

(51) International Patent Classification:
C12Q 1/68 (2006.01)(21) International Application Number:
PCT/US2010/058952(22) International Filing Date:
3 December 2010 (03.12.2010)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/266,733 4 December 2009 (04.12.2009) US(71) Applicant (for all designated States except US): **DUKE UNIVERSITY** [US/US]; 2812 Erwin Road, Suite 306, Durham, NC 27705 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **DAVE, Sandeep** [US/US]; Duke University, 2812 Erwin Road, Suite 306, Durham, NC 27705 (US). **JACOBS, Cassandra** [US/US]; Duke University, 2812 Erwin Road, Suite 306, Durham, NC 27705 (US).(74) Agent: **SINGER, Christopher, P.**; Michael Best & Friedrich LLP, 100 East Wisconsin Avenue, Suite 3300, Milwaukee, WI 53202-4108 (US).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

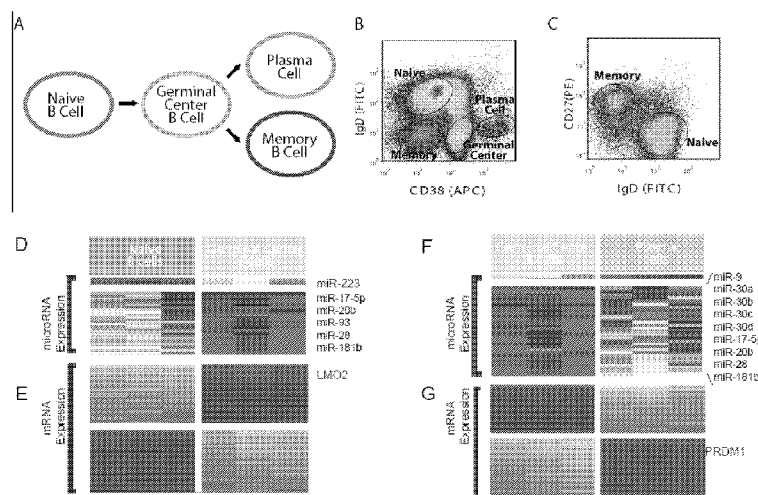
Published:

— without international search report and to be republished upon receipt of that report (Rule 48.2(g))

— with sequence listing part of description (Rule 5.2(a))

(54) Title: MICRORNA AND USE THEREOF IN IDENTIFICATION OF B CELL MALIGNANCIES

Figure 1



(57) Abstract: Disclosed are nucleic acid sequences, including microRNA sequences and cDNA sequences, as well as vectors, DNA libraries, microarrays, and recombinant cells comprising the nucleic acid sequences described herein. Methods of determining the B cell stage from which a B cell malignancy is derived. Methods of identifying B cell malignancies are also provided. Methods of diagnosing B cell malignancies are provided. Such methods comprise, in certain embodiments, detecting one or more microRNAs or cDNAs as disclosed herein.

MICRORNA AND USE THEREOF IN IDENTIFICATION OF B CELL MALIGNANCIES

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is related to and claims the benefit of priority of U.S. Provisional Application Serial No. 61/266,733, filed December 4, 2009, which is incorporated herein by reference.

STATEMENT OF GOVERNMENT SUPPORT

[0002] This invention was made with United States government support from the National Institutes of Health grant no. K12-CA-100639. The United States government has certain rights in this invention.

SEQUENCE LISTING

[0003] The sequence listing is filed with the application in electronic format only and is incorporated by reference herein. The sequence listing text file "WO_ASFILED_SequenceListing.txt" was created on December 3, 2010, and is 262,254 bytes in size.

BACKGROUND

[0004] Naive B cells migrate through the circulation to lymphoid organs where they undergo the T cell-dependent germinal center reaction. Adaptive immunity is acquired as specific antigen-reactive germinal center B cells differentiate into the major effector B cells of the adaptive immune system: memory cells and plasma cells. *See, e.g.*, Figure 1A. Although the role of specific transcription factors in mature B cell differentiation has been examined (*see* Nutt et al. *Nature*. 1999;401:556-562; Chang et al. *Proc Natl Acad Sci U S A*. 1996;93:6947-6952; Turner et al. *Cell*. 1994;77:297-306; Shaffer et al., *Immunity*. 2004;21:81-93; and Schebesta et al. *Curr Opin Immunol*. 2002;14:216-223), mechanisms regulating such transcription factors during mature B cell differentiation are largely unknown.

[0005] Many malignancies derived from mature B cells are known and are believed to constitute the majority of leukemias and lymphomas. Such malignancies appear to reflect defined stages of normal B cell differentiation. Diagnosis of leukemias and lymphomas can be particularly difficult because of their shared lineage. These cancers frequently display overlapping morphologies, genetic abnormalities, and expression of surface markers, which can complicate the diagnosis. However, the distinction of these tumors is clinically important

because there are important differences in the treatments and expected response to treatment. Thus methods that improve the accuracy of their diagnosis should provide to improved outcomes for these patients.

[0006] MicroRNAs are commonly 18-22 nucleotide-long RNA molecules that regulate expression of genes. There is an increasing recognition of the role of microRNAs in oncogenesis, lineage-selection, and immune cell function, including early B cell differentiation. See Calin et al. *N Engl J Med.* 2005;353:1793-1801; O'Donnell et al. *Nature.* 2005;435:839-843; Chen et al. *Science.* 2004;303:83-86; Lim et al. *Nature.* 2005;433:769-773; Li et al. *Cell.* 2007;129:147-161; Xiao et al., *Nat Immunol.* 2008;9:405-414; Baltimore et al. *Nat Immunol.* 2008;9:839-845; and Ventura et al. *Cell.* 2008;132:875-886. However, the full extent and function of microRNA expression during mature B cell differentiation and in B cell malignancies are not known.

[0007] Correct diagnosis of B cell malignancies is important from both a clinical standpoint and from the standpoint of setting appropriate patient expectations. A misdiagnosed B cell malignancy may lead to an inappropriate therapy, which can unnecessarily endanger the patient's life and/or be an ineffective treatment for the B cell malignancy. As an example, the diagnostic distinction of Burkitt lymphoma (BL) from diffuse large B cell lymphomas (DLBCLs) can be difficult because of overlapping morphology, immunophenotype and cytogenetics. Burkitt lymphoma tumors are molecularly distinct from DLBCL, however. The difficulty and importance of obtaining the correct diagnosis in BL was highlighted by the experience of a multicenter clinical trial, CALGB trial#925119, in which nearly half of the 100 patients with an assigned diagnosis of BL were found to have another diagnosis upon further pathology review.

[0008] If diagnosed and treated appropriately, nearly 80% of patients with BL can be cured with intensive (high dose) chemotherapy regimens. Thus, a misclassification of BL as DLBCL can result in a missed opportunity to cure the malignancy. On the other hand, misclassification of DLBCL as BL leads to unnecessarily morbidity from intensive chemotherapy regimens. Thus, methods that improve the diagnosis of BL, and other B cell malignancies, can provide better outcomes in patients.

[0009] DLBCLs can also be subclassified into two different B cell malignancies, activated B-cell (ABC) DLBCL and germinal center B cell like (GCB) DLBCL. There are at least two important clinical applications for the molecular sub-grouping of DLBCL patients. First, the prognostic information could inform the choices and expectations of patients and their physicians. Second, the important molecular differences in these subgroups form the basis of

testing different targeted therapies in these patients. The possibility of a differential response to therapy among ABC and GCB DLBCLs is supported by data that suggest that the benefit of receiving a proteasome inhibitor, bortozemib, is predominantly limited to those patients who have ABC DLBCL. However, the clinical distinction of the subgroups of DLBCL using immunohistochemistry is difficult with current methods distinguishing GCB DLBCL from non-GCB DLBCL with limited success.

[0010] Mature B cell differentiation is important for the development of adaptive immunity. The process is also of interest because B cell malignancies are common and retain a number of features derived from their normal counterpart B cell subsets. Unlike other maturation pathways in the hematopoietic and other cell lineages, successive stages of mature B cells do not simply signify progressive differentiation away from the stem cell stage. Rather, each stage represents a specialized state with specific functions. Thus, germinal center (GC) cells interact with CD4 T cells and dendritic cells and undergo somatic hypermutation and Ig-heavy chain class-switching. On the other hand, plasma cells secrete immunoglobulin, while memory cells are primed to proliferate and differentiate into plasma cells upon repeat contact with antigen. The specialized functions demand a finely tuned program of gene regulation.

[0011] MicroRNAs represent a novel class of biomarkers that provide new opportunities for clinical translation. First, intact microRNAs can be isolated from tissues preserved using standard methods, such as formalin fixed, paraffin embedded (FFPE) tissue. Thus, microRNA-based biomarkers could be easy to translate to clinical use. Second, microRNAs can be readily assayed using real-time PCR and other methods available in conventional pathology.

SUMMARY

[0012] In an aspect the disclosure provides an isolated nucleic acid molecule having at least 80% sequence identity to any one of SEQ ID NOs: 763-1350 or 1565 or a complementary sequence thereof. Embodiments provide for sequence identity of at least 90% or 95%.

[0013] In an aspect the disclosure provides an isolated nucleic acid molecule comprises any one of SEQ ID NOs: 763-1350 or 1565 or a complementary sequence thereof. Embodiments provide for isolated nucleic acid molecules comprising a primary miRNA, a precursor miRNA, a mature miRNA, or a DNA molecule coding therefore. Embodiments further provide for a cDNA molecule comprising sequence that corresponds to a miRNA sequence of any one of SEQ ID NOs: 763-1350 or 1565.

[0014] Aspects of the disclosure provide compositions, pharmaceutical compositions, vectors, host cells, and DNA libraries comprising at least one nucleic acid molecule described herein.

[0015] In an aspect the disclosure provides a method of determining the B cell stage of a B cell malignancy in a subject comprising determining the level of expression of at least one microRNA in a sample comprising a B cell taken from the subject relative the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in Table 4.

[0016] In an aspect the disclosure provides a method of identifying a B cell malignancy in a subject comprising determining the level of expression of at least one microRNA in a sample comprising a B cell taken from the subject relative the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in Table 4.

[0017] In an aspect the disclosure provides a method of diagnosing a B cell malignancy in a subject comprising determining the level of expression of at least one microRNA in a sample comprising a B cell taken from the subject relative the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in Table 4.

[0018] In an aspect the disclosure provides a method of identifying a B cell malignancy in a subject comprising determining the level of expression of at least one microRNA in a sample comprising a B cell taken from the subject relative the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in any one of Tables 7 to 35.

[0019] In an aspect the disclosure provides a method of diagnosing a B cell malignancy in a subject comprising determining the level of expression of at least one microRNA in a sample comprising a B cell taken from the subject relative to the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in any one of Tables 7 to 35.

[0020] Embodiments of these aspects provide for identification or diagnosis of a B cell malignancy selected from chronic lymphocytic leukemia, follicular lymphoma, Hodgkin's lymphoma, activated B-cell diffuse large B cell lymphoma (DLBCL), germinal center-like DLBCL, and Burkitt lymphoma.

[0021] In an aspect the disclosure provides a method of determining whether a B cell malignancy in a sample is Burkitt lymphoma, activated B cell-like diffuse large B cell lymphoma (DLBCL), or germinal center-like DLBCL, comprising determining the level of expression of at least one microRNA in the sample relative to the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from

the microRNAs listed in Table 10, column “BL miRNA list”; Table 14, column “BL High”; Table 11; Table 14, column “ABC High”; Table 10, column “GCB miRNA list”; Table 14, column “GCB High”; Table 32, or Table 35.

[0022] In an aspect the disclosure provides a method of determining whether a B cell malignancy in a sample is Burkitt lymphoma, activated B cell-like diffuse large B cell lymphoma (DLBCL), or germinal center-like DLBCL, comprising determining the level of expression of at least one microRNA in the sample relative to the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in at least one column labeled “GCBvsBL” or “GCBvsABC” in Table 7 or “ABCvsBL” in Table 8.

[0023] In an aspect the disclosure provides a method of determining whether a B cell malignancy in a sample is activated B cell-like diffuse large B cell lymphoma (DLBCL), or germinal center-like DLBCL, comprising determining the level of expression of at least one microRNA in the sample relative to the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in Table 35.

[0024] In an aspect the disclosure provides a microarray comprising miRNA-specific probe oligonucleotides wherein at least one miRNA-specific probe oligonucleotide is specific for a sequence of SEQ ID NOs: 763-1350 or 1565, or any combination thereof.

[0025] In an aspect the disclosure provides a kit comprising at least one primer sequence that can detect any one of SEQ ID NOs: 763-1350 or 1565, or a combination thereof.

[0026] In an aspect the disclosure provides a kit comprising at least one isolated nucleic acid molecule having a sequence of any one of SEQ ID NOs: 1351-1564.

[0027] In an aspect, the disclosure provides a method of identifying a B cell malignancy comprising determining the level of expression of at least one microRNA selected from the microRNAs listed in Table 4. In certain embodiments, a method comprises determining the level of expression of at least one microRNA selected from the microRNAs listed in Tables 7-35.

[0028] Other aspects and embodiments will be apparent to one of skill in the art in light of the following detailed description.

DESCRIPTION OF THE FIGURES

[0029] Figure 1 shows that mature B cell subsets demonstrate distinct microRNA profiles. Figure 1A is a diagram showing the overall schema of mature B cell differentiation. Figure 1B

shows selection of B cell subsets using flow cytometry. Figure 1C shows the distinction between naive and memory B cells based on IgD and CD27 expression using flow cytometry. Figure 1D shows relative expression of microRNA in the naive to germinal center B cell transition. Figure 1E shows relative expression of mRNA in the naive to germinal center B cell transition. Figure 1F shows relative expression of microRNA in the germinal center B cell to plasma cell transition. Figure 1G shows relative expression of mRNA in the germinal center B cell to plasma cell transition. Figure 1H shows relative expression of microRNA in the germinal center B cell to memory B cell transition. Figure 1I shows relative expression of mRNA in the germinal center B cell to memory B cell transition. In Figures 1D, 1F, and 1H, miRNAs that were, on average, at least 2-fold differentially expressed at a false discovery rate of less than 5% are shown according to the color scale. In Figures 1E, 1G, and 1I, mRNAs that were, on average, at least 2-fold differentially expressed at a false discovery rate of less than 1% are shown according to the color scale. Figure 1J shows that expression of certain microRNA processing genes, DGCR8, DICER1, EIF2C2, DROSHA, and XP05 is unchanged among the B cell subsets ($P > 0.1$ in all cases).

[0030] Figure 2 shows experimental validation of the interaction of miR-223, which is expressed highly in naive and memory B cells compared to germinal center B cells, and targets the transcription factor LM02. Figure 2A shows base-pairing of the 3'UTR of the LM02 gene with nucleotides 1-8 of miR-223. This 8-mer is highly conserved across a number of species and serves as a potential binding site for miR-223. Figure 2B shows the effects of over-expression of miR-223 in germinal center lymphoma-derived BJAB cells in 3 separate experiments. Figure 2C shows the relative LM02 protein expression from a representative experiment (from 3 replicates) transfecting a scrambled control versus a precursor for miR-223 in BJAB cells. Figure 2D shows average expression of LM02 relative to Actin over three Western blots of BJAB cells transfected with a scrambled control versus a precursor for miR-223. Figure 2E shows luciferase activity in BJAB cells transfected with a vector comprising either a luciferase gene coupled to the 3'UTR of the LM02 gene or a luciferase gene coupled to the 3'UTR of the LM02 gene with the miR-223 binding site mutated, and cotransfected with miR-223.

[0031] Figure 3 shows experimental validation of the interaction of miR-9 and miR-30, which are expressed highly in germinal center B cells compared to plasma cells and target the transcription factor PRDM1. Figure 3A shows base-pairing of the 3'UTR of the PRDM1 gene with the 5' seed region of miR-9 and the miR-30 family. Figure 3B shows the effects of over-expressing miR-9 and 2 members of the miR-30 family, miR-30b and miR-30d, in plasma cell

myeloma-derived U266 cells in 3 separate experiments. Figure 3C shows the relative PRDM1 protein expression from a representative experiment (from 3 replicates) transfecting a scrambled control versus a precursor for miR-9, miR-30b, or miR-30d in U266 cells. Figure 3D shows the average expression of PRDM1 relative to Actin over three Western blots of U266 cells transfected with a scrambled control versus a precursor for miR-9, miR-30b, or miR-30d. ($P < 0.05$ for miR-30b and miR-30d, $P = 0.08$ for miR-9.) Figure 3E shows repression of luciferase activity from the PRDM1 3'UTR construct by overexpression of miR-9, miR-30b, and miR-30d wild-type and mutant sequences.

[0032] Figure 4 shows that expression of microRNAs in normal B cells is conserved in certain B cell malignancies. Figure 4A shows lineage prediction of both IgV mutated and unmutated chronic lymphocytic leukemia, germinal center B cell derived DLBCL, and Burkitt lymphoma based on differential expression of microRNAs in normal naïve B cells and germinal center B cells (microRNAs depicted in Figure 1D). Figure 4B shows miRNAs that were found to be differentially expressed ($P < 0.05$) in malignant cells and normal cells as discussed in Example 5. Figure 4C shows cloning frequency of miRNAs in unselected mature B cells ($N = 3$) and certain B cell malignancies ($N = 42$) from a previously published study ("sequencing data"), as discussed in Example 5. Figure 4D shows differentially expressed miRNAs that distinguish Burkitt lymphoma, activated B cell-like (ABC) diffuse large B cell lymphoma (DLBCL), germinal center-like DLBCL (GCB DLBCL), and chronic lymphocytic leukemia. Predictor miRNAs from each pair-wise comparison that distinguish each entity are shown in the boxes.

[0033] Figure 5 shows the distribution of miRNAs present in B-cell subsets.

[0034] Figure 6 shows that certain microRNA targets are expressed at lower levels. Figure 6A shows density plots of the expression frequency of predicted mRNA targets of miRNAs expressed highly in germinal center B cells compared to naïve cells. Figure 6B shows density plots of the expression frequency of predicted mRNA targets of miRNAs expressed highly in germinal center B cells compared to plasma cells. Figure 6C shows density plots of the expression frequency of predicted mRNA targets of miRNAs expressed highly in the germinal center B cells compared to memory B cells.

[0035] Figure 7 shows that differentially expressed transcription factors are frequently microRNA targets. In Figure 7A, the left panel indicates the proportion of transcription factors that are differentially expressed in the naïve to germinal center B-cell transition that are also predicted targets of differentially expressed miRNAs. The right panel indicates the proportion of transcription factors that are not differentially expressed and also are predicted targets of differentially expressed miRNA in that stage-transition. The p-value indicates the results of a

chi-squared test for the enrichment of predicted miRNA targets among the differentially expressed transcription factors. Figure 7B shows a similar analysis of the germinal center to plasma cell transition. Figure 7C shows a similar analysis of the germinal center to memory cell transition.

[0036] Figure 8 shows that Mybl transcript levels decrease with miR-223 overexpression. Figure 8A shows base-pairing of the 3'UTR of the MYBL1 gene with nucleotides 2-8 of miR-223. This 7-mer is highly conserved across a number of species and serves as a potential binding site for miR-223. Figure 8B shows the effects of over-expression of miR-223 in germinal center lymphoma-derived BJAB cells in 3 separate experiments.

[0037] Figure 9 shows the specificity of real-time PCR probes for members of the miR-30 family.

[0038] Figure 10 shows the results of leave one out cross validation applied to the predictors for Burkitt lymphoma, chronic lymphocytic leukemia, activated B-cell diffuse large B-cell lymphoma, and germinal center B-cell DLBCL.

[0039] Figure 11 shows differentially expressed miRNAs that distinguish activated B cell-like diffuse large B cell lymphoma (DLBCL), germinal center-like DLBCL (GCB DLBCL), Burkitt lymphoma, chronic lymphocytic leukemia, follicular lymphoma, and Hodgkin's lymphoma. Predictor miRNAs from each pair-wise comparison that distinguish each entity are shown in the boxes.

DETAILED DESCRIPTION

[0040] All patent and non-patent literature references that are cited herein are incorporated herein by reference in their entirety.

[0041] In a general sense, the disclosure relates to nucleic acid sequences, such as microRNAs (miRNA), as well as to the identification and analysis of microRNA expression levels and/or patterns in B cells. Through concomitant microRNA and mRNA profiling, the inventors have identified regulatory roles for microRNAs at each stage in mature B cell differentiation. This provides methods identifying microRNA-mediated regulation of oncogenes and key transcription factors in B cell differentiation. This work establishes the landscape of normal microRNA expression in mature B cells and its role in regulating normal B cell differentiation. Further, our work demonstrates that in contrast to the described down-regulation in other malignancies, stage-specific microRNAs are retained in B cell malignancies. The lineage of common B cell malignancies can be predicted based upon miRNA profiles of normal B cells, pointing to a role for microRNAs in the maintenance of mature B cell phenotypes in normal and malignant B cells.

[0042] In an aspect, the disclosure relates to an isolated nucleic acid molecule comprising: (a) a nucleotide sequence as shown in Table 32; (b) a nucleotide sequence which is the complement of (a), (c) a nucleotide sequence comprising a sequence identity of at least 80%, (e.g., 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or at least 99%), to a sequence of (a) or (b) and/or (d) a nucleotide sequence which hybridizes under stringent conditions to a sequence of (a), (b) and/or (c). In some embodiments, the identity of sequence (c) to a sequence of (a) or (b) is at least 90%. In other embodiments, the identity of sequence (c) to a sequence of (a) or (b) at least 95%. The percent identity can be calculated by any routine method used by one of skill in the art such as, for example, the methods described herein.

[0043] In embodiments, the isolated nucleic acid molecule relates to a miRNA molecule and analogs thereof, a miRNA precursor molecule, or a primary miRNA molecule, as well as to DNA molecules encoding miRNA, miRNA precursor, or primary miRNA molecules. Accordingly, in such embodiments, the isolated nucleic acid molecule can function as a miRNA molecule under suitable conditions. Suitable conditions include, but are not limited to, various buffer systems that approximate physiologically relevant ionic concentrations and pHs, as well as physiological conditions.

[0044] In some embodiments, the nucleic acid molecule comprises a sequence that hybridizes to a nucleotide sequence as shown in Table 32, a complementary sequence thereof or a nucleic acid molecule having at least 80% sequence identity under stringent hybridization conditions. The basic parameters affecting the choice of hybridization conditions and guidance for devising suitable conditions are set forth by Sambrook, et al. (*See*, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.; and *Current Protocols in Molecular Biology*, 1995, Ausubel et al., eds., John Wiley & Sons, Inc.), and can be readily determined by those of ordinary skill in the art based on, for example, the length and/or base composition of the DNA. Generally, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, or less than about 500 mM NaCl and 50 mM trisodium citrate, or even less than about 250 mM NaCl and 25 mM trisodium citrate. High stringency hybridization conditions can be obtained by adding an amount of organic solvent (e.g., at least about 35% to about 50% formamide). Stringent temperature conditions will ordinarily include temperatures of at least about 30°C, (e.g., at least about 37°C, 42°C, 45°C, 50°C, or 55°C). Varying additional parameters, such as hybridization time, the concentration of detergent (e.g., 0.1-1.0% sodium dodecyl sulfate (SDS)), and the inclusion or exclusion of carrier DNA (e.g., about 100-200 µg/ml denatured

salmon sperm DNA (ssDNA)), are well known to those skilled in the art. Stringent hybridization conditions are known in the art and include non-limiting examples such as, washing for 1 hr in 300 mM NaCl, 30 mM trisodium citrate and 0.1% SDS at 45-50°C; washing for 1 h in 300 mM NaCl, 30 mM trisodium citrate and 0.1% SDS at 45-50°C; in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 µg/ml denatured salmon sperm DNA (ssDNA) at 37°C; or in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50% formamide, and 200 µg/ml ssDNA at 42°C. Useful variations on these conditions will be readily apparent to those skilled in the art.

[0045] The isolated nucleic acid molecules provided herein suitably have a length of from about 18 to about 100 nucleotides. In embodiments wherein the isolated nucleic acid molecules are miRNAs, the lengths of the miRNAs are suitably in an expected range for the particular type of miRNA molecule. For example, mature miRNAs are typically from about 15 to about 28 nucleotides in length, and suitably have a length of about 19 to about 24 nucleotides (e.g., 19, 20, 21, 22, 23, or 24 nucleotides). Precursor miRNAs typically comprise the mature miRNA sequence and contain a stem-loop structure, suitably of length of about 50 to about 90 nucleotides (e.g., 50, 55, 60, 65, 70, 75, 80, 85, or 90 nucleotides). Primary miRNAs (e.g., a primary transcript comprising a precursor miRNA) can suitably have a length of greater than 100 nucleotides.

[0046] The nucleic acid molecules can be provided in either a single-stranded or double-stranded form. Typically, a miRNA as such is identified as a single-stranded molecule, while the precursor miRNA is typically at least partially self-complementary and capable of forming double-stranded portions, e.g. stem- and loop-structures. DNA molecules encoding the miRNA and miRNA precursor molecules (e.g., expression vectors, cloning vectors, and the like) are typically double-stranded. The individual nucleic acids that comprise the isolated nucleic acid molecules can be selected from RNA, DNA, or nucleic acid analog molecules, such as chemically modified sugar (e.g., 2'-modified (2'-F, 2'-OMe, etc.) or backbone (e.g., phosphorothioates), or cap (e.g., 5'- and/or 3'-abasic groups) moieties of ribonucleotides or deoxyribonucleotides. Other nucleic acid analogs, such as peptide nucleic acids (PNA) or locked nucleic acids (LNA), are also suitable in various embodiments described herein. In some embodiments the nucleic acid molecules can comprise any combination of nucleic acid analog(s).

[0047] While many of the nucleic acid molecules in the Tables are identified as RNA sequences, e.g., miRNAs, the disclosure of those sequences should be understood to encompass the corresponding DNA (e.g., cDNA) sequences, wherein the uracil (U) nucleotides

of the disclosed RNAs are substituted by thymidine (T) nucleotides in the corresponding DNA. One of skill in the art is able to generate such DNA sequences (e.g., cDNA) through routine microbiological techniques known in the art such as, for example, reverse transcription using methods that incorporate the reverse transcriptase enzyme.

[0048] In another aspect, the disclosure provides a recombinant expression vector comprising a recombinant nucleic acid sequence operatively linked to an expression control sequence, wherein expression of the recombinant nucleic acid sequence provides a miRNA sequence, a precursor miRNA sequence, or a primary miRNA sequence as described herein. The resulting sequence (e.g., primary or precursor miRNAs) can optionally be further processed to provide the miRNA sequence. In embodiments, the recombinant expression vector comprises at least one sequence in Table 32. Any suitable expression vector can be used such as, for example, a DNA vector (e.g., viral vector, plasmid, etc.). In some embodiments the expression vector is selected for expression in a eukaryotic cell such as, for example, a mammalian cell. One of skill in the art will be able to select an appropriate vector based on the particular application and/or expression system to be employed.

[0049] Thus, embodiments provide nucleic acid constructs in the form of plasmids, vectors, transcription or expression cassettes which comprise at least one nucleotide sequence encoding a miRNA described herein, or fragments thereof, and a suitable promoter region. Suitable vectors can be chosen or constructed, which contain appropriate regulatory sequences, such as promoter sequences, terminator sequences, polyadenylation sequences, enhancer sequences, marker genes and other sequences as desired. Vectors can be plasmids, phage (e.g. phage, or phagemid) or viral (e.g. lentivirus, adenovirus, AAV) or any other appropriate vector. For further details see, for example, *Molecular Cloning: a Laboratory Manual*: 2nd edition, Sambrook et al., 1989, Cold Spring Harbor Laboratory Press.

[0050] Relatedness of Nucleic Acid Molecules/Sequences

[0051] The term "identity" refers to a relationship between the sequences of two or more two or more nucleic acid molecules, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between amino acid or nucleic acid molecule sequences, as the case may be, as determined by the match between strings of nucleotide or amino acid sequences. "Identity" measures the percent of identical matches between two or more sequences with gap alignments addressed by a particular mathematical model or computer programs (i.e., "algorithms").

[0052] Identity of related nucleic acid molecules can be readily calculated by known methods, including but not limited to those described in *Computational Molecular Biology*, Lesk, A. M.,

ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part 1, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M. Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., SIAM J. Applied Math., 48:1073 (1988).

[0053] Non-limiting methods for determining identity are designed to give the largest match between the sequences tested. Methods to determine identity are codified in publicly available computer programs. Preferred computer program methods to determine identity between two sequences include, but are not limited to, the GCG program package, including GAP (Devereux, et al., Nucleic Acids Research 12:387 [1984]; Genetics Computer Group, University of Wisconsin, Madison, Wis.), BLASTN, and FASTA (Atschul et al., J. Molec. Biol. 215:403-410 [1990]). The BLAST X program is publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul et al., NCB NLM NIH Bethesda, Md. 20894; Altschul et al., J. Mol. Biol. 215:403-410 [1990]). The well known Smith Waterman algorithm may also be used to determine identity.

[0054] Exemplary parameters for nucleic acid molecule sequence comparison include the following:

[0055] Algorithm: Needleman and Wunsch, J. Mol Biol. 48:443-453 (1970)

[0056] Comparison matrix: matches=+10, mismatch=0

[0057] Gap Penalty: 50

[0058] Gap Length Penalty: 3

[0059] The GAP program is also useful with the above parameters. The aforementioned parameters are the default parameters for nucleic acid molecule comparisons.

[0060] Other exemplary algorithms, gap opening penalties, gap extension penalties, comparison matrices, thresholds of similarity, etc. can be used by those of skill in the art, including those set forth in the Program Manual, Wisconsin Package, Version 9, September 1997. The particular choices to be made will depend on the specific comparison to be made, such as DNA to DNA or RNA to DNA; and additionally, whether the comparison is between given pairs of sequences (in which case GAP or BestFit are generally preferred) or between one sequence and a large database of sequences (in which case FASTA or BLASTA are preferred).

[0061] In an aspect, the disclosure provides a vector comprising the isolated polynucleotide as described herein such as, for example one or more of SEQ ID NOs 773-1046 or 1450-1542.

In embodiments, the vector can be any type of vector that finds use as a vehicle to transfer foreign genetic material into a cell. Non-limiting examples of vectors include plasmids, viral vectors (e.g., derived from lentivirus, adenovirus, adeno-associated virus (AAV), retrovirus, etc.), bacteriophage, cosmids, and artificial chromosomes. In embodiments, the vector can be an expression (or expression constructs) for driving expression of the polynucleotide in a target cell. Vectors and methods for inserting them into a target cell are known in the art [*See, e.g., Sambrook et al., 1989*].

[0062] In an aspect, the disclosure provides recombinant cells that comprise the vectors and/or polynucleotides described herein. The cells can be any cell suitable as a host for recombinant nucleic acid molecules, and selected based on well known techniques. Techniques for generating and maintaining recombinant cells are known in the art, such as those described in Sambrook et al., 1989.

[0063] The term “B cell malignancy,” as used herein, refers to a malignancy derived from any stage of B cell, including, but not limited to, naïve cells, germinal center cells, memory B cells, and plasma cells. Examples of B cell malignancies include, but are not limited to, mantle cell lymphoma, follicular lymphoma, Hodgkin’s lymphoma, Burkitt lymphoma, germinal center B-cell like diffuse large B cell lymphoma (DLBCL), chronic lymphocytic leukemia, small lymphocytic lymphoma, lymphoplasmacytic lymphoma, multiple myeloma, and activated B-cell like DLBCL.

[0064] In an aspect, the disclosure provides a method of distinguishing B cell malignancies on the basis of the B-cell origin. In certain embodiments, methods of diagnosing B cell malignancies on the basis of the B-cell origin are provided. In certain such embodiments, a B cell malignancy is determined to be derived from a particular B-cell stage. The B-cell origin of a B cell malignancy may be determined, in certain embodiments, by detecting one or more microRNAs that can be used to distinguish B-cell stages. Certain exemplary B-cell stages include, but are not limited to, naïve cells, germinal center cells, memory B cells, and plasma cells. Certain exemplary microRNAs that can be used to distinguish B-cell stages are shown in Table 4. In various embodiments, the method comprises detecting at least one, at least two, at least five, at least 10, at least 20, at least 30, at least 50, at least 75, or at least 100 microRNAs.

[0065] In certain embodiments, a panel of microRNAs is selected that will allow determination of the B cell stage from which a B cell malignancy is derived. For example, in certain embodiments, two or more microRNAs from Table 4 are selected such that detection of the levels of those microRNAs in a B cell malignancy will indicate whether the B cell malignancy is derived from naïve, germinal center, plasma, or memory B cells. In various embodiments,

the panel of microRNAs comprises at least one, at least two, at least five, at least 10, at least 20, at least 30, at least 50, at least 75, or at least 100 microRNAs from Table 4. One skilled in the art can select a suitable panel of microRNAs, including one or more microRNAs from Table 4, according to the intended use of the panel.

[0066] As described throughout the disclosure, the methods herein can include detecting one or a plurality of miRNAs. When the term “at least” is used in association with a number (e.g., “at least 20”) that term will be understood to include 20 as well as optionally any integer after 20 and up to and including the total number of microRNAs disclosed herein.

[0067] In some embodiments, a B cell malignancy derived from naïve cells is mantle cell lymphoma. In other embodiments, a B cell malignancy derived from germinal center cells includes, but is not limited to, follicular lymphoma, Hodgkin’s lymphoma, Burkitt lymphoma, or germinal center B-cell like diffuse large B cell lymphoma (DLBCL). In other embodiments, a B cell malignancy derived from memory B cells includes, but is not limited to, chronic lymphocytic leukemia or small lymphocytic lymphoma. In some embodiments, a B cell malignancy derived from plasma cells includes, but is not limited to, multiple myeloma or activated B-cell DLBCL.

[0068] Certain B cell malignancies can be difficult to distinguish using current methodologies. In extreme cases, almost any B cell malignancy can be confused with another. As illustrative examples, Burkitt lymphoma and DLBCLs are often confused. Similarly, mantle cell lymphoma and small lymphocytic lymphoma can also be confused. Burkitt lymphoma and germinal center DLBCL are both derived from germinal center cells, while activated B-cell DLBCL is derived from plasma cells. Thus, if a B cell malignancy appears to be Burkitt lymphoma or a DLBCL, in certain embodiments, microRNA analysis can be used to narrow down the B cell malignancy to either a germinal center cell-derived B cell malignancy or a plasma cell-derived B cell malignancy. If the B cell malignancy is plasma-cell derived, then it may be activated B-cell DLBCL.

[0069] Thus, in certain embodiments, when the identity of a particular B cell malignancy has been narrowed down to two or more possible B cell malignancies, and at least two of those B cell malignancies are derived from different B cell stages, microRNAs that distinguish certain B cell stages can be used to further narrow down the identity of the B cell malignancy. In certain embodiments, microRNAs that distinguish certain B cell stages can be used to identify the B cell malignancy. One or more such microRNAs can be selected, in certain embodiments, from the microRNAs in Table 4. One skilled in the art can select a suitable set of microRNAs, including at least one microRNA from Table 4, for distinguishing particular B cell stages.

[0070] In an aspect, the disclosure provides a method of identifying a B cell malignancy comprising detecting one or a plurality of microRNAs. In certain embodiments, the method can provide a diagnosis of a B cell malignancy. In certain embodiments, one or more microRNAs that are characteristic of a particular B cell malignancy are used to identify the B cell malignancy. In certain embodiments, the identity of the B cell malignancy is first narrowed down to a list of two or more particular B cell malignancies using, for example, tumor morphology and/or immunohistochemistry and/or microRNA detection, e.g., to determine the B cell stage from which the tumor is derived. Certain exemplary microRNAs that can be used to identify B cell malignancies are shown in the Tables (e.g., Tables 7-35).

[0071] In certain embodiments, methods of identifying B cell malignancies comprise detecting one or more microRNAs from one or more of Tables 7 to 15, and Appendix B, Tables 16 to 30. That is, in certain embodiments, a panel of microRNAs is selected that will identify a B cell malignancy as being one of a particular selection of B cell malignancies. As a non-limiting example, a panel of microRNAs can be designed to identify a B cell malignancy as one of Burkitt lymphoma, ABC DLBCL, or GCB DLBCL. In certain such embodiments, the panel of microRNAs comprises at least one microRNA from Table 10, column "BL miRNA list" and/or Table 14, column "BL High"; at least one microRNA from Table 11 and/or Table 14, column "ABC High"; and at least one microRNA from Table 10, column "GCB miRNA list" and/or Table 14, column "GCB High".

[0072] When other methods indicate a particular identity for a B cell malignancy, in certain embodiments, microRNAs can be used to confirm that identification. Thus, for example, if a B cell malignancy is believed to be a Burkitt lymphoma, that identification can be confirmed by determining the expression level of one or more microRNAs listed in Table 10, column "BL miRNA list" and/or Table 14, column "BL High". Similarly, if a B cell malignancy is believed to be ABC DLBCL, that identification can be confirmed by determining the expression level of one or more microRNAs listed in Table 11 and/or Table 14, column "ABC High". If a B cell malignancy is believed to be GCB DLBCL, that identification can be confirmed by determining the expression level of one or more microRNAs listed in Table 10, column "GCB miRNA list" and/or Table 14, column "GCB High". If a B cell malignancy is believed to be chronic lymphocytic leukemia, that identification can be confirmed by determining the expression level of one or more microRNAs listed in Table 12 and/or Table 15, column "CLL High". If a B cell malignancy is believed to be Hodgkin's lymphoma, that identification can be confirmed by determining the expression level of one or more microRNAs listed in Table 13 and/or Table 15, column "HL High". If a B cell malignancy is believed to be follicular

lymphoma, that identification can be confirmed by determining the expression level of one or more microRNAs listed in Table 10, column "FL miRNA list" and/or Table 15, column "FL High".

[0073] In certain embodiments, when the identity of a B cell malignancy has been narrowed down to two B cell malignancies selected from Burkitt lymphoma, GCB DLBCL, ABC DLBCL, chronic lymphocytic leukemia, follicular lymphoma, and Hodgkin's lymphoma, the identity of the B cell malignancy can be determined by detecting one or more microRNAs from Tables 16 to 30.

[0074] As discussed in the Examples, the miRNAs described herein as differentially expressed in a B cell malignancy have been identified with high confidence, and thus, identification of one miRNA is adequate to perform the methods of identification and diagnosis disclosed herein. Accordingly, in various embodiments, the methods can comprise detecting at least one, at least two, at least five, at least 10, at least 20, at least 30, or at least 50 microRNAs in order to narrow down the identity of, or identify, a B cell malignancy.

[0075] As noted above, the treatment regimens and prognoses for the various B cell malignancies can differ significantly. Thus, determining the correct identity and/or origin of a B cell malignancy can be important for selecting an effective therapy and/or setting appropriate patient expectations.

[0076] B cell malignancy samples may be obtained and prepared using methods known in the art. One skilled in the art can select an appropriate method of obtaining a B cell malignancy sample according to various parameters, such as the age, size, medical history, and/or identity of the patient. One skilled in the art can select an appropriate method of preparing a B cell malignancy sample for analysis according to the B cell malignancy sample source, size, quality, and/or intended use. For example, in certain embodiments, a B cell malignancy sample is prepared in a manner that preserves microRNAs in the sample as much as practicable under the circumstances.

[0077] MicroRNAs can be detected using any method known in the art. Exemplary methods of detecting microRNAs include, but are not limited to, hybridization-based methods and amplification-based methods. Certain exemplary detection methods include, but are not limited to, arrays (including microarrays and bead-based arrays), in situ hybridization, Northern blotting, TaqMan probes, RT-PCR, real-time PCR, and direct sequencing. One skilled in the art can select a suitable detection method according to the sample source, size, quality, and/or particular application.

[0078] In certain embodiments, real-time PCR is employed to determine the expression level of a microRNA. In some embodiments a miRNA is considered present in a subpopulation if the cycling time (CT) is less than 36 in all three biological replicates, and a CT greater than 36 is undetected.

[0079] In certain embodiments, the expression level of a microRNA in a sample is determined relative to a control sample. A control sample may be selected, in various embodiments, because it is expected to have either high or low expression of the microRNA.

[0080] In certain embodiments, the expression level of a microRNA may be normalized to the expression level of a polynucleotide that is expected to be expressed at similar levels in several different cell types and/or at constant levels in the cell type being analyzed.

[0081] In certain embodiments, an identified miRNA from Tables 7-35 is used to distinguish one of the six exemplified B cell malignancies from the other malignancies. A “high” and a “low” in Tables 10 to 13 refer to at least a 2-fold difference in the expression of the identified miRNA when one lymphoma is compared to other lymphomas and benign lymph nodes.

[0082] In embodiments, mRNA levels can be profiled by using a microarray. In some embodiments, array elements with median signal intensities of less than 7 log₂ units across samples are removed from analysis. In embodiments, a gene is considered for further analysis if it is on-average 2-fold or higher differentially expressed in a binary comparison of B cell subsets and expressed in at least one of the two B cell subsets being compared.

[0083] In an embodiment, the level of at least one miRNA is measured by reverse transcribing RNA from a test sample obtained from a subject to provide a set of target oligodeoxynucleotides, hybridizing the target oligodeoxynucleotides to one or more miRNA-specific probe oligonucleotides (e.g., a microarray that comprises miRNA-specific probe oligonucleotides) to provide a hybridization profile for the test sample, and comparing the test sample hybridization profile to a hybridization profile generated from a control sample. An alteration in the signal of at least one miRNA in the test sample relative to the control sample is indicative of the subject either having, or being at risk for developing, a B-cell malignancy. In an embodiment, the signal of at least one miRNA is upregulated, relative to the signal generated from the control sample. In another embodiment, the signal of at least one miRNA is down-regulated, relative to the signal generated from the control sample. In some embodiments, the microarray comprises miRNA-specific probe oligonucleotides for a substantial portion of all known human miRNAs. In a further embodiment, the microarray comprises miRNA-specific probe oligonucleotides for one or more miRNAs selected from the group consisting of SEQ ID NOs: 763-1350, or 1565 and any combination thereof.

[0084] The microarray can be prepared from gene-specific oligonucleotide probes generated from known miRNA sequences. The array may contain two different oligonucleotide probes for each miRNA, one containing the active, mature sequence and the other being specific for the precursor of the miRNA. The array may also contain controls, such as one or more mouse sequences differing from human orthologs by only a few bases, which can serve as controls for hybridization stringency conditions. tRNAs and other RNAs (e.g., rRNAs, mRNAs) from both species may also be printed on the microchip, providing an internal, relatively stable, positive control for specific hybridization. One or more appropriate controls for non-specific hybridization may also be included on the microchip. For this purpose, sequences are selected based upon the absence of any homology with any known miRNAs.

[0085] The microarray may be fabricated using techniques known in the art. For example, probe oligonucleotides of an appropriate length, e.g., 40 nucleotides, are 5'-amine modified at position C6 and printed using commercially available microarray systems. Labeled cDNA corresponding to the target RNA sequence(s) is prepared by reverse transcribing the target RNA with labeled primer. Following first strand synthesis, the RNA/DNA hybrids are denatured to degrade the RNA templates. The labeled target cDNAs thus prepared are then hybridized to the microarray chip under typical hybridizing conditions. At positions on the array where the immobilized probe DNA recognizes a complementary target cDNA in the sample, hybridization occurs. The labeled target cDNA marks the exact position on the array where binding occurs, allowing automatic detection and quantification. The output consists of a list of hybridization events, indicating the relative abundance of specific cDNA sequences, and therefore the relative abundance of the corresponding complementary miRNAs, in the patient sample.

[0086] In an aspect, the disclosure relates to kits. Such kits can be used in methods of identifying a miRNA or mRNA described herein; an expression level or expression pattern of one or more miRNA(s) or mRNA(s) described herein; and/or identifying a B-cell malignancy. In some embodiments the kit can provide a diagnosis of a B-cell type and or a B-cell malignancy. In some embodiments the kit can differentiate one B-cell malignancy from other B-cell malignancies (e.g., ABC-DLBCL from GBC-DLBCL), and can provide information useful to a medical professional regarding a preferred course of therapeutic treatment. Suitably, a kit can comprise an isolated nucleic acid molecule or a plurality of isolated nucleic acid molecules as described herein (e.g., a sequence complementary to any of the miRNAs disclosed in the Tables). In embodiments, the isolated nucleic acid molecule can comprise a sequence of one or more RT-PCR target sequences, primers directed thereto, or a sequence

complementary thereto. The kit can also include adapter nucleic acid molecules (e.g., universal adapter molecules for attachment to expressed miRNAs/mRNAs for reverse transcription and amplification); appropriate buffer systems and reagents, detectable labels, an energy source (e.g., ATP), and other agents and components that can be used in performing analysis of miRNA expression (e.g., in RT-PCR, deep sequencing, or microarray-based methods). Kits also include instructions for use.

[0087] It will be understood that any numerical value recited herein includes all values from the lower value to the upper value. For example, if a concentration range is stated as 1% to 50%, it is intended that values such as 2% to 40%, 10% to 30%, or 1% to 3%, etc., are expressly enumerated in this specification. These are only examples of what is specifically intended, and all possible combinations of numerical values between the lowest value and the highest value enumerated are to be considered to be expressly stated in this application.

[0088] In an aspect, the disclosure provides a DNA library comprising one or more miRNA sequences from Tables 4-5, or 6-33. In a related aspect, the disclosure provides a method for generating such a DNA library. In an embodiment the library comprises a cDNA library that includes sequences derived from a sample of the miRNAs or, in addition or alternatively, the mRNA purified from a particular source such as, for example, a collection of cells, a particular tissue, or an entire organism. In embodiments, the source of the cDNA library is a B cell, such as a B cell in any stage (e.g., naïve, germinal center, memory, activated, or plasma, etc.) or a B cell malignancy (e.g., mantle cell lymphoma, follicular lymphoma, Hodgkin's lymphoma, Burkitt lymphoma, germinal center B-cell like diffuse large B cell lymphoma (DLBCL), chronic lymphocytic leukemia, small lymphocytic lymphoma, lymphoplasmacytic lymphoma, multiple myeloma, and activated B-cell like DLBCL). Typically, the isolated miRNA (or mRNA) is converted to a DNA template by reverse transcription, and comprises the cDNA version of the expressed RNA (e.g., miRNA or mRNA). Thus, a library can represent the cDNA version of the active "transcriptome" in a particular source under the physiological, developmental, or environmental conditions that existed when the miRNA/mRNA was purified.

[0089] In an embodiment, the library comprises a miRNA sequence described in Tables 4-5; 7-33. In embodiments, the library comprises at least one of SEQ ID NOs 763-1350 or 1565, and any combination thereof. In an embodiment, the library comprises a collection of miRNA sequences comprising SEQ ID NOs 763-1350 or 1565. In embodiments the library can be used to identify and/or differentiate a B-cell malignancy from other B-cell malignancies. In

such embodiments, the library comprises at least one miRNA sequence selected from those listed in any of Tables 4 or 7-35.

[0090] As used herein, a "library" is a collection of DNA sequences that is stored and propagated in a population of microorganisms through standard molecular cloning processes. A DNA library can be of any type such as, for example, a cDNA library (formed from reverse-transcribed RNA) or a genomic library (formed from genomic DNA). The DNA library can be used in any routine application or technique known in the art (e.g., gene discovery; cloning of full-length cDNAs to identify/study gene function; miRNA/mRNA expression in different cells or tissues; splice variants in different cells or tissues) and, in some embodiments, can depend on the source of the original DNA fragments. In embodiments, the library can be used to isolate, characterize, and/or quantify the actively expressed miRNA in a population of cells such as, for example, B-cells or B-cell malignancies. In some embodiments, the library can be used to study miRNA-protein interactions or miRNA-based regulation of protein expression or activity.

[0091] Any known method of library preparation can be used to make the library described herein, including the methods described in the detailed description and non-limiting Examples. Further general techniques can be based on the methods and techniques known in the art, (see, e.g., RNA Methodologies: A Laboratory Guide for Isolation and Characterization (R.E. Farrell, Academic Press, 1998); cDNA Library Protocols (Cowell & Austin, eds., Humana Press; Functional Genomics (Hunt & Livesey, eds., 2000); and the Annual Review of Genomics and Human Genetics (E. Lander, ed., yearly publications by Annual Reviews). Suitably, the nucleotide sequences of interest in a library are preserved as inserts in a plasmid or the genome of a bacteriophage that has been used to infect bacterial cells. There are differences in the cloning vectors and techniques used in library preparation, but in general each DNA fragment is uniquely inserted into a cloning vector and the pool of recombinant DNA molecules is then transferred into a population of bacteria or yeast such that each organism contains on average one construct (vector + insert). The DNA molecules are copied and propagated along with the population of organisms in culture (thus, effectively, "cloned"). Accordingly, in some embodiments, the term "library" can refer to a population of organisms, each of which carries a DNA molecule inserted into a cloning vector, or alternatively to the collection of all of the cloned vector molecules.

[0092] An "increased level" of expression, as used herein, refers to a level of expression that is at least 2-fold greater than the level of expression in a control cell type or tissue. In various embodiments, the level of expression is at least 2.5-fold, at least 3-fold, at least 5-fold, or at

least 10-fold, greater than the level of expression in a control cell. Exemplary control cells and tissues include, but are not limited to, normal cells, benign lymph nodes, and other B cell malignancies. In certain embodiments, benign lymph nodes are used as a control tissue. Such benign lymph node tissue contains a variety of cell types.

[0093] A “decreased level” of expression, as used herein, refers to a level of expression that is less than 50% of the level of expression in a control cell.

[0094] The term “differentially expressed” or “differential expression” relates to a difference in the observed or detected level of expression of a biomolecule such as, for example, nucleic acids (e.g., a polynucleotide, mRNA, miRNA, etc.) or amino acid sequence (e.g., protein, polypeptide, etc.) in a test sample relative to the observed or detected level of expression of the same biomolecule in a control sample or other reference (e.g., a previously established reference level). The difference in expression can be either an increase or a decrease in the expression of the biomolecule in the test sample relative to the control sample.

[0095] The Examples that follow provide further illustration of certain aspects and embodiments described in the foregoing description. These illustrative Examples should not be interpreted as limiting the scope of the appended claims.

EXAMPLES

Example 1: Materials and Methods

Patient sample processing

[0096] B cell populations were obtained from young patients undergoing routine tonsillectomy using a protocol approved by the Clinical Center at the National Institutes of Health. Patient tonsils were disaggregated and separated by Ficoll. The mononuclear cell layer was harvested, washed in PBS, and resuspended in ACK lysing buffer to remove small numbers of red blood cells. After a wash and resuspension with 10 ml of PBS with 10% Bovine Serum Albumin, cells were counted and 200 million were stained with fluorochrome-tagged monoclonal antibodies to CD19, IgD, CD38 and CD27. The specific monoclonal antibodies employed were anti-CD19-PE-Cy5.5, anti-IgD-FITC, anti-CD27-PE, and anti-CD38-APC, all from BD Biosciences and BD Pharmingen (San Jose California). Cells were sorted using the MoFlo Cell sorter (Dako Cytomation, Colorado Springs, CO) into naive B cells (CD19+IgD+CD27⁻CD38⁺), germinal center B cells (CD19+IgD+CD38⁺⁺), memory B cells (CD19+IgD⁻CD27⁺CD38^{dim}) and plasma cells (CD19^{dim}IgD⁻CD27⁺⁺CD38⁺⁺⁺). Three replicates of each B cell subset were obtained from separate patients. The sample purity was verified by FACS and found to be over 90% in all cases.

[0097] Tumor specimens were obtained from patients who were examined under a protocol approved by the Duke University Medical Center Institutional Review Board. The pathologic diagnosis of the samples was verified prior to analysis. Samples from patients with diffuse large B cell lymphoma were further subclassified as described previously. See Hans et al. (2004) *Blood* 103: 275-282. Chronic lymphocytic leukemia samples were processed and purified as described previously. See Volkheimer et al. (2007) *Blood* 109: 1559-1567. Total RNA was extracted using the phenol-chloroform method to preserve miRNAs, using Ambion reagents.

microRNA profiling using multiplexed real-time PCR

[0098] MiRNA expression profiling was conducted using the Applied Biosystems 384-well multiplexed real-time PCR assay using 400ng of total RNA. Eight reactions, each containing 50ng of RNA and a multiplex looped primer pool with endogenous small nucleolar (sno)-RNA controls, were used to reverse-transcribe the miRNAs in parallel fashion. Each completed reaction was loaded onto the 384-well plate per manufacturer's instructions, and real-time PCR was run on the ABI 7900HT Prism. For each 384-well plate, we used the automatically determined cycle-threshold (CT) using the SDS 2.2.1 software (Applied Biosystems). Consistent with manufacturer recommendations, we considered CT greater than 36 as undetected. A miRNA was considered to be present in a subpopulation if the CT was less than 36 in all three biological replicates. The probes deemed to be present were normalized to the average expression of a sno-RNA control. The expression values were calculated as $2^{-\Delta CT}$, then median centered to 500 and log2-transformed.

Gene expression (mRNA) profiling using microarrays

[0099] Gene expression profiling and normalization were performed using methods identical to those we have described previously. See Dave et al. (2004) *N. Engl. J. Med.* 351: 2159-2169. Array elements with median signal intensities of less than 7 log2 units across the samples were removed from analysis, in order to exclude poorly measured genes and genes not appreciably expressed in the samples. Genes that were on-average 2-fold or higher differentially expressed in a binary comparison of B cell subsets, and appreciably expressed in at least one of the 2 B cell subsets being compared, were selected for further analysis as described below. The data have been deposited in the publicly available Gene Expression Omnibus database (GSE12366).

MiRNA profiling using microarray

[00100] MiRNA expression profiling from human B cell malignancies was conducted using up to 1 µg of total RNA from sample and reference (normal lymph node), which were

labeled with Cy3 or Cy5 fluorescent dyes, using the miRNA/LNA labeling kit (Exiqon, Denmark). The fluorescently labeled samples were combined and hybridized to a miRNA microarray (v.10.0, Exiqon, Denmark), in a nitrogen atmosphere. The micro array slides were scanned with GenePix 4100 Scanner. The quantified signals were normalized using the global Lowess algorithm, using Genespring (Agilent) software. The intensity values for multiple spots were averaged and the normalized values were log2-transformed. Missing values were replaced with the lowest value for analysis.

MiRNA target prediction

[00101] Annotated genes on the U133plus 2.0 array were matched to the miRNA target list downloaded from TargetScan (www.targetscan.org). For the purpose of this study, a target gene was defined by the presence of a seed sequence match (nucleotides 2-8) and conservation of the seed sequence and 3'UTR in humans, dog, rat, mouse and chicken. Additional conservation was examined in miRNA target genes selected for experimental validation. The distribution of the mRNA expression for these genes was plotted as a density plot using the Splus statistical software (Insightful Corporation). The difference in distribution between the B cell subsets was calculated using a two-sample, 1-sided Kolmogorov-Smirnov test to examine the hypothesis that being a miRNA target conferred repression in the appropriate population (consistent with the known biology of miRNA effects).

[00102] The 3'UTRs of LM02, MYBL1 and PRDM1 were aligned using Blastz alignment of Human, Chimp, Mouse, Rat, Dog, Chicken, Frog (Xenopus) and Zebrafish, and were displayed using the UCSC genome browser. The conservation of miR-223 seed sequence and the 3'UTRs of LM02 and MYBL1, as well as that of the miR-30 family and miR-9 on PRDM1, were thus verified.

Western blot

[00103] RIPA Lysis buffer (1x phosphate-buffered saline [PBS], 1 % Nonidet P-40, 0.5% sodium deoxycholate, 0.1 % SDS, 10 mM phenylmethylsulfonyl fluoride, 1 µg/mL aprotinin, and 100 mM sodium orthovanadate) was added to 750,000 cells and incubated on ice for 30 minutes. The mixture was spun down and the supernatant was transferred to a new tube as the whole cell extract. A total of 20 µg of cell lysate was separated on a 4 - 18 % Tris-Bis NuPAGE gel (Invitrogen) and transferred using the iBlot transfer device (Invitrogen) program 3 for 7 minutes (LM02 detection) or program 2 for 6 minutes (PRDM1). The blots were probed using 1:200 mouse-anti-LM02 (Santa Cruz Biotechnologies SC-65736), 1:750 mouse-anti-Blimp-1 (Santa Cruz Biotechnologies SC-66015) or 1:5000 goat-anti-B-actin (Santa Cruz Biotechnologies SC-47778) for 1 hour at room temperature. The antibodies were detected

using 1:10,000 goat-anti-mouse horseradish peroxidase conjugated antibodies (Santa Cruz Biotechnologies). Western Blotting Luminol Reagent (Santa Cruz Biotechnologies) was used to visualize the bands corresponding to each antibody.

Single miRNA/mRNA expression using real-time polymerase chain reaction (RT - PCR)

[00104] With 10ng of RNA per reaction, miRNAs of interest were reverse-transcribed with ABI individual stem-loop primers designed to detect only mature miRNA, and measured by Taqman real-time PCR normalized to the small nucleolar RNA, RNU48. In order to assess mRNA expression using RT-PCR, 1µg of RNA was reverse-transcribed with the ABI High Capacity cDNA Reverse Transcription kit. Gene expression was measured with exon-spanning Taqman probes, and normalized to beta-2 micro globulin expression.

Cell culture

[00105] BJAB and H929 were cultured in RPMI (Gibco) supplemented with 10% fetal bovine serum, and U266 was cultured in RPMI supplemented with 15% fetal bovine serum. 293T cells were grown in DMEM media (Gibco) with 10% FBS. All cell lines were grown in 37°C humidified cell culture incubators with CO₂ maintained at 5%.

MiRNA functional analysis

MicroRNA transfection

[00106] miRNAs of interest were over-expressed in cell lines of interest by transfecting the appropriate miRNA precursors (Ambion) at 100 nanomoles using Amaxa's Nucleofector system. In particular, BJAB was transfected with Nucleofector solution T, program T-016, U266 with Nucleofector C, program X-005, and H929 with Nucleofector V, program T-001. 1.5 million cells were used per transfection and mixed with appropriate miRNA precursors (Ambion) for a concentration of 100 nM.

Statistical Analysis

Identifying differentially expressed miRNA and mRNA

[00107] MiRNAs were considered to be differentially expressed if the mean signal was changed at least 2-fold and a false discovery rate (q) was less than 5% using Significance Analysis of Microarrays (SAM) with 1000 permutations. See Tusher et al. *Proc Natl Acad Sci U S A*. 2001;98:5116-5121.

[00108] Differentially expressed genes (mRNA) in Naive versus Germinal Center, Germinal Center versus Plasma Cells, and Germinal Center versus Memory Cells comparisons were identified using SAM. Genes that were 2-fold differentially expressed at a false discovery

rate (q) less than 1% with 1000 permutations were identified as significantly differentially expressed.

Transcription factors and miRNA target genes

[00109] Transcription factors were identified based on the gene ontology (GO search term “transcription factor”) and matched to the probes of the Affymetrix U133plus 2.0 microarray. Of the total of 938 transcription factor genes thus identified, we selected 364 genes that were differentially expressed in at least one of the B cell stage transitions. We evaluated the breakdown of the differentially expressed transcription factors among miRNA targets versus non targets. The p-values were computed using a chi-square test separately in each B cell stage-transition.

B cell malignancy sample classification

[00110] The top 50 most differentially expressed miRNAs ($P < 0.01$) in each pair-wise B cell malignancy type comparison were chosen as the initial predictor. Singular value decomposition was applied to reduce the list to 20 most informative miRNAs in each pair-wise comparison. See West et al. *Proc Natl Acad Sci U S A.* 2001; 98:11462-11467. A Bayesian logistic regression was performed in Matlab (Mathworks) using the 20-predictor miRNAs for each pair-wise comparison. Each sample was tested using the microRNA-based predictor in a leave-one-out fashion to determine the accuracy of each prediction. For a sample to be classified as a particular B cell malignancy (or normal) type, it had to be predicted as such in every pair-wise comparison.

Normal B cell stage classification of B cell malignancies

[00111] We constructed a Bayesian predictor to distinguish normal naive from germinal center B cells based on the 32 miRNAs depicted in Figure 1D. We then applied the predictor without optimization to the microarray data generated for GCB DLCL, Burkitt lymphoma and chronic lymphocytic leukemia to render a Bayesian prediction of lineage; i.e. naive versus germinal center B cell.

Western Blot Quantitative Analysis

[00112] Western blot scans were quantified using NIH ImageJ software. For each experiment, the ratios of protein of interest (LM02, PRDMI) to Actin were determined and mean centered to 100 across the experiment. The average and standard deviation of these values across the three experiments were calculated and displayed relative to the scrambled control expression.

Luciferase Indicator Assay Quantitative Analysis

[00113] Firefly luciferase reporter constructs were created in the pL/SV40/GL3 vector for the LMO2 3'UTR and the LMO2 3'UTR with the predicted miR-223 binding site mutated, as described below. Mature microRNA expression of a pL/CMV/eGFP vector coding for pri-miR-223 from the 3'UTR of EGFP of the vector was confirmed by Taqman-real time PCR in transfected 293T cells. gl3 activity was normalized in dual luciferase assays to pL/SV40/RLuc, with which it was cotransfected. The PRDMI 3'UTR was also cloned into the pL/SV40/GL3 vector. microRNA expression vectors and their respective seed sequence mutants were created for miR-9-2, miR-30b, and miR-30d.

LMO2

[00114] The LMO2 3'UTR was PCR-amplified from BJAB cDNA using primers 1 and 2 (SEQ ID NOs: 1 and 2, respectively) and ligated into the XhoI and XbaI sites of the previously described lentiviral vector pL/SV40/GL3, which expresses firefly luciferase. *See Tusher et al. Proc Natl Acad Sci U S A. 2001; 98:5116-5121.* As a control, an LMO2 3'UTR mutant was created using mutant PCR primers 3 and 4 and then outer primers 1 and 2. The resulting fragment was also placed into the XhoI and XbaI sites of pL/SV40/GL3. In this LMO2 3'UTR mutant, the seed match predicted to bind to nucleotides 2-8 of miR-223 is converted from 5'AACUGAC 3' to 5'AACAGUC 3'. To create a miR-223 expression vector, a ~350 nucleotide-long fragment of pri-miR-223, encompassing the pre-miRNA stem loop in its middle, was PCR-amplified from genomic BJAB DNA with primers 6 and 7 (SEQ ID NOs. 6 and 7) and ligated into the XhoI and XbaI sites of the pL/CMV/eGFP vector. This pL/CMV/eGFP vector was generated by ligating a fragment containing the CMV promoter and the EGFP ORF into the BamHI and XhoI sites of the previously described lentiviral backbone pL. *See Tusher et al. Proc Natl Acad Sci U S A. 2001; 98:5116-5121.* The expression of miR-223 from the 3'UTR of EGFP in the resulting vector was confirmed by Taqman real time PCR in transfected 293T cells.

[00115] For luciferase indicator assays, 293T cells plated in 24 well plates were transfected using FUGENE6 as follows:

Table 1: Luciferase indicator assay compositions

2.5ng pL/SV40/GL3 2.5ng pL/SV40/RLuc 0.4µg pL/CMV/eGFP/miR-223	2.5ng pL/SV40/GL3/LMO2 UTR 2.5ng pL/SV40/RLuc 0.4µg pL/CMV/eGFP/miR-223	2.5ng pL/SV40/GL3/ LMO2 seed mut 2.5ng pL/SV40/RLuc 0.4µg pL/CMV/eGFP/miR-223
--	---	---

2.5ng pL/SV40/GL3 2.5ng pL/SV40/RLuc 0.4µg pL/CMV/eGFP	2.5ng pL/SV40/GL3/LMO2 UTR 2.5ng pL/SV40/RLuc 0.4µg pL/CMV/eGFP	2.5ng pL/SV40/GL3/LMO2 seed mut 2.5ng pL/SV40/RLuc 0.4µg pL/CMV/eGFP
--	--	---

[00116] Reporter expression was evaluated by dual luciferase assays (Promega) 48 hours post-transfection. Firefly Luciferase (GL3) to internal control Renilla Luciferase (RLuc) ratios from 293T cells transfected with pL/CMV/eGFP/miR-223 were divided by those obtained from 293T transfected with the pL/CMV/eGFP vector control. The average and standard deviation were taken across five experiments for the pL/SV40/gl3 empty, LM02, and LM02 mutant vectors.

[00117] Firefly Luciferase (GL3) activity readings of the PRDM1 3'UTR construct were divided by internal control Renilla Luciferase (RLuc) activity readings. The average and standard deviation of these ratios across three experiments were calculated and scaled relative to the empty vector (pL/CMV/eGFP) transfection.

Table 2: LM02 primer sequences

Primer SEQ ID	description	Sequence (5'→3')
1543	LM02 3'UTR, FW	ATATCTCGAGGCCCGAGTCCCCGGGCATCTTTGG
1544	LM02 3'UTR, REV	ATATATCTAGACTACACACGACAAATACTTTG
1545	LM02 3'UTR seed mutant, FW	CAGCCCATCCATAGTAACAGTCATGATTAGCAGAAGAAAGG
1546	LM02 3'UTR seed mutant, REV	CCTTTCTTCTGCTAATCATGACTGTTACTATGGATGGGCTG
1547	pri-mir-223, FW	ATATCTCGAGGGTCACATCTCCCAGGAAGATC
1548	pri-mir-223, REV	ATATATCTAGAAGCACTCTCATGGTGTGTGTAG

PRDM1

[00118] The PRDM1 3'UTR was PCR-amplified from BJAB genomic DNA in two reactions using primer pairs 7 and 8 in one reaction, and 9 and 10 in another (SEQ ID NOs: 7 to 10, respectively). The two fragments were then ligated together into the XhoI and NotI sites of pL/SV40/GL3 to generate the entire PRDM1 3'UTR. microRNA expression vectors were created as described above for mir-9-2, mir-30b, and mir-30d with the primers listed below. Again, over-expression from the 3'UTR of EGFP in the resulting vector was confirmed by Taqman real-time PCR in transfected 293T cells. For the PRDM1 luciferase assays, we used the sequences listed below to PCR-mutate the seed sequence of the microRNA expression vectors rather than the PRDM1 3'UTR, which had numerous seed sequence binding sites.

Table 3: PRDM1 primer sequences

Primer SEQ ID:	description	sequence
1549	PRDM1 3'UTR piece 1, FW	AGAGACTCGAGGATTTTCAGAAAACACTTATTT

1550	PRDM1 3'UTR piece 1, REV	TTGCTTCTCTAGAGGAGAAAC
1551	PRDM1 3'UTR piece 2, FW	GTTTCTCCTCTAGAGAAGCAA
1552	PRDM1 3'UTR piece 2, REV	AGAGAGCGGCCGCAGGGGAGAGACAAATTGCATTG
1553	pri-mir-9-2, FW	AGAGACTCGAGATAAAAGGAGGAATCTTAAG
1554	pri-mir-9-2, REV	AGAGAGCGGCCGCGAAAAAACAACAAAAACAA
1555	pri-mir-30b, FW	AGAGAGCGGCCGCCCGATTGAGTCTTGCCCTCAT
1556	pri-mir-30b, REV	AGAGAGAATTCAATGGTCTCACATTTCCAAC
1557	pri-mir-30d, FW	AGAGAGCGGCCGCATGTACAGCTATTGTTTCAG
1558	pri-mir-30d, REV	AGAGAGAATTTCGAGTAAAGAATGCAGCTA
1559	pri-mir-9-2 seed mutant, FW	GGAAGCGAGTTGTTATCTATGCTTATCTAGCTGTATGAGT
1560	pri-mir-9-2 seed mutant, REV	ACTCATACAGCTAGATAAGCATAGATAACAACCTCGCTTCC
1561	pri-mir-30b seed mutant, FW	ACCAAGTTTCAGTTCATGTTAAGATCCTACACTCAGCTGT
1562	pri-mir-30b seed mutant, REV	ACAGCTGAGTGTAGGATCTTAACATGAACTGAACTTGGT
1563	pri-mir-30d seed mutant, FW	CAGAAAGTCTGTTGTTGTTAAGATCCCCGACTGGAAGCTG
1564	pri-mir-30d seed mutant, REV	CAGCTTCCAGTCGGGGATCTTAACAACAACAGACTTTCTG

[00119] Luciferase assays were carried out in a manner similar to those described for LMO2.

IgVH mutation Status of Chronic Lymphocytic Leukemia Samples

[00120] IgVH mutation status was determined as described in Volkheimer et al. (*Blood*. 2007; 109:1559-1567) using genomic DNA. In brief, genomic DNA was isolated from purified CLL cells and isolated using the GenElute Mammalian DNA extraction Kit from Sigma (St. Louis, MO) according to the manufacturer's instructions. DNA was amplified using nested PCR primers. PCR products were electrophoresed, purified, and sequenced using an automated DNA sequencer (Applied Biosystems, Foster City, CA) with the BigDye Terminator kit (Perkin Elmer, Boston, MA). Forward and reverse sequences were aligned into a single resolved sequence using Sequencher 4.1 software (Gene Codes Corporation, Ann Arbor, MI), and then aligned with germline sequences derived from DNA Plot on the V BASE directory website (<http://vbase.mrc-cpe.cam.ac.uk/>). The percent sequence identity was calculated by dividing the number of mutations from FR1 to FR3 by the total number of nucleotides in this region. Samples were considered somatically mutated if they had greater than 2% mutations in this region.

Example 2: Mature B cell Stages Display Characteristic Patterns of MicroRNA Expression

[00121] Mature B cell subsets can be defined by the expression of surface CD19, IgD, CD38, and CD27, and were obtained by fluorescence activated cell sorting of tonsils from young individuals undergoing routine tonsillectomy. See Figures 1B and 1C. Cells were previously gated on CD19 positive cells. Naive and memory B cells were distinguished from germinal center and plasma cells based on surface CD38 and IgD expression.

[00122] To determine whether mature B cell subsets had unique patterns of microRNA (miRNA) expression, we used a 384-well multiplexed real time polymerase chain reaction (RT-PCR) assay (Applied Biosystems) that allowed measurement of all 365 miRNAs in miRBase 9.2. *See* Chen et al. *Nucleic Acids Res.* 2005; 33:e179; and He et al. *Nature.* 2007; 447:1130-1134. We detected a total of 113 unique miRNAs in the B cell populations. *See* Table 4. This detection frequency compares favorably to the identification of 71 unique miRNAs (45 miRNAs with more than one clone) through the examination of 3101 sequences cloned from unselected CD19-positive mature B cells. *See* Landgraf et al. *Cell.* 2007; 129:1401-1414. We identified differentially expressed miRNAs in mature B cell subsets using a false discovery rate of less than 5%. *See* Figures 1D, 1F, and 1H. The complete list of assayed miRNAs found to be expressed in the B cell populations is shown in Tables 4 and 5.

[00123] In Table 4, normalized expression values for B-cell subsets are shown, along with significance analysis of microarrays q values. Empty microRNA expression cells indicate below-threshold values, defined as RT-QPCR Ct values greater than 36 or undetected. SAM q values greater than 5 were considered non-significant and not displayed.

