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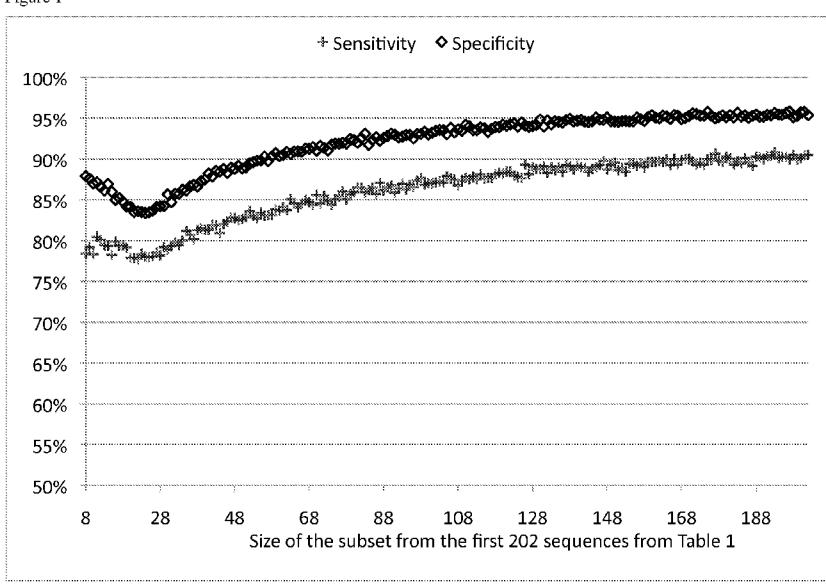
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(54) Title: METHODS AND KITS FOR DIAGNOSING COLORECTAL CANCER

Figure 1



The graph plots Sensitivity (marked with '+' symbols) and Specificity (marked with diamond symbols) against the size of the subset of sequences. The x-axis represents the size of the subset, ranging from 8 to 188. The y-axis represents percentages from 50% to 100%. Both sensitivity and specificity increase as the subset size increases, with specificity generally higher than sensitivity. Both curves stabilize around 95% as the subset size reaches approximately 140.

Size of the subset	Sensitivity (%)	Specificity (%)
8	80	88
28	78	85
48	82	89
68	85	91
88	88	93
108	90	94
128	92	95
148	93	95
168	94	95
188	95	95

(57) Abstract: The invention pertains to a method for early detection and screening of colorectal cancer in human subjects based on RNA isolated from blood obtained from said subject. According to the invention, the abundance of at least 3, 5, 8, 30, 60, 102, 202, 55, 1002 or 1002 RNAs listed in tables 1 to 13 is measured. Using the invention, an accurate and noninvasive screening and diagnosis tool for colorectal cancer is provided with a sensitivity of at least 80 % and a specificity of 85 % that has high clinical utility and the potential for broad adoption.

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## Methods And Kits For Diagnosing Colorectal Cancer

The invention pertains to a method for diagnosing or detecting colorectal cancer in human subjects based on ribonucleic acid (RNA), in particular based on RNA from blood.

### Background

Colorectal cancer (CRC) is the second-leading cause of cancer-related deaths in the United States. Each year, approximately 150,000 people are diagnosed with CRC and almost 60,000 people die from the disease.

CRC arises from the mucosa forming the inner lining of colon and rectum. Like any other mucosa, it needs to be regenerated and proliferates at a high rate (about one third of all fecal matter are mucosa cells), and is thus susceptible to abnormal growth, *i.e.*, neoplasia and/or dysplasia. In fact, abnormal colonic mucosal growth can be detected in about 40 % of all persons over the age of 55 years. The development of neoplasia into cancer is a well-established concept in the biomedical sciences; and is termed adenoma-carcinoma-sequence (ACS).

Pathologists classify abnormal mucosal growth into four categories with increasing severity: 1) Low-grade intraepithelial neoplasia (LIEN) or adenoma, which occurs in more than 30 %; 2) high-grade intraepithelial neoplasia (HIEN) or advanced adenoma, occurring in more than 2 %; 3) carcinoma in situ (CIS or pTis), where the cancerous growth is still confined to the mucosa; and 4) CRC, where the cancerous growth has invaded the submucosa. CRC is diagnosed with an incidence rate of about 1 % in persons over the age of 55 years with an average risk for the disease. The lifetime risk of developing CRC is estimated to be 1 in 18 persons (Cancer Statistics 2009: A Presentation From the American Cancer Society; 2009, American Cancer Society, Inc.).

After primary diagnosis of CRC, the spread/stage of the disease is classified according to the guidelines set forth by the “Union International Contre le Cancer” (UICC). UICC-stage 0 includes CIS only. UICC-stages I and II are comprised of the localized stages, whereas UICC-stage III describes CRC where tumor cells have metastasized into regional lymph

nodes. The worst case is UICC-stage IV; it describes CRC which has metastasized into other organ(s), usually liver (~75 %), peritoneum (~22 %), and/or lung (~21 %).

In 2008, the cancer registry in the state of Brandenburg/Germany documented 1591 patients with newly diagnosed CRC and stage information. They were staged into UICC-stage I: 22.6 %, UICC-stage II: 29.2 %, UICC-stage III: 28.9 %, and UICC-stage IV: 19.0 %. Relative five year survival-rates by UICC-stage were: I: 90.5%, II: 78.8%, III: 60.6%, and IV: 9.3%.

The U.S. National Institutes of Health (<http://seer.cancer.gov>) reported for the period 1999 to 2006 216,332 patients diagnosed with CRC with localized disease (UICC-stage I and II): 39 %, regional disease (UICC stage III): 37 % and distant disease (UICC-stage IV): 19 %. Relative five year survival-rates by stage were: localized (UICC-stages I and II): 90.4 %, regional (UICC stage III): 60.5 %, and distant (UICC-stage IV): 11.6 %. However, the statistics of the U.S. National Institutes of Health do not cover the U.S. population, while the data from the cancer registry in the state of Brandenburg/Germany do.

Current technologies to detect mucosal neoplasia (polyps/adenoma) and CRC can be categorized into three classes:

- I) ***in-vitro diagnostics* (IVDs)** – a specimen/sample (blood, stool, or urine) is taken from the test person and analyzed for one or more biomarkers as surrogate markers for colorectal neoplasia/cancer. Exemplary tests include guaiac fecal occult blood test (gFOBT) or immunological fecal occult blood test (iFOBT), detection of tumor DNA-chains (deoxyribonucleic acid chains) in stool samples, detection of specific methylated tumor DNA-chains in stool samples, detection of specific free methylated DNA-chains in blood plasma, detection of elevated and/or lowered amounts of specific proteins in blood samples, or detection of elevated and/or lowered amounts of specific RNA-chains in blood samples;
- II) **imaging methods without interventional capabilities** such as X-ray, double contrast barium enema (DCBE), video capsule endoscopy, or computed tomographic colonography;
- III) **imaging methods with interventional capabilities** such as flexible sigmoidoscopy, colonoscopy, laparoscopy, or open surgery.

To obtain a definitive diagnosis of colorectal neoplasia/cancer, an invasive procedure is typically required. The procedure requires taking a sample of the visibly abnormal tissue growth (neoplasia/cancer) and having a person of skill in the art of pathology examine this sample, who will then decide (diagnose) whether this sample was taken from a neoplasia/cancer or not (Sternberg's Diagnostic Surgical Pathology (5<sup>th</sup> Edition). Mills SE, Carter D, Greenson JK, Reuter V, Stoler MH. Lippincott Williams & Wilkins (LWW), 2009).

In response to the high incidence and mortality rate of patients with CRC, the American Cancer Society issued the following statement: "There are significant updates to the guidelines for colorectal cancer screening. Two new tests are now recommended as options for colorectal cancer screening. They are stool DNA (sDNA) and computerized tomographic colonography (also known as "virtual colonoscopy"). For the first time, screening tests are grouped into categories based on performance characteristics: those that primarily detect cancer early and those that can also detect precancerous polyps. Tests that primarily detect cancer early are fecal (stool) tests, including guaiac-based and immunochemical-based fecal occult blood tests (gFOBT & FIT), and stool DNA tests (sDNA). Tests that detect both precancerous polyps and cancer include flexible sigmoidoscopy, colonoscopy, the double contrast barium enema, and computerized tomographic colonography (also known as virtual colonoscopy). It is the strong opinion of the expert panel that colon cancer prevention should be the primary goal of colorectal cancer screening. Exams that are designed to detect both early cancer and precancerous polyps should be encouraged if resources are available and patients are willing to undergo an invasive test." (Cancer Statistics 2009: A Presentation From the American Cancer Society; ©2009, American Cancer Society, Inc.). A review of current CRC screening in Europe can be found in: Zavoral M, Suchanek S, Zavada F, Dusek L, Muzik J, Seifert B, Fric P. Colorectal cancer screening in Europe. World J Gastroenterol. 2009 Dec 21; 15: 5907-15.

However, each of the tests for the detection of mucosal neoplasias (polyps/adenomas) and CRC has limitations.

For example, the imaging methods (with or without interventional capabilities) require preparation time for the test subject, specialized equipment, and specialized medical personnel. Therefore, colonoscopy and flexible sigmoidoscopy are used only in wealthy

economies such as the U.S., Switzerland, and Germany as primary screening tools for early detection of CRC. Even in the U.K., France, Italy or Spain, IVDs, in most instances gFOBT, are used as a primary screening tool for colorectal cancer. Only patients with a positive IVD test result are referred to colonoscopy.

Recently, a screening program for CRC using gFOBT was initiated in the United Kingdom. All eligible persons were contacted via mail, and a test kit was delivered. Yet, just about 50 % of all contacted people complied. The willingness of patients to undergo gFOBT testing in Germany has dropped from 8.2 million tests in 2001 to 4.6 million tests in 2007 (Projekt wissenschaftliche Begleitung von Früherkennungs-Koloskopien in Deutschland, Berichtszeitraum 2008 - 6. Jahresbericht, im Auftrag des GKV - Spitzenverbands und der Kassenärztlichen Bundesvereinigung Version 1.1, Stand: 19. Februar 2010, Zentralinstitut für die kassenärztliche Versorgung in der Bundesrepublik Deutschland). In the U.S., about 24.01 % of all eligible patients underwent gFOBT-screening in 2000, in 2005 the rate dropped to 17.07 % (U.S. National Cancer Institute, <http://progressreport.cancer.gov>).

Thus, the clinical utility of all stool-based CRC-screening is limited because individuals in the CRC screening population are simply unwilling to take the test repeatedly, unless they have no other choice.

The U.S. National Institutes of Health reported that compliance with endoscopy (flexible sigmoidoscopy or colonoscopy) is dependent on the education and income of the population; by 2005 37.66 % of persons with less than high school education, 46.27 % of persons with high school education, and 57.52 % of persons with higher than high school education had ever had an endoscopy (not defined to CRC screening purposes).

Colonoscopy is an invasive procedure, which is not only inconvenient but may be associated with health risks. Approximately 3 % of the individuals over 55 years undergoing colonoscopy for screening purposes have heavy bleeding incidences. Additionally, in 2 of 1,000 individuals perforation of the colon occurs. Emergency operations must be performed to correct both heavy bleeding and perforation. As a result, 2 of 10,000 individuals who undergo colonoscopy will die from these complications. The relatively high rate of accidents in combination with the time consuming bowel cleaning procedure has led to a low adoption

of colonoscopy as a screening tool even in those countries where colonoscopy is paid by the health insurances.

Thus, the overall clinical utility of all endoscopy-based CRC-screening is also limited, because it is only offered in a few countries, a high percentage of the CRC screening population is unwilling to take the test, and because of the complications associated with the test.

Therefore, the clinical utility of a test for detection of colorectal neoplasia depends not only on its performance characteristics, *i.e.*, sensitivity and specificity, but on acceptance by the patients, the medical community, and, of course, the private or public health care system that has to pay for the test.

A blood test would have the highest chance of acceptance by patients, at least in Europe, the U.S., and Japan. In terms of the medical community, a blood test would also have the highest chance of acceptance, in particular if sensitivity and specificity are convincingly high, if there is no need for preparation time, if the blood need not be processed immediately but can be shipped to a central laboratory, if the test is accepted by local regulatory authorities, and if the test is commercially available. A high level of acceptance of a test can only be achieved if the test is endorsed by CRC screening guidelines and by the general health care system.

Although blood-based colon cancer screening has been attempted, each previously reported test is inherently limited in its respective specificity and sensitivity.

For example, Han et al., (Clin Cancer Res 2008; 14, 455-460; also: WO 2007/048074 A1) reported the discovery and validation of a five-gene expression (messenger RNA) signature for detection of colorectal carcinoma. Basically, the 37 candidate genes for the signature were selected from microarray data of 16 CRC cases and 15 controls. These 37 candidate genes were evaluated on a second set of 115 samples (58 CRC, 57 controls) using quantitative real-time PCR, validating 17 genes as differentially expressed. A further gene selection step using the PCR-results revealed the 5 gene signature, which was validated on a third set of 102 samples. The predictive power of these five genes, which was evaluated using a fourth set of 92 samples, correctly identifying 88 % (30 of 34) of CRC samples and only 64 % (27 of 42)

of non-CRC samples. The intermediate zone contained 16 samples. The performance parameters are compiled into table A.

**Table A:** Estimates and Exact Confidence Limits of GeneNews ColonSentry™ Test

Performance Parameter	N <sub>C</sub>	N	Estimate	Exact Two-Sided 95 % CI-Limits	
				Lower	Upper
Sensitivity	30	34	0.88	0.725	0.967
Specificity	27	42	0.64	0.480	0.784
Positive Predictive Value	30	45	0.67	0.510	0.800
Negative Predictive Value	27	31	0.87	0.702	0.964
Correct Classification Rate	57	76	0.75	0.637	0.842

N<sub>C</sub> = Number of correctly classified cases; CI = Confidence interval; Exact confidence limits were computed using the proc FREQ of the statistics program SAS.

Provided that patients of the last validation set were a random selection of the screening population, applying the performance on a hypothetical set of 10,000 patients with an incidence of one percent and computing the performance parameters of this test yields the results shown in table B.

**Table B:** Estimates and Exact Confidence Limits of GeneNews ColonSentry™ Test applied to a Hypothetical Set of 10000 Persons

Performance Parameter	N <sub>C</sub>	N	Estimate	Exact Two-Sided 95 % CI-Limits	
				Lower	Upper
Sensitivity	73	100	0.73	0.632	0.814
Specificity	6979	9900	0.70	0.696	0.714
Positive Predictive Value	73	2994	0.02	0.019	0.031
Negative Predictive Value	6979	7006	1.00	0.994	0.997
Correct Classification Rate	7052	10000	0.71	0.696	0.714

N<sub>C</sub> = Number of correctly classified cases; CI = Confidence interval; Exact confidence limits were computed using the proc FREQ of the statistics program SAS.

However, based on the data provided by Han, 1,739 of 10,000 patients would have an “intermediate result”. In clinical practice, this would mean that these 1,739 patients would have to undergo colonoscopy to clarify their state. However, in this computation, these 1,739 patients were regarded as having been predicted as low risk. The main disadvantage of the ColonSentry test is its relatively low sensitivity of 73 % and its low specificity of 70 %.

Applied to a screening population of 1 million individuals this means that 2,700 individuals with undetected CRC will not be detected by the test. In addition, 300,000 individuals (30 %) are diagnosed as false positive, which need to be followed up by colonoscopy. The combination of a relatively high false negative rate of 27 % with a high false positive rate of 30 % reduces the clinical utility of this test and impedes acceptance by the medical community and the screening population itself.

Epigenomics AG, Germany, has a CE-marked test, Epi proColon®, in the market that measures the methylation status of the Septin-9 gene and is based on detection of free somatic tumor DNA in blood serum.

**Table C:** Estimates and Exact Confidence Limits of Epi proColon® Test

Performance Parameter	N <sub>C</sub>	N	Estimate	Exact Two-Sided 95% CI-Limits	
				Lower	Upper
Sensitivity	69	103	0.67	0.570	0.759
Specificity	135	154	0.88	0.814	0.924
Positive Predictive Value	69	88	0.78	0.684	0.865
Negative Predictive Value	135	169	0.80	0.730	0.856
Correct Classification Rate	204	257	0.79	0.739	0.842

N<sub>C</sub> = Number of correctly classified cases; CI = Confidence interval; Exact confidence limits were computed using the proc FREQ of the statistics program SAS.

The product performance figures of Epi proColon® displayed in table C are cited from the companies' website ([www.epigenomics.com](http://www.epigenomics.com)). Table D shows the figures when the performance of the test is applied to a hypothetical screening population. Though the Epi proColon® test performs better than GeneNews' test in some performance parameters its overall sensitivity for all four stages of CRC is only 67 %. This means that if 10,000 individuals are screened and the prevalence of CRC in the screening population is approximately 1 %, so that 33 individuals with CRC will be missed by the test. Applied to a screening population of 1 million individuals (3.7 % of the German screening population or 1.3% of the US screening population) 3,300 individuals with CRC will not be detected by the test. This high false negative rate limits significantly the clinical utility of the Epi proColon® test. The false negative rate of patients with early stage CRC (UICC I and II) that will be missed is even higher.

**Table D:** Estimates and Exact Confidence Limits of Epi proColon® Test applied to a Hypothetical Set of 10,000 Persons

Performance Parameter	N <sub>C</sub>	N	Estimate	Exact Two-Sided 95% CI-Limits	
				Lower	Upper
Sensitivity	67	100	0.67	0.569	0.761
Specificity	8679	9900	0.88	0.870	0.883
Positive Predictive Value	67	1288	0.05	0.041	0.066
Negative Predictive Value	8679	8712	1.00	0.995	0.997
Correct Classification Rate	8746	10000	0.87	0.868	0.881

N<sub>C</sub> = Number of correctly classified cases; CI = Confidence interval; Exact confidence limits were computed using the proc FREQ of the statistics program SAS.

Another blood-based test developed by OncoMethylome Science (Liege, Belgium) measures the methylation status of two Genes FOXE1 and SYNE1. The sensitivity of this two-marker test for all four stages of CRC is 56 %, while the specificity is 91 % (ESMO meeting, Berlin, Germany, September 2009)

All three blood tests have a significant false negative rate and do not detect a significant number of patients with CRC. The ColonSentry test has a low specificity of 70 % and burdens colonoscopy facilities with a high number of false-positive test results.

Thus, there is a clear clinical need for an improved blood-based test for screening, detecting, or diagnosing colorectal cancer with high sensitivity and high specificity, which is minimally invasive so as to permit more widespread testing of the population to indicate the presence of colorectal cancer with high accuracy and therefore with a high clinical utility, and to ensure greater adherence to recommended protocols. Further, the identification of biomarkers, such as RNAs for use in such a minimally-invasive test would fulfill a longstanding need in the art.

### Brief description of the invention

The present invention provides methods and kits for diagnosing, detecting, and screening for colorectal cancer. Particularly, the invention provides for preparing RNA expression profiles of patient blood samples, the RNA expression profiles being indicative of the presence or

absence of colorectal cancer. The invention further provides for evaluating the patient RNA expression profiles for the presence or absence of one or more RNA expression signatures that are indicative of colorectal cancer.

The inventors have surprisingly found that a sensitivity of at least 75 %, and a specificity of at least 85 %, is reached if and only if at least 8 RNAs are measured that are chosen from the RNAs listed in table 1. In other words, measuring 8 RNAs is necessary and sufficient for the detection of colon cancer in a human subject based on RNA from a blood sample obtained from said subject by measuring the abundance of at least 8 RNAs in the sample, that are chosen from the RNAs listed in table 1, and concluding based on the measured abundance whether the subject has colon cancer or not.

In one aspect, the invention provides a method for preparing RNA expression profiles that are indicative of the presence or absence of colorectal cancer. The RNA expression profiles are prepared from patient blood samples. The number of transcripts in the RNA expression profile may be selected so as to offer a convenient and cost effective means for screening samples for the presence or absence of colorectal cancer with high sensitivity and high specificity. Generally, the RNA expression profile includes the expression level or “abundance” of from 8 to about 3000 transcripts. In certain embodiments, the expression profile includes the RNA levels of 2500 transcripts or less, 2002 transcripts or less, 1500 transcripts or less, 1002 transcripts or less, 502 transcripts or less, 250 transcripts or less, 102 transcripts or less, or 50 transcripts or less.

In such embodiments, the profile may contain the expression level of at least 8 RNAs that are indicative of the presence or absence of colorectal cancer, and specifically, as selected from table 1, or may contain the expression level of at least 10 or at least 30 RNAs selected from table 1. Where larger profiles are desired, the profile may contain the expression level or abundance of at least about 60, at least 102, at least 202, at least 502, at least 1002 RNAs, or 2002 RNAs that are indicative of the presence or absence of colorectal cancer, and such RNAs may be selected from table 1. The identities and/or combinations of genes and/or transcripts that make up or are included in expression profiles are disclosed in tables 1 to 13. In particular embodiments, the genes or transcripts include those listed in table 8 or table 13.

Such RNA expression profiles in accordance with this aspect may be evaluated for the presence or absence of an RNA expression signature indicative of colorectal cancer. Generally, the sequential addition of transcripts from table 1 to the expression profile provides for higher sensitivity and/or specificity for the detection of colorectal cancer. For example, the sensitivity of the methods provided herein may be at least 75 %, or at least 80 %, or at least 85 %, or at least 90 %. The specificity of the method may be at least 85 %, or at least 90 %.

In a second aspect, the invention provides a method for detecting, diagnosing, or screening for colorectal cancer. In this aspect the method comprises preparing an RNA expression profile by measuring the abundance of at least 8 RNAs in a patient blood sample, where the abundance of such RNAs are indicative of the presence or absence of colorectal cancer. The RNAs may be selected from the RNAs listed in table 1, and optionally also from the RNAs listed in table 2, and exemplary sets of such RNAs are disclosed in tables 3 to 13. The method further comprises evaluating the profile for the presence or absence of an RNA expression signature indicative of colorectal cancer, to thereby conclude whether the patient has or does not have colorectal cancer. The method generally provides a sensitivity for the detection of colorectal cancer of at least about 75 %, while providing a specificity of at least about 85 %.

In various embodiments, the method comprises determining the abundance of at least 30 RNAs, at least 60 RNAs, at least 102 RNAs, at least 202 RNAs, at least 502 RNAs, at least 1002 RNAs, or of at least 2002 RNAs chosen from the RNAs listed in table 1, and as exemplified in tables 3 to 13, and optionally one or more RNAs from table 2 in addition thereto, as exemplified in table 3, and then classifying the sample as being indicative of colorectal cancer, or not being indicative of colorectal cancer.

In other aspects, the invention provides kits and custom arrays for preparing the gene expression profiles, and for determining the presence or absence of colorectal cancer.

### Detailed description of the invention

The invention provides methods and kits for screening, diagnosing, and detecting colorectal cancer in human patients (subjects). “Colorectal cancer” (CRC) refers to both colorectal adenoma and colorectal carcinoma.

A colorectal adenoma is characterized by atypical growth of epithelial cells in mucosal tissue, i.e. neoplasia. Hypercellularity with enlarged, hyperchromatic nuclei, varying degrees of nuclear stratification, nuclear polymorphisms, and loss of polarity are the histologically defining features. In colorectal adenoma, this abnormal growth is confined to the mucosa; a synonym of adenoma is intraepithelial neoplasia (IEN). If this atypical growth of epithelial cells extends/invades through the muscularis mucosae, the muscle layer under the mucosa, with destruction of the usual anatomical wall, the pathologist terms this atypical growth a colorectal carcinoma.

The distinction between high- (HIEN) and low-grade (LIEN) intraepithelial neoplasia refers to the extent of the defining features.

A patient with CRC is traditionally defined as having undergone surgery/resection of colon and/or rectum for CRC and whose resection specimen has undergone examination by a board certified pathologist, who has diagnosed a colorectal carcinoma as defined above. A patient with CRC may have undergone complete colonoscopy of colon and rectum during which the examining physician has taken a sample of suspect tissue, which in turn has undergone examination by a board-certified pathologist, who has diagnosed a colorectal carcinoma as defined above. A synonym for a patient with CRC is “CRC-case” or simply “case.”

A patient without CRC is traditionally a person that has undergone complete colonoscopy during which the examining physician, an endoscopist, has noted no abnormal tissue growth. A synonym for a patient without CRC is “non-CRC-case” or “control.” This however does not exclude that this person has any other carcinoma.

A patient with HIEN is traditionally a person that has undergone surgery/resection of colon and/or rectum for suspected CRC and whose resection specimen has undergone examination

by a board certified pathologist, who has diagnosed a high-grade intraepithelial neoplasia as defined above. Alternatively, a patient with HIEN may be a person that has undergone complete colonoscopy of colon and rectum during which the examining physician has taken a sample of suspect tissue, which in turn has undergone examination by a board certified pathologist, who has diagnosed a high-grade intraepithelial neoplasia as defined above. A synonym for a person with HIEN is “HIEN-case” or “HIEN.”

A patient with LIEN is traditionally a person that has undergone surgery/resection of colon and/or rectum for suspected CRC and whose resection specimen has undergone examination by a board certified pathologist, who has diagnosed a high-grade intraepithelial neoplasia. Alternatively, a patient with LIEN is a person that has undergone complete colonoscopy of colon and rectum during which the examining physician has taken a sample of suspect tissue, which in turn has undergone examination by a board certified pathologist, who has diagnosed a low-grade intraepithelial neoplasia as defined above. A synonym for a person with LIEN “is LIEN-case” or “LIEN.”

As disclosed herein, the present invention provides methods and kits for screening patient samples for those that are positive for CRC, that is, in the absence of colonoscopy and/or surgery or resection of colon or rectum with pathologist’s examination.

The invention relates to the determination of the abundance of RNAs to detect a colorectal cancer in a human subject, wherein the determination of the abundance is based on RNA obtained (or isolated) from whole blood of the subject or from blood cells of the subject. For example, the sample may be obtained using PAXgene (QIAGEN) or an equivalent RNA isolation system. The measurement of the abundance of RNAs in the sample is preferably performed together, i.e. sequentially or preferably simultaneously. The blood sample preferably does not contain cancer cells. Preferably, the sample comprises or consists of white blood cells.

In various aspects, the invention involves preparing an RNA expression profile from a patient sample. The method may comprise isolating RNA from whole blood, and detecting the abundance or relative abundance of selected transcripts. As used herein, the terms RNA “abundance” and RNA “expression” are used interchangeably. The “RNAs” may be defined

by reference to an expressed gene, or by reference to a transcript, or by reference to a particular oligonucleotide probe for detecting the RNA (or cDNA derived therefrom), each of which is listed in table 1 for 2002 RNAs, and in table 2 for 750 RNAs that are indicative of the presence or absence of colorectal cancer. Specifically, table 1 lists such RNAs by probe ID, gene symbol, and Transcript ID, and such nucleotide sequences are publicly accessible. Table 1A gives the fold change in expression levels for the genes/transcripts listed in table 1, when measured in 64 control cases, and 55 CRC positive cases. Table 2, listing RNAs that can be measured in addition to the RNAs of table 1, lists RNAs by probe ID, gene symbol, and Transcript ID, and such nucleotide sequences are publicly accessible.

The number of transcripts in the RNA expression profile may be selected so as to offer a convenient and cost effective means for screening samples for the presence or absence of colorectal cancer with high sensitivity and high specificity. For example, the RNA expression profile may include the expression level or “abundance” of from 8 to about 3000 transcripts. In certain embodiments, the expression profile includes the RNA levels of 2500 transcripts or less, 2002 transcripts or less, 1500 transcripts or less, 1002 transcripts or less, 502 transcripts or less, 250 transcripts or less, 202 transcripts or less, 100 transcripts or less, or 50 transcripts or less. Such profiles may be prepared, for example, using custom microarrays or multiplex gene expression assays as described in detail herein.

In such embodiments, the profile may contain the expression level of at least 8 RNAs that are indicative of the presence or absence of colorectal cancer, and specifically, as selected from table 1, or may contain the expression level of at least 8, at least 10 or at least 30 RNAs selected from table 1. Where larger profiles are desired, the profile may contain the expression level or abundance of at least 60, 102, 202, 502, 1002 RNAs, or 2002 RNAs that are indicative of the presence or absence of colorectal cancer, and such RNAs may be selected from table 1, possibly together with one or more RNAs selected from table 2. Such RNAs may be defined by gene, or by transcript ID, or by probe ID, as set forth in table 1 and table 2.

The identities of genes and/or transcripts that make up, or are included in exemplary expression profiles are disclosed in tables 1 to 13. As shown herein, profiles selected from the RNAs of table 1, optionally together with RNAs of table 2, support the detection of

colorectal cancer with high sensitivity and high specificity. An exemplary selection of RNAs for the RNA expression profile is shown in table 8 and in table 3.

In some embodiments, the expression profile includes the abundance of one or more intergenic RNAs. As used herein, “intergenic RNA” or “an intergenic RNA sequence” is a transcript of table 1 whose abundance in a probe is determined that does not correspond to a known gene or transcript. Such sequences are listed in table 13.

Thus, in various embodiments, the abundance of at least 8, at least 30, at least 60, at least 102, at least 202, at least 502, at least 1002, or at least 2002 distinct RNAs are measured, in order to arrive at a reliable diagnosis of colon cancer. The set of RNAs may comprise, consist essentially of, or consist of, a set or subset of RNAs exemplified in any one of tables 1 to 13. The term “consists essentially of” in this context allows for the expression level of additional transcripts to be determined that are not differentially expressed in colorectal cancer subjects, and which may therefore be used as positive or negative expression level controls or for normalization of expression levels between samples.

Such RNA expression profiles may be evaluated for the presence or absence of an RNA expression signature indicative of colorectal cancer. Generally, the sequential addition of transcripts from table 1 to the expression profile provides for higher sensitivity and/or specificity for the detection of colorectal cancer. For example, the sensitivity of the methods provided herein may be at least 75 %, or at least 80 %, or at least 85 %, or at least 90 %. The specificity of the method may be at least 85 %, or at least 90 %.

The present invention provides an in-vitro diagnostic test system (IVD) that is trained (as described further below) for the detection of a colorectal cancer. For example, in order to determine whether a patient has colorectal cancer, reference RNA abundance values for colon cancer positive and negative samples are determined. The RNAs can be quantitatively measured on an adequate set of training samples comprising cases and controls, and with adequate clinical information on carcinoma status, applying adequate quality control measures, and on an adequate set of test samples, for which the detection is yet to be made. With such quantitative values for the RNAs and the clinical data for the training samples, a

classifier can be trained and applied to the test samples to calculate the probability of the presence or non-presence of the colorectal carcinoma.

Various classification schemes are known for classifying samples between two or more classes or groups, and these include, without limitation: Naïve Bayes, Support Vector Machines, Nearest Neighbors, Decision Trees, Logistics, Artificial Neural Networks, and Rule-based schemes. In addition, the predictions from multiple models can be combined to generate an overall prediction. Thus, a classification algorithm or “class predictor” may be constructed to classify samples. The process for preparing a suitable class predictor is reviewed in R. Simon, Diagnostic and prognostic prediction using gene expression profiles in high-dimensional microarray data, British Journal of Cancer (2003) 89, 1599-1604, which review is hereby incorporated by reference.

In this context, the invention teaches an in-vitro diagnostic test system (IVD) that is trained in the detection of a colorectal cancer referred to above, comprising at least 8 RNAs, which can be quantitatively measured on an adequate set of training samples comprising cases and controls, with adequate clinical information on carcinoma status, applying adequate quality control measures, and on an adequate set of test samples, for which the detection yet has to be made. Given the quantitative values for the RNAs and the clinical data for the training samples, a classifier can be trained and applied to the test samples to calculate the probability of the presence or absence of the colorectal carcinoma.

The present invention provides methods for detecting, diagnosing, or screening for colorectal cancer in a human subject with a sensitivity and specificity not previously described for a blood-based method (see Figs. 1 to 4). Specifically, the sensitivity of the methods provided herein is at least 75 %, at least 80 %, at least 85 %, or at least 90 %. The specificity of the methods is at least 85 %, or at least 90 %, for example, when determined with samples of at least 122 patients with CRC and adequate samples (e.g., at least 109) of normal individuals without CRC are tested.

In another embodiment, further RNAs than the at least 8 RNAs listed in table 1 can be used according to the invention, namely preferably the RNAs listed in table 2. Put differently, the measurement of any combination of at least 8 RNAs listed in table 1 can be combined with

the measurement of any combination of at least 1 RNA listed in table 2. In a preferred embodiment, the number of RNAs from table 2 used is not greater than the number of RNAs used of in table 1. For example, when 8 (10, 20) RNAs are used of table 1, not more than 8 (10, 20) RNAs of table 2 are used in addition. In further preferred embodiments, at least 8, at least 10, at least 20, at least 60, at least 100, at least 200, or at least 500 RNAs from table 2 are used together with RNAs selected from table 1.

Without wishing to be bound by any particular theory, the above finding may be due to the fact that an organism such as a human systemically reacts to the development of a colorectal tumor by altering the expression levels of genes in different pathways. The formation of cancerous tumor cells from a nonmalignant adenoma or nonmalignant polyps, the formation of high-grade intraepithelial neoplasias and the further growth and development of cancer of different stages may trigger differential expression of genes in white blood cells that are involved in both adaptive and innate immune responses, for example wound healing, inflammatory response and antibody production pathways. Although the change in expression (abundance) might be small for each gene in a particular signature, measuring a set of at least 8 genes, preferably even larger numbers such as 100, 202, 1002, 2002 or even more RNAs, for example at least 10, at least 100, at least 200, at least 1000, or at least 2000 RNAs at the same time, and optionally together with RNAs listed in table 2, allows for the detection of colorectal cancer in a human with high sensitivity and high specificity.

In this context, an RNA obtained from a subject's blood sample, i.e. an RNA biomarker, is an RNA molecule with a particular base sequence whose presence within a blood sample from a human subject can be quantitatively measured. The measurement can be based on a part of the RNA molecule, namely a part of the RNA molecule that has a certain base sequence, which allows for its detection and thereby allows for the measurement of its abundance in a sample. The measurement can be by methods known in the art, for example analysis on a solid phase device, or in solution (for example, by RT-PCR). Probes for the particular RNAs can either be bought commercially, or designed based on the respective RNA sequence.

In the method of the invention, the abundance of several RNA molecules (e.g. mRNA or pre-spliced RNA, intron-lariat RNA, micro RNA, small nuclear RNA, or fragments thereof) is determined in a relative or an absolute manner, wherein an absolute measurement of RNA

abundance is preferred. The RNA abundance is, if applicable, compared with that of other individuals, or with multivariate quantitative thresholds.

The determination of the abundance of the RNAs described herein is performed from blood samples using quantitative methods. In particular, RNA is isolated from a blood sample obtained from a human subject that is to undergo CRC testing. Although the examples described herein use microarray-based methods, the invention is not limited thereto. For example, RNA abundance can be measured by *in situ* hybridization, amplification assays such as the polymerase chain reaction (PCR), sequencing, or microarray-based methods. Other methods that can be used include polymerase-based assays, such as RT-PCR (e.g., TAQMAM), hybridization-based assays, such as DNA microarray analysis, as well as direct mRNA capture with branched DNA (QUANTIGENE) or HYBRID CAPTURE (DIGENE).

In certain embodiments, the invention employs a microarray. A "microarray" includes a specific set of probes, such as oligonucleotides and/or cDNAs (e.g., expressed sequence tags, "ESTs") corresponding in whole or in part, and/or continuously or discontinuously, to regions of RNAs that can be extracted from a blood sample of a human subject. The probes are bound to a solid support. The support may be selected from beads (magnetic, paramagnetic, etc.), glass slides, and silicon wafers. The probes can correspond in sequence to the RNAs of the invention such that hybridization between the RNA from the subject sample (or cDNA derived therefrom) and the probe occurs. In the microarray embodiments, the sample RNA can optionally be amplified before hybridization to the microarray. Prior to hybridization, the sample RNA is fluorescently labeled. Upon hybridization to the array and excitation at the appropriate wavelength, fluorescence emission is quantified. Fluorescence emission for each particular RNA is directly correlated with the amount of the particular RNA in the sample. The signal can be detected and together with its location on the support can be used to determine which probe hybridized with RNA from the subject's blood sample.

Accordingly, in certain aspects, the invention is directed to a kit or microarray for detecting the level of expression or abundance of RNAs in the subject's blood sample, where this "profile" allows for the conclusion of whether the subject has colorectal cancer or not (at a level of accuracy described herein). In another aspect, the invention relates to a probe set that allows for the detection of the RNAs associated with CRC. If these particular RNAs are

present in a sample, they (or corresponding cDNA) will hybridize with their respective probe (i.e., a complementary nucleic acid sequence), which will yield a detectable signal. Probes are designed to minimize cross reactivity and false positives. In one embodiment, the probes used are given e.g. in table 1 and table 2 as so-called Affymetrix probe set ID numbers. An Affymetrix probe set ID number is an identifier that refers to a set of probes selected to represent expressed sequences on an array. An Affymetrix probe set ID number identifies each probe present on the array, as known to a person of skill in the art. From the sequence defined by an Affymetrix probe set ID number, the sequence of an RNA hybridizing with the probe can be deduced.

Thus, the invention in certain aspects provides a microarray, which generally comprises a solid support and a set of oligonucleotide probes. The set of probes generally contains from 8 to about 3,000 probes, including at least 8 probes selected from table 1 or 8, and in addition may optionally contain a set of probes from table 2. In certain embodiments, the set contains 2002 probes or less, or 1000 probes or less, 500 probes or less, or 202 probes or less. In various embodiments, at least 10, at least 30, or at least 100 probes are listed in table 1 or table 8. The set of probes may comprise, or consist essentially of, the probes listed in table 8, with optionally one or more probes from table 2. Alternatively, the set of probes includes probes that hybridize to a combination of RNAs exemplified in any one of table 4, table 5, table 6, table 7, table 8, table 9, table 10, table 11, table 12, or table 13. The microarray may comprise, e.g., about 100,000 probes, some of which may be probes for providing reference data. For example, the microarray may comprise about 10,000 to 100,000 probes providing reference data, together with the probes of table 1 and optionally table 2.

In another embodiment, the microarray may comprise further probes for detecting RNAs listed in table 2. In certain embodiments, the set of oligonucleotide probes comprises 700 probes or less, 500 probes or less, or 200 probes or less for detecting RNAs listed in table 2.

The conclusion whether the subject has colorectal cancer or not is preferably reached on the basis of a classification algorithm, which can be developed using e.g. a random forest method, a support vector machine (SVM), or a K-nearest neighbor method (K-NN), such as a 3-nearest neighbor method (3-NN), as known in the art.

From the cross-classification of the true disease state (Positive = patient with CRC and Negative = patient without CRC) as determined by a physician and the test result as determined by the classification algorithm, the following measures for binary tests can be derived (Sullivan MS. *The Statistical Evaluation of Medical Tests for Classification and Prediction*. Oxford University Press, 2003), see table E. An example is given in table F.

**Table E:** Cross-Classification of True Disease State by Test Result

Test Result	True Disease State		Total
	Negative	Positive	
Negative	$n_{11}$	$n_{12}$	$n_{1\Sigma}$
Positive	$n_{21}$	$n_{22}$	$n_{2\Sigma}$
Total	$n_{\Sigma 1}$	$n_{\Sigma 2}$	$n_{\Sigma\Sigma}$

**Table F:** Example of a Cross-Classification of True Disease State by Test Result

Test Result	True Disease State		Total
	Negative	Positive	
Negative	30	10	40
Positive	20	70	90
Total	50	80	130

“Sensitivity” ( $S^+$  or true positive fraction (TPF)) refers to the count of positive test results among all true positive disease states divided by the count of all true positive disease states; in terms of table E this reads:  $S^+ = n_{22} / n_{\Sigma 2}$ ; the result from table F would read:  $S^+ = 70 / 80 = 0.875$ . “Specificity” ( $S^-$  or true negative fraction (TNF)) refers to the count of negative test results among all true negative disease states divided by the count of all true negative disease states; in terms of table E this reads:  $S^- = n_{11} / n_{\Sigma 1}$ ; the result from table F would read:  $S^- = 30 / 50 = 0.6$ . “Correct Classification Rate” (CCR or true fraction (TF)) refers to the sum of the count of positive test results among all true positive disease states and count of negative test results among all true negative disease states divided by all the sum of all cases; in terms of table E this reads:  $CCR = (n_{11} + n_{22}) / n_{\Sigma\Sigma}$ ; the result from table F would read:  $CCR = (30 + 70) / 130 \approx 0.769230769$ . The measures  $S^+$ ,  $S^-$ , and CCR address the question: To what degree does the test reflect the true disease state?

“Positive Predictive Value” (PV<sup>+</sup> or PPV) refers to the count of true positive disease states among all positive test results divided by the count of all positive test results; in terms of table E

this reads:  $PV^+ = n_{22} / n_{2\Sigma}$ ; the result from table F would read:  $PV^+ = 70 / 90 \approx 0.777777778$ . “Negative Predictive Value” ( $PV^-$  or  $NPV$ ) refers to the count of true negative disease states among all negative test results divided by the count of all negative test results; in terms of table E this reads:  $PV^- = n_{11} / n_{1\Sigma}$ ; the result from table F would read:  $PV^- = 30 / 40 = 0.75$ . The predictive values address the question: How likely is the disease given the test results?

Exact or asymptotic confidence limits (CI) for these rates or fractions can be computed using the commercially available software package SAS (SAS Institute Inc., Cary, NC, USA; [www.sas.com](http://www.sas.com)) or the publicly available software package R ([www.r-project.org](http://www.r-project.org)) (for literature reference see: Agresti A, Caffo B. Simple and effective confidence intervals for proportions and differences of proportions from adding two successes and two failures. *The American Statistician*: 54: 280-288, 2000).

The preferred RNA molecules that can be used in combinations described herein for diagnosing and detecting colorectal cancer in a subject according to the invention can be found in table 1 and table 2. The inventors have shown that the selection of at least 8 or more RNAs of the markers listed in table 1 can be used to diagnose or detect colorectal cancer in a subject using a blood sample from that subject. The RNA molecules that can be used for detecting, screening and diagnosing colorectal cancer are selected from the RNAs provided in table 2 (optionally together with RNAs provided in table 1), 3, 4, 5, 6, 7 or 8. Also, the RNAs (e.g., at least 8, at least 10, at least 30, or more) can be selected from table 8.

Specifically, the method of the invention comprises at least the following steps: measuring the abundance of at least 8 RNAs (preferably 8 RNAs or 10 RNAs) in the sample, that are chosen from the RNAs listed in table 1, and concluding, based on the measured abundance, whether the subject has colorectal cancer or not. Measuring the abundance of RNAs may comprise isolating RNA from blood samples as described, and hybridizing the RNA or cDNA prepared therefrom to a microarray. Alternatively, other methods for determining RNA levels may be employed.

Similarly, the abundance of at least 8 RNAs (preferably up to 29 RNAs), of at least 30 RNAs (preferably up to 59 RNAs), of at least 60 RNAs (preferably up to 101 RNAs), of at least 102 RNAs (preferably up to 201 RNAs), of at least 202 RNAs (preferably up to 501 RNAs), of at

least 502 RNAs (preferably ob to 1001 RNAs), of at least 1002 RNAs (preferably up to 2001 RNAs), or of at least 2002 RNAs that are chosen from the RNAs listed in table 1 can be measured in the method of the invention. In a preferred embodiment, the abundance of at least 8 RNAs (preferably up to 29 RNAs), of at least 30 RNAs (preferably up to 59 RNAs), of at least 60 RNAs (preferably up to 101 RNAs), of at least 102 RNAs (preferably up to 201 RNAs), of at least 202 RNAs (preferably up to 501 RNAs), or of at least 502 RNAs (preferably ob to 750 RNAs) that are chosen from the RNAs listed in table 2 can be measured in the method of the invention together with RNAs listed in table 1.

Three examples of a set of 8 RNAs of which the abundance can be measured in the method of the invention are listed in table 4 with the following performance data:

	Sensitivity	Specificity
Sig. 1	84.0%	94.0%
Sig. 2	83.6%	96.9%
Sig. 3	81.8%	98.4%

Three examples of a set of 30 RNAs of which the abundance can be measured in the method of the invention are listed in table 5 with the following performance data:

	Sensitivity	Specificity
Sig. 1	83.6%	85.9%
Sig. 2	92.7%	98.4%
Sig. 3	96.4%	98.4%

Three examples of a set of 60 RNAs of which the abundance can be measured in the method of the invention are listed in table 6 with the following performance data:

	Sensitivity	Specificity
Sig. 1	92.7%	92.2%
Sig. 2	94.6%	99.4%
Sig. 3	92.7%	98.4%

Two examples of a set of 102 RNAs of which the abundance can be measured in the method of the invention are listed in table 7 with the following performance data:

	Sensitivity	Specificity
Sig. 1	89.1%	95.3%
Sig. 2	94.5%	96.9%
Sig. 3	94.5%	96.9%

An example for a set of 202 RNAs of which the abundance can be measured in the method of the invention is listed in table 8. This set of 202 RNAs is particularly preferred. The performance data is as follows:

	Sensitivity	Specificity
Sig. 1	90.1%	95.3%
Sig. 2	90.1%	98.4%
Sig. 3	92.7%	100%

An example for a set of 502 RNAs of which the abundance can be measured in the method of the invention is listed in table 9 with the following performance data:

	Sensitivity	Specificity
Sig. 1	90.1%	96.6%
Sig. 2	90.1%	98.4%
Sig. 3	94.5%	98.4%

An example for a set of 1002 RNAs of which the abundance can be measured in the method of the invention is listed in table 10 with the following performance data:

	Sensitivity	Specificity
Sig. 1	92.7%	96.9%
Sig. 2	94.6%	98.4%
Sig. 3	92.7%	98.4%

An example for a set of 2002 RNAs of which the abundance can be measured in the method of the invention is listed in table 1.

In a further embodiment of the invention, using the example of 202 RNAs, the inventors have shown that the method of the invention is very robust in its performance. Specifically, the inventors have shown that from the set of 202 RNAs as listed in table 8, replacements of individual members of the set, enlargements of the set to up to 10 times, 8 times, 6 times, 4 times or 2 times the original set size (in the present example, 202 RNAs) with arbitrary other RNAs (also of RNAs not listed in table 1), or subtractions of individual RNAs from the original set of RNAs can be performed without reducing the performance (sensitivity and specificity) of the detection method of the invention.

