Supplementary Report 1:
Genes of interest marked by vector integration
All Patients (CLL & ALL) and
Response Groups (CR/PRtd & PR/NR)

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 40 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	102	*/* 19.6	*/* 13.73	/ 0.000	*/* 8.82	*/* 9.80	/ 0.980
Depletion	93	*/* 20.4	*/* 10.75	/ 0.000	/ 6.45	*/* 8.60	/ 1.075
Abundance	132	*/* 20.5	/ 5.30	/ 0.000	*/* 8.33	/ 4.55	/ 0.758
Longitudinal	226	*/* 25.2	*/* 11.95	/ 0.442	*/* 11.95	*/* 11.50	*/* 1.327
Composite	404	*/* 20.8	*/* 9.41	/ 0.248	*/* 10.15	*/* 8.91	*/ 0.743

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: 9.1%
- Tumor Suppressors: 4.83%
- Lymphoma Related: 0.16%
- COSMIC Related: 3.55%
- TCGA Related: 2.73%
- Clonal Hematopoiesis Related: 0.17%

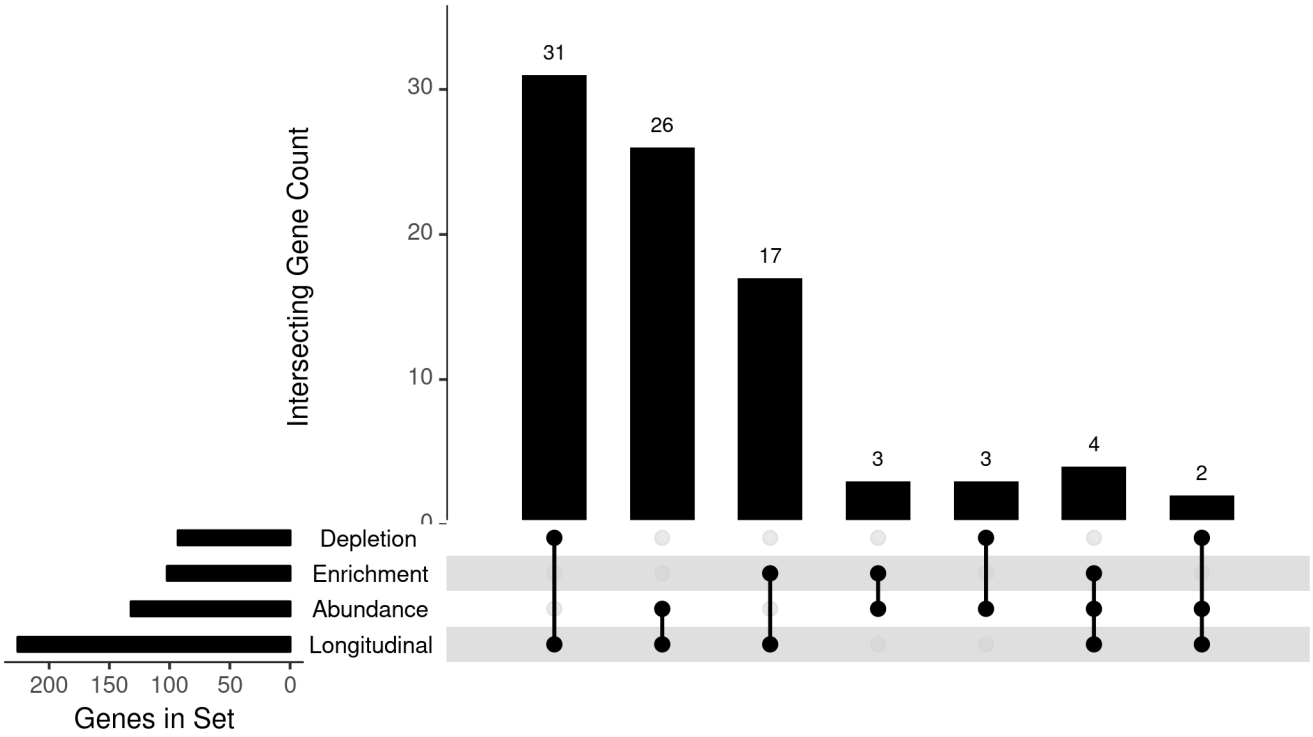

Figure 1: Intersecting gene lists identified through the various selection criteria.

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	12	75.1	27	360	EAL
UBAP2L	12	65.9	30	180	EAL
PTBP1	8	106.0	47	360	EAL
TET2	6	196.7	814	1584	EAL

Table 3: GO Biological Process. Top 7 per group. Total genes considered: 400

Group	GO ID	GO Term	Term Size	Gene Count	Adjusted P-value
1	GO:0016569	covalent chromatin modification	465	44	0.0000000
	GO:0016570	histone modification	377	39	0.0000000
	GO:0018205	peptidyl-lysine modification	321	35	0.0000000
	GO:0043414	macromolecule methylation	246	18	0.0105314
	GO:0006479	protein methylation	152	16	0.0003423
	GO:0008213	protein alkylation	152	16	0.0003423
	GO:0033044	regulation of chromosome organization	256	16	0.0459150
2	GO:0030155	regulation of cell adhesion	473	29	0.0075886
	GO:0030036	actin cytoskeleton organization	451	25	0.0361005
	GO:0032101	regulation of response to external stimulus	446	24	0.0472901
	GO:0051493	regulation of cytoskeleton organization	352	23	0.0109070
	GO:0097435	supramolecular fiber organization	423	23	0.0479028
	GO:0001667	ameboidal-type cell migration	227	18	0.0045494
	GO:0018209	peptidyl-serine modification	230	18	0.0053341
3	GO:1903827	regulation of cellular protein localization	464	31	0.0011936
	GO:0010256	endomembrane system organization	337	30	0.0000050
	GO:0080135	regulation of cellular response to stress	488	29	0.0111990
	GO:0032386	regulation of intracellular transport	428	27	0.0075800
	GO:0019439	aromatic compound catabolic process	438	24	0.0459150
	GO:0006913	nucleocytoplasmic transport	369	22	0.0260492
	GO:0051169	nuclear transport	375	22	0.0309496
4	GO:0006511	ubiquitin-dependent protein catabolic process	497	30	0.0078741
	GO:0010498	proteasomal protein catabolic process	384	24	0.0146571
	GO:0051656	establishment of organelle localization	350	23	0.0103342
	GO:0016050	vesicle organization	309	21	0.0108760
	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	342	20	0.0435799
	GO:0048193	Golgi vesicle transport	294	18	0.0410830
	GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	226	15	0.0376575
5	GO:0006281	DNA repair	454	27	0.0155672
	GO:0046649	lymphocyte activation	472	25	0.0486966
	GO:0071396	cellular response to lipid	369	23	0.0185046
	GO:0048729	tissue morphogenesis	396	23	0.0291836
	GO:0071407	cellular response to organic cyclic compound	411	23	0.0433384
	GO:0043009	chordate embryonic development	351	22	0.0207332
	GO:0009792	embryo development ending in birth or egg hatching	354	22	0.0229064
6	GO:0006397	mRNA processing	409	30	0.0002838
	GO:0008380	RNA splicing	360	22	0.0231729
	GO:1903311	regulation of mRNA metabolic process	231	17	0.0123267
	GO:0000375	RNA splicing, via transesterification reactions	279	17	0.0459150
	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	277	17	0.0459150
	GO:0000398	mRNA splicing, via spliceosome	277	17	0.0459150
	GO:0050684	regulation of mRNA processing	97	8	0.0478579

