

Genes of interest marked by vector integration
— Patients and
Response Groups CR/PRtd & PR/NR

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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 178 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** Longitudinal gene of interest are those that have insertion sites in at least 3 different positions in at least 3 patients. Additionally, a cutoff of at least 10 independent sonic breaks is imposed and only the top 100by average of last time point for the 3 latest insertion sites are selected.

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	418	*/ 11.7	/ 6.70	/ 0.000	*/ 8.61	*/ 6.70	/ 0.478
Depletion	402	*/ 15.9	*/ 7.21	*/ 0.995	*/ 9.20	*/ 7.21	/ 0.000
Abundance	184	*/ 21.7	/ 7.07	/ 0.000	*/ 10.87	*/ 7.61	*/ 1.087
Longitudinal	100	*/ 14.0	/ 7.00	/ 0.000	*/ 9.00	*/ 6.00	/ 0.000
Composite	655	*/ 14.0	*/ 6.56	/ 0.000	*/ 8.70	*/ 7.02	*/ 0.611

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 identified 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: 8.34%
- Tumor Suppressors: 4.68%
- Lymphoma Related: 0.14%
- COSMIC Related: 3.05%
- TCGA Related: 2.39%
- Clonal Hematopoiesis Related: 0.14%

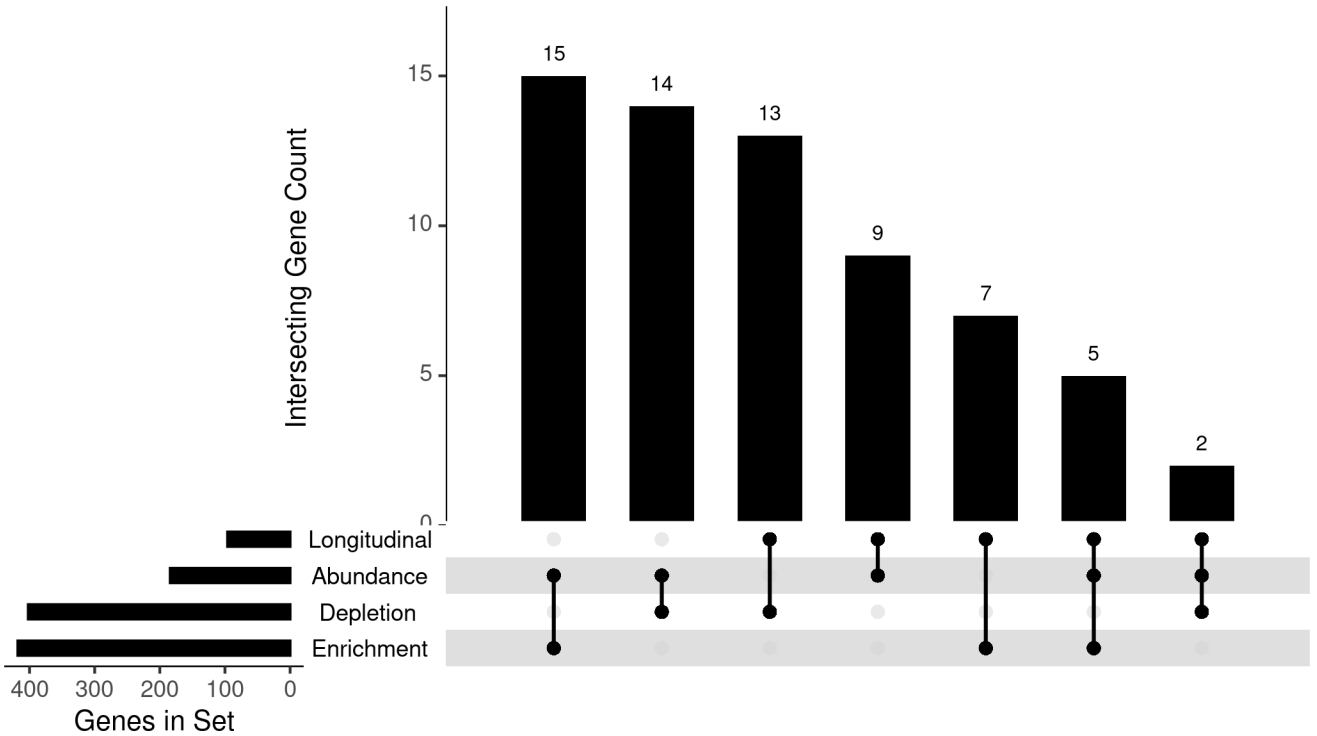


Figure 1: Intersecting gene lists identified through the various selection criteria.

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
ANKRD11	66	25.1	25	2555	EAL
RNF213	63	21.8	76	2190	EAL
ADD1	60	24.5	43	2008	EAL
FOXP1	54	33.3	49	3285	EAL
NELL2	45	42.5	441	4015	EAL

Table 3: GO Biological Process. Top 7 per group. Total genes considered: 847

Group	GO ID	GO Term	Term Size	Gene Count	Adjusted P-value
1	GO:0009792	embryo development ending in birth or egg hatching	451	30	0.0401352
	GO:0043009	chordate embryonic development	448	30	0.0401352
	GO:0007507	heart development	405	29	0.0263419
	GO:0001701	in utero embryonic development	271	21	0.0384766
	GO:0060537	muscle tissue development	282	21	0.0401352
	GO:0014706	striated muscle tissue development	157	16	0.0086340
	GO:0048738	cardiac muscle tissue development	145	13	0.0401352
2	GO:0016570	histone modification	387	33	0.0006695
	GO:0002764	immune response-regulating signaling pathway	475	33	0.0221772
	GO:0007264	small GTPase mediated signal transduction	470	31	0.0401352
	GO:0002521	leukocyte differentiation	406	28	0.0401352
	GO:0018205	peptidyl-lysine modification	352	27	0.0147417
	GO:0002768	immune response-regulating cell surface receptor signaling pathway	341	26	0.0195388
	GO:0030099	myeloid cell differentiation	317	25	0.0149999
3	GO:0044772	mitotic cell cycle phase transition	495	35	0.0136676
	GO:1901987	regulation of cell cycle phase transition	442	33	0.0077482
	GO:0051223	regulation of protein transport	456	30	0.0438861
	GO:0060271	cilium assembly	351	29	0.0035124
	GO:0044782	cilium organization	360	29	0.0051358
	GO:0010256	endomembrane system organization	412	29	0.0317821
	GO:1901990	regulation of mitotic cell cycle phase transition	354	28	0.0083582
4	GO:0006397	mRNA processing	459	35	0.0038361
	GO:0008380	RNA splicing	403	31	0.0069513
	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	311	25	0.0126797
	GO:0000398	mRNA splicing, via spliceosome	311	25	0.0126797
	GO:0000375	RNA splicing, via transesterification reactions	314	25	0.0137517
	GO:1903311	regulation of mRNA metabolic process	309	24	0.0221237
	GO:0006482	protein demethylation	29	5	0.0332242
5	GO:0048729	tissue morphogenesis	496	33	0.0396011
	GO:0002009	morphogenesis of an epithelium	425	31	0.0147675
	GO:0070646	protein modification by small protein removal	278	21	0.0401352
	GO:0016579	protein deubiquitination	262	20	0.0401352
	GO:0035567	non-canonical Wnt signaling pathway	136	15	0.0054508
	GO:2000027	regulation of animal organ morphogenesis	144	14	0.0242289
	GO:0001738	morphogenesis of a polarized epithelium	127	12	0.0401352
6	GO:0006281	DNA repair	497	33	0.0401352
	GO:0000724	double-strand break repair via homologous recombination	105	11	0.0333618
	GO:0000725	recombinational repair	106	11	0.0360969
	GO:2001251	negative regulation of chromosome organization	72	8	0.0446444
	GO:0031577	spindle checkpoint signaling	34	5	0.0446444
	GO:0032205	negative regulation of telomere maintenance	34	5	0.0446444

Integration Frequency (Enrichment)

Table 4: Table of top 50 genes with the most frequent clonal enrichment of patients samples..

Gene	Num. Patients	Time 0 Sites	Patient Sites	Onco-Related	Frequency Increase (%)
LOC101927550	8	2	10	FALSE	837.6
PPP2R3A	10	3	12	FALSE	650.1
PTPRT	8	3	12	TRUE	650.1
GFRA1	10	3	11	FALSE	587.6
LTBP1	11	3	11	FALSE	587.6
CNTN5	10	4	13	FALSE	509.5
MICAL3	15	5	16	FALSE	500.1
ATP9A	11	4	12	FALSE	462.6
LOC100499484-C9ORF174	11	4	12	FALSE	462.6
MIR4435-2HG	13	5	15	FALSE	462.6
LOC100499484	11	4	12	FALSE	462.6
RLIM	11	5	13	FALSE	387.6
KIAA1217	10	5	13	FALSE	387.6
LINGO2	11	5	13	FALSE	387.6
WDYHV1	6	4	10	FALSE	368.8
NAALAD2	9	4	10	FALSE	368.8
ZFYVE26	9	4	10	TRUE	368.8
PMS2P7	10	5	12	FALSE	350.1
PPP1R11	10	6	14	FALSE	337.6
CSMD1	41	12	28	FALSE	337.6
CP	8	5	11	FALSE	312.6
CDV3	7	5	11	FALSE	312.6
TMEM50B	10	5	11	FALSE	312.6
KIAA0930	7	5	11	FALSE	312.6
EEPD1	10	5	11	FALSE	312.6
FDX1	10	6	13	FALSE	306.3
TTC7B	12	6	13	FALSE	306.3
PDCD6	11	6	13	TRUE	306.3
HHAT	10	6	13	FALSE	306.3
PTCHD1-AS	12	7	15	FALSE	301.8
AGAP1	15	8	17	FALSE	298.5
PLD2	8	5	10	FALSE	275.0
CBWD3	9	5	10	FALSE	275.0
LOC339862	12	6	12	FALSE	275.0
NEBL	9	5	10	FALSE	275.0
DOCK1	9	5	10	FALSE	275.0
TMEM132D	8	5	10	FALSE	275.0
BBS4	10	5	10	FALSE	275.0
CCPG1	9	5	10	FALSE	275.0
LINC01170	8	6	12	FALSE	275.0
LARGE1	14	8	16	FALSE	275.0
ANKS1B	9	5	10	FALSE	275.0
MIR590	9	5	10	FALSE	275.0
ATL1	9	5	10	FALSE	275.0
RAI14	8	5	10	FALSE	275.0
TENM2	12	6	12	FALSE	275.0
NRXN3	17	9	18	FALSE	275.0
RHEB	13	10	19	FALSE	256.3
DNAAF4-CCPG1	18	10	19	FALSE	256.3
ABHD10	15	9	17	FALSE	254.2

Integration Frequency (Depletion)

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

Gene	Num. Patients	Time 0 sites	Patient Sites	Onco-Related	Frequency Increase (%)
RUVBL2	9	105	13	TRUE	-76.8
LONP1	13	98	13	FALSE	-75.1
CD4	15	166	23	FALSE	-74.0
STAG2	7	81	12	TRUE	-72.2
PTPN11	8	61	10	TRUE	-69.3
AKAP8	8	66	11	FALSE	-68.7
SF3B2	20	180	30	FALSE	-68.7
IL6R	9	71	12	FALSE	-68.3
HSPA1B	5	59	10	FALSE	-68.2
EIF4A3	9	57	10	FALSE	-67.1
UBTF	9	68	12	FALSE	-66.9
SNRNP200	7	55	10	FALSE	-65.9
TADA2A	8	66	13	FALSE	-63.1
WIPF1	14	80	16	FALSE	-62.5
TBC1D10C	15	100	20	FALSE	-62.5
ABCA7	14	99	20	FALSE	-62.1
TNFSF12-TNFSF13	12	69	14	FALSE	-62.0
DGAT1	11	81	17	FALSE	-60.6
ZSCAN10	10	66	14	FALSE	-60.2
LOC102724050	9	47	10	FALSE	-60.1
APOBEC3D	8	47	10	FALSE	-60.1
ZBTB45	9	47	10	FALSE	-60.1
MTBP	8	61	13	FALSE	-60.0
SHISA5	7	61	13	FALSE	-60.0
SDF4	19	137	30	FALSE	-58.9
EMB	9	50	11	FALSE	-58.7
C6orf48	8	54	12	FALSE	-58.3
GPAA1	8	54	12	FALSE	-58.3
LOC106660606	13	81	18	FALSE	-58.3
CD48	6	45	10	FALSE	-58.3
FZR1	11	58	13	FALSE	-58.0
RBM10	6	49	11	FALSE	-57.9
GPD2	14	80	18	FALSE	-57.8
KPNB1	20	124	28	FALSE	-57.7
PGP	15	106	24	FALSE	-57.5
PYCR3	6	44	10	FALSE	-57.4
PTK2	15	83	19	FALSE	-57.1
CD247	9	48	11	FALSE	-57.0
LOC105369632	16	100	23	FALSE	-56.9
SNORD48	8	51	12	FALSE	-55.9
SGTA	11	72	17	FALSE	-55.7
NTHL1	15	72	17	FALSE	-55.7
NAPSB	10	46	11	FALSE	-55.2
ARHGAP17	9	50	12	FALSE	-55.0
NUTF2	9	54	13	FALSE	-54.9
RPLP2	10	54	13	FALSE	-54.9
RETREG3	21	141	34	FALSE	-54.8
LOC101927018	10	66	16	FALSE	-54.5
PTPRCAP	10	66	16	FALSE	-54.5
MSL1	14	70	17	FALSE	-54.5

Genes with the Most Abundant Clones

Table 6: Table of top 50 Genes containing the highest abundant clones.

Gene	Num. Patients	Peak Abundance	Peak Rel. Abund.	Clonal Gini Index	Onco-Related
TET2	35	858	100.000	0.908	TRUE
PATL1	20	629	27.089	0.920	FALSE
KCTD3	16	626	26.960	0.917	FALSE
PIKFYVE	23	460	28.636	0.903	FALSE
NELL2	46	441	14.853	0.761	FALSE
GLCC1	29	425	14.315	0.864	FALSE
SRCAP	47	402	37.996	0.760	FALSE
MTMR3	41	280	8.163	0.743	TRUE
C1orf159	52	176	11.210	0.600	FALSE
IFNGR2	7	173	45.583	0.827	TRUE
RC3H1	38	164	5.556	0.694	FALSE
PCNX1	44	156	1.064	0.660	FALSE
PPP6R3	65	154	5.435	0.417	FALSE
UHRF1	27	150	9.554	0.718	FALSE
SSH2	47	146	6.288	0.500	FALSE
RSRC1	27	115	1.472	0.680	FALSE
WDR7	44	113	44.841	0.619	FALSE
MAPK14	44	98	1.282	0.547	TRUE
SNHG12	3	98	5.738	0.711	FALSE
ZZEF1	53	92	50.000	0.430	FALSE
MGA	46	91	14.286	0.475	FALSE
RPA3	22	90	4.678	0.728	FALSE
AQR	20	88	7.660	0.747	FALSE
LEF1	35	86	3.704	0.508	TRUE
MAN1B1	36	85	18.931	0.579	FALSE
ZNF573	14	85	68.750	0.765	FALSE
LINC01473	12	84	8.179	0.779	FALSE
CARD8	57	82	8.171	0.368	TRUE
BCAS3	40	81	32.143	0.559	TRUE
IQCB1	16	80	2.857	0.765	FALSE
KANSL1	44	79	3.300	0.425	FALSE
WWOX	30	78	69.027	0.605	TRUE
RNF213	63	76	2.857	0.355	TRUE
DNAJC13	32	73	0.562	0.588	FALSE
EXOSC10	15	69	0.768	0.670	FALSE
ATP2A2	25	67	2.885	0.592	FALSE
TRIO	19	66	2.571	0.663	TRUE
SEC31A	19	65	3.226	0.614	FALSE
SMAP2	29	65	3.704	0.604	FALSE
GPN1	7	63	1.817	0.748	FALSE
EARS2	6	60	28.169	0.763	FALSE
LINC01322	1	57	3.631	0.000	FALSE
JMJD6	12	54	4.545	0.671	FALSE
CLK4	47	53	6.077	0.328	FALSE
DERL2	21	52	14.286	0.596	FALSE
MEMO1	22	52	4.762	0.653	FALSE
PTBP1	44	52	4.478	0.407	TRUE
KDM5D	16	51	6.977	0.635	FALSE
FOXP1	57	49	36.567	0.312	TRUE
PPP3CC	44	49	52.128	0.359	FALSE

Longitudinal Observation

Table 7: Table of top 50 genes identified by longitudinal observations of patients samples.

Gene	t3avg	Time Span	Longest Time	Num. Timepoints	Patients	Sites	Max Abund.	Max RelAbund	Onco-Related
MIR6724-1	3190.00	1460.0	3285.0	3	4	6	2	33.33%	FALSE
MIR6724-2	3190.00	1460.0	3285.0	3	4	6	2	33.33%	FALSE
MIR6724-3	3190.00	1460.0	3285.0	3	4	6	2	33.33%	FALSE
MIR6724-4	3190.00	1460.0	3285.0	3	4	6	2	33.33%	FALSE
CTSS	2920.00	0.0	2920.0	1	46	75	2	3.45%	FALSE
ARFRP1	2859.17	547.5	4015.0	2	70	135	4	4%	FALSE
RTKL1	2859.17	547.5	4015.0	2	46	79	4	3.64%	FALSE
RTKL1-TNFRSF6B	2859.17	547.5	4015.0	2	46	79	4	3.64%	FALSE
TNFRSF6B	2859.17	547.5	4015.0	2	6	6	4	3.64%	TRUE
LOC100507412	2757.67	1460.0	3285.0	3	4	6	2	33.33%	FALSE
MIR6724-1	2757.67	1460.0	3285.0	3	4	6	2	33.33%	FALSE
MIR6724-2	2757.67	1460.0	3285.0	3	4	6	2	33.33%	FALSE
MIR6724-3	2757.67	1460.0	3285.0	3	4	6	2	33.33%	FALSE
MIR6724-4	2757.67	1460.0	3285.0	3	4	6	2	33.33%	FALSE
P14KA	2676.67	1432.0	4015.0	4	105	264	9	2%	FALSE
ZBTB8OS	2555.00	2105.0	2555.0	2	33	54	3	1.92%	FALSE
ZNF251	2372.50	182.5	4015.0	2	110	684	43	19%	FALSE
CDK19	2372.50	7.0	4015.0	2	34	40	3	5.77%	FALSE
KANSL1	2311.67	129.0	4015.0	3	101	399	79	3.3%	FALSE
CYTH1	2250.83	14.0	4015.0	2	125	790	30	7.56%	FALSE
RFX2	2129.17	182.5	4015.0	2	81	215	9	31.03%	TRUE
ANKRD11	2068.33	730.0	2555.0	4	127	795	25	6.56%	FALSE
VMP1	2068.33	46.0	2920.0	3	115	592	28	11.11%	FALSE
PTDSS2	2067.50	7.0	4015.0	2	72	140	11	1.59%	FALSE
TMEM241	2063.33	0.0	3000.0	1	27	34	2	3.45%	FALSE
PSMD13	2033.33	21.0	3000.0	2	119	661	19	3.7%	FALSE
ZNF44	2007.50	547.5	2007.5	2	72	142	9	6.72%	FALSE
P4HB	2001.67	14.0	3000.0	2	113	412	18	26.87%	FALSE
DENND1B	1946.67	730.0	2555.0	4	83	206	5	4.55%	FALSE
CSMD1	1946.67	597.0	2190.0	3	52	39	14	100%	FALSE
MIR1268A	1946.67	21.0	2555.0	2	127	830	6	3.08%	FALSE
ADD1	1946.67	14.0	2007.5	3	114	420	43	18.09%	FALSE
SLC9A7	1915.00	285.0	3285.0	2	54	95	10	5.71%	FALSE
MTOR	1913.33	360.0	2555.0	4	95	290	29	15.43%	TRUE
MACROD2	1911.67	14.0	3000.0	2	46	72	3	1.82%	FALSE
SHISA6	1911.67	0.0	3000.0	1	10	11	1	20%	FALSE
LAMA3	1861.00	0.0	3000.0	1	17	19	2	0.6%	FALSE
HSF5	1855.00	1825.0	3650.0	3	82	157	35	15.79%	FALSE
MTMR4	1855.00	1825.0	3650.0	3	24	27	5	3.33%	FALSE
TBC1D22A	1834.33	0.0	3650.0	1	62	101	4	3.33%	FALSE
SLC1A2	1834.33	0.0	3650.0	1	12	13	2	3.33%	FALSE
RAB11FIP3	1825.00	166.0	4015.0	3	111	567	7	2.6%	FALSE
UNKL	1825.00	15.0	2555.0	2	96	265	7	3.64%	FALSE
RELB	1825.00	14.0	1825.0	2	56	101	15	3.85%	TRUE
ZNF212	1795.83	0.0	3000.0	1	10	10	1	0.98%	FALSE
SMG1P2	1761.67	21.0	2372.5	2	112	360	11	10.78%	FALSE
RHOA	1733.33	23.0	2555.0	2	91	284	5	2.44%	TRUE
ERC1	1703.33	122.0	2007.5	3	111	322	10	4.24%	TRUE
MROH1	1703.33	46.0	1825.0	4	133	1774	12	6.86%	FALSE
HIVEP3	1703.33	23.0	4015.0	2	69	147	14	1.53%	TRUE

