

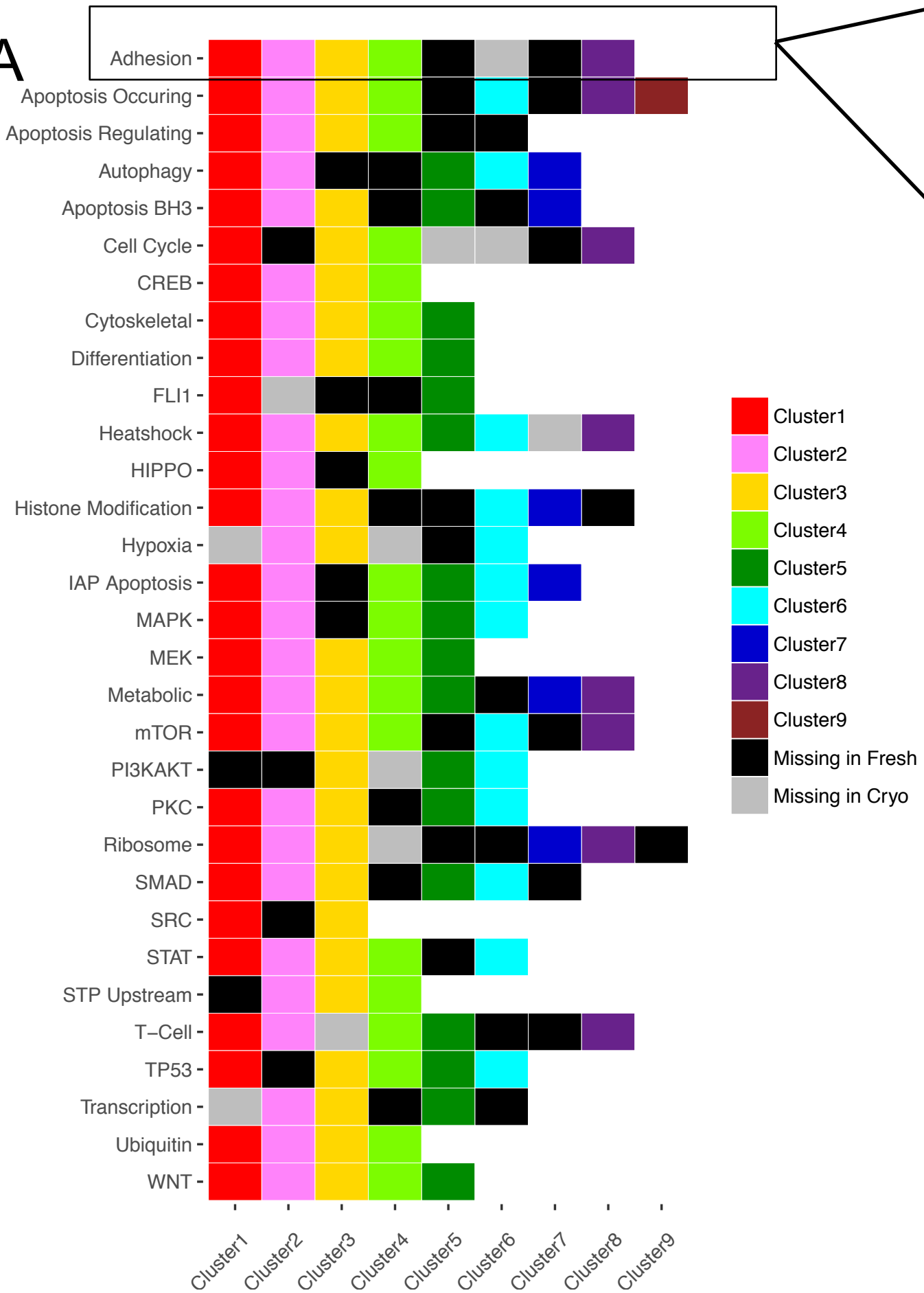
## Supplemental Figures, Tables & Tutorial

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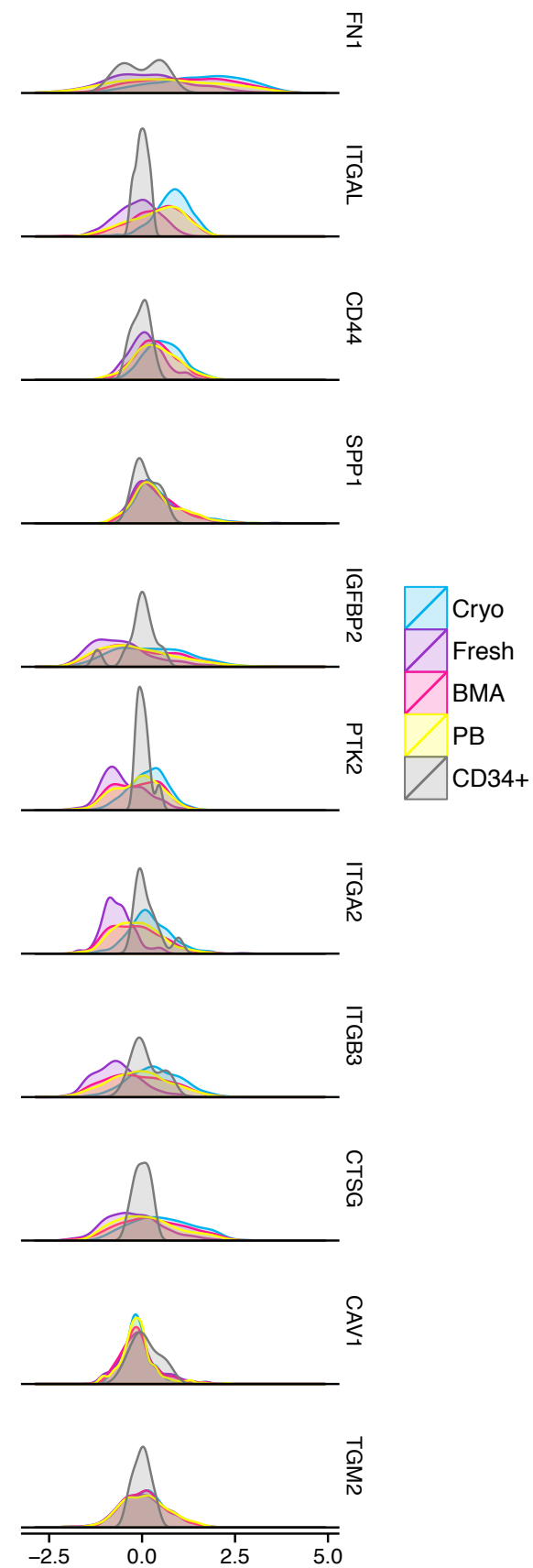
Example demo files (main.csv & pathway.csv) provided

**Figure S1. Proteomic differences between fresh and cryopreserved samples. (A)** Antibodies from the RPPA were grouped into 31 functional groups (shown as rows), and cluster analysis (Progeny Clustering with K-means) was performed using all samples (fresh and cryopreserved) to identify recurrent functional patterns (shown as columns). Functional patterns that only occur in cryopreserved samples (missing in fresh) were colored in black, whereas patterns that only occur in fresh samples (missing in cryo) were colored in grey. **(B)** Proteins from the *Adhesion group* were shown as an example to demonstrate varied expression distributions by sample source (i.e. peripheral blood (labeled “PB”) or bone marrow (labeled “BM”)) and processing technique (whether protein was prepared from fresh or previously cryopreserved cells (labeled “Cryo”). The protein expression distributions in cryopreserved bone marrow CD34+ cells from healthy subjects (labeled “CD34+”) were also shown in comparison. See **Table S1** for the functional group category and sample source comparison statistics for each protein.

# A

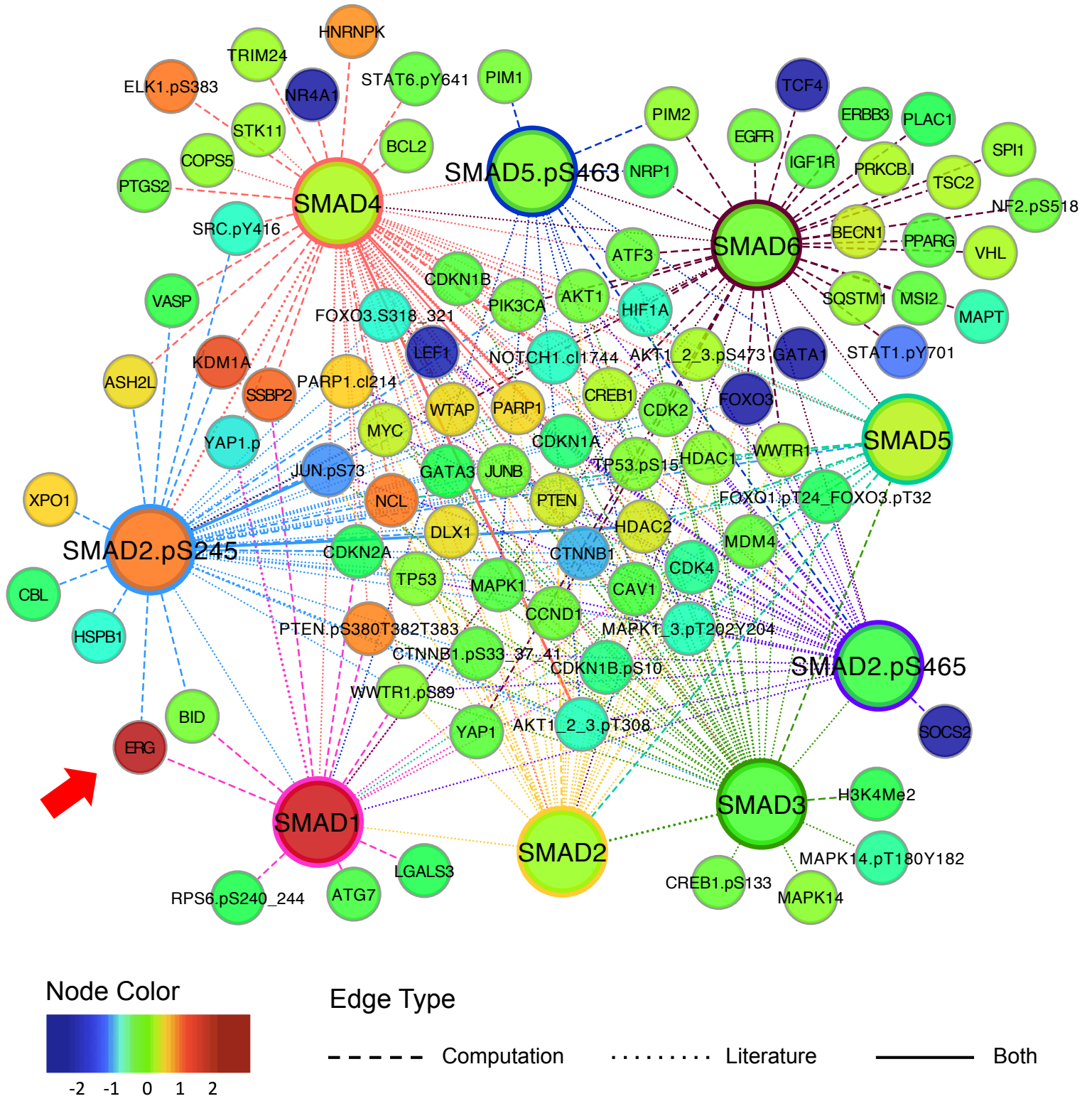


# B

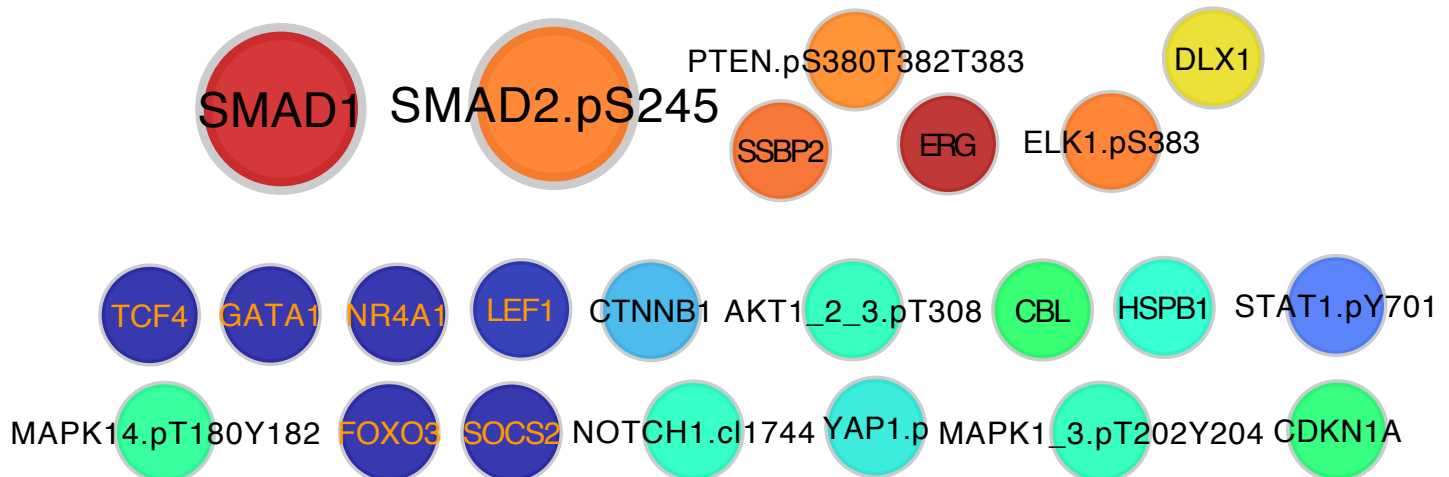


**Figure S2. Protein networks for discovering potential drug targets beyond individual functional groups.** (A) The protein network for *SMAD-P5* demonstrates the interactions (shown as edges) and expression levels (shown as node colors) of the SMAD proteins (shown in large nodes) and proteins that directly associate with them (shown in small nodes). Highlighted by a red arrow, ERG with abnormally high expression level can serve a potential drug target as an alternative to targeting SMAD2.p and SMAD1. (B) Proteins with abnormally high and low expressions compared to the normal range were selected and can potentially be tested as drug targets. The node color reflects the relative expression levels compared to that in control samples.