Table 4: MicroRNAs detected in at least one B-cell subset

	Naïve average	Germinal Center average	Plasma Cell average	Memory average	qNaive vs Germinal Center	qGerminal Center vs Plasma Cell	qGerminal Center vs Memory
hsa-let-7a	11.7	9.2		11.2			1.4
hsa-let-7b	10.3	9.0	7.7	11.3			0.0
hsa-let-7c	7.3			7.2			
hsa-let-7d	9.0	9.0		10.0			
hsa-let-7f	10.3	7.6	8.4	10.2			0.0
hsa-let-7g	13.1	10.3	10.5	14.0	0.0		0.0
hsa-miR-100				7.4			
hsa-miR-101	8.4			10.0			
hsa-miR-103	9.7	11.4	9.8	10.8	0.0	0.0	
hsa-miR-106b	11.7	12.5	11.6	12.7			
hsa-miR-125a			6.7	8.3			
hsa-miR-125b		6.3		7.3			
hsa-miR-130b	7.8	9.8	8.6	10.2	3.6	4.5	
hsa-miR-132		7.5		8.9			
hsa-miR-133b	7.7	7.7	7.2	7.3			
hsa-miR-140	10.8	12.0	11.1	12.0	4.7		
hsa-miR-141	7.0			6.2			
hsa-miR-142-3p	16.9	17.0	15.3	18.0		1.1	
hsa-miR-142-5p	11.7	11.0	9.8	13.4			2.1
hsa-miR-146a	10.1	14.0	14.0	14.6	0.0		
hsa-miR-146b	9.2	9.2	8.1	10.5			2.1
hsa-miR-148a	6.7	9.4	11.9	9.0	0.0		
hsa-miR-148b	6.4			8.5			
hsa-miR-151	8.2	9.6	6.6	9.0	1.5	0.0	
hsa-miR-152	6.4		9.7	6.6			
hsa-miR-155	14.2	14.6	15.0	15.6			
hsa-miR-15a	10.2	10.1	7.8	10.8		2.0	
hsa-miR-15b	11.2	14.0	12.6	12.9	0.0	2.8	
hsa-miR-16	16.7	17.3	17.1	17.1			
hsa-miR-17-3p				9.1			
hsa-miR-17-5p	8.8	11.5	8.9	9.4	0.0	0.0	0.0
hsa-miR-181b	9.0	11.7	10.8	9.3	0.0		0.0
hsa-miR-181d	8.2	10.6	8.5	9.0	0.0	1.1	
hsa-miR-182			8.7	8.7			
hsa-miR-186	8.8	9.2	8.7	9.7			
hsa-miR-18a	5.7	8.9	6.8	7.4	0.0	0.0	
hsa-miR-191	11.9	12.7	12.4	13.3			
hsa-miR-192	9.1	9.0	8.8	10.1			
hsa-miR-193b				6.6			
hsa-miR-194	6.8	7.4	4.9	9.5		2.0	4.7
hsa-miR-195	10.3	8.7	8.8	9.2			
hsa-miR-197	9.7	10.5	8.7	11.0		0.0	
hsa-miR-199a*				7.0			
hsa-miR-19a	9.7	12.8	11.9	11.1	0.0		
hsa-miR-19b	14.0	15.6	14.9	15.0	0.8		
hsa-miR-200a	6.5			6.8			
hsa-miR-200b				7.5			
hsa-miR-200c	9.0	9.6		9.7			

hsa-miR-203	7.9			7.6			
hsa-miR-20a	12.5	14.9	12.2	13.8	0.0	0.0	
hsa-miR-20b	8.4	11.0	8.0	8.5	0.0	1.1	0.0
hsa-miR-21	12.6	13.0	11.2	15.1		2.8	2.1
hsa-miR-210	9.2	11.1	10.7	10.2	0.8		
hsa-miR-214				7.6			
hsa-miR-22			8.3	7.4			
hsa-miR-221				6.9			
hsa-miR-222	11.4	11.6	7.8	12.7		0.0	4.7
hsa-miR-223	13.7	10.4	9.6	14.6	0.0		0.0
hsa-miR-23a				8.7			
hsa-miR-23b				6.2			
hsa-miR-24	11.7	11.8	12.8	13.4			2.1
hsa-miR-25	9.7	10.8	8.8	11.2		2.8	
hsa-miR-26a	14.7	13.6	14.2	16.3			0.0
hsa-miR-26b	12.6	12.1	12.0	14.1			3.4
hsa-miR-27a		6.5		11.1			0.0
hsa-miR-27b				7.2			
hsa-miR-28	9.4	13.3	8.4	10.3	0.0	0.0	0.0
hsa-miR-296	6.9	8.1	6.6	7.9	0.0	2.0	
hsa-miR-29a	13.4	11.7	13.5	15.0			0.0
hsa-miR-29c	11.2	8.7	12.3	13.3	1.5	2.6	0.0
hsa-miR-301	6.0	9.6	7.7	7.9	0.0	0.0	
hsa-miR-30a-3p		8.2					
hsa-miR-30a-5p	11.9	12.6	11.3	13.0		2.0	
hsa-miR-30b	11.7	12.6	11.2	13.0		2.8	
hsa-miR-30c	13.0	13.9	12.7	14.3		4.5	
hsa-miR-30d	10.8	11.9	10.1	12.1	3.8	0.0	
hsa-miR-30e-3p	8.3	9.0	6.8	9.9		0.0	
hsa-miR-30e-5p	12.5	8.1	10.2	14.8			0.0
hsa-miR-31				9.0			
hsa-miR-32	8.4		7.0	10.5			
hsa-miR-320	10.1	8.2	10.3	10.5	1.5	2.6	0.0
hsa-miR-324-3p	8.8	9.9	9.0	9.5			
hsa-miR-324-5p	8.0			7.8			
hsa-miR-328	8.1	8.6	7.4	8.7		2.8	
hsa-miR-331	9.4	12.6	12.0	10.8	0.0		2.6
hsa-miR-335	6.3			6.9			
hsa-miR-339	7.3		5.7	8.9			
hsa-miR-342	12.7	12.5	10.6	13.1		0.0	
hsa-miR-345	6.8	7.1	7.8	8.6			3.4
hsa-miR-361				8.3			
hsa-miR-365	6.0	7.8	8.3	8.4	0.0		
hsa-miR-374	8.0	8.9	10.4	9.8			
hsa-miR-423	8.0	9.7	7.6	8.7	0.0	0.0	
hsa-miR-425				6.9			
hsa-miR-425-5p	8.7	11.6	9.7	10.2	0.0	0.0	
hsa-miR-484	11.5	12.3	12.9	12.0			
hsa-miR-486	7.0	8.8	9.9	9.6	3.8		
hsa-miR-532	7.0			7.8			

hsa-miR-545			5.5	6.3			
hsa-miR-572		7.7		6.8			
hsa-miR-629	6.7	7.3	7.2	9.0			1.4
hsa-miR-646		6.0		7.3			
hsa-miR-650		8.8	11.4	8.0			
hsa-miR-659		7.6	6.0	6.8			
hsa-miR-660	9.5		8.6	10.1			
hsa-miR-7	6.1			5.8			
hsa-miR-9		7.8	6.8	6.2		2.8	
hsa-miR-9*			6.4	6.5			
hsa-miR-92	14.5	15.8	14.2	15.5	3.6	0.0	
hsa-miR-93	11.5	14.6	10.5	12.3	0.0	0.0	0.0
hsa-miR-98	6.3	5.0	5.0	7.8			2.1
hsa-miR-99a				7.3			
hsa-miR-99b				6.8			

Table 5: miRNAs measured using the multiplex RT-PCR assay, but not consistently detected in any B-cell population

hsa-let-7e	hsa-miR-383	hsa-miR-376a	hsa-miR-566
hsa-miR-10a	hsa-miR-198	hsa-miR-376b	hsa-miR-551b
hsa-miR-10b	hsa-miR-224	hsa-miR-380-5p	hsa-miR-569
hsa-miR-34a	hsa-miR-299-5p	hsa-miR-410	hsa-miR-570
hsa-miR-34b	hsa-miR-409-5p	hsa-miR-412	hsa-miR-548a
hsa-miR-34c	hsa-miR-432	hsa-miR-432	hsa-miR-586
hsa-miR-107	hsa-miR-433	hsa-miR-512-5p	hsa-miR-587
hsa-miR-181c	hsa-miR-485-5p	hsa-miR-199a	hsa-miR-548b
hsa-miR-215	hsa-miR-489	hsa-miR-199b	hsa-miR-588
hsa-miR-218	hsa-miR-494	hsa-miR-219	hsa-miR-589
hsa-miR-372	hsa-miR-506	hsa-miR-323	hsa-miR-550
hsa-miR-375	hsa-miR-508	hsa-miR-338	hsa-miR-591
hsa-miR-378	hsa-miR-521	hsa-miR-368	hsa-miR-593
hsa-miR-137	hsa-miR-134	hsa-miR-373	hsa-miR-596
hsa-miR-200a	hsa-miR-147	hsa-miR-373	hsa-miR-597
hsa-miR-1	hsa-miR-149	hsa-miR-382	hsa-miR-622
hsa-miR-183	hsa-miR-153	hsa-miR-424	hsa-miR-599
hsa-miR-302a	hsa-miR-187	hsa-miR-448	hsa-miR-600
hsa-miR-302c	hsa-miR-190	hsa-miR-450	hsa-miR-624
hsa-miR-302d	hsa-miR-193a	hsa-miR-451	hsa-miR-601
hsa-miR-367	hsa-miR-196a	hsa-miR-452	hsa-miR-626
hsa-miR-369-5p	hsa-miR-196b	hsa-miR-452	hsa-miR-548d
hsa-miR-449	hsa-miR-205	hsa-miR-453	hsa-miR-639
hsa-miR-497	hsa-miR-208	hsa-miR-485-3p	hsa-miR-613
hsa-miR-501	hsa-miR-213	hsa-miR-488	hsa-miR-614
hsa-miR-509	hsa-miR-220	hsa-miR-490	hsa-miR-615
hsa-miR-510	hsa-miR-325	hsa-miR-492	hsa-miR-616
hsa-miR-511	hsa-miR-326	hsa-miR-493	hsa-miR-548c
hsa-miR-514	hsa-miR-337	hsa-miR-503	hsa-miR-617
hsa-miR-515-3p	hsa-miR-340	hsa-miR-504	hsa-miR-642
hsa-miR-515-5p	hsa-miR-380-3p	hsa-miR-505	hsa-miR-618
hsa-miR-517a	hsa-miR-422b	hsa-miR-507	hsa-miR-644
hsa-miR-517b	hsa-miR-422a	hsa-miR-513	hsa-miR-647
hsa-miR-517c	hsa-miR-429	hsa-miR-516-5p	hsa-miR-649
hsa-miR-518a	hsa-miR-491	hsa-miR-517	hsa-miR-661
hsa-miR-518b	hsa-miR-496	hsa-miR-518c	hsa-miR-662
hsa-miR-518c	hsa-miR-500	hsa-miR-518f	hsa-miR-449b
hsa-miR-518d	hsa-miR-502	hsa-miR-519b	hsa-miR-653
hsa-miR-518e	hsa-miR-105	hsa-miR-519c	hsa-miR-411
hsa-miR-520a	hsa-miR-122a	hsa-miR-519d	hsa-miR-654
hsa-miR-520b	hsa-miR-124a	hsa-miR-519e	hsa-miR-575
hsa-miR-520c	hsa-miR-126	hsa-miR-522	hsa-miR-576
hsa-miR-520d	hsa-miR-128b	hsa-miR-523	hsa-miR-578
hsa-miR-520e	hsa-miR-129	hsa-miR-524	hsa-miR-579
hsa-miR-520f	hsa-miR-130a	hsa-miR-526b	hsa-miR-580

hsa-miR-520g	hsa-miR-139	hsa-miR-96	hsa-miR-585
hsa-miR-520h	hsa-miR-143	hsa-miR-651	hsa-miR-512-3p
hsa-miR-95	hsa-miR-145	hsa-miR-376a	hsa-miR-631
hsa-miR-126	hsa-miR-182	hsa-miR-542-5p	hsa-miR-363
hsa-miR-127	hsa-miR-185	hsa-miR-544	hsa-miR-487b
hsa-miR-133a	hsa-miR-189	hsa-miR-656	hsa-miR-645
hsa-miR-135a	hsa-miR-18b	hsa-miR-549	hsa-miR-556
hsa-miR-135b	hsa-miR-202	hsa-miR-657	hsa-miR-558
hsa-miR-184	hsa-miR-202	hsa-miR-658	hsa-miR-627
hsa-miR-204	hsa-miR-299-3p	hsa-miR-652	hsa-miR-630
hsa-miR-206	hsa-miR-302a	hsa-miR-551a	hsa-miR-603
hsa-miR-211	hsa-miR-302b	hsa-miR-552	hsa-miR-606
hsa-miR-216	hsa-miR-302b	hsa-miR-553	hsa-miR-607
hsa-miR-217	hsa-miR-302c	hsa-miR-554	hsa-miR-608
hsa-miR-330	hsa-miR-329	hsa-miR-555	hsa-miR-609
hsa-miR-371	hsa-miR-33	hsa-miR-562	hsa-miR-633
hsa-miR-379	hsa-miR-362	hsa-miR-563	hsa-miR-565*
hsa-miR-381	hsa-miR-369-3p	hsa-miR-564	hsa-miR-594*

miRNAs marked with * were not used in analyses because they have been reclassified as non-miRNAs.

[00124] The B cell subsets were profiled for gene expression at the whole genome level, as described previously. *See Dave et al. N Engl J Med.* 2004; 351:2159-2169. At each stage, we identified differentially expressed genes as those genes with a mean two-fold difference in expression and a false-discovery rate of less than 1%. *See Figures 1E, 1G, and 1I.* Genes that we found to be differentially expressed in each stage-transition were consistent with previous studies that examined gene expression in B cell subsets using microarrays with fewer probes, an overlap that was found to be highly statistically significant ($P < 0.001$, chi-squared test). *See, e.g., Klein et al. Proc Natl Acad Sci U S A.* 2003; 100:2639-2644; and Shaffer et al. *Immunity.* 2001; 15: 375-385.

[00125] In the naïve→germinal center (GC) B cell transition, we identified 32 miRNAs that were differentially expressed. Interestingly, all but 4 miRNAs were found to be expressed more highly in GC cells than in naïve B cells. *See Figure 1D.* We confirmed the mRNA expression patterns of several genes that are known to be differentially expressed in the transition including BCL6, MME, MYBL1, as well as LM02. *See Figure 1E.* LM02 was found to be expressed more highly in germinal center B cells compared to both naïve B cells and memory B cells. *See Figures 1E and 1I.* In the GC→plasma cell transition, we found 33 miRNAs that were differentially expressed. Once again, we noted a striking asymmetry, with all but 2 miRNAs found to be expressed highly in GC cells, but down-regulated in plasma cells. *See Figure 1F.* We also confirmed that the plasma cell-specific genes, PRDMI (Figure 1G), XBPI and IRF4

were highly differentially expressed in our experiments. In the GC→memory B cell transition, there was a preponderance of the 27 significant miRNAs expressed at higher levels in memory cells. See Figure 1H. Five miRNAs were expressed highly in GC cells compared to all the other B cell types. These included 3 members of the miR-17~92 cluster (miR-17-5p, miR-20b, miR-93), as well as miR-28 and miR-181b.

[00126] The expression pattern of all the miRNAs that were measurable in at least one of the B cell subsets is summarized in Figure 5. Notably, there were no differences in the expression of genes involved in miRNA processing, including *DICER1*, *DROSHA*, *XP05* (exportin5), *EIF2C2* (ag02) and *DGCR8*, among the B cell subsets. See Figure 1J.

[00127] Separately, we examined the expression of predicted target genes of differentially expressed microRNAs. We also found that predicted mRNA target genes of microRNAs expressed highly in GC cells were expressed at lower levels in GC cells compared to other stages. See Figure 6 and Appendix A. Figure 6A shows density plots of the expression frequency of predicted mRNA targets of microRNAs expressed highly in germinal center B cells compared to naive cells. mRNAs from Fig. 1E that were also predicted targets of the miRNAs (N=830) were plotted for both naive cells and germinal center B cells. The depicted p-value was calculated using a 1-sided Kolmogorov-Smirnov test. Figure 6B shows density plots of the expression frequency of predicted mRNA targets of miRNAs expressed highly in germinal center B cells compared to plasma cells. mRNAs from Fig. 1G that were also predicted targets of the miRNAs (N=1098) were plotted for both plasma cells and germinal center B cells. The depicted p-value was calculated using a 1-sided Kolmogorov-Smirnov test. Figure 6C shows density plots of the expression frequency of predicted mRNA targets of miRNAs expressed highly in the germinal center B cells compared to memory B cells. mRNAs from Fig. 1I that were also predicted targets of the miRNAs (N=269) were plotted for both naive cells and germinal center B cells. The depicted p-value was calculated using a 1-sided Kolmogorov-Smirnov test.

[00128] In the naïve to germinal center transition (see Figure 6A), genes with at least a two-fold change in expression were analyzed by SAM using a false discovery rate of less than 1% (Larsson et. al, *BMC Bioinformatics*. 2005; 6:129), depicted in Figure 1E. From that list of significantly differentially expressed genes, we determined those that were predicted targets of miRNAs (defined as genes with 3'UTR sequence complementarity to microRNA nucleotides 2-

7) that were expressed more highly in germinal center cells. The gene expression distribution of those mRNA targets was graphed for naïve B Cells (blue curve) and germinal center B cells (orange curve). Thus, in Fig. 6A, we show genes differentially expressed between naïve and germinal center B cells that are also predicted targets of miRNA expressed more highly in germinal center B cells. We observe that the expression of these microRNA target genes is lower in germinal center B cells compared to naïve B cells.

[00129] A similar analysis was carried out for the transitions from germinal center to plasma cell (Figure 6B) and germinal center to memory cell (Fig. 6C). In all three cases examined, the distribution of germinal center miRNA target gene expression is statistically significantly lower (leftward shift of orange curve), which suggests a possible gene regulatory role for the miRNAs that are more highly expressed in germinal center cells. We note that the observed lower expression of the miRNA target genes could, however, also be caused by other factors such as downstream effects of particular transcription factors. The complete set of genes plotted in Figure 6 is listed in Appendix A.

[00130] Finally, we found that a higher proportion of differentially expressed transcription factors are predicted microRNA targets. See Figure 7. Table 6 shows differentially expressed transcription factors, with the average level of expression for each in naïve, germinal center, plasma, and memory cells. Transcription factors for which the significance analysis showed a q value of 0 are indicated.

Table 6: Differentially-expressed transcription factors

ID	NAME	Naïve average	Germinal Center average	Plasma Cell average	Memory average	Naïve vs GC: q value	GC vs PC: q value	GC vs Mem: q value
1	AHR	8.9	10.33	8.36	10.38	0	0	
2	APBB2	6.86	7.87	7.35	6.39	0		0
3	ARID1A	12.3	12.22	11.11	12.17		0	
4	ARID3A	8.03	6.9	9.81	8.76	0	0	0
5	ARNTL	9.47	8.4	8.23	9.7	0		0
6	ATF7	7.83	8.97	8.23	8.44	0		
7	BACH1	10.68	9.97	11.76	10.59		0	
8	BHLHB3	11.11	8.05	13.26	13.26	0	0	0
9	BPTF	12.23	12.46	11.34	11.86		0	
10	BTG1	15.88	14.95	13.94	15.28		0	
11	CASP8AP2	10.17	10.55	9.44	10.22		0	
12	CBL	11.07	11.69	10.26	11.04		0	
13	CBX4	12.23	12.36	13.69	12.68		0	
14	CCNE1	7.86	9.18	8.87	7.66	0		0
15	CDH1	5.85	3.85	10.26	4.91		0	
16	CITED2	9.11	9.88	12.56	9.22		0	
17	CLOCK	9.85	7.68	9.91	9.62	0	0	0
18	CREB5	4.91	5.46	7.24	6.95		0	
19	CREBL1	7.53	6.97	8.06	8.09			0
20	CREBL2	10.18	9.95	11.1	10.79		0	
21	CSDA	12.12	8.59	10.1	8.98	0	0	
22	DEK	12.73	14.09	10.29	13.15	0	0	
23	DLX2	6.08	4.66	7.04	7.08		0	0
24	DR1	11.83	11.97	10.65	12.1		0	
25	DTX1	10.98	11.6	10.55	9.62		0	0
26	DYRK1B	6.32	5.92	7.61	4.96		0	
27	E2F1	7.01	8.37	7.95	7.21	0		0
28	EGR1	11.92	13.24	13.77	12.75	0		
29	EGR2	10.21	10.43	8.07	10.4		0	
30	EGR3	11.59	9.35	8.24	10.62	0	0	0
31	ELF1	12.39	12.7	11.34	12.55		0	
32	ELL	7.12	7.83	9.17	7.59		0	
33	ELL2	9.25	8.23	13.6	9.27		0	
34	EPAS1	7.1	7.02	8.39	7.5		0	
35	ETS1	14.25	14.4	12.62	14.17		0	
36	ETS2	6.37	7.5	5.66	4.9	0	0	0
37	ETV1	8.19	6.9	7.38	7.06	0		
38	ETV4	5.99	5.42	7.15	6.09		0	
39	ETV6	10.36	7.14	8.89	10.43	0	0	0
40	FHL2	4.82	7.77	6.82	5.65	0		0
41	FLNA	9.95	9.2	8.57	11.03			0
42	FOS	12.35	11.25	13.34	11.23	0	0	
43	FOSB	10.13	7.21	11.05	10.79	0	0	0
44	FOXC1	6.81	5.84	7.39	6.59		0	
45	FOXF2	7.05	4.83	6.37	5.84	0		
46	FOXJ2	10.01	8.38	9.97	9.85	0	0	0
47	FOXK2	8.94	8.4	9.63	8.71		0	
48	GATA3	8.05	7.76	8.51	9.6			0
49	GATA6	7.08	5.41	7.59	6.26	0	0	

50	GCN5L2	10.18	8.97	8.9	10.36	0		0
51	GLI2	6.93	7.26	7.52	6.09			0
52	GPX3	6.72	5.92	7.61	5.58		0	
53	HCLS1	13.94	14.42	13.12	13.92		0	
54	HIPK2	9.36	8.66	11.04	10.85		0	0
55	HMGA1	11.26	12.47	10.36	10.86	0	0	0
56	HMGB1	15.47	16.36	14.98	14.97		0	0
57	HMGB2	12.96	15.78	12.73	13.36	0	0	0
58	HOXA1	5.36	7.7	7.23	7.64	0		
59	HOXA5	7.03	8.32	8.36	7.54	0		
60	HOXB4	8.2	7.58	9.27	8.01		0	
61	HOXB9	7.4	6.2	8.41	6.87		0	
62	HOXC11	6.6	6.4	7.88	6.21		0	
63	HOXC8	7.05	5.48	6.88	6.71	0		
64	ID4	6.49	5.93	7.79	6.41		0	
65	ILF3	11.26	11.94	10.71	10.99		0	
66	IRAK1	12.19	11.48	12.8	11.96		0	
67	IRF4	11.16	9.28	13.66	10.51	0	0	0
68	ISL1	6.98	5.91	7.6	6.11		0	
69	JAZF1	11.93	10.65	7.49	11.31	0	0	
70	JMJD1C	12.34	12.34	11.11	12.56		0	
71	JUN	12.14	9.34	12.7	12.16	0	0	0
72	JUNB	11.62	9.72	10.84	11.37	0		0
73	KLF11	8.08	5.94	6.88	8.39	0		0
74	KLF2	12.61	9.1	11.7	12.61	0	0	0
75	KLF4	10.04	7.57	9.09	7.49	0	0	
76	KLF5	7.08	5.26	6.14	5.07	0		
77	KLF6	12.06	11.33	9.24	12.40		0	0
78	KLF7	9.36	8.35	8.88	9.8			0
79	KLF9	9.47	7.34	6.64	9.27	0		0
80	LITAF	12.52	10.18	11.82	12.49	0	0	0
81	LMO1	6.86	4.75	7.16	6.88		0	
82	MAF	8.05	9.95	8.25	10.83	0	0	
83	MAFB	6.58	7.3	8.56	7.29		0	
84	MAML3	8.05	10.85	9.07	7.04	0	0	0
85	MDFIC	12.06	13.67	13.6	13.08	0		
86	MEIS2	7.45	7.15	7.56	5.29			0
87	MEN1	10.79	11.33	10.49	10.23			0
88	MITF	7.51	8.05	8.01	6.41			0
89	MTF1	10.08	9.92	8.86	10.5		0	
90	MXD1	9.07	7.59	9.62	8.9	0	0	0
91	MXI1	10.63	7.85	11.1	9.42	0	0	0
92	MYB	6.97	8.62	5.61	7.99	0	0	
93	MYBL1	9.68	14.13	10.02	9.72	0	0	0
94	MYBL2	9.07	12.41	9.12	8.52	0	0	0
95	NAT14	6.62	7.66	7.33	7.63	0		
96	NF1	9.23	10.46	11.21	9.88	0		
97	NFAT5	11.71	12.09	10.72	11.77		0	
98	NFATC4	6.36	7.92	8.96	5.71	0		0
99	NFIX	8.09	7.43	8.67	7.37		0	
100	NFKB1	11.91	11.9	10.7	11.55		0	
101	NFYC	10.2	10.27	9.03	10.03		0	
102	NR3C2	8.85	5.58	4.91	8.41	0		0

103	NR6A1	9.1	6.03	6.42	7.62	0		0
104	NRIP1	11.79	10.3	10.33	11.20	0		
105	PAX3	7.01	5.55	5.01	5.96	0		
106	PHF1	11.85	10.69	12.26	11.45	0	0	
107	POU3F1	6.08	7.52	6.86	7.52	0		
108	POU4F1	5.62	8.85	8.46	7.53	0		0
109	POU4F2	7.09	5.72	7.21	5.1	0	0	
110	PPARD	11.23	9.98	10.29	10.69	0		
111	PPARG	7.79	7.22	6.74	5.47			0
112	PPARGC1B	6.89	6.09	6.51	7.91			0
113	PRDM1	8.49	9.15	14.1	9.33		0	
114	PRDM4	10.48	9.81	9.76	10.83			0
115	PROX1	7.18	6.38	7.89	5.54		0	
116	RAN	13.46	14.57	12.39	13.78	0	0	
117	RSF1	10.05	9.1	9.56	10.18			0
118	RUNX1T1	7.37	5.95	6.63	6.34	0		
119	RUNX2	8.75	7.91	10.22	9.75		0	0
120	RUNX3	11.8	11.13	10.26	12.47			0
121	RXRA	9.07	7.15	8.81	8.32	0	0	0
122	SAP30	8.22	9.91	9.28	8.33	0		0
123	SCMH1	8.48	9.69	9.65	8.62	0		0
124	SCML1	10.32	8.48	7.81	7.91	0		
125	SCML2	10.33	8.76	9.27	8.96	0		
126	SF1	11.72	11.44	10.36	11.37		0	
127	SLAH2	10.35	12.34	10.57	9.90	0	0	0
128	SLC2A4RG	8.25	8.98	7.4	8.91		0	
129	SMAD1	5.91	8.1	6.34	7.33	0	0	
130	SMAD2	10.45	11.57	10.8	10.98	0		
131	SMAD3	10.72	9.23	7.74	10.54	0	0	0
132	SMARCA2	11.14	10.12	10.79	11.19	0		0
133	SOLH	8.78	7.88	8.7	9.03			0
134	SOX4	8.99	9.14	9.17	10.2			0
135	SOX5	9.3	10.47	7.33	9.08	0	0	0
136	SOX9	6.72	8.42	8.18	7.03	0		0
137	SP4	11.26	10.14	9.58	11.75	0		0
138	SRCAP	8.58	8.06	6.96	8.38		0	
139	SREBF1	8.23	8.36	6.56	5.89		0	0
140	STAT5B	10.35	10.95	9.73	10.7		0	
141	SUFU	7.12	6.03	7.84	7.62		0	0
142	SUPT16H	11.12	11.35	9.6	10.71		0	
143	SUPT3H	7.77	6.3	8.05	8.35	0	0	0
144	TARDBP	12.31	12.72	11.49	11.91		0	
145	TBP	10.55	10.14	9.09	10.38		0	
146	TBX3	5.67	6.05	7.89	5.53		0	
147	TCEA1	13.31	15	14.05	13.6	0		0
148	TCERG1	12.29	12.5	11.46	12.04		0	
149	TCF7	10.21	10.82	9.97	12.61			0
150	TFAP2A	6.7	5.54	8.26	6.88		0	
151	TFAP4	7.28	5.29	5.42	5.13	0		
152	TFDP1	10.95	12.9	10.49	11.36	0	0	0
153	TFEB	11.56	11.15	9.49	11.77		0	
154	THRA	7.41	7.26	8.48	7.05		0	
155	THRB	7.45	7.51	6.11	6.29		0	0

156	TLE1	9.19	7.74	9.63	9.13	0	0	0
157	TMF1	10.76	9.68	10.71	10.42	0		
158	TSC22D3	13.22	11.26	12.67	13.4	0	0	0
159	UHRF1	9.23	12.22	8.72	8.96	0	0	0
160	VEZF1	10.98	11.45	9.94	10.81		0	
161	XBP1	10.1	10.74	15.84	10.65		0	
162	YBX1	14.79	15.31	14.2	14.53		0	
163	YWHAH	8.94	10.82	9.09	9.36	0	0	0
164	YWHAZ	13.38	13.62	12.61	13.62		0	
165	ZFP36L1	14.07	12.89	10.09	13.87	0	0	
166	ZHX3	8.29	7.76	7.47	6.66			0
167	ZNF207	12.29	13.51	12.69	12.54	0		
168	ZNF217	11.68	10.77	9.73	11.61		0	
169	ZNF219	6.13	6.11	8.42	6.48		0	
170	ZNF238	13.05	11.27	10.08	12.54	0	0	0
171	ZNF3	8.86	7.27	8.75	8.89	0	0	0
172	ZNF367	7.97	10.99	8.04	8.22	0	0	0
173	ZNF398	10.39	9.28	10.47	10.25	0	0	

Example 3: MiR-223 regulates LM02 in the naive ~ germinal center and germinal center ~ memory cell transitions

[00131] MiR-223 has previously been described as being important in the commitment to myeloid lineage. See Chen et al. *Science*. 2004; 303:83-86; Johnnidis et al. *Nature*. 2008; 451:1125-1129. We found miR-223 to be expressed at nearly 8-fold higher levels in both naive and memory cells compared to GC cells. This miRNA has a highly conserved sequence complementarity to the 3'UTR of 2 transcription factors that are expressed highly during GC cell differentiation: LM02 (Figure 2A) and MYBL1 (Figure 8A). Higher expression of miR-223 in the naive B cell stage could inhibit the untimely expression of these transcription factors until the cell is ready to undergo the germinal center reaction.

[00132] We evaluated the effects of miR-223 expression on its predicted target gene, LM02, by transfecting precursors of miR-223 into a cell line derived from GC cell lymphoma cells (BIAB). Over-expression of miR-223 resulted in a consistent down-regulation of LM02 at the transcript level compared to a transfection with a scrambled control with no sequence complementarity to the human genome. See Figure 2B. In that figure, the blue bars depict expression of LM02 24 hours after transfection with a scrambled control that does not possess complementarity to the human genome. The orange bars depict the expression of LM02 24 hours after transfection with a precursor for miR-223. The expression of LM02 was consistently lower in the cells treated with the miR-223 precursor, and the results were statistically significant ($P < 0.05$ in all cases,

student's t-test). There was no effect on the expression of a non-target control, beta-2 micro globulin in these experiments (data not shown). Over-expression of miR-223 also resulted in a consistent down-regulation of LM02 at the protein level compared to a transfection with a scrambled control with no sequence complementarity to the human genome. *See* Figure 2C. We quantified the results of 3 separate experiments examining LM02 protein expression and found consistent down-regulation of LM02 in cells treated with miR-223 compared to cells transfected with scrambled controls. *See* Figure 2D. Those results that were statistically significant ($P < 0.05$, student's t-test). The extent of down-regulation of LM02 mRNA and protein by miR-223 was comparable, suggesting that miR-223 regulation of LM02 occurs predominantly at the mRNA level. Similarly, over-expression of miR-223 resulted in a down-regulation of MYBL1 transcripts. *See* Figure 8B. In that figure, the blue bars depict expression of MYBL1 mRNA 24 hours after transfection with a scrambled control that does not possess complementarity to the human genome. The orange bars depict the expression of Mybl1 24 hours after transfection with a precursor for miR-223. The expression of LMO2 was consistently lower in the cells treated with the miR-223 precursor ($P < 0.05$ in all cases).

[00133] As additional validation, we investigated whether the miR-223 had a direct effect on LM02 by cloning the 3'UTR sequence of LM02 3' to the firefly luciferase ORF (*Fluc*). *See* Gottwein et al. *Nature*. 2007; 450:1096-1099. The resulting constructs and the unmodified vector were co-transfected into 293T cells along with a Renilla luciferase internal control and pL-CMV-eGFP constructs expressing either no miRNA or miR-223. *Fluc* expression from constructs bearing LM02 3' UTR sequences were differentially down-regulated by miR-223 compared to those with mutated seed sequences; the seed sequence mutant construct had consistently diminished miR-223 repression compared to the wild-type construct in 5 separate experiments. *See* Figure 2E. Those results were statistically significant ($P < 0.05$, student's t-test). These observations provide evidence for an inhibitory role for miR-223 in regulating the transcription factor LM02.

[00134] Activation of LM02 has been associated with the development of leukemia in patients undergoing gene therapy. Hacein-Bey-Abina et al. *Science*. 2003;302:415-419. On the other hand, higher expression of PRDM1 alone is sufficient to induce plasma cell-differentiation. Turner et al. *Cell*. 1994;77:297-306. Inappropriate expression of such genes must be effectively turned off for a cell to maintain its state. This mode of regulation is reflected in the effects of

miR-223, miR-9 and miR-30, which turn off the inappropriate expression of LM02 and PRDM1 and might promote state maintenance and inhibition of lymphomagenesis.

[00135] On the other hand, our data also identify a number of instances in which miRNAs are co-expressed with their predicted targets. It is possible that such interactions within the cell help to stabilize a defined expression level by dampening fluctuations. For example, in GC cells, we found that miR-181b was strongly co-expressed with its predicted target, BCL6. Such interactions could also be important in B cell stage maintenance and curbing the oncogenic potential of genes involved in B cell differentiation. See Cattoretti et al. *Cancer Cell*. 2005;7:445-455; Dorsett et al. *Immunity*. 2008;28:630-638.

Example 4: MiR-9 and the miR-30 family regulate *PRDM1* (blimp-1) in the germinal center → plasma cell transition

[00136] In the GC → plasma cell transition, we observed that several members of the miR-30 family were expressed at 2-fold or higher levels in GC cells. See Figure 1F. The transcription factor PRDM1 is an essential regulator of plasma cell differentiation. Martins et al. *Annu Rev Immunol*. 2008; 26:133-169. The miR-30 family comprises 5 members (miR-30a, 30b, 30c, 30d and 30e), of which 4 (all except 30e) were found to be expressed at higher levels in GC cells compared to plasma cells. Control transfection experiments documented good specificity of the RT-PCR probes for individual members of the miR-30 family with no discernible cross-hybridization. See Figure 9. Three separate transfection experiments using high concentrations of miR-30b precursors are shown in the left panel with measurement of miR-30b and miR-30d. Similar experiments were performed with precursors for miR-30d (right panel).

[00137] The 3'UTR of PRDM1 contains 3 highly conserved binding sites complementary to the seed sequence of members of the miR-30 family, as well as 3 binding sites for the seed sequence of miR-9, 2 of which are highly conserved across multiple species. See Figure 3A. The 3'UTR region of PRDM1 complementary to miR-30 is shown in red. The 3 sites are complementary to nucleotides 2-8 (UTR position 408), nucleotides 1-8 (UTR position 2370) and nucleotides 2-8 (UTR position 2383) on the miRNA, respectively. The 3'UTR region of PRDM1 complementary to miR-9 is shown in green. The 3 sites are complementary to nucleotides 1-7 (UTR position 1459), nucleotides 2-8 (UTR position 2108) and nucleotides 2-8 (UTR position 2323) on the miRNA respectively. These sites are highly conserved across a number of species, with the exception of one miR-9 site (UTR position 1459) that is only present in humans.

[00138] To evaluate the effects of the miR-30 family and miR-9 on PRDM1 expression in plasma cells, we introduced precursors of miR-9, miR-30b and miR-30d into the U266 multiple myeloma (plasma cell) cell line. Overexpression of miR-30 family members miR-30b and miR-30d, as well as miR-9, had no effect on PRDM1 at the mRNA level. *See* Figure 3B. In that figure, the blue bars depict expression of PRDM1 24 hours after transfection with a scrambled control with no complementarity to the human genome. The magenta bars depict the expression of PRDM1 24 hours after transfection with a hairpin precursor for miR-30b, while the red bars depict the expression of PRDM1 24 hours after transfection with a hairpin precursor for miR-30d. The green bars depict the expression of PRDM1 24 hours after transfection with a hairpin precursor for miR-9. By contrast, there was a consistent down-regulation of PRDM1 at the protein level. *See* Figures 3C and 3D. Those results were statistically significant in each case ($P < 0.05$, student's t-test), except for the transfections with the precursor to miR-9 ($P = 0.08$, student's t-test). Overexpression of each of those microRNAs had an average knockdown effect of around 40%. These exclusively post-transcriptional effects of miR-9 and miR-30 on PRDM1 expression are consistent with one mechanism of miRNA regulation that has been described previously in other systems. *See, e.g.,* O'Donnell et al. *Nature*. 2005; 435:839-843; Gottwein et al. *Nature*. 2007; 450:1096-1099; Selbach et al. *Nature*. 2008; 455:58-63; and Baek et al. *Nature*. 2008; 455:64-71. There was no effect on the expression of a non-target control (Actin).

[00139] Additionally, luciferase reporter activity of the PRDM1 3'UTR construct was decreased by overexpression of miR-9, miR-30b, and miR-30d, but not their respective seed sequence mutants. *See* Figure 3E, which shows the average of three experiments. The down-regulation of the luciferase reporter signal and its restoration in the mutant constructs was found to be statistically significant in each of the 3 microRNAs: miR-9, miR-30b and miR-30d ($P < 0.05$, student's t-test). The luciferase reporter activity level was rescued to the activity level of the empty vector control when the seed sequence of the microRNAs was mutated.

[00140] The combined effect of 5 different microRNA species (miR-30a, miR-30b, miR-30c, miR-30d and miR-9) is likely to be more potent than that of a single microRNA. The role of mutual repression of BCL6 and PRDM1 in the germinal center to plasma cell differentiation as been described previously. *See* Martins et al. *Immunol*. 2008; 26:133-169. Our data suggest that microRNAs may bolster the effects of BCL6 in the inhibition of PRDM1.

[00141] Our data show that members of the miR-17~92 family are consistently expressed in GC cells and may play a role in mature B cell differentiation. Interestingly, the miR-17~92 family has been implicated in early B cell differentiation and mice lacking the loci that encode these miRNAs have arrested early B cell development. *See Ventura et al. Cell. 2008;132:875-886.* The expression patterns of the miR-17~92 family suggest that the regulatory motifs embedded in the interaction of this miRNA family and its targets might have an additional function in regulating mature B cell differentiation.

[00142] A striking observation in this study is the high degree of asymmetry observed in relative expression of miRNAs in GC cells compared to naive and plasma cells. At least 2 hypotheses could account for these findings. First, miRNA expression may promote a highly regulated state that enables GC cells to interact with T cells and antigen presenting cells, and to leave the GC cells poised for differentiation into memory or plasma cells. Second, miRNAs expressed highly in naive and plasma cells may be underrepresented in current miRNA libraries. Such libraries are often constructed from lymph nodes, which are typically enriched in GC cells. High throughput sequencing of sorted populations of B cells could reveal novel miRNAs that are highly expressed in those populations. Interestingly, a larger number of miRNAs were highly expressed in memory cells compared to GC cells. This observation might stem from the fact that memory cells are known to be heterogeneous (Sanz et al. *Semin Immunol.* 2008;20:67-82) and standard methods used to select memory cells may capture a diverse group of memory subpopulations.

Example 5: MiRNAs and B cell malignancies

[00143] To examine the expression of B cell stage-specific microRNAs in B cell malignancies, we undertook miRNA profiling of 75 tissue samples derived from normal lymph nodes (N=5) as well as patients with B cell malignancies including the molecular subsets of diffuse large B cell lymphoma (DLBCL; *see Rosenwald et al. N Engl J Med.* 2002; 346:1937-1947), germinal center B cell-like (GCB) DLBCL (N=20) and activated B cell-like (ABC) DLBCL (N=20), as well as cases of IgV mutated and unmutated chronic lymphocytic leukemia (N=20) and Burkitt lymphoma (N=10).

[00144] We constructed a Bayesian predictor from miRNAs that distinguished normal memory B cells from GC cells. *See Figure 1H.* We tested the predictor in the B cell malignancies derived from germinal center B cells (Burkitt lymphoma and GCB DLBCL) along with chronic

lymphocytic leukemia, which is thought to arise from memory B cells. *See Klein et al. J Exp Med.* 2001; 194:1625-1638. Using leave one out cross-validation, we found that the predictor constructed from miRNAs expressed in normal B cells was able to correctly identify the B cell specific stage of the B cell malignancy type in over 95% of the cases. *See Figure 4A.*

[00145] An interesting aspect regarding the role of miRNAs in malignancies is their reported down-regulation in a number of malignancies compared to normal cells from the same lineage. *See Lu et al. Nature.* 2005;435:834-838. To further examine this effect in B cell malignancies, we examined the expression of 113 miRNAs that we had identified in normal B cells. *See Table 4, above.* Of the 113 miRNAs, 103 were detected using the microarrays that we used to profile B cell malignancies and normal lymph nodes. We applied a 2-sided student's t-test to evaluate the relative expression of those 103 miRNAs in B cell malignancies (N=60) and normal lymph nodes (N=5). 34 miRNAs were differentially expressed ($P<0.05$) at higher levels in malignant cells and 9 miRNAs were expressed more highly in normal cells. 60 miRNAs were not differentially expressed. *See Figure 4B.*

[00146] As additional validation, we examined miRNA cloning frequencies for sequences cloned from normal and malignant B cells. *See Landgraf et al. Cell.* 2007; 129:1401-1414. MiRNAs for which a sequence was identified in at least 2 of the 3 available normal B cell samples were used in the analysis. We applied a 2-sided student's t-test ($P<0.05$) to compare the differential cloning frequency of the miRNAs between normal B cells (N=3) and a variety of mature B cell malignancy patient samples and cell lines (N=42). In all, we found 56 miRNAs that were consistently expressed in normal B cells. We found 13 of those 56 miRNAs were differentially expressed ($P<0.05$) between normal and malignant B cells, of which 12 miRNAs were expressed more highly in malignant cells and 1 miRNA was expressed more highly in normal cells. *See Figure 4C.* In order to avoid effects from tumor-infiltrating non-malignant cells, we repeated the analysis with 20 chronic lymphocytic leukemia samples in the malignant group. The results were similar to those obtained with the larger set of malignancies (data not shown).

[00147] These results demonstrate that miRNAs are not down-regulated in B cell malignancies compared to normal B cells and that normal B cell stage-specific miRNAs are maintained in B cell malignancies.

[00148] MicroRNA profiling also revealed that each B cell malignancy type had a distinctive pattern of miRNA expression. *See* Figure 4D. In order to evaluate the ability of miRNA profiles to distinguish different B cell malignancy types, we constructed Bayesian predictors from the most highly differentially expressed miRNAs for each pair-wise comparison. *See* Tables 7, 8, and 9.

Table 7: Predictor microRNAs that distinguish germinal center B-cell (GCB) DLBCL from Burkitt Lymphoma, activated B-cell (ABC) DLBCL, and chronic lymphocytic leukemia

GCBvsBL	GCBvsABC	GCBvsCLL
hsa-miR-146a	hsa-miR-142-3p	hsa-miR-126
hsa-miR-154	hsa-miR-16	hsa-miR-130a
hsa-miR-155	hsa-miR-184	hsa-miR-10b
hsa-miR-184	hsa-miR-191	hsa-miR-154
hsa-miR-29b	hsa-miR-19a	hsa-miR-193b
hsa-miR-29c	hsa-miR-19b	hsa-miR-199a-3p
hsa-miR-363	hsa-miR-299-5p	hsa-miR-365
hsa-miR-503	hsa-miR-32	hsa-miR-99b
hsa-miR-519c-5p	hsa-miR-30e*	hsa-miR-143
hsa-miR-301a	hsa-miR-151-5p	hsa-miR-585
hsa-miR-152	hsa-miR-583	hsa-miR-193a-5p
hsa-miR-30b*	mghev-miR-MI-7-5p	hsa-miR-886-5p
hsa-miR-590-5p	hsa-miR-142-5p	hsa-miR-100
hsa-miR-149*	hsa-miR-106b	hsa-miR-768-5p
hsa-miR-300	hsa-miR-30e	hsa-miR-145
hsa-miR-625*	hsa-miR-140-3p	hsa-miR-943
kshv-miR-K12-3	hsa-miR-20a	hsa-miR-371-5p
hsa-miR-28-5p	hsa-miR-526b*	hsa-miR-675
hsa-miR-25*	hsa-miR-28-5p	hsa-miR-150
ebv-miR-BHRF1-2	hsa-miR-30c	hsa-miR-181a

BL=Burkitt lymphoma, ABC=activated B-cell DLBCL, CLL=chronic lymphocytic lymphoma

Table 8: Predictor microRNAs that distinguish activated B-cell (ABC) DLBCL from Burkitt Lymphoma and chronic lymphocytic leukemia

ABCvsBL	ABCvsCLL
hsa-miR-182	hsa-miR-193b
hsa-miR-377	hsa-miR-99b
hsa-miR-660	hsa-miR-551a
hsa-miR-595	mghev-miR-MI-7-3p
ebv-miR-BART10	hsa-miR-585
hsa-miR-532-5p	hsa-miR-617
hsa-miR-200c*	hsa-miR-629*
hsa-miR-362-3p	hsa-miR-575
hsa-miR-455-3p	kshv-miR-K12-6-5p
hsa-miR-128	hsa-miR-193a-5p
hsa-miR-21*	hsa-miR-30e

hsa-miR-589	hsa-miR-296-3p
hsa-miR-135a*	hsa-miR-518b
hsa-miR-532-3p	hsa-miR-492
hsa-miR-548d-5p	hsa-miR-220c
hsa-miR-652	hsa-miR-326
hsa-miR-150*	hsa-miR-671-5p
hsa-miR-330-5p	hsa-miR-340*
hsa-miR-339-3p	hsa-miR-150
hsa-miR-502-3p	hsa-miR-193b*
BL=Burkitt lymphoma, CLL=chronic lymphocytic lymphoma.	

Table 9: Predictor microRNAs that distinguish Burkitt lymphoma from chronic lymphocytic leukemia

BLvsCLL

hsa-miR-130b
 hsa-miR-154
 hsa-miR-155
 hsa-miR-29b
 hsa-miR-29c
 hsa-miR-637
 hsa-miR-658
 hsa-miR-193a-5p
 hsa-miR-886-5p
 hsa-miR-768-5p
 hsa-miR-101
 hsa-miR-933
 hsa-miR-371-5p
 hsa-miR-675
 hsa-miR-150
 hsa-miR-874
 hsa-miR-181a
 hsa-miR-30c
 ebv-miR-BHRF1-2
 hsa-miR-628-3p

CLL=chronic lymphocytic lymphoma

[00149] We tested the performance of the predictor using leave-one-out cross-validation applied to the predictors for Burkitt lymphoma, chronic lymphocytic leukemia, activated B-cell diffuse large B-cell lymphoma, and germinal center B-cell DLBCL. For a sample prediction to be correct, it had to be classified correctly in each pair-wise comparison with all remaining entities. We found it to be over 90% accurate in the identification of each entity. *See Figure 10.*

[00150] We next expanded the analysis to include follicular lymphoma and Hodgkin's lymphoma. We included the samples from the earlier study and we undertook miRNA profiling of the following additional samples: normal lymph nodes (N=5) and patients with germinal

center B cell-like (GCB) DLBCL (N=10), activated B cell-like (ABC) DLBCL (N=10), chronic lymphocytic leukemia (N=10), Burkitt lymphoma (N=10), follicular lymphoma (N=10), and Hodgkin's lymphoma (N=9). As before, microRNA profiling revealed that each B cell malignancy type had a distinctive pattern of miRNA expression. See Figure 11.

[00151] From that data, we identified microRNAs that can be used to distinguish each of the six B cell malignancies analyzed from the other five. Lists of those microRNAs, and whether they are expressed in high levels or low levels relative to the other 5 B cell malignancies, are shown in Tables 10 through 13. In certain embodiments, each of those microRNAs could be used to distinguish one of the six B cell malignancies from the other five. High and low in the table refer to at least a 2 fold difference when compared to other lymphomas and benign lymph nodes.

Table 10: Predictor microRNAs that distinguish Burkitt lymphoma, germinal center B-cell (GCB) DLBCL, and follicular lymphoma from all other B cell malignancies in the study

BL miRNA list	BL vs others	GCB miRNA list	GCB vs others	FL miRNA list	FL vs others
hsa-miR-106a	High	hsa-miR-93/mmu-miR-93/rno-miR-93	High	hsa-miR-96/mmu-miR-96/rno-miR-96	High
hsa-miR-17/mmu-miR-17/rno-miR-17-5p/rno-miR-17	High	hsa-miR-886-3p	High	hsa-miR-138/mmu-miR-138/rno-miR-138	High
hsa-miR-628-3p	High	hsa-miR-365/mmu-miR-365/rno-miR-365	High	hsa-miR-342-5p/mmu-miR-342-5p/rno-miR-342-5p	High
hsa-miR-193a-5p	High	hsa-miR-378/mmu-miR-378/rno-miR-378	High	hsa-miR-337-3p	High
hsa-miR-371-5p	High	hsa-miR-320/mmu-miR-320/rno-miR-320	High	hsa-miR-301a/mmu-miR-301a/rno-miR-301a	High
hsa-miR-20a/mmu-miR-20a/rno-miR-20a	High	hsa-miR-103/mmu-miR-103/rno-miR-103	High	hsa-miR-922	High
hsa-miR-23a/mmu-miR-23a/rno-miR-23a	Low	hsa-miR-637	High	hsa-miR-744/mmu-miR-744	High
hsa-miR-27a/mmu-miR-27a/rno-miR-27a	Low	hsa-miR-148a/mmu-miR-148a	High	hsa-miR-221*	High
hsa-miR-34b/mmu-miR-34b-3p	Low	hsa-miR-199a-3p/hsa-miR-199b-3p/mmu-miR-199a-3p/rno-miR-199a-3p	High	hsa-miR-215	High
hsa-miR-21/mmu-miR-21/rno-miR-21	Low	hsa-miR-126*/mmu-miR-126-5p/rno-miR-126*	High	hsa-miR-197/mmu-miR-197	High
hsa-miR-29a/mmu-miR-29a/rno-miR-29a	Low	kshv-miR-K12-6-3p	High	hsa-miR-92b/mmu-miR-92b/rno-miR-92b	High

BL miRNA list	BL vs others	GCB miRNA list	GCB vs others	FL miRNA list	FL vs others
hsa-let-7b/mmu-let-7b/rno-let-7b	Low	hsa-miR-125a-5p/mmu-miR-125a-5p/rno-miR-125a-5p	High	hsa-miR-218-2*/mmu-miR-218-2*/rno-miR-218*	High
hsa-let-7f/mmu-let-7f/rno-let-7f	Low	hsa-miR-551b/mmu-miR-551b/rno-miR-551b	Low	hsa-miR-636	High
hsa-miR-29b/mmu-miR-29b/rno-miR-29b	Low	hsa-miR-923	Low	hsa-miR-600	High
hsa-miR-549	Low			kshv-miR-K12-7	High
hsa-miR-374a	Low			hsa-miR-194/mmu-miR-194/rno-miR-194	High
hsa-miR-513a-5p	Low			hsa-miR-524-5p	High
hsa-miR-148a/mmu-miR-148a	Low			hsa-miR-22*/mmu-miR-22*/rno-miR-22*	High
hsa-miR-223/mmu-miR-223/rno-miR-223	Low			hsa-miR-34c-5p/mmu-miR-34c/rno-miR-34c	High
hsa-miR-138-1*/mmu-miR-138*/rno-miR-138*	Low			hsa-miR-151-3p	High
hsa-miR-342-3p/mmu-miR-342-3p/rno-miR-342-3p	Low			hsa-miR-425/mmu-miR-425/rno-miR-425	High
hsa-miR-146b-5p/mmu-miR-146b/rno-miR-146b	Low			ebv-miR-BART16	High
hsa-miR-195/mmu-miR-195/rno-miR-195	Low			hsa-miR-20b*	High
hsa-miR-103/mmu-miR-103/rno-miR-103	Low			hsa-miR-574-3p/mmu-miR-574-3p	High
hsa-miR-888*	Low			hsa-miR-155*	High
hsa-miR-363/mmu-miR-363/rno-miR-363	Low			hsa-miR-374b*	High
hsa-miR-140-3p/mmu-miR-140*/rno-miR-140*	Low			hsa-miR-497/mmu-miR-497/rno-miR-497	High
hsa-miR-191/mmu-miR-191/rno-miR-191	Low			hsa-miR-708/mmu-miR-708/rno-miR-708	High
hsa-miR-768-5p	Low			hsa-miR-92a/mmu-miR-92a/rno-miR-92a	High
hsa-miR-222/mmu-miR-222/rno-miR-222	Low			hsa-miR-361-3p	High
hsa-miR-668/mmu-miR-668	Low			hsa-miR-513a-3p	High
hsa-miR-221/mmu-miR-221/rno-miR-221	Low			hsa-miR-934	High

BL miRNA list	BL vs others	GCB miRNA list	GCB vs others	FL miRNA list	FL vs others
hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	Low			hsa-miR-363*/rno-miR-363*	High
hsa-miR-29c/mmu-miR-29c/rno-miR-29c	Low			mghev-miR-M1-3	High
hsa-miR-146a/mmu-miR-146a/rno-miR-146a	Low			hsa-miR-129*	High
hsa-miR-154/mmu-miR-154/rno-miR-154	Low			hsa-miR-148b/mmu-miR-148b/rno-miR-148b-3p	High
hsa-miR-215	Low			hsa-miR-493	High
hsa-miR-487b/mmu-miR-487b/rno-miR-487b	Low			hsa-miR-151-5p/mmu-miR-151-5p/rno-miR-151	High
hsa-miR-155	Low			hsa-miR-146b-3p	High
				hsa-miR-886-5p	High
				hsa-miR-331-3p/mmu-miR-331-3p/rno-miR-331	High
				hsa-miR-574-5p/mmu-miR-574-5p	High
				hsa-miR-424	High
				hsa-miR-152/mmu-miR-152/rno-miR-152	High
				hsa-miR-302a/mmu-miR-302a	High
				hsa-miR-181a/mmu-miR-181a/rno-miR-181a	High
				hsa-miR-509-5p	High
				hsa-let-7d/mmu-let-7d/rno-let-7d	High
				hsa-miR-18b	High
				hsa-miR-620	High
				hsa-miR-18a/mmu-miR-18a/rno-miR-18a	High
				hsa-miR-298	High
				hsa-miR-98/mmu-miR-98/rno-miR-98	High
				hsa-miR-576-3p	High
				hsa-miR-374b/mmu-miR-374/rno-miR-374	High
				hsa-miR-32*	High
				hsa-miR-302d*	High
				ebv-miR-BART17-5p	High
				hsa-miR-620	High
				hsa-miR-665	High

BL miRNA list	BL vs others	GCB miRNA list	GCB vs others	FL miRNA list	FL vs others
				hsa-miR-185/mmu-miR-185/rno-miR-185	High
				hsa-miR-34b/mmu-miR-34b-3p	High
				hsa-let-7e/mmu-let-7e/rno-let-7e	High

Table 11: Predictor microRNAs that distinguish activated B-cell (ABC) DLBCL from all other B cell malignancies in the study

ABC miRNA list	ABC vs others	ABC miRNA list (con't)	ABC vs others	ABC miRNA list (con't)	ABC vs others
hsa-miR-126/mmu-miR-126-3p/rno-miR-126	High	hsa-miR-300	Low	hsa-miR-30e*/mmu-miR-30e*/rno-miR-30e*	Low
hsa-miR-125b/mmu-miR-125b-5p/rno-miR-125b-5p	High	hsa-miR-620	Low	hsa-miR-183*/mmu-miR-183*	Low
hsa-miR-145/mmu-miR-145/rno-miR-145	High	hsa-miR-130b*/mmu-miR-130b*	Low	hsa-miR-144*	Low
hsa-miR-22/mmu-miR-22/rno-miR-22	High	hsa-miR-20b/mmu-miR-20b/rno-miR-20b-5p	Low	hsa-miR-574-3p/mmu-miR-574-3p	Low
hsa-miR-21/mmu-miR-21/rno-miR-21	High	kshv-miR-K12-3	Low	hsa-miR-889	Low
hsa-miR-199a-3p/hsa-miR-199b-3p/mmu-miR-199a-3p/mmu-miR-199b/rno-miR-199a-3p	High	hsa-miR-28-3p/rno-miR-28*	Low	hsa-miR-525-5p	Low
hsa-miR-24/mmu-miR-24/rno-miR-24	High	hsa-miR-557	Low	kshv-miR-K12-8	Low
hsa-miR-143/mmu-miR-143/rno-miR-143	High	hsa-miR-150/mmu-miR-150/rno-miR-150	Low	hsa-miR-32/mmu-miR-32/rno-miR-32	Low
hsa-miR-23b/mmu-miR-23b/rno-miR-23b	High	hsa-miR-98/mmu-miR-98/rno-miR-98	Low	hsa-miR-938	Low
hsa-miR-23a/mmu-miR-23a/rno-miR-23a	High	hsa-miR-486-5p/mmu-miR-486-5p	Low	hsa-miR-198	Low
hsa-miR-142-3p/mmu-miR-142-3p/rno-miR-142-3p	High	hsa-miR-518a-5p/hsa-miR-527	Low	hsa-miR-186/mmu-miR-186/rno-miR-186	Low
hsa-let-7a/mmu-let-7a/rno-let-7a	High	hsa-miR-302d*	Low	hsa-miR-18a/mmu-miR-18a/rno-miR-18a	Low

ABC miRNA list	ABC vs others	ABC miRNA list (con't)	ABC vs others	ABC miRNA list (con't)	ABC vs others
hsa-miR-146b-5p/mmu-miR-146b/rno-miR-146b	High	hsa-miR-516a-5p	Low	hsa-miR-516b	Low
hsa-miR-27a/mmu-miR-27a/rno-miR-27a	High	hsa-miR-148b/mmu-miR-148b/rno-miR-148b-3p	Low	hsa-miR-625*	Low
hsa-miR-30a/mmu-miR-30a/rno-miR-30a	High	hsa-miR-25*	Low	hsa-miR-551b*	Low
hsa-miR-27b/mmu-miR-27b/rno-miR-27b	High	hsa-miR-374b/mmu-miR-374/rno-miR-374	Low	hsa-miR-885-5p	Low
hsa-let-7c/mmu-let-7c/rno-let-7c	High	hsa-miR-638	Low	hsa-miR-891a	Low
hsa-miR-921	Low	hsa-miR-302a/mmu-miR-302a	Low	hsa-miR-340/mmu-miR-340-5p/rno-miR-340-5p	Low
ebv-miR-BHRF1-2	Low	hsa-miR-99b*/mmu-miR-99b*/rno-miR-99b*	Low	hsa-let-7d/mmu-let-7d/rno-let-7d	Low
hsa-miR-199a-5p/mmu-miR-199a-5p/rno-miR-199a-5p	Low	hsa-miR-29c*/mmu-miR-29c*/rno-miR-29c*	Low	hsa-miR-151-5p/mmu-miR-151-5p/rno-miR-151	Low
hsa-miR-768-5p	Low	hsa-miR-138/mmu-miR-138/rno-miR-138	Low	hsa-miR-18b	Low
hsa-miR-491-3p	Low	hsa-miR-766	Low	ebv-miR-BHRF1-1	Low
hsa-miR-185/mmu-miR-185/rno-miR-185	Low	hsa-miR-488	Low	hsa-miR-510	Low
ebv-miR-BART17-5p	Low	hsa-miR-498	Low	hsa-miR-625	Low
hsa-miR-32*	Low	hsa-miR-339-5p/mmu-miR-339-5p/rno-miR-339-5p	Low	mghv-miR-M1-8	Low
hsa-miR-335/mmu-miR-335-5p/rno-miR-335	Low	hsa-miR-193b*	Low	ebv-miR-BART19-3p	Low
hsa-miR-149*	Low	hsa-miR-299-5p/mmu-miR-299*/rno-miR-299	Low	hsa-miR-147	Low
hsa-miR-576-3p	Low	ebv-miR-BART8*	Low	hsa-miR-28-5p/mmu-miR-28/rno-miR-28	Low
hsa-miR-214/mmu-miR-214/rno-miR-214	Low	hsa-miR-107/mmu-miR-107/rno-miR-107	Low	ebv-miR-BART13	Low
hsa-miR-184/mmu-miR-184/rno-miR-184	Low	hsa-miR-519e*	Low	hsa-miR-25/mmu-miR-25/rno-miR-25	Low

ABC miRNA list	ABC vs others	ABC miRNA list (con't)	ABC vs others	ABC miRNA list (con't)	ABC vs others
hsa-miR-520d-5p hsa-miR-518c*	Low	hsa-miR-146b-3p hsa-miR-552	Low	hsa-miR-519d hsa-miR-361-5p/mmu-miR-361/rno-miR-361	Low
hsa-miR-801/mmu-miR-801	Low	hsa-miR-509-5p	Low	hsa-miR-331-3p/mmu-miR-331-3p/rno-miR-331	Low
hsa-miR-298	Low	hsa-miR-574-5p/mmu-miR-574-5p	Low	hsa-miR-423-3p/mmu-miR-423-3p/rno-miR-423	Low
hsa-miR-634	Low	hsa-miR-524-5p	Low	hsa-miR-93/mmu-miR-93/rno-miR-93	Low
hsa-miR-583	Low	mghv-miR-M1-7-5p	Low		
hsa-miR-187*	Low	hsa-miR-659	Low		
hsa-miR-30d/mmu-miR-30d/rno-miR-30d	Low	hcmv-miR-UL148D	Low		
hsa-miR-129-5p/mmu-miR-129-5p/rno-miR-129	Low	hsa-miR-92a/mmu-miR-92a/rno-miR-92a	Low		

Table 12: Predictor microRNAs that distinguish chronic lymphocytic leukemia from all other B cell malignancies in the study

CLL miRNA list	CLL vs others	CLL miRNA list (con't)	CLL vs others	CLL miRNA list (con't)	CLL vs others
hsa-miR-30e*/mmu-miR-30e*/rno-miR-30e*	High	hsa-miR-199a-5p/mmu-miR-199a-5p/rno-miR-199a-5p	High	hsa-miR-185*	Low
hsa-miR-32/mmu-miR-32/rno-miR-32	High	hsa-miR-649	High	hsa-miR-503	Low
hsa-let-7g/mmu-let-7g	High	hsa-miR-191/mmu-miR-191/rno-miR-191	High	hsa-miR-126*/mmu-miR-126-5p/rno-miR-126*	Low
hsa-miR-186/mmu-miR-186/rno-miR-186	High	hsa-miR-30e/mmu-miR-30e/rno-miR-30e	High	hsa-miR-10b/mmu-miR-10b/rno-miR-10b	Low
hsa-miR-140-5p/mmu-miR-140/rno-miR-140	High	hsa-miR-107/mmu-miR-107/rno-miR-107	High	hsa-miR-628-3p	Low
hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	High	hsa-miR-93/mmu-miR-93/rno-miR-93	High	hsa-miR-422a	Low
hsa-miR-	High	hsa-miR-29c/mmu-	High	hsa-miR-193a-5p	Low

CLL miRNA list	CLL vs others	CLL miRNA list (con't)	CLL vs others	CLL miRNA list (con't)	CLL vs others
487b/mmu-miR-487b/rno-miR-487b		miR-29c/rno-miR-29c			
hsa-miR-150/mmu-miR-150/rno-miR-150	High	hsa-miR-541*	High	hsa-miR-143/mmu-miR-143/rno-miR-143	Low
hsa-miR-147	High	hsa-miR-888*	High	hsa-miR-371-5p	Low
hsa-miR-486-5p/mmu-miR-486	High	hsa-miR-549	High	hsa-miR-100/mmu-miR-100/rno-miR-100	Low
hsa-miR-144*		hsa-miR-19a/mmu-miR-19a/rno-miR-19a	High	hsa-miR-365/mmu-miR-365/rno-miR-365	Low
hsa-miR-154/mmu-miR-154/rno-miR-154	High	hsa-miR-342-3p/mmu-miR-342-3p/rno-miR-342-3p	High	hsa-miR-145/mmu-miR-145/rno-miR-145	Low
hsa-miR-28-5p/mmu-miR-28/rno-miR-28	High	hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p	High	kshv-miR-K12-6-3p	Low
hsa-miR-299-5p/mmu-miR-299*/rno-miR-299	High	hsa-miR-801/mmu-miR-801	High	ebv-miR-BART6-3p	Low
hsa-miR-33a/mmu-miR-33/rno-miR-33	High	hsa-let-7i/mmu-let-7i/rno-let-7i	High	hsa-miR-220c	Low
hsa-miR-363/mmu-miR-363/rno-miR-363	High	hsa-miR-26a/mmu-miR-26a/rno-miR-26a	High	hsa-miR-519c-5p/hsa-miR-519b-5p/hsa-miR-523*/hsa-miR-518e*/hsa-miR-522*/hsa-miR-519a*	Low
hsa-miR-891a	High	hsa-miR-15a/mmu-miR-15a	High	hsa-miR-130a/mmu-miR-130a/rno-miR-130a	Low
hsa-miR-768-5p	High	hsa-miR-195/mmu-miR-195/rno-miR-195	High	hsa-miR-424	Low
hsa-miR-361-5p/mmu-miR-361/rno-miR-361	High	hsa-miR-106b/mmu-miR-106b/rno-miR-106b	High	hsa-miR-483-5p	Low
hsa-miR-519d	High	hsa-miR-26b/mmu-miR-26b/rno-miR-26b	High	hsa-miR-193b	Low
hsa-miR-335/mmu-miR-335-5p/rno-miR-335	High	hsa-miR-15b/mmu-miR-15b/rno-miR-15b	High	hsa-miR-637	Low
hsa-miR-668/mmu-miR-668	High	hsa-miR-222/mmu-miR-222/rno-miR-222	High	hsa-miR-920	Low
hsa-let-7f/mmu-let-7f/rno-let-7f	High	hsa-miR-185/mmu-miR-185/rno-miR-185	High	hsa-miR-488	Low

CLL miRNA list	CLL vs others	CLL miRNA list (con't)	CLL vs others	CLL miRNA list (con't)	CLL vs others
hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	High	hsa-miR-550	High	ebv-miR-BHRF1-2	Low
hsa-miR-223/mmu-miR-223/rno-miR-223	High	hsa-let-7e/mmu-let-7e/rno-let-7e	Low	hsa-miR-526b	Low
hsa-miR-140-3p/mmu-miR-140*/rno-miR-140*	High	hsa-miR-24/mmu-miR-24/rno-miR-24	Low	hsa-miR-126/mmu-miR-126-3p/rno-miR-126	Low
hsa-miR-144/mmu-miR-144/rno-miR-144	High	hsa-miR-30c-2*/mmu-miR-30c-2*/rno-miR-30c-2*	Low	hsa-miR-943	Low
hsa-miR-638	High	hsa-miR-765	Low	hsa-miR-199a-3p/hsa-miR-199b-3p/mmu-miR-199a-3p/mmu-miR-199b/rno-miR-199a-3p	Low
hsa-miR-30d/mmu-miR-30d/rno-miR-30d	High	mghv-miR-M1-4	Low	mghv-miR-M1-3	Low
hsa-miR-423-3p/mmu-miR-423-3p/rno-miR-423	High	hsa-miR-933	Low	hsa-miR-934	Low
hsa-miR-155	High	hsa-miR-620	Low	hsa-miR-886-5p	Low
hsa-miR-101/mmu-miR-101a/rno-miR-101a	High	hsa-miR-30b*	Low	hsa-miR-200b*/mmu-miR-200b*	Low
hsa-miR-20b/mmu-miR-20b/rno-miR-20b-5p	High	hsa-miR-658	Low	hsa-miR-485-3p/mmu-miR-485*	Low
hsa-miR-374a	High	hsa-miR-10a/mmu-miR-10a/rno-miR-10a-5p	Low	hsa-miR-181a/mmu-miR-181a/rno-miR-181a	Low
hsa-miR-25/mmu-miR-25/rno-miR-25	High	hsa-miR-665	Low	hsa-miR-125b/mmu-miR-125b-5p/rno-miR-125b-5p	Low

Table 13: Predictor microRNAs that distinguish Hodgkin's lymphoma from all other B cell malignancies in the study

HL miRNA list	HL vs others	HL miRNA list (con't)	HL vs others	HL miRNA list (con't)	HL vs others
hsa-miR-338-5p/mmu-miR-338-5p/rno-miR-338*	High	hsa-miR-500*	High	hsa-miR-502-3p	High
hsa-miR-433/mmu-miR-433/rno-miR-433	High	hsa-miR-24-2*/mmu-miR-24-2*/rno-miR-24-2*	High	hsa-miR-29c*/mmu-miR-29c*/rno-miR-29c*	High

HL miRNA list	HL vs others	HL miRNA list (con't)	HL vs others	HL miRNA list (con't)	HL vs others
hsa-miR-552		hsa-miR-382/mmu-miR-382/rno-miR-382		hsa-miR-937	
	High		High		High
hsa-miR-202	High	ebv-miR-BART8*	High	hsa-miR-515-5p	High
hsa-miR-299-3p		hsa-miR-125b-2*/rno-miR-125b*	High	hsa-miR-153/mmu-miR-153/rno-miR-153	High
hsa-miR-509-3-5p	High	hsa-miR-194*	High	hsa-miR-519e*	High
hsa-miR-490-5p		hsa-miR-297/mmu-miR-297a	High	hsa-miR-128/mmu-miR-128/rno-miR-128	High
hsa-miR-508-5p	High	hsa-miR-610	High	hsa-miR-516b	High
hsa-miR-181a-2*		hsa-miR-575		hsa-miR-532-5p/mmu-miR-532-5p/rno-miR-532-5p	High
	High		High	kshv-miR-K12-8	High
hsa-miR-663	High	hsa-miR-21*	High	hsa-miR-455-3p	
hsa-miR-326/mmu-miR-326/rno-miR-326	High	hsa-miR-936			High
hsa-miR-542-3p/mmu-miR-542-3p/rno-miR-542-3p	High	kshv-miR-K12-6-5p	High	hsa-miR-27a*/mmu-miR-27a*/rno-miR-27a*	High
hsa-miR-492	High	hsa-miR-553	High	hsa-miR-510	High
hsa-miR-584		hsa-miR-652/mmu-miR-652/rno-miR-652	High	hsa-miR-505/rno-miR-505	
	High		High		High
hsa-miR-654-5p		hsa-miR-877/mmu-miR-877/rno-miR-877	High	hsa-miR-187*	
	High		High		High
ebv-miR-BART20-3p		hsa-miR-526a/hsa-miR-520c-5p/hsa-miR-518d-5p	High	hsa-miR-498	
	High	hsa-miR-122*	High		High
hsa-miR-542-5p/mmu-miR-542-5p/rno-miR-542-5p	High		High	hsa-miR-625	
ebv-miR-BART9*	High	hsa-miR-576-5p	High		High
	High	mghv-miR-M1-6	High	hsa-miR-129-5p/mmu-miR-129-5p/rno-miR-129	High
hsa-miR-124/mmu-miR-124/rno-miR-124	High		High	ebv-miR-BHRF1-2	
hsa-miR-551a	High	hsa-miR-551b*	High		High
hsa-miR-208a/mmu-miR-208a/rno-miR-208		hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	High	hsa-miR-143*	High
	High		High	kshv-miR-K12-3	
hsa-miR-220b		hsa-miR-137/mmu-miR-137/rno-miR-137	High	hsa-miR-660	High
	High		High		High

HL miRNA list	HL vs others	HL miRNA list (con't)	HL vs others	HL miRNA list (con't)	HL vs others
hsa-miR-615-3p/mmu-miR-615-3p	High	ebv-miR-BART18-3p	High	hsa-miR-25*	High
hsa-miR-135a*/mmu-miR-135a*	High	hsa-miR-452	High	hsa-miR-29a*/mmu-miR-29a*/rno-miR-29a*	High
hiv1-miR-H1	High	hsa-miR-23a*/rno-miR-23a*	High	hsa-miR-422a	High
hsa-miR-124*/mmu-miR-124*/rno-miR-124*	High	hsa-miR-617	High	hsa-miR-518a-5p/hsa-miR-527	High
hsa-miR-502-5p	High	hsa-miR-550*	High	hsa-miR-519c-5p/hsa-miR-519b-5p/hsa-miR-523*/hsa-miR-518e*/hsa-miR-522*/hsa-miR-519a*	High
hsa-miR-92b*	High	hsa-miR-557	High	hsa-miR-28-3p/rno-miR-28*	High
hsa-miR-518a-3p	High	hsa-miR-331-5p/mmu-miR-331-5p	High	hsa-miR-300	High
hsa-miR-377*	High	hsa-miR-296-5p/mmu-miR-296-5p/rno-miR-296*	High	hsa-miR-130a/mmu-miR-130a/rno-miR-130a	High
hsa-miR-125a-3p/mmu-miR-125a-3p/rno-miR-125a-3p	High	mghv-miR-M1-2	High	hsa-miR-583	High
hsa-miR-30c-1*/mmu-miR-30c-1*/rno-miR-30c-1*	High	ebv-miR-BART6-3p	High	hsa-miR-149*	High
hsa-miR-650	High	hsa-miR-518b	High	hsa-miR-184/mmu-miR-184/rno-miR-184	High
hsa-miR-629	High	hsa-miR-99b/mmu-miR-99b/rno-miR-99b	High	hsa-miR-625*	High
hsa-miR-296-3p/mmu-miR-296-3p/rno-miR-296	High	hsa-miR-525-5p	High	hsa-miR-99a/mmu-miR-99a/rno-miR-99a	High
hsa-miR-425*/mmu-miR-425*	High	hsa-miR-589	High	hsa-miR-199b-5p	High
hsa-miR-514	High	hsa-miR-7-2*	High	hsa-miR-513a-5p	High
hsa-miR-519e	High	hsa-miR-490-3p/mmu-miR-490	High	hsa-miR-494/mmu-miR-494/rno-miR-494	High
hsa-miR-938	High	hsa-miR-150*/mmu-miR-150*	High	mghv-miR-M1-4	High
hsa-miR-340*/mmu-miR-340-3p/rno-miR-340-3p	High	hsa-miR-17*/rno-miR-17-3p	High	hsa-miR-634	High

HL miRNA list	HL vs others	HL miRNA list (con't)	HL vs others	HL miRNA list (con't)	HL vs others
hsa-miR-657	High	hsa-miR-509-3p	High	hsa-miR-923	High
hsa-miR-9*/mmu-miR-9*/rno-miR-9*	High	ebv-miR-BHRF1-1	High	hsa-miR-503	High
ebv-miR-BART7*		hsa-miR-183*/mmu-miR-183*		ebv-miR-BART2-3p	
	High		High		High
hsa-miR-612	High	hsa-miR-635	High	hsa-miR-520d-5p	High
hsa-miR-640		hsa-miR-130b/mmu-miR-130b/rno-miR-130b	High	hsa-miR-30b*	
	High	mghv-miR-M1-8			High
hsa-miR-623	High	hsa-miR-887	High	hsa-miR-30c-2*/mmu-miR-30c-2*/rno-miR-30c-2*	High
hsa-miR-99b*/mmu-miR-99b*/rno-miR-99b*	High			hsa-miR-658	
hsa-miR-645		hsa-miR-210/mmu-miR-210/rno-miR-210	High	hsa-miR-921	High
	High	hsa-miR-766	High		High
hsa-miR-484/mmu-miR-484/rno-miR-484	High		High	hsa-miR-423-5p/mmu-miR-423-5p	High
hsa-miR-376a*		hsa-miR-671-5p/mmu-miR-671-5p	High	hsa-miR-933	High
	High	hsa-miR-659	High		High
hsa-miR-345	High			hsa-miR-23b/mmu-miR-23b/rno-miR-23b	Low
hsa-miR-586		hsa-miR-330-5p/mmu-miR-330/rno-miR-330	High	hsa-miR-27b/mmu-miR-27b/rno-miR-27b	Low
	High	hsa-miR-323-3p/mmu-miR-323-3p/rno-miR-323	High	hsa-miR-550	
hsa-miR-622	High	ebv-miR-BART13	High		Low
hsa-miR-206/mmu-miR-206/rno-miR-206	High		High	hsa-let-7a/mmu-let-7a/rno-let-7a	Low
hcmv-miR-US25-1*	High	ebv-miR-BART5	High	hsa-miR-24/mmu-miR-24/rno-miR-24	Low
	High	hsa-miR-602	High	hsa-miR-451/mmu-miR-451/rno-miR-451	Low
hsa-miR-302c*	High	hcmv-miR-UL148D		hsa-miR-30a/mmu-miR-30a/rno-miR-30a	
hsa-miR-106b*/mmu-miR-106b*/rno-miR-106b*	High		High		Low
hsa-miR-500	High	hsa-miR-373*	High	hsa-miR-20b/mmu-miR-20b/rno-miR-20b-5p	Low

HL miRNA list	HL vs others	HL miRNA list (con't)	HL vs others	HL miRNA list (con't)	HL vs others
hsa-miR-890	High	hsa-miR-526b	High	hsa-miR-26a/mmu-miR-26a/rno-miR-26a	Low
hsa-miR-10a*/mmu-miR-10a*/rno-miR-10a-3p	High	hsa-miR-328/mmu-miR-328/rno-miR-328	High	hsa-miR-26b/mmu-miR-26b/rno-miR-26b	Low
kshv-miR-K12-1	High	hsa-miR-874/mmu-miR-874/rno-miR-874	High	hsa-miR-101/mmu-miR-101a/rno-miR-101a	Low
hsa-miR-629*	High	ebv-miR-BART19-3p	High	hsa-miR-106b/mmu-miR-106b/rno-miR-106b	Low
hsa-miR-193b*	High	hsa-miR-595	High	hsa-miR-16/mmu-miR-16/rno-miR-16	Low
ebv-miR-BHRF1-3	High	hsa-miR-889	High	hsa-miR-29b/mmu-miR-29b/rno-miR-29b	Low
hsa-miR-183/mmu-miR-183/rno-miR-183	High	mghv-miR-M1-7-5p	High	hsa-miR-768-3p	Low
hsa-let-7b*/mmu-let-7b*/rno-let-7b*	High	hsa-miR-483-5p	High	hsa-miR-30e/mmu-miR-30e/rno-miR-30e	Low
hsa-miR-409-5p/mmu-miR-409-5p/rno-miR-409-5p	High	hsa-miR-487b/mmu-miR-487b/rno-miR-487b	High	hsa-miR-106a	Low
hsa-miR-585	High	hsa-miR-675	High	hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p	Low
hsa-miR-526b*	High	hsa-miR-220c	High	hsa-miR-144/mmu-miR-144/rno-miR-144	Low
hsa-miR-337-3p	High	mghv-miR-M1-7-3p	High	hsa-miR-17/mmu-miR-17/rno-miR-17-5p/rno-miR-17	Low
hsa-miR-212/mmu-miR-212/rno-miR-212	High	hsa-miR-485-3p/mmu-miR-485*	High	hsa-miR-15b/mmu-miR-15b/rno-miR-15b	Low
hsa-miR-548b-3p	High	hsa-miR-198	High	hsa-miR-30c/mmu-miR-30c/rno-miR-30c	Low
hcmv-miR-UL112	High	hsa-miR-483-3p	High	hsa-miR-142-3p/mmu-miR-142-3p/rno-miR-142-3p	Low
hsa-miR-601	High	hcmv-miR-UL70-3p	High	hsa-miR-20a/mmu-miR-20a/rno-miR-20a	Low
hsa-let-7d*/mmu-let-7d*/rno-let-7d*	High	hsa-miR-149/mmu-miR-149	High	hsa-miR-30b/mmu-miR-30b/rno-miR-30b-5p	Low
hsa-miR-181b/mmu-miR-181b/rno-miR-181b	High	hsa-miR-516a-5p	High	hsa-miR-19a/mmu-miR-19a/rno-miR-19a	Low
hsa-miR-195*	High	hsa-miR-145*/mmu-miR-145*	High	hsa-miR-19b/mmu-miR-19b/rno-miR-19b	Low

HL miRNA list	HL vs others	HL miRNA list (con't)	HL vs others	HL miRNA list (con't)	HL vs others
kshv-miR-K12-5	High	hsa-miR-656	High		

[00152] From the data in Tables 10 through 13, we identified subsets of microRNAs that are sufficient to distinguish each of the six B cell malignancies from the other five. We selected only microRNAs that are expressed more highly in the selected B cell malignancy. Those microRNAs are listed in Tables 14 and 15. In certain embodiments, each of the microRNAs listed in Tables 14 and 15 can be used to distinguish one B cell malignancy from the other five.

