Supplementary Report 4:
Genes of interest marked by vector integration
Response Group CR/PRtd only (CLL & ALL Patients)

Contents

Summary

Lentiviral vectors integrate into genomes of targeted host cells (Tcells). These genomic locations of vector integrations are identifiable through integration site sequencing. Abundances of individual cell clones can be inferred by the sonicLength method (**Berry *et al.* 2012**).

In this report, we mined the data collected from integration site sequencing for 20 CART treated subjects. We constructed 4 gene lists based on: 1 & 2) increased / decreased integration site occurrence in patient samples relative to the initial transduction product, 3) peak clonal abundance, and 4) longitudinal clonal persistence. More about each of these criteria is below:

- **Integration Frequency** is the rate at which integration sites are observed within a gene. This is compared between patient samples and the initial transduction product to score enrichment or depletion during growth in patients. The top of genes with higher patient sample integration frequency over transduction samples were chosen for study (p-value <= 0.05 after exclusion of genes with clones from less than 2 patients and less than 10 observed clones).
- **Clonal Abundance** can be determined during analysis by quantifying the number of sites of linker ligation associated with each unique integration site. This method is further described in **Berry *et al.* 2012**. This allows clonal expansion to be quantified. The top 1% of the genes were selected for study based on their maximal peak clonal abundance.
- **Longitudinal Observation** of clones is the quantification of observed timespans and last observed timepoints. The maximum value for clones within a gene were considered for characterization of the gene in this analysis. Genes were only considered if there were 10 or more integration sites isolated from at least two different patient samples. Genes were also not considered if they only consited of clones which were observed once or the last observed timepoint was less than 90 days from initial infusion.

A point to keep in mind through all this analysis is that integration sites are sampled from a larger population. It would be rare for all integration sites in a sample to be represented in the sequence data.

Table 1: Summary of each filtering criteria.

Criteria	Gene Count	Onco Related1 (%)	Tumor Suppressors (%)	Lymphoma Related2 (%)	COSMIC Related3 (%)	TCGA Related4 (%)	Clonal Hema. Related5 (%)
Enrichment	278	*/* 21.2	*/* 11.15	/ 0.360	*/* 12.23	*/* 9.35	*/* 1.079
Depletion	4	/ 0.0	/ 0.00	/ 0.000	/ 0.00	/ 0.00	/ 0.000
Abundance	119	*/* 20.2	/ 5.88	/ 0.000	*/* 9.24	/ 5.04	/ 0.840
Longitudinal	208	*/* 25.5	*/* 12.02	/ 0.481	*/* 12.50	*/* 12.02	*/* 1.442
Composite	501	*/* 20.2	*/* 9.38	/ 0.200	*/* 10.78	*/* 8.18	/ 0.599

Table 1 summarizes the size and contents of each criteria gene list identified by the various methods. Significance of overlap between lists are displayed by asterisks before the percent of genes identifed from the criteria list which overlap with the column specified group. The asterisk to the left of the "/" indicates a p-value below 0.05 *before* multiple comparison corrections, while an asterisk to the right of the "/" indicates a p-value below 0.05 *after* multiple comparison corrections. Significance was tested using Fishers Exact test and multiple comparison corrections were made using a Benjamini-Hochberg (FDR) method for each criteria based list.

Percent of all analyzed transcription units associated with each list as as follows:

- Onco Related: 9.41%
- Tumor Suppressors: 4.91%
- Lymphoma Related: 0.16%
- COSMIC Related: 3.78%
- TCGA Related: 2.88%
- Clonal Hematopoiesis Related: 0.18%

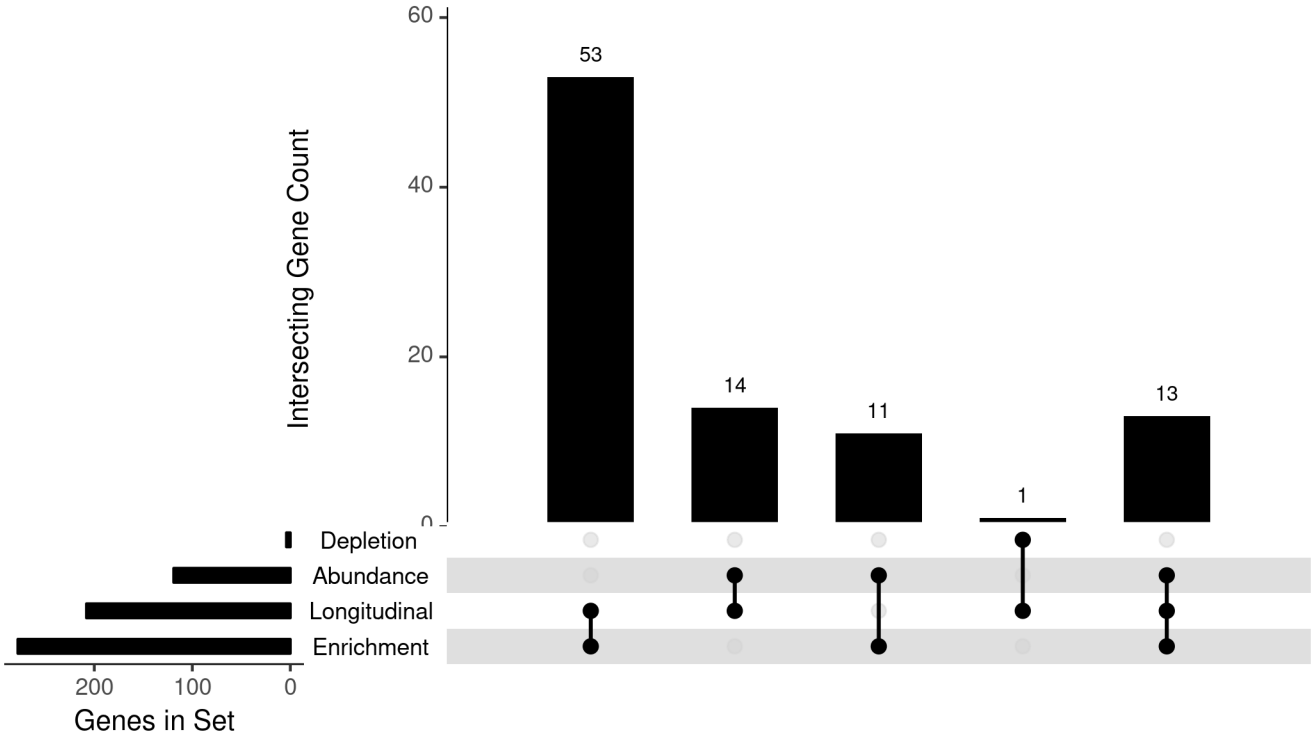

Figure 1: Intersecting gene lists identified through the various selection criteria.

Table 2: The most consistently observed genes from filtering by various criteria. The 'Criteria.' column is a count of how many times the gene was identified by these methods, while the 'Patients' column notes how many specimens collected from patients have had integration sites within the noted gene.

Gene	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
VAV1	13	110.6	37	180	EAL
RNF157	12	77.8	28	180	EAL
AKAP13	11	340.6	27	360	EAL
CARD8	11	74.4	79	180	EAL
ZZEF1	11	64.4	56	360	EAL
CRAMP1	10	53.1	30	548	EAL
PAFAH1B1	10	110.7	30	360	EAL
SRCAP	10	137.3	373	360	EAL
UBAP2L	10	235.7	30	180	EAL
ST13	8	153.7	29	180	EAL
CLK4	7	259.0	53	120	EAL
PTBP1	7	316.1	47	360	EAL
TET2	5	450.8	814	1584	EAL