Table 4: KEGG Pathway analysis. Top 10 per group. Total genes considered: 194

Group	KEGG ID	Description	Term Size	Gene Count	Adjusted P-value
1	path:hsa04024	cAMP signaling pathway	144	12	0.0294960
	path:hsa04720	Long-term potentiation	51	9	0.0007749
	path:hsa05415	Diabetic cardiomyopathy	139	9	0.0984754
	path:hsa04114	Oocyte meiosis	100	8	0.0638464
	path:hsa04921	Oxytocin signaling pathway	114	8	0.0908859
	path:hsa04916	Melanogenesis	61	7	0.0294960
	path:hsa03015	mRNA surveillance pathway	78	7	0.0564334
	path:hsa04310	Wnt signaling pathway	108	7	0.1130745
	path:hsa04360	Axon guidance	143	7	0.2348481
	path:hsa05012	Parkinson disease	196	7	0.4576448
2	path:hsa05200	Pathways in cancer	360	17	0.1384452
	path:hsa04919	Thyroid hormone signaling pathway	94	11	0.0031118
	path:hsa05165	Human papillomavirus infection	236	11	0.2038296
	path:hsa04140	Autophagy - animal	125	10	0.0396036
	path:hsa05203	Viral carcinogenesis	162	10	0.0988748
	path:hsa05206	MicroRNAs in cancer	189	10	0.1389458
	path:hsa00310	Lysine degradation	54	9	0.0007749
	path:hsa05225	Hepatocellular carcinoma	107	9	0.0396036
	path:hsa04714	Thermogenesis	168	9	0.1466238
	path:hsa05202	Transcriptional misregulation in cancer	113	8	0.0907861
3	path:hsa05022	Pathways of neurodegeneration - multiple diseases	347	17	0.1131964
	path:hsa05014	Amyotrophic lateral sclerosis	286	14	0.1384452
	path:hsa04010	MAPK signaling pathway	207	13	0.0739102
	path:hsa04144	Endocytosis	218	13	0.0882540
	path:hsa05131	Shigellosis	200	12	0.0908859
	path:hsa04120	Ubiquitin mediated proteolysis	132	11	0.0307649
	path:hsa04141	Protein processing in endoplasmic reticulum	143	11	0.0396036
	path:hsa05163	Human cytomegalovirus infection	166	10	0.1030116
	path:hsa05166	Human T-cell leukemia virus 1 infection	174	9	0.1598659
	path:hsa05016	Huntington disease	235	9	0.4019883
4	path:hsa05205	Proteoglycans in cancer	133	12	0.0180244
	path:hsa04810	Regulation of actin cytoskeleton	160	9	0.1343722
	path:hsa04014	Ras signaling pathway	158	7	0.3073857
	path:hsa04912	GnRH signaling pathway	68	6	0.0739102
	path:hsa04650	Natural killer cell mediated cytotoxicity	90	6	0.1131964
	path:hsa04926	Relaxin signaling pathway	94	6	0.1343722
	path:hsa04015	Rap1 signaling pathway	143	6	0.3536542
	path:hsa05208	Chemical carcinogenesis - reactive oxygen species	145	6	0.3619719
	path:hsa04510	Focal adhesion	148	6	0.3774230
	path:hsa04062	Chemokine signaling pathway	130	5	0.4202321
5	path:hsa03018	RNA degradation	70	5	0.1131964
	path:hsa03040	Spliceosome	117	5	0.3536542

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 (%)
HERC2	6	3	10	FALSE	518.1
PIP5K1A	9	4	13	FALSE	502.7
RAB11FIP2	9	4	12	FALSE	456.3
NUP107	9	4	12	FALSE	456.3
HSF2	8	5	14	FALSE	419.2
PDCD10	9	4	11	FALSE	410.0
LRPPRC	10	6	15	FALSE	363.6
RAD23B	7	4	10	TRUE	363.6
RBM27	6	5	12	FALSE	345.1
PIKFYVE	10	5	12	FALSE	345.1
ABLIM1	6	5	11	FALSE	308.0
CAMKMT	6	5	11	FALSE	308.0
TMTC3	6	6	13	FALSE	301.8
ARHGAP12	6	5	10	FALSE	270.9
ATG5	9	10	19	FALSE	252.3
GNA12	6	6	11	TRUE	240.0
ATE1	7	6	11	FALSE	240.0
PPP4R2	7	6	11	FALSE	240.0
BCKDHB	7	6	11	FALSE	240.0
FRG1BP	9	8	14	FALSE	224.5
MACROD2	7	8	14	FALSE	224.5
FUS	5	7	12	TRUE	217.9
UCHL3	7	7	12	FALSE	217.9
CPEB2	11	10	17	FALSE	215.2
HELLS	10	10	17	FALSE	215.2
KDM4A	9	10	17	FALSE	215.2
SNRPA	5	6	10	FALSE	209.1
LUC7L2	8	6	10	FALSE	209.1
USP9Y	7	6	10	FALSE	209.1
CDK8	7	6	10	FALSE	209.1
BZW2	6	6	10	FALSE	209.1
RBPJ	9	6	10	FALSE	209.1
IKZF2	8	8	13	TRUE	201.3
FUNDC2	6	8	13	FALSE	201.3
PDE12	7	8	13	FALSE	201.3
URI1	9	13	21	FALSE	199.6
TET2	6	10	16	TRUE	196.7
FANCL	5	7	11	FALSE	191.4
PRKN	7	7	11	FALSE	191.4
LOC101929095	12	13	20	FALSE	185.3
ASCC3	8	22	33	FALSE	178.2
WWP1	9	15	22	TRUE	172.0
GMDS	12	13	19	FALSE	171.0
BRWD3	6	9	13	TRUE	167.9
ECD	6	9	13	FALSE	167.9
KIF20B	9	9	13	FALSE	167.9
PHF3	10	14	20	FALSE	164.9
RBM39	11	14	20	TRUE	164.9
NDFIP2	6	12	17	FALSE	162.7
MTREX	9	12	17	FALSE	162.7

Integration Frequency (Depletion)

Table 6: Table of top 50 genes with the most frequent clonal depletion.

Gene	Num. Patients	TDN Sites	Patient Sites	Onco-Related	Frequency Increase (%)
RNPS1	6	146	17	FALSE	-78.4
EXOC2	5	66	10	FALSE	-71.9
LSM2	7	73	13	FALSE	-67.0
NOSIP	10	158	31	FALSE	-63.6
SFI1	6	56	11	FALSE	-63.6
ZNF598	5	56	11	FALSE	-63.6
UBE2J2	7	69	14	FALSE	-62.4
ZBTB4	6	49	10	FALSE	-62.2
WDR90	8	53	11	FALSE	-61.5
IP6K1	11	139	29	FALSE	-61.3
EIF2B3	10	81	17	FALSE	-61.1
STK11	7	47	10	TRUE	-60.5
WNK1	6	70	15	FALSE	-60.3
PLEC	10	105	23	FALSE	-59.4
NARFL	9	54	12	FALSE	-58.8
PRKAR2A	6	58	13	FALSE	-58.4
HAGH	5	53	12	FALSE	-58.0
GRAP2	6	44	10	FALSE	-57.9
IFT140	8	83	19	FALSE	-57.5
CCND3	10	82	19	TRUE	-57.0
CNOT6	5	47	11	FALSE	-56.6
DIDO1	6	42	10	FALSE	-55.8
QRICH1	8	92	22	FALSE	-55.7
PSMB9	9	54	13	FALSE	-55.4
PCBP3	4	41	10	FALSE	-54.8
PCED1B	6	45	11	TRUE	-54.7
TAP2	8	49	12	TRUE	-54.6
HORMAD2	8	93	23	FALSE	-54.1
TSC2	9	88	22	TRUE	-53.6
RPRD2	6	44	11	FALSE	-53.6
ZGPAT	11	98	25	FALSE	-52.7
HCG20	9	90	23	FALSE	-52.6
RAB40C	7	43	11	FALSE	-52.6
FAM222B	4	39	10	FALSE	-52.5
FKBP5	13	126	33	FALSE	-51.4
RBM14-RBM4	7	42	11	FALSE	-51.4
ABHD16A	9	38	10	FALSE	-51.2
MCM3AP	6	38	10	FALSE	-51.2
MIR5096	6	49	13	FALSE	-50.8
MTMR3	6	45	12	TRUE	-50.5
MROH1	13	291	78	FALSE	-50.3
SEPT2	7	41	11	TRUE	-50.2
TC2N	5	37	10	FALSE	-49.9
TRAF2	10	103	28	FALSE	-49.6
CEACAM21	9	73	20	FALSE	-49.2
RBM4	9	47	13	FALSE	-48.7
ADCK5	6	47	13	FALSE	-48.7
RNF216	9	54	15	TRUE	-48.5
PRRC2A	7	61	17	FALSE	-48.3
ASCC1	7	43	12	FALSE	-48.2