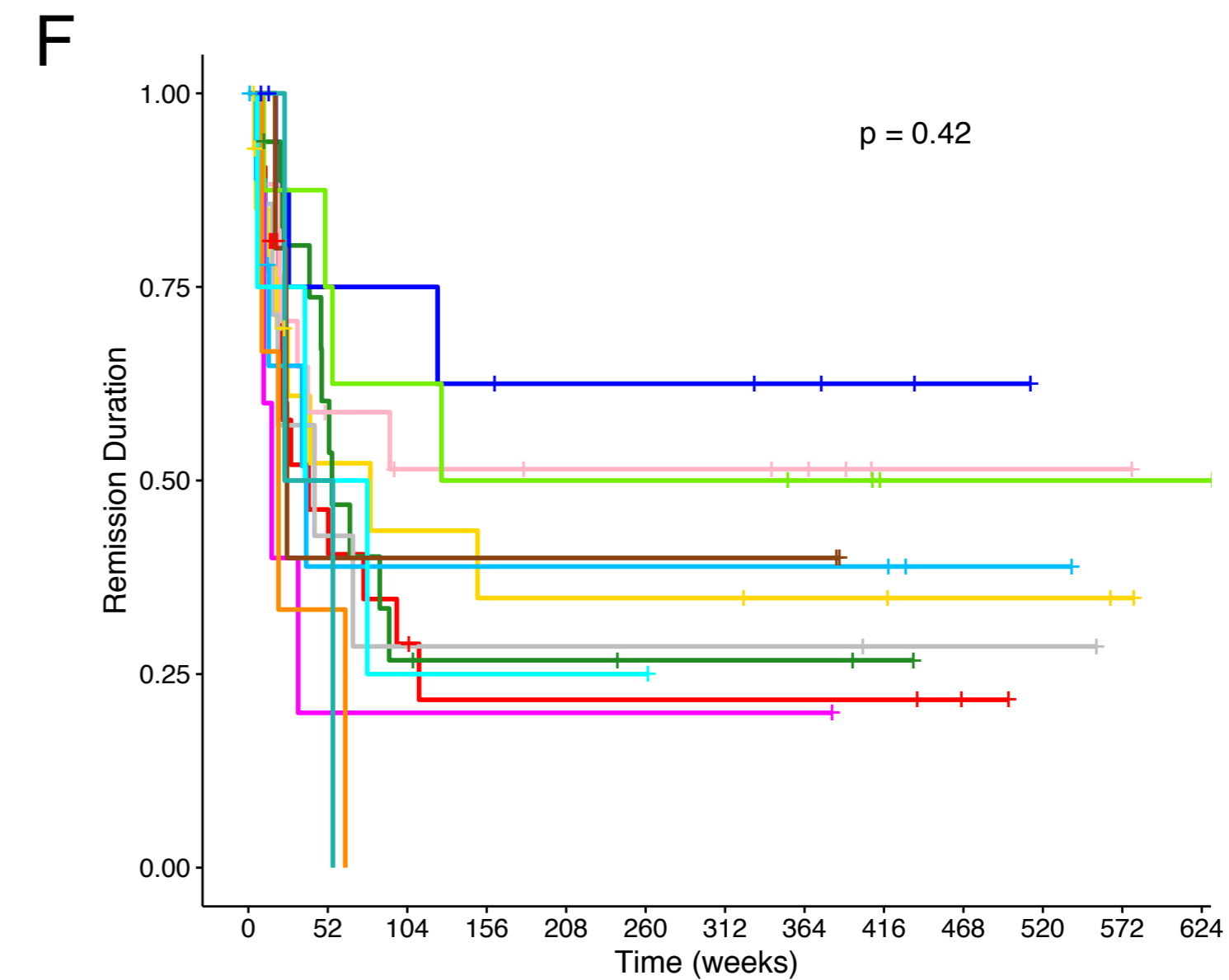
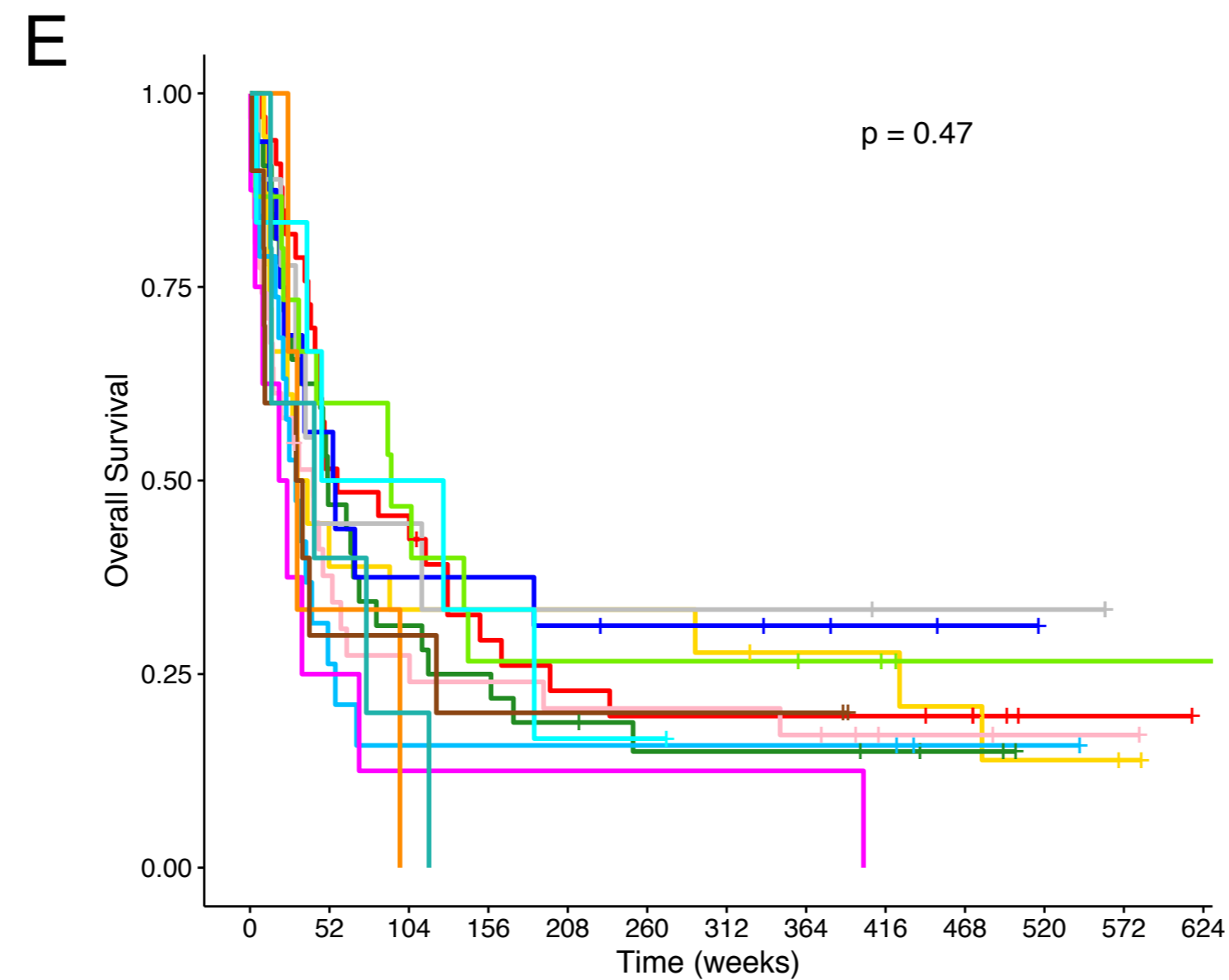
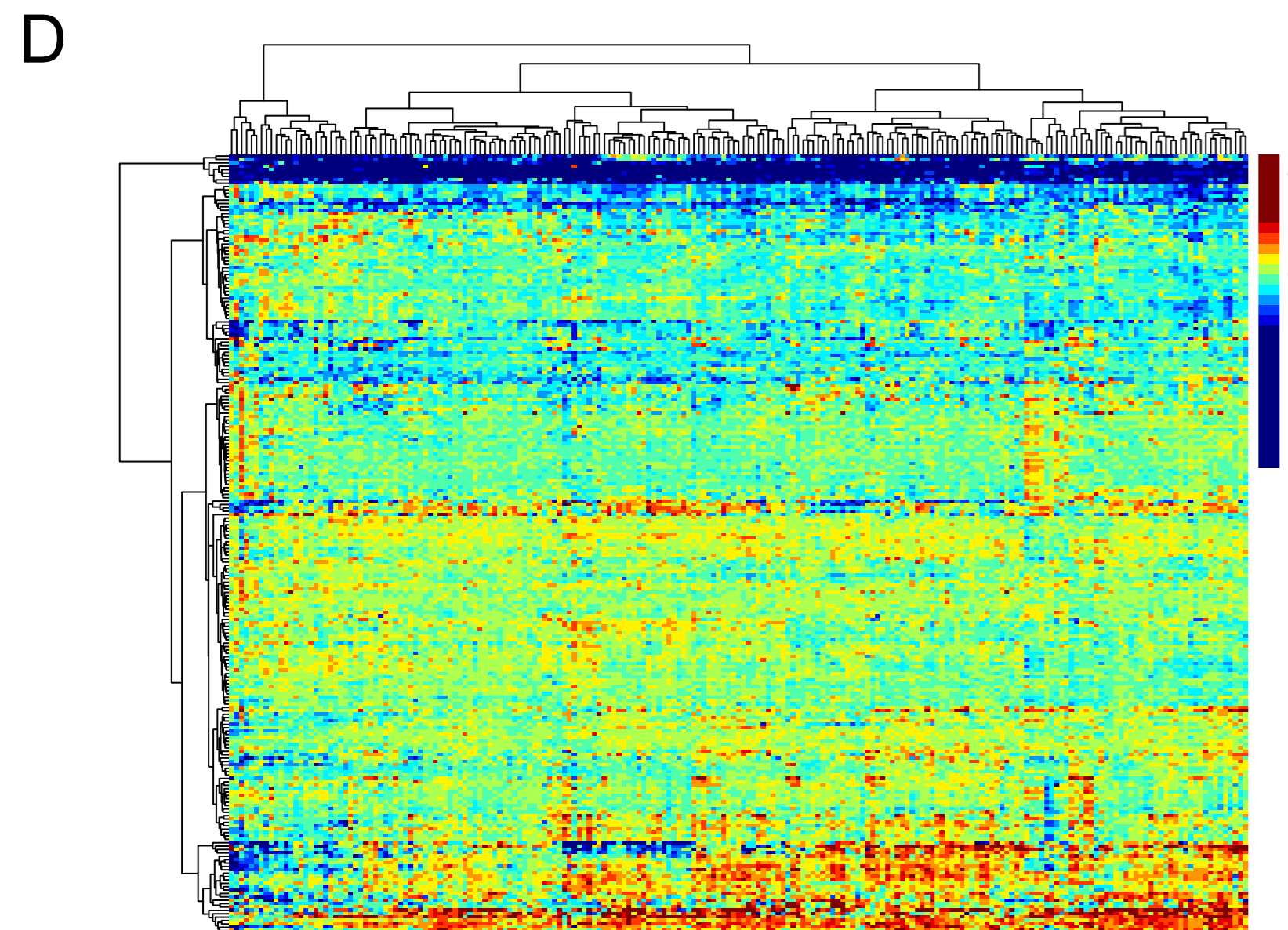
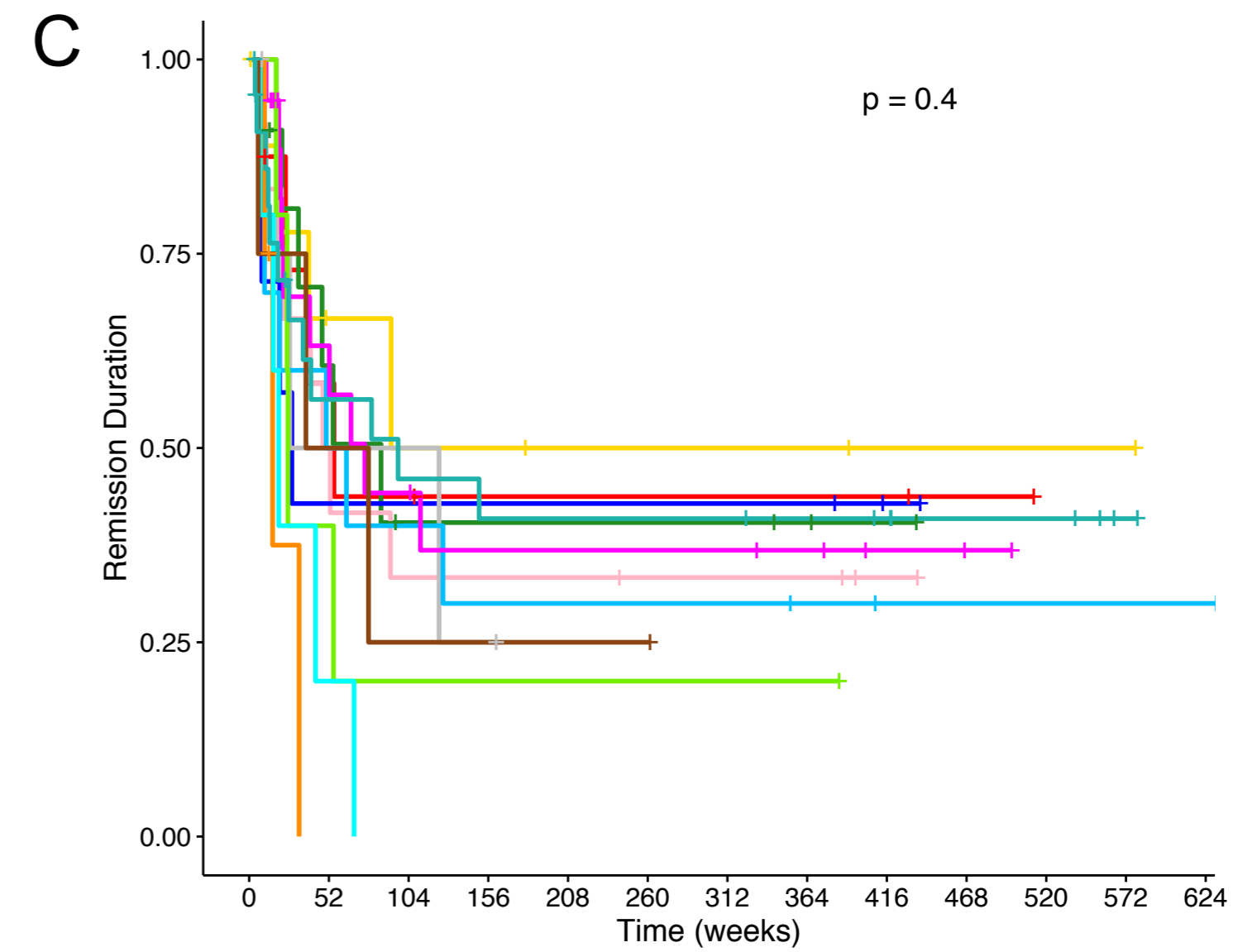
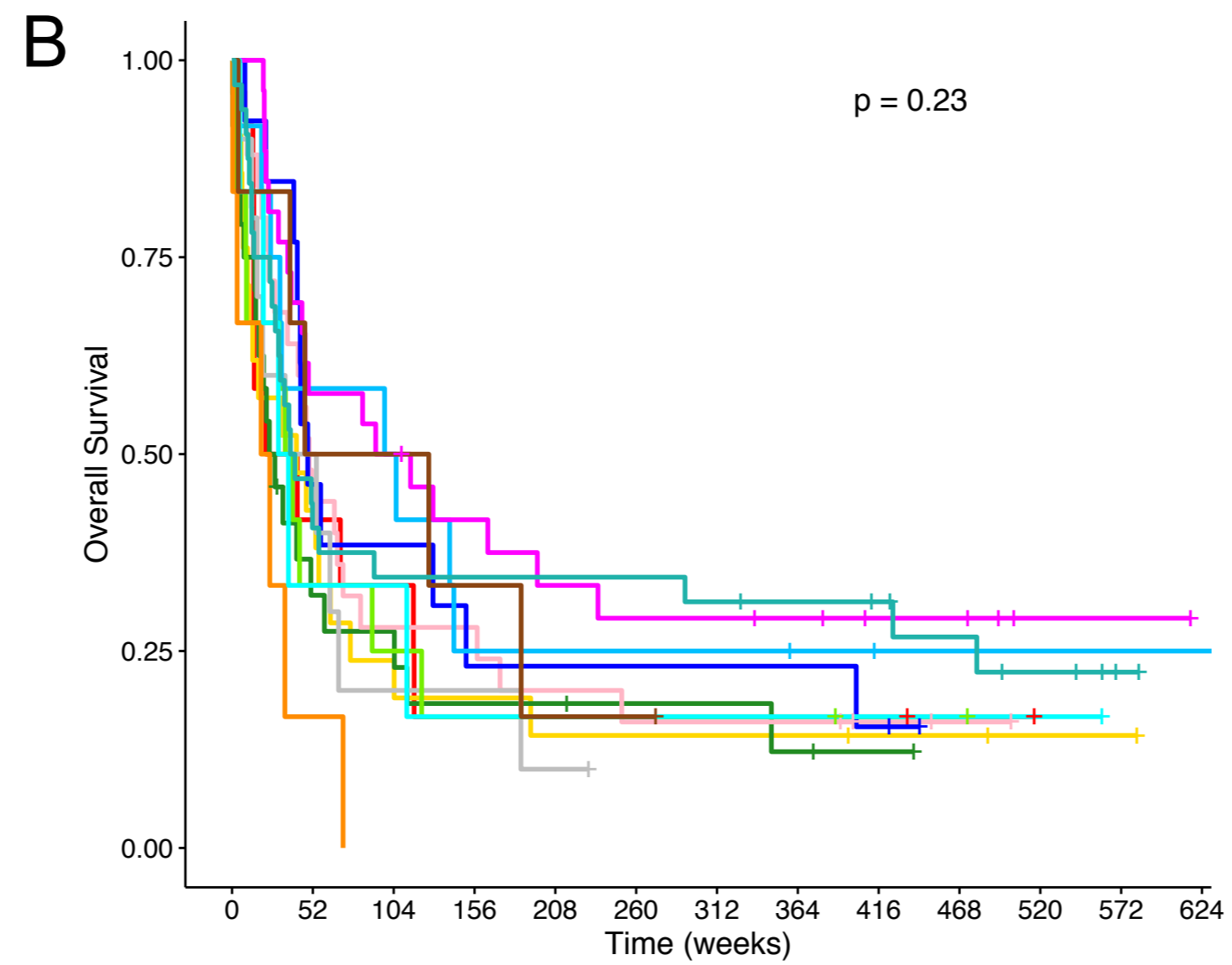
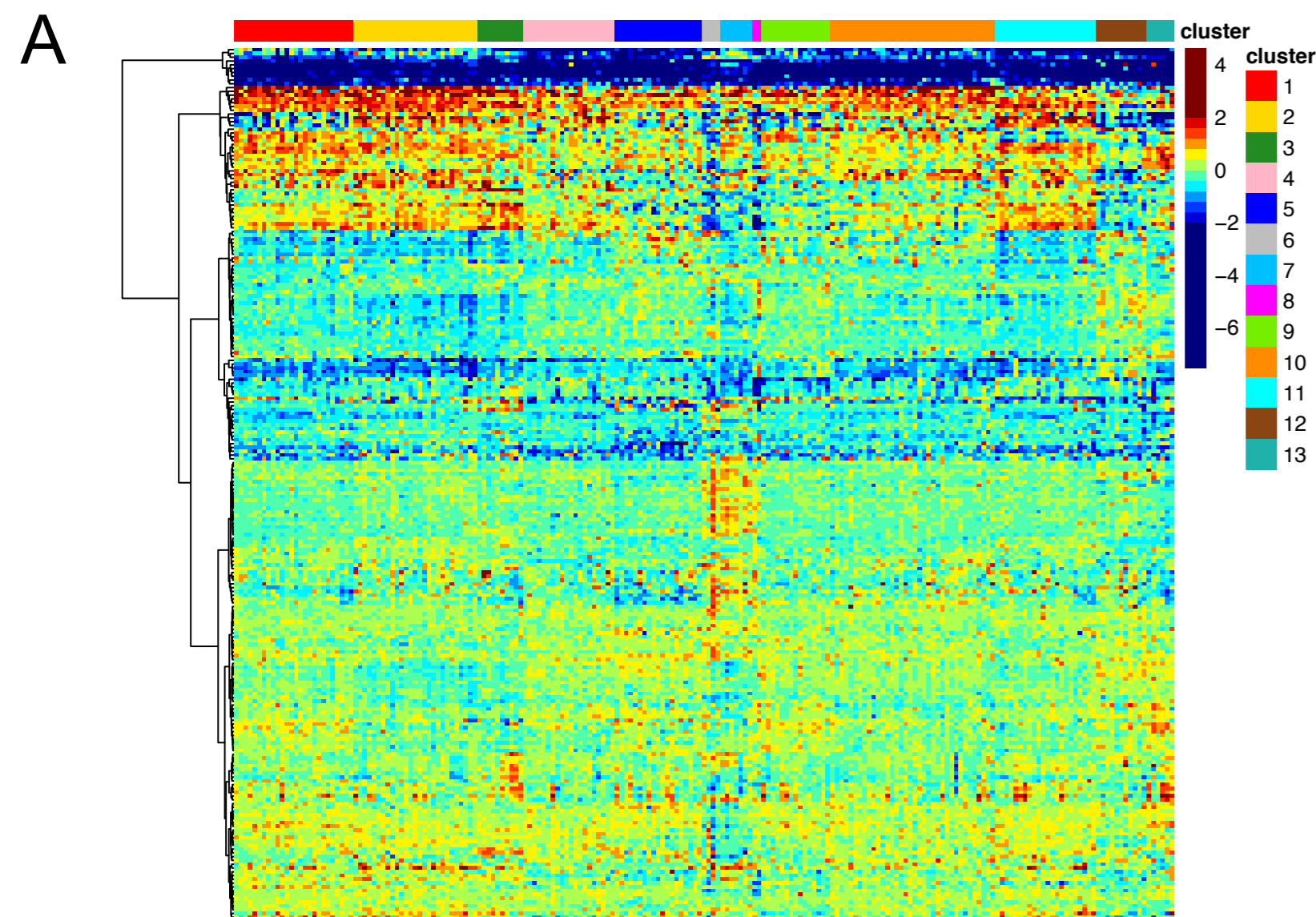
A



B



**Figure S3. Results from clustering patients based on protein expression levels.** (A) Clustering results of patients (columns) using k-means clustering, where proteins (rows) were ordered based on hierarchical clustering with ward linkage. (B) Patients' overall survival based on the k-means clustering memberships (p-value = 0.23). (C) Patients' remission duration based on the k-means clustering memberships (p-value = 0.4). (D) Clustering results using hierarchical clustering with ward linkage, where columns are patients and rows are proteins. (E) Patients' overall survival based on the hierarchical clustering memberships (p-value = 0.47). (F) Patients' remission duration based on the hierarchical clustering memberships (p-value = 0.42). The clusters identified by both k-means and hierarchical clustering are less prognostic in comparison to the clustering generated with the MetaGalaxy analysis (see **Figure 4**), in which the signatures are prognostic for overall survival (p-value = 0.00009) and remission duration (p-value = 0.03). n = 205 for all graphs. p-values shown for log-rank test, one-sided.

