

Supplemental Table 1: Clinical characteristics for newly diagnosed AML patients (n=67).

# AML	age	sex	karyotype	t(8;21)	inv(16)	t(15;17)	t(9;11)	FLT3 ITD	FLT3 TKD	CEBPA	NRAS	NPM1
1	32.8	m	CBF	WT	MUT	WT	WT	WT	WT	WT	WT	WT
2	55.2	w	normal	WT	WT	WT	WT	WT	WT	MUT		MUT
3	61.4	m	del12/normal					MUT	WT	WT		MUT
4	56.1	m	normal	WT	WT	WT	WT	WT	MUT	WT		MUT
5	21.0	m	CBF	WT	MUT	WT	WT	WT	WT	WT	WT	WT
6	57.0	m										
7	50.8	m	normal	WT	WT	WT	WT	WT	MUT	WT		MUT
8	46.1	m	normal	WT	WT	WT	WT	MUT	WT	WT		MUT
9	73.6	w	normal	WT	WT	WT	WT	MUT	WT			MUT
10	46.9	w	normal	WT	WT	WT	WT	MUT	WT	WT		WT
11	32.6	m	inv3; -7	WT	WT	WT	WT	WT	WT	WT		WT
12	76.5	m	normal	WT	WT	WT	WT	WT	WT	WT		MUT
13	47.8	w	normal	WT	WT	WT	WT	MUT	WT	WT		MUT
14	55.9	m	normal	WT	WT	WT	WT	WT	WT	MUT		WT
15	57.5	m	del13	WT	WT	WT	WT	MUT	WT	WT		WT
16	23.7	w	normal	WT	WT	WT	WT	WT	MUT	MUT		WT
17	81.7	w	normal	WT	WT	WT	WT	WT	WT	WT		WT
18	58.5	w	+8	WT	WT	WT	WT	MUT	WT	WT		WT
19	48.5	m	normal	WT	WT	WT	WT	WT	WT	WT		WT
20	44.6	w	normal	WT	WT	WT	WT	MUT	WT	WT		MUT
21	66.9	m	complex	WT	WT	WT	WT	WT	WT			WT
22		m										
23	61.0	m	t(2;14)	WT	WT	WT	WT	MUT	WT			WT
24	26.8	w	+21	WT	WT	WT	WT	WT	WT	MUT		WT
25	33.8	m	CBF	WT	MUT	WT	WT	WT	WT	WT		WT
26	53.5	w	normal	WT	WT	WT	WT	WT	MUT	WT		MUT
27	57.0	w	CBF	WT		WT	WT	WT	WT	WT		WT
28	30.8	w	normal	WT	WT	WT	WT	WT	WT	MUT		WT
29	31.6	w	normal	WT	WT	WT	WT	WT	MUT	WT		MUT
30	58.2	m	normal	WT	WT	WT	WT	WT	WT	WT		MUT
31	28.1	w	CBF	WT	MUT	WT	WT	WT	WT	WT		WT
32	62.2	w	normal	WT	WT	WT	WT	MUT	WT			MUT
33	28.8	m	complex	WT	WT	WT	WT	WT	WT	WT		WT
34	66.6	w	normal	WT	WT	WT	WT	MUT	WT			MUT
35	65.8	m	+8 +4	WT	WT	WT	WT	WT	WT			WT
36	41.8	m	normal	WT	WT	WT	WT	MUT	WT	WT		WT
37	20.3	m	+11	WT	WT	WT	WT	WT	WT			WT
38	75.0	w	normal	WT	WT	WT	WT	MUT	WT			MUT
39	49.6	m	normal	WT	WT	WT	WT	WT	MUT	WT		MUT
40	68.2	m	normal	WT	WT	WT	WT	WT	WT			WT
41												
42	39.5	m	normal	WT	WT	WT	WT	MUT	WT	WT		MUT
43	46.5	w	normal	WT	WT	WT	WT	MUT	WT	WT		MUT
44	71.4	w	normal	WT	WT	WT	WT	MUT	WT			WT
45	61.8	w	t(7;15); t(9;22)	WT	WT	WT	WT	WT	WT			WT
46	71.7	m	normal	WT	WT	WT	WT	MUT	WT			MUT
47	58.2	w	t(15;17)	WT	WT	MUT	WT	WT	WT	WT		WT
48	70.2	w	complex	WT	WT	WT	WT	WT	WT			WT
49	46.6	w	CBF	WT	MUT	WT	WT	WT	WT			WT
50	66.8	w	normal	WT	WT	WT	WT	WT	WT			WT
51	52.1	w	CBF	MUT	WT	WT	WT	WT	WT	WT		WT
52	78.0	w	normal	WT	WT	WT	WT	WT	WT			MUT
53	68.3	m	complex	WT	WT	WT	WT	WT	WT			WT
54	47.7	m	normal	WT	WT	WT	WT	WT	WT	WT		MUT
55	50.6	m		WT	WT	WT	WT	WT	WT	WT		MUT
56												
57	68.7	m	normal	WT	WT	WT	WT	MUT	WT			MUT
58	41.2	w	CBF									
59												
60												
61	57.6	m	normal	WT	WT	WT	WT	MUT	WT	WT		MUT
62	69.5	m	normal	WT	WT	WT	WT	WT	WT			WT
63	72.0	w	normal	WT	WT	WT	WT	WT	WT			WT
64	33.0	m	CBF	WT	MUT	WT	WT	WT	WT	WT		WT
65	76.8	w	normal	WT	WT	WT	WT	WT	WT			MUT
66	70.8	w	+13	WT	WT	WT	WT	WT	WT			WT
67	58.7	m	normal	WT	WT	WT	WT	MUT	WT			MUT