Table 14: Predictor microRNAs that distinguish activated B-cell (ABC) DLBCL, germinal center B-cell like (GCB) DLBCL, and Burkitt lymphoma

ABC High	GCB High	BL High
hsa-miR-22/mmu-miR-22/rno-miR-22	hsa-miR-93/mmu-miR-93/rno-miR-93	hsa-miR-628-3p
hsa-miR-21/mmu-miR-21/rno-miR-21	hsa-miR-103/mmu-miR-103/rno-miR-103	
hsa-miR-24/mmu-miR-24/rno-miR-24	hsa-miR-320/mmu-miR-320/rno-miR-320	
hsa-miR-23b/mmu-miR-23b/rno-miR-23b	hsa-miR-125a-5p/mmu-miR-125a-5p/rno-miR-125a-5p	
hsa-miR-23a/mmu-miR-23a/rno-miR-23a		
hsa-let-7a/mmu-let-7a/rno-let-7a		
hsa-let-7c/mmu-let-7c/rno-let-7c		

Table 15: Predictor microRNAs that distinguish chronic lymphocytic leukemia, follicular lymphoma, and Hodgkin's lymphoma

CLL High	FL High	HL High
hsa-miR-32/mmu-miR-32/rno-miR-32	hsa-miR-152/mmu-miR-152/rno-miR-152	hsa-miR-498
hsa-miR-150/mmu-miR-150/rno-miR-150	hsa-miR-885-5p	hsa-miR-525-5p
hsa-miR-140-5p/mmu-miR-140/rno-miR-140	hsv1-miR-H1	hsa-miR-551b*
hsa-let-7g/mmu-let-7g	hsa-miR-548d-5p	hsa-miR-340*/mmu-miR-340-3p/rno-miR-340-3p
hsa-miR-154/mmu-miR-154/rno-miR-154	hsa-miR-488	hsa-miR-494/mmu-miR-494/rno-miR-494
hsa-miR-486-5p/mmu-miR-486	ebv-miR-BART16	hsa-miR-183*/mmu-miR-183*
hsa-miR-101/mmu-miR-101a/rno-miR-101a	hsa-miR-22*/mmu-miR-22*/rno-miR-22*	hsa-miR-659
hsa-miR-30e/mmu-miR-30e/rno-miR-30e	hsa-miR-513a-3p	hsa-miR-193b*

CLL High	FL High	HL High
hsa-miR-768-5p	hsa-miR-708/mmu-miR-708/rno-miR-708	hsa-miR-766
hsa-miR-363/mmu-miR-363/rno-miR-363	hsa-miR-425/mmu-miR-425/rno-miR-425	hsa-miR-516a-5p
hsa-miR-668/mmu-miR-668	hsa-miR-337-3p	hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p
hsa-miR-147	ebv-miR-BART17-5p	ebv-miR-BART6-3p
hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	hsa-miR-221*	ebv-miR-BART8*
hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p	hsa-miR-92b/mmu-miR-92b/rno-miR-92b	hsa-miR-509-3-5p
hsa-miR-199a-5p/mmu-miR-199a-5p/rno-miR-199a-5p	hsa-miR-197/mmu-miR-197	hsa-miR-602
hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	hsa-miR-32*	ebv-miR-BHRF1-1
hsa-miR-891a	hsa-miR-342-5p/mmu-miR-342-5p/rno-miR-342-5p	mghv-miR-M1-2
hsa-miR-550	hsa-miR-524-5p	hsa-miR-145*/mmu-miR-145*
hsa-miR-801/mmu-miR-801	hsa-miR-34c-5p/mmu-miR-34c/rno-miR-34c	hsa-miR-296-5p/mmu-miR-296-5p/rno-miR-296*
hsa-miR-549	hsa-let-7e/mmu-let-7e/rno-let-7e	hsa-miR-17*/rno-miR-17-3p
hsa-miR-888*	hsa-miR-151-3p	hsa-miR-452
	hsa-miR-744/mmu-miR-744	hsa-miR-326/mmu-miR-326/rno-miR-326
	hsa-miR-574-3p/mmu-miR-574-3p	hsa-miR-652/mmu-miR-652/rno-miR-652
	hsa-miR-600	hsa-miR-623
	hsa-miR-20b*	hsa-miR-194*
	hsa-miR-194/mmu-miR-194/rno-miR-194	hsa-miR-125a-3p/mmu-miR-125a-3p/rno-miR-125a-3p
	hsa-miR-363*/rno-miR-363*	hsa-miR-10a*/mmu-miR-10a*/rno-miR-10a-3p
	hsa-miR-155*	hsa-miR-519e
	hsa-miR-34b/mmu-miR-34b-3p	hsa-miR-502-5p
	hsa-miR-922	hsa-miR-124*/mmu-miR-124*/rno-miR-124*
	hsa-miR-497/mmu-miR-497/rno-miR-497	hsa-miR-345
	hsa-miR-493	hsa-miR-584
	hsa-miR-138/mmu-miR-138/rno-miR-138	hsa-miR-650
	hsa-miR-215	hsa-miR-202
	hsa-miR-302a/mmu-miR-302a	hsa-miR-548b-3p
	hsa-miR-96/mmu-miR-96/rno-miR-96	hsa-miR-492

CLL High	FL High	HL High
	hsa-miR-218-2*/mmu-miR-218-2*/rno-miR-218*	hsa-miR-135a*/mmu-miR-135a*
	kshv-miR-K12-7	ebv-miR-BART20-3p
	hsa-miR-301a/mmu-miR-301a/rno-miR-301a	hsa-miR-586
		hsa-miR-338-5p/mmu-miR-338-5p/rno-miR-338*
		hsa-miR-92b*
		hiv1-miR-H1
		hsa-miR-508-5p
		hsa-miR-542-5p/mmu-miR-542-5p/rno-miR-542-5p
		hsa-miR-490-5p
		hsa-miR-663
		hsa-miR-433/mmu-miR-433/rno-miR-433

[00153] Finally, we identified sets of microRNAs that can distinguish between each pair of B cell malignancies in the study. Lists of those microRNAs are shown in Appendix B, Tables 16 to 30. In certain embodiments, each of the listed microRNAs is sufficient to distinguish between the two B cell malignancies listed in the table description.

[00154] The consistent expression of a number of miRNAs in a diverse set of B cell malignancies suggests a role for miRNAs in the maintenance of tumor phenotype. Assays for stage-specific B cell markers such as BCL6, a marker for GC cells, are essential in the clinical diagnosis of B cell malignancies. Our data suggest that stage-specific biology in B cell malignancies is retained at the miRNA level. Recent work has demonstrated the utility of gene expression profiling in reliably distinguishing closely related B cell malignancies. See Hummel et al. *N Engl J Med.* 2006;354:2419-2430; Dave et al. *N Engl J Med.* 2006;354:2431-2442. However, clinical translation of gene expression profiling has proved to be difficult because of the need for freshly frozen tissue. Since intact miRNAs can be isolated from tissues preserved using standard methods (see, e.g., Doleshal et al. *J Mol Diagn.* 2008;10:203-211; Xi et al. *Rna.* 2007;13:1668-1674), diagnostic methods based upon miRNA profiles could be fairly easy to translate to clinical use.

[00155] Interestingly, in contrast to a previous study (Lu et al. *Nature* 2005;435:834-838), we did not note a decrease in the expression of the total number or overall expression levels of miRNAs in B cell malignancies compared to normal lymph nodes. Although B cell

malignancies maintain the expression of a number of stage-specific miRNAs, their miRNA expression patterns are clearly deranged compared to normal lymph nodes. The consequences of altered miRNA expression in B cell tumors would be important to explore in future studies.

[00156] In conclusion, our study demonstrates that mature B cell subsets have distinct patterns of microRNA expression, suggesting a role for miRNAs in B cell differentiation. We provide experimental evidence that transcription factors such as LM02 and PRDMI are direct targets of differentially expressed miRNAs. B cell malignancies demonstrate a distinct pattern of miRNA expression that could be useful in distinguishing morphologically identical subtypes of these tumors. The conserved expression of stage-specific microRNAs in normal and malignant B cells suggests a role for microRNAs in the maintenance of the mature B cell phenotype.

Example 6: Differential expression of miRNAs in ABC DLBCL vs. GCB DLBCL malignancies

[00157] As discussed above, microRNAs have shown promise as biomarkers in a number of malignancies. Diffuse large B cell lymphoma (DLBCL) is the most common form of lymphoma and is known to comprise at least 2 molecularly distinct subgroups with different responses to standard therapy. These two distinct subgroups are typically identified as ABC DLBCL and GC (or GCB) DLBCL.

[00158] However, the current methods used to distinguish GCB from non GCB DLBCL are limited fashion and can yield inconsistent results. While gene expression profiling remains the gold standard for distinguishing these 2 molecular subgroups it is not routinely performed in clinical laboratories. In an effort to expand and improve the existing analytical options we sought to develop microRNA-based assays. We created RNA libraries from 31 different samples and performed deep sequencing analysis to identify the present miRNAs.

Small RNA library creation and deep sequencing

[00159] Total RNA was extracted from the 31 samples using the phenol-chloroform method to preserve microRNAs, using Ambion reagents. Total RNA (typically 5µg) from each sample was run on denaturing polyacrylamide-urea gels. The ~17-25 nucleotide RNAs were excised from the gel, ligated to sequencing adaptors on both ends and reverse transcribed. The resulting cDNA library was PCR-amplified for 15 cycles and gel purified on 6% acrylamide gel. The gel-purified

amplicon quality and quantity were analyzed on a 6% acrylamide gel relative to oligonucleotides of known concentration and size. 120 µl of 1-4 pM library were loaded on to the Illumina cluster station, where DNA molecules were attached to high-density universal adaptors in the flow cells and amplified. The DNA clusters generated via this process were sequenced with sequencing-by-synthesis technology, where successive high-resolution images of the four-color fluorescence excitation dependent on the base incorporated during each cycle were captured. Sequencing reads were generated for each of the 31 samples and base calls were rendered using Illumina software. All the primary sequencing data and gene expression data is publicly available through the GEO archive through accession GSE22898.

[00160] The small RNA libraries from the 31 samples which were subjected to massively parallel, high-throughput sequencing using the Illumina platform generated a total of 328 million separate reads. Our approach to analyzing the sequences and discovering microRNAs broadly follows a previously described method (see, Zheng, Q., et al. GOEAST: a web-based software toolkit for Gene Ontology enrichment analysis, *Nucleic acids Res.* 2008;36 (Web Server issue:W358-363). All bioinformatics analyses were performed using a cluster of 1024 Linux computer nodes. Preprocessing was carried out using locally written Shell and Perl scripts.

[00161] From the raw sequences generated by high-throughput sequencing, the 3'- and 5'-adaptor sequences were trimmed. Low quality sequences were identified as those sequencing reads that contained stretches of consecutive identical bases or uncalled nucleotides (N) in the first 12 bases and sequencing reads shorter than 17 nucleotides. To minimize redundancy, reads were initially curtailed to the first 22 nucleotides and identical sequences were represented with a single fasta entry for analysis. Each unique sequence was mapped to the reference genome (Ensembl, build 50) and reads were filtered such that only perfect alignments (full length, 100% identity) were retained. Reads that aligned to more than five positions in the genome and reads that overlapped with the UCSC RNA genes were identified and excluded from microRNA analysis.

Identification and analysis of the captured miRNA sequences

[00162] Sequences that occurred 20 or more times in at least one sample were consolidated and annotated for the 31 samples. Genomic loci that overlapped with microRNAs described in

miRBase (version 13) were identified as known microRNAs (see Table 31). The remaining genomic loci were identified as encoding candidate novel microRNAs (see Table 32).

[00163] The vast majority (96%) of the candidate novel microRNAs were found in more than one sample, with only a small minority of microRNAs were expressed exclusively in a specific B cell subset or malignancy. Many of the microRNAs that we identified in normal and malignant B cells were expressed at ten-fold or higher levels in these non B cell cases. These findings suggest that the microRNAs we have identified are broadly expressed and may have roles in a number of diverse tissue types.

miRNA profiling using real-time PCR

[00164] miRNA expression profiling was conducted using the Applied Biosystems 384-well multiplexed real-time PCR assay using 400ng of total RNA. Eight reactions, each containing 50ng of RNA and a multiplex looped primer pool with endogenous small nucleolar (sno)-RNA controls, were used to reverse-transcribe the miRNAs in parallel fashion (see Tables 33 and 34 for primers). The completed reactions were loaded onto the 384-well plate per manufacturer's instructions, and real-time PCR was run on the ABI 7900HT Prism instrument. For each 384-well plate, we used the automatically determined cycle-threshold (C_T) using the SDS 2.2.1 software (Applied Biosystems). Consistent with manufacturer recommendations, a C_T greater than 35 was treated as undetected. The probes deemed to be present were normalized to the average expression of a sno-RNA control. The expression values were calculated as $2^{-\Delta C_T}$, then median centered to 500 and log2-transformed.

[00165] For further validation of the deep sequencing results, we selected candidate novel microRNAs (see Table 34) that were detectably measured in at the sequencing data from least one of four diffuse large B cell lymphoma (DLBCL) cases. Using stem-loop reverse transcription (Ashburner, M., et al., *Nat Genet.* (2000); 25(1):25-29) for quantitative PCR, we tested the expression of the candidate microRNAs in 101 primary tumors from patients with DLBCL and found that about 92% were detectably measured by real-time PCR in at least 10% of these cases, suggesting that real-time PCR reproducibly identifies microRNAs that are expressed in lymphomas. We also used real-time PCR to measure the expression of known microRNAs (see Table 33) in the same 101 samples and found that over 90% of these were also detected in at

least 10% of the cases using real-time PCR. We found that six of the seven RT-PCR constructs that targeted RNA hairpins that had low probability of being a microRNA resulted in no detectable signal. These results suggest that our assays have high specificity for microRNAs and that the computational predictions based on our sequencing data correctly identified microRNAs.

Differentiating ABC DLBCL vs. GCB DLBCL malignancies

[00166] Gene expression profiling of patients with DLBCL has demonstrated that the tumors comprise at least two distinct diseases with different response rates to standard chemotherapy regimens (Chen, C., et al., *Nucleic Acids Res.* (2005);33(20):e179). We hypothesized that microRNAs might be used to make this clinically important distinction for which gene expression profiling remains the gold standard. We performed gene expression profiling on 101 DLBCL cases and further subdivided these cases into the molecular subgroups.

[00167] Tumor samples from 101 patients with diffuse large B cell lymphoma were obtained at the time of diagnosis and freshly frozen. These cases were profiled using Affymetrix Gene 1.0 ST arrays. The molecular subgroups were distinguished using a Bayesian approach described previously (Ambros, V., et al., *RNA* (2003);9(3):277-279).

[00168] We found that 25 microRNAs with the highest t-statistic were equally efficacious as the gene expression profiling in differentiating the two groups of DLBCL with over 95% overlap between the classifications rendered by the two methods, using leave out one cross-validation (see Table 35). Interestingly, a subset of these 25 predictor microRNAs was candidate novel microRNAs, suggesting a biological and clinical relevance for these candidate novel microRNAs in DLBCL tumors.

[00169] Our work provides an exhaustive identification of the microRNAs in normal and malignant B cells; that is a prerequisite to the delineation of their role. Further, we have developed a comprehensive framework that spans the identification of microRNAs from deep sequencing data to measuring their expression using real-time PCR and validating their expression in primary human tumors.

[00170] It is also conceivable that some of the low-abundance microRNAs that we have identified in our study may be expressed at higher levels in other development stages or in other

cell types. This notion is confirmed by our examination of the novel microRNAs in non B cell data. For instance, a number of the microRNAs that we discovered were also present at 10-fold or higher levels in cell lines derived from breast cancer and cervical cancer, suggesting that the microRNAs that we have discovered in B cells have broad biological significance.

Deep sequencing reveals a novel miRNA cluster that regulates the TGF- β pathway

[00171] Although microRNAs appear to be distributed throughout the genome, a number of microRNAs have been found in clusters such as miR-17-92 that are transcribed from a single primary transcript and cleaved into the individual microRNAs by the enzyme DROSHA. We found 2 separate clusters of candidate novel microRNAs on chromosome 9 and chromosome 14 (within the IgH locus), respectively. The first cluster was previously annotated as a hypothetical gene *LOC100130622*, and subsequently discarded from Refseq when no associated protein was identified. Our data demonstrate that this cluster (miR-2355), conserved only in primates, encodes 6 separate microRNAs: has-miR-2355a-1, has-miR-2356-1, has-miR-2355a-2, has-miR-2356-2, hsa-miR2355a-3, and hsa-miR-2355b (see Table 32 for sequence).

[00172] In order to evaluate whether the microRNAs encoded in these clusters originate from the same primary transcript, we took KMS12 multiple myeloma cells which express these microRNAs and used siRNA to knock-down the expression of the microRNA processing enzyme Drosha. This enzyme acts at the first step of microRNA processing by cleaving microRNA precursors from the primary transcript. We found that decreased Drosha expression was associated with increased accumulation of primary transcripts of both the miR-17-92 cluster as well as the novel miR-2355 cluster. MicroRNAs from miR-2355 cluster were found to be expressed more highly in normal germinal center (GC) B cells compared to memory cells.

[00173] The microRNAs of this cluster all share the same seed sequence, suggesting that they target the same genes. Among the computationally predicted targets of this microRNA cluster, we identified SMAD2 and SMAD3 which are well known mediators of the TGF-beta signaling pathway. We noted that gene expression of both SMAD2 and SMAD3 in our set of 101 DLBCLs were inversely correlated with this cluster ($P < 0.001$, correlation test). Gene set enrichment analysis revealed that expression of the TGF-beta pathway in DLBCL samples varied inversely with the expression of the microRNA cluster, with a higher expression of the microRNA

associated with a lower expression of the pathway ($P < 10^{-6}$), which has been noted as a factor in the biology of these tumors.

Table 31: miRNAs identified by deep sequencing analysis.

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
1	CUGGCAAGCUACUGCCUUGCU	hsa-let-7*	hsa-let-7i	hsa-let-7i*	MIMAT0004585	CUGGCAAGCUACUGCCUUGCU	393
2	CCACGGAUGUUUGAGCAUGUGC	hsa-mir-105-1*	hsa-mir-105-1	hsa-mir-105*	MIMAT0004516	ACGGAUGUUUGAGCAUGUGCUA	394
3	CCACGGAUGUUUGAGCAUGUGC	hsa-mir-105-2*	hsa-mir-105-2	hsa-mir-105*	MIMAT0004516	ACGGAUGUUUGAGCAUGUGCUA	395
4	UACUGCAAUGUAAAGCACUUCUU	hsa-mir-106a*	hsa-mir-106a	hsa-mir-106a*	MIMAT0004517	CUGCAAUGUAAAGCACUUCUAC	396
5	CAUUAUUACUUUUUGGUACGCG	hsa-mir-126*	hsa-mir-126	hsa-mir-126*	MIMAT0000444	CAUUAUUACUUUUUGGUACGCG	397
6	AAGCCCUUACCCCAAAAAGUUAU	hsa-mir-129*	hsa-mir-129-1	hsa-mir-129*	MIMAT0004548	AAGCCCUUACCCCAAAAAGUUAU	398
7	AAGCCCUUACCCCAAAAAGCAU	hsa-mir-129-2*	hsa-mir-129-2	hsa-mir-129-3p	MIMAT0004605	AAGCCCUUACCCCAAAAAGCAU	399
8	UCUACAGUGCACGUGUCUCCAG	hsa-mir-139-5p	hsa-mir-139	hsa-mir-139-5p	MIMAT0000250	UCUACAGUGCACGUGUCUCCAG	400
9	CUGGUACAGGCCUGGGGACAG	hsa-mir-150*	hsa-mir-150	hsa-mir-150*	MIMAT0004610	CUGGUACAGGCCUGGGGACAG	401
10	ACUGCAGUGAAGGCACUUGUAG	hsa-mir-17*	hsa-mir-17	hsa-mir-17*	MIMAT0000071	ACUGCAGUGAAGGCACUUGUAG	402
11	UGAAUUACCGAAGGGCCAUAA	hsa-mir-183*	hsa-mir-183	hsa-mir-183*	MIMAT0004560	GUGAAUUACCGAAGGGCCAUAA	403
12	AGGGGCGGCUUUCUUGGUC	hsa-mir-185*	hsa-mir-185	hsa-mir-185*	MIMAT0004611	AGGGGCGGCUUUCUUGGUC	404
13	ACUGCCCUAAGUCUCCUUCUGG	hsa-mir-18a*	hsa-mir-18a	hsa-mir-18a*	MIMAT0002891	ACUGCCCUAAGUCUCCUUCUGG	405
14	AACUGGCCUACAAAGUCCAGU	hsa-mir-193a-3p	hsa-mir-193a	hsa-mir-193a-3p	MIMAT0000459	AACUGGCCUACAAAGUCCAGU	406
15	CGGGUUUUUGAGGGCGAGAUGA	hsa-mir-193b*	hsa-mir-193b	hsa-mir-193b*	MIMAT0004767	CGGGUUUUUGAGGGCGAGAUGA	407
16	CCCAGUGUUCAGACUACCUUGUC	hsa-mir-199a-2*	hsa-mir-199a-2	hsa-mir-199a-5p	MIMAT0000231	CCCAGUGUUCAGACUACCUUGUC	408

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
17	UAGUUUUGCAUAGUUGCACUAC	hsa-mir-19a*	hsa-mir-19a	hsa-mir-19a*	MIMAT0004490	AGUUUUUGCAUAGUUGCACUACA	409
18	AGUUUUGCAGGUUUGCAUCCAGC	hsa-mir-19b-1*	hsa-mir-19b-1	hsa-mir-19b-1*	MIMAT0004491	AGUUUUUGCAGGUUUGCAUCCAGC	410
19	ACUGUAGUAUGGGCACUCCAG	hsa-mir-20b*	hsa-mir-20b	hsa-mir-20b*	MIMAT0004752	ACUGUAGUAUGGGCACUCCAG	411
20	ACCUGGCAUACAAUGUAGAUUU	hsa-mir-221*	hsa-mir-221	hsa-mir-221*	MIMAT0004568	ACCUGGCAUACAAUGUAGAUUU	412
21	GGGUUCCUGGCAUGCUGAUUU	hsa-mir-23b*	hsa-mir-23b	hsa-mir-23b*	MIMAT0004587	UGGGUCCUGGCAUGCUGAUUU	413
22	AGCGGAGACUUGGGCAAUUG	hsa-mir-25*	hsa-mir-25	hsa-mir-25*	MIMAT0004498	AGCGGAGACUUGGGCAAUUG	414
23	AGAGCUUAGCUGAUUGGUGAAC	hsa-mir-27b*	hsa-mir-27b	hsa-mir-27b*	MIMAT0004588	AGAGCUUAGCUGAUUGGUGAAC	415
24	CUGGGAGGUGGAUGUUUACUUC	hsa-mir-30b*	hsa-mir-30b	hsa-mir-30b*	MIMAT0004589	CUGGGAGGUGGAUGUUUACUUC	416
25	CUGGGAGAGGGUUGUUUACUCC	hsa-mir-30c-1*	hsa-mir-30c-1	hsa-mir-30c-1*	MIMAT0004674	CUGGGAGAGGGUUGUUUACUCC	417
26	CUGGGAGAAGGCUGUUUACUCU	hsa-mir-30c-2*	hsa-mir-30c-2	hsa-mir-30c-2*	MIMAT0004550	CUGGGAGAAGGCUGUUUACUCU	418
27	CUUUCAGUCGGAUGUUUACAGC	hsa-mir-30e*	hsa-mir-30e	hsa-mir-30e*	MIMAT0000693	CUUUCAGUCGGAUGUUUACAGC	419
28	UCCUGUCCUCCAGGAGCUCACG	hsa-mir-339-5p	hsa-mir-339	hsa-mir-339-5p	MIMAT0000764	UCCUGUCCUCCAGGAGCUCACG	420
29	UCUCACACAGAAUUGCACC CGU	hsa-mir-342-3p	hsa-mir-342	hsa-mir-342-3p	MIMAT0000753	UCUCACACAGAAUUGCACC CGU	421
30	AAUCAGCAAGUAUACUGCCCUA	hsa-mir-34a*	hsa-mir-34a	hsa-mir-34a*	MIMAT0004557	CAAUCAGCAAGUAUACUGCCCU	422
31	UCCCCCAGGUGAUUUCUGAUUU	hsa-mir-361-3p	hsa-mir-361	hsa-mir-361-3p	MIMAT0004682	UCCCCCAGGUGAUUUCUGAUUU	423
32	AAUCCUUGGAACCUAGGUGUGAGU	hsa-mir-362-5p	hsa-mir-362	hsa-mir-362-5p	MIMAT0000705	AAUCCUUGGAACCUAGGUGUGAGU	424

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
33	AGGGACUUUCAGGGGCAGCUGU	hsa-mir-365-2*	hsa-mir-365-2	hsa-mir-365*	MIMAT0009199	AGGGACUUUCAGGGGCAGCUGU	425
34	CUUAUCAGAUUGUAUUGUAAUU	hsa-mir-374a*	hsa-mir-374a	hsa-mir-374a*	MIMAT0004688	CUUAUCAGAUUGUAUUGUAAUU	426
35	CUUAGCAGGUUGUAUUUAUCAUU	hsa-mir-374b*	hsa-mir-374b	hsa-mir-374b*	MIMAT0004956	CUUAGCAGGUUGUAUUUAUCAUU	427
36	AGGUUACCCGAGCAACUUUGCAU	hsa-mir-409-5p	hsa-mir-409	hsa-mir-409-5p	MIMAT0001638	AGGUUACCCGAGCAACUUUGCAU	428
37	CAAAACGUGAGGGCGCUCUAU	hsa-mir-424*	hsa-mir-424	hsa-mir-424*	MIMAT0004749	CAAAACGUGAGGGCGCUCUAU	429
38	UAUGUGCCUUUGGACUACAUCG	hsa-mir-455-5p	hsa-mir-455	hsa-mir-455-5p	MIMAT0003150	UAUGUGCCUUUGGACUACAUCG	430
39	GUCAUACACGGCUCUCUCUCU	hsa-mir-485-3p	hsa-mir-485	hsa-mir-485-3p	MIMAT0002176	GUCAUACACGGCUCUCUCUCU	431
40	UGUCUUACUCCUCAGGCACAU	hsa-mir-550-1*	hsa-mir-550-1	hsa-mir-550*	MIMAT0003257	UGUCUUACUCCUCAGGCACAU	432
41	UGUCUUACUCCUCAGGCACAU	hsa-mir-550-2*	hsa-mir-550-2	hsa-mir-550*	MIMAT0003257	UGUCUUACUCCUCAGGCACAU	433
42	GAAAUCAAGCGUGGGUGAGACC	hsa-mir-551b*	hsa-mir-551b	hsa-mir-551b*	MIMAT0004794	GAAAUCAAGCGUGGGUGAGACC	434
43	AUUCUAAUUUCUCCACGUCUUU	hsa-mir-576-5p	hsa-mir-576	hsa-mir-576-5p	MIMAT0003241	AUUCUAAUUUCUCCACGUCUUU	435
44	UCAGAACAAUUGCCGGUUCGCCAGA	hsa-mir-589*	hsa-mir-589	hsa-mir-589*	MIMAT0003256	UCAGAACAAUUGCCGGUUCGCCAGA	436
45	GAGCUUAUUAUAAAAGUGCAG	hsa-mir-590-5p	hsa-mir-590	hsa-mir-590-5p	MIMAT0003258	GAGCUUAUUAUAAAAGUGCAG	437
46	GGGGGUCCCCGGUGUCUGGAUC	hsa-mir-615-5p	hsa-mir-615	hsa-mir-615-5p	MIMAT0004804	GGGGGUCCCCGGUGUCUGGAUC	438
47	GACUUAJAGAAUUUCCCCCUCA	hsa-mir-625*	hsa-mir-625	hsa-mir-625*	MIMAT0004808	GACUUAJAGAAUUUCCCCCUCA	439
48	UGGUGGGCCGAGAACAUUGUC	hsa-mir-654-5p	hsa-mir-654	hsa-mir-654-5p	MIMAT0003330	UGGUGGGCCGAGAACAUUGUC	440

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
49	AGGAAGCCUGGAGGGGCGUGGAG	hsa-mir-671-5p	hsa-mir-671	hsa-mir-671-5p	MIMAT0003880	AGGAAGCCUGGAGGGGCGUGGAG	441
50	AACUAGACUGUGAGGCUUCUAGA	hsa-mir-708*	hsa-mir-708	hsa-mir-708*	MIMAT0004927	CAACUAGACUGUGAGGCUUCUAG	442
51	CAACAAAUCACAGUCUGCCAUA	hsa-mir-7-1*	hsa-mir-7-1	hsa-mir-7-1*	MIMAT0004553	CAACAAAUCACAGUCUGCCAUA	443
52	AUAAAGCUAGAUAAACCGAAAGU	hsa-mir-9-1*	hsa-mir-9-1	hsa-mir-9-1*	MIMAT0000442	AUAAAGCUAGAUAAACCGAAAGU	444
53	AUAAAGCUAGAUAAACCGAAAGU	hsa-mir-9-2*	hsa-mir-9-2	hsa-mir-9-2*	MIMAT0000442	AUAAAGCUAGAUAAACCGAAAGU	445
54	AGGACGGGACGCGGUGCAGUG	hsa-mir-92b*	hsa-mir-92b	hsa-mir-92b*	MIMAT0004792	AGGACGGGACGCGGUGCAGUG	446
55	AUAAAGCUAGAUAAACCGAAAGU	hsa-mir-9-3*	hsa-mir-9-3	hsa-mir-9-3*	MIMAT0000442	AUAAAGCUAGAUAAACCGAAAGU	447
56	UGAGGUAGUAGGUUGUAUAGUU	hsa-let-7a-2	hsa-let-7a-2	hsa-let-7a	MIMAT0000062	UGAGGUAGUAGGUUGUAUAGUU	448
57	UGAGGUAGUAGGUUGUAUAGUU	hsa-let-7a-3	hsa-let-7a-3	hsa-let-7a	MIMAT0000062	UGAGGUAGUAGGUUGUAUAGUU	449
58	UGAGGUAGUAGGUUGUAUAGUU	hsa-let-7c	hsa-let-7c	hsa-let-7c	MIMAT0000064	UGAGGUAGUAGGUUGUAUAGUU	450
59	UGAGGUAGGAGGUUGUAUAGUU	hsa-let-7e	hsa-let-7e	hsa-let-7e	MIMAT0000066	UGAGGUAGGAGGUUGUAUAGUU	451
60	UGAGGUAGUAGAUUGUAUAGUU	hsa-let-7f-1	hsa-let-7f-1	hsa-let-7f	MIMAT0000067	UGAGGUAGUAGAUUGUAUAGUU	452
61	UGAGGUAGUAGUUUGUACAGUU	hsa-let-7g	hsa-let-7g	hsa-let-7g	MIMAT0000414	UGAGGUAGUAGUUUGUACAGUU	453
62	UGAGGUAGUAGUUUGUCUGUU	hsa-let-7i	hsa-let-7i	hsa-let-7i	MIMAT0000415	UGAGGUAGUAGUUUGUCUGUU	454
63	AACCCGUAUAGUCCGAACUUGUG	hsa-mir-100	hsa-mir-100	hsa-mir-100	MIMAT0000098	AACCCGUAUAGUCCGAACUUGUG	455
64	UACAGUACUGUGAUAAACUGAA	hsa-mir-101-1	hsa-mir-101-1	hsa-mir-101	MIMAT0000099	UACAGUACUGUGAUAAACUGAA	456
65	GUACAGUACUGUGAUAAACUGAA	hsa-mir-101-2	hsa-mir-101-2	hsa-mir-101	MIMAT0000099	UACAGUACUGUGAUAAACUGAA	457
66	AGCAGCAUUGUACAGGGCUAUGA	hsa-mir-103-1	hsa-mir-103-1	hsa-mir-103	MIMAT0000101	AGCAGCAUUGUACAGGGCUAUGA	458

SEQ. ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
67	AGCAGCAUUGUACAGGGCUAUGA	hsa-mir-103-2	hsa-mir-103-2	hsa-mir-103	MIMAT0000101	AGCAGCAUUGUACAGGGCUAUGA	4589
68	AAUAGCUCAGACUCCUGUGGUG	hsa-mir-105-1	hsa-mir-105-1	hsa-mir-105	MIMAT0000102	UCAAUUGCUCAGACUCCUGUGGU	460
69	AAUAGCUCAGACUCCUGUGGUG	hsa-mir-105-2	hsa-mir-105-2	hsa-mir-105	MIMAT0000102	UCAAUUGCUCAGACUCCUGUGGU	461
70	AAAAGUGCUUACAGUGCAGGUAG	hsa-mir-106a	hsa-mir-106a	hsa-mir-106a	MIMAT0000103	AAAAGUGCUUACAGUGCAGGUAG	462
71	UAAAGUGCUGACAGUGCAGAU	hsa-mir-106b	hsa-mir-106b	hsa-mir-106b	MIMAT0000680	UAAAGUGCUGACAGUGCAGAU	463
72	AGCAGCAUUGUACAGGGCUAUGA	hsa-mir-107	hsa-mir-107	hsa-mir-107	MIMAT0000104	AGCAGCAUUGUACAGGGCUAUGA	464
73	UACCCUGUAGAUCCGAAUUUGUG	hsa-mir-10a	hsa-mir-10a	hsa-mir-10a	MIMAT0000253	UACCCUGUAGAUCCGAAUUUGUG	465
74	UACCCUGUAGAACCGAAUUUGUG	hsa-mir-10b	hsa-mir-10b	hsa-mir-10b	MIMAT0000254	UACCCUGUAGAACCGAAUUUGUG	466
75	UGGAAUGUAAAAGAAGUAUGUAU	hsa-mir-1-1	hsa-mir-1-1	hsa-mir-1	MIMAT00000416	UGGAAUGUAAAAGAAGUAUGUAU	467
76	UGGAAUGUAAAAGAAGUAUGUAU	hsa-mir-1-2	hsa-mir-1-2	hsa-mir-1	MIMAT00000416	UGGAAUGUAAAAGAAGUAUGUAU	468
77	UGGAGUGUGACAAUGGUGUUUG	hsa-mir-122	hsa-mir-122	hsa-mir-122	MIMAT0000421	UGGAGUGUGACAAUGGUGUUUG	469
78	UAGGCACGCGGUGAAUGCC	hsa-mir-124-1	hsa-mir-124-1	hsa-mir-124	MIMAT0000422	UAGGCACGCGGUGAAUGCC	470
79	UAGGCACGCGGUGAAUGCC	hsa-mir-124-2	hsa-mir-124-2	hsa-mir-124	MIMAT0000422	UAGGCACGCGGUGAAUGCC	471
80	UAGGCACGCGGUGAAUGCC	hsa-mir-124-3	hsa-mir-124-3	hsa-mir-124	MIMAT0000422	UAGGCACGCGGUGAAUGCC	472
81	ACCCGUCCCGUUCGUCCCGGGA	hsa-mir-1247	hsa-mir-1247	hsa-mir-1247	MIMAT0005899	ACCCGUCCCGUUCGUCCCGGGA	473

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
82	ACGGUGGUGGGAUGUGGCCUUU	hsa-mir-1250	hsa-mir-1250	hsa-mir-1250	MIMAT0005902	ACGGUGGUGGGAUGUGGCCUUU	474
83	AGAGGAAAUUGAAUUAUUA	hsa-mir-1252	hsa-mir-1252	hsa-mir-1252	MIMAT0005944	AGAGGAAAUUGAAUUAUUA	475
84	AGCCUGGAAGCUGGAGCCUGCAGU	hsa-mir-1254	hsa-mir-1254	hsa-mir-1254	MIMAT0005905	AGCCUGGAAGCUGGAGCCUGCAGU	476
85	AGGAUGAGCAAAAGAAUGAUU	hsa-mir-1255a	hsa-mir-1255a	hsa-mir-1255a	MIMAT0005906	AGGAUGAGCAAAAGAAUGAUU	477
86	AGGCAUUGACUUCUCACUAGCU	hsa-mir-1256	hsa-mir-1256	hsa-mir-1256	MIMAT0005907	AGGCAUUGACUUCUCACUAGCU	478
87	CGUACCGUGAGUAAUUAUGCG	hsa-mir-126	hsa-mir-126	hsa-mir-126	MIMAT0000445	UCGUACCGUGAGUAAUUAUGCG	479
88	AUGGGUAAUUUGUAGAAGGAU	hsa-mir-1262	hsa-mir-1262	hsa-mir-1262	MIMAT0005914	AUGGGUAAUUUGUAGAAGGAU	480
89	AUGGUACCCUGGCAUACUGAGU	hsa-mir-1263	hsa-mir-1263	hsa-mir-1263	MIMAT0005915	AUGGUACCCUGGCAUACUGAGU	481
90	CAGGAUGUGGCAAGUGUUGUU	hsa-mir-1265	hsa-mir-1265	hsa-mir-1265	MIMAT0005918	CAGGAUGUGGCAAGUGUUGUU	482
91	CCUCAGGGCUGUAGAACAGGGCU	hsa-mir-1266	hsa-mir-1266	hsa-mir-1266	MIMAT0005920	CCUCAGGGCUGUAGAACAGGGCU	483
92	CUGGACUGAGCCGUGCUACUGG	hsa-mir-1269	hsa-mir-1269	hsa-mir-1269	MIMAT0005923	CUGGACUGAGCCGUGCUACUGG	484
93	CUGGAGAUUUGGAAGAGCUGUGU	hsa-mir-1270	hsa-mir-1270	hsa-mir-1270	MIMAT0005924	CUGGAGAUUUGGAAGAGCUGUGU	485
94	CUUGGCACCUAGCAAGCACUCA	hsa-mir-1271	hsa-mir-1271	hsa-mir-1271	MIMAT0005796	CUUGGCACCUAGCAAGCACUCA	486
95	UCGGAUCCGUCUGAGCUUGGCU	hsa-mir-127-3p	hsa-mir-127-3p	hsa-mir-127-3p	MIMAT0000446	UCGGAUCCGUCUGAGCUUGGCU	487
96	UACGUAGAUUAUUAUGAUUUU	hsa-mir-1277	hsa-mir-1277	hsa-mir-1277	MIMAT0005933	UACGUAGAUUAUUAUGAUUUU	488
97	UAGUACUGGCAUUAUCAUUAU	hsa-mir-1278	hsa-mir-1278	hsa-mir-1278	MIMAT0005936	UAGUACUGGCAUUAUCAUUAU	489

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
98	UCACAGUGAACCGGUCUCUUU	hsa-mir-128-1	hsa-mir-128-1	hsa-mir-128	MIMAT0000424	UCACAGUGAACCGGUCUCUUU	490
99	UCACAGUGAACCGGUCUCUUU	hsa-mir-128-2	hsa-mir-128-2	hsa-mir-128	MIMAT0000424	UCACAGUGAACCGGUCUCUUU	491
100	CUUUUUGCGGUCUGGGCUUGC	hsa-mir-129-1	hsa-mir-129-1	hsa-mir-129-5p	MIMAT0000242	CUUUUUGCGGUCUGGGCUUGC	492
101	CUUUUUGCGGUCUGGGCUUGC	hsa-mir-129-2	hsa-mir-129-2	hsa-mir-129-5p	MIMAT0000242	CUUUUUGCGGUCUGGGCUUGC	493
102	UGUGAGGUUGGCAUUGUUGUCU	hsa-mir-1294	hsa-mir-1294	hsa-mir-1294	MIMAT0005884	UGUGAGGUUGGCAUUGUUGUCU	494
103	UUAGGCCGAGAUUCUGGGUGA	hsa-mir-1295	hsa-mir-1295	hsa-mir-1295	MIMAT0005885	UUAGGCCGAGAUUCUGGGUGA	495
104	UUCAUUCGGCUGUCCAGAUUA	hsa-mir-1298	hsa-mir-1298	hsa-mir-1298	MIMAT0005800	UUCAUUCGGCUGUCCAGAUUA	496
105	UUGCAGCUGCCUGGGAGUGACUUC	hsa-mir-1301	hsa-mir-1301	hsa-mir-1301	MIMAT0005797	UUGCAGCUGCCUGGGAGUGACUUC	497
106	CGGUUUGAGGCUACAGUGAGAU	hsa-mir-1304	hsa-mir-1304	hsa-mir-1304	MIMAT0005892	UUUGAGGCUACAGUGAGAUUG	498
107	ACGUUGGCUCUGGGUGUG	hsa-mir-1306	hsa-mir-1306	hsa-mir-1306	MIMAT0005950	ACGUUGGCUCUGGGUGUG	499
108	ACUCGGCGUGGCGUCGGUCGUG	hsa-mir-1307	hsa-mir-1307	hsa-mir-1307	MIMAT0005951	ACUCGGCGUGGCGUCGGUCGUG	500
109	CAGUGCAAUGUUAAAAGGGCAU	hsa-mir-130a	hsa-mir-130a	hsa-mir-130a	MIMAT0000425	CAGUGCAAUGUUAAAAGGGCAU	501
110	CAGUGCAAUGAUGAAAGGGCAU	hsa-mir-130b	hsa-mir-130b	hsa-mir-130b	MIMAT0000691	CAGUGCAAUGAUGAAAGGGCAU	502
111	UACAGUCUACAGCCAUUGGUCG	hsa-mir-132	hsa-mir-132	hsa-mir-132	MIMAT0000426	UACAGUCUACAGCCAUUGGUCG	503
112	ACCGUGGCUUUCGAUUGUUACU	hsa-mir-132*	hsa-mir-132	hsa-mir-132*	MIMAT0004594	ACCGUGGCUUUCGAUUGUUACU	504
113	UGUGACUGGUUGACCAGAGGGG	hsa-mir-134	hsa-mir-134	hsa-mir-134	MIMAT0000447	UGUGACUGGUUGACCAGAGGGG	505

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
114	UAUGGCUUUUCAUUCUUAUGUGA	hsa-mir-135b	hsa-mir-135b	hsa-mir-135b	MIMAT0000758	UAUGGCUUUUCAUUCUUAUGUGA	506
115	ACUCCAUUUUUUUUGAUGAUGGA	hsa-mir-136	hsa-mir-136	hsa-mir-136	MIMAT0000448	ACUCCAUUUUUUUUGAUGAUGGA	507
116	AGCUGGUGUUGUGAAUACAGGCCG	hsa-mir-138-1	hsa-mir-138-1	hsa-mir-138	MIMAT0000430	AGCUGGUGUUGUGAAUACAGGCCG	508
117	AGCUGGUGUUGUGAAUACAGGCCG	hsa-mir-138-2	hsa-mir-138-2	hsa-mir-138	MIMAT0000430	AGCUGGUGUUGUGAAUACAGGCCG	509
118	UGGAGACGGGCCCUUGUGGAG	hsa-mir-139-3p	hsa-mir-139	hsa-mir-139-3p	MIMAT0004552	GGAGACGGGCCCUUGUGGAGU	510
119	UACCACAGGGUAGAACACCGG	hsa-mir-140-3p	hsa-mir-140	hsa-mir-140-3p	MIMAT0004597	UACCACAGGGUAGAACACCGG	511
120	UACACUGUCUGGUAAAAGAUGG	hsa-mir-141	hsa-mir-141	hsa-mir-141	MIMAT0000432	UACACUGUCUGGUAAAAGAUGG	512
121	CCCAUAAAGUAGAAAGCACU	hsa-mir-142	hsa-mir-142	hsa-mir-142-5p	MIMAT0000433	CAUAAAGUAGAAAGCACUACU	513
122	UGAGAUGAAGCACUGUAGCUC	hsa-mir-143	hsa-mir-143	hsa-mir-143	MIMAT0000435	UGAGAUGAAGCACUGUAGCUC	514
123	GGAUAUCAUAUACUGUAAG	hsa-mir-144	hsa-mir-144	hsa-mir-144*	MIMAT0004600	GGAUAUCAUAUACUGUAAG	515
124	GUCCAGUUUUUCCAGGAUCCCU	hsa-mir-145	hsa-mir-145	hsa-mir-145	MIMAT0000437	GUCCAGUUUUUCCAGGAUCCCU	516
125	UGAGAACUGAAUUCUUGGGUU	hsa-mir-146a	hsa-mir-146a	hsa-mir-146a	MIMAT0000449	UGAGAACUGAAUUCUUGGGUU	517
126	UGAGAACUGAAUUCUUGGGUU	hsa-mir-146b	hsa-mir-146b	hsa-mir-146b-5p	MIMAT0002809	UGAGAACUGAAUUCUUGGGUU	518
127	UCAGUGCACUACAGAAUUUGU	hsa-mir-148a	hsa-mir-148a	hsa-mir-148a	MIMAT0000243	UCAGUGCACUACAGAAUUUGU	519
128	UCAGUGCAUCACAGAAUUUGU	hsa-mir-148b	hsa-mir-148b	hsa-mir-148b	MIMAT0000759	UCAGUGCAUCACAGAAUUUGU	520
129	UCUCCCAACCCUUGUACACAGUG	hsa-mir-150	hsa-mir-150	hsa-mir-150	MIMAT0000451	UCUCCCAACCCUUGUACACAGUG	521

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
130	CUAGACUGAAGCUCCUUGAGG	hsa-mir-151-3p	hsa-mir-151	hsa-mir-151-3p	MIMAT0000757	CUAGACUGAAGCUCCUUGAGG	522
131	UCAGUGCAUGACAGAACUUGG	hsa-mir-152	hsa-mir-152	hsa-mir-152	MIMAT0000438	UCAGUGCAUGACAGAACUUGG	523
132	UUAAUGCUAAUCGUGAUAGGGGU	hsa-mir-155	hsa-mir-155	hsa-mir-155	MIMAT0000646	UUAAUGCUAAUCGUGAUAGGGGU	524
133	UAGCAGCACAUAAUGGUUUGUG	hsa-mir-15a	hsa-mir-15a	hsa-mir-15a	MIMAT0000068	UAGCAGCACAUAAUGGUUUGUG	525
134	UAGCAGCACAUCAUGGUUUACA	hsa-mir-15b	hsa-mir-15b	hsa-mir-15b	MIMAT0000417	UAGCAGCACAUCAUGGUUUACA	526
135	UAGCAGCACGUAAAUUUGGCG	hsa-mir-16-1	hsa-mir-16-1	hsa-mir-16	MIMAT0000069	UAGCAGCACGUAAAUUUGGCG	527
136	UAGCAGCACGUAAAUUUGGCG	hsa-mir-16-2	hsa-mir-16-2	hsa-mir-16	MIMAT0000069	UAGCAGCACGUAAAUUUGGCG	528
137	CAAAGUGCUACAGUGCAGGUAG	hsa-mir-17	hsa-mir-17	hsa-mir-17	MIMAT0000070	CAAAGUGCUACAGUGCAGGUAG	529
138	AACAUUCAAACGCUGUCGGUGAGU	hsa-mir-181a-1	hsa-mir-181a-1	hsa-mir-181a	MIMAT0000256	AACAUUCAAACGCUGUCGGUGAGU	530
139	AACAUUCAAACGCUGUCGGUGAGU	hsa-mir-181a-2	hsa-mir-181a-2	hsa-mir-181a	MIMAT0000256	AACAUUCAAACGCUGUCGGUGAGU	531
140	AACAUUCAAUUGCUGUCGGUGGGU	hsa-mir-181b-1	hsa-mir-181b-1	hsa-mir-181b	MIMAT0000257	AACAUUCAAUUGCUGUCGGUGGGU	532
141	AACAUUCAAUUGCUGUCGGUGGGU	hsa-mir-181b-2	hsa-mir-181b-2	hsa-mir-181b	MIMAT0000257	AACAUUCAAUUGCUGUCGGUGGGU	533
142	AACAUUCAAACCUUGUCGGUGAGU	hsa-mir-181c	hsa-mir-181c	hsa-mir-181c	MIMAT0000258	AACAUUCAAACCUUGUCGGUGAGU	534
143	AACAUUCAAUUGUUGUCGGUGGGU	hsa-mir-181d	hsa-mir-181d	hsa-mir-181d	MIMAT0002821	AACAUUCAAUUGUUGUCGGUGGGU	535
144	UUUGGCAUUGGUAGAACUCACACU	hsa-mir-182	hsa-mir-182	hsa-mir-182	MIMAT0000259	UUUGGCAUUGGUAGAACUCACACU	536
145	UAUGGCACUGGUAGAAUUCACU	hsa-mir-183	hsa-mir-183	hsa-mir-183	MIMAT0000261	UAUGGCACUGGUAGAAUUCACU	537

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
146	UGGACGGAGAACUGUAAGGGU	hsa-mir-184	hsa-mir-184	hsa-mir-184	MIMAT0000454	UGGACGGAGAACUGUAAGGGU	538
147	UGGAGAGAAAGGCAGUUCUGA	hsa-mir-185	hsa-mir-185	hsa-mir-185	MIMAT0000455	UGGAGAGAAAGGCAGUUCUGA	539
148	CAAGAAUUCUCCUUUUGGGCU	hsa-mir-186	hsa-mir-186	hsa-mir-186	MIMAT0000456	CAAGAAUUCUCCUUUUGGGCU	540
149	CAUCCUUGCAUGGUGGAGGG	hsa-mir-188-5p	hsa-mir-188	hsa-mir-188-5p	MIMAT0000457	CAUCCUUGCAUGGUGGAGGG	541
150	UAAGGUGCAUCUAGUGCAGAUAG	hsa-mir-18a	hsa-mir-18a	hsa-mir-18a	MIMAT0000072	UAAGGUGCAUCUAGUGCAGAUAG	542
151	CAACGGAAUCCCAAAAGCAGCUG	hsa-mir-191	hsa-mir-191	hsa-mir-191	MIMAT0000440	CAACGGAAUCCCAAAAGCAGCUG	543
152	CUGACCUAUGAAUUGACAGCC	hsa-mir-192	hsa-mir-192	hsa-mir-192	MIMAT0000222	CUGACCUAUGAAUUGACAGCC	544
153	UGGGUCUUUGCGGGCGAGAUGA	hsa-mir-193a-5p	hsa-mir-193a	hsa-mir-193a-5p	MIMAT0004614	UGGGUCUUUGCGGGCGAGAUGA	545
154	AACUGGCCUCAAAGUCCCGCU	hsa-mir-193b	hsa-mir-193b	hsa-mir-193b	MIMAT0002819	AACUGGCCUCAAAGUCCCGCU	546
155	UGUACAGCAACUCCAUUGUGGA	hsa-mir-194-1	hsa-mir-194	hsa-mir-194	MIMAT0000460	UGUACAGCAACUCCAUUGUGGA	547
156	UAGCAGCACAGAAAUUUGGC	hsa-mir-195	hsa-mir-195	hsa-mir-195	MIMAT0000461	UAGCAGCACAGAAAUUUGGC	548
157	UAGGUAGUUUCAUGUUGUUGGG	hsa-mir-196a-1	hsa-mir-196a	hsa-mir-196a	MIMAT0000226	UAGGUAGUUUCAUGUUGUUGGG	549
158	UAGGUAGUUUCAUGUUGUUGGG	hsa-mir-196a-2	hsa-mir-196a-2	hsa-mir-196a	MIMAT0000226	UAGGUAGUUUCAUGUUGUUGGG	550
159	UAGGUAGUUUCCUGUUGUUGGG	hsa-mir-196b	hsa-mir-196b	hsa-mir-196b	MIMAT0001080	UAGGUAGUUUCCUGUUGUUGGG	551
160	UUCACCACCUUCUCCACCCAGC	hsa-mir-197	hsa-mir-197	hsa-mir-197	MIMAT0000227	UUCACCACCUUCUCCACCCAGC	552
161	ACAGUAGUCUGCACAUGGUUA	hsa-mir-199a-1	hsa-mir-199a-1	hsa-mir-199a-3p	MIMAT0000232	ACAGUAGUCUGCACAUGGUUA	553

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
162	ACAGUAGUCUGCACAUUGGUUA	hsa-mir-199a-2	hsa-mir-199a-2	hsa-mir-199a-3p	MIMAT0000232	ACAGUAGUCUGCACAUUGGUUA	554
163	ACAGUAGUCUGCACAUUGGUUA	hsa-mir-199b	hsa-mir-199b	hsa-mir-199b-3p	MIMAT00004563	ACAGUAGUCUGCACAUUGGUUA	555
164	UGUGCAAUUCUAUGCAAAACUGA	hsa-mir-19a	hsa-mir-19a	hsa-mir-19a	MIMAT00000073	UGUGCAAUUCUAUGCAAAACUGA	556
165	UGUGCAAUUCUAUGCAAAACUGA	hsa-mir-19b-1	hsa-mir-19b-1	hsa-mir-19b	MIMAT00000074	UGUGCAAUUCUAUGCAAAACUGA	557
166	UGUGCAAUUCUAUGCAAAACUGA	hsa-mir-19b-2	hsa-mir-19b-2	hsa-mir-19b	MIMAT00000074	UGUGCAAUUCUAUGCAAAACUGA	558
167	UAAACACUGUCUGGUAAACGAUGU	hsa-mir-200a	hsa-mir-200a	hsa-mir-200a	MIMAT00000682	UAAACACUGUCUGGUAAACGAUGU	559
168	UAAUACUGCCUGGUAAUUGAUGA	hsa-mir-200b	hsa-mir-200b	hsa-mir-200b	MIMAT0000318	UAAUACUGCCUGGUAAUUGAUGA	560
169	UAAUACUGCCGGGUAUUGAUGGA	hsa-mir-200c	hsa-mir-200c	hsa-mir-200c	MIMAT00000617	UAAUACUGCCGGGUAUUGAUGGA	561
170	UUCUUAUGCAUUAUACUUCUUUG	hsa-mir-202*	hsa-mir-202	hsa-mir-202*	MIMAT0002810	UUCUUAUGCAUUAUACUUCUUUG	562
171	GUGAAAUUUUAGGACCACUAG	hsa-mir-203	hsa-mir-203	hsa-mir-203	MIMAT0000264	GUGAAAUUUUAGGACCACUAG	563
172	UUCUUUUUGUCAUCCUAUGCCU	hsa-mir-204	hsa-mir-204	hsa-mir-204	MIMAT0000265	UUCUUUUUGUCAUCCUAUGCCU	564
173	UCCUUAUUCACCGGAGUCUG	hsa-mir-205	hsa-mir-205	hsa-mir-205	MIMAT0000266	UCCUUAUUCACCGGAGUCUG	565
174	UGGAAUGUAAGGAAGUGUGUGG	hsa-mir-206	hsa-mir-206	hsa-mir-206	MIMAT0000462	UGGAAUGUAAGGAAGUGUGUGG	566
175	UAAAGUGCUUAUAGUGCAGGUAG	hsa-mir-20a	hsa-mir-20a	hsa-mir-20a	MIMAT00000075	UAAAGUGCUUAUAGUGCAGGUAG	567
176	CAAAGUGCUUAUAGUGCAGGUAG	hsa-mir-20b	hsa-mir-20b	hsa-mir-20b	MIMAT0001413	CAAAGUGCUUAUAGUGCAGGUAG	568
177	UAGCUUAUCAGACUGAUGUUGA	hsa-mir-21	hsa-mir-21	hsa-mir-21	MIMAT00000076	UAGCUUAUCAGACUGAUGUUGA	569

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
178	CUGUGCGUGUGACAGCGGCUGA	hsa-mir-210	hsa-mir-210	hsa-mir-210	MIMAT0000267	CUGUGCGUGUGACAGCGGCUGA	570
179	UACAGUCUCCAGUCACGGCC	hsa-mir-212	hsa-mir-212	hsa-mir-212	MIMAT0000269	UACAGUCUCCAGUCACGGCC	571
180	ACAGCAGGCACAGACAGGCAGU	hsa-mir-214	hsa-mir-214	hsa-mir-214	MIMAT0000271	ACAGCAGGCACAGACAGGCAGU	572
181	UGACCUAUGAAUUGACAG	hsa-mir-215	hsa-mir-215	hsa-mir-215	MIMAT0000272	AUGACCUAUGAAUUGACAGAC	573
182	AAUUCUCUGCAGGCAAAUGUGA	hsa-mir-216b	hsa-mir-216b	hsa-mir-216b	MIMAT0004959	AAUUCUCUGCAGGCAAAUGUGA	574
183	AUACUGCAUCAGGGAACUGAUUG	hsa-mir-217	hsa-mir-217	hsa-mir-217	MIMAT0000274	UACUGCAUCAGGGAACUGAUUGA	575
184	AGAGUUGAGUCUGGACGUCCCG	hsa-mir-219-1	hsa-mir-219-1	hsa-mir-219-1-3p	MIMAT0004567	AGAGUUGAGUCUGGACGUCCCG	576
185	AAGCUGCCAGUUGAAGAACUGU	hsa-mir-22	hsa-mir-22	hsa-mir-22	MIMAT0000077	AAGCUGCCAGUUGAAGAACUGU	577
186	AGCUACAUUGUCUGCGGGUUUC	hsa-mir-221	hsa-mir-221	hsa-mir-221	MIMAT0000278	AGCUACAUUGUCUGCGGGUUUC	578
187	AGCUACAUCUGGCUACUGGGU	hsa-mir-222	hsa-mir-222	hsa-mir-222	MIMAT0000279	AGCUACAUCUGGCUACUGGGU	579
188	CGUGAUUUUGACAAGCUGAGUU	hsa-mir-223*	hsa-mir-223	hsa-mir-223*	MIMAT0004570	CGUGAUUUUGACAAGCUGAGUU	580
189	CAAGUCACUAGUGGUUCCGUU	hsa-mir-224	hsa-mir-224	hsa-mir-224	MIMAT0000281	CAAGUCACUAGUGGUUCCGUU	581
190	AUCACAUUGCCAGGGAUUUCC	hsa-mir-23a	hsa-mir-23a	hsa-mir-23a	MIMAT0000078	AUCACAUUGCCAGGGAUUUCC	582
191	AUCACAUUGCCAGGGAUUUACC	hsa-mir-23b	hsa-mir-23b	hsa-mir-23b	MIMAT0000418	AUCACAUUGCCAGGGAUUUACC	583
192	UGGCUCAGUUCAGCAGGAACAG	hsa-mir-24-1	hsa-mir-24-1	hsa-mir-24	MIMAT0000080	UGGCUCAGUUCAGCAGGAACAG	584
193	UGGCUCAGUUCAGCAGGAACAG	hsa-mir-24-2	hsa-mir-24-2	hsa-mir-24	MIMAT0000080	UGGCUCAGUUCAGCAGGAACAG	585

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
194	CAUUGCACUUGUCUGGUCUGA	hsa-mir-25	hsa-mir-25	hsa-mir-25	MIMAT0000081	CAUUGCACUUGUCUGGUCUGA	586
195	UUCAAGUAAUCCAGGAUAGGCU	hsa-mir-26a-1	hsa-mir-26a-1	hsa-mir-26a	MIMAT0000082	UUCAAGUAAUCCAGGAUAGGCU	587
196	UUCAAGUAAUCCAGGAUAGGCU	hsa-mir-26a-2	hsa-mir-26a-2	hsa-mir-26a	MIMAT0000082	UUCAAGUAAUCCAGGAUAGGCU	588
197	UUCAAGUAAUCCAGGAUAGGU	hsa-mir-26b	hsa-mir-26b	hsa-mir-26b	MIMAT0000083	UUCAAGUAAUCCAGGAUAGGU	589
198	UUCACAGUGGCUAAGUCCGC	hsa-mir-27a	hsa-mir-27a	hsa-mir-27a	MIMAT0000084	UUCACAGUGGCUAAGUCCGC	590
199	UUCACAGUGGCUAAGUUCUGC	hsa-mir-27b	hsa-mir-27b	hsa-mir-27b	MIMAT00000419	UUCACAGUGGCUAAGUUCUGC	591
200	CACUAGAUUGUGAGCUCCUGGA	hsa-mir-28	hsa-mir-28	hsa-mir-28-3p	MIMAT0004502	CACUAGAUUGUGAGCUCCUGGA	592
201	GAGGGUUGGGUGGAGGCUCUCC	hsa-mir-296-3p	hsa-mir-296	hsa-mir-296-3p	MIMAT0004679	GAGGGUUGGGUGGAGGCUCUCC	593
202	AUGGUUUACCGUCCCAUACA	hsa-mir-299-5p	hsa-mir-299	hsa-mir-299-5p	MIMAT0002890	UGGUUUACCGUCCCAUACA	594
203	UAGCACCAUCUGAAAUCCGGUUA	hsa-mir-29a	hsa-mir-29a	hsa-mir-29a	MIMAT0000086	UAGCACCAUCUGAAAUCCGGUUA	595
204	UAGCACCAUUUGAAAUACAGUGUU	hsa-mir-29b-1	hsa-mir-29b-1	hsa-mir-29b	MIMAT0000100	UAGCACCAUUUGAAAUACAGUGUU	596
205	UAGCACCAUUUGAAAUACAGUGUU	hsa-mir-29b-2	hsa-mir-29b-2	hsa-mir-29b	MIMAT0000100	UAGCACCAUUUGAAAUACAGUGUU	597
206	UAGCACCAUUUGAAAUCCGGUUA	hsa-mir-29c	hsa-mir-29c	hsa-mir-29c	MIMAT0000681	UAGCACCAUUUGAAAUCCGGUUA	598
207	CAGUGCAAUGAUUUUGUCAAAGC	hsa-mir-301b	hsa-mir-301b	hsa-mir-301b	MIMAT0004958	CAGUGCAAUGAUUUUGUCAAAGC	599
208	UGUAAACAUCUCCGACUGGAAG	hsa-mir-30a	hsa-mir-30a	hsa-mir-30a	MIMAT0000087	UGUAAACAUCUCCGACUGGAAG	600
209	UGUAAACAUCUCCACACUCAGCU	hsa-mir-30b	hsa-mir-30b	hsa-mir-30b	MIMAT0000420	UGUAAACAUCUCCACACUCAGCU	601

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
210	UGUAAACAUCUACACUCUCAGC	hsa-mir-30c-1	hsa-mir-30c-1	hsa-mir-30c	MIMAT0000244	UGUAAACAUCUACACUCUCAGC	602
211	UGUAAACAUCUACACUCUCAGC	hsa-mir-30c-2	hsa-mir-30c-2	hsa-mir-30c	MIMAT0000244	UGUAAACAUCUACACUCUCAGC	603
212	UGUAAACAUCUACACUCUGGAAG	hsa-mir-30d	hsa-mir-30d	hsa-mir-30d	MIMAT0000245	UGUAAACAUCUACACUCUGGAAG	604
213	UGUAAACAUCUACACUCUGGAAG	hsa-mir-30e	hsa-mir-30e	hsa-mir-30e	MIMAT0000692	UGUAAACAUCUACACUCUGGAAG	605
214	AGGCAAGAUCUGGCAUAGCU	hsa-mir-31	hsa-mir-31	hsa-mir-31	MIMAT0000089	AGGCAAGAUCUGGCAUAGCU	606
215	UAUUGCACAUUACUAAAGUUGCA	hsa-mir-32	hsa-mir-32	hsa-mir-32	MIMAT0000090	UAUUGCACAUUACUAAAGUUGCA	607
216	AAAAGCUGGUUGAGAGGGCGA	hsa-mir-320a	hsa-mir-320a	hsa-mir-320a	MIMAT0000510	AAAAGCUGGUUGAGAGGGCGA	608
217	AAAAGCUGGUUGAGAGGGCGAA	hsa-mir-320b-1	hsa-mir-320b-1	hsa-mir-320b	MIMAT00005792	AAAAGCUGGUUGAGAGGGCGAA	609
218	AAAAGCUGGUUGAGAGGGCGAA	hsa-mir-320b-2	hsa-mir-320b-2	hsa-mir-320b	MIMAT00005792	AAAAGCUGGUUGAGAGGGCGAA	610
219	AAAAGCUGGUUGAGAGGGGU	hsa-mir-320c-1	hsa-mir-320c-1	hsa-mir-320c	MIMAT00005793	AAAAGCUGGUUGAGAGGGGU	611
220	AAAAGCUGGUUGAGAGGGGU	hsa-mir-320c-2	hsa-mir-320c-2	hsa-mir-320c	MIMAT00005793	AAAAGCUGGUUGAGAGGGGU	612
221	AAAAGCUGGUUGAGAGGGA	hsa-mir-320d-1	hsa-mir-320d-1	hsa-mir-320d	MIMAT00006764	AAAAGCUGGUUGAGAGGGA	613
222	AAAAGCUGGUUGAGAGGGA	hsa-mir-320d-2	hsa-mir-320d-2	hsa-mir-320d	MIMAT00006764	AAAAGCUGGUUGAGAGGGA	614
223	CACAUUACACGGUCGACCUCU	hsa-mir-323	hsa-mir-323	hsa-mir-323-3p	MIMAT0000755	CACAUUACACGGUCGACCUCU	615
224	CGCAUCCCCUAGGGCAUUGGUGU	hsa-mir-324	hsa-mir-324	hsa-mir-324-5p	MIMAT0000761	CGCAUCCCCUAGGGCAUUGGUGU	616
225	CUGGCCUUCUCUGCCCUUCCGU	hsa-mir-328	hsa-mir-328	hsa-mir-328	MIMAT0000752	CUGGCCUUCUCUGCCCUUCCGU	617

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
226	GCAAAGCACACGGCCUGCAGAGA	hsa-mir-330	hsa-mir-330	hsa-miR-330-3p	MIMAT0000751	GCAAAGCACACGGCCUGCAGAGA	618
227	GCCCCUGGGCCUAUCCUAGAA	hsa-mir-331	hsa-mir-331	hsa-miR-331-3p	MIMAT0000760	GCCCCUGGGCCUAUCCUAGAA	619
228	UCAAGAGCAAUAACGAAAAUUGU	hsa-mir-335	hsa-mir-335	hsa-miR-335	MIMAT0000765	UCAAGAGCAAUAACGAAAAUUGU	620
229	UCCAGCAUCAGUGAUUUUGUUG	hsa-mir-338	hsa-mir-338	hsa-miR-338-3p	MIMAT0000763	UCCAGCAUCAGUGAUUUUGUUG	621
230	UGAGGCCUCGACGACAGAGCCG	hsa-mir-339-3p	hsa-mir-339	hsa-miR-339-3p	MIMAT0004702	UGAGGCCUCGACGACAGAGCCG	622
231	GUGCAUUGUAGUUGCAUUGCA	hsa-mir-33a	hsa-mir-33a	hsa-miR-33a	MIMAT0000091	GUGCAUUGUAGUUGCAUUGCA	623
232	GUGCAUUGCUGUUGCAUUGC	hsa-mir-33b	hsa-mir-33b	hsa-miR-33b	MIMAT0003301	GUGCAUUGCUGUUGCAUUGC	624
233	UUUAAAAGCAAUGAGACUGAUU	hsa-mir-340	hsa-mir-340	hsa-miR-340	MIMAT0004692	UUUAAAAGCAAUGAGACUGAUU	625
234	AGGGGUGCUAUCUGUGAUUGA	hsa-mir-342-5p	hsa-mir-342	hsa-miR-342-5p	MIMAT0004694	AGGGGUGCUAUCUGUGAUUGA	626
235	GCUGACUCCUAGUCCAGGGCUC	hsa-mir-345	hsa-mir-345	hsa-miR-345	MIMAT0000772	GCUGACUCCUAGUCCAGGGCUC	627
236	UGGCAGUGUCUUAGCUGGUUGU	hsa-mir-34a	hsa-mir-34a	hsa-miR-34a	MIMAT0000255	UGGCAGUGUCUUAGCUGGUUGU	628
237	AGGCAGUGUCAUUAAGCUGAUUG	hsa-mir-34b*	hsa-mir-34b	hsa-miR-34b*	MIMAT0000685	UAGGCAGUGUCAUUAAGCUGAUUG	629
238	AGGCAGUGUAGUUAAGCUGAUUGC	hsa-mir-34c-5p	hsa-mir-34c	hsa-miR-34c-5p	MIMAT0000686	AGGCAGUGUAGUUAAGCUGAUUGC	630
239	UUUACAGAAUCCUCCAGGGGUAC	hsa-mir-361-5p	hsa-mir-361	hsa-miR-361-5p	MIMAT0000703	UUUACAGAAUCCUCCAGGGGUAC	631
240	AACACACCUAUUCAAAGGAUUA	hsa-mir-362-3p	hsa-mir-362	hsa-miR-362-3p	MIMAT0004683	AACACACCUAUUCAAAGGAUUA	632
241	AAUUGCACGGUAUCCAUCUGUA	hsa-mir-363	hsa-mir-363	hsa-miR-363	MIMAT0000707	AAUUGCACGGUAUCCAUCUGUA	633

SEQ ID NO.	SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
242	242	UAAUGCCCCUAAAAAUCCUUUAU	hsa-mir-365-2	hsa-mir-365-2	hsa-miR-365	MIMAT0000710	UAAUGCCCCUAAAAAUCCUUUAU	634
243	243	AAUAAUAUCAUGGUUGAUCUUU	hsa-mir-369	hsa-mir-369	hsa-miR-369-3p	MIMAT0000721	AAUAAUAUCAUGGUUGAUCUUU	635
244	244	GCCUGCUGGGGUGGAACCUUGGU	hsa-mir-370	hsa-mir-370	hsa-miR-370	MIMAT0000722	GCCUGCUGGGGUGGAACCUUGGU	636
245	245	ACUCAAACUGUGGGGGCACU	hsa-mir-371	hsa-mir-371	hsa-miR-371-5p	MIMAT0004687	ACUCAAACUGUGGGGGCACU	637
246	246	UUAUAAUACAACCUAGUAAGUG	hsa-mir-374a	hsa-mir-374a	hsa-miR-374a	MIMAT0000727	UUAUAAUACAACCUAGUAAGUG	638
247	247	AUAUAAUACAACCUAGUAAGUG	hsa-mir-374b	hsa-mir-374b	hsa-miR-374b	MIMAT0004955	AUAUAAUACAACCUAGUAAGUG	639
248	248	UUUGUUCGUUCGGCUCGCGUGA	hsa-mir-375	hsa-mir-375	hsa-miR-375	MIMAT0000728	UUUGUUCGUUCGGCUCGCGUGA	640
249	249	AGAGGUUGCCCUUGGUGAAUUC	hsa-mir-377*	hsa-mir-377	hsa-miR-377*	MIMAT0004689	AGAGGUUGCCCUUGGUGAAUUC	641
250	250	ACUGGACUUGGAGUCAGAAGG	hsa-mir-378	hsa-mir-378	hsa-miR-378	MIMAT0000732	ACUGGACUUGGAGUCAGAAGG	642
251	251	UGGUAGACUAUGGAACGUAGG	hsa-mir-379	hsa-mir-379	hsa-miR-379	MIMAT0000733	UGGUAGACUAUGGAACGUAGG	643
252	252	UAUACAAGGGCAAGCUCUCUGU	hsa-mir-381	hsa-mir-381	hsa-miR-381	MIMAT0000736	UAUACAAGGGCAAGCUCUCUGU	644
253	253	GAAGUUGUUCGUGGUGGAUUCG	hsa-mir-382	hsa-mir-382	hsa-miR-382	MIMAT0000737	GAAGUUGUUCGUGGUGGAUUCG	645
254	254	AGAUCAAGGGUGAUUGUGGCU	hsa-mir-383	hsa-mir-383	hsa-miR-383	MIMAT0000738	AGAUCAAGGGUGAUUGUGGCU	646
255	255	CGAAUGUUCGCGGUGAACCCC	hsa-mir-409-3p	hsa-mir-409	hsa-miR-409-3p	MIMAT0001639	GAAUGUUCGCGGUGAACCCC	647
256	256	AAUAAACACAGAUGGCCUGU	hsa-mir-410	hsa-mir-410	hsa-miR-410	MIMAT0002171	AAUAAACACAGAUGGCCUGU	648
257	257	AUAGUAGACCGUAUAGCGUACG	hsa-mir-411	hsa-mir-411	hsa-miR-411	MIMAT0003329	UAGUAGACCGUAUAGCGUACG	649

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
258	AUCAACAGACAUAAUUGGGCGC	hsa-mir-421	hsa-mir-421	hsa-mir-421	MIMAT0003339	AUCAACAGACAUAAUUGGGCGC	650
259	UGAGGGGCAGAGAGCGACUUAU	hsa-mir-423	hsa-mir-423	hsa-mir-423-5p	MIMAT0004748	UGAGGGGCAGAGAGCGACUUAU	651
260	CAGCAGCAAUUAUGUUUUGAA	hsa-mir-424	hsa-mir-424	hsa-mir-424	MIMAT0001341	CAGCAGCAAUUAUGUUUUGAA	652
261	UAAUACUGUCUGGUAACCGU	hsa-mir-429	hsa-mir-429	hsa-mir-429	MIMAT0001536	UAAUACUGUCUGGUAACCGU	653
262	UCUUGGAGUAGGUCAUUGGGUGG	hsa-mir-432	hsa-mir-432	hsa-mir-432	MIMAT0002814	UCUUGGAGUAGGUCAUUGGGUGG	654
263	AUCAUGAUGGGCUCUCGGUGU	hsa-mir-433	hsa-mir-433	hsa-mir-433	MIMAT0001627	AUCAUGAUGGGCUCUCGGUGU	655
264	UUGCAUAUGAGGAUGUCCCAU	hsa-mir-448	hsa-mir-448	hsa-mir-448	MIMAT0001532	UUGCAUAUGAGGAUGUCCCAU	656
265	UGCAGUGUAUUGUAGCUGGU	hsa-mir-449a	hsa-mir-449a	hsa-mir-449a	MIMAT0001541	UGCAGUGUAUUGUAGCUGGU	657
266	AGCAGUGUAUUGUAGCUGGC	hsa-mir-449b	hsa-mir-449b	hsa-mir-449b	MIMAT0003327	AGCAGUGUAUUGUAGCUGGC	658
267	UUUUGCGAUGUGUCCUAAUAU	hsa-mir-450a-1	hsa-mir-450a-1	hsa-mir-450a	MIMAT0001545	UUUUGCGAUGUGUCCUAAUAU	659
268	UUUUGCGAUGUGUCCUAAUAU	hsa-mir-450a-2	hsa-mir-450a-2	hsa-mir-450a	MIMAT0001545	UUUUGCGAUGUGUCCUAAUAU	660
269	UUUUGCAAUAUGUCCUGAAUA	hsa-mir-450b-5p	hsa-mir-450b	hsa-mir-450b-5p	MIMAT0004909	UUUUGCAAUAUGUCCUGAAUA	661
270	AACUGUUUGCAGAGGAAACUGA	hsa-mir-452	hsa-mir-452	hsa-mir-452	MIMAT0001635	AACUGUUUGCAGAGGAAACUGA	662
271	UAGUGCAAUAUUGCUUAUAGGGU	hsa-mir-454	hsa-mir-454	hsa-mir-454	MIMAT0003885	UAGUGCAAUAUUGCUUAUAGGGU	663
272	GCAGUCCAUGGGCAUAUACAC	hsa-mir-455-3p	hsa-mir-455	hsa-mir-455-3p	MIMAT0004784	GCAGUCCAUGGGCAUAUACAC	664
273	AAGACGGGAGGAAAGAGGGAG	hsa-mir-483-5p	hsa-mir-483	hsa-mir-483-5p	MIMAT0004761	AAGACGGGAGGAAAGAGGGAG	665

