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ketA B-cell receptor-related gene signature predicts survival in mantle cell lymphoma: results from the "Fondazione Italiana Linfomi" MCL-0208 trial

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Abstract

Mantle cell lymphoma patients have variable clinical courses, ranging from indolent cases not requiring immediate treatment to aggressive, rapidly progressing diseases. Thus, diagnostic tools capable to stratify patients according to their risk of relapse and death are warranted. The study included 83 samples from the "Fondazione Italiana Linfomi" MCL-0208 clinical trial. Through gene expression profiling and quantitative real-time PCR we analyzed 46 peripheral blood and 43 formalin-fixed paraffin-embedded lymph node samples. A prediction model to classify patients was developed. By analyzing the transcriptome of 27 peripheral blood samples, two subgroups characterized by a differential expression of genes from the B-cell receptor pathway (B-cell receptor^{low} and B-cell receptor^{high}) were identified. The prediction model based on the quantitative real-time PCR values of six representative genes (*AKT3*, *BCL2*, *BTK*, *CD79B*, *PIK3CD*, and *SYK*), was used to classify the 83 cases (43 B-cell receptor^{low} and 40 B-cell receptor^{high}). The B-cell receptor^{high} signature associated with shorter progression-free survival (P=0.0074), selected the mantle cell lymphoma subgroup with the shortest progression-free survival and overall survival (P=0.0014 and P=0.029) in combination with high (≥30%) Ki-67 staining, and was independent predictor of short progression-free survival along with the "Mantle Cell Lymphoma International Prognostic Index"-c score. Moreover, the clinical impact of the 6-gene signature related to the B-cell receptor pathway identified mantle cell lymphoma subset with shorter progression-free survival intervals also in an external independent mantle cell lymphoma cohort homogenously treated with different schedules. In conclusion, this 6-gene signature associates with a poor clinical response in the context of the MCL-0208 clinical trial. NCT02354313

Introduction

Mantle cell lymphoma (MCL) is a distinctive B cell malignancy accounting for 5-10% of all lymphomas,[1-3] whose molecular hallmark and initiating oncogenic event, the t(11;14)(q13;q32) translocation, leads to constitutive overexpression of the proto-oncogene cyclin D1 (CCND1).[2,4]

Once considered as uniformly characterized by a poor prognosis, MCL has been demonstrated to have unexpectedly variable clinical courses, ranging from indolent cases not requiring immediate treatment to aggressive, rapidly progressing disease.[2,5-10] Even among patients requiring treatment, prognosis is highly heterogeneous, with patients experiencing prolonged remissions and others rapidly relapsing even after cytarabine-containing induction regimens followed by autologous transplantation. Thus, diagnostic tools capable to stratify MCL patients in different risk classes are warranted, in order to direct treatment strategies.[11] For this reason, many attempts have been made to identify clinical, histologic, and molecular markers that allow the stratification of patients according to their risk of relapse and death.[12-25]

In addition to the clinical MCL prognostic score (MCL-International Prognostic Index, MIPI)[12,14] capable to stratify patients into risk groups with different overall survival,[14] the Ki-67 proliferation index has been proposed as one of the most powerful and independent predictor of survival in MCL even in the context of prospective trials and modern therapies,[5,13,26] and for these reasons integrated in the so-called MIPI-c score.[13,26] Moreover, effective prognostic discrimination is achieved by post-treatment response monitoring by PET-scan and minimal residue disease. Furthermore, a seminal study identified a specific signature associated with proliferation as the strongest predictor of overall survival in a large MCL series.[20] In this context, a cohort of 20 proliferation-associated genes constructed on the basis of gene expression analysis was demonstrated to be superior to other molecular markers.[20] Since approaches based on microarray technology cannot be still applied for routine clinical purposes, a PCR-based surrogate method investigating expression of five genes has been proposed and applied to paraffin-embedded tissues.[18]

Recent evidences suggest that the B-cell receptor (BCR) pathway may contribute to the pathogenesis of several histological types of B-cell non-Hodgkin lymphomas, including MCL.[27-30] The importance of BCR signaling pathway in B-cell malignancy pathogenesis has driven interest in the use of small-molecule inhibitors of BCR-associated kinases, potentially preventing the activation of one or more of the distal BCR signaling pathway proteins.[28,31]

In the present study, we developed a survival predictive model for younger patients with advanced MCL, treated in the context of the “Fondazione Italiana Linfomi” (FIL) MCL-0208 phase III randomized clinical trial. Notably, this model, based upon the quantitative evaluation of six genes, mostly from BCR pathway, as selected from a gene expression profile (GEP) of peripheral blood (PB) MCL cells, and applicable to formalin-fixed paraffin-embedded (FFPE) tissue specimens, predicts poor response in the context of FIL-MCL-0208 trial.

Methods

Primary MCL cases

The study included 83 out of 300 samples of adult patients aged<66 years with advanced stage MCL, enrolled in the "FIL-MCL-0208" prospective, multicenter, phase III randomized clinical trial (NCT02354313),[32] divided as follows: i) a panel of 27 PB samples utilized for GEP upon positive sorting of the clonal $CD5^+/CD19^+$ MCL cells; ii) an additional panel of 19 PB samples utilized for quantitative real time PCR (qRT-PCR) of the identified gene signature in the purified MCL cell component; iii) a panel of 43 lymph nodes (LN) samples utilized for qRT-PCR of the identified gene signature; in this LN panel 6 samples had a matched PB sample. The clinical and histo-pathological details of the 83 MCL cases used in this study are reported in Table 1. No significant differences were found between the 83 cases entering the study *versus* the 217 remaining cases enrolled in the clinical trial in term of median age, MIPI score, Ki-67 index and PFS intervals (Table S1 and Figure S1). No differences were observed between PB and LN MCL samples regarding the clinical and biological parameters (not shown). All patients were treated according to the FIL-MCL-0208 clinical trial as reported in Figure S2.

MCL diagnosis was prospectively confirmed by centralized histological review according to the 2008 WHO criteria.[3,33] All patients provided informed consent in accordance with Institutional Review Board requirements (0016331-BZ 09/02/2010) and declaration of Helsinki and protocol consent included use of MRD sample leftovers for the study.

All the procedures employed for RNA extraction, GEP and downstream analyses, qRT-PCR, analyses and qRT-PCR validations were done following standard protocols, as reported previously.[34-37] Details are reported in Supplemental Information. Microarray data are available in Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/) under accession numbers GSE89447. Cases used for these procedures were reported in Table S2.

Validation procedures

The 6-gene signature was tested in the MCL cohort described by Saba et al,[30] enrolled in another clinical trial (NCT00114738), by using the sum of the array gene expression values, as reported.[30]

Gene signatures related to MCL outcome were retrieved from previous papers,[30,38] and imported in the GeneSpring GX and tested in the present cohort with GEP data available.

Statistical analysis

Overall survival (OS) was computed from trial registration to death as a result of any cause, censored at the latest follow-up in patients who were still alive. Progression-free survival (PFS) was computed from trial registration to progression or death as a result of any cause, censored at the latest tumor assessment if no progression was observed. Clinical correlations, performed with the MedCalc v9.5 software, were made using Kaplan-Meier plots and log-rank test. The Cox proportional model was chosen for multivariable analysis. Clinical outcome results were updated as of January 2017.[32] Investigators are still blinded to investigation arm as the study primary endpoint is currently still not met.

Results

GEP Identifies MCL Patients with Distinct Expression of Genes Belonging to the BCR Pathway

Global GEP was performed in purified MCL cells from 27 PB samples. As shown in Figure 1A, an unsupervised analysis performed by principal component analysis (PCA) divided the cohort in two groups of 14 cases and 13 cases, respectively. Consistently, a hierarchical clustering, which was run with all the GEP features, split MCL cases into two major groups perfectly resembling the PCA groups (Figure 1B).

Supervised analysis according to the PCA classification defined a gene expression signature composed by 922 probes, 713 up-regulated and 209 down-regulated in group-2 *versus* group-1 samples (Table S3 and Figure 1C).

Pathway analysis revealed that "Antigen processing and presentation" and "B cell receptor signaling pathway" were among the top ranked pathways enriched in group-2 category (Table S4). Similar results were obtained by GSEA which highlighted a constitutive overexpression of genes related to the BCR signaling pathways in the context of group-2 patients (Figure 2A and Table S5). Therefore, hereafter the two PCA groups were identified as BCR^{low} (group-1) and BCR^{high} (group-2).

A 6-Gene Signature Identifies BCR^{low} and BCR^{high} MCL samples

Having identified two different groups of MCL patients at diagnosis with a different expression of genes related to the BCR pathway, we overlapped the genes included in the gene sets related to BCR pathway (115 probes), and the differentially expressed genes (922 probes) to create a reduced signature (Figure 2B). In this way, 18 probes corresponding to 15 genes, all overexpressed in BCR^{high} cases were identified (Figure 2B). Among these genes, a subgroup of six genes (*AKT3*, *BCL2*, *BTK*, *CD79B*, *PIK3CD*, and *SYK*) was selected for further validations due to their direct involvement in the BCR pathway and/or the existence of drugs targeting the related proteins. As shown in Figure 2C, a hierarchical cluster using only these six genes was able to discriminate patients belonging to the BCR^{low} or BCR^{high} groups.

Development of a qRT-PCR-Based Predictor for BCR^{low} and BCR^{high} in MCL Samples

By analyzing the expression levels of the selected six genes in the same 27 MCL PB samples by qRT-PCR approach, a strict correlation with GEP data was found (Figure S3B). Moreover, the 27 MCL cases were randomly divided into a training set (17 cases; 8 BCR^{low} and 9 BCR^{high} samples) and a validation set (10 cases; 6 BCR^{low} and 4 BCR^{high} samples) to develop and test a decision tree (DT) model based qRT-PCR data capable to categorize patients in one of the two categories. As reported in Figure 2 D-E and Table S2, the DT model based on qRT-PCR data correctly classified 16/17 cases belonging to the training set and 10/10 cases of the validation cohort, and allowed the classification of 19 additional PB samples screened with qRT-PCR (9 BCR^{low} and 10 BCR^{high}, Table S2).

Association between BCR Categories and Biological and Clinical Parameters

Collectively, the 6-gene signature was re-evaluated by setting up a validated qRT-PCR approach (see Supplemental Information and Table S6) in PB samples from 46 MCL cases, 23 identified as BCR^{low} and 23 as BCR^{high}. By correlating the BCR groups with the available biological parameters, no association was found between the 6-gene signature and IGHV gene status (P=0.93, Figure S4A and Table S2); Ki-67 expression, white blood cells, hemoglobin, lymphocytes, platelets, and neutrophils count (data not shown). The only significant difference was between the BCR classification and LDH levels; as shown in Figure S4B, BCR^{high} cases showed higher level of LDH respect to BCR^{low} MCL (416.6±191.6 *versus* 292.2±127.4, P=0.023).

Clinically, MCL patients classified as BCR^{high}, experienced shorter PFS respect to BCR^{low} MCL cases (median PFS: 21.6 months *versus* not reached, P=0.0375; Figure 3).

Application of the 6-Gene Signature to LN samples from MCL patients

To evaluate the capability of the 6-gene signature to identify different subgroups also in the context of MCL LN cases, we tested our qRT-PCR approach in a series of 43 LN samples preserved as FFPE LN specimens. Thirty-five (81%) out of 43 samples were amplifiable for all six genes, and as reported in Table S2, using a DT model based on qRT-PCR values from FFPE, 23 cases were classified as BCR^{low} and 20 classified as BCR^{high}. Notably, for 6 out of 43 LN samples, a PB matched sample was available, and by comparing qRT-PCR results performed on PB samples and

LN FFPE samples from these cases, a good concordance was overall observed, although FFPE samples generally amplified at higher Ct values (Figure S5). Of note, 5 out of 6 these MCL cases were consistently classified. The misclassified case was considered as BCR^{low} according to GEP data. Also in the context of LN samples, no correlation was found between the different biological parameters and BCR groups (not shown).

By merging the MCL cases analyzed either in PB or in LN, a total of 83 cases were collected, 43 BCR^{low} and 40 BCR^{high}. As shown in Figure 4A, BCR^{high} patients had a shorter PFS with respect to BCR^{low} patients (median PFS: 42.1 months versus not reached, P=0.0074). Being Ki-67 a well-known prognosticator in MCL,[26] we combined the BCR groups with the prognostic groups defined by Ki-67 score. As reported in Figure 4B, cases with high Ki-67 (≥30% of Ki-67 expressing cells) and classified in the BCR^{high} group experienced the shortest PFS, while cases classified as BCR^{low} had similar longer PFS intervals irrespective to the high or low Ki-67 score (median PFS: 20.5 months versus not reached for all the other combinations; P=0.0014). Consistently, multivariable analysis carried out by including the BCR signature and the MIPI-c categories selected the BCR^{high} and the high risk MIPI-c category as independent predictor of PFS (Table 2). Regarding OS, while the BCR readout failed to identify groups with different OS intervals, possibly due to the low rate of events and short follow-up (Figure 4C), the combination of high Ki-67 score and a BCR^{high} 6-gene signature was able again to select the MCL subgroup with the shortest OS (46.7 versus not reached; P=0.029; Figure 4D).

Validations of BCR Signature

To verify whether the BCR signature maintained its prognostic impact in an independent set of patients, we used the gene expression data of MCL LN biopsies reported by Saba et al.[30] Also in this different setting a high expression of the 6-gene signature, as in the context of BCR^{high} cases, identified a MCL patients subset with inferior PFS (P=0.049; Figure S6).

In another set of analyses, by taking advantage of our 27 MCL cases with GEP data available, we correlated our BCR signature with other MCL signatures with proven clinical impact.[30,38] As reported in Figure S7A, the BCR signature reported in Saba et al,[30] divided MCL cases in two groups exactly corresponding to our BCR definition (Figure S7B).[30] Similarly, the 17 genes of the proliferation signature reported by Scott et al,[38] split our MCL cases in 3 different groups resembling the 3 different groups originally defined (Figure S8A). In this context, the shortest PFS

and OS intervals were observed in the third group characterized by higher expression of genes related to proliferation and a BCR^{high} phenotype in keeping with our findings (Figure S8 A-C).

Discussion

In this study, we demonstrated that a BCR-derived signature based upon the differential expression of six genes correlated with shorter PFS intervals in the context of a phase III, prospective clinical trial (FIL-MCL-0208) for younger MCL patients receiving R-CHOP induction, followed by high-dose cytarabine and autologous stem cell transplantation (NCT023541313).[32]

Notably, the BCR-related 6-gene signature reported here was able to identify MCL subset with shorter PFS intervals also in the context of an external independent MCL cohort homogenously treated with different schedules.[30] On the other hand, when the signature described by Saba et al,[30] and Scott et al,[38] were applied to our MCL cases, the patients subsets with the worse prognosis turned out particularly enriched in BCR^{high} cases, even though these signatures did not include any gene from our signature. Therefore, although composed by genes located up-stream the BCR machinery, our signature was able to identify cases with an active BCR pathway as defined by other signature.[30] In this regard, however, experiments with primary MCL cases and/or MCL cell lines Combinating the BCR stimulation with the use of specific BCR inhibitors should be performed to investigate the contribution of the 6-gene signatures described here to the actual activation of the BCR pathway.

Again in agreement with this line of reasoning, BCR^{high} samples presented a significant up-regulation of *PAX5* (see GEP data, Table S3), a gene whose product is known to prevent plasma cell differentiation thus preserving the capacity to respond to antigen-induced activation and proliferation.[39] Taken together these data corroborate recent findings of ongoing active BCR signaling in MCL cell in vivo,[29,30] and further underline the role of antigen stimulation in the ontogeny of MCL as suggested by the skewed *IGVH* gene repertoire found in MCL cells.[40]

In order to discriminate between BCR^{low} and BCR^{high} MCL samples, we developed a DT model based upon the expression of the selected six genes[28] This DT model was applied in an independent cohort of PB samples and then to a further series of FFPE LN samples, thus demonstrating that two MCL subsets with different expression levels of BCR-related genes could be recognized also in the LN compartment, mirroring the PB. Altogether, by combining data from the PB and LN compartments, MCL cases classified as BCR^{high}, showed higher LDH levels and shorter PFS respect to BCR^{low} patients, suggesting that activation of BCR signaling drives tumor proliferation and determines clinical outcome of MCL patients which is in keeping with recent findings.[30]

By combining the predictive capacity of the 6-gene BCR signature with the Ki-67 index, we identified a particularly unfavorable category (BCR^{high}, and high Ki-67) with a substantially shorter PFS and OS respect to the other groups. Consistently, the BCR^{high} signature turned out independent prognosticator along with the high risk MIPI-c category for short PFS by multivariate analysis. There is no indication that the validity of the model may be affected by the different recruitment site (PB *versus* LN), or by different sample storage (frozen *versus* FFPE) because the main clinical parameters were equally distributed between the different series (PB/frozen *versus* LN/FFPE; R.B., unpublished observation). In this regard, an important feature of this model/assay is its applicability to both PB and LN FFPE samples, having therefore the chance to combine results of qRT-PCR with Ki-67 staining in all the cases.

Our data underscore the increasing importance of BCR-related genes in the pathogenesis and development of MCL, further underlined by the clinical significance of drugs specifically targeting genes belonging to this pathway. In particular, therapeutic targeting of BTK,[41] can be rationally exploited in lymphoid malignancies proved to be addicted to an antigen-dependent BCR-mediated active signaling. However, despite the relative high response rate to single agent ibrutinib in relapsed/refractory MCL, it remained unclear why some patients showed pronounced responses, while others received little therapeutic benefit.[31,42] The BCR-related signature, here described, may provide molecular insights explaining the divergent responses of MCL patients to ibrutinib, although other causes of primary resistance might be related to gene mutations in the other pathways, e.g. NF-kB pathway and epigenetic modifiers, as recently reported.[43,44]

In conclusion, in the present study we developed a survival model for patients with MCL composed by six genes (*AKT3*, *BTK*, *CD79B*, *PIK3CD*, *SYK*, *BCL2*) whose expression can be easily investigated by qRT-PCR and also in FFPE specimens. The signature was associated with a poor clinical response in the context of a high-dose chemo-immuno therapy regimen, and might be therefore considered for application/validations in future clinical trials.

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Ref Type: Abstract

Table 1. Characteristics of 83 MCL cases entering the study

	Samples
Number of cases	83
Median age (range)	56 (28-65)
Ratio male/female (%)	57/26 (68)
Abnormal LDH (%)	45/29 (39)
Median WBC (10^{-9}/L)	13.7
Typical Morphology	74
Blastoid Morphology	5
Median Proliferation Index (Ki-67 staining), %	20.0 (0-99)
MIPI-c class	
Low	38 (46%)
Low/intermediate	23 (28%)
High/intermediate	11 (13%)
High	6 (7%)
na	5 (6%)
Median Survival, months (range)	34.7 (1.4-73.4)
Median Progression Free Survival, months (range)	31.3 (1.4-73.4)

WBC, White Blood Count; LDH, lactate dehydrogenase; na, not available.

Table 2. Cox regression analysis on MCL cases

	Univariable		Multivariable	
Variable	HR (95%CI)	p value	HR (95%CI)	p value
BCR signature				
BCR high	2.81 (1.28 to 6.19)	0.01	3.48 (1.47 to 8.25)	0.005
MIPI-C				
Low/intermediate	1.5 (0.6 to 3.73)	0.384		
High/intermediate	1.41 (0.45 to 4.43)	0.557		
High	3.46 (1.1 to 10.91)	0.034	4.17 (1.3 to 13.34)	0.016

Multivariable Cox regression analyses of PFS was performed by including the 6-gene BCR categorization and the MIPI-c score as defined by Hoster et al [13].

HR, Hazard ratio; CI, Confidence Interval; BCR, B Cell Receptor; MIPI-c, MCL International Prognostic Index combined.

Figure legends

Figure 1. Gene Expression Profile (GEP) analysis of 27 MCL samples. A) Principal Component Analysis (PCA) scores represented in a 3D scatter plot. One point per array/sample is shown. Black line indicates separation between PCA classes. B) Hierarchical clustering of 14 group1 cases and 13 group2 cases, using 50 739 probes, is shown. C) Hierarchical clustering of 14 group1 cases and 13 group2 cases, using the 922 differentially expressed probes, is shown. Color codes for gene expression values refer to mean centered log-ratio values.

Figure 2. 6-gene signature and Decision Tree (DT) prediction model. A) GEP data of BCR^{low} and BCR^{high} MCL samples were tested using Gene set enrichment analysis (GSEA). Reported are the significantly gene sets differentially expressed and related to the B-Cell Receptor (BCR) pathway. B) Venn diagram derived by merging the differentially expressed probes and the genes belonging to the BCR related gene sets. In bold genes selected as the 6-gene signature. C) Hierarchical clustering of 14 BCR^{low} cases and 13 BCR^{high} cases, using the six gene values, is shown. Color codes for gene expression values refer to mean centered log-ratio values. D) Hierarchical clustering of 8 BCR^{low} cases and 9 BCR^{high} cases belonging to the training set of DT prediction model, using the six gene qRT-PCR values, is shown. E) Hierarchical clustering of 6 BCR^{low} cases and 4 BCR^{high} cases belonging to the validation set of DT prediction model, using the six gene qRT-PCR values, is shown. Bar under the heat-map refers to prediction generated by the DT prediction model. Color codes for gene expression values refer to mean centered log-ratio values.

Figure 3. BCR^{high} MCL group is associated with a worse clinical outcome. Kaplan-Meier curves obtained by comparing PFS intervals of 23 BCR^{low} MCL cases with 23 BCR^{high} MCL cases. The number of patients in each group is reported under relative categories; P value refers to log-rank test.

Figure 4. BCR^{high} MCL group is associated with a worse clinical outcome (overall series). A) Kaplan-Meier curves obtained by comparing PFS intervals of 43 BCR^{low} MCL cases with 40 BCR^{high} MCL cases. B) Kaplan-Meier curves obtained by comparing PFS intervals of 19 BCR^{low} and low Ki-67 MCL cases, with 20 BCR^{low} and high Ki-67 MCL cases, with 21 BCR^{high} and Ki-67

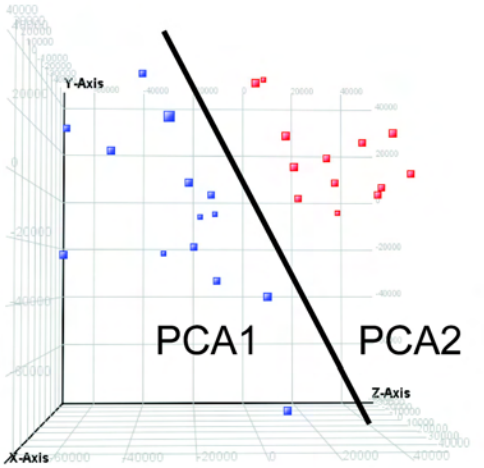
low MCL cases, with 10 BCR^{high} and Ki-67 high MCL cases. C) Kaplan-Meier curves obtained by comparing OS intervals of 43 BCR^{low} MCL cases with 40 BCR^{high} MCL cases. D) Kaplan-Meier curves obtained by comparing OS intervals of 19 BCR^{low} and low Ki-67 MCL cases, with 20 BCR^{low} and high Ki-67 MCL cases, with 21 BCR^{high} and Ki-67 low MCL cases, with 10 BCR^{high} and Ki-67 high MCL cases. The number of patients in each group is reported under relative categories; P value refers to log-rank test.

Figure 1

A

BCR^{low}

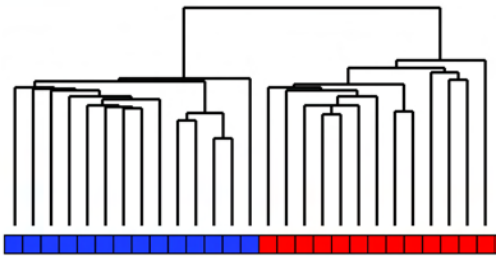
BCR^{high}



B

BCR^{low}

BCR^{high}



C

BCR^{low}

BCR^{high}

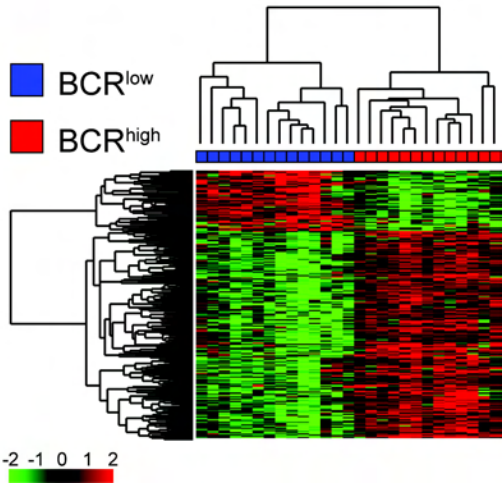
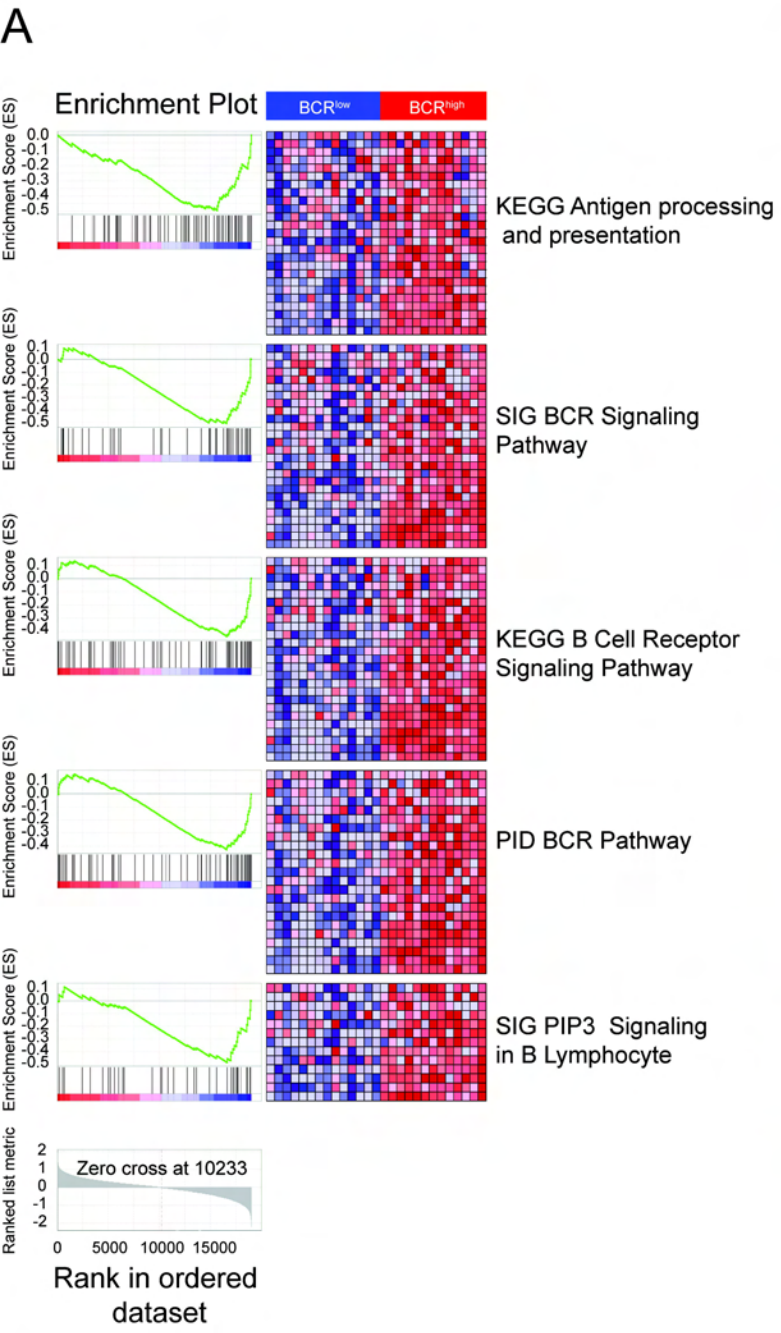
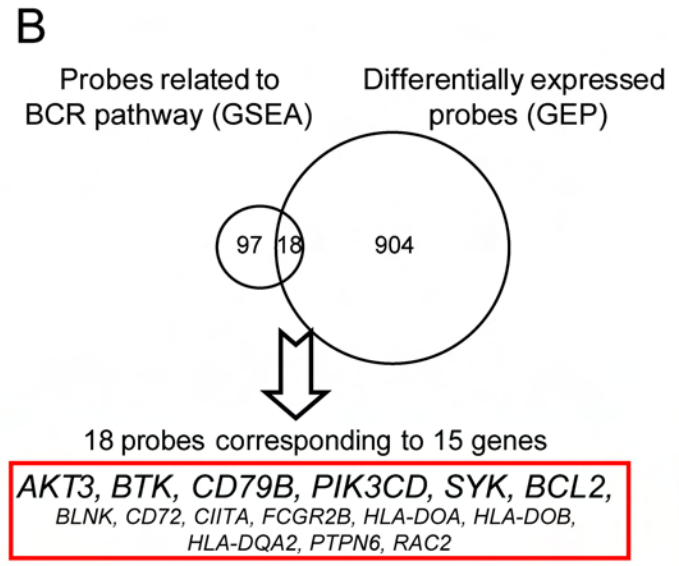
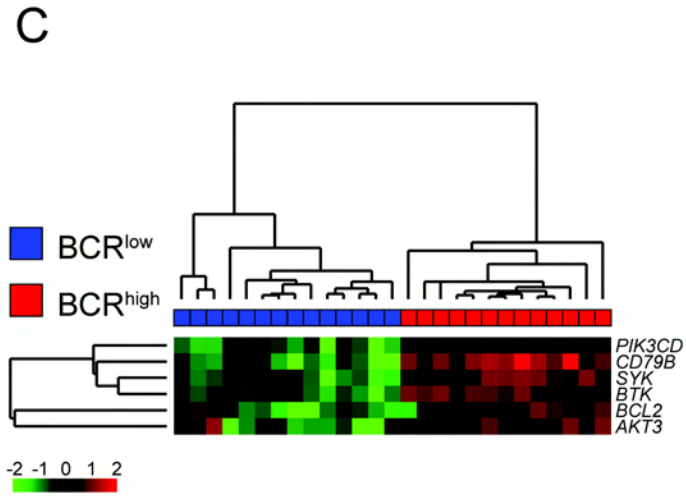
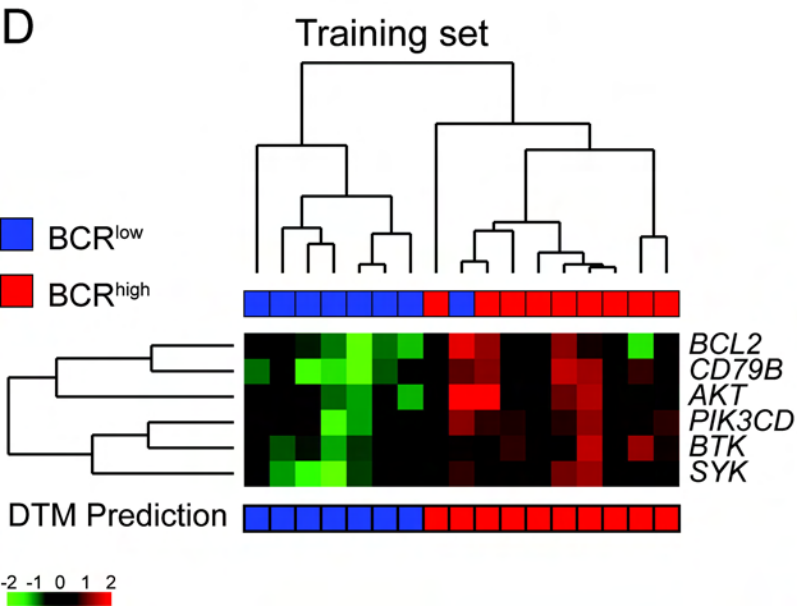


Figure 2


A
Enrichment Plot
BCR^low
BCR^high
Enrichment Score (ES)
KEGG Antigen processing and presentation
SIG BCR Signaling Pathway
KEGG B Cell Receptor Signaling Pathway
PID BCR Pathway
SIG PIP3 Signaling in B Lymphocyte
Ranked list metric
Zero cross at 10233
Rank in ordered dataset