Samples

Sample Info					Clone info			Population info				
GTSP	Time(d)	timePoint	cellType	patient	Clones	Unique	Max Clone	Shannon	Gini	Chao1	Simpson	UC50
GTSP5967	365	m12	Blood	0101	27	17	29.63%	2.526	0.322	36	0.122	4
GTSP5968	913	m30	Blood	0202	27	22	14.81%	2.968	0.170	212	0.062	9
GTSP5969	274	m9	Blood	0303	18	13	16.67%	2.447	0.222	36	0.099	5
GTSP5970	365	m12	Blood	0505	28	22	10.71%	2.979	0.185	193	0.059	9
GTSP5971	730	m24	Blood	0606	11	10	18.18%	2.272	0.082	28	0.107	5
GTSP5972	274	m9	Blood	0707	7	7	14.29%	1.946	0.000	28	0.143	4
GTSP5973	365	m12	Blood	0808	10	9	20%	2.164	0.089	23	0.120	5
GTSP3617	0	d0	Tcell	35418-1635418-16	1726	1412	0.93%	7.153	0.163	7073	0.001	550
GTSP3618	21	d21	Blood	35418-1635418-16	1091	591	4.4%	5.869	0.398	1666	0.007	107
GTSP3619	23	d23	Blood	35418-1635418-16	3714	1576	4.42%	6.799	0.449	2819	0.004	277
GTSP1853	0	d0	Tcell	C34-CXCR4-01.G1-TDN34	1382	1014	0.43%	6.805	0.218	3121	0.001	324
GTSP1855	7	d7	Blood	C34-CXCR4-0134	6	6	16.67%	1.792	0.000	21	0.167	4
GTSP1856	28	d28	Cells	C34-CXCR4-0134	2	2	50%	0.693	0.000	3	0.500	2
GTSP1857	138	d138	Cells	C34-CXCR4-0134	5	5	20%	1.609	0.000	15	0.200	3
GTSP1858	0	d0	Tcell	C34-CXCR4-02.G1-TDN34	3719	3437	0.13%	8.112	0.071	25360	0.000	1578
GTSP1861	28	d28	Cells	C34-CXCR4-0234	6	6	16.67%	1.792	0.000	21	0.167	4
GTSP2297	140	d140	Cells	C34-CXCR4-0234	1	1	100%	0.000	0.000	1	1.000	1
GTSP2299	0	d0	Tcell	C34-CXCR4-0334	5234	4739	0.08%	8.426	0.087	27908	0.000	2123
GTSP2301	7	d7	Blood	C34-CXCR4-0334	793	742	1.39%	6.539	0.064	88951	0.002	346
GTSP2302	28	d28	Cells	C34-CXCR4-0334	156	92	8.97%	4.208	0.349	603	0.023	18
GTSP1863	0	d0	Tcell	C34-CXCR4-04.G1-TDN34	4041	3472	0.12%	8.095	0.124	14969	0.000	1452
GTSP1865	7	d7	Blood	C34-CXCR4-0434	50	22	16%	2.731	0.429	74	0.086	5
GTSP1866	28	d28	Cells	C34-CXCR4-0434	338	265	2.37%	5.405	0.201	6049	0.006	97
GTSP2304	210	d210	Cells	C34-CXCR4-0434	6	4	33.33%	1.330	0.167	4	0.278	2
GTSP2305	0	d0	Tcell	C34-CXCR4-0534	7358	6934	0.08%	8.821	0.055	64225	0.000	3256
GTSP2307	7	d7	Blood	C34-CXCR4-0534	152	81	9.87%	4.051	0.383	435	0.026	15
GTSP2308	28	d28	Cells	C34-CXCR4-0534	591	475	0.85%	6.068	0.172	2087	0.003	180
GTSP2309	140	d140	Cells	C34-CXCR4-0534	3	3	33.33%	1.099	0.000	6	0.333	2
GTSP2310	0	d0	Tcell	C34-CXCR4-0634	6444	6115	0.06%	8.698	0.049	65744	0.000	2894
GTSP2313	28	d28	Cells	C34-CXCR4-0634	206	126	8.25%	4.415	0.357	744	0.022	24
GTSP5436	1095	y3	Blood	CHOP03712-03	6	6	16.67%	1.792	0.000	21	0.167	4
GTSP6004	1095	y3	Blood	CHOP03712-03	6	3	66.67%	0.868	0.333	4	0.500	1
GTSP6006	1703	d1703	Tumor Bx1	CHOP03712-03	2	2	50%	0.693	0.000	3	0.500	2
GTSP6007	1703	d1703	Tumor Bx2	CHOP03712-03	3	3	33.33%	1.099	0.000	6	0.333	2
GTSP6005	1825	y5	Blood	CHOP03712-03	3	2	66.67%	0.637	0.167	2	0.556	1
GTSP5999	183	m6	Blood	CHOP03712-29	1	1	100%	0.000	0.000	1	1.000	1
GTSP6001	183	m6	BM	CHOP03712-29	219	162	4.11%	4.930	0.226	561	0.009	53
GTSP6000	183	m6	Skin Bx	CHOP03712-29	27	21	14.81%	2.936	0.190	55	0.062	8
GTSP5415	1278	y3.5	Blood	CHOP03712-47	2	2	50%	0.693	0.000	3	0.500	2
GTSP5433	1278	y3.5	Blood	CHOP04409-01	94	17	25.53%	2.041	0.633	44	0.176	3
GTSP6003	852	m28	Blood	CHOP04409-02	86	41	19.77%	3.144	0.466	165	0.077	5
GTSP5432	1095	y3	Blood	CHOP04409-02	9	9	11.11%	2.197	0.000	45	0.111	5
GTSP5438	1460	y4	Blood	CHOP04409-02	52	21	50%	2.126	0.549	89	0.267	2
GTSP6010	4015	y11	Blood	CHOP04409-02	100	53	19%	3.583	0.368	79	0.053	13
GTSP5435	1278	y3.5	Blood	CHOP04409-10	4	2	75%	0.562	0.250	2	0.625	1
GTSP5974	365	m12	Blood	CHOP10	24	21	12.5%	2.983	0.115	106	0.056	10
GTSP5975	548	m18	Blood	CHOP11	22	21	9.09%	3.028	0.043	116	0.050	11
GTSP5976	548	m18	Blood	CHOP12	33	32	6.06%	3.454	0.029	264	0.032	16
GTSP5812	7	d7	Blood	CHOP16	4804	4697	0.08%	8.445	0.022	122227	0.000	2296
GTSP5811	10	d10	Blood	CHOP16	5658	5371	0.09%	8.566	0.049	66418	0.000	2543
GTSP5813	14	d14	Blood	CHOP16	14081	13326	0.04%	9.473	0.051	166316	0.000	6286
GTSP5072	183	m6	Blood	CHOP18415-02	17	15	11.76%	2.670	0.102	41	0.073	7
GTSP5073	365	m12	Blood	CHOP18415-02	3	3	33.33%	1.099	0.000	6	0.333	2
GTSP5407	1095	y3	Blood	CHOP18415-02	1	1	100%	0.000	0.000	1	1.000	1
GTSP5417	1278	y3.5	Blood	CHOP18415-02	7	6	28.57%	1.748	0.119	11	0.184	3
GTSP5423	1460	y4	Blood	CHOP18415-02	4	3	50%	1.040	0.167	4	0.375	2
GTSP5074	91	m3	Blood	CHOP18415-03	6	4	50%	1.242	0.250	7	0.333	2
GTSP5075	365	m12	Blood	CHOP18415-03	213	61	28.17%	2.739	0.670	229	0.147	3
GTSP5409	1095	y3	Blood	CHOP18415-03	1	1	100%	0.000	0.000	1	1.000	1
GTSP5076	91	m3	Blood	CHOP18415-04	2	2	50%	0.693	0.000	3	0.500	2
GTSP5078	91	m3	Blood	CHOP18415-05	14	12	21.43%	2.404	0.131	67	0.102	6
GTSP5079	365	m12	Blood	CHOP18415-05	11	6	45.45%	1.540	0.348	9	0.273	2
GTSP5418	1278	y3.5	Blood	CHOP18415-05	9	5	55.56%	1.303	0.356	11	0.358	1
GTSP5430	1825	y5	Blood	CHOP18415-05	15	7	33.33%	1.709	0.362	10	0.218	2
GTSP5080	365	m12	Blood	CHOP18415-06	1	1	100%	0.000	0.000	1	1.000	1
GTSP5412	1095	y3	Blood	CHOP18415-06	1	1	100%	0.000	0.000	1	1.000	1
GTSP5081	91	m3	Blood	CHOP18415-07	3	3	33.33%	1.099	0.000	6	0.333	2
GTSP5082	365	m12	Blood	CHOP18415-07	3	2	66.67%	0.637	0.167	2	0.556	1
GTSP5083	91	m3	Blood	CHOP18415-08	3	3	33.33%	1.099	0.000	6	0.333	2
GTSP5084	365	m12	Blood	CHOP18415-08	130	126	3.85%	4.806	0.031	7876	0.009	62
GTSP5410	1095	y3	Blood	CHOP18415-08	1	1	100%	0.000	0.000	1	1.000	1
GTSP5085	91	m3	Blood	CHOP18415-09	42	34	9.52%	3.408	0.174	179	0.040	14
GTSP5086	365	m12	Blood	CHOP18415-09	1	1	100%	0.000	0.000	1	1.000	1
GTSP5088	365	m12	Blood	CHOP18415-10	1	1	100%	0.000	0.000	1	1.000	1
GTSP5089	91	m3	Blood	CHOP18415-11	2	2	50%	0.693	0.000	3	0.500	2
GTSP5420	1278	y3.5	Blood	CHOP18415-16	3	3	33.33%	1.099	0.000	6	0.333	2
GTSP5425	1460	y4	Blood	CHOP18415-16	115	85	13.04%	4.136	0.248	560	0.030	28
GTSP5426	1642	y4.5	Blood	CHOP18415-16	8	6	37.5%	1.667	0.208	16	0.219	3
GTSP5429	1825	y5	Blood	CHOP18415-16	9	8	22.22%	2.043	0.097	18	0.136	4
GTSP5096	365	m12	Blood	CHOP18415-19	20	17	15%	2.762	0.135	70	0.070	8
GTSP5413	1095	y3	Blood	CHOP18415-19	48	40	16.67%	3.496	0.161	392	0.046	17
GTSP5414	1095	y3	Blood	CHOP18415-20	7	4	57.14%	1.154	0.321	7	0.388	1
GTSP5424	1460	y4	Blood	CHOP18415-20	3	3	33.33%	1.099	0.000	6	0.333	2
GTSP5814	7	d7	Peripheral Blood	CHOP19	4834	4753	0.06%	8.459	0.017	170645	0.000	2337
GTSP5817	7	d7	Peripheral Blood	CHOP19	7044	6895	0.07%	8.830	0.021	174578	0.000	3374
GTSP5818	7	d7	Peripheral Blood	CHOP19	13707	13492	0.04%	9.503	0.015	461608	0.000	6639
GTSP5815	10	d10	Peripheral Blood	CHOP19	4102	3936	0.12%	8.260	0.039	60090	0.000	1886
GTSP5816	10	d10	Peripheral Blood	CHOP19	3974	3865	0.1%	8.248	0.027	83565	0.000	1879
GTSP5977	365	y1	Blood	CHOP34	113	32	69.03%	1.671	0.689	102	0.480	1
GTSP5978	365	y1	Blood	CHOP34	13	10	23.08%	2.205	0.192	24	0.124	4

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Sample Info					Clone info			Population info				
GTSP	Time(d)	timePoint	cellType	patient	Clones	Unique	Max Clone	Shannon	Gini	Chao1	Simpson	UC50
GTSP5979	365	y1	Blood	CHOP34	55	45	5.45%	3.736	0.154	140	0.026	18
GTSP5980	365	y1	Blood	CHOP34	8	7	25%	1.906	0.107	14	0.156	4
GTSP5981	365	y1	Blood	CHOP34	15	14	13.33%	2.616	0.062	53	0.076	7
GTSP5982	365	y1	Blood	CHOP34	110	82	8.18%	4.242	0.222	261	0.019	28
GTSP5983	365	y1	Blood	CHOP34	9	9	11.11%	2.197	0.000	45	0.111	5
GTSP5984	365	y1	Blood	CHOP34	189	149	6.88%	4.810	0.197	708	0.013	55
GTSP5985	365	y1	Blood	CHOP34	145	127	2.07%	4.797	0.110	534	0.009	55
GTSP0630	0	d0	Tcell	CHOP959-100	181	160	1.65%	5.029	0.105	786	0.007	70
GTSP0643	0	d0	Tcells:CAR+	CHOP959-100	4337	4266	0.09%	8.352	0.016	139861	0.000	2098
GTSP0631	13	d13	Blood	CHOP959-100	1043	938	0.48%	6.798	0.093	6217	0.001	417
GTSP0632	15	d15	Blood	CHOP959-100	846	752	0.58%	6.572	0.102	4384	0.002	330
GTSP0633	28	d28	Blood	CHOP959-100	115	115	0.87%	4.745	0.000	6670	0.009	58
GTSP4274	28	d28	BM	CHOP959-100	399	378	1%	5.911	0.050	4179	0.003	179
GTSP4275	91	m3	Blood	CHOP959-100	64	62	3.12%	4.116	0.030	652	0.017	31
GTSP4276	91	m3	BM	CHOP959-100	302	255	1.66%	5.471	0.137	994	0.005	105
GTSP0645	0	d0	Tcell	CHOP959-101	5405	3791	0.18%	8.086	0.248	11262	0.000	1089
GTSP0644	0	d0	Tcells:CAR+	CHOP959-101	3186	3089	0.09%	8.024	0.030	52939	0.000	1497
GTSP4277	10	d10	Blood	CHOP959-101	1865	1820	0.27%	7.496	0.024	43486	0.001	888
GTSP1413	28	d28	Blood	CHOP959-101	287	208	3.11%	5.161	0.239	675	0.008	65
GTSP4278	28	d28	BM	CHOP959-101	176	165	1.7%	5.081	0.059	1358	0.006	78
GTSP0646	61	m2	Blood	CHOP959-101	15	13	13.33%	2.523	0.113	31	0.084	6
GTSP0634	0	d0	Tcell	CHOP959-103	1302	1253	0.23%	7.118	0.036	17794	0.001	603
GTSP4279	0	d0	Tcell	CHOP959-103	2513	2223	0.16%	7.668	0.101	8933	0.000	967
GTSP0635	14	d14	Blood	CHOP959-103	66	46	12.12%	3.619	0.264	125	0.037	14
GTSP4280	15	d15	Blood	CHOP959-103	97	92	2.06%	4.503	0.049	716	0.011	44
GTSP0636	28	d28	Blood	CHOP959-103	1	1	100%	0.000	0.000	1	1.000	1
GTSP4281	0	d0	Tcell	CHOP959-104	1837	1785	0.16%	7.476	0.028	32484	0.001	867
GTSP4282	10	d10	Blood	CHOP959-104	1048	1030	0.38%	6.930	0.017	33129	0.001	507
GTSP4283	0	d0	Tcell	CHOP959-105	2626	2349	0.19%	7.714	0.097	15208	0.000	1037
GTSP4284	10	d10	Blood	CHOP959-105	5052	2650	0.16%	7.768	0.257	3308	0.000	845
GTSP4285	0	d0	Tcell	CHOP959-108	1591	1427	0.31%	7.215	0.096	9787	0.001	632
GTSP4286	6	d6	Blood	CHOP959-108	397	286	7.56%	5.258	0.270	5245	0.012	88
GTSP4287	0	d0	Tcell	CHOP959-110	1086	778	1.2%	6.488	0.243	2686	0.002	236
GTSP4288	10	d10	Blood	CHOP959-110	82	56	8.54%	3.791	0.281	326	0.031	16
GTSP4289	0	d0	Tcell	CHOP959-111	5368	5071	0.07%	8.509	0.053	51910	0.000	2388
GTSP4290	10	d10	Blood	CHOP959-111	1424	1101	0.35%	6.911	0.187	3165	0.001	390
GTSP0653	0	d0	Tcell	CHOP959-112	4043	3930	0.12%	8.265	0.027	75593	0.000	1909
GTSP4442	0	d0	Tcell	CHOP959-112	2750	2731	0.07%	7.910	0.007	186537	0.000	1357
GTSP0652	0	d0	Tcells:CAR+	CHOP959-112	5142	5030	0.08%	8.514	0.021	125083	0.000	2460
GTSP4443	14	d14	Blood	CHOP959-112	175	147	1.71%	4.934	0.135	468	0.008	60
GTSP1414	28	d28	Blood	CHOP959-112	162	104	3.7%	4.442	0.296	446	0.015	25
GTSP4444	28	d28	BM	CHOP959-112	41	37	7.32%	3.566	0.091	224	0.030	17
GTSP4445	91	m3	Blood	CHOP959-112	100	92	3%	4.484	0.076	823	0.012	43
GTSP4446	0	d0	Tcell	CHOP959-113	7414	6749	0.05%	8.785	0.081	36352	0.000	3043
GTSP4447	15	d15	Blood	CHOP959-113	5134	5077	0.06%	8.528	0.011	247630	0.000	2511
GTSP4448	28	d28	Blood	CHOP959-113	131	104	4.58%	4.556	0.170	262	0.012	39
GTSP4449	28	d28	BM	CHOP959-113	91	82	4.4%	4.347	0.094	1057	0.014	37
GTSP4450	0	d0	Tcell	CHOP959-114	6500	5691	0.06%	8.606	0.107	21021	0.000	2442
GTSP4451	10	d10	Blood	CHOP959-114	1271	1246	0.24%	7.119	0.019	38670	0.001	611
GTSP4452	28	d28	Blood	CHOP959-114	1122	753	0.62%	6.471	0.262	2034	0.002	203
GTSP4453	28	d28	BM	CHOP959-114	338	212	2.66%	5.125	0.312	1081	0.008	47
GTSP4454	0	d0	Tcell	CHOP959-115	4975	4316	0.12%	8.318	0.117	18617	0.000	1829
GTSP4455	10	d10	Blood	CHOP959-115	780	526	0.77%	6.109	0.263	1619	0.003	139
GTSP0640	0	d0	Tcell	CHOP959-117	1335	1107	0.44%	6.934	0.149	4156	0.001	440
GTSP4456	0	d0	Tcell	CHOP959-117	3620	3443	0.14%	8.122	0.047	45486	0.000	1634
GTSP4457	10	d10	Blood	CHOP959-117	4406	3089	0.36%	7.882	0.245	7953	0.000	887
GTSP0641	14	d14	Blood	CHOP959-117	676	547	0.88%	6.211	0.167	2079	0.002	210
GTSP0642	25	d25	Blood	CHOP959-117	173	148	5.75%	4.866	0.138	1312	0.011	62
GTSP1415	25	d25	Blood	CHOP959-117	298	183	3.65%	4.920	0.334	918	0.011	37
GTSP4458	25	d25	Blood	CHOP959-117	407	304	1.97%	5.549	0.227	1870	0.005	101
GTSP4459	0	d0	Tcell	CHOP959-118	12062	11721	0.03%	9.357	0.028	244302	0.000	5691
GTSP4460	7	d7	Blood	CHOP959-118	5828	4893	0.12%	8.437	0.136	16112	0.000	1980
GTSP4461	28	d28	Blood	CHOP959-118	186	123	5.91%	4.503	0.309	1033	0.017	31
GTSP4462	28	d28	BM	CHOP959-118	429	323	3.73%	5.578	0.226	2927	0.006	109
GTSP4463	0	d0	Tcell	CHOP959-120	6464	5248	0.09%	8.497	0.156	15165	0.000	2017
GTSP4464	14	d14	Blood	CHOP959-120	2878	2693	0.17%	7.872	0.061	23970	0.000	1255
GTSP4465	28	d28	Blood	CHOP959-120	68	56	7.35%	3.902	0.164	694	0.025	23
GTSP4466	28	d28	BM	CHOP959-120	116	75	5.17%	4.110	0.295	215	0.021	19
GTSP4467	0	d0	Tcell	CHOP959-121	5368	4114	0.09%	8.244	0.181	9237	0.000	1431
GTSP4468	10	d10	Blood	CHOP959-121	1178	1035	0.34%	6.895	0.108	4687	0.001	447
GTSP4469	28	d28	Blood	CHOP959-121	25	21	12%	2.976	0.141	72	0.056	9
GTSP4470	28	d28	BM	CHOP959-121	59	32	8.47%	3.251	0.337	64	0.047	8
GTSP4471	0	d0	Tcell	CHOP959-123	6908	4597	0.12%	8.297	0.255	10047	0.000	1306
GTSP4472	10	d10	Blood	CHOP959-123	2210	1580	0.45%	7.202	0.245	7712	0.001	476
GTSP4473	28	d28	Blood	CHOP959-123	119	106	2.52%	4.623	0.098	470	0.010	47
GTSP4474	28	d28	BM	CHOP959-123	135	127	2.22%	4.819	0.056	1147	0.008	60
GTSP4475	0	d0	Tcell	CHOP959-125	4811	4179	0.06%	8.294	0.113	14989	0.000	1774
GTSP4476	10	d10	Blood	CHOP959-125	5073	4868	0.08%	8.473	0.039	71367	0.000	2332
GTSP4477	28	d28	Blood	CHOP959-125	664	622	0.75%	6.400	0.061	7057	0.002	291
GTSP4478	28	d28	BM	CHOP959-125	980	841	0.41%	6.684	0.122	2956	0.001	352
GTSP4479	91	m3	Blood	CHOP959-125	195	187	1.03%	5.216	0.039	1957	0.006	90
GTSP4480	91	m3	BM	CHOP959-125	292	238	2.05%	5.368	0.166	1066	0.006	93
GTSP4403	0	d0	Tcell	CHOP959-127	1482	1336	0.27%	7.160	0.089	7055	0.001	596
GTSP4404	10	d10	Blood	CHOP959-127	1635	1319	0.31%	7.102	0.166	5302	0.001	502
GTSP4405	28	d28	Blood	CHOP959-127	102	79	5.88%	4.212	0.205	364	0.019	29
GTSP4406	0	d0	Tcell	CHOP959-128	1084	1054	0.18%	6.950	0.027	17950	0.001	513
GTSP4407	14	d14	Blood	CHOP959-128	410	370	1.71%	5.849	0.093	3052	0.003	166
GTSP4408	28	d28	Blood	CHOP959-128	257	206	8.17%	5.105	0.188	1422	0.012	78
GTSP4409	28	d28	BM	CHOP959-128	118	83	6.78%	4.239	0.253	238	0.019	25
GTSP4410	0	d0	Tcell	CHOP959-131	3947	3891	0.1%	8.260	0.014	184043	0.000	1918
GTSP4411	10	d10	Blood	CHOP959-131	1437	1416	0.14%	7.250	0.014	45612	0.001	698
GTSP4412	0	d0	Tcell	CHOP959-132	1460	1264	0.27%	7.096	0.116	4550	0.001	535
GTSP4413	7	d7	Blood	CHOP959-132	728	696	0.55%	6.525	0.042	9634	0.002	333

