.73	0.65	-	0.00	0.68	0.00	0.01	0.04	0.013	
346359		7	13	6		21		9			0.07	25		89	08	5		
8																		
rf:2789																		
391	0.68	0.011	0.01	0.007	0.65	0.00	0.64	0.6	0.66	0.65	0.47	0.02	0.65	0.01	0.01	0.03	0.008	
246183		7	19	8		93		7				40		51	02	2		
7																		
svm:24																		
61837	0.68	0.012	0.00	0.007	0.71	0.00	0.70	0.7	0.72	0.71	0.06	0.00	0.67	0.01	0.01	0.01	0.005	
300535		2	19	8		04		3				07		36	04	7		
7																		
nb:3463																		
598	0.68	0.012	0.05	0.010	0.65	0.00	0.55	0.7	0.69	0.63	0.50	0.01	0.67	0.01	0.01	0.07	0.030	
246183		6	05	9		93		6				03		20	40	4		
7																		
svm:34																		
63598	0.68	0.012	0.00	0.002	0.70	0.00	0.64	0.7	0.72	0.68	0.12	0.00	0.65	0.01	0.00	0.55	0.051	
246183		6	48	2		09		6				18		15	49	3		
7																		
knn:346																		
3598	0.68	0.012	0.05	0.003	0.67	0.00	0.55	0.7	0.72	0.63	0.51	0.00	0.70	0.00	0.00	0.02	0.005	
295644		8	11	3		46		9				79		63	53	4		
2																		
rf:3414																		
753	0.68	0.013	0.00	0.002	0.67	0.00	0.67	0.6	0.67	0.67	0.42	0.01	0.72	0.00	0.00	0.08	0.012	
346359		3	53	9		46		7				09		57	46	2		
8																		
rf:3139																		
092	0.68	0.013	0.00	0.013	0.64	0.01	0.55	0.7	0.67	0.62	0.54	0.02	0.67	0.01	0.01	0.01	0.003	
278939		3	53	9		78		3				60		82	73	7		
1																		
nb:3463																		
598	0.68	0.013	0.00	0.004	0.70	0.00	0.55	0.8	0.78	0.65	0.50	0.00	0.68	0.00	0.00	0.05	0.028	
306677		6	48	1		09		5				06		35	70	3		
0																		
nb:2478																		
155	0.67	0.014	0.09	0.006	0.64	0.01	0.48	0.7	0.70	0.60	0.51	0.02	0.69	0.00	0.00	0.01	0.006	
295644		1	65	8		78		9				23		65	99	3		
2																		

nb:2512 364 295644 2	0.67	0.014 1	0.02 47	0.008 5	0.67	0.00 46	0.58	0.7 6	0.70	0.64	0.51	0.00 76	0.70	0.01 13	0.01 13	0.03 3	0.007
rpart:34 63598 295644 2	0.67	0.014 3	0.02 55	0.022 0	0.59	0.08 76	0.67	0.5 2	0.58	0.61	0.49	0.27 96	0.67	0.05 56	0.02 51	0.45 2	0.164
rpart:23 32285 313909 2	0.65	0.014 5	0.09 66	0.013 0	0.65	0.00 93	0.70	0.6 1	0.64	0.67	0.49	0.01 34	0.67	0.01 65	0.01 51	0.00 3	0.002
rpart:24 78155 313909 2	0.65	0.014 5	0.09 66	0.013 0	0.65	0.00 93	0.70	0.6 1	0.64	0.67	0.49	0.01 34	0.67	0.01 65	0.01 51	0.00 3	0.002
rpart:31 39092 236432 5	0.65	0.014 5	0.09 66	0.013 0	0.65	0.00 93	0.70	0.6 1	0.64	0.67	0.49	0.01 34	0.67	0.01 65	0.01 51	0.00 3	0.002
rpart:31 39092 278939 1	0.65	0.014 5	0.09 66	0.013 0	0.65	0.00 93	0.70	0.6 1	0.64	0.67	0.49	0.01 34	0.67	0.01 65	0.01 51	0.00 3	0.002
rpart:31 39092 295644 2	0.65	0.014 5	0.09 66	0.013 0	0.65	0.00 93	0.70	0.6 1	0.64	0.67	0.49	0.01 34	0.67	0.01 65	0.01 51	0.00 3	0.002
rpart:31 39092 306677 0	0.65	0.014 5	0.09 66	0.013 0	0.65	0.00 93	0.70	0.6 1	0.64	0.67	0.49	0.01 34	0.67	0.01 65	0.01 51	0.00 3	0.002
nb:2789 391 346359 8	0.67	0.014 7	0.02 47	0.008 9	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.48	0.00 35	0.67	0.00 74	0.01 29	0.03 8	0.015
nb:2956 442 265151 5	0.67	0.014 7	0.00 48	0.015 0	0.62	0.03 20	0.55	0.7 0	0.64	0.61	0.44	0.04 60	0.70	0.01 65	0.02 12	0.14 0	0.016
nb:2956 442 300535 7	0.67	0.014 7	0.05 05	0.010 8	0.65	0.00 93	0.58	0.7 3	0.68	0.63	0.48	0.01 39	0.73	0.01 15	0.01 39	0.01 0	0.005
nb:3139 092 295644 2	0.67	0.014 7	0.05 05	0.020 3	0.64	0.01 78	0.64	0.6 4	0.64	0.64	0.46	0.03 85	0.71	0.02 42	0.02 42	0.01 4	0.006
rf:3139 092 300535 7	0.67	0.015 0	0.01 19	0.001 9	0.67	0.00 46	0.67	0.6 7	0.67	0.67	0.62	0.00 43	0.73	0.00 35	0.00 36	0.00 1	0.001
nb:3139 092 265151 5	0.67	0.015 2	0.01 13	0.002 7	0.67	0.00 46	0.39	0.9 4	0.87	0.61	0.52	0.00 01	0.70	0.00 14	0.00 63	0.02 9	0.006
svm:27 89391 265151 5	0.67	0.015 2	0.01 13	0.009 3	0.67	0.00 46	0.58	0.7 6	0.70	0.64	- 0.32	0.00 45	0.66	0.00 79	0.01 46	0.06 9	0.012
svm:27 89391	0.67	0.015 2	0.00 48	0.007 4	0.70	0.00 09	0.61	0.7 9	0.74	0.67	- 0.15	0.00 06	0.67	0.00 76	0.01 03	0.03 8	0.015

306677 0 knn:332 6487 251236 4	0.67	0.015 3	0.02 55	0.022 7	0.58	0.13 39	0.33	0.8 2	0.65	0.55	0.54	0.13 16	0.66	0.02 01	0.03 01	0.20 8	0.055
knn:341 4753 313909 2	0.67	0.015 7	0.09 66	0.022 9	0.64	0.01 78	0.73	0.5 5	0.62	0.67	0.46	0.03 36	0.70	0.03 52	0.02 70	0.02 7	0.011
knn:346 3598 265151 5	0.67	0.016 3	0.44 78	0.009 0	0.61	0.05 44	0.33	0.8 8	0.73	0.57	0.70	0.04 78	0.69	0.01 93	0.01 31	0.06 6	0.017
svm:31 39092 246183 7	0.67	0.016 4	0.02 47	0.019 3	0.65	0.00 93	0.73	0.5 8	0.63	0.68	- 0.25	0.02 20	0.67	0.03 44	0.02 28	0.03 4	0.011
svm:34 63598 236432 5	0.67	0.017 0	0.00 19	0.002 8	0.71	0.00 04	0.58	0.8 5	0.79	0.67	0.01	0.00 04	0.68	0.00 58	0.00 49	0.08 6	0.009
knn:247 8155 278939 1	0.67	0.017 3	0.09 66	0.030 1	0.64	0.01 78	0.45	0.8 2	0.71	0.60	0.54	0.00 97	0.65	0.02 93	0.03 44	0.05 3	0.010
rf:3414 753 278939 1	0.67	0.017 3	0.01 19	0.010 1	0.68	0.00 21	0.64	0.7 3	0.70	0.67	0.50	0.00 43	0.70	0.01 72	0.01 28	0.04 5	0.011
svm:23 32285 278939 1	0.67	0.017 6	0.09 65	0.018 3	0.64	0.01 78	0.45	0.8 2	0.71	0.60	- 0.01	0.01 45	0.66	0.01 41	0.02 26	0.04 5	0.017
knn:346 3598 300535 7	0.67	0.018 4	0.09 66	0.014 4	0.61	0.05 44	0.39	0.8 2	0.68	0.57	0.58	0.06 32	0.67	0.02 33	0.01 85	0.18 9	0.012
rpart:23 32285 246183 7	0.66	0.018 6	0.05 11	0.036 8	0.67	0.00 46	0.61	0.7 3	0.69	0.65	0.59	0.01 08	0.62	0.05 59	0.03 94	0.09 4	0.031
nb:2458 376 295644 2	0.67	0.018 9	0.00 48	0.005 2	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.46	0.00 96	0.68	0.01 01	0.00 86	0.13 0	0.024
nb:2789 391 306677 0	0.67	0.018 9	0.00 48	0.009 0	0.67	0.00 46	0.61	0.7 3	0.69	0.65	0.44	0.00 53	0.68	0.00 61	0.01 31	0.03 5	0.021
svm:24 78155 278939 1	0.67	0.018 9	0.05 05	0.007 9	0.61	0.05 44	0.55	0.6 7	0.62	0.59	- 0.13	0.08 94	0.68	0.00 48	0.01 20	0.01 7	0.009
rf:2364 325 265151 5	0.67	0.019 2	0.09 66	0.006 7	0.64	0.01 78	0.36	0.9 1	0.80	0.59	0.73	0.00 18	0.68	0.00 36	0.01 13	0.16 3	0.064
svm:33 26487 306677 0	0.67	0.019 6	0.01 13	0.028 5	0.56	0.19 45	0.36	0.7 6	0.60	0.54	- 0.35	0.38 33	0.66	0.01 44	0.03 64	0.14 0	0.252

svm:34 63598 251236 4	0.67	0.019 6	0.00 19	0.004 0	0.71	0.00 04	0.61	0.8 2	0.77	0.68	0.02	0.00 09	0.66	0.00 88	0.00 64	0.19 3	0.021
rf:3414 753 265151 5	0.67	0.019 6	0.02 55	0.004 7	0.64	0.01 78	0.64	0.6 4	0.64	0.64	0.35	0.02 88	0.71	0.00 42	0.00 75	0.13 4	0.035
knn:233 2285 295644 2	0.66	0.020 8	0.00 53	0.016 6	0.65	0.00 93	0.52	0.7 9	0.71	0.62	0.53	0.01 64	0.68	0.02 50	0.01 97	0.07 2	0.016
rf:3414 753 233228 5	0.67	0.021 0	0.05 11	0.012 2	0.65	0.00 93	0.52	0.7 9	0.71	0.62	0.58	0.01 12	0.70	0.01 75	0.01 50	0.14 0	0.028
svm:25 12364 295644 2	0.66	0.021 0	0.05 05	0.012 2	0.67	0.00 46	0.58	0.7 6	0.70	0.64	0.04	0.00 76	0.67	0.01 55	0.01 53	0.03 6	0.008
knn:332 6487 236432 5	0.66	0.021 1	0.02 55	0.034 7	0.58	0.13 39	0.24	0.9 1	0.73	0.55	0.61	0.06 82	0.67	0.02 78	0.04 06	0.19 5	0.111
rf:3414 753 295644 2	0.67	0.021 3	0.02 55	0.016 1	0.64	0.01 78	0.55	0.7 3	0.67	0.62	0.50	0.02 96	0.71	0.02 24	0.01 93	0.06 5	0.015
rf:3326 487 245837 6	0.66	0.021 7	0.09 66	0.008 6	0.64	0.01 78	0.33	0.9 4	0.85	0.58	0.60	0.00 33	0.67	0.00 91	0.01 34	0.13 6	0.051
knn:246 1837 306677 0	0.66	0.022 4	0.17 17	0.036 1	0.55	0.26 93	0.30	0.7 9	0.59	0.53	0.64	0.45 52	0.67	0.05 63	0.04 14	0.27 3	0.108
svm:34 63598 295644 2	0.66	0.022 5	0.02 47	0.009 9	0.64	0.01 78	0.48	0.7 9	0.70	0.60	0.02	0.02 16	0.68	0.01 62	0.01 31	0.06 0	0.011
rpart:31 39092 265151 5	0.66	0.022 6	0.17 17	0.021 9	0.62	0.03 20	0.64	0.6 1	0.62	0.63	0.45	0.04 07	0.70	0.01 47	0.02 55	0.16 1	0.032
rf:2789 391 295644 2	0.66	0.022 8	0.05 11	0.017 9	0.61	0.05 44	0.52	0.7 0	0.63	0.59	0.48	0.06 66	0.65	0.02 52	0.02 13	0.04 0	0.011
knn:306 6770 295644 2	0.66	0.023 3	0.02 55	0.014 3	0.59	0.08 76	0.48	0.7 0	0.62	0.58	0.49	0.11 26	0.69	0.01 63	0.01 78	0.02 8	0.008
knn:233 2285 306677 0	0.66	0.023 4	0.01 19	0.004 1	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.52	0.00 47	0.71	0.00 48	0.00 63	0.04 4	0.014
rpart:24 58376 251236 4	0.66	0.023 6	0.02 55	0.008 3	0.62	0.03 20	0.61	0.6 4	0.63	0.62	0.50	0.07 60	0.65	0.02 27	0.01 09	0.44 1	0.026
nb:3326 487	0.66	0.024 1	0.05 05	0.017 3	0.58	0.13 39	0.24	0.9 1	0.73	0.55	0.57	0.06 82	0.69	0.00 78	0.02 54	0.12 3	0.139

[illegible]

rf:2458 376 251236 4	0.66	0.026 1	0.01 19	0.012 8	0.68	0.00 21	0.55	0.8 2	0.75	0.64	0.55	0.00 58	0.64	0.02 92	0.01 67	0.41 2	0.019
rf:3463 598 265151 5	0.66	0.026 4	0.00 53	0.001 1	0.68	0.00 21	0.61	0.7 6	0.71	0.66	0.31	0.00 13	0.71	0.00 15	0.00 28	0.10 0	0.019
nb:3463 598 265151 5	0.66	0.026 7	0.01 13	0.004 9	0.67	0.00 46	0.45	0.8 8	0.79	0.62	0.49	0.00 10	0.69	0.00 41	0.00 94	0.15 6	0.024
svm:24 78155 295644 2	0.66	0.026 7	0.09 65	0.025 8	0.61	0.05 44	0.55	0.6 7	0.62	0.59	0.06	0.12 74	0.68	0.03 45	0.02 91	0.04 5	0.010
svm:27 89391 300535 7	0.66	0.026 7	0.02 47	0.121 4	0.65	0.00 93	0.55	0.7 6	0.69	0.63	- 0.28	0.01 23	0.64	0.13 15	0.13 87	0.44 1	0.099
rf:2461 837 306677 0	0.66	0.027 4	0.01 19	0.010 4	0.65	0.00 93	0.55	0.7 6	0.69	0.63	0.57	0.01 49	0.64	0.01 47	0.01 30	0.10 4	0.023
svm:33 26487 341475 3	0.66	0.027 6	0.02 47	0.029 4	0.55	0.26 93	0.36	0.7 3	0.57	0.53	- 0.18	0.55 64	0.68	0.02 07	0.03 53	0.14 7	0.214
rf:3414 753 251236 4	0.66	0.027 8	0.02 55	0.015 9	0.61	0.05 44	0.45	0.7 6	0.65	0.58	0.57	0.11 46	0.72	0.02 50	0.01 92	0.29 0	0.038
rf:3414 753 313909 2	0.66	0.028 3	0.02 55	0.018 5	0.65	0.00 93	0.73	0.5 8	0.63	0.68	0.52	0.02 00	0.68	0.03 03	0.02 21	0.03 0	0.007
svm:29 56442 300535 7	0.66	0.028 6	0.01 13	0.046 7	0.68	0.00 21	0.76	0.6 1	0.66	0.71	- 0.28	0.00 43	0.70	0.05 38	0.05 48	0.19 4	0.014
knn:346 3598 246183 7	0.66	0.028 6	0.05 11	0.024 3	0.62	0.03 20	0.45	0.7 9	0.68	0.59	0.54	0.03 90	0.67	0.02 55	0.02 76	0.07 3	0.047
rf:2478 155 265151 5	0.66	0.028 8	0.17 17	0.018 6	0.61	0.05 44	0.36	0.8 5	0.71	0.57	0.58	0.02 58	0.65	0.01 35	0.02 41	0.30 3	0.140
svm:23 64325 265151 5	0.66	0.029 5	0.09 65	0.015 7	0.64	0.01 78	0.36	0.9 1	0.80	0.59	0.25	0.01 00	0.69	0.01 69	0.02 10	0.12 0	0.016
svm:24 61837 236432 5	0.66	0.029 5	0.00 19	0.030 9	0.70	0.00 09	0.64	0.7 6	0.72	0.68	0.07	0.00 07	0.64	0.03 36	0.03 53	0.03 8	0.034
nb:3326 487 278939 1	0.65	0.030 5	0.09 65	0.023 3	0.58	0.13 39	0.33	0.8 2	0.65	0.55	0.47	0.14 35	0.66	0.01 06	0.03 15	0.08 3	0.077
knn:251 2364	0.65	0.031 2	0.01 19	0.009 8	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.54	0.00 68	0.67	0.01 52	0.01 25	0.04 8	0.009

295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.031 4	0.05 11	0.019 2	0.67	0.00 46	0.52	0.8 2	0.74	0.63	0.54	0.00 28	0.67	0.02 30	0.02 32	0.08 7	0.013
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.032 6	0.00 48	0.014 3	0.70	0.00 09	0.70	0.7 0	0.70	0.70	0.43	0.00 23	0.66	0.01 27	0.01 79	0.03 2	0.017
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.032 6	0.05 05	0.057 3	0.61	0.05 44	0.48	0.7 3	0.64	0.59	0.05	0.08 37	0.66	0.05 78	0.06 59	0.18 7	0.062
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.032 7	0.00 53	0.002 6	0.68	0.00 21	0.52	0.8 5	0.77	0.64	0.52	0.00 26	0.72	0.00 35	0.00 46	0.06 5	0.016
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.032 8	0.02 55	0.032 1	0.59	0.08 76	0.48	0.7 0	0.62	0.58	0.53	0.10 57	0.66	0.03 66	0.03 52	0.06 3	0.020
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.033 5	0.02 55	0.025 4	0.59	0.08 76	0.48	0.7 0	0.62	0.58	0.56	0.08 66	0.66	0.02 21	0.02 82	0.00 4	0.004
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.033 7	0.05 05	0.025 7	0.62	0.03 20	0.55	0.7 0	0.64	0.61	0.47	0.03 65	0.68	0.02 47	0.02 98	0.07 6	0.033
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.033 7	0.01 13	0.009 2	0.67	0.00 46	0.85	0.4 8	0.62	0.76	0.14	0.00 95	0.65	0.02 51	0.01 37	0.02 6	0.003
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.033 7	0.02 47	0.007 8	0.64	0.01 78	0.39	0.8 8	0.76	0.59	- 0.10	0.00 43	0.64	0.00 83	0.01 29	0.38 3	0.039
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.034 8	0.05 05	0.020 4	0.61	0.05 44	0.52	0.7 0	0.63	0.59	0.03	0.10 41	0.68	0.03 33	0.02 34	0.11 3	0.020
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.036 0	0.09 66	0.043 9	0.59	0.08 76	0.82	0.3 6	0.56	0.67	0.41	0.12 45	0.62	0.07 88	0.04 84	0.11 7	0.019
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.037 2	0.09 65	0.038 0	0.62	0.03 20	0.45	0.7 9	0.68	0.59	0.16	0.03 86	0.68	0.03 64	0.04 41	0.32 4	0.023
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.65	0.038 3	0.09 66	0.021 5	0.64	0.01 78	0.55	0.7 3	0.67	0.62	0.55	0.03 10	0.68	0.02 86	0.02 46	0.15 0	0.040
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.64	0.038 8	0.64 65	0.034 4	0.59	0.08 76	0.61	0.5 8	0.59	0.59	0.50	0.24 30	0.59	0.05 74	0.03 81	0.16 0	0.056
295644 2 knn:278 9391 346359 8 nb:2789 391 246183 7 svm:24 61837 306677 0 knn:233 2285 265151 5 knn:246 1837 295644 2 rpart:23 64325 300535 7 nb:3066 770 295644 2 svm:24 58376 313909 2 svm:30 66770 265151 5 svm:34 14753 236432 5 rf:2458 376 246183 7 svm:34 63598 265151 5 rf:3414 753 306677 0 knn:245 8376 247815 5 rpart:30 66770 295644 2	0.62	0.038 9	0.28 68	0.037 1	0.62	0.03 20	0.45	0.7 9	0.68	0.59	0.50	0.02 96	0.65	0.03 34	0.04 03	0.04 2	0.023

knn:233 2285 246183 7	0.65	0.039 5	0.01 19	0.011 4	0.70	0.00 09	0.64	0.7 6	0.72	0.68	0.50	0.00 21	0.69	0.01 33	0.01 42	0.07 1	0.021
nb:3326 487 246183 7	0.65	0.039 6	0.05 05	0.020 2	0.65	0.00 93	0.61	0.7 0	0.67	0.64	0.39	0.02 51	0.66	0.01 10	0.02 63	0.09 0	0.101
svm:24 58376 295644 2	0.65	0.039 6	0.09 65	0.024 7	0.61	0.05 44	0.42	0.7 9	0.67	0.58	0.15	0.14 76	0.68	0.06 05	0.02 87	0.14 1	0.017
svm:24 61837 251236 4	0.65	0.040 9	0.05 05	0.050 0	0.65	0.00 93	0.55	0.7 6	0.69	0.63	- 0.07	0.02 17	0.61	0.08 16	0.05 39	0.26 1	0.079
svm:33 26487 346359 8	0.65	0.040 9	0.05 05	0.035 4	0.55	0.26 93	0.36	0.7 3	0.57	0.53	- 0.32	0.55 64	0.66	0.01 76	0.04 31	0.16 3	0.291
svm:30 66770 295644 2	0.65	0.042 2	0.09 65	0.031 2	0.61	0.05 44	0.55	0.6 7	0.62	0.59	- 0.18	0.07 00	0.67	0.02 92	0.03 55	0.06 8	0.029
rpart:25 12364 300535 7	0.64	0.043 5	0.44 78	0.059 5	0.58	0.13 39	0.52	0.6 4	0.59	0.57	0.53	0.20 51	0.65	0.05 81	0.06 16	0.04 6	0.017
rf:2461 837 295644 2	0.64	0.044 1	0.05 11	0.024 3	0.65	0.00 93	0.64	0.6 7	0.66	0.65	0.43	0.02 70	0.64	0.04 12	0.02 72	0.10 3	0.025
nb:3463 598 295644 2	0.64	0.044 9	0.05 05	0.029 7	0.67	0.00 46	0.58	0.7 6	0.70	0.64	0.50	0.00 93	0.69	0.03 54	0.03 37	0.08 6	0.026
rf:3326 487 346359 8	0.64	0.045 4	0.02 55	0.008 6	0.67	0.00 46	0.61	0.7 3	0.69	0.65	0.32	0.01 13	0.69	0.00 78	0.01 27	0.14 7	0.066
rf:3139 092 236432 5	0.64	0.045 4	0.05 11	0.044 5	0.62	0.03 20	0.76	0.4 8	0.60	0.67	0.46	0.04 97	0.66	0.05 95	0.04 82	0.03 3	0.006
rpart:24 58376 341475 3	0.62	0.046 3	0.28 68	0.044 6	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.52	0.05 14	0.66	0.05 45	0.04 67	0.20 3	0.046
rpart:34 14753 233228 5	0.62	0.046 3	0.28 68	0.044 6	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.52	0.05 14	0.66	0.05 45	0.04 67	0.20 3	0.046
rpart:34 14753 236432 5	0.62	0.046 3	0.28 68	0.044 6	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.52	0.05 14	0.66	0.05 45	0.04 67	0.20 3	0.046
rpart:34 14753 247815 5	0.62	0.046 3	0.28 68	0.044 6	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.52	0.05 14	0.66	0.05 45	0.04 67	0.20 3	0.046
rpart:34 14753	0.62	0.046 3	0.28 68	0.044 6	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.52	0.05 14	0.66	0.05 45	0.04 67	0.20 3	0.046

251236 4 rpart:34 14753 278939 1	0.62	0.046 3	0.28 68	0.044 6	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.52	0.05 14	0.66	0.05 45	0.04 67	0.20 3	0.046
rpart:34 14753 295644 2	0.62	0.046 3	0.28 68	0.044 6	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.52	0.05 14	0.66	0.05 45	0.04 67	0.20 3	0.046
rpart:34 14753 300535 7	0.62	0.046 3	0.28 68	0.044 6	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.52	0.05 14	0.66	0.05 45	0.04 67	0.20 3	0.046
rpart:34 14753 306677 0	0.62	0.046 3	0.28 68	0.044 6	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.52	0.05 14	0.66	0.05 45	0.04 67	0.20 3	0.046
rpart:34 14753 313909 2	0.62	0.046 3	0.28 68	0.044 6	0.62	0.03 20	0.52	0.7 3	0.65	0.60	0.52	0.05 14	0.66	0.05 45	0.04 67	0.20 3	0.046
rf:2461 837 251236 4	0.64	0.047 5	0.09 66	0.035 0	0.64	0.01 78	0.61	0.6 7	0.65	0.63	0.49	0.05 22	0.63	0.05 17	0.03 83	0.25 5	0.043
svm:24 61837 295644 2	0.64	0.047 8	0.17 29	0.044 7	0.55	0.26 93	0.91	0.1 8	0.53	0.67	14.3 1	0.34 48	0.59	0.10 62	0.05 72	0.25 5	0.065
rpart:24 78155 251236 4	0.64	0.048 5	0.09 66	0.106 0	0.61	0.05 44	0.58	0.6 4	0.61	0.60	0.56	0.10 25	0.55	0.12 74	0.10 54	0.90 2	0.497
rpart:33 26487 233228 5	0.58	0.048 7	0.84 32	0.046 4	0.58	0.13 39	0.18	0.9 7	0.86	0.54	0.57	0.00 72	0.59	0.01 01	0.07 75	0.31 8	0.319
rpart:33 26487 236432 5	0.58	0.048 7	0.84 32	0.046 4	0.58	0.13 39	0.18	0.9 7	0.86	0.54	0.57	0.00 72	0.59	0.01 01	0.07 75	0.31 8	0.319
rpart:33 26487 247815 5	0.58	0.048 7	0.84 32	0.046 4	0.58	0.13 39	0.18	0.9 7	0.86	0.54	0.57	0.00 72	0.59	0.01 01	0.07 75	0.31 8	0.319
rpart:33 26487 251236 4	0.58	0.048 7	0.84 32	0.046 4	0.58	0.13 39	0.18	0.9 7	0.86	0.54	0.57	0.00 72	0.59	0.01 01	0.07 75	0.31 8	0.319
rpart:33 26487 278939 1	0.58	0.048 7	0.84 32	0.046 4	0.58	0.13 39	0.18	0.9 7	0.86	0.54	0.57	0.00 72	0.59	0.01 01	0.07 75	0.31 8	0.319
rpart:33 26487 295644 2	0.58	0.048 7	0.84 32	0.046 4	0.58	0.13 39	0.18	0.9 7	0.86	0.54	0.57	0.00 72	0.59	0.01 01	0.07 75	0.31 8	0.319
rpart:33 26487 300535 7	0.58	0.048 7	0.84 32	0.046 4	0.58	0.13 39	0.18	0.9 7	0.86	0.54	0.57	0.00 72	0.59	0.01 01	0.07 75	0.31 8	0.319

rpart:33 26487 306677 0	0.58	0.048 7	0.84 32	0.046 4	0.58	0.13 39	0.18	0.9 7	0.86	0.54	0.57	0.00 72	0.59	0.01 01	0.07 75	0.31 8	0.319
rpart:33 26487 341475 3	0.58	0.048 7	0.84 32	0.046 4	0.58	0.13 39	0.18	0.9 7	0.86	0.54	0.57	0.00 72	0.59	0.01 01	0.07 75	0.31 8	0.319
rpart:33 26487 346359 8	0.58	0.048 7	0.84 32	0.046 4	0.58	0.13 39	0.18	0.9 7	0.86	0.54	0.57	0.00 72	0.59	0.01 01	0.07 75	0.31 8	0.319
svm:24 78155 313909 2	0.64	0.049 3	0.02 47	0.017 6	0.59	0.08 76	0.64	0.5 5	0.58	0.60	0.32	0.17 98	0.66	0.03 30	0.02 32	0.02 0	0.004
rf:3463 598 306677 0	0.64	0.049 7	0.01 19	0.010 2	0.65	0.00 93	0.45	0.8 5	0.75	0.61	0.60	0.01 41	0.68	0.01 59	0.01 37	0.33 2	0.035
knn:233 2285 247815 5	0.64	0.049 8	0.00 53	0.007 6	0.70	0.00 09	0.61	0.7 9	0.74	0.67	0.51	0.00 11	0.68	0.01 17	0.01 00	0.09 3	0.012
nb:2458 376 247815 5	0.80	0.000 0	0.00 01	0.000 1	0.67	0.00 46	0.45	0.8 8	0.79	0.62	0.50	0.00 25	0.78	0.00 03	0.00 08	0.03 0	0.005
knn:247 8155 236432 5	0.79	0.000 0	0.00 09	0.000 0	0.70	0.00 09	0.61	0.7 9	0.74	0.67	0.53	0.00 08	0.77	0.00 01	0.00 02	0.00 1	0.001
svm:23 32285 300535 7	0.79	0.000 0	0.00 01	0.000 2	0.71	0.00 04	0.64	0.7 9	0.75	0.68	- 0.14	0.00 07	0.77	0.00 06	0.00 09	0.00 9	0.003
svm:24 58376 233228 5	0.78	0.000 1	0.00 07	0.000 1	0.73	0.00 01	0.67	0.7 9	0.76	0.70	- 0.24	0.00 03	0.77	0.00 04	0.00 05	0.03 3	0.007
svm:24 78155 236432 5	0.78	0.000 1	0.00 00	0.000 0	0.71	0.00 04	0.70	0.7 3	0.72	0.71	0.19	0.00 08	0.75	0.00 03	0.00 02	0.00 6	0.002
nb:2332 285 247815 5	0.78	0.000 1	0.00 01	0.000 6	0.67	0.00 46	0.55	0.7 9	0.72	0.63	0.50	0.00 58	0.75	0.00 09	0.00 19	0.01 8	0.005
svm:23 32285 251236 4	0.78	0.000 1	0.00 07	0.000 2	0.71	0.00 04	0.64	0.7 9	0.75	0.68	- 0.12	0.00 07	0.77	0.00 05	0.00 08	0.01 0	0.004
svm:24 58376 236432 5	0.78	0.000 1	0.00 02	0.000 1	0.71	0.00 04	0.61	0.8 2	0.77	0.68	- 0.10	0.00 05	0.78	0.00 05	0.00 06	0.02 7	0.004
nb:3414 753 247815 5	0.78	0.000 1	0.00 02	0.000 2	0.68	0.00 21	0.61	0.7 6	0.71	0.66	0.49	0.00 29	0.76	0.00 02	0.00 09	0.00 8	0.002
nb:2458 376	0.77	0.000 1	0.00 02	0.000 2	0.70	0.00 09	0.61	0.7 9	0.74	0.67	0.45	0.00 17	0.77	0.00 05	0.00 10	0.03 1	0.008

236432																		
5																		
nb:2478																		
155	0.77	0.000	0.00	0.000	0.71	0.00	0.73	0.7	0.71	0.72	0.44	0.00	0.77	0.00	0.00	0.00	0.00	0.001
300535		1	07	1		04		0				06		01	06	0		
7																		
nb:2458																		
376	0.77	0.000	0.00	0.000	0.67	0.00	0.52	0.8	0.74	0.63	0.50	0.00	0.74	0.00	0.00	0.05	0.012	
233228		1	07	2		46		2				98		07	10	9		
5																		

Performance of pairwise combinations of the 15 markers across different metrics for the Recurrence endpoint. All classifiers have an Wilcox P-value ≤ 0.05 .

TABLE 12

CLASSIFIER	AUC	WILCOX P- VALUE	KS P- VALUE	T-TEST P- VALUE	PPV	NPV	CUTOFF	KM P- VALUE	UVA HR P- VALUE	UVA OR P- VALUE
rpart:3326487 2458376	0.70	0.0172	0.2259	0.0114	0.50	0.82	0.41	0.0264	0.0061	0.0200
nb:3326487 3414753	0.70	0.0373	0.0330	0.0630	0.42	0.66	0.41	0.5225	0.0124	0.0872
nb:3326487 2332285	0.70	0.0373	0.0451	0.0412	0.54	0.71	0.37	0.0771	0.0088	0.0617
nb:3326487 2478155	0.73	0.0166	0.0192	0.0146	0.53	0.73	0.40	0.0456	0.0015	0.0343
knn:3326487 2478155	0.68	0.0287	0.1722	0.0256	0.56	0.78	0.50	0.0130	0.0197	0.0300
knn:3326487 3139092	0.69	0.0452	0.0453	0.0354	0.67	0.76	0.48	0.0051	0.0180	0.0448
rpart:3326487 3139092	0.67	0.0483	0.4356	0.0282	0.50	0.76	0.41	0.0643	0.0099	0.0380
rf:3326487 2789391	0.69	0.0466	0.0637	0.0266	0.56	0.76	0.33	0.0236	0.0071	0.0389
knn:3326487 2789391	0.71	0.0251	0.1494	0.0526	0.60	0.67	0.54	0.1140	0.0144	0.0736
svm:3326487 2789391	0.70	0.0373	0.0861	0.0460	0.50	0.72	-0.44	0.1119	0.0173	0.0582
rpart:3326487 2461837	0.68	0.0287	0.1722	0.0256	0.56	0.78	0.47	0.0308	0.0405	0.0300
nb:3326487 2512364	0.70	0.0324	0.0546	0.0306	0.52	0.80	0.38	0.0339	0.0106	0.0444
knn:3326487 2512364	0.71	0.0233	0.0991	0.0391	0.45	0.67	0.50	0.4034	0.0216	0.0509
nb:3326487 2364325	0.69	0.0428	0.1781	0.0361	0.50	0.74	0.37	0.0894	0.0060	0.0595
nb:3326487 3066770	0.69	0.0458	0.0273	0.0729	0.56	0.69	0.41	0.1145	0.0184	0.0979
rpart:3326487 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
rf:2458376 3414753	0.75	0.0090	0.0721	0.0058	0.67	0.76	0.58	0.0038	0.0048	0.0114
nb:2458376 3414753	0.76	0.0055	0.0139	0.0027	0.75	0.73	0.48	0.0084	0.0006	0.0129
svm:2458376 3414753	0.72	0.0225	0.0652	0.0229	0.44	0.68	0.08	0.3676	0.0152	0.0305
rf:2458376 2332285	0.78	0.0023	0.0139	0.0025	0.46	0.85	0.30	0.0487	0.0025	0.0081
nb:2458376 2332285	0.77	0.0035	0.0497	0.0024	0.67	0.76	0.44	0.0039	0.0005	0.0111
knn:2458376 2332285	0.72	0.0212	0.0721	0.0170	0.56	0.76	0.50	0.0331	0.0097	0.0246
rpart:2458376 2332285	0.69	0.0216	0.1340	0.0187	0.52	0.83	0.48	0.0167	0.0273	0.0252
svm:2458376 2332285	0.79	0.0019	0.0243	0.0009	0.64	0.78	-0.40	0.0074	0.0003	0.0058
rf:2458376 2478155	0.79	0.0024	0.0538	0.0010	0.50	0.87	0.49	0.0222	0.0030	0.0055
nb:2458376 2478155	0.85	0.0001	0.0002	0.0003	0.71	0.71	0.50	0.0101	0.0001	0.0068
knn:2458376 2478155	0.76	0.0050	0.0380	0.0024	0.80	0.77	0.83	0.0004	0.0051	0.0063
rpart:2458376 2478155	0.69	0.0216	0.1340	0.0187	0.52	0.83	0.48	0.0167	0.0273	0.0252
svm:2458376 2478155	0.80	0.0012	0.0069	0.0011	0.63	0.80	0.30	0.0042	0.0016	0.0043

nb:2458376 3139092	0.73	0.0166	0.0273	0.0038	0.86	0.74	0.49	0.0021	0.0012	0.0160
rpart:2458376 3139092	0.69	0.0216	0.1340	0.0187	0.52	0.83	0.48	0.0167	0.0273	0.0252
rf:2458376 2789391	0.76	0.0063	0.0062	0.0004	0.77	0.82	0.54	0.0001	0.0006	0.0028
nb:2458376 2789391	0.71	0.0243	0.0032	0.0029	0.70	0.74	0.49	0.0026	0.0006	0.0112
rpart:2458376 2789391	0.69	0.0216	0.1340	0.0187	0.52	0.83	0.48	0.0167	0.0273	0.0252
rf:2458376 3463598	0.73	0.0160	0.0317	0.0017	1.00	0.76	0.64	0.0000	0.0011	0.0072
knn:2458376 3463598	0.76	0.0062	0.0380	0.0004	0.86	0.74	0.53	0.0006	0.0004	0.0058
rpart:2458376 3463598	0.71	0.0043	0.0721	0.0028	0.73	0.77	0.53	0.0012	0.0032	0.0069
rf:2458376 2461837	0.70	0.0397	0.1112	0.0359	0.45	0.83	0.42	0.0728	0.0493	0.0454
nb:2458376 2461837	0.69	0.0489	0.0110	0.0101	0.45	0.74	0.37	0.2061	0.0049	0.0206
knn:2458376 2461837	0.69	0.0475	0.3486	0.0609	0.45	0.74	0.45	0.2061	0.0650	0.0662
rpart:2458376 2461837	0.68	0.0287	0.1722	0.0256	0.56	0.78	0.47	0.0308	0.0405	0.0300
nb:2458376 2512364	0.78	0.0021	0.0032	0.0014	0.75	0.73	0.52	0.0040	0.0008	0.0077
knn:2458376 2512364	0.74	0.0109	0.1154	0.0035	0.48	0.81	0.46	0.0656	0.0044	0.0100
svm:2458376 2512364	0.77	0.0031	0.0024	0.0008	0.69	0.79	0.19	0.0011	0.0007	0.0041
rf:2458376 2364325	0.80	0.0015	0.0076	0.0010	0.69	0.79	0.53	0.0008	0.0013	0.0038
nb:2458376 2364325	0.78	0.0026	0.0101	0.0020	0.62	0.75	0.45	0.0148	0.0006	0.0087
knn:2458376 2364325	0.74	0.0130	0.0991	0.0079	0.57	0.74	0.50	0.0377	0.0062	0.0140
rpart:2458376 2364325	0.69	0.0216	0.1340	0.0187	0.52	0.83	0.48	0.0167	0.0273	0.0252
svm:2458376 2364325	0.79	0.0017	0.0055	0.0016	0.62	0.75	-0.21	0.0148	0.0012	0.0066
rf:2458376 3066770	0.73	0.0130	0.0451	0.0131	0.60	0.77	0.53	0.0097	0.0129	0.0210
nb:2458376 3066770	0.76	0.0046	0.0299	0.0020	0.70	0.74	0.45	0.0066	0.0003	0.0096
knn:2458376 3066770	0.73	0.0153	0.1494	0.0059	0.60	0.77	0.50	0.0082	0.0065	0.0128
rpart:2458376 3066770	0.69	0.0216	0.1340	0.0187	0.52	0.83	0.48	0.0167	0.0273	0.0252
svm:2458376 3066770	0.76	0.0046	0.0299	0.0029	0.64	0.78	0.13	0.0070	0.0056	0.0076
rf:2458376 2956442	0.70	0.0336	0.0637	0.0179	0.59	0.79	0.51	0.0096	0.0176	0.0245
knn:2458376 2956442	0.70	0.0326	0.1910	0.0173	0.54	0.71	0.52	0.0974	0.0127	0.0258
rpart:2458376 2956442	0.76	0.0051	0.0473	0.0131	0.60	0.77	0.50	0.0103	0.0124	0.0185
rf:2458376 3005357	0.74	0.0127	0.0453	0.0099	0.53	0.77	0.50	0.0300	0.0104	0.0158
nb:2458376 3005357	0.74	0.0093	0.0714	0.0039	0.75	0.73	0.50	0.0040	0.0015	0.0130
knn:2458376 3005357	0.74	0.0117	0.0751	0.0073	0.56	0.78	0.47	0.0192	0.0098	0.0125
rpart:2458376 3005357	0.69	0.0216	0.1340	0.0187	0.52	0.83	0.48	0.0167	0.0273	0.0252
svm:2458376 3005357	0.75	0.0072	0.0101	0.0053	0.67	0.72	0.11	0.0202	0.0063	0.0123
nb:2458376 2651515	0.70	0.0348	0.0497	0.0080	0.67	0.76	0.42	0.0030	0.0007	0.0211
knn:2458376 2651515	0.75	0.0073	0.0076	0.0036	0.41	0.75	0.37	0.2759	0.0013	0.0101
rpart:2458376 2651515	0.71	0.0161	0.1976	0.0117	0.52	0.80	0.39	0.0291	0.0032	0.0185
svm:2458376 2651515	0.70	0.0348	0.0714	0.0137	0.59	0.79	-0.29	0.0101	0.0077	0.0207
nb:3414753 2332285	0.79	0.0017	0.0036	0.0038	0.67	0.76	0.45	0.0039	0.0010	0.0125
svm:3414753 2332285	0.76	0.0060	0.0299	0.0076	0.69	0.79	-0.01	0.0007	0.0060	0.0128
rf:3414753 2478155	0.81	0.0013	0.0028	0.0015	0.56	1.00	0.28	0.0008	0.0027	0.0049
nb:3414753 2478155	0.83	0.0003	0.0005	0.0003	0.59	0.79	0.46	0.0069	0.0001	0.0031
knn:3414753 2478155	0.72	0.0213	0.1494	0.0200	0.50	0.76	0.45	0.0581	0.0107	0.0276
svm:3414753 2478155	0.81	0.0006	0.0014	0.0005	0.58	0.82	-0.34	0.0062	0.0002	0.0035

nb:3414753 3139092	0.73	0.0130	0.0652	0.0055	0.56	0.78	0.43	0.0163	0.0017	0.0133
svm:3414753 3139092	0.72	0.0194	0.0177	0.0276	0.50	0.76	-0.22	0.0666	0.0211	0.0332
rf:3414753 2789391	0.71	0.0255	0.0277	0.0161	0.63	0.80	0.50	0.0020	0.0143	0.0217
nb:3414753 2789391	0.73	0.0166	0.0177	0.0042	0.61	0.83	0.43	0.0039	0.0008	0.0114
knn:3414753 2789391	0.77	0.0034	0.0277	0.0010	0.67	0.81	0.46	0.0007	0.0006	0.0040
svm:3414753 2789391	0.72	0.0194	0.0177	0.0063	0.55	0.81	-0.31	0.0177	0.0013	0.0143
nb:3414753 3463598	0.69	0.0428	0.0405	0.0086	0.64	0.78	0.46	0.0035	0.0022	0.0189
knn:3414753 3463598	0.71	0.0281	0.0453	0.0055	0.67	0.76	0.50	0.0064	0.0067	0.0118
rpart:3414753 3463598	0.71	0.0043	0.0721	0.0028	0.73	0.77	0.53	0.0012	0.0032	0.0069
svm:3414753 3463598	0.73	0.0130	0.0139	0.0051	0.63	0.80	-0.14	0.0026	0.0047	0.0096
nb:3414753 2461837	0.71	0.0302	0.0221	0.0127	0.59	0.79	0.45	0.0141	0.0085	0.0199
rpart:3414753 2461837	0.72	0.0119	0.0721	0.0041	0.73	0.77	0.57	0.0039	0.0107	0.0083
nb:3414753 2512364	0.77	0.0031	0.0043	0.0013	0.57	0.85	0.44	0.0045	0.0010	0.0052
knn:3414753 2512364	0.77	0.0045	0.0332	0.0034	0.64	0.78	0.51	0.0030	0.0037	0.0079
svm:3414753 2512364	0.78	0.0026	0.0043	0.0007	0.60	0.86	-0.19	0.0018	0.0003	0.0044
rf:3414753 2364325	0.71	0.0264	0.0164	0.0142	0.63	0.80	0.49	0.0026	0.0123	0.0199
nb:3414753 2364325	0.78	0.0028	0.0127	0.0024	0.58	0.82	0.45	0.0042	0.0010	0.0083
knn:3414753 2364325	0.71	0.0258	0.0847	0.0125	0.60	0.77	0.48	0.0056	0.0063	0.0190
nb:3414753 3066770	0.74	0.0093	0.0101	0.0025	0.64	0.73	0.47	0.0135	0.0005	0.0088
knn:3414753 3066770	0.74	0.0105	0.1910	0.0054	0.70	0.74	0.54	0.0030	0.0031	0.0126
knn:3414753 2956442	0.70	0.0310	0.0637	0.0313	0.54	0.71	0.50	0.0667	0.0161	0.0380
svm:3414753 2956442	0.70	0.0373	0.0451	0.0223	0.53	0.75	-0.30	0.0546	0.0096	0.0304
nb:3414753 3005357	0.75	0.0086	0.0055	0.0045	0.61	0.83	0.43	0.0026	0.0022	0.0106
knn:3414753 3005357	0.78	0.0029	0.0115	0.0072	0.53	0.73	0.51	0.0503	0.0054	0.0127
nb:3414753 2651515	0.72	0.0179	0.0299	0.0038	0.56	0.76	0.41	0.0220	0.0001	0.0144
rpart:3414753 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
rf:2332285 2478155	0.81	0.0011	0.0199	0.0004	0.48	0.86	0.37	0.0343	0.0007	0.0040
nb:2332285 2478155	0.85	0.0001	0.0001	0.0008	0.67	0.76	0.47	0.0026	0.0002	0.0050
rpart:2332285 2478155	0.78	0.0017	0.0141	0.0013	0.53	0.77	0.55	0.0434	0.0029	0.0045
rf:2332285 3139092	0.73	0.0172	0.0062	0.0158	0.48	0.81	0.33	0.0656	0.0114	0.0237
nb:2332285 3139092	0.76	0.0046	0.0017	0.0034	0.67	0.76	0.48	0.0039	0.0011	0.0109
knn:2332285 3139092	0.70	0.0315	0.0076	0.0062	0.64	0.78	0.48	0.0025	0.0041	0.0111
svm:2332285 3139092	0.76	0.0050	0.0006	0.0059	0.52	0.80	-0.26	0.0204	0.0049	0.0110
rf:2332285 2789391	0.76	0.0065	0.0034	0.0027	0.65	0.83	0.44	0.0010	0.0023	0.0068
nb:2332285 2789391	0.73	0.0153	0.0043	0.0056	0.67	0.76	0.47	0.0039	0.0014	0.0134
knn:2332285 2789391	0.78	0.0023	0.0052	0.0082	0.60	0.71	0.55	0.0299	0.0039	0.0147
rpart:2332285 2789391	0.73	0.0046	0.0332	0.0031	0.61	0.83	0.50	0.0031	0.0073	0.0061
svm:2332285 2789391	0.75	0.0072	0.0451	0.0056	0.67	0.76	-0.01	0.0039	0.0022	0.0115
rf:2332285 3463598	0.75	0.0077	0.0134	0.0011	0.71	0.81	0.41	0.0003	0.0009	0.0045
nb:2332285 3463598	0.73	0.0166	0.0139	0.0051	0.75	0.79	0.47	0.0003	0.0015	0.0141
knn:2332285 3463598	0.75	0.0068	0.0637	0.0094	0.58	0.82	0.50	0.0087	0.0106	0.0196
rpart:2332285 3463598	0.71	0.0043	0.0721	0.0028	0.73	0.77	0.53	0.0012	0.0032	0.0069
svm:2332285 3463598	0.71	0.0243	0.0060	0.0014	0.75	0.79	-0.14	0.0003	0.0018	0.0048

rf:2332285 2461837	0.73	0.0154	0.0380	0.0448	0.42	0.71	0.26	0.4266	0.0550	0.0511
nb:2332285 2461837	0.71	0.0261	0.0273	0.0104	0.60	0.77	0.46	0.0163	0.0049	0.0181
rpart:2332285 2461837	0.69	0.0409	0.1494	0.0578	0.45	0.71	0.38	0.3591	0.1003	0.0627
svm:2332285 2461837	0.77	0.0042	0.0243	0.0058	0.53	0.77	-0.28	0.0447	0.0136	0.0105
nb:2332285 2512364	0.79	0.0015	0.0028	0.0021	0.67	0.76	0.51	0.0039	0.0011	0.0070
svm:2332285 2512364	0.80	0.0010	0.0008	0.0009	0.67	0.76	-0.10	0.0039	0.0005	0.0046
rf:2332285 2364325	0.75	0.0083	0.0538	0.0042	0.64	0.78	0.49	0.0037	0.0031	0.0095
nb:2332285 2364325	0.77	0.0031	0.0299	0.0036	0.69	0.79	0.47	0.0005	0.0013	0.0105
rpart:2332285 2364325	0.69	0.0191	0.1154	0.0163	0.55	0.81	0.51	0.0131	0.0210	0.0212
svm:2332285 2364325	0.79	0.0017	0.0192	0.0023	0.67	0.76	-0.02	0.0039	0.0014	0.0068
nb:2332285 3066770	0.75	0.0079	0.0101	0.0034	0.62	0.75	0.44	0.0135	0.0008	0.0117
svm:2332285 3066770	0.79	0.0019	0.0022	0.0020	0.67	0.76	-0.25	0.0039	0.0011	0.0070
svm:2332285 2956442	0.76	0.0060	0.0157	0.0060	0.67	0.76	-0.17	0.0039	0.0028	0.0129
rf:2332285 3005357	0.75	0.0090	0.0290	0.0104	0.48	0.78	0.30	0.0663	0.0056	0.0171
nb:2332285 3005357	0.76	0.0046	0.0028	0.0051	0.64	0.73	0.49	0.0123	0.0017	0.0131
knn:2332285 3005357	0.68	0.0493	0.1976	0.1346	0.52	0.80	0.39	0.0184	0.0971	0.1374
rpart:2332285 3005357	0.69	0.0333	0.3906	0.0381	0.53	0.75	0.50	0.0343	0.0206	0.0427
svm:2332285 3005357	0.81	0.0006	0.0022	0.0018	0.67	0.76	-0.22	0.0039	0.0010	0.0068
rf:2332285 2651515	0.73	0.0143	0.0397	0.0052	0.73	0.77	0.44	0.0002	0.0008	0.0120
nb:2332285 2651515	0.76	0.0050	0.0060	0.0028	0.82	0.80	0.44	0.0000	0.0002	0.0105
rpart:2332285 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
rf:2478155 3139092	0.78	0.0030	0.0277	0.0033	0.63	0.80	0.66	0.0011	0.0047	0.0076
nb:2478155 3139092	0.82	0.0005	0.0017	0.0002	0.61	0.83	0.45	0.0013	0.0001	0.0025
knn:2478155 3139092	0.78	0.0033	0.0991	0.0025	0.55	0.81	0.48	0.0094	0.0052	0.0069
svm:2478155 3139092	0.71	0.0261	0.0393	0.0193	0.50	0.92	-0.08	0.0100	0.0245	0.0290
rf:2478155 2789391	0.83	0.0005	0.0015	0.0003	0.55	0.81	0.47	0.0177	0.0008	0.0022
nb:2478155 2789391	0.79	0.0019	0.0079	0.0009	0.63	0.80	0.47	0.0020	0.0002	0.0045
knn:2478155 2789391	0.74	0.0100	0.0453	0.0163	0.69	0.79	0.54	0.0004	0.0067	0.0239
rpart:2478155 2789391	0.73	0.0046	0.0332	0.0031	0.61	0.83	0.50	0.0031	0.0073	0.0061
svm:2478155 2789391	0.74	0.0120	0.0060	0.0035	0.55	0.81	-0.23	0.0177	0.0006	0.0097
rf:2478155 3463598	0.83	0.0006	0.0015	0.0005	0.50	1.00	0.27	0.0050	0.0014	0.0037
nb:2478155 3463598	0.76	0.0046	0.0367	0.0014	0.62	0.75	0.48	0.0072	0.0004	0.0065
knn:2478155 3463598	0.73	0.0130	0.0397	0.0103	0.52	0.83	0.44	0.0214	0.0138	0.0176
rpart:2478155 3463598	0.71	0.0043	0.0721	0.0028	0.73	0.77	0.53	0.0012	0.0032	0.0069
svm:2478155 3463598	0.79	0.0017	0.0101	0.0010	0.57	0.85	0.13	0.0088	0.0071	0.0045
rf:2478155 2461837	0.75	0.0094	0.0562	0.0033	0.60	0.77	0.64	0.0244	0.0127	0.0088
nb:2478155 2461837	0.77	0.0031	0.0079	0.0019	0.58	0.82	0.44	0.0080	0.0012	0.0060
knn:2478155 2461837	0.73	0.0159	0.0141	0.0010	0.54	1.00	0.42	0.0017	0.0068	0.0098
rpart:2478155 2461837	0.68	0.0287	0.1722	0.0256	0.56	0.78	0.47	0.0308	0.0405	0.0300
svm:2478155 2461837	0.71	0.0281	0.0221	0.0151	0.52	0.83	-0.02	0.0242	0.0338	0.0221
rf:2478155 2512364	0.70	0.0359	0.0453	0.0374	0.46	0.80	0.43	0.1188	0.0465	0.0459
nb:2478155 2512364	0.83	0.0002	0.0014	0.0002	0.55	0.81	0.47	0.0094	0.0002	0.0023
knn:2478155 2512364	0.75	0.0074	0.0164	0.0037	0.58	0.82	0.50	0.0038	0.0026	0.0080

rf:2478155 2364325	0.86	0.0002	0.0003	0.0001	0.58	1.00	0.43	0.0004	0.0004	0.0018
nb:2478155 2364325	0.82	0.0004	0.0017	0.0002	0.58	0.82	0.46	0.0042	0.0001	0.0027
knn:2478155 2364325	0.83	0.0005	0.0052	0.0001	0.67	0.81	0.53	0.0003	0.0002	0.0012
rpart:2478155 2364325	0.68	0.0491	0.1199	0.0331	0.44	0.75	0.53	0.2860	0.0645	0.0425
svm:2478155 2364325	0.84	0.0002	0.0002	0.0002	0.65	0.90	-0.01	0.0001	0.0006	0.0020
rf:2478155 3066770	0.79	0.0020	0.0080	0.0008	0.54	0.88	0.38	0.0035	0.0024	0.0040
nb:2478155 3066770	0.83	0.0003	0.0043	0.0002	0.65	0.83	0.44	0.0010	0.0000	0.0021
knn:2478155 3066770	0.79	0.0022	0.0172	0.0010	0.54	1.00	0.45	0.0017	0.0019	0.0059
rpart:2478155 3066770	0.76	0.0015	0.0141	0.0008	0.56	0.94	0.47	0.0013	0.0127	0.0078
svm:2478155 3066770	0.75	0.0079	0.0069	0.0097	0.57	0.89	-0.03	0.0039	0.0131	0.0145
rf:2478155 2956442	0.77	0.0043	0.0172	0.0015	0.55	0.84	0.45	0.0077	0.0022	0.0058
nb:2478155 2956442	0.72	0.0194	0.0791	0.0097	0.50	0.76	0.43	0.0755	0.0032	0.0168
knn:2478155 2956442	0.73	0.0139	0.1783	0.0157	0.54	0.71	0.52	0.0697	0.0100	0.0218
rpart:2478155 2956442	0.76	0.0015	0.0141	0.0008	0.56	0.94	0.47	0.0013	0.0127	0.0078
svm:2478155 2956442	0.69	0.0428	0.1100	0.0449	0.47	0.73	-0.18	0.1612	0.0257	0.0508
rf:2478155 3005357	0.77	0.0051	0.0277	0.0018	0.59	0.79	0.66	0.0031	0.0032	0.0057
nb:2478155 3005357	0.81	0.0008	0.0101	0.0006	0.58	0.82	0.44	0.0036	0.0002	0.0036
knn:2478155 3005357	0.79	0.0020	0.0380	0.0025	0.52	0.88	0.41	0.0065	0.0020	0.0081
svm:2478155 3005357	0.81	0.0009	0.0079	0.0011	0.58	0.82	-0.07	0.0036	0.0013	0.0039
nb:2478155 2651515	0.80	0.0012	0.0032	0.0005	0.77	0.82	0.45	0.0000	0.0000	0.0048
knn:2478155 2651515	0.78	0.0035	0.0011	0.0002	0.63	0.80	0.46	0.0008	0.0001	0.0016
rpart:2478155 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
svm:2478155 2651515	0.69	0.0400	0.1175	0.0257	0.47	0.69	-0.29	0.2121	0.0045	0.0352
rf:3139092 2789391	0.71	0.0246	0.0094	0.0141	0.59	0.79	0.53	0.0077	0.0128	0.0205
nb:3139092 2789391	0.73	0.0166	0.0139	0.0061	0.59	0.79	0.44	0.0077	0.0017	0.0135
knn:3139092 2789391	0.70	0.0363	0.0277	0.0068	0.63	0.80	0.48	0.0020	0.0045	0.0116
rpart:3139092 3463598	0.71	0.0043	0.0721	0.0028	0.73	0.77	0.53	0.0012	0.0032	0.0069
nb:3139092 2461837	0.69	0.0400	0.0221	0.0238	0.61	0.83	0.43	0.0042	0.0200	0.0311
rpart:3139092 2461837	0.68	0.0287	0.1722	0.0256	0.56	0.78	0.47	0.0308	0.0405	0.0300
svm:3139092 2461837	0.71	0.0243	0.0595	0.0230	0.53	0.77	0.02	0.0746	0.0377	0.0296
nb:3139092 2512364	0.75	0.0079	0.0017	0.0034	0.58	0.82	0.47	0.0050	0.0025	0.0085
nb:3139092 2364325	0.75	0.0072	0.0079	0.0051	0.58	0.82	0.44	0.0042	0.0024	0.0114
knn:3139092 2364325	0.72	0.0211	0.0637	0.0124	0.59	0.79	0.54	0.0052	0.0126	0.0174
svm:3139092 2364325	0.75	0.0079	0.0079	0.0070	0.55	0.81	-0.15	0.0103	0.0051	0.0128
nb:3139092 3066770	0.74	0.0102	0.0101	0.0053	0.64	0.78	0.46	0.0041	0.0019	0.0124
knn:3139092 3066770	0.72	0.0215	0.0847	0.0105	0.64	0.78	0.51	0.0041	0.0103	0.0164
svm:3139092 3066770	0.72	0.0209	0.0177	0.0192	0.58	0.82	-0.21	0.0056	0.0161	0.0260
nb:3139092 2956442	0.70	0.0348	0.0273	0.0432	0.53	0.77	0.43	0.0324	0.0241	0.0506
knn:3139092 2956442	0.70	0.0348	0.0332	0.0715	0.43	0.77	0.38	0.1932	0.0504	0.0784
svm:3139092 2956442	0.75	0.0066	0.0017	0.0351	0.50	0.79	-0.04	0.0399	0.0237	0.0435
nb:3139092 3005357	0.72	0.0225	0.0022	0.0078	0.63	0.80	0.47	0.0022	0.0047	0.0142
knn:3139092 3005357	0.70	0.0320	0.0751	0.0244	0.52	0.83	0.41	0.0157	0.0155	0.0321
svm:3139092 3005357	0.72	0.0225	0.0101	0.0151	0.58	0.82	0.12	0.0050	0.0149	0.0220

rf:2789391 3463598	0.74	0.0104	0.0277	0.0034	0.67	0.81	0.43	0.0008	0.0029	0.0076
nb:2789391 3463598	0.71	0.0302	0.0194	0.0130	0.50	0.74	0.44	0.0782	0.0032	0.0218
knn:2789391 3463598	0.74	0.0117	0.0453	0.0062	0.69	0.79	0.54	0.0007	0.0056	0.0124
rpart:2789391 3463598	0.71	0.0043	0.0721	0.0028	0.73	0.77	0.53	0.0012	0.0032	0.0069
svm:2789391 3463598	0.71	0.0302	0.0139	0.0130	0.50	0.74	-0.32	0.0782	0.0055	0.0200
rf:2789391 2461837	0.73	0.0143	0.0637	0.0105	0.56	0.78	0.47	0.0308	0.0166	0.0154
nb:2789391 2461837	0.69	0.0458	0.0221	0.0202	0.55	0.81	0.40	0.0177	0.0116	0.0273
knn:2789391 2461837	0.72	0.0192	0.0991	0.0147	0.60	0.77	0.49	0.0106	0.0108	0.0209
rpart:2789391 2461837	0.68	0.0287	0.1722	0.0256	0.56	0.78	0.47	0.0308	0.0405	0.0300
svm:2789391 2461837	0.69	0.0400	0.0177	0.0371	0.58	0.82	-0.07	0.0103	0.0377	0.0437
rf:2789391 2512364	0.74	0.0113	0.0164	0.0030	0.61	0.83	0.48	0.0031	0.0044	0.0067
nb:2789391 2512364	0.76	0.0050	0.0101	0.0024	0.65	0.83	0.48	0.0013	0.0015	0.0068
rpart:2789391 2512364	0.73	0.0046	0.0332	0.0031	0.61	0.83	0.50	0.0031	0.0073	0.0061
svm:2789391 2512364	0.74	0.0093	0.0221	0.0086	0.59	0.79	-0.33	0.0138	0.0104	0.0143
rf:2789391 2364325	0.77	0.0047	0.0290	0.0038	0.53	0.77	0.45	0.0338	0.0058	0.0081
nb:2789391 2364325	0.74	0.0102	0.0861	0.0045	0.56	0.78	0.47	0.0187	0.0017	0.0108
knn:2789391 2364325	0.78	0.0033	0.0847	0.0044	0.64	0.78	0.50	0.0030	0.0035	0.0090
rpart:2789391 2364325	0.73	0.0046	0.0332	0.0031	0.61	0.83	0.50	0.0031	0.0073	0.0061
svm:2789391 2364325	0.74	0.0111	0.0595	0.0052	0.53	0.77	-0.26	0.0391	0.0016	0.0123
rf:2789391 3066770	0.75	0.0089	0.0062	0.0044	0.53	0.77	0.35	0.0338	0.0030	0.0088
nb:2789391 3066770	0.73	0.0153	0.0079	0.0053	0.56	0.78	0.43	0.0157	0.0010	0.0125
knn:2789391 3066770	0.78	0.0028	0.0229	0.0007	0.75	0.79	0.47	0.0002	0.0004	0.0039
rpart:2789391 3066770	0.73	0.0046	0.0332	0.0031	0.61	0.83	0.50	0.0031	0.0073	0.0061
svm:2789391 3066770	0.73	0.0130	0.0079	0.0048	0.56	0.78	-0.30	0.0157	0.0026	0.0099
rf:2789391 2956442	0.75	0.0097	0.0473	0.0087	0.58	0.82	0.44	0.0080	0.0087	0.0138
knn:2789391 2956442	0.74	0.0122	0.1154	0.0109	0.53	0.73	0.50	0.0596	0.0055	0.0172
rpart:2789391 2956442	0.73	0.0046	0.0332	0.0031	0.61	0.83	0.50	0.0031	0.0073	0.0061
svm:2789391 2956442	0.70	0.0324	0.0079	0.0151	0.71	0.81	0.08	0.0003	0.0109	0.0218
rf:2789391 3005357	0.76	0.0074	0.0229	0.0072	0.52	0.80	0.41	0.0200	0.0066	0.0125
nb:2789391 3005357	0.74	0.0102	0.0330	0.0071	0.53	0.75	0.45	0.0411	0.0027	0.0132
rpart:2789391 3005357	0.73	0.0046	0.0332	0.0031	0.61	0.83	0.50	0.0031	0.0073	0.0061
svm:2789391 3005357	0.79	0.0017	0.0001	0.0644	0.68	0.91	-0.28	0.0000	0.0473	0.1003
rf:2789391 2651515	0.75	0.0097	0.0751	0.0045	0.75	0.73	0.57	0.0005	0.0008	0.0118
nb:2789391 2651515	0.75	0.0079	0.0101	0.0035	0.63	0.80	0.43	0.0013	0.0001	0.0119
knn:2789391 2651515	0.76	0.0062	0.0453	0.0032	0.60	0.77	0.45	0.0077	0.0017	0.0076
rpart:2789391 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
svm:2789391 2651515	0.74	0.0111	0.0055	0.0072	0.59	0.79	-0.38	0.0044	0.0008	0.0172
rf:3463598 2461837	0.74	0.0114	0.0277	0.0181	0.55	0.81	0.47	0.0140	0.0275	0.0247
rpart:3463598 2461837	0.68	0.0287	0.1722	0.0256	0.56	0.78	0.47	0.0308	0.0405	0.0300
rf:3463598 2512364	0.72	0.0230	0.0637	0.0100	0.75	0.73	0.62	0.0111	0.0124	0.0203
nb:3463598 2512364	0.75	0.0079	0.0060	0.0056	0.82	0.80	0.53	0.0000	0.0032	0.0122
knn:3463598 2512364	0.76	0.0061	0.0538	0.0048	0.67	0.69	0.61	0.1293	0.0067	0.0155
rpart:3463598 2512364	0.71	0.0043	0.0721	0.0028	0.73	0.77	0.53	0.0012	0.0032	0.0069

rf:3463598 2364325	0.72	0.0179	0.0110	0.0036	0.67	0.76	0.58	0.0056	0.0039	0.0086
nb:3463598 2364325	0.70	0.0348	0.0299	0.0129	0.60	0.77	0.48	0.0088	0.0059	0.0207
knn:3463598 2364325	0.73	0.0139	0.0847	0.0052	0.67	0.76	0.53	0.0060	0.0043	0.0103
rpart:3463598 2364325	0.71	0.0043	0.0721	0.0028	0.73	0.77	0.53	0.0012	0.0032	0.0069
knn:3463598 3066770	0.75	0.0075	0.0380	0.0014	0.73	0.77	0.48	0.0018	0.0016	0.0063
rpart:3463598 3066770	0.71	0.0043	0.0721	0.0028	0.73	0.77	0.53	0.0012	0.0032	0.0069
svm:3463598 3066770	0.69	0.0458	0.0139	0.0077	0.73	0.77	-0.24	0.0018	0.0009	0.0188
rf:3463598 2956442	0.76	0.0065	0.0164	0.0053	0.55	0.81	0.42	0.0195	0.0109	0.0098
knn:3463598 2956442	0.70	0.0303	0.1291	0.0129	0.62	0.75	0.51	0.0162	0.0097	0.0195
rpart:3463598 2956442	0.69	0.0436	0.0991	0.0517	0.48	0.75	0.49	0.1720	0.0707	0.0565
svm:3463598 2956442	0.69	0.0400	0.1436	0.0239	0.58	0.72	-0.04	0.0495	0.0170	0.0313
rf:3463598 3005357	0.70	0.0383	0.1722	0.0213	0.48	0.78	0.41	0.0663	0.0185	0.0278
nb:3463598 3005357	0.72	0.0209	0.0861	0.0148	0.53	0.77	0.44	0.0277	0.0075	0.0228
rpart:3463598 3005357	0.71	0.0043	0.0721	0.0028	0.73	0.77	0.53	0.0012	0.0032	0.0069
rpart:3463598 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
nb:2461837 2512364	0.74	0.0102	0.0221	0.0071	0.61	0.83	0.47	0.0042	0.0082	0.0125
knn:2461837 2512364	0.73	0.0139	0.0094	0.0155	0.48	0.81	0.48	0.0589	0.0220	0.0224
rf:2461837 2364325	0.73	0.0178	0.0751	0.0134	0.57	0.74	0.55	0.0511	0.0225	0.0188
nb:2461837 2364325	0.75	0.0079	0.0127	0.0105	0.56	0.78	0.43	0.0157	0.0082	0.0178
knn:2461837 2364325	0.74	0.0100	0.0453	0.0078	0.58	0.82	0.50	0.0042	0.0129	0.0138
rpart:2461837 2364325	0.68	0.0287	0.1722	0.0256	0.56	0.78	0.47	0.0308	0.0405	0.0300
svm:2461837 2364325	0.73	0.0130	0.0055	0.0264	0.63	0.80	0.07	0.0038	0.0351	0.0341
nb:2461837 3066770	0.70	0.0373	0.0127	0.0179	0.56	0.76	0.44	0.0264	0.0112	0.0254
svm:2461837 3066770	0.71	0.0243	0.0367	0.0274	0.54	0.71	0.15	0.1021	0.0236	0.0333
rf:2461837 2956442	0.70	0.0347	0.0991	0.0439	0.56	0.76	0.47	0.0465	0.0525	0.0494
rpart:2461837 2956442	0.68	0.0287	0.1722	0.0256	0.56	0.78	0.47	0.0308	0.0405	0.0300
rf:2461837 3005357	0.69	0.0423	0.0473	0.0446	0.50	0.74	0.46	0.0958	0.0522	0.0495
nb:2461837 3005357	0.74	0.0102	0.0055	0.0271	0.53	0.73	0.46	0.0651	0.0240	0.0333
knn:2461837 3005357	0.76	0.0063	0.0094	0.0025	0.60	0.86	0.44	0.0035	0.0068	0.0063
rpart:2461837 3005357	0.68	0.0287	0.1722	0.0256	0.56	0.78	0.47	0.0308	0.0405	0.0300
svm:2461837 3005357	0.71	0.0281	0.0127	0.0407	0.61	0.83	0.06	0.0042	0.0476	0.0467
nb:2461837 2651515	0.72	0.0194	0.0139	0.0117	0.53	0.77	0.41	0.0335	0.0026	0.0219
nb:2512364 2364325	0.79	0.0019	0.0017	0.0011	0.61	0.83	0.48	0.0015	0.0007	0.0042
knn:2512364 2364325	0.71	0.0265	0.2825	0.0277	0.60	0.71	0.70	0.0500	0.0377	0.0357
rpart:2512364 2364325	0.71	0.0117	0.0751	0.0093	0.55	0.84	0.48	0.0100	0.0188	0.0147
svm:2512364 2364325	0.76	0.0046	0.0017	0.0035	0.58	0.82	-0.30	0.0042	0.0032	0.0082
nb:2512364 3066770	0.79	0.0017	0.0055	0.0015	0.65	0.83	0.47	0.0006	0.0013	0.0053
knn:2512364 3066770	0.80	0.0015	0.0241	0.0008	0.64	0.78	0.53	0.0054	0.0015	0.0043
svm:2512364 3066770	0.77	0.0035	0.0043	0.0041	0.60	0.86	-0.01	0.0016	0.0062	0.0094
nb:2512364 2956442	0.71	0.0281	0.1100	0.0220	0.53	0.77	0.44	0.0324	0.0138	0.0286
svm:2512364 2956442	0.69	0.0400	0.1209	0.0289	0.57	0.74	0.05	0.0316	0.0172	0.0356
nb:2512364 3005357	0.76	0.0046	0.0177	0.0030	0.59	0.79	0.48	0.0049	0.0024	0.0073
knn:2512364 3005357	0.71	0.0293	0.0380	0.0479	0.42	0.68	0.50	0.4168	0.0312	0.0537

nb:2512364 2651515	0.77	0.0042	0.0079	0.0018	0.67	0.81	0.45	0.0007	0.0001	0.0092
rpart:2512364 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
nb:2364325 3066770	0.78	0.0023	0.0032	0.0019	0.50	0.82	0.40	0.0334	0.0004	0.0079
knn:2364325 3066770	0.76	0.0064	0.0110	0.0009	0.86	0.74	0.57	0.0001	0.0004	0.0069
rpart:2364325 3066770	0.69	0.0191	0.1154	0.0163	0.55	0.81	0.51	0.0131	0.0210	0.0212
svm:2364325 3066770	0.77	0.0031	0.0017	0.0015	0.52	0.83	-0.44	0.0176	0.0011	0.0057
rf:2364325 2956442	0.72	0.0222	0.0277	0.0214	0.63	0.80	0.48	0.0032	0.0129	0.0279
nb:2364325 2956442	0.70	0.0324	0.0101	0.0322	0.64	0.78	0.48	0.0031	0.0175	0.0398
knn:2364325 2956442	0.71	0.0266	0.1154	0.0284	0.57	0.74	0.54	0.0249	0.0235	0.0347
rpart:2364325 2956442	0.69	0.0191	0.1154	0.0163	0.55	0.81	0.51	0.0131	0.0210	0.0212
svm:2364325 2956442	0.71	0.0302	0.0101	0.0245	0.62	0.75	-0.09	0.0162	0.0172	0.0308
nb:2364325 3005357	0.75	0.0079	0.0101	0.0056	0.65	0.83	0.46	0.0007	0.0033	0.0112
knn:2364325 3005357	0.72	0.0179	0.0277	0.0100	0.61	0.83	0.50	0.0014	0.0076	0.0159
svm:2364325 3005357	0.74	0.0093	0.0101	0.0068	0.61	0.83	0.03	0.0016	0.0063	0.0124
nb:2364325 2651515	0.72	0.0225	0.0946	0.0069	0.53	0.75	0.43	0.0550	0.0006	0.0170
knn:2364325 2651515	0.71	0.0219	0.1783	0.0136	0.83	0.71	0.61	0.0000	0.0023	0.0272
rpart:2364325 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
knn:3066770 2956442	0.72	0.0188	0.1663	0.0214	0.50	0.70	0.49	0.1243	0.0129	0.0300
rf:3066770 3005357	0.72	0.0238	0.0751	0.0161	0.50	0.82	0.33	0.0265	0.0107	0.0227
nb:3066770 3005357	0.75	0.0072	0.0127	0.0042	0.58	0.72	0.48	0.0264	0.0019	0.0100
knn:3066770 3005357	0.75	0.0072	0.0164	0.0101	0.58	0.72	0.52	0.0264	0.0069	0.0156
svm:3066770 3005357	0.75	0.0079	0.0055	0.0069	0.61	0.83	-0.07	0.0026	0.0066	0.0122
nb:3066770 2651515	0.74	0.0102	0.0079	0.0030	0.50	0.76	0.38	0.0414	0.0001	0.0132
rpart:3066770 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
svm:3066770 2651515	0.69	0.0458	0.1436	0.0118	0.53	0.75	-0.63	0.0409	0.0018	0.0225
rf:2956442 2651515	0.72	0.0185	0.0453	0.0084	0.52	0.80	0.29	0.0163	0.0007	0.0200
nb:2956442 2651515	0.71	0.0261	0.0055	0.0275	0.50	0.82	0.37	0.0223	0.0040	0.0400
knn:2956442 2651515	0.77	0.0036	0.0241	0.0136	0.57	0.74	0.47	0.0253	0.0060	0.0216
rpart:2956442 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
nb:3005357 2651515	0.73	0.0141	0.0221	0.0049	0.52	0.83	0.38	0.0139	0.0003	0.0134
rpart:3005357 2651515	0.63	0.0399	0.5592	0.0362	0.71	0.71	0.56	0.0007	0.0025	0.0508
svm:3005357 2651515	0.69	0.0400	0.1367	0.0381	0.47	0.73	-0.67	0.1165	0.0036	0.0531

Performance of pairwise combinations of the 15 markers across different metrics for the Recurrence endpoint for LNI negative patients. All classifiers have a Wilcox P-value ≤ 0.05

TABLE 13

CLASSIFIER	AUC	WILCO X P- VALUE	KS P- VALUE	T-TEST P- VALUE	PPV	NPV	CUTOFF	KM P- VALUE	UVA HR P- VALUE	UVA OR P- VALUE
knn:3326487 2478155	0.81	0.010	0.056	0.005	0.67	0.91	0.50	0.01	0.03	0.02
rf:3326487 3139092	0.79	0.043	0.128	0.051	0.10	0.40	0.49	0.02	0.05	0.07
rf:2458376 2512364	0.84	0.014	0.025	0.007	0.43	0.83	0.45	0.31	0.02	0.03
nb:2458376 2512364	0.78	0.046	0.036	0.021	0.50	0.88	0.41	0.10	0.04	0.05

svm:2458376 2512364	0.78	0.046	0.025	0.039	0.56	0.82	-0.06	0.08	0.03	0.05
nb:2458376 2364325	0.79	0.037	0.137	0.047	0.50	0.80	0.42	0.16	0.07	0.06
svm:2458376 2364325	0.81	0.024	0.073	0.042	0.50	0.80	-0.27	0.16	0.06	0.06
nb:2458376 3066770	0.79	0.037	0.203	0.033	0.44	0.73	0.39	0.44	0.05	0.05
nb:3414753 2512364	0.78	0.046	0.137	0.069	0.50	0.80	0.48	0.11	0.08	0.08
rf:2478155 2461837	0.79	0.043	0.115	0.074	0.43	0.83	0.36	0.30	0.13	0.09
rf:2478155 2512364	0.93	0.001	0.001	0.003	0.55	0.89	0.45	0.05	0.02	0.04
rpart:2478155 2512364	0.76	0.049	0.439	0.055	0.75	0.75	0.56	0.04	0.05	0.08
rpart:3139092 2512364	0.79	0.037	0.050	0.053	0.46	0.86	0.49	0.22	0.09	0.08
rf:2461837 2512364	0.82	0.019	0.025	0.008	0.56	0.82	0.51	0.15	0.04	0.02
rpart:2461837 2512364	0.76	0.045	0.115	0.015	0.71	0.85	0.63	0.03	0.06	0.03
svm:2461837 2512364	0.81	0.024	0.054	0.003	1.00	0.76	0.78	0.03	0.03	0.06
rf:2512364 2364325	0.78	0.047	0.115	0.044	0.55	0.89	0.44	0.04	0.04	0.06
knn:2512364 2364325	0.87	0.007	0.026	0.005	0.50	1.00	0.30	0.05	0.01	0.03
svm:2512364 3066770	0.80	0.030	0.046	0.049	0.57	0.77	0.37	0.08	0.06	0.06
rf:2512364 2956442	0.79	0.037	0.046	0.031	0.63	0.83	0.56	0.02	0.04	0.06
rf:2512364 3005357	0.84	0.014	0.025	0.015	0.60	0.90	0.51	0.01	0.02	0.04
knn:2512364 3005357	0.80	0.034	0.216	0.031	0.50	0.88	0.39	0.07	0.03	0.05
rf:2512364 2651515	0.85	0.014	0.026	0.014	0.57	0.77	0.65	0.09	0.02	0.03
knn:2512364 2651515	0.77	0.050	0.050	0.029	0.83	0.86	0.70	0.00	0.01	0.05
svm:2512364 2651515	0.79	0.037	0.073	0.046	0.71	0.85	0.25	0.00	0.04	0.06
rpart:3326487 2458376 3139092	0.77	0.044	0.238	0.036	0.17	0.38	0.51	0.04	0.05	0.05
knn:3326487 2512364 2651515	0.78	0.027	0.287	0.017	0.50	1.00	0.17	0.04	0.00	0.07
rpart:3326487 2364325 3066770	0.21	0.027	0.373	0.081	0.14	0.54	0.40	0.20	0.15	0.11
nb:2458376 3414753 2512364	0.78	0.046	0.137	0.032	0.55	0.89	0.41	0.05	0.05	0.05
knn:2458376 3414753 2512364	0.79	0.037	0.262	0.031	0.55	0.89	0.49	0.05	0.05	0.05
svm:2458376 3414753 2512364	0.79	0.037	0.054	0.030	0.50	0.80	0.25	0.20	0.05	0.05
hdda:2458376 3414753 2364325	0.78	0.046	0.094	0.035	0.75	0.75	0.53	0.06	0.06	0.06
nb:2458376 3414753 2651515	0.78	0.046	0.073	0.027	0.71	0.85	0.37	0.01	0.03	0.04
rf:2458376 2332285 2512364	0.85	0.011	0.012	0.017	0.46	0.86	0.41	0.18	0.03	0.04
hdda:2458376 2332285 2651515	0.80	0.030	0.036	0.052	0.67	0.79	0.47	0.04	0.05	0.07
rf:2458376 2478155 2789391	0.78	0.047	0.143	0.033	0.60	0.73	0.59	0.15	0.04	0.06
svm:2458376 2478155 2789391	0.82	0.019	0.094	0.016	0.56	0.82	-0.04	0.10	0.03	0.04
rf:2458376 2478155 2512364	0.81	0.029	0.064	0.015	0.58	1.00	0.52	0.01	0.03	0.04
knn:2458376 2478155 3066770	0.78	0.045	0.115	0.039	0.55	0.89	0.43	0.05	0.07	0.06
nb:2458376 2478155 2651515	0.78	0.046	0.012	0.058	0.67	0.79	0.39	0.02	0.04	0.08

knn:2458376 2478155 2651515	0.80	0.030	0.238	0.019	0.63	0.83	0.50	0.05	0.03	0.04
rf:2458376 2789391 2512364	0.79	0.039	0.115	0.028	0.71	0.85	0.59	0.01	0.04	0.05
rf:2458376 3463598 2512364	0.80	0.030	0.012	0.025	0.43	0.83	0.39	0.33	0.03	0.08
svm:2458376 3463598 2512364	0.80	0.030	0.054	0.011	0.63	0.83	-0.26	0.02	0.02	0.04
rf:2458376 2461837 2512364	0.79	0.039	0.115	0.019	0.71	0.85	0.59	0.02	0.05	0.05
knn:2458376 2461837 2512364	0.78	0.047	0.128	0.034	0.56	0.82	0.51	0.15	0.07	0.05
rpart:2458376 2461837 2364325	0.84	0.015	0.128	0.026	0.44	1.00	0.33	0.14	0.07	0.07
rf:2458376 2512364 2364325	0.84	0.016	0.022	0.010	0.80	0.80	0.68	0.01	0.01	0.03
nb:2458376 2512364 2364325	0.80	0.030	0.137	0.024	0.63	0.83	0.49	0.03	0.04	0.04
svm:2458376 2512364 2364325	0.88	0.005	0.017	0.009	0.67	0.79	0.39	0.04	0.02	0.03
rf:2458376 2512364 3066770	0.89	0.003	0.005	0.009	0.71	0.85	0.56	0.01	0.02	0.04
nb:2458376 2512364 3066770	0.79	0.037	0.137	0.029	0.50	0.80	0.39	0.13	0.05	0.05
knn:2458376 2512364 3066770	0.79	0.038	0.262	0.029	0.56	0.82	0.48	0.06	0.04	0.05
svm:2458376 2512364 3066770	0.82	0.019	0.094	0.011	0.57	0.77	0.28	0.20	0.03	0.03
rf:2458376 2512364 3005357	0.79	0.037	0.137	0.021	0.67	0.79	0.62	0.01	0.01	0.04
nb:2458376 2512364 3005357	0.78	0.046	0.169	0.028	0.55	0.89	0.38	0.06	0.05	0.05
rpart:2458376 2512364 3005357	0.77	0.044	0.439	0.039	0.56	0.82	0.50	0.05	0.05	0.05
svm:2458376 2512364 3005357	0.78	0.046	0.137	0.029	0.46	0.86	-0.27	0.18	0.04	0.05
rf:2458376 2512364 2651515	0.82	0.022	0.022	0.019	0.80	0.80	0.66	0.00	0.02	0.04
knn:2458376 2512364 2651515	0.89	0.003	0.003	0.001	0.67	0.79	0.83	0.01	0.01	0.01
nb:2458376 2364325 2651515	0.78	0.046	0.137	0.061	0.50	0.80	0.35	0.16	0.03	0.08
knn:2458376 2364325 2651515	0.81	0.022	0.216	0.038	0.50	0.88	0.50	0.10	0.02	0.08
nb:2458376 3066770 3005357	0.78	0.046	0.111	0.048	0.57	0.77	0.42	0.14	0.07	0.06
knn:2458376 3066770 3005357	0.80	0.035	0.216	0.023	0.67	0.79	0.53	0.07	0.04	0.04
nb:2458376 3066770 2651515	0.80	0.030	0.073	0.021	0.67	0.79	0.37	0.04	0.02	0.04
svm:2458376 3066770 2651515	0.82	0.019	0.012	0.013	0.67	0.79	1.14	0.07	0.05	0.03
hdda:3414753 2478155 2512364	0.79	0.037	0.046	0.106	0.44	0.73	0.49	0.39	0.11	0.12
svm:3414753 2512364 2364325	0.78	0.046	0.073	0.065	0.50	0.80	0.27	0.13	0.05	0.08
hdda:3414753 2512364 3066770	0.78	0.046	0.111	0.100	0.44	0.73	0.49	0.39	0.11	0.11

svm:3414753 2512364 3066770	0.79	0.037	0.054	0.040	0.50	0.80	-0.22	0.11	0.04	0.06
rf:3414753 2512364 2956442	0.79	0.039	0.143	0.065	0.57	0.77	0.66	0.12	0.06	0.08
knn:3414753 2512364 3005357	0.79	0.038	0.287	0.039	0.57	0.77	0.55	0.14	0.06	0.05
rpart:2332285 2478155 3463598	0.82	0.019	0.050	0.007	0.71	0.85	0.52	0.01	0.01	0.02
rf:2332285 2478155 2512364	0.84	0.016	0.022	0.013	0.55	0.89	0.46	0.06	0.03	0.04
rf:2332285 2512364 2364325	0.79	0.037	0.073	0.040	0.56	0.82	0.48	0.06	0.04	0.06
rpart:2332285 2512364 2364325	0.79	0.034	0.128	0.064	0.44	1.00	0.53	0.12	0.10	0.15
rpart:2332285 2512364 3066770	0.81	0.016	0.128	0.011	0.60	0.90	0.58	0.02	0.04	0.03
rf:2332285 2512364 3005357	0.79	0.039	0.128	0.058	0.56	0.82	0.52	0.06	0.06	0.07
rf:2478155 3463598 2512364	0.81	0.024	0.054	0.008	0.55	0.89	0.34	0.05	0.01	0.04
rpart:2478155 3463598 2512364	0.82	0.019	0.050	0.002	0.83	0.86	0.62	0.00	0.01	0.01
rf:2478155 2461837 2512364	0.86	0.008	0.012	0.012	0.46	0.86	0.36	0.18	0.04	0.04
rf:2478155 2512364 2364325	0.87	0.006	0.012	0.006	0.67	0.91	0.53	0.01	0.01	0.03
svm:2478155 2512364 2364325	0.78	0.046	0.111	0.034	0.57	0.77	0.26	0.07	0.02	0.05
rf:2478155 2512364 3066770	0.86	0.010	0.050	0.005	0.55	0.89	0.42	0.05	0.01	0.03
rf:2478155 2512364 2956442	0.80	0.030	0.094	0.022	0.60	0.90	0.42	0.02	0.03	0.04
rf:2478155 2512364 3005357	0.89	0.006	0.050	0.008	0.50	1.00	0.40	0.04	0.04	0.04
rf:2478155 2512364 2651515	0.84	0.017	0.050	0.023	0.56	0.82	0.50	0.08	0.03	0.04
svm:2478155 2364325 3066770	0.79	0.037	0.036	0.044	0.57	0.77	0.14	0.12	0.05	0.06
svm:2478155 2364325 3005357	0.78	0.046	0.046	0.080	0.63	0.83	-0.01	0.02	0.06	0.09
knn:2478155 3066770 3005357	0.78	0.045	0.287	0.072	0.56	0.82	0.47	0.06	0.08	0.08
knn:3139092 2461837 2651515	0.85	0.012	0.019	0.013	0.43	0.83	0.36	0.33	0.02	0.04
rpart:3139092 2512364 3005357	0.78	0.044	0.050	0.037	0.63	0.83	0.56	0.03	0.05	0.05
rf:2789391 2461837 2512364	0.81	0.024	0.046	0.033	0.50	0.80	0.43	0.24	0.08	0.05
rf:2789391 2512364 2364325	0.80	0.030	0.017	0.054	0.50	0.71	0.66	0.28	0.06	0.07
rf:2789391 2512364 2956442	0.79	0.037	0.036	0.068	0.50	0.71	0.64	0.28	0.08	0.08
svm:2789391 3066770 2651515	0.78	0.046	0.036	0.106	0.60	0.73	0.13	0.07	0.06	0.12
rf:3463598 2461837 2512364	0.80	0.030	0.054	0.008	0.80	0.80	0.59	0.04	0.03	0.03
rpart:3463598 2461837 2956442	0.79	0.036	0.238	0.042	0.67	0.79	0.55	0.05	0.07	0.06

rf:3463598 2512364 3005357	0.79	0.037	0.025	0.023	0.46	0.86	0.33	0.13	0.02	0.06
rf:2461837 2512364 2364325	0.79	0.039	0.143	0.027	0.55	0.89	0.42	0.06	0.05	0.05
svm:2461837 2512364 3005357	0.80	0.030	0.094	0.036	0.56	0.82	-0.12	0.12	0.06	0.05
rf:2461837 2512364 2651515	0.78	0.046	0.012	0.044	0.60	0.90	0.45	0.02	0.05	0.06
rf:2512364 2364325 3066770	0.80	0.030	0.036	0.036	0.60	0.73	0.67	0.09	0.03	0.05
rf:2512364 2364325 2956442	0.85	0.014	0.026	0.012	0.71	0.85	0.58	0.01	0.02	0.03
rf:2512364 2364325 3005357	0.79	0.037	0.073	0.037	0.55	0.89	0.48	0.03	0.03	0.05
rf:2512364 3066770 2956442	0.79	0.037	0.046	0.055	0.57	0.77	0.58	0.12	0.06	0.07
knn:2512364 3066770 3005357	0.79	0.040	0.128	0.051	0.63	0.83	0.51	0.03	0.06	0.06
svm:2512364 3066770 3005357	0.80	0.030	0.111	0.018	0.56	0.82	0.04	0.06	0.03	0.04
rf:2512364 2956442 2651515	0.79	0.043	0.128	0.112	0.60	0.90	0.35	0.02	0.06	0.13
rpart:2512364 2956442 2651515	0.89	0.005	0.022	0.002	0.50	1.00	0.33	0.05	0.03	0.03
svm:2512364 3005357 2651515	0.80	0.030	0.025	0.090	0.41	1.00	-2.69	0.22	0.09	0.13
knn:3326487 2458376 2332285 3005357	0.79	0.038	0.128	0.094	0.57	0.77	0.47	0.14	0.11	0.11
rpart:3326487 3414753 2478155 3066770	0.21	0.027	0.373	0.081	0.14	0.54	0.40	0.20	0.15	0.11
rf:3326487 2478155 3463598 2512364	0.78	0.047	0.102	0.065	0.63	0.83	0.41	0.02	0.05	0.08
svm:3326487 2478155 3066770 2651515	0.78	0.046	0.036	0.209	0.40	0.80	-0.13	0.51	0.27	0.23
hdda:3326487 3463598 2512364 3066770	0.82	0.019	0.046	0.010	0.23	0.43	0.46	0.10	0.01	0.04
svm:3326487 2512364 3066770 2651515	0.82	0.019	0.012	0.052	0.67	0.91	-0.14	0.01	0.07	0.07
hdda:2458376 3414753 2332285 2364325	0.78	0.046	0.094	0.051	0.57	0.77	0.48	0.14	0.08	0.07
svm:2458376 3414753 2332285 2364325	0.79	0.037	0.094	0.065	0.57	0.77	0.08	0.14	0.09	0.08
svm:2458376 3414753 2478155 2512364	0.78	0.046	0.203	0.042	0.50	0.80	0.05	0.20	0.06	0.06
nb:2458376 3414753 2478155 3066770	0.78	0.046	0.046	0.079	0.57	0.77	0.40	0.12	0.08	0.09
rpart:2458376 3414753 3139092 2512364	0.78	0.043	0.216	0.069	0.55	0.89	0.59	0.06	0.11	0.09
hdda:2458376 3414753 3463598 2364325	0.78	0.046	0.094	0.031	0.75	0.75	0.53	0.06	0.05	0.06
rpart:2458376 3414753 2461837 2512364	0.84	0.013	0.056	0.004	0.67	0.91	0.55	0.01	0.04	0.02
hdda:2458376 3414753 2512364 2364325	0.80	0.030	0.094	0.036	0.75	0.75	0.53	0.06	0.06	0.06
nb:2458376 3414753 2512364 2364325	0.80	0.030	0.111	0.038	0.63	0.83	0.46	0.03	0.05	0.05
svm:2458376 3414753 2512364 2364325	0.80	0.030	0.073	0.028	0.56	0.82	0.38	0.06	0.03	0.04

svm:2458376 3414753 2512364 3066770	0.84	0.014	0.054	0.004	0.54	1.00	-0.29	0.02	0.01	0.03
rpart:2458376 3414753 2512364 3005357	0.77	0.044	0.439	0.039	0.56	0.82	0.50	0.05	0.05	0.05
rf:2458376 3414753 2512364 2651515	0.83	0.019	0.115	0.024	0.56	0.82	0.54	0.04	0.03	0.05
nb:2458376 3414753 2512364 2651515	0.80	0.030	0.073	0.020	0.63	0.83	0.38	0.03	0.03	0.04
nb:2458376 3414753 2364325 3066770	0.78	0.046	0.094	0.073	0.57	0.77	0.45	0.14	0.08	0.08
nb:2458376 3414753 3066770 2651515	0.81	0.024	0.046	0.028	0.63	0.83	0.34	0.03	0.04	0.04
rf:2458376 2332285 2478155 2512364	0.85	0.014	0.008	0.014	0.55	0.89	0.49	0.05	0.03	0.04
svm:2458376 2332285 2478155 2364325	0.78	0.046	0.094	0.063	0.57	0.77	0.01	0.14	0.09	0.07
rpart:2458376 2332285 3139092 2461837	0.84	0.015	0.128	0.025	0.41	1.00	0.23	0.20	0.08	0.05
rf:2458376 2332285 2789391 2512364	0.78	0.046	0.094	0.041	0.57	0.77	0.59	0.14	0.07	0.06
rf:2458376 2332285 3463598 2512364	0.78	0.046	0.054	0.028	0.46	0.86	0.38	0.20	0.03	0.06
hdda:2458376 2332285 3463598 2651515	0.78	0.046	0.094	0.057	0.50	0.71	0.47	0.31	0.05	0.08
hdda:2458376 2332285 2461837 2651515	0.78	0.046	0.036	0.066	0.50	0.88	0.42	0.13	0.06	0.08
rf:2458376 2332285 2512364 2364325	0.81	0.024	0.036	0.022	0.63	0.83	0.59	0.03	0.04	0.04
svm:2458376 2332285 2512364 2364325	0.79	0.037	0.111	0.036	0.56	0.82	0.18	0.06	0.05	0.05
nb:2458376 2332285 2512364 3066770	0.78	0.046	0.094	0.095	0.50	0.75	0.41	0.25	0.12	0.10
rf:2458376 2332285 2512364 3005357	0.82	0.019	0.025	0.015	0.56	0.82	0.56	0.06	0.03	0.04
rf:2458376 2332285 2512364 2651515	0.86	0.011	0.022	0.019	0.75	0.92	0.55	0.00	0.03	0.04
hdda:2458376 2332285 2364325 2651515	0.78	0.046	0.169	0.058	0.50	0.88	0.42	0.13	0.05	0.08
svm:2458376 2332285 3066770 3005357	0.78	0.046	0.046	0.090	0.50	0.75	-0.29	0.25	0.11	0.10
hdda:2458376 2332285 2956442 2651515	0.78	0.046	0.073	0.041	0.75	0.75	0.50	0.02	0.04	0.06
rf:2458376 2478155 2789391 2512364	0.84	0.014	0.036	0.010	0.47	1.00	0.40	0.07	0.02	0.05
knn:2458376 2478155 2461837 2651515	0.81	0.025	0.022	0.040	0.75	0.92	0.50	0.00	0.07	0.06
rf:2458376 2478155 2512364 2364325	0.85	0.011	0.012	0.012	0.50	1.00	0.43	0.04	0.02	0.04
nb:2458376 2478155 2512364 2364325	0.79	0.037	0.073	0.039	0.56	0.82	0.38	0.06	0.04	0.05
svm:2458376 2478155 2512364 2364325	0.80	0.030	0.111	0.036	0.57	0.77	0.24	0.16	0.06	0.06
rf:2458376 2478155 2512364 3066770	0.85	0.012	0.056	0.006	0.47	1.00	0.36	0.07	0.01	0.03
nb:2458376 2478155 2512364 3066770	0.79	0.037	0.137	0.047	0.50	0.75	0.39	0.25	0.05	0.06
knn:2458376 2478155 2512364 3066770	0.80	0.029	0.056	0.016	0.67	0.91	0.50	0.01	0.05	0.03

svm:2458376 2478155 2512364 3066770	0.89	0.003	0.017	0.003	0.63	0.83	0.16	0.05	0.02	0.02
rf:2458376 2478155 2512364 2956442	0.78	0.046	0.137	0.029	0.46	0.86	0.43	0.18	0.04	0.05
rf:2458376 2478155 2512364 3005357	0.82	0.022	0.056	0.019	0.47	1.00	0.33	0.07	0.02	0.05
rf:2458376 2478155 2512364 2651515	0.82	0.019	0.036	0.016	0.55	0.89	0.50	0.04	0.03	0.04
knn:2458376 2478155 2512364 2651515	0.78	0.046	0.262	0.049	0.67	0.79	0.55	0.02	0.04	0.06
knn:2458376 2478155 2364325 2651515	0.79	0.042	0.238	0.046	0.63	0.83	0.48	0.03	0.03	0.06
svm:2458376 2478155 2364325 2651515	0.78	0.046	0.073	0.045	0.67	0.79	-0.16	0.04	0.04	0.06
nb:2458376 2478155 3066770 3005357	0.79	0.037	0.111	0.062	0.50	0.75	0.35	0.25	0.07	0.07
knn:2458376 2478155 3066770 3005357	0.77	0.049	0.262	0.076	0.50	0.75	0.46	0.25	0.09	0.08
knn:2458376 2478155 3066770 2651515	0.81	0.026	0.102	0.009	0.67	0.79	0.50	0.04	0.02	0.03
rpart:2458376 3139092 2512364 2364325	0.77	0.047	0.050	0.122	0.45	0.78	0.52	0.31	0.15	0.13
nb:2458376 3139092 2512364 3066770	0.78	0.046	0.137	0.058	0.50	0.80	0.37	0.13	0.07	0.07
nb:2458376 3139092 2512364 2651515	0.78	0.046	0.073	0.028	0.56	0.82	0.39	0.06	0.03	0.05
rf:2458376 2789391 2512364 2364325	0.84	0.014	0.017	0.022	0.67	0.91	0.53	0.01	0.03	0.05
svm:2458376 2789391 2512364 2364325	0.79	0.037	0.036	0.026	0.67	0.91	0.45	0.01	0.01	0.07
rf:2458376 2789391 2512364 3066770	0.81	0.024	0.005	0.022	0.67	0.91	0.52	0.01	0.04	0.05
knn:2458376 2789391 2512364 3005357	0.77	0.050	0.262	0.067	0.50	0.75	0.49	0.25	0.09	0.08
rf:2458376 2789391 2512364 2651515	0.84	0.017	0.022	0.031	0.60	0.90	0.52	0.02	0.03	0.06
knn:2458376 2789391 3066770 2651515	0.81	0.010	0.056	0.005	0.67	0.91	0.50	0.01	0.03	0.02
rf:2458376 3463598 2461837 2512364	0.81	0.024	0.007	0.032	0.46	0.86	0.43	0.18	0.05	0.07
rpart:2458376 3463598 2461837 2512364	0.79	0.037	0.216	0.044	0.56	0.82	0.62	0.09	0.08	0.06
svm:2458376 3463598 2461837 3005357	0.80	0.030	0.111	0.030	0.44	0.73	-0.20	0.44	0.05	0.05
hdda:2458376 3463598 2512364 2364325	0.78	0.046	0.137	0.034	0.75	0.75	0.53	0.06	0.05	0.06
rf:2458376 3463598 2512364 2364325	0.80	0.030	0.094	0.018	0.60	0.90	0.52	0.01	0.02	0.06
knn:2458376 3463598 2512364 2364325	0.77	0.043	0.475	0.035	0.50	0.88	0.50	0.16	0.05	0.06
svm:2458376 3463598 2512364 2364325	0.82	0.019	0.012	0.024	0.60	0.73	0.06	0.21	0.04	0.05
rf:2458376 3463598 2512364 3066770	0.81	0.026	0.050	0.020	0.45	0.78	0.44	0.22	0.02	0.08
svm:2458376 3463598 2512364 3066770	0.88	0.005	0.005	0.003	0.64	1.00	-0.45	0.00	0.01	0.03
knn:2458376 3463598 2512364 3005357	0.85	0.013	0.026	0.011	0.56	0.82	0.50	0.07	0.03	0.03

rf:2458376 3463598 2512364 2651515	0.78	0.047	0.056	0.061	0.67	0.91	0.43	0.01	0.04	0.08
rf:2458376 2461837 2512364 2364325	0.78	0.047	0.216	0.040	0.55	0.89	0.50	0.06	0.07	0.06
knn:2458376 2461837 2512364 2956442	0.80	0.033	0.287	0.109	0.50	0.75	0.52	0.25	0.12	0.11
knn:2458376 2461837 2512364 3005357	0.79	0.039	0.102	0.039	0.55	0.89	0.49	0.06	0.07	0.06
rf:2458376 2461837 2512364 2651515	0.78	0.047	0.115	0.031	0.71	0.85	0.60	0.02	0.07	0.05
nb:2458376 2461837 2512364 2651515	0.78	0.046	0.073	0.022	0.55	0.89	0.34	0.06	0.04	0.05
knn:2458376 2461837 2512364 2651515	0.79	0.035	0.128	0.096	0.50	0.88	0.45	0.11	0.10	0.12
rf:2458376 2512364 2364325 3066770	0.85	0.013	0.022	0.007	0.67	0.91	0.52	0.01	0.01	0.03
nb:2458376 2512364 2364325 3066770	0.82	0.019	0.046	0.041	0.63	0.83	0.45	0.03	0.05	0.05
svm:2458376 2512364 2364325 3066770	0.84	0.014	0.025	0.004	0.83	0.86	0.75	0.00	0.01	0.02
rf:2458376 2512364 2364325 3005357	0.84	0.014	0.073	0.024	0.50	0.88	0.49	0.07	0.02	0.05
nb:2458376 2512364 2364325 3005357	0.80	0.030	0.169	0.042	0.56	0.82	0.43	0.07	0.06	0.06
knn:2458376 2512364 2364325 3005357	0.79	0.035	0.511	0.015	0.57	0.77	0.64	0.08	0.01	0.06
svm:2458376 2512364 2364325 3005357	0.79	0.037	0.073	0.037	0.56	0.82	0.39	0.07	0.06	0.06
nb:2458376 2512364 2364325 2651515	0.78	0.046	0.169	0.029	0.63	0.83	0.40	0.03	0.03	0.04
nb:2458376 2512364 3066770 3005357	0.79	0.037	0.137	0.039	0.56	0.82	0.36	0.06	0.06	0.05
svm:2458376 2512364 3066770 3005357	0.79	0.037	0.137	0.028	0.56	0.82	-0.22	0.06	0.04	0.05
rf:2458376 2512364 3066770 2651515	0.89	0.003	0.003	0.010	0.75	0.75	0.66	0.03	0.02	0.03
nb:2458376 2512364 3066770 2651515	0.82	0.019	0.073	0.019	0.56	0.82	0.34	0.06	0.02	0.04
rf:2458376 2512364 2956442 3005357	0.78	0.046	0.137	0.030	0.55	0.89	0.47	0.03	0.04	0.05
rf:2458376 2512364 3005357 2651515	0.84	0.014	0.017	0.060	0.57	0.77	0.64	0.07	0.04	0.07
nb:2458376 2512364 3005357 2651515	0.80	0.030	0.054	0.023	0.63	0.83	0.38	0.03	0.03	0.04
nb:2458376 2364325 3066770 2651515	0.78	0.046	0.094	0.052	0.57	0.77	0.41	0.08	0.04	0.06
hdda:3414753 2478155 3463598 2512364	0.78	0.046	0.111	0.122	0.44	0.73	0.48	0.39	0.13	0.13
rpart:3414753 2478155 3463598 2512364	0.80	0.030	0.050	0.003	0.83	0.86	0.61	0.00	0.01	0.01
svm:3414753 2478155 2512364 2364325	0.78	0.046	0.111	0.079	0.56	0.82	-0.07	0.06	0.07	0.09
rf:3414753 2478155 2512364 3066770	0.80	0.036	0.143	0.056	0.50	0.80	0.44	0.11	0.06	0.07
knn:3414753 2478155 2512364 3066770	0.78	0.046	0.064	0.102	0.50	0.75	0.54	0.25	0.10	0.11
svm:3414753 2478155 2512364 3066770	0.81	0.024	0.111	0.022	0.57	0.77	0.78	0.09	0.02	0.04

svm:3414753 2478155 3066770 2651515	0.78	0.046	0.073	0.052	0.63	0.83	-0.09	0.03	0.06	0.07
rpart:3414753 2478155 2956442 3005357	0.79	0.032	0.262	0.021	0.50	1.00	0.46	0.04	0.04	0.07
rpart:3414753 3139092 3463598 2512364	0.78	0.043	0.216	0.069	0.55	0.89	0.59	0.06	0.11	0.09
rpart:3414753 3139092 2512364 3066770	0.78	0.043	0.216	0.069	0.55	0.89	0.59	0.06	0.11	0.09
rpart:3414753 3139092 2512364 3005357	0.78	0.043	0.216	0.069	0.55	0.89	0.59	0.06	0.11	0.09
svm:3414753 2789391 2461837 2512364	0.86	0.008	0.025	0.002	0.71	0.85	0.63	0.01	0.01	0.02
knn:3414753 3463598 2461837 2651515	0.77	0.049	0.262	0.041	0.55	0.89	0.50	0.05	0.08	0.06
rpart:3414753 2461837 2512364 3066770	0.79	0.029	0.115	0.013	0.71	0.85	0.63	0.03	0.05	0.02
rf:3414753 2461837 2512364 3005357	0.83	0.019	0.064	0.058	0.50	0.75	0.54	0.25	0.07	0.07
rpart:3414753 2461837 2512364 3005357	0.79	0.029	0.115	0.013	0.71	0.85	0.63	0.03	0.05	0.02
svm:3414753 2512364 2364325 3066770	0.78	0.046	0.094	0.082	0.56	0.82	-0.17	0.06	0.08	0.09
svm:3414753 2512364 3066770 3005357	0.84	0.014	0.046	0.073	0.56	0.82	0.00	0.06	0.08	0.08
rf:3414753 2512364 2956442 3005357	0.79	0.037	0.169	0.044	0.63	0.83	0.55	0.02	0.05	0.06
rpart:3414753 2512364 2956442 2651515	0.78	0.045	0.287	0.039	0.56	0.82	0.61	0.10	0.06	0.06
svm:3414753 2512364 3005357 2651515	0.78	0.046	0.073	0.019	0.71	0.85	0.09	0.01	0.02	0.04
rpart:2332285 2478155 2789391 3463598	0.81	0.027	0.216	0.061	0.57	0.77	0.43	0.15	0.08	0.07
rf:2332285 2478155 3463598 2512364	0.84	0.017	0.050	0.016	0.80	0.80	0.52	0.02	0.02	0.05
rf:2332285 2478155 2512364 2364325	0.82	0.019	0.036	0.015	0.63	0.83	0.51	0.02	0.01	0.03
rf:2332285 2478155 2512364 3066770	0.81	0.026	0.064	0.030	0.56	0.82	0.46	0.06	0.03	0.06
rf:2332285 2478155 2512364 2956442	0.79	0.043	0.056	0.028	0.60	0.90	0.46	0.02	0.05	0.05
rf:2332285 2478155 2512364 3005357	0.79	0.043	0.128	0.030	0.60	0.90	0.49	0.01	0.04	0.05
rf:2332285 3463598 2956442 3005357	0.79	0.037	0.017	0.074	0.50	0.75	0.49	0.37	0.10	0.09
knn:2332285 3463598 3005357 2651515	0.82	0.016	0.238	0.009	0.63	0.83	0.50	0.01	0.01	0.03
rpart:2332285 2512364 2364325 3066770	0.80	0.025	0.128	0.013	0.60	0.90	0.59	0.02	0.04	0.03
svm:2332285 2512364 2364325 3066770	0.82	0.019	0.073	0.023	0.56	0.82	0.24	0.06	0.03	0.04
rf:2332285 2512364 2364325 2956442	0.80	0.030	0.046	0.030	0.55	0.89	0.46	0.06	0.04	0.05
rf:2332285 2512364 2364325 3005357	0.80	0.036	0.115	0.050	0.50	0.80	0.51	0.13	0.05	0.07
knn:2332285 2512364 2956442 3005357	0.77	0.048	0.439	0.117	0.50	0.75	0.51	0.25	0.13	0.12
rpart:2478155 3139092 3463598 2512364	0.84	0.014	0.050	0.029	0.55	0.89	0.54	0.07	0.08	0.06

svm:2478155 3139092 2461837 2651515	0.84	0.014	0.007	0.053	0.35	0.67	-0.76	0.98	0.04	0.08
rpart:2478155 3139092 2512364 3066770	0.84	0.014	0.050	0.046	0.55	0.89	0.62	0.06	0.10	0.07
rf:2478155 3139092 2512364 2956442	0.78	0.047	0.022	0.102	0.40	0.80	0.33	0.46	0.12	0.12
rpart:2478155 3139092 2512364 2956442	0.77	0.049	0.216	0.063	0.50	0.88	0.46	0.11	0.09	0.08
rpart:2478155 2789391 3463598 2512364	0.79	0.040	0.216	0.035	0.67	0.79	0.48	0.06	0.05	0.05
rf:2478155 2789391 2461837 2512364	0.78	0.046	0.073	0.048	0.55	0.89	0.43	0.06	0.09	0.06
svm:2478155 2789391 2461837 2512364	0.78	0.046	0.073	0.028	0.71	0.85	0.47	0.01	0.01	0.08
rf:2478155 2789391 2512364 2364325	0.82	0.019	0.017	0.018	0.67	0.91	0.49	0.01	0.03	0.04
rf:2478155 2789391 2512364 3066770	0.79	0.037	0.036	0.030	0.67	0.91	0.42	0.01	0.05	0.05
rf:2478155 3463598 2461837 2512364	0.82	0.024	0.056	0.028	0.46	0.86	0.42	0.18	0.06	0.05
rpart:2478155 3463598 2461837 2512364	0.79	0.036	0.115	0.016	0.71	0.85	0.54	0.01	0.05	0.03
rf:2478155 3463598 2512364 2364325	0.84	0.014	0.046	0.010	0.50	0.71	0.55	0.25	0.01	0.04
rpart:2478155 3463598 2512364 2364325	0.82	0.019	0.050	0.002	0.83	0.86	0.62	0.00	0.01	0.01
rf:2478155 3463598 2512364 3066770	0.80	0.030	0.137	0.022	0.56	0.82	0.41	0.09	0.02	0.07
rf:2478155 3463598 2512364 2956442	0.81	0.026	0.022	0.012	0.60	0.90	0.44	0.03	0.03	0.03
rf:2478155 3463598 2512364 3005357	0.79	0.043	0.143	0.012	0.67	0.79	0.49	0.06	0.01	0.05
rf:2478155 2461837 2512364 2364325	0.78	0.046	0.137	0.037	0.43	0.83	0.33	0.30	0.07	0.06
rf:2478155 2461837 2512364 2956442	0.81	0.026	0.056	0.021	0.55	0.89	0.43	0.05	0.04	0.04
rf:2478155 2512364 2364325 3066770	0.85	0.014	0.022	0.006	0.67	0.91	0.46	0.01	0.01	0.03
svm:2478155 2512364 2364325 3066770	0.78	0.046	0.111	0.039	0.44	0.73	0.05	0.47	0.05	0.06
rf:2478155 2512364 2364325 2956442	0.84	0.014	0.012	0.006	0.67	0.91	0.49	0.01	0.01	0.02
rf:2478155 2512364 2364325 2651515	0.81	0.024	0.046	0.040	0.60	0.90	0.44	0.02	0.02	0.06
rf:2478155 2512364 3066770 2956442	0.85	0.011	0.036	0.013	0.50	0.88	0.38	0.10	0.03	0.04
rf:2478155 2512364 3066770 3005357	0.81	0.024	0.036	0.014	0.63	0.83	0.54	0.02	0.02	0.03
svm:2478155 2512364 3066770 3005357	0.78	0.046	0.111	0.037	0.56	0.82	0.09	0.06	0.04	0.06
rf:2478155 2512364 3066770 2651515	0.78	0.047	0.115	0.088	0.60	0.90	0.33	0.02	0.04	0.11
svm:2478155 2512364 3066770 2651515	0.80	0.030	0.017	0.043	0.60	0.73	-0.01	0.07	0.02	0.06
rf:2478155 2512364 2956442 3005357	0.82	0.024	0.056	0.008	0.58	1.00	0.43	0.01	0.02	0.03
rpart:2478155 2512364 2956442 3005357	0.77	0.036	0.262	0.028	0.50	1.00	0.44	0.04	0.16	0.17

rf:2478155 2512364 2956442 2651515	0.80	0.032	0.128	0.030	0.55	0.89	0.45	0.05	0.04	0.05
rpart:2478155 2512364 2956442 2651515	0.79	0.034	0.128	0.015	0.60	0.90	0.62	0.02	0.05	0.04
svm:2478155 2512364 3005357 2651515	0.80	0.030	0.094	0.029	0.56	0.82	-0.08	0.06	0.03	0.04
rpart:3139092 2789391 3463598 2512364	0.78	0.044	0.050	0.184	0.46	0.86	0.53	0.22	0.24	0.19
knn:3139092 2789391 2461837 2651515	0.81	0.021	0.050	0.009	0.83	0.86	0.50	0.00	0.01	0.03
svm:3139092 3463598 2461837 3005357	0.79	0.037	0.036	0.116	0.40	0.80	-0.38	0.46	0.14	0.14
knn:3139092 3463598 2461837 2651515	0.77	0.025	0.128	0.018	0.60	0.90	0.50	0.03	0.06	0.04
svm:3139092 3463598 2461837 2651515	0.84	0.014	0.012	0.011	0.55	0.89	-0.08	0.06	0.01	0.05
rpart:3139092 3463598 2512364 3066770	0.84	0.014	0.022	0.008	0.60	0.90	0.52	0.04	0.04	0.03
rpart:3139092 3463598 2512364 3005357	0.83	0.016	0.022	0.005	0.75	0.92	0.54	0.00	0.03	0.02
knn:3139092 3463598 3066770 2651515	0.74	0.045	0.238	0.036	0.63	0.83	0.50	0.05	0.08	0.05
knn:3139092 2512364 3066770 3005357	0.80	0.034	0.216	0.029	0.67	0.79	0.59	0.05	0.04	0.05
rpart:3139092 2512364 2956442 3005357	0.78	0.044	0.050	0.037	0.63	0.83	0.56	0.03	0.05	0.05
svm:3139092 2512364 2956442 2651515	0.78	0.046	0.257	0.056	0.14	0.54	-0.18	0.18	0.07	0.08
rf:2789391 2461837 2512364 2364325	0.79	0.037	0.046	0.030	0.50	0.80	0.50	0.24	0.06	0.05
rf:2789391 2461837 2512364 2651515	0.79	0.043	0.128	0.032	0.55	0.89	0.44	0.06	0.08	0.05
rf:2789391 2512364 2364325 3066770	0.81	0.029	0.026	0.093	0.50	0.71	0.60	0.28	0.09	0.10
rf:2789391 2512364 2364325 2956442	0.82	0.022	0.026	0.042	0.50	0.71	0.61	0.28	0.05	0.06
rf:3463598 2461837 2512364 2364325	0.81	0.024	0.046	0.020	0.56	0.82	0.48	0.15	0.03	0.05
rf:3463598 2461837 2512364 2956442	0.79	0.037	0.073	0.015	0.63	0.83	0.49	0.07	0.04	0.03
rf:3463598 2512364 2364325 2956442	0.87	0.009	0.026	0.013	0.67	0.71	0.75	0.20	0.02	0.05
rf:3463598 2512364 3066770 3005357	0.78	0.047	0.056	0.030	0.50	0.88	0.34	0.07	0.02	0.06
rf:3463598 2512364 2956442 3005357	0.85	0.011	0.017	0.006	0.58	1.00	0.41	0.01	0.02	0.03
knn:3463598 2956442 3005357 2651515	0.78	0.046	0.238	0.086	0.50	0.71	0.53	0.33	0.08	0.09
rf:2461837 2512364 2364325 3066770	0.78	0.046	0.203	0.046	0.67	0.79	0.60	0.05	0.06	0.06
rf:2461837 2512364 2364325 2956442	0.78	0.047	0.128	0.043	0.50	0.75	0.55	0.25	0.06	0.06
rf:2461837 2512364 2364325 2651515	0.78	0.046	0.025	0.037	0.55	0.89	0.42	0.06	0.05	0.06
rf:2461837 2512364 2956442 3005357	0.79	0.037	0.094	0.038	0.50	0.75	0.55	0.25	0.06	0.05
rf:2461837 2512364 3005357 2651515	0.80	0.030	0.005	0.079	0.67	0.91	0.42	0.01	0.10	0.09

svm:2512364 2364325 3066770 2956442	0.78	0.046	0.036	0.074	0.71	0.85	0.89	0.01	0.09	0.09
svm:2512364 2364325 3066770 3005357	0.81	0.024	0.036	0.022	0.71	0.85	0.65	0.01	0.02	0.04
rf:2512364 3066770 2956442 3005357	0.80	0.030	0.036	0.026	0.63	0.83	0.59	0.02	0.03	0.04
rf:2512364 2956442 3005357 2651515	0.82	0.024	0.026	0.030	0.58	1.00	0.36	0.01	0.03	0.05
knn:2512364 2956442 3005357 2651515	0.77	0.043	0.439	0.030	0.56	0.82	0.50	0.07	0.05	0.06
rpart:2512364 2956442 3005357 2651515	0.80	0.031	0.143	0.019	0.63	0.83	0.56	0.03	0.03	0.03
svm:2512364 2956442 3005357 2651515	0.82	0.019	0.046	0.032	0.71	0.85	0.13	0.01	0.05	0.05