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	8	814	0.989	0.923	TRUE
KCTD3	4	589	0.265	0.745	FALSE
PATL1	4	578	0.260	0.793	FALSE
PIKFYVE	10	410	0.273	0.890	FALSE
SRCAP	11	373	0.357	0.896	FALSE
MTMR3	6	261	0.041	0.876	TRUE
PCNX1	11	153	0.010	0.827	FALSE
PPP6R3	15	149	0.040	0.717	FALSE
SSH2	10	137	0.062	0.792	FALSE
RSRC1	9	109	0.014	0.812	FALSE
SNHG12	2	96	0.057	0.646	FALSE
MAPK14	9	91	0.018	0.774	TRUE
RPA3	5	87	0.020	0.783	FALSE
ZNF573	3	86	0.610	0.677	FALSE
MGA	13	85	0.013	0.746	FALSE
AQR	5	84	0.022	0.798	FALSE
LEF1	9	84	0.038	0.765	TRUE
LINC01473	3	82	0.075	0.643	FALSE
CARD8	14	79	0.056	0.681	TRUE
IQCB1	5	79	0.028	0.752	FALSE
DNAJC13	9	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	6	61	0.025	0.769	TRUE
ZZEF1	13	56	0.333	0.614	FALSE
CLK4	8	53	0.036	0.653	FALSE
IFNGR2	2	53	0.722	0.635	TRUE
JMJD6	2	53	0.015	0.755	FALSE
KDM5D	8	51	0.017	0.745	FALSE
UBR1	10	48	0.421	0.686	FALSE
MEMO1	6	47	0.006	0.741	FALSE
PTBP1	8	47	0.043	0.660	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	2	43	0.003	0.708	FALSE
RASEF	2	43	0.005	0.622	FALSE
UXT-AS1	2	43	0.039	0.477	FALSE
ADD1	10	42	0.011	0.594	FALSE
GRB2	12	42	0.017	0.554	TRUE
KIFC1	7	42	0.003	0.694	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	13	33	15	FALSE
PTPRA	1555.0	1825.0	3	9	36	4	FALSE
TET2	1464.0	1584.0	7	6	16	814	TRUE
UBR1	1277.5	1825.0	4	10	18	48	FALSE
COX6B1	825.0	1095.0	3	10	18	5	FALSE
CCDC57	642.5	912.5	2	15	40	6	FALSE
KMT5B	642.5	912.5	2	13	32	7	FALSE
MACF1	519.5	547.5	3	14	34	11	TRUE
DNMT1	365.0	912.5	2	14	74	13	TRUE
STXBP5	350.0	360.0	4	11	21	8	FALSE
CASK	346.0	547.5	2	8	17	5	FALSE
RPTOR	346.0	360.0	2	19	96	11	FALSE
DIP2A	346.0	360.0	2	14	41	25	FALSE
PTBP1	346.0	360.0	2	8	20	47	TRUE
MIR4745	346.0	360.0	2	7	13	47	FALSE
ZZEF1	332.0	360.0	5	13	51	56	FALSE
SRCAP	332.0	360.0	5	11	23	373	FALSE
SNORA30	332.0	360.0	5	7	10	373	FALSE
OGDH	332.0	360.0	4	5	12	17	FALSE
WDR82	277.5	547.5	3	10	25	7	TRUE
PIP5K1A	277.5	547.5	2	9	13	3	FALSE
EP400P1	260.0	270.0	3	6	18	5	FALSE
HSF1	256.0	270.0	3	13	48	10	FALSE
BOP1	256.0	270.0	3	12	35	10	TRUE
FNBP1	256.0	270.0	2	10	35	5	TRUE
ACOX1	256.0	270.0	2	8	19	2	FALSE
PDS5B	256.0	270.0	2	8	16	10	TRUE
PIK3C3	180.0	360.0	3	12	33	5	FALSE
IQGAP1	166.0	180.0	3	11	22	5	FALSE
SNAPC4	166.0	180.0	2	10	21	7	FALSE
UBE2J2	166.0	180.0	2	7	14	2	FALSE
SSH2	152.0	1095.0	4	10	30	137	FALSE
CARD8	152.0	270.0	4	14	44	79	TRUE
MED13	152.0	270.0	4	13	27	21	FALSE
LEF1	152.0	180.0	4	9	18	84	TRUE
VAV1	152.0	180.0	3	14	80	37	TRUE
STAG1	136.0	912.5	2	9	14	6	TRUE
PPP6R2	136.0	180.0	2	14	45	15	FALSE
RTTN	136.0	150.0	2	9	16	6	FALSE
MAPK8IP3	130.0	270.0	2	12	34	5	FALSE
SMG1	122.0	150.0	3	14	41	7	FALSE
INPP4B	122.0	150.0	3	13	32	3	FALSE
PIAS1	122.0	150.0	3	11	24	6	FALSE
DDX60	122.0	150.0	3	10	16	22	FALSE
ZNRD1ASP	122.0	150.0	3	6	14	4	FALSE
DPYD	122.0	150.0	2	14	36	22	FALSE
RUNX1	110.0	360.0	2	9	19	1	TRUE
ASH1L	106.0	1825.0	2	14	51	5	FALSE
WWOX	106.0	1095.0	3	6	12	5	TRUE
RFX2	106.0	360.0	2	7	14	9	TRUE

