Table S1. Main characteristics of the selected oncogenomic portals

Database	Data source	Sites of analyzed cancer	Oncogenomic data	Link
Oncomine	TCGA, Cancer data from literature	Bd; Br; Bra; Cer; Clr; Eso; HN; Kd; Lng; Lvr; Lymph; Ov; Pnc; also: cancer cell lines	Drug sensitivity,cancer histology,clinical outcome, tissue, pathology, subtype, molecular subtype, patient treatment response	https://www.oncomine.org
Prognoscan	Cancer data from literature	Bd; Bld; Br; Bra; Clr; EA; Eso; HN; Kd; Lng; Lymph; Ov; Prst; Sk; ST;	Survival analyses	http://www.abren.net/PrognoScan
STRING	Protein, gene from literature	Gene, gene from literature	Structure	http://STRINGdb.org
cBioPortal	AMC, CCRC, BGI, British Columbia, Broad, Broad/ Cornell, CCLE, CLCGP, Genentech, ICGC, JHU, Michigan, MSK, NCCS, NUS, PCGP, Pfizer UHK, Riken, Sanger, Singapore, TCGA, TSP, UTokyo, Yale	ACC; Bd; Bld; Br; Bra; Chl; Clr; Eso; HN; Kd; Lng; Lvr Lymph; MM; Npx; Ov; Pnc; Prst; Sk; ST; Stc; Thr; Utr; also: cancer cell lines	Mutations, putative copy number alterations; mRNA expression, protein/ phosphoproteinlevel; survival analyses	http://www.cbioportal.org/
DAVID	-	Signal pathway	GO terms, annotation terms, BioCarta & KEGG pathway, interacting proteins, gene-disease associations, protein functional domains and motifs	https://david.ncifcrf.gov/home.jsp
GEPIA	TCGA, GTEx projects	ACC; BLCA; BRCA; CESC; CHOL; COAD; DLBC; ESCA; GBM; HNSC; KICH; KIRC; KIRP; LAML; LGG; LIHC; LUAD; LUSC; MESO; OV; PAAD; PCPG; PRAD; READ; SARC; SKCM; STAD; TGCT; THCA; THYM; UCEC; UCS; UVM	Analyzing the RNA sequencing expression	http://gepia.cancerpku.cn/about.html
SurvExpress	TCGA		Survival analyses	http://bioinformatica.mty.itesm.mx:8080/Biomatec/SurvivaX.jsp
Kplan meier plotter		Bra; Gast; Lng; Ov; Lvr;	Survival analyses	http://kmplot.com/analysis/index.php?p=service

Table S1. Continued

Database	Data source	Sites of analyzed cancer	Oncogenomic data	Link
R2	TCGA	Genomics Analysis and Visualization Platform	Gene expression and survival analyses	https://hgserver1.amc.nl/cgi-bin/r2/main.cgi?&species=hs

ACC: adenoid cystic carcinoma, AMC: asan medical center, Bd: bladder, Bld: blood, BGI: beijing genomics institute, Br: breast, Bra: brain, Chl: cholangiocarcinoma, Clr: colorectal, CLCGP: clinical lung cancer genome project, DAVID: the database for annotation, visualization and integrated discovery, EA: eye and adnexa, Eso: esophagus, GTEx: genotype-tissue expression, HN: head and neck, Kd: kidney, Gast: Gastric, Lng: lung, Lvr: liver and biliary tract, Lymph: Lymphoma, MSK: memorial sloan-kettering cancer center, Npx: nasopharynx, Ov: ovary, Pnc: pancreas, Prst: prostate, Sk: skin, ST: soft tissues, Stc: stomach, Thr: thyroid, Utr: uterine, BLCA: Bladder Urothelial Carcinoma, BRCA: Breast invasive carcinoma, CESC: Cervical squamous cell carcinoma and endocervical adenocarcinoma, CHOL: Cholangio carcinoma, COAD: Colon adenocarcinoma, DLBC: Lymphoid Neoplasm Diffuse Large B-cell Lymphoma, Cer: cervix, ESCA: Esophageal carcinoma, GBM: Glioblastoma multiforme, HNSC: Head and Neck squamous cell carcinoma, Kd: kidney, ICGC: international cancer genome consortium, JHU: johns hopkins university, KICH: Kidney Chromophobe, KIRC: Kidney renal clear cell carcinoma, KIRP: Kidney renal papillary cell carcinoma, LAML: Acute Myeloid Leukemia, LGG: Brain Lower Grade Glioma, LIHC: Liver hepatocellular carcinoma, lng: lung, LUAD: Lung adenocarcinoma, LUSC: Lung squamous cell carcinoma, Lvr: liver, NCCS: national cancer centre of singapore, NUS: national university of singapore, PCGP: washington university pediatric cancer genome project, MESO: Mesothelioma, OV: Ovarian serous cystadenocarcinoma, PAAD: Pancreatic adenocarcinoma, PCPG: Pheochromocytoma and Paraganglioma, Pnc: pancreas, PRAD: Prostate adenocarcinoma, READ: Rectum adenocarcinoma, SARC: Sarcoma, SKCM: Skin Cutaneous Melanoma, STAD: Stomach adenocarcinoma, STRING: search tool for recurring instances of neighboring genes, TGCT: Testicular Germ Cell Tumors, THCA: Thyroid carcinoma, THYM: Thymoma, TSP: tumor sequencing project, UCEC: Uterine Corpus Endometrial Carcinoma, UCS: Uterine Carcinosarcoma, UHK: university of hong kong, UVM: Uveal Melanoma.

Table S2. C-MYC expression in cancers (Oncomine database)