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Sample Info					Clone info			Population info				
GTSP	Time(d)	timePoint	cellType	patient	Clones	Unique	Max Clone	Shannon	Gini	Chao1	Simpson	UC50
GTSP4414	28	d28	Blood	CHOP959-132	37	9	64.86%	1.259	0.643	30	0.452	1
GTSP0655	0	d0	Tcell	CHOP959-133	5939	5871	0.05%	8.673	0.011	265042	0.000	2902
GTSP4415	0	d0	Tcell	CHOP959-133	2890	2537	0.14%	7.798	0.106	9669	0.000	1093
GTSP0654	0	d0	Tcells:CAR+	CHOP959-133	5911	5805	0.05%	8.659	0.018	180820	0.000	2850
GTSP4416	10	d10	Blood	CHOP959-133	978	939	0.31%	6.826	0.039	16742	0.001	451
GTSP1416	28	d28	Blood	CHOP959-133	154	105	4.49%	4.465	0.270	336	0.015	29
GTSP4417	28	d28	Blood	CHOP959-133	182	170	2.2%	5.102	0.063	1780	0.006	80
GTSP4418	0	d0	Tcell	CHOP959-136	3350	2904	0.15%	7.928	0.115	10457	0.000	1230
GTSP4419	17	d17	Blood	CHOP959-136	3073	1756	2.47%	6.928	0.392	7706	0.003	285
GTSP4420	28	d28	Blood	CHOP959-136	171	141	4.68%	4.818	0.163	787	0.011	56
GTSP4421	28	d28	BM	CHOP959-136	84	63	4.76%	4.049	0.198	146	0.020	22
GTSP4422	91	m3	Blood	CHOP959-136	35	20	22.86%	2.639	0.373	80	0.105	4
GTSP4423	0	d0	Tcell	CHOP959-138	2446	2390	0.16%	7.769	0.022	59354	0.000	1168
GTSP4424	14	d14	Blood	CHOP959-138	2603	2268	0.15%	7.682	0.112	8519	0.000	967
GTSP4425	28	d28	Blood	CHOP959-138	196	180	2.04%	5.158	0.076	1158	0.006	83
GTSP4426	0	d0	Tcell	CHOP959-139	275	242	2.55%	5.427	0.110	1210	0.005	105
GTSP4427	7	d7	Blood	CHOP959-139	2954	2603	0.14%	7.823	0.104	10727	0.000	1127
GTSP4428	28	d28	Blood	CHOP959-139	63	51	6.35%	3.818	0.173	381	0.026	20
GTSP4429	28	d28	BM	CHOP959-139	136	111	5.15%	4.593	0.168	628	0.012	44
GTSP4430	0	d0	Tcell	CHOP959-140	1384	1294	0.29%	7.138	0.061	11380	0.001	603
GTSP4431	10	d10	Blood	CHOP959-140	2948	2419	0.2%	7.726	0.149	7053	0.000	946
GTSP4432	28	d28	Blood	CHOP959-140	187	159	1.6%	5.004	0.133	789	0.007	66
GTSP4433	0	d0	Tcell	CHOP959-141	3553	3438	0.14%	8.127	0.032	71521	0.000	1662
GTSP4434	10	d10	Blood	CHOP959-141	2897	2425	0.28%	7.732	0.139	8036	0.000	977
GTSP4435	28	d28	Blood	CHOP959-141	99	89	5.05%	4.425	0.096	770	0.014	40
GTSP4436	28	d28	BM	CHOP959-141	109	87	8.26%	4.314	0.185	364	0.018	33
GTSP4437	0	d0	Tcell	CHOP959-143	1813	1581	0.28%	7.319	0.112	6203	0.001	675
GTSP4438	14	d14	Blood	CHOP959-143	1364	1334	0.22%	7.187	0.022	32896	0.001	653
GTSP4439	28	d28	Blood	CHOP959-143	2027	1936	0.25%	7.546	0.043	29467	0.001	923
GTSP4441	91	m3	Blood	CHOP959-143	425	401	0.71%	5.970	0.054	4191	0.003	189
GTSP4440	91	m3	BM	CHOP959-143	1047	928	0.38%	6.794	0.100	3791	0.001	405
GTSP4481	0	d0	Tcell	CHOP959-144	4107	4056	0.07%	8.303	0.012	186648	0.000	2003
GTSP4482	7	d7	Blood	CHOP959-144	1126	1048	0.36%	6.926	0.065	8059	0.001	486
GTSP4483	0	d0	Tcell	CHOP959-145	4525	3852	0.13%	8.207	0.125	12218	0.000	1590
GTSP4484	10	d10	Blood	CHOP959-145	1302	1173	0.31%	7.030	0.090	6032	0.001	523
GTSP4485	0	d0	Tcell	CHOP959-146	4766	4713	0.06%	8.454	0.011	222009	0.000	2331
GTSP4486	10	d10	Blood	CHOP959-146	2268	2219	0.13%	7.696	0.021	58458	0.000	1086
GTSP4487	28	d28	Blood	CHOP959-146	235	141	11.06%	4.420	0.374	642	0.027	24
GTSP4488	28	d28	BM	CHOP959-146	314	246	4.78%	5.292	0.205	2721	0.008	90
GTSP4489	0	d0	Tcell	CHOP959-147	12868	12182	0.05%	9.386	0.051	130703	0.000	5749
GTSP4490	14	d14	Blood	CHOP959-147	307	261	1.3%	5.503	0.132	1094	0.004	108
GTSP4491	0	d0	Tcell	CHOP959-148	1562	1232	0.38%	7.037	0.171	3158	0.001	452
GTSP4492	14	d14	Blood	CHOP959-148	1451	1224	0.41%	7.038	0.139	5289	0.001	499
GTSP4493	28	d28	Blood	CHOP959-148	656	557	0.61%	6.253	0.135	2682	0.002	230
GTSP4494	28	d28	BM	CHOP959-148	618	488	0.81%	6.106	0.175	1463	0.002	180
GTSP4495	0	d0	Tcell	CHOP959-149	2721	2529	0.18%	7.807	0.066	20442	0.000	1169
GTSP4496	10	d10	Blood	CHOP959-149	3554	3397	0.14%	8.112	0.043	44160	0.000	1621
GTSP4497	28	d28	Blood	CHOP959-149	200	138	2.5%	4.780	0.252	414	0.010	39
GTSP4498	0	d0	Tcell	CHOP959-150	3378	3179	0.15%	8.039	0.056	31889	0.000	1491
GTSP4499	7	d7	Blood	CHOP959-150	213	160	2.82%	4.949	0.212	588	0.008	54
GTSP4500	0	d0	Tcell	CHOP959-151	3384	2866	0.12%	7.908	0.129	9280	0.000	1175
GTSP4501	10	d10	Blood	CHOP959-151	1847	1735	0.27%	7.430	0.058	20803	0.001	812
GTSP4502	0	d0	Tcell	CHOP959-152	848	673	0.71%	6.431	0.171	1917	0.002	250
GTSP4503	14	d14	Blood	CHOP959-152	140	128	3.57%	4.801	0.082	1148	0.009	59
GTSP4504	0	d0	Tcell	CHOP959-153	1165	1022	0.34%	6.882	0.109	4709	0.001	440
GTSP4505	10	d10	Blood	CHOP959-153	1554	1494	0.19%	7.294	0.037	20988	0.001	718
GTSP4506	28	d28	Blood	CHOP959-153	9	7	33.33%	1.831	0.190	22	0.185	3
GTSP4507	28	d28	BM	CHOP959-153	1012	843	0.4%	6.673	0.143	2964	0.001	338
GTSP4508	0	d0	Tcell	CHOP959-154	3228	2757	0.15%	7.875	0.123	8703	0.000	1144
GTSP4509	7	d7	Blood	CHOP959-154	206	186	1.46%	5.188	0.089	1011	0.006	84
GTSP4510	0	d0	Tcell	CHOP959-155	1594	1317	0.31%	7.119	0.146	4007	0.001	521
GTSP4511	14	d14	Blood	CHOP959-155	394	315	1.52%	5.660	0.173	1068	0.004	119
GTSP4512	0	d0	Tcell	CHOP959-156	3228	2862	0.12%	7.918	0.101	12650	0.000	1249
GTSP4513	14	d14	Blood	CHOP959-156	599	585	0.5%	6.362	0.023	13147	0.002	286
GTSP4514	28	d28	Blood	CHOP959-156	197	142	6.6%	4.640	0.263	847	0.017	44
GTSP4515	28	d28	BM	CHOP959-156	49	43	4.08%	3.722	0.105	138	0.025	19
GTSP4516	0	d0	Tcell	CHOP959-157	3080	2987	0.1%	7.990	0.029	55568	0.000	1448
GTSP4517	7	d7	Blood	CHOP959-157	22	19	13.64%	2.878	0.124	87	0.062	9
GTSP3263	0	d0	Tcell	CHOP959-158	11372	11124	0.05%	9.308	0.021	285819	0.000	5439
GTSP3264	0	d0	alpha-beta T cells	CHOP959-158	7767	6483	0.06%	8.722	0.137	19075	0.000	2600
GTSP3265	0	d0	gamma-delta T cells	CHOP959-158	16268	16018	0.04%	9.675	0.015	569615	0.000	7885
GTSP3266	7	d7	Blood	CHOP959-158	817	619	0.61%	6.347	0.185	1314	0.002	211
GTSP3268	7	d7	Blood	CHOP959-158	202	114	4.46%	4.512	0.331	294	0.014	27
GTSP3269	14	d14	Blood	CHOP959-158	297	190	4.38%	4.907	0.326	996	0.012	42
GTSP3267	28	d28	Blood	CHOP959-158	278	205	7.19%	4.977	0.252	2137	0.014	67
GTSP3270	28	d28	Blood	CHOP959-158	41	21	17.07%	2.718	0.388	141	0.087	4
GTSP3271	548	m18	Blood	CHOP959-158	102	64	8.82%	3.865	0.328	329	0.030	14
GTSP4518	0	d0	Tcell	CHOP959-159	899	891	0.22%	6.789	0.009	44158	0.001	442
GTSP4519	10	d10	Blood	CHOP959-159	232	191	5.6%	5.104	0.165	1149	0.009	76
GTSP4520	0	d0	Tcell	CHOP959-160	2004	1943	0.2%	7.559	0.030	36199	0.001	942
GTSP4521	17	d17	Blood	CHOP959-160	5603	5069	0.09%	8.495	0.087	27914	0.000	2268
GTSP4522	28	d28	Blood	CHOP959-160	3622	3535	0.08%	8.161	0.023	77990	0.000	1725
GTSP4523	28	d28	BM	CHOP959-160	2161	2113	0.14%	7.647	0.022	51817	0.000	1033
GTSP4524	91	m3	Blood	CHOP959-160	489	416	0.82%	5.972	0.130	1552	0.003	172
GTSP4525	183	m6	Blood	CHOP959-160	206	175	3.4%	5.064	0.141	1303	0.008	73
GTSP4526	274	m9	Blood	CHOP959-160	215	203	1.86%	5.287	0.053	2056	0.005	96
GTSP4527	365	m12	Blood	CHOP959-160	219	166	5.48%	4.967	0.205	436	0.009	57
GTSP4528	456	m15	Blood	CHOP959-160	144	111	4.86%	4.595	0.194	312	0.012	40
GTSP4529	0	d0	Tcell	CHOP959-161	2028	1993	0.2%	7.590	0.017	63986	0.001	980
GTSP4530	7	d7	Blood	CHOP959-161	1917	1732	0.26%	7.421	0.087	8995	0.001	774
GTSP4531	0	d0	Tcell	CHOP959-162	580	523	0.69%	6.219	0.090	3130	0.002	234
GTSP4532	10	d10	Blood	CHOP959-162	1831	1588	0.71%	7.305	0.120	7817	0.001	673
GTSP4533	0	d0	Tcell	CHOP959-163	886	770	0.45%	6.598	0.115	3046	0.001	328

(continued)

Sample Info					Clone info			Population info				
GTSP	Time(d)	timePoint	cellType	patient	Clones	Unique	Max Clone	Shannon	Gini	Chao1	Simpson	UC50
GTSP4534	14	d14	Blood	CHOP959-163	219	208	1.37%	5.315	0.048	2671	0.005	99
GTSP4535	0	d0	Tcell	CHOP959-165	2033	1773	0.2%	7.437	0.110	6517	0.001	757
GTSP4536	7	d7	Blood	CHOP959-165	779	668	0.77%	6.454	0.122	2240	0.002	279
GTSP4537	0	d0	Tcell	CHOP959-166	1727	1674	0.29%	7.408	0.030	37600	0.001	811
GTSP4538	14	d14	Blood	CHOP959-166	94	72	3.19%	4.191	0.188	186	0.017	26
GTSP4539	0	d0	Tcell	CHOP959-168	2656	2263	0.23%	7.667	0.129	8590	0.001	936
GTSP4540	7	d7	Blood	CHOP959-168	600	589	0.33%	6.372	0.018	14485	0.002	290
GTSP4541	28	d28	Blood	CHOP959-168	247	227	3.64%	5.358	0.079	2807	0.006	104
GTSP4542	0	d0	Tcell	CHOP959-169	2441	2292	0.16%	7.713	0.058	19976	0.000	1072
GTSP4543	10	d10	Blood	CHOP959-169	2828	2388	0.14%	7.727	0.130	7196	0.000	975
GTSP4544	28	d28	Blood	CHOP959-169	9	7	22.22%	1.889	0.159	10	0.160	3
GTSP4545	28	d28	BM	CHOP959-169	35	20	40%	2.421	0.399	65	0.180	3
GTSP4546	0	d0	Tcell	CHOP959-171	2763	2709	0.11%	7.896	0.019	74773	0.000	1328
GTSP4547	14	d14	Blood	CHOP959-171	411	338	3.89%	5.686	0.164	1702	0.005	133
GTSP4548	28	d28	Blood	CHOP959-171	252	15	44.84%	1.416	0.779	60	0.324	2
GTSP4549	0	d0	Tcell	CHOP959-172	2003	1954	0.15%	7.567	0.024	47531	0.001	953
GTSP4550	28	d28	Blood	CHOP959-172	235	184	2.98%	5.100	0.188	598	0.007	67
GTSP4551	0	d0	Tcell	CHOP959-174	2496	2133	0.2%	7.616	0.123	7050	0.001	886
GTSP4552	7	d7	Blood	CHOP959-174	18	13	16.67%	2.476	0.205	22	0.093	5
GTSP2982	0	d0	Tcell	CHOP959-175	261	250	1.15%	5.502	0.041	3865	0.004	120
GTSP4553	0	d0	Tcell	CHOP959-175	4041	3611	0.12%	8.155	0.095	16148	0.000	1591
GTSP2983	0	d0	alpha-beta T cells	CHOP959-175	1791	1534	0.28%	7.274	0.128	7058	0.001	639
GTSP2984	0	d0	gamma-delta T cells	CHOP959-175	871	690	1.15%	6.413	0.186	3359	0.002	255
GTSP2985	7	d7	Blood	CHOP959-175	719	578	1.53%	6.218	0.181	4650	0.003	219
GTSP4554	7	d7	Blood	CHOP959-175	1006	859	0.4%	6.706	0.124	2840	0.001	357
GTSP2986	21	d21	Blood	CHOP959-175	118	58	24.58%	3.427	0.456	403	0.077	8
GTSP2987	28	d28	Blood	CHOP959-175	9	4	33.33%	1.311	0.194	4	0.284	2
GTSP2988	28	d28	BM	CHOP959-175	347	275	3.46%	5.437	0.195	3678	0.006	102
GTSP2990	365	m12	BM	CHOP959-175	1	1	100%	0.000	0.000	1	1.000	1
GTSP2991	456	m15	Blood	CHOP959-175	10	7	30%	1.834	0.229	12	0.180	3
GTSP2780	7	d7	Blood	IRB82603534	62	38	12.9%	3.356	0.334	183	0.049	8
GTSP2781	28	d28	DNA	IRB82603534	237	182	6.33%	5.020	0.208	618	0.010	64
GTSP0573	0	d0	Tcell	UPCC03712-03	727	538	1.5%	6.134	0.226	1949	0.003	175
GTSP1203	14	d14	Blood	UPCC03712-03	2199	1513	1.67%	7.070	0.274	5198	0.001	414
GTSP0567	14	d14	Tcells:CAR+CD8-	UPCC03712-03	7782	3502	1.47%	7.554	0.473	8679	0.001	460
GTSP0568	14	d14	Tcells:CAR+CD8+	UPCC03712-03	15690	6803	1.78%	8.162	0.482	16608	0.001	877
GTSP1204	21	d21	Blood	UPCC03712-03	1123	656	4.17%	6.030	0.371	2141	0.006	124
GTSP0574	28	d28	Blood	UPCC03712-03	123	86	7.32%	4.207	0.273	406	0.022	25
GTSP2921	28	d28	Blood	UPCC03712-03	528	356	2.84%	5.646	0.282	1147	0.005	93
GTSP2922	28	d28	BM	UPCC03712-03	918	651	1.96%	6.227	0.262	2706	0.003	193
GTSP1235	61	m2	Blood	UPCC03712-03	390	267	3.57%	5.338	0.281	1461	0.007	73
GTSP1236	122	m4	Blood	UPCC03712-03	279	211	3.57%	5.156	0.225	1614	0.008	72
GTSP2923	183	m6	Blood	UPCC03712-03	435	353	9.89%	5.489	0.186	8634	0.014	136
GTSP2924	183	m6	BM	UPCC03712-03	181	124	6.08%	4.588	0.279	768	0.014	34
GTSP2925	274	m9	Blood	UPCC03712-03	49	22	12.24%	2.847	0.366	61	0.070	6
GTSP2926	365	y1	Blood	UPCC03712-03	3	2	66.67%	0.637	0.167	2	0.556	1
GTSP0575	0	d0	Tcell	UPCC03712-04	2014	1496	0.44%	7.181	0.217	4806	0.001	490
GTSP1206	14	d14	Blood	UPCC03712-04	363	276	2.16%	5.493	0.206	899	0.005	95
GTSP1207	21	d21	Blood	UPCC03712-04	1003	577	8.18%	5.705	0.395	2564	0.013	93
GTSP0576	28	d28	Blood	UPCC03712-04	190	125	7.29%	4.549	0.304	584	0.016	31
GTSP2927	28	d28	Blood	UPCC03712-04	359	220	6.96%	4.976	0.349	847	0.015	44
GTSP2928	28	d28	BM	UPCC03712-04	1035	603	6.86%	5.809	0.384	2103	0.010	106
GTSP2929	61	m2	Blood	UPCC03712-04	184	136	4.35%	4.699	0.240	1139	0.013	45
GTSP0577	0	d0	Tcell	UPCC03712-06	1050	1028	0.38%	6.926	0.021	29280	0.001	504
GTSP1238	14	d14	Blood	UPCC03712-06	1123	894	0.53%	6.693	0.179	3781	0.001	333
GTSP0569	14	d14	Tcells:CAR+CD8-	UPCC03712-06	434	270	2.98%	5.329	0.322	828	0.007	62
GTSP0570	14	d14	Tcells:CAR+CD8+	UPCC03712-06	2342	2002	0.25%	7.540	0.128	8626	0.001	832
GTSP0578	28	d28	Blood	UPCC03712-06	159	151	1.86%	4.993	0.049	2239	0.007	72
GTSP2275	28	d28	BM	UPCC03712-06	280	232	2.11%	5.345	0.157	1382	0.006	93
GTSP2276	183	m6	Blood	UPCC03712-06	329	279	3.24%	5.471	0.147	9024	0.006	115
GTSP2277	274	m9	Blood	UPCC03712-06	135	96	3.65%	4.389	0.251	610	0.016	29
GTSP2278	274	m9	BM	UPCC03712-06	111	69	7.14%	4.043	0.292	124	0.022	19
GTSP2279	365	y1	Blood	UPCC03712-06	193	154	3.57%	4.892	0.187	1485	0.010	58
GTSP2280	365	y1	BM	UPCC03712-06	217	185	5.24%	5.077	0.142	2665	0.009	77
GTSP2281	548	y1.5	Blood	UPCC03712-06	361	219	14.29%	4.731	0.375	1502	0.030	39
GTSP2282	730	y2	Blood	UPCC03712-06	63	34	15.38%	3.175	0.389	109	0.062	6
GTSP2283	912	y2.5	Blood	UPCC03712-06	114	52	42.11%	2.893	0.512	154	0.186	4
GTSP2284	1095	y3	Blood	UPCC03712-06	129	83	25.19%	3.766	0.346	1033	0.075	19
GTSP2285	1825	y5	Blood	UPCC03712-06	18	11	33.33%	2.139	0.323	20	0.160	3
GTSP0579	0	d0	Tcell	UPCC03712-08	516	332	1.9%	5.578	0.299	1117	0.005	80
GTSP0580	28	d28	Blood	UPCC03712-08	5	5	20%	1.609	0.000	15	0.200	3
GTSP2930	14	d14	Blood	UPCC03712-09	57	18	28.07%	2.424	0.496	40	0.129	3
GTSP0581	0	d0	Tcell	UPCC03712-11	1966	1560	0.45%	7.253	0.177	5229	0.001	578
GTSP0582	21	d21	Blood	UPCC03712-11	5	4	40%	1.332	0.150	6	0.280	2
GTSP0583	23	d23	Blood	UPCC03712-11	194	176	2.5%	5.088	0.090	4964	0.007	80
GTSP0584	25	d25	Blood	UPCC03712-11	108	57	14.29%	3.607	0.410	238	0.047	10
GTSP2931	25	d25	Blood	UPCC03712-11	449	88	38.53%	2.671	0.757	266	0.192	2
GTSP0585	28	d28	Blood	UPCC03712-11	69	53	10%	3.759	0.217	269	0.034	19
GTSP2932	28	d28	Blood	UPCC03712-11	283	89	45.58%	2.786	0.659	373	0.226	2
GTSP2933	28	d28	BM	UPCC03712-11	21	12	23.81%	2.331	0.274	14	0.116	4
GTSP0586	36	d36	Blood	UPCC03712-11	4	4	25%	1.386	0.000	10	0.250	3
GTSP2934	61	m2	BM	UPCC03712-11	112	80	15.18%	4.052	0.268	563	0.035	25
GTSP2935	152	d152	Blood	UPCC03712-11	1	1	100%	0.000	0.000	1	1.000	1
GTSP2936	913	m30	Blood	UPCC03712-11	4	4	25%	1.386	0.000	10	0.250	3
GTSP0587	0	d0	Tcell	UPCC03712-12	1975	1335	0.55%	6.993	0.278	5352	0.001	348
GTSP0588	28	d28	Blood	UPCC03712-12	25	22	12%	3.032	0.111	117	0.053	10
GTSP0589	0	d0	Tcell	UPCC03712-14	973	859	0.41%	6.712	0.104	3895	0.001	373
GTSP2938	21	d21	Blood	UPCC03712-14	37	31	8.11%	3.344	0.146	409	0.040	13
GTSP0590	28	d28	Blood	UPCC03712-14	42	38	6.82%	3.593	0.089	236	0.029	18
GTSP0591	0	d0	Tcell	UPCC03712-16	834	816	0.47%	6.694	0.021	23702	0.001	400
GTSP1215	10	d10	Tcell	UPCC03712-16	298	256	1.99%	5.468	0.130	1488	0.005	108
GTSP1216	14	d14	Blood	UPCC03712-16	1117	1002	0.35%	6.867	0.094	6052	0.001	444
GTSP0592	28	d28	Blood	UPCC03712-16	226	200	1.3%	5.249	0.105	1137	0.006	88

(continued)

Sample Info					Clone info			Population info				
GTSP	Time(d)	timePoint	cellType	patient	Clones	Unique	Max Clone	Shannon	Gini	Chao1	Simpson	UC50
GTSP2939	28	d28	BM	UPCC03712-16	179	174	1.12%	5.149	0.027	2540	0.006	85
GTSP1240	61	m2	Blood	UPCC03712-16	378	278	4.18%	5.407	0.239	1164	0.007	90
GTSP2941	91	m3	Blood	UPCC03712-16	43	43	2.33%	3.761	0.000	946	0.023	22
GTSP2940	91	m3	BM	UPCC03712-16	86	86	1.16%	4.454	0.000	3741	0.012	44
GTSP2942	122	m4	Blood	UPCC03712-16	31	30	6.45%	3.389	0.031	233	0.034	15
GTSP2943	152	m5	Blood	UPCC03712-16	22	22	4.55%	3.091	0.000	253	0.045	12
GTSP2944	183	m6	Blood	UPCC03712-16	13	13	7.69%	2.565	0.000	91	0.077	7
GTSP2945	183	m6	BM	UPCC03712-16	41	40	4.88%	3.680	0.024	410	0.026	20
GTSP0593	0	d0	Tcell	UPCC03712-17	665	534	0.9%	6.190	0.170	1851	0.002	202
GTSP2946	21	d21	Blood	UPCC03712-17	3	1	100%	0.000	0.000	1	1.000	1
GTSP0594	28	d28	Blood	UPCC03712-17	42	39	4.76%	3.639	0.066	196	0.027	19
GTSP0595	0	d0	Tcell	UPCC03712-18	571	554	0.52%	6.305	0.029	9582	0.002	269
GTSP1219	14	d14	Blood	UPCC03712-18	2726	2450	0.47%	7.752	0.094	16567	0.000	1088
GTSP1220	21	d21	Blood	UPCC03712-18	3669	2177	4.18%	7.071	0.375	8003	0.004	390
GTSP0596	28	d28	Blood	UPCC03712-18	349	278	3.36%	5.450	0.191	1980	0.006	104
GTSP2947	28	d28	BM	UPCC03712-18	184	147	5.43%	4.820	0.188	998	0.011	56
GTSP1241	61	m2	Blood	UPCC03712-18	51	32	15.69%	3.094	0.339	221	0.071	7
GTSP2948	91	m3	Blood	UPCC03712-18	11	11	9.09%	2.398	0.000	66	0.091	6
GTSP2949	122	m4	Blood	UPCC03712-18	1	1	100%	0.000	0.000	1	1.000	1
GTSP0597	0	d0	Tcell	UPCC03712-20	3256	2411	0.24%	7.661	0.218	7529	0.001	784
GTSP0598	28	d28	Blood	UPCC03712-20	44	40	6.82%	3.646	0.085	262	0.028	19
GTSP0599	0	d0	Tcell	UPCC03712-22	1973	1533	0.4%	7.242	0.185	4397	0.001	547
GTSP1209	10	d10	Tcell	UPCC03712-22	294	248	5.1%	5.355	0.150	3569	0.007	102
GTSP1210	14	d14	Tcell	UPCC03712-22	247	198	3.94%	5.158	0.180	954	0.007	75
GTSP0600	28	d28	Blood	UPCC03712-22	38	35	7.89%	3.514	0.075	299	0.032	17
GTSP2992	28	d28	Blood	UPCC03712-22	66	46	24.24%	3.375	0.292	498	0.075	14
GTSP0601	0	d0	Tcell	UPCC03712-25	3391	2454	0.26%	7.670	0.230	7429	0.001	759
GTSP0602	28	d28	Blood	UPCC03712-25	29	20	31.03%	2.638	0.291	96	0.122	6
GTSP1222	0	d0	Tcell	UPCC03712-29	3477	3183	0.17%	8.029	0.079	23384	0.000	1445
GTSP1223	14	d14	Blood	UPCC03712-29	319	229	2.5%	5.275	0.240	778	0.006	70
GTSP2993	21	d21	Blood	UPCC03712-29	713	513	1.54%	6.080	0.238	1610	0.003	157
GTSP1224	28	d28	Blood	UPCC03712-29	739	556	1.62%	6.161	0.219	2264	0.003	187
GTSP2994	28	d28	BM	UPCC03712-29	1197	826	1.84%	6.502	0.266	2567	0.002	228
GTSP2995	91	m3	Blood	UPCC03712-29	145	95	7.59%	4.295	0.301	303	0.020	23
GTSP2996	91	m3	BM	UPCC03712-29	516	332	3.88%	5.493	0.317	1460	0.007	75
GTSP2998	122	m4	Blood	UPCC03712-29	173	75	15.03%	3.747	0.486	314	0.045	10
GTSP2997	152	m5	Blood	UPCC03712-29	92	49	8.7%	3.630	0.362	137	0.034	11
GTSP2999	183	m6	Blood	UPCC03712-29	189	119	5.29%	4.523	0.317	538	0.015	26
GTSP3000	183	m6	BM	UPCC03712-29	146	81	5.48%	4.165	0.340	240	0.020	19
GTSP3001	0	d0	Tcell	UPCC03712-30	4231	3970	0.17%	8.259	0.059	40353	0.000	1855
GTSP3002	14	d14	Blood	UPCC03712-30	227	142	6.17%	4.686	0.321	595	0.014	31
GTSP3003	28	d28	Blood	UPCC03712-30	81	27	41.98%	2.419	0.579	198	0.198	2
GTSP3004	0	d0	Tcell	UPCC03712-31	8523	8214	0.06%	8.999	0.035	128698	0.000	3953
GTSP3005	14	d14	Blood	UPCC03712-31	192	148	13.02%	4.616	0.224	2094	0.025	53
GTSP3006	0	d0	Tcell	UPCC03712-40	7971	7048	0.06%	8.813	0.105	36797	0.000	3063
GTSP3007	21	d21	Blood	UPCC03712-40	861	525	1.86%	5.991	0.328	1866	0.004	116
GTSP3008	28	d28	Blood	UPCC03712-40	284	186	2.82%	4.985	0.300	1602	0.009	45
GTSP3009	28	d28	BM	UPCC03712-40	430	263	1.86%	5.339	0.318	687	0.006	63
GTSP3010	0	d0	Tcell	UPCC03712-43	5491	4693	0.09%	8.392	0.129	21560	0.000	1948
GTSP3011	14	d14	Blood	UPCC03712-43	3520	2570	0.37%	7.726	0.222	7207	0.001	811
GTSP3012	28	d28	Blood	UPCC03712-43	237	144	3.38%	4.779	0.303	447	0.010	36
GTSP3013	28	d28	BM	UPCC03712-43	223	136	3.59%	4.632	0.335	1608	0.013	26
GTSP3014	61	m2	Blood	UPCC03712-43	152	117	5.26%	4.604	0.209	838	0.013	42
GTSP1211	0	d0	Tcell	UPCC03712-45	2277	2089	0.22%	7.608	0.077	15578	0.001	951
GTSP1212	14	d14	Tcell	UPCC03712-45	945	525	19.83%	5.382	0.399	1374	0.042	96
GTSP0571	14	d14	Tcells:CAR+CD8-	UPCC03712-45	55	33	12.73%	3.180	0.348	208	0.059	6
GTSP0572	14	d14	Tcells:CAR+CD8+	UPCC03712-45	3168	1579	14.46%	6.385	0.456	5134	0.022	195
GTSP1213	21	d21	Blood	UPCC03712-45	439	217	28.64%	4.308	0.466	630	0.086	26
GTSP1405	28	d28	Blood	UPCC03712-45	414	220	10.36%	4.769	0.428	964	0.023	31
GTSP3015	28	d28	BM	UPCC03712-45	280	185	11.07%	4.831	0.309	693	0.019	46
GTSP3016	91	m3	Blood	UPCC03712-45	55	45	10.91%	3.676	0.169	240	0.032	18
GTSP3017	122	m4	Blood	UPCC03712-45	60	33	18.33%	3.081	0.397	208	0.072	5
GTSP3018	152	m5	Blood	UPCC03712-45	55	33	41.82%	2.696	0.388	529	0.185	6
GTSP3019	0	d0	Tcell	UPCC03712-47	4437	4051	0.11%	8.270	0.081	28782	0.000	1833
GTSP3020	11	d11	Blood	UPCC03712-47	3155	2484	0.19%	7.726	0.180	8272	0.000	907
GTSP3022	28	d28	Blood	UPCC03712-47	785	493	1.02%	6.019	0.293	1426	0.003	124
GTSP3021	28	d28	BM	UPCC03712-47	1026	692	0.88%	6.361	0.271	2495	0.002	180
GTSP3023	91	m3	Blood	UPCC03712-47	174	147	2.87%	4.893	0.144	1012	0.009	61
GTSP3024	91	m3	BM	UPCC03712-47	187	123	5.88%	4.562	0.300	662	0.015	30
GTSP3025	122	m4	Blood	UPCC03712-47	334	249	3.89%	5.281	0.237	2085	0.008	83
GTSP3026	152	m5	Blood	UPCC03712-47	189	146	8.47%	4.742	0.216	2340	0.015	52
GTSP3027	183	m6	Blood	UPCC03712-47	85	49	8.24%	3.669	0.328	189	0.032	12
GTSP3028	183	m6	BM	UPCC03712-47	289	155	11.76%	4.252	0.444	1190	0.039	15
GTSP3029	274	m9	Blood	UPCC03712-47	168	135	5.36%	4.725	0.186	1073	0.013	52
GTSP3030	365	m12	Blood	UPCC03712-47	87	78	5.75%	4.278	0.100	978	0.016	35
GTSP3228	0	d0	Tcell	UPCC03712-48	4175	3957	0.17%	8.262	0.050	40878	0.000	1870
GTSP3229	28	d28	Blood	UPCC03712-48	43	19	13.95%	2.700	0.375	30	0.082	5
GTSP3230	28	d28	BM	UPCC03712-48	29	11	34.48%	2.059	0.426	14	0.175	3
GTSP3231	0	d0	Tcell	UPCC03712-51	2321	2140	0.22%	7.636	0.073	15652	0.001	980
GTSP3232	28	d28	Blood	UPCC03712-51	16	12	25%	2.339	0.219	34	0.117	5
GTSP3233	61	m2	Blood	UPCC03712-51	178	175	1.12%	5.158	0.017	3852	0.006	87
GTSP3234	0	d0	Tcell	UPCC03712-55	2472	2356	0.12%	7.746	0.045	26855	0.000	1121
GTSP3235	28	d28	Blood	UPCC03712-55	106	98	3.77%	4.533	0.073	1555	0.012	46
GTSP3236	0	d0	Tcell	UPCC03712-57	1691	1541	0.3%	7.303	0.082	9959	0.001	696
GTSP3237	28	d28	Blood	UPCC03712-57	9	6	33.33%	1.677	0.241	9	0.210	2
GTSP3238	28	d28	BM	UPCC03712-57	52	48	5.77%	3.824	0.074	1083	0.024	23
GTSP3239	0	d0	Tcell	UPCC03712-58	943	924	0.32%	6.821	0.020	23700	0.001	453
GTSP3240	28	d28	Blood	UPCC03712-58	41	21	31.71%	2.556	0.430	61	0.135	3
GTSP3241	28	d28	BM	UPCC03712-58	65	40	10.77%	3.412	0.331	205	0.045	8
GTSP3242	0	d0	Tcell	UPCC03712-59	1708	1569	0.35%	7.324	0.076	11269	0.001	716
GTSP3244	28	d28	Blood	UPCC03712-59	94	31	52.13%	2.194	0.626	356	0.285	1
GTSP3243	28	d28	BM	UPCC03712-59	100	46	9%	3.556	0.385	96	0.036	11
GTSP3245	0	d0	Tcell	UPCC03712-60	3384	3075	0.18%	7.990	0.085	21464	0.000	1384