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	12	75.1	27	7.0	EAL
UBAP2L	chr1	154,215,171	154,276,510	12	65.9	30	7.0	EAL
PTBP1	chr19	792,391	817,327	8	106.0	47	346.0	EAL
TET2	chr4	105,140,874	105,284,803	6	196.7	814	1464.0	EAL
LUC7L	chr16	183,968	234,482	17	-20.9	30	7.0	AL
PPP3CA	chr4	101,018,429	101,352,471	17	118.2	6	46.0	EL
JPT2	chr16	1,673,276	1,707,072	16	2.7	23	46.0	AL
ANKRD11	chr16	89,262,620	89,495,561	15	10.4	23	7.0	AL
PPP6R3	chr11	68,455,717	68,620,333	15	56.3	149	14.0	EA
RNF157	chr17	76,137,452	76,245,311	15	-21.7	28	14.0	AL
SEC16A	chr9	136,435,095	136,488,759	15	-8.9	29	46.0	AL
CARD8	chr19	48,203,085	48,260,946	14	-30.3	79	152.0	DAL
CRAMP1	chr16	1,609,639	1,682,908	14	13.8	30	18.0	AL
DIP2A	chr21	46,453,948	46,575,013	14	-20.8	25	346.0	AL
PAFAH1B1	chr17	2,588,628	2,690,615	14	-4.7	30	7.0	AL
SMG1P1	chr16	22,432,007	22,497,220	14	135.4	3	100.0	EL
VAV1	chr19	6,767,667	6,862,366	14	26.8	37	152.0	AL
KDM6A	chrX	44,868,174	45,117,612	13	100.9	9	106.0	EL
ZZEF1	chr17	3,999,444	4,147,959	13	5.1	56	332.0	AL
GMDS	chr6	1,618,799	2,250,634	12	171.0	8	14.0	EL
GRB2	chr17	75,313,075	75,410,709	12	-14.8	42	14.0	AL
JMJD1C	chr10	63,162,220	63,527,075	12	107.7	5	7.0	EL
PIK3C3	chr18	41,950,197	42,086,482	12	144.8	5	180.0	EL
PRKACB	chr1	84,072,974	84,243,498	12	73.1	4	7.0	EL
XPO5	chr6	43,517,329	43,581,075	12	0.2	26	22.0	AL
EYA3	chr1	27,965,343	28,093,637	11	117.4	7	32.0	EL
PIAS1	chr15	68,049,178	68,196,466	11	93.5	6	122.0	EL
SRCAP	chr16	30,694,140	30,745,129	11	4.0	373	332.0	AL
ST13	chr22	40,819,534	40,862,008	11	53.5	29	7.0	AL
USP25	chr21	15,725,024	15,885,071	11	98.2	10	46.0	EL
HELLS	chr10	94,540,766	94,607,099	10	215.2	15	106.0	EL
PIKFYVE	chr2	208,261,266	208,363,751	10	345.1	410	14.0	EA
SSH2	chr17	29,620,938	29,935,228	10	-20.5	137	152.0	AL
UBR1	chr15	42,937,899	43,111,088	10	-22.4	48	1277.5	AL
FAM13A	chr4	88,720,953	89,062,195	9	136.0	1	7.0	EL
LEF1	chr4	108,042,544	108,173,956	9	-1.8	84	152.0	AL
MAPK14	chr6	36,022,676	36,116,236	9	21.5	91	7.0	AL
MCPH1	chr8	6,401,591	6,653,505	9	159.6	9	7.0	EL
PIP5K1A	chr1	151,193,543	151,254,531	9	502.7	3	277.5	EL
RSRC1	chr3	158,105,051	158,549,835	9	23.6	109	106.0	AL
SMURF2	chr17	64,539,616	64,667,268	9	-36.8	27	7.0	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
CLK4	chr5	178,597,663	178,632,053	8	52.3	53	106.0	AL
HERC4	chr10	67,916,898	68,080,346	8	33.9	35	106.0	AL
PDCD4	chr10	110,866,794	110,905,006	8	36.6	26	14.0	AL
MIR4745	chr19	799,939	810,001	7	141.1	47	346.0	EL
BRWD3	chrX	80,664,487	80,814,734	6	167.9	6	7.0	EL
ECD	chr10	73,129,523	73,173,095	6	167.9	24	1.0	EA
MAD1L1	chr7	1,810,791	2,237,948	6	-2.9	35	46.0	AL
MTMR3	chr22	29,878,168	30,035,868	6	-50.5	261	106.0	DAL
MTOR	chr1	11,101,530	11,267,551	6	-7.3	29	90.0	AL
NDFIP2	chr13	79,476,123	79,561,077	6	162.7	8	46.0	EL
PA2G4	chr12	56,099,318	56,118,910	6	48.4	38	14.0	AL
FANCA	chr16	89,732,550	89,821,657	20	16.0	21	15.0	L
NPLOC4	chr17	81,551,884	81,642,153	19	-33.7	16	46.0	DL
RPTOR	chr17	80,539,824	80,971,373	19	0.0	11	346.0	L
KDM2A	chr11	67,114,268	67,263,079	18	-35.4	7	50.0	DL
CBFB	chr16	67,024,146	67,106,055	16	66.9	14	22.0	E
EP300	chr22	41,087,609	41,185,077	16	13.1	6	46.0	L
PACS1	chr11	66,065,352	66,249,747	16	-41.1	5	46.0	DL
TRAPPC10	chr21	44,007,324	44,111,551	16	-17.4	7	14.0	L
UTRN	chr6	144,286,736	144,858,034	16	13.8	6	22.0	L
CCDC57	chr17	82,096,469	82,217,829	15	-46.2	6	642.5	DL
CREBBP	chr16	3,720,054	3,885,120	15	33.3	5	46.0	L
EHMT1	chr9	137,613,991	137,841,126	15	-5.3	3	50.0	L
NSD1	chr5	177,128,078	177,305,213	15	-32.0	6	62.0	DL
ASH1L	chr1	155,330,260	155,567,533	14	-34.8	5	106.0	DL
ATF7IP	chr12	14,360,631	14,507,935	14	18.4	8	7.0	L
DNMT1	chr19	10,128,343	10,200,135	14	-24.6	13	365.0	DL
DPYD	chr1	97,072,743	97,926,059	14	-7.3	22	122.0	L
EPB41	chr1	28,882,090	29,125,046	14	52.7	7	14.0	E
FCHSD2	chr11	72,831,744	73,147,098	14	-14.7	5	22.0	L
MACF1	chr1	39,079,166	39,492,138	14	-35.7	11	519.5	DL
PPP6R2	chr22	50,338,316	50,450,089	14	-32.7	15	136.0	DL
RABEP1	chr17	5,277,262	5,391,339	14	-4.1	26	14.0	A
SETD2	chr3	47,011,407	47,168,977	14	2.8	17	22.0	L
SMARCC1	chr3	47,580,887	47,786,915	14	-4.4	3	7.0	L
SMG1	chr16	18,799,852	18,931,404	14	-22.4	7	122.0	L
SUPT3H	chr6	44,821,729	45,383,051	14	45.5	8	14.0	L
VPS13D	chr1	12,225,038	12,517,046	14	54.5	3	0.0	E
VPS8	chr3	184,807,142	185,057,614	14	79.0	10	46.0	E
CYTH1	chr17	78,669,046	78,787,342	13	-35.4	4	7.0	DL
ELP4	chr11	31,504,728	31,789,525	13	113.3	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
FKBP5	chr6	35,568,584	35,733,583	13	-51.4	15	1555.0	DL
HSF1	chr8	144,286,568	144,319,726	13	-39.0	10	256.0	DL
INPP4B	chr4	142,018,159	142,851,535	13	-11.4	3	122.0	L
KMT5B	chr11	68,149,862	68,218,772	13	7.9	7	642.5	L
LRBA	chr4	150,259,658	151,020,497	13	42.4	17	106.0	L
MECP2	chrX	154,016,812	154,102,731	13	-31.0	12	99.0	DL
MED13	chr17	61,937,604	62,070,282	13	-1.8	21	152.0	L
MROH1	chr8	144,143,015	144,266,940	13	-50.3	5	46.0	DL
NF1	chr17	31,089,926	31,382,677	13	17.3	14	14.0	L
PBRM1	chr3	52,540,351	52,690,850	13	-24.7	14	7.0	L
PELP1	chr17	4,666,383	4,709,337	13	73.5	3	14.0	E
RAB11FIP3	chr16	420,667	527,481	13	-40.3	7	46.0	DL
SAFB2	chr19	5,581,998	5,627,927	13	-3.7	13	22.0	L
SF1	chr11	64,759,603	64,783,844	13	27.2	16	14.0	L
ARHGAP15	chr2	143,124,329	143,773,352	12	-1.7	7	5.0	L
BOP1	chr8	144,257,045	144,296,438	12	-32.4	10	256.0	L
CAPN1	chr11	65,176,214	65,217,006	12	-26.4	2	46.0	L
CHD4	chr12	6,565,081	6,612,433	12	26.3	19	7.0	L
CUX1	chr7	101,810,903	102,288,958	12	151.7	3	0.0	E
GBE1	chr3	81,484,698	81,766,799	12	155.0	9	46.0	E
LOC101929095	chr4	14,999,941	15,432,914	12	185.3	14	22.0	E
MAPK8IP3	chr16	1,701,182	1,775,317	12	-41.1	5	130.0	DL
MGA	chr15	41,655,411	41,774,943	12	11.3	85	46.0	A
MIR5096	chr17	4,136,088	4,245,637	12	-29.4	9	14.0	DL
PARP8	chr5	50,660,898	50,851,522	12	0.8	4	14.0	L
