Supplementary Report 2:
Genes of interest marked by vector integration
CLL Patients only (CR/PRtd & PR/NR Response Groups)

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 29 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	64	*/* 25.00	*/* 12.50	/ 0.000	/ 7.81	*/* 9.38	/ 1.562
Depletion	38	/ 7.89	/ 10.53	/ 0.000	/ 2.63	/ 7.89	/ 0.000
Abundance	120	*/* 20.83	/ 5.83	/ 0.000	*/* 9.17	/ 5.00	/ 0.833
Longitudinal	208	*/* 25.48	*/* 12.02	/ 0.481	*/* 12.50	*/* 12.02	*/* 1.442
Composite	343	*/* 22.16	*/* 8.75	/ 0.292	*/* 10.50	*/* 9.33	*/ 0.875

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%

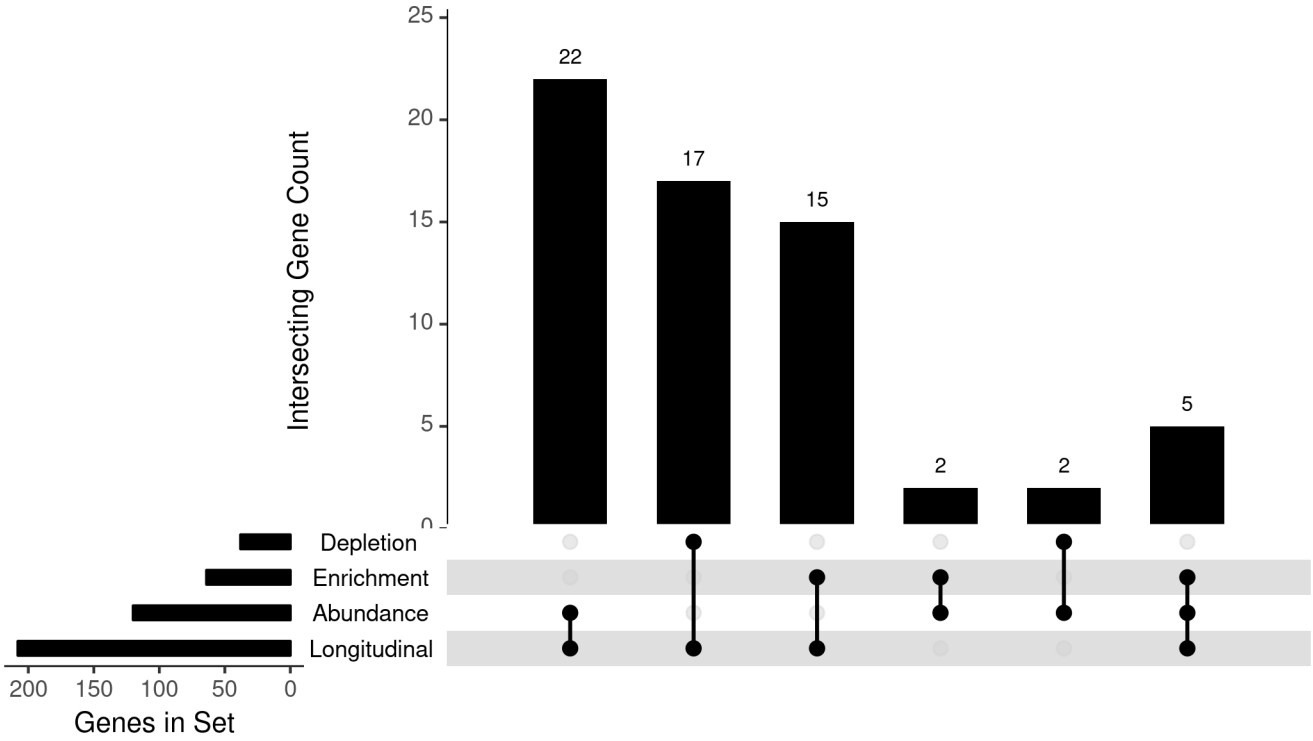

Figure 1: Intersecting gene lists identified through the various selection criteria.

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
AKAP13	11	191.5	27	360	EAL
UBAP2L	10	122.1	30	180	EAL
CLK4	7	137.5	53	120	EAL
PTBP1	7	175.3	47	360	EAL
TET2	5	264.4	814	1584	EAL

Table 3: GO Biological Process. Top 7 per group. Total genes considered: 314

Group	GO ID	GO Term	Term Size	Gene Count	Adjusted P-value
1	GO:0045861	negative regulation of proteolysis	182	13	0.0209024
	GO:0009895	negative regulation of catabolic process	187	13	0.0235506
	GO:0031330	negative regulation of cellular catabolic process	153	12	0.0176957
	GO:0061136	regulation of proteasomal protein catabolic process	138	11	0.0209024
	GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	97	8	0.0387819
	GO:0036503	ERAD pathway	71	7	0.0228095
	GO:0042177	negative regulation of protein catabolic process	84	7	0.0457042
2	GO:0016569	covalent chromatin modification	436	41	0.0000000
	GO:0016570	histone modification	353	36	0.0000000
	GO:0018205	peptidyl-lysine modification	297	30	0.0000000
	GO:0071396	cellular response to lipid	338	22	0.0055700
	GO:0048545	response to steroid hormone	248	16	0.0209024
	GO:0043414	macromolecule methylation	230	15	0.0231731
	GO:0033044	regulation of chromosome organization	243	15	0.0372852
3	GO:0051223	regulation of protein transport	495	33	0.0001555
	GO:1903827	regulation of cellular protein localization	429	26	0.0053968
	GO:0032386	regulation of intracellular transport	389	25	0.0031168
	GO:0080135	regulation of cellular response to stress	457	25	0.0209024
	GO:0006913	nucleocytoplasmic transport	342	23	0.0028779
	GO:0051169	nuclear transport	346	23	0.0033542
	GO:0006281	DNA repair	432	23	0.0334440
4	GO:0034330	cell junction organization	182	12	0.0417958
	GO:0007160	cell-matrix adhesion	131	11	0.0154991
	GO:0034329	cell junction assembly	139	11	0.0209024
	GO:0007162	negative regulation of cell adhesion	148	11	0.0267311
	GO:0001952	regulation of cell-matrix adhesion	66	9	0.0012082
	GO:0010810	regulation of cell-substrate adhesion	114	9	0.0352756
	GO:0007044	cell-substrate junction assembly	63	7	0.0169736
5	GO:0051640	organelle localization	483	27	0.0129509
	GO:0010256	endomembrane system organization	325	26	0.0000570
	GO:0120031	plasma membrane bounded cell projection assembly	440	23	0.0392466
	GO:0030031	cell projection assembly	442	23	0.0412216
	GO:0044770	cell cycle phase transition	449	23	0.0417958
	GO:0044772	mitotic cell cycle phase transition	425	22	0.0432627
	GO:0051656	establishment of organelle localization	319	20	0.0140352
6	GO:0030155	regulation of cell adhesion	424	27	0.0021359
	GO:0032101	regulation of response to external stimulus	402	25	0.0049258
	GO:0042110	T cell activation	314	19	0.0209024
	GO:0061061	muscle structure development	348	19	0.0417958
	GO:0030099	myeloid cell differentiation	234	18	0.0026869
	GO:0009314	response to radiation	317	18	0.0404364
	GO:0002521	leukocyte differentiation	291	17	0.0381858