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Sample Info					Clone info			Population info				
GTSP	Time(d)	timePoint	cellType	patient	Clones	Unique	Max Clone	Shannon	Gini	Chao1	Simpson	UC50
GTSP3246	28	d28	Blood	UPCC03712-60	46	12	71.74%	1.249	0.670	57	0.524	1
GTSP3247	28	d28	BM	UPCC03712-60	4	4	25%	1.386	0.000	10	0.250	3
GTSP3248	0	d0	Tcell	UPCC03712-61	3305	3037	0.18%	7.983	0.076	23410	0.000	1385
GTSP3249	28	d28	Blood	UPCC03712-61	511	370	2.15%	5.761	0.232	1056	0.004	115
GTSP3250	28	d28	BM	UPCC03712-61	443	310	2.26%	5.529	0.265	2880	0.005	89
GTSP3251	61	m2	Blood	UPCC03712-61	334	248	3.89%	5.316	0.234	2130	0.007	82
GTSP3252	91	m3	Blood	UPCC03712-61	23	21	8.7%	3.015	0.079	78	0.051	10
GTSP3253	91	m3	BM	UPCC03712-61	270	170	6.3%	4.787	0.335	2780	0.014	36
GTSP3254	122	m4	Blood	UPCC03712-61	499	417	4.61%	5.803	0.161	16377	0.006	168
GTSP3255	152	m5	Blood	UPCC03712-61	152	41	21.71%	2.998	0.578	99	0.091	4
GTSP1196	0	d0	Tcell	UPCC04409-01	3401	3228	0.12%	8.058	0.049	37980	0.000	1528
GTSP0734	13	d13	Blood	UPCC04409-01	2720	1318	1.65%	6.634	0.449	3739	0.003	183
GTSP0561	14	d14	Tcells:CAR+CD8-	UPCC04409-01	442	329	3.34%	5.612	0.229	1979	0.005	109
GTSP0562	14	d14	Tcells:CAR+CD8+	UPCC04409-01	3456	1533	2.31%	6.670	0.490	4554	0.003	171
GTSP1406	28	d28	Blood	UPCC04409-01	35	34	5.71%	3.516	0.028	298	0.030	17
GTSP3256	28	d28	BM	UPCC04409-01	271	189	7.38%	4.923	0.281	1389	0.014	54
GTSP1225	61	m2	Blood	UPCC04409-01	11	11	9.09%	2.398	0.000	66	0.091	6
GTSP1226	91	m3	Blood	UPCC04409-01	544	502	4.93%	6.079	0.077	41257	0.004	231
GTSP1197	274	m9	Blood	UPCC04409-01	441	357	6.58%	5.616	0.185	7350	0.008	137
GTSP1198	365	y1	Blood	UPCC04409-01	92	55	18.09%	3.525	0.373	1231	0.057	10
GTSP1227	456	m15	Blood	UPCC04409-01	20	10	50%	1.775	0.440	24	0.280	2
GTSP1199	548	m18	Blood	UPCC04409-01	407	300	5.3%	5.310	0.255	4178	0.011	97
GTSP1200	639	m21	Blood	UPCC04409-01	174	65	17.71%	3.392	0.553	194	0.071	6
GTSP2141	1095	y3	Blood	UPCC04409-01	178	83	26.09%	3.442	0.508	704	0.098	6
GTSP2142	1460	y4	Blood	UPCC04409-01	133	47	36.57%	2.643	0.612	867	0.177	2
GTSP1201	1825	y5	Blood	UPCC04409-01	389	264	10%	4.937	0.315	5410	0.024	70
GTSP2143	1825	y5	Blood	UPCC04409-01	161	37	27.68%	2.606	0.664	79	0.139	3
GTSP2144	2008	y5.5	Blood	UPCC04409-01	154	62	29.49%	3.168	0.555	307	0.112	4
GTSP2667	2920	y8	Blood	UPCC04409-01	29	20	17.24%	2.803	0.267	60	0.077	6
GTSP3257	3042	m100	Blood	UPCC04409-01	167	129	9.58%	4.562	0.220	1914	0.020	46
GTSP3272	3285	y9	Blood	UPCC04409-01	35	25	11.43%	3.080	0.235	59	0.055	8
GTSP3819	3650	y10	Blood	UPCC04409-01	30	30	3.33%	3.401	0.000	465	0.033	16
GTSP1173	0	d0	Tcell	UPCC04409-02	1204	1166	0.25%	7.048	0.031	20530	0.001	565
GTSP0735	28	d28	Blood	UPCC04409-02	996	205	20.28%	3.217	0.758	629	0.125	3
GTSP3258	28	d28	BM	UPCC04409-02	1017	155	21.44%	2.951	0.804	494	0.131	3
GTSP0563	28	d28	Tcells:CAR+CD8-	UPCC04409-02	1057	311	38%	3.550	0.686	1410	0.161	3
GTSP0564	28	d28	Tcells:CAR+CD8+	UPCC04409-02	2321	232	27.09%	2.918	0.857	615	0.156	2
GTSP1228	50	d50	Blood	UPCC04409-02	2257	380	16.87%	3.758	0.791	1406	0.080	4
GTSP3260	122	m4	Blood	UPCC04409-02	331	105	20.85%	3.453	0.630	480	0.085	4
GTSP3259	122	m4	BM	UPCC04409-02	621	278	14.17%	4.484	0.531	2190	0.042	13
GTSP1229	152	m5	Blood	UPCC04409-02	122	32	19.67%	2.770	0.589	51	0.101	4
GTSP1166	183	m6	Blood	UPCC04409-02	156	69	16.67%	3.476	0.513	620	0.064	6
GTSP3261	183	m6	BM	UPCC04409-02	252	91	17.86%	3.652	0.572	306	0.059	7
GTSP1167	365	y1	Blood	UPCC04409-02	53	17	33.96%	2.237	0.544	44	0.168	3
GTSP3262	365	m12	Blood	UPCC04409-02	138	33	29.71%	2.630	0.634	67	0.133	3
GTSP1168	456	m15	Blood	UPCC04409-02	164	84	15.7%	3.779	0.453	705	0.050	9
GTSP1169	548	m18	Blood	UPCC04409-02	284	164	31.34%	3.941	0.417	6366	0.106	23
GTSP1170	639	m21	Blood	UPCC04409-02	78	41	10.13%	3.376	0.391	150	0.048	8
GTSP1171	730	y2	Blood	UPCC04409-02	228	135	19.21%	4.101	0.397	4136	0.055	22
GTSP1172	973	m32	Blood	UPCC04409-02	76	34	44.74%	2.501	0.527	499	0.217	2
GTSP2145	1460	y4	Blood	UPCC04409-02	185	61	49.46%	2.659	0.623	179	0.254	2
GTSP2146	1642	y4.5	Blood	UPCC04409-02	415	343	5.52%	5.570	0.170	18548	0.008	136
GTSP2147	1825	y5	Blood	UPCC04409-02	149	71	28%	3.510	0.469	204	0.091	9
GTSP2148	2008	y5.5	Blood	UPCC04409-02	110	67	10%	3.908	0.336	332	0.030	14
GTSP2149	2190	y6	Blood	UPCC04409-02	122	66	9.84%	3.831	0.389	301	0.033	12
GTSP2150	2372	y6.5	Blood	UPCC04409-02	101	47	14.71%	3.388	0.451	187	0.054	7
GTSP2151	2555	y7	Blood	UPCC04409-02	240	171	11.43%	4.762	0.273	1446	0.021	52
GTSP1407	0	d0	Tcell	UPCC04409-03	2617	2078	0.27%	7.548	0.176	7145	0.001	770
GTSP0736	11	d11	Blood	UPCC04409-03	32	27	15.62%	3.171	0.148	177	0.053	12
GTSP1408	28	d28	Blood	UPCC04409-03	786	752	2.29%	6.560	0.043	46694	0.002	360
GTSP0737	0	d0	Tcell	UPCC04409-05	925	822	0.53%	6.658	0.103	5353	0.001	360
GTSP0738	17	d17	Blood	UPCC04409-05	273	136	6.57%	4.492	0.419	345	0.019	23
GTSP1175	21	d21	Blood	UPCC04409-05	221	155	10.18%	4.652	0.282	977	0.022	45
GTSP1409	28	d28	Blood	UPCC04409-05	108	54	11.01%	3.579	0.420	249	0.043	9
GTSP0739	0	d0	Tcell	UPCC04409-06	4408	4079	0.09%	8.283	0.070	31517	0.000	1876
GTSP1410	28	d28	Blood	UPCC04409-06	2	1	100%	0.000	0.000	1	1.000	1
GTSP0741	0	d0	Tcell	UPCC04409-07	2412	2266	0.21%	7.699	0.058	22885	0.000	1061
GTSP0742	1	d1	Blood	UPCC04409-07	14	9	26.67%	2.008	0.286	30	0.163	3
GTSP1411	28	d28	Blood	UPCC04409-07	8	5	50%	1.386	0.300	11	0.312	2
GTSP0603	0	d0	Tcell	UPCC04409-09	4076	2666	0.34%	7.698	0.284	8246	0.001	669
GTSP0744	10	d10	Blood	UPCC04409-09	1378	1098	0.36%	6.923	0.169	3308	0.001	410
GTSP0565	14	d14	Tcells:CAR+CD8-	UPCC04409-09	253	217	1.98%	5.324	0.124	766	0.005	91
GTSP0566	14	d14	Tcells:CAR+CD8+	UPCC04409-09	3985	2920	0.82%	7.791	0.233	9504	0.001	928
GTSP0604	28	d28	Blood	UPCC04409-09	1319	852	1.35%	6.464	0.314	5463	0.002	193
GTSP3279	28	d28	Blood	UPCC04409-09	3252	2512	0.62%	7.685	0.201	9979	0.001	887
GTSP3280	28	d28	BM	UPCC04409-09	3036	2446	0.46%	7.685	0.174	10453	0.001	929
GTSP1232	61	m2	Blood	UPCC04409-09	423	325	4.22%	5.603	0.210	1540	0.006	114
GTSP3281	91	m3	Blood	UPCC04409-09	235	119	6.38%	4.401	0.408	506	0.019	22
GTSP3282	91	m3	BM	UPCC04409-09	378	294	3.44%	5.520	0.203	1754	0.006	106
GTSP1233	152	m5	Blood	UPCC04409-09	283	243	3.52%	5.352	0.137	6884	0.006	102
GTSP1234	183	m6	Blood	UPCC04409-09	42	29	19.05%	3.131	0.273	80	0.063	9
GTSP1177	274	m9	Blood	UPCC04409-09	22	21	9.09%	3.028	0.043	116	0.050	11
GTSP1178	365	y1	Blood	UPCC04409-09	134	32	63.43%	1.839	0.708	116	0.409	1
GTSP3283	365	m12	BM	UPCC04409-09	16	6	68.75%	1.124	0.521	16	0.492	1
GTSP0605	0	d0	Tcell	UPCC04409-10	1350	1033	0.81%	6.805	0.206	4044	0.001	359
GTSP0606	10	d10	Blood	UPCC04409-10	26	23	11.54%	3.078	0.107	128	0.050	11
GTSP0607	28	d28	Blood	UPCC04409-10	11	10	18.18%	2.272	0.082	28	0.107	5
GTSP1603	28	d28	Blood	UPCC04409-10	432	385	4.61%	5.804	0.107	14261	0.005	170
GTSP1604	63	d63	Blood	UPCC04409-10	147	85	8%	4.114	0.362	442	0.024	16
GTSP1605	92	d92	Blood	UPCC04409-10	17	14	17.65%	2.558	0.155	47	0.087	6
GTSP0608	120	d120	Blood	UPCC04409-10	121	21	83.47%	0.943	0.787	211	0.698	1
GTSP0746	121	d121	Blood	UPCC04409-10	400	4	99%	0.066	0.741	4	0.980	1
GTSP0560	121	d121	Tcells:CAR+CD8+	UPCC04409-10	965	106	88.82%	0.864	0.882	1857	0.791	1

(continued)

Sample Info					Clone info			Population info				
GTSP	Time(d)	timePoint	cellType	patient	Clones	Unique	Max Clone	Shannon	Gini	Chao1	Simpson	UC50
GTSP1606	147	d147	Blood	UPCC04409-10	416	27	93.75%	0.437	0.900	352	0.879	1
GTSP0609	204	d204	Blood	UPCC04409-10	62	14	77.42%	1.108	0.717	47	0.604	1
GTSP0610	442	d442	Blood	UPCC04409-10	17	12	35.29%	2.201	0.270	67	0.163	4
GTSP1607	442	d442	Blood	UPCC04409-10	95	45	25.24%	2.845	0.502	906	0.140	2
GTSP0611	801	d801	Blood	UPCC04409-10	20	13	40%	2.164	0.323	79	0.190	4
GTSP1608	801	d801	Blood	UPCC04409-10	96	51	28.16%	3.210	0.441	524	0.107	6
GTSP1609	1584	d1584	PBL	UPCC04409-10	48	28	16%	3.052	0.347	98	0.065	6
GTSP0747	0	d0	Tcell	UPCC04409-12	1143	1132	0.26%	7.028	0.010	64020	0.001	561
GTSP1180	9	d9	Blood	UPCC04409-12	131	102	3.79%	4.486	0.200	649	0.014	37
GTSP0748	14	d14	Blood	UPCC04409-12	1321	1088	0.53%	6.909	0.155	4436	0.001	428
GTSP0613	28	d28	Blood	UPCC04409-12	375	319	1.6%	5.689	0.135	1451	0.004	132
GTSP1183	61	m2	Blood	UPCC04409-12	179	144	4.44%	4.834	0.180	1499	0.010	55
GTSP0749	0	d0	Tcell	UPCC04409-14	723	575	0.69%	6.251	0.180	2565	0.002	214
GTSP0750	14	d14	Blood	UPCC04409-14	5	5	20%	1.609	0.000	15	0.200	3
GTSP0614	0	d0	Tcell	UPCC04409-17	2039	1660	0.34%	7.322	0.164	6925	0.001	641
GTSP0752	10	d10	Blood	UPCC04409-17	455	368	1.96%	5.794	0.172	1742	0.004	141
GTSP0615	28	d28	Blood	UPCC04409-17	29	29	3.45%	3.367	0.000	435	0.034	15
GTSP0616	0	d0	Tcell	UPCC04409-18	393	274	3.54%	5.367	0.273	1810	0.007	78
GTSP0754	1	d1	Blood	UPCC04409-18	2	2	50%	0.693	0.000	3	0.500	2
GTSP0617	28	d28	Blood	UPCC04409-18	30	18	22.58%	2.543	0.352	70	0.116	4
GTSP0755	0	d0	Tcell	UPCC04409-22	996	982	0.2%	6.884	0.014	32184	0.001	485
GTSP1187	10	d10	Blood	UPCC04409-22	220	162	4.46%	4.847	0.246	1449	0.012	53
GTSP1188	14	d14	Blood	UPCC04409-22	3653	3004	0.35%	7.906	0.160	14819	0.000	1178
GTSP0619	28	d28	Blood	UPCC04409-22	190	178	1.05%	5.159	0.059	1231	0.006	84
GTSP3284	28	d28	BM	UPCC04409-22	579	432	1.21%	5.956	0.208	1224	0.003	143
GTSP1190	61	m2	Blood	UPCC04409-22	263	214	2.63%	5.254	0.169	1065	0.006	83
GTSP1191	91	m3	Blood	UPCC04409-22	174	102	22.41%	3.905	0.398	939	0.063	16
GTSP1192	122	m4	Blood	UPCC04409-22	88	75	5.56%	4.232	0.136	444	0.017	32
GTSP1193	152	m5	Blood	UPCC04409-22	22	22	4.55%	3.091	0.000	253	0.045	12
GTSP3285	180	d180	Blood	UPCC04409-22	4	1	100%	0.000	0.000	1	1.000	1
GTSP0620	0	d0	Tcell	UPCC04409-23	1542	1216	0.39%	7.008	0.180	4195	0.001	446
GTSP0621	28	d28	Blood	UPCC04409-23	35	27	14.29%	3.167	0.199	73	0.051	10
GTSP0757	0	d0	Tcell	UPCC04409-25	564	555	0.35%	6.313	0.016	15434	0.002	274
GTSP0758	14	d14	Blood	UPCC04409-25	276	246	4.33%	5.392	0.106	4174	0.006	109
GTSP0624	0	d0	Tcell	UPCC04409-26	936	923	0.32%	6.821	0.014	42465	0.001	456
GTSP0625	28	d28	Blood	UPCC04409-26	7	6	28.57%	1.748	0.119	11	0.184	3
GTSP0626	0	d0	Tcell	UPCC04409-27	1061	1045	0.28%	6.945	0.015	41888	0.001	515
GTSP0627	28	d28	Blood	UPCC04409-27	6	4	50%	1.242	0.250	7	0.333	2
GTSP0628	0	d0	Tcell	UPCC04409-29	203	195	1.46%	5.256	0.038	2706	0.005	94
GTSP0629	28	d28	Blood	UPCC04409-29	1233	1219	0.16%	7.101	0.011	49580	0.001	603
GTSP2648	0	d0	Tcell	UPCC18415-01	1952	1816	0.26%	7.475	0.066	15003	0.001	841
GTSP2649	0	d0	Tcell	UPCC18415-02	1479	1357	0.34%	7.179	0.077	9574	0.001	618
GTSP3288	28	d28	Blood	UPCC18415-02	485	338	1.86%	5.643	0.260	1448	0.005	96
GTSP3289	28	d28	BM	UPCC18415-02	388	291	2.06%	5.507	0.224	2333	0.005	98
GTSP3290	91	m3	Blood	UPCC18415-02	9	4	44.44%	1.215	0.306	5	0.333	2
GTSP2650	0	d0	Tcell	UPCC18415-03	2945	2818	0.14%	7.926	0.041	36921	0.000	1346
GTSP3291	28	d28	Blood	UPCC18415-03	55	27	25.45%	2.913	0.392	39	0.092	6
GTSP3292	28	d28	BM	UPCC18415-03	43	20	18.6%	2.614	0.429	50	0.101	4
GTSP2651	0	d0	Tcell	UPCC18415-04	3958	3836	0.1%	8.240	0.030	65598	0.000	1858
GTSP3293	28	d28	Blood	UPCC18415-04	44	12	54.55%	1.623	0.617	48	0.334	1
GTSP3294	28	d28	BM	UPCC18415-04	24	10	25%	2.087	0.350	20	0.146	3
GTSP2652	0	d0	Tcell	UPCC18415-05	1560	1451	0.32%	7.250	0.066	12536	0.001	672
GTSP3296	28	d28	Blood	UPCC18415-05	26	15	19.23%	2.482	0.328	70	0.104	4
GTSP3295	28	d28	BM	UPCC18415-05	16	9	25%	2.047	0.292	12	0.148	3
GTSP2653	0	d0	Tcell	UPCC18415-06	2957	2808	0.14%	7.918	0.048	34251	0.000	1330
GTSP3298	28	d28	Blood	UPCC18415-06	67	25	26.87%	2.759	0.468	41	0.104	5
GTSP3297	28	d28	BM	UPCC18415-06	122	90	7.38%	4.268	0.244	880	0.020	30
GTSP3299	91	m3	BM	UPCC18415-06	19	8	31.58%	1.840	0.375	11	0.191	2
GTSP3300	183	m6	Blood	UPCC18415-06	5	2	60%	0.673	0.100	2	0.520	1
GTSP3301	183	m6	BM	UPCC18415-06	25	17	20%	2.620	0.278	62	0.094	5
GTSP3302	274	m9	Blood	UPCC18415-06	18	7	38.89%	1.672	0.397	8	0.235	2
GTSP3303	304	m10	Blood	UPCC18415-06	10	4	30%	1.314	0.150	4	0.280	2
GTSP2654	0	d0	Tcell	UPCC18415-07	2522	2437	0.2%	7.782	0.033	50797	0.000	1177
GTSP3304	28	d28	Blood	UPCC18415-07	20	12	35%	2.176	0.342	24	0.165	3
GTSP3305	28	d28	BM	UPCC18415-07	100	71	11%	3.984	0.268	376	0.030	22
GTSP2655	0	d0	Tcell	UPCC18415-08	3064	2891	0.13%	7.945	0.054	30666	0.000	1360
GTSP3549	28	d28	Blood	UPCC18415-08	2	2	50%	0.693	0.000	3	0.500	2
GTSP3548	28	d28	BM	UPCC18415-08	1	1	100%	0.000	0.000	1	1.000	1
GTSP2656	0	d0	Tcell	UPCC18415-09	2358	2216	0.17%	7.677	0.057	23086	0.000	1038
GTSP3550	28	d28	Blood	UPCC18415-09	145	91	4.14%	4.373	0.265	158	0.015	27
GTSP3551	28	d28	BM	UPCC18415-09	487	304	2.05%	5.483	0.313	1196	0.006	69
GTSP2657	0	d0	Tcell	UPCC18415-10	2338	2221	0.21%	7.684	0.048	26327	0.000	1053
GTSP3552	28	d28	BM	UPCC18415-10	1	1	100%	0.000	0.000	1	1.000	1
GTSP2658	0	d0	Tcell	UPCC18415-11	3907	3725	0.13%	8.203	0.045	47817	0.000	1772
GTSP3555	28	d28	Blood	UPCC18415-11	32	11	37.5%	1.990	0.466	14	0.195	2
GTSP3554	28	d28	BM	UPCC18415-11	7	5	28.57%	1.550	0.171	6	0.224	2
GTSP2659	0	d0	Tcell	UPCC18415-12	2732	2547	0.18%	7.816	0.064	20420	0.000	1182
GTSP3556	28	d28	Blood	UPCC18415-12	373	247	3.49%	5.266	0.293	1193	0.007	61
GTSP3557	28	d28	BM	UPCC18415-12	748	503	1.87%	5.953	0.294	3144	0.004	130
GTSP3562	365	m12	Blood	UPCC18415-12	5	3	40%	1.055	0.133	3	0.360	2
GTSP2660	0	d0	Tcell	UPCC18415-13	3928	3812	0.08%	8.234	0.029	67801	0.000	1849
GTSP3563	28	d28	Blood	UPCC18415-13	37	31	5.41%	3.386	0.131	74	0.036	13
GTSP3564	28	d28	BM	UPCC18415-13	95	70	5.26%	4.100	0.228	298	0.020	23
GTSP3565	91	m3	Blood	UPCC18415-13	100	61	24%	3.569	0.365	392	0.071	12
GTSP3568	365	m12	Blood	UPCC18415-13	8	7	25%	1.906	0.107	14	0.156	4
GTSP3567	365	m12	BM	UPCC18415-13	11	6	45.45%	1.540	0.348	9	0.273	2
GTSP2661	0	d0	Tcell	UPCC18415-15	3330	2989	0.18%	7.956	0.094	18022	0.000	1325
GTSP3570	28	d28	Blood	UPCC18415-15	2	2	50%	0.693	0.000	3	0.500	2
GTSP2662	0	d0	Tcell	UPCC18415-16	2016	1905	0.2%	7.530	0.052	19392	0.001	898
GTSP3571	28	d28	Blood	UPCC18415-16	70	51	7.14%	3.799	0.227	181	0.027	17
GTSP3572	28	d28	BM	UPCC18415-16	8	7	25%	1.906	0.107	14	0.156	4
GTSP2663	0	d0	Tcell	UPCC18415-17	3441	3336	0.12%	8.099	0.030	65144	0.000	1616
GTSP3573	10	d10	Blood	UPCC18415-17	411	290	1.7%	5.491	0.255	1749	0.005	85

