

Supporting Information

Dual targeting of AMRC12 and *Malassezia globosa* disrupts MYC liquid condensates-driven nuclear pore complex biogenesis in neuroblastoma

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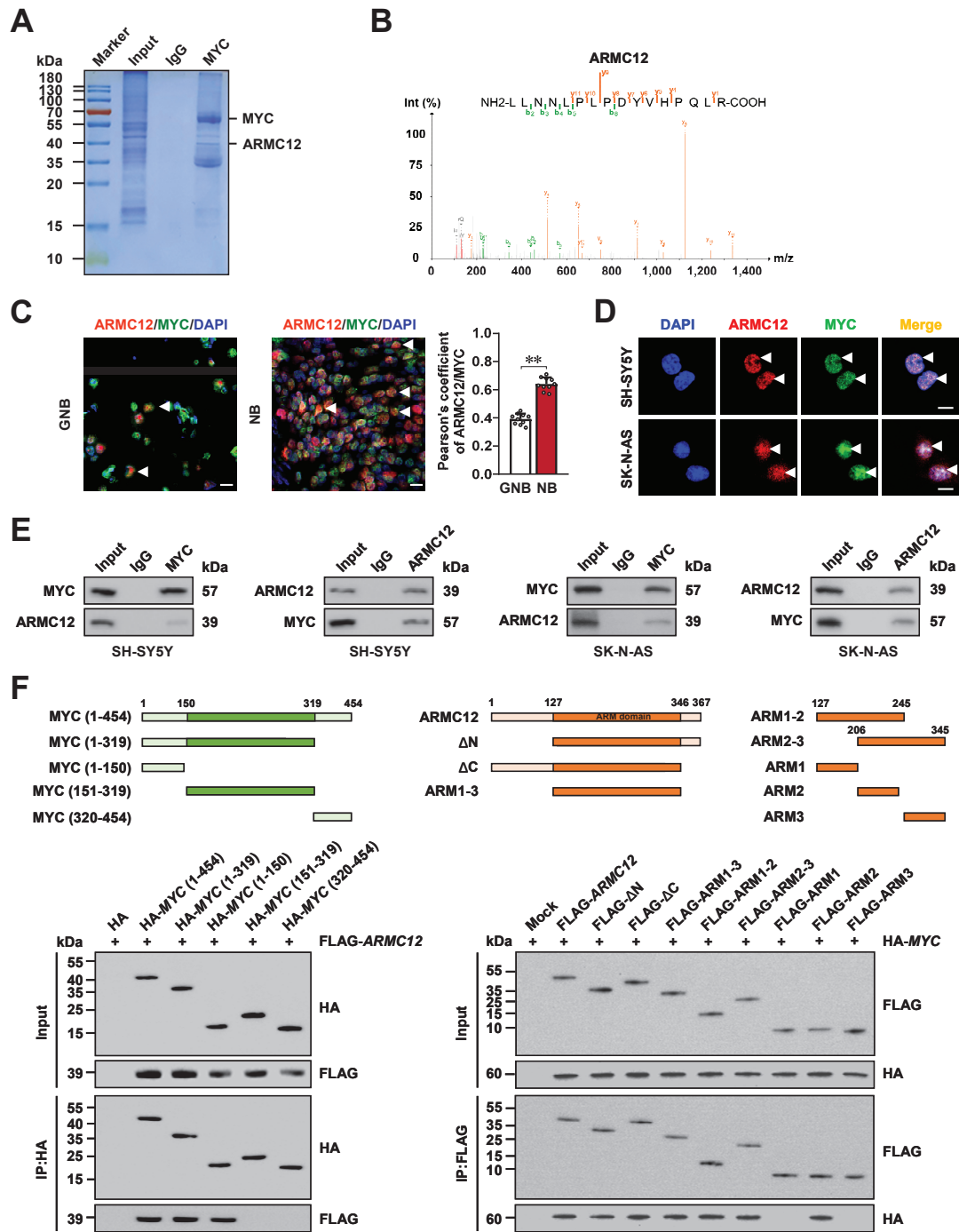


Figure S1. ARMC12 interacts with MYC in NB. (A) Coomassie blue staining showing the proteins pulled down by MYC-specific antibody from SH-SY5Y cell lysates. (B) Mass spectrometry assay of ARMC12 peptide pulled down by MYC-specific antibody from SH-SY5Y cell lysates. (C) Representative images (left panel) and quantification (right panel) of immunofluorescence assay revealing the co-localization of ARMC12 and MYC (arrowheads) in ganglioneuroblastoma (GNB) or NB specimens ($n = 5$), with nuclei staining with DAPI. Scale bars: 50 μ m. (D) Representative images of immunofluorescence assay showing co-localization of ARMC12 and MYC (arrowheads) in SH-SY5Y and SK-N-AS cells, with nuclei staining with DAPI. Scale bars: 10 μ m. (E) Co-IP and western blot assays indicating endogenous interaction between ARMC12 and MYC in SH-SY5Y and SK-N-AS cells. (F) Co-IP and western blot assays indicating the protein levels of ARMC12 and MYC in SK-N-BE(2) cells transfected with FLAG-tagged *ARMC12* and HA-tagged *MYC* truncation constructs. Student's t test compared the difference in C. ** $P < 0.01$. Data are shown as mean $\pm$ s.e.m. (error bars) or representative of three independent experiments in A and C-F.

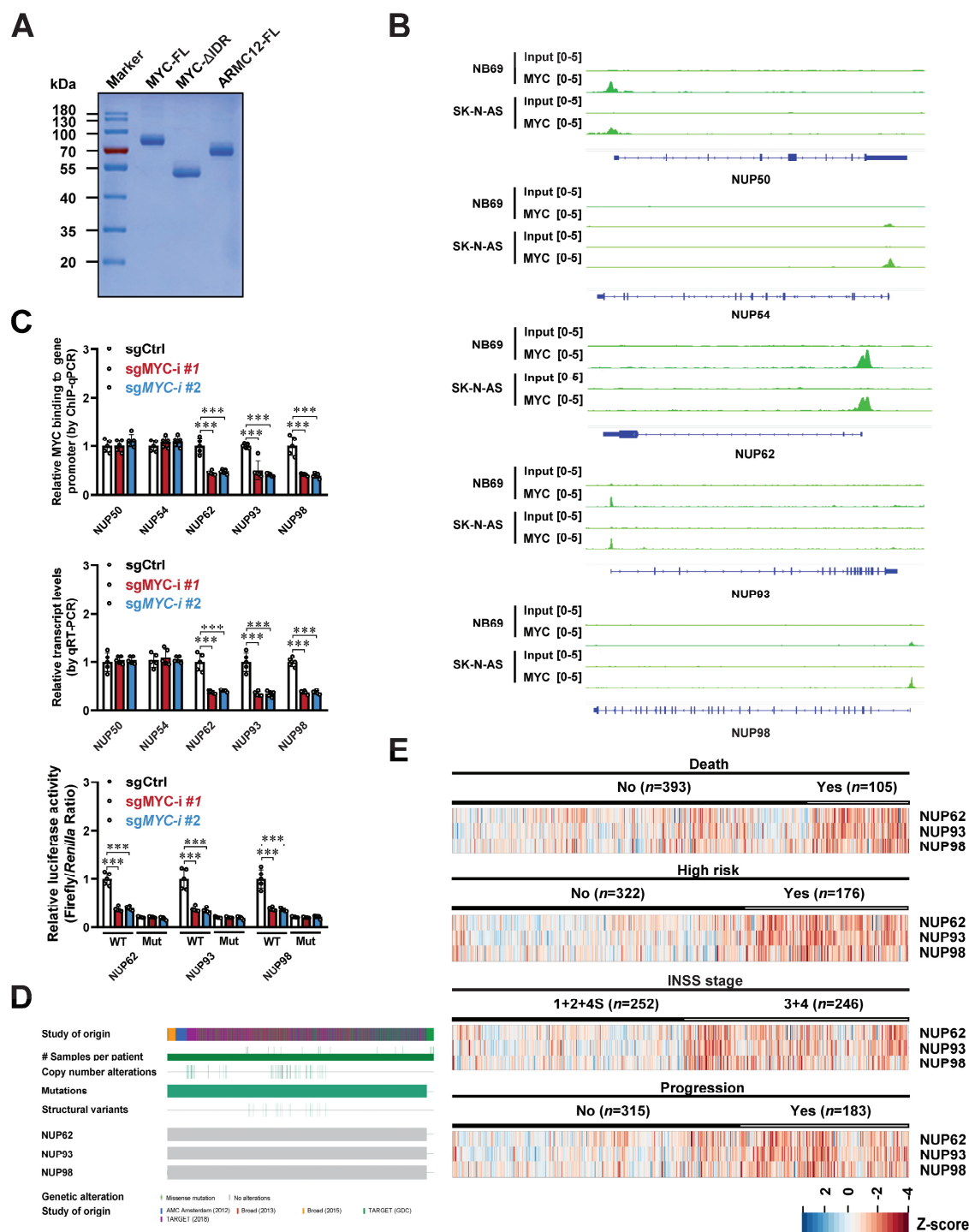


Figure S2. MYC facilitates expression of NPC components in NB. (A) Coomassie blue staining showing the purity of recombinant full-length (FL) or IDR-deficient (Δ IDR) MYC-EGFP and ARMC12-mCherry. (B) Mining of a public ChIP-seq dataset (GSE138295) revealing endogenous enrichment of MYC on promoter regions of *NUP50*, *NUP54*, *NUP62*, *NUP93*, and *NUP98* in NB cells. (C) ChIP-qPCR (normalized to input, $n = 5$), real-time qRT-PCR (normalized to β -actin, $n = 5$), and dual-luciferase ($n = 5$) assays indicating the MYC enrichment, transcript levels, and activity of promoter luciferase reporter containing wild-type (WT) or mutant (Mut) MYC binding sites of *NUP62*, *NUP93*, or *NUP98* in SH-SY5Y stably transfected with control sgRNA (sgCtrl), sgMYC-i #1, or sgMYC-i #2. (D) Mining of cBioportal database (<https://www.cbioportal.org/>) showing no missense mutation, nonsense mutation, insertion, or deletion of *NUP62*, *NUP93*, and *NUP98* gene in 2001 NB cases. (E) Heatmap indicating the expression of *NUP62*, *NUP93*, and *NUP98* gene in 498 NB cases (GSE62564) with different status of death, high risk, INSS stage, or progression. One-way ANOVA compared the difference in C. *** $P < 0.001$. Data are shown as mean $\pm$ s.e.m. (error bars) or representative of three independent experiments in C.