Cancer	Cancer subtype	p-value	Fold change	Rank (%)	Sample	Reference
Brain and CNS cancer	Malignant Glioma, NOS	3.51E-09	184.367	1	85	1
	Classic Medulloblastoma	1.45E-15	85.004	1	85	1
	Anaplastic Oligodendroglioma	2.41E-10	4.87	1	33	2
	Oligodendroglioma	2.52E-05	−2.105	2	42	2
Breast	Invasive Breast Carcinoma	1.54E-19	2.222	2	59	3
	Mixed Lobular and Ductal Breast Carcinoma	5.05E-10	−3.351	1	593	3
	Intraductal Cribriform Breast Adenocarcinoma	2.98E-12	3.224	1	593	3
	Invasive Lobular Breast Carcinoma	4.39E-11	−2.915	5	593	3
	Tubular Breast Carcinoma	6.52E-25	−3.015	5	2,136	4
Colorectal	Rectal Adenoma	1.27E-05	4.686	6	64	5
	Colon Adenoma	1.14E-08	9.287	1	40	6
	Colon Carcinoma	1.17E-08	6.484	4	40	6
	Colorectal Carcinoma	1.84E-12	6.801	3	82	7
Head and neck	Nasopharyngeal Carcinoma	9.25E-06	2.383	4	41	8
	Head and Neck Squamous Cell Carcinoma	8.93E-08	2.281	6	54	9
Kidney	Clear Cell Renal Cell Carcinoma	1.86E-06	3.112	3	67	10
	Clear Cell Renal Cell Carcinoma	9.42E-05	6.714	8	20	11
Leukemia	Chronic Lymphocytic Leukemia	4.66E-14	−3.637	1	336	12
	Chronic Lymphocytic Leukemia	1.04E-06	−6.468	4	102	13
	Chronic Lymphocytic Leukemia	3.34E-05	−2.795	7	120	14
Liver	Hepatocellular Carcinoma	2.06E-11	−2.214	6	197	15
Lymphoma	Burkitt's Lymphoma	5.22E-07	5.06	4	336	16
	Diffuse Large B-Cell Lymphoma	4.65E-06	2.431	5	336	16
	Follicular Lymphoma	3.96E-05	−2.25	2	120	17
	Cutaneous Follicular Lymphoma	5.48E-05	−2.068	1	27	18
Myeloma	Multiple Myeloma	1.57E-08	2.683	6	131	19
Prostate	Prostate Carcinoma	1.62E-05	2.535	1	19	20
	Prostate Carcinoma	7.27E-05	2.954	1	35	21
	Prostate Carcinoma	2.59E-09	2.276	1	122	22
	Prostate Carcinoma	5.63E-09	2.183	3	112	23
	Prostate Carcinoma	2.57E-05	2.195	3	101	24
Sarcoma	Leiomyosarcoma	1.19E-08	−9.976	2	158	25
	Pleomorphic Liposarcoma	2.45E-06	−5.303	3	158	25
	Dedifferentiated Liposarcoma	6.82E-06	−4.378	5	158	25
	Myxofibrosarcoma	2.10E-06	−5.699	5	158	25
Others	Teratoma, NOS	4.22E-09	4.536	3	107	26
	Testicular Seminoma	2.49E-06	−2.244	6	539	27

CNS: central nervous system, MYC: cellular myelocytomatosis oncogene, NOS: not otherwise specified.

Table S3. The association of C-MYC expression and the survival in cancer patients (PrognoScan database)

Cancer type	N	Cox p-value	HR	Endpoint	Dataset	Probe ID
Colorectal	55	0.001411	0	Overall survival	GSE17537	244089_at
	55	0.010481	0	Disease free survival	GSE17537	244089_at
	145	0.01759	0.03	Disease free survival	GSE17536	244089_at
	177	0.020065	0.06	Disease specific survival	GSE17536	244089_at
	49	0.043557	0.1	Disease specific Survival	GSE17537	244089_at
	177	0.021105	0	Overall survival	GSE17536	244089_at
Brain	74	0.000713	0.58	Overall survival	GSE4412-GPL96	202431_s_at
	50	0.002642	0.36	Overall survival	MGH-glioma	37724_at
	50	0.003811	0.49	Overall survival	MGH-glioma	1973_s_at
	50	0.008081	0.31	Overall survival	MGH-glioma	1827_s_at
	67	0.01552	8.04	Overall survival	GSE16581	202431_s_at
	74	0.043054	1.43	Overall survival	GSE4412-GPL97	244089_at
Lung	50	0.002894	2.41	Overall survival	GSE4716-GPL3694	202431_s_at
	79	0.012102	1.64	Overall survival	jacob-00182-HLM	202431_s_at
	204	0.015408	1.65	Relapse free survival	GSE31210	202431_s_at
	117	0.016083	0.35	Overall survival	GSE13213	244089_at
	2,437	0.3178	0.72	Overall survival	GSE14814	202431_s_at
	2,437	0.5936	0.86	Overall survival	GSE19188	202431_s_at
Breast	198	0.023791	1.26	Relapse free survival	GSE7390	202431_s_at
	77	0.041334	0.01	Distant metastasis free survival	GSE9195	244089_at
	155	0.047484	1.29	Overall survival	GSE9893	7035
		0.008081	0.31	Overall survival	MGH-glioma	7035
Blood	163	0.036089	0.77	Overall survival	GSE12417-GPL96	202431_s_at
Eye	63	0.032114	0	Distant metastasis free survival	GSE22138	244089_at

ID: identification, MYC: cellular myelocytomatosis oncogene, N: number.

Table S4. The alteration frequency of a five-gene signature (MYC, BCL2, TP53, MYB, JUN) in cancers (cBioPortal)

Cancer	Data source	N	Frequency (%)	Amplification (%N)	Deletion (%N)	Mutation (%N)	Multiple alteration (%N)
Ovarian	TCGA	316	91.46%	3.16% (10)	0.63% (2)	44.94% (142)	42.72% (135)
Esophagus	TCGA	184	86.96%	2.17% (4)	1.63% (3)	52.17% (96)	30.98% (57)
Head & Neck	TCGA	504	74.60%	1.79% (9)	0.6% (3)	57.94% (292)	14.29% (72)
Pancreas	TCGA	149	71.81%	2.01% (3)	-	51.01% (76)	18.79% (28)
Colorectal	TCGA	220	58.64%	2.27% (5)	1.36% (3)	50% (110)	5% (11)
NEP	Trento/cornell/ Broad2016	107	57.01%	31.78% (34)	0.93% (1)	8.41% (9)	15.89% (17)
Lung adeno	TCGA	230	54.35%	5.22% (12)	1.74% (4)	38.26% (88)	9.13% (21)

Table S5. The percentages of alterations in MYC, BCL2, TP53, MYB, and JUN genes (cBioPortal)

Cancer	MYC	BCL2	TP53	MYB	JUN
Ovarian	41.0%	4.0%	48.0%	2.5%	5.0%
Esophagus	27.0%	8.0%	84.0%	8.0%	1.1%
Head & Neck	13.0%	4.0%	72.0%	1.4%	0.8%
Pancreas	14.0%	5.0%	70.0%	2.0%	0.0%
Colorectal	6.0%	2.3%	55.0%	1.4%	0.0%
NEP	53.0%	9.0%	29.0%	12.0%	21.0%
Lung adeno	8.0%	2.9%	50.0%	2.0%	1.6%

Table S6. The alteration frequency of an eight - gene signature (MYC, BCL2, TP53, MYB, JUN, CDK4, CDKN1A and CDKN2A) in cancers (cBioPortal)

