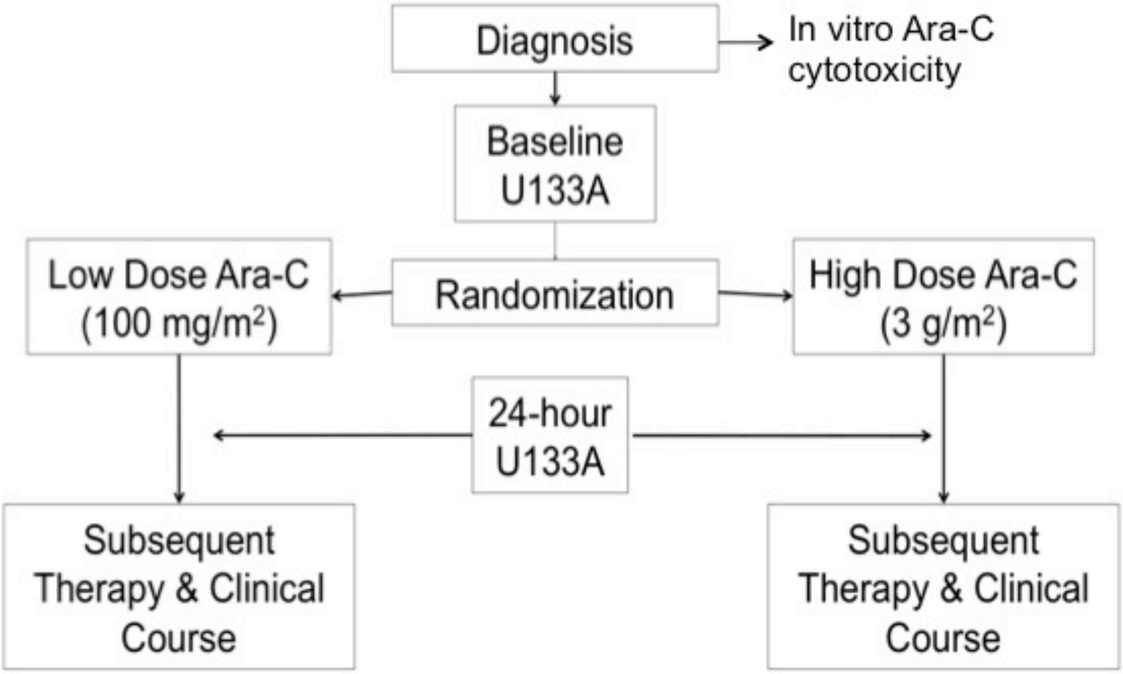

Supplementary Figure 1S. Schematic showing overall study design.

Supplementary Table 1. List of genes with distinct pattern of expression differences between post-Ara_C between LDAC and HDAC arms (p<0.001).

probeid	Gene.Symbo	Gene Name	Stat	perm.p	q value
220443_s_at	VAX2	ventral anterior homeobox 2	3.3690	0.0006	1
210139_s_at	PMP22	peripheral myelin protein 22	3.2498	0.0003	1
200730_s_at	PTP4A1	protein tyrosine phosphatase type IVA, member 1	3.1901	0.0008	1
201148_s_at	TIMP3	TIMP metallopeptidase inhibitor 3	3.0709	0.0009	1
203241_at	UVRAG	UV radiation resistance associated gene	-3.1901	0.0004	1
221376_at	FGF17	fibroblast growth factor 17	-3.1901	0.0006	1
216698_x_at	OR7E47P	olfactory receptor, family 7, subfamily E, member 47 pseudogene	-3.3094	0.0006	1
221378_at	CER1	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)	-3.4883	0.0004	1

A positive z-statistic indicates that (arm A) had a greater median expression change than Arm B.

Supplementary Table 2S. PROMISE analysis identified genes change in expression post ara-C to be predictive of beneficial or deterimental patterns of association with clinical endpoints in AML patients.