In particular, in one aspect of the invention, the abundance of at least 202 RNAs is measured, wherein at least 152 of the 202 measured RNAs are chosen from the group of RNAs that are listed in table 1 and are referred to therein as SEQ ID NOs. 1 to 202, and up to 50 of the remaining measured RNAs are chosen from the group of RNAs that are listed in table 1 and are referred to therein as SEQ ID NOs. 203 to 2002 (preferred are those shown in table 11), thereby replacing a fraction of the RNAs that were originally chosen.

Performance data of the resulting sets is as follows:

	Sensitivity	Specificity
Sig. 1	85.5%	93.8%
Sig. 2	90.1%	89.1%
Sig. 3	98.4%	98.4%

In one embodiment, at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50 RNAs from table 8 are substituted with distinct RNAs listed in table 1.

In yet another embodiment, up to 70, up to 65, up to 60, up to 55, up to 50, up to 45, up to 40, up to 35, up to 30, up to 25, up to 20, up to 15 or up to 10 RNAs from table 8 are substituted with distinct RNAs listed in table 1.

In yet another aspect of the invention, the abundance of at least 1002 RNAs is measured, wherein at least 952 of the 1002 measured RNAs are chosen from the group of RNAs that are listed in table 1 and are referred to therein as SEQ ID NOs. 1 to 1002, and up to 50 of the remaining RNAs are chosen from the group of RNAs that are listed in table 1 and that are referred to therein as SEQ ID NOs. 1003 to 2002 (preferred are those shown in table 12).

Performance data of three examples of resulting sets are:

	Sensitivity	Specificity
Sig. 1	92.7%	96.9%
Sig. 2	94.5%	98.4%
Sig. 3	94.5%	98.4%

When the wording “at least a number of RNAs” is used, this refers to a minimum number of RNAs that are measured. It is possible to use up to 10,000 or 20,000 genes in the invention, a fraction of which can be RNAs listed in table 1. In preferred embodiments of the invention, abundance of up to 5,000, 2,500, 2,000, 1,000, 500, 250, 100, 80, 70, 60, 50, 40, 30, 20, 10, 5, 4, 3, 2, or 1 RNA of randomly chosen RNAs that are not listed in table 1 is measured in addition to RNAs of table 1 (or subsets thereof).

In a preferred embodiment, only RNAs that are mentioned in table 1 are measured.

In one aspect of the invention, a combination of at least two of the following markers can be excluded from the scope of the invention: BCNPI, CD163, CDA, MS4A1, BANK1, and MCG20553. In another aspect of the invention, a combination of at least four of the following markers can be excluded from the scope of the invention: LGALS8, VEGFA, RNF114, PHF20, SPN, AKAP13, PDZK1IP1, S100A6, CTSB, CD163, and CD302.

In another aspect of the invention, intergenic sequences were surprisingly found that can be used to detect colorectal cancer in a human subject based on RNA from blood. Without wishing to be bound by theory, it is possible that these intergenic sequences are part of pre-

spliced mRNAs, alternative polyadenylation sites or part of not yet known transcripts and reflect differences in expression of the respective genes and the complexity of the transcriptome. These intergenic sequences can be found in table 1 and are characterized by the absence of a gene symbol and RefSeq Transcript ID; they are also summarized in table 13. Examples of signatures consisting only of intergenic sequences are shown, together with sensitivity and specificity values, in figure 4.

In a preferred embodiment, signatures of only intergenic sequences of table 13 are used as RNA. In particular, sets of at least 8, at least 30, at least 50, at least 60, at least 102, at least 202, at least 302, at least 402, such as 50, 100, 200, 400, or 408 intergenic RNAs can be used (see also figure 4). It is particularly surprising that non-coding RNAs can be used to detect or diagnose CRC in a subject.

Accordingly, the invention also relates to a method for the detection of colorectal cancer in a human subject based on RNA from a blood sample obtained from the subject, comprising measuring the abundance of at least 8 RNAs in the form of intergenic sequences in the sample, that are chosen from the intergenic RNAs listed in table 1 and 13 (i.e., without a gene symbol and RefSeq Transcript ID) or that are listed in table 13. In another embodiment, the present invention is directed to a method for the detection or screening of colorectal cancer in a human subject. The method entails measuring the abundance of at most 3 RNAs in the form of intergenic sequences. In a particular embodiment, the 3 RNAs are chosen from the intergenic RNAs listed in tables 1 or 13.

The present invention, in one embodiment, is directed to diagnosing and screening for CRC by measuring the abundance of intergenic RNAs, particularly the intergenic RNAs listed in table 13, or a subset thereof. For example, in one embodiment, a method of diagnosing or screening for CRC can comprise measuring the abundance of at least 10, at least 20, at least 30, at least 40, at least 50, at least 100, at least 150, at least 200, at least 250, at least 300, at least 350, at least 400 or all 408 of the intergenic sequences provided in table 13 (see also Figure 4).

In another embodiment, a custom microarray is provided with oligonucleotide probes, designed to detect some or all of the intergenic RNAs provided in table 13. For example, in

one embodiment, a microarray is provided which includes oligonucleotide probes designed to hybridize to at least 10, at least 20, at least 30, at least 40, at least 50, at least 100, at least 150, at least 200, at least 250, at least 300, at least 350, at least 400 or all 408 intergenic RNA sequences (or cDNA derived therefrom) provided in table 13.

The expression profile or abundance of RNA markers for colorectal cancer, for example the at least 8 RNAs described above, (or more RNAs as disclosed above and herein), is determined preferably by measuring the quantity of the transcribed RNA of the marker gene. This quantity of the mRNA of the marker gene can be determined for example through chip technology (microarray), (RT-) PCR (for example also on fixated material), Northern hybridization, dot-blotting, sequencing, or in situ hybridization.

The microarray technology, which is most preferred, allows for the simultaneous measurement of RNA abundance of up to many thousand RNAs and is therefore an important tool for determining differential expression (or differences in RNA abundance), in particular between two biological samples or groups of biological samples. In order to apply the microarray technology, the RNAs of the sample need to be amplified and labeled and the hybridization and detection procedure can be performed as known to a person of skill in the art.

As will be understood by those of ordinary skill in the art, the analysis can also be performed through single reverse transcriptase-PCR, competitive PCR, real time PCR, differential display RT-PCR, Northern blot analysis, sequencing, and other related methods. In general, the larger the number of markers is that are to be measured, the more preferred is the use of the microarray technology. However, multiplex PCR, for example, real time multiplex PCR is known in the art and is amenable for use with the present invention, in order to detect the presence of 2 or more genes or RNA simultaneously.

The RNA whose abundance is measured in the method of the invention can be mRNA, cDNA, unspliced RNA, or its fragments. Measurements can be performed using the complementary DNA (cDNA) or complementary RNA (cRNA), which is produced on the basis of the RNA to be analyzed, e.g. using microarrays. A great number of different arrays as well as their manufacture are known to a person of skill in the art and are described for

example in the U.S. Patent Nos. 5,445,934; 5,532,128; 5,556,752; 5,242,974; 5,384,261; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,472,672; 5,527,681; 5,529,756; 5,545,331; 5,554,501; 5,561,071; 5,571,639; 5,593,839; 5,599,695; 5,624,711; 5,658,734; and 5,700,637, each of which is hereby incorporated in its entireties.

Preferably the decision whether the subject has colon cancer comprises the step of training a classification algorithm on an adequate training set of cases and controls and applying it to RNA abundance data that was experimentally determined based on the blood sample from the human subject to be diagnosed. The classification method can be a random forest method, a support vector machine (SVM), or a K-nearest neighbor method (K-NN), such as 3-NN.

For the development of a model that allows for the classification for a given set of biomarkers, such as RNAs, methods generally known to a person of skill in the art are sufficient, i.e., new algorithms need not be developed.

The major steps of such a model are:

- 1) condensation of the raw measurement data (for example combining probes of a microarray to probeset data, and/or normalizing measurement data against common controls);
- 2) training and applying a classifier (i.e. a mathematical model that generalizes properties of the different classes (carcinoma vs. healthy individual) from the training data and applies them to the test data resulting in a classification for each test sample).

For example, the raw data from microarray hybridizations can first be condensed with FARMS as shown by Hochreiter (2006, Bioinformatics 22(8): 943-9). Alternative methods for condensation such as Robust Multi-Array Analysis (RMA, GC-RMA, see Irizarry et al (2003). Exploration, Normalization, and Summaries of High Density Oligonucleotide Array Probe Level Data. Biostatistics. 4, 249–264) can be used. Similar to condensation, classification of the test data set through a support-vector-machine or other classification algorithms is known to a person of skill in the art, like for example classification and regression trees, penalized logistic regression, sparse linear discriminant analysis, Fisher linear discriminant analysis, K-nearest neighbors, shrunken centroids, and artificial neural networks (see Wladimir Wapnik: The Nature of Statistical Learning Theory, Springer Verlag, New York, NY, USA, 1995; Berhard Schölkopf, Alex Smola: Learning with Kernels: Support

Vector Machines, Regularization, Optimization, and Beyond, MIT Press, Cambridge, MA, 2002; S. Kotsiantis, Supervised Machine Learning: A Review of Classification Techniques, *Informatica Journal* 31 (2007) 249-268).

The key component of these classifier training and classification techniques is the choice of RNA biomarkers that are used as input to the classification algorithm.

In a further aspect, the invention refers to the use of a method as described above and herein for the detection of colorectal cancer in a human subject, based on RNA from a blood sample.

In a further aspect, the invention also refers to the use of a microarray for the detection of colorectal cancer in a human subject based on RNA from a blood sample. According to the invention, such a use can comprise measuring the abundance of at least 8 RNAs (or more, as described above and herein) that are listed in table 1, optionally together with at least one RNA from table 2. Accordingly, the microarray comprises at least 8 probes for measuring the abundance of the at least 8 RNAs. It is preferred that the microarray has a set of 11 probes for each RNA, but 1 or 3 probes for each RNA are also preferred. Commercially available microarrays, such as from Affymetrix, may be used. Alternatively, at most 8, at most 10, or at most 20 RNAs are measured in a sample, in order to detect or diagnose CRC.

In another embodiment, the abundance of the at least 8 RNAs is measured by multiplex RT-PCR. In a further embodiment, the RT-PCR includes real time detection, e.g., with fluorescent probes such as Molecular beacons or TaqMan® probes.

In a preferred embodiment, the microarray comprises probes for measuring only RNAs that are listed in table 1 (or subsets thereof).

In yet a further aspect, the invention also refers to a kit for the detection of colorectal cancer in a human subject based on RNA obtained from a blood sample. Such a kit comprises a means for measuring the abundance of at least 8 RNAs that are chosen from the RNAs listed in table 1, optionally together with at least one RNA from table 2. In a further embodiment, the at least 8 RNAs are chosen from the RNAs listed in any of the tables provided herein, for example, the RNAs are chosen from table 8 or 3. The kit may further comprise a means for

measuring the abundance of at least one RNA that is chosen from the RNAs listed in table 2. The means for measuring expression can be probes that allow for the detection of RNA in the sample or primers that allow for the amplification of RNA in the sample. Ways to devise probes and primers for such a kit are known to a person of skill in the art.

Further, the invention refers to the use of a kit as described above and herein for the detection of colorectal cancer in a human subject based on RNA from a blood sample comprising means for measuring the abundance of at least 8 RNAs that are chosen from the RNAs listed in table 1, and optionally further means for measuring the abundance of at least 1 RNA that is chosen from the RNAs listed in table 2. Such a use may comprise the following steps: contacting at least one component of the kit with RNA from a blood sample from a human subject, measuring the abundance of at least 8 RNAs (or more as described above and herein) that are chosen from the RNAs listed in table 1 using the means for measuring the abundance of at least 8 RNAs, and concluding, based on the measured abundance, whether the subject has colorectal cancer.

In yet a further aspect, the invention also refers to a method for preparing an RNA expression profile that is indicative of the presence or absence of colorectal cancer, comprising: isolating RNA from a whole blood sample, and determining the level or abundance of from 8 to about 3000 RNAs, including at least 8 RNAs selected from table 1, optionally further including at least 1 RNA selected from table 2.

Preferably, the expression profile contains the level or abundance of 2002 RNAs or less, of 1002 RNAs or less, of 502 RNAs or less, or of 202 RNAs or less. Further, it is preferred that at least 10 RNAs, at least 30 RNAs, at least 102 RNAs are listed in table 1 or table 8. It is preferred that the expression profile includes the level or abundance of the RNAs listed in table 8. It is also preferred that the expression profile also includes the level or abundance of RNAs listed in table 2.

In a further preferred embodiment of the method, the abundance of at least 50 RNAs provided in table 13 is measured. Another preferred embodiment of the method comprises determining the presence or absence of an RNA expression signature indicative of colorectal cancer.

In yet a further aspect, the invention also refers to a microarray, comprising a solid support and a set of oligonucleotide probes, the set containing from 8 to about 3,000 probes, and including at least 8 probes selected from table 1 or 8. Preferably, the set contains 2002 probes or less, 1000 probes or less, 500 probes or less, or 202 probes or less. At least 10 probes can be those listed in table 1 or table 8. At least 30 probes can be those listed in table 1 or table 8. In another embodiment, at least 102 probes are listed in table 1 or table 8. Further, it is preferred that the set of probes is listed in table 8. In another embodiment of the microarray, it contains at least 50 probes from table 13. Further, it is preferred that the set of probes also contains probes for detecting RNAs listed in table 2.

Features of the invention that were described herein in combination with a method, a microarray, a kit, or a use also refer, if applicable, to all other aspects of the invention.

## Tables

Table 1 shows a list of 2002 RNAs that are differentially expressed in several human subjects with colorectal cancer in comparison to subject without colorectal cancer. Each marker is characterized by a SEQ ID NO., by an Affymetrix probe set ID, and, if applicable, a HUGO ID and a Ref. Seq ID. The first 202 RNAs shown are an exemplary set of RNAs and are also shown in table 8.

Table 1A shows the changes of expression level (abundance) between cases and controls for all 2002 RNAs listed in table 1. The data was derived from 119 samples, 55 CRC cases and 64 controls. In the third column, the log-2 fold change is shown, and in the fourth column, the non-log fold change is shown.

The numbers in the third column represent the differences of cases (events) and controls (non-events) in log2 steps. For example, a value of 0.53 for the first probe set (SEQ ID No.1) means an expression increase by  $2^{0.53}$ -fold for events vs. non-events. In other words, the events had a 144 % expression (see fourth column) with respect to non-events, i.e. 44 % more RNA ( $0.44 = 2^{0.53}-1$ ,  $1.44 = 2^{0.53}$ ).

Table 2 shows a list of 750 RNAs that are differentially expressed in several human subjects with colorectal cancer in comparison to subjects without colorectal cancer. Each marker is characterized by a SEQ ID NO., by a probe set ID, and, if applicable, a gene symbol and a primary transcript ID. According to the invention, the abundance of at least 8 RNAs from the list of RNAs shown in table 1 is measured, optionally together with a number of RNAs taken from the list of RNAs of table 2. Examples of signatures consisting of RNAs from table 1 and table 2 are given in table 3.

Table 3 shows nine exemplary subsets consisting of RNAs listed in table 1 and table 2 (“combination signatures”).

It was found that any group of 8 or more RNAs from table 1 can be supplemented by a subset of RNAs from table 2. Combination signatures 1 through 9 of table 3 show exemplary combinations of subsets from tables 1 and 2 with at least 8 RNAs from table 1. Three different sizes of sets were used:

- less than 100 RNAs in combination signatures 1, 2, and 3

- 100 to 500 RNAs in combination signatures 4, 5, and 6
- 500 to 1000 RNAs in combination signatures 7, 8, and 9.

In each of these three size ranges, the first set was balanced in favor of RNAs from table 1 regarding RNA numbers, the second was balanced between numbers of RNAs of table 1 and table 2, and the third set was balanced in favor of table 2.

The following table shows the subset sizes for combination signatures 1 through 9 of table 3:

Combination signature	Number of RNAs from	
	Table 1	Table 2
1	22	8
2	8	8
3	8	24
4	256	101
5	100	100
6	91	261
7	620	275
8	275	272
9	269	633

The performance of the combination signature, determined as average over 1000 test runs, where each time randomly chosen 15 percent of the samples were used as test set, is as follows:

Combination signature	Sensitivity	Specificity
1	80.8%	85.4%
2	83.6%,	87.0%
3	77.3%,	81.5%
4	88.5%,	96.1%
5	90.4%,	92.3%
6	88.6%,	94.8%

7	90.9%,	96.3%
8	87.8%,	96.0%
9	88.7%,	95.9%

Table 4 shows three exemplary subsets of 8 RNAs of the RNAs listed in table 1. Performance (obtained using the leave-one-out method) (specificity / sensitivity): Sig1: 84 % / 94 %, Sig2: 83.6 % / 96.9 %, Sig3: 81.8 % / 98.45 %.

Table 5 shows three exemplary subsets of 30 RNAs of the RNAs listed in table 1. Performance (obtained using the leave-one-out method) (specificity / sensitivity): Sig1: 83.6 % / 85.9 %, Sig2: 92.7 % / 98.4 %; Sig3: 96.4 % / 98.4 %.

Table 6 shows three exemplary subsets of 60 RNAs of the RNAs listed in table 1. Performance (obtained using the leave-one-out method) (specificity / sensitivity): Sig 1: 92.7 % / 92.2 %, Sig 2: 94.6 % / 98.4 %, Sig 3: 92.7 % / 98.4 %.

Table 7 shows two exemplary subsets of 102 RNAs of the RNAs listed in table 1. Performance (obtained using the leave-one-out method) (specificity / sensitivity): Sig 1: 89.1 % / 95.3 %, Sig 2: 94.5 % / 96.9 %, Sig 3: 94.5 % / 96.9 %

Table 8 shows one exemplary subsets of 202 RNAs of the RNAs listed in table 1. Performance (specificity / sensitivity): Sig.1: 90.1 % / 95.3 %; Sig.2: 90.1 % / 98.4 %; Sig.3: 92.7 % / 100 %).

Table 9 shows one exemplary subsets of 502 RNAs of the RNAs listed in table 1. Performance (specificity / sensitivity): Sig.1: 90.1 % / 96.9 %, Sig.2: 90.1 % / 98.4 %; Sig.3: 94.5 % / 98.4 %.

Table 10 shows one exemplary subset of 1002 RNAs of the RNAs listed in table 1. Performance (obtained using the leave-one-out method) (specificity / sensitivity): Sig1: 92.7 % / 96.9 %, Sig2: 94.6 % / 98.4 %, Sig3: 92.7 % / 98.4 %.

Table 11 shows an exemplary set of RNAs for substitution of 50 RNAs from a set of 202 RNAs. Performance (obtained using the leave-one-out method) (specificity / sensitivity): Exchange 1: 85.5 % / 93.8 %, Exchange 2: 90.1 % / 89.1 %, Exchange 3: 98.4 % / 98.4 %.

Table 12 shows an exemplary set of RNAs for substitution of 50 RNAs from a set of 1002 RNAs. Performance (obtained using the leave-one-out method) (specificity / sensitivity): Exchange 1: 92.7 % / 96.9 %, Exchange 2: 94.5 % / 98.4 %, Exchange 3: 94.5 % / 98.4 %.

Table 13 shows a subset of the RNAs listed in table 1, namely those 408 RNAs that comprise an intergenic sequence or consist of an intergenic sequence. These RNAs are listed in table 1 without a gene name. Examples for performances of signatures consisting of RNAs from table 13 are shown in figure 4.

## Figures

**Figure 1** is a graph showing various RNA colorectal cancer signatures as a function of performance. The x-axis shows the number of RNAs in each particular signature subset. The subset length is varied along the x-axis from 8 to 202 (the full set). The y-axis shows performance of the subset. Performance is shown in terms of sensitivity (percentage of real carcinomas that were properly classified; lower values (squares)) and specificity ((percentage of real health controls that were properly classified; upper values (diamonds)) scaled from 50 % to 100 %. These are retrospective examinations of the 202 set. As the figure shows, reduced sets compared to the full set appear to have excellent performance. For each subset size, the performance was measured for 1000 randomly chosen subsets based on leave-16 %-out runs: the subset is trained on 84 % and applied to the remaining 16 %. The average performance over all the 16 % tests is shown.

**Figure 2** is a graph showing the performance of RNA colorectal cancer signatures, each having 202 RNAs. Various RNAs from the first signature in table 8 (first column) were replaced with random subsets of RNA markers from table 1 that are not listed in table 8. The number of replacements is given along the x-axis and performance is given on the y-axis. Performance of the method of detecting CRC is shown in terms of sensitivity (percentage of real carcinomas that were properly classified; lower values (squares)) and specificity (percentage of real health controls that were properly classified upper values (diamonds)) scaled from 50 % to 100 %. For each subset size, the performance was measured for 1000 randomly chosen subsets based on leave-16%-out runs: the subset is trained on 84 % and applied to the remaining 16 %. The average performance over all the 16 % tests is shown. As the figure shows, replacements do not alter the performance of the signature given in table 8.

**Figure 3** is a graph showing the performance of RNA colorectal cancer signatures. The signatures each contain the RNAs from table 8, and also include additional RNAs from table 1 that are not in table 8. The resulting signature contains the original 202 elements and the new elements. The extension size (original length + length of addition) is varied along the x-axis from 202 to 2002. Performance (y-axis) is shown in terms of sensitivity (percentage of real carcinomas that were properly classified; lower values (squares)) and specificity (percentage of real health controls that were properly classified; upper values (diamonds)),

scaled from 50 % to 100 %. These are retrospective examinations of the 202 set. As the figure demonstrates, larger sets compared to the set with 202 RNAs appear to have excellent performance. For each subset size, the performance was measured for 1000 randomly chosen subsets based on leave-16 %-out runs: the subset is trained on 84 % and applied to the remaining 16 %. The average performance over all the 16 % tests is shown.

**Figure 4** is a graph showing the performance of RNA colorectal cancer signatures of 50, 100, 200, and 400 RNAs, wherein the RNAs are all intergenic sequences. The signatures each contain the RNAs from table 13. The performance of, from left to right, the first 50, 100, 200, and 400 RNAs is shown. Each light column (on the left of each pair of two columns) represents the sensitivity, each dark column (on the right of each pair of two columns) represents the specificity for each signature.

## Examples

### Materials and Methods

#### Study Protocol

All results described herein are based on a prospective, clinical-diagnostic study protocol entitled “Früherkennung kolorektaler Karzinome mit Hilfe von RNA-basierten Expression-Signaturen aus Blut - Eine multizentrische, diagnostische Studie zur Entwicklung und Validierung von Genexpressions-Signaturen zur Früherkennung kolorektaler Karzinome - Version CRC.SCR.2.BR.1 vom 06. Januar 2009” in accordance with the Guideline for Good Clinical Practice (Directive 75/318/EEC) July 1996, version July 2002 (<http://www.emea.eu.int/pdfs/human/ich/013595en.pdf>). This study protocol was reviewed and approved by the local ethics authority, the “Ethik-Kommission der Landesärztekammer Brandenburg” on January 14<sup>th</sup> 2009. All persons entered into this study gave written informed consent that their blood samples and associated clinical data could be used for this research endeavor. Moreover, the persons gave written, informed consent that samples and clinical data could be audited by regulatory authorities if the research results would be used in a performance evaluation study (according to German law (Gesetz über Medizinprodukte)).

This study was designed as a cohort study. One cohort, the colonoscopy cohort, included persons undergoing colonoscopy. The second cohort, the surgery cohort, included patients scheduled for surgery for suspected colorectal carcinoma.

The inclusion criteria for the colonoscopy cohort were: 1) Willingness to undergo complete colonoscopy; 2) At least 55 years of age; 3) Ability to give written, informed consent; 4) Written informed consent after information about the study was given by a physician. The exclusion criteria for the colonoscopy cohort were: 1) Rectoscopy, sigmoidoscopy, or colonoscopy during the last five years prior to inclusion into the study; 2) Treatment of a malignant disease during the last five years prior to inclusion into the study, except for malignoma with low metastatic potential such as basalioma in situ of the skin.

The inclusion criteria for the surgery cohort were: 1) Age at initial diagnosis at least 18 years of age; 2) Ability to give written, informed consent; 3) (Suspected) Diagnosis of colorectal

carcinoma UICC-stage I to IV; 4) Surgery is planned in such a fashion that staging according to UICC-criteria is feasible; 5) No treatment prior to surgery; 6) No treatment for a malignant disease during the last five years prior to inclusion into the study; 7) No other disease that lowers life expectancy below one year; 8) Regular follow-up examinations have to be possible; 9) Written informed consent after information about the study was given by a physician.

#### Blood Drawing and Blood Sample Storage

In the colonoscopy cohort, blood was drawn after written, informed consent and prior to bowel cleaning and change of medication if necessary. In the surgery cohort, blood was drawn after written, informed consent and prior to removal of the resected tissue from the body of the patient by the surgeon. In both cohorts, colonoscopy cohort and surgery cohort, blood was drawn into PAXgene™ blood tubes (Becton Dickinson). The tubes were stored within four hours in a freezer at -20 °C until transport to the laboratory on dry ice, where the tubes were stored again in a freezer at -20 °C until RNA-extraction.

#### Sample Sizes

The study protocol initially stipulated the use of 220 blood samples from the colonoscopy cohort and 220 blood samples from the surgery cohort for the discovery of the signatures. However, the study protocol was open to changes depending on the results of the discovery process. Additionally, the study protocol initially stipulated the use 220 blood samples from the colonoscopy cohort and 220 blood samples from the surgery cohort for prospective performance evaluation purposes. Again, these sample sizes were open and amenable to change.

#### Quality Control of Clinical Data

All clinical data of all included persons from both cohorts were checked directly from the patient's medical records and entered into study databases, as prescribed in the study protocol. Each item in the study databases were checked independently by two persons. Patients of both cohorts together with their blood samples were withdrawn if any violation of the inclusion or exclusion criteria cited above was detected. In particular for the colonoscopy cohort, all samples and their associated clinical data were excluded from all analyses if the

colonoscopy was found to be not complete. Moreover, blood samples were destroyed and clinical data were deleted if the patient decided to withdraw his/her informed consent.

#### RNA extraction

Total RNA extraction from blood was performed using the QIAGEN PAXgene Blood miRNA Kit together with the QIAcube® robot according to the manufacturer's instructions. The RNA obtained is therefore sometimes referred to as PAX-RNA.

Before starting RNA extraction, the buffers BM3 and BM4 were mixed with the specified amount of 96-100 % Ethanol. Furthermore, the DNase I (1500 Kunitz units) was dissolved in 550 µl of RNase free water.

After thawing, the PAX-blood tubes were turned several times to ensure proper mixing and left over night (or minimal two hours) at room temperature. Then, the tubes were centrifuged for 10 minutes at 4000 x g using a swing out bucket. Next, the supernatant was carefully removed from each tube, and the pellets were washed (vortexing until complete resuspension) with 4 ml RNase free water. After centrifuging again for 10 minutes at 4000 x g, the pellets were resuspended in 350 µl buffer BR1 and transferred to 2 ml processing tubes. The opened tubes were then loaded into the rotor adapters of the centrifuge. Subsequently, all buffers were placed on the respective spots of the reagent bottle holder. After closing the lid, the PAXgene Blood miRNA Part A protocol was started. When it was finished, the instrument door was opened, the RNA containing tubes were closed and subsequently placed on the shaker adaptor. After closing the instrument door again, the PAXgene Blood miRNA Part B protocol was started. When the program was finished, concentration was determined by UV-absorption measurement and the samples were stored at -70 °C until use.

For understanding of underlying principles of the automatic procedure the manual protocol is briefly described below. There is no difference between the two methods until the resuspension of the pellet.

To the resuspended pellet 300 µl binding buffer (BR2) and 40 µl proteinase K solution was added and mixed by vortexing for 5 seconds. Incubation follows for 10 minutes at 55 °C using a shaker-incubator at 400–1400 rpm. After incubation, the temperature of the shaker–

incubator is set to 65 °C. The lysate is pipetted directly into a PAXgene Shredder spin column (lilac) placed in a 2 ml processing tube and centrifuged for 3 minutes at maximum speed (don't not to exceed 20,000 x g). The entire supernatant of the flow-through fraction was carefully transferred the to a fresh 1.5 ml microcentrifuge tube without disturbing the pellet in the processing tube. 350 µl ethanol (96–100%, purity grade p.a.) was added and mixed by vortexing. The mixture is briefly (1–2 seconds at 500–1000 x g) centrifuged to remove drops from the inside of the tube Lid. 700 µl of the sample is pipetted into the PAXgene RNA spin column (red) placed in a 2 ml processing tube, and centrifuged for 1 minute at 8,000–20,000 x g. The spin column was placed in a new 2 ml processing tube (PT), and the old processing tube containing flow-through discarded. Subsequently, the remaining sample was pipetted into the PAXgene RNA spin column, and centrifuged for 1 minute at 8,000–20,000 x g. The spin column was placed in a new 2 ml processing tube and the old processing tube containing flow-through again discarded. Subsequently, 350 µl wash buffer 1 (BR3) was pipetted into the PAXgene RNA spin column. After centrifugation for 1 minute at 8000–20,000 x g the spin column was placed in a new 2 ml processing tube and the old processing tube containing the flow-through again discarded. 10 µl DNase I stock solution is added to 70 µl DNA digestion buffer in a 1.5 ml microcentrifuge tube and mixed by gently flicking the tube followed by a brief centrifugation to collect residual liquid from the sides of the tube. The DNase I incubation mix (80 µl) was pipetted directly onto the PAXgene RNA spin column membrane, and placed on the benchtop (20–30 °C) for 15 minutes. After Incubation, 350 µl wash buffer 1 (BR3) is pipetted into the PAXgene RNA spin column and centrifuged for 1 minute at 8000–20,000 x g. The spin column was placed in a new 2 ml processing tube and the old processing tube containing flow-through again discarded. 500 µl wash buffer 2 (BR4) was pipetted into the PAXgene RNA spin column and centrifuged for 1 minute at 8,000–20,000 x g. The spin column was placed in a new 2 ml processing tube and the old processing tube containing flow-through again discarded. Another 500 µl wash buffer 2 (BR4) was added to the PAXgene RNA spin column and centrifuged for 3 minutes at 8,000–20,000 x g. The spin column is placed in a new 2 ml processing tube and the old processing tube containing flow-through again discarded. The column is centrifuged for 1 minute at 8,000–20,000 x g. The processing tube is discarded and the column was placed on a 1.5 ml microcentrifuge tube. 40 µl elution buffer (BR5) directly pipetted onto the PAXgene RNA spin column membrane and subsequently centrifuged for 1 minute at 8,000–20,000 x g to elute the RNA. The elution step is repeated using again 40 µl elution buffer (BR5) and the

same 1.5 ml microcentrifuge tube. The RNA is denatured for 5 minutes at 65 °C in the shaker–incubator (see above) without shaking.

The quality control is performed on the Agilent Bioanalyzer.

Total RNA (100 ng) was labeled and hybridized onto Affymetrix U133Plus 2.0 GeneChips (Affymetrix; Santa Clara, CA) according to the manufacturer's instructions. Briefly, the 100 ng total RNA was used for cDNA synthesis with the Ovation® Whole Blood system (Nugen, San Carlos, CA 94070). After SPIA™ Amplification the cDNA was purified with a QIAquick PCR purification spin column (QIAGEN, Hilden) and then subjected to Biotin labeling with the FL-Ovation™ cDNA Biotin Module V2 (Nugen).

5 µg cDNA was then added into the hybridization cocktail and the cocktail was applied to the probe array cartridge. After 16 hours hybridization, the array was washed with Affymetrix fluidics station 450. The array was then scanned with Affymetrix® GeneChip® Scanner. Hybridization signals were collected with the Affymetrix GCOS software (version 1.4), using the default settings and imported into R (Bioconductor package)

#### Recruitment

499 persons scheduled for colonoscopy were recruited into the study; RNA blood samples were taken prior to colonoscopy. The recruitment period for the non-CRC patients lasted from February 9, 2009 until April 3, 2009. In parallel, RNA blood samples were taken from patients with (suspected) diagnosis of CRC prior or during surgery for CRC.

#### Discovery Set-Up

##### Sample Selection for RNA-Extraction

The selection criteria of CRC-cases included availability of UICC stage information and the check that the patients did not fulfill any exclusion criteria for the MSKK-study. At this time clinical data of the non-CRC case were not available. Hence, the first 240 patients of the study were selected.

Altogether, 480 PAX-RNA samples, 240 from non-CRC persons and 240 from CRC patients, were randomized into the discovery set. Additionally, the order of processing by the laboratory was randomized. A drop-out rate of 10 %, or 20 cases in each group, was assumed.

### Results of RNA-Extraction

From the RNA-extraction samples, 14 samples (2.92 %) showed RNA integrity numbers (RIN) lower than 3.5, which rendered these samples unfit for microarray hybridization.

### Selection of Samples for Microarray Hybridization

Based on the results of RNA extraction and clinical information about UICC-stages and complete colonoscopy in case of non-CRC cases, 428 samples were authorized for microarray hybridization. The vast majority of drop-outs were incomplete colonoscopies.

### Microarray Pseudonymization

A pseudonymization procedure was set-up at the beginning of the hybridization. On each day microarrays were hybridized, the system administrator removed the raw scan image files from the scan computer system and placed them in a directory. The system administrator applied the program (GCOS) to compute the expression (abundance) values from the raw image data and stored the computed expression values of each probe in a so-called .CEL-file. When the days' microarray production was complete and the probe expression values were all computed, the system administrator informed the project leader that the days' production was ready for pseudonymization. Through a program, the original .CEL-file was copied and the filename was stored within the .CEL-file, and was exchanged with a pseudonym.

Moreover, the date and time of the scan which are also stored in the .CEL-file was also replaced, since from date and time of scan the sample would be identifiable. Lastly, the pseudonomized .CEL-files was copied into a directory accessible by the bioinformatics group and authorizes these .CEL-files for microarray quality control.

### Microarray Quality Control

The microarray data authorized for quality control were checked according to a Standard Operating Procedure (SOP), and a report was given to the project leader. As of now, two

scans of 128 scans (1.56 %; exact two-sided 95 % CI: 0.19 % – 5.53 %), one of a MAQC control sample and one of a clinical sample did not pass quality control.

### Discovery Procedure

In brief, all raw measurement data from microarray hybridizations scheduled for a discovery (i.e., from samples selected for discovery, and measurements that passed quality control) were condensed together with the FARMS algorithm as shown by Hochreiter et al 2006 ("A new summarization method for Affymetrix probe level data." *Bioinformatics* 2006 22(8):943-949, doi:10.1093/bioinformatics/btl033), and filtered using IN/I calls shown by Talloen et al., 2007 ("I/NI-calls for the exclusion of non-informative genes: a highly effective filtering tool for microarray data." *Bioinformatics* 2007; 23(21): 2897-2902 doi:10.1093/bioinformatics/btm478). During this discovery, FARMS version 1.4 was used as part of the statistical software systems R (version 2.9.0) and Bioconductor (version 1.6) (for this software, see <http://cran.r-project.org/>, <http://www.r-project.org/> and <http://www.bioconductor.org>, also Ross Ihaka and Robert Gentleman. R: A language for data analysis and graphics. *Journal of Computational and Graphical Statistics*, 5(3): 299-314, 1996; Gentleman et al 2005: *Bioinformatics and Computational Biology Solutions Using R and Bioconductor*, Springer, New York, NY).

The resulting condensed array data were then partitioned into groups of samples in a double nested bootstrap approach (Efron (1979) Bootstrap Methods--Another Look at the Jackknifing, *Ann. Statist.* 7, 1-6). In the outer loop of this bootstrap, the samples were partitioned into an outer test set and an outer training set. In the inner bootstrap loop, this outer training set was partitioned again into an inner training set and an inner test set.

On the inner training set, probeset relevance was estimated through a decision-tree-analysis. The influence of each feature was determined from its contribution to the classification error: In case the error of a probeset increases due to the permutation of the values of a probeset while the values of all other probesets remain unchanged, this probeset is weighted more strongly.

The relevance evaluations of the individual inner loops were combined for each external loop and the chosen probesets were used to train a support vector machine (Bernhard Schölkopf,

Alex Smola: *Learning with Kernels: Support Vector Machines, Regularization, Optimization, and Beyond*, MIT Press, Cambridge, MA, 2002, also see citations above). This classifier was trained on the outer training set (which was already used for its feature selection) and applied to the outer test set of samples. For this classification, the same methods and parameters were used as for the intended application on external data (for example as part of validation): the details are described below as application for the RNAs of the invention. The whole external loop of the bootstrap procedure is a simulation of later classification of unknown data. Its average performance over all external loops gives a prospective estimate of the performance of the classification procedure (mainly based on the chosen biomarker set). The common mistake of overfitting, i.e., the overly optimistic evaluation of a classification method on its discovery set, is thereby avoided.

Finally, the results of all inner loops and of all external loops were combined to form a common biomarker set with prospective estimates of performance.

### Application of the Invention

A number of RNAs that result from the discovery above can be used with state of the art classification methods as described in the cited literature and as known by a person of skill in the art. As any classification, it will require a representative training set, which the inventors obtained through a clinical study fulfilling the requirements described above. Part of the training set is the necessary clinical information (carcinoma patient or healthy control, as defined by the clinical study). Similar to the clinical requirements, this description of the algorithmic part of the application of the invention also presupposes the described lab process and quality controls were applied.

The training set of microarray raw data was condensed by the same method as the discovery set in the section “Discovery Procedure” above: the FARMS condensation algorithm, preferentially version 1.4 (available at <http://www.bioinf.jku.at/software/farms/farms.html> from the author of the software, citations to the publication of this algorithm see above). A standard implementation of support vector machines, such as the one contained in Bioconductor’s (see references above) package for machine learning “e1071” with parameter “kernel” set to “linear” (preferential version for this package is 1.5-19).

It is important not to present the classification information on the training data as numeric data, but as categorical data. This can be ensured by passing the corresponding arguments as an R “factor” (for example as in “`svm(..., as.factor(clinicalData),...)`”). Otherwise this `svm` algorithm will use the wrong type of classification.

To apply this `svm`, using the same software package, to any kind of new microarray data, a condensation step is necessary just as for the discovery data. It is possible to simply reapply the condensation method above to each individual new sample in combination with the whole discovery set. This first method approximates the preferential method well, which is to explicitly compute a condensation model or parameter based on the discovery data and apply it to the test data. This can be done with the software package `on.farms`, preferentially version 1.4.1, available from the author (see references above). The application of the described `svm` to the thus condensed test data produces the desired decision value.

The embodiments illustrated and discussed in this specification are intended only to teach those skilled in the art the one way to make and use the invention. Modifications and variation of the above-described embodiments of the invention are possible without departing from the invention, as appreciated by those skilled in the art in light of the above teachings. It is therefore understood that, within the scope of the claims and their equivalents, the invention may be practiced otherwise than as specifically described.

Table 1, page 1

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1	1560255_at	C10ORF31	XR_041926
2	238712_at	---	---
3	227970_at	GPR157	NM_024980
4	237056_at	INSC	NM_001042536.1
5	241981_at	FAM20A	NM_017565.2
6	223974_at	MGC11082	XR_079560.1
7	241415_at	---	---
8	1565544_at	RNF141	NM_016422.3
9	216693_x_at	HDGFRP3	NM_016073.2
10	1570264_at	---	---
11	221044_s_at	TRIM6-TRIM34	NM_001003818.1
12	203658_at	SLC25A20	NM_000387
13	213390_at	ZC3H4	NM_015168.1
14	224832_at	DUSP16	NM_030640
15	212642_s_at	HIVEP2	NM_006734.3
16	225005_at	PHF13	NM_153812.2
17	242167_at	---	---
18	221143_at	RPA4	NM_013347.3
19	243824_at	---	---
20	222139_at	KIAA1466	AB040899
21	237315_at	---	---
22	238360_s_at	---	---
23	239571_at	---	---
24	232356_at	---	---
25	224645_at	EIF4EBP2	NM_004096.4
26	1556110_at	---	---
27	234842_at	TRA@	---
28	212017_at	FAM168B	NM_001009993.2
29	226772_s_at	SAP30L	NM_024632.5
30	1552648_a_at	TNFRSF10A	NM_003844.2
31	225840_at	TEF	NM_003216.2
32	202657_s_at	SERTAD2	NM_014755.2
33	231764_at	CHRAC1	NM_017444.4
34	232513_x_at	C20ORF107	NM_001013646
35	233283_at	---	---
36	206983_at	CCR6	NM_031409.3
37	243654_at	---	---
38	223558_at	C9ORF80	NM_021218.1
39	225263_at	HS6ST1	NM_004807.2
40	1563497_at	USP25	NM_013396.3
41	237655_at	---	---

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
42	230571_at	PLLP	NM_015993
43	238439_at	ANKRD22	NM_144590.2
44	200666_s_at	DNAJB1	NM_006145.1
45	235024_at	PHF17	NM_199320.2
46	244025_at	ITPRIP	NM_033397.2
47	217868_s_at	METTL9	NM_001077180.1
48	236229_at	ZNF814	NM_001144989.1
49	202365_at	UNC119B	NM_001080533.1
50	208741_at	SAP18	NM_005870.4
51	226585_at	NEIL2	NM_001135747.1
52	219938_s_at	PSTPIP2	NM_024430.3
53	1554557_at	ATP11B	NM_014616.1
54	244492_at	---	---
55	243303_at	---	---
56	216112_at	---	---
57	225494_at	DYNLL2	NM_080677.2
58	239363_at	C9ORF80	NM_021218.1
59	1563975_at	RNF130	NM_018434.4
60	242917_at	RASGEF1A	NM_145313.2
61	240661_at	LOC284475	---
62	226547_at	MYST3	NM_001099413.1
63	231259_s_at	CCND2	NM_001759.3
64	210281_s_at	ZMYM2	NM_003453.2
65	235543_at	IRF2	---
66	202656_s_at	SERTAD2	NM_014755
67	243399_at	HAAO	NM_012205.2
68	205321_at	EIF2S3	NM_001415.3
69	230738_at	HIST2H4B	NM_001034077.4
70	234302_s_at	ALKBH5	NM_017758.3
71	231309_at	GNA12	NM_007353.2
72	201751_at	JOSD1	NM_014876.5
73	221654_s_at	USP3	NM_006537.2
74	235058_at	GPN2	NM_018066.3
75	203609_s_at	ALDH5A1	NM_170740.1
76	239845_at	---	---
77	223637_s_at	C11ORF56	NM_032127.3
78	228156_at	---	---
79	243509_at	---	---
80	238053_at	DHRSX	NM_145177.2
81	240733_at	---	---
82	235421_at	MAP3K8	NM_005204.2

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
83	204787_at	VSIG4	NM_007268.2
84	212806_at	PRUNE2	NM_015225.2
85	200759_x_at	NFE2L1	NM_003204.2
86	213174_at	TTC9	NM_015351.1
87	205181_at	ZNF193	NM_006299.3
88	242306_at	---	---
89	1562321_at	PDK4	NM_002612.3
90	201578_at	PODXL	NM_005397.3
91	1554132_a_at	FAM190B	NM_018999
92	225545_at	EEF2K	NM_013302.3
93	228811_at	TMEM8B	NM_001042590.1
94	203879_at	PIK3CD	NM_005026.3
95	201170_s_at	BHLHE40	NM_003670.2
96	215322_at	---	---
97	1562110_at	---	---
98	226804_at	FAM20A	NM_017565
99	1554116_s_at	PARP11	NM_020367.4
100	237942_at	---	---
101	219671_at	HPCAL4	NM_016257.2
102	210104_at	MED6	NM_005466.2
103	212097_at	CAV1	NM_001172895
104	1558761_a_at	FAM120AO_S	NM_198841.2
105	215888_at	PDS5B	NM_015032.2
106	208823_s_at	CDK16	NM_006201
107	201731_s_at	TPR	NM_00329
108	220131_at	FXYD7	NM_022006.1
109	216233_at	CD163	NM_004244.4
110	236629_at	C1ORF69	NM_001010867.2
111	1562260_at	---	---
112	33494_at	ETFDH	NM_004453
113	228068_at	GOLGA7B	NM_001010917.1
114	222640_at	DNMT3A	NM_022552.3
115	239077_at	GALNACT2	NM_018590
116	207040_s_at	ST13	NM_003932.3
117	228723_at	---	---
118	1562031_at	JAK2	NM_004972
119	218771_at	PANK4	NM_018216.1
120	219906_at	FLJ10213	NM_018029.3
121	217286_s_at	NDRG3	NM_032013.2
122	235777_at	ANKRD44	NM_153697.1
123	218625_at	NRN1	NM_016588.2

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
124	1567213_at	PNN	NM_002687.3
125	243276_at	ALS2CL	NM_147129.2
126	215210_s_at	DLST	NM_001933.3
127	207339_s_at	LTB	NM_002341.1
128	202533_s_at	DHFR	NM_000791.3
129	230267_at	WSB1	NM_015626.8
130	218168_s_at	CABC1	NM_020247.4
131	222844_s_at	SRR	NM_021947.1
132	233264_at	---	---
133	214501_s_at	H2AFY	NM_001040158.1
134	203505_at	ABCA1	NM_005502.2
135	203556_at	ZHX2	NM_014943.3
136	226474_at	NLRC5	NM_032206.3
137	215640_at	TBC1D2B	NM_015079.5
138	243902_at	---	---
139	208109_s_at	C15ORF5	NR_026813.1
140	220905_at	---	---
141	201259_s_at	SYPL1	NM_006754.2
142	221908_at	RNFT2	NM_001109903.1
143	205379_at	CBR3	NM_001236.3
144	229374_at	EPHA4	NM_004438.3
145	1569666_s_at	---	---
146	228216_at	SERPINC1	NM_000488
147	240217_s_at	GMEB1	NM_024482.1
148	218287_s_at	EIF2C1	NM_012199.2
149	218517_at	PHF17	NM_024900
150	244796_at	GLS	NM_014905.3
151	233976_at	---	---
152	233647_s_at	CDADC1	NM_030911.1
153	239489_at	UBLCP1	NM_145049.3
154	238923_at	SPOP	NM_001007226.1
155	237018_at	AKAP13	NM_007200.3
156	240176_at	---	---
157	200860_s_at	CNOT1	NM_016284.3
158	212639_x_at	TUBA1C	NM_032704.3
159	201236_s_at	BTG2	NM_006763.2
160	205857_at	SLC18A2	NM_003054.3
161	228603_at	ACTR3	NM_005721.3
162	238728_at	MRPS23	NM_016070.2
163	216729_at	---	---
164	206674_at	FLT3	NM_004119.2