B
Probes related to BCR pathway (GSEA)
Differentially expressed probes (GEP)
97
18
904
18 probes corresponding to 15 genes
AKT3, BTK, CD79B, PIK3CD, SYK, BCL2,
BLNK, CD72, CIITA, FCGR2B, HLA-DOA, HLA-DOB,
HLA-DQA2, PTPN6, RAC2


C
BCR^low
BCR^high
PIK3CD
CD79B
SYK
BTK
BCL2
AKT3
-2 -1 0 1 2


D
Training set
BCR^low
BCR^high
BCL2
CD79B
AKT
PIK3CD
BTK
SYK
DTM Prediction
-2 -1 0 1 2

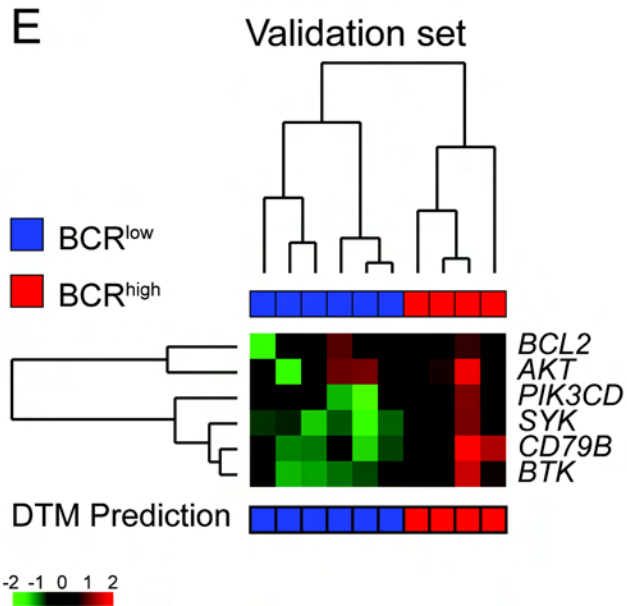
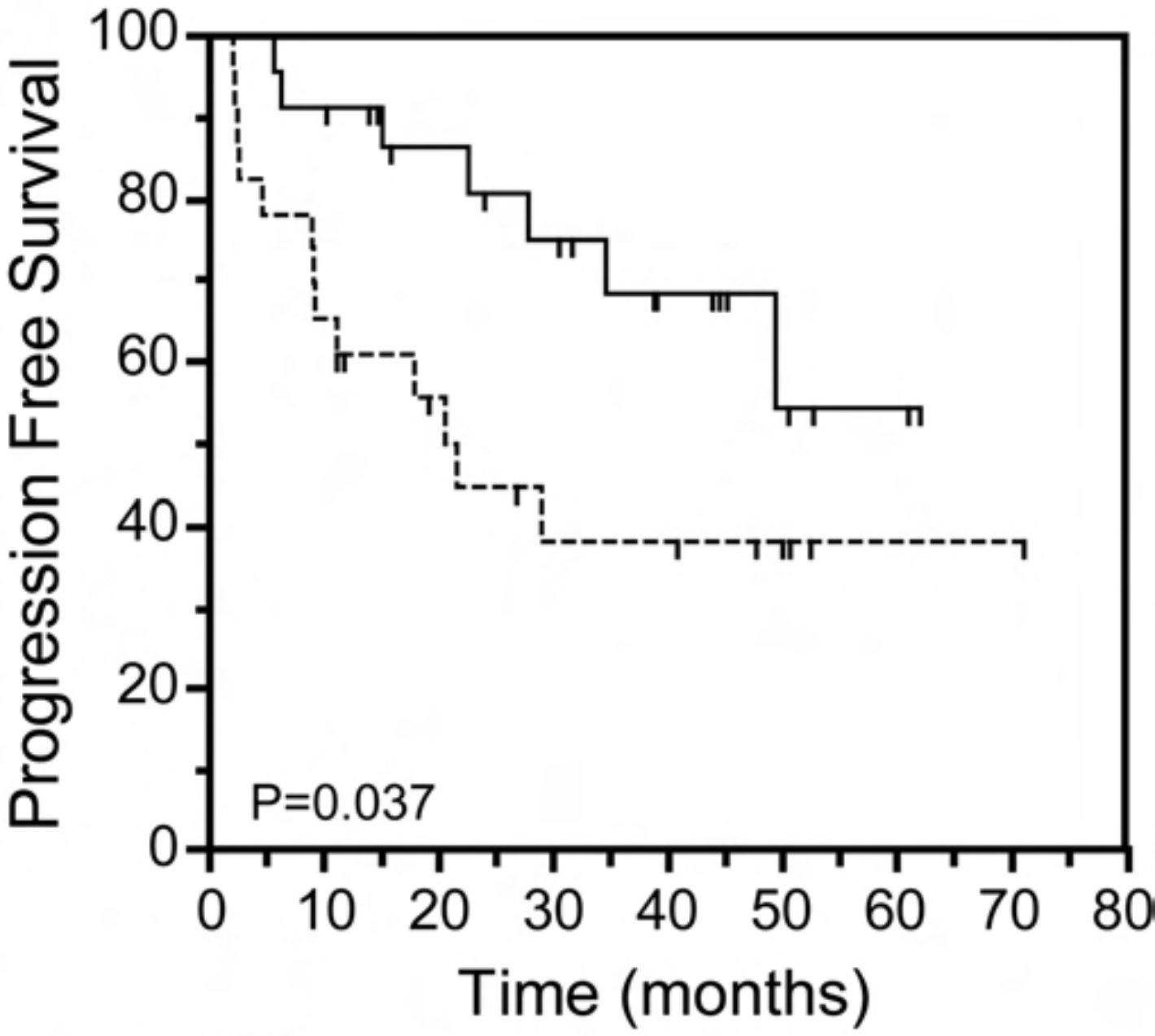

E
Validation set
BCR^low
BCR^high
BCL2
AKT
PIK3CD
SYK
CD79B
BTK
DTM Prediction
-2 -1 0 1 2

Figure 3

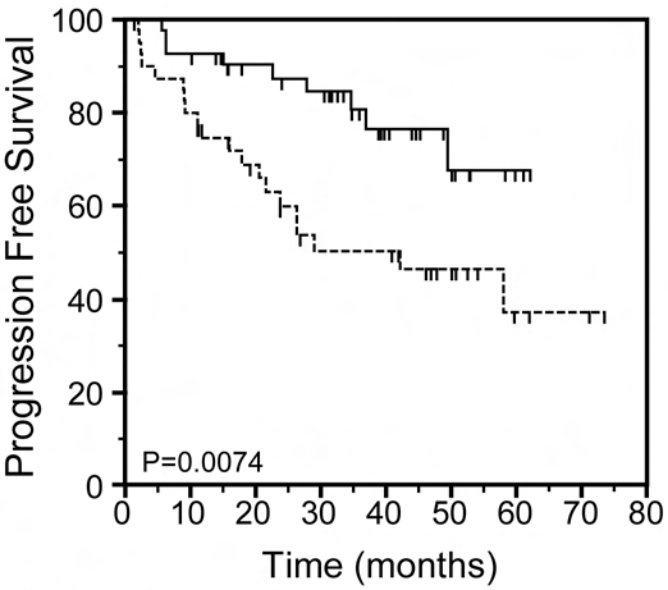


Number at risk

Group: BCR^{low} ——				
23	16	8	2	0
Group: BCR^{high} ----				
23	10	6	1	0

Figure 4

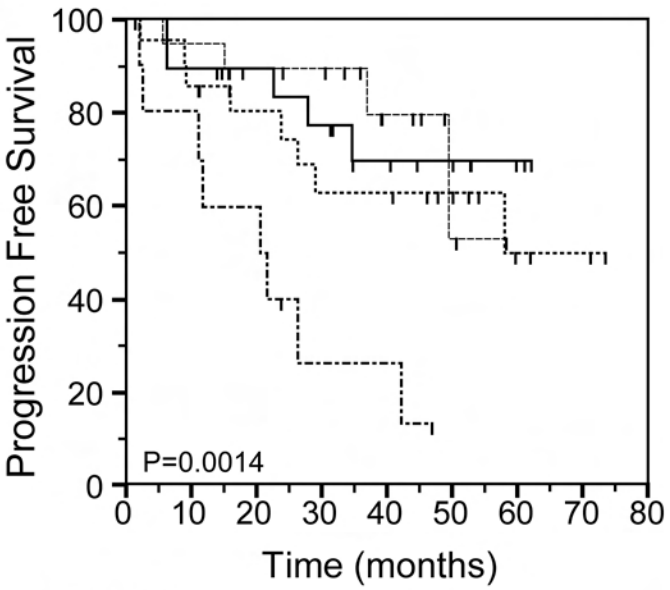
A



Number at risk

Group: BCR^{low}	43	32	14	2	0
Group: BCR^{high}	40	23	15	3	0

B



Number at risk

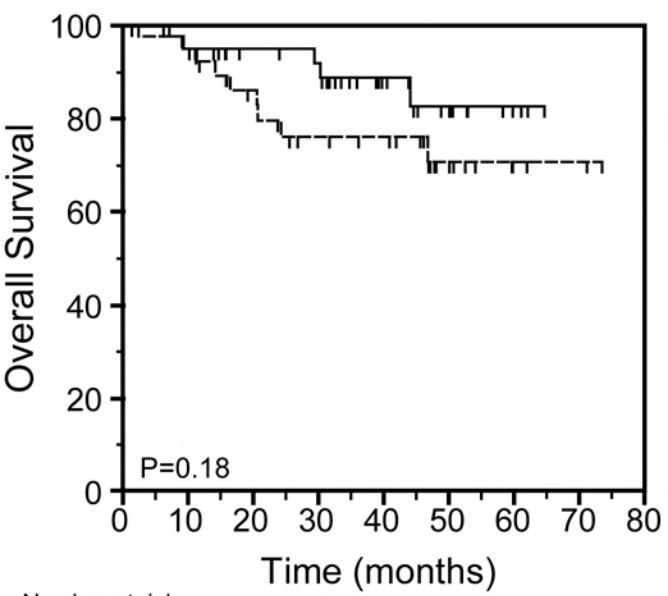
Group: BCR^{low} and low Ki67	19	15	8	2	0
Group: BCR^{low} and high Ki67	20	14	6	0	0
Group: BCR^{high} and low Ki67	21	14	11	3	0
Group: BCR^{high} and high Ki67	10	6	2	0	0

BCR^{high} and high Ki67 vs BCR^{high} and low Ki67 P=0.0148

BCR^{high} and high Ki67 vs BCR^{low} and high Ki67 P=0.0007

BCR^{high} and high Ki67 vs BCR^{low} and low Ki67 P=0.0026

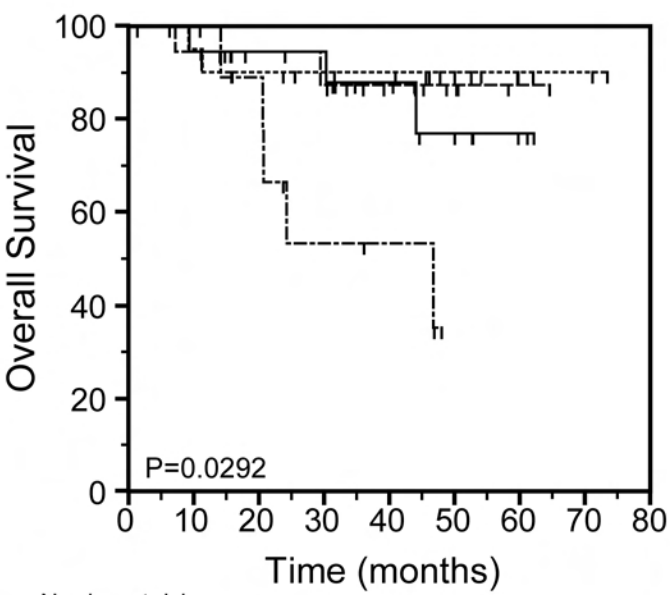
C



Number at risk

Group: BCR^{low}	43	33	17	3	0
Group: BCR^{high}	40	27	18	3	0

D



Number at risk

Group: BCR^{low} and low Ki67	19	15	10	2	0
Group: BCR^{low} and high Ki67	20	15	7	1	0
Group: BCR^{high} and low Ki67	21	15	12	3	0
Group: BCR^{high} and high Ki67	10	8	3	0	0

BCR^{high} and high Ki67 vs BCR^{high} and low Ki67 P=0.049

BCR^{high} and high Ki67 vs BCR^{low} and high Ki67 P=0.0242

BCR^{high} and high Ki67 vs BCR^{low} and low Ki67 P=0.021

A B-cell receptor-related gene signature predicts survival in Mantle Cell Lymphoma: results from the FIL-MCL-0208 trial

- **Supplemental Methods**

- **Supplemental Figure Legends**

- **Supplemental Figures:**
  - **Figure S1. Cases entering the study.**
  - **Figure S2. Flowchart describing the Fondazione Italiana Linfomi (FIL)-MCL-0208 randomized Italian clinical trial.**
  - **Figure S3. Analysis of the 6-gene signature using array and qRT-PCR values.**
  - **Figure S4. BCR and biological parameters.**
  - **Figure S5. Correlation between qRT-PCR calculated on PB and FFPE MCL samples.**
  - **Figure S6. Validation of BCR signature in an external cohort.**
  - **Figure S7. Validation with an external signature.**
  - **Figure S8. Validation with an external signature.**
  - **Figure S9. Reproducibility of RNA extraction and qRT-PCR methods.**

- **Supplemental Tables:**
  - **Table S1. Features of the study population.**
  - **Table S2. BCR categorization according to GEP or qRT-PCR experiments.**
  - **Table S3. Differentially expressed genes between BCR^{low} and BCR^{high} MCL cells.**
  - **Table S4. Pathway and GO categories differentially represented in BCR^{low} and BCR^{high} MCL cells.**
  - **Table S5. Gene Set upregulated in BCR^{high} MCL cells respect to BCR^{low} MCL cells according to Gene Set Enrichment Analysis (GSEA).**
  - **Table S6. qRT-PCR details.**

Methods

RNA extraction and GEP

The purity of purified clonal $CD5^+/CD19^+$ MCL cells, using a cell sorting FACSAriaIII (BD Biosciences, Franklin Lakes, NJ), always exceeded 95%. Total RNA was extracted using the TRIZOL Reagent (Thermo Fisher Scientific) according to protocol. In the case of FFPE MCL samples, RNA extraction was performed strictly following the RecoverAll Total Nucleic Acid Isolation Kit for FFPE (Thermo Fisher Scientific) instructions. RNA was checked using the Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA), as reported previously.[1-4]

GEP and data mining tools

GEP was performed with 150 ng total RNA labeled with Cyanine(Cy)-3 dye.[1,2] Cy3-labeled RNA was hybridized to the Whole Human Genome (8x60) oligo microarray (Agilent Technologies) and analyzed with an Agilent Microarray Scanner (Agilent Technologies) and with the Agilent Feature Extraction Software 10.7.3 (Agilent Technologies), as reported previously.[1-4] Microarray data are available in Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE89447.

Gene Expression Profiling (GEP) data mining tools

GEP data were analyzed using the GeneSpring GX 12.7 software (Agilent Technologies, Santa Clara, CA); pre-processing and pre-filtering steps were carried out according to Agilent instruction. To identify the differentially expressed genes, t statistic was applied and P values were then adjusted for multiple testing with Benjamini and Hochberg's method to control the false discovery rate. Differentially expressed genes were identified according to an adjusted P value ≤ 0.01 and a fold change at least equal to 3. GEP results were visualized using the Cluster and Tree View programs (Eisen Laboratory, Stanford University).[5] The biological functions of genes were investigated using Onto-Tools.[3] Significant gene ontology pathways differentially expressed were selected for having a P value of at least 0.05, and containing at least five genes per category. Gene Set Enrichment Analysis (GSEA)[1,2,4,6] was used to identify the putative genes sets involved in gene deregulation from the online database available at the GSEA Web site

(http://www.broadinstitute.org/gsea/). Enriched or over-represented genes sets between BCR^{low} and BCR^{high} MCL samples were identified using 1 000 permutations of the phenotype labels. Venn diagram was constructed using genes belonging to the different gene sets related to B-Cell Receptor (BCR) pathway and having a significant enrichment score after conversion into Agilent probes and merged with probes differentially expressed with an adjusted P value ≤ 0.01 and a fold change at least equal to 3.

Quantitative real-time PCR (qRT-PCR)

First strand cDNA synthesis was performed by using ImProm-II Reverse Transcription System (Promega) following the manufacturer's instructions, using 150 ng of RNA with 0.5 ug/reaction of Random primers. Expression of specific genes was evaluated with the Gene Expression assay kit (Integrated DNA Technologies, Coralville, IA) using 1 x FastStart Universal Probe Master Mix ROX (ROCHE).[1,2] All qRT-PCR experiments were performed on a Bio-Rad CFX96 (Bio-Rad Laboratories, Hercules, CA). Thermocycling was performed as follow: 95°C for 10 min; 40 cycles of 95°C for 15 s, 60°C for 1 min. The relative amount of each gene was computed using the equation $2^{-\Delta Ct}$, where $\Delta Ct=(Ctgene - Ct\beta 2M)$. Fold-change between classes was calculated as reported.[1,2] Amplification efficiency for each probe was calculated with a standard curve generated using a cDNA from a cell line. Four different 10 fold dilutions were used to construct the relative standard curves. For each qRT-PCR assays a $R^2>0.98$ and a slope between -3.28 and -3.39 was observed. For details related to primer and probe sequences, amplicon length and efficiency see Table S6.

In order to test the reproducibility for RNA isolation and qRT-PCR experiments, we isolated RNA material from four different samples in triplicate, and we tested the reproducibility of each qRT-PCR assay. A minimum variation among the mean of each replicate related to a single assay was observed (Figure S9A). Accordingly, the relative amount of each gene, normalized as above described, presented minimum variation (Figure S9B).

Generation of Prediction Model

We used the Decision Tree (DT) model implemented by GeneSpringGX 12.7 (Agilent Technologies). Briefly, the goal of DT model is to create a model that predicts as outcome the class

to which the data belongs. GeneSpring implements Axis Parallel Decision Trees where decisions at each step are made using one single feature of the many features present. The decision points in a decision tree are called internal nodes. A sample gets classified by following the appropriate path down the decision tree. All samples which follow the same path down the tree are said to be at the same leaf. The tree building process continues until each leaf has purity above a certain specified threshold, i.e., of all samples which are associated with this leaf, at least a certain fraction comes from one class. Once the tree building process is done, a pruning process is used to prune off portions of the tree to reduce chances of over-fitting.

Prediction models were built based on the expression profile of the 6-gene signature (*AKT3*, *BCL-2*, *BTK*, *CD79b*, *PIK3CD*, *SYK*) of conditions BCR^{low} and BCR^{high}. The input data set is divided into a training dataset (17 samples) and a validation dataset (10 samples) as reported in Fig. 2D-E and Table S2. As parameter we selected pessimistic error for pruning methods, Gini functions, Global allowable leaf impurity percentage, and N-Fold cross validation with 10 fold and 100 repeats.

In the case of qRT-PCR values on FFPE samples, being hierarchical cluster again able to split samples in two different group resembling BCR^{low} (low expression of the 6-gene signature) and BCR^{high} (high expression of the 6-gene signature) categories, we decided to use 16 samples with low or high expression of the 6-gene signature as training dataset for the construction of DT model based (see Table S2 for training samples). Accordingly to this model we assigned each FFPE MCL samples to a different BCR category as reported in Table S2.

References

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2 Dal BM, D'Agaro T, Gobessi S et al. The SIRT1/TP53 axis is activated upon B-cell receptor triggering via miR-132 up-regulation in chronic lymphocytic leukemia cells. Oncotarget. 2015;6(22):19102-19117.

3 Draghici S, Khatri P, Martins RP, Ostermeier GC, Krawetz SA. Global functional profiling of gene expression. Genomics. 2003;81(2):98-104.

4 Subramanian A, Tamayo P, Mootha VK et al. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. Proc Natl Acad Sci U S A. 2005;102(43):15545-15550.

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Figure legends

Figure S1. Cases entering the study. A) Kaplan-Meier curves obtained by comparing PFS intervals of 83 MCL cases entering the biological study (median PFS not reached) with 218 MCL cases not entering the biological study (median PFS 57.9 months). B) Kaplan-Meier curves obtained by comparing OS intervals of 83 MCL cases entering the biological study (median OS not reached) with 218 MCL cases not entering the biological study (median OS not reached). The number of patients included in each group is reported under relative categories; the reported P value refers to log-rank test.

Figure S2. Flowchart describing the Fondazione Italiana Linfomi (FIL)-MCL-0208 randomized Italian clinical trial.

Figure S3. Analysis of the 6-gene signature using array and qRT-PCR values. Correlation between GEP and qRT-PCR. Log2 ratios of array data are plotted in comparison with log2 of 2-ΔCt values obtained from qRT-PCR Gene Expression Assays (Integrated DNA Technologies, Coralville, IA). β2M was used as housekeeping gene. The reported P and R^2 values refer to correlation test.

Figure S4. BCR and biological parameters. A) Correlation between BCR categories and IGHV mutational status. P values indicate $\chi 2$ test. B) Levels of lactic dehydrogenase (LDH). Box plots display levels of LDH in 21 BCR^{low} MCL cases (273.9±113.4) and 21 BCR^{high} MCL cases (398.6±186.3). P value indicates Mann-Whitney test.

Figure S5. Correlation between qRT-PCR calculated on PB and FFPE MCL samples. Graph lines reporting the normalized qRT-PCR values calculated on PB or LN specimens for each samples. Blue line refers to PB samples; red line refers to LN samples. The reported Ic values refer to interclass correlation coefficient.

Figure S6. Validation of BCR signature in an external cohort. Validation of the 6-gene BCR signature in an external cohort. Probabilities of PFS were evaluated in a validation cohort of 34 MCL cases., as reported by Saba et al.[7] The separation of the 34 patients into 9 BCR^{high} and 25 BCR^{low} according to the sum of the expressione of the 6 genes, as obtained by GEP data, was based on statistical analyses computing the optimal cutoff point, i.e. the lowest P-value. The number of patients in each group is reported; P value refers to log-rank test.

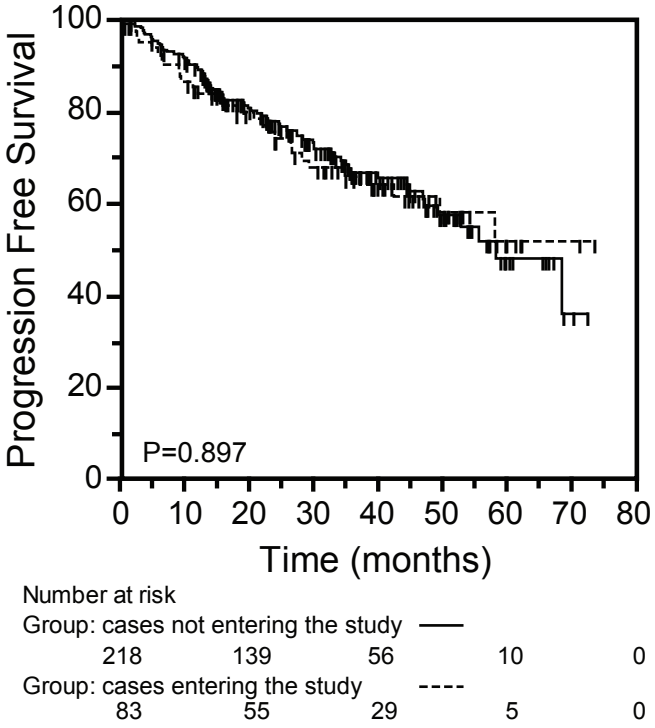
Figure S7. Validation with external signature. Hierarchical clustering of 14 BCR^{low} cases (blue bar under the horizontal dendrogram) and 13 BCR^{high} cases (red bar under the horizontal dendrogram), using the BCR signature retrieved by Saba et al., is shown. The reported P value refers to log-rank test. B) Levels of BCR activation according to Saba et al. Box plots display levels of BCR activation in 14 BCR^{low} MCL cases and 13 BCR^{high} MCL cases. P value indicates Mann-Whitney test.

Figure S8. Validation with external signature. A) Hierarchical clustering of 14 BCR^{low} cases (blue bar under the horizontal dendrogram) and 13 BCR^{high} cases (red bar under the horizontal dendrogram) using the BCR signature retrieved by Scott et al., is shown. Color codes for gene expression values refer to mean centered log-ratio values. B) Kaplan-Meier curves obtained by comparing PFS intervals of 13 Group 1 MCL cases (median PFS not reached), with 7 Group 2 MCL cases (median PFS 49.3 months), with 7 Group 3 MCL cases (median PFS 9.1 months). C) Kaplan-Meier curves obtained by comparing OS intervals of 13 Group 1 MCL cases (median OS not reached), with 7 Group 2 MCL cases (median OS not reached), with 7 Group 3 MCL cases (median OS 16.4 months). The number of patients included in each group is reported under relative categories; the reported P value refers to log-rank test.

Figure S9. Reproducibility of RNA extraction and qRT-PCR methods. A) Bars reported the Ct value for each gene belonging to 6-gene signature. B) Bars reported the normalize value for each gene belonging to 6-gene signature. In all graphs data represent mean ± standard deviation of three replicates for each sample.

Figure S1

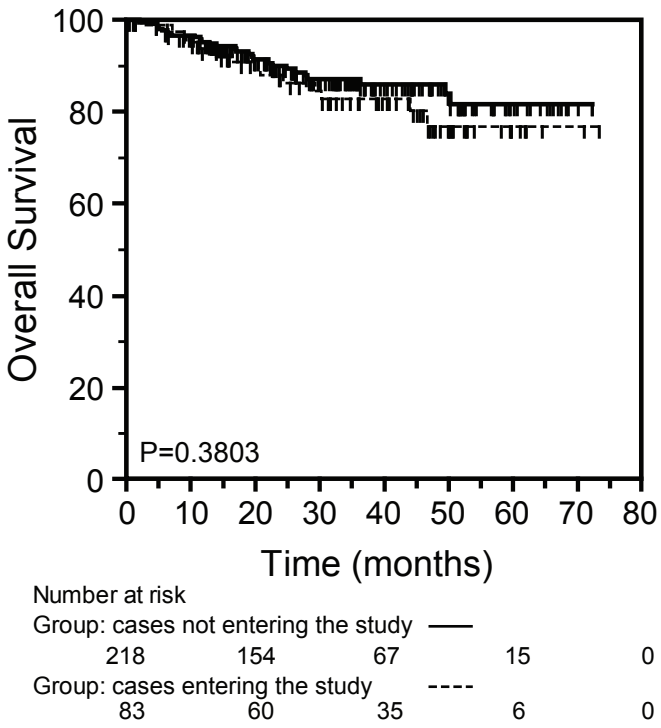
A



Number at risk

Group: cases not entering the study ——				
218	139	56	10	0
Group: cases entering the study ----				
83	55	29	5	0

B



Number at risk

Group: cases not entering the study ——				
218	154	67	15	0
Group: cases entering the study ----				
83	60	35	6	0

Figure S2

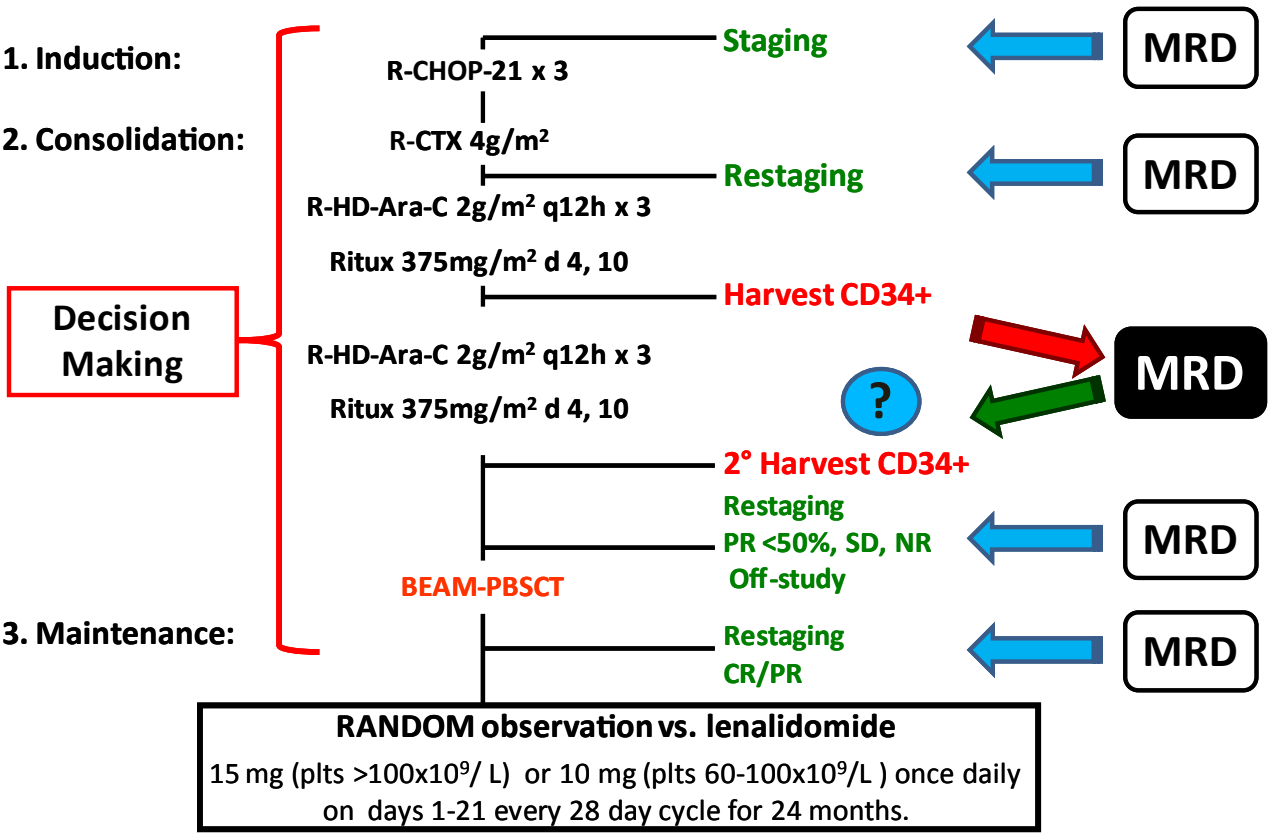

1. Induction:
R-CHOP-21 x 3
Staging
MRD
2. Consolidation:
R-CTX 4g/m²
Restaging
MRD
R-HD-Ara-C 2g/m² q12h x 3
Ritux 375mg/m² d 4, 10
Harvest CD34+
Decision Making
R-HD-Ara-C 2g/m² q12h x 3
Ritux 375mg/m² d 4, 10
?
MRD
2° Harvest CD34+
Restaging
PR <50%, SD, NR
Off-study
MRD
BEAM-PBSCT
3. Maintenance:
Restaging
CR/PR
MRD
RANDOM observation vs. lenalidomide
15 mg (plts >100x10⁹/ L) or 10 mg (plts 60-100x10⁹/L) once daily on days 1-21 every 28 day cycle for 24 months.