Performance of pairwise, threewise and fourwise combinations of the 15 markers across different metrics for the
Recurrence endpoint for pT2 patients (organ-confined disease). All classifiers have a Wilcox P-value ≤ 0.05

TABLE 14

CLASSIFIER	AUC	WILCOX P-VALUE	KS P- VALUE	T-TEST P- VALUE	PPV	NPV	CUTOFF	KM P- VALUE	UVA HR P-VALUE	UVA OR P- VALUE
knn:2458376 2364325	0.80	0.022	0.137	0.030	0.83	0.38	0.53	0.32	0.11	0.05
rf:2458376 3005357	0.77	0.046	0.051	0.026	0.86	0.45	0.52	0.21	0.15	0.04
rpart:2478155 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:3139092 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:2512364 3005357	0.77	0.040	0.097	0.066	0.92	0.50	0.50	0.05	0.11	0.08
rpart:2512364 3005357	0.79	0.026	0.068	0.012	0.91	0.43	0.62	0.11	0.03	0.03
rpart:2364325 3005357	0.77	0.038	0.097	0.032	0.88	0.63	0.37	0.02	0.07	0.05
rpart:3066770 3005357	0.81	0.010	0.097	0.006	0.92	0.50	0.56	0.03	0.02	0.02
rpart:2956442 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:3005357 2651515	0.80	0.023	0.016	0.015	0.92	0.50	0.45	0.05	0.09	0.03
knn:3005357 2651515	0.76	0.045	0.137	0.062	0.89	0.38	0.50	0.53	0.37	0.08
knn:3326487 2332285 2512364	0.75	0.046	0.292	0.029	0.87	0.50	0.50	0.20	0.13	0.05
rpart:3326487 2364325 3005357	0.75	0.049	0.097	0.093	0.88	0.35	0.58	0.08	0.03	0.12
rpart:3326487 3066770 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:3326487 3005357 2651515	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01
svm:2458376 2332285 3139092	0.78	0.034	0.043	0.103	0.84	0.67	-0.28	0.09	0.19	0.11
knn:2458376 2332285 3005357	0.79	0.028	0.126	0.035	0.81	0.44	0.50	0.45	0.20	0.05
rpart:2458376 2332285 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02

svm:2458376										
2478155 2461837	0.76	0.047	0.046	0.021	0.50	0.13	-0.59	0.05	0.13	0.07
rpart:2458376										
2478155 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:2458376										
3139092 3463598	0.77	0.035	0.089	0.056	0.77	0.67	0.32	0.27	0.15	0.08
knn:2458376										
3139092 3005357	0.78	0.036	0.219	0.029	0.78	0.43	0.48	0.52	0.10	0.05
rpart:2458376										
3139092 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:2458376										
2512364 2956442	0.81	0.017	0.126	0.013	0.92	0.50	0.50	0.09	0.08	0.03
rf:2458376										
2512364 3005357	0.80	0.023	0.016	0.032	0.83	0.32	0.70	0.72	0.14	0.05
knn:2458376										
2512364 3005357	0.80	0.023	0.236	0.016	0.90	0.40	0.61	0.63	0.17	0.04
svm:2458376										
2512364 3005357	0.77	0.041	0.043	0.028	0.87	0.50	-0.05	0.19	0.17	0.04
rf:2458376										
2512364 2651515	0.76	0.047	0.043	0.043	0.92	0.46	0.56	0.18	0.27	0.06
knn:2458376										
2364325 3005357	0.81	0.021	0.097	0.010	0.86	0.45	0.51	0.16	0.08	0.02
rpart:2458376										
2364325 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:2458376										
2364325 2651515	0.80	0.023	0.034	0.026	0.93	0.60	0.50	0.03	0.19	0.04
rpart:2458376										
3066770 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
svm:2458376										
3066770 2651515	0.80	0.021	0.043	0.019	0.92	0.46	1.16	0.37	0.15	0.04
rf:2458376										
3005357 2651515	0.80	0.023	0.051	0.028	0.83	0.32	0.72	0.94	0.29	0.05
rpart:2458376										
3005357 2651515	0.80	0.024	0.068	0.038	0.92	0.46	0.49	0.09	0.13	0.06
svm:3414753										
2478155 2651515	0.78	0.034	0.008	0.105	0.70	0.20	-0.16	0.57	0.09	0.12
rf:3414753										
2512364 3005357	0.76	0.049	0.097	0.043	0.89	0.38	0.62	0.37	0.16	0.06
rpart:3414753										
2512364 3005357	0.80	0.019	0.068	0.017	0.92	0.46	0.44	0.06	0.05	0.04
knn:3414753										
2512364 2651515	0.77	0.035	0.074	0.023	0.85	0.42	0.50	0.42	0.16	0.04
rpart:3414753										
2364325 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:3414753										
2956442 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:3414753										
3005357 2651515	0.79	0.032	0.025	0.023	0.80	0.30	0.70	0.70	0.24	0.04
svm:2332285										
3139092 2461837	0.76	0.047	0.020	0.039	0.93	0.55	0.16	0.05	0.06	0.06
knn:2332285										
3139092 2512364	0.78	0.029	0.313	0.012	0.89	0.38	0.70	0.23	0.06	0.03
rpart:2332285										
2789391 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:2332285										
2512364 2651515	0.76	0.048	0.292	0.040	0.87	0.50	0.55	0.19	0.26	0.05
rpart:2332285										
3066770 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:2332285										
3005357 2651515	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01
svm:2478155										
3139092 3005357	0.79	0.029	0.014	0.048	0.70	0.20	-0.15	0.48	0.02	0.07

svm:2478155										
2512364 3005357	0.76	0.047	0.068	0.040	0.91	0.43	0.45	0.17	0.10	0.06
rpart:2478155										
2956442 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:2478155										
3005357 2651515	0.81	0.021	0.016	0.034	0.86	0.33	0.56	0.91	0.28	0.06
rpart:2478155										
3005357 2651515	0.76	0.046	0.034	0.016	0.91	0.43	0.60	0.17	0.07	0.04
knn:3139092										
3463598 2956442	0.82	0.013	0.089	0.010	0.83	0.57	0.50	0.10	0.01	0.02
rpart:3139092										
2364325 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:3139092										
3066770 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:3139092										
2956442 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:2789391										
3463598 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:2789391										
2512364 3005357	0.76	0.027	0.068	0.008	0.93	0.55	0.48	0.01	0.01	0.02
svm:2789391										
2512364 3005357	0.76	0.047	0.005	0.251	0.83	0.38	-0.27	0.32	0.44	0.25
rpart:2789391										
2956442 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:2789391										
3005357 2651515	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01
rf:3463598										
2512364 3005357	0.77	0.046	0.051	0.037	0.89	0.38	0.67	0.22	0.12	0.06
svm:3463598										
2956442 3005357	0.77	0.041	0.026	0.185	0.92	0.46	-0.27	0.15	0.58	0.20
rf:3463598										
3005357 2651515	0.80	0.021	0.014	0.044	0.89	0.38	0.61	0.50	0.28	0.07
knn:3463598										
3005357 2651515	0.76	0.044	0.381	0.026	0.89	0.38	0.70	0.46	0.21	0.05
svm:2461837										
2512364 3066770	0.77	0.041	0.130	0.030	0.80	0.60	-3.54	0.16	0.13	0.05
rf:2461837										
2512364 2651515	0.76	0.047	0.020	0.052	0.88	0.63	0.35	0.05	0.28	0.06
svm:2461837										
3066770 3005357	0.78	0.034	0.111	0.296	0.76	0.50	-4.24	0.31	0.21	0.31
rf:2461837										
3005357 2651515	0.79	0.032	0.074	0.050	0.86	0.45	0.45	0.18	0.22	0.07
rpart:2512364										
2364325 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:2512364										
2956442 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:2512364										
3005357 2651515	0.81	0.018	0.003	0.017	0.93	0.60	0.37	0.02	0.18	0.04
rpart:2512364										
3005357 2651515	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01
knn:2364325										
3005357 2651515	0.77	0.044	0.236	0.059	0.86	0.33	0.61	0.91	0.45	0.08
rpart:3066770										
2956442 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:3066770										
3005357 2651515	0.79	0.032	0.025	0.075	0.88	0.35	0.59	0.73	0.38	0.11
rf:2956442										
3005357 2651515	0.79	0.029	0.020	0.035	0.93	0.60	0.39	0.01	0.16	0.05
rpart:3326487										
2458376 2364325	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
rpart:3326487	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02

2458376 3066770											
3005357											
rf:3326487											
2458376 3005357	0.76	0.049	0.074	0.067	0.88	0.35	0.64	0.50	0.31	0.09	
2651515											
rpart:3326487											
3414753 3139092	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
rpart:3326487											
3414753 2512364	0.82	0.007	0.068	0.004	0.93	0.55	0.55	0.01	0.01	0.02	
3005357											
rpart:3326487											
3414753 3066770	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
rpart:3326487											
3414753 2956442	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
svm:3326487											
2332285 3139092	0.80	0.021	0.020	0.050	0.90	0.40	0.53	0.23	0.02	0.06	
2512364											
rf:3326487											
2478155 3005357	0.79	0.029	0.025	0.117	0.88	0.35	0.59	0.73	0.45	0.14	
2651515											
rpart:3326487											
3139092 3463598	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
rpart:3326487											
2789391 2512364	0.82	0.007	0.068	0.004	0.93	0.55	0.55	0.01	0.01	0.02	
3005357											
rpart:3326487											
2789391 3066770	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
rf:3326487											
2789391 3005357	0.78	0.034	0.014	0.112	0.86	0.33	0.65	0.91	0.42	0.13	
2651515											
rf:3326487											
3463598 3005357	0.76	0.049	0.074	0.129	0.86	0.33	0.62	0.91	0.47	0.15	
2651515											
knn:3326487											
2461837 3066770	0.73	0.043	0.219	0.036	0.92	0.46	0.50	0.07	0.07	0.06	
2651515											
rpart:3326487											
2512364 2364325	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
rf:3326487											
2512364 3005357	0.84	0.008	0.001	0.018	0.88	0.35	0.55	0.44	0.14	0.04	
2651515											
rf:3326487											
2364325 3005357	0.78	0.037	0.025	0.106	0.88	0.35	0.50	0.73	0.43	0.13	
2651515											
rpart:3326487											
2364325 3005357	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01	
2651515											
rf:3326487											
3066770 3005357	0.77	0.046	0.051	0.101	0.89	0.38	0.54	0.54	0.37	0.12	
2651515											
rpart:3326487											
3066770 3005357	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01	
2651515											
rf:3326487											
2956442 3005357	0.78	0.037	0.051	0.176	0.80	0.33	0.46	0.99	0.51	0.18	
2651515											

rpart:3326487 2956442 3005357 2651515	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01
rpart:2458376 3414753 2332285 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:2458376 3414753 2478155 2789391	0.75	0.048	0.457	0.037	0.55	0.14	0.50	0.10	0.04	0.06
rpart:2458376 3414753 3139092 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:2458376 3414753 2512364 3005357	0.76	0.047	0.068	0.041	0.92	0.46	0.54	0.13	0.23	0.06
knn:2458376 3414753 2364325 3005357	0.76	0.048	0.097	0.031	0.86	0.45	0.53	0.39	0.18	0.05
rpart:2458376 3414753 2364325 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:2458376 3414753 3066770 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:2458376 3414753 3005357 2651515	0.77	0.040	0.074	0.050	0.86	0.33	0.69	0.91	0.38	0.07
knn:2458376 3414753 3005357 2651515	0.77	0.041	0.074	0.017	0.82	0.50	0.43	0.36	0.21	0.03
rpart:2458376 2332285 2478155 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:2458376 2332285 3139092 2512364	0.84	0.008	0.051	0.007	0.91	0.43	0.64	0.32	0.11	0.03
svm:2458376 2332285 3139092 2512364	0.77	0.041	0.033	0.024	0.87	0.50	0.04	0.11	0.09	0.04
svm:2458376 2332285 2512364 2956442	0.76	0.047	0.056	0.048	0.92	0.50	-0.09	0.10	0.24	0.06
rf:2458376 2332285 2512364 2651515	0.76	0.047	0.043	0.058	0.88	0.56	0.47	0.08	0.31	0.07
knn:2458376 2332285 2364325 3005357	0.81	0.017	0.174	0.019	0.87	0.50	0.50	0.19	0.15	0.03
rpart:2458376 2332285 3066770 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:2458376 2332285 3005357 2651515	0.85	0.008	0.007	0.005	0.93	0.60	0.45	0.02	0.10	0.03
rpart:2458376 2332285 3005357 2651515	0.79	0.025	0.097	0.044	0.91	0.43	0.56	0.16	0.12	0.06
rpart:2458376 2478155 2789391 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:2458376 2478155 2512364	0.76	0.049	0.051	0.090	0.93	0.55	0.55	0.03	0.28	0.10

2651515										
knn:2458376										
2478155 2364325	0.79	0.031	0.051	0.022	0.87	0.50	0.51	0.19	0.11	0.04
3005357										
knn:2458376										
2478155 3066770	0.78	0.034	0.051	0.051	0.90	0.40	0.61	0.75	0.47	0.07
2651515										
rf:2458376										
2478155 3005357	0.76	0.047	0.095	0.047	0.86	0.33	0.63	0.91	0.37	0.07
2651515										
rpart:2458376										
3139092 2789391	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
knn:2458376										
3139092 3463598	0.86	0.005	0.046	0.004	0.88	0.63	0.50	0.06	0.01	0.02
2956442										
svm:2458376										
3139092 3463598	0.81	0.017	0.020	0.026	0.93	0.55	0.04	0.04	0.08	0.04
2956442										
rf:2458376										
3139092 3463598	0.77	0.043	0.016	0.058	0.90	0.40	0.56	0.17	0.23	0.08
2651515										
knn:2458376										
3139092 2512364	0.78	0.035	0.137	0.012	0.91	0.43	0.61	0.15	0.07	0.03
3005357										
rpart:2458376										
3139092 2364325	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
knn:2458376										
3139092 2364325	0.80	0.024	0.097	0.024	0.80	0.60	0.35	0.25	0.22	0.04
2651515										
svm:2458376										
3139092 2364325	0.76	0.047	0.068	0.066	0.85	0.42	-0.13	0.75	0.48	0.08
2651515										
rpart:2458376										
3139092 2956442	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
rf:2458376										
2789391 3005357	0.76	0.047	0.014	0.066	0.85	0.42	0.44	0.58	0.33	0.08
2651515										
rpart:2458376										
3463598 2512364	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
rpart:2458376										
3463598 2364325	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
rpart:2458376										
3463598 3066770	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
rpart:2458376										
3463598 2956442	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
rf:2458376										
3463598 3005357	0.81	0.017	0.014	0.019	0.92	0.50	0.51	0.16	0.22	0.04
2651515										
rf:2458376										
2461837 3005357	0.77	0.043	0.025	0.033	0.86	0.45	0.50	0.18	0.18	0.05
2651515										
rf:2458376										
2512364 2364325	0.80	0.023	0.016	0.030	0.92	0.50	0.49	0.12	0.31	0.05
2651515										

knn:2458376 2512364 3066770 3005357	0.79	0.027	0.126	0.019	0.89	0.38	0.64	0.25	0.09	0.04
rpart:2458376 2512364 3066770 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:2458376 2512364 2956442 3005357	0.78	0.033	0.025	0.067	0.85	0.42	0.54	0.34	0.22	0.08
rf:2458376 2512364 3005357 2651515	0.84	0.008	0.001	0.008	0.93	0.55	0.43	0.04	0.09	0.03
knn:2458376 2512364 3005357 2651515	0.78	0.033	0.051	0.033	0.86	0.45	0.50	0.32	0.26	0.05
knn:2458376 2364325 3066770 2651515	0.77	0.035	0.126	0.052	0.92	0.50	0.50	0.08	0.34	0.07
knn:2458376 2364325 2956442 3005357	0.81	0.021	0.174	0.027	0.85	0.42	0.51	0.34	0.11	0.04
rpart:2458376 2364325 2956442 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:2458376 2364325 3005357 2651515	0.83	0.012	0.008	0.025	0.86	0.33	0.62	0.91	0.30	0.05
knn:2458376 2364325 3005357 2651515	0.77	0.045	0.051	0.026	0.88	0.56	0.45	0.13	0.18	0.04
svm:2458376 2364325 3005357 2651515	0.81	0.017	0.046	0.013	0.87	0.50	-0.04	0.22	0.14	0.03
rf:2458376 3066770 3005357 2651515	0.80	0.021	0.046	0.039	0.86	0.33	0.68	0.91	0.33	0.06
rf:2458376 2956442 3005357 2651515	0.79	0.029	0.008	0.038	0.92	0.50	0.45	0.09	0.25	0.06
svm:3414753 2332285 3139092 2512364	0.78	0.034	0.085	0.053	0.83	0.57	-0.12	0.09	0.03	0.05
knn:3414753 2332285 2512364 3005357	0.76	0.046	0.219	0.033	0.92	0.46	0.59	0.18	0.17	0.05
knn:3414753 2332285 2512364 2651515	0.76	0.040	0.219	0.041	0.81	0.44	0.50	0.28	0.10	0.05
rpart:3414753 2478155 3463598 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:3414753 2478155 3005357 2651515	0.77	0.040	0.097	0.072	0.88	0.35	0.57	0.73	0.41	0.10
rpart:3414753 3139092 2789391 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:3414753 3139092 2461837 3005357	0.78	0.032	0.219	0.056	0.92	0.46	0.61	0.07	0.06	0.08
knn:3414753 3139092 2364325	0.76	0.046	0.570	0.019	0.83	0.38	0.59	0.43	0.09	0.04

3005357											
rf:3414753											
3139092 3005357	0.79	0.027	0.016	0.015	0.88	0.63	0.43	0.06	0.13	0.03	
2651515											
rf:3414753											
2789391 2512364	0.76	0.047	0.085	0.064	0.83	0.57	0.36	0.10	0.31	0.08	
2651515											
rf:3414753											
2512364 3005357	0.79	0.025	0.020	0.040	0.75	0.29	0.82	0.59	0.29	0.06	
2651515											
rpart:3414753											
2364325 3066770	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
rf:3414753											
2364325 3005357	0.77	0.042	0.025	0.108	0.88	0.35	0.49	0.73	0.48	0.14	
2651515											
rf:3414753											
3066770 3005357	0.78	0.034	0.033	0.050	0.86	0.33	0.69	0.91	0.32	0.07	
2651515											
knn:3414753											
3066770 3005357	0.75	0.027	0.174	0.021	0.88	0.56	0.50	0.09	0.10	0.03	
2651515											
rpart:3414753											
3066770 3005357	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01	
2651515											
rpart:2332285											
2478155 2512364	0.82	0.007	0.068	0.004	0.93	0.55	0.55	0.01	0.01	0.02	
3005357											
knn:2332285											
3139092 2789391	0.77	0.044	0.292	0.035	0.87	0.50	0.50	0.20	0.15	0.05	
2512364											
rpart:2332285											
3139092 2789391	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
svm:2332285											
3139092 3463598	0.77	0.041	0.043	0.058	0.89	0.38	0.78	0.22	0.24	0.07	
2461837											
svm:2332285											
3139092 3463598	0.76	0.047	0.095	0.029	0.82	0.50	0.10	0.22	0.06	0.04	
2512364											
knn:2332285											
3139092 3463598	0.75	0.050	0.174	0.065	0.90	0.40	0.70	0.13	0.20	0.08	
2956442											
knn:2332285											
3139092 3463598	0.78	0.035	0.292	0.027	0.82	0.50	0.50	0.24	0.18	0.04	
3005357											
rpart:2332285											
3139092 3463598	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
svm:2332285											
3139092 2461837	0.78	0.034	0.043	0.021	0.92	0.50	0.20	0.01	0.02	0.05	
2512364											
svm:2332285											
3139092 2461837	0.79	0.029	0.043	0.043	0.77	0.67	-0.61	0.27	0.14	0.07	
2651515											
knn:2332285											
3139092 2512364	0.77	0.044	0.097	0.033	0.87	0.50	0.52	0.19	0.21	0.05	
2364325											
svm:2332285											
3139092 2512364	0.77	0.041	0.130	0.026	0.80	0.60	-0.78	0.18	0.09	0.05	
2364325											

svm:2332285 3139092 2512364 3005357	0.78	0.034	0.068	0.043	0.83	0.57	0.03	0.09	0.03	0.05
svm:2332285 3139092 2512364 2651515	0.78	0.034	0.056	0.039	0.86	0.45	-0.14	0.30	0.06	0.05
knn:2332285 3139092 2364325 2651515	0.77	0.038	0.126	0.041	0.78	0.43	0.44	0.65	0.29	0.06
knn:2332285 3139092 2956442 2651515	0.77	0.040	0.457	0.029	0.86	0.45	0.50	0.35	0.19	0.05
rpart:2332285 2789391 3463598 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
svm:2332285 2789391 2512364 2364325	0.83	0.012	0.020	0.013	0.92	0.46	-0.08	0.15	0.07	0.04
rpart:2332285 3463598 2956442 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:2332285 3463598 3005357 2651515	0.78	0.034	0.051	0.031	0.87	0.50	0.44	0.19	0.21	0.05
rpart:2332285 2512364 3066770 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:2332285 2512364 2956442 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rf:2332285 2512364 3005357 2651515	0.80	0.023	0.016	0.017	0.93	0.60	0.41	0.02	0.17	0.03
knn:2332285 2512364 3005357 2651515	0.82	0.008	0.016	0.017	0.94	0.67	0.50	0.00	0.10	0.03
rpart:2332285 2364325 3066770 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:2332285 2364325 3005357 2651515	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01
rpart:2332285 2956442 3005357 2651515	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01
rpart:2478155 3139092 2789391 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
svm:2478155 3139092 3463598 2956442	0.78	0.034	0.043	0.168	1.00	0.29	5.96	0.00	0.01	0.11
rpart:2478155 3139092 3463598 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
knn:2478155 3139092 2364325 3005357	0.80	0.024	0.236	0.009	0.80	0.60	0.44	0.25	0.12	0.03
rpart:2478155 2789391 3066770 3005357	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
rpart:2478155 2789391 2956442	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02

3005357											
rf:2478155											
2789391 3005357	0.78	0.034	0.014	0.094	0.88	0.35	0.48	0.73	0.44	0.12	
2651515											
rpart:2478155											
3463598 2512364	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
rpart:2478155											
3463598 3066770	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
rpart:2478155											
3463598 2956442	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
rf:2478155											
3463598 3005357	0.80	0.023	0.034	0.048	0.89	0.38	0.60	0.32	0.32	0.07	
2651515											
svm:2478155											
2461837 2512364	0.76	0.047	0.130	0.029	0.89	0.38	0.30	0.26	0.09	0.05	
3066770											
rpart:2478155											
2512364 2364325	0.77	0.036	0.068	0.072	0.79	0.50	0.43	0.30	0.12	0.08	
3005357											
svm:2478155											
2512364 2364325	0.78	0.034	0.043	0.056	0.83	0.32	2.30	0.71	0.29	0.08	
2651515											
rpart:2478155											
2512364 2956442	0.76	0.045	0.068	0.056	0.88	0.35	0.62	0.48	0.21	0.08	
2651515											
rf:2478155											
2512364 3005357	0.83	0.009	0.001	0.013	0.93	0.55	0.46	0.03	0.14	0.03	
2651515											
knn:2478155											
2512364 3005357	0.76	0.042	0.068	0.045	0.93	0.55	0.50	0.04	0.08	0.06	
2651515											
rpart:2478155											
2512364 3005357	0.81	0.018	0.007	0.007	0.93	0.55	0.53	0.06	0.05	0.02	
2651515											
svm:2478155											
2512364 3005357	0.80	0.021	0.008	0.027	0.92	0.50	0.18	0.10	0.19	0.04	
2651515											
rpart:2478155											
2364325 3066770	0.81	0.010	0.097	0.006	0.92	0.50	0.56	0.03	0.02	0.02	
3005357											
rpart:2478155											
2364325 2956442	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02	
3005357											
rf:2478155											
2364325 3005357	0.83	0.012	0.014	0.076	0.88	0.35	0.55	0.73	0.41	0.11	
2651515											
svm:2478155											
2364325 3005357	0.77	0.041	0.008	0.073	0.91	0.43	0.16	0.21	0.56	0.09	
2651515											
rpart:2478155											
3066770 2956442	0.81	0.010	0.097	0.006	0.92	0.50	0.56	0.03	0.02	0.02	
3005357											
rf:2478155											
3066770 3005357	0.81	0.021	0.034	0.045	0.86	0.33	0.66	0.91	0.32	0.07	
2651515											
knn:2478155											
3066770 3005357	0.77	0.038	0.097	0.075	0.88	0.35	0.58	0.73	0.40	0.09	
2651515											

rpart:2478155										
2956442 3005357	0.77	0.040	0.034	0.011	0.92	0.46	0.61	0.09	0.03	0.03
2651515										
knn:3139092										
2789391 2512364	0.77	0.042	0.097	0.038	0.86	0.45	0.50	0.16	0.15	0.05
2364325										
knn:3139092										
2789391 2364325	0.78	0.034	0.137	0.028	0.82	0.36	0.54	0.45	0.10	0.05
3005357										
knn:3139092										
3463598 2461837	0.75	0.027	0.174	0.021	0.88	0.56	0.50	0.05	0.06	0.03
3066770										
svm:3139092										
3463598 2461837	0.76	0.047	0.130	0.043	0.92	0.46	0.21	0.09	0.22	0.06
3066770										
rpart:3139092										
3463598 2364325	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
svm:3139092										
3463598 2956442	0.79	0.029	0.056	0.033	0.92	0.46	0.06	0.14	0.17	0.05
2651515										
svm:3139092										
2461837 2364325	0.76	0.047	0.174	0.065	0.82	0.36	0.16	0.81	0.29	0.08
2651515										
svm:3139092										
2461837 2956442	0.79	0.029	0.008	0.103	0.83	0.32	0.63	0.93	0.50	0.12
2651515										
knn:3139092										
2512364 2364325	0.77	0.041	0.292	0.028	0.87	0.50	0.51	0.19	0.11	0.04
3005357										
svm:3139092										
2364325 3005357	0.79	0.025	0.012	0.018	1.00	0.50	0.17	0.01	0.04	0.05
2651515										
rpart:3139092										
3066770 2956442	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
rf:2789391										
3463598 2512364	0.77	0.041	0.020	0.072	0.91	0.43	0.46	0.29	0.18	0.09
3005357										
rpart:2789391										
3463598 3066770	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
rf:2789391										
3463598 3005357	0.79	0.029	0.014	0.036	0.83	0.38	0.50	0.48	0.25	0.06
2651515										
knn:2789391										
3463598 3005357	0.79	0.030	0.097	0.026	0.87	0.50	0.41	0.09	0.16	0.04
2651515										
rf:2789391										
2512364 3005357	0.81	0.020	0.003	0.012	0.94	0.86	0.26	0.00	0.14	0.03
2651515										
svm:2789391										
2364325 3066770	0.77	0.041	0.033	0.023	0.85	0.42	-0.10	0.30	0.18	0.04
2651515										
rpart:2789391										
2364325 2956442	0.77	0.011	0.097	0.007	0.88	0.63	0.44	0.02	0.03	0.02
3005357										
rpart:2789391										
2364325 3005357	0.85	0.007	0.025	0.002	0.93	0.60	0.48	0.02	0.04	0.01
2651515										
svm:2789391										
2364325 3005357	0.79	0.029	0.005	0.167	0.83	0.32	0.07	0.99	0.65	0.19

2651515

rpart:2789391

3066770 2956442 0.77 0.011 0.097 0.007 0.88 0.63 0.44 0.02 0.03 0.02

3005357

rpart:2789391

3066770 3005357 0.85 0.007 0.025 0.002 0.93 0.60 0.48 0.02 0.04 0.01

2651515

rf:2789391

2956442 3005357 0.76 0.047 0.014 0.051 0.86 0.33 0.53 0.91 0.32 0.07

2651515

rpart:2789391

2956442 3005357 0.85 0.007 0.025 0.002 0.93 0.60 0.48 0.02 0.04 0.01

2651515

svm:3463598

2461837 2512364 0.82 0.014 0.026 0.049 1.00 0.44 0.41 0.15 0.36 0.07

3005357

rpart:3463598

2512364 2364325 0.76 0.044 0.126 0.050 0.86 0.45 0.46 0.12 0.08 0.06

3005357

rf:3463598

2512364 2364325 0.79 0.029 0.008 0.049 0.90 0.40 0.58 0.23 0.25 0.07

2651515

rpart:3463598

2512364 3066770 0.77 0.042 0.068 0.029 0.87 0.50 0.41 0.05 0.03 0.04

3005357

rpart:3463598

2512364 2956442 0.77 0.011 0.097 0.007 0.88 0.63 0.44 0.02 0.03 0.02

3005357

rf:3463598

2512364 3005357 0.83 0.012 0.003 0.016 0.94 0.75 0.41 0.00 0.17 0.03

2651515

rpart:3463598

2512364 3005357 0.81 0.018 0.007 0.007 0.93 0.55 0.53 0.06 0.05 0.02

2651515

rpart:3463598

2364325 2956442 0.77 0.011 0.097 0.007 0.88 0.63 0.44 0.02 0.03 0.02

3005357

knn:3463598

2364325 2956442 0.78 0.035 0.137 0.028 0.79 0.36 0.50 0.83 0.25 0.04

2651515

rf:3463598

2364325 3005357 0.78 0.034 0.012 0.054 0.85 0.42 0.44 0.37 0.30 0.07

2651515

rpart:3463598

2364325 3005357 0.85 0.007 0.025 0.002 0.93 0.60 0.48 0.02 0.04 0.01

2651515

rpart:3463598

3066770 2956442 0.77 0.011 0.097 0.007 0.88 0.63 0.44 0.02 0.03 0.02

3005357

rf:3463598

3066770 3005357 0.78 0.034 0.097 0.062 0.85 0.42 0.49 0.34 0.35 0.08

2651515

svm:2461837

2512364 3066770 0.77 0.041 0.111 0.027 0.80 0.60 -2.92 0.16 0.16 0.04

2956442

svm:2461837

2512364 3066770 0.76 0.047 0.174 0.052 0.80 0.60 -3.14 0.11 0.13 0.07

3005357

svm:2461837

2364325 3066770 0.81 0.017 0.043 0.017 0.93 0.55 -0.16 0.02 0.06 0.04

2651515

knn:2461837 2364325 3005357 2651515	0.79	0.021	0.236	0.013	0.87	0.50	0.50	0.11	0.05	0.03
svm:2461837 2364325 3005357 2651515	0.79	0.025	0.068	0.013	0.85	0.42	0.04	0.08	0.04	0.03
rf:2512364 2364325 3066770 3005357	0.77	0.041	0.043	0.033	0.92	0.46	0.57	0.13	0.07	0.05
rpart:2512364 2364325 3066770 3005357	0.77	0.042	0.068	0.029	0.87	0.50	0.41	0.05	0.03	0.04
rf:2512364 2364325 3066770 2651515	0.76	0.049	0.034	0.070	0.88	0.35	0.62	0.73	0.38	0.09
rf:2512364 2364325 3005357 2651515	0.83	0.012	0.001	0.007	0.94	0.75	0.36	0.00	0.10	0.02
svm:2512364 2364325 3005357 2651515	0.79	0.025	0.043	0.023	0.88	0.63	-0.25	0.03	0.13	0.04
rf:2512364 2956442 3005357 2651515	0.83	0.012	0.003	0.015	0.93	0.60	0.38	0.01	0.13	0.03
knn:2512364 2956442 3005357 2651515	0.76	0.043	0.357	0.045	0.83	0.32	0.83	0.73	0.20	0.07
rpart:2512364 2956442 3005357 2651515	0.76	0.045	0.016	0.023	0.91	0.43	0.62	0.29	0.19	0.04
svm:2512364 2956442 3005357 2651515	0.79	0.025	0.033	0.086	0.92	0.46	0.15	0.06	0.36	0.07
rf:2364325 3066770 3005357 2651515	0.81	0.021	0.025	0.026	0.88	0.35	0.61	0.73	0.22	0.05
knn:2364325 3066770 3005357 2651515	0.76	0.043	0.137	0.034	0.86	0.33	0.70	0.66	0.33	0.06
svm:2364325 3066770 3005357 2651515	0.79	0.029	0.068	0.020	0.83	0.38	0.27	0.71	0.15	0.04
rf:2364325 2956442 3005357 2651515	0.79	0.027	0.025	0.075	0.88	0.35	0.54	0.73	0.36	0.10
rf:3066770 2956442 3005357 2651515	0.77	0.043	0.025	0.073	0.86	0.33	0.64	0.91	0.36	0.10

Performance of pairwise, three wise and four wise combinations of the 15 markers across different metrics for the

Recurrence endpoint for LNI positive patients. All classifiers have a Wilcox P-value <=0.05

TABLE 15

CLASSIFIER	AUC	WILCOX P- VALUE	KS P- VALUE	T-TEST P- VALUE	PPV	NPV	CUTOFF	KM P- VALUE	UVA HR P- VALUE	UVA OR P- VALUE
rf:3326487 2458376	0.70	0.020	0.018	0.013	0.83	0.53	0.55	0.04	0.02	0.02
nb:3326487 2458376	0.72	0.012	0.078	0.019	0.86	0.56	0.49	0.02	0.02	0.03
knn:3326487 2458376	0.67	0.047	0.104	0.018	0.85	0.55	0.51	0.04	0.03	0.03

rpart:3326487 2458376	0.75	0.002	0.014	0.001	0.77	0.70	0.41	0.00	0.00	0.00
svm:3326487 2458376	0.71	0.014	0.078	0.016	0.80	0.55	0.18	0.06	0.04	0.02
nb:3326487 3414753	0.73	0.008	0.018	0.019	0.80	0.50	0.54	0.08	0.01	0.03
svm:3326487 3414753	0.67	0.047	0.148	0.056	0.67	0.48	-0.18	0.45	0.04	0.06
nb:3326487 2332285	0.76	0.002	0.004	0.010	0.80	0.55	0.48	0.03	0.01	0.02
knn:3326487 2332285	0.68	0.039	0.081	0.012	0.91	0.54	0.53	0.01	0.01	0.02
svm:3326487 2332285	0.72	0.011	0.063	0.019	0.69	0.50	-0.21	0.25	0.01	0.03
nb:3326487 2478155	0.74	0.005	0.036	0.008	0.80	0.50	0.54	0.07	0.00	0.02
nb:3326487 3139092	0.70	0.021	0.014	0.028	0.71	0.50	0.49	0.15	0.01	0.04
knn:3326487 3139092	0.70	0.022	0.014	0.028	0.69	0.50	0.52	0.20	0.03	0.03
rpart:3326487 3139092	0.71	0.008	0.075	0.008	0.73	0.65	0.41	0.01	0.00	0.01
nb:3326487 2789391	0.67	0.049	0.208	0.030	0.80	0.50	0.52	0.09	0.01	0.04
rf:3326487 3463598	0.68	0.038	0.019	0.015	0.81	0.64	0.39	0.01	0.02	0.02
nb:3326487 3463598	0.68	0.037	0.036	0.026	0.80	0.50	0.56	0.07	0.01	0.04
nb:3326487 2461837	0.68	0.044	0.089	0.033	0.69	0.48	0.49	0.30	0.01	0.04
rpart:3326487 2461837	0.68	0.019	0.118	0.017	0.74	0.61	0.47	0.01	0.02	0.02
nb:3326487 2512364	0.72	0.012	0.044	0.013	0.69	0.48	0.50	0.34	0.01	0.02
knn:3326487 2512364	0.69	0.032	0.098	0.031	0.80	0.50	0.58	0.07	0.04	0.04
rf:3326487 2364325	0.73	0.008	0.038	0.006	0.83	0.53	0.56	0.02	0.01	0.01
nb:3326487 2364325	0.74	0.006	0.020	0.007	0.90	0.53	0.54	0.01	0.00	0.02
knn:3326487 2364325	0.69	0.030	0.092	0.032	0.89	0.51	0.61	0.01	0.04	0.04
svm:3326487 2364325	0.70	0.023	0.101	0.032	0.75	0.50	0.03	0.16	0.03	0.04
nb:3326487 3066770	0.69	0.030	0.101	0.039	0.80	0.50	0.55	0.07	0.02	0.05
nb:3326487 3005357	0.75	0.003	0.003	0.015	0.67	0.47	0.50	0.40	0.01	0.03
svm:3326487 3005357	0.70	0.018	0.018	0.036	0.67	0.48	0.07	0.30	0.04	0.04
rpart:3326487 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
rf:2458376 3414753	0.75	0.004	0.010	0.002	0.79	0.59	0.52	0.02	0.01	0.00
nb:2458376 3414753	0.78	0.001	0.003	0.002	0.85	0.55	0.56	0.03	0.01	0.01
rpart:2458376 3414753	0.65	0.040	0.261	0.037	0.76	0.55	0.52	0.04	0.04	0.04
rf:2458376 2332285	0.76	0.002	0.001	0.001	0.80	0.71	0.42	0.00	0.01	0.00
nb:2458376 2332285	0.80	0.000	0.001	0.001	0.83	0.61	0.48	0.01	0.00	0.00

knn:2458376 2332285	0.70	0.017	0.098	0.020	0.76	0.60	0.50	0.02	0.02	0.03
rpart:2458376 2332285	0.73	0.002	0.014	0.001	0.77	0.70	0.48	0.00	0.01	0.00
svm:2458376 2332285	0.81	0.000	0.001	0.000	0.85	0.65	-0.15	0.00	0.00	0.00
rf:2458376 2478155	0.69	0.027	0.032	0.021	0.71	0.59	0.60	0.06	0.07	0.03
nb:2458376 2478155	0.83	0.000	0.000	0.001	0.85	0.55	0.53	0.03	0.00	0.01
rpart:2458376 2478155	0.73	0.002	0.014	0.001	0.77	0.70	0.48	0.00	0.01	0.00
svm:2458376 2478155	0.73	0.008	0.047	0.005	0.71	0.56	0.09	0.12	0.02	0.01
nb:2458376 3139092	0.78	0.001	0.004	0.003	0.81	0.57	0.49	0.03	0.01	0.01
rpart:2458376 3139092	0.73	0.002	0.014	0.001	0.77	0.70	0.48	0.00	0.01	0.00
svm:2458376 3139092	0.68	0.037	0.004	0.003	0.76	0.76	0.25	0.00	0.01	0.01
rf:2458376 2789391	0.75	0.004	0.002	0.001	0.87	0.58	0.57	0.00	0.00	0.00
nb:2458376 2789391	0.72	0.010	0.001	0.006	0.87	0.58	0.49	0.00	0.01	0.01
rpart:2458376 2789391	0.73	0.002	0.014	0.001	0.77	0.70	0.48	0.00	0.01	0.00
rf:2458376 3463598	0.75	0.005	0.001	0.001	0.85	0.65	0.54	0.00	0.00	0.00
nb:2458376 3463598	0.70	0.021	0.001	0.005	0.93	0.61	0.51	0.00	0.01	0.01
knn:2458376 3463598	0.73	0.007	0.001	0.000	0.94	0.66	0.54	0.00	0.00	0.00
rpart:2458376 3463598	0.71	0.006	0.040	0.004	0.80	0.62	0.53	0.01	0.01	0.01
svm:2458376 3463598	0.67	0.049	0.005	0.009	0.88	0.62	0.12	0.00	0.03	0.01
nb:2458376 2461837	0.71	0.014	0.007	0.007	0.88	0.62	0.48	0.00	0.01	0.01
knn:2458376 2461837	0.74	0.006	0.081	0.006	0.69	0.60	0.45	0.05	0.01	0.01
rpart:2458376 2461837	0.68	0.019	0.118	0.017	0.74	0.61	0.47	0.01	0.02	0.02
svm:2458376 2461837	0.69	0.028	0.123	0.037	0.67	0.55	0.11	0.13	0.07	0.04
nb:2458376 2512364	0.76	0.002	0.007	0.003	0.87	0.58	0.52	0.01	0.01	0.01
knn:2458376 2512364	0.73	0.008	0.024	0.004	0.87	0.58	0.58	0.01	0.01	0.01
svm:2458376 2512364	0.71	0.015	0.005	0.024	0.88	0.62	0.12	0.00	0.03	0.03
rf:2458376 2364325	0.80	0.001	0.000	0.000	0.88	0.62	0.65	0.00	0.00	0.00
nb:2458376 2364325	0.79	0.001	0.000	0.001	0.86	0.56	0.53	0.01	0.01	0.01
knn:2458376 2364325	0.82	0.000	0.006	0.000	0.88	0.60	0.53	0.00	0.00	0.00
rpart:2458376 2364325	0.73	0.002	0.014	0.001	0.77	0.70	0.48	0.00	0.01	0.00
svm:2458376 2364325	0.79	0.001	0.000	0.001	0.88	0.60	0.03	0.00	0.00	0.00
rf:2458376 3066770	0.71	0.016	0.038	0.023	0.71	0.59	0.46	0.07	0.06	0.03

nb:2458376 3066770	0.72	0.010	0.007	0.008	0.86	0.56	0.52	0.02	0.02	0.02
knn:2458376 3066770	0.72	0.013	0.066	0.009	0.76	0.60	0.50	0.02	0.04	0.02
rpart:2458376 3066770	0.73	0.002	0.014	0.001	0.77	0.70	0.48	0.00	0.01	0.00
svm:2458376 3066770	0.74	0.005	0.013	0.007	0.79	0.59	0.20	0.02	0.03	0.01
rf:2458376 2956442	0.73	0.009	0.011	0.004	0.81	0.64	0.48	0.01	0.02	0.01
nb:2458376 2956442	0.68	0.042	0.007	0.014	0.83	0.61	0.46	0.00	0.03	0.02
knn:2458376 2956442	0.75	0.004	0.019	0.002	0.83	0.61	0.55	0.00	0.01	0.01
rpart:2458376 2956442	0.79	0.001	0.002	0.003	0.79	0.59	0.57	0.01	0.01	0.01
svm:2458376 2956442	0.68	0.037	0.059	0.039	0.75	0.53	-0.04	0.19	0.11	0.04
rf:2458376 3005357	0.78	0.002	0.006	0.001	0.78	0.65	0.50	0.00	0.00	0.00
nb:2458376 3005357	0.79	0.001	0.003	0.002	0.87	0.58	0.50	0.01	0.01	0.01
knn:2458376 3005357	0.78	0.001	0.006	0.001	0.75	0.64	0.48	0.01	0.00	0.00
rpart:2458376 3005357	0.73	0.002	0.014	0.001	0.77	0.70	0.48	0.00	0.01	0.00
svm:2458376 3005357	0.77	0.002	0.001	0.001	0.82	0.59	0.06	0.01	0.01	0.00
rf:2458376 2651515	0.72	0.013	0.030	0.007	0.86	0.56	0.55	0.01	0.02	0.01
nb:2458376 2651515	0.73	0.006	0.017	0.010	0.89	0.51	0.58	0.09	0.03	0.02
knn:2458376 2651515	0.77	0.002	0.001	0.001	0.86	0.71	0.46	0.00	0.00	0.00
rpart:2458376 2651515	0.74	0.003	0.030	0.002	0.76	0.67	0.39	0.01	0.00	0.00
svm:2458376 2651515	0.73	0.006	0.016	0.006	0.77	0.63	-0.22	0.01	0.02	0.01
rf:3414753 2332285	0.69	0.028	0.040	0.014	0.81	0.57	0.57	0.01	0.02	0.02
nb:3414753 2332285	0.79	0.001	0.001	0.003	0.79	0.53	0.55	0.06	0.00	0.01
rpart:3414753 2332285	0.65	0.040	0.261	0.037	0.76	0.55	0.52	0.04	0.04	0.04
svm:3414753 2332285	0.75	0.003	0.002	0.001	0.85	0.65	-0.01	0.00	0.00	0.00
rf:3414753 2478155	0.75	0.004	0.006	0.003	0.78	0.57	0.67	0.02	0.01	0.01
nb:3414753 2478155	0.80	0.000	0.001	0.001	0.81	0.64	0.49	0.00	0.00	0.00
knn:3414753 2478155	0.71	0.015	0.118	0.017	0.63	0.57	0.40	0.30	0.03	0.02
rpart:3414753 2478155	0.65	0.040	0.261	0.037	0.76	0.55	0.52	0.04	0.04	0.04
svm:3414753 2478155	0.77	0.002	0.001	0.001	0.75	0.64	-0.23	0.02	0.00	0.00
rf:3414753 3139092	0.70	0.021	0.006	0.009	0.76	0.67	0.52	0.01	0.02	0.01
nb:3414753 3139092	0.78	0.001	0.000	0.002	0.74	0.56	0.49	0.03	0.00	0.01
knn:3414753 3139092	0.71	0.016	0.058	0.025	0.73	0.65	0.43	0.02	0.04	0.03

rpart:3414753 3139092	0.65	0.040	0.261	0.037	0.76	0.55	0.52	0.04	0.04	0.04
svm:3414753 3139092	0.76	0.002	0.001	0.001	0.76	0.67	0.14	0.01	0.01	0.00
rf:3414753 2789391	0.71	0.017	0.019	0.009	0.77	0.63	0.47	0.01	0.01	0.01
nb:3414753 2789391	0.72	0.012	0.010	0.006	0.90	0.53	0.56	0.00	0.00	0.01
knn:3414753 2789391	0.75	0.004	0.009	0.001	0.88	0.62	0.50	0.00	0.00	0.00
rpart:3414753 2789391	0.65	0.040	0.261	0.037	0.76	0.55	0.52	0.04	0.04	0.04
svm:3414753 2789391	0.72	0.011	0.010	0.010	0.70	0.63	-0.42	0.03	0.01	0.02
rf:3414753 3463598	0.71	0.016	0.019	0.004	0.78	0.65	0.52	0.01	0.01	0.01
nb:3414753 3463598	0.73	0.007	0.005	0.003	0.81	0.64	0.49	0.00	0.00	0.01
knn:3414753 3463598	0.70	0.020	0.006	0.004	0.81	0.64	0.50	0.00	0.02	0.01
rpart:3414753 3463598	0.71	0.006	0.040	0.004	0.80	0.62	0.53	0.01	0.01	0.01
svm:3414753 3463598	0.73	0.009	0.005	0.004	0.82	0.67	0.04	0.00	0.01	0.01
nb:3414753 2461837	0.74	0.005	0.007	0.004	0.77	0.63	0.45	0.00	0.00	0.01
rpart:3414753 2461837	0.69	0.021	0.118	0.014	0.78	0.57	0.57	0.01	0.01	0.02
nb:3414753 2512364	0.75	0.003	0.000	0.002	0.83	0.70	0.48	0.00	0.00	0.01
knn:3414753 2512364	0.77	0.002	0.001	0.001	0.89	0.64	0.55	0.00	0.00	0.00
rpart:3414753 2512364	0.65	0.040	0.261	0.037	0.76	0.55	0.52	0.04	0.04	0.04
svm:3414753 2512364	0.76	0.003	0.000	0.001	0.86	0.68	0.00	0.00	0.00	0.00
rf:3414753 2364325	0.73	0.010	0.011	0.002	0.78	0.65	0.50	0.01	0.01	0.00
nb:3414753 2364325	0.78	0.001	0.001	0.001	0.83	0.70	0.45	0.00	0.00	0.00
knn:3414753 2364325	0.75	0.003	0.012	0.001	0.83	0.61	0.48	0.00	0.00	0.00
rpart:3414753 2364325	0.65	0.040	0.261	0.037	0.76	0.55	0.52	0.04	0.04	0.04
svm:3414753 2364325	0.67	0.049	0.026	0.041	0.68	0.52	-0.05	0.20	0.06	0.05
rf:3414753 3066770	0.67	0.046	0.118	0.026	0.74	0.56	0.53	0.06	0.03	0.03
nb:3414753 3066770	0.71	0.013	0.020	0.006	0.82	0.59	0.50	0.00	0.00	0.01
knn:3414753 3066770	0.73	0.007	0.066	0.010	0.81	0.57	0.57	0.01	0.01	0.02
rpart:3414753 3066770	0.65	0.040	0.261	0.037	0.76	0.55	0.52	0.04	0.04	0.04
rf:3414753 2956442	0.70	0.019	0.019	0.013	0.80	0.62	0.42	0.00	0.02	0.02
nb:3414753 2956442	0.72	0.012	0.016	0.012	0.77	0.63	0.45	0.01	0.02	0.02
knn:3414753 2956442	0.73	0.009	0.011	0.012	0.78	0.57	0.50	0.01	0.01	0.02
rpart:3414753 2956442	0.65	0.040	0.261	0.037	0.76	0.55	0.52	0.04	0.04	0.04

svm:3414753 2956442	0.73	0.008	0.016	0.010	0.79	0.59	-0.23	0.01	0.01	0.02
rf:3414753 3005357	0.74	0.006	0.022	0.004	0.79	0.59	0.50	0.01	0.01	0.01
nb:3414753 3005357	0.77	0.002	0.001	0.002	0.78	0.65	0.46	0.00	0.00	0.00
knn:3414753 3005357	0.79	0.001	0.005	0.001	0.77	0.63	0.50	0.01	0.00	0.00
rpart:3414753 3005357	0.65	0.040	0.261	0.037	0.76	0.55	0.52	0.04	0.04	0.04
rf:3414753 2651515	0.68	0.038	0.054	0.010	0.86	0.56	0.58	0.01	0.02	0.02
nb:3414753 2651515	0.74	0.005	0.051	0.006	0.85	0.55	0.50	0.02	0.01	0.02
rpart:3414753 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
rf:2332285 2478155	0.75	0.004	0.013	0.003	0.76	0.67	0.57	0.01	0.02	0.01
nb:2332285 2478155	0.82	0.000	0.000	0.001	0.85	0.65	0.46	0.00	0.00	0.00
knn:2332285 2478155	0.70	0.019	0.003	0.002	0.85	0.65	0.51	0.00	0.01	0.01
rpart:2332285 2478155	0.71	0.013	0.086	0.011	0.64	0.56	0.55	0.25	0.03	0.02
svm:2332285 2478155	0.69	0.030	0.033	0.011	0.71	0.56	-0.14	0.10	0.01	0.02
rf:2332285 3139092	0.75	0.005	0.006	0.002	0.78	0.74	0.43	0.00	0.00	0.00
nb:2332285 3139092	0.80	0.000	0.000	0.002	0.80	0.62	0.49	0.01	0.00	0.01
knn:2332285 3139092	0.72	0.013	0.001	0.002	0.81	0.64	0.50	0.00	0.01	0.00
rpart:2332285 3139092	0.72	0.004	0.030	0.003	0.76	0.67	0.49	0.00	0.01	0.01
svm:2332285 3139092	0.78	0.001	0.001	0.000	0.78	0.74	-0.11	0.00	0.00	0.00
rf:2332285 2789391	0.72	0.011	0.012	0.005	0.87	0.58	0.54	0.00	0.01	0.01
nb:2332285 2789391	0.75	0.004	0.001	0.004	0.84	0.63	0.45	0.00	0.00	0.01
knn:2332285 2789391	0.74	0.005	0.018	0.001	0.82	0.59	0.51	0.01	0.00	0.00
svm:2332285 2789391	0.68	0.040	0.047	0.010	0.86	0.56	-0.01	0.01	0.01	0.02
rf:2332285 3463598	0.76	0.003	0.006	0.001	0.78	0.65	0.42	0.01	0.00	0.00
nb:2332285 3463598	0.75	0.003	0.001	0.002	0.86	0.68	0.47	0.00	0.00	0.01
knn:2332285 3463598	0.71	0.013	0.104	0.015	0.86	0.56	0.64	0.01	0.03	0.02
rpart:2332285 3463598	0.71	0.006	0.040	0.004	0.80	0.62	0.53	0.01	0.01	0.01
svm:2332285 3463598	0.76	0.003	0.000	0.000	0.85	0.65	0.04	0.00	0.00	0.00
rf:2332285 2461837	0.72	0.011	0.019	0.019	0.67	0.58	0.39	0.10	0.02	0.02
nb:2332285 2461837	0.75	0.003	0.001	0.002	0.85	0.65	0.47	0.00	0.00	0.01
knn:2332285 2461837	0.70	0.020	0.005	0.005	0.81	0.64	0.49	0.00	0.00	0.01
rpart:2332285 2461837	0.68	0.027	0.081	0.053	0.79	0.59	0.59	0.01	0.04	0.06

svm:2332285 2461837	0.74	0.005	0.013	0.003	0.72	0.62	-0.16	0.02	0.01	0.01
nb:2332285 2512364	0.76	0.002	0.001	0.002	0.89	0.67	0.51	0.00	0.00	0.00
knn:2332285 2512364	0.72	0.012	0.001	0.003	0.89	0.67	0.56	0.00	0.01	0.01
svm:2332285 2512364	0.82	0.000	0.001	0.000	0.85	0.65	-0.12	0.00	0.00	0.00
rf:2332285 2364325	0.76	0.003	0.002	0.001	0.85	0.65	0.49	0.00	0.00	0.00
nb:2332285 2364325	0.78	0.001	0.001	0.001	0.89	0.67	0.50	0.00	0.00	0.00
knn:2332285 2364325	0.72	0.013	0.006	0.003	0.82	0.67	0.48	0.00	0.00	0.01
rpart:2332285 2364325	0.74	0.001	0.011	0.001	0.79	0.68	0.51	0.00	0.00	0.00
svm:2332285 2364325	0.81	0.000	0.001	0.000	0.89	0.67	0.02	0.00	0.00	0.00
nb:2332285 3066770	0.75	0.004	0.003	0.003	0.84	0.63	0.49	0.00	0.00	0.01
knn:2332285 3066770	0.72	0.012	0.012	0.003	0.83	0.61	0.52	0.00	0.00	0.01
svm:2332285 3066770	0.81	0.000	0.001	0.001	0.81	0.64	-0.18	0.00	0.00	0.00
nb:2332285 2956442	0.74	0.006	0.009	0.008	0.82	0.59	0.50	0.01	0.01	0.01
knn:2332285 2956442	0.71	0.012	0.008	0.011	0.82	0.59	0.53	0.01	0.02	0.02
svm:2332285 2956442	0.78	0.001	0.001	0.001	0.80	0.62	-0.16	0.01	0.00	0.00
rf:2332285 3005357	0.80	0.001	0.001	0.000	0.74	0.68	0.39	0.01	0.00	0.00
nb:2332285 3005357	0.80	0.000	0.001	0.001	0.84	0.63	0.48	0.00	0.00	0.00
knn:2332285 3005357	0.71	0.013	0.050	0.010	0.77	0.63	0.50	0.01	0.02	0.02
rpart:2332285 3005357	0.74	0.003	0.038	0.006	0.79	0.59	0.44	0.00	0.00	0.01
svm:2332285 3005357	0.83	0.000	0.000	0.000	0.85	0.65	-0.12	0.00	0.00	0.00
rf:2332285 2651515	0.75	0.003	0.008	0.002	0.88	0.62	0.49	0.00	0.00	0.01
nb:2332285 2651515	0.78	0.001	0.001	0.003	0.87	0.58	0.51	0.01	0.01	0.01
knn:2332285 2651515	0.70	0.021	0.008	0.002	0.88	0.60	0.53	0.00	0.01	0.01
rpart:2332285 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
svm:2332285 2651515	0.72	0.010	0.016	0.004	0.76	0.55	-0.11	0.05	0.01	0.01
rf:2478155 3139092	0.71	0.014	0.011	0.002	0.69	0.65	0.55	0.04	0.01	0.01
nb:2478155 3139092	0.78	0.001	0.007	0.001	0.81	0.64	0.49	0.00	0.00	0.00
knn:2478155 3139092	0.77	0.002	0.014	0.001	0.75	0.64	0.50	0.01	0.01	0.00
rpart:2478155 3139092	0.72	0.004	0.030	0.003	0.76	0.67	0.49	0.00	0.01	0.01
svm:2478155 3139092	0.71	0.017	0.010	0.006	0.65	0.50	0.54	0.50	0.02	0.01
rf:2478155 2789391	0.76	0.003	0.035	0.003	0.74	0.56	0.59	0.04	0.01	0.01

nb:2478155 2789391	0.74	0.005	0.030	0.004	0.80	0.55	0.50	0.02	0.00	0.01
knn:2478155 2789391	0.69	0.024	0.125	0.019	0.80	0.55	0.54	0.02	0.02	0.03
svm:2478155 2789391	0.69	0.025	0.030	0.011	0.74	0.56	-0.06	0.04	0.01	0.02
rf:2478155 3463598	0.74	0.007	0.014	0.003	0.80	0.62	0.67	0.01	0.02	0.01
nb:2478155 3463598	0.75	0.003	0.005	0.001	0.78	0.57	0.52	0.04	0.00	0.00
knn:2478155 3463598	0.71	0.014	0.047	0.014	0.66	0.73	0.44	0.09	0.07	0.02
rpart:2478155 3463598	0.71	0.006	0.040	0.004	0.80	0.62	0.53	0.01	0.01	0.01
nb:2478155 2461837	0.76	0.002	0.000	0.002	0.80	0.62	0.49	0.00	0.00	0.01
knn:2478155 2461837	0.68	0.040	0.071	0.008	0.69	0.82	0.42	0.02	0.03	0.01
rpart:2478155 2461837	0.68	0.019	0.118	0.017	0.74	0.61	0.47	0.01	0.02	0.02
nb:2478155 2512364	0.77	0.001	0.001	0.001	0.78	0.65	0.50	0.01	0.00	0.00
knn:2478155 2512364	0.77	0.002	0.005	0.001	0.79	0.68	0.50	0.00	0.01	0.00
rf:2478155 2364325	0.80	0.001	0.000	0.000	0.70	0.77	0.49	0.02	0.00	0.00
nb:2478155 2364325	0.81	0.000	0.000	0.000	0.85	0.65	0.49	0.00	0.00	0.00
knn:2478155 2364325	0.85	0.000	0.002	0.000	0.84	0.63	0.55	0.00	0.00	0.00
svm:2478155 2364325	0.81	0.000	0.000	0.000	0.79	0.68	0.27	0.00	0.00	0.00
rf:2478155 3066770	0.69	0.030	0.086	0.015	0.67	0.69	0.37	0.05	0.05	0.02
nb:2478155 3066770	0.76	0.002	0.002	0.002	0.84	0.63	0.49	0.00	0.00	0.01
knn:2478155 3066770	0.70	0.020	0.223	0.010	0.67	0.55	0.50	0.17	0.04	0.02
rpart:2478155 3066770	0.69	0.004	0.086	0.003	0.69	0.82	0.47	0.02	0.03	0.01
rf:2478155 2956442	0.70	0.023	0.058	0.015	0.69	0.65	0.47	0.04	0.05	0.02
nb:2478155 2956442	0.71	0.017	0.059	0.008	0.81	0.57	0.52	0.02	0.01	0.01
knn:2478155 2956442	0.75	0.004	0.075	0.003	0.78	0.57	0.52	0.03	0.01	0.01
rpart:2478155 2956442	0.69	0.004	0.086	0.003	0.69	0.82	0.47	0.02	0.03	0.01
svm:2478155 2956442	0.68	0.040	0.047	0.029	0.74	0.56	0.09	0.08	0.05	0.03
rf:2478155 3005357	0.75	0.004	0.011	0.001	0.76	0.67	0.66	0.01	0.01	0.00
nb:2478155 3005357	0.80	0.000	0.002	0.000	0.79	0.68	0.44	0.00	0.00	0.00
knn:2478155 3005357	0.80	0.001	0.019	0.000	0.69	0.71	0.41	0.02	0.00	0.00
rpart:2478155 3005357	0.71	0.005	0.038	0.003	0.74	0.68	0.44	0.01	0.01	0.01
svm:2478155 3005357	0.79	0.001	0.002	0.000	0.79	0.68	-0.07	0.00	0.00	0.00
rf:2478155 2651515	0.68	0.035	0.189	0.029	0.83	0.53	0.66	0.04	0.05	0.04

nb:2478155 2651515	0.75	0.004	0.022	0.003	0.92	0.58	0.51	0.01	0.01	0.01
knn:2478155 2651515	0.71	0.013	0.004	0.003	0.88	0.62	0.52	0.00	0.01	0.01
rpart:2478155 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
svm:2478155 2651515	0.68	0.033	0.030	0.033	0.63	0.48	-0.29	0.63	0.07	0.04
rf:3139092 2789391	0.73	0.010	0.014	0.007	0.78	0.57	0.57	0.02	0.01	0.01
nb:3139092 2789391	0.73	0.008	0.013	0.007	0.76	0.60	0.45	0.01	0.00	0.01
knn:3139092 2789391	0.72	0.010	0.032	0.004	0.71	0.59	0.44	0.04	0.01	0.01
rpart:3139092 2789391	0.72	0.004	0.030	0.003	0.76	0.67	0.49	0.00	0.01	0.01
rf:3139092 3463598	0.72	0.010	0.014	0.005	0.70	0.69	0.43	0.02	0.02	0.01
nb:3139092 3463598	0.73	0.006	0.007	0.005	0.77	0.63	0.48	0.01	0.01	0.01
knn:3139092 3463598	0.75	0.004	0.014	0.002	0.77	0.70	0.47	0.00	0.01	0.00
rpart:3139092 3463598	0.71	0.006	0.040	0.004	0.80	0.62	0.53	0.01	0.01	0.01
svm:3139092 3463598	0.72	0.012	0.014	0.036	0.67	0.69	-0.14	0.04	0.05	0.04
nb:3139092 2461837	0.73	0.008	0.003	0.006	0.76	0.60	0.46	0.01	0.01	0.01
rpart:3139092 2461837	0.68	0.019	0.118	0.017	0.74	0.61	0.47	0.01	0.02	0.02
svm:3139092 2461837	0.68	0.035	0.022	0.028	0.76	0.60	0.03	0.02	0.04	0.03
nb:3139092 2512364	0.76	0.002	0.003	0.002	0.76	0.60	0.48	0.01	0.00	0.00
rf:3139092 2364325	0.72	0.012	0.014	0.007	0.74	0.61	0.54	0.04	0.02	0.01
nb:3139092 2364325	0.80	0.000	0.001	0.001	0.83	0.70	0.45	0.00	0.00	0.00
knn:3139092 2364325	0.76	0.002	0.001	0.001	0.81	0.64	0.52	0.00	0.00	0.00
rpart:3139092 2364325	0.72	0.004	0.030	0.003	0.76	0.67	0.49	0.00	0.01	0.01
svm:3139092 2364325	0.80	0.000	0.001	0.000	0.80	0.71	-0.15	0.00	0.00	0.00
nb:3139092 3066770	0.73	0.009	0.009	0.008	0.73	0.58	0.46	0.03	0.01	0.01
knn:3139092 3066770	0.74	0.006	0.006	0.004	0.73	0.58	0.51	0.03	0.01	0.01
rpart:3139092 3066770	0.72	0.004	0.030	0.003	0.76	0.67	0.49	0.00	0.01	0.01
svm:3139092 3066770	0.73	0.008	0.003	0.007	0.75	0.64	0.01	0.01	0.01	0.01
rf:3139092 2956442	0.67	0.049	0.030	0.032	0.76	0.67	0.50	0.00	0.06	0.04
nb:3139092 2956442	0.71	0.016	0.020	0.018	0.74	0.61	0.45	0.03	0.02	0.02
knn:3139092 2956442	0.74	0.005	0.005	0.003	0.75	0.72	0.44	0.00	0.01	0.01
rpart:3139092 2956442	0.72	0.004	0.030	0.003	0.76	0.67	0.49	0.00	0.01	0.01
svm:3139092 2956442	0.75	0.004	0.003	0.006	0.76	0.67	-0.02	0.00	0.01	0.01

rf:3139092 3005357	0.71	0.015	0.013	0.001	0.74	0.61	0.56	0.01	0.00	0.00
nb:3139092 3005357	0.77	0.002	0.000	0.001	0.78	0.74	0.44	0.00	0.00	0.00
knn:3139092 3005357	0.73	0.007	0.001	0.001	0.77	0.87	0.43	0.00	0.00	0.00
rpart:3139092 3005357	0.71	0.005	0.038	0.003	0.74	0.68	0.44	0.01	0.01	0.01
svm:3139092 3005357	0.75	0.004	0.000	0.002	0.76	0.67	0.14	0.00	0.00	0.00
nb:3139092 2651515	0.69	0.028	0.022	0.009	0.86	0.56	0.50	0.01	0.01	0.02
rpart:3139092 2651515	0.68	0.031	0.189	0.032	0.68	0.57	0.45	0.06	0.03	0.04
rf:2789391 3463598	0.73	0.008	0.019	0.005	0.79	0.59	0.50	0.01	0.01	0.01
nb:2789391 3463598	0.71	0.013	0.005	0.010	0.79	0.59	0.49	0.01	0.01	0.02
knn:2789391 3463598	0.71	0.014	0.032	0.009	0.83	0.61	0.54	0.00	0.02	0.01
rpart:2789391 3463598	0.71	0.006	0.040	0.004	0.80	0.62	0.53	0.01	0.01	0.01
svm:2789391 3463598	0.72	0.012	0.005	0.008	0.81	0.64	-0.07	0.00	0.01	0.01
rf:2789391 2461837	0.72	0.012	0.030	0.012	0.73	0.58	0.47	0.03	0.01	0.02
nb:2789391 2461837	0.69	0.028	0.007	0.015	0.78	0.65	0.42	0.00	0.01	0.02
knn:2789391 2461837	0.74	0.005	0.081	0.004	0.79	0.59	0.50	0.01	0.00	0.01
rpart:2789391 2461837	0.68	0.019	0.118	0.017	0.74	0.61	0.47	0.01	0.02	0.02
rf:2789391 2512364	0.71	0.015	0.050	0.010	0.77	0.63	0.45	0.00	0.01	0.01
nb:2789391 2512364	0.72	0.010	0.005	0.007	0.75	0.64	0.44	0.01	0.01	0.01
svm:2789391 2512364	0.72	0.012	0.036	0.031	0.74	0.56	-0.31	0.03	0.04	0.04
rf:2789391 2364325	0.74	0.005	0.047	0.006	0.71	0.56	0.45	0.04	0.01	0.01
nb:2789391 2364325	0.74	0.004	0.005	0.003	0.78	0.65	0.43	0.00	0.00	0.01
knn:2789391 2364325	0.79	0.001	0.019	0.001	0.88	0.60	0.49	0.00	0.00	0.00
svm:2789391 2364325	0.73	0.007	0.005	0.005	0.78	0.65	-0.26	0.00	0.00	0.01
rf:2789391 3066770	0.70	0.021	0.012	0.014	0.76	0.60	0.51	0.02	0.01	0.02
nb:2789391 3066770	0.69	0.030	0.004	0.017	0.87	0.58	0.50	0.00	0.01	0.02
knn:2789391 3066770	0.78	0.001	0.005	0.001	0.88	0.62	0.46	0.00	0.00	0.00
svm:2789391 3066770	0.70	0.022	0.003	0.012	0.89	0.64	-0.01	0.00	0.01	0.02
rf:2789391 2956442	0.69	0.027	0.098	0.021	0.74	0.56	0.48	0.04	0.03	0.03
nb:2789391 2956442	0.68	0.040	0.047	0.032	0.78	0.57	0.49	0.02	0.03	0.04
knn:2789391 2956442	0.67	0.050	0.118	0.027	0.80	0.55	0.54	0.02	0.02	0.04
rf:2789391 3005357	0.75	0.004	0.008	0.002	0.75	0.72	0.34	0.00	0.00	0.00

nb:2789391 3005357	0.74	0.006	0.011	0.005	0.77	0.63	0.44	0.00	0.00	0.01
svm:2789391 3005357	0.70	0.023	0.016	0.032	0.78	0.57	-0.24	0.02	0.06	0.05
rf:2789391 2651515	0.75	0.005	0.081	0.005	0.86	0.56	0.56	0.01	0.01	0.01
nb:2789391 2651515	0.70	0.021	0.013	0.015	0.85	0.55	0.49	0.03	0.02	0.03
knn:2789391 2651515	0.73	0.007	0.026	0.007	0.88	0.60	0.48	0.00	0.02	0.01
rpart:2789391 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
svm:2789391 2651515	0.69	0.026	0.013	0.019	0.79	0.59	-0.32	0.02	0.02	0.03
rf:3463598 2461837	0.68	0.034	0.092	0.029	0.71	0.67	0.47	0.02	0.05	0.03
nb:3463598 2461837	0.71	0.014	0.020	0.014	0.76	0.60	0.47	0.01	0.01	0.02
rpart:3463598 2461837	0.68	0.019	0.118	0.017	0.74	0.61	0.47	0.01	0.02	0.02
svm:3463598 2461837	0.69	0.030	0.059	0.015	0.74	0.61	0.12	0.02	0.07	0.02
rf:3463598 2512364	0.68	0.034	0.104	0.017	0.81	0.57	0.61	0.03	0.04	0.02
nb:3463598 2512364	0.74	0.005	0.001	0.004	0.81	0.64	0.51	0.00	0.01	0.01
knn:3463598 2512364	0.72	0.010	0.011	0.009	0.85	0.55	0.61	0.05	0.03	0.02
rpart:3463598 2512364	0.71	0.006	0.040	0.004	0.80	0.62	0.53	0.01	0.01	0.01
svm:3463598 2512364	0.69	0.032	0.004	0.007	0.85	0.65	0.07	0.00	0.02	0.01
rf:3463598 2364325	0.75	0.004	0.005	0.001	0.85	0.65	0.57	0.00	0.01	0.00
nb:3463598 2364325	0.75	0.004	0.001	0.001	0.89	0.67	0.51	0.00	0.00	0.00
knn:3463598 2364325	0.79	0.001	0.001	0.000	0.88	0.62	0.53	0.00	0.00	0.00
rpart:3463598 2364325	0.71	0.006	0.040	0.004	0.80	0.62	0.53	0.01	0.01	0.01
svm:3463598 2364325	0.70	0.020	0.001	0.003	0.89	0.67	0.04	0.00	0.01	0.01
rf:3463598 3066770	0.68	0.040	0.011	0.019	0.79	0.59	0.55	0.02	0.04	0.02
nb:3463598 3066770	0.71	0.016	0.003	0.010	0.84	0.63	0.50	0.00	0.01	0.02
knn:3463598 3066770	0.76	0.002	0.005	0.001	0.89	0.64	0.54	0.00	0.00	0.00
rpart:3463598 3066770	0.71	0.006	0.040	0.004	0.80	0.62	0.53	0.01	0.01	0.01
svm:3463598 3066770	0.72	0.012	0.003	0.006	0.85	0.65	-0.29	0.00	0.00	0.01
rf:3463598 2956442	0.70	0.019	0.024	0.011	0.70	0.63	0.44	0.03	0.03	0.02
nb:3463598 2956442	0.69	0.030	0.028	0.022	0.76	0.60	0.49	0.02	0.03	0.03
knn:3463598 2956442	0.71	0.016	0.054	0.004	0.82	0.59	0.53	0.01	0.01	0.01
svm:3463598 2956442	0.70	0.023	0.036	0.010	0.79	0.59	-0.11	0.01	0.02	0.02
rf:3463598 3005357	0.74	0.006	0.008	0.002	0.75	0.64	0.48	0.01	0.01	0.01

nb:3463598 3005357	0.76	0.002	0.009	0.002	0.79	0.59	0.50	0.01	0.00	0.01
rpart:3463598 3005357	0.71	0.006	0.040	0.004	0.80	0.62	0.53	0.01	0.01	0.01
rf:3463598 2651515	0.69	0.027	0.019	0.004	0.80	0.55	0.54	0.04	0.01	0.01
nb:3463598 2651515	0.69	0.028	0.010	0.013	0.80	0.55	0.50	0.05	0.03	0.02
knn:3463598 2651515	0.69	0.023	0.304	0.025	0.69	0.48	0.70	0.35	0.07	0.03
rpart:3463598 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
nb:2461837 2512364	0.73	0.008	0.016	0.005	0.78	0.65	0.46	0.00	0.01	0.01
knn:2461837 2512364	0.72	0.010	0.008	0.009	0.78	0.65	0.50	0.00	0.01	0.01
rf:2461837 2364325	0.74	0.005	0.015	0.002	0.84	0.63	0.54	0.00	0.00	0.00
nb:2461837 2364325	0.77	0.001	0.001	0.002	0.84	0.63	0.49	0.00	0.00	0.00
knn:2461837 2364325	0.73	0.007	0.024	0.006	0.83	0.61	0.59	0.00	0.01	0.01
rpart:2461837 2364325	0.68	0.019	0.118	0.017	0.74	0.61	0.47	0.01	0.02	0.02
svm:2461837 2364325	0.71	0.015	0.002	0.009	0.83	0.70	-0.20	0.00	0.01	0.01
nb:2461837 3066770	0.70	0.023	0.026	0.015	0.78	0.57	0.49	0.01	0.01	0.02
svm:2461837 3066770	0.70	0.023	0.018	0.062	0.67	0.50	0.15	0.25	0.06	0.08
nb:2461837 2956442	0.67	0.047	0.036	0.031	0.77	0.63	0.43	0.01	0.03	0.04
knn:2461837 2956442	0.70	0.020	0.024	0.019	0.72	0.54	0.53	0.07	0.02	0.02
rpart:2461837 2956442	0.68	0.019	0.118	0.017	0.74	0.61	0.47	0.01	0.02	0.02
rf:2461837 3005357	0.70	0.024	0.022	0.008	0.74	0.61	0.45	0.01	0.01	0.01
nb:2461837 3005357	0.74	0.005	0.003	0.007	0.75	0.58	0.46	0.01	0.01	0.01
knn:2461837 3005357	0.75	0.003	0.005	0.001	0.80	0.71	0.44	0.00	0.00	0.00
rpart:2461837 3005357	0.68	0.019	0.118	0.017	0.74	0.61	0.47	0.01	0.02	0.02
svm:2461837 3005357	0.71	0.015	0.003	0.011	0.80	0.71	-0.07	0.00	0.01	0.02
rf:2461837 2651515	0.67	0.046	0.125	0.042	0.75	0.58	0.53	0.02	0.05	0.05
nb:2461837 2651515	0.72	0.010	0.017	0.010	0.87	0.58	0.48	0.00	0.01	0.02
svm:2461837 2651515	0.68	0.040	0.176	0.027	0.68	0.52	-0.30	0.27	0.04	0.04
nb:2512364 2364325	0.76	0.002	0.000	0.001	0.79	0.68	0.44	0.00	0.00	0.00
rpart:2512364 2364325	0.69	0.011	0.075	0.009	0.73	0.65	0.48	0.02	0.02	0.01
svm:2512364 2364325	0.74	0.005	0.000	0.001	0.83	0.70	-0.20	0.00	0.00	0.00
nb:2512364 3066770	0.74	0.004	0.003	0.004	0.77	0.63	0.47	0.01	0.01	0.01
knn:2512364 3066770	0.75	0.004	0.026	0.002	0.80	0.62	0.53	0.01	0.00	0.01

svm:2512364 3066770	0.72	0.012	0.013	0.014	0.75	0.64	-0.01	0.02	0.02	0.02
nb:2512364 2956442	0.71	0.016	0.047	0.012	0.79	0.59	0.50	0.01	0.02	0.02
svm:2512364 2956442	0.70	0.021	0.047	0.015	0.79	0.59	0.04	0.01	0.02	0.02
nb:2512364 3005357	0.76	0.003	0.005	0.002	0.81	0.64	0.50	0.00	0.00	0.00
knn:2512364 3005357	0.67	0.050	0.335	0.056	0.67	0.52	0.50	0.24	0.07	0.06
nb:2512364 2651515	0.75	0.003	0.005	0.005	0.69	0.65	0.39	0.02	0.01	0.01
knn:2512364 2651515	0.68	0.039	0.178	0.037	0.75	0.58	0.50	0.06	0.06	0.04
rpart:2512364 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
nb:2364325 3066770	0.76	0.003	0.002	0.002	0.88	0.62	0.50	0.00	0.00	0.01
knn:2364325 3066770	0.78	0.001	0.009	0.001	0.88	0.62	0.52	0.00	0.00	0.00
rpart:2364325 3066770	0.74	0.001	0.011	0.001	0.79	0.68	0.51	0.00	0.00	0.00
svm:2364325 3066770	0.75	0.004	0.002	0.001	0.84	0.63	0.01	0.00	0.00	0.00
rf:2364325 2956442	0.75	0.004	0.006	0.003	0.83	0.61	0.55	0.00	0.01	0.01
nb:2364325 2956442	0.72	0.010	0.004	0.006	0.83	0.61	0.49	0.00	0.01	0.01
knn:2364325 2956442	0.74	0.006	0.019	0.004	0.82	0.59	0.54	0.01	0.01	0.01
rpart:2364325 2956442	0.74	0.001	0.011	0.001	0.79	0.68	0.51	0.00	0.00	0.00
svm:2364325 2956442	0.74	0.004	0.004	0.004	0.81	0.57	0.04	0.02	0.01	0.01
rf:2364325 3005357	0.77	0.002	0.008	0.000	0.76	0.67	0.47	0.01	0.00	0.00
nb:2364325 3005357	0.79	0.001	0.000	0.000	0.86	0.68	0.48	0.00	0.00	0.00
knn:2364325 3005357	0.79	0.001	0.001	0.000	0.89	0.67	0.54	0.00	0.00	0.00
rpart:2364325 3005357	0.70	0.015	0.038	0.010	0.74	0.68	0.37	0.01	0.02	0.01
svm:2364325 3005357	0.78	0.001	0.000	0.000	0.86	0.71	0.10	0.00	0.00	0.00
rf:2364325 2651515	0.74	0.006	0.050	0.008	0.86	0.56	0.58	0.01	0.01	0.02
nb:2364325 2651515	0.77	0.001	0.001	0.002	0.89	0.51	0.56	0.03	0.01	0.01
knn:2364325 2651515	0.71	0.013	0.275	0.020	0.90	0.53	0.61	0.01	0.03	0.03
rpart:2364325 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
svm:2364325 2651515	0.71	0.014	0.020	0.014	0.85	0.55	0.24	0.06	0.04	0.02
nb:3066770 2956442	0.67	0.047	0.063	0.036	0.71	0.56	0.47	0.05	0.04	0.04
knn:3066770 2956442	0.70	0.020	0.043	0.015	0.72	0.54	0.49	0.07	0.02	0.02
rpart:3066770 2956442	0.66	0.028	0.223	0.025	0.80	0.55	0.50	0.02	0.02	0.03
svm:3066770 2956442	0.67	0.047	0.123	0.036	0.71	0.52	-0.08	0.13	0.04	0.04

rf:3066770 3005357	0.74	0.006	0.018	0.002	0.76	0.60	0.59	0.01	0.00	0.01
nb:3066770 3005357	0.76	0.003	0.002	0.004	0.76	0.55	0.50	0.01	0.00	0.01
knn:3066770 3005357	0.74	0.005	0.030	0.006	0.78	0.57	0.50	0.01	0.01	0.01
rpart:3066770 3005357	0.70	0.011	0.038	0.009	0.73	0.58	0.56	0.04	0.02	0.01
svm:3066770 3005357	0.75	0.003	0.005	0.003	0.79	0.59	0.12	0.01	0.01	0.01
nb:3066770 2651515	0.70	0.018	0.013	0.014	0.90	0.53	0.54	0.01	0.02	0.03
rpart:3066770 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
rf:2956442 3005357	0.72	0.012	0.018	0.015	0.71	0.56	0.46	0.07	0.03	0.02
nb:2956442 3005357	0.71	0.015	0.028	0.014	0.79	0.59	0.48	0.01	0.02	0.02
rpart:2956442 3005357	0.71	0.005	0.038	0.003	0.74	0.68	0.44	0.01	0.01	0.01
svm:2956442 3005357	0.67	0.047	0.033	0.117	0.73	0.65	-0.28	0.03	0.20	0.13
rf:2956442 2651515	0.72	0.012	0.015	0.006	0.90	0.53	0.58	0.04	0.01	0.01
nb:2956442 2651515	0.69	0.028	0.020	0.025	0.86	0.49	0.61	0.17	0.05	0.03
knn:2956442 2651515	0.76	0.003	0.047	0.008	0.76	0.55	0.48	0.05	0.02	0.02
rpart:2956442 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
rf:3005357 2651515	0.73	0.009	0.008	0.006	0.74	0.61	0.45	0.03	0.01	0.01
nb:3005357 2651515	0.77	0.002	0.007	0.002	0.89	0.51	0.56	0.03	0.00	0.01
knn:3005357 2651515	0.70	0.019	0.133	0.022	0.67	0.50	0.50	0.35	0.05	0.03
rpart:3005357 2651515	0.66	0.018	0.189	0.015	0.85	0.55	0.56	0.01	0.02	0.03
svm:3005357 2651515	0.71	0.013	0.036	0.026	0.74	0.61	-0.45	0.03	0.06	0.03

Performance of pairwise, threewise and fourwise combinations of the 15 markers across different metrics for the Recurrence endpoint for the subset of patients that excludes pT2 (organ confined disease) cases. All classifiers have a Wilcox P-value ≤ 0.05

[00339] Example 3: A 1,425 Biomarker Library is Prognostic for Muscle Invasive Bladder Cancer Recurrence.

[00340] In order to define, from the entire set of 1.4 million features available in the array, a comprehensive library of prognostic markers for the recurrence of muscle invasive bladder cancer, features were selected based on the pooled dataset (n=199) presented in Example 1 as follows. Features having an AUC greater or equal than 0.6, a Wilcox p-value less or equal than 0.05 and a MFD greater or equal than 1.25 (or MFD less or equal 0.8) were kept. Features with one or more probes deemed unreliable, unmappable or features having less than 4 probes were removed. After applying these steps,

1,440 markers remained, of which 15 corresponded to the markers already presented in Example 1 (Table 2B). The remaining markers are presented in Table 16. The markers listed in Table 16 were statistically significant for the differential expression between patients with and without bladder cancer recurrence post-cystectomy. Accordingly, Table 16 provides a biomarker library for muscle invasive bladder cancer recurrence. Gene Ontology enrichment assessment of these markers showed that they are highly enriched for multiple biological processes including translation, splicing and cell cycle progression among others processes (Table 17).

[00341] Table 18 shows the performance of 1,425 biomarkers of the present invention across various metrics for the recurrence endpoint on the pooled discovery and validation cohort (n = 199). Additionally, the good performance of these markers is demonstrated within a clinically relevant set of patients, such as those with negative lymph node involvement (Table 19). Based on the multiple metrics shown in Table 18, these results demonstrate that the library of 1,440 markers of the present invention are useful for prognosing, diagnosing, and predicting the recurrence of muscle invasive bladder cancer.

[00342] In addition to the good performance of these markers as univariable predictors, pairwise combinations of the markers (pairwise classifiers) through a machine learning algorithm results in enhanced performance. As shown in Table 20, pairwise classifiers show statistically significant performance when predicting recurrence within the subset of patients with positive lymph node involvement based on Wilcox P-value and a number of other metrics. Each classifier in Table 20 is described by the machine learning algorithm that combines the markers (column 'classifier') as well as the probeset ID number of the corresponding markers as provided by Affymetrix (<http://www.affymetrix.com/analysis/index.affx>; Table 16). These classifiers were trained and tuned in the discover cohort (n = 133) and the performance on the positive lymph node involvement patients from the validation set is indicated. When dichotomization is necessary for a performance metric, the classifier scores are dichotomized using unsupervised clustering in the pamr package. The machine learning algorithms used are Naïve Bayes (NB), recursive Partitioning (Rpart), Support Vector Machines (SVMs), Random Forest (RF) and K Nearest Neighbors (KNN). These machine learning algorithms were executed with default parameters using packages rpart 4.1-0, HDclassif 1.2.2, randomForest 4.6-7, caret 5.15-61, cluster 1.14.3, e1071 1.6-1, class 7.3-5 in R. Each classifier generates a score between 0 and 1, except for SVM which generates a score from $-\infty$ to $+\infty$; in all cases, higher score values indicate higher probability of recurrence.

[00343] These results showed that the methods and markers of the present invention are useful for prognosing muscle invasive bladder cancer recurrence. These results further showed that the methods and markers of the present invention are useful for diagnosing, prognosing, determining the progression of cancer, or predicting benefit from therapy in a subject having cancer.

TABLE 16

SEQ ID NO	AFFYMET RIX PROBESE T ID	GENES	CATEGORY	CHRO MOSO ME	START	END	STRA ND
SEQ ID NO. 16	2318654	VAMP3	Non-coding(UTR)	chr1	7841394	7841457	+
SEQ ID NO. 17	2318755	PARK7	Non-coding(UTR)	chr1	8045210	8045305	+
SEQ ID NO. 18	2320062	TARDBP	Coding	chr1	11082181	11082249	+
SEQ ID NO. 19	2321661	TMEM51	Non-coding(UTR)	chr1	15546921	15546958	+
SEQ ID NO. 20	2322383	C1orf144	Non-coding(UTR)	chr1	16722804	16722848	+
SEQ ID NO. 21	2325809	TMEM50A	Non-coding(UTR)	chr1	25687219	25687391	+
SEQ ID NO. 22	2327494	SNHG3	Non-coding(ncTranscript)	chr1	28836076	28836118	+
SEQ ID NO. 23	2327865	PTPRU	Non-coding(UTR)	chr1	29653253	29653286	+
SEQ ID NO. 24	2328504	KHDRBS1	Non-coding(UTR)	chr1	32509334	32509457	+
SEQ ID NO. 25	2328507	KHDRBS1	Non-coding(Intronic)	chr1	32510473	32510602	+
SEQ ID NO. 26	2329019	RBBP4	Coding	chr1	33145365	33145408	+
SEQ ID NO. 27	2329798	ZMYM4	Coding	chr1	35858255	35858285	+
SEQ ID NO. 28	2330704	ZC3H12A	Non-coding(UTR)	chr1	37949930	37949963	+
SEQ ID NO. 29	2331419	MACF1	Coding	chr1	39888103	39888203	+
SEQ ID NO. 30	2331842	ZMPSTE24	Non-coding(UTR)	chr1	40759698	40759778	+
SEQ ID NO. 31	2332192	CTPS	Non-coding(UTR)	chr1	41478182	41478210	+
SEQ ID NO. 32	2332740	PPIH	Non-coding(UTR)	chr1	43142355	43142406	+
SEQ ID NO. 33	2334302	UROD	Non-coding(UTR)	chr1	45481172	45481224	+
SEQ ID NO. 34	2336960	TMEM59	Non-coding(Exonic Antisense)	chr1	54497388	54497746	+
SEQ ID NO. 35	2339310	INADL	Non-coding(UTR)	chr1	62628807	62628976	+
SEQ ID NO. 36	2342617	ACADM	Non-coding(UTR)	chr1	76229076	76229135	+
SEQ ID NO. 37	2345634	PKN2	Coding	chr1	89206755	89206948	+
SEQ ID NO. 38	2345663	PKN2	Non-coding(Intronic)	chr1	89262619	89262697	+
SEQ ID NO. 39	2345666	PKN2	Coding	chr1	89270538	89270576	+
SEQ ID NO. 40	2346911	RPL5	Coding	chr1	93307350	93307383	+
SEQ ID NO. 41	2346912	RPL5	Non-coding(UTR)	chr1	93307433	93307475	+
SEQ ID NO. 42	2347108	DR1	Non-coding(UTR)	chr1	93826315	93826475	+
SEQ ID NO. 43	2348819	CCDC76	Non-coding(UTR)	chr1	100615958	100616029	+
SEQ ID NO. 44	2350305	PRPF38B	Coding	chr1	109242408	109242557	+
SEQ ID NO. 45	2350371	STXBP3	Coding	chr1	109325090	109325138	+
SEQ ID NO. 46	2352268	CAPZA1	Non-coding(UTR)	chr1	113212895	113214104	+
SEQ ID NO. 47	2353492	ATPIA1	Coding	chr1	116926636	116926663	+
SEQ ID NO. 48	2358275	RPRD2	Coding	chr1	150432735	150432779	+

SEQ ID NO. 49	2358923	PSMB4	Non-coding(UTR)	chr1	15137431 7	15137438 7	+
SEQ ID NO. 50	2359857	INTS3	Coding	chr1	15373522 6	15373530 7	+
SEQ ID NO. 51	2360078	C1orf43	Non-coding(Exonic Antisense)	chr1	15417923 2	15417978 5	+
SEQ ID NO. 52	2360119	UBAP2L	Coding	chr1	15422763 5	15422775 2	+
SEQ ID NO. 53	2360120	UBAP2L	Coding	chr1	15422776 3	15422779 0	+
SEQ ID NO. 54	2360340	UBE2Q1	Non-coding(Exonic Antisense)	chr1	15452257 6	15452281 1	+
SEQ ID NO. 55	2360716	SLC50A1	Non-coding(UTR)	chr1	15511125 2	15511130 1	+
SEQ ID NO. 56	2360962	ASH1L	Non-coding(Exonic Antisense)	chr1	15549097 7	15549132 4	+
SEQ ID NO. 57	2361031	MSTO1	Non-coding(UTR)	chr1	15558468 2	15558471 5	+
SEQ ID NO. 58	2363064	DCAF8	Non-coding(Exonic Antisense)	chr1	16018656 3	16018659 4	+
SEQ ID NO. 59	2363334	F11R	Non-coding(Exonic Antisense)	chr1	16096606 6	16096628 6	+
SEQ ID NO. 60	2363956	ATF6	Coding	chr1	16182301 4	16182304 6	+
SEQ ID NO. 61	2365991	MPZL1	Coding	chr1	16775712 9	16775715 8	+
SEQ ID NO. 62	2367178	PRRC2C	Coding	chr1	17149258 0	17149265 0	+
SEQ ID NO. 63	2367214	PRRC2C	Coding	chr1	17154849 9	17154853 2	+
SEQ ID NO. 64	2367236	PRRC2C	Non- coding(Intronic)	chr1	17145710 6	17145715 7	+
SEQ ID NO. 65	2369830	chr1+:179888850- 179889162	Non- coding(Intergenic)	chr1	17988885 0	17988916 2	+
SEQ ID NO. 66	2370014	QSOX1	Non-coding(UTR)	chr1	18016717 1	18016722 2	+
SEQ ID NO. 67	2371291	SMG7	Coding	chr1	18351135 7	18351147 3	+
SEQ ID NO. 68	2371339	ARPC5	Non-coding(Exonic Antisense)	chr1	18359553 2	18359559 1	+
SEQ ID NO. 69	2371796	IVNS1ABP	Non-coding(Exonic Antisense)	chr1	18528029 2	18528043 6	+
SEQ ID NO. 70	2373002	CDC73	Coding	chr1	19318157 3	19318160 6	+
SEQ ID NO. 71	2375035	ELF3	Non-coding(UTR)	chr1	20198515 9	20198519 8	+
SEQ ID NO. 72	2375037	ELF3	Non-coding(UTR)	chr1	20198625 1	20198628 7	+
SEQ ID NO. 73	2375675	BTG2	Non-coding(UTR)	chr1	20327863 1	20327870 4	+
SEQ ID NO. 74	2375780	ATP2B4	Non-coding(UTR)	chr1	20371316 4	20371319 5	+
SEQ ID NO. 75	2375850	ZC3H11A	Coding	chr1	20381637 2	20381652 5	+
SEQ ID NO. 76	2375890	SNRPE	Non-coding(UTR)	chr1	20383916 0	20383918 5	+
SEQ ID NO. 77	2377473	CD46	Non- coding(ncTranscript)	chr1	20794068 9	20794092 4	+
SEQ ID NO. 78	2377508	CD46	Non-coding(UTR)	chr1	20796866 9	20796879 9	+
SEQ ID NO. 79	2378615	RCOR3	Coding	chr1	21146901	21146904	+

					8	8	
SEQ ID NO. 80	2379787	SMYD2	Coding	chr1	21449802 1	21449805 0	+
SEQ ID NO. 81	2383763	ARF1	Non-coding(UTR)	chr1	22828590 9	22828615 6	+
SEQ ID NO. 82	2389076	FAM36A	Non-coding(Intronic)	chr1	24500591 8	24500624 8	+
SEQ ID NO. 83	2389079	FAM36A	Non-coding(UTR)	chr1	24500664 1	24500681 4	+
SEQ ID NO. 84	2389084	NCRNA00201	Non-coding(Intronic Antisense)	chr1	24501024 4	24501031 3	+
SEQ ID NO. 85	2389086	NCRNA00201	Non-coding(Intronic Antisense)	chr1	24501095 7	24501108 6	+
SEQ ID NO. 86	2389817	SCCPDH	Non-coding(UTR)	chr1	24693061 9	24693072 3	+
SEQ ID NO. 87	2394560	RPL22	Non-coding(UTR)	chr1	6245095	6245147	-
SEQ ID NO. 88	2395192	ERRFI1	Non-coding(Intronic)	chr1	8077370	8078230	-
SEQ ID NO. 89	2395195	ERRFI1	Non-coding(Intronic)	chr1	8081604	8082267	-
SEQ ID NO. 90	2396421	MASP2	Coding	chr1	11086948	11086983	-
SEQ ID NO. 91	2400180	CAMK2N1	Non-coding(UTR)	chr1	20810077	20810117	-
SEQ ID NO. 92	2400323	HP1BP3	Non-coding(UTR)	chr1	21069239	21069434	-
SEQ ID NO. 93	2401277	chr1:-23614583-23614893	Non-coding(Intergenic)	chr1	23614583	23614893	-
SEQ ID NO. 94	2401288	HNRNPR	Non-coding(UTR)	chr1	23636701	23636918	-
SEQ ID NO. 95	2401350	TCEA3	Non-coding(UTR)	chr1	23707883	23707923	-
SEQ ID NO. 96	2401368	TCEA3	Coding	chr1	23735157	23735185	-
SEQ ID NO. 97	2402210	TMEM50A	Non-coding(Exonic Antisense)	chr1	25687170	25687537	-
SEQ ID NO. 98	2405379	AK2	Coding	chr1	33478681	33478714	-
SEQ ID NO. 99	2406094	SFPQ	Coding	chr1	35654644	35654687	-
SEQ ID NO. 100	2406148	KIAA0319L	Non-coding(UTR)	chr1	35899093	35899130	-
SEQ ID NO. 101	2407134	MEAF6	Non-coding(UTR)	chr1	37958790	37958867	-
SEQ ID NO. 102	2408880	FOXJ3	Coding	chr1	42660561	42660688	-
SEQ ID NO. 103	2410112	MUTYH	Non-coding(UTR)	chr1	45794927	45794963	-
SEQ ID NO. 104	2410528	POMGNT1	Coding	chr1	46654372	46654408	-
SEQ ID NO. 105	2412669	TXNDC12	Non-coding(UTR)	chr1	52485854	52485894	-
SEQ ID NO. 106	2413580	TMEM59	Non-coding(UTR)	chr1	54497716	54497788	-
SEQ ID NO. 107	2414030	USP24	Coding	chr1	55608416	55608446	-
SEQ ID NO. 108	2414960	TACSTD2	Non-coding(UTR)	chr1	59041241	59041545	-
SEQ ID NO. 109	2417788	SRSF11	Non-coding(Exonic Antisense)	chr1	70717148	70717519	-
SEQ ID NO. 110	2418028	ZRANB2	Coding	chr1	71542488	71542559	-
SEQ ID NO. 111	2419242	FUBP1	Non-coding(ncTranscript)	chr1	78412683	78413071	-
SEQ ID NO. 112	2419247	FUBP1	Non-coding(ncTranscript)	chr1	78413793	78413946	-
SEQ ID NO. 113	2419276	FUBP1	Coding	chr1	78429939	78430038	-
SEQ ID NO. 114	2420740	SYDE2	Non-coding(UTR)	chr1	85624387	85624416	-
SEQ ID NO. 115	2420839	DDAH1	Non-coding(UTR)	chr1	85784191	85784259	-

SEQ ID NO. 116	2421273	RP4-604K5.1	Non-coding(UTR)	chr1	87328509	87329064	-
SEQ ID NO. 117	2421274	RP4-604K5.1	Coding	chr1	87329188	87329229	-
SEQ ID NO. 118	2421932	GBP2	Non-coding(UTR)	chr1	89573754	89573847	-
SEQ ID NO. 119	2422519	ZNF644	Non-coding(UTR)	chr1	91381226	91381289	-
SEQ ID NO. 120	2423200	RPL5	Non-coding(Exonic Antisense)	chr1	93303053	93303092	-
SEQ ID NO. 121	2427009	SORT1	Non-coding(UTR)	chr1	10985222 7	10985226 5	-
SEQ ID NO. 122	2427501	HBXIP	Non-coding(UTR)	chr1	11094396 1	11094404 4	-
SEQ ID NO. 123	2427978	ATP5F1	Non-coding(Exonic Antisense)	chr1	11200380 9	11200384 9	-
SEQ ID NO. 124	2428394	CAPZA1	Non-coding(Exonic Antisense)	chr1	11321352 1	11321410 5	-
SEQ ID NO. 125	2429071	TRIM33	Non-coding(UTR)	chr1	11493859 2	11493906 1	-
SEQ ID NO. 126	2429119	TRIM33	Non-coding(Intronic)	chr1	11496930 1	11496966 2	-
SEQ ID NO. 127	2429168	BCAS2	Coding	chr1	11511082 1	11511085 0	-
SEQ ID NO. 128	2429282	CSDE1	Non-coding(UTR)	chr1	11526044 4	11526056 6	-
SEQ ID NO. 129	2429309	CSDE1	Coding	chr1	11527526 9	11527538 1	-
SEQ ID NO. 130	2429310	CSDE1	Coding	chr1	11527637 7	11527646 6	-
SEQ ID NO. 131	2433376	ACP6	Non-coding(UTR)	chr1	14711919 3	14711922 4	-
SEQ ID NO. 132	2434721	LASS2	Non-coding(UTR)	chr1	15093778 0	15093785 4	-
SEQ ID NO. 133	2435391	S100A10	Non-coding(UTR)	chr1	15195551 6	15195563 8	-
SEQ ID NO. 134	2437095	KRTCAP2	Non-coding(UTR)	chr1	15514188 8	15514191 5	-
SEQ ID NO. 135	2437537	RP11-29H23.5	Non-coding(ncTranscript)	chr1	15558463 1	15558465 8	-
SEQ ID NO. 136	2437538	RP11-29H23.5	Non-coding(Intronic)	chr1	15558467 5	15558471 0	-
SEQ ID NO. 137	2437680	GON4L	Coding	chr1	15574095 0	15574099 9	-
SEQ ID NO. 138	2437775	KIAA0907	Coding	chr1	15589165 2	15589170 7	-
SEQ ID NO. 139	2439041	RP11-367J7.4	Non-coding(Exonic Antisense)	chr1	15767893 7	15767903 1	-
SEQ ID NO. 140	2440149	COPA	Coding	chr1	16025996 3	16025999 2	-
SEQ ID NO. 141	2440513	TSTD1	Non-coding(UTR)	chr1	16100743 4	16100746 6	-
SEQ ID NO. 142	2442702	CREG1	Non-coding(UTR)	chr1	16751055 4	16751102 5	-
SEQ ID NO. 143	2443917	PRRC2C	Non-coding(Exonic Antisense)	chr1	17149258 4	17149284 8	-
SEQ ID NO. 144	2444488	GAS5	Non-coding(ncTranscript)	chr1	17383381 3	17383384 2	-
SEQ ID NO. 145	2444489	GAS5,SNORD80	Non-coding(ncTranscript)	chr1	17383384 4	17383396 8	-
SEQ ID NO. 146	2448289	TPR	Coding	chr1	18631643 1	18631656 0	-
SEQ ID NO. 147	2448313	TPR	Coding	chr1	18634010 2	18634013 7	-

SEQ ID NO. 148	2450669	TMEM9	Non-coding(UTR)	chr1	20110390 5	20110393 4	-
SEQ ID NO. 149	2451314	KDM5B	Non-coding(UTR)	chr1	20269785 1	20269812 4	-
SEQ ID NO. 150	2452652	NUCKS1	Coding	chr1	20569306 3	20569309 0	-
SEQ ID NO. 151	2452655	NUCKS1	Coding	chr1	20569870 6	20569874 5	-
SEQ ID NO. 152	2457626	BROX	Non-coding(Exonic Antisense)	chr1	22290682 3	22290687 1	-
SEQ ID NO. 153	2458075	PARP1	Non- coding(Intronic)	chr1	22456352 4	22456362 1	-
SEQ ID NO. 154	2458381	ENAH	Coding	chr1	22570037 5	22570041 4	-
SEQ ID NO. 155	2458503	PARP1	Non- coding(Intronic)	chr1	22597714 9	22597717 3	-
SEQ ID NO. 156	2459655	RHOA	Non-coding(Exonic Antisense)	chr1	22888232 9	22888237 0	-
SEQ ID NO. 157	2461827	ARID4B	Coding	chr1	23538315 0	23538326 5	-
SEQ ID NO. 158	2461828	ARID4B	Coding	chr1	23538367 4	23538384 1	-
SEQ ID NO. 159	2462178	NID1	Non-coding(UTR)	chr1	23613915 6	23613926 1	-
SEQ ID NO. 160	2464496	NCRNA00201	Non- coding(Intronic)	chr1	24501024 7	24501064 5	-
SEQ ID NO. 161	2464505	HNRNPU	Non-coding(UTR)	chr1	24501642 0	24501644 9	-
SEQ ID NO. 162	2464514	HNRNPU,NCRN A00201	Coding	chr1	24501775 2	24501778 9	-
SEQ ID NO. 163	2464537	HNRNPU	Coding	chr1	24502258 7	24502267 2	-
SEQ ID NO. 164	2468935	CPSF3	Coding	chr2	9580633	9580745	+
SEQ ID NO. 165	2469568	ATP6V1C2	Non-coding(UTR)	chr2	10923651	10923817	+
SEQ ID NO. 166	2473241	NCOA1	Coding	chr2	24962301	24962395	+
SEQ ID NO. 167	2473624	RAB10	Non-coding(UTR)	chr2	26358253	26358315	+
SEQ ID NO. 168	2474147	TMEM214	Non-coding(UTR)	chr2	27264519	27264553	+
SEQ ID NO. 169	2474700	GPN1	Coding	chr2	27873018	27873055	+
SEQ ID NO. 170	2474770	MRPL33	Non-coding(UTR)	chr2	28002513	28002557	+
SEQ ID NO. 171	2475647	YPEL5	Non-coding(UTR)	chr2	30383149	30383365	+
SEQ ID NO. 172	2476316	BIRC6	Coding	chr2	32707551	32707640	+
SEQ ID NO. 173	2476408	BIRC6	Non-coding(UTR)	chr2	32843548	32843578	+
SEQ ID NO. 174	2477341	AC007390.5	Coding	chr2	37428785	37428822	+
SEQ ID NO. 175	2478839	EML4	Non-coding(UTR)	chr2	42559443	42559634	+
SEQ ID NO. 176	2479729	SLC3A1	Non- coding(Intronic)	chr2	44546007	44546621	+
SEQ ID NO. 177	2480989	EPCAM	Non-coding(UTR)	chr2	47614066	47614142	+
SEQ ID NO. 178	2481178	MSH6	Non-coding(UTR)	chr2	48034001	48034074	+
SEQ ID NO. 179	2482593	SPTBN1	Coding	chr2	54882207	54882334	+
SEQ ID NO. 180	2482624	SPTBN1	Non-coding(UTR)	chr2	54896727	54896801	+
SEQ ID NO. 181	2483047	CCDC104	Non-coding(UTR)	chr2	55772160	55772187	+
SEQ ID NO. 182	2484558	AHSA2	Non-coding(UTR)	chr2	61405713	61405771	+
SEQ ID NO. 183	2484807	COMMD1	Non-coding(UTR)	chr2	62363157	62363187	+