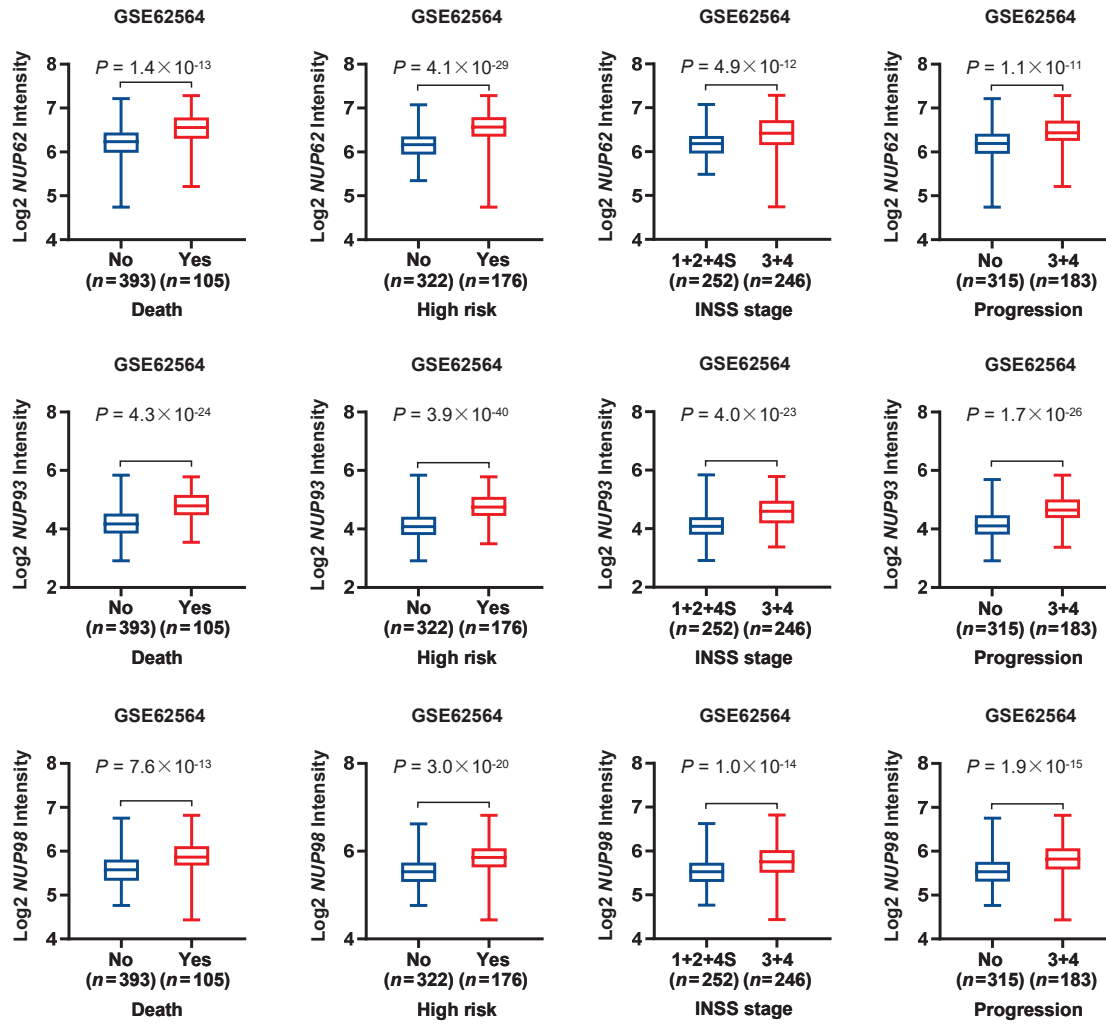


Figure S3. Expression profiles of NPC components in NB. Box plot indicating the expression levels of *NUP62*, *NUP93*, and *NUP98* in 498 NB cases (GSE62564) with different status of death, high risk, INSS stage, or progression. Mann-Whitney U test (for non-normal distributions) compared the difference.

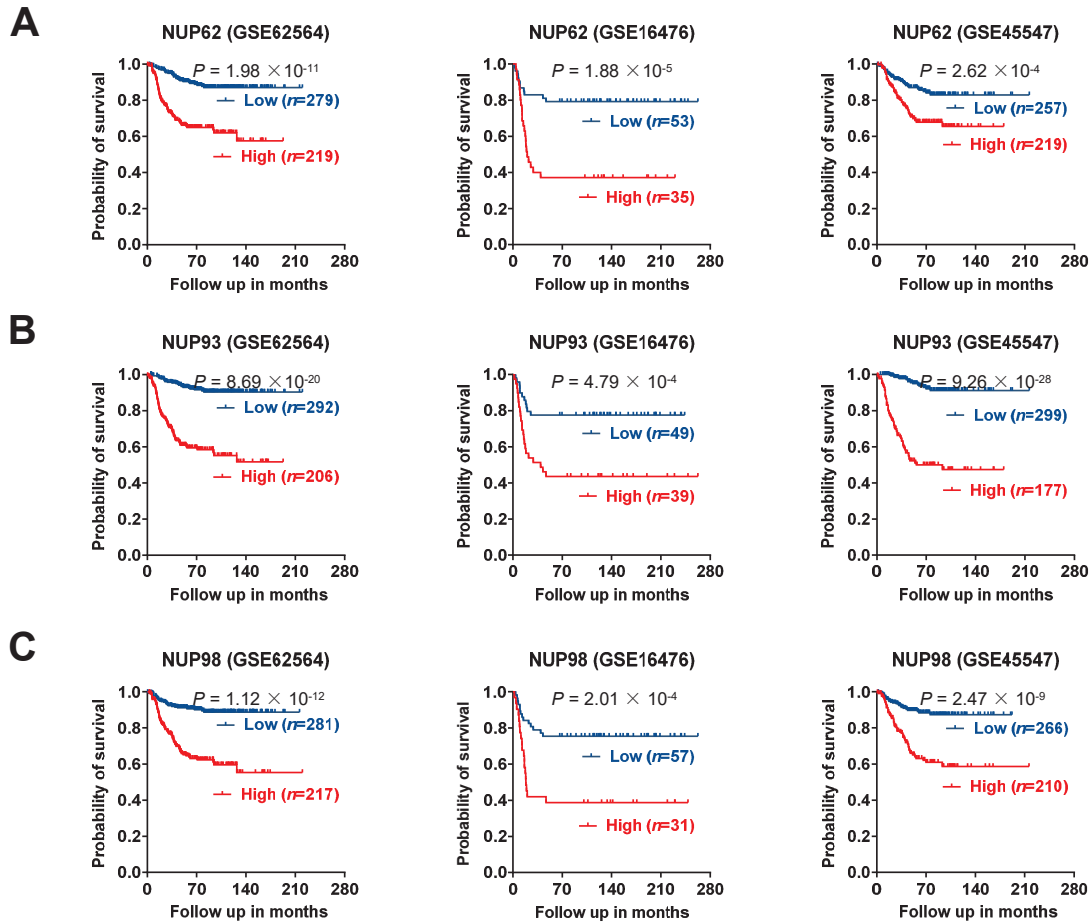


Figure S4. Prognostic values of NPC components in NB. Kaplan-Meier curve showing overall survival of 498 (GSE62564), 88 (GSE16476), and 649 (GSE45547) NB patients with high or low expression of *NUP62* (A, cutoff values = 6.34, 8.19 and 14.38), *NUP93* (B, cutoff values = 4.44, 6.61 and 10.89), or *NUP98* (C, cutoff values = 5.69, 6.78 and 10.98). Log-rank test for survival comparison.

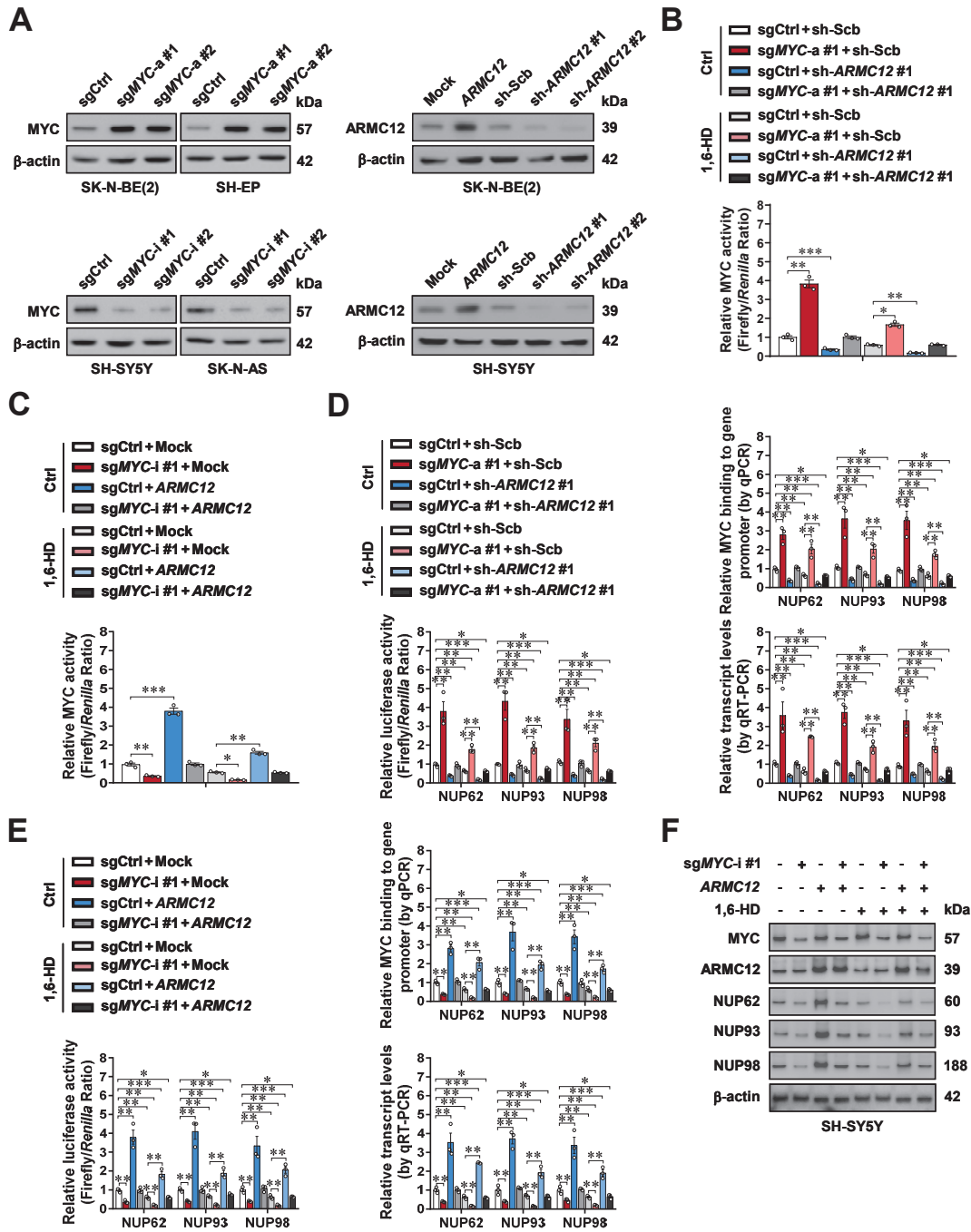


Figure S5. ARMC12 facilitates MYC-mediated gene expression and NPC biogenesis in NB cells. (A) Western blot assay showing the levels of MYC or ARMC12 in NB cells stably transfected with control sgRNA (sgCtrl), sgMYC-a #1, sgMYC-a #2, sgMYC-i #1, sgMYC-i #2, empty vector (mock), *ARMC12*, scramble shRNA (sh-Scb), sh-*ARMC12* #1, or sh-*ARMC12* #2. (B and C) Dual-luciferase assay indicating the MYC activity in SH-N-BE(2) cells stably transfected with sgCtrl, sgMYC-a #1, sgMYC-i #1, sh-Scb, sh-*ARMC12* #1, mock, or *ARMC12*, and those treated with vehicle or 10% 1,6-HD ($n = 3$). (D-F) ChIP-qPCR (D, E, normalized to input, $n = 3$), dual-luciferase (D, E, $n = 3$), and real-time qRT-PCR (D, E, normalized to β -actin, $n = 3$), and western blot (F) assays indicating the MYC enrichment, promoter activity, transcript levels, and protein expression of *NUP62*, *NUP93*, or *NUP98* in SH-N-BE(2) cells stably transfected with sgCtrl, sgMYC-a #1, sgMYC-i #1, sh-Scb, sh-*ARMC12* #1, mock, or *ARMC12*, and those treated with vehicle or 10% 1,6-HD. One-way ANOVA compared the difference in B-E. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. Data are shown as mean $\pm$ s.e.m. (error bars) or representative of three independent experiments in A-F.