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
274	UCAGGCUCAGUCCCCUCCCGAU	hsa-mir-484	hsa-mir-484	hsa-mir-484	MIMAT0002174	UCAGGCUCAGUCCCCUCCCGAU	666
275	AGAGGCUGGCCGUGAUAUUC	hsa-mir-485-5p	hsa-mir-485	hsa-mir-485-5p	MIMAT0002175	AGAGGCUGGCCGUGAUAUUC	667
276	UCCUGUACUGAGCUGCCCCGAG	hsa-mir-486-5p	hsa-mir-486	hsa-mir-486-5p	MIMAT0002177	UCCUGUACUGAGCUGCCCCGAG	668
277	AAUCGUACAGGGGUCAUCCACUU	hsa-mir-487b	hsa-mir-487b	hsa-mir-487b	MIMAT0003180	AAUCGUACAGGGGUCAUCCACUU	669
278	CCCAGAUAAUGGCACUCUCAA	hsa-mir-488*	hsa-mir-488	hsa-mir-488*	MIMAT0002804	CCCAGAUAAUGGCACUCUCAA	670
279	UUGUACAUGGUAGGCUUUCUU	hsa-mir-493*	hsa-mir-493	hsa-mir-493*	MIMAT0002813	UUGUACAUGGUAGGCUUUCUU	671
280	UGAAACAUAACACGGGAAACCUC	hsa-mir-494	hsa-mir-494	hsa-mir-494	MIMAT0002816	UGAAACAUAACACGGGAAACCUC	672
281	AAACAAACAUGGUGCACUUCUU	hsa-mir-495	hsa-mir-495	hsa-mir-495	MIMAT0002817	AAACAAACAUGGUGCACUUCUU	673
282	CAGCAGCACACUGUGGUUUUGU	hsa-mir-497	hsa-mir-497	hsa-mir-497	MIMAT0002820	CAGCAGCACACUGUGGUUUUGU	674
283	UUAAGACUUGCAGUGAUGUUU	hsa-mir-499-5p	hsa-mir-499	hsa-mir-499-5p	MIMAT0002870	UUAAGACUUGCAGUGAUGUUU	675
284	AUGCACCUGGGCAAGGAUUCUG	hsa-mir-500*	hsa-mir-500	hsa-mir-500*	MIMAT0002871	AUGCACCUGGGCAAGGAUUCUG	676
285	AAUGCACCUGGGCAAGGAUUCU	hsa-mir-501-3p	hsa-mir-501	hsa-mir-501-3p	MIMAT0004774	AAUGCACCUGGGCAAGGAUUCU	677
286	AAUGCACCUGGGCAAGGAUUCA	hsa-mir-502-3p	hsa-mir-502	hsa-mir-502-3p	MIMAT0004775	AAUGCACCUGGGCAAGGAUUCA	678
287	UAGCAGCGGGAACAGUUCUGCAG	hsa-mir-503	hsa-mir-503	hsa-mir-503	MIMAT0002874	UAGCAGCGGGAACAGUUCUGCAG	679
288	AGACCCUGGUCUGCACUCUAUC	hsa-mir-504	hsa-mir-504	hsa-mir-504	MIMAT0002875	AGACCCUGGUCUGCACUCUAUC	680
289	GGGAGCCAGGAAGUAUUGAUGU	hsa-mir-505*	hsa-mir-505	hsa-mir-505*	MIMAT0004776	GGGAGCCAGGAAGUAUUGAUGU	681

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
290	UGAUUGUAGCCUUUUGGAGUAGA	hsa-mir-508-3p	hsa-mir-508	hsa-mir-508-3p	MIMAT0002880	UGAUUGUAGCCUUUUGGAGUAGA	682
291	UACUGCAGACGUGGCAAUCAUG	hsa-mir-509-3-5p	hsa-mir-509-3	hsa-mir-509-3-5p	MIMAT0004975	UACUGCAGACGUGGCAAUCAUG	683
292	UUCACAGGGAGGUGUCAU	hsa-mir-513a-1	hsa-mir-513a-1	hsa-mir-513a-5p	MIMAT0002877	UUCACAGGGAGGUGUCAU	684
293	UUCACAGGGAGGUGUCAU	hsa-mir-513a-2	hsa-mir-513a-2	hsa-mir-513a-5p	MIMAT0002877	UUCACAGGGAGGUGUCAU	685
294	UUCACAAAGGAGGUGUCAUUUAU	hsa-mir-513b	hsa-mir-513b	hsa-mir-513b	MIMAT0005788	UUCACAAAGGAGGUGUCAUUUAU	686
295	UUCUCAAGGAGGUGUCGUUUUAU	hsa-mir-513c	hsa-mir-513c	hsa-mir-513c	MIMAT0005789	UUCUCAAGGAGGUGUCGUUUUAU	687
296	CAUGCCUUGAGUGUAGGACCGU	hsa-mir-532	hsa-mir-532	hsa-mir-532-5p	MIMAT0002888	CAUGCCUUGAGUGUAGGACCGU	688
297	UGUGACAGAUUGAUACUGAAA	hsa-mir-542-3p	hsa-mir-542	hsa-mir-542-3p	MIMAT0003389	UGUGACAGAUUGAUACUGAAA	689
298	AAACAUUCGCGGUGCACUUCUU	hsa-mir-543	hsa-mir-543	hsa-mir-543	MIMAT0004954	AAACAUUCGCGGUGCACUUCUU	690
299	CAAAACUGGCAAUUACUUUUUGC	hsa-mir-548a-1	hsa-mir-548a-1	hsa-mir-548a-3p	MIMAT0003251	CAAAACUGGCAAUUACUUUUUGC	691
300	CAAAACUGGCAAUUACUUUUUGC	hsa-mir-548a-2	hsa-mir-548a-2	hsa-mir-548a-3p	MIMAT0003251	CAAAACUGGCAAUUACUUUUUGC	692
301	CAAAACUGGCAAUUACUUUUUGC	hsa-mir-548a-3	hsa-mir-548a-3	hsa-mir-548a-3p	MIMAT0003251	CAAAACUGGCAAUUACUUUUUGC	693
302	CAAGAACCUACAGUUGCUUUUUGU	hsa-mir-548b-3p	hsa-mir-548b	hsa-mir-548b-3p	MIMAT0003254	CAAGAACCUACAGUUGCUUUUUGU	694
303	AAAAACUGAGACUACUUUUUGCA	hsa-mir-548e	hsa-mir-548e	hsa-mir-548e	MIMAT0005874	AAAAACUGAGACUACUUUUUGCA	695
304	AAAAGUAAUCGCGGUUUUUUGUC	hsa-mir-548h-1	hsa-mir-548h-1	hsa-mir-548h	MIMAT0005928	AAAAGUAAUCGCGGUUUUUUGUC	696
305	AAAAGUAAUCGCGGUUUUUUGUC	hsa-mir-548h-2	hsa-mir-548h-2	hsa-mir-548h	MIMAT0005928	AAAAGUAAUCGCGGUUUUUUGUC	697

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
306	AAAAGUAAUCGCGGUUUUUGUC	hsa-mir-548h-3	hsa-mir-548h-3	hsa-mir-548h	MIMAT0005928	AAAAGUAAUCGCGGUUUUUGUC	698
307	AAAAGUAAUCGCGGUUUUUGUC	hsa-mir-548h-4	hsa-mir-548h-4	hsa-mir-548h	MIMAT0005928	AAAAGUAAUCGCGGUUUUUGUC	699
308	AAAAGUAAUUGCGGUUUUUGGU	hsa-mir-548j	hsa-mir-548j	hsa-mir-548j	MIMAT0005875	AAAAGUAAUUGCGGUUUUUGGU	700
309	AAAAGUACUUGCGGAUUUUGCU	hsa-mir-548k	hsa-mir-548k	hsa-mir-548k	MIMAT0005882	AAAAGUACUUGCGGAUUUUGCU	701
310	AAAAGUAAUUGCGGUUUUUGUC	hsa-mir-548l	hsa-mir-548l	hsa-mir-548l	MIMAT0005889	AAAAGUAAUUGCGGUUUUUGUC	702
311	CAAAGUAAUUGUGGAUUUUGU	hsa-mir-548n	hsa-mir-548n	hsa-mir-548n	MIMAT0005916	CAAAGUAAUUGUGGAUUUUGU	703
312	AGUGCCUGAGGGAGUAAGAGCCC	hsa-mir-550-1	hsa-mir-550-1	hsa-mir-550	MIMAT0004800	AGUGCCUGAGGGAGUAAGAGCCC	704
313	AGUGCCUGAGGGAGUAAGAGCCC	hsa-mir-550-2	hsa-mir-550-2	hsa-mir-550	MIMAT0004800	AGUGCCUGAGGGAGUAAGAGCCC	705
314	GCGACCAUACUUGGUUUUCAG	hsa-mir-551b	hsa-mir-551b	hsa-mir-551b	MIMAT0003233	GCGACCAUACUUGGUUUUCAG	706
315	CACGCUCAUGCACACACCCACA	hsa-mir-574-3p	hsa-mir-574-3p	hsa-mir-574-3p	MIMAT0003239	CACGCUCAUGCACACACCCACA	707
316	AAGAUUGGAAAAAUUGGAAUC	hsa-mir-576-3p	hsa-mir-576-3p	hsa-mir-576-3p	MIMAT0004796	AAGAUUGGAAAAAUUGGAAUC	708
317	GUAGUAAAAAUUUGGUACCUG	hsa-mir-577	hsa-mir-577	hsa-mir-577	MIMAT0003242	UAGUAAAAAUUUGGUACCUG	709
318	UACUGGUUGAACAAACUGAAC	hsa-mir-582-3p	hsa-mir-582-3p	hsa-mir-582-3p	MIMAT0004797	UACUGGUUGAACAAACUGAAC	710
319	UUACAGUUGUUAACACAGUUACU	hsa-mir-582-5p	hsa-mir-582-5p	hsa-mir-582-5p	MIMAT0003247	UUACAGUUGUUAACACAGUUACU	711
320	UUUUGGUUUUGCCUGGGACUGAG	hsa-mir-584	hsa-mir-584	hsa-mir-584	MIMAT0003249	UUUUGGUUUUGCCUGGGACUGAG	712

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase Mature/Minor ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
321	UGAGAACACGUCUCUCUGAG	hsa-mir-589	hsa-mir-589	hsa-mir-589	MIMAT0004799	UGAGAACACGUCUCUCUGAG	713
322	UAAUUUUUAUGUAUAAGCUAGU	hsa-mir-590-3p	hsa-mir-590	hsa-mir-590-3p	MIMAT0004801	UAAUUUUUAUGUAUAAGCUAGU	714
323	UACGUCAUCGUUGUCAUCGUCA	hsa-mir-598	hsa-mir-598	hsa-mir-598	MIMAT0003266	UACGUCAUCGUUGUCAUCGUCA	715
324	UCCGAGCCUGGGUCUCCCUUU	hsa-mir-615-3p	hsa-mir-615	hsa-mir-615-3p	MIMAT0003283	UCCGAGCCUGGGUCUCCCUUU	716
325	AAGUCAUUUGAGGGUUUGAGCA	hsa-mir-616	hsa-mir-616	hsa-mir-616	MIMAT0004805	AGUCAUUUGAGGGUUUGAGCAG	717
326	AAACUCUACUUGUCCUUCUGAGU	hsa-mir-618	hsa-mir-618	hsa-mir-618	MIMAT0003287	AAACUCUACUUGUCCUUCUGAGU	718
327	AGGGGAAAGUUCUAUAGUCC	hsa-mir-625	hsa-mir-625	hsa-mir-625	MIMAT0003294	AGGGGAAAGUUCUAUAGUCC	719
328	AUGCUGACAUUUUACUAGAGG	hsa-mir-628-5p	hsa-mir-628	hsa-mir-628-5p	MIMAT0004809	AUGCUGACAUUUUACUAGAGG	720
329	UGGGUUUACGUUGGGAGAACU	hsa-mir-629	hsa-mir-629	hsa-mir-629	MIMAT0004810	UGGGUUUACGUUGGGAGAACU	721
330	AAAGACAUAGGAUAGAGUCACCUC	hsa-mir-641	hsa-mir-641	hsa-mir-641	MIMAT0003311	AAAGACAUAGGAUAGAGUCACCUC	722
331	ACACUUGUAUGCUAGCUCAGGU	hsa-mir-643	hsa-mir-643	hsa-mir-643	MIMAT0003313	ACUUGUAUGCUAGCUCAGGUAG	723
332	UUUAGGAUAAGCUUGACUUUUUG	hsa-mir-651	hsa-mir-651	hsa-mir-651	MIMAT0003321	UUUAGGAUAAGCUUGACUUUUUG	724
333	AAUGGCGCCACUAGGGUUGUG	hsa-mir-652	hsa-mir-652	hsa-mir-652	MIMAT0003322	AAUGGCGCCACUAGGGUUGUG	725
334	UAUGUCUGCUGACCAUCACCUU	hsa-mir-654-3p	hsa-mir-654	hsa-mir-654-3p	MIMAT0004814	UAUGUCUGCUGACCAUCACCUU	726
335	UACCCAUGCAUAUCGGAGUUG	hsa-mir-660	hsa-mir-660	hsa-mir-660	MIMAT0003338	UACCCAUGCAUAUCGGAGUUG	727

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
336	UCCGGUUCUCAGGGCUCCACC	hsa-mir-671-3p	hsa-mir-671	hsa-mir-671-3p	MIMAT0004819	UCCGGUUCUCAGGGCUCCACC	728
337	AAGGAGCUUACAAUCUAGCUGGG	hsa-mir-708	hsa-mir-708	hsa-mir-708	MIMAT0004926	AAGGAGCUUACAAUCUAGCUGGG	729
338	UGGAAGACUAGUGAUUUUUGUUGU	hsa-mir-7-1	hsa-mir-7-1	hsa-mir-7	MIMAT0000252	UGGAAGACUAGUGAUUUUUGUUGU	730
339	UGGAAGACUAGUGAUUUUUGUUGU	hsa-mir-7-2	hsa-mir-7-2	hsa-mir-7	MIMAT0000252	UGGAAGACUAGUGAUUUUUGUUGU	731
340	UGGAAGACUAGUGAUUUUUGUUGU	hsa-mir-7-3	hsa-mir-7-3	hsa-mir-7	MIMAT0000252	UGGAAGACUAGUGAUUUUUGUUGU	732
341	CGGCUCUGGGUCUGUGGGGA	hsa-mir-760	hsa-mir-760	hsa-mir-760	MIMAT0004957	CGGCUCUGGGUCUGUGGGGA	733
342	UGCACCAUGGUUGUCUGAGCAUG	hsa-mir-767-5p	hsa-mir-767	hsa-mir-767-5p	MIMAT0003882	UGCACCAUGGUUGUCUGAGCAUG	734
343	UGAGACCUCUGGGUUCUGAGCU	hsa-mir-769-5p	hsa-mir-769	hsa-mir-769-5p	MIMAT0003886	UGAGACCUCUGGGUUCUGAGCU	735
344	GCAGGAACUUGUGAGUCUCCU	hsa-mir-873	hsa-mir-873	hsa-mir-873	MIMAT0004953	GCAGGAACUUGUGAGUCUCCU	736
345	CUGCCUGGCCCGAGGGACCGA	hsa-mir-874	hsa-mir-874	hsa-mir-874	MIMAT0004911	CUGCCUGGCCCGAGGGACCGA	737
346	GUAGAGGAGAUUGGCGCAGGG	hsa-mir-877	hsa-mir-877	hsa-mir-877	MIMAT0004949	GUAGAGGAGAUUGGCGCAGGG	738
347	GUGAACGGCGCCAUUCCCGAGG	hsa-mir-887	hsa-mir-887	hsa-mir-887	MIMAT0004951	GUGAACGGCGCCAUUCCCGAGG	739
348	UUAUAUCGGACAAACCAUUGU	hsa-mir-889	hsa-mir-889	hsa-mir-889	MIMAT0004921	UUAUAUCGGACAAACCAUUGU	740
349	UGCAACGAACCUUGAGCCACUGA	hsa-mir-891a	hsa-mir-891a	hsa-mir-891a	MIMAT0004902	UGCAACGAACCUUGAGCCACUGA	741
350	CACUGUGUCCUUUCUGCGUAG	hsa-mir-892a	hsa-mir-892a	hsa-mir-892a	MIMAT0004907	CACUGUGUCCUUUCUGCGUAG	742
351	UCUUUGGUUAUCUAGCUGUAUGA	hsa-mir-9-1	hsa-mir-9-1	hsa-mir-9	MIMAT0000441	UCUUUGGUUAUCUAGCUGUAUGA	743

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
352	UCUUUGGUUAUCUAGCUGUAUGA	hsa-mir-9-2	hsa-mir-9-2	hsa-mir-9	MIMAT0000441	UCUUUGGUUAUCUAGCUGUAUGA	744
353	UAUUGCACUUGUCCCCGGCCUGU	hsa-mir-92a-1	hsa-mir-92a-1	hsa-mir-92a	MIMAT0000092	UAUUGCACUUGUCCCCGGCCUGU	745
354	UAUUGCACUUGUCCCCGGCCUGU	hsa-mir-92a-2	hsa-mir-92a-2	hsa-mir-92a	MIMAT0000092	UAUUGCACUUGUCCCCGGCCUGU	746
355	UAUUGCACUUGUCCCCGGCCUCC	hsa-mir-92b	hsa-mir-92b	hsa-mir-92b	MIMAT0003218	UAUUGCACUUGUCCCCGGCCUCC	747
356	CAAAGUGCUGUUGCGCAGGUAG	hsa-mir-93	hsa-mir-93	hsa-mir-93	MIMAT0000093	CAAAGUGCUGUUGCGCAGGUAG	748
357	UCUUUGGUUAUCUAGCUGUAUGA	hsa-mir-9-3	hsa-mir-9-3	hsa-mir-9	MIMAT0000441	UCUUUGGUUAUCUAGCUGUAUGA	749
358	AAGGCAGGCCCCCGCUCUCC	hsa-mir-940	hsa-mir-940	hsa-mir-940	MIMAT0004983	AAGGCAGGCCCCCGCUCUCC	750
359	UUCUCUGUUUGGCCAUGUGUG	hsa-mir-942	hsa-mir-942	hsa-mir-942	MIMAT0004985	UUCUCUGUUUGGCCAUGUG	751
360	AAUUUAUUGUACAUCGGAUGAG	hsa-mir-944	hsa-mir-944	hsa-mir-944	MIMAT0004987	AAUUUAUUGUACAUCGGAUGAG	752
361	UUCAACGGGUUUUAUUGAGCA	hsa-mir-95	hsa-mir-95	hsa-mir-95	MIMAT0000094	UUCAACGGGUUUUAUUGAGCA	753
362	UUUGGCACUAGCACAUUUUUUGCU	hsa-mir-96	hsa-mir-96	hsa-mir-96	MIMAT0000095	UUUGGCACUAGCACAUUUUUUGCU	754
363	UGAGGUAGUAAGUUGUAUUUGUU	hsa-mir-98	hsa-mir-98	hsa-mir-98	MIMAT0000096	UGAGGUAGUAAGUUGUAUUUGUU	755
364	AACCCGUAGAUCCGAUCUUGUG	hsa-mir-99a	hsa-mir-99a	hsa-mir-99a	MIMAT0000097	AACCCGUAGAUCCGAUCUUGUG	756
365	CACCCGUAGAACCGACCUUGCG	hsa-mir-99b	hsa-mir-99b	hsa-mir-99b	MIMAT0000689	CACCCGUAGAACCGACCUUGCG	757
366	AACAUAGAGGAAAUUCCACGU	hsa-mir-376c	hsa-mir-376c	hsa-mir-376c		AACAUAGAGGAAAUUCCACGU	758
367	AUCAUAGAGGAAAUUCCAUUGUU	hsa-mir-376b	hsa-mir-376b	hsa-mir-376b		AUCAUAGAGGAAAUUCCAUUGUU	759

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
368	UGGUGGCCGCGAGAACAUUGUC	hsa-mir-654	hsa-mir-654	hsa-mir-654		UGGUGGCCGCGAGAACAUUGUC	760
369	AUCAUAGAGGAAAAUCCACGU	hsa-mir-376a-2	hsa-mir-376a-2	hsa-mir-376a-2		AUCAUAGAGGAAAAUCCACGU	761
370	AUCAUAGAGGAAAAUCCACGU	hsa-mir-376a-1	hsa-mir-376a-1	hsa-mir-376a-1		AUCAUAGAGGAAAAUCCACGU	762
371	AAAACCGUCUAGUACAGUUGU	hsa-mir-1537					
372	AUAUACAGGGGAGACUCUCAU	hsa-mir-1185-2					
373	CCUAGAAUGGGGAUUGUGG	hsa-mir-1301*					
374	AGCGAGACCUCACUCUACAAU	hsa-mir-1303					
375	UCGACCGGACCUCGACCGGUC	hsa-mir-1307*					
376	AUGUAGGGAUGGAAGCCAUCAA	hsa-mir-135a-2					
377	CUCACUGAACAAUGAAUGCAA	hsa-mir-181b-1*					
378	CGGGUAGAGGGGCGAGUGGGAG	hsa-mir-197*					
379	GCUGGGAAGGCAAGGGACGU	hsa-mir-204*					
380	ACCUUGGCUCUAGACUGCUUAC	hsa-mir-212*					
381	GCUCUGACUUUUUGCACUACU	hsa-mir-301a					
382	AGGACUUUUUGGGGCGAGAUU	hsa-mir-365-1					
383	UUGGGGACAUUUUGCAUUCAU	hsa-mir-450a-2*					
384	AAUGUGUAGCAAAAAGACAGA	hsa-mir-511-1-3p					
385	AAUGUGUAGCAAAAAGACAGA	hsa-mir-511-2-3p					
386	AUCAUACAAGGACAAUUUCUUU	hsa-mir-539					
387	AAAGGUAAUUGCAGUUUUUCCC	hsa-mir-570					
388	UCGCGGUUUUGGCCAGAUACG	hsa-mir-579					

SEQ ID NO.	Mature Sequence Captured	Putative Mature/Minor miRNA ID	miRBase ID	miRBase Mature/Minor ID	miRBase Mature/Minor Accession Number	miRBase Mature/Minor Sequence	SEQ ID NO.
389	AGAAAGGCACUAUGAGAUUUAGA	hsa-mir-605					
390	AGACACAUUUGGAGAGGGAACC	hsa-mir-642					
391	AGGACCUUCCCUUGAACCAAGGA	hsa-mir-659					
392	AUAUACAGGGGGGAGACUCUUAU	hsa-mir-1185-1					

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
777	AAAAGUAAUCGCGGUUUUUGUC	hsa-mir-548h-5	hsa-mir-548h-5	1071	acAAAAGUAAUCGCGGUUUUUGUCaUUaUacUUUUaUacUgUcUaaacacccggUUgcUUUUUgc
778	AAAAGUAAUUGUGGAUUUUUGCU	hsa-mir-548r-1	hsa-mir-548ab	1072	aUGUUGgUgcAAAAAGUAAUUGUGUGGAUUUUUGCUaUUaUcUgUaUUUaUUUgUaaUgcUaaaccccgcaaUgUUUUUgUgcacc aacc
779	AAAAGUAAUUGUGGAUUUUUGCU	hsa-mir-548r-2	hsa-mir-548ab	1073	UGUUGgUgcAAAAAGUAAUUGUGUGGAUUUUUGCUaUUaUcUgUaUUUaUUUgUaaUgcUaaaccccgcaaUgUUUUUgUgcacc aacc
780	UGUCUUACUCCUCAGGCACAU	hsa-miR-550-3*	pending	1074	cUggUgcagUgcUgagggagUaagagUccUgUgUgUgUgUgUaagaUagUGUCUUACUCCUCAGGCACAUcUcUcaa
781	GGUGGGCUUCCCGGAGGG	hsa-mir-2221	hsa-mir-4417	1075	gaaacaaccaGGUGGGCUUCCCGGAGGGcggaataccaccgcgcagcaUccagggcUcaccUaccacgUUUg
782	GAAGCGGUGGCGGGCUG	hsa-mir-2222	pending	1076	gaggcgccUagcgccaUUUUGUgggagcGAAGCGGGUGGCUUGGCGUgcgcUUG
783	CACUGCAGGACUCAGCAG	hsa-mir-2223	hsa-mir-4418	1077	UggUUUUUgUcUcUgagUgacccgUggUgUgUgUgUgggagUCACUGCAGGACUCAGCAGGaaUUC
784	UGAGGGAGGAGACUGCA	hsa-mir-2224	hsa-mir-4419a	1078	UggUggUgUgUgcUcUgUgUcUgUgUcUcUgggagggcUGAGGGAGGAGACUGCAGUgagUggagUcacgccacUg
785	ACUGGACUUGGAGCCAGAAG	hsa-mir-2225	hsa-mir-378f	1079	gUcaggUccUggagUcccaUagUUUUCaggcUgcUaaacaacagaaacgacACUGGACUUGGAGCCAGAAAGUcUUggg
786	GUCACUGAUGUCUGUAGCUGAG	hsa-mir-2226	hsa-mir-4420	1080	cUcUUGgUaUgaacaUcUgUgUgUcUgUcUcUgUgUgcagggagcagagUCACUGAUGUCUGUAGCUGAGGac
787	GAUGAGGAUGGAUAGCAAGGAA	hsa-mir-2227	hsa-mir-3605	1081	cUggccUcUgUgcUggagUacUUUaUacgUgUaaUUGUgAUUAGGAUGGAUAGCAAGGAacgcg
788	ACCUGUCUGUGAAAGGAGCUA	hsa-mir-2228	hsa-mir-4421	1082	cUgggUcUccUUUcUgcUgagagUUGaacacUUGUUGggagAACCUUGUCUGUGGAAAGGAGCUAccUac
789	AAAAGCAUCAGGAAGUACCCA	hsa-mir-2229	hsa-mir-4422	1083	agUUcUUcUgcagacAAAAGCAUCAGGAAAGUACCCCAcUaUgUaccagUggggccUcUgUgUgcUcUgUaUUGcagaggagcc
790	UGCCUGGAACAUAUAGGGGACU	hsa-mir-2230-1	hsa-mir-3116-2	1084	UccUUUaUUGagUcccUacUaUgUcUccaggcaccUacgaUaccagUGCCUGGAACAUAUAGGGGACUcaUaaUaaUgU
791	UGCCUGGAACAUAUAGGGGACU	hsa-mir-2230-2	hsa-mir-3116-1	1085	ccUUUaUUGagUcccUacUaUgUcUccaggcaccUacgaUaccagUGCCUGGAACAUAUAGGGGACUcaUaaUaaUgUagUccUcUcagcaUcUaUgUcUaUgggcUUGggUccUgga gUGGAUUAAAAACAAUUGGAGGU
792	UGGAUUAAAAACAAUGGAGG	hsa-mir-2231	pending	1086	

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
809	UAGUGGAUGAUGCACUCUGUC	hsa-mir-2248	hsa-mir-3681	1103	cUacUuccagUAGUGGAUGAUGCACUCUGUCagggccaa cUgUgcacacagUgcUUcaUccacUacUggaagUgU
810	AGGCUGGAGUGAGCGGAG	hsa-mir-2249	hsa-mir-4430	1104	gUgAGGCUGGAGUGAGCGGAGaUcgUaccacUgcacUcca accUggUga
811	GAAACGACAAUGACUUUUUGCA	hsa-mir-2250	hsa-mir-548ad	1105	cUgUUaggUUggUgcaaaagUaaUUgUggUUUUUUgaaaagUa acUUGgcGAAACACAAUGACUUUUUGCAccaaUcUaaUa c
812	GCGACUCUGAAACUAGAAGGU	hsa-mir-2251	hsa-mir-4431	1106	UggUUUUGCGACUCUGAAACUAGAAGGUUUUaUgacUgg gcaUUUcUcacccaaUgccccaaUaUgaaUcUUUcUagUUgUc agagUcaUUaacc
813	AGAAGGCUGGAGCGCGCGGU	hsa-mir-2252	pending	1107	gcacUgcccUcUgagggcgUUacUccggcUUcUccaUagaggg cggAGAAGGCUGGAGCGCGCGGUga
814	AAAGACUCUGCAAGAUGCCU	hsa-mir-2253	hsa-mir-4432	1108	gcaUcUUgagagcgUUccaaUgcgacaccUcUagagUgUcaU ccccUagaaUgUcaccUUggAAAGACUCUGCAAGAUGCCU
815	ACAGGAGUGGGGUGGGACAU	hsa-mir-2254	hsa-mir-4433	1109	caUccUcUUacgUccccccccUcUgUUUcUgUgUgaaU aUUcaAACAGAGUGGGGUGGGACAUaaggaggaaUa
816	AGGAGAAUAAGUAGAA	hsa-mir-2255	hsa-mir-4434	1110	UcacUUUAGGAGAGUAAAGUAGAAcUUUggUUUUUcaa cUUUUcUacagUgU
817	AUGGCCAGAGCUCACACAGAGG	hsa-mir-2256	hsa-mir-4435-1	1111	aggcagcaaaUUGGCCAGAGCUCACACAGGGAUgagUgca cUUcaccUgcagUgUgacUcagcagggccaacagaUgcUa
818	GCAGGACAGGCAGAAUGGGAU	hsa-mir-2257	hsa-mir-4436	1112	gccUcacUUUUUcUcUaUgUcUgccccUgccccUcgaaUcUgCU ccacgaUUUggGACAGGCAGGCAAGGUAaagUgaggg a
819	AUCAGGCUUGUGGAUUGGGA	hsa-mir-2258	hsa-mir-3127	1113	ggccccAUCAGGCUUGUGGAUUGGGAaggagaaggagcgc UUccccUUcUgcaggccUgcUgggUg
820	AUGGCCAGAGCUCACACAGAGG	hsa-mir-2259	hsa-mir-4435-2	1114	gcaaaUGGCCAGAGCUCACACAGGGAUgagUgcacUuc accUgcagUgUgacUcagcagggccaacagaUgcU
821	UGAGGAUAUGGCAGGGAAGGGG	hsa-mir-2260	hsa-mir-3679	1115	atgUggUGAGGAUAUGGCAGGGAAGGGGagUUUccccUc UaUUccccUUccccagUaaUcUcaUcaUgc
822	AGGAGGUUGGUGUGGAUU	hsa-mir-2261	pending	1116	UaUgAGGAGGUUGGUGUGGAUUcUgUgaaagaaaagaa ggggaatacUaaUUUUUcUaUU
823	UUGGAAGACAUGGAGCAUGAGG	hsa-mir-2262	pending	1117	UUUUUGGAAGACAUGGAGCAUGAGGUaagUgccUagaUcc UcaaacacUUGccUccaccUaUgcUUccaggU

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
824	UCUGGCAAGUAAAAACUCUCA	hsa-mir-2263	hsa-mir-3128	1118	cUuccUCUGGCAAGUAAAAACUCUCAUUUUUccUuaaaa aaUgagagUUUUUacUgcaalUaggaaa
825	UGGGCUCAGGGUACAAAGGUU	hsa-mir-2264	hsa-mir-4437	1119	acUUUgUgcaUUgggUcccaagaggagggaUgacccUUGUGG GCUCAGGGUACAAAGGUU
826	CAAAAACUGCAAUUACUUUCA	hsa-mir-2265-1	hsa-mir-548ae-1	1120	gcagUUUUUgccaUUaagUgCGUUUUUgccaUUaUaaUg gCAAAAACUGCAAUUACUUUCAcaccUgc
827	CAAAAACUGCAAUUACUUUCA	hsa-mir-2265-2	hsa-mir-548ae-2	1121	UgUgcaaaagUaaUUgUgUUUUUgUcaUUUuaaaagUaaUg gCAAAAACUGCAAUUACUUUCAcacc
828	GCUGCACCGGAGACUGGGUAA	hsa-mir-2266-1	hsa-mir-3130-1	1122	acUUgUcaUgUcUUaccagUcUccggUgcagccUgUUgUcaa ggCUGCACCGGAGACUGGGUAAgacaUgacaagc
829	GCUGCACCGGAGACUGGGUAA	hsa-mir-2266-2	hsa-mir-3130-2	1123	UgUcUUaccagUcUccggUgcagccUgacaacagGCUGCAC CGGAGACUGGGUAAgacaUgacaagUU
830	AUCCCCAGAUACAAGGACAAU	hsa-mir-2267	hsa-mir-2355	1124	cgUgUcAUCCCCAGAUACAAGGACAAUaUgcUaUuaUa aUcgUaUggcaUgUcUcUgUgUUUggaUaaUacU
831	AUUGUCCUUGCUGUUUGGAGAU	hsa-mir-2267*	pending	1125	cgUgUcAUCCCCAGAUACAAGGACAAUaUgcUaUuaUaUcg UaUggcAUUUGCUGUUUGGAGAUaaUacU
832	CACAGGCUUAGAAAAGACAGU	hsa-mir-2268	hsa-mir-4438	1126	UaagUgUaaacUuaaggacUgUcUUUUUcUaaagccUgUgcccUU gccUUUcUUUgGCACAGGCUUAGAAAAGACAGUcUUua agUUUacacUUC
833	UCGAGGACUGGUGGAAGGGCCU	hsa-mir-2269	hsa-mir-3131	1127	UcUcagagUCGAGGACUGGUGGAAGGGCCUUccccUca gaccaaggcccUggccccagcUUcUUcUcagagU
834	GUGACUGAUACCUUGGAGGCAU	hsa-mir-2270	hsa-mir-4439	1128	ccaGUGACUGAUACCUUGGAGGCAUUUUUcUcUaagaUac acacaaagcaaaUgcccUcUaaggUaUcagUUUaccaggcca
835	AGGGCUGGACUCAGCGCGGAG	hsa-mir-2271	pending	1129	gCgagAGGGCUGGACUCAGCGCGGAGcUggcUgCUGgc cUcagUUcUgcccUcUgUccaggUccUUGUga
836	UGUCGUGGGGUUGCUGGCUUG	hsa-mir-2272	hsa-mir-4440	1130	cUcUcaccagcaagUgCagUggggcUUGcUggcUUgCaccgUg acUcccUcUcaccagcaagUGUCUGGGGCUUGCUGGCU UGcUcUgUgaagU
837	ACAGGGAGGAGAUUGUA	hsa-mir-2273	hsa-mir-4441	1131	cagagUcUccUUcUgUgUacaggaggagacUgUacUgagagaU agUcagaUccgcaUgUUagagcagagUcUccUcgUgUACAG GGAGGAGAUUGUAC
838	ACUGGACUUGGAGGCAGAA	hsa-mir-2274	hsa-mir-378b	1132	UggUcaUUGagUcUcUcagagcUagUggaaagagACUGGACU UGGAGGCAGAAagaccc

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
839	GCCGGACAAGAGGGGAGG	hsa-mir-2275	hsa-mir-4442	1133	gccccUcccUcUcUcccccggUgUgcaaaUgUgUgUgcggUgUUaUGCCGGACAGAGGGAGGUG
840	AUACACAUACACGAACACACA	hsa-mir-2276	hsa-mir-466	1134	aUgUgUgUaUaUgUgUgUgUgcaUgUgUgUaUaUgUgUgUaUaUaUgUacacAUACACAUACACGCACACACACAUAaUaUgcac
841	UUGGAGGCGUGGUUUU	hsa-mir-2277	hsa-mir-4443	1135	ggUggggUUUGGAGGCGUGGUUUUaagaaccUaUcccUUUcUagccccUgagca
842	AAUUCUUUGUAGAUAACCCGG	hsa-mir-2278	hsa-mir-3938	1136	cgaUcacUagaUUaUcUacaagggaUUUUUUUUUUuaaUUUaaaaAAUUCUUUGUAGAUAACCCGGUggUca
843	AAGACUGGAGACAAAAGUGGGAG	hsa-mir-2279	pending	1137	CACCACCAAAUUCUCCAGGGGCUcUGUUGAAUUCGUAAGGAUGUGCAGCUCAUUAAGACUGGAGACAAAGUGGGAG
844	CUGACUGAAUAGGUAGGGUCAU	hsa-mir-2280	hsa-mir-3136	1138	aaaCUGACUGAAUAGGUAGGGUCAUUUUUucUgUgacUgcacUbgggcccgccUcUccUcUcggUcccaUaUugaaCU CGAUUGGAAGAGCGCagUccggUcUcaaa
845	CUCGAGUUGGAAGAGGCG	hsa-mir-2281	hsa-mir-4444	1139	UuccUgCAGAUUUUUUUUUGCCGUGCAagUUUaagUUUUUgcacggcaaaagaacaaUccagagggU
846	AGAUUUUUUUUUUGCCGUGCA	hsa-mir-2282	hsa-mir-4445	1140	UUccUgcagaUgUUUcUUUUUgcccUgcaagUUUuaagUUUUGCACGGCAAAGAAACAAUCCAgagggU
847	CACGGCAAAAGAAACAAUCCA	hsa-mir-2282*	has-mir-4445	1141	cUggUccaUUUcccUgccauUcccUUGgcUucaUUUacUcc CAGGGCUGGCAGUGACAUUGGUUcaa
848	CAGGGCUGGCAGUGACAUGGGU	hsa-mir-2283	hsa-mir-4446	1142	gUcUcUagagcaUggUUUcUcaUcaUUUgacUacUgaUacU UggggUcagaUaaUgUUUUGUGUGGGGGGUGUUUGUUU gcaUUgUaggaU
849	GGUGGGGCGUGUUGUUU	hsa-mir-2284	hsa-mir-4447	1143	gggcaUUGGGGAGGUGUGGAGUCAGCAUggggcUagggc cccgcgcUgacctcgccUcUcccgagcUlg
850	UGGGGAGGUGUGGAGUCAGCAU	hsa-mir-2285	pending	1144	accUlagagcacUUUacUgagUccUUUgUUcUcUacUagUUU gUagUagUUcgUaGCAGAGAACAAAGGACUCACUGUaaUg gUgcUcagga
851	GCAGAGAACAAAGGACUCAGU	hsa-mir-2286	hsa-mir-3919	1145	aggagUgaccaaaagataagagUgcgagccUUcUaUUaUgcccag acagggccaccagagGGCUCCUUUGGUUCUAGGGGUaaUgcca agcagccccUcggcggccccggggggcggcggcggUgccccGCCG GGGCUGCGCAGGCACagggc
852	GGCUCCUUGGUUCUAGGGGUA	hsa-mir-2287	hsa-mir-4448	1146	
853	CGUCCCGGGGCGUGCGGAGGCA	hsa-mir-2288	hsa-mir-4449	1147	

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
854	AAAGGUAUUUGGUUUCUGC	hsa-mir-2289-1	hsa-mir-548ag-1	1148	gUcAAAAGUAUUUGGUUUCUGCUUUUaaaggUaaUggcaaaUaUuaUacUUUacUUUUGcaccaca
855	AAAGGUAUUUGGUUUCUGC	hsa-mir-2289-2	hsa-mir-548ag-2	1149	UgcAAAGGUAAUUGUGGUUUUCUGCcaUUGaaaagUaaaggcaagaaccUcaaUUaccUUUUGcgagc
856	UGGGGAUUUGGAGAAGUGGUGA	hsa-mir-2290	hsa-mir-4450	1150	UgUcUGGGGAUUUGGAGAAGUGGUGAgcgagcagUcUUUggcaccaUcUccccUggUuccCUgggcU
857	AAAAAGUAUUGCAGUGUUUG	hsa-mir-2291	hsa-mir-548ah	1151	aggUUGglUgcAAAAGUGAUUGCAGUGUUUUGccaaUaaaaUgUaaUgacaaaaaacUgcagUUacUUUUGcaccagccc
858	UGGUAGAGCUGAGGACA	hsa-mir-2292	hsa-mir-4451	1152	UcUgUaccUcagcUUUgUccccaccaaacacUuccacaUgUUUgUcUGGUAGAGCUGAGGACAgc
859	UUGAAUUUCUUGGCCUUAAGUGAU	hsa-mir-2293	hsa-mir-4452	1153	UggaUcacUUGaggccaaagUgcagagcUgUagUgUgcacagccUUGAAUUUCUUGGCCUUAAAGUGAUccc
860	UAGGAGCUCAACAGAU GCCUGU	hsa-mir-2294	hsa-mir-3139	1154	UcagagUAGGAGCUCACAGAU GCCUGUgacUgaaUaaacabggUaUcgcagagcUUUUGUUaUgU
861	AGCUUUUGGGAAUUCAGGUAG	hsa-mir-2295	hsa-mir-3140	1155	UgUccUcUgUagggUaccUgaaUaaccaaaagtUUUaUgUaUucUgaagUUaUgaaaaUaagAGCUUUUGGGAAUUCAGGUAGUcaggagUgacU
862	GAGCUUGGUUCUGUAGCGGUU	hsa-mir-2296	hsa-mir-4453	1156	UggaGAGCUUGGUUCUGUAGCGGUUUUccUUGggggcaggUgggagUgcUccUUUgggaggaaggagggcccgcgUcUUcagg
863	GGAUCCGAGUCACGCACCCA	hsa-mir-2297	hsa-mir-4454	1157	ccGGAUCCGAGUCACGCACCCAaaUUUcaUgUcgUgUccgUgUgaagagaccacca
864	CAAAGUGAUCGUGGUUUUUUG	hsa-mir-2298	hsa-mir-548t	1158	gUggUgCAAAAAGUGAUCGUGGUUUUUUGCaUUUUUUUaaUgacaaaaccacaaUUacUUUUGcaccaca
865	AGGGUGUGUGUUUUUU	hsa-mir-2299	hsa-mir-4455	1159	agaAGGGUGUGUGUUUUUccUgagaaUaagagaaggaaUgacagccaaaUUCUca
866	CCUGGUGGCUUCCUUUU	hsa-mir-2300	hsa-mir-4456	1160	aUgaaCCUGGUGGCUUCCUUUccUgggaggaagUUagggUuca
867	UCACAAGGUUUUGACUGGCGUA	hsa-mir-2301	hsa-mir-4457	1161	BgagUacUccagUcaaUaccgUgUgagUUagaaaaUgUcUgCACAAAGUAUUGACUGGCGUAUca
868	AGAGGUAGGUGUGGAAGAA	hsa-mir-2302	hsa-mir-4458	1162	gagcgcacAGAGGUAGGUGUGGAAGAAagUgaaacacUaUUUagUUUUUagUUacacUcUgcUgUgUgUgUgUg
869	CCAGGAGCGGAGGAGGUGGAG	hsa-mir-2303	hsa-mir-4459	1163	acCCAGGAGCGGAGGAGGUGGAGgUUgUcagUgagccaagUcUgUggcacUgacUccagccUgggg

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
870	GUGGAGGACUGAGAGGUGAG	hsa-mir-2304	pending	1164	aUgaUGUGGAGGACUGAGAGGUGAGGcagUUUUGcccc gUgcUgcccUUUccaccggUUaagaccUccaaaaUcga
871	ACUGACAGGAGAGCAUUUUUGA	hsa-mir-2305	hsa-mir-3660	1165	ggacaaaaUuaaaaUgcUcUcUgUcUaUgUaaUagUUcaUa UgggcACUGACAGGAGAGCAUUUUUGAcUUUUGUca
872	AGCGGGGCGUGAGCGCUGCCAG	hsa-mir-2306	hsa-mir-2277	1166	ggUUcacUggUgcUgcUuccUgccccUgAGCGGGGCGUGA GCGCUGCCAGUcagcg
873	AAGCUCGGGGCGCUCGGGCGUGU	hsa-mir-2307	pending	1167	gcUtagUcagcUggggccgcUcagcUcUcggagUaggAAGCUCG GGCGCUCGGGCGUGUaaggagccc
874	AUAGUGGUUGUGAAUUUACCUU	hsa-mir-2308	hsa-mir-4460	1168	gUUUUUUGccccAUAGUGGUUGUGAAUUUACCUUcUccU cUUUgCagUgaUaaaggaggUaaaUUcacaaccacUgUgggcag aaac
875	GAUUGAGACUAGUAGGGGCUAGGC	hsa-mir-2309	hsa-mir-4461	1169	gagUaggcUUUaggUUaUgUacgUagUcUaggccaUacgUgUU ggagAUUUGAGACUAGUAGGGGCUAGGGCcUacUg
876	CUACCCAGGAUGCCAGCAUAG	hsa-mir-2310	pending	1171	aUagcUggUUggcaUcUcUggccccUggUUcaUgccaacUcUUG UgUUgaCUACCCAGGAUGCCAGCAUAGUUgc
877	ACUGGACUUGGUGUCAGAUAGG	hsa-mir-2311	hsa-mir-378h	1171	acaggaacACUGGACUUGGUGUCAGAUAGGgaUgagccccUg gcUcUgUUUcUcUagcagcaUcUgaUcUUGagcUagUcUacUgg
878	GACAAUGAUGAGAAGACCUGAG	hsa-mir-2312	pending	1172	ggGACAAUGAUGAGAAGACCUGAGAUUUgCagccccca gccccUgggUUcaagUcccagcUcUacccccUcUUGggcccc
879	ACCGCUCGAUCUUGGGACC	hsa-mir-2313	pending	1173	gUUUcACCGCUCGAUCUUGGGACCcaccgcUgccccUcagcU ccgagUccagggcgaggUaagggcUggagUcggggcaggga
880	UAGUGGAUGAGGAGACUCGGU	hsa-mir-2314	hsa-mir-3691	1174	aUUgagggcacUgggUAGUGGAUGAGGAGACUCGGUacc cacUgcUgagggUggggagccaagUcUgcgUcaUccUcUccUcag UgcccUcaaa
881	CUCGGAGCGUUAGAGAUGGA	hsa-mir-2315	pending	1175	gUUCUGGGAGCGUUAGAGAUGGAGacUaacgUcUUccaa gggagaUUgcgUcUccacUUUcaccUggUacUgagag
882	GGCUGGAGCGAGUGCAGUGGUG	hsa-mir-2316	hsa-mir-3135b	1176	UgccccGGCUGGAGCGAGUGCAGUGGUGGcagUccU agcUcacUgcagccUcgaacUccUgggcu
883	UCAGGUGUGGAAACUGAGGCAG	hsa-mir-2317	hsa-mir-3934	1177	UUUUACAGGUGUGGAAACUGAGGCAGgagggcagUgaagUa acUUGcUcagUUGcagagcUgggaagU
884	UGACACGGAGGGUGGCUUGGGAA	hsa-mir-2318	hsa-mir-4462	1178	cUUcccagcUgccccUaagUcagagUggcUUUcUUGACACGG AGGGUGGCUUGGGAAa
885	GAAGAUUGGUGUGUGUGAGGGA	hsa-mir-2319	pending	1179	ggUGAAGAUUGGUGUGUGUGAGGGAaagggaUgcagagc ccUgcccagcaccaccUccUaUg

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
886	AAAGACUGCAAUUACUUUUGCG	hsa-mir-2320	hsa-mir-548u	1180	aUggUgcaaaagUaaUgUggUUUUUUUUUcUUUacUUUUUaaUaaggcAAAAGACUCGCAAUUACUUUUUUGCGcca
887	GAGACUGGGGUGGGGCC	hsa-mir-2321	hsa-mir-4463	1181	aaUagaUUaUUggUcaccaccUccagUUUcUgaaUUUgUaGACUGGGGUGGGGCCUgagaaUUUgjc
888	AAGGUUUGGAUGAUGCAAUA	hsa-mir-2322	hsa-mir-4464	1182	ggaaccUUagUAAAGGUUUUGGAUAGAUAGCAUAaagUaUgUccatcagcUgaaggacaUacUUUaUUgcaUgUaUccaaaccUUacUaaUUca
889	AAAGGUAAUUGCAGUUUUUCCCC	hsa-mir-2323	hsa-mir-548ai	1183	gUaUUaggUUggUgcAAAGGUAAUUGCAGUUUUUCCCCaUUUaaaaUaUggaaaaaaaUcacaUUacUUUUUUGcaUcaaUcUaaUaa
890	AGGGGACCAAAGAGAUAAUAG	hsa-mir-2324	hsa-mir-3144	1184	gaaacUacacUUUaAGGGGACCAAAGAGAUAAUAAUAGaUaUcagcUaccUaUaUaccUgUcggUcUcUUUaaagUgUaUgUUa
891	UAAAAACUGCAAUUACUUUUA	hsa-mir-2325-1	hsa-mir-548aj-1	1185	aUUggUgUaaaaUaaUUgCaggUUaUgCcaUUaaaaUaaUaUggUaUUAAAAACUCGCAAUUACUUUUUAAcUacUaac
892	UAAAAACUGCAAUUACUUUUA	hsa-mir-2325-2	hsa-mir-548aj-2	1186	aaggUaUUaggUUggUgcaaaagUaaUUgCagUUUUUUUgCuaUUacUUUUaaUggUAAAAACUCGCAAUUACUUUUUAAcacaUaccUaaUaUUUa
893	CUCAAGUAGUCUGACCAGGGGA	hsa-mir-2326	hsa-mir-4465	1187	caUgUgUccccUggcacgcUaUUUgaggUUUacUaUaggaaCUCAAAGUAGUCUGACCAAGGGGACacaUga
894	UCUGGCUGAGGAGGAAGUGGAG	hsa-mir-2327-1	pending	1188	gcUcUagUagccacagccaUccccUagagggaUCUGGCGUGAGGAGGAAGUGGAGg
895	UCUGGCUGAGGAGGAAGUGGAG	hsa-mir-2327-2	pending	1189	ccgcccUcagUggcUUccUccacagccaccUccggagggaUCUGGCGUGAGGAGGAAGUGGAGgUgcUg
896	GGCGACAAAACGAGACCCUGU	hsa-mir-2328	hsa-mir-1273c	1190	cUgGGCGACAAAACGAGACCCUGUcUUUUUUUUUUUUUcUgagacagagUcUcgUucUgUUGcccaa
897	GGGUGCGGGCGCGGGG	hsa-mir-2329	hsa-mir-4466	1191	acgcGGGUGCGGCGCGGGGUGaagaccaccggcccgccgcgcggcccgccga
898	CCUGCUGGUCAGGAGUGGAUAC	hsa-mir-2330	hsa-mir-3692	1192	ggcaUUCCUCUGGUCAGGAGUGGAUACUgaggcaUagUaUacagUUccacacUgacacUgcagaagUgga
899	CAUGCUGGAUAGAAAGAAUGG	hsa-mir-2331	hsa-mir-3146	1193	aUUUUcUUUgUcUaagUcccUucUUUUcUaUccUagUaUaacUUgaagaaUUcaaaUagUCAUGCUAGGAUAGAAAGAAUGGacUUGcccaaggagaa

[illegible]

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
915	CCCUGGGUUCUGAGGACAUG	hsa-mir-2346	pending	1209	aUgcUgCCCUGGGUUCUGAGGACAUGcUcUgacUccccUgaUgUccUcUgUUccUcaggUgcUgggcga
916	CAAGGGACCAAGCAUUAUUAU	hsa-mir-2347	hsa-mir-4475	1210	aUcUcaaUgagUgUgUgUcUaaUgacUcaUagUCAAGG GACCAAGCAUUAUUAUgaa
917	CAGGAAGGAUUUAGGGACAGGC	hsa-mir-2348	hsa-mir-4476	1211	aaaagccUgUccccUaagUccccUccagagcUccagagUUggUgc CAGGAAGGAUUUAGGGACAGGCUUUUg
918	CUAUUAAGGACAUUUUGUGAUUC	hsa-mir-2349	hsa-mir-4477a	1212	UccUccUcccaUcaaUcacaaaUgUccUbaaUggcaUUUuaagg aUUGCUAUUAAGGACAUUUUGUGAUUCacggaggaggU
919	AUUAAGGACAUUUUGUGAUUGAU	hsa-mir-2350	hsa-mir-4477b	1213	accUccUccccUgaaUcacaaaUgUccUbaaUagcaUccUuaa aUgccaUUUAAGGACAUUUUGUGAUUgaggaggaggga
920	AAAAGGCAUAAAACCAAGACA	hsa-mir-2351-1	hsa-mir-3910-2	1214	cUUUUUUUgUgUcUgUcUgUgUUUUUaUgcccUUUUaUg UgcccUgaaUaUAAAAAGGCAUAAAACCAAGACAagcaacag aaaaac
921	AAAAGGCAUAAAACCAAGACA	hsa-mir-2351-2	hsa-mir-3910-1	1215	cUgUcagUUUUUcUgUgUgUcUcUgUUUUUaUgUccUU UUaUaUcaaggcacUAAAAGGCAUAAAACCAAGACAagc aaca
922	GAGGCUGAGCUGAGGAG	hsa-mir-2352	hsa-mir-4478	1216	ggccGAGGCUGAGCUGAGGAGGccUccaaaccUgUagacagg gUcaUgcagUacUagggggcagccUcaUccccUgcagcccUggcc
923	CUGGGAGGUGUGAUUUUGUGGU	hsa-mir-2353	hsa-mir-3689c	1217	gggagagUgUgaUaUcUgUgUcUcUgggagUgUgaUaUcUg gUcUcUGGGGAGGUGUGAUUUUGUGUUccU
924	UAAAAACUGCAUUUACUUUC	hsa-mir-2354-1	hsa-mir-548x-2	1218	aUgccaalUaUUagUgUggcacaagaUaaUgUggcUUUUG ccaUuaaaagUaaUgUUA AAAACUGCAUUACUUUCgUgc caaccUaaUaUUUgUgUg
925	UAAAAACUGCAUUUACUUUC	hsa-mir-2354-2	hsa-mir-548x-1	1219	agUgcaaaagUaaUugcagUUUUUgUgUacUUUcUcaaUcgU AAAAACUGCAUUACUUUCacacc
926	UGUGAUAUCAUGGUUCCUGGGA	hsa-mir-2355-1	hsa-mir-3689a	1220	gcUcccUgggagUgUGAUUAUCAUGGUUUCCUGGGAGgUg UgaUccUgUgcUuccUgggagUgUgaUaUcUgUggUUccUgg gagg
927	GGGAGGUGUGAUCUCACACUCG	has-mir-2356-1	hsa-mir-3689d-1	1221	UGGGAGGUGUGAUCUCACACUCGcUgggagUgUgcUaU cgUcUUccccgggagUgUgaUccUgUcUcUUccUg
928	CUGGGAGGUGUGAUUUUGUGGU	mir-2355-2*	has-mir-3689b-1	1222	gggagUgUGAUUAUCAUGGUUUCCUGGGAGgUgUgaUccc gUgcUUcCUGGGAGGUGUGAUUUUGUGUUccU
929	UGUGAUAUCAUGGUUCCUGGGA	hsa-mir-2355-2	hsa-mir-3689b-1	1223	gggagUgUGAUUAUCAUGGUUUCCUGGGAGgUgUgaUccc gUgcUUcCUGGGAGGUGUGAUUUUGUGUUccU

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
930	GGGAGGUGUGAUCACACUCG	has-mir-2356-2	hsa-mir-3689d-2	1224	acUUGGAGGUGUGAUCACACUCGcUgggaggUgUgcUaUccUuccUgggagglUgaUccUgUucUuccUgagcg
931	UGUGAUUAUCAUGGUUCCUGGGA	hsa-mir-2355-3	has-mir-3689b-2	1225	gggaggUGUGAUUAUCAUGGUUCCUGGAGglUaUgaUaUcUgUggUUccUlgggagglUgaUcccgUgcUcccU
932	UGUGAUUAUCGUGCUUCCUGGGA	hsa-mir-2355b	hsa-mir-3689f	1226	aggUGUGAUUAUCGUGCUUCCUGGGAcgUgUgaUgcUgUgcUuccUgggagglUgaUucccacUc
933	CGCGGGCGGUGCUCGGAGCAG	hsa-mir-2356	hsa-mir-4479	1227	gaaaccaagUccgagcgUggcUggcggggaaaagUcgggaacgC GCGGGCCGUGCUGGAGCAGcgcca
934	CCAGGCUCUCGAGUGGGAACU	hsa-mir-2357a	hsa-mir-3155a	1228	ccUgUuccgggcaUccaccUcccacUgcagagccUggggagccggag agcUcccUuccCAGGCUCUCGAGUGGGAACUgaUgccUgg aacagU
935	CCAGGCUCUCGAGUGGGA	hsa-mir-2357b	hsa-mir-3155b	1229	ccacUgcagagccUgggaaggagcUgUccggcUccCCAGGCCUC UGCAGUGGGAGU
936	AAAAGUAACUGCGGUUUUUGA	hsa-mir-2358	hsa-mir-548ak	1230	gUgcAAAAAGUAACUGCGGUUUUUUGagaagUaaUUgaaaa ccgcaaUUacUUUUJgcag
937	AGCCAAGUGGAAGUUACUUUA	hsa-mir-2359	hsa-mir-4480	1231	gcagaggUgagUugaccUccacaggggccaccaggagUaagUAG CCAAGUGGAAGUUACUUUAccUcUgU
938	GGAGUGGGCUGGUGGUU	hsa-mir-2360	hsa-mir-4481	1232	GGAGUGGGCUGGUGGUUUUUUaagaggaaaggagaccUa agcUagcacalbgagcacgcUc
939	GAGCGAUCCGAGGGACUG	hsa-mir-2361	pending	1233	cggcUUccccggUccccggUgcUgaggagagAGCGAUCCCGAG GGACUGgcgcgc
940	AAGGCUUCCUCUCUGCAGGAC	hsa-mir-2362-1	hsa-mir-3158-2	1234	acaUaUUcagggcggUccUgcagagaggaaagcccUUccaaUacc UgUaagcagAAGGGCUUCCUCUCUGCAGGACcggccUgaa UaaUga
941	AAGGCUUCCUCUCUGCAGGAC	hsa-mir-2362-2	hsa-mir-3158-1	1235	gggaUcaUUaUUcagggcggUccUgcagagaggaaagcccUUcUgc UUacaggUaUUggAAAGGGCUUCCUCUCUGCAGGACcggcc UgaalUaalUgUaaUca
942	AACCCAGUGGGCUAUGGAA AUG	hsa-mir-2363	hsa-mir-4482	1236	agUgagAACCCAGUGGGCUAUGGAAAUUGUgUggaagaU ggcaUUUUcUaUUUcUcagUggggcUcUUacc
943	GGGGUGGUCUGUUGUUG	hsa-mir-2364	hsa-mir-4483	1237	aaaaaacacaUacUUagUgcaUaccUaUaaUaUUaGGGG UGGUCUGUUGUUGUUUUUcU
944	AAAAGCGGAGAGCCCCA	hsa-mir-2365	hsa-mir-4484	1238	gggUUUcUcUgcccUUUUUUUccaaUgaaaaUaacgaaaccU gUUaUUUcccaUUGagggggAAAAAGCGGGGAGAGAGCCCC A

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
945	UGGCUGUUGAGGGGGCAGGCU	hsa-mir-2366	pending	1239	ggagccagcccUccUcccgcaccaacaacUUGgagcacUUGaccUUUGGCUGUUGAGGGGGCAGGCUcg
946	UAACGGCCGCGGUACCCUAA	hsa-mir-2367	hsa-mir-4485	1240	agaggcacccUgccccagUgacUgagUUUAACGGCCGCGGGUACCCUAAcUgUgca
947	UAGGAUUACAAGUGUCGGCCAC	hsa-mir-2368	hsa-mir-3159	1241	ccUAGGAUUACAAGUGUCGGCCACcgggcUgggcacagUggcUcacgccUgUaaUucccagc
948	GCUGGGCGAGGCUGGCA	hsa-mir-2369	hsa-mir-4486	1242	gcaUGCUGGGCGAGGCUGGCAUcUagcacagggcgUagaUgcUUGcUcUgccaUUGcaalUga
949	AGAGCUGGCUGAAGGGCAG	hsa-mir-2370	hsa-mir-4487	1243	acUgUcUUcagccAGAGCUGGCUGAAGGGGCAGaagggaacUgUcUcUcagccagcUggcUgaaggcgaga
950	AGGGGGCGGGCUCCGGCG	hsa-mir-2371	hsa-mir-4488	1244	ggUAGGGGGCGGGCUCCGGCGcUgggacccacUaggggUggcgccUUGggccgccccgcc
951	GCCGAGAGUCUCGGGGUU	hsa-mir-2372	pending	1245	UcGCCGAGAGUCUCGGGGUUUcUcUgUcUcaacagUgcUUGgacggaaaccggcg
952	UGGGGCUAGUGAUGCAGGACG	hsa-mir-2373	hsa-mir-4489	1246	gggggUGGGGCUAGUGAUGCAGGACGcUggggacUgggagUggagaagUccUgcccUgacccUgUccca
953	UGUGACUUUAAGGGAAUUGCG	hsa-mir-2374	hsa-mir-3164	1247	UggaaacUGUGACUUUAAGGGAAUUGCGCcacagcagaccUgcaacUcaUgcccUUUgUcUUGaagUcgagUUUccc
954	UCUCAGGAGUAAAGACAGAGUU	hsa-mir-2375	hsa-mir-3664	1248	aacUUGaaggUagggacUcUgUcUUcacUcaUgagUaccUUcUcaacagcUcUCUCAGGAGUAAAGACAGAGUUcccUaccUUcaacUgU
955	AGGUGGAUGCAAUGUGACCUCA	hsa-mir-2376	hsa-mir-3165	1249	caAGGUGGAUGCAAUGUGACCUCAacUcUUGgUccUcUgaggUcacacUUGUaUccaccUUa
956	AACGGCAAUGACUUUUUGUACCA	hsa-mir-2377	hsa-mir-548a1	1250	ggUcggUgcaaaagUaaUUgUcUUUUUUgccaUUaaaaUaaUggcaUUaaaagUaaUggcaaaACGGCAAUGACUUUUUGUACCAaUcUaaUaUcU
957	UCUGGUAAGAGAUUUGGGCAUA	hsa-mir-2378	hsa-mir-4490	1251	aUagUUUcUgcaaUgcUcaaaUcUcUggccaaagaccagaacUaaUggUcUCUGGUAAGAGAUUUUGGGCAUAUUAgaacUaaUaa
958	AAUGUGGACUGGUGACCAAA	hsa-mir-2379-1	hsa-mir-4491	1252	acaUUUggUcacaccagUccacaUUaaagUggaccagacaaUaUAAUUGUGGACUGGUGUGACCAAAa
959	AAUGUGGACUGGUGACCAAA	hsa-mir-2379-2	pending	1253	accUggacaUUUggUcacaccagUccacaUUaaagUggaccagacaaUaUUAAUUGUGGACUGGUGACCAAAagUccagc

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
960	GGGCGUGGGCGCGCC	hsa-mir-2380	hsa-mir-4492	1254	cUgcagcglgUcUUcUccaggcccccgcgggacagacacacggaca agUcccgcccaGGGCUGGGCGCGGCCCagccgg
961	AGAAGGCCUUUCCAUCUCUGU	hsa-mir-2381	hsa-mir-4493	1255	ccagagaUeggaagggccUUccggUgaUUAUcacagccaUgcccUU UaccUccAGAAAGCCUUUCCAUCUCUGUc
962	CCAGACUGUGGCUGACCAGAGG	hsa-mir-2382	hsa-mir-4494	1256	agUUUUJagUUaccclluggUcalUcUvgcaglUcUgaaaaUacaaa UggaatauuuccAGACUGUGGCUGACCAAGGUaaUaacUgaa acc
963	AGGAGAAGCAGGAGCUGU	hsa-mir-2383	pending	1257	cUGAGGAGAACGCAGGAGCUGUcUUUgguUacaUUcaggUcac Ug
964	AAUGUAAAACAGGCUUUUUGCU	hsa-mir-2384	hsa-mir-4495	1258	aagaAAUGUAAAAACAGGCUUUUUGCUcagUggagUUaUUUU UgagcaaaaagcUUaUUUacaUUUcUg
965	GAGGAACUGAAGCUGAGAGGG	hsa-mir-2385	hsa-mir-4496	1259	ACAUCAGCUCAUAAUAAUCCUCGAAGCUGCUCUUUAGAA AUGAGAAACUGAAGCUGAGAGGG
966	CUCCGGGACGGCUGGGC	hsa-mir-2386	hsa-mir-4497	1260	acCUCGGGACGGCUGGGCGccggcgccgggagaUccgcgcU UcUgaaUccggccggccggccggcccgUccggcccgggUc
967	UGGGCUGGCAGGGCAAGUGCUG	hsa-mir-2387	hsa-mir-4498	1261	agggcUUGGGCUGGCAGGGCAAUGUCUGCagalUcUUUgUc UaagcagccccUggcuUggalUcUacca
968	GAGGCUGAAGGAAGAUGG	hsa-mir-2388	hsa-mir-4419b	1262	cUcaggcUcagUggUgcaUgcUUaUlagUccagccacUcUGA GGCUGAAGGAAGAUGGCcUUGagccU
969	AAGACUGAGAGGAGGGA	hsa-mir-2389	hsa-mir-4499	1263	AAGACUGAGAGGAGGGAacUggUgagUugUacaUagaaa UgcUUUucUaacUccUugUcUcagUcUgUUU
970	UGAGGUAGUAGUUUCUU	hsa-mir-2390	hsa-mir-4500	1264	caggagagaaaagUacUgccccagaagcUaaagUgUagaUcaaacgc aUaaUggcUGAGGUAGUAGUUUcUUgaacUU
971	CGGCUGGGAGCGCAGGCGUCGG	hsa-mir-2391	pending	1265	ggCGGCUGGGAGCGCGGCGGUGcgagaccUggagacg ggcaUgggggggc-UgcggcUgcUggcUgUg
972	UAUGUGACCUCGGAUGAAUCA	hsa-mir-2392	hsa-mir-4501	1266	UAUGUGACCUCGGAUGAAUAcUgaaaUaUgUcUgagcU UcUgUUUucaUcagaUgUcacaUUUU
973	GCUGAUGAUGGUGCUGAAG	hsa-mir-2393	hsa-mir-4502	1267	agccUUUagcaagUUGuaaUcUUUUUgUgaUggagggUcU UgccUccaUgggggaUgGCUGAUGAUGAUGGUGCUGAAG c
974	AGAUGUAUGGAUCUCUGUAU	hsa-mir-2394	hsa-mir-3171	1268	gAGAUGUAUGGAUCUCUGUAUAUaUcUaUaUaUaUgUgUg aUaUaUaUaUUrcaUaaalUcUa

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
975	UUUAAAGCAGGAAAUAGAAUUUA	hsa-mir-2395	hsa-mir-4503	1269	acaaUgUagaUaUUUAAGCAGGAAAUAGAAUUUAcaUaUaaaUUUcUaUUUgUUUcUaUUUcUcUgcUUaaaaUaUcUacaUUgc
976	UGUGACAAUAGAGAUGAACAU	hsa-mir-2396	hsa-mir-4504	1270	cUaagaUaaUgUccUccaggUUcaUcUcUgUgUcaUUUgUggcaUggaccaUUUGUGACAAUAGAGAUGAACAUGGaggaUaUUaUcUUaa
977	AGGUGGGGUGGACGGA	hsa-mir-2397	hsa-mir-4505	1271	ggAGGCGUGGCGUGGACGGACacccggccUccacUUUcUgUggcaggUaccUccUccaUgUcgcccgccUug
978	AAUGGGUGGUCUGAGGCAA	hsa-mir-2398	hsa-mir-4506	1272	UggccUcUggcaUcagaccaUcUgggUUcaagUUUgUgUcUcUcUUaUgAAUUGGUGUCUGAGGCAAgUggUcU
979	UAGGAUGGGGUGAGAGGUG	hsa-mir-2399	hsa-mir-2392	1273	aUggUcccUccaaUccagccaUuccUcagaccaggUggcUcccagcaccacccaggcUgUAGGAUGGGGUGAGAGGUGcUag
980	CUGGGUUGGGCUGGGCUGGG	hsa-mir-2400	hsa-mir-4507	1274	UcUgggcUgagcagcUgggUuaagccagcUGGGGUUGGGCGUGGGCUGGGU
981	AAGGACUGGAGUGGAUUGGGU	hsa-mir-2401	pending	1275	ggAAGGGACUGGAGUGGAUUGGGUacaUcUaUUaUaUgUggagaccUacUacaaccgUcccUcaagagUcgagUcacc
982	AAGGGCUGGAGUGGAUUGGGG	hsa-mir-2402	pending	1276	cUggUgaaUcUgggUcgcgcagcccccagggAAGGGGCGUGGAUGGAUUGGGGaaaUccaU
983	GCGGGGCGGGCGCG	hsa-mir-2403	hsa-mir-4508	1277	aggaccacGCGGGGCGUGGCGCGGgagcagcUgggUgcaUgcgcUgcccggcagcUgcaaggcgccg
984	ACUAAAGGAUAUAGAAGGUUUU	hsa-mir-2404-1	hsa-mir-4509-1	1278	cUUUaaUacUaUcUcaaACUAAAGGAUAUAGAAGGUUUUccccUUUcUcUUggcccUgaaaccUUcUgUaUcccUUUaUUUUgagaUagUaUUagaa
985	ACUAAAGGAUAUAGAAGGUUUU	hsa-mir-2404-2	hsa-mir-4509-2	1279	cUUUaaUacUaUcUcaaACUAAAGGAUAUAGAAGGUUUUccccUUUcUcUUggcccUgaaaccUUcUgUaUcccUUUaUUUUgagaUagUaUUagaa
986	ACUAAAGGAUAUAGAAGGUUUU	hsa-mir-2404-3	hsa-mir-4509-3	1280	cUUUaaUacUaUcUcaaACUAAAGGAUAUAGAAGGUUUUccccUUUcUcUUggcccUgaaaccUUcUgUaUcccUUUaUUUUgagaUagUaUUagaa
987	AAGCAUACUGUUAACCGAAAU	hsa-mir-2405	hsa-mir-3942	1281	cUcaagAAGCAUAUCUGUUUACCUGAAAAUaggcUgcgagaUaacagUaUUUcagaUaacagUaUUaUcUcUUUgaa
988	UGAGGGAGUAGGAUGUAUGGUU	hsa-mir-2406	hsa-mir-4510	1282	gUgUaUgUGAGGGGAGUAGGAUGUAUGGUUgUgUaUgacaacUacaUcUUUUUcUcacaacagacag

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
989	GAAGAACUGUUGCAUUUGCCCU	hsa-mir-2407	hsa-mir-4511	1283	aaaaaaagggaagAACUGUUGCAUUUGCCCUgcac UcagUUUgacagggUaaaUgcaaUagUUcUUUuccUUU UUUUUa
990	CAGGGCCUCACUGUAUCGCCCA	hsa-mir-2408	hsa-mir-4512	1284	cUagcccgaggcaUaUagUgagaccUgcUcUacaAAAAUU gagaCAGGGCCUCACUGUAUCGCCCAggcUgga
991	AGACUGACGGCUGGAGGCCCAU	hsa-mir-2409	hsa-mir-4513	1285	aUUCUagUgggAGACUGACGGCUGGAGGCCCAUaagc UgUcUaaaacUcggccccagaaUUUcUggUcUccccacUUcag aac
992	ACAGGCAGGAUUGGGGAA	hsa-mir-2410	hsa-mir-4514	1286	gUUGagACAGGCAGGAUUGGGGAAacaUcUUUuaccUgc UcUcUgcccUgUUUUUaga
993	AGGACUGGACUCCCCGGCAGCCC	hsa-mir-2411	hsa-mir-4515	1287	gcggaggUgUaacAGGACUGGACUCCCCGGCAGCCCcraggg cagggcgUggggagcUggUccUagcUcagcgcUccccgga
994	UAGUGAGUAGAGAUAGCAGAGC	hsa-mir-2412	hsa-mir-3174	1288	agcgUuaccUggUAGUGAGUAGAGAUAGCAGAGCccUgg gcUccUcagcaaacUacUgggaUcUgca
995	ACUGGCCUGGACUACCGGGGG	hsa-mir-2413	hsa-mir-3176	1289	UcUgagcUccccagcUcggccacacUccccgggaUccccaggg ACUGGCCUGGACUACCGGGGGUggcggc
996	GGGAGAAGGGUCCGGGC	hsa-mir-2414	hsa-mir-4516	1290	aGGGAGAAGGGUCCGGGGCagggaggcagggcagggcUcUgg ggUggggggUcUgUgagUcagccacggcUcUgcccacgUcUcccc
997	UGGGGGGAGCUUCCGGAGGCC	hsa-mir-2415-1	hsa-mir-3180-1	1291	agcUcUcagacgcUccccacgUcgcaUgcggccccgggaaacgcgU GGGGGGGAGCUUCCGGAGGCCcc
998	UGGGGGGAGCUUCCGGAGGCC	hsa-mir-2415-2	hsa-mir-3180-2	1292	agcUcUcagacgcUccccacgUcgcaUgcggccccgggaaacgcgU GGGGGGGAGCUUCCGGAGGCCcc
999	UGGGGGGAGCUUCCGGAGGCC	hsa-mir-2415-3	hsa-mir-3180-3	1293	agcUcUcagacgcUccccacgUcgcaUgcggccccgggaaacgcgU GGGGGGGAGCUUCCGGAGGCCcc
1000	UGGGGGGAGCUUCCGGAGGCC	hsa-mir-2415-4	hsa-mir-3180-4	1294	agcUcUcagacgcUccccacgUcgcaUgcggccccgggaaacgcgU GGGGGGGAGCUUCCGGAGGCCcc
1001	UGGGGGGAGCUUCCGGAGGCC	hsa-mir-2415-5	hsa-mir-3180-5	1295	agcUcUcagacgcUccccacgUcgcaUgcggccccgggaaacgcgU GGGGGGGAGCUUCCGGAGGCCcc
1002	CUCGUGGGCUCUGGCCACGGC	hsa-mir-2416	hsa-mir-3677	1296	UggagggaUuagggcagUggccagagcccUgcagUgcUgggcaUg ggcUUUCUGUGGGCUCUGGCCACGGCCUgagcUccUcc
1003	AGAGGGGUGAAAAUUUAAACGU	hsa-mir-2417-1	hsa-mir-3179-1	1297	gccaggaUcacagcUuUaaaaUaacacUccUUcUgcUgUgccc UUacagcagUAGAGGGGGUGAAAAUUUAAACGUcUgUga UccUgggg