Table 4: KEGG Pathway analysis. Top 10 per group. Total genes considered: 156

Group	KEGG ID	Description	Term Size	Gene Count	Adjusted P-value
1	path:hsa05022	Pathways of neurodegeneration - multiple diseases	316	14	0.1869642
	path:hsa04010	MAPK signaling pathway	195	12	0.0667815
	path:hsa05131	Shigellosis	186	10	0.1251238
	path:hsa05014	Amyotrophic lateral sclerosis	262	10	0.3376286
	path:hsa05163	Human cytomegalovirus infection	154	9	0.1023397
	path:hsa05167	Kaposi sarcoma-associated herpesvirus infection	124	8	0.0956112
	path:hsa04141	Protein processing in endoplasmic reticulum	134	8	0.1086580
	path:hsa05132	Salmonella infection	188	7	0.3807339
	path:hsa05010	Alzheimer disease	245	7	0.5621436
	path:hsa05168	Herpes simplex virus 1 infection	357	6	0.9246679
2	path:hsa04070	Phosphatidylinositol signaling system	83	7	0.0486522
	path:hsa00562	Inositol phosphate metabolism	62	6	0.0471307
3	path:hsa04024	cAMP signaling pathway	131	10	0.0458569
	path:hsa04720	Long-term potentiation	49	8	0.0014174
	path:hsa04114	Oocyte meiosis	96	8	0.0458569
	path:hsa05415	Diabetic cardiomyopathy	124	8	0.0956112
	path:hsa04916	Melanogenesis	56	7	0.0180511
	path:hsa04310	Wnt signaling pathway	99	7	0.0851782
	path:hsa05152	Tuberculosis	109	7	0.1023397
	path:hsa04120	Ubiquitin mediated proteolysis	126	7	0.1479512
	path:hsa04020	Calcium signaling pathway	143	6	0.3154989
	path:hsa05012	Parkinson disease	176	6	0.4519734
4	path:hsa04140	Autophagy - animal	120	10	0.0368957
	path:hsa05205	Proteoglycans in cancer	128	10	0.0458569
	path:hsa04144	Endocytosis	205	10	0.1712077
	path:hsa05225	Hepatocellular carcinoma	100	9	0.0368957
	path:hsa04714	Thermogenesis	154	9	0.1023397
	path:hsa00310	Lysine degradation	48	8	0.0014174
	path:hsa04915	Estrogen signaling pathway	78	7	0.0458569
	path:hsa04072	Phospholipase D signaling pathway	107	7	0.1010930
	path:hsa04810	Regulation of actin cytoskeleton	151	7	0.2369929
	path:hsa04151	PI3K-Akt signaling pathway	225	6	0.6001654
5	path:hsa05200	Pathways in cancer	340	15	0.1771734
	path:hsa04919	Thyroid hormone signaling pathway	91	11	0.0014174
	path:hsa05203	Viral carcinogenesis	147	9	0.0978172
	path:hsa05166	Human T-cell leukemia virus 1 infection	166	9	0.1251238
	path:hsa05206	MicroRNAs in cancer	168	9	0.1293045
	path:hsa05165	Human papillomavirus infection	224	9	0.3109450
	path:hsa04935	Growth hormone synthesis, secretion and action	83	8	0.0368957
	path:hsa05016	Huntington disease	214	8	0.3732704
	path:hsa05164	Influenza A	111	7	0.1058513
	path:hsa05161	Hepatitis B	117	7	0.1251238

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	871.8
MCPH1	8	2	13	TRUE	531.7
BACH2	7	2	12	TRUE	483.1
NDFIP2	6	3	17	FALSE	450.7
GAK	8	3	17	TRUE	450.7
GNA12	6	2	11	TRUE	434.5
FANCL	5	2	11	FALSE	434.5
IKZF2	6	2	11	TRUE	434.5
PIKFYVE	9	2	11	FALSE	434.5
PAPOLA	6	3	16	FALSE	418.3
FAM117B	6	5	25	FALSE	385.9
CD55	9	3	14	TRUE	353.5
EP400P1	6	4	18	FALSE	337.3
FUNDC2	6	3	13	FALSE	321.1
NDUFV2	9	3	13	FALSE	321.1
GPHN	8	3	13	TRUE	321.1
RAB11FIP2	9	3	12	FALSE	288.7
PDS5B	8	4	16	TRUE	288.7
TAF2	7	4	16	FALSE	288.7
UHRF1BP1	8	3	12	FALSE	288.7
RBM39	10	5	19	TRUE	269.3
TET2	5	4	15	TRUE	264.4
LRPPRC	10	4	15	FALSE	264.4
HSF2	8	4	14	FALSE	240.1
MACROD2	7	4	14	FALSE	240.1
SLK	9	4	14	FALSE	240.1
PELP1	11	8	26	FALSE	215.8
ZFAND3	9	4	13	FALSE	215.8
KDM4A	8	5	16	FALSE	211.0
HELLS	9	5	16	FALSE	211.0
RNF10	8	5	16	FALSE	211.0
RASA1	7	7	22	TRUE	205.4
TANC2	8	6	18	FALSE	191.5
YWHAE	8	7	21	TRUE	191.5
ATG5	8	6	18	FALSE	191.5
AKAP13	11	11	33	TRUE	191.5
TNKS	5	5	15	FALSE	191.5
SACM1L	8	6	18	FALSE	191.5
ASCC3	7	11	32	FALSE	182.7
SEPT7	7	6	17	FALSE	175.3
PTBP1	7	6	17	TRUE	175.3
PUM1	9	7	19	FALSE	163.8
CLEC16A	10	12	32	FALSE	159.1
FOCAD	8	8	21	FALSE	155.1
PIAS1	8	8	21	FALSE	155.1
CHD1	6	7	18	FALSE	149.9
JMJD1C	12	11	28	FALSE	147.4
GBE1	10	8	20	FALSE	142.9
ABCD2	8	10	25	FALSE	142.9

Integration Frequency (Depletion)

Table 6: Table of top 38 genes with the most frequent clonal depletion.

