

Supplementary Materials

Mutations of epigenetic regulatory genes are common in thymic carcinomas

Yisong Wang^{1,2}, Anish Thomas¹, Christopher Lau¹, Arun Rajan¹, Yuelin Zhu¹, J. Keith Killian¹, Iacopo Petrini¹, Trung Pham¹, Betsy Morrow¹, Xiaogang Zhong², Paul S. Meltzer¹, Giuseppe Giaccone^{1,2}

¹Center for Cancer Research, National Cancer Institute, Bethesda, MD 20892; ²Lombardi Comprehensive Cancer Center, Georgetown University, Washington DC 20007

Table S1. List of 197 cancer-associated genes

ABL1	DKK3	JAK2	PTPN11	VIM
ACN9	DLD	JAK3	RB1	WT1
ACVR1B	DMBT1	KDR	REEP5	WTS
AKT1	DNMT3A	KIT	RET	XRCC1
ALK	DPYD	KRAS	RNF139	ZNF135
APC	EGF	KRT20	RNF2	
ARHGEF2	EGFR	MAG11	RPS15	
ARID1A	EGR3	MAP2K4	RUNX1	
ASXL1	EIF4G2	MEN1	SCLC1	
ATM	EML4	MET	SDHA	
ATRX	ENO1	MGMT	SDHAF1	
BAG3	ENO2	MIB1	SDHAF2	
BAI3	ERBB2	MKI67	SDHB	
BAP1	ERBB3	MLH1	SDHC	
BCAN	ERBB4	MPL	SDHD	
BCL2	ERG	MSH2	SELT	
BRAF	EZH2	MSH6	SETD2	
BRCA1	F10	MUC1	SLC38A1	
BRCA2	FAM123B	MUC17	SLC6A2	
CA12	FBXW7	MUC2	SLTM	
CA9	FGFR1	MUC3A	SMAD4	
CALU	FGFR2	MUTYH	SMARCA4	
CARD11	FGFR3	MVP	SMARCB1	
CBL	FH	MYC	SMO	
CCND1	FHIT	MYD88	SMOX	
CD34	FLCN	NAT1	SMUG1	
CDC73	FLT3	NAT2	SOCS1	
CDH1	FOXL2	NES	SRC	
CDK4	FZR1	NF1	SST	
CDKN2A	GATA1	NF2	STC1	
CDX2	GATA2	NOTCH1	STK11	
CEACAM7	GATA3	NOTCH2	SUFU	
CEBPA	GFAP	NPM1	SYP	
CES3	GNA11	NRAS	TCF7L2	
CHDM	GNAQ	PBRM1	TET2	
CRLF2	GNAS	PCNA	TFE3	
CSF1R	GRP	PDGFRA	TFEB	
CSF3	GSTM1	PDZD4	TMEM97	
CTNNA1	HIVEP3	PGR	TNFAIP3	
CTNNB1	HNF1A	PHOX2B	TNFSF13	
CUL2	HRAS	PIK3CA	TP53	
CYLD	IDH1	PMS2	TPD52L2	
CYP1A1	IDH2	PPP2R1A	TPM4	
DAXX	IFNA1	PRCC	TSC1	
DCC	IGKV1D-43	PRKAR1A	TSC2	
DES	IL2	PTCH1	TSHR	
DIRAS1	ITGB5	PTEN	TYK2	
DIRC2	JAK1	PTGS2	VHL	

Sample ID	WHO histotype	Gene symbol	Chromosome	Position	Ref nt	Change nt	Variant allele frequency	Effect	AA Change	Transcript Ensembl ID	Exon #	AA Length	COSMIC/abSNP IDs	Sift score	Ppr2 score	Interpro domain	Uniprot ID	Sanger seq confirmation
1010016	TC	HRAS	chr11	533874	A	T	0.592	Missense	Q61L	ENST00000451590	3	189	COSM99664/rs121913253	0.01	benign	Small_GTP-binding_protein_domain	P01112;P01112	Confirmed
1010016	TC	SDHA	chr5	224571	G	T	0.151	Missense	A83S	ENST00000264932	3	664		0.01	benign	Fumarate_reductase/succinate_dehydrogenase_B_avoprotein_N	EPBLJ5,B4DYNS,D6RFM5,P3104,QJ5GQW8	Confirmed
