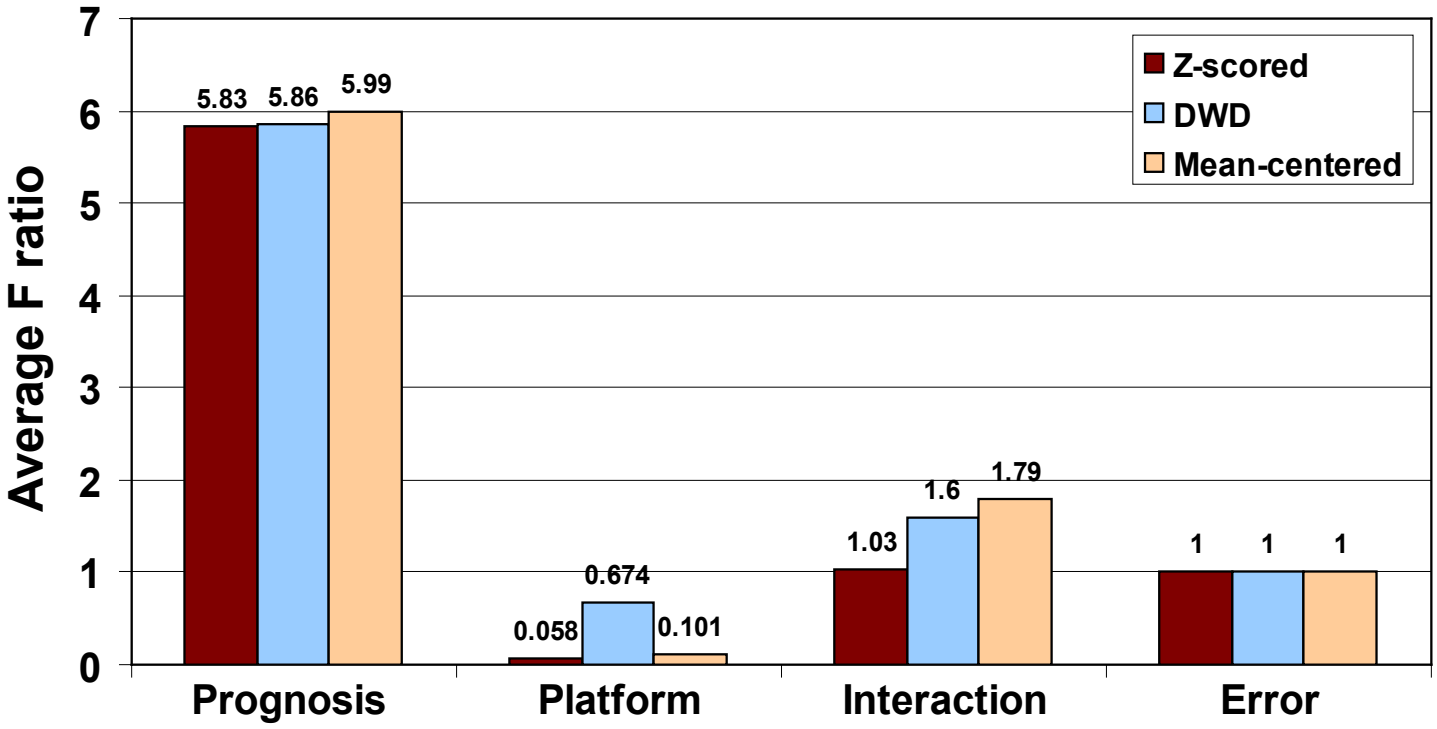
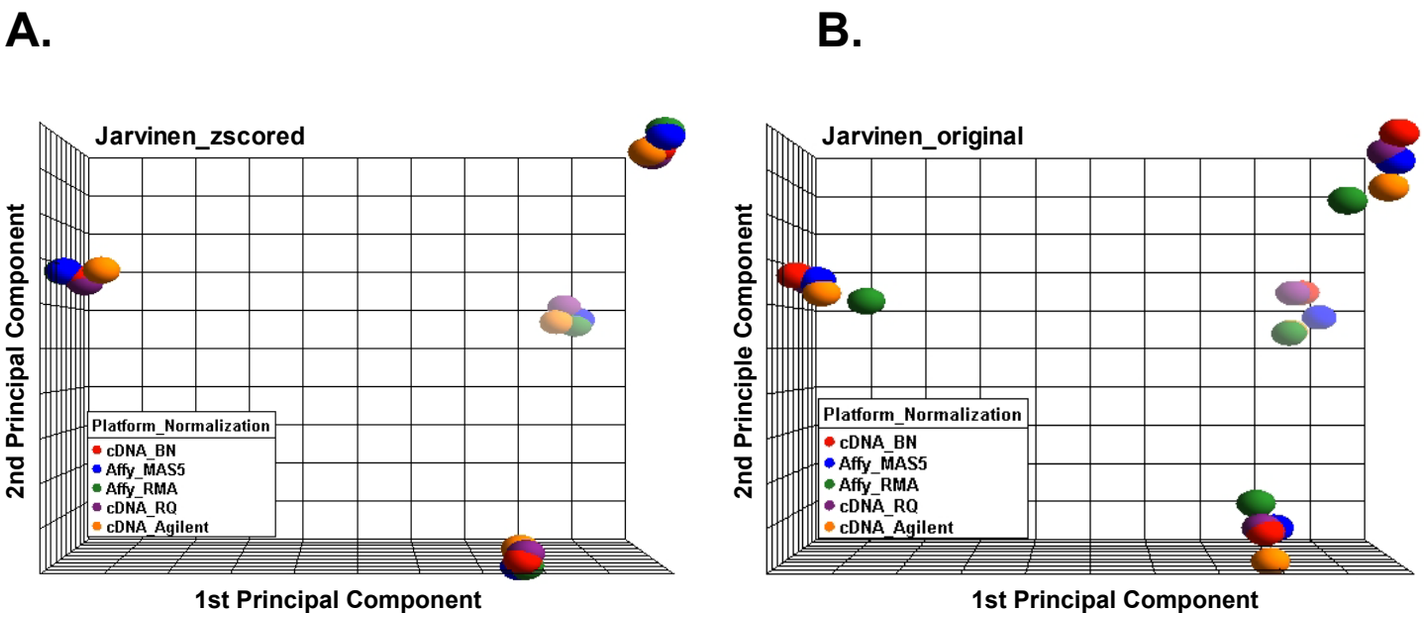
Supplemental Fig 1.