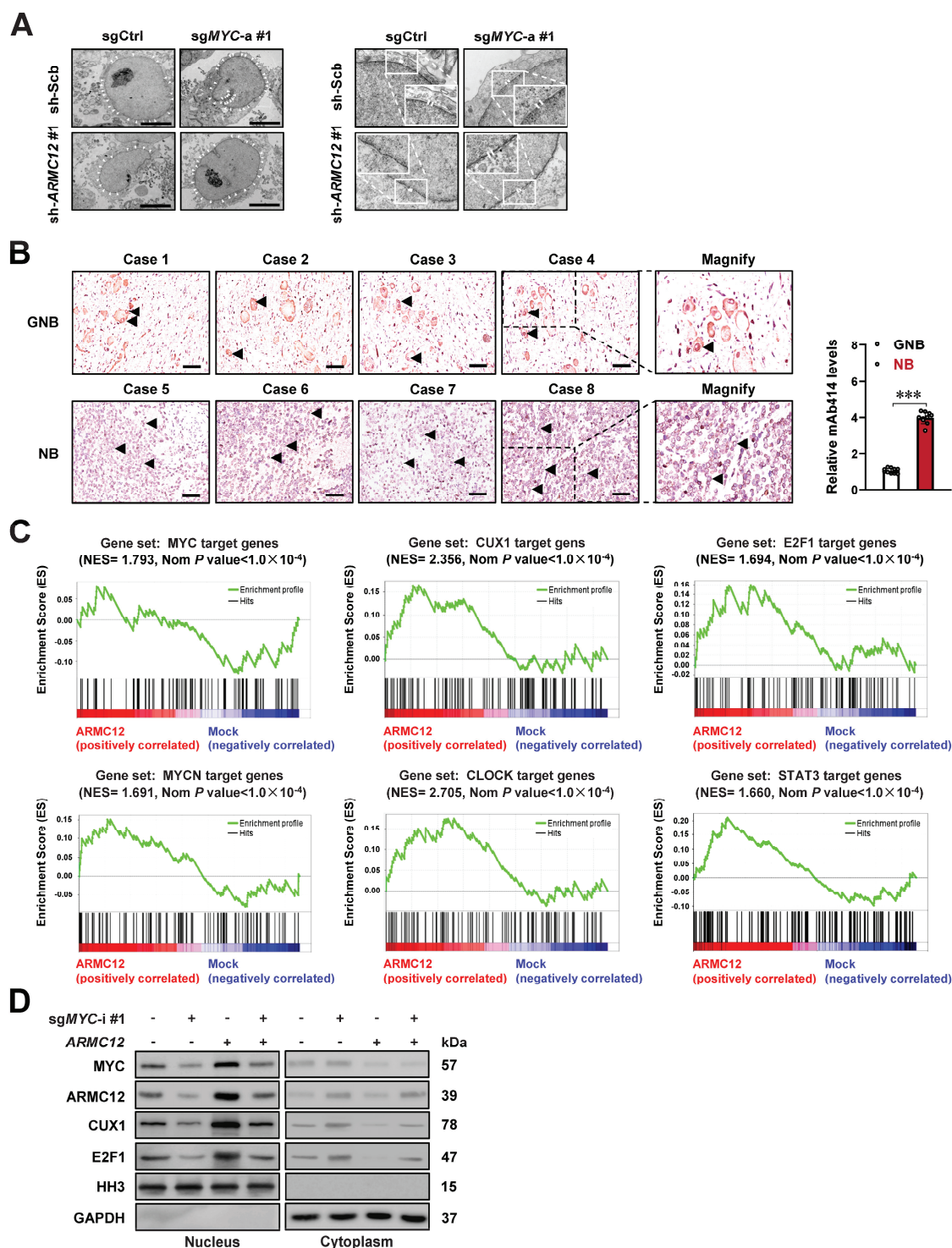


Figure S6. ARMC12 cooperates with MYC to facilitate nuclear transport of transcriptional regulators in NB cells. (A) Transmission electron microscopy indicating the NPC numbers and nuclear envelope (NE) spacing (arrowheads) in SH-N-BE(2) cells stably transfected with control sgRNA (sgCtrl), sgMYC-a #1, scramble shRNA (sh-Scb), or sh-ARMC12 #1, and those treated with vehicle or 10% 1,6-HD. (B) Representative images (left panel) and quantification (right panel) of immunohistochemistry using mAb414 indicating the expression of NPC at nuclear envelope (arrowheads) in GNB and NB tissues ($n = 10$). Scale bars: 100 μ m. (C) GSEA of transcriptional regulators for altered genes in SK-N-BE(2) cells stably transfected with empty vector (mock) or ARMC12. (D) Western blot assay showing the nuclear or cytoplasmic distribution of MYC, ARMC12, CUX1, or E2F1 in SH-SY5Y cells stably transfected with control sgRNA (sgCtrl), sgMYC-i #1, mock, or ARMC12. Student's t -test compared the difference in B. *** $P < 0.001$. Data are shown as mean $\pm$ s.e.m. (error bars) or representative of three independent experiments in A, B and D.

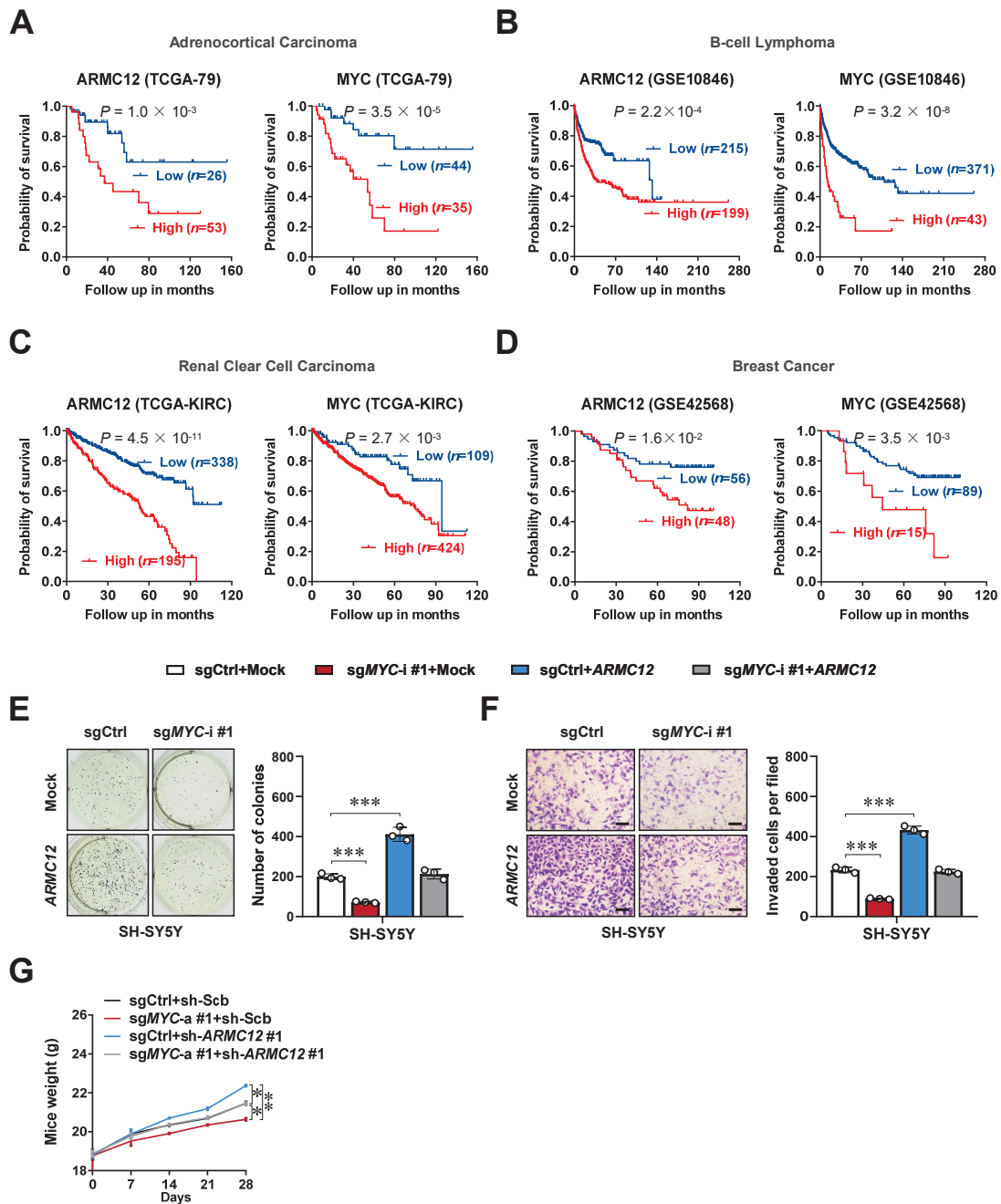
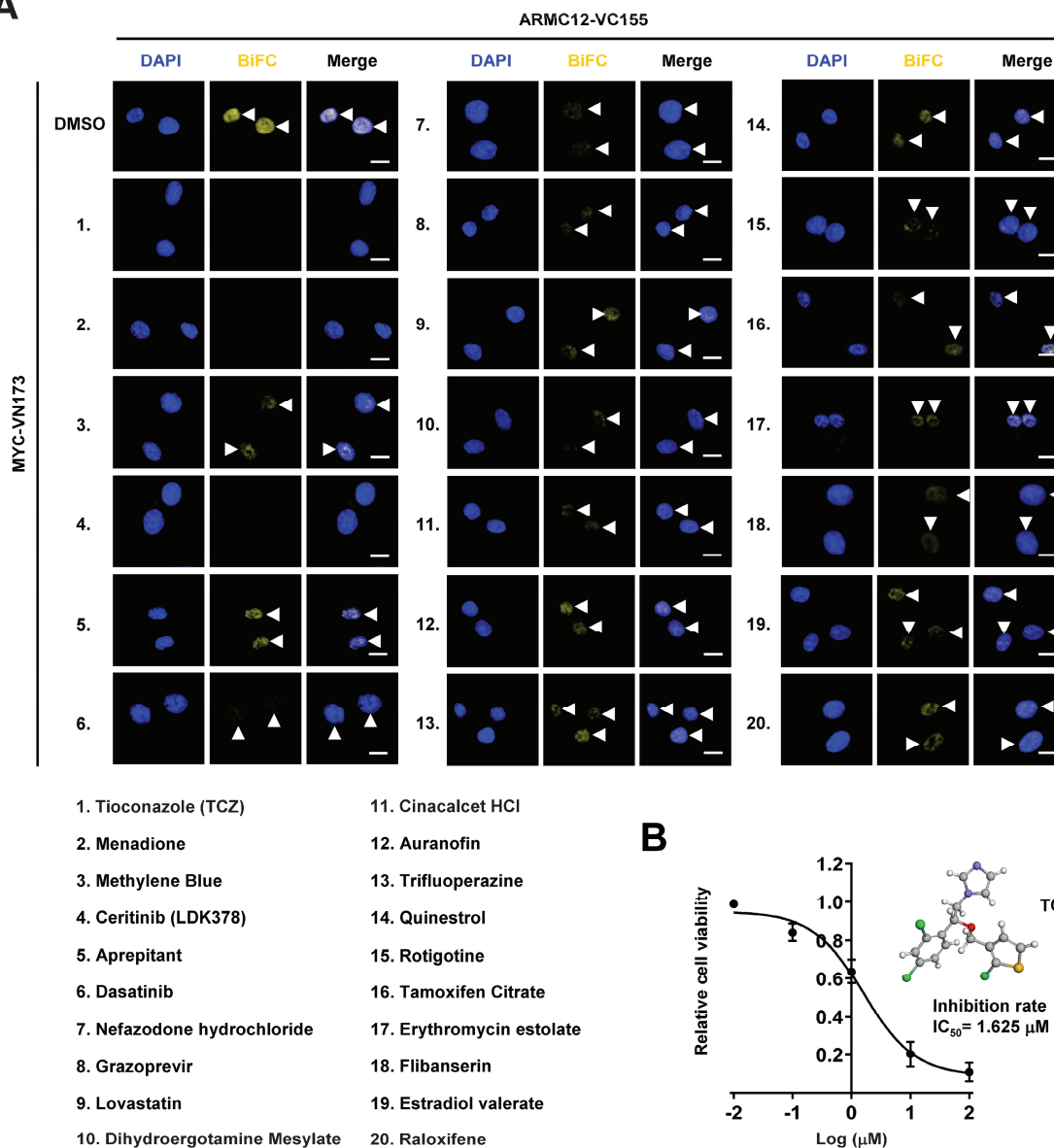


Figure S7. ARMC12 cooperates with MYC to exert oncogenic functions. (A-D) Kaplan-Meier curve showing overall survival of patients suffering from adrenocortical carcinoma (A, cutoff values = 4.08 and 8.84), B-cell lymphoma (B, cutoff values = 4.45 and 10.31), renal clear cell carcinoma (C, cutoff values = 2.44 and 10.22), or breast cancer (D, cutoff values = 3.83 and 8.96) with high or low expression levels of *ARMC12* or *MYC*. (E and F) Representative images (left panel) and quantification (right panel) of soft agar (E) and Matrigel invasion (F) assays showing the growth and invasion of SH-SY5Y cells stably transfected with control sgRNA (sgCtrl), sgMYC-i #1, empty vector (mock), or *ARMC12* ($n = 3$). Scale bars: 50 μ m. (G) Body weight of nude mice receiving vein tail injection of SK-N-BE(2) cells stably transfected with sgCtrl, sgMYC-a #1, sh-Scb, or sh-*ARMC12* #1 ($n = 5$ per group). Log-rank test for survival comparison in A-D. One-way ANOVA compared the difference in E-G. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. Data are shown as mean $\pm$ s.e.m. (error bars) or representative of three independent experiments in E-G.