1010016	TC	TP53	chr17	7578532	T	A	0.333	Missense	M133K	ENST00000289305	5	393	COSM437606	0	damaging	p53_DNA-binding_domain_(1).p53-like_transcription_factor_DNA-binding_(1).p53/RUNT-type_transcription_factor_DNA-binding_domain_(1)	B4E095,P04637-2,P04637-3,EPPT15,P04637,Q1MSWB,E7E,QX7	ND
1010016	AB	RUNX1	chr21	36171607	G	A	0.284	Nonsense	R320*	ENST00000437180	8	480	COSM41699					ND
1010018	AB	TET2	chr4	106156391	TAGA	T	0.243	Frameshift deletion	E452 del	ENST00000513237	3	2023						Confirmed
1010019	TNEC	CTNNB1	chr3	41266137	C	G	0.416	Missense	S45C	ENST00000396185	3	781	COSM5669/rs121913409	0	damaging		P35222	ND
1010024	TC	SETD2	chr3	47165698	TG	T	0.196	Frameshift deletion	H143 fs	ENST00000409792	3	2564						Confirmed
1010024	TC	TP53	chr17	7578717	C	T	0.222	Missense	P27S	ENST00000289305	3	393	COSM1167902	0.05	damaging	p53_transactivation_domain_(1)	E7EMR8,P04637-2,P04637-3,EPPT15,P04637,Q1MSWB,E7E,QX7	ND
1010056	TC	CYLD	chr16	50815317	CTT	C	0.292	Frameshift deletion	L560 fs	ENST00000311559	11	956						Confirmed
1010056	TC	DCC	chr18	50731625	C	G	0.153	Missense	S538C	ENST00000442544	10	1447		0	damaging	Fibronectin_type_III_(4)_immunoglobulin-like_fold_(1)	E7EQM8,B4DYX2,P43146	Confirmed
1010075	B2	DCC	chr18	50278519	G	A	0.314	Missense	A63T	ENST00000442544	2	1447		0.01	damaging	Immunoglobulin_subtype_(1)_immunoglobulin-like_(1)_immunoglobulin-like_fold_(1)	P43146	Confirmed
1010075	B2	EGFR	chr7	55259554	CAGA	C	0.233	Frameshift deletion	E871 del	ENST00000275493	21	1210						Confirmed
1010075	B2	ERG	chr21	39755553	CG	C	0.183	Frameshift deletion	P411fs	ENST00000398919	12	486	COSM1414058					ND
1010075	B2	HRAS	chr11	533548	G	A	0.228	Missense	D119N	ENST00000451590	4	189	COSM99643	0	damaging	Small_GTP-binding_protein_domain_(1)	P01112-2;P01112	Confirmed
1010075	B2	MAGI1	chr3	65367573	G	A	0.362	Missense	R894W	ENST00000402939	16	1462	COSM222818	0.07	damaging		ABK18,Q96QZ7-4,Q96QZ7-5,Q96QZ7-2,Q96QZ7-6	Confirmed
1010075	B2	PRCC	chr1	156761496	A	G	0.347	Missense	Y364C	ENST00000271236	4	491		0.04	damaging		None;Q92733	ND
1010075	B2	SDHA	chr5	256468	C	A	0.275	Missense	P643H	ENST00000264932	15	664		0	damaging	Fumarate_reductase/succinate_dehydrogenase_B_avoprotein-like_C-terminal_(1).Fumarate_reductase/succinate_dehydrogenase_avoprotein_C-terminal_(1)_None	EPBLJ5,B3KYA5,D6RFM5,P3104,QNone	Confirmed
1010075	B2	SETD2	chr3	47142948	C	T	0.384	Missense	G1672E	ENST00000409792	8	2564		0	damaging	SET_domain_(1)	FZ2317,Q9BYW2	Confirmed