Table 3: GO Biological Process. Top 6 per group. Total genes considered: 446

Group	GO ID	GO Term	Term Size	Gene Count	Adjusted P-value
1	GO:0016569	covalent chromatin modification	436	52	0.0000000
	GO:0016570	histone modification	353	45	0.0000000
	GO:0018205	peptidyl-lysine modification	297	41	0.0000000
	GO:0033044	regulation of chromosome organization	243	22	0.0106821
	GO:0043414	macromolecule methylation	230	21	0.0113995
	GO:0006479	protein methylation	142	19	0.0001516
2	GO:0043632	modification-dependent macromolecule catabolic process	477	39	0.0016006
	GO:0006511	ubiquitin-dependent protein catabolic process	464	38	0.0018954
	GO:0019941	modification-dependent protein catabolic process	469	38	0.0023447
	GO:0010498	proteasomal protein catabolic process	360	30	0.0064831
	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	325	26	0.0206822
	GO:0034976	response to endoplasmic reticulum stress	203	17	0.0437244
3	GO:0071407	cellular response to organic cyclic compound	387	32	0.0049674
	GO:0060322	head development	430	30	0.0476302
	GO:0071396	cellular response to lipid	338	29	0.0049976
	GO:0007420	brain development	407	29	0.0409789
	GO:0043009	chordate embryonic development	316	25	0.0271696
	GO:0009792	embryo development ending in birth or egg hatching	319	25	0.0303990
4	GO:0006397	mRNA processing	394	37	0.0001266
	GO:0010608	posttranscriptional regulation of gene expression	402	34	0.0023145
	GO:0006913	nucleocytoplasmic transport	342	32	0.0005569
	GO:0051169	nuclear transport	346	32	0.0006778
	GO:0019439	aromatic compound catabolic process	398	29	0.0332963
	GO:0046700	heterocycle catabolic process	394	28	0.0477359
5	GO:0051640	organelle localization	483	36	0.0127430
	GO:0010256	endomembrane system organization	325	31	0.0005086
	GO:0044770	cell cycle phase transition	449	31	0.0487192
	GO:0051656	establishment of organelle localization	319	29	0.0020083
	GO:0000226	microtubule cytoskeleton organization	384	28	0.0357725
	GO:0097435	supramolecular fiber organization	388	28	0.0405686
6	GO:0030155	regulation of cell adhesion	424	34	0.0057642
	GO:0043547	positive regulation of GTPase activity	490	34	0.0335019
	GO:0007265	Ras protein signal transduction	249	20	0.0394239
	GO:0001667	ameboidal-type cell migration	199	19	0.0111995
	GO:0018105	peptidyl-serine phosphorylation	197	18	0.0211385
	GO:0018209	peptidyl-serine modification	207	18	0.0332963
7	GO:0051223	regulation of protein transport	495	41	0.0008073
	GO:1903827	regulation of cellular protein localization	429	37	0.0008073
	GO:0032386	regulation of intracellular transport	389	32	0.0053911
	GO:0033157	regulation of intracellular protein transport	259	26	0.0008563
	GO:0034504	protein localization to nucleus	257	21	0.0332963
	GO:0051170	nuclear import	200	18	0.0246751

Table 4: KEGG Pathway analysis. Top 9 per group. Total genes considered: 209

Group	KEGG ID	Description	Term Size	Gene Count	Adjusted P-value
1	path:hsa04024	cAMP signaling pathway	131	12	0.0985244
	path:hsa00310	Lysine degradation	48	9	0.0023145
	path:hsa04310	Wnt signaling pathway	99	9	0.1206771
	path:hsa04114	Oocyte meiosis	96	9	0.1206771
	path:hsa04720	Long-term potentiation	49	8	0.0128656
	path:hsa04921	Oxytocin signaling pathway	109	8	0.2365007
	path:hsa05012	Parkinson disease	176	8	0.5810597
	path:hsa04916	Melanogenesis	56	7	0.0906693
	path:hsa04020	Calcium signaling pathway	143	7	0.5128703
2	path:hsa05022	Pathways of neurodegeneration - multiple diseases	316	18	0.2949414
	path:hsa04120	Ubiquitin mediated proteolysis	126	16	0.0023145
	path:hsa05014	Amyotrophic lateral sclerosis	262	15	0.3080526
	path:hsa04010	MAPK signaling pathway	195	14	0.1659765
	path:hsa04144	Endocytosis	205	14	0.1801055
	path:hsa04141	Protein processing in endoplasmic reticulum	134	13	0.0693902
	path:hsa05131	Shigellosis	186	11	0.3104519
	path:hsa05202	Transcriptional misregulation in cancer	105	10	0.1039590
	path:hsa05010	Alzheimer disease	245	9	0.7157590
3	path:hsa05200	Pathways in cancer	340	16	0.5139562
	path:hsa04919	Thyroid hormone signaling pathway	91	13	0.0023145
	path:hsa05166	Human T-cell leukemia virus 1 infection	166	12	0.1790553
	path:hsa05206	MicroRNAs in cancer	168	12	0.1801055
	path:hsa05203	Viral carcinogenesis	147	11	0.1767306
	path:hsa05016	Huntington disease	214	11	0.4500675
	path:hsa05165	Human papillomavirus infection	224	10	0.5840418
	path:hsa05167	Kaposi sarcoma-associated herpesvirus infection	124	9	0.2238980
	path:hsa04935	Growth hormone synthesis, secretion and action	83	8	0.1206771
4	path:hsa05205	Proteoglycans in cancer	128	13	0.0528221
	path:hsa04810	Regulation of actin cytoskeleton	151	11	0.1801055
	path:hsa05163	Human cytomegalovirus infection	154	10	0.2795651
	path:hsa04660	T cell receptor signaling pathway	80	8	0.1206771
	path:hsa04015	Rap1 signaling pathway	137	8	0.3640239
	path:hsa05135	Yersinia infection	101	7	0.2872758
	path:hsa04022	cGMP-PKG signaling pathway	107	7	0.3080526
	path:hsa05417	Lipid and atherosclerosis	137	6	0.5938126
	path:hsa04510	Focal adhesion	143	6	0.6269290
5	path:hsa05225	Hepatocellular carcinoma	100	10	0.0985244
	path:hsa04140	Autophagy - animal	120	10	0.1408152
	path:hsa04915	Estrogen signaling pathway	78	7	0.1659765
	path:hsa04926	Relaxin signaling pathway	88	7	0.2113832
	path:hsa04371	Apelin signaling pathway	95	7	0.2443199
	path:hsa04910	Insulin signaling pathway	101	7	0.2872758
	path:hsa04072	Phospholipase D signaling pathway	107	7	0.3080526
	path:hsa04014	Ras signaling pathway	149	7	0.5587694
	path:hsa05168	Herpes simplex virus 1 infection	357	6	0.9939354

Integration Frequency (Enrichment)

Table 5: Table of top 50 genes with the most frequent clonal enrichment.

Gene	Num. Patients	TDN Sites	Patient Sites	Onco-Related	Frequency Increase (%)
RBM27	6	0	12	FALSE	Inf
AGL	4	1	10	FALSE	1368.7
MCPH1	8	2	13	TRUE	854.7
BACH2	7	2	12	TRUE	781.2
NDFIP2	6	3	17	FALSE	732.3
GAK	8	3	17	TRUE	732.3
IKZF2	6	2	11	TRUE	707.8
GNA12	6	2	11	TRUE	707.8
FANCL	5	2	11	FALSE	707.8
PIKFYVE	9	2	11	FALSE	707.8
PAPOLA	6	3	16	FALSE	683.3
FAM117B	6	5	25	FALSE	634.4
CD55	9	3	14	TRUE	585.4
EP400P1	6	4	18	FALSE	560.9
FUNDC2	6	3	13	FALSE	536.4
GPHN	8	3	13	TRUE	536.4
NDUFV2	9	3	13	FALSE	536.4
UHRF1BP1	8	3	12	FALSE	487.5
RAB11FIP2	9	3	12	FALSE	487.5
TAF2	7	4	16	FALSE	487.5
PDS5B	8	4	16	TRUE	487.5
RBM39	10	5	19	TRUE	458.1
LRPPRC	10	4	15	FALSE	450.8
TET2	5	4	15	TRUE	450.8
FUS	4	3	11	TRUE	438.5
PIP5K1A	7	3	11	FALSE	438.5
LPXN	5	3	11	FALSE	438.5
RBMS1	7	3	11	FALSE	438.5
EEF2	8	3	11	FALSE	438.5
SLK	9	4	14	FALSE	414.0
MACROD2	7	4	14	FALSE	414.0
HSF2	8	4	14	FALSE	414.0
SIPA1L1	6	3	10	FALSE	389.6
VPS9D1	7	3	10	FALSE	389.6
GARS	4	3	10	FALSE	389.6
NSRP1	6	3	10	FALSE	389.6
SLBP	7	3	10	FALSE	389.6
PDCD10	8	3	10	FALSE	389.6
BZW2	6	3	10	FALSE	389.6
NAA16	6	3	10	FALSE	389.6
UBR3	5	3	10	FALSE	389.6
PELP1	11	8	26	FALSE	377.3
ZFAND3	9	4	13	FALSE	377.3
RNF10	8	5	16	FALSE	370.0
KDM4A	8	5	16	FALSE	370.0
HELLS	9	5	16	FALSE	370.0
RASA1	7	7	22	TRUE	361.6
PCMTD2	6	4	12	FALSE	340.6
ZNF512	9	4	12	FALSE	340.6
SYNJ1	5	4	12	FALSE	340.6

Integration Frequency (Depletion)

Table 6: Table of top 4 genes with the most frequent clonal depletion.

Gene	Num. Patients	TDN Sites	Patient Sites	Onco-Related	Frequency Increase (%)
RNPS1	5	69	16	FALSE	-65.9
EXOC2	5	34	10	FALSE	-56.8
EIF2B3	8	42	14	FALSE	-51.0
MROH1	8	142	71	FALSE	-26.6

Genes with the Most Abundant Clones

Table 7: Table of top 50 Genes containing the highest abundant clones.