Gene	Num. Patients	TDN Sites	Patient Sites	Onco-Related	Frequency Increase (%)
RNPS1	5	69	16	FALSE	-77.5
EXOC2	5	34	10	FALSE	-71.4
EIF2B3	8	42	14	FALSE	-67.6
NARFL	7	25	10	FALSE	-61.1
USP34	5	25	10	FALSE	-61.1
TRAF2	8	53	22	FALSE	-59.7
QRICH1	6	45	19	FALSE	-59.0
UBE2J2	7	33	14	FALSE	-58.8
HAGH	5	28	12	FALSE	-58.4
IP6K1	9	60	26	FALSE	-57.9
BCAS3	6	23	10	TRUE	-57.7
NOSIP	9	64	28	FALSE	-57.5
SFI1	5	22	10	FALSE	-55.8
ZNF598	4	22	10	FALSE	-55.8
NPEPPS	9	26	12	FALSE	-55.1
WDR90	8	23	11	FALSE	-53.5
PPP3CC	7	27	13	FALSE	-53.2
LSM2	7	27	13	FALSE	-53.2
WNK1	5	28	14	FALSE	-51.4
IFT140	6	32	16	FALSE	-51.4
TSC2	8	42	21	TRUE	-51.4
MROH1	8	142	71	FALSE	-51.4
PLEC	8	37	19	FALSE	-50.1
HCG20	7	38	20	FALSE	-48.9
MIR5096	8	35	19	FALSE	-47.2
NFKBIL1	6	31	17	FALSE	-46.7
ANKFY1	8	36	20	FALSE	-46.0
RAB11FIP3	10	54	30	FALSE	-46.0
ZGPAT	10	41	23	FALSE	-45.5
FKBP5	11	53	30	FALSE	-45.0
SIRT3	10	37	21	FALSE	-44.8
HSF1	12	76	45	FALSE	-42.5
MAPK8IP3	10	52	31	FALSE	-42.1
CCDC57	11	53	33	FALSE	-39.5
ASH1L	12	66	46	FALSE	-32.3
PACS1	12	150	105	FALSE	-32.0
DNMT1	11	91	65	TRUE	-30.6
NPLOC4	14	217	155	FALSE	-30.6