Figure S3

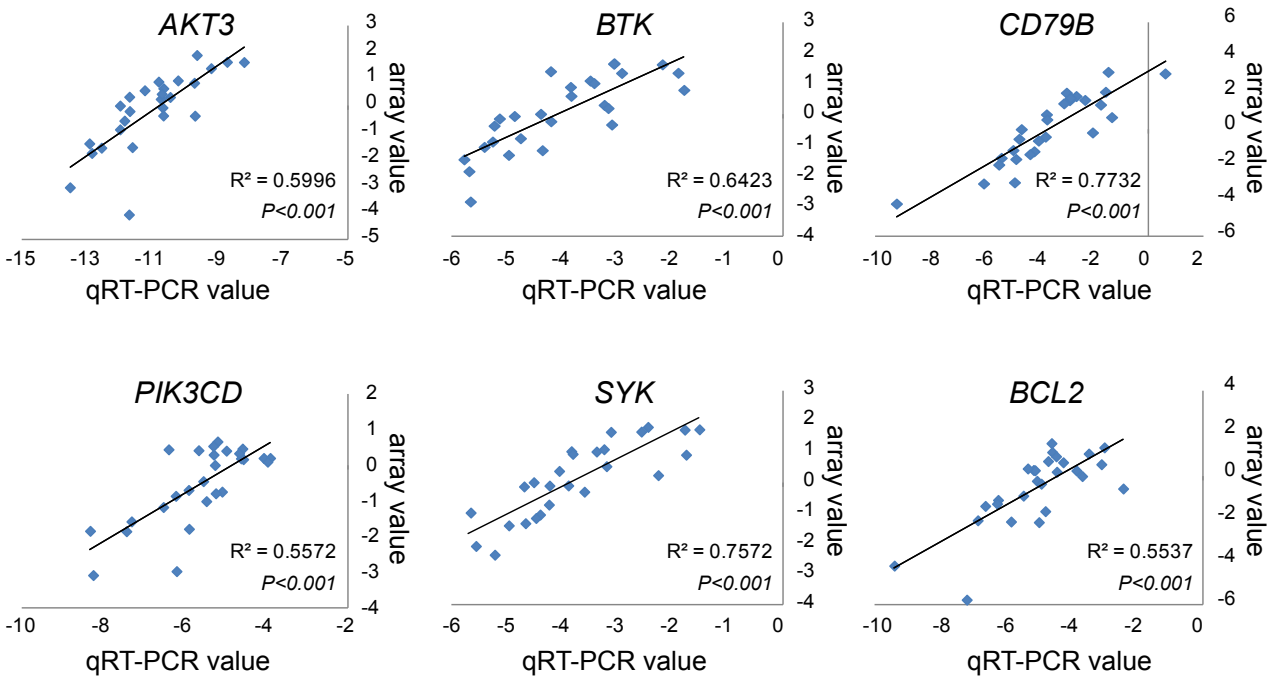
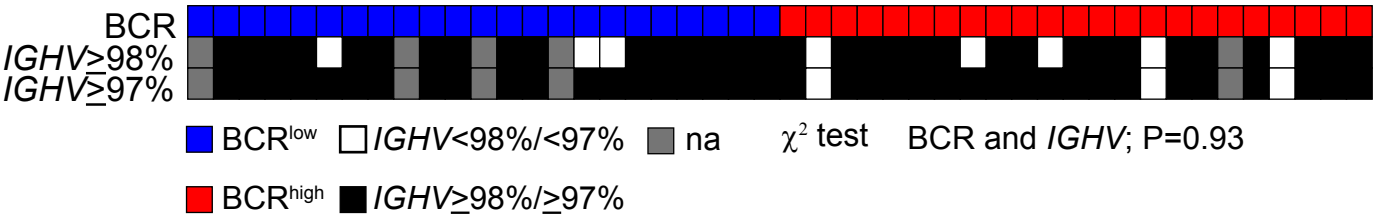

AKT3
R² = 0.5996
P<0.001
array value
qRT-PCR value
BTK
R² = 0.6423
P<0.001
array value
qRT-PCR value
CD79B
R² = 0.7732
P<0.001
array value
qRT-PCR value
PIK3CD
R² = 0.5572
P<0.001
array value
qRT-PCR value
SYK
R² = 0.7572
P<0.001
array value
qRT-PCR value
BCL2
R² = 0.5537
P<0.001
array value
qRT-PCR value

Figure S4

A


BCR
IGHV≥98%
IGHV≥97%
BCRlow
IGHV<98%/<97%
na
χ2 test
BCR and IGHV; P=0.93
BCRhigh
IGHV≥98%/≥97%

B

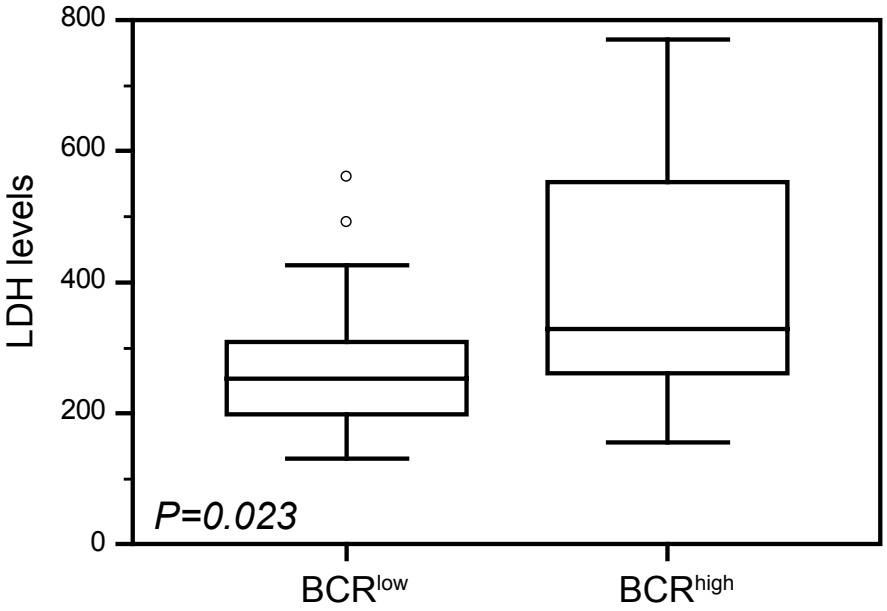
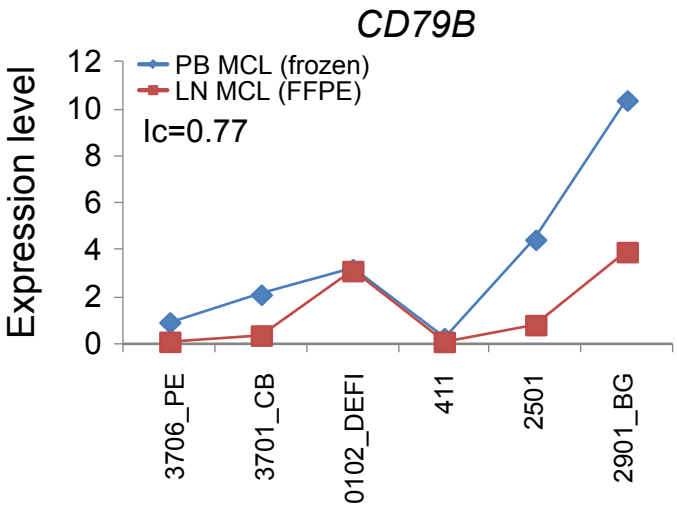
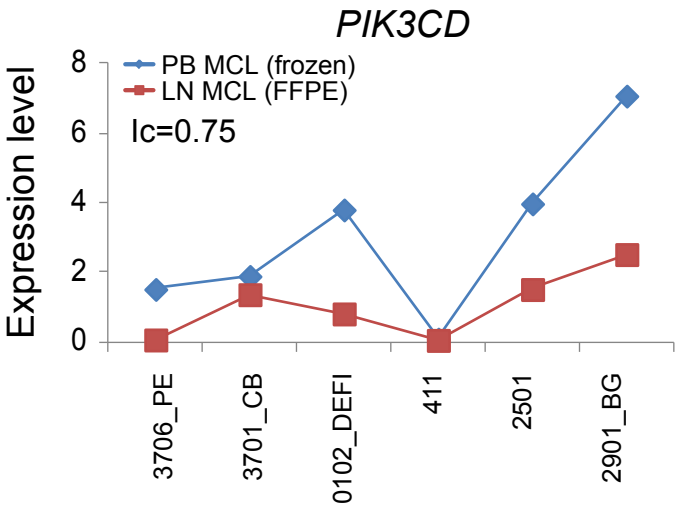
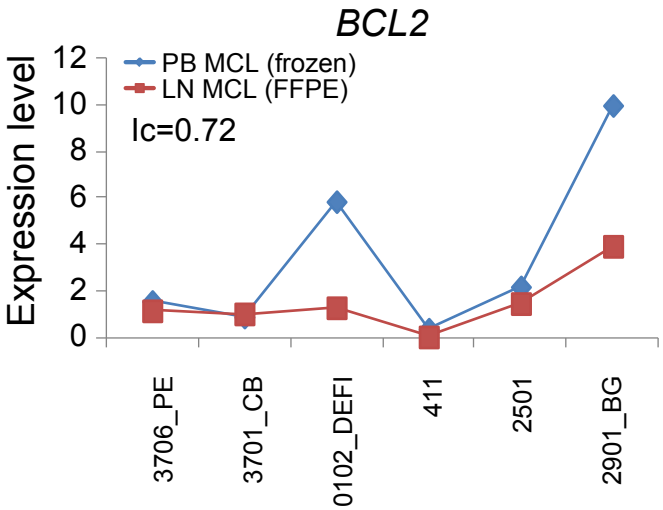
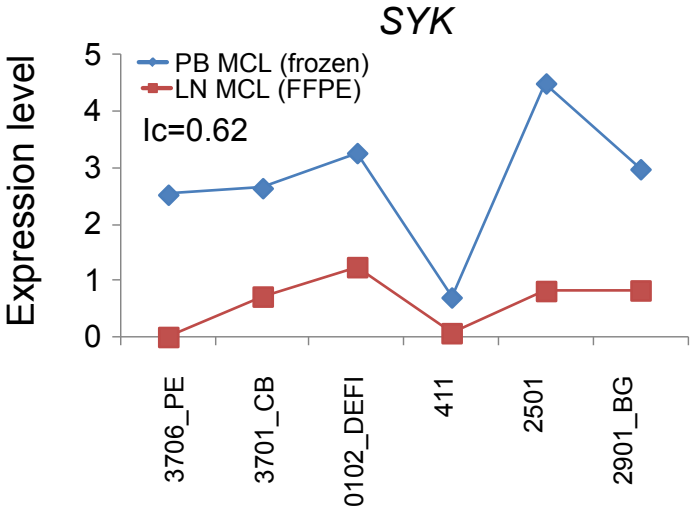

800
600
400
200
0
LDH levels
P=0.023
BCRlow
BCRhigh

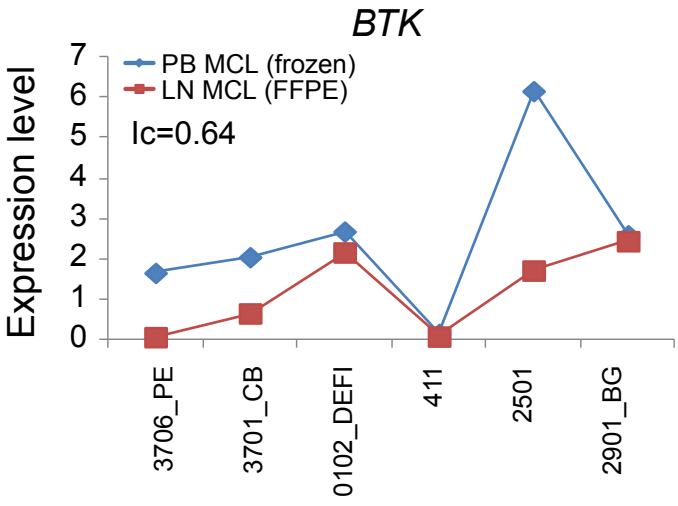
Figure S5


CD79B
PB MCL (frozen)
LN MCL (FFPE)
Ic=0.77
Expression level
12
10
8
6
4
2
0
3706_PE
3701_CB
0102_DEFI
411
2501
2901_BG


PIK3CD
PB MCL (frozen)
LN MCL (FFPE)
Ic=0.75
Expression level
8
6
4
2
0
3706_PE
3701_CB
0102_DEFI
411
2501
2901_BG


BCL2
PB MCL (frozen)
LN MCL (FFPE)
Ic=0.72
Expression level
12
10
8
6
4
2
0
3706_PE
3701_CB
0102_DEFI
411
2501
2901_BG


SYK
PB MCL (frozen)
LN MCL (FFPE)
Ic=0.62
Expression level
5
4
3
2
1
0
3706_PE
3701_CB
0102_DEFI
411
2501
2901_BG


BTK
PB MCL (frozen)
LN MCL (FFPE)
Ic=0.64
Expression level
7
6
5
4
3
2
1
0
3706_PE
3701_CB
0102_DEFI
411
2501
2901_BG

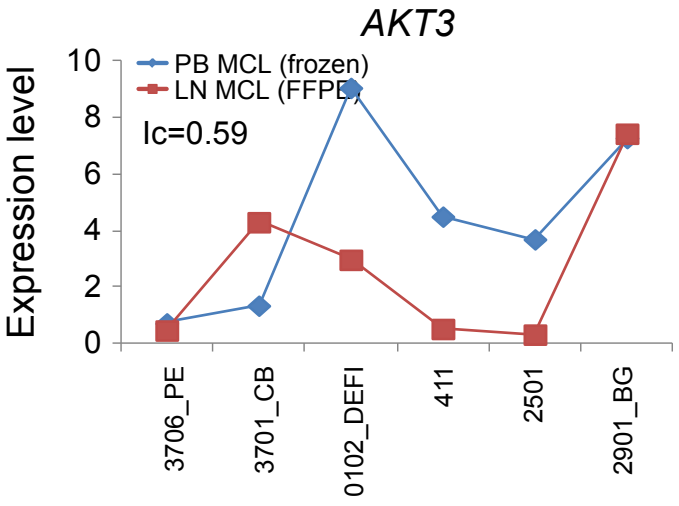

AKT3
PB MCL (frozen)
LN MCL (FFPE)
Ic=0.59
Expression level
10
8
6
4
2
0
3706_PE
3701_CB
0102_DEFI
411
2501
2901_BG

Figure S6

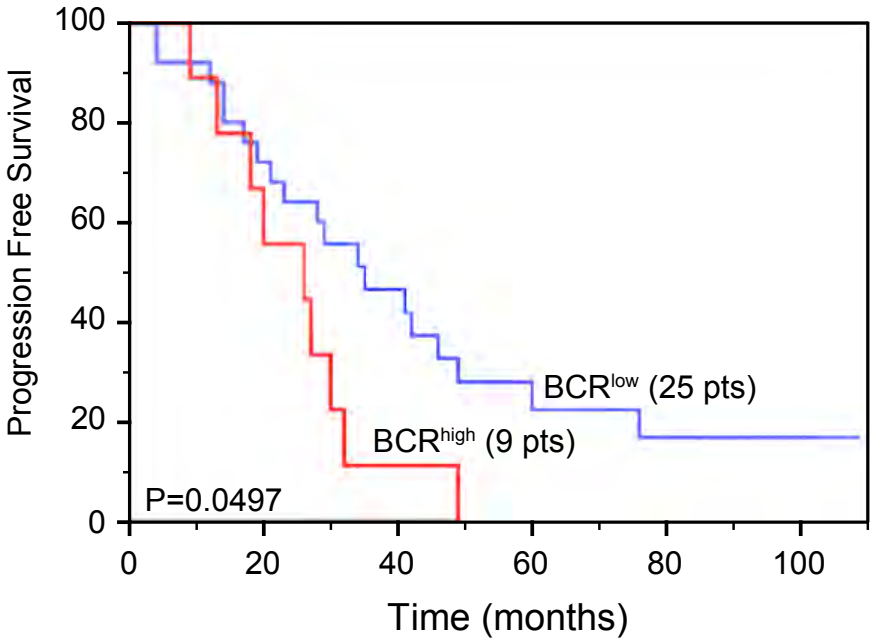

Progression Free Survival
100
80
60
40
20
0
0
20
40
60
80
100
Time (months)
BCR^low (25 pts)
BCR^high (9 pts)
P=0.0497

Figure S7

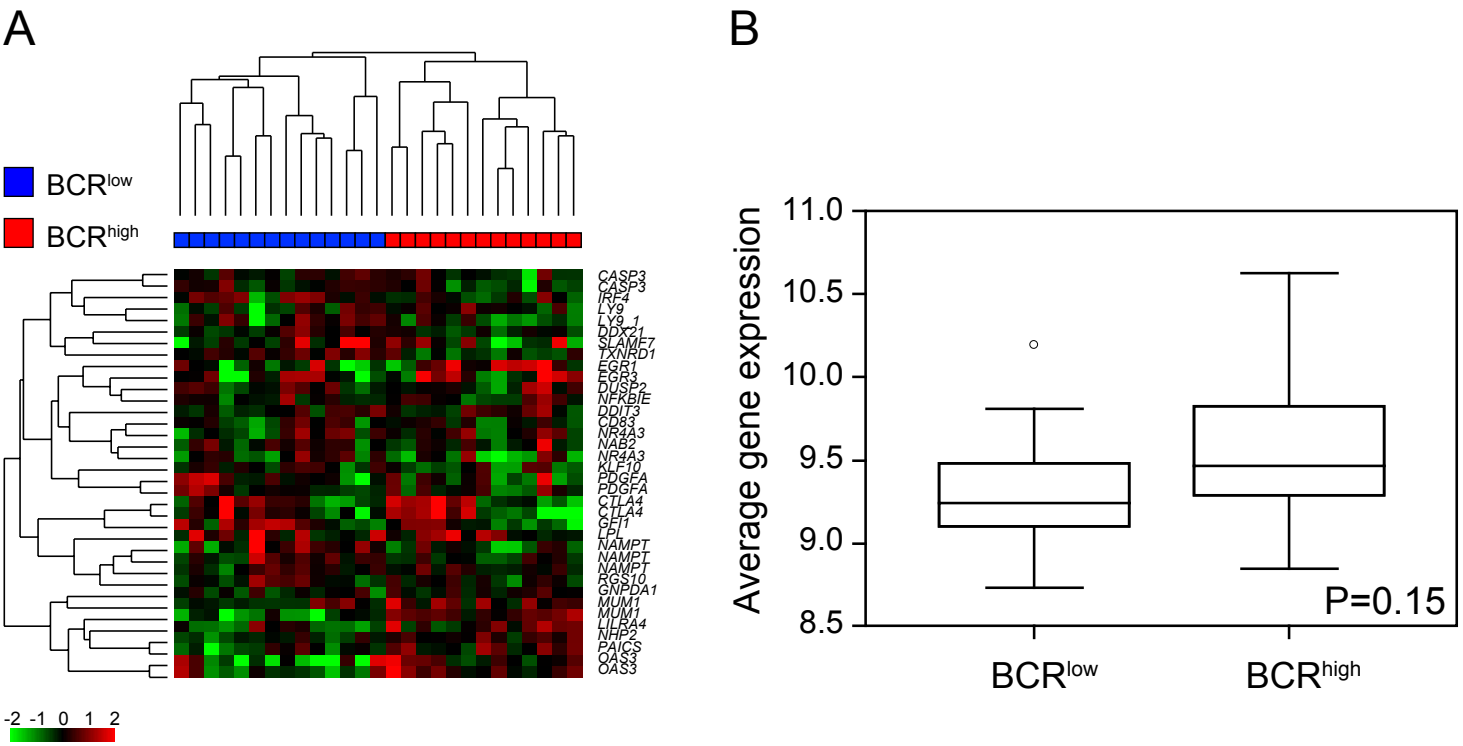
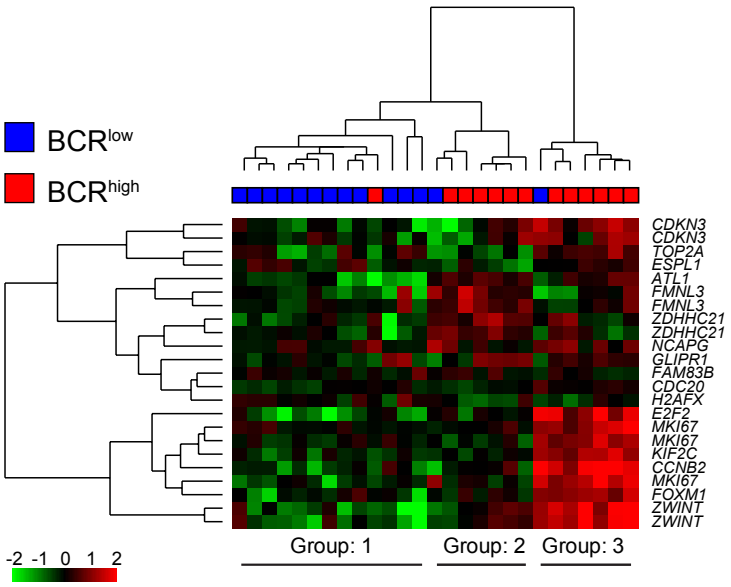
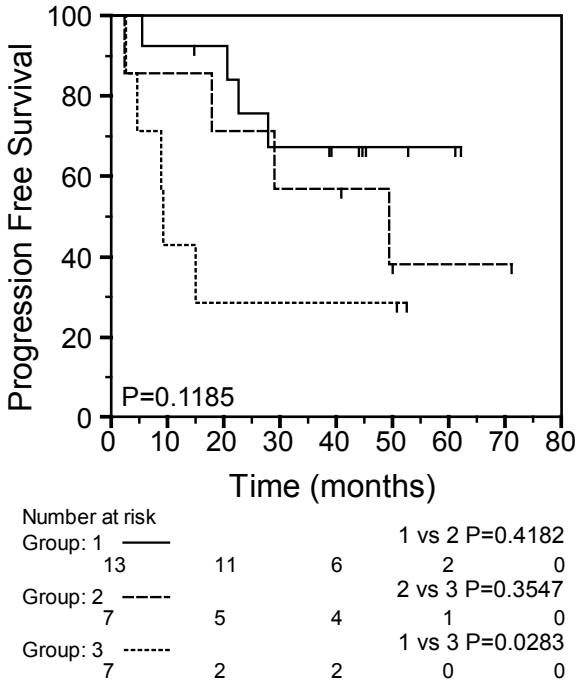

A
BCRlow
BCRhigh
CASP3
CASP3
IRF4
LY9
LY9_1
DDX21
SLAMF7
TXNRD1
EGR1
EGR3
DUSP2
NFKBIE
DDIT3
CD83
NR4A3
NAB2
NR4A3
KLF10
PDGFA
PDGFA
CTLA4
CTLA4
GFI1
LPL
NAMPT
NAMPT
NAMPT
RGS10
GNPDA1
MUM1
MUM1
LILRA4
NHP2
PAICS
OAS3
OAS3
-2 -1 0 1 2
B
Average gene expression
11.0
10.5
10.0
9.5
9.0
8.5
P=0.15
BCRlow
BCRhigh

Figure S8

A



B

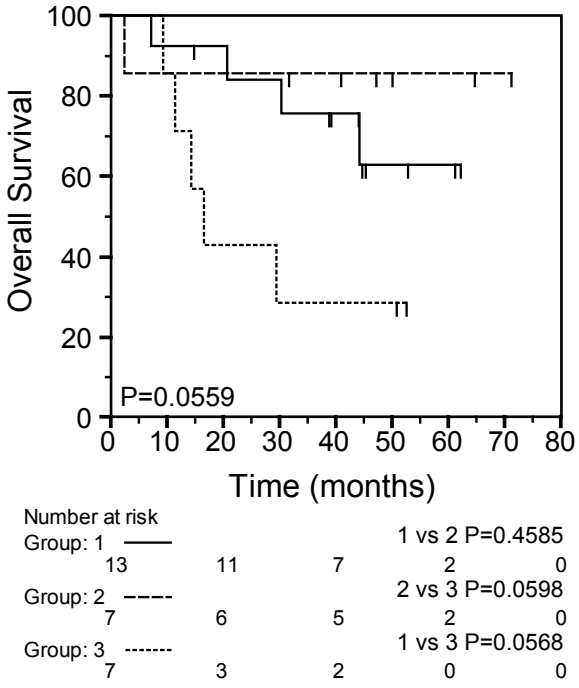


Number at risk

Group: 1	13	11	6	2	0
Group: 2	7	5	4	1	0
Group: 3	7	2	2	0	0

1 vs 2 P=0.4182
2 vs 3 P=0.3547
1 vs 3 P=0.0283

C



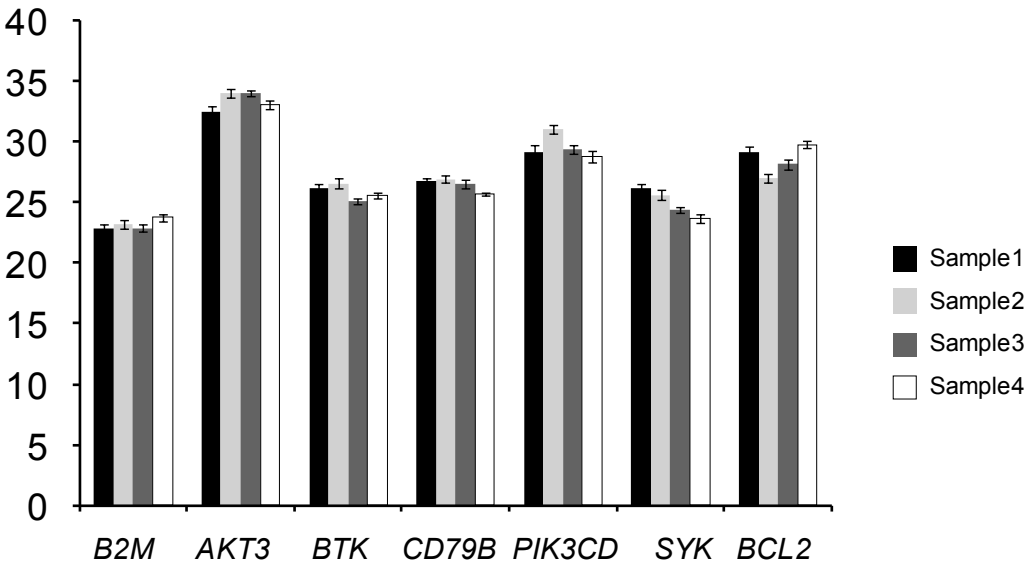
Number at risk

Group: 1	13	11	7	2	0
Group: 2	7	6	5	2	0
Group: 3	7	3	2	0	0

1 vs 2 P=0.4585
2 vs 3 P=0.0598
1 vs 3 P=0.0568

Figure S9

A


40
35
30
25
20
15
10
5
0
B2M
AKT3
BTK
CD79B
PIK3CD
SYK
BCL2
Sample1
Sample2
Sample3
Sample4

B

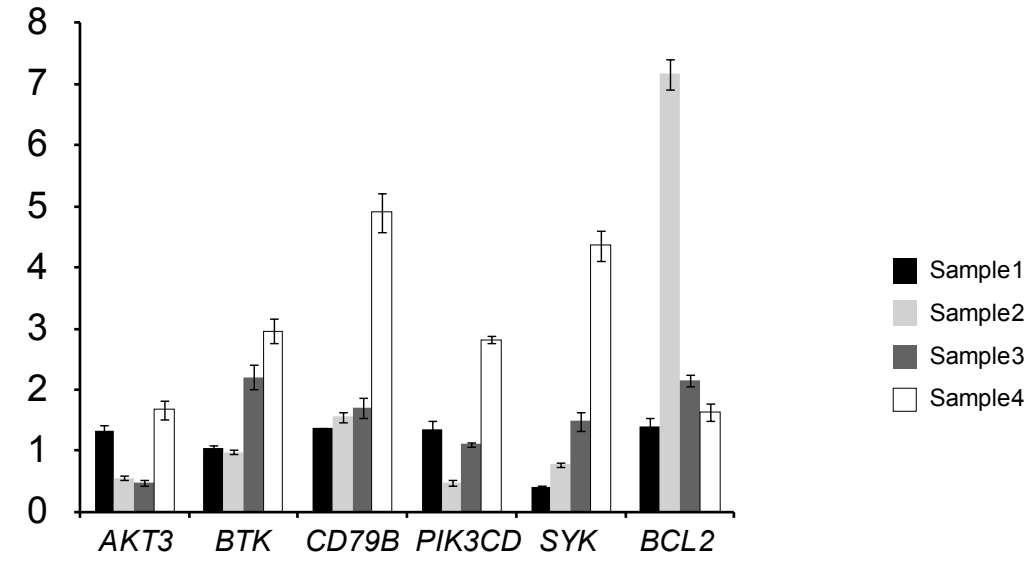

8
7
6
5
4
3
2
1
0
AKT3
BTK
CD79B
PIK3CD
SYK
BCL2
Sample1
Sample2
Sample3
Sample4

Table S1. Features of the study population

	Cases entering the study	Cases not entering the study	p value
N. of cases	83	217	
Median age, years	54.3	55.9	ns
Male	70%	81%	0.041
Stage IV	99%	92%	ns
MIPI (n=83/n=217)			
Low	47%	58%	
Intermediate	35%	28%	ns
High	18%	14%	
Ki67 ≥30% (n=70/n=167)	43%	52%	ns
Follow-up, years	3.1	2.8	ns
2-years PFS	78%	74%	ns

Abbreviation: ns, not significant ($p<0.05$); MIPI, Mantle Cell Lymphoma International Prognostic Index; PFS, progression free survival.