1010075	B2	SRC	chr20	36031706	G	A	0.259	Missense	E513K	ENST00000260723	13	536		0.01	benign	Serine-threonine/tyrosine-protein_kinase_(1).Protein_kinase-like_domain_(1).Tyrosine-protein_kinase_catalytic_domain_(1).Protein_kinase_catalytic_domain_(1)	P12931	ND
1010075	B2	TP53	chr17	7577139	G	A	0.237	Missense	R267W	ENST00000289305	8	393	COSM1640829/rs55832599	0	damaging	p53_DNA-binding_domain_(1).p53-like_transcription_factor_DNA-binding_(1).p53/RUNT-type_transcription_factor_DNA-binding_domain_(1)	P04637-2;P04637-3;P04637,Q1MSWB	ND
1010089	TC	BAP1	chr3	52443729	C	G	0.421	Splice site donor		ENST00000406980	2	729						Confirmed
1010089	TC	BRC42	chr13	32912496	A	T	0.286	Missense	E1335V	ENST00000380152	11	3418		0.01	damaging		P51567	ND
1010089	TC	PBRM1	chr3	32588866	G	GA	0.49	Frameshift insertion	L1494 fs	ENST00000296302	27	1689						Confirmed
1010089	TC	TP53	chr17	7577538	C	T	0.447	Missense	R248Q	ENST00000289305	7	393	COSM99020/rs11540652	0.01	damaging	p53_DNA-binding_domain_(1).p53-like_transcription_factor_DNA-binding_(1).p53/RUNT-type_transcription_factor_DNA-binding_domain_(1)	P04637-2;P04637-3;EPPT15,P04637,Q1MSWB,E7E,QX7	Confirmed
1010103	TC	CYLD	chr16	50815156	G	C	0.787	Splice site acceptor		ENST00000311559	11	956						Confirmed
1010103	TC	TET2	chr4	106197112	CAATTA	C	0.256	Frameshift deletion	L1816_D1821 del	ENST00000513237	11	2023						Confirmed

1010103	TC	TET2	chr4	106183006	G	T	0.471	Splice site donor		ENST00000513237	8	2023	COSM87147					Confirmed	
1010109	TC	ASXL1	chr20	31022297	C	A	0.279	Nonsense	C584*	ENST00000375687	13	1541	COSM110708					Confirmed	
1010109	TC	PIK3CA	chr3	178936091	G	A	0.19	Missense	E545K	ENST00000263967	10	1068	COSM763_r10488600_3	0	damaging	Phosphoinositide 3-kinase_accessory_PP2K_domain_(3)Armadillo-type_fold_(1)	P42336	Confirmed	
1010112	TC	MEN1	chr11	64577330	A	A	0.381	Frameshift insertion	S84 fs	ENST00000394376	3	615						Confirmed	
1010137	TC	SETD2	chr3	47158121	C	G	0.61	Missense	M152H	ENST00000409792	4	2564		0	damaging	AWS_(2)	FZ2317,Q9BYW2	ND	
1010137	TC	SETD2	chr3	47164736	G	C	0.637	Missense	E464G	ENST00000409792	3	2564		0	benign		FZ2317,Q9BYW2	ND	
1010137	TC	SETD2	chr3	47162075	C	T	0.726	Missense	D1351N	ENST00000409792	3	2564		0.21	benign		FZ2317,Q9BYW2	Confirmed	