Cancer	Data source	N	Frequency (%)	Amplification (%N)	Deletion (%N)	Mutation (%N)	Multiple alteration (%N)
Ovarian	TCGA	316	92.41%	3.8% (12)	0.95% (3)	41.14% (130)	46.52% (147)
Esophagus	TCGA	184	91.30%	2.17% (4)	3.8% (7)	26.64% (49)	58.7% (108)
Brain	TCGA	273	87.55%	10.62% (29)	45.79% (125)	12.09% (33)	19.05% (52)
Pancreas	TCGA	149	83.22%	2.01% (3)	8.05% (12)	37.58% (56)	35.57% (53)
Head & Neck	TCGA	504	81.94%	1.79% (9)	6.94% (35)	38.69% (195)	34.52% (174)
NEP	trento/cornell/Broad2016	107	60.75%	32.71% (35)	3.74% (4)	8.41% (9)	15.89% (17)
Colorectal	MSK	138	81.88%	-	-	81.88% (113)	-
Lung	TCGA	178	95.51%	2.25% (4)	6.18% (11)	53.37% (95)	33.71% (60)
Liver	TCGA	366	52.73%	12.57% (46)	5.19% (19)	24.32% (89)	10.66% (39)
Uterine	TCGA	55	96.36%	3.64% (2)	-	63.64% (35)	29.09% (16)
Breast	BCCRC Xenograft	29	86.21%	44.83% (13)	-	10.34% (3)	31.03% (9)
Sarcoma	TCGA	248	75.81%	22.98% (57)	16.13% (40)	27.42% (68)	9.27% (23)

BCCRC: BC cancer research centre.

Table S7. The percentages of alterations in MYC, BCL2, TP53, MYB, JUN, CDK4, CDKN1A and CDKN2A genes (cBioPortal)

Cancer	MYC	BCL2	TP53	MYB	JUN	CDK4	CDKN1A	CDKN2A
Ovarian	41.0%	4.0%	48.0%	2.5%	5.0%	2.0%	7.0%	6.0%
Esophagus	27.0%	8.0%	84.0%	8.0%	1.1%	0.5%	5.0%	51.0%
Brain	12.0%	4.0%	52.0%	4.0%	0.4%	10.0%	2.6%	57.0%
Pancreas	14.0%	5.0%	70.0%	2.0%	0.0%	3.0%	0.0%	46.0%
Head & Neck	13.0%	4.0%	72.0%	1.4%	0.8%	1.6%	0.4%	54.0%
NEP	53.0%	9.0%	29.0%	12.0%	21.0%	22.0%	18.0%	21.0%
Colorectal	4.0%	1.1%	64.0%	0.6%	2.1%	0.7%	0.5%	2.3%
Lung	8.0%	1.7%	61.0%	1.8%	1.2%	4.0%	1.2%	21.0%
Liver	8.0%	0.2%	29.0%	1.2%	0.4%	0.8%	2.8%	6.0%
Uterine	13.0%	1.6%	42.0%	3.0%	0.9%	0.6%	2.2%	0.6%
Breast	23.0%	2.2%	37.0%	3.0%	1.9%	1.6%	1.1%	5.0%
Sarcoma	4.0%	3.0%	28.0%	4.0%	8.0%	19.0%	1.6%	11.0%

Table S8. MYCL expression in cancers (Oncomine database)

Cancer	Cancer subtype	p-value	Fold change	Rank (%)	Sample	Reference
Bladder	Superficial Bladder Cancer	9.72E-08	2.833	5	60	1
	Superficial Bladder Cancer	1.12E-13	7.004	6	157	2
Brain and CNS cancer	Astrocytoma	9.00E-09	7.858	1	51	3
	Desmoplastic Medulloblastoma	1.65E-05	53.343	1	85	4
	Classic Medulloblastoma	3.11E-10	26.743	2	85	4
	Glioblastoma	1.18E-05	−2.372	1	54	5
Colorectal	Colon Carcinoma	5.71E-08	−2.761	3	40	6
Lung	Squamous Cell Lung Carcinoma	4.93E-05	2.076	3	73	7
	Lung Adenocarcinoma	6.69E-06	−3.195	9	96	8
Blood	Centroblastic Lymphoma	1.23E-09	3.866	6	336	9
	Diffuse Large B-Cell Lymphoma	6.07E-05	2.285	8	336	9
	Cutaneous Melanoma	7.58E-06	−3.917	1	87	10
	Cutaneous Melanoma	5.20E-12	−4.088	2	70	11
Ovary	Ovarian Serous Cystadenocarcinoma	1.08E-07	2.886	3	594	12
Pancreas	Pancreatic Adenocarcinoma	5.36E-05	−54.832	6	27	13
Others	Seminoma, NOS	1.43E-09	3.962	2	107	14
	Yolk Sac Tumor, NOS	4.38E-06	2.573	4	107	14
	Embryonal Carcinoma, NOS	8.23E-07	2.094	8	107	14
	Testicular Seminoma	2.10E-06	2.262	6	107	15

Table S9. The association of MYCL expression and the survival in cancer patients (PrognoScan database)

Cancer type	N	p-value	HR	Endpoint	Dataset	Probe ID
Brain	74	0.000771	0.36	Overall Survival	GSE4412-GPL96	214058_at
	50	0.011936	0.12	Overall Survival	MGH-glioma	1490_at
	77	0.029505	0.55	Overall Survival	GSE4271-GPL96	214058_at
Colorectal	226	0.00367	0.59	Disease Free Survival	GSE14333	214058_at
Ovarian	110	0.012935	0.76	Overall Survival	GSE17260	A_24_P156757
	110	0.035615	0.53	Overall Survival	GSE17260	A_23_P160668
Lung	178	0.013358	0.62	Overall Survival	jacob-00182-UM	214058_at
	104	0.04063	0.48	Overall Survival	jacob-00182-MSK	214058_at
		0.011134	1.00	Overall Survival	GSE13213	214058_at
Breast	286	0.013913	0.6	Distant Metastasis Free Survival	GSE2034	214058_at
	54	0.022941	0.13	Disease Free Survival	GSE7378	214058_at
Blood	158	0.017034	0.21	Overall Survival	GSE4475	214058_at

MGH: the massachusetts general hospital, UM: university of michigan cancer center.

Table S10. The alteration frequency of a five-gene signature (MYCL, TP53, RLF, PPIE, and COL9A2) in cancers (cBioPortal)

Cancer	Data source	N	Frequency (%)	Amplification (%N)	Deletion (%N)	Mutation (%N)	Multiple alteration (%N)
Ovarian	TCGA pub	316	96.20%	-	0.32% (1)	84.49% (267)	84.49% (267)
Esophagus	TCGA	184	84.78%	-	1.09% (2)	78.26% (144)	78.26% (144)
Head & Neck	TCGA	504	73.02%	0.2% (1)	0.4% (2)	70.44% (355)	70.44% (355)
Pancreas	TCGA	149	70.47%	-	-	69.8% (104)	69.8% (104)
Colorectal	TCGA	220	58.18%	-	0.91% (2)	0.45% (1)	0.45% (1)

COL9A2: collagen type Ⅸ alpha 2, PPIE: petidylprolyl isomerase E, RLF: rearranged MYCL fusion.