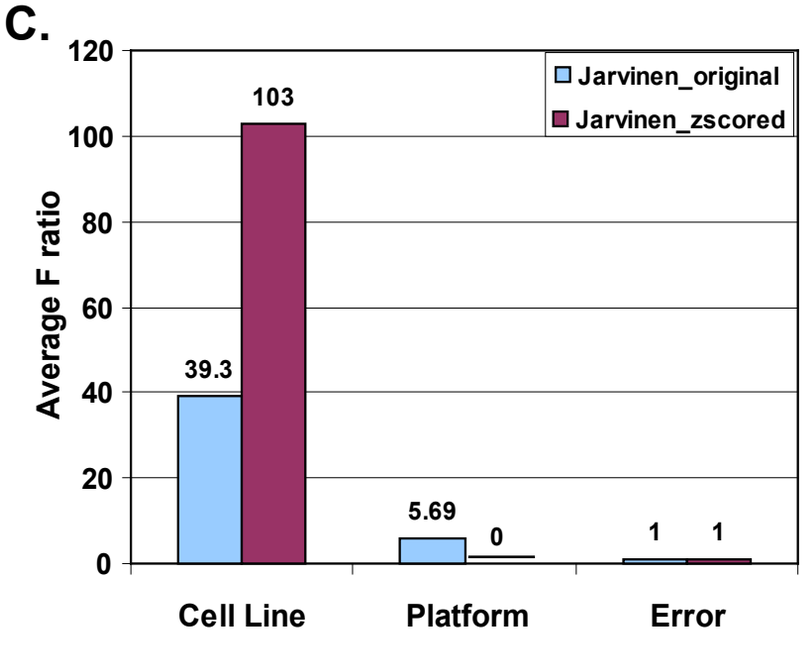


Supplemental Fig 1. Comparison of three bias removing methods. The data sets of 42 neuroblastoma samples from cDNA and Affymetrix platforms were combined after the normalization and using one of bias removing methods (z-score standardization, distance weighted discrimination (DWD) [1], and mean-centered method) to remove the effect of platform. DWD was performed using software available at https://genome.unc.edu/pubsup/dwd. The sources of variation from the ANOVA analysis showed that all these methods worked well with z-score standardization method showed better than other two methods because of lower interaction and platform effect.

[1] M. Benito, J. Parker, Q. Du, J. Wu, D. Xiang, C.M. Perou, and J.S. Marron, Adjustment of systematic microarray data biases. Bioinformatics 20 (2004) 105-14.

Supplemental Fig 2.



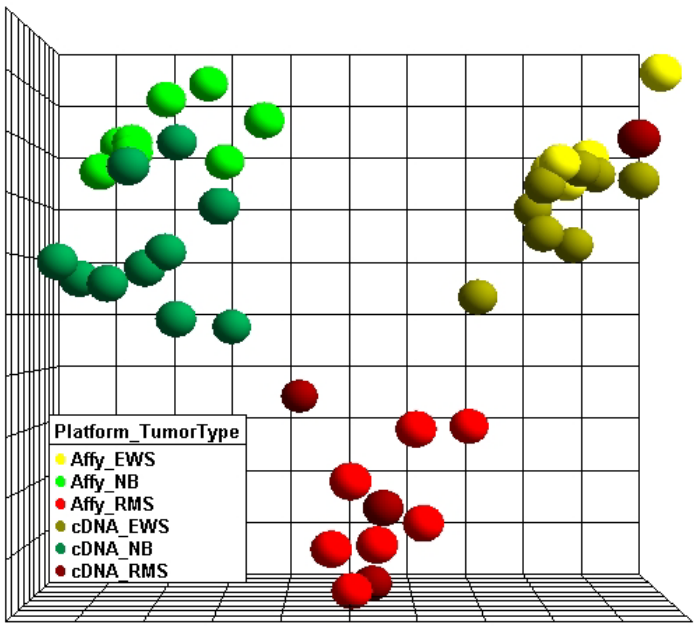


Supplemental Fig 2. Validation of the integrative method in a breast cancer data set. A published breast cancer dataset [2] contains four breast cancer cell lines on three different microarray platforms with different normalization methods, there are total 20 combinations of cell line type, platform and normalization method. The labels are as follows: cDNA_BN, custom-printed cDNA platform and data filtered with Bayesian networks and normalized with Lowess; cDNA_RQ, custom-printed cDNA platform and data filtered with ratio quality and normalized with ratio statistics; cDNA_Agilent, Agilent cDNA platform and Agilent normalization; Affy_MAS5, Affymetrix U95-Av2 platform and MAS5 normalization; Affy_RMA, Affymetrix U95-Av2 platform and RMA normalization. The Unigene ID was used as a common identifier and probes with the same Uingene ID were averaged [2]. **A.** Loading plot of top three principal components of data processed with z-score standardization. **B.** Loading plot of top three principal components of data without z-score standardization. **C.** Sources of variation in two-way ANOVA analysis. The data processed with z-score standardization result in lower platform effect and higher cell line difference.