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
165	238025_at	MLKL	NM_152649.2
166	203255_at	FBXO11	NM_025133.3
167	213294_at	CCDC75	NM_174931.2
168	215209_at	SEC24D	NM_014822.2
169	208030_s_at	ADD1	NM_176801.1
170	238570_at	ZNF611	NM_030972.2
171	232164_s_at	EPPK1	NM_031308.1
172	209828_s_at	IL16	NM_172217.2
173	222526_at	GATAD2A	NM_017660.3
174	203366_at	POLG	NM_002693.2
175	242319_at	DGKG	NM_001080745.1
176	223846_at	AZI2	NM_022461.3
177	234402_at	TRD@	M18414
178	32042_at	ENOX2	NM_182314.1
179	225478_at	MFHAS1	NM_004225.2
180	229754_at	---	---
181	243514_at	---	---
182	213484_at	ADD2	NM_001617.2
183	208744_x_at	HSPH1	NM_006644.2
184	1558592_at	---	---
185	239462_at	ZNF284	NM_001037813.2
186	212399_s_at	VGLL4	NM_014667.2
187	236013_at	CACNA1E	NM_000721.2
188	211986_at	AHNAK	NM_001620.1
189	242803_at	---	---
190	217815_at	SUPT16H	NM_007192.3
191	219120_at	C2ORF44	NM_025203.2
192	242780_at	VAPA	NM_003574.5
193	242695_at	---	---
194	1570394_at	XRN1	NM_019001.3
195	221639_x_at	HNRNPU	NM_031844.2
196	217185_s_at	ZNF259	NM_003904.3
197	1568964_x_at	SPN	NM_001030288.1
198	1556942_at	---	---
199	200594_x_at	HNRNPU	NM_031844.2
200	1559739_at	CHPT1	NM_020244.2
201	232157_at	SPRY3	NM_005840.1
202	224855_at	PYCR2	NM_013328.2
203	200796_s_at	MCL1	NM_021960
204	201747_s_at	SAFB	NM_002967
205	205781_at	C16orf7	NM_004913

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
206	201032_at	BLCAP	NM_006698
207	226687_at	PRPF40A	NM_017892
208	207253_s_at	UBN1	NM_001079514
209	222310_at	SFRS15	NM_001145444
210	203218_at	MAPK9	NM_001135044
211	203409_at	DDB2	NM_000107
212	217857_s_at	RBM8A	NM_005105
213	212428_at	KIAA0368	NM_001080398
214	213266_at	TUBGCP4	NM_014444
215	201652_at	COPS5	NM_006837
216	204211_x_at	EIF2AK2	NM_001135651
217	201051_at	ANP32A	NM_006305
218	230998_at	---	---
219	230664_at	H2BFM	NM_001164416
220	200979_at	PDHA1	NM_000284
221	228623_at	---	---
222	200767_s_at	FAM120A	NM_014612
223	201721_s_at	LAPTM5	NM_006762
224	200030_s_at	SLC25A3	NM_002635
225	215828_at	---	---
226	237943_at	---	---
227	1569369_at	ZFYVE28	NM_020972
228	204216_s_at	ZC3H14	NM_001160103
229	202796_at	SYNPO	NM_001109974
230	226656_at	CRTAP	NM_006371
231	212234_at	ASXL1	NM_015338
232	209715_at	CBX5	NM_001127321
233	200016_x_at	HNRNPA1	NM_002136
234	209078_s_at	TXN2	NM_012473
235	204275_at	SOLH	NM_005632
236	1566501_at	---	---
237	228091_at	STX17	NM_017919
238	1554096_a_at	RBM33	NM_053043
239	209358_at	TAF11	NM_005643
240	1554628_at	ZNF57	NM_173480
241	203379_at	RPS6KA1	NM_001006665
242	1569999_at	---	---
243	232628_at	---	---
244	219004_s_at	C21orf45	NM_018944
245	222043_at	CLU	NM_001831
246	212527_at	PPPDE2	NM_015704

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
247	235114_x_at	HOOK3	NM_032410
248	232188_at	AKAP13	NM_006738
249	209735_at	ABCG2	NM_004827
250	207604_s_at	SLC4A7	NM_003615
251	224990_at	C4orf34	NM_174921
252	235840_at	---	---
253	232648_at	PSMA3	NM_002788
254	220213_at	TSHZ2	NM_173485
255	218912_at	GCC1	NM_024523
256	219963_at	DUSP13	NM_001007271
257	214783_s_at	ANXA11	NM_001157
258	213836_s_at	WIPI1	NM_017983
259	202184_s_at	NUP133	NM_018230
260	237317_at	---	---
261	214016_s_at	SFPQ	NM_005066
262	236901_at	---	---
263	204025_s_at	PDCD2	NM_002598
264	208740_at	SAP18	NM_005870
265	201083_s_at	BCLAF1	NM_001077440
266	208087_s_at	ZBP1	NM_001160417
267	202941_at	NDUFV2	NM_021074
268	215545_at	---	---
269	201088_at	KPNA2	NM_002266
270	1556007_s_at	---	---
271	212859_x_at	MT1E	NM_175617
272	204245_s_at	RPP14	NM_001098783
273	210965_x_at	CDC2L5	NM_003718
274	204116_at	IL2RG	NM_000206
275	219409_at	SNIP1	NM_024700
276	204962_s_at	CENPA	NM_001042426
277	221535_at	LSG1	NM_018385
278	228200_at	ZNF252	NR_023392
279	203905_at	PARN	NM_001134477
280	212415_at	38961	NM_015129
281	232427_at	ZNF224	NM_013398
282	226052_at	BRD4	NM_014299
283	227346_at	IKZF1	NM_006060
284	201588_at	TXNL1	NM_004786
285	1561880_a_at	SIGLEC16	NR_002825
286	221529_s_at	PLVAP	NM_031310
287	224686_x_at	LRRC37A2	NM_001006607

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
288	201762_s_at	PSME2	NM_002818
289	210732_s_at	LGALS8	NM_006499
290	229897_at	ZNF641	NM_152320
291	203836_s_at	MAP3K5	NM_005923
292	220439_at	RIN3	NM_024832
293	213193_x_at	TRBC1	---
294	225125_at	MMGT1	NM_173470
295	1555884_at	PSMD6	NM_014814
296	210277_at	AP4S1	NM_001128126
297	223946_at	MED23	NM_004830
298	212346_s_at	MXD4	NM_006454
299	203799_at	CD302	NM_014880
300	228158_at	LOC645166	NR_027238
301	238140_at	ARV1	NM_022786
302	236703_at	NT5C2	NM_001134373
303	1565651_at	ARF1	NM_001024226
304	200988_s_at	PSME3	NM_005789
305	206652_at	ZMYM5	NM_001039649
306	202717_s_at	CDC16	NM_001078645
307	1554424_at	FIP1L1	NM_001134937
308	231557_at	---	---
309	1557520_a_at	---	---
310	200751_s_at	HNRNPC	NM_001077442
311	209299_x_at	PPIL2	NM_014337
312	238704_at	---	---
313	1555906_s_at	C3orf23	NM_001029839
314	232034_at	LOC203274	---
315	1568907_at	---	---
316	232330_at	C7orf44	NM_018224
317	1563687_a_at	FRYL	NM_015030
318	226107_at	---	---
319	214472_at	HIST1H2AD	NM_003530
320	208978_at	CRIP2	NM_001312
321	222975_s_at	CSDE1	NM_001007553
322	232569_at	---	---
323	230735_at	---	---
324	203497_at	MED1	NM_004774
325	219138_at	RPL14	NM_001034996
326	200815_s_at	PAFAH1B1	NM_000430
327	233545_at	INPP5D	NM_001017915
328	208876_s_at	PAK2	NM_002577

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
329	204533_at	CXCL10	NM_001565
330	241752_at	SLC8A1	NM_001112800
331	202768_at	FOSB	NM_001114171
332	234991_at	ZXDC	NM_001040653
333	228818_at	---	---
334	218805_at	GIMAP5	NM_018384
335	219001_s_at	DCAF10	NM_024345
336	202386_s_at	KIAA0430	NM_014647
337	228624_at	TMEM144	NM_018342
338	236971_at	---	---
339	202840_at	TAF15	NM_003487
340	209124_at	MYD88	NM_002468
341	210136_at	MBP	NM_001025081
342	202003_s_at	ACAA2	NM_006111
343	238788_at	LOC494150	---
344	243598_at	---	---
345	222909_s_at	BAG4	NM_004874
346	218641_at	LOC65998	NM_001144936
347	239104_at	MGC42157	XR_017710
348	1558354_s_at	---	---
349	238257_at	MLLT10	NM_001009569
350	1568830_at	IRAK3	NM_001142523
351	231937_at	---	---
352	212766_s_at	ISG20L2	NM_030980
353	1569652_at	MLLT3	NM_004529
354	223832_s_at	CAPNS2	NM_032330
355	227249_at	NDE1	NM_001143979
356	209162_s_at	PRPF4	NM_004697
357	210943_s_at	LYST	NM_000081
358	213963_s_at	SAP30	NM_003864
359	233079_at	MERTK	NM_006343
360	242945_at	FAM20A	NM_017565
361	239213_at	SERPINB1	NM_030666
362	226229_s_at	SSU72	NM_014188
363	212124_at	ZMIZ1	NM_020338
364	224357_s_at	MS4A4A	NM_024021
365	236273_at	NBPF1	NM_017940
366	204526_s_at	TBC1D8	NM_001102426
367	233263_at	---	---
368	209907_s_at	ITSN2	NM_006277
369	201880_at	ARIH1	NM_005744

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
370	218448_at	C20orf11	NM_017896
371	243631_at	MPHOSPH8	NM_017520
372	238026_at	RPL35A	NM_000996
373	218454_at	PLBD1	NM_024829
374	202172_at	VEZF1	NM_007146
375	209161_at	PRPF4	NM_004697
376	201470_at	GSTO1	NM_004832
377	206335_at	GALNS	NM_000512
378	204061_at	PRKX	NM_005044
379	203368_at	CRELD1	NM_001031717
380	235309_at	RPS15A	NM_001019
381	226874_at	KLHL8	NM_020803
382	217905_at	C10orf119	NM_024834
383	215175_at	PCNX	NM_014982
384	1555793_a_at	ZFP82	NM_133466
385	235681_at	---	---
386	243315_at	---	---
387	205475_at	SCRG1	NM_007281
388	239902_at	---	---
389	216134_at	FRMD4B	NM_015123
390	235119_at	TAF3	NM_031923
391	1553333_at	C1orf161	NM_152367
392	203113_s_at	EEF1D	NM_001130053
393	235518_at	SLC8A1	NM_001112800
394	217555_at	SMC1A	NM_006306
395	227854_at	---	---
396	225613_at	MAST4	NM_015183
397	201739_at	SGK1	NM_001143676
398	201960_s_at	MYCBP2	NM_015057
399	221571_at	TRAF3	NM_003300
400	221819_at	RAB35	NM_006861
401	203298_s_at	JARID2	NM_004973
402	1558459_s_at	LOC401320	XM_379482
403	57516_at	ZNF764	NM_033410
404	202714_s_at	KIAA0391	NM_014672
405	1559614_at	FLJ38773	XR_001008
406	223027_at	SNX9	NM_016224
407	201927_s_at	PKP4	NM_001005476
408	200699_at	KDELR2	NM_001100603
409	223189_x_at	MLL5	NM_018682
410	215507_x_at	---	---

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
411	219385_at	SLAMF8	NM_020125
412	218039_at	NUSAP1	NM_001129897
413	1567101_at	---	---
414	1563629_a_at	---	---
415	217894_at	KCTD3	NM_016121
416	212814_at	AHCYL2	NM_001130720
417	205692_s_at	CD38	NM_001775
418	233186_s_at	BANP	NM_017869
419	219308_s_at	AK5	NM_012093
420	1556750_at	LOC153577	---
421	203676_at	GNS	NM_002076
422	234865_at	LOC100293705	XM_002346051
423	209555_s_at	CD36	NM_000072
424	200633_at	UBB	NM_018955
425	203065_s_at	CAV1	NM_001753
426	235959_at	---	---
427	218047_at	OSBPL9	NM_024586
428	218358_at	CRELD2	NM_001135101
429	228138_at	ZNF498	NM_145115
430	226913_s_at	SOX8	NM_014587
431	1560705_at	---	---
432	232821_at	GTSF1L	NM_001008901
433	239679_at	---	---
434	237953_at	---	---
435	220560_at	C11orf21	NM_001142946
436	220797_at	METT10D	NM_024086
437	219112_at	RAPGEF6	NM_001164386
438	235061_at	PPM1K	NM_152542
439	212945_s_at	MGA	NM_001080541
440	218232_at	C1QA	NM_015991
441	213604_at	TCEB3	NM_003198
442	229659_s_at	---	---
443	212794_s_at	KIAA1033	NM_015275
444	218969_at	Magmas	NM_016069
445	1555487_a_at	ACTR3B	NM_001040135
446	207129_at	CA5B	NM_007220
447	244578_at	LCP2	NM_005565
448	225407_at	MBP	NM_001025081
449	230515_at	---	---
450	232559_at	---	---
451	244726_at	---	---

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
452	238644_at	MYSM1	NM_001085487
453	203240_at	FCGBP	NM_003890
454	236399_at	---	---
455	223492_s_at	LRRFIP1	NM_001137550
456	203234_at	UPP1	NM_003364
457	213260_at	FOXC1	NM_001453
458	216142_at	---	---
459	233072_at	NTNG2	NM_032536
460	228660_x_at	SEMA4F	NM_004263
461	238107_at	---	---
462	201376_s_at	HNRNPF	NM_001098204
463	210317_s_at	YWHAE	NM_006761
464	218426_s_at	RNF216	NM_207111
465	239637_at	---	---
466	224336_s_at	DUSP16	NM_030640
467	244659_at	LOC100131015	XM_001726042
468	1555950_a_at	CD55	NM_000574
469	219284_at	HSPBAP1	NM_024610
470	236007_at	AKAP10	NM_007202
471	212601_at	ZZEF1	NM_015113
472	233781_s_at	RIF1	NM_018151
473	238109_at	---	---
474	201305_x_at	ANP32B	NM_006401
475	210592_s_at	SAT1	NM_002970
476	204140_at	TPST1	NM_003596
477	227599_at	C3orf59	NM_178496
478	1554287_at	TRIM4	NM_033017
479	243470_at	---	---
480	1562898_at	---	---
481	239287_at	---	---
482	1558938_at	---	---
483	1557780_at	---	---
484	207734_at	LAX1	NM_001136190
485	214595_at	KCNG1	NM_002237
486	236982_at	---	---
487	1555608_at	CAPRIN2	NM_001002259
488	228923_at	S100A6	NM_014624
489	207968_s_at	MEF2C	NM_001131005
490	203927_at	NFKBIE	NM_004556
491	222306_at	---	---
492	203130_s_at	KIF5C	NM_004522

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
493	219498_s_at	BCL11A	NM_018014
494	1557224_at	---	---
495	223313_s_at	MAGED4	NM_001098800
496	1555180_at	LOC100132686	XR_078450
497	203632_s_at	GPRC5B	NM_016235
498	220387_s_at	HHLA3	NM_001031693
499	217791_s_at	ALDH18A1	NM_001017423
500	1559479_at	PI4K2B	NM_018323
501	1554600_s_at	LMNA	NM_005572
502	1569792_a_at	C12orf72	NM_001135863
503	235071_at	WDR92	NM_138458
504	243334_at	CACNA1D	NM_000720
505	234848_at	---	---
506	201489_at	PPIF	NM_005729
507	210189_at	HSPA1L	NM_005527
508	221816_s_at	PHF11	NM_001040443
509	231319_x_at	KIF9	NM_001134878
510	202863_at	SP100	NM_001080391
511	235699_at	REM2	NM_173527
512	211930_at	HNRNPA3	NM_194247
513	228349_at	---	---
514	224516_s_at	CXXC5	NM_016463
515	204099_at	SMARCD3	NM_001003801
516	221589_s_at	ALDH6A1	NM_005589
517	1569617_at	OSBP2	NM_030758
518	212904_at	LRRC47	NM_020710
519	203007_x_at	LYPLA1	NM_006330
520	236165_at	MSL3	NM_006800
521	229404_at	TWIST2	NM_057179
522	222234_s_at	DBNDD1	NM_001042610
523	200659_s_at	PHB	NM_002634
524	226668_at	WDSUB1	NM_001128212
525	219669_at	CD177	NM_020406
526	208778_s_at	TCP1	NM_001008897
527	203320_at	SH2B3	NM_005475
528	226802_s_at	LOC96610	NR_027293
529	1565928_at	---	---
530	212259_s_at	PBXIP1	NM_020524
531	231816_s_at	UBE2Q1	NM_017582
532	228184_at	DISP1	NM_032890
533	222821_s_at	GEMIN7	NM_001007269

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
534	217722_s_at	NGRN	NM_001033088
535	1566171_at	RFFL	NM_001017368
536	233219_at	---	---
537	1565894_at	---	---
538	1569599_at	SAMSN1	NM_022136
539	206761_at	CD96	NM_005816
540	1556253_s_at	---	---
541	1564053_a_at	YTHDF3	NM_152758
542	229199_at	SCN9A	NM_002977
543	226734_at	EIF4E2	NM_004846
544	226447_at	ASH1L	NM_018489
545	202985_s_at	BAG5	NM_001015048
546	208180_s_at	HIST1H4H	NM_003543
547	217995_at	SQRDL	NM_021199
548	234172_at	---	---
549	205169_at	RBBP5	NM_005057
550	212387_at	TCF4	NM_001083962
551	213293_s_at	TRIM22	NM_006074
552	244536_at	---	---
553	232306_at	CDH26	NM_021810
554	212838_at	DNMBP	NM_015221
555	235033_at	NPEPL1	NM_024663
556	203460_s_at	PSEN1	NM_000021
557	209409_at	GRB10	NM_001001549
558	216527_at	---	---
559	1554453_at	HNRPLL	NM_001142650
560	226775_at	ENY2	NM_020189
561	211152_s_at	HTRA2	NM_013247
562	235825_at	---	---
563	212594_at	PDCD4	NM_014456
564	206059_at	ZNF91	NM_003430
565	214184_at	NPFF	NM_003717
566	205392_s_at	CCL14	NM_004166
567	213046_at	PABPN1	NM_004643
568	234883_x_at	TRBV7-3	---
569	228650_at	---	---
570	227112_at	TMCC1	NM_001017395
571	217431_x_at	CYBB	NM_000397
572	202095_s_at	BIRC5	NM_001012270
573	206026_s_at	TNFAIP6	NM_007115
574	226651_at	HOMER1	NM_004272

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
575	240859_at	---	---
576	1555634_a_at	LILRA5	NM_021250
577	235207_at	---	---
578	231695_at	---	---
579	213524_s_at	GOS2	NM_015714
580	212318_at	TNPO3	NM_012470
581	227329_at	ZBTB46	NM_025224
582	203050_at	TP53BP1	NM_001141979
583	219975_x_at	OLAH	NM_001039702
584	215671_at	PDE4B	NM_001037339
585	231260_at	BC036928	---
586	217513_at	C17orf60	NM_001085423
587	1556339_a_at	---	---
588	208774_at	CSNK1D	NM_001893
589	221536_s_at	LSG1	NM_018385
590	231641_at	FJ10213	NM_018029
591	202551_s_at	CRIM1	NM_016441
592	204110_at	HNMT	NM_001024074
593	201235_s_at	BTG2	NM_006763
594	219633_at	TTPAL	NM_001039199
595	227055_at	METTL7B	NM_152637
596	234427_at	TRAJ17	---
597	239819_at	---	---
598	230762_at	---	---
599	201651_s_at	PAC SIN2	NM_007229
600	244579_at	---	---
601	233476_at	---	---
602	1562576_at	---	---
603	227589_at	PITPN C1	NM_012417
604	209062_x_at	NCOA3	NM_006534
605	236755_at	TBC1D23	NM_018309
606	223608_at	EFCAB2	NM_001143943
607	204079_at	TPST2	NM_001008566
608	238789_at	KANK1	NM_015158
609	213172_at	TTC9	NM_015351
610	224582_s_at	NUCKS1	NM_022731
611	243796_at	LOC100293 311	XM_002345033
612	213567_at	---	---
613	242197_x_at	CD36	NM_000072
614	244177_at	---	---
615	210873_x_at	APOBEC3A	NM_145699

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
616	238929_at	SFRS2B	NM_032102
617	229756_at	---	---
618	224681_at	GNA12	NM_007353
619	242423_x_at	---	---
620	219300_s_at	CNTNAP2	NM_014141
621	209477_at	EMD	NM_000117
622	203088_at	FBLN5	NM_006329
623	242947_at	---	---
624	210609_s_at	TP53I3	NM_004881
625	203660_s_at	PCNT	NM_006031
626	213755_s_at	---	---
627	216297_at	---	---
628	1559375_s_at	---	---
629	217866_at	CPSF7	NM_001136040
630	223337_at	SDCCAG10	NM_005869
631	221524_s_at	RRAGD	NM_021244
632	216614_at	---	---
633	220342_x_at	EDEM3	NM_025191
634	218883_s_at	MLF1IP	NM_024629
635	217486_s_at	ZDHHC17	NM_015336
636	236572_at	---	---
637	203188_at	B3GNT1	NM_006876
638	1564231_at	IFT80	NM_020800
639	209765_at	ADAM19	NM_023038
640	202902_s_at	CTSS	NM_004079
641	224369_s_at	FBXO38	NM_030793
642	218876_at	TPPP3	NM_015964
643	240099_at	---	---
644	228119_at	LRCH3	NM_032773
645	239130_at	---	---
646	1560971_a_at	---	---
647	222820_at	TNRC6C	NM_001142640
648	243476_at	NF1	NM_000267
649	1558697_a_at	KIAA0430	NM_014647
650	1558046_x_at	LOC100132 864	XM_001713861
651	241275_at	CAPZA1	NM_006135
652	209425_at	AMACR	NM_014324
653	228835_at	---	---
654	237901_at	---	---
655	234785_at	---	---
656	1557193_at	---	---

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
657	244447_at	---	---
658	204950_at	CARD8	NM_014959
659	227410_at	FAM43A	NM_153690
660	205500_at	C5	NM_001735
661	228394_at	STK10	NM_005990
662	1561206_at	KLHL8	NM_020803
663	48808_at	DHFR	NM_000791
664	228253_at	LOXL3	NM_032603
665	227501_at	---	---
666	226674_at	SHISA4	NM_198149
667	202290_at	PDAP1	NM_014891
668	237062_at	---	---
669	1554665_at	ZNF586	NM_017652
670	237082_at	---	---
671	201206_s_at	RRBP1	NM_001042576
672	1561615_s_at	SLC8A1	NM_001112800
673	201783_s_at	RELA	NM_001145138
674	212180_at	CRKL	NM_005207
675	220289_s_at	AIM1L	NM_001039775
676	225157_at	MLXIP	NM_014938
677	237627_at	---	---
678	203052_at	C2	NM_000063
679	215030_at	GRSF1	NM_001098477
680	208629_s_at	HADHA	NM_000182
681	201757_at	NDUFS5	NM_004552
682	232251_at	NUDT16P	NR_002949
683	228468_at	MASTL	NM_032844
684	226989_at	RGMB	NM_001012761
685	1556257_at	LOC645513	XR_078309
686	223194_s_at	SLC22A23	NM_015482
687	212166_at	XPO7	NM_001100161
688	240233_at	---	---
689	1563053_at	LOC729083	XM_001133289
690	1568915_at	---	---
691	223121_s_at	SFRP2	NM_003013
692	204067_at	SUOX	NM_000456
693	226313_at	C10orf35	NM_145306
694	206636_at	RASA2	NM_006506
695	212457_at	TFE3	NM_006521
696	1553856_s_at	P2RY10	NM_014499
697	230885_at	SPG7	NM_003119

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
698	231357_at	CLEC12B	NM_001129998
699	241956_at	---	---
700	201596_x_at	KRT18	NM_000224
701	244026_at	---	---
702	211072_x_at	TUBA1B	NM_006082
703	230619_at	ARNT	NM_001668
704	1554833_at	MCTP2	NM_001159643
705	212388_at	USP24	NM_015306
706	1566809_a_at	---	---
707	235310_at	GCET2	NM_001008756
708	211003_x_at	TGM2	NM_004613
709	230036_at	SAMD9L	NM_152703
710	239391_at	FAM120AO_S	NM_198841
711	214243_s_at	SERHL	NM_014509
712	240806_at	RPL15	NM_002948
713	1554447_at	LOC554203	NR_024582
714	242501_at	---	---
715	209865_at	SLC35A3	NM_012243
716	238961_s_at	FNDC3A	NM_001079673
717	1557465_at	RP11-327P2.4	NR_027047
718	1562608_at	---	---
719	214394_x_at	EEF1D	NM_001130053
720	230796_at	LOC440900	XR_041709
721	220546_at	MLL	NM_005933
722	210640_s_at	GPER	NM_001039966
723	1562745_at	---	---
724	1556323_at	CUGBP2	NM_001025076
725	213208_at	KIAA0240	NM_015349
726	201143_s_at	EIF2S1	NM_004094
727	202087_s_at	CTSL1	NM_001912
728	1558279_a_at	KDSR	NM_002035
729	223591_at	RNF135	NM_032322
730	202005_at	ST14	NM_021978
731	242031_at	---	---
732	204889_s_at	NEURL	NM_004210
733	217701_x_at	---	---
734	213774_s_at	---	---
735	235288_at	---	---
736	204222_s_at	GLIPR1	NM_006851
737	214513_s_at	CREB1	NM_004379

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
738	201678_s_at	C3orf37	NM_001006109
739	1563348_at	---	---
740	1561306_s_at	STRC	NM_153700
741	223733_s_at	PPP4R1L	NR_003505
742	203308_x_at	HPS1	NM_000195
743	232121_at	TRDMT1	NM_004412
744	1556211_a_at	---	---
745	232033_at	USP37	NM_020935
746	202601_s_at	HTATSF1	NM_001163280
747	212680_x_at	PPP1R14B	NM_138689
748	1563466_at	MYLK	NM_053025
749	219676_at	ZSCAN16	NM_025231
750	1558586_at	ZNF33B	NM_006955
751	230886_at	---	---
752	240144_at	DNASE1	NM_005223
753	1560034_a_at	---	---
754	221223_x_at	CISH	NM_013324
755	200999_s_at	CKAP4	NM_006825
756	235456_at	---	---
757	214766_s_at	AHCTF1	NM_015446
758	202706_s_at	UMPS	NM_000373
759	233176_at	---	---
760	227449_at	EPHA4	NM_004438
761	225655_at	UHRF1	NM_001048201
762	236024_at	GPM6A	NM_005277
763	207654_x_at	DR1	NM_001938
764	236094_at	TCF7L2	NM_001146274
765	230166_at	KIAA1958	NM_133465
766	229008_at	WDR60	NM_018051
767	210817_s_at	CALCOCO2	NM_005831
768	1560069_at	PLEKHM3	NM_001080475
769	236113_at	---	---
770	202794_at	INPP1	NM_001128928
771	231174_s_at	---	---
772	1559459_at	LOC613266	NM_001033516
773	238892_at	---	---
774	203803_at	PCYOX1	NM_016297
775	221801_x_at	NEFL	NM_006158
776	222449_at	PMEPA1	NM_020182
777	202954_at	UBE2C	NM_007019
778	1568997_at	---	---

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
779	228769_at	ZSCAN22	NM_181846
780	1557119_a_at	ZNF575	NM_174945
781	200857_s_at	NCOR1	NM_006311
782	234082_at	---	---
783	243819_at	---	---
784	206632_s_at	APOBEC3B	NM_004900
785	203430_at	HEBP2	NM_014320
786	1555626_a_at	SLAMF1	NM_003037
787	1559618_at	LOC100129447	XM_001719594
788	1555058_a_at	LPGAT1	NM_014873
789	221253_s_at	TXND5	NM_001145549
790	219493_at	SHCBP1	NM_024745
791	238607_at	ZNF296	NM_145288
792	215411_s_at	TRAF3IP2	NM_001164281
793	203616_at	POLB	NM_002690
794	206075_s_at	CSNK2A1	NM_001895
795	232953_at	C20orf69	NM_001104925
796	226652_at	USP3	NM_006537
797	222413_s_at	MLL3	NM_170606
798	214814_at	YTHDC1	NM_001031732
799	228983_at	---	---
800	215342_s_at	RABGAP1L	NM_001035230
801	227737_at	SRPRB	NM_021203
802	233033_at	ZEB2	NM_014795
803	209378_s_at	FAM190B	NM_018999
804	209105_at	NCOA1	NM_003743
805	221833_at	LONP2	NM_031490
806	239516_at	---	---
807	205798_at	IL7R	NM_002185
808	200868_s_at	RNF114	NM_018683
809	1564639_at	LOC389906	XM_001713861
810	203633_at	CPT1A	NM_001031847
811	223588_at	THAP2	NM_031435
812	202349_at	TOR1A	NM_000113
813	200600_at	MSN	NM_002444
814	201196_s_at	AMD1	NM_001033059
815	208642_s_at	XRCC5	NM_021141
816	231340_at	---	---
817	210253_at	HTATIP2	NM_001098520
818	212624_s_at	CHN1	NM_001025201
819	228478_at	---	---

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
820	1569154_a_at	---	---
821	1553857_at	IGSF22	NM_173588
822	224567_x_at	MALAT1	NR_002819
823	221215_s_at	RIPK4	NM_020639
824	200710_at	ACADVL	NM_000018
825	220302_at	MAK	NM_005906
826	214499_s_at	BCLAF1	NM_001077440
827	238836_at	---	---
828	213256_at	MARCH3	NM_178450
829	226095_s_at	ATXN1L	NM_001137675
830	203816_at	DGUOK	NM_080916
831	209307_at	SWAP70	NM_015055
832	201144_s_at	EIF2S1	NM_004094
833	236707_at	DAPP1	NM_014395
834	240703_s_at	HERC1	NM_003922
835	229720_at	BAG1	NM_004323
836	238037_at	LMLN	NM_001136049
837	200597_at	EIF3A	NM_003750
838	207563_s_at	OGT	NM_181672
839	241441_at	---	---
840	217961_at	SLC25A38	NM_017875
841	225696_at	COPS7B	NM_022730
842	211721_s_at	ZNF551	NM_138347
843	212095_s_at	MTUS1	NM_001001924
844	242857_at	---	---
845	241421_at	---	---
846	225119_at	CHMP4B	NM_176812
847	243375_at	---	---
848	202239_at	PARP4	NM_006437
849	200819_s_at	RPS15	NM_001018
850	237218_at	---	---
851	1570124_at	---	---
852	217225_x_at	NOMO1	NM_001004060
853	215220_s_at	TPR	NM_003292
854	228899_at	LOC100132 884	XR_078381
855	222880_at	AKT3	NM_005465
856	218820_at	C14orf132	NR_023938
857	223892_s_at	TMBIM4	NM_016056
858	229907_at	---	---
859	209536_s_at	EHD4	NM_139265
860	240899_at	---	---

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
861	221267_s_at	FAM108A1	NM_001130111
862	216069_at	---	---
863	215390_at	---	---
864	224583_at	COTL1	NM_021149
865	205248_at	DOPEY2	NM_005128
866	227820_at	TBC1D25	NM_002536
867	208934_s_at	LGALS8	NM_006499
868	229364_at	LOC646870	XR_040282
869	222073_at	COL4A3	NM_000091
870	219757_s_at	C14orf101	NM_017799
871	226013_at	TRAK1	NM_001042646
872	239922_at	CCDC142	NM_032779
873	242966_x_at	---	---
874	224229_s_at	AKT3	NM_005465
875	218464_s_at	C17orf63	NM_001077498
876	204924_at	TLR2	NM_003264
877	228532_at	C1orf162	NM_174896
878	1560060_s_at	VPS37C	NM_017966
879	1559282_at	---	---
880	217380_s_at	XPNPEP1	NM_020383
881	223002_s_at	XRN2	NM_012255
882	229145_at	C10orf104	NM_173473
883	224911_s_at	DCBLD2	NM_080927
884	205466_s_at	HS3ST1	NM_005114
885	203907_s_at	IQSEC1	NM_001134382
886	232645_at	LOC153684	NR_015447
887	233575_s_at	TLE4	NM_007005
888	200019_s_at	FAU	NM_001997
889	225738_at	RAPGEF1	NM_005312
890	1561018_at	---	---
891	236460_at	---	---
892	217518_at	MYOF	NM_013451
893	212836_at	POLD3	NM_006591
894	213264_at	PCBP2	NM_001098620
895	1557852_at	---	---
896	202708_s_at	HIST2H2BE	NM_003528
897	231763_at	POLR3A	NM_007055
898	223259_at	ORMDL3	NM_139280
899	213729_at	PRPF40A	NM_017892
900	219978_s_at	NUSAP1	NM_001129897
901	222674_at	C9orf114	NM_016390

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
902	223363_at	PSMG3	NM_001134340
903	221188_s_at	CIDEB	NM_014430
904	223059_s_at	FAM107B	NM_031453
905	220557_s_at	PACS1	NM_018026
906	219576_at	MAP7D3	NM_024597
907	204326_x_at	MT1X	NM_005952
908	235575_at	---	---
909	201256_at	COX7A2L	NM_004718
910	226645_at	KLF2	NM_016270
911	1559050_at	HCG27	NR_026791
912	212114_at	LOC552889	NM_001136262
913	209948_at	KCNMB1	NM_004137
914	236407_at	KCNE1	NM_000219
915	240481_at	---	---
916	208195_at	TTN	NM_003319
917	203728_at	BAK1	NM_001188
918	227684_at	S1PR2	NM_004230
919	236002_at	---	---
920	204270_at	SKI	NM_003036
921	202345_s_at	FABP5	NM_001444
922	219745_at	TMEM180	NM_024789
923	235802_at	PLD4	NM_138790
924	230375_at	SFRS18	NM_015491
925	219066_at	PPCDC	NM_021823
926	1560339_s_at	NAP1L4	NM_005969
927	203110_at	PTK2B	NM_004103
928	219630_at	PDZK1IP1	NM_005764
929	244307_s_at	---	---
930	238758_at	---	---
931	214917_at	PRKAA1	NM_006251
932	218276_s_at	SAV1	NM_021818
933	228193_s_at	C13orf15	NM_014059
934	227037_at	PLD6	NM_178836
935	225831_at	LUZP1	NM_001142546
936	237210_at	NFRKB	NM_001143835
937	221206_at	PMS2	NM_000535
938	221499_s_at	STX16	NM_001001433
939	222217_s_at	SLC27A3	NM_024330
940	238523_at	KLHL36	NM_024731
941	202048_s_at	CBX6	NM_014292
942	212856_at	GRAMD4	NM_015124

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
943	225759_x_at	CLMN	NM_024734
944	217606_at	---	---
945	200973_s_at	TSPAN3	NM_005724
946	230970_at	---	---
947	228932_at	---	---
948	209338_at	TFCP2	NM_005653
949	205758_at	CD8A	NM_001145873
950	225065_x_at	NCRNA00188	NM_152350
951	203358_s_at	EZH2	NM_004456
952	209375_at	XPC	NM_001145769
953	232489_at	CCDC76	NM_019083
954	239723_at	---	---
955	1552641_s_at	ATAD3A	NM_018188
956	1558220_at	MUC20	NM_001098516
957	239960_x_at	LYRM7	NM_181705
958	225212_at	SLC25A25	NM_001006641
959	214815_at	TRIM33	NM_015906
960	212135_s_at	ATP2B4	NM_001001396
961	232952_at	---	---
962	1556053_at	DNAJC7	NM_001144766
963	232346_at	LOC388692	NR_027002
964	228967_at	EIF1	NM_005801
965	239556_at	LOC645513	XR_078309
966	226863_at	FAM110C	NM_001077710
967	229810_at	---	---
968	236669_at	---	---
969	222480_at	UBE2Q1	NM_017582
970	228281_at	C11orf82	NM_145018
971	216945_x_at	PASK	NM_015148
972	207434_s_at	FXYD2	NM_001127489
973	201674_s_at	AKAP1	NM_003488
974	239037_at	GNAS	NM_000516
975	1560434_x_at	CLTA	NM_001076677
976	244556_at	LCP2	NM_005565
977	1552386_at	GAPT	NM_152687
978	222906_at	FLVCR1	NM_014053
979	1554057_at	LOC645676	NR_027023
980	204512_at	HIVEP1	NM_002114
981	210512_s_at	VEGFA	NM_001025366
982	223816_at	SLC46A2	NM_033051
983	239251_at	---	---

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
984	208998_at	UCP2	NM_003355
985	213810_s_at	LOC100292682	XM_002345924
986	207194_s_at	ICAM4	NM_001039132
987	226372_at	CHST11	NM_018413
988	201792_at	AEBP1	NM_001129
989	221203_s_at	YEATS2	NM_018023
990	1562019_at	NT5DC4	XM_001715677
991	205613_at	SYT17	NM_016524
992	221581_s_at	LAT2	NM_014146
993	244834_at	C1orf134	---
994	201557_at	VAMP2	NM_014232
995	225549_at	DDX6	NM_004397
996	201800_s_at	OSBP	NM_002556
997	202548_s_at	ARHGEF7	NM_001113511
998	222243_s_at	TOB2	NM_016272
999	2028_s_at	E2F1	NM_005225
1000	223000_s_at	F11R	NM_016946
1001	222282_at	---	---
1002	230252_at	LPAR5	NM_001142961
1003	227152_at	C12orf35	NM_018169
1004	242877_at	---	---
1005	236908_at	---	---
1006	201365_at	OAZ2	NM_002537
1007	241117_at	LOXHD1	NM_001145472
1008	230663_at	---	---
1009	209579_s_at	MBD4	NM_003925
1010	1562007_at	---	---
1011	222672_at	LYRM4	NM_020408
1012	206842_at	KCND1	NM_004979
1013	213034_at	QSK	NM_025164
1014	203764_at	DLGAP5	NM_001146015
1015	239014_at	CCAR1	NM_018237
1016	204029_at	CELSR2	NM_001408
1017	204711_at	KIAA0753	NM_014804
1018	221595_at	---	---
1019	1552671_a_at	SLC9A7	NM_032591
1020	226066_at	MITF	NM_000248
1021	1553364_at	PNPLA1	NM_001145716
1022	224653_at	EIF4EBP2	NM_004096
1023	1564435_a_at	KRT72	NM_001146225
1024	229253_at	THEM4	NM_053055

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1025	222044_at	PCIF1	NM_022104
1026	241705_at	ABCA5	NM_018672
1027	228469_at	PPID	NM_005038
1028	204858_s_at	TYMP	NM_001113755
1029	201621_at	NBL1	NM_005380
1030	234492_at	---	---
1031	212906_at	GRAMD1B	NM_020716
1032	231116_at	---	---
1033	232782_at	---	---
1034	224978_s_at	USP36	NM_025090
1035	225471_s_at	AKT2	NM_001626
1036	1556496_a_at	---	---
1037	224717_s_at	C19orf42	NM_024104
1038	241819_at	TNFSF8	NM_001244
1039	202286_s_at	TACSTD2	NM_002353
1040	219198_at	GTF3C4	NM_012204
1041	202800_at	SLC1A3	NM_004172
1042	208003_s_at	NFAT5	NM_001113178
1043	36030_at	IFFO1	NM_001039670
1044	219826_at	ZNF419	NM_001098491
1045	214005_at	GGCX	NM_000821
1046	241669_x_at	PRKD2	NM_001079880
1047	227122_at	ZNF791	NM_153358
1048	205560_at	PCSK5	NM_006200
1049	1564378_a_at	---	---
1050	240721_at	---	---
1051	228306_at	CNIH4	NM_014184
1052	202074_s_at	OPTN	NM_001008211
1053	210559_s_at	CDC2	NM_001130829
1054	206873_at	CA6	NM_001215
1055	225221_at	---	---
1056	213180_s_at	GOSR2	NM_001012511
1057	200622_x_at	CALM3	NM_005184
1058	229413_s_at	---	---
1059	220466_at	CCDC15	NM_025004
1060	229817_at	ZNF608	NM_020747
1061	238417_at	PGM2L1	NM_173582
1062	240845_at	---	---
1063	238016_s_at	LOC100129105	---
1064	226765_at	SPTBN1	NM_003128
1065	217856_at	RBM8A	NM_005105

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1066	220865_s_at	PDSS1	NM_014317
1067	232588_at	STAG1	NM_005862
1068	201736_s_at	MARCH6	NM_005885
1069	1561195_at	---	---
1070	236422_at	---	---
1071	209118_s_at	TUBA1A	NM_006009
1072	229622_at	FAM132B	XM_001130886
1073	227490_at	WDFY2	NM_052950
1074	226517_at	BCAT1	NM_005504
1075	230405_at	C5orf56	NM_001013717
1076	201543_s_at	SAR1A	NM_001142648
1077	200855_at	C20orf191	NM_006311
1078	209193_at	PIM1	NM_002648
1079	216857_at	---	---
1080	225207_at	PDK4	NM_002612
1081	203969_at	PEX3	NM_003630
1082	243444_at	SRD5A3	NM_024592
1083	227091_at	CCDC146	NM_020879
1084	1007_s_at	DDR1	NM_001954
1085	205493_s_at	DPYSL4	NM_006426
1086	208304_at	CCR3	NM_001837
1087	210470_x_at	NONO	NM_001145408
1088	210947_s_at	MSH3	NM_002439
1089	218561_s_at	LYRM4	NM_020408
1090	208613_s_at	FLNB	NM_001164317
1091	227436_at	OTUD7B	NM_020205
1092	242729_at	---	---
1093	237387_at	---	---
1094	206005_s_at	KIAA1009	NM_014895
1095	218807_at	VAV3	NM_001079874
1096	219371_s_at	KLF2	NM_016270
1097	243858_at	---	---
1098	219412_at	RAB38	NM_022337
1099	233224_at	---	---
1100	226571_s_at	PTPRS	NM_002850
1101	212828_at	SYNJ2	NM_003898
1102	239212_at	LTV1	NM_032860
1103	241763_s_at	FBXO32	NM_058229
1104	1570566_at	LOC100292 875	XM_002345815
1105	1554985_at	ZNF396	NM_145756
1106	202291_s_at	MGP	NM_000900

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1107	235308_at	ZBTB20	NM_015642
1108	219433_at	BCOR	NM_001123383
1109	230023_at	NSUN4	NM_199044
1110	204578_at	HISPPD2A	NM_001024463
1111	212599_at	AUTS2	NM_001127231
1112	236836_at	---	---
1113	234088_at	---	---
1114	222667_s_at	ASH1L	NM_018489
1115	231221_at	CLEC16A	NM_015226
1116	202449_s_at	RXRA	NM_002957
1117	209455_at	FBXW11	NM_012300
1118	1554237_at	SDCCAG8	NM_006642
1119	1556352_at	---	---
1120	205844_at	VNN1	NM_004666
1121	1562453_at	---	---
1122	1552613_s_at	CDC42SE2	NM_001038702
1123	225204_at	PPTC7	NM_139283
1124	209806_at	HIST1H2BK	NM_080593
1125	240154_at	---	---
1126	239464_at	---	---
1127	1555370_a_at	CAMTA1	NM_015215
1128	225004_at	TMEM101	NM_032376
1129	226893_at	ABL2	NM_001100108
1130	202190_at	CSTF1	NM_001033521
1131	202369_s_at	TRAM2	NM_012288
1132	243973_at	---	---
1133	242862_x_at	---	---
1134	236327_at	---	---
1135	235778_s_at	ANKRD44	NM_153697
1136	229686_at	P2RY8	NM_178129
1137	213924_at	MPPE1	NM_023075
1138	239792_at	LOC440288	XM_001714156
1139	206560_s_at	MIA	NM_006533
1140	225654_at	NSD1	NM_022455
1141	228570_at	BTBD11	NM_001017523
1142	231064_s_at	---	---
1143	238126_at	---	---
1144	212995_x_at	FAM128B	NM_025029
1145	214617_at	PRF1	NM_001083116
1146	208269_s_at	ADAM28	NM_014265
1147	1568717_a_at	FKBP15	NM_015258

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1148	1558854_a_at	---	---
1149	241938_at	QKI	NM_006775
1150	215099_s_at	RXRB	NM_021976
1151	230100_x_at	PAK1	NM_001128620
1152	202464_s_at	PFKFB3	NM_001145443
1153	225454_at	CCDC124	NM_001136203
1154	1558201_s_at	SLC4A1AP	NM_018158
1155	239597_at	---	---
1156	228772_at	HNMT	NM_001024074
1157	227722_at	RPS23	NM_001025
1158	243340_at	---	---
1159	217769_s_at	POMP	NM_015932
1160	228308_at	FKBP11	NM_001143781
1161	204233_s_at	CHKA	NM_001277
1162	204440_at	CD83	NM_001040280
1163	204184_s_at	ADRBK2	NM_005160
1164	212099_at	RHOB	NM_004040
1165	212504_at	DIP2C	NM_014974
1166	220266_s_at	KLF4	NM_004235
1167	227750_at	KALRN	NM_001024660
1168	203157_s_at	GLS	NM_014905
1169	202804_at	ABCC1	NM_004996
1170	242752_at	---	---
1171	219799_s_at	DHRS9	NM_001142270
1172	236191_at	---	---
1173	230725_at	---	---
1174	212137_at	LARP1	NM_015315
1175	238135_at	AGTRAP	NM_001040194
1176	207079_s_at	MED6	NM_005466
1177	203973_s_at	CEBPD	NM_005195
1178	228778_at	---	---
1179	240798_at	---	---
1180	244347_at	---	---
1181	231093_at	FCRL3	NM_052939
1182	231435_at	C7orf34	NM_178829
1183	244280_at	---	---
1184	224549_x_at	---	---
1185	228516_at	CDAN1	NM_138477
1186	233218_at	---	---
1187	1560297_at	---	---
1188	227114_at	RNF214	NM_001077239