Table S2. BCR categorization

Sample	Sex	Starting Material	Training/ Validation dataset on PB	Training/ Validation dataset on FFPE	BCR category	Classification according to DT model on PB samples	Classification according to DT model on FFPE samples	IGHV UM/M	LDH Abnormal	Ki67 2 groups
101	Female	LN			BCRhigh		BCRhigh	M	No	0
104	Male	LN		T	BCRlow		BCRlow	nd	na	0
106	Male	LN			BCRhigh		BCRhigh	UM	Yes	2
401	Male	LN			BCRhigh		BCRhigh	UM	No	0
402	Male	LN		T	BCRlow		BCRlow	M	No	0
405	Male	LN		T	BCRhigh		BCRhigh	UM	No	0
406	Male	LN		T	BCRhigh		BCRhigh	nd	No	0
413	Male	LN		T	BCRhigh		BCRhigh	UM	Yes	2
417	Male	LN			BCRlow		BCRlow	M	Yes	0
418	Male	LN			BCRlow		BCRlow	nd	No	0
420	Male	LN		T	BCRlow		BCRlow	M	Yes	2
509	Male	LN			BCRlow		BCRlow	UM	Yes	2
514	Female	LN			BCRlow		BCRlow	UM	No	2
518	Male	LN			BCRlow		BCRlow	UM	No	2
521	Male	LN		T	BCRlow		BCRlow	nd	na	2
1002	Male	LN		T	BCRhigh		BCRhigh	nd	No	0
1102	Female	LN			BCRhigh		BCRhigh	UM	No	0
1305	Female	LN		T	BCRhigh		BCRhigh	UM	Yes	0
1308	Female	LN		T	BCRhigh		BCRhigh	UM	No	2
1403	Male	LN		T	BCRhigh		BCRhigh	nd	No	2
1702	Male	LN			BCRlow		BCRlow	UM	No	2
2302	Female	LN			BCRlow		BCRlow	M	No	0
2402	Male	LN			BCRhigh		BCRhigh	UM	No	0
2403	Male	LN		T	BCRhigh		BCRhigh	nd	Yes	0
2503	Male	LN			BCRlow		BCRlow	nd	No	0
2902	Male	LN			BCRhigh		BCRhigh	UM	No	2
3003	Female	LN			BCRlow		BCRlow	UM	No	0
3006	Male	LN			BCRlow		BCRlow	UM	Yes	0
3008	Female	LN			BCRlow		BCRlow	UM	Yes	2
3702	Male	LN			BCRhigh		BCRhigh	UM	No	0
3705	Male	LN			BCRlow		BCRlow	UM	Yes	2
3708	Female	LN		T	BCRhigh		BCRhigh	nd	No	0
4002	Female	LN			BCRlow		BCRlow	nd	Yes	2
4402	Male	LN		T	BCRlow		BCRlow	nd	No	0
4404	Male	LN			BCRhigh		BCRhigh	UM	No	0
4702	Male	LN		T	BCRlow		BCRlow	nd	No	2
5101	Male	LN		T	BCRlow		BCRlow	nd	No	na
105	Male	PB			BCRhigh	BCRhigh		UM	Yes	2
205	Female	PB	V		BCRlow	BCRlow		UM	na	na
301	Male	PB	T		BCRhigh	BCRhigh		M	na	0
306	Male	PB			BCRhigh	BCRhigh		UM	No	0
404	Male	PB	T		BCRlow	BCRlow		UM	Yes	2
408	Female	PB	V		BCRlow	BCRlow		UM	No	0
409	Male	PB	V		BCRlow	BCRlow		UM	Yes	0
410	Male	PB	T		BCRhigh	BCRhigh		UM	No	0
412	Female	PB	V		BCRhigh	BCRhigh		UM	Yes	0
505	Male	PB	V		BCRlow	BCRlow		UM	Yes	2
506	Male	PB	T		BCRhigh	BCRhigh		UM	No	0
507	Male	PB	T		BCRlow	BCRlow		UM	Yes	0
511	Male	PB			BCRlow	BCRlow		nd	No	2
513	Male	PB			BCRhigh	BCRhigh		UM	Yes	0
601	Male	PB	T		BCRhigh	BCRhigh		M	Yes	0
604	Male	PB	V		BCRhigh	BCRhigh		UM	No	2
610	Male	PB			BCRhigh	BCRhigh		UM	Yes	0
703	Male	PB	V		BCRhigh	BCRhigh		M	Yes	0
707	Male	PB	V		BCRhigh	BCRhigh		UM	Yes	0
802	Female	PB	T		BCRhigh	BCRhigh		UM	No	0
1201	Female	PB	V		BCRlow	BCRlow		UM	No	0
1307	Female	PB			BCRlow	BCRlow		UM	No	0
1309	Male	PB			BCRhigh	BCRhigh		UM	Yes	na
1513	Male	PB			BCRlow	BCRlow		nd	No	0
1606	Female	PB			BCRhigh	BCRhigh		M	Yes	na
1701	Female	PB	T		BCRlow	BCRlow		UM	No	2
1901	Female	PB	T		BCRhigh	BCRhigh		UM	No	0
2001	Male	PB	T		BCRlow	BCRlow		UM	Yes	0
2103	Female	PB			BCRlow	BCRlow		nd	na	na
2301	Male	PB	T		BCRlow	BCRlow		M	No	0
2310	Female	PB			BCRlow	BCRlow		M	Yes	2
2602	Male	PB	T		BCRlow	BCRlow		UM	No	0
3304	Female	PB	T		BCRlow	BCRlow		UM	No	2
3401	Male	PB			BCRhigh	BCRhigh		UM	Yes	2

4103	Male	PB		BCRhigh	BCRhigh		UM	No	2
4301	Female	PB	V	BCRlow	BCRlow		UM	Yes	2
4305	Male	PB		BCRhigh	BCRhigh		UM	na	na
4703	Female	PB		BCRlow	BCRlow		UM	No	2
5202	Male	PB		BCRlow	BCRlow		UM	No	0
5206	Female	PB		BCRhigh	BCRhigh		UM	na	na
102	Male	PB/LN	T	BCRlow	BCRhigh	BCRlow	nd	Yes	2
411	Male	PB/LN		BCRlow	BCRlow	BCRlow	M	No	0
2501	Male	PB/LN	T	BCRhigh	BCRhigh	BCRhigh	UM	No	0
2901	Male	PB/LN	T	BCRhigh	BCRhigh	BCRhigh	nd	na	2
3701	Female	PB/LN	T	BCRhigh	BCRhigh	BCRhigh	M	No	0
3706	Male	PB/LN		BCRlow	BCRlow	BCRlow	UM	na	2

PB: Peripheral Blood; LN: Lymph Node; DT: Decision Tree model; UM: Unmutated IGHV; M: Mutated IGHV; nd: not done; na: not available; T: Training dataset; V: Validation dataset.

Table S3. Differentially expressed genes between BCRlow and BCRhigh MCL cells

ProbeName	GeneSymbol	Description	Fold change (BCRhigh vs BCRlow)	Regulation (BCRhigh vs BCRlow)	Position in Heatmap
A_23_P131899	SDCBP2	Homo sapiens syndecan binding protein (syntenin) 2 (SDCBP2), transcript variant 1, mRNA [NM_080489]	3.837	down	1
A_33_P3254331	CTRC	Homo sapiens chymotrypsin C (caldecrin) (CTRC), mRNA [NM_007272]	4.126	down	2
A_33_P3310070	FOXK2	Homo sapiens forkhead box K2 (FOXK2), mRNA [NM_004514]	4.114	down	3
A_33_P3651911	na	cancer susceptibility candidate 7 (non-protein coding) [Source:HGNC Symbol;Acc:HGNC:48905] [ENST00000560295]	5.803	down	4
A_23_P112159	AGO2	Homo sapiens argonaute RISC catalytic component 2 (AGO2), transcript variant 1, mRNA [NM_012154]	6.121	down	5
A_23_P62642	CFAP45	Homo sapiens cilia and flagella associated protein 45 (CFAP45), mRNA [NM_012337]	6.836	down	6
A_33_P3393684	VSIG8	Homo sapiens V-set and immunoglobulin domain containing 8 (VSIG8), mRNA [NM_001013661]	7.906	down	7
A_23_P356616	ABTB2	Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA [NM_145804]	3.503	down	8
A_33_P3274647	CAMK2A	Homo sapiens calcium/calmodulin-dependent protein kinase II alpha (CAMK2A), transcript variant 1, mRNA [NM_015981]	9.697	down	9
A_24_P781615	AOC4P	Homo sapiens amine oxidase, copper containing 4, pseudogene (AOC4P), non-coding RNA [NR_002773]	4.222	down	10
A_33_P3374190	INPP5A	Homo sapiens inositol polyphosphate-5-phosphatase, 40kDa (INPP5A), mRNA [NM_005539]	7.494	down	11
A_24_P26897	INPP5A	Homo sapiens inositol polyphosphate-5-phosphatase, 40kDa (INPP5A), mRNA [NM_005539]	5.480	down	12
A_21_P0011503	na	ens	8.473	down	13
A_33_P3287068	MTUS2-AS1	Homo sapiens MTUS2 antisense RNA 1 (MTUS2-AS1), long non-coding RNA [NR_046378]	9.289	down	14
A_23_P163639	ANKRD11	Homo sapiens ankyrin repeat domain 11 (ANKRD11), transcript variant 2, mRNA [NM_013275]	4.157	down	15
A_24_P363278	MAK	Homo sapiens male germ cell-associated kinase (MAK), transcript variant 1, mRNA [NM_005906]	3.620	down	16
A_23_P154688	SLC4A11	Homo sapiens solute carrier family 4, sodium borate transporter, member 11 (SLC4A11), transcript variant 2, mRNA [NM_032034]	3.149	down	17
A_21_P0001690	lnc-IFI44-2	LNCipedia lincRNA (lnc-IFI44-2), lincRNA [lnc-IFI44-2:1]	3.691	down	18
A_23_P204801	SLC41A2	Homo sapiens solute carrier family 41 (magnesium transporter), member 2 (SLC41A2), mRNA [NM_032148]	3.424	down	19
A_33_P3415596	na	ens	4.343	down	20
A_33_P3225091	NUMBL	Homo sapiens numb homolog (Drosophila)-like (NUMBL), transcript variant 1, mRNA [NM_004756]	6.128	down	21
A_23_P74887	SDC3	Homo sapiens syndecan 3 (SDC3), mRNA [NM_014654]	4.002	down	22
A_33_P3241884	SDC3	Homo sapiens syndecan 3 (SDC3), mRNA [NM_014654]	3.200	down	23
A_33_P3223116	HIPK2	homeodomain interacting protein kinase 2 [Source:HGNC Symbol;Acc:HGNC:14402] [ENST00000342645]	4.150	down	24
A_33_P3223121	HIPK2	Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), transcript variant 2, mRNA [NM_001113239]	3.908	down	25
A_21_P0010208	na	0	3.171	down	26
A_23_P317756	ACSM3	Homo sapiens acyl-CoA synthetase medium-chain family member 3 (ACSM3), transcript variant 2, mRNA [NM_202000]	3.580	down	27
A_23_P305616	LOC652276	Homo sapiens potassium channel tetramerization domain containing 5 pseudogene (LOC652276), non-coding RNA [NR_015441]	3.592	down	28
A_33_P3343828	lnc-CEMP1-1	Homo sapiens cDNA FLJ44722 fis, clone BRACE3022847. [AK126677]	3.513	down	29
A_21_P0008871	FLJ42627	Homo sapiens uncharacterized LOC645644 (FLJ42627), long non-coding RNA [NR_024492]	3.690	down	30
A_33_P3354796	FLJ42627	Homo sapiens uncharacterized LOC645644 (FLJ42627), long non-coding RNA [NR_024492]	3.676	down	31
A_33_P3871347	SNED1	Homo sapiens sushi, nidogen and EGF-like domains 1 (SNED1), mRNA [NM_001080437]	3.168	down	32
A_19_P00317171	CASC8	Homo sapiens cancer susceptibility candidate 8 (non-protein coding) (CASC8), transcript variant 2, long non-coding RNA [NR_024393]	3.149	down	33
A_24_P281975	GNPTAB	Homo sapiens N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits (GNPTAB), mRNA [NM_024312]	3.258	down	34
A_33_P3640690	ZEB1	Homo sapiens zinc finger E-box binding homeobox 1 (ZEB1), transcript variant 1, mRNA [NM_001128128]	3.521	down	35
A_33_P3229702	WFIKKN1	Homo sapiens WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1 (WFIKKN1), mRNA [NM_053284]	6.968	down	36
A_33_P3325723	CHN1	Homo sapiens chimerin 1 (CHN1), transcript variant 1, mRNA [NM_001822]	4.822	down	37
A_33_P3432135	EPHA1-AS1	Homo sapiens EPHA1 antisense RNA 1 (EPHA1-AS1), long non-coding RNA [NR_033897]	3.884	down	38
A_33_P3265855	PRR5-ARHGAP8	Homo sapiens PRR5-ARHGAP8 readthrough (PRR5-ARHGAP8), mRNA [NM_181334]	3.359	down	39
A_33_P3250671	TCF7	Homo sapiens transcription factor 7 (T-cell specific, HMG-box) (TCF7), transcript variant 1, mRNA [NM_003202]	3.457	down	40
A_23_P132760	TRH	Homo sapiens thyrotropin-releasing hormone (TRH), mRNA [NM_007117]	3.349	down	41
A_23_P79247	PGAP1	Homo sapiens post-GPI attachment to proteins 1 (PGAP1), mRNA [NM_024989]	3.345	down	42
A_33_P3312735	PGAP1	Homo sapiens post-GPI attachment to proteins 1 (PGAP1), mRNA [NM_024989]	3.272	down	43
A_33_P3257312	ATG2A	Homo sapiens autophagy related 2A (ATG2A), mRNA [NM_015104]	3.403	down	44
A_23_P361820	ATG2A	Homo sapiens autophagy related 2A (ATG2A), mRNA [NM_015104]	3.902	down	45
A_24_P4816	GABARAPL1	Homo sapiens GABA(A) receptor-associated protein like 1 (GABARAPL1), mRNA [NM_031412]	5.891	down	46
A_33_P3812669	GABARAPL1	Homo sapiens GABA(A) receptor-associated protein like 1 (GABARAPL1), mRNA [NM_031412]	4.634	down	47
A_33_P3263538	na	nuclear paraspeckle assembly transcript 1 (non-protein coding) [Source:HGNC Symbol;Acc:HGNC:30815] [ENST00000501122]	3.721	down	48
A_23_P132027	SPAG4	Homo sapiens sperm associated antigen 4 (SPAG4), mRNA [NM_003116]	3.765	down	49
A_33_P3324765	CSNK1D	Homo sapiens casein kinase 1, delta (CSNK1D), transcript variant 1, mRNA [NM_001893]	3.278	down	50
A_33_P3309491	PTPRU	Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 3, mRNA [NM_005704]	13.763	down	51
A_23_P208334	PDE4A	Homo sapiens phosphodiesterase 4A, cAMP-specific (PDE4A), transcript variant 4, mRNA [NM_006202]	5.526	down	52
A_19_P00315493	LOC145474	Homo sapiens uncharacterized LOC145474 (LOC145474), long non-coding RNA [NR_027046]	3.640	down	53
A_19_P00809708	LOC145474	Homo sapiens uncharacterized LOC145474 (LOC145474), long non-coding RNA [NR_027046]	4.110	down	54
A_23_P94552	TMEM2	Homo sapiens transmembrane protein 2 (TMEM2), transcript variant 1, mRNA [NM_013390]	4.044	down	55
A_23_P142389	LSR	Homo sapiens lipolysis stimulated lipoprotein receptor (LSR), transcript variant 2, mRNA [NM_205834]	4.581	down	56
A_33_P3266923	LMTK2	Homo sapiens lemur tyrosine kinase 2 (LMTK2), mRNA [NM_014916]	3.194	down	57
A_33_P3265394	WDR74	WD repeat domain 74 [Source:HGNC Symbol;Acc:HGNC:25529] [ENST00000538098]	3.738	down	58
A_21_P0004458	lnc-ARSI-1	LNCipedia lincRNA (lnc-ARSI-1), lincRNA [lnc-ARSI-1:1]	10.111	down	59
A_21_P0003035	lnc-RNF7-1	LNCipedia lincRNA (lnc-RNF7-1), lincRNA [lnc-RNF7-1:1]	3.751	down	60
A_33_P3404676	AMOT	angiomotin [Source:HGNC Symbol;Acc:HGNC:17810] [ENST00000371958]	3.162	down	61
A_23_P102950	RSPH1	Homo sapiens radial spoke head 1 homolog (Chlamydomonas) (RSPH1), transcript variant 1, mRNA [NM_080860]	3.726	down	62

A_33_P3343972	RSPH1	Homo sapiens radial spoke head 1 homolog (Chlamydomonas) (RSPH1), transcript variant 1, mRNA [NM_080860]	4.224	down	63
A_23_P129157	NEIL1	Homo sapiens nei endonuclease VIII-like 1 (E. coli) (NEIL1), transcript variant 2, mRNA [NM_024608]	4.258	down	64
A_21_P0006912	lnc-SMC3-1	LNCipedia lincRNA (lnc-SMC3-1), lincRNA [lnc-SMC3-1:2]	4.582	down	65
A_21_P0010580	XLOC_l2_000657	BROAD Institute lincRNA (XLOC_l2_000657), lincRNA [TCONS_l2_00000881]	3.487	down	66
A_33_P3396578	GRK5	Homo sapiens G protein-coupled receptor kinase 5, mRNA (cDNA clone IMAGE:3912936), with apparent retained intron. [BC018116]	4.271	down	67
A_21_P0006893	lnc-KIF20B-5	LNCipedia lincRNA (lnc-KIF20B-5), lincRNA [lnc-KIF20B-5:1]	3.154	down	68
A_33_P3250895	PSMB11	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 11 (PSMB11), mRNA [NM_001099780]	3.377	down	69
A_21_P0007975	LINC00424	long intergenic non-protein coding RNA 424 [Source:HGNC Symbol;Acc:HGNC:42815] [ENST00000413124]	3.647	down	70
A_21_P0007497	LINC01234	Homo sapiens long intergenic non-protein coding RNA 1234 (LINC01234), transcript variant 1, long non-coding RNA [NR_110026]	5.040	down	71
A_23_P58729	SLC34A1	Homo sapiens solute carrier family 34 (type II sodium/phosphate cotransporter), member 1 (SLC34A1), transcript variant 1, mRNA [NM_003052]	4.726	down	72
A_21_P0013289	LOC646588	PREDICTED: Homo sapiens uncharacterized LOC646588 (LOC646588), transcript variant X2, misc_RNA [XR_426148]	3.693	down	73
A_21_P0013485	XLOC_l2_014217	BROAD Institute lincRNA (XLOC_l2_014217), lincRNA [TCONS_l2_00027780]	4.303	down	74
A_33_P3303474	CYP4A11	Homo sapiens cytochrome P450, family 4, subfamily A, polypeptide 11 (CYP4A11), mRNA [NM_000778]	3.278	down	75
A_21_P0001471	lnc-ZBTB17-2	LNCipedia lincRNA (lnc-ZBTB17-2), lincRNA [lnc-ZBTB17-2:1]	3.221	down	76
A_21_P0007041	LINC00200	long intergenic non-protein coding RNA 200 [Source:HGNC Symbol;Acc:HGNC:30974] [ENST00000583117]	3.901	down	77
A_33_P3313283	CILP2	Homo sapiens cartilage intermediate layer protein 2 (CILP2), mRNA [NM_153221]	3.459	down	78
A_23_P412389	FGF18	Homo sapiens fibroblast growth factor 18 (FGF18), mRNA [NM_003862]	3.103	down	79
A_33_P3235262	PIP5KL1	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase-like 1 (PIP5KL1), transcript variant 1, mRNA [NM_001135219]	3.750	down	80
A_23_P25994	LGMN	Homo sapiens legumain (LGMN), transcript variant 2, mRNA [NM_001008530]	4.178	down	81
A_33_P3799936	ARHGEF10L	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10-like (ARHGEF10L), transcript variant 1, mRNA [NM_018125]	3.247	down	82
A_33_P3409159	SLC22A23	Homo sapiens solute carrier family 22, member 23 (SLC22A23), transcript variant 1, mRNA [NM_015482]	4.156	down	83
A_23_P396858	FZD8	Homo sapiens frizzled class receptor 8 (FZD8), mRNA [NM_031866]	3.244	down	84
A_24_P832426	B3GALTL	Homo sapiens beta 1,3-galactosyltransferase-like (B3GALTL), mRNA [NM_194318]	4.267	down	85
A_33_P3413098	LOC100129550	Homo sapiens uncharacterized LOC100129550 (LOC100129550), long non-coding RNA [NR_024618]	3.394	down	86
A_23_P315571	RFTN1	Homo sapiens raftlin, lipid raft linker 1 (RFTN1), mRNA [NM_015150]	4.643	down	87
A_21_P0013889	na	raftlin, lipid raft linker 1 pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:23971] [ENST00000442584]	3.864	down	88
A_32_P41026	SC5D	Homo sapiens sterol-C5-desaturase (SC5D), transcript variant 2, mRNA [NM_001024956]	3.155	down	89
A_23_P328206	DNMBP	Homo sapiens dynamin binding protein (DNMBP), mRNA [NM_015221]	4.108	down	90
A_33_P3347035	na	Homo sapiens cDNA clone IMAGE:7262526, with apparent retained intron. [BC069659]	5.251	down	91
A_33_P3390708	TMEM2	Homo sapiens transmembrane protein 2 (TMEM2), transcript variant 1, mRNA [NM_013390]	5.721	down	92
A_24_P324405	ANKRD11	Homo sapiens ankyrin repeat domain 11 (ANKRD11), transcript variant 2, mRNA [NM_013275]	3.639	down	93
A_23_P80778	DIRC2	Homo sapiens disrupted in renal carcinoma 2 (DIRC2), mRNA [NM_032839]	4.040	down	94
A_23_P166297	ABCG1	Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 5, mRNA [NM_207627]	4.285	down	95
A_21_P0005231	na	0	3.230	down	96
A_23_P203743	GAB2	Homo sapiens GRB2-associated binding protein 2 (GAB2), transcript variant 2, mRNA [NM_012296]	5.934	down	97
A_23_P154526	GRB14	Homo sapiens growth factor receptor-bound protein 14 (GRB14), transcript variant 1, mRNA [NM_004490]	3.751	down	98
A_21_P0007219	lnc-AP000769.1-1	LNCipedia lincRNA (lnc-AP000769.1-1), lincRNA [lnc-AP000769.1-1:1]	6.459	down	99
A_23_P101905	APC2	Homo sapiens adenomatosis polyposis coli 2 (APC2), mRNA [NM_005883]	5.499	down	100
A_33_P3415052	NIPAL4	Homo sapiens NIPA-like domain containing 4 (NIPAL4), transcript variant 2, mRNA [NM_001172292]	3.778	down	101
A_33_P3401753	FFAR3	Homo sapiens free fatty acid receptor 3 (FFAR3), mRNA [NM_005304]	4.966	down	102
A_33_P3298810	FFAR3	Homo sapiens free fatty acid receptor 3 (FFAR3), mRNA [NM_005304]	5.254	down	103
A_23_P127824	TNNT3	Homo sapiens troponin T type 3 (skeletal, fast) (TNNT3), transcript variant 3, mRNA [NM_001042780]	3.149	down	104
A_33_P3382229	TNNT3	Homo sapiens troponin T type 3 (skeletal, fast) (TNNT3), transcript variant 5, mRNA [NM_001297646]	5.933	down	105
A_23_P431933	CAMKK1	Homo sapiens calcium/calmodulin-dependent protein kinase kinase 1, alpha (CAMKK1), transcript variant 1, mRNA [NM_032294]	4.313	down	106
A_24_P292929	CAMKK1	Homo sapiens calcium/calmodulin-dependent protein kinase kinase 1, alpha (CAMKK1), transcript variant 3, mRNA [NM_172207]	4.297	down	107
A_23_P325631	SKI	Homo sapiens v-ski avian sarcoma viral oncogene homolog (SKI), mRNA [NM_003036]	3.953	down	108
A_24_P285032	IDS	Homo sapiens iduronate 2-sulfatase (IDS), transcript variant 2, mRNA [NM_006123]	4.071	down	109
A_32_P205944	RGPD5	Homo sapiens RANBP2-like and GRIP domain containing 5 (RGPD5), transcript variant 1, mRNA [NM_005054]	3.175	down	110
A_23_P360316	FUT3	Homo sapiens fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group) (FUT3), transcript variant 1, mRNA [NM_000149]	3.739	down	111
A_24_P179044	SNX9	Homo sapiens sorting nexin 9 (SNX9), mRNA [NM_016224]	8.235	down	112
A_24_P276873	ERMN	ermin, ERM-like protein [Source:HGNC Symbol;Acc:HGNC:29208] [ENST00000409395]	5.065	down	113
A_33_P3250165	ERMN	ermin, ERM-like protein [Source:HGNC Symbol;Acc:HGNC:29208] [ENST00000411762]	4.371	down	114
A_24_P335620	SLC7A5	Homo sapiens solute carrier family 7 (amino acid transporter light chain, L system), member 5 (SLC7A5), mRNA [NM_003486]	6.363	down	115
A_23_P20494	NDRG1	Homo sapiens N-myc downstream regulated 1 (NDRG1), transcript variant 2, mRNA [NM_006096]	5.034	down	116
A_23_P143016	ARID5A	Homo sapiens AT rich interactive domain 5A (MRF1-like) (ARID5A), mRNA [NM_212481]	3.357	down	117
A_33_P3389342	ARID5A	Homo sapiens AT rich interactive domain 5A (MRF1-like) (ARID5A), mRNA [NM_212481]	3.363	down	118
A_23_P170290	TMEM57	Homo sapiens transmembrane protein 57 (TMEM57), transcript variant 1, mRNA [NM_018202]	3.150	down	119
A_21_P0009331	TMEM92-AS1	Homo sapiens TMEM92 antisense RNA 1 (TMEM92-AS1), long non-coding RNA [NR_125805]	9.689	down	120
A_21_P0009196	TMEM92-AS1	Homo sapiens TMEM92 antisense RNA 1 (TMEM92-AS1), long non-coding RNA [NR_125805]	10.987	down	121
A_23_P58506	ELL2	Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA [NM_012081]	4.228	down	122
A_33_P3401428	TMEM38B	Homo sapiens transmembrane protein 38B (TMEM38B), mRNA [NM_018112]	3.138	down	123
A_23_P139919	CHST11	Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), transcript variant 1, mRNA [NM_018413]	3.154	down	124
A_21_P0002056	na	0	3.469	down	125
A_33_P3294679	SMCR5	Homo sapiens Smith-Magenis syndrome chromosome region, candidate 5 (non-protein coding) (SMCR5), long non-coding RNA [NR_024007]	3.943	down	126

A_33_P3339531	CHADL	Homo sapiens chondroadherin-like (CHADL), mRNA [NM_138481]	3.440	down	127
A_23_P5853	SAG	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA [NM_000541]	3.534	down	128
A_23_P426305	AOC3	Homo sapiens amine oxidase, copper containing 3 (AOC3), transcript variant 1, mRNA [NM_003734]	4.095	down	129
A_33_P3279353	AZU1	Homo sapiens azurocidin 1 (AZU1), mRNA [NM_001700]	5.458	down	130
A_23_P19030	ARSI	Homo sapiens arylsulfatase family, member I (ARSI), mRNA [NM_001012301]	19.301	down	131
A_33_P3239527	LOC100128517	Homo sapiens cDNA FLJ44820 fis, clone BRACE3046049. [AK126772]	5.197	down	132
A_33_P3226367	lnc-CD44-1	LNCipedia lincRNA (lnc-CD44-1), lincRNA [lnc-CD44-1:1]	8.220	down	133
A_33_P3299416	GRASP	Homo sapiens GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein (GRASP), transcript variant 1, mRNA [NM_181711]	3.124	down	134
A_33_P3336592	KLF13	Homo sapiens cDNA FLJ45109 fis, clone BRAWH3034097. [AK127052]	3.429	down	135
A_21_P0009442	LINC01540	Homo sapiens long intergenic non-protein coding RNA 1540 (LINC01540), transcript variant 1, long non-coding RNA [NR_110429]	3.465	down	136
A_33_P3361896	LOC100127994	Homo sapiens cDNA FLJ45631 fis, clone CHONS2001797. [AK127538]	3.342	down	137
A_24_P286951	PLEKHS1	Homo sapiens pleckstrin homology domain containing, family S member 1 (PLEKHS1), transcript variant 4, mRNA [NM_024889]	3.508	down	138
A_33_P3309832	PLEKHS1	Homo sapiens pleckstrin homology domain containing, family S member 1 (PLEKHS1), transcript variant 1, mRNA [NM_182601]	3.606	down	139
A_33_P3232677	na	0	3.122	down	140
A_21_P0013391	na	0	4.124	down	141
A_23_P39550	TMEM163	Homo sapiens transmembrane protein 163 (TMEM163), mRNA [NM_030923]	5.852	down	142
A_21_P0004840	lnc-CD83-2	LNCipedia lincRNA (lnc-CD83-2), lincRNA [lnc-CD83-2:1]	4.882	down	143
A_23_P9869	CNDP1	Homo sapiens carnosine dipeptidase 1 (metallopeptidase M20 family) (CNDP1), mRNA [NM_032649]	4.912	down	144
A_33_P3281473	FAM83A-AS1	Homo sapiens FAM83A antisense RNA 1 (FAM83A-AS1), long non-coding RNA [NR_024479]	3.239	down	145
A_33_P3301351	RBM44	Homo sapiens RNA binding motif protein 44 (RBM44), mRNA [NM_001080504]	3.484	down	146
A_33_P3374087	RBM44	Homo sapiens RNA binding motif protein 44 (RBM44), mRNA [NM_001080504]	4.292	down	147
A_33_P3543133	LINC00641	Homo sapiens long intergenic non-protein coding RNA 641 (LINC00641), transcript variant 1, long non-coding RNA [NR_038970]	3.383	down	148
A_32_P137920	RSPH4A	Homo sapiens radial spoke head 4 homolog A (Chlamydomonas) (RSPH4A), transcript variant 1, mRNA [NM_001010892]	3.613	down	149
A_24_P520767	LOC149351	0	3.446	down	150
A_23_P148541	CTAG1A	Homo sapiens cancer/testis antigen 1A (CTAG1A), mRNA [NM_139250]	3.802	down	151
A_24_P128442	TBX15	Homo sapiens T-box 15 (TBX15), mRNA [NM_152380]	3.910	down	152
A_21_P0001044	LINC01031	Homo sapiens long intergenic non-protein coding RNA 1031 (LINC01031), long non-coding RNA [NR_125789]	3.337	down	153
A_21_P0010389	na	Homo sapiens cDNA FLJ46287 fis, clone TESTI4032375. [AK128164]	3.642	down	154
A_33_P3224819	SLC45A4	Homo sapiens solute carrier family 45, member 4 (SLC45A4), transcript variant 1, mRNA [NM_001286646]	7.139	down	155
A_23_P209320	PER2	Homo sapiens period circadian clock 2 (PER2), mRNA [NM_022817]	3.272	down	156
A_23_P411162	PER2	Homo sapiens period circadian clock 2 (PER2), mRNA [NM_022817]	3.187	down	157
A_24_P380311	CAMK2A	Homo sapiens calcium/calmodulin-dependent protein kinase II alpha (CAMK2A), transcript variant 1, mRNA [NM_015981]	7.602	down	158
A_23_P54996	TEX14	Homo sapiens testis expressed 14 (TEX14), transcript variant 1, mRNA [NM_198393]	15.998	down	159
A_23_P401106	PDE2A	Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), transcript variant 1, mRNA [NM_002599]	9.232	down	160
A_24_P20200	PLEKHB2	Homo sapiens pleckstrin homology domain containing, family B (evectins) member 2 (PLEKHB2), transcript variant 8, mRNA [NM_001267066]	3.255	down	161
A_23_P21560	FAM49A	Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA [NM_030797]	4.068	down	162
A_33_P3236392	PVRL4	Homo sapiens poliovirus receptor-related 4 (PVRL4), mRNA [NM_030916]	3.696	down	163
A_24_P149713	ZBTB43	Homo sapiens zinc finger and BTB domain containing 43 (ZBTB43), transcript variant 1, mRNA [NM_014007]	3.884	down	164
A_23_P122662	GFOD1	Homo sapiens glucose-fructose oxidoreductase domain containing 1 (GFOD1), transcript variant 1, mRNA [NM_018988]	3.152	down	165
A_33_P3418000	RELL1	Homo sapiens RELT-like 1 (RELL1), transcript variant 2, mRNA [NM_001085399]	4.505	down	166
A_24_P322474	PDE4A	Homo sapiens phosphodiesterase 4A, cAMP-specific (PDE4A), transcript variant 4, mRNA [NM_006202]	7.198	down	167
A_23_P5903	SLCO4A1	Homo sapiens solute carrier organic anion transporter family, member 4A1 (SLCO4A1), mRNA [NM_016354]	7.906	down	168
A_32_P5251	RARA	Homo sapiens retinoic acid receptor, alpha (RARA), transcript variant 2, mRNA [NM_001024809]	3.576	down	169
A_23_P128375	FAM222A	Homo sapiens family with sequence similarity 222, member A (FAM222A), mRNA [NM_032829]	4.295	down	170
A_33_P3294801	na	Homo sapiens cDNA FLJ40672 fis, clone THYMU2021509. [AK097991]	3.654	down	171
A_33_P3245126	na	0	3.351	down	172
A_23_P301304	FGFR1	Homo sapiens fibroblast growth factor receptor 1 (FGFR1), transcript variant 1, mRNA [NM_023110]	4.341	down	173
A_23_P372923	FGFR1	Homo sapiens fibroblast growth factor receptor 1 (FGFR1), transcript variant 13, mRNA [NM_001174066]	3.133	down	174
A_24_P82155	ANKDD1A	ankyrin repeat and death domain containing 1A [Source:HGNC Symbol;Acc:HGNC:28002] [ENST00000620154]	3.180	down	175
A_23_P210763	JAG1	Homo sapiens jagged 1 (JAG1), mRNA [NM_000214]	4.692	down	176
A_23_P76823	ADSSL1	Homo sapiens adenylosuccinate synthase like 1 (ADSSL1), transcript variant 1, mRNA [NM_199165]	3.315	down	177
A_24_P253003	WNT11	Homo sapiens wingless-type MMTV integration site family, member 11 (WNT11), mRNA [NM_004626]	3.374	down	178
A_33_P3813128	SEMA3F	Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F (SEMA3F), mRNA [NM_004186]	3.736	down	179
A_24_P389916	LRRC32	Homo sapiens leucine rich repeat containing 32 (LRRC32), transcript variant 1, mRNA [NM_005512]	6.504	down	180
A_33_P3351249	CXCL16	Homo sapiens chemokine (C-X-C motif) ligand 16 (CXCL16), transcript variant 2, mRNA [NM_001100812]	3.928	down	181
A_33_P3623118	lnc-MGAT1-1	Homo sapiens cDNA FLJ30091 fis, clone BNGH41000017. [AK054653]	3.436	down	182
A_23_P37484	CHSY1	Homo sapiens chondroitin sulfate synthase 1 (CHSY1), mRNA [NM_014918]	3.122	down	183
A_23_P218626	NEU4	Homo sapiens sialidase 4 (NEU4), transcript variant 1, mRNA [NM_080741]	6.189	down	184
A_23_P348121	FOSL2	Homo sapiens FOS-like antigen 2 (FOSL2), mRNA [NM_005253]	7.252	down	185
A_23_P139786	OASL	Homo sapiens 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 1, mRNA [NM_003733]	4.360	down	186
A_23_P10559	AATK	Homo sapiens apoptosis-associated tyrosine kinase (AATK), transcript variant 1, mRNA [NM_001080395]	7.568	down	187
A_24_P96961	SPSB1	Homo sapiens splA/ryanodine receptor domain and SOCS box containing 1 (SPSB1), mRNA [NM_025106]	5.773	down	188
A_23_P134935	DUSP4	Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 1, mRNA [NM_001394]	4.493	down	189
A_23_P85922	BMP8A	Homo sapiens bone morphogenetic protein 8a (BMP8A), mRNA [NM_181809]	11.433	down	190