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	6	814	0.989	0.918	TRUE
KCTD3	3	589	0.265	0.663	FALSE
PATL1	4	578	0.260	0.793	FALSE
PIKFYVE	9	410	0.273	0.885	FALSE
SRCAP	10	373	0.357	0.896	FALSE
MTMR3	4	261	0.041	0.859	TRUE
PCNX1	10	153	0.010	0.825	FALSE
PPP6R3	12	149	0.040	0.733	FALSE
SSH2	8	137	0.062	0.805	FALSE
RSRC1	8	109	0.014	0.812	FALSE
SNHG12	2	96	0.057	0.646	FALSE
MAPK14	7	91	0.006	0.784	TRUE
RPA3	4	87	0.020	0.752	FALSE
ZNF573	3	86	0.610	0.677	FALSE
MGA	11	85	0.013	0.754	FALSE
AQR	4	84	0.022	0.790	FALSE
LEF1	7	84	0.038	0.771	TRUE
LINC01473	3	82	0.075	0.643	FALSE
CARD8	11	79	0.056	0.702	TRUE
IQCB1	5	79	0.028	0.752	FALSE
DNAJC13	8	71	0.004	0.765	FALSE
EXOSC10	4	70	0.008	0.776	FALSE
ATP2A2	8	67	0.030	0.749	FALSE
SEC31A	5	66	0.004	0.736	FALSE
GPN1	2	62	0.017	0.711	FALSE
SMAP2	5	61	0.004	0.758	FALSE
TRIO	6	61	0.025	0.769	TRUE
ZZEF1	11	56	0.333	0.626	FALSE
CLK4	7	53	0.036	0.659	FALSE
IFNGR2	2	53	0.722	0.635	TRUE
JMJD6	2	53	0.015	0.755	FALSE
KDM5D	7	51	0.017	0.747	FALSE
UBR1	7	48	0.421	0.722	FALSE
MEMO1	5	47	0.006	0.733	FALSE
PTBP1	7	47	0.043	0.672	TRUE
DYNC1H1	8	44	0.003	0.709	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	1	43	0.003	0.609	FALSE
RASEF	2	43	0.005	0.622	FALSE
UXT-AS1	2	43	0.039	0.477	FALSE
ADD1	8	42	0.011	0.608	FALSE
GRB2	9	42	0.017	0.592	TRUE
KIFC1	6	42	0.003	0.697	FALSE
TAC3	2	42	0.018	0.477	FALSE
ZNF92	3	42	0.031	0.707	FALSE
ACTL6A	1	40	0.003	0.000	FALSE
ATP6V1G2-DDX39B	11	40	0.005	0.621	FALSE
PHF12	2	40	0.014	0.670	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
AKAP13	chr15	85,375,615	85,754,358	11	191.5	27	7.0	EAL
UBAP2L	chr1	154,215,171	154,276,510	10	122.1	30	7.0	EAL
CLK4	chr5	178,597,663	178,632,053	7	137.5	53	106.0	EAL
PTBP1	chr19	792,391	817,327	7	175.3	47	346.0	EAL
TET2	chr4	105,140,874	105,284,803	5	264.4	814	1464.0	EAL
PPP3CA	chr4	101,018,429	101,352,471	14	84.1	5	46.0	EL
LUC7L	chr16	183,968	234,482	13	-10.1	30	7.0	AL
VAV1	chr19	6,767,667	6,862,366	13	39.4	37	152.0	AL
JMJD1C	chr10	63,162,220	63,527,075	12	147.4	5	7.0	EL
PPP6R3	chr11	68,455,717	68,620,333	12	87.2	149	14.0	EA
RNF157	chr17	76,137,452	76,245,311	12	17.6	28	14.0	AL
SMG1P1	chr16	22,432,007	22,497,220	12	115.2	3	100.0	EL
CARD8	chr19	48,203,085	48,260,946	11	15.4	79	152.0	AL
SUPT3H	chr6	44,821,729	45,383,051	11	90.1	8	14.0	EL
XPO5	chr6	43,517,329	43,581,075	11	31.9	26	22.0	AL
ZZEF1	chr17	3,999,444	4,147,959	11	8.7	56	332.0	AL
CRAMP1	chr16	1,609,639	1,682,908	10	1.3	30	18.0	AL
DIP2A	chr21	46,453,948	46,575,013	10	-15.0	25	346.0	AL
EYA3	chr1	27,965,343	28,093,637	10	122.1	7	32.0	EL
NF1	chr17	31,089,926	31,382,677	10	94.4	14	14.0	EL
PAFAH1B1	chr17	2,588,628	2,690,615	10	39.4	30	7.0	AL
PIK3C3	chr18	41,950,197	42,086,482	10	142.9	5	180.0	EL
SRCAP	chr16	30,694,140	30,745,129	10	57.0	373	332.0	AL
GRB2	chr17	75,313,075	75,410,709	9	-22.3	42	14.0	AL
HELLS	chr10	94,540,766	94,607,099	9	211.0	15	106.0	EL
NDUFV2	chr18	9,097,629	9,139,345	9	321.1	15	22.0	EL
PIKFYVE	chr2	208,261,266	208,363,751	9	434.5	410	14.0	EA
SMURF2	chr17	64,539,616	64,667,268	9	32.5	27	7.0	AL
USP25	chr21	15,725,024	15,885,071	9	110.6	10	46.0	EL
MCPH1	chr8	6,401,591	6,653,505	8	531.7	9	7.0	EL
PDCD4	chr10	110,866,794	110,905,006	8	36.0	26	14.0	AL
PDS5B	chr13	32,581,426	32,783,020	8	288.7	10	256.0	EL
PIAS1	chr15	68,049,178	68,196,466	8	155.1	6	122.0	EL
RSRC1	chr3	158,105,051	158,549,835	8	-2.8	109	106.0	AL
SSH2	chr17	29,620,938	29,935,228	8	-15.8	137	152.0	AL
ST13	chr22	40,819,534	40,862,008	8	67.9	29	7.0	AL
LEF1	chr4	108,042,544	108,173,956	7	-2.8	84	152.0	AL
MAPK14	chr6	36,022,676	36,116,236	7	37.7	91	7.0	AL
UBR1	chr15	42,937,899	43,111,088	7	-45.1	48	1277.5	AL
