

Xenograft production

CB17/Icr female scid-/- female mice (Taconic Farms, Germantown NY), were used to propagate kidney/rhabdoid tumors, sarcomas (Ewing, osteosarcoma, rhabdomyosarcoma), neuroblastoma, and non-glioblastoma brain tumors. All tumors were maintained subcutaneously, with the exception of two neuroblastoma samples (intra adrenal; X108, X107). Human leukemia cells were propagated by intravenous inoculation in female non-obese diabetic (NOD)/scid-/- female mice as described previously (1). Xenograft samples were removed, care was taken to remove any necrotic tissue before the tissue was snap-frozen in liquid nitrogen. Samples were acquired through the Pediatric Preclinical Testing Program established by the NCI. An additional primary tumor set consisting of 19 EWS (plus 3 cell lines; see Supplemental Table 2), 22 RMS (plus 3 cell lines), and 30 NB (plus 12 NB cell lines) was also analyzed. EWS, RMS, and NB tumor samples were collected from four different centers. The clinical and histological diagnosis was performed at the hospital where the tumors were obtained. Tumor samples were surgical specimens and snap-frozen in liquid nitrogen according to local procedures.

References

1. Lock RB, Liem N, Farnsworth ML, *et al.* The nonobese diabetic/severe combined immunodeficient (NOD/SCID) mouse model of childhood acute lymphoblastic leukemia reveals intrinsic differences in biologic characteristics at diagnosis and relapse. *Blood* 2002;99(11):4100-8.