Table S11. The alteration frequency of a seven-gene signature (MYCL, TP53, RLF, PPIE, COL9A2, IER5, and GLI4) in cancers (cBioPortal)

Cancer	Data source	N	Frequency (%)	Amplification (%N)	Deletion (%N)	Mutation (%N)	Multiple alteratio (%N)
Ovarian	TCGA pub	316	96.20%	-	0.32% (1)	62.03% (196)	33.86% (107)
Esophagus	TCGA	184	85.87%	1.09% (2)	1.09% (2)	62.5% (115)	21.2% (39)
Head & Neck	TCGA	504	75.20%	2.38% (12)	0.4% (2)	62.3% (314)	10.12% (51)
Pancreas	TCGA	149	72.48%	2.01% (3)	-	57.72% (86)	12.75% (19)
Colorectal	TCGA	220	60.45%	1.82% (4)	0.91% (2)	53.64% (118)	4.09% (9)
Liver	TCGA	366	50.82%	15.57% (57)	1.91% (7)	23.5% (86)	9.84% (36)
Lung	UCOLOGNE	110	93.64%	-	-	93.64% (103)	-

IER5: immediate early response 5, GLI4: GLI family zinc finger 4, UCOLOGNE: university of cologne.

Table S12. The percentages of alterations in MYCL, TP53, RLF, PPIE, and COL9A2 genes (cBioPortal)

Cancer	MYCL	TP53	RLF	PPIE	COL9A2
Ovarian	10.0%	96.0%	10.0%	10.0%	10.0%
Esophagus	5.0%	84.0%	8.0%	4.0%	5.0%
Head & Neck	2.0%	72.0%	4.0%	1.6%	2.8%
Pancreas	0.0%	70.0%	1.3%	0.0%	0.0%
Colorectal	0.9%	55.0%	5.0%	0.5%	1.4%

Table S13. The percentages of alterations in MYCL, TP53, RLF, PPIE, COL9A2, IER5, and GLI4 genes(cBioPortal)

Cancer	MYCL	TP53	RLF	PPIE	COL9A2	IER5	GLI4
Ovarian	10.0%	96.0%	10.0%	10.0%	10.0%	3.0%	23.0%
Esophagus	5.0%	84.0%	8.0%	4.0%	5.0%	2.7%	15.0%
Head & Neck	2.0%	72.0%	4.0%	1.6%	2.8%	0.8%	12.0%
Pancreas	0.0%	70.0%	1.3%	0.0%	0.0%	2.7%	12.0%
Colorectal	0.9%	55.0%	5.0%	0.5%	1.4%	0.5%	5.0%
Liver	2.0%	41.0%	2.9%	1.5%	1.9%	6.0%	12.0%
Lung	1.5%	61.0%	4.0%	1.5%	2.7%	4%	5%

Table S14. MYCN expression in cancers (Oncomine database)

Cancer	Cancer subtype	p-value	Fold change	Rank (%)	Sample	Reference
Bladder	Superficial Bladder Cancer	4.72E-05	2.15	2	110	1
Colorectal	Rectal Adenocarcinoma	5.73E-13	2.382	8	237	2
	Cecum Adenocarcinoma	2.71E-08	2.244	9	237	2
	Colon Adenoma	4.07E-10	4.575	8	64	3
	Rectal Adenocarcinoma	1.31E-15	2.11	9	130	4
Kidney	Clear Cell Renal Cell Carcinoma	8.04E-08	−9.492	2	20	5
Leukemia	Acute Adult T-Cell Leukemia/Lymphoma	1.16E-14	42.025	1	47	6
	Chronic Adult T-Cell Leukemia/Lymphoma	6.93E-10	11.886	1	47	6
	Acute Myeloid Leukemia	4.86E-71	2.607	1	2,096	7
	T-Cell Childhood Acute Lymphoblastic Leukemia	8.19E-06	4.301	3	288	8
Lymphoma	Acute Adult T-Cell Leukemia/Lymphoma	1.16E-14	42.025	1	47	9
	Chronic Adult T-Cell Leukemia/Lymphoma	6.93E-10	11.886	1	47	9
	Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma	2.90E-10	−2.105	2	136	10
	Activated B-Cell-Like Diffuse Large B-Cell Lymphoma	2.17E-10	−2.11	4	136	10
	Diffuse Large B-Cell Lymphoma	8.18E-11	−2.082	9	136	10
Ovarian	Ovarian Serous Cystadenocarcinoma	3.08E-06	3.25	6	594	11
Myeloma	Smoldering Myeloma	7.44E-05	−2.674	2	78	12
	Monoclonal Gammopathy of Undetermined Significance	5.79E-05	−2.362	6	78	12
Others	Skin Basal Cell Carcinoma	1.16E-05	3.051	3	87	13
	Yolk Sac Tumor, NOS	6.11E-06	3.388	4	107	14
	Mixed Germ Cell Tumor, NOS	2.35E-09	3.108	6	107	14
	Seminoma, NOS	6.65E-07	4.852	7	107	14
	Testicular Seminoma	7.58E-06	2.123	8	74	15

Table S15. The association of MYCN expression and the survival in cancer patients (PrognoScan database)