EP400P1	chr12	132,079,282	132,131,340	6	337.3	5	260.0	EL
HERC4	chr10	67,916,898	68,080,346	6	-10.9	35	106.0	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
MTOR	chr1	11,101,530	11,267,551	6	2.9	29	90.0	AL
NDFIP2	chr13	79,476,123	79,561,077	6	450.7	8	46.0	EL
PA2G4	chr12	56,099,318	56,118,910	5	52.7	38	14.0	AL
FANCA	chr16	89,732,550	89,821,657	15	28.6	21	15.0	L
JPT2	chr16	1,673,276	1,707,072	15	36.8	23	46.0	L
RPTOR	chr17	80,539,824	80,971,373	15	16.3	11	346.0	L
KDM2A	chr11	67,114,268	67,263,079	14	-24.2	7	50.0	L
NPLOC4	chr17	81,551,884	81,642,153	14	-30.6	16	46.0	DL
ANKRD11	chr16	89,262,620	89,495,561	13	28.5	23	7.0	L
EHMT1	chr9	137,613,991	137,841,126	13	39.7	3	50.0	L
EP300	chr22	41,087,609	41,185,077	13	71.5	6	46.0	L
NSD1	chr5	177,128,078	177,305,213	13	-25.8	6	62.0	L
RABEP1	chr17	5,277,262	5,391,339	13	15.6	26	14.0	A
UTRN	chr6	144,286,736	144,858,034	13	-7.0	6	22.0	L
VPS8	chr3	184,807,142	185,057,614	13	118.7	10	46.0	E
ASH1L	chr1	155,330,260	155,567,533	12	-32.3	5	106.0	DL
DPYD	chr1	97,072,743	97,926,059	12	-25.4	22	122.0	L
HSF1	chr8	144,286,568	144,319,726	12	-42.5	10	256.0	DL
MACF1	chr1	39,079,166	39,492,138	12	-29.3	11	519.5	L
MED13	chr17	61,937,604	62,070,282	12	68.4	21	152.0	L
PACS1	chr11	66,065,352	66,249,747	12	-32.0	5	46.0	DL
SMG1	chr16	18,799,852	18,931,404	12	-29.8	7	122.0	L
BOP1	chr8	144,257,045	144,296,438	11	-28.2	10	256.0	L
CCDC57	chr17	82,096,469	82,217,829	11	-39.5	6	642.5	DL
CREBBP	chr16	3,720,054	3,885,120	11	21.5	5	46.0	L
DNMT1	chr19	10,128,343	10,200,135	11	-30.6	13	365.0	DL
FKBP5	chr6	35,568,584	35,733,583	11	-45.0	15	1555.0	DL
GMDS	chr6	1,618,799	2,250,634	11	118.7	8	14.0	L
INPP4B	chr4	142,018,159	142,851,535	11	-17.5	3	122.0	L
PELP1	chr17	4,666,383	4,709,337	11	215.8	3	14.0	E
PPP6R2	chr22	50,338,316	50,450,089	11	-28.0	15	136.0	L
SEC16A	chr9	136,435,095	136,488,759	11	-12.9	29	46.0	A
SF1	chr11	64,759,603	64,783,844	11	22.2	16	14.0	L
TRAPPC10	chr21	44,007,324	44,111,551	11	-0.3	7	14.0	L
USP15	chr12	62,255,339	62,414,721	11	45.8	14	15.0	L
VPS13D	chr1	12,225,038	12,517,046	11	74.9	3	0.0	E
ZNF407	chr18	74,625,962	75,070,672	11	110.6	3	1.0	E
ARHGAP15	chr2	143,124,329	143,773,352	10	45.8	7	5.0	L
ATF7IP	chr12	14,360,631	14,507,935	10	9.9	8	7.0	L
CHD4	chr12	6,565,081	6,612,433	10	53.4	19	7.0	L
CLEC16A	chr16	10,939,487	11,187,189	10	159.1	9	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
CYTH1	chr17	78,669,046	78,787,342	10	-23.6	4	7.0	L
DDX42	chr17	63,769,188	63,824,317	10	42.0	6	14.0	L
GBE1	chr3	81,484,698	81,766,799	10	142.9	9	46.0	E
GLCCI1	chr7	7,963,742	8,094,079	10	8.6	4	84.0	L
KDM6A	chrX	44,868,174	45,117,612	10	86.3	9	106.0	L
KMT5B	chr11	68,149,862	68,218,772	10	-6.4	7	642.5	L
LRBA	chr4	150,259,658	151,020,497	10	32.2	17	106.0	L
LRPPRC	chr2	43,881,223	44,001,005	10	264.4	7	0.0	E
MAPK8IP3	chr16	1,701,182	1,775,317	10	-42.1	5	130.0	DL
MECP2	chrX	154,016,812	154,102,731	10	-9.6	12	99.0	L
MGA	chr15	41,655,411	41,774,943	10	64.5	85	46.0	A
NCOA1	chr2	24,579,476	24,775,701	10	-7.2	3	22.0	L
PBRM1	chr3	52,540,351	52,690,850	10	-16.2	14	7.0	L
PCNX1	chr14	70,902,404	71,120,382	10	-23.1	153	14.0	A
PRKACB	chr1	84,072,974	84,243,498	10	39.7	4	7.0	L
RAB11FIP3	chr16	420,667	527,481	10	-46.0	7	46.0	DL
RBM39	chr20	35,698,608	35,747,336	10	269.3	2	14.0	E
SAFB2	chr19	5,581,998	5,627,927	10	-6.9	13	22.0	L
SETD2	chr3	47,011,407	47,168,977	10	32.8	17	22.0	L
SMARCC1	chr3	47,580,887	47,786,915	10	-11.1	3	7.0	L
SMG6	chr17	2,054,838	2,308,775	10	-16.7	16	7.0	L
SRRM2	chr16	2,747,328	2,776,412	10	87.4	32	1.0	A
ZGPAT	chr20	63,702,441	63,741,142	10	-45.5	5	7.0	DL
ZNF251	chr8	144,715,908	144,760,585	10	-22.6	21	22.0	L