A. PROMISE 3 (PR3) analysis utilizing 3 endpoints LC50, MRD22 and EFS

ProbeID	Gene.Symbol	Gene Name	LC50. stat	MRD22. stat	EFS. stat	PROMISE. stat	LC50 p vaule	MRD22 p value	EFS p value	PROMISE 3 (PR3) p value	BH95_q	PC06_q	Risk p value
201088_at	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1); karyopherin alpha-2 subunit lik	0.708	0.568	0.290	-0.522	0.044	0.006	0.136	0.000	0.000	0.000	0.171
203699_s_at	DIO2	deiodinase, iodothyronine, type II	-0.708	-0.468	-0.506	0.561	0.040	0.026	0.009	0.000	0.000	0.000	0.472
205547_s_at	TAGLN	transgelin	-0.773	-0.462	-0.447	0.561	0.030	0.026	0.020	0.000	0.000	0.000	0.662
205569_at	LAMP3	lysosomal-associated membrane protein 3	-0.773	-0.406	-0.614	0.598	0.028	0.060	0.001	0.000	0.000	0.000	0.686
206160_at	APOBEC2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	-0.602	-0.531	-0.493	0.542	0.110	0.010	0.010	0.000	0.000	0.000	0.245
207366_at	KCNS1	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1	-0.773	-0.365	-0.448	0.529	0.024	0.085	0.020	0.000	0.000	0.000	0.879
209668_x_at	CES2	carboxylesterase 2 (intestine, liver)	-0.773	-0.537	-0.253	0.521	0.030	0.008	0.203	0.000	0.000	0.000	0.658
210119_at	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	-0.773	-0.586	-0.331	0.564	0.027	0.004	0.090	0.000	0.000	0.000	0.531
220849_at	FLJ22659	hypothetical LOC100132472; hypothetical LOC79999; hypothetical LOC388436	-0.838	-0.291	-0.549	0.559	0.007	0.177	0.004	0.000	0.000	0.000	0.719
221793_at	DOCK6	dedicator of cytokinesis 6	-0.708	-0.400	-0.650	0.586	0.043	0.064	0.000	0.000	0.000	0.000	0.886
201053_s_at	PSMF1	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	0.773	0.403	0.306	-0.494	0.027	0.057	0.116	0.000	0.153	0.118	0.842
205444_at	ATP2A1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	-0.773	-0.523	-0.349	0.548	0.029	0.011	0.071	0.000	0.153	0.118	0.259
207780_at	CYLC2	cylicin, basic protein of sperm head cytoskeleton 2	-0.708	-0.435	-0.460	0.534	0.042	0.041	0.017	0.000	0.153	0.118	0.858
212436_at	TRIM33	tripartite motif-containing 33	-0.602	-0.478	-0.668	0.583	0.116	0.024	0.000	0.000	0.153	0.118	0.983
216708_x_at	IGL2	cytoskeleton associated protein 2	-0.643	-0.520	-0.411	0.525	0.096	0.013	0.033	0.000	0.153	0.118	0.638
217330_at	DISC1	disrupted in schizophrenia 1	-0.643	-0.307	-0.607	0.519	0.097	0.152	0.001	0.000	0.153	0.118	0.284
221999_at	VRK3	vaccinia related kinase 3	-0.838	-0.504	-0.233	0.525	0.008	0.017	0.246	0.000	0.153	0.118	0.388
38447_at	ADRBK1	adrenergic, beta, receptor kinase 1	-0.643	-0.400	-0.546	0.530	0.091	0.059	0.003	0.000	0.153	0.118	0.809
208429_x_at	HNF4A	hepatocyte nuclear factor 4, alpha	-0.659	-0.277	-0.549	0.495	0.066	0.200	0.004	0.000	0.217	0.192	0.854
211920_at	CFB	complement factor B	-0.643	-0.450	-0.408	0.500	0.097	0.031	0.032	0.000	0.217	0.192	0.943