Cancer type	N	p-value	HR	Endpoint	Dataset	Probe ID
Brain	74	0.000001	5.66	Overall Survival	GSE4412-GPL97	234376_at
	74	0.004832	1.88	Overall Survival	GSE4412-GPL97	234872_at
	74	0.011182	0.57	Overall Survival	GSE4412-GPL97	234169_at
	74	0.030068	1.89	Overall Survival	GSE4412-GPL96	211377_x_at
Colorectal	226	0.000097	0.73	Disease Free Survival	GSE14333	209757_s_at
	49	0.000641	0.01	Disease Specific Survival	GSE17537	234376_at
	177	0.012113	0.07	Disease Specific Survival	GSE17536	234872_at
	177	0.014569	0.17	Overall Survival	GSE17536	234376_at
	55	0.021063	0.04	Disease Free Survival	GSE17537	234376_at
	55	0.024013	0.07	Overall Survival	GSE17537	234376_at
	177	0.031349	0.17	Disease Specific Survival	GSE17536	234376_at
	177	0.033407	0.07	Disease Specific Survival	GSE17536	211377_x_at
	145	0.036677	0.49	Disease Free Survival	GSE17536	209757_s_at
	177	0.039265	0.15	Overall Survival	GSE17536	234872_at
	49	0.048066	0.05	Disease Specific Survival	GSE17537	242026_at
	177	0.048692	0.19	Overall Survival	GSE17536	211377_x_at
	49	0.025185	170.29	Disease Specific Survival	GSE17537	234872_at
	62	0.016533	4.61	Overall Survival	GSE12945	209757_s_at
Breast	159	0.000672	4.16	Disease Specific Survival	GSE1456-GPL97	234376_at
	159	0.000735	3.57	Relapse Free Survival	GSE1456-GPL97	234376_at
	155	0.002998	0.18	Relapse Free Survival	GSE9893	1683
	159	0.004516	3.11	Overall Survival	GSE1456-GPL97	234376_at
	249	0.012234	1.32	Overall Survival	GSE4922-GPL97	234169_at
	159	0.013889	1.55	Disease Free Survival	GSE1456-GPL96	209757_s_at
	236	0.01458	1.40	Disease Specific Survival	GSE3494-GPL97	234169_at
	200	0.021837	1.82	Distant Metastasis Free Survival	GSE11121	211377_x_at
	204	0.033144	1.15	Relapse Free Survival	GSE12276	209757_s_at
	236	0.03341	2.65	Disease Specific Survival	GSE3494-GPL97	234376_at
	159	0.035472	1.38	Relapse Free Survival	GSE1456-GPL96	209757_s_at
	115	0.037299	1.79	Distant Metastasis Free Survival	GSE19615	209757_s_at
	249	0.045677	2.17	Disease Free Survival	GSE4922-GPL97	234376_at
Lung	204	0.001616	0.53	Relapse Free Survival	GSE31210	234376_at
	117	0.003596	0.53	Overall Survival	GSE13213	A_23_P303390
	204	0.008722	0.48	Overall Survival	GSE31210	234376_at
	90	0.009374	1.76	Disease Specific Survival	GSE14814	209757_s_at
	138	0.023862	0.00	Relapse Free Survival	GSE8894	234815_at
	138	0.030613	0.04	Relapse Free Survival	GSE8894	234169_at
	111	0.036569	1.37	Overall Survival	GSE3141	234376_at
	204	0.042469	0.62	Overall Survival	GSE31210	234815_at
	111	0.044855	1.30	Overall Survival	GSE3141	209757_s_at
	138	0.049294	0.00	Relapse Free Survival	GSE8894	234253_at
Blood	559	0.00467	1.23	Disease Specific Survival	GSE2658	209757_s_at
	180	0.014006	1.97	Overall Survival	GSE16131-GPL96	211377_x_at
	79	0.016344	0.12	Overall Survival	GSE12417-GPL570	234815_at
	79	0.018702	0.16	Overall Survival	GSE12417-GPL570	242026_at
	559	0.029309	0.81	Disease Specific Survival	GSE2658	234815_at
	79	0.032612	0.18	Overall Survival	GSE12417-GPL570	234872_at
	79	0.048649	0.23	Overall Survival	GSE12417-GPL570	234169_at
	559	0.040315	0.89	Disease Specific Survival	GSE2658	234376_at
Skin	38	0.009468	0.49	Overall Survival	GSE19234	234376_at

Table S15. Continued

Cancer type	N	p-value	HR	Endpoint	Dataset	Probe ID
Ovarian	133	0.010856	0.49	Overall Survival	DUKE-OC	211377_x_at
	185	0.022213	0.42	Disease Free Survival	GSE26712	211377_x_at
	185	0.036437	0.75	Disease Free Survival	GSE26712	209757_s_at
	185	0.040045	0.43	Overall Survival	GSE26712	211377_x_at
	185	0.04014	0.73	Overall Survival	GSE26712	209757_s_at
Eye	63	0.012605	0.00	Distant Metastasis Free Survival	GSE22138	234872_at
	63	0.012737	0.00	Distant Metastasis Free Survival	GSE22138	211377_x_at
	63	0.044845	0.00	Distant Metastasis Free Survival	GSE22138	234298_at

Table S16. The alteration frequency of a five-gene signature (MYCN, NDRG1, NTRK1, PTEN, and TP53) in cancers (cBioPortal)

Cancer	Data source	N	Frequency (%)	Amplification (%N)	Deletion (%N)	Mutation (%N)	Multiple alteration (%N)
Ovarian	TCGA	316	91.46%	3.16% (10)	0.32% (1)	45.89% (145)	42.09% (133)
Esophagus	TCGA	184	88.04%	1.63% (3)	2.17% (4)	63.04% (116)	21.2% (39)
Uterine	TCGA	242	88.02%	0.83% (2)	1.24% (3)	73.97% (179)	11.98% (29)
Head & Neck	TCGA	504	76.98%	1.79% (9)	1.79% (9)	61.71% (311)	11.71% (59)
pancreas	TCGA	149	73.15%	2.68% (4)	-	55.7% (83)	14.77% (22)
NEP	NOS	63	66.67%	38.1% (24)	7.94% (5)	4.76% (3)	15.87% (10)
Colorectal	MSKCC	138	83.33%	-	-	83.33% (115)	-
Brain	UCSF	61	91.80%	-	-	91.8% (56)	-
Lung	UCOLOGNE	110	93.64%	-	-	93.64% (103)	-
Liver	TCGA	366	54.37%	18.58% (68)	1.64% (6)	20.77% (76)	13.39% (49)
Breast	BCCRC Xenograft	29	86.21%	37.93% (11)	-	34.48% (10)	13.79% (4)
Sarcoma	TCGA	248	52.42%	6.05% (15)	10.48% (26)	29.84% (74)	6.05% (15)

UCSF: university of california, san francisco.

Table S17. The percentages of alterations in N-MYC, NDRG1, NTRK1, PTEN, and TP53 genes (cBioPortal)

Cancer	MYCN	NDRG1	NTRK1	PTEN	TP53
Ovarian	4.0%	38.0%	7.0%	6.0%	58.0%
Esophagus	2.2%	16.0%	7.0%	8.0%	84.0%
Uterine	5.0%	7.0%	9.0%	67.0%	28.0%
Head & Neck	0.8%	10.0%	1.8%	6.0%	72.0%
pancreas	1.3%	12.0%	5.0%	2.0%	70.0%
NEP	19.0%	52.0%	32.0%	31.0%	29.0%
Colorectal	1.5%	1.1%	3.0%	7.0%	64.0%
Brain	0.7%	0.4%	0.6%	12.0%	30.0%
Lung	1.9%	5.0%	7.0%	6.0%	61.0%
Liver	1.5%	8.0%	6.0%	3.0%	298.0%
Breast	1.3%	21.0%	16.0%	8.0%	37.0%
Sarcoma	0.2%	2.9%	6.0%	6.0%	28.0%

Table S18. The alteration frequency of a seven-gene signature (MYCN, NDRG1, NTRK1, PTEN, TP53, CCND1, and VEGFA) in cancers (cBioPortal)