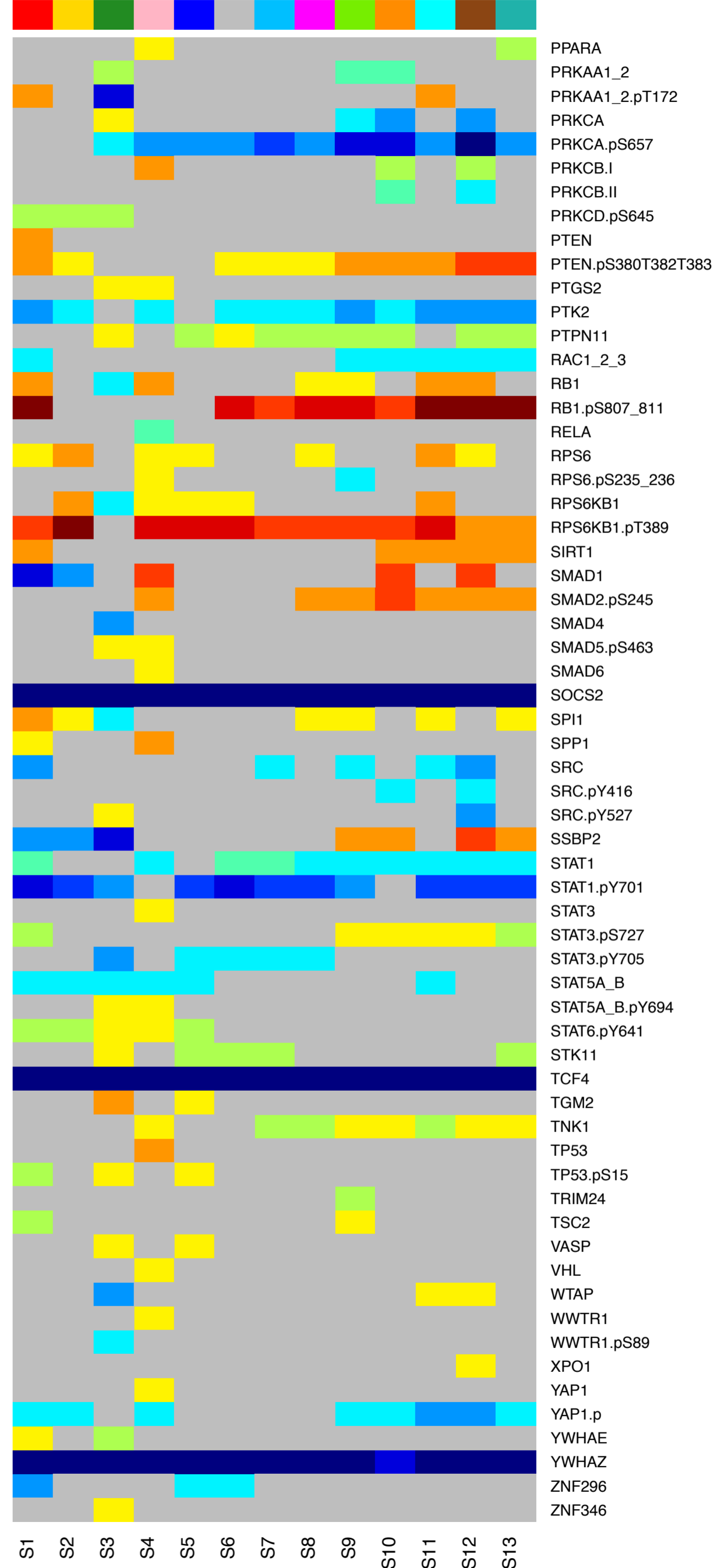
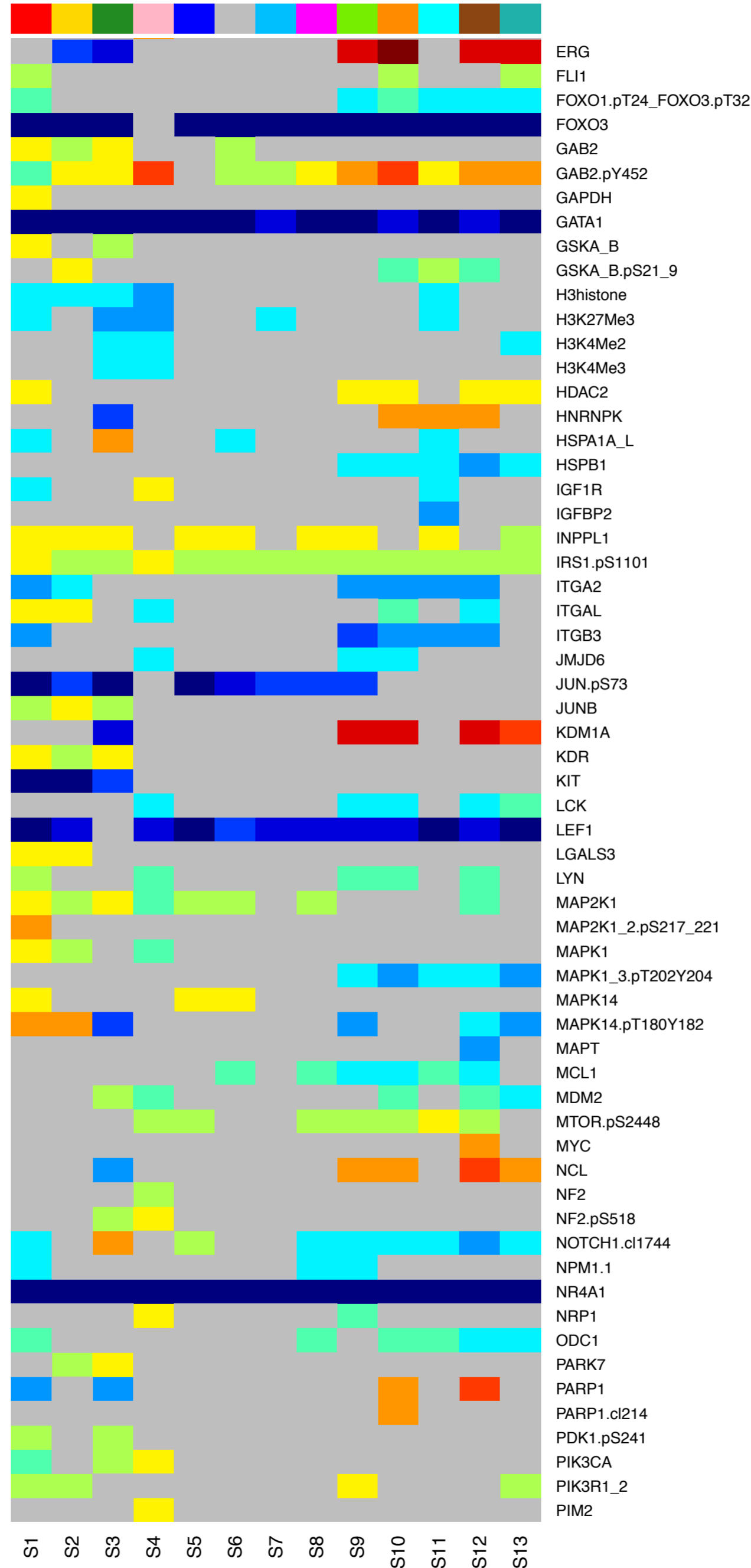
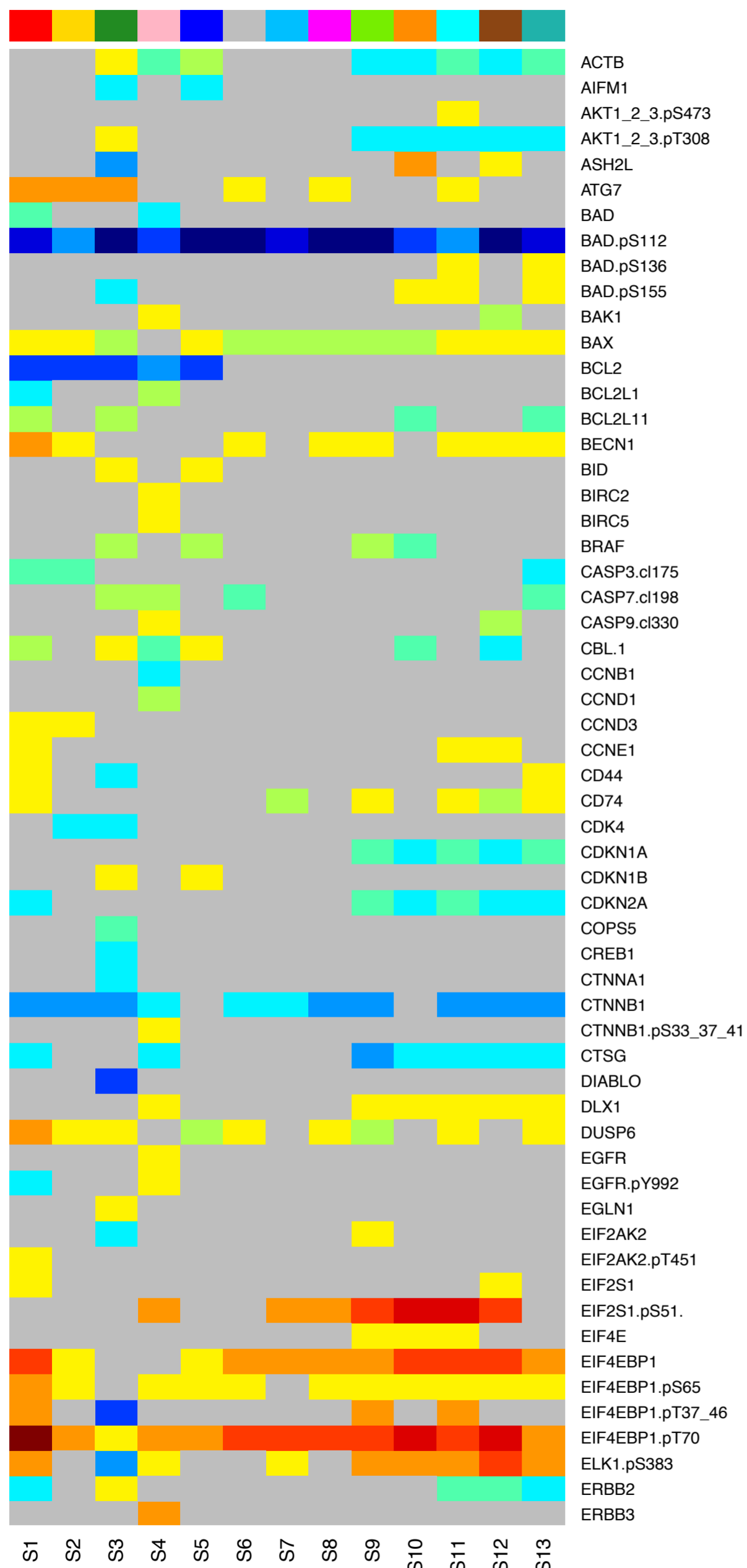


**Figure S4. Kaplan-Meier curves from training and testing data.** The four plots display overall survival curves from the training set (upper left), overall survival curves from the testing set (upper right), remission duration curves from the training set (lower left) and remission duration curves from the testing set (lower right). In either overall survival or remission duration, the three signature groups (favorable, intermediate and unfavorable) display consistent outcome between the training and the testing set. Training sample size (n = 102); testing samples size (n = 103). p-values shown for log-rank test, one-sided.

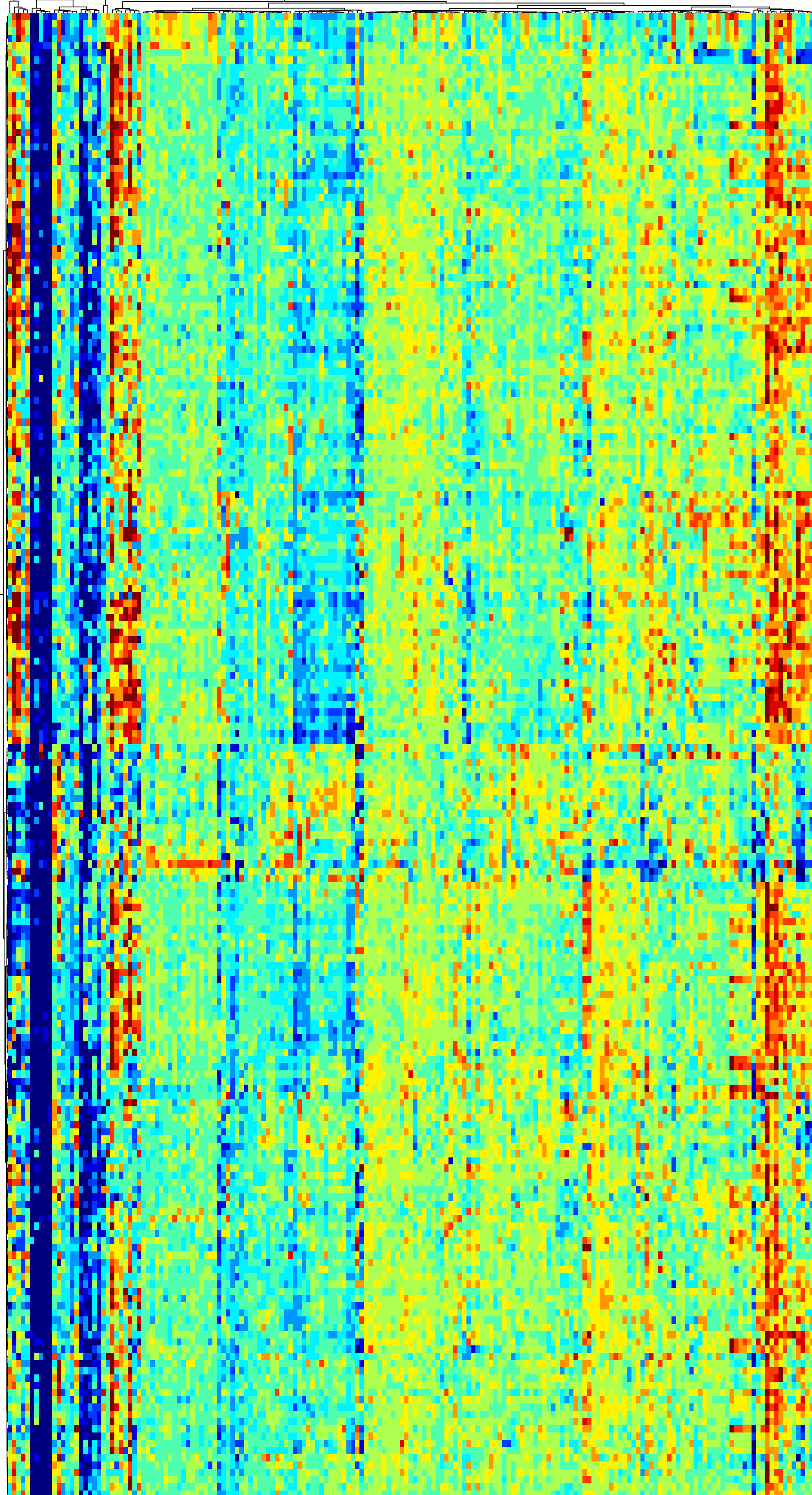
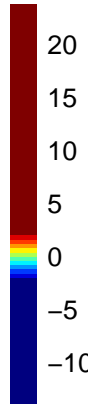




**Figure S5. Potential drug targets for signatures.** The heatmap shows the mean expression levels of potential drug targets (rows) in each signature (columns). A cell is marked in grey if the protein is not a target in that signature. Note that only proteins that are targets for at least one signature are included, and proteins that are not targets for any of the signatures are excluded. The signature color at the top corresponds to the signature color in **Figure 4A**.



**Figure S6. Clustering of cell lines together with AML patient samples.** In the heatmap, the columns are proteins and the rows are samples. To distinguish cell lines from patients, we labeled all cell lines (text at the right of the heatmap), whereas we kept all patient samples unlabeled. Hierarchical clustering was applied to both the rows and columns, and the proteins and samples were ordered by the clustering result. It is clear that all cell lines (at the bottom) were separated from all patient samples (at the top) from the clustering. This was true for all the cell lines, regardless of lineage (AML or ALL), or for mycoplasma infected cell lines (n=17) and their uninfected counterparts.



OCIA1M3 inducible HIF1a ODD mut  
OCIA1M3 TRE TGM2 control  
OCIA1M3 708 ppp2R2A shRNA  
OCIA1M3 NS-IPp2R2A shRNA  
OCIA1M3 stat1 R132H  
OCIA1M3 PLK3 wt pool #1  
OCIA1M3 IBH1 wt pool #2 1A  
OCIA1M3 stat3A N642H  
OCIA1M3 stat3A N642H H4F  
OCIA1M3 stat3A N642H  
OCIA1M3 ITD treated  
OCIA1M3 ITD vec  
Mv1 treated  
Mv2 treated  
OCIA1M3 550 TGM2-overexp  
OCIA1M3 TRE TGM2  
OCIA1M3 F53 shRNA  
OCIA1M3 F53 vector  
OCIA1M3 p100SSAA  
Mv1-11  
Mv2-11  
Mv4-11 IBH1 R132H  
Mv4-11 wt(vector)  
GM00131 treated  
M00m13 F53 KD  
M00m13 F53 vector  
M00m14  
M00m14 (AML-ML2)  
Mv1-1  
Mv2-1 treated  
KCG-1 treated  
Leko-1  
BS2-11 treated  
HFB0  
HFB0-1  
HFB0-1 TRE TGM2  
HFB0-1 treated TGM2 control  
HFB0-1  
Mv2-80  
Mv2-80 treated  
Mv2 treated  
TAC ichikawa  
Daudi  
Daudi treated  
OCIA1M3 Bcl2 overexpression  
OCIA1M3 Bcl2 vector  
OCIA1M3 treated  
XBVIS treated  
XBVIS STI w/STI  
XBVIS STI treated w/o STI  
XBVIS STI w/o STI  
XBVIS STI w/o STI  
R01116  
Barmos  
VNO8226  
kasumi-1  
kasumi-1  
kasumi-1 treated  
Mv1e  
V1e  
OCIA1M5 PLKO CTGF  
OCIA1M5 PLKO-NS-shRNA(control)  
Mv1-1 treated  
Mv1-13 treated  
Mv1-13 treated  
Nalm6 treated  
Nalm6 treated  
U937  
U937  
XBM3  
XBM3-K1 (label:KOPTI) (Teresa label: KOPTI ALL)  
OCIA1-1  
KCG-1  
Jurkat 19.2 Caspase8 mut  
Jurkat  
Jurkat treated  
OCIA1-1 CEM  
M013  
M013  
M014

**Table S1. Antibody nomenclature table.** This table consists of five parts with the first being a protein name “Rosetta Stone” showing the HUGO, MiMI and the RPPA modified HUGO protein name abbreviation, the full protein name, the PTM site and consequence. The second part lists the manufacturer of each antibody along with their antibody name, catalog number, and the primary and secondary antibody concentrations utilized. The third section lists which protein functional group each antibody was assigned to. The fourth section records the p-values (corrected for multiple testing to control the FDR at 5%) and effect sizes for the comparison of sample sources (i.e. blood vs. marrow). The last section indicates the p-values (two-sided t-test, corrected for multiple testing to control the FDR at 5%) and effect sizes for the comparison of processing procedures (i.e. cryopreserved vs. fresh). Last two columns: Blood (n = 282) vs. Marrow (n = 387); Cryo (n = 377) vs. Fresh (n = 292).

Protein Name Rosetta Stone					RPPA Staining Details						Functional Category	Blood vs. Marrow		Cryo vs. Fresh	
RPPA Antibody Name	Huge Name (added with PTMs)	MiMI Name	Full Name/Description from GeneCards	Functional Effect of Phosphorylation	Common Name Mfg Claimed Target	Manufacturer	Catalog#	Anti-body Source	Anti-body Dilution	2nd Ab dilution	Functional Group	p-value	Cohen's d	p-value	Cohen's d
ACTB	ACTB	ACTB	Actin Beta		Actin(β)	Sigma	A5441	mouse	2000	20000	cytoskeletal	0.0964	0.129	0.0000	0.796
AIFM1	AIFM1	AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1		AIF	Santa Cruz	sc-13116	mouse	250		ApopReg	0.6740	0.033	0.0000	0.595
AKT1	AKT1	AKT1	v-akt murine thymoma viral oncogene homolog 1		AKT1	Cell Signaling	9272	Rabbit	150	15000	pi3kakt	0.3743	-0.069	0.0000	-0.817
AKT1_2_3.pS473	AKT1/AKT2/AKT3-phosphoser473	AKT1	v-akt murine thymoma viral oncogene homolog 1	Activation	AKT-P473(Ser)	Cell Signaling	9271	Rabbit	50	15000	pi3kakt	0.3823	-0.068	0.0000	-0.624
AKT1_2_3.pT308	AKT1/AKT2/AKT3-phosphoThr308	AKT1	v-akt murine thymoma viral oncogene homolog 1	Activation	AKT-P308(Thr)	Cell Signaling	9275	Rabbit	50	15000	pi3kakt	0.8142	0.018	0.0000	0.912
ASH2L	ASH2L	ASH2L	ash2 (absent, small, or homeotic)-like (Drosophila)		Ash2L	Cell Signaling	5019	Rabbit	5000	15000	histone	0.6513	-0.035	0.0000	-1.016
ASNS	ASNS	ASNS	asparagine synthetase (glutamine-hydrolyzing)		ASNS	Sigma	HPA029318	Rabbit	500	15000	metabolic	0.5779	0.043	0.0000	-0.395
ATF3	ATF3	ATF3	activating transcription factor 3		ATF3	Abcam	ab87213	Rabbit	500	15000	autophagy, creb	0.4265	0.061	0.0017	0.234
ATG7	ATG7	ATG7	autophagy related 7		ATG7	Cell Signaling	8558	Rabbit	500	15000	autophagy	0.5886	-0.042	0.0002	-0.292
BAD	BAD	BAD	BCL2-associated agonist of cell death		Bad	Cell Signaling	9292	Rabbit	100	15000	BH3	0.1154	0.124	0.0000	-0.390
BAD_pS112	BAD-phospho Ser112	BAD	BCL2-associated agonist of cell death	Inactivation	Bad-p112(Ser)	Cell Signaling	9291	Rabbit	100	15000	BH3	0.1662	-0.107	0.6886	0.030
BAD_pS136	BAD-phospho Ser136	BAD	BCL2-associated agonist of cell death	Inactivation	Bad-p136(Ser)	Cell Signaling	9295	Rabbit	50	15000	BH3	0.6238	0.037	0.0000	-0.558
BAD_pS155	BAD-phospho Ser155	BAD	BCL2-associated agonist of cell death	Inactivation	Bad-p155(Ser)	Cell Signaling	9297	Rabbit	100	15000	BH3	0.4066	-0.066	0.7822	0.022
BAK1	BAK1	BAK1	BCL2-antagonist/killer 1		Bak	Cell Signaling	3792	Rabbit	50	15000	BH3	0.6487	0.035	0.0000	1.122
BAX	BAX	BAX	BCL2-associated X protein		Bax	Cell Signaling	2772	Rabbit	100	15000	BH3	0.1208	-0.122	0.5601	0.045
BCL2	BCL2	BCL2	B-cell CLL/lymphoma 2		Bcl2	DAKO	M0887	mouse	200	15000	BH3	0.6868	-0.032	0.0000	0.478
BCL2L1	BCL2L1	BCL2L1	BCL2-like 1		Bcl-XL	Cell Signaling	2762	Rabbit	500	20000	BH3	0.0992	0.131	0.0000	0.869