CD55	chr1	207,316,471	207,365,966	9	353.5	4	0.0	E
COX6B1	chr19	35,643,222	35,663,784	9	3.3	5	825.0	L
CSNK1D	chr17	82,237,660	82,278,742	9	-19.0	8	7.0	L
DDX60	chr4	168,211,290	168,323,807	9	62.0	22	122.0	L
DENND1B	chr1	197,499,748	197,780,493	9	-27.1	3	7.0	L
DIP2B	chr12	50,499,984	50,753,667	9	2.6	4	7.0	L
DLG1	chr3	197,037,559	197,304,272	9	5.0	8	7.0	L
FNBP1	chr9	129,882,186	130,048,194	9	-18.2	5	256.0	L
FOXJ3	chr1	42,171,538	42,340,877	9	27.5	12	7.0	L
FRYL	chr4	48,492,362	48,785,299	9	17.6	24	14.0	A
GANAB	chr11	62,619,825	62,651,726	9	9.9	6	7.0	L
HNRNPUL2	chr11	62,707,624	62,732,385	9	-10.0	9	76.0	L
IL4I1	chr19	49,884,655	49,934,539	9	-36.8	5	46.0	L
IQGAP1	chr15	90,383,240	90,507,243	9	-29.3	5	166.0	L
KIAA1468	chr18	62,182,290	62,312,122	9	23.1	17	46.0	L
MED13L	chr12	115,953,575	116,282,186	9	35.0	38	7.0	A
NBEAL1	chr2	203,009,878	203,222,994	9	66.6	11	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
NOSIP	chr19	49,550,467	49,585,572	9	-57.5	29	0.0	DA
NUP214	chr9	131,120,560	131,239,670	9	8.6	8	106.0	L
PARP8	chr5	50,660,898	50,851,522	9	-21.5	4	14.0	L
PLEKHA5	chr12	19,124,691	19,381,399	9	16.6	2	7.0	L
POLA2	chr11	65,256,851	65,303,685	9	-16.7	9	7.0	L
POT1	chr7	124,817,385	124,934,983	9	10.1	26	0.0	A
PUM1	chr1	30,926,505	31,070,717	9	163.8	5	0.0	E
RAB11FIP2	chr10	117,999,915	118,051,884	9	288.7	19	1.0	E
RNF216	chr7	5,615,040	5,786,730	9	-41.7	15	106.0	L
RUNX1	chr21	34,782,800	35,054,298	9	130.8	1	110.0	L
SLC6A16	chr19	49,284,634	49,330,217	9	20.5	2	14.0	L
SLK	chr10	103,962,184	104,034,233	9	240.1	13	1.0	E
SMCHD1	chr18	2,650,886	2,810,017	9	-33.5	4	7.0	L
TARSL2	chr15	101,648,751	101,729,442	9	191.5	22	7.0	L
TCF20	chr22	42,155,012	42,288,927	9	-2.8	10	7.0	L
TRAPPC8	chr18	31,824,172	31,948,128	9	21.5	4	7.0	L
UBAC2	chr13	99,195,424	99,391,499	9	45.8	4	14.0	L
UBR4	chr1	19,069,505	19,215,252	9	136.0	8	7.0	L
VPS52	chr6	33,245,271	33,276,965	9	1.6	10	106.0	L
ZFAND3	chr6	37,814,530	38,159,623	9	215.8	5	46.0	E
ABCD2	chr12	39,546,219	39,625,041	8	142.9	8	14.0	E
ADD1	chr4	2,838,856	2,935,075	8	-6.6	42	7.0	A
AP2B1	chr17	35,582,262	35,731,417	8	62.0	13	90.0	L
ARIH1	chr15	72,469,325	72,591,555	8	51.2	5	7.0	L
ASXL2	chr2	25,728,752	25,883,516	8	-39.8	3	7.0	L
ATG5	chr6	106,179,476	106,330,820	8	191.5	2	0.0	E
ATP2A2	chr12	110,276,226	110,356,092	8	70.1	67	22.0	A
CAMK2D	chr4	113,446,031	113,766,927	8	2.0	9	106.0	L
CAMK4	chr5	111,218,652	111,499,884	8	3.3	9	7.0	L
CDKAL1	chr6	20,529,456	21,237,403	8	-13.1	5	106.0	L
DAZAP1	chr19	1,402,568	1,440,687	8	-10.9	2	4.0	L
DNAJC13	chr3	132,412,659	132,544,032	8	94.4	71	7.0	A
DYNC1H1	chr14	101,959,527	102,055,798	8	94.4	44	7.0	A
ERC1	chr12	986,207	1,500,933	8	8.6	4	7.0	L
FAM13A	chr4	88,720,953	89,062,195	8	80.5	1	7.0	L
FOCAD	chr9	20,653,308	21,000,955	8	155.1	17	7.0	E
GAK	chr4	844,274	937,390	8	450.7	4	14.0	E
GPHN	chr14	66,502,406	67,186,808	8	321.1	2	0.0	E
HNRNPUL1	chr19	41,257,475	41,312,783	8	84.6	4	14.0	L
HSF2	chr6	122,394,550	122,438,119	8	240.1	15	14.0	E
KDM4A	chr1	43,645,125	43,710,518	8	211.0	7	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
KMT2C	chr7	152,129,924	152,441,005	8	-23.6	4	7.0	L
MIR5096	chr17	4,136,088	4,245,637	8	-47.2	9	14.0	DL
MOB3A	chr19	2,066,035	2,101,270	8	55.5	2	22.0	L
MROH1	chr8	144,143,015	144,266,940	8	-51.4	5	46.0	DL
MUM1	chr19	1,349,976	1,383,431	8	-26.0	4	90.0	L
NCOA3	chr20	47,496,856	47,661,877	8	2.0	6	7.0	L
NEAT1	chr11	65,417,797	65,450,538	8	-2.8	4	22.0	L
NELL2	chr12	44,503,274	44,918,928	8	20.0	2	4.0	L
PHF20L1	chr8	132,770,357	132,853,807	8	36.0	4	22.0	L
PLEC	chr8	143,910,146	143,981,745	8	-50.1	11	22.0	DL
POGZ	chr1	151,397,723	151,464,465	8	52.7	26	0.0	A
PTPRA	chr20	2,859,194	3,043,669	8	10.6	4	1555.0	L