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
1004	AGAAGGGGUGAAUUUAAAACGU	hsa-mir-2417-2	hsa-mir-3179-2	1298	gaUcacagagUUUaaUUUaacUccUcUgcUgUgcUUaca gUcagUAGAAAGGGUGAAUUUAAAACGUCUgUgaUccUggg
1005	AGAAGGGGUGAAUUUAAAACGU	hsa-mir-2417-3	hsa-mir-3179-3	1299	gccaggUcacagagUUUaaUUUaacUccUcUgcUgUgc UUacagcagUAGAAGGGGUGAAUUUAAAACGUCUgUga UccUgg
1006	AAAUUAUGAUGAAACUCACAGCUG AG	hsa-mir-2418	hsa-mir-4517	1300	aggUAAAUUAUGAUGAAACUCACAGCUGAGagagcUUagca agUagcUaaaggccagagcUUgUUUggggUggUgUggcUg
1007	GCUCAGGGAUGAUAAACUGUGCUG AGA	hsa-mir-2419	hsa-mir-4518	1301	UgggggaaaagUgcUggggaUUgaUUagUgaUgcUgcUggggga acggggGCUCACAGGGAUGAUAAACUGUGCUGAGAGccccU
1008	CAGCAGUGCGCAGGGCUG	hsa-mir-2420	hsa-mir-4519	1302	aaccUCAGCAGUGCGCAGGGGUGcacUgUcUccgUcUgcgg ccUgcagUaagcgggUa
1009	UUGGACAGAAACACGCAGGAA	hsa-mir-2421	hsa-mir-4520	1303	gUgUgcccaccUgcgUgUUUUUcUgUcCaUUcagaaaaaggaaUU UGGACAGAAACACGCAGGAagaaggaa
1010	GCUAAGGAAGUCCUGUGCUCAG	hsa-mir-2422	hsa-mir-4521	1304	UcgGCUAAGGAAGUCCUGUGCUCAGUUUUUgUagcaUca aaacUaggaUUUcUcUgUUUac
1011	CUGGACUGAGCCAUAGCUACUGG	hsa-mir-2423	hsa-mir-1269b	1305	UbagggUUUCUGGACUGAGCCAUAGCUACUGGcUUcUcUg gUUcUccagcUUacagaUggcUUaUcaUgggaccUcU
1012	UGACUCUGCCUGUAGGCCGGU	hsa-mir-2424	hsa-mir-4522	1306	gcggggcUgUccUggggggccUcgcaagggggaggaUccagccccaggcU ggUUccgcUGACUCUGCCUGUAGGCCGGGUGggcUcUUcU
1013	GACCGAGAGGGCCUCGGCUGU	hsa-mir-2425	hsa-mir-4523	1307	gcggggGACCGAGAGGGCCUCGGCUGUgUgaggacUagagg cggcgagggccggggcgUUccccga
1014	UAGAGGCUGGAUAGAGAUUCU	hsa-mir-2426	pending	1308	aUUUUAGAGGCUGGAUAGAGAUUCUUGaggcUUGgaa gagUaagggaUcccUUUaUcUgUccUcUaggag
1015	UAGCCUUCAGAUUUUGGUGUUU	hsa-mir-2427	hsa-mir-3614	1309	UggaUcUgaaggcUgccccUUUgUcUcUgUggggUAGCCUUCA GAUCUUGGUGUUUUU
1016	CCACUUGGAUCUGAAGGCUGCC	hsa-mir-2427*	has-mir-3614	1310	UgggCCACUUGGAUCUGAAGGCUGCCcUUUgUcUcUgUg gggUagccUUcagaUcUUggUgUUUUU
1017	AUAGCAGCAUGAACCUUCUCU	hsa-mir-2428	hsa-mir-4524	1311	gaacgAUAGCAGCAUGAACCUUCUCACUgcagaaUaUU UUgagacaggcUUaUgcUgcUaUccUuca
1018	UGAGACAGGCUUAUGCUGCUAU	hsa-mir-2428*	has-mir-4524	1312	ggaaacgaUagcagcaUgaaccUgUcUcacUgcagaaUaUUUU GAGACAGGCUUAUGCUGCUAUcUUca

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
1019	GGGGGAUGUGCAUGGUGGU	hsa-mir-2429	hsa-mir-4525	1313	gUcagaGGGGGAUGUGCAUGGUGGUUgbbggUgbbgcUgc cUgUggbaccaaUcagcgUgcacUUcccccaccUgaa
1020	CAGGAGGUGAAUGGUUCUGUC	hsa-mir-2430	pending	1314	cUUagcUcccUggbcUUcagcccUUUUUcCAGGGGAGGUGAA UGGUUCUGUCUcgc
1021	GCUGACAGCAGGCGUGGCCGCU	hsa-mir-2431	hsa-mir-4526	1315	UgcggUgacaUcagggccragUcccUgcUgUcaUgUccccaggUga cgUgcUggGCGUGACAGCAGGCGUGGCCGCGUaacgUcacUg Uc
1022	UGGUCUGCAAAGAGAUGACUGU	hsa-mir-2432	hsa-mir-4527	1316	ccagaagUGGUCUGCAAAGAGAUGACUGUGaaUccaagaU ccacaUcagcUcUgUgcUgcccUacaUcUga
1023	UCAUUUAUUAUGUAUCUGGAC	hsa-mir-2433	hsa-mir-4528	1317	UaUUcUacUgagagUacagaUcUUUaUaUaUaUaUgaUcaUUa UaUgUaUgaUgagaUCAUUUAUUAUGUAUGAUCUGGACacc cagUagaaUc
1024	AUUGGACUGCUGAUGGCCCGU	hsa-mir-2434	hsa-mir-4529	1318	aUgacaggccaUcagcagUccaaUgaagacaUgaagaccacaaUgU cUUcAUUGGACUGCUGAUGGCCCGUcacUggga
1025	UUUGAGGGUGUGGAAGACAUC	hsa-mir-2435	pending	1319	cUccacaUUUGAGGGUGUGGAAGACAUCUgbbcccaacUcU gaUcUcUUcaUcUacccccaggacUggga
1026	CCCAGCAGGACGGGAGCG	hsa-mir-2436	hsa-mir-4530	1320	cgaccgcaccccgcaagcUgggUcaaggagCCCAGCAGGACG GGAGCGcggcgc
1027	AUGGAGAAGGCUUCUGA	hsa-mir-2437	hsa-mir-4531	1321	gccUaggagUccUUGgUcagUggggacAUGGAGAAGGCUUC UGAgga
1028	AAAAGCUGGGUUGAGAA	hsa-mir-2438	hsa-mir-320e	1322	gccUUcUcUcccagUUcUcUcUggagUcggggAAAAAGCUG GGUUGAGAAggUgaaaaa
1029	UGGAAGGUAGACGGCCAGAGAG	hsa-mir-2439	hsa-mir-3190	1323	ggUcaccUgUcUggccagcUacgUccccacggcccUgUcagUg UGGAAGGUAGACGGCCAGAGAGgUgaccc
1030	UCUGGGAGGUUGUAGCAGUGGA	hsa-mir-2440	hsa-mir-3192	1324	aggaagggaUUcUUGGGAGGUUGUAGCAGUGGAaaaaagUU cUUUUcUcUcUcUgUcggcccUcUcagcUcUUUcUcUcUg acagaCCCCGGGGAGCCCGGgUgaaUcUcUggUaUcUcU gggUgUcUgga
1031	CCCCGGGAGCCCGCGG	hsa-mir-2441	hsa-mir-4532	1325	UgagaaUgUGGAAGGAGGUUGCCCGGACGCGUgcUggcUgc cUUccagcUccacUUcccUUUcUcUcUcUcUcUcUcUc
1032	UGGAAGGAGGUUGCCGACGCU	hsa-mir-2442	hsa-mir-4533	1326	cggUUgUgUgcaaaaggUaaUUGUgguUUcUgccaUUGaaagUa aaggCAAGAACCUCUAAUACCUUUUGCagcgaccU
1033	CAAGAACCUCAAUUACCUUUGC	hsa-mir-2443	pending	1327	UcgaaggAAUCUGAAGGCGCACAAAGGUUUgUgUcUcUcUc UacagUccaccUcUgcUacUcagUcUgcUcUgUg
1034	AAUCUGAGAAAGCGCACAAAGGU	hsa-mir-2444	has-mir-3200	1328	

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
1035	CACCUUGCGUACUCAGGUCUG	hsa-mir-2444*	hsa-mir-3200	1329	UcagaggaaUcUgagaagcgcaacaaggUUUgUgUccaaUacag UccaCACCUUGCGUACUCAGGUCUGcUgU
1036	GGAGGAACCUUGGAGCUUCGGC	hsa-mir-2445	hsa-mir-3928	1330	ggcUgaagcUcUaaggUUccgcUgcggcgaggaagcGGAGGA ACCUUGGAGCUUCGGCa
1037	GGAUGGAGGAGGGGUCU	hsa-mir-2446	hsa-mir-4534	1331	UgUgalUgacccccUuccagagccaataUaccagGGAUUGGAG GAGGGUCUUGggUacU
1038	ACUGGACUAGGAGUCAGAAGG	hsa-mir-2447	hsa-mir-378i	1332	888agCACUGGACUAGGAGUCAGAAGGUggagUUcUg88g UgcUgUUUUUcccacUcUUGggccUlgggcaUgUUcUg
1039	GUGGACCUGGCCGGAC	hsa-mir-2448	hsa-mir-4535	1333	aacUgggUcccagUcUUcacagUUggUUcUgacacGUGGGAC CUGGCUGGGACGaUgUg
1040	ACCUGGACCCAGCGUAGACAAA	hsa-mir-2449	hsa-mir-3690	1334	ccACCUGGACCCAGCGUAGACAAAgaggUgUUUcUacUcc aUaUcUaccUggaccagUgU
1041	CAAAAACUGCAGUUACUUUUGU	hsa-mir-2450	hsa-mir-548am	1335	agUUGUgcaaaaagUaaUgvcggUUUUUgvcgUcgaaaaUaa UgGCAAAACUCUGAGUUACUUUUUGUaccaUg
1042	UUGGGCUGGGCUGGGUUGGG	hsa-mir-2451	hsa-mir-1587	1336	UUUGGCUGGGCUGGGUUGGGCragUUcUUcUgcUggac UaccUgUgaccagc
1043	UGUGGUAGAUUAUAGCACGAU	hsa-mir-2452	hsa-mir-4536	1337	aUgUgUggUagaUaUaUgcacUgUaUaUaaacaUaaUGUGG UAGAUUAUAGCACGAUaUag
1044	AGAGGGAAAGAACAUCAA	hsa-mir-2453	pending	1338	aUggUgUUUgcccUccUucaUccgcaaggcaUcUgaUgccccaga agUUaggaaggUccUUGgggAGAGGGAAAGAACAUCAAa cgcUgacUcUUcaatcUcaggacUUGcabaaUUaaUggaaUg CUGUCCUAAAGUUUUGAGUUgUgca
1045	CUGUCCUAAAGGUUGUUGAGUU	hsa-mir-2454	hsa-mir-676	1339	caUUaggUUggUgcAAAAAGCAUUGUGGUUUUUUgCcUa UaaaagUaaUggcaaaaacgcgaUUccUUUUGcaccacccUaa U
1046	AAAAGCAUUGUGGUUUUUUG	hsa-mir-2455	hsa-mir-548an	1340	cacUcgcgUcgggccagcgcccgggccUgcgggccCGGGCGGCG GCUGUGUUGCGCagUc
1047	CGGGCGGGCUGUGUUGCGCA	hsa-mir-2456	pending	1341	UUaUUaaUaugGAAGGAGAGAGCUUUUaaUgaUUgga gUcaUUUUUcagagcaUUaaagcUcUUcUcccUUccaUaUUaa Ugu
1048	UAUGGAAGGAGAGACUUUA	hsa-mir-2457	hsa-mir-3202-1	1342	UgcgcGGCGGGGACGGCGAUUGGUcgcUaUgUgUggUg ccaccggcgccggcUccgcccgcc
1049	CGGGGGGACGGCAUUGGU	hsa-mir-1908	hsa-mir-1908	1343	gcaaaeggUggcagcaaggaaagcagggUccUaaggUgUgUCC UCCUGCCCCUUGCUGUAGacUUUUGg
1050	CCUCCUGCCCUCUUGCUGUAG	hsa-mir-1976	pending	1344	

SEQ ID NO.	Mature Sequence Captured	Temporary Assigned miRNA ID	miRBase ID	SEQ ID NO.	miRNA Precursor Sequence
1051	UGAGCCGAGCUGAGCUUAGCUG	hsa-mir-2457	hsa-mir-4537	1345	UGAGCCGAGCUGAGCUUAGCUGggcUgagcUa accagggcUgggcUgagcUgggcUgagcUgagcUgagc
1052	GAGCUUGGAUGAGCUGGGCUGA	hsa-mir-2458	hsa-mir-4538	1346	GAGCUUGGAUGAGCUGGGCUGAacUgggcUggg gUgagcUgggcUgggcUgagUgagccaggcUgaU cUgggcUgag
1053	GCUGAACUGGGCUGAGCUGGGC	hsa-mir-2459	hsa-mir-4539	1347	UgagcUgggcUcUgclUgclUgclUgclUgagcagggcU gaGCUGAACUGGGCUGAGCUGGGC
1054	CUGGGCUGAAUGACAGUGAUGAG	hsa-mir-2460	pending	1348	gUcaagUcagaacacaggccaggUagagcccUgUccaaac CUGGGCUGAAUGACAGUGAUGAG
1055	GGGAGCCGGGCUGUGAGAGGA	hsa-mir-2461	pending	1349	cUcUUUgagccUggcUggcUggcUggcUggcaggUc aUcUgUagggccaccacacagcUcUUUccUucccUc cUcUcUccaGGGAGCCGGGCUGUGAGAGGA
1056	UUAGUCCUGCCUGAGGUUUA	hsa-mir-2462	hsa-mir-4540	1350	aagcUgcaUggaccaggacUggcaccUUGggccUU AGUCCUGCCUGAGGUUUA

Table 33: Primers for Reverse Transcription for a subset of the known miRNAs identified by deep sequencing analysis.

SEQ ID NO.	Putative Major/Minor miRNA ID	Mature Sequence Captured	Primer for reverse transcription of miRNA	SEQ ID NO.
7	hsa-mir-129-2*	AAGCCCUUACCCCAAAAAGCAU	AAGCCCTTACCCCAAAAAGCAT	1351
22	hsa-mir-25*	AGGCGGAGACUUGGGCAAUUG	AGGCGGAGACTTGGGCAATTG	1352
24	hsa-mir-30b*	CUGGGAGGUGGAUGUUUACUUC	CTGGGAGGTGGATGTTTACTTC	1353
26	hsa-mir-30c-2*	CUGGGAGAAGGCUGUUUACUCU	CTGGGAGAAGGCTGTTTACTCT	1354
27	hsa-mir-30e*	CUUUCAGUCGGAUGUUUACAGC	CTTTCAGTCGGATGTTTACAGC	1355
29	hsa-mir-342-3p	UCUCACACAGAAUUCGCACCCGU	TCTCACACAGAAATCGCACCCGT	1356
56	hsa-let-7a-2	UGAGGUAGUAGGUUGUAUAGUU	TGAGGTAGTAGGTTGTATAGTT	1357
57	hsa-let-7a-3	UGAGGUAGUAGGUUGUAUAGUU	TGAGGTAGTAGGTTGTATAGTT	1358
58	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	TGAGGTAGTAGGTTGTATGGTT	1359
63	hsa-mir-100	AACCCGUAGAUCCGAACUUGUG	AACCCGTAGATCCGAACCTGTG	1360
64	hsa-mir-101-1	UACAGUACUGUGAUAAACUGAA	TACAGTACTGTGATAACTGAA	1361
65	hsa-mir-101-2	GUACAGUACUGUGAUAAACUGAA	TACAGTACTGTGATAACTGAA	1362
66	hsa-mir-103-1	AGCAGCAUUGUACAGGGCUAUGA	AGCAGCATTGTACAGGGCTATGA	1363
67	hsa-mir-103-2	AGCAGCAUUGUACAGGGCUAUGA	AGCAGCATTGTACAGGGCTATGA	1364
70	hsa-mir-106a	AAAAGUGCUUACAGUGCAGGUAG	AAAAGTGCTTACAGTGCAGGTAG	1365
71	hsa-mir-106b	UAAAGUGCUGACAGUGCAGAU	TAAAGTGCTGACAGTGCAGAT	1366
72	hsa-mir-107	AGCAGCAUUGUACAGGGCUAUGA	AGCAGCATTGTACAGGGCTATCA	1367
73	hsa-mir-10a	UACCCUGUAGAACC GAUUUUGUG	TACCTGTAGATCCGAATTTGTG	1368
74	hsa-mir-10b	UACCCUGUAGAACC GAUUUUGUG	TACCTGTAGAACC GAATTTGTG	1369
98	hsa-mir-128-1	UCACAGUGAACCGGUCUCUUU	TCACAGTGAACCGGTCTCTTT	1370
99	hsa-mir-128-2	UCACAGUGAACCGGUCUCUUU	TCACAGTGAACCGGTCTCTTT	1371
100	hsa-mir-129-1	CUUUUUGCGGUCUGGGCUUGC	CTTTTTCGGTCTGGGCTTGC	1372
101	hsa-mir-129-2	CUUUUUGCGGUCUGGGCUUGC	CTTTTTCGGTCTGGGCTTGC	1373
103	hsa-mir-1295	UUAGGCCGCAGAUUCGGGUGA	TTAGGCCGCAGATCTGGGTGA	1374
119	hsa-mir-140-3p	UACCACAGGGUAGAACCACGG	TACCACAGGGTAGAACCACGG	1375
122	hsa-mir-143	UGAGAUGAAGCACUGUAGCUC	TGAGATGAAGCACTGTAGCTC	1376
125	hsa-mir-146a	UGAGAACUGAAUCCAUGGGUU	TGAGAACTGAATTCATGGGTT	1377
126	hsa-mir-146b	UGAGAACUGAAUCCAUGGGCU	TGAGAACTGAATTCATAGGCT	1378
127	hsa-mir-148a	UCAGUGCACUACAGAACUUUGU	TCAGTGCACACAGAACCTTGT	1379
130	hsa-mir-151-3p	CUAGACUGAAGCUCCUUGAGG	CTAGACTGAAGCTCCTTGAGG	1380
131	hsa-mir-152	UCAGUGCAUGACAGAACUUGG	TCAGTGCATGACAGAACCTGG	1381
132	hsa-mir-155	UUAAUGCUAAUCGUGAUAGGGGU	TTAATGCTAATCGTGATAGGGGT	1382
133	hsa-mir-15a	UAGCAGCACAUAAUGGUUUUGUG	TAGCAGCACATAATGGTTTGTG	1383
134	hsa-mir-15b	UAGCAGCACAUCAUGGUUUACA	TAGCAGCACATCATGGTTTACA	1384
135	hsa-mir-16-1	UAGCAGCACGUAAAUAUUGGCG	TAGCAGCACGTAAATATTGGCG	1385
136	hsa-mir-16-2	UAGCAGCACGUAAAUAUUGGCG	TAGCAGCACGTAAATATTGGCG	1386
137	hsa-mir-17	CAAAGUGCUUACAGUGCAGGUAG	CAAAGTGCTTACAGTGCAGGTAG	1387

138	hsa-mir-181a-1	AACAUUCAACGCUGUCGGUGAGU	AACATTCAACGCTGTCGGTGAGT	1388
139	hsa-mir-181a-2	AACAUUCAACGCUGUCGGUGAGU	AACATTCAACGCTGTCGGTGAGT	1389
140	hsa-mir-181b-1	AACAUUCAUUGCUGUCGGUGGGU	AACATTCATTGCTGTCGGTGGG	1390
141	hsa-mir-181b-2	AACAUUCAUUGCUGUCGGUGGGU	AACATTCATTGCTGTCGGTGGG	1391
142	hsa-mir-181c	AACAUUCAACCGUCGGUGAGU	AACATTCAACCTGTCGGTGAGT	1392
143	hsa-mir-181d	AACAUUCAUUGUUGUCGGUGGGU	AACATTCATTGTTGTCGGTGGGT	1393
147	hsa-mir-185	UGGAGAGAAAGGCAGUCCUGA	TGGAGAGAAAGGCAGTTCCTGA	1394
150	hsa-mir-18a	UAAGGUGCAUCUAGUGCAGAUAG	TAAGGTGCATCTAGTGCAGATAG	1395
151	hsa-mir-191	CAACGGAUCCCAAAGCAGCUG	CAACGGAATCCCAAAGCAGCTG	1396
152	hsa-mir-192	CUGACCUAUGAAUUGACAGCC	CTGACCTATGAATTGACAGCC	1397
153	hsa-mir-193a-5p	UGGGUCUUUGCGGGCGAGAUGA	TGGGTCTTTGCGGGCGAGATGA	1398
159	hsa-mir-196b	UAGGUAGUUUCCUGUUGUUGGG	TAGGTAGTTTCTGTTGTTGGG	1399
160	hsa-mir-197	UUCACCACCUUCCACCCAGC	TTCACCACCTTCTCCACCCAGC	1400
163	hsa-mir-199b	ACAGUAGUCUGCAUUGGUUA	ACAGTAGTCTGCACATTGGTTA	1401
164	hsa-mir-19a	UGUGCAAAUCUUAUGCAAAACUGA	TGTGCAAATCTATGCAAACTGA	1402
175	hsa-mir-20a	UAAAGUGCUUUAUGUGCAGGUAG	TAAAGTGCTTATAGTGCAGGTAG	1403
176	hsa-mir-20b	CAAAGUGCUCAUAGUGCAGGUAG	CAAAGTGCTCATAGTGCAGGTAG	1404
186	hsa-mir-221	AGCUACAUCUGUCUGGGUUUC	AGCTACATTGTCTGCTGGGTTTC	1405
187	hsa-mir-222	AGCUACAUCUGGCUACUGGGU	AGCTACATCTGGTACTGGGT	1406
190	hsa-mir-23a	AUCACAUUGCCAGGGAUUUC	ATCACATTGCCAGGGATTTC	1407
194	hsa-mir-25	CAUUGCACUUGUCUCGGUCUGA	CATTGCACTGTCTCGGTCTGA	1408
195	hsa-mir-26a-1	UUCAAGUAAUCCAGGAUAGGCU	TTCAAGTAATCCAGGATAGGCT	1409
196	hsa-mir-26a-2	UUCAAGUAAUCCAGGAUAGGCU	TTCAAGTAATCCAGGATAGGCT	1410
197	hsa-mir-26b	UUCAAGUAAUCCAGGAUAGGU	TTCAAGTAATCCAGGATAGGT	1411
198	hsa-mir-27a	UUCACAGUGGCUAAGUCCGC	TTACAGTGGCTAAGTCCGC	1412
203	hsa-mir-29a	UAGCACAUCUGAAUCCGUUA	TAGCACCATCTGAAATCGGTTA	1413
208	hsa-mir-30a	UGUAAACAUCUCCAGCUGGAAG	TGTAAACATCCTCGACTGGAAG	1414
209	hsa-mir-30b	UGUAAACAUCUCCAGCUGCU	TGTAAACATCCTACACTCAGCT	1415
210	hsa-mir-30c-1	UGUAAACAUCUCCAGCUCAGC	TGTAAACATCCTACACTCTCAGC	1416
211	hsa-mir-30c-2	UGUAAACAUCUCCAGCUCAGC	TGTAAACATCCTACACTCTCAGC	1417
212	hsa-mir-30d	UGUAAACAUCUCCAGCUGGAAG	TGTAAACATCCTCGACTGGAAG	1418
213	hsa-mir-30e	UGUAAACAUCUCCAGCUGGAAG	TGTAAACATCCTGACTGGAAG	1419
216	hsa-mir-320a	AAAAGCUGGGUUGAGAGGGCGA	AAAAGCTGGGTTGAGAGGGCGA	1420
217	hsa-mir-320b-1	AAAAGCUGGGUUGAGAGGGCAA	AAAAGCTGGGTTGAGAGGGCAA	1421
218	hsa-mir-320b-2	AAAAGCUGGGUUGAGAGGGCAA	AAAAGCTGGGTTGAGAGGGCAA	1422
227	hsa-mir-331	GCCCCUGGGCCUAUCCUAGAA	GCCCCTGGGCCTATCCTAGAA	1423
231	hsa-mir-33a	GUGCAUUGUAGUUGCAUUGCA	GTGCATTGTAGTTGCATTGCA	1424
233	hsa-mir-340	UUUAAAGCAUAGAGACUGAUU	TTATAAAGCAATGAGACTGATT	1425
236	hsa-mir-34a	UGGCAGUGUCUAGCUGGUUGU	TGGCAGTGTCTTAGCTGGTTGT	1426
239	hsa-mir-361-5p	UUUUCAGAAUCUCCAGGGGUAC	TTATCAGAATCTCCAGGGGTAC	1427
241	hsa-mir-363	AAUUGCACGGUAUCCAUCUGUA	AATTGCACGGTATCCATCTGTA	1428

242	hsa-mir-365-2	UAAUGCCCCUAAAAUCCUUUAU	TAATGCCCTAAAAATCCTTAT	1429
246	hsa-mir-374a	UUUAUUAACAACCUGAUUAGUG	TTATAATACAACCTGATAAGTG	1430
250	hsa-mir-378	ACUGGACUUGGAGUCAGAAGG	ACTGGACTTGGAGTCAGAAGG	1431
259	hsa-mir-423	UGAGGGGCAGAGAGCGAGACUUU	TGAGGGGCAGAGAGCGAGACTTT	1432
265	hsa-mir-449a	UGGCAGUGUAUUGUUAGCUGGU	TGGCAGTGTATTGTTAGCTGGT	1433
287	hsa-mir-503	UAGCAGCGGGAACAGUUCUGCAG	TAGCAGCGGGAACAGTTCTGCAG	1434
296	hsa-mir-532	CAUGCCUUGAGUGUAGGACCGU	CATGCCTTGAGTGTAGGACCGT	1435
316	hsa-mir-576-3p	AAGAUGUGGAAAAUUGGAAUC	AAGATGTGGAAAAATTGGAATC	1436
327	hsa-mir-625	AGGGGGAAAGUUCUAUAGUCC	AGGGGGAAAGTTCTATAGTCC	1437
338	hsa-mir-7-1	UGGAAGACUAGUGAUUUUGUUGU	TGGAAGACTAGTGATTTTGTGT	1438
339	hsa-mir-7-2	UGGAAGACUAGUGAUUUUGUUGU	TGGAAGACTAGTGATTTTGTGT	1439
340	hsa-mir-7-3	UGGAAGACUAGUGAUUUUGUUGU	TGGAAGACTAGTGATTTTGTGT	1440
345	hsa-mir-874	CUGCCUGGCCCGAGGGACCGA	CTGCCCTGGCCCGAGGGACCGA	1441
351	hsa-mir-9-1	UCUUUGGUUAUCUAGCUGUAUGA	TCTTGTTATCTAGCTGTATGA	1442
352	hsa-mir-9-2	UCUUUGGUUAUCUAGCUGUAUGA	TCTTGTTATCTAGCTGTATGA	1443
353	hsa-mir-92a-1	UAUUGCACUUGUCCCGGCCUGU	TATTGCACTGTCCCGGCCCTGT	1444
354	hsa-mir-92a-2	UAUUGCACUUGUCCCGGCCUGU	TATTGCACTGTCCCGGCCCTGT	1445
356	hsa-mir-93	CAAAGUGCUGUUCGUGCAGGUAG	CAAAGTGCTGTCGTGCAGGTAG	1446
357	hsa-mir-9-3	UCUUUGGUUAUCUAGCUGUAUGA	TCTTGTTATCTAGCTGTATGA	1447
364	hsa-mir-99a	AACCCGUAGAUCCGAUCUUGUG	AACCCGTAGATCCGATCTTGTG	1448
387	hsa-mir-570	AAAGGUAAUUGCAGUUUUUCCC	AAAGGTAATTGCAGTTTTCCCA	1449

Table 34: Primers for Reverse Transcription of a subset of novel miRNAs identified by deep sequencing analysis.

SEQ ID NO.	Temporary Assigned miRNA ID	Mature Sequence Captured	Primer for Reverse Transcription of miRNA	SEQ ID NO.
773	hsa-miR-378c	ACUGGACUUGGAGUCAGGA	ACTGGACTTGGAGTCAGGA	1450
774	hsa-mir-449c	AGGCAGUGUAUUGCUAGCGGCU	AGGCAGTGTATTGCTAGCGGCTGT	1451
775	hsa-mir-500-2	UGCACCCAGGCAAGGAUUCUGC	TGCACCCAGGCAAGGATTCTGC	1452
784	hsa-mir-2224	UGAGGGAGGAGACUGCA	TGAGGGAGGAGACTGCA	1453
785	hsa-mir-2225	ACUGGACUUGGAGCCAGAAG	ACTGGACTTGGAGCCAGAAG	1454
786	hsa-mir-2226	GUCACUGAUGUCUGUAGCUGAG	GTCAGTGTCTGTAGCTGAGACGG	1455
787	hsa-mir-2227	GAUGAGGAUGGAUAGCAAGGAA	GATGAGGATGGATAGCAAGGAAG	1456
789	hsa-mir-2229	AAAAGCAUCAGGAAGUACCCA	AAAAGCATCAGGAAGTACCCA	1457
796	hsa-mir-2235	GUCAAAUGAAGGGCUGAUCACG	GTCAAATGAAGGGCTGATCACGAAATA	1458
798	hsa-mir-2237	AGAGUUAACUAAAAUGGACUA	AGAGTTAACTCAAAATGGACTA	1459
799	hsa-mir-2238	UGUUGGGAUUCAGCAGGACCAU	TGTTGGGATTCAGCAGGACCATT	1460
800	hsa-mir-2239	UAAAUAGAGUAGGCAAAGGACA	TAAATAGAGTAGGCAAAGGACA	1461
805	hsa-mir-2244	AAGAGGAAGAAUUGGCUUGUUC	AAGAGGAAGAAATGGCTGGTTCTCAG	1462
809	hsa-mir-2248	UAGUGGAUGAUGCACUCUGUGC	TAGTGGATGATGCACTCTGTGC	1463
814	hsa-mir-2253	AAAGACUCUGCAAGAUGCCU	AAAGACTCTGAAGATGCCT	1464
816	hsa-mir-2255	AGGAGAAGUAAAGUAGAA	AGGAGAAGTAAAGTAGAA	1465
817	hsa-mir-2256	AUGGCCAGAGCUCACACAGAGG	ATGGCCAGAGCTCACACAGAGG	1466
819	hsa-mir-2258	AUCAGGGCUUGUGGAAUGGGAA	ATCAGGGCTTGGAATGGGAAG	1467

SEQ ID NO:	Temporary Assigned miRNA ID	Mature Sequence Captured	Primer for Reverse Transcription of miRNA	SEQ ID NO.
820	hsa-mir-2259	AUGGCCAGAGCUACACAGAGG	ATGGCCAGAGCTCACACAGAGG	1468
821	hsa-mir-2260	UGAGGAUAUUGGCAGGGAAGGGG	TGAGGATATGGCAGGGAAGGGGA	1469
825	hsa-mir-2264	UGGGCUCAGGGUACAAAGGUU	TGGGCTCAGGGTACAAAGGTTC	1470
828	hsa-mir-2266-1	GCUGCACCGGAGACUGGGUAA	GCTGCACCGGAGACTGGGTAA	1471
829	hsa-mir-2266-2	GCUGCACCGGAGACUGGGUAA	GCTGCACCGGAGACTGGGTAA	1472
836	hsa-mir-2272	UGUCGUGGGGCUUGCUGGCUUG	TGTCGTGGGGCTTGCTGGCTTG	1473
838	hsa-mir-2274	ACUGGACUUGGAGGCAGAA	ACTGGACTTGGAGGCAGAA	1474
841	hsa-mir-2277	UUGGAGGCGUGGGUUUU	TTGGAGGCGTGGGTTTT	1475
844	hsa-mir-2280	CUGACUGAAUAGGUAGGGUCAU	CTGACTGAATAGGTAGGGTCAT	1476
846	hsa-mir-2282	AGAUUGUUUCUUUUGCCGUGCA	AGATTGTTCTTTGCCGTGCA	1477
847	hsa-mir-2282*	CACGGCAAAAGAAACAAUCCA	CACGGCAAAAGAAACAATCCA	1478
848	hsa-mir-2283	CAGGGCUGGCAGUGACAUGGGU	CAGGGCTGGCAGTGACATGGGT	1479
849	hsa-mir-2284	GGUGGGGGCUGUUGUUU	GGTGGGGGCTGTTGTTT	1480
850	hsa-mir-2285	UGGGGAGGUGUGGAGUCAGCAU	TGGGGAGGTGTGGAGTCAGCATG	1481
852	hsa-mir-2287	GGCUCCUUGGUCUAGGGGUA	GGCTCCTTGGTCTAGGGGTA	1482
856	hsa-mir-2290	UGGGGAUUUGGAGAAGUGGUGA	TGGGGATTGGAGAAGTGGTGA	1483
857	hsa-mir-2291	AAAAGUGAUUGCAGUGUUUG	AAAAGTGATTGCAGTGTTCGCC	1484
860	hsa-mir-2294	UAGGAGCUCAACAGAUGCCUGU	TAGGAGCTCAACAGATGCCTGT	1485
861	hsa-mir-2295	AGCUUUUGGGAUUUCAGGUAG	AGCTTTTGGGAATTCAGGTAG	1486
864	hsa-mir-2298	CAAAAGUGAUCGUGGUUUUUG	CAAAAGTGATCGTGGTTTTTG	1487
865	hsa-mir-2299	AGGGUGUGUGUGUUUUU	AGGGTGTGTGTGTTTTT	1488
871	hsa-mir-2305	ACUGACAGGAGAGCAUUUUGA	ACTGACAGGAGAGCATTTTGA	1489
874	hsa-mir-2308	AUAGUGGUUGUGAAUUUACCUU	ATAGTGGTTGTGAATTTACCTTC	1490
876	hsa-mir-2310	CUACCCAGGAUGCCAGCAUAG	CTACCCAGGATGCCAGCATAGTT	1491
877	hsa-mir-2311	ACUGGACUUGGUGUCAGAUUG	ACTGGACTTGGTGTGATGTTG	1492
880	hsa-mir-2314	UAGUGGAUGAUGGAGACUCGGU	TAGTGGATGATGGAGACTCGGT	1493
888	hsa-mir-2322	AAGGUUUGGAUAGAUGCAAUA	AAGGTTTGGATAGATGCAATA	1494
889	hsa-mir-2323	AAAGGUAAUUGCAGUUUUUCCC	AAAGGTAATTGCAGTTTTTCCA	1495
890	hsa-mir-2324	AGGGGACCAAAGAGAUUAUAG	AGGGGACCAAAGAGATATATAG	1496
896	hsa-mir-2328	GGCGACAAAACGAGACCCUGU	GGCGACAAAACGAGACCCTGTC	1497
897	hsa-mir-2329	GGGUGCGGGCCGGCGGGG	GGGTGCGGGCCGGCGGGGT	1498
899	hsa-mir-2331	CAUGCUAGGAUAGAAAGAAUGG	CATGCTAGGATAGAAAGAAATGG	1499
901	hsa-mir-2333	GCAAAGUGAUGAGUAAUACUGG	GCAAAGTGATGAGTAATACTGG	1500
915	hsa-mir-2346	CCCUGGGGUUCUGAGGACAUG	CCCTGGGGTTCTGAGGACATG	1501
917	hsa-mir-2348	CAGGAAGGAUUUAGGGACAGGC	CAGGAAGGATTTAGGGACAGGC	1502
919	hsa-mir-2350	AUUAAGGACAUUUGUGAUUGAU	ATTAAGGACATTTGTGATTGAT	1503
920	hsa-mir-2351-1	AAAAGGCAUAAAACCAAGACA	AAAAGGCATAAAACCAAGACA	1504
921	hsa-mir-2351-2	AAAAGGCAUAAAACCAAGACA	AAAAGGCATAAAACCAAGACA	1505
924	hsa-mir-2354-1	UAAAAACUGCAAUUACUUUC	TAAAACTGCAATTACTTTC	1506
926	hsa-mir-2355-1	UGUGAUUAUCAUGGUUCCUGGGA	TGTGATATCATGGTTCCTGGGA	1507

SEQ ID NO.	Temporary Assigned miRNA ID	Mature Sequence Captured	Primer for Reverse Transcription of miRNA	SEQ ID NO.
929	hsa-mir-2355-2	UGUGAUUAUCAUGGUUCCUGGGA	TGTGATATCATGGTTCCTGGGA	1508
931	hsa-mir-2355-3	UGUGAUUAUCAUGGUUCCUGGGA	TGTGATATCATGGTTCCTGGGA	1509
932	hsa-mir-2355b	UGUGAUUAUCGUGCUUCCUGGGA	TGTGATATCGTGCTTCCTGGGA	1510
936	hsa-mir-2358	AAAAGUAAACUGCGGUUUUUGA	AAAAGTAACTGCGGTTTTTGA	1511
938	hsa-mir-2360	GGAGUGGGCUGGUGGUU	GGAGTGGGCTGGTGGTT	1512
940	hsa-mir-2362-1	AAGGGCUUCCUCUCUGCAGGAC	AAGGGCTTCCTCTCTGCAGGAC	1513
941	hsa-mir-2362-2	AAGGGCUUCCUCUCUGCAGGAC	AAGGGCTTCCTCTCTGCAGGAC	1514
949	hsa-mir-2370	AGAGCUGGCUGAAGGGCAG	AGAGCTGGCTGAAGGGCAG	1515
953	hsa-mir-2374	UGUGACUUUAAGGGAAAUGGCG	TGTGACTTTAAGGGAAATGGCG	1516
954	hsa-mir-2375	UCUCAGGAGUAAAGACAGAGUU	TCTCAGGAGTAAAGACAGAGTT	1517
955	hsa-mir-2376	AGGUGGAUGCAAUGUGACCUCA	AGGTGGATGCAATGTGACCTCA	1518
977	hsa-mir-2397	AGGCUGGGCUGGGACGGA	AGGCTGGGCTGGGACGGA	1519
979	hsa-mir-2399	UAGGAUGGGGGUGAGAGGUG	TAGGATGGGGGTGAGAGGTG	1520
988	hsa-mir-2406	UGAGGGAGUAGGAUGUAUGGUU	TGAGGGAGTAGGATGTATGGTT	1521
991	hsa-mir-2409	AGACUGACGGCUGGAGGCCCAU	AGACTGACGGCTGGAGGCCCAT	1522
994	hsa-mir-2412	UAGUGAGUUAGAGAUGCAGAGC	TAGTGAGTTAGAGATGCAGAGC	1523
996	hsa-mir-2414	GGGAGAAGGGUCGGGGC	GGGAGAAGGGTCGGGGC	1524
1002	hsa-mir-2416	CUCGUGGGCUCUGGCCACGGC	CTCGTGGGCTCTGGCCACGGCC	1525
1003	hsa-mir-2417-1	AGAAGGGGUGAAAUUUAAACGU	AGAAGGGGTGAAATTTAAACGT	1526
1004	hsa-mir-2417-2	AGAAGGGGUGAAAUUUAAACGU	AGAAGGGGTGAAATTTAAACGT	1527
1005	hsa-mir-2417-3	AGAAGGGGUGAAAUUUAAACGU	AGAAGGGGTGAAATTTAAACGT	1528
1007	hsa-mir-2419	GCUCAGGGAUGAUAAACUGUGCUGAGA	GCTCAGGGATGATACTGTGCTGAGA	1529
1011	hsa-mir-2423	CUGGACUGAGCCAUGCACUGG	CTGGACTGAGCCATGCTACTGG	1530
1017	hsa-mir-2428	AUAGCAGCAUGAACCGUCUCA	ATAGCAGCATGAACCTGTCTCA	1531
1018	hsa-mir-2428*	UGAGACAGGCUUAUGCUGCUAU	TGAGACAGGCTTATGCTGTAT	1532
1022	hsa-mir-2432	UGGUCUGCAAAGAGAUGACUGU	TGGTCTGCAAAGAGATGACTGTG	1533
1025	hsa-mir-2435	UUGGAGGGUGUGGAAGACAUC	TTGGAGGGTGTGGAAGACATC	1534
1027	hsa-mir-2437	AUGGAGAAGGCUUCUGA	ATGGAGAAGGCTTCTGA	1535
1028	hsa-mir-2438	AAAAGCUGGGUUGAGAA	AAAAGCTGGGTTGAGAAG	1536
1029	hsa-mir-2439	UGGAAGGUAGACGGCCAGAGAG	TGGAAGGTAGACGGCCAGAGAG	1537
1030	hsa-mir-2440	UCUGGGAGGUUGUAGCAGUGGA	TCTGGGAGGTTGTAGCAGTGGA	1538
1036	hsa-mir-2445	GGAGGAACCUUGGAGCUUCGGC	GGAGGAACCTTGAGCTTCGCA	1539
1038	hsa-mir-2447	ACUGGACUAGGAGUCAGAAGG	ACTGGACTAGGAGTCAGAAGG	1540
1041	hsa-mir-2450	CAAAAACUGCAGUUACUUUUUGU	CAAAAACCTGCAGTTACTTTTGT	1541
1046	hsa-mir-2455	AAAAGGCAUUGUGGUUUUUUG	AAAAGGCATTGTGGTTTTTG	1542

Table 35: miRNAs that differentiate ABC DLBCL vs. GCB DLBCL

MicroRNA	FoldChange ABC vs. GCB	pVal ABC vs. GCB
UGGUCUGCAAAGAGAUGACUGUG (SEQ ID NO. 1565)	-4.30138	0.001335
CAAAAACUGCAGUUACUUUUGU (SEQ ID NO. 1041)	-3.52085	0.022949
UGGGGAUUUGGAGAAGUGGUGA (SEQ ID NO. 856)	-2.8374	0.000753
hsa-miR-129-3p	-2.48708	7.39E-05
ACUGGACUUGGUGUCAGAUGG (SEQ ID NO. 877)	-1.3712	0.01173
hsa-miR-196b	-1.28463	0.032606
hsa-miR-9	-1.00737	0.003176
hsa-miR-28-5p	-0.82319	0.00026
hsa-miR-365	-0.78573	0.032749
hsa-miR-185	-0.75345	0.044082
hsa-miR-199b-3p	-0.74898	0.015518
hsa-miR-152	-0.67388	0.001282
hsa-miR-23a	-0.65979	0.028732
hsa-miR-193a-5p	-0.54233	0.031154
hsa-miR-27a	-0.49729	0.027207
hsa-miR-331-3p	-0.47573	0.0128
hsa-miR-301a	-0.45261	0.014231
hsa-miR-128	-0.4224	0.024065
AGAUUGUUUCUUUUGCCGUGCA (SEQ ID NO. 846)	0.557435	0.02141
hsa-miR-625	0.747299	0.01813
hsa-miR-155	0.781901	0.024175
hsa-miR-20b	0.986918	0.000746
GGCUCCUUGGUCUAGGGGUA (SEQ ID NO. 852)	1.945372	0.002596
UAGUGAGUUAGAGAUGCAGAGC (SEQ ID NO. 994)	2.347695	0.009081
CAGGAAGGAUUUAGGGACAGGC (SEQ ID NO. 917)	2.519326	0.04483

*The 3'-end G of SEQ ID NO. 1565 is optionally omitted (providing SEQ ID NO. 1022).

Appendix A: Average expression of the genes depicted in Fig. 6*

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
1	VPS37B	10.60	4.58	4.58	9.71		
2	SCN3A	9.50	3.98				
3	NT5E	10.76	5.69				
4	TBC1D9	12.03	7.03	7.03	11.19	7.03	12.88
5	MAP7					1.64	8.03
6	SPRY1	10.40	5.72				
7	TNFSF12	8.11	3.54			3.54	7.55
8	SOCS3	9.00	4.48	4.48	9.39		
9	EDG1	11.43	6.91			6.91	8.69
10	CTGF	7.62	3.30	3.30	9.65		
11	FAM46A	10.65	6.46			6.46	8.29
12	MOBK12B	11.63	7.45				
13	DNMT3A	10.56	6.44	6.44	7.85		
14	BHLHB2	10.75	6.64			6.64	10.96
15	LAMC1	9.85	5.80	5.80	9.67		
16	CD69	13.27	9.40			9.40	12.27
17	PLEKHA1	10.95	7.20				
18	PTGDR	7.20	3.46				
19	TXNIP	14.89	11.20	11.20	13.39	11.20	15.10
20	SIDT1	11.52	7.86	7.86	9.38		
21	LY6E	8.57	4.92	4.92	7.39		
22	IGF1R	8.73	5.13				
23	PRICKLE1	11.68	8.09	8.09	9.69		
24	CSDA	12.12	8.59	8.59	10.10		
25	KLF2	12.61	9.10	9.10	11.70		
26	ELOVL2	7.32	3.86				
27	CCND2	12.06	8.61			8.61	11.53
28	LASS6	10.29	6.86	6.86	9.42	6.86	9.48
29	DUSP6	11.93	8.53			8.53	10.19
30	CUGBP2	14.28	10.93			10.93	14.29
31	PTPRO	9.64	6.32			6.32	8.63
32	PHF16	10.33	7.04				
33	NR3C2	8.85	5.58				
34	CRTC3	12.56	9.32	9.32	11.11		
35	ADAMTS6	7.68	4.45				
36	ETV6	10.36	7.14	7.14	8.89	7.14	10.43
37	LRR17			3.10	7.49		
38	FAM46C	12.18	8.98	8.98	14.76	8.98	10.54
39	SATB2	7.20	4.02	4.02	7.60		
40	RNF125	9.00	5.83				
41	ST6GALNAC3	8.12	4.96				
42	LARGE	9.05	5.89	5.89	8.73		
43	ZNF276	9.39	6.25				
44	KCNA3			4.83	9.82		
45	BCL2	10.89	7.76			7.76	11.41
46	MTSS1	12.92	9.82			9.82	12.05
47	NR6A1	9.10	6.03			6.03	7.62
48	BHLHB3	11.11	8.05	8.05	13.26	8.05	13.26
49	MYO10	7.22	4.19				
50	ITM2C			6.44	13.85		

*Empty cells indicate values not appreciably measured.

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
51	C18orf1	9.49	6.47	6.47	8.63		
52	FXVD7	7.36	4.35				
53	DUSP8	7.96	4.96	4.96	8.41	4.96	7.75
54	BTBD3	7.41	4.42				
55	TMEPAI	11.15	8.20	8.20	11.03		
56	ANTXR2	9.90	6.97				
57	FOSB	10.13	7.21	7.21	11.05		
58	TMCC3	8.23	5.31	5.31	7.09	5.31	8.05
59	ARL4C	11.31	8.41			8.41	10.32
60	ZMYND11	11.33	8.43	8.43	11.34	8.43	11.68
61	RHOBTB1	7.33	4.48				
62	JUN	12.14	9.34	9.34	12.70		
63	SKI	10.46	7.67			7.67	10.68
64	TMEM121	7.07	4.29				
65	IL13RA1	8.99	6.21				
66	KIF13B			6.23	9.01		
67	BHLHB5			4.26	7.39		
68	PGM2L1	10.35	7.65				
69	C14orf4	12.11	9.47	9.47	11.01	9.47	11.65
70	PDE4B	12.38	9.74	9.74	11.60		
71	PDE7B	8.64	6.03				
72	BCL9L	9.37	6.77	6.77	8.61		
73	PCDH9	10.32	7.73				
74	ARHGAP5	10.44	7.86	7.86	9.11	7.86	9.85
75	KIAA0802	9.18	6.61	6.61	7.91	6.61	7.89
76	ITGB4	7.48	4.91				
77	NOTCH2NL			7.17	8.95		
78	CDC42BPA	7.32	4.77				
79	SPG20	9.25	6.73				
80	KLF4	10.04	7.57	7.57	9.09		
81	AHNAK	9.34	6.87	6.87	9.56	6.87	11.51
82	FCHSD1	9.15	6.69				
83	KIAA1622			3.94	7.67		
84	PLXNC1	10.92	8.48				
85	TMEM150	8.39	5.96				
86	ACVR2A	7.81	5.38	5.38	8.63	5.38	7.40
87	KALRN			5.61	7.64		
88	ANK2	7.69	5.28	5.28	7.54	5.28	7.00
89	FLJ14213	7.61	5.21	5.21	7.97		
90	CHPT1	10.92	8.52				
91	TCF2			5.69	7.82		
92	FGF5			5.41	7.52		
93	SLC12A6	12.18	9.80	9.80	11.09		
94	MGC17330	11.53	9.16				
95	NR4A2	10.21	7.85	7.85	9.21	7.85	10.54
96	SLC39A10	11.06	8.70				
97	LITAF	12.52	10.18	10.18	11.82		
98	AKT3	9.32	6.99			6.99	9.25
99	PDCD4	12.89	10.57			10.57	13.33
100	STMN3	10.03	7.72				

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
101	SIDT2	13.13	10.85				
102	GRIA3	7.04	4.77				
103	EML4	12.83	10.57				
104	DIP2B	11.26	8.99			8.99	10.77
105	FBN1			4.89	8.17		
106	FAM84B	9.21	6.96				
107	EGR3	11.59	9.35	9.35	8.24	9.35	10.62
108	CTHRC1			4.25	11.94		
109	RRAGD	7.69	5.46				
110	MACF1	12.88	10.66				
111	FOXF2	7.05	4.83				
112	GAB1	8.01	5.81	5.81	10.91		
113	ST18			4.42	7.40		
114	ZFP36L2	13.78	11.59	11.59	13.43	11.59	14.05
115	GAB2	8.29	6.12	6.12	9.02		
116	CHST11	11.17	8.99	8.99	10.28		
117	CLOCK	9.85	7.68	7.68	9.91	7.68	9.62
118	PREX1	10.07	7.90			7.90	11.16
119	KLF11	8.08	5.94			5.94	8.39
120	PTGER4	11.66	9.53				
121	KLF9	9.47	7.34			7.34	9.27
122	FLJ37078	7.55	5.42	5.42	7.49		
123	ODZ2	7.20	5.08	5.08	7.25	5.08	7.22
124	SESN3	11.24	9.11	9.11	7.60		
125	PDK4	7.22	5.09				
126	CNTNAP3	7.35	5.23	5.23	7.10		
127	DUSP1	13.34	11.22				
128	MARCKS	11.19	9.07	9.07	11.05	9.07	12.21
129	SPRY4	7.02	4.91				
130	LMO1			4.75	7.16		
131	MTUS1	7.77	5.66	5.66	8.16		
132	ADCY9	8.01	5.91	5.91	7.74		
133	SLC17A6			3.80	7.06		
134	NOX4	7.45	5.37	5.37	7.22		
135	UTRN			9.46	10.97		
136	ZBTB10	8.50	6.45				
137	SLC26A7	8.37	6.32	6.32	7.89		
138	PNRC1	13.14	11.09				
139	LLGL2			6.83	9.29		
140	CHST1	7.15	5.12				
141	CREB3L2	10.53	8.51	8.51	13.30		
142	DDIT4	12.69	10.68				
143	C20orf108	8.82	6.80	6.80	10.19		
144	CDH1			3.85	10.26		
145	TFAP4	7.28	5.29				
146	SLC38A2	13.57	11.58	11.58	13.74	11.58	13.17
147	SESN1	9.84	7.87	7.87	9.13		
148	YPEL2	10.18	8.20			8.20	10.04
149	GRASP	8.47	6.50				
150	TSC22D3	13.22	11.26	11.26	12.67		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
151	ATP11A	9.70	7.75	7.75	9.50		
152	L3MBTL3	10.61	8.66			8.66	10.06
153	SORT1	7.61	5.67	5.67	8.11		
154	CAV1			4.80	9.11		
155	RXRA	9.07	7.15	7.15	8.81		
156	CRELD1	8.40	6.48	6.48	8.26		
157	RBMS1	12.40	10.49	10.49	8.80		
158	LYST	10.90	8.99				
159	PIP5K1B	9.61	7.70	7.70	9.97		
160	JUNB	11.62	9.72				
161	MBOAT1					4.80	7.27
162	IRF4	11.16	9.28	9.28	13.66		
163	LIFR			4.62	7.08		
164	MORC3	11.25	9.37				
165	MBP	11.91	10.05	10.05	8.61		
166	SRC			4.98	7.98		
167	ALS2CR13	11.79	9.93	9.93	8.89	9.93	11.47
168	MYH1			4.40	7.37		
169	DUSP3	9.36	7.50	7.50	9.16		
170	HLX1	7.14	5.28			5.28	7.65
171	CDKN1A	9.09	7.23	7.23	8.97	7.23	8.43
172	SOC5	10.00	8.15				
173	PPP1R9A			5.14	7.35		
174	TGFB2	12.81	10.99			10.99	12.63
175	LRRC16	8.47	6.66				
176	ZNF629	8.17	6.35	6.35	8.58		
177	RPS6KA5	11.75	9.95			9.95	11.48
178	SATB1	12.79	10.99	10.99	9.06		
179	SEMA4C	7.38	5.59	5.59	8.49	5.59	7.14
180	ULK1	7.79	5.99	5.99	8.72	5.99	8.06
181	STX3	8.88	7.09	7.09	8.91		
182	BAMBI					4.81	7.26
183	MAP3K5	10.63	8.84	8.84	7.66	8.84	10.71
184	KIAA1147	11.70	9.91			9.91	11.53
185	SBK1			5.20	7.04		
186	RYS3	7.80	6.02	6.02	8.27		
187	ZNF238	13.05	11.27	11.27	10.08	11.27	12.54
188	IL12A			5.65	7.26		
189	SLC2A3	12.00	10.23			10.23	11.89
190	GFPT2			3.39	7.18		
191	GOS2	7.72	5.96				
192	LYRM5	10.29	8.53	8.53	10.93		
193	SSH2	11.67	9.91			9.91	11.85
194	NRP1	7.44	5.69	5.69	7.22		
195	LMLN	8.92	7.19				
196	UCP3	7.71	5.99				
197	TMEM166	7.31	5.60				
198	CACNA1I	7.46	5.76	5.76	7.06		
199	PHOSPHO1			3.55	7.10		
200	CRM1	9.79	8.11			8.11	9.32

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
201	GATA6			5.41	7.59		
202	SACS	10.06	8.39			8.39	10.54
203	CDKN1B	12.91	11.24	11.24	14.41		
204	CACNA2D2			5.25	7.57	5.25	7.93
205	MKRN3			3.65	7.10		
206	MTFR1	10.40	8.74	8.74	7.34	8.74	10.15
207	GALNT3	10.19	8.54				
208	RPS6KA3	12.07	10.42			10.42	11.48
209	DTNA			5.47	7.86		
210	MAGI2	7.04	5.40	5.40	7.42		
211	FOXJ2	10.01	8.38	8.38	9.97	8.38	9.85
212	KIAA0513			5.29	8.44	5.29	7.36
213	NDRG1			7.75	10.02		
214	AKAP7	10.16	8.54				
215	CD72	13.74	12.12				
216	IGFBP5	7.30	5.69	5.69	7.59		
217	REPS2	7.51	5.92	5.92	7.60		
218	PRDM12	7.17	5.57				
219	ZNF3	8.86	7.27	7.27	8.75		
220	TLL2			4.88	7.01		
221	PCNX	9.77	8.19				
222	ARHGAP24	11.31	9.73	9.73	8.65	9.73	11.32
223	THRAP2	11.31	9.73				
224	RNF11	9.72	8.15	8.15	11.08		
225	HOXC8	7.05	5.48				
226	SCML2	10.33	8.76				
227	BMPR2	9.70	8.14			8.14	10.06
228	STAC			5.27	7.20		
229	C10orf54	9.12	7.56	7.56	10.16		
230	FBXL17	9.51	7.95	7.95	9.36		
231	CBX7	10.87	9.32			9.32	10.96
232	UBE2W	9.80	8.25	8.25	9.76	8.25	9.38
233	ProSAPiP1			4.12	7.54		
234	UBL3	10.73	9.18	9.18	11.27	9.18	11.03
235	TTYH3	7.35	5.81	5.81	8.16		
236	PUNC			5.39	8.85	5.39	7.30
237	GDF11	7.01	5.47	5.47	7.70		
238	LMX1A			5.25	7.43		
239	TIMP2	7.51	5.97	5.97	7.69	5.97	7.40
240	NHLH2			3.93	7.35		
241	CLCF1	10.50	8.98				
242	ITGB3	7.66	6.14				
243	TMEM132E			3.93	7.20		
244	KCTD17	7.45	5.94	5.94	7.33		
245	ChGn	7.75	6.24	6.24	8.36		
246	DIP2C	9.25	7.75				
247	DKFZp667G2110	8.79	7.28	7.28	9.25		
248	CSNK1G3	10.84	9.34			9.34	10.70
249	NRIP1	11.79	10.30				
250	SMAD3	10.72	9.23	9.23	7.74	9.23	10.54

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
251	SHOX2	7.05	5.57				
252	LDLRAP1			6.80	9.84	6.80	8.59
253	SUPT3H	7.77	6.30	6.30	8.05		
254	KCNN2	7.18	5.70				
255	DLL1	7.37	5.90				
256	CEND1	7.72	6.26				
257	NOTCH1	10.90	9.45				
258	TLE1			7.74	9.63		
259	FCHO2	8.75	7.30				
260	JPH4	7.12	5.67	5.67	7.60		
261	KCNMB2	7.16	5.72				
262	KHDRBS2	7.17	5.73				
263	LEFTY1			4.38	7.21		
264	ST3GAL5	10.59	9.15				
265	LGR4			5.30	7.29		
266	FNDCC8			4.25	8.01		
267	NPTXR			5.87	7.65		
268	PRICKLE2			5.47	7.47		
269	GRIA4			5.19	7.04		
270	RHOB	8.66	7.23	7.23	9.56		
271	ZADH2	8.65	7.22				
272	ZBTB41	9.73	8.31			8.31	9.42
273	GPRASP2			6.00	7.35		
274	SYS1	10.79	9.36				
275	RUNX1T1	7.37	5.95				
276	DLX2			4.66	7.04		
277	SLC30A7	11.58	10.17				
278	PER1	8.82	7.40				
279	NTSC3	12.67	11.25				
280	PDE3A	11.62	10.21				
281	OCRL	8.07	6.66			6.66	8.04
282	PSD3	7.99	6.60				
283	LPHN1	7.80	6.41				
284	TNRC6B	11.87	10.48			10.48	11.77
285	SNN	12.03	10.64	10.64	8.91	10.64	12.10
286	HERPUD2	11.56	10.18				
287	UBQLNL	7.45	6.07				
288	HES7	7.37	5.99				
289	GALNT2	10.08	8.69	8.69	10.63		
290	CAMKK1	8.45	7.07				
291	ELN			5.44	7.18		
292	ICK	8.09	6.72	6.72	8.01		
293	POU4F2	7.09	5.72	5.72	7.21		
294	GAS2	7.13	5.76	5.76	7.81		
295	ARHGEF3	10.11	8.75			8.75	11.04
296	ZBTB4	11.45	10.09			10.09	11.78
297	CHD7	12.14	10.78			10.78	12.08
298	TMEM45B			5.97	7.61		
299	CLDN11			5.74	7.22		
300	PTPN1	10.85	9.51				

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
301	PHF20	12.00	10.67				
302	VAV3			10.44	7.84		
303	CARKL	8.38	7.06	7.06	8.94		
304	TRIM36			5.43	7.77		
305	CTLA4			6.57	7.95		
306	POLK	9.69	8.38	8.38	10.55		
307	WSB1	13.22	11.91			11.91	13.02
308	ALS2CR2	9.87	8.57	8.57	10.14		
309	PLK2			4.94	7.13		
310	SRPK2	10.83	9.53			9.53	11.13
311	ARRDC2	10.86	9.55				
312	IER5	13.10	11.80				
313	EPN1	8.95	7.66	7.66	9.07		
314	SLC20A2	9.45	8.16				
315	DLG4			4.23	7.22		
316	TMTC2			6.16	7.92		
317	ETV1	8.19	6.90				
318	JAZF1	11.93	10.65	10.65	7.49		
319	VAV2	10.22	8.94				
320	C15orf27	7.19	5.91				
321	FYCO1	9.75	8.47				
322	KIAA0789	7.27	6.00				
323	OBFC2A	9.94	8.66			8.66	10.94
324	MCF2	7.19	5.92				
325	KIAA2018	11.77	10.50	10.50	9.50		
326	MTMR10	10.75	9.48				
327	FAM63B			6.03	7.83	6.03	7.95
328	SNF1LK	10.20	8.93			8.93	10.18
329	ZNF385	8.89	7.63				
330	SESTD1	11.05	9.78				
331	SLC31A2			5.41	9.13		
332	PCMTD1	12.03	10.76	10.76	12.44		
333	NBEA	8.06	6.81	6.81	8.02	6.81	8.35
334	ZNF295			9.24	10.61		
335	SIPA1L3	10.81	9.57				
336	CC2D1B	9.11	7.87				
337	PRKAG2			7.12	8.42		
338	PKD1	9.04	7.81				
339	CNTNAP2	7.54	6.32				
340	FNBP1L	7.90	6.67				
341	HEXIM1	10.27	9.05			9.05	10.24
342	C19orf2	12.29	11.07				
343	MYLIP	11.62	10.41			10.41	11.81
344	SLC11A2	9.27	8.06				
345	CLU	9.92	8.71				
346	GCN5L2	10.18	8.97				
347	DKFZP564J0863	10.85	9.65			9.65	11.11
348	CNNM2	7.85	6.64	6.64	8.07		
349	CDC42SE1	12.07	10.87			10.87	12.18
350	HOXB9			6.20	8.41		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
351	NFATC3	11.39	10.19				
352	UNC84B	11.12	9.93	9.93	8.59		
353	DUSP5			6.23	9.44		
354	ING1	11.35	10.17				
355	ITM2B			11.23	13.62		
356	FAM53B	11.67	10.49				
357	ZFP36L1	14.07	12.89	12.89	10.09		
358	NIPA1	9.75	8.57			8.57	10.07
359	GALNT1	10.93	9.76	9.76	11.12		
360	MYPN			4.25	7.32		
361	ITPK1	10.03	8.86				
362	TTYH2	7.90	6.73				
363	DOCK10	10.80	9.63			9.63	11.53
364	C14orf28	9.18	8.01	8.01	9.58	8.01	9.50
365	RP11-130N24.1			4.76	7.62		
366	FGF12			5.82	7.33		
367	ATP2B2	7.93	6.76				
368	PPP1R9B	9.77	8.60				
369	PPP3CA	13.50	12.33			12.33	13.86
370	TFAP2A			5.54	8.26		
371	CYLD	10.91	9.75				
372	PHF1	11.85	10.69	10.69	12.26		
373	NEBL	7.98	6.82	6.82	8.08		
374	ACIN1	12.04	10.89			10.89	11.99
375	SPTBN1	12.28	11.14	11.14	12.53	11.14	12.42
376	VAMP4	10.81	9.67	9.67	11.18		
377	DNAJB9	10.80	9.66	9.66	15.21	9.66	11.03
378	ZDHHC2	11.55	10.42				
379	TRJO	10.57	9.43				
380	TMEM25			6.24	8.57		
381	TAF9B	10.82	9.69				
382	ARID3A	8.03	6.90	6.90	9.81		
383	KIAA0182	10.68	9.55				
384	RPS6KA2	8.61	7.49				
385	C3orf58	11.47	10.34				
386	CAST	11.94	10.82				
387	SH3PXD2A	8.46	7.34				
388	RAB6B			5.93	7.36		
389	RNF141	11.47	10.35				
390	SP4	11.26	10.14				
391	ARMCX2	9.44	8.32	8.32	9.54		
392	ZNF398	10.39	9.28				
393	PBX3	9.69	8.58	8.58	7.00		
394	FOS	12.35	11.25	11.25	13.34		
395	FHOD3			6.40	7.94		
396	C20orf59	10.11	9.01	9.01	10.92		
397	FAM117A	11.67	10.57	10.57	12.06	10.57	11.64
398	ATP8B2	8.58	7.49	7.49	10.87	7.49	8.88
399	UXS1	9.53	8.43				
400	GOLGA8A	12.84	11.74	11.74	13.14	11.74	13.05