214598_at	CLDN8	claudin 8	-0.708	-0.579	-0.309	0.532	0.043	0.004	0.114	0.000	0.217	0.192	0.435
217857_s_at	RBM8A	RNA binding motif protein 8A	0.708	0.325	0.530	-0.521	0.042	0.133	0.005	0.000	0.217	0.192	0.476
202585_s_at	NFX1	nuclear transcription factor, X-box binding 1	-0.773	-0.326	-0.427	0.509	0.027	0.132	0.028	0.000	0.278	0.254	0.941
209966_x_at	ESRRG	estrogen-related receptor gamma	-0.667	-0.417	-0.472	0.519	0.050	0.049	0.013	0.000	0.278	0.254	0.355
213078_x_at	AGPAT7	lysophosphatidylcholine acyltransferase 4	-0.838	-0.291	-0.372	0.500	0.008	0.172	0.052	0.000	0.278	0.254	0.498
212265_at	QKI	quaking homolog, KH domain RNA binding (mouse)	0.708	0.391	0.372	-0.490	0.042	0.068	0.059	0.000	0.312	0.273	0.779
212570_at	ENDOD1	endonuclease domain containing 1	-0.449	-0.541	-0.512	0.501	0.251	0.010	0.006	0.000	0.312	0.273	0.603
212885_at	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	0.838	0.493	0.126	-0.486	0.009	0.019	0.518	0.000	0.312	0.273	0.265
215114_at	SENP3	SUMO1/sentrin/SMT3 specific peptidase 3	-0.708	-0.391	-0.409	0.503	0.043	0.067	0.035	0.000	0.312	0.273	0.907
38398_at	MADD	MAP-kinase activating death domain	-0.838	-0.262	-0.377	0.492	0.006	0.219	0.052	0.000	0.312	0.273	0.546
45572_s_at	GGA1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	-0.773	-0.334	-0.339	0.482	0.028	0.120	0.083	0.000	0.312	0.273	0.713
206242_at	TM4SF5	transmembrane 4 L six family member 5	-0.513	-0.488	-0.493	0.498	0.185	0.021	0.010	0.001	0.317	0.279	0.969
206841_at	PDE6H	phosphodiesterase 6H, cGMP-specific, cone, gamma	-0.838	-0.593	-0.072	0.501	0.005	0.003	0.717	0.001	0.317	0.279	0.094
208674_x_at	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	0.773	0.434	0.271	-0.493	0.026	0.041	0.168	0.001	0.317	0.279	0.810
209556_at	NCDN	neurochondrin	-0.773	-0.444	-0.301	0.506	0.024	0.035	0.127	0.001	0.317	0.279	0.994
216294_s_at	KIAA1109	KIAA1109	-0.838	-0.428	-0.256	0.508	0.007	0.044	0.190	0.001	0.317	0.279	0.796
219041_s_at	REPIN1	replication initiator 1	0.773	0.322	0.364	-0.486	0.030	0.139	0.059	0.001	0.317	0.279	0.599
219967_at	MRM1	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	-0.384	-0.714	-0.434	0.511	0.333	0.000	0.022	0.001	0.317	0.279	0.348
206421_s_at	SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	-0.513	-0.505	-0.446	0.488	0.185	0.015	0.020	0.001	0.329	0.294	0.618
207239_s_at	PCTK1	PCTAIRE protein kinase 1	-0.269	-0.437	-0.707	0.471	0.498	0.042	0.000	0.001	0.329	0.294	0.560
209476_at	TXNDC	thioredoxin-related transmembrane protein 1	0.838	0.377	0.257	-0.491	0.009	0.078	0.192	0.001	0.329	0.294	0.910
211896_s_at	DCN	decorin	-0.838	-0.380	-0.215	0.478	0.007	0.072	0.282	0.001	0.329	0.294	0.367
213209_at	TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 6	-0.773	-0.161	-0.520	0.485	0.029	0.463	0.007	0.001	0.338	0.304	0.450