Gene	Num. Patients	Peak Abundance	Peak Rel. Abund.	Clonal Gini Index	Onco-Related
TET2	7	814	0.989	0.920	TRUE
KCTD3	3	589	0.265	0.663	FALSE
PATL1	3	578	0.260	0.745	FALSE
PIKFYVE	8	410	0.273	0.878	FALSE
SRCAP	10	373	0.357	0.896	FALSE
MTMR3	5	261	0.041	0.872	TRUE
PCNX1	10	153	0.010	0.828	FALSE
PPP6R3	11	149	0.040	0.745	FALSE
SSH2	8	137	0.062	0.805	FALSE
RSRC1	7	109	0.014	0.811	FALSE
SNHG12	2	96	0.057	0.646	FALSE
MAPK14	8	91	0.018	0.784	TRUE
RPA3	4	87	0.011	0.767	FALSE
ZNF573	3	86	0.610	0.677	FALSE
MGA	10	85	0.013	0.762	FALSE
AQR	4	84	0.022	0.790	FALSE
LEF1	8	84	0.038	0.770	TRUE
LINC01473	2	82	0.075	0.488	FALSE
CARD8	11	79	0.056	0.700	TRUE
IQCB1	4	79	0.028	0.713	FALSE
DNAJC13	6	71	0.004	0.764	FALSE
EXOSC10	4	70	0.008	0.776	FALSE
ATP2A2	8	67	0.030	0.749	FALSE
SEC31A	6	66	0.004	0.752	FALSE
GPN1	2	62	0.017	0.711	FALSE
SMAP2	6	61	0.004	0.768	FALSE
TRIO	5	61	0.025	0.770	TRUE
ZZEF1	10	56	0.333	0.632	FALSE
CLK4	8	53	0.036	0.653	FALSE
JMJD6	2	53	0.015	0.755	FALSE
KDM5D	5	51	0.017	0.741	FALSE
UBR1	8	48	0.421	0.715	FALSE
MEMO1	4	47	0.006	0.722	FALSE
PTBP1	6	47	0.043	0.680	TRUE
DYNC1H1	6	44	0.003	0.721	FALSE
NGDN	3	44	0.005	0.623	FALSE
EIF2AK4	3	43	0.003	0.659	FALSE
MSH5-SAPCD1	4	43	0.039	0.708	FALSE
POLG2	2	43	0.003	0.708	FALSE
RASEF	1	43	0.005	0.477	FALSE
UXT-AS1	2	43	0.039	0.477	FALSE
ADD1	8	42	0.006	0.605	FALSE
GRB2	10	42	0.017	0.566	TRUE
KIFC1	7	42	0.003	0.694	FALSE
TAC3	2	42	0.018	0.477	FALSE
ZNF92	2	42	0.003	0.690	FALSE
ACTL6A	1	40	0.003	0.000	FALSE
ATP6V1G2-DDX39B	8	40	0.005	0.656	FALSE
PHF12	2	40	0.014	0.670	FALSE
MICAL2	1	39	0.028	0.000	FALSE

Longitudinal Observation

Table 8: Table of top 50 genes identified by longitudinal observations.

Gene	Time Span	Longest Time	Obs. Count	Num. Patients	Patient Sites	Peak Abund.	Onco-Related
FKBP5	1555.0	1825.0	4	11	30	15	FALSE
PTPRA	1555.0	1825.0	3	8	33	4	FALSE
TET2	1464.0	1584.0	7	5	15	814	TRUE
UBR1	1277.5	1825.0	4	7	13	48	FALSE
COX6B1	825.0	1095.0	3	9	17	5	FALSE
CCDC57	642.5	912.5	2	11	33	6	FALSE
KMT5B	642.5	912.5	2	10	26	7	FALSE
MACF1	519.5	547.5	3	12	32	11	TRUE
DNMT1	365.0	912.5	2	11	65	13	TRUE
STXBP5	350.0	360.0	4	8	15	8	FALSE
CASK	346.0	547.5	2	7	16	5	FALSE
RPTOR	346.0	360.0	2	15	85	11	FALSE
DIP2A	346.0	360.0	2	10	35	25	FALSE
PTBP1	346.0	360.0	2	7	17	47	TRUE
MIR4745	346.0	360.0	2	6	10	47	FALSE
ZZEF1	332.0	360.0	5	11	47	56	FALSE
SRCAP	332.0	360.0	5	10	21	373	FALSE
OGDH	332.0	360.0	4	4	10	17	FALSE
WDR82	277.5	547.5	3	7	20	7	TRUE
PIP5K1A	277.5	547.5	2	7	11	3	FALSE
EP400P1	260.0	270.0	3	6	18	5	FALSE
HSF1	256.0	270.0	3	12	45	10	FALSE
BOP1	256.0	270.0	3	11	34	10	TRUE
FNBP1	256.0	270.0	2	9	32	5	TRUE
PDS5B	256.0	270.0	2	8	16	10	TRUE
ACOX1	256.0	270.0	2	7	15	2	FALSE
PIK3C3	180.0	360.0	3	10	30	5	FALSE
IQGAP1	166.0	180.0	3	9	16	5	FALSE
SNAPC4	166.0	180.0	2	7	18	7	FALSE
UBE2J2	166.0	180.0	2	7	14	2	FALSE
SSH2	152.0	1095.0	4	8	26	137	FALSE
MED13	152.0	270.0	4	12	26	21	FALSE
CARD8	152.0	180.0	4	11	38	79	TRUE
LEF1	152.0	180.0	4	7	15	84	TRUE
VAV1	152.0	180.0	3	13	76	37	TRUE
STAG1	136.0	912.5	2	8	13	6	TRUE
PPP6R2	136.0	180.0	2	11	40	15	FALSE
RTTN	136.0	150.0	2	8	15	6	FALSE
MAPK8IP3	130.0	270.0	2	10	31	5	FALSE
SMG1	122.0	150.0	3	12	39	7	FALSE
INPP4B	122.0	150.0	3	11	28	3	FALSE
PIAS1	122.0	150.0	3	8	21	6	FALSE
DDX60	122.0	150.0	3	9	15	22	FALSE
ZNRD1ASP	122.0	150.0	3	6	14	4	FALSE
DPYD	122.0	150.0	2	12	33	22	FALSE
RUNX1	110.0	360.0	2	9	19	1	TRUE
ASH1L	106.0	1825.0	2	12	46	5	FALSE
WWOX	106.0	1095.0	3	5	11	5	TRUE
RFX2	106.0	360.0	2	7	14	9	TRUE
PPFIA1	106.0	270.0	4	5	11	20	FALSE

Reference Data

The NCBI RefGenes data set was used to identify gene regions (hg38) while genes identified as onco-related were from the Bushman Lab curated list of **onco-related genes**.

Gene Ontologies were extracted from the `GO.db` R-package (v3.4.1). KEGG pathways were acquired via interfacing with the KEGG web-server API through the `KEGGREST` R-package (v1.16.1). Gene lists, including RefSeq genes used for annotation of integration sites, were standardized to HGNC gene symbols (date: 2018-02-07). Groups identified in GO and KEGG analyses were determined from Jaccard distances between identified terms, followed by modularity-optimizing clustering from a weighted-undirected graph using a Louvain algorithm (**Blondel *et al.* 2008**). Terms within groups of GO or KEGG terms have greater overlap of gene lists between themselves that between terms found in other groups. This method was implemented to help reduce the functional redundancy commonly observed in GO and overlapping pathways observed with KEGG.

Comprehensive Genes of Interest Table

Table 9: Table of all genes identified within analysis.