(continued)

Sample Info					Clone info			Population info				
GTSP	Time(d)	timePoint	cellType	patient	Clones	Unique	Max Clone	Shannon	Gini	Chao1	Simpson	UC50
GTSP2664	0	d0	Tcell	UPCC18415-18	3695	3597	0.11%	8.176	0.026	79582	0.000	1750
GTSP3575	28	d28	Blood	UPCC18415-18	27	23	11.11%	3.071	0.132	86	0.051	10
GTSP3574	28	d28	BM	UPCC18415-18	20	16	15%	2.692	0.169	42	0.075	7
GTSP2665	0	d0	Tcell	UPCC18415-19	4270	4164	0.09%	8.324	0.024	97111	0.000	2030
GTSP3577	28	d28	Blood	UPCC18415-19	18	12	22.22%	2.351	0.250	19	0.111	4
GTSP3576	28	d28	BM	UPCC18415-19	46	31	13.04%	3.229	0.279	181	0.051	9
GTSP3579	91	m3	Blood	UPCC18415-19	7	5	42.86%	1.475	0.229	11	0.265	2
GTSP3578	91	m3	BM	UPCC18415-19	6	5	33.33%	1.561	0.133	8	0.222	3
GTSP3580	122	m4	Blood	UPCC18415-19	77	55	7.79%	3.871	0.233	137	0.025	17
GTSP2666	0	d0	Tcell	UPCC18415-20	4421	4236	0.14%	8.332	0.040	64915	0.000	2026
GTSP3581	28	d28	Blood	UPCC18415-20	75	54	10.67%	3.768	0.253	195	0.033	17
GTSP3582	28	d28	BM	UPCC18415-20	12	11	16.67%	2.369	0.076	34	0.097	6
GTSP3583	61	m2	Blood	UPCC18415-20	19	14	15.79%	2.552	0.199	25	0.086	5
GTSP3507	0	d0	Tcell	UPCC25416-07	1374	1214	0.36%	7.047	0.107	6846	0.001	528
GTSP3508	7	d7	Blood	UPCC25416-07	658	408	1.67%	5.807	0.303	1071	0.004	102
GTSP3820	14	d14	Blood	UPCC25416-07	126	101	3.17%	4.518	0.174	458	0.012	39
GTSP3509	91	m3	Blood	UPCC25416-07	407	299	1.97%	5.545	0.230	1203	0.005	96
GTSP3821	91	m3	Blood	UPCC25416-07	381	256	4.46%	5.209	0.302	1302	0.010	66
GTSP3510	0	d0	Tcell	UPCC25416-35	620	455	0.97%	5.994	0.222	1451	0.003	146
GTSP3511	7	d7	Blood	UPCC25416-35	231	160	11.69%	4.619	0.295	1304	0.025	45
GTSP3512	183	m6	Blood	UPCC25416-35	21	11	23.81%	2.174	0.346	22	0.138	3
GTSP3822	274	m9	Blood	UPCC25416-35	77	48	10.39%	3.684	0.289	103	0.032	13
GTSP3513	0	d0	Tcell	UPCC25416-39	2254	1979	0.27%	7.535	0.111	10947	0.001	853
GTSP3514	10	d10	Blood	UPCC25416-39	1267	976	0.32%	6.799	0.185	2537	0.001	343
GTSP3823	28	d28	Blood	UPCC25416-39	511	280	3.91%	5.259	0.385	921	0.009	51
GTSP3515	183	m6	Blood	UPCC25416-39	346	253	1.45%	5.402	0.226	903	0.005	81
GTSP3824	183	m6	Blood	UPCC25416-39	1570	453	11.21%	5.001	0.612	819	0.027	29
GTSP2950	0	d0	Tcell	UPCC32816-02	15475	11698	0.04%	9.266	0.200	34739	0.000	3961
GTSP2951	10	d10	Blood	UPCC32816-02	146	123	3.42%	4.708	0.147	886	0.011	51
GTSP2952	0	d0	Tcell	UPCC32816-04	7273	7150	0.04%	8.868	0.017	236243	0.000	3514
GTSP2953	10	d10	Blood	UPCC32816-04	181	161	1.66%	5.037	0.100	847	0.007	71
GTSP2954	0	d0	Tcell	UPCC32816-05	9476	9379	0.03%	9.142	0.010	477868	0.000	4642
GTSP2955	10	d10	FFPE	UPCC32816-05	6	2	50%	0.693	0.000	2	0.500	2
GTSP2956	0	d0	Tcell	UPCC32816-06	8257	8150	0.04%	9.000	0.013	376575	0.000	4022
GTSP2957	7	d7	Blood	UPCC32816-06	251	213	1.99%	5.267	0.141	2272	0.006	88
GTSP4261	28	d28	Blood	UPCC32816-08	1	1	100%	0.000	0.000	1	1.000	1
GTSP4263	10	d10	Blood	UPCC32816-11	2	2	50%	0.693	0.000	3	0.500	2
GTSP4266	14	d14	Blood	UPCC32816-12	3	3	33.33%	1.099	0.000	6	0.333	2
GTSP2683	0	d0	Tcell	p32816-099	13031	12823	0.03%	9.452	0.016	474110	0.000	6308
GTSP2684	10	d10	Blood	p32816-099	2857	2756	0.21%	7.904	0.034	49100	0.000	1328
GTSP2685	21	d21	Blood	p32816-099	1691	1349	4.14%	6.900	0.194	11230	0.003	504
GTSP2686	28	d28	Blood	p32816-099	2969	1348	14.85%	5.595	0.528	8612	0.044	67
GTSP9999	30	m1	T-cells	testPatient	4	1	100%	0.000	0.000	1	1.000	1