217830_s_at	NSFL1C	NSFL1 (p97) cofactor (p47)	-0.773	-0.260	-0.390	0.474	0.030	0.227	0.043	0.001	0.338	0.304	0.483
219704_at	YBX2	Y box binding protein 2	-0.472	-0.558	-0.443	0.491	0.214	0.007	0.020	0.001	0.338	0.304	0.763
220538_at	ADM2	adrenomedullin 2	-0.643	-0.421	-0.419	0.494	0.094	0.045	0.028	0.001	0.338	0.304	0.692
221001_at	LOC647835	chromosome 15 open reading frame 49	-0.594	-0.503	-0.337	0.478	0.126	0.017	0.086	0.001	0.338	0.304	0.091
221047_s_at	MARK1	MAP/microtubule affinity-regulating kinase 1	-0.594	-0.465	-0.438	0.499	0.126	0.029	0.024	0.001	0.338	0.304	0.320
40189_at	SET	SET nuclear oncogene; similar to SET translocation	0.773	0.514	0.156	-0.481	0.027	0.015	0.436	0.001	0.338	0.304	0.220
211147_s_at	P2RXL1	purinergic receptor P2X, ligand-gated ion channel, 6	-0.773	-0.336	-0.285	0.465	0.027	0.115	0.147	0.001	0.339	0.308	0.944
212168_at	RBM12	RNA binding motif protein 12; copine I	0.838	0.338	0.223	-0.467	0.007	0.117	0.257	0.001	0.339	0.308	0.484
216443_at	LUZP2	leucine zipper protein 2	-0.602	-0.626	-0.235	0.488	0.120	0.001	0.236	0.001	0.339	0.308	0.226
218476_at	POMT1	protein-O-mannosyltransferase 1	-0.708	-0.501	-0.196	0.468	0.043	0.014	0.325	0.001	0.339	0.308	0.439
49327_at	SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	-0.708	-0.530	-0.246	0.495	0.042	0.011	0.214	0.001	0.339	0.308	0.339
49878_at	PEX16	peroxisomal biogenesis factor 16	-0.513	-0.704	-0.251	0.489	0.197	0.000	0.201	0.001	0.339	0.308	0.459
202231_at	PCID1	eukaryotic translation initiation factor 3, subunit M	0.773	0.457	0.179	-0.470	0.029	0.030	0.367	0.001	0.345	0.318	0.907
202621_at	IRF3	interferon regulatory factor 3	-0.838	-0.274	-0.304	0.472	0.006	0.199	0.120	0.001	0.345	0.318	0.743
216272_x_at	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	-0.838	-0.301	-0.298	0.479	0.006	0.163	0.132	0.001	0.345	0.318	0.859
216540_at	TRA@	T cell receptor alpha constant; T cell receptor alpha locus; T cell receptor alpha variab	-0.602	-0.292	-0.547	0.480	0.115	0.177	0.004	0.001	0.345	0.318	0.849
220977_x_at	EPB41L5	erythrocyte membrane protein band 4.1 like 5	-0.773	-0.247	-0.417	0.479	0.027	0.259	0.030	0.001	0.345	0.318	0.309
1494_f_at	CYP2A6	cytochrome P450, family 2, subfamily A, polypeptide 6	-0.838	-0.165	-0.432	0.478	0.007	0.459	0.025	0.001	0.348	0.322	0.516
205981_s_at	ING2	inhibitor of growth family, member 2	0.773	0.400	0.229	-0.467	0.028	0.057	0.245	0.001	0.348	0.322	0.837
213664_at	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system	-0.773	-0.320	-0.389	0.494	0.029	0.136	0.045	0.001	0.348	0.322	0.342
215579_at	APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	-0.342	-0.681	-0.381	0.468	0.384	0.000	0.050	0.001	0.348	0.322	0.066