BCL2L11	BCL2L11	BCL2L11	BCL2-like 11 (apoptosis facilitator)		Bim	Epitomics	1036-1	Rabbit	200	15000	BH3	0.6561	-0.035	0.0000	1.095
BECN1	BECN1	BECN1	beclin 1, autophagy related		Beclin-1	Cell Signaling	3738	Rabbit	500	15000	autophagy	0.0336	-0.165	0.0268	-0.164
BID	BID	BID	BH3 interacting domain death agonist		Bid	Cell Signaling	2002	Rabbit	250	15000	BH3	0.2264	-0.094	0.0563	-0.145
BIRC2	BIRC2	BIRC2	baculoviral IAP repeat containing 2		CIAP-1	Upstate	07-759	Rabbit	200	15000	IAP	0.7987	-0.020	0.0000	0.350
BIRC5	BIRC5	BIRC5	baculoviral IAP repeat containing 5		Survivin	Cell Signaling	2802	Rabbit	50	15000	IAP	0.0003	-0.285	0.3249	-0.077
BMI1	BMI1	BMI1	<i>BMI1</i> polycomb ring finger oncogene		Bmi-1	Cell Signaling	2830	Rabbit	150	15000	histone	0.7572	0.024	0.0000	0.668
BRAF	BRAF	BRAF	v-raf murine sarcoma viral oncogene homolog B		Raf-B	Santa Cruz	sc5284	mouse	100	15000	mek	0.7902	-0.021	0.0000	-1.098
BRD4	BRD4	BRD4			BRD4	Epitomics	5716-1	Rabbit	250	15000	histone	0.3519	-0.073	0.0048	-0.224
CASP3	CASP3	CASP3	caspase 3, apoptosis-related cysteine peptidase		caspase 3	Cell Signaling	9662	Rabbit	250	15000	ApopOccur	0.5420	-0.048	0.0000	-0.989
CASP3.c1175	CASP3 cleaved	CASP3	caspase 3, apoptosis-related cysteine peptidase		Caspase 3 cleaved Asp175	Cell Signaling	9661	Rabbit	100	15000	ApopOccur	0.8579	0.014	0.0039	-0.230
CASP7.c1198	CASP7 cleaved Asp198	CASP7	caspase 7, apoptosis-related cysteine peptidase		Caspase 7 cleaved Asp198	Cell Signaling	9491	Rabbit	250	15000	ApopOccur	0.3148	0.079	0.0001	0.323
CASP8	CASP8	CASP8	caspase 8, apoptosis-related cysteine peptidase		Caspase 8	Cell Signaling	9746	mouse	250	15000	ApopOccur	0.2870	0.084	0.2364	0.089
CASP9.c1315	CASP9 cleaved Asp315	CASP9	caspase 9, apoptosis-related cysteine peptidase		Caspase 9 cleaved Asp315	Cell Signaling	9505	Rabbit	250	15000	ApopOccur	0.8805	-0.012	0.4320	0.062
CASP9.c1330	CASP9 cleaved Asp330	CASP9	caspase 9, apoptosis-related cysteine peptidase		Caspase 9 cleaved Asp330	Cell Signaling	9501	Rabbit	250	15000	ApopOccur	0.5689	0.045	0.0000	0.873
CAV1	CAV1	CAV1	caveolin 1, caveolae protein, 22kDa		Caveolin-1	Cell Signaling	3238	Rabbit	100	15000	adhesion	0.9300	-0.007	0.6507	-0.036
CBL	CBL	CBL	<i>Cbl</i> proto-oncogene, E3 ubiquitin protein ligase		Cbl-c	BD sciences	610441	mouse	1000	15000	ubiquitin	0.3865	-0.068	0.0000	1.023
CCNB1	CCNB1	CCNB1	cyclin B1		Cyclin B1	Santa Cruz	SC245	mouse	100	15000	celcycle	0.0167	-0.185	0.0000	0.626
CCND1	CCND1	CCND1	cyclin D1		Cyclin D1(M-20)	Santa Cruz	sc718	Rabbit	500	15000	celcycle	0.4544	-0.058	0.0000	0.558
CCND3	CCND3	CCND3	cyclin D3		Cyclin D3	Cell Signaling	2936	mouse	100	15000	celcycle	0.4060	-0.064	0.0000	-0.400
CCNE1	CCNE1	CCNE1	cyclin E1		Cyclin E	Santa Cruz	sc-247	Rabbit	100	15000	celcycle	0.3551	-0.072	0.0559	0.150
CCNE2	CCNE2	CCNE2	cyclin E2		Cyclin E2	Cell Signaling	1142	Rabbit	250	15000	celcycle	0.6465	-0.036	0.0000	-0.491
CD44	CD44	CD44	<i>CD44</i> molecule (Indian blood group)		CD44.Epi	Epitomics	1998-1	Rabbit	2000	15000	adhesion	0.7581	0.025	0.0000	0.877
CD74	CD74	CD74	<i>CD74</i> molecule, major histocompatibility complex, class II invariant chain		CD74	Santa Cruz	sc-6262	mouse	300	15000	tcell	0.3866	-0.068	0.0000	0.451
CDK1	CDK1	CDC2	cyclin-dependent kinase 1		CDC2	calbiochem	cc01	mouse	200	15000	celcycle	0.2448	-0.090	0.0000	-0.416
CDK2	CDK2	CDK2	cyclin-dependent kinase 2		CDK2	Santa Cruz	SC6248		200	15000	celcycle	0.8857	0.011	0.0000	-0.631
CDK4	CDK4	CDK4	cyclin-dependent kinase 4		CDK4	Cell Signaling	2906	mouse	200	15000	celcycle	0.7873	-0.021	0.0000	-0.517
CDKN1A	CDKN1A	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)		P21/Waf	Cell Signaling	2946	mouse	250	10000	celcycle	0.9823	0.002	0.0000	0.982
CDKN1B	CDKN1B	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)		P27	Santa Cruz	sc-528	Rabbit	250	15000	celcycle	0.7480	-0.025	0.0130	0.201
CDKN1B.pS10	CDKN1B PhosphoSer10	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	Apoptosis altered	P27ps10	Epitomics	2187-1	Rabbit	500	15000	celcycle	0.0100	0.203	0.0000	0.483
CDKN2A	CDKN2A	CDKN2A	cyclin-dependent kinase inhibitor 2A		P16	santa Cruz	sc468	Rabbit	5000	15000	celcycle	0.1593	0.110	0.0000	0.726

CLPP	CLPP	CLPP	caseinolytic mitochondrial matrix peptidase proteolytic subunit		CLPP	Abcam	124822	Rabbit	1000	15000	histone	0.5881	-0.043	0.0000	0.822
COPS5	COPS5	COPS5	COP9 signalosome subunit 5		JAB1	Santa Cruz	sc-13157	mouse	300	15000	ubiquitin	0.0333	0.166	0.0000	-1.139
CREB1	CREB1	CREB1	cAMP responsive element binding protein 1		CREB	Epitomics	1496-1	Rabbit	2000	15000	creb	0.4912	-0.056	0.0008	0.251
CREB1.pS133	CREB2 phospho Ser133	CREB1	cAMP responsive element binding protein 1	Activation	CREB-p(ser133)	Epitomics	1113-1	Rabbit	2000	15000	creb	0.4939	-0.054	0.0104	-0.203
CTNNA1	CTNNA1	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa		Catenin-alpha	calbiochem	CA1030	mouse	75	15000	wnt	0.9015	0.010	0.0076	0.209
CTNNB1	CTNNB1	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa		Catenin-beta	Cell Signaling	9562	Rabbit	50	15000	wnt	0.0009	-0.256	0.0431	0.159
CTNNB1.pS33_37_41	CTNNB1-phospho Ser33/37/Thr41	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	Leads to degradation	catenin-beta phospho-	Cell Signaling	9561	Rabbit	500	15000	wnt	0.5061	0.053	0.0877	0.128
CTSG	CTSG	CTSG	cathepsin G		CTSG	Abcam	ab8816	sheep	500	30000	adhesion	0.0144	-0.190	0.0000	0.962
DIABLO	DIABLO	DIABLO	<i>blo</i> , IAP-binding mitochondrial protein		Smac/Diablo	Cell Signaling	2954	mouse	500	15000	IAP	0.7975	-0.020	0.0000	0.641
DLX1	DLX1	DLX1	distal-less homeobox 1		DLX1	Abnova	H00001745-M01	mouse	1000	15000	transcription	0.5635	0.045	0.0001	-0.304
DUSP6	DUSP6	DUSP6	dual specificity phosphatase 6		DUSP6	abcam	ab76310	Rabbit	3000	15000	mek	0.1256	0.120	0.1900	0.104
EGFR	EGFR	EGFR	Epidermal growth factor receptor		EGFR	Santa Cruz	sc-03	Rabbit	500	20000	mtor, STP	0.9740	-0.003	0.0000	0.491
EGFR.pY992	EGFR-phospho Tyr992	EGFR	Epidermal growth factor receptor	Activation	EGFR-p tyr992	Cell Signaling	2235	Rabbit	50	15000	mtor	0.1042	0.129	0.0000	0.352
EGLN1	EGLN1	EGLN1	egl-9 family hypoxia-inducible factor 1		EglN1	Millipore	05-1327	mouse	500	5000	hypoxia	0.0799	0.139	0.0000	-0.423
EIF2AK2	EIF2AK2	EIF2AK2	ryotic translation initiation factor 2-alpha kinase 2		PRKR(EIF2AK2)	Abnova	H00005610-M02	mouse	5000	15000	transcription	0.4336	0.061	0.0000	-1.329
EIF2AK2.pT451	EIF2AK2.phospho Thr 451	EIF2AK2	ryotic translation initiation factor 2-alpha kinase 2	Activation	PRKRpTh451(EIF2AK2)	invitrogen	44-668G	Rabbit	1500	15000	transcription	0.8923	0.010	0.0000	0.434
EIF2S1	EIF2S1	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa		eIF2	Cell Signaling	9722	Rabbit	3000	15000	transcription	0.9015	-0.010	0.0000	-1.628
EIF2S1.pS51	EIF2S1-phospho Ser51	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	Stabalizes	phospho-eIF2-alpha	Cell Signaling	9721	Rabbit	250	15000	transcription	0.4258	-0.062	0.0000	-0.912
EIF4E	EIF4E	EIF4E	otic translation initiation factor 4E		eIF4E	Cell Signaling	9742	Rabbit	200	15000	transcription	0.7838	-0.021	0.0000	-1.736
EIF4EBP1	EIF4EBP1	EIF4EBP1	proliferation-associated 2G4, 38kDa		EBP1	Cell Signaling	9452	Rabbit	500	15000	s6rp	0.2127	-0.097	0.0000	-1.790
EIF4EBP1.pS65	EIF4EBP1.phospho Ser S65	EIF4EBP1	proliferation-associated 2G4, 38kDa	Inactivation	EBP1.pser65	Cell Signaling	9456	Rabbit	400	15000	s6rp	0.0570	-0.147	0.0000	-1.224
EIF4EBP1.pT37_46	EIF4EBP1.phospho Thr T37 & 46	EIF4EBP1	proliferation-associated 2G4, 38kDa	Inactivation	EBP1.pthr37_46	Cell Signaling	9459	Rabbit	1000	15000	s6rp	0.0137	-0.193	0.0000	-1.028
EIF4EBP1.pT70	EIF4EBP1.phospho Thr T70	EIF4EBP1	proliferation-associated 2G4, 38kDa	Inactivation	EBP1.pthr70	Cell Signaling	9455	Rabbit	200	15000	s6rp	0.0000	-0.328	0.0000	-1.569
ELK1.pS383	ELK1-phospho Ser383	ELK1	<i>ELK1</i> , member of ETS oncogene family	Activation	EIK(phospho-ser383)	Cell Signaling	9181	Rabbit	100	15000	mek, pi3kakt	0.0853	-0.136	0.0002	-0.287
ERBB2	ERBB2	ERBB2	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2		HER2/Erb2	Cell Signaling	2242	Rabbit	250	15000	STP	0.1443	0.116	0.0030	0.237
ERBB2.pY1248	ERBB2-phospho Tyr1248	ERBB2	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2	Activation	HER2(p-Tyr1248)	Upstate	06-229	Rabbit	1500	15000	STP	0.5560	0.046	0.0003	-0.287
ERBB3	ERBB3	ERBB3	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3		HER3	Upstate	05-390	mouse	500	15000	STP	0.2394	0.093	0.0002	0.288



ERG	ERG	EGR1	early growth response 1		ERG1/2/3	Santa Cruz	sc-353	Rabbit	1000	15000	transcription	0.9473	-0.005	0.0000	-1.146
FLI1	Fli1	FLI1	Fli-1 proto-oncogene, ETS transcription factor		Fli	Dennis Watson		Rabbit	2000	15000	fli1, histone	0.7253	0.028	0.0000	-0.763
FN1	FN1	FN1	fibronectin 1		Fibronectin	Epitomics	1574	Rabbit	30000	15000	adhesion	0.0000	-0.373	0.0000	1.249
FOXO1.pT24_FOXO3.pT32	FOXO1-phospho thr24/FOXO3-phospho thr32	FOXO1	forkhead box O1	Inactivation	FoxO1a/3a	Cell Signaling	9464	Rabbit	500	15000	cellcycle, pi3kakt	0.2335	0.094	0.1729	0.110
FOXO3	FOXO3	FOXO3	forkhead box O3		FoxO3a	Cell Signaling	9467	Rabbit	500	20000	cellcycle, pi3kakt	0.1311	-0.118	0.0000	1.537
FOXO3.S318_321	FOXO3-phospho Ser318/321	FOXO3	forkhead box O3	Inactivation	FKHRL1/FoxO3a (P-Ser 318/321)	Cell Signaling	9465	Rabbit	10000	15000	cellcycle, pi3kakt	0.0987	0.131	0.5286	0.049
GAB2	GAB2	GAB2	GRB2-associated binding protein 2		Gab2	Cell Signaling	3239	Rabbit	500	15000	pi3kakt	0.6883	-0.032	0.0000	-0.912
GAB2.pY452	GAB2-phospho Tyr452	GAB2	GRB2-associated binding protein 2	Tyr452 is a potential binding site of p85, the regulatory subunit of PI3 kinase.	Gab2-pTyr452	Cell Signaling	3882	Rabbit	100	15000	pi3kakt	0.8325	0.017	0.0000	-0.832
GAPDH	GAPDH	GAPDH	glyceraldehyde-3-phosphate dehydrogenase		GAPDH	Cell Signaling	4300	mouse	2000	15000	metabolic	0.1393	0.115	0.0000	-1.365
GATA1	GATA1	GATA1	GATA binding protein 1 (globin transcription factor 1)		GATA-1	Cell Signaling	3535	Rabbit	1000	15000	differentiation, transcription	0.0000	-0.513	0.4038	0.064
GATA3	GATA3	GATA3	GATA binding protein 3		Gata3	BD bioscience	558686	mouse	500	15000	differentiation, transcription	0.1692	0.107	0.0000	1.910
GSKA_B	GSKA/GSKB	GSK3A	glycogen synthase kinase 3 alpha		GSK3	santa Cruz	sc-7291	mouse	200	15000	autophagy, pi3kakt	0.0922	0.133	0.0000	-1.793
GSKA_B.pS21_9	GSKA/GSKB-phospho Ser21/9	GSK3A	glycogen synthase kinase 3 alpha	Inactivation	GSK3a/B(p-ser21/9)	Cell Signaling	9331	Rabbit	200	15000	autophagy, pi3kakt	0.1380	-0.115	0.0000	-0.348
H3histone	HIST3H3	HIST3H3	histone cluster 3, H3		H3histone	active motif	39163	Rabbit	1500000	40000	histone	0.8604	0.014	0.0000	1.050
H3K27Me3	HIST3H3-K27-Me3	HIST3H3	histone cluster 3, H3, Lysine 27 methylation 3	Repression	H3K27Me3	active motif	61017	mouse	3000	40000	histone	0.0660	0.147	0.0000	1.037
H3K4Me2	HIST3H3-K4-Me2	HIST3H3	histone cluster 3, H3, Lysine 4 methylation 2	Repression	H3K4Me2	active motif	39141	Rabbit	8000	20000	histone	0.2023	0.102	0.0000	1.043
H3K4Me3	HIST3H3-K4-Me3	HIST3H3	histone cluster 3, H3, Lysine 4 methylation 3	Repression	H3K4Me3	active motif	39159	Rabbit	7000	20000	histone	0.7350	0.027	0.0000	0.995
HDAC1	HDAC1	HDAC1	histone deacetylase 1		HDAC1	Imgenex	IM-337	Rabbit	400	20000	histone	0.1937	0.100	0.0345	-0.165
HDAC2	HDAC2	HDAC2	histone deacetylase 2		HDAC2	Santa Cruz	sc-7899	Rabbit	1000	15000	histone	0.6995	0.030	0.0000	-0.565
HDAC3	HDAC3	HDAC3	histone deacetylase 3		HDAC3	Cell Signaling	2632	Rabbit	100	15000	histone	0.2363	0.091	0.0297	0.161
HIF1A	HIF1A	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)		HIF-1a	BD pharmingen	610959	mouse	50	15000	hypoxia	0.3670	0.069	0.0000	-0.388
HNRNPK	HNRNPK	HNRNPK	rogenous nuclear ribonucleoprotein K		hnRNPk	Santa Cruz	sc-28380	mouse	5000	15000	histone	0.4864	-0.054	0.0000	-1.146
HSP90AA1_B1	HSP90AA1/HSP90AB1	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1		HSP90	Cell Signaling	4875	Rabbit	500	15000	heatshock	0.1229	-0.118	0.0000	-1.282
HSPA1A_L	HSPA1A/HSPA1L	HSPA1A	heat shock 70kDa protein 1A		HSP70	Cell Signaling	4872	Rabbit	250	15000	heatshock	0.1369	0.118	0.1743	0.108
HSPB1	HSPB1	HSPB1	heat shock 27kDa protein 1		HSP27	Cell Signaling	2402	mouse	100	15000	heatshock	0.7967	0.020	0.0000	0.581
IGF1R	IGF1R	IGF1R	insulin-like growth factor 1 receptor		IGF-1 receptor beta	Cell Signaling	3027	Rabbit	1000	15000	STP	0.9536	-0.005	0.9688	0.003