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 (v3.14). KEGG pathways were acquired via interfacing with the KEGG web-server API through the `KEGGREST` R-package (v1.34.1). 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 than 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
ANKRD11	chr16	89,262,620	89,495,561	66	25.1	25	730.0	EAL
RNF213	chr17	80,255,860	80,403,781	63	21.8	76	15.0	EAL
ADD1	chr4	2,838,856	2,935,075	60	24.5	43	14.0	EAL
FOXP1	chr3	70,949,713	71,588,989	54	33.3	49	2745.0	EAL
NELL2	chr12	44,503,274	44,918,928	45	42.5	441	62.0	EAL
VAV1	chr19	6,767,667	6,862,366	72	29.7	37	602.0	EA
RNF157	chr17	76,137,452	76,245,311	67	-3.0	39	18.0	AL
PPP6R3	chr11	68,455,717	68,620,333	65	56.5	154	62.0	EA
PAFAH1B1	chr17	2,588,628	2,690,615	61	21.3	33	60.0	EA
ZNF251	chr8	144,715,908	144,760,585	60	-4.0	43	182.5	AL
CYTH1	chr17	78,669,046	78,787,342	58	-19.3	30	14.0	DAL
SUPT3H	chr6	44,821,729	45,383,051	57	40.0	31	14.0	EA
SAE1	chr19	47,125,822	47,215,636	56	20.2	24	76.0	EA
MED13L	chr12	115,953,575	116,282,186	54	34.7	38	14.0	EA
VMP1	chr17	59,702,464	59,847,255	54	-32.0	28	46.0	DAL
ZZEF1	chr17	3,999,444	4,147,959	54	-0.9	92	2527.0	AL
AKAP13	chr15	85,375,615	85,754,358	48	32.1	27	15.0	EA
CLK4	chr5	178,597,663	178,632,053	47	48.6	53	166.0	EA
SRCAP	chr16	30,694,140	30,745,129	47	14.2	402	2162.0	AL
KANSL1	chr17	46,024,915	46,230,374	44	-15.1	79	129.0	AL
PTBP1	chr19	792,391	817,327	44	39.1	52	351.0	EA
MTOR	chr1	11,101,530	11,267,551	42	-13.7	29	360.0	AL
CSMD1	chr8	2,930,352	4,999,806	41	337.6	8	597.0	EL
SRRM2	chr16	2,747,328	2,776,412	40	31.6	33	18.0	EA
KMT2D	chr12	49,013,974	49,060,324	35	97.8	33	76.0	EA
CENPP	chr9	92,320,467	92,620,155	31	49.4	3	0.0	EL
HSF5	chr17	58,415,166	58,493,401	30	-9.8	35	1825.0	AL
ZNF44	chr19	12,266,809	12,299,899	27	-6.2	9	547.5	AL
RMND5A	chr2	86,715,290	86,783,041	23	100.9	25	7.0	EA
CNTNAP2	chr7	146,111,360	148,425,996	21	104.6	2	0.0	EL
PPP1R2	chr3	195,509,421	195,548,401	21	41.9	24	1905.0	AL
RBFOX1	chr16	6,014,130	7,718,338	19	79.7	8	0.0	EL
MACROD2	chr20	13,990,499	16,058,196	18	77.4	2	14.0	EL
SIMC1	chr5	176,233,358	176,350,991	18	87.5	2	0.0	EL
TRIO	chr5	14,138,701	14,515,204	13	96.0	66	166.0	EA
C19orf48	chr19	50,792,692	50,809,853	12	137.5	28	46.0	EA
TENM2	chr5	167,279,837	168,269,157	12	275.0	1	0.0	EL
POLG2	chr17	64,472,784	64,502,066	11	87.5	41	14.0	EA
NPLOC4	chr17	81,551,884	81,642,153	81	-17.5	23	1432.0	DL
PACS1	chr11	66,065,352	66,249,747	78	-25.9	24	1925.0	DA
FANCA	chr16	89,732,550	89,821,657	76	-6.2	28	547.5	A
MROH1	chr8	144,143,015	144,266,940	74	-26.4	12	46.0	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
LUC7L	chr16	183,968	234,482	65	-10.6	39	17.0	A
MIR1268A	chr9	128,347,046	128,667,136	64	-15.6	6	15.0	DL
SEC16A	chr9	136,435,095	136,488,759	63	4.3	29	166.0	A
DIP2A	chr21	46,453,948	46,575,013	62	-2.4	27	351.0	A
EP300	chr22	41,087,609	41,185,077	62	83.8	6	46.0	E
PSMD13	chr11	231,807	257,984	62	-18.8	19	14.0	DL
RABEP1	chr17	5,277,262	5,391,339	62	-2.3	27	76.0	A
SMG1P5	chr16	30,280,017	30,340,374	61	21.8	5	14.0	E
SMARCC1	chr3	47,580,887	47,786,915	60	-4.7	4	7.0	L
CBFB	chr16	67,024,146	67,106,055	59	58.1	14	22.0	E
CRAMP1	chr16	1,609,639	1,682,908	59	15.5	31	62.0	A
CREBBP	chr16	3,720,054	3,885,120	58	45.6	5	46.0	E
KLF12	chr13	73,681,011	74,138,929	58	22.5	16	122.0	E
CARD8	chr19	48,203,085	48,260,946	57	-18.8	82	332.0	DA
NOSIP	chr19	49,550,467	49,585,572	56	-28.0	31	3.0	DA
RAB11FIP3	chr16	420,667	527,481	55	-10.0	5	166.0	L
SMG1P2	chr16	29,540,010	29,618,717	55	12.7	11	14.0	L
SMG1P1	chr16	22,432,007	22,497,220	54	62.0	3	100.0	E
UBR2	chr6	42,559,021	42,698,505	54	-15.2	24	14.0	A
FNBP1	chr9	129,882,186	130,048,194	53	-25.9	24	256.0	DA
IFT140	chr16	1,505,426	1,617,108	53	-26.1	27	62.0	DA
C1orf159	chr1	1,076,817	1,121,356	52	-14.5	176	150.0	A
LPP	chr3	188,148,872	188,895,671	52	58.8	10	22.0	E
RASA2	chr3	141,482,046	141,620,363	52	39.4	7	14.0	E
CCNF	chr16	2,424,390	2,463,858	51	-5.6	6	917.5	L
SLC38A10	chr17	81,239,810	81,300,339	51	-4.6	26	92.0	A
ZNF34	chr8	144,767,223	144,792,345	51	-8.6	34	166.0	A
ATM	chr11	108,217,831	108,374,099	50	25.0	7	18.0	E
DDX17	chr22	38,478,437	38,511,340	50	25.6	5	62.0	E
GRB2	chr17	75,313,075	75,410,709	50	10.9	44	14.0	A
KDM6A	chrX	44,868,174	45,117,612	50	94.9	14	166.0	E
PELP1	chr17	4,666,383	4,709,337	50	35.3	5	14.0	E
UBAP2L	chr1	154,215,171	154,276,510	50	18.4	31	7.0	A
P4HB	chr17	81,838,157	81,865,668	49	-25.7	18	14.0	DL
PHF14	chr7	10,968,871	11,174,623	49	28.8	5	69.0	E
PHIP	chr6	78,929,418	79,083,298	49	35.6	5	14.0	E
PPP3CA	chr4	101,018,429	101,352,471	49	41.6	6	166.0	E
TAOK1	chr17	29,385,924	29,556,903	49	-11.3	24	76.0	A
CCDC91	chr12	28,185,426	28,555,166	47	31.8	5	18.0	E
HTT	chr4	3,069,680	3,248,960	47	12.9	25	62.0	A
SSH2	chr17	29,620,938	29,935,228	47	-1.3	146	166.0	A
ZNF276	chr16	89,715,367	89,745,924	47	-1.5	24	702.0	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
IMMP2L	chr7	110,658,049	111,567,517	46	-20.7	4	14.0	DL
STIM2	chr4	26,855,690	27,030,381	46	42.9	5	80.0	E
ERC1	chr12	986,207	1,500,933	45	-9.7	10	122.0	L
SNX13	chr7	17,785,760	17,945,508	45	34.7	9	14.0	E
VPS8	chr3	184,807,142	185,057,614	45	27.7	10	46.0	E
ARHGEF18	chr19	7,390,112	7,477,485	44	38.2	5	14.0	E
KMT2C	chr7	152,129,924	152,441,005	44	37.7	9	365.0	E
MAPK14	chr6	36,022,676	36,116,236	44	20.3	98	14.0	A
MGA	chr15	41,655,411	41,774,943	44	-3.9	91	256.0	A
PCNX1	chr14	70,902,404	71,120,382	44	-8.7	156	32.0	A
PI4KA	chr22	20,702,690	20,863,812	44	-19.2	9	1432.0	L
PPP3CC	chr8	22,435,969	22,546,144	44	-27.7	49	0.0	DA
RUNX2	chr6	45,323,316	45,556,082	44	46.9	8	14.0	E
WDR7	chr18	56,646,384	57,034,805	44	4.1	113	0.0	A
DIDO1	chr20	62,872,737	62,942,952	43	18.6	40	0.0	A
DNM2	chr19	10,713,052	10,836,910	43	12.9	48	2.0	A
FAM117B	chr2	202,630,177	202,774,757	43	34.2	6	169.0	E
LSM14A	chr19	34,167,446	34,234,515	43	34.1	4	2.0	E
YWHAЕ	chr17	1,339,539	1,405,262	43	22.4	26	18.0	A
ZCCHC7	chr9	37,115,471	37,363,148	43	32.1	7	80.0	E
AP2A1	chr19	49,761,922	49,812,112	42	-28.3	3	70.0	DL
DAZAP1	chr19	1,402,568	1,440,687	42	37.1	9	18.0	E
PHF3	chr6	63,630,801	63,720,522	42	56.3	7	122.0	E
SMURF2	chr17	64,539,616	64,667,268	42	-0.3	27	18.0	A
WDR90	chr16	644,362	672,829	42	-30.7	3	62.0	DL
XPO5	chr6	43,517,329	43,581,075	42	7.8	25	22.0	A
AP3B1	chr5	77,997,325	78,299,755	41	51.2	4	76.0	E
ATF7IP	chr12	14,360,631	14,507,935	41	27.6	8	69.0	E
C2CD3	chr11	74,007,713	74,176,019	41	-21.9	4	1979.5	DL
CNOT6L	chr4	77,708,386	77,824,390	41	40.6	7	62.0	E
KDM4C	chr9	6,715,862	7,180,648	41	10.7	27	14.0	A
MBD5	chr2	148,016,010	148,518,475	41	43.9	5	0.0	E
MTMR3	chr22	29,878,168	30,035,868	41	-21.3	280	256.0	A
ROCK1	chr18	20,944,741	21,116,851	41	44.9	14	166.0	E
UBA2	chr19	34,423,362	34,474,893	41	41.1	4	14.0	E
USP47	chr11	11,836,422	11,964,325	41	31.7	5	14.0	E
BCAS3	chr17	60,672,774	61,397,838	40	-8.2	81	106.0	A
ERBIN	chr5	65,921,553	66,086,023	40	40.2	7	18.0	E
LCOR	chr10	96,827,259	96,991,212	40	69.1	4	14.0	E
NUDCD3	chr7	44,377,365	44,495,786	40	37.7	5	69.0	E
PCM1	chr8	17,917,856	18,034,948	40	38.0	11	166.0	E
RHOA	chr3	49,354,135	49,417,097	40	-18.8	5	0.0	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
ZNF250	chr8	144,871,950	144,906,461	40	-12.2	6	0.0	L
LOC101929095	chr4	14,999,941	15,432,914	39	46.8	14	92.0	E
MALAT1	chr11	65,492,737	65,511,512	39	-15.8	14	2745.0	L
SFI1	chr22	31,491,138	31,623,551	39	-27.5	24	14.0	DA
TALAM1	chr11	65,494,311	65,512,432	39	-10.3	14	2745.0	L
FRYL	chr4	48,492,362	48,785,299	38	12.3	24	14.0	A
MAN1B1	chr9	137,081,926	137,114,187	38	-6.6	85	5.0	A
RBM39	chr20	35,698,608	35,747,336	38	34.6	5	256.0	E
RNGTT	chr6	88,604,896	88,968,629	38	42.4	5	14.0	E
ST13	chr22	40,819,534	40,862,008	38	2.2	29	18.0	A
ATF7	chr12	53,502,855	53,631,415	37	-30.9	32	166.0	DA
ATXN1	chr6	16,294,111	16,766,490	37	64.9	4	18.0	E
CDC73	chr1	193,116,957	193,259,812	37	37.0	18	14.0	E
KHDC4	chr1	155,908,042	155,939,442	37	13.0	35	4.0	A
MASCRNA	chr11	65,501,116	65,511,174	37	16.8	14	2745.0	L
PDS5B	chr13	32,581,426	32,783,020	37	33.9	11	256.0	E
AUH	chr9	91,208,814	91,366,969	36	7.4	24	14.0	A
CDK17	chr12	96,273,260	96,405,588	36	59.7	5	14.0	E
CPEB2	chr4	14,997,673	15,075,153	36	44.4	14	92.0	E
KAT6A	chr8	41,924,478	42,057,026	36	34.9	5	0.0	E
NCBP3	chr17	3,801,750	3,851,251	36	37.2	7	69.0	E
PDE3B	chr11	14,638,722	14,877,058	36	0.6	36	32.0	A
XRN2	chr20	21,298,283	21,394,825	36	47.5	6	152.0	E
ABCD2	chr12	39,546,219	39,625,041	35	34.2	8	166.0	E
ATF1	chr12	50,759,005	50,826,160	35	76.7	5	14.0	E
CPSF1	chr8	144,388,230	144,414,349	35	-27.7	43	14.0	DA
DDX39B	chr6	31,525,218	31,547,475	35	30.4	4	0.0	E
GRAP2	chr22	39,896,081	39,978,342	35	-32.3	4	4.0	DL
IPO7	chr11	9,379,621	9,453,127	35	42.1	6	422.0	E
KMT2B	chr19	35,713,018	35,743,880	35	-8.5	36	22.0	A
LEF1	chr4	108,042,544	108,173,956	35	5.8	86	602.0	A
PRDM2	chr1	13,695,239	13,830,079	35	40.1	6	62.0	E
SMC5	chr9	70,253,961	70,359,873	35	38.8	11	7.0	E
SNORD117	chr6	31,531,373	31,541,449	35	39.6	4	0.0	E
TANC2	chr17	63,004,536	63,432,706	35	33.9	12	13.0	E
UBR1	chr15	42,937,899	43,111,088	35	-19.1	48	1277.5	A
UNKL	chr16	1,358,204	1,419,720	35	3.0	7	15.0	L
DENND1A	chr9	123,374,653	123,935,138	34	57.2	12	92.0	E
LOC100288798	chr12	46,378,675	46,657,579	34	39.6	3	166.0	E
LRPPRC	chr2	43,881,223	44,001,005	34	145.2	7	0.0	E
MIR4745	chr19	799,939	810,001	34	39.3	52	351.0	E
PLEKHA1	chr10	122,369,577	122,437,355	34	70.2	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
POT1	chr7	124,817,385	124,934,983	34	23.8	28	0.0	A
SEMA3A	chr7	83,953,342	84,199,901	34	45.2	4	7.0	E
TCF12	chr15	56,913,089	57,296,261	34	60.2	5	14.0	E
ZNF791	chr19	12,605,917	12,634,862	34	26.9	28	14.0	A
ATL3	chr11	63,619,081	63,676,974	33	3.1	26	46.0	A
HIVEP1	chr6	12,007,490	12,169,999	33	63.8	5	7.0	E
PDCD4	chr10	110,866,794	110,905,006	33	17.7	26	14.0	A
PITPNB	chr22	27,846,668	27,924,306	33	55.2	4	2.0	E
PLPPR3	chr19	807,487	826,952	33	46.9	6	4.0	E
RFX2	chr19	5,988,163	6,115,653	33	-10.1	9	182.5	L
SEPT9	chr17	77,276,409	77,505,596	33	-29.8	30	7.0	DA
TIAM1	chr21	31,113,417	31,563,977	33	80.9	15	14.0	E
TLE4	chr9	79,566,772	79,731,881	33	56.3	4	17.0	E
TMLHE	chrX	155,484,010	155,617,961	33	65.9	5	30.0	E
AP2A2	chr11	920,808	1,017,245	32	-12.2	6	0.0	L
ATG5	chr6	106,179,476	106,330,820	32	85.0	3	14.0	E
CHD8	chr14	21,380,193	21,442,298	32	57.8	16	76.0	E
DCAF6	chr1	167,931,558	168,080,843	32	65.3	5	14.0	E
DNAJC13	chr3	132,412,659	132,544,032	32	34.9	73	166.0	A
EFR3A	chr8	131,899,087	132,018,639	32	46.6	7	15.0	E
MAP4K3	chr2	39,244,265	39,442,312	32	11.7	26	46.0	A
NSMCE1	chr16	27,219,993	27,273,792	32	46.4	4	7.0	E
RC3H1	chr1	173,926,083	173,998,072	32	25.8	10	0.0	A
RPAP3	chr12	47,656,931	47,711,061	32	39.3	6	14.0	E
ZMYND11	chr10	129,464	259,637	32	52.7	8	14.0	E
ZNF148	chr3	125,220,668	125,380,354	32	61.5	6	18.0	E
DENND1B	chr1	197,499,748	197,780,493	31	-10.3	5	730.0	L
RABGAP1	chr9	122,936,008	123,109,868	31	16.7	31	14.0	A
SMAD2	chr18	47,828,094	47,936,146	31	48.1	7	18.0	E
STAG3	chr7	100,172,723	100,219,387	31	-6.2	36	0.0	A
UTY	chrY	13,243,378	13,485,670	31	55.6	8	18.0	E
WAC	chr10	28,527,587	28,628,112	31	79.1	4	4.0	E
DHX15	chr4	24,522,464	24,589,561	30	83.8	3	0.0	E
DYNC1H1	chr14	101,959,527	102,055,798	30	28.0	46	14.0	A
ECI1	chr16	2,234,871	2,256,601	30	-19.6	25	3.0	A
GNA13	chr17	65,004,288	65,061,802	30	48.3	2	0.0	E
MAD1L1	chr7	1,810,791	2,237,948	30	0.7	37	46.0	A
MIR3187	chr19	808,583	818,653	30	69.1	6	4.0	E
MKL2	chr16	14,066,312	14,271,779	30	40.6	10	7.0	E
ORC4	chr2	147,925,396	148,026,604	30	114.3	3	0.0	E
TET2	chr4	105,140,874	105,284,803	30	30.6	858	1464.0	A
ATP9B	chr18	79,064,274	79,383,282	29	32.0	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
CCSER2	chr10	84,323,588	84,523,521	29	17.2	27	76.0	A
CEP128	chr14	80,491,477	80,944,540	29	67.0	3	152.0	E
GLCCI1	chr7	7,963,742	8,094,079	29	-2.3	425	84.0	A
HERC4	chr10	67,916,898	68,080,346	29	-22.0	37	166.0	A
PHF20	chr20	35,767,000	35,955,366	29	-32.7	39	14.0	DA
POLR3K	chr16	41,978	58,632	29	-7.3	7	14.0	L
PUM2	chr2	20,243,691	20,355,850	29	55.8	8	32.0	E
RB1CC1	chr8	52,617,457	52,719,466	29	48.2	6	152.0	E
RBM25	chr14	73,053,512	73,126,368	29	46.2	3	14.0	E
SNORD84	chr6	31,536,100	31,546,178	29	54.6	4	0.0	E
SUZ12	chr17	31,932,009	32,006,045	29	31.7	36	547.5	A
UHRF1	chr19	4,898,079	4,967,154	29	-7.7	150	18.0	A
AKAP9	chr7	91,935,874	92,115,673	28	-7.2	27	166.0	A
CD96	chr3	111,537,078	111,670,991	28	3.0	7	129.0	L
GOLGA3	chr12	132,763,908	132,833,840	28	62.0	4	7.0	E
ITSN2	chr2	24,197,865	24,365,528	28	68.4	2	120.0	E
LARP4B	chr10	801,913	936,705	28	68.0	7	1.0	E
NDUFV2	chr18	9,097,629	9,139,345	28	63.3	15	92.0	E
RAB28	chr4	13,362,722	13,489,365	28	44.0	14	120.0	E
SMAP2	chr1	40,368,705	40,428,326	28	33.5	65	14.0	A
SNORA30	chr16	30,705,536	30,715,665	28	56.8	402	2162.0	E
STARD7	chr2	96,179,860	96,213,835	28	56.8	3	0.0	E
STXBP4	chr17	54,963,764	55,169,088	28	57.5	3	14.0	E
WWOX	chr16	78,094,412	79,217,667	28	32.1	78	106.0	A
ARL15	chr5	53,879,783	54,315,573	27	62.0	3	0.0	E
DDX60	chr4	168,211,290	168,323,807	27	52.7	23	1797.0	E
HELLS	chr10	94,540,766	94,607,099	27	62.3	16	256.0	E
KCNIP4	chr4	20,723,615	21,953,751	27	93.4	2	0.0	E
MCPH1	chr8	6,401,591	6,653,505	27	57.4	9	253.0	E
PTDSS2	chr11	443,267	496,400	27	-27.6	11	7.0	L
RSRC1	chr3	158,105,051	158,549,835	27	8.6	115	106.0	A
TAF2	chr8	119,725,773	119,837,834	27	101.9	8	1.0	E
TRIM33	chr1	114,387,776	114,516,160	27	55.7	17	106.0	E
YWHAZ	chr8	100,913,575	100,958,395	27	55.6	3	0.0	E
ANKRD46	chr8	100,504,751	100,564,786	26	34.9	25	7.0	A
CASC15	chr6	21,661,443	22,199,387	26	69.2	4	7.0	E
CLIP1	chr12	122,266,433	122,427,569	26	-18.6	4	14.0	L
DDX10	chr11	108,660,024	108,945,930	26	64.5	3	14.0	E
EHBP1	chr2	62,668,850	63,051,486	26	15.2	3	0.0	L
IL12RB1	chr19	18,053,994	18,103,816	26	-20.9	9	14.0	L
LUC7L2	chr7	139,335,358	139,428,457	26	79.4	4	14.0	E
TSR1	chr17	2,317,687	2,342,384	26	42.5	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
ABLM1	chr10	114,426,109	114,773,225	25	72.5	6	14.0	E
AMMECR1	chrX	110,189,185	110,445,233	25	87.5	2	62.0	E
ARFRP1	chr20	63,693,641	63,713,013	25	3.0	4	547.5	L
DENND6A	chr3	57,620,453	57,698,089	25	80.2	4	0.0	E
DNAJC1	chr10	21,751,547	22,008,721	25	6.3	38	14.0	A
ELMO1	chr7	36,847,905	37,454,326	25	-26.7	38	46.0	A
IPO8	chr12	30,623,980	30,700,995	25	16.1	24	62.0	A
KIF16B	chr20	16,267,103	16,578,434	25	74.7	8	0.0	E
PPP4R2	chr3	72,991,742	73,074,201	25	163.9	4	76.0	E
PRPF40A	chr2	152,646,592	152,722,461	25	69.8	5	14.0	E
PSMC4	chr19	39,966,004	39,986,764	25	62.0	2	0.0	E
RNPC3	chr1	103,520,955	103,560,237	25	62.0	5	159.0	E
ANKS1A	chr6	34,884,260	35,096,413	24	56.3	6	14.0	E
ATP2A2	chr12	110,276,226	110,356,092	24	-4.2	67	602.0	A
CDC27	chr17	47,112,696	47,194,312	24	-30.9	3	18.0	DL
CDYL2	chr16	80,592,898	80,809,278	24	105.7	5	14.0	E
EXOSC6	chr16	70,245,230	70,256,930	24	93.6	6	7.0	E
PRH1-PRR4	chr12	10,840,848	11,176,625	24	87.5	5	152.0	E
SNORD91B	chr17	2,324,124	2,334,210	24	87.5	4	0.0	E
UPF2	chr10	11,915,021	12,048,170	24	79.4	4	0.0	E
USP16	chr21	29,019,616	29,059,486	24	190.7	2	4.0	E
USP36	chr17	78,790,651	78,845,527	24	48.2	4	79.0	E
ABI1	chr10	26,741,595	26,866,087	23	58.1	11	0.0	E
DDX39B-AS1	chr6	31,537,303	31,548,138	23	75.8	4	0.0	E
ECHDC1	chr6	127,283,711	127,348,609	23	81.5	2	0.0	E
EED	chr11	86,239,383	86,283,810	23	71.2	6	76.0	E
FAM3C	chr7	121,343,850	121,401,368	23	77.1	3	14.0	E
GOLPH3L	chr1	150,641,224	150,702,196	23	-39.3	24	7.0	DA
HELQ	chr4	83,402,342	83,460,883	23	165.7	2	0.0	E
MALT1	chr18	58,666,385	58,755,139	23	28.1	24	332.0	A
NUCB2	chr11	17,271,717	17,336,865	23	177.8	4	14.0	E
PA2G4	chr12	56,099,318	56,118,910	23	33.9	38	1.0	A
PIKFYVE	chr2	208,261,266	208,363,751	23	28.9	460	14.0	A
POGZ	chr1	151,397,723	151,464,465	23	-20.6	27	14.0	A
PRH1	chr12	10,875,960	11,176,623	23	87.5	5	152.0	E
RAB18	chr10	27,499,173	27,547,237	23	39.4	25	14.0	A
RANBP10	chr16	67,718,065	67,811,652	23	-20.5	28	73.0	A
SDHC	chr1	161,309,375	161,369,745	23	8.7	5	1175.0	L
SLC9A7	chrX	46,594,250	46,764,172	23	-4.7	10	285.0	L
SNORD105B	chr19	10,104,748	10,114,840	23	73.5	14	1.0	E
SNORD37	chr19	3,977,506	3,987,572	23	81.8	3	0.0	E
USP11	chrX	47,227,914	47,253,328	23	111.0	4	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
ZBTB44	chr11	130,221,678	130,319,712	23	70.5	3	2.0	E
ATE1	chr10	121,735,420	121,933,801	22	63.5	18	256.0	E
DERL2	chr17	5,466,250	5,491,230	22	4.5	52	7.0	A
FMR1	chrX	147,906,950	147,956,127	22	130.8	6	0.0	E
FRG1CP	chr20	28,575,632	28,607,665	22	124.0	5	0.0	E
GID8	chr20	62,933,088	62,953,475	22	63.5	2	791.0	E
HIVEP3	chr1	41,501,364	42,040,925	22	-29.5	14	1.0	L
MED1	chr17	39,399,284	39,456,274	22	81.8	3	14.0	E
PAM	chr5	102,749,782	103,036,104	22	-21.9	34	337.0	A
PRH1-TAS2R14	chr12	10,932,405	11,176,623	22	68.3	5	152.0	E
PTPN22	chr1	113,808,810	113,876,759	22	64.1	3	0.0	E
RAB11FIP2	chr10	117,999,915	118,051,884	22	68.8	19	14.0	E
RAP1GAP2	chr17	2,771,920	3,042,741	22	114.3	10	30.0	E
RPA3	chr7	7,631,562	7,723,607	22	45.3	90	106.0	A
RSBN1L	chr7	77,691,425	77,784,803	22	30.1	31	15.0	A
SLC25A13	chr7	96,115,219	96,327,147	22	73.1	6	7.0	E
SYNJ1	chr21	32,623,758	32,733,040	22	65.6	4	0.0	E
TBC1D22A	chr22	46,757,616	47,180,699	22	-4.8	4	0.0	L
TBC1D22B	chr6	37,252,703	37,337,970	22	74.1	3	0.0	E
ARRDC3	chr5	91,363,631	91,388,373	21	76.8	5	7.0	E
CDK8	chr13	26,249,103	26,410,236	21	123.6	2	0.0	E
CPSF2	chr14	92,116,953	92,169,199	21	87.5	6	80.0	E
FAR1	chr11	13,663,658	13,737,346	21	87.5	4	14.0	E
MEMO1	chr2	31,862,809	32,016,052	21	-34.8	52	14.0	A
MRE11	chr11	94,412,300	94,498,908	21	71.9	5	0.0	E
PAXBP1	chr21	32,728,898	32,776,858	21	83.0	10	14.0	E
RFC3	chr13	33,813,068	33,971,558	21	87.5	3	0.0	E
RRP1B	chr21	43,654,550	43,701,079	21	56.3	3	0.0	E
SMG1P7	chr16	70,214,580	70,231,033	21	107.6	3	14.0	E
SMURF1	chr7	99,022,434	99,149,120	21	61.4	3	0.0	E
SNORD91A	chr17	2,325,278	2,335,370	21	72.8	4	0.0	E
SNX4	chr3	125,441,643	125,525,214	21	67.3	6	0.0	E
SOS2	chr14	50,112,120	50,236,693	21	-47.3	4	2.0	DL
VPS37A	chr8	17,241,891	17,303,024	21	93.6	11	0.0	E
ZNF207	chr17	32,345,137	32,375,449	21	54.4	3	46.0	E
AQR	chr15	34,851,350	34,974,794	20	-14.8	88	14.0	A
COG3	chr13	45,459,894	45,541,698	20	74.1	3	0.0	E
ECD	chr10	73,129,523	73,173,095	20	34.5	24	1.0	A
FANCC	chr9	95,094,053	95,322,709	20	95.7	4	256.0	E
IL7R	chr5	35,851,874	35,884,603	20	63.5	5	122.0	E
PATL1	chr11	59,631,715	59,674,038	20	18.6	629	1432.0	A
PPHLN1	chr12	42,321,144	42,453,620	20	2.3	4	0.0	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
PSME4	chr2	53,859,066	53,975,840	20	16.3	29	0.0	A
RAD23B	chr9	107,278,235	107,337,194	20	87.5	4	7.0	E
SLC7A6	chr16	68,259,515	68,306,823	20	-22.5	5	0.0	L
SNRPA	chr19	40,745,853	40,770,392	20	100.5	20	7.0	E