RABGAP1L	chr1	174,154,413	175,000,308	12	51.1	3	46.0	L
SMG6	chr17	2,054,838	2,308,775	12	-30.9	16	7.0	DL
SRRM2	chr16	2,747,328	2,776,412	12	45.3	32	1.0	A
USP15	chr12	62,255,339	62,414,721	12	49.4	14	15.0	L
ZNF34	chr8	144,767,223	144,792,345	12	-25.8	23	1.0	A
AP3B1	chr5	77,997,325	78,299,755	11	111.9	5	0.0	E
CDKAL1	chr6	20,529,456	21,237,403	11	6.0	5	106.0	L
CLEC16A	chr16	10,939,487	11,187,189	11	70.8	9	0.0	E
CPEB2	chr4	14,997,673	15,075,153	11	215.2	14	22.0	E
CSNK1D	chr17	82,237,660	82,278,742	11	-25.8	8	7.0	L
DDX42	chr17	63,769,188	63,824,317	11	-7.3	6	14.0	L
DIP2B	chr12	50,499,984	50,753,667	11	-34.0	4	7.0	L
DLG1	chr3	197,037,559	197,304,272	11	-2.4	8	7.0	L
GLCCI1	chr7	7,963,742	8,094,079	11	37.4	4	84.0	L
HNRNPUL2	chr11	62,707,624	62,732,385	11	-20.1	9	76.0	L
IQGAP1	chr15	90,383,240	90,507,243	11	-9.3	5	166.0	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
KMT2C	chr7	152,129,924	152,441,005	11	-1.5	5	7.0	L
MED13L	chr12	115,953,575	116,282,186	11	15.4	38	7.0	A
NCOA1	chr2	24,579,476	24,775,701	11	-0.5	3	22.0	L
PCNX1	chr14	70,902,404	71,120,382	11	-9.4	153	14.0	A
POT1	chr7	124,817,385	124,934,983	11	46.8	26	0.0	A
RBM39	chr20	35,698,608	35,747,336	11	164.9	2	14.0	E
SMCHD1	chr18	2,650,886	2,810,017	11	-17.6	4	7.0	L
STK4	chr20	44,961,473	45,084,977	11	-7.3	23	11.0	A
STXBP5	chr6	147,199,357	147,395,476	11	49.8	8	350.0	L
UBR4	chr1	19,069,505	19,215,252	11	11.3	8	7.0	L
ZGPAT	chr20	63,702,441	63,741,142	11	-52.7	5	7.0	DL
ZNF251	chr8	144,715,908	144,760,585	11	-22.9	21	22.0	L
ZNF407	chr18	74,625,962	75,070,672	11	109.6	3	1.0	E
ADD1	chr4	2,838,856	2,935,075	10	-5.6	42	7.0	A
ARIH1	chr15	72,469,325	72,591,555	10	85.4	5	7.0	L
ATF7	chr12	53,502,855	53,631,415	10	-9.8	32	1.0	A
CAMK2D	chr4	113,446,031	113,766,927	10	17.1	9	106.0	L
CLTC	chr17	59,614,688	59,701,956	10	107.3	3	1.0	E
COX6B1	chr19	35,643,222	35,663,784	10	-4.6	5	825.0	L
DDX60	chr4	168,211,290	168,323,807	10	111.9	22	122.0	L
DENND1B	chr1	197,499,748	197,780,493	10	-15.2	3	7.0	L
FAM117B	chr2	202,630,177	202,774,757	10	68.6	6	14.0	E
FNBP1	chr9	129,882,186	130,048,194	10	-27.1	5	256.0	L
FOXJ3	chr1	42,171,538	42,340,877	10	29.2	12	7.0	L
FRYL	chr4	48,492,362	48,785,299	10	27.2	24	14.0	A
IL4I1	chr19	49,884,655	49,934,539	10	-36.7	5	46.0	DL
KIAA1468	chr18	62,182,290	62,312,122	10	34.3	17	46.0	L
LOC101926943	chr7	74,683,936	74,733,918	10	106.0	7	0.0	E
LRPPRC	chr2	43,881,223	44,001,005	10	363.6	7	0.0	E
MOB3A	chr19	2,066,035	2,101,270	10	-12.2	2	22.0	L
NBEAL1	chr2	203,009,878	203,222,994	10	72.2	11	14.0	L
NELL2	chr12	44,503,274	44,918,928	10	39.1	2	4.0	L
NOSIP	chr19	49,550,467	49,585,572	10	-63.6	29	0.0	DA
PHF3	chr6	63,630,801	63,720,522	10	164.9	7	4.0	E
PLEC	chr8	143,910,146	143,981,745	10	-59.4	11	22.0	DL
PLEKHA5	chr12	19,124,691	19,381,399	10	41.8	2	7.0	L
COP1	chr1	175,939,825	176,212,244	10	125.2	3	14.0	E
RUNX2	chr6	45,323,316	45,556,082	10	94.3	8	14.0	E
SLC6A16	chr19	49,284,634	49,330,217	10	-8.7	2	14.0	L
SNAPC4	chr9	136,370,568	136,403,437	10	29.8	7	166.0	L
SNX13	chr7	17,785,760	17,945,508	10	85.4	5	14.0	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
TANC2	chr17	63,004,536	63,432,706	10	105.0	11	7.0	E
TCF20	chr22	42,155,012	42,288,927	10	-7.3	10	7.0	L
TRAPPC8	chr18	31,824,172	31,948,128	10	49.8	4	7.0	L
UBAC2	chr13	99,195,424	99,391,499	10	36.0	4	14.0	L
VMP1	chr17	59,702,464	59,847,255	10	-36.2	28	46.0	DA
VPS52	chr6	33,245,271	33,276,965	10	-9.2	10	106.0	L
WDR82	chr3	52,249,421	52,283,643	10	3.0	7	277.5	L
ZFC3H1	chr12	71,604,600	71,668,969	10	136.0	4	0.0	E
ADK	chr10	74,146,184	74,714,303	9	-16.1	3	7.0	L
AP2B1	chr17	35,582,262	35,731,417	9	39.1	13	90.0	L
ASXL2	chr2	25,728,752	25,883,516	9	-41.0	3	7.0	L
ATG5	chr6	106,179,476	106,330,820	9	252.3	2	0.0	E
BCAS3	chr17	60,672,774	61,397,838	9	-34.8	2	7.0	L
C6orf106	chr6	34,582,279	34,701,850	9	-11.9	3	46.0	L
CAMK4	chr5	111,218,652	111,499,884	9	4.3	9	7.0	L
DAP3	chr1	155,684,090	155,744,009	9	131.8	2	0.0	E
DAZAP1	chr19	1,402,568	1,440,687	9	-32.6	2	4.0	L
DNAJC13	chr3	132,412,659	132,544,032	9	98.7	71	7.0	A
ERC1	chr12	986,207	1,500,933	9	3.5	4	7.0	L
FOCAD	chr9	20,653,308	21,000,955	9	140.0	17	7.0	E
FRG1BP	chr20	30,372,163	30,424,842	9	224.5	4	7.0	E
GAK	chr4	844,274	937,390	9	156.8	4	14.0	E
GANAB	chr11	62,619,825	62,651,726	9	-19.6	6	7.0	L
GPBP1L1	chr1	45,622,303	45,691,630	9	-38.2	2	46.0	L
GPHN	chr14	66,502,406	67,186,808	9	131.8	2	0.0	E
HNRNPUL1	chr19	41,257,475	41,312,783	9	68.6	4	14.0	L
HTT	chr4	3,069,680	3,248,960	9	6.0	25	1.0	A
KDM4A	chr1	43,645,125	43,710,518	9	215.2	7	0.0	E
KIF20B	chr10	89,696,589	89,779,943	9	167.9	13	0.0	E
LCOR	chr10	96,827,259	96,991,212	9	113.3	4	0.0	E
MUM1	chr19	1,349,976	1,383,431	9	-43.7	4	90.0	DL
NAA38	chr17	7,851,680	7,890,388	9	-36.3	15	14.0	DL
NDUFV2	chr18	9,097,629	9,139,345	9	119.2	15	22.0	L
NEAT1	chr11	65,417,797	65,450,538	9	2.0	4	22.0	L
NEMP1	chr12	57,050,642	57,083,791	9	-16.9	10	46.0	L
NUP107	chr12	68,681,950	68,750,814	9	456.3	4	0.0	E
NUP214	chr9	131,120,560	131,239,670	9	-2.1	8	106.0	L
PDCD10	chr3	167,678,905	167,739,863	9	410.0	4	0.0	E
PHF20L1	chr8	132,770,357	132,853,807	9	54.5	4	22.0	L
POGZ	chr1	151,397,723	151,464,465	9	23.6	26	0.0	A
POLA2	chr11	65,256,851	65,303,685	9	-20.5	9	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
PTPRA	chr20	2,859,194	3,043,669	9	-13.3	4	1555.0	L
RAB11FIP2	chr10	117,999,915	118,051,884	9	456.3	19	1.0	E
RBPJ	chr4	26,314,709	26,440,130	9	209.1	2	0.0	E
RNF216	chr7	5,615,040	5,786,730	9	-48.5	15	106.0	DL
ROCK1	chr18	20,944,741	21,116,851	9	93.9	13	14.0	E
RTTN	chr18	69,998,805	70,210,726	9	2.3	6	136.0	L
RUNX1	chr21	34,782,800	35,054,298	9	6.8	1	110.0	L
SEPT7	chr7	35,795,985	35,912,105	9	107.3	10	7.0	E
MTREX	chr5	55,302,747	55,430,581	9	162.7	6	0.0	E
SNTB1	chr8	120,530,744	120,817,069	9	147.3	3	4.0	E
SPEN	chr1	15,842,863	15,945,455	9	2.3	2	7.0	L