IGFBP2	IGFBP2	IGFBP2	insulin-like growth factor binding protein 2, 36kDa		IGFBP-2	Cell Signaling	3922	Rabbit	250	15000	adhesion	0.6565	-0.035	0.0000	0.883
INPP5D	INPP5D	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa		SHIP1	Santa Cruz	SC-8425	mouse	250	15000	mtor	0.7708	-0.022	0.0000	-0.749
INPPL1	INPPL1	INPPL1	inositol polyphosphate phosphatase-like 1		SHIP2	Cell Signaling	2730	Rabbit	300	15000	mtor	0.5815	-0.043	0.0001	-0.303
IRS1_pS1101	IRS1-phosphoser1101	IRS1	insulin receptor substrate 1	Inhibition	IRS-1-p(ser1101)	Cell Signaling	2385	Rabbit	250	15000	mtor, tp53	0.1163	-0.120	0.0000	0.347
ITGA2	ITGA2	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)		CD49b	BD Transduction Lab	611016	mouse	500	15000	adhesion	0.5572	0.045	0.0000	1.619
ITGAL	ITGAL	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)		CD11a	BD Transduction Lab	610826	mouse	500	15000	adhesion	0.5836	-0.043	0.0000	1.789
ITGB3	ITGB3	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)		Integrin-beta3	Cell Signaling	4702	Rabbit	250	15000	adhesion	0.5481	0.047	0.0000	1.517
JMJD6	JMJD6	JMJD6	jumonji domain containing 6		JMJD6	Abcam	ab50720	Rabbit	1000	20000	histone	0.5229	0.049	0.0000	0.708
JUN_pS73	JUN-phosphoser73	JUN	jun proto-oncogene	Activation	Jun-C-phosphoser73	Cell Signaling	9164	Rabbit	100	10000	transcription	0.1456	0.114	0.0000	-0.989
JUNB	JUNB	JUNB	jun B proto-oncogene		Jun-B	Cell Signaling	3755	Rabbit	100	15000	transcription	0.0460	0.160	0.0034	0.229
KDM1A	KDM1A	KDM1A	lysine (K)-specific demethylase 1A		LSD1	Cell Signaling	2184	Rabbit	3000	15000	histone	0.1172	-0.123	0.0000	-1.114
KDR	KDR	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)		VEGFR2	Cell Signaling	2479	Rabbit	700	15000	hypoxia	0.0865	0.134	0.0140	-0.194
KIT	KIT	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog		Kit-C	Epitomics	1522	Rabbit	1000	15000	mek, STP	0.0007	-0.260	0.0000	-0.601
LCK	LCK	LCK	lymphocyte-specific protein tyrosine kinase		Lck	Cell Signaling	2752	Rabbit	50	15000	tccl	0.0550	0.151	0.0000	2.029
LEF1	LEF1	LEF1	lymphoid enhancer-binding factor 1		LEF1	Cell Signaling	2230	Rabbit	1000	15000	wnt	0.0036	0.232	0.0000	0.654
LGALS3	LGALS3	LGALS3	lectin, galactoside-binding, soluble, 3		Galectin-3	Santa Cruz	sc-32790	mouse	250	15000	tccl	0.1909	0.103	0.0000	0.401
LYN	LYN	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog		Lyn	Cell Signaling	2732	Rabbit	250	15000	mek, STP	0.1827	0.106	0.0000	0.925
MAP2K1	MAP2K1	MAP2K1	mitogen-activated protein kinase kinase 1		MEK	Cell Signaling	9122	Rabbit	2000	10000	mapk	0.7990	-0.020	0.9237	-0.007
MAP2K1_2_pS217_221	MAP2K1/MAP2K2-phosphoser217/221	MAP2K1	mitogen-activated protein kinase kinase 1	Activation	MEK(p-ser217/221)	Cell Signaling	9121	Rabbit	1000	15000	mapk	0.3554	0.073	0.0000	0.352
MAPK1	MAPK1	MAPK1	mitogen-activated protein kinase 1		Erk2	Santa Cruz	Sc-154	Rabbit	2000	15000	mapk	0.1481	0.113	0.0015	-0.240
MAPK1_3_pT202Y204	MAPK1/MAPK3-phosphoThr202/Tyr204	MAPK1	mitogen-activated protein kinase 1	Activation	Erk-p42/44(Thr202/Tyr204)	Cell Signaling	9101	Rabbit	400	15000	mapk	0.5190	0.051	0.0000	0.518
MAPK14	MAPK14	MAPK14	mitogen-activated protein kinase 14		P38	Cell Signaling	9212	Rabbit	200		mapk	0.2260	-0.095	0.0000	-0.815
MAPK14_pT180Y182	MAPK14-p180p182	MAPK14	mitogen-activated protein kinase 14	Activation	P38p180p182	Cell Signaling	9211	Rabbit	10	15000	mapk	0.2214	-0.096	0.2806	-0.084
MAPK9	MAPK9	MAPK9	mitogen-activated protein kinase 9		JNK2	Cell Signaling	4672	Rabbit	25	15000	mapk, stat	0.4195	-0.064	0.0000	-1.098
MAPT	MAPT	MAPT	microtubule-associated protein tau		Tau	Upstate	05-348	mouse	150	15000	cytoskeletal	0.2708	0.088	0.0000	-0.541
MCL1	MCL1	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)		MCL1	BD pharmingen	559027	mouse	50	15000	BH3	0.0999	0.125	0.0000	0.628
MDM2	MDM2	MDM2	MDM2 oncogene, E3 ubiquitin protein ligase		MDM2	Santa Cruz	sc813	Rabbit	5000	15000	tp53	0.4832	-0.056	0.0000	0.740

MDM4	MDM4	MDM4	<i>Mdm4</i> p53 binding protein homolog (mouse)		MDM4	Bethly lab	A300-287A	Rabbit	5000	15000	tp53	0.0621	0.146	0.1703	0.106
MET_pY1230_1234_1235	MET-phospho Py1230/1234/1235	MET	<i>met</i> proto-oncogene	Activation	C-Met-pTyr 1230/1234/1235	Biosource	44-888G	Rabbit	250	20000	STP	0.0123	-0.193	0.0000	0.488
MTOR	MTOR	FRAP1	mechanistic target of rapamycin (serine/threonine kinase)		mTor	Cell Signaling	2983	Rabbit	200	10000	mtor	0.5073	0.117	0.0000	0.158
MTOR.pS2448	MTOR-phospho Ser2448	FRAP1	mechanistic target of rapamycin (serine/threonine kinase)	Activation	mTor(p-Ser2448)	Cell Signaling	2971	Rabbit	100	15000	mtor	0.0395	0.052	0.0000	-0.548
MYC	MYC	MYC	<i>v-myc</i> avian myelocytomatosis viral oncogene homolog		Myc	Cell Signaling	9402	Rabbit	100	15000	celcycle, transcription	0.0076	-0.161	0.0000	0.569
NCL	NCL	NCL	nucleolin		C23 (nucleolin)	Santa Cruz	sc8031	mouse	200	15000	flil, histone	0.7710	-0.205	0.0000	-0.382
NF2	NF2	NF2	neurofibromin 2 (merlin)		NF2	Santa Cruz	sc332	Rabbit	500	15000	cytoskeletal, hippo	0.0028	0.023	0.5829	-1.327
NF2.pS518	NF2-phospho ser518	NF2	neurofibromin 2 (merlin)	Inactivation	pNF2(ser518)	chemicon	AB5607	Rabbit	500	15000	cytoskeletal, hippo	0.0889	-0.234	0.0000	-0.043
NOL3	ARC	ARC	activity-regulated cytoskeleton-associated protein		ARC	Imgenex	IMG-171	Rabbit	2000	15000	ApopReg,BH3	0.6040	0.135	0.0059	0.365
NOTCH1.c11744	NOTCH1 cleaved val11744	NOTCH1	notch 1	Activation	Notch1-cleaved (Val11744)	Cell Signaling	4147	Rabbit	400	15000	tcell	0.0000	-0.041	0.8618	0.217
NOTCH3	NOTCH3	NOTCH3	notch 3		Notch3	santa Cruz	sc5593	Rabbit	200	15000	tcell	0.2132	0.332	0.0000	0.014
NPM1	NPM1	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)		NPM	invitrogen	32-5200	mouse	10000	15000	histone	0.6235	-0.093	0.1202	0.597
NPM1.3542	NPM1mut AA3542	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)		NPM1.3542	Cell Signaling	3542	Rabbit	1000	15000	flil	0.1976	-0.038	0.0000	-0.122
NR4A1	NR4A1	NR4A1	nuclear receptor subfamily 4, group A, member 1		Nur77	Imgenex	IMG-528	Rabbit	200	15000	transcription	0.7442	-0.100	0.0000	-0.935
NRP1	NRP1	NRP1	neuropilin 1		NRP1(neuropilin)	Santa Cruz	SC-5307	mouse	10	20000	cytoskeletal	0.0121	0.025	0.0000	-0.909
ODC1	ODC1	ODC1	ornithine decarboxylase 1		ODC	Shantz/Lisa Lab			500	15000	metabolic	0.0773	0.201	0.0000	0.344
PARK7	PARK7	PARK7	parkinson protein 7		DJ-1	Private-Andreeff		Rabbit	500	15000	autophagy	0.1003	-0.135	0.0000	1.023
PARP1	PARP1	PARP1	poly (ADP-ribose) polymerase 1		PARP	Cell Signaling	9542	Rabbit	200	15000	ApopOccur	0.2141	0.130	0.0000	-1.579
PARP1.c1214	PARP1-cleaved Asp 214	PARP1	poly (ADP-ribose) polymerase 1	Activation	PARP(cleaved Asp214)	Cell Signaling	9541	Rabbit	100	15000	ApopOccur	0.3728	0.096	0.2080	-0.488
PDK1	PDK1	PDK1	pyruvate dehydrogenase kinase, isozyme 1		PDK1	Cell Signaling	3062	Rabbit	200	15000	mtor	0.4773	0.069	0.0016	0.099
PDK1.pS241	PDK1-phospho ser241	PDK1	pyruvate dehydrogenase kinase, isozyme 1	Activation	PDK1-p241(Ser)	Cell Signaling	3061	Rabbit	500	15000	mtor	0.7411	0.056	0.5279	0.243
PIK3CA	PIK3CA	PIK3CA	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha		PI3 K p110-alpha	Epitomics	1683-1	Rabbit	200	15000	mtor	0.3452	0.026	0.0000	-0.050
PIK3R1_2	PIK3R1/PIK3R2	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)		PI3 K p85	Cell Signaling	4292	Rabbit	20	15000	mtor	0.0674	0.074	0.0000	0.749
PIM1	PIM1	PIM1	pim-1 oncogene		PIM1	Santa Cruz	sc-13153	mouse	100	15000	differentiation	0.0576	-0.137	0.0065	-0.305
PIM2	PIM2	PIM2	pim-2 oncogene		PIM2	Cell Signaling	4730	Rabbit	200	15000	differentiation	0.0107	0.145	0.0000	-0.211
PPARA	PPARA	PPARA	peroxisome proliferator-activated receptor alpha		PPARA	boster Bio	PA1412	Rabbit	0.5ug/ul	30000	metabolic	0.7654	0.197	0.0000	0.396
PPARG	PPARG	PPARG	peroxisome proliferator-activated receptor gamma		PPARγ	Santa Cruz	sc7273	mouse	75	15000	differentiation	0.1336	0.126	0.6570	0.985

PPP2R2A_B_C_D	PPP2R2D/PPP2R2A/PPP2R2B/PPP2R2C	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4		PP2A-B55	Santa Cruz	sc-18330	goat	500	15000	STP	0.5336	-0.023	0.0000	0.531
PRKAA1_2	PRKAA1/PRKAA2	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit		AMPK $\alpha$	cell signaling	2532	Rabbit	200	15000	autophagy	0.2778	0.116	0.0000	0.034
PRKAA1_2_pT172	PRKAA1/PRKAA2-phospho Thr172	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	Activation	AMPK $\alpha$ P(Thr172)	cell signaling	2535	Rabbit	200	15000	autophagy	0.3911	-0.047	0.0000	-0.911
PRKCA	PRKCA	PRKCA	protein kinase C, alpha		PKC $\alpha$	Upstate	05-154	mouse	2000	15000	pkc	0.4760	-0.084	0.0000	0.531
PRKCA.pS657	PRKCA-phosphoser657	PRKCA	protein kinase C, alpha	Activation	PKC $\alpha$ -p657(Ser)	Upstate	06-822	Rabbit	1000	20000	pkc	0.1128	-0.067	0.0000	-0.540
PRKCB.I	PRKCB	PRKCB	protein kinase C, beta		PKC $\beta$ I	Santa Cruz	sc8049	mouse	300	20000	pkc	0.3429	0.056	0.0520	1.239
PRKCB.II	PRKCB	PRKCB	protein kinase C, beta		PKC $\beta$ II	Santa Cruz	13149	mouse	200	15000	pkc	0.2902	0.124	0.0000	0.739
PRKCD.pS645	PRKCD-phospho Ser645	PRKCD	protein kinase C, delta		PKC $\delta$ -645(Ser)	Upstate	07-875	Rabbit	200	30000	pkc	0.0277	0.073	0.0000	-0.155
PRKCD.pS664	PRKCD-phospho Ser664	PRKCD	protein kinase C, delta		PKC $\delta$ -p664(Ser)	Upstate	07-874	Rabbit	250	30000	pkc	0.0644	0.082	0.0000	1.445
PRKCD.pT507	PRKCD-phospho Thr507	PRKCD	protein kinase C, delta	Activation	PKC $\delta$ -507(Thr)	Santa Cruz	sc11770	Goat	1000	30000	pkc	0.6354	-0.168	0.0000	0.904
PTEN	PTEN	PTEN	phosphatase and tensin homolog		PTEN	Upstate	07-016	Rabbit	400	15000	mtor	0.5910	0.146	0.0000	0.926
PTEN.pS380T382T383	PTEN	PTEN	phosphatase and tensin homolog	Inactivation	PTEN-p(380/382/383)	Cell Signaling	9554	Rabbit	500	15000	mtor	0.2099	-0.038	0.0000	0.711
PTGS2	PTGS2	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)		cox-2	Epitomics	2169-1	Rabbit	250	15000	metabolic	0.4956	-0.042	0.0000	-0.948
PTK2	PTK2	PTK2	protein tyrosine kinase 2		Fak	Cell Signaling	3285	Rabbit	500	15000	adhesion	0.6867	-0.099	0.0000	-0.961
PTPN11	PTPN11	PTPN11	protein tyrosine phosphatase, non-receptor type 11		SHP-2	Epitomics	1590-1	Rabbit	500	15000	STP	0.0386	0.054	0.0000	0.535
RAC1_2_3	RAC1/RAC2/RAC3	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)		Rac1/2/3	Cell Signaling	2465	Rabbit	500	15000	mek	0.0028	0.031	0.0000	1.237
RB1	RB1	RB1	retinoblastoma 1		Rb	BD PharMingen	554136	mouse	100	15000	cellcycle	0.0527	0.163	0.0000	-1.639
RB1.pS807_811	RB1-phosphoser807/811	RB1	retinoblastoma 1	Inactivation	Rb (P-Ser807/811)	Cell Signaling	9308	Rabbit	250	15000	cellcycle	0.0000	-0.233	0.0000	0.991
RELA	RELA	NFKB1	v-rel avian reticuloendotheliosis viral oncogene homolog A		NF-kB p65	Cell Signaling	3034	Rabbit	500	15000	pkc	0.5268	-0.152	0.0000	-1.006
RPS6	RPS6	RPS6	ribosomal protein S6		S6 Ribosomal protein	Cell Signaling	2217	Rabbit	250	15000	s6rp	0.0003	-0.639	0.0001	-1.611
RPS6.pS235_236	RPS6-phosphoser235/236	RPS6	ribosomal protein S6	Activation	S6 Ribosomal protein(phosphoser235/236)	Cell Signaling	2211	Rabbit	1500-2000	15000	s6rp	0.0000	-0.050	0.0000	0.625
RPS6.pS240_244	RPS6-phosphoser240/244	RPS6	ribosomal protein S6	Activation	S6 Ribosomal protein(phosphoser240/244)	Cell Signaling	2215	Rabbit	750-1000	15000	s6rp	0.3893	-0.281	0.0000	-0.307
RPS6KB1	RPS6KB1	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1		p70S6K	Cell Signaling	9202	Rabbit	250	15000	s6rp	0.0000	-0.501	0.3723	-0.418
RPS6KB1.pT389	RPS6KB1-phospho thr389	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	Activation	p70S6K(p-thr389)	Cell Signaling	9205	Rabbit	250	15000	s6rp	0.0000	-0.069	0.0857	0.727

SFN	SFN	SFN	stratifin		X14.3.3Sigma	Upstate	05-632	mouse	200	15000	tp53	0.7464	-0.357	0.0000	0.070
SIRT1	SIRT1	SIRT1	sirtuin 1		SIRT1	Abcam	ab32441	Rabbit	1000	15000	histone	0.1331	-0.421	0.0000	-0.134
SMAD1	SMAD1	SMAD1	SMAD family member 1		smad1	Epitomics	1649-1	Rabbit	200	15000	smad	0.1681	-0.025	0.0000	-0.519
SMAD2	SMAD2	SMAD2	SMAD family member 2		SMAD2	Cell Signaling	5339	Rabbit	5000	15000	smad	0.6904	-0.117	0.0000	-0.674
SMAD2.pS245	SMAD2.p245	SMAD2	SMAD family member 2	Activation	Smad2-pS245/250/255	Cell Signaling	3104	Rabbit	500	15000	smad	0.7130	0.108	0.0000	-1.214
SMAD2.pS465	SMAD2.pS465	SMAD2	SMAD family member 2	Activation	Smad2-pS465/467	Cell Signaling	3108	Rabbit	1000	15000	smad	0.8132	-0.031	0.0079	-0.811
SMAD3	SMAD3	SMAD3	SMAD family member 3		SMAD3	Cell Signaling	9523	Rabbit	500	15000	smad	0.7179	-0.029	0.0020	-0.953
SMAD4	SMAD4	SMAD4	SMAD family member 4		smad4	Santa Cruz	sc7966	mouse	1000	15000	smad	0.6291	-0.018	0.0000	-0.202
SMAD5	SMAD5	SMAD5	SMAD family member 5		SMAD5	epitomics	1682-1	Rabbit	1000	15000	smad	0.5207	0.028	0.0000	-0.245
SMAD5.pS463	SMAD5pS463	SMAD5	SMAD family member 5	Activation	Smad5-pS463/465	epitomics	2224-1	Rabbit	500	15000	smad	0.6227	-0.038	0.0000	-1.145
SMAD6	SMAD6	SMAD6	SMAD family member 6		Smad6	Cell Signaling	9519	Rabbit	100	15000	smad	0.4579	-0.050	0.0000	-0.938
SOCS2	SOCS2	SOCS2	suppressor of cytokine signaling 2		SOCS2	Abcam	ab92847	Rabbit	200	15000	STP	0.5535	-0.037	0.0002	0.508
SPI1	SPI1	SPI1	spleen focus forming virus (SFFV) proviral integration oncogene		PU.1	Cell Signaling	2258	Rabbit	5000	15000	transcription	0.0677	0.056	0.0049	0.309
SPP1	SPP1	SPP1	secreted phosphoprotein 1		Osteopontin	Santa Cruz	sc-21742	mouse	500	15000	adhesion	0.9421	0.045	0.0075	-0.274
SQSTM1	SQSTM1	SQSTM1	sequestosome 1		P62	Santa Cruz	sc-28359	mouse	250	15000	autophagy	0.6072	-0.146	0.0000	-0.217
SRC	SRC	SRC	v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog		Src	Upstate	05-184	mouse	600	15000	src	0.1605	-0.006	0.0000	0.205
SRC.pY416	SRC-phosphoty416	SRC	v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog	Activation	Src(phosphoty416)	Cell Signaling	2101	Rabbit	400	15000	src	0.5570	0.040	0.0000	-0.442
SRC.pY527	SRC-phosphoty527	SRC	v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog	Inactivation	Src(phosphoty527)	Cell Signaling	2105	Rabbit	100	15000	src	0.2572	0.109	0.0000	1.422
SSBP2	SSBP2	SSBP2	single-stranded DNA binding protein 2		SSBP2-I(alpha)	Private-Nagarajan		Rabbit	1000	15000	differentiation	0.8414	0.045	0.0000	1.948
STAT1	STAT1	STAT1	signal transducer and activator of transcription 1, 91kDa		stat1	Cell Signaling	9172		250	15000	stat	0.8608	0.089	0.0000	1.241
STAT1.pY701	STAT1-phosphoty701	STAT1	signal transducer and activator of transcription 1, 91kDa	Activation	Stat1(phospho-tyr701)	Cell Signaling	9171	Rabbit	100	15000	stat	0.1893	0.016	0.0021	-1.031
STAT3	STAT3	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)		Stat3	Upstate	06-596	Rabbit	50	15000	stat	0.4588	0.014	0.0000	0.767
STAT3.pS727	STAT3-phosphoser727	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	Activation	Stat3-p727(Ser)	Cell Signaling	9134	Rabbit	100	15000	stat	0.7732	0.101	0.2176	0.239
STAT3.pY705	STAT3-phosphoty705	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	Activation	Stat3-p705(Tyr)	Cell Signaling	9131	Rabbit	500	15000	stat	0.1145	0.058	0.0012	-0.433
STAT5A_B	STAT5A/STAT5B	STAT5A	signal transducer and activator of transcription 5A		Stat5	Cell Signaling	9352	Rabbit	250	15000	stat	0.4673	-0.022	0.0000	0.092