USPL1	chr13	30,612,678	30,665,770	20	80.8	3	14.0	E
DCUN1D4	chr4	51,837,999	51,921,837	19	3.8	33	106.0	A
DMD	chrX	31,114,227	33,344,609	19	74.1	4	7.0	E
ENTHD1	chr22	39,738,043	39,898,790	19	-49.2	2	0.0	DL
FANCL	chr2	58,154,242	58,246,380	19	159.6	5	15.0	E
MICU3	chr8	17,022,237	17,127,639	19	93.4	4	14.0	E
MPP6	chr7	24,568,345	24,698,703	19	82.5	7	0.0	E
N4BP1	chr16	48,533,725	48,615,209	19	31.8	31	106.0	A
OPA1	chr3	193,588,143	193,702,811	19	12.5	3	0.0	A
PLCL1	chr2	197,799,701	198,154,884	19	-32.6	24	14.0	DA
POM121	chr7	72,874,334	72,956,440	19	73.6	30	14.0	A
RBPJ	chr4	26,314,709	26,440,130	19	93.8	2	0.0	E
RELB	chr19	44,996,448	45,043,198	19	-14.3	15	14.0	L
SEC31A	chr4	82,813,508	82,905,571	19	12.0	65	14.0	A
UBE2E2	chr3	23,198,292	23,595,805	19	82.3	2	0.0	E
ZBTB8OS	chr1	32,615,822	32,655,590	19	61.7	3	2105.0	L
CEP57L1	chr6	109,090,152	109,168,912	18	87.5	2	0.0	E
CHMP2B	chr3	87,222,262	87,260,548	18	-0.7	30	11.0	A
CSDE1	chr1	114,711,912	114,763,050	18	191.7	2	0.0	E
DNAAF4-CCPG1	chr15	55,350,222	55,503,584	18	256.3	13	1.0	E
GTPBP10	chr7	90,341,664	90,396,455	18	118.8	14	69.0	E
GUSBP1	chr5	21,454,479	21,594,372	18	81.3	1	0.0	E
GZMB	chr14	24,625,955	24,639,269	18	164.7	13	14.0	E
ING3	chr7	120,945,762	120,980,657	18	87.5	3	0.0	E
KCTD9	chr8	25,422,847	25,463,468	18	102.5	7	7.0	E
METTL23	chr17	76,721,829	76,738,881	18	76.8	54	1.0	E
PDCD11	chr10	103,391,654	103,451,262	18	25.0	27	152.0	A
PRKD2	chr19	46,669,315	46,722,127	18	-8.9	24	92.0	A
RNF219	chr13	78,609,285	78,664,179	18	87.5	2	0.0	E
RTEL1	chr20	63,652,809	63,701,253	18	-13.2	4	547.5	L
RTEL1-TNFRSF6B	chr20	63,652,809	63,703,698	18	-13.2	4	547.5	L
RUFY2	chr10	68,336,106	68,412,294	18	80.0	5	0.0	E
SLC35E2	chr1	1,719,837	1,750,999	18	58.4	4	73.0	E
SNRNP25	chr16	48,828	62,669	18	23.1	4	14.0	L
ZBTB10	chr8	80,480,618	80,531,265	18	74.6	2	14.0	E
ATL2	chr2	38,288,956	38,383,584	17	80.0	4	0.0	E
CPEB3	chr10	92,043,639	92,296,118	17	150.0	2	0.0	E
DIS3	chr13	72,750,401	72,787,128	17	94.7	2	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
DYNC2H1	chr11	103,104,430	103,484,863	17	73.8	6	0.0	E
EIF2AK4	chr15	39,929,123	40,040,596	17	8.8	47	7.0	A
FRG1DP	chr20	29,075,389	29,101,832	17	127.0	3	0.0	E
INTS9	chr8	28,762,657	28,895,181	17	141.1	2	0.0	E
LOC102723780	chr22	10,935,596	10,966,529	17	136.9	2	0.0	E
MFSD14B	chr9	94,369,550	94,465,920	17	87.5	2	0.0	E
NRXN3	chr14	78,165,372	79,873,290	17	275.0	2	0.0	E
SART3	chr12	108,517,213	108,566,389	17	116.4	2	0.0	E
SNAP25-AS1	chr20	10,018,811	10,224,506	17	131.6	3	1.0	E
SNED1	chr2	240,993,837	241,099,228	17	87.5	9	0.0	E
SUGCT	chr7	40,129,975	40,865,767	17	117.1	5	0.0	E
ZNF644	chr1	90,910,299	91,027,255	17	60.7	17	14.0	E
ANKEF1	chr20	10,029,998	10,061,762	16	111.0	3	1.0	E
DPP10	chr2	114,437,357	115,850,752	16	141.1	1	0.0	E
EIF4H	chr7	74,169,375	74,202,099	16	150.0	2	2.0	E
GNAI1	chr7	80,129,823	80,224,409	16	109.6	2	0.0	E
GXYLT1	chr12	42,076,845	42,149,871	16	51.5	4	92.0	L
IQCB1	chr3	121,764,760	121,840,079	16	-13.1	80	15.0	A
MRPS30	chr5	44,803,924	44,820,516	16	142.7	2	4.0	E
SGPP1	chr14	63,679,215	63,733,095	16	125.0	4	14.0	E
ABHD10	chr3	111,973,875	111,998,368	15	254.2	3	1.0	E
ACOT7	chr1	6,259,271	6,398,766	15	112.5	2	0.0	E
AGAP1	chr2	235,489,088	236,136,800	15	298.5	2	0.0	E
CAAP1	chr9	26,835,684	26,897,828	15	5.2	27	46.0	A
CALN1	chr7	71,774,490	72,417,375	15	237.5	1	0.0	E
CD109	chr6	73,691,084	73,833,317	15	-28.9	30	0.0	A
EXOSC10	chr1	11,061,612	11,104,910	15	-3.1	69	7.0	A
GALNT10	chr5	154,185,734	154,425,983	15	87.5	3	0.0	E
GBP2	chr1	89,101,132	89,131,159	15	155.7	4	0.0	E
GFM1	chr3	158,639,527	158,697,571	15	106.3	3	14.0	E
HBP1	chr7	107,163,960	107,207,529	15	98.6	3	1.0	E
IRF8	chr16	85,894,167	85,927,605	15	97.4	3	0.0	E
JMJD6	chr17	76,707,831	76,731,799	15	33.9	54	1.0	A
KRBOX4	chrX	46,442,188	46,479,639	15	165.7	2	0.0	E
LRP1B	chr2	140,226,426	142,136,701	15	164.7	4	0.0	E
MICAL3	chr22	17,782,649	18,029,559	15	500.1	1	0.0	E
MIR1268A	chr19	2,997,812	3,069,714	15	-35.8	3	62.0	DL
NT5C3A	chr7	33,009,112	33,067,797	15	87.5	2	0.0	E
PPAT	chr4	56,388,362	56,440,636	15	130.8	2	0.0	E
RAB5A	chr3	19,942,079	19,990,175	15	105.4	8	60.0	E
SLX4	chr16	3,576,182	3,616,606	15	105.4	4	22.0	E
SRGAP2	chr1	206,200,428	206,469,443	15	77.7	2	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
ADSS	chr1	244,403,491	244,457,134	14	95.3	16	0.0	E
ATG4A	chrX	108,086,666	108,159,671	14	251.6	14	0.0	E
CTSS	chr1	150,725,195	150,770,957	14	-11.8	2	0.0	L
DNAH3	chr16	20,928,110	21,164,441	14	251.6	3	14.0	E
EYS	chr6	63,714,979	65,712,225	14	87.5	4	0.0	E
GOLT1B	chr12	21,496,764	21,523,403	14	241.0	2	0.0	E
HCFC2	chr12	104,059,457	104,111,526	14	111.0	4	1.0	E
IKZF1	chr7	50,299,082	50,410,100	14	-27.3	6	0.0	A
ITGAM	chr16	31,254,966	31,337,892	14	150.0	3	0.0	E
KLRC3	chr12	10,407,314	10,425,595	14	87.5	5	11.0	E
LANCL1	chr2	210,426,248	210,481,775	14	-3.4	4	22.0	L
LARGE1	chr22	33,267,860	33,925,428	14	275.0	1	0.0	E
OTUD6B	chr8	91,065,195	91,092,095	14	129.2	3	14.0	E
PPA1	chr10	70,197,829	70,238,434	14	87.5	10	0.0	E
PPWD1	chr5	65,558,235	65,592,549	14	111.0	4	14.0	E
RAVER1	chr19	10,311,212	10,338,638	14	-36.4	24	14.0	A
UBE2Z	chr17	48,903,368	48,934,060	14	181.3	3	7.0	E
XPO1	chr2	61,472,933	61,543,283	14	15.4	27	106.0	A
ZNF568	chr19	36,911,328	37,002,932	14	15.4	34	0.0	A
ZNF573	chr19	37,733,301	37,784,590	14	-29.2	85	730.0	A
ARL5A	chr2	151,795,965	151,833,495	13	138.7	3	4.0	E
CD8B	chr2	86,810,336	86,866,924	13	116.4	2	15.0	E
CDK1	chr10	60,773,330	60,799,852	13	223.9	4	14.0	E
CNTN4	chr3	2,093,865	3,062,961	13	162.5	2	0.0	E
DGCR2	chr22	19,031,281	19,127,454	13	87.5	6	7.0	E
DLG2	chr11	83,450,012	85,632,270	13	162.5	1	0.0	E
GPN1	chr2	27,623,647	27,655,846	13	-24.4	63	15.0	A
GREB1L	chr18	21,237,241	21,531,112	13	181.3	1	0.0	E
GUSBP11	chr22	23,633,487	23,722,423	13	107.3	2	62.0	E
HAUS2	chr15	42,543,812	42,574,992	13	141.1	3	14.0	E
KIAA1958	chr9	112,481,967	112,670,311	13	111.0	4	0.0	E
LOC101927178	chr14	35,076,080	35,118,130	13	87.5	3	14.0	E
MIR4435-2HG	chr2	111,190,865	111,500,161	13	462.6	2	0.0	E
MPP5	chr14	67,236,294	67,341,061	13	25.0	23	0.0	L
NOP58	chr2	202,260,715	202,308,661	13	181.3	3	11.0	E
PALLD	chr4	168,492,065	168,933,457	13	181.3	1	0.0	E
PNPLA4	chrX	7,893,762	7,932,739	13	98.6	3	0.0	E
PPP2R3C	chr14	35,080,467	35,127,543	13	80.0	11	7.0	E
PTPN23	chr3	47,375,981	47,418,441	13	-9.7	5	0.0	L
RAD17	chr5	69,364,296	69,419,801	13	87.5	14	0.0	E
RHEB	chr7	151,461,011	151,524,924	13	256.3	3	0.0	E
SERPINI1	chr3	167,730,643	167,830,569	13	120.6	7	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
SLC2A1	chr1	42,920,374	42,964,176	13	87.5	3	22.0	E
STX19	chr3	94,009,370	94,033,610	13	97.9	3	7.0	E
TBP	chr6	170,549,332	170,577,870	13	111.0	4	0.0	E
TGFBR2	chr3	30,601,501	30,699,141	13	-13.7	32	14.0	A
UBN1	chr16	4,842,630	4,887,401	13	98.6	4	0.0	E
VCPIP1	chr8	66,625,252	66,672,217	13	130.8	6	0.0	E
ZNF718	chr4	119,475	207,306	13	-25.0	27	152.0	A
AGBL4	chr1	48,527,854	50,028,954	12	200.0	2	0.0	E
ANKRD27	chr19	32,592,000	32,680,196	12	221.5	5	0.0	E
CDK19	chr6	110,604,977	110,820,885	12	12.5	3	7.0	L
CLCN6	chr1	11,801,095	11,848,144	12	145.2	3	0.0	E
ERC2	chr3	55,503,310	56,473,363	12	130.8	1	0.0	E
GGT6	chr17	4,551,926	4,565,596	12	134.4	3	14.0	E
HSPA13	chr21	14,366,115	14,388,188	12	150.0	2	92.0	E
HSPA14	chr10	14,833,159	14,876,741	12	111.0	2	0.0	E
KATNBL1	chr15	34,135,673	34,215,096	12	127.7	3	0.0	E
KCTD3	chr1	215,562,378	215,626,821	12	4.2	5	14.0	A
KIF26B	chr1	245,149,984	245,708,126	12	221.5	1	0.0	E
LOC339862	chr3	17,957,571	18,273,918	12	275.0	1	0.0	E
MBP	chr18	76,973,832	77,137,818	12	137.5	6	14.0	E
MIR7108	chr19	2,429,913	2,440,000	12	150.0	3	14.0	E
MRPL14	chr6	44,108,453	44,132,491	12	172.8	2	14.0	E
MTRF1L	chr6	152,982,365	153,007,815	12	155.7	2	0.0	E
MYO10	chr5	16,656,906	16,941,276	12	212.5	4	0.0	E
NDE1	chr16	15,638,266	15,731,351	12	-18.2	34	11.0	A
PSMA2	chr7	42,911,860	42,937,206	12	111.0	3	14.0	E
PTCHD1-AS	chrX	22,188,004	23,298,146	12	301.8	1	0.0	E
SGCD	chr5	156,321,756	156,772,787	12	228.2	5	0.0	E
TDRD7	chr9	97,407,019	97,501,123	12	112.5	3	0.0	E
TTC7B	chr14	90,535,587	90,821,417	12	306.3	1	0.0	E
AARSD1	chr17	42,945,525	42,969,498	11	191.7	3	0.0	E
ATP9A	chr20	51,591,774	51,773,411	11	462.6	1	0.0	E
BMPRI1A	chr10	86,751,638	86,930,188	11	150.0	3	0.0	E
CBWD1	chr9	116,037	184,075	11	141.1	2	0.0	E
CDH12	chr5	21,745,865	22,858,622	11	221.5	2	0.0	E
CDH18	chr5	19,468,045	20,580,873	11	170.9	3	7.0	E
CHN2	chr7	29,141,546	29,519,335	11	143.8	2	0.0	E
FLJ42627	chr16	2,633,981	2,651,129	11	194.7	1	0.0	E
FN3KRP	chr17	82,711,705	82,733,017	11	138.7	2	0.0	E
GOLIM4	chr3	168,003,672	168,100,925	11	189.8	20	7.0	E
HCG27	chr6	31,192,759	31,208,968	11	143.8	5	0.0	E
HVCN1	chr12	110,643,685	110,694,812	11	116.4	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
KDM5D	chrY	19,700,414	19,749,939	11	-0.4	2	14.0	A
LINGO2	chr9	27,943,085	29,218,000	11	387.6	2	17.0	E
LOC100499484	chr9	97,233,425	97,302,314	11	462.6	2	0.0	E
LOC100499484-C9ORF174	chr9	97,233,425	97,382,295	11	462.6	2	0.0	E
LTBP1	chr2	32,942,301	33,404,508	11	587.6	1	0.0	E
MICAL2	chr11	12,105,575	12,268,790	11	-25.0	40	15.0	A
MIGA2	chr9	129,031,510	129,077,082	11	87.5	3	7.0	E
NAA50	chr3	113,711,459	113,751,299	11	251.6	1	0.0	E
OAS2	chr12	112,973,468	113,016,723	11	150.0	2	7.0	E
OSBPL10	chr3	31,655,824	31,986,850	11	150.0	2	0.0	E
PDCD6	chr5	266,620	319,974	11	306.3	8	0.0	E
RLIM	chrX	74,577,975	74,619,626	11	387.6	3	152.0	E
SCARNA26A	chr1	155,674,107	155,684,255	11	109.6	2	14.0	E
SHANK2	chr11	70,462,855	71,229,796	11	181.3	1	0.0	E
SNORD88A	chr19	50,794,438	50,804,535	11	165.7	28	46.0	E
SNORD88B	chr19	50,794,028	50,804,125	11	165.7	28	46.0	E
SNRNP40	chr1	31,254,567	31,301,797	11	191.7	8	46.0	E
ST3GAL5	chr2	85,834,147	85,894,034	11	96.9	7	0.0	E
SUSD3	chr9	93,053,687	93,090,136	11	155.7	1	0.0	E
TEC	chr4	48,130,782	48,274,797	11	181.3	3	0.0	E
TMEM263	chr12	106,950,721	106,979,037	11	134.4	3	2.0	E
XKR6	chr8	10,891,145	11,206,366	11	25.0	3	0.0	L
YWHAG	chr7	76,321,790	76,364,025	11	204.7	1	0.0	E
ZW10	chr11	113,728,182	113,778,763	11	145.2	12	14.0	E
BBS4	chr15	72,681,178	72,743,476	10	275.0	1	0.0	E
CHD1L	chr1	147,168,193	147,300,766	10	76.5	26	1.0	A
CNTN5	chr11	99,015,975	100,363,885	10	509.5	2	0.0	E
CTNNB1	chr3	41,194,423	41,245,453	10	107.3	5	0.0	E
DTL	chr1	212,030,552	212,110,006	10	138.7	3	0.0	E
EEPD1	chr7	36,148,226	36,306,543	10	312.6	1	14.0	E
ABRAXAS2	chr10	124,796,784	124,841,670	10	167.9	2	0.0	E
FDX1	chr11	110,424,936	110,469,884	10	306.3	4	0.0	E
GFRA1	chr10	116,051,930	116,278,645	10	587.6	1	0.0	E
HHAT	chr1	210,323,251	210,681,296	10	306.3	3	0.0	E
KIAA1217	chr10	23,689,745	24,552,848	10	387.6	1	0.0	E
KLHL9	chr9	21,324,670	21,340,432	10	194.7	4	0.0	E
LRRC9	chr14	59,914,712	60,068,559	10	212.5	1	0.0	E
MTMR4	chr17	58,484,531	58,522,890	10	50.0	5	1825.0	L
NGDN	chr14	23,464,688	23,483,193	10	100.9	44	166.0	A
NUDT22	chr11	64,221,257	64,235,016	10	143.8	1	0.0	E
PHF12	chr17	28,900,252	28,956,490	10	-53.8	42	166.0	DA
PMS2P7	chr7	75,315,771	75,364,038	10	350.1	1	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
PPP1R11	chr6	30,062,154	30,075,331	10	337.6	3	0.0	E
PPP2R3A	chr3	135,960,672	136,152,910	10	650.1	1	0.0	E
RGL4	chr22	23,685,860	23,704,176	10	167.9	2	62.0	E
SNORD97	chr11	10,796,466	10,806,608	10	155.7	1	0.0	E
TMEM241	chr18	23,291,014	23,442,969	10	31.3	2	0.0	L
TMEM50B	chr21	33,427,485	33,485,009	10	312.6	1	0.0	E
TPST1	chr7	66,200,271	66,365,451	10	243.8	2	7.0	E
TTLL11	chr9	121,816,924	122,098,606	10	170.9	1	0.0	E
GALNT17	chr7	71,127,536	71,718,601	10	143.8	1	0.0	E
ANKS1B	chr12	98,729,790	99,989,654	9	275.0	1	0.0	E
ATL1	chr14	50,528,081	50,638,066	9	275.0	2	0.0	E
MRPS30-DT	chr5	44,739,327	44,813,793	9	243.8	2	4.0	E
C12orf29	chr12	88,030,490	88,055,160	9	167.9	3	0.0	E
CBWD3	chr9	68,236,944	68,305,035	9	275.0	2	0.0	E
CCPG1	chr15	55,350,222	55,413,510	9	275.0	13	1.0	E
DCLRE1C	chr10	14,899,610	14,959,432	9	181.3	2	0.0	E
DNAJB6	chr7	157,332,015	157,422,439	9	191.7	2	14.0	E
DOCK1	chr10	126,900,408	127,457,517	9	275.0	2	0.0	E
FAM98A	chr2	33,578,660	33,604,362	9	248.3	1	0.0	E
HPS3	chr3	149,124,583	149,178,196	9	116.4	4	46.0	E
IQCJ-SCHIP1	chr3	159,064,251	159,902,366	9	87.5	1	0.0	L
LOC101927151	chr19	27,788,466	27,811,780	9	33.9	35	46.0	A
LOC101929243	chr6	34,691,153	34,702,471	9	221.5	3	0.0	E
LOC730100	chr2	51,027,600	52,412,917	9	212.5	1	0.0	E
MAGI2	chr7	78,012,056	79,458,574	9	167.9	1	0.0	E
MIR590	chr7	74,186,197	74,196,294	9	275.0	1	2.0	E
NAALAD2	chr11	90,129,649	90,197,611	9	368.8	2	0.0	E
NCOR2	chr12	124,319,410	124,572,464	9	150.0	1	0.0	E
NEBL	chr10	20,774,973	21,179,187	9	275.0	3	0.0	E
NECAB1	chr8	90,786,692	90,964,402	9	212.5	4	0.0	E
QRSL1	chr6	106,624,565	106,673,417	9	138.7	3	14.0	E
RGS6	chr14	71,927,099	72,571,530	9	167.9	1	0.0	E
SPTLC3	chr20	13,003,978	13,171,764	9	194.7	2	14.0	E
THSD4	chr15	71,136,448	71,788,383	9	212.5	1	0.0	E
TMEM138	chr11	61,357,000	61,374,503	9	167.9	2	0.0	E
ZFYVE26	chr14	67,741,519	67,821,589	9	368.8	1	0.0	E
ZNF273	chr7	64,898,241	64,936,577	9	167.9	2	0.0	E
C20orf196	chr20	5,745,386	5,869,407	8	-16.7	1	0.0	A
CNTN1	chr12	40,687,441	41,077,411	8	275.0	1	0.0	L
CP	chr3	149,157,409	149,227,045	8	312.6	2	0.0	E
CREB5	chr7	28,294,320	28,830,894	8	150.0	2	0.0	E
DEPDC1	chr1	68,469,151	68,502,221	8	243.8	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
DNAJC27	chr2	24,938,635	24,977,094	8	212.5	2	0.0	E
EARS2	chr16	23,517,012	23,562,375	8	56.3	60	0.0	A
ECT2L	chr6	138,791,110	138,909,070	8	212.5	1	0.0	E
FAM104A	chr17	73,202,352	73,237,394	8	248.3	1	0.0	E
GCLM	chr1	93,880,199	93,914,598	8	167.9	2	14.0	E
GPAT4	chr8	41,573,187	41,630,001	8	212.5	2	0.0	E
GPR132	chr14	105,044,388	105,070,550	8	-34.8	29	0.0	A
IRS2	chr13	109,748,836	109,791,567	8	212.5	3	0.0	E
LINC00597	chr15	77,218,907	77,230,404	8	167.9	3	0.0	E
LINC01170	chr5	124,054,793	124,443,520	8	275.0	2	69.0	E
LMBR1L	chr12	49,092,139	49,115,900	8	167.9	1	0.0	E
LOC101927550	chr7	99,008,164	99,041,479	8	837.6	4	0.0	E
MTSS1	chr8	124,545,769	124,733,507	8	212.5	1	0.0	E
PLD2	chr17	4,802,100	4,828,432	8	275.0	2	106.0	E
PTPRT	chr20	42,067,751	43,194,917	8	650.1	1	0.0	E
RAI14	chr5	34,651,327	34,837,612	8	275.0	1	0.0	E
SEC23B	chr20	18,502,543	18,566,415	8	-1.3	29	0.0	A
SHISA6	chr17	11,236,422	11,569,063	8	743.9	1	0.0	L
STOM	chr9	121,333,987	121,375,304	8	138.7	4	0.0	E
SYN3	chr22	32,507,552	33,063,391	8	167.9	1	0.0	E
TMEM132D	chr12	129,066,725	129,908,667	8	275.0	1	0.0	E
TMEM63B	chr6	44,121,913	44,160,519	8	400.1	27	422.0	A
ZNF717	chr3	75,724,960	75,790,583	8	221.5	2	14.0	E
CDV3	chr3	133,568,589	133,595,274	7	312.6	5	0.0	E
CPA6	chr8	67,417,169	67,751,385	7	212.5	2	0.0	E
KARS	chr16	75,622,723	75,652,687	7	-11.8	25	14.0	A
KIAA0930	chr22	45,187,241	45,245,769	7	312.6	1	0.0	E
LAMA3	chr18	23,684,442	23,960,065	7	68.8	1	0.0	L
NTAN1	chr16	15,032,852	15,061,079	7	194.7	2	0.0	E
PPEF1	chrX	18,685,925	18,832,916	7	228.2	3	0.0	L
SNAP29	chr22	20,854,003	20,896,213	7	-6.2	27	14.0	A
ZEB2	chr2	144,379,374	144,525,391	7	-18.0	7	46.0	A
ZNF224	chr19	44,089,328	44,114,830	7	53.4	16	0.0	L
ZNF92	chr7	65,368,798	65,406,135	7	87.5	44	166.0	A
ACTL6A	chr3	179,557,879	179,593,405	6	20.6	41	14.0	A
APOL2	chr22	36,221,208	36,244,954	6	150.0	2	0.0	E
CPS1	chr2	210,472,681	210,684,107	6	2.3	2	0.0	L
RETREG2	chr2	219,173,189	219,190,475	6	45.9	2	0.0	A
NTM	chr11	131,365,475	132,341,822	6	181.3	1	0.0	L
PMS2P7	chr7	73,001,079	73,021,375	6	87.5	8	0.0	E
RBAK	chr7	5,040,820	5,074,488	6	-6.2	29	7.0	A
SLC1A2	chr11	35,246,204	35,425,063	6	118.8	2	0.0	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
SNHG12	chr1	28,573,537	28,586,854	6	162.5	98	1614.5	A
TAC3	chr12	57,004,996	57,021,560	6	-39.7	44	166.0	A
WDYHV1	chr8	123,411,724	123,453,090	6	368.8	1	0.0	E
ZNF212	chr7	149,234,650	149,260,609	6	181.3	1	0.0	L
C5	chr9	120,947,335	121,080,174	5	-27.9	33	0.0	A
HRH1	chr3	11,132,092	11,268,253	5	134.4	36	0.0	A
IFNGR2	chr21	33,397,895	33,442,521	5	462.6	173	39.0	A
PIK3R2	chr19	18,148,177	18,175,533	5	-48.9	27	0.0	A
CRTAP	chr3	33,108,957	33,152,773	4	368.8	35	14.0	A
LINC01473	chr2	186,028,533	186,091,317	4	7.2	84	39.0	A
LOC100507412	chr21	8,375,664	8,416,091	4	Inf	2	1460.0	L
MIR6724-1	chr21	8,383,361	8,437,621	4	Inf	2	1460.0	L
MIR6724-2	chr21	8,383,361	8,437,621	4	Inf	2	1460.0	L
MIR6724-3	chr21	8,383,361	8,437,621	4	Inf	2	1460.0	L
MIR6724-4	chr21	8,383,361	8,437,621	4	Inf	2	1460.0	L
RASEF	chr9	82,974,584	83,068,128	4	650.1	47	46.0	A
DNAJB5	chr9	34,984,640	35,003,433	3	7.2	1	14.0	A
LOC100507412	chr21	8,192,619	8,233,092	3	837.6	2	1460.0	L
MIR6724-1	chr21	8,200,314	8,254,596	3	837.6	2	1460.0	L
MIR6724-2	chr21	8,200,314	8,254,596	3	837.6	2	1460.0	L
MIR6724-3	chr21	8,200,314	8,254,596	3	837.6	2	1460.0	L
MIR6724-4	chr21	8,200,314	8,254,596	3	837.6	2	1460.0	L
RHOD	chr11	67,051,817	67,077,017	3	275.0	34	912.5	A
RTCA-AS1	chr1	100,259,741	100,271,174	3	462.6	27	0.0	A
TNFRSF6B	chr20	63,691,650	63,703,698	3	87.5	4	547.5	L
MIR1268A	chr15	28,320,482	28,505,841	2	87.5	1	0.0	DL
UXT-AS1	chrX	47,653,832	47,665,111	2	-37.5	45	7.0	A
CXorf67	chrX	51,401,914	51,413,837	1	-37.5	2	0.0	A
FFAR2	chr19	35,444,714	35,456,767	1	-37.5	3	0.0	A
KCNC2	chr12	75,035,077	75,214,748	1	-73.2	1	0.0	A
LINC01322	chr3	165,201,959	165,518,728	1	87.5	57	0.0	A
KDM2A	chr11	67,114,268	67,263,079	78	-27.1	11	92.0	D
ASH1L	chr1	155,330,260	155,567,533	73	-27.6	8	130.0	D
RPTOR	chr17	80,539,824	80,971,373	73	-14.0	11	351.0	D
PPP6R2	chr22	50,338,316	50,450,089	69	-21.1	17	136.0	D
DNMT1	chr19	10,128,343	10,200,135	67	-12.4	16	182.5	D
HSF1	chr8	144,286,568	144,319,726	64	-20.8	13	256.0	D
MECP2	chrX	154,016,812	154,102,731	61	-20.7	16	99.0	D
FKBP5	chr6	35,568,584	35,733,583	60	-22.4	17	642.5	D
NFATC3	chr16	68,080,365	68,234,259	59	-17.4	7	76.0	D
MAPK8IP3	chr16	1,701,182	1,775,317	57	-23.2	5	1592.5	D
CCDC57	chr17	82,096,469	82,217,829	55	-26.5	7	642.5	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
HORMAD2	chr22	30,075,068	30,182,075	55	-25.3	5	130.0	D
RBM6	chr3	49,935,043	50,082,252	55	-30.6	13	14.0	D
IP6K1	chr3	49,719,294	49,791,540	54	-39.1	3	2.0	D
NAA38	chr17	7,851,680	7,890,388	54	-15.0	18	166.0	D
QRICH1	chr3	49,024,706	49,099,373	54	-38.8	7	18.0	D
TRAF2	chr9	136,881,512	136,931,615	53	-36.1	6	106.0	D
ARHGAP15	chr2	143,124,329	143,773,352	52	-17.8	7	14.0	D
CAPN1	chr11	65,176,214	65,217,006	51	-30.8	5	46.0	D
IKZF3	chr17	39,752,714	39,869,188	51	-20.7	8	62.0	D
INPP4B	chr4	142,018,159	142,851,535	51	-23.6	4	122.0	D
MIR5096	chr17	4,136,088	4,245,637	51	3.2	12	14.0	D
ARIH2	chr3	48,913,819	48,990,538	50	-19.0	5	14.0	D
IL4I1	chr19	49,884,655	49,934,539	50	-27.8	6	166.0	D
PRR12	chr19	49,586,642	49,631,439	50	-34.4	5	18.0	D
NARFL	chr16	724,754	746,038	49	-28.8	4	22.0	D