1010137	TC	SMARCA4	chr19	11132513	C	T	0.392	Missense	T910M	ENST00000358026	19	1679	COSM86025	0	damaging	DEAD-like_helicase_(2)SNF2-related_(1)	B1ABZ6,B1ABZ4,B1ABZ7,Q9HBD4,B1ABZ5,B4E0F1,A7EE21,P51532	Confirmed	
1010137	TC	TP53	chr17	7577093	C	G	0.8	Missense	R282P	ENST00000269305	8	393	COSM44306	0	damaging	p53_DNA-binding_domain_(1),p53-like_transcription_factor_DNA-binding_(1),p53/RUN1-type_transcription_factor_DNA-binding_domain_(1)	P04637-2,P04637-3,P04637,Q1MSW8	Confirmed	
1010144	TC	BAP1	chr3	52438585	C	C	0.389	Frameshift insertion	A378TW fs	ENST00000406080	12	729						Confirmed	
1010144	TC	KIT	chr4	55593589	T	G	0.311	Inframe deletion	553YEVQ556 del	ENST000002088135	11	976					Kinase domain	Confirmed	
1010148	TC	NF1	chr17	29652841	C	G	0.161	Missense	F1613L	ENST00000358273	37	2639		0.4	damaging	Cellular_retinoid_acyl-binding_triple_function_C-terminal_C2Armadillo-type_fold_(1)	Q59FX3,P21359-2,P21359	ND	
1010148	TC	NF1	chr17	29556328	T	G	0.271	Missense	L899V	ENST00000358273	21	2639	COSM1479419	0.13	damaging	Armadillo-type_fold_(1)	E1P657,P21359-2,P21359	ND	
1010148	TC	SETD2	chr3	47108587	T	C	0.639	Missense	K2028E	ENST00000409792	13	2564						FZ2317,Q9BYW2	ND
1010148	TC	TP53	chr17	7578403	C	T	0.658	Missense	C176Y	ENST00000269305	5	393	COSM1649384	0	damaging	p53_DNA-binding_domain_(1),p53-like_transcription_factor_DNA-binding_(1),p53/RUN1-type_transcription_factor_DNA-binding_domain_(1)	B4E095,P04637-2,P04637-3,E9PF15,P04637,Q1MSW8,ETE QX7	Confirmed	
1010152	TC	TP53	chr17	7577580	T	C	0.649	Missense	Y234C	ENST00000269305	7	393	COSM10725	0	damaging	p53_DNA-binding_domain_(1),p53-like_transcription_factor_DNA-binding_(1),p53/RUN1-type_transcription_factor_DNA-binding_domain_(1)	P04637-2,P04637-3,E9PF15,P04637,Q1MSW8,ETE QX7	Confirmed	
1010153	TC	ASXL1	chr20	31022615	T	A	0.231	Nonsense	Y700*	ENST00000375687	13	1541	COSM133574					Confirmed	
1010153	TC	DNMT3A	chr2	25458691	TC	T	0.268	Frameshift deletion	F827 fs	ENST00000321117	22	912	COSM53096					Confirmed	
1010153	TC	DNMT3A	chr2	25464666	T	G	0.226	Missense	Y683D	ENST00000321117	17	912		0.01	damaging		Q9Y6K1,E9PEB8	Confirmed	
1010153	TC	TP53	chr17	7575525	G	T	0.541	Nonsense	C135*	ENST00000269305	5	393	COSM44319					Confirmed	
1010168	B1	ASXL1	chr20	31022782	A	C	0.194	Missense	D756A	ENST00000375687	13	1541		0.53	benign		A6N26,Q8IKJ9	ND	
1010168	B1	PDGFRA	chr4	55195653	C	A	0.2	Nonsense	Y1018*	ENST00000257290	22	1089						ND	