RNF10	chr12	120,529,328	120,582,594	8	211.0	7	1.0	E
RTTN	chr18	69,998,805	70,210,726	8	-8.9	6	136.0	L
SACM1L	chr3	45,684,240	45,750,425	8	191.5	11	0.0	E
SLX4IP	chr20	10,430,302	10,633,034	8	66.6	3	7.0	L
STAG1	chr3	136,332,156	136,757,403	8	152.7	6	136.0	L
STXBP5	chr6	147,199,357	147,395,476	8	-8.9	8	350.0	L
TANC2	chr17	63,004,536	63,432,706	8	191.5	11	7.0	E
TONSL	chr8	144,423,779	144,449,429	8	-32.4	7	7.0	L
UHRF1BP1	chr6	34,787,016	34,882,514	8	288.7	4	0.0	E
VMP1	chr17	59,702,464	59,847,255	8	-2.8	28	46.0	A
YWHAE	chr17	1,339,539	1,405,262	8	191.5	2	0.0	E
ACOX1	chr17	75,936,510	75,984,434	7	-30.6	2	256.0	L
ASCC3	chr6	100,503,194	100,886,372	7	182.7	4	7.0	E
ATF7	chr12	53,502,855	53,631,415	7	12.1	32	1.0	A
ATP8A1	chr4	42,403,374	42,662,105	7	19.6	4	14.0	L
BACH2	chr6	89,921,527	90,301,908	7	483.1	2	0.0	E
C6orf106	chr6	34,582,279	34,701,850	7	-2.8	3	46.0	L
CASK	chrX	41,509,935	41,928,034	7	29.6	5	346.0	L
CCDC47	chr17	63,740,249	63,778,728	7	-42.8	6	22.0	L
CDC73	chr1	193,116,957	193,259,812	7	123.5	19	7.0	E
GATAD2B	chr1	153,799,906	153,927,975	7	6.9	2	7.0	L
HTT	chr4	3,069,680	3,248,960	7	-2.8	25	1.0	A
KLRG1	chr12	8,945,043	9,015,744	7	-40.6	3	7.0	L
LSM2	chr6	31,792,391	31,811,984	7	-53.2	2	14.0	DL
MACROD2	chr20	13,990,499	16,058,196	7	240.1	1	0.0	E
MAP4K3	chr2	39,244,265	39,442,312	7	-2.8	15	46.0	L
NAA38	chr17	7,851,680	7,890,388	7	-34.5	15	14.0	L
NBAS	chr2	15,161,907	15,566,348	7	-19.0	4	106.0	L
NEMP1	chr12	57,050,642	57,083,791	7	113.8	10	46.0	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
NUP62	chr19	49,901,825	49,934,731	7	-42.3	5	46.0	L
PIP5K1A	chr1	151,193,543	151,254,531	7	256.3	3	277.5	L
PPP1R16A	chr8	144,472,981	144,507,121	7	-10.3	4	7.0	L
PRKCA	chr17	66,297,807	66,815,744	7	51.2	7	7.0	L
RAD51B	chr14	67,814,778	68,688,106	7	-2.8	2	22.0	L
RASA1	chr5	87,263,252	87,396,926	7	205.4	3	0.0	E
RFX2	chr19	5,988,163	6,115,653	7	13.4	9	106.0	L
SEPT7	chr7	35,795,985	35,912,105	7	175.3	10	7.0	E
SNAPC4	chr9	136,370,568	136,403,437	7	34.6	7	166.0	L
SPEN	chr1	15,842,863	15,945,455	7	4.7	2	7.0	L
SPG7	chr16	89,503,387	89,562,768	7	-28.7	10	7.0	L
SYNE1	chr6	152,116,683	152,642,399	7	-2.8	22	46.0	L
SYNE2	chr14	63,847,964	64,231,451	7	12.1	8	22.0	L
TAF2	chr8	119,725,773	119,837,834	7	288.7	8	1.0	E
THEMIS	chr6	127,703,193	127,923,631	7	-35.2	5	106.0	L
TTC21B	chr2	165,868,361	165,958,838	7	-9.8	5	46.0	L
UBE2J2	chr1	1,248,911	1,278,854	7	-58.8	2	166.0	DL
UBR5	chr8	102,247,273	102,417,689	7	29.6	19	7.0	L
VRK3	chr19	49,971,466	50,030,548	7	-43.0	2	7.0	L
WDR82	chr3	52,249,421	52,283,643	7	-11.7	7	277.5	L
YTHDF3	chr8	63,163,552	63,217,788	7	8.0	13	7.0	L
ANXA1	chr9	73,146,730	73,175,394	6	62.0	5	14.0	L
ATP9B	chr18	79,064,274	79,383,282	6	18.8	2	7.0	L
BAG6	chr6	31,634,027	31,657,700	6	-19.0	36	46.0	A
BCAS3	chr17	60,672,774	61,397,838	6	-57.7	2	7.0	DL
BRWD3	chrX	80,664,487	80,814,734	6	80.5	6	7.0	L
CHD1	chr5	98,850,203	98,931,534	6	149.9	8	1.0	E
CHMP2B	chr3	87,222,262	87,260,548	6	24.9	24	7.0	A
CLASP2	chr3	33,491,245	33,723,213	6	57.9	5	7.0	L
DERL2	chr17	5,466,250	5,491,230	6	55.5	37	0.0	A
DNAJC1	chr10	21,751,547	22,008,721	6	-22.3	38	7.0	A
DOT1L	chr19	2,159,148	2,237,578	6	-18.2	6	14.0	L
FAM117B	chr2	202,630,177	202,774,757	6	385.9	6	14.0	E
FUNDC2	chrX	155,021,788	155,061,916	6	321.1	9	46.0	E
GNA12	chr7	2,723,105	2,849,325	6	434.5	2	0.0	E
IKZF2	chr2	212,994,685	213,156,609	6	434.5	1	0.0	E
MIR4745	chr19	799,939	810,001	6	142.9	47	346.0	L
MIR5096	chr1	15,866,148	15,910,467	6	18.8	2	7.0	DL
MIR5096	chr22	37,663,025	38,029,093	6	-25.7	6	7.0	DL
MMP23A	chr1	1,627,779	1,706,808	6	4.7	17	14.0	L
NFKBIL1	chr6	31,541,850	31,563,829	6	-46.7	4	7.0	DL