STAT5A_B.pY694	STAT5A/STAT5 B phospho Tyr694	STAT5A	signal transducer and activator of transcription 5A	Activation	Stat5(phospho-Tyr694)	Cell Signaling	9351	Rabbit	100	15000	stat	0.1052	0.121	0.0000	0.251
STAT6.pY641	STAT6-phospho tyr641	STAT6	signal transducer and activator of transcription 6, interleukin-4 induced	Activation	Stat6(phospho-tyr641)	Cell Signaling	9361	Rabbit	100	10000	stat	0.9019	0.055	0.0000	-0.642
STK11	STK11	STK11	serine/threonine kinase 11		LKB1/STK11	Cell Signaling	3050	Rabbit	500	15000	autophagy	0.7446	0.127	0.0000	0.622
STMN1	STMN1	STMN1	stathmin 1		Stathmin	epitomics	1972-1	Rabbit	30000	15000	fli1	0.0124	-0.010	0.0000	0.420
TCF4	TCF4	TCF4	transcription factor 4		TCF-4	Santa Cruz	sc8632	goat	400	15000	transcription	0.9364	-0.026	0.0000	-0.803
TGM2	TGM2	TGM2	transglutaminase 2		TG2	Abcam	ab2386	mouse	2000	30000	adhesion	0.5722	-0.193	0.1825	-2.355
TNK1	TNK1	TNK1	tyrosine kinase, non-receptor, 1		TNK1	Agent	AP7722a	Rabbit	400	15000	mek	0.1014	-0.006	0.0004	1.070
TP53	TP53	TP53	tumor protein p53		TP53	Cell Signaling	9282	Rabbit	1000	15000	ApopReg, tp53	0.3966	0.045	0.0050	0.105
TP53.pS15	TP53-pS15	TP53	tumor protein p53	Blocks MDM2 binding	TP53(phospho Ser 15)	Cell Signaling	9284	Rabbit	250	15000	ApopReg, tp53	0.8883	0.131	0.0000	-0.278
TRIM24	TRIM24	TRIM24	tripartite motif containing 24		TRIM24	Novus	NB100-2597	Rabbit	1000	15000	histone, tp53, ubiquitin	0.2333	-0.066	0.0000	-0.219
TRIM62	TRIM62	TRIM62	tripartite motif containing 62		TRIM62	from Dr. Quintas-cardama	DEAR1	mouse	150	15000	ubiquitin	0.5946	-0.011	0.0026	0.471
TSC2	TSC2	TSC2	tuberous sclerosis 2		TSC2	epitomic	1613-1	Rabbit	500	15000	autophagy, mtor	0.2358	0.094	0.0000	-0.642
VASP	VASP	VASP	vasodilator-stimulated phosphoprotein		VASP	Cell Signaling	3112	Rabbit	250	15000	hypoxia	0.1090	0.041	0.0000	-0.224
VHL	VHL	VHL	von Hippel-Lindau tumor suppressor, E3 ubiquitin protein ligase		VHL	Novus	NB100-485	Rabbit	2000	15000	hypoxia	0.5126	-0.092	0.0000	-0.925
WTAP	WTAP	WTAP	Wilms tumor 1 associated protein		WTAP	sanjay bansal	from UTSA	Rabbit	10000	15000	cellcycle, fli1, histone	0.0855	0.126	0.0000	0.847
WWTR1	TAZ	TAZ	WW Domain Containing Transcription Regulator 1/Transcriptional Coactivator With PDZ-Binding Motif		TAZ	Abcam	ab3961	Rabbit	1000	15000	hippo	0.1509	-0.051	0.1403	-1.664
WWTR1.pS89	TAZ-phospho Ser89	TAZ	WW Domain Containing Transcription Regulator 1/Transcriptional Coactivator With PDZ-Binding Motif	Inactivation	TAZ p-Ser89	Santa Cruz	sc17610R	Rabbit	150	15000	hippo	0.0000	-0.138	0.0000	-0.463
XIAP	XIAP	BIRC4	X-linked inhibitor of apoptosis		XIAP	Cell Signaling	2042	Rabbit	100	15000	IAP	0.8860	0.110	0.0000	-0.111
XPO1	XPO1	XPO1	exportin 1 (CRM1 homolog, yeast)		CRM1	Santa Cruz	sc-5595	Rabbit	2000	15000	cytoskeletal	0.7656	0.349	0.0003	-0.436
YAP1	YAP1	YAP1	Yes-associated protein 1		YAP	Cell Signaling	4912	Rabbit	100	15000	ApopReg, hippo	0.7281	0.011	0.0011	-0.460
YAP1.p	YAP1 phospho Serine 127	YAP1	Yes-associated protein 1	Inactivation	YAP-p(ser127)	Cell Signaling	4911	Rabbit	500	15000	ApopReg, hippo	0.5198	0.023	0.0000	-0.276
YWHAE	YWHAE	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide		X14.3.3Epsilon	Santa Cruz	sc-23957	mouse	200	15000	tp53	0.1673	0.027	0.0416	0.257
YWHAZ	YWHAZ	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide		14-3-3-zeta	chemicon	AB9746	Rabbit	750	20000	tp53	0.0998	-0.050	0.0092	1.333
ZNF296	ZNF296	ZNF296	zinc finger protein 296		ZNF342	abcam	ab51265	Rabbit	1000	15000	transcription	0.2069	-0.107	0.0000	-0.161

ZNF346	ZNF346	ZNF346	zinc finger protein 346		JAZ111	May-UFL		Rabbit	1000	15000	transcription	0.0305	0.127	0.0986	0.194
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**Table S2. Correlation between post-translational modifications (PTMs) and total protein expression levels. PCC: Pearson correlation coefficient. n = 205.**

Post-translational Modifications	Total Proteins	PCC	p-value
BAD.pS112	BAD	-0.293	0.000
GAB2.pY452	GAB2	-0.142	0.042
CTNNB1.pS33 37 41	CTNNB1	-0.083	0.238
BAD.pS155	BAD	-0.077	0.272
FOXO3.S318 321	FOXO3	-0.075	0.287
BAD.pS136	BAD	-0.030	0.668
EIF2AK2.pT451	EIF2AK2	-0.024	0.730
STAT1.pY701	STAT1	-0.021	0.764
AKT1 2 3.pT308	AKT1	-0.017	0.814
ERBB2.pY1248	ERBB2	-0.012	0.866
EIF4EBP1.pS65	EIF4EBP1	0.009	0.893
EGFR.pY992	EGFR	0.023	0.747
RPS6.pS235 236	RPS6	0.035	0.623
YAP1.p	YAP1	0.064	0.362
STAT5A B.pY694	STAT5A B	0.069	0.329
PRKAA1 2.pT172	PRKAA1 2	0.070	0.318
EIF2S1.pS51.	EIF2S1	0.087	0.216
SMAD2.pS465	SMAD2	0.094	0.181
STAT3.pY705	STAT3	0.095	0.177
STAT3.pS727	STAT3	0.111	0.115
SMAD2.pS245	SMAD2	0.118	0.092
MAPK14.pT180Y182	MAPK14	0.138	0.048
NF2.pS518	NF2	0.141	0.043
MAP2K1 2.pS217 221	MAP2K1	0.161	0.021
AKT1 2 3.pS473	AKT1	0.192	0.006
MAPK1 3.pT202Y204	MAPK1	0.200	0.004
CDKN1B.pS10	CDKN1B	0.206	0.003
GSKA B.pS21 9	GSKA B	0.256	0.000
RPS6.pS240 244	RPS6	0.292	0.000
MTOR.pS2448	MTOR	0.293	0.000
WWTR1.pS89	WWTR1	0.315	0.000
TP53.pS15	TP53	0.324	0.000
SMAD5.pS463	SMAD5	0.344	0.000
CREB1.pS133	CREB1	0.379	0.000
EIF4EBP1.pT37 46	EIF4EBP1	0.380	0.000
CASP3.cl175	CASP3	0.385	0.000



EIF4EBP1.pT70	EIF4EBP1	0.406	0.000
H3K27Me3	H3histone	0.478	0.000
PDK1.pS241	PDK1	0.509	0.000
H3K4Me3	H3histone	0.618	0.000
RB1.pS807 811	RB1	0.657	0.000
H3K4Me2	H3histone	0.697	0.000
SRC.pY416	SRC	0.739	0.000
PRKCA.pS657	PRKCA	0.798	0.000
SRC.pY527	SRC	0.804	0.000
PTEN.pS380T382T383	PTEN	0.835	0.000
RPS6KB1.pT389	RPS6KB1	0.890	0.000

**Table S3. Functional group memberships.**

Functional Group	Antibodies
Adhesion	CAV1, TGM2, ITGB3, ITGA2, FN1, PTK2, IGFBP2, ITGAL, SPP1, CD44, CTSG
ApopOccur	CASP3, CASP3.cl175, CASP7.cl198, CASP8, CASP9.cl315, CASP9.cl330, PARP1, PARP1.cl214
ApopReg	AIFM1, NOL3, YAP1, YAP1.p, TP53, TP53.pS15
autophagy	PARK7, GSKA_B, TSC2, STK11, GSKA_B.pS21_9, ATG7, BECN1, ATF3, PRKAA1_2, PRKAA1_2.pT172, SQSTM1
BH3	NOL3, BAD, BAD.pS155, BAD.pS112, BAD.pS136, BAK1, BCL2, BCL2L1, BCL2L11, BID, BAX, MCL1
cellcycle	CCNB1, CCND1, CCND3, CCNE1, CDK1, CDK2, CDK4, CDKN1A, CDKN2A, FOXO3.S318_321, MYC, CDKN1B, CCNE2, FOXO1.pT24_FOXO3.pT32, CDKN1B.pS10, RB1, WTAP, FOXO3, RB1.pS807_811
creb	ATF3, CREB1, CREB1.pS133
cytoskeletal	XPO1, MAPT, NRPI, NF2.pS518, NF2, ACTB
differentiation	GATA1, GATA3, PIM1, PIM2, PPARG, SSBP2
fli1	NCL, NPM1.3542, STMN1, WTAP, FLI1
heatshock	HSP90AA1_B1, HSPB1, HSPA1A_L
hippo	WWTR1.pS89, YAP1, NF2.pS518, WWTR1, NF2, YAP1.p
histone	H3K4Me3, H3K4Me2, H3histone, BMI1, HDAC3, KDM1A, ASH2L, WTAP, FLI1, NCL, HNRNPK, HDAC1, TRIM24, SIRT1, HDAC2, H3K27Me3, CLPP, JMJD6, NPM1, BRD4
hypoxia	VASP, VHL, EGLN1, HIF1A, KDR
IAP	BIRC2, BIRC5, DIABLO, XIAP
mapk	MAP2K1, MAP2K1_2.pS217_221, MAPK1, MAPK1_3.pT202Y204, MAPK14, MAPK14.pT180Y182, MAPK9
mek	DUSP6, BRAF, ELK1.pS383, RAC1_2_3, TNK1, KIT, LYN
metabolic	ASNS, ODC1, PPARA, PTGS2, GAPDH
mtor	MTOR, MTOR.pS2448, PDK1, PDK1.pS241, PIK3CA, PIK3R1_2, PTEN, PTEN.pS380T382T383, TSC2, EGFR, EGFR.pY992, INPP5D, INPPL1, IRS1.pS1101
pi3kakt	AKT1, AKT1_2_3.pS473, AKT1_2_3.pT308, ELK1.pS383, FOXO1.pT24_FOXO3.pT32, FOXO3, FOXO3.S318_321, GAB2, GAB2.pY452, GSKA_B, GSKA_B.pS21_9
pkc	PRKCD.pS664, PRKCD.pS645, PRKCD.pT507 PRKCB.I, PRKCB.II, PRKCA.pS657, PRKCA, RELA
s6rp	RPS6, RPS6.pS235_236, RPS6.pS240_244, EIF4EBP1, EIF4EBP1.pS65, EIF4EBP1.pT37_46, EIF4EBP1.pT70, RPS6KB1, RPS6KB1.pT389
smad	SMAD6, SMAD4, SMAD2.pS245, SMAD3, SMAD5, SMAD2, SMAD5.pS463, SMAD2.pS465, SMAD1
src	SRC, SRC.pY416, SRC.pY527
stat	MAPK9, STAT3.pY705, STAT3.pS727, STAT1.pY701, STAT5A_B.pY694, STAT6.pY641, STAT5A_B, STAT1, STAT3
STP	ERBB2, ERBB2.pY1248, ERBB3, IGF1R, EGFR, MET.pY1230_1234_1235, PTPN11, PPP2R2A_B_C_D, KIT, LYN, SOCS2
tcell	CD74, LCK, LGALS3, NOTCH1.cl1744, NOTCH3
tp53	YWHAE, IRS1.pS1101, SFN, TRIM24, MDM4, MDM2, TP53.pS15, TP53, YWHAZ
transcription	GATA3, ZNF296, NR4A1, JUN.pS73, MYC, ERG, EIF2AK2.pT451, EIF2AK2, EIF4E, EIF2S1, TCF4, EIF2S1.pS51., GATA1, JUNB, ZNF346, SPI1, DLX1
ubiquitin	TRIM24, COPS5, CBL, TRIM62
wnt	LEF1, CTNNB1, CTNNB1.pS33_37_41, CTNNA1

**Table S4. Constellation memberships for functional patterns.**

Constellation	Functional Pattern
1	cellcycle.C5
2	fli1.C2
2	hippo.C2
2	src.C2
2	ubiquitin.C2
3	adhesion.C5
3	ApopOccur.C1
3	ApopReg.C2
3	autophagy.C5
3	BH3.C5
3	cellcycle.C4
3	creb.C2
3	cytoskeletal.C2
3	differentiation.C2
3	histone.C2
3	hypoxia.C1
3	mapk.C1
3	mek.C3
3	metabolic.C1
3	mtor.C4
3	pi3kakt.C4
3	pkc.C5
3	s6rp.C4
3	stat.C5
3	STP.C1
3	tcell.C1
3	tp53.C2
3	transcription.C1
3	wnt.C4
4	heatshock.C8
5	differentiation.C3
5	mek.C4
5	pkc.C1
5	smad.C4
5	STP.C3
5	tcell.C6
5	transcription.C3

6	ApopReg.C3
6	fli1.C1
6	hippo.C1
6	histone.C1
6	hypoxia.C3
6	mek.C1
6	pi3kakt.C1
6	src.C1
6	ubiquitin.C1
7	adhesion.C2
7	ApopOccur.C3
7	ApopReg.C1
7	autophagy.C2
7	BH3.C2
7	cellcycle.C3
7	creb.C1
7	cytoskeletal.C1
7	differentiation.C5
7	heatshock.C5
7	IAP.C1
7	mapk.C4
7	metabolic.C3
7	mtor.C2
7	pkc.C2
7	s6rp.C3
7	s6rp.C6
7	smad.C3
7	STP.C2
7	tp53.C1
7	tp53.C3
7	transcription.C4
7	wnt.C2
8	adhesion.C3
8	ApopOccur.C4
8	ApopOccur.C7
8	autophagy.C1
8	BH3.C1
8	creb.C3

8	differentiation.C1
8	heatshock.C3
8	histone.C5
8	hypoxia.C2
8	IAP.C2
8	IAP.C4
8	mek.C5
8	mtor.C3
8	pi3kakt.C2
8	pkc.C3
8	smad.C5
8	stat.C4
8	tcell.C4
9	adhesion.C1
9	ApopOccur.C2
9	BH3.C3
9	BH3.C4
9	cytoskeletal.C4
9	heatshock.C2
9	hypoxia.C4
9	IAP.C5
9	mapk.C2
9	mapk.C3
9	mapk.C5
9	metabolic.C2
9	metabolic.C4
9	mtor.C1
9	s6rp.C2
9	smad.C1
9	stat.C1
9	stat.C2
9	stat.C3
9	tcell.C3
9	tcell.C5
9	ubiquitin.C3
9	wnt.C3
10	ApopOccur.C5
10	ApopReg.C4
10	autophagy.C3
10	autophagy.C4

10	cellcycle.C1
10	cellcycle.C6
10	cytoskeletal.C5
10	heatshock.C1
10	heatshock.C7
10	hippo.C3
10	histone.C4
10	IAP.C6
10	metabolic.C5
10	metabolic.C6
10	metabolic.C7
10	mtor.C5
10	mtor.C6
10	pi3kakt.C3
10	s6rp.C1
10	s6rp.C5
10	tp53.C4
10	transcription.C2
10	wnt.C1
10	wnt.C5
11	adhesion.C4
11	adhesion.C6
11	ApopOccur.C6
11	cellcycle.C2
11	creb.C4
11	cytoskeletal.C3
11	differentiation.C4
11	fli1.C3
11	heatshock.C4
11	heatshock.C6
11	histone.C3
11	hypoxia.C5
11	IAP.C3
11	mek.C2
11	pkc.C4
11	smad.C2
11	tcell.C2
11	tp53.C5
11	ubiquitin.C4

**Table S5. Functional pattern memberships for cell lines.**

cell_line	mycoplasma	disease	adhesion	ApoptOcur	ApoptReg	autophagy	BH3	cellcycle	creb	cytoskeletal	differentiatio	flil	heatshock	hippo	histone	hypoxia	IAP	mapk	mek	metabolic	mtor	pi3kakt	pke	s6rp	smad	src	stat	STP	tecl	tp53	transcription	ubiquitin	wnt
Blin-1	neg	BCP-ALL	7	7	5	6	6	7	5	2	6	4	9	2	6	3	2	6	6	8	7	5	4	7	6	3	6	4	7	6	3	5	6
BV173	pos	B cell precursor leukemia	7	8	5	6	3	7	5	6	2	1	9	1	1	3	1	6	6	8	7	5	6	7	2	3	6	4	7	6	5	1	6
BV173	neg	B cell precursor leukemia	7	8	5	6	6	7	5	4	5	4	9	1	6	3	2	6	6	8	7	5	5	7	1	3	6	4	6	6	5	5	6
BV173 treated	neg	B cell precursor leukemia	7	8	5	6	2	7	5	6	5	4	9	4	1	6	2	6	6	8	7	5	4	7	2	2	6	4	7	6	1	1	6
CCRF-CEM	neg	leukemia, T lymphoblast	7	4	5	6	2	7	5	4	6	4	3	2	6	6	7	6	6	8	7	1	3	7	6	3	6	4	7	6	5	5	6
Daudi	pos	b lymphoblast,Burkitt's lymphoma	7	8	5	6	6	7	1	6	6	3	9	1	6	3	2	6	6	8	7	5	6	7	6	3	6	4	1	6	5	5	6
Daudi	neg	b lymphoblast,Burkitt's lymphoma	7	8	5	6	6	7	5	6	5	4	9	1	6	6	2	6	6	8	7	5	6	7	6	3	6	4	6	6	5	5	2
RPMI8226			7	8	5	6	6	7	5	1	6	3	9	1	6	6	7	6	6	8	7	5	6	7	6	3	6	4	1	6	5	5	4
GM00131	2nd-neg	lymphoblastoid cell line	7	8	5	5	1	7	1	6	4	4	3	2	6	6	2	6	6	8	7	5	6	7	6	3	6	4	7	6	5	1	2
GM00131 treated	neg	lymphoblastoid cell line	7	8	5	5	6	7	5	4	4	4	9	4	1	6	2	6	6	8	2	5	6	7	6	3	6	4	7	6	5	3	1
HL-60	pos	leukemia, AML M2	7	1	5	6	6	7	5	6	6	4	9	1	6	3	2	2	6	8	7	5	1	7	6	3	6	4	1	6	5	5	5
HL-60	neg	leukemia, AML M2	7	8	5	5	6	7	5	6	6	4	9	1	6	6	2	6	6	8	7	5	2	7	6	3	6	4	1	6	5	5	5
HL60	neg	leukemia, AML M2	7	8	5	5	6	7	2	4	6	1	9	1	6	3	7	2	6	8	7	5	6	7	6	1	6	4	1	6	5	3	5
HL-60 treated	neg	leukemia, AML M2	7	7	5	6	6	5	5	6	6	4	9	1	6	2	7	2	6	8	7	5	6	7	6	3	6	4	7	6	5	5	1
HL-60 TRE TGM2	neg	leukemia, AML M2	7	8	5	5	6	7	5	6	6	1	9	1	6	6	1	1	6	8	7	5	4	7	6	3	6	4	1	6	5	5	6
HL-60 TRE TGM2 control	neg	leukemia, AML M2	7	8	5	5	6	7	5	6	6	1	2	1	6	6	7	1	6	8	7	5	4	7	6	3	6	4	7	6	5	5	6
Jeko-1	neg	lymphoma	7	8	5	6	2	7	5	1	5	4	9	1	6	6	7	6	6	8	7	5	6	7	6	3	6	4	7	6	5	5	5
Jurkat	2nd-neg	leukemia T-ALL	7	8	5	6	6	7	5	6	6	2	9	2	6	6	2	6	6	8	7	5	6	7	6	3	6	4	7	6	5	5	6
Jurkat treated	neg	leukemia T-ALL	7	8	5	6	6	7	1	4	6	4	3	1	6	6	7	6	6	8	7	5	6	7	6	3	6	4	7	6	5	5	6
Jurkat I9.2 Caspase8 mut	neg	leukemia T-ALL	7	8	5	6	6	7	5	4	6	4	3	4	6	6	2	6	6	8	7	5	6	7	2	3	6	4	7	6	5	1	6
K562	pos	leukemia, CML	7	8	5	6	6	7	5	1	6	4	9	2	6	6	2	6	6	8	7	5	6	7	6	3	6	4	1	6	5	5	6
K562	neg	leukemia, CML	7	8	5	6	6	7	2	2	6	4	9	1	6	6	7	6	6	8	7	5	6	7	6	3	6	4	1	1	5	5	6