SEQ ID NO. 184	2485214	MDH1	Non-coding(UTR)	chr2	63834172	63834310	+
SEQ ID NO. 185	2485276	UGP2	Coding	chr2	64111133	64111216	+
SEQ ID NO. 186	2487216	ANTXR1	Non-coding(UTR)	chr2	69475036	69475067	+
SEQ ID NO. 187	2487645	PCBP1	Non-coding(UTR)	chr2	70315979	70316219	+
SEQ ID NO. 188	2488150	ZNF638	Coding	chr2	71591148	71591240	+
SEQ ID NO. 189	2489030	ACTG2	Non-coding(UTR)	chr2	74146720	74146765	+
SEQ ID NO. 190	2489435	HTRA2	Non-coding(UTR)	chr2	74760238	74760277	+
SEQ ID NO. 191	2491645	MAT2A	Non-coding(UTR)	chr2	85771254	85771283	+
SEQ ID NO. 192	2492101	KDM3A	Coding	chr2	86705731	86705762	+
SEQ ID NO. 193	2492833	THNSL2	Non-coding(UTR)	chr2	88486099	88486137	+
SEQ ID NO. 194	2495140	ACTR1B	Non-coding(Exonic Antisense)	chr2	98272473	98272513	+
SEQ ID NO. 195	2498988	GCC2	Coding	chr2	10906751 8	10906756 7	+
SEQ ID NO. 196	2507241	CCNT2	Non-coding(Intronic)	chr2	13570408 5	13570412 3	+
SEQ ID NO. 197	2507514	UBXN4	Coding	chr2	13651941 0	13651948 1	+
SEQ ID NO. 198	2507533	UBXN4	Non-coding(UTR)	chr2	13654063 2	13654087 0	+
SEQ ID NO. 199	2512351	MARCH7	Coding	chr2	16060431 7	16060434 6	+
SEQ ID NO. 200	2512363	MARCH7	Non-coding(Intronic)	chr2	16062108 7	16062113 6	+
SEQ ID NO. 201	2512959	GCA	Non-coding(UTR)	chr2	16321746 2	16321760 4	+
SEQ ID NO. 202	2515085	GORASP2	Coding	chr2	17181817 3	17181825 9	+
SEQ ID NO. 203	2517330	HNRNPA3	Non-coding(UTR)	chr2	17808594 7	17808597 1	+
SEQ ID NO. 204	2518193	UBE2E3	Non-coding(Intronic)	chr2	18192065 2	18192078 9	+
SEQ ID NO. 205	2518707	NCKAP1	Non-coding(Exonic Antisense)	chr2	18378964 2	18379048 6	+
SEQ ID NO. 206	2525095	CREB1	Non-coding(UTR)	chr2	20846257 2	20846263 1	+
SEQ ID NO. 207	2527206	RPL37A	Coding	chr2	21736608 3	21736612 7	+
SEQ ID NO. 208	2527635	ARPC2	Non-coding(Intronic)	chr2	21910858 6	21910871 3	+
SEQ ID NO. 209	2532844	ATG16L1	Non-coding(UTR)	chr2	23420425 0	23420427 8	+
SEQ ID NO. 210	2534447	LRRFIP1	Coding	chr2	23867195 7	23867201 9	+
SEQ ID NO. 211	2537112	SH3YL1	Non-coding(UTR)	chr2	218176	218541	-
SEQ ID NO. 212	2539775	ITGB1BP1	Non-coding(UTR)	chr2	9546826	9546962	-
SEQ ID NO. 213	2540221	NOL10	Non-coding(UTR)	chr2	10711789	10711820	-
SEQ ID NO. 214	2544180	AC008073.5	Non-coding(UTR)	chr2	24290483	24290599	-
SEQ ID NO. 215	2544185	AC008073.5	Coding	chr2	24296946	24296980	-
SEQ ID NO. 216	2544295	ITSN2	Coding	chr2	24498610	24498679	-
SEQ ID NO. 217	2544306	ITSN2	Coding	chr2	24516558	24516637	-
SEQ ID NO. 218	2546279	SPDYA.PPP1CB	Non-coding(Exonic Antisense)	chr2	29025630	29025776	-
SEQ ID NO. 219	2549323	MAP4K3	Coding	chr2	39552666	39552755	-

SEQ ID NO. 220	2550840	LRPPRC	Coding	chr2	44170831	44170960	-
SEQ ID NO. 221	2550842	LRPPRC	Coding	chr2	44173258	44173355	-
SEQ ID NO. 222	2550964	PREPL	Non-coding(UTR)	chr2	44546148	44546608	-
SEQ ID NO. 223	2552021	EPCAM	Non-coding(Exonic Antisense)	chr2	47613985	47614122	-
SEQ ID NO. 224	2553312	PSME4	Coding	chr2	54127114	54127147	-
SEQ ID NO. 225	2553583	RTN4	Non-coding(UTR)	chr2	55199333	55199382	-
SEQ ID NO. 226	2553585	RTN4	Non-coding(UTR)	chr2	55199483	55199611	-
SEQ ID NO. 227	2553595	RTN4	Coding	chr2	55200957	55200996	-
SEQ ID NO. 228	2553907	CCDC104	Non-coding(Exonic Antisense)	chr2	55771450	55771480	-
SEQ ID NO. 229	2554001	PNPT1	Coding	chr2	55899130	55899157	-
SEQ ID NO. 230	2555279	USP34	Non-coding(UTR)	chr2	61414634	61414669	-
SEQ ID NO. 231	2555281	USP34	Coding	chr2	61415253	61415312	-
SEQ ID NO. 232	2555288	USP34	Coding	chr2	61417424	61417531	-
SEQ ID NO. 233	2555330	USP34	Non-coding(Intronic)	chr2	61452805	61453037	-
SEQ ID NO. 234	2555409	USP34	Coding	chr2	61575369	61575420	-
SEQ ID NO. 235	2555411	USP34	Coding	chr2	61575891	61575998	-
SEQ ID NO. 236	2555416	USP34	Coding	chr2	61597633	61597690	-
SEQ ID NO. 237	2555507	XPO1	Coding	chr2	61712955	61713067	-
SEQ ID NO. 238	2555522	XPO1	Coding	chr2	61725848	61725908	-
SEQ ID NO. 239	2556229	VPS54	Coding	chr2	64126624	64126660	-
SEQ ID NO. 240	2558208	AAK1	Coding	chr2	69754363	69754404	-
SEQ ID NO. 241	2558313	ANXA4	Non-coding(Exonic Antisense)	chr2	70053082	70053422	-
SEQ ID NO. 242	2558519	TIA1	Non-coding(UTR)	chr2	70439751	70439835	-
SEQ ID NO. 243	2559293	EXOC6B	Coding	chr2	72707745	72707845	-
SEQ ID NO. 244	2562334	MAT2A	Non-coding(Exonic Antisense)	chr2	85771249	85771273	-
SEQ ID NO. 245	2565264	SNRNP200	Non-coding(UTR)	chr2	96940504	96940591	-
SEQ ID NO. 246	2575142	POLR2D	Non-coding(UTR)	chr2	12860426 0	12860428 8	-
SEQ ID NO. 247	2577959	DARS	Non-coding(UTR)	chr2	13666432 5	13666478 4	-
SEQ ID NO. 248	2581588	PRPF40A	Coding	chr2	15353558 5	15353562 3	-
SEQ ID NO. 249	2583054	BAZ2B	Coding	chr2	16025534 0	16025538 8	-
SEQ ID NO. 250	2583056	BAZ2B	Coding	chr2	16025711 4	16025714 5	-
SEQ ID NO. 251	2583249	MARCH7	Non-coding(Exonic Antisense)	chr2	16062483 9	16062502 4	-
SEQ ID NO. 252	2583609	RBMS1	Non-coding(UTR)	chr2	16112982 8	16112987 3	-
SEQ ID NO. 253	2584845	COBLL1	Coding	chr2	16557893 5	16557897 3	-
SEQ ID NO. 254	2588838	NFE2L2	Coding	chr2	17809668 6	17809671 4	-
SEQ ID NO. 255	2590750	NCKAP1	Non-coding(UTR)	chr2	18378982 5	18379038 9	-
SEQ ID NO. 256	2590802	NCKAP1	Coding	chr2	18386770 9	18386774 4	-

SEQ ID NO. 257	2591635	COL3A1	Non-coding(Exonic Antisense)	chr2	18987379 9	18987391 3	-
SEQ ID NO. 258	2591638	COL3A1	Non-coding(Exonic Antisense)	chr2	18987657 1	18987730 1	-
SEQ ID NO. 259	2593447	PGAP1	Coding	chr2	19776734 4	19776745 8	-
SEQ ID NO. 260	2593692	SF3B1	Coding	chr2	19826543 9	19826547 3	-
SEQ ID NO. 261	2593714	SF3B1	Coding	chr2	19828323 4	19828328 7	-
SEQ ID NO. 262	2593758	HSPD1	Coding	chr2	19835940 4	19835943 3	-
SEQ ID NO. 263	2594506	CLK1	Coding	chr2	20171935 2	20171941 7	-
SEQ ID NO. 264	2596691	FAM119A	Non-coding(UTR)	chr2	20844611 0	20844614 0	-
SEQ ID NO. 265	2597013	IDH1	Non-coding(UTR)	chr2	20910112 6	20910138 2	-
SEQ ID NO. 266	2598267	FN1	Non-coding(UTR)	chr2	21622602 7	21622606 1	-
SEQ ID NO. 267	2598289	FN1	Coding	chr2	21623702 7	21623706 0	-
SEQ ID NO. 268	2598781	RPL37A,AC07332 1.5	Non-coding(Exonic Antisense)	chr2	21736606 7	21736610 1	-
SEQ ID NO. 269	2599342	ARPC2	Non-coding(Exonic Antisense)	chr2	21911892 9	21911904 0	-
SEQ ID NO. 270	2599903	C2orf24	Non-coding(UTR)	chr2	22003663 2	22003669 1	-
SEQ ID NO. 271	2606647	MYEOV2	Non-coding(UTR)	chr2	24107027 3	24107037 9	-
SEQ ID NO. 272	2607152	HDLBP	Coding	chr2	24218648 5	24218654 8	-
SEQ ID NO. 273	2607374	DTYMK	Non-coding(UTR)	chr2	24261520 2	24261529 7	-
SEQ ID NO. 274	2609635	SETD5	Non-coding(ncTranscript)	chr3	9473392	9473435	+
SEQ ID NO. 275	2609657	SETD5	Coding	chr3	9482211	9482361	+
SEQ ID NO. 276	2609668	SETD5	Coding	chr3	9486849	9486982	+
SEQ ID NO. 277	2610353	chr3+:10195215- 10195245	Non-coding(Intergenic)	chr3	10195215	10195245	+
SEQ ID NO. 278	2611083	PPARG	Non-coding(Intronic)	chr3	12400965	12401103	+
SEQ ID NO. 279	2614100	UBE2E1	Coding	chr3	23929058	23929154	+
SEQ ID NO. 280	2614135	RPL15	Non-coding(UTR)	chr3	23961672	23961706	+
SEQ ID NO. 281	2614137	RPL15	Non-coding(UTR)	chr3	23962179	23962307	+
SEQ ID NO. 282	2615656	STT3B	Non-coding(UTR)	chr3	31678984	31679087	+
SEQ ID NO. 283	2616071	CNOT10	Non-coding(UTR)	chr3	32815151	32815180	+
SEQ ID NO. 284	2616248	FBXL2	Non-coding(Intronic)	chr3	33429931	33430929	+
SEQ ID NO. 285	2617578	MYD88	Non-coding(UTR)	chr3	38184424	38184480	+
SEQ ID NO. 286	2618656	RPL14	Non-coding(UTR)	chr3	40503816	40503845	+
SEQ ID NO. 287	2619365	NKTR	Non-coding(Intronic)	chr3	42666725	42666819	+
SEQ ID NO. 288	2625632	APPL1	Coding	chr3	57290985	57291016	+
SEQ ID NO. 289	2625643	APPL1	Coding	chr3	57301770	57301820	+
SEQ ID NO. 290	2625893	SLMAP	Non-coding(UTR)	chr3	57914855	57914884	+

SEQ ID NO. 291	2627951	RP11-714G12.1	Non-coding(ncTranscript)	chr3	65673641	65673667	+
SEQ ID NO. 292	2633534	C3orf26	Non-coding(UTR)	chr3	99897391	99897425	+
SEQ ID NO. 293	2633651	NIT2	Non-coding(UTR)	chr3	10007412	10007418	+
SEQ ID NO. 294	2638377	LRRC58	Non-coding(Exonic Antisense)	chr3	12004898	12004916	+
SEQ ID NO. 295	2638451	NDUFB4	Coding	chr3	12032108	12032111	+
SEQ ID NO. 296	2638452	NDUFB4	Non-coding(UTR)	chr3	12032112	12032116	+
SEQ ID NO. 297	2641575	COPG	Non-coding(UTR)	chr3	12899654	12899660	+
SEQ ID NO. 298	2643579	CEP63	Non-coding(UTR)	chr3	13428043	13428058	+
SEQ ID NO. 299	2645294	SLC25A36	Non-coding(UTR)	chr3	14068522	14068527	+
SEQ ID NO. 300	2646066	U2SURP	Coding	chr3	14274177	14274188	+
SEQ ID NO. 301	2646085	U2SURP	Coding	chr3	14275773	14275777	+
SEQ ID NO. 302	2647361	WWTR1	Non-coding(Exonic Antisense)	chr3	14923510	14923542	+
SEQ ID NO. 303	2647678	TSC22D2	Non-coding(Intronic)	chr3	15014390	15014395	+
SEQ ID NO. 304	2647775	EIF2A	Coding	chr3	15029346	15029349	+
SEQ ID NO. 305	2647779	EIF2A	Coding	chr3	15030098	15030101	+
SEQ ID NO. 306	2648202	MBNL1	Coding	chr3	15217706	15217709	+
SEQ ID NO. 307	2651521	MECOM	Non-coding(Intronic Antisense)	chr3	16904812	16904840	+
SEQ ID NO. 308	2652021	chr3+:170114495-170114579	Non-coding(Intergenic)	chr3	17011449	17011457	+
SEQ ID NO. 309	2654335	TTC14	Coding	chr3	18032800	18032812	+
SEQ ID NO. 310	2654874	ATP11B	Coding	chr3	18260537	18260548	+
SEQ ID NO. 311	2654878	ATP11B	Coding	chr3	18261452	18261455	+
SEQ ID NO. 312	2655475	DVL3	Non-coding(UTR)	chr3	18389114	18389134	+
SEQ ID NO. 313	2655509	AP2M1	Non-coding(UTR)	chr3	18390179	18390182	+
SEQ ID NO. 314	2655678	PSMD2	Coding	chr3	18402416	18402420	+
SEQ ID NO. 315	2656791	EIF4A2	Non-coding(UTR)	chr3	18650757	18650765	+
SEQ ID NO. 316	2658354	OPA1	Coding	chr3	19333258	19333269	+
SEQ ID NO. 317	2658632	HES1	Non-coding(UTR)	chr3	19385616	19385628	+
SEQ ID NO. 318	2663553	NUP210	Non-coding(UTR)	chr3	13357767	13357827	-
SEQ ID NO. 319	2666503	TOP2B	Coding	chr3	25659949	25659979	-
SEQ ID NO. 320	2666519	TOP2B	Coding	chr3	25668695	25668787	-
SEQ ID NO. 321	2666524	TOP2B	Coding	chr3	25671534	25671588	-
SEQ ID NO. 322	2669316	GOLGA4	Non-coding(Exonic Antisense)	chr3	37365990	37366061	-

SEQ ID NO. 323	2669571	MYD88	Non-coding(Exonic Antisense)	chr3	38184382	38184448	-
SEQ ID NO. 324	2670438	chr3-:41197321-41197352	Non-coding(Intergenic)	chr3	41197321	41197352	-
SEQ ID NO. 325	2672775	C3orf75	Non-coding(UTR)	chr3	47537138	47537165	-
SEQ ID NO. 326	2674243	RHOA	Non-coding(UTR)	chr3	49396583	49396613	-
SEQ ID NO. 327	2675269	NPRL2	Non-coding(UTR)	chr3	50384946	50384986	-
SEQ ID NO. 328	2675802	PCBP4	Non-coding(UTR)	chr3	51991509	51991574	-
SEQ ID NO. 329	2676931	RP11-884K10.5	Non-coding(UTR)	chr3	53919264	53919310	-
SEQ ID NO. 330	2677655	C3orf63	Non-coding(UTR)	chr3	56656912	56656956	-
SEQ ID NO. 331	2677695	C3orf63	Non-coding(Intronic)	chr3	56702382	56702424	-
SEQ ID NO. 332	2680511	MAG11,RP11-175F9.3	Non-coding(Intronic)	chr3	65887126	65887154	-
SEQ ID NO. 333	2682663	PPP4R2	Non-coding(Exonic Antisense)	chr3	73116009	73116260	-
SEQ ID NO. 334	2685954	CPOX	Non-coding(UTR)	chr3	98298317	98298425	-
SEQ ID NO. 335	2691756	GOLGB1	Coding	chr3	12141741 6	12141754 7	-
SEQ ID NO. 336	2692111	DTX3L	Non-coding(Exonic Antisense)	chr3	12229304 6	12229326 5	-
SEQ ID NO. 337	2694407	RPN1	Coding	chr3	12834559 5	12834563 0	-
SEQ ID NO. 338	2694648	CNBP	Non-coding(UTR)	chr3	12888833 6	12888840 0	-
SEQ ID NO. 339	2694649	CNBP	Non-coding(UTR)	chr3	12888847 1	12888873 1	-
SEQ ID NO. 340	2695413	MRPL3	Non-coding(UTR)	chr3	13118125 8	13118135 4	-
SEQ ID NO. 341	2700507	COMMD2	Coding	chr3	14946846 5	14946849 7	-
SEQ ID NO. 342	2700829	SIAH2	Non-coding(UTR)	chr3	15045893 4	15045899 7	-
SEQ ID NO. 343	2701289	MBNL1	Non-coding(Intronic Antisense)	chr3	15204648 0	15204674 3	-
SEQ ID NO. 344	2702329	CCNL1	Non-coding(UTR)	chr3	15686564 9	15686577 5	-
SEQ ID NO. 345	2703240	KPNA4	Coding	chr3	16022595 6	16022598 6	-
SEQ ID NO. 346	2704511	MECOM	Non-coding(Intronic)	chr3	16903188 0	16903200 2	-
SEQ ID NO. 347	2704898	PHC3	Non-coding(Intronic)	chr3	16980800 0	16980821 5	-
SEQ ID NO. 348	2704935	PHC3	Coding	chr3	16988916 8	16988923 7	-
SEQ ID NO. 349	2705001	chr3-:170112099-170112278	Non-coding(Intergenic)	chr3	17011209 9	17011227 8	-
SEQ ID NO. 350	2706322	TBL1XR1	Non-coding(UTR)	chr3	17673978 7	17674027 6	-
SEQ ID NO. 351	2706324	TBL1XR1	Non-coding(UTR)	chr3	17674113 4	17674122 6	-
SEQ ID NO. 352	2707780	DCUN1D1	Coding	chr3	18266504 6	18266507 4	-
SEQ ID NO. 353	2708798	RP11-110C15.4	Non-coding(ncTranscript)	chr3	18513562 7	18513565 7	-
SEQ ID NO. 354	2709489	RFC4	Coding	chr3	18650775 8	18650781 7	-

SEQ ID NO. 355	2710214	LPP	Non-coding(Exonic Antisense)	chr3	18859505 2	18859526 3	-
SEQ ID NO. 356	2710217	LPP	Non-coding(Exonic Antisense)	chr3	18859621 2	18859630 4	-
SEQ ID NO. 357	2711689	ATP13A3	Coding	chr3	19416919 9	19416935 7	-
SEQ ID NO. 358	2712424	TNK2	Non-coding(UTR)	chr3	19559024 3	19559028 4	-
SEQ ID NO. 359	2713075	NCBP2	Non-coding(UTR)	chr3	19666229 8	19666235 9	-
SEQ ID NO. 360	2713262	DLG1	Coding	chr3	19686515 4	19686525 8	-
SEQ ID NO. 361	2713269	DLG1	Coding	chr3	19687662 5	19687665 6	-
SEQ ID NO. 362	2714106	PIGG	Non-coding(UTR)	chr4	533179	533289	+
SEQ ID NO. 363	2715470	RNF4	Non-coding(UTR)	chr4	2517539	2517569	+
SEQ ID NO. 364	2715717	ADD1	Non-coding(UTR)	chr4	2931743	2931773	+
SEQ ID NO. 365	2720693	SLIT2	Non-coding(UTR)	chr4	20622128	20622155	+
SEQ ID NO. 366	2724050	KLF3	Non-coding(UTR)	chr4	38700710	38702100	+
SEQ ID NO. 367	2724565	PABPC1P1	Non-coding(ncTranscript)	chr4	39975424	39975454	+
SEQ ID NO. 368	2726514	OCIAD1	Coding	chr4	48859230	48859373	+
SEQ ID NO. 369	2727970	EXOC1	Non-coding(UTR)	chr4	56771127	56771164	+
SEQ ID NO. 370	2730701	MOBK1A	Coding	chr4	71844873	71844981	+
SEQ ID NO. 371	2731872	USO1	Coding	chr4	76722241	76722353	+
SEQ ID NO. 372	2732403	CCNG2	Coding	chr4	78081887	78082066	+
SEQ ID NO. 373	2735017	SPARCL1	Non-coding(Exonic Antisense)	chr4	88394536	88394668	+
SEQ ID NO. 374	2736295	SMARCAD1	Coding	chr4	95198175	95198297	+
SEQ ID NO. 375	2738963	OSTC	Non-coding(UTR)	chr4	10958860 1	10958872 3	+
SEQ ID NO. 376	2743194	PGRMC2	Non-coding(Exonic Antisense)	chr4	12919133 7	12919209 9	+
SEQ ID NO. 377	2744632	NAA15	Coding	chr4	14028293 9	14028303 0	+
SEQ ID NO. 378	2745687	SMARCA5	Coding	chr4	14446502 6	14446510 5	+
SEQ ID NO. 379	2754300	IRF2	Non-coding(Exonic Antisense)	chr4	18530898 3	18530925 1	+
SEQ ID NO. 380	2757037	CTBP1	Non-coding(UTR)	chr4	1205264	1205300	-
SEQ ID NO. 381	2763813	DHX15	Non-coding(UTR)	chr4	24529196	24529350	-
SEQ ID NO. 382	2766634	PDS5A	Coding	chr4	39878690	39878768	-
SEQ ID NO. 383	2770195	AASDH	Non-coding(UTR)	chr4	57204490	57204521	-
SEQ ID NO. 384	2770473	IGFBP7.RP11-738E22.2	Non-coding(UTR)	chr4	57897402	57897479	-
SEQ ID NO. 385	2771759	UBA6	Coding	chr4	68506869	68506938	-
SEQ ID NO. 386	2773129	ANKRD17	Non-coding(Intronic)	chr4	74079054	74079088	-
SEQ ID NO. 387	2774054	SCARB2	Non-coding(UTR)	chr4	77081059	77081265	-
SEQ ID NO. 388	2775592	HNRPD	Coding	chr4	83350409	83350477	-
SEQ ID NO. 389	2775758	SEC31A	Non-coding(UTR)	chr4	83739819	83739846	-
SEQ ID NO. 390	2776094	FAM175A	Coding	chr4	84383985	84384015	-
SEQ ID NO. 391	2777492	FAM13A	Non-coding(UTR)	chr4	89647632	89647659	-

SEQ ID NO. 392	2779488	H2AFZ	Non-coding(UTR)	chr4	10086925 9	10086928 3	-
SEQ ID NO. 393	2779639	PPP3CA	Non-coding(UTR)	chr4	10194459 5	10194462 9	-
SEQ ID NO. 394	2779995	UBE2D3	Non-coding(UTR)	chr4	10371715 1	10371728 2	-
SEQ ID NO. 395	2780545	PPA2	Non-coding(UTR)	chr4	10629078 8	10629085 4	-
SEQ ID NO. 396	2783475	C4orf3	Non-coding(UTR)	chr4	12021822 8	12021828 8	-
SEQ ID NO. 397	2789554	SH3D19	Non-coding(UTR)	chr4	15209672 7	15209678 4	-
SEQ ID NO. 398	2790573	PLRG1	Non-coding(UTR)	chr4	15545768 7	15545772 8	-
SEQ ID NO. 399	2797449	FAT1	Coding	chr4	18756089 1	18756092 7	-
SEQ ID NO. 400	2801338	CTD-2001E22.2	Non-coding(ncTranscript)	chr5	9550353	9550381	+
SEQ ID NO. 401	2801556	CCT5	Non-coding(UTR)	chr5	10265042	10265108	+
SEQ ID NO. 402	2801679	MARCH6	Coding	chr5	10433706	10433796	+
SEQ ID NO. 403	2802506	TRIO	Coding	chr5	14358400	14358435	+
SEQ ID NO. 404	2805739	RP11-36C20.1	Non-coding(ncTranscript)	chr5	33162531	33162567	+
SEQ ID NO. 405	2806859	NIPBL	Coding	chr5	36984905	36985298	+
SEQ ID NO. 406	2806912	NIPBL	Coding	chr5	37045613	37045670	+
SEQ ID NO. 407	2807658	AC008810.1	Non-coding(Exonic Antisense)	chr5	40761189	40761495	+
SEQ ID NO. 408	2809146	PELO	Non-coding(UTR)	chr5	52097805	52097849	+
SEQ ID NO. 409	2810487	GPBP1	Coding	chr5	56531793	56531821	+
SEQ ID NO. 410	2812307	PPWD1	Non-coding(UTR)	chr5	64883290	64883318	+
SEQ ID NO. 411	2812500	ERBB2IP	Coding	chr5	65374321	65374358	+
SEQ ID NO. 412	2812573	SREK1	Coding	chr5	65460623	65460704	+
SEQ ID NO. 413	2817404	PAPD4	Coding	chr5	78919159	78919265	+
SEQ ID NO. 414	2817457	PAPD4	Non-coding(UTR)	chr5	78982421	78982452	+
SEQ ID NO. 415	2818271	RPS23	Non-coding(Exonic Antisense)	chr5	81573522	81573652	+
SEQ ID NO. 416	2818964	COX7C	Non-coding(UTR)	chr5	85916491	85916564	+
SEQ ID NO. 417	2822274	PAM	Non-coding(UTR)	chr5	10236534 2	10236537 2	+
SEQ ID NO. 418	2823066	EFNA5	Non-coding(Intronic Antisense)	chr5	10697495 5	10697498 5	+
SEQ ID NO. 419	2823854	WDR36	Coding	chr5	11045678 9	11045683 9	+
SEQ ID NO. 420	2824899	AP3S1	Non-coding(UTR)	chr5	11524943 2	11524961 0	+
SEQ ID NO. 421	2828112	HINT1	Non-coding(Exonic Antisense)	chr5	13049507 2	13049510 4	+
SEQ ID NO. 422	2828637	RAD50	Coding	chr5	13193905 2	13193915 6	+
SEQ ID NO. 423	2828642	RAD50	Coding	chr5	13194500 0	13194507 7	+
SEQ ID NO. 424	2829255	SKP1,PPP2CA	Non-coding(Exonic Antisense)	chr5	13353306 2	13353325 8	+
SEQ ID NO. 425	2829555	C5orf24	Non-coding(UTR)	chr5	13419529 9	13419538 2	+
SEQ ID NO. 426	2829679	CTC-203F4.1	Non-	chr5	13467020	13467039	+

			coding(Intronic)		6	3	
SEQ ID NO. 427	2831231	PAIP2	Non-coding(UTR)	chr5	13870498 8	13870532 9	+
SEQ ID NO. 428	2831557	C5orf32	Non-coding(UTR)	chr5	13962333 4	13962337 1	+
SEQ ID NO. 429	2836687	SAP30L	Non-coding(UTR)	chr5	15383560 0	15383566 7	+
SEQ ID NO. 430	2840638	NPM1	Coding	chr5	17083230 6	17083233 0	+
SEQ ID NO. 431	2843280	TMED9	Non-coding(UTR)	chr5	17702303 5	17702309 9	+
SEQ ID NO. 432	2844248	CANX	Non-coding(UTR)	chr5	17915757 3	17915762 3	+
SEQ ID NO. 433	2844250	CANX	Non-coding(UTR)	chr5	17915786 4	17915789 4	+
SEQ ID NO. 434	2848258	CCT5	Non-coding(Exonic Antisense)	chr5	10264858	10265070	-
SEQ ID NO. 435	2848472	DAP	Non-coding(UTR)	chr5	10679387	10679458	-
SEQ ID NO. 436	2851973	DROSHA	Coding	chr5	31401461	31401522	-
SEQ ID NO. 437	2854808	RPL37	Coding	chr5	40834283	40834312	-
SEQ ID NO. 438	2854809	RPL37	Coding	chr5	40834313	40834356	-
SEQ ID NO. 439	2855289	SEPP1	Non-coding(UTR)	chr5	42800001	42800083	-
SEQ ID NO. 440	2855291	SEPP1	Non-coding(UTR)	chr5	42800241	42800298	-
SEQ ID NO. 441	2855292	SEPP1	Non-coding(UTR)	chr5	42800506	42800717	-
SEQ ID NO. 442	2857172	DHX29	Coding	chr5	54589903	54589952	-
SEQ ID NO. 443	2862162	TNPO1	Non-coding(Exonic Antisense)	chr5	72161442	72161545	-
SEQ ID NO. 444	2862377	BTF3	Non-coding(Exonic Antisense)	chr5	72801222	72801281	-
SEQ ID NO. 445	2865063	RPS23	Non-coding(UTR)	chr5	81571901	81571927	-
SEQ ID NO. 446	2868141	ERAP1	Non-coding(UTR)	chr5	96110219	96110633	-
SEQ ID NO. 447	2877518	HSPA9	Coding	chr5	13789309 1	13789317 6	-
SEQ ID NO. 448	2878261	PFDN1	Coding	chr5	13966106 4	13966111 5	-
SEQ ID NO. 449	2882121	SPARC	Non-coding(UTR)	chr5	15104204 6	15104226 4	-
SEQ ID NO. 450	2888344	RNF44	Non-coding(UTR)	chr5	17595372 4	17595381 0	-
SEQ ID NO. 451	2893822	DSP	Coding	chr6	7578699	7578774	+
SEQ ID NO. 452	2893942	TXNDC5,MUTED	Non-coding(Exonic Antisense)	chr6	7881819	7881943	+
SEQ ID NO. 453	2896978	FAM8A1	Non-coding(UTR)	chr6	17611895	17611944	+
SEQ ID NO. 454	2898531	ALDH5A1	Non-coding(UTR)	chr6	24537390	24537418	+
SEQ ID NO. 455	2902010	DDR1	Non-coding(UTR)	chr6	30867773	30867802	+
SEQ ID NO. 456	2902011	DDR1	Coding	chr6	30867849	30867902	+
SEQ ID NO. 457	2905137	SRSF3	Non-coding(UTR)	chr6	36570141	36570256	+
SEQ ID NO. 458	2906968	PRICKLE4,TOM M6	Non-coding(UTR)	chr6	41757493	41757600	+
SEQ ID NO. 459	2908048	TJAP1	Non-coding(UTR)	chr6	43474171	43474248	+
SEQ ID NO. 460	2909471	CD2AP	Coding	chr6	47580215	47580271	+
SEQ ID NO. 461	2910489	FBXO9	Coding	chr6	52938339	52938411	+
SEQ ID NO. 462	2914002	SENp6	Non-	chr6	76345055	76345281	+

			coding(Intronic)				
SEQ ID NO. 463	2914107	MYO6	Coding	chr6	76576694	76576822	+
SEQ ID NO. 464	2916383	SLC35A1	Non-coding(UTR)	chr6	88222005	88222043	+
SEQ ID NO. 465	2916976	CASP8AP2	Coding	chr6	90565189	90565242	+
SEQ ID NO. 466	2918543	SFRS18	Non-coding(Exonic Antisense)	chr6	99846655	99846962	+
SEQ ID NO. 467	2918547	SFRS18	Non-coding(Exonic Antisense)	chr6	99848935	99849230	+
SEQ ID NO. 468	2922232	MARCKS	Non-coding(UTR)	chr6	11418305 4	11418314 5	+
SEQ ID NO. 469	2922235	MARCKS	Non-coding(UTR)	chr6	11418455 0	11418462 7	+
SEQ ID NO. 470	2926222	RPS12	Coding	chr6	13313864 6	13313867 5	+
SEQ ID NO. 471	2929946	STXBP5	Non-coding(Intronic)	chr6	14766927 8	14766930 5	+
SEQ ID NO. 472	2930652	TAB2	Non-coding(UTR)	chr6	14973266 1	14973270 5	+
SEQ ID NO. 473	2932399	SCAF8	Coding	chr6	15512650 4	15512658 8	+
SEQ ID NO. 474	2932428	SCAF8	Non-coding(UTR)	chr6	15515516 4	15515519 1	+
SEQ ID NO. 475	2933660	TMEM181	Coding	chr6	15900197 3	15900201 0	+
SEQ ID NO. 476	2936963	MLLT4	Coding	chr6	16837053 1	16837058 2	+
SEQ ID NO. 477	2940827	TXNDC5,MUTED	Non-coding(UTR)	chr6	7881828	7882072	-
SEQ ID NO. 478	2942512	RANBP9	Coding	chr6	13625915	13625996	-
SEQ ID NO. 479	2944070	DEK	Non-coding(UTR)	chr6	18224463	18224675	-
SEQ ID NO. 480	2944963	SOX4	Non-coding(Exonic Antisense)	chr6	21598569	21598785	-
SEQ ID NO. 481	2946479	HMGH4	Non-coding(Exonic Antisense)	chr6	26546937	26547116	-
SEQ ID NO. 482	2947592	TRIM27	Coding	chr6	28876750	28876789	-
SEQ ID NO. 483	2948592	TUBB	Non-coding(Exonic Antisense)	chr6	30691418	30691448	-
SEQ ID NO. 484	2948596	FLOT1	Non-coding(UTR)	chr6	30695520	30695552	-
SEQ ID NO. 485	2949053	DDX39B	Non-coding(ncTranscript)	chr6	31500977	31501368	-
SEQ ID NO. 486	2949061	XXbac-BPG296P20.16,DX39B	Coding	chr6	31504283	31504313	-
SEQ ID NO. 487	2951060	C6orf1	Non-coding(UTR)	chr6	34214199	34214278	-
SEQ ID NO. 488	2956077	TNFRSF21	Coding	chr6	47252104	47252155	-
SEQ ID NO. 489	2958402	DST	Coding	chr6	56394805	56394917	-
SEQ ID NO. 490	2961302	COX7A2	Coding	chr6	75947554	75947636	-
SEQ ID NO. 491	2966293	SFRS18	Non-coding(UTR)	chr6	99864226	99864304	-
SEQ ID NO. 492	2966378	CCNC	Non-coding(UTR)	chr6	99990291	99990460	-
SEQ ID NO. 493	2967164	HACE1	Non-coding(UTR)	chr6	10517656 0	10517677 7	-
SEQ ID NO. 494	2967323	PREP	Non-coding(UTR)	chr6	10572561 0	10572564 3	-
SEQ ID NO. 495	2968257	SNX3	Coding	chr6	10858196 4	10858199 7	-

SEQ ID NO. 496	2968653	SESNI	Non-coding(UTR)	chr6	10930767 0	10930772 7	-
SEQ ID NO. 497	2974195	MED23	Coding	chr6	13190789 7	13190795 0	-
SEQ ID NO. 498	2974332	CTGF	Non-coding(UTR)	chr6	13226939 0	13226942 5	-
SEQ ID NO. 499	2975686	BCLAF1	Non-coding(UTR)	chr6	13658081 4	13658117 8	-
SEQ ID NO. 500	2975709	BCLAF1	Coding	chr6	13659426 0	13659429 6	-
SEQ ID NO. 501	2976368	PERP	Non-coding(UTR)	chr6	13841203 2	13841208 4	-
SEQ ID NO. 502	2977521	FUCA2	Non-coding(UTR)	chr6	14381662 5	14381666 0	-
SEQ ID NO. 503	2981918	EZR	Non-coding(UTR)	chr6	15918743 7	15918755 9	-
SEQ ID NO. 504	2982323	SOD2	Non-coding(UTR)	chr6	16010044 9	16010052 0	-
SEQ ID NO. 505	2982385	TCPI	Coding	chr6	16020025 2	16020028 2	-
SEQ ID NO. 506	2984576	SFT2D1	Non-coding(UTR)	chr6	16673352 6	16673368 2	-
SEQ ID NO. 507	2985813	THBS2	Non-coding(UTR)	chr6	16961744 9	16961765 4	-
SEQ ID NO. 508	2985965	WDR27	Non-coding(UTR)	chr6	16985731 7	16985735 0	-
SEQ ID NO. 509	2988895	AIMP2	Non-coding(UTR)	chr7	6063363	6063418	+
SEQ ID NO. 510	2988896	AIMP2	Non-coding(UTR)	chr7	6063425	6063456	+
SEQ ID NO. 511	2989720	AC007128.1,AC0 07009.1	Non- coding(ncTranscript)	chr7	8302393	8302437	+
SEQ ID NO. 512	2991248	AHR	Coding	chr7	17373588	17373738	+
SEQ ID NO. 513	2991263	AHR	Non-coding(UTR)	chr7	17382754	17383243	+
SEQ ID NO. 514	2991264	AHR	Non-coding(UTR)	chr7	17383478	17384186	+
SEQ ID NO. 515	2993622	HNRNPA2B1	Non-coding(Exonic Antisense)	chr7	26230040	26230071	+
SEQ ID NO. 516	2993644	CBX3	Non-coding(UTR)	chr7	26242591	26242618	+
SEQ ID NO. 517	2993659	CBX3	Non-coding(UTR)	chr7	26252158	26252837	+
SEQ ID NO. 518	2994371	TAX1BP1	Non- coding(Intronic)	chr7	27841295	27841322	+
SEQ ID NO. 519	2995598	AQP1	Non-coding(UTR)	chr7	30965061	30965090	+
SEQ ID NO. 520	2997143	SEPT7	Coding	chr7	35930330	35930354	+
SEQ ID NO. 521	3002667	EGFR	Non- coding(ncTranscript)	chr7	55111601	55111721	+
SEQ ID NO. 522	3003180	GBAS	Non-coding(UTR)	chr7	56067815	56067843	+
SEQ ID NO. 523	3004652	chr7+:64171405- 64171435	Non- coding(Intergenic)	chr7	64171405	64171435	+
SEQ ID NO. 524	3011652	EEF1A1P28	Non- coding(ncTranscript)	chr7	88269706	88269736	+
SEQ ID NO. 525	3011846	STEAP1	Non-coding(UTR)	chr7	89794089	89794119	+
SEQ ID NO. 526	3012405	AKAP9	Coding	chr7	91624943	91625038	+
SEQ ID NO. 527	3012428	AKAP9	Coding	chr7	91670017	91670138	+
SEQ ID NO. 528	3012438	AKAP9	Coding	chr7	91682056	91682090	+
SEQ ID NO. 529	3012452	AKAP9	Coding	chr7	91700231	91700287	+

SEQ ID NO. 530	3012453	AKAP9	Coding	chr7	91700288	91700319	+
SEQ ID NO. 531	3013190	CASD1	Coding	chr7	94147516	94147581	+
SEQ ID NO. 532	3013468	PON2	Non-coding(Intronic Antisense)	chr7	95042749	95042946	+
SEQ ID NO. 533	3013685	SLC25A13	Non-coding(Exonic Antisense)	chr7	95749570	95749793	+
SEQ ID NO. 534	3014422	TRRAP	Coding	chr7	98493399	98493443	+
SEQ ID NO. 535	3015985	SRRT	Coding	chr7	100486179	100486273	+
SEQ ID NO. 536	3017629	MLL5	Coding	chr7	104746413	104746442	+
SEQ ID NO. 537	3017826	RINT1	Non-coding(UTR)	chr7	105208082	105208113	+
SEQ ID NO. 538	3021760	WASL	Non-coding(Exonic Antisense)	chr7	123324045	123324364	+
SEQ ID NO. 539	3022682	SND1	Non-coding(UTR)	chr7	127732585	127732630	+
SEQ ID NO. 540	3027555	NDUFB2	Non-coding(UTR)	chr7	140406369	140406414	+
SEQ ID NO. 541	3027926	SSBP1	Coding	chr7	141443718	141443782	+
SEQ ID NO. 542	3027936	SSBP1	Non-coding(UTR)	chr7	141450185	141450241	+
SEQ ID NO. 543	3037391	KDELR2	Non-coding(UTR)	chr7	6502522	6502596	-
SEQ ID NO. 544	3037406	KDELR2	Coding	chr7	6513851	6513887	-
SEQ ID NO. 545	3037950	RPA3	Non-coding(UTR)	chr7	7676584	7676627	-
SEQ ID NO. 546	3039980	AHR	Non-coding(Exonic Antisense)	chr7	17382756	17383093	-
SEQ ID NO. 547	3039983	AHR	Non-coding(Exonic Antisense)	chr7	17384068	17384200	-
SEQ ID NO. 548	3040116	SNX13	Coding	chr7	17915324	17915397	-
SEQ ID NO. 549	3041262	TOMM7	Non-coding(UTR)	chr7	22852644	22852678	-
SEQ ID NO. 550	3042004	CYCS	Non-coding(UTR)	chr7	25162509	25162708	-
SEQ ID NO. 551	3042424	HNRNPA2B1	Non-coding(UTR)	chr7	26229786	26229921	-
SEQ ID NO. 552	3042426	HNRNPA2B1	Non-coding(UTR)	chr7	26230047	26230074	-
SEQ ID NO. 553	3042429	HNRNPA2B1	Non-coding(UTR)	chr7	26230678	26230737	-
SEQ ID NO. 554	3042430	HNRNPA2B1	Non-coding(UTR)	chr7	26230767	26230996	-
SEQ ID NO. 555	3042437	HNRNPA2B1	Non-coding(UTR)	chr7	26231796	26231958	-
SEQ ID NO. 556	3042453	HNRNPA2B1	Coding	chr7	26236208	26236278	-
SEQ ID NO. 557	3048780	TMED4	Non-coding(UTR)	chr7	44617913	44617943	-
SEQ ID NO. 558	3048870	H2AFV	Non-coding(UTR)	chr7	44866413	44866768	-
SEQ ID NO. 559	3053384	chr7:-64435274-64435303	Non-coding(Intergenic)	chr7	64435274	64435303	-
SEQ ID NO. 560	3056395	EIF4H	Non-coding(Exonic Antisense)	chr7	73611210	73611234	-
SEQ ID NO. 561	3060052	DMTF1	Non-coding(Exonic Antisense)	chr7	86824937	86825415	-
SEQ ID NO. 562	3061054	AC000120.7,KRIT1	Non-coding(UTR)	chr7	91829356	91829670	-
SEQ ID NO. 563	3061144	ANKIB1	Non-coding(Exonic Antisense)	chr7	92029299	92029375	-
SEQ ID NO. 564	3061758	COL1A2	Non-coding(Exonic Antisense)	chr7	94058608	94058723	-

SEQ ID NO. 565	3062023	PON2	Non-coding(ncTranscript)	chr7	95041837	95042319	-
SEQ ID NO. 566	3064354	SRRT	Non-coding(Exonic Antisense)	chr7	100486138	100486258	-
SEQ ID NO. 567	3075645	chr7-:138912234-138912268	Non-coding(Intergenic)	chr7	138912234	138912268	-
SEQ ID NO. 568	3076355	NDUFB2	Non-coding(Intronic Antisense)	chr7	140419154	140419193	-
SEQ ID NO. 569	3076393	BRAF	Coding	chr7	140501240	140501268	-
SEQ ID NO. 570	3076490	MRPS33	Non-coding(UTR)	chr7	140705974	140706021	-
SEQ ID NO. 571	3081625	LMBR1	Non-coding(UTR)	chr7	156475639	156475683	-
SEQ ID NO. 572	3087828	PCM1	Coding	chr8	17810521	17810685	+
SEQ ID NO. 573	3087930	ASAH1	Non-coding(Exonic Antisense)	chr8	17924332	17924610	+
SEQ ID NO. 574	3088570	ATP6V1B2	Non-coding(UTR)	chr8	20079154	20079183	+
SEQ ID NO. 575	3092505	RBPMS	Non-coding(UTR)	chr8	30404975	30405013	+
SEQ ID NO. 576	3094309	PROSC	Non-coding(UTR)	chr8	37637241	37637268	+
SEQ ID NO. 577	3096162	IKBKB	Non-coding(UTR)	chr8	42189466	42189790	+
SEQ ID NO. 578	3096409	HOOK3	Coding	chr8	42862996	42863063	+
SEQ ID NO. 579	3096979	KIAA0146	Coding	chr8	48309034	48309125	+
SEQ ID NO. 580	3099780	SDCBP	Non-coding(UTR)	chr8	59495253	59495349	+
SEQ ID NO. 581	3100230	RAB2A	Non-coding(UTR)	chr8	61533537	61533612	+
SEQ ID NO. 582	3107638	DPY19L4	Coding	chr8	95795948	95795975	+
SEQ ID NO. 583	3108472	MTDH	Coding	chr8	98731359	98731417	+
SEQ ID NO. 584	3108501	LAPTM4B	Coding	chr8	98828334	98828363	+
SEQ ID NO. 585	3108938	VPS13B	Coding	chr8	100160128	100160223	+
SEQ ID NO. 586	3111090	AC090579.1	Coding	chr8	107719006	107719178	+
SEQ ID NO. 587	3111116	AC090579.1	Non-coding(UTR)	chr8	107764863	107764893	+
SEQ ID NO. 588	3112517	EIF3H	Non-coding(Exonic Antisense)	chr8	117657108	117657268	+
SEQ ID NO. 589	3114370	FAM91A1	Coding	chr8	124792239	124792277	+
SEQ ID NO. 590	3114664	NDUFB9	Non-coding(UTR)	chr8	125562138	125562181	+
SEQ ID NO. 591	3124536	FDFT1	Non-coding(Exonic Antisense)	chr8	11696124	11696400	-
SEQ ID NO. 592	3126094	ASAH1	Non-coding(UTR)	chr8	17913971	17914068	-
SEQ ID NO. 593	3128680	SDAD1P1	Non-coding(ncTranscript)	chr8	26238141	26238174	-
SEQ ID NO. 594	3129955	TMEM66	Coding	chr8	29923504	29923543	-
SEQ ID NO. 595	3131973	WHSC1L1	Coding	chr8	38205449	38205479	-
SEQ ID NO. 596	3132336	TM2D2	Non-coding(UTR)	chr8	38848290	38848319	-
SEQ ID NO. 597	3133528	RP11-598P20.5,HOOK3	Non-coding(Exonic Antisense)	chr8	42882619	42882650	-
SEQ ID NO. 598	3134184	PRKDC	Coding	chr8	48852116	48852256	-
SEQ ID NO. 599	3136352	RP11-17A4.1	Non-coding(Exonic Antisense)	chr8	57501108	57501163	-

SEQ ID NO. 600	3137586	ASPH	Non-coding(UTR)	chr8	62537157	62537642	-
SEQ ID NO. 601	3138886	SNHG6	Non-coding(ncTranscript)	chr8	67834852	67834955	-
SEQ ID NO. 602	3138980	COP55	Non-coding(UTR)	chr8	67955322	67955454	-
SEQ ID NO. 603	3139053	ARFGEF1	Coding	chr8	68112673	68112748	-
SEQ ID NO. 604	3139926	TRAM1	Coding	chr8	71510160	71510244	-
SEQ ID NO. 605	3141863	TPD52	Non-coding(UTR)	chr8	80948831	80948859	-
SEQ ID NO. 606	3145023	KIAA1429	Non-coding(UTR)	chr8	95500766	95500848	-
SEQ ID NO. 607	3145956	RPL30	Coding	chr8	99054030	99054078	-
SEQ ID NO. 608	3145966	RPL30	Coding	chr8	99057186	99057310	-
SEQ ID NO. 609	3146538	POLR2K	Non-coding(Exonic Antisense)	chr8	10116609 6	10116616 5	-
SEQ ID NO. 610	3146566	RNF19A	Non-coding(UTR)	chr8	10126931 7	10126952 1	-
SEQ ID NO. 611	3146788	PABPC1	Non-coding(UTR)	chr8	10171524 1	10171545 4	-
SEQ ID NO. 612	3146799	PABPC1	Coding	chr8	10172142 1	10172144 5	-
SEQ ID NO. 613	3147328	UBR5	Coding	chr8	10326986 0	10326993 2	-
SEQ ID NO. 614	3148628	EIF3E	Coding	chr8	10924051 5	10924054 4	-
SEQ ID NO. 615	3149768	EIF3H	Non-coding(UTR)	chr8	11765708 7	11765722 1	-
SEQ ID NO. 616	3149773	EIF3H	Coding	chr8	11766105 8	11766115 9	-
SEQ ID NO. 617	3149864	RAD21	Coding	chr8	11786889 8	11786892 8	-
SEQ ID NO. 618	3151480	C8orf76	Non-coding(UTR)	chr8	12423225 7	12423228 5	-
SEQ ID NO. 619	3152560	FAM84B	Non-coding(UTR)	chr8	12756485 6	12756502 1	-
SEQ ID NO. 620	3153532	ASAP1	Coding	chr8	13119948 7	13119951 6	-
SEQ ID NO. 621	3157388	TOP1MT	Non-coding(UTR)	chr8	14439153 9	14439161 0	-
SEQ ID NO. 622	3157461	ZC3H3	Non-coding(UTR)	chr8	14451983 1	14451986 4	-
SEQ ID NO. 623	3157723	FAM83H	Non-coding(UTR)	chr8	14480611 8	14480619 6	-
SEQ ID NO. 624	3157847	NRBP2	Non-coding(UTR)	chr8	14491592 3	14491601 5	-
SEQ ID NO. 625	3164299	DENND4C	Non-coding(UTR)	chr9	19373469	19374005	+
SEQ ID NO. 626	3165138	RP11-370B11.1	Non-coding(ncTranscript)	chr9	22748070	22748104	+
SEQ ID NO. 627	3165799	IFT74	Coding	chr9	27018647	27018685	+
SEQ ID NO. 628	3166029	chr9+:27943648-27943678	Non-coding(Intergenic)	chr9	27943648	27943678	+
SEQ ID NO. 629	3166735	DNAJA1	Coding	chr9	33038903	33038998	+
SEQ ID NO. 630	3167990	RP11-156G14.6	Non-coding(ncTranscript)	chr9	35592905	35592943	+
SEQ ID NO. 631	3168127	GBA2	Non-coding(Exonic Antisense)	chr9	35738843	35738870	+
SEQ ID NO. 632	3169011	FRMPD1	Coding	chr9	37735573	37735720	+
SEQ ID NO. 633	3174268	SMC5	Coding	chr9	72967152	72967246	+

SEQ ID NO. 634	3174441	C9orf85	Non-coding(UTR)	chr9	74588315	74588354	+
SEQ ID NO. 635	3175632	VPS13A	Coding	chr9	79895103	79895154	+
SEQ ID NO. 636	3175657	VPS13A	Coding	chr9	79936422	79936637	+
SEQ ID NO. 637	3178635	SECISBP2	Coding	chr9	91949555	91949616	+
SEQ ID NO. 638	3183178	SLC44A1	Non-coding(UTR)	chr9	10815202 7	10815205 9	+
SEQ ID NO. 639	3190449	CERCAM.AL359 091.1	Coding	chr9	13119959 4	13119962 3	+
SEQ ID NO. 640	3192674	GTF3C5	Coding	chr9	13592923 7	13592932 8	+
SEQ ID NO. 641	3197644	ERMP1	Non-coding(UTR)	chr9	5784578	5784615	-
SEQ ID NO. 642	3199457	ZDHHC21	Non-coding(UTR)	chr9	14617270	14617297	-
SEQ ID NO. 643	3199485	ZDHHC21.AL390 732.1	Non- coding(Intronic)	chr9	14679025	14679408	-
SEQ ID NO. 644	3200638	HAUS6	Coding	chr9	19087118	19087151	-
SEQ ID NO. 645	3200711	DENND4C	Non-coding(Exonic Antisense)	chr9	19373580	19373641	-
SEQ ID NO. 646	3200718	RPS6	Coding	chr9	19376535	19376564	-
SEQ ID NO. 647	3200725	RPS6	Coding	chr9	19378719	19378755	-
SEQ ID NO. 648	3203822	UBAP2	Coding	chr9	33996241	33996307	-
SEQ ID NO. 649	3205039	RP11-327L3.5	Non- coding(ncTranscript)	chr9	35971885	35971912	-
SEQ ID NO. 650	3205424	ZCCHC7	Non-coding(Intronic Antisense)	chr9	37193836	37193865	-
SEQ ID NO. 651	3212146	UBQLN1	Non-coding(UTR)	chr9	86275826	86276211	-
SEQ ID NO. 652	3212163	UBQLN1	Coding	chr9	86294773	86294919	-
SEQ ID NO. 653	3214671	IARS	Coding	chr9	94973097	94973125	-
SEQ ID NO. 654	3214699	IARS	Coding	chr9	95012528	95012559	-
SEQ ID NO. 655	3219683	C9orf5	Non-coding(UTR)	chr9	11177749 6	11177753 1	-
SEQ ID NO. 656	3219711	C9orf5	Coding	chr9	11182263 9	11182272 1	-
SEQ ID NO. 657	3219891	PTPN3	Non-coding(UTR)	chr9	11214054 5	11214061 0	-
SEQ ID NO. 658	3220159	TXN	Non-coding(UTR)	chr9	11300633 4	11300636 1	-
SEQ ID NO. 659	3222054	ATP6V1G1	Non-coding(Exonic Antisense)	chr9	11736047 9	11736062 4	-
SEQ ID NO. 660	3222984	RP11-442A13.1	Non- coding(ncTranscript)	chr9	12084534 9	12084539 1	-
SEQ ID NO. 661	3223876	RAB14	Non-coding(UTR)	chr9	12394311 0	12394346 4	-
SEQ ID NO. 662	3225580	PBX3	Non-coding(Intronic Antisense)	chr9	12852625 9	12852630 3	-
SEQ ID NO. 663	3226470	GOLGA2	Coding	chr9	13102856 7	13102859 5	-
SEQ ID NO. 664	3227646	UCK1	Non-coding(UTR)	chr9	13439920 2	13439922 9	-
SEQ ID NO. 665	3233387	C10orf18	Non-coding(UTR)	chr10	5805626	5805670	+
SEQ ID NO. 666	3234175	ATP5C1	Non-coding(UTR)	chr10	7849648	7849732	+
SEQ ID NO. 667	3235500	CDC123	Coding	chr10	12292460	12292553	+
SEQ ID NO. 668	3237000	VIM	Non-coding(UTR)	chr10	17279281	17279308	+
SEQ ID NO. 669	3237001	VIM	Non-coding(UTR)	chr10	17279361	17279398	+

SEQ ID NO. 670	3239927	ABI1	Non-coding(Exonic Antisense)	chr10	27036907	27037562	+
SEQ ID NO. 671	3239982	YME1L1	Non-coding(Exonic Antisense)	chr10	27399495	27399646	+
SEQ ID NO. 672	3240135	RAB18	Non-coding(UTR)	chr10	27828060	27828089	+
SEQ ID NO. 673	3240409	WAC	Coding	chr10	28899657	28899737	+
SEQ ID NO. 674	3240425	WAC	Non-coding(UTR)	chr10	28909409	28909439	+
SEQ ID NO. 675	3241499	KIF5B	Non-coding(Exonic Antisense)	chr10	32299937	32300224	+
SEQ ID NO. 676	3241506	KIF5B	Non-coding(Exonic Antisense)	chr10	32321635	32321697	+
SEQ ID NO. 677	3243292	HSD17B7P2	Non-coding(ncTranscript)	chr10	38667320	38667344	+
SEQ ID NO. 678	3250201	VPS26A	Non-coding(UTR)	chr10	70932578	70932609	+
SEQ ID NO. 679	3251409	DDIT4	Non-coding(UTR)	chr10	74035646	74035717	+
SEQ ID NO. 680	3252608	VDAC2	Non-coding(UTR)	chr10	76990904	76990928	+
SEQ ID NO. 681	3253445	RPS24	Coding	chr10	79795283	79795370	+
SEQ ID NO. 682	3253863	ZMIZ1	Non-coding(UTR)	chr10	81076140	81076245	+
SEQ ID NO. 683	3255269	GHITM	Non-coding(UTR)	chr10	85912224	85912254	+
SEQ ID NO. 684	3257404	KIF20B	Non-coding(UTR)	chr10	91534618	91534656	+
SEQ ID NO. 685	3258021	BTAFL	Non-coding(UTR)	chr10	93790008	93790053	+
SEQ ID NO. 686	3259678	LCOR	Non-coding(UTR)	chr10	98719067	98719119	+
SEQ ID NO. 687	3261550	GBF1	Coding	chr10	10401982 5	10401985 6	+
SEQ ID NO. 688	3262470	SLK	Coding	chr10	10577855 8	10577866 4	+
SEQ ID NO. 689	3263804	SMC3	Coding	chr10	11234232 1	11234239 5	+
SEQ ID NO. 690	3264697	TCF7L2	Coding	chr10	11491148 4	11491151 2	+
SEQ ID NO. 691	3264726	TCF7L2	Non-coding(UTR)	chr10	11492738 6	11492741 9	+
SEQ ID NO. 692	3275175	GDI2	Coding	chr10	5842593	5842621	-
SEQ ID NO. 693	3276455	KIN	Coding	chr10	7822227	7822261	-
SEQ ID NO. 694	3277709	UPF2	Coding	chr10	12041905	12041992	-
SEQ ID NO. 695	3279906	VIM	Non-coding(Exonic Antisense)	chr10	17279228	17279424	-
SEQ ID NO. 696	3280961	DNAJC1	Non-coding(Intronic)	chr10	22268411	22268452	-
SEQ ID NO. 697	3282022	ABI1	Non-coding(UTR)	chr10	27037123	27037168	-
SEQ ID NO. 698	3282170	ANKRD26	Coding	chr10	27342283	27342313	-
SEQ ID NO. 699	3282215	YME1L1	Non-coding(UTR)	chr10	27399405	27399460	-
SEQ ID NO. 700	3282220	YME1L1	Non-coding(UTR)	chr10	27400692	27400769	-
SEQ ID NO. 701	3282254	YME1L1	Coding	chr10	27434387	27434415	-
SEQ ID NO. 702	3284025	KIF5B	Coding	chr10	32326449	32326532	-
SEQ ID NO. 703	3284217	ITGB1	Coding	chr10	33218756	33218953	-
SEQ ID NO. 704	3284603	PARD3	Non-coding(UTR)	chr10	34400052	34400096	-
SEQ ID NO. 705	3284665	PARD3	Non-coding(UTR)	chr10	34601224	34601273	-
SEQ ID NO. 706	3294341	DNAJC9,MRPS16	Non-coding(UTR)	chr10	75008616	75008693	-
SEQ ID NO. 707	3294501	PPP3CB	Non-coding(UTR)	chr10	75196574	75196612	-

SEQ ID NO. 708	3298980	GLUD1	Non-coding(UTR)	chr10	88810786	88810903	-
SEQ ID NO. 709	3301222	PDLIM1	Non-coding(UTR)	chr10	96997343	96997375	-
SEQ ID NO. 710	3301703	ZNF518A	Non-coding(Exonic Antisense)	chr10	97919238	97919382	-
SEQ ID NO. 711	3301858	TM9SF3	Non-coding(UTR)	chr10	98277891	98277925	-
SEQ ID NO. 712	3301863	TM9SF3	Non-coding(UTR)	chr10	98281306	98281546	-
SEQ ID NO. 713	3302047	LCOR	Non-coding(Exonic Antisense)	chr10	98723611	98724126	-
SEQ ID NO. 714	3304013	MGEA5	Non-coding(UTR)	chr10	10354422 9	10354429 2	-
SEQ ID NO. 715	3304626	NT5C2	Non-coding(UTR)	chr10	10484782 0	10484790 4	-
SEQ ID NO. 716	3304652	NT5C2	Coding	chr10	10486099 2	10486108 2	-
SEQ ID NO. 717	3307940	ABLM1	Non-coding(UTR)	chr10	11619088 4	11619091 8	-
SEQ ID NO. 718	3308532	KIAA1598	Coding	chr10	11870001 9	11870007 0	-
SEQ ID NO. 719	3309267	EIF3A	Coding	chr10	12081645 1	12081655 2	-
SEQ ID NO. 720	3311304	FAM53B	Non-coding(Intronic)	chr10	12637008 0	12637012 1	-
SEQ ID NO. 721	3317557	AC131971.3	Non-coding(ncTranscript)	chr11	2965724	2965773	+
SEQ ID NO. 722	3325714	EIF3M	Coding	chr11	32623308	32623345	+
SEQ ID NO. 723	3325963	HIPK3	Non-coding(UTR)	chr11	33378433	33378548	+
SEQ ID NO. 724	3326246	CAPRIN1	Non-coding(UTR)	chr11	34122068	34122389	+
SEQ ID NO. 725	3326465	EHF	Non-coding(Intronic)	chr11	34644499	34644527	+
SEQ ID NO. 726	3329941	FNBP4	Non-coding(Exonic Antisense)	chr11	47738349	47738675	+
SEQ ID NO. 727	3331532	CTNND1,RP11-691N7.7,RP11-691N7.6	Non-coding(Intronic)	chr11	57530665	57530828	+
SEQ ID NO. 728	3331573	CTNND1	Coding	chr11	57577586	57577659	+
SEQ ID NO. 729	3331613	C11orf31,RP11-691N7.6	Non-coding(UTR)	chr11	57510340	57510456	+
SEQ ID NO. 730	3331614	C11orf31	Non-coding(UTR)	chr11	57510457	57510487	+
SEQ ID NO. 731	3333687	NXF1	Non-coding(Exonic Antisense)	chr11	62559649	62559673	+
SEQ ID NO. 732	3334162	OTUB1	Non-coding(UTR)	chr11	63765054	63765087	+
SEQ ID NO. 733	3334515	PRDX5	Non-coding(UTR)	chr11	64089219	64089254	+
SEQ ID NO. 734	3335173	MALAT1	Non-coding(ncTranscript)	chr11	65268541	65268772	+
SEQ ID NO. 735	3335176	MALAT1	Non-coding(ncTranscript)	chr11	65269878	65270060	+
SEQ ID NO. 736	3335178	MALAT1	Non-coding(ncTranscript)	chr11	65270566	65270941	+
SEQ ID NO. 737	3335179	MALAT1	Non-coding(ncTranscript)	chr11	65271104	65271134	+
SEQ ID NO. 738	3335181	MALAT1	Non-coding(ncTranscript)	chr11	65271308	65271537	+
SEQ ID NO. 739	3335182	MALAT1	Non-coding(ncTranscript)	chr11	65271622	65271671	+

SEQ ID NO. 740	3335187	MALAT1	Non-coding(ncTranscript)	chr11	65272277	65272473	+
SEQ ID NO. 741	3335188	MALAT1	Non-coding(ncTranscript)	chr11	65272569	65272745	+
SEQ ID NO. 742	3335189	MALAT1	Non-coding(ncTranscript)	chr11	65272758	65272932	+
SEQ ID NO. 743	3335191	MALAT1	Non-coding(ncTranscript)	chr11	65273073	65273133	+
SEQ ID NO. 744	3335231	NEAT1	Non-coding(ncTranscript)	chr11	65198362	65198453	+
SEQ ID NO. 745	3337724	PPP6R3	Non-coding(UTR)	chr11	68380696	68382033	+
SEQ ID NO. 746	3338618	CTTN	Non-coding(UTR)	chr11	70282540	70282638	+
SEQ ID NO. 747	3341466	C11orf67	Non-coding(UTR)	chr11	77583362	77583395	+
SEQ ID NO. 748	3341504	NDUFC2	Non-coding(Exonic Antisense)	chr11	77780928	77781047	+
SEQ ID NO. 749	3344853	KIAA1731	Non-coding(UTR)	chr11	93463465	93463495	+
SEQ ID NO. 750	3344889	C11orf54	Non-coding(UTR)	chr11	93496161	93496200	+
SEQ ID NO. 751	3345453	ENDOD1	Non-coding(UTR)	chr11	94865773	94865801	+
SEQ ID NO. 752	3347691	ATM	Coding	chr11	10813802 3	10813805 0	+
SEQ ID NO. 753	3352533	ARHGEF12	Coding	chr11	12027845 0	12027852 0	+
SEQ ID NO. 754	3352561	ARHGEF12	Coding	chr11	12031613 1	12031617 3	+
SEQ ID NO. 755	3352585	ARHGEF12	Coding	chr11	12033599 5	12033607 0	+
SEQ ID NO. 756	3352925	SC5DL	Coding	chr11	12117818 7	12117822 0	+
SEQ ID NO. 757	3354966	NAPIL1P1	Non-coding(ncTranscript)	chr11	12593816 3	12593820 3	+
SEQ ID NO. 758	3356173	APLP2	Non-coding(UTR)	chr11	13001387 7	13001413 3	+
SEQ ID NO. 759	3358364	PDDC1	Coding	chr11	767235	767266	-
SEQ ID NO. 760	3359382	KCNQ1	Non-coding(Intronic Antisense)	chr11	2717173	2717259	-
SEQ ID NO. 761	3362739	EIF4G2	Coding	chr11	10821117	10821149	-
SEQ ID NO. 762	3362742	EIF4G2	Coding	chr11	10821676	10821713	-
SEQ ID NO. 763	3362745	EIF4G2	Coding	chr11	10821991	10822194	-
SEQ ID NO. 764	3362763	EIF4G2	Non-coding(ncTranscript)	chr11	10825209	10825432	-
SEQ ID NO. 765	3362773	EIF4G2	Non-coding(ncTranscript)	chr11	10828449	10828622	-
SEQ ID NO. 766	3362943	ZBED5	Non-coding(UTR)	chr11	10874366	10874401	-
SEQ ID NO. 767	3363519	TEAD1	Non-coding(Exonic Antisense)	chr11	12965256	12965362	-
SEQ ID NO. 768	3363981	PSMA1	Non-coding(UTR)	chr11	14526493	14526586	-
SEQ ID NO. 769	3364729	RPS13	Coding	chr11	17096711	17096738	-
SEQ ID NO. 770	3364770	PIK3C2A	Coding	chr11	17112883	17112975	-
SEQ ID NO. 771	3364800	PIK3C2A	Non-coding(Intronic)	chr11	17150520	17150651	-
SEQ ID NO. 772	3368920	CAPRIN1	Non-coding(Exonic Antisense)	chr11	34121109	34121645	-
SEQ ID NO. 773	3371737	CKAP5	Coding	chr11	46780476	46780582	-
SEQ ID NO. 774	3372461	FNBP4	Non-coding(UTR)	chr11	47738082	47738123	-

SEQ ID NO. 775	3375309	CYBASC3	Non-coding(UTR)	chr11	61116287	61116314	-
SEQ ID NO. 776	3375752	AHNAK	Coding	chr11	62288763	62288870	-
SEQ ID NO. 777	3375863	MTA2	Non-coding(UTR)	chr11	62360703	62360739	-
SEQ ID NO. 778	3376090	RP11-831H9.16,HNRNP UL2	Coding	chr11	62482992	62483073	-
SEQ ID NO. 779	3376775	STIP1	Non-coding(Exonic Antisense)	chr11	63971039	63971068	-
SEQ ID NO. 780	3377457	ZNHIT2	Non-coding(UTR)	chr11	64883876	64883909	-
SEQ ID NO. 781	3377464	FAU	Non-coding(UTR)	chr11	64888125	64888152	-
SEQ ID NO. 782	3377621	NEAT1	Non-coding(Exonic Antisense)	chr11	65197863	65198674	-
SEQ ID NO. 783	3377623	NEAT1	Non-coding(Exonic Antisense)	chr11	65199459	65199866	-
SEQ ID NO. 784	3377625	NEAT1	Non-coding(Exonic Antisense)	chr11	65200367	65201041	-
SEQ ID NO. 785	3377632	NEAT1	Non-coding(Exonic Antisense)	chr11	65204836	65204978	-
SEQ ID NO. 786	3377633	NEAT1	Non-coding(Exonic Antisense)	chr11	65205053	65205164	-
SEQ ID NO. 787	3377659	MALAT1	Non-coding(Exonic Antisense)	chr11	65271852	65272483	-
SEQ ID NO. 788	3377660	MALAT1	Non-coding(Exonic Antisense)	chr11	65272684	65273443	-
SEQ ID NO. 789	3379122	RPL37P2	Non- coding(ncTranscript)	chr11	67450210	67450359	-
SEQ ID NO. 790	3379574	PPP6R3	Non-coding(Exonic Antisense)	chr11	68382665	68382760	-
SEQ ID NO. 791	3382981	RSF1	Coding	chr11	77383104	77383245	-
SEQ ID NO. 792	3382984	RSF1	Coding	chr11	77387892	77388043	-
SEQ ID NO. 793	3383148	NDUFC2	Coding	chr11	77780919	77780950	-
SEQ ID NO. 794	3383149	NDUFC2	Coding	chr11	77780951	77781016	-
SEQ ID NO. 795	3384489	CCDC90B	Coding	chr11	82984696	82984729	-
SEQ ID NO. 796	3384495	CCDC90B	Coding	chr11	82985729	82985759	-
SEQ ID NO. 797	3385045	SYTL2	Non-coding(UTR)	chr11	85406077	85406206	-
SEQ ID NO. 798	3385178	chr11:-85668255- 85668284	Non- coding(Intergenic)	chr11	85668255	85668284	-
SEQ ID NO. 799	3386816	TAF1D	Non-coding(UTR)	chr11	93463398	93463437	-
SEQ ID NO. 800	3387176	CWC15	Non- coding(ncTranscript)	chr11	94696550	94696588	-
SEQ ID NO. 801	3387436	FAM76B	Non- coding(ncTranscript)	chr11	95512328	95512401	-
SEQ ID NO. 802	3388633	TMEM123	Non-coding(UTR)	chr11	10226897 5	10226923 0	-
SEQ ID NO. 803	3393789	RP11-770J1.5	Non- coding(Intronic)	chr11	11826980 9	11826988 4	-
SEQ ID NO. 804	3394076	RPS25	Coding	chr11	11888818 6	11888821 0	-
SEQ ID NO. 805	3394529	PVRL1	Non- coding(Intronic)	chr11	11956112 0	11956115 7	-
SEQ ID NO. 806	3395420	HSPA8	Non-coding(UTR)	chr11	12292837 3	12292844 1	-
SEQ ID NO. 807	3395427	HSPA8	Coding	chr11	12292936 6	12292942 5	-
SEQ ID NO. 808	3400152	WNK1	Non-	chr12	997620	997790	+

			coding(Intronic)				
SEQ ID NO. 809	3402624	NCAPD2	Non-coding(UTR)	chr12	6640984	6641092	+
SEQ ID NO. 810	3402667	CHD4	Non-coding(Exonic Antisense)	chr12	6679340	6679405	+
SEQ ID NO. 811	3402720	COPS7A	Non-coding(UTR)	chr12	6840982	6841012	+
SEQ ID NO. 812	3406062	ATF7IP	Coding	chr12	14578178	14578407	+
SEQ ID NO. 813	3407177	PLEKHA5	Non-coding(Intronic)	chr12	19462808	19462891	+
SEQ ID NO. 814	3407275	AEBP2	Non-coding(UTR)	chr12	19673066	19673136	+
SEQ ID NO. 815	3409292	PPFIBP1	Coding	chr12	27845759	27845805	+
SEQ ID NO. 816	3412651	ANO6	Coding	chr12	45822918	45822963	+
SEQ ID NO. 817	3414226	TMBIM6	Non-coding(UTR)	chr12	50158602	50158686	+
SEQ ID NO. 818	3416068	PCBP2	Coding	chr12	53862564	53862605	+
SEQ ID NO. 819	3416501	HNRNPA1	Non-coding(UTR)	chr12	54678679	54679003	+
SEQ ID NO. 820	3417160	CDK2	Non-coding(UTR)	chr12	56366537	56366564	+
SEQ ID NO. 821	3417666	ATP5B	Non-coding(Exonic Antisense)	chr12	57032010	57032118	+
SEQ ID NO. 822	3418209	MARS	Non-coding(UTR)	chr12	57910381	57910412	+
SEQ ID NO. 823	3419262	MON2	Coding	chr12	62895382	62895464	+
SEQ ID NO. 824	3419622	RP11-415112.6	Non-coding(ncTranscript)	chr12	64216729	64216755	+
SEQ ID NO. 825	3421154	RAP1B	Non-coding(UTR)	chr12	69054240	69054272	+
SEQ ID NO. 826	3421223	NUP107	Non-coding(UTR)	chr12	69136358	69136416	+
SEQ ID NO. 827	3421350	MDM2	Non-coding(UTR)	chr12	69237819	69237941	+
SEQ ID NO. 828	3421492	CPSF6	Non-coding(UTR)	chr12	69663759	69663896	+
SEQ ID NO. 829	3421652	CCT2	Coding	chr12	69986764	69986823	+
SEQ ID NO. 830	3421668	CCT2	Non-coding(UTR)	chr12	69995199	69995277	+
SEQ ID NO. 831	3427811	TMPO	Non-coding(UTR)	chr12	98944024	98944069	+
SEQ ID NO. 832	3427812	TMPO	Non-coding(UTR)	chr12	98944093	98944124	+
SEQ ID NO. 833	3428711	CHPT1	Non-coding(UTR)	chr12	10212272 4	10212279 0	+
SEQ ID NO. 834	3428712	CHPT1	Non-coding(UTR)	chr12	10212280 1	10212283 2	+
SEQ ID NO. 835	3429794	KIAA1033	Coding	chr12	10553810 6	10553823 3	+
SEQ ID NO. 836	3430575	PWP1	Non-coding(UTR)	chr12	10810605 8	10810620 8	+
SEQ ID NO. 837	3431352	TCHP	Non-coding(UTR)	chr12	11035583 5	11035587 1	+
SEQ ID NO. 838	3431686	PPP1CC	Non-coding(Exonic Antisense)	chr12	11115775 1	11115852 7	+
SEQ ID NO. 839	3432171	MAPKAPK5	Non-coding(UTR)	chr12	11233115 5	11233122 7	+
SEQ ID NO. 840	3432352	PTPN11	Coding	chr12	11291547 2	11291552 6	+
SEQ ID NO. 841	3435860	TMED2	Coding	chr12	12407492 0	12407496 9	+
SEQ ID NO. 842	3435864	TMED2	Non-coding(UTR)	chr12	12408174 9	12408252 7	+
SEQ ID NO. 843	3436017	TCTN2	Non-coding(UTR)	chr12	12419282 7	12419290 6	+
SEQ ID NO. 844	3436264	ZNF664	Non-coding(UTR)	chr12	12449993 0	12449995 8	+

SEQ ID NO. 845	3438044	RAN	Non-coding(UTR)	chr12	13136069 9	13136073 7	+
SEQ ID NO. 846	3445545	PLBD1	Non-coding(UTR)	chr12	14656642	14656700	-
SEQ ID NO. 847	3445674	WBP11	Non-coding(UTR)	chr12	14939813	14939844	-
SEQ ID NO. 848	3445750	MGP	Coding	chr12	15035935	15035980	-
SEQ ID NO. 849	3446488	RP11-841C19.6	Non-coding(ncTranscript)	chr12	19610131	19610161	-
SEQ ID NO. 850	3446869	LDHB	Non-coding(UTR)	chr12	21788309	21788372	-
SEQ ID NO. 851	3446885	LDHB	Coding	chr12	21796891	21796927	-
SEQ ID NO. 852	3452256	SLC38A1	Coding	chr12	46594896	46594950	-
SEQ ID NO. 853	3452262	SLC38A1	Coding	chr12	46598093	46598153	-
SEQ ID NO. 854	3452324	SLC38A2	Non-coding(UTR)	chr12	46752021	46752132	-
SEQ ID NO. 855	3452349	SLC38A2	Non-coding(Intronic)	chr12	46759827	46760034	-
SEQ ID NO. 856	3454729	DAZAP2	Non-coding(Exonic Antisense)	chr12	51637043	51637499	-
SEQ ID NO. 857	3456599	SMUG1	Non-coding(UTR)	chr12	54575266	54575301	-
SEQ ID NO. 858	3457550	ANKRD52	Non-coding(UTR)	chr12	56631625	56631704	-
SEQ ID NO. 859	3458494	R3HDM2	Coding	chr12	57690242	57690331	-
SEQ ID NO. 860	3461302	RAP1B	Non-coding(Exonic Antisense)	chr12	69054237	69054275	-
SEQ ID NO. 861	3461431	CPSF6	Non-coding(Intronic Antisense)	chr12	69660063	69660148	-
SEQ ID NO. 862	3462710	KRR1	Coding	chr12	75895562	75895592	-
SEQ ID NO. 863	3462846	NAPIL1	Non-coding(UTR)	chr12	76440105	76440134	-
SEQ ID NO. 864	3462861	NAPIL1	Coding	chr12	76443241	76443271	-
SEQ ID NO. 865	3462867	NAPIL1	Coding	chr12	76447550	76447578	-
SEQ ID NO. 866	3462868	NAPIL1	Coding	chr12	76447613	76447637	-
SEQ ID NO. 867	3462884	NAPIL1	Coding	chr12	76462692	76462753	-
SEQ ID NO. 868	3462988	OSBPL8	Coding	chr12	76796488	76796545	-
SEQ ID NO. 869	3463596	PPP1R12A	Coding	chr12	80189429	80189478	-
SEQ ID NO. 870	3463603	PPP1R12A	Coding	chr12	80192274	80192363	-
SEQ ID NO. 871	3464009	CCDC59	Non-coding(UTR)	chr12	82746826	82746850	-
SEQ ID NO. 872	3465251	LUM	Non-coding(UTR)	chr12	91497423	91497674	-
SEQ ID NO. 873	3465252	LUM	Non-coding(UTR)	chr12	91497768	91497898	-
SEQ ID NO. 874	3465278	DCN	Non-coding(UTR)	chr12	91539375	91539470	-
SEQ ID NO. 875	3466861	CDK17	Coding	chr12	96692676	96692724	-
SEQ ID NO. 876	3467642	UHRF1BP1L	Non-coding(UTR)	chr12	10043087 3	10043090 3	-
SEQ ID NO. 877	3468015	ARL1	Coding	chr12	10178941 8	10178944 8	-
SEQ ID NO. 878	3469369	APPL2	Coding	chr12	10560193 6	10560196 8	-
SEQ ID NO. 879	3471177	ATP2A2	Non-coding(Exonic Antisense)	chr12	11076080 4	11076087 7	-
SEQ ID NO. 880	3471377	PPP1CC	Coding	chr12	11115774 8	11115800 8	-
SEQ ID NO. 881	3471379	PPP1CC	Non-coding(UTR)	chr12	11115830 4	11115880 5	-
SEQ ID NO. 882	3472092	RPL6	Coding	chr12	11284375 6	11284378 8	-

SEQ ID NO. 883	3473482	FBXO21	Non-coding(UTR)	chr12	11758162 3	11758171 6	-
SEQ ID NO. 884	3474494	COX6A1	Non-coding(Exonic Antisense)	chr12	12087838 4	12087840 8	-
SEQ ID NO. 885	3474937	ANAPC5	Non-coding(UTR)	chr12	12174618 7	12174621 9	-
SEQ ID NO. 886	3475623	CLIP1	Coding	chr12	12281287 4	12281296 0	-
SEQ ID NO. 887	3475737	RSRC2	Coding	chr12	12300346 7	12300355 2	-
SEQ ID NO. 888	3476294	RP11-338K17.8	Non-coding(ncTranscript)	chr12	12419288 1	12419291 1	-
SEQ ID NO. 889	3480098	PSPC1	Non-coding(Intronic Antisense)	chr13	20288513	20288582	+
SEQ ID NO. 890	3480100	PSPC1	Non-coding(Intronic Antisense)	chr13	20289439	20289587	+
SEQ ID NO. 891	3480173	ZMYM2	Coding	chr13	20625705	20625738	+
SEQ ID NO. 892	3480201	ZMYM2	Coding	chr13	20660015	20660105	+
SEQ ID NO. 893	3480203	ZMYM2	Non-coding(UTR)	chr13	20660684	20660800	+
SEQ ID NO. 894	3480685	MRP63	Non-coding(UTR)	chr13	21751366	21751479	+
SEQ ID NO. 895	3480856	RP11-149B7.3	Non-coding(Intronic)	chr13	21949514	21949608	+
SEQ ID NO. 896	3481480	MIPEP	Non-coding(Exonic Antisense)	chr13	24304376	24304486	+
SEQ ID NO. 897	3482124	PABPC3	Coding	chr13	25671061	25671086	+
SEQ ID NO. 898	3482915	GTF3A	Non-coding(UTR)	chr13	28009740	28009770	+
SEQ ID NO. 899	3482916	GTF3A	Non-coding(UTR)	chr13	28009783	28009821	+
SEQ ID NO. 900	3483215	EEF1A1P3	Non-coding(ncTranscript)	chr13	28790004	28790032	+
SEQ ID NO. 901	3484743	N4BP2L2	Non-coding(Exonic Antisense)	chr13	33091777	33091983	+
SEQ ID NO. 902	3484750	N4BP2L2	Non-coding(Intronic Antisense)	chr13	33100404	33100549	+
SEQ ID NO. 903	3484756	N4BP2L2	Non-coding(Intronic Antisense)	chr13	33108310	33108639	+
SEQ ID NO. 904	3484762	N4BP2L2	Non-coding(Exonic Antisense)	chr13	33110810	33111128	+
SEQ ID NO. 905	3485891	EXOSC8	Non-coding(UTR)	chr13	37583482	37583513	+
SEQ ID NO. 906	3489010	ITM2B	Non-coding(UTR)	chr13	48835362	48835441	+
SEQ ID NO. 907	3489011	ITM2B	Non-coding(UTR)	chr13	48835461	48835490	+
SEQ ID NO. 908	3494193	LMO7	Coding	chr13	76378428	76378461	+
SEQ ID NO. 909	3497656	MBNL2	Coding	chr13	98043613	98043670	+
SEQ ID NO. 910	3497658	MBNL2	Non-coding(UTR)	chr13	98046231	98046350	+
SEQ ID NO. 911	3497823	IPO5	Coding	chr13	98658384	98658526	+
SEQ ID NO. 912	3498048	FARP1	Non-coding(UTR)	chr13	99101993	99102022	+
SEQ ID NO. 913	3498445	UBAC2	Non-coding(UTR)	chr13	10003853 7	10003862 8	+
SEQ ID NO. 914	3498523	TM9SF2	Coding	chr13	10018172 9	10018175 9	+
SEQ ID NO. 915	3498537	TM9SF2	Coding	chr13	10019382 8	10019385 9	+
SEQ ID NO. 916	3498977	PCCA	Non-coding(UTR)	chr13	10118261 3	10118266 6	+
SEQ ID NO. 917	3499545	TPP2	Coding	chr13	10332864 7	10332872 7	+

SEQ ID NO. 918	3500408	ARGLU1	Non-coding(Exonic Antisense)	chr13	10721088 9	10721122 6	+
SEQ ID NO. 919	3501216	COL4A1	Non-coding(Exonic Antisense)	chr13	11080136 6	11080252 1	+
SEQ ID NO. 920	3501217	COL4A1	Non-coding(Exonic Antisense)	chr13	11080255 7	11080262 2	+
SEQ ID NO. 921	3501555	ANKRD10,RP11-120J20.2	Non-coding(Intronic Antisense)	chr13	11155012 6	11155026 3	+
SEQ ID NO. 922	3503211	CDC16	Non-coding(UTR)	chr13	11503804 9	11503814 1	+
SEQ ID NO. 923	3505453	MIPEP	Non-coding(UTR)	chr13	24304376	24304406	-
SEQ ID NO. 924	3506941	GTF3A	Non-coding(Exonic Antisense)	chr13	28009271	28009319	-
SEQ ID NO. 925	3508731	N4BP2L2	Non-coding(UTR)	chr13	33091139	33091739	-
SEQ ID NO. 926	3508732	N4BP2L2	Non-coding(UTR)	chr13	33091797	33091904	-
SEQ ID NO. 927	3508761	N4BP2L2	Non-coding(UTR)	chr13	33112755	33112784	-
SEQ ID NO. 928	3509912	FAM48A	Non-coding(UTR)	chr13	37583472	37583574	-
SEQ ID NO. 929	3509913	FAM48A	Non-coding(UTR)	chr13	37583672	37583718	-
SEQ ID NO. 930	3510070	POSTN	Coding	chr13	38137470	38137505	-
SEQ ID NO. 931	3510382	C13orf23	Coding	chr13	39591637	39591681	-
SEQ ID NO. 932	3512558	TPT1	Coding	chr13	45914196	45914249	-
SEQ ID NO. 933	3513710	FNDC3A	Non-coding(Intronic Antisense)	chr13	49743307	49743495	-
SEQ ID NO. 934	3517677	KLF5	Non-coding(Intronic Antisense)	chr13	73639022	73639125	-
SEQ ID NO. 935	3517683	KLF5	Non-coding(Exonic Antisense)	chr13	73651458	73651592	-
SEQ ID NO. 936	3518501	MYCBP2	Non-coding(UTR)	chr13	77618823	77618901	-
SEQ ID NO. 937	3519136	RBM26	Coding	chr13	79908511	79908559	-
SEQ ID NO. 938	3521962	MBNL2	Non-coding(Exonic Antisense)	chr13	98046114	98046289	-
SEQ ID NO. 939	3524627	ARGLU1	Coding	chr13	10720941 6	10720947 8	-
SEQ ID NO. 940	3524630	ARGLU1	Non-coding(ncTranscript)	chr13	10720998 0	10721097 8	-
SEQ ID NO. 941	3524631	ARGLU1	Non-coding(Intronic)	chr13	10721104 7	10721110 3	-
SEQ ID NO. 942	3525314	COL4A1	Non-coding(UTR)	chr13	11080132 3	11080139 1	-
SEQ ID NO. 943	3525317	COL4A1	Non-coding(UTR)	chr13	11080200 9	11080204 9	-
SEQ ID NO. 944	3525320	COL4A1	Non-coding(UTR)	chr13	11080265 9	11080270 3	-
SEQ ID NO. 945	3525547	CARS2	Non-coding(UTR)	chr13	11129377 0	11129380 1	-
SEQ ID NO. 946	3525702	ANKRD10	Coding	chr13	11154645 9	11154650 9	-
SEQ ID NO. 947	3525704	ANKRD10	Non-coding(Intronic)	chr13	11154656 2	11154661 5	-
SEQ ID NO. 948	3525710	ANKRD10,RP11-120J20.2	Non-coding(Intronic)	chr13	11155045 8	11155079 8	-
SEQ ID NO. 949	3526383	PCID2	Non-coding(UTR)	chr13	11383214 5	11383217 3	-
SEQ ID NO. 950	3527530	PNP	Non-coding(UTR)	chr14	20945198	20945234	+

SEQ ID NO. 951	3528208	chr14+:22219841-22219898	Non-coding(Intergenic)	chr14	22219841	22219898	+
SEQ ID NO. 952	3529094	PABPN1	Coding	chr14	23793174	23793252	+
SEQ ID NO. 953	3531094	SCFD1	Non-coding(UTR)	chr14	31204908	31204938	+
SEQ ID NO. 954	3531491	ARHGAP5	Non-coding(UTR)	chr14	32559824	32559857	+
SEQ ID NO. 955	3533452	PNN	Coding	chr14	39649881	39650067	+
SEQ ID NO. 956	3534950	KLHDC2	Non-coding(UTR)	chr14	50249686	50249814	+
SEQ ID NO. 957	3535917	PSMC6	Non-coding(UTR)	chr14	53194359	53194390	+
SEQ ID NO. 958	3536669	MAPK11P1L	Non-coding(Intronic)	chr14	55521391	55521561	+
SEQ ID NO. 959	3536745	LGALS3	Non-coding(UTR)	chr14	55612028	55612094	+
SEQ ID NO. 960	3536931	KTN1	Coding	chr14	56079043	56079161	+
SEQ ID NO. 961	3536934	KTN1	Coding	chr14	56084718	56084852	+
SEQ ID NO. 962	3536938	KTN1	Coding	chr14	56094637	56094745	+
SEQ ID NO. 963	3536943	KTN1	Coding	chr14	56103204	56103241	+
SEQ ID NO. 964	3536948	KTN1	Coding	chr14	56107121	56107158	+
SEQ ID NO. 965	3536949	KTN1	Coding	chr14	56107654	56107685	+
SEQ ID NO. 966	3536951	KTN1	Coding	chr14	56108443	56108473	+
SEQ ID NO. 967	3536992	KTN1	Coding	chr14	56138319	56138348	+
SEQ ID NO. 968	3536994	KTN1	Coding	chr14	56138552	56138592	+
SEQ ID NO. 969	3537787	PSMA3	Non-coding(Intronic)	chr14	58736530	58737088	+
SEQ ID NO. 970	3537795	PSMA3	Non-coding(UTR)	chr14	58738645	58738676	+
SEQ ID NO. 971	3537796	PSMA3	Non-coding(UTR)	chr14	58738678	58738711	+
SEQ ID NO. 972	3539104	HIF1A	Non-coding(UTR)	chr14	62213835	62214927	+
SEQ ID NO. 973	3539877	SYNE2	Coding	chr14	64608087	64608217	+
SEQ ID NO. 974	3543929	ZNF410	Non-coding(UTR)	chr14	74398925	74398960	+
SEQ ID NO. 975	3544473	TMED10	Non-coding(Exonic Antisense)	chr14	75600819	75601043	+
SEQ ID NO. 976	3544890	C14orf179	Non-coding(UTR)	chr14	76549980	76550008	+
SEQ ID NO. 977	3545534	C14orf156	Coding	chr14	78183857	78183893	+
SEQ ID NO. 978	3549043	GOLGA5	Coding	chr14	93273192	93273296	+
SEQ ID NO. 979	3550451	PAPOLA	Non-coding(UTR)	chr14	97031464	97031570	+
SEQ ID NO. 980	3550453	PAPOLA	Non-coding(UTR)	chr14	97032230	97033320	+
SEQ ID NO. 981	3550455	PAPOLA	Non-coding(UTR)	chr14	97033359	97033402	+
SEQ ID NO. 982	3552937	DYNC1H1	Coding	chr14	10250066 2	10250072 1	+
SEQ ID NO. 983	3552938	DYNC1H1	Coding	chr14	10250073 7	10250078 8	+
SEQ ID NO. 984	3556198	HNRNPC	Non-coding(Intronic)	chr14	21711637	21711681	-
SEQ ID NO. 985	3556224	HNRNPC	Non-coding(Intronic)	chr14	21715371	21715455	-
SEQ ID NO. 986	3556278	HNRNPC	Non-coding(Intronic)	chr14	21724188	21724274	-
SEQ ID NO. 987	3556420	METTL3	Non-coding(UTR)	chr14	21966312	21966385	-
SEQ ID NO. 988	3558292	SDR39U1	Non-coding(UTR)	chr14	24909005	24909035	-
SEQ ID NO. 989	3559519	STRN3	Coding	chr14	31388179	31388221	-

SEQ ID NO. 990	3559556	STRN3	Non-coding(Intronic)	chr14	31494313	31494364	-
SEQ ID NO. 991	3562436	chr14-:43624685-43624788	Non-coding(Intergenic)	chr14	43624685	43624788	-
SEQ ID NO. 992	3563349	KLHDC2	Non-coding(Exonic Antisense)	chr14	50249079	50249817	-
SEQ ID NO. 993	3563970	MAP4K5	Coding	chr14	50930810	50930847	-
SEQ ID NO. 994	3566596	C14orf37	Non-coding(Intronic)	chr14	58732098	58732170	-
SEQ ID NO. 995	3566603	C14orf37	Non-coding(Intronic)	chr14	58738232	58738695	-
SEQ ID NO. 996	3566648	C14orf37	Non-coding(Intronic)	chr14	58745642	58745917	-
SEQ ID NO. 997	3566657	TIMM9	Non-coding(UTR)	chr14	58875404	58875448	-
SEQ ID NO. 998	3566993	JKAMP	Non-coding(Exonic Antisense)	chr14	59971339	59971383	-
SEQ ID NO. 999	3569346	PIGH	Non-coding(UTR)	chr14	68056048	68056249	-
SEQ ID NO. 1000	3569757	ZFP36L1	Non-coding(UTR)	chr14	69254887	69255185	-
SEQ ID NO. 1001	3569759	ZFP36L1	Non-coding(UTR)	chr14	69255920	69256161	-
SEQ ID NO. 1002	3569819	ACTN1	Non-coding(UTR)	chr14	69341254	69341307	-
SEQ ID NO. 1003	3570456	COX16	Non-coding(UTR)	chr14	70792813	70792939	-
SEQ ID NO. 1004	3573155	SPTLC2	Non-coding(UTR)	chr14	77978379	77978415	-
SEQ ID NO. 1005	3576551	SMEK1	Non-coding(UTR)	chr14	91924009	91924055	-
SEQ ID NO. 1006	3576567	SMEK1	Coding	chr14	91929149	91929176	-
SEQ ID NO. 1007	3576712	TC2N	Non-coding(UTR)	chr14	92248983	92249066	-
SEQ ID NO. 1008	3576730	TC2N	Coding	chr14	92278706	92278866	-
SEQ ID NO. 1009	3576939	NDUFB1	Non-coding(UTR)	chr14	92582506	92582534	-
SEQ ID NO. 1010	3576940	NDUFB1	Coding	chr14	92582542	92582573	-
SEQ ID NO. 1011	3577874	DICER1	Non-coding(UTR)	chr14	95556680	95556725	-
SEQ ID NO. 1012	3577898	DICER1	Coding	chr14	95573945	95574043	-
SEQ ID NO. 1013	3577911	DICER1	Coding	chr14	95583981	95584063	-
SEQ ID NO. 1014	3578431	PAPOLA	Non-coding(Exonic Antisense)	chr14	97032931	97033315	-
SEQ ID NO. 1015	3580188	HSP90AA1	Coding	chr14	10254957 5	10254960 8	-
SEQ ID NO. 1016	3580204	HSP90AA1	Coding	chr14	10255234 4	10255246 1	-
SEQ ID NO. 1017	3580587	CDC42BPB	Coding	chr14	10347847 1	10347850 3	-
SEQ ID NO. 1018	3580953	C14orf2	Non-coding(UTR)	chr14	10437887 4	10437890 2	-
SEQ ID NO. 1019	3589660	SRP14	Non-coding(Exonic Antisense)	chr15	40327993	40328048	+
SEQ ID NO. 1020	3590159	ZFYVE19	Non-coding(UTR)	chr15	41106724	41106757	+
SEQ ID NO. 1021	3590352	AC012652.1	Coding	chr15	41554969	41555013	+
SEQ ID NO. 1022	3591851	CASC4	Coding	chr15	44615169	44615209	+
SEQ ID NO. 1023	3591858	CASC4	Coding	chr15	44624186	44624269	+
SEQ ID NO. 1024	3591985	EIF3J	Non-coding(UTR)	chr15	44853865	44853895	+
SEQ ID NO. 1025	3592046	B2M	Non-coding(UTR)	chr15	45010076	45010140	+
SEQ ID NO. 1026	3592047	B2M	Non-coding(UTR)	chr15	45010149	45010306	+

SEQ ID NO. 1027	3592395	SPATA5L1	Non-coding(UTR)	chr15	45713540	45713570	+
SEQ ID NO. 1028	3593171	DUT	Non-coding(UTR)	chr15	48634495	48634524	+
SEQ ID NO. 1029	3594101	TMOD3	Non-coding(UTR)	chr15	52203518	52204078	+
SEQ ID NO. 1030	3595811	ADAM10	Non-coding(Exonic Antisense)	chr15	58936101	58936173	+
SEQ ID NO. 1031	3595872	FAM63B	Coding	chr15	59146705	59146747	+
SEQ ID NO. 1032	3596235	RPS3AP6	Non-coding(ncTranscript)	chr15	60061048	60061073	+
SEQ ID NO. 1033	3597406	TPM1	Coding	chr15	63363335	63363371	+
SEQ ID NO. 1034	3597468	RPS27L	Non-coding(Exonic Antisense)	chr15	63448685	63448718	+
SEQ ID NO. 1035	3597671	USP3	Non-coding(Intronic)	chr15	63863224	63863330	+
SEQ ID NO. 1036	3598717	RPL4	Non-coding(Exonic Antisense)	chr15	66792495	66792526	+
SEQ ID NO. 1037	3599449	FEM1B	Non-coding(UTR)	chr15	68588065	68588154	+
SEQ ID NO. 1038	3602509	UBE2Q2	Coding	chr15	76165783	76165852	+
SEQ ID NO. 1039	3605249	BTBD1	Non-coding(Exonic Antisense)	chr15	83685253	83685989	+
SEQ ID NO. 1040	3606117	PDE8A	Coding	chr15	85660888	85661024	+
SEQ ID NO. 1041	3606409	AKAP13	Coding	chr15	86228040	86228071	+
SEQ ID NO. 1042	3608201	IQGAP1	Non-coding(UTR)	chr15	91043485	91044457	+
SEQ ID NO. 1043	3609166	chr15+:93441269-93441296	Non-coding(Intergenic)	chr15	93441269	93441296	+
SEQ ID NO. 1044	3615597	TJPI	Coding	chr15	29993813	29993887	-
SEQ ID NO. 1045	3615604	TJPI	Coding	chr15	30000769	30001056	-
SEQ ID NO. 1046	3615659	TJPI	Coding	chr15	30064323	30064365	-
SEQ ID NO. 1047	3615989	MTMR10	Non-coding(UTR)	chr15	31231241	31231375	-
SEQ ID NO. 1048	3621014	RP11-473C18.1	Non-coding(ncTranscript)	chr15	43408169	43408193	-
SEQ ID NO. 1049	3623329	SECISBP2L	Non-coding(UTR)	chr15	49280903	49280978	-
SEQ ID NO. 1050	3624199	DMXL2	Coding	chr15	51828398	51828822	-
SEQ ID NO. 1051	3624533	MYO5C	Coding	chr15	52511971	52512014	-
SEQ ID NO. 1052	3624702	ARPP19	Non-coding(UTR)	chr15	52842989	52843020	-
SEQ ID NO. 1053	3625565	NEDD4	Coding	chr15	56144633	56144664	-
SEQ ID NO. 1054	3626570	ADAM10	Coding	chr15	58889656	58889693	-
SEQ ID NO. 1055	3626585	ADAM10	Coding	chr15	58913702	58913746	-
SEQ ID NO. 1056	3626730	SLTM	Coding	chr15	59186138	59186165	-
SEQ ID NO. 1057	3627045	GTF2A2	Non-coding(UTR)	chr15	59931155	59931320	-
SEQ ID NO. 1058	3628011	VPS13C	Coding	chr15	62223290	62223365	-
SEQ ID NO. 1059	3628052	VPS13C	Coding	chr15	62277071	62277198	-
SEQ ID NO. 1060	3628057	VPS13C	Coding	chr15	62299573	62299653	-
SEQ ID NO. 1061	3628471	RPS27L	Non-coding(UTR)	chr15	63446088	63446161	-
SEQ ID NO. 1062	3628924	FAM96A	Non-coding(UTR)	chr15	64364822	64365114	-
SEQ ID NO. 1063	3630191	RPL4	Coding	chr15	66793304	66793342	-
SEQ ID NO. 1064	3631414	UACA	Coding	chr15	70963386	70963413	-
SEQ ID NO. 1065	3632170	HEXA	Non-coding(UTR)	chr15	72636242	72636274	-

SEQ ID NO. 1066	3633110	ULK3	Non-coding(UTR)	chr15	75128476	75128503	-
SEQ ID NO. 1067	3633223	COX5A	Non-coding(UTR)	chr15	75212727	75212760	-
SEQ ID NO. 1068	3633226	COX5A	Coding	chr15	75219110	75219150	-
SEQ ID NO. 1069	3634074	TSPAN3	Non-coding(UTR)	chr15	77338406	77338505	-
SEQ ID NO. 1070	3643958	IFT140	Non-coding(Intronic Antisense)	chr16	1605465	1605543	+
SEQ ID NO. 1071	3645267	SRRM2	Coding	chr16	2809141	2809173	+
SEQ ID NO. 1072	3645314	SRRM2	Coding	chr16	2821320	2821352	+
SEQ ID NO. 1073	3645591	AC108134.1	Non-coding(UTR)	chr16	3082688	3082721	+
SEQ ID NO. 1074	3647535	PMM2	Non-coding(UTR)	chr16	8943097	8943149	+
SEQ ID NO. 1075	3648373	GSPT1	Non-coding(Exonic Antisense)	chr16	11965914	11966088	+
SEQ ID NO. 1076	3651472	THUMPDI	Non-coding(Exonic Antisense)	chr16	20745035	20745197	+
SEQ ID NO. 1077	3653349	RBBP6	Coding	chr16	24572962	24573036	+
SEQ ID NO. 1078	3653673	LCMT1	Non-coding(UTR)	chr16	25189503	25189534	+
SEQ ID NO. 1079	3655101	ATP2A1	Coding	chr16	28915742	28915771	+
SEQ ID NO. 1080	3658610	chr16+:34329397-34329426	Non-coding(Intergenic)	chr16	34329397	34329426	+
SEQ ID NO. 1081	3659201	PHKB	Coding	chr16	47674954	47674997	+
SEQ ID NO. 1082	3659319	LONP2	Coding	chr16	48295347	48295482	+
SEQ ID NO. 1083	3660917	CHD9	Coding	chr16	53256556	53256653	+
SEQ ID NO. 1084	3660927	CHD9	Coding	chr16	53269097	53269212	+
SEQ ID NO. 1085	3665635	CTCF	Non-coding(UTR)	chr16	67673041	67673073	+
SEQ ID NO. 1086	3666111	NFATC3	Non-coding(UTR)	chr16	68262372	68262449	+
SEQ ID NO. 1087	3666869	NFAT5	Non-coding(UTR)	chr16	69738402	69738519	+
SEQ ID NO. 1088	3668992	CFDP1	Non-coding(Exonic Antisense)	chr16	75445798	75445831	+
SEQ ID NO. 1089	3671113	HSD17B2	Non-coding(UTR)	chr16	82132049	82132091	+
SEQ ID NO. 1090	3677863	CREBBP	Coding	chr16	3832776	3832921	-
SEQ ID NO. 1091	3679601	USP7	Coding	chr16	9002201	9002297	-
SEQ ID NO. 1092	3683054	SMG1	Non-coding(UTR)	chr16	18816225	18816252	-
SEQ ID NO. 1093	3685080	USP31	Coding	chr16	23113641	23113757	-
SEQ ID NO. 1094	3687262	CDIPT	Non-coding(UTR)	chr16	29869699	29869726	-
SEQ ID NO. 1095	3687792	DCTPP1	Non-coding(UTR)	chr16	30435055	30435119	-
SEQ ID NO. 1096	3690089	DNAJA2	Non-coding(UTR)	chr16	46990519	46990548	-
SEQ ID NO. 1097	3692857	AMFR	Non-coding(UTR)	chr16	56395400	56395436	-
SEQ ID NO. 1098	3693546	CSNK2A2	Non-coding(Intronic)	chr16	58197918	58197957	-
SEQ ID NO. 1099	3693711	CNOT1	Coding	chr16	58580290	58580397	-
SEQ ID NO. 1100	3693737	CNOT1	Coding	chr16	58612675	58612766	-
SEQ ID NO. 1101	3693746	CNOT1	Coding	chr16	58621684	58621741	-
SEQ ID NO. 1102	3696670	NFAT5	Non-coding(Exonic Antisense)	chr16	69735142	69735208	-
SEQ ID NO. 1103	3697925	KIAA0174	Non-coding(Intronic Antisense)	chr16	71956876	71957154	-
SEQ ID NO. 1104	3699559	CFDP1	Coding	chr16	75445743	75445831	-

SEQ ID NO. 1105	3701588	chr16:-81422942-81422986	Non-coding(Intergenic)	chr16	81422942	81422986	-
SEQ ID NO. 1106	3705531	GLOD4	Non-coding(Exonic Antisense)	chr17	662604	662642	+
SEQ ID NO. 1107	3707211	PSMB6	Non-coding(UTR)	chr17	4701718	4701745	+
SEQ ID NO. 1108	3708006	TXNDC17	Non-coding(UTR)	chr17	6546346	6546406	+
SEQ ID NO. 1109	3709275	CHD3	Coding	chr17	7801317	7801402	+
SEQ ID NO. 1110	3710735	MAP2K4	Non-coding(UTR)	chr17	12044587	12044730	+
SEQ ID NO. 1111	3714102	ALDH3A2	Non-coding(UTR)	chr17	19578985	19579015	+
SEQ ID NO. 1112	3715142	WSB1	Non-coding(UTR)	chr17	25639650	25640711	+
SEQ ID NO. 1113	3715434	NLK	Non-coding(UTR)	chr17	26523346	26523402	+
SEQ ID NO. 1114	3716021	NUFIP2	Non-coding(Exonic Antisense)	chr17	27584395	27585068	+
SEQ ID NO. 1115	3716674	SUZ12P	Non-coding(ncTranscript)	chr17	29061929	29061961	+
SEQ ID NO. 1116	3716757	CRLF3	Non-coding(Exonic Antisense)	chr17	29109181	29110227	+
SEQ ID NO. 1117	3717647	ZNF207	Coding	chr17	30688498	30688534	+
SEQ ID NO. 1118	3717681	ZNF207	Non-coding(UTR)	chr17	30703222	30704388	+
SEQ ID NO. 1119	3717684	ZNF207	Non-coding(UTR)	chr17	30707067	30707332	+
SEQ ID NO. 1120	3718837	TAF15	Non-coding(UTR)	chr17	34174149	34174181	+
SEQ ID NO. 1121	3719123	ZNHIT3	Non-coding(UTR)	chr17	34851541	34851568	+
SEQ ID NO. 1122	3720778	MSL1	Non-coding(UTR)	chr17	38292930	38292996	+
SEQ ID NO. 1123	3720990	TOP2A	Non-coding(Exonic Antisense)	chr17	38551732	38551789	+
SEQ ID NO. 1124	3722990	GPATCH8	Non-coding(Exonic Antisense)	chr17	42544382	42544480	+
SEQ ID NO. 1125	3723305	NMT1	Non-coding(UTR)	chr17	43183284	43183313	+
SEQ ID NO. 1126	3726811	LUC7L3	Non-coding(UTR)	chr17	48829837	48829910	+
SEQ ID NO. 1127	3728316	chr17+:55758561-55758676	Non-coding(Intergenic)	chr17	55758561	55758676	+
SEQ ID NO. 1128	3729194	CLTC	Coding	chr17	57743467	57743600	+
SEQ ID NO. 1129	3729227	CLTC	Non-coding(UTR)	chr17	57771220	57771523	+
SEQ ID NO. 1130	3732475	BPTF	Coding	chr17	65905772	65905867	+
SEQ ID NO. 1131	3732477	BPTF	Coding	chr17	65906998	65907253	+
SEQ ID NO. 1132	3732479	BPTF	Coding	chr17	65908073	65908103	+
SEQ ID NO. 1133	3732480	BPTF	Coding	chr17	65908105	65908152	+
SEQ ID NO. 1134	3734754	NUP85	Non-coding(UTR)	chr17	73231775	73231813	+
SEQ ID NO. 1135	3734863	KIAA0195	Non-coding(UTR)	chr17	73496070	73496097	+
SEQ ID NO. 1136	3737304	RNF213	Coding	chr17	78286838	78286959	+
SEQ ID NO. 1137	3737985	ACTG1	Non-coding(Exonic Antisense)	chr17	79477609	79477714	+
SEQ ID NO. 1138	3738300	ANAPC11	Non-coding(UTR)	chr17	79858058	79858126	+
SEQ ID NO. 1139	3739125	FN3KRP	Non-coding(UTR)	chr17	80685795	80685853	+
SEQ ID NO. 1140	3739523	RPH3AL	Non-coding(UTR)	chr17	62308	62338	-
SEQ ID NO. 1141	3740129	YWHAE	Non-coding(UTR)	chr17	1247864	1247932	-
SEQ ID NO. 1142	3740130	YWHAE	Non-coding(UTR)	chr17	1247937	1247962	-

SEQ ID NO. 1143	3744423	RPL26	Coding	chr17	8280885	8280918	-
SEQ ID NO. 1144	3746953	NCOR1	Coding	chr17	16041478	16041507	-
SEQ ID NO. 1145	3746967	NCOR1	Coding	chr17	16055260	16055312	-
SEQ ID NO. 1146	3747223	UBB,AC093484.6	Non-coding(Exonic Antisense)	chr17	16285909	16285939	-
SEQ ID NO. 1147	3748953	ALDH3A2	Non-coding(Exonic Antisense)	chr17	19578961	19579027	-
SEQ ID NO. 1148	3750786	SPAG5	Non-coding(UTR)	chr17	26904610	26904639	-
SEQ ID NO. 1149	3752711	MYO1D	Non-coding(UTR)	chr17	30819629	30819657	-
SEQ ID NO. 1150	3754530	ACACA	Coding	chr17	35538144	35538267	-
SEQ ID NO. 1151	3754741	DDX52	Non-coding(UTR)	chr17	35974190	35974305	-
SEQ ID NO. 1152	3756204	TOP2A	Coding	chr17	38552572	38552698	-
SEQ ID NO. 1153	3759590	PLCD3	Non-coding(UTR)	chr17	43189041	43189118	-
SEQ ID NO. 1154	3760197	KIAA1267	Non-coding(Intronic)	chr17	44229099	44229138	-
SEQ ID NO. 1155	3761752	ZNF652	Non-coding(Intronic)	chr17	47371242	47371658	-
SEQ ID NO. 1156	3762575	SPAG9	Coding	chr17	49098531	49098605	-
SEQ ID NO. 1157	3764121	SRSF1	Non-coding(UTR)	chr17	56080881	56081053	-
SEQ ID NO. 1158	3764125	SRSF1	Non-coding(UTR)	chr17	56082334	56082402	-
SEQ ID NO. 1159	3764127	SRSF1	Non-coding(UTR)	chr17	56082659	56082766	-
SEQ ID NO. 1160	3764884	PTRH2	Non-coding(UTR)	chr17	57774692	57774781	-
SEQ ID NO. 1161	3764921	TMEM49	Non-coding(Intronic Antisense)	chr17	57916786	57917067	-
SEQ ID NO. 1162	3765738	MED13	Coding	chr17	60072562	60072692	-
SEQ ID NO. 1163	3765761	MED13	Coding	chr17	60112841	60112917	-
SEQ ID NO. 1164	3765767	MED13	Coding	chr17	60129924	60130040	-
SEQ ID NO. 1165	3766896	DDX5	Coding	chr17	62496067	62496341	-
SEQ ID NO. 1166	3768039	HELZ	Coding	chr17	65110458	65110513	-
SEQ ID NO. 1167	3768121	PSMD12	Coding	chr17	65343474	65343574	-
SEQ ID NO. 1168	3768258	BPTF	Non-coding(Exonic Antisense)	chr17	65900527	65900955	-
SEQ ID NO. 1169	3769780	SLC39A11	Non-coding(UTR)	chr17	70642090	70642140	-
SEQ ID NO. 1170	3770244	RPL38	Non-coding(Exonic Antisense)	chr17	72205375	72205399	-
SEQ ID NO. 1171	3770564	ATP5H	Non-coding(UTR)	chr17	73034985	73035011	-
SEQ ID NO. 1172	3770565	ATP5H	Coding	chr17	73035028	73035125	-
SEQ ID NO. 1173	3770746	AC011933.1,GRB2	Non-coding(UTR)	chr17	73314175	73314221	-
SEQ ID NO. 1174	3771039	WBP2	Non-coding(UTR)	chr17	73841911	73841967	-
SEQ ID NO. 1175	3771094	TRIM65	Non-coding(UTR)	chr17	73885066	73885127	-
SEQ ID NO. 1176	3771337	EXOC7	Non-coding(UTR)	chr17	74077120	74077149	-
SEQ ID NO. 1177	3776189	SMCHD1	Coding	chr18	2694604	2694691	+
SEQ ID NO. 1178	3776219	SMCHD1	Coding	chr18	2729285	2729399	+
SEQ ID NO. 1179	3776236	SMCHD1	Coding	chr18	2760668	2760737	+
SEQ ID NO. 1180	3776446	MYL12A	Non-coding(UTR)	chr18	3256140	3256174	+
SEQ ID NO. 1181	3776461	MYL12B	Non-coding(UTR)	chr18	3277954	3277997	+
SEQ ID NO. 1182	3778266	ANKRD12	Coding	chr18	9208709	9208785	+