217773_s_at	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	0.513	0.497	0.406	-0.472	0.185	0.018	0.035	0.001	0.348	0.322	0.878

B. PROMISE 2 (PR2) analysis utilizing 2 clinical endpoints (MRD22 and EFS)

ProbeID	Gene.Symbol		MRD22. stat	EFS.stat	PROMISE. stat	MRD22 p value	EFS p value	PROMISE 2 (PR2) p value	BH95_q	PC06_q	Risk p value		
221212_x_at	PB1	polybromo 1	-0.613	-0.635	0.624	0.003	0.001	0.000	0.000	0.000	0.212		
221365_at	MLNR	motilin receptor	-0.611	-0.529	0.570	0.002	0.004	0.000	0.000	0.000	0.284		
212436_at	TRIM33	tripartite motif-containing 33	-0.478	-0.668	0.573	0.024	0.000	0.000	0.635	0.548	0.983		
219967_at	MRM1	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	-0.714	-0.434	0.574	0.000	0.022	0.000	0.635	0.548	0.348		
207239_s_at	PCTK1	PCTAIRE protein kinase 1	-0.437	-0.707	0.572	0.042	0.000	0.000	0.662	0.613	0.560		
212671_s_at	HLA-DQA1	similar to hCG2042724; similar to HLA class II histocompatibility antigen, DQ(1) alpha	0.556	0.533	-0.545	0.007	0.004	0.000	0.662	0.613	0.889		
215835_at	SCARB1	scavenger receptor class B, member 1	-0.665	-0.390	0.527	0.001	0.045	0.000	0.662	0.613	0.191		
212570_at	ENDOD1	endonuclease domain containing 1	-0.541	-0.512	0.527	0.010	0.006	0.000	0.662	0.626	0.603		
215579_at	APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	-0.681	-0.381	0.531	0.000	0.050	0.000	0.662	0.626	0.066		
216546_s_at	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	-0.544	-0.524	0.534	0.009	0.005	0.000	0.662	0.626	0.090		
217315_s_at	KLK13	kallikrein-related peptidase 13	-0.562	-0.547	0.554	0.006	0.003	0.000	0.662	0.626	1.000		
218901_at	PLSCR4	phospholipid scramblase 4	-0.570	-0.497	0.534	0.005	0.009	0.000	0.662	0.626	0.197		
220874_at	---	astrotactin 2	-0.577	-0.461	0.519	0.006	0.013	0.000	0.662	0.626	0.971		
215479_at	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin)	-0.568	-0.468	0.518	0.005	0.013	0.001	0.662	0.636	0.980		
216809_at	CYLC1	cylicin, basic protein of sperm head cytoskeleton 1	-0.675	-0.434	0.554	0.001	0.025	0.001	0.662	0.636	0.095		
205569_at	LAMP3	lysosomal-associated membrane protein 3	-0.406	-0.614	0.510	0.060	0.001	0.001	0.662	0.649	0.686		
206160_at	APOBEC2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	-0.531	-0.493	0.512	0.010	0.010	0.001	0.662	0.649	0.245		
211524_at	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	-0.611	-0.413	0.512	0.002	0.031	0.001	0.662	0.649	0.279		
215473_at	LOC388458	hypothetical gene supported by BC040718	-0.570	-0.483	0.527	0.006	0.011	0.001	0.662	0.649	0.905		
216994_s_at	RUNX2	runt-related transcription factor 2	-0.668	-0.354	0.511	0.001	0.066	0.001	0.662	0.649	0.193		
220986_s_at	TIGD6	tigger transposable element derived 6	-0.486	-0.578	0.532	0.021	0.002	0.001	0.662	0.649	0.912		
216005_at	TNC	tenascin C	-0.713	-0.329	0.521	0.000	0.088	0.001	0.662	0.664	0.236		
219602_s_at	FAM38B	family with sequence similarity 38, member B	-0.466	-0.562	0.514	0.031	0.003	0.001	0.662	0.664	0.697		
220053_at	GDF3	growth differentiation factor 3	-0.482	-0.556	0.519	0.023	0.003	0.001	0.662	0.664	0.363		
221793_at	DOCK6	dedicator of cytokinesis 6	-0.400	-0.650	0.525	0.064	0.000	0.001	0.662	0.664	0.886		
202196_s_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	-0.444	-0.594	0.519	0.037	0.002	0.001	0.671	0.674	0.700		
207242_s_at	GRIK1	glutamate receptor, ionotropic, kainate 1	-0.733	-0.296	0.514	0.000	0.134	0.001	0.671	0.674	0.102		
215766_at	GSTA1	glutathione S-transferase alpha 1	-0.608	-0.438	0.523	0.003	0.023	0.001	0.678	0.709	0.613		
215825_at	---		-0.675	-0.359	0.517	0.000	0.067	0.001	0.678	0.709	0.349		
220345_at	LRRTM4	leucine rich repeat transmembrane neuronal 4	-0.568	-0.476	0.522	0.006	0.014	0.001	0.678	0.709	0.220		
222172_at	NPAS3	neuronal PAS domain protein 3	-0.434	-0.627	0.530	0.042	0.001	0.001	0.678	0.709	0.841		
220584_at	FLJ22184	hypothetical protein FLJ22184	-0.639	-0.375	0.507	0.001	0.052	0.001	0.684	0.717	0.721		
221915_s_at	RANBP1	similar to RAN binding protein 1; RAN binding protein 1	-0.533	-0.509	0.521	0.011	0.007	0.001	0.684	0.717	0.636		