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
401	SUFU			6.03	7.84		
402	NAGPA	9.32	8.23				
403	MLLT6	11.70	10.61				
404	CPEB4	9.46	8.36	8.36	12.21		
405	TMEM50B	10.67	9.58	9.58	11.41	9.58	10.63
406	AMPD3	11.65	10.56	10.56	8.76		
407	SIX5			5.19	7.53		
408	MMP16			5.66	7.47		
409	LBH	11.87	10.79	10.79	8.83		
410	POM121					9.60	11.26
411	ATP8B1	11.93	10.86	10.86	8.88		
412	ARHGAP29			3.75	7.60		
413	ZNF395			11.78	10.76		
414	CRY2					6.50	8.01
415	BIN1			10.68	9.67		
416	PSAP			11.24	13.41	11.24	12.71
417	ISL1			5.91	7.60		
418	DNAJB5	8.04	6.97				
419	KIAA0284			6.42	8.79		
420	RBM35B	11.44	10.38				
421	ADCY7	11.53	10.47				
422	ARRDC3					9.46	10.68
423	MICAL1	11.72	10.67				
424	MTHFR	10.31	9.26				
425	HOOK3	8.57	7.53	7.53	6.52		
426	EFNB3			5.16	7.79		
427	ARHGAP12	9.86	8.82				
428	LMBR1L	9.33	8.29				
429	FGF7			5.88	7.86		
430	USP2			5.50	7.52		
431	SMARCA2	11.14	10.12				
432	ELL2			8.23	13.60		
433	C1orf26			7.06	10.01		
434	CXCR4			14.61	13.45		
435	HDGFRP3			5.58	7.39		
436	BNC2			6.18	7.72		
437	YPEL3			10.16	11.81	10.16	11.47
438	PPFIA3			4.58	8.06		
439	DLGAP4			9.34	10.68		
440	ZBTB7A					9.84	11.10
441	D4S234E			5.90	7.38		
442	FNDC3A			9.41	13.60		
443	FOXC1			5.84	7.39		
444	KIF26B			5.55	7.30		
445	NAV2			6.26	7.90		
446	DDX3Y			8.07	10.38		
447	FGD1			7.31	6.06		
448	HTR4			7.26	9.01	7.26	8.40
449	C22orf31			5.67	8.10		
450	RNF44			11.48	10.14		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
451	GALNAC4S-6ST			10.43	12.71		
452	CCNT2					10.15	11.23
453	CHIC1					8.91	10.02
454	NNAT			5.97	8.19	5.97	7.84
455	CTDP1			6.81	8.26		
456	BTG1			14.95	13.94		
457	CMTM4			5.27	7.81		
458	GOLGA8B					11.37	12.63
459	HBP1			10.07	12.13		
460	GDPD1					6.35	7.61
461	CDYL			9.31	10.61	9.31	10.50
462	ZNF217			10.77	9.73		
463	KIF5A			6.13	7.75		
464	C1QL1			5.80	8.11		
465	SOLH					7.88	9.03
466	ZC3H6					9.81	10.96
467	LATS2			7.61	10.19		
468	COL18A1			6.46	7.85		
469	C11orf24			9.89	11.07		
470	SCUBE3			6.14	7.88		
471	SEMA4G			5.57	7.81		
472	FOXP1			12.31	10.84		
473	TRIB2			10.62	9.61		
474	LOC285382			5.35	7.20		
475	RUNX2			7.91	10.22		
476	LOC196463			4.16	7.52		
477	LPGAT1			10.57	7.99		
478	RASSF2			12.52	10.93		
479	IRF1			9.86	11.60		
480	RAB40B			7.31	10.89		
481	CTDSPL			6.37	7.83		
482	CLCN4					7.44	6.39
483	CACNB1			6.41	8.20		
484	SYNGR1			8.45	10.40		
485	ST8SLA4					10.67	11.81
486	PLD3			7.63	10.59		
487	FOXO3A			10.17	12.41		
488	TSPAN33			10.49	9.38		
489	HIST1H4F			6.20	8.08		
490	LAPTM4A					12.05	13.06
491	PRKCB1			12.14	10.50		
492	PROX1			6.38	7.89		
493	CDK5R1			10.12	7.78		
494	MAP3K9			7.96	9.13		
495	GPX3			5.92	7.61		
496	GNS			8.79	11.06		
497	ARL15			8.27	6.51		
498	OXR1			9.21	11.17	9.21	10.25
499	AAK1			7.38	9.54	7.38	8.47
500	SH3PX3			6.72	8.58		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
501	MS4A7			10.55	8.35		
502	FLJ20273			5.96	11.23	5.96	8.65
503	ISCU			12.01	13.55		
504	ITGA2			5.70	7.60		
505	ME1			5.87	7.89		
506	LRP1			4.92	7.04		
507	ZNF652					9.66	10.81
508	TRAK1			11.07	9.85		
509	SLC8A1			6.27	7.83		
510	C1orf119					10.76	11.98
511	KLF6			11.33	9.24	11.33	12.40
512	TRIM2			6.22	8.20		
513	USP3			11.11	12.51		
514	ARID5B					11.02	12.48
515	RASD1			6.15	9.32		
516	ZCCHC2			10.63	8.93		
517	LEFTY2					5.08	7.03
518	BACH1			9.97	11.76		
519	IRAK1			11.48	12.80		
520	RP11-217H1.1			10.76	13.04		
521	HLCS			6.54	8.45		
522	NAGK			10.94	12.14		
523	CELSR2			6.26	7.89		
524	PCBP4			7.75	9.08		
525	FLJ25476					9.49	10.72
526	TPP1			12.10	11.06		
527	ACVR1			7.95	9.31		
528	EHD3					8.99	10.35
529	FAM80B			9.35	8.02		
530	SPRYD3			8.19	9.51		
531	PRDM4					9.81	10.83
532	C6orf134			7.92	5.60		
533	HSP90B1			12.04	16.36		
534	DYNC1H1			5.98	7.33		
535	NFIX			7.43	8.67		
536	DOCK4					5.96	7.97
537	ZNF287			7.09	8.47		
538	XRN1			10.92	12.37		
539	YES1			6.39	8.60		
540	RBM35A			8.19	9.44		
541	HOXB4			7.58	9.27		
542	OTUD7B			7.24	8.57		
543	CELSR3					6.83	8.39
544	RHOC					7.71	8.84
545	ZNF607			8.10	6.95		
546	XYLT1			10.28	8.78	10.28	8.86
547	FAM89B			9.16	10.75		
548	OSBPL8			12.99	11.66		
549	SRCRB4D			6.82	8.67		
550	RASL12			5.05	8.07		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
551	NAG8			8.39	9.78		
552	MAN1A2			10.83	12.15		
553	PPARA					8.59	9.65
554	CLDN12			6.66	8.39		
555	ID4			5.93	7.79		
556	HECTD2			7.98	6.80		
557	EFCAB4A			5.93	8.96		
558	CREBL1					6.97	8.09
559	SARM1					6.98	8.29
560	MIDN			8.48	7.29		
561	EMB			10.48	8.65		
562	FO XK2			8.40	9.63		
563	INADL			6.87	8.44		
564	KCNAB1			6.26	9.76		
565	MAP3K8			10.92	9.60		
566	C8orf58			7.89	5.62		
567	SLC4A7			9.82	8.52	9.82	10.90
568	RAB8B			12.46	10.92		
569	C10orf118			8.93	10.20		
570	CRTC2			9.37	7.94		
571	KLC2			7.31	9.19		
572	SRCAP			8.06	6.96		
573	CNTFR			7.15	8.67		
574	SPTBN2			4.75	7.11		
575	SMAD7					8.69	9.93
576	NDFIP1			9.10	10.95		
577	BCL11A			14.03	10.63		
578	SFXN5			7.26	8.87		
579	RIMBP2			5.93	8.33		
580	FUT8			8.62	11.08		
581	PSEN2			5.86	9.17		
582	MAP6			5.22	7.37		
583	FOXO1A			11.53	10.14		
584	BTG2			11.81	13.82		
585	C10orf56			6.93	9.30		
586	MAPK1			12.06	10.36		
587	ZBTB47			6.63	8.12		
588	GOSR2			9.73	11.07		
589	ZFP90			10.15	8.92		
590	RALGPS1			8.02	9.38		
591	DGKI			4.77	7.39		
592	RGL2			11.08	9.55		
593	PAK6			5.90	8.55		
594	DMXL1			11.85	10.31		
595	TMEM113			12.28	11.03		
596	SNX24			6.75	8.53		
597	HOXA3			5.99	8.27		
598	SAMD4A			9.84	8.36		
599	WDR45			9.88	12.43		
600	TLOC1			12.91	14.52		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
601	LARP2			7.64	11.50		
602	DTX2			7.60	6.20		
603	ITGA9					7.53	6.32
604	FASTK			10.04	11.22		
605	TAOK2			7.47	6.37		
606	CRTAP					9.78	11.08
607	SERTAD2			11.91	10.82		
608	TBP			10.14	9.09		
609	IQGAP2			7.26	11.19	7.26	8.93
610	RASGEF1B			6.23	8.01		
611	PIP5K2B			9.69	8.53		
612	PRRC1			10.32	11.92		
613	RHPN2			6.73	8.21		
614	DYRK1B			5.92	7.61		
615	ADCY2			5.98	7.97		
616	C12orf34			5.61	7.09		
617	GMPR			5.35	8.15		
618	PAK2			10.86	9.66		
619	KIAA1539			8.12	9.49		
620	PLAGL1			10.03	6.68		
621	LCORL			9.74	11.29		
622	BCL9			7.21	9.16		
623	CPEB2					9.09	10.23
624	TMEM59			12.10	14.75		
625	TRIP10			7.17	9.36		
626	CCPG1			8.38	11.86		
627	NDE1			10.71	9.30		
628	ZDHHC21			9.38	8.11		
629	STOX2			5.87	7.66		
630	RAB4B			10.63	8.66		
631	LRRFIP1			13.25	11.99		
632	OSBP			10.10	11.39		
633	RAB6A			10.76	12.27		
634	RHOV			4.88	7.19		
635	SLC39A14			8.80	11.00		
636	ADARB1			10.05	7.69		
637	ESPN			6.85	8.19		
638	SEC31A			11.64	13.61		
639	PJA2			10.85	11.99		
640	SYNGR3			9.01	7.56		
641	LOC339745			11.94	10.54		
642	NEDD9			11.23	12.48		
643	COL23A1			5.41	7.02		
644	PIP5K3			11.93	10.79		
645	PTPRG			7.30	8.49		
646	DAB2IP			5.61	8.30		
647	MAPRE3			5.80	8.60		
648	SQSTM1			10.05	11.45		
649	RAB6C			10.88	12.04		
650	FAM57A			7.58	6.18		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
651	YPEL5			12.41	13.78		
652	TTN			9.61	7.03		
653	HTRA3			5.62	8.02		
654	CHST2			7.80	12.49		
655	BAZ1A			11.43	10.06		
656	LRFN5					7.38	6.21
657	MBNL1			14.10	12.62		
658	MLL2			10.93	9.89		
659	SF1			11.44	10.36		
660	FRMPD1			4.80	7.06		
661	PPP2R5B			7.60	9.12		
662	RNF43			10.04	8.01		
663	GAP43			5.07	7.49		
664	NOMO1			11.11	14.31		
665	VEGFA			7.79	9.36		
666	C22orf5			8.75	11.38		
667	AKAP11			11.79	10.64		
668	INSIG2			9.46	11.32		
669	PDIK1L			9.11	10.72		
670	TMEM4			10.93	13.32		
671	LMNA			7.80	9.75		
672	TP53INP1			11.84	14.14		
673	NAV1			6.96	8.31		
674	SPTY2D1			9.25	10.77		
675	CREBL2			9.95	11.10		
676	MFAP3L			5.90	7.46		
677	REXO2			10.96	13.71		
678	SPTBN4			6.77	8.22		
679	NOMO2			9.74	12.94		
680	PTEN			12.78	11.40		
681	FBXL16			6.86	9.56		
682	GPM6A			7.87	6.15	7.87	6.67
683	PRX			6.76	8.91		
684	HOXC11			6.40	7.88		
685	KIAA0329			8.27	9.87		
686	PAFAH1B1			11.68	10.33		
687	C20orf174			9.58	7.27		
688	MTPN			13.87	12.17		
689	TMED5			12.25	14.41		
690	FURIN			8.03	9.54		
691	ELAVL3			4.66	8.01		
692	SH2B3			10.31	8.87		
693	LIN28B			5.99	7.58		
694	KIAA1033			12.65	11.38		
695	TMEM28			4.95	7.14		
696	TBC1D15			10.30	11.52		
697	GOLGA4			10.11	11.71		
698	STX1A			5.63	7.82		
699	SLC40A1					6.87	8.27
700	KIAA1815			9.18	7.93		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
701	HNT			5.53	7.09		
702	PDE11A			5.72	7.82		
703	TGFBR3			7.84	9.52		
704	MTF1			9.92	8.86		
705	MAN1A1			9.99	13.65		
706	THRA			7.26	8.48		
707	CBLB			11.46	9.08		
708	SLC35F1			6.29	8.16		
709	FOXP4			8.52	7.30		
710	ELOVL5			13.83	12.78		
711	NMUR1			4.13	7.31		
712	ITPR1			12.06	9.69		
713	CDCA7L			11.95	10.33		
714	RASSF1					9.35	10.69
715	IL1RAPL1			6.42	8.18		
716	AUH			9.37	11.19		
717	DIAPH1			11.52	9.74		
718	ENSA			12.33	11.22		
719	FAM43A			10.62	9.39		
720	CSMD3			4.79	7.58		
721	SLC25A37			10.10	8.69		
722	SLC33A1			9.78	12.19		
723	CNOT6			9.98	8.93		
724	GRID1			7.05	8.80		
725	C21orf91			11.51	10.18		
726	ITPKB			11.28	8.91		
727	CP			5.89	7.41		
728	HMBOX1			10.05	8.50		
729	ARID1A			12.22	11.11		
730	C5orf5			11.86	10.38		
731	TMSB4X			16.86	15.10		
732	EPAS1			7.02	8.39		
733	HPS3			11.65	10.16		
734	DKK1			6.16	7.86		
735	ZNF282			7.89	5.40		
736	AP3D1			11.29	12.84		
737	DERL1			11.69	13.43		
738	C5orf13			9.89	7.62		
739	CCNG2			13.32	11.64		
740	PGRMC2			9.44	11.38		
741	ARF6			13.60	12.55		
742	TMEM110			7.75	9.24		
743	FAM13A1			7.11	9.69		
744	BRMS1L			8.58	10.18		
745	TRAM1			12.52	15.17		
746	CALU			9.42	11.20		
747	GOLPH3			11.55	12.81		
748	MAP3K7			11.14	10.06		
749	ABCG4			6.90	8.22		
750	NELF			8.75	7.70		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
751	ADIPOR1			9.67	10.92		
752	INSR			8.48	11.62		
753	GRM5					6.24	7.65
754	TFG			10.76	12.30		
755	USP48			11.91	13.09		
756	CLCN6			9.26	7.48		
757	ZNF219			6.11	8.42		
758	C7orf43					8.34	6.62
759	NFKB1			11.90	10.70		
760	ARF3			11.11	9.87		
761	JMJD1C			12.34	11.11		
762	ROD1			13.13	11.42		
763	OXSRI			10.69	9.15		
764	ERGIC2			10.86	12.81		
765	EIF4E3			7.61	9.87		
766	SEC24A			10.05	12.85		
767	SPRED1			7.19	5.77		
768	HNRPH3			12.60	11.38		
769	ZDHHC7			10.34	9.05		
770	HNRPA1			16.14	15.14		
771	TMED2			12.01	14.26		
772	VASP			10.60	8.60		
773	CHD4			11.40	10.31		
774	RTN4RL1			5.48	8.36		
775	PPP1R12A			12.03	10.97		
776	SGK3			9.58	11.68		
777	ARHGAP17			12.37	8.62		
778	GORASP2			11.28	13.30		
779	C2orf44			8.38	6.72		
780	FAM116A			11.12	10.08		
781	SSR1			12.75	14.73		
782	MYH9			11.24	9.89		
783	PIK3CD			12.99	10.03		
784	DAZAP2			14.26	13.23		
785	SEL1L			10.74	14.04		
786	LOC388284			7.05	8.32		
787	THRB			7.51	6.11	7.51	6.29
788	MGAT2			11.91	14.44		
789	C8orf13			9.35	6.47		
790	PDZD2			7.00	4.39		
791	DERL2			10.74	12.75		
792	ZCCHC5					7.39	6.27
793	NFYC			10.27	9.03		
794	GLUD2			8.88	7.58		
795	ESR1			7.55	9.88		
796	NRP2			6.51	8.13		
797	NUS1			10.01	11.53		
798	BIRC6			12.15	10.94		
799	ARID3B			7.83	9.22		
800	STCH			10.16	13.88		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
801	SLC7A11			6.32	8.00		
802	OSBPL5			7.91	9.22	7.91	6.62
803	IGFBP3			5.60	7.61		
804	LNPEP			13.72	11.05		
805	ZNRF1			8.18	9.68		
806	DDAH1			7.96	5.87		
807	ERG			4.07	7.49		
808	APLP2					10.90	8.38
809	ZNFX1			10.14	8.93		
810	GPM6B			8.66	6.69		
811	BLCAP			11.49	10.10		
812	SRP68			11.47	12.88		
813	PIK3AP1			14.12	11.74		
814	ANKRD28			11.00	12.46		
815	KCNH8			8.27	4.80		
816	KIAA0430			12.43	10.61		
817	PPP2R1B			9.84	8.41		
818	TMED9			11.62	13.82		
819	CTNNBIP1			7.31	8.89		
820	PPP2R5D			9.51	7.92		
821	CBX4			12.36	13.69		
822	AKAP6			7.38	5.55	7.38	4.93
823	C2orf30			10.72	13.84		
824	DR1			11.97	10.65		
825	MTDH			12.46	13.96		
826	ETS1			14.40	12.62		
827	EPHA8			6.12	8.10		
828	ANKRD13B					7.23	5.85
829	C4orf16			8.83	7.70		
830	SOX4					9.14	10.20
831	SLC12A2			10.23	9.01		
832	IER3IP1			11.35	12.56		
833	DST			7.02	8.34		
834	WRNIP1			11.03	9.49		
835	CLCC1			9.63	11.48		
836	B4GALT6			7.90	6.82		
837	BTBD10			10.12	8.07		
838	SDC1			7.05	12.14		
839	C10orf12			10.32	8.40		
840	ZDHHC3			9.80	8.78		
841	GNAI2			10.86	9.27		
842	HNRPU			13.82	12.47		
843	GNAZ					8.86	7.26
844	ALG9			8.93	10.97		
845	FBXL10			11.75	10.43		
846	ARID4B			12.19	10.96		
847	PPP1R3F			6.19	7.79		
848	EPB49			6.49	7.94		
849	PCNP			12.91	11.74		
850	PCYT1B			11.35	9.77		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
851	RAB14			11.64	10.41		
852	TCERG1			12.50	11.46		
853	MKNK2			14.87	12.67		
854	COL4A3					8.78	12.23
855	HNRPA0			12.50	11.36		
856	P2RX4			8.88	10.29		
857	JUP			9.23	5.70		
858	EGR2			10.43	8.07		
859	SUPT16H			11.35	9.60		
860	PNRC2			13.93	11.64		
861	SRPR			11.87	13.89		
862	BPTF			12.46	11.34		
863	RBM16			12.05	10.52		
864	YWHAZ			13.62	12.61		
865	EDEM3			11.01	12.76		
866	C12orf23			11.18	12.40		
867	DOC2A			3.96	7.21		
868	SETD2			11.54	10.39		
869	FAM98A			10.91	12.10		
870	C13orf18			13.25	9.86		
871	BRP44L			10.48	11.91		
872	CCDC6			11.25	9.82		
873	GLCCI1			12.22	15.19		
874	PLEKHH1			7.03	9.25		
875	SMEK1			11.38	10.37		
876	ANKRD9			4.70	8.61		
877	CSNK1E			8.86	11.48		
878	DCUN1D3			7.48	5.95		
879	LTB			14.66	9.91		
880	EOMES			7.30	6.14		
881	PARP8			10.81	8.69		
882	ABCD1			7.12	8.49		
883	HOXA10			5.56	7.32		
884	RNPS1			12.60	11.25		
885	AYTL2			12.08	10.79		
886	FLJ20699			5.74	8.80		
887	SAPS1			11.43	9.76		
888	SYNJ1			8.36	9.64		
889	ZNF403			12.06	10.91		
890	KPNB1			13.37	12.26		
891	ISOC1			9.67	10.98		
892	HYOU1			9.95	11.85		
893	ZNF706			12.83	14.30		
894	HDLBP			10.60	13.37		
895	ELF1			12.70	11.34		
896	TM9SF4			8.66	10.55		
897	RAB8A			11.94	10.88		
898	MORF4L2			12.94	14.69		
899	SERP1			13.31	15.16		
900	ADAMTS5			5.71	7.31		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
901	TRIOBP			11.23	10.18		
902	ZNF664			11.32	12.57		
903	RAB11FIP1			11.78	9.03		
904	MYO18A			8.06	6.19		
905	DUSP10			10.13	8.70		
906	ATXN1			6.66	10.65	6.66	10.25
907	EPB41L4B			6.12	7.95		
908	CNTNAP1			6.51	9.06		
909	SLC17A7			6.47	8.01		
910	SPCS2			13.75	15.53		
911	CCNC			12.68	14.10		
912	WDR77			10.67	8.83		
913	GMFB			12.03	10.70		
914	ITGA6			6.72	10.51		
915	CASP8AP2			10.55	9.44		
916	SEC24D			8.79	11.88		
917	CBX1			12.16	10.96		
918	TBX3			6.05	7.89		
919	NFAT5			12.09	10.72		
920	ATP6V1B2			10.73	9.53		
921	ACTG1			16.72	14.81		
922	RND3			7.31	5.65		
923	HNRPUL1			11.97	10.58		
924	TJP1			7.18	10.59		
925	RAPGEF4			5.25	8.09		
926	RGMA			5.65	7.42		
927	NAPIL1			14.70	12.60		
928	TARDBP			12.72	11.49		
929	DAZAP1			12.74	11.30		
930	ZNF609			8.26	6.94	8.26	9.52
931	ARL1			10.44	12.41		
932	ERC2			7.03	5.97		
933	PDE4A			7.65	9.22		
934	CSK			12.83	10.59		
935	IMPAD1			8.44	10.05		
936	PNN			13.75	12.48		
937	DCP2			13.06	10.74		
938	PIK3R3			6.34	7.82		
939	RAB1A			13.59	14.83		
940	CENTB2			12.39	10.97		
941	SPTAN1			11.48	9.79		
942	DNAJC8			12.25	11.00		
943	UNC13B			6.70	8.35		
944	DHX15			14.19	12.99		
945	VEZF1			11.45	9.94		
946	DHDDS			8.74	10.05		
947	FAM55C			8.19	9.74		
948	USP37			8.89	7.60		
949	MMD			11.68	10.32		
950	HCLS1			14.42	13.12		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
951	KIAA1370			13.30	14.72		
952	GANC			8.31	6.12		
953	SSRP1			11.34	10.27		
954	G3BP1			12.24	10.55		
955	BAAT			4.91	7.24		
956	FNDC3B			8.27	14.34		
957	FBXW7			10.21	12.19		
958	SPECC1L			10.27	7.66		
959	YBX1			15.31	14.20		
960	YAP1			7.23	5.61		
961	ARF4			12.09	14.23		
962	PNKD			10.86	9.79		
963	CLEC2D			11.96	10.90		
964	XPO1			13.81	11.82		
965	TRAM2			9.38	12.80		
966	MITF					8.05	6.41
967	CFL1			16.37	14.09		
968	CREB5			5.46	7.24		
969	GREM1			4.48	7.14		
970	LONRF1			11.26	10.00		
971	NME7			9.37	8.30		
972	PMAP1			12.26	10.75		
973	KLHL14			11.89	10.84		
974	AOF1			9.33	7.96	9.33	8.28
975	SMPD3			5.90	7.83		
976	RGL1			6.66	8.04		
977	LYPD6			5.38	7.39		
978	STAT5B			10.95	9.73		
979	C10orf6			10.04	8.44		
980	CLDND1			10.72	12.01		
981	DUSP9			5.59	7.70		
982	SLC36A1			8.53	7.23		
983	PAM			8.90	10.86		
984	GHR			5.87	7.56		
985	CBL			11.69	10.26		
986	CENTG2			5.96	7.39		
987	BACH2			13.68	9.35	13.68	11.88
988	NUP153			12.33	10.55		
989	CPD			8.37	9.72		
990	APLN			8.58	6.47		
991	RFXDC2			11.67	10.00		
992	GABRB2			5.58	8.10		
993	NOMO3			5.39	7.39		
994	RHOJ			6.41	7.75		
995	PRDM1			9.15	14.10		
996	IGSF3			7.62	5.91		
997	UBE2A			12.47	11.47		
998	KBTBD8			12.82	9.73	12.82	11.71
999	PRR15			7.27	5.94	7.27	4.67
1000	ILF3			11.94	10.71		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
1001	WIPF1			13.81	12.41		
1002	GCNT2			11.01	8.49		
1003	DBNL			10.43	8.48		
1004	C14orf43			10.14	8.01		
1005	MID1IP1			9.16	8.11		
1006	LIMD2			10.43	8.88		
1007	HNRPK			14.49	12.95	14.49	13.46
1008	ZNF697			5.74	8.07		
1009	TSHZ3			7.31	5.32		
1010	MBNL2			11.88	13.47		
1011	ELL			7.83	9.17		
1012	MAFB			7.30	8.56		
1013	GGA2			13.25	10.77		
1014	C20orf121			10.01	8.93		
1015	CDC2L6			11.52	9.69		
1016	TOB2			11.39	9.58		
1017	MAP4K4			12.04	10.41		
1018	FAM102A			11.41	10.18		
1019	ITGB3BP			11.86	10.76		
1020	HIVEP1			10.35	9.05		
1021	NUDT21			12.51	11.11		
1022	EIF4A1					14.02	12.98
1023	TSPAN14			8.38	6.31		
1024	SLC2A4RG			8.98	7.40		
1025	DGKZ			9.74	7.85		
1026	PTPN9			9.30	7.85		
1027	BCL7A			11.33	10.10		
1028	LSM14A			12.74	11.19		
1029	GNB2			11.50	10.12		
1030	SLC6A6			11.35	8.51		
1031	TACC1			13.21	11.62		
1032	LIMK2			9.80	8.12		
1033	ACVR2B			6.69	8.33		
1034	SCC-112			12.25	10.55		
1035	PTBP1			13.38	12.19	13.38	12.21
1036	CITED2			9.88	12.56		
1037	SNX5			14.17	13.16		
1038	ACTR2			15.12	13.32		
1039	OSBPL3			10.59	12.84		
1040	SFRS1			14.60	13.24		
1041	ADM			7.24	11.10		
1042	PFKFB3			11.91	10.01		
1043	FNBP1			13.61	12.25		
1044	MTMR2			10.53	9.06		
1045	DDHD1					10.18	8.74
1046	HSPA5			13.70	16.32		
1047	PTK2			12.12	8.33		
1048	UBE2I			13.17	11.22		
1049	SNAP23			13.78	12.23		
1050	MTERFD2			10.53	8.59		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
1051	COTL1			13.89	10.14		
1052	PHACTR2			8.65	6.86		
1053	GLRA2			5.93	7.69		
1054	NUTF2			10.39	9.26		
1055	TSGA14			9.52	8.03		
1056	FKBP1A			12.16	10.89	12.16	10.82
1057	LRRC1			8.82	7.68		
1058	PDIA6			13.07	14.91		
1059	YWHAQ			14.50	12.99		
1060	ACHE			5.59	8.29		
1061	KRAS			12.36	10.49		
1062	FAM107B			13.87	12.55		
1063	CCDC117					11.03	9.56
1064	WDR1			13.38	11.36		
1065	HMGB1			16.36	14.98	16.36	14.97
1066	CCND3			12.69	9.79		
1067	SUV39H1					9.28	8.07
1068	RANBP5					11.94	10.87
1069	SLC25A33			10.24	9.00		
1070	EDNRA			5.94	7.12		
1071	RAB11A			12.94	11.73		
1072	DDEF1			11.98	10.54		
1073	CXorf15			11.84	10.47		
1074	C4orf34			13.65	10.16		
1075	SLC44A1			11.10	13.50		
1076	EIF2AK3			12.29	13.83		
1077	RAP1B			14.21	13.21		
1078	CDK2			10.20	8.73	10.20	9.01
1079	JDP2			7.94	5.97		
1080	GSTCD			8.86	7.85		
1081	TNKS2			10.95	9.62	10.95	9.62
1082	FUZ			7.15	8.96	7.15	8.19
1083	SYPL1			13.56	10.87		
1084	EIF4H					13.07	12.02
1085	PIP5K2A			9.65	8.06		
1086	RGS2			11.61	14.48		
1087	ARF5					10.35	9.13
1088	JAKMIP2			8.57	6.96		
1089	RABGAP1			12.19	9.65	12.19	10.85
1090	LRIG1	9.76	10.77			10.77	9.16
1091	CLTA			13.08	11.71		
1092	APBB2					7.87	6.39
1093	SMC1A			12.88	11.33		
1094	CDC27	9.86	10.88				
1095	STT3A	8.64	9.66				
1096	ZFAND6	12.01	13.04	13.04	11.95		
1097	BZRAP1			8.43	7.15		
1098	DPP3	9.41	10.44	10.44	8.39		
1099	CNIH	11.94	12.98				
1100	TMEM16F	9.42	10.46				

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
1101	ARHGEF7	11.99	13.03	13.03	11.18	13.03	11.60
1102	CAMTA1	10.60	11.64				
1103	PFN1	14.03	15.08				
1104	USP12	10.18	11.23				
1105	AZIN1	11.24	12.29				
1106	GNA13	13.89	14.94	14.94	13.37		
1107	RCOR1	10.46	11.51	11.51	9.96		
1108	USP1			13.36	11.52		
1109	VANGL1			7.47	9.15		
1110	CAPZB	11.85	12.91				
1111	CDV3	13.86	14.91				
1112	ABI1	11.61	12.67	12.67	10.96		
1113	ST5	7.21	8.28				
1114	TTL	8.63	9.69	9.69	8.03		
1115	ANP32E	12.76	13.82	13.82	12.19		
1116	USP7	12.27	13.34				
1117	BCL11B	7.20	8.27			8.27	9.68
1118	OAZ2	8.98	10.06				
1119	PPP2CA	12.04	13.12			13.12	11.89
1120	TSC1	10.58	11.66				
1121	CTDSPL2	9.81	10.90	10.90	9.51	10.90	9.68
1122	NEDD4L	7.81	8.90				
1123	NAT13	12.06	13.16				
1124	ASF1A	9.54	10.64				
1125	DPF1			7.18	8.50	7.18	5.84
1126	RAN	13.46	14.57	14.57	12.39		
1127	ELAVL1	11.66	12.77	12.77	11.43		
1128	GRHL1			5.76	7.24		
1129	SMAD2	10.45	11.57				
1130	IQWD1	9.70	10.83			10.83	9.73
1131	ETS2			7.50	5.66		
1132	CDC25B	10.04	11.18				
1133	USP32	10.65	11.78			11.78	10.75
1134	EED	11.76	12.90	12.90	11.50		
1135	CTNND2			5.93	7.81		
1136	SHROOM3	7.86	9.01			9.01	6.05
1137	PSCD3	6.43	7.57				
1138	ATF7	7.83	8.97				
1139	CDK6	10.31	11.46				
1140	GCH1			12.59	10.17		
1141	AP3S1	11.95	13.12				
1142	ARL6IP1	12.03	13.20	13.20	11.51		
1143	TBC1D1	11.00	12.17			12.17	10.01
1144	ATP2A2	10.75	11.92			11.92	10.76
1145	SORL1	12.49	13.67	13.67	10.58		
1146	SOX5	9.30	10.47	10.47	7.33	10.47	9.08
1147	KIAA1411	8.65	9.83				
1148	KIAA0922	12.43	13.61	13.61	10.86	13.61	12.35
1149	SSX2IP	7.82	9.00			9.00	7.49
1150	SNRPD1	11.85	13.04				

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
1151	EDD1	11.23	12.42				
1152	BLMH	9.01	10.21				
1153	PTPLB	11.32	12.52				
1154	SLC25A27					7.44	3.28
1155	PGAM1	12.40	13.61	13.61	12.55		
1156	HMGA1	11.26	12.47	12.47	10.36		
1157	EDEM1	11.34	12.55				
1158	PRPF38A	10.27	11.48	11.48	10.00		
1159	DCUN1D1	9.82	11.03				
1160	ROBO1	7.43	8.64				
1161	LRRC59			11.26	12.65		
1162	ZNF207	12.29	13.51				
1163	GTDC1	9.19	10.42	10.42	9.35		
1164	C1orf121	10.47	11.70				
1165	NF1	9.23	10.46				
1166	CUL3	12.98	14.21	14.21	12.80	14.21	12.99
1167	B4GALT5	8.74	9.97	9.97	8.08	9.97	8.71
1168	GADD45A	8.14	9.37	9.37	11.74		
1169	RASD2			5.53	7.35		
1170	CD4	6.76	8.01	8.01	6.11		
1171	WWC1			6.16	7.88		
1172	DUSP2	9.43	10.69	10.69	9.18		
1173	TP53INP2	8.44	9.70	9.70	8.53	9.70	8.00
1174	NRAS	8.89	10.16				
1175	TFRC	12.12	13.39	13.39	11.88		
1176	MASTL	8.76	10.03	10.03	8.23	10.03	8.64
1177	USP6	9.12	10.39			10.39	9.25
1178	VGLL4	10.30	11.57	11.57	10.16		
1179	C10orf78	8.93	10.21				
1180	BTG3	9.87	11.16				
1181	TMOD2	8.64	9.93	9.93	6.94		
1182	HOXA5	7.03	8.32				
1183	AK2	10.33	11.62				
1184	MAP2K1	10.41	11.71	11.71	10.69	11.71	10.61
1185	CASP3	10.16	11.47				
1186	STK40	9.30	10.60	10.60	8.13		
1187	GRHL3			5.20	7.46		
1188	SLC25A4	8.65	9.96				
1189	KLHDC5	9.52	10.83				
1190	SAMHD1	9.72	11.03				
1191	PHLPP	7.93	9.24			9.24	7.58
1192	CCNE1	7.86	9.18				
1193	EGR1	11.92	13.24				
1194	PIM1	9.44	10.76			10.76	8.87
1195	HECW1	6.49	7.81				
1196	CHAC1			6.73	8.76		
1197	P4HA2	6.84	8.18				
1198	PPM1E	6.59	7.92				
1199	KIAA0746	13.65	14.98				
1200	LOC401720			6.33	7.63		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
1201	CAPN5	5.90	7.24				
1202	DYNLL1	12.69	14.03				
1203	EHMT1	10.40	11.75				
1204	RIC8B	7.54	8.89				
1205	GRIN1			7.40	8.93		
1206	DEK	12.73	14.09	14.09	10.29		
1207	E2F1	7.01	8.37			8.37	7.21
1208	FAM45A	10.66	12.02				
1209	VAMP1	11.10	12.47				
1210	LTBP1	7.23	8.61				
1211	SOCS1	9.18	10.56	10.56	9.25		
1212	ZCCHC14	6.98	8.36				
1213	KLHL3	8.04	9.43				
1214	RET	5.90	7.29	7.29	5.99		
1215	CUTL1	10.33	11.72	11.72	10.67	11.72	10.50
1216	RBL1	7.58	8.98	8.98	7.52	8.98	7.97
1217	TOP1	11.47	12.87				
1218	GPD1L	7.94	9.35				
1219	SAR1B	9.03	10.46	10.46	12.55		
1220	MTF2	11.84	13.27	13.27	11.18		
1221	ANP32B			15.53	14.21		
1222	CIT	8.19	9.63	9.63	7.43	9.63	7.77
1223	POU3F1	6.08	7.52				
1224	MTMR12	11.44	12.89	12.89	11.13	12.89	11.60
1225	MBOAT2	6.73	8.17			8.17	6.25
1226	DOCK9	9.28	10.73				
1227	ZAK	8.60	10.05	10.05	8.21		
1228	LOC152485	11.05	12.51	12.51	10.56		
1229	HNRPA3			14.33	12.26		
1230	LMNB1			10.63	8.78		
1231	ZFYVE21	8.42	9.90				
1232	TXNDC5			12.47	16.40		
1233	UBE2G1	11.36	12.84				
1234	KIF23	7.44	8.93	8.93	5.57	8.93	6.64
1235	DPYSL2	9.98	11.46	11.46	9.03		
1236	ATP5G3	12.15	13.64				
1237	GLRX5	10.08	11.57				
1238	NLK	10.41	11.92				
1239	ARL6IP6	10.51	12.02	12.02	10.43		
1240	CNNM4	6.17	7.68	7.68	5.21		
1241	TBC1D4	9.12	10.64	10.64	8.94		
1242	CD163			5.49	7.00		
1243	PKD2	8.17	9.71			9.71	7.48
1244	DIAPH3	8.23	9.77	9.77	8.34		
1245	RAD23B	10.65	12.20			12.20	10.54
1246	DCAMKL2	5.53	7.08	7.08	5.88		
1247	LMBR1	7.22	8.77				
1248	RRAS2	11.24	12.79	12.79	11.03		
1249	MYO1D	6.31	7.88	7.88	10.07		
1250	KLHL5	10.57	12.15	12.15	10.43	12.15	10.80

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
1251	EPS15	12.32	13.91			13.91	12.70
1252	FASLG	5.47	7.06				
1253	H2AFY	12.56	14.16				
1254	LIMA1	8.47	10.07	10.07	9.06		
1255	CDCA4	8.92	10.52	10.52	9.16		
1256	HAS3	5.70	7.31	7.31	6.15		
1257	HRBL	5.96	7.57	7.57	6.35	7.57	5.97
1258	SYAP1	9.71	11.32			11.32	9.76
1259	MDFIC	12.06	13.67				
1260	FAM76B	11.27	12.89	12.89	10.52		
1261	SNTB2	8.22	9.85	9.85	8.64		
1262	ARL3	8.92	10.55				
1263	GPR124	5.50	7.14				
1264	BCL2L11	10.79	12.43			12.43	11.14
1265	RNF103			12.03	13.23		
1266	MYB	6.97	8.62	8.62	5.61		
1267	PKM2	11.21	12.87				
1268	VCL	8.92	10.57	10.57	8.25		
1269	RBBP7	12.45	14.11	14.11	12.96	14.11	12.70
1270	LBR	12.86	14.53	14.53	12.16	14.53	12.50
1271	RRBP1	6.97	8.64	8.64	11.94		
1272	GABRB3	5.33	7.00				
1273	SGCB	7.78	9.45	9.45	8.22		
1274	FAM81A	6.61	8.30	8.30	5.44		
1275	RAB15	5.75	7.44				
1276	SOX9	6.72	8.42				
1277	SAP30	8.22	9.91				
1278	BRWD1	8.60	10.30	10.30	8.72	10.30	9.04
1279	KCNMA1	7.47	9.17	9.17	10.42		
1280	WHSC1	9.67	11.37	11.37	9.60		
1281	CCDC126	9.36	11.09				
1282	GRAMD1C	7.83	9.57				
1283	PHF19	8.98	10.73	10.73	9.18		
1284	ADAM23	7.02	8.77	8.77	7.00		
1285	C9orf150	5.38	7.13				
1286	ZNF572	6.52	8.30	8.30	6.82		
1287	STK39	9.38	11.15	11.15	9.40		
1288	SMS	9.73	11.54				
1289	DMD	8.96	10.77	10.77	9.32		
1290	C1orf83	6.15	7.96				
1291	MFHAS1	9.80	11.61	11.61	9.36		
1292	STXBP1			6.57	7.79		
1293	CPNE2	5.44	7.27	7.27	4.84		
1294	MYH10	7.07	8.90			8.90	7.85
1295	CALM3	9.63	11.46	11.46	10.30		
1296	EFNB2	7.01	8.85				
1297	ACTN1	5.89	7.74				
1298	RBMS3	5.67	7.51				
1299	ACOT7			9.70	7.83		
1300	RKHD1			5.92	7.77		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
1301	LRRK1	9.74	11.62			11.62	10.12
1302	PTCH1	7.70	9.58				
1303	MGLL	7.30	9.18	9.18	10.57	9.18	8.06
1304	YWHAH	8.94	10.82	10.82	9.09		
1305	PDE4D	6.78	8.66				
1306	MAF	8.05	9.95	9.95	8.25		
1307	PTGER3	5.18	7.09			7.09	6.06
1308	PRKCD	9.49	11.40				
1309	CCDC64	8.15	10.07	10.07	7.55		
1310	RASL11A			7.89	6.65		
1311	KPNA2	11.18	13.09	13.09	11.78	13.09	11.55
1312	GPR137B	8.65	10.58			10.58	9.36
1313	TIAM1	6.97	8.90				
1314	TFDP1	10.95	12.90	12.90	10.49		
1315	SSBP2	10.47	12.42	12.42	10.32		
1316	REEP1	5.64	7.61				
1317	MAP2	7.85	9.83			9.83	7.75
1318	HOXA9	5.15	7.12				
1319	SCRN1			11.81	9.54		
1320	LOC129607	8.79	10.78	10.78	9.33	10.78	9.45
1321	SIAH2	10.35	12.34	12.34	10.57		
1322	DKFZP564O0823	6.96	8.95				
1323	POLQ	8.30	10.30	10.30	8.98	10.30	7.83
1324	KLF15	5.88	7.88	7.88	9.36	7.88	6.74
1325	PXDN	8.36	10.37				
1326	BTBD12	8.06	10.08	10.08	8.56		
1327	PHF6	11.19	13.21	13.21	11.96	13.21	12.09
1328	SLC41A2	5.67	7.68				
1329	HN1	9.87	11.92	11.92	9.85	11.92	10.58
1330	ZNF608	8.98	11.07	11.07	9.74		
1331	RNGTT	10.32	12.45				
1332	RAP2A	10.35	12.47				
1333	LIMK1	5.18	7.36			7.36	5.05
1334	SMAD1	5.91	8.10	8.10	6.34		
1335	NCOA7	10.39	12.58				
1336	PRDM15	10.29	12.49				
1337	PELI1	10.67	12.88				
1338	PLS1	5.43	7.65			7.65	4.53
1339	RAB23	6.14	8.36				
1340	NAPIL5	7.40	9.63	9.63	8.30	9.63	8.34
1341	DNER	6.90	9.14				
1342	LRRC42	7.58	9.83				
1343	ID2	7.74	9.99				
1344	IBRDC2	9.98	12.24	12.24	8.84	12.24	9.94
1345	DNMT1	11.21	13.50				
1346	STAC3	5.74	8.02	8.02	7.01		
1347	HMGB3	8.20	10.50	10.50	8.80	10.50	8.08
1348	BMPRI1A	6.75	9.06				
1349	SGK	10.06	12.37				
1350	CBX2	6.06	8.37	8.37	6.38		

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
1351	LRRC20	5.69	8.03				
1352	LRRC4	4.81	7.15	7.15	5.05		
1353	HOXA1	5.36	7.70				
1354	LRRC62	4.95	7.30				
1355	ATAD2	9.00	11.34	11.34	8.44	11.34	9.37
1356	MOBK1A	9.73	12.08	12.08	9.13	12.08	10.12
1357	LOC220594	10.06	12.41			12.41	10.07
1358	ZNF804A	6.14	8.51				
1359	C1orf113	5.99	8.36			8.36	5.74
1360	FMNL2	6.58	8.96				
1361	H2AFX			12.49	10.60		
1362	ATP1B1	5.60	8.03				
1363	GPT2	6.54	8.97				
1364	PSRC1			9.89	7.46		
1365	SLC25A35	5.23	7.68				
1366	LHFPL2	8.94	11.41				
1367	UBE2J1	11.34	13.81			13.81	12.22
1368	TBC1D8B	5.43	7.91	7.91	6.89		
1369	SGPP1	10.96	13.46	13.46	11.28		
1370	C11orf9	4.74	7.24				
1371	BCL6	12.29	14.82	14.82	10.60	14.82	11.78
1372	ANUBL1	8.12	10.66			10.66	8.78
1373	MTA3	8.37	10.92				
1374	PGBD5	4.87	7.45			7.45	5.87
1375	LPP	11.00	13.59	13.59	10.07	13.59	10.89
1376	NDFIP2	7.39	9.99				
1377	STMN1			11.76	9.03		
1378	PITPNC1	8.77	11.42	11.42	10.00		
1379	SH3RF1	7.37	10.05	10.05	8.10		
1380	ASF1B	8.56	11.25	11.25	7.91	11.25	8.27
1381	FLJ20186	12.06	14.82	14.82	12.05		
1382	SLC16A2			8.08	5.17		
1383	PEX5	9.12	11.90	11.90	9.50		
1384	ECT2	7.45	10.23	10.23	7.70	10.23	7.63
1385	MAML3	8.05	10.85				
1386	TEAD1	4.42	7.24				
1387	HMGB2	12.96	15.78	15.78	12.73	15.78	13.36
1388	NCALD	5.15	7.97				
1389	RGC32	7.75	10.62				
1390	PPP1R3C	4.18	7.06				
1391	DEPDC1B			9.96	7.11		
1392	WEE1	10.11	13.01	13.01	10.32	13.01	11.84
1393	FHL2	4.82	7.77				
1394	ITGB8	4.70	7.66				
1395	SLC1A1			10.86	8.88		
1396	FAM83D	7.36	10.32				
1397	UHRF1			12.22	8.72		
1398	C7orf41	4.94	7.95	7.95	6.29		
1399	ZBTB8	5.58	8.59	8.59	11.07		
1400	ZNF367	7.97	10.99	10.99	8.04	10.99	8.22

ID	Gene Name	Naïve vs Germinal Center		Germinal Center vs Plasma		Germinal Center vs Memory	
		Naïve Average	GC Average	GC average	PC Average	GC Average	Memory Average
1401	CDC25A	6.03	9.09	9.09	6.81		
1402	CHEK1	7.59	10.68	10.68	7.72		
1403	CDCA7	10.61	13.76	13.76	10.16	13.76	11.06
1404	FGF13	4.55	7.69				
1405	SSBP3	6.20	9.35				
1406	EZH2	9.40	12.57	12.57	10.22		
1407	TNFSF11	5.18	8.36	8.36	5.91	8.36	9.78
1408	PACSLN1	5.16	8.35				
1409	RRM2	10.59	13.82	13.82	9.47	13.82	10.79
1410	POU4F1	5.62	8.85				
1411	MYBL2	9.07	12.41	12.41	9.12		
1412	KIAA1212	8.46	11.81			11.81	8.55
1413	CCNE2	7.30	10.66	10.66	8.02	10.66	8.03
1414	IGF2BP3	7.92	11.34	11.34	9.93	11.34	9.55
1415	PRKAR2B	6.17	9.66	9.66	8.16		
1416	CADPS	5.04	8.58	8.58	6.18		
1417	ANKRD15	6.97	10.52			10.52	7.58
1418	DAAM1	9.33	12.92				
1419	MAP1B	4.05	7.68	7.68	5.03	7.68	6.23
1420	AFF2	6.32	10.00				
1421	E2F7	5.66	9.37	9.37	6.53	9.37	6.89
1422	PRC1	8.37	12.08				
1423	ENPP5	3.54	7.26	7.26	4.97		
1424	E2F8	7.68	11.41				
1425	MED12L	7.82	11.59	11.59	7.46	11.59	10.57
1426	LOC162073	6.30	10.08				
1427	LRRC32	4.14	7.93	7.93	6.61	7.93	4.95
1428	DMXL2	6.57	10.38	10.38	6.61	10.38	7.76
1429	FLJ20366	7.86	11.68	11.68	7.62	11.68	9.86
1430	TOX	9.05	12.88	12.88	11.27		
1431	MME			11.56	10.33		
1432	FGD6	7.63	11.73	11.73	9.12		
1433	MYBL1	9.68	14.13	14.13	10.02	14.13	9.72

Table 16: Predictor microRNAs that distinguish activated B-cell (ABC) DLBCL from germinal center B-cell (GCB) DLBC

ABC vs GCB	Higher in
hsa-miR-93/mmu-miR-93/rno-miR-93	GCB
hsa-miR-331-3p/mmu-miR-331-3p/rno-miR-331	GCB
hsa-miR-129*	GCB
hsa-miR-423-3p/mmu-miR-423-3p/rno-miR-423	GCB
hsa-miR-28-5p/mmu-miR-28/rno-miR-28	GCB
mghv-miR-M1-7-3p	GCB
hsa-miR-518b	GCB
ebv-miR-BHRF1-1	GCB
hsa-miR-140-5p/mmu-miR-140/rno-miR-140	GCB
hsa-miR-505*	GCB
hsa-miR-675	GCB
hsa-miR-198	GCB
hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	GCB
hsa-miR-361-5p/mmu-miR-361/rno-miR-361	GCB
ebv-miR-BART8*	GCB

Table 17: Predictor microRNAs that distinguish activated B-cell (ABC) DLBCL from Burkitt lymphoma

ABC vs BL	Higher in	ABC vs BL (con't)	Higher in
hsa-miR-155	ABC	hsa-miR-142-3p/mmu-miR-142-3p/rno-miR-142-3p	ABC
hsa-miR-29c/mmu-miR-29c/rno-miR-29c	ABC	hsa-let-7a/mmu-let-7a/rno-let-7a	ABC
hsa-miR-146b-5p/mmu-miR-146b/rno-miR-146b	ABC	hsa-miR-30b/mmu-miR-30b/rno-miR-30b-5p	ABC
hsa-miR-29b/mmu-miR-29b/rno-miR-29b	ABC	hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p	ABC
hsa-miR-22/mmu-miR-22/rno-miR-22	ABC	hsa-miR-34b/mmu-miR-34b-3p	ABC
hsa-miR-21/mmu-miR-21/rno-miR-21	ABC	hsa-miR-16/mmu-miR-16/rno-miR-16	ABC
hsa-miR-768-3p	ABC	hsa-miR-30c/mmu-miR-30c/rno-miR-30c	ABC
hsa-miR-145/mmu-miR-145/rno-miR-145	ABC	hsa-let-7c/mmu-let-7c/rno-let-7c	ABC
hsa-miR-29a/mmu-miR-29a/rno-miR-29a	ABC	hsa-miR-550	ABC
hsa-miR-30e/mmu-miR-30e/rno-miR-30e	ABC	hsa-miR-921	BL
hsa-miR-26a/mmu-miR-26a/rno-miR-26a	ABC	hsa-miR-30c-2*/mmu-miR-30c-2*/rno-miR-30c-2*	BL
hsa-miR-101/mmu-miR-101a/rno-miR-101a	ABC	hsa-miR-933	BL
hsa-miR-24/mmu-miR-24/rno-miR-24	ABC	hsa-miR-658	BL
hsa-miR-26b/mmu-miR-26b/rno-miR-26b	ABC	hsa-miR-628-3p	BL
hsa-miR-27a/mmu-miR-27a/rno-miR-27a	ABC	hsa-miR-503	BL
hsa-miR-27b/mmu-miR-27b/rno-miR-27b	ABC	hsa-miR-193a-5p	BL
hsa-miR-23b/mmu-miR-23b/rno-miR-23b	ABC	hsa-miR-30b*	BL
hsa-miR-23a/mmu-miR-23a/rno-miR-23a	ABC	hsa-miR-93/mmu-miR-93/rno-miR-93	BL
hsa-miR-125b/mmu-miR-125b-5p/rno-miR-125b-5p	ABC	hsa-miR-18b	BL
hsa-miR-30a/mmu-miR-30a/rno-miR-30a	ABC	hsa-miR-18a/mmu-miR-18a/rno-miR-18a	BL
		hsa-miR-874/mmu-miR-874/rno-miR-874	BL

Table 18: Predictor microRNAs that distinguish activated B-cell (ABC) DLBCL from chronic lymphocytic leukemia

ABC vs CLL	Higher in	ABC vs CLL (con't)	Higher in	ABC vs CLL (con't)	Higher in
hsa-miR-125b/mmu-miR-125b-5p/rno-miR-125b-5p	ABC	hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p	CLL	hsa-miR-340/mmu-miR-340-5p/rno-miR-340-5p	CLL
hsa-miR-126/mmu-miR-126-3p/rno-miR-126	ABC	hsa-miR-101/mmu-miR-101a/rno-miR-101a	CLL	hsa-miR-331-3p/mmu-miR-331-3p/rno-miR-331	CLL
hsa-miR-199a-3p/hsa-miR-199b-3p/mmu-miR-199a-3p/mmu-miR-199b-3p/rno-miR-199a-3p	ABC	hsa-miR-185/mmu-miR-185/rno-miR-185	CLL	hsa-miR-151-5p/mmu-miR-151-5p/rno-miR-151	CLL
hsa-miR-145/mmu-miR-145/rno-miR-145	ABC	hsa-miR-888*	CLL	hsa-miR-636	CLL
hsa-miR-143/mmu-miR-143/rno-miR-143	ABC	hsa-miR-199a-5p/mmu-miR-199a-5p/rno-miR-199a-5p	CLL	hsa-miR-33a/mmu-miR-33/rno-miR-33	CLL
hsa-miR-637	ABC	hsa-miR-668/mmu-miR-668	CLL	hsa-miR-486-5p/mmu-miR-486	CLL
hsa-miR-371-5p	ABC	hsa-miR-549	CLL	hsa-miR-150/mmu-miR-150/rno-miR-150	CLL
kshv-miR-K12-6-3p	ABC	hsa-miR-801/mmu-miR-801	CLL	hsa-miR-25/mmu-miR-25/rno-miR-25	CLL
hsa-miR-628-3p	ABC	hsa-miR-649	CLL	hsa-miR-331-5p/mmu-miR-331-5p	CLL
hsa-miR-126*/mmu-miR-126-5p/rno-miR-126*	ABC	hsa-miR-625*	CLL	hsa-miR-299-5p/mmu-miR-299*/rno-miR-299	CLL
hsa-miR-193a-5p	ABC	hsa-miR-140-3p/mmu-miR-140*/rno-miR-140*	CLL	hsa-miR-891a	CLL
hsa-miR-21/mmu-miR-21/rno-miR-21	ABC	hsa-let-7f/mmu-let-7f/rno-let-7f	CLL	hsa-miR-144*	CLL
hsa-miR-24/mmu-miR-24/rno-miR-24	ABC	hsa-miR-768-5p	CLL	hsa-miR-363*/rno-miR-363*	CLL
hsa-miR-503	ABC	hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	CLL	hsa-miR-93/mmu-miR-93/rno-miR-93	CLL
hsa-miR-23a/mmu-miR-23a/rno-miR-23a	ABC	ebv-miR-BART13	CLL	hsa-miR-423-3p/mmu-miR-423-3p/rno-miR-423	CLL
hsa-miR-23b/mmu-miR-23b/rno-miR-23b	ABC	hsa-miR-339-5p/mmu-miR-339-5p/rno-miR-339-5p	CLL	hsa-let-7g/mmu-let-7g	CLL
hsa-miR-22/mmu-miR-22/rno-miR-22	ABC	hsa-miR-20b/mmu-miR-20b/rno-miR-20b-5p	CLL	hsa-miR-28-5p/mmu-miR-28/rno-miR-28	CLL

ABC vs CLL	Higher in	ABC vs CLL (con't)	Higher in	ABC vs CLL (con't)	Higher in
hsa-miR-665		hsa-miR-335/mmu- miR-335-5p/rno-miR- 335		hsa-miR-20b*	
hsa-let-7c/mmu-let-7c/rno- let-7c	ABC	mghv-miR-M1-8	CLL	hsa-miR-140- 5p/mmu-miR- 140/rno-miR-140	CLL
hsa-miR-658	ABC	hsa-miR-30d/mmu- miR-30d/rno-miR-30d	CLL	hsa-miR-519d	CLL
hsa-let-7a/mmu-let-7a/rno- let-7a	ABC	hsa-miR-363/mmu- miR-363/rno-miR-363	CLL	hsa-miR-147	CLL
mghv-miR-M1-4	ABC	hsa-miR-361-3p	CLL	hsa-miR-487b/mmu- miR-487b/rno-miR- 487b	CLL
hsa-miR-933	ABC	hsa-miR-107/mmu- miR-107/rno-miR-107	CLL	hsa-miR-361- 5p/mmu-miR- 361/rno-miR-361	CLL
hsa-miR-550	CLL	hsa-miR-154/mmu- miR-154/rno-miR-154	CLL	hsa-miR-186/mmu- miR-186/rno-miR- 186	CLL
hsa-miR-30e/mmu-miR- 30e/rno-miR-30e	CLL	hsa-miR-638	CLL	hsa-miR-32/mmu- miR-32/rno-miR-32	CLL
				hsa-miR-129*	CLL
				hsa-miR-30e*/mmu- miR-30e*/rno-miR- 30e*	CLL
				hsa-miR-196a*/mmu- miR-196a*/rno-miR- 196a*	CLL

Table 19: Predictor microRNAs that distinguish activated B-cell (ABC) DLBCL from follicular lymphoma

ABC vs FL	Higher in	ABC vs FL (con't)	Higher in	ABC vs FL (con't)	Higher in
hsa-miR-938	ABC	hsa-miR-518b	FL	hsa-miR-98/mmu-miR-98	FL
hsa-miR-183*/mmu-miR-183*	ABC	hsa-miR-194/mmu-miR-194	FL	hsa-let-7g/mmu-let-7g	FL
hsa-miR-197/mmu-miR-197	ABC	hsa-miR-647	FL	hsa-miR-302a/mmu-miR-302a	FL
hsa-miR-382/mmu-miR-382	ABC	kshv-miR-K12-6-5p	FL	hsa-miR-625*	FL
hsa-miR-20b*	ABC	hsa-miR-622	FL	hsa-miR-30b*	FL
hsa-miR-524-5p	ABC	hsa-miR-516b	FL	hsa-miR-30b/mmu-miR-30b/rno-miR-30b-5p	FL
hsa-miR-337-3p	ABC	hsa-miR-675	FL	hsa-miR-377*	FL
hsa-miR-600	ABC	hsa-miR-526b	FL	hsa-miR-106b*/mmu-miR-106b*/rno-miR-106b*	FL
hsa-miR-96/mmu-miR-96	ABC	hsa-miR-671-5p/mmu-miR-671-5p	FL	hsa-miR-181a-2*	FL
mghev-miR-M1-8	ABC	hsa-miR-18a/mmu-miR-18a/rno-miR-18a	FL	hsa-miR-887	FL
hsa-miR-29c*/mmu-miR-29c*/rno-miR-29c*	ABC	hsa-miR-18b	FL	hsa-miR-208a/mmu-miR-208a/rno-miR-208	FL
hsa-miR-575	ABC	hsa-miR-181b/mmu-miR-181b/rno-miR-181b	FL	ebv-miR-BART7*	FL
hsa-miR-518a-3p	ABC	hsa-miR-215	FL	hsa-miR-7-2*	FL
hsa-miR-361-5p/mmu-miR-361/rno-miR-361	ABC	hsa-miR-153/mmu-miR-153/rno-miR-153	FL	hsa-miR-155*	FL
hsa-miR-193b*	ABC	hsa-miR-625	FL	hsa-miR-513a-3p	FL
hsa-miR-340*/mmu-miR-340-3p/rno-miR-340-3p	ABC	hsa-miR-510	FL	kshv-miR-K12-7	FL
hsa-miR-708/mmu-miR-708/rno-miR-708	ABC	hsa-miR-519d	FL	hsa-miR-299-3p	FL
hsa-miR-129*	ABC	mghev-miR-M1-7-3p	FL	hsa-miR-218-2*/mmu-miR-218-2*/rno-miR-218*	FL
hsa-miR-525-5p	ABC	hsa-miR-485-3p/mmu-miR-485*	FL	hsa-miR-130b*/mmu-miR-130b*	FL
hsa-miR-497/mmu-miR-497/rno-miR-497	FL	hsa-miR-483-5p	FL	hsa-miR-620	FL

ABC vs FL	Higher in	ABC vs FL (con't)	Higher in	ABC vs FL (con't)	Higher in
hsa-miR-22*/mmu-miR-22*/rno-miR-22*	FL	hsa-miR-140-5p/mmu-miR-140/rno-miR-140	FL	hsa-miR-33a/mmu-miR-33/rno-miR-33	FL
hsa-miR-130b/mmu-miR-130b/rno-miR-130b	FL	hsa-miR-921	FL	hsa-miR-7/mmu-miR-7a/rno-miR-7a	FL
hsa-miR-551b*	FL	hsa-miR-186/mmu-miR-186/rno-miR-186	FL	ebv-miR-BART6-3p	FL
hsa-miR-331-3p/mmu-miR-331-3p/rno-miR-331	FL	hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	FL	hsa-miR-22/mmu-miR-22/rno-miR-22	FL
ebv-miR-BART13	FL	hsa-miR-381/mmu-miR-381/rno-miR-381	FL	hsa-miR-199b-5p	FL
hsa-miR-877/mmu-miR-877/rno-miR-877	FL	hsa-miR-620	FL	hsa-miR-768-3p	FL
hsa-miR-636	FL	hsa-miR-152/mmu-miR-152/rno-miR-152	FL	hsa-miR-494/mmu-miR-494/rno-miR-494	FL
hsa-miR-922	FL	hsa-miR-766	FL	hsa-miR-602	FL
hsa-miR-198	FL	mghev-miR-M1-7-5p	FL	hsa-miR-125b-2*/rno-miR-125b*	FL
hsa-miR-342-5p/mmu-miR-342-5p/rno-miR-342-5p	FL	hsa-miR-374b/mmu-miR-374/rno-miR-374	FL	hsa-miR-300	FL
hsa-miR-585	FL	hsa-let-7c/mmu-let-7c/rno-let-7c	FL	hsa-let-7e/mmu-let-7e/rno-let-7e	FL
ebv-miR-BART8*	FL	kshv-miR-K12-8	FL	hsa-miR-298	FL
hsa-miR-617	FL	mghev-miR-M1-3	FL	hsa-miR-576-3p	FL
hsa-miR-221*	FL	hsa-miR-920	FL	hsa-miR-187*	FL
hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	FL	hsa-miR-519e*	FL	hsa-miR-365/mmu-miR-365/rno-miR-365	FL
hsa-miR-93/mmu-miR-93/rno-miR-93	FL	hsa-miR-147	FL	hsa-miR-518a-5p/hsa-miR-527	FL
hsa-miR-363*/rno-miR-363*	FL	hsa-miR-424	FL	hsa-miR-302d*	FL
hsa-miR-744/mmu-miR-744	FL	hsa-miR-193b	FL	hsa-miR-105	FL
hsa-miR-659	FL	ebv-miR-BART19-3p	FL	hsa-miR-126/mmu-miR-126-3p/rno-miR-126	FL
hsa-miR-490-3p/mmu-miR-490	FL	hsa-miR-146b-3p	FL	hsa-miR-107/mmu-miR-107/rno-miR-107	FL
hsa-let-7d/mmu-let-7d/rno-let-7d	FL	hsa-miR-30c/mmu-miR-30c/rno-miR-30c	FL	hsa-miR-299-5p/mmu-miR-299*/rno-miR-299	FL

ABC vs FL	Higher in	ABC vs FL (con't)	Higher in	ABC vs FL (con't)	Higher in
hsa-miR-361-3p		hsa-miR-30a/mmu-miR-30a/rno-miR-30a		hsa-miR-28-3p/rno-miR-28*	
ebv-miR-BHRF1-1	FL	hsa-miR-939	FL	hsa-miR-21/mmu-miR-21/rno-miR-21	FL
hsa-miR-92b/mmu-miR-92b/rno-miR-92b	FL	hsa-let-7a/mmu-let-7a/rno-let-7a	FL	hsa-miR-27b/mmu-miR-27b/rno-miR-27b	FL
hsa-miR-151-5p/mmu-miR-151-5p/rno-miR-151	FL	hsa-miR-122*	FL	hsa-miR-516a-5p	FL
hsa-miR-144*		hsa-miR-206/mmu-miR-206/rno-miR-206		hsa-miR-129-5p/mmu-miR-129-5p/rno-miR-129	FL
hsa-miR-425/mmu-miR-425/rno-miR-425	FL	ebv-miR-BART18-3p	FL	hsa-miR-583	FL
hsa-miR-138/mmu-miR-138/rno-miR-138	FL	hsa-miR-183/mmu-miR-183/rno-miR-183	FL	hsa-miR-483-3p	FL
hsa-miR-92a/mmu-miR-92a/rno-miR-92a	FL	hsa-miR-9*/mmu-miR-9*/rno-miR-9*	FL	hsa-miR-326/mmu-miR-326/rno-miR-326	FL
hsa-miR-151-3p	FL	kshv-miR-K12-1	FL	hsa-miR-548d-5p	FL
hsa-miR-25/mmu-miR-25/rno-miR-25	FL	hsa-miR-34c-5p/mmu-miR-34c/rno-miR-34c	FL	hsa-miR-629	FL
hsa-miR-509-3-5p	FL	hsa-miR-934	FL	ebv-miR-BART5	FL
hsa-miR-30e*/mmu-miR-30e*/rno-miR-30e*	FL	hsa-miR-890	FL	hsa-miR-665	FL
hsa-miR-28-5p/mmu-miR-28/rno-miR-28	FL	hsa-miR-514	FL	hsa-miR-493	FL
hsa-miR-200b*/mmu-miR-200b*	FL	hsa-miR-297/mmu-miR-297a	FL	hsa-miR-484/mmu-miR-484/rno-miR-484	FL
hsa-miR-148b/mmu-miR-148b/rno-miR-148b-3p	FL	hsa-miR-553	FL	hsa-miR-645	FL
hsa-miR-488	FL	hsa-miR-765	FL	hsa-miR-452	FL
hsa-miR-99b/mmu-miR-99b/rno-miR-99b	FL	hsa-let-7b*/mmu-let-7b*/rno-let-7b*	FL	hsa-miR-518c*	FL
hsa-miR-339-5p/mmu-miR-339-5p/rno-miR-339-5p	FL	hsa-miR-500*	FL	hsa-miR-24-2*/mmu-miR-24-2*/rno-miR-24-2*	FL
hsv1-miR-H1	FL	hsa-miR-601	FL	hsa-miR-124/mmu-miR-124/rno-miR-124	FL
hsa-miR-32/mmu-miR-32/rno-miR-32	FL	ebv-miR-BHRF1-3	FL	hsa-miR-184/mmu-miR-184/rno-miR-184	FL
hsa-miR-885-5p	FL	hsa-miR-296-3p/mmu-miR-296-3p/rno-miR-296	FL	hsa-miR-27a*/mmu-miR-27a*/rno-miR-27a*	FL
hsa-miR-630	FL	hsa-miR-574-5p/mmu-miR-574-5p	FL	hsa-miR-25*	FL

ABC vs FL	Higher in	ABC vs FL (con't)	Higher in	ABC vs FL (con't)	Higher in
ebv-miR-BART16		hsa-miR-409-5p/mmu-miR-409-5p/rno-miR-409-5p		hsa-miR-34b/mmu-miR-34b-3p	
hsa-miR-505*	FL	hsa-miR-195*	FL	ebv-miR-BART17-5p	FL
hsa-miR-374b*	FL	hsa-miR-635	FL	hsa-miR-658	FL
hsa-miR-574-3p/mmu-miR-574-3p		hsa-miR-542-3p/mmu-miR-542-3p/rno-miR-542-3p/hcmv-miR-US25-1*		hsa-miR-212/mmu-miR-212/rno-miR-212	
	FL		FL		FL
hsa-miR-874/mmu-miR-874/rno-miR-874	FL		FL	hsa-miR-99a/mmu-miR-99a/rno-miR-99a	FL
hsa-miR-423-3p/mmu-miR-423-3p/rno-miR-423	FL	mg hv-miR-M1-2	FL	hsa-miR-801/mmu-miR-801	FL
hsa-miR-889	FL	hsa-miR-509-5p	FL	hsa-miR-491-3p	FL
hcmv-miR-UL148D		hsa-miR-340/mmu-miR-340-5p/rno-miR-340-5p		hsa-miR-551b/mmu-miR-551b/rno-miR-551b	
	FL		FL		FL
hsa-miR-487b/mmu-miR-487b/rno-miR-487b	FL	hsa-miR-891a	FL	hsa-miR-214/mmu-miR-214/rno-miR-214	FL
hsa-miR-552		hsa-miR-23a/mmu-miR-23a/rno-miR-23a		hsa-miR-30e/mmu-miR-30e/rno-miR-30e	
	FL		FL		FL
hsa-miR-220b		hsa-miR-19b/mmu-miR-19b/rno-miR-19b		hsa-miR-888*	
	FL		FL		FL
hsa-miR-551a	FL	hsa-miR-515-5p	FL	hsa-miR-505/rno-miR-505	FL
hsa-let-7d*/mmu-let-7d*/rno-let-7d*		hsa-miR-23b/mmu-miR-23b/rno-miR-23b		hsa-miR-27a/mmu-miR-27a/rno-miR-27a	
	FL		FL		FL
kshv-miR-K12-5	FL	hsa-miR-498	FL	hsa-miR-15a/mmu-miR-15a	FL
hsa-miR-629*	FL	hsa-miR-886-5p	FL	hsa-miR-20a/mmu-miR-20a/rno-miR-20a	FL
hsa-miR-99b*/mmu-miR-99b*/rno-miR-99b*	FL	hsa-miR-220c	FL	kshv-miR-K12-3	FL
hsa-miR-615-3p/mmu-miR-615-3p		hsa-miR-10a/mmu-miR-10a/rno-miR-10a-5p		hsa-miR-455-3p	
	FL		FL		FL
hsa-miR-657	FL	hsa-miR-32*	FL	hsa-miR-486-5p/mmu-miR-486	FL
hsa-miR-301a/mmu-miR-301a/rno-miR-301a	FL	hsa-miR-24/mmu-miR-24/rno-miR-24	FL		

Table 20: Predictor microRNAs that distinguish activated B-cell (ABC) DLBCL from Hodgkin's lymphoma

ABC vs HL	Higher in	ABC vs HL (con't)	Higher in	ABC vs HL (con't)	Higher in
hsa-miR-19b/mmu-miR-19b/rno-miR-19b	ABC	hsa-miR-934	HL	hsa-miR-488	HL
hsa-miR-30b/mmu-miR-30b/rno-miR-30b-5p	ABC	hsa-miR-328/mmu-miR-328/rno-miR-328	HL	hsa-miR-125a-3p/mmu-miR-125a-3p/rno-miR-125a-3p	HL
hsa-miR-142-3p/mmu-miR-142-3p/rno-miR-142-3p	ABC	hsa-miR-187*	HL	hsa-miR-24-2*/mmu-miR-24-2*/rno-miR-24-2*	HL
hsa-miR-768-3p	ABC	kshv-miR-K12-3	HL	hsa-miR-484/mmu-miR-484/rno-miR-484	HL
hsa-miR-30c/mmu-miR-30c/rno-miR-30c	ABC	hsa-miR-373*	HL	hsa-miR-106b*/mmu-miR-106b*/rno-miR-106b*	HL
hsa-miR-29b/mmu-miR-29b/rno-miR-29b	ABC	hsa-miR-96/mmu-miR-96/rno-miR-96	HL	hsa-miR-600	HL
hsa-miR-24/mmu-miR-24/rno-miR-24	ABC	hsa-miR-186/mmu-miR-186/rno-miR-186	HL	hsa-let-7b*/mmu-let-7b*/rno-let-7b*	HL
hsa-miR-22/mmu-miR-22/rno-miR-22	ABC	hsa-miR-886-5p	HL	hsa-miR-302c*	HL
hsa-miR-30e/mmu-miR-30e/rno-miR-30e	ABC	hsa-miR-424	HL	hsa-miR-20b*	HL
hsa-miR-30a/mmu-miR-30a/rno-miR-30a	ABC	hsa-miR-147	HL	hsa-miR-524-5p	HL
hsa-miR-26b/mmu-miR-26b/rno-miR-26b	ABC	hsa-miR-340/mmu-miR-340-5p/rno-miR-340-5p	HL	hsa-miR-505*	HL
hsa-miR-26a/mmu-miR-26a/rno-miR-26a	ABC	hsa-miR-129-5p/mmu-miR-129-5p/rno-miR-129	HL	hsa-miR-542-5p/mmu-miR-542-5p/rno-miR-542-5p	HL
hsa-miR-15a/mmu-miR-15a	ABC	hsa-miR-25*	HL	hsa-miR-557	HL
hsa-miR-16/mmu-miR-16/rno-miR-16	ABC	hsa-miR-193b	HL	hsa-miR-183/mmu-miR-183/rno-miR-183	HL
hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p	ABC	hsa-miR-574-5p/mmu-miR-574-5p	HL	hsa-miR-122*	HL
hsa-miR-29a/mmu-miR-29a/rno-miR-29a	ABC	hsa-miR-589	HL	hsa-miR-675	HL
hsa-miR-101/mmu-miR-101a/rno-miR-101a	ABC	hsa-miR-339-5p/mmu-miR-339-5p/rno-miR-339-5p	HL	hsv1-miR-H1	HL
hsa-miR-126/mmu-miR-126-3p/rno-miR-126	ABC	hsa-miR-34c-5p/mmu-miR-34c/rno-miR-34c	HL	hsa-miR-99b/mmu-miR-99b/rno-miR-99b	HL

ABC vs HL	Higher in	ABC vs HL (con't)	Higher in	ABC vs HL (con't)	Higher in
hsa-miR-451/mmu-miR-451/rno-miR-451	ABC	hsa-miR-891a	HL	hsa-miR-766	HL
hsa-let-7a/mmu-let-7a/rno-let-7a	ABC	hsa-miR-18a/mmu-miR-18a/rno-miR-18a	HL	hsa-miR-409-5p/mmu-miR-409-5p/rno-miR-409-5p/ebv-miR-BART20-3p	HL
hsa-miR-23b/mmu-miR-23b/rno-miR-23b	ABC	hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	HL	hsa-miR-129*	HL
hsa-miR-21/mmu-miR-21/rno-miR-21	ABC	hsa-miR-17*/rno-miR-17-3p	HL	mghv-miR-M1-7-5p	HL
hsa-miR-29c/mmu-miR-29c/rno-miR-29c	ABC	hsa-miR-296-5p/mmu-miR-296-5p/rno-miR-296*	HL	hsa-miR-671-5p/mmu-miR-671-5p/hsa-miR-629	HL
hsa-miR-20a/mmu-miR-20a/rno-miR-20a	ABC	hsa-miR-25/mmu-miR-25/rno-miR-25	HL	hsa-miR-553	HL
hsa-miR-27b/mmu-miR-27b/rno-miR-27b	ABC	hsa-miR-509-5p	HL	hsa-let-7d*/mmu-let-7d*/rno-let-7d*	HL
hsa-miR-23a/mmu-miR-23a/rno-miR-23a	ABC	hsa-miR-550*	HL	hsa-miR-601	HL
hsa-miR-27a/mmu-miR-27a/rno-miR-27a	ABC	hsa-miR-708/mmu-miR-708/rno-miR-708	HL	hsa-miR-645	HL
hsa-miR-550	ABC	hsa-miR-146b-3p	HL	hsa-miR-221*	HL
hsa-let-7c/mmu-let-7c/rno-let-7c	ABC	hsa-miR-625*	HL	hsa-miR-874/mmu-miR-874/rno-miR-874	HL
hsa-miR-34b/mmu-miR-34b-3p	ABC	hsa-miR-210/mmu-miR-210/rno-miR-210	HL	hsa-miR-890	HL
hsa-miR-933	HL	hsa-miR-93/mmu-miR-93/rno-miR-93	HL	hsa-miR-492	HL
hsa-miR-30c-2*/mmu-miR-30c-2*/rno-miR-30c-2*	HL	hsa-miR-548b-3p	HL	hsa-miR-629*	HL
hsa-miR-503	HL	hsa-miR-652/mmu-miR-652/rno-miR-652	HL	hsa-miR-635	HL
hsa-miR-765	HL	hsa-miR-153/mmu-miR-153/rno-miR-153	HL	hsa-miR-130b/mmu-miR-130b/rno-miR-130b	HL
hsa-miR-658	HL	mghv-miR-M1-3	HL	hsa-miR-197/mmu-miR-197	HL
hsa-miR-620	HL	hsa-miR-194*	HL	hsa-miR-654-5p	HL
hsa-miR-921	HL	hsa-miR-23a*/rno-miR-23a*	HL	hsa-miR-518b	HL
hsa-miR-30b*	HL	hsa-miR-943	HL	hsa-miR-889	HL
mghv-miR-M1-4	HL	hsa-let-7d/mmu-let-7d/rno-let-7d	HL	hsa-miR-584	HL
hsa-miR-939	HL	hsa-miR-498	HL	hsa-miR-198	HL
hsa-miR-494/mmu-miR-494/rno-miR-494	HL	hsa-miR-381/mmu-miR-381/rno-miR-381	HL		
hsa-miR-32*	HL	hsa-miR-586	HL		

ABC vs HL	Higher in	ABC vs HL (con't)	Higher in	ABC vs HL (con't)	Higher in
hsa-miR-491-3p	HL	hsa-miR-137/mmu-miR-137/rno-miR-137	HL	hsa-miR-636	HL
hsa-miR-10a/mmu-miR-10a/rno-miR-10a-5p	HL	hsa-miR-610	HL	hsa-miR-630	HL
hsa-miR-33a/mmu-miR-33/rno-miR-33	HL	hsa-miR-920	HL	hsa-miR-490-5p	HL
hsa-miR-99a/mmu-miR-99a/rno-miR-99a	HL	hsa-miR-936	HL	hsa-miR-663	HL
hsa-miR-199b-5p	HL	hsa-miR-744/mmu-miR-744	HL	hcmv-miR-UL148D	HL
hsa-miR-365/mmu-miR-365/rno-miR-365	HL	ebv-miR-BART5	HL	hsa-miR-337-3p	HL
hsa-miR-520d-5p	HL	hsa-miR-21*	HL	hsa-miR-9*/mmu-miR-9*/rno-miR-9*	HL
hsa-miR-518c*	HL	hsa-miR-516a-5p	HL	hsa-miR-200b*/mmu-miR-200b*	HL
hsa-miR-32/mmu-miR-32/rno-miR-32	HL	hsa-miR-576-5p	HL	ebv-miR-BART9*	HL
hsa-miR-214/mmu-miR-214/rno-miR-214	HL	mghv-miR-M1-6	HL	hsa-miR-342-5p/mmu-miR-342-5p/rno-miR-342-5p	HL
hsa-miR-98/mmu-miR-98/rno-miR-98	HL	hsa-miR-425/mmu-miR-425/rno-miR-425	HL	hsa-miR-206/mmu-miR-206/rno-miR-206	HL
hsa-miR-302d*	HL	hsa-miR-220c	HL	hcmv-miR-US25-1*	HL
hsa-miR-30e*/mmu-miR-30e*/rno-miR-30e*	HL	hsa-miR-10a*/mmu-miR-10a*/rno-miR-10a-3p	HL	hsa-miR-659	HL
hsa-miR-374b/mmu-miR-374/rno-miR-374	HL	hsa-miR-452	HL	hsa-miR-514	HL
hsa-miR-29a*/mmu-miR-29a*/rno-miR-29a*	HL	hsa-miR-345	HL	kshv-miR-K12-6-5p	HL
hsa-miR-532-5p/mmu-miR-532-5p/rno-miR-532-5p	HL	hsa-miR-29c*/mmu-miR-29c*/rno-miR-29c*	HL	hsa-miR-508-5p	HL
hsa-miR-149*	HL	hsa-miR-887	HL	hsa-miR-377*	HL
hsa-miR-422a	HL	hsa-miR-7-2*	HL	ebv-miR-BART16	HL
ebv-miR-BHRF1-2	HL	hsa-miR-363*/rno-miR-363*	HL	hsa-miR-181b/mmu-miR-181b/rno-miR-181b	HL
hsa-miR-634	HL	hsa-miR-22*/mmu-miR-22*/rno-miR-22*	HL	hsa-miR-622	HL
hsa-miR-143*	HL	hsa-miR-922	HL	kshv-miR-K12-1	HL
hsa-miR-620	HL	hsa-miR-92b*	HL	hsa-miR-490-3p/mmu-miR-490	HL
hsa-miR-660	HL	hsa-miR-526a/hsa-miR-520c-5p/hsa-miR-518d-5p	HL	hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	HL

ABC vs HL	Higher in	ABC vs HL (con't)	Higher in	ABC vs HL (con't)	Higher in
hsa-miR-140-5p/mmu-miR-140/rno-miR-140	HL	hsa-miR-574-3p/mmu-miR-574-3p	HL	hsa-miR-124/mmu-miR-124/rno-miR-124	HL
hsa-miR-28-5p/mmu-miR-28/rno-miR-28	HL	hsa-miR-92a/mmu-miR-92a/rno-miR-92a	HL	hsa-miR-657	HL
hsa-miR-519c-5p/hsa-miR-519b-5p/hsa-miR-523*/hsa-miR-518e*/hsa-miR-522*/hsa-miR-519a*	HL	hsa-miR-423-3p/mmu-miR-423-3p/rno-miR-423	HL	ebv-miR-BHRF1-3	HL
hsa-miR-505/rno-miR-505	HL	hsa-miR-526b	HL	kshv-miR-K12-5	HL
hsa-miR-184/mmu-miR-184/rno-miR-184	HL	hsa-miR-526b*	HL	hsa-miR-487b/mmu-miR-487b/rno-miR-487b	HL
hsa-miR-107/mmu-miR-107/rno-miR-107	HL	ebv-miR-BART6-3p	HL	hsa-miR-183*/mmu-miR-183*	HL
hsa-miR-298	HL	hsa-miR-92b/mmu-miR-92b/rno-miR-92b	HL	hsa-miR-297/mmu-miR-297a	HL
hsa-miR-455-3p	HL	hsa-miR-519e*	HL	hsa-miR-885-5p	HL
hsa-miR-638	HL	hiv1-miR-H1	HL	hsa-miR-296-3p/mmu-miR-296-3p/rno-miR-296	HL
hsa-miR-502-3p	HL	hsa-miR-623	HL	ebv-miR-BART19-3p	HL
hsa-miR-149/mmu-miR-149	HL	hsa-miR-483-5p	HL	hsa-miR-617	HL
hsa-miR-583	HL	mghev-miR-M1-2	HL	hsa-miR-519d	HL
hsa-miR-105	HL	mghev-miR-M1-7-3p	HL	hsa-miR-195*	HL
hsa-miR-128/mmu-miR-128/rno-miR-128	HL	hsa-miR-519e	HL	hsa-miR-575	HL
hsa-miR-656	HL	hsa-miR-361-5p/mmu-miR-361/rno-miR-361	HL	hsa-miR-208a/mmu-miR-208a/rno-miR-208	HL
hsa-miR-497/mmu-miR-497/rno-miR-497	HL	hsa-miR-650	HL	hsa-miR-647	HL
hsa-miR-152/mmu-miR-152/rno-miR-152	HL	hsa-miR-361-3p	HL	hsa-miR-525-5p	HL
hsa-miR-151-5p/mmu-miR-151-5p/rno-miR-151	HL	hsa-miR-374b*	HL	ebv-miR-BART8*	HL
hsa-miR-148b/mmu-miR-148b/rno-miR-148b-3p	HL	kshv-miR-K12-8	HL	hsa-miR-340*/mmu-miR-340-3p/rno-miR-340-3p	HL
hsa-miR-300	HL	hsa-miR-150*/mmu-miR-150*	HL	hsa-miR-220b	HL
hsa-miR-144*	HL	hsa-miR-425*/mmu-miR-425*	HL	hsa-miR-382/mmu-miR-382/rno-miR-382	HL
hsa-miR-145*/mmu-miR-145*	HL	hsa-miR-135a*/mmu-miR-135a*	HL	hsa-miR-585	HL

ABC vs HL	Higher in	ABC vs HL (con't)	Higher in	ABC vs HL (con't)	Higher in
hcmv-miR-UL70-3p		hsa-miR-612		hsa-miR-877/mmu-miR-877/rno-miR-877	
hsa-miR-28-3p/rno-miR-28*	HL	hsa-miR-212/mmu-miR-212/rno-miR-212	HL	hsa-miR-99b*/mmu-miR-99b*/rno-miR-99b*	HL
hsa-miR-27a*/mmu-miR-27a*/rno-miR-27a*	HL	hsa-miR-125b-2*/rno-miR-125b*	HL	ebv-miR-BHRF1-1	HL
hsa-miR-194/mmu-miR-194/rno-miR-194	HL	hcmv-miR-UL112	HL	hsa-miR-326/mmu-miR-326/rno-miR-326	HL
hsa-miR-130b*/mmu-miR-130b*	HL	hsa-miR-500	HL	ebv-miR-BART7*	HL
hsa-miR-548d-5p	HL	hsa-miR-502-5p	HL	hsa-miR-615-3p/mmu-miR-615-3p	HL
hsa-miR-937	HL	ebv-miR-BART18-3p	HL	mghv-miR-M1-8	HL
hsa-miR-7/mmu-miR-7a/rno-miR-7a	HL	hsa-miR-625	HL	hsa-miR-193b*	HL
hsa-miR-518a-5p/hsa-miR-527	HL	hsa-miR-138/mmu-miR-138/rno-miR-138	HL	ebv-miR-BART13	HL
hsa-miR-323-3p/mmu-miR-323-3p/rno-miR-323	HL	hsa-miR-500*	HL	hsa-miR-433/mmu-miR-433/rno-miR-433	HL
hsa-miR-215	HL	hsa-miR-124*/mmu-miR-124*/rno-miR-124*	HL	hsa-miR-202	HL
hsa-miR-513a-3p	HL	hsa-miR-516b	HL	hsa-miR-551b*	HL
hsa-miR-595	HL	hsa-miR-30c-1*/mmu-miR-30c-1*/rno-miR-30c-1*	HL	hsa-miR-551a	HL
hsa-miR-515-5p	HL	hsa-miR-331-5p/mmu-miR-331-5p	HL	hsa-miR-542-3p/mmu-miR-542-3p/rno-miR-542-3p	HL
hsa-miR-483-3p	HL	hsa-miR-510	HL	hsa-miR-338-5p/mmu-miR-338-5p/rno-miR-338*	HL
hsa-miR-330-5p/mmu-miR-330/rno-miR-330	HL	hsa-miR-376a*	HL	hsa-miR-299-3p	HL
hsa-miR-18b	HL	hsa-miR-640	HL	hsa-miR-518a-3p	HL
hsa-miR-509-3p	HL	hsa-miR-331-3p/mmu-miR-331-3p/rno-miR-331	HL	hsa-miR-181a-2*	HL
hsa-miR-151-3p	HL	hsa-miR-602	HL	hsa-miR-938	HL
		hsa-miR-485-3p/mmu-miR-485*	HL	hsa-miR-509-3-5p	HL
				hsa-miR-552	HL

Table 21: Predictor microRNAs that distinguish germinal center B-cell like (GCB) DLBCL from Burkitt lymphoma