A_23_P34835	LMNA	Homo sapiens lamin A/C (LMNA), transcript variant 2, mRNA [NM_005572]	6.395	down	191
A_33_P3408762	LMNA	Homo sapiens lamin A/C (LMNA), transcript variant 6, mRNA [NM_001282625]	7.222	down	192
A_23_P106024	JAG2	Homo sapiens jagged 2 (JAG2), transcript variant 1, mRNA [NM_002226]	4.044	down	193
A_33_P3312676	na	myelin transcription factor 1 [Source:RefSeq peptide;Acc:NP_004526] [ENST00000621996]	8.594	down	194
A_33_P3233906	RAMP1	Homo sapiens receptor (G protein-coupled) activity modifying protein 1 (RAMP1), mRNA [NM_005855]	13.457	down	195
A_23_P50946	RAMP1	Homo sapiens receptor (G protein-coupled) activity modifying protein 1 (RAMP1), mRNA [NM_005855]	10.041	down	196
A_24_P51909	CPLX1	Homo sapiens complexin 1 (CPLX1), mRNA [NM_006651]	4.868	down	197
A_21_P0006238	lnc-RXRA-1	LNCipedia lincRNA (lnc-RXRA-1), lincRNA [lnc-RXRA-1:1]	3.894	down	198
A_33_P3417150	P2RY1	Homo sapiens purinergic receptor P2Y, G-protein coupled, 1 (P2RY1), mRNA [NM_002563]	3.417	down	199
A_33_P3238626	na	Homo sapiens cDNA FLJ41497 fis, clone BRTHA2006075. [AK123491]	3.102	down	200
A_32_P175301	DENND3	Homo sapiens DENN/MADD domain containing 3 (DENND3), mRNA [NM_014957]	5.813	down	201
A_33_P3783812	C8orf60	Homo sapiens cDNA FLJ12193 fis, clone MAMMA1000856. [AK022255]	5.868	down	202
A_33_P3321130	DENND3	DENN/MADD domain containing 3 [Source:HGNC Symbol;Acc:HGNC:29134] [ENST00000520482]	5.856	down	203
A_23_P93938	NACAD	Homo sapiens NAC alpha domain containing (NACAD), mRNA [NM_001146334]	3.194	down	204
A_21_P0010687	XLOC_l2_000018	BROAD Institute lincRNA (XLOC_l2_000018), lincRNA [TCONS_l2_00001952]	4.453	down	205
A_21_P0010689	XLOC_l2_000018	BROAD Institute lincRNA (XLOC_l2_000018), lincRNA [TCONS_l2_00001954]	5.387	down	206
A_24_P291826	SYTL3	Homo sapiens synaptotagmin-like 3 (SYTL3), transcript variant 3, mRNA [NM_001009991]	3.755	down	207
A_23_P316974	SYNJ2	Homo sapiens synaptojanin 2 (SYNJ2), transcript variant 1, mRNA [NM_003898]	3.776	down	208
A_21_P0009211	na	ys84c11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:221492 5', mRNA sequence [H92146]	3.300	down	209
A_23_P373724	PPFIBP1	Homo sapiens PTPRF interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1), transcript variant 1, mRNA [NM_003622]	5.509	up	210
A_23_P75441	NUDT22	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 22 (NUDT22), transcript variant 1, mRNA [NM_032344]	4.008	up	211
A_23_P103486	CYP2J2	Homo sapiens cytochrome P450, family 2, subfamily J, polypeptide 2 (CYP2J2), mRNA [NM_000775]	5.107	up	212
A_33_P3259183	FAM78B	Homo sapiens family with sequence similarity 78, member B (FAM78B), mRNA [NM_001017961]	3.448	up	213
A_33_P3346771	AK9	adenylate kinase 9 [Source:HGNC Symbol;Acc:HGNC:33814] [ENST00000466992]	5.040	up	214
A_24_P73075	TTC12	Homo sapiens tetratricopeptide repeat domain 12 (TTC12), mRNA [NM_017868]	3.842	up	215
A_23_P145541	FIG4	Homo sapiens FIG4 phosphoinositide 5-phosphatase (FIG4), mRNA [NM_014845]	4.578	up	216
A_23_P149259	TMEM79	Homo sapiens transmembrane protein 79 (TMEM79), transcript variant 1, mRNA [NM_032323]	3.729	up	217
A_33_P3320272	TMEM79	Homo sapiens transmembrane protein 79 (TMEM79), transcript variant 1, mRNA [NM_032323]	4.782	up	218
A_33_P3256113	GUSBP1	Homo sapiens glucuronidase, beta pseudogene 1 (GUSBP1), transcript variant 1, non-coding RNA [NR_027026]	3.781	up	219
A_33_P3220919	ADRBK2	Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA [NM_005160]	4.308	up	220
A_33_P3356361	SRP14-AS1	Homo sapiens SRP14 antisense RNA1 (head to head) (SRP14-AS1), transcript variant 1, long non-coding RNA [NR_040059]	6.041	up	221
A_33_P3386117	RER1	Homo sapiens retention in endoplasmic reticulum sorting receptor 1 (RER1), mRNA [NM_007033]	3.523	up	222
A_32_P29118	SEMA3D	Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D (SEMA3D), mRNA [NM_152754]	7.700	up	223
A_23_P209962	SMC6	Homo sapiens structural maintenance of chromosomes 6 (SMC6), transcript variant 2, mRNA [NM_024624]	3.788	up	224
A_21_P0001216	lnc-C1orf186-1	EST643 human nasopharynx Homo sapiens cDNA, mRNA sequence [CD684123]	6.965	up	225
A_33_P3334443	FAM69A	Homo sapiens family with sequence similarity 69, member A (FAM69A), transcript variant 4, mRNA [NM_001252271]	3.276	up	226
A_24_P941359	FAM65B	Homo sapiens family with sequence similarity 65, member B (FAM65B), transcript variant 1, mRNA [NM_014722]	3.360	up	227
A_33_P3303146	ATG4C	Homo sapiens autophagy related 4C, cysteine peptidase (ATG4C), transcript variant 1, mRNA [NM_032852]	4.357	up	228
A_33_P3358923	BTLA	Homo sapiens B and T lymphocyte associated (BTLA), transcript variant 1, mRNA [NM_181780]	4.615	up	229
A_33_P3412900	CBLN3	Homo sapiens cerebellin 3 precursor (CBLN3), mRNA [NM_001039771]	3.680	up	230
A_32_P180315	CCDC180	Homo sapiens coiled-coil domain containing 180 (CCDC180), mRNA [NM_020893]	4.490	up	231
A_33_P3302563	LOC100129408	Homo sapiens cDNA FLJ46023 fis, clone SPLEN2021991. [AK127916]	3.910	up	232
A_21_P0000185	LOC100505549	Homo sapiens uncharacterized LOC100505549 (LOC100505549), mRNA [NM_001242804]	3.299	up	233
A_21_P0001575	lnc-NOTCH2-2	LNCipedia lincRNA (lnc-NOTCH2-2), lincRNA [lnc-NOTCH2-2:1]	5.100	up	234
A_24_P289178	C16orf74	Homo sapiens chromosome 16 open reading frame 74 (C16orf74), mRNA [NM_206967]	3.963	up	235
A_23_P50775	LRFN3	Homo sapiens leucine rich repeat and fibronectin type III domain containing 3 (LRFN3), mRNA [NM_024509]	3.168	up	236
A_23_P30900	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2 [Source:HGNC Symbol;Acc:HGNC:4943] [ENST00000552745]	5.537	up	237
A_23_P352266	BCL2	Homo sapiens B-cell CLL/lymphoma 2 (BCL2), transcript variant alpha, mRNA [NM_000633]	3.304	up	238
A_32_P92505	LCLAT1	Homo sapiens lysocardiolipin acyltransferase 1 (LCLAT1), transcript variant 1, mRNA [NM_182551]	3.400	up	239
A_23_P391228	MANEAL	Homo sapiens mannosidase, endo-alpha-like (MANEAL), transcript variant 1, mRNA [NM_001031740]	3.224	up	240
A_33_P3413483	SORD	sorbitol dehydrogenase [Source:HGNC Symbol;Acc:HGNC:11184] [ENST00000267814]	3.253	up	241
A_24_P481824	DPY19L4	Homo sapiens dpy-19-like 4 (C. elegans) (DPY19L4), mRNA [NM_181787]	3.205	up	242
A_23_P340188	FAM122C	Homo sapiens family with sequence similarity 122C (FAM122C), transcript variant 2, mRNA [NM_138819]	3.865	up	243
A_33_P3315425	METTL4	Homo sapiens methyltransferase like 4 (METTL4), mRNA [NM_022840]	3.511	up	244
A_23_P28733	RBL1	Homo sapiens retinoblastoma-like 1 (RBL1), transcript variant 1, mRNA [NM_002895]	3.191	up	245
A_32_P85813	RAP1GDS1	Homo sapiens RAP1, GTP-GDP dissociation stimulator 1 (RAP1GDS1), transcript variant 1, mRNA [NM_001100426]	3.481	up	246
A_24_P190877	TRMT1L	Homo sapiens tRNA methyltransferase 1 homolog (S. cerevisiae)-like (TRMT1L), transcript variant 1, mRNA [NM_030934]	4.070	up	247
A_24_P145047	ZNF609	Homo sapiens zinc finger protein 609 (ZNF609), mRNA [NM_015042]	3.570	up	248
A_23_P130856	CEP89	Homo sapiens centrosomal protein 89kDa (CEP89), mRNA [NM_032816]	3.554	up	249
A_23_P80902	KIF15	Homo sapiens kinesin family member 15 (KIF15), mRNA [NM_020242]	5.393	up	250
A_23_P19816	RNF32	Homo sapiens ring finger protein 32 (RNF32), transcript variant 3, mRNA [NM_030936]	3.735	up	251
A_23_P127915	STK33	Homo sapiens serine/threonine kinase 33 (STK33), transcript variant 1, mRNA [NM_030906]	8.482	up	252
A_23_P157527	LRRCC1	Homo sapiens leucine rich repeat and coiled-coil centrosomal protein 1 (LRRCC1), mRNA [NM_033402]	5.072	up	253
A_24_P110983	AKT3	Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (AKT3), transcript variant 1, mRNA [NM_005465]	3.105	up	254
A_24_P88801	NPHP1	Homo sapiens nephronophthisis 1 (juvenile) (NPHP1), transcript variant 1, mRNA [NM_000272]	3.502	up	255

A_33_P3260125	LDLRAD2	Homo sapiens low density lipoprotein receptor class A domain containing 2 (LDLRAD2), mRNA [NM_001013693]	4.256	up	256
A_21_P0005196	LOC101927902	PREDICTED: Homo sapiens uncharacterized LOC101927902 (LOC101927902), ncRNA [XR_242326]	3.777	up	257
A_21_P0010465	lnc-APOBEC3F-1	LNCipedia lincRNA (lnc-APOBEC3F-1), lincRNA [lnc-APOBEC3F-1:1]	3.867	up	258
A_23_P321160	ZNF594	Homo sapiens zinc finger protein 594 (ZNF594), mRNA [NM_032530]	3.236	up	259
A_33_P3327956	ZNF605	Homo sapiens zinc finger protein 605 (ZNF605), transcript variant 1, mRNA [NM_183238]	3.507	up	260
A_21_P0008768	LOC101929641	PREDICTED: Homo sapiens uncharacterized LOC101929641 (LOC101929641), ncRNA [XR_243223]	4.158	up	261
A_23_P201731	TRAF5	Homo sapiens TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA [NM_004619]	6.152	up	262
A_24_P710730	SMA4	Homo sapiens glucuronidase, beta pseudogene (SMA4), transcript variant 2, non-coding RNA [NR_024054]	3.371	up	263
A_23_P304511	ZNF397	Homo sapiens zinc finger protein 397 (ZNF397), transcript variant 2, mRNA [NM_032347]	3.951	up	264
A_23_P434430	ZNF439	Homo sapiens zinc finger protein 439 (ZNF439), mRNA [NM_152262]	5.647	up	265
A_23_P22672	ALG13	Homo sapiens ALG13, UDP-N-acetylglucosaminyltransferase subunit (ALG13), transcript variant 7, mRNA [NM_001257231]	3.239	up	266
A_33_P3323218	CARF	Homo sapiens calcium responsive transcription factor (CARF), transcript variant 2, mRNA [NM_024744]	3.553	up	267
A_24_P363087	C5orf45	Homo sapiens chromosome 5 open reading frame 45 (C5orf45), transcript variant 1, mRNA [NM_016175]	3.156	up	268
A_24_P168398	ZNF177	Homo sapiens zinc finger protein 177 (ZNF177), transcript variant 3, mRNA [NM_003451]	8.146	up	269
A_23_P416751	ZNF610	Homo sapiens zinc finger protein 610 (ZNF610), transcript variant 3, mRNA [NM_173530]	4.020	up	270
A_23_P250245	CD72	Homo sapiens CD72 molecule (CD72), mRNA [NM_001782]	4.453	up	271
A_23_P356139	FAM178A	Homo sapiens family with sequence similarity 178, member A (FAM178A), transcript variant 1, mRNA [NM_018121]	3.340	up	272
A_33_P3420204	CRTC1	Homo sapiens CREB regulated transcription coactivator 1 (CRTC1), transcript variant 3, mRNA [NM_001098482]	3.300	up	273
A_21_P0007489	LOC100507616	PREDICTED: Homo sapiens uncharacterized LOC100507616 (LOC100507616), transcript variant X1, ncRNA [XR_110328]	5.104	up	274
A_32_P356316	HLA-DOA	Homo sapiens major histocompatibility complex, class II, DO alpha (HLA-DOA), mRNA [NM_002119]	3.902	up	275
A_23_P251705	ARHGEF9	Homo sapiens Cdc42 guanine nucleotide exchange factor (GEF) 9 (ARHGEF9), transcript variant 1, mRNA [NM_015185]	3.230	up	276
A_24_P344961	AMOT	Homo sapiens angiomotin (AMOT), transcript variant 2, mRNA [NM_133265]	4.503	up	277
A_33_P3311917	na	Q6JHZ7_HUMAN (Q6JHZ7) HCV-NS5ATP5 binding protein 1, partial (29%) [THC2537043]	3.571	up	278
A_23_P110288	GSTCD	Homo sapiens glutathione S-transferase, C-terminal domain containing (GSTCD), transcript variant 2, mRNA [NM_024751]	3.857	up	279
A_23_P501435	CSRP2BP	Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant 1, mRNA [NM_020536]	3.620	up	280
A_32_P396186	TRIM66	Homo sapiens tripartite motif containing 66 (TRIM66), mRNA [NM_014818]	3.644	up	281
A_23_P418431	C6orf164	Homo sapiens chromosome 6 open reading frame 164 (C6orf164), long non-coding RNA [NR_026784]	3.488	up	282
A_24_P807031	ATP6AP1L	Homo sapiens ATPase, H+ transporting, lysosomal accessory protein 1-like (ATP6AP1L), mRNA [NM_001017971]	4.119	up	283
A_23_P52082	INTS7	Homo sapiens integrator complex subunit 7 (INTS7), transcript variant 1, mRNA [NM_015434]	4.605	up	284
A_33_P3321657	HSPG2	Homo sapiens heparan sulfate proteoglycan 2 (HSPG2), transcript variant 1, mRNA [NM_001291860]	3.109	up	285
A_23_P50786	CLIP3	Homo sapiens CAP-GLY domain containing linker protein 3 (CLIP3), transcript variant 2, mRNA [NM_015526]	4.295	up	286
A_23_P155857	NUDT6	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 6 (NUDT6), transcript variant 2, mRNA [NM_198041]	6.013	up	287
A_33_P3241786	ADD2	Homo sapiens adducin 2 (beta) (ADD2), transcript variant 2, mRNA [NM_017482]	5.772	up	288
A_33_P3241782	ADD2	Homo sapiens adducin 2 (beta) (ADD2), transcript variant 1, mRNA [NM_001617]	4.248	up	289
A_23_P159907	MAGED4B	Homo sapiens melanoma antigen family D, 4B (MAGED4B), transcript variant 1, mRNA [NM_030801]	3.960	up	290
A_19_P00810465	KCNA6	Homo sapiens potassium channel, voltage gated shaker related subfamily A, member 6 (KCNA6), mRNA [NM_002235]	3.199	up	291
A_23_P111635	STYXL1	Homo sapiens serine/threonine/tyrosine interacting-like 1 (STYXL1), mRNA [NM_016086]	3.630	up	292
A_24_P185604	NDRG3	Homo sapiens NDRG family member 3 (NDRG3), transcript variant 1, mRNA [NM_032013]	3.974	up	293
A_32_P154223	LINC01431	Homo sapiens long intergenic non-protein coding RNA 1431 (LINC01431), long non-coding RNA [NR_109884]	3.345	up	294
A_32_P465742	PIP5K1B	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), transcript variant 2, mRNA [NM_003558]	8.084	up	295
A_32_P211045	DHFR	Homo sapiens dihydrofolate reductase (DHFR), transcript variant 1, mRNA [NM_000791]	6.917	up	296
A_23_P1676	TMEM218	Homo sapiens transmembrane protein 218 (TMEM218), transcript variant 1, mRNA [NM_001258243]	9.116	up	297
A_23_P217114	ALAD	Homo sapiens aminolevulinate dehydratase (ALAD), mRNA [NM_000031]	3.427	up	298
A_33_P3300092	NDST1	Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 (NDST1), transcript variant 1, mRNA [NM_001543]	4.819	up	299
A_23_P401084	ZNF575	Homo sapiens zinc finger protein 575 (ZNF575), mRNA [NM_174945]	5.194	up	300
A_23_P146637	SIGMAR1	Homo sapiens sigma non-opioid intracellular receptor 1 (SIGMAR1), transcript variant 1, mRNA [NM_005866]	5.066	up	301
A_23_P115356	AKR7A2	Homo sapiens aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) (AKR7A2), mRNA [NM_003689]	4.752	up	302
A_23_P5731	FAHD2A	Homo sapiens fumarylacetoacetate hydrolase domain containing 2A (FAHD2A), mRNA [NM_016044]	4.102	up	303
A_23_P151075	ARHGDIB	Homo sapiens Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB), mRNA [NM_001175]	3.158	up	304
A_33_P3329467	STYXL1	Homo sapiens serine/threonine/tyrosine interacting-like 1 (STYXL1), mRNA [NM_016086]	4.149	up	305
A_23_P258093	AGPAT1	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 1 (AGPAT1), transcript variant 1, mRNA [NM_006411]	3.165	up	306
A_23_P124927	RGS14	Homo sapiens regulator of G-protein signaling 14 (RGS14), mRNA [NM_006480]	4.359	up	307
A_23_P42746	NCF1	Homo sapiens neutrophil cytosolic factor 1 (NCF1), mRNA [NM_000265]	3.257	up	308
A_23_P91140	PECR	Homo sapiens peroxisomal trans-2-enoyl-CoA reductase (PECR), mRNA [NM_018441]	6.125	up	309
A_33_P3337019	LOC728975	PREDICTED: Homo sapiens uncharacterized LOC728975 (LOC728975), misc_RNA [XR_247237]	4.550	up	310
A_23_P71855	C5	Homo sapiens complement component 5 (C5), mRNA [NM_001735]	3.238	up	311
A_23_P61487	LRRC20	Homo sapiens leucine rich repeat containing 20 (LRRC20), transcript variant 3, mRNA [NM_018205]	7.468	up	312
A_24_P168416	PRDX2	Homo sapiens peroxiredoxin 2 (PRDX2), mRNA [NM_005809]	3.833	up	313
A_23_P502654	SHMT1	Homo sapiens serine hydroxymethyltransferase 1 (soluble) (SHMT1), transcript variant 1, mRNA [NM_004169]	4.491	up	314
A_33_P3632937	LOC100131262	PREDICTED: Homo sapiens uncharacterized LOC100131262 (LOC100131262), misc_RNA [XR_132952]	3.665	up	315
A_33_P3337931	na	0	6.831	up	316
A_33_P3843415	WDR11-AS1	Homo sapiens WDR11 antisense RNA 1 (WDR11-AS1), long non-coding RNA [NR_033850]	4.817	up	317
A_32_P216548	LDLRAP1	Homo sapiens low density lipoprotein receptor adaptor protein 1 (LDLRAP1), mRNA [NM_015627]	3.328	up	318

A_23_P258221	ABCC5	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5), transcript variant 1, mRNA [NM_005688]	5.243	up	319
A_33_P3317948	TP73-AS1	Homo sapiens TP73 antisense RNA 1 (TP73-AS1), transcript variant 1, long non-coding RNA [NR_033711]	4.382	up	320
A_23_P76529	ITGB7	Homo sapiens integrin, beta 7 (ITGB7), transcript variant 1, mRNA [NM_000889]	3.579	up	321
A_19_P00320723	SRP14-AS1	Homo sapiens SRP14 antisense RNA1 (head to head) (SRP14-AS1), transcript variant 1, long non-coding RNA [NR_040059]	6.579	up	322
A_33_P3298062	ABCC5	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5), transcript variant 2, mRNA [NM_001023587]	10.762	up	323
A_23_P170978	ZNF692	Homo sapiens zinc finger protein 692 (ZNF692), transcript variant 2, mRNA [NM_017865]	4.191	up	324
A_23_P397543	LINC00174	Homo sapiens long intergenic non-protein coding RNA 174 (LINC00174), long non-coding RNA [NR_026873]	5.221	up	325
A_33_P3212172	SNX22	Homo sapiens sorting nexin 22 (SNX22), transcript variant 1, mRNA [NM_024798]	12.078	up	326
A_32_P95914	MMS22L	Homo sapiens MMS22-like, DNA repair protein (MMS22L), mRNA [NM_198468]	6.498	up	327
A_33_P3305482	EIF2B3	Homo sapiens eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa (EIF2B3), transcript variant 1, mRNA [NM_020365]	5.174	up	328
A_23_P92543	SCFD2	Homo sapiens sec1 family domain containing 2 (SCFD2), mRNA [NM_152540]	3.300	up	329
A_23_P2223	MYL6B	Homo sapiens myosin, light chain 6B, alkali, smooth muscle and non-muscle (MYL6B), transcript variant 2, mRNA [NM_002475]	3.432	up	330
A_33_P3405334	GM2A	Homo sapiens GM2 ganglioside activator (GM2A), transcript variant 1, mRNA [NM_000405]	5.418	up	331
A_23_P29836	TMEM42	transmembrane protein 42 [Source:HGNC Symbol;Acc:HGNC:28444] [ENST00000477126]	3.771	up	332
A_23_P160992	FMO4	Homo sapiens flavin containing monooxygenase 4 (FMO4), mRNA [NM_002022]	7.359	up	333
A_33_P3336422	ZBED5-AS1	Homo sapiens ZBED5 antisense RNA 1 (ZBED5-AS1), long non-coding RNA [NR_034137]	5.761	up	334
A_33_P3415211	MPV17	Homo sapiens MpV17 mitochondrial inner membrane protein (MPV17), mRNA [NM_002437]	3.322	up	335
A_33_P3357087	MPV17	Homo sapiens MpV17 mitochondrial inner membrane protein (MPV17), mRNA [NM_002437]	3.548	up	336
A_33_P3388312	SKAP2	src kinase associated phosphoprotein 2 [Source:HGNC Symbol;Acc:HGNC:15687] [ENST00000345317]	6.037	up	337
A_24_P89843	CYHR1	Homo sapiens cysteine/histidine-rich 1 (CYHR1), transcript variant 2, mRNA [NM_032687]	4.398	up	338
A_23_P1775	DPAGT1	Homo sapiens dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase) (DPAGT1), mRNA [NM_001382]	4.625	up	339
A_23_P105409	MAP3K12	Homo sapiens mitogen-activated protein kinase kinase kinase 12 (MAP3K12), transcript variant 2, mRNA [NM_006301]	3.467	up	340
A_33_P3252794	GLI4	Homo sapiens GLI family zinc finger 4 (GLI4), mRNA [NM_138465]	3.314	up	341
A_23_P64828	OAS1	Homo sapiens 2'-5'-oligoadenylate synthetase 1, 40/46kDa (OAS1), transcript variant 2, mRNA [NM_002534]	6.161	up	342
A_23_P148807	CDC7	Homo sapiens cell division cycle 7 (CDC7), transcript variant 1, mRNA [NM_003503]	4.570	up	343
A_21_P0011476	CHEK2	Homo sapiens checkpoint kinase 2 (CHEK2), transcript variant 3, mRNA [NM_001005735]	5.260	up	344
A_23_P117494	MTHFD1	Homo sapiens methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase (MTHFD1), mRNA [NM_005956]	3.607	up	345
A_21_P0008517	LOC100506476	Homo sapiens uncharacterized LOC100506476 (LOC100506476), long non-coding RNA [NR_109995]	4.436	up	346
A_21_P0014231	lnc-WDR34-1	LNCipedia lincRNA (lnc-WDR34-1), lincRNA [lnc-WDR34-1:1]	3.372	up	347
A_24_P405205	ATP2B4	Homo sapiens ATPase, Ca++ transporting, plasma membrane 4 (ATP2B4), transcript variant 1, mRNA [NM_001001396]	3.631	up	348
A_23_P64898	KLRG1	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA [NM_005810]	4.193	up	349
A_21_P0014077	LOC100505666	Homo sapiens uncharacterized LOC100505666 (LOC100505666), transcript variant 1, long non-coding RNA [NR_040772]	3.115	up	350
A_24_P355493	LHPP	Homo sapiens phospholysine phosphohistidine inorganic pyrophosphate phosphatase (LHPP), transcript variant 1, mRNA [NM_022126]	3.251	up	351
A_23_P24616	SIAE	Homo sapiens sialic acid acetylesterase (SIAE), transcript variant 1, mRNA [NM_170601]	3.459	up	352
A_24_P212539	GALM	Homo sapiens galactose mutarotase (aldose 1-epimerase) (GALM), mRNA [NM_138801]	3.121	up	353
A_33_P3273436	GALM	Homo sapiens galactose mutarotase (aldose 1-epimerase) (GALM), mRNA [NM_138801]	3.194	up	354
A_23_P210015	PTPN18	Homo sapiens protein tyrosine phosphatase, non-receptor type 18 (brain-derived) (PTPN18), transcript variant 1, mRNA [NM_014369]	3.454	up	355
A_24_P306720	FOXN3-AS1	Homo sapiens FOXN3 antisense RNA 1 (FOXN3-AS1), long non-coding RNA [NR_036500]	3.502	up	356
A_24_P139943	HS1BP3	Homo sapiens HCLS1 binding protein 3 (HS1BP3), mRNA [NM_022460]	3.167	up	357
A_23_P130515	CEACAM3	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 3 (CEACAM3), transcript variant 1, mRNA [NM_001815]	3.845	up	358
A_23_P148473	IL2RG	Homo sapiens interleukin 2 receptor, gamma (IL2RG), mRNA [NM_000206]	3.179	up	359
A_33_P3396607	UGDH	Homo sapiens UDP-glucose 6-dehydrogenase (UGDH), transcript variant 1, mRNA [NM_003359]	5.443	up	360
A_33_P3327822	SH3BGR	Homo sapiens SH3 domain binding glutamate-rich protein (SH3BGR), transcript variant 1, mRNA [NM_007341]	3.274	up	361
A_21_P0006453	lnc-ZMYM3-1	LNCipedia lincRNA (lnc-ZMYM3-1), lincRNA [lnc-ZMYM3-1:1]	4.017	up	362
A_23_P139396	C11orf73	Homo sapiens chromosome 11 open reading frame 73 (C11orf73), transcript variant 1, mRNA [NM_016401]	3.742	up	363
A_23_P134714	HRSP12	Homo sapiens heat-responsive protein 12 (HRSP12), mRNA [NM_005836]	5.662	up	364
A_33_P3232544	na	0	3.270	up	365
A_23_P256413	CMTM7	Homo sapiens CKLF-like MARVEL transmembrane domain containing 7 (CMTM7), transcript variant 1, mRNA [NM_138410]	3.134	up	366
A_23_P402319	GAPT	GRB2-binding adaptor protein, transmembrane [Source:HGNC Symbol;Acc:HGNC:26588] [ENST00000318469]	3.850	up	367
A_33_P3282489	GCNT1	Homo sapiens glucosaminyl (N-acetyl) transferase 1, core 2 (GCNT1), transcript variant 1, mRNA [NM_001097634]	4.942	up	368
A_23_P98565	MS4A14	Homo sapiens membrane-spanning 4-domains, subfamily A, member 14 (MS4A14), transcript variant 1, mRNA [NM_032597]	5.130	up	369
A_23_P322756	TET1	Homo sapiens tet methylcytosine dioxygenase 1 (TET1), mRNA [NM_030625]	3.387	up	370
A_33_P3308332	PLEKHB1	Homo sapiens pleckstrin homology domain containing, family B (evectins) member 1 (PLEKHB1), transcript variant 1, mRNA [NM_021200]	5.359	up	371
A_32_P224522	SLC25A23	Homo sapiens solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23 (SLC25A23), mRNA [NM_024103]	4.070	up	372
A_23_P20427	RHOBTB2	Homo sapiens Rho-related BTB domain containing 2 (RHOBTB2), transcript variant 3, mRNA [NM_015178]	5.691	up	373
A_23_P375922	COL19A1	Homo sapiens collagen, type XIX, alpha 1 (COL19A1), mRNA [NM_001858]	3.951	up	374
A_21_P0009429	lnc-NEDD4L-2	Homo sapiens cDNA FLJ45655 fis, clone CTONG2012425. [AK127562]	3.445	up	375
A_32_P167705	AGBL2	Homo sapiens ATP/GTP binding protein-like 2 (AGBL2), mRNA [NM_024783]	4.125	up	376
A_24_P211565	C1QTNF6	Homo sapiens C1q and tumor necrosis factor related protein 6 (C1QTNF6), transcript variant 1, mRNA [NM_031910]	3.487	up	377
A_33_P3408938	LILRP2	Homo sapiens leukocyte immunoglobulin-like receptor pseudogene 2 (LILRP2), non-coding RNA [NR_003061]	4.201	up	378
A_24_P157370	IL17RB	Homo sapiens interleukin 17 receptor B (IL17RB), mRNA [NM_018725]	4.447	up	379
A_24_P13083	TSPAN18	Homo sapiens tetraspanin 18 (TSPAN18), mRNA [NM_130783]	3.167	up	380
A_33_P3413038	PLXNB3	Homo sapiens plexin B3 (PLXNB3), transcript variant 2, mRNA [NM_001163257]	3.116	up	381