SEQ ID NO. 1183	3778629	VAPA	Non-coding(UTR)	chr18	9954382	9954461	+
SEQ ID NO. 1184	3778630	VAPA	Non-coding(UTR)	chr18	9954599	9954786	+
SEQ ID NO. 1185	3779850	CEP192	Coding	chr18	13042229	13042330	+
SEQ ID NO. 1186	3781686	RIOK3	Coding	chr18	21043933	21043978	+
SEQ ID NO. 1187	3781689	RIOK3	Coding	chr18	21044236	21044277	+
SEQ ID NO. 1188	3783364	DSC2	Non-coding(Exonic Antisense)	chr18	28645981	28646054	+
SEQ ID NO. 1189	3787934	ACAA2	Non-coding(Exonic Antisense)	chr18	47309906	47309967	+
SEQ ID NO. 1190	3789817	NARS	Non-coding(Exonic Antisense)	chr18	55267984	55268652	+
SEQ ID NO. 1191	3795442	HSBP1L1	Non-coding(Intronic)	chr18	77726702	77726744	+
SEQ ID NO. 1192	3796554	MYL12A	Non-coding(Exonic Antisense)	chr18	3253291	3253318	-
SEQ ID NO. 1193	3798470	VAPA	Non-coding(Exonic Antisense)	chr18	9954382	9954673	-
SEQ ID NO. 1194	3800623	ROCK1	Non-coding(UTR)	chr18	18529985	18530009	-
SEQ ID NO. 1195	3804170	RPRD1A	Coding	chr18	33605587	33605638	-
SEQ ID NO. 1196	3804202	SLC39A6	Non-coding(UTR)	chr18	33689334	33689516	-
SEQ ID NO. 1197	3806255	ATP5A1	Non-coding(UTR)	chr18	43664158	43664210	-
SEQ ID NO. 1198	3806256	ATP5A1	Coding	chr18	43664262	43664314	-
SEQ ID NO. 1199	3807476	C18orf32	Non-coding(UTR)	chr18	47008582	47008661	-
SEQ ID NO. 1200	3807570	ACAA2	Non-coding(UTR)	chr18	47310009	47310100	-
SEQ ID NO. 1201	3807629	MYO5B	Coding	chr18	47405315	47405362	-
SEQ ID NO. 1202	3808602	MBD2	Non-coding(UTR)	chr18	51681249	51681283	-
SEQ ID NO. 1203	3809343	TXNL1	Non-coding(UTR)	chr18	54270079	54270117	-
SEQ ID NO. 1204	3809673	NARS	Non-coding(UTR)	chr18	55267919	55268047	-
SEQ ID NO. 1205	3809834	ATP8B1	Coding	chr18	55319275	55319401	-
SEQ ID NO. 1206	3813298	CYB5A	Non-coding(UTR)	chr18	71920626	71920814	-
SEQ ID NO. 1207	3813299	CYB5A	Coding	chr18	71920819	71920861	-
SEQ ID NO. 1208	3815669	CIRBP	Non-coding(UTR)	chr19	1273068	1273101	+
SEQ ID NO. 1209	3816402	OAZ1	Non-coding(UTR)	chr19	2273334	2273365	+
SEQ ID NO. 1210	3820658	SLC44A2	Non-coding(UTR)	chr19	10755194	10755225	+
SEQ ID NO. 1211	3820705	ILF3	Non-coding(UTR)	chr19	10796289	10796443	+
SEQ ID NO. 1212	3820721	ILF3	Non-coding(UTR)	chr19	10803046	10803074	+
SEQ ID NO. 1213	3820752	QTRT1	Non-coding(UTR)	chr19	10823990	10824021	+
SEQ ID NO. 1214	3822055	CALR	Coding	chr19	13050910	13050952	+
SEQ ID NO. 1215	3825428	UPF1	Non-coding(UTR)	chr19	18978996	18979030	+
SEQ ID NO. 1216	3829039	PDCD5	Coding	chr19	33078171	33078199	+
SEQ ID NO. 1217	3829810	UBA2	Non-coding(UTR)	chr19	34960742	34960773	+
SEQ ID NO. 1218	3831128	WDR62	Non-coding(UTR)	chr19	36595963	36596001	+
SEQ ID NO. 1219	3831280	ZNF146	Non-coding(UTR)	chr19	36729581	36729635	+
SEQ ID NO. 1220	3835412	AC084219.1	Non-coding(Intronic Antisense)	chr19	44593725	44593755	+
SEQ ID NO. 1221	3837493	GLTSCR2	Coding	chr19	48259945	48259974	+
SEQ ID NO. 1222	3838612	RPS11	Coding	chr19	50000777	50000849	+

SEQ ID NO. 1223	3838790	SCAF1	Coding	chr19	50161065	50161099	+
SEQ ID NO. 1224	3840344	ZNF808	Coding	chr19	53056690	53056733	+
SEQ ID NO. 1225	3841271	CNOT3	Coding	chr19	54647403	54647485	+
SEQ ID NO. 1226	3843668	ZNF587	Non-coding(UTR)	chr19	58375789	58375813	+
SEQ ID NO. 1227	3845710	AP3D1	Non-coding(UTR)	chr19	2100996	2101030	-
SEQ ID NO. 1228	3846115	AES	Non-coding(UTR)	chr19	3052943	3053123	-
SEQ ID NO. 1229	3846291	C19orf29	Coding	chr19	3610671	3610894	-
SEQ ID NO. 1230	3846561	EEF2	Coding	chr19	3981383	3981450	-
SEQ ID NO. 1231	3846784	UBXN6	Non-coding(UTR)	chr19	4445025	4445062	-
SEQ ID NO. 1232	3847357	LONPI	Non-coding(UTR)	chr19	5691860	5691889	-
SEQ ID NO. 1233	3849774	chr19::9671051-9671089	Non-coding(Intergenic)	chr19	9671051	9671089	-
SEQ ID NO. 1234	3849776	chr19::9671562-9671894	Non-coding(Intergenic)	chr19	9671562	9671894	-
SEQ ID NO. 1235	3850502	AC011475.2	Non-coding(UTR)	chr19	10762558	10762816	-
SEQ ID NO. 1236	3851604	DHPS	Non-coding(UTR)	chr19	12786536	12786648	-
SEQ ID NO. 1237	3851902	CALR	Non-coding(Exonic Antisense)	chr19	13050901	13050963	-
SEQ ID NO. 1238	3854371	MRPL34	Non-coding(Exonic Antisense)	chr19	17417528	17417592	-
SEQ ID NO. 1239	3855101	C19orf50	Non-coding(Exonic Antisense)	chr19	18680064	18680145	-
SEQ ID NO. 1240	3856046	chr19::19900909-19901230	Non-coding(Intergenic)	chr19	19900909	19901230	-
SEQ ID NO. 1241	3857120	ZNF91	Coding	chr19	23545201	23545314	-
SEQ ID NO. 1242	3857884	CTC-448F2.1	Non-coding(ncTranscript)	chr19	30447703	30447769	-
SEQ ID NO. 1243	3862168	FBL	Non-coding(UTR)	chr19	40325111	40325177	-
SEQ ID NO. 1244	3862473	AKT2	Non-coding(UTR)	chr19	40737024	40737088	-
SEQ ID NO. 1245	3867099	KDELRI	Coding	chr19	48887509	48887616	-
SEQ ID NO. 1246	3869659	ZNF83	Coding	chr19	53117048	53117096	-
SEQ ID NO. 1247	3869971	ZNF320	Non-coding(Intronic)	chr19	53428386	53428415	-
SEQ ID NO. 1248	3870593	TSEN34	Non-coding(Exonic Antisense)	chr19	54697315	54697498	-
SEQ ID NO. 1249	3872197	chr19::57806251-57806283	Non-coding(Intergenic)	chr19	57806251	57806283	-
SEQ ID NO. 1250	3872208	chr19::57815574-57815765	Non-coding(Intergenic)	chr19	57815574	57815765	-
SEQ ID NO. 1251	3874114	PTPRA	Coding	chr20	2967446	2967484	+
SEQ ID NO. 1252	3874280	ITPA	Non-coding(UTR)	chr20	3204423	3204497	+
SEQ ID NO. 1253	3875278	CRLS1	Non-coding(UTR)	chr20	6018636	6018682	+
SEQ ID NO. 1254	3878051	DSTN	Non-coding(UTR)	chr20	17587973	17588000	+
SEQ ID NO. 1255	3878053	DSTN	Non-coding(UTR)	chr20	17588715	17588815	+
SEQ ID NO. 1256	3879490	XRN2	Coding	chr20	21314576	21314607	+
SEQ ID NO. 1257	3881731	TM9SF4	Non-coding(UTR)	chr20	30755023	30755057	+

SEQ ID NO. 1258	3881914	ASXL1	Coding	chr20	31025076	31025127	+
SEQ ID NO. 1259	3882710	CHMP4B	Non-coding(UTR)	chr20	32442082	32442156	+
SEQ ID NO. 1260	3882867	ITCH	Coding	chr20	32996498	32996582	+
SEQ ID NO. 1261	3883424	ERGIC3	Coding	chr20	34144991	34145020	+
SEQ ID NO. 1262	3883533	RBM39	Non-coding(Exonic Antisense)	chr20	34326915	34327120	+
SEQ ID NO. 1263	3883537	RBM39	Non-coding(Exonic Antisense)	chr20	34328294	34328562	+
SEQ ID NO. 1264	3883987	C20orf24	Non-coding(UTR)	chr20	35240820	35240910	+
SEQ ID NO. 1265	3884147	RPN2	Non-coding(UTR)	chr20	35869831	35869970	+
SEQ ID NO. 1266	3884334	CTNBNB1	Non-coding(Intronic)	chr20	36345727	36345755	+
SEQ ID NO. 1267	3884673	RALGAPB	Coding	chr20	37153421	37153451	+
SEQ ID NO. 1268	3884709	RALGAPB	Non-coding(Intronic)	chr20	37196054	37196487	+
SEQ ID NO. 1269	3885711	LPIN3	Non-coding(UTR)	chr20	39989186	39989218	+
SEQ ID NO. 1270	3886656	YWHAB	Non-coding(UTR)	chr20	43535667	43535846	+
SEQ ID NO. 1271	3886907	PIGT	Coding	chr20	44049169	44049270	+
SEQ ID NO. 1272	3887661	NCOA3	Coding	chr20	46251022	46251063	+
SEQ ID NO. 1273	3888081	ARFGEF2	Coding	chr20	47587735	47587844	+
SEQ ID NO. 1274	3888182	CSEIL	Non-coding(UTR)	chr20	47713056	47713100	+
SEQ ID NO. 1275	3888253	DDX27	Non-coding(UTR)	chr20	47860499	47860571	+
SEQ ID NO. 1276	3888289	NCRNA00275	Non-coding(ncTranscript)	chr20	47905708	47905750	+
SEQ ID NO. 1277	3888494	RNF114	Coding	chr20	48568679	48568737	+
SEQ ID NO. 1278	3888936	DPM1	Non-coding(Exonic Antisense)	chr20	49551434	49551628	+
SEQ ID NO. 1279	3889140	ATP9A	Non-coding(Exonic Antisense)	chr20	50213352	50214559	+
SEQ ID NO. 1280	3889782	PFDN4	Non-coding(UTR)	chr20	52835863	52835936	+
SEQ ID NO. 1281	3891221	GNAS	Coding	chr20	57470705	57470737	+
SEQ ID NO. 1282	3891257	GNAS	Non-coding(UTR)	chr20	57485961	57486084	+
SEQ ID NO. 1283	3892672	RPS21	Coding	chr20	60962934	60962970	+
SEQ ID NO. 1284	3894074	PCMTD2	Non-coding(UTR)	chr20	62907409	62907536	+
SEQ ID NO. 1285	3894508	RP4-545L17.7.PSMF1	Non-coding(Exonic Antisense)	chr20	1147867	1148150	-
SEQ ID NO. 1286	3894602	FKBP1A	Non-coding(UTR)	chr20	1349656	1349683	-
SEQ ID NO. 1287	3895000	SNRPB	Non-coding(UTR)	chr20	2442340	2442373	-
SEQ ID NO. 1288	3896202	PCNA	Non-coding(UTR)	chr20	5095649	5095739	-
SEQ ID NO. 1289	3898306	SEL1L2	Non-coding(ncTranscript)	chr20	13908674	13908801	-
SEQ ID NO. 1290	3901666	C20orf3	Non-coding(UTR)	chr20	24943603	24943644	-
SEQ ID NO. 1291	3902984	CDK5RAP1	Non-coding(UTR)	chr20	31946673	31946723	-
SEQ ID NO. 1292	3903290	EIF2S2	Non-coding(UTR)	chr20	32677392	32677416	-
SEQ ID NO. 1293	3904028	chr20:-34146096-34146124	Non-coding(Intergenic)	chr20	34146096	34146124	-
SEQ ID NO. 1294	3904029	FER1L4.AL389875.1	Non-coding(UTR)	chr20	34146544	34146635	-
SEQ ID NO. 1295	3904255	RBM39	Coding	chr20	34317239	34317283	-

SEQ ID NO. 1296	3904257	RBM39	Coding	chr20	34317385	34317431	-
SEQ ID NO. 1297	3904276	RBM39	Non-coding(ncTranscript)	chr20	34327102	34327246	-
SEQ ID NO. 1298	3904281	RBM39	Non-coding(ncTranscript)	chr20	34328529	34328635	-
SEQ ID NO. 1299	3906196	CHD6	Coding	chr20	40083276	40083334	-
SEQ ID NO. 1300	3907788	SLC35C2	Non-coding(UTR)	chr20	44978376	44978406	-
SEQ ID NO. 1301	3908789	STAU1	Non-coding(UTR)	chr20	47729881	47730036	-
SEQ ID NO. 1302	3909376	ADNP	Non-coding(Intronic)	chr20	49531572	49531914	-
SEQ ID NO. 1303	3911474	VAPB	Non-coding(Exonic Antisense)	chr20	57020464	57020567	-
SEQ ID NO. 1304	3911564	STX16,RP11-261P9.5	Non-coding(Exonic Antisense)	chr20	57252189	57252339	-
SEQ ID NO. 1305	3911706	GNAS	Non-coding(Exonic Antisense)	chr20	57470704	57470737	-
SEQ ID NO. 1306	3911738	GNAS	Non-coding(Exonic Antisense)	chr20	57485755	57485993	-
SEQ ID NO. 1307	3911801	ATP5E	Coding	chr20	57605376	57605455	-
SEQ ID NO. 1308	3911815	SLMO2	Non-coding(UTR)	chr20	57608287	57608462	-
SEQ ID NO. 1309	3913564	DIDO1	Coding	chr20	61536907	61536953	-
SEQ ID NO. 1310	3915125	USP25	Coding	chr21	17202860	17202896	+
SEQ ID NO. 1311	3917896	SOD1	Non-coding(UTR)	chr21	33041107	33041153	+
SEQ ID NO. 1312	3918586	IFNARI	Coding	chr21	34715912	34715982	+
SEQ ID NO. 1313	3918651	IFNGR2	Non-coding(Intronic)	chr21	34804818	34804850	+
SEQ ID NO. 1314	3918723	SON	Coding	chr21	34927046	34927291	+
SEQ ID NO. 1315	3918734	SON	Coding	chr21	34931543	34931653	+
SEQ ID NO. 1316	3919024	MRPS6	Non-coding(UTR)	chr21	35515288	35515318	+
SEQ ID NO. 1317	3920401	TTC3	Coding	chr21	38466361	38466389	+
SEQ ID NO. 1318	3920456	TTC3	Coding	chr21	38555078	38555116	+
SEQ ID NO. 1319	3920487	TTC3	Non-coding(UTR)	chr21	38574158	38575271	+
SEQ ID NO. 1320	3922023	FAM3B	Coding	chr21	42717624	42717654	+
SEQ ID NO. 1321	3922993	PKNOX1	Coding	chr21	44445014	44445052	+
SEQ ID NO. 1322	3924758	DIP2A	Non-coding(UTR)	chr21	47989552	47989586	+
SEQ ID NO. 1323	3925641	NRIP1	Non-coding(UTR)	chr21	16333709	16333966	-
SEQ ID NO. 1324	3926090	CXADR	Non-coding(Exonic Antisense)	chr21	18940282	18940430	-
SEQ ID NO. 1325	3927180	ATP5J	Non-coding(UTR)	chr21	27096864	27096895	-
SEQ ID NO. 1326	3927228	APP	Non-coding(UTR)	chr21	27253137	27253203	-
SEQ ID NO. 1327	3927229	APP	Non-coding(UTR)	chr21	27253256	27253928	-
SEQ ID NO. 1328	3928670	TIAM1	Coding	chr21	32490760	32490873	-
SEQ ID NO. 1329	3929943	ATP5O,AP000304.12	Coding	chr21	35279673	35279756	-
SEQ ID NO. 1330	3934699	PTTG1IP	Coding	chr21	46271504	46271534	-
SEQ ID NO. 1331	3935246	LSS,AP001468.2	Non-coding(UTR)	chr21	47609049	47609184	-
SEQ ID NO. 1332	3935301	MCM3AP	Non-coding(UTR)	chr21	47655078	47655109	-
SEQ ID NO. 1333	3936897	MRPL40	Non-coding(UTR)	chr22	19423556	19423583	+
SEQ ID NO. 1334	3939407	SMARCB1	Non-coding(UTR)	chr22	24176665	24176692	+

SEQ ID NO. 1335	3942668	TUG1	Non-coding(ncTranscript)	chr22	31372108	31372178	+
SEQ ID NO. 1336	3945331	DDX17	Non-coding(Exonic Antisense)	chr22	38881930	38881962	+
SEQ ID NO. 1337	3945370	CBY1	Non-coding(UTR)	chr22	39069809	39069840	+
SEQ ID NO. 1338	3946374	ADSL,RP5-1042K10.13	Coding	chr22	40762454	40762500	+
SEQ ID NO. 1339	3946589	XPNPEP3,RBX1	Non-coding(UTR)	chr22	41368540	41368588	+
SEQ ID NO. 1340	3946677	EP300	Coding	chr22	41566534	41566575	+
SEQ ID NO. 1341	3953804	PI4KA	Coding	chr22	21161651	21161735	-
SEQ ID NO. 1342	3956591	XBP1	Non-coding(UTR)	chr22	29190562	29190620	-
SEQ ID NO. 1343	3957262	SF3A1	Non-coding(UTR)	chr22	30730186	30730263	-
SEQ ID NO. 1344	3959259	RBFOX2	Non-coding(Intronic)	chr22	36334548	36334674	-
SEQ ID NO. 1345	3959453	MYH9	Non-coding(UTR)	chr22	36677371	36677403	-
SEQ ID NO. 1346	3960634	DDX17	Non-coding(UTR)	chr22	38880599	38880760	-
SEQ ID NO. 1347	3961482	ADSL,RP5-1042K10.13	Non-coding(Exonic Antisense)	chr22	40762473	40762565	-
SEQ ID NO. 1348	3962268	NDUFA6	Non-coding(UTR)	chr22	42482152	42482181	-
SEQ ID NO. 1349	3962596	AL049757.3	Non-coding(ncTranscript)	chr22	43172653	43172678	-
SEQ ID NO. 1350	3969510	OFD1	Coding	chrX	13787185	13787222	+
SEQ ID NO. 1351	3969511	OFD1	Non-coding(UTR)	chrX	13787252	13787317	+
SEQ ID NO. 1352	3970894	PDHA1	Coding	chrX	19377802	19377939	+
SEQ ID NO. 1353	3974757	USP9X	Coding	chrX	41043776	41043927	+
SEQ ID NO. 1354	3974789	USP9X	Coding	chrX	41082579	41082644	+
SEQ ID NO. 1355	3981154	OGT	Coding	chrX	70783211	70783337	+
SEQ ID NO. 1356	3981752	NCRNA00183	Non-coding(ncTranscript)	chrX	73219683	73219763	+
SEQ ID NO. 1357	3981906	MIR374AHG	Non-coding(Intronic Antisense)	chrX	73491128	73491377	+
SEQ ID NO. 1358	3982421	COX7B	Non-coding(UTR)	chrX	77160796	77160836	+
SEQ ID NO. 1359	3985558	NGFRAP1	Non-coding(UTR)	chrX	10263293 0	10263296 8	+
SEQ ID NO. 1360	3985635	TCEAL4	Non-coding(UTR)	chrX	10284227 4	10284242 2	+
SEQ ID NO. 1361	3986857	COL4A5	Non-coding(UTR)	chrX	10793998 8	10794072 4	+
SEQ ID NO. 1362	3987532	ALG13	Non-coding(UTR)	chrX	11100374 7	11100385 4	+
SEQ ID NO. 1363	3988214	RP11-27G9.1	Non-coding(ncTranscript)	chrX	11609742 3	11609747 4	+
SEQ ID NO. 1364	3989205	MCTS1	Non-coding(UTR)	chrX	11974613 3	11974622 4	+
SEQ ID NO. 1365	3989770	STAG2	Coding	chrX	12319698 5	12319705 3	+
SEQ ID NO. 1366	3991722	HPRT1	Non-coding(UTR)	chrX	13363451 7	13363466 0	+
SEQ ID NO. 1367	3993347	CDR1	Non-coding(Exonic Antisense)	chrX	13986584 5	13986591 1	+
SEQ ID NO. 1368	3993349	CDR1	Non-coding(Exonic Antisense)	chrX	13986645 6	13986650 4	+
SEQ ID NO. 1369	4004822	DYNLT3	Non-coding(UTR)	chrX	37698478	37698663	-
SEQ ID NO. 1370	4007593	SLC35A2	Non-coding(UTR)	chrX	48760908	48760940	-

SEQ ID NO. 1371	4009318	HUWE1	Non-coding(UTR)	chrX	53559796	53559831	-
SEQ ID NO. 1372	4009451	HUWE1	Coding	chrX	53654361	53654464	-
SEQ ID NO. 1373	4011604	IGBP1	Non-coding(Exonic Antisense)	chrX	69385996	69386136	-
SEQ ID NO. 1374	4011967	OGT	Non-coding(Exonic Antisense)	chrX	70765919	70766276	-
SEQ ID NO. 1375	4012169	RPS4X	Coding	chrX	71495419	71495459	-
SEQ ID NO. 1376	4012627	MIR374AHG	Non-coding(Intronic)	chrX	73473183	73473384	-
SEQ ID NO. 1377	4012632	MIR374AHG	Non-coding(Intronic)	chrX	73477308	73477534	-
SEQ ID NO. 1378	4012759	chrX:-73429697-73429730	Non-coding(Intergenic)	chrX	73429697	73429730	-
SEQ ID NO. 1379	4013274	ATRX	Coding	chrX	76937974	76938071	-
SEQ ID NO. 1380	4013282	ATRX	Coding	chrX	76939315	76939355	-
SEQ ID NO. 1381	4015535	HNRNPA1P27	Non-coding(ncTranscript)	chrX	10014321	10014325	-
SEQ ID NO. 1382	4016549	TCEAL4	Non-coding(Exonic Antisense)	chrX	10284227	10284239	-
SEQ ID NO. 1383	4016573	MORF4L2	Non-coding(UTR)	chrX	10293049	10293052	-
SEQ ID NO. 1384	4019367	PGRMC1	Non-coding(Exonic Antisense)	chrX	11837754	11837812	-
SEQ ID NO. 1385	4019418	CXorf56	Non-coding(UTR)	chrX	11867216	11867218	-
SEQ ID NO. 1386	4019610	NDUFA1	Non-coding(Exonic Antisense)	chrX	11901052	11901060	-
SEQ ID NO. 1387	4020462	THOC2	Non-coding(Intronic)	chrX	12275208	12275238	-
SEQ ID NO. 1388	4024375	CDR1	Non-coding(UTR)	chrX	13986554	13986557	-
SEQ ID NO. 1389	4024376	CDR1	Non-coding(UTR)	chrX	13986564	13986573	-
SEQ ID NO. 1390	4024377	CDR1	Coding	chrX	13986582	13986585	-
SEQ ID NO. 1391	4024378	CDR1	Coding	chrX	13986588	13986592	-
SEQ ID NO. 1392	4024379	CDR1	Coding	chrX	13986593	13986597	-
SEQ ID NO. 1393	4030986	NCRNA00185	Non-coding(Intronic Antisense)	chrY	21152685	21153560	+
SEQ ID NO. 1394	4034997	DDX3Y	Non-coding(Exonic Antisense)	chrY	15030062	15030179	-
SEQ ID NO. 1395	4035834	NCRNA00185	Non-coding(Intronic)	chrY	21152548	21152618	-
SEQ ID NO. 1396	4035835	NCRNA00185	Non-coding(Intronic)	chrY	21152684	21152813	-
SEQ ID NO. 1397	4035838	NCRNA00185	Non-coding(Intronic)	chrY	21154041	21154065	-
SEQ ID NO. 1398	4035839	CD24P4	Non-coding(ncTranscript)	chrY	21154244	21154350	-
SEQ ID NO. 1399	4040526	ANAPC11	Non-coding(UTR)	chr17	79858058	79858126	+
SEQ ID NO. 1400	4041367	P4HB	Coding	chr17	79813023	79813113	-
SEQ ID NO. 1401	4041822	DVL1	Non-coding(Exonic Antisense)	chr1	1270724	1270751	+
SEQ ID NO. 1402	4043125	MIA3	Non-coding(UTR)	chr1	22283916	22283919	+
SEQ ID NO. 1403	4044199	MRPL20	Non-coding(UTR)	chr1	1337315	1337437	-

SEQ ID NO. 1404	4044413	PNRC2	Non-coding(Exonic Antisense)	chr1	24289858	24289900	-
SEQ ID NO. 1405	4047577	RNF4	Non-coding(UTR)	chr4	2517539	2517569	+
SEQ ID NO. 1406	4052399	SNRNP35	Non-coding(ncTranscript)	chr12	12395676 5	12395689 0	+
SEQ ID NO. 1407	4055295	ATRX	Coding	chrX	76939261	76939355	-
SEQ ID NO. 1408	4055302	ATRX	Coding	chrX	76937669	76938071	-
SEQ ID NO. 1409	2720180	LAP3	Non-coding(UTR)	chr4	17609540	17609571	+
SEQ ID NO. 1410	2347642	SLC44A3	Coding	chr1	95294064	95294116	+
SEQ ID NO. 1411	2395344	RERE	Non-coding(Intronic)	chr1	8626188	8626254	-
SEQ ID NO. 1412	2397069	DHRS3	Non-coding(Intronic)	chr1	12675869	12676175	-
SEQ ID NO. 1413	2430377	AL122007.1	Non-coding(Exonic Antisense)	chr1	11840613 1	11840665 2	-
SEQ ID NO. 1414	2448270	TPR	Coding	chr1	18630226 4	18630248 4	-
SEQ ID NO. 1415	2553581	EML6	Non-coding(Exonic Antisense)	chr2	55198361	55198412	-
SEQ ID NO. 1416	2600700	EPHA4	Non-coding(UTR)	chr2	22229019 3	22229066 4	-
SEQ ID NO. 1417	2624519	CACNA1D	Coding	chr3	53839020	53839140	+
SEQ ID NO. 1418	2651846	GPR160	Non-coding(Intronic)	chr3	16976024 1	16976028 0	+
SEQ ID NO. 1419	2682441	RYBP	Coding	chr3	72428191	72428278	-
SEQ ID NO. 1420	2704512	MECOM	Non-coding(Intronic)	chr3	16903990 6	16904002 9	-
SEQ ID NO. 1421	2704702	MECOM	Non-coding(Intronic)	chr3	16924543 4	16924547 9	-
SEQ ID NO. 1422	2902832	C2,XXbac-BPG116M5.17,CFB	Coding	chr6	31912504	31912533	+
SEQ ID NO. 1423	2918558	RP11-98I9.4	Non-coding(Intronic)	chr6	99874240	99874405	+
SEQ ID NO. 1424	3031661	ABP1	Non-coding(Intronic)	chr7	15054894 4	15054900 9	+
SEQ ID NO. 1425	3212761	AGTPBP1	Non-coding(Intronic)	chr9	88262440	88262595	-
SEQ ID NO. 1426	3268183	TACC2	Non-coding(Intronic)	chr10	12399565 1	12399569 2	+
SEQ ID NO. 1427	3472753	chr12:-115105073-115105114	Non-coding(Intergenic)	chr12	11510507 3	11510511 4	-
SEQ ID NO. 1428	3501557	ANKRD10	Non-coding(Intronic Antisense)	chr13	11155167 1	11155200 5	+
SEQ ID NO. 1429	3543621	NUMB	Non-coding(Intronic Antisense)	chr14	73924866	73924936	+
SEQ ID NO. 1430	3551833	YY1	Non-coding(Intronic)	chr14	10073182 8	10073263 4	+
SEQ ID NO. 1431	3562041	PNN	Non-coding(Exonic Antisense)	chr14	39650300	39650740	-
SEQ ID NO. 1432	3661099	RBL2	Coding	chr16	53514479	53514525	+
SEQ ID NO. 1433	3667907	DHX38	Coding	chr16	72131593	72131680	+
SEQ ID NO. 1434	3701840	MPHOSPH6	Non-coding(UTR)	chr16	82182086	82182335	-
SEQ ID NO. 1435	3840609	ZNF347	Non-coding(Intronic Antisense)	chr19	53653851	53653898	+
SEQ ID NO. 1436	3889144	ATP9A	Non-coding(Exonic Antisense)	chr20	50217042	50217277	+

SEQ ID NO. 1437	3889625	TSHZ2,AL354993 .1	Coding	chr20	52105591	52105740	+
SEQ ID NO. 1438	3897081	PLCB1	Non-coding(Intronic Antisense)	chr20	8419858	8419910	-
SEQ ID NO. 1439	3902441	DEFB121	Coding	chr20	29993912	29993949	-
SEQ ID NO. 1440	4026042	GABRE	Non- coding(ncTranscript)	chrX	15114041 4	15114060 7	-

1,425 prognostic markers for MIBC recurrence. For each marker, the Affymetrix Probeset ID, associated gene, category and chromosomal location based on hg19 human genome version is indicated.

TABLE 17

Term	Benjamini P-value	Term	Benjamini P-value
GO:0016071~mRNA metabolic process	0.000000	GO:0006259~DNA metabolic process	0.01
GO:0006396~RNA processing	0.000000	GO:0051276~chromosome organization	0.01
GO:0006412~translation	0.000000	GO:0009201~ribonucleoside triphosphate biosynthetic process	0.01
GO:0006397~mRNA processing	0.000000	GO:0006754~ATP biosynthetic process	0.01
GO:0046907~intracellular transport	0.000000	GO:0006406~mRNA export from nucleus	0.02
GO:0008380~RNA splicing	0.000000	GO:0046034~ATP metabolic process	0.02
GO:0006414~translational elongation	0.000000	GO:0006325~chromatin organization	0.02
GO:0015031~protein transport	0.000004	GO:0006511~ubiquitin-dependent protein catabolic process	0.02
GO:0045184~establishment of protein localization	0.000006	GO:0009199~ribonucleoside triphosphate metabolic process	0.03
GO:0006403~RNA localization	0.000005	GO:0043631~RNA polyadenylation	0.03
GO:0051168~nuclear export	0.000007	GO:0016568~chromatin modification	0.03
GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	0.000007	GO:0006119~oxidative phosphorylation	0.03
GO:0000375~RNA splicing, via transesterification reactions	0.000007	GO:0009206~purine ribonucleoside triphosphate biosynthetic process	0.03
GO:0000398~nuclear mRNA splicing, via spliceosome	0.000007	GO:0006974~response to DNA damage stimulus	0.03
GO:0008104~protein localization	0.000007	GO:0010605~negative regulation of macromolecule metabolic process	0.03
GO:0006913~nucleocytoplasmic transport	0.000009	GO:0009144~purine nucleoside triphosphate metabolic process	0.03

GO:0051236~establishment of RNA localization	0.00009	GO:0033554~cellular response to stress	0.03
GO:0050657~nucleic acid transport	0.00009	GO:0009145~purine nucleoside triphosphate biosynthetic process	0.03
GO:0050658~RNA transport	0.00009	GO:0070647~protein modification by small protein conjugation or removal	0.03
GO:0007049~cell cycle	0.00009	GO:0051603~proteolysis involved in cellular protein catabolic process	0.03
GO:0051169~nuclear transport	0.0001	GO:0009260~ribonucleotide biosynthetic process	0.03
GO:0006405~RNA export from nucleus	0.0001	GO:0006892~post-Golgi vesicle-mediated transport	0.04
GO:0006886~intracellular protein transport	0.0003	GO:0030518~steroid hormone receptor signaling pathway	0.04
GO:0044265~cellular macromolecule catabolic process	0.0004	GO:0044257~cellular protein catabolic process	0.04
GO:0070727~cellular macromolecule localization	0.0007	GO:0022618~ribonucleoprotein complex assembly	0.04
GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport	0.0007	GO:0034220~ion transmembrane transport	0.04
GO:0009057~macromolecule catabolic process	0.001	GO:0030163~protein catabolic process	0.04
GO:0034613~cellular protein localization	0.001	GO:0015985~energy coupled proton transport, down electrochemical gradient	0.04
GO:0022402~cell cycle process	0.001	GO:0015986~ATP synthesis coupled proton transport	0.04
GO:0000278~mitotic cell cycle	0.002	GO:0006457~protein folding	0.04
GO:0051028~mRNA transport	0.004	GO:0006091~generation of precursor metabolites and energy	0.04
GO:0009141~nucleoside triphosphate metabolic process	0.005	GO:0022403~cell cycle phase	0.04
GO:0006605~protein targeting	0.01	GO:0006461~protein complex assembly	0.04
GO:0022613~ribonucleoprotein complex biogenesis	0.01	GO:0070271~protein complex biogenesis	0.04
GO:0009142~nucleoside triphosphate biosynthetic process	0.01	GO:0009152~purine ribonucleotide biosynthetic process	0.04
GO:0043933~macromolecular complex subunit organization	0.01	GO:0009205~purine ribonucleoside triphosphate metabolic process	0.04
GO:0065003~macromolecular complex assembly	0.01		

Gene Ontology enrichment of the prognostic markers selected. P-values shown are after correction for multiple testing using Benjamini-Hochberg method.

TABLE 18

Affymetrix Probeset ID	AU C	WILCOX P- VALU E	MF D	AC CU RA CY	ACCU RACY P- VALU E	SEN SITI VIT Y	SPE CIF ICI TY	PP V	NP V	CU TO FF	KMP- VALU E	UVA HR P- VALU E	UVA OR P- VALU E	MV A HR P- VA LU E	MV A OR P- VAL UE
2318654	0.61	0.0104	1.28	0.61	0.0028	0.64	0.57	0.61	0.61	7.84	0.0046	0.0149	0.0103	0.2	0.022
2318755	0.62	0.0034	1.53	0.64	0.0001	0.6	0.68	0.66	0.63	5.42	0.0001	0.0027	0.0029	0.02	0.006
2320062	0.62	0.003	1.26	0.62	0.0011	0.62	0.61	0.62	0.61	4.99	0.0006	0.0029	0.0045	0.02	0.008
2321661	0.62	0.0034	1.34	0.62	0.0007	0.65	0.59	0.62	0.62	6.56	0.0021	0.0045	0.0025	0.05	0.006
2322383	0.61	0.0074	1.35	0.6	0.0042	0.6	0.6	0.61	0.6	5.28	0.0032	0.0095	0.009	0.05	0.019
2325809	0.61	0.0052	1.29	0.62	0.0011	0.63	0.6	0.62	0.61	6.05	0.001	0.0064	0.0056	0.15	0.046
2327494	0.62	0.0039	1.35	0.62	0.0011	0.63	0.6	0.62	0.61	6.48	0.0017	0.0027	0.0022	0.06	0.005
2327865	0.63	0.002	1.43	0.61	0.0018	0.65	0.57	0.61	0.62	5.32	0.0011	0.0014	0.0016	0.08	0.013
2328504	0.63	0.0019	1.31	0.63	0.0002	0.64	0.62	0.64	0.63	6.57	0.0006	0.0032	0.0013	0.04	0.003
2328507	0.64	0.0009	1.29	0.59	0.0138	0.46	0.72	0.63	0.56	5.28	0.009	0.004	0.0027	0.21	0.025
2329019	0.61	0.0089	1.29	0.61	0.0018	0.61	0.61	0.62	0.61	6.44	0.0011	0.0074	0.0071	0.11	0.014
2329798	0.62	0.004	1.45	0.6	0.0042	0.55	0.65	0.62	0.59	4.91	0.0066	0.0086	0.0065	0.1	0.053
2330704	0.6	0.0122	1.32	0.58	0.0276	0.59	0.56	0.58	0.57	5.04	0.0429	0.0159	0.0114	0.13	0.022
2331419	0.62	0.0043	1.28	0.58	0.0197	0.49	0.68	0.61	0.56	4.59	0.0151	0.012	0.0062	0.87	0.12
2331842	0.61	0.0103	1.32	0.6	0.0042	0.54	0.66	0.63	0.59	6	0.0052	0.009	0.0077	0.22	0.065
2332192	0.65	0.0004	1.6	0.61	0.0018	0.57	0.65	0.63	0.6	4.91	0.0009	0.0005	0.0005	0.06	0.011
2332740	0.64	0.0006	1.31	0.61	0.0018	0.5	0.72	0.65	0.59	3.65	0.001	0.0007	0.0014	0.02	0.004
2334302	0.62	0.0044	1.31	0.62	0.0011	0.62	0.61	0.62	0.61	6.23	0.0023	0.0051	0.0035	0.12	0.008
2336960	0.64	0.0005	1.26	0.62	0.0007	0.61	0.63	0.63	0.61	6.56	0.0005	0.0009	0.0006	0.08	0.009
2339310	0.61	0.0055	1.35	0.61	0.0018	0.53	0.69	0.64	0.59	4.5	0.0017	0.0071	0.0062	0.15	0.028
2342617	0.62	0.0034	1.27	0.58	0.0276	0.45	0.71	0.62	0.56	4.65	0.0382	0.0211	0.0088	0.15	0.012
2345634	0.64	0.0006	1.36	0.6	0.0064	0.62	0.57	0.6	0.6	4.71	0.0046	0.0003	0.0005	0.02	0.002
2345663	0.67	0	1.25	0.64	0.0001	0.68	0.59	0.63	0.64	4.43	0.0006	0	0	0.03	0.001
2345666	0.61	0.0092	1.33	0.6	0.0064	0.53	0.66	0.62	0.58	4.06	0.0021	0.0116	0.0152	0.16	0.101
2346911	0.62	0.0041	1.34	0.62	0.0011	0.55	0.68	0.64	0.6	7.34	0.0011	0.0042	0.0043	0.51	0.118
2346912	0.63	0.0017	1.34	0.56	0.0681	0.41	0.72	0.6	0.54	3.86	0.1027	0.0139	0.0051	0.23	0.032
2347108	0.62	0.004	1.33	0.6	0.0064	0.51	0.68	0.63	0.58	5.73	0.0064	0.0068	0.0049	0.13	0.036
2348819	0.63	0.0014	1.33	0.63	0.0002	0.63	0.63	0.64	0.63	5.92	0.0002	0.0019	0.0013	0.14	0.011
2350305	0.62	0.0032	1.31	0.63	0.0004	0.63	0.62	0.63	0.62	5.19	0.0005	0.0026	0.0025	0.26	0.085
2350371	0.67	0.0001	1.28	0.61	0.0028	0.47	0.76	0.66	0.58	4.38	0.0012	0.0002	0.0001	0.05	0.016
2352268	0.63	0.0015	1.27	0.61	0.0028	0.57	0.64	0.62	0.59	6.23	0.0028	0.0026	0.0032	0.06	0.01
2353492	0.6	0.0139	1.25	0.59	0.0095	0.61	0.57	0.6	0.59	5.83	0.0151	0.0102	0.0144	0.11	0.025
2358275	0.64	0.0009	1.25	0.62	0.0011	0.56	0.67	0.64	0.6	4.26	0.0009	0.001	0.0018	0.06	0.067
2358923	0.61	0.0058	1.39	0.65	0	0.69	0.6	0.64	0.66	6.94	0	0.0052	0.0046	0.07	0.009
2359857	0.65	0.0003	1.32	0.63	0.0004	0.6	0.65	0.64	0.62	4.36	0.0006	0.0009	0.0005	0.03	0.008
2360078	0.65	0.0003	1.29	0.61	0.0018	0.54	0.68	0.64	0.59	7.33	0.0018	0.0003	0.0005	0.03	0.002
2360119	0.64	0.0006	1.26	0.65	0	0.64	0.65	0.66	0.64	7.33	0.0001	0.0005	0.0005	0.02	0.004

2360120	0.65	0.0002	1.25	0.61	0.0018	0.61	0.61	0.62	0.61	7.06	0.001	0.0001	0.0002	0.01	0.001
2360340	0.64	0.0004	1.26	0.65	0	0.57	0.72	0.68	0.62	5.7	0	0.0004	0.0006	0.02	0.012
2360716	0.61	0.0054	1.26	0.62	0.0011	0.7	0.53	0.61	0.63	7.26	0.0018	0.0082	0.0061	0.12	0.016
2360962	0.64	0.0005	1.34	0.64	0.0001	0.61	0.66	0.65	0.63	5.34	0.0001	0.0004	0.0005	0.02	0.003
2361031	0.61	0.0082	1.27	0.59	0.0138	0.51	0.66	0.61	0.57	3.26	0.0065	0.0304	0.025	0.12	0.06
2363064	0.64	0.0006	1.27	0.62	0.0011	0.62	0.61	0.62	0.61	6.56	0.0014	0.0006	0.0005	0.04	0.003
2363334	0.6	0.0138	1.25	0.56	0.0681	0.54	0.58	0.57	0.55	5.05	0.0524	0.0144	0.0146	0.43	0.19
2363956	0.63	0.0012	1.26	0.61	0.0018	0.51	0.71	0.65	0.59	4.39	0.0046	0.0069	0.0039	0.27	0.052
2365991	0.61	0.0091	1.48	0.59	0.0138	0.55	0.62	0.6	0.58	4.71	0.0136	0.0237	0.0154	0.16	0.044
2367178	0.65	0.0002	1.41	0.64	0.0001	0.61	0.66	0.65	0.63	5.15	0.0001	0.0006	0.0004	0.06	0.005
2367214	0.61	0.0062	1.42	0.6	0.0064	0.61	0.58	0.6	0.59	4.86	0.0052	0.0079	0.0065	0.1	0.017
2367236	0.6	0.0119	1.3	0.61	0.0028	0.6	0.61	0.62	0.6	5.7	0.0027	0.0067	0.0095	0.37	0.135
2369830	0.65	0.0002	1.41	0.59	0.0138	0.54	0.63	0.6	0.57	4.65	0.0121	0.0008	0.0008	0.07	0.021
2370014	0.63	0.0022	1.27	0.6	0.0064	0.57	0.62	0.61	0.59	4.41	0.0047	0.001	0.0021	0.13	0.058
2371291	0.66	0.0001	1.27	0.6	0.0042	0.5	0.7	0.64	0.58	5.49	0.0025	0.0001	0.0003	0.04	0.018
2371339	0.63	0.0021	1.34	0.6	0.0064	0.54	0.65	0.62	0.58	4.45	0.0045	0.012	0.0094	0.1	0.026
2371796	0.65	0.0002	1.31	0.59	0.0095	0.5	0.68	0.62	0.57	5.76	0.004	0.0003	0.0005	0.02	0.005
2373002	0.62	0.0042	1.38	0.6	0.0042	0.51	0.69	0.63	0.58	4.06	0.0014	0.02	0.019	0.05	0.025
2375035	0.65	0.0002	1.41	0.62	0.0007	0.51	0.73	0.67	0.6	4.75	0.0002	0.0001	0.0001	0.02	0.002
2375037	0.65	0.0002	1.25	0.62	0.0007	0.59	0.65	0.64	0.61	6.97	0.0013	0.0003	0.0002	0.05	0.003
2375675	0.63	0.0014	1.37	0.62	0.0011	0.59	0.64	0.63	0.61	5.35	0.0024	0.0035	0.0013	0.18	0.014
2375780	0.61	0.0102	1.36	0.58	0.0197	0.53	0.63	0.6	0.57	6.05	0.0192	0.0159	0.012	0.15	0.013
2375850	0.64	0.0006	1.26	0.64	0.0001	0.65	0.63	0.65	0.64	6.63	0.0001	0.0008	0.0009	0.09	0.014
2375890	0.61	0.0058	1.28	0.6	0.0042	0.67	0.53	0.6	0.61	6.77	0.0035	0.0059	0.0046	0.11	0.009
2377473	0.65	0.0004	1.34	0.6	0.0064	0.5	0.69	0.63	0.58	5.02	0.0034	0.0007	0.0008	0.05	0.003
2377508	0.64	0.0005	1.52	0.63	0.0002	0.68	0.58	0.63	0.64	5.81	0.0001	0.0003	0.0005	0.01	0.002
2378615	0.61	0.0057	1.29	0.57	0.0513	0.47	0.67	0.59	0.55	3.72	0.0199	0.0089	0.0238	0.03	0.072
2379787	0.62	0.0024	1.3	0.62	0.0007	0.71	0.53	0.61	0.64	4.58	0.0012	0.0041	0.003	0.2	0.038
2383763	0.62	0.0045	1.3	0.6	0.0064	0.59	0.6	0.61	0.59	6.42	0.0072	0.0039	0.0049	0.06	0.013
2389076	0.62	0.0028	1.34	0.61	0.0018	0.53	0.69	0.64	0.59	4.92	0.0007	0.0025	0.0032	0.18	0.014
2389079	0.64	0.0006	1.29	0.6	0.0064	0.5	0.7	0.63	0.58	4.6	0.0082	0.001	0.0011	0.05	0.01
2389084	0.61	0.0105	1.27	0.62	0.0011	0.48	0.77	0.68	0.59	5.19	0.0002	0.0033	0.0064	0.05	0.031
2389086	0.64	0.0004	1.27	0.6	0.0064	0.54	0.65	0.62	0.58	5.44	0.0037	0.0005	0.0007	0.03	0.02
2389817	0.65	0.0002	1.3	0.61	0.0018	0.55	0.67	0.64	0.59	7.1	0.0021	0.0008	0.0007	0.05	0.004
2394560	0.61	0.0062	1.62	0.61	0.0028	0.63	0.58	0.61	0.61	5.1	0.002	0.0071	0.0053	0.07	0.01
2395192	0.62	0.0035	1.35	0.61	0.0018	0.53	0.69	0.64	0.59	6.14	0.0007	0.0013	0.0023	0.01	0.005
2395195	0.64	0.0006	1.26	0.62	0.0007	0.52	0.72	0.66	0.6	5.43	0.0002	0.001	0.0015	0.01	0.004
2396421	0.63	0.0019	1.27	0.61	0.0018	0.6	0.62	0.62	0.6	4.26	0.0007	0.0024	0.0032	0	0.003
2400180	0.63	0.0016	1.29	0.61	0.0018	0.5	0.72	0.65	0.59	6.32	0.0014	0.0008	0.0012	0.07	0.022
2400323	0.63	0.0011	1.3	0.58	0.0276	0.43	0.73	0.62	0.55	4.31	0.0167	0.0015	0.0025	0.1	0.041
2401277	0.65	0.0002	1.26	0.62	0.0007	0.52	0.72	0.66	0.6	2.91	0.0004	0.0002	0.0005	0.01	0

2401288	0.64	0.0005	1.26	0.63	0.0004	0.69	0.56	0.62	0.64	5.91	0.0002	0.0005	0.0007	0.01	0.002
2401350	0.65	0.0004	1.37	0.63	0.0002	0.63	0.63	0.64	0.63	5.21	0.0001	0.0005	0.0005	0.02	0.002
2401368	0.65	0.0002	1.38	0.65	0	0.59	0.71	0.68	0.63	4.69	0	0	0.0001	0.02	0.021
2402210	0.64	0.0004	1.25	0.62	0.0007	0.57	0.67	0.64	0.61	5.89	0.0004	0.0012	0.0012	0.04	0.006
2405379	0.63	0.0013	1.35	0.61	0.0028	0.58	0.63	0.62	0.6	5.61	0.0026	0.0017	0.0016	0.03	0.008
2406094	0.63	0.0018	1.43	0.62	0.0007	0.6	0.64	0.64	0.61	6.24	0.0003	0.0014	0.0019	0.08	0.015
2406148	0.6	0.0136	1.36	0.63	0.0004	0.71	0.54	0.62	0.65	5.88	0.0009	0.0208	0.0132	0.22	0.034
2407134	0.61	0.0063	1.35	0.61	0.0028	0.56	0.65	0.63	0.59	4.55	0.0013	0.0034	0.0046	0.08	0.027
2408880	0.61	0.0062	1.26	0.58	0.0276	0.49	0.67	0.6	0.56	4.83	0.0153	0.0024	0.0069	0.02	0.024
2410112	0.63	0.0015	1.38	0.6	0.0042	0.66	0.54	0.6	0.61	5.4	0.0056	0.0016	0.001	0.02	0.002
2410528	0.62	0.0043	1.29	0.62	0.0007	0.72	0.52	0.61	0.65	6.06	0.0004	0.0046	0.0058	0.05	0.011
2412669	0.62	0.0038	1.35	0.59	0.0095	0.53	0.65	0.61	0.58	4.74	0.0137	0.0096	0.0064	0.1	0.019
2413580	0.63	0.0015	1.27	0.6	0.0042	0.53	0.67	0.63	0.58	5.1	0.0023	0.0068	0.0044	0.12	0.021
2414030	0.63	0.0015	1.43	0.61	0.0028	0.55	0.66	0.63	0.59	4.8	0.0039	0.0031	0.002	0.04	0.007
2414960	0.64	0.001	1.4	0.59	0.0138	0.54	0.63	0.6	0.57	4.87	0.0112	0.0005	0.0014	0.02	0.012
2417788	0.61	0.0067	1.29	0.6	0.0042	0.54	0.66	0.63	0.59	4.95	0.0017	0.0071	0.0069	0.19	0.047
2418028	0.62	0.0035	1.28	0.64	0.0001	0.6	0.68	0.66	0.63	5.64	0.0001	0.0028	0.0029	0.08	0.017
2419242	0.65	0.0002	1.35	0.6	0.0042	0.46	0.76	0.66	0.57	4.58	0.002	0.0006	0.0004	0.1	0.008
2419247	0.61	0.0076	1.3	0.6	0.0042	0.52	0.68	0.63	0.58	5.26	0.0031	0.0063	0.0047	0.54	0.073
2419276	0.65	0.0002	1.29	0.62	0.0007	0.64	0.6	0.63	0.62	5.81	0.0009	0.0004	0.0003	0.06	0.004
2420740	0.61	0.0086	1.39	0.57	0.038	0.52	0.62	0.59	0.56	4.21	0.0444	0.0104	0.0087	0.34	0.078
2420839	0.6	0.0113	1.3	0.62	0.0011	0.5	0.74	0.67	0.59	4.79	0.0006	0.0042	0.0044	0.18	0.079
2421273	0.64	0.0009	1.28	0.62	0.0007	0.54	0.7	0.65	0.6	6.21	0.0004	0.0009	0.0009	0.08	0.007
2421274	0.63	0.0013	1.32	0.63	0.0002	0.51	0.76	0.68	0.6	4.85	0.0001	0.0014	0.0015	0.25	0.034
2421932	0.61	0.006	1.27	0.61	0.0018	0.69	0.53	0.6	0.63	6.69	0.0041	0.0152	0.0062	0.27	0.014
2422519	0.62	0.0039	1.32	0.63	0.0004	0.57	0.68	0.65	0.61	4.68	0.0005	0.0052	0.004	0.18	0.02
2423200	0.65	0.0003	1.35	0.62	0.0007	0.62	0.62	0.63	0.62	7.02	0.0009	0.0003	0.0003	0.09	0.005
2427009	0.6	0.0108	1.45	0.59	0.0138	0.54	0.63	0.6	0.57	3.93	0.0112	0.0106	0.0105	0.04	0.01
2427501	0.64	0.001	1.48	0.6	0.0064	0.57	0.62	0.61	0.59	4.97	0.0075	0.0015	0.0015	0.11	0.013
2427978	0.63	0.0022	1.29	0.63	0.0004	0.62	0.63	0.64	0.62	6.01	0.0005	0.0032	0.0022	0.03	0.009
2428394	0.65	0.0003	1.31	0.65	0	0.59	0.7	0.67	0.63	6.29	0	0.0005	0.0003	0.05	0.004
2429071	0.62	0.0028	1.25	0.57	0.038	0.5	0.64	0.59	0.56	4.26	0.0596	0.0113	0.0054	0.05	0.006
2429119	0.65	0.0003	1.33	0.62	0.0011	0.57	0.66	0.64	0.6	5.45	0.0025	0.0008	0.0005	0.05	0.001
2429168	0.61	0.0075	1.39	0.57	0.0513	0.51	0.62	0.58	0.55	3.73	0.047	0.0176	0.0208	0.34	0.201
2429282	0.66	0.0001	1.32	0.62	0.0007	0.53	0.71	0.66	0.6	5	0.0005	0.0002	0.0002	0.04	0.007
2429309	0.63	0.0015	1.28	0.62	0.0011	0.62	0.61	0.62	0.61	6.71	0.0015	0.0011	0.001	0.11	0.009
2429310	0.64	0.0005	1.56	0.63	0.0004	0.65	0.6	0.63	0.63	5.66	0.0005	0.0005	0.0005	0.05	0.006
2433376	0.61	0.0063	1.29	0.64	0.0001	0.63	0.64	0.65	0.63	4.93	0.0001	0.0174	0.0114	0.08	0.013
2434721	0.63	0.001	1.26	0.6	0.0064	0.53	0.66	0.62	0.58	5.68	0.007	0.0015	0.0013	0.17	0.046
2435391	0.62	0.0031	1.27	0.61	0.0018	0.53	0.69	0.64	0.59	6.45	0.0006	0.0025	0.0049	0.01	0.01
2437095	0.61	0.0074	1.3	0.6	0.0042	0.65	0.55	0.6	0.61	6.32	0.005	0.0125	0.008	0.13	0.02

2437537	0.62	0.0027	1.37	0.6	0.0042	0.53	0.67	0.63	0.58	5.11	0.0031	0.0049	0.0035	0.49	0.153
2437538	0.65	0.0004	1.4	0.62	0.0007	0.71	0.53	0.61	0.64	6.07	0.0007	0.0006	0.0003	0.03	0.001
2437680	0.65	0.0004	1.3	0.61	0.0028	0.55	0.66	0.63	0.59	4.57	0.002	0.002	0.0015	0.08	0.037
2437775	0.62	0.0023	1.34	0.59	0.0095	0.48	0.71	0.63	0.57	4.27	0.0094	0.0051	0.0042	0.43	0.119
2439041	0.64	0.0009	1.27	0.62	0.0007	0.57	0.67	0.64	0.61	4.7	0.0005	0.0019	0.0014	0.18	0.071
2440149	0.6	0.0128	1.26	0.58	0.0197	0.53	0.63	0.6	0.57	4.89	0.0115	0.0112	0.0172	0.12	0.075
2440513	0.63	0.0015	1.27	0.61	0.0018	0.73	0.49	0.6	0.64	8	0.0021	0.0024	0.0023	0.06	0.005
2442702	0.63	0.0011	1.34	0.62	0.0011	0.53	0.7	0.65	0.59	5.39	0.0007	0.0022	0.002	0.03	0.006
2443917	0.63	0.0021	1.31	0.61	0.0028	0.53	0.68	0.64	0.59	4.6	0.0037	0.0035	0.0023	0.36	0.05
2444488	0.6	0.0142	1.3	0.6	0.0064	0.49	0.71	0.64	0.57	3.88	0.0038	0.0109	0.0118	0.27	0.055
2444489	0.62	0.0042	1.3	0.56	0.0681	0.41	0.72	0.6	0.54	4.28	0.0584	0.01	0.0111	0.29	0.075
2448289	0.64	0.0007	1.31	0.65	0	0.63	0.67	0.67	0.64	3.57	0.0001	0.0072	0.0037	0.12	0.026
2448313	0.63	0.0019	1.41	0.59	0.0095	0.5	0.68	0.62	0.57	4.02	0.0037	0.0022	0.0035	0.04	0.014
2450669	0.63	0.0019	1.41	0.6	0.0042	0.64	0.56	0.6	0.6	4.96	0.0033	0.0014	0.0012	0.02	0.003
2451314	0.61	0.0073	1.34	0.59	0.0095	0.54	0.64	0.61	0.58	4.6	0.0095	0.0029	0.0048	0.06	0.013
2452652	0.65	0.0002	1.4	0.65	0	0.69	0.6	0.64	0.66	6.12	0.0001	0.0002	0.0001	0.01	0.001
2452655	0.61	0.0053	1.41	0.61	0.0018	0.52	0.7	0.65	0.59	4.82	0.0005	0.002	0.0064	0.04	0.049
2457626	0.65	0.0003	1.28	0.64	0.0001	0.59	0.69	0.67	0.62	5.46	0	0.0012	0.0007	0.23	0.043
2458075	0.62	0.0033	1.46	0.59	0.0095	0.53	0.65	0.61	0.58	5.43	0.0052	0.0036	0.0043	0.05	0.016
2458381	0.62	0.0035	1.26	0.57	0.038	0.51	0.63	0.59	0.56	5.01	0.0397	0.003	0.0038	0.17	0.039
2458503	0.64	0.0005	1.3	0.62	0.0007	0.63	0.61	0.63	0.62	5.95	0.0007	0.0006	0.0005	0.04	0.004
2459655	0.63	0.0011	1.3	0.61	0.0028	0.56	0.65	0.63	0.59	6.21	0.0011	0.001	0.0011	0.08	0.013
2461827	0.66	0.0001	1.33	0.65	0	0.61	0.69	0.67	0.64	5.1	0	0.0004	0.0004	0.03	0.003
2461828	0.63	0.0011	1.26	0.6	0.0042	0.56	0.64	0.62	0.59	5.38	0.0039	0.0014	0.0012	0.06	0.005
2462178	0.61	0.0099	1.3	0.57	0.0513	0.5	0.63	0.59	0.55	4.63	0.0735	0.005	0.0071	0.09	0.018
2464496	0.65	0.0003	1.55	0.64	0.0001	0.58	0.69	0.66	0.62	5.59	0.0001	0.0001	0.0003	0.01	0.001
2464505	0.64	0.0006	1.28	0.61	0.0018	0.58	0.64	0.63	0.6	6.37	0.0019	0.0007	0.0007	0.04	0.005
2464514	0.63	0.002	1.28	0.62	0.0011	0.6	0.63	0.63	0.61	5.79	0.001	0.0023	0.0018	0.07	0.012
2464537	0.62	0.0042	1.34	0.65	0	0.62	0.68	0.67	0.64	5.63	0	0.003	0.0032	0.15	0.011
2468935	0.6	0.0107	1.27	0.58	0.0197	0.56	0.6	0.59	0.57	4.61	0.0509	0.0299	0.01	0.29	0.034
2469568	0.64	0.0006	1.29	0.61	0.0028	0.49	0.73	0.65	0.58	4.39	0.0014	0.0039	0.0036	0.09	0.031
2473241	0.67	0.0001	1.25	0.63	0.0002	0.56	0.7	0.66	0.61	4.78	0.0003	0.0002	0.0002	0.07	0.013
2473624	0.64	0.0009	1.57	0.63	0.0002	0.62	0.64	0.64	0.62	5.03	0.0003	0.0011	0.0007	0.01	0.001
2474147	0.61	0.0063	1.28	0.6	0.0064	0.67	0.52	0.59	0.61	6.87	0.0067	0.0054	0.0067	0.08	0.042
2474700	0.65	0.0003	1.34	0.64	0.0001	0.69	0.59	0.64	0.65	5.15	0.0001	0.0006	0.0004	0.05	0.005
2474770	0.64	0.0006	1.29	0.64	0.0001	0.64	0.64	0.65	0.64	6.1	0.0001	0.0011	0.0005	0.02	0.002
2475647	0.61	0.0101	1.28	0.58	0.0276	0.48	0.68	0.61	0.56	5.08	0.0463	0.0278	0.0158	0.29	0.094
2476316	0.66	0.0001	1.25	0.64	0.0001	0.57	0.7	0.67	0.62	4.91	0.0001	0.0004	0.0004	0.09	0.007
2476408	0.63	0.0022	1.53	0.63	0.0004	0.61	0.64	0.64	0.62	4.89	0.0003	0.0013	0.0017	0.02	0.006
2477341	0.6	0.0128	1.26	0.6	0.0042	0.61	0.59	0.61	0.6	5.26	0.0028	0.0224	0.0138	0.3	0.047
2478839	0.62	0.005	1.25	0.62	0.0007	0.61	0.63	0.63	0.61	6.44	0.001	0.008	0.0045	0.09	0.006

2479729	0.64	0.0004	1.3	0.61	0.0028	0.66	0.55	0.6	0.61	5.19	0.0021	0.0006	0.0005	0.02	0.002
2480989	0.63	0.0011	1.31	0.57	0.038	0.45	0.7	0.61	0.55	4.89	0.0197	0.0019	0.0016	0.03	0.003
2481178	0.64	0.0007	1.44	0.63	0.0002	0.6	0.66	0.65	0.62	4.99	0.0003	0.001	0.0008	0.02	0.002
2482593	0.63	0.0012	1.33	0.61	0.0018	0.56	0.66	0.63	0.6	5.41	0.0011	0.0023	0.002	0.03	0.005
2482624	0.63	0.0014	1.25	0.63	0.0002	0.72	0.54	0.62	0.65	6.89	0.0003	0.0019	0.0015	0.03	0.003
2483047	0.61	0.0058	1.34	0.59	0.0095	0.57	0.61	0.6	0.58	4.92	0.0052	0.01	0.0104	0.06	0.013
2484558	0.65	0.0003	1.42	0.64	0.0001	0.49	0.8	0.71	0.6	4.17	0	0.0002	0.0003	0.03	0.002
2484807	0.62	0.0035	1.25	0.6	0.0042	0.71	0.49	0.59	0.62	6.47	0.0057	0.0048	0.0023	0.01	0.001
2485214	0.6	0.0136	1.3	0.58	0.0276	0.54	0.61	0.59	0.57	5.47	0.0351	0.0224	0.0135	0.08	0.009
2485276	0.61	0.0085	1.29	0.59	0.0138	0.54	0.63	0.6	0.57	4.36	0.0166	0.0417	0.0294	0.31	0.1
2487216	0.61	0.0063	1.39	0.58	0.0276	0.51	0.64	0.6	0.56	5.37	0.0365	0.0035	0.0042	0.13	0.024
2487645	0.63	0.0015	1.27	0.63	0.0004	0.57	0.68	0.65	0.61	5.9	0.0005	0.0034	0.0019	0.09	0.011
2488150	0.65	0.0002	1.27	0.62	0.0011	0.61	0.62	0.63	0.61	5.02	0.0012	0.0001	0.0002	0.02	0.007
2489030	0.62	0.0043	1.28	0.59	0.0138	0.53	0.64	0.61	0.57	5.84	0.0133	0.0086	0.0042	0.29	0.035
2489435	0.63	0.0019	1.25	0.63	0.0002	0.65	0.61	0.63	0.63	6.02	0.0002	0.0021	0.0016	0.01	0.003
2491645	0.64	0.0006	1.27	0.62	0.0007	0.62	0.62	0.63	0.62	6.38	0.0005	0.0009	0.0007	0.04	0.007
2492101	0.63	0.0013	1.25	0.6	0.0064	0.5	0.69	0.63	0.58	3.78	0.0078	0.0014	0.003	0.04	0.01
2492833	0.61	0.0066	1.34	0.59	0.0138	0.55	0.62	0.6	0.58	5.88	0.0047	0.0018	0.0054	0.04	0.089
2495140	0.63	0.0015	1.43	0.62	0.0011	0.65	0.58	0.62	0.62	4.83	0.0013	0.002	0.0016	0.08	0.006
2498988	0.61	0.006	1.3	0.58	0.0197	0.48	0.69	0.62	0.56	4.48	0.0246	0.0105	0.011	0.13	0.028
2507241	0.66	0.0001	1.4	0.61	0.0028	0.51	0.7	0.64	0.58	5.19	0.0019	0.0004	0.0004	0.05	0.005
2507514	0.62	0.0031	1.25	0.58	0.0197	0.53	0.63	0.6	0.57	6.15	0.0392	0.0044	0.0034	0.02	0.003
2507533	0.64	0.0005	1.25	0.64	0.0001	0.64	0.64	0.65	0.64	6.62	0.0001	0.0005	0.0004	0.04	0.003
2512351	0.62	0.0024	1.29	0.62	0.0007	0.56	0.68	0.65	0.6	4.68	0.0009	0.0053	0.0049	0.08	0.02
2512363	0.62	0.0044	1.3	0.57	0.038	0.5	0.64	0.59	0.56	3.74	0.0309	0.0093	0.0079	0.05	0.01
2512959	0.63	0.0013	1.26	0.6	0.0064	0.56	0.63	0.61	0.58	3.93	0.0045	0.0039	0.0033	0.04	0.013
2515085	0.63	0.0017	1.27	0.63	0.0004	0.63	0.62	0.63	0.62	7.13	0.0003	0.001	0.0016	0.03	0.017
2517330	0.64	0.0009	1.31	0.6	0.0042	0.45	0.77	0.66	0.57	4.33	0.0023	0.0035	0.0028	0.13	0.025
2518193	0.63	0.0013	1.27	0.63	0.0004	0.71	0.54	0.62	0.65	5.44	0.0005	0.0029	0.0024	0.15	0.008
2518707	0.63	0.0018	1.29	0.59	0.0138	0.54	0.63	0.6	0.57	5.24	0.0072	0.0009	0.0024	0.03	0.034
2525095	0.65	0.0003	1.29	0.62	0.0007	0.58	0.66	0.64	0.61	5.56	0.001	0.0014	0.001	0.09	0.004
2527206	0.63	0.0016	1.29	0.6	0.0042	0.69	0.51	0.59	0.62	8.09	0.0037	0.0025	0.0023	0.09	0.008
2527635	0.62	0.0033	1.25	0.58	0.0197	0.52	0.64	0.6	0.57	4.94	0.0205	0.0046	0.0041	0.06	0.007
2532844	0.62	0.0051	1.26	0.59	0.0138	0.5	0.68	0.62	0.57	4.66	0.017	0.0122	0.009	0.26	0.059
2534447	0.63	0.0014	1.29	0.62	0.0011	0.51	0.72	0.66	0.59	5.77	0.001	0.0027	0.0018	0.06	0.009
2537112	0.64	0.0007	1.35	0.63	0.0002	0.65	0.61	0.63	0.63	6.32	0.0002	0.0006	0.0009	0.03	0.011
2539775	0.63	0.0011	1.33	0.61	0.0028	0.5	0.72	0.65	0.58	4.61	0.0023	0.0024	0.0016	0.09	0.011
2540221	0.62	0.0038	1.32	0.63	0.0004	0.67	0.58	0.62	0.63	6.24	0.0008	0.0033	0.0023	0.05	0.007
2544180	0.62	0.0041	1.27	0.62	0.0007	0.62	0.62	0.63	0.62	6.55	0.0006	0.0047	0.0028	0.04	0.003
2544185	0.6	0.0107	1.27	0.55	0.1438	0.35	0.76	0.59	0.53	4.72	0.0545	0.0234	0.0369	0.14	0.11
2544295	0.61	0.0059	1.43	0.59	0.0138	0.54	0.63	0.6	0.57	4.66	0.0201	0.011	0.0081	0.39	0.11

2544306	0.62	0.0045	1.25	0.59	0.0138	0.43	0.76	0.64	0.56	5.45	0.015	0.014	0.0103	0.49	0.177
2546279	0.62	0.0029	1.49	0.62	0.0007	0.64	0.6	0.63	0.62	5.03	0.0014	0.0063	0.003	0.11	0.009
2549323	0.62	0.0032	1.34	0.59	0.0095	0.52	0.66	0.62	0.58	4.74	0.0102	0.0024	0.0049	0.03	0.015
2550840	0.62	0.0035	1.27	0.63	0.0004	0.54	0.71	0.66	0.6	4.91	0.0001	0.0043	0.006	0.1	0.022
2550842	0.62	0.0034	1.33	0.59	0.0138	0.5	0.67	0.61	0.57	3.67	0.0178	0.0125	0.0106	0.09	0.023
2550964	0.67	0	1.27	0.64	0.0001	0.61	0.67	0.66	0.63	5.74	0.0001	0.0001	0.0001	0.02	0.001
2552021	0.63	0.0017	1.5	0.61	0.0018	0.53	0.69	0.64	0.59	4.86	0.0011	0.0028	0.002	0.06	0.006
2553312	0.63	0.002	1.27	0.63	0.0004	0.63	0.62	0.63	0.62	5.72	0.0004	0.0023	0.0021	0.12	0.015
2553583	0.63	0.0012	1.27	0.6	0.0042	0.71	0.49	0.59	0.62	7.2	0.0063	0.0019	0.0014	0.05	0.004
2553585	0.63	0.0013	1.71	0.61	0.0018	0.52	0.7	0.65	0.59	5.48	0.0006	0.0006	0.001	0.04	0.011
2553595	0.62	0.0031	1.38	0.6	0.0042	0.57	0.63	0.62	0.59	5.43	0.0024	0.0023	0.0029	0.07	0.015
2553907	0.63	0.0012	1.31	0.59	0.0095	0.47	0.72	0.64	0.57	4.28	0.0043	0.0028	0.0039	0.19	0.052
2554001	0.63	0.0018	1.42	0.6	0.0042	0.5	0.71	0.64	0.58	3.88	0.0009	0.0015	0.0025	0.06	0.037
2555279	0.62	0.004	1.36	0.6	0.0064	0.56	0.63	0.61	0.58	5.6	0.0113	0.0095	0.0048	0.2	0.024
2555281	0.64	0.0006	1.29	0.58	0.0197	0.45	0.72	0.63	0.56	4.35	0.0033	0.0021	0.0029	0.01	0.007
2555288	0.62	0.0028	1.29	0.6	0.0064	0.5	0.69	0.63	0.58	4.4	0.0026	0.0029	0.0052	0.11	0.052
2555330	0.65	0.0004	1.28	0.6	0.0042	0.45	0.77	0.66	0.57	4.24	0.0025	0.0011	0.0012	0.21	0.039
2555409	0.62	0.0046	1.31	0.61	0.0028	0.52	0.69	0.64	0.59	4.36	0.0011	0.0022	0.0053	0.05	0.013
2555411	0.64	0.0008	1.46	0.62	0.0007	0.62	0.62	0.63	0.62	5.58	0.0008	0.0008	0.0007	0.15	0.016
2555416	0.64	0.0004	1.27	0.62	0.0007	0.53	0.71	0.66	0.6	5.26	0.0006	0.0007	0.0008	0.2	0.039
2555507	0.61	0.0068	1.25	0.53	0.2618	0.3	0.78	0.58	0.52	4.25	0.2445	0.0242	0.0249	0.19	0.039
2555522	0.62	0.0026	1.26	0.62	0.0007	0.69	0.55	0.61	0.64	5.18	0.0018	0.0044	0.004	0.07	0.03
2556229	0.62	0.0024	1.39	0.6	0.0064	0.52	0.67	0.62	0.58	4.22	0.0064	0.0048	0.0049	0.17	0.037
2558208	0.62	0.003	1.26	0.6	0.0064	0.5	0.7	0.63	0.58	4.27	0.0027	0.0032	0.0055	0.01	0.021
2558313	0.65	0.0003	1.28	0.63	0.0004	0.55	0.7	0.66	0.61	5.59	0.0003	0.0003	0.0003	0.01	0.002
2558519	0.63	0.002	1.35	0.64	0.0001	0.61	0.66	0.65	0.63	5.68	0.0001	0.0015	0.0015	0.21	0.018
2559293	0.65	0.0004	1.27	0.63	0.0004	0.52	0.73	0.67	0.6	5.19	0.0002	0.0004	0.0008	0.03	0.02
2562334	0.65	0.0004	1.3	0.65	0	0.66	0.63	0.65	0.65	6.84	0	0.0003	0.0003	0.02	0.004
2565264	0.64	0.0006	1.33	0.64	0.0001	0.68	0.6	0.64	0.65	7.48	0.0001	0.0005	0.0003	0.02	0.001
2575142	0.6	0.0129	1.32	0.58	0.0197	0.5	0.66	0.61	0.57	4.65	0.0195	0.0287	0.019	0.06	0.016
2577959	0.64	0.0009	1.27	0.59	0.0138	0.48	0.7	0.62	0.57	3.97	0.0115	0.0024	0.0026	0.06	0.022
2581588	0.61	0.0061	1.28	0.57	0.038	0.54	0.6	0.59	0.56	4.26	0.0358	0.0105	0.0101	0.06	0.027
2583054	0.64	0.0009	1.28	0.62	0.0011	0.65	0.58	0.62	0.62	6.29	0.0018	0.0014	0.0009	0.03	0.003
2583056	0.65	0.0003	1.35	0.65	0	0.62	0.67	0.66	0.63	4.37	0.0001	0.0016	0.0006	0.12	0.009
2583249	0.61	0.0102	1.31	0.59	0.0138	0.5	0.67	0.61	0.57	4.69	0.0143	0.009	0.0093	0.06	0.017
2583609	0.6	0.012	1.32	0.59	0.0138	0.54	0.63	0.6	0.57	5.38	0.0137	0.0112	0.0102	0.1	0.025
2584845	0.64	0.001	1.3	0.63	0.0004	0.63	0.62	0.63	0.62	6	0.0002	0.0006	0.0013	0.01	0.004
2588838	0.61	0.0058	1.27	0.57	0.038	0.51	0.63	0.59	0.56	5.09	0.0173	0.0064	0.0114	0.18	0.11
2590750	0.64	0.0008	1.42	0.64	0.0001	0.59	0.68	0.66	0.62	5.38	0	0.0011	0.0014	0.02	0.014
2590802	0.62	0.0046	1.51	0.65	0	0.6	0.69	0.67	0.63	7	0	0.0023	0.0027	0.07	0.011
2591635	0.6	0.0145	1.25	0.6	0.0042	0.6	0.6	0.61	0.6	6.9	0.0046	0.0107	0.017	0.18	0.053

2591638	0.61	0.0052	1.36	0.62	0.0011	0.53	0.7	0.65	0.59	6.82	0.0005	0.0027	0.0054	0.09	0.016
2593447	0.61	0.0059	1.32	0.58	0.0197	0.5	0.67	0.61	0.56	4.62	0.0131	0.0105	0.0139	0.11	0.031
2593692	0.61	0.0064	1.35	0.58	0.0197	0.54	0.62	0.6	0.57	5.2	0.0159	0.006	0.0044	0.02	0.002
2593714	0.61	0.0093	1.31	0.59	0.0095	0.51	0.67	0.62	0.57	4.97	0.0075	0.0075	0.0121	0.11	0.03
2593758	0.61	0.0063	1.53	0.63	0.0004	0.66	0.59	0.63	0.63	4.96	0.0002	0.0023	0.004	0.07	0.029
2594506	0.61	0.0077	1.31	0.61	0.0018	0.51	0.71	0.65	0.59	4.28	0.0016	0.0292	0.0191	0.33	0.084
2596691	0.63	0.0017	1.28	0.63	0.0004	0.69	0.56	0.62	0.64	4.81	0.0007	0.0048	0.0028	0.03	0.005
2597013	0.64	0.0009	1.28	0.61	0.0028	0.56	0.65	0.63	0.59	4.94	0.0039	0.0014	0.001	0.02	0.003
2598267	0.6	0.0108	1.25	0.6	0.0042	0.61	0.59	0.61	0.6	6.26	0.0053	0.0044	0.0126	0.07	0.026
2598289	0.63	0.002	1.29	0.58	0.0197	0.47	0.7	0.62	0.56	5.73	0.0298	0.0015	0.0035	0.02	0.004
2598781	0.63	0.0021	1.26	0.64	0.0001	0.68	0.59	0.63	0.64	8.61	0.0002	0.0027	0.0024	0.09	0.007
2599342	0.61	0.0055	1.4	0.6	0.0042	0.51	0.69	0.63	0.58	5.58	0.005	0.0074	0.0064	0.05	0.01
2599903	0.61	0.0085	1.37	0.59	0.0138	0.51	0.66	0.61	0.57	4.45	0.0279	0.0131	0.0066	0.17	0.017
2606647	0.6	0.0122	1.25	0.58	0.0276	0.61	0.54	0.58	0.58	6.59	0.0576	0.0127	0.0076	0.18	0.019
2607152	0.62	0.0037	1.3	0.61	0.0018	0.58	0.64	0.63	0.6	6.07	0.0039	0.0044	0.004	0.14	0.024
2607374	0.6	0.012	1.34	0.56	0.0889	0.42	0.7	0.59	0.54	5.08	0.0849	0.026	0.0232	0.06	0.042
2609635	0.62	0.003	1.3	0.61	0.0028	0.63	0.58	0.61	0.61	4.58	0.003	0.0027	0.0032	0.08	0.019
2609657	0.63	0.0021	1.36	0.63	0.0004	0.53	0.72	0.67	0.6	5.28	0.0002	0.0012	0.0018	0.06	0.023
2609668	0.61	0.0055	1.25	0.61	0.0028	0.62	0.59	0.61	0.6	5.62	0.0024	0.0041	0.0082	0.12	0.038
2610353	0.6	0.0138	1.33	0.6	0.0064	0.6	0.59	0.6	0.59	5.54	0.0054	0.0091	0.012	0.2	0.055
2611083	0.62	0.0037	1.26	0.6	0.0064	0.42	0.79	0.67	0.57	5.68	0.0019	0.002	0.0032	0.25	0.04
2614100	0.61	0.0051	1.33	0.62	0.0007	0.53	0.71	0.66	0.6	5.7	0.0002	0.0025	0.0052	0.02	0.01
2614135	0.65	0.0003	1.33	0.61	0.0028	0.53	0.68	0.64	0.59	5.24	0.0038	0.0006	0.0006	0.05	0.002
2614137	0.61	0.0082	1.32	0.6	0.0064	0.53	0.66	0.62	0.58	5.83	0.0051	0.007	0.006	0.14	0.036
2615656	0.63	0.0013	1.33	0.6	0.0064	0.53	0.66	0.62	0.58	5.53	0.0034	0.0032	0.003	0.07	0.024
2616071	0.63	0.0019	1.46	0.62	0.0011	0.53	0.7	0.65	0.59	4.56	0.0005	0.0018	0.0024	0.05	0.018
2616248	0.62	0.0026	1.32	0.6	0.0064	0.52	0.67	0.62	0.58	4.93	0.0108	0.0114	0.0044	0.48	0.04
2617578	0.61	0.0057	1.33	0.59	0.0095	0.68	0.5	0.58	0.6	5.79	0.018	0.011	0.0056	0.16	0.012
2618656	0.63	0.0014	1.36	0.61	0.0018	0.68	0.54	0.61	0.62	5.73	0.0025	0.0022	0.0013	0.02	0.002
2619365	0.63	0.0011	1.34	0.62	0.0011	0.58	0.65	0.63	0.6	4.86	0.0012	0.0023	0.0025	0.13	0.03
2625632	0.65	0.0004	1.3	0.6	0.0042	0.59	0.61	0.61	0.59	4.15	0.0049	0.0009	0.0006	0.04	0.004
2625643	0.65	0.0002	1.33	0.62	0.0007	0.58	0.66	0.64	0.61	5.84	0.0008	0.0004	0.0003	0.06	0.005
2625893	0.64	0.0007	1.37	0.58	0.0276	0.44	0.72	0.62	0.55	3.76	0.0209	0.0035	0.003	0.02	0.01
2627951	0.67	0	1.33	0.63	0.0002	0.5	0.77	0.69	0.6	4.23	0.0001	0.0002	0.0002	0.01	0.001
2633534	0.63	0.0014	1.25	0.57	0.038	0.43	0.72	0.61	0.55	4.54	0.0237	0.0035	0.003	0.01	0.004
2633651	0.63	0.0021	1.27	0.62	0.0011	0.55	0.68	0.64	0.6	5.83	0.0011	0.0034	0.0027	0.03	0.004
2638377	0.63	0.0018	1.26	0.58	0.0276	0.48	0.68	0.61	0.56	4.37	0.015	0.0052	0.0046	0.05	0.014
2638451	0.62	0.0048	1.29	0.62	0.0011	0.62	0.61	0.62	0.61	7.12	0.0011	0.0033	0.0028	0.1	0.013
2638452	0.61	0.0067	1.32	0.6	0.0064	0.67	0.52	0.59	0.61	6.87	0.0087	0.005	0.0036	0.03	0.006
2641575	0.61	0.0097	1.28	0.6	0.0064	0.56	0.63	0.61	0.58	5.25	0.0063	0.0196	0.0121	0.16	0.047
2643579	0.62	0.0045	1.28	0.6	0.0064	0.53	0.66	0.62	0.58	4.81	0.0052	0.0038	0.0044	0.23	0.093

2645294	0.65	0.0002	1.46	0.66	0	0.6	0.71	0.69	0.64	5.72	0	0.0001	0.0001	0.03	0.003
2646066	0.61	0.0088	1.25	0.62	0.0007	0.65	0.59	0.62	0.62	5.06	0.0009	0.0173	0.0143	0.08	0.023
2646085	0.64	0.0007	1.51	0.63	0.0004	0.67	0.58	0.62	0.63	5.34	0.0005	0.0005	0.0005	0.05	0.004
2647361	0.63	0.0011	1.36	0.63	0.0004	0.54	0.71	0.66	0.6	5.39	0.0003	0.002	0.0016	0.29	0.087
2647678	0.65	0.0003	1.3	0.64	0.0001	0.54	0.73	0.68	0.61	4.48	0	0.0003	0.0007	0	0.003
2647775	0.6	0.0125	1.32	0.6	0.0042	0.52	0.68	0.63	0.58	5.37	0.0011	0.0055	0.0089	0.4	0.074
2647779	0.62	0.0042	1.3	0.6	0.0042	0.55	0.65	0.62	0.59	4.39	0.0024	0.0018	0.0045	0	0.002
2648202	0.62	0.0028	1.27	0.63	0.0004	0.65	0.6	0.63	0.63	4.61	0.0004	0.0084	0.0074	0.15	0.054
2651521	0.66	0.0001	1.31	0.64	0.0001	0.56	0.71	0.67	0.61	4.58	0	0.0001	0.0002	0.06	0.005
2652021	0.65	0.0004	1.47	0.63	0.0004	0.54	0.71	0.66	0.6	5.18	0.0004	0.0004	0.0006	0.06	0.008
2654335	0.66	0.0002	1.41	0.61	0.0018	0.51	0.71	0.65	0.59	5.41	0.0005	0.0002	0.0002	0.04	0.003
2654874	0.64	0.0008	1.3	0.65	0	0.63	0.67	0.67	0.64	5.77	0	0.0021	0.001	0.11	0.012
2654878	0.61	0.0102	1.25	0.55	0.1438	0.42	0.68	0.58	0.53	4.05	0.1136	0.0115	0.0178	0.12	0.042
2655475	0.66	0.0001	1.34	0.63	0.0004	0.59	0.66	0.65	0.61	5.11	0.0002	0.0001	0.0001	0.02	0.002
2655509	0.64	0.0008	1.27	0.61	0.0028	0.63	0.58	0.61	0.61	8.77	0.0046	0.0008	0.0008	0.02	0.002
2655678	0.61	0.0062	1.26	0.61	0.0028	0.59	0.62	0.62	0.6	5.74	0.0011	0.003	0.0057	0.05	0.018
2656791	0.64	0.001	1.25	0.61	0.0018	0.65	0.57	0.61	0.62	7.16	0.0018	0.0013	0.0009	0.06	0.005
2658354	0.64	0.0009	1.26	0.66	0	0.63	0.68	0.67	0.64	5.21	0	0.0019	0.0013	0.23	0.039
2658632	0.66	0.0001	1.33	0.65	0	0.66	0.64	0.66	0.65	4.88	0	0	0.0001	0.02	0.002
2663553	0.61	0.0056	1.4	0.61	0.0018	0.5	0.73	0.66	0.59	4.84	0.0002	0.0024	0.0065	0.08	0.092
2666503	0.61	0.0086	1.34	0.63	0.0002	0.58	0.68	0.66	0.61	5.98	0.0002	0.0068	0.0069	0.45	0.125
2666519	0.62	0.0027	1.26	0.62	0.0007	0.52	0.72	0.66	0.6	6.48	0.0007	0.003	0.0025	0.28	0.053
2666524	0.62	0.003	1.42	0.6	0.0064	0.54	0.65	0.62	0.58	4.57	0.0053	0.0014	0.0021	0.21	0.036
2669316	0.6	0.0107	1.45	0.61	0.0028	0.55	0.66	0.63	0.59	4.88	0.0028	0.008	0.0072	0.34	0.119
2669571	0.64	0.001	1.33	0.63	0.0004	0.59	0.66	0.65	0.61	5.12	0.0011	0.0057	0.0023	0.07	0.012
2670438	0.62	0.0034	0.79	0.37	1	0.43	0.32	0.39	0.35	4.25	0.0015	0.0286	0.0075	0.28	0.004
2672775	0.61	0.0088	1.43	0.59	0.0095	0.63	0.55	0.59	0.59	4.95	0.0084	0.0064	0.0081	0.11	0.022
2674243	0.6	0.0141	1.33	0.62	0.0007	0.71	0.53	0.61	0.64	5.72	0.0008	0.0118	0.009	0.08	0.008
2675269	0.62	0.0041	1.39	0.58	0.0276	0.48	0.68	0.61	0.56	4.13	0.017	0.0135	0.0141	0.2	0.045
2675802	0.62	0.0039	1.34	0.61	0.0018	0.58	0.64	0.63	0.6	5.78	0.0016	0.0034	0.0028	0.13	0.032
2676931	0.6	0.0124	1.33	0.6	0.0042	0.59	0.61	0.61	0.59	6.33	0.0046	0.0174	0.0107	0.28	0.029
2677655	0.63	0.0015	1.31	0.65	0	0.66	0.64	0.66	0.65	5.9	0	0.0031	0.0013	0.14	0.006
2677695	0.68	0	1.37	0.61	0.0028	0.48	0.74	0.66	0.58	4.48	0.0007	0	0.0001	0	0
2680511	0.62	0.0024	1.26	0.63	0.0004	0.6	0.65	0.64	0.62	3.39	0.0001	0.0064	0.0067	0.03	0.018
2682663	0.63	0.0021	1.29	0.65	0	0.58	0.72	0.69	0.63	6.34	0	0.0023	0.0018	0.14	0.011
2685954	0.6	0.0132	1.25	0.57	0.0513	0.44	0.7	0.6	0.55	3.66	0.031	0.0321	0.0608	0.15	0.125
2691756	0.64	0.0007	1.27	0.62	0.0007	0.6	0.64	0.64	0.61	4.72	0.0003	0.0011	0.0011	0	0.001
2692111	0.64	0.0004	1.51	0.64	0.0001	0.59	0.68	0.66	0.62	5.09	0.0001	0.0009	0.0006	0.03	0.009
2694407	0.65	0.0004	1.28	0.59	0.0138	0.54	0.63	0.6	0.57	4	0.0096	0.0005	0.001	0.02	0.008
2694648	0.62	0.0049	1.33	0.6	0.0042	0.64	0.56	0.6	0.6	5.51	0.0049	0.0047	0.0042	0.05	0.011
2694649	0.64	0.0009	1.44	0.61	0.0018	0.61	0.61	0.62	0.61	5.62	0.0025	0.0013	0.0012	0.1	0.015

2695413	0.66	0.0001	1.25	0.62	0.0011	0.53	0.7	0.65	0.59	5.99	0.0007	0.0004	0.0002	0.07	0.005
2700507	0.62	0.0026	1.29	0.56	0.0681	0.46	0.67	0.59	0.55	5.39	0.0471	0.002	0.0035	0.13	0.146
2700829	0.64	0.0009	1.35	0.59	0.0095	0.53	0.65	0.61	0.58	5.18	0.0112	0.0027	0.0026	0.03	0.004
2701289	0.62	0.0026	1.26	0.63	0.0004	0.61	0.64	0.64	0.62	5.43	0.0004	0.0061	0.0033	0.2	0.026
2702329	0.61	0.0058	1.37	0.6	0.0042	0.57	0.63	0.62	0.59	4.76	0.0026	0.0048	0.0058	0.31	0.103
2703240	0.63	0.002	1.55	0.6	0.0064	0.47	0.73	0.64	0.57	4.57	0.0025	0.0021	0.0033	0.06	0.02
2704511	0.67	0	1.26	0.65	0	0.56	0.73	0.69	0.62	3.5	0	0	0	0.02	0.001
2704898	0.64	0.0006	1.36	0.59	0.0095	0.51	0.67	0.62	0.57	4.15	0.0071	0.0009	0.0009	0.12	0.01
2704935	0.63	0.002	1.25	0.63	0.0004	0.62	0.63	0.64	0.62	7.15	0.0003	0.0006	0.0011	0.03	0.015
2705001	0.66	0.0001	1.48	0.63	0.0002	0.58	0.68	0.66	0.61	6.26	0.0002	0	0.0001	0.01	0.001
2706322	0.61	0.0062	1.34	0.62	0.0011	0.59	0.64	0.63	0.61	5.01	0.0005	0.0044	0.0053	0.24	0.057
2706324	0.61	0.0103	1.29	0.61	0.0028	0.58	0.63	0.62	0.6	6.1	0.0029	0.0068	0.0076	0.09	0.014
2707780	0.62	0.0029	1.35	0.59	0.0095	0.55	0.63	0.61	0.58	5.34	0.0181	0.003	0.003	0.21	0.033
2708798	0.64	0.0007	1.33	0.62	0.0007	0.65	0.59	0.62	0.62	7.58	0.0012	0.0015	0.0017	0.07	0.007
2709489	0.64	0.0006	1.33	0.62	0.0007	0.54	0.7	0.65	0.6	5.65	0.0001	0.0012	0.0013	0.03	0.011
2710214	0.62	0.0049	1.26	0.59	0.0095	0.52	0.66	0.62	0.58	4.4	0.0132	0.0067	0.0045	0.59	0.087
2710217	0.67	0	1.37	0.64	0.0001	0.49	0.81	0.72	0.6	5.18	0	0	0	0.06	0.002
2711689	0.62	0.0029	1.26	0.6	0.0064	0.5	0.69	0.63	0.58	4.5	0.0032	0.0015	0.0042	0.06	0.035
2712424	0.62	0.0041	1.29	0.62	0.0011	0.64	0.59	0.62	0.62	6.2	0.0015	0.0033	0.003	0.11	0.012
2713075	0.61	0.0078	1.36	0.61	0.0028	0.64	0.57	0.61	0.61	6.22	0.0019	0.0061	0.0057	0.11	0.017
2713262	0.64	0.0007	1.31	0.64	0.0001	0.58	0.69	0.66	0.62	4.43	0.0001	0.0008	0.0014	0.05	0.011
2713269	0.66	0.0001	1.35	0.62	0.0007	0.54	0.7	0.65	0.6	5.51	0.0003	0.0002	0.0002	0.07	0.005
2714106	0.61	0.0082	1.32	0.59	0.0095	0.54	0.64	0.61	0.58	4.38	0.0105	0.0303	0.017	0.32	0.039
2715470	0.61	0.0068	1.41	0.6	0.0064	0.66	0.53	0.59	0.6	5.57	0.0084	0.006	0.005	0.07	0.009
2715717	0.62	0.0027	1.58	0.61	0.0028	0.67	0.54	0.6	0.62	5.55	0.003	0.0036	0.0026	0.06	0.007
2720693	0.63	0.0014	1.37	0.59	0.0138	0.43	0.76	0.64	0.56	4.6	0.0053	0.0039	0.0035	0.12	0.065
2724050	0.64	0.0008	1.28	0.61	0.0028	0.5	0.71	0.65	0.58	5.76	0.0009	0.001	0.0012	0.05	0.012
2724565	0.66	0.0001	1.29	0.62	0.0011	0.65	0.58	0.62	0.62	8.25	0.0011	0.0001	0.0001	0.02	0.003
2726514	0.64	0.0005	1.34	0.61	0.0028	0.55	0.66	0.63	0.59	4.4	0.0022	0.0026	0.0013	0.05	0.006
2727970	0.62	0.0039	1.49	0.63	0.0004	0.63	0.62	0.63	0.62	5.1	0.0004	0.0037	0.0023	0.11	0.02
2730701	0.63	0.0014	1.27	0.58	0.0276	0.5	0.66	0.6	0.56	4.34	0.0546	0.0052	0.0028	0.16	0.025
2731872	0.61	0.0067	1.31	0.58	0.0197	0.44	0.73	0.63	0.56	4.68	0.0137	0.0064	0.006	0.15	0.039
2732403	0.62	0.0029	1.34	0.6	0.0064	0.59	0.6	0.61	0.59	4.85	0.0092	0.0024	0.0043	0.07	0.037
2735017	0.64	0.0005	1.37	0.59	0.0095	0.47	0.72	0.64	0.57	5.03	0.0071	0.0023	0.0012	0.41	0.085
2736295	0.63	0.0015	1.26	0.57	0.038	0.47	0.68	0.6	0.55	4.72	0.0306	0.0028	0.0034	0.16	0.058
2738963	0.62	0.0029	1.27	0.6	0.0042	0.54	0.66	0.63	0.59	5.3	0.0058	0.0042	0.0039	0.05	0.01
2743194	0.67	0	1.29	0.65	0	0.66	0.63	0.65	0.65	6.83	0.0001	0	0.0001	0.01	0.001
2744632	0.6	0.0148	1.25	0.6	0.0042	0.49	0.72	0.64	0.58	4.28	0.0023	0.0143	0.0221	0.19	0.352
2745687	0.61	0.0063	1.28	0.6	0.0064	0.54	0.65	0.62	0.58	5.03	0.0098	0.0112	0.008	0.22	0.035
2754300	0.64	0.0009	1.3	0.61	0.0018	0.52	0.7	0.65	0.59	4.52	0.0033	0.0064	0.0023	0.45	0.075
2757037	0.62	0.0027	1.29	0.62	0.0011	0.7	0.53	0.61	0.63	7.15	0.0011	0.0031	0.0035	0.04	0.005

2763813	0.6	0.0108	1.35	0.58	0.0197	0.45	0.72	0.63	0.56	4.04	0.0062	0.0072	0.0128	0.18	0.15
2766634	0.64	0.0006	1.31	0.63	0.0002	0.65	0.61	0.63	0.63	4.74	0.0004	0.0013	0.0013	0.08	0.014
2770195	0.6	0.0144	1.25	0.54	0.2178	0.45	0.63	0.56	0.53	3.41	0.3483	0.0313	0.0237	0.19	0.027
2770473	0.63	0.0012	1.29	0.62	0.0007	0.57	0.67	0.64	0.61	6.83	0.0008	0.0014	0.0009	0.21	0.02
2771759	0.63	0.0022	1.27	0.6	0.0042	0.52	0.68	0.63	0.58	5.04	0.0084	0.0049	0.0025	0.04	0.005
2773129	0.63	0.0011	1.34	0.59	0.0138	0.62	0.55	0.59	0.59	4.18	0.0179	0.0023	0.0014	0.12	0.027
2774054	0.62	0.0048	1.33	0.6	0.0042	0.49	0.72	0.64	0.58	4.26	0.0032	0.0173	0.0105	0.17	0.023
2775592	0.62	0.0034	1.26	0.6	0.0042	0.59	0.61	0.61	0.59	5.07	0.0035	0.0017	0.0031	0.12	0.046
2775758	0.61	0.007	1.32	0.62	0.0011	0.7	0.53	0.61	0.63	6.83	0.0015	0.0111	0.0091	0.13	0.015
2776094	0.61	0.0083	1.27	0.6	0.0064	0.51	0.68	0.63	0.58	4.3	0.0137	0.0369	0.0113	0.2	0.01
2777492	0.6	0.0141	1.27	0.56	0.0889	0.39	0.73	0.6	0.54	4.01	0.0641	0.0153	0.0223	0.22	0.077
2779488	0.63	0.0012	1.25	0.63	0.0004	0.61	0.64	0.64	0.62	6.49	0.0003	0.0009	0.0011	0.04	0.006
2779639	0.63	0.0014	1.45	0.61	0.0018	0.63	0.59	0.62	0.61	5.62	0.0018	0.0019	0.0012	0.05	0.005
2779995	0.61	0.0056	1.26	0.61	0.0028	0.56	0.65	0.63	0.59	5.44	0.0037	0.005	0.0035	0.12	0.014
2780545	0.62	0.0033	1.4	0.61	0.0028	0.55	0.66	0.63	0.59	4.57	0.0035	0.0062	0.0052	0.17	0.037
2783475	0.64	0.0006	1.32	0.64	0.0001	0.73	0.54	0.62	0.66	6.56	0.0003	0.0012	0.0005	0.05	0.001
2789554	0.61	0.0079	1.27	0.59	0.0095	0.5	0.69	0.63	0.57	5.86	0.0085	0.0066	0.0081	0.1	0.072
2790573	0.61	0.0069	1.28	0.61	0.0018	0.65	0.57	0.61	0.62	6.28	0.0029	0.0076	0.0037	0.04	0.004
2797449	0.64	0.0007	1.28	0.62	0.0007	0.55	0.69	0.65	0.6	6.42	0.0004	0.0011	0.0009	0.07	0.013
2801338	0.62	0.0034	1.43	0.61	0.0028	0.52	0.69	0.64	0.59	4.71	0.0012	0.0021	0.0032	0.12	0.045
2801556	0.63	0.0022	1.3	0.61	0.0028	0.64	0.57	0.61	0.61	6.84	0.0027	0.0014	0.0016	0.01	0.004
2801679	0.63	0.0014	1.32	0.61	0.0028	0.61	0.6	0.61	0.6	6.25	0.0027	0.0007	0.0014	0.01	0.005
2802506	0.64	0.0004	1.3	0.63	0.0004	0.62	0.63	0.64	0.62	4.57	0.0001	0.0002	0.001	0.01	0.017
2805739	0.62	0.004	1.28	0.59	0.0095	0.5	0.68	0.62	0.57	4.4	0.0082	0.006	0.0061	0.09	0.024
2806859	0.66	0.0001	1.28	0.62	0.0007	0.54	0.7	0.65	0.6	6.23	0.0004	0.0001	0.0001	0.01	0.002
2806912	0.62	0.0032	1.3	0.6	0.0042	0.53	0.67	0.63	0.58	6.08	0.0043	0.0037	0.003	0.14	0.019
2807658	0.64	0.0005	1.27	0.6	0.0064	0.5	0.69	0.63	0.58	5.22	0.0033	0.0007	0.0008	0.07	0.008
2809146	0.61	0.0071	1.43	0.62	0.0011	0.61	0.62	0.63	0.61	5.52	0.0018	0.0083	0.0055	0.14	0.037
2810487	0.6	0.0114	1.26	0.61	0.0028	0.55	0.66	0.63	0.59	4.07	0.0007	0.0066	0.0152	0.3	0.315
2812307	0.61	0.0075	1.37	0.59	0.0138	0.5	0.67	0.61	0.57	4.53	0.0223	0.0159	0.0104	0.13	0.02
2812500	0.63	0.0017	1.33	0.57	0.038	0.46	0.69	0.61	0.55	3.64	0.0507	0.0039	0.0034	0.17	0.023
2812573	0.63	0.0013	1.25	0.6	0.0064	0.6	0.59	0.6	0.59	7.18	0.0067	0.0014	0.0011	0.07	0.006
2817404	0.61	0.0067	1.49	0.61	0.0028	0.53	0.68	0.64	0.59	4.52	0.0034	0.009	0.007	0.29	0.036
2817457	0.64	0.0007	1.5	0.6	0.0064	0.51	0.68	0.63	0.58	5.07	0.0037	0.0015	0.0011	0.03	0.007
2818271	0.6	0.0132	1.25	0.63	0.0002	0.57	0.69	0.66	0.61	6.77	0.0002	0.022	0.0269	0.47	0.07
2818964	0.63	0.0019	1.37	0.63	0.0002	0.71	0.55	0.62	0.65	6.65	0.0002	0.0025	0.002	0.06	0.006
2822274	0.6	0.0113	1.43	0.58	0.0276	0.5	0.66	0.6	0.56	5.18	0.0299	0.0195	0.0143	0.15	0.035
2823066	0.64	0.0007	1.33	0.61	0.0028	0.44	0.79	0.68	0.57	3.93	0.0011	0.0034	0.0021	0.24	0.062
2823854	0.61	0.0066	1.43	0.6	0.0042	0.62	0.58	0.61	0.6	6.28	0.003	0.0028	0.0036	0.09	0.026
2824899	0.63	0.0021	1.31	0.61	0.0028	0.52	0.69	0.64	0.59	4.62	0.0015	0.0025	0.0045	0.1	0.034
2828112	0.63	0.002	1.54	0.62	0.0007	0.66	0.58	0.62	0.63	5.66	0.0006	0.0016	0.0019	0.04	0.007

2828637	0.6	0.0123	1.3	0.61	0.0018	0.55	0.67	0.64	0.59	5.38	0.0004	0.0021	0.007	0.13	0.068
2828642	0.63	0.0019	1.42	0.59	0.0095	0.53	0.65	0.61	0.58	4.58	0.0105	0.002	0.0024	0.13	0.023
2829255	0.64	0.0008	1.28	0.62	0.0011	0.47	0.78	0.68	0.58	5.09	0.0007	0.0012	0.0011	0.09	0.024
2829555	0.61	0.0076	1.26	0.59	0.0095	0.48	0.71	0.63	0.57	5.17	0.0037	0.0043	0.0066	0.12	0.058
2829679	0.62	0.0037	1.26	0.61	0.0028	0.58	0.63	0.62	0.6	5.77	0.0035	0.0021	0.0024	0.05	0.007
2831231	0.62	0.0034	1.25	0.58	0.0276	0.52	0.63	0.6	0.56	6.06	0.0213	0.004	0.0045	0.1	0.034
2831557	0.63	0.0011	1.38	0.61	0.0028	0.61	0.6	0.61	0.6	6.54	0.0037	0.0009	0.0006	0.02	0.001
2836687	0.61	0.0085	1.29	0.6	0.0064	0.63	0.56	0.6	0.6	4.96	0.006	0.0061	0.0074	0.03	0.015
2840638	0.61	0.0057	1.33	0.61	0.0028	0.6	0.61	0.62	0.6	4.59	0.0023	0.0053	0.0072	0.2	0.032
2843280	0.61	0.0099	1.37	0.61	0.0028	0.64	0.57	0.61	0.61	5.82	0.0017	0.0084	0.0073	0.03	0.009
2844248	0.61	0.0103	1.38	0.62	0.0011	0.64	0.59	0.62	0.62	5.94	0.0022	0.008	0.0046	0.09	0.01
2844250	0.61	0.0063	1.36	0.59	0.0095	0.65	0.53	0.59	0.6	5.71	0.0115	0.0052	0.0043	0.1	0.014
2848258	0.62	0.0027	1.32	0.56	0.0889	0.44	0.68	0.59	0.54	5.15	0.0478	0.0024	0.0038	0.07	0.039
2848472	0.62	0.0042	1.6	0.65	0	0.63	0.66	0.66	0.64	5.69	0	0.0017	0.0018	0.03	0.009
2851973	0.64	0.0006	1.29	0.61	0.0028	0.56	0.65	0.63	0.59	4.78	0.002	0.0007	0.001	0.01	0.004
2854808	0.64	0.0009	1.58	0.63	0.0002	0.66	0.6	0.63	0.63	6.05	0.0003	0.0006	0.0008	0.05	0.007
2854809	0.63	0.0011	1.27	0.63	0.0004	0.61	0.64	0.64	0.62	8.1	0.0003	0.0006	0.0009	0.06	0.008
2855289	0.62	0.0024	1.29	0.58	0.0276	0.48	0.68	0.61	0.56	5.6	0.0568	0.0088	0.0057	0.05	0.006
2855291	0.63	0.0011	1.41	0.62	0.0011	0.53	0.7	0.65	0.59	4.74	0.0015	0.0034	0.0021	0.06	0.009
2855292	0.62	0.0044	1.27	0.62	0.0007	0.57	0.67	0.64	0.61	5.57	0.0013	0.009	0.006	0.08	0.011
2857172	0.62	0.0041	1.4	0.6	0.0064	0.58	0.61	0.61	0.59	5.05	0.0067	0.0035	0.0032	0.2	0.037
2862162	0.61	0.0079	1.28	0.62	0.0007	0.62	0.62	0.63	0.62	4.45	0.0004	0.0172	0.0192	0.16	0.049
2862377	0.61	0.0068	1.3	0.64	0.0001	0.66	0.61	0.64	0.64	7.95	0.0003	0.0059	0.0047	0.1	0.009
2865063	0.62	0.003	1.34	0.62	0.0011	0.65	0.58	0.62	0.62	6.34	0.0018	0.0028	0.0027	0.09	0.008
2868141	0.62	0.0029	1.28	0.63	0.0004	0.59	0.66	0.65	0.61	5.75	0.0002	0.0021	0.0033	0.04	0.006
2877518	0.61	0.0092	1.28	0.6	0.0042	0.62	0.58	0.61	0.6	5.41	0.0057	0.0083	0.0089	0.16	0.042
2878261	0.62	0.0029	1.29	0.63	0.0002	0.63	0.63	0.64	0.63	5.98	0.0001	0.0011	0.0025	0.05	0.015
2882121	0.63	0.001	1.26	0.6	0.0042	0.57	0.63	0.62	0.59	7.76	0.0045	0.0009	0.0015	0.04	0.004
2888344	0.6	0.0148	1.3	0.57	0.038	0.51	0.63	0.59	0.56	4.55	0.05	0.0191	0.0135	0.2	0.072
2893822	0.61	0.0089	1.26	0.59	0.0095	0.45	0.74	0.64	0.57	4.91	0.0028	0.01	0.0211	0.08	0.045
2893942	0.61	0.0078	1.31	0.58	0.0276	0.53	0.62	0.59	0.56	6.54	0.0371	0.0132	0.0084	0.14	0.019
2896978	0.62	0.0027	1.36	0.59	0.0138	0.48	0.7	0.62	0.57	4.8	0.0165	0.0112	0.0042	0.2	0.011
2898531	0.63	0.001	1.28	0.58	0.0276	0.67	0.48	0.57	0.59	5.33	0.0173	0.0012	0.0016	0.05	0.009
2902010	0.65	0.0003	1.26	0.63	0.0002	0.58	0.68	0.66	0.61	6.44	0.0002	0.0002	0.0003	0.05	0.005
2902011	0.62	0.0024	1.45	0.63	0.0004	0.68	0.57	0.62	0.64	5.66	0.0007	0.0014	0.0013	0.07	0.01
2905137	0.63	0.0022	1.31	0.6	0.0042	0.47	0.74	0.65	0.57	4.98	0.002	0.0011	0.0016	0.01	0.002
2906968	0.61	0.0101	1.28	0.6	0.0064	0.57	0.62	0.61	0.59	5.8	0.0118	0.0121	0.0081	0.15	0.011
2908048	0.62	0.0041	1.27	0.62	0.0011	0.7	0.53	0.61	0.63	4.51	0.0008	0.005	0.0058	0.07	0.031
2909471	0.6	0.014	1.26	0.58	0.0276	0.55	0.6	0.59	0.57	5	0.0413	0.0243	0.019	0.28	0.07
2910489	0.63	0.0015	1.25	0.61	0.0028	0.6	0.61	0.62	0.6	5.4	0.0045	0.0036	0.0026	0.05	0.008
2914002	0.64	0.0008	1.31	0.59	0.0095	0.47	0.72	0.64	0.57	4.56	0.0045	0.0015	0.0016	0.02	0.003