1010174	TC	CDKN2A	chr9	21970917	G	C	0.342	Frameshift insertion	A147 fs	ENST00000304494	2	157	COSM33804					Confirmed	
1010174	TC	TP53	chr17	7578655	G	A	0.42	Nonsense	Q331*	ENST00000269305	9	393	COSM288612					Confirmed	
1010174	TC	WT1	chr11	32417949	T	A	0.232	Missense	V300E	ENST00000332351	7	517					None_Wilm&apoptosis_(1),tumour_protein_N-terminal_(1)	None,P19544-8,P19544,P19544-7,B3KSA5,P19544-6	Confirmed
1010184	B3	PTGS2	chr1	186643487	A	G	0.161	Stop codon	T605Q	ENST00000367468	10	604						ND	
1010188	TC	APC	chr5	112179388	T	A	0.306	Missense	D2690E	ENST00000268376	17	2843					EB-1_binding_(1)	Q4LE70,P25064	ND
1010198	TC	ATM	chr11	108186757	G	A	0.306	Missense	E2039K	ENST00000452508	43	3056	COSM1561120	0	damaging	PKC-related_kinase_(1),Armadillo-type_fold_(1)	Q13315	ND	
1010198	TC	ATM	chr11	108115727	C	T	0.384	Missense	P282L	ENST00000452508	8	3056	COSM1350746	0	damaging	Armadillo-type_fold_(1)	Q13315	ND	
1010198	TC	OCC	chr18	50977010	C	T	0.437	Missense	R1124C	ENST00000442544	23	1447						P43146	ND
1010198	TC	EML4	chr2	42509964	T	C	0.321	Missense	Y276H	ENST00000401738	9	992					HELP_(1),Quinoliprotein_alcohol_dehydrogenase-like_(1)	B5MCW9,Q9HC35	ND
1010198	TC	FLCN	chr17	17119708	TG	T	0.208	Frameshift deletion	H429fs	ENST00000285071	11	579	r80338683						ND
1010198	TC	MLH1	chr3	37089163	G	T	0.442	Nonsense	E629*	ENST00000231790	16	756						ND	
1010198	TC	NES	chr1	156642803	TG	T	0.225	Frameshift deletion	P392 fs	ENST00000368223	4	1621	COSM1334916						ND
1010198	TC	NF2	chr22	30000022	G	C	0.474	Frameshift deletion	S12 del	ENST00000338641	1	595	COSM22361						ND
1010198	TC	TCF7L2	chr10	114912188	C	T	0.241	Missense	R420W	ENST00000545257	11	619	COSM1560964	0	damaging	High_mobility_group_C2ZKWA,C2ZLJ8,C2ZLJ9,C2ZLJ10,C2ZLJ11,C2ZLJ12,C2ZLJ13,C2ZLJ14,C2ZLJ15,C2ZLJ16,C2ZLJ17,C2ZLJ18,C2ZLJ19,C2ZLJ20,C2ZLJ21,C2ZLJ22,C2ZLJ23,C2ZLJ24,C2ZLJ25,C2ZLJ26,C2ZLJ27,C2ZLJ28,C2ZLJ29,C2ZLJ30,C2ZLJ31,C2ZLJ32,C2ZLJ33,C2ZLJ34,C2ZLJ35,C2ZLJ36,C2ZLJ37,C2ZLJ38,C2ZLJ39,C2ZLJ40,C2ZLJ41,C2ZLJ42,C2ZLJ43,C2ZLJ44,C2ZLJ45,C2ZLJ46,C2ZLJ47,C2ZLJ48,C2ZLJ49,C2ZLJ50,C2ZLJ51,C2ZLJ52,C2ZLJ53,C2ZLJ54,C2ZLJ55,C2ZLJ56,C2ZLJ57,C2ZLJ58,C2ZLJ59,C2ZLJ60,C2ZLJ61,C2ZLJ62,C2ZLJ63,C2ZLJ64,C2ZLJ65,C2ZLJ66,C2ZLJ67,C2ZLJ68,C2ZLJ69,C2ZLJ70,C2ZLJ71,C2ZLJ72,C2ZLJ73,C2ZLJ74,C2ZLJ75,C2ZLJ76,C2ZLJ77,C2ZLJ78,C2ZLJ79,C2ZLJ80,C2ZLJ81,C2ZLJ82,C2ZLJ83,C2ZLJ84,C2ZLJ85,C2ZLJ86,C2ZLJ87,C2ZLJ88,C2ZLJ89,C2ZLJ90,