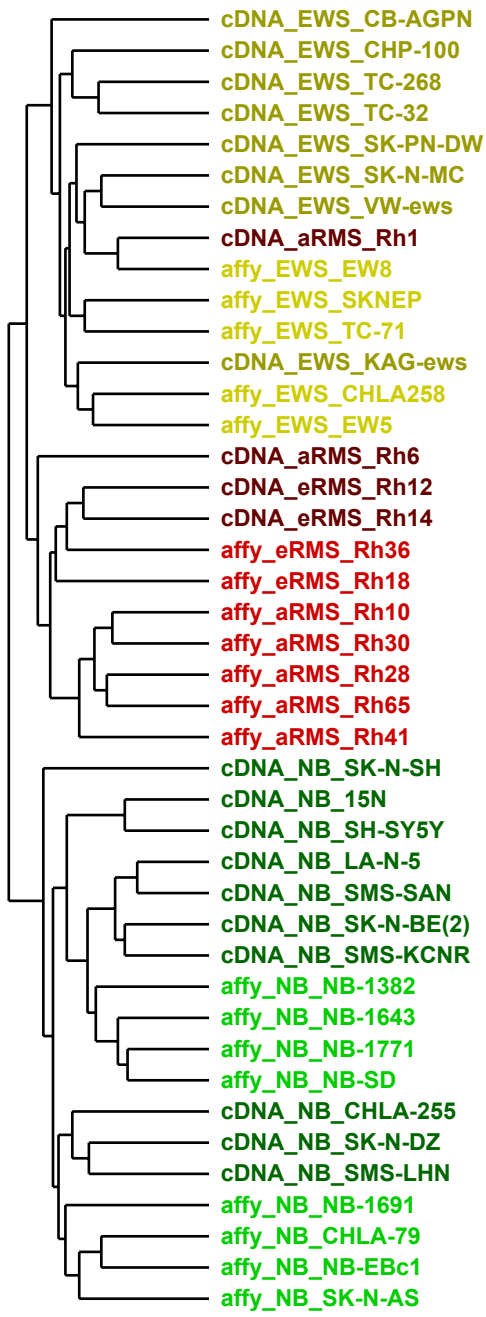
[2] A.K. Jarvinen, S. Hautaniemi, H. Edgren, P. Auvinen, J. Saarela, O.P. Kallioniemi, and O. Monni, Are data from different gene expression microarray platforms comparable? Genomics 83 (2004) 1164-8.

Supplemental Fig 3.

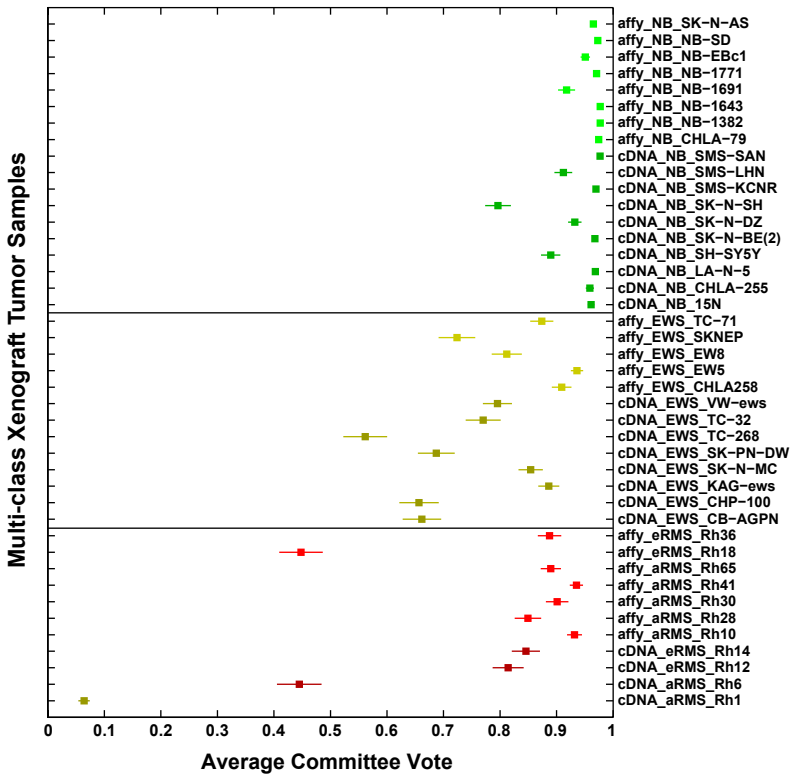
A.



B.



C.



Supplemental Fig 3. Validation of the integrative method in preclinical pediatric xenograft datasets. Datasets of total 42 experiments of preclinical pediatric xenograft samples, with 22 experiments on custom cDNA array [3] and 20 experiments on Affymetrix human U133plus2 array platform [4] consist of three pediatric cancer types: Neuroblastoma (NB), Rhabdomyosarcoma (RMS) and Ewing's sarcoma (EWS) (Supplemental Table 4). The cDNA expression ratio between test RNA and reference RNA on each microarray were normalized using a pin-based normalization method. For Affymetrix genechip, .CEL files were exported from Affymetrix GCOS software and normalized by GC-RMA in R [5]. The Unigene ID was used as a common identifier between two platforms and probes with the same Uingene ID were averaged; a total of 11847 Unigenes were common to both platforms and used for analysis. The data from each platform was z-score standardized and then combined for analysis. The sample labels are shown as follows: platform-cancer type-sample name. **A.** Loading plot of top three principal components of the 42 experiments using all 11847 Unigenes demonstrates the separation of three types of cancers except two samples. Platform effect is not seen after standardization. **B.** Hierarchical clustering analysis using all 11847 Unigenes showed the experiments are clustering according to cancer types except cDNA_aRMS_Rh1. Rh1 was initially diagnosed as embryonal rhabdomyosarcoma, however review by other has reclassified it as primitive neuroectoderma tumor, which is a member of Ewing's family of tumors [6]. **C.** Classification of the samples from ANN analysis using the leave-one-out strategy. A sample is classified to a cancer category according to its highest committee vote (average of all ANN outputs). Plotted is its committee vote for each sample. The perfectly classified sample would be plotted with a vote = 1. Different cancer categories were displayed in color as red for RMS, yellow for EWS and green for NB. cDNA_aRMS_Rh1 was labeled in yellow due to misclassification. See Supplemental Table 3 for ANN diagnosis and the committee votes.