2914107	0.67	0	1.26	0.65	0	0.54	0.76	0.7	0.62	4.52	0.0001	0.0006	0.0006	0.06	0.009
2916383	0.61	0.0088	1.26	0.58	0.0197	0.62	0.54	0.58	0.58	5.79	0.0218	0.0129	0.0103	0.37	0.063
2916976	0.61	0.0055	1.26	0.59	0.0095	0.48	0.71	0.63	0.57	4.23	0.003	0.007	0.0089	0.16	0.036
2918543	0.63	0.0012	1.3	0.62	0.0007	0.6	0.64	0.64	0.61	4.74	0.0004	0.0036	0.0022	0.09	0.012
2918547	0.64	0.0006	1.38	0.61	0.0018	0.58	0.64	0.63	0.6	6.5	0.0013	0.0005	0.0005	0.04	0.003
2922232	0.63	0.0014	1.27	0.6	0.0042	0.5	0.71	0.64	0.58	5.15	0.003	0.0058	0.003	0.42	0.047
2922235	0.61	0.0052	1.27	0.59	0.0095	0.49	0.7	0.63	0.57	4.54	0.0118	0.0449	0.0191	0.14	0.024
2926222	0.64	0.0005	1.42	0.62	0.0007	0.65	0.59	0.62	0.62	7.41	0.0007	0.0005	0.0004	0.03	0.002
2929946	0.63	0.0021	1.28	0.61	0.0028	0.5	0.71	0.65	0.58	5.67	0.0008	0.0018	0.0024	0.11	0.034
2930652	0.64	0.0009	1.3	0.61	0.0018	0.6	0.62	0.62	0.6	6.46	0.0023	0.0023	0.001	0.17	0.016
2932399	0.63	0.0022	1.25	0.6	0.0064	0.51	0.68	0.63	0.58	4.77	0.0094	0.0045	0.0023	0.22	0.047
2932428	0.61	0.0057	1.37	0.58	0.0276	0.48	0.68	0.61	0.56	4.49	0.0327	0.0118	0.0092	0.14	0.043
2933660	0.64	0.0005	1.26	0.66	0	0.65	0.66	0.67	0.65	5.65	0	0.0009	0.0009	0.17	0.023
2936963	0.6	0.0118	1.31	0.57	0.0513	0.44	0.7	0.6	0.55	3.91	0.0437	0.0364	0.0354	0.56	0.204
2940827	0.62	0.0039	1.3	0.6	0.0064	0.57	0.62	0.61	0.59	5.47	0.0054	0.0081	0.0057	0.1	0.013
2942512	0.63	0.0014	1.26	0.58	0.0197	0.5	0.67	0.61	0.56	6.1	0.0094	0.0033	0.0028	0.09	0.032
2944070	0.63	0.0014	1.54	0.61	0.0018	0.6	0.62	0.62	0.6	5.64	0.0011	0.0019	0.0016	0.16	0.033
2944963	0.66	0.0001	1.27	0.62	0.0007	0.57	0.67	0.64	0.61	7.12	0.0008	0.0003	0.0003	0.02	0.002
2946479	0.63	0.0012	1.28	0.6	0.0042	0.5	0.7	0.64	0.58	4.37	0.0049	0.0062	0.0046	0.2	0.041
2947592	0.64	0.0005	1.33	0.63	0.0004	0.59	0.66	0.65	0.61	4.54	0.0003	0.0003	0.0005	0	0.001
2948592	0.63	0.0013	1.3	0.61	0.0028	0.63	0.58	0.61	0.61	5.64	0.0019	0.0013	0.0012	0.06	0.008
2948596	0.6	0.0126	1.25	0.59	0.0138	0.61	0.56	0.59	0.59	4.34	0.0226	0.0211	0.0164	0.07	0.018
2949053	0.63	0.0023	1.4	0.63	0.0004	0.62	0.63	0.64	0.62	4.81	0.0002	0.0014	0.0023	0.05	0.01
2949061	0.61	0.0103	1.36	0.61	0.0028	0.56	0.65	0.63	0.59	4.82	0.0016	0.0056	0.0094	0.22	0.129
2951060	0.61	0.0083	1.26	0.6	0.0042	0.65	0.55	0.6	0.61	6.61	0.0083	0.008	0.0046	0.09	0.006
2956077	0.63	0.0022	1.28	0.6	0.0042	0.5	0.7	0.64	0.58	5.37	0.0038	0.001	0.0026	0.05	0.039
2958402	0.65	0.0002	1.32	0.61	0.0018	0.52	0.7	0.65	0.59	5.05	0.0005	0.0009	0.0016	0.04	0.026
2961302	0.61	0.0086	1.32	0.63	0.0004	0.7	0.55	0.62	0.64	5.56	0.0007	0.0083	0.0078	0.09	0.025
2966293	0.63	0.002	1.33	0.62	0.0011	0.55	0.68	0.64	0.6	4.26	0.0006	0.0023	0.0019	0.17	0.013
2966378	0.62	0.0045	1.28	0.6	0.0042	0.62	0.58	0.61	0.6	5.81	0.0052	0.008	0.0048	0.2	0.039
2967164	0.62	0.0029	1.27	0.62	0.0007	0.53	0.71	0.66	0.6	4.09	0.0005	0.0074	0.0048	0.6	0.095
2967323	0.61	0.0085	1.33	0.57	0.038	0.49	0.66	0.6	0.56	4.67	0.0674	0.0113	0.0083	0.05	0.008
2968257	0.63	0.0011	1.28	0.62	0.0007	0.62	0.62	0.63	0.62	5.01	0.0003	0.0018	0.0016	0.03	0.014
2968653	0.61	0.0055	1.33	0.6	0.0042	0.56	0.64	0.62	0.59	5.14	0.0024	0.006	0.0053	0.21	0.025
2974195	0.61	0.0079	1.26	0.62	0.0011	0.7	0.53	0.61	0.63	6.73	0.0012	0.0135	0.0134	0.1	0.016
2974332	0.61	0.0066	1.53	0.6	0.0042	0.59	0.61	0.61	0.59	4.95	0.0103	0.0105	0.0062	0.07	0.011
2975686	0.63	0.0017	1.28	0.63	0.0004	0.63	0.62	0.63	0.62	5.93	0.0008	0.0034	0.0016	0.12	0.004
2975709	0.61	0.0069	1.28	0.57	0.0513	0.5	0.63	0.59	0.55	4.81	0.0755	0.014	0.0119	0.16	0.023
2976368	0.61	0.0066	1.38	0.62	0.0007	0.55	0.69	0.65	0.6	5.16	0.0003	0.011	0.0111	0.26	0.088
2977521	0.61	0.0096	1.28	0.61	0.0018	0.7	0.52	0.6	0.63	6.52	0.0025	0.0156	0.0105	0.11	0.01
2981918	0.61	0.0091	1.4	0.59	0.0095	0.5	0.68	0.62	0.57	5.26	0.0096	0.0156	0.0111	0.05	0.018

2982323	0.61	0.0076	1.33	0.6	0.0042	0.61	0.59	0.61	0.6	6.64	0.0043	0.0078	0.0077	0.18	0.028
2982385	0.63	0.0011	1.45	0.61	0.0028	0.59	0.62	0.62	0.6	4.39	0.0093	0.0032	0.0011	0.19	0.005
2984576	0.61	0.0075	1.32	0.58	0.0197	0.51	0.65	0.6	0.57	4.1	0.0341	0.0075	0.0049	0.32	0.069
2985813	0.62	0.0044	1.43	0.6	0.0042	0.47	0.74	0.65	0.57	4.6	0.0017	0.0139	0.0132	0.45	0.127
2985965	0.65	0.0002	1.27	0.63	0.0004	0.55	0.7	0.66	0.61	6.33	0.0003	0.0004	0.0003	0.03	0.001
2988895	0.65	0.0003	1.28	0.6	0.0064	0.51	0.68	0.63	0.58	4.59	0.0042	0.0012	0.0014	0.03	0.01
2988896	0.62	0.0035	1.26	0.59	0.0138	0.73	0.44	0.57	0.61	7.15	0.0195	0.0055	0.0033	0.11	0.008
2989720	0.65	0.0004	1.33	0.61	0.0028	0.59	0.62	0.62	0.6	4.81	0.0026	0.001	0.0005	0.17	0.018
2991248	0.6	0.0125	1.26	0.59	0.0095	0.55	0.63	0.61	0.58	7.21	0.0102	0.0105	0.0087	0.61	0.119
2991263	0.66	0.0001	1.3	0.64	0.0001	0.59	0.69	0.67	0.62	7.03	0.0001	0.0004	0.0003	0.21	0.012
2991264	0.64	0.0009	1.44	0.61	0.0018	0.53	0.69	0.64	0.59	5.75	0.0016	0.0023	0.0012	0.4	0.039
2993622	0.63	0.0019	1.27	0.61	0.0028	0.64	0.57	0.61	0.61	5.13	0.0047	0.0024	0.0023	0.06	0.01
2993644	0.62	0.0038	1.34	0.62	0.0007	0.69	0.55	0.61	0.64	4.61	0.0006	0.0025	0.0037	0.03	0.013
2993659	0.67	0	1.42	0.64	0.0001	0.61	0.67	0.66	0.63	5.71	0.0001	0.0001	0.0001	0.01	0.001
2994371	0.6	0.013	1.3	0.59	0.0138	0.51	0.66	0.61	0.57	3.82	0.0373	0.0501	0.0192	0.87	0.102
2995598	0.6	0.0117	1.27	0.59	0.0138	0.53	0.64	0.61	0.57	5.35	0.0202	0.0287	0.011	0.15	0.03
2997143	0.64	0.0008	1.27	0.59	0.0138	0.49	0.69	0.62	0.57	4.85	0.0092	0.0019	0.0028	0.14	0.035
3002667	0.61	0.0053	1.27	0.61	0.0028	0.56	0.65	0.63	0.59	6.14	0.0026	0.0052	0.008	0.14	0.067
3003180	0.61	0.0068	1.29	0.57	0.038	0.5	0.65	0.6	0.56	4.11	0.0332	0.0094	0.0068	0.42	0.07
3004652	0.65	0.0002	1.41	0.6	0.0064	0.5	0.69	0.63	0.58	4.86	0.0052	0.0014	0.0007	0.08	0.006
3011652	0.61	0.0057	1.25	0.6	0.0064	0.54	0.65	0.62	0.58	6.99	0.005	0.0031	0.0033	0.07	0.01
3011846	0.6	0.0118	1.26	0.59	0.0138	0.48	0.7	0.62	0.57	4.59	0.01	0.0056	0.0081	0.18	0.093
3012405	0.66	0.0001	1.28	0.65	0	0.61	0.68	0.67	0.63	6.96	0.0001	0.0001	0.0001	0.04	0.003
3012428	0.67	0	1.29	0.64	0.0001	0.59	0.68	0.66	0.62	5.6	0.0001	0	0.0001	0.02	0.003
3012438	0.62	0.0046	1.3	0.57	0.038	0.46	0.69	0.61	0.55	4.08	0.0341	0.0025	0.0029	0.11	0.047
3012452	0.63	0.0014	1.4	0.59	0.0095	0.5	0.68	0.62	0.57	4.98	0.0071	0.0009	0.0012	0.09	0.015
3012453	0.64	0.001	1.31	0.64	0.0001	0.59	0.69	0.67	0.62	6.58	0	0.0006	0.001	0.07	0.007
3013190	0.62	0.0039	1.28	0.61	0.0018	0.5	0.73	0.66	0.59	4.85	0.0014	0.0075	0.0059	0.16	0.045
3013468	0.66	0.0001	1.4	0.63	0.0004	0.59	0.66	0.65	0.61	5.57	0.0003	0.0002	0.0001	0.05	0.006
3013685	0.62	0.0033	1.26	0.61	0.0028	0.53	0.68	0.64	0.59	5.07	0.0021	0.0046	0.0027	0.04	0.008
3014422	0.62	0.0036	1.37	0.63	0.0004	0.53	0.72	0.67	0.6	3.79	0.0002	0.0033	0.0096	0.12	0.104
3015985	0.61	0.0063	1.25	0.61	0.0028	0.64	0.57	0.61	0.61	6.89	0.0034	0.0081	0.0084	0.09	0.015
3017629	0.6	0.0114	1.28	0.55	0.1438	0.37	0.73	0.59	0.53	3.64	0.1043	0.0347	0.0366	0.22	0.076
3017826	0.6	0.0122	1.36	0.6	0.0064	0.58	0.61	0.61	0.59	5.59	0.007	0.0129	0.0081	0.05	0.006
3021760	0.66	0.0001	1.33	0.64	0.0001	0.53	0.76	0.69	0.61	4.96	0	0.0001	0.0002	0	0.002
3022682	0.62	0.0024	1.3	0.62	0.0011	0.59	0.64	0.63	0.61	6.47	0.0007	0.0035	0.0022	0.02	0.002
3027555	0.63	0.0017	1.55	0.63	0.0004	0.7	0.55	0.62	0.64	6.41	0.0004	0.001	0.0009	0.02	0.002
3027926	0.63	0.0018	1.31	0.62	0.0007	0.56	0.68	0.65	0.6	5.93	0.0005	0.0013	0.0017	0.06	0.016
3027936	0.62	0.0049	1.34	0.61	0.0018	0.72	0.5	0.6	0.64	6.19	0.0027	0.0043	0.0024	0.11	0.013
3037391	0.63	0.0019	1.36	0.59	0.0095	0.47	0.72	0.64	0.57	4.16	0.0082	0.0159	0.0093	0.23	0.036
3037406	0.63	0.0022	1.3	0.63	0.0002	0.71	0.55	0.62	0.65	7.23	0.0004	0.0017	0.0021	0.02	0.004

3037950	0.61	0.0088	1.45	0.59	0.0138	0.53	0.64	0.61	0.57	3.82	0.0091	0.0095	0.0132	0.03	0.016
3039980	0.63	0.0011	1.37	0.64	0.0001	0.62	0.65	0.65	0.63	6.37	0.0001	0.0007	0.0009	0.15	0.016
3039983	0.6	0.0108	1.39	0.59	0.0138	0.58	0.59	0.6	0.58	5.64	0.0152	0.0074	0.006	0.44	0.07
3040116	0.64	0.001	1.43	0.64	0.0001	0.56	0.72	0.68	0.62	4.91	0	0.0011	0.0009	0.32	0.033
3041262	0.65	0.0004	1.43	0.63	0.0004	0.62	0.63	0.64	0.62	6.49	0.0003	0.0003	0.0003	0.06	0.003
3042004	0.62	0.005	1.35	0.62	0.0007	0.6	0.64	0.64	0.61	5.41	0.0007	0.0084	0.0067	0.29	0.039
3042424	0.63	0.0015	1.63	0.63	0.0002	0.63	0.63	0.64	0.63	5.85	0.0002	0.0012	0.001	0.06	0.004
3042426	0.62	0.0048	1.28	0.62	0.0011	0.61	0.62	0.63	0.61	6.11	0.0011	0.0035	0.0035	0.09	0.008
3042429	0.63	0.0017	1.27	0.59	0.0095	0.5	0.68	0.62	0.57	4.85	0.0061	0.0038	0.0043	0.32	0.123
3042430	0.64	0.0007	1.55	0.61	0.0028	0.62	0.59	0.61	0.6	5.62	0.0028	0.0009	0.0006	0.1	0.008
3042437	0.67	0.0001	1.35	0.66	0	0.64	0.67	0.67	0.65	6.81	0	0.0001	0.0001	0.01	0
3042453	0.64	0.0008	1.29	0.6	0.0064	0.49	0.71	0.64	0.57	3.84	0.0035	0.0021	0.0037	0.05	0.059
3048780	0.63	0.002	1.51	0.61	0.0018	0.62	0.6	0.62	0.61	4.61	0.0014	0.0025	0.0024	0.06	0.012
3048870	0.66	0.0001	1.36	0.62	0.0007	0.53	0.71	0.66	0.6	5.06	0.0003	0.0004	0.0002	0.01	0.002
3053384	0.68	0	1.58	0.64	0.0001	0.54	0.74	0.69	0.61	3.95	0	0	0	0.03	0.005
3056395	0.64	0.0005	1.27	0.64	0.0001	0.64	0.63	0.64	0.63	7.15	0.0001	0.0005	0.0006	0.05	0.011
3060052	0.64	0.0006	1.29	0.58	0.0276	0.44	0.72	0.62	0.55	3.77	0.0132	0.0022	0.0025	0.12	0.02
3061054	0.64	0.0007	1.26	0.62	0.0011	0.51	0.72	0.66	0.59	4.72	0.0005	0.0024	0.0014	0.14	0.011
3061144	0.62	0.0037	1.41	0.61	0.0028	0.52	0.69	0.64	0.59	4.89	0.002	0.0053	0.0065	0.07	0.027
3061758	0.64	0.0006	1.3	0.63	0.0002	0.58	0.68	0.66	0.61	5.26	0.0001	0.0011	0.0032	0.05	0.029
3062023	0.64	0.0006	1.26	0.64	0.0001	0.55	0.73	0.68	0.62	5.86	0	0.0002	0.0005	0.01	0.002
3064354	0.62	0.0028	1.3	0.63	0.0004	0.67	0.58	0.62	0.63	5.88	0.0005	0.003	0.002	0.07	0.006
3075645	0.62	0.0049	1.37	0.61	0.0028	0.64	0.57	0.61	0.61	5.92	0.0025	0.0062	0.006	0.16	0.027
3076355	0.67	0	1.49	0.61	0.0018	0.57	0.65	0.63	0.6	5.8	0.0019	0.0001	0	0.02	0.001
3076393	0.63	0.001	1.34	0.62	0.0007	0.54	0.7	0.65	0.6	4.19	0	0.0001	0.0009	0.01	0.038
3076490	0.63	0.0023	1.3	0.63	0.0004	0.61	0.64	0.64	0.62	6.59	0.0006	0.0037	0.0015	0.03	0.002
3081625	0.61	0.0064	1.26	0.59	0.0095	0.53	0.65	0.61	0.58	4.98	0.0063	0.0072	0.006	0.34	0.057
3087828	0.64	0.001	1.26	0.6	0.0064	0.5	0.69	0.63	0.58	5.49	0.0048	0.0012	0.0014	0.07	0.005
3087930	0.63	0.0022	1.36	0.62	0.0011	0.55	0.68	0.64	0.6	5.84	0.0022	0.0047	0.0026	0.09	0.014
3088570	0.6	0.0133	1.27	0.6	0.0064	0.63	0.56	0.6	0.6	5.28	0.0096	0.022	0.0139	0.1	0.013
3092505	0.61	0.0051	1.39	0.62	0.0007	0.65	0.59	0.62	0.62	5.8	0.0008	0.0048	0.0039	0.15	0.035
3094309	0.62	0.0029	1.57	0.58	0.0197	0.58	0.58	0.59	0.58	4.85	0.03	0.0054	0.0035	0.12	0.012
3096162	0.64	0.0005	1.31	0.62	0.0011	0.54	0.69	0.65	0.6	5.09	0.0022	0.0015	0.0008	0.04	0.005
3096409	0.63	0.0012	1.47	0.64	0.0001	0.5	0.79	0.71	0.61	4.9	0	0.0013	0.0016	0.01	0.003
3096979	0.66	0.0001	1.31	0.64	0.0001	0.6	0.68	0.66	0.63	5.57	0.0001	0.0002	0.0001	0.13	0.01
3099780	0.62	0.005	1.31	0.6	0.0042	0.6	0.6	0.61	0.6	5.8	0.0072	0.0074	0.0052	0.08	0.021
3100230	0.65	0.0004	1.35	0.63	0.0004	0.6	0.65	0.64	0.62	5.98	0.0006	0.0009	0.0007	0.05	0.009
3107638	0.61	0.0092	1.26	0.57	0.038	0.44	0.71	0.61	0.55	4.45	0.0104	0.0052	0.0122	0.24	0.085
3108472	0.65	0.0003	1.29	0.63	0.0004	0.59	0.66	0.65	0.61	6.54	0.0004	0.0004	0.0004	0.02	0.003
3108501	0.65	0.0003	1.27	0.61	0.0028	0.5	0.71	0.65	0.58	4.39	0.0047	0.0031	0.0017	0.19	0.031
3108938	0.61	0.0062	1.26	0.59	0.0138	0.55	0.62	0.6	0.58	4.59	0.0103	0.0101	0.0126	0.33	0.117

3111090	0.64	0.0008	1.28	0.64	0.0001	0.57	0.71	0.67	0.62	5.61	0	0.0003	0.0008	0.06	0.016
3111116	0.61	0.0073	1.37	0.61	0.0018	0.57	0.65	0.63	0.6	5.39	0.0008	0.0037	0.0051	0.22	0.042
3112517	0.63	0.0011	1.37	0.61	0.0018	0.58	0.64	0.63	0.6	6.28	0.0018	0.0009	0.0009	0.05	0.004
3114370	0.61	0.0054	1.27	0.58	0.0276	0.45	0.71	0.62	0.56	4.57	0.0231	0.0084	0.0093	0.46	0.124
3114664	0.6	0.0106	1.28	0.58	0.0197	0.53	0.63	0.6	0.57	5.06	0.0149	0.0158	0.0109	0.12	0.036
3124536	0.63	0.0021	1.28	0.63	0.0002	0.64	0.62	0.64	0.63	6.2	0.0004	0.0027	0.0023	0.01	0.002
3126094	0.63	0.002	1.31	0.64	0.0001	0.71	0.56	0.63	0.65	7.39	0.0002	0.0023	0.0012	0.06	0.006
3128680	0.61	0.008	1.35	0.57	0.038	0.54	0.6	0.59	0.56	5.38	0.0588	0.0095	0.0093	0.31	0.101
3129955	0.64	0.0007	1.3	0.62	0.0011	0.58	0.65	0.63	0.6	5.98	0.001	0.0015	0.0013	0.06	0.006
3131973	0.65	0.0003	1.31	0.64	0.0001	0.56	0.71	0.67	0.61	6.31	0.0001	0.0008	0.0006	0.07	0.006
3132336	0.61	0.0066	1.37	0.61	0.0018	0.53	0.69	0.64	0.59	4.42	0.0017	0.0249	0.0137	0.03	0.003
3133528	0.63	0.0014	1.3	0.62	0.0011	0.5	0.74	0.67	0.59	4.39	0.0004	0.001	0.0018	0.03	0.006
3134184	0.62	0.0035	1.27	0.57	0.038	0.39	0.77	0.63	0.55	3.84	0.0303	0.0046	0.0058	0.72	0.365
3136352	0.64	0.0009	1.31	0.62	0.0011	0.56	0.67	0.64	0.6	7.14	0.0007	0.0008	0.0013	0.03	0.006
3137586	0.63	0.0016	1.27	0.61	0.0028	0.62	0.59	0.61	0.6	6.36	0.0059	0.0023	0.0015	0.1	0.011
3138886	0.62	0.0028	1.25	0.58	0.0276	0.52	0.63	0.6	0.56	5.47	0.0263	0.0025	0.0028	0.14	0.023
3138980	0.6	0.0114	1.27	0.61	0.0028	0.6	0.61	0.62	0.6	5.6	0.0026	0.0142	0.0085	0.15	0.023
3139053	0.6	0.0142	1.28	0.62	0.0011	0.54	0.69	0.65	0.6	5.19	0.0009	0.0174	0.0166	0.44	0.07
3139926	0.66	0.0001	1.36	0.64	0.0001	0.56	0.72	0.68	0.62	5.9	0	0.0001	0.0002	0.03	0.014
3141863	0.62	0.0029	1.62	0.6	0.0042	0.54	0.66	0.63	0.59	3.89	0.0051	0.0093	0.0067	0.1	0.014
3145023	0.61	0.007	1.25	0.59	0.0095	0.52	0.66	0.62	0.58	5.1	0.0132	0.0084	0.0063	0.34	0.117
3145956	0.63	0.0021	1.27	0.63	0.0002	0.68	0.58	0.63	0.64	8.34	0.0004	0.0061	0.0046	0.15	0.011
3145966	0.63	0.001	1.26	0.63	0.0004	0.6	0.65	0.64	0.62	5.71	0.0006	0.0014	0.0012	0.13	0.012
3146538	0.61	0.0052	1.25	0.58	0.0197	0.47	0.7	0.62	0.56	4.01	0.0178	0.0178	0.0184	0.13	0.03
3146566	0.62	0.0027	1.35	0.61	0.0028	0.5	0.71	0.65	0.58	5.22	0.0012	0.0022	0.0033	0.05	0.014
3146788	0.62	0.0027	1.29	0.62	0.0007	0.6	0.64	0.64	0.61	7.65	0.0006	0.0018	0.0019	0.2	0.036
3146799	0.64	0.0005	1.25	0.63	0.0002	0.68	0.58	0.63	0.64	8.6	0.0004	0.0006	0.0007	0.09	0.011
3147328	0.62	0.0042	1.34	0.61	0.0028	0.56	0.65	0.63	0.59	5.1	0.0013	0.0018	0.0041	0.05	0.019
3148628	0.62	0.0031	1.38	0.6	0.0042	0.49	0.72	0.64	0.58	4.19	0.0029	0.0055	0.006	0.14	0.024
3149768	0.61	0.0076	1.39	0.62	0.0011	0.6	0.63	0.63	0.61	6.2	0.0016	0.0083	0.0058	0.16	0.018
3149773	0.65	0.0004	1.35	0.62	0.0007	0.58	0.66	0.64	0.61	4.81	0.001	0.0006	0.0005	0.15	0.009
3149864	0.65	0.0004	1.51	0.65	0	0.66	0.63	0.65	0.65	5.25	0	0.0003	0.0003	0.04	0.006
3151480	0.63	0.0014	1.75	0.62	0.0007	0.55	0.69	0.65	0.6	5.21	0.0004	0.0007	0.0006	0.04	0.005
3152560	0.61	0.0077	1.26	0.6	0.0064	0.53	0.66	0.62	0.58	4.5	0.0084	0.0181	0.0075	0.64	0.1
3153532	0.6	0.012	1.32	0.6	0.0042	0.53	0.67	0.63	0.58	4.96	0.0059	0.0179	0.0145	0.15	0.045
3157388	0.61	0.0102	1.43	0.6	0.0042	0.63	0.57	0.6	0.6	6.08	0.0055	0.0093	0.0074	0.18	0.024
3157461	0.61	0.0058	1.46	0.61	0.0028	0.66	0.55	0.6	0.61	5.23	0.0022	0.0053	0.0047	0.04	0.008
3157723	0.62	0.0037	1.34	0.62	0.0007	0.65	0.59	0.62	0.62	5.9	0.0006	0.0025	0.0025	0.1	0.028
3157847	0.63	0.0011	1.4	0.6	0.0042	0.53	0.67	0.63	0.58	5.48	0.0085	0.0016	0.0009	0.19	0.021
3164299	0.63	0.0019	1.3	0.63	0.0004	0.55	0.7	0.66	0.61	4.81	0.0002	0.0028	0.0036	0.18	0.061
3165138	0.64	0.0006	1.41	0.63	0.0004	0.59	0.66	0.65	0.61	4.24	0.0001	0.0013	0.0015	0.03	0.015

3165799	0.65	0.0004	1.44	0.61	0.0028	0.52	0.69	0.64	0.59	5.26	0.0015	0.0005	0.0004	0.03	0.002
3166029	0.63	0.0011	0.79	0.39	0.9996	0.41	0.38	0.4	0.38	4.13	0.0029	0.0021	0.0016	0.01	0.007
3166735	0.63	0.0015	1.47	0.62	0.0011	0.63	0.6	0.62	0.61	5.52	0.0011	0.0037	0.0025	0.07	0.013
3167990	0.64	0.0008	1.5	0.62	0.0011	0.54	0.69	0.65	0.6	6.06	0.0016	0.0009	0.0007	0.1	0.012
3168127	0.61	0.0096	1.25	0.6	0.0064	0.48	0.72	0.64	0.57	3.78	0.0076	0.0273	0.0127	0.65	0.149
3169011	0.71	0	0.79	0.35	1	0.24	0.47	0.32	0.37	3.13	0	0	0	0	0
3174268	0.67	0.0001	1.26	0.59	0.0095	0.47	0.72	0.64	0.57	5.25	0.0034	0.0001	0.0002	0.01	0.003
3174441	0.62	0.0043	1.29	0.59	0.0095	0.5	0.68	0.62	0.57	5.43	0.0199	0.0101	0.0054	0.34	0.023
3175632	0.65	0.0004	1.47	0.62	0.0011	0.64	0.59	0.62	0.62	5.06	0.0011	0.0003	0.0005	0.05	0.01
3175657	0.61	0.0094	1.28	0.58	0.0276	0.52	0.63	0.6	0.56	5.56	0.0345	0.0166	0.0136	0.56	0.149
3178635	0.63	0.001	1.43	0.59	0.0095	0.5	0.68	0.62	0.57	4.19	0.0078	0.0027	0.0032	0.06	0.019
3183178	0.6	0.0107	1.41	0.59	0.0095	0.53	0.65	0.61	0.58	4.45	0.0073	0.0055	0.0089	0.03	0.013
3190449	0.62	0.0043	1.32	0.59	0.0138	0.58	0.59	0.6	0.58	6.01	0.0129	0.0034	0.0056	0.09	0.038
3192674	0.6	0.0111	1.28	0.59	0.0138	0.52	0.65	0.61	0.57	4.88	0.0094	0.0146	0.0198	0.13	0.081
3197644	0.63	0.0013	1.39	0.58	0.0276	0.62	0.53	0.58	0.58	5.72	0.0406	0.0017	0.0014	0.03	0.006
3199457	0.63	0.0017	1.47	0.62	0.0007	0.55	0.69	0.65	0.6	4.76	0.0011	0.0025	0.0016	0.11	0.012
3199485	0.61	0.0069	1.29	0.61	0.0018	0.48	0.76	0.67	0.58	4.41	0.0008	0.0045	0.0045	0.18	0.048
3200638	0.62	0.0039	1.44	0.6	0.0042	0.56	0.64	0.62	0.59	4.43	0.004	0.0037	0.0028	0.76	0.074
3200711	0.61	0.0066	1.25	0.6	0.0064	0.51	0.68	0.63	0.58	5.69	0.0046	0.0081	0.0054	0.35	0.043
3200718	0.65	0.0004	1.28	0.59	0.0138	0.51	0.66	0.61	0.57	6.59	0.017	0.0004	0.0005	0.03	0.001
3200725	0.65	0.0002	1.35	0.62	0.0007	0.55	0.69	0.65	0.6	7.06	0.0007	0.0001	0.0002	0.04	0.004
3203822	0.62	0.0043	1.31	0.6	0.0042	0.61	0.59	0.61	0.6	4.86	0.0039	0.0058	0.0048	0.12	0.02
3205039	0.65	0.0004	1.26	0.63	0.0004	0.58	0.67	0.65	0.61	5.83	0.0004	0.0006	0.0007	0.02	0.004
3205424	0.62	0.0031	1.34	0.62	0.0011	0.52	0.71	0.65	0.59	4.24	0.0007	0.0068	0.0044	0.19	0.041
3212146	0.61	0.0078	1.36	0.62	0.0007	0.57	0.67	0.64	0.61	5.88	0.0007	0.0063	0.005	0.12	0.012
3212163	0.62	0.0032	1.38	0.62	0.0011	0.59	0.64	0.63	0.61	4.68	0.0009	0.0016	0.0024	0.02	0.008
3214671	0.63	0.0011	1.32	0.63	0.0004	0.63	0.62	0.63	0.62	4.48	0.0007	0.0013	0.0018	0.04	0.01
3214699	0.63	0.0015	1.31	0.63	0.0002	0.54	0.72	0.67	0.61	4.42	0.0001	0.003	0.0055	0.02	0.017
3219683	0.62	0.0032	1.33	0.6	0.0042	0.54	0.66	0.63	0.59	4.95	0.0036	0.0051	0.0057	0.25	0.056
3219711	0.67	0	1.55	0.6	0.0042	0.47	0.74	0.65	0.57	3.71	0.0008	0	0.0001	0	0
3219891	0.63	0.0016	1.53	0.61	0.0028	0.58	0.63	0.62	0.6	5.22	0.0021	0.0012	0.0017	0.03	0.007
3220159	0.62	0.0041	1.32	0.61	0.0018	0.64	0.58	0.61	0.61	7.14	0.0025	0.0055	0.0033	0.07	0.006
3222054	0.64	0.0008	1.3	0.62	0.0011	0.49	0.76	0.67	0.59	5.58	0.0004	0.0009	0.001	0.04	0.013
3222984	0.61	0.0078	1.26	0.54	0.2178	0.38	0.7	0.57	0.52	4.6	0.2985	0.0144	0.0113	0.32	0.046
3223876	0.63	0.0021	1.29	0.62	0.0007	0.57	0.67	0.64	0.61	5	0.0003	0.0015	0.0018	0.02	0.003
3225580	0.62	0.0045	1.26	0.58	0.0276	0.47	0.69	0.61	0.56	3.59	0.0542	0.0619	0.0186	0.25	0.029
3226470	0.63	0.0013	1.33	0.61	0.0028	0.51	0.7	0.64	0.58	3.52	0.0009	0.001	0.0024	0.01	0.004
3227646	0.63	0.0016	1.29	0.6	0.0042	0.59	0.61	0.61	0.59	5.96	0.0031	0.0022	0.0017	0.02	0.005
3233387	0.64	0.0005	1.56	0.65	0	0.66	0.64	0.66	0.65	5.55	0	0.0008	0.0003	0.07	0.004
3234175	0.61	0.007	1.33	0.61	0.0018	0.66	0.56	0.61	0.62	6.78	0.0022	0.0055	0.0052	0.1	0.021
3235500	0.63	0.0019	1.27	0.6	0.0042	0.55	0.65	0.62	0.59	4.55	0.0084	0.0074	0.0038	0.09	0.007

3237000	0.61	0.0092	1.34	0.59	0.0095	0.63	0.55	0.59	0.59	6.38	0.0102	0.015	0.01	0.3	0.041
3237001	0.61	0.0052	1.32	0.6	0.0042	0.65	0.55	0.6	0.61	7.77	0.0072	0.0096	0.0077	0.23	0.021
3239927	0.61	0.0054	1.25	0.6	0.0064	0.58	0.61	0.61	0.59	4.62	0.0068	0.0067	0.0058	0.06	0.017
3239982	0.64	0.0007	1.28	0.6	0.0042	0.51	0.69	0.63	0.58	6.06	0.0028	0.0016	0.0012	0.07	0.006
3240135	0.63	0.0018	1.28	0.59	0.0095	0.47	0.72	0.64	0.57	4.18	0.004	0.0057	0.005	0.08	0.022
3240409	0.66	0.0001	1.27	0.64	0.0001	0.57	0.71	0.67	0.62	7.78	0.0001	0.0002	0.0002	0.02	0.001
3240425	0.64	0.0005	1.29	0.61	0.0018	0.68	0.54	0.61	0.62	6.52	0.0018	0.0017	0.0011	0.06	0.006
3241499	0.63	0.0021	1.29	0.59	0.0095	0.5	0.69	0.63	0.57	4.32	0.0037	0.0026	0.0036	0.03	0.008
3241506	0.63	0.0011	1.3	0.62	0.0007	0.55	0.69	0.65	0.6	5.12	0.0003	0.0012	0.0012	0.09	0.029
3243292	0.65	0.0003	1.4	0.63	0.0004	0.57	0.68	0.65	0.61	5.85	0.0003	0.0003	0.0002	0.01	0.001
3250201	0.6	0.0125	1.57	0.59	0.0095	0.57	0.61	0.6	0.58	4.58	0.009	0.0224	0.0123	0.37	0.035
3251409	0.62	0.0042	1.28	0.62	0.0007	0.51	0.73	0.67	0.6	5.7	0.0003	0.001	0.0025	0.04	0.005
3252608	0.62	0.0037	1.29	0.61	0.0018	0.56	0.66	0.63	0.6	4.94	0.0012	0.0025	0.0036	0.12	0.094
3253445	0.65	0.0002	1.32	0.63	0.0002	0.65	0.61	0.63	0.63	7.12	0.0003	0.0003	0.0003	0.11	0.015
3253863	0.62	0.0043	1.28	0.59	0.0138	0.51	0.66	0.61	0.57	5.05	0.0232	0.0042	0.0032	0.14	0.02
3255269	0.61	0.0092	1.27	0.62	0.0007	0.57	0.67	0.64	0.61	6.42	0.0005	0.0081	0.007	0.25	0.021
3257404	0.6	0.0115	1.33	0.54	0.2178	0.38	0.7	0.57	0.52	4.85	0.2778	0.133	0.0798	0.19	0.03
3258021	0.65	0.0002	1.45	0.65	0	0.65	0.65	0.66	0.65	5.48	0	0.0005	0.0003	0.06	0.005
3259678	0.61	0.0092	1.35	0.59	0.0138	0.49	0.69	0.62	0.57	5.5	0.0074	0.0044	0.0071	0.1	0.029
3261550	0.62	0.0026	1.39	0.61	0.0028	0.5	0.71	0.65	0.58	4.53	0.0018	0.0046	0.0044	0.13	0.038
3262470	0.64	0.0006	1.27	0.59	0.0095	0.54	0.64	0.61	0.58	5.26	0.0133	0.0011	0.0012	0.11	0.028
3263804	0.63	0.0012	1.27	0.6	0.0064	0.55	0.64	0.62	0.58	5.78	0.0024	0.0014	0.0018	0.04	0.005
3264697	0.64	0.0007	1.31	0.62	0.0011	0.52	0.71	0.65	0.59	5.76	0.0009	0.0014	0.001	0.07	0.009
3264726	0.62	0.0024	1.59	0.59	0.0138	0.58	0.59	0.6	0.58	5.41	0.0154	0.0029	0.0019	0.15	0.017
3275175	0.63	0.0016	1.29	0.61	0.0028	0.54	0.67	0.63	0.59	5.15	0.0039	0.0025	0.002	0.12	0.013
3276455	0.62	0.0049	1.26	0.56	0.0681	0.43	0.7	0.6	0.54	3.84	0.0363	0.0135	0.0157	0.07	0.079
3277709	0.66	0.0001	1.33	0.66	0	0.58	0.73	0.69	0.63	4.68	0	0.0005	0.0004	0.06	0.009
3279906	0.62	0.0026	1.26	0.57	0.038	0.59	0.55	0.58	0.57	7.48	0.0556	0.0034	0.0028	0.08	0.009
3280961	0.62	0.0042	1.35	0.59	0.0138	0.48	0.7	0.62	0.57	4.37	0.0237	0.0174	0.0068	0.22	0.042
3282022	0.61	0.0058	1.4	0.58	0.0197	0.55	0.61	0.6	0.57	4.5	0.0225	0.0106	0.0065	0.34	0.048
3282170	0.63	0.0015	1.28	0.62	0.0011	0.57	0.66	0.64	0.6	3.58	0.0004	0.0032	0.0047	0.04	0.013
3282215	0.61	0.0067	1.49	0.59	0.0138	0.54	0.63	0.6	0.57	4.73	0.0203	0.0096	0.0069	0.07	0.006
3282220	0.63	0.0013	1.51	0.63	0.0002	0.59	0.67	0.65	0.62	5.09	0.0002	0.0016	0.001	0.03	0.003
3282254	0.62	0.0034	1.3	0.61	0.0028	0.6	0.61	0.62	0.6	5.13	0.0035	0.0036	0.0034	0.05	0.01
3284025	0.64	0.0009	1.33	0.63	0.0004	0.48	0.79	0.7	0.59	5.03	0.0001	0.0013	0.0011	0.05	0.01
3284217	0.64	0.0009	1.27	0.63	0.0002	0.69	0.57	0.63	0.64	6.48	0.0005	0.0008	0.0009	0.01	0.002
3284603	0.61	0.006	1.28	0.58	0.0197	0.53	0.63	0.6	0.57	5.47	0.0264	0.0095	0.007	0.15	0.026
3284665	0.62	0.0039	1.33	0.58	0.0276	0.54	0.61	0.59	0.57	5.97	0.0194	0.0033	0.0044	0.25	0.072
3294341	0.6	0.0107	1.39	0.6	0.0064	0.53	0.66	0.62	0.58	4.2	0.0055	0.0118	0.0091	0.08	0.012
3294501	0.63	0.0017	1.32	0.63	0.0002	0.61	0.65	0.65	0.62	4.97	0.0002	0.0032	0.0027	0.07	0.022
3298980	0.61	0.0095	1.34	0.62	0.0011	0.52	0.71	0.65	0.59	4.05	0.0018	0.03	0.0241	0.35	0.153

3301222	0.6	0.0138	1.33	0.6	0.0042	0.68	0.52	0.59	0.61	6.14	0.0063	0.0187	0.0112	0.29	0.034
3301703	0.6	0.014	1.34	0.61	0.0028	0.49	0.73	0.65	0.58	3.72	0.0038	0.0107	0.0074	0.32	0.041
3301858	0.6	0.0134	1.28	0.58	0.0276	0.39	0.78	0.64	0.55	4.07	0.0142	0.0254	0.0172	0.16	0.033
3301863	0.62	0.0033	1.36	0.63	0.0004	0.63	0.62	0.63	0.62	7.19	0.0008	0.0056	0.0027	0.22	0.012
3302047	0.67	0.0001	1.35	0.62	0.0011	0.53	0.7	0.65	0.59	5.12	0.0006	0.0001	0.0002	0.03	0.003
3304013	0.62	0.0031	1.29	0.61	0.0028	0.64	0.57	0.61	0.61	6.38	0.0046	0.0037	0.0025	0.1	0.005
3304626	0.61	0.0076	1.25	0.6	0.0042	0.5	0.7	0.64	0.58	5.73	0.0021	0.0052	0.0043	0.17	0.031
3304652	0.65	0.0003	1.38	0.6	0.0064	0.49	0.71	0.64	0.57	4.91	0.0031	0.0002	0.0004	0.09	0.011
3307940	0.61	0.0096	1.28	0.58	0.0276	0.5	0.65	0.6	0.56	3.98	0.0357	0.0117	0.009	0.15	0.03
3308532	0.62	0.0038	1.26	0.56	0.0889	0.4	0.72	0.6	0.54	5.32	0.033	0.0273	0.0286	0.23	0.05
3309267	0.6	0.0121	1.32	0.59	0.0138	0.57	0.6	0.6	0.58	5.15	0.006	0.0079	0.0119	0.12	0.043
3311304	0.65	0.0002	1.3	0.61	0.0028	0.45	0.78	0.67	0.58	3.87	0.0022	0.0017	0.0007	0.07	0.003
3317557	0.65	0.0002	1.35	0.57	0.0513	0.43	0.71	0.61	0.55	3.97	0.0488	0.0074	0.0035	0	0.001
3325714	0.61	0.0053	1.29	0.58	0.0197	0.47	0.7	0.62	0.56	4.46	0.0169	0.007	0.0057	0.27	0.036
3325963	0.64	0.0006	1.43	0.63	0.0004	0.65	0.6	0.63	0.63	5.49	0.0006	0.0017	0.0006	0.05	0.004
3326246	0.63	0.0022	1.26	0.59	0.0138	0.42	0.77	0.65	0.56	4.09	0.0088	0.0082	0.0071	0.08	0.035
3326465	0.66	0.0001	1.43	0.61	0.0028	0.54	0.67	0.63	0.59	3.43	0.0021	0.0001	0.0002	0.06	0.004
3329941	0.64	0.0008	1.3	0.62	0.0011	0.57	0.66	0.64	0.6	4.95	0.0005	0.0002	0.0008	0.03	0.013
3331532	0.66	0.0001	1.29	0.64	0.0001	0.6	0.68	0.66	0.63	6.28	0.0001	0.0001	0.0001	0.01	0
3331573	0.62	0.0025	1.43	0.63	0.0002	0.63	0.63	0.64	0.63	5.1	0.0002	0.0008	0.001	0.09	0.016
3331613	0.65	0.0002	1.26	0.63	0.0004	0.55	0.7	0.66	0.61	6.82	0.0004	0.0003	0.0002	0.01	0.001
3331614	0.64	0.0006	1.36	0.63	0.0004	0.72	0.53	0.61	0.65	6.9	0.0006	0.0014	0.0008	0.03	0.002
3333687	0.6	0.0109	1.29	0.59	0.0138	0.58	0.59	0.6	0.58	5.39	0.021	0.0263	0.0172	0.22	0.06
3334162	0.64	0.0007	1.31	0.61	0.0028	0.5	0.72	0.65	0.58	5.02	0.0008	0.0003	0.001	0.05	0.066
3334515	0.62	0.003	1.26	0.6	0.0042	0.67	0.53	0.6	0.61	7.13	0.0057	0.0025	0.0022	0.02	0.002
3335173	0.66	0.0001	1.47	0.62	0.0007	0.67	0.57	0.62	0.63	6.87	0.0011	0.0001	0.0001	0.02	0.002
3335176	0.65	0.0003	1.38	0.61	0.0028	0.6	0.61	0.62	0.6	6.73	0.0032	0.0003	0.0003	0.02	0.002
3335178	0.65	0.0003	1.31	0.62	0.0007	0.62	0.62	0.63	0.62	7	0.0004	0.0002	0.0003	0.01	0.002
3335179	0.65	0.0002	1.46	0.63	0.0002	0.6	0.66	0.65	0.62	5.84	0.0002	0.0002	0.0002	0.01	0.002
3335181	0.65	0.0002	1.29	0.61	0.0018	0.69	0.53	0.6	0.63	8.16	0.0027	0.0008	0.0008	0.03	0.003
3335182	0.64	0.0004	1.29	0.62	0.0007	0.67	0.57	0.62	0.63	8.91	0.001	0.0008	0.0009	0.03	0.003
3335187	0.65	0.0002	1.38	0.64	0.0001	0.69	0.59	0.64	0.65	8.55	0.0001	0.0004	0.0005	0.03	0.002
3335188	0.65	0.0003	1.27	0.63	0.0002	0.7	0.56	0.62	0.65	9.15	0.0004	0.0007	0.0005	0.03	0.003
3335189	0.62	0.0037	1.29	0.59	0.0138	0.59	0.58	0.59	0.58	5.87	0.0145	0.0018	0.0036	0.05	0.023
3335191	0.65	0.0004	1.32	0.62	0.0011	0.65	0.58	0.62	0.62	8.92	0.0014	0.0007	0.0012	0.04	0.005
3335231	0.64	0.0006	1.27	0.63	0.0004	0.75	0.5	0.61	0.66	7.56	0.0005	0.0008	0.0006	0.03	0.004
3337724	0.64	0.0006	1.26	0.64	0.0001	0.64	0.64	0.65	0.64	7.12	0.0001	0.0012	0.0005	0.09	0.003
3338618	0.65	0.0002	1.36	0.65	0	0.62	0.67	0.66	0.63	7.42	0	0.0003	0.0003	0.02	0.003
3341466	0.63	0.0017	1.25	0.63	0.0002	0.68	0.58	0.63	0.64	5.33	0.0002	0.0021	0.0027	0.09	0.033
3341504	0.64	0.0009	1.5	0.6	0.0042	0.58	0.62	0.61	0.59	5.8	0.0053	0.0011	0.0009	0.05	0.005
3344853	0.62	0.005	1.6	0.6	0.0042	0.63	0.57	0.6	0.6	4.8	0.0033	0.0048	0.0032	0.07	0.009

3344889	0.62	0.0049	1.34	0.59	0.0138	0.49	0.69	0.62	0.57	3.99	0.0097	0.0046	0.0044	0.11	0.017
3345453	0.61	0.0074	1.57	0.6	0.0064	0.55	0.64	0.62	0.58	5.32	0.0054	0.0092	0.0078	0.11	0.047
3347691	0.61	0.0072	1.26	0.59	0.0138	0.55	0.62	0.6	0.58	6.2	0.0155	0.0116	0.0059	0.14	0.02
3352533	0.67	0	1.25	0.63	0.0002	0.69	0.57	0.63	0.64	5.45	0.0005	0.0001	0.0001	0.02	0.001
3352561	0.62	0.0051	1.32	0.62	0.0007	0.6	0.64	0.64	0.61	4.61	0.0012	0.0063	0.005	0.15	0.027
3352585	0.61	0.0063	1.34	0.62	0.0011	0.7	0.53	0.61	0.63	5.69	0.0011	0.0066	0.0071	0.08	0.019
3352925	0.62	0.0027	1.32	0.62	0.0011	0.57	0.66	0.64	0.6	3.22	0.0009	0.0009	0.0012	0.04	0.004
3354966	0.62	0.003	1.29	0.62	0.0011	0.61	0.62	0.63	0.61	7.42	0.0013	0.0043	0.0041	0.1	0.013
3356173	0.62	0.0045	1.3	0.6	0.0042	0.56	0.64	0.62	0.59	4.84	0.0026	0.0039	0.0045	0.02	0.011
3358364	0.64	0.0004	1.4	0.63	0.0004	0.71	0.54	0.62	0.65	5.9	0.0004	0.0005	0.0003	0.02	0.002
3359382	0.64	0.0006	1.35	0.6	0.0042	0.49	0.72	0.64	0.58	4.53	0.0026	0.0004	0.0008	0.12	0.013
3362739	0.62	0.0023	1.42	0.6	0.0064	0.52	0.67	0.62	0.58	4.72	0.0043	0.0022	0.0026	0.01	0.01
3362742	0.65	0.0002	1.56	0.64	0.0001	0.66	0.62	0.64	0.64	5.09	0.0001	0.0003	0.0004	0.02	0.009
3362745	0.61	0.007	1.39	0.6	0.0042	0.56	0.64	0.62	0.59	5.36	0.0023	0.0051	0.0054	0.08	0.024
3362763	0.67	0	1.25	0.62	0.0007	0.54	0.7	0.65	0.6	5.41	0.0006	0.0002	0.0001	0.01	0.001
3362773	0.64	0.001	1.28	0.61	0.0018	0.55	0.67	0.64	0.59	7.19	0.0012	0.0013	0.0008	0.06	0.003
3362943	0.62	0.0049	1.47	0.61	0.0018	0.58	0.64	0.63	0.6	5.08	0.0014	0.0056	0.004	0.1	0.01
3363519	0.61	0.0099	1.31	0.63	0.0004	0.6	0.65	0.64	0.62	4.57	0	0.0093	0.017	0.03	0.065
3363981	0.6	0.0113	1.29	0.58	0.0276	0.47	0.69	0.61	0.56	3.66	0.0122	0.0376	0.043	0.14	0.055
3364729	0.61	0.0056	1.36	0.56	0.0681	0.49	0.64	0.58	0.55	4.73	0.0521	0.0049	0.0071	0.14	0.118
3364770	0.64	0.0006	1.28	0.6	0.0064	0.52	0.67	0.62	0.58	4.25	0.0074	0.0011	0.0008	0.06	0.012
3364800	0.64	0.0006	1.32	0.64	0.0001	0.58	0.69	0.66	0.62	3.64	0.0001	0.002	0.001	0.08	0.017
3368920	0.6	0.011	1.34	0.6	0.0064	0.55	0.64	0.62	0.58	5.71	0.0113	0.0142	0.0091	0.13	0.018
3371737	0.61	0.0063	1.25	0.61	0.0028	0.57	0.64	0.62	0.59	6.25	0.0034	0.0073	0.0052	0.13	0.018
3372461	0.61	0.0093	1.39	0.57	0.0513	0.47	0.67	0.59	0.55	3.62	0.0298	0.0243	0.0231	0.05	0.019
3375309	0.6	0.0134	1.54	0.6	0.0064	0.62	0.57	0.6	0.6	4.78	0.0149	0.0179	0.0088	0.18	0.018
3375752	0.66	0.0001	1.3	0.61	0.0018	0.6	0.62	0.62	0.6	5.1	0.0026	0.0006	0.0004	0.02	0.003
3375863	0.63	0.0016	1.3	0.61	0.0018	0.58	0.64	0.63	0.6	4.63	0.0048	0.0035	0.0017	0.04	0.005
3376090	0.64	0.0005	1.42	0.62	0.0007	0.64	0.6	0.63	0.62	5.66	0.0009	0.0004	0.0004	0.07	0.009
3376775	0.62	0.0036	1.25	0.59	0.0095	0.62	0.56	0.59	0.59	5.6	0.0068	0.0043	0.0049	0.09	0.021
3377457	0.61	0.0057	1.58	0.62	0.0007	0.62	0.62	0.63	0.62	4.79	0.0002	0.0042	0.0044	0.04	0.008
3377464	0.62	0.004	1.36	0.63	0.0004	0.65	0.6	0.63	0.63	6.05	0.0004	0.0034	0.0024	0.09	0.013
3377621	0.64	0.0005	1.42	0.62	0.0011	0.68	0.55	0.61	0.63	6.62	0.0015	0.0003	0.0004	0.03	0.007
3377623	0.63	0.0016	1.37	0.6	0.0064	0.64	0.55	0.6	0.6	6.65	0.0059	0.0009	0.0011	0.04	0.008
3377625	0.63	0.0017	1.31	0.61	0.0028	0.73	0.48	0.59	0.64	6.78	0.0033	0.0021	0.0019	0.1	0.01
3377632	0.64	0.001	1.37	0.59	0.0095	0.66	0.52	0.59	0.6	6.13	0.0099	0.0008	0.0009	0.03	0.004
3377633	0.61	0.0054	1.26	0.59	0.0095	0.53	0.65	0.61	0.58	6.83	0.0047	0.0024	0.005	0.08	0.038
3377659	0.65	0.0004	1.29	0.61	0.0018	0.65	0.57	0.61	0.62	9.15	0.0022	0.0009	0.0011	0.04	0.003
3377660	0.64	0.0006	1.29	0.63	0.0004	0.66	0.59	0.63	0.63	7.82	0.0004	0.0011	0.0013	0.04	0.004
3379122	0.62	0.0028	1.44	0.61	0.0018	0.67	0.55	0.61	0.62	6.31	0.0018	0.0035	0.0029	0.07	0.007
3379574	0.61	0.0069	1.36	0.6	0.0042	0.55	0.65	0.62	0.59	4.73	0.0024	0.0056	0.0057	0.13	0.019

3382981	0.66	0.0001	1.29	0.62	0.0011	0.6	0.63	0.63	0.61	5.13	0.0008	0.0002	0.0002	0.01	0.003
3382984	0.64	0.0004	1.32	0.6	0.0042	0.57	0.63	0.62	0.59	5.6	0.0036	0.0006	0.0007	0.05	0.011
3383148	0.63	0.0011	1.39	0.62	0.0007	0.69	0.55	0.61	0.64	6.75	0.0009	0.0017	0.0012	0.02	0.002
3383149	0.61	0.0056	1.47	0.58	0.0197	0.59	0.57	0.59	0.58	5.88	0.0217	0.0051	0.0047	0.09	0.013
3384489	0.64	0.0008	1.41	0.61	0.0018	0.57	0.65	0.63	0.6	5.19	0.0022	0.0009	0.0009	0.02	0.002
3384495	0.62	0.0035	1.35	0.63	0.0004	0.64	0.61	0.63	0.63	4.38	0.0011	0.0121	0.0058	0.41	0.051
3385045	0.65	0.0002	1.27	0.6	0.0042	0.43	0.79	0.67	0.57	3.72	0.0004	0.0002	0.0008	0.01	0.004
3385178	0.6	0.0107	1.34	0.6	0.0064	0.53	0.66	0.62	0.58	4.08	0.0055	0.0123	0.011	0.23	0.067
3386816	0.64	0.0009	1.33	0.61	0.0018	0.56	0.66	0.63	0.6	7.1	0.0036	0.0021	0.0009	0.06	0.003
3387176	0.61	0.009	1.26	0.59	0.0095	0.48	0.71	0.63	0.57	4.06	0.0173	0.0177	0.0116	0.48	0.068
3387436	0.64	0.0004	1.29	0.61	0.0028	0.54	0.67	0.63	0.59	5.92	0.0032	0.0011	0.0004	0.02	0.002
3388633	0.64	0.0005	1.31	0.65	0	0.58	0.72	0.69	0.63	5.36	0	0.0006	0.0005	0.03	0.006
3393789	0.62	0.0033	1.38	0.63	0.0004	0.61	0.64	0.64	0.62	5.27	0.0008	0.0028	0.0022	0.08	0.006
3394076	0.65	0.0002	1.28	0.64	0.0001	0.59	0.69	0.67	0.62	7.04	0.0001	0.0002	0.0003	0.04	0.003
3394529	0.6	0.0109	1.35	0.59	0.0138	0.53	0.64	0.61	0.57	4.77	0.0115	0.0238	0.0278	0.58	0.288
3395420	0.61	0.0057	1.37	0.61	0.0018	0.64	0.58	0.61	0.61	6.13	0.0033	0.0052	0.0057	0.11	0.016
3395427	0.62	0.0026	1.29	0.62	0.0007	0.59	0.65	0.64	0.61	5.82	0.0004	0.0026	0.0032	0.05	0.015
3400152	0.62	0.0024	1.26	0.6	0.0042	0.58	0.62	0.61	0.59	4.91	0.0069	0.0035	0.0021	0.16	0.022
3402624	0.61	0.0103	1.25	0.58	0.0276	0.51	0.64	0.6	0.56	5.13	0.0325	0.0107	0.0113	0.04	0.018
3402667	0.63	0.0021	1.25	0.59	0.0095	0.6	0.58	0.6	0.59	5.61	0.0058	0.0017	0.002	0.01	0.003
3402720	0.63	0.0012	1.4	0.61	0.0018	0.58	0.64	0.63	0.6	5.64	0.0021	0.0023	0.0015	0.04	0.004
3406062	0.63	0.0018	1.29	0.64	0.0001	0.57	0.7	0.67	0.62	4.22	0.0002	0.0021	0.002	0.06	0.005
3407177	0.64	0.0005	1.25	0.54	0.2178	0.34	0.74	0.58	0.52	3.85	0.1199	0.0007	0.0022	0.08	0.029
3407275	0.61	0.0068	1.28	0.56	0.0681	0.46	0.67	0.59	0.55	5.5	0.0872	0.0085	0.0089	0.38	0.1
3409292	0.61	0.0081	1.31	0.63	0.0002	0.59	0.67	0.65	0.62	5.99	0.0002	0.0054	0.0088	0.25	0.06
3412651	0.63	0.0015	1.31	0.6	0.0042	0.48	0.73	0.65	0.58	5.63	0.0043	0.0023	0.0018	0.03	0.005
3414226	0.64	0.0007	1.4	0.65	0	0.67	0.62	0.65	0.65	6.01	0	0.0006	0.0004	0.01	0.001
3416068	0.65	0.0003	1.34	0.62	0.0011	0.63	0.6	0.62	0.61	5.69	0.001	0.0002	0.0004	0.01	0.005
3416501	0.6	0.0141	1.26	0.6	0.0064	0.49	0.71	0.64	0.57	4.91	0.0061	0.025	0.02	0.24	0.076
3417160	0.64	0.0004	1.38	0.62	0.0011	0.61	0.62	0.63	0.61	6.47	0.0013	0.0004	0.0005	0.01	0.002
3417666	0.64	0.0005	1.31	0.58	0.0276	0.55	0.6	0.59	0.57	6.07	0.0331	0.0008	0.0006	0.02	0.003
3418209	0.62	0.0041	1.34	0.6	0.0064	0.55	0.64	0.62	0.58	4.18	0.006	0.0085	0.0083	0.06	0.018
3419262	0.63	0.0021	1.29	0.62	0.0007	0.54	0.7	0.65	0.6	5.76	0.0005	0.0031	0.0026	0.06	0.011
3419622	0.64	0.0009	1.35	0.62	0.0011	0.6	0.63	0.63	0.61	4.99	0.0005	0.0004	0.0007	0.04	0.024
3421154	0.62	0.0037	1.42	0.59	0.0095	0.65	0.53	0.59	0.6	5.74	0.0115	0.0039	0.0032	0.07	0.007
3421223	0.61	0.0062	1.58	0.61	0.0018	0.56	0.66	0.63	0.6	4.69	0.0017	0.0054	0.0035	0.09	0.015
3421350	0.63	0.0014	1.39	0.6	0.0064	0.57	0.62	0.61	0.59	5.56	0.0042	0.001	0.0009	0.04	0.009
3421492	0.61	0.006	1.25	0.6	0.0064	0.48	0.72	0.64	0.57	4.45	0.0054	0.0103	0.005	0.13	0.024
3421652	0.61	0.0085	1.31	0.61	0.0028	0.62	0.59	0.61	0.6	6.32	0.0035	0.0138	0.0078	0.2	0.016
3421668	0.64	0.001	1.3	0.58	0.0276	0.42	0.74	0.63	0.55	4.63	0.0331	0.0093	0.0031	0.04	0.017
3427811	0.61	0.0086	1.3	0.61	0.0018	0.54	0.68	0.64	0.59	3.76	0.0018	0.0186	0.0167	0.04	0.01

3427812	0.65	0.0002	1.51	0.6	0.0042	0.6	0.6	0.61	0.6	5.2	0.0055	0.0004	0.0003	0	0
3428711	0.66	0.0002	1.34	0.62	0.0011	0.46	0.79	0.69	0.58	4.49	0.0002	0.0011	0.0009	0.01	0.004
3428712	0.62	0.0025	1.31	0.58	0.0276	0.45	0.71	0.62	0.56	4.48	0.0242	0.0169	0.0072	0.18	0.028
3429794	0.62	0.003	1.26	0.62	0.0007	0.59	0.65	0.64	0.61	5.44	0.0006	0.0053	0.006	0.1	0.023
3430575	0.62	0.0025	1.26	0.61	0.0018	0.54	0.68	0.64	0.59	6.53	0.0021	0.0033	0.0034	0.07	0.02
3431352	0.6	0.0111	1.31	0.6	0.0042	0.58	0.62	0.61	0.59	5.54	0.0047	0.0188	0.0099	0.13	0.011
3431686	0.64	0.0007	1.27	0.64	0.0001	0.55	0.72	0.67	0.61	5.54	0.0002	0.0014	0.0008	0.05	0.004
3432171	0.64	0.0006	1.42	0.64	0.0001	0.63	0.64	0.65	0.63	5.86	0.0002	0.0005	0.0003	0.04	0.002
3432352	0.62	0.0049	1.26	0.58	0.0197	0.52	0.64	0.6	0.57	5.27	0.0135	0.0039	0.0068	0.06	0.018
3435860	0.64	0.0008	1.4	0.64	0.0001	0.67	0.6	0.64	0.64	4.87	0.0001	0.0008	0.001	0.03	0.006
3435864	0.64	0.0006	1.28	0.59	0.0138	0.5	0.67	0.61	0.57	6.2	0.0067	0.0005	0.0009	0.01	0.009
3436017	0.62	0.0025	1.25	0.59	0.0138	0.56	0.61	0.6	0.58	5.68	0.0145	0.004	0.0035	0.02	0.008
3436264	0.62	0.0031	1.48	0.6	0.0064	0.56	0.63	0.61	0.58	4.23	0.0064	0.0047	0.0035	0.03	0.003
3438044	0.61	0.0098	1.38	0.59	0.0095	0.48	0.71	0.63	0.57	4.94	0.0063	0.0105	0.0116	0.2	0.105
3445545	0.61	0.0065	1.27	0.59	0.0095	0.54	0.64	0.61	0.58	5.51	0.0066	0.0105	0.0078	0.12	0.02
3445674	0.64	0.0008	1.36	0.6	0.0064	0.47	0.73	0.64	0.57	3.86	0.0016	0.0034	0.0036	0.01	0.007
3445750	0.64	0.0009	1.3	0.6	0.0064	0.43	0.78	0.66	0.57	4.94	0.003	0.001	0.0008	0.47	0.142
3446488	0.61	0.0055	1.34	0.58	0.0197	0.58	0.58	0.59	0.58	5.85	0.0292	0.0049	0.0051	0.34	0.056
3446869	0.61	0.0097	1.25	0.6	0.0064	0.61	0.58	0.6	0.59	7.86	0.0106	0.0086	0.007	0.05	0.006
3446885	0.61	0.006	1.26	0.57	0.0513	0.48	0.66	0.59	0.55	4.75	0.0338	0.0069	0.0077	0.02	0.02
3452256	0.63	0.0022	1.34	0.62	0.0007	0.65	0.59	0.62	0.62	5.46	0.0014	0.0028	0.0021	0.05	0.017
3452262	0.63	0.0011	1.41	0.61	0.0028	0.56	0.65	0.63	0.59	4.74	0.0035	0.0018	0.0018	0.08	0.034
3452324	0.62	0.0036	1.31	0.61	0.0018	0.56	0.66	0.63	0.6	5.71	0.001	0.0029	0.0046	0.15	0.046
3452349	0.67	0	1.25	0.62	0.0007	0.51	0.73	0.67	0.6	6.28	0.0004	0.0001	0.0001	0.12	0.011
3454729	0.62	0.0024	1.26	0.61	0.0018	0.58	0.64	0.63	0.6	7.12	0.0011	0.0022	0.0025	0.08	0.01
3456599	0.63	0.0015	1.4	0.62	0.0011	0.59	0.64	0.63	0.61	4.31	0.0007	0.0019	0.0024	0.04	0.015
3457550	0.64	0.0008	1.27	0.64	0.0001	0.57	0.7	0.67	0.62	6.92	0.0002	0.0008	0.0006	0.05	0.008
3458494	0.63	0.0011	1.28	0.62	0.0011	0.56	0.67	0.64	0.6	5.36	0.0004	0.0003	0.0007	0	0.002
3461302	0.63	0.0021	1.4	0.6	0.0042	0.59	0.61	0.61	0.59	6.08	0.0057	0.0033	0.0023	0.05	0.003
3461431	0.68	0	1.28	0.66	0	0.6	0.71	0.69	0.64	4.02	0	0	0	0	0.001
3462710	0.61	0.0055	1.28	0.59	0.0095	0.54	0.64	0.61	0.58	6.36	0.0099	0.01	0.0079	0.1	0.025
3462846	0.62	0.0037	1.34	0.57	0.0513	0.52	0.61	0.58	0.56	4.1	0.0946	0.0243	0.0079	0.21	0.016
3462861	0.6	0.0107	1.26	0.56	0.0681	0.51	0.61	0.58	0.55	5.04	0.0861	0.017	0.0147	0.14	0.022
3462867	0.65	0.0003	1.31	0.62	0.0007	0.68	0.56	0.62	0.63	7.41	0.0009	0.0006	0.0005	0.02	0.001
3462868	0.63	0.0011	1.26	0.58	0.0197	0.46	0.71	0.62	0.56	4.64	0.0393	0.007	0.0029	0.21	0.024
3462884	0.65	0.0002	1.3	0.62	0.0007	0.5	0.74	0.67	0.59	5.57	0.0004	0.0008	0.0004	0.05	0.002
3462988	0.64	0.0005	1.34	0.62	0.0007	0.69	0.55	0.61	0.64	5.34	0.0008	0.0007	0.0005	0.01	0.003
3463596	0.68	0	1.29	0.64	0.0001	0.52	0.76	0.69	0.61	6.46	0.0001	0	0	0.01	0
3463603	0.67	0	1.27	0.63	0.0002	0.56	0.7	0.66	0.61	4.05	0.0001	0.0003	0.0006	0.01	0.002
3464009	0.61	0.0058	1.27	0.63	0.0004	0.66	0.59	0.63	0.63	4.22	0.001	0.0295	0.0147	0.47	0.096
3465251	0.63	0.0021	1.36	0.6	0.0042	0.5	0.7	0.64	0.58	5.2	0.0027	0.0046	0.0045	0.12	0.023

3465252	0.61	0.007	1.47	0.62	0.0011	0.61	0.62	0.63	0.61	6.33	0.0022	0.0053	0.0044	0.15	0.018
3465278	0.63	0.002	1.29	0.53	0.31	0.31	0.76	0.56	0.51	5.11	0.3312	0.0161	0.0179	0.3	0.166
3466861	0.62	0.0027	1.27	0.6	0.0042	0.46	0.76	0.66	0.57	4.55	0.0009	0.0015	0.0034	0.13	0.04
3467642	0.63	0.002	1.36	0.61	0.0028	0.59	0.62	0.62	0.6	5.79	0.0024	0.0056	0.0029	0.1	0.015
3468015	0.63	0.0018	1.39	0.62	0.0011	0.52	0.71	0.65	0.59	4.88	0.0003	0.0019	0.0029	0.04	0.009
3469369	0.65	0.0004	1.27	0.6	0.0042	0.48	0.73	0.65	0.58	3.12	0.0033	0.0013	0.0016	0.01	0.012
3471177	0.6	0.0141	1.26	0.59	0.0138	0.5	0.67	0.61	0.57	4.52	0.008	0.0075	0.0107	0.23	0.184
3471377	0.64	0.0008	1.45	0.64	0.0001	0.6	0.68	0.66	0.63	6.02	0.0001	0.0003	0.0004	0.05	0.003
3471379	0.62	0.0035	1.27	0.58	0.0197	0.49	0.68	0.61	0.56	4.35	0.0131	0.0067	0.0081	0.51	0.146
3472092	0.62	0.0043	1.29	0.61	0.0018	0.65	0.57	0.61	0.62	7.95	0.0025	0.0042	0.0034	0.12	0.009
3473482	0.62	0.0043	1.3	0.57	0.038	0.46	0.69	0.61	0.55	4.38	0.0518	0.0078	0.0068	0.11	0.02
3474494	0.65	0.0004	1.33	0.62	0.0007	0.65	0.59	0.62	0.62	6.29	0.0019	0.0008	0.0005	0.04	0.004
3474937	0.61	0.0079	1.26	0.58	0.0276	0.52	0.63	0.6	0.56	5.34	0.0197	0.0188	0.0152	0.06	0.009
3475623	0.61	0.0058	1.26	0.57	0.038	0.46	0.69	0.61	0.55	4.6	0.0285	0.0095	0.0102	0.1	0.017
3475737	0.62	0.004	1.25	0.64	0.0001	0.55	0.72	0.67	0.61	4.86	0.0001	0.0043	0.0066	0.07	0.046
3476294	0.62	0.0029	1.38	0.61	0.0028	0.61	0.6	0.61	0.6	5.71	0.0039	0.0046	0.0034	0.06	0.004
3480098	0.66	0.0002	1.45	0.6	0.0064	0.55	0.64	0.62	0.58	4.26	0.0031	0.0001	0.0002	0.06	0.007
3480100	0.63	0.0016	1.25	0.58	0.0276	0.48	0.68	0.61	0.56	3.35	0.016	0.0014	0.002	0.02	0.01
3480173	0.63	0.0014	1.25	0.6	0.0042	0.51	0.69	0.63	0.58	5.38	0.002	0.0014	0.0018	0.07	0.01
3480201	0.65	0.0003	1.37	0.62	0.0007	0.62	0.62	0.63	0.62	5.14	0.0006	0.0003	0.0004	0.09	0.009
3480203	0.62	0.003	1.27	0.59	0.0138	0.59	0.58	0.59	0.58	5.88	0.0211	0.007	0.004	0.18	0.008
3480685	0.63	0.002	1.3	0.63	0.0002	0.66	0.6	0.63	0.63	7	0.0002	0.0025	0.0022	0.03	0.005
3480856	0.67	0.0001	1.29	0.61	0.0018	0.58	0.64	0.63	0.6	6.68	0.0039	0.0002	0.0001	0.02	0.003
3481480	0.64	0.0008	1.35	0.61	0.0018	0.59	0.63	0.63	0.6	4.71	0.0028	0.0042	0.0017	0.05	0.001
3482124	0.61	0.0063	1.28	0.59	0.0138	0.51	0.66	0.61	0.57	5.98	0.0166	0.0035	0.0051	0.36	0.126
3482915	0.62	0.0047	1.43	0.62	0.0007	0.53	0.71	0.66	0.6	4.94	0.0002	0.007	0.0076	0.03	0.004
3482916	0.61	0.0061	1.56	0.63	0.0004	0.63	0.62	0.63	0.62	4.71	0.0004	0.0041	0.0031	0.1	0.014
3483215	0.64	0.0006	1.27	0.62	0.0007	0.62	0.62	0.63	0.62	7.97	0.0005	0.0006	0.0008	0.03	0.003
3484743	0.65	0.0004	1.32	0.66	0	0.63	0.68	0.67	0.64	6.65	0	0.0004	0.0003	0.02	0.001
3484750	0.65	0.0002	1.48	0.64	0.0001	0.6	0.68	0.66	0.63	5.16	0.0001	0.0004	0.0003	0.01	0.002
3484756	0.64	0.0009	1.27	0.62	0.0011	0.55	0.68	0.64	0.6	5.07	0.0005	0.0007	0.0008	0.1	0.018
3484762	0.66	0.0001	1.33	0.64	0.0001	0.58	0.7	0.67	0.62	6.04	0	0.0001	0.0001	0.01	0.001
3485891	0.61	0.0092	1.54	0.59	0.0095	0.56	0.62	0.61	0.58	4.59	0.0142	0.0118	0.0077	0.16	0.012
3489010	0.62	0.0034	1.38	0.58	0.0276	0.56	0.59	0.59	0.57	5.21	0.0421	0.0074	0.0052	0.07	0.019
3489011	0.62	0.0026	1.33	0.61	0.0018	0.7	0.52	0.6	0.63	7.21	0.0034	0.0043	0.0025	0.11	0.007
3494193	0.61	0.0096	1.39	0.61	0.0018	0.62	0.6	0.62	0.61	5.2	0.001	0.0067	0.01	0.06	0.028
3497656	0.6	0.0148	1.36	0.6	0.0064	0.53	0.66	0.62	0.58	3.74	0.0131	0.0094	0.0103	0.12	0.051
3497658	0.64	0.0009	1.27	0.64	0.0001	0.59	0.68	0.66	0.62	6.46	0.0001	0.001	0.001	0.02	0.001
3497823	0.65	0.0003	1.31	0.61	0.0018	0.55	0.67	0.64	0.59	4.76	0.0017	0.0009	0.0007	0.02	0.003
3498048	0.63	0.0014	1.36	0.59	0.0138	0.45	0.73	0.63	0.56	4.52	0.0084	0.0006	0.0008	0.04	0.002
3498445	0.64	0.0007	1.31	0.63	0.0004	0.62	0.63	0.64	0.62	5.36	0.0006	0.0006	0.0008	0.05	0.007

3498523	0.66	0.0001	1.67	0.65	0	0.65	0.64	0.65	0.64	5.42	0.0001	0.0004	0.0002	0.02	0.002
3498537	0.62	0.0033	1.26	0.59	0.0138	0.51	0.66	0.61	0.57	5.14	0.0083	0.0041	0.0041	0.13	0.025
3498977	0.64	0.0008	1.34	0.59	0.0095	0.61	0.57	0.6	0.59	5.28	0.013	0.001	0.0006	0.02	0.001
3499545	0.62	0.0024	1.29	0.63	0.0002	0.62	0.64	0.64	0.62	5.41	0.0003	0.0029	0.0029	0.06	0.006
3500408	0.61	0.0076	1.3	0.59	0.0095	0.53	0.65	0.61	0.58	5.14	0.0086	0.0039	0.006	0.1	0.013
3501216	0.64	0.0009	1.29	0.59	0.0095	0.55	0.63	0.61	0.58	6.18	0.0181	0.001	0.0017	0.04	0.006
3501217	0.65	0.0002	1.34	0.61	0.0028	0.63	0.58	0.61	0.61	6.24	0.0049	0.0002	0.0003	0.01	0.002
3501555	0.68	0	1.51	0.63	0.0002	0.57	0.69	0.66	0.61	5.52	0.0002	0.0001	0	0.01	0
3503211	0.65	0.0002	1.27	0.62	0.0007	0.56	0.68	0.65	0.6	6.53	0.0006	0.0003	0.0003	0.02	0.003
3505453	0.61	0.0073	1.56	0.6	0.0042	0.55	0.65	0.62	0.59	4.72	0.0119	0.01	0.0045	0.12	0.008
3506941	0.62	0.0043	1.38	0.61	0.0028	0.56	0.65	0.63	0.59	4.83	0.0038	0.0043	0.0049	0.13	0.027
3508731	0.65	0.0002	1.35	0.58	0.0197	0.33	0.85	0.69	0.55	4.44	0.0019	0.0006	0.0009	0.03	0.006
3508732	0.61	0.0077	1.28	0.62	0.0011	0.54	0.69	0.65	0.6	5.69	0.0006	0.0062	0.0072	0.15	0.043
3508761	0.65	0.0002	1.31	0.63	0.0004	0.61	0.64	0.64	0.62	6.68	0.0003	0.0002	0.0004	0.02	0.006
3509912	0.64	0.0008	1.48	0.61	0.0018	0.61	0.61	0.62	0.61	3.92	0.0015	0.0034	0.0022	0.04	0.004
3509913	0.61	0.0085	1.32	0.6	0.0064	0.5	0.69	0.63	0.58	4.02	0.0082	0.0161	0.0134	0.16	0.035
3510070	0.61	0.0082	1.25	0.61	0.0018	0.5	0.72	0.65	0.59	7.05	0.0005	0.0024	0.0073	0.07	0.017
3510382	0.64	0.0005	1.37	0.61	0.0028	0.56	0.65	0.63	0.59	5.76	0.0032	0.0005	0.0007	0.01	0.002
3512558	0.64	0.001	1.28	0.59	0.0095	0.65	0.53	0.59	0.6	7.23	0.0117	0.001	0.001	0.07	0.005
3513710	0.62	0.0028	1.29	0.59	0.0138	0.5	0.68	0.62	0.57	4.27	0.0154	0.0068	0.0034	0.09	0.013
3517677	0.65	0.0002	1.45	0.61	0.0018	0.37	0.87	0.74	0.57	4.15	0.0001	0.0001	0.0002	0.03	0.003
3517683	0.67	0	1.25	0.64	0.0001	0.53	0.76	0.69	0.61	5.6	0	0.0001	0.0003	0.01	0.003
3518501	0.62	0.0038	1.35	0.59	0.0138	0.49	0.69	0.62	0.57	4.62	0.0038	0.013	0.0114	0.03	0.01
3519136	0.63	0.001	1.35	0.63	0.0004	0.53	0.72	0.67	0.6	4.81	0.0003	0.0022	0.0017	0.13	0.012
3521962	0.61	0.0059	1.27	0.61	0.0028	0.49	0.73	0.65	0.58	5.22	0.0007	0.003	0.0042	0.29	0.079
3524627	0.62	0.0044	1.26	0.6	0.0042	0.54	0.66	0.63	0.59	5.82	0.0032	0.0044	0.0055	0.07	0.013
3524630	0.6	0.0141	1.31	0.6	0.0064	0.53	0.66	0.62	0.58	4.61	0.0078	0.02	0.0214	0.45	0.127
3524631	0.64	0.0007	1.39	0.61	0.0018	0.58	0.64	0.63	0.6	4.94	0.0015	0.0007	0.0005	0.08	0.005
3525314	0.65	0.0003	1.37	0.62	0.0007	0.61	0.63	0.63	0.61	6.22	0.0007	0.0004	0.0004	0.02	0.001
3525317	0.65	0.0002	1.47	0.59	0.0095	0.55	0.63	0.61	0.58	5.43	0.0188	0.0002	0.0002	0.01	0
3525320	0.63	0.0016	1.38	0.6	0.0042	0.56	0.64	0.62	0.59	5.97	0.0074	0.0009	0.0012	0.1	0.019
3525547	0.61	0.0079	1.26	0.6	0.0042	0.67	0.53	0.6	0.61	5.66	0.0108	0.0083	0.0065	0.07	0.007
3525702	0.62	0.0024	1.37	0.62	0.0011	0.54	0.69	0.65	0.6	5.08	0.001	0.0037	0.002	0.11	0.011
3525704	0.65	0.0002	1.32	0.61	0.0018	0.67	0.55	0.61	0.62	4.82	0.0019	0.0004	0.0003	0.03	0.006
3525710	0.64	0.0005	1.29	0.64	0.0001	0.62	0.65	0.65	0.63	8.03	0.0002	0.0006	0.0004	0.03	0.001
3526383	0.63	0.0019	1.25	0.59	0.0095	0.46	0.73	0.64	0.57	3.04	0.0052	0.0499	0.0366	0.13	0.027
3527530	0.62	0.0034	1.33	0.6	0.0064	0.6	0.59	0.6	0.59	4.61	0.0063	0.0049	0.0036	0.01	0.002
3528208	0.6	0.0135	1.35	0.6	0.0064	0.56	0.63	0.61	0.58	4.77	0.0043	0.0318	0.0225	0.46	0.13
3529094	0.62	0.0039	1.28	0.62	0.0011	0.62	0.61	0.62	0.61	4.74	0.002	0.0044	0.0045	0.14	0.031
3531094	0.63	0.0013	1.33	0.57	0.038	0.5	0.64	0.59	0.56	5.34	0.0448	0.0041	0.0028	0.21	0.032
3531491	0.65	0.0003	1.47	0.63	0.0002	0.54	0.72	0.67	0.61	4.11	0.0001	0.0003	0.0003	0.1	0.007

3533452	0.64	0.0009	1.37	0.62	0.0007	0.64	0.6	0.63	0.62	6.32	0.001	0.0009	0.0009	0.03	0.002
3534950	0.68	0	1.41	0.65	0	0.61	0.68	0.67	0.63	6.12	0	0	0	0.01	0.001
3535917	0.61	0.0084	1.25	0.59	0.0138	0.5	0.67	0.61	0.57	4.79	0.0108	0.0196	0.0119	0.09	0.016
3536669	0.64	0.0006	1.26	0.65	0	0.52	0.79	0.72	0.62	6.07	0	0.0005	0.0005	0.01	0.001
3536745	0.64	0.0004	1.41	0.59	0.0095	0.5	0.68	0.62	0.57	4.96	0.0209	0.0025	0.0011	0.04	0.008
3536931	0.63	0.0021	1.29	0.59	0.0095	0.56	0.62	0.61	0.58	7.39	0.009	0.0024	0.0027	0.12	0.021
3536934	0.61	0.0084	1.29	0.62	0.0007	0.6	0.64	0.64	0.61	4.7	0.0008	0.0072	0.0078	0.08	0.019
3536938	0.61	0.0072	1.32	0.6	0.0042	0.57	0.63	0.62	0.59	5.98	0.007	0.0051	0.0062	0.12	0.039
3536943	0.66	0.0001	1.31	0.63	0.0002	0.6	0.66	0.65	0.62	5.91	0.0001	0	0.0001	0.01	0.001
3536948	0.64	0.0006	1.26	0.6	0.0064	0.53	0.66	0.62	0.58	6.2	0.0065	0.0005	0.0009	0.04	0.013
3536949	0.61	0.0058	1.52	0.6	0.0042	0.6	0.6	0.61	0.6	5.83	0.0056	0.003	0.0036	0.03	0.007
3536951	0.62	0.0038	1.49	0.59	0.0095	0.55	0.63	0.61	0.58	4.41	0.011	0.004	0.0045	0.04	0.014
3536992	0.61	0.0055	1.32	0.58	0.0276	0.48	0.68	0.61	0.56	3.98	0.0599	0.006	0.004	0.21	0.026
3536994	0.64	0.0007	1.32	0.62	0.0007	0.57	0.67	0.64	0.61	6.35	0.0012	0.001	0.0007	0.05	0.003
3537787	0.65	0.0004	1.29	0.65	0	0.55	0.74	0.69	0.62	5.2	0	0.0004	0.0003	0.1	0.008
3537795	0.6	0.0107	1.61	0.61	0.0028	0.63	0.58	0.61	0.61	5.36	0.0027	0.0086	0.0055	0.06	0.008
3537796	0.62	0.0047	1.5	0.59	0.0095	0.63	0.55	0.59	0.59	4.67	0.0113	0.0098	0.0057	0.03	0.004
3539104	0.63	0.0019	1.25	0.58	0.0197	0.52	0.64	0.6	0.57	6.42	0.0328	0.002	0.002	0.04	0.005
3539877	0.63	0.0014	1.34	0.6	0.0064	0.52	0.67	0.62	0.58	4.21	0.0136	0.0089	0.0043	0.07	0.018
3543929	0.64	0.0004	1.31	0.6	0.0064	0.66	0.53	0.59	0.6	6.37	0.0111	0.0007	0.0003	0.03	0.002
3544473	0.62	0.0024	1.3	0.61	0.0018	0.57	0.65	0.63	0.6	6.47	0.0017	0.0036	0.0026	0.03	0.003
3544890	0.61	0.0079	1.41	0.58	0.0197	0.53	0.63	0.6	0.57	4.49	0.0381	0.0078	0.0065	0.55	0.132
3545534	0.61	0.0052	1.37	0.61	0.0018	0.62	0.6	0.62	0.61	6.34	0.0022	0.0048	0.0038	0.04	0.005
3549043	0.61	0.0101	1.29	0.58	0.0276	0.51	0.64	0.6	0.56	5.29	0.0412	0.0149	0.0115	0.34	0.072
3550451	0.62	0.0044	1.37	0.63	0.0004	0.62	0.63	0.64	0.62	5.63	0.0003	0.0025	0.004	0.05	0.009
3550453	0.64	0.0009	1.26	0.63	0.0002	0.58	0.68	0.66	0.61	5.12	0.0002	0.0008	0.0013	0.06	0.038
3550455	0.61	0.0055	1.25	0.57	0.0513	0.42	0.72	0.61	0.55	3.91	0.0535	0.0147	0.0106	0.41	0.12
3552937	0.61	0.01	1.3	0.58	0.0197	0.56	0.6	0.59	0.57	4.66	0.0167	0.008	0.0155	0.22	0.153
3552938	0.61	0.0065	1.31	0.57	0.038	0.51	0.63	0.59	0.56	5.16	0.0371	0.0054	0.0083	0.04	0.02
3556198	0.64	0.0004	1.26	0.61	0.0018	0.56	0.66	0.63	0.6	7.24	0.001	0.0007	0.0005	0.05	0.007
3556224	0.65	0.0003	1.28	0.62	0.0007	0.62	0.62	0.63	0.62	5.68	0.0011	0.0009	0.0005	0.06	0.002
3556278	0.63	0.0019	1.34	0.61	0.0018	0.45	0.79	0.68	0.58	4.31	0.0008	0.002	0.0015	0.05	0.008
3556420	0.61	0.0066	1.35	0.61	0.0028	0.57	0.64	0.62	0.59	4.26	0.003	0.0071	0.0058	0.19	0.024
3558292	0.64	0.0008	1.32	0.62	0.0007	0.69	0.55	0.61	0.64	6.56	0.0009	0.0015	0.0011	0.03	0.003
3559519	0.64	0.0007	1.31	0.59	0.0138	0.42	0.77	0.65	0.56	4.33	0.0104	0.0009	0.0007	0.18	0.005
3559556	0.6	0.0117	1.25	0.58	0.0276	0.48	0.68	0.61	0.56	4.19	0.0242	0.0098	0.014	0.12	0.011
3562436	0.7	0	1.31	0.64	0.0001	0.49	0.81	0.72	0.6	3.49	0	0	0.0001	0.05	0.002
3563349	0.65	0.0004	1.26	0.63	0.0004	0.53	0.72	0.67	0.6	4.98	0.0001	0.0005	0.0007	0.04	0.009
3563970	0.62	0.0038	1.27	0.57	0.0513	0.46	0.68	0.6	0.55	4.02	0.0384	0.0049	0.0049	0.13	0.029
3566596	0.63	0.0019	1.39	0.62	0.0007	0.63	0.61	0.63	0.62	6.08	0.0005	0.0017	0.0015	0.02	0.002
3566603	0.6	0.0136	1.34	0.59	0.0138	0.64	0.53	0.59	0.59	5.5	0.0183	0.0177	0.0122	0.09	0.012

3566648	0.61	0.0076	1.26	0.58	0.0276	0.46	0.7	0.61	0.56	4.37	0.028	0.0061	0.0076	0.12	0.015
3566657	0.62	0.0033	1.32	0.6	0.0064	0.48	0.72	0.64	0.57	4.58	0.0013	0.0018	0.0042	0.01	0.012
3566993	0.61	0.007	1.29	0.58	0.0276	0.55	0.6	0.59	0.57	5.09	0.0416	0.0098	0.0087	0.08	0.022
3569346	0.65	0.0003	1.39	0.62	0.0007	0.52	0.72	0.66	0.6	4.98	0.0007	0.0003	0.0004	0.04	0.007
3569757	0.65	0.0002	1.32	0.61	0.0018	0.54	0.68	0.64	0.59	6.32	0.0019	0.0006	0.0003	0.02	0.001
3569759	0.65	0.0003	1.25	0.61	0.0018	0.57	0.65	0.63	0.6	5.88	0.0018	0.0003	0.0004	0.01	0.004
3569819	0.64	0.0006	1.31	0.61	0.0018	0.56	0.66	0.63	0.6	5.21	0.003	0.0022	0.0017	0.18	0.027
3570456	0.61	0.0066	1.25	0.61	0.0028	0.64	0.57	0.61	0.61	5.71	0.0039	0.0099	0.0077	0.06	0.009
3573155	0.6	0.0135	1.26	0.57	0.0513	0.53	0.6	0.58	0.56	4.88	0.058	0.0281	0.0173	0.22	0.031
3576551	0.61	0.0053	1.29	0.59	0.0095	0.65	0.53	0.59	0.6	5.7	0.0219	0.0069	0.0042	0.08	0.009
3576567	0.65	0.0003	1.43	0.62	0.0007	0.51	0.73	0.67	0.6	4.66	0.0001	0.0003	0.0006	0.01	0.004
3576712	0.62	0.0027	1.44	0.6	0.0064	0.51	0.68	0.63	0.58	4.77	0.0039	0.0016	0.0019	0.09	0.046
3576730	0.62	0.0031	1.38	0.6	0.0064	0.56	0.63	0.61	0.58	5.46	0.0092	0.0027	0.0025	0.11	0.066
3576939	0.63	0.0022	1.4	0.61	0.0028	0.68	0.53	0.6	0.62	5.89	0.003	0.0023	0.001	0.06	0.002
3576940	0.64	0.001	1.32	0.61	0.0028	0.56	0.65	0.63	0.59	5.96	0.0033	0.0018	0.0012	0.07	0.008
3577874	0.66	0.0001	1.42	0.62	0.0011	0.59	0.64	0.63	0.61	4.39	0.0022	0.0004	0.0002	0	0
3577898	0.63	0.0022	1.33	0.63	0.0002	0.63	0.63	0.64	0.63	5.37	0.0002	0.0017	0.0015	0.04	0.007
3577911	0.65	0.0002	1.29	0.64	0.0001	0.56	0.72	0.68	0.62	5.09	0	0.0002	0.0006	0.02	0.006
3578431	0.64	0.0005	1.3	0.63	0.0004	0.55	0.7	0.66	0.61	4.99	0.0004	0.0008	0.0007	0.06	0.004
3580188	0.61	0.0066	1.29	0.58	0.0276	0.52	0.63	0.6	0.56	5.28	0.027	0.0034	0.0083	0.04	0.038
3580204	0.61	0.0096	1.27	0.61	0.0018	0.55	0.67	0.64	0.59	6.72	0.0008	0.0056	0.006	0.05	0.013
3580587	0.62	0.0024	1.32	0.59	0.0095	0.52	0.66	0.62	0.58	3.5	0.0054	0.0029	0.0049	0.29	0.226
3580953	0.63	0.0015	1.27	0.58	0.0197	0.71	0.45	0.57	0.6	7.14	0.0262	0.006	0.005	0.09	0.008
3589660	0.61	0.0093	1.29	0.58	0.0276	0.46	0.7	0.61	0.56	4.64	0.0305	0.0167	0.0135	0.52	0.111
3590159	0.62	0.0042	1.29	0.6	0.0064	0.62	0.57	0.6	0.6	5.62	0.0063	0.0034	0.004	0.01	0.002
3590352	0.62	0.003	1.27	0.57	0.0513	0.51	0.62	0.58	0.55	5.27	0.0812	0.0043	0.0045	0.21	0.11
3591851	0.63	0.0014	1.28	0.6	0.0042	0.59	0.61	0.61	0.59	4.89	0.0054	0.001	0.0013	0.13	0.021
3591858	0.68	0	1.28	0.62	0.0011	0.58	0.65	0.63	0.6	7.39	0.0017	0.0001	0	0.02	0
3591985	0.6	0.0128	1.25	0.6	0.0042	0.59	0.61	0.61	0.59	5.29	0.0034	0.0101	0.0121	0.07	0.026
3592046	0.61	0.0056	1.37	0.62	0.0007	0.64	0.6	0.63	0.62	5.82	0.0021	0.01	0.0046	0.2	0.027
3592047	0.63	0.0015	1.29	0.63	0.0002	0.7	0.56	0.62	0.65	6.69	0.0003	0.004	0.0012	0.05	0.004
3592395	0.61	0.0101	1.27	0.55	0.1438	0.42	0.68	0.58	0.53	4.01	0.1404	0.0068	0.0123	0.05	0.011
3593171	0.62	0.0029	1.64	0.62	0.0007	0.61	0.63	0.63	0.61	5.39	0.0009	0.0019	0.0013	0.07	0.011
3594101	0.61	0.0059	1.28	0.6	0.0042	0.46	0.76	0.66	0.57	4.57	0.0026	0.026	0.0227	0.1	0.043
3595811	0.63	0.0023	1.26	0.61	0.0028	0.61	0.6	0.61	0.6	4.89	0.0018	0.0015	0.0027	0.38	0.146
3595872	0.62	0.0041	1.42	0.61	0.0028	0.6	0.61	0.62	0.6	5.13	0.0011	0.0028	0.0033	0.04	0.011
3596235	0.68	0	1.28	0.63	0.0002	0.6	0.66	0.65	0.62	3.58	0.0001	0	0.0001	0.01	0.002
3597406	0.61	0.0059	1.29	0.6	0.0064	0.6	0.59	0.6	0.59	6.28	0.0055	0.0033	0.0053	0.22	0.069
3597468	0.61	0.0067	1.25	0.58	0.0276	0.59	0.56	0.58	0.57	6.2	0.0178	0.0033	0.0069	0.06	0.029
3597671	0.66	0.0001	1.32	0.6	0.0042	0.58	0.62	0.61	0.59	5.41	0.0041	0	0.0001	0.05	0.009
3598717	0.63	0.0016	1.36	0.61	0.0028	0.64	0.57	0.61	0.61	6.44	0.0032	0.0032	0.0024	0.1	0.007

3599449	0.61	0.009	1.32	0.61	0.0018	0.54	0.68	0.64	0.59	4.41	0.0019	0.0148	0.009	0.58	0.1
3602509	0.65	0.0002	1.3	0.63	0.0002	0.67	0.59	0.63	0.64	5.42	0.0003	0.0004	0.0003	0.01	0.003
3605249	0.63	0.0014	1.3	0.61	0.0028	0.65	0.56	0.61	0.61	5.41	0.0036	0.001	0.0011	0.02	0.011
3606117	0.61	0.0075	1.25	0.61	0.0018	0.5	0.73	0.66	0.59	4.63	0.0008	0.0037	0.0055	0.09	0.101
3606409	0.66	0.0001	1.43	0.63	0.0002	0.63	0.63	0.64	0.63	5.58	0.0001	0.0001	0.0001	0.02	0.002
3608201	0.62	0.0046	1.25	0.6	0.0042	0.54	0.66	0.63	0.59	5.04	0.0027	0.0027	0.0042	0.04	0.026
3609166	0.63	0.0011	1.35	0.62	0.0011	0.59	0.64	0.63	0.61	5.15	0.0006	0.0015	0.0011	0.04	0.004
3615597	0.63	0.0016	1.26	0.62	0.0011	0.56	0.67	0.64	0.6	4.92	0.0003	0.0023	0.0031	0.01	0.012
3615604	0.63	0.0012	1.26	0.62	0.0007	0.5	0.74	0.67	0.59	6.26	0.0004	0.0024	0.0012	0.04	0.011
3615659	0.62	0.0038	1.29	0.62	0.0011	0.58	0.65	0.63	0.6	4.57	0.0012	0.0047	0.0039	0.05	0.023
3615989	0.61	0.0062	1.26	0.59	0.0138	0.55	0.62	0.6	0.58	4.52	0.0284	0.0038	0.0033	0.02	0.005
3621014	0.66	0.0001	1.44	0.63	0.0004	0.52	0.73	0.67	0.6	5.45	0.0001	0.0001	0.0001	0.02	0.003
3623329	0.64	0.001	1.38	0.63	0.0004	0.53	0.72	0.67	0.6	5.71	0.0002	0.0005	0.0007	0.02	0.007
3624199	0.64	0.0005	1.25	0.61	0.0018	0.54	0.68	0.64	0.59	6.12	0.0038	0.0012	0.0009	0.02	0.006
3624533	0.66	0.0001	1.33	0.63	0.0002	0.57	0.69	0.66	0.61	4.65	0.0001	0	0.0001	0	0.002
3624702	0.61	0.0078	1.33	0.58	0.0197	0.52	0.64	0.6	0.57	3.93	0.0249	0.0115	0.0083	0.08	0.014
3625565	0.62	0.0026	1.32	0.59	0.0095	0.44	0.76	0.65	0.56	3.93	0.0036	0.0079	0.0143	0.28	0.258
3626570	0.63	0.0016	1.29	0.61	0.0018	0.53	0.69	0.64	0.59	4.56	0.0007	0.0009	0.0014	0.09	0.009
3626585	0.63	0.0011	1.25	0.61	0.0018	0.58	0.64	0.63	0.6	5.82	0.0029	0.0008	0.0009	0.05	0.005
3626730	0.63	0.0016	1.44	0.62	0.0007	0.57	0.67	0.64	0.61	5.14	0.0006	0.0014	0.0015	0.06	0.01
3627045	0.64	0.0008	1.25	0.6	0.0064	0.49	0.71	0.64	0.57	5.25	0.001	0.0014	0.0018	0.01	0.011
3628011	0.61	0.0101	1.25	0.58	0.0197	0.47	0.7	0.62	0.56	4.75	0.0188	0.0111	0.0146	0.21	0.09
3628052	0.61	0.0059	1.25	0.59	0.0138	0.5	0.67	0.61	0.57	5.4	0.0128	0.006	0.0068	0.23	0.053
3628057	0.64	0.0006	1.26	0.62	0.0007	0.48	0.78	0.69	0.59	5.07	0.0002	0.0014	0.0008	0.05	0.007
3628471	0.64	0.0005	1.45	0.61	0.0018	0.6	0.62	0.62	0.6	6.06	0.0036	0.0008	0.0005	0.02	0.002
3628924	0.64	0.0007	1.31	0.58	0.0276	0.48	0.68	0.61	0.56	4.63	0.0344	0.0026	0.002	0.02	0.006
3630191	0.64	0.0006	1.38	0.64	0.0001	0.61	0.67	0.66	0.63	6.32	0.0001	0.0003	0.0005	0.02	0.002
3631414	0.65	0.0004	1.27	0.63	0.0002	0.45	0.83	0.73	0.59	4.2	0	0.0001	0.0005	0	0.002
3632170	0.6	0.0111	1.41	0.6	0.0064	0.63	0.56	0.6	0.6	6.09	0.0067	0.0096	0.0083	0.04	0.007
3633110	0.63	0.0012	1.37	0.58	0.0276	0.53	0.62	0.59	0.56	4.04	0.0305	0.0037	0.003	0.05	0.012
3633223	0.61	0.006	1.27	0.6	0.0042	0.66	0.54	0.6	0.61	6.33	0.0043	0.0053	0.0044	0.09	0.016
3633226	0.62	0.0024	1.41	0.6	0.0064	0.51	0.68	0.63	0.58	4.11	0.0033	0.0009	0.0018	0.01	0.009
3634074	0.62	0.0027	1.42	0.62	0.0011	0.64	0.59	0.62	0.62	5.31	0.0012	0.0034	0.0022	0.17	0.014
3643958	0.61	0.0075	1.32	0.59	0.0138	0.55	0.62	0.6	0.58	5.77	0.0187	0.0111	0.0076	0.22	0.024
3645267	0.64	0.0004	1.3	0.61	0.0018	0.65	0.57	0.61	0.62	7.04	0.0013	0.0004	0.0004	0.01	0.001
3645314	0.63	0.0022	1.34	0.61	0.0028	0.7	0.51	0.6	0.63	5.55	0.0041	0.0019	0.0017	0.02	0.005
3645591	0.63	0.0013	1.28	0.59	0.0095	0.59	0.59	0.6	0.59	4.87	0.0096	0.0049	0.0036	0.15	0.032
3647535	0.62	0.0031	1.31	0.61	0.0028	0.58	0.63	0.62	0.6	5.33	0.0025	0.0039	0.0041	0.1	0.02
3648373	0.62	0.0032	1.26	0.58	0.0276	0.5	0.65	0.6	0.56	4.62	0.0323	0.0045	0.0067	0.12	0.02
3651472	0.64	0.0008	1.26	0.61	0.0018	0.55	0.67	0.64	0.59	5.07	0.0009	0.0015	0.0015	0.03	0.005
3653349	0.63	0.0018	1.29	0.6	0.0042	0.55	0.65	0.62	0.59	4.92	0.002	0.0025	0.0042	0.1	0.068

3653673	0.63	0.0012	1.37	0.64	0.0001	0.65	0.62	0.64	0.64	6.32	0.0001	0.0011	0.0008	0.01	0.001
3655101	0.61	0.0092	1.56	0.61	0.0028	0.55	0.66	0.63	0.59	4.47	0.0037	0.0034	0.0039	0.09	0.026
3658610	0.66	0.0001	1.31	0.63	0.0004	0.54	0.71	0.66	0.6	5.67	0.0002	0	0.0001	0.01	0.001
3659201	0.6	0.0133	1.35	0.58	0.0276	0.51	0.64	0.6	0.56	5.34	0.0158	0.0172	0.0231	0.23	0.038
3659319	0.66	0.0001	1.46	0.64	0.0001	0.58	0.69	0.66	0.62	5.09	0.0002	0.0003	0.0002	0.03	0.003
3660917	0.62	0.005	1.26	0.59	0.0095	0.55	0.63	0.61	0.58	3.05	0.013	0.0215	0.0106	0.28	0.04
3660927	0.6	0.0107	1.26	0.57	0.0513	0.43	0.71	0.61	0.55	4.12	0.0105	0.0094	0.0164	0.13	0.091
3665635	0.61	0.0057	1.41	0.59	0.0138	0.61	0.56	0.59	0.59	5.24	0.0062	0.0036	0.0042	0.05	0.009
3666111	0.64	0.0006	1.27	0.63	0.0002	0.49	0.79	0.7	0.6	4.28	0.0001	0.0011	0.0009	0.02	0.004
3666869	0.64	0.0006	1.64	0.64	0.0001	0.56	0.71	0.67	0.61	4.89	0.0001	0.0004	0.0004	0.08	0.014
3668992	0.61	0.0051	1.3	0.6	0.0064	0.53	0.66	0.62	0.58	4.44	0.0017	0.0021	0.0043	0.1	0.046
3671113	0.62	0.004	1.28	0.57	0.0513	0.41	0.73	0.61	0.55	4.96	0.029	0.0021	0.0071	0.02	0.016
3677863	0.64	0.0005	1.27	0.61	0.0028	0.52	0.69	0.64	0.59	5.25	0.0045	0.0033	0.0019	0.08	0.016
3679601	0.62	0.0027	1.28	0.58	0.0276	0.5	0.66	0.6	0.56	4.47	0.0241	0.0027	0.0045	0.06	0.023
3683054	0.62	0.0028	1.53	0.63	0.0004	0.68	0.57	0.62	0.64	5.14	0.0004	0.0014	0.0014	0.11	0.01
3685080	0.61	0.0075	1.29	0.58	0.0276	0.49	0.67	0.6	0.56	3.73	0.0218	0.0017	0.0044	0.1	0.05
3687262	0.63	0.0014	1.27	0.63	0.0004	0.71	0.54	0.62	0.65	8.12	0.0006	0.0018	0.0013	0.09	0.008
3687792	0.62	0.0033	1.5	0.6	0.0042	0.57	0.63	0.62	0.59	5.65	0.0075	0.0026	0.0022	0.1	0.012
3690089	0.62	0.0026	1.41	0.58	0.0197	0.55	0.61	0.6	0.57	5.33	0.0218	0.0042	0.0027	0.1	0.006
3692857	0.61	0.0071	1.28	0.59	0.0138	0.54	0.63	0.6	0.57	5.34	0.0126	0.0105	0.007	0.38	0.066
3693546	0.62	0.005	1.31	0.57	0.038	0.58	0.56	0.58	0.57	5.36	0.0226	0.0063	0.0072	0.11	0.053
3693711	0.62	0.0025	1.35	0.59	0.0138	0.52	0.65	0.61	0.57	4.97	0.0113	0.003	0.0038	0.07	0.015
3693737	0.62	0.0031	1.26	0.65	0	0.65	0.64	0.65	0.64	7.19	0.0001	0.004	0.0026	0.18	0.038
3693746	0.64	0.0009	1.29	0.56	0.0889	0.36	0.77	0.61	0.54	5.2	0.0493	0.0037	0.0064	0.18	0.113
3696670	0.62	0.005	1.35	0.62	0.0007	0.55	0.69	0.65	0.6	5.01	0.0007	0.0069	0.0065	0.17	0.028
3697925	0.63	0.0021	1.27	0.59	0.0095	0.52	0.66	0.62	0.58	4.75	0.0147	0.0013	0.0017	0.21	0.033
3699559	0.64	0.0008	1.26	0.62	0.0011	0.56	0.67	0.64	0.6	4.82	0.0006	0.0008	0.0011	0.03	0.009
3701588	0.64	0.0008	1.26	0.6	0.0064	0.59	0.6	0.61	0.59	5.75	0.0205	0.0051	0.0014	0.09	0.006
3705531	0.61	0.0094	1.37	0.57	0.038	0.42	0.73	0.62	0.55	4.01	0.0426	0.0248	0.02	0.18	0.017
3707211	0.62	0.0046	1.43	0.6	0.0064	0.56	0.63	0.61	0.58	5.42	0.0079	0.0084	0.0048	0.07	0.009
3708006	0.6	0.0126	1.37	0.62	0.0011	0.66	0.57	0.61	0.62	6.34	0.0019	0.0052	0.0044	0.09	0.014
3709275	0.62	0.0033	1.29	0.59	0.0138	0.52	0.65	0.61	0.57	5.13	0.0077	0.0019	0.0031	0.09	0.023
3710735	0.65	0.0004	1.29	0.63	0.0002	0.66	0.6	0.63	0.63	4.04	0.0006	0.0016	0.0008	0.14	0.021
3714102	0.62	0.0038	1.28	0.58	0.0197	0.57	0.59	0.59	0.57	5	0.0398	0.0065	0.0033	0.18	0.011
3715142	0.66	0.0002	1.37	0.63	0.0004	0.61	0.64	0.64	0.62	5.39	0.0006	0.0001	0.0002	0.09	0.012
3715434	0.61	0.0101	1.26	0.59	0.0138	0.54	0.63	0.6	0.57	4.69	0.0183	0.0153	0.0116	0.2	0.07
3716021	0.63	0.0022	1.36	0.61	0.0018	0.61	0.61	0.62	0.61	4.77	0.002	0.0014	0.002	0.13	0.022
3716674	0.6	0.0113	1.26	0.59	0.0138	0.56	0.61	0.6	0.58	5.17	0.0244	0.022	0.0142	0.41	0.084
3716757	0.64	0.0009	1.28	0.65	0	0.62	0.68	0.67	0.64	5.39	0	0.0016	0.0019	0.03	0.004
3717647	0.67	0	1.27	0.65	0	0.54	0.76	0.7	0.62	5.34	0	0.0003	0.0002	0.07	0.004
3717681	0.62	0.0038	1.31	0.62	0.0007	0.55	0.69	0.65	0.6	5.48	0.0008	0.0033	0.0033	0.31	0.099

3717684	0.63	0.001	1.28	0.64	0.0001	0.6	0.68	0.66	0.63	6.96	0.0001	0.0019	0.001	0.13	0.008
3718837	0.63	0.0014	1.26	0.6	0.0042	0.78	0.42	0.58	0.65	6.39	0.0051	0.0033	0.0026	0.06	0.004
3719123	0.61	0.0091	1.68	0.59	0.0138	0.5	0.67	0.61	0.57	4.59	0.0069	0.007	0.0075	0.19	0.028
3720778	0.62	0.0033	1.33	0.63	0.0002	0.57	0.69	0.66	0.61	5.66	0.0002	0.0041	0.0028	0.23	0.034
3720990	0.63	0.0011	1.27	0.6	0.0042	0.54	0.66	0.63	0.59	7	0.0022	0.0013	0.0024	0.04	0.008
3722990	0.63	0.0013	1.27	0.61	0.0018	0.51	0.71	0.65	0.59	4	0.0018	0.0025	0.002	0.03	0.003
3723305	0.62	0.0029	1.39	0.59	0.0138	0.61	0.56	0.59	0.59	5.33	0.0215	0.0039	0.0029	0.07	0.014
3726811	0.63	0.0016	1.46	0.59	0.0138	0.52	0.65	0.61	0.57	4.63	0.0154	0.0035	0.0028	0.26	0.038
3728316	0.64	0.0005	1.26	0.62	0.0007	0.58	0.66	0.64	0.61	5.83	0.0016	0.0017	0.0005	0.26	0.009
3729194	0.62	0.003	1.33	0.59	0.0095	0.54	0.64	0.61	0.58	4.39	0.0188	0.0049	0.0046	0.08	0.016
3729227	0.63	0.0023	1.35	0.62	0.0011	0.58	0.65	0.63	0.6	6.23	0.0018	0.003	0.0022	0.03	0.005
3732475	0.65	0.0002	1.39	0.63	0.0004	0.56	0.69	0.66	0.61	5.12	0.0003	0.0004	0.0003	0.03	0.003
3732477	0.62	0.0024	1.27	0.62	0.0007	0.55	0.69	0.65	0.6	4.33	0.0002	0.0017	0.004	0.07	0.024
3732479	0.63	0.0019	1.27	0.61	0.0028	0.53	0.68	0.64	0.59	6.12	0.0033	0.0027	0.002	0.22	0.023
3732480	0.67	0	1.35	0.61	0.0018	0.51	0.71	0.65	0.59	3.5	0.0014	0.0002	0.0002	0.03	0.001
3734754	0.63	0.0016	1.62	0.6	0.0042	0.64	0.56	0.6	0.6	5.01	0.0037	0.0015	0.001	0.01	0.002
3734863	0.61	0.0056	1.38	0.58	0.0276	0.55	0.6	0.59	0.57	5.95	0.021	0.0037	0.0053	0.04	0.016
3737304	0.63	0.002	1.3	0.63	0.0004	0.54	0.71	0.66	0.6	5.7	0.0003	0.0059	0.0043	0.13	0.013
3737985	0.61	0.0053	1.28	0.62	0.0011	0.64	0.59	0.62	0.62	6.8	0.0015	0.0049	0.0044	0.08	0.014
3738300	0.61	0.0064	1.29	0.62	0.0011	0.68	0.55	0.61	0.63	6.91	0.0018	0.0069	0.004	0.06	0.007
3739125	0.63	0.0012	1.56	0.61	0.0028	0.55	0.66	0.63	0.59	4.25	0.0031	0.0042	0.0026	0.07	0.016
3739523	0.63	0.0014	1.39	0.6	0.0064	0.5	0.7	0.63	0.58	5.3	0.0048	0.0024	0.0017	0.26	0.064
3740129	0.64	0.0008	1.46	0.63	0.0004	0.65	0.6	0.63	0.63	5.47	0.0004	0.0007	0.0006	0	0.001
3740130	0.63	0.002	1.58	0.61	0.0028	0.57	0.64	0.62	0.59	5.15	0.002	0.0026	0.0024	0.03	0.007
3744423	0.61	0.0064	1.3	0.63	0.0002	0.67	0.59	0.63	0.64	7.58	0.0002	0.0092	0.0084	0.23	0.029
3746953	0.61	0.006	1.27	0.57	0.038	0.45	0.7	0.61	0.55	4.11	0.0237	0.0041	0.0099	0.12	0.047
3746967	0.6	0.0135	1.3	0.59	0.0095	0.48	0.71	0.63	0.57	5.09	0.0068	0.0232	0.0125	0.08	0.016
3747223	0.64	0.0006	1.38	0.66	0	0.6	0.71	0.69	0.64	6.51	0	0.0006	0.0005	0.03	0.002
3748953	0.6	0.0133	1.32	0.58	0.0276	0.56	0.59	0.59	0.57	4.8	0.0439	0.0129	0.0097	0.11	0.019
3750786	0.61	0.0093	1.35	0.62	0.0011	0.68	0.55	0.61	0.63	5.19	0.001	0.0102	0.007	0.11	0.011
3752711	0.6	0.0111	1.34	0.61	0.0028	0.7	0.51	0.6	0.63	5.53	0.0019	0.0084	0.0089	0.04	0.009
3754530	0.64	0.0005	1.32	0.62	0.0011	0.59	0.64	0.63	0.61	4.86	0.0006	0.0003	0.0006	0.01	0.003
3754741	0.6	0.0117	1.29	0.6	0.0064	0.56	0.63	0.61	0.58	4.08	0.0102	0.0456	0.0305	0.13	0.023
3756204	0.61	0.0078	1.25	0.6	0.0064	0.54	0.65	0.62	0.58	6.24	0.0028	0.006	0.0078	0.05	0.013
3759590	0.62	0.0027	1.29	0.59	0.0138	0.52	0.65	0.61	0.57	4.14	0.0165	0.0052	0.0048	0.12	0.032
3760197	0.62	0.0029	1.32	0.57	0.0513	0.6	0.53	0.57	0.57	4.46	0.0636	0.0068	0.004	0.21	0.022
3761752	0.63	0.002	1.26	0.6	0.0064	0.54	0.65	0.62	0.58	4.7	0.0225	0.0101	0.0028	0.48	0.041
3762575	0.64	0.0006	1.42	0.58	0.0197	0.55	0.61	0.6	0.57	5.23	0.0256	0.0013	0.001	0.06	0.015
3764121	0.63	0.0014	1.32	0.61	0.0028	0.64	0.57	0.61	0.61	6.19	0.0044	0.0018	0.0014	0.04	0.004
3764125	0.63	0.0019	1.26	0.62	0.0007	0.62	0.62	0.63	0.62	5.95	0.0005	0.0012	0.0012	0.03	0.004
3764127	0.62	0.0032	1.27	0.62	0.0011	0.55	0.68	0.64	0.6	4.63	0.0011	0.012	0.0069	0.29	0.106