Supplemental Table 1

Sample	Source Name	Source	Diagnosis	Xenograft Type
Leukemia				
ALL_X86	ALL-2	Lock	ALL B-precursor	direct transplantation
ALL_X87	ALL-3	Lock	ALL B-precursor	direct transplantation
ALL_X88	ALL-4	Lock	ALL B-precursor	direct transplantation
ALL_X89	ALL-7	Lock	ALL B-precursor	direct transplantation
ALL_X91	ALL-10	Lock	ALL B-precursor	direct transplantation
ALL_X92	ALL-11	Lock	ALL B-precursor	direct transplantation
ALL_X94	ALL-17	Lock	ALL B-precursor	direct transplantation
ALL_X95	ALL-19	Lock	ALL B-precursor	direct transplantation
ALL_X90	ALL-8	Lock	ALL T-cell ALL	direct transplantation
ALL_X93	ALL-16	Lock	ALL T-cell ALL	direct transplantation
Rhabdomyosarcoma				
ARMS_X2	Rh41	Houghton	ARMS	direct transplantation
ARMS_X26	Rh1	Houghton	ARMS	cell culture
ARMS_X27	Rh10	Houghton	ARMS	direct transplantation
ARMS_X3	Rh6	Houghton	ARMS	direct transplantation
ARMS_X34	Rh28	Houghton	ARMS	direct transplantation
ARMS_X35	Rh30	Houghton	ARMS	direct transplantation
ERMS_X1	Rh36	Houghton	ERMS	direct transplantation
ERMS_X28	Rh12	Houghton	ERMS	direct transplantation
ERMS_X32	Rh14	Houghton	ERMS	direct transplantation
ERMS_X33	Rh18	Houghton	ERMS	direct transplantation
Ependymoma				
EP_X14	SJ-BT36	Houghton	Ependymoma	direct transplantation
EP_X22	SJ-BT41	Houghton	Ependymoma	direct transplantation
EP_X24	SJ-BT43	Houghton	Ependymoma	direct transplantation
EP_X29	SJ-BT44	Houghton	Ependymoma	direct transplantation
Medulloblastoma				
MB_X10	SJ-BT31	Houghton	Medulloblastoma	direct transplantation
MB_X30	SJ-BT45	Houghton	Medulloblastoma	direct transplantation
MB_X31	SJ-BT46	Houghton	Medulloblastoma	direct transplantation
MB_X38	SJ-BT47	Houghton	Medulloblastoma	direct transplantation
MB_X41	SJ-BT50	Houghton	Medulloblastoma	direct transplantation
MB_X8	SJ-BT28	Houghton	Medulloblastoma	direct transplantation
Ewing's Sarcoma				
EWS_X109	KAG-EWS	Khanna	EWS	cell culture
EWS_X110	VW-EWS	Khanna	EWS	cell culture
EWS_X65	CB-AGPN	Reynolds	EWS	cell culture
EWS_X68	CHP-100	Reynolds	EWS	cell culture
EWS_X70	SK-N-MC	Reynolds	EWS	cell culture
EWS_X71	TC-268	Reynolds	EWS	cell culture
EWS_X72	TC-32	Reynolds	EWS	cell culture
EWS_X73	TC-71	Reynolds	EWS	cell culture
EWS_X77	SK-PN-DW	Reynolds	EWS	cell culture
Neuroblastoma				
NB_X105	SH-SY5Y	Thiele	NB	cell culture
NB_X106	15N (LA-N-1)	Thiele	NB	cell culture
NB_X107	SK-N-AS	Reynolds	NB	cell culture
NB_X108	SMS-KCNR	Thiele	NB	cell culture
NB_X16	NB-1643	Houghton	NB	cell culture
NB_X17	NB-1691	Houghton	NB	cell culture
NB_X18	SNB-1771	Houghton	NB	cell culture
NB_X19	NB-EB	Houghton	NB	cell culture
NB_X25	NB-SD	Houghton	NB	cell culture
NB_X37	NB-1382	Houghton	NB	cell culture
NB_X61	CHLA-255	Reynolds	NB	cell culture
NB_X62	SMS-LHN	Reynolds	NB	cell culture
NB_X64	SK-N-AS	Reynolds	NB	cell culture
NB_X66	JHAN	Reynolds	NB	cell culture
NB_X67	SK-N-BE(2)	Reynolds	NB	cell culture
NB_X74	SK-N-SH	Reynolds	NB	cell culture
NB_X75	SMS-KCNR	Reynolds	NB	cell culture
NB_X78	SK-N-DZ	Reynolds	NB	cell culture
NB_X79	LA-N-5	Reynolds	NB	cell culture
NB_X80	SMS-SAN	Reynolds	NB	cell culture
Osteosarcoma				
OS_X36	OS160	Gorlick	Osteosarcoma	direct transplantation
OS_X53	SJ-OS1	Houghton	Osteosarcoma	direct transplantation
OS_X54	SJ-OS2	Houghton	Osteosarcoma	direct transplantation
OS_X56	SJ-OS8	Houghton	Osteosarcoma	direct transplantation
OS_X57	SJ-OS10	Houghton	Osteosarcoma	direct transplantation
OS_X58	SJ-OS17	Houghton	Osteosarcoma	direct transplantation
OS_X59	SJ-OS21	Houghton	Osteosarcoma	direct transplantation
OS_X60	SJ-OS29	Houghton	Osteosarcoma	direct transplantation
Wilms' Tumor				
WT_X43	SJ-WT10	Houghton	Medulloblastoma	direct transplantation
WT_X44	SJ-WT11	Houghton	Wilms' tumor	direct transplantation
WT_X46	SJ-WT13	Houghton	Wilms' tumor	direct transplantation
WT_X48	SJ-WT5	Houghton	Wilms' tumor	direct transplantation
WT_X49	SJ-WT6	Houghton	Wilms' tumor	direct transplantation
WT_X50	SJ-WT7	Houghton	Wilms' tumor	direct transplantation
WT_X51	SJ-WT8	Houghton	Ependymoma	direct transplantation
WT_X52	SJ-WT9	Houghton	Wilms' tumor	direct transplantation

Supplemental Table 2**Tumors**

Sample	Source Name	Source	Diagnosis
Rhabdomyosarcoma			
aRMS-T30	200002P2054	CHTN	ARMS
aRMS-T31	200002P2065	CHTN	ARMS
aRMS-T33	200003P4067	CHTN	ARMS
aRMS-T35	200004P2174	CHTN	ARMS
aRMS-T38	9709P144	CHTN	ARMS
aRMS-T39	200008P6027	CHTN	ARMS
aRMS-T51	200007P1049	CHTN	ARMS
aRMS-T57	9807P117	CHTN	ARMS
aRMS-T59	9807P332	CHTN	ARMS
aRMS-T61	9808P189	CHTN	ARMS
aRMS-T65	9903P605	CHTN	ARMS
eRMS-T32	200003P2080	CHTN	ERMS
eRMS-T37	9911P1241	CHTN	ERMS
eRMS-T55	9609P032	CHTN	ERMS
eRMS-T62	9705P060	CHTN	ERMS
RMS-T104	93-08-110	CHTN	RMS
RMS-T11	91-04-EE02	CHTN	RMS
RMS-T12	93-08-110	CHTN	RMS
RMS-T14	9901C114C	CHTN	RMS
RMS-T15	96-06-A154	CHTN	RMS
RMS-T18	12Y30a	CHTN	RMS