[3] C.C. Whiteford, S. Bilke, B.T. Greer, Q. Chen, T.A. Braunschweig, N. Cenacchi, J.S. Wei, M.A. Smith, P. Houghton, C. Morton, C.P. Reynolds, R. Lock, R. Gorlick, C. Khanna, C.J. Thiele, M. Takikita, D. Catchpoole, S.M. Hewitt, and J. Khan, Credentialing preclinical pediatric xenograft models using gene expression and tissue microarray analysis. Cancer Res 67 (2007) 32-40.
[4] G. Neale, X. Su, C.L. Morton, D. Phelps, R. Gorlick, R.B. Lock, C.P. Reynolds, J.M. Maris, H.S. Friedman, J. Dome, J. Khoury, T.J. Triche, R.C. Seeger, R. Gilbertson, J. Khan, M.A. Smith, P.J. Houghton. Molecular characterization of the pediatric preclinical testing panel. Clinical Cancer Res (in Press)
[5] Z. Wu, and R.A. Irizarry, Preprocessing of oligonucleotide array data. Nat Biotechnol 22 (2004) 656-8.
[6] C.L. Morton, P.M. Potter: Rhabdomyosarcoma-specific expression of the herpes simplex virus thymidine kinase gene confers sensitivity to ganciclovir. J Pharmacol Exp Ther 1998, 286(2):1066-1073.

Supplemental Table 1. Neuroblastoma samples used in the study

Sample label	Year of Diagnosis	Sample Source	Age at Diagnosis (yrs)	INSS Stage	MYCN Amplification Status	Shimada Histology	COG Risk Stratification	Years of Survival	Clinical Outcome
St1_NA_NB17_A	2000	2	1.2	1	NA	F	L	3.5	A
St1_NA_NB208_A	1995	1	0.8	1	NA	F	L	4.8	A
St1_NA_NB221_A	1997	1	0.4	1	NA	F	L	5.7	A
St1_NA_NB237_A	1999	1	4.1	1	NA	F	L	3.2	A
St1_NA_NB29_A	1998	2	0.3	1	NA	F	L	5.1	A
St1_NA_NB33_A	1998	2	1.4	1	NA	F	L	4.8	A
St1_NA_NB34_A	1997	2	1.2	1	NA	F	L	5.2	A
St1_NA_NB7_A	1998	2	1.3	1	NA	-	L	5.2	A
St1_NA_NB77_A	1994	2	0.2	1	NA	-	L	9.7	A
St1_NA_NB9_A	1996	2	1.1	1	NA	-	L	7.1	A
St2_NA_NB220_A	1997	1	0.4	2	NA	F	L	6	A
St2_NA_NB231_A	1998	1	0.5	2	NA	F	L	4	A
St2_NA_NB232_A	1998	1	0.1	2	NA	F	L	4.3	A
St2_NA_NB235_A	1999	1	0.4	2	NA	F	L	3.2	A
St3_NA_NB201_A	1994	1	1.5	3	NA	UF	H	7.4	A
St3_NA_NB215_A	1996	1	1.2	3	NA	F	I	7.3	A
St3_NA_NB216_A	1996	1	0.6	3	NA	-	I	6.8	A
St3_NA_NB61_A	1997	2	1.4	3	NA	F	I	6.3	A
St4_A_NB14_A	2000	2	0.9	4	AMP	-	H	3.2	A
St4_NA_NB24_A	2000	2	0.6	4	NA	F	I	3	A
St4_NA_NB269_A	1997	3	0.8	4	NA	-	I	5.3	A
St4_NA_NB282_A	1999	1	4.6	4	NA	UF	H	3.3	A
St4_NA_NB30_A	1997	2	0.9	4	NA	F	I	5.9	A
St4_NA_NB31_A	1997	2	1.4	4	NA	F	H	6.7	A
St4_NA_NB32_A	1998	2	1.2	4	NA	F	H	5.7	A
St4_NA_NB35_A	1997	2	2.6	4	NA	-	H	6.5	A
St2_NA_NB18_D	2000	2	1.8	2	NA	-	L	1.4	D
St3_A_NB72_D	1994	2	3	3	AMP	-	H	1	D
St3_A_NB75_D	1998	2	1	3	AMP	F	H	3	D
St4_A_NB21_D	2000	2	5.2	4	AMP	-	H	0.6	D
St4_A_NB265_D	1996	3	1.8	4	AMP	-	H	2	D
St4_A_NB266_D	1996	3	2	4	AMP	-	H	0	D
St4_A_NB27_D	2000	2	10.5	4	AMP	UF	H	1.4	D
St4_A_NB278_D	1999	1	1.7	4	AMP	UF	H	0.8	D
St4_NA_NB205_D	1995	1	3.9	4	NA	-	H	2.3	D
St4_NA_NB206_D	1995	1	3.3	4	NA	UF	H	5.8	D
St4_NA_NB207_D	1995	1	4.4	4	NA	-	H	3.1	D
St4_NA_NB210_D	1996	1	2.3	4	NA	UF	H	1.1	D
St4_NA_NB275_D	1995	1	1.2	4	NA	UF	H	1	D
St4_NA_NB283_D	1999	1	5.5	4	NA	UF	H	4	D
St4_NA_NB69_D	1992	2	4.4	4	NA	-	H	0.5	D
St4_NA_NB8_D	1998	2	4.6	4	NA	-	H	1.8	D

NOTE:

Sample Source: 1= Cooperative Human Tissue Network (CHTN, Ohio, USA); 2=German Cancer Research Center (GCRC); 3=The Children's Hospital at Westmead (CHW, Australia). INSS= International Neuroblastoma Staging System.

MYCN amplification status: AMP=amplification; NA= not amplified. Shimada Histology: F=favorable, "-"= not known, UF= unfavorable.

COG risk stratification: H=high-risk; I=intermediate-risk; L=low-risk. Ave. ANN Vote= average ANN committee votes.

Clinical Outcome: A= alive without event; D= deceased due to NB disease.