STAG1	chr3	136,332,156	136,757,403	9	29.8	6	136.0	L
TARSL2	chr15	101,648,751	101,729,442	9	71.2	22	7.0	L
THEMIS	chr6	127,703,193	127,923,631	9	-16.0	5	106.0	L
TONSL	chr8	144,423,779	144,449,429	9	-29.9	7	7.0	L
TTC21B	chr2	165,868,361	165,958,838	9	15.9	5	46.0	L
TUT1	chr11	62,570,044	62,596,637	9	-31.3	5	7.0	L
URI1	chr19	29,918,643	30,021,612	9	199.6	6	1.0	E
WWP1	chr8	86,337,764	86,472,949	9	172.0	4	7.0	E
ZC3H13	chr13	45,949,464	46,057,778	9	152.9	6	46.0	E
ABCD2	chr12	39,546,219	39,625,041	8	131.8	8	14.0	E
ACOX1	chr17	75,936,510	75,984,434	8	-21.7	2	256.0	L
ASCC3	chr6	100,503,194	100,886,372	8	178.2	4	7.0	E
ATP2A2	chr12	110,276,226	110,356,092	8	12.9	67	22.0	A
ATP8A1	chr4	42,403,374	42,662,105	8	33.5	4	14.0	L
AUH	chr9	91,208,814	91,366,969	8	29.0	23	7.0	A
CASK	chrX	41,509,935	41,928,034	8	-4.5	5	346.0	L
DOT1L	chr19	2,159,148	2,237,578	8	-18.1	6	14.0	L
DYNC1H1	chr14	101,959,527	102,055,798	8	71.2	44	7.0	A
EED	chr11	86,239,383	86,283,810	8	136.0	6	14.0	E
HSF2	chr6	122,394,550	122,438,119	8	419.2	15	14.0	E
IKZF2	chr2	212,994,685	213,156,609	8	201.3	1	0.0	E
KLRG1	chr12	8,945,043	9,015,744	8	-11.0	3	7.0	L
LUC7L2	chr7	139,335,358	139,428,457	8	209.1	4	14.0	E
MAP4K3	chr2	39,244,265	39,442,312	8	29.8	15	46.0	L
MMP23A	chr1	1,627,779	1,706,808	8	5.1	17	14.0	L
NBAS	chr2	15,161,907	15,566,348	8	6.0	4	106.0	L
NCOA3	chr20	47,496,856	47,661,877	8	-35.1	6	7.0	L
NUP62	chr19	49,901,825	49,934,731	8	-40.1	5	46.0	DL
PDS5B	chr13	32,581,426	32,783,020	8	85.4	10	256.0	L
PPP1R16A	chr8	144,472,981	144,507,121	8	-36.6	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
RAD51B	chr14	67,814,778	68,688,106	8	-21.5	2	22.0	L
RBL2	chr16	53,429,419	53,496,648	8	102.3	8	14.0	L
SLX4IP	chr20	10,430,302	10,633,034	8	102.3	3	7.0	L
SPG7	chr16	89,503,387	89,562,768	8	-30.5	10	7.0	L
SYNE2	chr14	63,847,964	64,231,451	8	65.9	8	22.0	L
UBE2L3	chr22	21,544,446	21,629,034	8	52.7	3	7.0	L
UBR5	chr8	102,247,273	102,417,689	8	21.2	19	7.0	L
VPS28	chr8	144,418,600	144,433,563	8	9.1	7	7.0	L
VRK3	chr19	49,971,466	50,030,548	8	-34.6	2	7.0	L
YTHDF3	chr8	63,163,552	63,217,788	8	70.0	13	7.0	L
ANXA1	chr9	73,146,730	73,175,394	7	155.0	5	14.0	L
ATE1	chr10	121,735,420	121,933,801	7	240.0	14	46.0	E
BCKDHB	chr6	80,101,609	80,351,270	7	240.0	3	0.0	E
CCDC47	chr17	63,740,249	63,778,728	7	-42.1	6	22.0	L
CDC73	chr1	193,116,957	193,259,812	7	150.9	19	7.0	E
CDK8	chr13	26,249,103	26,410,236	7	209.1	1	0.0	E
CHMP2B	chr3	87,222,262	87,260,548	7	85.4	24	7.0	A
CLASP2	chr3	33,491,245	33,723,213	7	36.6	5	7.0	L
DERL2	chr17	5,466,250	5,491,230	7	48.4	37	0.0	A
DNAJC1	chr10	21,751,547	22,008,721	7	4.3	38	7.0	A
GATAD2B	chr1	153,799,906	153,927,975	7	-43.3	2	7.0	DL
GTDC1	chr2	143,941,013	144,337,534	7	138.4	9	7.0	E
INO80	chr15	40,973,880	41,121,246	7	-25.8	3	14.0	L
KMT2D	chr12	49,013,974	49,060,324	7	12.6	33	0.0	A
LSM2	chr6	31,792,391	31,811,984	7	-67.0	2	14.0	DL
MACROD2	chr20	13,990,499	16,058,196	7	224.5	1	0.0	E
MATR3	chr5	139,268,751	139,336,677	7	125.2	6	1.0	E
MIR5096	chr1	15,866,148	15,910,467	7	11.3	2	7.0	DL
NFKBIL1	chr6	31,541,850	31,563,829	7	-47.0	4	7.0	DL
OPRM1	chr6	154,005,495	154,251,867	7	20.0	3	14.0	L
PAG1	chr8	80,962,810	81,117,068	7	-13.9	2	32.0	L
PCNT	chr21	46,319,121	46,450,769	7	6.0	5	4.0	L
PDE12	chr3	57,551,246	57,661,480	7	201.3	3	0.0	E
PDE7A	chr8	65,709,333	65,846,734	7	-10.5	4	7.0	L
PHACTR4	chr1	28,364,581	28,505,369	7	-38.2	3	22.0	L
PPP4R2	chr3	72,991,742	73,074,201	7	240.0	2	7.0	E
PRKCA	chr17	66,297,807	66,815,744	7	62.3	7	7.0	L
PRKN	chr6	161,342,557	162,732,802	7	191.4	3	0.0	E
RAD23B	chr9	107,278,235	107,337,194	7	363.6	2	0.0	E
RASA1	chr5	87,263,252	87,396,926	7	140.0	3	0.0	E
RFX2	chr19	5,988,163	6,115,653	7	-33.4	9	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
RIPOR2	chr6	24,799,280	25,047,288	7	-16.3	10	7.0	L
SNORA30	chr16	30,705,536	30,715,665	7	54.5	373	332.0	L
SPPL3	chr12	120,757,509	120,909,352	7	-35.5	9	14.0	L
SYNE1	chr6	152,116,683	152,642,399	7	36.6	22	46.0	L
TCF25	chr16	89,868,585	89,916,384	7	-35.1	5	106.0	L
UBE2J2	chr1	1,248,911	1,278,854	7	-62.4	2	166.0	DL
UCHL3	chr13	75,544,479	75,611,020	7	217.9	6	7.0	E
UNKL	chr16	1,358,204	1,419,720	7	15.9	7	15.0	L
USP9Y	chrY	12,696,230	12,865,843	7	209.1	4	18.0	E
ZNF473	chr19	50,020,892	50,053,774	7	-7.3	3	22.0	L
ABLIM1	chr10	114,426,109	114,773,225	6	308.0	6	14.0	E
ARHGAP12	chr10	31,800,397	31,933,876	6	270.9	3	14.0	E
ATP9B	chr18	79,064,274	79,383,282	6	13.3	2	7.0	L
BAG6	chr6	31,634,027	31,657,700	6	-32.2	36	46.0	A
BZW2	chr7	16,641,133	16,711,523	6	209.1	6	0.0	E
CAMKMT	chr2	44,356,903	44,777,592	6	308.0	9	0.0	E
CEP85L	chr6	118,455,771	118,715,075	6	-15.7	3	46.0	L
EP400P1	chr12	132,079,282	132,131,340	6	66.9	5	260.0	L
EVL	chr14	99,966,474	100,149,236	6	-23.3	4	7.0	L
FUNDC2	chrX	155,021,788	155,061,916	6	201.3	9	46.0	E
GNA12	chr7	2,723,105	2,849,325	6	240.0	2	0.0	E
HERC2	chr15	28,106,036	28,327,152	6	518.1	4	1.0	E
HSF5	chr17	58,415,166	58,493,401	6	-7.3	34	1.0	A
MARF1	chr16	15,589,368	15,648,166	6	75.7	17	106.0	L
KIFC1	chr6	33,386,535	33,414,922	6	-2.9	42	7.0	A
MBD3	chr19	1,571,670	1,597,761	6	58.9	2	7.0	L
MIR5096	chr22	37,663,025	38,029,093	6	-50.8	6	7.0	DL
N4BP1	chr16	48,533,725	48,615,209	6	85.4	32	106.0	A
OXCT1	chr5	41,725,064	41,875,689	6	54.5	3	7.0	L
PAPOLA	chr14	96,497,375	96,572,116	6	128.2	3	0.0	E
PHF20	chr20	35,767,000	35,955,366	6	-24.7	38	7.0	A
PPFIA1	chr11	70,265,699	70,389,501	6	23.6	20	106.0	L
PPP1CB	chr2	28,746,747	28,807,940	6	-25.8	23	22.0	A
PTGES3	chr12	56,658,340	56,693,408	6	-47.0	23	1.0	A
RAB18	chr10	27,499,173	27,547,237	6	29.8	24	7.0	A
RBM27	chr5	146,198,599	146,294,221	6	345.1	3	0.0	E
RPRD2	chr1	150,359,110	150,481,565	6	-53.6	6	14.0	DL
RSBN1L	chr7	77,691,425	77,784,803	6	48.4	31	1.0	A
SEC23A	chr14	39,026,918	39,108,528	6	33.9	7	7.0	L
SEC31A	chr4	82,813,508	82,905,571	6	29.8	66	7.0	A
SFI1	chr22	31,491,138	31,623,551	6	-63.6	24	7.0	DA