Ewing's Sarcoma

EWS-T142	9512P350SP3	CHTN	EWS
EWS-T143	9601P007SP1	CHTN	EWS
EWS-T144	9607P075	CHTN	EWS
EWS-T145	9704P013	CHTN	EWS
EWS-T146	9706P044	CHTN	EWS
EWS-T147	9708P076	CHTN	EWS
EWS-T154	9810P202	CHTN	EWS
EWS-T156	9904P6008	CHTN	EWS
EWS-T157	9910P6003	CHTN	EWS
EWS-T181	1	CHW	EWS
EWS-T182	2	CHW	EWS
EWS-T183	3	CHW	EWS
EWS-T184	4	CHW	EWS
EWS-T185	5	CHW	EWS
EWS-T186	6	CHW	EWS
EWS-T187	7	CHW	EWS
EWS-T189	8	CHW	EWS
EWS-T190	9	CHW	EWS
EWS-T191	98-10-A040A	CHTN	EWS

Neuroblastoma

NB-T14	NB-14	GCRC	NB
NB-T21	NB-21	GCRC	NB
NB-T243	10	CHW	NB
NB-T249	11	CHW	NB
NB-T250	12	CHW	NB
NB-T251	13	CHW	NB
NB-T252	14	CHW	NB
NB-T254	15	CHW	NB
NB-T257	16	CHW	NB
NB-T266	17	CHW	NB
NB-T27	NB-27	GCRC	NB
NB-T28	NB-28	GCRC	NB
NB-T284	200207P6101	CHTN	NB
NB-T285	200207P6108	CHTN	NB
NB-T407	95-004	CHLA	NB
NB-T207	9508P027	CHTN	NB
NB-T401	92-174	CHLA	NB
NB-T210	9601P035	CHTN	NB
NB-T275	9511P314	CHTN	NB
NB-T283	200207P6099	CHTN	NB
NB-T287	200208P6007	CHTN	NB
NB-T202	9412P013	CHTN	NB
NB-T30	NB-30	GCRC	NB
NB-T31	NB-31	GCRC	NB
NB-T32	NB-32	GCRC	NB
NB-T65	NB-65	GCRC	NB
NB-T67	NB-67	GCRC	NB
NB-T69	NB-69	GCRC	NB
NB-T8	NB-8	GCRC	NB
NB-T88	NB-88	GCRC	NB

Cell Lines

Sample	Source Name	Source	Diagnosis
Neuroblastoma			
NB-C1	GILIN	ICLC	NB
NB-C2	IMR-32	ATCC	NB
NB-C3	IMR-5	ICLC	NB
NB-C4	SK-N-FI	ATCC	NB
NB-C5	CHP134	NCI	NB
NB-C6	SMS-KCNR	NCI	NB
NB-C7	LA-N-5	NCI	NB
NB-C8	SK-N-BE2	ATCC	NB
NB-C9	SK-N-DZ	ATCC	NB
NB-C10	SH-SY5Y	ATCC	NB
NB-C11	SK-N-AS	ATCC	NB
NB-C12	SK-N-SH	ATCC	NB