A



B

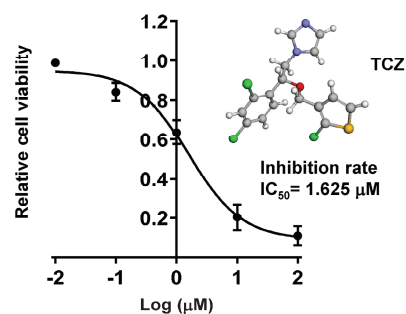


Figure S8. Screening of inhibitors targeting ARMC12-MYC interaction. (A) Representative images of BiFC assay showing the impact of indicated chemical agents on interaction between ARMC12 and MYC (arrowheads) in SH-SY5Y cells. (B) MTT colorimetric assay indicating the viability of SH-SY5Y cells treated with different doses of TCZ as indicated. Data are shown as mean $\pm$ s.e.m. (error bars) or representative of three independent experiments in A and B.

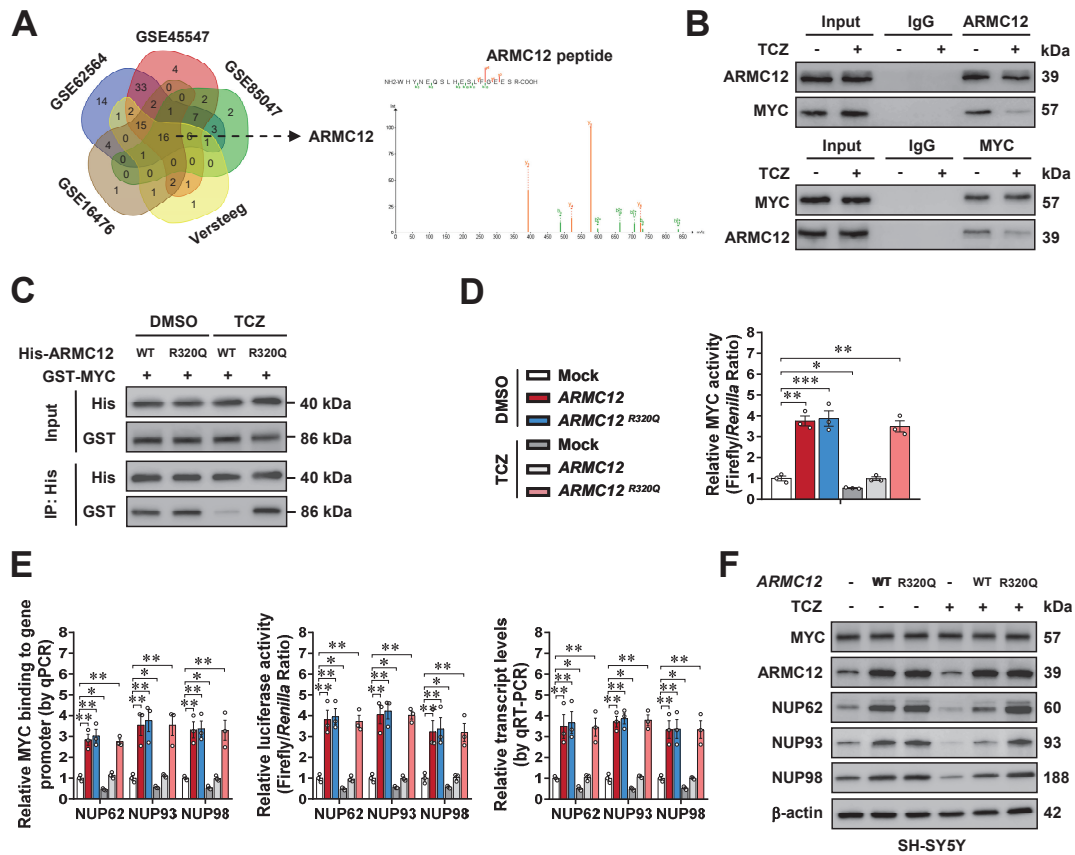


Figure S9. TCZ binds with ARMC12 to disrupt its interaction with MYC. (A) Venn diagram (left panel) and peptide in mass spectrometry (right panel) showing the identification of proteins within SH-SY5Y cell lysates binding to NHS magnetic beads covalently conjugated with TCZ (20 μ M), and those consistently associated with survival of 498 (GSE62564), 649 (GSE45547), 283 (GSE85047), 122 (Versteeg), and 88 (GSE16476) NB patients. (B) Co-IP and western blot assays revealing the interaction between ARMC12 and MYC in SK-N-AS cells treated with DMSO or TCZ (20 μ M). (C) Co-IP and western blot assay indicating the binding of wild-type or R320Q mutant His-tagged ARMC12 to GST-tagged MYC protein incubated with DMSO or TCZ (20 μ M). (D) Dual-luciferase assay indicating the MYC activity in SH-SY5Y cells stably transfected with empty vector (mock), *ARMC12*, or *ARMC12* mutant (R320Q), and those treated with DMSO or TCZ (20 μ M, $n = 3$). (E and F) ChIP-qPCR (E, normalized to input, $n = 3$), dual-luciferase (E, $n = 3$), and real-time qRT-PCR (E, normalized to β -actin, $n = 3$), and western blot (F) assays indicating the MYC enrichment, promoter activity, transcript levels, and protein expression of NUP62, NUP93, or NUP98 in SH-SY5Y cells stably transfected with mock, *ARMC12*, or *ARMC12* mutant (R320Q), and those treated with DMSO or TCZ (20 μ M). One-way ANOVA compared the difference in D and E. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. Data are shown as mean $\pm$ s.e.m. (error bars) or representative of three independent experiments in B-F.

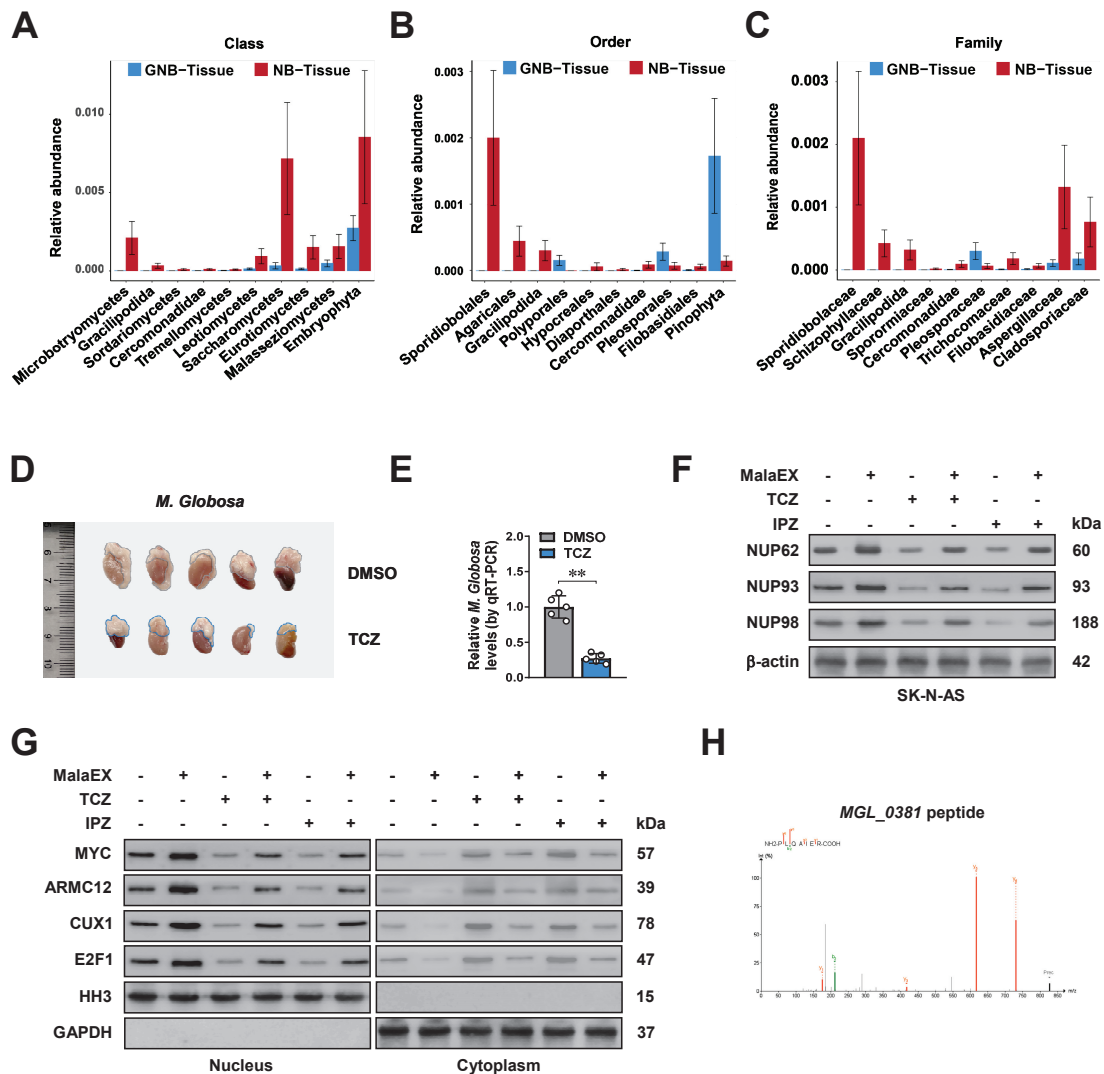


Figure S10. *M. globosa* extracellular vesicles facilitates NPC biogenesis and tumorigenesis. (A-C) Mycobiome analysis using 18S rRNA sequencing indicating the class (A), and order (B), or family (C) of fungi within GNB and NB tissues. (D) Representative images of xenograft tumors of SH-SY5Y cells under renal capsule of NSG mice receiving oral gavage of Amphotericin B, *M. globosa*, and intraperitoneal injection of TCZ (60 mg/kg/day). (E) Real-time qRT-PCR assay indicating the levels (normalized to β -actin, $n = 5$) of *M. globosa* 18S rRNA within xenograft tumors of SH-SY5Y cells under renal capsule of NSG mice receiving oral gavage of Amphotericin B, *M. globosa*, and intraperitoneal injection of TCZ (60 mg/kg/day). (F) Western blot assay showing the expression of NUP62, NUP93, and NUP98 in SK-N-AS cells treated with MalaEX, TCZ (20 μ M), or UU-T02 (1.0 μ M). (G) Western blot assay showing the nuclear or cytoplasmic distribution of MYC, ARMC12, CUX1, or E2F1 in SK-N-AS cells treated with MalaEX, TCZ (20 μ M), or UU-T02 (1.0 μ M). (H) Peptide of MGL_0381 in mass spectrometry assay of protein content within MalaEX. Student's *t*-test compared the difference in E. ** $P < 0.01$. Data are shown as mean $\pm$ s.e.m. (error bars) or representative of three independent experiments in E-G.