Supplemental Table 2: Clinical, cytogenetic and molecular genetic characteristics of primary AML samples (n=12) profiled on microarrays to obtain BV6 response associated signature.

# AML	age	sex	karyotype	t(15;17)	t(9;11)	FLT3 ITD	FLT3 TKD	CEBPA	NPM1	BV6 response group	ara-C response group
3	61	m	del12/normal	n.a.	n.a.	MUT	WT	WT	MUT	sensitive	resistant
18	58	w	+8	WT	WT	MUT	WT	WT	WT	sensitive	sensitive
29	32	w	normal	WT	WT	WT	MUT	WT	MUT	sensitive	sensitive
49	47	w	CBF	WT	WT	WT	WT	n.a.	WT	sensitive	sensitive
54	48	m	normal	WT	WT	WT	WT	WT	MUT	sensitive	sensitive
65	77	w	normal	WT	WT	WT	WT	n.a.	MUT	sensitive	intermediate
2	55	w	normal	WT	WT	WT	WT	MUT	MUT	resistant	n.a.
12	76	m	normal	WT	WT	WT	WT	WT	MUT	resistant	resistant
15	58	m	del13	WT	WT	MUT	WT	WT	WT	resistant	n.a.
24	27	w	+21	WT	WT	WT	WT	MUT	WT	resistant	sensitive
27	57	w	CBF	WT	WT	WT	WT	WT	WT	resistant	resistant
37	20	m	+11	WT	WT	WT	WT	n.a.	WT	resistant	resistant

Supplemental Table 4: Differentially regulated Biocarta pathways among BV6- and DMSO-treated primary AML samples, according to LS/KS permutation testing (Pathway comparison). Light grey script indicated pathways not significant in LS/KS testing, but in GSA test.