A_19_P00318174	LOC100506014	0	3.110	up	382
A_19_P00802098	LOC100506014	0	3.989	up	383
A_33_P3367112	lnc-SIRT4-1	602713021F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853452 5', mRNA sequence [BG758909]	3.296	up	384
A_19_P00322432	LOC100506014	0	3.231	up	385
A_19_P00316666	LOC100506014	0	3.359	up	386
A_21_P0007481	LINC00944	Homo sapiens long intergenic non-protein coding RNA 944 (LINC00944), long non-coding RNA [NR_033878]	3.629	up	387
A_23_P9255	SYK	Homo sapiens spleen tyrosine kinase (SYK), transcript variant 1, mRNA [NM_003177]	4.092	up	388
A_21_P0000642	LINC00959	Homo sapiens long intergenic non-protein coding RNA 959 (LINC00959), long non-coding RNA [NR_034125]	3.357	up	389
A_21_P0000641	LINC00959	Homo sapiens long intergenic non-protein coding RNA 959 (LINC00959), long non-coding RNA [NR_034125]	3.220	up	390
A_23_P20852	AUH	Homo sapiens AU RNA binding protein/enoyl-CoA hydratase (AUH), mRNA [NM_001698]	3.760	up	391
A_21_P0013825	STAU2	Homo sapiens staufen double-stranded RNA binding protein 2 (STAU2), transcript variant 1, mRNA [NM_001164380]	3.103	up	392
A_23_P364766	SLX4IP	Homo sapiens SLX4 interacting protein (SLX4IP), mRNA [NM_001009608]	6.415	up	393
A_21_P0000893	IQCH-AS1	Homo sapiens IQCH antisense RNA 1 (IQCH-AS1), transcript variant 1, long non-coding RNA [NR_040051]	7.245	up	394
A_24_P143686	SPIDR	Homo sapiens scaffolding protein involved in DNA repair (SPIDR), transcript variant 1, mRNA [NM_001080394]	3.390	up	395
A_23_P48771	C14orf159	Homo sapiens chromosome 14 open reading frame 159 (C14orf159), transcript variant 3, mRNA [NM_024952]	4.827	up	396
A_23_P30069	DDX60L	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like (DDX60L), transcript variant 1, mRNA [NM_001012967]	4.454	up	397
A_23_P258251	ENOX2	Homo sapiens ecto-NOX disulfide-thiol exchanger 2 (ENOX2), transcript variant 2, mRNA [NM_182314]	3.714	up	398
A_23_P93499	TFB1M	Homo sapiens transcription factor B1, mitochondrial (TFB1M), mRNA [NM_016020]	4.198	up	399
A_33_P3214456	PDSS2	Homo sapiens prenyl (decaprenyl) diphosphate synthase, subunit 2 (PDSS2), mRNA [NM_020381]	3.909	up	400
A_23_P134167	PDSS2	Homo sapiens prenyl (decaprenyl) diphosphate synthase, subunit 2 (PDSS2), mRNA [NM_020381]	5.249	up	401
A_23_P382043	NT5DC1	Homo sapiens 5'-nucleotidase domain containing 1 (NT5DC1), mRNA [NM_152729]	3.295	up	402
A_33_P3324904	na	0	3.236	up	403
A_23_P401700	APBB1IP	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein (APBB1IP), mRNA [NM_019043]	4.277	up	404
A_24_P32520	RNF214	Homo sapiens ring finger protein 214 (RNF214), transcript variant 1, mRNA [NM_001077239]	3.271	up	405
A_23_P55948	PRR12	Homo sapiens proline rich 12 (PRR12), mRNA [NM_020719]	3.114	up	406
A_24_P379512	PIGK	Homo sapiens phosphatidylinositol glycan anchor biosynthesis, class K (PIGK), mRNA [NM_005482]	4.943	up	407
A_24_P759674	OBFC1	Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 1 (OBFC1), mRNA [NM_024928]	3.204	up	408
A_24_P45451	SLAMF6	Homo sapiens SLAM family member 6 (SLAMF6), transcript variant 2, mRNA [NM_052931]	4.857	up	409
A_33_P3303857	SLAMF6	Homo sapiens SLAM family member 6 (SLAMF6), transcript variant 1, mRNA [NM_001184714]	4.605	up	410
A_23_P201319	DISP1	Homo sapiens dispatched homolog 1 (Drosophila) (DISP1), mRNA [NM_032890]	5.283	up	411
A_23_P133075	TBCK	Homo sapiens TBC1 domain containing kinase (TBCK), transcript variant 4, mRNA [NM_033115]	3.324	up	412
A_23_P433369	HEATR5A	Homo sapiens HEAT repeat containing 5A (HEATR5A), mRNA [NM_015473]	4.292	up	413
A_23_P412186	ZNF252P	Homo sapiens zinc finger protein 252, pseudogene (ZNF252P), non-coding RNA [NR_023392]	4.083	up	414
A_23_P156390	JAKMIP2	Homo sapiens janus kinase and microtubule interacting protein 2 (JAKMIP2), transcript variant 3, mRNA [NM_014790]	5.589	up	415
A_33_P3255290	JAKMIP2	Homo sapiens janus kinase and microtubule interacting protein 2 (JAKMIP2), transcript variant 3, mRNA [NM_014790]	4.560	up	416
A_21_P0004864	na	PREDICTED: Homo sapiens uncharacterized LOC102724851 (LOC102724851), transcript variant X1, ncRNA [XR_427900]	5.428	up	417
A_21_P0004862	LOC102724851	PREDICTED: Homo sapiens uncharacterized LOC102724851 (LOC102724851), transcript variant X2, ncRNA [XR_427901]	3.922	up	418
A_33_P3272090	PDE4DIP	Homo sapiens phosphodiesterase 4D interacting protein (PDE4DIP), transcript variant 1, mRNA [NM_014644]	3.364	up	419
A_23_P205913	SLC24A1	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1), transcript variant 1, mRNA [NM_004727]	3.435	up	420
A_23_P126605	TMOD4	Homo sapiens tropomodulin 4 (muscle) (TMOD4), mRNA [NM_013353]	3.336	up	421
A_33_P3251332	HEATR5A	Homo sapiens HEAT repeat containing 5A (HEATR5A), mRNA [NM_015473]	4.693	up	422
A_21_P0010661	XLOC_l2_001196	BROAD Institute lincRNA (XLOC_l2_001196), lincRNA [TCONS_l2_00001624]	3.220	up	423
A_24_P860797	PAIP2B	Homo sapiens poly(A) binding protein interacting protein 2B (PAIP2B), mRNA [NM_020459]	6.717	up	424
A_23_P133279	FAM173B	Homo sapiens family with sequence similarity 173, member B (FAM173B), transcript variant 1, mRNA [NM_199133]	5.741	up	425
A_33_P3384078	AK9	Homo sapiens cDNA FLJ16163 fis, clone BRCAN2014229. [AK131244]	4.356	up	426
A_24_P678418	DICER1-AS1	Homo sapiens DICER1 antisense RNA 1 (DICER1-AS1), long non-coding RNA [NR_015415]	5.360	up	427
A_23_P356526	TRIM5	Homo sapiens tripartite motif containing 5 (TRIM5), transcript variant gamma, mRNA [NM_033092]	4.729	up	428
A_24_P141629	FAM111A	Homo sapiens family with sequence similarity 111, member A (FAM111A), transcript variant 1, mRNA [NM_022074]	4.393	up	429
A_33_P3341616	GVINP1	Homo sapiens GTPase, very large interferon inducible pseudogene 1 (GVINP1), non-coding RNA [NR_003945]	5.417	up	430
A_23_P384056	CCDC14	Homo sapiens coiled-coil domain containing 14 (CCDC14), mRNA [NM_022757]	5.218	up	431
A_33_P3394234	ZNF133	Homo sapiens zinc finger protein 133 (ZNF133), transcript variant 1, mRNA [NM_003434]	4.354	up	432
A_32_P209960	CIITA	Homo sapiens class II, major histocompatibility complex, transactivator (CIITA), transcript variant 2, mRNA [NM_000246]	5.437	up	433
A_33_P3421351	TRAF3IP3	Homo sapiens TRAF3 interacting protein 3 (TRAF3IP3), transcript variant 2, mRNA [NM_001287754]	3.563	up	434
A_33_P3336622	ALDH3A2	Homo sapiens aldehyde dehydrogenase 3 family, member A2 (ALDH3A2), transcript variant 1, mRNA [NM_001031806]	4.037	up	435
A_23_P55011	SLC38A10	Homo sapiens solute carrier family 38, member 10 (SLC38A10), transcript variant 1, mRNA [NM_001037984]	3.571	up	436
A_23_P146111	NIPAL2	Homo sapiens NIPA-like domain containing 2 (NIPAL2), mRNA [NM_024759]	4.230	up	437
A_33_P3398448	PARP10	Homo sapiens poly (ADP-ribose) polymerase family, member 10 (PARP10), mRNA [NM_032789]	3.939	up	438
A_23_P127367	POLD4	Homo sapiens polymerase (DNA-directed), delta 4, accessory subunit (POLD4), transcript variant 1, mRNA [NM_021173]	3.225	up	439
A_33_P3216955	ANAPC16	Homo sapiens anaphase promoting complex subunit 16 (ANAPC16), transcript variant 1, mRNA [NM_001242546]	4.852	up	440
A_24_P279797	MRI1	Homo sapiens methylthioribose-1-phosphate isomerase 1 (MRI1), transcript variant 1, mRNA [NM_001031727]	4.936	up	441
A_24_P329065	BTN3A1	Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), transcript variant 1, mRNA [NM_007048]	3.574	up	442
A_24_P252078	BTN3A2	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), transcript variant 1, mRNA [NM_007047]	4.132	up	443

A_23_P155376	CRELD1	Homo sapiens cysteine-rich with EGF-like domains 1 (CRELD1), transcript variant 2, mRNA [NM_015513]	3.111	up	444
A_23_P390172	RNASEL	Homo sapiens ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent) (RNASEL), mRNA [NM_021133]	4.402	up	445
A_32_P14610	PDLIM5	Homo sapiens PDZ and LIM domain 5 (PDLIM5), transcript variant 1, mRNA [NM_006457]	4.654	up	446
A_23_P369666	ZMYND8	zinc finger, MYND-type containing 8 [Source:HGNC Symbol;Acc:HGNC:9397] [ENST00000468376]	3.159	up	447
A_33_P3416881	C2orf27A	Homo sapiens chromosome 2 open reading frame 27A (C2orf27A), mRNA [NM_013310]	4.206	up	448
A_21_P0000682	LHX4-AS1	Homo sapiens LHX4 antisense RNA 1 (LHX4-AS1), long non-coding RNA [NR_037642]	3.174	up	449
A_23_P34644	FCGR2B	Homo sapiens Fc fragment of IgG, low affinity IIb, receptor (CD32) (FCGR2B), transcript variant 1, mRNA [NM_004001]	4.806	up	450
A_33_P3418170	DDX58	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (DDX58), mRNA [NM_014314]	3.339	up	451
A_33_P3252499	CFAP44	Homo sapiens cilia and flagella associated protein 44 (CFAP44), transcript variant 1, mRNA [NM_001164496]	3.228	up	452
A_32_P213661	CCDC122	Homo sapiens coiled-coil domain containing 122 (CCDC122), mRNA [NM_144974]	3.689	up	453
A_23_P501877	ZFP64	Homo sapiens ZFP64 zinc finger protein (ZFP64), transcript variant 1, mRNA [NM_018197]	3.524	up	454
A_33_P3317880	ZNF252P	Homo sapiens zinc finger protein 252, pseudogene (ZNF252P), non-coding RNA [NR_023392]	4.553	up	455
A_23_P82047	STXBP5	Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), transcript variant 2, mRNA [NM_001127715]	3.101	up	456
A_23_P425304	SUFU	Homo sapiens suppressor of fused homolog (Drosophila) (SUFU), transcript variant 1, mRNA [NM_016169]	3.413	up	457
A_33_P3369058	LRRK2	Homo sapiens leucine-rich repeat kinase 2 (LRRK2), mRNA [NM_198578]	4.240	up	458
A_21_P0000049	DISC1	Homo sapiens disrupted in schizophrenia 1 (DISC1), transcript variant b, mRNA [NM_001164538]	3.451	up	459
A_23_P336198	GLCCI1	Homo sapiens glucocorticoid induced transcript 1 (GLCCI1), mRNA [NM_138426]	4.648	up	460
A_21_P0014183	LOC100505921	Homo sapiens uncharacterized LOC100505921 (LOC100505921), long non-coding RNA [NR_110018]	3.408	up	461
A_33_P3253687	GVINP1	Homo sapiens GTPase, very large interferon inducible pseudogene 1 (GVINP1), non-coding RNA [NR_003945]	6.823	up	462
A_24_P349196	CCDC30	Homo sapiens coiled-coil domain containing 30 (CCDC30), mRNA [NM_001080850]	4.552	up	463
A_23_P381714	CA13	Homo sapiens carbonic anhydrase XIII (CA13), mRNA [NM_198584]	5.394	up	464
A_23_P78595	CEACAM21	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 21 (CEACAM21), transcript variant 2, mRNA [NM_033543]	3.124	up	465
A_24_P945228	CYP4V2	Homo sapiens cytochrome P450, family 4, subfamily V, polypeptide 2 (CYP4V2), mRNA [NM_207352]	4.436	up	466
A_33_P3219840	ZNRD1-AS1	Homo sapiens ZNRD1 antisense RNA 1 (ZNRD1-AS1), long non-coding RNA [NR_026751]	3.762	up	467
A_33_P3373348	AFF3	AF4/FMR2 family, member 3 [Source:HGNC Symbol;Acc:HGNC:6473] [ENST00000483600]	3.155	up	468
A_21_P0014736	LOC100506538	PREDICTED: Homo sapiens uncharacterized LOC100506538 (LOC100506538), ncRNA [XR_426345]	3.112	up	469
A_21_P0006615	na	0	5.478	up	470
A_33_P3268838	CPEB1	Homo sapiens cytoplasmic polyadenylation element binding protein 1 (CPEB1), transcript variant 5, mRNA [NM_001288819]	3.309	up	471
A_24_P712562	C17orf67	Homo sapiens chromosome 17 open reading frame 67 (C17orf67), mRNA [NM_001085430]	3.304	up	472
A_23_P382705	TMTC2	Homo sapiens transmembrane and tetratricopeptide repeat containing 2 (TMTC2), mRNA [NM_152588]	3.305	up	473
A_23_P24716	TMEM132A	Homo sapiens transmembrane protein 132A (TMEM132A), transcript variant 1, mRNA [NM_017870]	3.857	up	474
A_21_P0005688	lnc-RP11-150O12.5.	LNCipedia lincRNA (lnc-RP11-150O12.5.1-2), lincRNA [lnc-RP11-150O12.5.1-2:1]	4.168	up	475
A_23_P109452	CHEK2	Homo sapiens checkpoint kinase 2 (CHEK2), transcript variant 3, mRNA [NM_001005735]	3.781	up	476
A_33_P3221999	GSDMB	Homo sapiens gasdermin B (GSDMB), transcript variant 3, mRNA [NM_001165958]	3.211	up	477
A_23_P153524	C19orf73	Homo sapiens chromosome 19 open reading frame 73 (C19orf73), mRNA [NM_018111]	3.302	up	478
A_33_P3335522	FCRL5	Homo sapiens Fc receptor-like 5 (FCRL5), transcript variant 2, mRNA [NM_001195388]	3.174	up	479
A_24_P290751	DTX1	Homo sapiens deltex 1, E3 ubiquitin ligase (DTX1), mRNA [NM_004416]	5.928	up	480
A_23_P204998	FARP1	Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA [NM_005766]	3.297	up	481
A_23_P71624	PAX5	Homo sapiens paired box 5 (PAX5), transcript variant 1, mRNA [NM_016734]	3.171	up	482
A_23_P373464	AFF3	Homo sapiens AF4/FMR2 family, member 3 (AFF3), transcript variant 1, mRNA [NM_002285]	3.252	up	483
A_33_P3350259	FAM129C	Homo sapiens family with sequence similarity 129, member C (FAM129C), transcript variant 2, mRNA [NM_001098524]	3.345	up	484
A_23_P345799	FAM129C	Homo sapiens family with sequence similarity 129, member C (FAM129C), transcript variant 1, mRNA [NM_173544]	3.534	up	485
A_24_P206317	HDAC9	Homo sapiens histone deacetylase 9 (HDAC9), transcript variant 1, mRNA [NM_058176]	4.792	up	486
A_23_P404162	HDAC9	Homo sapiens histone deacetylase 9 (HDAC9), transcript variant 3, mRNA [NM_014707]	3.916	up	487
A_23_P303803	C19orf18	Homo sapiens chromosome 19 open reading frame 18 (C19orf18), mRNA [NM_152474]	3.732	up	488
A_21_P0011696	LINC00665	Homo sapiens long intergenic non-protein coding RNA 665 (LINC00665), transcript variant 2, long non-coding RNA [NR_038279]	4.408	up	489
A_23_P214208	CNR1	Homo sapiens cannabinoid receptor 1 (brain) (CNR1), transcript variant 2, mRNA [NM_033181]	5.830	up	490
A_23_P252155	STRBP	Homo sapiens spermatid perinuclear RNA binding protein (STRBP), transcript variant 1, mRNA [NM_018387]	3.272	up	491
A_24_P64344	BLNK	Homo sapiens B-cell linker (BLNK), transcript variant 1, mRNA [NM_013314]	5.093	up	492
A_33_P3363637	BLNK	Homo sapiens B-cell linker (BLNK), transcript variant 1, mRNA [NM_013314]	4.897	up	493
A_23_P41194	LRRC34	Homo sapiens leucine rich repeat containing 34 (LRRC34), transcript variant 3, mRNA [NM_153353]	3.962	up	494
A_21_P0000091	LRRC34	Homo sapiens leucine rich repeat containing 34 (LRRC34), transcript variant 1, mRNA [NM_001172780]	3.250	up	495
A_33_P3406567	MS4A1	Homo sapiens membrane-spanning 4-domains, subfamily A, member 1 (MS4A1), transcript variant 1, mRNA [NM_152866]	3.723	up	496
A_23_P370830	KLHL14	Homo sapiens kelch-like family member 14 (KLHL14), mRNA [NM_020805]	3.278	up	497
A_24_P694820	lnc-ZNF236-1	LNCipedia lincRNA (lnc-ZNF236-1), lincRNA [lnc-ZNF236-1:5]	8.274	up	498
A_23_P147245	OSBPL10	Homo sapiens oxysterol binding protein-like 10 (OSBPL10), transcript variant 1, mRNA [NM_017784]	3.552	up	499
A_23_P312920	POU2AF1	Homo sapiens POU class 2 associating factor 1 (POU2AF1), mRNA [NM_006235]	3.726	up	500
A_33_P3335511	FCRL5	Homo sapiens Fc receptor-like 5 (FCRL5), transcript variant 2, mRNA [NM_001195388]	5.250	up	501
A_21_P0010658	FCRL5	Homo sapiens Fc receptor-like 5 (FCRL5), transcript variant 2, mRNA [NM_001195388]	4.522	up	502
A_33_P3335525	FCRL5	Fc receptor-like 5 [Source:HGNC Symbol;Acc:HGNC:18508] [ENST00000368189]	4.960	up	503
A_33_P3335506	FCRL5	Fc receptor-like 5 [Source:HGNC Symbol;Acc:HGNC:18508] [ENST00000368190]	5.355	up	504
A_23_P201211	FCRL5	Homo sapiens Fc receptor-like 5 (FCRL5), transcript variant 1, mRNA [NM_031281]	6.043	up	505
A_21_P0010993	LOC101929174	PREDICTED: Homo sapiens uncharacterized LOC101929174 (LOC101929174), ncRNA [XR_424270]	4.341	up	506
A_21_P0010991	LOC101929174	PREDICTED: Homo sapiens uncharacterized LOC101929174 (LOC101929174), ncRNA [XR_424270]	3.575	up	507
A_21_P0000840	PXN-AS1	Homo sapiens PXN antisense RNA 1 (PXN-AS1), long non-coding RNA [NR_038924]	3.780	up	508

A_33_P3340655	KLHL32	Homo sapiens kelch-like family member 32 (KLHL32), transcript variant 1, mRNA [NM_052904]	3.354	up	509
A_24_P374634	STAU2	Homo sapiens staufen double-stranded RNA binding protein 2 (STAU2), transcript variant 1, mRNA [NM_001164380]	3.296	up	510
A_23_P82351	BBS9	Homo sapiens Bardet-Biedl syndrome 9 (BBS9), transcript variant 2, mRNA [NM_198428]	3.319	up	511
A_33_P3234764	na	Homo sapiens cDNA FLJ27410 fis, clone WMC04875. [AK130920]	3.250	up	512
A_21_P0010989	XLOC_l2_002433	BROAD Institute lincRNA (XLOC_l2_002433), lincRNA [TCONS_l2_00004704]	3.238	up	513
A_23_P143981	FBLN2	Homo sapiens fibulin 2 (FBLN2), transcript variant 1, mRNA [NM_001004019]	4.990	up	514
A_23_P21495	FCGBP	Homo sapiens Fc fragment of IgG binding protein (FCGBP), mRNA [NM_003890]	4.944	up	515
A_23_P98645	DCHS1	Homo sapiens dachsous cadherin-related 1 (DCHS1), mRNA [NM_003737]	3.800	up	516
A_23_P110941	GSTA4	Homo sapiens glutathione S-transferase alpha 4 (GSTA4), mRNA [NM_001512]	4.308	up	517
A_33_P3257903	GSTA4	Homo sapiens glutathione S-transferase alpha 4 (GSTA4), mRNA [NM_001512]	5.687	up	518
A_24_P178631	na	Homo sapiens cDNA FLJ14761 fis, clone NT2RP3003302. [AK027667]	5.086	up	519
A_24_P149124	NREP	Homo sapiens neuronal regeneration related protein (NREP), transcript variant 1, mRNA [NM_004772]	7.061	up	520
A_33_P3391290	NREP	Homo sapiens neuronal regeneration related protein (NREP), transcript variant 11, mRNA [NM_001142483]	6.475	up	521
A_33_P3287907	ZBED3-AS1	Homo sapiens ZBED3 antisense RNA 1 (ZBED3-AS1), long non-coding RNA [NR_024398]	4.519	up	522
A_21_P0004869	LOC100131289	Homo sapiens uncharacterized LOC100131289 (LOC100131289), long non-coding RNA [NR_038929]	11.701	up	523
A_32_P74752	LOC100131289	Homo sapiens uncharacterized LOC100131289 (LOC100131289), long non-coding RNA [NR_038929]	8.340	up	524
A_21_P0009669	lnc-ZNF682-1	LNCipedia lincRNA (lnc-ZNF682-1), lincRNA [lnc-ZNF682-1:1]	3.286	up	525
A_33_P3213962	OR13A1	Homo sapiens olfactory receptor, family 13, subfamily A, member 1 (OR13A1), mRNA [NM_001004297]	6.106	up	526
A_23_P328034	C20orf96	Homo sapiens chromosome 20 open reading frame 96 (C20orf96), transcript variant 1, mRNA [NM_153269]	3.494	up	527
A_32_P68533	FAM161A	Homo sapiens family with sequence similarity 161, member A (FAM161A), transcript variant 2, mRNA [NM_032180]	3.345	up	528
A_24_P115007	ALDH5A1	Homo sapiens aldehyde dehydrogenase 5 family, member A1 (ALDH5A1), transcript variant 1, mRNA [NM_170740]	3.786	up	529
A_33_P3391275	LINC00494	Homo sapiens long intergenic non-protein coding RNA 494 (LINC00494), long non-coding RNA [NR_026958]	3.246	up	530
A_33_P3256725	PIP5K1B	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), transcript variant 3, mRNA [NM_001278253]	8.483	up	531
A_24_P349965	TCF19	Homo sapiens transcription factor 19 (TCF19), transcript variant 1, mRNA [NM_007109]	4.533	up	532
A_23_P31765	PKIA	Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor alpha (PKIA), transcript variant 1, mRNA [NM_006823]	3.599	up	533
A_23_P316150	IFT80	Homo sapiens intraflagellar transport 80 (IFT80), transcript variant 1, mRNA [NM_020800]	3.452	up	534
A_24_P943613	TBC1D1	Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), transcript variant 1, mRNA [NM_015173]	3.482	up	535
A_24_P365365	TCF3	Homo sapiens transcription factor 3 (TCF3), transcript variant 1, mRNA [NM_003200]	3.286	up	536
A_33_P3369844	CD24	Homo sapiens CD24 molecule (CD24), transcript variant 1, mRNA [NM_013230]	4.024	up	537
A_24_P941625	ZNF70	Homo sapiens zinc finger protein 70 (ZNF70), mRNA [NM_021916]	5.370	up	538
A_23_P57417	MMP11	Homo sapiens matrix metallopeptidase 11 (stromelysin 3) (MMP11), mRNA [NM_005940]	6.973	up	539
A_32_P90483	STXBP4	Homo sapiens syntaxin binding protein 4 (STXBP4), mRNA [NM_178509]	3.469	up	540
A_24_P284584	ZNF559	Homo sapiens zinc finger protein 559 (ZNF559), transcript variant 2, mRNA [NM_032497]	3.940	up	541
A_33_P3234989	IFT81	Homo sapiens intraflagellar transport 81 (IFT81), transcript variant 1, mRNA [NM_014055]	6.803	up	542
A_21_P0014472	na	ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (13%) [THC2757892]	5.306	up	543
A_23_P357717	TCL1A	Homo sapiens T-cell leukemia/lymphoma 1A (TCL1A), transcript variant 1, mRNA [NM_021966]	7.591	up	544
A_23_P125618	GABRA3	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 3 (GABRA3), mRNA [NM_000808]	3.886	up	545
A_19_P00806490	TET1	Homo sapiens tet methylcytosine dioxygenase 1 (TET1), mRNA [NM_030625]	4.225	up	546
A_23_P38154	FDXR	Homo sapiens ferredoxin reductase (FDXR), transcript variant 2, mRNA [NM_004110]	3.356	up	547
A_21_P0014820	na	endogenous retrovirus group K3, member 1 [Source:HGNC Symbol;Acc:HGNC:30466] [ENST00000413518]	3.857	up	548
A_32_P175715	MEIG1	Homo sapiens meiosis/spermiogenesis associated 1 (MEIG1), mRNA [NM_001080836]	4.969	up	549
A_23_P212241	CHL1	Homo sapiens cell adhesion molecule L1-like (CHL1), transcript variant 1, mRNA [NM_006614]	8.090	up	550
A_21_P0009109	lnc-FAM65A-1	LNCipedia lincRNA (lnc-FAM65A-1), lincRNA [lnc-FAM65A-1:1]	3.722	up	551
A_21_P0010270	na	0	8.706	up	552
A_21_P0010269	lnc-AF165138.7.1-3	LNCipedia lincRNA (lnc-AF165138.7.1-3), lincRNA [lnc-AF165138.7.1-3:2]	4.246	up	553
A_33_P3273723	na	Homo sapiens cDNA FLJ26029 fis, clone PNC05018. [AK129540]	3.124	up	554
A_33_P3288824	H2AFB3	Homo sapiens H2A histone family, member B3 (H2AFB3), mRNA [NM_080720]	3.158	up	555
A_21_P0013802	TMLHE	Homo sapiens trimethyllysine hydroxylase, epsilon (TMLHE), transcript variant 1, mRNA [NM_018196]	4.118	up	556
A_23_P348281	TCEANC2	Homo sapiens transcription elongation factor A (SII) N-terminal and central domain containing 2 (TCEANC2), mRNA [NM_153035]	3.894	up	557
A_21_P0013638	KGFLP1	Homo sapiens fibroblast growth factor 7 pseudogene (KGFLP1), transcript variant 1, non-coding RNA [NR_047527]	4.959	up	558
A_23_P10232	BANK1	Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), transcript variant 1, mRNA [NM_017935]	3.758	up	559
A_23_P392476	AK9	Homo sapiens adenylate kinase 9 (AK9), transcript variant 1, mRNA [NM_001145128]	3.717	up	560
A_23_P313632	FUT8	Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), transcript variant 1, mRNA [NM_178155]	4.143	up	561
A_23_P328621	UBQLNL	Homo sapiens ubiquilin-like (UBQLNL), mRNA [NM_145053]	3.901	up	562
A_23_P24623	ELP4	Homo sapiens elongator acetyltransferase complex subunit 4 (ELP4), transcript variant 1, mRNA [NM_019040]	3.717	up	563
A_23_P93464	BCKDHB	Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (BCKDHB), transcript variant 2, mRNA [NM_000056]	4.260	up	564
A_33_P3352873	BCKDHB	Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (BCKDHB), transcript variant 2, mRNA [NM_000056]	4.522	up	565
A_23_P33720	FARS2	Homo sapiens phenylalanyl-tRNA synthetase 2, mitochondrial (FARS2), mRNA [NM_006567]	3.493	up	566
A_24_P72518	AHCYL2	Homo sapiens adenosylhomocysteinase-like 2 (AHCYL2), transcript variant 1, mRNA [NM_015328]	3.813	up	567
A_24_P194886	EHBP1	Homo sapiens EH domain binding protein 1 (EHBP1), transcript variant 1, mRNA [NM_015252]	3.625	up	568
A_24_P71244	PIK3CD	Homo sapiens phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit delta (PIK3CD), mRNA [NM_005026]	3.176	up	569
A_33_P3384543	POMGNT1	Homo sapiens protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-) (POMGNT1), transcript variant 2, mRNA [NM_001243766]	3.158	up	570
A_23_P136196	TBC1D19	Homo sapiens TBC1 domain family, member 19 (TBC1D19), transcript variant 1, mRNA [NM_018317]	3.943	up	571
A_32_P71113	SCAI	Homo sapiens suppressor of cancer cell invasion (SCAI), transcript variant 1, mRNA [NM_173690]	3.795	up	572