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

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
SMAP2	chr1	40,368,705	40,428,326	6	-7.3	61	7.0	A
TMTC3	chr12	88,137,295	88,204,887	6	301.8	2	0.0	E
TNKS	chr8	9,550,934	9,787,346	6	162.7	8	7.0	E
TRIM33	chr1	114,387,776	114,516,160	6	104.0	17	106.0	L
UBE2F-SCLY	chr2	237,961,944	238,104,413	6	-7.3	6	46.0	L
WWOX	chr16	78,094,412	79,217,667	6	39.1	5	106.0	L
ZNRD1ASP	chr6	29,996,010	30,066,189	6	-7.3	4	122.0	L
ANKRD46	chr8	100,504,751	100,564,786	5	-14.4	24	7.0	A
AQR	chr15	34,851,350	34,974,794	5	23.6	84	14.0	A
CNOT6	chr5	180,489,398	180,583,405	5	-56.6	2	7.0	DL
CSNK1G1	chr15	64,160,516	64,361,259	5	-19.4	8	7.0	L
ELMO1	chr7	36,847,905	37,454,326	5	-38.2	34	46.0	A
FANCL	chr2	58,154,242	58,246,380	5	191.4	6	0.0	E
FUS	chr16	31,175,109	31,199,871	5	217.9	12	0.0	E
IQCB1	chr3	121,764,760	121,840,079	5	85.4	79	15.0	A
KDM5D	chrY	19,700,414	19,749,939	5	178.2	2	14.0	A
MAP2K2	chr19	4,085,321	4,129,129	5	-32.0	2	106.0	L
MEMO1	chr2	31,862,809	32,016,052	5	-51.2	47	7.0	A
MIR5096	chr1	235,507,822	235,723,113	5	116.3	1	0.0	DL
NAP1L1	chr12	76,039,744	76,090,033	5	196.7	23	7.0	A
NHLRC2	chr10	113,849,631	113,917,506	5	44.2	23	7.0	A
OGDH	chr7	44,601,521	44,714,070	5	-44.4	17	332.0	L
POM121	chr7	72,874,334	72,956,440	5	224.5	29	1.0	A
QKI	chr6	163,409,642	163,583,596	5	45.7	3	7.0	L
RMND5A	chr2	86,715,290	86,783,041	5	15.9	26	0.0	A
RPA3	chr7	7,631,562	7,723,607	5	85.4	87	106.0	A
SEPT9	chr17	77,276,409	77,505,596	5	-57.6	27	7.0	A
SNRPA	chr19	40,745,853	40,770,392	5	209.1	19	7.0	E
STAG3	chr7	100,172,723	100,219,387	5	-11.3	35	0.0	A
STX8	chr17	9,245,470	9,580,958	5	-2.4	4	7.0	L
XPO1	chr2	61,472,933	61,543,283	5	85.4	25	106.0	A
AKAP9	chr7	91,935,874	92,115,673	4	-1.8	25	0.0	A
CAAP1	chr9	26,835,684	26,897,828	4	-7.3	27	46.0	A
EHMT1	chr9	137,758,021	137,769,772	4	131.8	1	0.0	L
EXOSC10	chr1	11,061,612	11,104,910	4	-0.1	70	7.0	A
GOLPH3L	chr1	150,641,224	150,702,196	4	-53.6	24	7.0	A
ITM2B	chr13	48,228,137	48,267,096	4	-7.3	23	7.0	A
MSH5-SAPCD1	chr6	31,734,947	31,769,847	4	-62.9	43	7.0	A
PATL1	chr11	59,631,715	59,674,038	4	-7.3	578	332.0	A
PDCD11	chr10	103,391,654	103,451,262	4	6.0	27	152.0	A
PDE3B	chr11	14,638,722	14,877,058	4	2.3	35	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
RABGAP1	chr9	122,936,008	123,109,868	4	6.0	29	7.0	A
TRIO	chr5	14,138,701	14,515,204	4	332.7	61	106.0	A
CHD1L	chr1	147,168,193	147,300,766	3	641.8	25	1.0	A
DCUN1D4	chr4	51,837,999	51,921,837	3	-22.7	32	106.0	A
EIF2AK4	chr15	39,929,123	40,040,596	3	54.5	43	7.0	A
GPN1	chr2	27,623,647	27,655,846	3	11.3	62	1.0	A
KCTD3	chr1	215,562,378	215,626,821	3	39.1	1	0.0	A
LOC101927151	chr19	27,788,466	27,811,780	3	456.3	31	46.0	A
NGDN	chr14	23,464,688	23,483,193	3	39.1	44	0.0	A
POLG2	chr17	64,472,784	64,502,066	3	116.3	43	7.0	A
PRKD2	chr19	46,669,315	46,722,127	3	-45.5	24	22.0	A
SNAP29	chr22	20,854,003	20,896,213	3	147.3	27	7.0	A
ZNF573	chr19	37,733,301	37,784,590	3	-25.8	86	735.0	A
C20orf196	chr20	5,745,386	5,869,407	2	-47.0	1	0.0	A
CRTAP	chr3	33,108,957	33,152,773	2	270.9	35	7.0	A
GRSF1	chr4	70,810,781	70,844,910	2	Inf	23	0.0	A
JMJD6	chr17	76,707,831	76,731,799	2	164.9	53	1.0	A
LINC01473	chr2	186,028,533	186,091,317	2	Inf	82	7.0	A
PHF12	chr17	28,900,252	28,956,490	2	-42.9	40	106.0	A
RASEF	chr9	82,974,584	83,068,128	2	Inf	43	46.0	A
SNHG12	chr1	28,573,537	28,586,854	2	456.3	96	332.0	A
TAC3	chr12	57,004,996	57,021,560	2	-71.5	42	7.0	A
TGFBR2	chr3	30,601,501	30,699,141	2	23.6	31	7.0	A
ACTL6A	chr3	179,557,879	179,593,405	1	-69.1	40	0.0	A
C19orf48	chr19	50,792,692	50,809,853	1	-53.6	28	46.0	A
CD109	chr6	73,691,084	73,833,317	1	-85.7	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	-7.3	24	0.0	A
LOC101927501	chrX	43,171,993	43,231,598	1	Inf	23	1.0	A
MICAL2	chr11	12,105,575	12,268,790	1	-73.5	39	15.0	A
RBAK-RBAKDN	chr7	5,040,820	5,078,223	1	-53.6	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	85.4	43	7.0	A
ZNF92	chr7	65,368,798	65,406,135	1	Inf	42	7.0	A
TNRC6B	chr22	40,039,816	40,340,808	17	-29.3	10	46.0	D
RBM6	chr3	49,935,043	50,082,252	15	-31.8	7	1.0	D
MIR1268A	chr9	128,347,046	128,667,136	14	-29.8	4	1.0	D
NFATC3	chr16	68,080,365	68,234,259	14	-30.6	4	4.0	D
CCNL2	chr1	1,380,710	1,404,338	13	-32.6	8	22.0	D
NUP188	chr9	128,942,692	129,012,096	13	-38.9	12	1.0	D
IKZF3	chr17	39,752,714	39,869,188	12	-38.2	4	46.0	D