GCBvsBL	Higher in	GCB vs BL (con't)	Higher in
hsa-miR-129*		hsa-miR-140-3p/mmu-miR-140*/rno-miR-140*	GCB
hsa-miR-28-5p/mmu-miR-28/rno-miR-28	GCB	hsa-miR-148a/mmu-miR-148a	GCB
hsa-miR-155	GCB	hsa-miR-365/mmu-miR-365/rno-miR-365	GCB
hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	GCB	hsa-miR-29c/mmu-miR-29c/rno-miR-29c	GCB
hsa-miR-146a/mmu-miR-146a/rno-miR-146a	GCB	hsa-miR-30d/mmu-miR-30d/rno-miR-30d	GCB
hsa-miR-331-3p/mmu-miR-331-3p/rno-miR-331	GCB	hsa-miR-214/mmu-miR-214/rno-miR-214	GCB
hsa-miR-215	GCB	hsa-miR-146b-5p/mmu-miR-146b/rno-miR-146b	GCB
hsa-miR-600	GCB	hsa-miR-342-3p/mmu-miR-342-3p/rno-miR-342-3p	GCB
mghev-miR-M1-7-3p	GCB	hsa-miR-374a	GCB
hsa-miR-107/mmu-miR-107/rno-miR-107	GCB	hsa-miR-223/mmu-miR-223/rno-miR-223	GCB
hsa-miR-886-3p	GCB	hsa-miR-29b/mmu-miR-29b/rno-miR-29b	GCB
hsa-miR-140-5p/mmu-miR-140/rno-miR-140	GCB	hsa-miR-21/mmu-miR-21/rno-miR-21	GCB
hsa-miR-154/mmu-miR-154/rno-miR-154	GCB	hsa-miR-29a/mmu-miR-29a/rno-miR-29a	GCB
hsa-miR-103/mmu-miR-103/rno-miR-103	GCB	hsa-miR-23b/mmu-miR-23b/rno-miR-23b	GCB
hsa-let-7g/mmu-let-7g	GCB	hsa-miR-24/mmu-miR-24/rno-miR-24	GCB
hsa-miR-222/mmu-miR-222/rno-miR-222	GCB	hsa-miR-26a/mmu-miR-26a/rno-miR-26a	GCB
hsa-miR-221/mmu-miR-221/rno-miR-221	GCB	hsa-miR-26b/mmu-miR-26b/rno-miR-26b	GCB
hsa-miR-320/mmu-miR-320/rno-miR-320	GCB	hsa-miR-34b/mmu-miR-34b-3p	GCB
		hsa-miR-503	BL
		hsa-miR-30b*	BL

Table 22: Predictor microRNAs that distinguish germinal center B-cell like (GCB) DLBCL from chronic lymphocytic leukemia

GCB vs CLL	Higher in	GCB vs CLL (con't)	Higher in	GCB vs CLL (con't)	Higher in
hsa-miR-181a/mmu-miR-181a/rno-miR-181a	GCB	hsa-miR-100/mmu-miR-100/rno-miR-100	GCB	hsa-miR-374a	CLL
hsa-miR-886-5p	GCB	hsa-miR-371-5p	GCB	hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p	CLL
mghv-miR-M1-7-3p	GCB	hsa-miR-193a-5p	GCB	hsa-miR-29c/mmu-miR-29c/rno-miR-29c	CLL
hsa-miR-934	GCB	hsa-miR-628-3p	GCB	hsa-miR-140-3p/mmu-miR-140*/rno-miR-140*	CLL
mghv-miR-M1-3	GCB	hsa-miR-185*	GCB	hsa-miR-30e/mmu-miR-30e/rno-miR-30e	CLL
hsa-miR-485-3p/mmu-miR-485*	GCB	hsa-miR-10b/mmu-miR-10b/rno-miR-10b	GCB	hsa-miR-801/mmu-miR-801	CLL
hsa-miR-125b/mmu-miR-125b-5p/rno-miR-125b-5p	GCB	hsa-miR-665	GCB	hsa-miR-768-3p	CLL
hsa-miR-637	GCB	hsa-miR-503	GCB	hsa-miR-549	CLL
hsa-miR-365/mmu-miR-365/rno-miR-365	GCB	hsa-miR-642	GCB	hsa-miR-199a-5p/mmu-miR-199a-5p/rno-miR-199a-5p	CLL
hsa-miR-505*	GCB	hsa-miR-658	GCB	hsa-miR-223/mmu-miR-223/rno-miR-223	CLL
hsa-miR-199a-3p/hsa-miR-199b-3p/mmu-miR-199a-3p/mmu-miR-199b/rno-miR-199a-3p	GCB	hsa-miR-21/mmu-miR-21/rno-miR-21	GCB	hsa-miR-101/mmu-miR-101a/rno-miR-101a	CLL
hsa-miR-675	GCB	hsa-miR-23a/mmu-miR-23a/rno-miR-23a	GCB	hsa-miR-888*	CLL
hsa-miR-424	GCB	hsa-miR-125a-5p/mmu-miR-125a-5p/rno-miR-125a-5p	GCB	hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	CLL
ebv-miR-BHRF1-2	GCB	hsa-miR-24/mmu-miR-24/rno-miR-24	GCB	hsa-miR-519d	CLL
hsa-miR-519c-5p/hsa-miR-519b-5p/hsa-miR-523*/hsa-miR-518e*/hsa-miR-522*/hsa-miR-519a*	GCB	hsa-miR-23b/mmu-miR-23b/rno-miR-23b	GCB	hsa-miR-154/mmu-miR-154/rno-miR-154	CLL

GCB vs CLL	Higher in	GCB vs CLL (con't)	Higher in	GCB vs CLL (con't)	Higher in
hsa-miR-130a/mmu-miR-130a/rno-miR-130a	GCB	hsa-miR-620	GCB	hsa-miR-638	CLL
hsa-miR-943	GCB	hsa-miR-933	GCB	hsa-miR-668/mmu-miR-668	CLL
hsa-miR-126/mmu-miR-126-3p/rno-miR-126	GCB	hsa-miR-30b*	GCB	hsa-miR-891a	CLL
hsa-miR-193b	GCB	hsa-miR-22/mmu-miR-22/rno-miR-22	GCB	hsa-miR-768-5p	CLL
hsa-miR-198	GCB	hsa-let-7e/mmu-let-7e/rno-let-7e	GCB	hsa-miR-140-5p/mmu-miR-140/rno-miR-140	CLL
hsa-miR-200b*/mmu-miR-200b*	GCB	mghev-miR-M1-4	GCB	hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	CLL
kshv-miR-K12-6-3p	GCB	hsa-miR-149*	GCB	hsa-miR-150/mmu-miR-150/rno-miR-150	CLL
hsa-miR-220c	GCB	hsa-miR-765	GCB	hsa-let-7g/mmu-let-7g	CLL
hsa-miR-374b*	GCB	hsa-let-7c/mmu-let-7c/rno-let-7c	GCB	hsa-miR-363/mmu-miR-363/rno-miR-363	CLL
hsa-miR-518b	GCB	hsa-miR-423-5p/mmu-miR-423-5p	CLL	hsa-miR-486-5p/mmu-miR-486	CLL
hsa-miR-920	GCB	hsa-miR-32*	CLL	hsa-miR-32/mmu-miR-32/rno-miR-32	CLL
hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	GCB	hsa-miR-34b/mmu-miR-34b-3p	CLL	hsa-miR-147	CLL
ebv-miR-BART8*	GCB	hsa-miR-551b/mmu-miR-551b/rno-miR-551b	CLL	hsa-miR-20b*	CLL
ebv-miR-BART16	GCB	hsa-let-7i/mmu-let-7i/rno-let-7i	CLL	hsa-miR-487b/mmu-miR-487b/rno-miR-487b	CLL
hsa-miR-630	GCB	hsa-miR-29a/mmu-miR-29a/rno-miR-29a	CLL	hsa-miR-636	CLL
hsa-miR-483-5p	GCB	hsa-miR-138-1*/mmu-miR-138*/rno-miR-138*	CLL	hsa-miR-144*	CLL
hsa-miR-422a	GCB	hsa-miR-29b/mmu-miR-29b/rno-miR-29b	CLL	hsa-miR-186/mmu-miR-186/rno-miR-186	CLL
hsa-miR-526b	GCB	hsa-miR-191/mmu-miR-191/rno-miR-191	CLL	hsa-miR-30e*/mmu-miR-30e*/rno-miR-30e*	CLL
hsa-miR-145/mmu-miR-145/rno-miR-145	GCB	hsa-miR-26b/mmu-miR-26b/rno-miR-26b	CLL	hsa-miR-331-5p/mmu-miR-331-5p	CLL
hsa-miR-126*/mmu-miR-126-5p/rno-miR-126*	GCB	hsa-miR-26a/mmu-miR-26a/rno-miR-26a	CLL		

GCB vs CLL	Higher in	GCB vs CLL (con't)	Higher in	GCB vs CLL (con't)	Higher in
hsa-miR-143/mmu-miR-143/rno-miR-143	GCB	hsa-miR-550	CLL		

Table 23: Predictor microRNAs that distinguish germinal center B-cell like (GCB) DLBCL from follicular lymphoma

GCB vs FL	Higher in	GCB vs FL (con't)	Higher in	GCB vs FL (con't)	Higher in
hsa-miR-378/mmu-miR-378/rno-miR-378	GCB	hcmv-miR-UL148D	FL	hsa-miR-425/mmu-miR-425/rno-miR-425	FL
hsa-miR-20b/mmu-miR-20b/rno-miR-20b-5p	GCB	hsa-miR-497/mmu-miR-497/rno-miR-497	FL	hsa-miR-99b*/mmu-miR-99b*/rno-miR-99b*	FL
hsa-miR-19b/mmu-miR-19b/rno-miR-19b	GCB	ebv-miR-BART13	FL	hsa-miR-513a-3p	FL
hsa-miR-106a	GCB	ebv-miR-BART16	FL	hsa-miR-206/mmu-miR-206/rno-miR-206	FL
hsa-miR-17/mmu-miR-17/rno-miR-17-5p/rno-miR-17	GCB	hsa-miR-125b-2*/rno-miR-125b*	FL	hsa-miR-155*	FL
hsa-miR-93/mmu-miR-93/rno-miR-93	GCB	hsa-miR-490-3p/mmu-miR-490	FL	hsa-miR-181b/mmu-miR-181b/rno-miR-181b	FL
hsa-miR-20a/mmu-miR-20a/rno-miR-20a	GCB	hsa-miR-99b/mmu-miR-99b/rno-miR-99b	FL	hsa-miR-299-3p	FL
hsa-miR-23b/mmu-miR-23b/rno-miR-23b	GCB	hsa-miR-339-5p/mmu-miR-339-5p/rno-miR-339-5p	FL	hsa-miR-218-2*/mmu-miR-218-2*/rno-miR-218*	FL
hsa-miR-23a/mmu-miR-23a/rno-miR-23a	GCB	hsa-miR-574-3p/mmu-miR-574-3p	FL	mghv-miR-M1-8	FL
hsa-miR-22/mmu-miR-22/rno-miR-22	GCB	hsa-miR-515-5p	FL	ebv-miR-BART18-3p	FL
hsa-miR-19a/mmu-miR-19a/rno-miR-19a	GCB	hsa-miR-877/mmu-miR-877/rno-miR-877	FL	hsa-miR-708/mmu-miR-708/rno-miR-708	FL
hsa-miR-320/mmu-miR-320/rno-miR-320	GCB	hsa-miR-208a/mmu-miR-208a/rno-miR-208	FL	hsa-miR-409-5p/mmu-miR-409-5p/rno-miR-409-5p	FL
hsa-miR-106b/mmu-miR-106b/rno-miR-106b	GCB	hcmv-miR-US25-1*	FL	hsa-miR-553	FL
hsa-miR-103/mmu-miR-103/rno-miR-103	GCB	hsa-miR-326/mmu-miR-326/rno-miR-326	FL	hsa-miR-361-3p	FL
hsa-miR-30c/mmu-miR-30c/rno-miR-30c	GCB	hsa-miR-488	FL	hsa-miR-296-3p/mmu-miR-296-3p/rno-miR-296	FL
ebv-miR-BHRF1-2	GCB	hsa-miR-629	FL	ebv-miR-BHRF1-3	FL

GCB vs FL	Higher in	GCB vs FL (con't)	Higher in	GCB vs FL (con't)	Higher in
hsa-miR-125a-5p/mmu-miR-125a-5p/rno-miR-125a-5p	GCB	hsa-miR-24-2*/mmu-miR-24-2*/rno-miR-24-2*	FL	hsa-miR-34c-5p/mmu-miR-34c/rno-miR-34c	FL
hsa-let-7a/mmu-let-7a/rno-let-7a	GCB	hsa-miR-124/mmu-miR-124/rno-miR-124	FL	hsa-let-7b*/mmu-let-7b*/rno-let-7b*	FL
hsa-miR-628-3p	GCB	hsa-miR-493	FL	hsa-miR-301a/mmu-miR-301a/rno-miR-301a	FL
hsa-let-7c/mmu-let-7c/rno-let-7c	GCB	hsv1-miR-H1	FL	hsa-miR-122*	FL
hsa-miR-423-5p/mmu-miR-423-5p	FL	hsa-miR-484/mmu-miR-484/rno-miR-484	FL	hsa-miR-183/mmu-miR-183/rno-miR-183	FL
hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	FL	hsa-miR-483-3p	FL	kshv-miR-K12-5	FL
ebv-miR-BART2-3p	FL	hsa-miR-27a*/mmu-miR-27a*/rno-miR-27a*	FL	hsa-miR-552	FL
hsa-miR-138-1*/mmu-miR-138*/rno-miR-138*	FL	hsa-miR-144*	FL	hsa-miR-151-3p	FL
hsa-miR-768-5p	FL	hsa-miR-617	FL	hsa-miR-194/mmu-miR-194/rno-miR-194	FL
hsa-miR-30b*	FL	hsa-miR-377*	FL	hsa-miR-585	FL
hsa-miR-494/mmu-miR-494/rno-miR-494	FL	hsa-miR-363*/rno-miR-363*	FL	hsa-miR-340*/mmu-miR-340-3p/rno-miR-340-3p	FL
hsa-miR-583	FL	hsa-miR-148b/mmu-miR-148b/rno-miR-148b-3p	FL	hsa-let-7d*/mmu-let-7d*/rno-let-7d*	FL
hsa-miR-185/mmu-miR-185/rno-miR-185	FL	kshv-miR-K12-1	FL	hsa-miR-622	FL
hsa-miR-765	FL	hsa-miR-7/mmu-miR-7a/rno-miR-7a	FL	hsa-miR-575	FL
hsa-miR-34b/mmu-miR-34b-3p	FL	hsa-miR-193b*	FL	hsa-miR-514	FL
hsa-miR-921	FL	hsa-miR-542-3p/mmu-miR-542-3p/rno-miR-542-3p	FL	hsa-miR-92b/mmu-miR-92b/rno-miR-92b	FL
hsa-miR-551b/mmu-miR-551b/rno-miR-551b	FL	hsa-miR-601	FL	hsa-miR-551a	FL
hsa-miR-549	FL	hsa-miR-106b*/mmu-miR-106b*/rno-miR-106b*	FL	hsa-miR-221*	FL
hsa-miR-939	FL	hsa-miR-7-2*	FL	hsa-miR-922	FL
hsa-miR-302d*	FL	kshv-miR-K12-6-5p	FL	hsa-miR-938	FL
ebv-miR-BART17-5p	FL	hsa-miR-645	FL	hsa-miR-615-3p/mmu-miR-615-3p	FL
hsa-miR-801/mmu-miR-801	FL	hsa-miR-524-5p	FL	hsa-miR-220b	FL
hsa-miR-888*	FL	hsa-miR-548d-5p	FL		

GCB vs FL	Higher in	GCB vs FL (con't)	Higher in	GCB vs FL (con't)	Higher in
hsa-miR-620	FL	hsa-miR-9*/mmu-miR-9*/rno-miR-9*	FL	hsa-miR-744/mmu-miR-744	FL
hsa-miR-576-3p	FL	hsa-miR-92a/mmu-miR-92a/rno-miR-92a	FL	hsa-miR-657	FL
hsa-miR-32*	FL	hsa-miR-22*/mmu-miR-22*/rno-miR-22*	FL	hsa-miR-382/mmu-miR-382/rno-miR-382	FL
hsa-miR-574-5p/mmu-miR-574-5p	FL	hsa-miR-500*	FL	hsa-miR-518a-3p	FL
hsa-miR-505/rno-miR-505	FL	hsa-miR-890	FL	hsa-miR-138/mmu-miR-138/rno-miR-138	FL
hsa-miR-885-5p	FL	hsa-miR-297/mmu-miR-297a	FL	hsa-miR-636	FL
hsa-miR-455-3p	FL	hsa-miR-197/mmu-miR-197	FL	hsa-miR-96/mmu-miR-96/rno-miR-96	FL
hsa-miR-152/mmu-miR-152/rno-miR-152	FL	hsa-miR-20b*	FL	hsa-miR-509-3-5p	FL
hsa-miR-200b*/mmu-miR-200b*	FL	hsa-miR-629*	FL	hsa-miR-337-3p	FL
mghev-miR-M1-2	FL	hsa-miR-887	FL	hsa-miR-342-5p/mmu-miR-342-5p/rno-miR-342-5p	FL

Table 24: Predictor microRNAs that distinguish germinal center B-cell like (GCB) DLBCL from Hodgkin's lymphoma

GCB vs HL	Higher in	GCB vs HL (con't)	Higher in	GCB vs HL (con't)	Higher in
hsa-miR-19b/mmu-miR-19b/rno-miR-19b	GCB	hsa-miR-130b/mmu-miR-130b/rno-miR-130b	HL	hsa-miR-744/mmu-miR-744	HL
hsa-miR-19a/mmu-miR-19a/rno-miR-19a	GCB	hsa-miR-671-5p/mmu-miR-671-5p	HL	kshv-miR-K12-6-5p	HL
hsa-miR-106a	GCB	hsa-miR-525-5p	HL	hcmv-miR-US25-1*	HL
hsa-miR-20b/mmu-miR-20b/rno-miR-20b-5p	GCB	hsa-miR-505/rno-miR-505	HL	hsa-miR-21*	HL
hsa-miR-17/mmu-miR-17/rno-miR-17-5p/rno-miR-17	GCB	hsa-miR-488	HL	mghev-miR-M1-6	HL
hsa-miR-15b/mmu-miR-15b/rno-miR-15b	GCB	hsa-miR-766	HL	mghev-miR-M1-8	HL
hsa-miR-20a/mmu-miR-20a/rno-miR-20a	GCB	hsa-miR-20b*	HL	hsa-miR-10a*/mmu-miR-10a*/rno-miR-10a-3p	HL
hsa-miR-30b/mmu-miR-30b/rno-miR-30b-5p	GCB	hsa-miR-339-5p/mmu-miR-339-5p/rno-miR-339-5p	HL	hsa-miR-345	HL
hsa-miR-142-3p/mmu-miR-142-3p/rno-miR-142-3p	GCB	hsa-miR-524-5p	HL	hsa-miR-887	HL

GCB vs HL	Higher in	GCB vs HL (con't)	Higher in	GCB vs HL (con't)	Higher in
hsa-miR-30c/mmu-miR-30c	GCB	hsa-miR-455-3p	HL	hsa-miR-193b*	HL
hsa-miR-378/mmu-miR-378	GCB	hsa-miR-92a/mmu-miR-92a	HL	hsa-miR-122*	HL
hsa-miR-93/mmu-miR-93	GCB	hsa-miR-502-3p	HL	kshv-miR-K12-5	HL
hsa-miR-106b/mmu-miR-106b	GCB	hsa-miR-210/mmu-miR-210	HL	hsa-miR-92b*	HL
hsa-miR-374a	GCB	hsv1-miR-H1	HL	hsa-miR-526b*	HL
hsa-miR-24/mmu-miR-24	GCB	ebv-miR-BART6-3p	HL	hsa-miR-553	HL
hsa-miR-29b/mmu-miR-29b	GCB	hsa-miR-490-3p/mmu-miR-490	HL	hsa-miR-601	HL
hsa-miR-22/mmu-miR-22	GCB	hsa-miR-149/mmu-miR-149	HL	hiv1-miR-H1	HL
hsa-miR-142-5p/mmu-miR-142-5p	GCB	hsa-miR-128/mmu-miR-128	HL	hsa-miR-623	HL
hsa-miR-30e/mmu-miR-30e	GCB	hsa-miR-635	HL	hsa-miR-519e	HL
hsa-miR-30a/mmu-miR-30a	GCB	hcmv-miR-UL148D	HL	hsa-miR-650	HL
hsa-miR-30d/mmu-miR-30d	GCB	hsa-miR-373*	HL	hsa-miR-575	HL
hsa-miR-23b/mmu-miR-23b	GCB	hsa-miR-647	HL	hsa-miR-629*	HL
hsa-miR-16/mmu-miR-16	GCB	hsa-miR-197/mmu-miR-197	HL	hsa-miR-890	HL
hsa-miR-191/mmu-miR-191	GCB	hsa-miR-602	HL	hsa-miR-150*/mmu-miR-150*	HL
hsa-miR-15a/mmu-miR-15a	GCB	hsa-miR-656	HL	hsa-miR-425*/mmu-miR-425*	HL
hsa-miR-26b/mmu-miR-26b	GCB	hsa-miR-874/mmu-miR-874	HL	hsa-miR-135a*/mmu-miR-135a*	HL
hsa-miR-23a/mmu-miR-23a	GCB	ebv-miR-BART19-3p	HL	hsa-miR-612	HL
hsa-let-7a/mmu-let-7a/rno-let-7a	GCB	hsa-miR-551b*	HL	hsa-miR-636	HL
hsa-miR-103/mmu-miR-103	GCB	hsa-miR-96/mmu-miR-96	HL	hsa-miR-500	HL
hsa-miR-140-3p/mmu-miR-140*/rno-miR-140*	GCB	hsa-miR-889	HL	hsa-miR-502-5p	HL
hsa-miR-154/mmu-miR-154	GCB	hsa-miR-425/mmu-miR-425	HL	hsa-miR-9*/mmu-miR-9*/rno-miR-9*	HL
hsa-miR-320/mmu-miR-320	GCB	hsa-miR-34c-5p/mmu-miR-34c/rno-miR-34c	HL	hsa-miR-500*	HL

GCB vs HL	Higher in	GCB vs HL (con't)	Higher in	GCB vs HL (con't)	Higher in
hsa-miR-550		hcmv-miR-UL70-3p		hsa-miR-124*/mmu-miR-124*/rno-miR-124*	HL
hsa-miR-125a-5p/mmu-miR-125a-5p/rno-miR-125a-5p	GCB	hsa-miR-27a*/mmu-miR-27a*/rno-miR-27a*	HL	hsa-miR-30c-1*/mmu-miR-30c-1*/rno-miR-30c-1*	HL
hsa-let-7c/mmu-let-7c/rno-let-7c	GCB	hsa-miR-194/mmu-miR-194/rno-miR-194	HL	hsa-miR-99b*/mmu-miR-99b*/rno-miR-99b*	HL
hsa-miR-185/mmu-miR-185/rno-miR-185	GCB	hsa-miR-17*/rno-miR-17-3p	HL	hsa-miR-331-5p/mmu-miR-331-5p	HL
hsa-miR-658	HL	hsa-miR-548d-5p	HL	hsa-miR-206/mmu-miR-206/rno-miR-206	HL
hsa-miR-549	HL	hsa-miR-7/mmu-miR-7a/rno-miR-7a	HL	hsa-miR-376a*	HL
hsa-miR-634	HL	hsa-miR-877/mmu-miR-877/rno-miR-877	HL	hsa-miR-585	HL
hsa-miR-551b/mmu-miR-551b/rno-miR-551b	HL	hsa-miR-22*/mmu-miR-22*/rno-miR-22*	HL	hsa-miR-640	HL
hsa-miR-518c*	HL	hsa-miR-323-3p/mmu-miR-323-3p/rno-miR-323	HL	hsa-miR-377*	HL
hsa-miR-888*	HL	hsa-miR-708/mmu-miR-708/rno-miR-708	HL	hsa-miR-125a-3p/mmu-miR-125a-3p/rno-miR-125a-3p	HL
hsa-miR-765	HL	hsa-miR-513a-3p	HL	hsa-miR-24-2*/mmu-miR-24-2*/rno-miR-24-2*	HL
hsa-miR-423-5p/mmu-miR-423-5p	HL	hsa-miR-595	HL	hsa-miR-484/mmu-miR-484/rno-miR-484	HL
hsa-miR-30c-2*/mmu-miR-30c-2*/rno-miR-30c-2*	HL	hsa-miR-922	HL	hsa-miR-106b*/mmu-miR-106b*/rno-miR-106b*	HL
hsa-miR-503	HL	hsa-miR-515-5p	HL	hsa-let-7b*/mmu-let-7b*/rno-let-7b*	HL
hsa-miR-921	HL	hsa-miR-99b/mmu-miR-99b/rno-miR-99b	HL	hsa-miR-302c*	HL
hsa-miR-520d-5p	HL	hsa-miR-483-3p	HL	hsa-miR-542-5p/mmu-miR-542-5p/rno-miR-542-5p	HL
hsa-miR-574-5p/mmu-miR-574-5p	HL	hsa-miR-330-5p/mmu-miR-330/rno-miR-330	HL	hsa-miR-622	HL
hsa-miR-32*	HL	hsa-miR-509-3p	HL	ebv-miR-BHRF1-3	HL
hsa-miR-939	HL	hsa-miR-151-3p	HL	hsa-miR-181a-2*	HL

GCB vs HL	Higher in	GCB vs HL (con't)	Higher in	GCB vs HL (con't)	Higher in
ebv-miR-BART2-3p		ebv-miR-BART13		hsa-miR-183/mmu-miR-183/rno-miR-183	
ebv-miR-BHRF1-2	HL	hsa-miR-617	HL	hsa-miR-409-5p/mmu-miR-409-5p/rno-miR-409-5p	HL
hsa-miR-583	HL	hsa-miR-328/mmu-miR-328/rno-miR-328	HL	ebv-miR-BART20-3p	HL
hsa-miR-30b*	HL	hsa-miR-361-3p	HL	hsa-miR-629	HL
hsa-miR-149*	HL	hsa-miR-138/mmu-miR-138/rno-miR-138	HL	hsa-let-7d*/mmu-let-7d*/rno-let-7d*	HL
mghev-miR-M1-4	HL	ebv-miR-BART7*	HL	hsa-miR-645	HL
hsa-miR-513a-5p	HL	hsa-miR-589	HL	hsa-miR-492	HL
hsa-miR-494/mmu-miR-494/rno-miR-494	HL	hsa-miR-576-5p	HL	hsa-miR-654-5p	HL
hsa-miR-498		hsa-miR-452		hsa-miR-208a/mmu-miR-208a/rno-miR-208	HL
hsa-miR-485-3p/mmu-miR-485*	HL	hsa-miR-7-2*	HL	hsa-miR-584	HL
hsa-miR-129-5p/mmu-miR-129-5p/rno-miR-129	HL	hsa-miR-296-5p/mmu-miR-296-5p/rno-miR-296*	HL	hsa-miR-382/mmu-miR-382/rno-miR-382	HL
hsa-miR-25*		hsa-miR-550*		hsa-miR-340*/mmu-miR-340-3p/rno-miR-340-3p	HL
hsa-miR-923	HL	hsa-miR-92b/mmu-miR-92b/rno-miR-92b	HL	hsa-miR-490-5p	HL
hsa-miR-519d	HL	kshv-miR-K12-1	HL	hsa-miR-663	HL
hsa-miR-516a-5p	HL	hsa-miR-526a/hsa-miR-520c-5p/hsa-miR-518d-5p	HL	hsa-miR-337-3p	HL
hsa-miR-99a/mmu-miR-99a/rno-miR-99a	HL	mghev-miR-M1-2	HL	hsa-miR-518a-3p	HL
hsa-miR-943	HL	hsa-miR-548b-3p	HL	ebv-miR-BART9*	HL
hsa-miR-885-5p	HL	hsa-miR-297/mmu-miR-297a	HL	hsa-miR-342-5p/mmu-miR-342-5p/rno-miR-342-5p	HL
ebv-miR-BHRF1-1	HL	hsa-miR-195*	HL	hsa-miR-514	HL
hsa-miR-152/mmu-miR-152/rno-miR-152	HL	hsa-miR-652/mmu-miR-652/rno-miR-652	HL	hsa-miR-508-5p	HL
ebv-miR-BART8*		hsa-miR-221*		hsa-miR-124/mmu-miR-124/rno-miR-124	HL
hsa-miR-200b*/mmu-miR-200b*	HL	hsa-miR-194*	HL	hsa-miR-657	HL

GCB vs HL	Higher in	GCB vs HL (con't)	Higher in	GCB vs HL (con't)	Higher in
hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	HL	hsa-miR-23a*/rno-miR-23a*	HL	hsa-miR-938	HL
hsa-miR-526b	HL	hsa-miR-125b-2*/rno-miR-125b*	HL	hsa-miR-296-3p/mmu-miR-296-3p/rno-miR-296	HL
hsa-miR-29a*/mmu-miR-29a*/rno-miR-29a*	HL	hsa-miR-212/mmu-miR-212/rno-miR-212	HL	hsa-miR-551a	HL
hsa-miR-532-5p/mmu-miR-532-5p/rno-miR-532-5p	HL	ebv-miR-BART18-3p	HL	hsa-miR-542-3p/mmu-miR-542-3p/rno-miR-542-3p	HL
hsa-miR-183*/mmu-miR-183*	HL	hsa-miR-586	HL	hsa-miR-220b	HL
hsa-miR-659	HL	hsa-miR-137/mmu-miR-137/rno-miR-137	HL	hsa-miR-326/mmu-miR-326/rno-miR-326	HL
hsa-miR-145*/mmu-miR-145*	HL	hsa-miR-610	HL	hsa-miR-615-3p/mmu-miR-615-3p	HL
mghev-miR-M1-7-5p	HL	hcmv-miR-UL112	HL	hsa-miR-433/mmu-miR-433/rno-miR-433	HL
hsa-miR-143*	HL	hsa-miR-181b/mmu-miR-181b/rno-miR-181b	HL	hsa-miR-202	HL
hsa-miR-660	HL	hsa-miR-936	HL	hsa-miR-338-5p/mmu-miR-338-5p/rno-miR-338*	HL
				hsa-miR-552	HL
				hsa-miR-299-3p	HL
				hsa-miR-509-3-5p	HL

Table 25: Predictor microRNAs that distinguish Burkitt lymphoma from chronic lymphocytic leukemia

BL vs CLL	Higher in	BL vs CLL (con't)	Higher in	BL vs CLL (con't)	Higher in
hsa-miR-874/mmu-miR-874/rno-miR-874	BL	hsa-miR-30b/mmu-miR-30b/rno-miR-30b-5p	CLL	hsa-miR-361-5p/mmu-miR-361/rno-miR-361	CLL
hsa-miR-125b/mmu-miR-125b-5p/rno-miR-125b-5p	BL	hsa-miR-34b/mmu-miR-34b-3p	CLL	hsa-miR-29c/mmu-miR-29c/rno-miR-29c	CLL
hsa-miR-126/mmu-miR-126-3p/rno-miR-126	BL	hsa-miR-801/mmu-miR-801	CLL	hsa-miR-147	CLL
ebv-miR-BHRF1-2	BL	hsa-miR-26b/mmu-miR-26b/rno-miR-26b	CLL	hsa-miR-361-3p	CLL

BL vs CLL	Higher in	BL vs CLL (con't)	Higher in	BL vs CLL (con't)	Higher in
hsa-miR-193b		hsa-let-7b/mmu-let-7b/rno-let-7b		hsa-miR-140-3p/mmu-miR-140*/rno-miR-140*	
	BL		CLL		CLL
hsa-miR-371-5p		hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p		hsa-miR-486-5p/mmu-miR-486	
	BL		CLL		CLL
hsa-miR-193a-5p		hsa-miR-26a/mmu-miR-26a/rno-miR-26a		hsa-miR-33a/mmu-miR-33/rno-miR-33	
	BL		CLL	hsa-miR-636	CLL
hsa-miR-628-3p		hsa-miR-29a/mmu-miR-29a/rno-miR-29a			CLL
	BL		CLL		CLL
hsa-miR-185*		hsa-miR-768-3p		hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	
	BL		CLL		CLL
hsa-miR-503		hsa-miR-199a-5p/mmu-miR-199a-5p/rno-miR-199a-5p		hsa-miR-144*	
	BL		CLL		CLL
hsa-miR-199a-3p/hsa-miR-199b-3p/mmu-miR-199a-3p/mmu-miR-199b/rno-miR-199a-3p		hsa-miR-30e/mmu-miR-30e/rno-miR-30e		hsa-miR-668/mmu-miR-668	
	BL		CLL		CLL
hsa-miR-143/mmu-miR-143/rno-miR-143		hsa-miR-29b/mmu-miR-29b/rno-miR-29b		hsa-miR-768-5p	
	BL		CLL		CLL
hsa-miR-130a/mmu-miR-130a/rno-miR-130a		hsa-miR-101/mmu-miR-101a/rno-miR-101a		hsa-miR-363/mmu-miR-363/rno-miR-363	
	BL		CLL		CLL
hsa-miR-145/mmu-miR-145/rno-miR-145		hsa-miR-138-1*/mmu-miR-138*/rno-miR-138*		hsa-miR-150/mmu-miR-150/rno-miR-150	
	BL		CLL	hsa-miR-519d	CLL
hsa-miR-30b*		hsa-miR-195/mmu-miR-195/rno-miR-195			CLL
	BL		CLL		CLL
hsa-miR-665		hsa-miR-549		hsa-miR-891a	
	BL		CLL		CLL
hsa-miR-658		hsa-miR-103/mmu-miR-103/rno-miR-103		hsa-miR-186/mmu-miR-186/rno-miR-186	
	BL		CLL	hsa-miR-331-5p/mmu-miR-331-5p	CLL
hsa-miR-933		hsa-miR-649		hsa-miR-28-5p/mmu-miR-28/rno-miR-28	
	BL		CLL		CLL
hsa-miR-30c-2*/mmu-miR-30c-2*/rno-miR-30c-2*		hsa-miR-335/mmu-miR-335-5p/rno-miR-335			CLL
	BL		CLL		CLL
hsa-miR-765		hsa-miR-342-3p/mmu-miR-342-3p/rno-miR-342-3p		hsa-miR-154/mmu-miR-154/rno-miR-154	
	BL		CLL		CLL
hsa-miR-620		hsa-miR-423-3p/mmu-miR-423-3p/rno-miR-423		hsa-miR-155	
	BL		CLL		CLL
hsa-miR-520d-5p		hsa-miR-222/mmu-miR-222/rno-miR-222		hsa-miR-363*/rno-miR-363*	
	BL		CLL		CLL
hsa-miR-494/mmu-miR-494/rno-miR-494		hsa-miR-374a		hsa-miR-32/mmu-miR-32/rno-miR-32	
	BL		CLL		CLL

BL vs CLL	Higher in	BL vs CLL (con't)	Higher in	BL vs CLL (con't)	Higher in
hsa-miR-551b/mmu-miR-551b/rno-miR-551b	CLL	hsa-miR-888*	CLL	hsa-miR-30e*/mmu-miR-30e*/rno-miR-30e*	CLL
hsa-miR-106b/mmu-miR-106b/rno-miR-106b	CLL	hsa-miR-30d/mmu-miR-30d/rno-miR-30d	CLL	hsa-miR-140-5p/mmu-miR-140/rno-miR-140	CLL
hsa-miR-30c/mmu-miR-30c/rno-miR-30c	CLL	hsa-miR-299-5p/mmu-miR-299*/rno-miR-299	CLL	hsa-let-7g/mmu-let-7g	CLL
hsa-miR-16/mmu-miR-16/rno-miR-16	CLL	hsa-miR-107/mmu-miR-107/rno-miR-107	CLL	hsa-miR-20b*	CLL
hsa-miR-27a/mmu-miR-27a/rno-miR-27a	CLL	hsa-miR-105	CLL	hsa-miR-129*	CLL
hsa-miR-27b/mmu-miR-27b/rno-miR-27b	CLL	hsa-let-7f/mmu-let-7f/rno-let-7f	CLL	hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	CLL
hsa-miR-550	CLL	hsa-miR-191/mmu-miR-191/rno-miR-191	CLL	hsa-miR-487b/mmu-miR-487b/rno-miR-487b	CLL
hsa-miR-30a/mmu-miR-30a/rno-miR-30a	CLL	hsa-miR-223/mmu-miR-223/rno-miR-223	CLL		

Table 26: Predictor microRNAs that distinguish Burkitt lymphoma from follicular lymphoma

BL vs FL	Higher in	BL vs FL (con't)	Higher in	BL vs FL (con't)	Higher in
hsa-miR-17/mmu-miR-17/rno-miR-17-5p/rno-miR-17	BL	hsa-miR-493	FL	hsa-miR-574-3p/mmu-miR-574-3p	FL
hsa-miR-106a	BL	hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	FL	hsa-miR-615-3p/mmu-miR-615-3p	FL
hsa-miR-19b/mmu-miR-19b/rno-miR-19b	BL	hsa-miR-200b*/mmu-miR-200b*	FL	hsa-miR-28-5p/mmu-miR-28/rno-miR-28	FL
hsa-miR-20a/mmu-miR-20a/rno-miR-20a	BL	hsa-miR-484/mmu-miR-484/rno-miR-484	FL	hsa-miR-934	FL
hsa-miR-19a/mmu-miR-19a/rno-miR-19a	BL	hsa-miR-483-3p	FL	hsa-miR-151-5p/mmu-miR-151-5p/rno-miR-151	FL
hsa-miR-628-3p	BL	hsa-miR-516b	FL	hsa-miR-885-5p	FL
hsa-miR-503	BL	hsa-miR-125b-2*/rno-miR-125b*	FL	hsa-miR-409-5p/mmu-miR-409-5p/rno-miR-409-5p	FL
hsa-miR-371-5p	BL	hsa-miR-490-3p/mmu-miR-490	FL	hsa-let-7d*/mmu-let-7d*/rno-let-7d*	FL
hsa-miR-106b/mmu-miR-106b/rno-miR-106b	BL	hsa-miR-140-5p/mmu-miR-140/rno-miR-140	FL	hsa-miR-155	FL

BL vs FL	Higher in	BL vs FL (con't)	Higher in	BL vs FL (con't)	Higher in
hsa-miR-30c-2*/mmu-miR-30c-2*/rno-miR-30c-2*	BL	hsa-miR-877/mmu-miR-877/rno-miR-877	FL	hsa-let-7b*/mmu-let-7b*/rno-let-7b*	FL
ebv-miR-BART2-3p	FL	hsa-miR-381/mmu-miR-381/rno-miR-381	FL	hsa-miR-7-2*	FL
hsa-let-7e/mmu-let-7e/rno-let-7e	FL	hsa-miR-193b*	FL	hsa-miR-221*	FL
hsa-miR-551b/mmu-miR-551b/rno-miR-551b	FL	hsa-miR-635	FL	hsa-miR-9*/mmu-miR-9*/rno-miR-9*	FL
hsa-miR-26b/mmu-miR-26b/rno-miR-26b	FL	hsa-miR-542-3p/mmu-miR-542-3p/rno-miR-542-3p	FL	hsa-miR-122*	FL
hsa-miR-26a/mmu-miR-26a/rno-miR-26a	FL	hsa-miR-181a-2*	FL	hsa-miR-130b/mmu-miR-130b/rno-miR-130b	FL
hsa-miR-620	FL	hsa-miR-32/mmu-miR-32/rno-miR-32	FL	hsa-miR-183/mmu-miR-183/rno-miR-183	FL
hsa-miR-801/mmu-miR-801	FL	hsa-miR-105	FL	hsa-miR-92a/mmu-miR-92a/rno-miR-92a	FL
ebv-miR-BART17-5p	FL	hsa-miR-488	FL	hsa-miR-890	FL
hsa-miR-29a/mmu-miR-29a/rno-miR-29a	FL	hsa-miR-505*	FL	hsa-miR-938	FL
hsa-miR-34b/mmu-miR-34b-3p	FL	ebv-miR-BART16	FL	kshv-miR-K12-7	FL
hsa-miR-32*	FL	hsa-miR-891a	FL	hsa-miR-629*	FL
hsa-miR-29b/mmu-miR-29b/rno-miR-29b	FL	hsa-miR-221/mmu-miR-221/rno-miR-221	FL	hsa-miR-922	FL
hsa-miR-649	FL	hsa-miR-7/mmu-miR-7a/rno-miR-7a	FL	kshv-miR-K12-5	FL
hsa-miR-576-3p	FL	hsa-miR-299-3p	FL	hsa-miR-197/mmu-miR-197	FL
hsa-miR-302a/mmu-miR-302a	FL	hsa-miR-575	FL	hsa-miR-552	FL
hsa-miR-365/mmu-miR-365/rno-miR-365	FL	hsa-miR-585	FL	hsa-miR-151-3p	FL
hsa-miR-148a/mmu-miR-148a	FL	hsa-miR-30e*/mmu-miR-30e*/rno-miR-30e*	FL	hsa-miR-194/mmu-miR-194/rno-miR-194	FL
hsa-miR-146b-5p/mmu-miR-146b/rno-miR-146b	FL	hcmv-miR-US25-1*	FL	hsa-miR-218-2*/mmu-miR-218-2*/rno-miR-218*	FL
hsa-miR-505/rno-miR-505	FL	hsa-miR-708/mmu-miR-708/rno-miR-708	FL	hsa-miR-181b/mmu-miR-181b/rno-miR-181b	FL
hsa-miR-33a/mmu-miR-33/rno-miR-33	FL	hsv1-miR-H1	FL	ebv-miR-BART18-3p	FL
hsa-miR-455-3p	FL	hsa-let-7g/mmu-let-7g	FL	hsa-miR-34c-5p/mmu-miR-34c/rno-miR-34c	FL

BL vs FL	Higher in	BL vs FL (con't)	Higher in	BL vs FL (con't)	Higher in
hsa-miR-374b/mmu-miR-374/rno-miR-374	FL	hsa-miR-146a/mmu-miR-146a/rno-miR-146a	FL	hsa-miR-622	FL
hsa-miR-214/mmu-miR-214/rno-miR-214	FL	ebv-miR-BART8*	FL	hsa-miR-514	FL
hsa-miR-138-1*/mmu-miR-138*/rno-miR-138*	FL	hsa-miR-106b*/mmu-miR-106b*/rno-miR-106b*	FL	hsa-miR-657	FL
hsa-miR-140-3p/mmu-miR-140*/rno-miR-140*	FL	hsa-miR-601	FL	hsa-miR-518a-3p	FL
hsa-miR-212/mmu-miR-212/rno-miR-212	FL	hsa-miR-553	FL	hsa-miR-647	FL
hsa-miR-29c/mmu-miR-29c/rno-miR-29c	FL	hsa-miR-518b	FL	hsa-miR-22*/mmu-miR-22*/rno-miR-22*	FL
hsa-miR-888*	FL	hsa-miR-548d-5p	FL	hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	FL
hsa-miR-222/mmu-miR-222/rno-miR-222	FL	hsa-miR-382/mmu-miR-382/rno-miR-382	FL	kshv-miR-K12-1	FL
hsa-miR-152/mmu-miR-152/rno-miR-152	FL	hsa-miR-630	FL	hsa-miR-425/mmu-miR-425/rno-miR-425	FL
hsa-miR-183*/mmu-miR-183*	FL	hsa-miR-144*	FL	hsa-miR-361-3p	FL
hsa-miR-768-5p	FL	hsa-miR-519d	FL	hsa-miR-220b	FL
hsa-miR-107/mmu-miR-107/rno-miR-107	FL	mghv-miR-M1-3	FL	hsa-miR-744/mmu-miR-744	FL
hsa-miR-574-5p/mmu-miR-574-5p	FL	hsa-miR-497/mmu-miR-497/rno-miR-497	FL	hsa-miR-551a	FL
hsa-miR-154/mmu-miR-154/rno-miR-154	FL	hsa-miR-524-5p	FL	hsa-miR-301a/mmu-miR-301a/rno-miR-301a	FL
hsa-miR-620	FL	hsa-miR-500*	FL	hsa-miR-92b/mmu-miR-92b/rno-miR-92b	FL
hsa-miR-886-5p	FL	hsa-miR-920	FL	hsa-miR-487b/mmu-miR-487b/rno-miR-487b	FL
hsa-miR-208a/mmu-miR-208a/rno-miR-208	FL	hsa-miR-297/mmu-miR-297a	FL	hsa-miR-363*/rno-miR-363*	FL
hsa-miR-374b*	FL	hsa-miR-509-3-5p	FL	hsa-miR-337-3p	FL
hsa-miR-525-5p	FL	hsa-miR-340*/mmu-miR-340-3p/rno-miR-340-3p	FL	hsa-miR-636	FL
hsa-miR-363/mmu-miR-363/rno-miR-363	FL	hsa-miR-99b*/mmu-miR-99b*/rno-miR-99b*	FL	hsa-miR-600	FL
hsa-miR-99b/mmu-miR-99b/rno-miR-99b	FL	hsa-miR-887	FL	hsa-miR-138/mmu-miR-138/rno-miR-138	FL

BL vs FL	Higher in	BL vs FL (con't)	Higher in	BL vs FL (con't)	Higher in
hsa-miR-148b/mmu-miR-148b/rno-miR-148b-3p	FL	hsa-miR-331-3p/mmu-miR-331-3p/rno-miR-331	FL	hsa-miR-96/mmu-miR-96/rno-miR-96	FL
kshv-miR-K12-6-5p	FL	hsa-miR-206/mmu-miR-206/rno-miR-206	FL	hsa-miR-20b*	FL
hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	FL	hsa-miR-377*	FL	hsa-miR-342-5p/mmu-miR-342-5p/rno-miR-342-5p	FL
hsa-miR-526b	FL	mghev-miR-M1-8	FL	hsa-miR-215	FL
hsa-miR-629	FL	hsa-miR-513a-3p	FL	hsa-miR-129*	FL
hsa-miR-617	FL	hsa-miR-146b-3p	FL		
hsa-miR-124/mmu-miR-124/rno-miR-124	FL	hsa-miR-155*	FL		

Table 27: Predictor microRNAs that distinguish Burkitt lymphoma from Hodgkin's lymphoma

BL vs HL	Higher in	BL vs HL (con't)	Higher in	BL vs HL (con't)	Higher in
hsa-miR-19b/mmu-miR-19b/rno-miR-19b	BL	hsa-miR-937	HL	hsa-miR-526a/hsa-miR-520c-5p/hsa-miR-518d-5p	HL
hsa-miR-19a/mmu-miR-19a/rno-miR-19a	BL	ebv-miR-BART13	HL	kshv-miR-K12-5	HL
hsa-miR-17/mmu-miR-17/rno-miR-17-5p/rno-miR-17	BL	hsa-miR-7/mmu-miR-7a/rno-miR-7a	HL	hsa-miR-340*/mmu-miR-340-3p/rno-miR-340-3p	HL
hsa-miR-106a	BL	hsa-miR-210/mmu-miR-210/rno-miR-210	HL	hsa-let-7d*/mmu-let-7d*/rno-let-7d*	HL
hsa-miR-20a/mmu-miR-20a/rno-miR-20a	BL	hsa-miR-490-3p/mmu-miR-490	HL	hsa-miR-92b/mmu-miR-92b/rno-miR-92b	HL
hsa-miR-106b/mmu-miR-106b/rno-miR-106b	BL	hsa-miR-221*	HL	hsa-miR-518b	HL
hsa-miR-30c/mmu-miR-30c/rno-miR-30c	BL	hsa-miR-92a/mmu-miR-92a/rno-miR-92a	HL	hiv1-miR-H1	HL
hsa-miR-551b/mmu-miR-551b/rno-miR-551b	HL	hsa-miR-183*/mmu-miR-183*	HL	hsa-miR-623	HL
hsa-miR-921	HL	hsa-miR-513a-3p	HL	hsa-miR-645	HL
ebv-miR-BART2-3p	HL	hsa-miR-575	HL	hsa-miR-601	HL
hsa-miR-32*	HL	hsa-miR-595	HL	hsa-miR-519e	HL
hsa-miR-494/mmu-miR-494/rno-miR-494	HL	hsa-miR-920	HL	hsa-miR-650	HL
hsa-miR-29c/mmu-miR-29c/rno-miR-29c	HL	hsa-miR-483-3p	HL	hsa-miR-361-3p	HL
hsa-miR-923	HL	hsa-miR-330-5p/mmu-miR-330/rno-miR-330	HL	hsa-miR-150*/mmu-miR-150*	HL

BL vs HL	Higher in	BL vs HL (con't)	Higher in	BL vs HL (con't)	Higher in
hsa-miR-199b-5p		hsa-miR-525-5p		hsa-miR-425*/mmu-miR-425*	HL
hsa-miR-148a/mmu-miR-148a	HL	hsa-miR-99b/mmu-miR-99b/rno-miR-99b	HL	hsa-miR-135a*/mmu-miR-135a*	HL
hsa-miR-130a/mmu-miR-130a/rno-miR-130a	HL	hsa-miR-509-3p	HL	hsa-miR-518a-3p	HL
hsa-miR-154/rno-miR-154	HL	hsa-miR-151-3p	HL	hsa-miR-612	HL
hsa-miR-151-5p/mmu-miR-151-5p/rno-miR-151	HL	ebv-miR-BHRF1-1	HL	hsa-miR-212/mmu-miR-212/rno-miR-212	HL
hsa-miR-28-5p/mmu-miR-28/rno-miR-28	HL	hsa-miR-630	HL	hsa-miR-125b-2*/rno-miR-125b*	HL
hsa-miR-365/mmu-miR-365/rno-miR-365	HL	mghev-miR-M1-7-3p	HL	hsa-miR-500	HL
hsa-miR-602	HL	hsa-miR-328/mmu-miR-328/rno-miR-328	HL	hsa-miR-663	HL
hsa-miR-222/mmu-miR-222/rno-miR-222	HL	hsa-miR-452	HL	hsa-miR-647	HL
hsa-miR-214/mmu-miR-214/rno-miR-214	HL	hsa-miR-635	HL	hsa-miR-502-5p	HL
hsa-miR-144*	HL	ebv-miR-BART5	HL	ebv-miR-BART18-3p	HL
hsa-miR-107/mmu-miR-107/rno-miR-107	HL	hsa-miR-373*	HL	hsa-miR-99b*/mmu-miR-99b*/rno-miR-99b*	HL
hsa-miR-497/mmu-miR-497/rno-miR-497	HL	hsa-miR-96/mmu-miR-96/rno-miR-96	HL	ebv-miR-BART7*	HL
hsa-let-7g/mmu-let-7g	HL	hsa-miR-382/mmu-miR-382/rno-miR-382	HL	hsa-miR-500*	HL
hsa-miR-146a/mmu-miR-146a/rno-miR-146a	HL	hsa-miR-155	HL	hsa-miR-124*/mmu-miR-124*/rno-miR-124*	HL
hsa-miR-186/mmu-miR-186/rno-miR-186	HL	hsa-miR-197/mmu-miR-197	HL	hsa-miR-206/mmu-miR-206/rno-miR-206	HL
hsa-miR-886-5p	HL	kshv-miR-K12-6-5p	HL	hsa-miR-615-3p/mmu-miR-615-3p	HL
hsa-miR-152/mmu-miR-152/rno-miR-152	HL	hcmv-miR-UL112	HL	hsa-miR-30c-1*/mmu-miR-30c-1*/rno-miR-30c-1*	HL
hsa-miR-29a*/mmu-miR-29a*/rno-miR-29a*	HL	hsa-miR-551b*	HL	hsa-miR-331-5p/mmu-miR-331-5p	HL
hsa-miR-140-5p/mmu-miR-140/rno-miR-140	HL	hsa-miR-877/mmu-miR-877/rno-miR-877	HL	hcmv-miR-US25-1*	HL

BL vs HL	Higher in	BL vs HL (con't)	Higher in	BL vs HL (con't)	Higher in
hsa-miR-532-5p/mmu-miR-532-5p/rno-miR-532-5p	HL	hsa-miR-589	HL	hsa-miR-326/mmu-miR-326/rno-miR-326	HL
hsa-miR-145*/mmu-miR-145*	HL	hsa-miR-936	HL	hsa-miR-181b/mmu-miR-181b/rno-miR-181b	HL
hsa-miR-515-5p	HL	hsa-miR-34c-5p/mmu-miR-34c/rno-miR-34c	HL	hsa-miR-376a*	HL
hsa-miR-153/mmu-miR-153/rno-miR-153	HL	hsa-miR-885-5p	HL	hsa-miR-433/mmu-miR-433/rno-miR-433	HL
hsa-miR-513a-5p	HL	ebv-miR-BART6-3p	HL	hsa-miR-640	HL
hsa-miR-516a-5p	HL	hsa-miR-585	HL	hsa-miR-938	HL
hsa-miR-660	HL	hsa-miR-302c*	HL	hsa-miR-508-5p	HL
hsa-miR-29c*/mmu-miR-29c*/rno-miR-29c*	HL	hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	HL	hsa-miR-484/mmu-miR-484/rno-miR-484	HL
hsa-miR-505/rno-miR-505	HL	hsa-miR-195*	HL	hsa-miR-106b*/mmu-miR-106b*/rno-miR-106b*	HL
hsa-miR-455-3p	HL	hsa-miR-17*/rno-miR-17-3p	HL	hsa-miR-600	HL
hsa-miR-519e*	HL	hsa-miR-296-5p/mmu-miR-296-5p/rno-miR-296*	HL	hsa-let-7b*/mmu-let-7b*/rno-let-7b*	HL
hsa-miR-502-3p	HL	hsa-miR-550*	HL	hsa-miR-20b*	HL
hsa-miR-922	HL	ebv-miR-BHRF1-3	HL	hsa-miR-622	HL
hsa-miR-524-5p	HL	hsa-miR-296-3p/mmu-miR-296-3p/rno-miR-296	HL	hsa-miR-657	HL
hsa-miR-483-5p	HL	hsa-miR-526b*	HL	hsa-miR-183/mmu-miR-183/rno-miR-183	HL
hsa-miR-708/mmu-miR-708/rno-miR-708	HL	hsa-miR-548b-3p	HL	hsa-miR-409-5p/mmu-miR-409-5p/rno-miR-409-5p	HL
hsa-miR-498	HL	hsa-miR-652/mmu-miR-652/rno-miR-652	HL	ebv-miR-BART20-3p	HL
ebv-miR-BART19-3p	HL	hsa-miR-297/mmu-miR-297a	HL	ebv-miR-BART8*	HL
hsa-miR-149/mmu-miR-149	HL	hsa-miR-553	HL	hsa-miR-129*	HL
hsa-miR-574-3p/mmu-miR-574-3p	HL	hsa-miR-194*	HL	hsa-miR-629	HL
hsa-miR-659	HL	hsa-miR-23a*/rno-miR-23a*	HL	hsa-miR-890	HL
hsa-miR-331-3p/mmu-miR-331-3p/rno-miR-331	HL	hsa-miR-130b/mmu-miR-130b/rno-miR-130b	HL	hsa-miR-208a/mmu-miR-208a/rno-miR-208	HL

BL vs HL	Higher in	BL vs HL (con't)	Higher in	BL vs HL (con't)	Higher in
hsa-miR-105	HL	hsa-miR-586	HL	hsa-miR-492	HL
hsa-miR-128/mmu-miR-128/rno-miR-128	HL	hsa-miR-137/mmu-miR-137/rno-miR-137	HL	hsa-miR-629*	HL
hsa-miR-200b*/mmu-miR-200b*	HL	hsa-miR-610	HL	hsa-miR-654-5p	HL
hsa-miR-381/mmu-miR-381/rno-miR-381	HL	mghev-miR-M1-8	HL	hsa-miR-584	HL
hsa-miR-766	HL	hsa-miR-193b*	HL	hsa-miR-636	HL
hsa-miR-557	HL	hsa-miR-519d	HL	hsa-miR-490-5p	HL
ebv-miR-BART16		hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	HL	hsa-miR-337-3p	
	HL	hsa-miR-744/mmu-miR-744	HL	hsa-miR-9*/mmu-miR-9*/rno-miR-9*	HL
hsa-miR-488	HL	hsa-miR-138/mmu-miR-138/rno-miR-138	HL	ebv-miR-BART9*	HL
hsa-miR-516b	HL	hsa-miR-21*	HL	hsa-miR-509-3-5p	HL
mghev-miR-M1-2	HL	hsa-miR-576-5p	HL	hsa-miR-342-5p/mmu-miR-342-5p/rno-miR-342-5p	HL
hsa-miR-891a	HL	hsa-miR-125a-3p/mmu-miR-125a-3p/rno-miR-125a-3p	HL	hsa-miR-514	HL
hsa-miR-221/mmu-miR-221/rno-miR-221	HL	mghev-miR-M1-6	HL	hsa-miR-377*	HL
hsa-miR-146b-3p	HL	hsa-miR-425/mmu-miR-425/rno-miR-425	HL	kshv-miR-K12-1	HL
hsa-miR-526b	HL	hsa-miR-10a*/mmu-miR-10a*/rno-miR-10a-3p	HL	hsa-miR-124/mmu-miR-124/rno-miR-124	HL
mghev-miR-M1-3	HL	hsa-miR-215	HL	hsa-miR-542-3p/mmu-miR-542-3p/rno-miR-542-3p	HL
hsa-miR-505*	HL	hsa-miR-345	HL	hsa-miR-220b	HL
hsv1-miR-H1	HL	hsa-miR-887	HL	hsa-miR-299-3p	HL
hcmv-miR-UL70-3p	HL	hsa-miR-7-2*	HL	hsa-miR-181a-2*	HL
hsa-miR-24-2*/mmu-miR-24-2*/rno-miR-24-2*	HL	hsa-miR-122*	HL	hsa-miR-202	HL
hsa-miR-617	HL	hsa-miR-363*/rno-miR-363*	HL	hsa-miR-487b/mmu-miR-487b/rno-miR-487b	HL
hsa-miR-194/mmu-miR-194/rno-miR-194	HL	hsa-miR-22*/mmu-miR-22*/rno-miR-22*	HL	hsa-miR-551a	HL
hsa-miR-934	HL	hsa-miR-542-5p/mmu-miR-542-5p/rno-miR-542-5p	HL	hsa-miR-338-5p/mmu-miR-338-5p/rno-miR-338*	HL
hsa-miR-220c	HL	hsa-miR-92b*	HL	hsa-miR-552	HL
hsa-miR-548d-5p	HL				

Table 28: Predictor microRNAs that distinguish chronic lymphocytic leukemia from follicular lymphoma

CLL vs FL	Higher in	CLL vs FL (con't)	Higher in	CLL vs FL (con't)	Higher in
hsa-miR-331-5p/mmu-miR-331-5p	CLL	hsa-miR-620	FL	hsa-miR-9*/mmu-miR-9*/rno-miR-9*	FL
hsa-miR-144/mmu-miR-144/rno-miR-144	CLL	hsa-miR-99a/mmu-miR-99a/rno-miR-99a	FL	hsa-miR-509-3-5p	FL
hsa-miR-150/mmu-miR-150/rno-miR-150	CLL	hsa-miR-371-5p	FL	hsa-miR-518b	FL
hsa-miR-140-5p/mmu-miR-140/rno-miR-140	CLL	hsa-miR-452	FL	hsa-miR-183*/mmu-miR-183*	FL
hsa-miR-335/mmu-miR-335-5p/rno-miR-335	CLL	hsa-miR-126*/mmu-miR-126-5p/rno-miR-126*	FL	hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	FL
hsa-miR-186/mmu-miR-186/rno-miR-186	CLL	hsa-miR-298	FL	hsa-miR-183/mmu-miR-183/rno-miR-183	FL
hsa-miR-486-5p/mmu-miR-486	CLL	hsa-miR-193a-5p	FL	hsa-miR-890	FL
hsa-miR-154/mmu-miR-154/rno-miR-154	CLL	hsa-miR-583	FL	hsa-miR-153/mmu-miR-153/rno-miR-153	FL
hsa-miR-223/mmu-miR-223/rno-miR-223	CLL	hsa-miR-143/mmu-miR-143/rno-miR-143	FL	hsa-miR-874/mmu-miR-874/rno-miR-874	FL
hsa-miR-299-5p/mmu-miR-299*/rno-miR-299	CLL	hsa-miR-665	FL	hsa-miR-220c	FL
hsa-let-7g/mmu-let-7g	CLL	hsa-miR-505/rno-miR-505	FL	hsa-miR-99b*/mmu-miR-99b*/rno-miR-99b*	FL
hsa-miR-32/mmu-miR-32/rno-miR-32	CLL	hsa-miR-199b-5p	FL	hsa-miR-193b*	FL
hsa-miR-30e*/mmu-miR-30e*/rno-miR-30e*	CLL	hsa-miR-28-3p/rno-miR-28*	FL	hsa-miR-629*	FL
hsa-miR-147	CLL	hsa-miR-422a	FL	hcmv-miR-UL148D	FL
hsa-miR-20b/mmu-miR-20b/rno-miR-20b-5p	CLL	hsa-miR-515-5p	FL	ebv-miR-BART7*	FL
hsa-miR-101/mmu-miR-101a/rno-miR-101a	CLL	hsa-miR-455-3p	FL	hsa-miR-99b/mmu-miR-99b/rno-miR-99b	FL
hsa-let-7f/mmu-let-7f/rno-let-7f	CLL	hsa-miR-10a/mmu-miR-10a/rno-miR-10a-5p	FL	hsa-miR-206/mmu-miR-206/rno-miR-206	FL
hsa-miR-30e/mmu-miR-30e/rno-miR-30e	CLL	hsa-miR-300	FL	hsa-miR-381/mmu-miR-381/rno-miR-381	FL
hsa-miR-668/mmu-miR-668	CLL	ebv-miR-BART5	FL	hsa-miR-194/mmu-miR-194/rno-miR-194	FL
hsa-miR-768-5p	CLL	hsa-miR-10b/mmu-miR-10b/rno-miR-10b	FL	hsa-miR-525-5p	FL

CLL vs FL	Higher in	CLL vs FL (con't)	Higher in	CLL vs FL (con't)	Higher in
hsa-miR-19a/mmu-miR-19a/rno-miR-19a	CLL	hsa-miR-212/mmu-miR-212/rno-miR-212	FL	hsa-miR-193b	FL
hsa-miR-199a-5p/mmu-miR-199a-5p/rno-miR-199a-5p	CLL	hsa-miR-145/mmu-miR-145/rno-miR-145	FL	hsa-miR-497/mmu-miR-497/rno-miR-497	FL
hsa-miR-638	CLL	hsa-miR-187*	FL	ebv-miR-BART18-3p	FL
hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	CLL	ebv-miR-BHRF1-1	FL	hsa-miR-424	FL
hsa-miR-19b/mmu-miR-19b/rno-miR-19b	CLL	ebv-miR-BHRF1-2	FL	hsa-miR-553	FL
hsa-miR-30d/mmu-miR-30d/rno-miR-30d	CLL	hsa-miR-126/mmu-miR-126-3p/rno-miR-126	FL	hsa-let-7d*/mmu-let-7d*/rno-let-7d*	FL
hsa-miR-363/mmu-miR-363/rno-miR-363	CLL	hsa-miR-130b*/mmu-miR-130b*	FL	hsa-miR-34c-5p/mmu-miR-34c/rno-miR-34c	FL
hsa-miR-374a	CLL	hsa-miR-326/mmu-miR-326/rno-miR-326	FL	ebv-miR-BHRF1-3	FL
hsa-miR-140-3p/mmu-miR-140*/rno-miR-140*	CLL	mgshv-miR-M1-2	FL	kshv-miR-K12-6-5p	FL
hsa-miR-185/mmu-miR-185/rno-miR-185	CLL	kshv-miR-K12-6-3p	FL	hsa-miR-551a	FL
hsa-miR-106b/mmu-miR-106b/rno-miR-106b	CLL	hsa-miR-516b	FL	hsa-miR-195*	FL
hsa-miR-106a	CLL	hsa-miR-519e*	FL	hsa-miR-551b*	FL
hsa-miR-191/mmu-miR-191/rno-miR-191	CLL	mgshv-miR-M1-7-3p	FL	hsa-miR-514	FL
hsa-miR-17/mmu-miR-17/rno-miR-17	CLL	hsa-miR-629	FL	hsa-miR-552	FL
hsa-let-7i/mmu-let-7i/rno-let-7i	CLL	hsa-miR-24-2*/mmu-miR-24-2*/rno-miR-24-2*	FL	hsa-miR-122*	FL
hsa-miR-20a/mmu-miR-20a/rno-miR-20a	CLL	hsa-miR-943	FL	hsa-miR-92b/mmu-miR-92b/rno-miR-92b	FL
hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p	CLL	hsa-miR-124/mmu-miR-124/rno-miR-124	FL	hsa-miR-22*/mmu-miR-22*/rno-miR-22*	FL
hsa-miR-768-3p	CLL	hsa-miR-365/mmu-miR-365/rno-miR-365	FL	hsa-miR-635	FL
hsa-miR-30b/mmu-miR-30b/rno-miR-30b-5p	CLL	hsa-miR-493	FL	kshv-miR-K12-1	FL
hsa-miR-891a	CLL	hsa-miR-29c*/mmu-miR-29c*/rno-miR-29c*	FL	hsa-miR-483-5p	FL
hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	CLL	hsa-miR-602	FL	hsa-miR-340*/mmu-miR-340-3p/rno-miR-340-3p	FL

CLL vs FL	Higher in	CLL vs FL (con't)	Higher in	CLL vs FL (con't)	Higher in
hsa-miR-29c/mmu-miR-29c	CLL	hsa-miR-484/mmu-miR-484/rno-miR-484	FL	hsa-miR-615-3p/mmu-miR-615-3p	FL
hsa-miR-28-5p/mmu-miR-28/rno-miR-28	CLL	hsa-miR-483-3p	FL	hsa-miR-505*	FL
hsa-miR-30a/mmu-miR-30a/rno-miR-30a	CLL	hsa-miR-125b-2*/rno-miR-125b*	FL	hsa-miR-622	FL
hsa-miR-155	CLL	hsa-miR-675	FL	hsa-miR-181b/mmu-miR-181b/rno-miR-181b	FL
hsa-miR-361-5p/mmu-miR-361/rno-miR-361	CLL	mghev-miR-M1-7-5p	FL	hsa-miR-886-5p	FL
hsa-miR-15a/mmu-miR-15a	CLL	hsa-miR-152/mmu-miR-152/rno-miR-152	FL	hsa-miR-885-5p	FL
hsa-miR-26a/mmu-miR-26a/rno-miR-26a	CLL	hsa-miR-27a*/mmu-miR-27a*/rno-miR-27a*	FL	hsa-miR-220b	FL
hsa-miR-30c/mmu-miR-30c/rno-miR-30c	CLL	hsa-miR-542-3p/mmu-miR-542-3p/rno-miR-542-3p	FL	hsa-miR-524-5p	FL
hsa-miR-541*	CLL	hsa-miR-100/mmu-miR-100/rno-miR-100	FL	hsa-miR-382/mmu-miR-382/rno-miR-382	FL
hsa-miR-26b/mmu-miR-26b/rno-miR-26b	CLL	hsa-miR-208a/mmu-miR-208a/rno-miR-208	FL	hsa-miR-744/mmu-miR-744	FL
hsa-miR-519d	CLL	hsa-miR-766	FL	hsv1-miR-H1	FL
hsa-miR-15b/mmu-miR-15b/rno-miR-15b	CLL	hsa-miR-637	FL	hsa-miR-526b	FL
hsa-miR-550	CLL	hsa-miR-519c-5p/hsa-miR-519b-5p/hsa-miR-523*/hsa-miR-518e*/hsa-miR-522*/hsa-miR-519a*	FL	hsa-miR-657	FL
hsa-miR-29b/mmu-miR-29b/rno-miR-29b	CLL	hsa-miR-409-5p/mmu-miR-409-5p/rno-miR-409-5p	FL	hsa-miR-130b/mmu-miR-130b/rno-miR-130b	FL
hsa-miR-29a/mmu-miR-29a/rno-miR-29a	CLL	hsa-miR-199a-3p/hsa-miR-199b-3p/mmu-miR-199a-3p/mmu-miR-199b/rno-miR-199a-3p	FL	hsa-miR-181a/mmu-miR-181a/rno-miR-181a	FL
hsa-miR-103/mmu-miR-103/rno-miR-103	CLL	hsa-miR-106b*/mmu-miR-106b*/rno-miR-106b*	FL	hsa-miR-301a/mmu-miR-301a/rno-miR-301a	FL
hsa-miR-423-3p/mmu-miR-423-3p/rno-miR-423	CLL	hsa-miR-130a/mmu-miR-130a/rno-miR-130a	FL	hsa-miR-490-3p/mmu-miR-490	FL
hsa-miR-549	CLL	hsa-miR-645	FL	hsa-miR-485-3p/mmu-miR-485*	FL

CLL vs FL	Higher in	CLL vs FL (con't)	Higher in	CLL vs FL (con't)	Higher in
hsa-miR-107/mmu-miR-107/rno-miR-107	CLL	hsa-miR-548d-5p	FL	hsa-miR-297/mmu-miR-297a	FL
hsa-miR-888*	CLL	hsa-miR-671-5p/mmu-miR-671-5p	FL	hsa-miR-630	FL
hsa-miR-801/mmu-miR-801	CLL	hsa-miR-574-3p/mmu-miR-574-3p	FL	hsa-miR-877/mmu-miR-877/rno-miR-877	FL
hsa-miR-149*	FL	hsa-miR-125b/mmu-miR-125b-5p/rno-miR-125b-5p	FL	kshv-miR-K12-5	FL
hsa-miR-634	FL	hsa-miR-500*	FL	hsa-miR-617	FL
ebv-miR-BART2-3p	FL	hsa-miR-425/mmu-miR-425/rno-miR-425	FL	mghv-miR-M1-3	FL
hsa-miR-921	FL	ebv-miR-BART8*	FL	hsa-miR-920	FL
hsa-miR-494/mmu-miR-494/rno-miR-494	FL	hsa-miR-377*	FL	hsa-miR-585	FL
hsa-miR-933	FL	hsa-miR-513a-3p	FL	hsa-miR-374b*	FL
mghv-miR-M1-4	FL	hsa-miR-181a-2*	FL	hsa-miR-215	FL
hsa-let-7e/mmu-let-7e/rno-let-7e	FL	hsa-miR-938	FL	hsa-miR-342-5p/mmu-miR-342-5p/rno-miR-342-5p	FL
hsa-miR-939	FL	hsa-miR-155*	FL	hsa-miR-934	FL
hsa-miR-518c*	FL	hsa-miR-218-2*/mmu-miR-218-2*/rno-miR-218*	FL	hsa-miR-575	FL
hsa-miR-32*	FL	hsa-miR-198	FL	hsa-miR-488	FL
hsa-miR-491-3p	FL	hsa-miR-151-3p	FL	ebv-miR-BART16	FL
hsa-miR-185/mmu-miR-185/rno-miR-185	FL	hsa-miR-299-3p	FL	hsa-miR-647	FL
hsa-miR-765	FL	hcmv-miR-US25-1*	FL	hsa-miR-138/mmu-miR-138/rno-miR-138	FL
ebv-miR-BART17-5p	FL	hsa-miR-708/mmu-miR-708/rno-miR-708	FL	hsa-miR-221*	FL
hsa-miR-576-3p	FL	hsa-miR-659	FL	hsa-miR-200b*/mmu-miR-200b*	FL
hsa-miR-658	FL	hsa-miR-600	FL	hsa-miR-337-3p	FL
hsa-miR-503	FL	hsa-miR-601	FL	hsa-miR-922	FL
hsa-miR-30b*	FL	hsa-miR-296-3p/mmu-miR-296-3p/rno-miR-296	FL	hsa-miR-197/mmu-miR-197	FL
hsa-miR-302a/mmu-miR-302a	FL	hsa-let-7b*/mmu-let-7b*/rno-let-7b*	FL	hsa-miR-96/mmu-miR-96/rno-miR-96	FL
hsa-miR-628-3p	FL	ebv-miR-BART6-3p	FL	hsa-miR-518a-3p	FL
hsa-miR-642	FL	hsa-miR-7-2*	FL		

Table 29: Predictor microRNAs that distinguish Burkitt lymphoma from Hodgkin's lymphoma

CLL vs HL	Higher in	CLL vs HL (con't)	Higher in	CLL vs HL (con't)	Higher in
hsa-miR-32/mmu-miR-32/rno-miR-32	CLL	hsa-miR-145/mmu-miR-145/rno-miR-145	HL	hsa-miR-886-5p	HL
hsa-miR-30e*/mmu-miR-30e*/rno-miR-30e*	CLL	hsa-miR-128/mmu-miR-128/rno-miR-128	HL	hsa-miR-500	HL
hsa-let-7g/mmu-let-7g	CLL	hsa-miR-532-5p/mmu-miR-532-5p/rno-miR-532-5p	HL	hsa-miR-502-5p	HL
hsa-miR-144/mmu-miR-144/rno-miR-144	CLL	hsa-miR-143*	HL	ebv-miR-BART18-3p	HL
hsa-miR-140-5p/mmu-miR-140/rno-miR-140	CLL	hsa-miR-28-3p/rno-miR-28*	HL	hsa-miR-198	HL
hsa-miR-19a/mmu-miR-19a/rno-miR-19a	CLL	hsa-miR-130b*/mmu-miR-130b*	HL	hsa-miR-500*	HL
hsa-miR-154/mmu-miR-154/rno-miR-154	CLL	hsa-miR-505/rno-miR-505	HL	hsa-miR-342-5p/mmu-miR-342-5p/rno-miR-342-5p	HL
hsa-miR-150/mmu-miR-150/rno-miR-150	CLL	hsa-miR-25*	HL	hsa-miR-124*/mmu-miR-124*/rno-miR-124*	HL
hsa-miR-28-5p/mmu-miR-28/rno-miR-28	CLL	hsa-miR-574-3p/mmu-miR-574-3p	HL	hsa-miR-30c-1*/mmu-miR-30c-1*/rno-miR-30c-1*	HL
hsa-miR-363/mmu-miR-363/rno-miR-363	CLL	hsa-miR-455-3p	HL	hsa-miR-220c	HL
hsa-miR-101/mmu-miR-101a/rno-miR-101a	CLL	kshv-miR-K12-3	HL	hsa-miR-376a*	HL
hsa-miR-299-5p/mmu-miR-299*/rno-miR-299	CLL	hsa-miR-516b	HL	hsa-miR-640	HL
hsa-miR-768-5p	CLL	kshv-miR-K12-8	HL	hcmv-miR-UL148D	HL
hsa-miR-19b/mmu-miR-19b/rno-miR-19b	CLL	hsa-miR-502-3p	HL	hsa-miR-659	HL
hsa-miR-30e/mmu-miR-30e/rno-miR-30e	CLL	kshv-miR-K12-6-3p	HL	hsa-miR-934	HL
hsa-miR-20b/mmu-miR-20b/rno-miR-20b-5p	CLL	hsa-miR-129-5p/mmu-miR-129-5p/rno-miR-129	HL	hsa-miR-125a-3p/mmu-miR-125a-3p/rno-miR-125a-3p	HL
hsa-miR-374a	CLL	hsa-miR-515-5p	HL	hsa-miR-885-5p	HL
hsa-let-7f/mmu-let-7f/rno-let-7f	CLL	hsa-miR-199a-3p/hsa-miR-199b-3p/mmu-miR-199a-3p/mmu-miR-199b/rno-miR-199a-3p	HL	hsa-miR-24-2*/mmu-miR-24-2*/rno-miR-24-2*	HL
hsa-miR-335/mmu-miR-335-5p/rno-miR-335	CLL	hsa-miR-149/mmu-miR-149	HL	hsa-miR-484/mmu-miR-484/rno-miR-484	HL