Supplemental Table 2. FDR report

Variable Name	Cutoff Value	No. of Significant p-values
p-value(Platform)	4.02E-06	0
p-value(Prognosis)	0.016	3632
p-value(Platform*Prognosis)	8.44E-05	21

Supplemental Table 3. GO analysis of the significant genes

Expression	System	Gene Category	p-value	Bonferroni(p<0.01)
High in Dead	GO Cellular Component	intracellular	3.13E-20	5.49E-17
	GO Cellular Component	mitochondrion	5.71E-14	1.00E-10
	GO Biological Process	metabolism	7.40E-13	1.30E-09
	GO Cellular Component	ribonucleoprotein complex	1.12E-09	1.97E-06
	GO Biological Process	mitotic cell cycle	9.53E-09	1.67E-05
	GO Cellular Component	nucleolus	1.18E-08	2.08E-05
	GO Molecular Function	structural constituent of ribosome	4.31E-08	7.56E-05
	GO Cellular Component	nucleus	1.20E-07	2.11E-04
	GO Cellular Component	cytoplasm	1.43E-07	2.51E-04
	GO Biological Process	biosynthesis	7.78E-07	1.37E-03
	GO Biological Process	RNA metabolism	9.87E-07	1.73E-03
	GO Biological Process	RNA processing	1.13E-06	1.99E-03
	GO Biological Process	DNA metabolism	1.65E-06	2.90E-03
	GO Biological Process	nucleobase\, nucleoside\, nucleotide and nucleic acid metabolism	2.22E-06	3.90E-03
	GO Cellular Component	cell	2.27E-06	3.99E-03
	GO Biological Process	macromolecule biosynthesis	3.38E-06	5.93E-03
	GO Biological Process	cell cycle	4.39E-06	7.71E-03
	GO Cellular Component	ribosome	5.48E-06	9.62E-03
	GO Biological Process	protein biosynthesis	5.67E-06	9.95E-03
High in Alive	GO Molecular Function	signal transducer activity	5.85E-06	7.13E-03

Supplemental Table 4. Pediatric xenograft samples used in the study

Name	Tumor Line	Histological Diagnosis	ANN Diagnosis	Data source	ANN committee vote		
					RMS	EWS	NB
cDNA_aRMS_Rh1	Rh1	aRMS	EWS **	Whiteford et al [14]	0.06	0.96	0.03
cDNA_aRMS_Rh6	Rh6	aRMS	RMS	Whiteford et al [14]	0.44	0.37	0.30
cDNA_eRMS_Rh12	Rh12	eRMS	RMS	Whiteford et al [14]	0.81	0.09	0.19
cDNA_eRMS_Rh14	Rh14	eRMS	RMS	Whiteford et al [14]	0.85	0.07	0.18
cDNA_EWS_CB-AGPN	CB-AGPN	EWS	EWS	Whiteford et al [14]	0.30	0.66	0.12
cDNA_EWS_CHP-100	CHP-100	EWS	EWS	Whiteford et al [14]	0.48	0.66	0.02
cDNA_EWS_KAG-ews	KAG-ews	EWS	EWS	Whiteford et al [14]	0.16	0.89	0.02
cDNA_EWS_SK-N-MC	SK-N-MC	EWS	EWS	Whiteford et al [14]	0.18	0.85	0.03
cDNA_EWS_SK-PN-DW	SK-PN-DW	EWS	EWS	Whiteford et al [14]	0.36	0.69	0.04
cDNA_EWS_TC-268	TC-268	EWS	EWS	Whiteford et al [14]	0.35	0.56	0.20
cDNA_EWS_TC-32	TC-32	EWS	EWS	Whiteford et al [14]	0.20	0.77	0.14
cDNA_EWS_VW-ews	VW-ews	EWS	EWS	Whiteford et al [14]	0.35	0.80	0.02
cDNA_NB_15N	15N (LA-N-1)	NB	NB	Whiteford et al [14]	0.14	0.02	0.96
cDNA_NB_CHLA-255	CHLA-255	NB	NB	Whiteford et al [14]	0.07	0.05	0.96
cDNA_NB_LA-N-5	LA-N-5	NB	NB	Whiteford et al [14]	0.07	0.01	0.97
cDNA_NB_SH-SY5Y	SH-SY5Y	NB	NB	Whiteford et al [14]	0.23	0.03	0.89
cDNA_NB_SK-N-BE(2)	SK-N-BE(2)	NB	NB	Whiteford et al [14]	0.04	0.03	0.97
cDNA_NB_SK-N-DZ	SK-N-DZ	NB	NB	Whiteford et al [14]	0.20	0.02	0.93
cDNA_NB_SK-N-SH	SK-N-SH	NB	NB	Whiteford et al [14]	0.32	0.09	0.80
cDNA_NB_SMS-KCNR	SMS_KCNR	NB	NB	Whiteford et al [14]	0.06	0.02	0.97
cDNA_NB_SMS-LHN	SMS-LHN	NB	NB	Whiteford et al [14]	0.13	0.06	0.91
cDNA_NB_SMS-SAN	SMS-SAN	NB	NB	Whiteford et al [14]	0.03	0.02	0.98
affy_aRMS_Rh10	Rh10	aRMS	RMS	Neale et al (in submission)	0.93	0.09	0.03
affy_aRMS_Rh28	Rh28	aRMS	RMS	Neale et al (in submission)	0.85	0.13	0.11
affy_aRMS_Rh30	Rh30	aRMS	RMS	Neale et al (in submission)	0.90	0.05	0.08
affy_aRMS_Rh41	Rh41	aRMS	RMS	Neale et al (in submission)	0.94	0.11	0.03
affy_aRMS_Rh65	Rh65	aRMS	RMS	Neale et al (in submission)	0.89	0.10	0.07
affy_eRMS_Rh18	Rh18	eRMS	RMS	Neale et al (in submission)	0.45	0.43	0.23
affy_eRMS_Rh36	Rh36	eRMS	RMS	Neale et al (in submission)	0.89	0.09	0.08
affy_EWS_CHLA258	CHLA258	EWS	EWS	Neale et al (in submission)	0.05	0.91	0.15
affy_EWS_EW5	EW5	EWS	EWS	Neale et al (in submission)	0.06	0.94	0.06
affy_EWS_EW8	EW8	EWS	EWS	Neale et al (in submission)	0.21	0.81	0.04
affy_EWS_SKNEP	SKNEP	EWS	EWS	Neale et al (in submission)	0.26	0.72	0.10
affy_EWS_TC-71	TC-71	EWS	EWS	Neale et al (in submission)	0.09	0.87	0.08
affy_NB_CHLA-79	CHLA-79	NB	NB	Neale et al (in submission)	0.02	0.04	0.97
affy_NB_NB-1382	NB-1382	NB	NB	Neale et al (in submission)	0.02	0.04	0.98
affy_NB_NB-1643	NB-1643	NB	NB	Neale et al (in submission)	0.02	0.04	0.98
affy_NB_NB-1691	NB-1691	NB	NB	Neale et al (in submission)	0.07	0.10	0.92
affy_NB_NB-1771	NB-1771	NB	NB	Neale et al (in submission)	0.03	0.04	0.97
affy_NB_NB-EBc1	NB-EBc1	NB	NB	Neale et al (in submission)	0.04	0.07	0.95
affy_NB_NB-SD	NB-SD	NB	NB	Neale et al (in submission)	0.03	0.04	0.97
affy_NB_SK-N-AS	SK-N-AS	NB	NB	Neale et al (in submission)	0.03	0.06	0.97