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1189	204373_s_at	CEP350	NM_014810
1190	226190_at	MAP3K13	NM_004721
1191	224564_s_at	RTN3	NM_006054
1192	214483_s_at	ARFIP1	NM_001025593
1193	209248_at	GHITM	NM_014394
1194	204576_s_at	CLUAP1	NM_015041
1195	209467_s_at	MKNK1	NM_001135553
1196	242970_at	DIP2B	NM_173602
1197	230233_at	---	---
1198	212560_at	SORL1	NM_003105
1199	228786_at	LOC387647	NR_003930
1200	211368_s_at	CASP1	NM_001223
1201	202958_at	PTPN9	NM_002833
1202	244262_x_at	---	---
1203	244647_at	---	---
1204	223457_at	COPG2	NM_012133
1205	219260_s_at	C17orf81	NM_015362
1206	236832_at	LOC221442	NR_026938
1207	1552307_a_at	TTC39C	NM_001135993
1208	201336_at	VAMP3	NM_004781
1209	AFFX-HUMISGF3A/M97935_MB_at	STAT1	NM_007315
1210	227080_at	ZNF697	NM_001080470
1211	227486_at	NT5E	NM_002526
1212	206413_s_at	TCL1B	NM_004918
1213	237120_at	KRT77	NM_175078
1214	207091_at	P2RX7	NM_002562
1215	226815_at	C3orf31	NM_138807
1216	219025_at	CD248	NM_020404
1217	227182_at	SUSD3	NM_145006
1218	214877_at	CDKAL1	NM_017774
1219	218997_at	POLR1E	NM_022490
1220	240861_at	---	---
1221	204592_at	DLG4	NM_001128827
1222	213406_at	WSB1	NM_015626
1223	227707_at	MYLIP	NM_013262
1224	237538_at	---	---
1225	218262_at	RMND5B	NM_022762
1226	232283_at	LYSMD1	NM_001136543
1227	212249_at	PIK3R1	NM_181504
1228	213672_at	MARS	NM_004990

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1229	210052_s_at	TPX2	NM_012112
1230	229893_at	FRMD3	NM_174938
1231	222482_at	LOC100129321	NM_001009955
1232	203129_s_at	KIF5C	NM_004522
1233	203418_at	CCNA2	NM_001237
1234	225091_at	ZCCHC3	NM_033089
1235	240718_at	LRMP	NM_006152
1236	81737_at	---	---
1237	209360_s_at	RUNX1	NM_001001890
1238	210912_x_at	GSTM4	NM_000850
1239	203716_s_at	DPP4	NM_001935
1240	225095_at	SPTLC2	NM_004863
1241	213048_s_at	---	---
1242	40016_g_at	MAST4	NM_015183
1243	224965_at	GNG2	NM_053064
1244	207623_at	ABCF2	NM_005692
1245	226171_at	ZDHHC3	NM_001135179
1246	241242_at	---	---
1247	207535_s_at	NFKB2	NM_001077493
1248	239522_at	IL12RB1	NM_005535
1249	215191_at	---	---
1250	212161_at	AP2A2	NM_012305
1251	1562280_at	---	---
1252	209122_at	PLIN2	NM_001122
1253	229305_at	MLF1IP	NM_024629
1254	210407_at	PPM1A	NM_021003
1255	226614_s_at	FAM167A	NM_053279
1256	1555679_a_at	RTN4IP1	NM_032730
1257	224697_at	DCAF5	NM_003861
1258	222262_s_at	ETNK1	NM_001039481
1259	227331_at	ZNF740	NM_001004304
1260	227259_at	CD47	NM_001025079
1261	222000_at	C1orf174	NM_207356
1262	205603_s_at	DIAPH2	NM_006729
1263	213021_at	GOSR1	NM_001007024
1264	210149_s_at	ATP5H	NM_001003785
1265	240793_at	TTN	NM_003319
1266	200089_s_at	RPL4	NM_000968
1267	217834_s_at	SYNCRIP	NM_001159673
1268	234396_at	---	---
1269	1566001_at	---	---

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1270	236742_at	---	---
1271	240231_at	---	---
1272	200664_s_at	DNAJB1	NM_006145
1273	212671_s_at	HLA-DQA1	NM_002122
1274	207536_s_at	TNFRSF9	NM_001561
1275	232218_at	---	---
1276	205545_x_at	DNAJC8	NM_014280
1277	239654_at	CHD9	NM_025134
1278	223907_s_at	PINX1	NM_017884
1279	233483_at	TBC1D27	XM_002343481
1280	1556643_at	LOC100128718	---
1281	209502_s_at	BAIAP2	NM_001144888
1282	232720_at	LINGO2	NM_152570
1283	227138_at	CRTAP	NM_006371
1284	1559895_x_at	---	---
1285	203554_x_at	PTTG1	NM_004219
1286	220305_at	MAVS	NM_020746
1287	229966_at	EWSR1	NM_001163285
1288	230435_at	LOC375190	NM_001145710
1289	220000_at	SIGLEC5	NM_003830
1290	1558094_s_at	C3orf19	NM_016474
1291	233157_x_at	CCDC114	NM_144577
1292	205067_at	IL1B	NM_000576
1293	212662_at	PVR	NM_001135768
1294	213028_at	NFRKB	NM_001143835
1295	224836_at	TP53INP2	NM_021202
1296	210648_x_at	SNX3	NM_003795
1297	1558105_a_at	---	---
1298	210153_s_at	ME2	NM_002396
1299	212650_at	EHBP1	NM_001142614
1300	209281_s_at	ATP2B1	NM_001001323
1301	239307_at	---	---
1302	213902_at	ASAH1	NM_001127505
1303	1559835_at	---	---
1304	240070_at	TIGIT	NM_173799
1305	222396_at	HN1	NM_001002032
1306	211781_x_at	---	---
1307	219179_at	DACT1	NM_001079520
1308	207072_at	IL18RAP	NM_003853
1309	224919_at	MRPS6	NM_032476
1310	231547_at	ZBTB37	NM_001122770

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1311	227476_at	LPGAT1	NM_014873
1312	218584_at	TCTN1	NM_001082537
1313	209714_s_at	CDKN3	NM_001130851
1314	230354_at	---	---
1315	228831_s_at	GNG7	NM_052847
1316	237522_at	FAS	NM_000043
1317	212663_at	FKBP15	NM_015258
1318	226336_at	PPIA	NM_021130
1319	242673_at	---	---
1320	232784_at	---	---
1321	205232_s_at	PAFAH2	NM_000437
1322	201364_s_at	OAZ2	NM_002537
1323	1558143_a_at	BCL2L11	NM_006538
1324	1569906_s_at	PHF20	NM_016436
1325	244332_at	---	---
1326	242082_at	MMAB	NM_052845
1327	212154_at	SDC2	NM_002998
1328	1569207_s_at	TCP11L2	NM_152772
1329	232257_s_at	---	---
1330	239060_at	---	---
1331	1563075_s_at	---	---
1332	208645_s_at	RPS14	NM_001025070
1333	244035_at	---	---
1334	227402_s_at	UTP23	NM_032334
1335	230921_s_at	---	---
1336	227790_at	UBE2CBP	NM_198920
1337	242582_at	---	---
1338	1553405_a_at	CSMD1	NM_033225
1339	244886_at	LOC389641	XM_374260
1340	228762_at	LFNG	NM_001040167
1341	220231_at	C7orf16	NM_001145123
1342	202341_s_at	TRIM2	NM_001130067
1343	208054_at	HERC4	NM_015601
1344	228003_at	RAB30	NM_014488
1345	243534_at	CC2D2B	NM_001001732
1346	212573_at	ENDOD1	NM_015036
1347	230063_at	ZNF264	NM_003417
1348	204165_at	WASF1	NM_001024934
1349	238279_x_at	---	---
1350	201842_s_at	EFEMP1	NM_001039348
1351	223132_s_at	TRIM8	NM_030912

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1352	244043_at	---	---
1353	206043_s_at	ATP2C2	NM_014861
1354	208653_s_at	CD164	NM_001142401
1355	238596_at	C10orf4	NM_145246
1356	231907_at	ABL2	NM_001100108
1357	1557478_at	---	---
1358	1558906_a_at	---	---
1359	243404_at	---	---
1360	243526_at	WDR86	NM_198285
1361	205531_s_at	GLS2	NM_013267
1362	241702_at	---	---
1363	223821_s_at	SUSD4	NM_001037175
1364	242232_at	---	---
1365	221573_at	C7orf25	NM_001099858
1366	1569492_at	---	---
1367	227897_at	---	---
1368	231809_x_at	PCDCD7	NM_005707
1369	226982_at	ELL2	NM_012081
1370	214876_s_at	TUBGCP5	NM_001102610
1371	226957_x_at	RALBP1	NM_006788
1372	204251_s_at	CEP164	NM_014956
1373	229881_at	KLF12	NM_007249
1374	205039_s_at	IKZF1	NM_006060
1375	214000_s_at	RGS10	NM_001005339
1376	204454_at	LDOC1	NM_012317
1377	229821_at	---	---
1378	202166_s_at	PPP1R2	NM_006241
1379	228177_at	CREBBP	NM_001079846
1380	233063_s_at	---	---
1381	204173_at	MYL6B	NM_002475
1382	206513_at	AIM2	NM_004833
1383	218949_s_at	QRSL1	NM_018292
1384	204167_at	BTD	NM_000060
1385	221256_s_at	HDHD3	NM_031219
1386	220239_at	KLHL7	NM_001031710
1387	201307_at	40787	NM_018243
1388	232530_at	PLD1	NM_001130081
1389	226519_s_at	AGXT2L2	NM_153373
1390	219298_at	ECHDC3	NM_024693
1391	209134_s_at	RPS6	NM_001010
1392	219529_at	CLIC3	NM_004669

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1393	202759_s_at	AKAP2	NM_001004065
1394	232829_at	OR52K3P	---
1395	1559391_s_at	---	---
1396	203605_at	SRP54	NM_001146282
1397	232636_at	SLTRK4	NM_173078
1398	201061_s_at	STOM	NM_004099
1399	222633_at	TBL1XR1	NM_024665
1400	214710_s_at	CCNB1	NM_031966
1401	231866_at	LNPEP	NM_005575
1402	208619_at	DDB1	NM_001923
1403	1566039_a_at	---	---
1404	202891_at	NIT1	NM_005600
1405	229334_at	RUFY3	NM_001037442
1406	214686_at	ZNF266	NM_006631
1407	1565358_at	RARA	NM_000964
1408	243924_at	LOC100127980	XM_001720119
1409	225007_at	---	---
1410	213285_at	TMEM30B	NM_001017970
1411	206592_s_at	AP3D1	NM_001077523
1412	221909_at	RNFT2	NM_001109903
1413	218746_at	TAPBPL	NM_018009
1414	235927_at	XPO1	NM_003400
1415	240089_at	---	---
1416	1554292_a_at	UHRF1BP1L	NM_001006947
1417	208636_at	ACTN1	NM_001102
1418	206342_x_at	IDS	NM_000202
1419	217374_x_at	TARP	NM_001003799
1420	223527_s_at	CDADC1	NM_030911
1421	209686_at	S100B	NM_006272
1422	242364_x_at	LOC100131096	XM_001720907
1423	201523_x_at	UBE2N	NM_003348
1424	202348_s_at	TOR1A	NM_000113
1425	1558847_at	---	---
1426	220363_s_at	ELMO2	NM_133171
1427	234860_at	---	---
1428	232095_at	---	---
1429	211984_at	CALM1	NM_006888
1430	201053_s_at	PSMF1	NM_006814
1431	207332_s_at	TFRC	NM_001128148
1432	235942_at	LOC401629	NR_002160

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1433	218361_at	GOLPH3L	NM_018178
1434	205757_at	ENTPD5	NM_001249
1435	220606_s_at	C17orf48	NM_020233
1436	209642_at	BUB1	NM_004336
1437	203264_s_at	ARHGEF9	NM_015185
1438	236193_at	HIST1H2BC	NM_003526
1439	229274_at	GNAS	NM_000516
1440	225661_at	IFNAR1	NM_000629
1441	202070_s_at	IDH3A	NM_005530
1442	201286_at	SDC1	NM_001006946
1443	237229_at	JMJD5	NM_001145348
1444	221776_s_at	BRD7	NM_013263
1445	218312_s_at	ZSCAN18	NM_001145542
1446	230444_at	---	---
1447	205708_s_at	TRPM2	NM_003307
1448	224794_s_at	CERCAM	NM_016174
1449	240237_at	---	---
1450	225834_at	FAM72A	NM_001100910
1451	218064_s_at	AKAP8L	NM_014371
1452	229592_at	---	---
1453	209445_x_at	C7orf44	NM_018224
1454	208517_x_at	BTF3	NM_001037637
1455	217677_at	PLEKHA2	NM_021623
1456	210812_at	XRCC4	NM_003401
1457	224756_s_at	BAT5	NM_021160
1458	1559059_s_at	ZNF611	NM_001161499
1459	225609_at	GSR	NM_000637
1460	242691_at	---	---
1461	204785_x_at	IFNAR2	NM_000874
1462	233191_at	RUFY2	NM_001042417
1463	225987_at	STEAP4	NM_024636
1464	212010_s_at	CDV3	NM_001134422
1465	229398_at	RAB18	NM_021252
1466	234819_at	---	---
1467	230440_at	ZNF469	NM_001127464
1468	1557186_s_at	TPCN1	NM_001143819
1469	222651_s_at	TRPS1	NM_014112
1470	212881_at	PIAS4	NM_015897
1471	226546_at	---	---
1472	243201_at	HNRNPH2	NM_001032393
1473	204254_s_at	VDR	NM_000376

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1474	244070_at	SYNE1	NM_015293
1475	210622_x_at	CDK10	NM_001098533
1476	217620_s_at	PIK3CB	NM_006219
1477	238573_at	---	---
1478	201777_s_at	KIAA0494	NM_014774
1479	231598_x_at	---	---
1480	202055_at	KPNA1	NM_002264
1481	226856_at	MUSTN1	NM_205853
1482	1553858_at	ZBTB3	NM_024784
1483	235446_at	---	---
1484	242064_at	SDK2	NM_001144952
1485	239574_at	---	---
1486	204069_at	MEIS1	NM_002398
1487	212390_at	PDE4DIP	NM_001002810
1488	AFFX-hum_alu_at	---	---
1489	212933_x_at	RPL13	NM_000977
1490	212547_at	BRD3	NM_007371
1491	241202_at	---	---
1492	1562067_at	---	---
1493	1566427_at	---	---
1494	211717_at	ANKRD40	NM_052855
1495	1552485_at	LACTB	NM_032857
1496	209345_s_at	PI4K2A	NM_018425
1497	232722_at	RNASET2	NM_003730
1498	225755_at	KLHDC8B	NM_173546
1499	209541_at	IGF1	NM_000618
1500	230669_at	RASA2	NM_006506
1501	217207_s_at	BTNL3	NM_197975
1502	230442_at	MTHFSD	NM_001159377
1503	200983_x_at	CD59	NM_000611
1504	217232_x_at	HBB	NM_000518
1505	202738_s_at	PHKB	NM_000293
1506	218773_s_at	MSRB2	NM_012228
1507	213343_s_at	GDPD5	NM_030792
1508	233880_at	RNF213	NM_020914
1509	214377_s_at	CTRL	NM_001907
1510	211324_s_at	RGPD5	NM_001037866
1511	219055_at	SRBD1	NM_018079
1512	237389_at	---	---
1513	225729_at	C6orf89	NM_152734
1514	221521_s_at	GINS2	NM_016095

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1515	1559449_a_at	ZNF254	NM_203282
1516	1565674_at	FCGR2A	NM_001136219
1517	241933_at	QRSL1	NM_018292
1518	215559_at	ABCC6	NM_001079528
1519	221928_at	ACACB	NM_001093
1520	226051_at	SELM	NM_080430
1521	1566166_at	---	---
1522	225208_s_at	FAM103A1	NM_031452
1523	243675_at	---	---
1524	239944_at	---	---
1525	58780_s_at	FLJ10357	NM_018071
1526	235030_at	FAM55C	NM_001134456
1527	239783_at	---	---
1528	1555580_at	---	---
1529	238494_at	TRAF3IP1	NM_001139490
1530	1558719_s_at	RPAIN	NM_001033002
1531	41660_at	CELSR1	NM_014246
1532	210971_s_at	ARNTL	NM_001030272
1533	201825_s_at	SCCPDH	NM_016002
1534	217727_x_at	VPS35	NM_018206
1535	203725_at	GADD45A	NM_001924
1536	225490_at	ARID2	NM_152641
1537	231023_at	CARS2	NM_024537
1538	224524_s_at	ASB3	NM_001164165
1539	232959_at	---	---
1540	237133_at	---	---
1541	218391_at	SNF8	NM_007241
1542	227060_at	RELT	NM_032871
1543	200606_at	DSP	NM_001008844
1544	219681_s_at	RAB11FIP1	NM_001002233
1545	225638_at	C1orf31	NM_001012985
1546	227957_at	GSN	NM_000177
1547	239560_at	---	---
1548	208936_x_at	LGALS8	NM_006499
1549	226334_s_at	AHSA2	NM_152392
1550	238750_at	---	---
1551	225061_at	DNAJA4	NM_001130182
1552	228096_at	C1orf151	NM_001032363
1553	209709_s_at	HMMR	NM_001142556
1554	207277_at	CD209	NM_001144893
1555	212448_at	NEDD4L	NM_001144964

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1556	229734_at	LOC283174	NR_024344
1557	237332_at	---	---
1558	228069_at	FAM54A	NM_001099286
1559	1553978_at	LOC729991	NM_001145783
1560	205042_at	GNE	NM_001128227
1561	229820_at	LOC440993	XR_039810
1562	1554513_s_at	CCDC123	NM_032816
1563	221877_at	IRGQ	NM_001007561
1564	208696_at	CCT5	NM_012073
1565	240554_at	AKAP8L	NM_014371
1566	201589_at	SMC1A	NM_006306
1567	235824_at	---	---
1568	232375_at	---	---
1569	242384_at	---	---
1570	203155_at	SETDB1	NM_001145415
1571	243092_at	LOC100290367	XM_002347376
1572	232045_at	PHACTR1	NM_030948
1573	1554710_at	KCNMB1	NM_004137
1574	237104_at	---	---
1575	231223_at	CSMD1	NM_033225
1576	1553920_at	C9orf84	NM_001080551
1577	225901_at	PTPMT1	NM_001143984
1578	212975_at	DENND3	NM_014957
1579	1554365_a_at	PPP2R5C	NM_001161725
1580	215495_s_at	SAMD4A	NM_001161576
1581	206521_s_at	GTF2A1	NM_015859
1582	215032_at	RREB1	NM_001003698
1583	226879_at	HVCN1	NM_001040107
1584	221582_at	HIST3H2A	NM_033445
1585	225276_at	GSPT1	NM_001130006
1586	1560520_at	LOC401312	---
1587	214997_at	SCAI	NM_001144877
1588	220393_at	LGSN	NM_001143940
1589	230952_at	LOC730092	NR_003370
1590	242279_at	---	---
1591	222592_s_at	ACSL5	NM_016234
1592	209426_s_at	AMACR	NM_014324
1593	231099_at	FKBP15	NM_015258
1594	206860_s_at	MIOS	NM_019005
1595	208628_s_at	YBX1	NM_004559
1596	1566447_at	CD6	NM_006725

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1597	236298_at	PDSS1	NM_014317
1598	237426_at	SP100	NM_001080391
1599	230000_at	RNF213	NM_020914
1600	221815_at	ABHD2	NM_007011
1601	234747_at	C4orf41	NM_021942
1602	236149_at	---	---
1603	209357_at	CITED2	NM_006079
1604	225111_s_at	NAPB	NM_022080
1605	226270_at	EXOC2	NM_018303
1606	210858_x_at	ATM	NM_000051
1607	212320_at	TUBB	NM_178014
1608	214464_at	CDC42BPA	NM_003607
1609	205619_s_at	MEOX1	NM_001040002
1610	225606_at	BCL2L11	NM_006538
1611	217774_s_at	TRMT112	NM_016404
1612	228219_s_at	UPB1	NM_016327
1613	243958_at	---	---
1614	208503_s_at	GATAD1	NM_021167
1615	227170_at	ZNF316	XR_078353
1616	201698_s_at	SFRS9	NM_003769
1617	239698_at	---	---
1618	1555904_at	---	---
1619	217825_s_at	UBE2J1	NM_016021
1620	240247_at	---	---
1621	218108_at	UBR7	NM_001100417
1622	1559688_at	LOC400581	NM_001129778
1623	218125_s_at	CCDC25	NM_018246
1624	226666_at	DAAM1	NM_014992
1625	230027_s_at	MRPL43	NM_032112
1626	205227_at	IL1RAP	NM_002182
1627	228513_at	TMEM219	NM_001083613
1628	1552677_a_at	DIP2A	NM_001146114
1629	215796_at	---	---
1630	201903_at	UQCRC1	NM_003365
1631	1560869_a_at	---	---
1632	234852_at	---	---
1633	227708_at	EEF1A1	NM_001402
1634	1552807_a_at	SIGLEC10	NM_033130
1635	229844_at	---	---
1636	204992_s_at	PFN2	NM_002628
1637	227613_at	ZNF331	NM_001079906

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1638	243579_at	MSI2	NM_138962
1639	210146_x_at	LILRB2	NM_001080978
1640	202433_at	SLC35B1	NM_005827
1641	209870_s_at	APBA2	NM_001130414
1642	224698_at	ESYT2	NM_020728
1643	207617_at	DDX3X	NM_001356
1644	203445_s_at	CTDSP2	NM_005730
1645	235761_at	---	---
1646	238546_at	SLC8A1	NM_001112800
1647	1554536_at	DPYD	NM_000110
1648	200701_at	NPC2	NM_006432
1649	1558722_at	ZNF252	NR_023392
1650	239033_at	---	---
1651	201003_x_at	RNPEP	NM_001032288
1652	228984_at	ATPGD1	NM_020811
1653	217025_s_at	DBN1	NM_004395
1654	232826_at	---	---
1655	241692_at	---	---
1656	205826_at	MYOM2	NM_003970
1657	242079_at	RGS12	NM_002926
1658	242014_at	---	---
1659	205612_at	MMRN1	NM_007351
1660	225546_at	EEF2K	NM_013302
1661	1559284_at	---	---
1662	202583_s_at	RANBP9	NM_005493
1663	225673_at	MYADM	NM_001020818
1664	1556072_at	C22orf37	XR_040827
1665	201190_s_at	PITPNA	NM_006224
1666	218751_s_at	FBXW7	NM_001013415
1667	209069_s_at	H3F3B	NM_005324
1668	210285_x_at	WTAP	NM_004906
1669	209131_s_at	SNAP23	NM_003825
1670	222491_at	HGSNAT	NM_152419
1671	213198_at	ACVR1B	NM_004302
1672	233006_at	38231	NM_004574
1673	1555408_at	BAGE2	NM_181704
1674	243558_at	---	---
1675	228373_at	C16orf72	NM_014117
1676	231578_at	GBP1	NM_002053
1677	241233_x_at	C21orf81	NR_027270
1678	213851_at	TMEM110	NM_198563

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1679	219269_at	HMBOX1	NM_001135726
1680	222276_at	---	---
1681	217741_s_at	ZFAND5	NM_001102420
1682	202080_s_at	TRAK1	NM_001042646
1683	224406_s_at	FCRL5	NM_031281
1684	220987_s_at	C11orf17	NM_020642
1685	230618_s_at	---	---
1686	213274_s_at	CTSB	NM_001908
1687	229202_at	---	---
1688	237009_at	---	---
1689	228125_at	ZNF397OS	NM_001112734
1690	225820_at	PHF17	NM_024900
1691	218348_s_at	ZC3H7A	NM_014153
1692	232883_at	---	---
1693	209006_s_at	C1orf63	NM_020317
1694	211269_s_at	IL2RA	NM_000417
1695	240415_at	---	---
1696	231219_at	CMTM1	NM_052999
1697	226931_at	TMTC1	NM_175861
1698	243720_at	CMIP	NM_030629
1699	208780_x_at	VAPA	NM_003574
1700	213788_s_at	NCRNA00094	NR_015427
1701	200806_s_at	HSPD1	NM_002156
1702	217810_x_at	LARS	NM_020117
1703	219489_s_at	NXN	NM_022463
1704	227201_at	LOC643837	NR_015368
1705	202732_at	PKIG	NM_007066
1706	206777_s_at	CRYBB2	NM_000496
1707	1568680_s_at	YTHDC2	NM_022828
1708	224163_s_at	DMAP1	NM_001034023
1709	1559658_at	C15orf29	NM_024713
1710	228645_at	SNHG9	NR_003142
1711	238946_at	---	---
1712	202898_at	SDC3	NM_014654
1713	1566485_at	---	---
1714	1554112_a_at	ULK2	NM_001142610
1715	214583_at	RSC1A1	NM_006511
1716	1556202_at	SRGAP2	NM_001042758
1717	212169_at	FKBP9	NM_007270
1718	200950_at	ARPC1A	NM_006409
1719	201009_s_at	TXNIP	NM_006472

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1720	201060_x_at	STOM	NM_004099
1721	244633_at	---	---
1722	231973_s_at	ANAPC1	NM_022662
1723	215013_s_at	USP34	NM_014709
1724	237461_at	NLRP7	NM_001127255
1725	227793_at	---	---
1726	238952_x_at	ZNF829	NM_001037232
1727	228806_at	RORC	NM_001001523
1728	204826_at	CCNF	NM_001761
1729	214132_at	ATP5C1	NM_001001973
1730	213119_at	SLC36A1	NM_078483
1731	1558795_at	LOC728052	XM_001717850
1732	222760_at	ZNF703	NM_025069
1733	211742_s_at	EVI2B	NM_006495
1734	243356_at	FAM7A3	NR_026859
1735	203063_at	PPM1F	NM_014634
1736	207922_s_at	MAEA	NM_001017405
1737	228314_at	LRRC8C	NM_032270
1738	214137_at	PTPRJ	NM_001098503
1739	216234_s_at	PRKACA	NM_002730
1740	242551_at	---	---
1741	207610_s_at	EMR2	NM_013447
1742	1559205_s_at	---	---
1743	217292_at	MTMR7	NM_004686
1744	231055_at	---	---
1745	217984_at	RNASET2	NM_003730
1746	216370_s_at	TKTL1	NM_001145933
1747	37433_at	PIAS2	NM_004671
1748	201141_at	GPNMB	NM_001005340
1749	226816_s_at	KIAA1143	NM_020696
1750	239175_at	---	---
1751	209158_s_at	CYTH2	NM_004228
1752	203588_s_at	TFDP2	NM_006286
1753	212823_s_at	PLEKHG3	NM_015549
1754	202822_at	LPP	NM_005578
1755	1561058_at	---	---
1756	225802_at	TOP1MT	NM_052963
1757	213931_at	ID2	NM_002166
1758	223666_at	SNX5	NM_014426
1759	201827_at	SMARCD2	NM_001098426
1760	235052_at	ZNF792	NM_175872

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1761	227579_at	---	---
1762	228105_at	---	---
1763	236292_at	RNF130	NM_018434
1764	219550_at	ROBO3	NM_022370
1765	242216_at	---	---
1766	229544_at	---	---
1767	227533_at	---	---
1768	209442_x_at	ANK3	NM_001149
1769	37145_at	GNLY	NM_006433
1770	225680_at	LRWD1	NM_152892
1771	209239_at	NFKB1	NM_003998
1772	213579_s_at	EP300	NM_001429
1773	213073_at	ZFYVE26	NM_015346
1774	206855_s_at	HYAL2	NM_003773
1775	205277_at	PRDM2	NM_001007257
1776	214076_at	GFOD2	NM_030819
1777	1558167_a_at	MGC16275	NR_026914
1778	1568574_x_at	SPP1	NM_000582
1779	224298_s_at	UBAC2	NM_001144072
1780	230795_at	---	---
1781	221765_at	UGCG	NM_003358
1782	201668_x_at	MARCKS	NM_002356
1783	1556432_at	---	---
1784	227203_at	FBXL17	NM_001163315
1785	208743_s_at	YWHAB	NM_003404
1786	212008_at	UBXN4	NM_014607
1787	220072_at	CSPP1	NM_001077204
1788	1563467_at	---	---
1789	224639_at	UNQ1887	NM_139015
1790	230480_at	PIWIL4	NM_152431
1791	1562013_a_at	---	---
1792	204909_at	DDX6	NM_004397
1793	209824_s_at	ARNTL	NM_001030272
1794	206409_at	TIAM1	NM_003253
1795	208174_x_at	ZRSR2	NM_005089
1796	211015_s_at	HSPA4	NM_002154
1797	208658_at	PDIA4	NM_004911
1798	213801_x_at	RPSA	NM_001012321
1799	225634_at	ZC3HAV1	NM_020119
1800	215356_at	TDRD12	NM_001110822
1801	213688_at	CALM1	NM_006888

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<i>SEQ ID No.</i>	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1802	200933_x_at	RPS4X	NM_001007
1803	242270_at	---	---
1804	210036_s_at	KCNH2	NM_000238
1805	229822_at	---	---
1806	232739_at	SPIB	NM_003121
1807	201219_at	CTBP2	NM_001083914
1808	1560457_x_at	LSDP5	NM_001013706
1809	1558372_at	---	---
1810	1568851_at	---	---
1811	225849_s_at	SFT2D1	NM_145169
1812	1557257_at	BCL10	NM_003921
1813	231283_at	MGAT4A	NM_001160154
1814	239154_at	---	---
1815	212523_s_at	KIAA0146	NM_001080394
1816	231922_at	ZNF276	NM_001113525
1817	213514_s_at	DIAPH1	NM_001079812
1818	205129_at	NPM3	NM_006993
1819	230997_at	TTC21A	NM_001105513
1820	208705_s_at	EIF5	NM_001969
1821	203939_at	NT5E	NM_002526
1822	217770_at	PIGT	NM_015937
1823	233787_at	C6orf163	NM_001010868
1824	241621_at	SMCHD1	NM_015295
1825	1553750_a_at	FAM76B	NM_144664
1826	211018_at	LSS	NM_001001438
1827	200693_at	YWHAQ	NM_006826
1828	218662_s_at	NCAPG	NM_022346
1829	220990_s_at	MIR21	NM_030938
1830	232149_s_at	NSMAF	NM_001144772
1831	232012_at	CAPN1	NM_005186
1832	1562825_at	---	---
1833	233800_at	---	---
1834	242806_at	---	---
1835	1557544_at	CCDC147	NM_001008723
1836	203923_s_at	CYBB	NM_000397
1837	217978_s_at	UBE2Q1	NM_017582
1838	220940_at	ANKRD36B	NM_025190
1839	221711_s_at	C19orf62	NM_001033549
1840	222087_at	PVT1	NR_003367
1841	213201_s_at	TNNT1	NM_001126132
1842	219178_at	QTRTD1	NM_024638

<i>SEQ ID No.</i>	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1843	213535_s_at	UBE2I	NM_003345
1844	204039_at	CEBPA	NM_004364
1845	215754_at	SCARB2	NM_005506
1846	232284_at	PSMD6	NM_014814
1847	204214_s_at	RAB32	NM_006834
1848	219765_at	ZNF329	NM_024620
1849	201938_at	CDK2AP1	NM_004642
1850	230009_at	FAM118B	NM_024556
1851	239427_at	---	---
1852	214717_at	DKFZp434H 1419	---
1853	239755_at	---	---
1854	208322_s_at	ST3GAL1	NM_003033
1855	227910_at	XPNPEP3	NM_022098
1856	225382_at	ZNF275	NM_001080485
1857	220167_s_at	TP53TG3	NM_001099687
1858	1561884_at	CEPT1	NM_001007794
1859	206332_s_at	IFI16	NM_005531
1860	220193_at	C1orf113	NM_001162530
1861	237623_at	CST3	NM_000099
1862	209410_s_at	GRB10	NM_001001549
1863	214481_at	HIST1H2AM	NM_003514
1864	236511_at	---	---
1865	226184_at	FMNL2	NM_052905
1866	222955_s_at	FAM45A	NM_207009
1867	226840_at	H2AFY	NM_001040158
1868	227931_at	INO80D	NM_017759
1869	231837_at	USP28	NM_020886
1870	232180_at	UGP2	NM_001001521
1871	227305_s_at	SMCR8	NM_144775
1872	237597_at	---	---
1873	1555963_x_at	B3GNT7	NM_145236
1874	211874_s_at	MYST4	NM_012330
1875	208541_x_at	TFAM	NM_003201
1876	242868_at	---	---
1877	227522_at	CMBL	NM_138809
1878	207324_s_at	DSC1	NM_004948
1879	1560109_s_at	---	---
1880	231644_at	---	---
1881	1554360_at	FCHSD2	NM_014824
1882	239988_at	---	---
1883	201898_s_at	UBE2A	NM_003336

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SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1884	1555420_a_at	KLF7	NM_003709
1885	209691_s_at	DOK4	NM_018110
1886	213596_at	CASP4	NM_001225
1887	243767_at	---	---
1888	218014_at	NUP85	NM_024844
1889	208179_x_at	KIR2DL3	NM_014511
1890	230761_at	---	---
1891	217100_s_at	UBXN7	NM_015562
1892	242066_at	---	---
1893	232927_at	---	---
1894	217933_s_at	LAP3	NM_015907
1895	205929_at	GPA33	NM_005814
1896	234049_at	hCG_19905 47	NR_024361
1897	225435_at	SSR1	NM_003144
1898	203560_at	GGH	NM_003878
1899	1555427_s_at	SYNCRIP	NM_001159673
1900	215127_s_at	RBMS1	NM_002897
1901	1561211_at	---	---
1902	226509_at	ZNF641	NM_152320
1903	228088_at	SESTD1	NM_178123
1904	218126_at	FAM82A2	NM_018145
1905	1559052_s_at	PAK2	NM_002577
1906	203311_s_at	ARF6	NM_001663
1907	232646_at	TTC17	NM_018259
1908	218907_s_at	LRRC61	NM_001142928
1909	232744_x_at	---	---
1910	213310_at	EIF2C2	NM_012154
1911	222900_at	NRIP3	NM_020645
1912	1552607_at	NCRNA002 04	NR_027401
1913	232237_at	MDGA1	NM_153487
1914	1558310_s_at	hCG_20391 48	XR_078315
1915	233794_at	---	---
1916	207276_at	CDR1	NM_004065
1917	228719_at	ZSWIM7	NM_001042697
1918	200076_s_at	C19orf50	NM_024069
1919	209750_at	NR1D2	NM_001145425
1920	243033_at	TWF1	NM_002822
1921	226210_s_at	MEG3	NR_002766
1922	228434_at	BTNL9	NM_152547

SEQ ID No.	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1923	204497_at	ADCY9	NM_001116
1924	203339_at	SLC25A12	NM_003705
1925	229980_s_at	SNX5	NM_014426
1926	213531_s_at	RAB3GAP1	NM_012233
1927	201487_at	CTSC	NM_001114173
1928	215169_at	SLC35E2	NM_182838
1929	203342_at	TIMM17B	NM_005834
1930	222879_s_at	POLH	NM_006502
1931	239866_at	---	---
1932	209110_s_at	RGL2	NM_004761
1933	214083_at	PPP2R5C	NM_001161725
1934	205770_at	GSR	NM_000637
1935	219684_at	RTP4	NM_022147
1936	206448_at	ZNF365	NM_014951
1937	222230_s_at	ACTR10	NM_018477
1938	1553689_s_at	METTL6	NM_152396
1939	226032_at	CASP2	NM_032982
1940	242858_at	---	---
1941	241590_at	---	---
1942	207113_s_at	TNF	NM_000594
1943	234886_at	TRBV24-1	---
1944	205978_at	KL	NM_004795
1945	243213_at	STAT3	NM_003150
1946	236668_at	---	---
1947	230683_at	ANKRD60	XM_001134442
1948	217747_s_at	RPS9	NM_001013
1949	1560228_at	SNAI3	NM_178310
1950	233571_x_at	PPDPF	NM_024299
1951	222214_at	---	---
1952	220079_s_at	USP48	NM_001032730
1953	233401_at	---	---
1954	223566_s_at	BCOR	NM_001123383
1955	221964_at	TULP3	NM_001160408
1956	212337_at	TUG1	NR_002323
1957	201192_s_at	PITPNA	NM_006224
1958	223217_s_at	NFKBIZ	NM_001005474
1959	243955_at	---	---
1960	231810_at	BRI3BP	NM_080626
1961	218627_at	DRAM1	NM_018370
1962	205728_at	ODZ1	NM_001163278
1963	238425_at	---	---

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<i>SEQ ID No.</i>	Probe Set ID	Gene Symbol	RefSeq Transcript ID
1964	202299_s_at	HBXIP	NM_006402
1965	203659_s_at	TRIM13	NM_001007278
1966	207735_at	RNF125	NM_017831
1967	233979_s_at	ESPN	NM_031475
1968	226300_at	MED19	NM_153450
1969	222307_at	LOC282997	NR_026932
1970	1559699_at	C20orf74	NM_020343
1971	239937_at	ZNF207	NM_001032293
1972	211022_s_at	ATRX	NM_000489
1973	203567_s_at	TRIM38	NM_006355
1974	203054_s_at	TCTA	NM_022171
1975	202905_x_at	NBN	NM_002485
1976	237870_at	LOC285771	---
1977	232044_at	RBBP6	NM_006910
1978	201931_at	ETFA	NM_000126
1979	203694_s_at	DHX16	NM_001164239
1980	224652_at	CCNY	NM_145012
1981	221978_at	HLA-F	NM_001098478
1982	243995_at	PTAR1	NM_001099666
1983	225925_s_at	USP48	NM_001032730
1984	204750_s_at	DSC2	NM_004949
1985	226606_s_at	GTPBP5	NM_015666
1986	232141_at	U2AF1	NM_001025203
1987	227535_at	C15orf24	NM_020154
1988	1553829_at	C2orf58	NR_027252
1989	208853_s_at	CANX	NM_001024649
1990	212020_s_at	MKI67	NM_001145966
1991	225205_at	KIF3B	NM_004798
1992	232724_at	MS4A6A	NM_022349
1993	221139_s_at	CSAD	NM_015989
1994	210495_x_at	FN1	NM_002026
1995	210910_s_at	POMZP3	NM_012230
1996	1555920_at	CBX3	NM_007276
1997	220980_s_at	ADPGK	NM_031284
1998	1556601_a_at	SPATA13	NM_153023
1999	215236_s_at	PICALM	NM_001008660
2000	240031_at	MSRA	NM_001135670
2001	234980_at	TMEM56	NM_152487
2002	1556865_at	---	---

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<i>SEQ ID No.</i>	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1	1560255_at	0,53	144%
2	238712_at	0,29	122%
3	227970_at	-0,55	68%
4	237056_at	0,94	192%
5	241981_at	0,86	182%
6	223974_at	0,59	151%
7	241415_at	0,31	124%
8	1565544_at	0,56	147%
9	216693_x_at	0,44	136%
10	1570264_at	0,39	131%
11	221044_s_at	0,19	114%
12	203658_at	0,39	131%
13	213390_at	-0,11	93%
14	224832_at	-0,37	77%
15	212642_s_at	-0,33	80%
16	225005_at	-0,22	86%
17	242167_at	0,33	126%
18	221143_at	0,32	125%
19	243824_at	0,62	154%
20	222139_at	0,66	158%
21	237315_at	0,37	129%
22	238360_s_at	0,28	121%
23	239571_at	0,38	130%
24	232356_at	0,24	118%
25	224645_at	-0,22	86%
26	1556110_at	-0,21	86%
27	234842_at	-0,21	86%
28	212017_at	-0,24	85%
29	226772_s_at	0,23	117%
30	1552648_a_at	-0,32	80%
31	225840_at	-0,35	78%
32	202657_s_at	-0,27	83%
33	231764_at	-0,22	86%
34	232513_x_at	0,42	134%
35	233283_at	0,46	138%
36	206983_at	-0,69	62%
37	243654_at	0,61	153%

<i>SEQ ID No.</i>	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
38	223558_at	-0,33	80%
39	225263_at	-0,16	90%
40	1563497_at	0,25	119%
41	237655_at	0,65	157%
42	230571_at	-0,28	82%
43	238439_at	1,42	268%
44	200666_s_at	-0,18	88%
45	235024_at	-0,21	86%
46	244025_at	0,15	111%
47	217868_s_at	0,23	117%
48	236229_at	0,43	135%
49	202365_at	-0,24	85%
50	208741_at	-0,20	87%
51	226585_at	-0,30	81%
52	219938_s_at	0,34	127%
53	1554557_at	0,35	127%
54	244492_at	0,50	141%
55	243303_at	0,23	117%
56	216112_at	0,29	122%
57	225494_at	-0,32	80%
58	239363_at	-0,31	81%
59	1563975_at	0,67	159%
60	242917_at	0,55	146%
61	240661_at	0,37	129%
62	226547_at	-0,10	93%
63	231259_s_at	-0,51	70%
64	210281_s_at	0,27	121%
65	235543_at	0,33	126%
66	202656_s_at	-0,18	88%
67	243399_at	0,44	136%
68	205321_at	-0,32	80%
69	230738_at	0,39	131%
70	234302_s_at	-0,17	89%
71	231309_at	-0,33	80%
72	201751_at	-0,22	86%
73	221654_s_at	0,08	106%
74	235058_at	-0,26	84%

<i>SEQ ID No.</i>	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
75	203609_s_at	-0,41	75%
76	239845_at	0,31	124%
77	223637_s_at	0,26	120%
78	228156_at	0,23	117%
79	243509_at	0,33	126%
80	238053_at	0,45	137%
81	240733_at	0,31	124%
82	235421_at	0,21	116%
83	204787_at	0,71	164%
84	212806_at	1,21	231%
85	200759_x_at	-0,08	95%
86	213174_at	-0,48	72%
87	205181_at	0,23	117%
88	242306_at	0,21	116%
89	1562321_at	0,60	152%
90	201578_at	0,10	107%
91	1554132_a_at	-0,21	86%
92	225545_at	-0,31	81%
93	228811_at	-0,47	72%
94	203879_at	-0,08	95%
95	201170_s_at	-0,43	74%
96	215322_at	0,38	130%
97	1562110_at	0,43	135%
98	226804_at	0,62	154%
99	1554116_s_at	0,45	137%
100	237942_at	0,24	118%
101	219671_at	-0,62	65%
102	210104_at	-0,16	90%
103	212097_at	0,69	161%
104	1558761_a_at	0,29	122%
105	215888_at	0,24	118%
106	208823_s_at	-0,22	86%
107	201731_s_at	-0,18	88%
108	220131_at	-0,34	79%
109	216233_at	0,60	152%
110	236629_at	-0,36	78%
111	1562260_at	0,34	127%

Table 1A, page 2

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
112	33494_at	0,18	113%
113	228068_at	-0,17	89%
114	222640_at	-0,17	89%
115	239077_at	0,41	133%
116	207040_s_at	-0,26	84%
117	228723_at	0,22	116%
118	1562031_at	0,66	158%
119	218771_at	-0,13	91%
120	219906_at	0,23	117%
121	217286_s_at	-0,17	89%
122	235777_at	0,20	115%
123	218625_at	0,91	188%
124	1567213_at	0,30	123%
125	243276_at	-0,43	74%
126	215210_s_at	-0,23	85%
127	207339_s_at	-0,32	80%
128	202533_s_at	0,12	109%
129	230267_at	0,35	127%
130	218168_s_at	-0,30	81%
131	222844_s_at	-0,32	80%
132	233264_at	0,33	126%
133	214501_s_at	0,15	111%
134	203505_at	0,54	145%
135	203556_at	-0,15	90%
136	226474_at	0,14	110%
137	215640_at	0,29	122%
138	243902_at	0,64	156%
139	208109_s_at	0,15	111%
140	220905_at	0,21	116%
141	201259_s_at	-0,20	87%
142	221908_at	-0,41	75%
143	205379_at	-0,66	63%
144	229374_at	-0,39	76%
145	1569666_s_at	0,59	151%
146	228216_at	0,26	120%
147	240217_s_at	-0,12	92%
148	218287_s_at	-0,20	87%
149	218517_at	-0,13	91%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
150	244796_at	0,22	116%
151	233976_at	0,21	116%
152	233647_s_at	0,31	124%
153	239489_at	0,27	121%
154	238923_at	-0,18	88%
155	237018_at	0,13	109%
156	240176_at	0,40	132%
157	200860_s_at	-0,16	90%
158	212639_x_at	-0,09	94%
159	201236_s_at	-0,16	90%
160	205857_at	0,38	130%
161	228603_at	0,28	121%
162	238728_at	-0,25	84%
163	216729_at	0,40	132%
164	206674_at	0,55	146%
165	238025_at	0,16	112%
166	203255_at	0,07	105%
167	213294_at	0,34	127%
168	215209_at	0,29	122%
169	208030_s_at	-0,12	92%
170	238570_at	-0,20	87%
171	232164_s_at	-0,70	62%
172	209828_s_at	-0,23	85%
173	222526_at	-0,23	85%
174	203366_at	-0,17	89%
175	242319_at	0,47	139%
176	223846_at	0,31	124%
177	234402_at	-0,60	66%
178	32042_at	-0,18	88%
179	225478_at	-0,37	77%
180	229754_at	0,36	128%
181	243514_at	0,34	127%
182	213484_at	-0,59	66%
183	208744_x_at	-0,45	73%
184	1558592_at	0,15	111%
185	239462_at	-0,32	80%
186	212399_s_at	-0,16	90%
187	236013_at	0,86	182%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
188	211986_at	-0,18	88%
189	242803_at	0,16	112%
190	217815_at	-0,07	95%
191	219120_at	-0,25	84%
192	242780_at	0,27	121%
193	242695_at	0,19	114%
194	1570394_at	0,43	135%
195	221639_x_at	-0,54	69%
196	217185_s_at	-0,21	86%
197	1568964_x_at	-0,22	86%
198	1556942_at	0,40	132%
199	200594_x_at	-0,16	90%
200	1559739_at	0,35	127%
201	232157_at	0,31	124%
202	224855_at	-0,21	86%
203	200796_s_at	-0,26	84%
204	201747_s_at	-0,12	92%
205	205781_at	0,29	122%
206	201032_at	-0,15	90%
207	226687_at	0,11	108%
208	207253_s_at	-0,08	95%
209	222310_at	-0,04	97%
210	203218_at	0,17	113%
211	203409_at	-0,03	98%
212	217857_s_at	-0,09	94%
213	212428_at	-0,14	91%
214	213266_at	-0,11	93%
215	201652_at	0,08	106%
216	204211_x_at	0,25	119%
217	201051_at	-0,03	98%
218	230998_at	0,06	104%
219	230664_at	-0,09	94%
220	200979_at	-0,07	95%
221	228623_at	-0,02	99%
222	200767_s_at	0,01	101%
223	201721_s_at	0,00	100%
224	200030_s_at	-0,07	95%
225	215828_at	-0,04	97%