CLL vs HL	Higher in	CLL vs HL (con't)	Higher in	CLL vs HL (con't)	Higher in
hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p	CLL	hsa-miR-889	HL	hsa-miR-106b*/mmu-miR-106b*/rno-miR-106b*	HL
hsa-miR-486-5p/mmu-miR-486	CLL	hsa-miR-637	HL	hsa-miR-505*	HL
hsa-miR-33a/mmu-miR-33/rno-miR-33	CLL	hsa-miR-600	HL	hsa-let-7b*/mmu-let-7b*/rno-let-7b*	HL
hsa-miR-30b/mmu-miR-30b/rno-miR-30b-5p	CLL	hsa-miR-151-3p	HL	hsa-miR-302c*	HL
hsa-miR-768-3p	CLL	hsa-miR-656	HL	hsa-miR-542-5p/mmu-miR-542-5p/rno-miR-542-5p	HL
hsa-miR-668/mmu-miR-668	CLL	hsa-miR-497/mmu-miR-497/rno-miR-497	HL	hsv1-miR-H1	HL
hsa-miR-15b/mmu-miR-15b/rno-miR-15b	CLL	hsa-miR-152/mmu-miR-152/rno-miR-152	HL	mghv-miR-M1-3	HL
hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	CLL	hsa-miR-100/mmu-miR-100/rno-miR-100	HL	hsa-miR-183/mmu-miR-183/rno-miR-183	HL
hsa-miR-140-3p/mmu-miR-140*/rno-miR-140*	CLL	hsa-miR-425/mmu-miR-425/rno-miR-425	HL	hsa-miR-122*	HL
hsa-miR-29b/mmu-miR-29b/rno-miR-29b	CLL	hsa-miR-145*/mmu-miR-145*	HL	hsa-miR-183*/mmu-miR-183*	HL
hsa-miR-29c/mmu-miR-29c/rno-miR-29c	CLL	hsa-miR-365/mmu-miR-365/rno-miR-365	HL	hsa-miR-675	HL
hsa-miR-186/mmu-miR-186/rno-miR-186	CLL	hsa-miR-422a	HL	hsa-miR-99b/mmu-miR-99b/rno-miR-99b	HL
hsa-miR-106a	CLL	hcmv-miR-UL70-3p	HL	hsa-miR-874/mmu-miR-874/rno-miR-874	HL
hsa-miR-26a/mmu-miR-26a/rno-miR-26a	CLL	hsa-miR-27a*/mmu-miR-27a*/rno-miR-27a*	HL	ebv-miR-BART20-3p	HL
hsa-miR-106b/mmu-miR-106b/rno-miR-106b	CLL	hsa-miR-194/mmu-miR-194/rno-miR-194	HL	hsa-miR-483-5p	HL
hsa-miR-17/mmu-miR-17/rno-miR-17-5p/rno-miR-17	CLL	hsa-miR-548d-5p	HL	hsa-miR-671-5p/mmu-miR-671-5p	HL
hsa-miR-191/mmu-miR-191/rno-miR-191	CLL	hsa-miR-187*	HL	hsa-miR-629	HL
hsa-miR-20a/mmu-miR-20a/rno-miR-20a	CLL	hsa-miR-323-3p/mmu-miR-323-3p/rno-miR-323	HL	hsa-miR-553	HL
hsa-miR-30c/mmu-miR-30c/rno-miR-30c	CLL	hsa-miR-708/mmu-miR-708/rno-miR-708	HL	hsa-let-7d*/mmu-let-7d*/rno-let-7d*	HL

CLL vs HL	Higher in	CLL vs HL (con't)	Higher in	CLL vs HL (con't)	Higher in
hsa-miR-26b/mmu-miR-26b/rno-miR-26b		hsa-miR-29c*/mmu-miR-29c*/rno-miR-29c*		hsa-miR-601	
hsa-miR-147	CLL	hsa-miR-513a-3p	HL	hsa-miR-645	HL
hsa-miR-15a/mmu-miR-15a	CLL	hsa-miR-595	HL	hsa-miR-920	HL
hsa-miR-30d/mmu-miR-30d/rno-miR-30d	CLL	hsa-miR-483-3p	HL	hsa-miR-525-5p	HL
hsa-miR-199a-5p/mmu-miR-199a-5p/rno-miR-199a-5p	CLL	hsa-miR-330-5p/mmu-miR-330/rno-miR-330	HL	hsa-miR-221*	HL
hsa-miR-29a/mmu-miR-29a/rno-miR-29a	CLL	hsa-miR-519e*	HL	hsa-miR-890	HL
hsa-miR-223/mmu-miR-223/rno-miR-223	CLL	hsa-miR-509-3p	HL	hsa-miR-492	HL
hsa-miR-30a/mmu-miR-30a/rno-miR-30a	CLL	hsa-miR-328/mmu-miR-328/rno-miR-328	HL	hsa-miR-629*	HL
hsa-miR-16/mmu-miR-16/rno-miR-16	CLL	hsa-miR-373*	HL	hsa-miR-635	HL
hsa-miR-451/mmu-miR-451/rno-miR-451	CLL	hsa-miR-96/mmu-miR-96/rno-miR-96	HL	hsa-miR-130b/mmu-miR-130b/rno-miR-130b	HL
hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	CLL	hsa-miR-215	HL	hsa-miR-197/mmu-miR-197	HL
hsa-miR-550	CLL	hsa-miR-589	HL	hsa-miR-654-5p	HL
hsa-miR-342-3p/mmu-miR-342-3p/rno-miR-342-3p	CLL	hsa-miR-34c-5p/mmu-miR-34c/rno-miR-34c	HL	hsa-miR-518b	HL
hsa-miR-195/mmu-miR-195/rno-miR-195	CLL	hsa-miR-125b/mmu-miR-125b-5p/rno-miR-125b-5p	HL	hsa-miR-382/mmu-miR-382/rno-miR-382	HL
hsa-miR-801/mmu-miR-801	CLL	hsa-miR-130a/mmu-miR-130a/rno-miR-130a	HL	hsa-miR-584	HL
hsa-miR-541*		hsa-miR-519c-5p/hsa-miR-519b-5p/hsa-miR-523*/hsa-miR-518e*/hsa-miR-522*/hsa-miR-519a*		hsa-miR-99b*/mmu-miR-99b*/rno-miR-99b*	
hsa-let-7i/mmu-let-7i/rno-let-7i	CLL	mghv-miR-M1-7-5p	HL	hsa-miR-630	HL
hsa-miR-155	CLL	hsa-miR-516a-5p	HL	hsa-miR-490-5p	HL
hsa-miR-185/mmu-miR-185/rno-miR-185	CLL	hsa-miR-424	HL	hsa-miR-663	HL
hsa-miR-891a	CLL	hsa-miR-17*/rno-miR-17-3p	HL	hsa-miR-337-3p	HL
hsa-miR-138-1*/mmu-miR-138*/rno-miR-138*	CLL	hsa-miR-296-5p/mmu-miR-296-5p/rno-miR-296*	HL	hsa-miR-9*/mmu-miR-9*/rno-miR-9*	HL
hsa-miR-27b/mmu-miR-27b/rno-miR-27b	CLL	hsa-miR-550*	HL	hsa-miR-202	HL

CLL vs HL	Higher in	CLL vs HL (con't)	Higher in	CLL vs HL (con't)	Higher in
hsa-miR-361-5p/mmu-miR-361/rno-miR-361	CLL	hsa-miR-210/mmu-miR-210/rno-miR-210	HL	ebv-miR-BART16	HL
hsa-miR-129*	CLL	hsa-miR-92b/mmu-miR-92b/rno-miR-92b	HL	ebv-miR-BART9*	HL
hsa-miR-638	CLL	hsa-miR-548b-3p	HL	hsa-miR-193b*	HL
hsa-miR-34b/mmu-miR-34b-3p	CLL	hsa-miR-652/mmu-miR-652/rno-miR-652	HL	ebv-miR-BART8*	HL
hsa-miR-107/mmu-miR-107/rno-miR-107	CLL	hsa-miR-138/mmu-miR-138/rno-miR-138	HL	hsa-miR-206/mmu-miR-206/rno-miR-206	HL
hsa-miR-549	CLL	hsa-miR-194*	HL	hcmv-miR-US25-1*	HL
hsa-miR-888*	CLL	hsa-miR-23a*/rno-miR-23a*	HL	hsa-miR-514	HL
hsa-miR-423-3p/mmu-miR-423-3p/rno-miR-423	CLL	hsa-miR-153/mmu-miR-153/rno-miR-153	HL	kshv-miR-K12-6-5p	HL
hsa-let-7e/mmu-let-7e/rno-let-7e	HL	hsa-miR-586	HL	hsa-miR-488	HL
hsa-miR-125a-5p/mmu-miR-125a-5p/rno-miR-125a-5p	HL	hsa-miR-137/mmu-miR-137/rno-miR-137	HL	hsa-miR-508-5p	HL
hsa-miR-576-3p	HL	hsa-miR-610	HL	hsa-miR-551b*	HL
hsa-miR-513a-5p	HL	hsa-miR-381/mmu-miR-381/rno-miR-381	HL	hsa-miR-377*	HL
ebv-miR-BART17-5p	HL	hsa-miR-936	HL	ebv-miR-BART6-3p	HL
hsa-miR-185/mmu-miR-185/rno-miR-185	HL	hsa-miR-744/mmu-miR-744	HL	hsa-miR-181b/mmu-miR-181b/rno-miR-181b	HL
hsa-miR-921	HL	ebv-miR-BART5	HL	hsa-miR-526b	HL
hsa-miR-518c*	HL	ebv-miR-BHRF1-1	HL	hsa-miR-622	HL
hsa-miR-520d-5p	HL	hsa-miR-21*	HL	kshv-miR-K12-1	HL
hsa-miR-939	HL	hsa-miR-576-5p	HL	hsa-miR-485-3p/mmu-miR-485*	HL
hsa-miR-634	HL	mghv-miR-M1-6	HL	hsa-miR-490-3p/mmu-miR-490	HL
hsa-miR-491-3p	HL	hsa-miR-193b	HL	hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	HL
ebv-miR-BART2-3p	HL	hsa-miR-10a*/mmu-miR-10a*/rno-miR-10a-3p	HL	hsa-miR-124/mmu-miR-124/rno-miR-124	HL
hsa-miR-30c-2*/mmu-miR-30c-2*/rno-miR-30c-2*	HL	hsa-miR-524-5p	HL	hsa-miR-657	HL
hsa-miR-765	HL	hsa-miR-452	HL	ebv-miR-BHRF1-3	HL
hsa-miR-923	HL	hsa-miR-345	HL	hsa-miR-542-3p/mmu-miR-542-3p/rno-miR-542-3p	HL
hsa-miR-620	HL	hsa-miR-7-2*	HL	kshv-miR-K12-5	HL

CLL vs HL	Higher in	CLL vs HL (con't)	Higher in	CLL vs HL (con't)	Higher in
hsa-miR-933		hsa-miR-409- 5p/mmu-miR-409- 5p/rno-miR-409-5p		hsa-miR-943	
hsa-miR-143/mmu-miR- 143/rno-miR-143	HL	hsa-miR-557	HL	hsa-miR-551a	HL
hsa-miR-494/mmu-miR- 494/rno-miR-494	HL	hsa-miR-181a/mmu- miR-181a/rno-miR- 181a	HL	hsa-miR-297/mmu- miR-297a	HL
hsa-miR-665		hsa-miR-22*/mmu- miR-22*/rno-miR-22*		hsa-miR-296- 3p/mmu-miR-296- 3p/rno-miR-296	HL
hsa-miR-642	HL	hsa-miR-922	HL	hsa-miR-617	HL
hsa-miR-126*/mmu-miR- 126-5p/rno-miR-126*	HL	hsa-miR-92b*	HL	hsa-miR-195*	HL
hsa-miR-658	HL	hsa-miR-938	HL	hsa-miR-575	HL
hsa-miR-149*		hsa-miR-526a/hsa- miR-520c-5p/hsa- miR-518d-5p		hsa-miR-208a/mmu- miR-208a/rno-miR- 208	HL
hsa-miR-30b*	HL	hsa-miR-526b*	HL	hsa-miR-647	HL
mghev-miR-M1-4	HL	ebv-miR-BHRF1-2	HL	hsa-miR-509-3-5p	HL
hsa-miR-99a/mmu-miR- 99a/rno-miR-99a		hiv1-miR-H1		hsa-miR-340*/mmu- miR-340-3p/rno- miR-340-3p	HL
hsa-miR-193a-5p	HL	hsa-miR-623	HL	hsa-miR-220b	HL
hsa-miR-498		mghev-miR-M1-2		hsa-miR- 200b*/mmu-miR- 200b*	HL
hsa-miR-628-3p	HL	mghev-miR-M1-7-3p	HL	hsa-miR-585	HL
hsa-miR-185*		hsa-miR-519e		hsa-miR-877/mmu- miR-877/rno-miR- 877	HL
hsa-miR-371-5p	HL	hsa-miR-650	HL	hsa-miR-326/mmu- miR-326/rno-miR- 326	HL
hsa-miR-199b-5p	HL	hsa-miR-766	HL	ebv-miR-BART7*	HL
hsa-miR-126/mmu-miR- 126-3p/rno-miR-126	HL	hsa-miR-602	HL	hsa-miR-615- 3p/mmu-miR-615-3p	HL
hsa-miR-503		hsa-miR-425*/mmu- miR-425*		hsa-miR-433/mmu- miR-433/rno-miR- 433	HL
hsa-miR-10a/mmu-miR- 10a/rno-miR-10a-5p	HL	hsa-miR- 135a*/mmu-miR- 135a*	HL	hsa-miR-338- 5p/mmu-miR-338- 5p/rno-miR-338*	HL
hsa-miR-300	HL	hsa-miR-612	HL	hsa-miR-299-3p	HL
hsa-miR-583		hsa-miR-212/mmu- miR-212/rno-miR- 212		hsa-miR-518a-3p	
hsa-miR-518a-5p/hsa- miR-527	HL	hsa-miR-125b- 2*/rno-miR-125b*	HL	hsa-miR-181a-2*	HL
hsa-miR-10b/mmu-miR- 10b/rno-miR-10b	HL	hcmv-miR-UL112	HL	hsa-miR-552	HL
		hsa-miR-374b*	HL		

Table 30: Predictor microRNAs that distinguish follicular lymphoma from Hodgkin's lymphoma

FL vs HL	Higher in	FL vs HL (con't)	Higher in	FL vs HL (con't)	Higher in
hsa-miR-301a/mmu-miR-301a/rno-miR-301a	FL	mg hv-miR-M1-7-5p	HL	ebv-miR-BHRF1-2	HL
kshv-miR-K12-7	FL	hsa-miR-498	HL	hsa-miR-145*/mmu-miR-145*	HL
hsa-miR-96/mmu-miR-96/rno-miR-96	FL	hsa-miR-525-5p	HL	hsa-miR-296-5p/mmu-miR-296-5p/rno-miR-296*	HL
hsa-miR-151-5p/mmu-miR-151-5p/rno-miR-151	FL	hsa-miR-520d-5p	HL	hsa-miR-17*/rno-miR-17-3p	HL
hsa-miR-28-5p/mmu-miR-28/rno-miR-28	FL	hsa-miR-551b*	HL	hsa-miR-452	HL
hsa-miR-302a/mmu-miR-302a	FL	hsa-miR-340*/mmu-miR-340-3p/rno-miR-340-3p	HL	hsa-miR-943	HL
hsa-miR-215	FL	hsa-miR-889	HL	hsa-miR-326/mmu-miR-326/rno-miR-326	HL
hsa-miR-15b/mmu-miR-15b/rno-miR-15b	FL	hsa-miR-494/mmu-miR-494/rno-miR-494	HL	hsa-miR-652/mmu-miR-652/rno-miR-652	HL
hsa-miR-29b/mmu-miR-29b/rno-miR-29b	FL	hsa-miR-874/mmu-miR-874/rno-miR-874	HL	hsa-miR-623	HL
hsa-miR-138/mmu-miR-138/rno-miR-138	FL	hsa-miR-30c-2*/mmu-miR-30c-2*/rno-miR-30c-2*	HL	hsa-miR-194*	HL
hsa-miR-363/mmu-miR-363/rno-miR-363	FL	hsa-miR-183*/mmu-miR-183*	HL	hsa-miR-557	HL
hsa-miR-142-5p/mmu-miR-142-5p/rno-miR-142-5p	FL	hsa-miR-25*	HL	hsa-miR-125a-3p/mmu-miR-125a-3p/rno-miR-125a-3p	HL
hsa-miR-19a/mmu-miR-19a/rno-miR-19a	FL	hsa-miR-513a-5p	HL	hsa-miR-425*/mmu-miR-425*	HL
hsa-miR-497/mmu-miR-497/rno-miR-497	FL	hsa-miR-198	HL	hsa-miR-10a*/mmu-miR-10a*/rno-miR-10a-3p	HL
hsa-miR-144*	FL	hsa-miR-659	HL	hsa-miR-323-3p/mmu-miR-323-3p/rno-miR-323	HL
hsa-miR-16/mmu-miR-16/rno-miR-16	FL	mg hv-miR-M1-4	HL	hsa-miR-519e	HL
hsa-miR-138-1*/mmu-miR-138*/rno-miR-138*	FL	hsa-miR-129-5p/mmu-miR-129-5p/rno-miR-129-5p	HL	hsa-miR-502-5p	HL
hsa-miR-768-5p	FL	ebv-miR-BART13	HL	hsa-miR-124*/mmu-miR-124*/rno-miR-124*	HL
hsa-miR-30c/mmu-miR-30c/rno-miR-30c	FL	hsa-miR-193b*	HL	hsa-miR-345	HL
hsa-miR-129*	FL	hsa-miR-422a	HL	hsa-miR-584	HL
hsa-miR-801/mmu-miR-801	FL	hsa-miR-503	HL	hsa-miR-654-5p	HL

FL vs HL	Higher in	FL vs HL (con't)	Higher in	FL vs HL (con't)	Higher in
hsa-miR-34b/mmu-miR-34b-3p	FL	kshv-miR-K12-3	HL	hsa-miR-331-5p/mmu-miR-331-5p	HL
hsa-miR-363*/rno-miR-363*	FL	hsa-miR-766	HL	hsa-miR-650	HL
hsa-miR-20b*	FL	hsa-miR-516a-5p	HL	hsa-miR-202	HL
hsa-miR-550		hsa-miR-125b-1*/mmu-miR-125b-3p/rno-miR-125b-3p	HL	hsa-miR-548b-3p	
hsa-miR-600	FL	hsa-miR-149*	HL	hsa-miR-492	HL
hsa-miR-196a*/mmu-miR-196a*/rno-miR-196a*	FL	ebv-miR-BART6-3p	HL	hsa-miR-135a*/mmu-miR-135a*	HL
hsa-miR-574-3p/mmu-miR-574-3p	FL	ebv-miR-BART19-3p	HL	ebv-miR-BART20-3p	HL
hsa-miR-620	FL	hsa-miR-671-5p/mmu-miR-671-5p	HL	hsa-miR-586	HL
hsa-miR-331-3p/mmu-miR-331-3p/rno-miR-331	FL	ebv-miR-BART8*	HL	hsa-miR-338-5p/mmu-miR-338-5p/rno-miR-338*	HL
hsa-let-7e/mmu-let-7e/rno-let-7e	FL	hsa-miR-509-3-5p	HL	hsa-miR-92b*	HL
hsa-miR-524-5p	FL	hsa-miR-602	HL	hiv1-miR-H1	HL
hsa-miR-197/mmu-miR-197	FL	ebv-miR-BHRF1-1	HL	hsa-miR-508-5p	HL
hsa-miR-24-1*/mmu-miR-24-1*/rno-miR-24-1*	FL	mghv-miR-M1-7-3p	HL	hsa-miR-542-5p/mmu-miR-542-5p/rno-miR-542-5p	HL
hsa-miR-519e*	HL	mghv-miR-M1-2	HL	hsa-miR-490-5p	HL
hsa-miR-628-3p	HL	hsa-miR-675	HL	hsa-miR-663	HL
				hsa-miR-433/mmu-miR-433/rno-miR-433	HL

CLAIMS

We claim:

1. An isolated nucleic acid molecule having at least 80% sequence identity to any one of SEQ ID NOs: 763-1350 or 1565 or a complementary sequence thereof.
2. The isolated nucleic acid molecule of claim 1, wherein the sequence identity is at least 90%.
3. The isolated nucleic acid molecule of claim 1, wherein the sequence identity is at least 95%.
4. The isolated nucleic acid molecule of claim 1, wherein the nucleic acid sequence comprises any one of SEQ ID NOs: 763-1350 or 1565 or a complementary sequence thereof.
5. The nucleic acid molecule of any of claims 1-4, which is a miRNA precursor molecule having the sequence of SEQ ID NOs: 763-1350 or 1565, or a DNA molecule coding the miRNA.
6. The nucleic acid molecule of any of claims 1-4, which is single-stranded.
7. The nucleic acid molecule of any of claims 1-4, which is at least partially double-stranded.
8. The nucleic acid molecule of any of claims 1-4, which is selected from RNA or DNA molecules.
9. The isolated nucleic acid molecule of any of claims 1-4, wherein the nucleic acid molecule is a cDNA that corresponds to any one of SEQ ID NOs: 763-1350 or 1565.
10. The nucleic acid molecule of claim 8, comprising at least one modified nucleotide analog.

11. A composition comprising at least one nucleic acid molecule of any of claims 1-10 and a carrier or vehicle.
12. The composition of claim 11 wherein the carrier or vehicle is a pharmaceutically acceptable carrier or vehicle suitable for diagnostic applications.
13. The composition of claims 11-12 wherein carrier or vehicle is a pharmaceutically acceptable carrier or vehicle is suitable for therapeutic applications.
14. The composition of claim 12, wherein the nucleic acid molecule is suitable as a marker or a modulator of a B cell malignancy.
15. A recombinant expression vector comprising at least one nucleic acid molecule of any of claims 1-10.
16. A cell comprising the recombinant expression vector of claim 15.
17. A method of determining the B cell stage of a B cell malignancy in a subject comprising determining the level of expression of at least one microRNA in a sample comprising a B cell taken from the subject relative the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in Table 4.
18. The method of claim 17, wherein at least one microRNA selected from the microRNAs in Table 4 has a q value of less than 5 in at least one of the last three columns of Table 4.
19. A method of identifying a B cell malignancy in a subject comprising determining the level of expression of at least one microRNA in a sample comprising a B cell taken from the subject relative the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in Table 4.

20. A method of diagnosing a B cell malignancy in a subject comprising determining the level of expression of at least one microRNA in a sample comprising a B cell taken from the subject relative the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in Table 4.

21. The method of claim 20, wherein the B cell malignancy is one of at least two potential B cell malignancies, wherein at least two of the potential B cell malignancies are derived from different B cell stages.

22. A method of identifying a B cell malignancy in a subject comprising determining the level of expression of at least one microRNA in a sample comprising a B cell taken from the subject relative the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in any one of Tables 7 to 35.

23. The method of claim 22, wherein the B cell malignancy is selected from chronic lymphocytic leukemia, follicular lymphoma, Hodgkin's lymphoma, activated B-cell diffuse large B cell lymphoma (DLBCL), germinal center-like DLBCL, and Burkitt lymphoma.

24. A method of diagnosing a B cell malignancy in a subject comprising determining the level of expression of at least one microRNA in a sample comprising a B cell taken from the subject relative to the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in any one of Tables 7 to 35.

25. The method of claim 24, wherein the B cell malignancy is selected from chronic lymphocytic leukemia, follicular lymphoma, Hodgkin's lymphoma, activated B-cell diffuse large B cell lymphoma (DLBCL), germinal center-like DLBCL, and Burkitt lymphoma.

26. A method of determining whether a B cell malignancy in a sample is Burkitt lymphoma, activated B cell-like diffuse large B cell lymphoma (DLBCL), or germinal center-like DLBCL, comprising determining the level of expression of at least one microRNA in the sample relative

to the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in Table 10, column “BL miRNA list”; Table 14, column “BL High”; Table 11; Table 14, column “ABC High”; Table 10, column “GCB miRNA list”; Table 14, column “GCB High”; Table 32, or Table 35.

27. The method of claim 26, comprising determining the level of expression of at least one microRNA selected from the microRNAs listed in Table 10, column “BL miRNA list”, and Table 14, column “BL High”; determining the level of expression of at least one microRNA selected from the microRNAs listed in Table 11 and Table 14, column “ABC High”; and determining the level of expression of at least one microRNA selected from the microRNAs listed in Table 10, column “GCB miRNA list”, and Table 14, column “GCB High”.

28. A method of determining whether a B cell malignancy in a sample is Burkitt lymphoma, activated B cell-like diffuse large B cell lymphoma (DLBCL), or germinal center-like DLBCL, comprising determining the level of expression of at least one microRNA in the sample relative to the level of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in at least one column labeled “GCBvsBL” or “GCBvsABC” in Table 7 or “ABCvsBL” in Table 8.

29. The method of claim 28, wherein at least one microRNA is listed in no more than two columns selected from the columns labeled “GCBvsBL” or “GCBvsABC” in Table 7 or “ABCvsBL” in Table 8.

30. The method of claim 27, wherein at least one microRNA is listed in only one column selected from the columns labeled “GCBvsBL” or “GCBvsABC” in Table 7 or “ABCvsBL” in Table 8.

31. A method of determining whether a B cell malignancy in a sample is activated B cell-like diffuse large B cell lymphoma (DLBCL), or germinal center-like DLBCL, comprising determining the level of expression of at least one microRNA in the sample relative to the level

of expression of the at least one microRNA in a control sample, wherein the at least one microRNA is selected from the microRNAs listed in Table 35.

32. A microarray comprising miRNA-specific probe oligonucleotides wherein at least one miRNA-specific probe oligonucleotide is specific for a sequence of SEQ ID NOs: 763-1350 or 1565, or any combination thereof.

33. The microarray of claim 32 wherein the microarray further comprises miRNA-specific probes oligonucleotides for the miRNA sequences in Tables 4 or 7-35.

34. The microarray of claim 32 wherein the microarray comprises miRNA-specific probes oligonucleotides for SEQ ID NOs: 763-1350 or 1565.

35. A kit comprising at least one primer sequence that can detect any one of SEQ ID NOs: 763-1350 or 1565, or a combination thereof.

36. A kit comprising at least one isolated nucleic acid molecule having a sequence of any one of SEQ ID NOs: 1351-1564.

37. The kit of either of claims 35-36, further comprising enzymes and reagents that are adequate for performing an RT-PCR reaction.

38. A kit comprising the isolated nucleic acid molecule of any of claims 1-10.

39. A DNA library comprising at least one isolated nucleic acid molecule of any one of SEQ ID NOs: 763-1350 or 1565.

40. A DNA library comprising the nucleic acid sequences listed in Table 32.

41. The DNA library of any of claims 39-40 comprising at least one cDNA sequence corresponding to an RNA of SEQ ID NOs: 763-1350 or 1565, or any combination thereof.

Figure 1

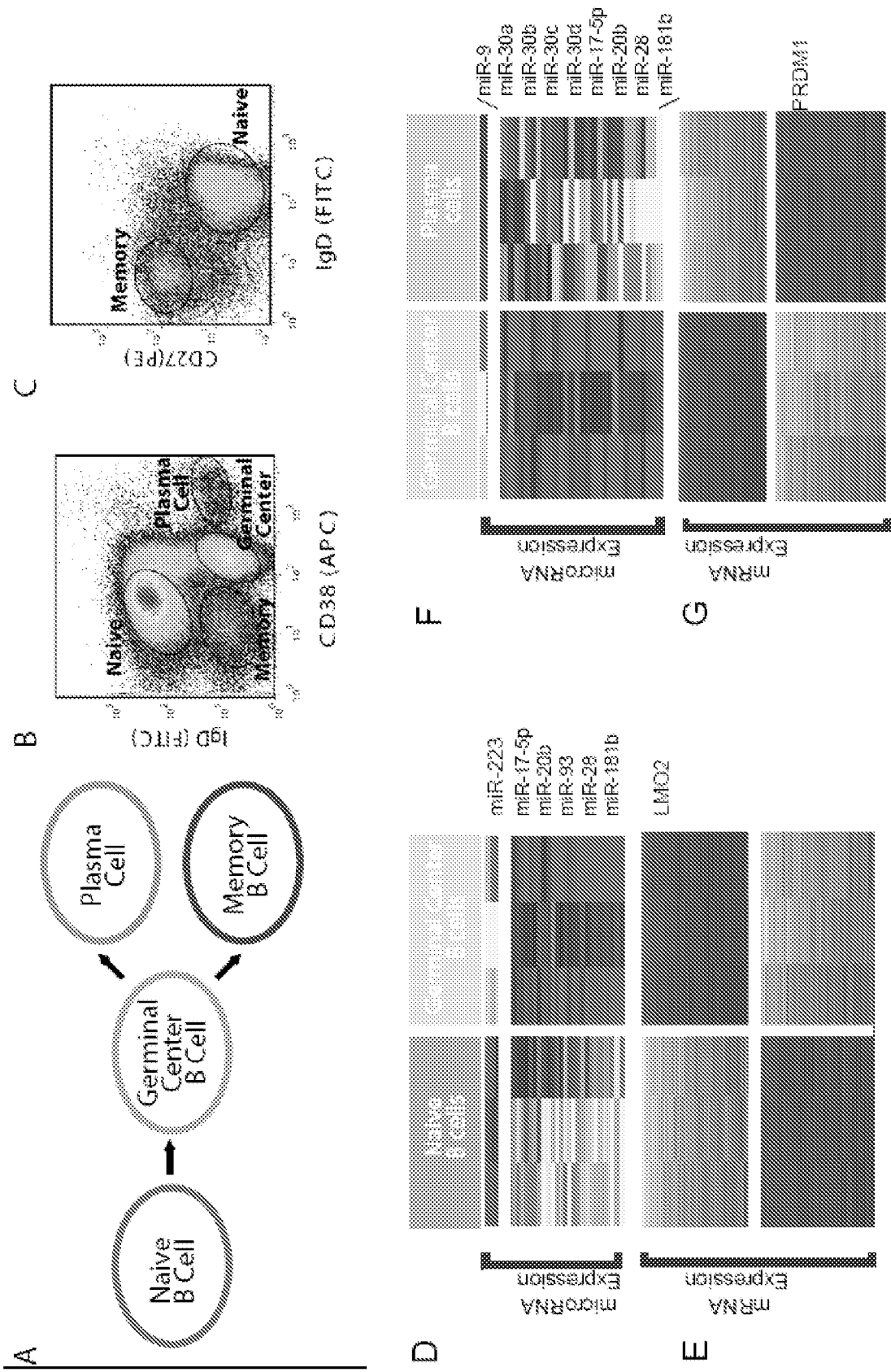


Figure 1 (con't)

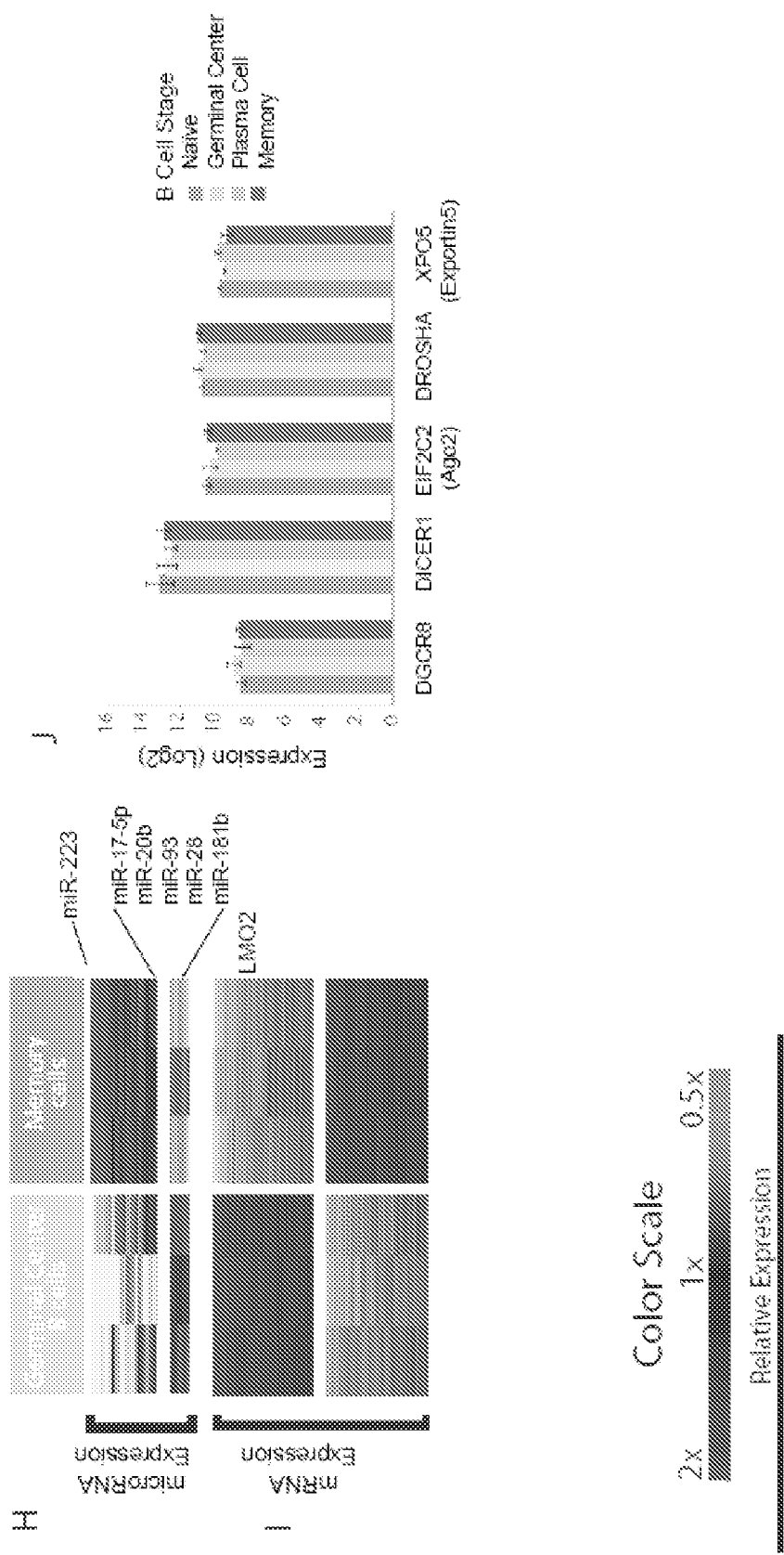


Figure 2

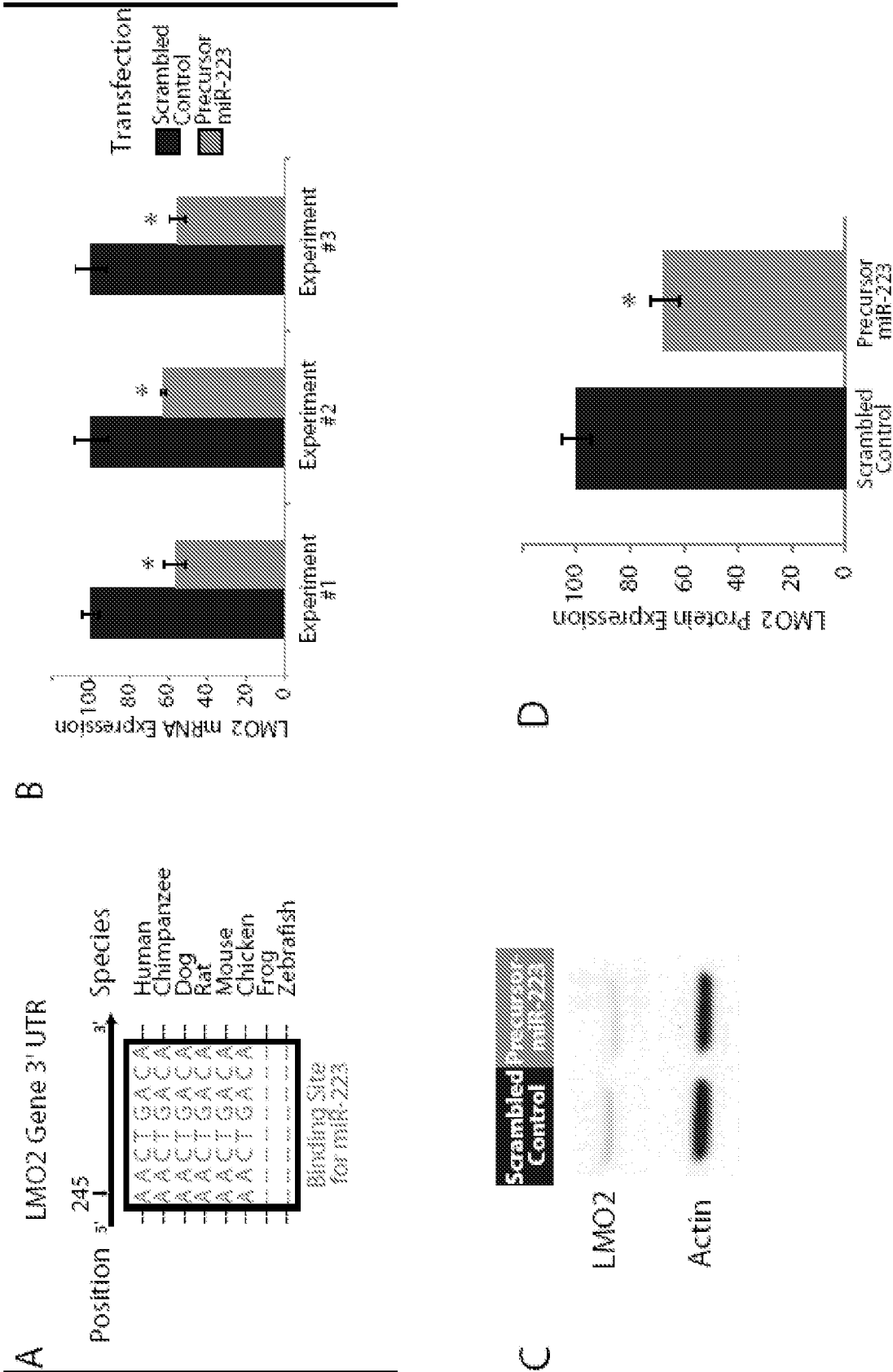


Figure 2 (con't)

E

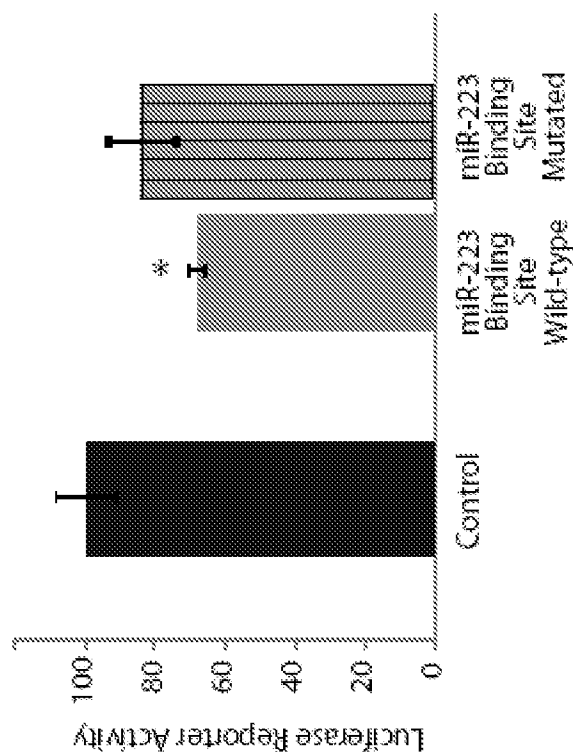
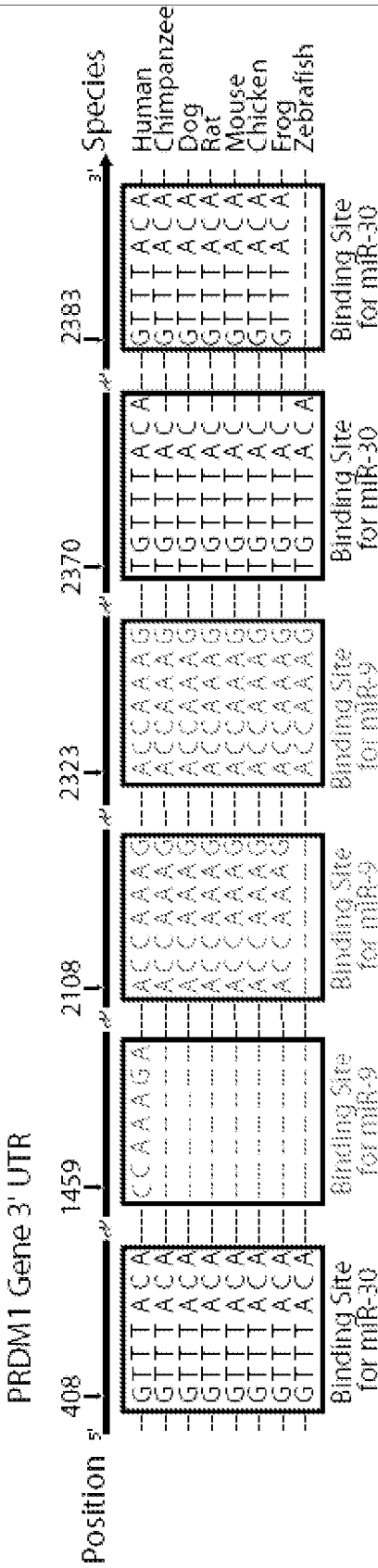


Figure 3
A



B

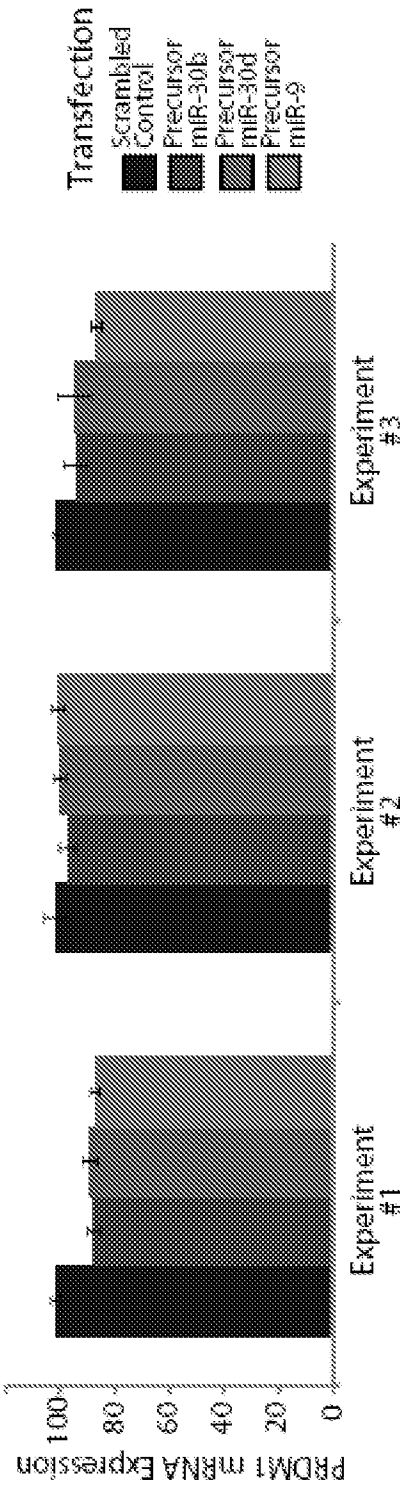


Figure 3 (con't)

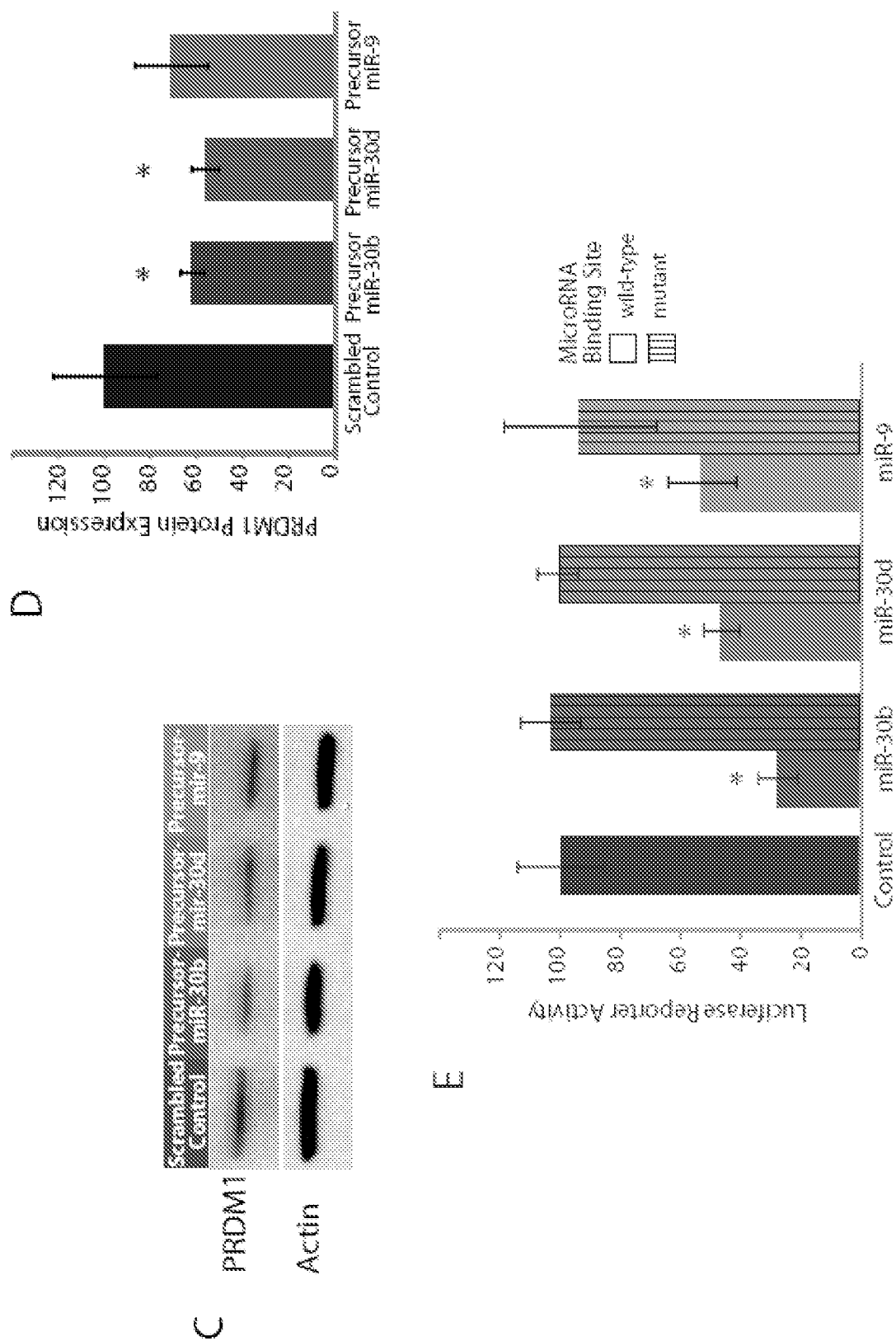


Figure 4

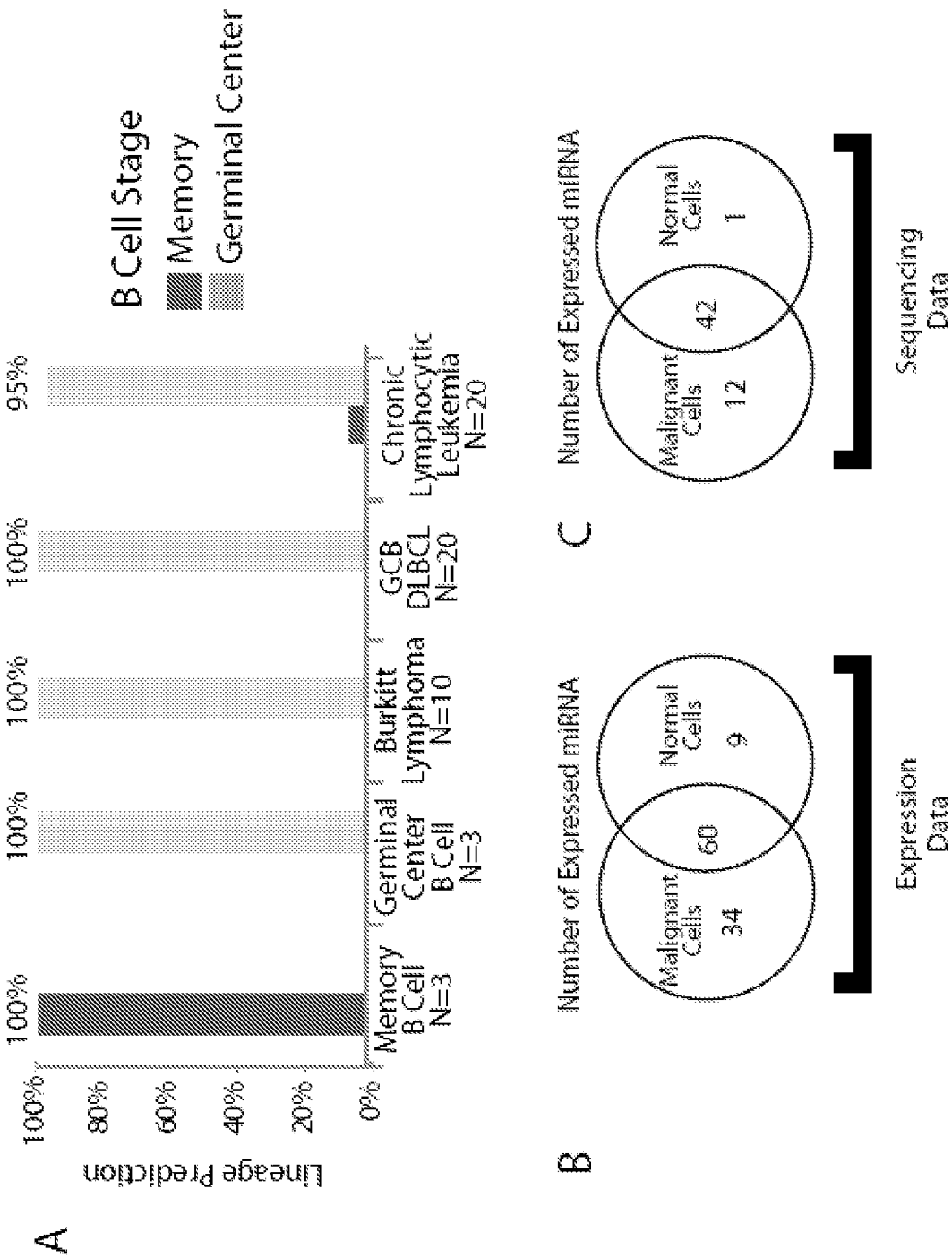


Figure 4 (con't)
D

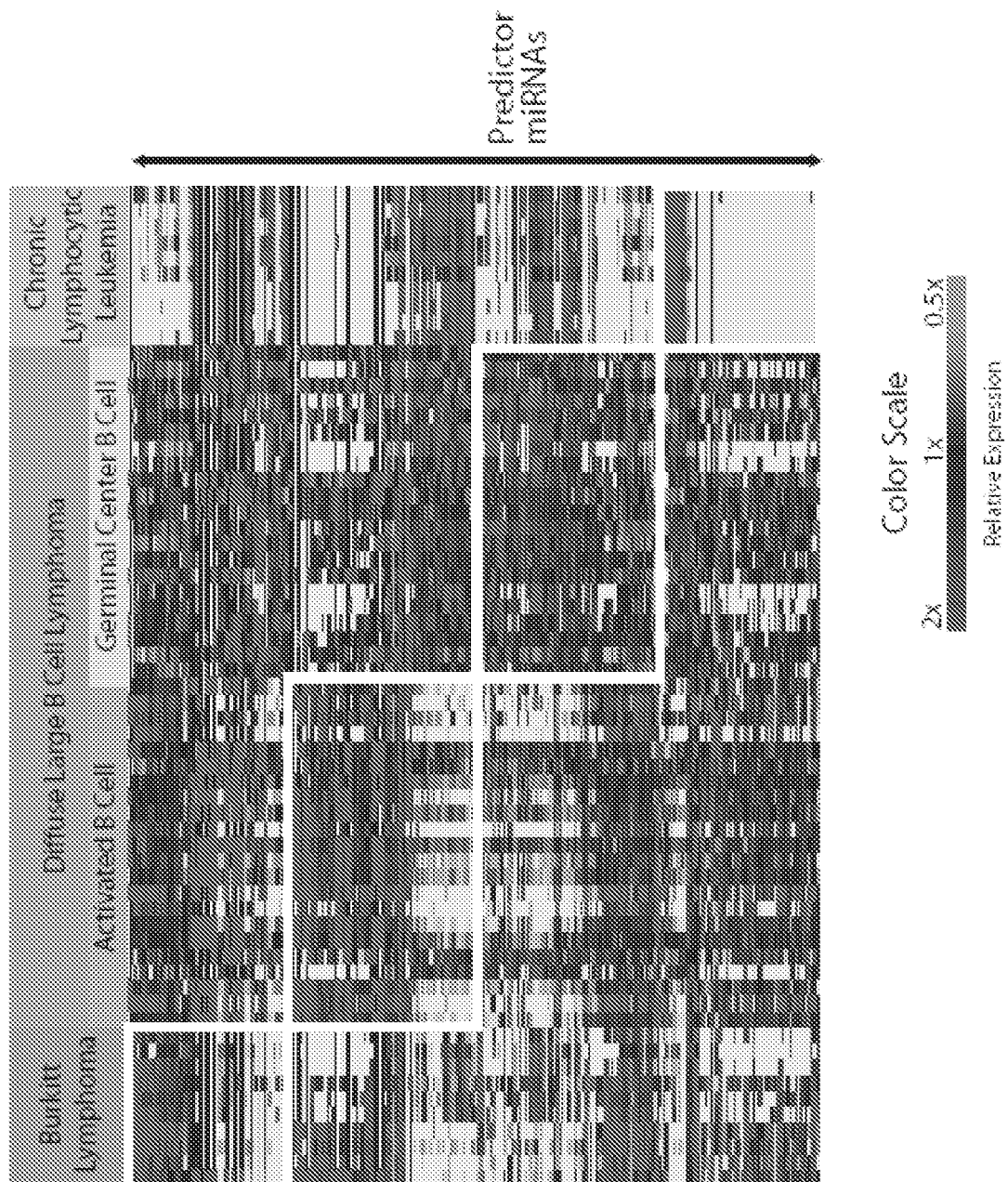


Figure 5

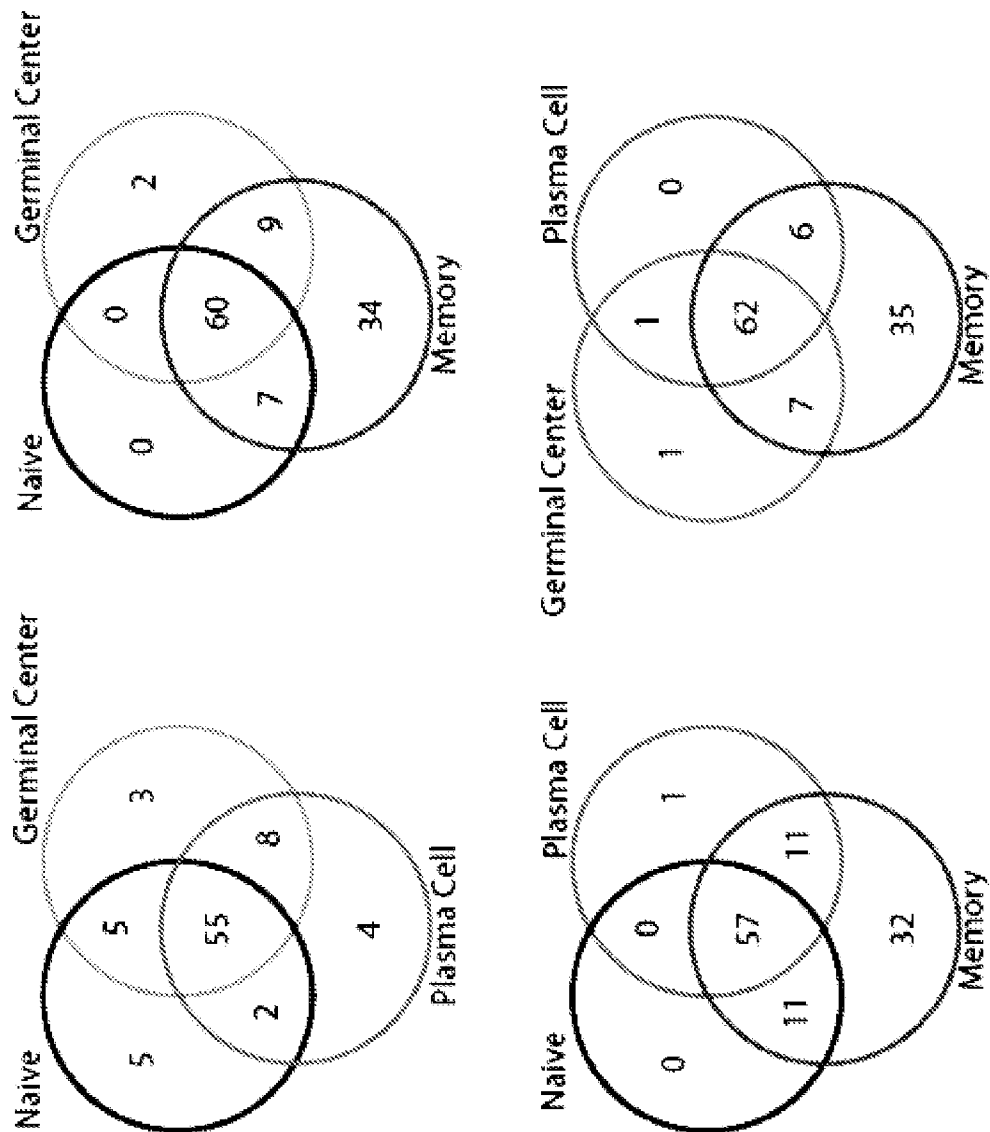


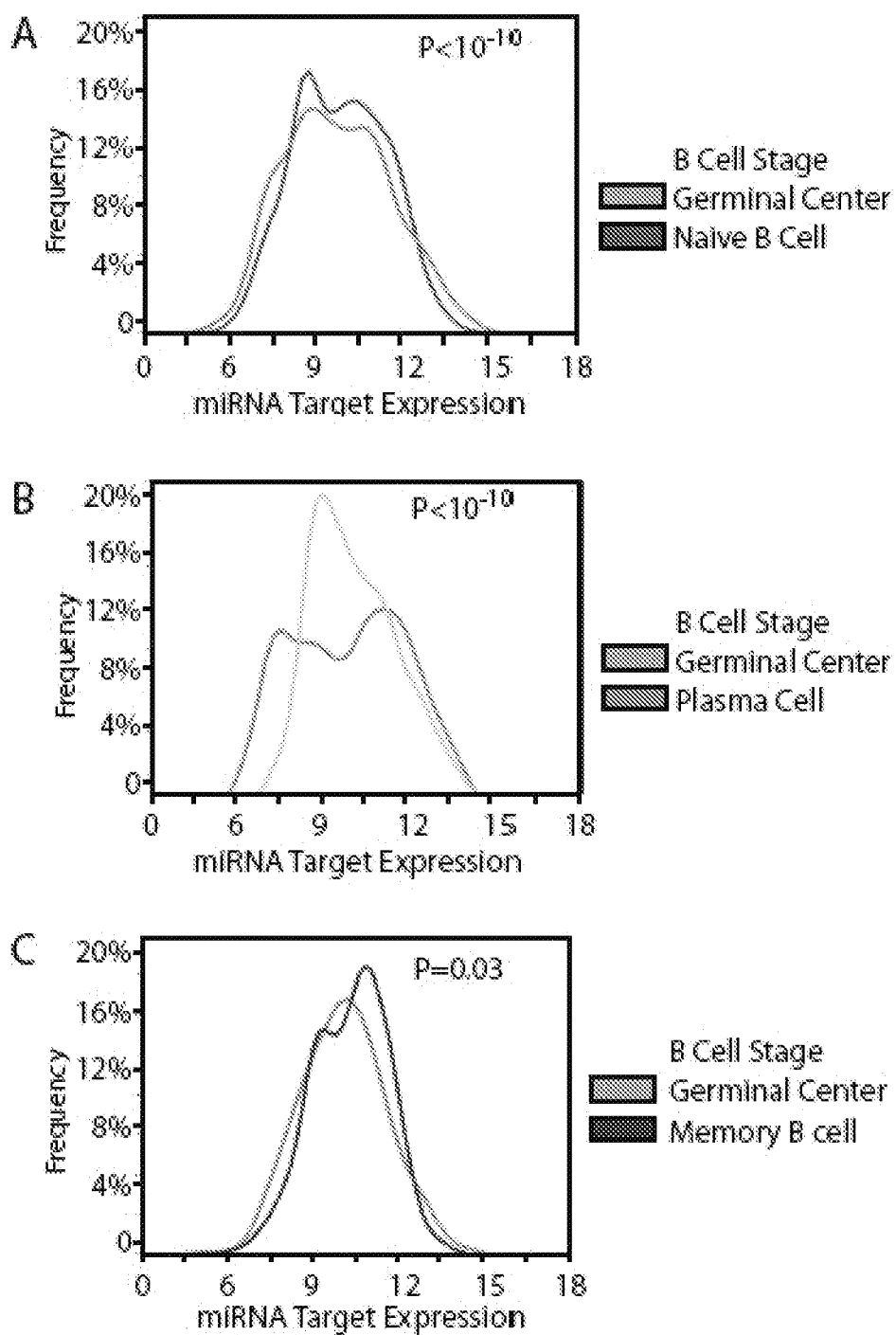
Figure 6

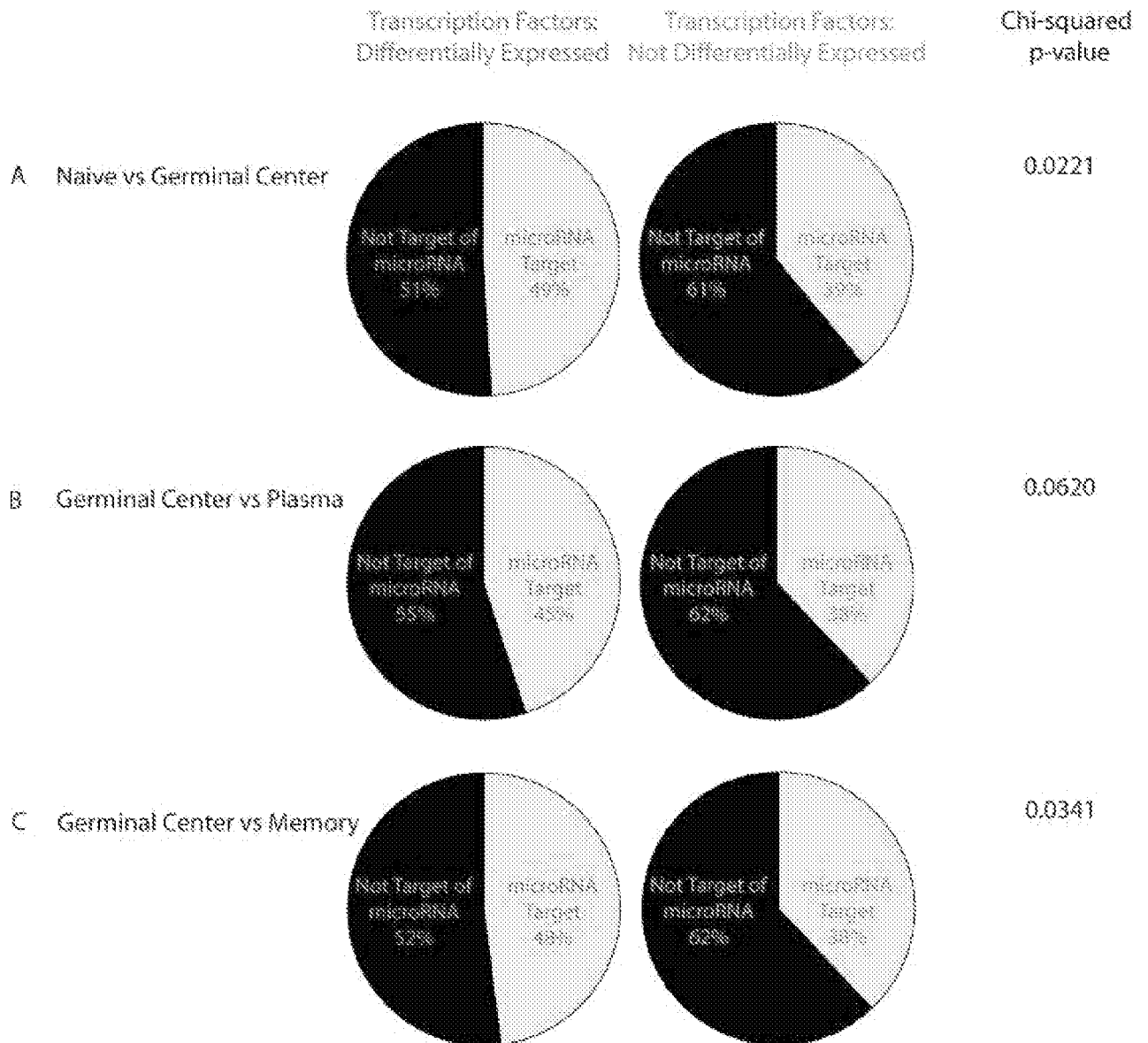
Figure 7

Figure 8

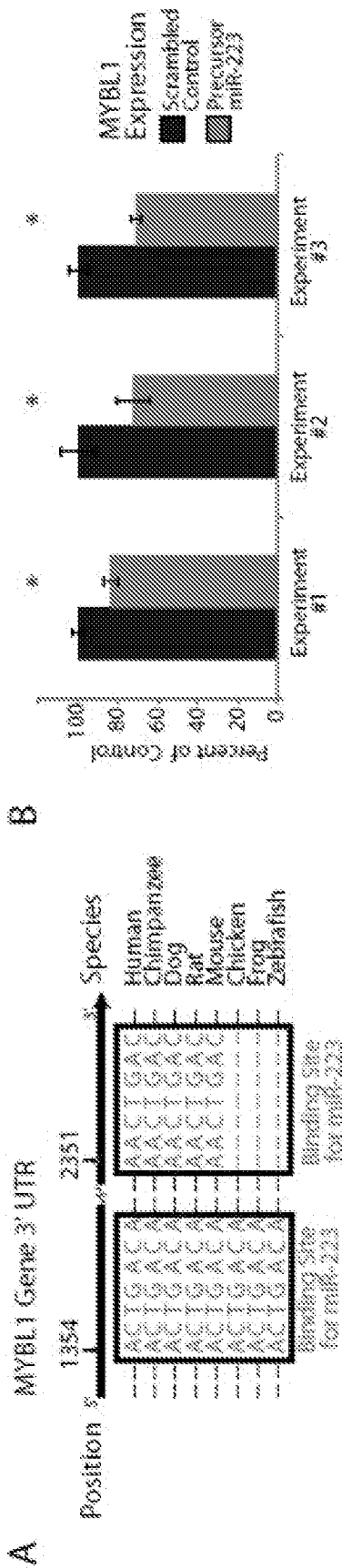


Figure 9

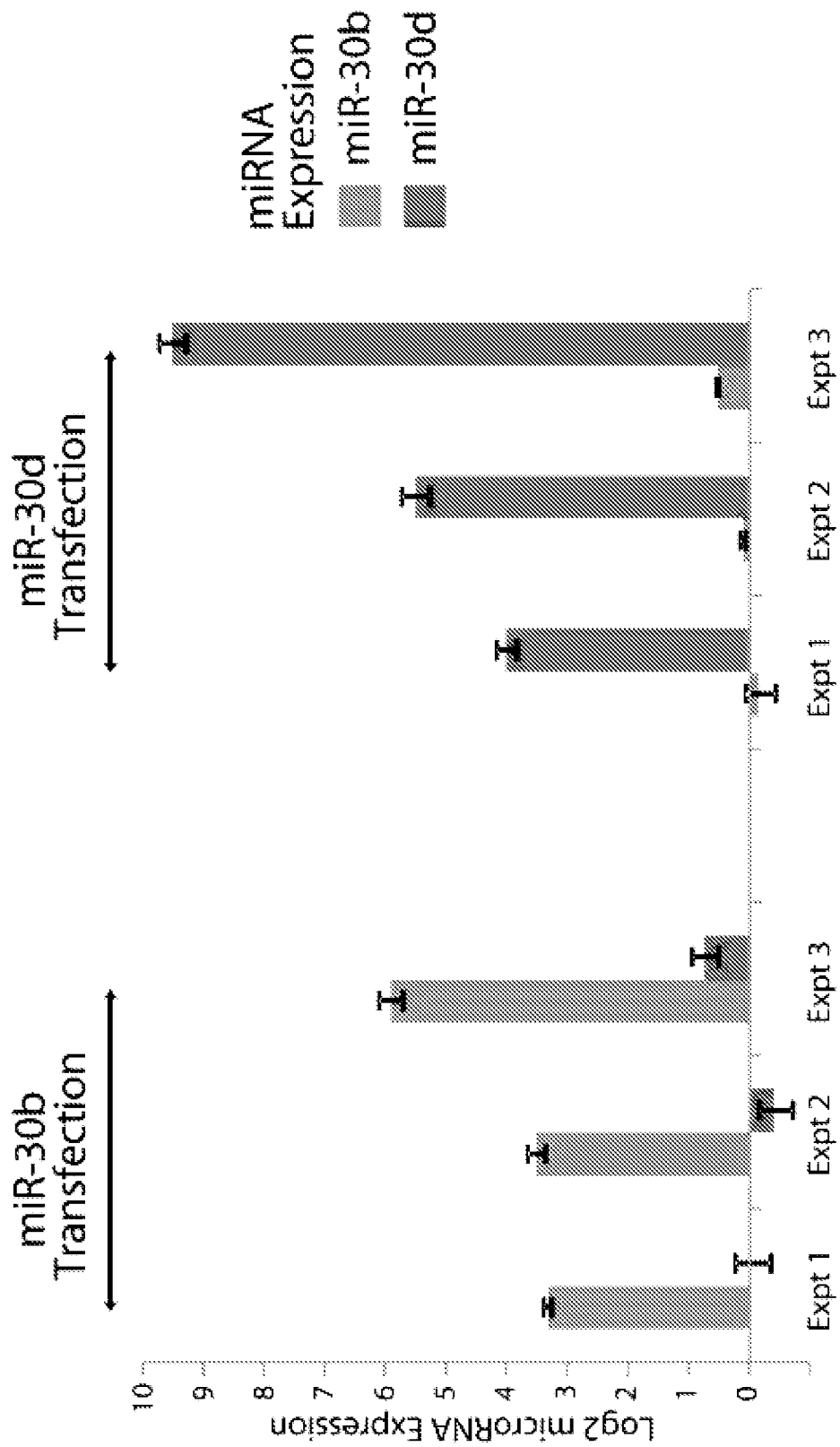


Figure 10

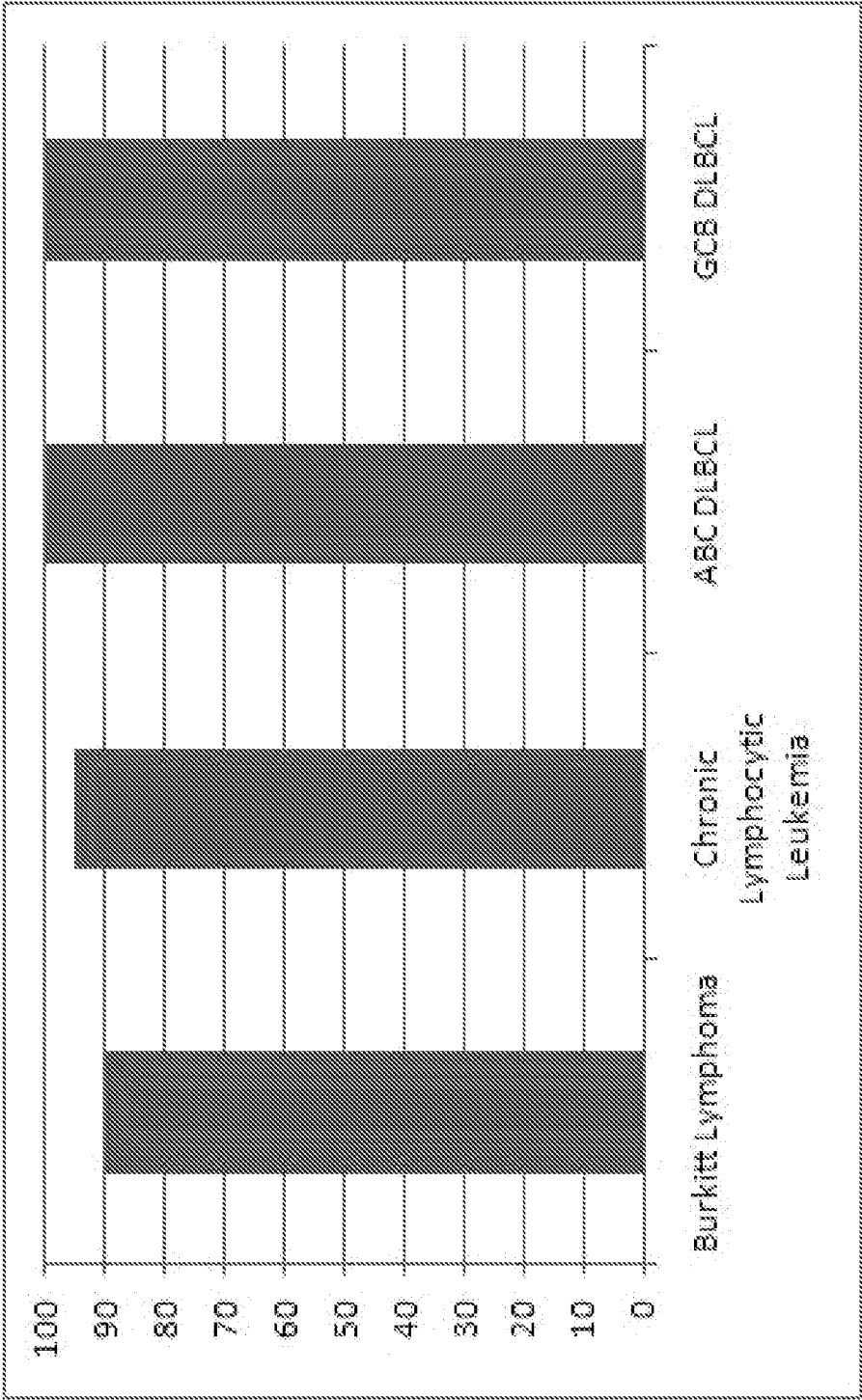


Figure 11