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
VAV1	chr19	6,767,667	6,862,366	13	110.6	37	152.0	EAL
RNF157	chr17	76,137,452	76,245,311	12	77.8	28	14.0	EAL
AKAP13	chr15	85,375,615	85,754,358	11	340.6	27	7.0	EAL
CARD8	chr19	48,203,085	48,260,946	11	74.4	79	152.0	EAL
ZZEF1	chr17	3,999,444	4,147,959	11	64.4	56	332.0	EAL
CRAMP1	chr16	1,609,639	1,682,908	10	53.1	30	18.0	EAL
PAFAH1B1	chr17	2,588,628	2,690,615	10	110.7	30	7.0	EAL
SRCAP	chr16	30,694,140	30,745,129	10	137.3	373	332.0	EAL
UBAP2L	chr1	154,215,171	154,276,510	10	235.7	30	7.0	EAL
ST13	chr22	40,819,534	40,862,008	8	153.7	29	7.0	EAL
CLK4	chr5	178,597,663	178,632,053	7	259.0	53	106.0	EAL
PTBP1	chr19	792,391	817,327	7	316.1	47	346.0	EAL
TET2	chr4	105,140,874	105,284,803	5	450.8	814	1464.0	EAL
FANCA	chr16	89,732,550	89,821,657	15	94.3	21	15.0	EL
JPT2	chr16	1,673,276	1,707,072	15	106.7	23	46.0	EL
RPTOR	chr17	80,539,824	80,971,373	15	75.8	11	346.0	EL
PPP3CA	chr4	101,018,429	101,352,471	14	178.3	5	46.0	EL
ANKRD11	chr16	89,262,620	89,495,561	13	94.2	23	7.0	EL
EHMT1	chr9	137,613,991	137,841,126	13	111.1	3	50.0	EL
EP300	chr22	41,087,609	41,185,077	13	159.2	6	46.0	EL
LUC7L	chr16	183,968	234,482	13	35.9	30	7.0	AL
RABEP1	chr17	5,277,262	5,391,339	13	74.7	26	14.0	EA
JMJD1C	chr10	63,162,220	63,527,075	12	273.9	5	7.0	EL
MED13	chr17	61,937,604	62,070,282	12	154.6	21	152.0	EL
PPP6R3	chr11	68,455,717	68,620,333	12	182.9	149	14.0	EA
SMG1P1	chr16	22,432,007	22,497,220	12	225.2	3	100.0	EL
CREBBP	chr16	3,720,054	3,885,120	11	83.6	5	46.0	EL
GMDS	chr6	1,618,799	2,250,634	11	230.5	8	14.0	EL
SF1	chr11	64,759,603	64,783,844	11	84.6	16	14.0	EL
SUPT3H	chr6	44,821,729	45,383,051	11	187.4	8	14.0	EL
USP15	chr12	62,255,339	62,414,721	11	120.3	14	15.0	EL
XPO5	chr6	43,517,329	43,581,075	11	99.3	26	22.0	AL
ARHGAP15	chr2	143,124,329	143,773,352	10	120.3	7	5.0	EL
CHD4	chr12	6,565,081	6,612,433	10	131.9	19	7.0	EL
DDX42	chr17	63,769,188	63,824,317	10	114.7	6	14.0	EL
DIP2A	chr21	46,453,948	46,575,013	10	28.5	25	346.0	AL
EYA3	chr1	27,965,343	28,093,637	10	235.7	7	32.0	EL
KDM6A	chrX	44,868,174	45,117,612	10	181.5	9	106.0	EL
LRBA	chr4	150,259,658	151,020,497	10	99.7	17	106.0	EL
MGA	chr15	41,655,411	41,774,943	10	148.6	85	46.0	EA
NF1	chr17	31,089,926	31,382,677	10	193.7	14	14.0	EL

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
PIK3C3	chr18	41,950,197	42,086,482	10	267.2	5	180.0	EL
PRKACB	chr1	84,072,974	84,243,498	10	111.1	4	7.0	EL
SETD2	chr3	47,011,407	47,168,977	10	100.7	17	22.0	EL
SRRM2	chr16	2,747,328	2,776,412	10	183.3	32	1.0	EA
DDX60	chr4	168,211,290	168,323,807	9	144.8	22	122.0	EL
GRB2	chr17	75,313,075	75,410,709	9	17.5	42	14.0	AL
HELLS	chr10	94,540,766	94,607,099	9	370.0	15	106.0	EL
MED13L	chr12	115,953,575	116,282,186	9	104.0	38	7.0	EA
NDUFV2	chr18	9,097,629	9,139,345	9	536.4	15	22.0	EL
PIKFYVE	chr2	208,261,266	208,363,751	9	707.8	410	14.0	EA
RUNX1	chr21	34,782,800	35,054,298	9	248.8	1	110.0	EL
SLC6A16	chr19	49,284,634	49,330,217	9	82.1	2	14.0	EL
SMURF2	chr17	64,539,616	64,667,268	9	100.3	27	7.0	AL
TARSL2	chr15	101,648,751	101,729,442	9	340.6	22	7.0	EL
UBAC2	chr13	99,195,424	99,391,499	9	120.3	4	14.0	EL
UBR4	chr1	19,069,505	19,215,252	9	256.7	8	7.0	EL
USP25	chr21	15,725,024	15,885,071	9	218.2	10	46.0	EL
AP2B1	chr17	35,582,262	35,731,417	8	144.8	13	90.0	EL
ATP2A2	chr12	110,276,226	110,356,092	8	157.0	67	22.0	EA
DNAJC13	chr3	132,412,659	132,544,032	8	193.7	71	7.0	EA
DYNC1H1	chr14	101,959,527	102,055,798	8	193.7	44	7.0	EA
FAM13A	chr4	88,720,953	89,062,195	8	172.8	1	7.0	EL
HNRNPUL1	chr19	41,257,475	41,312,783	8	179.1	4	14.0	EL
MCPH1	chr8	6,401,591	6,653,505	8	854.7	9	7.0	EL
MOB3A	chr19	2,066,035	2,101,270	8	135.0	2	22.0	EL
PDCD4	chr10	110,866,794	110,905,006	8	105.6	26	14.0	AL
PDS5B	chr13	32,581,426	32,783,020	8	487.5	10	256.0	EL
PIAS1	chr15	68,049,178	68,196,466	8	285.5	6	122.0	EL
RSRC1	chr3	158,105,051	158,549,835	8	46.9	109	106.0	AL
SSH2	chr17	29,620,938	29,935,228	8	27.3	137	152.0	AL
STAG1	chr3	136,332,156	136,757,403	8	281.9	6	136.0	EL
LEF1	chr4	108,042,544	108,173,956	7	46.9	84	152.0	AL
MAPK14	chr6	36,022,676	36,116,236	7	108.1	91	7.0	AL
NEMP1	chr12	57,050,642	57,083,791	7	223.1	10	46.0	EL
PIP5K1A	chr1	151,193,543	151,254,531	7	438.5	3	277.5	EL
UBR1	chr15	42,937,899	43,111,088	7	-17.0	48	1277.5	AL
BRWD3	chrX	80,664,487	80,814,734	6	172.8	6	7.0	EL
EP400P1	chr12	132,079,282	132,131,340	6	560.9	5	260.0	EL
HERC4	chr10	67,916,898	68,080,346	6	34.6	35	106.0	AL
MIR4745	chr19	799,939	810,001	6	267.2	47	346.0	EL
MTOR	chr1	11,101,530	11,267,551	6	55.5	29	90.0	AL

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
NDFIP2	chr13	79,476,123	79,561,077	6	732.3	8	46.0	EL
PCNT	chr21	46,319,121	46,450,769	6	223.1	5	4.0	EL
TRIM33	chr1	114,387,776	114,516,160	6	303.9	17	106.0	EL
UBE2L3	chr22	21,544,446	21,629,034	6	193.7	3	7.0	EL
ECD	chr10	73,129,523	73,173,095	5	340.6	24	1.0	EA
MARF1	chr16	15,589,368	15,648,166	5	212.1	17	106.0	EL
PA2G4	chr12	56,099,318	56,118,910	5	130.8	38	14.0	AL
PPFIA1	chr11	70,265,699	70,389,501	5	169.3	20	106.0	EL
STAG3	chr7	100,172,723	100,219,387	5	169.3	35	0.0	EA
EHMT1	chr9	137,758,021	137,769,772	4	144.8	1	0.0	EL
KDM2A	chr11	67,114,268	67,263,079	14	14.5	7	50.0	L
NPLOC4	chr17	81,551,884	81,642,153	14	4.9	16	46.0	L
SARNP	chr12	55,747,462	55,822,756	14	136.6	5	22.0	E
SMG1P5	chr16	30,280,017	30,340,374	14	88.2	5	14.0	E
TNRC6C	chr17	77,999,236	78,113,835	14	75.2	6	22.0	E
CBFB	chr16	67,024,146	67,106,055	13	98.3	14	22.0	E
NSD1	chr5	177,128,078	177,305,213	13	12.2	6	62.0	L
UTRN	chr6	144,286,736	144,858,034	13	40.5	6	22.0	L
VPS8	chr3	184,807,142	185,057,614	13	230.5	10	46.0	E
ASH1L	chr1	155,330,260	155,567,533	12	2.4	5	106.0	L
DPYD	chr1	97,072,743	97,926,059	12	12.7	22	122.0	L
HSF1	chr8	144,286,568	144,319,726	12	-13.0	10	256.0	L
MACF1	chr1	39,079,166	39,492,138	12	6.8	11	519.5	L
PACS1	chr11	66,065,352	66,249,747	12	2.8	5	46.0	L
PSMD13	chr11	231,807	257,984	12	77.8	18	1.0	E
SAFB	chr19	5,618,034	5,673,478	12	58.2	17	0.0	E
SMG1	chr16	18,799,852	18,931,404	12	6.1	7	122.0	L
ZNF276	chr16	89,715,367	89,745,924	12	77.5	3	1.0	E
BOP1	chr8	144,257,045	144,296,438	11	8.6	10	256.0	L
CCDC57	chr17	82,096,469	82,217,829	11	-8.6	6	642.5	L
DIAPH2	chrX	96,679,662	97,605,598	11	95.8	20	46.0	E
DNMT1	chr19	10,128,343	10,200,135	11	4.9	13	365.0	L
FKBP5	chr6	35,568,584	35,733,583	11	-16.9	15	1555.0	L
FOXP1	chr3	70,949,713	71,588,989	11	88.0	4	14.0	E
FXR2	chr17	7,586,229	7,619,897	11	86.4	12	14.0	E
INPP4B	chr4	142,018,159	142,851,535	11	24.6	3	122.0	L
PELP1	chr17	4,666,383	4,709,337	11	377.3	3	14.0	E
PPP6R2	chr22	50,338,316	50,450,089	11	8.8	15	136.0	L
SEC16A	chr9	136,435,095	136,488,759	11	31.7	29	46.0	A
SNORD117	chr6	31,531,373	31,541,449	11	98.7	40	14.0	E
TRAPPC10	chr21	44,007,324	44,111,551	11	50.6	7	14.0	L