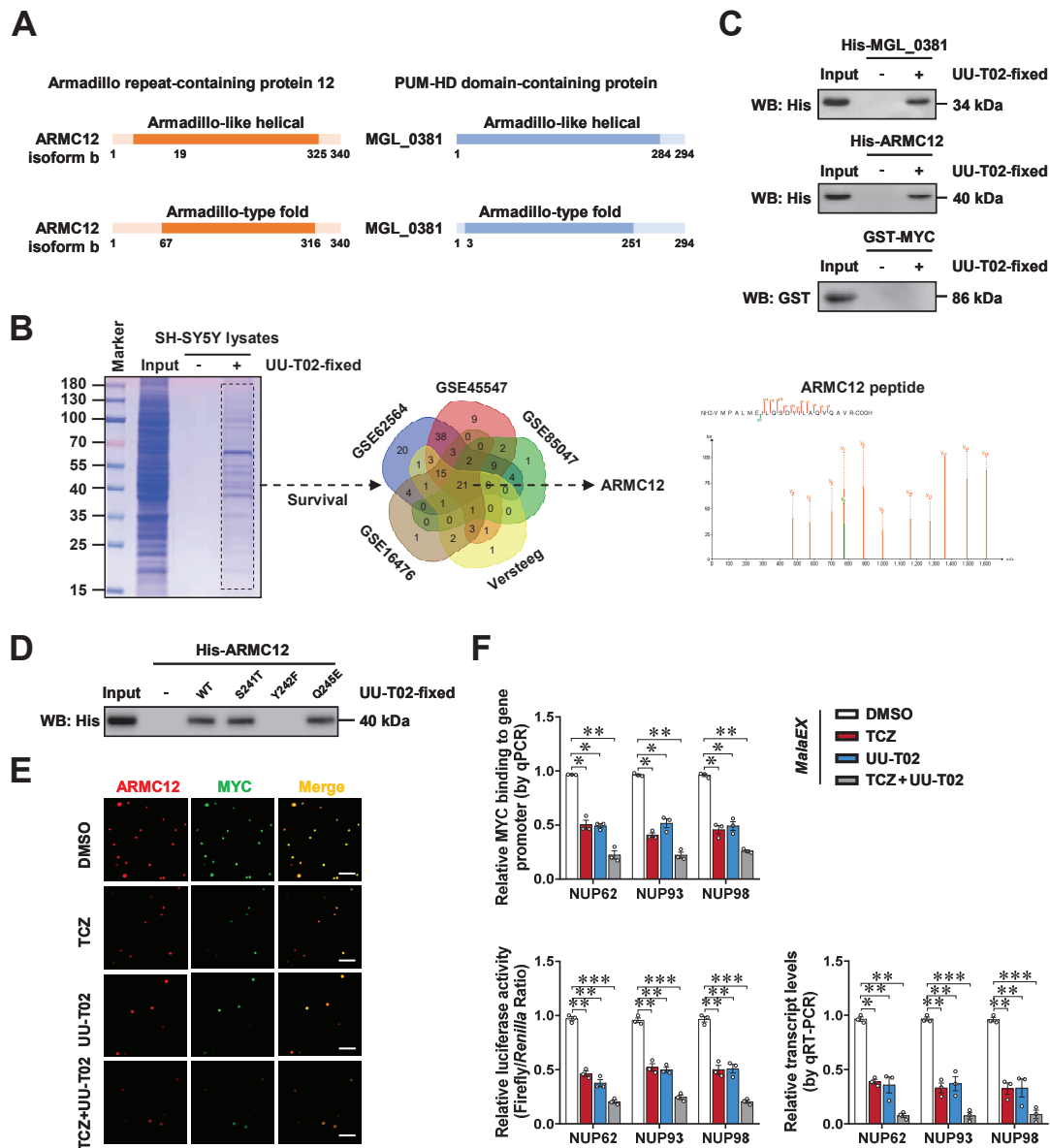


Figure S11. TCZ and UU-T02 suppress liquid condensates and activity of MYC in NB cells. **A**, Schematic illustration showing the domains of ARMC12 and MGL_0381 proteins. **B**, Coomassie blue staining (left panel) and Venn diagram (middle panel), and peptide in mass spectrometry (right panel) revealing the binding of proteins within SH-SY5Y cell lysates to NHS magnetic beads covalently conjugated with UU-T02 (1.0 μ M), and those consistently associated with survival of 498 (GSE62564), 649 (GSE45547), 283 (GSE85047), 122 (Versteeg), and 88 (GSE16476) NB patients. **C**, Western blot assay indicating the affinity of recombinant His-tagged MGL_0381, His-tagged ARMC12, or GST-tagged MYC to NHS beads covalently conjugated with UU-T02 (1.0 μ M). **D**, Western blot assay indicating the affinity of recombinant wild-type or mutant (S241T, Y242F, Q245E) ARMC12 protein to NHS beads covalently conjugated with UU-T02 (1.0 μ M). **E**, Representative images indicating the liquid droplet formation of ARMC12-mCherry and MYC-EGFP *in vitro*, and those incubated with DMSO, TCZ (20 μ M), or UU-T02 (1.0 μ M). Scale bars: 10 μ m. **F**, ChIP-qPCR (normalized to input, $n = 3$), dual-luciferase ($n = 3$), and real-time qRT-PCR (normalized to β -actin, $n = 3$) assays indicating the MYC enrichment, promoter activity, and transcript levels of *NUP62*, *NUP93*, or *NUP98* in SK-N-AS cells treated with MalaEx, TCZ (20 μ M), or UU-T02 (1.0 μ M). One-way ANOVA compared the difference in **F**. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. Data are shown as mean $\pm$ s.e.m. (error bars) or representative of three independent experiments in **B-F**.

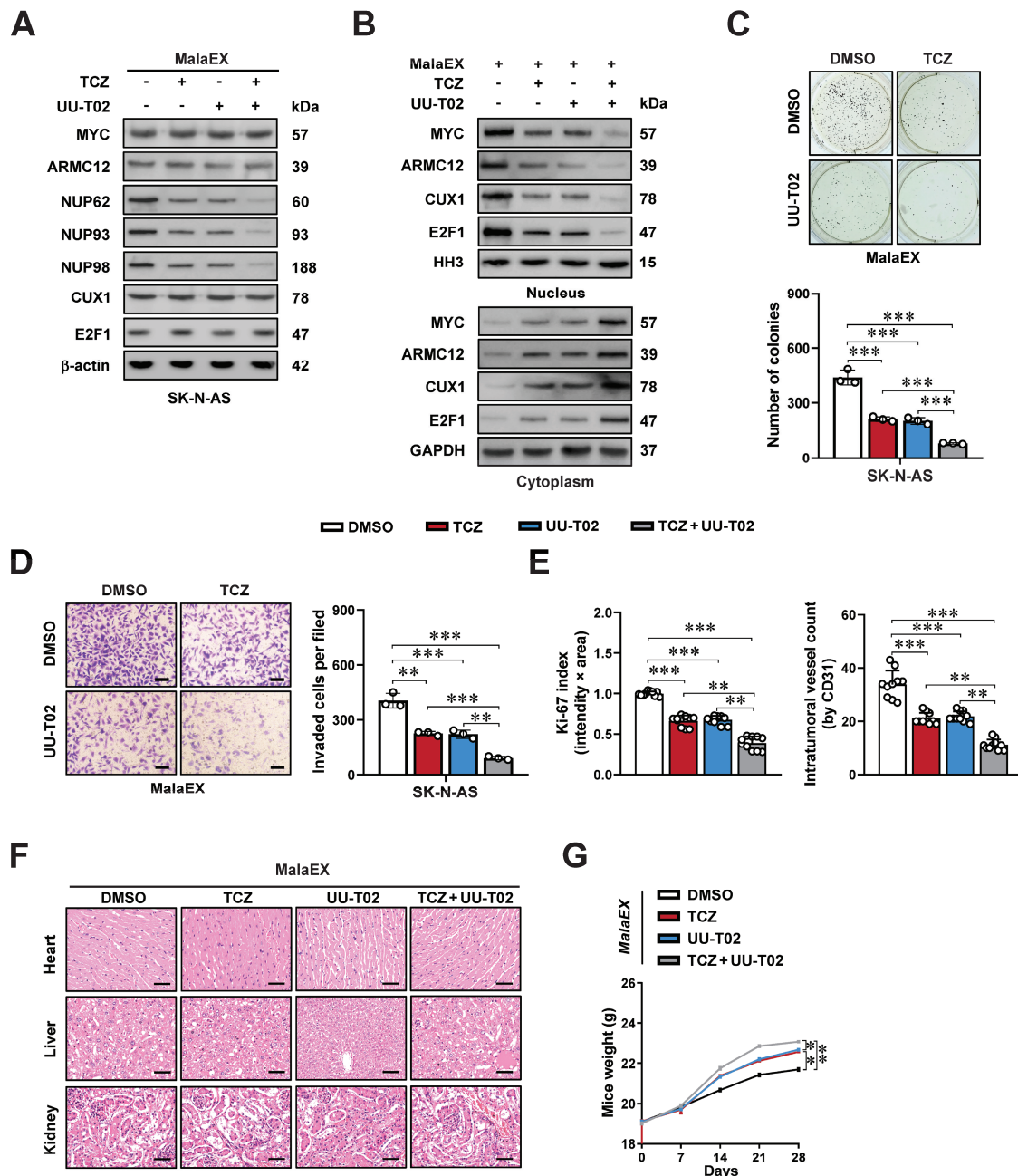


Figure S12. Synergetic targeting MGL_0381 and AMRC12-facilitated MYC transactivation inhibits NPC biogenesis, growth, and invasion of NB cells. **A** and **B**, Western blot assay indicating the protein expression of MYC, ARMC12, NUP62, NUP93, NUP98, CUX1, or E2F1 and nuclear or cytoplasmic distribution of MYC, ARMC12, CUX1, or E2F1 in SK-N-AS cells treated with MalaEx, TCZ (20 μ M), or UU-T02 (1.0 μ M). **C** and **D**, Representative images and quantification of soft agar (**C**) and Matrigel invasion (**D**) assays showing the growth and invasion of SK-N-AS cells treated with MalaEx, TCZ (20 μ M), or UU-T02 (1.0 μ M, $n = 3$). Scale bars: 50 μ m. **E**, Quantification of Ki-67 or CD31 immunostaining within subcutaneous xenograft tumors formed by SH-SY5Y cells in nude mice that received administration of MalaEx, TCZ (60 mg/kg/day), or UU-T02 (60 mg/kg/day, $n = 5$ per group). **F**, HE staining showing the morphological changes of heart, liver, and kidney tissues of nude mice with SH-SY5Y-formed subcutaneous xenograft tumors and administration of MalaEx, TCZ (60 mg/kg/day), or UU-T02 (60 mg/kg/day). **G**, Body weight of nude mice treated with tail vein injection of SH-SY5Y cells in nude mice that received administration of MalaEx, TCZ (60 mg/kg/day), or UU-T02 (60 mg/kg/day, $n = 5$ per group). One-way ANOVA compared the difference in **C-E** and **G**. * $P < 0.01$, ** $P < 0.01$, *** $P < 0.001$. Data are shown as mean $\pm$ s.e.m. (error bars) or representative of three independent experiments in **A-G**.