Note:

1. ** Rh1 was intially diagnosied as eRMS, however review by others has reclassified it as primitive neuroectoderma tumor, which is a member of the Ewing's family of tumors [6].
2. Abbreviations: aRMS, alveolar rhabdomyosarcoma; eRMS, embryonal rhabdomyosarcoma; EWS, Ewings sarcoma; NB, neuroblastoma.

Supplemental Table 5: Genes with significant interaction between prognosis and platform

UGCluster	Gene Symbol	CloneID	probeset	p-value(Platform * Prognosis)
Hs.293798	ZNF436	196824	226114_at_B	4.54E-07
Hs.473838	DSCR2	843224	203405_at_A	7.18E-07
Hs.632368	EXOSC10	841179	207541_s_at_A	4.61E-06
Hs.410965	DGCR6	471266	208024_s_at_A	7.57E-06
Hs.154276	BACH1	1638852	234315_at_B	1.09E-05
Hs.200016	NUDT11	53162	219855_at_A	1.34E-05
Hs.591704	BTC	1535554	207326_at_A	1.53E-05
Hs.522699	COX7B	35612	202110_at_A	2.16E-05
Hs.442291	LOC345222	1751293	237434_x_at_B	2.50E-05
Hs.525752	KLF13	251529	225390_s_at_B	2.62E-05
Hs.472564	C20orf52	1635665	224972_at_B	3.34E-05
Hs.437072	CNIH2	32226	230070_at_B	3.35E-05
Hs.505806	PBXIP1	366042	212259_s_at_A	3.44E-05
Hs.83190	FASN	179276	212218_s_at_A	3.70E-05
Hs.206770	ZBTB22	49319	213081_at_A	4.37E-05
Hs.109212	KLHL17	190915	229792_at_B	4.39E-05
Hs.128330	---	1586060	236411_at_B	4.42E-05
Hs.521568	GCNT1	2800783	239761_at_B	4.80E-05
Hs.189716	NDUFAB1	782635	202077_at_A	5.67E-05
Hs.555978	RABEP2	342158	77508_r_at_A	6.19E-05
Hs.513984	FLII	826204	212025_s_at_A	7.41E-05
Hs.512767	DKFZP761H1710	124143	221273_s_at_A	9.25E-05
Hs.379754	LOC340061	81662	224916_at_B	9.53E-05
Hs.417628	CRHR1	44692	208593_x_at_A	0.000106586
Hs.7036	NAGK	2511663	218231_at_A	0.000107878
Hs.632380	GALE	711768	202528_at_A	0.000151759
Hs.544767	---	251417	243989_at_B	0.000189463
Hs.534334	NOL1	280970	214427_at_A	0.000190984
Hs.410830	C21orf70	1557018	243750_x_at_B	0.0001927
Hs.24054	JAGN1	1636756	223104_at_B	0.000194335
Hs.73677	RFX1	611964	226786_at_B	0.000197967
Hs.534870	---	1502186	239081_at_B	0.000204763
Hs.367690	C15orf17	195346	224798_s_at_B	0.00021968
Hs.90280	ATIC	449020	208758_at_A	0.000223524
Hs.279761	CHMP4A	76252	218572_at_A	0.000255838
Hs.508958	STXBP6	788524	220995_at_A	0.000285238
Hs.523718	SFN	2027515	33322_i_at_A	0.000287124
Hs.104134	HMX1	2017947	207353_s_at_A	0.000300168
Hs.507290	KARCA1	795851	227582_at_B	0.000303173
Hs.534375	B3GALT4	1601661	210205_at_A	0.000304245
Hs.129711	HAVCR1	2779608	207052_at_A	0.000309808
Hs.104650	FLJ10292	1664710	222776_at_B	0.00031552
Hs.591803	C6orf142	251769	235377_at_B	0.000343315
Hs.469316	LOC643085	207275	229224_x_at_B	0.000401426
Hs.244590	BTBD3	866633	243462_s_at_B	0.000406624
Hs.201918	HIPK3	1580803	207764_s_at_A	0.000463301
Hs.249718	EIF4E	1580219	201437_s_at_A	0.000487709
Hs.143873	S100A10	756595	238909_at_B	0.000499164
Hs.589427	PCOLN3	261971	201933_at_A	0.000519157