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
VPS13D	chr1	12,225,038	12,517,046	11	164.4	3	0.0	E
ZNF407	chr18	74,625,962	75,070,672	11	218.2	3	1.0	E
ATF7IP	chr12	14,360,631	14,507,935	10	66.0	8	7.0	L
CBLB	chr3	105,650,460	105,874,422	10	100.3	4	7.0	E
CLEC16A	chr16	10,939,487	11,187,189	10	291.7	9	0.0	E
CUX1	chr7	101,810,903	102,288,958	10	212.1	3	0.0	E
CYTH1	chr17	78,669,046	78,787,342	10	15.4	4	7.0	L
DDX10	chr11	108,660,024	108,945,930	10	193.7	3	14.0	E
EPB41	chr1	28,882,090	29,125,046	10	140.3	7	14.0	E
FCHSD2	chr11	72,831,744	73,147,098	10	72.0	5	22.0	E
GBE1	chr3	81,484,698	81,766,799	10	267.2	9	46.0	E
GLCCI1	chr7	7,963,742	8,094,079	10	64.2	4	84.0	L
KLF12	chr13	73,681,011	74,138,929	10	133.7	12	14.0	E
KMT5B	chr11	68,149,862	68,218,772	10	41.4	7	642.5	L
LRPPRC	chr2	43,881,223	44,001,005	10	450.8	7	0.0	E
MAPK8IP3	chr16	1,701,182	1,775,317	10	-12.4	5	130.0	L
MECP2	chrX	154,016,812	154,102,731	10	36.6	12	99.0	L
MGEA5	chr10	101,779,442	101,823,465	10	218.2	4	0.0	E
MIR6767	chr16	2,440,391	2,450,457	10	140.3	3	1.0	E
NCOA1	chr2	24,579,476	24,775,701	10	40.2	3	22.0	L
PBRM1	chr3	52,540,351	52,690,850	10	26.6	14	7.0	L
PCNX1	chr14	70,902,404	71,120,382	10	16.3	153	14.0	A
PHF14	chr7	10,968,871	11,174,623	10	125.2	3	7.0	E
PRPF6	chr20	63,976,077	64,038,100	10	120.3	9	0.0	E
RAB11FIP3	chr16	420,667	527,481	10	-18.4	7	46.0	L
RANBP9	chr6	13,616,497	13,716,564	10	167.0	6	7.0	E
RBM39	chr20	35,698,608	35,747,336	10	458.1	2	14.0	E
RBM5	chr3	50,083,907	50,123,964	10	135.0	10	1.0	E
RNF213	chr17	80,255,860	80,403,781	10	66.5	6	15.0	E
SAFB2	chr19	5,581,998	5,627,927	10	40.8	13	22.0	L
SIN3A	chr15	75,364,378	75,460,783	10	124.6	6	0.0	E
SMARCC1	chr3	47,580,887	47,786,915	10	34.4	3	7.0	L
SMG6	chr17	2,054,838	2,308,775	10	25.9	16	7.0	L
SUPT5H	chr19	39,440,545	39,481,668	10	157.0	3	0.0	E
VPS13B	chr8	99,008,265	99,882,586	10	67.9	5	0.0	E
XPO6	chr16	28,092,975	28,216,918	10	146.7	2	7.0	E
ZGPAT	chr20	63,702,441	63,741,142	10	-17.6	5	7.0	L
ZNF251	chr8	144,715,908	144,760,585	10	17.0	21	22.0	L
AKAP8L	chr19	15,375,047	15,424,121	9	157.0	3	0.0	E
AP3B1	chr5	77,997,325	78,299,755	9	157.0	3	0.0	E
CD55	chr1	207,316,471	207,365,966	9	585.4	4	0.0	E

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
CHD2	chr15	92,895,320	93,033,007	9	109.8	7	0.0	E
COX6B1	chr19	35,643,222	35,663,784	9	56.1	5	825.0	L
CPEB2	chr4	14,997,673	15,075,153	9	242.7	14	22.0	E
CSNK1D	chr17	82,237,660	82,278,742	9	22.4	8	7.0	L
DENND1B	chr1	197,499,748	197,780,493	9	10.2	3	7.0	L
DIP2B	chr12	50,499,984	50,753,667	9	55.0	4	7.0	L
DLG1	chr3	197,037,559	197,304,272	9	58.6	8	7.0	L
EIF4G3	chr1	20,801,291	21,181,888	9	102.8	3	0.0	E
ELP4	chr11	31,504,728	31,789,525	9	140.3	4	0.0	E
FNBP1	chr9	129,882,186	130,048,194	9	23.7	5	256.0	L
FOXJ3	chr1	42,171,538	42,340,877	9	92.8	12	7.0	L
FRYL	chr4	48,492,362	48,785,299	9	77.8	24	14.0	A
GANAB	chr11	62,619,825	62,651,726	9	66.0	6	7.0	L
GTF2I	chr7	74,652,664	74,765,692	9	193.7	7	0.0	E
HERC1	chr15	63,603,617	63,838,948	9	132.5	4	1.0	E
HNRNPUL2	chr11	62,707,624	62,732,385	9	36.0	9	76.0	L
IL4I1	chr19	49,884,655	49,934,539	9	-4.5	5	46.0	L
IQGAP1	chr15	90,383,240	90,507,243	9	6.8	5	166.0	L
KIAA1468	chr18	62,182,290	62,312,122	9	86.0	17	46.0	L
LOC101926943	chr7	74,683,936	74,733,918	9	193.7	7	0.0	E
LOC101929095	chr4	14,999,941	15,432,914	9	235.7	14	22.0	E
MARK3	chr14	103,380,363	103,508,829	9	80.3	15	14.0	E
NBEAL1	chr2	203,009,878	203,222,994	9	151.8	11	14.0	L
NOSIP	chr19	49,550,467	49,585,572	9	-35.7	29	0.0	A
NUP214	chr9	131,120,560	131,239,670	9	64.2	8	106.0	L
PAN3	chr13	28,133,505	28,300,338	9	127.0	8	14.0	E
PARP8	chr5	50,660,898	50,851,522	9	18.6	4	14.0	L
PLEKHA5	chr12	19,124,691	19,381,399	9	76.2	2	7.0	L
POLA2	chr11	65,256,851	65,303,685	9	25.9	9	7.0	L
POT1	chr7	124,817,385	124,934,983	9	66.5	26	0.0	A
PUM1	chr1	30,926,505	31,070,717	9	298.7	5	0.0	E
RAB11FIP2	chr10	117,999,915	118,051,884	9	487.5	19	1.0	E
COP1	chr1	175,939,825	176,212,244	9	172.8	3	14.0	E
RNF216	chr7	5,615,040	5,786,730	9	-11.9	15	106.0	L
SENP6	chr6	75,596,508	75,723,285	9	101.9	3	0.0	E
MTREX	chr5	55,302,747	55,430,581	9	212.1	6	0.0	E
SLK	chr10	103,962,184	104,034,233	9	414.0	13	1.0	E
SMCHD1	chr18	2,650,886	2,810,017	9	0.5	4	7.0	L
SYNRG	chr17	37,509,796	37,614,438	9	120.3	10	46.0	E
TCF20	chr22	42,155,012	42,288,927	9	46.9	10	7.0	L
TRAPPC8	chr18	31,824,172	31,948,128	9	83.6	4	7.0	L