A_23_P133359	ZFP2	Homo sapiens ZFP2 zinc finger protein (ZFP2), mRNA [NM_030613]	5.540	up	573
A_23_P126757	INTS3	Homo sapiens integrator complex subunit 3 (INTS3), mRNA [NM_023015]	3.681	up	574
A_23_P140427	EVL	Homo sapiens Enah/Vasp-like (EVL), mRNA [NM_016337]	4.564	up	575
A_23_P54556	MKL2	Homo sapiens MKL/myocardin-like 2 (MKL2), mRNA [NM_014048]	4.805	up	576
A_23_P33154	STAU2	Homo sapiens staufen double-stranded RNA binding protein 2 (STAU2), transcript variant 5, mRNA [NM_014393]	4.333	up	577
A_23_P97810	na	poly (ADP-ribose) glycohydrolase [Source:HGNC Symbol;Acc:HGNC:8605] [ENST00000614063]	3.191	up	578
A_23_P138125	FAIM3	Homo sapiens Fas apoptotic inhibitory molecule 3 (FAIM3), transcript variant 1, mRNA [NM_005449]	4.519	up	579
A_33_P3351101	TYSND1	Homo sapiens trypsin domain containing 1 (TYSND1), transcript variant 1, mRNA [NM_173555]	4.252	up	580
A_33_P3327333	IRF3	Homo sapiens interferon regulatory factor 3 (IRF3), transcript variant 3, mRNA [NM_001197123]	3.120	up	581
A_24_P333421	ZNF862	Homo sapiens zinc finger protein 862 (ZNF862), mRNA [NM_001099220]	3.884	up	582
A_33_P3210965	TCTN1	Homo sapiens tectonic family member 1 (TCTN1), transcript variant 1, mRNA [NM_001082538]	3.331	up	583
A_21_P0010860	LINC00202-1	Homo sapiens long intergenic non-protein coding RNA 202-1 (LINC00202-1), long non-coding RNA [NR_026795]	3.457	up	584
A_21_P0000702	STX18-AS1	Homo sapiens STX18 antisense RNA 1 (head to head) (STX18-AS1), long non-coding RNA [NR_037888]	3.940	up	585
A_23_P389692	KIAA1328	Homo sapiens KIAA1328 (KIAA1328), mRNA [NM_020776]	4.489	up	586
A_33_P3256425	BICD1	Homo sapiens bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA [NM_001714]	4.919	up	587
A_33_P3343957	EHBP1	Homo sapiens EH domain binding protein 1 (EHBP1), transcript variant 1, mRNA [NM_015252]	3.103	up	588
A_33_P3305531	METTL15	Homo sapiens methyltransferase like 15 (METTL15), transcript variant 3, mRNA [NM_001297775]	3.764	up	589
A_23_P346982	DTWD2	Homo sapiens DTW domain containing 2 (DTWD2), mRNA [NM_173666]	3.971	up	590
A_23_P14458	L3HYPDH	Homo sapiens L-3-hydroxyproline dehydratase (trans-) (L3HYPDH), mRNA [NM_144581]	4.646	up	591
A_23_P436526	SLC25A42	Homo sapiens solute carrier family 25, member 42 (SLC25A42), mRNA [NM_178526]	3.274	up	592
A_19_P00319698	na	KIAA1328 [Source:HGNC Symbol;Acc:HGNC:29248] [ENST00000601437]	3.499	up	593
A_32_P86245	EFHC1	Homo sapiens EF-hand domain (C-terminal) containing 1 (EFHC1), transcript variant A, mRNA [NM_018100]	4.187	up	594
A_32_P167471	CLMN	Homo sapiens calmin (calponin-like, transmembrane) (CLMN), mRNA [NM_024734]	3.754	up	595
A_21_P0004811	lnc-AL035696.1-2	LNCipedia lincRNA (lnc-AL035696.1-2), lincRNA [lnc-AL035696.1-2:1]	10.310	up	596
A_23_P20363	ZC2HC1A	Homo sapiens zinc finger, C2HC-type containing 1A (ZC2HC1A), mRNA [NM_016010]	3.265	up	597
A_21_P0014689	LOC100506974	PREDICTED: Homo sapiens uncharacterized LOC100506974 (LOC100506974), ncRNA [XR_111668]	3.121	up	598
A_23_P343900	na	immunoglobulin heavy variable 5-78 (pseudogene) [Source:HGNC Symbol;Acc:HGNC:5660] [ENST00000450948]	5.753	up	599
A_33_P3240182	na	immunoglobulin heavy variable 5-51 [Source:HGNC Symbol;Acc:HGNC:5659] [ENST00000390626]	4.587	up	600
A_33_P3278137	RPL31P11	Homo sapiens ribosomal protein L31 pseudogene 11 (RPL31P11), non-coding RNA [NR_002595]	3.699	up	601
A_23_P205348	TCL6	Homo sapiens T-cell leukemia/lymphoma 6 (non-protein coding) (TCL6), long non-coding RNA [NR_028288]	4.057	up	602
A_23_P363203	TCL6	Homo sapiens T-cell leukemia/lymphoma 6 (non-protein coding) (TCL6), long non-coding RNA [NR_028288]	4.499	up	603
A_33_P3401342	lnc-TCL1B-1	Homo sapiens T-cell leukemia/lymphoma 6, mRNA (cDNA clone MGC:52120 IMAGE:5923478), complete cds. [BC041075]	5.397	up	604
A_33_P3222728	ZKSCAN7	Homo sapiens zinc finger with KRAB and SCAN domains 7 (ZKSCAN7), transcript variant 5, mRNA [NM_001288592]	4.814	up	605
A_21_P0012741	lnc-LARP1B-2	Homo sapiens cDNA FLJ41533 fis, clone BRTHA2016179. [AK123527]	3.472	up	606
A_33_P3362696	RIC8B	Homo sapiens RIC8 guanine nucleotide exchange factor B (RIC8B), mRNA [NM_018157]	3.208	up	607
A_33_P3449397	METTL3	Homo sapiens methyltransferase like 3 (METTL3), mRNA [NM_019852]	3.334	up	608
A_33_P3218980	ENTPD1	Homo sapiens ectonucleoside triphosphate diphosphohydrolase 1 (ENTPD1), transcript variant 1, mRNA [NM_001776]	3.369	up	609
A_23_P4714	MIA	Homo sapiens melanoma inhibitory activity (MIA), transcript variant 1, mRNA [NM_006533]	5.170	up	610
A_23_P423482	FAM81A	Homo sapiens family with sequence similarity 81, member A (FAM81A), mRNA [NM_152450]	5.927	up	611
A_33_P3299254	VPREB3	Homo sapiens pre-B lymphocyte 3 (VPREB3), mRNA [NM_013378]	5.645	up	612
A_33_P3401990	VPREB3	Homo sapiens pre-B lymphocyte 3 (VPREB3), mRNA [NM_013378]	5.531	up	613
A_33_P3236734	CLEC17A	Homo sapiens C-type lectin domain family 17, member A (CLEC17A), transcript variant 1, mRNA [NM_001204118]	3.507	up	614
A_32_P79434	PTPRN2	Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA [NM_002847]	4.862	up	615
A_23_P103803	FCRL3	Homo sapiens Fc receptor-like 3 (FCRL3), mRNA [NM_052939]	5.504	up	616
A_33_P3368334	FCRL3	Fc receptor-like 3 [Source:HGNC Symbol;Acc:HGNC:18506] [ENST00000480682]	7.939	up	617
A_23_P360804	CPNE5	Homo sapiens copine V (CPNE5), mRNA [NM_020939]	6.361	up	618
A_24_P319647	FCRL2	Homo sapiens Fc receptor-like 2 (FCRL2), transcript variant 1, mRNA [NM_030764]	5.609	up	619
A_23_P160751	FCRL2	Homo sapiens Fc receptor-like 2 (FCRL2), transcript variant 1, mRNA [NM_030764]	5.745	up	620
A_33_P3294504	FCRL1	Homo sapiens Fc receptor-like 1 (FCRL1), transcript variant 2, mRNA [NM_001159397]	3.942	up	621
A_23_P149368	FCRL1	Homo sapiens Fc receptor-like 1 (FCRL1), transcript variant 1, mRNA [NM_052938]	5.905	up	622
A_23_P208182	SIGLEC10	Homo sapiens sialic acid binding Ig-like lectin 10 (SIGLEC10), transcript variant 1, mRNA [NM_033130]	3.303	up	623
A_23_P156562	CRIP3	Homo sapiens cysteine-rich protein 3 (CRIP3), mRNA [NM_206922]	4.784	up	624
A_21_P0012439	TRANK1	Homo sapiens tetratricopeptide repeat and ankyrin repeat containing 1 (TRANK1), mRNA [NM_014831]	3.205	up	625
A_33_P3306823	ZNF846	Homo sapiens zinc finger protein 846 (ZNF846), mRNA [NM_001077624]	3.774	up	626
A_33_P3337981	FIG4	Homo sapiens FIG4 phosphoinositide 5-phosphatase (FIG4), mRNA [NM_014845]	3.764	up	627
A_21_P0002653	ASXL2	additional sex combs like transcriptional regulator 2 [Source:HGNC Symbol;Acc:HGNC:23805] [ENST00000435504]	3.398	up	628
A_23_P311640	AGFG2	Homo sapiens ArfGAP with FG repeats 2 (AGFG2), mRNA [NM_006076]	3.636	up	629
A_21_P0012221	ANKRD20A11P	Homo sapiens ankyrin repeat domain 20 family, member A11, pseudogene (ANKRD20A11P), non-coding RNA [NR_027270]	3.204	up	630
A_23_P209799	MYO7B	Homo sapiens myosin VIIB (MYO7B), mRNA [NM_001080527]	4.700	up	631
A_32_P161033	lnc-RP3-377D14.1.1	Homo sapiens, clone IMAGE:6155889, mRNA. [BC043411]	4.307	up	632
A_23_P21673	FOCAD	Homo sapiens focadhesin (FOCAD), mRNA [NM_017794]	3.909	up	633
A_21_P0014186	LOC101927811	Homo sapiens uncharacterized LOC101927811 (LOC101927811), transcript variant 1, long non-coding RNA [NR_110119]	4.547	up	634
A_23_P152047	SCAMP5	Homo sapiens secretory carrier membrane protein 5 (SCAMP5), transcript variant 3, mRNA [NM_138967]	3.946	up	635
A_33_P3211968	lnc-TCL1B-2	human full-length cDNA clone CS0DG006YJ19 of B cells (Ramos cell line) of Homo sapiens (human). [BX247990]	6.978	up	636
A_21_P0000769	LOC100505622	Homo sapiens uncharacterized LOC100505622 (LOC100505622), long non-coding RNA [NR_038332]	3.159	up	637

A_33_P3421728	DGKG	Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), transcript variant 1, mRNA [NM_001346]	3.819	up	638
A_33_P3366175	LOC100130298	Homo sapiens hCG1816373-like (LOC100130298), long non-coding RNA [NR_034003]	4.806	up	639
A_32_P167904	ZNF681	Homo sapiens zinc finger protein 681 (ZNF681), mRNA [NM_138286]	4.404	up	640
A_33_P3226212	JAM2	Homo sapiens junctional adhesion molecule 2 (JAM2), transcript variant 3, mRNA [NM_001270408]	7.402	up	641
A_21_P0014373	lnc-ZNF667-2	Homo sapiens mRNA; cDNA DKFZp686A1999 (from clone DKFZp686A1999). [BX647249]	3.541	up	642
A_33_P3336587	LOC283710	Homo sapiens uncharacterized LOC283710 (LOC283710), mRNA [NM_001243538]	5.461	up	643
A_33_P3482534	LOC613266	Homo sapiens hypothetical LOC613266, mRNA (cDNA clone IMAGE:5222345). [BC043571]	4.954	up	644
A_23_P121396	DNAJC19	Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 19 (DNAJC19), transcript variant 1, mRNA [NM_145261]	3.897	up	645
A_33_P3231367	ATXN10	Homo sapiens ataxin 10 (ATXN10), transcript variant 1, mRNA [NM_013236]	4.113	up	646
A_24_P142269	HIRIP3	Homo sapiens HIRA interacting protein 3 (HIRIP3), transcript variant 1, mRNA [NM_003609]	4.269	up	647
A_23_P91487	RWDD2B	Homo sapiens RWD domain containing 2B (RWDD2B), mRNA [NM_016940]	4.816	up	648
A_23_P151368	N6AMT2	Homo sapiens N-6 adenine-specific DNA methyltransferase 2 (putative) (N6AMT2), mRNA [NM_174928]	6.011	up	649
A_23_P97736	NCDN	Homo sapiens neurochondrin (NCDN), transcript variant 3, mRNA [NM_014284]	6.451	up	650
A_33_P3368301	BOLA3	Homo sapiens bolA family member 3 (BOLA3), transcript variant 1, mRNA [NM_212552]	3.941	up	651
A_23_P42802	PDIA4	Homo sapiens protein disulfide isomerase family A, member 4 (PDIA4), mRNA [NM_004911]	3.683	up	652
A_23_P102517	PDE6D	Homo sapiens phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D), transcript variant 1, mRNA [NM_002601]	4.271	up	653
A_23_P211850	ABHD6	Homo sapiens abhydrolase domain containing 6 (ABHD6), mRNA [NM_020676]	4.557	up	654
A_23_P149813	RSU1	Homo sapiens Ras suppressor protein 1 (RSU1), transcript variant 1, mRNA [NM_012425]	3.256	up	655
A_23_P318604	CYHR1	cysteine/histidine-rich 1 [Source:HGNC Symbol;Acc:HGNC:17806] [ENST00000528663]	3.824	up	656
A_23_P97221	ZNF691	Homo sapiens zinc finger protein 691 (ZNF691), transcript variant 2, mRNA [NM_015911]	3.276	up	657
A_23_P120931	APOBEC3C	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C (APOBEC3C), mRNA [NM_014508]	4.117	up	658
A_23_P357101	APOBEC3F	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F (APOBEC3F), transcript variant 1, mRNA [NM_145298]	3.868	up	659
A_23_P37144	DTD2	Homo sapiens D-tyrosyl-tRNA deacylase 2 (putative) (DTD2), mRNA [NM_080664]	3.327	up	660
A_23_P95823	NSMCE1	Homo sapiens non-SMC element 1 homolog (S. cerevisiae) (NSMCE1), mRNA [NM_145080]	3.826	up	661
A_33_P3215059	NSMCE1	Homo sapiens non-SMC element 1 homolog (S. cerevisiae) (NSMCE1), mRNA [NM_145080]	3.386	up	662
A_23_P216630	SLC44A1	Homo sapiens solute carrier family 44 (choline transporter), member 1 (SLC44A1), transcript variant 1, mRNA [NM_080546]	3.158	up	663
A_23_P65830	HDDC3	Homo sapiens HD domain containing 3 (HDDC3), transcript variant 2, mRNA [NM_198527]	3.204	up	664
A_23_P15305	PRPSAP1	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), mRNA [NM_002766]	4.139	up	665
A_24_P57730	MRPL52	Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 4, mRNA [NM_181304]	6.435	up	666
A_23_P97932	MSRB2	Homo sapiens methionine sulfoxide reductase B2 (MSRB2), mRNA [NM_012228]	3.522	up	667
A_24_P818529	na	ribonuclease H2, subunit C pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:24117] [ENST00000454281]	3.192	up	668
A_23_P166248	RCAN1	Homo sapiens regulator of calcineurin 1 (RCAN1), transcript variant 1, mRNA [NM_004414]	3.599	up	669
A_24_P192805	CARD17	Homo sapiens caspase recruitment domain family, member 17 (CARD17), mRNA [NM_001007232]	3.362	up	670
A_23_P92261	ECE2	Homo sapiens endothelin converting enzyme 2 (ECE2), transcript variant 3, mRNA [NM_032331]	3.172	up	671
A_24_P184388	LRTOMT	Homo sapiens leucine rich transmembrane and O-methyltransferase domain containing (LRTOMT), transcript variant 1, mRNA [NM_145309]	4.114	up	672
A_33_P3286046	DPCD	Homo sapiens deleted in primary ciliary dyskinesia homolog (mouse) (DPCD), mRNA [NM_015448]	3.133	up	673
A_23_P252201	EAF2	Homo sapiens ELL associated factor 2 (EAF2), mRNA [NM_018456]	3.601	up	674
A_23_P3602	NUDT7	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 7 (NUDT7), transcript variant 3, mRNA [NM_001243657]	3.965	up	675
A_21_P0013589	LINC01504	Homo sapiens long intergenic non-protein coding RNA 1504 (LINC01504), transcript variant 2, long non-coding RNA [NR_110953]	3.537	up	676
A_23_P125668	SLC25A43	Homo sapiens solute carrier family 25, member 43 (SLC25A43), mRNA [NM_145305]	3.260	up	677
A_33_P3386765	ABHD14A	Homo sapiens abhydrolase domain containing 14A (ABHD14A), mRNA [NM_015407]	3.882	up	678
A_33_P3283713	ABHD14A	Homo sapiens abhydrolase domain containing 14A (ABHD14A), mRNA [NM_015407]	3.498	up	679
A_33_P3353816	ITGA4	Homo sapiens integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4), mRNA [NM_000885]	3.164	up	680
A_23_P56505	ITGA4	Homo sapiens integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4), mRNA [NM_000885]	3.382	up	681
A_24_P306443	LOC100233156	Homo sapiens tektin 4 pseudogene (LOC100233156), transcript variant 1, non-coding RNA [NR_037871]	3.162	up	682
A_19_P00315584	LOC100130691	Homo sapiens uncharacterized LOC100130691 (LOC100130691), long non-coding RNA [NR_026966]	4.676	up	683
A_24_P400172	LOC100130691	Homo sapiens uncharacterized LOC100130691 (LOC100130691), long non-coding RNA [NR_026966]	4.813	up	684
A_19_P00315583	LOC100130691	Homo sapiens uncharacterized LOC100130691 (LOC100130691), long non-coding RNA [NR_026966]	4.019	up	685
A_23_P140876	ABCA3	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA [NM_001089]	4.707	up	686
A_23_P251680	COMT	Homo sapiens catechol-O-methyltransferase (COMT), transcript variant 1, mRNA [NM_000754]	3.208	up	687
A_33_P3398897	QDPR	Homo sapiens quinoid dihydropteridine reductase (QDPR), mRNA [NM_000320]	3.707	up	688
A_33_P3379091	SYNGR1	Homo sapiens synaptogyrin 1 (SYNGR1), transcript variant 1b, mRNA [NM_145731]	3.315	up	689
A_32_P114284	IKZF2	Homo sapiens IKAROS family zinc finger 2 (Helios) (IKZF2), transcript variant 2, mRNA [NM_001079526]	4.210	up	690
A_21_P0000089	ZFYVE28	Homo sapiens zinc finger, FYVE domain containing 28 (ZFYVE28), transcript variant 6, mRNA [NM_001172660]	3.145	up	691
A_23_P126836	TNFSF4	Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (TNFSF4), transcript variant 1, mRNA [NM_003326]	3.889	up	692
A_23_P162486	PTPN6	Homo sapiens protein tyrosine phosphatase, non-receptor type 6 (PTPN6), transcript variant 1, mRNA [NM_002831]	3.461	up	693
A_24_P228717	RAC2	Homo sapiens ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) (RAC2), mRNA [NM_002872]	3.902	up	694
A_23_P218770	RAC2	Homo sapiens ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) (RAC2), mRNA [NM_002872]	4.093	up	695
A_23_P78108	ALDOC	Homo sapiens aldolase C, fructose-bisphosphate (ALDOC), mRNA [NM_005165]	3.162	up	696
A_24_P852756	HLA-DQA2	Homo sapiens major histocompatibility complex, class II, DQ alpha 2 (HLA-DQA2), mRNA [NM_020056]	3.768	up	697
A_21_P0002674	FLJ42351	Homo sapiens uncharacterized LOC400999 (FLJ42351), long non-coding RNA [NR_033871]	3.236	up	698
A_23_P887	IKBKE	Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon (IKBKE), transcript variant 1, mRNA [NM_014002]	3.164	up	699
A_23_P42144	PEX6	Homo sapiens peroxisomal biogenesis factor 6 (PEX6), mRNA [NM_000287]	4.714	up	700

A_21_P0000047	DISC1	Homo sapiens disrupted in schizophrenia 1 (DISC1), transcript variant g, mRNA [NM_001164544]	4.182	up	701
A_23_P40821	HPS3	Homo sapiens Hermansky-Pudlak syndrome 3 (HPS3), mRNA [NM_032383]	3.106	up	702
A_23_P83028	RECK	Homo sapiens reversion-inducing-cysteine-rich protein with kazal motifs (RECK), mRNA [NM_021111]	3.700	up	703
A_33_P3741059	na	Homo sapiens mRNA; cDNA DKFZp667K053 (from clone DKFZp667K053). [AL832882]	4.667	up	704
A_21_P0007122	ZBED5-AS1	Homo sapiens ZBED5 antisense RNA 1 (ZBED5-AS1), long non-coding RNA [NR_034137]	6.525	up	705
A_33_P3415216	MPV17	Homo sapiens MpV17 mitochondrial inner membrane protein (MPV17), mRNA [NM_002437]	3.625	up	706
A_21_P0014888	na	BC009371 adipocyte-specific adhesion molecule {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (13%) [THC2642479]	3.289	up	707
A_24_P182539	ATG4C	Homo sapiens autophagy related 4C, cysteine peptidase (ATG4C), transcript variant 1, mRNA [NM_032852]	3.153	up	708
A_21_P0002185	lnc-EFR3B-3	LNCipedia lincRNA (lnc-EFR3B-3), lincRNA [lnc-EFR3B-3:7]	3.121	up	709
A_23_P406350	MFSD3	Homo sapiens major facilitator superfamily domain containing 3 (MFSD3), transcript variant 1, mRNA [NM_138431]	4.501	up	710
A_33_P3245908	C10orf128	Homo sapiens chromosome 10 open reading frame 128 (C10orf128), transcript variant 5, mRNA [NM_001288743]	3.766	up	711
A_23_P216655	TRIM14	Homo sapiens tripartite motif containing 14 (TRIM14), transcript variant 1, mRNA [NM_014788]	3.197	up	712
A_24_P55250	HDDC2	Homo sapiens HD domain containing 2 (HDDC2), mRNA [NM_016063]	3.197	up	713
A_23_P137848	MRPL24	Homo sapiens mitochondrial ribosomal protein L24 (MRPL24), transcript variant 1, mRNA [NM_145729]	4.168	up	714
A_23_P6535	KLHDC7B	Homo sapiens kelch domain containing 7B (KLHDC7B), mRNA [NM_138433]	3.343	up	715
A_23_P131653	PIGF	Homo sapiens phosphatidylinositol glycan anchor biosynthesis, class F (PIGF), transcript variant 1, mRNA [NM_002643]	3.805	up	716
A_24_P49383	AAMDC	Homo sapiens adipogenesis associated, Mth938 domain containing (AAMDC), mRNA [NM_024684]	4.607	up	717
A_24_P341019	TMEM230	Homo sapiens transmembrane protein 230 (TMEM230), transcript variant 2, mRNA [NM_001009924]	3.981	up	718
A_23_P17490	TMEM230	Homo sapiens transmembrane protein 230 (TMEM230), transcript variant 2, mRNA [NM_001009924]	3.575	up	719
A_23_P359904	PDDC1	Homo sapiens Parkinson disease 7 domain containing 1 (PDDC1), mRNA [NM_182612]	4.370	up	720
A_24_P245246	PIP4K2B	Homo sapiens phosphatidylinositol-5-phosphate 4-kinase, type II, beta (PIP4K2B), mRNA [NM_003559]	3.808	up	721
A_23_P146209	RNF170	Homo sapiens ring finger protein 170 (RNF170), transcript variant 2, mRNA [NM_030954]	4.263	up	722
A_32_P129968	ZNF284	zinc finger protein 284 [Source:HGNC Symbol;Acc:HGNC:13078] [ENST00000421176]	4.609	up	723
A_33_P3361417	C6orf57	Homo sapiens chromosome 6 open reading frame 57 (C6orf57), mRNA [NM_145267]	3.328	up	724
A_33_P3271755	SIRT5	Homo sapiens sirtuin 5 (SIRT5), transcript variant 2, mRNA [NM_031244]	3.199	up	725
A_24_P40594	HOMEZ	Homo sapiens homeobox and leucine zipper encoding (HOMEZ), mRNA [NM_020834]	3.636	up	726
A_23_P88753	TSR3	Homo sapiens TSR3, 20S rRNA accumulation, homolog (S. cerevisiae) (TSR3), mRNA [NM_001001410]	3.182	up	727
A_33_P3246007	APOA1BP	Homo sapiens apolipoprotein A-I binding protein (APOA1BP), mRNA [NM_144772]	3.583	up	728
A_23_P61960	ATP6V0E2	Homo sapiens ATPase, H+ transporting V0 subunit e2 (ATP6V0E2), transcript variant 1, mRNA [NM_145230]	3.176	up	729
A_24_P75072	SMUG1	Homo sapiens single-strand-selective monofunctional uracil-DNA glycosylase 1 (SMUG1), transcript variant 1, mRNA [NM_014311]	3.739	up	730
A_23_P34307	PIGK	Homo sapiens phosphatidylinositol glycan anchor biosynthesis, class K (PIGK), mRNA [NM_005482]	4.905	up	731
A_23_P201035	GBA	Homo sapiens glucosidase, beta, acid (GBA), transcript variant 2, mRNA [NM_001005741]	3.233	up	732
A_23_P123454	NUDT18	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 18 (NUDT18), mRNA [NM_024815]	3.472	up	733
A_24_P370670	ZMYM6NB	Homo sapiens ZMYM6 neighbor (ZMYM6NB), mRNA [NM_001195156]	3.161	up	734
A_23_P431569	LOC100049716	Homo sapiens uncharacterized LOC100049716 (LOC100049716), long non-coding RNA [NR_122124]	3.237	up	735
A_33_P3261610	POLR3GL	Homo sapiens polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like (POLR3GL), mRNA [NM_032305]	3.115	up	736
A_23_P23855	POLR3GL	Homo sapiens polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like (POLR3GL), mRNA [NM_032305]	3.363	up	737
A_23_P56759	KRCC1	Homo sapiens lysine-rich coiled-coil 1 (KRCC1), mRNA [NM_016618]	5.416	up	738
A_23_P350574	FCRLB	Homo sapiens Fc receptor-like B (FCRLB), transcript variant 1, mRNA [NM_001002901]	3.831	up	739
A_33_P3244117	STARD9	StAR-related lipid transfer (START) domain containing 9 [Source:HGNC Symbol;Acc:HGNC:19162] [ENST00000568493]	5.388	up	740
A_21_P0011317	XLOC_l2_004640	BROAD Institute lincRNA (XLOC_l2_004640), lincRNA [TCONS_l2_00008603]	4.070	up	741
A_33_P3329898	STARD9	StAR-related lipid transfer (START) domain containing 9 [Source:HGNC Symbol;Acc:HGNC:19162] [ENST00000564158]	6.349	up	742
A_23_P38677	SLMO1	Homo sapiens slowmo homolog 1 (Drosophila) (SLMO1), transcript variant 2, mRNA [NM_006553]	4.329	up	743
A_21_P0011320	XLOC_l2_004640	BROAD Institute lincRNA (XLOC_l2_004640), lincRNA [TCONS_l2_00008608]	4.518	up	744
A_23_P348298	SAC3D1	Homo sapiens SAC3 domain containing 1 (SAC3D1), mRNA [NM_013299]	3.423	up	745
A_23_P421401	PDGFRB	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB), mRNA [NM_002609]	3.382	up	746
A_24_P225616	RRM2	Homo sapiens ribonucleotide reductase M2 (RRM2), transcript variant 2, mRNA [NM_001034]	3.467	up	747
A_23_P408955	E2F2	Homo sapiens E2F transcription factor 2 (E2F2), mRNA [NM_004091]	3.640	up	748
A_23_P379614	OIP5	Homo sapiens Opa interacting protein 5 (OIP5), mRNA [NM_007280]	6.188	up	749
A_23_P115482	UBE2T	Homo sapiens ubiquitin-conjugating enzyme E2T (UBE2T), mRNA [NM_014176]	3.469	up	750
A_33_P3313796	CCDC34	Homo sapiens coiled-coil domain containing 34 (CCDC34), transcript variant 1, mRNA [NM_030771]	6.087	up	751
A_32_P221256	MGC70870	Homo sapiens C-terminal binding protein 2 pseudogene (MGC70870), non-coding RNA [NR_003682]	3.296	up	752
A_33_P3330099	ARSD	Homo sapiens arylsulfatase D (ARSD), mRNA [NM_001669]	3.511	up	753
A_33_P3357322	SMC2	Homo sapiens structural maintenance of chromosomes 2 (SMC2), transcript variant 1, mRNA [NM_001042550]	3.318	up	754
A_23_P48585	SALL2	Homo sapiens spalt-like transcription factor 2 (SALL2), transcript variant 1, mRNA [NM_005407]	4.469	up	755
A_23_P11862	C1orf112	Homo sapiens chromosome 1 open reading frame 112 (C1orf112), mRNA [NM_018186]	3.825	up	756
A_33_P3369153	KIF3C	Homo sapiens kinesin family member 3C (KIF3C), mRNA [NM_002254]	4.126	up	757
A_21_P0007523	DDX11-AS1	Homo sapiens DDX11 antisense RNA 1 (DDX11-AS1), long non-coding RNA [NR_038927]	5.120	up	758
A_21_P0001702	lnc-CHD1L-1	LNCipedia lincRNA (lnc-CHD1L-1), lincRNA [lnc-CHD1L-1:3]	3.602	up	759
A_24_P106112	PKD2	Homo sapiens polycystic kidney disease 2 (autosomal dominant) (PKD2), mRNA [NM_000297]	4.008	up	760
A_32_P150891	DIAPH3	Homo sapiens diaphanous-related formin 3 (DIAPH3), transcript variant 1, mRNA [NM_001042517]	4.090	up	761
A_23_P251421	CDCA7	Homo sapiens cell division cycle associated 7 (CDCA7), transcript variant 1, mRNA [NM_031942]	7.153	up	762
A_23_P48088	CD27	Homo sapiens CD27 molecule (CD27), mRNA [NM_001242]	3.293	up	763