Hs.522615	NDP	878835	206022_at_A	0.000608928
Hs.109059	MRPL12	1636069	203931_s_at_A	0.000620437
Hs.372840	APBB1	184022	202652_at_A	0.000636672
Hs.465818	ADAMTS10	2760176	230341_x_at_B	0.000661722
Hs.7884	SLCO2B1	2491247	211557_x_at_A	0.000664768
Hs.86970	C8orf53	1466942	227836_at_B	0.000679764
Hs.590939	TFPT	1605473	218996_at_A	0.000688456
Hs.269571	MYCNOS	1031203	216188_at_A	0.000689978
Hs.596918	GABPB2	1557288	227406_at_B	0.000735758
Hs.133534	KSR1	1636511	235252_at_B	0.00075609
Hs.505337	CLDN5	243181	204482_at_A	0.000758694
Hs.103315	ZNF384	588559	212369_at_A	0.000792367
Hs.526975	LARS2	172495	34764_at_A	0.00086895
Hs.26550	RXRG	358433	205954_at_A	0.000880736
Hs.534342	RNF5	2557375	209111_at_A	0.000972887
Hs.73739	HTR7	46611	236281_x_at_B	0.000982293
Hs.73986	CLK2	713080	203229_s_at_A	0.000991503
Hs.437957	Magmas	502277	218969_at_A	0.000992242
Hs.25040	ZNF239	2324268	206261_at_A	0.00100944
Hs.527909	EDG7	784200	220816_at_A	0.00104979
Hs.193557	---	767164	242321_at_B	0.00106155
Hs.65734	ARNTL	50519	210971_s_at_A	0.00106632
Hs.593575	---	858375	229351_at_B	0.00110962
Hs.586945	---	1688746	238442_at_B	0.00111697
Hs.31210	BCL3	755923	204908_s_at_A	0.00112043
Hs.514038	FLOT2	156386	211299_s_at_A	0.00114366
Hs.198003	SARDH	1870053	210862_s_at_A	0.00114543
Hs.273621	CNP	46786	208912_s_at_A	0.00115361
Hs.513726	GBP5	841492	229625_at_B	0.0011609
Hs.326941	SCIN	240430	222272_x_at_A	0.00116955
Hs.90875	RABIF	360168	204477_at_A	0.00117244
Hs.123116	SLC12A1	1553719	220281_at_A	0.00121199
Hs.45002	RAC3	281978	206103_at_A	0.00121744
Hs.505924	HMGA2	261204	208025_s_at_A	0.00125147
Hs.489354	MUC3B	2229550	217117_x_at_A	0.00127737
Hs.524496	C1orf113	769002	220193_at_A	0.00131056
Hs.310893	CSDC2	51221	209981_at_A	0.00131058
Hs.503716	DCUN1D5	625933	223151_at_B	0.00137811
Hs.134726	C18orf24	564981	217640_x_at_A	0.00142054
Hs.632415	PLK3	825080	215462_at_A	0.00145432
Hs.281707	PUM1	229969	201165_s_at_A	0.00155902
Hs.143751	MMP11	487296	203878_s_at_A	0.00160134
Hs.111732	FCGBP	154172	203240_at_A	0.00164612
Hs.523080	C10orf56	489509	212419_at_A	0.00166941
Hs.79033	QPCT	711918	205174_s_at_A	0.0017007
Hs.490394	TAS2R5	815110	231757_at_B	0.00170334
Hs.380704	FGF11	49284	227271_at_B	0.00175473
Hs.517029	C20orf102	192419	226973_at_B	0.00178436
Hs.98367	SOX17	770979	219993_at_A	0.00178985
Hs.128292	---	1637316	230960_at_B	0.00189156
Hs.501898	MRVI1	323780	224550_s_at_B	0.00192401
Hs.118400	FSCN1	2566856	201564_s_at_A	0.00198235

Hs.191215	PSCD1	814546	202879_s_at_A	0.00200133
Hs.160550	SLC43A2	135654	228918_at_B	0.00201623
Hs.327179	SLC17A3	1323539	207298_at_A	0.00204119
Hs.582050	THAP9	1845627	230185_at_B	0.00204277
Hs.467862	KIAA1240	39574	232908_at_B	0.00204481
Hs.11042	PDZD11	810402	223037_at_B	0.00212046
Hs.538438	LOC653468	487938	243937_x_at_B	0.00216299
Hs.235795	LOC643424	413089	229635_at_B	0.00217257
Hs.95260	FAM8A1	2312236	203420_at_A	0.00220256
Hs.367833	SLC28A2	1416142	216432_at_A	0.0022158
Hs.220529	CEACAM5	586706	201884_at_A	0.00229044
Hs.288382	C16orf56	773284	218148_at_A	0.0022924
Hs.591336	SESN1	813584	218346_s_at_A	0.00231147
Hs.531254	LRRIQ1	279826	223817_at_B	0.00237437
Hs.443140	LOC201181	32782	241383_at_B	0.0024119
Hs.591536	RSC1A1	151251	214583_at_A	0.00251805
Hs.284232	PLEKHG5	136317	227142_at_B	0.00252084
Hs.98967	ATP6V0A4	1917784	220197_at_A	0.00256873
Hs.71428	C9orf18	743481	229976_at_B	0.00259936
Hs.150557	KLF9	302549	203543_s_at_A	0.00268543
Hs.591158	ART4	1715418	207220_at_A	0.00270206
Hs.88045	---	1625160	230312_at_B	0.00270588
Hs.489786	CFTR	2498575	234702_x_at_B	0.0027061
Hs.254113	POLRMT	827129	203783_x_at_A	0.00279353
Hs.303870	KCNC1	1859326	208477_at_A	0.00283522
Hs.445534	PER1	120108	202861_at_A	0.00295769
Hs.515340	LRP3	2018820	204381_at_A	0.00297396
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Hs.524953	KL	897271	205978_at_A	0.00309471
Hs.591088	IL11RA	811920	204773_at_A	0.00314535
Hs.596942	---	280381	244389_at_B	0.00314854
Hs.33102	TFAP2B	363144	215686_x_at_A	0.00318807
Hs.158852	LMAN2L	842851	221274_s_at_A	0.00321999
Hs.436061	IRF1	740476	202531_at_A	0.0034116
Hs.94107	GSTA2	248545	242478_at_B	0.00346223
Hs.503048	IGHMBP2	1569465	31861_at_A	0.00346758
Hs.476306	WDR51A	462333	234749_s_at_B	0.00346913
Hs.521651	STMN2	2306752	203001_s_at_A	0.00348316
Hs.526920	RTDR1	52802	229977_at_B	0.00350156
Hs.534052	ZFP36	23804	201531_at_A	0.00362276
Hs.415172	RABL4	431632	205037_at_A	0.00363469
Hs.525006	NUFIP1	240223	205135_s_at_A	0.00364875
Hs.479396	RBPSUH	129725	229540_at_B	0.0036757
Hs.4276	BHLHB9	26259	213709_at_A	0.00370192
Hs.584852	MAB21L2	866660	210302_s_at_A	0.00378539
Hs.534513	FLJ20021	269820	228832_at_B	0.00379927
Hs.513530	TGFB1I1	811848	209651_at_A	0.00380735
Hs.435302	ZNF3	511814	219605_at_A	0.00383719
Hs.363087	FLJ12684	45629	219987_at_A	0.00400395
Hs.19193	LOC400043	796495	226582_at_B	0.00401599
Hs.131810	---	1655450	230256_at_B	0.00402004
Hs.631562	PLA2G4C	2556649	209785_s_at_A	0.00404735