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
TRPC4AP	chr20	34,997,403	35,097,815	9	212.1	3	0.0	E
UBE2I	chr16	1,304,152	1,332,018	9	120.3	4	50.0	E
VPS52	chr6	33,245,271	33,276,965	9	53.5	10	106.0	L
VPS53	chr17	503,667	719,856	9	226.4	6	0.0	E
ZCCHC7	chr9	37,115,471	37,363,148	9	148.6	7	46.0	E
ZFAND3	chr6	37,814,530	38,159,623	9	377.3	5	46.0	E
ZMYM4	chr1	35,263,966	35,426,944	9	157.0	3	0.0	E
ZNF512	chr2	27,577,968	27,628,215	9	340.6	2	0.0	E
ZNF609	chr15	64,494,419	64,691,067	9	193.7	6	0.0	E
ABCD2	chr12	39,546,219	39,625,041	8	267.2	8	14.0	E
ACSF3	chr16	89,088,808	89,160,846	8	115.4	4	0.0	E
ADD1	chr4	2,838,856	2,935,075	8	41.2	42	7.0	A
ANKHD1	chr5	140,396,813	140,544,856	8	125.2	6	7.0	E
ARID4B	chr1	235,161,894	235,333,219	8	167.0	6	0.0	E
ARIH1	chr15	72,469,325	72,591,555	8	128.5	5	7.0	L
ASXL2	chr2	25,728,752	25,883,516	8	-9.1	3	7.0	L
ATG5	chr6	106,179,476	106,330,820	8	340.6	2	0.0	E
BRWD1	chr21	39,180,477	39,318,786	8	153.7	4	14.0	E
CAMK2D	chr4	113,446,031	113,766,927	8	54.2	9	106.0	L
CAMK4	chr5	111,218,652	111,499,884	8	56.1	9	7.0	L
CDKAL1	chr6	20,529,456	21,237,403	8	31.4	5	106.0	L
CHAF1A	chr19	4,397,662	4,448,397	8	89.7	7	7.0	E
CHD3	chr17	7,879,804	7,917,757	8	179.1	3	0.0	E
CLTC	chr17	59,614,688	59,701,956	8	161.1	3	1.0	E
DAP3	chr1	155,684,090	155,744,009	8	252.5	2	0.0	E
DAZAP1	chr19	1,402,568	1,440,687	8	34.6	2	4.0	L
EED	chr11	86,239,383	86,283,810	8	311.2	6	14.0	E
EEF2	chr19	3,971,055	3,990,463	8	438.5	3	0.0	E
ERC1	chr12	986,207	1,500,933	8	64.2	4	7.0	L
FOCAD	chr9	20,653,308	21,000,955	8	285.5	17	7.0	E
GAK	chr4	844,274	937,390	8	732.3	4	14.0	E
GCN1	chr12	120,122,209	120,199,710	8	144.8	3	1.0	E
GIGYF2	chr2	232,692,304	232,865,577	8	214.7	2	0.0	E
GPHN	chr14	66,502,406	67,186,808	8	536.4	2	0.0	E
HNRNPR	chr1	23,299,689	23,349,364	8	235.7	7	46.0	E
HSF2	chr6	122,394,550	122,438,119	8	414.0	15	14.0	E
KDM4A	chr1	43,645,125	43,710,518	8	370.0	7	0.0	E
KIAA1109	chr4	122,165,602	122,367,759	8	120.3	19	1.0	E
KMT2C	chr7	152,129,924	152,441,005	8	15.4	4	7.0	L
KMT2E	chr7	105,009,189	105,119,085	8	140.3	3	0.0	E
LCOR	chr10	96,827,259	96,991,212	8	115.4	4	0.0	E

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
MIR5096	chr17	4,136,088	4,245,637	8	-20.3	9	14.0	L
MROH1	chr8	144,143,015	144,266,940	8	-26.6	5	46.0	DL
MUM1	chr19	1,349,976	1,383,431	8	11.9	4	90.0	L
NAA35	chr9	85,936,141	86,030,462	8	267.2	8	1.0	E
NCOA3	chr20	47,496,856	47,661,877	8	54.2	6	7.0	L
NEAT1	chr11	65,417,797	65,450,538	8	46.9	4	22.0	L
NELL2	chr12	44,503,274	44,918,928	8	81.4	2	4.0	L
PCM1	chr8	17,917,856	18,034,948	8	107.3	11	14.0	E
PDCD10	chr3	167,678,905	167,739,863	8	389.6	4	0.0	E
PDLIM5	chr4	94,446,856	94,673,227	8	252.5	3	4.0	E
PHF20L1	chr8	132,770,357	132,853,807	8	105.6	4	22.0	L
PLEC	chr8	143,910,146	143,981,745	8	-24.6	11	22.0	L
POGZ	chr1	151,397,723	151,464,465	8	130.8	26	0.0	A
PPIP5K2	chr5	103,115,247	103,209,911	8	172.8	3	0.0	E
PTPRA	chr20	2,859,194	3,043,669	8	67.1	4	1555.0	L
RASA2	chr3	141,482,046	141,620,363	8	115.4	7	14.0	E
RNF10	chr12	120,529,328	120,582,594	8	370.0	7	1.0	E
RRN3P2	chr16	29,069,841	29,121,717	8	144.8	2	4.0	E
RTTN	chr18	69,998,805	70,210,726	8	37.7	6	136.0	L
SACM1L	chr3	45,684,240	45,750,425	8	340.6	11	0.0	E
SEC24A	chr5	134,643,784	134,732,911	8	193.7	1	0.0	E
SLX4IP	chr20	10,430,302	10,633,034	8	151.8	3	7.0	L
SRP68	chr17	76,033,774	76,077,526	8	115.4	12	0.0	E
STIM2	chr4	26,855,690	27,030,381	8	132.5	2	4.0	E
STRN3	chr14	30,888,798	31,031,401	8	169.3	3	7.0	E
STXBP5	chr6	147,199,357	147,395,476	8	37.7	8	350.0	L
SYMPK	chr19	45,810,441	45,868,290	8	193.7	3	1.0	E
TANC2	chr17	63,004,536	63,432,706	8	340.6	11	7.0	E
TONSL	chr8	144,423,779	144,449,429	8	2.2	7	7.0	L
TOP1	chr20	41,023,817	41,129,486	8	242.7	2	0.0	E
UHRF1BP1	chr6	34,787,016	34,882,514	8	487.5	4	0.0	E
URI1	chr19	29,918,643	30,021,612	8	193.7	6	1.0	E
VAV3	chr1	107,566,159	107,969,923	8	135.0	1	0.0	E
VMP1	chr17	59,702,464	59,847,255	8	46.9	28	46.0	A
YLPM1	chr14	74,758,365	74,842,310	8	214.7	19	14.0	E
YWHAE	chr17	1,339,539	1,405,262	8	340.6	2	0.0	E
ZC3H13	chr13	45,949,464	46,057,778	8	311.2	6	46.0	E
ZFC3H1	chr12	71,604,600	71,668,969	8	340.6	4	0.0	E
ZNF148	chr3	125,220,668	125,380,354	8	153.7	6	7.0	E
ACOX1	chr17	75,936,510	75,984,434	7	4.9	2	256.0	L
ASCC3	chr6	100,503,194	100,886,372	7	327.3	4	7.0	E