PBRM1	chr3	52,540,351	52,690,850	49	-19.0	13	14.0	D
SIRT3	chr11	210,029	241,362	49	-24.9	4	1.0	D
AKAP8L	chr19	15,375,047	15,424,121	48	-22.0	8	62.0	D
CCND3	chr6	41,929,932	42,053,894	48	-25.6	4	14.0	D
GANAB	chr11	62,619,825	62,651,726	48	-24.3	7	14.0	D
SP1	chr12	53,375,194	53,421,442	47	-26.3	10	0.0	D
WNK1	chr12	747,922	916,452	47	-37.0	5	152.0	D
ZGPAT	chr20	63,702,441	63,741,142	47	-22.3	10	15.0	D
HCG20	chr6	30,761,824	30,797,250	46	-26.2	8	152.0	D
ITGAL	chr16	30,467,661	30,528,185	46	-20.9	14	14.0	D
TSC2	chr16	2,042,894	2,093,720	46	-25.7	4	22.0	D
DEAF1	chr11	639,219	700,754	45	-21.4	15	7.0	D
FOXK2	chr17	82,514,717	82,609,607	44	-21.7	19	0.0	D
HNRNPM	chr19	8,439,827	8,494,118	44	-22.7	12	14.0	D
EIF2B3	chr1	44,845,521	44,991,722	43	-38.9	6	69.0	D
MEIOB	chr16	1,828,982	1,877,178	43	-29.1	9	1.0	D
NUP62	chr19	49,901,825	49,934,731	43	-30.6	6	166.0	D
POLD1	chr19	50,379,322	50,423,018	43	-20.8	20	14.0	D
RNPS1	chr16	2,248,115	2,273,412	43	-50.8	6	11.0	D
VAR5	chr6	31,772,519	31,800,935	43	-32.8	6	0.0	D
CTCF	chr16	67,557,406	67,644,185	42	-18.6	8	152.0	D
DENND4A	chr15	65,654,122	65,797,293	42	-21.3	10	14.0	D
UBE2J2	chr1	1,248,911	1,278,854	42	-42.6	9	166.0	D
USP4	chr3	49,272,143	49,345,103	42	-32.3	3	14.0	D
SPATS2	chr12	49,361,904	49,532,426	41	-26.1	6	18.0	D
NARF	chr17	82,453,183	82,493,267	40	-26.3	6	15.0	D
STAT3	chr17	42,308,324	42,393,495	40	-36.4	2	7.0	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
TMEM204	chr16	1,523,740	1,560,580	40	-32.7	27	62.0	D
MGAT4A	chr2	98,614,105	98,736,126	39	-19.3	5	7.0	D
RIPOR2	chr6	24,799,280	25,047,288	38	-32.0	11	7.0	D
FLT3LG	chr19	49,469,208	49,491,231	37	-32.8	17	3.0	D
GLE1	chr9	128,499,691	128,547,301	37	-28.5	4	1.0	D
LRRC14	chr8	144,512,964	144,530,175	37	-28.9	2	0.0	D
RAB40C	chr16	584,356	634,273	37	-35.6	6	11.0	D
STK11	chr19	1,200,798	1,233,435	37	-25.0	6	80.0	D
ASXL2	chr2	25,728,752	25,883,516	36	-23.6	4	152.0	D
CDK12	chr17	39,456,510	39,539,565	36	-28.3	3	14.0	D
CNOT6	chr5	180,489,398	180,583,405	36	-24.6	3	7.0	D
HAGH	chr16	1,804,102	1,832,194	36	-23.3	7	62.0	D
INTS11	chr1	1,306,584	1,329,687	36	-30.1	6	14.0	D
NFKBIL1	chr6	31,541,850	31,563,829	36	-30.2	3	0.0	D
PPP1R16A	chr8	144,472,981	144,507,121	36	-32.8	4	14.0	D
RECQL4	chr8	144,506,283	144,522,826	36	-23.1	4	0.0	D
TONSL	chr8	144,423,779	144,449,429	36	-41.4	13	7.0	D
ADCK5	chr8	144,369,014	144,398,238	35	-39.6	8	422.0	D
AHRR	chr5	299,175	443,290	35	-23.5	7	7.0	D
CRTC3	chr15	90,524,885	90,650,345	35	-30.9	5	0.0	D
FAHD1	chr16	1,822,223	1,845,202	35	-25.8	2	18.0	D
GATAD2B	chr1	153,799,906	153,927,975	35	-34.9	8	7.0	D
MAP4	chr3	47,845,689	48,094,279	35	-24.6	5	46.0	D
VPS52	chr6	33,245,271	33,276,965	35	-28.7	3	0.0	D
VRK3	chr19	49,971,466	50,030,548	35	-34.7	4	7.0	D
WASF2	chr1	27,399,225	27,495,187	35	-29.5	4	122.0	D
ARNT	chr1	150,804,704	150,881,768	34	-27.1	14	14.0	D
LPCAT3	chr12	6,971,184	7,023,538	34	-35.8	5	14.0	D
MIR5096	chr22	37,663,025	38,029,093	34	-36.1	7	7.0	D
SNHG9	chr16	1,959,995	1,970,504	34	-28.1	3	0.0	D
ANTXR2	chr4	79,896,616	80,078,472	33	-41.5	4	7.0	D
LSM2	chr6	31,792,391	31,811,984	33	-38.0	4	90.0	D
TESPA1	chr12	54,943,302	54,989,746	33	-31.7	4	0.0	D
MAML2	chr11	95,971,592	96,348,180	32	-36.5	6	14.0	D
MYH9	chr22	36,276,276	36,393,067	32	-38.3	3	0.0	D
NPRL3	chr16	80,804	143,698	32	-31.8	6	136.0	D
TALDO1	chr11	742,431	770,024	32	-30.1	6	14.0	D
BRD4	chr19	15,232,489	15,337,543	31	-33.0	5	0.0	D
EXOC2	chr6	480,137	698,141	31	-53.1	5	0.0	D
KMT2A	chr11	118,431,489	118,531,824	31	-28.6	4	18.0	D
NUMA1	chr11	71,997,863	72,085,693	31	-26.5	3	0.0	D
RBM26	chr13	79,313,867	79,411,221	31	-27.1	3	7.0	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
SNORA78	chr16	1,960,183	1,970,310	31	-29.7	3	0.0	D
ARHGEF6	chrX	136,660,550	136,786,344	30	-33.2	5	7.0	D
LRRC24	chr8	144,517,376	144,532,032	30	-29.7	2	0.0	D
RHOT2	chr16	663,082	679,174	30	-31.9	3	92.0	D
TBL3	chr16	1,967,062	1,983,750	30	-29.2	3	0.0	D
ZNF83	chr19	52,607,364	52,695,581	30	-33.4	4	0.0	D
LINC01128	chr1	822,590	864,446	29	-35.5	4	0.0	D
LINC01619	chr12	91,979,975	92,147,831	29	-31.4	5	0.0	D
PCNX3	chr11	65,611,311	65,642,439	29	-32.5	20	1.0	D
PSMB9	chr6	32,849,160	32,864,851	29	-30.8	3	0.0	D
SIK3	chr11	116,838,401	117,103,415	29	-28.0	9	14.0	D
ANK3	chr10	60,021,297	60,738,526	28	-52.3	6	7.0	D
DPF2	chr11	65,328,753	65,359,260	28	-35.2	5	3.0	D
HBS1L	chr6	134,955,382	135,059,898	28	-35.5	4	166.0	D
RBL1	chr20	36,991,350	37,101,215	28	-34.4	5	0.0	D
RPL13A	chr19	49,482,553	49,497,307	28	-29.7	17	0.0	D
RUFY1	chr5	179,545,560	179,615,026	28	-30.8	3	0.0	D
STX5	chr11	62,801,859	62,837,091	28	-37.1	3	7.0	D
TAPBP	chr6	33,294,694	33,319,387	28	-25.6	3	14.0	D
CD27-AS1	chr12	6,434,000	6,456,517	27	-48.3	3	62.0	D
HAGHL	chr16	721,935	734,715	27	-36.7	4	0.0	D
MIR5096	chr1	15,866,148	15,910,467	27	5.4	3	7.0	D
PPP3CB	chr10	73,431,427	73,501,024	27	-30.3	7	14.0	D
SMARCA4	chr19	10,955,921	11,067,282	27	-28.7	4	18.0	D
TAP2	chr6	32,816,832	32,843,823	27	-36.8	7	2.0	D
TNPO2	chr19	12,694,193	12,728,996	27	-30.3	4	7.0	D
XRCC6	chr22	41,616,162	41,669,048	27	-35.0	2	0.0	D
ABCF1	chr6	30,566,392	30,596,532	26	-40.9	5	0.0	D
ALYREF	chr17	81,882,834	81,896,586	26	-32.5	5	343.0	D
ANKRD13D	chr11	67,284,290	67,307,484	26	-42.3	6	2.0	D
HGS	chr17	81,678,931	81,707,121	26	-40.2	6	130.0	D
LOC100294145	chr6	32,889,175	32,908,758	26	-31.2	2	7.0	D
MIR6727	chr1	1,307,501	1,317,566	26	-33.3	6	14.0	D
SS18	chr18	26,011,252	26,096,217	26	-29.5	3	18.0	D
UNK	chr17	75,779,838	75,830,805	26	-34.1	10	14.0	D
BAZ2A	chr12	56,590,595	56,641,379	25	-27.5	9	14.0	D
CDK13	chr7	39,945,359	40,102,134	25	-31.3	2	14.0	D
FLYWCH1	chr16	2,906,978	2,956,208	25	-34.3	8	0.0	D
NCAPH2	chr22	50,503,215	50,529,780	25	-45.6	22	1.0	D
ATF6	chr1	161,761,243	161,969,070	24	-29.5	4	0.0	D
GIMAP7	chr7	150,509,856	150,526,073	24	-37.5	2	0.0	D
BICRAL	chr6	42,741,957	42,873,560	24	-32.8	4	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
MAP2K2	chr19	4,085,321	4,129,129	24	-39.9	9	106.0	D
MRPL12	chr17	81,698,369	81,712,526	24	-41.5	12	1285.0	D
NUP98	chr11	3,670,009	3,802,792	24	-42.2	6	0.0	D
PIEZO1	chr16	88,710,337	88,790,220	24	-28.1	2	14.0	D
ZNF16	chr8	144,925,357	144,955,888	24	-43.9	3	0.0	D
ABHD16A	chr6	31,681,948	31,708,360	23	-31.0	2	7.0	D
EIF3L	chr22	37,844,371	37,893,782	23	-45.9	7	7.0	D
EPPK1	chr8	143,852,318	143,883,464	23	-36.1	3	0.0	D
FAM222B	chr17	28,750,977	28,847,839	23	-31.6	6	0.0	D
IP6K2	chr3	48,683,002	48,722,278	23	-30.7	6	4.0	D
MIR6893	chr8	144,430,550	144,440,619	23	-47.3	6	0.0	D
PKD1	chr16	2,083,709	2,140,898	23	-35.8	3	7.0	D
RELA	chr11	65,648,595	65,667,972	23	-35.7	4	0.0	D
USP9X	chrX	41,080,634	41,241,579	23	-45.0	4	2.0	D
VPS51	chr11	65,091,114	65,116,860	23	-43.4	3	32.0	D
BCL2	chr18	63,118,345	63,324,380	22	-39.7	4	14.0	D
DEDD2	chr19	42,193,592	42,225,152	22	-34.4	2	0.0	D
DEF6	chr6	35,292,817	35,326,771	22	-43.0	3	14.0	D
EMG1	chr12	6,965,780	7,002,428	22	-36.8	3	0.0	D
ITPKB	chr1	226,626,689	226,744,175	22	-30.7	8	0.0	D
LASP1	chr17	38,864,858	38,926,770	22	-30.1	9	0.0	D
MAP3K14	chr17	45,258,118	45,322,064	22	-49.6	3	0.0	D
MDC1	chr6	30,694,806	30,722,681	22	-40.2	3	0.0	D
MDC1-AS1	chr6	30,698,066	30,718,184	22	-35.8	3	0.0	D
MZF1-AS1	chr19	58,554,185	58,579,797	22	-34.2	2	0.0	D
NCR3	chr6	31,583,882	31,597,985	22	-49.1	7	2.0	D
PTBP3	chr9	112,212,714	112,338,664	22	-41.2	2	0.0	D
SPATA5	chr4	122,918,069	123,324,449	22	-43.4	19	332.0	D
STAU2	chr8	73,415,368	73,752,708	22	-29.7	5	7.0	D
VPS28	chr8	144,418,600	144,433,563	22	-44.0	13	7.0	D
ANKRD28	chr3	15,662,235	15,864,546	21	-35.8	6	14.0	D
BPTF	chr17	67,820,663	67,989,378	21	-33.7	6	2.0	D
CAPN7	chr3	15,201,225	15,257,916	21	-49.4	5	0.0	D
RETREG3	chr17	42,574,507	42,614,427	21	-54.8	4	0.0	D
IL27RA	chr19	14,026,739	14,057,905	21	-43.9	4	2.0	D
LOC105371038	chr16	643,457	654,313	21	-32.0	2	0.0	D
MARCH6	chr5	10,348,638	10,445,388	21	-44.2	2	4.0	D
MCM3AP	chr21	46,230,124	46,290,394	21	-39.1	11	92.0	D
NEK7	chr1	198,151,977	198,327,418	21	-35.9	3	14.0	D
PNKP	chr19	49,856,202	49,872,565	21	-31.3	9	0.0	D
PTOV1	chr19	49,845,734	49,865,744	21	-31.2	9	0.0	D
PYM1	chr12	55,896,412	55,932,913	21	-44.9	5	2.0	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
SH3GL1	chr19	4,355,366	4,405,568	21	-52.8	2	14.0	D
ARHGAP4	chrX	153,902,375	153,931,260	20	-36.7	4	0.0	D
EIF4B	chr12	53,001,257	53,047,215	20	-38.3	3	2.0	D
FASN	chr17	82,073,337	82,103,230	20	-38.7	12	2.0	D
KPNB1	chr17	47,644,837	47,688,638	20	-57.7	2	7.0	D
MIR1234	chr8	144,395,085	144,405,165	20	-37.0	43	14.0	D
MIR6849	chr8	144,395,276	144,405,345	20	-38.5	43	14.0	D
MVP	chr16	29,815,393	29,853,039	20	-36.9	2	0.0	D
NOTCH1	chr9	136,489,432	136,550,786	20	-34.1	5	14.0	D
OTUD5	chrX	48,917,025	48,963,386	20	-39.1	2	0.0	D
SF3B2	chr11	66,047,344	66,073,911	20	-68.7	4	1.0	D
TNRC6A	chr16	24,724,727	24,831,226	20	-47.0	3	1.0	D
ARHGDIA	chr17	81,862,718	81,876,406	19	-50.2	2	14.0	D
ASPSCR1	chr17	81,972,545	82,022,406	19	-43.0	4	912.5	D
BTBD2	chr19	1,980,447	2,020,703	19	-36.7	4	14.0	D
CAMTA2	chr17	4,962,991	4,992,665	19	-35.5	3	0.0	D
DMC1	chr22	38,513,948	38,575,196	19	-39.5	2	0.0	D
ELF1	chr13	40,926,918	41,024,372	19	-32.9	4	18.0	D
EMSY	chr11	76,440,024	76,557,899	19	-45.7	3	0.0	D
ERN1	chr17	64,038,029	64,135,142	19	-49.8	4	0.0	D
GYS1	chr19	48,963,124	48,998,353	19	-35.3	3	0.0	D
LOC100130987	chr11	67,312,838	67,396,687	19	-50.0	2	0.0	D
MIR3681HG	chr2	12,002,115	12,583,348	19	-41.7	14	14.0	D
POU2F2	chr19	42,081,109	42,137,473	19	-36.3	7	92.0	D
PRKCH	chr14	61,316,442	61,555,980	19	-42.2	2	7.0	D
PRPF8	chr17	1,645,628	1,689,882	19	-38.1	3	0.0	D
RNF24	chr20	3,922,308	4,020,591	19	-42.0	5	0.0	D
SDF4	chr1	1,211,907	1,237,067	19	-58.9	3	0.0	D
TYK2	chr19	10,345,527	10,385,572	19	-49.3	2	0.0	D
CARNS1	chr11	67,410,677	67,430,607	18	-49.3	2	7.0	D
HNRNPLL	chr2	38,558,185	38,608,036	18	-48.9	2	1.0	D
KIAA0355	chr19	34,249,550	34,360,566	18	-36.7	4	0.0	D
LBHD1	chr11	62,657,816	62,676,769	18	-42.9	6	166.0	D
PTOV1-AS2	chr19	49,851,464	49,864,289	18	-34.7	9	0.0	D
RLF	chr1	40,156,368	40,245,921	18	-33.7	4	0.0	D
SLAMF6	chr1	160,480,029	160,528,262	18	-40.4	2	0.0	D
SPHK2	chr19	48,614,290	48,635,406	18	-45.2	4	0.0	D
TRAF7	chr16	2,150,797	2,183,129	18	-39.4	3	0.0	D
ZC3H4	chr19	47,059,189	47,118,752	18	-44.1	2	0.0	D
CTDSPL2	chr15	44,422,380	44,532,231	17	-40.1	4	0.0	D
DACH1	chr13	71,432,965	71,872,192	17	-36.0	1	0.0	D
EME2	chr16	1,768,227	1,781,238	17	-40.2	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
IL32	chr16	3,060,311	3,074,819	17	-49.4	3	0.0	D
LST1	chr6	31,581,178	31,593,909	17	-51.7	7	2.0	D
OBSCN	chr1	228,203,129	228,383,874	17	-53.6	7	0.0	D
PITPNM1	chr11	67,486,767	67,510,372	17	-45.0	2	0.0	D
PPP1R10	chr6	30,595,399	30,622,307	17	-36.1	2	0.0	D
RFX1	chr19	13,956,529	14,011,322	17	-39.3	2	0.0	D
RPS6KB2	chr11	67,423,463	67,440,408	17	-42.2	2	7.0	D
TSEN34	chr19	54,185,267	54,199,536	17	-32.6	2	0.0	D
ZNF584	chr19	58,403,673	58,423,325	17	-43.5	3	0.0	D
AMBRA1	chr11	46,391,411	46,599,069	16	-35.3	3	0.0	D
ARL3	chr10	102,668,726	102,719,433	16	-40.2	3	2.0	D
BRAT1	chr7	2,532,809	2,560,758	16	-45.6	2	0.0	D
BSCL2	chr11	62,685,261	62,714,619	16	-38.9	3	0.0	D
CARD8-AS1	chr19	48,250,674	48,263,193	16	-35.6	8	46.0	D
CDR2	chr16	22,340,935	22,379,617	16	-36.8	3	0.0	D
GIMAP1-GIMAP5	chr7	150,711,556	150,748,649	16	-47.1	5	0.0	D
LINC00243	chr6	30,807,865	30,835,659	16	-40.7	2	0.0	D
LOC105369632	chr12	6,870,764	6,894,358	16	-56.9	3	0.0	D
MMP25	chr16	3,041,680	3,065,723	16	-40.5	3	0.0	D
NSD2	chr4	1,866,395	1,987,207	16	-47.9	2	0.0	D
OPA3	chr19	45,522,766	45,589,864	16	-48.4	4	0.0	D
RNF43	chr17	58,347,499	58,422,582	16	-44.0	3	76.0	D
RPL18	chr19	48,610,326	48,624,418	16	-50.9	2	0.0	D
STX12	chr1	27,768,182	27,829,452	16	-42.7	4	14.0	D
TAF1	chrX	71,361,238	71,535,525	16	-53.8	2	0.0	D
TBC1D24	chr16	2,470,145	2,510,733	16	-42.7	2	0.0	D
BCL7C	chr16	30,829,040	30,899,302	15	-45.3	2	0.0	D
BISPR	chr19	17,400,685	17,420,736	15	-41.2	4	0.0	D
C11orf98	chr11	62,657,816	62,670,216	15	-47.4	6	166.0	D
C8orf82	chr8	144,521,218	144,534,074	15	-41.2	2	0.0	D
CD27	chr12	6,439,884	6,456,718	15	-47.4	2	0.0	D
CD4	chr12	6,784,471	6,825,810	15	-74.0	5	0.0	D
CLPB	chr11	72,287,425	72,439,684	15	-45.0	2	0.0	D
COG6	chr13	39,650,626	39,796,665	15	-38.4	6	2.0	D
EHBP1L1	chr11	65,571,037	65,597,645	15	-44.5	13	0.0	D
IKZF4	chr12	56,015,904	56,043,435	15	-40.0	2	0.0	D
LTB	chr6	31,575,558	31,587,425	15	-38.3	7	2.0	D
MIR5690	chr6	35,659,716	35,669,789	15	-43.2	2	0.0	D
MVB12A	chr19	17,400,685	17,430,339	15	-42.7	4	0.0	D
NTHL1	chr16	2,034,814	2,052,869	15	-55.7	1	0.0	D
PGP	chr16	2,206,601	2,219,821	15	-57.5	10	14.0	D
PRRG2	chr19	49,576,329	49,596,008	15	-44.4	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
PTK2	chr8	140,653,381	141,006,313	15	-57.1	10	46.0	D
TAPBP1	chr12	6,447,010	6,467,322	15	-40.0	2	0.0	D
TBC1D10C	chr11	67,398,912	67,415,090	15	-62.5	2	0.0	D
ABCA7	chr19	1,035,102	1,070,571	14	-62.1	2	0.0	D
ACTG1	chr17	81,504,970	81,517,866	14	-38.4	2	80.0	D
ELL	chr19	18,437,662	18,527,127	14	-42.5	2	0.0	D
GPD2	chr2	156,430,452	156,591,403	14	-57.8	2	14.0	D
INTS5	chr11	62,641,847	62,658,302	14	-38.3	2	0.0	D
KCTD13	chr16	29,901,335	29,931,232	14	-50.8	2	0.0	D
MIR4479	chr9	136,881,732	136,891,803	14	-45.0	2	0.0	D
MSL1	chr17	40,117,536	40,141,791	14	-54.5	4	0.0	D
SCYL1	chr11	65,520,076	65,543,711	14	-40.4	3	14.0	D
USP12	chr13	27,061,149	27,176,896	14	-46.1	3	0.0	D
WIPF1	chr2	174,554,573	174,687,899	14	-62.5	1	0.0	D
ZNF655	chr7	99,553,421	99,581,456	14	-47.5	3	0.0	D
CDT1	chr16	88,798,777	88,814,258	13	-41.4	1	0.0	D
GRAMD1A	chr19	34,989,783	35,031,471	13	-49.5	2	18.0	D
HSPBP1	chr19	55,257,221	55,285,383	13	-37.5	4	0.0	D
LOC105371184	chr16	673,517	684,777	13	-44.3	2	0.0	D
LOC106660606	chr16	2,263,662	2,278,072	13	-58.3	2	0.0	D
LONP1	chr19	5,686,833	5,725,452	13	-75.1	5	106.0	D
PTPN6	chr12	6,941,576	6,966,316	13	-50.7	5	7.0	D
SEC11A	chr15	84,664,536	84,721,460	13	-53.1	4	136.0	D
TMBIM6	chr12	49,736,509	49,769,934	13	-51.4	4	14.0	D
ABCA3	chr16	2,270,877	2,345,746	12	-51.7	2	0.0	D
C15orf41	chr15	36,574,602	36,815,260	12	-46.4	4	7.0	D
CSGALNACT1	chr8	19,399,160	19,687,750	12	-54.3	2	0.0	D
DSTNP2	chr12	6,879,681	6,890,786	12	-53.1	3	0.0	D
GFOD2	chr16	67,669,532	67,724,370	12	-51.3	22	932.0	D
MCM3AP-AS1	chr21	46,224,230	46,256,701	12	-39.2	8	92.0	D
MIR5096	chr1	235,507,822	235,723,113	12	59.4	1	0.0	D
NGLY1	chr3	25,713,943	25,795,039	12	-42.0	3	0.0	D
PDCD2L	chr19	34,399,397	34,431,167	12	-42.0	4	0.0	D
RNF34	chr12	121,395,082	121,429,352	12	-40.5	3	0.0	D
SCAMP2	chr15	74,838,729	74,878,379	12	-45.3	1	0.0	D
SNUPN	chr15	75,593,082	75,631,378	12	-50.5	4	0.0	D
TNFSF12-TNFSF13	chr17	7,544,057	7,566,608	12	-62.0	5	0.0	D
COQ8B	chr19	40,686,528	40,721,885	11	-52.0	2	0.0	D
DGAT1	chr8	144,309,582	144,331,919	11	-60.6	4	22.0	D
DGKA	chr12	55,926,161	55,959,023	11	-38.4	3	14.0	D
EXOSC4	chr8	144,073,618	144,085,648	11	-50.0	5	0.0	D
FYTTD1	chr3	197,744,552	197,789,446	11	-49.2	4	14.0	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
FZR1	chr19	3,501,296	3,541,757	11	-58.0	2	0.0	D
GNA15	chr19	3,131,031	3,168,769	11	-47.5	3	0.0	D
LCP2	chr5	170,241,232	170,302,842	11	-53.1	2	2.0	D
LTBP3	chr11	65,533,558	65,563,228	11	-43.7	4	0.0	D
MAP1S	chr19	17,714,451	17,739,515	11	-37.5	5	14.0	D
MED16	chr19	862,961	898,218	11	-52.3	4	0.0	D
NCLN	chr19	3,180,876	3,214,575	11	-40.5	4	0.0	D
SGTA	chr19	2,749,713	2,788,356	11	-55.7	2	0.0	D
SH2D3C	chr9	127,733,316	127,783,769	11	-45.6	3	0.0	D
TATDN2	chr3	10,243,492	10,286,222	11	-37.5	3	14.0	D
TYMP	chr22	50,520,752	50,535,085	11	-53.9	3	0.0	D
ACAP3	chr1	1,287,383	1,312,889	10	-50.9	2	0.0	D
CENPBD1P1	chr19	58,570,398	58,589,395	10	-50.7	2	0.0	D
DPP4	chr2	161,987,244	162,079,542	10	-43.1	2	0.0	D
EFTUD2	chr17	44,845,286	44,904,625	10	-51.1	7	0.0	D
HSPA1L	chr6	31,804,618	31,820,058	10	-47.7	4	90.0	D
LIX1L	chr1	145,928,423	145,963,019	10	-43.4	2	0.0	D
LOC101927018	chr17	28,921,274	28,949,748	10	-54.5	42	166.0	D
NAPSB	chr19	50,328,799	50,349,748	10	-55.2	1	0.0	D
PTPRCAP	chr11	67,430,509	67,442,682	10	-54.5	2	0.0	D
PTPRJ	chr11	47,975,557	48,175,842	10	-54.0	2	0.0	D
RAB27A	chr15	55,197,965	55,294,815	10	-45.6	4	18.0	D
RPLP2	chr11	804,935	817,876	10	-54.9	2	0.0	D
ZSCAN10	chr16	3,083,890	3,104,317	10	-60.2	1	0.0	D
ARHGAP17	chr16	24,914,383	25,020,378	9	-55.0	1	0.0	D
BRICD5	chr16	2,204,252	2,216,068	9	-53.1	1	14.0	D
CD247	chr1	167,425,639	167,523,610	9	-57.0	2	0.0	D
CERS5	chr12	50,124,305	50,172,533	9	-45.9	2	0.0	D
EIF4A3	chr17	80,130,213	80,152,183	9	-67.1	2	0.0	D
EMB	chr5	50,391,196	50,446,400	9	-58.7	2	0.0	D
ENTPD1-AS1	chr10	95,748,205	96,095,235	9	-53.1	3	7.0	D
GIMAP1	chr7	150,711,556	150,729,280	9	-52.1	1	0.0	D
IL6R	chr1	154,400,192	154,474,450	9	-68.3	5	22.0	D
LOC102724050	chr12	54,348,690	54,472,030	9	-60.1	2	0.0	D
MIR762HG	chr16	30,870,459	30,900,218	9	-49.2	2	0.0	D
MLST8	chr16	2,200,176	2,214,417	9	-54.0	1	14.0	D
NHEJ1	chr2	219,070,323	219,165,865	9	-50.9	4	0.0	D
NUTF2	chr16	67,841,731	67,877,566	9	-54.9	12	0.0	D
PPT2-EGFL8	chr6	32,148,998	32,173,285	9	-52.3	3	62.0	D
RNF31	chr14	24,141,874	24,165,661	9	-51.7	3	0.0	D
RUVBL2	chr19	48,988,447	49,020,995	9	-76.8	2	0.0	D
SNORA52	chr11	806,680	816,814	9	-48.9	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
TMEM219	chr16	29,957,029	29,978,052	9	-45.3	2	0.0	D
UBTF	chr17	44,200,032	44,226,626	9	-66.9	2	0.0	D
VBP1	chrX	155,192,006	155,244,841	9	-46.8	3	0.0	D
ZBTB45	chr19	58,508,529	58,546,712	9	-60.1	1	0.0	D
AKAP8	chr19	15,348,520	15,384,801	8	-68.7	1	0.0	D
APOBEC3D	chr22	39,016,112	39,038,251	8	-60.1	1	0.0	D
C6orf48	chr6	31,829,914	31,844,766	8	-58.3	2	0.0	D
CSAD	chr12	53,152,662	53,185,909	8	-54.1	2	0.0	D
DHX16	chr6	30,648,118	30,678,053	8	-51.2	4	0.0	D
GPAA1	chr8	144,077,620	144,091,216	8	-58.3	5	0.0	D
KDELR1	chr19	48,377,569	48,396,553	8	-52.1	1	0.0	D
MFSD12	chr19	3,539,198	3,562,584	8	-49.7	2	0.0	D
MTBP	chr8	120,440,397	120,528,635	8	-60.0	2	0.0	D
NME3	chr16	1,765,319	1,776,709	8	-47.7	2	0.0	D
PTPN11	chr12	112,413,897	112,514,918	8	-69.3	2	0.0	D
PTPRO	chr12	15,317,256	15,603,331	8	-54.3	2	18.0	D
SNORD48	chr6	31,830,262	31,840,326	8	-55.9	2	0.0	D
TADA2A	chr17	37,401,885	37,482,121	8	-63.1	3	0.0	D
EGFL8	chr6	32,159,604	32,173,285	7	-51.9	3	62.0	D
FOSL1	chr11	65,887,135	65,905,526	7	-45.3	1	0.0	D
PLXNA3	chrX	154,453,280	154,478,646	7	-50.7	1	0.0	D
RRM2B	chr8	102,199,500	102,244,118	7	-50.7	3	106.0	D
SHISA5	chr3	48,462,797	48,509,826	7	-60.0	1	0.0	D
SNRNP200	chr2	96,269,335	96,310,569	7	-65.9	1	0.0	D
STAG2	chrX	123,955,559	124,107,655	7	-72.2	6	0.0	D
CD48	chr1	160,673,745	160,716,851	6	-58.3	1	0.0	D
PYCR3	chr8	143,598,223	143,614,614	6	-57.4	1	0.0	D
RBM10	chrX	47,140,217	47,191,815	6	-57.9	4	0.0	D
HSPA1B	chr6	31,822,734	31,835,254	5	-68.2	2	0.0	D