Table 1A, page 3

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
226	237943_at	0,16	112%
227	1569369_at	-0,01	99%
228	204216_s_at	-0,05	97%
229	202796_at	-0,31	81%
230	226656_at	-0,24	85%
231	212234_at	-0,16	90%
232	209715_at	-0,14	91%
233	200016_x_at	-0,06	96%
234	209078_s_at	-0,07	95%
235	204275_at	-0,04	97%
236	1566501_at	0,12	109%
237	228091_at	-0,02	99%
238	1554096_a_at	0,08	106%
239	209358_at	-0,03	98%
240	1554628_at	-0,10	93%
241	203379_at	0,00	100%
242	1569999_at	-0,04	97%
243	232628_at	0,01	101%
244	219004_s_at	-0,16	90%
245	222043_at	0,13	109%
246	212527_at	0,18	113%
247	235114_x_at	0,06	104%
248	232188_at	0,37	129%
249	209735_at	0,19	114%
250	207604_s_at	-0,12	92%
251	224990_at	0,04	103%
252	235840_at	0,01	101%
253	232648_at	0,12	109%
254	220213_at	-0,49	71%
255	218912_at	-0,14	91%
256	219963_at	0,67	159%
257	214783_s_at	0,01	101%
258	213836_s_at	0,40	132%
259	202184_s_at	-0,14	91%
260	237317_at	0,26	120%
261	214016_s_at	-0,04	97%
262	236901_at	0,47	139%
263	204025_s_at	-0,02	99%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
264	208740_at	-0,19	88%
265	201083_s_at	0,01	101%
266	208087_s_at	0,29	122%
267	202941_at	0,07	105%
268	215545_at	0,17	113%
269	201088_at	0,21	116%
270	1556007_s_at	0,29	122%
271	212859_x_at	0,53	144%
272	204245_s_at	-0,20	87%
273	210965_x_at	0,01	101%
274	204116_at	-0,12	92%
275	219409_at	-0,20	87%
276	204962_s_at	0,27	121%
277	221535_at	-0,27	83%
278	228200_at	-0,21	86%
279	203905_at	-0,19	88%
280	212415_at	-0,20	87%
281	232427_at	0,13	109%
282	226052_at	-0,06	96%
283	227346_at	-0,09	94%
284	201588_at	0,03	102%
285	1561880_a_at	0,42	134%
286	221529_s_at	-0,54	69%
287	224686_x_at	-0,11	93%
288	201762_s_at	0,08	106%
289	210732_s_at	0,28	121%
290	229897_at	0,35	127%
291	203836_s_at	0,05	104%
292	220439_at	0,34	127%
293	213193_x_at	-0,21	86%
294	225125_at	-0,09	94%
295	1555884_at	0,25	119%
296	210277_at	0,04	103%
297	223946_at	0,59	151%
298	212346_s_at	-0,12	92%
299	203799_at	0,11	108%
300	228158_at	0,07	105%
301	238140_at	-0,21	86%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
302	236703_at	0,35	127%
303	1565651_at	0,19	114%
304	200988_s_at	-0,19	88%
305	206652_at	0,15	111%
306	202717_s_at	-0,03	98%
307	1554424_at	-0,23	85%
308	231557_at	0,51	142%
309	1557520_a_at	0,09	106%
310	200751_s_at	-0,13	91%
311	209299_x_at	-0,13	91%
312	238704_at	-0,32	80%
313	1555906_s_at	0,07	105%
314	232034_at	0,47	139%
315	1568907_at	0,31	124%
316	232330_at	0,21	116%
317	1563687_a_at	-0,21	86%
318	226107_at	0,31	124%
319	214472_at	0,52	143%
320	208978_at	-0,34	79%
321	222975_s_at	-0,08	95%
322	232569_at	0,46	138%
323	230735_at	0,36	128%
324	203497_at	-0,21	86%
325	219138_at	-0,05	97%
326	200815_s_at	0,03	102%
327	233545_at	0,14	110%
328	208876_s_at	-0,07	95%
329	204533_at	0,63	155%
330	241752_at	0,38	130%
331	202768_at	-0,47	72%
332	234991_at	0,29	122%
333	228818_at	-0,32	80%
334	218805_at	-0,19	88%
335	219001_s_at	0,25	119%
336	202386_s_at	-0,11	93%
337	228624_at	0,53	144%
338	236971_at	0,29	122%
339	202840_at	-0,15	90%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
340	209124_at	0,10	107%
341	210136_at	-0,16	90%
342	202003_s_at	0,18	113%
343	238788_at	-0,11	93%
344	243598_at	0,26	120%
345	222909_s_at	0,19	114%
346	218641_at	0,14	110%
347	239104_at	0,31	124%
348	1558354_s_at	0,14	110%
349	238257_at	0,34	127%
350	1568830_at	0,67	159%
351	231937_at	0,25	119%
352	212766_s_at	-0,12	92%
353	1569652_at	-0,22	86%
354	223832_s_at	0,48	139%
355	227249_at	-0,19	88%
356	209162_s_at	-0,18	88%
357	210943_s_at	0,19	114%
358	213963_s_at	0,54	145%
359	233079_at	0,28	121%
360	242945_at	0,78	172%
361	239213_at	0,39	131%
362	226229_s_at	-0,18	88%
363	212124_at	-0,19	88%
364	224357_s_at	0,47	139%
365	236273_at	-0,42	75%
366	204526_s_at	0,30	123%
367	233263_at	0,25	119%
368	209907_s_at	0,12	109%
369	201880_at	-0,03	98%
370	218448_at	-0,15	90%
371	243631_at	0,12	109%
372	238026_at	-0,28	82%
373	218454_at	0,27	121%
374	202172_at	0,02	101%
375	209161_at	-0,18	88%
376	201470_at	0,14	110%
377	206335_at	0,15	111%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
378	204061_at	-0,43	74%
379	203368_at	-0,24	85%
380	235309_at	-0,28	82%
381	226874_at	0,33	126%
382	217905_at	0,41	133%
383	215175_at	0,23	117%
384	1555793_a_at	-0,39	76%
385	235681_at	0,32	125%
386	243315_at	0,28	121%
387	205475_at	0,51	142%
388	239902_at	0,07	105%
389	216134_at	0,32	125%
390	235119_at	-0,21	86%
391	1553333_at	0,35	127%
392	203113_s_at	-0,18	88%
393	235518_at	0,32	125%
394	217555_at	-0,26	84%
395	227854_at	0,29	122%
396	225613_at	-0,25	84%
397	201739_at	-0,28	82%
398	201960_s_at	-0,16	90%
399	221571_at	-0,25	84%
400	221819_at	-0,19	88%
401	203298_s_at	-0,12	92%
402	1558459_s_at	0,18	113%
403	57516_at	-0,23	85%
404	202714_s_at	-0,37	77%
405	1559614_at	0,26	120%
406	223027_at	-0,35	78%
407	201927_s_at	-0,44	74%
408	200699_at	-0,13	91%
409	223189_x_at	-0,10	93%
410	215507_x_at	-0,20	87%
411	219385_at	0,31	124%
412	218039_at	0,28	121%
413	1567101_at	0,58	149%
414	1563629_a_at	0,22	116%
415	217894_at	0,28	121%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
416	212814_at	-0,10	93%
417	205692_s_at	0,37	129%
418	233186_s_at	-0,17	89%
419	219308_s_at	-0,57	67%
420	1556750_at	0,25	119%
421	203676_at	0,34	127%
422	234865_at	-0,81	57%
423	209555_s_at	0,40	132%
424	200633_at	-0,06	96%
425	203065_s_at	0,40	132%
426	235959_at	0,22	116%
427	218047_at	0,21	116%
428	218358_at	0,01	101%
429	228138_at	-0,28	82%
430	226913_s_at	-0,62	65%
431	1560705_at	0,27	121%
432	232821_at	-0,41	75%
433	239679_at	-0,03	98%
434	237953_at	-0,34	79%
435	220560_at	0,18	113%
436	220797_at	-0,11	93%
437	219112_at	-0,17	89%
438	235061_at	-0,36	78%
439	212945_s_at	-0,22	86%
440	218232_at	0,60	152%
441	213604_at	-0,18	88%
442	229659_s_at	-0,56	68%
443	212794_s_at	0,17	113%
444	218969_at	0,08	106%
445	1555487_a_at	-0,11	93%
446	207129_at	-0,28	82%
447	244578_at	0,28	121%
448	225407_at	-0,08	95%
449	230515_at	-0,18	88%
450	232559_at	0,19	114%
451	244726_at	0,15	111%
452	238644_at	0,24	118%
453	203240_at	-0,81	57%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
454	236399_at	0,43	135%
455	223492_s_at	0,22	116%
456	203234_at	0,18	113%
457	213260_at	0,40	132%
458	216142_at	0,14	110%
459	233072_at	0,37	129%
460	228660_x_at	-0,11	93%
461	238107_at	0,38	130%
462	201376_s_at	-0,15	90%
463	210317_s_at	-0,18	88%
464	218426_s_at	-0,15	90%
465	239637_at	0,15	111%
466	224336_s_at	-0,25	84%
467	244659_at	0,18	113%
468	1555950_a_at	0,17	113%
469	219284_at	0,24	118%
470	236007_at	0,12	109%
471	212601_at	-0,10	93%
472	233781_s_at	0,15	111%
473	238109_at	0,34	127%
474	201305_x_at	-0,15	90%
475	210592_s_at	0,10	107%
476	204140_at	0,71	164%
477	227599_at	-0,42	75%
478	1554287_at	0,29	122%
479	243470_at	0,08	106%
480	1562898_at	0,31	124%
481	239287_at	-0,67	63%
482	1558938_at	0,22	116%
483	1557780_at	0,18	113%
484	207734_at	-0,46	73%
485	214595_at	-0,63	65%
486	236982_at	0,41	133%
487	1555608_at	-0,30	81%
488	228923_at	0,20	115%
489	207968_s_at	-0,43	74%
490	203927_at	-0,06	96%
491	222306_at	-0,03	98%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
492	203130_s_at	-0,49	71%
493	219498_s_at	-0,34	79%
494	1557224_at	0,18	113%
495	223313_s_at	-0,35	78%
496	1555180_at	0,35	127%
497	203632_s_at	-0,83	56%
498	220387_s_at	-0,33	80%
499	217791_s_at	-0,13	91%
500	1559479_at	0,48	139%
501	1554600_s_at	-0,17	89%
502	1569792_a_at	0,29	122%
503	235071_at	-0,32	80%
504	243334_at	0,37	129%
505	234848_at	-0,72	61%
506	201489_at	-0,21	86%
507	210189_at	0,16	112%
508	221816_s_at	0,07	105%
509	231319_x_at	-0,14	91%
510	202863_at	0,18	113%
511	235699_at	0,28	121%
512	211930_at	-0,11	93%
513	228349_at	0,24	118%
514	224516_s_at	-0,35	78%
515	204099_at	0,34	127%
516	221589_s_at	-0,28	82%
517	1569617_at	-0,31	81%
518	212904_at	-0,19	88%
519	203007_x_at	0,25	119%
520	236165_at	0,25	119%
521	229404_at	0,78	172%
522	222234_s_at	-0,33	80%
523	200659_s_at	-0,14	91%
524	226668_at	0,28	121%
525	219669_at	1,64	312%
526	208778_s_at	-0,13	91%
527	203320_at	-0,18	88%
528	226802_s_at	-0,24	85%
529	1565928_at	-0,35	78%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
530	212259_s_at	-0,15	90%
531	231816_s_at	-0,27	83%
532	228184_at	-0,36	78%
533	222821_s_at	0,08	106%
534	217722_s_at	-0,18	88%
535	1566171_at	0,14	110%
536	233219_at	0,33	126%
537	1565894_at	0,27	121%
538	1569599_at	0,69	161%
539	206761_at	-0,40	76%
540	1556253_s_at	0,36	128%
541	1564053_a_at	0,08	106%
542	229199_at	0,31	124%
543	226734_at	-0,24	85%
544	226447_at	-0,12	92%
545	202985_s_at	-0,05	97%
546	208180_s_at	0,39	131%
547	217995_at	0,12	109%
548	234172_at	0,36	128%
549	205169_at	-0,13	91%
550	212387_at	-0,38	77%
551	213293_s_at	0,24	118%
552	244536_at	0,16	112%
553	232306_at	0,30	123%
554	212838_at	-0,18	88%
555	235033_at	0,33	126%
556	203460_s_at	0,07	105%
557	209409_at	0,38	130%
558	216527_at	0,19	114%
559	1554453_at	0,18	113%
560	226775_at	0,13	109%
561	211152_s_at	0,12	109%
562	235825_at	0,19	114%
563	212594_at	-0,14	91%
564	206059_at	-0,33	80%
565	214184_at	0,09	106%
566	205392_s_at	0,29	122%
567	213046_at	0,05	104%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
568	234883_x_at	-0,39	76%
569	228650_at	-0,25	84%
570	227112_at	-0,21	86%
571	217431_x_at	0,18	113%
572	202095_s_at	0,42	134%
573	206026_s_at	0,62	154%
574	226651_at	0,16	112%
575	240859_at	0,39	131%
576	1555634_a_at	0,48	139%
577	235207_at	0,12	109%
578	231695_at	0,36	128%
579	213524_s_at	0,83	178%
580	212318_at	0,08	106%
581	227329_at	-0,30	81%
582	203050_at	-0,22	86%
583	219975_x_at	1,02	203%
584	215671_at	0,33	126%
585	231260_at	-0,39	76%
586	217513_at	0,48	139%
587	1556339_a_at	0,33	126%
588	208774_at	-0,11	93%
589	221536_s_at	-0,10	93%
590	231641_at	0,29	122%
591	202551_s_at	0,22	116%
592	204110_at	0,22	116%
593	201235_s_at	-0,20	87%
594	219633_at	0,22	116%
595	227055_at	0,89	185%
596	234427_at	-0,59	66%
597	239819_at	0,20	115%
598	230762_at	0,33	126%
599	201651_s_at	-0,17	89%
600	244579_at	0,16	112%
601	233476_at	0,23	117%
602	1562576_at	0,50	141%
603	227589_at	-0,19	88%
604	209062_x_at	0,34	127%
605	236755_at	0,22	116%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
606	223608_at	0,51	142%
607	204079_at	0,15	111%
608	238789_at	-0,74	60%
609	213172_at	-0,43	74%
610	224582_s_at	-0,37	77%
611	243796_at	0,22	116%
612	213567_at	-0,05	97%
613	242197_x_at	0,27	121%
614	244177_at	-0,06	96%
615	210873_x_at	0,37	129%
616	238929_at	-0,28	82%
617	229756_at	0,40	132%
618	224681_at	-0,29	82%
619	242423_x_at	0,29	122%
620	219300_s_at	-0,91	53%
621	209477_at	-0,15	90%
622	203088_at	-0,74	60%
623	242947_at	-0,45	73%
624	210609_s_at	0,49	140%
625	203660_s_at	-0,22	86%
626	213755_s_at	-0,39	76%
627	216297_at	0,34	127%
628	1559375_s_at	0,36	128%
629	217866_at	-0,18	88%
630	223337_at	-0,03	98%
631	221524_s_at	0,37	129%
632	216614_at	0,15	111%
633	220342_x_at	0,17	113%
634	218883_s_at	0,36	128%
635	217486_s_at	0,28	121%
636	236572_at	0,27	121%
637	203188_at	-0,47	72%
638	1564231_at	-0,48	72%
639	209765_at	0,03	102%
640	202902_s_at	0,05	104%
641	224369_s_at	0,25	119%
642	218876_at	-0,66	63%
643	240099_at	0,31	124%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
644	228119_at	0,17	113%
645	239130_at	0,30	123%
646	1560971_a_at	-0,61	66%
647	222820_at	-0,35	78%
648	243476_at	0,15	111%
649	1558697_a_at	-0,14	91%
650	1558046_x_at	-0,18	88%
651	241275_at	0,37	129%
652	209425_at	-0,10	93%
653	228835_at	0,21	116%
654	237901_at	0,34	127%
655	234785_at	0,13	109%
656	1557193_at	0,24	118%
657	244447_at	0,22	116%
658	204950_at	0,13	109%
659	227410_at	-0,25	84%
660	205500_at	0,30	123%
661	228394_at	-0,20	87%
662	1561206_at	0,30	123%
663	48808_at	0,10	107%
664	228253_at	0,24	118%
665	227501_at	0,34	127%
666	226674_at	-0,54	69%
667	202290_at	-0,18	88%
668	237062_at	0,28	121%
669	1554665_at	0,15	111%
670	237082_at	-0,34	79%
671	201206_s_at	-0,04	97%
672	1561615_s_at	0,40	132%
673	201783_s_at	-0,07	95%
674	212180_at	-0,13	91%
675	220289_s_at	0,22	116%
676	225157_at	-0,23	85%
677	237627_at	-0,23	85%
678	203052_at	0,37	129%
679	215030_at	-0,21	86%
680	208629_s_at	-0,23	85%
681	201757_at	-0,03	98%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
682	232251_at	0,39	131%
683	228468_at	0,15	111%
684	226989_at	-0,73	60%
685	1556257_at	0,41	133%
686	223194_s_at	-0,40	76%
687	212166_at	-0,18	88%
688	240233_at	0,36	128%
689	1563053_at	-0,23	85%
690	1568915_at	0,25	119%
691	223121_s_at	-0,64	64%
692	204067_at	0,10	107%
693	226313_at	-0,49	71%
694	206636_at	0,15	111%
695	212457_at	0,01	101%
696	1553856_s_at	-0,44	74%
697	230885_at	-0,07	95%
698	231357_at	0,29	122%
699	241956_at	0,11	108%
700	201596_x_at	-0,19	88%
701	244026_at	0,22	116%
702	211072_x_at	-0,06	96%
703	230619_at	-0,19	88%
704	1554833_at	0,43	135%
705	212388_at	-0,06	96%
706	1566809_a_at	-0,38	77%
707	235310_at	-0,55	68%
708	211003_x_at	-0,47	72%
709	230036_at	0,34	127%
710	239391_at	0,10	107%
711	214243_s_at	-0,29	82%
712	240806_at	-0,39	76%
713	1554447_at	0,25	119%
714	242501_at	-0,25	84%
715	209865_at	-0,19	88%
716	238961_s_at	0,25	119%
717	1557465_at	0,35	127%
718	1562608_at	0,49	140%
719	214394_x_at	-0,08	95%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
720	230796_at	0,36	128%
721	220546_at	-0,07	95%
722	210640_s_at	0,53	144%
723	1562745_at	0,15	111%
724	1556323_at	0,31	124%
725	213208_at	-0,20	87%
726	201143_s_at	-0,28	82%
727	202087_s_at	0,26	120%
728	1558279_a_at	-0,21	86%
729	223591_at	0,15	111%
730	202005_at	0,20	115%
731	242031_at	0,24	118%
732	204889_s_at	-0,26	84%
733	217701_x_at	-0,59	66%
734	213774_s_at	-0,14	91%
735	235288_at	0,13	109%
736	204222_s_at	0,06	104%
737	214513_s_at	-0,13	91%
738	201678_s_at	-0,17	89%
739	1563348_at	0,11	108%
740	1561306_s_at	-0,44	74%
741	223733_s_at	0,44	136%
742	203308_x_at	0,00	100%
743	232121_at	0,24	118%
744	1556211_a_at	0,22	116%
745	232033_at	-0,23	85%
746	202601_s_at	-0,22	86%
747	212680_x_at	0,15	111%
748	1563466_at	-0,31	81%
749	219676_at	0,15	111%
750	1558586_at	-0,27	83%
751	230886_at	0,11	108%
752	240144_at	0,14	110%
753	1560034_a_at	0,20	115%
754	221223_x_at	-0,34	79%
755	200999_s_at	0,26	120%
756	235456_at	0,55	146%
757	214766_s_at	0,08	106%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
758	202706_s_at	-0,14	91%
759	233176_at	0,23	117%
760	227449_at	-0,56	68%
761	225655_at	0,32	125%
762	236024_at	-0,64	64%
763	207654_x_at	0,18	113%
764	236094_at	0,37	129%
765	230166_at	0,31	124%
766	229008_at	-0,32	80%
767	210817_s_at	0,09	106%
768	1560069_at	0,09	106%
769	236113_at	0,56	147%
770	202794_at	0,08	106%
771	231174_s_at	-0,34	79%
772	1559459_at	-0,14	91%
773	238892_at	0,23	117%
774	203803_at	-0,28	82%
775	221801_x_at	-0,68	62%
776	222449_at	-0,39	76%
777	202954_at	0,23	117%
778	1568997_at	-0,44	74%
779	228769_at	-0,12	92%
780	1557119_a_at	-0,32	80%
781	200857_s_at	-0,14	91%
782	234082_at	0,26	120%
783	243819_at	0,11	108%
784	206632_s_at	0,82	177%
785	203430_at	0,14	110%
786	1555626_a_at	-0,52	70%
787	1559618_at	-0,49	71%
788	1555058_a_at	0,40	132%
789	221253_s_at	0,30	123%
790	219493_at	0,19	114%
791	238607_at	-0,30	81%
792	215411_s_at	-0,19	88%
793	203616_at	0,15	111%
794	206075_s_at	-0,14	91%
795	232953_at	0,44	136%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
796	226652_at	0,10	107%
797	222413_s_at	-0,02	99%
798	214814_at	0,31	124%
799	228983_at	0,15	111%
800	215342_s_at	-0,32	80%
801	227737_at	-0,33	80%
802	233033_at	0,18	113%
803	209378_s_at	-0,21	86%
804	209105_at	-0,17	89%
805	221833_at	0,18	113%
806	239516_at	0,13	109%
807	205798_at	-0,42	75%
808	200868_s_at	0,14	110%
809	1564639_at	-0,46	73%
810	203633_at	0,20	115%
811	223588_at	-0,21	86%
812	202349_at	0,14	110%
813	200600_at	-0,05	97%
814	201196_s_at	-0,04	97%
815	208642_s_at	-0,05	97%
816	231340_at	0,28	121%
817	210253_at	0,14	110%
818	212624_s_at	-0,47	72%
819	228478_at	0,06	104%
820	1569154_a_at	-0,28	82%
821	1553857_at	-0,18	88%
822	224567_x_at	0,10	107%
823	221215_s_at	0,07	105%
824	200710_at	0,04	103%
825	220302_at	-0,18	88%
826	214499_s_at	-0,13	91%
827	238836_at	-0,36	78%
828	213256_at	-0,09	94%
829	226095_s_at	-0,08	95%
830	203816_at	-0,03	98%
831	209307_at	-0,32	80%
832	201144_s_at	-0,04	97%
833	236707_at	0,42	134%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
834	240703_s_at	-0,23	85%
835	229720_at	-0,15	90%
836	238037_at	-0,37	77%
837	200597_at	-0,22	86%
838	207563_s_at	0,20	115%
839	241441_at	0,16	112%
840	217961_at	-0,20	87%
841	225696_at	-0,18	88%
842	211721_s_at	-0,20	87%
843	212095_s_at	-0,38	77%
844	242857_at	-0,18	88%
845	241421_at	0,31	124%
846	225119_at	-0,29	82%
847	243375_at	0,34	127%
848	202239_at	0,08	106%
849	200819_s_at	-0,17	89%
850	237218_at	0,18	113%
851	1570124_at	0,16	112%
852	217225_x_at	-0,13	91%
853	215220_s_at	-0,11	93%
854	228899_at	0,10	107%
855	222880_at	-0,37	77%
856	218820_at	-0,52	70%
857	223892_s_at	0,03	102%
858	229907_at	0,51	142%
859	209536_s_at	-0,18	88%
860	240899_at	0,09	106%
861	221267_s_at	-0,05	97%
862	216069_at	0,26	120%
863	215390_at	-0,94	52%
864	224583_at	-0,05	97%
865	205248_at	-0,19	88%
866	227820_at	-0,13	91%
867	208934_s_at	0,16	112%
868	229364_at	0,17	113%
869	222073_at	-0,54	69%
870	219757_s_at	0,33	126%
871	226013_at	-0,19	88%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
872	239922_at	0,04	103%
873	242966_x_at	0,16	112%
874	224229_s_at	-0,18	88%
875	218464_s_at	-0,15	90%
876	204924_at	0,23	117%
877	228532_at	0,09	106%
878	1560060_s_at	-0,17	89%
879	1559282_at	0,38	130%
880	217380_s_at	0,26	120%
881	223002_s_at	-0,12	92%
882	229145_at	-0,10	93%
883	224911_s_at	0,35	127%
884	205466_s_at	-0,24	85%
885	203907_s_at	0,00	100%
886	232645_at	0,13	109%
887	233575_s_at	0,14	110%
888	200019_s_at	-0,09	94%
889	225738_at	-0,21	86%
890	1561018_at	0,26	120%
891	236460_at	-0,01	99%
892	217518_at	0,30	123%
893	212836_at	-0,07	95%
894	213264_at	-0,15	90%
895	1557852_at	0,40	132%
896	202708_s_at	0,14	110%
897	231763_at	-0,23	85%
898	223259_at	-0,28	82%
899	213729_at	0,08	106%
900	219978_s_at	0,19	114%
901	222674_at	-0,11	93%
902	223363_at	-0,19	88%
903	221188_s_at	0,23	117%
904	223059_s_at	-0,08	95%
905	220557_s_at	-0,37	77%
906	219576_at	-0,09	94%
907	204326_x_at	0,13	109%
908	235575_at	0,30	123%
909	201256_at	-0,01	99%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
910	226645_at	-0,22	86%
911	1559050_at	0,30	123%
912	212114_at	-0,18	88%
913	209948_at	0,17	113%
914	236407_at	0,65	157%
915	240481_at	0,16	112%
916	208195_at	-0,43	74%
917	203728_at	0,12	109%
918	227684_at	-0,35	78%
919	236002_at	0,17	113%
920	204270_at	-0,28	82%
921	202345_s_at	0,27	121%
922	219745_at	0,18	113%
923	235802_at	-0,44	74%
924	230375_at	0,12	109%
925	219066_at	-0,18	88%
926	1560339_s_at	-0,18	88%
927	203110_at	0,10	107%
928	219630_at	-0,30	81%
929	244307_s_at	0,13	109%
930	238758_at	0,15	111%
931	214917_at	0,10	107%
932	218276_s_at	-0,36	78%
933	228193_s_at	-0,28	82%
934	227037_at	-0,25	84%
935	225831_at	-0,26	84%
936	237210_at	0,17	113%
937	221206_at	-0,11	93%
938	221499_s_at	0,18	113%
939	222217_s_at	0,04	103%
940	238523_at	-0,23	85%
941	202048_s_at	-0,18	88%
942	212856_at	-0,12	92%
943	225759_x_at	0,29	122%
944	217606_at	0,24	118%
945	200973_s_at	-0,22	86%
946	230970_at	0,34	127%
947	228932_at	0,11	108%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
948	209338_at	-0,21	86%
949	205758_at	-0,18	88%
950	225065_x_at	-0,14	91%
951	203358_s_at	0,07	105%
952	209375_at	-0,07	95%
953	232489_at	-0,10	93%
954	239723_at	0,46	138%
955	1552641_s_at	-0,17	89%
956	1558220_at	0,21	116%
957	239960_x_at	-0,19	88%
958	225212_at	-0,15	90%
959	214815_at	0,11	108%
960	212135_s_at	-0,19	88%
961	232952_at	0,25	119%
962	1556053_at	0,07	105%
963	232346_at	0,22	116%
964	228967_at	-0,13	91%
965	239556_at	0,19	114%
966	226863_at	-0,18	88%
967	229810_at	-0,11	93%
968	236669_at	0,28	121%
969	222480_at	-0,14	91%
970	228281_at	0,42	134%
971	216945_x_at	-0,55	68%
972	207434_s_at	-0,44	74%
973	201674_s_at	-0,09	94%
974	239037_at	0,12	109%
975	1560434_x_at	0,20	115%
976	244556_at	0,11	108%
977	1552386_at	0,25	119%
978	222906_at	-0,24	85%
979	1554057_at	0,16	112%
980	204512_at	-0,13	91%
981	210512_s_at	0,49	140%
982	223816_at	0,23	117%
983	239251_at	0,30	123%
984	208998_at	-0,06	96%
985	213810_s_at	0,16	112%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
986	207194_s_at	-0,31	81%
987	226372_at	-0,11	93%
988	201792_at	-0,42	75%
989	221203_s_at	-0,18	88%
990	1562019_at	0,62	154%
991	205613_at	-0,39	76%
992	221581_s_at	0,04	103%
993	244834_at	-0,29	82%
994	201557_at	-0,12	92%
995	225549_at	-0,24	85%
996	201800_s_at	-0,11	93%
997	202548_s_at	-0,18	88%
998	222243_s_at	-0,18	88%
999	2028_s_at	0,29	122%
1000	223000_s_at	-0,10	93%
1001	222282_at	0,13	109%
1002	230252_at	-0,29	82%
1003	227152_at	0,10	107%
1004	242877_at	0,09	106%
1005	236908_at	0,32	125%
1006	201365_at	-0,08	95%
1007	241117_at	0,46	138%
1008	230663_at	0,10	107%
1009	209579_s_at	0,12	109%
1010	1562007_at	-0,28	82%
1011	222672_at	-0,23	85%
1012	206842_at	0,12	109%
1013	213034_at	-0,09	94%
1014	203764_at	0,40	132%
1015	239014_at	0,27	121%
1016	204029_at	-0,30	81%
1017	204711_at	0,05	104%
1018	221595_at	-0,21	86%
1019	1552671_a_at	-0,42	75%
1020	226066_at	0,35	127%
1021	1553364_at	0,57	148%
1022	224653_at	-0,11	93%
1023	1564435_a_at	-0,57	67%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1024	229253_at	-0,37	77%
1025	222044_at	0,18	113%
1026	241705_at	0,25	119%
1027	228469_at	0,20	115%
1028	204858_s_at	0,18	113%
1029	201621_at	-0,47	72%
1030	234492_at	0,26	120%
1031	212906_at	0,22	116%
1032	231116_at	0,35	127%
1033	232782_at	-0,15	90%
1034	224978_s_at	-0,24	85%
1035	225471_s_at	-0,06	96%
1036	1556496_a_at	0,22	116%
1037	224717_s_at	0,09	106%
1038	241819_at	0,20	115%
1039	202286_s_at	0,67	159%
1040	219198_at	-0,20	87%
1041	202800_at	0,48	139%
1042	208003_s_at	0,23	117%
1043	36030_at	0,11	108%
1044	219826_at	-0,10	93%
1045	214005_at	0,16	112%
1046	241669_x_at	-0,26	84%
1047	227122_at	0,05	104%
1048	205560_at	-0,20	87%
1049	1564378_a_at	0,25	119%
1050	240721_at	0,56	147%
1051	228306_at	0,20	115%
1052	202074_s_at	-0,23	85%
1053	210559_s_at	0,20	115%
1054	206873_at	-0,51	70%
1055	225221_at	0,01	101%
1056	213180_s_at	-0,15	90%
1057	200622_x_at	-0,08	95%
1058	229413_s_at	0,26	120%
1059	220466_at	-0,14	91%
1060	229817_at	0,48	139%
1061	238417_at	-0,06	96%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1062	240845_at	0,32	125%
1063	238016_s_at	0,17	113%
1064	226765_at	-0,23	85%
1065	217856_at	-0,14	91%
1066	220865_s_at	0,21	116%
1067	232588_at	0,10	107%
1068	201736_s_at	0,15	111%
1069	1561195_at	-0,29	82%
1070	236422_at	0,82	177%
1071	209118_s_at	-0,09	94%
1072	229622_at	0,78	172%
1073	227490_at	0,20	115%
1074	226517_at	0,60	152%
1075	230405_at	0,18	113%
1076	201543_s_at	0,15	111%
1077	200855_at	-0,08	95%
1078	209193_at	-0,13	91%
1079	216857_at	-0,62	65%
1080	225207_at	0,37	129%
1081	203969_at	-0,08	95%
1082	243444_at	-0,48	72%
1083	227091_at	0,36	128%
1084	1007_s_at	-0,47	72%
1085	205493_s_at	-0,62	65%
1086	208304_at	-0,43	74%
1087	210470_x_at	-0,14	91%
1088	210947_s_at	0,11	108%
1089	218561_s_at	-0,22	86%
1090	208613_s_at	-0,25	84%
1091	227436_at	-0,15	90%
1092	242729_at	0,30	123%
1093	237387_at	0,34	127%
1094	206005_s_at	0,25	119%
1095	218807_at	0,24	118%
1096	219371_s_at	-0,16	90%
1097	243858_at	0,25	119%
1098	219412_at	0,18	113%
1099	233224_at	-0,29	82%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1100	226571_s_at	-0,34	79%
1101	212828_at	-0,21	86%
1102	239212_at	-0,18	88%
1103	241763_s_at	0,12	109%
1104	1570566_at	0,37	129%
1105	1554985_at	0,24	118%
1106	202291_s_at	0,46	138%
1107	235308_at	-0,21	86%
1108	219433_at	-0,41	75%
1109	230023_at	-0,25	84%
1110	204578_at	-0,16	90%
1111	212599_at	-0,43	74%
1112	236836_at	0,22	116%
1113	234088_at	0,21	116%
1114	222667_s_at	0,06	104%
1115	231221_at	-0,15	90%
1116	202449_s_at	-0,16	90%
1117	209455_at	-0,09	94%
1118	1554237_at	0,22	116%
1119	1556352_at	0,04	103%
1120	205844_at	0,57	148%
1121	1562453_at	-0,56	68%
1122	1552613_s_at	-0,07	95%
1123	225204_at	-0,09	94%
1124	209806_at	0,16	112%
1125	240154_at	0,09	106%
1126	239464_at	0,54	145%
1127	1555370_a_at	-0,44	74%
1128	225004_at	-0,14	91%
1129	226893_at	-0,19	88%
1130	202190_at	-0,07	95%
1131	202369_s_at	-0,29	82%
1132	243973_at	-0,19	88%
1133	242862_x_at	0,09	106%
1134	236327_at	0,28	121%
1135	235778_s_at	0,20	115%
1136	229686_at	-0,13	91%
1137	213924_at	0,10	107%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1138	239792_at	-0,11	93%
1139	206560_s_at	-0,17	89%
1140	225654_at	-0,12	92%
1141	228570_at	-0,28	82%
1142	231064_s_at	0,17	113%
1143	238126_at	0,26	120%
1144	212995_x_at	-0,14	91%
1145	214617_at	-0,20	87%
1146	208269_s_at	-0,31	81%
1147	1568717_a_at	0,16	112%
1148	1558854_a_at	0,23	117%
1149	241938_at	0,16	112%
1150	215099_s_at	-0,15	90%
1151	230100_x_at	0,14	110%
1152	202464_s_at	0,13	109%
1153	225454_at	-0,14	91%
1154	1558201_s_at	0,13	109%
1155	239597_at	0,18	113%
1156	228772_at	0,34	127%
1157	227722_at	-0,52	70%
1158	243340_at	0,33	126%
1159	217769_s_at	0,07	105%
1160	228308_at	0,03	102%
1161	204233_s_at	0,12	109%
1162	204440_at	-0,39	76%
1163	204184_s_at	-0,04	97%
1164	212099_at	-0,25	84%
1165	212504_at	-0,45	73%
1166	220266_s_at	-0,28	82%
1167	227750_at	-0,47	72%
1168	203157_s_at	0,21	116%
1169	202804_at	-0,15	90%
1170	242752_at	-0,35	78%
1171	219799_s_at	0,46	138%
1172	236191_at	0,31	124%
1173	230725_at	0,22	116%
1174	212137_at	-0,15	90%
1175	238135_at	0,31	124%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1176	207079_s_at	-0,16	90%
1177	203973_s_at	0,18	113%
1178	228778_at	-0,22	86%
1179	240798_at	0,18	113%
1180	244347_at	-0,26	84%
1181	231093_at	-0,39	76%
1182	231435_at	0,41	133%
1183	244280_at	-0,33	80%
1184	224549_x_at	0,23	117%
1185	228516_at	-0,13	91%
1186	233218_at	0,11	108%
1187	1560297_at	0,14	110%
1188	227114_at	-0,25	84%
1189	204373_s_at	-0,16	90%
1190	226190_at	0,17	113%
1191	224564_s_at	0,06	104%
1192	214483_s_at	0,24	118%
1193	209248_at	0,04	103%
1194	204576_s_at	-0,25	84%
1195	209467_s_at	0,25	119%
1196	242970_at	0,25	119%
1197	230233_at	-0,10	93%
1198	212560_at	0,01	101%
1199	228786_at	-0,13	91%
1200	211368_s_at	0,20	115%
1201	202958_at	-0,13	91%
1202	244262_x_at	-0,24	85%
1203	244647_at	-0,14	91%
1204	223457_at	-0,11	93%
1205	219260_s_at	-0,39	76%
1206	236832_at	0,16	112%
1207	1552307_a_at	-0,24	85%
1208	201336_at	0,07	105%
1209	AFFX-HUMISGF3A/M97935_MB_at	0,31	124%
1210	227080_at	0,30	123%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1211	227486_at	-0,64	64%
1212	206413_s_at	-0,25	84%
1213	237120_at	-0,50	71%
1214	207091_at	0,01	101%
1215	226815_at	-0,22	86%
1216	219025_at	-0,35	78%
1217	227182_at	-0,22	86%
1218	214877_at	-0,39	76%
1219	218997_at	-0,23	85%
1220	240861_at	-0,50	71%
1221	204592_at	-0,02	99%
1222	213406_at	0,39	131%
1223	227707_at	0,25	119%
1224	237538_at	0,46	138%
1225	218262_at	-0,03	98%
1226	232283_at	0,14	110%
1227	212249_at	-0,16	90%
1228	213672_at	0,08	106%
1229	210052_s_at	0,15	111%
1230	229893_at	0,48	139%
1231	222482_at	-0,33	80%
1232	203129_s_at	-0,35	78%
1233	203418_at	0,14	110%
1234	225091_at	-0,18	88%
1235	240718_at	0,28	121%
1236	81737_at	0,34	127%
1237	209360_s_at	-0,08	95%
1238	210912_x_at	-0,37	77%
1239	203716_s_at	-0,41	75%
1240	225095_at	0,16	112%
1241	213048_s_at	-0,10	93%
1242	40016_g_at	-0,36	78%
1243	224965_at	0,21	116%
1244	207623_at	-0,37	77%
1245	226171_at	0,18	113%
1246	241242_at	0,15	111%
1247	207535_s_at	-0,32	80%
1248	239522_at	0,10	107%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1249	215191_at	0,27	121%
1250	212161_at	-0,12	92%
1251	1562280_at	0,11	108%
1252	209122_at	0,10	107%
1253	229305_at	0,28	121%
1254	210407_at	0,27	121%
1255	226614_s_at	-0,42	75%
1256	1555679_a_at	-0,28	82%
1257	224697_at	-0,17	89%
1258	222262_s_at	0,23	117%
1259	227331_at	-0,06	96%
1260	227259_at	-0,18	88%
1261	222000_at	-0,12	92%
1262	205603_s_at	0,18	113%
1263	213021_at	-0,12	92%
1264	210149_s_at	0,01	101%
1265	240793_at	0,35	127%
1266	200089_s_at	-0,04	97%
1267	217834_s_at	-0,10	93%
1268	234396_at	-0,68	62%
1269	1566001_at	-0,36	78%
1270	236742_at	0,06	104%
1271	240231_at	0,25	119%
1272	200664_s_at	-0,07	95%
1273	212671_s_at	-0,43	74%
1274	207536_s_at	-0,36	78%
1275	232218_at	-0,17	89%
1276	205545_x_at	-0,01	99%
1277	239654_at	0,13	109%
1278	223907_s_at	-0,19	88%
1279	233483_at	-0,33	80%
1280	1556643_at	0,10	107%
1281	209502_s_at	-0,31	81%
1282	232720_at	-0,18	88%
1283	227138_at	-0,22	86%
1284	1559895_x_at	-0,38	77%
1285	203554_x_at	0,26	120%
1286	220305_at	-0,14	91%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1287	229966_at	0,09	106%
1288	230435_at	0,20	115%
1289	220000_at	0,34	127%
1290	1558094_s_at	-0,14	91%
1291	233157_x_at	-0,22	86%
1292	205067_at	-0,27	83%
1293	212662_at	-0,28	82%
1294	213028_at	-0,14	91%
1295	224836_at	-0,23	85%
1296	210648_x_at	0,18	113%
1297	1558105_a_at	-0,10	93%
1298	210153_s_at	0,15	111%
1299	212650_at	-0,34	79%
1300	209281_s_at	-0,07	95%
1301	239307_at	-0,36	78%
1302	213902_at	0,33	126%
1303	1559835_at	0,32	125%
1304	240070_at	-0,36	78%
1305	222396_at	-0,06	96%
1306	211781_x_at	-0,37	77%
1307	219179_at	-0,69	62%
1308	207072_at	0,46	138%
1309	224919_at	-0,14	91%
1310	231547_at	0,27	121%
1311	227476_at	0,21	116%
1312	218584_at	-0,26	84%
1313	209714_s_at	0,27	121%
1314	230354_at	0,40	132%
1315	228831_s_at	-0,39	76%
1316	237522_at	0,39	131%
1317	212663_at	0,03	102%
1318	226336_at	-0,21	86%
1319	242673_at	-0,34	79%
1320	232784_at	0,18	113%
1321	205232_s_at	-0,14	91%
1322	201364_s_at	-0,13	91%
1323	1558143_a_at	-0,15	90%
1324	1569906_s_at	-0,11	93%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1325	244332_at	-0,29	82%
1326	242082_at	-0,29	82%
1327	212154_at	-0,32	80%
1328	1569207_s_at	-0,36	78%
1329	232257_s_at	0,44	136%
1330	239060_at	0,25	119%
1331	1563075_s_at	0,18	113%
1332	208645_s_at	-0,03	98%
1333	244035_at	-0,31	81%
1334	227402_s_at	-0,17	89%
1335	230921_s_at	-0,11	93%
1336	227790_at	-0,12	92%
1337	242582_at	0,37	129%
1338	1553405_a_at	-0,08	95%
1339	244886_at	-0,41	75%
1340	228762_at	-0,17	89%
1341	220231_at	-0,42	75%
1342	202341_s_at	-0,24	85%
1343	208054_at	0,22	116%
1344	228003_at	-0,32	80%
1345	243534_at	0,35	127%
1346	212573_at	0,06	104%
1347	230063_at	-0,09	94%
1348	204165_at	0,28	121%
1349	238279_x_at	0,12	109%
1350	201842_s_at	0,16	112%
1351	223132_s_at	-0,10	93%
1352	244043_at	-0,38	77%
1353	206043_s_at	0,29	122%
1354	208653_s_at	0,23	117%
1355	238596_at	0,27	121%
1356	231907_at	-0,21	86%
1357	1557478_at	0,12	109%
1358	1558906_a_at	-0,13	91%
1359	243404_at	0,13	109%
1360	243526_at	-0,39	76%
1361	205531_s_at	-0,30	81%
1362	241702_at	0,16	112%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1363	223821_s_at	-0,46	73%
1364	242232_at	0,29	122%
1365	221573_at	0,20	115%
1366	1569492_at	0,18	113%
1367	227897_at	-0,22	86%
1368	231809_x_at	-0,22	86%
1369	226982_at	0,28	121%
1370	214876_s_at	-0,38	77%
1371	226957_x_at	-0,08	95%
1372	204251_s_at	-0,13	91%
1373	229881_at	-0,53	69%
1374	205039_s_at	-0,27	83%
1375	214000_s_at	-0,08	95%
1376	204454_at	-0,45	73%
1377	229821_at	-0,73	60%
1378	202166_s_at	-0,05	97%
1379	228177_at	-0,08	95%
1380	233063_s_at	0,18	113%
1381	204173_at	0,14	110%
1382	206513_at	0,51	142%
1383	218949_s_at	-0,29	82%
1384	204167_at	-0,08	95%
1385	221256_s_at	-0,25	84%
1386	220239_at	0,22	116%
1387	201307_at	-0,23	85%
1388	232530_at	0,18	113%
1389	226519_s_at	0,07	105%
1390	219298_at	0,75	168%
1391	209134_s_at	-0,03	98%
1392	219529_at	-0,33	80%
1393	202759_s_at	-0,40	76%
1394	232829_at	0,42	134%
1395	1559391_s_at	0,34	127%
1396	203605_at	0,06	104%
1397	232636_at	0,28	121%
1398	201061_s_at	0,25	119%
1399	222633_at	0,03	102%
1400	214710_s_at	0,11	108%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1401	231866_at	-0,14	91%
1402	208619_at	-0,06	96%
1403	1566039_a_at	-0,46	73%
1404	202891_at	0,01	101%
1405	229334_at	-0,03	98%
1406	214686_at	-0,15	90%
1407	1565358_at	-0,17	89%
1408	243924_at	-0,37	77%
1409	225007_at	-0,15	90%
1410	213285_at	-0,17	89%
1411	206592_s_at	-0,09	94%
1412	221909_at	-0,36	78%
1413	218746_at	0,04	103%
1414	235927_at	0,15	111%
1415	240089_at	0,15	111%
1416	1554292_a_at	0,20	115%
1417	208636_at	-0,03	98%
1418	206342_x_at	-0,10	93%
1419	217374_x_at	0,23	117%
1420	223527_s_at	0,28	121%
1421	209686_at	0,20	115%
1422	242364_x_at	-0,33	80%
1423	201523_x_at	0,08	106%
1424	202348_s_at	0,20	115%
1425	1558847_at	-0,50	71%
1426	220363_s_at	0,08	106%
1427	234860_at	-0,36	78%
1428	232095_at	0,17	113%
1429	211984_at	-0,07	95%
1430	201053_s_at	-0,09	94%
1431	207332_s_at	0,20	115%
1432	235942_at	0,71	164%
1433	218361_at	0,08	106%
1434	205757_at	-0,23	85%
1435	220606_s_at	-0,15	90%
1436	209642_at	0,25	119%
1437	203264_s_at	-0,28	82%
1438	236193_at	0,29	122%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1439	229274_at	0,20	115%
1440	225661_at	-0,03	98%
1441	202070_s_at	-0,11	93%
1442	201286_at	0,35	127%
1443	237229_at	-0,42	75%
1444	221776_s_at	-0,10	93%
1445	218312_s_at	-0,37	77%
1446	230444_at	-0,14	91%
1447	205708_s_at	0,22	116%
1448	224794_s_at	0,03	102%
1449	240237_at	0,22	116%
1450	225834_at	0,41	133%
1451	218064_s_at	-0,21	86%
1452	229592_at	-0,11	93%
1453	209445_x_at	0,18	113%
1454	208517_x_at	-0,06	96%
1455	217677_at	-0,36	78%
1456	210812_at	0,30	123%
1457	224756_s_at	0,07	105%
1458	1559059_s_at	-0,29	82%
1459	225609_at	-0,23	85%
1460	242691_at	-0,20	87%
1461	204785_x_at	0,14	110%
1462	233191_at	-0,12	92%
1463	225987_at	0,20	115%
1464	212010_s_at	-0,10	93%
1465	229398_at	0,22	116%
1466	234819_at	-0,51	70%
1467	230440_at	-0,39	76%
1468	1557186_s_at	-0,13	91%
1469	222651_s_at	0,07	105%
1470	212881_at	-0,11	93%
1471	226546_at	-0,05	97%
1472	243201_at	0,24	118%
1473	204254_s_at	-0,10	93%
1474	244070_at	0,36	128%
1475	210622_x_at	-0,22	86%
1476	217620_s_at	0,19	114%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1477	238573_at	-0,31	81%
1478	201777_s_at	0,00	100%
1479	231598_x_at	0,24	118%
1480	202055_at	0,08	106%
1481	226856_at	0,11	108%
1482	1553858_at	-0,13	91%
1483	235446_at	-1,26	42%
1484	242064_at	-0,59	66%
1485	239574_at	0,49	140%
1486	204069_at	-0,37	77%
1487	212390_at	-0,46	73%
1488	AFFX- hum_alu_at	0,01	101%
1489	212933_x_at	-0,07	95%
1490	212547_at	-0,12	92%
1491	241202_at	-0,21	86%
1492	1562067_at	0,21	116%
1493	1566427_at	-0,47	72%
1494	211717_at	-0,22	86%
1495	1552485_at	0,31	124%
1496	209345_s_at	-0,14	91%
1497	232722_at	-0,24	85%
1498	225755_at	0,33	126%
1499	209541_at	0,21	116%
1500	230669_at	0,17	113%
1501	217207_s_at	1,46	275%
1502	230442_at	0,11	108%
1503	200983_x_at	0,29	122%
1504	217232_x_at	0,03	102%
1505	202738_s_at	0,07	105%
1506	218773_s_at	0,38	130%
1507	213343_s_at	-0,27	83%
1508	233880_at	0,25	119%
1509	214377_s_at	0,19	114%
1510	211324_s_at	0,47	139%
1511	219055_at	0,19	114%
1512	237389_at	-0,25	84%
1513	225729_at	-0,11	93%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1514	221521_s_at	0,21	116%
1515	1559449_a_at	-0,40	76%
1516	1565674_at	0,36	128%
1517	241933_at	-0,34	79%
1518	215559_at	0,17	113%
1519	221928_at	-0,32	80%
1520	226051_at	-0,20	87%
1521	1566166_at	0,11	108%
1522	225208_s_at	-0,07	95%
1523	243675_at	0,06	104%
1524	239944_at	0,30	123%
1525	58780_s_at	-0,22	86%
1526	235030_at	-0,20	87%
1527	239783_at	0,11	108%
1528	1555580_at	-0,32	80%
1529	238494_at	-0,28	82%
1530	1558719_s_at	-0,44	74%
1531	41660_at	-0,56	68%
1532	210971_s_at	0,10	107%
1533	201825_s_at	0,27	121%
1534	217727_x_at	-0,09	94%
1535	203725_at	0,47	139%
1536	225490_at	-0,18	88%
1537	231023_at	0,17	113%
1538	224524_s_at	0,08	106%
1539	232959_at	0,29	122%
1540	237133_at	0,24	118%
1541	218391_at	0,03	102%
1542	227060_at	0,16	112%
1543	200606_at	-0,72	61%
1544	219681_s_at	-0,07	95%
1545	225638_at	0,11	108%
1546	227957_at	-0,09	94%
1547	239560_at	0,29	122%
1548	208936_x_at	0,09	106%
1549	226334_s_at	0,12	109%
1550	238750_at	-0,34	79%
1551	225061_at	-0,17	89%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1552	228096_at	-0,28	82%
1553	209709_s_at	0,28	121%
1554	207277_at	-0,04	97%
1555	212448_at	-0,28	82%
1556	229734_at	-0,51	70%
1557	237332_at	0,15	111%
1558	228069_at	0,20	115%
1559	1553978_at	0,19	114%
1560	205042_at	-0,20	87%
1561	229820_at	0,08	106%
1562	1554513_s_at	-0,14	91%
1563	221877_at	-0,11	93%
1564	208696_at	-0,12	92%
1565	240554_at	0,03	102%
1566	201589_at	-0,15	90%
1567	235824_at	-0,46	73%
1568	232375_at	0,20	115%
1569	242384_at	0,32	125%
1570	203155_at	0,01	101%
1571	243092_at	0,07	105%
1572	232045_at	0,38	130%
1573	1554710_at	0,19	114%
1574	237104_at	0,13	109%
1575	231223_at	-0,32	80%
1576	1553920_at	0,44	136%
1577	225901_at	-0,04	97%
1578	212975_at	0,15	111%
1579	1554365_a_at	0,02	101%
1580	215495_s_at	0,27	121%
1581	206521_s_at	-0,11	93%
1582	215032_at	0,10	107%
1583	226879_at	-0,23	85%
1584	221582_at	-0,22	86%
1585	225276_at	-0,09	94%
1586	1560520_at	-0,61	66%
1587	214997_at	-0,38	77%
1588	220393_at	0,27	121%
1589	230952_at	-0,16	90%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1590	242279_at	0,15	111%
1591	222592_s_at	0,02	101%
1592	209426_s_at	-0,16	90%
1593	231099_at	0,16	112%
1594	206860_s_at	0,02	101%
1595	208628_s_at	-0,09	94%
1596	1566447_at	-0,32	80%
1597	236298_at	0,08	106%
1598	237426_at	0,15	111%
1599	230000_at	0,28	121%
1600	221815_at	-0,14	91%
1601	234747_at	0,03	102%
1602	236149_at	-0,34	79%
1603	209357_at	-0,16	90%
1604	225111_s_at	0,11	108%
1605	226270_at	-0,20	87%
1606	210858_x_at	-0,10	93%
1607	212320_at	-0,13	91%
1608	214464_at	-0,18	88%
1609	205619_s_at	-0,32	80%
1610	225606_at	-0,10	93%
1611	217774_s_at	-0,14	91%
1612	228219_s_at	0,38	130%
1613	243958_at	0,10	107%
1614	208503_s_at	0,09	106%
1615	227170_at	-0,18	88%
1616	201698_s_at	0,04	103%
1617	239698_at	0,17	113%
1618	1555904_at	0,12	109%
1619	217825_s_at	0,26	120%
1620	240247_at	0,08	106%
1621	218108_at	-0,07	95%
1622	1559688_at	-0,37	77%
1623	218125_s_at	-0,25	84%
1624	226666_at	-0,24	85%
1625	230027_s_at	-0,24	85%
1626	205227_at	-0,18	88%
1627	228513_at	0,03	102%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1628	1552677_a_at	0,03	102%
1629	215796_at	-0,61	66%
1630	201903_at	-0,18	88%
1631	1560869_a_at	0,06	104%
1632	234852_at	-0,23	85%
1633	227708_at	-0,24	85%
1634	1552807_a_at	-0,21	86%
1635	229844_at	-0,24	85%
1636	204992_s_at	-0,28	82%
1637	227613_at	-0,38	77%
1638	243579_at	-0,11	93%
1639	210146_x_at	0,20	115%
1640	202433_at	0,06	104%
1641	209870_s_at	-0,35	78%
1642	224698_at	-0,21	86%
1643	207617_at	-0,45	73%
1644	203445_s_at	-0,07	95%
1645	235761_at	0,15	111%
1646	238546_at	0,24	118%
1647	1554536_at	0,27	121%
1648	200701_at	0,01	101%
1649	1558722_at	0,05	104%
1650	239033_at	0,15	111%
1651	201003_x_at	0,03	102%
1652	228984_at	-0,45	73%
1653	217025_s_at	0,22	116%
1654	232826_at	0,20	115%
1655	241692_at	0,20	115%
1656	205826_at	-0,35	78%
1657	242079_at	-0,29	82%
1658	242014_at	0,16	112%
1659	205612_at	0,41	133%
1660	225546_at	-0,25	84%
1661	1559284_at	-0,31	81%
1662	202583_s_at	0,13	109%
1663	225673_at	-0,16	90%
1664	1556072_at	0,20	115%
1665	201190_s_at	-0,09	94%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1666	218751_s_at	-0,09	94%
1667	209069_s_at	-0,04	97%
1668	210285_x_at	0,13	109%
1669	209131_s_at	0,19	114%
1670	222491_at	-0,10	93%
1671	213198_at	0,19	114%
1672	233006_at	0,22	116%
1673	1555408_at	-0,12	92%
1674	243558_at	-0,32	80%
1675	228373_at	0,13	109%
1676	231578_at	0,50	141%
1677	241233_x_at	0,09	106%
1678	213851_at	0,06	104%
1679	219269_at	-0,05	97%
1680	222276_at	-0,27	83%
1681	217741_s_at	0,17	113%
1682	202080_s_at	-0,09	94%
1683	224406_s_at	-0,52	70%
1684	220987_s_at	-0,11	93%
1685	230618_s_at	-0,16	90%
1686	213274_s_at	-0,18	88%
1687	229202_at	-0,35	78%
1688	237009_at	0,28	121%
1689	228125_at	0,15	111%
1690	225820_at	-0,09	94%
1691	218348_s_at	-0,04	97%
1692	232883_at	0,08	106%
1693	209006_s_at	0,13	109%
1694	211269_s_at	-0,20	87%
1695	240415_at	0,24	118%
1696	231219_at	0,28	121%
1697	226931_at	0,72	165%
1698	243720_at	0,20	115%
1699	208780_x_at	0,05	104%
1700	213788_s_at	-0,09	94%
1701	200806_s_at	-0,27	83%
1702	217810_x_at	-0,23	85%
1703	219489_s_at	-0,30	81%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1704	227201_at	-0,23	85%
1705	202732_at	-0,36	78%
1706	206777_s_at	-0,17	89%
1707	1568680_s_at	0,09	106%
1708	224163_s_at	-0,23	85%
1709	1559658_at	0,13	109%
1710	228645_at	-0,11	93%
1711	238946_at	0,41	133%
1712	202898_at	0,36	128%
1713	1566485_at	-0,42	75%
1714	1554112_a_at	-0,15	90%
1715	214583_at	-0,19	88%
1716	1556202_at	0,23	117%
1717	212169_at	0,49	140%
1718	200950_at	-0,09	94%
1719	201009_s_at	-0,06	96%
1720	201060_x_at	0,18	113%
1721	244633_at	0,23	117%
1722	231973_s_at	-0,02	99%
1723	215013_s_at	0,07	105%
1724	237461_at	0,25	119%
1725	227793_at	0,09	106%
1726	238952_x_at	-0,33	80%
1727	228806_at	-0,35	78%
1728	204826_at	-0,22	86%
1729	214132_at	0,10	107%
1730	213119_at	0,22	116%
1731	1558795_at	0,41	133%
1732	222760_at	-0,48	72%
1733	211742_s_at	0,05	104%
1734	243356_at	0,26	120%
1735	203063_at	0,02	101%
1736	207922_s_at	0,10	107%
1737	228314_at	-0,19	88%
1738	214137_at	0,16	112%
1739	216234_s_at	-0,02	99%
1740	242551_at	-0,41	75%
1741	207610_s_at	-0,20	87%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1742	1559205_s_at	-0,49	71%
1743	217292_at	0,12	109%
1744	231055_at	0,11	108%
1745	217984_at	-0,05	97%
1746	216370_s_at	-0,11	93%
1747	37433_at	0,20	115%
1748	201141_at	-0,37	77%
1749	226816_s_at	-0,07	95%
1750	239175_at	0,27	121%
1751	209158_s_at	-0,11	93%
1752	203588_s_at	-0,04	97%
1753	212823_s_at	-0,13	91%
1754	202822_at	0,06	104%
1755	1561058_at	0,16	112%
1756	225802_at	-0,33	80%
1757	213931_at	0,12	109%
1758	223666_at	0,21	116%
1759	201827_at	-0,06	96%
1760	235052_at	-0,25	84%
1761	227579_at	-0,15	90%
1762	228105_at	0,03	102%
1763	236292_at	0,24	118%
1764	219550_at	-0,44	74%
1765	242216_at	0,12	109%
1766	229544_at	-0,25	84%
1767	227533_at	-0,23	85%
1768	209442_x_at	-0,36	78%
1769	37145_at	-0,24	85%
1770	225680_at	0,25	119%
1771	209239_at	-0,19	88%
1772	213579_s_at	-0,06	96%
1773	213073_at	-0,01	99%
1774	206855_s_at	0,15	111%
1775	205277_at	-0,14	91%
1776	214076_at	0,07	105%
1777	1558167_a_at	-0,15	90%
1778	1568574_x_at	-0,29	82%
1779	224298_s_at	-0,04	97%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1780	230795_at	0,37	129%
1781	221765_at	0,00	100%
1782	201668_x_at	-0,17	89%
1783	1556432_at	0,09	106%
1784	227203_at	-0,12	92%
1785	208743_s_at	-0,08	95%
1786	212008_at	0,17	113%
1787	220072_at	-0,20	87%
1788	1563467_at	0,22	116%
1789	224639_at	-0,07	95%
1790	230480_at	0,08	106%
1791	1562013_a_at	-0,13	91%
1792	204909_at	-0,08	95%
1793	209824_s_at	0,14	110%
1794	206409_at	-0,47	72%
1795	208174_x_at	-0,19	88%
1796	211015_s_at	-0,09	94%
1797	208658_at	-0,20	87%
1798	213801_x_at	-0,08	95%
1799	225634_at	0,08	106%
1800	215356_at	-0,15	90%
1801	213688_at	-0,20	87%
1802	200933_x_at	-0,06	96%
1803	242270_at	0,34	127%
1804	210036_s_at	-0,24	85%
1805	229822_at	-0,28	82%
1806	232739_at	-0,50	71%
1807	201219_at	0,17	113%
1808	1560457_x_at	0,16	112%
1809	1558372_at	0,14	110%
1810	1568851_at	0,46	138%
1811	225849_s_at	0,12	109%
1812	1557257_at	0,39	131%
1813	231283_at	-0,19	88%
1814	239154_at	0,07	105%
1815	212523_s_at	0,05	104%
1816	231922_at	-0,11	93%
1817	213514_s_at	-0,18	88%