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

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
UBE2G1	chr17	4,264,216	4,371,674	12	-33.8	3	14.0	D
FOXK2	chr17	82,514,717	82,609,607	11	-40.2	19	0.0	D
IP6K1	chr3	49,719,294	49,791,540	11	-61.3	2	1.0	D
RABL6	chr9	136,802,921	136,846,187	11	-36.7	11	0.0	D
CCND3	chr6	41,929,932	42,053,894	10	-57.0	3	0.0	D
EIF2B3	chr1	44,845,521	44,991,722	10	-61.1	6	1.0	D
R3HDM2	chr12	57,248,763	57,436,005	10	-41.0	2	0.0	D
RERE	chr1	8,347,403	8,822,640	10	-46.7	5	0.0	D
SP1	chr12	53,375,194	53,421,442	10	-47.9	10	0.0	D
STAT5B	chr17	42,194,176	42,281,406	10	-42.2	2	0.0	D
TRAF2	chr9	136,881,512	136,931,615	10	-49.6	4	46.0	D
ABHD16A	chr6	31,681,948	31,708,360	9	-51.2	6	0.0	D
CEACAM21	chr19	41,544,517	41,591,844	9	-49.2	2	0.0	D
HCG20	chr6	30,761,824	30,797,250	9	-52.6	4	22.0	D
ITGAL	chr16	30,467,661	30,528,185	9	-45.5	14	14.0	D
NARFL	chr16	724,754	746,038	9	-58.8	3	22.0	D
PSMB9	chr6	32,849,160	32,864,851	9	-55.4	2	0.0	D
RBM4	chr11	66,633,616	66,673,386	9	-48.7	6	11.0	D
TSC2	chr16	2,042,894	2,093,720	9	-53.6	1	22.0	D
HORMAD2	chr22	30,075,068	30,182,075	8	-54.1	4	7.0	D
IFT140	chr16	1,505,426	1,617,108	8	-57.5	3	7.0	D
PPP3CC	chr8	22,435,969	22,546,144	8	-48.1	3	0.0	D
QRICH1	chr3	49,024,706	49,099,373	8	-55.7	7	1.0	D
TAP2	chr6	32,816,832	32,843,823	8	-54.6	4	7.0	D
VARS	chr6	31,772,519	31,800,935	8	-47.3	5	46.0	D
WDR90	chr16	644,362	672,829	8	-61.5	3	0.0	D
ASCC1	chr10	72,091,031	72,222,134	7	-48.2	2	0.0	D
PRRC2A	chr6	31,615,672	31,642,777	7	-48.3	13	14.0	D
RAB40C	chr16	584,356	634,273	7	-52.6	3	0.0	D
RBM14-RBM4	chr11	66,611,581	66,651,473	7	-51.4	6	11.0	D
SEPT2	chr2	241,310,186	241,359,026	7	-50.2	8	0.0	D
STK11	chr19	1,200,798	1,233,435	7	-60.5	6	0.0	D
ADCK5	chr8	144,369,014	144,398,238	6	-48.7	2	0.0	D
BLM	chr15	90,712,326	90,820,462	6	-41.3	11	14.0	D
CPSF1	chr8	144,388,230	144,414,349	6	-42.2	4	0.0	D
DIDO1	chr20	62,872,737	62,942,952	6	-55.8	2	0.0	D
GRAP2	chr22	39,896,081	39,978,342	6	-57.9	4	4.0	D
MCM3AP	chr21	46,230,124	46,290,394	6	-51.2	8	22.0	D
PCED1B	chr12	47,074,602	47,241,663	6	-54.7	1	0.0	D
PRKAR2A	chr3	48,741,578	48,852,850	6	-58.4	2	7.0	D
RNPS1	chr16	2,248,115	2,273,412	6	-78.4	2	0.0	D

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

Gene	Chromosome	Start Pos.	End Pos.	Patients	Freq. Change (%)	Peak Abund.	Long. Obs.	Criteria
WASF2	chr1	27,399,225	27,495,187	6	-48.2	3	0.0	D
WNK1	chr12	747,922	916,452	6	-60.3	4	1.0	D
ZBTB4	chr17	7,454,365	7,489,249	6	-62.2	3	0.0	D
EXOC2	chr6	480,137	698,141	5	-71.9	4	0.0	D
HAGH	chr16	1,804,102	1,832,194	5	-58.0	6	14.0	D
MIR1268A	chr19	2,997,812	3,069,714	5	8.2	3	0.0	D
TC2N	chr14	91,774,751	91,872,536	5	-49.9	4	0.0	D
ZNF598	chr16	1,992,651	2,014,821	5	-63.6	3	0.0	D
FAM222B	chr17	28,750,977	28,847,839	4	-52.5	5	0.0	D
PCBP3	chr21	45,638,724	45,947,454	4	-54.8	2	0.0	D
MIR1268A	chr15	28,320,482	28,505,841	2	Inf	1	0.0	D