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
ATF7	chr12	53,502,855	53,631,415	7	69.5	32	1.0	A
ATP8A1	chr4	42,403,374	42,662,105	7	80.8	4	14.0	L
BACH2	chr6	89,921,527	90,301,908	7	781.2	2	0.0	E
C6orf106	chr6	34,582,279	34,701,850	7	46.9	3	46.0	L
CASK	chrX	41,509,935	41,928,034	7	95.8	5	346.0	L
CCDC47	chr17	63,740,249	63,778,728	7	-13.6	6	22.0	L
CDC73	chr1	193,116,957	193,259,812	7	237.8	19	7.0	E
CHD8	chr14	21,380,193	21,442,298	7	223.1	16	14.0	E
CLEC2D	chr12	9,664,707	9,704,555	7	214.7	6	1.0	E
COG5	chr7	107,196,743	107,569,514	7	256.7	7	46.0	E
CSNK2A1	chr20	477,693	548,838	7	135.0	7	0.0	E
DEPDC5	chr22	31,748,950	31,912,034	7	223.1	4	0.0	E
DNAJC5	chr20	63,890,101	63,941,031	7	120.3	2	7.0	E
FRG1BP	chr20	30,372,163	30,424,842	7	340.6	4	7.0	E
GATAD2B	chr1	153,799,906	153,927,975	7	61.6	2	7.0	L
GMCL1	chr2	69,824,605	69,886,395	7	311.2	4	0.0	E
HTT	chr4	3,069,680	3,248,960	7	46.9	25	1.0	A
KDM7A	chr7	140,079,745	140,181,941	7	242.7	5	7.0	E
KLRG1	chr12	8,945,043	9,015,744	7	-10.2	3	7.0	L
LSM2	chr6	31,792,391	31,811,984	7	-29.3	2	14.0	L
MACROD2	chr20	13,990,499	16,058,196	7	414.0	1	0.0	E
MAN1B1	chr9	137,081,926	137,114,187	7	83.6	20	5.0	E
MAP4K3	chr2	39,244,265	39,442,312	7	46.9	15	46.0	L
MATR3	chr5	139,268,751	139,336,677	7	212.1	6	1.0	E
MIA2	chr14	39,228,909	39,356,193	7	161.1	10	7.0	E
NAA15	chr4	139,296,466	139,395,781	7	212.1	11	0.0	E
NAA38	chr17	7,851,680	7,890,388	7	-0.9	15	14.0	L
NBAS	chr2	15,161,907	15,566,348	7	22.4	4	106.0	L
NUMA1	chr11	71,997,863	72,085,693	7	135.0	3	0.0	E
NUP62	chr19	49,901,825	49,934,731	7	-12.8	5	46.0	L
NUP88	chr17	5,379,832	5,424,739	7	129.5	4	0.0	E
PAPD4	chr5	79,607,419	79,691,648	7	281.9	2	0.0	E
PHF3	chr6	63,630,801	63,720,522	7	144.8	7	4.0	E
PMS2P1	chr7	100,315,639	100,341,307	7	193.7	10	0.0	E
PPP1R16A	chr8	144,472,981	144,507,121	7	35.6	4	7.0	L
PPP4R2	chr3	72,991,742	73,074,201	7	303.9	2	7.0	E
PRKCA	chr17	66,297,807	66,815,744	7	128.5	7	7.0	L
PRKN	chr6	161,342,557	162,732,802	7	303.9	3	0.0	E
PRPSAP1	chr17	76,305,735	76,359,149	7	149.7	2	46.0	E
RAD51B	chr14	67,814,778	68,688,106	7	46.9	2	22.0	L
RASA1	chr5	87,263,252	87,396,926	7	361.6	3	0.0	E

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
RBMS1	chr2	160,267,150	160,498,807	7	438.5	5	1.0	E
RFX2	chr19	5,988,163	6,115,653	7	71.3	9	106.0	L
ROCK1	chr18	20,944,741	21,116,851	7	105.6	13	14.0	E
RUNX2	chr6	45,323,316	45,556,082	7	248.8	8	14.0	E
SENP3-EIF4A1	chr17	7,556,991	7,584,006	7	157.0	5	46.0	E
SEPT7	chr7	35,795,985	35,912,105	7	316.1	10	7.0	E
SLBP	chr4	1,687,730	1,717,741	7	389.6	2	0.0	E
SMAD2	chr18	47,828,094	47,936,146	7	172.8	7	0.0	E
SNAPC4	chr9	136,370,568	136,403,437	7	103.4	7	166.0	L
SNTB1	chr8	120,530,744	120,817,069	7	172.8	3	4.0	E
SPEN	chr1	15,842,863	15,945,455	7	58.2	2	7.0	L
SPG7	chr16	89,503,387	89,562,768	7	7.7	10	7.0	L
SYNE1	chr6	152,116,683	152,642,399	7	46.9	22	46.0	L
SYNE2	chr14	63,847,964	64,231,451	7	69.5	8	22.0	L
TAF2	chr8	119,725,773	119,837,834	7	487.5	8	1.0	E
THEMIS	chr6	127,703,193	127,923,631	7	-2.1	5	106.0	L
TTC21B	chr2	165,868,361	165,958,838	7	36.4	5	46.0	L
UBE2J2	chr1	1,248,911	1,278,854	7	-37.7	2	166.0	L
UBE3A	chr15	25,332,248	25,444,028	7	149.7	10	0.0	E
UBR5	chr8	102,247,273	102,417,689	7	95.8	19	7.0	L
VPS9D1	chr16	89,702,132	89,725,986	7	389.6	5	0.0	E
VRK3	chr19	49,971,466	50,030,548	7	-13.9	2	7.0	L
WDR82	chr3	52,249,421	52,283,643	7	33.5	7	277.5	L
YTHDF3	chr8	63,163,552	63,217,788	7	63.2	13	7.0	L
ZNF81	chrX	47,831,901	47,927,256	7	175.4	7	7.0	E
ZNRF2	chr7	30,279,306	30,372,692	7	144.8	3	14.0	E
ANXA1	chr9	73,146,730	73,175,394	6	144.8	5	14.0	L
ARHGEF6	chrX	136,660,550	136,786,344	6	193.7	5	7.0	E
ATE1	chr10	121,735,420	121,933,801	6	267.2	14	46.0	E
ATP9B	chr18	79,064,274	79,383,282	6	79.5	2	7.0	L
BAG6	chr6	31,634,027	31,657,700	6	22.4	36	46.0	A
BCAS3	chr17	60,672,774	61,397,838	6	-36.1	2	7.0	L
BCKDHB	chr6	80,101,609	80,351,270	6	267.2	3	0.0	E
BIRC6	chr2	32,352,027	32,623,898	6	311.2	3	0.0	E
BUB1B	chr15	40,156,008	40,226,136	6	267.2	7	14.0	E
BZW2	chr7	16,641,133	16,711,523	6	389.6	6	0.0	E
CD96	chr3	111,537,078	111,670,991	6	252.5	6	0.0	E
CHD1	chr5	98,850,203	98,931,534	6	277.7	8	1.0	E
CHMP2B	chr3	87,222,262	87,260,548	6	88.8	24	7.0	A
CLASP2	chr3	33,491,245	33,723,213	6	138.7	5	7.0	L
CUL3	chr2	224,465,149	224,590,397	6	252.5	8	22.0	E

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
DERL2	chr17	5,466,250	5,491,230	6	135.0	37	0.0	A
DNAJC1	chr10	21,751,547	22,008,721	6	17.5	38	7.0	A
DOT1L	chr19	2,159,148	2,237,578	6	23.7	6	14.0	L
ERGIC2	chr12	29,335,645	29,386,210	6	169.3	3	0.0	E
FAM117B	chr2	202,630,177	202,774,757	6	634.4	6	14.0	E
FUNDC2	chrX	155,021,788	155,061,916	6	536.4	9	46.0	E
GNA12	chr7	2,723,105	2,849,325	6	707.8	2	0.0	E
GTDC1	chr2	143,941,013	144,337,534	6	256.7	9	7.0	E
IKZF2	chr2	212,994,685	213,156,609	6	707.8	1	0.0	E
MED12L	chr3	151,081,797	151,441,677	6	169.3	7	7.0	E
MIR5096	chr1	15,866,148	15,910,467	6	79.5	2	7.0	L
MIR5096	chr22	37,663,025	38,029,093	6	12.3	6	7.0	L
MMP23A	chr1	1,627,779	1,706,808	6	58.2	17	14.0	L
NAA16	chr13	41,306,204	41,382,030	6	389.6	2	1.0	E
NFKBIL1	chr6	31,541,850	31,563,829	6	-19.5	4	7.0	L
NSRP1	chr17	30,111,806	30,191,475	6	389.6	2	0.0	E
NUCB1	chr19	48,895,049	48,928,283	6	303.9	2	0.0	E
NUCB1-AS1	chr19	48,905,929	48,923,891	6	303.9	2	0.0	E
OPRM1	chr6	154,005,495	154,251,867	6	46.9	3	14.0	L
PAPOLA	chr14	96,497,375	96,572,116	6	683.3	3	0.0	E
PCMTD2	chr20	64,250,694	64,281,226	6	340.6	17	1.0	E
PDE12	chr3	57,551,246	57,661,480	6	303.9	3	0.0	E
PHACTR4	chr1	28,364,581	28,505,369	6	1.0	3	22.0	L
RAB28	chr4	13,362,722	13,489,365	6	172.8	12	0.0	E
RBM27	chr5	146,198,599	146,294,221	6	Inf	3	0.0	E
RIPOR2	chr6	24,799,280	25,047,288	6	46.9	10	7.0	L
RSBN1L	chr7	77,691,425	77,784,803	6	193.7	31	1.0	A
SEC23A	chr14	39,026,918	39,108,528	6	73.6	7	7.0	L
SHPRH	chr6	145,879,808	145,969,097	6	267.2	4	0.0	E
SIPA1L1	chr14	71,524,311	71,746,229	6	389.6	22	7.0	E
SPPL3	chr12	120,757,509	120,909,352	6	57.4	9	14.0	L
TCF25	chr16	89,868,585	89,916,384	6	-17.0	5	106.0	L
UBE2F-SCLY	chr2	237,961,944	238,104,413	6	34.6	6	46.0	L
UNKL	chr16	1,358,204	1,419,720	6	79.5	7	15.0	L
WWP1	chr8	86,337,764	86,472,949	6	177.4	3	7.0	E
ZNF473	chr19	50,020,892	50,053,774	6	4.9	3	22.0	L
ZNRD1ASP	chr6	29,996,010	30,066,189	6	128.5	4	122.0	L
BMP2K	chr4	78,771,377	78,917,187	5	303.9	3	0.0	E
CLEC2B	chr12	9,847,368	9,874,859	5	252.5	7	0.0	E
CSNK1G1	chr15	64,160,516	64,361,259	5	33.5	8	7.0	L
CYLD	chr16	50,737,049	50,806,935	5	172.8	3	7.0	E