3764884	0.61	0.0064	1.32	0.61	0.0028	0.61	0.6	0.61	0.6	5.36	0.0015	0.0062	0.0052	0.1	0.028
3764921	0.64	0.0007	1.4	0.6	0.0064	0.56	0.63	0.61	0.58	6.37	0.0159	0.0011	0.0008	0.04	0.005
3765738	0.61	0.0062	1.34	0.62	0.0011	0.53	0.7	0.65	0.59	4.6	0.0005	0.0068	0.0086	0.07	0.045
3765761	0.62	0.0042	1.25	0.61	0.0028	0.6	0.61	0.62	0.6	5.63	0.0021	0.0031	0.0039	0.25	0.083
3765767	0.61	0.008	1.31	0.58	0.0197	0.5	0.66	0.61	0.57	4	0.0195	0.0193	0.0184	0.2	0.141
3766896	0.61	0.0083	1.29	0.58	0.0276	0.5	0.66	0.6	0.56	4.94	0.0307	0.0178	0.0118	0.16	0.063
3768039	0.65	0.0003	1.35	0.62	0.0007	0.5	0.76	0.68	0.59	4.62	0.0001	0.001	0.0015	0.03	0.019
3768121	0.63	0.0014	1.25	0.6	0.0042	0.52	0.68	0.63	0.58	4.98	0.0029	0.0047	0.0035	0.07	0.031
3768258	0.63	0.0012	1.29	0.61	0.0018	0.59	0.63	0.63	0.6	4.37	0.0012	0.0029	0.002	0.16	0.029
3769780	0.63	0.0022	1.26	0.63	0.0004	0.59	0.66	0.65	0.61	6.27	0.0003	0.0029	0.002	0.11	0.015
3770244	0.62	0.0032	1.25	0.62	0.0007	0.53	0.71	0.66	0.6	8.23	0.0003	0.0023	0.0025	0.14	0.02
3770564	0.62	0.0028	1.36	0.62	0.0011	0.66	0.57	0.61	0.62	6.2	0.0008	0.0027	0.0023	0.06	0.015
3770565	0.6	0.0114	1.31	0.59	0.0095	0.56	0.62	0.61	0.58	6.42	0.006	0.0092	0.0084	0.17	0.041
3770746	0.62	0.0051	1.35	0.59	0.0095	0.57	0.61	0.6	0.58	6.91	0.0092	0.009	0.0056	0.11	0.019
3771039	0.61	0.0076	1.28	0.6	0.0064	0.48	0.72	0.64	0.57	5.11	0.0024	0.0074	0.0087	0.16	0.057
3771094	0.63	0.0022	1.43	0.6	0.0042	0.52	0.68	0.63	0.58	4.09	0.0056	0.0064	0.0027	0.12	0.015
3771337	0.61	0.0057	1.64	0.61	0.0018	0.59	0.63	0.63	0.6	4.64	0.0025	0.0081	0.0041	0.15	0.015
3776189	0.65	0.0002	1.36	0.63	0.0002	0.56	0.7	0.66	0.61	6.15	0.0001	0.0007	0.0004	0.01	0.002
3776219	0.6	0.0133	1.25	0.6	0.0064	0.49	0.71	0.64	0.57	4.26	0.0042	0.0223	0.0174	0.1	0.045
3776236	0.63	0.0014	1.29	0.58	0.0276	0.39	0.78	0.64	0.55	3.87	0.0368	0.0045	0.0024	0.04	0.014
3776446	0.61	0.0062	1.49	0.59	0.0138	0.53	0.64	0.61	0.57	4.89	0.0141	0.0091	0.0076	0.08	0.014
3776461	0.62	0.0027	1.25	0.6	0.0064	0.58	0.61	0.61	0.59	6.29	0.0082	0.0052	0.0035	0.03	0.005
3778266	0.66	0.0001	1.29	0.61	0.0018	0.57	0.65	0.63	0.6	6.28	0.0024	0.0004	0.0002	0.03	0.003
3778629	0.65	0.0003	1.41	0.64	0.0001	0.58	0.7	0.67	0.62	6.43	0.0001	0.0003	0.0003	0.04	0.003
3778630	0.63	0.0011	1.34	0.59	0.0138	0.63	0.54	0.59	0.59	6.04	0.0224	0.002	0.0011	0.09	0.012
3779850	0.62	0.0026	1.27	0.55	0.114	0.39	0.72	0.59	0.53	4.22	0.1004	0.007	0.007	0.1	0.04
3781686	0.6	0.0122	1.26	0.55	0.1438	0.42	0.68	0.58	0.53	3.38	0.0685	0.0308	0.0676	0.06	0.07
3781689	0.63	0.0012	1.29	0.59	0.0138	0.53	0.64	0.61	0.57	5.5	0.0105	0.0012	0.0018	0.01	0.003
3783364	0.61	0.0058	1.26	0.58	0.0197	0.56	0.6	0.59	0.57	6.36	0.0142	0.0052	0.0072	0.02	0.008
3787934	0.66	0.0001	1.31	0.64	0.0001	0.57	0.7	0.67	0.62	6.26	0.0001	0	0	0	0.001
3789817	0.62	0.004	1.34	0.59	0.0095	0.5	0.68	0.62	0.57	5.3	0.0081	0.0079	0.0062	0.12	0.012
3795442	0.64	0.0007	1.27	0.58	0.0197	0.49	0.68	0.61	0.56	4.08	0.0088	0.0003	0.0014	0.02	0.046
3796554	0.61	0.0067	1.3	0.57	0.038	0.44	0.71	0.61	0.55	4.53	0.0236	0.019	0.0175	0.18	0.093
3798470	0.67	0.0001	1.42	0.63	0.0004	0.58	0.67	0.65	0.61	5.95	0.0004	0.0001	0.0001	0.01	0.001
3800623	0.61	0.0083	1.25	0.59	0.0138	0.56	0.61	0.6	0.58	4.9	0.0186	0.0126	0.0094	0.5	0.12
3804170	0.64	0.0005	1.3	0.58	0.0197	0.54	0.62	0.6	0.57	4.46	0.0214	0.0009	0.0008	0.03	0.002
3804202	0.63	0.0012	1.3	0.62	0.0011	0.56	0.67	0.64	0.6	4.59	0.001	0.0036	0.0023	0.05	0.018
3806255	0.64	0.0006	1.31	0.62	0.0007	0.64	0.6	0.63	0.62	6.72	0.0012	0.001	0.0007	0.06	0.005
3806256	0.61	0.0078	1.27	0.59	0.0138	0.48	0.7	0.62	0.57	4.44	0.021	0.0108	0.0129	0.05	0.019
3807476	0.61	0.0059	1.29	0.61	0.0018	0.52	0.7	0.65	0.59	4.95	0.0012	0.0046	0.0056	0.15	0.039
3807570	0.63	0.0013	1.34	0.62	0.0007	0.52	0.72	0.66	0.6	4.16	0.0002	0.0001	0.0005	0.1	0.054

3807629	0.65	0.0002	1.36	0.62	0.0007	0.5	0.76	0.68	0.59	4.56	0.0001	0	0.0002	0.01	0.011
3808602	0.64	0.0007	1.39	0.63	0.0004	0.63	0.62	0.63	0.62	7.24	0.0006	0.001	0.0006	0.02	0.001
3809343	0.62	0.003	1.36	0.61	0.0028	0.65	0.56	0.61	0.61	5.43	0.003	0.0024	0.0022	0.04	0.008
3809673	0.64	0.0008	1.36	0.62	0.0007	0.65	0.59	0.62	0.62	6.29	0.0006	0.0012	0.0009	0.03	0.004
3809834	0.67	0.0001	1.26	0.62	0.0011	0.5	0.73	0.66	0.59	5.07	0.0026	0.0004	0.0002	0.01	0.002
3813298	0.65	0.0003	1.3	0.59	0.0095	0.52	0.66	0.62	0.58	5.9	0.0084	0.0003	0.0005	0.06	0.009
3813299	0.62	0.0024	1.27	0.57	0.0513	0.44	0.7	0.6	0.55	4.8	0.0317	0.0022	0.0051	0.23	0.094
3815669	0.61	0.0079	1.35	0.58	0.0197	0.56	0.6	0.59	0.57	4.76	0.0292	0.0071	0.0064	0.08	0.016
3816402	0.6	0.0146	1.38	0.61	0.0028	0.57	0.64	0.62	0.59	4.49	0.0023	0.0122	0.0123	0.06	0.022
3820658	0.62	0.0024	1.29	0.61	0.0018	0.73	0.49	0.6	0.64	6.03	0.0031	0.0037	0.0027	0.07	0.012
3820705	0.61	0.0061	1.25	0.58	0.0197	0.6	0.56	0.59	0.58	6.12	0.0264	0.0065	0.007	0.25	0.049
3820721	0.62	0.0034	1.27	0.6	0.0064	0.69	0.5	0.59	0.61	5.6	0.0088	0.0056	0.0055	0.15	0.028
3820752	0.61	0.007	1.3	0.59	0.0095	0.56	0.62	0.61	0.58	4.68	0.0118	0.0133	0.0064	0.11	0.014
3822055	0.62	0.0039	1.38	0.61	0.0028	0.57	0.64	0.62	0.59	5.92	0.0011	0.0019	0.0037	0.01	0.01
3825428	0.62	0.0049	1.39	0.58	0.0197	0.59	0.57	0.59	0.58	5.49	0.014	0.0069	0.0048	0.05	0.005
3829039	0.63	0.0021	1.35	0.6	0.0064	0.56	0.63	0.61	0.58	4.81	0.0068	0.0039	0.0028	0.06	0.007
3829810	0.64	0.0004	1.56	0.62	0.0011	0.65	0.58	0.62	0.62	5.69	0.0008	0.0007	0.0005	0.01	0
3831128	0.61	0.0067	1.65	0.62	0.0011	0.61	0.62	0.63	0.61	4.89	0.0009	0.0049	0.0041	0.04	0.006
3831280	0.62	0.0035	1.26	0.61	0.0018	0.6	0.62	0.62	0.6	7.53	0.0019	0.0036	0.0027	0.06	0.007
3835412	0.64	0.0005	1.59	0.61	0.0028	0.52	0.69	0.64	0.59	3.94	0.0027	0.0042	0.0035	0.08	0.016
3837493	0.64	0.0009	1.32	0.59	0.0138	0.54	0.63	0.6	0.57	5.56	0.0188	0.0012	0.001	0.12	0.024
3838612	0.61	0.0087	1.27	0.62	0.0007	0.54	0.7	0.65	0.6	5.73	0.001	0.008	0.0069	0.26	0.037
3838790	0.63	0.0014	1.28	0.61	0.0018	0.53	0.69	0.64	0.59	4.65	0.0008	0.0027	0.0021	0.04	0.004
3840344	0.65	0.0004	1.25	0.6	0.0042	0.55	0.65	0.62	0.59	5.88	0.0055	0.0004	0.0004	0.14	0.021
3841271	0.63	0.0012	1.32	0.62	0.0007	0.54	0.7	0.65	0.6	4.78	0.0003	0.0027	0.0029	0.07	0.022
3843668	0.66	0.0001	1.36	0.64	0.0001	0.54	0.74	0.69	0.61	4.86	0	0.0002	0.0002	0.05	0.006
3845710	0.63	0.0018	1.29	0.61	0.0028	0.73	0.48	0.59	0.64	6.23	0.0038	0.0025	0.0014	0.07	0.006
3846115	0.62	0.0043	1.3	0.62	0.0011	0.57	0.66	0.64	0.6	5.13	0.0009	0.0033	0.0039	0.09	0.032
3846291	0.61	0.0063	1.26	0.59	0.0138	0.55	0.62	0.6	0.58	4.67	0.0263	0.015	0.0083	0.16	0.055
3846561	0.63	0.0015	1.26	0.61	0.0028	0.67	0.54	0.6	0.62	7.21	0.0022	0.0027	0.0028	0.15	0.012
3846784	0.62	0.0043	1.4	0.61	0.0018	0.65	0.57	0.61	0.62	6.04	0.0023	0.0028	0.0026	0.04	0.006
3847357	0.62	0.0047	1.32	0.62	0.0007	0.71	0.53	0.61	0.64	6.54	0.0008	0.0051	0.0039	0.03	0.003
3849774	0.61	0.0106	1.27	0.59	0.0095	0.56	0.62	0.61	0.58	5.84	0.0138	0.0185	0.0112	0.29	0.051
3849776	0.63	0.0019	1.26	0.62	0.0011	0.5	0.73	0.66	0.59	5.51	0.0006	0.0016	0.0018	0.2	0.02
3850502	0.64	0.0009	1.37	0.62	0.0007	0.64	0.6	0.63	0.62	5.57	0.0006	0.0013	0.0009	0.02	0.001
3851604	0.6	0.0138	1.27	0.63	0.0004	0.69	0.56	0.62	0.64	6.74	0.0003	0.0134	0.0108	0.2	0.017
3851902	0.62	0.004	1.44	0.61	0.0028	0.57	0.64	0.62	0.59	5.47	0.0015	0.0018	0.0044	0.03	0.02
3854371	0.63	0.0019	1.48	0.62	0.0007	0.52	0.72	0.66	0.6	3.6	0.0002	0.004	0.0045	0.02	0.012
3855101	0.61	0.0056	1.27	0.6	0.0064	0.57	0.62	0.61	0.59	6.36	0.0085	0.0061	0.0059	0.04	0.006
3856046	0.62	0.0035	1.27	0.57	0.038	0.45	0.7	0.61	0.55	4.39	0.0496	0.0083	0.0058	0.4	0.053
3857120	0.62	0.0028	1.3	0.61	0.0028	0.5	0.71	0.65	0.58	4.45	0.0015	0.0019	0.0024	0.19	0.066

3857884	0.67	0	1.3	0.65	0	0.57	0.73	0.69	0.63	5.25	0	0.0001	0.0001	0.02	0.001
3862168	0.63	0.0019	1.29	0.61	0.0018	0.67	0.55	0.61	0.62	8.4	0.0033	0.0022	0.0013	0.05	0.004
3862473	0.63	0.0013	1.27	0.59	0.0095	0.6	0.58	0.6	0.59	6.39	0.0079	0.0022	0.001	0.08	0.006
3867099	0.6	0.0112	1.27	0.62	0.0011	0.56	0.67	0.64	0.6	5.68	0.0015	0.0098	0.008	0.36	0.097
3869659	0.62	0.0045	1.27	0.57	0.038	0.51	0.63	0.59	0.56	4.47	0.0826	0.0092	0.0061	0.36	0.128
3869971	0.64	0.0009	1.37	0.59	0.0095	0.47	0.72	0.64	0.57	5.08	0.0112	0.0011	0.0009	0.09	0.004
3870593	0.64	0.0005	1.27	0.64	0.0001	0.63	0.65	0.65	0.63	6.4	0.0002	0.0008	0.0004	0.02	0.001
3872197	0.62	0.0024	1.73	0.62	0.0007	0.58	0.66	0.64	0.61	5.31	0.0008	0.0029	0.0018	0.22	0.015
3872208	0.62	0.0049	1.26	0.6	0.0042	0.57	0.63	0.62	0.59	5.65	0.0066	0.006	0.0044	0.19	0.024
3874114	0.65	0.0003	1.29	0.62	0.0007	0.55	0.69	0.65	0.6	3.09	0.0008	0.0022	0.0016	0.12	0.015
3874280	0.63	0.002	1.3	0.62	0.0007	0.7	0.54	0.61	0.64	7.41	0.0005	0.0036	0.0027	0.05	0.003
3875278	0.6	0.0148	1.34	0.57	0.038	0.53	0.61	0.59	0.56	4.97	0.0509	0.0203	0.0126	0.64	0.09
3878051	0.61	0.0066	1.45	0.59	0.0095	0.57	0.61	0.6	0.58	4.6	0.0096	0.0081	0.0047	0.13	0.027
3878053	0.65	0.0003	1.37	0.64	0.0001	0.64	0.64	0.65	0.64	7.19	0.0001	0.0004	0.0003	0.03	0.003
3879490	0.62	0.0037	1.27	0.54	0.1784	0.45	0.64	0.56	0.53	3.33	0.2201	0.0103	0.0098	0.27	0.09
3881731	0.64	0.0009	1.56	0.6	0.0064	0.63	0.56	0.6	0.6	4.8	0.0063	0.0015	0.001	0.02	0.003
3881914	0.63	0.0016	1.27	0.61	0.0028	0.54	0.67	0.63	0.59	6.52	0.0015	0.0014	0.0027	0.05	0.019
3882710	0.62	0.0037	1.4	0.61	0.0018	0.64	0.58	0.61	0.61	6.49	0.0015	0.0028	0.0028	0.07	0.025
3882867	0.64	0.0009	1.46	0.62	0.0007	0.57	0.67	0.64	0.61	5.07	0.0005	0.0014	0.0016	0.09	0.037
3883424	0.68	0	1.3	0.64	0.0001	0.62	0.65	0.65	0.63	7.1	0.0001	0	0	0.01	0.001
3883533	0.64	0.0009	1.26	0.65	0	0.6	0.7	0.68	0.63	6.41	0	0.0011	0.0009	0.06	0.005
3883537	0.63	0.0015	1.31	0.62	0.0007	0.55	0.69	0.65	0.6	6.1	0.0003	0.0016	0.0015	0.1	0.012
3883987	0.65	0.0003	1.28	0.63	0.0004	0.62	0.63	0.64	0.62	5.89	0.0018	0.0006	0.0003	0.02	0.001
3884147	0.62	0.0026	1.34	0.6	0.0042	0.57	0.63	0.62	0.59	5.86	0.0055	0.0031	0.0032	0.06	0.006
3884334	0.65	0.0004	1.27	0.63	0.0002	0.57	0.69	0.66	0.61	3.63	0.0001	0.0033	0.0013	0.01	0.001
3884673	0.63	0.0017	1.31	0.62	0.0011	0.51	0.72	0.66	0.59	3.9	0.0002	0.0006	0.0019	0.04	0.009
3884709	0.65	0.0002	1.28	0.62	0.0007	0.53	0.71	0.66	0.6	5.2	0.0005	0.0003	0.0002	0.18	0.014
3885711	0.62	0.0035	1.27	0.62	0.0011	0.6	0.63	0.63	0.61	6.49	0.0008	0.0035	0.0045	0.02	0.004
3886656	0.61	0.006	1.33	0.61	0.0018	0.5	0.72	0.65	0.59	5.12	0.0015	0.0096	0.0062	0.42	0.045
3886907	0.62	0.0037	1.27	0.63	0.0002	0.54	0.72	0.67	0.61	6.13	0.0001	0.004	0.0055	0.08	0.011
3887661	0.61	0.0054	1.25	0.59	0.0095	0.46	0.73	0.64	0.57	3.99	0.0092	0.0063	0.0049	0.35	0.057
3888081	0.64	0.0007	1.28	0.61	0.0018	0.51	0.71	0.65	0.59	5.18	0.0008	0.0003	0.001	0.05	0.023
3888182	0.61	0.0071	1.35	0.62	0.0011	0.71	0.52	0.61	0.64	6.72	0.0013	0.0087	0.0045	0.12	0.009
3888253	0.64	0.0004	1.35	0.62	0.0011	0.56	0.67	0.64	0.6	6.09	0.0006	0.0006	0.0004	0.01	0.001
3888289	0.63	0.0019	1.45	0.61	0.0018	0.64	0.58	0.61	0.61	5.85	0.003	0.0014	0.0015	0.05	0.005
3888494	0.6	0.0106	1.27	0.59	0.0095	0.56	0.62	0.61	0.58	6.07	0.0145	0.0143	0.0089	0.09	0.012
3888936	0.63	0.0013	1.3	0.59	0.0138	0.54	0.63	0.6	0.57	5.44	0.0348	0.0048	0.0019	0.13	0.016
3889140	0.66	0.0001	1.25	0.64	0.0001	0.55	0.72	0.67	0.61	6.4	0	0	0.0001	0.03	0.012
3889782	0.62	0.0043	1.34	0.59	0.0138	0.46	0.72	0.63	0.56	4	0.0055	0.0063	0.0073	0.03	0.012
3891221	0.6	0.0125	1.36	0.62	0.0011	0.6	0.63	0.63	0.61	4.76	0.0015	0.0088	0.0108	0.2	0.03
3891257	0.66	0.0002	1.28	0.61	0.0018	0.6	0.62	0.62	0.6	7.82	0.003	0.0003	0.0003	0.03	0.001

3892672	0.64	0.0007	1.28	0.64	0.0001	0.6	0.67	0.66	0.62	8.08	0.0001	0.0005	0.0009	0.09	0.012
3894074	0.61	0.0066	1.25	0.58	0.0276	0.5	0.66	0.6	0.56	3.6	0.0363	0.0046	0.0073	0.08	0.01
3894508	0.63	0.0013	1.49	0.62	0.0011	0.59	0.64	0.63	0.61	5.67	0.0011	0.0014	0.0008	0.03	0.001
3894602	0.61	0.0089	1.4	0.6	0.0042	0.63	0.57	0.6	0.6	5.52	0.0046	0.008	0.0058	0.09	0.012
3895000	0.61	0.0069	1.31	0.63	0.0004	0.65	0.6	0.63	0.63	6.22	0.0008	0.0065	0.0048	0.06	0.012
3896202	0.6	0.0144	1.39	0.57	0.038	0.52	0.62	0.59	0.56	5.28	0.04	0.0192	0.0162	0.08	0.019
3898306	0.6	0.0122	1.29	0.58	0.0276	0.53	0.62	0.59	0.56	3.04	0.0448	0.0531	0.0268	0.49	0.237
3901666	0.6	0.0115	1.35	0.6	0.0064	0.65	0.54	0.59	0.6	6.28	0.0079	0.0126	0.0109	0.07	0.011
3902984	0.64	0.0009	1.34	0.59	0.0095	0.54	0.64	0.61	0.58	5.5	0.0097	0.0015	0.0015	0.03	0.014
3903290	0.65	0.0004	1.32	0.64	0.0001	0.62	0.65	0.65	0.63	6.67	0.0002	0.0004	0.0002	0.04	0.005
3904028	0.64	0.0004	1.39	0.54	0.1784	0.3	0.8	0.6	0.52	4.37	0.1663	0.0014	0.0027	0.44	0.225
3904029	0.64	0.0005	1.25	0.63	0.0004	0.58	0.67	0.65	0.61	8.51	0.0008	0.0002	0.0004	0.04	0.006
3904255	0.64	0.0006	1.27	0.63	0.0002	0.58	0.68	0.66	0.61	5.76	0.0004	0.0015	0.0011	0.08	0.013
3904257	0.64	0.0005	1.34	0.64	0.0001	0.69	0.59	0.64	0.65	6.17	0.0001	0.0007	0.0005	0.1	0.014
3904276	0.64	0.0005	1.28	0.61	0.0018	0.57	0.65	0.63	0.6	4.36	0.0014	0.0012	0.0019	0.03	0.023
3904281	0.61	0.0081	1.27	0.61	0.0028	0.47	0.76	0.66	0.58	5.04	0.0004	0.0023	0.0035	0.19	0.034
3906196	0.61	0.008	1.31	0.59	0.0095	0.58	0.6	0.6	0.58	4.26	0.0182	0.009	0.0083	0.61	0.127
3907788	0.61	0.007	1.45	0.62	0.0007	0.62	0.62	0.63	0.62	5.04	0.0003	0.0049	0.005	0.04	0.012
3908789	0.62	0.0024	1.34	0.63	0.0002	0.62	0.64	0.64	0.62	7.29	0.0004	0.0015	0.001	0.14	0.009
3909376	0.61	0.0077	1.25	0.58	0.0276	0.5	0.66	0.6	0.56	3.83	0.0184	0.0035	0.0033	0.3	0.032
3911474	0.64	0.0007	1.36	0.62	0.0007	0.62	0.62	0.63	0.62	6.7	0.0013	0.0011	0.0005	0.07	0.003
3911564	0.65	0.0002	1.37	0.67	0	0.63	0.7	0.69	0.65	6.02	0	0.0002	0.0002	0.04	0.003
3911706	0.64	0.0006	1.31	0.63	0.0002	0.61	0.65	0.65	0.62	5.56	0.0004	0.0008	0.0007	0.03	0.002
3911738	0.66	0.0001	1.3	0.63	0.0004	0.65	0.6	0.63	0.63	7.3	0.0015	0.0003	0.0002	0.02	0.001
3911801	0.63	0.0016	1.44	0.63	0.0002	0.65	0.61	0.63	0.63	5.91	0.0003	0.0007	0.0007	0.02	0.002
3911815	0.62	0.004	1.48	0.61	0.0018	0.55	0.67	0.64	0.59	5.48	0.003	0.003	0.0028	0.13	0.019
3913564	0.62	0.0029	1.31	0.57	0.038	0.55	0.59	0.58	0.56	4.58	0.0329	0.0065	0.004	0.19	0.068
3915125	0.64	0.0006	1.35	0.57	0.0513	0.38	0.77	0.62	0.54	4.05	0.0575	0.0031	0.0023	0.03	0.004
3917896	0.65	0.0003	1.38	0.62	0.0007	0.6	0.64	0.64	0.61	5.35	0.0006	0.0012	0.0007	0.03	0.003
3918586	0.62	0.0031	1.37	0.61	0.0028	0.45	0.78	0.67	0.58	4.15	0.0018	0.0015	0.0016	0.09	0.017
3918651	0.61	0.0095	1.27	0.59	0.0138	0.54	0.63	0.6	0.57	4.24	0.0113	0.0074	0.0075	0.13	0.032
3918723	0.64	0.0007	1.32	0.64	0.0001	0.61	0.67	0.66	0.63	6.09	0.0001	0.0007	0.0011	0.09	0.012
3918734	0.63	0.0016	1.31	0.62	0.0011	0.56	0.67	0.64	0.6	4.43	0.0003	0.0011	0.0021	0.28	0.102
3919024	0.63	0.0012	1.4	0.65	0	0.76	0.54	0.63	0.69	6.04	0.0001	0.0007	0.0004	0.02	0.001
3920401	0.63	0.0012	1.38	0.6	0.0042	0.5	0.71	0.64	0.58	4.26	0.0031	0.0037	0.0031	0.25	0.033
3920456	0.64	0.0008	1.26	0.62	0.0011	0.63	0.6	0.62	0.61	6.62	0.0009	0.001	0.0009	0.15	0.01
3920487	0.66	0.0001	1.28	0.61	0.0028	0.54	0.67	0.63	0.59	5.06	0.0025	0.0002	0.0003	0.07	0.015
3922023	0.61	0.0053	1.29	0.55	0.114	0.32	0.8	0.62	0.53	4.57	0.0529	0.0052	0.011	0.06	0.059
3922993	0.63	0.0021	1.36	0.61	0.0018	0.59	0.63	0.63	0.6	4.28	0.0014	0.0026	0.0057	0.22	0.128
3924758	0.61	0.008	1.27	0.55	0.1438	0.4	0.7	0.58	0.53	4.56	0.2256	0.0594	0.0262	0.99	0.182
3925641	0.66	0.0001	1.29	0.59	0.0138	0.43	0.76	0.64	0.56	5.51	0.0025	0.0009	0.0009	0.15	0.072

3926090	0.63	0.001	1.28	0.62	0.0011	0.48	0.77	0.68	0.59	4.4	0.0002	0.0008	0.001	0.15	0.027
3927180	0.6	0.0122	1.49	0.59	0.0095	0.54	0.64	0.61	0.58	4.11	0.0143	0.016	0.0108	0.29	0.049
3927228	0.62	0.0029	1.26	0.6	0.0042	0.76	0.44	0.58	0.64	6.24	0.0048	0.0042	0.0027	0.06	0.008
3927229	0.64	0.0009	1.42	0.62	0.0011	0.66	0.57	0.61	0.62	5.6	0.0025	0.0015	0.0009	0.06	0.009
3928670	0.63	0.0011	1.31	0.6	0.0064	0.59	0.6	0.61	0.59	5.2	0.008	0.0011	0.0015	0.07	0.022
3929943	0.63	0.0018	1.36	0.59	0.0095	0.59	0.59	0.6	0.59	6.67	0.008	0.0008	0.0013	0.1	0.018
3934699	0.6	0.0124	1.4	0.61	0.0028	0.6	0.61	0.62	0.6	4.71	0.0037	0.0141	0.0112	0.34	0.081
3935246	0.61	0.0089	1.41	0.63	0.0004	0.63	0.62	0.63	0.62	4.97	0.0002	0.0101	0.0106	0.04	0.024
3935301	0.61	0.007	1.26	0.63	0.0004	0.65	0.6	0.63	0.63	7.03	0.0005	0.009	0.0075	0.12	0.014
3936897	0.62	0.0029	1.36	0.6	0.0064	0.51	0.68	0.63	0.58	4.69	0.0095	0.0085	0.0039	0.31	0.019
3939407	0.61	0.0069	1.27	0.63	0.0004	0.69	0.56	0.62	0.64	6.85	0.0008	0.0078	0.0044	0.09	0.005
3942668	0.62	0.0029	1.27	0.62	0.0011	0.62	0.61	0.62	0.61	7.02	0.0021	0.0038	0.0022	0.13	0.005
3945331	0.62	0.0026	1.42	0.62	0.0011	0.67	0.56	0.61	0.63	4.9	0.0018	0.0031	0.0019	0.08	0.008
3945370	0.63	0.0017	1.38	0.61	0.0018	0.5	0.72	0.65	0.59	5.23	0.0007	0.0038	0.0023	0.16	0.036
3946374	0.61	0.008	1.27	0.59	0.0138	0.44	0.74	0.64	0.56	4.93	0.0071	0.0068	0.0074	0.03	0.004
3946589	0.6	0.0116	1.29	0.57	0.038	0.51	0.63	0.59	0.56	5.2	0.0496	0.0169	0.0147	0.18	0.084
3946677	0.61	0.0071	1.31	0.58	0.0197	0.5	0.67	0.61	0.56	4.18	0.0159	0.0107	0.0124	0.24	0.132
3953804	0.63	0.0019	1.28	0.62	0.0011	0.65	0.58	0.62	0.62	4.64	0.0018	0.0023	0.0028	0.08	0.013
3956591	0.62	0.0049	1.28	0.61	0.0028	0.66	0.55	0.6	0.61	7.26	0.0092	0.0106	0.0034	0.14	0.019
3957262	0.63	0.0011	1.47	0.61	0.0028	0.51	0.7	0.64	0.58	5.05	0.0034	0.0026	0.0015	0.09	0.016
3959259	0.63	0.0015	1.25	0.61	0.0018	0.62	0.6	0.62	0.61	5.32	0.0004	0.0005	0.002	0.06	0.023
3959453	0.62	0.004	1.34	0.59	0.0095	0.61	0.57	0.6	0.59	6.98	0.0147	0.0054	0.0038	0.08	0.008
3960634	0.66	0.0001	1.52	0.62	0.0007	0.64	0.6	0.63	0.62	5.96	0.0006	0.0002	0.0002	0.03	0.002
3961482	0.62	0.004	1.26	0.6	0.0064	0.6	0.59	0.6	0.59	5.66	0.0059	0.0037	0.0029	0.11	0.01
3962268	0.64	0.0007	1.65	0.62	0.0007	0.66	0.58	0.62	0.63	5.98	0.0009	0.0004	0.0004	0.02	0.002
3962596	0.65	0.0002	1.42	0.61	0.0028	0.6	0.61	0.62	0.6	5.63	0.0024	0.0002	0.0002	0.07	0.005
3969510	0.62	0.0041	1.32	0.62	0.0011	0.48	0.77	0.68	0.59	4.12	0.0003	0.0049	0.0061	0.13	0.05
3969511	0.64	0.0008	1.65	0.64	0.0001	0.64	0.64	0.65	0.64	5.23	0.0001	0.0003	0.0003	0.02	0.004
3970894	0.66	0.0001	1.32	0.63	0.0004	0.64	0.61	0.63	0.63	7.89	0.0006	0.0002	0.0002	0.01	0
3974757	0.61	0.0063	1.29	0.55	0.114	0.5	0.6	0.57	0.54	4.69	0.079	0.0048	0.0121	0.04	0.052
3974789	0.63	0.0017	1.43	0.62	0.0007	0.59	0.65	0.64	0.61	5.33	0.0008	0.0017	0.0013	0.09	0.01
3981154	0.63	0.0014	1.42	0.62	0.0011	0.55	0.68	0.64	0.6	4.28	0.0011	0.0013	0.0015	0.25	0.027
3981752	0.62	0.0038	1.32	0.58	0.0276	0.51	0.64	0.6	0.56	5.23	0.0256	0.0037	0.0035	0.84	0.17
3981906	0.63	0.0011	1.34	0.62	0.0011	0.58	0.65	0.63	0.6	6.58	0.0007	0.0011	0.0012	0.06	0.008
3982421	0.6	0.012	1.38	0.62	0.0007	0.61	0.63	0.63	0.61	5.83	0.0013	0.0116	0.0095	0.15	0.024
3985558	0.63	0.0011	1.31	0.63	0.0004	0.64	0.61	0.63	0.63	7.57	0.0005	0.0009	0.0009	0.01	0.001
3985635	0.66	0.0001	1.51	0.61	0.0018	0.58	0.64	0.63	0.6	4.97	0.0019	0.0006	0.0003	0.1	0.004
3986857	0.62	0.0031	1.31	0.57	0.038	0.46	0.69	0.61	0.55	5.54	0.0584	0.0041	0.0035	0.06	0.003
3987532	0.6	0.0126	1.45	0.57	0.038	0.52	0.62	0.59	0.56	4.8	0.0561	0.0214	0.0129	0.31	0.051
3988214	0.61	0.0053	1.32	0.62	0.0011	0.56	0.67	0.64	0.6	5.55	0.001	0.0153	0.0097	0.16	0.027
3989205	0.63	0.0019	1.27	0.61	0.0018	0.67	0.55	0.61	0.62	6.95	0.0029	0.0012	0.0009	0.01	0.002

3989770	0.62	0.0048	1.29	0.6	0.0064	0.46	0.74	0.65	0.57	3.76	0.0068	0.0071	0.0049	0.27	0.017
3991722	0.61	0.0083	1.44	0.61	0.0028	0.51	0.7	0.64	0.58	4.63	0.002	0.0173	0.0135	0.04	0.005
3993347	0.61	0.0081	1.27	0.59	0.0138	0.54	0.63	0.6	0.57	7.42	0.0204	0.0062	0.007	0.09	0.024
3993349	0.63	0.002	1.35	0.62	0.0007	0.66	0.58	0.62	0.63	7.12	0.0007	0.002	0.0021	0.05	0.014
4004822	0.63	0.0013	1.26	0.66	0	0.6	0.71	0.69	0.64	5.18	0	0.0026	0.0021	0.07	0.023
4007593	0.62	0.0049	1.44	0.59	0.0095	0.57	0.61	0.6	0.58	5.78	0.0124	0.0081	0.0045	0.16	0.023
4009318	0.62	0.0024	1.31	0.63	0.0002	0.71	0.55	0.62	0.65	7.98	0.0003	0.0028	0.002	0.08	0.008
4009451	0.63	0.0018	1.26	0.61	0.0018	0.55	0.67	0.64	0.59	4.75	0.0007	0.0031	0.0045	0.08	0.038
4011604	0.61	0.0051	1.3	0.6	0.0064	0.64	0.55	0.6	0.6	5.92	0.0062	0.0047	0.0047	0.08	0.012
4011967	0.62	0.0029	1.26	0.6	0.0042	0.55	0.65	0.62	0.59	6.66	0.0034	0.0017	0.0026	0.05	0.011
4012169	0.63	0.0016	1.29	0.63	0.0002	0.55	0.71	0.67	0.61	6.31	0.0003	0.0026	0.0022	0.12	0.008
4012627	0.64	0.0006	1.3	0.63	0.0002	0.56	0.7	0.66	0.61	6.17	0.0003	0.0009	0.0007	0.08	0.005
4012632	0.63	0.0022	1.27	0.61	0.0018	0.52	0.7	0.65	0.59	4.67	0.001	0.0024	0.0025	0.16	0.04
4012759	0.63	0.0011	1.46	0.6	0.0064	0.52	0.67	0.62	0.58	4.18	0.0062	0.0023	0.0022	0.15	0.017
4013274	0.64	0.0005	1.29	0.62	0.0011	0.53	0.7	0.65	0.59	4.28	0.001	0.002	0.0017	0.1	0.014
4013282	0.65	0.0002	1.43	0.6	0.0042	0.58	0.62	0.61	0.59	5.8	0.004	0.0002	0.0002	0.05	0.009
4015535	0.65	0.0003	1.29	0.64	0.0001	0.65	0.63	0.65	0.64	5.1	0.0001	0.0001	0.0004	0	0.001
4016549	0.65	0.0002	1.48	0.63	0.0002	0.52	0.74	0.68	0.6	5.33	0.0001	0.0003	0.0003	0.05	0.006
4016573	0.63	0.001	1.29	0.61	0.0018	0.6	0.62	0.62	0.6	7.57	0.0029	0.0007	0.0005	0.04	0.004
4019367	0.62	0.0035	1.25	0.62	0.0011	0.58	0.65	0.63	0.6	5.61	0.0008	0.0017	0.0027	0.08	0.02
4019418	0.65	0.0003	1.26	0.65	0	0.67	0.63	0.65	0.65	5.4	0.0001	0.003	0.0011	0.08	0.011
4019610	0.63	0.0016	1.3	0.62	0.0011	0.65	0.58	0.62	0.62	6.07	0.002	0.0027	0.0014	0.13	0.012
4020462	0.64	0.0005	1.26	0.58	0.0197	0.43	0.74	0.63	0.56	4.86	0.0209	0.0031	0.0015	0.06	0.002
4024375	0.62	0.0026	1.44	0.62	0.0011	0.64	0.59	0.62	0.62	5.55	0.0011	0.0022	0.0028	0.05	0.01
4024376	0.62	0.0026	1.41	0.62	0.0011	0.55	0.68	0.64	0.6	5.48	0.0007	0.0031	0.0043	0.06	0.022
4024377	0.61	0.0082	1.29	0.59	0.0095	0.61	0.57	0.6	0.59	6.83	0.0111	0.0085	0.0086	0.2	0.055
4024378	0.62	0.0032	1.53	0.6	0.0064	0.55	0.64	0.62	0.58	5.34	0.0059	0.0024	0.0038	0.05	0.036
4024379	0.64	0.0005	1.46	0.61	0.0018	0.59	0.63	0.63	0.6	6.42	0.0017	0.0004	0.0005	0.01	0.002
4030986	0.66	0.0001	1.42	0.63	0.0004	0.52	0.73	0.67	0.6	5.64	0.0002	0.0001	0.0001	0.03	0.003
4034997	0.64	0.0005	1.33	0.62	0.0011	0.55	0.68	0.64	0.6	4.38	0.0008	0.0008	0.0014	0.04	0.014
4035834	0.62	0.0043	1.28	0.57	0.038	0.64	0.5	0.57	0.58	6.53	0.0797	0.0152	0.0075	0.35	0.053
4035835	0.67	0	1.35	0.65	0	0.55	0.76	0.7	0.62	4.43	0	0	0.0001	0.04	0.009
4035838	0.63	0.0013	1.28	0.62	0.0011	0.53	0.7	0.65	0.59	6.9	0.0013	0.0023	0.0016	0.13	0.031
4035839	0.63	0.0015	1.27	0.61	0.0018	0.58	0.64	0.63	0.6	6.89	0.0023	0.0017	0.0012	0.12	0.039
4040526	0.64	0.0007	1.31	0.61	0.0018	0.67	0.55	0.61	0.62	7.04	0.0017	0.001	0.0006	0.01	0.002
4041367	0.61	0.0088	1.27	0.57	0.0513	0.51	0.62	0.58	0.55	4.39	0.0584	0.0126	0.0127	0.03	0.011
4041822	0.63	0.0016	1.31	0.6	0.0042	0.73	0.47	0.59	0.63	5.7	0.0031	0.0016	0.0018	0.05	0.01
4043125	0.61	0.0071	1.28	0.58	0.0276	0.53	0.62	0.59	0.56	4.38	0.0533	0.0202	0.0115	0.58	0.054
4044199	0.62	0.0039	1.26	0.62	0.0011	0.57	0.66	0.64	0.6	6.34	0.0007	0.0053	0.0065	0.2	0.082
4044413	0.62	0.003	1.28	0.63	0.0004	0.55	0.7	0.66	0.61	4.54	0.0006	0.0095	0.0041	0.27	0.054
4047577	0.61	0.0085	1.42	0.63	0.0004	0.67	0.58	0.62	0.63	6.05	0.0006	0.0089	0.0043	0.18	0.014

4052399	0.65	0.0002	1.42	0.65	0	0.57	0.72	0.68	0.62	5.66	0	0.0005	0.0004	0.07	0.006
4055295	0.65	0.0002	1.4	0.6	0.0042	0.55	0.65	0.62	0.59	6.06	0.0033	0.0003	0.0002	0.11	0.016
4055302	0.66	0.0001	1.27	0.61	0.0028	0.54	0.67	0.63	0.59	5.2	0.0022	0.0003	0.0003	0.01	0.003
2720180	0.58	0.0585	1.53	0.57	0.038	0.56	0.58	0.58	0.56	5.14	0.0794	0.1125	0.0625	0.41	0.046
2347642	0.69	0	1.12	0.62	0.0011	0.42	0.83	0.71	0.58	6.34	0.0001	0	0.0001	0	0.002
2395344	0.68	0	1.17	0.65	0	0.75	0.55	0.63	0.68	4.74	0	0	0	0.01	0
2397069	0.69	0	1.12	0.65	0	0.57	0.72	0.68	0.62	6.12	0	0	0	0	0.003
2430377	0.69	0	1.09	0.63	0.0004	0.59	0.66	0.65	0.61	5.44	0.0007	0.0001	0	0	0.001
2448270	0.68	0	1.08	0.63	0.0004	0.61	0.64	0.64	0.62	6.84	0.001	0.0001	0	0.01	0
2553581	0.7	0	1.15	0.63	0.0004	0.58	0.67	0.65	0.61	5.17	0.0003	0	0	0	0.001
2600700	0.69	0	1.14	0.63	0.0002	0.66	0.6	0.63	0.63	4.66	0.0005	0	0	0	0
2624519	0.68	0	1.08	0.62	0.0007	0.74	0.5	0.6	0.65	4.49	0.0014	0.0004	0.0001	0.02	0
2651846	0.68	0	1.17	0.64	0.0001	0.68	0.6	0.64	0.65	2.99	0.0001	0	0	0	0.002
2682441	0.68	0	1.14	0.65	0	0.57	0.73	0.69	0.63	6.35	0	0	0	0.01	0.001
2704512	0.69	0	1.11	0.6	0.0042	0.53	0.67	0.63	0.58	4.5	0.0047	0	0	0	0
2704702	0.68	0	1.11	0.65	0	0.68	0.61	0.64	0.65	7.75	0.0001	0	0.0001	0.04	0.004
2902832	0.68	0	0.97	0.39	0.9996	0.5	0.28	0.42	0.35	6.72	0.001	0	0.0001	0.01	0.001
2918558	0.68	0	1.17	0.61	0.0018	0.4	0.84	0.71	0.57	4.99	0.0004	0.0001	0	0.01	0
3031661	0.69	0	0.95	0.35	1	0.55	0.14	0.4	0.24	6.09	0	0.0001	0	0.01	0
3212761	0.68	0	1.18	0.63	0.0002	0.58	0.68	0.66	0.61	4.32	0.0002	0	0.0001	0	0
3268183	0.68	0	1.04	0.63	0.0004	0.46	0.81	0.71	0.59	6.98	0.0001	0	0	0	0.001
3472753	0.69	0	0.96	0.37	1	0.42	0.32	0.39	0.34	7.01	0.0006	0.0001	0.0001	0	0
3501557	0.68	0	1.23	0.64	0.0001	0.58	0.69	0.66	0.62	4.53	0.0003	0.0001	0	0.01	0
3543621	0.69	0	0.91	0.37	1	0.51	0.21	0.4	0.3	4.9	0.0001	0.0001	0	0.04	0.002
3551833	0.69	0	1.13	0.65	0	0.58	0.72	0.69	0.63	6.09	0	0	0	0	0
3562041	0.69	0	1.24	0.64	0.0001	0.57	0.71	0.67	0.62	6.37	0	0	0	0	0
3661099	0.69	0	1.09	0.63	0.0004	0.51	0.74	0.68	0.6	6.7	0.0003	0	0.0001	0.1	0.013
3667907	0.69	0	1.05	0.64	0.0001	0.56	0.72	0.68	0.62	8.01	0	0	0	0	0
3701840	0.68	0	1.09	0.61	0.0018	0.49	0.74	0.66	0.58	5.5	0.0009	0	0	0	0.001
3840609	0.69	0	1.21	0.63	0.0004	0.45	0.82	0.71	0.59	3.09	0.0001	0	0	0.02	0.004
3889144	0.7	0	1.13	0.64	0.0001	0.6	0.67	0.66	0.62	5.77	0	0	0	0	0
3889625	0.69	0	1.15	0.63	0.0002	0.58	0.68	0.66	0.61	5.32	0.0002	0	0	0	0
3897081	0.69	0	1.11	0.66	0	0.5	0.83	0.75	0.62	5.73	0	0	0	0.1	0.002
3902441	0.68	0	0.95	0.38	0.9999	0.47	0.3	0.41	0.35	6.22	0.0007	0.0001	0.0001	0.01	0.001
4026042	0.69	0	1.15	0.64	0.0001	0.61	0.66	0.65	0.63	7.8	0.0001	0	0	0.01	0.001

Performance of the 1,425 detected biomarkers across different metrics for the recurrence endpoint on the pooled discovery and validation cohort (n = 199). See Example 2 for explanation of metrics.

TABLE 19

Affymetrix Probeset ID	AUC	WILCOX P- VALUE	MFD	ACC URACY	ACCURACY P- VALUE	SENSI TIVITY	SPECIF ICITY	PPV	NPV	CUT OFF	KM P- VALUE	UVA HR P- VALUE	UVA OR P- VALUE
2318654	0.65	0.0052	1.33	0.64	0.5397	0.7	0.6	0.5	0.78	7.85	0.001	0.0038	0.005
2318755	0.63	0.0113	1.66	0.67	0.2627	0.6	0.71	0.54	0.75	5.57	0.0005	0.0043	0.007
2320062	0.65	0.0054	1.26	0.64	0.4669	0.6	0.67	0.51	0.74	5.23	0.0014	0.0043	0.009
2321661	0.65	0.006	1.43	0.64	0.5397	0.72	0.59	0.5	0.79	6.52	0.0012	0.0042	0.004
2322383	0.63	0.012	1.47	0.63	0.611	0.66	0.61	0.49	0.76	5.18	0.0017	0.0078	0.012
2325809	0.62	0.0233	1.38	0.61	0.7405	0.62	0.61	0.48	0.74	6.06	0.0111	0.0139	0.019
2327494	0.63	0.0164	1.38	0.63	0.611	0.68	0.6	0.49	0.77	6.31	0.0023	0.0069	0.008
2327865	0.64	0.0082	1.46	0.61	0.7405	0.66	0.59	0.48	0.75	5.34	0.0037	0.0031	0.005
2328504	0.67	0.0013	1.4	0.67	0.2627	0.7	0.65	0.53	0.79	6.54	0.0002	0.0013	0.001
2328507	0.68	0.0005	1.34	0.66	0.3262	0.47	0.77	0.54	0.72	5.36	0.0045	0.0019	0.002
2329019	0.65	0.004	1.3	0.64	0.5397	0.64	0.63	0.5	0.75	6.44	0.0016	0.0042	0.005
2329798	0.65	0.0049	1.53	0.64	0.5397	0.62	0.65	0.5	0.75	4.79	0.0055	0.0085	0.007
2330704	0.62	0.023	1.35	0.6	0.8429	0.64	0.57	0.46	0.73	4.95	0.0143	0.0153	0.018
2331419	0.65	0.0043	1.32	0.62	0.6786	0.47	0.71	0.48	0.7	4.58	0.0358	0.0118	0.009
2331842	0.61	0.0405	1.33	0.64	0.5397	0.6	0.66	0.5	0.74	5.92	0.0044	0.0215	0.030
2332192	0.67	0.0012	1.61	0.64	0.5397	0.51	0.71	0.5	0.72	5.14	0.0079	0.0023	0.003
2332740	0.66	0.002	1.48	0.67	0.206	0.57	0.73	0.55	0.75	3.69	0.0004	0.001	0.002
2334302	0.66	0.0028	1.33	0.67	0.2627	0.72	0.63	0.53	0.8	6.17	0.0001	0.0016	0.002
2336960	0.66	0.003	1.31	0.64	0.4669	0.62	0.66	0.51	0.75	6.62	0.0011	0.0018	0.002
2339310	0.64	0.0065	1.43	0.67	0.2627	0.55	0.73	0.54	0.74	4.64	0.0014	0.0039	0.005
2342617	0.64	0.0104	1.3	0.61	0.7405	0.51	0.67	0.47	0.71	4.46	0.0632	0.0188	0.015
2345634	0.66	0.0024	1.44	0.6	0.8429	0.64	0.57	0.46	0.73	4.69	0.0111	0.0009	0.002
2345663	0.7	0.0001	1.29	0.64	0.4669	0.74	0.59	0.51	0.8	4.44	0.0009	0.0001	0.000
2345666	0.6	0.0676	1.36	0.63	0.611	0.51	0.7	0.49	0.71	4.25	0.0106	0.0392	0.058
2346911	0.63	0.0141	1.27	0.64	0.4669	0.55	0.7	0.51	0.73	7.17	0.0048	0.0092	0.012
2346912	0.62	0.0189	1.37	0.61	0.7405	0.4	0.73	0.46	0.68	3.88	0.1237	0.0236	0.019
2347108	0.64	0.0096	1.34	0.63	0.611	0.45	0.73	0.49	0.7	6.04	0.0286	0.0121	0.014
2348819	0.66	0.0029	1.37	0.65	0.3949	0.64	0.66	0.52	0.76	5.97	0.0009	0.0031	0.003
2350305	0.62	0.0292	1.34	0.64	0.5397	0.62	0.65	0.5	0.75	5.19	0.0029	0.0131	0.021
2350371	0.65	0.0043	1.25	0.62	0.6786	0.38	0.76	0.47	0.68	4.47	0.0896	0.0057	0.005
2352268	0.69	0.0004	1.34	0.66	0.3262	0.64	0.67	0.53	0.76	6.24	0.0004	0.0005	0.00
2353492	0.63	0.017	1.27	0.64	0.5397	0.62	0.65	0.5	0.75	6.15	0.0021	0.0093	0.019
2358275	0.59	0.0819	1.25	0.63	0.611	0.53	0.68	0.49	0.72	4.26	0.0187	0.0715	0.088
2358923	0.64	0.0096	1.44	0.65	0.3949	0.7	0.62	0.52	0.78	6.94	0.0005	0.007	0.009
2359857	0.67	0.0017	1.33	0.66	0.3262	0.66	0.66	0.53	0.77	4.36	0.0006	0.005	0.004
2360078	0.66	0.0022	1.29	0.64	0.4669	0.55	0.7	0.51	0.73	7.34	0.0024	0.0011	0.003
2360119	0.66	0.0024	1.32	0.67	0.206	0.68	0.67	0.54	0.79	7.4	0.0001	0.0021	0.002
2360120	0.66	0.0021	1.25	0.62	0.6786	0.62	0.62	0.48	0.74	7.06	0.0072	0.0009	0.001
2360340	0.63	0.0115	1.28	0.67	0.206	0.55	0.74	0.55	0.74	5.72	0.0007	0.0066	0.00

2360716	0.63	0.0141	1.28	0.61	0.7405	0.77	0.52	0.48	0.8	7.12	0.0016	0.0166	0.0204
2360962	0.68	0.001	1.36	0.65	0.3949	0.6	0.68	0.52	0.75	5.51	0.0008	0.0006	0.0013
2361031	0.58	0.1168	1.15	0.61	0.7405	0.45	0.71	0.47	0.69	3.33	0.06	0.1638	0.1501
2363064	0.67	0.0012	1.29	0.61	0.7405	0.66	0.59	0.48	0.75	6.45	0.0075	0.001	0.0012
2363334	0.62	0.0233	1.29	0.57	0.9388	0.53	0.6	0.43	0.69	5.01	0.0894	0.0173	0.0279
2363956	0.68	0.0006	1.28	0.67	0.206	0.51	0.77	0.56	0.73	4.57	0.0017	0.0055	0.0064
2365991	0.62	0.0187	1.61	0.61	0.7405	0.6	0.62	0.47	0.73	4.56	0.0113	0.0352	0.0361
2367178	0.67	0.0016	1.6	0.64	0.4669	0.68	0.62	0.51	0.77	4.92	0.0008	0.0019	0.0025
2367214	0.64	0.0094	1.46	0.61	0.7405	0.66	0.59	0.48	0.75	4.86	0.0047	0.0077	0.0097
2367236	0.63	0.0177	1.32	0.63	0.611	0.66	0.61	0.49	0.76	5.6	0.0024	0.0109	0.0171
2369830	0.68	0.0009	1.47	0.66	0.3262	0.66	0.66	0.53	0.77	4.54	0.0004	0.0012	0.0018
2370014	0.65	0.0038	1.26	0.61	0.7405	0.62	0.61	0.48	0.74	4.18	0.0105	0.001	0.004
2371291	0.66	0.0026	1.37	0.63	0.611	0.55	0.67	0.49	0.72	5.26	0.0078	0.0022	0.0059
2371339	0.64	0.0078	1.36	0.63	0.611	0.55	0.67	0.49	0.72	4.45	0.0111	0.0198	0.0222
2371796	0.67	0.0016	1.31	0.63	0.611	0.51	0.7	0.49	0.71	5.7	0.0134	0.0023	0.0036
2373002	0.64	0.0076	1.46	0.66	0.3262	0.57	0.71	0.53	0.74	4.06	0.0005	0.0133	0.016
2375035	0.66	0.002	1.4	0.65	0.3949	0.53	0.72	0.52	0.73	4.75	0.0033	0.002	0.0027
2375037	0.69	0.0004	1.27	0.67	0.2627	0.66	0.67	0.53	0.77	6.88	0.0002	0.0004	0.0006
2375675	0.65	0.0056	1.35	0.62	0.6786	0.7	0.57	0.49	0.77	4.68	0.003	0.0091	0.0072
2375780	0.64	0.0079	1.44	0.62	0.6786	0.62	0.62	0.48	0.74	5.94	0.006	0.006	0.008
2375850	0.68	0.0009	1.27	0.67	0.206	0.66	0.68	0.54	0.78	6.85	0.0001	0.0005	0.001
2375890	0.65	0.0053	1.41	0.6	0.7956	0.68	0.56	0.47	0.75	6.85	0.0055	0.0038	0.0047
2377473	0.7	0.0002	1.43	0.6	0.7956	0.66	0.57	0.47	0.75	4.47	0.0072	0.0002	0.0005
2377508	0.68	0.0009	1.63	0.63	0.611	0.68	0.6	0.49	0.77	5.88	0.0016	0.0005	0.0011
2378615	0.61	0.0303	1.35	0.61	0.7405	0.51	0.67	0.47	0.71	3.71	0.0266	0.0335	0.0664
2379787	0.67	0.0017	1.36	0.61	0.7405	0.77	0.52	0.48	0.8	4.65	0.0021	0.0015	0.0019
2383763	0.64	0.0069	1.3	0.63	0.611	0.66	0.61	0.49	0.76	6.36	0.0026	0.0055	0.0087
2389076	0.66	0.0026	1.38	0.65	0.3949	0.57	0.7	0.52	0.74	4.92	0.0014	0.0017	0.0032
2389079	0.68	0.0006	1.36	0.67	0.206	0.49	0.78	0.56	0.73	4.81	0.0007	0.0007	0.0012
2389084	0.63	0.0185	1.34	0.67	0.2627	0.49	0.77	0.55	0.72	5.29	0.0014	0.0051	0.0095
2389086	0.64	0.0066	1.29	0.64	0.5397	0.55	0.68	0.5	0.73	5.34	0.0075	0.0083	0.0102
2389817	0.68	0.0007	1.33	0.66	0.3262	0.57	0.71	0.53	0.74	7.11	0.0016	0.0012	0.0018
2394560	0.64	0.0094	1.73	0.6	0.8429	0.62	0.59	0.46	0.73	5.1	0.0164	0.0088	0.0103
2395192	0.66	0.0025	1.49	0.67	0.2627	0.55	0.73	0.54	0.74	6.47	0.0004	0.0005	0.0016
2395195	0.67	0.0016	1.26	0.61	0.7405	0.62	0.61	0.48	0.74	5.06	0.0119	0.0019	0.0033
2396421	0.63	0.0112	1.33	0.61	0.7405	0.57	0.63	0.47	0.72	4.36	0.0155	0.0106	0.0129
2400180	0.64	0.0086	1.32	0.6	0.8429	0.57	0.61	0.46	0.71	5.75	0.0214	0.0027	0.0075
2400323	0.63	0.013	1.3	0.6	0.8429	0.45	0.68	0.45	0.68	3.94	0.1368	0.0079	0.0162
2401277	0.73	0	1.39	0.7	0.0837	0.62	0.74	0.58	0.77	2.96	0	0	0.0002
2401288	0.69	0.0005	1.27	0.63	0.611	0.72	0.57	0.49	0.78	5.94	0.0008	0.0003	0.0005
2401350	0.69	0.0005	1.52	0.64	0.5397	0.66	0.62	0.5	0.76	5.08	0.0009	0.0004	0.0007
2401368	0.64	0.0106	1.31	0.69	0.1164	0.43	0.84	0.61	0.72	5.17	0.0005	0.0018	0.0038
2402210	0.66	0.003	1.22	0.64	0.4669	0.7	0.61	0.51	0.78	5.56	0.0006	0.0046	0.0073

2405379	0.65	0.0037	1.4	0.64	0.4669	0.64	0.65	0.51	0.76	5.51	0.0013	0.0037	0.0051
2406094	0.64	0.0064	1.43	0.65	0.3949	0.64	0.66	0.52	0.76	6.24	0.0005	0.0041	0.0073
2406148	0.65	0.0059	1.44	0.64	0.4669	0.74	0.59	0.51	0.8	6.23	0.0003	0.0047	0.0048
2407134	0.63	0.0177	1.36	0.64	0.4669	0.57	0.68	0.51	0.74	4.7	0.0021	0.0096	0.0161
2408880	0.62	0.0205	1.33	0.6	0.8429	0.53	0.63	0.45	0.7	4.7	0.0531	0.0151	0.0246
2410112	0.65	0.0042	1.35	0.63	0.611	0.72	0.57	0.49	0.78	5.4	0.0013	0.003	0.0027
2410528	0.63	0.0126	1.26	0.6	0.7956	0.79	0.5	0.47	0.8	6.06	0.001	0.0094	0.0138
2412669	0.64	0.0092	1.32	0.63	0.611	0.55	0.67	0.49	0.72	4.75	0.0104	0.0112	0.0112
2413580	0.64	0.008	1.3	0.64	0.4669	0.57	0.68	0.51	0.74	5.02	0.0023	0.0102	0.0125
2414030	0.68	0.001	1.52	0.64	0.4669	0.62	0.66	0.51	0.75	4.78	0.0029	0.002	0.0019
2414960	0.62	0.0194	1.36	0.6	0.8429	0.6	0.6	0.46	0.72	4.59	0.0172	0.0064	0.0202
2417788	0.64	0.0075	1.42	0.64	0.4669	0.62	0.66	0.51	0.75	4.86	0.0005	0.0063	0.0107
2418028	0.66	0.002	1.29	0.68	0.1571	0.62	0.72	0.56	0.77	5.81	0.0002	0.0024	0.0028
2419242	0.69	0.0005	1.34	0.63	0.611	0.43	0.74	0.49	0.69	4.65	0.0341	0.0014	0.0018
2419247	0.6	0.0698	1.25	0.64	0.5397	0.49	0.72	0.5	0.71	5.37	0.0119	0.0363	0.0436
2419276	0.67	0.0016	1.31	0.64	0.4669	0.7	0.61	0.51	0.78	5.71	0.0004	0.0013	0.0024
2420740	0.65	0.0048	1.54	0.6	0.7956	0.53	0.65	0.46	0.71	3.96	0.0525	0.0024	0.0031
2420839	0.65	0.0036	1.34	0.66	0.3262	0.47	0.77	0.54	0.72	4.98	0.0043	0.0014	0.0027
2421273	0.67	0.0012	1.33	0.69	0.1164	0.64	0.72	0.57	0.78	6.06	0	0.0009	0.0014
2421274	0.64	0.0068	1.31	0.65	0.3949	0.6	0.68	0.52	0.75	4.52	0.0016	0.0095	0.0146
2421932	0.64	0.0072	1.31	0.61	0.7405	0.74	0.54	0.48	0.79	6.5	0.0028	0.011	0.0083
2422519	0.65	0.0044	1.41	0.64	0.4669	0.57	0.68	0.51	0.74	4.8	0.0038	0.0041	0.0064
2423200	0.65	0.0062	1.37	0.65	0.3949	0.68	0.63	0.52	0.78	6.89	0.0005	0.0027	0.0042
2427009	0.6	0.05	1.51	0.6	0.7956	0.53	0.65	0.46	0.71	4.01	0.0398	0.0192	0.0271
2427501	0.65	0.0046	1.65	0.65	0.3949	0.68	0.63	0.52	0.78	4.76	0.0006	0.0024	0.0045
2427978	0.66	0.0021	1.43	0.66	0.3262	0.64	0.67	0.53	0.76	6.15	0.0007	0.0014	0.0016
2428394	0.68	0.0007	1.36	0.71	0.0583	0.68	0.72	0.58	0.8	6.19	0	0.0007	0.0009
2429071	0.67	0.0016	1.26	0.62	0.6786	0.45	0.72	0.48	0.69	4.47	0.0691	0.0068	0.0059
2429119	0.69	0.0003	1.39	0.67	0.206	0.68	0.67	0.54	0.79	5.43	0.0001	0.0004	0.0006
2429168	0.63	0.0134	1.43	0.57	0.9388	0.47	0.63	0.42	0.68	3.82	0.2306	0.03	0.0506
2429282	0.69	0.0004	1.38	0.67	0.206	0.57	0.73	0.55	0.75	4.96	0.0003	0.0008	0.001
2429309	0.67	0.0015	1.37	0.64	0.5397	0.68	0.61	0.5	0.77	6.53	0.0012	0.0008	0.0016
2429310	0.66	0.0022	1.66	0.62	0.6786	0.68	0.59	0.48	0.76	5.42	0.003	0.0012	0.0021
2433376	0.63	0.0149	1.33	0.64	0.4669	0.64	0.65	0.51	0.76	4.99	0.0012	0.0188	0.0224
2434721	0.63	0.0121	1.34	0.58	0.914	0.53	0.61	0.44	0.69	5.46	0.1464	0.016	0.0175
2435391	0.65	0.0049	1.36	0.64	0.4669	0.53	0.71	0.51	0.73	6.56	0.0035	0.0041	0.0079
2437095	0.63	0.0139	1.32	0.58	0.914	0.64	0.55	0.45	0.73	6.33	0.0342	0.0142	0.0147
2437537	0.6	0.0541	1.3	0.61	0.7405	0.45	0.71	0.47	0.69	5.24	0.0806	0.0959	0.0881
2437538	0.68	0.0008	1.51	0.62	0.6786	0.72	0.56	0.49	0.78	6.29	0.0019	0.0011	0.0009
2437680	0.65	0.0062	1.37	0.65	0.3949	0.62	0.67	0.52	0.75	4.52	0.0011	0.0171	0.0171
2437775	0.62	0.0261	1.31	0.64	0.5397	0.49	0.72	0.5	0.71	4.15	0.0219	0.0254	0.0273
2439041	0.6	0.0511	1.28	0.61	0.7405	0.55	0.65	0.47	0.72	4.52	0.0389	0.0635	0.0547
2440149	0.64	0.0082	1.32	0.61	0.7405	0.55	0.65	0.47	0.72	4.93	0.0155	0.0091	0.0159

2440513	0.67	0.001	1.33	0.62	0.6786	0.74	0.55	0.49	0.79	8.24	0.0009	0.0019	0.0026
2442702	0.62	0.0233	1.3	0.64	0.4669	0.51	0.72	0.51	0.72	5.53	0.0042	0.0145	0.0234
2443917	0.66	0.0024	1.34	0.65	0.3949	0.55	0.71	0.52	0.73	4.71	0.003	0.0026	0.0034
2444488	0.62	0.0236	1.32	0.65	0.3949	0.49	0.74	0.52	0.72	3.92	0.0049	0.0118	0.0235
2444489	0.62	0.0197	1.32	0.6	0.7956	0.36	0.74	0.45	0.67	4.42	0.1867	0.0227	0.0376
2448289	0.61	0.0391	1.28	0.64	0.5397	0.43	0.76	0.5	0.7	4.08	0.0437	0.0535	0.051
2448313	0.66	0.0032	1.47	0.64	0.5397	0.53	0.7	0.5	0.72	4.09	0.0079	0.0034	0.0061
2450669	0.64	0.0072	1.49	0.6	0.8429	0.6	0.6	0.46	0.72	5.06	0.0236	0.0053	0.0068
2451314	0.63	0.0137	1.36	0.63	0.611	0.6	0.65	0.49	0.74	4.55	0.0069	0.0025	0.0074
2452652	0.67	0.0011	1.43	0.66	0.3262	0.72	0.62	0.52	0.8	6.12	0.0001	0.001	0.0012
2452655	0.63	0.0121	1.5	0.65	0.3949	0.55	0.71	0.52	0.73	4.93	0.0018	0.007	0.0169
2457626	0.68	0.0005	1.3	0.67	0.2627	0.51	0.76	0.55	0.73	5.73	0.0015	0.0011	0.0013
2458075	0.62	0.0219	1.51	0.64	0.5397	0.57	0.67	0.5	0.73	5.28	0.0031	0.0125	0.0211
2458381	0.62	0.0292	1.2	0.58	0.914	0.47	0.65	0.43	0.68	4.9	0.2056	0.0113	0.0215
2458503	0.66	0.0026	1.33	0.64	0.5397	0.68	0.61	0.5	0.77	5.73	0.0014	0.0015	0.0023
2459655	0.65	0.0053	1.23	0.62	0.6786	0.47	0.71	0.48	0.7	6.48	0.0268	0.0041	0.0067
2461827	0.67	0.0015	1.32	0.67	0.2627	0.6	0.71	0.54	0.75	5.09	0.0004	0.002	0.003
2461828	0.67	0.0018	1.35	0.64	0.4669	0.66	0.63	0.51	0.76	5.29	0.0014	0.0024	0.0028
2462178	0.64	0.0074	1.34	0.58	0.914	0.55	0.6	0.44	0.7	4.45	0.0924	0.0027	0.0068
2464496	0.69	0.0005	1.58	0.67	0.2627	0.68	0.66	0.53	0.78	5.38	0.0002	0.0004	0.0008
2464505	0.68	0.001	1.35	0.67	0.206	0.68	0.67	0.54	0.79	6.3	0.0001	0.0007	0.0011
2464514	0.66	0.0025	1.32	0.64	0.4669	0.66	0.63	0.51	0.76	5.72	0.001	0.0024	0.0028
2464537	0.66	0.0024	1.41	0.67	0.206	0.62	0.71	0.55	0.76	5.7	0.0001	0.0012	0.0021
2468935	0.62	0.0271	1.24	0.6	0.8429	0.47	0.67	0.45	0.69	4.85	0.1455	0.0219	0.0241
2469568	0.7	0.0002	1.37	0.69	0.1164	0.62	0.73	0.57	0.77	4.27	0.0001	0.0005	0.001
2473241	0.68	0.0005	1.25	0.64	0.4669	0.53	0.71	0.51	0.73	4.8	0.008	0.0015	0.0023
2473624	0.66	0.002	1.66	0.64	0.5397	0.66	0.62	0.5	0.76	4.93	0.0018	0.0013	0.0019
2474147	0.61	0.0369	1.36	0.58	0.914	0.66	0.54	0.45	0.73	6.87	0.0257	0.0254	0.0377
2474700	0.67	0.0016	1.36	0.64	0.5397	0.72	0.59	0.5	0.79	5.15	0.0005	0.0018	0.0023
2474770	0.69	0.0004	1.42	0.68	0.1571	0.7	0.67	0.55	0.8	6.05	0	0.0004	0.0005
2475647	0.6	0.0529	1.33	0.61	0.7405	0.49	0.68	0.47	0.7	4.98	0.0592	0.0594	0.0558
2476316	0.7	0.0002	1.26	0.65	0.3949	0.64	0.66	0.52	0.76	4.67	0.001	0.0007	0.0013
2476408	0.65	0.0039	1.53	0.64	0.5397	0.6	0.66	0.5	0.74	5.02	0.0034	0.002	0.0036
2477341	0.64	0.0097	1.43	0.6	0.7956	0.6	0.61	0.47	0.72	5.4	0.019	0.0104	0.0102
2478839	0.65	0.0049	1.32	0.65	0.3949	0.66	0.65	0.52	0.77	6.62	0.0008	0.0028	0.0033
2479729	0.67	0.0016	1.38	0.61	0.7405	0.72	0.55	0.48	0.78	5.13	0.003	0.0011	0.0012
2480989	0.69	0.0004	1.36	0.64	0.4669	0.47	0.74	0.51	0.71	4.92	0.0068	0.0002	0.0006
2481178	0.66	0.0032	1.43	0.67	0.2627	0.64	0.68	0.54	0.77	5.04	0.0005	0.0024	0.0026
2482593	0.66	0.0033	1.32	0.63	0.611	0.53	0.68	0.49	0.72	5.54	0.0104	0.0035	0.0051
2482624	0.67	0.0011	1.28	0.62	0.6786	0.72	0.56	0.49	0.78	7.06	0.0017	0.0009	0.0012
2483047	0.65	0.0057	1.51	0.59	0.8822	0.53	0.62	0.45	0.7	5.04	0.0678	0.0075	0.011
2484558	0.67	0.0013	1.39	0.67	0.206	0.49	0.78	0.56	0.73	4.17	0.0011	0.0069	0.0071
2484807	0.67	0.0014	1.32	0.59	0.8822	0.77	0.49	0.46	0.78	6.35	0.0048	0.0017	0.0016

2485214	0.64	0.008	1.39	0.62	0.6786	0.6	0.63	0.48	0.73	5.47	0.0091	0.0079	0.0085
2485276	0.63	0.0121	1.25	0.6	0.8429	0.49	0.66	0.45	0.69	4.49	0.0798	0.0433	0.0454
2487216	0.63	0.0113	1.49	0.63	0.611	0.6	0.65	0.49	0.74	5.06	0.0075	0.0064	0.0112
2487645	0.67	0.0015	1.34	0.67	0.206	0.62	0.71	0.55	0.76	5.91	0.0001	0.0018	0.0024
2488150	0.65	0.0058	1.21	0.61	0.7405	0.6	0.62	0.47	0.73	5.01	0.0208	0.0063	0.0102
2489030	0.64	0.0071	1.43	0.64	0.5397	0.6	0.66	0.5	0.74	5.64	0.004	0.0099	0.0075
2489435	0.67	0.0014	1.32	0.63	0.611	0.64	0.62	0.49	0.75	6.14	0.0036	0.002	0.0019
2491645	0.65	0.0046	1.3	0.64	0.5397	0.66	0.62	0.5	0.76	6.43	0.0014	0.0042	0.0048
2492101	0.65	0.0057	1.24	0.61	0.7405	0.62	0.61	0.48	0.74	3.51	0.0114	0.0024	0.0087
2492833	0.61	0.0415	1.38	0.6	0.7956	0.53	0.65	0.46	0.71	5.89	0.0251	0.0207	0.0408
2495140	0.66	0.002	1.53	0.64	0.5397	0.68	0.61	0.5	0.77	4.83	0.0015	0.0015	0.0021
2498988	0.66	0.003	1.46	0.65	0.3949	0.53	0.72	0.52	0.73	4.54	0.0042	0.0041	0.0073
2507241	0.68	0.0008	1.5	0.67	0.2627	0.57	0.72	0.54	0.75	5.06	0.0008	0.0013	0.0017
2507514	0.66	0.0035	1.37	0.64	0.4669	0.66	0.63	0.51	0.76	6.06	0.0016	0.0032	0.0051
2507533	0.67	0.0017	1.38	0.66	0.3262	0.68	0.65	0.52	0.78	6.67	0.0002	0.001	0.0016
2512351	0.65	0.0042	1.31	0.65	0.3949	0.66	0.65	0.52	0.77	4.43	0.0009	0.01	0.0116
2512363	0.64	0.0068	1.55	0.63	0.611	0.57	0.66	0.49	0.73	3.74	0.0081	0.0036	0.0051
2512959	0.64	0.009	1.26	0.59	0.8822	0.55	0.61	0.45	0.7	3.88	0.0675	0.0218	0.0201
2515085	0.64	0.0098	1.33	0.64	0.4669	0.66	0.63	0.51	0.76	6.98	0.0009	0.0051	0.0081
2517330	0.66	0.003	1.41	0.67	0.206	0.45	0.8	0.57	0.72	4.39	0.0013	0.0051	0.0069
2518193	0.68	0.0007	1.27	0.62	0.6786	0.77	0.54	0.49	0.8	5.52	0.001	0.0005	0.0009
2518707	0.64	0.0083	1.47	0.6	0.7956	0.57	0.62	0.47	0.72	5.24	0.0156	0.0031	0.0087
2525095	0.69	0.0004	1.37	0.67	0.206	0.6	0.72	0.55	0.76	5.7	0.0002	0.0005	0.0012
2527206	0.67	0.0015	1.32	0.6	0.8429	0.72	0.52	0.47	0.77	8.07	0.0048	0.0016	0.002
2527635	0.68	0.0005	1.36	0.61	0.7405	0.53	0.66	0.47	0.71	5.16	0.0273	0.0008	0.0011
2532844	0.63	0.0153	1.25	0.64	0.5397	0.49	0.72	0.5	0.71	4.77	0.0142	0.0131	0.0184
2534447	0.67	0.0013	1.42	0.69	0.1164	0.55	0.77	0.58	0.75	5.8	0.0001	0.0021	0.0025
2537112	0.64	0.0064	1.36	0.64	0.5397	0.66	0.62	0.5	0.76	6.32	0.0013	0.0042	0.0081
2539775	0.68	0.0008	1.46	0.67	0.206	0.51	0.77	0.56	0.73	4.74	0.0007	0.0011	0.002
2540221	0.64	0.01	1.48	0.63	0.611	0.66	0.61	0.49	0.76	6.42	0.0035	0.0057	0.007
2544180	0.66	0.0031	1.37	0.64	0.4669	0.66	0.63	0.51	0.76	6.73	0.001	0.0024	0.0026
2544185	0.6	0.0573	1.27	0.6	0.8429	0.32	0.76	0.43	0.66	4.66	0.2278	0.0756	0.1259
2544295	0.65	0.0044	1.56	0.64	0.4669	0.6	0.67	0.51	0.74	4.64	0.003	0.0075	0.0078
2544306	0.64	0.0078	1.36	0.63	0.611	0.49	0.71	0.49	0.71	5.25	0.0202	0.0174	0.0194
2546279	0.67	0.0019	1.58	0.67	0.2627	0.66	0.67	0.53	0.77	5.37	0.0003	0.0023	0.0021
2549323	0.62	0.0261	1.29	0.61	0.7405	0.53	0.66	0.47	0.71	4.71	0.0268	0.0109	0.0253
2550840	0.64	0.0107	1.25	0.66	0.3262	0.57	0.71	0.53	0.74	4.88	0.0006	0.0104	0.0193
2550842	0.63	0.012	1.34	0.6	0.8429	0.43	0.7	0.44	0.68	3.89	0.1429	0.0194	0.0269
2550964	0.7	0.0002	1.39	0.68	0.1571	0.62	0.72	0.56	0.77	5.94	0.0001	0.0002	0.0003
2552021	0.65	0.0057	1.53	0.65	0.3949	0.51	0.73	0.52	0.72	5.1	0.0037	0.0024	0.0035
2553312	0.65	0.0056	1.29	0.63	0.611	0.64	0.62	0.49	0.75	5.71	0.0039	0.0066	0.0065
2553583	0.67	0.0017	1.33	0.59	0.8822	0.74	0.5	0.46	0.77	7.07	0.009	0.002	0.0023
2553585	0.63	0.0128	1.75	0.66	0.3262	0.57	0.71	0.53	0.74	5.35	0.0009	0.0045	0.0077

2553595	0.66	0.0031	1.43	0.63	0.611	0.6	0.65	0.49	0.74	5.33	0.0044	0.0019	0.0033
2553907	0.66	0.0024	1.3	0.64	0.4669	0.45	0.76	0.51	0.7	4.47	0.008	0.002	0.0055
2554001	0.63	0.013	1.7	0.65	0.3949	0.53	0.72	0.52	0.73	3.88	0.0027	0.0089	0.0105
2555279	0.64	0.0084	1.42	0.62	0.6786	0.57	0.65	0.48	0.73	5.58	0.019	0.0103	0.0088
2555281	0.68	0.0005	1.51	0.66	0.3262	0.53	0.73	0.53	0.73	4.3	0.0012	0.0006	0.0011
2555288	0.65	0.0049	1.34	0.65	0.3949	0.6	0.68	0.52	0.75	4.22	0.0017	0.0059	0.0101
2555330	0.64	0.01	1.2	0.64	0.4669	0.38	0.79	0.51	0.69	4.29	0.0305	0.0048	0.0087
2555409	0.65	0.0056	1.39	0.68	0.1571	0.57	0.74	0.56	0.75	4.38	0.0001	0.0021	0.007
2555411	0.66	0.0022	1.51	0.63	0.611	0.68	0.6	0.49	0.77	5.34	0.0025	0.0013	0.0019
2555416	0.67	0.0014	1.36	0.66	0.3262	0.55	0.72	0.53	0.74	5.26	0.0015	0.0017	0.0034
2555507	0.63	0.0115	1.27	0.63	0.611	0.34	0.79	0.48	0.68	4.25	0.0667	0.0178	0.0274
2555522	0.65	0.0061	1.26	0.63	0.611	0.77	0.55	0.49	0.8	5.16	0.0011	0.0088	0.0087
2556229	0.65	0.0039	1.41	0.62	0.6786	0.55	0.66	0.48	0.72	4.17	0.0168	0.0085	0.0089
2558208	0.64	0.0092	1.28	0.67	0.2627	0.49	0.77	0.55	0.72	4.49	0.0011	0.0037	0.0087
2558313	0.64	0.0071	1.29	0.64	0.5397	0.64	0.63	0.5	0.75	5.23	0.0026	0.0029	0.0044
2558519	0.68	0.0005	1.39	0.68	0.1571	0.62	0.72	0.56	0.77	5.82	0.0001	0.0004	0.0007
2559293	0.61	0.0467	1.15	0.65	0.3949	0.47	0.76	0.52	0.71	5.3	0.0041	0.0244	0.0409
2562334	0.68	0.0007	1.33	0.66	0.3262	0.72	0.62	0.52	0.8	6.74	0.0002	0.0005	0.0008
2565264	0.57	0.0011	1.36	0.66	0.3262	0.72	0.62	0.52	0.8	7.58	0.0001	0.0008	0.0011
2575142	0.64	0.0084	1.49	0.65	0.3949	0.6	0.68	0.52	0.75	4.58	0.0017	0.0069	0.0074
2577959	0.65	0.006	1.32	0.67	0.206	0.47	0.79	0.56	0.72	4.14	0.0015	0.0085	0.0103
2581588	0.64	0.0106	1.32	0.58	0.914	0.55	0.6	0.44	0.7	4.27	0.0751	0.0171	0.0237
2583054	0.66	0.0032	1.33	0.64	0.5397	0.7	0.6	0.5	0.78	6.28	0.0012	0.0021	0.0029
2583056	0.67	0.0016	1.44	0.69	0.1164	0.7	0.68	0.56	0.8	4.41	0	0.0026	0.0027
2583249	0.63	0.0164	1.45	0.64	0.5397	0.55	0.68	0.5	0.73	4.69	0.0068	0.0125	0.0171
2583609	0.61	0.0382	1.33	0.6	0.7956	0.6	0.61	0.47	0.72	5.26	0.0229	0.0228	0.0302
2584845	0.68	0.0007	1.41	0.65	0.3949	0.66	0.65	0.52	0.77	6.12	0.0005	0.0006	0.0012
2588838	0.65	0.0058	1.3	0.67	0.2627	0.55	0.73	0.54	0.74	5.31	0.0003	0.0105	0.0173
2590750	0.64	0.0093	1.46	0.67	0.2627	0.62	0.7	0.54	0.76	5.42	0.0002	0.0062	0.0111
2590802	0.65	0.0055	1.6	0.67	0.2627	0.62	0.7	0.54	0.76	6.66	0.0002	0.002	0.0036
2591635	0.61	0.0472	1.31	0.6	0.8429	0.66	0.56	0.46	0.74	6.53	0.0108	0.0229	0.0396
2591638	0.64	0.0097	1.44	0.66	0.3262	0.64	0.67	0.53	0.76	6.56	0.0002	0.0034	0.0094
2593447	0.65	0.0044	1.37	0.63	0.611	0.55	0.67	0.49	0.72	4.58	0.0108	0.0066	0.0118
2593692	0.65	0.0052	1.56	0.62	0.6786	0.57	0.65	0.48	0.73	5.33	0.012	0.0033	0.0041
2593714	0.62	0.0236	1.31	0.61	0.7405	0.47	0.7	0.47	0.7	5.08	0.0502	0.0143	0.0259
2593758	0.61	0.0323	1.63	0.62	0.6786	0.66	0.6	0.48	0.75	4.96	0.0031	0.0086	0.0156
2594506	0.65	0.006	1.4	0.64	0.5397	0.57	0.67	0.5	0.73	4.18	0.007	0.0149	0.0127
2596691	0.65	0.0043	1.3	0.63	0.611	0.72	0.57	0.49	0.78	4.81	0.0017	0.007	0.0057
2597013	0.65	0.0043	1.32	0.59	0.8822	0.64	0.56	0.45	0.73	4.47	0.0208	0.0019	0.0039
2598267	0.64	0.0084	1.35	0.64	0.5397	0.68	0.61	0.5	0.77	6.26	0.0015	0.0032	0.0099
2598289	0.67	0.0014	1.46	0.67	0.2627	0.6	0.71	0.54	0.75	5.61	0.001	0.0008	0.0029
2598781	0.66	0.0031	1.3	0.64	0.4669	0.72	0.6	0.51	0.79	8.69	0.0005	0.0021	0.0028
2599342	0.66	0.0024	1.5	0.66	0.3262	0.57	0.71	0.53	0.74	5.64	0.0018	0.0033	0.0041

2599903	0.63	0.0155	1.47	0.63	0.611	0.57	0.66	0.49	0.73	4.36	0.0141	0.0094	0.0095
2606647	0.63	0.0151	1.36	0.6	0.8429	0.66	0.56	0.46	0.74	6.61	0.0171	0.0096	0.0108
2607152	0.64	0.0066	1.31	0.65	0.3949	0.66	0.65	0.52	0.77	6.02	0.0008	0.0046	0.0075
2607374	0.64	0.0086	1.37	0.62	0.6786	0.45	0.72	0.48	0.69	5.08	0.0487	0.0072	0.0108
2609635	0.65	0.0051	1.34	0.64	0.5397	0.68	0.61	0.5	0.77	4.55	0.0012	0.0052	0.0063
2609657	0.68	0.001	1.41	0.69	0.1164	0.64	0.72	0.57	0.78	5.09	0.0001	0.0006	0.0013
2609668	0.64	0.0074	1.29	0.63	0.611	0.68	0.6	0.49	0.77	5.61	0.0015	0.0077	0.0179
2610353	0.63	0.0177	1.37	0.6	0.8429	0.66	0.56	0.46	0.74	5.45	0.012	0.0113	0.0179
2611083	0.64	0.0093	1.27	0.64	0.4669	0.38	0.79	0.51	0.69	5.77	0.0163	0.0037	0.0079
2614100	0.65	0.0041	1.36	0.67	0.206	0.57	0.73	0.55	0.75	5.7	0.0003	0.0025	0.0056
2614135	0.64	0.0101	1.27	0.61	0.7405	0.51	0.67	0.47	0.71	5.24	0.0455	0.0078	0.0121
2614137	0.63	0.0118	1.44	0.65	0.3949	0.64	0.66	0.52	0.76	5.64	0.0012	0.0057	0.0055
2615656	0.62	0.03	1.25	0.58	0.914	0.51	0.62	0.44	0.69	5.34	0.1141	0.0366	0.0484
2616071	0.62	0.0194	1.47	0.64	0.4669	0.51	0.72	0.51	0.72	4.56	0.0043	0.0077	0.0167
2616248	0.65	0.0055	1.36	0.64	0.5397	0.53	0.7	0.5	0.72	5.09	0.0112	0.0054	0.0055
2617578	0.64	0.007	1.41	0.58	0.914	0.74	0.49	0.45	0.77	5.27	0.0116	0.0066	0.0071
2618656	0.67	0.0013	1.49	0.61	0.7405	0.7	0.56	0.48	0.77	5.76	0.0049	0.0015	0.0014
2619365	0.64	0.0078	1.38	0.64	0.4669	0.57	0.68	0.51	0.74	4.8	0.003	0.011	0.0141
2625632	0.62	0.0242	1.2	0.58	0.914	0.66	0.54	0.45	0.73	3.76	0.0335	0.0467	0.0408
2625643	0.7	0.0002	1.35	0.66	0.3262	0.53	0.73	0.53	0.73	6.21	0.0026	0.0005	0.0006
2625893	0.67	0.0017	1.41	0.63	0.611	0.45	0.73	0.49	0.7	3.81	0.0318	0.0037	0.0042
2627951	0.7	0.0002	1.37	0.69	0.1164	0.66	0.71	0.56	0.78	3.94	0	0.0005	0.0009
2633534	0.67	0.0015	1.3	0.63	0.611	0.45	0.73	0.49	0.7	4.58	0.0355	0.0017	0.0024
2633651	0.64	0.0069	1.4	0.66	0.3262	0.62	0.68	0.53	0.76	5.81	0.0004	0.0033	0.0053
2638377	0.65	0.0046	1.28	0.62	0.6786	0.49	0.7	0.48	0.7	4.39	0.0182	0.0047	0.0075
2638451	0.64	0.0073	1.29	0.64	0.5397	0.64	0.63	0.5	0.75	7.12	0.0018	0.0036	0.0057
2638452	0.64	0.0101	1.37	0.6	0.7956	0.72	0.54	0.47	0.77	6.85	0.0049	0.0069	0.0076
2641575	0.63	0.011	1.34	0.62	0.6786	0.57	0.65	0.48	0.73	5.27	0.0126	0.0137	0.0133
2643579	0.62	0.0194	1.29	0.65	0.3949	0.55	0.71	0.52	0.73	4.93	0.0019	0.0136	0.0179
2645294	0.67	0.0017	1.63	0.68	0.1571	0.6	0.73	0.56	0.76	5.95	0.0001	0.0006	0.0011
2646066	0.64	0.01	1.3	0.66	0.3262	0.7	0.63	0.52	0.79	5.12	0.0003	0.0124	0.0148
2646085	0.66	0.0026	1.54	0.62	0.6786	0.7	0.57	0.49	0.77	5.23	0.0029	0.0013	0.0022
2647361	0.64	0.007	1.46	0.66	0.3262	0.62	0.68	0.53	0.76	5.11	0.0005	0.0077	0.0102
2647678	0.65	0.0044	1.31	0.67	0.2627	0.55	0.73	0.54	0.74	4.46	0.0004	0.0031	0.0062
2647775	0.66	0.0028	1.39	0.66	0.3262	0.57	0.71	0.53	0.74	5.37	0.0006	0.0014	0.003
2647779	0.64	0.0107	1.32	0.6	0.7956	0.57	0.62	0.47	0.72	4.28	0.0257	0.0028	0.0081
2648202	0.62	0.0213	1.25	0.65	0.3949	0.47	0.76	0.52	0.71	5.46	0.0116	0.0259	0.0292
2651521	0.68	0.0006	1.35	0.7	0.0837	0.64	0.73	0.58	0.78	4.48	0	0.0003	0.0011
2652021	0.67	0.0016	1.51	0.67	0.2627	0.57	0.72	0.54	0.75	5.14	0.0005	0.001	0.0023
2654335	0.68	0.0007	1.38	0.64	0.4669	0.47	0.74	0.51	0.71	5.6	0.0075	0.0009	0.0014
2654874	0.67	0.001	1.34	0.68	0.1571	0.64	0.71	0.56	0.77	5.87	0.0001	0.0011	0.0014
2654878	0.67	0.0017	1.29	0.66	0.3262	0.45	0.78	0.54	0.71	4.18	0.0021	0.0006	0.0026
2655475	0.68	0.0008	1.39	0.67	0.206	0.57	0.73	0.55	0.75	5.38	0.0002	0.0007	0.0011

2655509	0.66	0.0023	1.3	0.63	0.611	0.7	0.59	0.49	0.77	8.77	0.0016	0.0012	0.0021
2655678	0.64	0.0097	1.31	0.62	0.6786	0.62	0.62	0.48	0.74	5.74	0.0036	0.004	0.01
2656791	0.66	0.0024	1.31	0.62	0.6786	0.72	0.56	0.49	0.78	6.96	0.0024	0.0025	0.0033
2658354	0.66	0.0032	1.23	0.67	0.2627	0.6	0.71	0.54	0.75	5.34	0.001	0.0033	0.0037
2658632	0.72	0	1.39	0.69	0.1164	0.64	0.72	0.57	0.78	5.01	0	0	0.0001
2663553	0.61	0.043	1.32	0.64	0.4669	0.47	0.74	0.51	0.71	4.81	0.0087	0.011	0.0206
2666503	0.61	0.0456	1.39	0.67	0.2627	0.57	0.72	0.54	0.75	6.15	0.0005	0.0167	0.027
2666519	0.64	0.0096	1.2	0.64	0.4669	0.45	0.76	0.51	0.7	6.7	0.0174	0.0067	0.0104
2666524	0.66	0.0031	1.47	0.63	0.611	0.53	0.68	0.49	0.72	4.57	0.0072	0.0013	0.0035
2669316	0.62	0.0271	1.55	0.64	0.5397	0.53	0.7	0.5	0.72	4.86	0.0115	0.0127	0.0154
2669571	0.67	0.0014	1.41	0.66	0.3262	0.64	0.67	0.53	0.76	5.11	0.001	0.0034	0.0029
2670438	0.68	0.0008	0.71	0.36	1	0.36	0.37	0.25	0.5	4.35	0.0086	0.0035	0.0013
2672775	0.63	0.0121	1.5	0.59	0.8822	0.6	0.59	0.45	0.72	4.97	0.0351	0.007	0.0121
2674243	0.63	0.0113	1.4	0.6	0.7956	0.7	0.55	0.47	0.76	5.96	0.0056	0.011	0.0127
2675269	0.61	0.0339	1.2	0.6	0.8429	0.45	0.68	0.45	0.68	4.13	0.1106	0.0587	0.0831
2675802	0.61	0.0315	1.34	0.63	0.611	0.55	0.67	0.49	0.72	5.9	0.0157	0.0202	0.0209
2676931	0.65	0.0051	1.37	0.64	0.5397	0.62	0.65	0.5	0.75	6.46	0.0021	0.0049	0.0057
2677655	0.63	0.0141	1.33	0.64	0.4669	0.64	0.65	0.51	0.76	5.91	0.002	0.0134	0.0126
2677695	0.69	0.0004	1.32	0.64	0.5397	0.49	0.72	0.5	0.71	4.41	0.0088	0.0003	0.0009
2680511	0.65	0.0036	1.33	0.69	0.1164	0.64	0.72	0.57	0.78	3.39	0	0.0021	0.0034
2682663	0.66	0.0024	1.34	0.68	0.1571	0.53	0.77	0.57	0.74	6.54	0.0001	0.0023	0.0036
2685954	0.62	0.0252	1.26	0.61	0.7405	0.38	0.74	0.46	0.68	3.8	0.072	0.0329	0.0816
2691756	0.67	0.001	1.31	0.64	0.4669	0.64	0.65	0.51	0.76	4.83	0.0011	0.0014	0.0018
2692111	0.67	0.0012	1.57	0.69	0.1164	0.66	0.71	0.56	0.78	5.09	0.0001	0.0022	0.0018
2694407	0.69	0.0005	1.32	0.64	0.5397	0.6	0.66	0.5	0.74	3.99	0.0032	0.0006	0.0021
2694648	0.64	0.0101	1.44	0.6	0.8429	0.62	0.59	0.46	0.73	5.7	0.024	0.0089	0.0113
2694649	0.65	0.004	1.45	0.61	0.7405	0.64	0.6	0.48	0.74	5.44	0.0085	0.0042	0.0064
2695413	0.66	0.0031	1.39	0.66	0.3262	0.53	0.73	0.53	0.73	6.08	0.001	0.0014	0.0026
2700507	0.63	0.0159	1.27	0.6	0.7956	0.43	0.71	0.45	0.68	5.32	0.0742	0.0166	0.0338
2700829	0.66	0.0023	1.39	0.61	0.7405	0.47	0.7	0.47	0.7	5.51	0.0397	0.003	0.0055
2701289	0.65	0.0045	1.31	0.65	0.3949	0.64	0.66	0.52	0.76	5.43	0.0009	0.0062	0.0058
2702329	0.61	0.0303	1.33	0.63	0.611	0.6	0.65	0.49	0.74	4.59	0.0064	0.0177	0.0298
2703240	0.65	0.0054	1.52	0.64	0.4669	0.47	0.74	0.51	0.71	4.59	0.0064	0.0037	0.0075
2704511	0.66	0.0023	1.23	0.67	0.206	0.55	0.74	0.55	0.74	3.46	0.0008	0.0006	0.0009
2704898	0.66	0.0026	1.37	0.62	0.6786	0.51	0.68	0.48	0.71	4.15	0.0193	0.0013	0.0029
2704935	0.64	0.0094	1.29	0.65	0.3949	0.66	0.65	0.52	0.77	7.15	0.0005	0.0039	0.0085
2705001	0.69	0.0004	1.54	0.67	0.206	0.64	0.7	0.55	0.77	6.2	0.0001	0.0001	0.0003
2706322	0.55	0.0049	1.36	0.66	0.3262	0.55	0.72	0.53	0.74	5.24	0.0006	0.0025	0.005
2706324	0.63	0.0132	1.36	0.66	0.3262	0.64	0.67	0.53	0.76	6.14	0.0005	0.0064	0.0107
2707780	0.66	0.0031	1.38	0.63	0.611	0.57	0.66	0.49	0.73	5.34	0.0092	0.0022	0.0048
2708798	0.67	0.0011	1.36	0.64	0.4669	0.7	0.61	0.51	0.78	7.58	0.0007	0.0012	0.0017
2709489	0.61	0.0382	1.25	0.64	0.5397	0.53	0.7	0.5	0.72	5.65	0.0044	0.0378	0.0499
2710214	0.65	0.0041	1.31	0.62	0.6786	0.45	0.72	0.48	0.69	4.56	0.0535	0.0046	0.0057

2710217	0.71	0.0001	1.4	0.69	0.1164	0.55	0.77	0.58	0.75	4.85	0.0002	0.0002	0.0003
2711689	0.63	0.0173	1.32	0.61	0.7405	0.57	0.63	0.47	0.72	4.1	0.0134	0.0191	0.0379
2712424	0.65	0.0052	1.44	0.64	0.4669	0.68	0.62	0.51	0.77	6.13	0.0013	0.0031	0.0037
2713075	0.64	0.0104	1.46	0.6	0.8429	0.6	0.6	0.46	0.72	6.49	0.0219	0.0063	0.0084
2713262	0.66	0.0024	1.34	0.67	0.206	0.62	0.71	0.55	0.76	4.38	0.0001	0.0037	0.0071
2713269	0.68	0.0005	1.35	0.64	0.4669	0.55	0.7	0.51	0.73	5.43	0.0032	0.0005	0.0009
2714106	0.64	0.007	1.29	0.58	0.914	0.34	0.72	0.41	0.66	4.95	0.4954	0.02	0.0209
2715470	0.63	0.0173	1.41	0.59	0.8822	0.72	0.51	0.46	0.76	5.36	0.0088	0.0119	0.0146
2715717	0.65	0.0038	1.77	0.6	0.7956	0.68	0.56	0.47	0.75	5.55	0.0062	0.0036	0.0045
2720693	0.66	0.0035	1.38	0.64	0.4669	0.47	0.74	0.51	0.71	4.42	0.0093	0.0129	0.0129
2724050	0.67	0.001	1.36	0.66	0.3262	0.57	0.71	0.53	0.74	5.65	0.0004	0.0004	0.0013
2724565	0.67	0.0017	1.35	0.64	0.5397	0.7	0.6	0.5	0.78	8.11	0.0011	0.0004	0.001
2726514	0.65	0.0051	1.34	0.62	0.6786	0.53	0.67	0.48	0.71	4.49	0.0198	0.0088	0.01
2727970	0.64	0.0101	1.48	0.63	0.611	0.64	0.62	0.49	0.75	5.17	0.004	0.0077	0.0084
2730701	0.64	0.0096	1.31	0.6	0.7956	0.45	0.7	0.46	0.69	4.41	0.0935	0.0163	0.0202
2731872	0.67	0.0015	1.49	0.65	0.3949	0.45	0.77	0.53	0.71	4.78	0.0066	0.0033	0.0041
2732403	0.63	0.0115	1.38	0.62	0.6786	0.64	0.61	0.48	0.75	4.77	0.0058	0.0054	0.0135
2735017	0.63	0.0118	1.36	0.63	0.611	0.43	0.74	0.49	0.69	4.91	0.0495	0.0377	0.0262
2736295	0.63	0.0153	1.41	0.64	0.5397	0.53	0.7	0.5	0.72	4.58	0.0078	0.011	0.0193
2738963	0.65	0.0052	1.4	0.64	0.4669	0.62	0.66	0.51	0.75	5.13	0.0033	0.0048	0.0064
2743194	0.68	0.0006	1.3	0.64	0.4669	0.68	0.62	0.51	0.77	6.67	0.0008	0.0001	0.0005
2744632	0.58	0.1112	1.25	0.62	0.6786	0.47	0.71	0.48	0.7	4.28	0.042	0.1095	0.147
2745687	0.65	0.0041	1.32	0.64	0.5397	0.57	0.67	0.5	0.73	5.03	0.0056	0.0086	0.0125
2754300	0.65	0.0045	1.29	0.64	0.4669	0.47	0.74	0.51	0.71	4.77	0.0171	0.0106	0.0088
2757037	0.66	0.003	1.35	0.61	0.7405	0.74	0.54	0.48	0.79	7.13	0.0017	0.005	0.0068
2763813	0.62	0.0282	1.34	0.61	0.7405	0.47	0.7	0.47	0.7	3.84	0.0581	0.0175	0.0303
2766634	0.66	0.0019	1.33	0.65	0.3949	0.7	0.62	0.52	0.78	4.74	0.0006	0.0022	0.0042
2770195	0.63	0.0121	1.29	0.64	0.5397	0.4	0.77	0.5	0.69	3.7	0.0313	0.0114	0.0156
2770473	0.66	0.0025	1.4	0.66	0.3262	0.64	0.67	0.53	0.76	6.63	0.0006	0.002	0.0023
2771759	0.68	0.0006	1.43	0.69	0.1164	0.55	0.77	0.58	0.75	5.36	0.0002	0.0003	0.0004
2773129	0.62	0.0221	1.32	0.59	0.8822	0.64	0.56	0.45	0.73	4.12	0.0343	0.0262	0.0211
2774054	0.64	0.0078	1.38	0.64	0.5397	0.43	0.76	0.5	0.7	4.42	0.037	0.0161	0.0109
2775592	0.6	0.0547	1.23	0.58	0.914	0.6	0.57	0.44	0.71	4.96	0.0661	0.023	0.0372
2775758	0.65	0.0055	1.41	0.61	0.7405	0.72	0.55	0.48	0.78	6.87	0.0025	0.0071	0.0101
2776094	0.64	0.0077	1.38	0.66	0.3262	0.62	0.68	0.53	0.76	4.13	0.0016	0.0434	0.0197
2777492	0.61	0.0327	1.31	0.64	0.5397	0.43	0.76	0.5	0.7	4	0.0178	0.009	0.0225
2779488	0.67	0.0011	1.39	0.67	0.206	0.64	0.7	0.55	0.77	6.72	0.0001	0.0004	0.001
2779639	0.66	0.0029	1.48	0.62	0.6786	0.64	0.61	0.48	0.75	5.71	0.0043	0.0028	0.003
2779995	0.63	0.0149	1.34	0.63	0.611	0.55	0.67	0.49	0.72	5.44	0.0121	0.0076	0.0095
2780545	0.67	0.0011	1.44	0.67	0.206	0.62	0.71	0.55	0.76	4.57	0.0002	0.0012	0.0022
2783475	0.67	0.0016	1.39	0.64	0.4669	0.72	0.6	0.51	0.79	6.7	0.0005	0.0013	0.0015
2789554	0.62	0.0227	1.17	0.61	0.7405	0.49	0.68	0.47	0.7	5.7	0.0366	0.0162	0.0293
2790573	0.63	0.0128	1.32	0.63	0.611	0.74	0.56	0.49	0.79	6.09	0.0012	0.0137	0.0111

2797449	0.65	0.0042	1.33	0.63	0.611	0.53	0.68	0.49	0.72	6.3	0.0131	0.005	0.0068
2801338	0.62	0.02	1.47	0.64	0.5397	0.51	0.71	0.5	0.72	4.65	0.0066	0.0168	0.0265
2801556	0.65	0.0044	1.34	0.6	0.7956	0.68	0.56	0.47	0.75	6.7	0.0063	0.0023	0.0036
2801679	0.66	0.0029	1.33	0.64	0.5397	0.66	0.62	0.5	0.76	6.36	0.002	0.0013	0.0026
2802506	0.69	0.0003	1.33	0.64	0.4669	0.74	0.59	0.51	0.8	4.36	0.0002	0.0003	0.0013
2805739	0.61	0.0356	1.21	0.6	0.7956	0.47	0.68	0.46	0.69	4.4	0.0679	0.0264	0.0409
2806859	0.68	0.0007	1.29	0.67	0.2627	0.64	0.68	0.54	0.77	6.08	0.0003	0.0003	0.0006
2806912	0.64	0.0109	1.34	0.63	0.611	0.57	0.66	0.49	0.73	5.86	0.0079	0.0078	0.012
2807658	0.69	0.0004	1.34	0.67	0.2627	0.57	0.72	0.54	0.75	5.22	0.0003	0.0002	0.0006
2809146	0.61	0.0303	1.43	0.62	0.6786	0.64	0.61	0.48	0.75	5.49	0.0056	0.0171	0.0207
2810487	0.61	0.0477	1.25	0.61	0.7405	0.47	0.7	0.47	0.7	4.2	0.0389	0.0321	0.0581
2812307	0.65	0.0046	1.46	0.64	0.5397	0.53	0.7	0.5	0.72	4.52	0.0133	0.015	0.0115
2812500	0.64	0.0078	1.6	0.64	0.4669	0.53	0.71	0.51	0.73	3.58	0.0058	0.0023	0.0051
2812573	0.64	0.0092	1.28	0.62	0.6786	0.68	0.59	0.48	0.76	7	0.0034	0.0044	0.0073
2817404	0.67	0.0019	1.66	0.67	0.206	0.57	0.73	0.55	0.75	4.65	0.0007	0.0042	0.0046
2817457	0.66	0.0031	1.66	0.64	0.5397	0.57	0.67	0.5	0.73	4.85	0.0067	0.0034	0.0035
2818271	0.63	0.0118	1.25	0.67	0.206	0.64	0.7	0.55	0.77	6.67	0.0001	0.0085	0.017
2818964	0.67	0.0014	1.4	0.63	0.611	0.72	0.57	0.49	0.78	6.77	0.0011	0.0018	0.002
2822274	0.61	0.0315	1.7	0.64	0.5397	0.6	0.66	0.5	0.74	5.01	0.0025	0.0132	0.0191
2823066	0.68	0.001	1.36	0.67	0.2627	0.43	0.8	0.56	0.71	4.03	0.003	0.0041	0.0047
2823854	0.63	0.0135	1.44	0.59	0.8822	0.64	0.56	0.45	0.73	6.26	0.0217	0.0078	0.0118
2824899	0.62	0.0265	1.26	0.63	0.611	0.49	0.71	0.49	0.71	4.63	0.0104	0.0181	0.0374
2828112	0.67	0.0015	1.61	0.66	0.3262	0.72	0.62	0.52	0.8	5.64	0.0001	0.001	0.0014
2828637	0.64	0.0103	1.26	0.63	0.611	0.53	0.68	0.49	0.72	5.51	0.0074	0.0022	0.0082
2828642	0.65	0.0056	1.52	0.62	0.6786	0.57	0.65	0.48	0.73	4.5	0.0113	0.0054	0.0087
2829255	0.65	0.0036	1.34	0.63	0.611	0.66	0.61	0.49	0.76	4.35	0.0048	0.0043	0.0056
2829555	0.57	0.1609	1.24	0.63	0.611	0.49	0.71	0.49	0.71	5.03	0.0191	0.0538	0.0889
2829679	0.65	0.006	1.33	0.64	0.5397	0.55	0.68	0.5	0.73	6.03	0.0078	0.0027	0.0045
2831231	0.64	0.0082	1.36	0.64	0.5397	0.57	0.67	0.5	0.73	6.17	0.0035	0.0071	0.0109
2831557	0.64	0.0076	1.4	0.6	0.7956	0.6	0.61	0.47	0.72	6.57	0.0219	0.0039	0.0047
2836687	0.63	0.0149	1.32	0.57	0.9388	0.66	0.52	0.44	0.73	4.88	0.0462	0.0081	0.0117
2840638	0.64	0.0094	1.31	0.61	0.7405	0.6	0.62	0.47	0.73	4.59	0.0129	0.0058	0.012
2843280	0.61	0.0373	1.33	0.57	0.9388	0.55	0.59	0.43	0.7	6.04	0.0824	0.028	0.0329
2844248	0.62	0.0187	1.52	0.64	0.4669	0.66	0.63	0.51	0.76	6.16	0.0012	0.0078	0.0093
2844250	0.64	0.0079	1.45	0.6	0.7956	0.66	0.57	0.47	0.75	5.75	0.0115	0.0063	0.0075
2848258	0.65	0.0039	1.35	0.6	0.8429	0.47	0.67	0.45	0.69	4.95	0.0619	0.003	0.0062
2848472	0.62	0.0278	1.67	0.64	0.5397	0.57	0.67	0.5	0.73	6.16	0.003	0.0097	0.014
2851973	0.66	0.0027	1.32	0.64	0.4669	0.62	0.66	0.51	0.75	4.77	0.0017	0.0024	0.0039
2854808	0.65	0.0036	1.65	0.64	0.5397	0.68	0.61	0.5	0.77	5.98	0.0013	0.0017	0.0029
2854809	0.67	0.0019	1.29	0.66	0.3262	0.66	0.66	0.53	0.77	8.1	0.0002	0.0007	0.0016
2855289	0.65	0.0043	1.55	0.64	0.4669	0.62	0.66	0.51	0.75	5.36	0.0037	0.0058	0.0065
2855291	0.66	0.0024	1.49	0.66	0.3262	0.6	0.7	0.53	0.75	4.63	0.0016	0.0023	0.0029
2855292	0.64	0.0083	1.33	0.67	0.2627	0.64	0.68	0.54	0.77	5.55	0.0004	0.0029	0.0047