Rhabdomyosarcoma

aRMS-C67	RH5	NCI	ARMS
aRMS-C68	RMS13	SJCRH	ARMS
eRMS-C29	RD	ATCC	ERMS

Ewing's Sarcoma

EWS-C192	TC71	NCI	EWS
EWS-C193	5838	NCI	EWS
EWS-C26	A673	NCI	EWS

Source Codes

CHTN: Cooperative Human Tissue Network

CHW: Children's Hospital Westmeade

GCRC: German Cancer Research Center

CHLA: Children's Hospital Los Angeles

ICLC: Interlab Cell Line Collection

ATCC: American Type Culture Collection

NCI: National Cancer Institute

SJCRH: St. Jude's Children's Research Hospital

Supplemental Table 3 Reverse ANN Classification

Sample	ANN committee vote			ANN Classification
	RMS	NB	EWS	
aRMS-T30	0.96	0.04	0.04	RMS
aRMS-T31	0.96	0.03	0.04	RMS
aRMS-T33	0.96	0.04	0.04	RMS
aRMS-T35	0.96	0.04	0.04	RMS
aRMS-T38	0.95	0.03	0.05	RMS
aRMS-T39	0.66	0.04	0.33	RMS
aRMS-T51	0.96	0.04	0.04	RMS
aRMS-T57	0.96	0.04	0.04	RMS
aRMS-T59	0.96	0.03	0.04	RMS
aRMS-T61	0.96	0.03	0.04	RMS
aRMS-T65	0.96	0.03	0.04	RMS
eRMS-T32	0.96	0.03	0.04	RMS
eRMS-T37	0.96	0.03	0.04	RMS
eRMS-T55	0.96	0.04	0.04	RMS
eRMS-T62	0.96	0.03	0.04	RMS
RMS-T104	0.96	0.03	0.04	RMS
RMS-T11	0.94	0.03	0.08	RMS
RMS-T12	0.95	0.03	0.05	RMS
RMS-T14	0.96	0.03	0.04	RMS
RMS-T15	0.76	0.04	0.23	RMS
RMS-T18	0.96	0.04	0.04	RMS
NB-T14	0.02	0.98	0.02	NB
NB-T21	0.02	0.98	0.02	NB
NB-T243	0.02	0.98	0.02	NB
NB-T249	0.03	0.98	0.02	NB
NB-T250	0.02	0.98	0.02	NB
NB-T251	0.03	0.98	0.02	NB
NB-T252	0.03	0.98	0.02	NB
NB-T254	0.03	0.98	0.02	NB
NB-T257	0.03	0.98	0.02	NB
NB-T266	0.06	0.96	0.02	NB
NB-T27	0.03	0.98	0.02	NB
NB-T28	0.03	0.98	0.02	NB
NB-T284	0.02	0.98	0.02	NB
NB-T285	0.02	0.98	0.02	NB
NB-T407	0.03	0.98	0.02	NB
NB-T207	0.03	0.98	0.02	NB
NB-T401	0.03	0.98	0.02	NB
NB-T210	0.03	0.98	0.02	NB
NB-T275	0.03	0.98	0.02	NB
NB-T283	0.03	0.98	0.02	NB
NB-T287	0.04	0.96	0.02	NB
NB-T202	0.03	0.98	0.02	NB
NB-T30	0.03	0.98	0.02	NB
NB-T31	0.03	0.98	0.02	NB
NB-T32	0.03	0.98	0.02	NB
NB-T65	0.03	0.98	0.02	NB
NB-T67	0.03	0.98	0.02	NB
NB-T69	0.03	0.98	0.02	NB
NB-T8	0.03	0.98	0.02	NB
NB-T88	0.03	0.98	0.02	NB
EWS-T142	0.04	0.03	0.97	EWS
EWS-T143	0.09	0.03	0.94	EWS
EWS-T144	0.04	0.03	0.96	EWS
EWS-T145	0.04	0.03	0.96	EWS
EWS-T146	0.05	0.03	0.96	EWS
EWS-T147	0.05	0.03	0.96	EWS
EWS-T154	0.04	0.03	0.96	EWS
EWS-T156	0.06	0.03	0.95	EWS
EWS-T157	0.04	0.03	0.96	EWS
EWS-T181	0.04	0.03	0.97	EWS
EWS-T182	0.04	0.03	0.96	EWS
EWS-T183	0.05	0.03	0.96	EWS
EWS-T184	0.03	0.03	0.97	EWS
EWS-T185	0.04	0.03	0.96	EWS
EWS-T186	0.11	0.03	0.92	EWS
EWS-T187	0.08	0.03	0.94	EWS
EWS-T189	0.04	0.03	0.96	EWS
EWS-T190	0.04	0.03	0.96	EWS
EWS-T191	0.04	0.03	0.96	EWS