C2ZLJ91,C2ZLJ92,C2ZLJ93,C2ZLJ94,C2ZLJ95,C2ZLJ96,C2ZLJ97,C2ZLJ98,C2ZLJ99,C2ZLJ100,C2ZLJ101,C2ZLJ102,C2ZLJ103,C2ZLJ104,C2ZLJ105,C2ZLJ106,C2ZLJ107,C2ZLJ108,C2ZLJ109,C2ZLJ110,C2ZLJ111,C2ZLJ112,C2ZLJ113,C2ZLJ114,C2ZLJ115,C2ZLJ116,C2ZLJ117,C2ZLJ118,C2ZLJ119,C2ZLJ120,C2ZLJ121,C2ZLJ122,C2ZLJ123,C2ZLJ124,C2ZLJ125,C2ZLJ126,C2ZLJ127,C2ZLJ128,C2ZLJ129,C2ZLJ130,C2ZLJ131,C2ZLJ132,C2ZLJ133,C2ZLJ134,C2ZLJ135,C2ZLJ136,C2ZLJ137,C2ZLJ138,C2ZLJ139,C2ZLJ140,C2ZLJ141,C2ZLJ142,C2ZLJ143,C2ZLJ144,C2ZLJ145,C2ZLJ146,C2ZLJ147,C2ZLJ148,C2ZLJ149,C2ZLJ150,C2ZLJ151,C2ZLJ152,C2ZLJ153,C2ZLJ154,C2ZLJ155,C2ZLJ156,C2ZLJ157,C2ZLJ158,C2ZLJ159,C2ZLJ160,C2ZLJ161,C2ZLJ162,C2ZLJ163,C2ZLJ164,C2ZLJ165,C2ZLJ166,C2ZLJ167,C2ZLJ168,C2ZLJ169,C2ZLJ170,C2ZLJ171,C2ZLJ172,C2ZLJ173,C2ZLJ174,C2ZLJ175,C2ZLJ176,C2ZLJ177,C2ZLJ178,C2ZLJ179,C2ZLJ180,C2ZLJ181,C2ZLJ182,C2ZLJ183,C2ZLJ184,C2ZLJ185,C2ZLJ186,C2ZLJ187,C2ZLJ188,C2ZLJ189,C2ZLJ190,C2ZLJ191,C2ZLJ192,C2ZLJ193,C2ZLJ194,C2ZLJ195,C2ZLJ196,C2ZLJ197,C2ZLJ198,C2ZLJ199,C2ZLJ200,C2ZLJ201,C2ZLJ202,C2ZLJ203,C2ZLJ204,C2ZLJ205,C2ZLJ206,C2ZLJ207,C2ZLJ208,C2ZLJ209,C2ZLJ210,C2ZLJ211,C2ZLJ212,C2ZLJ213,C2ZLJ214,C2ZLJ215,C2ZLJ216,C2ZLJ217,C2ZLJ218,C2ZLJ219,C2ZLJ220,C2ZLJ221,C2ZLJ222,C2ZLJ223,C2ZLJ224,C2ZLJ225,C2ZLJ226,C2ZLJ227,C2ZLJ228,C2ZLJ229,C2ZLJ230,C2ZLJ231,C2ZLJ232,C2ZLJ233,C2ZLJ234,C2ZLJ235,C2ZLJ236,C2ZLJ237,C2ZLJ238,C2ZLJ239,C2ZLJ240,C2ZLJ241,C2ZLJ242,C2ZLJ243,C2ZLJ244,C2ZLJ245,C2ZLJ246,C2ZLJ247,C2ZLJ248,C2ZLJ249,C2ZLJ250,C2ZLJ251,C2ZLJ252,C2ZLJ253,C2ZLJ254,C2ZLJ255,C2ZLJ256,C2ZLJ257,C2ZLJ258,C2ZLJ259,C2ZLJ260,C2ZLJ261,C2ZLJ262,C2ZLJ263,C2ZLJ264,C2ZLJ265,C2ZLJ266,C2ZLJ267,C2ZLJ268,C2ZLJ269,C2ZLJ270,C2ZLJ271,C2ZLJ272,C2ZLJ273,C2ZLJ274,C2ZLJ275,C2ZLJ276,C2ZLJ277,C2ZLJ278,C2ZLJ279,C2ZLJ280,C2ZLJ281,C2ZLJ282,C2ZLJ283,C2ZLJ284,C2ZLJ285,C2ZLJ286,C2ZLJ287,C2ZLJ288,C2ZLJ289,C2ZLJ290,C2ZLJ291,C2ZLJ292,C2ZLJ293,C2ZLJ294,C2ZLJ295,C2ZLJ296,C2ZLJ297,C2ZLJ298,C2ZLJ299,C2ZLJ300,C2ZLJ301,C2ZLJ302,C2ZLJ303,C2ZLJ304,C2ZLJ305,C2ZLJ306,C2ZLJ307,C2ZLJ308,C2ZLJ309,C2ZLJ310,C2ZLJ311,C2ZLJ312,C2ZLJ313,C2ZLJ314,C2ZLJ315,C2ZLJ316,C2ZLJ317,C2ZLJ318,C2ZLJ319,C2ZLJ320,C2ZLJ321,C2ZLJ322,C2ZLJ323,C2ZLJ324,C2ZLJ325,C2ZLJ326,C2ZLJ327,C2ZLJ328,C2ZLJ329,C2ZLJ330,C2ZLJ331,C2ZLJ332,C2ZLJ333,C2ZLJ334,C2ZLJ335,C2ZLJ336,C2ZLJ337,C2ZLJ338,C2ZLJ339,C2ZLJ340,C2ZLJ341,C2ZLJ342,C2ZLJ343,C2ZLJ344,C2ZLJ345,C2ZLJ346,C2ZLJ347,C2ZLJ348,C2ZLJ349,C2ZLJ350,C2ZLJ351,C2ZLJ352,C2ZLJ353,C2ZLJ354,C2ZLJ355,C2ZLJ356,C2ZLJ357,C2ZLJ358,C2ZLJ359,C2ZLJ360,C2ZLJ361,C2ZLJ362,C2ZLJ363,C2ZLJ364,C2ZLJ365,C2ZLJ366,C2ZLJ367,C2ZLJ368,C2ZLJ369,C2ZLJ370,C2ZLJ371,C2ZLJ372,C2ZLJ373,C2ZLJ374,C2ZLJ375,C2ZLJ376,C2ZLJ377,C2ZLJ378,C2ZLJ379,C2ZLJ380,C2ZLJ381,C2ZLJ382,C2ZLJ383,C2ZLJ384,C2ZLJ385,C2ZLJ386,C2ZLJ387,C2ZLJ388,C2ZLJ389,C2ZLJ390,C2ZLJ391,C2ZLJ392,C2ZLJ393,C2ZLJ394,C2ZLJ395,C2ZLJ396,C2ZLJ397,C2ZLJ398,C2ZLJ399,C2ZLJ400,C2ZLJ401,C2ZLJ402,C2ZLJ403,C2ZLJ404,C2ZLJ405,C2ZLJ406,C2ZLJ407,C2ZLJ408,C2ZLJ409,C2ZLJ410,C2ZLJ411,C2ZLJ412,C2ZLJ413,C2ZLJ414,C2ZLJ415,C2ZLJ416,C2ZLJ417,C2ZLJ418,C2ZLJ419,C2ZLJ420,C2ZLJ421,C2ZLJ422,C2ZLJ423,C2ZLJ424,C2ZLJ425,C2ZLJ426,C2ZLJ427,C2ZLJ428,C2ZLJ429,C2ZLJ430,C2ZLJ431,C2ZLJ432,C2ZLJ433,C2ZLJ434,C2ZLJ435,C2ZLJ436,C2ZLJ437,C2ZLJ438,C2ZLJ439,C2ZLJ440,C2ZLJ441,C2ZLJ442,C2ZLJ443,C2ZLJ444,C2ZLJ445,C2ZLJ446,C2ZLJ447,C2ZLJ448,C2ZLJ449,C2ZLJ450,C2ZLJ451,C2ZLJ452,C2ZLJ453,C2ZLJ454,C2ZLJ455,C2ZLJ456,C2ZLJ457,C2ZLJ458,C2ZLJ459,C2ZLJ460,C2ZLJ461,C2ZLJ462,C2ZLJ463,C2ZLJ464,C2ZLJ465,C2ZLJ466,C2ZLJ467,C2ZLJ468,C2ZLJ469,C2ZLJ470,C2ZLJ471,C2ZLJ472,C2ZLJ473,C2ZLJ474,C2ZLJ475,C2ZLJ476,C2ZLJ477,C2ZLJ478,C2ZLJ479,C2ZLJ480,C2ZLJ481,C2ZLJ482,C2ZLJ483,C2ZLJ484,C2ZLJ485,C2ZLJ486,C2ZLJ487,C2ZLJ488,C2ZLJ489,C2ZLJ490,C2ZLJ491,C2ZLJ492,C2ZLJ493,C2ZLJ494,C2ZLJ495,C2ZLJ496,C2ZLJ497,C2ZLJ498,C2ZLJ499,C2ZLJ500,C2ZLJ501,C2ZLJ502,C2ZLJ503,C2ZLJ504,C2ZLJ505,C2ZLJ506,C2ZLJ507,C2ZLJ508,C2ZLJ509,C2ZLJ510,C2ZLJ511,C2ZLJ512,C2ZLJ513,C2ZLJ514,C2ZLJ515,C2ZLJ516,C2ZLJ517,C2ZLJ518,C2ZLJ519,C2ZLJ520,C2ZLJ521,C2ZLJ522,C2ZLJ523,C2ZLJ524,C2ZLJ525,C2ZLJ526,C2ZLJ527,C2ZLJ528,C2ZLJ529,C2ZLJ530,C2ZLJ531,C2ZLJ532,C2ZLJ533,C2ZLJ534,C2ZLJ535,C2ZLJ536,C2ZLJ537,C2ZLJ538,C2ZLJ539,C2ZLJ540,C2ZLJ541,C2ZLJ542,C2ZLJ543,C2ZLJ544,C2ZLJ545,C2ZLJ546,C2ZLJ547,C2ZLJ548,C2ZLJ549,C2ZLJ550,C2ZLJ551,C2ZLJ552,C2ZLJ553,C2ZLJ554,C2ZLJ555,C2ZLJ556,C2ZLJ557,C2ZLJ558,C2ZLJ559,C2ZLJ560,C2ZLJ561,C2ZLJ562,C2ZLJ563,C2ZLJ564,C2ZLJ565,C2ZLJ566,C2ZLJ567,C2ZLJ568,C2ZLJ569,C2ZLJ570,C2ZLJ571,C2ZLJ572,C2ZLJ573,C2ZLJ574,C2ZLJ575,C2ZLJ576,C2ZLJ577,C2ZLJ578,C2ZLJ579,C2ZLJ580,C2ZLJ581,C2ZLJ582,C2ZLJ583,C2ZLJ584,C2ZLJ585,C2ZLJ586,C2ZLJ587,C2ZLJ588,C2ZLJ589,C2ZLJ590,C2ZLJ591,C2ZLJ592,C2ZLJ593,C2ZLJ594,C2ZLJ595,C2ZLJ596,C2ZLJ597,C2ZLJ598,C2ZLJ599,C2ZLJ600,C2ZLJ601,C2ZLJ602,C2ZLJ603,C2ZLJ604,C2ZLJ605,C2ZLJ606,C2ZLJ607,C2ZLJ608,C2ZLJ609,C2ZLJ610,C2ZLJ611,C2ZLJ612