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SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1818	205129_at	-0,09	94%
1819	230997_at	-0,27	83%
1820	208705_s_at	-0,06	96%
1821	203939_at	-0,58	67%
1822	217770_at	-0,07	95%
1823	233787_at	0,17	113%
1824	241621_at	0,15	111%
1825	1553750_a_at	0,13	109%
1826	211018_at	-0,36	78%
1827	200693_at	-0,02	99%
1828	218662_s_at	0,26	120%
1829	220990_s_at	0,07	105%
1830	232149_s_at	0,19	114%
1831	232012_at	0,03	102%
1832	1562825_at	0,33	126%
1833	233800_at	0,06	104%
1834	242806_at	-0,16	90%
1835	1557544_at	0,41	133%
1836	203923_s_at	0,20	115%
1837	217978_s_at	-0,07	95%
1838	220940_at	0,12	109%
1839	221711_s_at	-0,12	92%
1840	222087_at	-0,35	78%
1841	213201_s_at	0,32	125%
1842	219178_at	-0,11	93%
1843	213535_s_at	-0,17	89%
1844	204039_at	0,24	118%
1845	215754_at	0,04	103%
1846	232284_at	0,35	127%
1847	204214_s_at	0,23	117%
1848	219765_at	-0,32	80%
1849	201938_at	0,09	106%
1850	230009_at	0,16	112%
1851	239427_at	-0,38	77%
1852	214717_at	-0,12	92%
1853	239755_at	0,02	101%
1854	208322_s_at	-0,21	86%
1855	227910_at	0,06	104%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1856	225382_at	-0,25	84%
1857	220167_s_at	0,22	116%
1858	1561884_at	0,17	113%
1859	206332_s_at	0,12	109%
1860	220193_at	-0,09	94%
1861	237623_at	0,22	116%
1862	209410_s_at	0,53	144%
1863	214481_at	0,23	117%
1864	236511_at	0,19	114%
1865	226184_at	0,35	127%
1866	222955_s_at	-0,01	99%
1867	226840_at	0,17	113%
1868	227931_at	0,09	106%
1869	231837_at	-0,25	84%
1870	232180_at	0,07	105%
1871	227305_s_at	-0,10	93%
1872	237597_at	-0,29	82%
1873	1555963_x_at	-0,38	77%
1874	211874_s_at	-0,19	88%
1875	208541_x_at	-0,13	91%
1876	242868_at	0,37	129%
1877	227522_at	0,68	160%
1878	207324_s_at	-0,46	73%
1879	1560109_s_at	0,19	114%
1880	231644_at	0,52	143%
1881	1554360_at	0,17	113%
1882	239988_at	0,22	116%
1883	201898_s_at	0,07	105%
1884	1555420_a_at	-0,07	95%
1885	209691_s_at	0,01	101%
1886	213596_at	0,27	121%
1887	243767_at	0,13	109%
1888	218014_at	-0,17	89%
1889	208179_x_at	-0,29	82%
1890	230761_at	0,04	103%
1891	217100_s_at	-0,08	95%
1892	242066_at	0,17	113%
1893	232927_at	-0,01	99%

SEQ ID No.	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1894	217933_s_at	0,26	120%
1895	205929_at	-0,38	77%
1896	234049_at	-0,16	90%
1897	225435_at	-0,05	97%
1898	203560_at	0,37	129%
1899	1555427_s_at	0,04	103%
1900	215127_s_at	0,04	103%
1901	1561211_at	-0,17	89%
1902	226509_at	0,17	113%
1903	228088_at	0,17	113%
1904	218126_at	-0,02	99%
1905	1559052_s_at	-0,11	93%
1906	203311_s_at	-0,12	92%
1907	232646_at	-0,02	99%
1908	218907_s_at	0,12	109%
1909	232744_x_at	0,13	109%
1910	213310_at	-0,05	97%
1911	222900_at	-0,12	92%
1912	1552607_at	-0,06	96%
1913	232237_at	-0,01	99%
1914	1558310_s_at	0,13	109%
1915	233794_at	-0,33	80%
1916	207276_at	-0,11	93%
1917	228719_at	0,00	100%
1918	200076_s_at	0,01	101%
1919	209750_at	-0,30	81%
1920	243033_at	0,11	108%
1921	226210_s_at	-0,36	78%
1922	228434_at	-0,33	80%
1923	204497_at	-0,24	85%
1924	203339_at	0,10	107%
1925	229980_s_at	0,06	104%
1926	213531_s_at	-0,09	94%
1927	201487_at	0,11	108%
1928	215169_at	-0,16	90%
1929	203342_at	0,06	104%
1930	222879_s_at	-0,17	89%
1931	239866_at	-0,31	81%

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<i>SEQ ID No.</i>	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1932	209110_s_at	0,08	106%
1933	214083_at	-0,11	93%
1934	205770_at	0,19	114%
1935	219684_at	0,30	123%
1936	206448_at	-0,22	86%
1937	222230_s_at	0,10	107%
1938	1553689_s_at	0,12	109%
1939	226032_at	-0,04	97%
1940	242858_at	0,08	106%
1941	241590_at	0,22	116%
1942	207113_s_at	-0,24	85%
1943	234886_at	-0,52	70%
1944	205978_at	0,53	144%
1945	243213_at	0,19	114%
1946	236668_at	0,11	108%
1947	230683_at	0,24	118%
1948	217747_s_at	-0,07	95%
1949	1560228_at	0,18	113%
1950	233571_x_at	-0,37	77%
1951	222214_at	0,02	101%
1952	220079_s_at	0,08	106%
1953	233401_at	-0,20	87%
1954	223566_s_at	-0,39	76%
1955	221964_at	-0,20	87%

<i>SEQ ID No.</i>	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1956	212337_at	0,10	107%
1957	201192_s_at	-0,10	93%
1958	223217_s_at	0,20	115%
1959	243955_at	0,50	141%
1960	231810_at	-0,17	89%
1961	218627_at	0,28	121%
1962	205728_at	0,68	160%
1963	238425_at	-0,23	85%
1964	202299_s_at	0,09	106%
1965	203659_s_at	0,10	107%
1966	207735_at	-0,17	89%
1967	233979_s_at	-0,40	76%
1968	226300_at	-0,10	93%
1969	222307_at	-0,17	89%
1970	1559699_at	0,34	127%
1971	239937_at	0,10	107%
1972	211022_s_at	0,00	100%
1973	203567_s_at	0,08	106%
1974	203054_s_at	0,01	101%
1975	202905_x_at	0,21	116%
1976	237870_at	0,45	137%
1977	232044_at	0,07	105%
1978	201931_at	0,12	109%
1979	203694_s_at	-0,04	97%

<i>SEQ ID No.</i>	Probe Set ID	Log-2 Fold Chan ge	Non- Log Fold Chng.
1980	224652_at	-0,07	95%
1981	221978_at	0,08	106%
1982	243995_at	0,17	113%
1983	225925_s_at	0,12	109%
1984	204750_s_at	0,34	127%
1985	226606_s_at	0,33	126%
1986	232141_at	0,18	113%
1987	227535_at	0,04	103%
1988	1553829_at	0,30	123%
1989	208853_s_at	-0,11	93%
1990	212020_s_at	-0,02	99%
1991	225205_at	-0,14	91%
1992	232724_at	0,09	106%
1993	221139_s_at	0,21	116%
1994	210495_x_at	0,07	105%
1995	210910_s_at	-0,23	85%
1996	1555920_at	0,14	110%
1997	220980_s_at	0,08	106%
1998	1556601_a_at	0,29	122%
1999	215236_s_at	0,02	101%
2000	240031_at	0,24	118%
2001	234980_at	0,53	144%
2002	1556865_at	0,33	126%

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SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2003	201030_x_at	LDHB	NM_002300
2004	212300_at	TXLNA	NM_175852
2005	208781_x_at	SNX3	NM_003795
2006	234734_s_at	TNRC6A	NM_014494
2007	213297_at	RMND5B	NM_022762
2008	226220_at	METTL9	NM_001077180
2009	209127_s_at	SART3	NM_014706
2010	202022_at	ALDOC	NM_005165
2011	200066_at	IK	NM_006083
2012	236065_at	---	AA782826
2013	217234_s_at	EZR	NM_001111077
2014	222427_s_at	LARS	NM_020117
2015	230958_s_at	---	AA040716
2016	209721_s_at	IFFO1	NM_001039670
2017	239673_at	---	AA618177
2018	215543_s_at	LARGE	NM_004737
2019	203413_at	NELL2	NM_001145107
2020	1556451_at	---	AA741105
2021	1555355_a_at	ETS1	NM_001143820
2022	204178_s_at	RBM14	NM_002896
2023	236472_at	---	AA490889
2024	217911_s_at	BAG3	NM_004281
2025	226204_at	C22orf29	NM_024627
2026	244549_at	LOC100130212	ENST00000406220
2027	223219_s_at	CNOT10	NM_015442
2028	204089_x_at	MAP3K4	NM_005922
2029	39249_at	AQP3	NM_004925
2030	212660_at	PHF15	NM_015288
2031	230679_at	DCAF10	NM_024345
2032	206453_s_at	NDRG2	NM_016250
2033	205081_at	CRIP1	NM_001311
2034	201478_s_at	DKC1	NM_001142463
2035	221726_at	RPL22	NM_000983
2036	211750_x_at	TUBA1C	NM_032704
2037	223088_x_at	ECHDC1	NM_001002030
2038	217884_at	NAT10	NM_001144030
2039	214447_at	ETS1	NM_001143820
2040	227731_at	CNBP	NM_001127192
2041	218123_at	C21orf59	NM_021254
2042	1558525_at	---	AK095480
2043	218611_at	IER5	NM_016545
2044	211928_at	DYNC1H1	1
2045	212115_at	HN1L	NM_144570

SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2046	228585_at	ENTPD1	NM_001098175
2047	236172_at	LTB4R	NM_001143919
2048	229569_at	---	BC037328
2049	202724_s_at	FOXO1	NM_002015
2050	201173_x_at	NUDC	NM_006600
2051	211997_x_at	H3F3B	NM_005324
2052	204951_at	RHOH	NM_004310
2053	1557910_at	HSP90A	B1
2054	203082_at	BMS1	NM_014753
2055	230586_s_at	ZNF703	NM_025069
2056	212036_s_at	PNN	NM_002687
2057	217957_at	C16orf80	NM_013242
2058	202683_s_at	RNMT	NM_003799
2059	237340_at	SLC26A8	NM_052961
2060	208758_at	ATIC	NM_004044
2061	209671_x_at	TRA@	M12423
2062	239790_s_at	---	AI435437
2063	203956_at	MORC2	NM_014941
2064	213006_at	CEBDP	NM_005195
2065	205544_s_at	CR2	NM_001006658
2066	218667_at	PJA1	NM_001032396
2067	220690_s_at	DHRS7B	NM_015510
2068	223287_s_at	FOXP1	NM_001012505
2069	202521_at	CTCF	NM_006565
2070	1560797_s_at	---	BC042086
2071	204947_at	E2F1	NM_005225
2072	211623_s_at	FBL	NM_001436
2073	239196_at	ANKRD22	NM_144590
2074	223916_s_at	BCOR	NM_001123383
2075	228976_at	ICOSLG	NM_015259
2076	211949_s_at	NOLC1	NM_004741
2077	201677_at	C3orf37	NM_001006109
2078	201581_at	TMX4	NM_021156
2079	243798_at	---	AI436580
2080	1554413_s_at	RUNDCLB	NM_001012391
2081	202723_s_at	FOXO1	NM_002015
2082	208313_s_at	SF1	NM_004630
2083	219737_s_at	PCDH9	NM_020403
2084	202481_at	DHRS3	NM_004753
2085	32069_at	N4BP1	NM_153029
2086	200956_s_at	SSRP1	NM_003146
2087	233086_at	C20orf106	NM_001012971

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SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2088	212592_at	IGJ	NM_144646
2089	216863_s_at	MORC2	NM_014941
2090	202084_s_at	SEC14L1	NM_001039573
2091	235568_at	C19orf59	NM_174918
2092	201875_s_at	MPZL1	NM_001146191
2093	202577_s_at	DDX19A	NM_018332
2094	230656_s_at	CIRH1A	NM_032830
2095	212567_s_at	MAP4	NM_001134364
2096	205698_s_at	MAP2K6	NM_002758
2097	200997_at	RBM4	NM_002896
2098	208857_s_at	PCMT1	NM_005389
2099	242714_at	---	GENSCAN00000051549
2100	231584_s_at		AA977251
2101	201817_at	UBE3C	NM_014671
2102	206206_at	CD180	NM_005582
2103	224301_x_at	H2AFJ	NM_177925
2104	239292_at	---	AA243430
2105	200610_s_at		NCL
2106	219497_s_at	BCL11A	NM_018014
2107	213545_x_at	SNX3	NM_003795
2108	204745_x_at	MT1G	NM_005950
2109	217157_x_at	IGK@	XM_001715827
2110	200792_at	XRCC6	NM_001469
2111	227516_at	SF3A1	NM_001005409
2112	206472_s_at	TLE3	NM_001105192
2113	203634_s_at	CPT1A	NM_001031847
2114	235334_at	ST6GAL NAC3	NM_001160011
2115	206057_x_at		SPN
2116	200874_s_at	NOP56	NM_006392
2117	222895_s_at	BCL11B	NM_022898
2118	212009_s_at	STIP1	NM_006819
2119	210972_x_at	TRA@	AK026255
2120	217152_at	---	AK024136
2121	200632_s_at	NDRG1	NM_001135242
2122	208660_at	CS	NM_004077
2123	238006_at	SIN3A	NM_001145357
2124	226531_at	ORAI1	NM_032790
2125	209188_x_at	DR1	NM_001938
2126	209190_s_at	DIAPH1	NM_001079812
2127	210574_s_at	NUDC	NM_006600
2128	210555_s_at	NFATC3	NM_004555
2129	201998_at	ST6GAL1	NM_003032
2130	229735_s_at	---	AA283195

SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2131	200083_at	USP22	NM_015276
2132	200921_s_at	BTG1	NM_001731
2133	215343_at	CCDC88 C	NM_001080414
2134	211275_s_at		GYG1
2135	211643_x_at	IGK@	XM_001719095
2136	218143_s_at	SCAMP2	NM_005697
2137	211902_x_at	TRA@	AY360462
2138	219974_x_at	ECHDC1	NM_001002030
2139	225793_at	LIX1L	NM_153713
2140	210202_s_at	BIN1	NM_004305
2141	222435_s_at	UBE2J1	NM_016021
2142	203089_s_at	HTRA2	NM_013247
2143	201491_at	AHSA1	NM_012111
2144	219110_at	GAR1	NM_018983
2145	220948_s_at	ATP1A1	NM_000701
2146	223993_s_at	CNIH4	NM_014184
2147	215524_x_at	TRA@	AB305657
2148	222447_at	METTL9	NM_001077180
2149	243780_at	---	AK128410
2150	206461_x_at		MT1H
2151	200836_s_at	MAP4	NM_001134364
2152	1555677_s_at	SMC1A	NM_006306
2153	200067_x_at	SNX3	NM_003795
2154	203685_at	BCL2	NM_000633
2155	202354_s_at	GTF2F1	NM_002096
2156	212566_at	MAP4	NM_001134364
2157	213302_at	PFAS	NM_012393
2158	217378_x_at	LOC1001 30100	XM_001716310
2159	222481_at	FXC1	NM_012192
2160	228639_at	AA251347	
2161	237753_at	---	AA873230
2162	240698_s_at		AA987545
2163	224917_at	MIR21	AY699265
2164	243_g_at	MAP4	NM_001134364
2165	209604_s_at	GATA3	NM_001002295
2166	213957_s_at	CEP350	NM_014810
2167	225320_at	CCDC10 9A	NM_138357
2168	228926_s_at		SMARCA
2169	217170_at	2	NM_003070
2170	240656_at		ENST00000390443
2171	1554343_a_at	STAP1	NM_012108
2172	205530_at	ETFDH	NM_004453

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SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2173	200825_s_at	HYOU1	NM_001130991
2174	217437_s_at	TACC1	NM_001122824
2175	208649_s_at	VCP	NM_007126
2176	236279_at	---	AA614270
2177	237515_at	TMEM56	NM_152487
2178	205126_at	VRK2	NM_001130480
2179	212125_at	RANGAP1	NM_002883
2180	208577_at	HIST1H3C	NM_003531
2181	213620_s_at	ICAM2	NM_000873
2182	212741_at	MAOA	NM_000240
2183	212375_at	EP400	NM_015409
2184	212109_at	HN1L	NM_144570
2185	234681_s_at	CHD6	NM_032221
2186	218575_at	ANAPC1	NM_022662
2187	201176_s_at	ARCN1	NM_001142281
2188	222694_at	MGC2752	NR_026052
2189	212396_s_at	KIAA0090	NM_015047
2190	234964_at	TRD@	AK310675
2191	213360_s_at	POM121	NM_001099415
2192	214881_s_at	UBTF	NM_001076683
2193	206337_at	CCR7	NM_001838
2194	223304_at	SLC37A3	NM_032295
2195	1567214_a_at	PNN	NM_002687
2196	225135_at	SIN3A	NM_001145357
2197	204594_s_at	SMCR7L	NM_019008
2198	200005_at	EIF3D	NM_003753
2199	226423_at	PAQR8	NM_133367
2200	202032_s_at	MAN2A2	NM_006122
2201	216905_s_at	ST14	NM_021978
2202	225624_at	SNX29	NM_001080530
2203	206569_at	IL24	NM_006850
2204	218648_at	CRTC3	NM_001042574
2205	217497_at	TYMP	NM_001113755
2206	202518_at	BCL7B	NM_001707
2207	226987_at	RBM15B	NM_013286
2208	218091_at	AGFG1	NM_001135187
2209	235372_at	FCRLA	NM_032738
2210	225669_at	IFNAR1	NM_000629
2211	204643_s_at	ENOX2	NM_006375
2212	212424_at	PDCD11	NM_014976
2213	244015_at	---	AA704163
2214	222126_at	AGFG2	NM_006076

SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2215	210561_s_at	WSB1	NM_015626
2216	236796_at	---	AA129098
2217	243066_at	NPL	NM_030769
2218	1555261_at	---	AL832319
2219	204683_at	ICAM2	NM_000873
2220	218001_at	MRPS2	NM_016034
2221	209850_s_at	CDC42E_P2	NM_006779
2222	219722_s_at	GDPD3	NM_024307
2223	219599_at	EIF4B	NM_001417
2224	231296_at	---	ENST00000439273
2225	201614_s_at	RUVBL1	NM_003707
2226	243764_at	VSIG1	NM_182607
2227	242104_at	---	AA687144
2228	213646_x_at	TUBA1B	NM_006082
2229	222696_at	AXIN2	NM_004655
2230	242783_at	---	GENSCAN00000040863
2231	207819_s_at	ABCB4	NM_000443
2232	205861_at	SPIB	NM_003121
2233	224833_at	ETS1	NM_001143820
2234	201648_at	JAK1	NM_002227
2235	218754_at	NOL9	NM_024654
2236	239085_at	JDP2	NM_001135047
2237	225898_at	WDR54	NM_032118
2238	202953_at	C1QB	NM_000491
2239	217235_x_at	IGL@	AF026926
2240	240515_at	---	AA779991
2241	227307_at	TSPAN18	NM_001031730
2242	215797_at	TRAV8-3	X58769
2243	218865_at	MOSC1	NM_022746
2244	208723_at	USP11	NM_004651
2245	205445_at	PRL	NM_000948
2246	211300_s_at	TP53	NM_000546
2247	233124_s_at	ECHDC1	NM_001002030
2248	204642_at	S1PR1	NM_001400
2249	219717_at	DCAF16	NM_017741
2250	218619_s_at	SUV39H1	NM_003173
2251	202906_s_at	NBN	NM_002485
2252	224311_s_at	CAB39	NM_001130849
2253	221969_at	---	ENST00000358127
2254	229252_at	ATG9B	NM_173681
2255	1558662_s_at	BANK1	NM_001083907
2256	208623_s_at	EZR	NM_001111077

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SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2257	213087_s_at	EEF1D	NM_001130053
2258	242606_at	---	AA360683
2259	216528_at	---	AL049244
2260	200715_x_at	RPL13A	NM_012423
2261	217328_at	LOC100134017	XM_001717113
2262	227075_at	ELP3	NM_018091
2263	219880_at	---	AK026811
2264	212769_at	TLE3	NM_001105192
2265	228309_at	---	AF090935
2266	205297_s_at	CD79B	NM_000626
2267	227216_at	RLTPR	NM_001013838
2268	1562612_at	---	AK054812
2269	240156_at	---	AA417099
2270	235096_at	LEO1	NM_138792
2271	217480_x_at	LOC100287723	XM_001713971
2272	213590_at	SLC16A5	NM_004695
2273	206420_at	IGSF6	NM_005849
2274	229348_at	UBIAD1	NM_013319
2275	206126_at	CXCR5	NM_001716
2276	212770_at	TLE3	NM_001105192
2277	211161_s_at	COL3A1	NM_000090
2278	208663_s_at	TTC3	NM_001001894
2279	226055_at	ARRDC2	NM_001025604
2280	235965_at	---	BX648200
2281	200593_s_at	HNRNPU	NM_004501
2282	212480_at	CYTSA	NM_001145468
2283	200795_at	SPARCL1	NM_001128310
2284	219667_s_at	BANK1	NM_001083907
2285	48117_at	CCDC101	NM_138414
2286	209702_at	FTO	NM_001080432
2287	201217_x_at	RPL3	NM_000967
2288	208842_s_at	GORASP2	NM_015530
2289	1558215_s_at	UBTF	NM_001076683
2290	212039_x_at	RPL3	NM_000967
2291	207008_at	IL8RB	NM_001557
2292	208687_x_at	HSPA8	NM_006597
2293	217099_s_at	GEMIN4	NM_015721
2294	229093_at	NOS3	NM_000603
2295	200998_s_at	CKAP4	NM_006825
2296	224607_s_at	SRP68	NM_014230
2297	228181_at	SLC30A1	NM_021194
2298	227646_at	EBF1	NM_024007

SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2299	219108_x_at	DDX27	NM_001007559
2300	212076_at	MLL	NM_005933
2301	214179_s_at	NFE2L1	NM_003204
2302	201778_s_at	KIAA0494	NM_014774
2303	222915_s_at	BANK1	NM_001083907
2304	203611_at	TERF2	NM_005652
2305	214643_x_at	BIN1	NM_004305
2306	215176_x_at	LOC100291464	XM_002346408
2307	227336_at	DTX1	NM_004416
2308	210616_s_at	SEC31A	NM_001077206
2309	221575_at	SCLY	NM_016510
2310	219864_s_at	RCAN3	NM_013441
2311	204388_s_at	MAOA	NM_000240
2312	242309_at	---	AA424143
2313	209995_s_at	TCL1A	NM_001098725
2314	223246_s_at	STRBP	NM_018387
2315	208581_x_at	MT1X	NM_005952
2316	208664_s_at	TTC3	NM_001001894
2317	201115_at	POLD2	NM_001127218
2318	219999_at	MAN2A2	NM_006122
2319	205254_x_at	TCF7	NM_001134851
2320	225006_x_at	TH1L	NM_198976
2321	205255_x_at	TCF7	NM_001134851
2322	225110_at	OGFOD1	NM_018233
2323	231697_s_at	TMEM49	NM_030938
2324	225245_x_at	H2AFJ	NM_177925
2325	213351_s_at	TMCC1	NM_001017395
2326	201746_at	TP53	NM_000546
2327	223565_at	MGC29506	NM_016459
2328	209994_s_at	ABCB1	NM_000443
2329	217719_at	EIF3L	NM_016091
2330	203572_s_at	TAF6	NM_005641
2331	225352_at	SEC62	NM_003262
2332	1552773_at	CLEC4D	NM_080387
2333	209773_s_at	RRM2	NM_001034
2334	209004_s_at	FBXL5	NM_012161
2335	214439_x_at	BIN1	NM_004305
2336	230175_s_at	---	ENST00000500586
2337	235154_at	TAF3	NM_031923
2338	228496_s_at	CRIM1	NM_016441
2339	237071_at	---	A1342132
2340	227093_at	USP36	NM_025090

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SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2341	204484_at	PIK3C2B	NM_002646
2342	201027_s_at	EIF5B	NM_015904
2343	225865_x_at	TH1L	NM_198976
2344	225370_at	PYGO2	NM_138300
2345	202230_s_at	CHERP	NM_006387
2346	219997_s_at	COPS7B	NM_022730
2347	222920_s_at	KIAA0748	NM_001098815
2348	226602_s_at	BCR	NM_004327
2349	241613_at	---	AI254302
2350	1563674_at	FCRL2	NM_030764
2351	239377_at	EIF1AD	NM_032325
2352	216212_s_at	DKC1	NM_001142463
2353	224281_s_at	NGRN	NM_001033088
2354	221234_s_at	BACH2	NM_021813
2355	204197_s_at	RUNX3	NM_001031680
2356	221477_s_at	SOD2	NM_000636
2357	200910_at	CCT3	NM_001008800
2358	226121_at	DHRS13	NM_144683
2359	208858_s_at	ESYT1	NM_015292
2360	222686_s_at	CPPED1	NM_001099455
2361	209503_s_at	PSMC5	NM_002805
2362	201719_s_at	EPB41L2	NM_001135554
2363	229382_at	C1orf183	NM_019099
2364	212400_at	FAM102A	NM_001035254
2365	200965_s_at	ABLIM1	NM_001003407
2366	207094_at	IL8RA	NM_000634
2367	227770_at	---	AA702005
2368	1568852_x_at	---	BC045735
2369	1563209_a_at	MACROD2	NM_001033087
2370	224632_at	GPATCH4	NM_015590
2371	232981_s_at	SYNRG	NM_001163544
2372	203936_s_at	MMP9	NM_004994
2373	210156_s_at	PCMT1	NM_005389
2374	211313_s_at	BAZ1B	NM_032408
2375	214626_s_at	GANAB	NM_198334
2376	233312_at	ROPN1L	NM_031916
2377	242241_x_at	---	AW104358
2378	225583_at	UXS1	NM_025076
2379	201503_at	G3BP1	NM_005754
2380	229513_at	STRBP	NM_018387
2381	233261_at	EBF1	NM_024007
2382	213489_at	MAPRE2	NM_001143826

SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2383	225002_s_at	SUMF2	NM_001042469
2384	220384_at	TXND3	NM_016616
2385	208914_at	GGA2	NM_015044
2386	217230_at	EZR	NM_001111077
2387	200655_s_at	CALM1	NM_006888
2388	203500_at	GCDH	NM_000159
2389	228787_s_at	BCAS4	NM_001010974
2390	200671_s_at	SPTBN1	NM_003128
2391	224688_at	C7orf42	NM_017994
2392	218569_s_at	KBTBD4	NM_016506
2393	225296_at	ZNF317	NM_020933
2394	216652_s_at	DR1	NM_001938
2395	221741_s_at	YTHDF1	NM_017798
2396	211645_x_at	---	ENST000000390254
2397	209092_s_at	GLOD4	NM_016080
2398	217925_s_at	C6orf106	NM_022758
2399	200702_s_at	DDX24	NM_020414
2400	206177_s_at	ARG1	NM_000045
2401	216133_at	TRD@611	ENST000000443
2402	219122_s_at	THG1L	NM_017872
2403	213609_s_at	SEZ6L	NM_021115
2404	217821_s_at	WBP11	NM_016312
2405	200619_at	SF3B2	NM_006842
2406	218023_s_at	FAM53C	NM_001135647
2407	38340_at	HIP1R	NM_003959
2408	203747_at	AQP3	NM_004925
2409	213336_at	BAZ1B	NM_032408
2410	231553_s_at	MICAL3	NM_001122731
2411	228325_at	KIAA0146	NM_001080394
2412	221790_s_at	LDLRAP1	NM_015627
2413	201554_x_at	GYG1	NM_004130
2414	216207_x_at	IGKC	XM_001715827
2415	229934_at	---	DQ680071
2416	211456_x_at	MT1P2	AF333388
2417	204504_s_at	HIRIP3	NM_003609
2418	242722_at	LMO7	NM_005358
2419	1569932_at	NHSL2	NM_001013627
2420	226082_s_at	SFRS15	NM_001145444
2421	219073_s_at	OSBPL10	NM_017784
2422	226715_at	FOXK1	NM_001037165
2423	202474_s_at	HCFC1	NM_005334
2424	203980_at	FABP4	NM_001442

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SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2425	234370_at	VSIG1	NM_182607
2426	232035_at	HIST1H4_H	NM_003543
2427	217938_s_at	KCMF1	NM_020122
2428	201270_x_at	NUDCD3	NM_015332
2429	210948_s_at	LEF1	NM_001130713
2430	200022_at	RPL18	NM_000979
2431	208880_s_at	PRPF6	NM_012469
2432	208622_s_at	EZR	NM_001111077
2433	202926_at	NBAS	NM_015909
2434	226744_at	METT10_D	NM_024086
2435	236465_at	RNF175	NM_173662
2436	208875_s_at	PAK2	NM_002577
2437	231418_at	---	AA749348
2438	230865_at	LIX1	NM_153234
2439	203051_at	BAHD1	NM_014952
2440	217036_at	LOC100293679	XM_002345543
2441	230983_at	FAM129_C	NM_001098524
2442	212303_x_at	KHSRP	NM_003685
2443	210688_s_at	CPT1A	NM_001031847
2444	1555779_a_at	CD79A	NM_001783
2445	226069_at	PRICKLE1	NM_001144881
2446	210915_x_at	TRBC1	AF043180
2447	235281_x_at	AHNAK	NM_001620
2448	201934_at	WDR82	NM_025222
2449	200060_s_at	RNPS1	NM_006711
2450	200992_at	IPO7	NM_006391
2451	221822_at	CCDC101	NM_138414
2452	222169_x_at	SH2D3A	NM_005490
2453	1552541_at	TAGAP	NM_054114
2454	208598_s_at	HUWE1	NM_031407
2455	220370_s_at	USP36	NM_025090
2456	208960_s_at	KLF6	NM_001160124
2457	212069_s_at	BAT2L	NM_013318
2458	220078_at	USP48	NM_001032730
2459	201561_s_at	CLSTN1	NM_001009566
2460	201611_s_at	ICMT	NM_012405
2461	226163_at	ZBTB9	NM_152735
2462	212257_s_at	SMARCA2	NM_003070
2463	213349_at	TMCC1	NM_001017395
2464	206980_s_at	FLT3LG	NM_001459
2465	231662_at	ARG1	NM_000045

SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2466	212802_s_at	GAPVD1	NM_015635
2467	210125_s_at	BANF1	NM_001143985
2468	211073_x_at	RPL3	NM_000967
2469	222450_at	PMEPA1	NM_020182
2470	213145_at	FBXL14	NM_152441
2471	221744_at	DCAF7	NM_005828
2472	227344_at	IKZF1	NM_006060
2473	200895_s_at	FKBP4	NM_002014
2474	225876_at	NIPAL3	NM_020448
2475	1568987_at	MGC57346	NR_026680
2476	216981_x_at	SPN	NM_001030288
2477	1556055_at	---	U90905
2478	219528_s_at	BCL11B	NM_022898
2479	201892_s_at	IMPDH2	NM_000884
2480	212827_at	IGHM	BC009851
2481	227420_at	TNFAIP8_L1	NM_152362
2482	230245_s_at	LOC283663	NR_024433
2483	225487_at	TMEM18	NM_152834
2484	212617_at	ZNF609	NM_015042
2485	218149_s_at	ZNF395	NM_018660
2486	218764_at	PRKCH	NM_006255
2487	215621_s_at	IGHD	AK057614
2488	212313_at	CHMP7	NM_152272
2489	201999_s_at	DYNLT1	NM_006519
2490	1560538_at	---	BC033936
2491	39402_at	IL1B	NM_000576
2492	216873_s_at	ATP8B2	NM_001005855
2493	239827_at	C13orf15	NM_014059
2494	205527_s_at	GEMIN4	NM_015721
2495	1556737_at	LOC388387	NR_027254
2496	212098_at	LOC151162	NM_002410
2497	220326_s_at	FLJ10357	NM_018071
2498	225875_s_at	NIPAL3	NM_020448
2499	224187_x_at	HSPA8	NM_006597
2500	226481_at	VPRBP	NM_014703
2501	212145_at	MRPS27	NM_015084
2502	201164_s_at	PUM1	NM_001020658
2503	211478_s_at	DPP4	NM_001935
2504	220068_at	VPREB3	NM_013378
2505	219301_s_at	CNTNAP2	NM_014141
2506	243931_at	---	AA441806