Supplemental Table 4: Gene Ontology of 120 Highly Expressed Genes

GO ID	GO Term	# Array	# List	P
30554	adenyl nucleotide binding	820	28	0
5524	ATP binding	807	28	0
7049	cell cycle	534	46	0
75	cell cycle checkpoint	26	5	0
8151	cell growth and/or maintenance	2487	56	0
8283	cell proliferation	768	49	0
50875	cellular physiological process	2861	56	0
5694	chromosome	141	15	0
775	chromosome, pericentric region	21	5	0
910	cytokinesis	89	19	0
5659	delta DNA polymerase complex	4	3	0
5660	delta-DNA polymerase cofactor complex	3	3	0
9262	deoxyribonucleotide metabolism	5	3	0
6259	DNA metabolism	348	22	0
42575	DNA polymerase complex	5	3	0
6260	DNA replication	106	11	0
67	DNA replication and chromosome cycle	134	17	0
6270	DNA replication initiation	13	4	0
6261	DNA-dependent DNA replication	52	7	0
3887	DNA-directed DNA polymerase activity	19	4	0
82	G1/S transition of mitotic cell cycle	43	6	0
86	G2/M transition of mitotic cell cycle	35	6	0
43232	intracellular non-membrane-bound organelle	668	25	0
776	kinetochore	14	4	0
279	M phase	138	23	0
87	M phase of mitotic cell cycle	106	21	0
72	M phase specific microtubule process	18	5	0
15630	microtubule cytoskeleton	109	12	0
7067	mitosis	104	21	0
278	mitotic cell cycle	157	29	0
7093	mitotic checkpoint	10	4	0
7052	mitotic spindle assembly	12	4	0
43228	non-membrane-bound organelle	668	25	0
280	nuclear division	131	21	0
6139	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	1815	38	0
166	nucleotide binding	1050	30	0
5634	nucleus	2052	48	0
17076	purine nucleotide binding	1036	29	0
74	regulation of cell cycle	312	24	0
7088	regulation of mitosis	28	7	0
5819	spindle	39	10	0
7051	spindle assembly	12	4	0
9186	deoxyribonucleoside diphosphate metabolism	2	2	0.0001
9263	deoxyribonucleotide biosynthesis	2	2	0.0001
5622	intracellular	4258	65	0.0001
226	microtubule cytoskeleton organization and biogenesis	38	5	0.0001
90	mitotic anaphase	10	3	0.0001
9221	pyrimidine deoxyribonucleotide biosynthesis	2	2	0.0001
3824	catalytic activity	2922	49	0.0002
785	chromatin	74	6	0.0002
30261	chromosome condensation	11	3	0.0002
4693	cyclin-dependent protein kinase activity	11	3	0.0002
79	regulation of cyclin dependent protein kinase activity	29	4	0.0003
80	G1 phase of mitotic cell cycle	14	3	0.0004
43231	intracellular membrane-bound organelle	3073	50	0.0004
43227	membrane-bound organelle	3073	50	0.0004
3676	nucleic acid binding	1710	33	0.0004
9132	nucleoside diphosphate metabolism	3	2	0.0004
7582	physiological process	6369	83	0.0004
16772	transferase activity, transferring phosphorus-containing groups	617	17	0.0004
7059	chromosome segregation	15	3	0.0005
3677	DNA binding	1213	26	0.0005
30894	repilisome	15	3	0.0005
16740	transferase activity	956	22	0.0006
7017	microtubule-based process	65	5	0.0007
7094	mitotic spindle checkpoint	4	2	0.0007
9219	pyrimidine deoxyribonucleotide metabolism	4	2	0.0007
6221	pyrimidine nucleotide biosynthesis	16	3	0.0007
5856	cytoskeleton	427	13	0.0008
43229	intracellular organelle	3497	54	0.0008
43226	organelle	3497	54	0.0008
5657	replication fork	17	3	0.0008
6271	DNA strand elongation	5	2	0.0012
7076	mitotic chromosome condensation	5	2	0.0012
88	mitotic prophase	5	2	0.0012
42623	ATPase activity, coupled	194	8	0.0013
9309	amine biosynthesis	46	4	0.0016
16887	ATPase activity	202	8	0.0017
4674	protein serine/threonine kinase activity	300	10	0.0017
6220	pyrimidine nucleotide metabolism	22	3	0.0017
70	mitotic sister chromatid segregation	6	2	0.0018
819	sister chromatid segregation	6	2	0.0018
17111	nucleoside-triphosphatase activity	307	10	0.002
8094	DNA-dependent ATPase activity	24	3	0.0022
8152	metabolism	4277	61	0.0023
5663	DNA replication factor C complex	7	2	0.0024
5876	spindle microtubule	7	2	0.0024
9117	nucleotide metabolism	125	6	0.0025
5815	microtubule organizing center	26	3	0.0028
6281	DNA repair	129	6	0.0029
9165	nucleotide biosynthesis	89	5	0.0029
16462	pyrophosphatase activity	328	10	0.0032
16818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	331	10	0.0034
8652	amino acid biosynthesis	28	3	0.0035
16817	hydrolase activity, acting on acid anhydrides	332	10	0.0035
922	spindle pole	28	3	0.0035
9070	serine family amino acid biosynthesis	9	2	0.0041
9987	cellular process	4089	58	0.0044
19205	nucleobase, nucleoside, nucleotide kinase activity	33	3	0.0056
16301	kinase activity	536	13	0.0057
8026	ATP-dependent helicase activity	67	4	0.0063
9147	pyrimidine nucleoside triphosphate metabolism	12	2	0.0074
6974	response to DNA damage stimulus	156	6	0.0074
45859	regulation of protein kinase activity	71	4	0.0077
9719	response to endogenous stimulus	161	6	0.0086

Supplemental Figure 1: A representative example for the accumulated distribution of fluorescent intensities for mouse and human RNA co-hybridized on a human cDNA microarray.