Hs.494648	TEX10	824847	218104_at_A	0.00414888
Hs.436787	RP11-308D16.4	209518	242012_at_B	0.00417992
Hs.593315	---	73960	242203_at_B	0.00421896
Hs.577753	LARP4	1856516	212714_at_A	0.00422908
Hs.99405	---	813474	241138_at_B	0.00427032
Hs.633139	---	681891	235732_at_B	0.00431831
Hs.73800	SELP	2249736	206049_at_A	0.00436171
Hs.634038	---	815046	232739_at_B	0.00442129
Hs.530463	MGC3196	1543840	220934_s_at_A	0.00450403
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Hs.562457	KLRD1	1901363	207796_x_at_A	0.00454251
Hs.513145	NGRN	303105	224281_s_at_B	0.00455161
Hs.355952	LOC150223	809974	227042_at_B	0.00457655
Hs.274579	CNNM1	25159	220166_at_A	0.0046416
Hs.1755	FGF4	2908538	206783_at_A	0.0046629
Hs.490991	PINX1	824460	223907_s_at_B	0.00473955
Hs.149020	KIAA1772	431748	220340_at_A	0.00474388
Hs.74870	HLX1	1560977	214438_at_A	0.00481196
Hs.195710	ZNF503	810457	227195_at_B	0.00482116
Hs.381912	SPRY3	450396	232157_at_B	0.00487339
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Hs.249125	TLX3	1860115	208495_at_A	0.00495848
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Hs.343334	SPRYD3	49481	225134_at_B	0.00514948
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Hs.525015	---	841220	235211_at_B	0.00534531
Hs.63489	PTPN6	2307001	206687_s_at_A	0.00544254
Hs.520339	COL10A1	2421971	217428_s_at_A	0.00545792
Hs.591258	CD74	155916	209619_at_A	0.00551593
Hs.431109	STX8	1710829	204690_at_A	0.00553331
Hs.335049	GNAT3	1908423	216590_at_A	0.0055605
Hs.274363	NGB	25409	236677_at_B	0.00556257
Hs.632219	SOLH	2385051	204275_at_A	0.0057056
Hs.93670	NHN1	1558392	240535_at_B	0.00573606
Hs.437599	HPS5	194297	204544_at_A	0.00586425
Hs.88778	CBR1	711552	209213_at_A	0.00586962
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Hs.592928	---	714151	242705_x_at_B	0.00597367
Hs.8035	RASL11B	773142	219142_at_A	0.00604051
Hs.513230	MRPL28	1592276	204599_s_at_A	0.00606523
Hs.478741	C3orf21	1858159	226891_at_B	0.00606549
Hs.516802	KIF1A	221828	203850_s_at_A	0.00629812
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Hs.435761	PIAS3	2563108	203035_s_at_A	0.00651153
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Hs.388364	RNF175	37823	236465_at_B	0.00657396
Hs.50319	---	431792	239291_at_B	0.00662065
Hs.376071	CCND2	366412	200953_s_at_A	0.0066312
Hs.414099	TNRC5	809682	228369_at_B	0.00663825
Hs.13845	SLC25A20	247831	203658_at_A	0.00680868
Hs.102866	TKTL1	1543346	216370_s_at_A	0.00683912
Hs.43818	---	726767	237365_at_B	0.006941
Hs.516855	CENPB	809720	212437_at_A	0.00700593
Hs.544106	RNF180	321807	242033_at_B	0.00703337
Hs.1041	ROS1	840514	244363_at_B	0.00726074
Hs.132576	PAX9	1683351	207059_at_A	0.00739892
Hs.485572	SOCS2	491121	203373_at_A	0.00741224
Hs.479386	LOC389203	251806	225014_at_B	0.00758897
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Hs.173311	RPUSD2	131988	221940_at_A	0.0077078
Hs.132682	PSMB9	1456118	204279_at_A	0.00772003
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Hs.132994	CCDC69	549867	212886_at_A	0.00780983
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Hs.471067	LOC339483	772429	228593_at_B	0.00815189
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Hs.286261	WDR55	279496	219809_at_A	0.00853272
Hs.633147	---	365990	228700_at_B	0.008575
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Hs.407587	GNRHR	50593	216341_s_at_A	0.00862543
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Hs.526494	MGRN1	782147	212576_at_A	0.00874612
Hs.632547	COQ10B	626619	219397_at_A	0.00879677
Hs.418367	NMU	1703053	206023_at_A	0.00879699
Hs.66163	---	2273418	215421_at_A	0.00883517
Hs.546636	LOC402665	758360	244694_at_B	0.00889536
Hs.505004	TCEA2	730149	203919_at_A	0.00907566
Hs.164453	HECW1	42811	237295_at_B	0.00914099
Hs.439713	ZNF154	825464	242170_at_B	0.00915617
Hs.515104	STXBP2	196650	209367_at_A	0.00920113
Hs.146250	---	1880932	236821_at_B	0.00920682
Hs.72964	MKRN3	2169114	206585_at_A	0.00935199
Hs.75615	APOC2	809523	231561_s_at_B	0.00939594
Hs.89771	GCKR	66534	206867_at_A	0.00952321
Hs.3232	CYLC2	1292142	207780_at_A	0.00956707
Hs.262886	INPP5D	825604	203332_s_at_A	0.00970641
Hs.278036	LOC442512	1598759	244079_at_B	0.00972121
Hs.590970	AXL	49318	202686_s_at_A	0.00973432
Hs.91910	UNQ5831	23323	236701_at_B	0.00981169