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
ELMO1	chr7	36,847,905	37,454,326	5	6.8	34	46.0	A
EVL	chr14	99,966,474	100,149,236	5	13.0	4	7.0	L
FANCL	chr2	58,154,242	58,246,380	5	707.8	6	0.0	E
HIVEP1	chr6	12,007,490	12,169,999	5	169.3	1	0.0	E
HS2ST1	chr1	86,909,651	87,114,998	5	303.9	12	7.0	E
HSF5	chr17	58,415,166	58,493,401	5	46.9	34	1.0	A
IQCB1	chr3	121,764,760	121,840,079	5	144.8	79	15.0	A
KIFC1	chr6	33,386,535	33,414,922	5	46.9	42	7.0	A
KMT2D	chr12	49,013,974	49,060,324	5	7.7	33	0.0	A
LPXN	chr11	58,521,870	58,583,239	5	438.5	9	46.0	E
MBD3	chr19	1,571,670	1,597,761	5	267.2	2	7.0	E
MIR5096	chr1	235,507,822	235,723,113	5	157.0	1	0.0	L
N4BP1	chr16	48,533,725	48,615,209	5	291.7	32	106.0	A
PAG1	chr8	80,962,810	81,117,068	5	1.0	2	32.0	L
PDE7A	chr8	65,709,333	65,846,734	5	79.5	4	7.0	L
PHF20	chr20	35,767,000	35,955,366	5	7.7	38	7.0	A
PLPPR3	chr19	807,487	826,952	5	169.3	6	1.0	E
POM121	chr7	72,874,334	72,956,440	5	414.0	29	1.0	A
RELB	chr19	44,996,448	45,043,198	5	223.1	2	0.0	E
SEC31A	chr4	82,813,508	82,905,571	5	46.9	66	7.0	A
SEPT9	chr17	77,276,409	77,505,596	5	-16.1	27	7.0	A
SFI1	chr22	31,491,138	31,623,551	5	-33.2	24	7.0	A
SMAP2	chr1	40,368,705	40,428,326	5	120.3	61	7.0	A
STX8	chr17	9,245,470	9,580,958	5	109.8	4	7.0	L
SYNJ1	chr21	32,623,758	32,733,040	5	340.6	4	0.0	E
TNKS	chr8	9,550,934	9,787,346	5	340.6	8	7.0	E
TTC3	chr21	37,068,183	37,208,118	5	223.1	2	0.0	E
UBR3	chr2	169,822,507	170,089,129	5	389.6	11	46.0	E
WWOX	chr16	78,094,412	79,217,667	5	24.3	5	106.0	L
AGL	chr1	99,845,083	99,929,023	4	1368.7	4	0.0	E
ANKRD46	chr8	100,504,751	100,564,786	4	95.8	24	7.0	A
AQR	chr15	34,851,350	34,974,794	4	28.5	84	14.0	A
CAAP1	chr9	26,835,684	26,897,828	4	-8.2	27	46.0	A
CNOT6	chr5	180,489,398	180,583,405	4	22.4	2	7.0	L
DENND6A	chr3	57,620,453	57,698,089	4	267.2	3	0.0	E
EXOSC10	chr1	11,061,612	11,104,910	4	71.3	70	7.0	A
FAM13B	chr5	137,932,915	138,038,113	4	223.1	3	7.0	E
FUS	chr16	31,175,109	31,199,871	4	438.5	12	0.0	E
GARS	chr7	30,589,734	30,639,032	4	389.6	3	0.0	E
GOLPH3L	chr1	150,641,224	150,702,196	4	-26.6	24	7.0	A
KDM5D	chrY	19,700,414	19,749,939	4	144.8	2	14.0	A

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
MAD1L1	chr7	1,810,791	2,237,948	4	20.2	35	46.0	A
MAP2K2	chr19	4,085,321	4,129,129	4	46.9	2	106.0	L
MEMO1	chr2	31,862,809	32,016,052	4	-46.6	47	7.0	A
MSH5-SAPCD1	chr6	31,734,947	31,769,847	4	-51.0	43	7.0	A
MTMR3	chr22	29,878,168	30,035,868	4	-17.4	261	106.0	A
OGDH	chr7	44,601,521	44,714,070	4	-22.7	17	332.0	L
PATL1	chr11	59,631,715	59,674,038	4	95.8	578	332.0	A
PDCD11	chr10	103,391,654	103,451,262	4	193.7	27	152.0	A
PDE3B	chr11	14,638,722	14,877,058	4	95.8	35	7.0	A
PEX5	chr12	7,184,162	7,223,573	4	340.6	2	0.0	E
RAB18	chr10	27,499,173	27,547,237	4	17.5	24	7.0	A
RMND5A	chr2	86,715,290	86,783,041	4	Inf	26	0.0	A
RPA3	chr7	7,631,562	7,723,607	4	83.6	87	106.0	A
TMTC3	chr12	88,137,295	88,204,887	4	223.1	2	0.0	E
TRIO	chr5	14,138,701	14,515,204	4	928.1	61	106.0	A
XPO1	chr2	61,472,933	61,543,283	4	83.6	25	106.0	A
ZC3H7A	chr16	11,745,585	11,802,258	4	311.2	11	1.0	E
AKAP9	chr7	91,935,874	92,115,673	3	17.5	25	0.0	A
CHD1L	chr1	147,168,193	147,300,766	3	Inf	25	1.0	A
DCUN1D4	chr4	51,837,999	51,921,837	3	22.4	32	106.0	A
EIF2AK4	chr15	39,929,123	40,040,596	3	634.4	43	7.0	A
NGDN	chr14	23,464,688	23,483,193	3	120.3	44	0.0	A
PRKD2	chr19	46,669,315	46,722,127	3	144.8	24	22.0	A
RABGAP1	chr9	122,936,008	123,109,868	3	2.8	29	7.0	A
SNAP29	chr22	20,854,003	20,896,213	3	487.5	27	7.0	A
STT3B	chr3	31,527,500	31,642,622	3	252.5	6	0.0	E
ZNF573	chr19	37,733,301	37,784,590	3	17.5	86	735.0	A
C20orf196	chr20	5,745,386	5,869,407	2	-2.1	1	0.0	A
CRTAP	chr3	33,108,957	33,152,773	2	193.7	35	7.0	A
GPN1	chr2	27,623,647	27,655,846	2	46.9	62	1.0	A
JMJD6	chr17	76,707,831	76,731,799	2	193.7	53	1.0	A
KCTD3	chr1	215,562,378	215,626,821	2	-26.6	1	0.0	A
LINC01473	chr2	186,028,533	186,091,317	2	Inf	82	7.0	A
LOC101927151	chr19	27,788,466	27,811,780	2	193.7	31	46.0	A
PHF12	chr17	28,900,252	28,956,490	2	17.5	40	106.0	A
POLG2	chr17	64,472,784	64,502,066	2	83.6	43	7.0	A
RASEF	chr9	82,974,584	83,068,128	2	Inf	43	46.0	A
SNHG12	chr1	28,573,537	28,586,854	2	340.6	96	332.0	A
TAC3	chr12	57,004,996	57,021,560	2	-51.0	42	7.0	A
TGFBR2	chr3	30,601,501	30,699,141	2	193.7	31	7.0	A
ACTL6A	chr3	179,557,879	179,593,405	1	-70.6	40	0.0	A

Table 9: Table of all genes identified within analysis. *(continued)*

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
C19orf48	chr19	50,792,692	50,809,853	1	46.9	28	46.0	A
CD109	chr6	73,691,084	73,833,317	1	-81.6	32	0.0	A
KARS	chr16	75,622,723	75,652,687	1	46.9	24	0.0	A
MICAL2	chr11	12,105,575	12,268,790	1	-26.6	39	15.0	A
RBAK-RBAKDN	chr7	5,040,820	5,078,223	1	46.9	28	7.0	A
RTCA-AS1	chr1	100,259,741	100,271,174	1	Inf	27	0.0	A
UXT-AS1	chrX	47,653,832	47,665,111	1	Inf	43	7.0	A
ZNF92	chr7	65,368,798	65,406,135	1	Inf	42	7.0	A
EIF2B3	chr1	44,845,521	44,991,722	8	-51.0	6	1.0	D
EXOC2	chr6	480,137	698,141	5	-56.8	4	0.0	D
RNPS1	chr16	2,248,115	2,273,412	5	-65.9	2	0.0	D