Cancer	Data source	N	Frequency (%)	Amplification (% N)	Deletion (%N)	Mutation (%N)	Multiple alteration (%N)
Ovarian	TCGA	316	92.41%	4.11% (13)	0.32% (1)	41.46% (131)	46.52% (147)
Esophagus	TCGA	184	90.22%	3.26% (6)	2.17% (4)	32.61% (60)	52.17% (96)
Uterine	TCGA	242	88.84%	0.83% (2)	1.24% (3)	71.49% (173)	15.29% (37)
Head & Neck	TCGA	504	79.56%	3.77% (19)	1.98% (10)	43.85% (221)	29.96% (151)
pancreas	TCGA	149	73.15%	2.68% (4)	-	53.69% (80)	16.78% (25)
NEP	NOS	63	69.84%	41.27% (26)	7.94% (5)	4.76% (3)	15.87% (10)
Colorectal	MSKCC	138	83.33%	-	-	83.33% (115)	-
Brain	UCSF	61	91.80%	91.8% (56)	-	-	-
Lung	UCOLOGNE	110	93.64%	-	-	93.64% (103)	-
Liver	TCGA	366	59.02%	22.95% (84)	1.64% (6)	16.67% (61)	17.76% (65)
Sarcoma	TCGA	248	54.84%	8.06% (20)	10.24% (26)	28.23% (70)	8.06% (20)
Breast	BCCRC Xenograft	29	86.21%	37.93% (11)	-	20.69% (6)	27.59% (8)

Table S19. The percentages of alterations MYCN, NDRG1, NTRK1, PTEN, TP53, CCND1, and VEGFA genes (cBioPortal)

Cancer	MYCN	NDRG1	NTRK1	PTEN	TP53	CCND1	VEGFA
Ovarian	4.0%	38.0%	7.0%	6.0%	58.0%	7.0%	5.0%
Esophagus	2.2%	16.0%	7.0%	8.0%	84.0%	36.0%	14.0%
Uterine	5.0%	7.0%	9.0%	67.0%	28.0%	10.0%	2.9%
Head & Neck	0.8%	10.0%	1.8%	6.0%	72.0%	25.0%	1.4%
pancreas	1.3%	12.0%	5.0%	2.0%	70.0%	1.3%	2.0%
NEP	19.0%	52.0%	32.0%	31.0%	29.0%	27.0%	23.0%
Colorectal	1.5%	1.1%	3.0%	7.0%	64.0%	1.5%	1.0%
Brain	0.7%	0.4%	0.6%	12.0%	30.0%	0.4%	0.4%
Lung	1.9%	5.0%	7.0%	6.0%	61.0%	5.0%	1.8%
Liver	1.5%	8.0%	6.0%	3.0%	298.0%	4.0%	4.0%
Sarcoma	0.2%	2.9%	6.0%	6.0%	28.0%	3.0%	2.5%
Breast	1.3%	21.0%	16.0%	8.0%	37.0%	16.0%	2.0%