K562 treated	neg	leukemia, CML	7	8	5	6	6	7	5	2	6	4	9	4	6	6	7	6	6	8	7	5	6	7	6	3	6	4	1	6	5	5	6
kasumi-1	pos	leukemia, AML M2	7	8	5	1	6	7	5	6	6	4	9	2	6	3	2	1	6	8	7	1	6	7	2	3	6	4	1	6	3	5	5
kasumi-1	neg	leukemia, AML M2	7	8	5	5	6	7	5	6	3	4	9	1	6	6	2	1	6	8	7	5	6	7	1	3	4	4	1	6	5	5	6
kasumi-1 treated		leukemia, AML M2	7	8	5	2	6	7	5	4	6	4	9	1	6	6	7	6	6	8	7	4	6	7	2	3	6	4	1	6	3	5	2
KBM3	neg	leukemia, AML M5	7	8	5	2	6	7	5	4	6	2	3	2	6	6	7	2	6	8	7	5	1	7	6	3	6	4	7	6	5	5	5
KBM5	pos	leukemia, CML	7	8	5	6	6	7	5	6	6	1	9	1	6	2	1	6	6	8	7	5	4	4	2	3	6	4	7	6	5	5	5
KBM5	neg	leukemia, CML	7	8	5	6	6	7	5	6	6	1	9	4	6	2	2	1	6	8	7	5	6	4	2	3	6	4	7	6	5	5	6
KBM5 treated	neg	leukemia, CML	7	8	5	6	6	7	5	6	6	1	9	1	6	2	2	1	6	8	7	4	6	7	2	3	6	4	7	6	5	5	6
KBM5 STL, w/o STI	pos	CML T315I	7	2	5	6	6	7	5	6	6	3	9	1	1	2	1	5	6	8	7	1	6	7	6	3	6	4	7	6	5	5	6
KBM5 STL, w/STI	neg	CML T315I	7	7	5	2	6	7	1	6	6	3	9	1	1	3	7	5	6	8	7	1	6	7	6	3	6	4	7	6	5	3	6
KBM5 STL, w/o STI	neg	CML T315I	7	8	5	5	6	7	5	1	6	1	9	1	6	3	2	6	6	8	7	1	6	7	2	3	6	4	1	6	5	3	3
KBM5 STL treated, w/o STI	neg	CML T315I	7	8	5	5	6	7	5	6	6	3	9	1	6	3	7	2	6	8	7	4	6	7	6	3	6	4	2	6	5	3	6
KG-1	pos	leukemia, AML M3	7	1	5	6	6	7	5	6	6	4	9	2	6	6	2	2	6	8	7	1	6	4	6	3	6	4	7	6	5	5	5
KG1	neg	leukemia, AML M3	7	8	5	6	1	7	5	4	2	4	9	1	6	3	2	6	6	6	7	5	3	7	6	3	6	4	7	6	1	3	6
KG-1 treated	neg	leukemia, AML M3	7	8	5	5	2	7	2	4	6	4	9	4	6	6	2	2	6	8	7	5	6	4	6	1	2	4	7	6	5	5	5
KG-1 $\alpha$	neg	leukemia, AML M3	7	8	2	6	6	7	5	4	6	2	9	2	6	6	2	1	6	8	7	5	6	7	6	3	6	4	7	6	5	5	6
KOPTI-K1 (labe:KOP TI)	neg	T-ALL	7	2	5	6	6	7	3	6	6	4	9	2	6	6	1	6	6	2	7	1	6	7	6	3	6	4	7	6	5	5	6
MDSL	neg	MDS	7	8	5	6	6	7	5	6	6	1	3	1	6	6	2	6	6	8	7	5	6	7	2	3	2	4	7	6	5	2	6
MINO	neg	Mantle Cell Lymphoma	7	8	5	6	6	7	5	6	6	1	9	1	6	3	2	6	6	8	7	5	6	7	6	3	6	4	7	6	5	2	6
ML-1	pos	leukemia, AML M3	7	8	5	5	6	7	5	4	6	1	9	2	6	3	7	1	6	8	7	5	6	7	6	3	6	4	7	6	5	5	5
ML-1	neg	leukemia, AML M3	7	7	5	5	6	7	5	4	6	1	9	1	6	6	7	6	6	8	7	5	6	7	6	3	2	4	1	6	5	5	6
ML-1 treated	neg	leukemia, AML M3	7	8	5	6	6	7	2	6	6	4	9	1	6	6	7	6	6	8	7	5	6	7	6	3	6	4	1	6	5	5	6
ML-2 (AML-ML2)	neg	leukemia, AML M4	7	1	5	6	6	7	5	4	6	4	9	2	6	6	7	6	6	8	7	5	1	7	6	3	6	4	6	6	5	5	6
Mo7e	2nd-neg	leukemia, AML M7	7	8	5	6	6	7	5	2	6	3	9	4	6	6	7	6	1	8	7	5	6	7	6	3	6	4	7	6	5	5	1
Molm13	neg	leukemia, AML M5a	7	8	5	2	6	7	5	6	6	4	9	4	6	3	2	6	6	8	7	5	6	7	6	3	6	4	7	6	5	1	6
Molm13 P53 K/D	neg	leukemia, AML M5a	7	8	5	5	6	7	1	1	6	3	9	1	1	3	2	2	6	8	7	1	6	7	6	3	6	4	7	6	5	1	6
Molm13 P53 vector	neg	leukemia, AML M5a	7	8	5	5	6	7	5	1	6	3	9	1	6	3	2	2	6	8	7	1	6	7	6	1	6	4	7	6	5	1	5

Molm14	2nd-neg	leukemia, AML M5a	7	7	5	6	6	7	5	4	6	1	9	2	6	3	1	6	6	8	7	1	4	7	6	3	6	4	7	6	5	1	3
molm14	neg	leukemia, AML M5a	7	7	5	5	6	7	5	4	6	3	9	2	1	6	2	2	6	8	7	1	6	7	6	3	6	4	2	6	5	1	6
molm14 treated	neg	leukemia, AML M5a	7	8	5	6	6	7	5	4	6	3	9	4	6	3	7	6	6	8	7	1	6	7	6	3	6	4	7	6	5	5	3
molm16			7	8	5	1	6	7	5	4	6	1	9	4	1	6	7	6	6	8	7	4	6	7	6	3	6	4	1	6	5	1	1
molt3	neg	T lymphoblast, T-ALL	7	8	5	6	6	7	5	1	6	4	9	2	6	6	2	1	6	2	7	1	6	7	6	3	2	4	7	6	5	5	6
Molt4	neg	T lymphoblast, T-ALL	7	8	5	6	6	7	5	1	6	4	9	1	6	6	2	6	6	8	7	5	6	7	2	3	6	4	7	6	5	5	6
MR2	pos	APL	7	8	5	6	6	7	5	4	6	4	9	1	6	6	2	6	6	8	7	1	6	7	6	3	2	4	1	6	5	5	5
MR2 treated	neg	APL	7	8	5	6	6	7	5	4	6	4	9	1	6	6	7	1	6	8	7	5	6	7	6	2	2	4	1	6	5	5	6
MV4-11	pos	leukemia, AML M5	7	8	5	6	6	7	2	6	6	4	9	2	6	6	2	6	6	8	7	5	4	7	6	3	6	4	6	6	5	1	6
MV4-11	neg	leukemia, AML M5	7	8	5	2	6	7	2	6	6	4	3	2	6	6	2	6	6	8	7	5	4	7	6	3	6	4	7	6	5	3	6
MV4-11 treated		leukemia, AML M5	7	8	5	1	6	7	5	4	6	4	3	2	6	3	7	6	6	8	7	5	6	7	6	3	6	4	1	6	5	3	5
MV4-11 IDH1 R132H	neg	leukemia, AML M5	7	8	5	6	6	7	2	4	6	4	9	1	1	3	2	6	6	8	7	5	6	7	6	3	6	4	7	6	5	2	6
MV4-11 IDH1 wt(vector)	neg	leukemia, AML M5	7	8	5	2	6	7	2	4	6	4	3	1	6	6	2	6	6	8	7	5	6	7	6	3	2	4	7	6	5	5	6
Nalm6	pos	B-ALL	7	1	5	6	6	7	5	6	6	4	9	1	6	6	2	1	6	8	7	4	6	7	6	3	6	4	7	6	3	1	6
Nalm6 treated	neg	B-ALL	7	8	5	6	6	7	5	4	6	1	9	4	6	6	7	1	6	8	7	5	4	7	6	3	6	4	7	6	5	5	6
NB4	neg	leukemia, AML M3	7	8	5	1	1	7	5	4	6	1	9	1	6	6	1	1	6	8	7	1	6	7	6	3	2	4	1	6	5	3	5
OCIAML2	neg	leukemia, AML M4	7	8	5	6	6	7	1	4	6	1	9	4	6	6	1	6	6	8	7	5	6	7	6	3	6	4	1	6	5	5	6
OCIAML3	neg	leukemia, AML M4	7	8	5	6	6	7	5	6	6	3	9	1	1	3	2	6	6	8	7	4	6	7	6	3	6	4	7	6	5	1	2
OCIAML3 550 TGM2-overexp	neg	leukemia, AML M4	7	8	5	6	6	7	5	4	6	3	9	1	6	6	1	6	6	8	7	5	6	7	6	3	6	4	7	6	5	1	2
OCIAML3 708 ppp2R2A shRNA	neg	leukemia, AML M5	7	7	5	6	6	7	5	6	6	4	9	1	6	3	3	6	6	8	7	5	6	7	6	3	6	4	7	6	5	5	6
OCIAML3 709 ppp2R2A shRNA	neg	leukemia, AML M4	7	7	5	6	6	7	1	6	6	4	9	1	6	6	2	2	6	8	7	5	6	7	6	3	6	4	7	6	5	5	5
OCIAML3 Bcl2 overexpression	neg	leukemia, AML M4	7	8	5	6	6	7	1	4	6	4	9	4	6	6	1	1	6	8	7	5	6	7	6	3	6	4	7	6	5	5	3
OCIAML3 Bcl2 vector	neg	leukemia, AML M4	7	7	5	6	6	7	1	6	6	4	9	4	6	6	7	6	6	8	7	5	6	7	6	1	6	4	7	6	5	5	3
OCIAML3 IDH1 R132H	neg	leukemia, AML M4	7	8	5	5	6	7	5	6	6	4	9	1	1	3	2	2	6	8	7	5	6	7	6	3	6	4	7	6	5	5	2

OCIAML3 IDH1 wt(vector)	neg	leukemia, AML M4	7	8	5	6	6	7	5	4	6	4	9	1	6	6	2	6	6	8	7	5	6	7	6	3	6	4	7	6	5	3	2
OCIAML3 inducible HIF1a ODD mut	neg	leukemia, AML M4	7	8	5	2	6	7	5	6	6	3	9	1	1	6	7	6	6	8	7	5	6	7	6	3	6	4	7	6	5	5	2
OCIAML3 ITD	pos	leukemia, AML M4	7	8	5	6	6	7	1	4	6	4	9	4	6	6	2	2	6	8	7	5	6	7	6	3	6	4	7	6	5	3	3
OCIAML3 ITD treated	neg	leukemia, AML M4	7	8	5	6	6	7	1	6	6	4	9	4	6	6	2	2	6	8	7	5	6	7	6	3	6	4	7	6	5	5	6
OCIAML3 ITD vec	neg	leukemia, AML M4	7	8	5	6	6	7	5	6	6	4	3	4	6	6	1	2	6	8	7	5	6	7	6	3	6	4	7	6	5	5	3
OCIAML3 NS for ppp2R2A shRNA	neg	leukemia, AML M4	7	8	5	6	6	7	5	6	6	4	9	1	6	6	2	2	6	8	7	5	6	7	6	3	6	4	7	6	5	5	2
OCIAML3 p100SSAA	neg	leukemia, AML M4	7	8	5	6	6	7	5	4	6	4	9	1	6	6	2	2	6	8	7	5	6	7	6	3	6	4	7	6	5	1	5
OCIAML3 P53 shRNA	neg	leukemia, AML M4	7	8	5	6	6	7	5	6	6	4	9	1	6	6	2	5	6	8	7	5	6	7	6	3	6	4	7	6	5	1	6
OCIAML3 P53 vector	neg	leukemia, AML M4	7	8	5	6	6	7	5	6	6	4	9	1	6	6	2	6	6	8	7	5	6	7	6	3	6	4	7	6	5	5	6
OCIAML3 PI3K active pool #1	neg	leukemia, AML M4	7	7	5	6	6	7	5	4	6	1	9	1	6	6	2	6	6	8	7	5	6	7	6	3	6	4	7	6	5	3	6
OCIAML3 PI3K wt pool#2 1A	neg	leukemia, AML M4	7	8	5	6	6	7	5	4	6	4	9	1	6	6	1	6	6	8	7	5	6	7	6	3	6	4	7	6	5	3	2
OCIAML3 Stat5A	neg	leukemia, AML M4	7	8	5	6	6	7	5	4	6	3	3	4	6	3	2	6	6	8	7	5	6	7	6	3	6	4	7	6	5	3	2
OCIAML3 stat5A N642H	neg	leukemia, AML M4	7	7	5	6	6	7	5	6	6	3	9	1	1	6	7	2	6	8	7	5	6	7	6	3	6	4	7	6	5	5	6
OCIAML3 stat5A N642H H4F	neg	leukemia, AML M4	7	7	5	6	6	7	5	6	6	3	9	1	6	3	7	6	6	8	7	5	6	7	6	3	6	4	7	6	5	5	3
OCIAML3 stat5A wt	neg	leukemia, AML M4	7	8	5	6	6	7	5	6	6	3	9	1	6	3	7	2	6	8	7	5	6	7	6	3	6	4	7	6	5	3	2
OCIAML3 TRE TGM2	neg	leukemia, AML M4	7	8	5	6	6	7	5	4	6	1	9	1	1	6	2	2	6	8	7	5	6	7	6	3	6	4	6	6	5	5	5
OCIAML3 TRE TGM2 control	neg	leukemia, AML M4	7	1	5	2	6	7	5	6	6	1	9	1	6	3	7	6	6	8	7	5	6	7	6	3	6	4	6	6	5	3	5
OCIAML5	neg	leukemia, AML M4	7	8	5	6	6	7	5	4	6	1	9	4	6	6	7	6	6	8	7	5	6	7	2	3	2	4	7	6	5	3	6
P12 ichikawa	neg	T-ALL	7	8	5	5	6	7	1	6	6	4	3	2	1	6	7	6	6	8	7	4	6	7	6	1	6	4	7	6	5	5	6
Raji	pos	B lymphocyte, Burkitt's lymphoma	7	8	5	6	6	7	5	6	3	1	9	2	6	6	7	6	6	8	7	5	6	7	6	3	6	4	6	6	5	5	6
Raji	neg	B lymphocyte, Burkitt's lymphoma	7	8	5	6	6	7	5	1	6	4	9	2	6	6	7	6	6	8	7	5	4	7	6	3	6	4	6	6	5	1	6
Raji treated	neg	B lymphocyte, Burkitt's	7	8	5	6	6	7	5	1	6	4	9	2	6	6	2	6	6	8	7	5	4	7	6	3	6	4	6	6	5	1	6





**Table S6. Demographic information of patients overall and in each signature (S1-S13).**

Clinical Features		All	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
Sample Size	Count	205	9	12	11	11	27	17	20	28	6	17	22	14	11
Age.at.Dx	Mean	59.05	62.79	65.98	56.29	56.20	58.81	54.51	58.57	57.77	48.68	60.75	59.14	55.00	73.81
	SD	15.62	9.66	9.06	14.88	17.22	15.04	18.89	16.69	16.23	16.85	12.05	16.46	17.83	8.78
Gender	Female	50.7%	44.4%	41.7%	54.5%	54.5%	40.7%	52.9%	40.0%	60.7%	66.7%	64.7%	45.5%	42.9%	63.6%
	Male	49.3%	55.6%	58.3%	45.5%	45.5%	59.3%	47.1%	60.0%	39.3%	33.3%	35.3%	54.5%	57.1%	36.4%
FAB	M0	5.9%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	5.0%	7.1%	0.0%	17.6%	9.1%	14.3%	18.2%
	M1	12.7%	0.0%	0.0%	0.0%	0.0%	11.1%	11.8%	10.0%	7.1%	50.0%	23.5%	9.1%	42.9%	18.2%
	M2	33.2%	0.0%	0.0%	36.4%	45.5%	48.1%	47.1%	45.0%	39.3%	33.3%	29.4%	9.1%	28.6%	45.5%
	M4	28.3%	44.4%	50.0%	18.2%	27.3%	18.5%	41.2%	25.0%	39.3%	0.0%	23.5%	36.4%	14.3%	9.1%
	M5	12.2%	55.6%	41.7%	0.0%	0.0%	3.7%	0.0%	10.0%	7.1%	16.7%	0.0%	36.4%	0.0%	9.1%
	M6	2.0%	0.0%	0.0%	9.1%	9.1%	3.7%	0.0%	5.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	M7	2.4%	0.0%	8.3%	9.1%	9.1%	3.7%	0.0%	0.0%	0.0%	0.0%	0.0%	5.9%	0.0%	0.0%
	RAEBT	2.9%	0.0%	0.0%	27.3%	9.1%	7.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	NA	0.5%	0.0%	0.0%	0.0%	0.0%	3.7%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Cytogenetics	Favorable	10.7%	11.1%	0.0%	9.1%	18.2%	3.7%	23.5%	20.0%	17.9%	0.0%	5.9%	4.5%	7.1%	9.1%
	Intermediate	46.3%	33.3%	66.7%	27.3%	27.3%	44.4%	52.9%	40.0%	50.0%	83.3%	29.4%	50.0%	71.4%	36.4%
	Unfavorable	42.9%	55.6%	33.3%	63.6%	54.5%	51.9%	23.5%	40.0%	32.1%	16.7%	64.7%	45.5%	21.4%	54.5%
AHD	Yes	31.4%	22.2%	33.3%	45.5%	36.4%	48.1%	47.1%	35.0%	28.6%	0.0%	29.4%	13.6%	15.4%	27.3%
	No	68.6%	77.8%	66.7%	54.5%	63.6%	51.9%	52.9%	65.0%	71.4%	100.0%	70.6%	86.4%	84.6%	72.7%
ITD	N (tested)	196	9	11	10	9	26	16	18	28	6	16	22	14	11
	Mutant	23.0%	11.1%	9.1%	40.0%	11.1%	11.5%	12.5%	11.1%	35.7%	16.7%	37.5%	27.3%	50.0%	9.1%
	Wildtype	77.0%	88.9%	90.9%	60.0%	88.9%	88.5%	87.5%	88.9%	64.3%	83.3%	62.5%	72.7%	50.0%	90.9%
D835	N (tested)	196	9	11	10	9	26	16	18	28	6	16	22	14	11
	Mutant	9.7%	0.0%	0.0%	0.0%	0.0%	3.8%	12.5%	5.6%	10.7%	0.0%	0.0%	27.3%	21.4%	27.3%
	Wildtype	90.3%	100.0%	100.0%	100.0%	100.0%	96.2%	87.5%	94.4%	89.3%	100.0%	100.0%	72.7%	78.6%	72.7%
FLT3	N (tested)	196	9	11	10	9	26	16	18	28	6	16	22	14	11
	Mutant	29.6%	11.1%	9.1%	40.0%	11.1%	15.4%	25.0%	11.1%	39.3%	16.7%	37.5%	40.9%	71.4%	36.4%
	Wildtype	70.4%	88.9%	90.9%	60.0%	88.9%	84.6%	75.0%	88.9%	60.7%	83.3%	62.5%	59.1%	28.6%	63.6%
NPM1	N (tested)	165	9	7	7	7	21	15	17	23	4	17	19	12	7
	Mutant	22.4%	22.2%	28.6%	14.3%	14.3%	4.8%	6.7%	17.6%	21.7%	25.0%	23.5%	36.8%	58.3%	28.6%
	Wildtype	77.6%	77.8%	71.4%	85.7%	85.7%	95.2%	93.3%	82.4%	78.3%	75.0%	76.5%	63.2%	41.7%	71.4%