2857172	0.65	0.0054	1.58	0.64	0.4669	0.64	0.65	0.51	0.76	4.95	0.001	0.0029	0.0057
2862162	0.63	0.0166	1.26	0.64	0.4669	0.62	0.66	0.51	0.75	4.52	0.0014	0.0174	0.0248
2862377	0.64	0.0101	1.32	0.66	0.3262	0.7	0.63	0.52	0.79	7.96	0.0003	0.0059	0.007
2865063	0.64	0.0065	1.48	0.64	0.5397	0.7	0.6	0.5	0.78	6.19	0.001	0.0039	0.0059
2868141	0.64	0.0107	1.32	0.64	0.4669	0.62	0.66	0.51	0.75	5.73	0.0014	0.0056	0.0098
2877518	0.62	0.0245	1.31	0.64	0.5397	0.57	0.67	0.5	0.73	5.76	0.0045	0.0137	0.0243
2878261	0.65	0.004	1.3	0.62	0.6786	0.68	0.59	0.48	0.76	5.74	0.0012	0.0014	0.004
2882121	0.65	0.0039	1.36	0.64	0.5397	0.66	0.62	0.5	0.76	7.59	0.0011	0.0017	0.0038
2888344	0.61	0.0351	1.26	0.58	0.914	0.47	0.65	0.43	0.68	4.55	0.2339	0.0421	0.0391
2893822	0.61	0.0451	1.22	0.6	0.8429	0.36	0.73	0.44	0.67	5.07	0.175	0.0408	0.0892
2893942	0.63	0.0173	1.37	0.63	0.611	0.64	0.62	0.49	0.75	6.32	0.0041	0.017	0.0172
2896978	0.66	0.0035	1.37	0.64	0.5397	0.49	0.72	0.5	0.71	4.84	0.0241	0.0057	0.0038
2898531	0.63	0.018	1.32	0.53	0.9955	0.6	0.49	0.4	0.68	5.35	0.2482	0.009	0.0177
2902010	0.65	0.0062	1.28	0.65	0.3949	0.6	0.68	0.52	0.75	6.35	0.0015	0.0032	0.0052
2902011	0.63	0.018	1.49	0.63	0.611	0.68	0.6	0.49	0.77	5.59	0.0034	0.0066	0.0099
2905137	0.67	0.0013	1.39	0.69	0.1164	0.55	0.77	0.58	0.75	4.9	0.0001	0.0001	0.0007
2906968	0.64	0.0077	1.4	0.64	0.5397	0.66	0.62	0.5	0.76	5.69	0.0025	0.0046	0.0059
2908048	0.61	0.0378	1.33	0.57	0.9577	0.62	0.54	0.43	0.71	4.61	0.0579	0.0322	0.0492
2909471	0.63	0.0121	1.41	0.61	0.7405	0.6	0.62	0.47	0.73	5	0.0179	0.0165	0.0182
2910489	0.65	0.0062	1.26	0.6	0.8429	0.7	0.54	0.46	0.76	5.05	0.0087	0.0081	0.0108
2914002	0.65	0.0063	1.33	0.64	0.4669	0.49	0.73	0.51	0.71	4.56	0.0061	0.0033	0.005
2914107	0.71	0.0001	1.28	0.68	0.1571	0.74	0.65	0.55	0.82	4.16	0	0.0011	0.0018
2916383	0.62	0.0221	1.24	0.58	0.914	0.64	0.55	0.45	0.73	5.73	0.0307	0.018	0.0257
2916976	0.68	0.0007	1.44	0.68	0.1571	0.57	0.74	0.56	0.75	4.23	0	0.0008	0.0013
2918543	0.64	0.0075	1.33	0.64	0.5397	0.66	0.62	0.5	0.76	4.64	0.002	0.0096	0.0077
2918547	0.66	0.0024	1.46	0.63	0.611	0.62	0.63	0.49	0.74	6.45	0.0042	0.002	0.0028
2922232	0.63	0.0137	1.27	0.62	0.6786	0.45	0.72	0.48	0.69	5.15	0.0405	0.024	0.0242
2922235	0.66	0.003	1.4	0.64	0.4669	0.51	0.72	0.51	0.72	4.63	0.008	0.0105	0.0083
2926222	0.67	0.0012	1.46	0.65	0.3949	0.7	0.62	0.52	0.78	7.58	0.0005	0.001	0.0012
2929946	0.65	0.0048	1.29	0.64	0.4669	0.53	0.71	0.51	0.73	5.67	0.003	0.0044	0.0065
2930652	0.65	0.0052	1.44	0.63	0.611	0.62	0.63	0.49	0.74	6.5	0.005	0.0045	0.0055
2932399	0.6	0.0612	1.24	0.62	0.6786	0.51	0.68	0.48	0.71	4.8	0.0367	0.0637	0.0539
2932428	0.65	0.0059	1.52	0.65	0.3949	0.53	0.72	0.52	0.73	4.44	0.0035	0.0056	0.007
2933660	0.66	0.002	1.27	0.67	0.206	0.7	0.66	0.54	0.79	5.57	0.0001	0.002	0.004
2936963	0.64	0.0106	1.37	0.6	0.7956	0.4	0.72	0.45	0.68	3.97	0.1336	0.0447	0.057
2940827	0.65	0.0039	1.41	0.63	0.611	0.6	0.65	0.49	0.74	5.39	0.0044	0.0069	0.0076
2942512	0.62	0.0268	1.23	0.6	0.8429	0.49	0.66	0.45	0.69	5.96	0.056	0.0433	0.045
2944070	0.65	0.0059	1.47	0.63	0.611	0.6	0.65	0.49	0.74	5.68	0.0043	0.006	0.0075
2944963	0.68	0.0006	1.3	0.65	0.3949	0.62	0.67	0.52	0.75	7.11	0.0013	0.0004	0.0007
2946479	0.64	0.0071	1.4	0.64	0.4669	0.53	0.71	0.51	0.73	4.29	0.0076	0.0283	0.0289
2947592	0.66	0.0024	1.46	0.64	0.4669	0.6	0.67	0.51	0.74	4.7	0.0015	0.0005	0.0018
2948592	0.66	0.0031	1.33	0.6	0.8429	0.6	0.6	0.46	0.72	5.71	0.0251	0.0031	0.0039
2948596	0.65	0.0036	1.32	0.61	0.7405	0.68	0.57	0.48	0.76	4.3	0.0067	0.0052	0.0061

2949053	0.63	0.0173	1.41	0.63	0.611	0.6	0.65	0.49	0.74	4.92	0.0032	0.0108	0.0184
2949061	0.58	0.1101	1.27	0.6	0.8429	0.49	0.66	0.45	0.69	4.84	0.0833	0.0877	0.1248
2951060	0.63	0.0123	1.28	0.61	0.7405	0.7	0.56	0.48	0.77	6.58	0.0039	0.0073	0.0069
2956077	0.65	0.0046	1.3	0.64	0.4669	0.49	0.73	0.51	0.71	5.43	0.0069	0.0034	0.0085
2958402	0.65	0.0056	1.32	0.66	0.3262	0.55	0.72	0.53	0.74	5.07	0.0007	0.0143	0.0251
2961302	0.63	0.0149	1.4	0.62	0.6786	0.72	0.56	0.49	0.78	5.63	0.0018	0.0082	0.0107
2966293	0.63	0.0157	1.37	0.64	0.5397	0.55	0.68	0.5	0.73	4.28	0.0062	0.0149	0.0183
2966378	0.62	0.021	1.31	0.63	0.611	0.66	0.61	0.49	0.76	5.86	0.0035	0.0172	0.0181
2967164	0.63	0.0115	1.26	0.63	0.611	0.57	0.66	0.49	0.73	3.89	0.0053	0.0101	0.022
2967323	0.62	0.0258	1.43	0.64	0.4669	0.62	0.66	0.51	0.75	4.4	0.0038	0.0082	0.0127
2968257	0.61	0.0401	1.23	0.6	0.8429	0.57	0.61	0.46	0.71	5.01	0.0256	0.0424	0.0552
2968653	0.64	0.0103	1.37	0.63	0.611	0.57	0.66	0.49	0.73	5.14	0.0066	0.0094	0.0116
2974195	0.64	0.0094	1.25	0.6	0.7956	0.77	0.51	0.47	0.79	6.75	0.002	0.0091	0.0118
2974332	0.65	0.0041	1.67	0.64	0.5397	0.66	0.62	0.5	0.76	4.95	0.0036	0.0065	0.0052
2975686	0.67	0.0019	1.34	0.66	0.3262	0.68	0.65	0.52	0.78	5.93	0.0006	0.0017	0.0014
2975709	0.63	0.0166	1.27	0.62	0.6786	0.4	0.74	0.48	0.69	5.29	0.0671	0.0242	0.0287
2976368	0.63	0.0162	1.35	0.64	0.5397	0.47	0.73	0.5	0.71	5.49	0.012	0.0214	0.0372
2977521	0.64	0.0068	1.31	0.58	0.914	0.74	0.49	0.45	0.77	6.32	0.0093	0.0064	0.0074
2981918	0.63	0.0116	1.39	0.62	0.6786	0.51	0.68	0.48	0.71	5.26	0.0269	0.0118	0.0142
2982323	0.64	0.0098	1.39	0.63	0.611	0.68	0.6	0.49	0.77	6.6	0.0014	0.0067	0.008
2982385	0.68	0.001	1.48	0.63	0.611	0.6	0.65	0.49	0.74	4.49	0.0141	0.0011	0.0013
2984576	0.61	0.0303	1.39	0.61	0.7405	0.53	0.66	0.47	0.71	4.1	0.0315	0.0123	0.0164
2985813	0.64	0.0071	1.51	0.64	0.4669	0.55	0.7	0.51	0.73	4.14	0.0044	0.0268	0.0347
2985965	0.68	0.0006	1.28	0.66	0.3262	0.6	0.7	0.53	0.75	6.32	0.0007	0.0006	0.0007
2988895	0.66	0.0028	1.26	0.66	0.3262	0.68	0.65	0.52	0.78	4.25	0.0004	0.0048	0.0074
2988896	0.65	0.0039	1.31	0.58	0.914	0.74	0.49	0.45	0.77	7.44	0.0123	0.0049	0.005
2989720	0.66	0.0031	1.31	0.61	0.7405	0.47	0.7	0.47	0.7	5.09	0.0541	0.0021	0.0029
2991248	0.61	0.0307	1.26	0.62	0.6786	0.64	0.61	0.48	0.75	6.93	0.0056	0.0169	0.0238
2991263	0.68	0.0007	1.32	0.66	0.3262	0.68	0.65	0.52	0.78	6.56	0.0002	0.001	0.0017
2991264	0.65	0.0041	1.52	0.67	0.206	0.64	0.7	0.55	0.77	5.46	0.0001	0.0029	0.0046
2993622	0.64	0.007	1.32	0.6	0.8429	0.66	0.56	0.46	0.74	4.94	0.0201	0.0064	0.008
2993644	0.65	0.0054	1.32	0.6	0.8429	0.68	0.55	0.46	0.75	4.71	0.009	0.0037	0.0064
2993659	0.68	0.0007	1.48	0.67	0.2627	0.64	0.68	0.54	0.77	5.68	0.0004	0.0006	0.0009
2994371	0.62	0.0255	1.24	0.64	0.5397	0.49	0.72	0.5	0.71	3.95	0.0273	0.0382	0.0314
2995598	0.62	0.0242	1.25	0.6	0.8429	0.51	0.65	0.45	0.7	5.45	0.1016	0.0497	0.0309
2997143	0.67	0.0018	1.39	0.63	0.611	0.51	0.7	0.49	0.71	4.86	0.0105	0.0035	0.0077
3002667	0.64	0.0082	1.33	0.66	0.3262	0.64	0.67	0.53	0.76	6.08	0.0009	0.0073	0.0119
3003180	0.62	0.023	1.41	0.61	0.7405	0.51	0.67	0.47	0.71	4.09	0.0402	0.0098	0.013
3004652	0.68	0.0007	1.36	0.6	0.8429	0.38	0.72	0.44	0.67	5.1	0.2088	0.0054	0.0055
3011652	0.62	0.0213	1.28	0.65	0.3949	0.62	0.67	0.52	0.75	6.93	0.0014	0.0109	0.0145
3011846	0.62	0.0278	1.34	0.63	0.611	0.49	0.71	0.49	0.71	4.56	0.025	0.0101	0.0183
3012405	0.67	0.0011	1.25	0.67	0.206	0.66	0.68	0.54	0.78	6.88	0.0001	0.0008	0.0014
3012428	0.69	0.0003	1.24	0.62	0.6786	0.47	0.71	0.48	0.7	5.68	0.0424	0.0004	0.0015

3012438	0.61	0.0307	1.3	0.59	0.8822	0.45	0.67	0.44	0.68	4.06	0.2198	0.0154	0.02
3012452	0.64	0.0078	1.4	0.64	0.5397	0.51	0.71	0.5	0.72	4.94	0.0076	0.0029	0.0066
3012453	0.66	0.0024	1.33	0.67	0.206	0.62	0.71	0.55	0.76	6.58	0.0001	0.001	0.0025
3013190	0.63	0.0162	1.22	0.64	0.5397	0.47	0.73	0.5	0.71	4.93	0.0182	0.0196	0.0231
3013468	0.67	0.0019	1.46	0.64	0.5397	0.62	0.65	0.5	0.75	5.44	0.0023	0.0013	0.0022
3013685	0.61	0.0351	1.29	0.62	0.6786	0.51	0.68	0.48	0.71	5.2	0.0298	0.032	0.0298
3014422	0.6	0.0573	1.12	0.64	0.4669	0.43	0.77	0.51	0.7	4.18	0.0118	0.018	0.0587
3015985	0.64	0.0072	1.29	0.64	0.4669	0.64	0.65	0.51	0.76	7.05	0.001	0.0053	0.0069
3017629	0.63	0.0153	1.36	0.61	0.7405	0.36	0.76	0.46	0.67	3.67	0.1401	0.0342	0.0398
3017826	0.63	0.0159	1.43	0.62	0.6786	0.62	0.62	0.48	0.74	5.59	0.0059	0.0127	0.0135
3021760	0.69	0.0003	1.4	0.71	0.0394	0.62	0.77	0.6	0.78	4.95	0	0.0001	0.0005
3022682	0.65	0.0057	1.29	0.65	0.3949	0.66	0.65	0.52	0.77	6.44	0.0005	0.0043	0.0048
3027555	0.66	0.0025	1.57	0.62	0.6786	0.74	0.55	0.49	0.79	6.4	0.0011	0.0016	0.0021
3027926	0.65	0.0039	1.32	0.64	0.5397	0.57	0.67	0.5	0.73	5.95	0.0062	0.0033	0.005
3027936	0.64	0.0104	1.41	0.6	0.7956	0.74	0.52	0.47	0.78	6.19	0.0039	0.0071	0.0078
3037391	0.67	0.0018	1.41	0.63	0.611	0.49	0.71	0.49	0.71	4	0.0191	0.0109	0.011
3037406	0.64	0.0085	1.34	0.63	0.611	0.72	0.57	0.49	0.78	7.3	0.0014	0.0052	0.0096
3037950	0.63	0.0145	1.35	0.63	0.611	0.47	0.72	0.49	0.7	4.07	0.018	0.0129	0.0227
3039980	0.65	0.0062	1.41	0.67	0.2627	0.64	0.68	0.54	0.77	6.48	0.0001	0.0022	0.0055
3039983	0.62	0.0221	1.49	0.6	0.7956	0.62	0.6	0.47	0.73	5.59	0.0126	0.0115	0.0157
3040116	0.64	0.0088	1.49	0.66	0.3262	0.51	0.74	0.53	0.73	4.93	0.0022	0.0076	0.012
3041262	0.67	0.0011	1.53	0.64	0.5397	0.62	0.65	0.5	0.75	6.49	0.0024	0.0007	0.0012
3042004	0.64	0.007	1.41	0.67	0.2627	0.68	0.66	0.53	0.78	5.3	0.0001	0.0062	0.009
3042424	0.66	0.0026	1.71	0.66	0.3262	0.66	0.66	0.53	0.77	5.87	0.0005	0.0017	0.0018
3042426	0.65	0.0048	1.39	0.66	0.3262	0.7	0.63	0.52	0.79	5.98	0.0003	0.0026	0.0037
3042429	0.62	0.0213	1.27	0.61	0.7405	0.51	0.67	0.47	0.71	4.72	0.0405	0.0366	0.0432
3042430	0.65	0.004	1.65	0.63	0.611	0.68	0.6	0.49	0.77	5.36	0.002	0.0026	0.0026
3042437	0.71	0.0001	1.4	0.68	0.1571	0.68	0.68	0.55	0.79	6.83	0.0001	0.0001	0.0001
3042453	0.64	0.0085	1.35	0.64	0.4669	0.53	0.71	0.51	0.73	3.9	0.0064	0.0108	0.0159
3048780	0.65	0.0052	1.51	0.6	0.7956	0.6	0.61	0.47	0.72	4.61	0.0194	0.0044	0.0067
3048870	0.66	0.0022	1.36	0.65	0.3949	0.55	0.71	0.52	0.73	5.03	0.0027	0.0027	0.0028
3053384	0.64	0.009	1.44	0.64	0.5397	0.47	0.73	0.5	0.71	3.82	0.0193	0.0009	0.0025
3056395	0.65	0.0044	1.38	0.64	0.4669	0.66	0.63	0.51	0.76	7.19	0.0008	0.0028	0.0047
3060052	0.68	0.0008	1.21	0.64	0.5397	0.47	0.73	0.5	0.71	3.77	0.0123	0.0019	0.0037
3061054	0.68	0.0009	1.28	0.66	0.3262	0.51	0.74	0.53	0.73	4.74	0.0019	0.0014	0.0015
3061144	0.62	0.0242	1.42	0.65	0.3949	0.55	0.71	0.52	0.73	4.87	0.0031	0.0241	0.0325
3061758	0.66	0.0032	1.34	0.64	0.4669	0.6	0.67	0.51	0.74	5.24	0.0014	0.0081	0.0219
3062023	0.68	0.0009	1.29	0.68	0.1571	0.57	0.74	0.56	0.75	5.88	0.0002	0.0002	0.0007
3064354	0.65	0.0055	1.32	0.62	0.6786	0.66	0.6	0.48	0.75	5.87	0.0046	0.0043	0.0049
3075645	0.61	0.0461	1.39	0.6	0.7956	0.64	0.59	0.47	0.74	5.92	0.0083	0.0323	0.043
3076355	0.71	0.0001	1.56	0.65	0.3949	0.57	0.7	0.52	0.74	5.9	0.0017	0.0001	0.0001
3076393	0.61	0.0477	1.25	0.64	0.4669	0.51	0.72	0.51	0.72	4.07	0.0035	0.006	0.024
3076490	0.66	0.0031	1.31	0.65	0.3949	0.64	0.66	0.52	0.76	6.63	0.0011	0.0029	0.0027

3081625	0.62	0.0197	1.21	0.61	0.7405	0.49	0.68	0.47	0.7	5.04	0.0337	0.0079	0.0115
3087828	0.68	0.0008	1.42	0.65	0.3949	0.6	0.68	0.52	0.75	5.2	0.0012	0.0004	0.0009
3087930	0.65	0.0039	1.47	0.66	0.3262	0.6	0.7	0.53	0.75	5.85	0.0015	0.005	0.0046
3088570	0.64	0.0079	1.41	0.62	0.6786	0.66	0.6	0.48	0.75	5.46	0.0049	0.0097	0.0089
3092505	0.63	0.0112	1.44	0.6	0.8429	0.66	0.56	0.46	0.74	5.61	0.0182	0.0088	0.0101
3094309	0.66	0.003	1.7	0.6	0.8429	0.57	0.61	0.46	0.71	4.94	0.0336	0.002	0.0029
3096162	0.66	0.0028	1.41	0.69	0.1164	0.68	0.7	0.56	0.79	4.95	0.0001	0.0029	0.003
3096409	0.68	0.0009	1.55	0.7	0.0837	0.53	0.79	0.6	0.75	4.94	0.0001	0.0008	0.0016
3096979	0.68	0.0008	1.38	0.67	0.206	0.64	0.7	0.55	0.77	5.5	0.0001	0.0008	0.0015
3099780	0.65	0.0046	1.44	0.63	0.611	0.64	0.62	0.49	0.75	5.78	0.0064	0.0041	0.0034
3100230	0.65	0.0048	1.31	0.64	0.5397	0.62	0.65	0.5	0.75	5.87	0.0036	0.0034	0.0049
3107638	0.65	0.0049	1.32	0.64	0.5397	0.45	0.74	0.5	0.7	4.51	0.005	0.0014	0.0068
3108472	0.69	0.0003	1.35	0.67	0.2627	0.66	0.67	0.53	0.77	6.54	0.0002	0.0003	0.0007
3108501	0.69	0.0002	1.35	0.66	0.3262	0.6	0.7	0.53	0.75	4.16	0.0017	0.0005	0.0009
3108938	0.62	0.0216	1.28	0.63	0.611	0.62	0.63	0.49	0.74	4.56	0.003	0.0125	0.0266
3111090	0.64	0.009	1.28	0.66	0.3262	0.55	0.72	0.53	0.74	5.59	0.0012	0.0054	0.0113
3111116	0.6	0.0489	1.42	0.63	0.611	0.62	0.63	0.49	0.74	5.08	0.003	0.0154	0.0273
3112517	0.68	0.0008	1.42	0.64	0.4669	0.6	0.67	0.51	0.74	6.38	0.0016	0.0003	0.0007
3114370	0.62	0.0194	1.3	0.64	0.4669	0.51	0.72	0.51	0.72	4.48	0.0061	0.0088	0.0157
3114664	0.63	0.0162	1.29	0.62	0.6786	0.53	0.67	0.48	0.71	5.21	0.0142	0.0089	0.0132
3124536	0.65	0.0044	1.28	0.64	0.4669	0.62	0.66	0.51	0.75	6.5	0.0033	0.0049	0.0055
3126094	0.66	0.0024	1.44	0.63	0.611	0.77	0.55	0.49	0.8	7.1	0.0008	0.0019	0.0019
3128680	0.63	0.0145	1.32	0.58	0.914	0.53	0.61	0.44	0.69	5.38	0.1137	0.019	0.0232
3129955	0.66	0.0028	1.36	0.64	0.4669	0.62	0.66	0.51	0.75	5.98	0.0015	0.0023	0.0044
3131973	0.67	0.001	1.36	0.69	0.1164	0.6	0.74	0.57	0.76	6.31	0.0001	0.0009	0.0014
3132336	0.64	0.0088	1.48	0.66	0.3262	0.57	0.71	0.53	0.74	4.37	0.001	0.0078	0.011
3133528	0.71	0.0001	1.48	0.69	0.1164	0.55	0.77	0.58	0.75	4.42	0.0001	0	0.0002
3134184	0.58	0.1565	1.14	0.6	0.7956	0.3	0.78	0.44	0.66	3.84	0.2446	0.0721	0.1183
3136352	0.65	0.0046	1.3	0.6	0.8429	0.62	0.59	0.46	0.73	6.73	0.0216	0.0027	0.0052
3137586	0.68	0.0006	1.39	0.62	0.6786	0.68	0.59	0.48	0.76	6.25	0.0032	0.0007	0.001
3138886	0.63	0.0135	1.31	0.6	0.8429	0.57	0.61	0.46	0.71	5.27	0.0363	0.013	0.0198
3138980	0.64	0.0076	1.36	0.65	0.3949	0.64	0.66	0.52	0.76	5.71	0.0007	0.0066	0.0076
3139053	0.66	0.0026	1.34	0.67	0.2627	0.55	0.73	0.54	0.74	5.25	0.0009	0.0048	0.0066
3139926	0.66	0.0021	1.35	0.65	0.3949	0.53	0.72	0.52	0.73	5.76	0.0026	0.0026	0.0041
3141863	0.66	0.0019	1.69	0.66	0.3262	0.62	0.68	0.53	0.76	3.82	0.0005	0.002	0.003
3145023	0.52	0.02	1.34	0.64	0.5397	0.53	0.7	0.5	0.72	5.2	0.0102	0.014	0.0172
3145956	0.66	0.002	1.33	0.64	0.4669	0.72	0.6	0.51	0.79	8.36	0.0006	0.0039	0.0057
3145966	0.65	0.0046	1.25	0.64	0.4669	0.64	0.65	0.51	0.76	5.71	0.0012	0.0033	0.006
3146538	0.65	0.006	1.33	0.62	0.6786	0.49	0.7	0.48	0.7	3.95	0.0239	0.0116	0.0213
3146566	0.64	0.0075	1.48	0.69	0.1164	0.57	0.76	0.57	0.76	5.22	0.0001	0.0037	0.0074
3146788	0.62	0.0194	1.34	0.61	0.7405	0.64	0.6	0.48	0.74	7.33	0.0099	0.0095	0.0151
3146799	0.67	0.0014	1.3	0.64	0.5397	0.72	0.59	0.5	0.79	8.32	0.0009	0.0011	0.0023
3147328	0.63	0.0121	1.34	0.62	0.6786	0.62	0.62	0.48	0.74	4.93	0.0058	0.0062	0.0144

3148628	0.63	0.012	1.53	0.66	0.3262	0.51	0.74	0.53	0.73	4.22	0.0014	0.0064	0.0118
3149768	0.64	0.0092	1.46	0.65	0.3949	0.64	0.66	0.52	0.76	6.19	0.0008	0.0049	0.0065
3149773	0.68	0.0009	1.45	0.65	0.3949	0.64	0.66	0.52	0.76	4.72	0.001	0.0004	0.0011
3149864	0.67	0.0016	1.53	0.67	0.2627	0.72	0.63	0.53	0.8	5.14	0.0001	0.0011	0.0019
3151480	0.66	0.0031	1.84	0.65	0.3949	0.6	0.68	0.52	0.75	5.11	0.0013	0.0008	0.0016
3152560	0.61	0.0378	1.31	0.64	0.4669	0.55	0.7	0.51	0.73	4.37	0.0049	0.0181	0.0211
3153532	0.62	0.0285	1.32	0.64	0.5397	0.55	0.68	0.5	0.73	5.02	0.0088	0.0236	0.0297
3157388	0.64	0.0067	1.49	0.61	0.7405	0.66	0.59	0.48	0.75	6.08	0.007	0.0058	0.0066
3157461	0.64	0.01	1.61	0.6	0.7956	0.64	0.59	0.47	0.74	5.37	0.0123	0.0074	0.01
3157723	0.64	0.0084	1.4	0.64	0.5397	0.66	0.62	0.5	0.76	5.9	0.0017	0.0043	0.0068
3157847	0.66	0.0029	1.39	0.63	0.611	0.53	0.68	0.49	0.72	5.48	0.0188	0.0036	0.0035
3164299	0.64	0.0066	1.31	0.65	0.3949	0.43	0.78	0.53	0.7	5.08	0.0065	0.0123	0.0189
3165138	0.64	0.0068	1.44	0.6	0.8429	0.66	0.56	0.46	0.74	3.75	0.0136	0.0063	0.0097
3165799	0.69	0.0005	1.48	0.66	0.3262	0.6	0.7	0.53	0.75	5.16	0.0009	0.0005	0.0007
3166029	0.65	0.0052	0.81	0.4	1	0.4	0.39	0.28	0.53	4.13	0.0174	0.0086	0.01
3166735	0.66	0.0032	1.54	0.63	0.611	0.64	0.62	0.49	0.75	5.57	0.0039	0.0053	0.0066
3167990	0.69	0.0004	1.58	0.67	0.206	0.55	0.74	0.55	0.74	6.17	0.0007	0.0004	0.0006
3168127	0.6	0.0698	1.27	0.64	0.4669	0.49	0.73	0.51	0.71	3.79	0.0102	0.0707	0.0664
3169011	0.69	0.0004	0.83	0.41	1	0.23	0.51	0.22	0.54	3.15	0.0077	0.0004	0.0006
3174268	0.7	0.0002	1.28	0.67	0.2627	0.51	0.76	0.55	0.73	5.23	0.0007	0.0002	0.0007
3174441	0.65	0.0036	1.4	0.64	0.4669	0.57	0.68	0.51	0.74	5.29	0.0035	0.007	0.0081
3175632	0.66	0.0021	1.48	0.61	0.7405	0.7	0.56	0.48	0.77	4.82	0.0038	0.0021	0.0034
3175657	0.61	0.0331	1.17	0.6	0.7956	0.49	0.67	0.46	0.7	5.56	0.0853	0.0589	0.0601
3178635	0.66	0.0034	1.52	0.64	0.4669	0.57	0.68	0.51	0.74	4.07	0.0034	0.0076	0.011
3183178	0.62	0.0205	1.52	0.61	0.7405	0.53	0.66	0.47	0.71	4.5	0.0269	0.0077	0.0146
3190449	0.61	0.0369	1.38	0.6	0.8429	0.57	0.61	0.46	0.71	6.01	0.0237	0.0196	0.0375
3192674	0.62	0.0202	1.27	0.6	0.7956	0.4	0.72	0.45	0.68	5.28	0.0966	0.0252	0.039
3197644	0.64	0.0098	1.48	0.58	0.914	0.64	0.55	0.45	0.73	5.54	0.0283	0.0057	0.0086
3199457	0.65	0.0057	1.49	0.65	0.3949	0.6	0.68	0.52	0.75	4.81	0.0031	0.0032	0.004
3199485	0.63	0.0126	1.19	0.64	0.5397	0.43	0.76	0.5	0.7	4.52	0.0271	0.0073	0.0117
3200638	0.66	0.0032	1.68	0.64	0.4669	0.62	0.66	0.51	0.75	4.31	0.0008	0.0014	0.0031
3200711	0.62	0.0208	1.25	0.63	0.611	0.53	0.68	0.49	0.72	5.61	0.0125	0.0213	0.0227
3200718	0.66	0.0026	1.25	0.62	0.6786	0.62	0.62	0.48	0.74	6.15	0.0095	0.0019	0.0035
3200725	0.66	0.002	1.34	0.62	0.6786	0.68	0.59	0.48	0.76	6.37	0.0035	0.0013	0.0023
3203822	0.66	0.0032	1.31	0.61	0.7405	0.66	0.59	0.48	0.75	4.83	0.0072	0.0045	0.0063
3205039	0.63	0.0112	1.23	0.64	0.4669	0.6	0.67	0.51	0.74	5.79	0.0019	0.0132	0.0184
3205424	0.64	0.0064	1.38	0.65	0.3949	0.57	0.7	0.52	0.74	4.05	0.003	0.0104	0.009
3212146	0.66	0.0026	1.55	0.68	0.1571	0.64	0.71	0.56	0.77	5.88	0.0001	0.0008	0.0015
3212163	0.61	0.0315	1.4	0.63	0.611	0.6	0.65	0.49	0.74	4.68	0.0069	0.0117	0.0215
3214671	0.67	0.0016	1.33	0.64	0.5397	0.68	0.61	0.5	0.77	4.47	0.0021	0.0019	0.004
3214699	0.64	0.0076	1.29	0.67	0.2627	0.55	0.73	0.54	0.74	4.43	0.0007	0.0142	0.0278
3219683	0.64	0.008	1.34	0.61	0.7405	0.57	0.63	0.47	0.72	4.71	0.0234	0.0105	0.0178
3219711	0.66	0.0021	1.54	0.65	0.3949	0.51	0.73	0.52	0.72	3.71	0.0027	0.0011	0.004

3219891	0.67	0.0012	1.74	0.62	0.6786	0.6	0.63	0.48	0.73	5.21	0.0084	0.0012	0.0026
3220159	0.65	0.0062	1.42	0.62	0.6786	0.68	0.59	0.48	0.76	7.05	0.0028	0.006	0.0071
3222054	0.66	0.0027	1.42	0.67	0.206	0.51	0.77	0.56	0.73	5.59	0.0009	0.0016	0.0026
3222984	0.64	0.0075	1.3	0.61	0.7405	0.43	0.72	0.47	0.69	4.5	0.0689	0.0069	0.0103
3223876	0.65	0.0043	1.26	0.64	0.5397	0.57	0.67	0.5	0.73	5	0.0045	0.0042	0.0071
3225580	0.63	0.0128	1.26	0.61	0.7405	0.36	0.76	0.46	0.67	3.76	0.2566	0.0745	0.0409
3226470	0.63	0.0153	1.29	0.64	0.4669	0.57	0.68	0.51	0.74	3.35	0.0021	0.0092	0.0247
3227646	0.64	0.0097	1.4	0.62	0.6786	0.55	0.66	0.48	0.72	6.22	0.0143	0.0083	0.009
3233387	0.66	0.0022	1.67	0.66	0.3262	0.66	0.66	0.53	0.77	5.74	0.0004	0.0016	0.0014
3234175	0.63	0.0141	1.34	0.64	0.5397	0.7	0.6	0.5	0.78	6.78	0.0009	0.0075	0.0112
3235500	0.65	0.0052	1.32	0.64	0.5397	0.6	0.66	0.5	0.74	4.55	0.0052	0.0067	0.0072
3237000	0.63	0.0155	1.42	0.61	0.7405	0.68	0.57	0.48	0.76	6.47	0.0066	0.013	0.0135
3237001	0.66	0.0032	1.37	0.62	0.6786	0.7	0.57	0.49	0.77	7.62	0.0021	0.003	0.0041
3239927	0.6	0.05	1.16	0.59	0.8822	0.6	0.59	0.45	0.72	4.55	0.0439	0.0275	0.0453
3239982	0.64	0.0064	1.35	0.66	0.3262	0.6	0.7	0.53	0.75	5.78	0.0005	0.0045	0.0072
3240135	0.65	0.0041	1.38	0.64	0.5397	0.49	0.72	0.5	0.71	4.11	0.0108	0.0053	0.0075
3240409	0.7	0.0002	1.31	0.71	0.0583	0.68	0.72	0.58	0.8	7.67	0	0.0001	0.0002
3240425	0.67	0.0015	1.45	0.61	0.7405	0.7	0.56	0.48	0.77	6.55	0.0031	0.0028	0.0037
3241499	0.65	0.0063	1.46	0.64	0.5397	0.53	0.7	0.5	0.72	4.32	0.0036	0.004	0.0086
3241506	0.67	0.0017	1.32	0.6	0.7956	0.66	0.57	0.47	0.75	4.59	0.0085	0.0023	0.0038
3243292	0.65	0.004	1.46	0.67	0.2627	0.6	0.71	0.54	0.75	5.81	0.0003	0.0018	0.0029
3250201	0.63	0.012	1.62	0.62	0.6786	0.57	0.65	0.48	0.73	4.64	0.0073	0.0066	0.0083
3251409	0.68	0.0008	1.39	0.67	0.206	0.53	0.76	0.56	0.74	5.94	0.0003	0.0002	0.0011
3252608	0.63	0.0173	1.26	0.64	0.5397	0.55	0.68	0.5	0.73	4.94	0.0057	0.0122	0.0165
3253445	0.67	0.0016	1.32	0.64	0.5397	0.77	0.56	0.5	0.81	6.69	0.0007	0.0013	0.0022
3253863	0.65	0.0059	1.41	0.64	0.4669	0.55	0.7	0.51	0.73	5.07	0.0071	0.0015	0.0026
3255269	0.65	0.0037	1.35	0.67	0.2627	0.6	0.71	0.54	0.75	6.58	0.0005	0.0015	0.0025
3257404	0.64	0.0104	1.47	0.61	0.7405	0.47	0.7	0.47	0.7	4.78	0.0455	0.0629	0.0592
3258021	0.67	0.0011	1.5	0.65	0.3949	0.6	0.68	0.52	0.75	5.61	0.0019	0.0015	0.0017
3259678	0.61	0.0378	1.34	0.61	0.7405	0.45	0.71	0.47	0.69	5.5	0.0718	0.023	0.0354
3261550	0.58	0.1179	1.38	0.63	0.611	0.51	0.7	0.49	0.71	4.45	0.0181	0.1173	0.1286
3262470	0.63	0.0166	1.23	0.6	0.8429	0.55	0.62	0.46	0.71	5.11	0.0448	0.0149	0.0211
3263804	0.67	0.0017	1.25	0.64	0.4669	0.57	0.68	0.51	0.74	5.79	0.001	0.0013	0.0029
3264697	0.66	0.0033	1.37	0.67	0.2627	0.53	0.74	0.54	0.73	5.83	0.0009	0.0031	0.0046
3264726	0.63	0.0143	1.52	0.58	0.914	0.62	0.56	0.45	0.72	5.14	0.0323	0.01	0.0139
3275175	0.66	0.0035	1.37	0.64	0.4669	0.57	0.68	0.51	0.74	5.13	0.0045	0.0022	0.0035
3276455	0.63	0.0168	1.26	0.61	0.7405	0.43	0.72	0.47	0.69	3.86	0.0883	0.0323	0.0325
3277709	0.69	0.0003	1.36	0.71	0.0583	0.66	0.73	0.58	0.79	4.6	0	0.001	0.0018
3279906	0.65	0.0049	1.31	0.6	0.7956	0.72	0.54	0.47	0.77	7.18	0.0043	0.0036	0.0048
3280961	0.64	0.0076	1.37	0.63	0.611	0.49	0.71	0.49	0.71	4.34	0.0322	0.016	0.0113
3282022	0.61	0.0391	1.43	0.62	0.6786	0.62	0.62	0.48	0.74	4.4	0.0063	0.0275	0.037
3282170	0.64	0.0073	1.28	0.64	0.5397	0.55	0.68	0.5	0.73	3.64	0.0035	0.0091	0.0169
3282215	0.66	0.0021	1.64	0.64	0.5397	0.62	0.65	0.5	0.75	4.71	0.0032	0.0019	0.0026

3282220	0.69	0.0004	1.66	0.68	0.1571	0.6	0.73	0.56	0.76	5.4	0.0001	0.0003	0.0005
3282254	0.65	0.0052	1.32	0.64	0.5397	0.64	0.63	0.5	0.75	5.13	0.002	0.0035	0.0058
3284025	0.64	0.008	1.29	0.67	0.206	0.45	0.8	0.57	0.72	5.09	0.0011	0.0055	0.0091
3284217	0.67	0.0015	1.39	0.66	0.3262	0.74	0.61	0.52	0.81	6.6	0.0001	0.0006	0.0011
3284603	0.64	0.0096	1.31	0.63	0.611	0.57	0.66	0.49	0.73	5.47	0.008	0.0048	0.0083
3284665	0.65	0.0043	1.44	0.62	0.6786	0.57	0.65	0.48	0.73	5.98	0.005	0.0021	0.0049
3294341	0.64	0.0107	1.39	0.63	0.611	0.49	0.71	0.49	0.71	4.54	0.0169	0.0053	0.007
3294501	0.63	0.0126	1.35	0.64	0.5397	0.55	0.68	0.5	0.73	4.92	0.0073	0.0084	0.0116
3298980	0.62	0.0278	1.32	0.66	0.3262	0.55	0.72	0.53	0.74	4.08	0.0028	0.0389	0.0492
3301222	0.61	0.0387	1.34	0.61	0.7405	0.72	0.55	0.48	0.78	6.14	0.0021	0.0264	0.028
3301703	0.65	0.0052	1.4	0.68	0.1571	0.49	0.79	0.58	0.73	3.9	0.0005	0.0028	0.0045
3301858	0.62	0.0213	1.32	0.64	0.4669	0.36	0.8	0.52	0.69	4.2	0.0276	0.027	0.0287
3301863	0.65	0.0059	1.43	0.67	0.2627	0.72	0.63	0.53	0.8	7.07	0.0001	0.0041	0.0042
3302047	0.67	0.0014	1.37	0.64	0.5397	0.66	0.62	0.5	0.76	4.62	0.003	0.0024	0.0045
3304013	0.64	0.0101	1.31	0.62	0.6786	0.68	0.59	0.48	0.76	6.32	0.0039	0.0079	0.0103
3304626	0.62	0.0271	1.18	0.61	0.7405	0.47	0.7	0.47	0.7	5.7	0.0312	0.0162	0.024
3304652	0.67	0.0016	1.37	0.64	0.5397	0.47	0.73	0.5	0.71	4.89	0.0119	0.0012	0.0034
3307940	0.64	0.0096	1.32	0.61	0.7405	0.51	0.67	0.47	0.71	3.94	0.0428	0.0066	0.0098
3308532	0.63	0.0175	1.24	0.6	0.8429	0.34	0.74	0.43	0.66	5.37	0.187	0.1171	0.1202
3309267	0.62	0.0189	1.35	0.6	0.8429	0.64	0.57	0.46	0.73	4.83	0.0118	0.01	0.0202
3311304	0.68	0.0009	1.38	0.66	0.3262	0.47	0.77	0.54	0.72	3.87	0.0086	0.0027	0.0029
3317557	0.68	0.0007	1.35	0.63	0.611	0.45	0.73	0.49	0.7	3.97	0.0466	0.0078	0.0066
3325714	0.63	0.0155	1.25	0.6	0.7956	0.49	0.67	0.46	0.7	4.26	0.0761	0.012	0.0164
3325963	0.64	0.0078	1.48	0.64	0.5397	0.68	0.61	0.5	0.77	5.56	0.0015	0.0087	0.0072
3326246	0.62	0.0224	1.33	0.63	0.611	0.4	0.76	0.49	0.69	4.11	0.055	0.0349	0.0402
3326465	0.7	0.0001	1.43	0.65	0.3949	0.55	0.71	0.52	0.73	3.43	0.0027	0	0.0001
3329941	0.64	0.0067	1.3	0.65	0.3949	0.6	0.68	0.52	0.75	5	0.0017	0.0066	0.0127
3331532	0.7	0.0002	1.36	0.65	0.3949	0.66	0.65	0.52	0.77	6.06	0.001	0.0003	0.0003
3331573	0.61	0.041	1.32	0.64	0.5397	0.64	0.63	0.5	0.75	5.05	0.0021	0.0152	0.0247
3331613	0.69	0.0005	1.4	0.66	0.3262	0.62	0.68	0.53	0.76	6.7	0.0007	0.0005	0.0007
3331614	0.67	0.0018	1.44	0.63	0.611	0.77	0.55	0.49	0.8	6.86	0.0006	0.002	0.0023
3333687	0.62	0.0205	1.34	0.62	0.6786	0.6	0.63	0.48	0.73	5.33	0.0128	0.0251	0.0227
3334162	0.63	0.0164	1.32	0.64	0.5397	0.49	0.72	0.5	0.71	5.02	0.0131	0.0201	0.0302
3334515	0.66	0.0027	1.33	0.6	0.7956	0.72	0.54	0.47	0.77	7.19	0.0036	0.0021	0.0032
3335173	0.66	0.0022	1.61	0.64	0.5397	0.74	0.57	0.5	0.8	6.66	0.0005	0.0011	0.0012
3335176	0.64	0.0069	1.38	0.61	0.7405	0.64	0.6	0.48	0.74	6.61	0.0111	0.0053	0.0053
3335178	0.68	0.0006	1.38	0.64	0.4669	0.68	0.62	0.51	0.77	6.69	0.0005	0.0004	0.0006
3335179	0.67	0.0012	1.5	0.66	0.3262	0.66	0.66	0.53	0.77	5.65	0.0005	0.0009	0.0011
3335181	0.67	0.0014	1.34	0.6	0.8429	0.72	0.52	0.47	0.77	8.05	0.0062	0.0023	0.003
3335182	0.67	0.0014	1.31	0.64	0.5397	0.74	0.57	0.5	0.8	8.91	0.0006	0.0015	0.0023
3335187	0.67	0.0012	1.39	0.64	0.4669	0.72	0.6	0.51	0.79	8.46	0.0003	0.0013	0.0019
3335188	0.67	0.0015	1.29	0.64	0.4669	0.77	0.57	0.51	0.81	9.17	0.0003	0.0015	0.0019
3335189	0.63	0.0123	1.29	0.58	0.914	0.68	0.52	0.45	0.74	5.49	0.0282	0.0086	0.0146

3335191	0.66	0.0021	1.33	0.62	0.6786	0.7	0.57	0.49	0.77	8.73	0.0019	0.0013	0.0024
3335231	0.66	0.0027	1.45	0.61	0.7405	0.77	0.52	0.48	0.8	7.5	0.0017	0.0027	0.0031
3337724	0.68	0.0007	1.29	0.67	0.206	0.68	0.67	0.54	0.79	7.12	0.0001	0.0008	0.0009
3338618	0.67	0.0014	1.36	0.67	0.206	0.66	0.68	0.54	0.78	7.3	0.0001	0.001	0.0017
3341466	0.62	0.0275	1.23	0.61	0.7405	0.68	0.57	0.48	0.76	5.31	0.0056	0.0256	0.0366
3341504	0.67	0.0016	1.56	0.64	0.4669	0.66	0.63	0.51	0.76	5.61	0.0015	0.0008	0.0013
3344853	0.65	0.0044	1.68	0.63	0.611	0.62	0.63	0.49	0.74	5	0.0049	0.0031	0.0031
3344889	0.63	0.0162	1.44	0.62	0.6786	0.49	0.7	0.48	0.7	3.97	0.0201	0.0071	0.0143
3345453	0.6	0.0586	1.73	0.61	0.7405	0.55	0.65	0.47	0.72	5	0.0209	0.0264	0.0332
3347691	0.62	0.0255	1.31	0.6	0.7956	0.64	0.59	0.47	0.74	6	0.0102	0.0264	0.0231
3352533	0.68	0.0005	1.25	0.62	0.6786	0.7	0.57	0.49	0.77	5.44	0.0029	0.0006	0.0011
3352561	0.62	0.0292	1.25	0.64	0.5397	0.62	0.65	0.5	0.75	4.52	0.0069	0.0438	0.0471
3352585	0.63	0.0137	1.33	0.6	0.7956	0.74	0.52	0.47	0.78	5.69	0.0024	0.0081	0.0126
3352925	0.63	0.0147	1.33	0.64	0.5397	0.6	0.66	0.5	0.74	3.22	0.0034	0.0033	0.0069
3354966	0.65	0.0039	1.31	0.64	0.5397	0.68	0.61	0.5	0.77	7.27	0.0012	0.0031	0.004
3356173	0.63	0.0135	1.38	0.63	0.611	0.6	0.65	0.49	0.74	4.81	0.0066	0.0132	0.0137
3358364	0.66	0.0034	1.41	0.6	0.8429	0.72	0.52	0.47	0.77	5.54	0.0099	0.0036	0.0041
3359382	0.66	0.0029	1.4	0.66	0.3262	0.51	0.74	0.53	0.73	4.41	0.0012	0.0005	0.0021
3362739	0.65	0.0044	1.54	0.64	0.5397	0.6	0.66	0.5	0.74	4.54	0.0037	0.0028	0.0037
3362742	0.67	0.0014	1.61	0.64	0.5397	0.62	0.65	0.5	0.75	5.27	0.0029	0.0013	0.0021
3362745	0.62	0.0233	1.39	0.62	0.6786	0.6	0.63	0.48	0.73	5.25	0.005	0.0105	0.0174
3362763	0.66	0.0027	1.24	0.63	0.611	0.53	0.68	0.49	0.72	5.42	0.0192	0.0045	0.0045
3362773	0.67	0.0014	1.36	0.65	0.3949	0.62	0.67	0.52	0.75	7.19	0.001	0.0011	0.0012
3362943	0.65	0.0035	1.66	0.64	0.4669	0.62	0.66	0.51	0.75	4.96	0.0015	0.0023	0.003
3363519	0.62	0.0216	1.31	0.57	0.9388	0.62	0.55	0.44	0.71	4.13	0.0545	0.0285	0.0343
3363981	0.63	0.0113	1.31	0.64	0.4669	0.62	0.66	0.51	0.75	3.46	0.0023	0.0399	0.0533
3364729	0.6	0.0506	1.36	0.6	0.8429	0.53	0.63	0.45	0.7	4.33	0.0626	0.0548	0.0644
3364770	0.65	0.0036	1.41	0.64	0.5397	0.57	0.67	0.5	0.73	4.17	0.0077	0.0058	0.0055
3364800	0.63	0.0121	1.34	0.66	0.3262	0.57	0.71	0.53	0.74	3.63	0.0047	0.026	0.0109
3368920	0.65	0.0049	1.42	0.64	0.4669	0.62	0.66	0.51	0.75	5.77	0.0022	0.0049	0.0053
3371737	0.63	0.0113	1.28	0.64	0.5397	0.62	0.65	0.5	0.75	6.21	0.0021	0.0143	0.0175
3372461	0.66	0.0027	1.67	0.64	0.5397	0.51	0.71	0.5	0.72	3.75	0.0086	0.0055	0.0064
3375309	0.61	0.042	1.51	0.6	0.7956	0.64	0.59	0.47	0.74	4.89	0.0196	0.0433	0.0396
3375752	0.67	0.0019	1.32	0.64	0.5397	0.66	0.62	0.5	0.76	5.07	0.0017	0.0019	0.0029
3375863	0.65	0.0038	1.33	0.64	0.4669	0.57	0.68	0.51	0.74	4.77	0.0072	0.0039	0.0039
3376090	0.65	0.0036	1.39	0.64	0.4669	0.66	0.63	0.51	0.76	5.73	0.0012	0.0028	0.0039
3376775	0.65	0.004	1.26	0.58	0.914	0.68	0.52	0.45	0.74	5.44	0.0148	0.0042	0.0074
3377457	0.65	0.0044	1.7	0.64	0.5397	0.62	0.65	0.5	0.75	5.07	0.0025	0.0029	0.0042
3377464	0.65	0.0063	1.49	0.64	0.5397	0.64	0.63	0.5	0.75	6.16	0.0023	0.0035	0.0043
3377621	0.64	0.0064	1.64	0.61	0.7405	0.7	0.56	0.48	0.77	6.49	0.003	0.0037	0.0059
3377623	0.64	0.0103	1.48	0.6	0.8429	0.66	0.56	0.46	0.74	6.38	0.0113	0.0064	0.0097
3377625	0.65	0.0053	1.37	0.58	0.914	0.74	0.49	0.45	0.77	6.68	0.0104	0.0035	0.0045
3377632	0.64	0.0092	1.36	0.58	0.914	0.68	0.52	0.45	0.74	6.13	0.0192	0.0067	0.0092

3377633	0.61	0.0311	1.25	0.61	0.7405	0.53	0.66	0.47	0.71	6.84	0.0153	0.0164	0.0315
3377659	0.67	0.0013	1.3	0.63	0.611	0.7	0.59	0.49	0.77	9.07	0.0013	0.0008	0.001
3377660	0.66	0.0028	1.32	0.64	0.5397	0.7	0.6	0.5	0.78	7.75	0.0007	0.0022	0.0032
3379122	0.67	0.0013	1.52	0.63	0.611	0.72	0.57	0.49	0.78	6.2	0.0012	0.0013	0.0016
3379574	0.64	0.0079	1.44	0.65	0.3949	0.62	0.67	0.52	0.75	4.64	0.0006	0.0042	0.0073
3382981	0.65	0.0035	1.29	0.62	0.6786	0.62	0.62	0.48	0.74	5.05	0.0104	0.0046	0.006
3382984	0.67	0.0011	1.36	0.63	0.611	0.64	0.62	0.49	0.75	5.38	0.0025	0.001	0.0018
3383148	0.67	0.0011	1.47	0.63	0.611	0.72	0.57	0.49	0.78	6.79	0.0012	0.0015	0.0019
3383149	0.65	0.0046	1.57	0.62	0.6786	0.7	0.57	0.49	0.77	5.64	0.002	0.0022	0.0038
3384489	0.64	0.0064	1.53	0.64	0.4669	0.62	0.66	0.51	0.75	5.16	0.0021	0.0022	0.0038
3384495	0.65	0.0056	1.37	0.6	0.7956	0.72	0.54	0.47	0.77	4.1	0.0066	0.01	0.0102
3385045	0.65	0.0036	1.23	0.65	0.3949	0.45	0.77	0.53	0.71	3.67	0.0035	0.0018	0.0082
3385178	0.58	0.1362	1.29	0.6	0.7956	0.49	0.67	0.46	0.7	4.14	0.0565	0.1056	0.1188
3386816	0.65	0.0036	1.32	0.64	0.5397	0.55	0.68	0.5	0.73	7.23	0.0105	0.0051	0.0041
3387176	0.64	0.0104	1.29	0.64	0.5397	0.55	0.68	0.5	0.73	3.78	0.0099	0.0152	0.0211
3387436	0.66	0.0019	1.4	0.64	0.4669	0.62	0.66	0.51	0.75	5.79	0.0047	0.0057	0.0023
3388633	0.67	0.0015	1.37	0.67	0.206	0.64	0.7	0.55	0.77	5.23	0.0001	0.0018	0.002
3393789	0.67	0.0017	1.41	0.67	0.2627	0.62	0.7	0.54	0.76	5.4	0.0005	0.0019	0.0023
3394076	0.68	0.0008	1.31	0.69	0.1164	0.66	0.71	0.56	0.78	6.9	0	0.0007	0.0011
3394529	0.61	0.0323	1.32	0.63	0.611	0.6	0.65	0.49	0.74	4.77	0.0059	0.0226	0.032
3395420	0.65	0.0036	1.4	0.62	0.6786	0.68	0.59	0.48	0.76	6.13	0.0035	0.0025	0.0041
3395427	0.61	0.0323	1.25	0.64	0.5397	0.62	0.65	0.5	0.75	5.78	0.0021	0.0212	0.0335
3400152	0.64	0.0082	1.29	0.6	0.7956	0.6	0.61	0.47	0.72	4.87	0.0243	0.0097	0.0105
3402624	0.61	0.0323	1.25	0.61	0.7405	0.51	0.67	0.47	0.71	5.33	0.0387	0.03	0.0371
3402667	0.65	0.0059	1.25	0.6	0.7956	0.64	0.59	0.47	0.74	5.61	0.0086	0.0029	0.0051
3402720	0.64	0.0064	1.52	0.65	0.3949	0.64	0.66	0.52	0.76	5.58	0.0008	0.0034	0.0047
3406062	0.68	0.0007	1.35	0.71	0.0583	0.66	0.73	0.58	0.79	4.22	0	0.0008	0.0014
3407177	0.65	0.0061	1.27	0.61	0.7405	0.45	0.71	0.47	0.69	3.45	0.0396	0.003	0.0091
3407275	0.61	0.0445	1.28	0.57	0.9388	0.49	0.62	0.43	0.68	5.04	0.1771	0.0394	0.0555
3409292	0.63	0.0132	1.29	0.63	0.611	0.64	0.62	0.49	0.75	5.69	0.0028	0.0072	0.0183
3412651	0.65	0.0052	1.38	0.64	0.5397	0.55	0.68	0.5	0.73	5.41	0.0083	0.0059	0.0065
3414226	0.66	0.0027	1.47	0.68	0.1571	0.7	0.67	0.55	0.8	6.15	0	0.0011	0.0015
3416068	0.65	0.0049	1.28	0.62	0.6786	0.68	0.59	0.48	0.76	5.61	0.0025	0.0025	0.006
3416501	0.6	0.0668	1.26	0.64	0.5397	0.49	0.72	0.5	0.71	4.89	0.0185	0.0567	0.069
3417160	0.69	0.0004	1.49	0.64	0.4669	0.62	0.66	0.51	0.75	6.56	0.0023	0.0004	0.0006
3417666	0.69	0.0005	1.35	0.62	0.6786	0.62	0.62	0.48	0.74	5.97	0.0071	0.0007	0.0009
3418209	0.64	0.0066	1.4	0.62	0.6786	0.66	0.6	0.48	0.75	3.86	0.004	0.0086	0.0101
3419262	0.64	0.0066	1.3	0.64	0.4669	0.53	0.71	0.51	0.73	5.78	0.0052	0.0064	0.0087
3419622	0.61	0.0347	1.35	0.6	0.8429	0.6	0.6	0.46	0.72	4.81	0.0319	0.019	0.0313
3421154	0.64	0.009	1.42	0.59	0.8822	0.68	0.54	0.46	0.75	5.72	0.0154	0.0067	0.0081
3421223	0.64	0.0073	1.72	0.67	0.2627	0.55	0.73	0.54	0.74	5.06	0.001	0.0048	0.0044
3421350	0.65	0.006	1.42	0.61	0.7405	0.57	0.63	0.47	0.72	5.56	0.012	0.0031	0.0042
3421492	0.63	0.0182	1.31	0.66	0.3262	0.51	0.74	0.53	0.73	4.54	0.0027	0.0156	0.0146

3421652	0.64	0.0096	1.29	0.6	0.7956	0.53	0.65	0.46	0.71	6.73	0.027	0.0057	0.0071
3421668	0.67	0.0012	1.33	0.66	0.3262	0.47	0.77	0.54	0.72	4.65	0.0056	0.003	0.0027
3427811	0.63	0.0141	1.37	0.65	0.3949	0.53	0.72	0.52	0.73	3.88	0.0036	0.0185	0.0194
3427812	0.67	0.001	1.57	0.6	0.7956	0.62	0.6	0.47	0.73	5.18	0.0197	0.001	0.0013
3428711	0.66	0.0024	1.37	0.66	0.3262	0.45	0.78	0.54	0.71	4.49	0.0058	0.0029	0.004
3428712	0.65	0.0063	1.4	0.65	0.3949	0.47	0.76	0.52	0.71	4.45	0.0126	0.0096	0.0066
3429794	0.63	0.012	1.26	0.63	0.611	0.6	0.65	0.49	0.74	5.49	0.0079	0.0164	0.0221
3430575	0.62	0.0197	1.27	0.64	0.5397	0.57	0.67	0.5	0.73	6.41	0.0063	0.0155	0.0217
3431352	0.62	0.0205	1.32	0.62	0.6786	0.6	0.63	0.48	0.73	5.55	0.0128	0.0226	0.0185
3431686	0.66	0.0024	1.33	0.69	0.1164	0.62	0.73	0.57	0.77	5.51	0.0001	0.0029	0.003
3432171	0.66	0.0031	1.46	0.66	0.3262	0.66	0.66	0.53	0.77	5.85	0.0007	0.0016	0.0016
3432352	0.62	0.0282	1.29	0.6	0.7956	0.57	0.62	0.47	0.72	5.1	0.0177	0.018	0.0328
3435860	0.67	0.0011	1.51	0.64	0.4669	0.66	0.63	0.51	0.76	4.96	0.0007	0.0013	0.0025
3435864	0.66	0.0025	1.31	0.64	0.5397	0.7	0.6	0.5	0.78	5.62	0.0011	0.0011	0.0027
3436017	0.65	0.0036	1.33	0.64	0.5397	0.7	0.6	0.5	0.78	5.3	0.0015	0.0046	0.0056
3436264	0.66	0.0033	1.71	0.64	0.5397	0.64	0.63	0.5	0.75	3.99	0.0025	0.0022	0.003
3438044	0.63	0.0132	1.38	0.64	0.4669	0.49	0.73	0.51	0.71	4.94	0.0102	0.0134	0.0192
3445545	0.61	0.0319	1.31	0.64	0.5397	0.57	0.67	0.5	0.73	5.56	0.0025	0.0164	0.0259
3445674	0.67	0.0012	1.37	0.66	0.3262	0.45	0.78	0.54	0.71	4.05	0.0037	0.0133	0.0115
3445750	0.63	0.0126	1.34	0.65	0.3949	0.64	0.66	0.52	0.76	4.13	0.0012	0.0051	0.0066
3446488	0.64	0.0098	1.41	0.61	0.7405	0.64	0.6	0.48	0.74	5.7	0.007	0.0049	0.0083
3446869	0.66	0.0035	1.31	0.62	0.6786	0.7	0.57	0.49	0.77	7.73	0.0021	0.0021	0.0026
3446885	0.63	0.0112	1.3	0.6	0.8429	0.51	0.65	0.45	0.7	4.66	0.1091	0.0106	0.0108
3452256	0.64	0.0086	1.29	0.62	0.6786	0.68	0.59	0.48	0.76	5.45	0.0047	0.0083	0.0076
3452262	0.65	0.0039	1.49	0.64	0.4669	0.57	0.68	0.51	0.74	4.64	0.0051	0.0039	0.0044
3452324	0.63	0.0128	1.35	0.64	0.5397	0.6	0.66	0.5	0.74	5.58	0.0024	0.0102	0.0204
3452349	0.66	0.0028	1.18	0.64	0.4669	0.49	0.73	0.51	0.71	6.07	0.0064	0.0042	0.007
3454729	0.66	0.0032	1.29	0.64	0.5397	0.62	0.65	0.5	0.75	7.03	0.002	0.0019	0.0033
3456599	0.67	0.0017	1.52	0.63	0.611	0.55	0.67	0.49	0.72	4.38	0.0106	0.0011	0.0024
3457550	0.67	0.001	1.31	0.67	0.2627	0.57	0.72	0.54	0.75	7.1	0.0004	0.0006	0.001
3458494	0.65	0.0036	1.34	0.66	0.3262	0.62	0.68	0.53	0.76	5.37	0.0006	0.0016	0.0029
3461302	0.65	0.0036	1.44	0.63	0.611	0.64	0.62	0.49	0.75	6.12	0.0039	0.0042	0.0044
3461431	0.68	0.001	1.3	0.67	0.2627	0.66	0.67	0.53	0.77	3.87	0.0003	0.0002	0.0007
3462710	0.64	0.0109	1.31	0.63	0.611	0.6	0.65	0.49	0.74	6.28	0.0048	0.0092	0.0124
3462846	0.63	0.0115	1.35	0.61	0.7405	0.62	0.61	0.48	0.74	3.98	0.015	0.0156	0.0133
3462861	0.64	0.0065	1.33	0.63	0.611	0.68	0.6	0.49	0.77	4.84	0.0024	0.0101	0.0108
3462867	0.69	0.0004	1.35	0.62	0.6786	0.77	0.54	0.49	0.8	7.16	0.0011	0.0007	0.0008
3462868	0.67	0.0017	1.31	0.66	0.3262	0.51	0.74	0.53	0.73	4.64	0.0047	0.0059	0.0049
3462884	0.66	0.0031	1.32	0.66	0.3262	0.6	0.7	0.53	0.75	5.34	0.0008	0.0026	0.0031
3462988	0.67	0.0014	1.48	0.6	0.8429	0.66	0.56	0.46	0.74	5.48	0.0164	0.0015	0.0017
3463596	0.68	0.0008	1.29	0.67	0.206	0.51	0.77	0.56	0.73	6.43	0.0005	0.0006	0.0009
3463603	0.72	0	1.28	0.67	0.2627	0.36	0.84	0.57	0.7	4.81	0.0041	0.0001	0.0005
3464009	0.61	0.0405	1.33	0.62	0.6786	0.64	0.61	0.48	0.75	4.21	0.0069	0.0776	0.0787

3465251	0.66	0.0022	1.53	0.68	0.1571	0.66	0.7	0.55	0.78	4.84	0.0001	0.0045	0.0061
3465252	0.62	0.0261	1.62	0.65	0.3949	0.68	0.63	0.52	0.78	6.2	0.0006	0.0064	0.0095
3465278	0.63	0.0139	1.26	0.57	0.9388	0.26	0.76	0.38	0.64	5.12	0.7659	0.0836	0.1065
3466861	0.64	0.0109	1.34	0.65	0.3949	0.51	0.73	0.52	0.72	4.4	0.0021	0.0058	0.0164
3467642	0.64	0.0065	1.49	0.62	0.6786	0.62	0.62	0.48	0.74	5.63	0.0052	0.0061	0.0065
3468015	0.64	0.007	1.4	0.63	0.611	0.57	0.66	0.49	0.73	4.68	0.0087	0.0058	0.0106
3469369	0.64	0.0083	1.26	0.64	0.4669	0.4	0.78	0.51	0.7	3.35	0.042	0.0095	0.0114
3471177	0.64	0.0071	1.31	0.62	0.6786	0.49	0.7	0.48	0.7	4.56	0.0334	0.0041	0.0072
3471377	0.69	0.0004	1.69	0.69	0.1164	0.7	0.68	0.56	0.8	5.99	0	0.0001	0.0002
3471379	0.63	0.0182	1.31	0.61	0.7405	0.45	0.71	0.47	0.69	4.4	0.0397	0.0156	0.0335
3472092	0.64	0.0092	1.34	0.63	0.611	0.7	0.59	0.49	0.77	7.77	0.002	0.0052	0.0073
3473482	0.65	0.0045	1.33	0.63	0.611	0.49	0.71	0.49	0.71	4.29	0.0228	0.0043	0.0064
3474494	0.68	0.0008	1.36	0.66	0.3262	0.72	0.62	0.52	0.8	6.28	0.0003	0.0009	0.0012
3474937	0.62	0.0197	1.4	0.61	0.7405	0.55	0.65	0.47	0.72	5.34	0.0175	0.0218	0.0268
3475623	0.65	0.0059	1.29	0.64	0.4669	0.57	0.68	0.51	0.74	4.37	0.0023	0.0099	0.0158
3475737	0.64	0.0101	1.3	0.68	0.1571	0.57	0.74	0.56	0.75	4.9	0.0001	0.008	0.0139
3476294	0.65	0.0044	1.53	0.64	0.4669	0.68	0.62	0.51	0.77	5.56	0.0006	0.0026	0.0038
3480098	0.67	0.0017	1.57	0.64	0.5397	0.57	0.67	0.5	0.73	4.3	0.0023	0.0006	0.0014
3480100	0.67	0.0016	1.28	0.62	0.6786	0.49	0.7	0.48	0.7	3.34	0.0204	0.001	0.0033
3480173	0.66	0.0024	1.25	0.64	0.4669	0.47	0.74	0.51	0.71	5.63	0.0059	0.0029	0.0049
3480201	0.67	0.0014	1.4	0.64	0.4669	0.7	0.61	0.51	0.78	5.06	0.0005	0.0009	0.0018
3480203	0.65	0.0037	1.31	0.61	0.7405	0.66	0.59	0.48	0.75	5.79	0.0084	0.0036	0.0044
3480685	0.65	0.0042	1.3	0.64	0.4669	0.7	0.61	0.51	0.78	7.01	0.0005	0.0034	0.0054
3480856	0.7	0.0002	1.34	0.65	0.3949	0.6	0.68	0.52	0.75	6.74	0.0025	0.0002	0.0003
3481480	0.68	0.0005	1.37	0.66	0.3262	0.7	0.63	0.52	0.79	4.65	0.0003	0.0012	0.001
3482124	0.6	0.0729	1.32	0.6	0.7956	0.51	0.66	0.46	0.7	5.82	0.0443	0.0289	0.0537
3482915	0.65	0.0053	1.48	0.66	0.3262	0.55	0.72	0.53	0.74	4.94	0.0009	0.0086	0.0118
3482916	0.64	0.0073	1.62	0.68	0.1571	0.66	0.7	0.55	0.78	5.01	0	0.0021	0.0035
3483215	0.67	0.0015	1.28	0.65	0.3949	0.68	0.63	0.52	0.78	7.97	0.0003	0.0014	0.0022
3484743	0.67	0.0013	1.33	0.69	0.1164	0.68	0.7	0.56	0.79	6.76	0	0.0009	0.0015
3484750	0.66	0.0035	1.52	0.68	0.1571	0.7	0.67	0.55	0.8	4.99	0	0.002	0.0021
3484756	0.62	0.0248	1.32	0.61	0.7405	0.55	0.65	0.47	0.72	4.84	0.0186	0.0147	0.0182
3484762	0.68	0.0007	1.36	0.67	0.2627	0.62	0.7	0.54	0.76	5.98	0.0003	0.0008	0.0011
3485891	0.65	0.006	1.85	0.64	0.5397	0.6	0.66	0.5	0.74	4.72	0.0051	0.0036	0.0049
3489010	0.61	0.0331	1.43	0.59	0.8822	0.57	0.6	0.45	0.71	5.16	0.0525	0.0301	0.0337
3489011	0.66	0.0024	1.47	0.62	0.6786	0.77	0.54	0.49	0.8	7.21	0.001	0.0025	0.0028
3494193	0.63	0.017	1.45	0.61	0.7405	0.64	0.6	0.48	0.74	5.1	0.0042	0.0094	0.0158
3497656	0.59	0.0881	1.2	0.59	0.8822	0.49	0.65	0.44	0.69	3.62	0.1954	0.0862	0.0967
3497658	0.67	0.001	1.3	0.67	0.2627	0.66	0.67	0.53	0.77	6.29	0.0002	0.0011	0.0015
3497823	0.67	0.001	1.36	0.64	0.5397	0.6	0.66	0.5	0.74	4.65	0.0042	0.0028	0.0035
3498048	0.66	0.0019	1.4	0.61	0.7405	0.47	0.7	0.47	0.7	4.26	0.0419	0.0006	0.0016
3498445	0.64	0.0069	1.39	0.64	0.4669	0.64	0.65	0.51	0.76	5.51	0.0019	0.0031	0.0061
3498523	0.68	0.0007	1.74	0.66	0.3262	0.7	0.63	0.52	0.79	5.3	0.0004	0.0009	0.0008

3498537	0.65	0.0039	1.33	0.64	0.4669	0.55	0.7	0.51	0.73	5.07	0.0031	0.0031	0.0051
3498977	0.67	0.0015	1.56	0.58	0.914	0.64	0.55	0.45	0.73	5.18	0.0316	0.0015	0.0018
3499545	0.65	0.0042	1.28	0.64	0.4669	0.62	0.66	0.51	0.75	5.43	0.0024	0.0036	0.0052
3500408	0.62	0.02	1.37	0.64	0.5397	0.57	0.67	0.5	0.73	5.1	0.0036	0.0089	0.0195
3501216	0.66	0.0022	1.32	0.64	0.5397	0.64	0.63	0.5	0.75	5.99	0.0024	0.0019	0.0039
3501217	0.67	0.0012	1.36	0.62	0.6786	0.7	0.57	0.49	0.77	6.19	0.0024	0.0011	0.0023
3501555	0.72	0	1.55	0.67	0.206	0.66	0.68	0.54	0.78	5.52	0.0001	0.0001	0.0001
3503211	0.66	0.0027	1.33	0.65	0.3949	0.6	0.68	0.52	0.75	6.44	0.001	0.0012	0.0024
3505453	0.63	0.0137	1.59	0.63	0.611	0.6	0.65	0.49	0.74	4.58	0.0162	0.0158	0.0132
3506941	0.63	0.0166	1.46	0.64	0.4669	0.62	0.66	0.51	0.75	4.86	0.0017	0.0083	0.0156
3508731	0.66	0.0024	1.39	0.66	0.3262	0.34	0.84	0.55	0.69	4.35	0.011	0.0067	0.0093
3508732	0.64	0.0084	1.3	0.67	0.206	0.64	0.7	0.55	0.77	5.5	0.0001	0.0057	0.0103
3508761	0.64	0.0106	1.28	0.62	0.6786	0.68	0.59	0.48	0.76	6.3	0.0033	0.0061	0.0115
3509912	0.66	0.0024	1.65	0.66	0.3262	0.6	0.7	0.53	0.75	4.21	0.0007	0.0032	0.0047
3509913	0.63	0.0126	1.35	0.64	0.4669	0.53	0.71	0.51	0.73	4	0.0057	0.0109	0.0169
3510070	0.64	0.0107	1.27	0.63	0.611	0.55	0.67	0.49	0.72	6.7	0.005	0.0039	0.0138
3510382	0.66	0.0028	1.43	0.63	0.611	0.62	0.63	0.49	0.74	5.54	0.0067	0.0024	0.0031
3512558	0.67	0.0018	1.36	0.6	0.8429	0.7	0.54	0.46	0.76	7.03	0.0064	0.0012	0.002
3513710	0.64	0.0086	1.51	0.64	0.5397	0.55	0.68	0.5	0.73	4.27	0.0066	0.0133	0.0103
3517677	0.68	0.0008	1.53	0.71	0.0583	0.4	0.88	0.66	0.72	4.2	0.0001	0.0001	0.0006
3517683	0.69	0.0005	1.28	0.7	0.0837	0.6	0.76	0.58	0.77	5.37	0.0001	0.0008	0.0025
3518501	0.64	0.0066	1.34	0.64	0.5397	0.49	0.72	0.5	0.71	4.95	0.0085	0.011	0.0121
3519136	0.66	0.0031	1.29	0.64	0.4669	0.49	0.73	0.51	0.71	4.81	0.0103	0.0083	0.0112
3521962	0.62	0.0236	1.39	0.67	0.2627	0.51	0.76	0.55	0.73	5.23	0.0005	0.0157	0.0241
3524627	0.66	0.0033	1.32	0.62	0.6786	0.66	0.6	0.48	0.75	5.38	0.0027	0.0041	0.0065
3524630	0.61	0.0369	1.46	0.64	0.5397	0.53	0.7	0.5	0.72	4.55	0.008	0.0212	0.0347
3524631	0.63	0.0112	1.39	0.6	0.7956	0.64	0.59	0.47	0.74	4.7	0.0066	0.0065	0.0108
3525314	0.68	0.0008	1.47	0.64	0.5397	0.64	0.63	0.5	0.75	6.24	0.002	0.0007	0.0012
3525317	0.69	0.0003	1.62	0.64	0.4669	0.62	0.66	0.51	0.75	5.31	0.0025	0.0002	0.0004
3525320	0.67	0.0013	1.48	0.62	0.6786	0.64	0.61	0.48	0.75	5.79	0.0045	0.0008	0.0019
3525547	0.66	0.003	1.35	0.61	0.7405	0.74	0.54	0.48	0.79	5.55	0.0032	0.0028	0.0032
3525702	0.65	0.0036	1.35	0.65	0.3949	0.53	0.72	0.52	0.73	5.08	0.0037	0.0038	0.0041
3525704	0.66	0.0028	1.42	0.59	0.8822	0.66	0.55	0.46	0.74	4.7	0.0253	0.0025	0.0031
3525710	0.68	0.001	1.32	0.66	0.3262	0.68	0.65	0.52	0.78	7.86	0.0002	0.0005	0.0007
3526383	0.68	0.0005	1.35	0.67	0.2627	0.49	0.77	0.55	0.72	3.05	0.0011	0.004	0.0086
3527530	0.67	0.0011	1.46	0.64	0.5397	0.68	0.61	0.5	0.77	4.61	0.0018	0.0011	0.0014
3528208	0.63	0.0145	1.52	0.64	0.4669	0.6	0.67	0.51	0.74	4.78	0.0028	0.0168	0.0138
3529094	0.63	0.0166	1.29	0.61	0.7405	0.64	0.6	0.48	0.74	4.76	0.0114	0.0186	0.0247
3531094	0.65	0.0063	1.45	0.6	0.7956	0.53	0.65	0.46	0.71	5.15	0.0372	0.0062	0.0107
3531491	0.72	0	1.61	0.69	0.1164	0.53	0.78	0.58	0.74	4.24	0.0001	0	0
3533452	0.68	0.0009	1.43	0.65	0.3949	0.74	0.6	0.51	0.8	6.12	0.0002	0.0007	0.0011
3534950	0.67	0.0011	1.4	0.68	0.1571	0.64	0.71	0.56	0.77	6.09	0.0001	0.0004	0.0011
3535917	0.66	0.0032	1.36	0.63	0.611	0.53	0.68	0.49	0.72	4.82	0.013	0.0044	0.0046

3536669	0.7	0.0001	1.28	0.71	0.0394	0.55	0.8	0.62	0.76	6.23	0	0.0001	0.0003
3536745	0.65	0.0056	1.46	0.64	0.5397	0.53	0.7	0.5	0.72	4.96	0.0138	0.0079	0.0077
3536931	0.65	0.006	1.34	0.63	0.611	0.64	0.62	0.49	0.75	7.03	0.003	0.0022	0.0043
3536934	0.65	0.0036	1.33	0.64	0.5397	0.6	0.66	0.5	0.74	4.85	0.0026	0.0037	0.0064
3536938	0.61	0.0445	1.42	0.61	0.7405	0.6	0.62	0.47	0.73	5.85	0.0138	0.0162	0.0338
3536943	0.68	0.0005	1.33	0.65	0.3949	0.64	0.66	0.52	0.76	5.95	0.0005	0.0002	0.0006
3536948	0.64	0.0074	1.29	0.64	0.5397	0.62	0.65	0.5	0.75	5.94	0.0027	0.0033	0.0087
3536949	0.63	0.0151	1.57	0.62	0.6786	0.64	0.61	0.48	0.75	5.86	0.0063	0.0045	0.0082
3536951	0.65	0.0044	1.78	0.65	0.3949	0.66	0.65	0.52	0.77	4.39	0.0008	0.0022	0.0042
3536992	0.64	0.0074	1.39	0.64	0.5397	0.6	0.66	0.5	0.74	3.75	0.0062	0.0051	0.009
3536994	0.67	0.0013	1.37	0.64	0.5397	0.7	0.6	0.5	0.78	5.98	0.0015	0.0007	0.0012
3537787	0.67	0.0012	1.39	0.69	0.1164	0.55	0.77	0.58	0.75	5.2	0.0001	0.0005	0.0012
3537795	0.63	0.0159	1.68	0.63	0.611	0.64	0.62	0.49	0.75	5.68	0.0041	0.0085	0.0098
3537796	0.65	0.0054	1.94	0.6	0.8429	0.64	0.57	0.46	0.73	4.78	0.0173	0.0058	0.005
3539104	0.65	0.0061	1.35	0.61	0.7405	0.57	0.63	0.47	0.72	6.36	0.0133	0.0029	0.0051
3539877	0.66	0.0029	1.39	0.64	0.4669	0.53	0.71	0.51	0.73	4.25	0.0135	0.0097	0.0071
3543929	0.67	0.0017	1.36	0.6	0.7956	0.74	0.52	0.47	0.78	6.03	0.004	0.0017	0.0019
3544473	0.67	0.0014	1.4	0.65	0.3949	0.66	0.65	0.52	0.77	6.41	0.0005	0.0009	0.0015
3544890	0.62	0.0192	1.55	0.62	0.6786	0.45	0.72	0.48	0.69	4.77	0.0404	0.0098	0.0177
3545534	0.63	0.0115	1.4	0.64	0.5397	0.68	0.61	0.5	0.77	6.28	0.0015	0.0067	0.0096
3549043	0.63	0.0175	1.31	0.61	0.7405	0.55	0.65	0.47	0.72	5.16	0.0193	0.0161	0.0244
3550451	0.65	0.0045	1.43	0.63	0.611	0.62	0.63	0.49	0.74	5.73	0.0037	0.0017	0.0043
3550453	0.64	0.0094	1.29	0.65	0.3949	0.62	0.67	0.52	0.75	5.01	0.0018	0.0057	0.0108
3550455	0.63	0.0166	1.3	0.63	0.611	0.43	0.74	0.49	0.69	3.85	0.0424	0.0145	0.0172
3552937	0.63	0.0157	1.32	0.59	0.8822	0.53	0.62	0.45	0.7	4.68	0.0633	0.0091	0.0235
3552938	0.62	0.0236	1.39	0.58	0.914	0.53	0.61	0.44	0.69	5.07	0.0903	0.0166	0.0315
3556198	0.66	0.0032	1.33	0.65	0.3949	0.62	0.67	0.52	0.75	6.91	0.0007	0.002	0.0027
3556224	0.71	0.0001	1.35	0.66	0.3262	0.68	0.65	0.52	0.78	5.81	0.0004	0.0002	0.0002
3556278	0.68	0.0006	1.5	0.7	0.0837	0.53	0.79	0.6	0.75	4.27	0.0001	0.0002	0.0005
3556420	0.65	0.0044	1.44	0.65	0.3949	0.62	0.67	0.52	0.75	4.13	0.0013	0.0039	0.0049
3558292	0.65	0.006	1.37	0.62	0.6786	0.68	0.59	0.48	0.76	6.74	0.0039	0.0079	0.0089
3559519	0.67	0.0017	1.43	0.66	0.3262	0.45	0.78	0.54	0.71	4.32	0.0031	0.0009	0.0024
3559556	0.64	0.0097	1.38	0.64	0.5397	0.51	0.71	0.5	0.72	4.2	0.0092	0.0063	0.016
3562436	0.74	0	1.31	0.71	0.0583	0.47	0.84	0.63	0.73	3.52	0	0	0.0003
3563349	0.67	0.0014	1.27	0.67	0.206	0.6	0.72	0.55	0.76	4.86	0.0001	0.0024	0.0057
3563970	0.67	0.0015	1.52	0.64	0.4669	0.51	0.72	0.51	0.72	3.97	0.0056	0.001	0.002
3566596	0.65	0.0041	1.51	0.65	0.3949	0.68	0.63	0.52	0.78	6.11	0.0005	0.0017	0.0022
3566603	0.62	0.0197	1.43	0.61	0.7405	0.68	0.57	0.48	0.76	5.61	0.0052	0.0159	0.0172
3566648	0.64	0.0088	1.26	0.64	0.5397	0.47	0.73	0.5	0.71	4.44	0.0169	0.0083	0.0154
3566657	0.63	0.0137	1.18	0.64	0.4669	0.45	0.76	0.51	0.7	4.83	0.0054	0.0052	0.0162
3566993	0.63	0.0159	1.29	0.57	0.9388	0.66	0.52	0.44	0.73	4.8	0.0436	0.014	0.022
3569346	0.7	0.0001	1.38	0.67	0.206	0.51	0.77	0.56	0.73	5.02	0.0006	0.0002	0.0006
3569757	0.69	0.0003	1.46	0.68	0.1571	0.64	0.71	0.56	0.77	6.3	0.0001	0.0004	0.0005

3569759	0.66	0.0035	1.33	0.64	0.4669	0.64	0.65	0.51	0.76	5.73	0.0017	0.0027	0.0045
3569819	0.68	0.001	1.4	0.64	0.5397	0.66	0.62	0.5	0.76	4.92	0.0022	0.0025	0.0041
3570456	0.63	0.0145	1.32	0.58	0.914	0.66	0.54	0.45	0.73	5.49	0.0306	0.011	0.0165
3573155	0.63	0.0164	1.22	0.61	0.7405	0.47	0.7	0.47	0.7	5.19	0.0588	0.0201	0.0213
3576551	0.64	0.0096	1.31	0.6	0.8429	0.7	0.54	0.46	0.76	5.7	0.012	0.009	0.0098
3576567	0.67	0.0017	1.65	0.66	0.3262	0.55	0.72	0.53	0.74	4.59	0.0005	0.0006	0.0018
3576712	0.61	0.0445	1.31	0.6	0.7956	0.47	0.68	0.46	0.69	4.85	0.0503	0.0279	0.043
3576730	0.61	0.0364	1.55	0.64	0.5397	0.57	0.67	0.5	0.73	5.54	0.005	0.0107	0.0157
3576939	0.67	0.0018	1.51	0.61	0.7405	0.74	0.54	0.48	0.79	5.89	0.0016	0.0011	0.0012
3576940	0.67	0.0018	1.45	0.63	0.611	0.66	0.61	0.49	0.76	5.57	0.0032	0.0019	0.0028
3577874	0.69	0.0004	1.49	0.63	0.611	0.62	0.63	0.49	0.74	4.35	0.0064	0.0006	0.0007
3577898	0.64	0.01	1.43	0.66	0.3262	0.68	0.65	0.52	0.78	5.31	0.0003	0.0046	0.0062
3577911	0.69	0.0003	1.35	0.7	0.0837	0.62	0.74	0.58	0.77	5.07	0	0.0003	0.0013
3578431	0.68	0.0009	1.29	0.66	0.3262	0.49	0.76	0.53	0.72	5.19	0.0039	0.0016	0.0028
3580188	0.61	0.0335	1.25	0.62	0.6786	0.6	0.63	0.48	0.73	5.04	0.0065	0.0225	0.043
3580204	0.64	0.008	1.33	0.67	0.2627	0.6	0.71	0.54	0.75	6.87	0.0002	0.0045	0.0068
3580587	0.6	0.0535	1.22	0.63	0.611	0.45	0.73	0.49	0.7	3.6	0.0213	0.0342	0.0667
3580953	0.67	0.0017	1.3	0.57	0.9388	0.74	0.48	0.45	0.76	7.37	0.0157	0.0046	0.0061
3589660	0.63	0.0162	1.48	0.64	0.5397	0.55	0.68	0.5	0.73	4.41	0.0073	0.0165	0.0266
3590159	0.63	0.013	1.21	0.58	0.914	0.57	0.59	0.44	0.71	5.72	0.0615	0.0099	0.014
3590352	0.6	0.0729	1.26	0.57	0.9577	0.45	0.63	0.41	0.67	5.22	0.4343	0.1028	0.1181
3591851	0.66	0.002	1.31	0.64	0.5397	0.62	0.65	0.5	0.75	4.89	0.0035	0.0008	0.0021
3591858	0.7	0.0001	1.31	0.65	0.3949	0.68	0.63	0.52	0.78	7.12	0.0004	0.0001	0.0002
3591985	0.64	0.007	1.38	0.65	0.3949	0.66	0.65	0.52	0.77	5.29	0.0005	0.0064	0.0105
3592046	0.62	0.0245	1.38	0.64	0.5397	0.66	0.62	0.5	0.76	5.86	0.0025	0.0244	0.0217
3592047	0.66	0.0026	1.34	0.63	0.611	0.7	0.59	0.49	0.77	6.72	0.0017	0.0047	0.003
3592395	0.66	0.0033	1.34	0.6	0.7956	0.43	0.71	0.45	0.68	4.01	0.0895	0.0047	0.0109
3593171	0.63	0.0182	1.76	0.64	0.5397	0.62	0.65	0.5	0.75	5.31	0.0025	0.0067	0.0081
3594101	0.63	0.0164	1.38	0.67	0.206	0.53	0.76	0.56	0.74	4.51	0.0005	0.0316	0.0396
3595811	0.61	0.0307	1.26	0.61	0.7405	0.64	0.6	0.48	0.74	4.86	0.003	0.0156	0.0357
3595872	0.64	0.0094	1.5	0.61	0.7405	0.64	0.6	0.48	0.74	5.15	0.0047	0.0058	0.0088
3596235	0.67	0.0012	1.27	0.66	0.3262	0.68	0.65	0.52	0.78	3.4	0.0003	0.0026	0.0052
3597406	0.64	0.0098	1.34	0.63	0.611	0.66	0.61	0.49	0.76	6.07	0.0025	0.0037	0.0067
3597468	0.63	0.0118	1.29	0.6	0.7956	0.7	0.55	0.47	0.76	5.92	0.0027	0.0057	0.0115
3597671	0.67	0.0018	1.29	0.6	0.7956	0.55	0.63	0.46	0.71	5.39	0.0257	0.0006	0.0016
3598717	0.65	0.0054	1.37	0.6	0.7956	0.68	0.56	0.47	0.75	6.37	0.0085	0.0035	0.0043
3599449	0.64	0.0078	1.24	0.61	0.7405	0.45	0.71	0.47	0.69	4.69	0.0736	0.0165	0.0195
3602509	0.67	0.0012	1.32	0.61	0.7405	0.68	0.57	0.48	0.76	5.32	0.0057	0.0012	0.0022
3605249	0.65	0.0046	1.32	0.62	0.6786	0.7	0.57	0.49	0.77	5.35	0.0032	0.0048	0.005
3606117	0.55	0.3487	1.1	0.64	0.5397	0.45	0.74	0.5	0.7	4.66	0.0257	0.1812	0.2086
3606409	0.68	0.0008	1.67	0.67	0.206	0.72	0.65	0.54	0.8	5.41	0	0.0005	0.0009
3608201	0.63	0.0121	1.29	0.63	0.611	0.57	0.66	0.49	0.73	4.98	0.0065	0.012	0.0187
3609166	0.65	0.0054	1.43	0.64	0.4669	0.66	0.63	0.51	0.76	4.97	0.0009	0.0042	0.0054

3615597	0.63	0.0132	1.22	0.64	0.4669	0.6	0.67	0.51	0.74	4.79	0.0036	0.0201	0.0207
3615604	0.64	0.0096	1.26	0.67	0.2627	0.51	0.76	0.55	0.73	6.32	0.0019	0.0139	0.0115
3615659	0.64	0.0085	1.24	0.62	0.6786	0.57	0.65	0.48	0.73	4.57	0.0171	0.0098	0.0126
3615989	0.67	0.0017	1.33	0.66	0.3262	0.64	0.67	0.53	0.76	4.74	0.0007	0.0006	0.0013
3621014	0.64	0.0082	1.35	0.66	0.3262	0.49	0.76	0.53	0.72	5.5	0.0024	0.0039	0.0073
3623329	0.63	0.0145	1.44	0.67	0.206	0.6	0.72	0.55	0.76	5.65	0.0002	0.0028	0.0062
3624199	0.67	0.0017	1.26	0.64	0.5397	0.6	0.66	0.5	0.74	6	0.0079	0.006	0.0048
3624533	0.65	0.0043	1.34	0.66	0.3262	0.57	0.71	0.53	0.74	4.7	0.0013	0.002	0.0055
3624702	0.63	0.0112	1.41	0.64	0.4669	0.55	0.7	0.51	0.73	4.04	0.0038	0.0102	0.0119
3625565	0.59	0.0819	1.31	0.63	0.611	0.38	0.77	0.49	0.68	3.93	0.0315	0.1383	0.236
3626570	0.66	0.0024	1.42	0.64	0.4669	0.57	0.68	0.51	0.74	4.45	0.0014	0.0012	0.0035
3626585	0.64	0.0079	1.26	0.64	0.5397	0.62	0.65	0.5	0.75	5.84	0.0038	0.0044	0.0072
3626730	0.66	0.0031	1.48	0.65	0.3949	0.6	0.68	0.52	0.75	5.01	0.0014	0.0015	0.0026
3627045	0.65	0.0063	1.24	0.61	0.7405	0.45	0.71	0.47	0.69	5.25	0.0386	0.006	0.0096
3628011	0.65	0.0035	1.34	0.65	0.3949	0.64	0.66	0.52	0.76	4.38	0.001	0.0069	0.009
3628052	0.65	0.0049	1.33	0.66	0.3262	0.53	0.73	0.53	0.73	5.43	0.0016	0.0066	0.0109
3628057	0.67	0.0011	1.27	0.66	0.3262	0.47	0.77	0.54	0.72	5.14	0.0044	0.0029	0.0026
3628471	0.67	0.0017	1.57	0.65	0.3949	0.66	0.65	0.52	0.77	6.06	0.0012	0.0019	0.0018
3628924	0.66	0.0032	1.49	0.65	0.3949	0.53	0.72	0.52	0.73	4.6	0.0034	0.0059	0.0059
3630191	0.67	0.0013	1.44	0.67	0.206	0.68	0.67	0.54	0.79	6.28	0.0001	0.0005	0.0011
3631414	0.67	0.0012	1.27	0.7	0.0837	0.47	0.83	0.61	0.73	4.2	0.0001	0.0009	0.0028
3632170	0.64	0.0069	1.48	0.6	0.7956	0.72	0.54	0.47	0.77	5.68	0.004	0.0049	0.0059
3633110	0.64	0.0076	1.38	0.62	0.6786	0.6	0.63	0.48	0.73	3.97	0.0181	0.0128	0.0112
3633223	0.62	0.0265	1.27	0.6	0.8429	0.68	0.55	0.46	0.75	6.34	0.0105	0.0166	0.0227
3633226	0.63	0.018	1.53	0.63	0.611	0.55	0.67	0.49	0.72	3.92	0.0118	0.0061	0.0099
3634074	0.64	0.0094	1.51	0.62	0.6786	0.62	0.62	0.48	0.74	5.42	0.0068	0.0066	0.0094
3643958	0.64	0.0089	1.36	0.62	0.6786	0.62	0.62	0.48	0.74	5.59	0.0059	0.0115	0.013
3645267	0.63	0.0116	1.25	0.6	0.7956	0.74	0.52	0.47	0.78	6.59	0.0032	0.0073	0.0097
3645314	0.64	0.0079	1.36	0.58	0.914	0.7	0.51	0.45	0.75	5.52	0.0194	0.0077	0.0085
3645591	0.61	0.0477	1.17	0.57	0.9388	0.57	0.57	0.44	0.7	4.87	0.0798	0.0571	0.0696
3647535	0.63	0.0141	1.39	0.63	0.611	0.57	0.66	0.49	0.73	5.33	0.0054	0.0127	0.0195
3648373	0.62	0.0192	1.3	0.6	0.7956	0.51	0.66	0.46	0.7	4.56	0.0464	0.0213	0.0307
3651472	0.63	0.0125	1.31	0.63	0.611	0.55	0.67	0.49	0.72	5.07	0.0087	0.0118	0.0152
3653349	0.63	0.0134	1.29	0.64	0.4669	0.57	0.68	0.51	0.74	4.92	0.0024	0.0178	0.0289
3653673	0.66	0.0026	1.39	0.64	0.4669	0.72	0.6	0.51	0.79	6.18	0.0003	0.0019	0.0024
3655101	0.61	0.0373	1.62	0.64	0.5397	0.57	0.67	0.5	0.73	4.38	0.0052	0.0095	0.0167
3658610	0.68	0.0005	1.35	0.68	0.1571	0.6	0.73	0.56	0.76	5.67	0.0001	0.0001	0.0006
3659201	0.62	0.0224	1.38	0.63	0.611	0.55	0.67	0.49	0.72	5.26	0.0072	0.0173	0.0306
3659319	0.7	0.0002	1.51	0.68	0.1571	0.62	0.72	0.56	0.77	5.12	0.0002	0.0005	0.0007
3660917	0.66	0.0025	1.43	0.65	0.3949	0.68	0.63	0.52	0.78	2.94	0.0004	0.0073	0.0079
3660927	0.6	0.0506	1.23	0.6	0.7956	0.4	0.72	0.45	0.68	4.1	0.0736	0.0422	0.0706
3665635	0.66	0.0033	1.7	0.58	0.914	0.57	0.59	0.44	0.71	5.46	0.0453	0.0033	0.0052
3666111	0.68	0.0009	1.34	0.68	0.1571	0.55	0.76	0.57	0.75	4.13	0.0004	0.0007	0.0014

3666869	0.67	0.0013	1.75	0.68	0.1571	0.6	0.73	0.56	0.76	4.84	0.0002	0.0012	0.0015
3668992	0.61	0.0405	1.32	0.63	0.611	0.51	0.7	0.49	0.71	4.51	0.0096	0.0199	0.0326
3671113	0.59	0.0777	1.09	0.57	0.9577	0.38	0.67	0.4	0.65	4.65	0.5046	0.0513	0.0935
3677863	0.65	0.0042	1.33	0.65	0.3949	0.57	0.7	0.52	0.74	5.13	0.0038	0.0079	0.0075
3679601	0.62	0.02	1.24	0.59	0.8822	0.49	0.65	0.44	0.69	4.34	0.0902	0.0218	0.034
3683054	0.67	0.0019	1.65	0.64	0.5397	0.7	0.6	0.5	0.78	5.14	0.0011	0.0009	0.0015
3685080	0.6	0.05	1.31	0.62	0.6786	0.53	0.67	0.48	0.71	3.73	0.0116	0.0222	0.0435
3687262	0.66	0.0028	1.31	0.63	0.611	0.74	0.56	0.49	0.79	8.06	0.0009	0.0017	0.0019
3687792	0.62	0.0289	1.59	0.64	0.4669	0.66	0.63	0.51	0.76	5.54	0.0014	0.0098	0.0137
3690089	0.65	0.0037	1.4	0.62	0.6786	0.7	0.57	0.49	0.77	4.87	0.0027	0.0026	0.0037
3692857	0.64	0.0074	1.44	0.63	0.611	0.57	0.66	0.49	0.73	5.27	0.0051	0.0088	0.011
3693546	0.67	0.0016	1.42	0.62	0.6786	0.64	0.61	0.48	0.75	5.36	0.0037	0.0012	0.0023
3693711	0.66	0.0032	1.59	0.65	0.3949	0.72	0.61	0.52	0.79	4.56	0.0001	0.002	0.0038
3693737	0.65	0.0049	1.32	0.67	0.206	0.66	0.68	0.54	0.78	7.29	0.0002	0.0034	0.004
3693746	0.63	0.0116	1.38	0.64	0.4669	0.51	0.72	0.51	0.72	4.52	0.007	0.0136	0.0283
3696670	0.55	0.0049	1.36	0.67	0.2627	0.57	0.72	0.54	0.75	5.19	0.0007	0.0108	0.0113
3697925	0.67	0.0012	1.28	0.65	0.3949	0.55	0.71	0.52	0.73	4.78	0.0059	0.0016	0.0025
3699559	0.66	0.0021	1.28	0.62	0.6786	0.53	0.67	0.48	0.71	4.94	0.0137	0.0019	0.0032
3701588	0.65	0.0042	1.25	0.6	0.7956	0.57	0.62	0.47	0.72	5.79	0.0464	0.0105	0.0084
3705531	0.63	0.0155	1.5	0.65	0.3949	0.45	0.77	0.53	0.71	4.03	0.0055	0.007	0.0163
3707211	0.64	0.0089	1.5	0.64	0.4669	0.6	0.67	0.51	0.74	5.44	0.0026	0.0078	0.0077
3708006	0.64	0.0104	1.58	0.63	0.611	0.7	0.59	0.49	0.77	6.36	0.0013	0.0032	0.005
3709275	0.6	0.0517	1.31	0.6	0.8429	0.51	0.65	0.45	0.7	5.13	0.0444	0.0247	0.052
3710735	0.65	0.004	1.28	0.65	0.3949	0.7	0.62	0.52	0.78	3.96	0.0007	0.0101	0.0101
3714102	0.67	0.0018	1.4	0.62	0.6786	0.6	0.63	0.48	0.73	5.18	0.0103	0.0017	0.0022
3715142	0.67	0.0018	1.42	0.67	0.2627	0.68	0.66	0.53	0.78	5.36	0.0002	0.0009	0.0019
3715434	0.6	0.0586	1.23	0.6	0.8429	0.47	0.67	0.45	0.69	4.94	0.0832	0.0439	0.0499
3716021	0.65	0.0036	1.39	0.61	0.7405	0.68	0.57	0.48	0.76	4.6	0.0032	0.0022	0.0051
3716674	0.61	0.036	1.29	0.6	0.8429	0.62	0.59	0.46	0.73	5.02	0.0279	0.0424	0.043
3716757	0.66	0.0033	1.26	0.68	0.1571	0.57	0.74	0.56	0.75	5.68	0.0002	0.0027	0.0044
3717647	0.65	0.0038	1.3	0.68	0.1571	0.6	0.73	0.56	0.76	5.16	0.0001	0.0097	0.0109
3717681	0.61	0.0401	1.39	0.66	0.3262	0.57	0.71	0.53	0.74	5.44	0.0021	0.0178	0.0223
3717684	0.63	0.0157	1.36	0.67	0.206	0.64	0.7	0.55	0.77	7.02	0.0001	0.0087	0.0103
3718837	0.66	0.0025	1.31	0.57	0.9388	0.83	0.43	0.45	0.81	6.39	0.0049	0.0032	0.004
3719123	0.52	0.0192	1.63	0.63	0.611	0.49	0.71	0.49	0.71	4.59	0.0096	0.0043	0.01
3720778	0.64	0.0083	1.43	0.67	0.2627	0.6	0.71	0.54	0.75	5.65	0.0004	0.0037	0.0059
3720990	0.66	0.0031	1.28	0.64	0.5397	0.62	0.65	0.5	0.75	6.82	0.0019	0.0016	0.0042
3722990	0.65	0.0053	1.3	0.64	0.4669	0.55	0.7	0.51	0.73	3.96	0.0066	0.004	0.0049
3723305	0.66	0.0027	1.54	0.6	0.8429	0.64	0.57	0.46	0.73	5.32	0.0222	0.0034	0.0037
3726811	0.63	0.011	1.39	0.6	0.7956	0.47	0.68	0.46	0.69	4.59	0.095	0.0156	0.0193
3728316	0.66	0.0026	1.28	0.64	0.4669	0.6	0.67	0.51	0.74	5.72	0.004	0.0048	0.004
3729194	0.63	0.012	1.37	0.64	0.4669	0.6	0.67	0.51	0.74	4.31	0.0047	0.0118	0.015
3729227	0.65	0.0035	1.38	0.64	0.4669	0.66	0.63	0.51	0.76	6.03	0.0013	0.0027	0.0037

3732475	0.67	0.0019	1.42	0.69	0.1164	0.66	0.71	0.56	0.78	5.02	0	0.0006	0.0012
3732477	0.61	0.0382	1.27	0.65	0.3949	0.55	0.71	0.52	0.73	4.32	0.0012	0.0183	0.0408
3732479	0.64	0.0078	1.2	0.62	0.6786	0.57	0.65	0.48	0.73	6	0.0147	0.0057	0.0084
3732480	0.71	0.0001	1.49	0.67	0.2627	0.51	0.76	0.55	0.73	3.67	0.0008	0.0001	0.0003
3734754	0.65	0.0044	1.63	0.6	0.7956	0.68	0.56	0.47	0.75	4.84	0.0055	0.0031	0.0043
3734863	0.62	0.0227	1.4	0.58	0.914	0.57	0.59	0.44	0.71	5.91	0.0653	0.0115	0.0184
3737304	0.66	0.0026	1.32	0.66	0.3262	0.55	0.72	0.53	0.74	5.76	0.0017	0.0058	0.0062
3737985	0.64	0.0107	1.29	0.64	0.5397	0.57	0.67	0.5	0.73	7.3	0.006	0.0076	0.0105
3738300	0.65	0.0052	1.35	0.62	0.6786	0.72	0.56	0.49	0.78	7	0.0018	0.0041	0.0043
3739125	0.64	0.0075	1.68	0.64	0.5397	0.55	0.68	0.5	0.73	4.35	0.0074	0.009	0.0091
3739523	0.64	0.0064	1.39	0.63	0.611	0.49	0.71	0.49	0.71	5.32	0.0265	0.0046	0.0054
3740129	0.68	0.0009	1.51	0.65	0.3949	0.68	0.63	0.52	0.78	5.48	0.0005	0.0008	0.0011
3740130	0.66	0.0033	1.74	0.64	0.5397	0.6	0.66	0.5	0.74	5.11	0.0032	0.0031	0.004
3744423	0.62	0.0205	1.34	0.62	0.6786	0.68	0.59	0.48	0.76	7.41	0.0033	0.0187	0.0252
3746953	0.66	0.0035	1.49	0.63	0.611	0.55	0.67	0.49	0.72	3.92	0.0055	0.0024	0.0074
3746967	0.62	0.021	1.3	0.63	0.611	0.49	0.71	0.49	0.71	5.09	0.0174	0.0226	0.0226
3747223	0.66	0.0025	1.46	0.71	0.0394	0.68	0.73	0.59	0.8	6.51	0	0.0018	0.0026
3748953	0.65	0.0046	1.5	0.63	0.611	0.66	0.61	0.49	0.76	4.76	0.0036	0.0026	0.0032
3750786	0.64	0.0106	1.39	0.62	0.6786	0.68	0.59	0.48	0.76	5.19	0.0022	0.0074	0.0096
3752711	0.62	0.0208	1.43	0.58	0.914	0.7	0.51	0.45	0.75	5.53	0.0183	0.0168	0.0209
3754530	0.67	0.0013	1.41	0.67	0.206	0.68	0.67	0.54	0.79	4.81	0.0001	0.0012	0.0022
3754741	0.65	0.0052	1.32	0.62	0.6786	0.55	0.66	0.48	0.72	4.2	0.0157	0.0205	0.0226
3756204	0.65	0.0036	1.29	0.62	0.6786	0.55	0.66	0.48	0.72	6.43	0.0107	0.0024	0.0045
3759590	0.64	0.0077	1.26	0.6	0.7956	0.51	0.66	0.46	0.7	4.12	0.063	0.0076	0.0139
3760197	0.64	0.0084	1.36	0.57	0.9577	0.62	0.54	0.43	0.71	4.29	0.103	0.0105	0.0095
3761752	0.64	0.0082	1.34	0.64	0.5397	0.57	0.67	0.5	0.73	4.64	0.0083	0.0121	0.009
3762575	0.66	0.0024	1.36	0.6	0.7956	0.55	0.63	0.46	0.71	5.25	0.0315	0.0031	0.0044
3764121	0.65	0.004	1.38	0.6	0.7956	0.7	0.55	0.47	0.76	6.01	0.0048	0.0032	0.0045
3764125	0.65	0.0043	1.26	0.64	0.4669	0.68	0.62	0.51	0.77	5.95	0.0004	0.0022	0.0042
3764127	0.61	0.0396	1.27	0.62	0.6786	0.51	0.68	0.48	0.71	4.58	0.0399	0.0823	0.0646
3764884	0.62	0.0219	1.45	0.61	0.7405	0.62	0.61	0.48	0.74	5.24	0.0056	0.0094	0.0145
3764921	0.67	0.0011	1.45	0.64	0.5397	0.6	0.66	0.5	0.74	6.37	0.0063	0.001	0.0014
3765738	0.62	0.0285	1.26	0.64	0.5397	0.53	0.7	0.5	0.72	4.53	0.0067	0.0121	0.025
3765761	0.63	0.0177	1.33	0.61	0.7405	0.64	0.6	0.48	0.74	5.54	0.007	0.01	0.0168
3765767	0.6	0.0523	1.34	0.63	0.611	0.53	0.68	0.49	0.72	3.88	0.0161	0.0448	0.0597
3766896	0.63	0.0116	1.42	0.63	0.611	0.55	0.67	0.49	0.72	4.97	0.0094	0.0132	0.0153
3768039	0.65	0.0053	1.33	0.65	0.3949	0.45	0.77	0.53	0.71	4.65	0.0056	0.0125	0.0177
3768121	0.61	0.0387	1.2	0.64	0.5397	0.55	0.68	0.5	0.73	4.85	0.0059	0.0523	0.0601
3768258	0.68	0.0008	1.31	0.64	0.5397	0.6	0.66	0.5	0.74	4.37	0.0036	0.0021	0.0025
3769780	0.63	0.0153	1.28	0.63	0.611	0.62	0.63	0.49	0.74	6.1	0.003	0.01	0.014
3770244	0.64	0.0077	1.27	0.64	0.4669	0.6	0.67	0.51	0.74	7.96	0.0021	0.0042	0.0065
3770564	0.62	0.0248	1.39	0.59	0.8822	0.68	0.54	0.46	0.75	5.86	0.0126	0.0163	0.0233
3770565	0.61	0.0445	1.34	0.59	0.8822	0.64	0.56	0.45	0.73	6.17	0.0204	0.0246	0.0375

3770746	0.64	0.0079	1.38	0.63	0.611	0.62	0.63	0.49	0.74	6.91	0.0041	0.005	0.0051
3771039	0.58	0.1262	1.17	0.61	0.7405	0.45	0.71	0.47	0.69	4.99	0.0524	0.1338	0.1718
3771094	0.65	0.0061	1.54	0.63	0.611	0.51	0.7	0.49	0.71	4.22	0.0283	0.006	0.0058
3771337	0.63	0.0118	1.62	0.62	0.6786	0.57	0.65	0.48	0.73	4.57	0.014	0.0105	0.0118
3776189	0.67	0.0017	1.42	0.64	0.4669	0.7	0.61	0.51	0.78	5.63	0.0005	0.002	0.0023
3776219	0.61	0.0303	1.34	0.61	0.7405	0.51	0.67	0.47	0.71	4.14	0.0576	0.0301	0.029
3776236	0.62	0.0216	1.3	0.64	0.5397	0.38	0.78	0.5	0.69	3.83	0.0895	0.0201	0.0168
3776446	0.65	0.0063	1.83	0.61	0.7405	0.6	0.62	0.47	0.73	4.65	0.011	0.0043	0.0067
3776461	0.66	0.0035	1.38	0.61	0.7405	0.57	0.63	0.47	0.72	6.35	0.0166	0.0032	0.0038
3778266	0.69	0.0004	1.3	0.66	0.3262	0.62	0.68	0.53	0.76	6.28	0.0007	0.0007	0.0008
3778629	0.68	0.0006	1.5	0.67	0.2627	0.68	0.66	0.53	0.78	6.12	0.0002	0.0005	0.001
3778630	0.67	0.0016	1.42	0.59	0.8822	0.64	0.56	0.45	0.73	6.07	0.0233	0.0015	0.0022
3779850	0.65	0.0059	1.27	0.61	0.7405	0.3	0.79	0.45	0.66	4.46	0.2066	0.0216	0.0261
3781686	0.58	0.1481	1.2	0.57	0.9388	0.26	0.76	0.38	0.64	3.81	0.7859	0.2517	0.3776
3781689	0.65	0.0035	1.33	0.62	0.6786	0.55	0.66	0.48	0.72	5.5	0.0144	0.0028	0.0054
3783364	0.65	0.004	1.29	0.59	0.8822	0.57	0.6	0.45	0.71	6.36	0.0381	0.0027	0.0053
3787934	0.67	0.0013	1.31	0.67	0.2627	0.6	0.71	0.54	0.75	6.23	0.0006	0.0003	0.0008
3789817	0.65	0.0035	1.47	0.64	0.4669	0.6	0.67	0.51	0.74	5.01	0.002	0.0033	0.0053
3795442	0.63	0.0153	1.26	0.6	0.8429	0.43	0.7	0.44	0.68	4.16	0.1521	0.0254	0.0278
3796554	0.6	0.0529	1.21	0.57	0.9577	0.53	0.59	0.42	0.69	3.93	0.1323	0.0387	0.0638
3798470	0.67	0.0014	1.43	0.65	0.3949	0.55	0.71	0.52	0.73	6.12	0.0023	0.001	0.002
3800623	0.6	0.0619	1.27	0.59	0.8822	0.55	0.61	0.45	0.7	4.69	0.0615	0.0437	0.0506
3804170	0.65	0.004	1.33	0.61	0.7405	0.62	0.61	0.48	0.74	4.18	0.013	0.0044	0.0062
3804202	0.61	0.0356	1.29	0.62	0.6786	0.53	0.67	0.48	0.71	4.53	0.0156	0.0195	0.0308
3806255	0.66	0.0029	1.4	0.64	0.5397	0.68	0.61	0.5	0.77	6.51	0.0011	0.0018	0.0026
3806256	0.62	0.0197	1.3	0.62	0.6786	0.57	0.65	0.48	0.73	4.27	0.0173	0.0134	0.0211
3807476	0.64	0.0101	1.46	0.65	0.3949	0.57	0.7	0.52	0.74	4.79	0.0012	0.0045	0.0093
3807570	0.61	0.0369	1.14	0.63	0.611	0.36	0.78	0.49	0.68	4.41	0.0377	0.0102	0.0292
3807629	0.62	0.0189	1.2	0.64	0.5397	0.43	0.76	0.5	0.7	4.45	0.0242	0.004	0.0124
3808602	0.67	0.001	1.41	0.64	0.4669	0.7	0.61	0.51	0.78	7.12	0.0005	0.0009	0.0011
3809343	0.65	0.0062	1.42	0.59	0.8822	0.66	0.55	0.46	0.74	5.22	0.0186	0.0045	0.0064
3809673	0.64	0.0076	1.36	0.62	0.6786	0.68	0.59	0.48	0.76	6.13	0.0028	0.0056	0.0077
3809834	0.67	0.0012	1.27	0.66	0.3262	0.51	0.74	0.53	0.73	5.06	0.0065	0.0012	0.0017
3813298	0.66	0.0027	1.35	0.64	0.5397	0.51	0.71	0.5	0.72	5.9	0.01	0.0007	0.0025
3813299	0.6	0.05	1.17	0.6	0.7956	0.45	0.7	0.46	0.69	4.53	0.058	0.0182	0.0544
3815669	0.62	0.0224	1.42	0.58	0.914	0.64	0.55	0.45	0.73	4.46	0.0381	0.0168	0.0211
3816402	0.63	0.012	1.41	0.62	0.6786	0.6	0.63	0.48	0.73	4.6	0.0104	0.0143	0.0182
3820658	0.63	0.0147	1.29	0.57	0.9577	0.74	0.46	0.44	0.76	5.83	0.0247	0.0158	0.0184
3820705	0.63	0.0177	1.23	0.6	0.8429	0.62	0.59	0.46	0.73	6.02	0.0203	0.0154	0.0197
3820721	0.63	0.0132	1.3	0.58	0.914	0.7	0.51	0.45	0.75	5.6	0.0253	0.0141	0.0153
3820752	0.62	0.0285	1.22	0.6	0.8429	0.55	0.62	0.46	0.71	4.6	0.0444	0.038	0.0291
3822055	0.62	0.0296	1.37	0.61	0.7405	0.6	0.62	0.47	0.73	5.94	0.0089	0.0203	0.0324
3825428	0.65	0.0046	1.55	0.61	0.7405	0.64	0.6	0.48	0.74	5.55	0.006	0.0035	0.0041