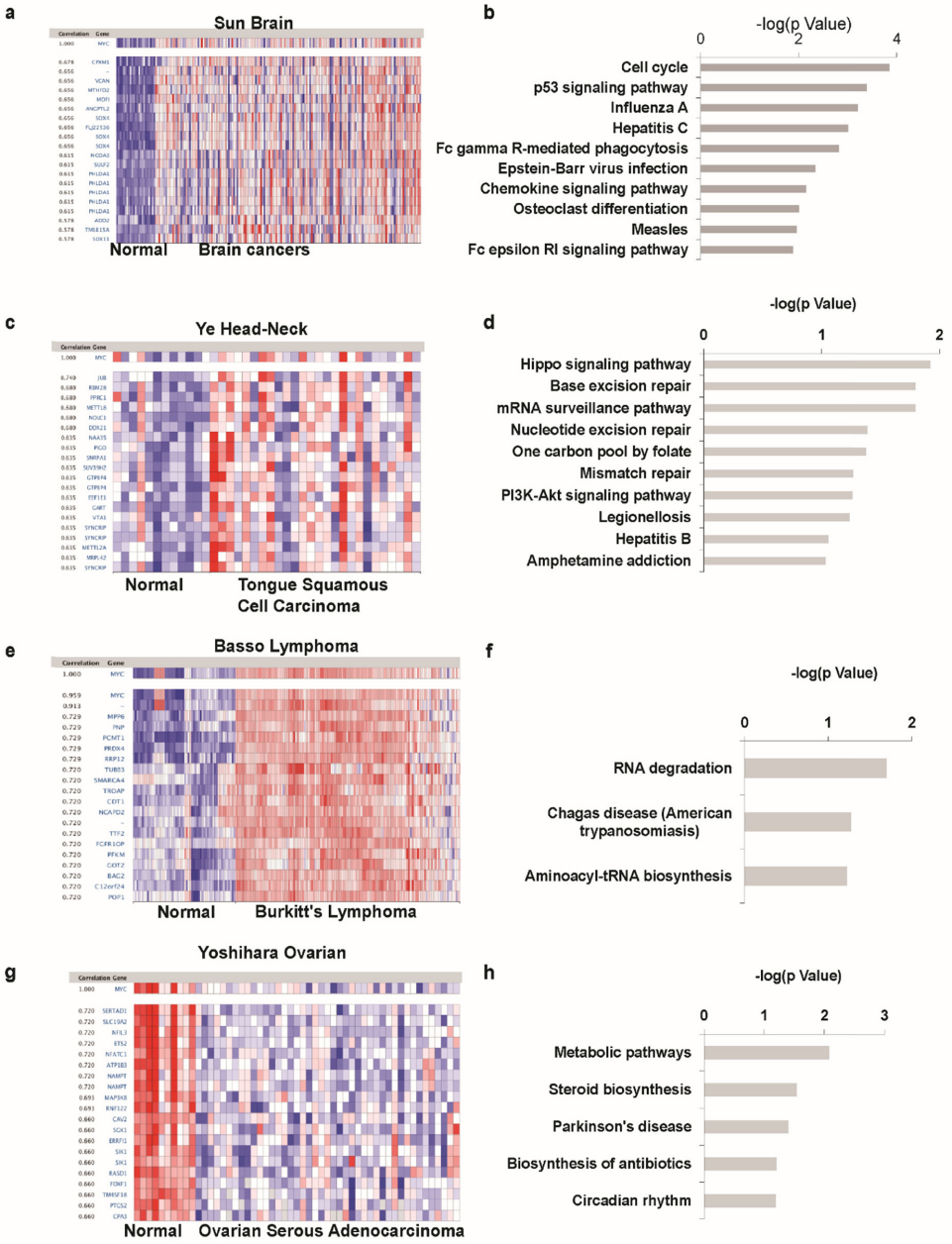

Fig. S1. Distribution of co-expression profiles and top gene ontology (GO) processes for MYC in various cancer types. (a) MYC was co-expressed with the indicated genes across a panel of 81 Glioblastoma, 19 Anaplastic Astrocytoma, 50 Oligodendroglioma, and 7 Diffuse Astrocytoma and 23 normal brain tissues. (b) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3000 genes in brain cancer. (c) MYC was co-expressed with the indicated genes across a panel of 26 tongue squamous cell carcinoma and 12 normal tongue tissues. (d) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3,000 genes in head and neck cancers. (e) MYC was co-expressed with the indicated genes across a panel of 127 Burkitt's Lymphoma and 58 normal lymphoid tissues. (f) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3,000 genes in lymphoma. (g) MYC was co-expressed with the indicated genes across a panel of 43 ovarian serous adenocarcinoma and 10 normal ovarian tissues. (h) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3,000 genes in ovarian cancer. The co-expression profiles of MYC were retrieved from cBioPortal web. Bar length represents the significance and negative logarithm of enrichment p-value.

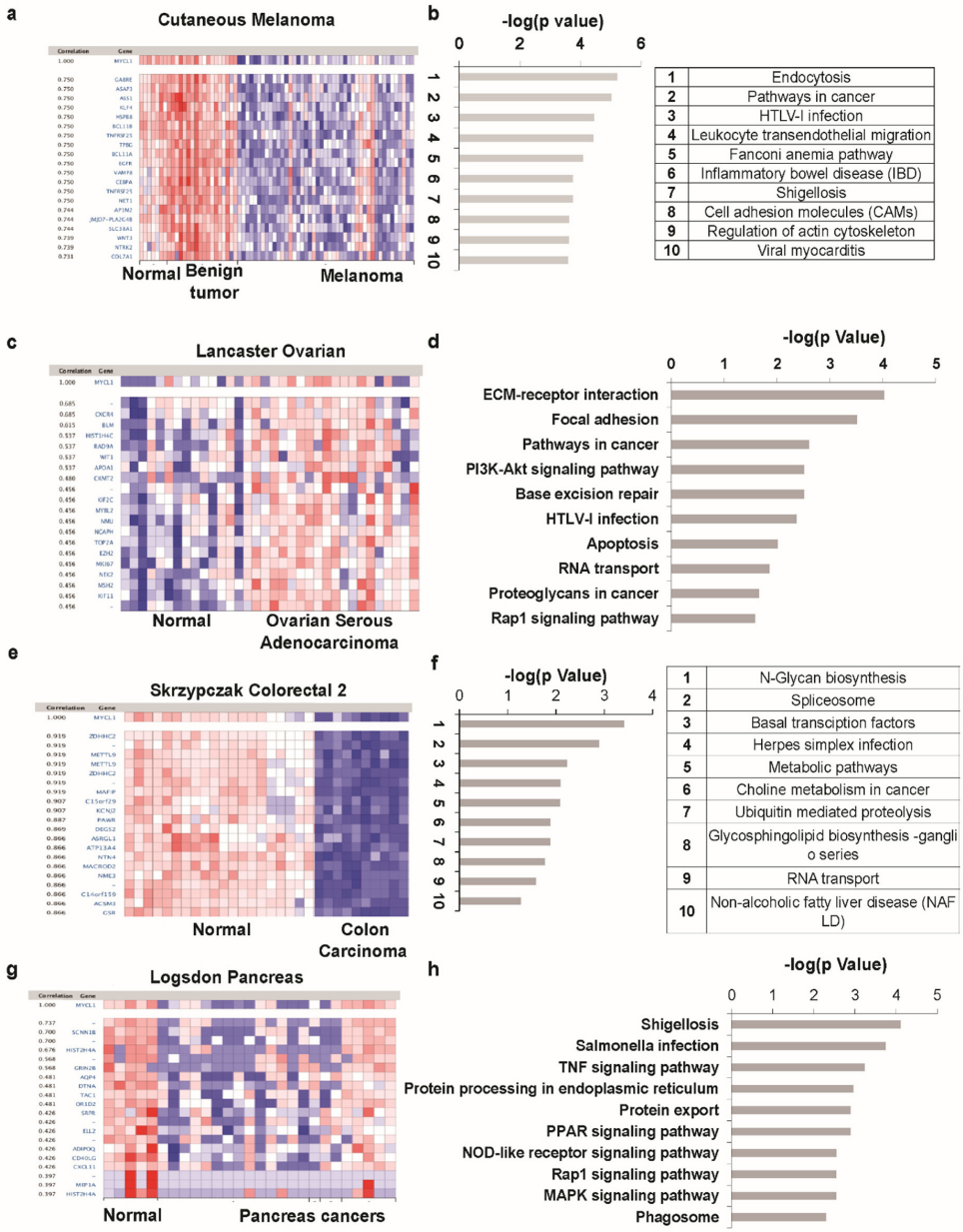

Fig. S2. Distribution of co-expression profiles and top gene ontology (GO) processes for MYCL in various cancer types. (a) MYCL was co-expressed with the indicated genes across a panel of 45 melanoma and normal skin tissues. (b) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3,000 genes in melanoma. (c) MYCL was co-expressed with the indicated genes across a panel of 31 ovarian serous adenocarcinoma and 3 normal ovarian tissues. (d) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3,000 genes in ovarian cancer. (e) MYCL was co-expressed with the indicated genes across a panel of 10 colon carcinoma and 20 normal colorectal tissues. (f) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3,000 genes in colon carcinoma. (g) MYCL was co-expressed with the indicated genes across a panel of 45 pancreatic cancers and 7 normal pancreas tissues. (h) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3,000 genes in pancreas cancers. The co-expression profiles of MYCL were retrieved from cBioPortal web. Bar length represents the significance and negative logarithm of enrichment p-value.