Table S1 Primer sets used for RT-PCR, ChIP and probe

Primer set	Primers Sequence	Product size (bp)	Application
ALADIN	Forward 5'-ACTGCCTTCATCCATCACCG-3' Reverse 5'-GCCGTCTTCACCCACTCAAA-3'	131	RT-PCR
DDX19	Forward 5'-GCTTTTCTCCGCCACCTTTG-3' Reverse 5'-TCCACCATCATCTCCCACT-3'	297	RT-PCR
ELYS	Forward 5'-CCTATTAGACGGCGTTACTG-3' Reverse 5'-CTATCAACCAAACCCCTGA-3'	170	RT-PCR
GLE1	Forward 5'-CCCTACGCAGTTCGACAAAA-3' Reverse 5'-CGTGCTCTACCACCCATCCA-3'	129	RT-PCR
NDC1	Forward 5'-TGCTGCTGTCAGTGGTAATA-3' Reverse 5'-CTGACTGGCCCTGGGTAT-3'	199	RT-PCR
RAE1	Forward 5'-GACCTCAGCAGTAACCAAGC-3' Reverse 5'-ATAGACAATCAGGCCCCCTCT-3'	246	RT-PCR
SEC13	Forward 5'-GAGGACATGATTACAGACG-3' Reverse 5'-GATAAGGATCTGCCCTCCA-3'	114	RT-PCR
SEH1	Forward 5'-CAGTGGTCTTTCAGCATGA-3' Reverse 5'-ATTCTCACATCTTTGGTCGC-3'	124	RT-PCR
TPR	Forward 5'-TCCACTGGCACTTTATCTAC-3' Reverse 5'-CACCTTGTCTCAATGTTGTC-3'	268	RT-PCR
NUP37	Forward 5'-TAATGTCAGCACACTGGTG-3' Reverse 5'-TGAGGATAACTGGACCGAG-3'	100	RT-PCR
NUP42	Forward 5'-CAATGGAGGAACAGGGTAAA-3' Reverse 5'-GACTGCTGCCAAATCCAAAT-3'	196	RT-PCR
NUP43	Forward 5'-CCTGGCAGTCCTTCTATAG-3' Reverse 5'-GGCTCATTTCCTTGTGTCT-3'	251	RT-PCR
NUP50	Forward 5'-ATAACCACTGCCCTCCCTTCG-3' Reverse 5'-GGCGGCCAACTGCTGTGATAG-3'	207	RT-PCR
NUP53	Forward 5'-CGATGACTCTTGGGTGACTG-3' Reverse 5'-CACTGCTTCCATAACACTT-3'	245	RT-PCR
NUP54	Forward 5'-TTGGCACAAACACGGGAAGT-3' Reverse 5'-CAGAAAGAGCACTCGCAGTA-3'	177	RT-PCR
NUP58	Forward 5'-GCAGTACAGGCAGCAGATTG-3' Reverse 5'-GGAGTGGTCCAGTAGTAAC-3'	288	RT-PCR
NUP62	Forward 5'-GGGGAAGTGGATTTTCTTTGGG-3' Reverse 5'-GCTCGATATGGCATTAGTGAGG-3'	131	RT-PCR
NUP75	Forward 5'-TGAAAGCCGTCCGCAACAAT-3' Reverse 5'-GCAAAACGCTTCTCCCGTA-3'	238	RT-PCR
NUP88	Forward 5'-AAAACCAGAGTCCAACCGAA-3' Reverse 5'-AAACAGGGGTGGATTATGC-3'	233	RT-PCR
NUP93	Forward 5'-TACTCAAGAAAGCGAGCCAAGC-3' Reverse 5'-AGCACAAAGGTCCACCAGGTTA-3'	157	RT-PCR
NUP98	Forward 5'-CAGTTTGTGGGTAGCCAGTCAG-3' Reverse 5'-AAGATGGATAGCCAGGGAGCGT-3'	207	RT-PCR
NUP107	Forward 5'-AGCGTTATTTTCAAGGGGATT-3' Reverse 5'-CTGCCGTTGTTTAAAGGTAT-3'	163	RT-PCR
POM121	Forward 5'-TTGGAGGACAAGAGCGATGC-3' Reverse 5'-GCGGCCCTGACTGTGATAAA-3'	283	RT-PCR
NUP133	Forward 5'-AAGCTTTGGACTTGTTGGA-3' Reverse 5'-AGAACTGGACCAGTTATCT-3'	110	RT-PCR
NUP153	Forward 5'-TGAAGCGAGCCCTTACATTG-3' Reverse 5'-TCCCTCGGGTTTCTTGAAGT-3'	299	RT-PCR
NUP155	Forward 5'-CACTGCTGCCTGTGATAGAG-3' Reverse 5'-ATACCATGAGACGGTGTTC-3'	210	RT-PCR
NUP160	Forward 5'-TTATGGCCTAGCAATCCTGG-3' Reverse 5'-GACACCAGGGATGTAGCAGT-3'	103	RT-PCR
NUP188	Forward 5'-GGTCAGGGTATGTCAAGTCA-3' Reverse 5'-ACGCACCACAGAGTCAGTCA-3'	164	RT-PCR
NUP205	Forward 5'-CTTCCAAGTGCAGATAGTG-3' Reverse 5'-GTAGCTCAGCTTTTAGGACA-3'	223	RT-PCR
NUP210	Forward 5'-TGGATGGACCCGAAAAGGTT-3' Reverse 5'-AGAGTTGTCGTGGAAGTGGA-3'	269	RT-PCR
NUP214	Forward 5'-GTCATTCTTGTCTCCGTT-3' Reverse 5'-CAGATGCTGCCAGCACTAAA-3'	280	RT-PCR
NUP358	Forward 5'-TTCTACACCGTCTCTACCA-3' Reverse 5'-AGGGGATGCTGAGTTACTGC-3'	184	RT-PCR
M. globosa	Forward 5'-GCTTCTTAGAGGGACTATTGG-3' Reverse 5'-GCTGATGACTCACGCTTACT-3'	229	RT-PCR
β-actin	Forward 5'-TGCCCATCTACGAGGGGTATG-3' Reverse 5'-TCTCCTTAATGTCACGCACGATT-3'	156	RT-PCR
NUP50	Forward 5'-GGACTCGTTCCCCTGCTCTACA-3' Reverse 5'-ACCCCTCGTTGCTGACATTTG-3'	109	ChIP
NUP54	Forward 5'-AACATCGTGAAACCCGTCTCT-3'	286	ChIP

	Reverse	5'-CTCTTGACCTCGTGATACGCCC-3'		
NUP62	Forward	5'-TTCGGCCACCGTACTACTTCT-3'	133	ChIP
	Reverse	5'-CGCTTACCTCTTCTCCAACTGC-3'		
NUP93	Forward	5'-GCCACGGTGTGCCAGTTCCTA-3'	146	ChIP
	Reverse	5'-ACGGACCTCGCCTTTCCCACTT-3'		
NUP98	Forward	5'-ACTCTTTGGACAGACAGACCTT-3'	286	ChIP
	Reverse	5'-AACTATTCGACCCTTTCCTTGC-3'		
M. globosa	Forward	5'-AATGAAGTATCGCCAGCACGAG-3'	NA	Probe

ALADIN, alacrima-achalasia-adrenal insufficiency neurologic disorder protein; DDX19, DEAD-box helicase 19; ELYS, Embryonic large molecule derived from Yolk sac; GLE1, GLE1 RNA export mediator homolog; NDC1, nuclear division cycle 1 homolog; RAE1, ribonucleic acid export 1; SEC13, SEC13 homolog, nuclear pore and COPII coat complex component; SEH1, SEH1 homolog; TPR, translocated promoter region, nuclear basket protein; NUP37, nucleoporin 37; NUP42, nucleoporin 42; NUP43, nucleoporin 43; NUP50, nucleoporin 50; NUP53, nucleoporin 53; NUP54, nucleoporin 54; NUP58, nucleoporin 58; NUP62, nucleoporin 62; NUP75, nucleoporin 75; NUP88, nucleoporin 88; NUP93, nucleoporin 93; NUP98, nucleoporin 98; NUP107, nucleoporin 107; POM121, POM121 transmembrane nucleoporin; NUP133, nucleoporin 133; NUP153, nucleoporin 153; NUP155, nucleoporin 155; NUP160, nucleoporin 160; NUP188, nucleoporin 188; NUP205, nucleoporin 205; NUP210, nucleoporin 210; NUP214, nucleoporin 214; NUP358, nucleoporin 358; M. globosa, Malassezia globosa; ChIP, chromatin immunoprecipitation.

Table S2 Primer sets used for constructs

Primer set	Primers	Sequence
pLenti-ARMC12	Forward	5'-CGCGGATCCATGGGCAAGAGCATCCCCCAATAC-3'
	Reverse	5'-GCGCACC GGTTTCCGTGTTTTTAAAGTAGGAACG-3'
pET28a-ARMC12	Forward	5'-GTGGACAGCAAATGGGTCGCGGATCCATGGGCAAGAGCATCCCCCA-3'
	Reverse	5'-GGTGGTGGTGGTGGTCTCGAGTGC GGCCGCTTCCGTGTTTTTAAAGTAGG-3'
pLenti-ARMC12 R320Q	Forward	5'-CTGGCAGACCAACTACTTGCCCTGGTCATCCACCCTGAGGAA-3'
pET28a-ARMC12 R320Q	Reverse	5'-GGGCAAGTAGTTGGTCTGCCAGTCGGGACTCTTCCCCAAAGA-3'
pET28a-ARMC12 S241T	Forward	5'-CGACTGCTGACCTACCTGGCACAGAAGAATGACCTTCTCTAT-3'
	Reverse	5'-GTGCCAGGTAGGTCAGCAGTCGTACGGCTTGACACCTGTGCCA-3'
pET28a-ARMC12 Y242F	Forward	5'-CTGCTGAGCTTCCTGGCACAGAAGAATGACCTTCTCTATGAC-3'
	Reverse	5'-TCTGTGCCAGGAAGCTCAGCAGTCGTACGGCTTGACACCTGTG-3'
pET28a-ARMC12 Q245E	Forward	5'-CTACCTGGCAGAGAAGAATGACCTTCTCTATGACATTCTCAA-3'
	Reverse	5'-GTCATTCTTCTCTGCCAGGTAGCTCAGCAGTCGTACGGCTTG-3'
pBiFC-VC155-ARMC12	Forward	5'-CCGGAATTCGGATGGGCAAGAGCATCCCCCAATAC-3'
	Reverse	5'-CGGGGTACCTTCCGTGTTTTTAAAGTAGGAACG-3'
pBiFC-VN173-MYC	Forward	5'-ATGCTGGATTTTTTTCGGGTAGTG-3'
	Reverse	5'-CGCACAAAGAGTCCGTAGCTGTTC-3'
pEGFP-N1-MYC	Forward	5'-CCCAAGCTTATGCTGGATTTTTTTCGGGTAGTG-3'
	Reverse	5'-CGCGGATCCCGCACAAAGAGTCCGTAGCTGTTC-3'
pEGFP-N1-MYC ΔIDR	Forward-1	5'-CCCAAGCTTATGCTGGATTTTTTTCGGGTAGTG-3'
	Reverse-1	5'-AGGGTGTGACGAGGTCATAGTTCCTGTTGGTGAA-3'
	Forward-2	5'-CTATGACCTCGTCACACCCTTCTCCCTTCGGGGA-3'
	Reverse-2	5'-GGTCACGCAGGGCCAGCTTCTCTGAGACGAGCTT-3'
	Forward-3	5'-GAAGCTGGCCCTGCGTGACCAGATCCCGGAGTTG-3'
pET28a-EGFP-MYC	Reverse-3	5'-CGCGGATCCCGCACAAAGAGTCCGTAGCTGTTC-3'
	Forward	5'-CCGGAATTCATGCTGGATTTTTTTCGGGT-3'
	Reverse	5'-CCCAAGCTTCGCACAAGAGTCCGTAGCT-3'
	Forward-1	5'-CCGGAATTCATGCTGGATTTTTTTCGGGT-3'
	Reverse-1	5'-AGGGTGTGACGAGGTCATAGTTCCTGTTGGTGAA-3'
pET28a-EGFP-MYC ΔIDR	Forward-2	5'-CTATGACCTCGTCACACCCTTCTCCCTTCGGGGA-3'
	Reverse-2	5'-GGTCACGCAGGGCCAGCTTCTCTGAGACGAGCTT-3'
	Forward-3	5'-GAAGCTGGCCCTGCGTGACCAGATCCCGGAGTTG-3'
	Reverse-3	5'-CCCAAGCTTCGCACAAGAGTCCGTAGCT-3'
	Forward	5'-TGGACAGCAAATGGGTCGCGGAATGGGCAAGAGCATCCCCCA-3'
pET28a-mCherry-ARMC12	Reverse	5'-GCCCTTGCTCACCATGGATCCTTCCGTGTTTTTAAAGTAGG-3'
	Forward	5'-CCCACGTGCATAGCACGTGCTATGCACGTGGATACACGTGGA-3'
pGL4.1-c-Myc luc	Reverse	5'-CATGGGGTGCACGTATCGTGCACGATACGTGCACCTATGGTGCACCTTCGA-3'
pGL3-NUP62 luc	Forward	5'-CGGGGTACCCAGCCCTTCAGCAATGTTATCCAC-3'
	Reverse	5'-CCCAAGCTTGCTCCACCTTCTTTCTTCAGCCG-3'
pGL3-NUP62 luc Mut	Forward	5'-AGCCAGAGCAAATCAGGGCAGGGAGGGTGGAGGAGGGTAGAGGGG-3'
	Reverse	5'-CTCCCTGCCCTGATTGCTCTGGCTCACAGCCCAGCTTCCTTCCT-3'
pGL3-NUP93 luc	Forward	5'-CGGGGTACCGGGCAGCAGGACAGGAATGAGTG-3'
	Reverse	5'-CCCAAGCTTGGAAGTATGAGCGGCGGGGTTCC-3'
pGL3-NUP93 luc Mut	Forward	5'-ACCCTTGATATACTACTATTATGGGGATTATAATTCAAGGTGAGATT-3'
	Reverse	5'-TCCCCATAATAGTAGTATATCAAGGGTGAGACCAGGTGGAGGTAACC-3'
pGL3-NUP98 luc	Forward	5'-CGGGGTACCGTGGGCCAGTCCCTTAGGGCATCT-3'
	Reverse	5'-CCCAAGCTTGTTGGGGAAGGGGAAGTGTGAGGAG-3'
pGL3-NUP98 luc Mut	Forward	5'-CTCAGGCTCCGACATCTGTCTGGGCGGGAAGTGC GGGCAGAGAGACT-3'
	Reverse	5'-CCGCCAGACAGATGTCGGAGCCTGAGGGCCCTCTTGAAGGTCTGT-3'