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SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2507	212376_s_at	EP400	NM_015409
2508	1556394_a_at	---	AI912646
2509	242808_at	---	ENST00000462248
2510	55692_at	ELMO2	NM_133171
		HSP90A	
2511	214359_s_at	B1	NM_007355
2512	218945_at	C16orf68	NM_024109
2513	202117_at	ARHGAP1	NM_004308
2514	206464_at	BMX	NM_001721
2515	202925_s_at	PLAGL2	NM_002657
2516	1555751_a_at	GEMIN7	NM_001007269
2517	200812_at	CCT7	NM_001009570
2518	200694_s_at	DDX24	NM_020414
2519	225141_at	---	CR607695
2520	228065_at	BCL9L	NM_182557
2521	201853_s_at	CDC25B	NM_004358
2522	226806_s_at	NFIA	NM_001134673
		CDC42E	
2523	214014_at	P2	NM_006779
2524	208895_s_at	DDX18	NM_006773
2525	203648_at	TATDN2	NM_014760
2526	212750_at	PPP1R16B	NM_015568
2527	205419_at	GPR183	NM_004951
2528	209251_x_at	TUBA1C	NM_032704
2529	213772_s_at	GGA2	NM_015044
2530	218564_at	RFWD3	NM_018124
2531	213079_at	TSR2	NM_058163
2532	200957_s_at	SSRP1	NM_003146
2533	208621_s_at	EZR	NM_001111077
2534	209927_s_at	C1orf77	NM_015607
2535	202093_s_at	PAF1	NM_019088
2536	203580_s_at	SLC7A6	NM_001076785
2537	226511_at	DCAF10	NM_024345
2538	208445_s_at	BAZ1B	NM_032408
2539	211938_at	EIF4B	NM_001417
2540	218031_s_at	FOXN3	NM_001085471
		PPP1R16B	
2541	41577_at		NM_015568
2542	221090_s_at	OGFOD1	NM_018233
2543	201303_at	EIF4A3	NM_014740
2544	221123_x_at	ZNF395	NM_018660
2545	1556006_s_at	CSNK1A1	NM_001025105
2546	200990_at	TRIM28	NM_005762
2547	202524_s_at	SPOCK2	NM_001134434

SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2548	229420_at	--	AK094885
2549	222439_s_at	THRAP3	NM_005119
2550	208614_s_at	FLNB	NM_001164317
2551	221780_s_at	DDX27	NM_017895
2552	209603_at	GATA3	NM_001002295
2553	221712_s_at	WDR74	NM_018093
2554	244313_at	CR1	NM_000573
2555	217755_at	HN1	NM_001002032
2556	211596_s_at	LRIG1	NM_015541
2557	213891_s_at	TCF4	NM_001083962
2558	211666_x_at	RPL3	NM_000967
2559	211430_s_at	IGH@	XM_001718220
		TMEM38A	
2560	222896_at		NM_024074
2561	1552772_at	CLEC4D	NM_080387
2562	202200_s_at	SRPK1	NM_003137
2563	201555_at	MCM3	NM_002388
2564	219419_at	C18orf22	NM_024805
		HIST2H2AA3	
2565	218280_x_at		NM_001040874
2566	244218_at	--	AI374686
2567	235401_s_at	FCRLA	NM_032738
		LOC728052	
2568	1558796_a_at		XM_001717850
2569	221549_at	GRWD1	NM_031485
2570	221733_s_at	GPATCH4	NM_015590
2571	202106_at	GOLGA3	NM_005895
2572	231377_at	CXorf65	NM_001025265
2573	200916_at	TAGLN2	NM_003564
2574	202123_s_at	ABL1	NM_005157
2575	225557_at	CSRNP1	NM_033027
2576	217767_at	C3	NM_000064
2577	205049_s_at	CD79A	NM_001783
2578	208644_at	PARP1	NM_001618
2579	211941_s_at	PEBP1	NM_002567
2580	218511_s_at	PNPO	NM_018129
2581	222352_at	--	CR621785
2582	202589_at	TYMS	NM_001071
2583	233126_s_at	OLAHL	NM_001039702
2584	224581_s_at	NUCKS1	NM_022731
2585	220730_at	ZNF778	NM_182531
2586	221558_s_at	LEF1	NM_001130713
2587	1555826_at	EPR1	NR_002219
2588	221528_s_at	ELMO2	NM_133171
		GORASP2	
2589	207812_s_at		NM_015530

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SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2590	219451_at	MSRB2	NM_012228
2591	226116_at	---	AK022602
2592	238071_at	LCN10	NM_001001712
2593	218728_s_at	CNIH4	NM_014184
2594	216262_s_at	TGIF2	NM_021809
2595	39854_r_at	LOC100293124	NM_020376
2596	213564_x_at	LDHB	NM_002300
2597	227855_at	FLJ10357	NM_018071
2598	201076_at	NHP2L1	NM_001003796
2599	206031_s_at	USP5	NM_001098536
2600	226122_at	PLEKHG1	NM_001029884
2601	214615_at	P2RY10	NM_014499
2602	239203_at	C7orf53	NM_001134468
2603	231830_x_at	RAB11FIP1	NM_001002233
2604	229721_x_at	DERL3	NM_001002862
2605	1563560_at	AHNAK	NM_001620
2606	219118_at	FKBP11	NM_001143781
2607	230489_at	CD5	NM_014207
2608	224732_at	CHTF8	NM_001039690
2609	200000_s_at	PRPF8	NM_006445
2610	215235_at	SPTAN1	NM_001130438
2611	225918_at	GLG1	NM_001145666
2612	214130_s_at	PDE4DIP	NM_001002810
2613	236402_at	---	AK124257
2614	212360_at	AMPD2	NM_004037
2615	200936_at	RPL8	NM_000973
2616	225562_at	RASA3	NM_007368
2617	206324_s_at	DAPK2	NM_014326
2618	201320_at	SMARCC2	NM_001130420
2619	201361_at	TMEM109	NM_024092
2620	214659_x_at	YLPM1	NM_019589
2621	240326_at	---	AA226458
2622	220507_s_at	UPB1	NM_016327
2623	39248_at	AQP3	NM_004925
2624	205841_at	JAK2	NM_004972
2625	219129_s_at	SAP30L	NM_001131062
2626	242422_at	---	AK128316
2627	242109_at	SYTL3	NM_001009991
2628	234013_at	TRD@	AY232281
2629	212348_s_at	KDM1	NM_001009999
2630	211105_s_at	NFATC1	NM_006162
2631	226311_at	---	BC098581

SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2632	200079_s_at	KARS	NM_001130089
2633	225796_at	PXK	NM_017771
2634	208611_s_at	SPTAN1	NM_001130438
2635	201090_x_at	TUBA1B	NM_006082
2636	225628_s_at	MLLT6	NM_005937
2637	214635_at	CLDN9	NM_020982
2638	228340_at	TLE3	NM_001105192
2639	213892_s_at	APRT	NM_000485
2640	212413_at	38961	NM_015129
2641	201075_s_at	SMARCC1	NM_003074
2642	200064_at	HSP90AB1	NM_007355
2643	213481_at	S100A13	NM_001024210
2644	209558_s_at	HIP1R	NM_003959
2645	202705_at	CCNB2	NM_004701
2646	241388_at	---	AK097885
2647	211816_x_at	FCAR	NM_002000
2648	231775_at	TNFRSF10A	NM_003844
2649	210338_s_at	HSPA8	NM_006597
2650	207628_s_at	WBSCR22	NM_017528
2651	57082_at	LDLRAP1	NM_015627
2652	234574_at	---	AK024563
2653	200706_s_at	LITAF	NM_001136472
2654	224837_at	FOXP1	NM_001012505
2655	223374_s_at	B3GALNT1	NM_001038628
2656	224603_at	---	BC042949
2657	228659_at	---	AL832516
2658	218153_at	CARS2	NM_024537
2659	211944_at	BAT2D1	NM_015172
2660	210809_s_at	POSTN	NM_001135934
2661	221891_x_at	HSPA8	NM_006597
2662	209670_at	TRAC	BC063385
2663	225130_at	ZRANB1	NM_017580
2664	225353_s_at	C1QC	NM_001114101
2665	202092_s_at	ARL2BP	NM_012106
2666	219526_at	C14orf169	NM_024644
2667	222186_at	ZFAND6	NM_019006
2668	212144_at	UNC84B	NM_015374
2669	212646_at	RFTN1	NM_015150
2670	222006_at	LETM1	NM_012318
2671	200057_s_at	NONO	NM_001145408
2672	202578_s_at	DDX19A	NM_018332

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SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
2673	214661_s_at	NOP14	NM_003703
2674	201490_s_at	PPIF	NM_005729
2675	205456_at	CD3E	NM_000733
2676	202870_s_at	CDC20	NM_001255
2677	241329_s_at	---	GENSCAN0000 0003786
2678	205238_at	TRMT2B	NM_024917
2679	207826_s_at	ID3	NM_002167
2680	243338_at	---	GENSCAN0000 0018368
2681	219892_at	TM6SF1	NM_001144903
2682	214129_at	PDE4DIP	NM_001002810
2683	201080_at	PIP4K2B	NM_003559
2684	234339_s_at	GLTSCR2	NM_015710
2685	221876_at	ZNF783	NR_015357
2686	54037_at	HPS4	NM_022081
2687	1560433_at	---	AI476295
2688	227198_at	AFF3	NM_001025108
2689	38521_at	CD22	NM_001771
2690	200045_at	ABCF1	NM_001025091
2691	226981_at	MLL	NM_005933
2692	1560257_at	---	AI908420
2693	229064_s_at	RCAN3	NM_013441
2694	1558186_s_at	CLLU1	NM_001025233
2695	203158_s_at	GLS	NM_014905
2696	206485_at	CD5	NM_014207
2697	221286_s_at	MGC29506	NM_016459
2698	202910_s_at	CD97	NM_001025160
2699	225852_at	ANKRD17	NM_032217
2700	214669_x_at	IGKC	AB159729
2701	217422_s_at	CD22	NM_001771
2702	1558185_at	CLLU1	NM_001025233
2703	208152_s_at	DDX21	NM_004728
2704	225145_at	NCOA5	NM_020967
2705	221011_s_at	LBH	NM_030915
2706	212641_at	HIVEP2	NM_006734
2707	220034_at	IRAK3	NM_001142523
2708	204581_at	CD22	NM_001771
2709	202845_s_at	RALBP1	NM_006788
2710	211058_x_at	TUBA1B	NM_006082
2711	227173_s_at	BACH2	NM_021813
2712	202523_s_at	SPOCK2	NM_001134434
2713	226733_at	PFKFB2	NM_001018053
2714	1557055_s_at	LOC6438	NR_015368

SEQ ID NO	Probe Set ID	Gene Symbol	Primary Transcript ID
		37	
2715	235460_at	SNX22	NM_024798
2716	33850_at	MAP4	NM_001134364
2717	223350_x_at	LIN7C	NM_018362
2718	200842_s_at	EPRS	NM_004446
2719	220476_s_at	C1orf183	NM_019099
2720	39318_at	TCL1A	NM_001098725
2721	213947_s_at	NUP210	NM_024923
2722	205173_x_at	CD58	NM_001144822
2723	200072_s_at	HNRNPM	NM_005968
2724	201356_at	SF3A1	NM_001005409
2725	204199_at	RALGPS1	NM_014636
2726	228898_s_at	SMARCB1	NM_001007468
2727	229072_at	---	AA456828
2728	218251_at	MID1IP1	NM_001098790
2729	225134_at	SPRYD3	NM_032840
2730	212185_x_at	MT2A	NM_005953
2731	202692_s_at	UBTF	NM_001076683
2732	241608_at	---	AI254302
2733	205926_at	IL27RA	NM_004843
2734	236437_at	---	AA779351
2735	209504_s_at	PLEKHB1	NM_001130033
2736	221651_x_at	IGK@	AJ010442
2737	222428_s_at	LARS	NM_020117
2738	203547_at	CD4	NM_000616
2739	211796_s_at	TRBC1	AF043179
2740	232867_at	---	AI916960
2741	210461_s_at	ABLIM1	NM_001003407
2742	214579_at	NIPAL3	NM_020448
2743	216457_s_at	SF3A1	NM_001005409
2744	227400_at	NFIX	NM_002501
2745	201183_s_at	CHD4	NM_001273
2746	208549_x_at	PTMAP7	AF170294
2747	229719_s_at	DERL3	NM_001002862
2748	203717_at	DPP4	NM_001935
2749	206621_s_at	EIF4H	NM_022170
2750	232165_at	EPPK1	NM_031308
2751	217760_at	TRIM44	NM_017583
2752	212139_at	GCN1L1	NM_006836

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**Combination  
Signature 1**

SEQ ID NO from Table 1	SEQ ID NO from Table 2
43	2125
54	2194
61	2473
103	2480
110	2488
149	2588
206	2635
337	2638
346	
457	
481	
572	
796	
826	
860	
903	
1007	
1154	
1175	
1245	
1426	

**Combination  
Signature 2**

SEQ ID NO from Table 1	SEQ ID NO from Table 2
89	2044
92	2416
149	2458
262	2473
269	2510
565	2538
617	2547
1311	2646

**Combination  
Signature 3**

SEQ ID NO from Table 1	SEQ ID NO from Table 2
6	2010
12	2021
15	2022
19	2121
36	2139
47	2172
112	2217

1732	
	118
	2282
	2301
	2323
	2340
	2345
	2349
	2496
	2509
	2511
	2538
	2547
	2550
	2616
	2642
	2711
	2712
	2732

**Combination  
Signature 4**

SEQ ID NO from Table 1	SEQ ID NO from Table 2
5	2008
6	2020
8	2031
9	2032
10	2039
11	2040
12	2060

Table 3, page 2

SEQ ID NO from Table 1	SEQ ID NO from Table 2
13	2065
14	2072
16	2107
19	2138
21	2146
22	2152
28	2160
29	2162
32	2179
34	2187
36	2189
37	2208
38	2211
43	2213
56	2226
60	2228
71	2234
72	2235
76	2236
77	2243
78	2244
79	2251
80	2253
86	2255
87	2263
89	2277
97	2282
99	2283
100	2291
101	2296
102	2309
105	2310
110	2312
112	2316
113	2318
115	2319
120	2323
129	2326
130	2339

SEQ ID NO from Table 1	SEQ ID NO from Table 2
131	2343
132	2348
134	2351
137	2365
141	2374
144	2386
145	2390
149	2408
151	2416
158	2423
164	2430
168	2431
175	2438
178	2441
180	2448
183	2470
187	2480
191	2481
196	2483
199	2484
201	2485
211	2489
244	2494
258	2499
262	2502
271	2503
274	2515
279	2521
285	2523
292	2528
293	2529
302	2538
314	2546
315	2571
331	2578
335	2591
336	2594
341	2603
342	2618

SEQ ID NO from Table 1	SEQ ID NO from Table 2
343	2630
346	2645
351	2646
355	2648
356	2650
372	2654
375	2661
377	2663
382	2669
386	2700
398	2711
399	2712
401	2715
406	2719
411	2732
416	2733
421	
422	
438	
439	
440	
444	
453	
456	
461	
462	
465	
469	
493	
496	
497	
505	
506	
524	
526	
533	
534	
543	
544	

Table 3, page 3

SEQ ID NO from Table 1	SEQ ID NO from Table 2
561	
566	
568	
569	
572	
579	
582	
599	
600	
602	
604	
613	
614	
617	
620	
624	
631	
642	
676	
677	
689	
690	
702	
707	
713	
718	
722	
730	
732	
745	
746	
760	
763	
769	
771	
783	
784	
785	
789	

SEQ ID NO from Table 1	SEQ ID NO from Table 2
799	
800	
814	
817	
824	
825	
826	
828	
851	
860	
865	
876	
877	
878	
883	
884	
890	
893	
903	
907	
910	
914	
923	
925	
951	
960	
964	
981	
987	
988	
991	
996	
1000	
1007	
1019	
1021	
1027	
1071	
1078	

SEQ ID NO from Table 1	SEQ ID NO from Table 2
1096	
1108	
1111	
1118	
1127	
1149	
1160	
1162	
1164	
1176	
1197	
1222	
1226	
1228	
1255	
1292	
1293	
1296	
1311	
1321	
1327	
1344	
1350	
1367	
1372	
1381	
1393	
1398	
1407	
1485	
1509	
1535	
1552	
1553	
1566	
1610	
1634	
1637	
1664	

Table 3, page 4

SEQ ID NO from Table 1	SEQ ID NO from Table 2
1667	///
1681	///
1717	///
1732	///
1740	///
1771	///
1810	///
1877	///
1898	///
1926	///
1932	///
1946	///
1961	///
1962	///
2001	///

Table 3, page 5

**Combination  
Signature 5**

SEQ ID NO from Table 1	SEQ ID NO from Table 2
3	2005
4	2047
8	2068
15	2074
19	2087
22	2101
23	2104
24	2127
30	2134
32	2138
36	2143
37	2147
38	2151
47	2155
51	2162
52	2163
56	2167
60	2190
61	2191
86	2212
87	2215
92	2218
93	2221
99	2226
100	2232
103	2238
107	2242
112	2247
118	2253
130	2266
136	2283
149	2288
154	2290
171	2293
183	2295
188	2301

199	2308
244	2309
258	2310
269	2323
285	2326
297	2334
302	2336
320	2340
331	2342
371	2345
375	2376
378	2385
397	2392
398	2415
399	2420
406	2427
412	2444
417	2453
422	2455
457	2459
461	2464
481	2467
506	2477
515	2489
518	2495
533	2499
561	2502
566	2504
569	2505
572	2513
609	2518
613	2522
617	2523
620	2542
642	2549
690	2550
702	2582
769	2586
785	2588
789	2605
799	2622
810	2634
824	2643

825	2654
826	2655
903	2657
923	2661
925	2665
932	2669
944	2672
997	2687
1010	2688
1038	2697
1043	2699
1096	2700
1118	2711
1175	2714
1296	2716
1407	2721
1535	2724
1611	2732
1681	2735
1732	2742
1946	2747

Table 3, page 6

**Combination  
Signature 6**

SEQ ID NO from Table 1	SEQ ID NO from Table 2
2	2008
3	2010
5	2013
6	2014
8	2021
12	2022
15	2032
16	2037
19	2039
30	2044
32	2045
34	2046
36	2047
37	2048
43	2049
44	2053
45	2058
47	2060
54	2061
79	2062
83	2068
86	2073
89	2074
92	2075
95	2077
100	2078
103	2081
107	2082
112	2086
118	2087
124	2088
130	2093
136	2095
149	2096
154	2097
157	2098

SEQ ID NO from Table 1	SEQ ID NO from Table 2
159	2100
171	2101
172	2104
183	2105
188	2108
196	2110
199	2111
206	2112
256	2116
258	2117
262	2119
269	2121
279	2125
297	2129
302	2130
331	2134
342	2137
356	2138
375	2139
397	2142
398	2143
406	2145
412	2150
417	2151
422	2152
448	2157
461	2160
506	2161
561	2162
566	2163
569	2165
570	2168
617	2169
624	2172
642	2184
696	2186
763	2187
769	2189
799	2191
810	2192
814	2194

SEQ ID NO from Table 1	SEQ ID NO from Table 2
824	2195
825	2196
826	2201
932	2202
944	2208
1010	2209
1096	2211
1106	2212
1118	2214
1311	2215
1426	2217
1535	2221
1611	2222
1681	2228
	2234
	2235
	2236
	2241
	2242
	2243
	2253
	2256
	2261
	2263
	2264
	2266
	2274
	2275
	2276
	2277
	2282
	2286
	2288
	2289
	2291
	2292
	2293
	2299
	2301
	2303
	2309

Table 3, page 7

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2312
	2315
	2319
	2321
	2323
	2326
	2327
	2333
	2339
	2340
	2341
	2342
	2345
	2349
	2351
	2354
	2357
	2359
	2364
	2365
	2373
	2375
	2376
	2383
	2384
	2385
	2386
	2389
	2390
	2391
	2394
	2398
	2400
	2401
	2409
	2415
	2416
	2420
	2421
	2423
	2425

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2428
	2429
	2431
	2432
	2434
	2441
	2444
	2448
	2458
	2459
	2460
	2461
	2469
	2472
	2473
	2474
	2477
	2478
	2479
	2480
	2485
	2488
	2489
	2494
	2495
	2496
	2498
	2502
	2503
	2504
	2509
	2510
	2511
	2515
	2518
	2519
	2523
	2531
	2532
	2533
	2538

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2539
	2540
	2543
	2546
	2547
	2550
	2551
	2564
	2570
	2571
	2574
	2578
	2582
	2588
	2594
	2601
	2603
	2604
	2606
	2607
	2611
	2616
	2620
	2622
	2627
	2630
	2631
	2634
	2635
	2638
	2641
	2642
	2646
	2649
	2654
	2656
	2662
	2670
	2671
	2672
	2675

Table 3, page 8

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2679
	2688
	2693
	2694
	2696
	2697
	2699
	2704
	2705
	2706
	2711
	2712
	2715
	2716
	2724
	2728
	2732
	2733
	2741
	2750

### Combination Signature 7

SEQ ID NO from Table 1	SEQ ID NO from Table 2
2	2005
3	2007
5	2010
8	2013
9	2014
10	2027
11	2039
13	2044
14	2046
16	2047
17	2048
19	2049
20	2050
21	2051

SEQ ID NO from Table 1	SEQ ID NO from Table 2
22	2052
23	2053
24	2055
28	2059
29	2061
30	2062
31	2065
32	2068
34	2073
35	2074
36	2075
37	2080
38	2081
40	2083
41	2084
42	2086
43	2087
45	2089
47	2093
48	2094
49	2095
51	2097
52	2098
54	2100
56	2103
58	2104
60	2106
61	2109
63	2110
69	2111
70	2116
71	2120
72	2127
74	2134
76	2142
77	2145
78	2147
79	2148
80	2150
83	2152

SEQ ID NO from Table 1	SEQ ID NO from Table 2
87	2153
89	2154
91	2155
92	2156
93	2157
95	2158
96	2160
97	2161
98	2162
99	2163
100	2164
101	2169
102	2172
103	2179
105	2180
107	2184
108	2190
109	2193
110	2195
111	2200
112	2203
115	2204
117	2206
118	2208
120	2209
121	2212
122	2213
123	2214
124	2215
125	2224
126	2225
127	2227
129	2228
130	2231
132	2232
133	2235
134	2236
136	2241
137	2247
138	2249

Table 3, page 9

SEQ ID NO from Table 1	SEQ ID NO from Table 2
139	2253
141	2254
145	2256
146	2270
148	2271
149	2274
153	2276
155	2278
157	2281
158	2283
159	2284
163	2286
164	2288
165	2289
168	2290
171	2293
174	2294
177	2295
178	2296
180	2298
183	2299
185	2300
186	2301
187	2306
188	2308
191	2312
193	2314
196	2319
197	2321
199	2327
201	2328
205	2335
206	2336
207	2337
211	2340
244	2342
255	2345
256	2346
258	2348
259	2349

SEQ ID NO from Table 1	SEQ ID NO from Table 2
262	2351
264	2352
269	2354
271	2359
272	2360
274	2367
275	2370
279	2373
281	2376
285	2382
286	2384
289	2385
292	2386
293	2389
297	2390
302	2391
304	2393
310	2398
312	2400
314	2404
315	2413
320	2414
322	2416
325	2420
329	2422
331	2423
333	2430
335	2431
336	2434
337	2436
340	2438
341	2441
342	2444
343	2445
346	2448
350	2450
351	2454
352	2456
355	2457
356	2458

SEQ ID NO from Table 1	SEQ ID NO from Table 2
358	2461
363	2463
371	2464
373	2468
375	2472
376	2473
377	2474
378	2475
380	2478
381	2484
382	2485
384	2489
385	2498
386	2500
389	2502
391	2503
392	2504
397	2505
398	2506
399	2509
401	2510
402	2511
404	2515
406	2518
408	2522
411	2523
412	2524
414	2531
416	2533
418	2534
419	2538
420	2539
421	2540
422	2545
423	2547
427	2558
430	2559
436	2562
438	2569
439	2571

Table 3, page 10

SEQ ID NO from Table 1	SEQ ID NO from Table 2
440	2574
444	2576
447	2578
448	2582
453	2585
454	2586
456	2587
457	2588
461	2591
462	2601
465	2603
466	2606
469	2607
476	2611
480	2616
481	2618
483	2620
485	2621
486	2622
488	2626
495	2628
496	2630
497	2632
498	2634
503	2638
504	2640
505	2641
507	2642
509	2643
513	2648
514	2649
526	2653
527	2654
530	2656
533	2659
534	2661
537	2663
538	2668
540	2669
544	2671

SEQ ID NO from Table 1	SEQ ID NO from Table 2
547	2673
550	2675
552	2676
553	2677
557	2679
561	2683
564	2687
565	2688
566	2695
568	2697
569	2703
570	2705
572	2710
579	2713
583	2705
598	2710
599	2713
603	2719
604	2730
607	2732
609	2741
610	
613	
614	
617	
620	
624	
628	
631	
636	
637	
638	
642	
646	
647	
653	
659	
661	
662	
663	

SEQ ID NO from Table 1	SEQ ID NO from Table 2
664	
666	
675	
676	
677	
678	
679	
680	
689	
690	
692	
693	
696	
707	
709	
712	
713	
714	
715	
718	
719	
722	
725	
728	
730	
732	
733	
744	
745	
746	
749	
750	
753	
755	
756	
759	
761	
763	
766	
769	

Table 3, page 11

SEQ ID NO from Table 1	SEQ ID NO from Table 2
770	
771	
783	
784	
785	
787	
789	
792	
796	
799	
800	
801	
804	
810	
814	
817	
825	
826	
829	
831	
837	
844	
845	
847	
851	
858	
860	
865	
869	
876	
877	
878	
881	
884	
888	
890	
892	
893	
902	
903	

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	907
	910
	916
	918
	921
	925
	932
	939
	940
	941
	944
	951
	954
	957
	960
	961
	967
	971
	975
	978
	981
	987
	988
	991
	994
	997
	999
	1000
	1002
	1007
	1010
	1013
	1014
	1018
	1019
	1021
	1034
	1038
	1043
	1064

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	1066
	1068
	1070
	1071
	1072
	1076
	1078
	1080
	1093
	1096
	1106
	1108
	1117
	1118
	1121
	1122
	1123
	1127
	1136
	1137
	1140
	1141
	1146
	1154
	1160
	1162
	1164
	1166
	1167
	1168
	1170
	1171
	1172
	1175
	1178
	1179
	1181
	1183
	1184
	1187

Table 3, page 12

SEQ ID NO from Table 1	SEQ ID NO from Table 2
1189	
1197	
1199	
1214	
1215	
1218	
1219	
1222	
1226	
1228	
1230	
1231	
1234	
1237	
1239	
1242	
1245	
1247	
1255	
1258	
1266	
1268	
1271	
1285	
1288	
1290	
1292	
1293	
1294	
1295	
1296	
1297	
1303	
1305	
1311	
1313	
1322	
1327	
1334	
1344	

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	1350
	1351
	1367
	1368
	1370
	1372
	1376
	1381
	1382
	1383
	1387
	1389
	1390
	1393
	1394
	1397
	1398
	1400
	1407
	1408
	1426
	1429
	1431
	1433
	1436
	1438
	1441
	1445
	1460
	1466
	1472
	1481
	1482
	1509
	1517
	1518
	1525
	1529
	1530
	1534

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	1535
	1536
	1543
	1544
	1549
	1550
	1552
	1553
	1564
	1566
	1567
	1568
	1571
	1572
	1583
	1584
	1586
	1587
	1602
	1605
	1610
	1611
	1612
	1619
	1624
	1626
	1627
	1629
	1634
	1637
	1640
	1641
	1644
	1663
	1664
	1666
	1681
	1682
	1685
	1690

Table 3, page 13

SEQ ID NO from Table 1	SEQ ID NO from Table 2
1692	
1701	
1717	
1719	
1724	
1731	
1732	
1740	
1747	
1756	
1757	
1767	
1771	
1774	
1778	
1789	
1809	
1817	
1821	
1848	
1862	
1866	
1876	
1877	
1878	
1884	
1893	
1895	
1898	
1906	
1921	
1923	
1925	
1932	
1946	
1947	
1948	
1954	
1959	
1961	

SEQ ID NO from Table 1	SEQ ID NO from Table 2
1962	
1969	
1976	
1981	
1983	
2001	

### Combination Signature 8

SEQ ID NO from Table 1	SEQ ID NO from Table 2
3	2005
4	2010
6	2017
9	2020
10	2021
11	2022
12	2023
14	2025
16	2026
17	2029
19	2032
22	2036
28	2037
29	2038
30	2040
32	2041
34	2043
41	2045
43	2049
47	2052
51	2060
52	2061
54	2069
56	2070
61	2071
69	2073
70	2075
71	2076

SEQ ID NO from Table 1	SEQ ID NO from Table 2
72	2077
74	2078
77	2081
78	2082
79	2083
86	2087
87	2089
89	2093
92	2095
93	2096
95	2100
98	2101
99	2105
100	2108
108	2111
112	2113
113	2116
118	2117
121	2118
124	2119
126	2123
127	2127
130	2129
134	2130
136	2138
137	2139
138	2142
145	2145
146	2147
149	2149
158	2150
159	2151
163	2153
178	2161
183	2162
188	2165
191	2168
206	2169
207	2171
211	2172
256	2183

Table 3, page 14

SEQ ID NO from Table 1	SEQ ID NO from Table 2
258	2187
271	2191
285	2195
292	2200
293	2201
297	2202
302	2203
312	2206
314	2207
315	2209
316	2211
336	2212
340	2214
341	2217
349	2218
350	2220
355	2221
356	2222
363	2224
371	2225
372	2226
378	2228
380	2231
382	2234
386	2236
389	2237
406	2239
411	2241
416	2243
417	2246
418	2251
419	2253
427	2256
438	2257
439	2261
440	2268
444	2270
448	2275
462	2276
465	2277
476	2282

SEQ ID NO from Table 1	SEQ ID NO from Table 2
485	2287
488	2290
493	2295
496	2296
497	2298
503	2303
506	2306
513	2316
524	2326
526	2335
552	2340
553	2341
561	2342
565	2345
566	2346
568	2351
569	2352
579	2354
599	2356
602	2357
603	2359
604	2364
606	2366
607	2367
613	2369
614	2374
617	2375
622	2376
628	2383
631	2385
637	2386
638	2388
647	2389
659	2390
663	2391
664	2392
679	2395
692	2398
693	2401
702	2404
707	2405

SEQ ID NO from Table 1	SEQ ID NO from Table 2
718	2415
719	2416
725	2421
730	2425
755	2427
760	2428
763	2429
766	2433
771	2435
789	2438
799	2441
810	2444
817	2450
824	2454
825	2455
826	2458
828	2459
831	2461
837	2464
851	2466
865	2467
876	2473
877	2475
884	2479
890	2480
892	2481
893	2482
902	2485
907	2486
914	2491
921	2495
944	2499
954	2515
978	2521
988	2524
991	2526
997	2528
999	2531
1002	2537
1005	2538
1019	2539

Table 3, page 15

SEQ ID NO from Table 1	SEQ ID NO from Table 2
1034	2541
1038	2542
1071	2545
1078	2546
1093	2547
1111	2549
1117	2550
1118	2551
1127	2556
1136	2558
1154	2567
1160	2569
1162	2570
1164	2573
1167	2574
1175	2585
1183	2586
1187	2588
1211	2598
1219	2601
1242	2603
1255	2604
1258	2605
1261	2606
1268	2607
1285	2610
1288	2616
1292	2621
1295	2622
1297	2624
1311	2628
1344	2631
1368	2632
1372	2633
1381	2635
1389	2643
1390	2646
1407	2647
1417	2654
1426	2655
1429	2659

SEQ ID NO from Table 1	SEQ ID NO from Table 2
1436	2661
1440	2662
1460	2665
1485	2666
1517	2668
1529	2669
1533	2670
1536	2671
1544	2674
1549	2676
1552	2679
1553	2683
1566	2688
1572	2692
1584	2694
1586	2695
1605	2696
1610	2697
1611	2698
1619	2701
1626	2703
1637	2705
1664	2706
1681	2711
1724	2713
1731	2715
1732	2716
1771	2719
1789	2722
1810	2724
1877	2726
1884	2727
1895	2732
1898	2733
1921	2735
1925	2738
1926	2741
1946	2748
1952	2751
1954	2752
1976	2753

SEQ ID NO from Table 1	SEQ ID NO from Table 2
2001	

Table 3, page 16

**Combination  
Signature 9**

SEQ ID NO from Table 1	SEQ ID NO from Table 2
2	2003
3	2005
4	2006
5	2007
6	2008
8	2009
11	2010
12	2013
14	2014
15	2015
16	2016
17	2017
19	2018
22	2020
23	2021
24	2022
28	2023
29	2025
30	2026
32	2027
34	2029
36	2030
37	2032
38	2034
41	2035
43	2036
44	2037
45	2038
47	2039
48	2040
51	2041
52	2042
54	2043
56	2044
60	2045
61	2046

SEQ ID NO from Table 1	SEQ ID NO from Table 2
69	2047
70	2048
72	2049
74	2050
76	2051
77	2052
79	2053
83	2054
86	2055
87	2056
89	2057
92	2058
93	2059
95	2060
98	2061
99	2062
100	2063
101	2065
102	2066
103	2067
107	2068
110	2069
112	2070
118	2071
121	2072
124	2073
126	2074
127	2075
129	2076
130	2077
132	2078
136	2080
137	2081
141	2082
144	2083
145	2084
149	2086
151	2087
154	2088
157	2089
158	2090

SEQ ID NO from Table 1	SEQ ID NO from Table 2
159	2093
164	2094
171	2095
172	2096
180	2097
183	2098
188	2099
196	2100
197	2101
199	2103
206	2104
244	2105
255	2106
256	2107
258	2108
262	2109
268	2110
269	2111
271	2112
279	2113
285	2114
292	2115
297	2116
302	2117
320	2118
331	2119
337	2120
342	2121
343	2123
346	2124
351	2125
355	2126
356	2127
360	2128
371	2129
373	2130
375	2131
377	2132
378	2133
385	2134
397	2137

Table 3, page 17

SEQ ID NO from Table 1	SEQ ID NO from Table 2
398	2138
399	2139
406	2141
412	2142
416	2143
417	2145
419	2146
421	2147
422	2148
438	2149
439	2150
444	2151
448	2152
453	2153
457	2154
461	2155
462	2156
465	2157
481	2158
485	2160
488	2161
505	2162
506	2163
515	2164
518	2165
524	2166
526	2167
533	2168
544	2169
550	2171
561	2172
565	2173
566	2177
568	2179
569	2180
570	2183
572	2184
579	2186
582	2187
583	2188
599	2189

SEQ ID NO from Table 1	SEQ ID NO from Table 2
609	2190
613	2191
617	2192
620	2193
624	2194
631	2195
638	2196
642	2197
646	2198
675	2200
690	2201
696	2202
702	2203
715	2204
730	2205
732	2206
746	2207
755	2208
761	2209
763	2210
769	2211
783	2212
784	2213
785	2214
789	2215
799	2216
810	2217
814	2218
817	2219
824	2220
825	2221
826	2222
831	2223
860	2224
865	2225
877	2226
884	2227
903	2228
907	2230
910	2231
914	2232

SEQ ID NO from Table 1	SEQ ID NO from Table 2
923	2234
925	2235
932	2236
944	2237
975	2238
978	2239
991	2240
996	2241
997	2242
999	2243
1000	2244
1010	2245
1038	2246
1043	2247
1068	2248
1072	2249
1096	2251
1106	2252
1117	2253
1118	2254
1136	2255
1154	2256
1164	2257
1175	2258
1184	2261
1197	2263
1219	2264
1234	2266
1242	2268
1285	2270
1292	2271
1293	2272
1296	2274
1303	2275
1311	2276
1350	2277
1390	2278
1398	2279
1407	2280
1426	2281
1436	2282

Table 3, page 18

SEQ ID NO from Table 1	SEQ ID NO from Table 2
1453	2283
1517	2284
1525	2285
1529	2286
1535	2287
1544	2288
1552	2289
1566	2290
1611	2291
1612	2292
1627	2293
1634	2294
1667	2295
1681	2296
1731	2297
1732	2298
1740	2299
1789	2300
1810	2301
1884	2303
1895	2304
1898	2306
1926	2307
1946	2308
1947	2309
1952	2310
1976	2312
2001	2314
	2315
	2316
	2317
	2318
	2319
	2321
	2323
	2324
	2325
	2326
	2327
	2328
	2329

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2331
	2332
	2333
	2334
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	2336
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	2341
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	2374
	2375
	2376

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2379
	2380
	2382
	2383
	2384
	2385
	2386
	2388
	2389
	2390
	2391
	2392
	2393
	2394
	2395
	2398
	2400
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Table 3, page 19

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2431
	2432
	2433
	2434
	2435
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	2439
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	2442
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	2469
	2470
	2472
	2473
	2474
	2475

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2476
	2477
	2478
	2479
	2480
	2481
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	2484
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	2487
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	2489
	2491
	2492
	2494
	2495
	2496
	2498
	2499
	2500
	2501
	2502
	2503
	2504
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	2511
	2512
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	2515
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	2518
	2519
	2520
	2521
	2522

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2523
	2524
	2525
	2526
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	2534
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	2573
	2574

Table 3, page 20

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2576
	2577
	2578
	2579
	2580
	2581
	2582
	2584
	2585
	2586
	2587
	2588
	2589
	2590
	2591
	2593
	2594
	2598
	2600
	2601
	2603
	2604
	2605
	2606
	2607
	2609
	2610
	2611
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	2615
	2616
	2618
	2619
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	2621
	2622
	2624
	2625
	2626
	2627

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2628
	2629
	2630
	2631
	2632
	2633
	2634
	2635
	2636
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	2639
	2640
	2641
	2642
	2643
	2645
	2646
	2647
	2648
	2649
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	2653
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	2672
	2673
	2674
	2675

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2676
	2677
	2679
	2681
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	2697
	2698
	2699
	2700
	2701
	2702
	2703
	2704
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	2721
	2722

Table 3, page 21

SEQ ID NO from Table 1	SEQ ID NO from Table 2
	2724
	2725
	2726
	2727
	2728
	2729
	2730
	2731
	2732
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	2750
	2751
	2752

Table 4, page 1

1st Signature of 8 (SEQ ID Nos.)	2nd Signature of 8 (SEQ ID Nos.)	3rd Signature of 8 (SEQ ID Nos.)
3	197	6
36	55	156
112	4	137
34	33	123
2	145	58
1	112	44
12	173	19
35	12	100

Table 5, page 1

1st Signature of 30 (SEQ ID Nos.)	2nd Signature of 30 (SEQ ID Nos.)	3rd Signature of 30 (SEQ ID Nos.)
112	111	113
2	32	112
3	132	25
1	149	26
12	114	152
34	56	57
35	41	40
36	54	133
5	46	127
7	86	31
115	113	119
37	83	134
14	69	161
118	76	182
121	5	138
8	175	141
15	165	162
10	99	124
127	197	143
39	16	35
17	55	74
9	45	160
18	202	66
124	103	101
38	60	96
4	44	62
40	78	78
19	117	169
20	31	137
130	176	197

Table 6, page 1

3rd Signature of 60 (SEQ ID Nos.)		
2nd Signature of 60 (SEQ ID Nos.)		
1st Signature of 60 (SEQ ID Nos.)		
6	104	172
43	65	121
27	30	35
16	53	72
115	173	159
24	189	190
17	16	162
19	92	86
133	82	77
14	7	147
12	22	157
18	193	182
30	164	188
9	33	155
121	160	63
8	188	146
21	48	151
107	98	7
58	192	137
41	43	15
46	13	88
57	156	148
40	41	105
35	133	83
11	57	142
45	70	169
7	117	174
31	180	25
34	185	114
20	158	24

3rd Signature of 60 (SEQ ID Nos.)		
2nd Signature of 60 (SEQ ID Nos.)		
1st Signature of 60 (SEQ ID Nos.)		
38	83	32
5	62	14
32	165	166
47	195	92
33	149	180
50	11	2
124	126	13
26	59	191
22	116	51
36	184	81
4	94	104
127	27	179
49	42	176
3	128	173
39	71	189
130	190	19
44	31	50
13	114	194
25	36	101
28	3	115
10	5	130
29	196	133
23	140	73
1	49	94
42	159	79
37	191	178
2	86	91
118	139	202
15	171	37
112	138	10

Table 7, page 1

3rd Signature of 102 (SEQ ID Nos.)		
2nd Signature of 102 (SEQ ID Nos.)		
1st Signature of 102 (SEQ ID Nos.)		
91	2	141
67	110	45
6	181	62
84	113	95
9	174	69
8	13	147
19	83	192
10	91	134
130	168	10
71	103	119
89	185	53
59	128	12
124	49	124
16	41	197
112	28	153
52	26	186
93	167	170
72	202	83
26	120	8
22	124	157
24	191	122
34	121	150
86	19	162
14	11	5
1	84	187
3	99	130
76	104	84
15	27	195
37	151	129
120	6	120
2	161	47
133	187	36
83	12	201
12	17	123
53	42	23
78	170	149
77	111	118
69	117	140
50	108	70
46	48	64
107	112	176
87	142	6
56	173	16
25	47	108
42	189	55
54	43	1
90	132	152
57	53	30
62	55	7
5	127	77
55	39	190
4	87	86
13	123	183
21	166	14
18	3	35
43	81	42
66	94	199
44	56	146
32	165	105
70	62	34
20	50	114
47	97	87
33	89	33
115	21	31
94	34	76
23	145	27
29	131	17
35	61	169
75	182	110
28	51	154
85	5	166
118	177	163

Table 7, page 2

3rd Signature of 102 (SEQ ID Nos.)		
2nd Signature of 102 (SEQ ID Nos.)		
1st Signature of 102 (SEQ ID Nos.)		
30	152	198
82	159	112
49	63	68
31	158	91
60	60	156
74	25	161
36	190	185
68	149	160
88	86	98
17	178	58
127	93	59
61	141	103
121	85	51
65	1	142
81	195	22

3rd Signature of 102 (SEQ ID Nos.)		
2nd Signature of 102 (SEQ ID Nos.)		
1st Signature of 102 (SEQ ID Nos.)		
64	129	171
80	101	11
73	76	132
63	70	167
58	52	131
7	126	2
40	138	80
103	95	60
27	66	44
45	196	94
109	200	180
41	40	65
11	144	196
38	24	89
39	44	102

Table 8, page 1

3rd Signature of 202 (SEQ ID Nos.)	2nd Signature of 202 (SEQ ID Nos.)	1st Signature of 202 (SEQ ID Nos.)	3rd Signature of 202 (SEQ ID Nos.)	2nd Signature of 202 (SEQ ID Nos.)	1st Signature of 202 (SEQ ID Nos.)
24	1461	1575	161	926	579
123	1589	1348	195	1711	1271
21	1995	931	190	905	1095
142	1983	1184	192	788	210
17	612	1549	38	1647	792
183	1710	1263	169	1210	1860
47	1024	733	125	1930	1245
178	1544	786	80	1788	80
144	956	1677	136	1646	1946
109	1740	102	128	1416	1107
105	1718	892	141	1793	590
69	1979	79	78	1893	1611
67	911	1592	146	1107	1468
181	1560	1147	95	1195	1200
172	90	184	6	1582	44
79	1454	1116	77	1859	1276
100	568	1420	115	1830	242
191	1365	668	113	1644	909
162	1008	828	174	646	1043
52	1190	158	166	1315	793
35	102	250	103	523	1360
51	1854	1073	19	132	1308
63	1494	286	39	184	734
72	1947	1563	130	724	1579
188	1364	30	60	412	840
133	1105	1727	120	216	112
66	1649	964	119	1703	1552
97	1480	1912	137	1769	1637
110	1103	662	148	988	217
68	762	207	32	689	1945
150	1741	1123	131	117	47
159	594	238	25	893	1664
99	355	367	167	1071	72
116	1303	1502	85	1036	762
46	889	1086	49	42	1079
16	896	183	57	1060	1092

Table 8, page 2

3rd Signature of 202 (SEQ ID Nos.)	31	1570	27
2nd Signature of 202 (SEQ ID Nos.)	3	337	362
1st Signature of 202 (SEQ ID Nos.)	1	1844	1673
3rd Signature of 202 (SEQ ID Nos.)	122	433	1806
2nd Signature of 202 (SEQ ID Nos.)	55	1241	1161
1st Signature of 202 (SEQ ID Nos.)	193	1880	518
3rd Signature of 202 (SEQ ID Nos.)	54	884	106
2nd Signature of 202 (SEQ ID Nos.)	163	1393	73
1st Signature of 202 (SEQ ID Nos.)	22	491	1652
3rd Signature of 202 (SEQ ID Nos.)	87	1384	1937
2nd Signature of 202 (SEQ ID Nos.)	58	1006	702
1st Signature of 202 (SEQ ID Nos.)	157	654	256
3rd Signature of 202 (SEQ ID Nos.)	50	857	493
2nd Signature of 202 (SEQ ID Nos.)	18	152	1118
1st Signature of 202 (SEQ ID Nos.)	202	69	839
3rd Signature of 202 (SEQ ID Nos.)	106	217	161
2nd Signature of 202 (SEQ ID Nos.)	37	62	572
1st Signature of 202 (SEQ ID Nos.)	96	190	896
3rd Signature of 202 (SEQ ID Nos.)	26	865	1418
2nd Signature of 202 (SEQ ID Nos.)	182	1700	1499
1st Signature of 202 (SEQ ID Nos.)	65	944	1311
3rd Signature of 202 (SEQ ID Nos.)	160	601	476
2nd Signature of 202 (SEQ ID Nos.)	74	763	1619
1st Signature of 202 (SEQ ID Nos.)	149	261	1975
3rd Signature of 202 (SEQ ID Nos.)	27	268	382
2nd Signature of 202 (SEQ ID Nos.)	134	1825	1726
1st Signature of 202 (SEQ ID Nos.)	2	591	85
3rd Signature of 202 (SEQ ID Nos.)	30	606	1882
2nd Signature of 202 (SEQ ID Nos.)	194	868	1832
1st Signature of 202 (SEQ ID Nos.)	42	1756	918
3rd Signature of 202 (SEQ ID Nos.)	201	501	835
2nd Signature of 202 (SEQ ID Nos.)	196	643	817
1st Signature of 202 (SEQ ID Nos.)	71	1588	1337
3rd Signature of 202 (SEQ ID Nos.)	34	1679	39
2nd Signature of 202 (SEQ ID Nos.)	124	1607	1626
1st Signature of 202 (SEQ ID Nos.)	156	506	1513
3rd Signature of 202 (SEQ ID Nos.)	53	1988	1560
2nd Signature of 202 (SEQ ID Nos.)	29	460	1849
1st Signature of 202 (SEQ ID Nos.)	126	623	202
3rd Signature of 202 (SEQ ID Nos.)	129	687	879
2nd Signature of 202 (SEQ ID Nos.)	84	1720	1411
1st Signature of 202 (SEQ ID Nos.)	94	1477	168
3rd Signature of 202 (SEQ ID Nos.)	36	1563	259
2nd Signature of 202 (SEQ ID Nos.)	76	1850	1906
1st Signature of 202 (SEQ ID Nos.)	88	1617	605
3rd Signature of 202 (SEQ ID Nos.)	20	1578	1852
2nd Signature of 202 (SEQ ID Nos.)	132	80	561
1st Signature of 202 (SEQ ID Nos.)	127	819	812