3829039	0.65	0.0043	1.47	0.63	0.611	0.53	0.68	0.49	0.72	5.01	0.0099	0.0038	0.006
3829810	0.66	0.0027	1.52	0.6	0.7956	0.66	0.57	0.47	0.75	5.69	0.0069	0.0026	0.0037
3831128	0.63	0.0147	1.71	0.64	0.4669	0.66	0.63	0.51	0.76	4.79	0.0007	0.0056	0.0076
3831280	0.64	0.0073	1.28	0.62	0.6786	0.62	0.62	0.48	0.74	7.53	0.0063	0.0038	0.0054
3835412	0.64	0.007	1.57	0.62	0.6786	0.51	0.68	0.48	0.71	3.89	0.026	0.0194	0.0239
3837493	0.63	0.0145	1.29	0.59	0.8822	0.53	0.62	0.45	0.7	5.53	0.081	0.015	0.0197
3838612	0.63	0.017	1.31	0.64	0.4669	0.57	0.68	0.51	0.74	5.57	0.0031	0.0112	0.0165
3838790	0.64	0.0073	1.23	0.63	0.611	0.45	0.73	0.49	0.7	4.89	0.0206	0.0103	0.0144
3840344	0.67	0.0014	1.39	0.61	0.7405	0.57	0.63	0.47	0.72	5.71	0.023	0.0007	0.0014
3841271	0.61	0.0307	1.24	0.63	0.611	0.47	0.72	0.49	0.7	4.87	0.0209	0.0269	0.0454
3843668	0.67	0.0013	1.32	0.66	0.3262	0.51	0.74	0.53	0.73	4.81	0.0019	0.0024	0.0037
3845710	0.66	0.0032	1.4	0.6	0.8429	0.74	0.51	0.47	0.78	6.23	0.0063	0.0046	0.0045
3846115	0.61	0.0477	1.36	0.65	0.3949	0.6	0.68	0.52	0.75	5.06	0.0019	0.035	0.043
3846291	0.61	0.0327	1.26	0.61	0.7405	0.57	0.63	0.47	0.72	4.48	0.0218	0.044	0.0396
3846561	0.64	0.008	1.29	0.6	0.8429	0.68	0.55	0.46	0.75	7.21	0.0082	0.0079	0.0119
3846784	0.63	0.0113	1.53	0.6	0.7956	0.7	0.55	0.47	0.76	5.8	0.0061	0.0049	0.0068
3847357	0.65	0.0041	1.41	0.62	0.6786	0.72	0.56	0.49	0.78	6.78	0.0021	0.0048	0.0053
3849774	0.61	0.0327	1.33	0.62	0.6786	0.51	0.68	0.48	0.71	6.01	0.0264	0.0369	0.0358
3849776	0.67	0.0019	1.32	0.66	0.3262	0.55	0.72	0.53	0.74	5.29	0.0016	0.0025	0.0039
3850502	0.67	0.0016	1.36	0.64	0.4669	0.7	0.61	0.51	0.78	5.58	0.0006	0.0018	0.0015
3851604	0.63	0.0141	1.29	0.63	0.611	0.68	0.6	0.49	0.77	6.87	0.0023	0.0116	0.0134
3851902	0.64	0.0089	1.45	0.64	0.4669	0.66	0.63	0.51	0.76	5.42	0.0008	0.0065	0.0118
3854371	0.65	0.0062	1.46	0.65	0.3949	0.47	0.76	0.52	0.71	3.76	0.006	0.0124	0.0185
3855101	0.65	0.0045	1.28	0.64	0.5397	0.66	0.62	0.5	0.76	6.28	0.0013	0.0035	0.0064
3856046	0.61	0.0364	1.3	0.61	0.7405	0.36	0.76	0.46	0.67	4.68	0.1657	0.0462	0.0432
3857120	0.6	0.0511	1.22	0.63	0.611	0.49	0.71	0.49	0.71	4.3	0.02	0.0261	0.0385
3857884	0.69	0.0003	1.32	0.69	0.1164	0.68	0.7	0.56	0.79	5.03	0	0.0003	0.0007
3862168	0.65	0.0048	1.3	0.62	0.6786	0.72	0.56	0.49	0.78	8.35	0.0018	0.0049	0.0058
3862473	0.64	0.0107	1.27	0.58	0.914	0.62	0.56	0.45	0.72	6.29	0.0381	0.0067	0.0061
3867099	0.61	0.0335	1.35	0.66	0.3262	0.6	0.7	0.53	0.75	5.64	0.0012	0.0235	0.0307
3869659	0.6	0.0676	1.33	0.6	0.7956	0.53	0.65	0.46	0.71	4.49	0.0612	0.064	0.0637
3869971	0.66	0.0027	1.45	0.65	0.3949	0.51	0.73	0.52	0.72	4.79	0.0054	0.0015	0.0027
3870593	0.67	0.0013	1.32	0.69	0.1164	0.7	0.68	0.56	0.8	6.4	0	0.0012	0.0015
3872197	0.66	0.0021	1.77	0.7	0.0837	0.7	0.7	0.57	0.8	5.29	0	0.0009	0.0011
3872208	0.64	0.0093	1.26	0.63	0.611	0.62	0.63	0.49	0.74	5.59	0.0056	0.0083	0.0088
3874114	0.62	0.0239	1.26	0.64	0.5397	0.53	0.7	0.5	0.72	3.09	0.0103	0.0407	0.0433
3874280	0.66	0.0033	1.36	0.62	0.6786	0.72	0.56	0.49	0.78	7.63	0.0019	0.0027	0.0032
3875278	0.61	0.0351	1.34	0.6	0.7956	0.6	0.61	0.47	0.72	4.85	0.0204	0.0204	0.0283
3878051	0.62	0.0216	1.56	0.64	0.5397	0.57	0.67	0.5	0.73	4.85	0.0043	0.0109	0.0122
3878053	0.68	0.0009	1.38	0.67	0.2627	0.7	0.65	0.53	0.79	7.19	0.0001	0.0006	0.0009
3879490	0.62	0.0194	1.31	0.61	0.7405	0.51	0.67	0.47	0.71	3.19	0.0306	0.0149	0.0286
3881731	0.66	0.0032	1.61	0.6	0.7956	0.66	0.57	0.47	0.75	4.79	0.0098	0.003	0.0032
3881914	0.62	0.0221	1.28	0.59	0.8822	0.6	0.59	0.45	0.72	6.02	0.0309	0.0181	0.0348

3882710	0.63	0.0143	1.48	0.61	0.7405	0.62	0.61	0.48	0.74	6.5	0.0107	0.01	0.0129
3882867	0.65	0.0042	1.48	0.65	0.3949	0.55	0.71	0.52	0.73	5.07	0.0034	0.0064	0.0082
3883424	0.69	0.0003	1.3	0.64	0.4669	0.66	0.63	0.51	0.76	6.99	0.0011	0.0003	0.0007
3883533	0.67	0.0016	1.31	0.7	0.0837	0.7	0.7	0.57	0.8	6.28	0	0.0012	0.0017
3883537	0.63	0.0126	1.35	0.64	0.4669	0.55	0.7	0.51	0.73	6.1	0.0035	0.0079	0.0117
3883987	0.69	0.0003	1.3	0.6	0.7956	0.81	0.49	0.48	0.82	5.1	0.001	0.0005	0.0006
3884147	0.66	0.0026	1.36	0.64	0.4669	0.66	0.63	0.51	0.76	5.72	0.0007	0.0034	0.0057
3884334	0.69	0.0004	1.33	0.64	0.5397	0.38	0.78	0.5	0.69	4.08	0.0538	0.0053	0.0029
3884673	0.61	0.0339	1.26	0.64	0.4669	0.45	0.76	0.51	0.7	4.09	0.0145	0.0108	0.0227
3884709	0.68	0.0006	1.26	0.68	0.1571	0.55	0.76	0.57	0.75	5.2	0.0002	0.0005	0.0008
3885711	0.62	0.0205	1.26	0.64	0.5397	0.72	0.59	0.5	0.79	6.2	0.0006	0.0116	0.0164
3886656	0.66	0.0027	1.42	0.65	0.3949	0.51	0.73	0.52	0.72	5.21	0.0059	0.005	0.006
3886907	0.67	0.0011	1.34	0.71	0.0583	0.62	0.76	0.59	0.78	6.13	0	0.0009	0.0025
3887661	0.64	0.0076	1.25	0.65	0.3949	0.47	0.76	0.52	0.71	3.9	0.0078	0.0067	0.011
3888081	0.65	0.0039	1.34	0.67	0.2627	0.57	0.72	0.54	0.75	5.12	0.0004	0.002	0.0055
3888182	0.65	0.0055	1.35	0.6	0.7956	0.74	0.52	0.47	0.78	6.68	0.003	0.006	0.0055
3888253	0.67	0.0016	1.34	0.66	0.3262	0.62	0.68	0.53	0.76	5.99	0.0005	0.0015	0.002
3888289	0.65	0.0044	1.52	0.63	0.611	0.7	0.59	0.49	0.77	5.77	0.002	0.0022	0.0035
3888494	0.63	0.0137	1.3	0.63	0.611	0.62	0.63	0.49	0.74	6.08	0.0054	0.0136	0.0152
3888936	0.63	0.0118	1.28	0.61	0.7405	0.55	0.65	0.47	0.72	5.35	0.0332	0.0155	0.014
3889140	0.68	0.0009	1.29	0.64	0.5397	0.62	0.65	0.5	0.75	6.04	0.0016	0.0001	0.0011
3889782	0.66	0.0031	1.5	0.63	0.611	0.53	0.68	0.49	0.72	3.77	0.0084	0.0023	0.0043
3891221	0.62	0.0197	1.39	0.62	0.6786	0.6	0.63	0.48	0.73	4.77	0.0144	0.0114	0.0191
3891257	0.69	0.0003	1.34	0.67	0.2627	0.7	0.65	0.53	0.79	7.71	0.0001	0.0002	0.0005
3892672	0.67	0.0015	1.27	0.66	0.3262	0.66	0.66	0.53	0.77	7.8	0.0003	0.0013	0.0033
3894074	0.62	0.0258	1.31	0.61	0.7405	0.53	0.66	0.47	0.71	3.6	0.0323	0.0068	0.0165
3894508	0.67	0.0011	1.54	0.66	0.3262	0.64	0.67	0.53	0.76	5.69	0.0005	0.0006	0.0008
3894602	0.63	0.011	1.47	0.62	0.6786	0.64	0.61	0.48	0.75	5.61	0.0054	0.0069	0.0081
3895000	0.64	0.0098	1.4	0.66	0.3262	0.66	0.66	0.53	0.77	6.34	0.0004	0.007	0.0085
3896202	0.61	0.0311	1.33	0.59	0.8822	0.51	0.63	0.44	0.69	5.28	0.0961	0.026	0.033
3898306	0.59	0.0845	1.27	0.6	0.8429	0.51	0.65	0.45	0.7	3.14	0.1419	0.3259	0.2322
3901666	0.63	0.0155	1.39	0.6	0.8429	0.68	0.55	0.46	0.75	6.28	0.0099	0.0147	0.0219
3902984	0.66	0.0031	1.41	0.61	0.7405	0.55	0.65	0.47	0.72	5.3	0.023	0.0045	0.0054
3903290	0.67	0.0016	1.36	0.66	0.3262	0.66	0.66	0.53	0.77	6.63	0.0004	0.0012	0.0012
3904028	0.63	0.0121	1.35	0.6	0.7956	0.26	0.8	0.43	0.65	4.19	0.4545	0.0146	0.0257
3904029	0.67	0.0017	1.31	0.68	0.1571	0.64	0.71	0.56	0.77	8.48	0.0002	0.0004	0.0012
3904255	0.66	0.0026	1.28	0.61	0.7405	0.66	0.59	0.48	0.75	5.33	0.0098	0.0063	0.0058
3904257	0.66	0.0025	1.33	0.64	0.4669	0.77	0.57	0.51	0.81	6.08	0.0002	0.0021	0.002
3904276	0.64	0.0074	1.25	0.61	0.7405	0.53	0.66	0.47	0.71	4.43	0.04	0.0169	0.0186
3904281	0.61	0.0311	1.23	0.64	0.4669	0.45	0.76	0.51	0.7	5.04	0.0066	0.0115	0.018
3906196	0.65	0.005	1.35	0.64	0.4669	0.64	0.65	0.51	0.76	4.26	0.0013	0.0033	0.0065
3907788	0.62	0.0197	1.49	0.63	0.611	0.68	0.6	0.49	0.77	4.76	0.0018	0.0149	0.0156
3908789	0.65	0.0037	1.33	0.67	0.2627	0.68	0.66	0.53	0.78	7.31	0.0002	0.0015	0.0018

3909376	0.61	0.0351	1.28	0.61	0.7405	0.49	0.68	0.47	0.7	3.78	0.0202	0.0082	0.0186
3911474	0.67	0.001	1.47	0.64	0.5397	0.68	0.61	0.5	0.77	6.61	0.0012	0.0006	0.0009
3911564	0.69	0.0004	1.46	0.72	0.0257	0.7	0.73	0.6	0.81	5.98	0	0.0001	0.0003
3911706	0.66	0.0028	1.33	0.67	0.206	0.64	0.7	0.55	0.77	5.67	0.0003	0.002	0.0035
3911738	0.69	0.0004	1.34	0.64	0.5397	0.74	0.57	0.5	0.8	7.01	0.0008	0.0005	0.0007
3911801	0.66	0.0032	1.5	0.64	0.4669	0.66	0.63	0.51	0.76	5.97	0.0009	0.0013	0.0025
3911815	0.63	0.0147	1.61	0.64	0.4669	0.64	0.65	0.51	0.76	5.17	0.0017	0.0056	0.0084
3913564	0.62	0.021	1.33	0.58	0.914	0.6	0.57	0.44	0.71	4.54	0.0681	0.0283	0.0207
3915125	0.68	0.0007	1.5	0.65	0.3949	0.45	0.77	0.53	0.71	3.94	0.0104	0.0006	0.0011
3917896	0.67	0.0013	1.51	0.64	0.4669	0.66	0.63	0.51	0.76	5.34	0.001	0.0018	0.0021
3918586	0.66	0.0029	1.54	0.69	0.1164	0.53	0.78	0.58	0.74	3.89	0.0002	0.0015	0.0026
3918651	0.6	0.0729	1.27	0.6	0.8429	0.55	0.62	0.46	0.71	4.26	0.0417	0.0294	0.047
3918723	0.67	0.0016	1.36	0.66	0.3262	0.7	0.63	0.52	0.79	5.83	0.0002	0.0011	0.0024
3918734	0.65	0.0045	1.42	0.64	0.4669	0.6	0.67	0.51	0.74	4.32	0.0012	0.0022	0.0053
3919024	0.66	0.0033	1.4	0.65	0.3949	0.81	0.56	0.51	0.84	6.04	0.0001	0.0017	0.0017
3920401	0.65	0.0051	1.49	0.65	0.3949	0.55	0.71	0.52	0.73	4.13	0.0024	0.0094	0.0119
3920456	0.65	0.0036	1.28	0.62	0.6786	0.7	0.57	0.49	0.77	6.29	0.0018	0.002	0.0031
3920487	0.65	0.004	1.33	0.64	0.4669	0.62	0.66	0.51	0.75	4.86	0.0025	0.0027	0.0048
3922023	0.63	0.0151	1.41	0.64	0.5397	0.34	0.8	0.5	0.68	4.47	0.0392	0.0078	0.0196
3922993	0.66	0.0023	1.4	0.66	0.3262	0.7	0.63	0.52	0.79	4.05	0.0002	0.0047	0.0096
3924758	0.66	0.0021	1.41	0.63	0.611	0.51	0.7	0.49	0.71	4.23	0.0233	0.0111	0.0087
3925641	0.66	0.0024	1.32	0.67	0.2627	0.45	0.79	0.55	0.71	5.47	0.0014	0.0037	0.0061
3926090	0.62	0.023	1.3	0.66	0.3262	0.47	0.77	0.54	0.72	4.34	0.003	0.0047	0.0076
3927180	0.62	0.0202	1.49	0.61	0.7405	0.55	0.65	0.47	0.72	4.11	0.0286	0.0124	0.0136
3927228	0.64	0.0068	1.32	0.58	0.914	0.79	0.46	0.46	0.79	6.3	0.0064	0.0086	0.0088
3927229	0.65	0.0049	1.42	0.63	0.611	0.74	0.56	0.49	0.79	5.47	0.001	0.0042	0.0039
3928670	0.65	0.0039	1.4	0.64	0.5397	0.66	0.62	0.5	0.76	5.02	0.0021	0.0024	0.0044
3929943	0.63	0.0128	1.38	0.6	0.7956	0.64	0.59	0.47	0.74	6.55	0.0101	0.004	0.0092
3934699	0.6	0.0511	1.4	0.62	0.6786	0.62	0.62	0.48	0.74	4.85	0.0096	0.0353	0.0411
3935246	0.6	0.0633	1.36	0.64	0.5397	0.64	0.63	0.5	0.75	4.96	0.0017	0.0527	0.0596
3935301	0.64	0.0103	1.34	0.64	0.4669	0.66	0.63	0.51	0.76	7.04	0.001	0.0068	0.0082
3936897	0.66	0.0022	1.63	0.65	0.3949	0.55	0.71	0.52	0.73	4.74	0.0033	0.0032	0.0033
3939407	0.66	0.0029	1.35	0.64	0.5397	0.72	0.59	0.5	0.79	6.88	0.0009	0.0024	0.0025
3942668	0.67	0.0015	1.35	0.64	0.4669	0.66	0.63	0.51	0.76	7.03	0.0015	0.0007	0.0011
3945331	0.65	0.0037	1.5	0.61	0.7405	0.62	0.61	0.48	0.74	5.07	0.0167	0.0063	0.0057
3945370	0.61	0.0477	1.38	0.65	0.3949	0.53	0.72	0.52	0.73	5.14	0.0021	0.0318	0.0333
3946374	0.66	0.0024	1.34	0.64	0.4669	0.45	0.76	0.51	0.7	4.9	0.0121	0.0033	0.005
3946589	0.61	0.0477	1.34	0.61	0.7405	0.57	0.63	0.47	0.72	5.01	0.0211	0.0465	0.0531
3946677	0.6	0.0517	1.3	0.61	0.7405	0.47	0.7	0.47	0.7	4.18	0.06	0.0388	0.0527
3953804	0.72	0	1.35	0.69	0.1164	0.7	0.68	0.56	0.8	4.78	0	0.0001	0.0003
3956591	0.63	0.0128	1.34	0.6	0.7956	0.66	0.57	0.47	0.75	7.26	0.0177	0.0148	0.0097
3957262	0.62	0.0197	1.44	0.64	0.5397	0.51	0.71	0.5	0.72	4.97	0.0151	0.0191	0.0191
3959259	0.63	0.0153	1.24	0.6	0.7956	0.6	0.61	0.47	0.72	5.24	0.0095	0.0044	0.0176

3959453	0.64	0.0075	1.41	0.6	0.7956	0.62	0.6	0.47	0.73	6.95	0.0154	0.0054	0.0077
3960634	0.69	0.0005	1.63	0.65	0.3949	0.68	0.63	0.52	0.78	5.83	0.0003	0.0004	0.0006
3961482	0.66	0.0026	1.4	0.61	0.7405	0.6	0.62	0.47	0.73	5.74	0.0085	0.0017	0.0028
3962268	0.66	0.0024	1.7	0.63	0.611	0.68	0.6	0.49	0.77	6.13	0.0022	0.0012	0.0019
3962596	0.68	0.0007	1.44	0.59	0.8822	0.62	0.57	0.45	0.72	5.26	0.0335	0.0009	0.0017
3969510	0.6	0.0592	1.18	0.63	0.611	0.38	0.77	0.49	0.68	4.28	0.0539	0.0442	0.062
3969511	0.62	0.0292	1.69	0.65	0.3949	0.62	0.67	0.52	0.75	5.24	0.0011	0.0074	0.0095
3970894	0.7	0.0002	1.38	0.67	0.2627	0.74	0.62	0.53	0.81	7.84	0.0001	0.0002	0.0003
3974757	0.63	0.018	1.25	0.57	0.9388	0.53	0.6	0.43	0.69	4.61	0.1211	0.0158	0.0363
3974789	0.65	0.0052	1.48	0.65	0.3949	0.64	0.66	0.52	0.76	5.33	0.0007	0.0037	0.0049
3981154	0.65	0.0044	1.57	0.64	0.4669	0.55	0.7	0.51	0.73	4.29	0.0038	0.0024	0.0047
3981752	0.61	0.0425	1.2	0.6	0.8429	0.49	0.66	0.45	0.69	5.23	0.0726	0.0207	0.0322
3981906	0.66	0.0028	1.38	0.67	0.2627	0.66	0.67	0.53	0.77	6.5	0.0002	0.0017	0.0024
3982421	0.62	0.0239	1.42	0.66	0.3262	0.66	0.66	0.53	0.77	5.88	0.0006	0.0114	0.0152
3985558	0.65	0.0056	1.35	0.65	0.3949	0.68	0.63	0.52	0.78	7.64	0.0003	0.0039	0.0055
3985635	0.69	0.0004	1.66	0.67	0.2627	0.68	0.66	0.53	0.78	4.81	0.0002	0.0007	0.0009
3986857	0.7	0.0002	1.48	0.66	0.3262	0.55	0.72	0.53	0.74	5.55	0.0029	0.0002	0.0004
3987532	0.62	0.0252	1.57	0.63	0.611	0.62	0.63	0.49	0.74	4.64	0.0043	0.0175	0.019
3988214	0.63	0.011	1.35	0.6	0.8429	0.62	0.59	0.46	0.73	5.28	0.0238	0.0204	0.0239
3989205	0.64	0.0069	1.36	0.64	0.5397	0.74	0.57	0.5	0.8	6.93	0.0005	0.0029	0.0042
3989770	0.69	0.0003	1.41	0.69	0.1164	0.6	0.74	0.57	0.76	3.58	0.0001	0.0006	0.001
3991722	0.68	0.0009	1.65	0.69	0.1164	0.64	0.72	0.57	0.78	4.63	0	0.0019	0.0021
3993347	0.64	0.0064	1.33	0.63	0.611	0.66	0.61	0.49	0.76	7.08	0.0023	0.0058	0.008
3993349	0.65	0.0058	1.34	0.6	0.7956	0.72	0.54	0.47	0.77	6.93	0.0038	0.0039	0.007
4004822	0.69	0.0003	1.29	0.65	0.3949	0.68	0.63	0.52	0.78	4.9	0.0005	0.0005	0.0009
4007593	0.62	0.0245	1.39	0.6	0.8429	0.55	0.62	0.46	0.71	5.8	0.0372	0.0264	0.0282
4009318	0.64	0.0064	1.33	0.63	0.611	0.77	0.55	0.49	0.8	7.87	0.0008	0.0037	0.0039
4009451	0.62	0.0265	1.28	0.64	0.4669	0.62	0.66	0.51	0.75	4.69	0.0012	0.0174	0.0331
4011604	0.63	0.0141	1.35	0.6	0.8429	0.68	0.55	0.46	0.75	5.87	0.0106	0.0075	0.0114
4011967	0.63	0.0151	1.27	0.64	0.4669	0.64	0.65	0.51	0.76	6.49	0.001	0.0109	0.0171
4012169	0.64	0.0073	1.29	0.67	0.206	0.6	0.72	0.55	0.76	6.4	0.0004	0.0052	0.0081
4012627	0.68	0.0008	1.39	0.68	0.1571	0.64	0.71	0.56	0.77	6.08	0.0001	0.0006	0.0009
4012632	0.61	0.0391	1.33	0.63	0.611	0.51	0.7	0.49	0.71	4.5	0.0112	0.0213	0.0316
4012759	0.64	0.007	1.56	0.64	0.5397	0.57	0.67	0.5	0.73	4.05	0.0056	0.0127	0.0139
4013274	0.65	0.0041	1.4	0.66	0.3262	0.57	0.71	0.53	0.74	4.21	0.0009	0.0074	0.0108
4013282	0.69	0.0004	1.52	0.65	0.3949	0.7	0.62	0.52	0.78	5.6	0.0004	0.0003	0.0005
4015535	0.64	0.0076	1.29	0.65	0.3949	0.6	0.68	0.52	0.75	5.28	0.0011	0.0035	0.0091
4016549	0.66	0.0031	1.48	0.67	0.2627	0.62	0.7	0.54	0.76	4.89	0.0004	0.0045	0.0074
4016573	0.66	0.0032	1.32	0.64	0.4669	0.64	0.65	0.51	0.76	7.61	0.0019	0.0023	0.0031
4019367	0.64	0.008	1.33	0.64	0.5397	0.66	0.62	0.5	0.76	5.5	0.0012	0.0038	0.0084
4019418	0.66	0.0024	1.26	0.64	0.5397	0.57	0.67	0.5	0.73	5.56	0.0056	0.0078	0.0058
4019610	0.64	0.0078	1.37	0.62	0.6786	0.74	0.55	0.49	0.79	5.86	0.0016	0.0072	0.0077
4020462	0.67	0.0012	1.26	0.63	0.611	0.36	0.78	0.49	0.68	5	0.0833	0.0045	0.0047

4024375	0.65	0.0051	1.48	0.62	0.6786	0.68	0.59	0.48	0.76	5.36	0.0037	0.0039	0.0058
4024376	0.64	0.0109	1.54	0.64	0.4669	0.6	0.67	0.51	0.74	5.29	0.0018	0.0106	0.0159
4024377	0.63	0.0141	1.31	0.6	0.8429	0.64	0.57	0.46	0.73	6.91	0.0175	0.0103	0.0137
4024378	0.62	0.0208	1.61	0.61	0.7405	0.57	0.63	0.47	0.72	5.3	0.0198	0.0133	0.0213
4024379	0.65	0.0039	1.49	0.64	0.4669	0.68	0.62	0.51	0.77	6.23	0.0008	0.0025	0.0038
4030986	0.7	0.0002	1.48	0.69	0.1164	0.6	0.74	0.57	0.76	5.29	0.0001	0.0002	0.0004
4034997	0.65	0.0056	1.39	0.66	0.3262	0.55	0.72	0.53	0.74	4.44	0.0019	0.0082	0.0113
4035834	0.64	0.0097	1.3	0.54	0.9881	0.66	0.48	0.42	0.71	6.32	0.1411	0.0154	0.016
4035835	0.67	0.0012	1.4	0.67	0.206	0.6	0.72	0.55	0.76	4.21	0.0003	0.0001	0.0007
4035838	0.63	0.0166	1.27	0.64	0.4669	0.51	0.72	0.51	0.72	7.03	0.0099	0.011	0.014
4035839	0.65	0.0058	1.31	0.63	0.611	0.57	0.66	0.49	0.73	6.89	0.0109	0.0056	0.0068
4040526	0.67	0.0013	1.37	0.62	0.6786	0.7	0.57	0.49	0.77	7.07	0.002	0.0013	0.0015
4041367	0.63	0.0147	1.28	0.58	0.914	0.51	0.62	0.44	0.69	4.36	0.151	0.0166	0.0219
4041822	0.65	0.0044	1.29	0.58	0.914	0.77	0.48	0.46	0.78	5.7	0.0066	0.0037	0.0051
4043125	0.65	0.0051	1.29	0.61	0.7405	0.55	0.65	0.47	0.72	4.38	0.0262	0.0108	0.0129
4044199	0.65	0.0056	1.22	0.64	0.4669	0.55	0.7	0.51	0.73	6.37	0.0034	0.0044	0.0069
4044413	0.63	0.0121	1.24	0.63	0.611	0.47	0.72	0.49	0.7	4.71	0.0241	0.0129	0.0129
4047577	0.63	0.0121	1.4	0.64	0.5397	0.74	0.57	0.5	0.8	5.82	0.0006	0.0086	0.0074
4052399	0.69	0.0003	1.46	0.69	0.1164	0.6	0.74	0.57	0.76	5.7	0.0001	0.0005	0.0008
4055295	0.7	0.0001	1.45	0.64	0.5397	0.62	0.65	0.5	0.75	5.94	0.0031	0.0002	0.0002
4055302	0.69	0.0004	1.29	0.69	0.1164	0.74	0.66	0.56	0.82	4.81	0	0.0005	0.001
2720180	0.61	0.0307	1.74	0.61	0.7405	0.66	0.59	0.48	0.75	4.96	0.0116	0.0244	0.0176
2347642	0.71	0.0001	1.11	0.69	0.1164	0.45	0.83	0.6	0.72	6.16	0.0001	0	0.0007
2395344	0.73	0	1.2	0.66	0.3262	0.83	0.56	0.52	0.85	4.69	0	0	0.0001
2397069	0.7	0.0002	1.15	0.69	0.1164	0.64	0.72	0.57	0.78	6.11	0	0	0.0002
2430377	0.63	0.0151	1.07	0.61	0.7405	0.53	0.66	0.47	0.71	5.43	0.034	0.0319	0.0413
2448270	0.68	0.0007	1.08	0.64	0.5397	0.62	0.65	0.5	0.75	6.9	0.005	0.0017	0.0021
2553581	0.67	0.0012	1.14	0.62	0.6786	0.66	0.6	0.48	0.75	4.92	0.0057	0.0005	0.0017
2600700	0.74	0	1.16	0.65	0.3949	0.72	0.61	0.52	0.79	4.7	0.0006	0	0.0001
2624519	0.7	0.0002	1.12	0.61	0.7405	0.72	0.55	0.48	0.78	4.56	0.0032	0.0005	0.0007
2651846	0.67	0.0011	1.16	0.64	0.5397	0.66	0.62	0.5	0.76	3.02	0.0017	0.0009	0.0024
2682441	0.69	0.0004	1.14	0.62	0.6786	0.74	0.55	0.49	0.79	5.91	0.001	0.0006	0.0015
2704512	0.74	0	1.16	0.66	0.3262	0.77	0.6	0.52	0.82	4.33	0.0001	0	0
2704702	0.74	0	1.11	0.64	0.4669	0.74	0.59	0.51	0.8	7.7	0.0004	0	0.0001
2902832	0.74	0	0.96	0.33	1	0.51	0.22	0.27	0.44	6.72	0.001	0	0.0001
2918558	0.71	0.0001	1.19	0.67	0.2627	0.4	0.82	0.56	0.71	5.01	0.0065	0.0005	0.0005
3031661	0.76	0	0.94	0.25	1	0.47	0.12	0.23	0.29	6.09	0	0	0
3212761	0.77	0	1.24	0.7	0.0837	0.77	0.66	0.56	0.83	4.25	0	0	0
3268183	0.66	0.0031	1.04	0.63	0.611	0.66	0.61	0.49	0.76	6.74	0.003	0.0036	0.0055
3472753	0.71	0.0001	0.94	0.33	1	0.36	0.32	0.23	0.46	7.02	0.0004	0.0002	0.0005
3501557	0.7	0.0002	1.22	0.66	0.3262	0.6	0.7	0.53	0.75	4.53	0.0023	0.0004	0.0005
3543621	0.65	0.0039	0.94	0.36	1	0.53	0.26	0.29	0.49	5.01	0.0111	0.0171	0.0139
3551833	0.7	0.0002	1.12	0.67	0.2627	0.6	0.71	0.54	0.75	6.09	0.0008	0.0003	0.0004

3562041	0.71	0.0001	1.27	0.7	0.0837	0.64	0.73	0.58	0.78	6.32	0	0.0002	0.0004
3661099	0.67	0.0016	1.08	0.66	0.3262	0.57	0.71	0.53	0.74	6.54	0.0022	0.0022	0.004
3667907	0.7	0.0002	1.06	0.63	0.611	0.6	0.65	0.49	0.74	7.88	0.0044	0.0003	0.0005
3701840	0.65	0.0042	1.1	0.64	0.4669	0.51	0.72	0.51	0.72	5.52	0.0072	0.0019	0.0036
3840609	0.66	0.0029	1.19	0.67	0.2627	0.4	0.82	0.56	0.71	3.06	0.0048	0.0042	0.0072
3889144	0.71	0.0001	1.13	0.64	0.4669	0.68	0.62	0.51	0.77	5.67	0.0004	0	0.0002
3889625	0.73	0	1.21	0.66	0.3262	0.66	0.66	0.53	0.77	5.21	0.0004	0	0
3897081	0.71	0.0001	1.15	0.71	0.0394	0.55	0.8	0.62	0.76	5.7	0	0.0002	0.0006
3902441	0.67	0.001	0.95	0.35	1	0.38	0.33	0.25	0.48	6.27	0.0007	0.0031	0.0047
4026042	0.66	0.0027	1.16	0.65	0.3949	0.55	0.71	0.52	0.73	7.94	0.0016	0.0004	0.0014

Performance of the 1,425 detected biomarkers across different metrics for the recurrence endpoint on the subset of patients with LNI negative (n = 129). See Example 2 for explanation of metrics.

TABLE 20

CLASSIFIER	AUC	WILC OX P- VALU E	KS P- VALU E	T- TEST P- VALU E	SE NSI TIV ITY	SPE CIF ICI TY	PP V	NP V	CUT OFF	KM P- VALU E	SU RV AU C	UVA HR P- VAL UE	UVA OR P- VAL UE
nb:3169011 3889144	0.94	0.0003	0.0002	0	0.89	0.86	0.94	0.75	0.48	0.001	0.92	0.003	0.007
knn:3169011 3840609	0.92	0.0013	0.0045	0.0001	0.83	0.86	0.94	0.67	0.53	0.0103	0.9	0.001	0.009
rf:3169011 3889144	0.92	0.0015	0.0007	0.0001	0.89	0.86	0.94	0.75	0.27	0.0013	0.94	0.004	0.01
nb:3169011 2553581	0.92	0.0005	0.0001	0.0005	0.78	1	1	0.64	0.54	0	0.89	0.002	0.011
svm:3169011 3889625	0.91	0.0008	0.0006	0.0003	0.72	1	1	0.58	0.39	0.0046	0.91	0.015	0.012
nb:3169011 3969511	0.87	0.003	0.0083	0.0016	0.83	0.86	0.94	0.67	0.54	0.0013	0.89	0.005	0.012
knn:3562041 2397069	0.87	0.0055	0.0464	0.0027	0.89	0.57	0.84	0.67	0.37	0.0167	0.85	0.006	0.012
knn:3969511 3962268	0.82	0.0049	0.0344	0.0023	0.78	0.86	0.93	0.6	0.5	0.0409	0.82	0.049	0.013
nb:3169011 3151480	0.87	0.0039	0.0018	0.0019	0.78	1	1	0.64	0.53	0.0005	0.87	0.003	0.013
svm:3169011 3661099	0.89	0.0018	0.0083	0.0006	0.72	0.86	0.93	0.55	0.23	0.0041	0.9	0.008	0.013
rf:3169011 2397069	0.86	0.0049	0.003	0.0012	0.89	0.86	0.94	0.75	0.47	0.001	0.89	0.003	0.013
nb:3169011 3498523	0.87	0.003	0.0048	0.002	0.72	0.86	0.93	0.55	0.56	0.0038	0.86	0.007	0.013
rf:3169011 3889625	0.87	0.0053	0.0227	0.0019	0.72	0.86	0.93	0.55	0.6	0.0301	0.87	0.02	0.013
nb:3169011 3212761	0.9	0.0014	0.0048	0.0018	0.72	1	1	0.58	0.54	0.0002	0.87	0.004	0.013
nb:3169011 3872197	0.87	0.003	0.0048	0.0021	0.72	0.86	0.93	0.55	0.53	0.0038	0.86	0.007	0.014
knn:3169011 3661099	0.9	0.0021	0.0073	0.0005	0.78	0.86	0.93	0.6	0.52	0.0207	0.87	0.014	0.014
nb:3169011 3831128	0.87	0.0039	0.0048	0.0035	0.72	0.86	0.93	0.55	0.54	0.0038	0.86	0.005	0.014
svm:3169011 3840609	0.93	0.0004	0.0006	0.0001	0.67	1	1	0.54	0.55	0.0017	0.92	0.001	0.015
nb:3169011	0.87	0.0039	0.0018	0.0015	0.78	1	1	0.64	0.57	0.0005	0.88	0.005	0.015

3501555

svm:3562041 3969511	0.82	0.0141	0.0325	0.0028	0.72	0.86	0.93	0.55	0.24	0.0231	0.83	0.03	0.015
svm:3169011 2553581	0.92	0.0005	0.0001	0.0005	0.61	1	1	0.5	0.46	0.0023	0.91	0.002	0.015
svm:3169011 3562041	0.94	0.0003	0.0001	0.0001	0.78	1	1	0.64	0.32	0.0005	0.93	0.001	0.015
nb:3169011 3962268	0.89	0.0018	0.0006	0.0014	0.72	1	1	0.58	0.55	0.0002	0.85	0.004	0.015
svm:3169011 3151480	0.87	0.0039	0.0018	0.0021	0.72	1	1	0.58	0.32	0.0002	0.86	0.004	0.016
rf:3169011 3501555	0.84	0.011	0.0104	0.0035	0.78	0.86	0.93	0.6	0.53	0.0054	0.85	0.008	0.016
nb:3169011 2553585	0.84	0.0076	0.0048	0.0029	0.72	1	1	0.58	0.55	0.0002	0.85	0.005	0.016
svm:3169011 3551833	0.9	0.0014	0.003	0.0002	0.72	0.86	0.93	0.55	0.38	0.0486	0.91	0.014	0.017
svm:3169011 3501555	0.87	0.0039	0.0018	0.0012	0.78	1	1	0.64	0.07	0.0005	0.86	0.004	0.017
rf:3562041 3719123	0.79	0.0316	0.0511	0.0052	0.89	0.71	0.89	0.71	0.44	0.0031	0.81	0.022	0.017
nb:3169011 3666869	0.84	0.0076	0.0018	0.0041	0.78	1	1	0.64	0.53	0.0005	0.85	0.005	0.018
nb:3169011 3551833	0.9	0.001	0.0083	0.0007	0.61	1	1	0.5	0.61	0.0055	0.88	0.003	0.018
knn:3169011 3501555	0.85	0.0075	0.0344	0.0035	0.78	0.86	0.93	0.6	0.53	0.0054	0.85	0.007	0.018
svm:3169011 3962268	0.87	0.003	0.0018	0.0008	0.72	1	1	0.58	0.26	0.0002	0.88	0.003	0.018
nb:3169011 3661099	0.85	0.0061	0.0202	0.0037	0.72	0.86	0.93	0.55	0.52	0.0041	0.86	0.009	0.018
knn:3169011 2553581	0.88	0.0043	0.0104	0.0025	0.89	0.57	0.84	0.67	0.47	0.0159	0.87	0.011	0.018
svm:2553581 3562041	0.79	0.0245	0.0431	0.0044	0.89	0.57	0.84	0.67	-0.02	0.026	0.79	0.038	0.018
svm:3562041 2397069	0.83	0.0116	0.0325	0.0059	0.83	0.71	0.88	0.63	-0.37	0.009	0.83	0.022	0.019
nb:3169011 3719123	0.83	0.0094	0.0048	0.0064	0.72	0.71	0.87	0.5	0.51	0.0266	0.82	0.009	0.019
nb:3169011 3840609	0.93	0.0004	0.0006	0.0003	0.61	1	1	0.5	0.64	0.0004	0.91	0.001	0.02
rf:3169011 3969511	0.89	0.0033	0.0104	0.001	0.67	1	1	0.54	0.66	0.0014	0.88	0.004	0.02
nb:3169011 3562041	0.94	0.0003	0.0006	0.0001	0.78	1	1	0.64	0.56	0.0005	0.92	0	0.02
rf:3169011 3840609	0.86	0.0064	0.0227	0.002	0.61	1	1	0.5	0.66	0.0001	0.88	0.001	0.021
svm:3169011 2553585	0.85	0.0061	0.0048	0.0038	0.67	1	1	0.54	0.42	0.0006	0.85	0.007	0.021
rf:3169011 3661099	0.9	0.0022	0.0164	0.0001	0.67	1	1	0.54	0.69	0.0013	0.89	0.003	0.021
nb:3169011 3031661	0.81	0.0171	0.0325	0.0085	0.83	0.71	0.88	0.63	0.47	0.0092	0.8	0.013	0.022
nb:3562041 3840609	0.82	0.0141	0.0684	0.0084	0.78	0.71	0.88	0.56	0.5	0.0379	0.8	0.037	0.022
nb:3169011 2624519	0.83	0.0094	0.0048	0.0058	0.72	1	1	0.58	0.56	0.0119	0.82	0.043	0.022
svm:3169011 3031661	0.81	0.0171	0.0325	0.0076	0.83	0.71	0.88	0.63	-0.12	0.0092	0.81	0.011	0.022
rpart:3169011 2553581	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022

rpart:3169011 3562041	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3661099	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3889625	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3151480	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3872197	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3719123	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3498523	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3969511	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3962268	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3831128	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 2624519	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3212761	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 3501555	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
rpart:3169011 2600700	0.79	0.0113	0.0679	0.0072	0.72	0.86	0.93	0.55	0.48	0.0038	0.79	0.008	0.022
knn:3169011 3551833	0.87	0.0044	0.0744	0.0013	0.5	1	1	0.44	0.61	0.0153	0.87	0.016	0.022
rf:3169011 3962268	0.84	0.01	0.0104	0.0085	0.72	0.71	0.87	0.5	0.45	0.0266	0.84	0.011	0.023
rf:3169011 3562041	0.92	0.0005	0.003	0.0003	0.61	1	1	0.5	0.62	0	0.91	0.001	0.023
rf:3169011 3498523	0.82	0.0141	0.0431	0.0071	0.72	0.86	0.93	0.55	0.61	0.0038	0.83	0.008	0.023
rf:3169011 2624519	0.85	0.0061	0.0018	0.0041	0.56	1	1	0.47	0.64	0.0117	0.84	0.019	0.023
rf:3562041 3661099	0.77	0.0426	0.0744	0.0055	0.78	0.71	0.88	0.56	0.61	0.0333	0.76	0.045	0.023
nb:3840609 3551833	0.83	0.0116	0.0431	0.0068	0.78	0.71	0.88	0.56	0.53	0.0262	0.84	0.031	0.023
rf:3169011 3719123	0.83	0.012	0.0227	0.0062	0.72	0.86	0.93	0.55	0.46	0.0038	0.82	0.006	0.023
rf:3169011 2600700	0.85	0.0084	0.0045	0.0051	0.67	1	1	0.54	0.51	0.0005	0.83	0.019	0.024
rf:3169011 3031661	0.79	0.0316	0.0464	0.0104	0.56	1	1	0.47	0.71	0.0084	0.81	0.014	0.026
svm:3889144 3661099	0.87	0.0039	0.0006	0.0023	0.72	1	1	0.58	-0.13	0.0207	0.87	0.034	0.026
nb:3169011 2397069	0.81	0.0171	0.0083	0.0081	0.61	0.86	0.92	0.46	0.58	0.0037	0.82	0.006	0.026
rf:3169011 2553581	0.9	0.0025	0.0018	0.0023	0.5	1	1	0.44	0.66	0.0022	0.89	0.003	0.026
svm:3169011 3212761	0.9	0.001	0.0048	0.0007	0.67	1	1	0.54	0.18	0.0004	0.9	0.003	0.027
rpart:3562436 3562041	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:2553581 3562041	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 3661099	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027

rpart:3562041 3551833	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 3151480	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 3872197	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 2553585	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 3719123	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 3498523	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 3962268	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 3831128	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 3666869	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 2624519	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 3212761	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
rpart:3562041 3501555	0.73	0.0198	0.2359	0.0142	0.89	0.57	0.84	0.67	0.46	0.0167	0.73	0.03	0.027
svm:3169011 3831128	0.83	0.0094	0.0118	0.0121	0.67	1	1	0.54	0.2	0.0004	0.83	0.006	0.028
svm:3169011 2397069	0.86	0.0049	0.0083	0.0043	0.61	0.86	0.92	0.46	0.5	0.0037	0.85	0.004	0.03
svm:2397069 3212761	0.8	0.0205	0.0563	0.004	0.44	1	1	0.41	0.61	0.0262	0.81	0.032	0.03
nb:3562041 3661099	0.81	0.0171	0.0264	0.0125	0.67	0.86	0.92	0.5	0.56	0.0405	0.82	0.038	0.03
knn:3169011 3212761	0.86	0.0056	0.0104	0.0044	0.56	1	1	0.47	0.64	0.0215	0.86	0.003	0.03
nb:3889144 3661099	0.87	0.0039	0.0006	0.0072	0.78	1	1	0.64	0.52	0.0066	0.87	0.047	0.031
knn:2553581 3562041	0.78	0.0318	0.0973	0.0159	0.89	0.57	0.84	0.67	0.39	0.026	0.79	0.033	0.031
rpart:3169011 3562436	0.79	0.0147	0.0679	0.0126	0.67	0.86	0.92	0.5	0.62	0.0109	0.79	0.014	0.032
svm:3562041 3872197	0.79	0.0245	0.0325	0.0225	0.78	0.71	0.88	0.56	-0.26	0.0288	0.8	0.031	0.033
nb:3661099 3031661	0.86	0.0049	0.0202	0.0127	0.5	1	1	0.44	0.59	0.0427	0.84	0.02	0.033
knn:3169011 2397069	0.78	0.0337	0.0511	0.0187	0.89	0.71	0.89	0.71	0.5	0.0107	0.78	0.026	0.034
rf:3169011 2553585	0.88	0.0044	0.0045	0.0012	0.67	1	1	0.54	0.56	0.0014	0.86	0.004	0.038
knn:3169011 3889144	0.83	0.0137	0.0104	0.0166	0.72	1	1	0.58	0.5	0.0016	0.82	0.027	0.04
rf:3169011 3562436	0.82	0.0141	0.0048	0.0241	0.67	1	1	0.54	0.67	0.0008	0.81	0.025	0.041
svm:2397069 3969511	0.82	0.0141	0.0563	0.007	0.5	1	1	0.44	0.24	0.0451	0.8	0.032	0.043
rpart:3889144 3889625	0.85	0.0061	0.0227	0.0023	0.67	1	1	0.54	0.5	0.018	0.85	0.028	0.045
knn:3889144 2397069	0.77	0.0363	0.2191	0.0301	0.61	0.86	0.92	0.46	0.5	0.0458	0.77	0.025	0.048

Performance across multiple metrics of pairwise combinations of markers selected from the library (Table 16, Table 18) in the subset of patients with positive lymph node involvement.

CLAIMS

What is claimed is:

1. A method of diagnosing, prognosing, determining progression of cancer, predicting a therapeutic regimen or predicting benefit from therapy in a subject having cancer, comprising:
 - (a) assaying an expression level in a sample from the subject for a plurality of targets, wherein the plurality of targets comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; and
 - (b) diagnosing, prognosing, determining progression of cancer, predicting a therapeutic regimen or predicting benefit from therapy in a subject having cancer based on the expression levels of the plurality of targets.
2. The method of claim 1, wherein the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.
3. The method of claim 1, wherein the cancer is a bladder cancer.
4. The method of claim 1, wherein the plurality of targets comprises a coding target.
5. The method of claim 4, wherein the coding target is an exonic sequence.
6. The method of claim 1, wherein the plurality of targets comprises a non-coding target.
7. The method of claim 6, wherein the non-coding target comprises an intronic sequence or partially overlaps an intronic sequence.
8. The method of claim 6, wherein the non-coding target comprises a sequence within the UTR or partially overlaps with a UTR sequence.
9. The method of any claim 1, wherein the target comprises a nucleic acid sequence.
10. The method of claim 9, wherein the nucleic acid sequence is a DNA sequence.
11. The method of claim 9, wherein the nucleic acid sequence is an RNA sequence.
12. The method of claim 1, wherein the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
13. The method of claim 1, wherein the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
14. The method of claim 1, wherein the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
15. The method of claim 1, wherein the plurality of targets comprises SEQ ID NOs: 1-15.

16. The method of claim 1, wherein the diagnosing, prognosing, determining progression of cancer, predicting therapeutic regimen or predicting benefit from therapy includes assessing the risk of cancer recurrence.
17. The method of claim 1, further comprising sequencing the plurality of targets.
18. The method of claim 1, further comprising hybridizing the plurality of targets to a solid support.
19. The method of claim 18, wherein the solid support is a bead or array.
20. A probe set for assessing a cancer status of a subject comprising a plurality of probes, wherein the probes in the set are capable of detecting an expression level of one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440, wherein the expression level determines the cancer status of the subject with at least 40% specificity.
21. The probe set of claim 20, wherein the one or more targets comprises SEQ ID NOs: 1-15.
22. The probe set of claim 20, wherein the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.
23. The probe set of claim 20, wherein the cancer is a bladder cancer.
24. The probe set of claim 20, wherein the probe set further comprises a probe capable of detecting an expression level of at least one coding target.
25. The probe set of claim 24, wherein the coding target is an exonic sequence.
26. The probe set of claim 20, wherein the probe set further comprises a probe capable of detecting an expression level of at least one non-coding target.
27. The probe set of claim 26, wherein the non-coding target is an intronic sequence or partially overlaps with an intronic sequence.
28. The probe set of claim 26, wherein the non-coding target is a UTR sequence or partially overlaps with a UTR sequence.
29. The probe set of claim 20, wherein assessing the cancer status includes assessing cancer recurrence risk.
30. The probe set of claim 20, wherein the target is a nucleic acid sequence.
31. The probe set of claim 30, wherein the nucleic acid sequence is a DNA sequence.
32. The probe set of claim 30, wherein the nucleic acid sequence is an RNA sequence.
33. The probe set of claim 20, wherein the probes are between about 15 nucleotides and about 500 nucleotides in length.
34. The probe set of claim 20, wherein the probes are at least 15 nucleotides in length.
35. The probe set of claim 20, wherein the probes are at least 25 nucleotides in length.

36. The probe set of claim 20, wherein the non-coding target is a non-coding RNA transcript and the non-coding RNA transcript is non-polyadenylated.
37. A system for analyzing a cancer, comprising:
- (a) a probe set comprising a plurality of target sequences, wherein
 - (i) the plurality of target sequences hybridizes to one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; or
 - (ii) the plurality of target sequences comprises one or more target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; and
 - (b) a computer model or algorithm for analyzing an expression level and/or expression profile of the target hybridized to the probe in a sample from a subject suffering from a cancer.
38. The system of claim 37, wherein the plurality of target sequences comprises SEQ ID NOs: 1-15
39. The system of claim 37, further comprising a label that specifically binds to the target, the probe, or a combination thereof.
40. The system of claim 37, wherein the plurality of target sequences comprises at least 5 target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
41. The system of claim 37, wherein the plurality of target sequences comprises at least 10 target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
42. The system of claim 37, wherein the plurality of target sequences comprises at least 15 target sequences selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
43. The system of claim 37, wherein the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.
44. A method of analyzing a cancer in an individual in need thereof, comprising:
- (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440; and
 - (b) comparing the expression profile from the sample to an expression profile of a control or standard.
45. The method of claim 44, wherein the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
46. The method of claim 44, wherein the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

47. The method of claim 44, wherein the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
48. The method of claim 44, wherein the plurality of targets comprises SEQ ID NOs: 1-15.
49. The method of claim 44, wherein the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.
50. The method of claim 44, further comprising providing diagnostic or prognostic information to the individual about the cancer based on the comparison.
51. The method of claim 44, further comprising diagnosing the individual with a cancer if the expression profile of the sample (a) deviates from the control or standard from a healthy individual or population of healthy individuals, or (b) matches the control or standard from an individual or population of individuals who have or have had the cancer.
52. The method of claim 44, further comprising predicting the susceptibility of the individual for developing a cancer based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer.
53. The method of claim 44, further comprising prescribing a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer.
54. The method of claim 44, further comprising altering a treatment regimen prescribed or administered to the individual based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer.
55. The method of claim 44, further comprising predicting the individual's response to a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer.

56. The method of claim 55, wherein the deviation is the expression level of one or more targets from the sample is greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals.
57. The method of claim 55, wherein the deviation is the expression level of one or more targets from the sample is at least about 30% greater than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals.
58. The method of claim 55, wherein the deviation is the expression level of one or more targets from the sample is less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals.
59. The method of claim 55, wherein the deviation is the expression level of one or more targets from the sample is at least about 30% less than the expression level of one or more targets from a control or standard derived from a healthy individual or population of healthy individuals.
60. The method of claim 44, further comprising using a machine to isolate the target or the probe from the sample.
61. The method of claim 44, further comprising contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof.
62. The method of claim 44, further comprising amplifying the target, the probe, or any combination thereof.
63. The method of claim 44, further comprising sequencing the target, the probe, or any combination thereof.
64. A method of diagnosing cancer in an individual in need thereof, comprising:
- (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440;
 - (b) comparing the expression profile from the sample to an expression profile of a control or standard; and
 - (c) diagnosing a cancer in the individual if the expression profile of the sample (i) deviates from the control or standard from a healthy individual or population of healthy individuals, or (ii) matches the control or standard from an individual or population of individuals who have or have had the cancer.
65. The method of claim 64, wherein the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
66. The method of claim 64, wherein the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

67. The method of claim 64, wherein the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
68. The method of claim 64, wherein the plurality of targets comprises SEQ ID NOs: 1-15
69. The method of claim 64, wherein the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.
70. The method of claim 64, further comprising a software module executed by a computer-processing device to compare the expression profiles.
71. The method of claim 64, further comprising using a machine to isolate the target or the probe from the sample.
72. The method of claim 64, further comprising contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof.
73. The method of claim 64, further comprising amplifying the target, the probe, or any combination thereof.
74. The method of claim 64, further comprising sequencing the target, the probe, or any combination thereof.
75. A method of predicting whether an individual is susceptible to developing a cancer, comprising:
- (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440;
 - (b) comparing the expression profile from the sample to an expression profile of a control or standard; and
 - (c) predicting the susceptibility of the individual for developing a cancer based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer.
76. The method of claim 75, wherein the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
77. The method of claim 75, wherein the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
78. The method of claim 75, wherein the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.

79. The method of claim 75, wherein the plurality of targets comprises SEQ ID NOs:1-15.
80. The method of claim 75, wherein the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.
81. The method of claim 75, further comprising a software module executed by a computer-processing device to compare the expression profiles.
82. The method of claim 75, further comprising using a machine to isolate the target or the probe from the sample.
83. The method of claim 75, further comprising contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof.
84. The method of claim 75, further comprising amplifying the target, the probe, or any combination thereof.
85. The method of claim 75, further comprising sequencing the target, the probe, or any combination thereof.
86. A method of predicting an individual's response to a treatment regimen for a cancer, comprising:
- (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440;
 - (b) comparing the expression profile from the sample to an expression profile of a control or standard; and
 - (c) predicting the individual's response to a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer.
87. The method of claim 86, wherein the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
88. The method of claim 86, wherein the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
89. The method of claim 86, wherein the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
90. The method of claim 86, wherein the plurality of targets comprises SEQ ID NOs:1-15.

91. The method of claim 86, wherein the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.
92. The method of claim 86, further comprising a software module executed by a computer-processing device to compare the expression profiles.
93. The method of claim 86, further comprising using a machine to isolate the target or the probe from the sample.
94. The method of claim 86, further comprising contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof.
95. The method of claim 86, further comprising amplifying the target, the probe, or any combination thereof.
96. The method of claim 86, further comprising sequencing the target, the probe, or any combination thereof.
97. A method of prescribing a treatment regimen for a cancer to an individual in need thereof, comprising:
- (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises one or more targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440;
 - (b) comparing the expression profile from the sample to an expression profile of a control or standard; and
 - (c) prescribing a treatment regimen based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer.
98. The method of claim 97, wherein the plurality of targets comprises at least 5 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
99. The method of claim 97, wherein the plurality of targets comprises at least 10 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
100. The method of claim 97, wherein the plurality of targets comprises at least 15 targets selected from Table 2B, Table 16 or SEQ ID NOs:1-1440.
101. The method of claim 97, wherein the plurality of targets comprises SEQ ID NOs:1-15.
102. The method of claim 97, wherein the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid

cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.

103. The method of claim 97, further comprising a software module executed by a computer-processing device to compare the expression profiles.

104. The method of claim 97, further comprising using a machine to isolate the target or the probe from the sample.

105. The method of claim 97, further comprising contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof.

106. The method of claim 97, further comprising amplifying the target, the probe, or any combination thereof.

107. The method of claim 97, further comprising sequencing the target, the probe, or any combination thereof.

108. The method of claim 97, further comprising converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit cancer recurrence.

109. The method of claim 97, wherein the target sequences are differentially expressed the cancer.

110. The method of claim 109, wherein the differential expression is dependent on aggressiveness.

111. The method of claim 97, wherein the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

112. A kit for analyzing a cancer, comprising:

(a) a probe set comprising a plurality of target sequences, wherein the plurality of target sequences comprises at least one target sequence listed in Table 2B, Table 16 or SEQ ID NOs:1-1440; and

(b) a computer model or algorithm for analyzing an expression level and/or expression profile of the target sequences in a sample.

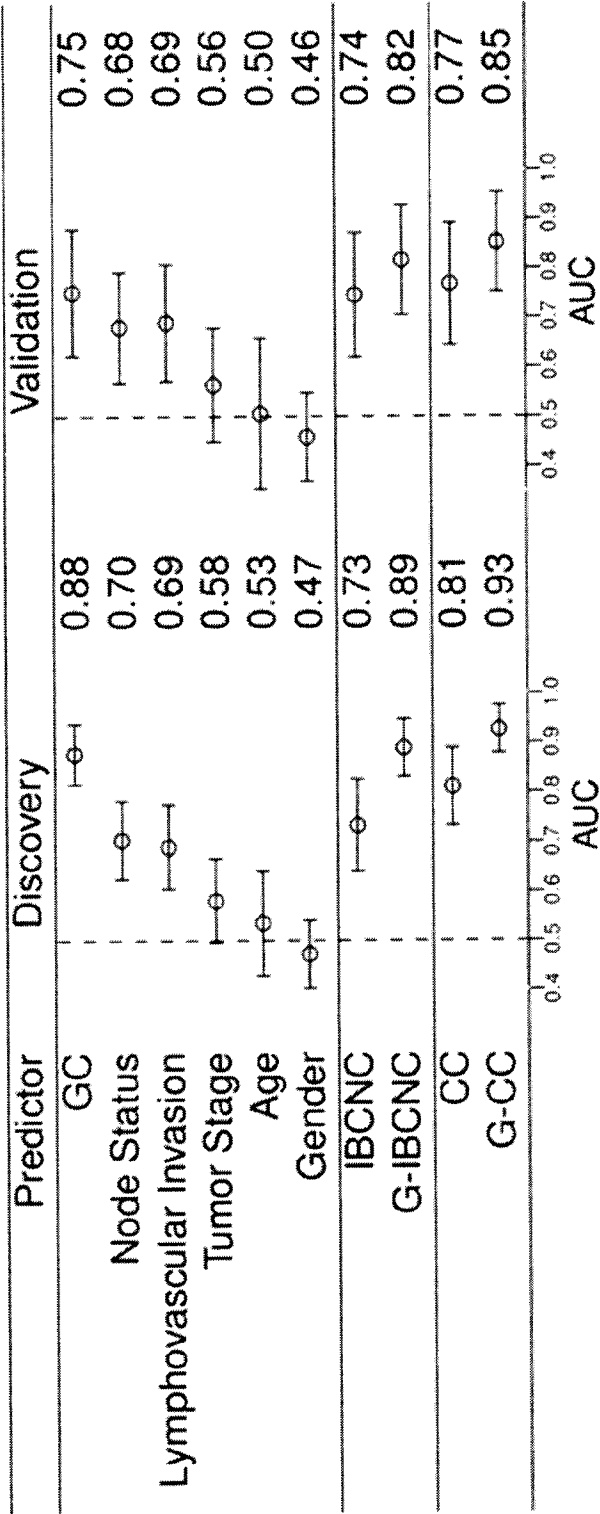
113. The kit of claim 112, further comprising a computer model or algorithm for correlating the expression level or expression profile with disease state or outcome.

114. The kit of claim 112, further comprising a computer model or algorithm for designating a treatment modality for the individual.

115. The kit of claim 112, further comprising a computer model or algorithm for normalizing expression level or expression profile of the target sequences.

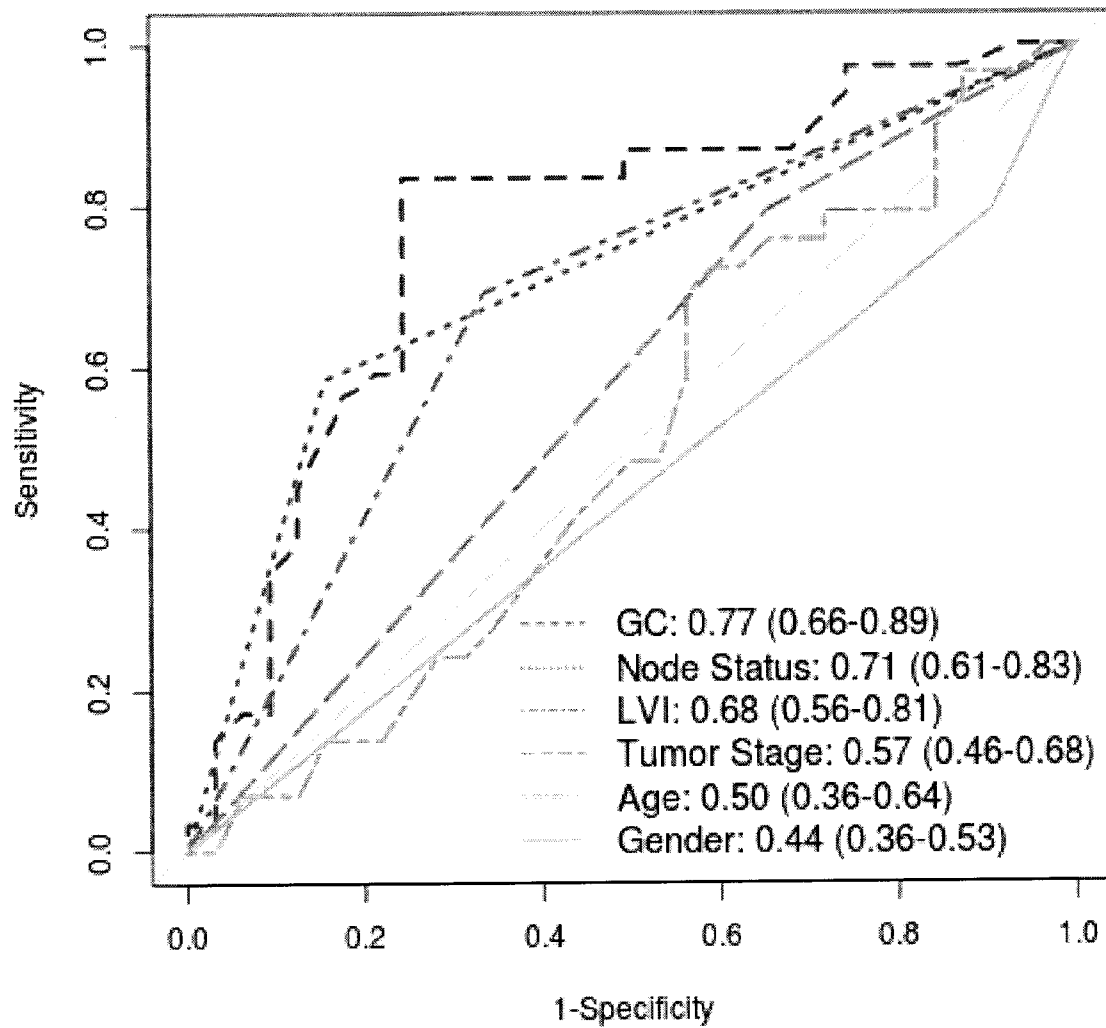
116. The kit of claim 112, further comprising a computer model or algorithm comprising a robust multichip average (RMA), frozen robust multichip average (fRMA), Single Channel Array Normalization (SCAN), ComBat (Combining Batches of gene expression), probe logarithmic intensity error estimation (PLIER), non-linear fit (NLFIT) quantile-based, nonlinear normalization, or a combination thereof.
117. The kit of claim 112, wherein the cancer is a bladder cancer.
118. The kit of claim 112, wherein the plurality of targets comprises SEQ ID NOs:1-15.

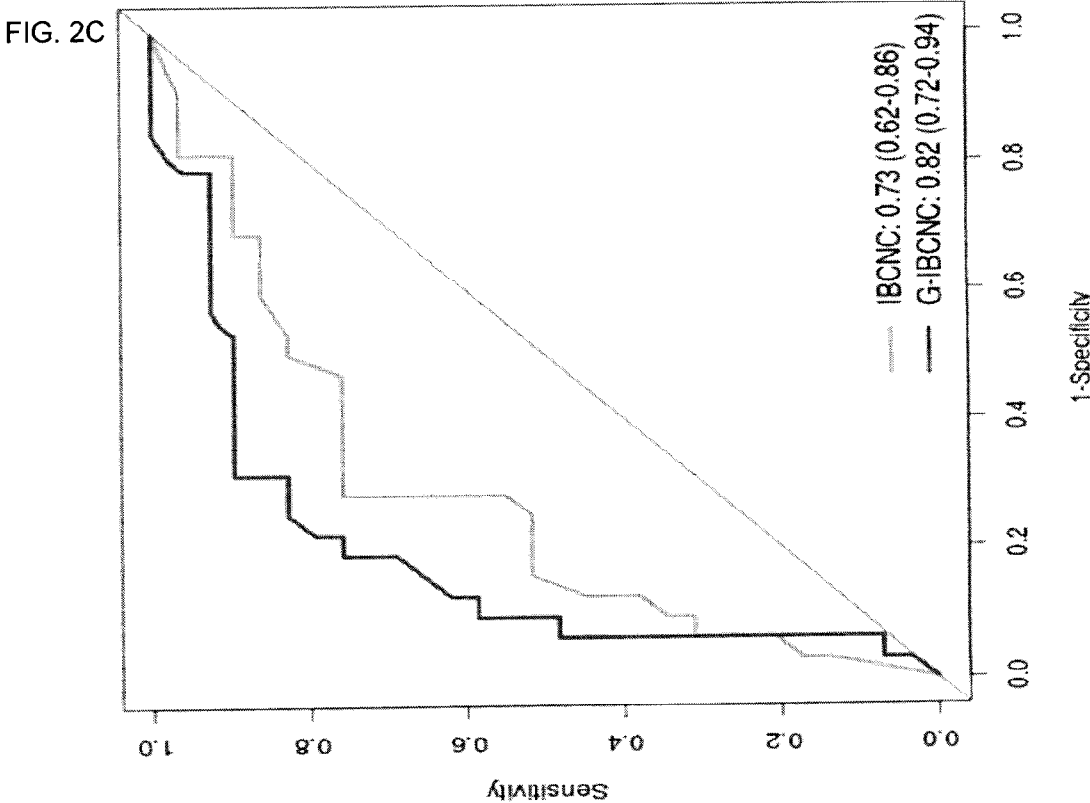
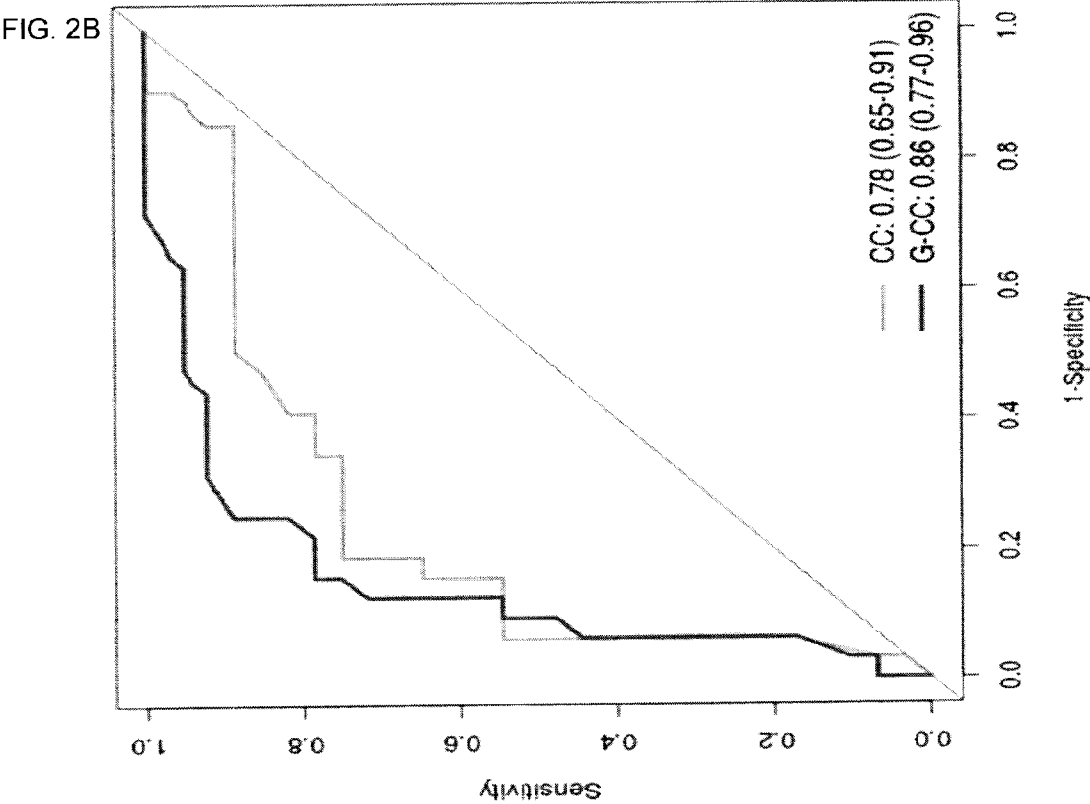
FIG. 1



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FIG. 2A





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FIG. 3A

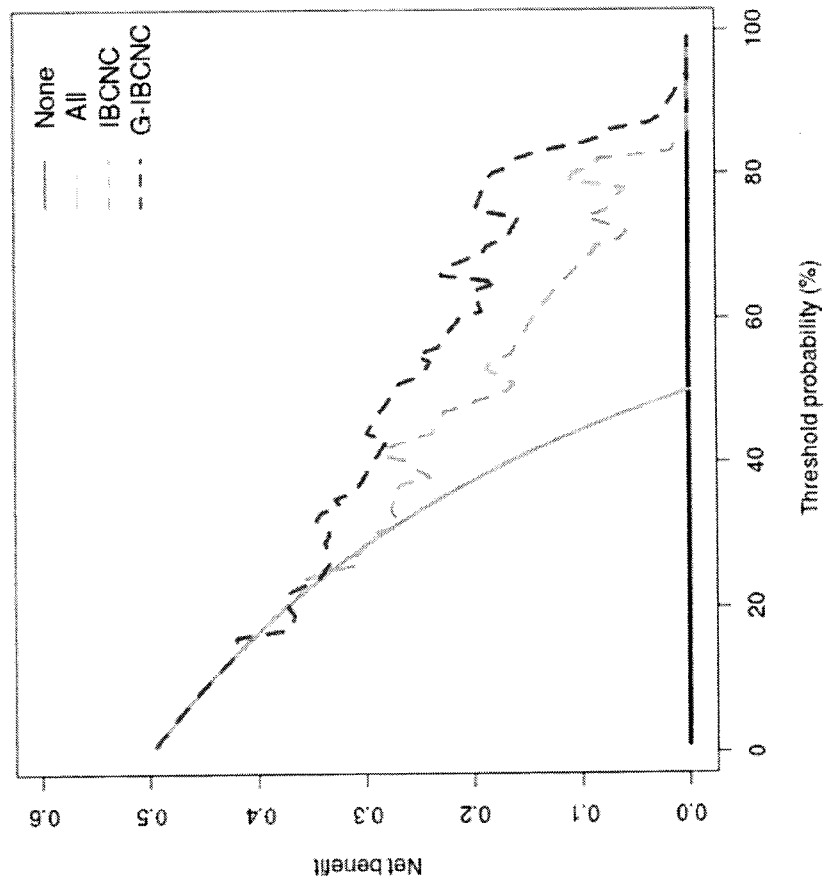


FIG. 3B

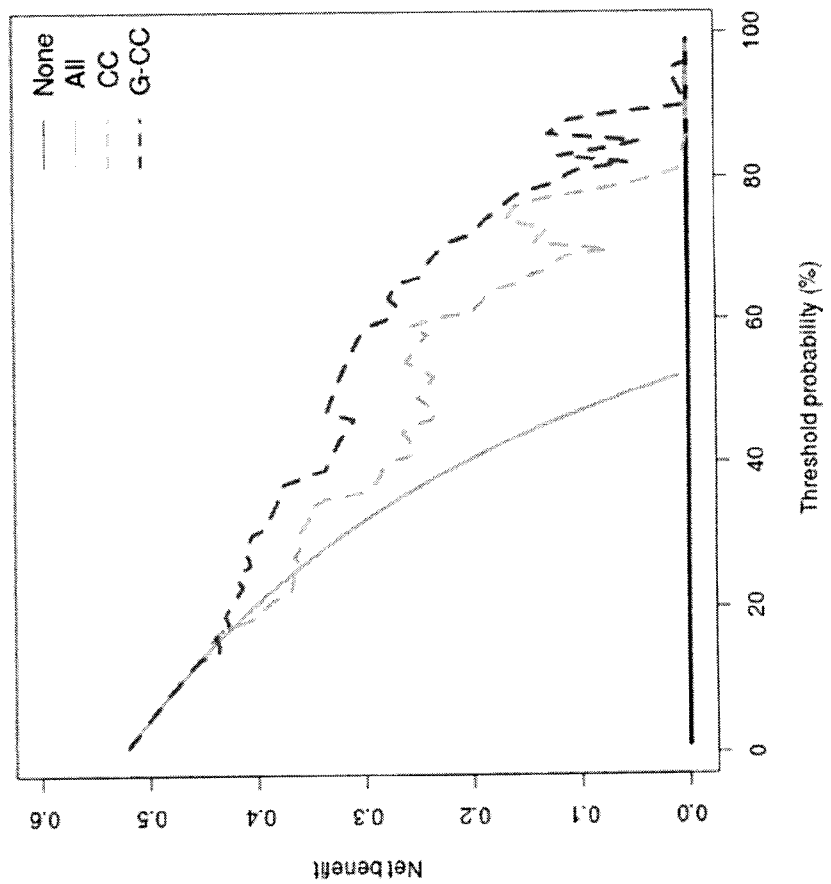


FIG. 4C

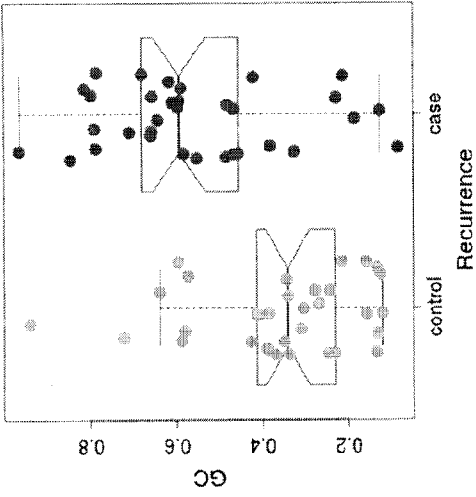


FIG. 4E

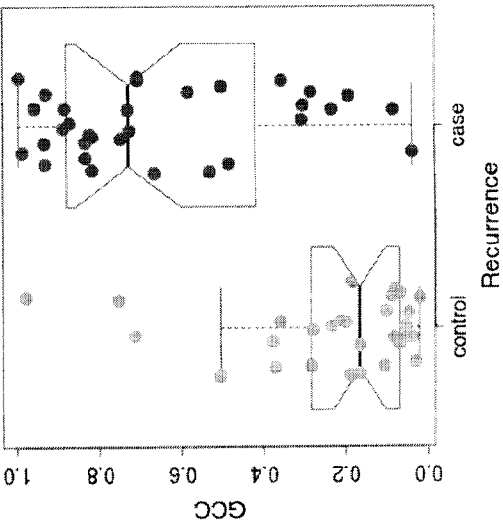


FIG. 4B

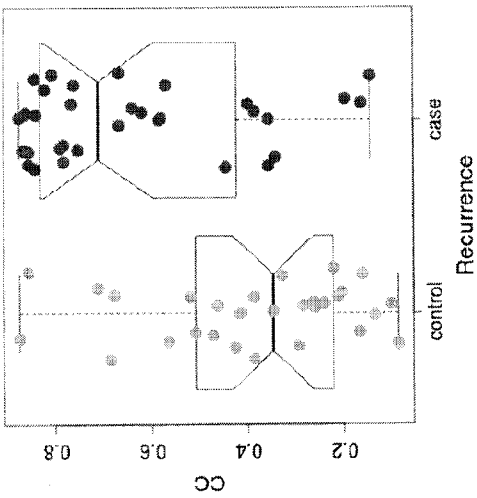


FIG. 4D

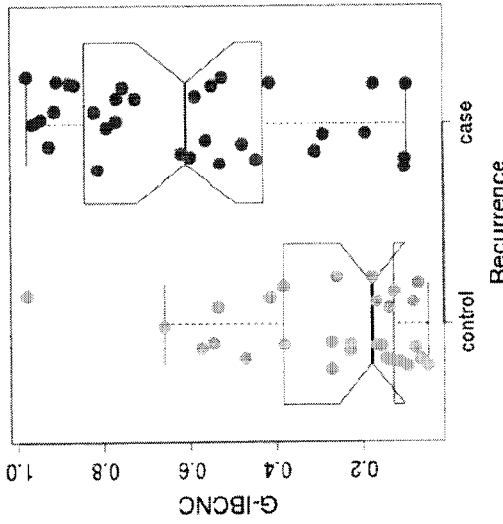


FIG. 4A

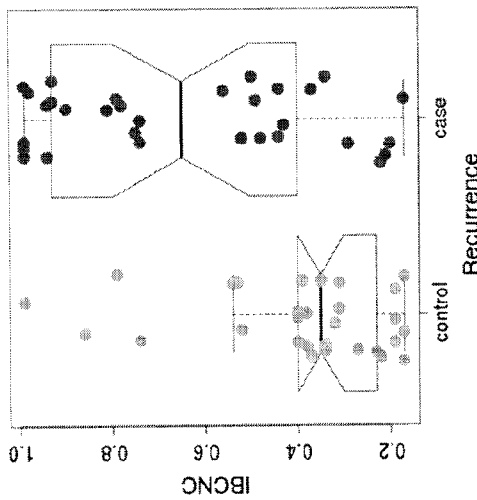


FIG. 5B

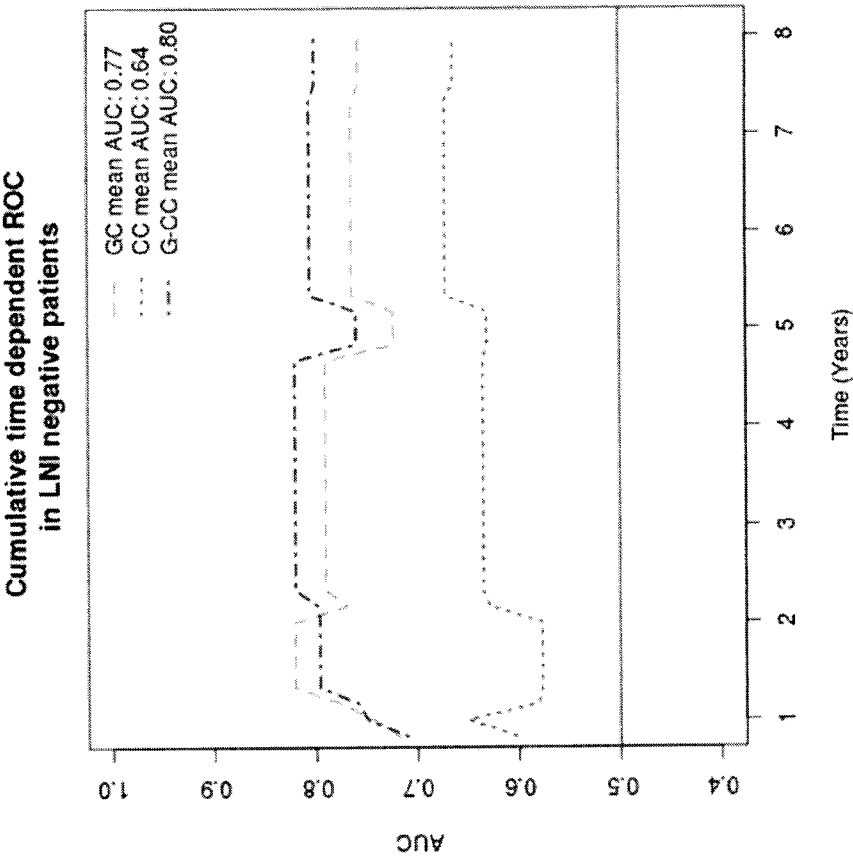
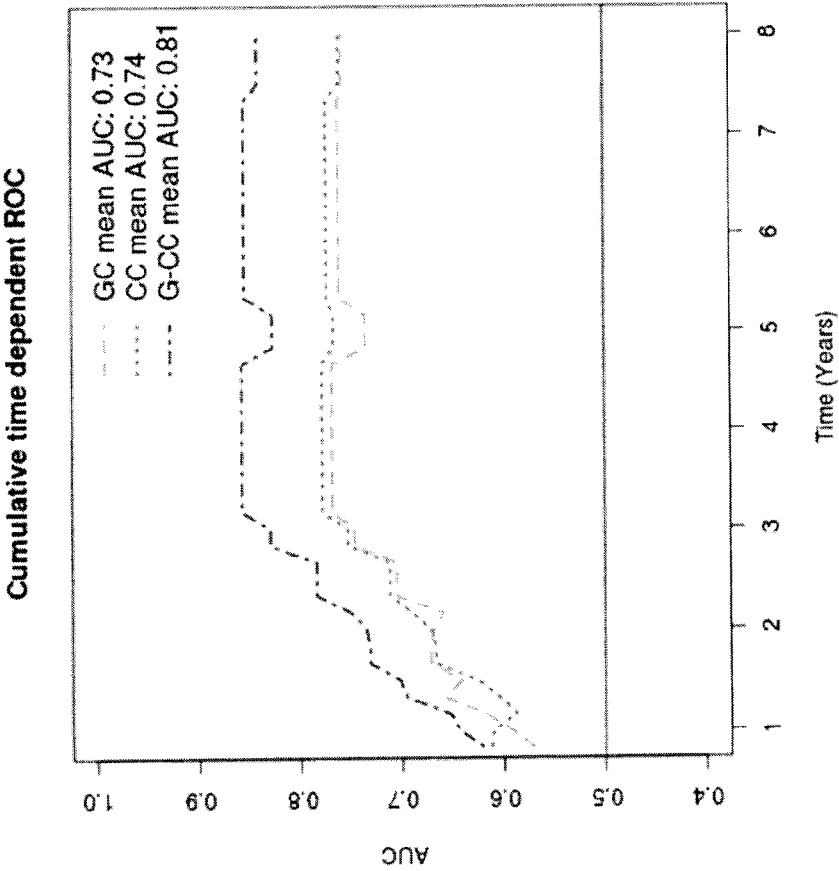


FIG. 5A



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FIG. 6

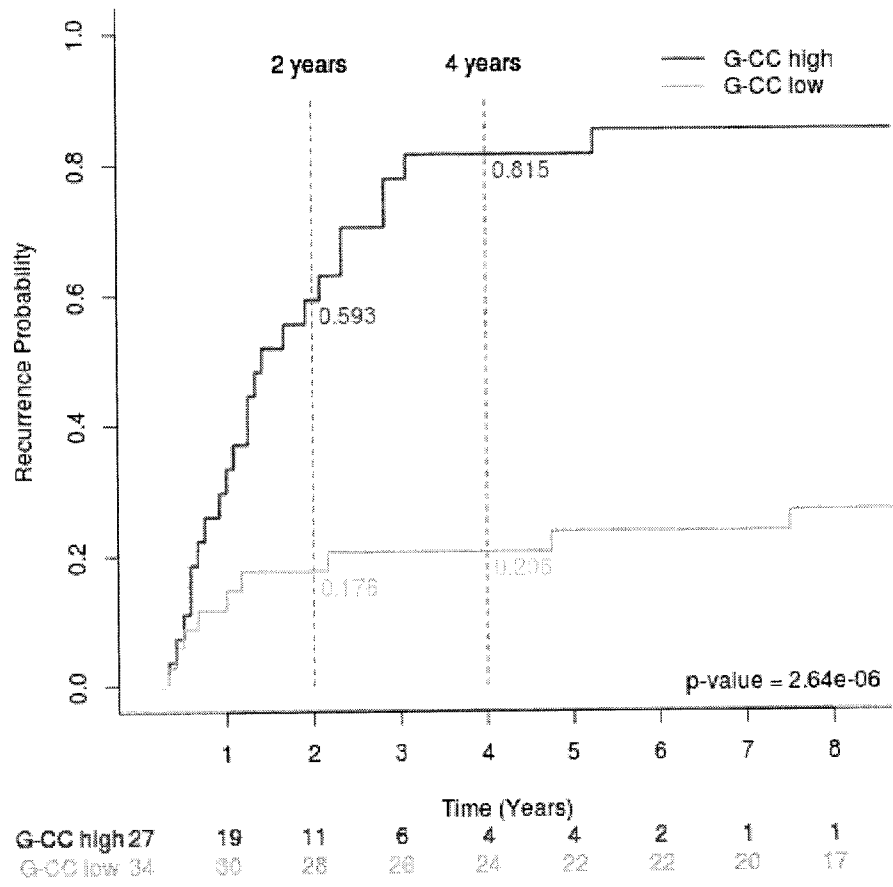


FIG. 7B

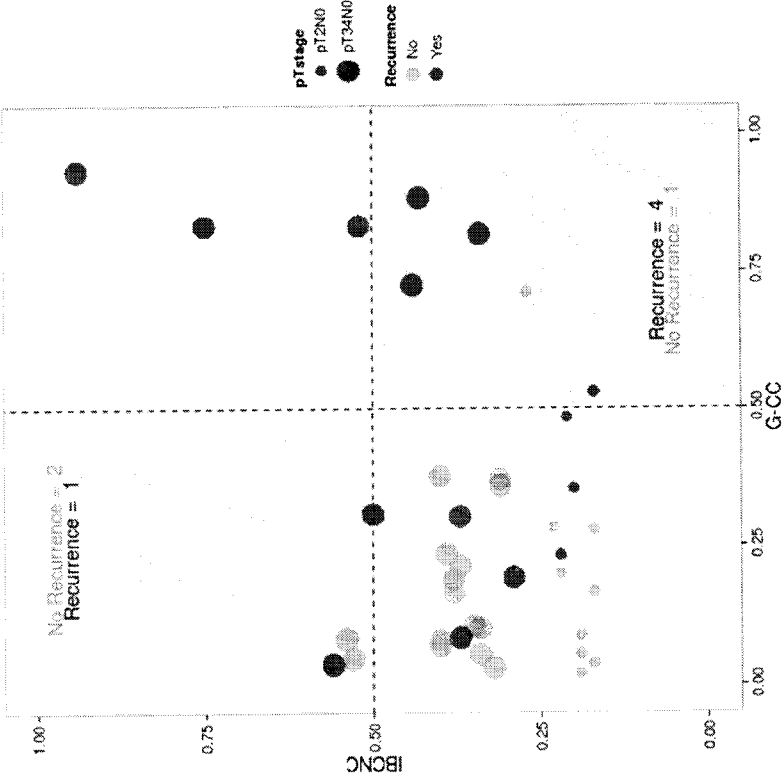


FIG. 7A

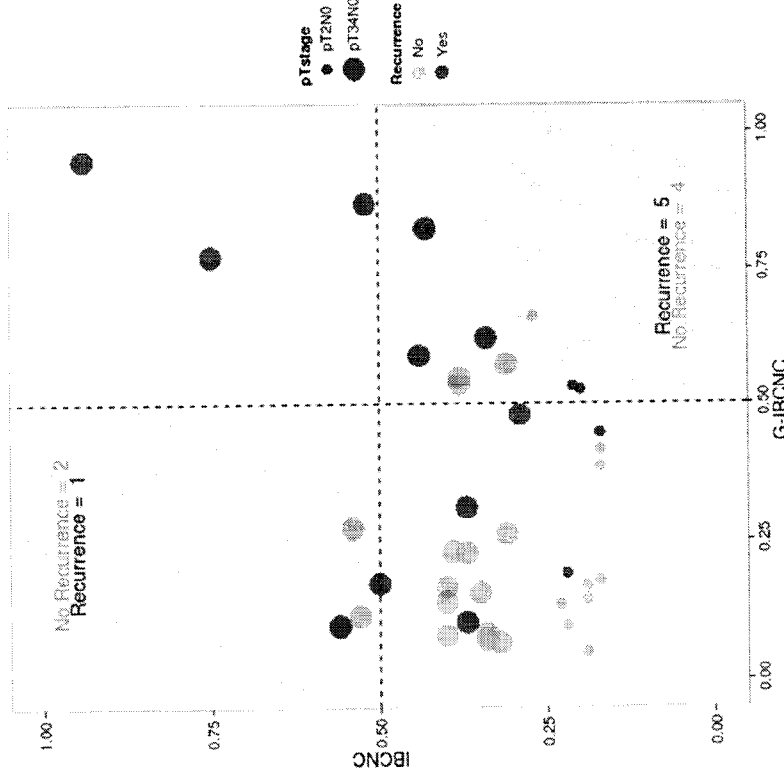


FIG. 8

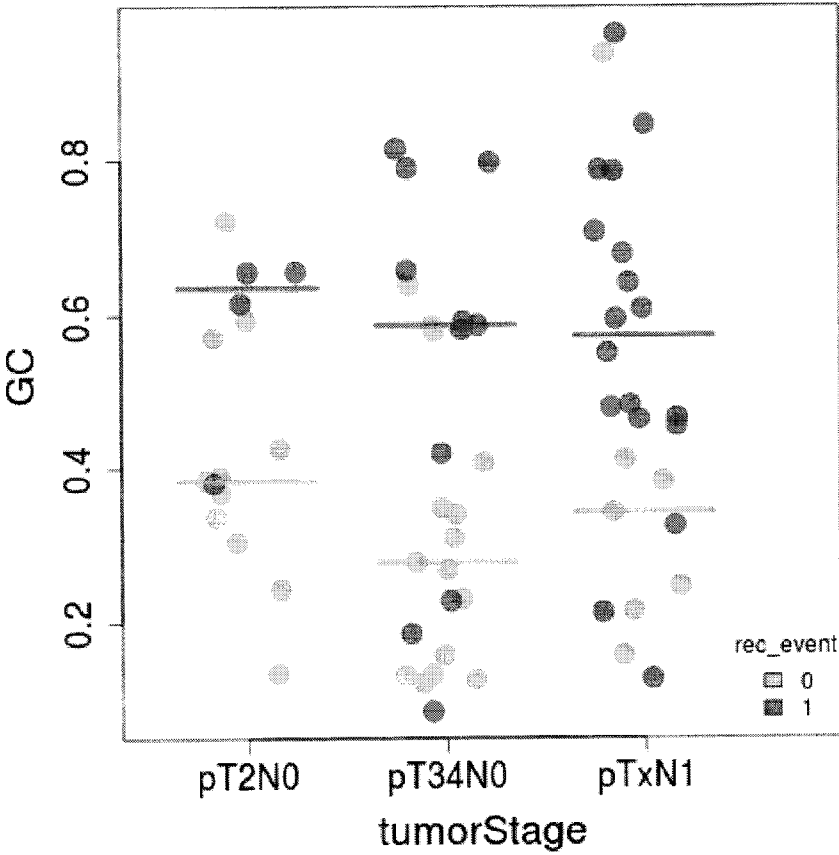


FIG. 9B

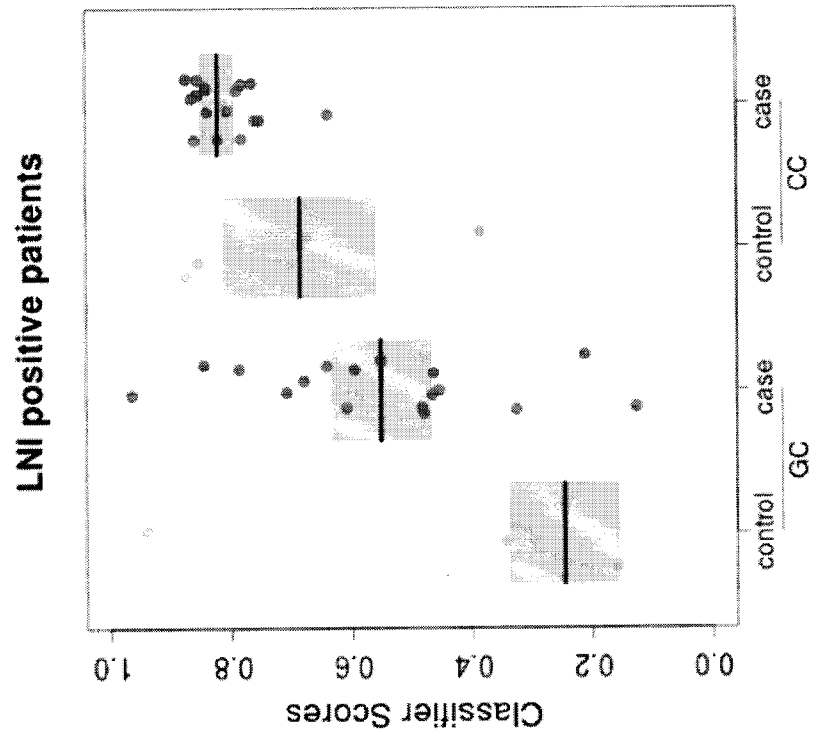


FIG. 9A

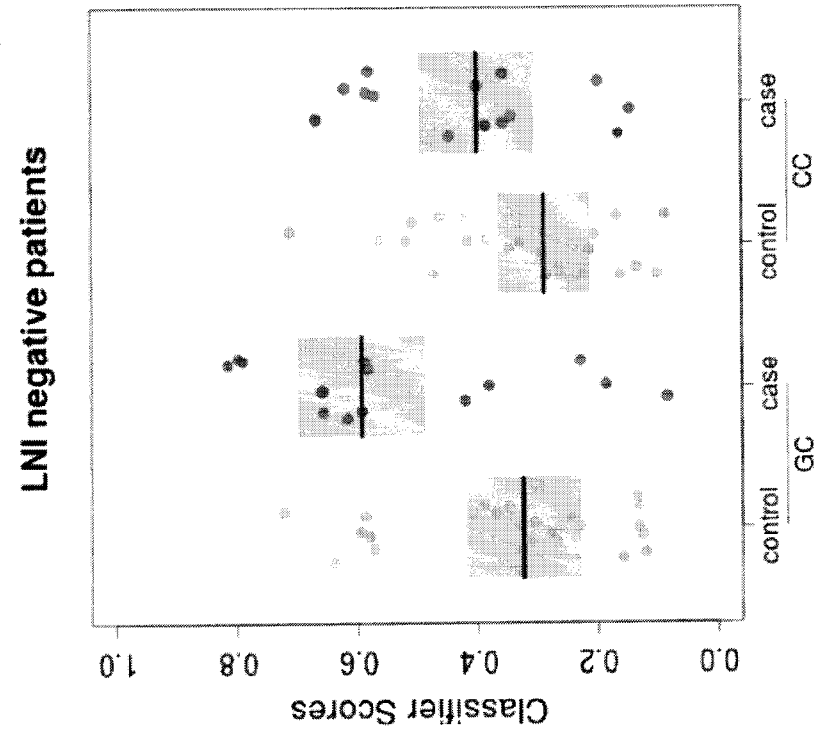


FIG. 10B

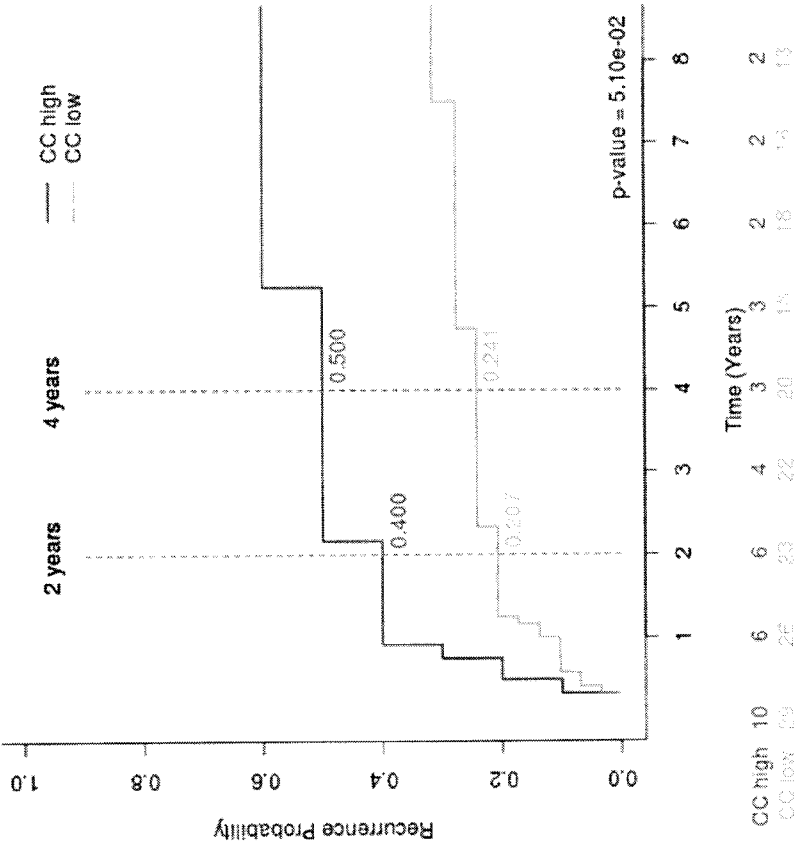
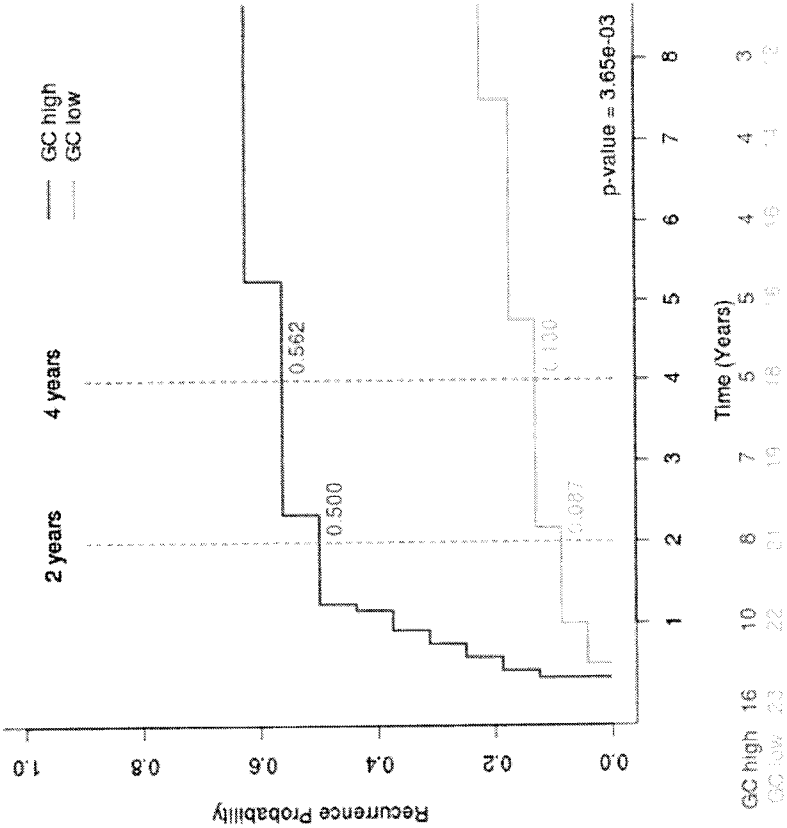


FIG. 10A



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FIG. 11

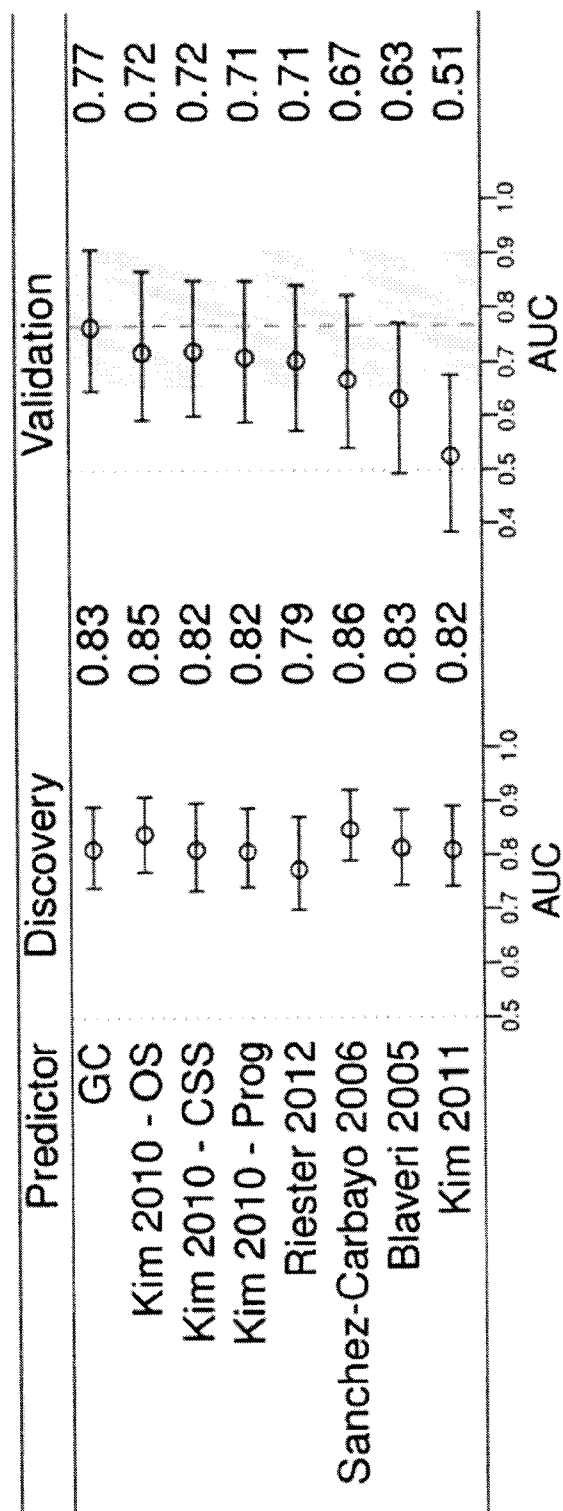
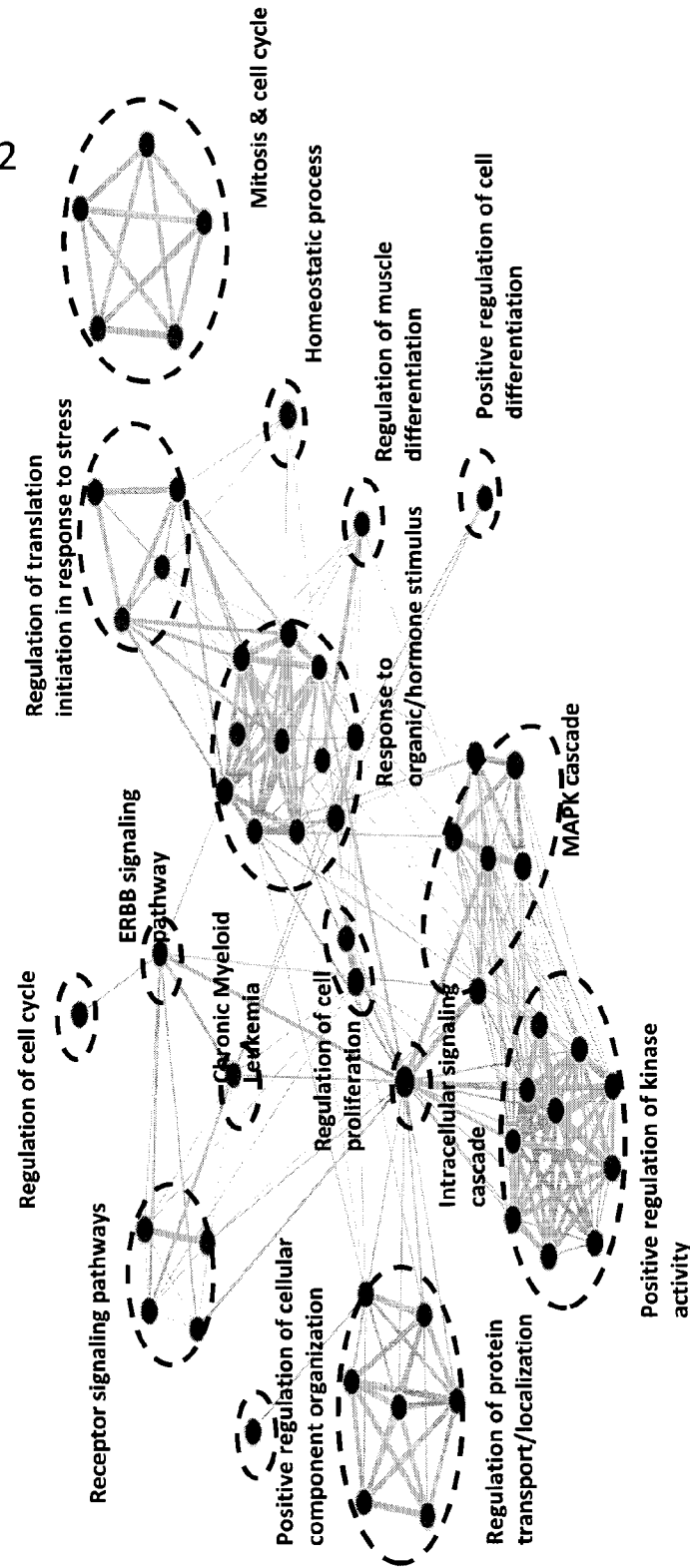


FIG. 12



INTERNATIONAL SEARCH REPORT

International application No.

PCT/CA2014/000787

A. CLASSIFICATION OF SUBJECT MATTER

IPC: **C12Q 1/68** (2006.01), **C40B 30/04** (2006.01), **G01N 33/48** (2006.01), **C40B 40/06** (2006.01)

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)

IPC: **C12Q 1/68** (2006.01), **C40B 30/04** (2006.01), **G01N 33/48** (2006.01), **C40B 40/06** (2006.01)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic database(s) consulted during the international search (name of database(s) and, where practicable, search terms used)

Canadian Patent Database, TotalPatent, PubMed, Google Scholar, Scopus

Keywords: bladder, cancer, classifier, gene expression, muscle, invasive, affymetrix

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SMITH, S.C. ET AL.: "A 20-gene model for molecular nodal staging of bladder cancer: development and prospective assessment" 1-February-2011, Lancet Oncology, vol. 12(2), pp. 137-43. ISSN 1470-2045 See entire document	1-118
A	WANG, R. ET AL.: "Development of a multiplex quantitative PCR signature to predict progression in non-muscle-invasive bladder cancer" 1-May-2009, Cancer Res. vol. 69(9), pp. 3810-8. ISSN 1538-7445 See entire document	1-118

☒ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:	"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
"A" document defining the general state of the art which is not considered to be of particular relevance	"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
"E" earlier application or patent but published on or after the international filing date	"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
"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)	"&" document member of the same patent family
"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	

Date of the actual completion of the international search
15 January 2015 (15-01-2015)Date of mailing of the international search report
04 February 2015 (04-02-2015)Name and mailing address of the ISA/CA
Canadian Intellectual Property Office
Place du Portage I, C114 - 1st Floor, Box PCT
50 Victoria Street
Gatineau, Quebec K1A 0C9
Facsimile No.: 001-819-953-2476

Authorized officer

Stephen Misener (819) 934-4548

INTERNATIONAL SEARCH REPORT

International application No.

PCT/CA2014/000787

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	ASANCHEZ-CARBAYO, M. ET AL.: "Defining molecular profiles of poor outcome in patients with invasive bladder cancer using oligonucleotide microarrays" 23-January-2006, J. Clin. Oncol. Vol. 24(5) pp. 778-89. ISSN: 1527-7755 See entire document	1-118
P, X	MITRA, A.P. ET AL.: "Discovery and Validation of Novel Expression Signature for Postcystectomy Recurrence in High-Risk Bladder Cancer" 24-October-2014, J. Natl. Cancer Inst., vol. 106(11), pp. 1-9. ISSN: 1460-2105 See entire document	1-118

Box No. I **Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)**

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

- a. ☒ forming part of the international application as filed:
 ☐ in the form of an Annex C/ST.25 text file.
 ☒ on paper or in the form of an image file.
- b. ☒ furnished together with the international application under PCT Rule 13ter.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.
- c. ☐ furnished subsequent to the international filing date for the purposes of international search only:
 ☐ in the form of an Annex C/ST.25 text file (Rule 13ter.1(a)).
 ☐ on paper or in the form of an image file (Rule 13ter.1(b) and Administrative Instructions, Section 713).
2. ☒ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.

PCT/CA2014/000787**Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of the 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. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claim Nos.: 1-118 (partially)
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:

See supplemental sheet

3. ☐ Claim 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 supplemental 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 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 claim 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 claim Nos.:

- 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.

Continuation of Box II:

The claims define a combinatorially large number of classifiers for use in diagnosing, prognosing, determining progression of cancer, predicting a therapeutic regimen or predicting a benefit from therapy in a subject having any possible type of cancer. All such classifiers are not supported by the description and fail to comply with the requirements of Article 6 of the PCT to such an extent that a meaningful search over the entire claimed scope is not possible.

An effort was nevertheless made by the ISA to identify subject matter on which a meaningful search could be performed. In view of the description, the subject matter apparently most important for the applicant is the combination of 15 markers as defined in Table 2B for use in determining progression of muscle invasive bladder cancer. The scope of the search and examination was therefore limited to the subject matter of claims 1-118 (all partially) specifically limited to targets consisting of SEQ ID NOs: 1-15 (Table 2B).

Continuation of Box III:

The application is directed to methods, probe sets, systems and kits for diagnosing, prognosing, determining progression of cancer, predicting a therapeutic regimen or predicting a benefit from therapy in a subject having any possible type of cancer using a combination of one or more of the markers selected from Table 2B, Table 16 or SEQ ID NOs: 1-1440. The only feature which might serve to unify the subject matter of the claims is the general concept of using combinations of one or more markers in expression-based diagnosis of cancer.

However, the use of combinations of one or more markers in expression-based diagnosis of cancer is well known in the prior art as disclosed in, for example, any one of Smith et al., Wang et al. or Asanchez-Carbayo et al. Thus the claims do not relate to a single inventive concept *a posteriori* contrary to Rule 13.1 of the PCT. Therefore the claims are directed to a plurality of alleged inventions wherein each specific combination of one or more markers as set forth in Table 2B, Table 16 or SEQ ID NOs: 1-1440 represents a separate invention.

The claims must be limited to one inventive concept as set out in Rule 13 of the PCT.