ARMC12, armadillo repeat containing 12; NUP62, nucleoporin 62; NUP93, nucleoporin 93; NUP98, nucleoporin 98; Mut, mutataion.

Table S3 Oligonucleotide sets used for short hairpin RNAs and small guide RNAs

Primer set	Sequence
sh-Scb	5'-AGGGATACAAGCATATACCACTCGAGTGGTATATGCTTGTATCCCTC-3' (sense); 5'-GAGGGATACAAGCATATACCACTCGAGTGGTATATGCTTGTATCCCT-3' (antisense)
sh- <i>ARMC12</i> #1	5'-CCGGTATGACCTTCTCTATGACATTCCTCGAGGAATGTCATAGAGAAGGTCATTTTTTG-3' (sense); 5'-GATCCAAAAAATGACCTTCTCTATGACATTCCTCGAGGAATGTCATAGAGAAGGTCATA-3' (antisense)
sh- <i>ARMC12</i> #2	5'-CCGGTGGCCATCAAGGCTGGCATAAACTCGAGTTTATGCCAGCCTTGATGGCCTTTTTG-3' (sense); 5'-GATCCAAAAAGGCCATCAAGGCTGGCATAAACTCGAGTTTATGCCAGCCTTGATGGCCA-3' (antisense)
sgMYC-a #1	5'-CACCGGGAGATCCGGAGCGAATAGGGGG-3' (sense); 5'-AAACCCCCCTATTCGCTCCGGATCTCCC-3' (antisense)
sgMYC-a #2	5'-CACCGGCTGTAGTAATTCCAGCGAGAGG-3' (sense); 5'-AAACCTCTCGCTGGAATTACTACAGCC-3' (antisense)
sgMYC-i #1	5'-CACCGCCTTGACAGCTGCTTAGACGC-3' (sense); 5'-AAACGCGTCTAAGCAGCTGCAAGGC-3' (antisense)
sgMYC-i #2	5'-CACCGTTTTTCGGGTAGTGGAAAACC-3' (sense); 5'-AAACGGTTTTCCACTACCCGAAAAC-3' (antisense)

ARMC12, armadillo repeat containing 12.

Table S4 Identification of MYC-binding proteins by mass spectrometry

Protein	log ₂ FC	Protein	log ₂ FC	Protein	log ₂ FC
KDM2A	8.20059	NOL11	1.92971	ZC3H13	1.31795
PURB	8.1986	XRCC1	1.9273	ESF1	1.30705
ETV6	7.56911	WDR36	1.88225	NOP58	1.305
MIOS	6.03426	PARP1	1.86231	HNRNPH3	1.2985
TMEM109	5.40402	SNU13	1.85505	CPSF6	1.29499
NOP10	5.07401	PTMA	1.85487	GTF2E2	1.28651
MAX	4.98669	NOL10	1.85283	DHX36	1.27755
PPIE	4.73516	DNTTIP2	1.81253	NCOA5	1.27537
GTF2F2	4.68745	SAFB	1.79753	PARP2	1.27411
PRPF38A	4.56863	RBMXL1	1.7973	UTP14A	1.26528
VIRMA	4.48085	PPAN	1.79305	UTP3	1.25495
CREM	4.21497	TBL3	1.78914	HMG13	1.25316
ARMC12	4.01901	UBTF	1.78144	CGAS	1.24841
IMP4	4.00298	WDR3	1.772	DNAJC9	1.24617
YTHDC2	3.90748	SEH1L	1.74661	GNL2	1.24464
PWP1	3.89115	ZC3H11A	1.73602	CFAP20	1.23541
DDX39A	3.85322	RB1	1.72604	DHX9	1.22827
NEDD8	3.7902	CDC27	1.72353	CHD1	1.219
JADE3	3.73508	NIPBL	1.72121	HMG20A	1.2145
NHP2	3.73076	MAU2	1.6974	TFAP2D	1.21351
TFAP4	3.68096	UTP15	1.68576	NLE1	1.20502
DDX10	3.65887	HNRNPC	1.66519	XRCC6	1.19855
PSME3IP1	3.61664	NOP2	1.66306	SRSF10	1.1944
ZCCHC10	3.48588	LMNA	1.64491	RPA3	1.18328
CPSF4	3.40326	RBMX	1.63334	HMG1	1.17856
VWA5A	3.21564	SPOUT1	1.62737	ATAD2B	1.16898
WDR76	3.20909	RFC1	1.62242	RPA1	1.16345
UBP1	3.18293	NOP56	1.62058	PTBP1	1.15866
PRPSAP2	3.17756	RPP30	1.61559	MAX	1.15657
BMS1	3.17619	UTP11	1.60724	EMG1	1.15528
HNRNPM	3.13878	SMARCA5	1.58606	SRRM1	1.15497
HMCES	3.13066	RALY	1.58389	TOP1	1.15036
DDX20	3.06295	ZNF280C	1.58355	NOP16	1.14694
WDR46	3.04008	SSRP1	1.57801	SNU13	1.14426
KRR1	2.99692	DDX27	1.57382	HNRNPA3	1.13966
CDK4	2.95993	RSF1	1.57147	EXOSC4	1.13942
POLE3	2.90998	AATF	1.56832	RBM6	1.13031
USP34	2.89794	NOP14	1.5642	AHCTF1	1.12925
RIF1	2.7932	BYSL	1.56143	HNRNPA1	1.12575
RBM28	2.73774	PUM3	1.55739	ILF3	1.12244
BAZ1A	2.71388	CLASRP	1.54435	XRCC5	1.1216
DUSP12	2.66371	FBL	1.50634	ZC3H14	1.12155
NCKIPSD	2.64937	KIF1C	1.50301	ILF2	1.11723
WDR55	2.64848	PDCD11	1.49694	SMCHD1	1.11069
OTX1	2.61372	RCL1	1.4906	RRP9	1.10873
CENPV	2.58762	BAZ2A	1.48954	HNRNPL	1.10475
NAA40	2.58025	INCENP	1.48893	RBM12B	1.10463
DCAF13	2.5576	XPC	1.48144	CBX3	1.10382
UTP4	2.55271	PFKFB2	1.47344	PTBP3	1.10247
RBM42	2.54947	TCF20	1.46615	U2AF2	1.09427
LIG3	2.52778	SUPT16H	1.46306	MATR3	1.09237
TRIM26	2.47445	HP1BP3	1.46015	BRX1	1.085
THOC5	2.47174	RPA2	1.45415	CEBPZ	1.08487
ZNF326	2.46776	STRBP	1.45287	HNRNPH2	1.08283
SMC6	2.45798	DRG1	1.44441	SRP14	1.08265
CDC73	2.41179	STAU2	1.43805	PTBP2	1.08259
MORF4L1	2.40773	GLYR1	1.42961	TFAP2A	1.0814
APTX	2.40655	DIDO1	1.42443	SRSF7	1.07972
SAFB2	2.3845	GPATCH4	1.42375	DHX15	1.07737
NONO	2.35717	PIIG	1.4129	TRA2A	1.06239
RBM15	2.32515	FGF2	1.40895	CBX5	1.06185
BAZ1B	2.27354	TOP2A	1.40601	CHD2	1.06068
TDRD3	2.26526	PNKP	1.4042	RCC1	1.0601
PAK1IP1	2.20825	C1orf131	1.40405	MECP2	1.05826
SMARCA1	2.17335	ATRAX	1.40401	HNRNPA0	1.05056
GAR1	2.16951	MSH3	1.40336	HNRNPR	1.04753
SFPQ	2.14266	MPHOSPH10	1.39633	LRRC47	1.04169
POLR3F	2.14252	H2AC21	1.38597	RRP12	1.04064
CUL2	2.13922	FOLR1	1.38571	POLA2	1.04007
DNAJB1	2.13466	CHD1L	1.38083	BANF1	1.03437
NSD2	2.12453	NOL7	1.3805	TFCP2	1.02782
ALKBH5	2.09317	IMP3	1.38001	ZEB1	1.02623
PAXBP1	2.08948	KAT7	1.37179	MACROH2A1	1.01823
UTP18	2.08902	PHIP	1.36294	TFIP11	1.01619
XIAP	2.08546	ZCCHC8	1.36212	SH3BGR13	1.01545
PINX1	2.00772	DDX18	1.35404	WDR82	1.01512
RPF2	1.99147	CBX8	1.35177	SAP18	1.01286
RPF1	1.98017	H1-10	1.3504	ARAP1	1.01215
TMPO	1.97512	CHTOP	1.33736	MDC1	1.00125
RRP7A	1.96172	DKC1	1.31802		

Table S5 Identification of target genes associated with outcome of NB

Up-regulated genes		Down-regulated genes
ALDH16A1	PRDX6	ALDH3A2
ARFIP2	PRKCSH	ARHGAP21
ARHGEF2	PRPF3	ATP6V1C1
ATP11C	PSMB5	ATP8A1
ATP13A1	PTGER2	BBS9
BAZ1A	REC8	BEND6
BRCA2	RECQL4	C9orf24
BRIP1	RPUSD2	CADM1
BRMS1	SEC13	CCDC146
BRPF1	SIAH2	CLTCL1
CD248	SLC1A5	CMAS
CDC25A	SLC25A22	CREBL2
CFL1	SLC30A3	DCAF6
CHEK2	SLC38A5	DERA
CITED1	SLC41A1	DLG1
CLMP	SMG8	EPB41L5
CNOT3	SNRPB	FAM131B
CYP27B1	SNRPF	FIG4
DAXX	SPATA5L1	FOXP1
DDR2	STAMBP	HECTD2
DGAT2	STK24	HP1BP3
DNAJB5	TBX2	HRK
DNTTIP2	TICAM1	ICA1L
DPF1	TMEM216	INPP5K
DTL	TMUB1	KATNAL1
DUSP4	TNFRSF10B	LRRC8C
DYRK3	TOP1MT	MAGI2
EMILIN1	TP53I11	MAP1A
FIBP	TRIB3	MTRF1
FTSJ1	TRIM28	MYO9A
GLA	YIF1A	PIP5KL1
GTPBP1	ZNF195	PPP3CB
HMGB2	ZNF317	PRKAG1
ING2	ZNF530	RAB2A
IPO4	ZNF581	RHOU
KDELRL1	ZNF668	RORB
KLHL25		SEC31B
LIG1		SHF
LSM7		SLC4A8
LY6E		SMIM14
MCM5		SPOPL
MED12		SPRYD7
MKRN3		SRR
MND1		SSX2IP
MRPL16		STX8
MYB		SYBU
NAE1		TCTA
NFATC3		TMCO3
NOB1		TMEM107
NUP50		TOM1L2
NUP54		TRPC1
NUP62		TSHZ2
NUP93		VPS4B
NUP98		ZC3H6
PLAGL2		
PNKP		
PNPT1		
POLD1		
PPP1R15B		
PRDX4		