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

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
OPRM1	chr6	154,005,495	154,251,867	6	-2.8	3	14.0	L
PAPOLA	chr14	96,497,375	96,572,116	6	418.3	3	0.0	E
PCNT	chr21	46,319,121	46,450,769	6	113.8	5	4.0	L
PHACTR4	chr1	28,364,581	28,505,369	6	-33.2	3	22.0	L
RBM27	chr5	146,198,599	146,294,221	6	Inf	3	0.0	E
RIPOR2	chr6	24,799,280	25,047,288	6	-2.8	10	7.0	L
RSBN1L	chr7	77,691,425	77,784,803	6	94.4	31	1.0	A
SEC23A	chr14	39,026,918	39,108,528	6	14.8	7	7.0	L
SPPL3	chr12	120,757,509	120,909,352	6	4.1	9	14.0	L
TCF25	chr16	89,868,585	89,916,384	6	-45.1	5	106.0	L
TRIM33	chr1	114,387,776	114,516,160	6	167.2	17	106.0	L
UBE2F-SCLY	chr2	237,961,944	238,104,413	6	-10.9	6	46.0	L
UBE2L3	chr22	21,544,446	21,629,034	6	94.4	3	7.0	L
UNKL	chr16	1,358,204	1,419,720	6	18.8	7	15.0	L
ZNF473	chr19	50,020,892	50,053,774	6	-30.6	3	22.0	L
ZNRD1ASP	chr6	29,996,010	30,066,189	6	51.2	4	122.0	L
CSNK1G1	chr15	64,160,516	64,361,259	5	-11.7	8	7.0	L
ECD	chr10	73,129,523	73,173,095	5	191.5	24	1.0	A
ELMO1	chr7	36,847,905	37,454,326	5	-29.3	34	46.0	A
EVL	chr14	99,966,474	100,149,236	5	-25.2	4	7.0	L
FANCL	chr2	58,154,242	58,246,380	5	434.5	6	0.0	E
HSF5	chr17	58,415,166	58,493,401	5	-2.8	34	1.0	A
IQCB1	chr3	121,764,760	121,840,079	5	62.0	79	15.0	A
MARF1	chr16	15,589,368	15,648,166	5	106.5	17	106.0	L
KIFC1	chr6	33,386,535	33,414,922	5	-2.8	42	7.0	A
KMT2D	chr12	49,013,974	49,060,324	5	-28.7	33	0.0	A
MIR5096	chr1	235,507,822	235,723,113	5	70.1	1	0.0	DL
N4BP1	chr16	48,533,725	48,615,209	5	159.1	32	106.0	A
PAG1	chr8	80,962,810	81,117,068	5	-33.2	2	32.0	L
PDE7A	chr8	65,709,333	65,846,734	5	18.8	4	7.0	L
PHF20	chr20	35,767,000	35,955,366	5	-28.7	38	7.0	A
POM121	chr7	72,874,334	72,956,440	5	240.1	29	1.0	A
PPFIA1	chr11	70,265,699	70,389,501	5	78.2	20	106.0	L
SEC31A	chr4	82,813,508	82,905,571	5	-2.8	66	7.0	A
SEPT9	chr17	77,276,409	77,505,596	5	-44.5	27	7.0	A
SFI1	chr22	31,491,138	31,623,551	5	-55.8	24	7.0	DA
SMAP2	chr1	40,368,705	40,428,326	5	45.8	61	7.0	A
STAG3	chr7	100,172,723	100,219,387	5	78.2	35	0.0	A
STX8	chr17	9,245,470	9,580,958	5	38.8	4	7.0	L
TNKS	chr8	9,550,934	9,787,346	5	191.5	8	7.0	E
WWOX	chr16	78,094,412	79,217,667	5	-17.8	5	106.0	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
AGL	chr1	99,845,083	99,929,023	4	871.8	4	0.0	E
ANKRD46	chr8	100,504,751	100,564,786	4	29.6	24	7.0	A
AQR	chr15	34,851,350	34,974,794	4	-15.0	84	14.0	A
CAAP1	chr9	26,835,684	26,897,828	4	-39.3	27	46.0	A
CNOT6	chr5	180,489,398	180,583,405	4	-19.0	2	7.0	L
EHMT1	chr9	137,758,021	137,769,772	4	62.0	1	0.0	L
EXOSC10	chr1	11,061,612	11,104,910	4	13.4	70	7.0	A
GOLPH3L	chr1	150,641,224	150,702,196	4	-51.4	24	7.0	A
KDM5D	chrY	19,700,414	19,749,939	4	62.0	2	14.0	A
MAD1L1	chr7	1,810,791	2,237,948	4	-20.5	35	46.0	A
MAP2K2	chr19	4,085,321	4,129,129	4	-2.8	2	106.0	L
MEMO1	chr2	31,862,809	32,016,052	4	-64.7	47	7.0	A
MSH5-SAPCD1	chr6	31,734,947	31,769,847	4	-67.6	43	7.0	A
MTMR3	chr22	29,878,168	30,035,868	4	-45.3	261	106.0	A
OGDH	chr7	44,601,521	44,714,070	4	-48.9	17	332.0	L
PATL1	chr11	59,631,715	59,674,038	4	29.6	578	332.0	A
PDCD11	chr10	103,391,654	103,451,262	4	94.4	27	152.0	A
PDE3B	chr11	14,638,722	14,877,058	4	29.6	35	7.0	A
RAB18	chr10	27,499,173	27,547,237	4	-22.3	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	21.5	87	106.0	A
TRIO	chr5	14,138,701	14,515,204	4	580.2	61	106.0	A
XPO1	chr2	61,472,933	61,543,283	4	21.5	25	106.0	A
AKAP9	chr7	91,935,874	92,115,673	3	-22.3	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	-19.0	32	106.0	A
EIF2AK4	chr15	39,929,123	40,040,596	3	385.9	43	7.0	A
NGDN	chr14	23,464,688	23,483,193	3	45.8	44	0.0	A
PRKD2	chr19	46,669,315	46,722,127	3	62.0	24	22.0	A
RABGAP1	chr9	122,936,008	123,109,868	3	-32.0	29	7.0	A
SNAP29	chr22	20,854,003	20,896,213	3	288.7	27	7.0	A
ZNF573	chr19	37,733,301	37,784,590	3	-22.3	86	735.0	A
C20orf196	chr20	5,745,386	5,869,407	2	-35.2	1	0.0	A
CRTAP	chr3	33,108,957	33,152,773	2	94.4	35	7.0	A
GPN1	chr2	27,623,647	27,655,846	2	-2.8	62	1.0	A
JMJD6	chr17	76,707,831	76,731,799	2	94.4	53	1.0	A
KCTD3	chr1	215,562,378	215,626,821	2	-51.4	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	94.4	31	46.0	A
PHF12	chr17	28,900,252	28,956,490	2	-22.3	40	106.0	A
POLG2	chr17	64,472,784	64,502,066	2	21.5	43	7.0	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
RASEF	chr9	82,974,584	83,068,128	2	Inf	43	46.0	A
SNHG12	chr1	28,573,537	28,586,854	2	191.5	96	332.0	A
TAC3	chr12	57,004,996	57,021,560	2	-67.6	42	7.0	A
TGFBR2	chr3	30,601,501	30,699,141	2	94.4	31	7.0	A
ACTL6A	chr3	179,557,879	179,593,405	1	-80.6	40	0.0	A
C19orf48	chr19	50,792,692	50,809,853	1	-2.8	28	46.0	A
CD109	chr6	73,691,084	73,833,317	1	-87.9	32	0.0	A
IFNGR2	chr21	33,397,895	33,442,521	1	Inf	53	15.0	A
KARS	chr16	75,622,723	75,652,687	1	-2.8	24	0.0	A
MICAL2	chr11	12,105,575	12,268,790	1	-51.4	39	15.0	A
RBAK-RBAKDN	chr7	5,040,820	5,078,223	1	-2.8	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
SIRT3	chr11	210,029	241,362	10	-44.8	4	1.0	D
IP6K1	chr3	49,719,294	49,791,540	9	-57.9	2	1.0	D
NPEPPS	chr17	47,517,956	47,628,276	9	-55.1	3	14.0	D
ANKFY1	chr17	4,158,817	4,268,995	8	-46.0	9	14.0	D
EIF2B3	chr1	44,845,521	44,991,722	8	-67.6	6	1.0	D
TRAF2	chr9	136,881,512	136,931,615	8	-59.7	4	46.0	D
TSC2	chr16	2,042,894	2,093,720	8	-51.4	1	22.0	D
WDR90	chr16	644,362	672,829	8	-53.5	3	0.0	D
HCG20	chr6	30,761,824	30,797,250	7	-48.9	4	22.0	D
NARFL	chr16	724,754	746,038	7	-61.1	3	22.0	D
PPP3CC	chr8	22,435,969	22,546,144	7	-53.2	3	0.0	D
IFT140	chr16	1,505,426	1,617,108	6	-51.4	3	7.0	D
QRICH1	chr3	49,024,706	49,099,373	6	-59.0	7	1.0	D
EXOC2	chr6	480,137	698,141	5	-71.4	4	0.0	D
HAGH	chr16	1,804,102	1,832,194	5	-58.4	6	14.0	D
RNPS1	chr16	2,248,115	2,273,412	5	-77.5	2	0.0	D
USP34	chr2	61,182,454	61,475,714	5	-61.1	2	0.0	D
WNK1	chr12	747,922	916,452	5	-51.4	4	1.0	D
ZNF598	chr16	1,992,651	2,014,821	4	-55.8	3	0.0	D