Table 9, page 1

3rd Signature of 502 (SEQ ID Nos.)	4	1977	1379
2nd Signature of 502 (SEQ ID Nos.)	348	603	759
1st Signature of 502 (SEQ ID Nos.)	438	1749	575
345	129	849	
100	1571	894	
433	869	1001	
209	158	422	
242	781	876	
443	451	1755	
389	1195	1267	
86	44	1589	
240	1656	1570	
201	693	75	
214	741	1332	
7	454	380	
200	1043	93	
97	1815	381	
133	1871	329	
132	1892	35	
207	1151	1411	
318	615	1866	
429	1351	1885	
283	1	1266	
194	215	853	
449	1181	1800	
333	35	738	
256	628	975	
384	252	1367	
468	504	708	
3	1986	391	
404	1028	229	
231	713	1382	
267	1121	20	
153	481	1994	
167	241	1058	
62	1854	435	
325	1613	616	
397	1984	1546	
154	304	776	

298	1071	608
246	56	1024
219	361	1773
301	1436	1031
35	1040	1709
96	598	183
310	316	1114
148	483	1603
198	266	1043
199	1681	1938
61	1750	1899
450	178	719
177	601	195
141	1995	993
453	1198	506
364	1402	1798
378	169	1913
363	1647	1084
289	1514	790
408	1486	1529
303	254	641
353	1533	1384
87	1403	111
230	1912	1421
452	441	609
367	1063	826
77	247	1301
475	1228	705
37	1467	251
204	815	873
244	295	206
206	1204	1200
27	736	1750
393	1470	412
178	565	365
275	1223	1809
195	1205	371
317	1787	1653
398	436	1760
461	494	1009
122	174	920
356	1926	1389

272	1876	765
321	1287	1614
308	433	900
300	1006	764
95	737	1363
375	1112	1152
221	1309	1315
352	756	335
306	589	519
324	813	1392
139	568	1088
277	1270	408
48	1318	766
335	431	1164
284	1585	287
498	1430	54
392	838	934
370	1299	278
445	1371	986
361	513	441
432	872	1021
373	1294	1435
460	1149	123
82	162	60
107	785	152
334	1566	25
169	1037	1371
131	1263	1901
417	943	1335
426	1334	1942
113	1745	1027
188	1747	1906
487	1473	267
264	1097	1010
407	986	1158
446	1714	1083
67	1225	1182
1	888	76
365	1895	1230
17	1464	1667
380	1762	1463
85	323	216

Table 9, page 2

127	1407	105
410	548	621
355	579	2001
109	195	1658
307	1328	313
282	1713	571
423	571	1248
33	1096	439
402	1622	274
280	1224	1306
478	1576	49
386	976	958
305	1343	396
269	1992	1249
176	634	681
420	538	1978
395	249	1453
156	1414	830
112	1943	558
220	550	230
56	775	1943
391	1924	1401
494	1577	1108
174	765	413
29	1268	579
42	1985	207
158	545	798
434	470	1234
481	703	1431
409	824	899
57	355	1949
173	747	192
441	1817	1920
405	96	338
55	768	237
455	460	1636
265	1748	383
259	188	660
309	166	1451
189	350	999
359	1732	1780
342	1799	1220
351	1216	1606

224	1551	461
222	508	1122
290	1822	731
285	1775	1604
211	1545	225
341	1671	1758
123	1573	801
302	1659	944
358	1274	1870
336	1187	1812
390	760	1506
14	1284	560
114	1484	1595
21	957	1692
422	364	1498
241	718	1975
245	203	890
44	1536	388
462	1095	370
486	1307	1542
286	1348	81
225	359	531
138	1910	201
488	715	1783
213	1376	971
437	730	1051
314	1709	1069
480	308	241
376	1540	1123
106	1827	1651
467	951	15
339	991	1731
46	342	1702
192	673	299
98	1581	1534
31	73	43
457	1129	1527
472	820	711
218	366	301
47	418	994
255	955	1831
357	1952	63
5	680	1283

493	1761	1341
331	1882	1
372	1185	1732
150	202	1372
49	859	200
496	275	188
316	1535	1608
183	31	494
444	1236	904
135	111	1399
160	417	737
40	1383	1250
50	925	175
456	529	131
9	732	755
330	15	680
346	704	1333
396	157	990
369	447	121
117	1013	1047
350	864	658
15	870	1221
312	1315	243
165	105	427
157	1010	1622
431	189	576
349	790	592
105	402	815
75	1633	835
184	584	805
412	1873	5
89	121	924
299	1726	1386
152	1690	1768
32	1756	308
329	1143	688
338	992	501
60	1250	1777
18	1293	172
401	1672	1116
276	1883	1867
474	733	1821
76	474	1710

418	1357	1521
115	1816	843
469	984	1243
52	186	813
379	973	179
151	235	141
274	1134	721
2	735	101
463	990	1716
458	1084	1408
208	383	614
11	1190	735
79	1721	349
387	1029	1837
34	1378	914
413	627	1403
501	1262	1744
196	1973	927
465	739	1344
126	641	563
45	327	1412
322	453	1240
252	834	420
332	1468	629
454	670	442
235	518	213
278	309	1192
129	750	389
237	287	421
243	4	1254
436	1354	1235
411	1668	1241
134	1249	350
26	1940	970
415	1265	1535
421	1434	1699
78	893	1825
430	963	1828
92	684	977
210	1499	1416
424	378	1223
144	558	695
203	463	470

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497	6	1447
400	766	310
228	619	1584
414	1918	312
382	632	880
130	980	502
257	742	864
388	432	1556
99	1483	342
215	546	1669
223	472	1966
343	421	174
6	230	487
51	438	1628
492	1132	648
500	1478	203
202	238	453
473	1723	247
263	344	1211
470	1421	122
294	744	1543
170	771	511
91	1176	741
250	1135	1205
428	1567	789
185	1044	240
136	525	1349
366	160	488
59	258	1841
464	1017	394
374	873	78
311	1278	277
88	1607	61
163	1260	249
251	829	1687
377	928	479
84	207	178
94	621	831
281	1426	935
439	660	1525
205	1488	281
186	920	536
368	1532	1959

119	1674	86
344	1534	341
360	917	922
394	1578	1457
101	1635	1097
36	810	983
81	1409	79
74	1502	1679
288	1120	1684
254	1425	1685
146	1077	907
381	850	724
459	1572	1933
260	1569	897
23	1242	407
8	1694	1611
466	1719	1273
304	1440	810
38	609	640
451	1711	395
416	949	1940
234	1565	1520
323	1905	374
482	245	1568
120	1087	34
447	1902	1299
13	48	399
232	29	1587
247	457	1854
296	1768	1893
143	857	1865
19	595	1366
495	878	1629
292	1373	1216
442	294	194
190	1625	1072
155	1152	9
383	142	678
271	1948	1918
175	734	33
181	1864	1955
287	580	1322
326	92	1533

162	288	508
64	664	1377
354	1459	739
385	1406	821
236	707	204
425	240	1226
362	996	1485
102	788	1561
128	1391	1153
137	1098	1696
297	1014	1953
25	757	164
72	332	357
111	1012	1413
484	587	38
266	1452	62
110	977	513
403	499	1659
168	216	1675
71	213	153
80	659	212
216	758	1450
121	257	1874
479	623	1713
347	1485	1061
125	1554	1476
268	576	1721
93	1030	1605
164	1598	1736
66	1061	529
291	1784	90
502	1221	1168
270	59	1142
124	1267	1537
293	1627	620
448	1167	354
30	1157	1785
179	1007	811
233	591	156
239	1410	1202
58	701	1580
427	1463	134
63	171	593

171	594	858
69	1442	37
262	389	1610
258	1950	1470
406	1291	1730
159	1907	1432
65	844	1956
328	1720	1930
319	1629	816
187	1501	1704
43	196	696
226	1011	823
118	1285	117
477	573	97
476	1300	431
142	1900	363
193	416	1574
172	1753	967
279	268	1137
197	1715	1862
340	1321	1718
73	133	544
149	840	1576
70	1826	1701
227	1489	67
419	1140	1062
147	1105	753
483	267	484
161	919	1139
182	1158	1186
68	170	541
499	581	1119
337	1757	1513
440	1481	1657
54	1651	1516
320	1050	1511
313	969	670
41	1173	1022
12	1465	140

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3rd Signature of 1002 (SEQ ID Nos.)	2nd Signature of 1002 (SEQ ID Nos.)	1st Signature of 1002 (SEQ ID Nos.)
378	2002	82
339	1375	1617
550	41	1424
211	30	509
186	784	674
163	1342	939
947	639	398
908	1887	797
58	1601	383
918	462	228
600	647	1107
771	1326	1564
853	343	930
203	1217	1266
887	476	954
329	1608	192
171	403	1010
714	1043	914
219	452	679
247	1833	1993
415	1278	304
510	882	1740
204	546	199
274	1259	1514
982	1322	1732
519	193	250
38	547	388
270	315	659
948	1028	980
566	1545	119
703	1984	1226
814	1873	728
953	302	597
761	43	140
745	1407	214

3rd Signature of 1002 (SEQ ID Nos.)	2nd Signature of 1002 (SEQ ID Nos.)	1st Signature of 1002 (SEQ ID Nos.)
645	448	1726
7	1401	1287
588	623	973
257	1533	1244
39	477	495
223	525	26
264	1042	533
488	465	725
828	799	496
333	1785	1647
161	112	73
433	1332	1438
940	383	1022
877	361	202
622	1265	295
79	1522	729
585	612	44
552	938	1949
616	1793	378
103	1479	205
556	310	1528
107	952	361
632	604	1207
612	113	1959
436	348	1479
420	796	1540
822	1712	443
81	1460	144
250	1697	1508
825	1359	365
866	1731	896
648	130	159
966	1100	127
928	526	489
289	889	673

3rd Signature of 1002 (SEQ ID Nos.)	2nd Signature of 1002 (SEQ ID Nos.)	1st Signature of 1002 (SEQ ID Nos.)
480	1655	1532
965	445	952
266	279	427
59	1578	63
330	63	1346
610	1353	113
541	1818	1283
624	1884	1952
462	1708	1261
647	1617	552
192	1749	384
555	829	459
188	1634	475
335	419	215
863	758	265
810	761	1136
513	577	1385
33	865	347
180	1879	1296
868	478	297
338	1456	65
823	1863	539
629	1365	847
438	1053	1642
244	153	262
395	1905	1182
345	413	601
873	675	1036
945	1685	93
150	1001	1580
368	1004	1432
123	493	323
830	125	1811
97	225	1004
468	1468	1449

3rd Signature of 1002 (SEQ ID Nos.)	2nd Signature of 1002 (SEQ ID Nos.)	1st Signature of 1002 (SEQ ID Nos.)
46	767	1410
669	181	1309
455	934	542
261	705	1888
845	1800	706
296	1510	1699
544	110	610
657	507	1838
370	1754	1240
551	1002	704
696	883	1995
73	551	35
278	731	876
786	1056	1389
442	1849	1021
871	644	1361
819	1895	1442
472	1742	1844
487	1603	1566
854	470	1868
509	1536	1378
396	1616	870
423	184	30
48	1255	1444
664	808	1945
342	1026	966
662	1083	592
405	1039	1612
376	514	642
141	1819	1364
962	1323	909
800	1339	599
72	1556	434
746	1038	430
633	1070	1308

Table 10, page 2

3rd Signature of 1002 (SEQ ID Nos.)		
2nd Signature of 1002 (SEQ ID Nos.)		
1st Signature of 1002 (SEQ ID Nos.)		
119	1193	169
730	549	875
685	1425	1900
707	762	1562
741	1133	737
198	839	455
282	1779	1704
527	242	25
197	933	1333
324	169	1546
605	492	694
2	176	469
650	1821	473
355	314	282
546	1307	1159
792	1674	71
677	1837	1277
672	1804	1891
540	685	1151
914	654	94
144	115	1737
958	1184	2000
725	1335	1889
813	6	668
308	1838	1724
327	509	1461
85	524	1954
636	1719	1000
213	846	822
978	561	128
973	1077	946
437	1775	1426
721	900	1023
659	1182	1836
222	71	1050
388	357	1675

3rd Signature of 1002 (SEQ ID Nos.)		
2nd Signature of 1002 (SEQ ID Nos.)		
1st Signature of 1002 (SEQ ID Nos.)		
949	436	1108
938	1660	1711
996	473	1967
466	1899	1295
915	481	224
142	1347	1753
712	1677	1904
248	719	796
90	562	1545
773	101	1695
842	989	1123
826	1201	471
31	725	1429
852	1331	1314
236	1600	415
54	906	252
434	32	734
312	33	1409
502	1563	1591
705	1748	1618
444	804	1106
379	1978	526
910	82	1550
848	1453	185
815	1264	1325
286	782	1423
493	1412	1256
11	1728	148
86	620	781
748	1572	1115
968	88	588
467	1564	1826
331	59	104
8	187	66
478	866	1855
747	389	1881

3rd Signature of 1002 (SEQ ID Nos.)		
2nd Signature of 1002 (SEQ ID Nos.)		
1st Signature of 1002 (SEQ ID Nos.)		
242	1862	274
359	1198	853
975	1764	181
254	1137	330
581	572	766
506	489	564
620	338	1656
389	394	672
542	1321	338
857	1834	332
209	369	219
162	888	1843
627	975	29
271	135	1221
439	432	135
559	406	1529
383	516	755
484	408	1217
639	177	888
386	1841	1791
457	1118	994
775	479	431
512	266	9
424	1174	1357
682	1612	1759
481	908	153
593	979	657
572	221	1222
276	427	774
569	827	273
533	580	152
537	1428	540
681	1009	1963
416	617	211
30	677	1513
373	1752	180

Table 10, page 3

3rd Signature of 1002 (SEQ ID Nos.)	2nd Signature of 1002 (SEQ ID Nos.)	1st Signature of 1002 (SEQ ID Nos.)	3rd Signature of 1002 (SEQ ID Nos.)	2nd Signature of 1002 (SEQ ID Nos.)	1st Signature of 1002 (SEQ ID Nos.)
285	971	1567	43	1475	380
357	211	1661	349	395	397
906	26	238	673	738	1480
34	126	821	343	307	1194
404	895	598	435	919	1575
959	1117	43	225	1580	283
365	674	1121	497	1932	556
983	1974	1065	214	849	118
1000	1311	1817	302	1444	1707
538	1360	1586	920	686	362
957	146	1493	35	1654	1876
584	1938	1042	695	95	354
147	334	14	922	1567	1497
943	1720	1766	753	446	970
781	751	1030	288	823	1506
642	942	1158	352	1023	968
611	1210	1630	456	1981	1286
140	779	1597	165	1413	1105
401	610	450	684	824	149
314	1073	1864	595	811	921
215	93	1196	284	4	887
414	155	849	892	1672	372
903	648	1898	543	892	385
1002	2001	284	851	133	544
183	1770	1565	750	352	577
220	69	600	665	1963	1001
260	1723	1748	838	366	1542
283	1145	582	25	340	364
839	56	895	932	1544	1806
601	1826	184	615	154	1533
762	1558	1197	990	1312	1668
674	1078	357	902	74	841
528	1998	967	891	36	1269
106	145	924	83	1761	1006
970	1109	778	26	598	1421
525	1084	108	68	1429	1684
			277	1075	1319

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			3rd Signature of 1002 (SEQ ID Nos.)
			2nd Signature of 1002 (SEQ ID Nos.)
			1st Signature of 1002 (SEQ ID Nos.)
752	1716	1970	679
754	1325	56	237
464	1514	173	268
744	599	504	602
654	1727	686	751
778	1403	1161	124
476	474	343	402
328	626	977	874
297	96	1847	191
924	1584	684	864
280	233	1957	927
794	1330	1700	976
233	1079	763	22
450	78	633	818
19	1705	519	738
23	978	77	909
52	1557	1834	208
690	1642	1344	606
418	1590	770	666
816	1664	1120	178
592	961	1925	740
55	1431	1734	964
177	1391	1321	795
118	1611	920	486
881	573	730	570
367	137	1126	419
759	141	186	495
421	1020	1964	767
56	1983	312	832
175	616	411	733
577	1096	1459	92
89	1159	1535	159
756	1035	1033	522
427	24	1894	769
255	1643	306	453
71	921	1097	13

			3rd Signature of 1002 (SEQ ID Nos.)
			2nd Signature of 1002 (SEQ ID Nos.)
			1st Signature of 1002 (SEQ ID Nos.)
			648

			3rd Signature of 1002 (SEQ ID Nos.)
			2nd Signature of 1002 (SEQ ID Nos.)
			1st Signature of 1002 (SEQ ID Nos.)
			1094

			3rd Signature of 1002 (SEQ ID Nos.)
			2nd Signature of 1002 (SEQ ID Nos.)
			1st Signature of 1002 (SEQ ID Nos.)
			1850

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3rd Signature of 1002 (SEQ ID Nos.)		
2nd Signature of 1002 (SEQ ID Nos.)		
1st Signature of 1002 (SEQ ID Nos.)		
51	1	1792
821	198	1398
901	1280	1690
586	1639	498
637	606	41
18	330	244
463	940	1912
708	267	1056
505	845	1472
960	1483	52
749	1589	799
122	798	1951
704	556	1104
240	1424	251
999	1551	1086
382	42	788
340	1835	546
997	1805	813
251	1454	114
371	281	608
604	1803	1401
346	625	401
717	163	874
723	1169	1721
808	1024	1327
154	2000	1054
1001	519	22
44	472	974
235	109	1162
483	418	81
477	948	964
74	232	1652
706	127	1960
931	1606	1289
377	1143	382
619	1408	1163

3rd Signature of 1002 (SEQ ID Nos.)		
2nd Signature of 1002 (SEQ ID Nos.)		
1st Signature of 1002 (SEQ ID Nos.)		
890	431	358
47	1650	732
390	1540	191
408	392	1779
783	372	293
907	213	1706
833	10	1183
804	399	873
597	1484	1781
265	1539	1510
776	255	662
135	1371	1416
176	55	1955
14	397	142
229	280	560
1	899	628
292	67	58
168	122	1602
120	1625	851
393	1714	688
831	1976	767
936	1271	1328
667	438	989
279	70	1853
430	164	1300
925	1386	1040
182	1214	1672
500	694	650
806	494	669
834	793	395
100	536	1915
190	296	579
93	868	1574
591	634	472
594	962	441
711	1823	1509

3rd Signature of 1002 (SEQ ID Nos.)		
2nd Signature of 1002 (SEQ ID Nos.)		
1st Signature of 1002 (SEQ ID Nos.)		
194	422	1386
944	1885	1743
790	966	1436
76	1679	16
520	1635	1692
364	1597	1940
287	1917	882
515	1814	445
21	373	233
698	874	48
429	1902	1974
969	859	1015
715	1562	1803
649	1626	740
136	1646	1969
580	1445	1141
239	1734	547
796	998	1623
989	1857	1246
530	913	641
319	1669	1638
777	321	1388
529	659	1330
807	965	736
791	1064	988
879	1665	1437
855	1314	848
809	358	1085
151	792	1578
42	1195	1659
575	681	107
399	523	1907
417	1336	1249
53	1911	1712
249	768	772
930	1943	1441

3rd Signature of 1002 (SEQ ID Nos.)		
2nd Signature of 1002 (SEQ ID Nos.)		
1st Signature of 1002 (SEQ ID Nos.)		
614	724	275
210	1107	1962
919	1369	1708
841	977	545
69	1878	223
17	691	217
886	1228	64
446	490	1592
148	237	1697
578	1662	237
858	277	1917
230	1276	363
531	27	1243
946	1231	1913
95	1209	645
670	1258	828
977	1929	521
356	755	1901
728	581	986
105	1903	814
954	1759	3
413	1729	993
867	1842	137
334	1699	1292
713	1535	1980
301	1304	1786
498	1250	517
217	1447	1556
917	49	1405
939	150	1336
3	1531	1531
504	835	867
36	1080	494
979	941	1746
252	680	206
683	914	1117

Table 10, page 6

3rd Signature of 1002 (SEQ ID Nos.)	2nd Signature of 1002 (SEQ ID Nos.)	1st Signature of 1002 (SEQ ID Nos.)	3rd Signature of 1002 (SEQ ID Nos.)	2nd Signature of 1002 (SEQ ID Nos.)	1st Signature of 1002 (SEQ ID Nos.)
303	1636	886	316	1194	178
734	1760	201	802	1400	1149
563	25	922	201	870	1068
394	1735	101	764	990	195
757	316	1869	820	83	1926
988	1443	1504	548	723	1559
138	1260	999	32	1913	1383
735	116	693	518	1613	1031
998	1115	1880	640	1364	676
511	1931	1076	193	1366	474
603	1261	374	579	683	890
884	272	1039	451	1449	1017
897	1298	303	293	1772	1832
269	76	791	112	704	655
850	944	1291	99	428	1896
347	584	451	499	1068	187
294	1893	638	134	907	1371
732	66	1213	207	1060	1044
353	655	623	935	1397	1549
801	365	32	607	1238	748
694	716	2002	560	400	311
561	236	110	166	1262	1648
344	1656	1349	306	1790	1348
785	805	318	57	1132	752
827	983	190	793	344	1083
470	1052	1408	152	294	277
126	709	1599	258	794	690
789	1518	555	325	1915	1833
817	1815	1415	760	894	1425
587	766	1172	398	195	745
700	645	1340	228	1094	913
916	576	717	121	1421	479
155	108	953	803	698	193
929	439	1608	295	837	530
608	324	1059	880	371	290
758	283	574	675	1163	1696

Table 10, page 7

3rd Signature of 1002 (SEQ ID Nos.)	2nd Signature of 1002 (SEQ ID Nos.)	1st Signature of 1002 (SEQ ID Nos.)	3rd Signature of 1002 (SEQ ID Nos.)	2nd Signature of 1002 (SEQ ID Nos.)	1st Signature of 1002 (SEQ ID Nos.)
933	1801	248	617	1062	1878
646	97	801	861	1965	1914
259	1710	1823	375	991	7
743	214	299	655	553	1783
626	1898	625	27	568	1463
547	956	1787	469	1122	1262
474	1949	1657	341	1799	1052
62	1361	46	232	1241	805
941	968	1687	362	592	270
956	1534	557	212	1789	1568
129	1114	1624	729	200	288
381	1393	333	812	1277	1830
91	1736	1941	653	903	756
737	558	1505	621	134	285
526	185	264	710	651	538
361	354	67	942	336	702
189	970	68	720	1771	1043
174	1512	1471	115	1478	714
534	144	1845	185	1283	392
447	1395	1110	836	1167	369
847	1337	541	458	1865	961
992	947	1956	726	123	1519
366	541	639	904	871	126
471	1224	1741	709	533	1411
565	1581	965	994	512	1092
28	460	155	701	364	89
508	173	1606	205	1741	727
400	1341	502	885	1552	460
160	1576	1391	460	1924	1547
61	1205	2	784	529	808
311	1532	1496	797	862	835
310	1340	1282	63	1427	247
718	754	245	678	1252	1874
173	1410	1443	116	332	1165
787	168	516	618	630	1720
893	1372	1164	661	511	402

Table 11, page 1

1 <sup>st</sup> Example for Exchange of 50 within 202		2 <sup>nd</sup> Example for Exchange of 50 within 202		3 <sup>rd</sup> Example for Exchange of 50 within 202	
Dropped	Added	Dropped	Added	Dropped	Added
64	451	43	1253	131	847
155	322	113	515	167	1396
162	483	151	815	53	390
72	449	160	508	55	1538
127	388	185	1256	179	1530
103	268	198	898	145	595
102	465	111	1943	82	451
63	236	67	1030	119	891
118	243	98	777	121	844
68	536	106	229	133	1348
44	426	164	927	60	1745
161	395	133	602	134	1631
38	479	8	1643	180	975
157	450	85	1910	42	585
36	218	5	1790	160	1571
120	260	145	1019	6	1215
109	226	93	1888	102	406
37	491	174	1580	72	642
184	529	131	1220	104	596
154	252	41	441	158	1878
169	308	152	1870	185	1456
96	482	20	1467	77	1453
115	458	197	1254	116	1414
144	473	42	314	20	1683
2	434	94	1686	5	771
188	312	171	1610	63	1306
65	486	116	216	1	217
124	315	189	1430	128	470
39	367	161	1514	152	1209
94	270	19	423	124	1253
107	242	6	305	39	1990
34	454	137	1017	79	1950
47	344	122	1101	135	1230
187	323	135	323	30	837
173	351	156	470	75	715
62	433	167	2002	61	709
166	221	53	753	149	1068

Table 11, page 2

1 <sup>st</sup> Example for Exchange of 50 within 202		2 <sup>nd</sup> Example for Exchange of 50 within 202		3 <sup>rd</sup> Example for Exchange of 50 within 202	
Dropped	Added	Dropped	Added	Dropped	Added
136	513	16	1029	202	952
133	338	100	1283	138	1603
45	505	65	479	7	1602
158	385	78	1491	110	582
121	494	143	1617	36	1499
31	386	186	1111	96	1285
130	225	199	1378	197	506
106	481	74	1909	9	1424
95	348	29	298	188	301
112	431	108	959	190	923
137	309	107	1688	166	657
43	461	2	347	144	1604
172	262	101	469	43	1852

Table 12, page 1

1 <sup>st</sup> Example for Exchange of 50 within 1002		2 <sup>nd</sup> Example for Exchange of 50 within 1002		3 <sup>rd</sup> Example for Exchange of 50 within 1002	
Dropped	Added	Dropped	Added	Dropped	Added
106	1070	33	1219	9	1711
45	1030	130	1932	16	1042
65	1050	50	1142	46	1722
124	1018	26	1528	121	1211
118	1155	3	1160	45	1985
169	1202	6	1847	7	1424
161	1049	17	1990	8	1007
144	1099	8	1477	4	1710
107	1158	25	1569	34	1398
187	1093	34	1044	35	1725
2	1119	15	1768	10	1585
130	1143	13	1052	43	1771
172	1036	9	1401	5	1341
68	1033	121	1962	42	1153
96	1172	16	1591	47	1513
39	1005	27	1525	18	1714
136	1241	2	1223	22	1178
115	1220	118	1734	3	1124
102	1246	1	1147	28	1807
133	1032	124	1577	14	1782
62	1069	45	1358	20	1571
127	1170	44	1531	19	1971
38	1079	5	1445	27	1975
166	1132	46	1772	25	1802
36	1268	35	1096	38	1762
63	1097	23	1200	57	1273
109	1179	11	1034	107	1363
94	1197	115	1251	115	1039
120	1236	58	1396	31	1769
173	1142	120	1210	23	1253
64	1173	39	1536	58	1943
31	1058	22	1767	39	1848
112	1183	107	1910	2	1564
137	1008	29	1352	40	1844
157	1112	42	1789	44	1898
154	1178	10	1928	112	1361
37	1121	14	1325	124	1800

Table 12, page 2

1 <sup>st</sup> Example for Exchange of 50 within 1002		2 <sup>nd</sup> Example for Exchange of 50 within 1002		3 <sup>rd</sup> Example for Exchange of 50 within 1002	
Dropped	Added	Dropped	Added	Dropped	Added
47	1270	49	1045	29	1135
184	1180	133	1833	37	1438
95	1249	20	1690	127	1501
103	1126	28	1250	32	1578
155	1224	37	1452	11	1750
188	1251	112	1460	33	1173
158	1113	38	1166	15	1839
72	1125	31	1312	17	1631
34	1269	19	1844	36	1008
162	1062	21	1821	12	1930
44	1203	43	1041	26	1291
43	1004	36	1507	118	1082
121	1148	32	1533	130	1526

Table 13, page 1

SEQ ID No.	SEQ ID No.	SEQ ID No.	SEQ ID No.	SEQ ID No.	SEQ ID No.
2	146	344	558	718	915
7	147	348	562	723	919
10	150	351	569	731	929
17	151	367	575	733	930
19	153	385	577	734	944
21	155	386	578	735	946
22	156	388	587	739	947
23	161	395	597	744	954
24	162	410	598	751	961
26	163	413	600	753	967
27	167	414	601	756	968
35	170	426	602	759	983
37	180	431	612	769	1001
41	181	433	614	771	1004
46	182	434	617	773	1005
48	184	442	619	778	1008
54	189	449	623	782	1010
55	193	450	626	783	1018
56	198	451	627	799	1030
58	218	454	628	806	1032
63	221	458	632	816	1033
65	225	461	636	819	1036
67	226	465	643	820	1049
74	236	473	645	827	1050
76	242	479	646	839	1055
78	243	480	653	844	1058
79	252	481	654	845	1062
81	260	482	655	847	1069
88	262	483	656	850	1070
93	268	486	657	851	1079
96	270	491	665	858	1092
97	308	494	668	860	1093
100	309	505	670	862	1097
111	312	513	677	863	1099
117	315	529	688	873	1112
129	318	536	690	879	1113
132	322	537	699	890	1119
138	323	540	701	891	1121
140	333	548	706	895	1125
145	338	552	714	908	1126

Table 13, page 2

SEQ ID No.	SEQ ID No.	SEQ ID No.	SEQ ID No.	SEQ ID No.	SEQ ID No.
1132	1268	1367	1527	1680	1814
1133	1269	1377	1528	1685	1832
1134	1270	1380	1539	1687	1833
1142	1271	1395	1540	1688	1834
1143	1275	1403	1547	1692	1851
1148	1284	1409	1550	1695	1853
1155	1297	1415	1557	1711	1864
1158	1301	1425	1567	1713	1872
1170	1303	1427	1568	1721	1876
1172	1306	1428	1569	1725	1879
1173	1314	1446	1574	1740	1880
1178	1319	1449	1590	1742	1882
1179	1320	1452	1602	1744	1887
1180	1325	1460	1613	1750	1890
1183	1329	1466	1617	1755	1892
1184	1330	1471	1618	1761	1893
1186	1331	1477	1620	1762	1901
1187	1333	1479	1629	1765	1909
1197	1335	1483	1631	1766	1915
1202	1337	1485	1632	1767	1931
1203	1349	1488	1635	1780	1940
1220	1352	1491	1645	1783	1941
1224	1357	1492	1650	1788	1946
1236	1358	1493	1654	1791	1951
1241	1359	1512	1655	1803	1953
1246	1362	1521	1658	1805	1959
1249	1364	1523	1661	1809	1963
1251	1366	1524	1674	1810	2002

## Claims

1. A method for the detection of colorectal cancer in a human subject based on RNA from a blood sample obtained from said subject, comprising:
  - measuring the abundance of at least 8 RNAs in the sample, that are chosen from the RNAs listed in table 1, and
  - concluding based on the measured abundance whether the subject has colorectal cancer.
2. The method of claim 1, wherein the abundance of at least 30 RNAs, of at least 60 RNAs, of at least 102 RNAs, of at least 202 RNAs, of at least 502 RNAs, of at least 1002 RNAs, or of at least 2002 RNAs that are chosen from the RNAs listed in table 1 is measured.
3. The method of claim 1, wherein the abundance of a set of 8 RNAs as listed in table 4 is measured.
4. The method of claim 2, wherein the abundance of a set of 30 RNAs as listed in table 5 is measured.
5. The method of claim 2, wherein the abundance of a set of 60 RNAs as listed in table 6 is measured.
6. The method of claim 42, wherein the abundance of a set of 102 RNAs as listed in table 7 is measured.
7. The method of claim 2, wherein the abundance of the 202 RNAs of table 8 is measured.
8. The method of claim 2, wherein the abundance of at least the 502 RNAs of table 9 is measured.
9. The method of claim 2, wherein the abundance of at least the 1002 RNAs of table 10 is measured.

10. The method of claim 2, wherein the abundance of at least the 2002 RNAs of table 1 is measured.

11. The method of claims 1, 2 and 7, wherein the abundance of at least 202 RNAs is measured, wherein

- at least 152 of the 202 measured RNAs are chosen from the group of RNAs that are listed in table 1 and are referred to therein as SEQ ID NOs. 1 to 202, and
- up to 50 of the remaining measured RNAs are chosen from the group of RNAs that are listed in table 1 and are referred to therein as SEQ ID NOs. 203 to 2002.

12. The method of claims 1, 2, and 9, wherein the abundance of at least 1002 RNAs is measured, wherein

- at least 952 of the 1002 measured RNAs are chosen from the group of RNAs that are listed in table 1 and are referred to therein as SEQ ID NOs. 1 to 1002, and
- up to 50 of the remaining RNAs are chosen from the group of RNAs that are listed in table 1 and are referred to therein as SEQ ID NOs. 1003 to 2002.

13. The method of claims 1 to 12, wherein the measuring of RNA abundance is performed using a microarray, a real-time polymerase chain reaction or sequencing.

14. The method of claims 1 to 13, wherein the decision whether the subject has colon cancer comprises the step of training a classification algorithm on a training set of cases and controls, and applying it to measured RNA abundance.

15. The method of claims 1 to 14, wherein the classification method is a random forest method, a support vector machine (SVM), or a K-nearest neighbor method (K-NN), such as a 3-nearest neighbor method (3-NN).

16. The method of claims 1 to 15, wherein the RNA is mRNA, cDNA, micro RNA, small nuclear RNA, unspliced RNA, or its fragments.

17. Use of a method of claims 1 to 16 for detection of colorectal cancer in a human subject based on RNA from a blood sample.
18. A microarray, comprising a solid support and a set of oligonucleotide probes, the set containing from 5 8 to about 3,000 probes, and including at least 8 probes selected from table 1 or 8.
19. Use of a microarray for detection of colorectal cancer in a human subject based on RNA from a blood sample, comprising measuring the abundance of at least 8 RNAs listed in table 1, wherein the microarray comprises at least 1 probe for measuring the abundance of each of at least 8 RNAs.
20. A kit for the detection of colorectal cancer in a human subject based on RNA obtained from a blood sample, comprising means for measuring the abundance of at least 8 RNAs that are chosen from the RNAs listed in table 1, preferably comprising means for exclusively measuring the abundance of RNAs that are chosen from table 1.
21. Use of a kit of claim 20 for the detection of colorectal cancer in a human subject based on RNA from a blood sample, comprising means for measuring the abundance of at least 8 RNAs that are chosen from the RNAs listed in table 1, comprising
  - measuring the abundance of at least 8 RNAs in a blood sample from a human subject, wherein the at least 8 RNAs are chosen from the RNAs listed in table 1, and
  - concluding based on the measured abundance whether the subject has colorectal cancer.
22. A method for preparing an RNA expression profile that is indicative of the presence or absence of colorectal cancer in a subject, comprising:
  - isolating RNA from a blood sample obtained from the subject, and
  - determining the abundance of from 8 to about 3000 RNAs, including at least 8 RNAs selected from table 1.

Figure 1

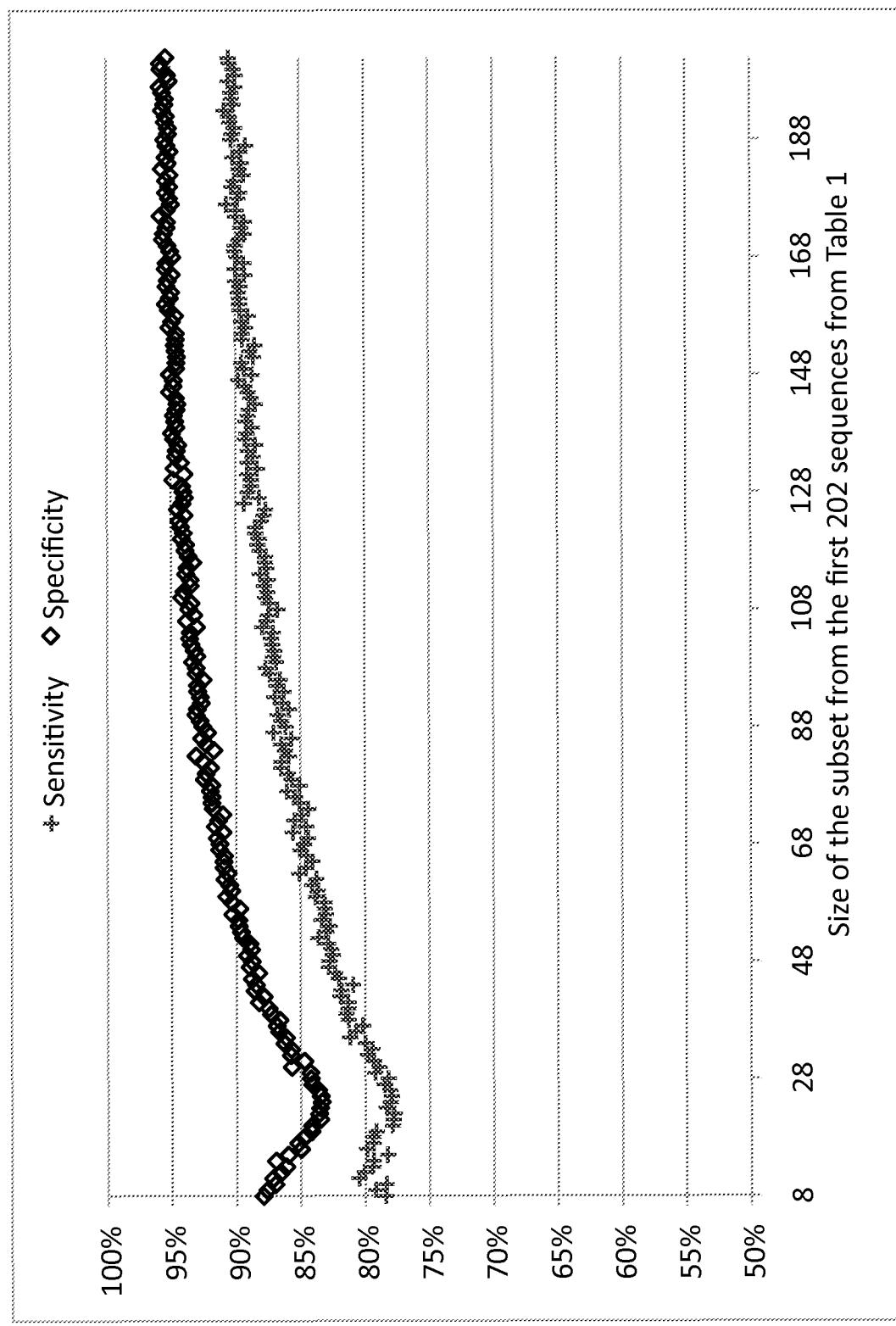


Figure 2

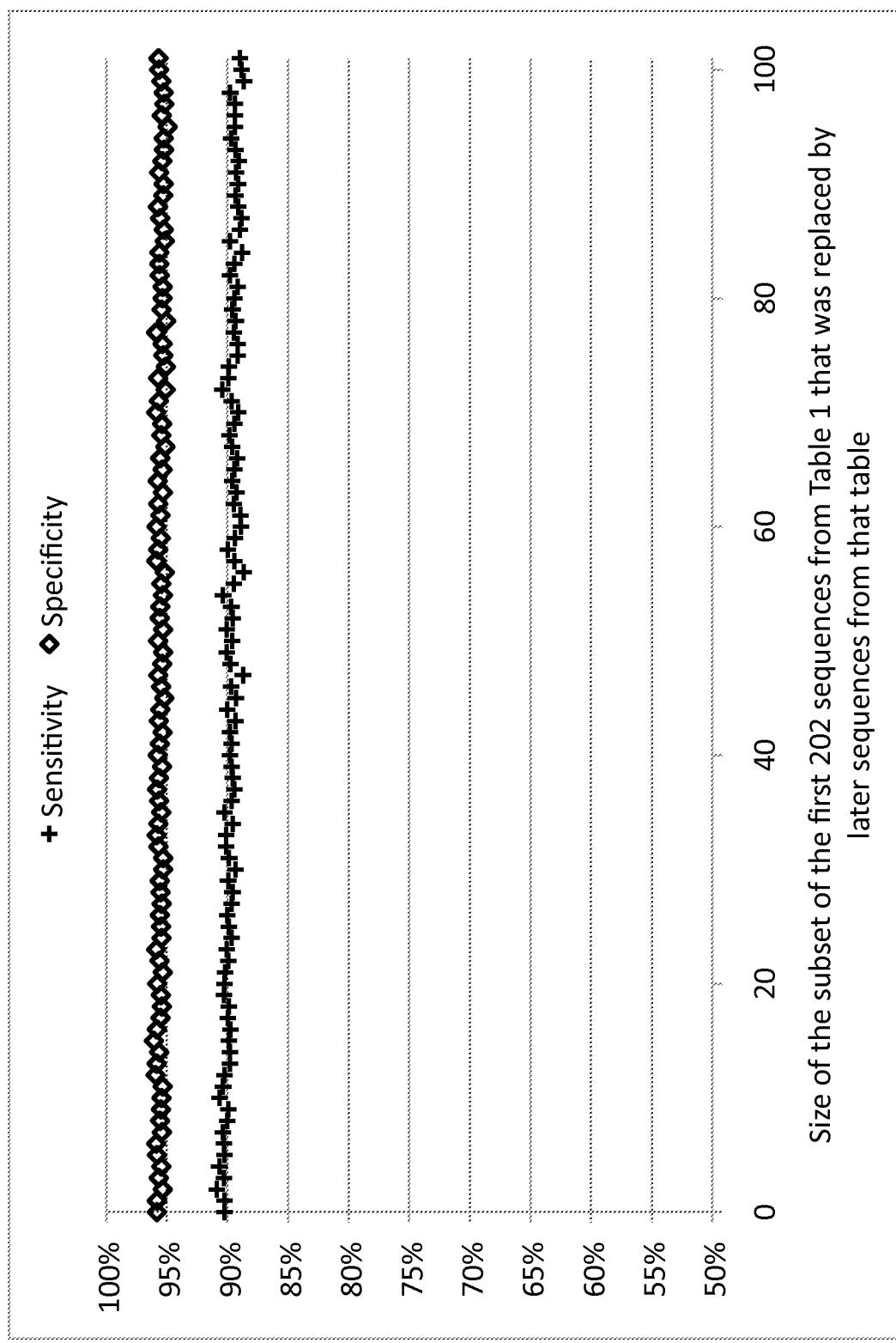


Figure 3

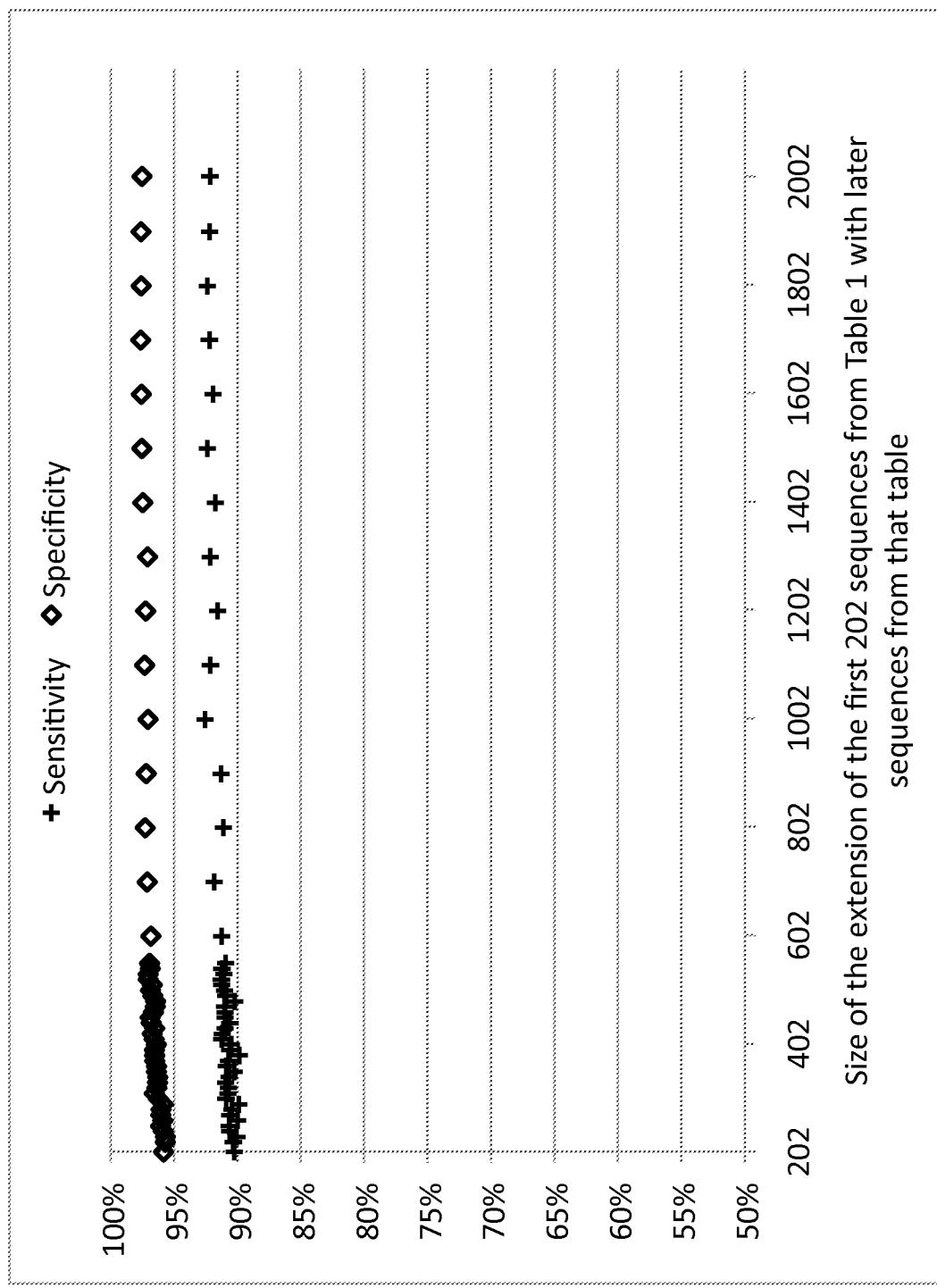


Figure 4

**Performance of the first 50 / 100 / 200 / 400 Sequences from Table 13**