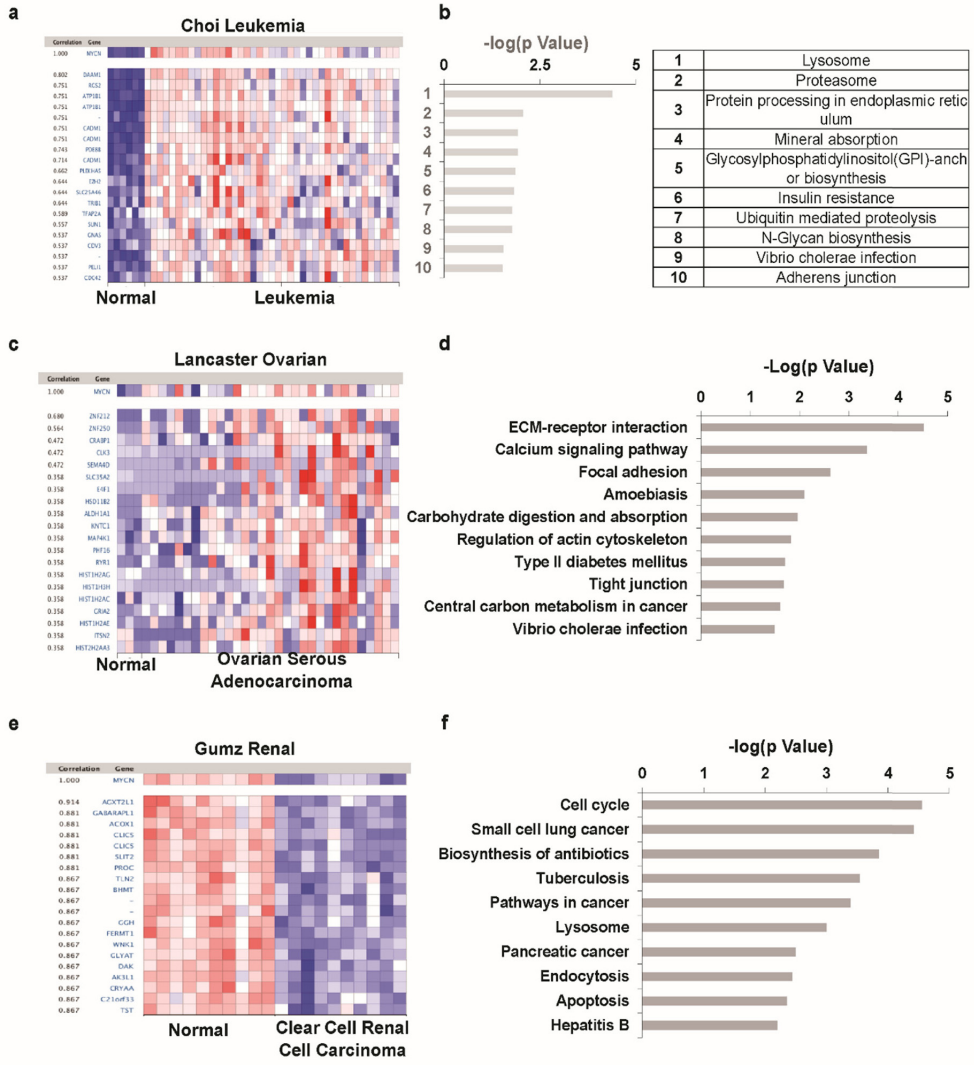

Fig. S3. Distribution of co-expression profiles and top gene ontology (GO) processes for MYCN in various cancer types. (a) MYCN was co-expressed with the indicated genes across a panel of 41 leukemia and 6 normal white blood cells. (b) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3,000 genes in blood cancer. (c) MYCN was co-expressed with the indicated genes across a panel of 31 ovarian serous adenocarcinoma and 3 normal ovarian tissues. (d) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3,000 genes in ovarian cancer. (e) MYCN was co-expressed with the indicated genes across a panel of 10 Clear cell renal cell carcinoma and 10 normal renal tissues. (f) Top significant GO processes were visualized by DAVID functional annotation web according to the co-expression profiles of 3,000 genes in kidney cancer. The co-expression profiles of C-MYC were retrieved from cBioPortal web. Bar length represents the significance and negative logarithm of enrichment p-value.

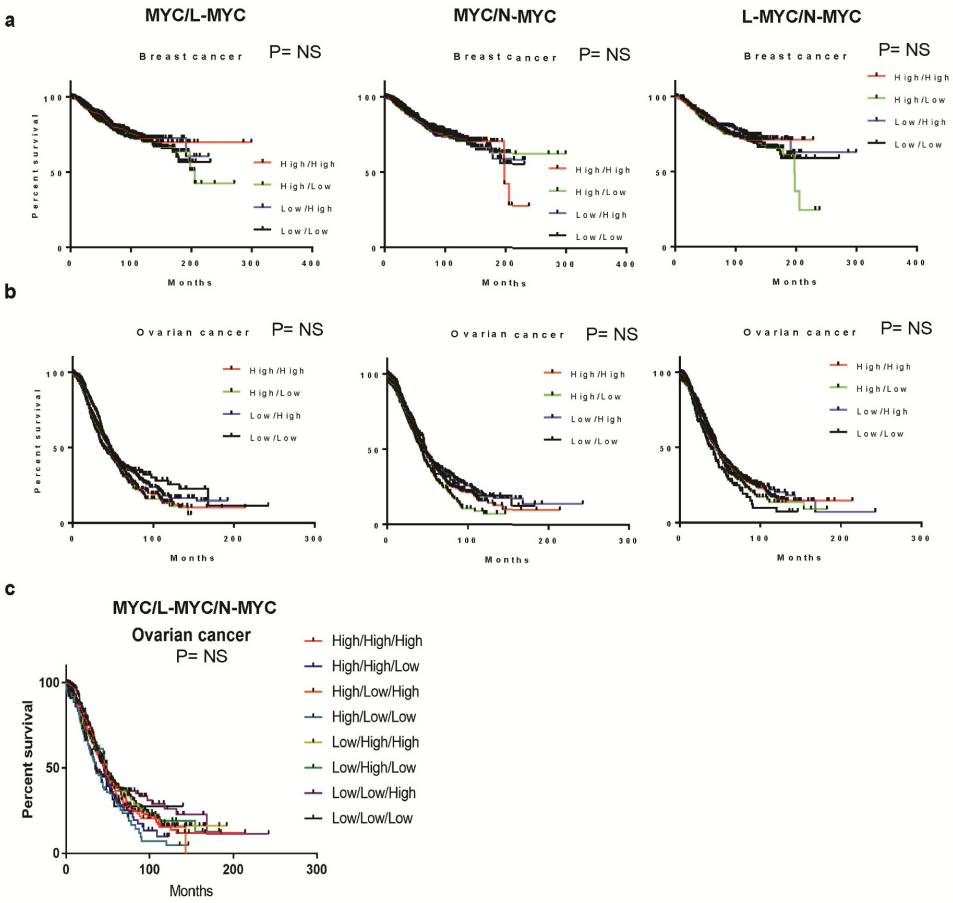

Fig. S4. The relationship between MYC family genes co-occurrence and Clinical outcomes in various types of cancer. Multivariate survival analysis of MYC/MYCL, MYC/MYCN, and MYCL/MYCN was performed using data from Kaplan-Meier Plotter in breast (a) and ovarian (b) cancers. Multivariate survival analysis of MYC/MYCL/MYCN was performed using data from Kaplan-Meier Plotter in ovarian cancer (c). All the survival curves were drown using Graph pad prism 7 software. The p-value=NS: non-significance.