,C2ZLJ613,C2ZLJ614,C2ZLJ615,C2ZLJ616,C2ZLJ617,C2ZLJ618,C2ZLJ619,C2ZLJ620,C2ZLJ621,C2ZLJ622,C2ZLJ623,C2ZLJ624,C2ZLJ625,C2ZLJ626,C2ZLJ627,C2ZLJ628,C2ZLJ629,C2ZLJ630,C2ZLJ631,C2ZLJ632,C2ZLJ633,C2ZLJ634,C2ZLJ635,C2ZLJ636,C2ZLJ637,C2ZLJ638,C2ZLJ639,C2ZLJ640,C2ZLJ641,C2ZLJ642,C2ZLJ643,C2ZLJ644,C2ZLJ645,C2ZLJ646,C2ZLJ647,C2ZLJ648,C2ZLJ649,C2ZLJ650,C2ZLJ651,C2ZLJ652,C2ZLJ653,C2ZLJ654,C2ZLJ655,C2ZLJ656,C2ZLJ657,C2ZLJ658,C2ZLJ659,C2ZLJ660,C2ZLJ661,C2ZLJ662,C2ZLJ663,C2ZLJ664,C2ZLJ665,C2ZLJ666,C2ZLJ667,C2ZLJ668,C2ZLJ669,C2ZLJ670,C2ZLJ671,C2ZLJ672,C2ZLJ673,C2ZLJ674,C2ZLJ675,C2ZLJ676,C2ZLJ677,C2ZLJ678,C2ZLJ679,C2ZLJ680,C2ZLJ681,C2ZLJ682,C2ZLJ683,C2ZLJ684,C2ZLJ685,C2ZLJ686,C2ZLJ687,C2ZLJ688,C2ZLJ689,C2ZLJ690,C2ZLJ691,C2ZLJ692,C2ZLJ693,C2ZLJ694,C2			

Table S3. Summary of CYLD somatic variations in thymic carcinomas

Sample ID	Positions on chr 16	Ref nt	Change nt	Effect	AA Change	Transcript Ensembl ID	AA Length	Sift score	Source
1010056	50815317	CTT	C	Frameshift deletion	L560 fs	ENST00000311559	956		this study
1010103	50815156	G	C	Splice site acceptor		ENST00000311559	956		this study
1010363	50820823	GCATCAG GATTT	G	Frameshift deletion	667EAASG F672 del	ENST00000311559	956		this study
1010376	50783936	G	T	Missense	R109S	ENST00000311559	956	0	this study
P-Thy002	50784106	A	G	Missesense	E166G	ENST00000569681	956	0.002	Nature Genetics
P-Thy002	50826571	A	T	Missesense	I584F	ENST00000568704	956	0.005	Nature Genetics
P-Thy002	50828337	A	G	Missesense	D710G	ENST00000568704	956	0.197	Nature Genetics
N-Thy011	50813914	C	T	Nonsense	Q490X	ENST00000566206	956		Nature Genetics
N-Thy004	50818352	CT	-CT	Frame shift indel	G462fs	ENST00000568704	956		Nature Genetics

ref nt, reference nucleotide; AA, amino acid; ID, identification number.
Nature Genetics, 46, 8, 844-9, 2014

Table S5. Pathway enrichment scores

Pathway	Significant	q-value	p-value
Chromatin Modification	TRUE	2.86E-17	6.78E-18
DNA Damage Control	TRUE	2.57E-11	1.22E-11
PI3K	TRUE	1.43E-09	1.02E-09
RAS	TRUE	1.49E-09	1.42E-09
Apoptosis	TRUE	1.02E-07	1.21E-07
APC	TRUE	1.02E-06	1.45E-06
Transcriptional Regulation	TRUE	0.010291726	0.019554279
STAT	TRUE	0.010291726	0.019554279
MAPK	FALSE	0.350877193	1
TGF-b	FALSE	0.350877193	1
NOTCH	FALSE	0.350877193	1
HH	FALSE	0.350877193	1

q values were calculated from the empirical p values of bootstrap estimation method (see Method section)