A_33_P3234202	DNASE1L3	Homo sapiens deoxyribonuclease I-like 3 (DNASE1L3), transcript variant 1, mRNA [NM_004944]	6.763	up	764
A_23_P120227	LBH	Homo sapiens limb bud and heart development (LBH), mRNA [NM_030915]	3.176	up	765
A_23_P29594	RPL39L	Homo sapiens ribosomal protein L39-like (RPL39L), mRNA [NM_052969]	5.154	up	766
A_24_P379820	ITM2C	Homo sapiens integral membrane protein 2C (ITM2C), transcript variant 1, mRNA [NM_030926]	4.789	up	767
A_24_P402690	ITM2C	Homo sapiens integral membrane protein 2C (ITM2C), transcript variant 1, mRNA [NM_030926]	5.317	up	768
A_23_P63789	ZWINT	Homo sapiens ZW10 interacting kinetochore protein (ZWINT), transcript variant 2, mRNA [NM_032997]	5.233	up	769
A_33_P3212994	ZWINT	Homo sapiens ZW10 interacting kinetochore protein (ZWINT), transcript variant 2, mRNA [NM_032997]	4.314	up	770
A_23_P26557	C16orf59	Homo sapiens chromosome 16 open reading frame 59 (C16orf59), mRNA [NM_025108]	4.543	up	771
A_33_P3317523	STMN1	Homo sapiens stathmin 1 (STMN1), transcript variant 1, mRNA [NM_203401]	3.754	up	772
A_33_P3423949	CBX2	Homo sapiens chromobox homolog 2 (CBX2), transcript variant 1, mRNA [NM_005189]	5.229	up	773
A_33_P3219256	BMPR1A	Homo sapiens bone morphogenetic protein receptor, type IA (BMPR1A), mRNA [NM_004329]	6.520	up	774
A_19_P00805548	BMPR1A	Homo sapiens bone morphogenetic protein receptor, type IA (BMPR1A), mRNA [NM_004329]	6.758	up	775
A_33_P3219475	MSANTD3-TMEFF1	Homo sapiens MSANTD3-TMEFF1 readthrough (MSANTD3-TMEFF1), mRNA [NM_001198812]	3.197	up	776
A_21_P0014379	ZNF793-AS1	Homo sapiens ZNF793 antisense RNA 1 (head to head) (ZNF793-AS1), long non-coding RNA [NR_110723]	3.108	up	777
A_19_P00808794	XLOC_l2_008221	BROAD Institute lincRNA (XLOC_l2_008221), lincRNA [TCONS_l2_00014842]	5.311	up	778
A_33_P3391476	CRYZ	Homo sapiens crystallin, zeta (quinone reductase) (CRYZ), transcript variant 1, mRNA [NM_001130042]	3.921	up	779
A_23_P39067	SPIB	Homo sapiens Spi-B transcription factor (Spi-1/PU.1 related) (SPIB), transcript variant 1, mRNA [NM_003121]	3.114	up	780
A_23_P104046	BPNT1	Homo sapiens 3'(2'), 5'-bisphosphate nucleotidase 1 (BPNT1), transcript variant 1, mRNA [NM_006085]	3.319	up	781
A_21_P0012929	XLOC_l2_012319	BROAD Institute lincRNA (XLOC_l2_012319), lincRNA [TCONS_l2_00023251]	3.598	up	782
A_23_P120860	NIPSNAP1	Homo sapiens nipsnap homolog 1 (C. elegans) (NIPSNAP1), transcript variant 1, mRNA [NM_003634]	3.825	up	783
A_23_P88904	NTHL1	Homo sapiens nth endonuclease III-like 1 (E. coli) (NTHL1), mRNA [NM_002528]	5.161	up	784
A_23_P59528	ACN9	Homo sapiens ACN9 homolog (S. cerevisiae) (ACN9), mRNA [NM_020186]	4.086	up	785
A_24_P148811	RUVBL1	Homo sapiens RuvB-like AAA ATPase 1 (RUVBL1), mRNA [NM_003707]	4.711	up	786
A_23_P164814	C19orf57	Homo sapiens chromosome 19 open reading frame 57 (C19orf57), mRNA [NM_024323]	3.163	up	787
A_23_P133770	CCDC167	Homo sapiens coiled-coil domain containing 167 (CCDC167), mRNA [NM_138493]	5.743	up	788
A_33_P3260100	CCDC167	Homo sapiens coiled-coil domain containing 167 (CCDC167), mRNA [NM_138493]	3.682	up	789
A_23_P31116	ACOT13	Homo sapiens acyl-CoA thioesterase 13 (ACOT13), transcript variant 1, mRNA [NM_018473]	3.399	up	790
A_21_P0014321	ATP2A1-AS1	Homo sapiens ATP2A1 antisense RNA 1 (ATP2A1-AS1), transcript variant 1, long non-coding RNA [NR_046287]	3.342	up	791
A_24_P343095	DHFR	Homo sapiens dihydrofolate reductase (DHFR), transcript variant 1, mRNA [NM_000791]	3.516	up	792
A_23_P32135	C9orf9	Homo sapiens chromosome 9 open reading frame 9 (C9orf9), mRNA [NM_018956]	4.538	up	793
A_33_P3764802	SIRT5	Homo sapiens sirtuin 5 (SIRT5), transcript variant 1, mRNA [NM_012241]	3.200	up	794
A_33_P3390778	TRIM46	Homo sapiens tripartite motif containing 46 (TRIM46), transcript variant 2, mRNA [NM_001256599]	7.981	up	795
A_23_P18413	TIMMDC1	Homo sapiens translocase of inner mitochondrial membrane domain containing 1 (TIMMDC1), mRNA [NM_016589]	3.460	up	796
A_23_P150009	ZDHHC16	Homo sapiens zinc finger, DHHC-type containing 16 (ZDHHC16), transcript variant 5, mRNA [NM_198046]	4.643	up	797
A_33_P3340025	GINS1	Homo sapiens GINS complex subunit 1 (Psf1 homolog) (GINS1), mRNA [NM_021067]	8.166	up	798
A_32_P1701	POLA1	Homo sapiens polymerase (DNA directed), alpha 1, catalytic subunit (POLA1), mRNA [NM_016937]	3.791	up	799
A_33_P3296372	EIF2B3	Homo sapiens eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa (EIF2B3), transcript variant 1, mRNA [NM_020365]	5.697	up	800
A_24_P73943	COX11	Homo sapiens COX11 cytochrome c oxidase copper chaperone (COX11), transcript variant 1, mRNA [NM_004375]	6.883	up	801
A_33_P3218584	POP5	Homo sapiens processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae) (POP5), transcript variant 1, mRNA [NM_015918]	4.298	up	802
A_23_P153098	HDHD2	Homo sapiens haloacid dehalogenase-like hydrolase domain containing 2 (HDHD2), mRNA [NM_032124]	8.984	up	803
A_23_P207517	PDK2	Homo sapiens pyruvate dehydrogenase kinase, isozyme 2 (PDK2), transcript variant 1, mRNA [NM_002611]	4.115	up	804
A_23_P90732	PNKD	Homo sapiens paroxysmal nonkinesigenic dyskinesia (PNKD), transcript variant 3, mRNA [NM_001077399]	6.650	up	805
A_21_P0000034	COX11	Homo sapiens COX11 cytochrome c oxidase copper chaperone (COX11), transcript variant 1, mRNA [NM_004375]	9.076	up	806
A_23_P111000	PSMB9	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 9 (PSMB9), mRNA [NM_002800]	4.735	up	807
A_21_P0013869	FIRRE	Homo sapiens firre intergenic repeating RNA element (FIRRE), long non-coding RNA [NR_026975]	4.800	up	808
A_21_P0013831	XLOC_l2_015821	BROAD Institute lincRNA (XLOC_l2_015821), lincRNA [TCONS_l2_00030598]	6.382	up	809
A_21_P0013832	FIRRE	Homo sapiens firre intergenic repeating RNA element (FIRRE), long non-coding RNA [NR_026975]	6.660	up	810
A_21_P0011391	CHEK2	Homo sapiens checkpoint kinase 2 (CHEK2), transcript variant 3, mRNA [NM_001005735]	4.916	up	811
A_21_P0011475	CHEK2	Homo sapiens checkpoint kinase 2 (CHEK2), transcript variant 3, mRNA [NM_001005735]	4.347	up	812
A_21_P0011474	CHEK2	Homo sapiens checkpoint kinase 2 (CHEK2), transcript variant 3, mRNA [NM_001005735]	5.076	up	813
A_23_P203115	TMEM25	Homo sapiens transmembrane protein 25 (TMEM25), transcript variant 1, mRNA [NM_032780]	3.792	up	814
A_33_P3400152	ENTPD1-AS1	Homo sapiens ENTPD1 antisense RNA 1 (ENTPD1-AS1), long non-coding RNA [NR_038444]	3.372	up	815
A_23_P207400	BRCA1	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant 2, mRNA [NM_007300]	7.853	up	816
A_33_P3301524	XRCC3	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 3 (XRCC3), transcript variant 1, mRNA [NM_001100119]	3.731	up	817
A_23_P53276	TIMELESS	Homo sapiens timeless circadian clock (TIMELESS), mRNA [NM_003920]	3.801	up	818
A_23_P207201	CD79B	Homo sapiens CD79b molecule, immunoglobulin-associated beta (CD79B), transcript variant 3, mRNA [NM_001039933]	9.246	up	819
A_33_P3383970	TLR10	Homo sapiens toll-like receptor 10 (TLR10), transcript variant 1, mRNA [NM_030956]	5.577	up	820
A_33_P3264846	SAMD9L	sterile alpha motif domain containing 9-like [Source:HGNC Symbol;Acc:HGNC:1349] [ENST00000610760]	7.353	up	821
A_23_P145874	SAMD9L	sterile alpha motif domain containing 9-like [Source:HGNC Symbol;Acc:HGNC:1349] [ENST00000411955]	6.081	up	822
A_23_P42080	TMEM14A	Homo sapiens transmembrane protein 14A (TMEM14A), mRNA [NM_014051]	4.647	up	823
A_24_P277155	HLTF	Homo sapiens helicase-like transcription factor (HLTF), transcript variant 1, mRNA [NM_003071]	3.575	up	824
A_23_P88222	PLD4	Homo sapiens phospholipase D family, member 4 (PLD4), mRNA [NM_138790]	8.007	up	825
A_23_P342131	CYB561A3	Homo sapiens cytochrome b561 family, member A3 (CYB561A3), transcript variant 2, mRNA [NM_153611]	3.550	up	826

A_23_P16078	PAFAH1B3	Homo sapiens platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa) (PAFAH1B3), transcript variant 2, mRNA [NM_002573]	3.412	up	827
A_33_P3372451	DNPH1	Homo sapiens 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 (DNPH1), transcript variant 2, mRNA [NM_199184]	4.573	up	828
A_33_P3258712	LOC101928000	PREDICTED: Homo sapiens uncharacterized LOC101928000 (LOC101928000), ncRNA [XR_243583]	3.267	up	829
A_33_P3304824	LINC00618	Homo sapiens long intergenic non-protein coding RNA 618 (LINC00618), long non-coding RNA [NR_104113]	3.328	up	830
A_19_P00320722	SRP14-AS1	Homo sapiens SRP14 antisense RNA1 (head to head) (SRP14-AS1), transcript variant 1, long non-coding RNA [NR_040059]	8.796	up	831
A_23_P66311	DNASE1	Homo sapiens deoxyribonuclease I (DNASE1), mRNA [NM_005223]	3.954	up	832
A_24_P296907	THAP8	Homo sapiens THAP domain containing 8 (THAP8), mRNA [NM_152658]	5.831	up	833
A_24_P925314	GM2A	Homo sapiens GM2 ganglioside activator (GM2A), transcript variant 1, mRNA [NM_000405]	3.427	up	834
A_23_P129064	GATM	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM), mRNA [NM_001482]	3.217	up	835
A_24_P417352	LOC102725284	immunoglobulin heavy constant mu [Source:HGNC Symbol;Acc:HGNC:5541] [ENST00000610838]	3.287	up	836
A_33_P3263317	na	Homo sapiens cDNA FLJ46564 fis, clone THYMU3040746, highly similar to Ig gamma-2 chain C region. [AK128421]	3.711	up	837
A_24_P276576	FCRLA	Homo sapiens Fc receptor-like A (FCRLA), transcript variant 2, mRNA [NM_032738]	15.711	up	838
A_23_P46039	FCRLA	Homo sapiens Fc receptor-like A (FCRLA), transcript variant 2, mRNA [NM_032738]	14.672	up	839
A_23_P217901	TSTD1	Homo sapiens thiosulfate sulfurtransferase (rhodanese)-like domain containing 1 (TSTD1), transcript variant 1, mRNA [NM_001113207]	4.731	up	840
A_23_P30736	HLA-DOB	Homo sapiens major histocompatibility complex, class II, DO beta (HLA-DOB), mRNA [NM_002120]	4.305	up	841
A_33_P3397910	lnc-RAB1A-1	ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (5%) [THC2680929]	3.461	up	842
A_23_P49988	KRTAP4-2	Homo sapiens keratin associated protein 4-2 (KRTAP4-2), mRNA [NM_033062]	3.223	up	843
A_21_P0002860	na	0	3.501	up	844
A_33_P3565787	PSMG3-AS1	Homo sapiens PSMG3 antisense RNA 1 (head to head) (PSMG3-AS1), transcript variant 1, long non-coding RNA [NR_027329]	3.163	up	845
A_23_P208961	MUM1	Homo sapiens melanoma associated antigen (mutated) 1 (MUM1), transcript variant 1, mRNA [NM_032853]	4.407	up	846
A_23_P86731	ZNF239	Homo sapiens zinc finger protein 239 (ZNF239), transcript variant 1, mRNA [NM_005674]	7.140	up	847
A_32_P24140	GAS2	Homo sapiens growth arrest-specific 2 (GAS2), transcript variant 1, mRNA [NM_005256]	5.144	up	848
A_33_P3371341	FAM66C	Homo sapiens family with sequence similarity 66, member C (FAM66C), long non-coding RNA [NR_026788]	4.237	up	849
A_33_P3238295	FAM66C	Homo sapiens family with sequence similarity 66, member C (FAM66C), long non-coding RNA [NR_026788]	3.833	up	850
A_21_P0000742	MYLK-AS1	Homo sapiens MYLK antisense RNA 1 (MYLK-AS1), transcript variant 1, long non-coding RNA [NR_038266]	5.233	up	851
A_33_P3271395	LOC100129534	Homo sapiens small nuclear ribonucleoprotein polypeptide N pseudogene (LOC100129534), non-coding RNA [NR_024489]	5.804	up	852
A_23_P92629	CWC27	Homo sapiens CWC27 spliceosome-associated protein homolog (S. cerevisiae) (CWC27), transcript variant 1, mRNA [NM_005869]	4.689	up	853
A_23_P147605	C11orf49	Homo sapiens chromosome 11 open reading frame 49 (C11orf49), transcript variant 1, mRNA [NM_001003676]	3.538	up	854
A_33_P3252369	TMEM182	Homo sapiens transmembrane protein 182 (TMEM182), mRNA [NM_144632]	7.132	up	855
A_24_P268729	HEMK1	Homo sapiens HemK methyltransferase family member 1 (HEMK1), mRNA [NM_016173]	6.326	up	856
A_23_P256835	TRAPPC12	Homo sapiens trafficking protein particle complex 12 (TRAPPC12), mRNA [NM_016030]	3.259	up	857
A_23_P420256	C2orf43	Homo sapiens chromosome 2 open reading frame 43 (C2orf43), transcript variant 1, mRNA [NM_021925]	8.585	up	858
A_24_P914513	BCKDHB	Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (BCKDHB), transcript variant 1, mRNA [NM_183050]	4.744	up	859
A_33_P3389298	ZNF30	Homo sapiens zinc finger protein 30 (ZNF30), transcript variant 1, mRNA [NM_001099438]	5.286	up	860
A_32_P151782	na	AGENCOURT_14064404 NIH_MGC_172 Homo sapiens cDNA 5', mRNA sequence [CD248433]	6.827	up	861
A_23_P39517	SRBD1	Homo sapiens S1 RNA binding domain 1 (SRBD1), mRNA [NM_018079]	3.404	up	862
A_24_P626931	UBE3D	ubiquitin protein ligase E3D [Source:HGNC Symbol;Acc:HGNC:21381] [ENST00000503942]	4.684	up	863
A_21_P0011592	LINC00910	Homo sapiens long intergenic non-protein coding RNA 910 (LINC00910), transcript variant 2, long non-coding RNA [NR_027412]	4.756	up	864
A_21_P0012925	XLOC_l2_012210	BROAD Institute lincRNA (XLOC_l2_012210), lincRNA [TCONS_l2_00023087]	3.984	up	865
A_24_P299355	GRAPL	Homo sapiens GRB2-related adaptor protein-like (GRAPL), mRNA [NM_001129778]	6.365	up	866
A_23_P23719	VPS45	Homo sapiens vacuolar protein sorting 45 homolog (S. cerevisiae) (VPS45), transcript variant 1, mRNA [NM_007259]	3.127	up	867
A_32_P133670	ANP32A	Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member A (ANP32A), mRNA [NM_006305]	3.143	up	868
A_33_P3275510	C20orf196	chromosome 20 open reading frame 196 [Source:HGNC Symbol;Acc:HGNC:26318] [ENST00000303142]	3.460	up	869
A_21_P0007119	FLJ37035	Homo sapiens uncharacterized LOC399821 (FLJ37035), long non-coding RNA [NR_033847]	3.456	up	870
A_23_P86100	KLHDC9	Homo sapiens kelch domain containing 9 (KLHDC9), transcript variant 2, mRNA [NM_001007255]	4.806	up	871
A_33_P3304963	LRRC27	Homo sapiens leucine rich repeat containing 27 (LRRC27), transcript variant 4, mRNA [NM_001143759]	4.508	up	872
A_23_P123086	PSMG3-AS1	Homo sapiens PSMG3 antisense RNA 1 (head to head) (PSMG3-AS1), transcript variant 1, long non-coding RNA [NR_027329]	4.243	up	873
A_24_P254551	ARHGEF9	Homo sapiens Cdc42 guanine nucleotide exchange factor (GEF) 9 (ARHGEF9), transcript variant 1, mRNA [NM_015185]	5.116	up	874
A_23_P315206	CCBL1	Homo sapiens cysteine conjugate-beta lyase, cytoplasmic (CCBL1), transcript variant 1, mRNA [NM_004059]	6.120	up	875
A_24_P398323	TRIM34	Homo sapiens tripartite motif containing 34 (TRIM34), transcript variant 4, mRNA [NM_001003827]	3.971	up	876
A_24_P573533	CBWD5	Homo sapiens COBW domain containing 5 (CBWD5), transcript variant 1, mRNA [NM_001024916]	3.310	up	877
A_24_P100830	AMN1	Homo sapiens antagonist of mitotic exit network 1 homolog (S. cerevisiae) (AMN1), transcript variant 3, mRNA [NM_001278412]	3.439	up	878
A_21_P0014380	na	PREDICTED: Homo sapiens uncharacterized LOC100507486 (LOC100507486), misc_RNA [XR_109525]	3.584	up	879
A_33_P3405743	CRYZ	Homo sapiens crystallin, zeta (quinone reductase) (CRYZ), transcript variant 1, mRNA [NM_001130042]	3.885	up	880
A_33_P3233273	LRRC61	Homo sapiens leucine rich repeat containing 61 (LRRC61), transcript variant 1, mRNA [NM_001142928]	3.951	up	881
A_23_P320717	COG4	Homo sapiens component of oligomeric golgi complex 4 (COG4), transcript variant 1, mRNA [NM_015386]	3.166	up	882
A_33_P3277514	BTK	Homo sapiens Bruton agammaglobulinemia tyrosine kinase (BTK), transcript variant 3, mRNA [NM_001287344]	3.806	up	883
A_23_P137139	BTK	Homo sapiens Bruton agammaglobulinemia tyrosine kinase (BTK), transcript variant 1, mRNA [NM_000061]	3.916	up	884
A_33_P3531828	LARS	Homo sapiens leucyl-tRNA synthetase (LARS), mRNA [NM_020117]	3.856	up	885
A_33_P3217834	SMARCAL1	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 (SMARCAL1), transcript variant 1, mRNA [NM_014140]	4.416	up	886

A_23_P96761	ACADM	Homo sapiens acyl-CoA dehydrogenase, C-4 to C-12 straight chain (ACADM), transcript variant 1, mRNA [NM_000016]	6.941	up	887
A_23_P332042	RECQL5	Homo sapiens RecQ protein-like 5 (RECQL5), transcript variant 1, mRNA [NM_004259]	3.990	up	888
A_33_P3210521	C2orf43	Homo sapiens chromosome 2 open reading frame 43 (C2orf43), transcript variant 1, mRNA [NM_021925]	6.877	up	889
A_23_P118406	C17orf62	Homo sapiens chromosome 17 open reading frame 62 (C17orf62), transcript variant 2, mRNA [NM_001033046]	3.389	up	890
A_23_P358470	PRIMPOL	Homo sapiens primase and polymerase (DNA-directed) (PRIMPOL), transcript variant 1, mRNA [NM_152683]	3.368	up	891
A_23_P90333	ZNF404	Homo sapiens zinc finger protein 404 (ZNF404), mRNA [NM_001033719]	7.140	up	892
A_23_P84922	HDAC8	Homo sapiens histone deacetylase 8 (HDAC8), transcript variant 1, mRNA [NM_018486]	3.149	up	893
A_33_P3235987	PIN4	Homo sapiens protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) (PIN4), transcript variant 1, mRNA [NM_006223]	3.296	up	894
A_24_P207139	PML	Homo sapiens promyelocytic leukemia (PML), transcript variant 1, mRNA [NM_033238]	3.845	up	895
A_23_P300076	IQCG	Homo sapiens IQ motif containing G (IQCG), transcript variant 1, mRNA [NM_032263]	3.837	up	896
A_23_P215070	CEP41	Homo sapiens centrosomal protein 41kDa (CEP41), transcript variant 1, mRNA [NM_018718]	5.563	up	897
A_23_P23102	ZSCAN20	Homo sapiens zinc finger and SCAN domain containing 20 (ZSCAN20), mRNA [NM_145238]	3.825	up	898
A_23_P92954	HSD17B4	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), transcript variant 2, mRNA [NM_000414]	3.112	up	899
A_23_P353717	RMI2	Homo sapiens RecQ mediated genome instability 2 (RMI2), mRNA [NM_152308]	4.385	up	900
A_32_P96692	POLH	Homo sapiens polymerase (DNA directed), eta (POLH), transcript variant 1, mRNA [NM_006502]	3.993	up	901
A_33_P3313830	LINC01184	Homo sapiens long intergenic non-protein coding RNA 1184 (LINC01184), long non-coding RNA [NR_015360]	3.709	up	902
A_21_P0000799	RNASEH1-AS1	Homo sapiens RNASEH1 antisense RNA 1 (RNASEH1-AS1), transcript variant 1, long non-coding RNA [NR_038430]	3.340	up	903
A_21_P0000800	RNASEH1-AS1	Homo sapiens RNASEH1 antisense RNA 1 (RNASEH1-AS1), transcript variant 3, long non-coding RNA [NR_038431]	3.252	up	904
A_24_P162287	CEP250	Homo sapiens centrosomal protein 250kDa (CEP250), mRNA [NM_007186]	3.166	up	905
A_23_P129014	EFCAB11	Homo sapiens EF-hand calcium binding domain 11 (EFCAB11), transcript variant 1, mRNA [NM_145231]	5.168	up	906
A_21_P0010470	lnc-MAPK8IP2-1	LNCipedia lincRNA (lnc-MAPK8IP2-1), lincRNA [lnc-MAPK8IP2-1:12]	3.256	up	907
A_21_P0014568	LOC100507616	PREDICTED: Homo sapiens uncharacterized LOC100507616 (LOC100507616), transcript variant X1, ncRNA [XR_110328]	3.421	up	908
A_33_P3407895	RINL	Homo sapiens Ras and Rab interactor-like (RINL), transcript variant 1, mRNA [NM_001195833]	3.469	up	909
A_23_P357104	ANXA6	Homo sapiens annexin A6 (ANXA6), transcript variant 1, mRNA [NM_001155]	4.033	up	910
A_23_P163143	ACYP1	Homo sapiens acylphosphatase 1, erythrocyte (common) type (ACYP1), transcript variant 4, mRNA [NM_001302617]	5.273	up	911
A_23_P334218	TBC1D31	Homo sapiens TBC1 domain family, member 31 (TBC1D31), transcript variant 1, mRNA [NM_145647]	3.718	up	912
A_24_P14260	CARD8	Homo sapiens caspase recruitment domain family, member 8 (CARD8), transcript variant 2, mRNA [NM_014959]	3.186	up	913
A_23_P58036	MCCC1	Homo sapiens methylcrotonoyl-CoA carboxylase 1 (alpha) (MCCC1), transcript variant 1, mRNA [NM_020166]	3.951	up	914
A_23_P155477	C3orf18	Homo sapiens chromosome 3 open reading frame 18 (C3orf18), transcript variant 1, mRNA [NM_016210]	4.289	up	915
A_23_P415021	METTL7A	Homo sapiens methyltransferase like 7A (METTL7A), mRNA [NM_014033]	5.115	up	916
A_23_P200838	KMO	Homo sapiens kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO), mRNA [NM_003679]	3.159	up	917
A_24_P77082	KMO	Homo sapiens kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO), mRNA [NM_003679]	4.662	up	918
A_24_P175612	SFXN2	Homo sapiens sideroflexin 2 (SFXN2), mRNA [NM_178858]	3.242	up	919
A_33_P3401647	PPP1R14A	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 14A (PPP1R14A), transcript variant 1, mRNA [NM_033256]	7.542	up	920
A_33_P3416712	LOC400958	Homo sapiens uncharacterized LOC400958 (LOC400958), long non-coding RNA [NR_036586]	5.611	up	921
A_23_P65983	CCDC102A	Homo sapiens coiled-coil domain containing 102A (CCDC102A), mRNA [NM_033212]	3.513	up	922

Differentially expressed genes were assessed by Moderated T-Test (see Supplemental Methods).

Table S4. Pathway and GO categories differentially represented in BCRlow and BCRhigh MCL cells

Rank	Function Name	Number of genes/pathway	P	Impact Factor
1	Antigen processing and presentation	5	0.03739	82.185
2	Phosphatidylinositol signaling system	6	0.00813	22.084
3	Adherens junction	5	0.03085	18.065
4	B cell receptor signaling pathway	10	0.00000	15.474
5	Regulation of actin cytoskeleton	11	0.01035	6.809
6	Fc epsilon RI signaling pathway	6	0.00866	6.569
7	Melanoma	6	0.00625	6.442
8	Cell adhesion molecules (CAMs)	7	0.03665	5.913
9	Colorectal cancer	6	0.01379	5.827
10	Acute myeloid leukemia	5	0.00975	5.813
11	Pathways in cancer	14	0.02175	5.456
12	Glioma	5	0.01674	5.44
13	Prostate cancer	6	0.01790	5.344

Table S5. Gene Set upregulated in BCRhigh MCL cells respect to BCRlow MCL cells according to Gene Set Enrichment Analysis (GSEA)

Gene Set Name	Gene Set Size	Enrichment Score	Normalized Enrichment Score	Nominal P-Value	FDR Q-Value
KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN	57	-0.64277	-2.45527	0.00000	0.00000
GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN	78	-0.57130	-2.32747	0.00000	0.00000
MOOTHA_VOXPHOS	84	-0.55872	-2.28949	0.00000	0.00028
BASSO_CD40_SIGNALING_DN	55	-0.58473	-2.25370	0.00000	0.00021
KEGG_DNA_REPLICATION	36	-0.63488	-2.20542	0.00000	0.00017
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	91	-0.52801	-2.18743	0.00000	0.00014
YU_MYC_TARGETS_DN	48	-0.58498	-2.17545	0.00000	0.00012
KANG_DOXORUBICIN_RESISTANCE_UP	49	-0.59507	-2.15912	0.00000	0.00031
PYEON_HPV_POSITIVE_TUMORS_UP	84	-0.51976	-2.13562	0.00000	0.00047
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	74	-0.53031	-2.12988	0.00000	0.00051
SANA_RESPONSE_TO_IFNG_UP	64	-0.54144	-2.10834	0.00000	0.00070
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	41	-0.57968	-2.09385	0.00000	0.00079
REACTOME_TELOMERE_MAINTENANCE	72	-0.51982	-2.08997	0.00000	0.00073
ISHIDA_E2F_TARGETS	47	-0.56699	-2.08842	0.00000	0.00067
CROONQUIST_IL6_DEPRIVATION_DN	90	-0.49985	-2.08417	0.00000	0.00069
REN_BOUND_BY_E2F	58	-0.52731	-2.05434	0.00000	0.00107
ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_DN	41	-0.55371	-2.00415	0.00000	0.00261
WAKASUGI_HAVE_ZNF143_BINDING_SITES	57	-0.52023	-2.00376	0.00159	0.00247
WIELAND_UP_BY_HBV_INFECTION	93	-0.48095	-2.00256	0.00000	0.00234
REACTOME_DNA_REPAIR	100	-0.48007	-1.98779	0.00000	0.00265
WOO_LIVER_CANCER_RECURRENCE_DN	55	-0.52017	-1.97602	0.00000	0.00297
KAUFFMANN_MELANOMA_RELAPSE_UP	57	-0.51877	-1.97578	0.00000	0.00283
REACTOME_G2_M_CHECKPOINTS	39	-0.55443	-1.97193	0.00000	0.00297
KEGG_PEROXISOME	61	-0.49775	-1.95369	0.00000	0.00373
KEGG_PYRIMIDINE_METABOLISM	86	-0.47361	-1.95241	0.00000	0.00369
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	67	-0.49561	-1.95205	0.00000	0.00354
ZHANG_TLX_TARGETS_UP	79	-0.48407	-1.94407	0.00000	0.00398
SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP	69	-0.48185	-1.92280	0.00000	0.00554
MORI_LARGE_PRE_BII_LYMPHOCYTE_DN	56	-0.50942	-1.91841	0.00000	0.00570
KEGG_TYPE_I_DIABETES_MELLITUS	36	-0.54784	-1.91498	0.00000	0.00560
BURTON_ADIPOGENESIS_3	89	-0.45991	-1.91036	0.00000	0.00572
RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP	86	-0.45730	-1.90216	0.00161	0.00621
REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	42	-0.52377	-1.90046	0.00000	0.00613
LEE_EARLY_T_LYMPHOCYTE_UP	81	-0.46723	-1.89848	0.00000	0.00615
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR	70	-0.47887	-1.89808	0.00000	0.00600
MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_UP	100	-0.45255	-1.89449	0.00000	0.00614
SIG_BCR_SIGNALING_PATHWAY	46	-0.50867	-1.87878	0.00000	0.00725
FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN	47	-0.51505	-1.87696	0.00000	0.00721
VERNELL_RETINOBLASTOMA_PATHWAY_UP	64	-0.48012	-1.87643	0.00164	0.00716
SONG_TARGETS_OF_IE86_CMV_PROTEIN	60	-0.48315	-1.87443	0.00000	0.00722
KEGG_NUCLEOTIDE_EXCISION_REPAIR	43	-0.51015	-1.87328	0.00164	0.00719
CROONQUIST_NRAS_SIGNALING_DN	66	-0.47718	-1.87134	0.00000	0.00724
RAMALHO_STEMNESS_DN	61	-0.48163	-1.87126	0.00000	0.00709
GRADE_METASTASIS_DN	42	-0.51037	-1.86763	0.00332	0.00730
PRAMOONJAGO_SOX4_TARGETS_DN	44	-0.51644	-1.86716	0.00000	0.00715
STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN	39	-0.52469	-1.85699	0.00000	0.00789
WINTER_HYPOXIA_DN	45	-0.50350	-1.85265	0.00000	0.00812
KLEIN_TARGETS_OF_BCR_ABL1_FUSION	39	-0.51916	-1.84838	0.00000	0.00834
WU_APOPTOSIS_BY_CDKN1A_VIA_TP53	46	-0.50415	-1.84734	0.00000	0.00822
REACTOME_MEIOTIC_RECOMBINATION	72	-0.46258	-1.84729	0.00000	0.00806
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	57	-0.48821	-1.84263	0.00163	0.00842
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQUOISE_DN	46	-0.51149	-1.84091	0.00000	0.00834
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	80	-0.45159	-1.83489	0.00000	0.00875
WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLESTEROL_UP	48	-0.49467	-1.82950	0.00000	0.00912
BROWNE_INTERFERON_RESPONSIVE_GENES	61	-0.46999	-1.82879	0.00000	0.00900
GRABARCZYK_BCL11B_TARGETS_DN	41	-0.51471	-1.82742	0.00169	0.00889
JAIN_NFKB_SIGNALING	72	-0.45657	-1.82466	0.00000	0.00911
MARTINEZ_RESPONSE_TO_TRABECTEDIN	45	-0.49161	-1.82280	0.00165	0.00915
KIM_GERMINAL_CENTER_T_HELPER_UP	54	-0.47593	-1.80912	0.00165	0.01068
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	47	-0.48685	-1.79712	0.00168	0.01224
MORI_IMMATURE_B_LYMPHOCYTE_UP	50	-0.48321	-1.79501	0.00491	0.01236
HUTTMANN_B_CLL_POOR_SURVIVAL_DN	50	-0.47818	-1.76558	0.00000	0.01688
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	71	-0.44228	-1.76109	0.00159	0.01771
PID_FANCONI_PATHWAY	45	-0.48904	-1.75872	0.00325	0.01799
JIANG_AGING_HYPOTHALAMUS_UP	43	-0.49043	-1.75646	0.00165	0.01819
CHICAS_RB1_TARGETS_LOW_SERUM	85	-0.41979	-1.74780	0.00000	0.01964
ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN	61	-0.44533	-1.74122	0.00320	0.02091
REACTOME_SYNTHESIS_OF_DNA	88	-0.42086	-1.73437	0.00157	0.02225
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	42	-0.47820	-1.72246	0.00162	0.02495
GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_UP	70	-0.43364	-1.71998	0.00000	0.02516
GAVIN_FOXP3_TARGETS_CLUSTER_P6	74	-0.43022	-1.71931	0.00324	0.02494
COATES_MACROPHAGE_M1_VS_M2_UP	64	-0.44386	-1.71656	0.00162	0.02543
KESHELAVA_MULTIPLE_DRUG_RESISTANCE	72	-0.42945	-1.71176	0.00318	0.02660
BURTON_ADIPOGENESIS_PEAK_AT_16HR	40	-0.48610	-1.68823	0.00498	0.03372
HOWLIN_PUBERTAL_MAMMARY_GLAND	46	-0.46024	-1.68665	0.00796	0.03382
REACTOME_TRNA_AMINOACYLATION	41	-0.46911	-1.67962	0.00659	0.03592
PID_BCR_5PATHWAY	64	-0.42934	-1.65977	0.00161	0.04395
OXFORD_RALA_OR_RALB_TARGETS_UP	46	-0.44430	-1.65210	0.00663	0.04706
ROSS_AML_WITH_MLL_FUSIONS	66	-0.41646	-1.64851	0.00000	0.04830
SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES	35	-0.48680	-1.64517	0.00336	0.04936

Table S6. qRT-PCR details

Gene name	SEQUENCE PRIMER 1	SEQUENCE PRIMER 2	SEQUENCE PROBE	Amplicon lenght	ID	R^2	Slope
AKT3	GCTTGTACCTCCTTTTAAACCTC	CATGCAGTCCATACCATCCTC	TGAGACAGATACTAGATATTTTGATGAAGAATTTACAGCT	130	Hs.PT.58.38907880	0.998	3.308
B2M	CCTGAATCTTTGGAGTACGCT	GGCATTCCTGAAGCTGACA	CTAAGGCCACGGAGCGAGACATC	118	B2M	0.997	3.280
BTK	TGTATAGCAAGTTCAGCAGCAA	ATCTCTCATATGGCATCTTCCC	CCCACATCAAAACCCCAAAAGCCC	93	Hs.PT.56a.38768830	0.996	3.323
CD79b	CAGCTGAGCCAGTACCAG	TGTGCCAAGGTGCTGAATC	5'AGCCAGATCGGAGGACCGG	73	Hs.PT.58.40462637	0.996	3.390
PIK3CD	TGCTCCAAAGACATCCAGTATC	GGCTTCGTTAAACTTCACTCG	TCTGTTTTCCCCAGTGCCAGGG	96	Hs.PT.58.39393086	0.984	3.377
SYK	CTGGAGCTTTGGAGTGTTGA	CGCTCTCCTTTCTCTAACATAGC	TGCCCATAGGAGAATGCTTCCCAC	105	Hs.PT.5839642284	0.997	3.346
BCL2	AGCCAGGAGAAATCAAACAGAG	GATGACTGAGTACCTGAACCG	CAGGATAACGGAGGCTGGGATGC	117	Hs.PT.56a.2905156	0.996	3.301

Note: ID, assay name according to IDT producer; R2, correlation coefficient; Slope, slope of the standar curve.