RAS	N (tested)	178	8	11	7	9	25	15	19	25	5	13	19	11	11
	Mutant	21.9%	37.5%	27.3%	14.3%	33.3%	20.0%	33.3%	31.6%	28.0%	40.0%	7.7%	10.5%	0.0%	9.1%
	Wildtype	78.1%	62.5%	72.7%	85.7%	66.7%	80.0%	66.7%	68.4%	72.0%	60.0%	92.3%	89.5%	100.0%	90.9%
IDH1	N (tested)	145	8	6	6	6	18	13	17	19	5	13	15	11	8
	Mutant	11.7%	0.0%	33.3%	16.7%	0.0%	11.1%	23.1%	11.8%	5.3%	0.0%	7.7%	20.0%	18.2%	0.0%
	Wildtype	88.3%	100.0%	66.7%	83.3%	100.0%	88.9%	76.9%	88.2%	94.7%	100.0%	92.3%	80.0%	81.8%	100.0%
IDH2	N (tested)	145	8	6	6	6	18	13	17	19	5	13	15	11	8
	Mutant	11.0%	12.5%	0.0%	16.7%	0.0%	16.7%	7.7%	11.8%	15.8%	20.0%	7.7%	13.3%	9.1%	0.0%
	Wildtype	89.0%	87.5%	100.0%	83.3%	100.0%	83.3%	92.3%	88.2%	84.2%	80.0%	92.3%	86.7%	90.9%	100.0%
IDH1.2	N (tested)	145	8	6	6	6	18	13	17	19	5	13	15	11	8
	Mutant	21.4%	12.5%	33.3%	16.7%	0.0%	27.8%	30.8%	23.5%	21.1%	20.0%	15.4%	26.7%	27.3%	0.0%
	Wildtype	78.6%	87.5%	66.7%	83.3%	100.0%	72.2%	69.2%	76.5%	78.9%	80.0%	84.6%	73.3%	72.7%	100.0%
DNMT3A	N (tested)	133	8	5	5	6	17	9	16	18	4	12	14	12	7
	Mutant	8.3%	0.0%	0.0%	20.0%	0.0%	11.8%	0.0%	0.0%	5.6%	0.0%	16.7%	28.6%	8.3%	0.0%
	Wildtype	91.7%	100.0%	100.0%	80.0%	100.0%	88.2%	100.0%	100.0%	94.4%	100.0%	83.3%	71.4%	91.7%	100.0%
P53	N (tested)	54	2	2	0	3	7	5	8	7	0	7	6	4	3
	Mutant	14.8%	0.0%	0.0%	NaN	0.0%	14.3%	0.0%	25.0%	14.3%	NaN	28.6%	0.0%	25.0%	33.3%
	Wildtype	85.2%	100.0%	100.0%	NaN	100.0%	85.7%	100.0%	75.0%	85.7%	NaN	71.4%	100.0%	75.0%	66.7%

**Table S7. Method implementation and parameter specification.**

Analysis	Method	Implementation	Parameters <sup>a</sup>
Cluster analysis in Functional Patterning	K-means	R	Iter.max=1000 (kmeans) Nstart=1000 (kmeans)
	Progeny Clustering <sup>b</sup>	R package “progenyclust” <sup>1</sup>	method=” both” (progenyClust)
Network construction	Known protein interaction query	STRING <sup>2</sup>	combined score >= 0.9
	Graphical lasso and StARS	R package “huge” <sup>3</sup>	Nlambda=100 (huge) Criterion=” starts” (huge.select) Stars.thresh=0.05 (huge.select)
	Network visualization	Cytoscape <sup>4</sup>	NA
Cluster analysis in Constellation Patterning	Block clustering	R package “blockcluster” <sup>5</sup>	Nbtry=20 (coclusterStrategy) Nbxem=20 (coclusterStrategy) Datatype=” binary” (cocluster)
	Progeny Clustering <sup>c</sup>	R package “progenyClust” customized for co-clustering <sup>d</sup>	#progenies per cluster block=25 (5 by 5) Iteration=50
Tree analysis	Decision tree	R package “rpart” <sup>6</sup>	minsplit=5 (rpart.control) cp=0.02 (rpart.control)
Other statistical analysis	Pearson Correlation, One-way ANOVA, Kaplan-Meier, Pearson’s Chi-squared test, Multiple testing correction (FDR)	R	NA

**References**

1. Hu, C. & Qutub, A. progenyClust: an R package for Progeny Clustering. *R J.* (2016).
2. Franceschini, A. *et al.* STRING v9. 1: protein-protein interaction networks, with increased coverage and integration. *Nucleic Acids Res.* **41**, D808-D815 (2013).
3. Zhao, T., Liu, H. & Roeder, K. The huge package for high-dimensional undirected graph estimation in r. *J. Mach. Learn. Res.* **13**, 1059-1062 (2012).
4. Shannon, P. *et al.* Cytoscape : A Software Environment for Integrated Models of Biomolecular Interaction Networks Cytoscape : A Software Environment for Integrated Models of Biomolecular Interaction Networks. *Genome Res.* 2498-2504 (2003).

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5. Bhatia, P., Iovleff, S. & Govaert, G. blockcluster: An R Package for Model Based Co-Clustering. (2014).
6. Therneau, T., Atkinson, B. & Ripley, B. rpart: Recursive partitioning. *R Packag. version* (2010).

## Notes

- a. Default parameter values are not specified.
- b. Clusters of too small a size were removed (with fewer than 5 fresh samples or clusters with fewer than 25% of the expected number of fresh samples), and samples in those clusters were re-assigned to clusters with the closest center.
- c. Progeny Clustering initially picked 14 signatures by 11 constellations as the optimal clustering solution (see Table S7). However, since Signature 9 contains only 2 patients (which is infeasible for subsequent statistical analyses), we combined Signature 9 with its most similar signature, Signature 8. This combination results in the final structure of 13 signatures as shown in Figure 3A.
- d. The progenyClust code was customized for co-clustering, in which progenies were first constructed for each 2-dimensional cluster block by bootstrapping values within the block, and were then randomly populated within 5 by 5 blocks for re-clustering. The clustering stability was assessed by the chances of progenies within the same blocks being re-clustered together.

**Table S8. Stability scores from Progeny Clustering for co-clustering.** The Progeny Clustering result showed that the structure of 14 signatures by 11 constellations is the optimal solution. Note that the final 13 signatures were derived from the original 14 by 11 co-clustering result by merging Signature 9 (of only 2 patients) with Signature 8 (the signature closest to Signature 9).

	6 Signatures	7 Signatures	8 Signatures	9 Signatures	10 Signatures	11 Signatures	12 Signatures	13 Signatures	14 Signatures	15 Signatures
8 Constellations	7.64	7.18	8.82	11.31	14.39	11.36	9.77	11.67	11.81	12.91
9 Constellations	6.54	8.27	10.92	12.99	12.62	13.77	12.80	12.33	15.87	19.79
10 Constellations	7.90	11.71	11.34	9.71	14.24	18.09	10.78	12.91	15.13	17.46
11 Constellations	9.56	12.16	12.37	15.31	16.27	14.90	19.83	13.05	32.60	16.89
12 Constellations	10.02	9.96	12.09	14.94	24.84	18.35	18.57	20.33	21.69	19.34

# Meta-Galaxy Analysis Online Tool Tutorial

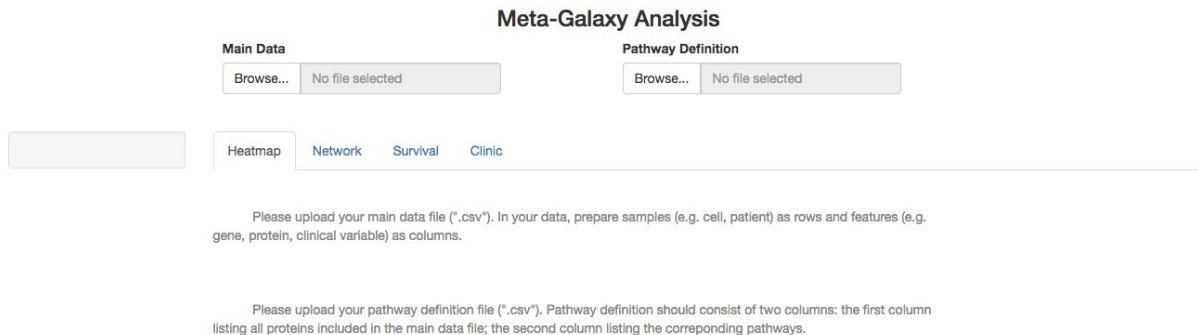
## Data Preparation

Before using the tool, please prepare your data in the following two “.csv” files:

- **Main Data.** This file should contain all sample measurements that you wish to analyze via the Meta-Galaxy analysis portal, including numeric measurements such as gene/protein expression (required), as well as clinical attributes such as survival and demographic information (optional, only required in the ‘Clinic’ module). The data should be structured, in which rows are samples and columns are measurements.
- **Pathway Definition.** This file should specify the pathway membership of each gene/protein contained in the main data file. The data should consist of two columns, with gene/protein names in the first column and their pathway names in the second column.

## Meta-Galaxy Analysis

Upon uploading the data files at the portal, the pathway names will be automatically parsed and populated in the left grey column box. By selecting a pathway name in the list, the portal will automatically start the analysis for that pathway.



**Meta-Galaxy Analysis**

Main Data Browse... No file selected

Pathway Definition Browse... No file selected

Heatmap Network Survival Clinic

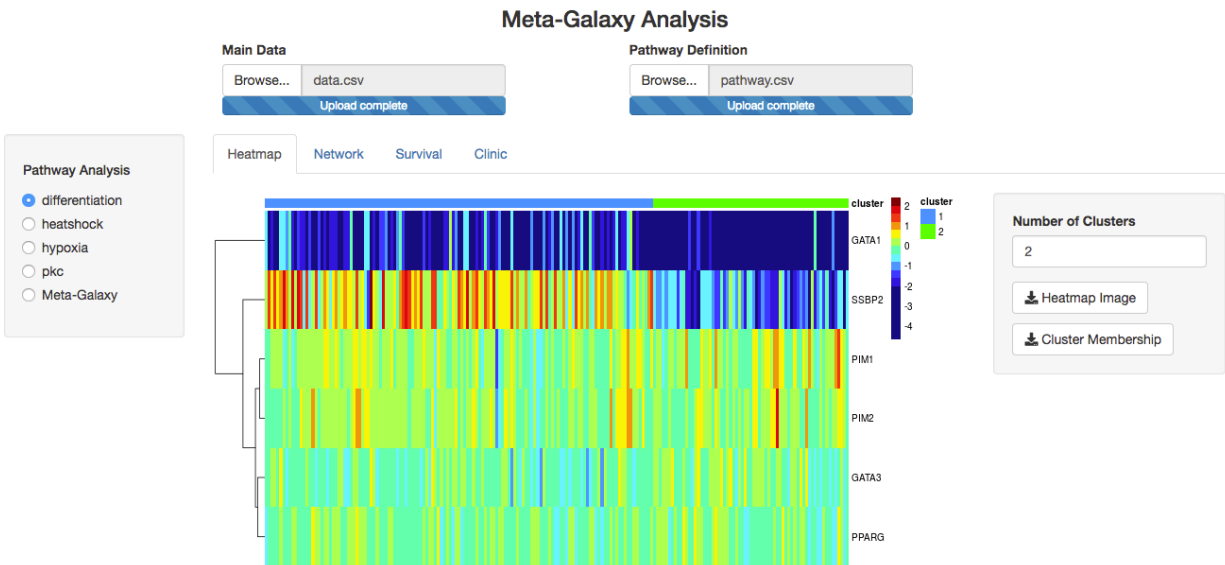
Please upload your main data file (\*.csv). In your data, prepare samples (e.g. cell, patient) as rows and features (e.g. gene, protein, clinical variable) as columns.

Please upload your pathway definition file (\*.csv). Pathway definition should consist of two columns: the first column listing all proteins included in the main data file; the second column listing the corresponding pathways.

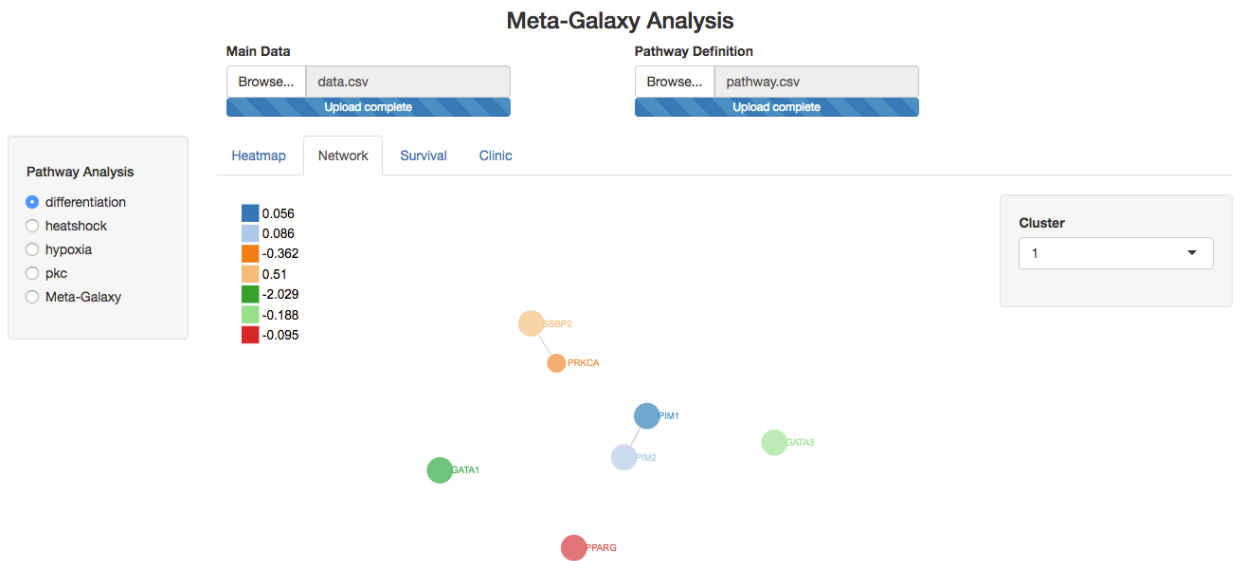
The portal offers four modules of analyses for each pathway: Heatmap, Network, Survival, Clinic. Users can select and switch between analysis modules by clicking on the tabs underneath the data upload panel. In each module, the analysis results (i.e. figures and tables) will be displayed in the central panel underneath the analysis tabs, whereas the grey panel on the right offers options to adjust parameters and download the figures/tables.

**Heatmap.** This module provides cluster analysis, which clusters samples based on the genes/proteins in the pathway using *k-means* algorithm and clusters genes/proteins using *hierarchical clustering (ward linkage)* algorithm. The optimal number of sample clusters,

determined using *Progeny Clustering* algorithm, are automatically shown. Users have the option to adjust the number of clusters, and download the figures as well as the cluster memberships.

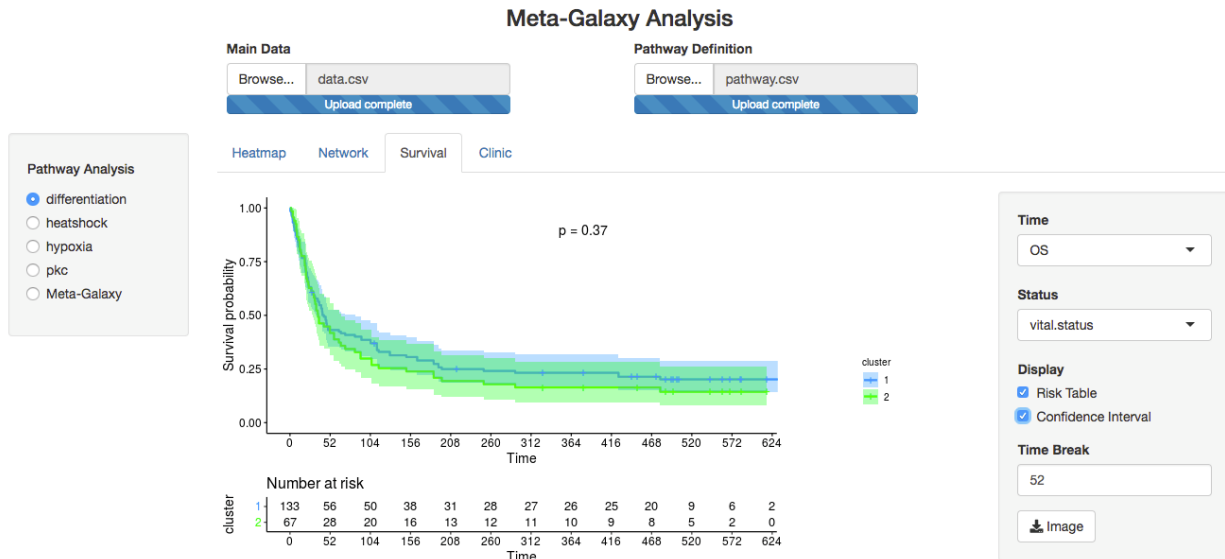


**Network.** This module provides network analysis, which uses the *glasso* algorithm to construct the network connections. The network will display all genes/proteins of the pathway (in a bigger node size), as well as genes/proteins from other pathways that are connected to the pathway (in a smaller node size). The node color indicates the median expression level of that gene/protein in the chosen cluster. Users have the option to zoom in and out of the network, move and adjust the network display, and select which cluster to look at.





**Survival.** This module provides survival analysis, which plots the *Kaplan-Meier* curves for survival stats. Users have the option to choose the variables for creating the survival curves, displaying risk table and confidence intervals, adjusting the time interval for the plot, and downloading the figure.



**Clinic.** This module analyzes relations between clinical variables and the clusters (as determined in the Heatmap module). Any categorical or numeric measurements except the gene/protein measurements will be automatically extracted and included in the analysis. Users have the option to select the clinical variables of interest, adjust the display length, search for a particular clinical variable, and download the table.

**Meta-Galaxy Analysis**

Main Data: data.csv (Upload complete)  
 Pathway Definition: pathway.csv (Upload complete)

Heatmap | Network | Survival | **Clinic**

Pathway Analysis:  
 differentiation  
 heatshock  
 hypoxia  
 pkc  
 Meta-Galaxy

Show 10 entries | Search:

Category	Type	Count	Freq	C1.freq	C2.freq	pvalue.all	C1.n	C2.n	pvalue
Total	Count	200	1	0.665	0.335	5e-04	133	67	5e-04
SEX	F	108	0.54	0.534	0.552	0.92337	71	37	0.00107
SEX	M	92	0.46	0.466	0.448		62	30	0.00085
PRIOR.MAL	NO	162	0.81	0.812	0.806	1	108	54	2e-05
PRIOR.MAL	YES	38	0.19	0.188	0.194		25	13	0.05158
FLT3	Mutant	66	0.333	0.382	0.239	0.06309	50	16	3e-05
FLT3	Wildtype	132	0.667	0.618	0.761		81	51	0.00902

Clinical Variables:  
 SEX  
 PRIOR.MAL  
 FLT3  
 Relapse  
 vital.status  
 Table

Showing 1 to 7 of 7 entries | Previous 1 Next