Biocarta Pathway	Pathway description	Number of genes	LS p-value	KS p-value	Efron-Tibshirani's GSA test p-value
pathways specifically deregulated in BV6 sensitive samples					
h DNAfragmentPathway	Apoptotic DNA fragmentation and tissue homeostasis	15	0.00003	0.04441	< 0.005
h smPathway	Spliceosomal Assembly	22	0.00003	0.04504	< 0.005
h il18Pathway	IL 18 Signaling Pathway	7	0.00136	0.00337	< 0.005
h rabPathway	Rab GTPases Mark Targets In The Endocytotic Machinery	25	0.00242	0.04861	< 0.005
h tnfr1Pathway	TNFR1 Signaling Pathway	37	0.0038	0.00918	< 0.005
h cpsfPathway	Polyadenylation of mRNA	9	0.00931	0.01273	< 0.005
h eif2Pathway	Regulation of eIF2	18	0.01638	0.01819	< 0.005
h d4gdiPathway	D4-GDI Signaling Pathway	21	0.02449	0.28193	< 0.005
h RacCycDPathway	Influence of Ras and Rho proteins on G1 to S Transition	34	0.02801	0.05138	< 0.005
h prc2Pathway	The PRC2 Complex Sets Long-term Gene Silencing Through Modification of Histone Tails	13	0.03252	0.10773	< 0.005
h bard1Pathway	BRCA1-dependent Ub-ligase activity	5	0.04497	0.08486	< 0.005
h caspasePathway	Caspase Cascade in Apoptosis	36	0.04637	0.51603	< 0.005
h aifPathway	Opposing roles of AIF in Apoptosis and Cell Survival	5	0.29515	0.46769	< 0.005
h nfkbPathway	NF-kB Signaling Pathway	25	0.42002	0.08742	< 0.005
pathways specifically deregulated in BV6 resistant samples					
h ctlPathway	CTL mediated immune response against target cells	16	0.00614	0.59215	< 0.005
h ionPathway	Ion Channel and Phorbol Esters Signaling Pathway	7	0.00849	0.02759	< 0.005
h agpcrPathway	Attenuation of GPCR Signaling	13	0.0099	0.00023	< 0.005
h chrebpPathway	ChREBP regulation by carbohydrates and cAMP	12	0.01466	0.00003	< 0.005
h raccPathway	Ion Channels and Their Functional Role in Vascular Endothelium	11	0.015	0.0001	< 0.005
h il2Pathway	IL 2 signaling pathway	22	0.01677	0.01018	< 0.005
h pdgfrPathway	PDGF Signaling Pathway	33	0.01736	0.00807	< 0.005
h mhcPathway	Antigen Processing and Presentation	14	0.0193	0.01398	< 0.005
h gcrPathway	Corticosteroids and cardioprotection	23	0.02473	0.001	< 0.005
h gsPathway	Activation of cAMP-dependent protein kinase, PKA	14	0.02478	0.00052	< 0.005
h plcePathway	Phospholipase C-epsilon pathway	15	0.0251	0.00014	< 0.005
h egfPathway	EGF Signaling Pathway	36	0.02617	0.00662	< 0.005
h pkcPathway	Activation of PKC through G protein coupled receptor	8	0.03227	0.02533	< 0.005
h cremPathway	Regulation of Spermatogenesis by CREM	8	0.0343	0.00133	< 0.005
h il4Pathway	IL 4 signaling pathway	7	0.03687	0.12185	< 0.005
h ifngPathway	IFN gamma signaling pathway	13	0.04199	0.09419	< 0.005
h myosinPathway	PKC-catalyzed phosphorylation of inhibitory phosphoprotein of myosin phosphatase	22	0.04362	0.01643	< 0.005
h cfrPathway	Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway	12	0.0482	0.00287	< 0.005
h stressPathway	TNF/Stress Related Signaling	31	0.04909	0.00733	< 0.005
h mPRPathway	How Progesterone Initiates the Oocyte Maturation	22	0.05098	0.01763	< 0.005
h tubbyPathway	G-Protein Signaling Through Tubby Proteins	8	0.05217	0.02533	< 0.005
h bArrestinPathway	?-arrestins in GPCR Desensitization	15	0.05415	0.00401	< 0.005
h nos1Pathway	Nitric Oxide Signaling Pathway	6	0.10852	0.03352	< 0.005
h ifnaPathway	IFN alpha signaling pathway	14	0.11202	0.02918	< 0.005
h ptenPathway	PTEN dependent cell cycle arrest and apoptosis	36	0.17184	0.04242	< 0.005
h barr-mapkPathway	Role of β -arrestins in the activation and targeting of MAP kinases	18	0.17544	0.03456	< 0.005
h atrbrcaPathway	Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility	23	0.5561	0.59134	< 0.005
pathways deregulated in both BV6 sensitive and resistant samples					
h setPathway	Granzyme A mediated Apoptosis Pathway	20	0.00001	0.01475	< 0.005
h glycolysisPathway	Glycolysis Pathway	17	0.00015	0.00047	0.115
h iresPathway	Internal Ribosome entry pathway	16	0.00016	0.03141	< 0.005
h eifPathway	Eukaryotic protein translation	25	0.00249	0.00867	< 0.005
h SARSPathway	SARS Coronavirus Protease	10	0.00338	0.24913	< 0.005
h ck1Pathway	Regulation of cdk1/cdk5 by type 1 glutamate receptors	11	0.01807	0.00065	< 0.005
h hifPathway	Hypoxia-Inducible Factor in the Cardiovascular System	26	0.03089	0.18056	< 0.005