Table S6 Screening of inhibitors targeting ARMC12-MYC interaction

MTT colorimetry		Dual-luciferase assay	
(S)-crizotinib	Duloxetine HCl	Primaquine Diphosphate	Tioconazole
Adapalene	Econazole	Proguanil	Aprepitant
Afatinib (BIBW2992)	Econazole nitrate	Protriptyline hydrochloride	Auranofin
Afatinib (BIBW2992) Dimaleate	Efavirenz	Quetiapine Fumarate	Ceritinib (LDK378)
Amiodarone HCl	Elvitegravir (GS-9137, JTK-303)	Quinestrol	Cinacalcet HCl
Amitriptyline	Enasidenib Mesylate	Raloxifene	Dasatinib
Amlodipine	Erythromycin estolate	Raloxifene HCl	Dihydroergotamine Mesylate
Amlodipine Besylate	Estradiol Cypionate	Rotigotine	Erythromycin estolate
Amlodipine maleate	Estradiol valerate	Salmeterol	Estradiol valerate
Anidulafungin (LY303366)	Ezetimibe	Salmeterol Xinafoate	Flibanserin
Aprepitant	Fedratinib (SAR302503, TG101348)	Sertaconazole nitrate	Grazoprevir
Asenapine maleate	Felodipine	Sertraline HCl	Lovastatin
Auranofin	Fingolimod	Simeprevir	Menadione
Azelastine HCl	Flibanserin	Simvastatin	Methylene Blue
BAF312 (Siponimod)	Fluoxetine HCl	Sulconazole Nitrate	Nefazodone hydrochloride
Bazedoxifene Acetate	Fluphenazine dihydrochloride	Sunitinib Malate	Quinestrol
Bazedoxifene HCl	Gefitinib (ZD1839)	Tacrolimus (FK506)	Raloxifene
Bepidil hydrochloride	Grazoprevir	Tafuprost	Rotigotine
Betamethasone Valerate	Hydroxyzine 2HCl	Tamoxifen	Tamoxifen Citrate
Brexiprazole	Ibrutinib (PCI-32765)	Tamoxifen Citrate	Trifluoperazine
Butoconazole	Indacaterol	Tegaserod Maleate	
Butoconazole nitrate	Indacaterol Maleate	Telotristat Etiprate (LX 1606 Hippurate)	
Calcipotriene	Ivacaftor (VX-770)	Terconazole	
Calcitriol	Ivermectin	Tezacaftor?(VX-661)	
Canagliflozin	Lansoprazole	Thioridazine hydrochloride	
Canagliflozin hemihydrate	Latanoprost	Thiothixene	
Candesartan Cilexetil	Lomitapide	Ticagrelor	
Carvedilol	Loperamide HCl	Tioconazole	
Carvedilol Phosphate	Loratadine	Toremifene Citrate	
Celecoxib	Lovastatin	Travoprost	
Ceritinib (LDK378)	Luliconazole	Triclosan	
Ceritinib dihydrochloride	Lusutrombopag	Trifluoperazine	
Chlorhexidine	Maprotiline HCl	Trifluoperazine 2HCl	
Chlorhexidine?2HCl	Mefloquine HCl	Triflupromazine hydrochloride	
Chloroxine	Menadione	Vilanterol Trifenate	
Chlorpromazine	Methylene Blue	Vilazodone	
Chlorpromazine HCl	Miconazole	Vinorelbine Tartrate	
Chlorprothixene	Miconazole Nitrate	Vortioxetine	
Cinacalcet	Mitotane	Vortioxetine (Lu AA21004) HBr	
Cinacalcet HCl	Montelukast		
Clemastine Fumarate	Montelukast Sodium		
Clioquinol	Moxidectin		
Clomipramine HCl	Nebivolol		
Clotrimazole	Nebivolol HCl		
Cobicistat (GS-9350)	Nefazodone hydrochloride		
Crizotinib (PF-02341066)	Netupitant		
Cyproheptadine hydrochloride	Nisoldipine		
Dacomitinib (PF299804, PF299)	Nortriptyline hydrochloride		
Dasatinib	Osimertinib (AZD9291)		
Dasatinib hydrochloride	Osimertinib mesylate		
Desipramine Hydrochloride	Ospemifene		
Desogestrel	Oxybutynin		
Dienestrol	Ozanimod (RPC1063)		
Dihydroergotamine Mesylate	Paroxetine HCl		
Doxazosin	Paroxetine mesylate		
Doxazosin Mesylate	Penbutolol Sulfate		
Doxercalciferol	Perphenazine		
Dronedarone	Pimavanserin		
Dronedarone HCl	Pimozide		
Duloxetine	Ponatinib (AP24534)		

Table S7 Identification of TCZ-binding proteins by mass spectrometry

Protein	log ₂ FC	Protein	log ₂ FC
ABHD11	3.61977528	MRPL51	4.41355784
ACAD10	2.69059883	MRPS14	4.3190597
ACSL6	7.73759139	MT-ATP6	5.44737132
ADD3	2.77414007	MTFR1L	1.75782611
AKTIP	2.65347884	MTG1	1.69780896
ALAS1	3.30379115	MTIF2	3.2860458
ALKBH2	3.11270156	MT-ND4	1.99556276
ANGEL2	1.90907936	NBEAL2	1.68014173
ANKRD11	3.77849481	NDUFAF6	3.45496546
AP3M2	2.45576453	NDUFS5	5.28094921
APOO	1.14847122	NDUFS7	5.03010422
ARMC12	6.98867069	NEBL	3.70231603
ATAD2	1.81283811	NEMF	2.72742317
ATG12	3.24571524	NHERF2	3.46409028
ATPAF2	3.93107175	NME4	2.37170434
BAZ2A	1.35701902	NOP10	3.86176969
BBX	4.91136001	NSMCE1	1.39330276
BPGM	4.7184945	NT5DC3	4.91580891
CC2D1B	2.66651895	NTHL1	2.53575404
CDC23	1.50112165	OTUB2	2.89586886
CENPU	2.09363868	OXSM	4.92887835
CLCC1	6.30074306	P3H3	4.5777604
CLN5	3.9068348	PACIN3	6.05560506
COA3	4.30543312	PAK4	2.5662295
COIL	1.83854219	PFKFB2	2.78809548
COL18A1	5.93242669	PGS1	2.35550688
COX6A1	2.83086337	PIK3R2	2.75
CRAT	1.13683865	PISD	5.07834637
CROT	3.07879794	PLG	2.4630962
CSNK1G3	1.35280752	POLR1H	1.07745908
CSPG4	2.29070123	PPP2R5E	3.48856561
CTSA	1.17390481	PRAF2	2.52030053
DACH1	4.24935427	PRKCD	4.64020128
DBR1	4.33421605	PTDSS1	2.94975976
DEPDC1B	1.95028045	PTGR3	4.58946427
DES	5.50358618	PYGM	5.13126199
DHODH	5.75573114	RAB3D	3.2316429
DOCK1	1.20595593	RARS2	2.9558212
DPCD	2.83690443	RASAL2	1.64130982
DPF2	6.29014061	RMND5A	4.36925657
DPP9	1.8418003	SELENOT	4.76405594
EHBP1L1	1.74516404	SLC25A12	1.98994761
ENDOV	1.33046354	SLC4A7	3.19712145
ENPP4	2.56307604	SLIT1	5.3538743
ENPP7	4.14113559	SMAP1	3.33809543
EPHA2	1.13255485	SMC5	1.146668
ERO1B	4.6645248	SMC6	4.85099336
EXOC1	2.6758868	SNCG	4.18367181
F8A1	2.54994637	SNX8	3.41991804
FAM13B	1.52335924	SPCS3	3.49222769
FASTKD2	4.95410854	SPOUT1	1.14085927
FASTKD5	4.88877669	SRR	3.59059324
FBXL18	2.44539299	STAT2	1.44108918
FECH	4.66739734	STX10	3.98002118
GAMT	4.79210405	STX4	3.67299653
GLDC	5.84761285	SUCLA2	3.54814372
GRPEL2	3.29615985	TAF2	2.25448522
GTF2E1	4.32612731	TIMM8B	3.52274964
H3C1	2.25378219	TMEM205	6.80145432
HAUS6	5.22934627	TRAPPC5	1.61723212
HDAC3	3.81930609	TRMT2B	2.5396186
HSPA2	3.96116039	UQCC1	3.11094234
IFT70B	1.89012137	XRCC4	3.04459332
IKBIP	4.90546218	YBEY	4.1041352
IMP4	1.2950141	ZNF512	2.50829678
IST1	5.9264137	ZNG1F	2.36477878
KATNA1	3.08550182		
KCTD1	2.34865574		
KXD1	2.92401997		
KYAT1	4.04208613		
LAMTOR2	1.32471535		
LBH	4.03744402		
LDB1	4.3099737		
LGALS3BP	3.85301745		
LIN37	1.99204048		
MBIP	3.97089556		
MEAK7	2.27618524		
MECR	3.93614069		
MRC2	3.50182415		
MRPL20	2.00333717		

Table S8 18S rRNA analysis of NB and GNB tissues

Phylum	GNB-Tissue	NB-Tissue	Genus	NB-Tissue	GNB-Tissue
Ascomycota	0.102826562	1.074615472	Aspergillus	0.007789891	0.000000000
Basidiomycota	0.064266601	0.414811699	Cercomonadidae	0.000000000	0.000389495
Cercozoa	0.004284440	0.061929634	Cladosporium	0.075561943	0.017527255
Gracilipodida	0.000000000	0.031549059	Filobasidium	0.000000000	0.001168484
Phragmoplastophyt	0.271477703	0.847929642	Gracilipodida	0.031549059	0.000000000
Vertebrata	99.55130228	97.46984338	Magnoliophyta	0.832739354	0.090362736
			Malassezia	0.153850348	0.046739346
			Mammalia	97.46984338	99.55130228
			Naganishia	0.006621407	0.000000000
			Pinophyta	0.015190288	0.181114967
			Preussia	0.001557978	0.000000000
			Rhodotorula	0.207990091	0.000000000
			Saccharomyces	0.706932614	0.031549059
			Schizophyllum	0.042065412	0.000000000
			Talaromyces	0.017916749	0.000778989

Table S9 Identification of UU-T02-binding proteins by mass spectrometry

Protein	log ₂ FC	Protein	log ₂ FC	Protein	log ₂ FC
ABHD11	3.21231979	LIN37	1.70257	STX10	4.07272641
ACAD10	3.23832264	LMBR1L	1.17633	STX4	3.92041893
ALAS1	4.27644756	LRATD2	4.52896	SUCLA2	3.81367739
ALG12	2.3117023	MBIP	3.60028	SUN1	6.67942939
ALG6	2.26013307	MBLAC2	1.45482	TAF2	2.3696954
ALKBH2	2.85252474	MEAK7	2.21353	TAF9B	1.21062407
ANGEL2	1.98590377	MECR	4.75746	TATDN3	1.00305677
ANKRD11	4.29730618	MIOS	2.83367	TMED7	2.32572033
ANKRD28	2.44511034	MLYCD	3.66279	TMEM205	7.64855216
AP3M2	2.36262245	MPRIIP	4.34749	TMEM256	6.48984145
APOO	1.47990832	MRC2	3.84443	TRAPPC5	1.35306168
APOOL	5.72863524	MRPL16	1.68968	TRIT1	3.00090694
ARMC12	8.0264864	MRPL20	1.56476	TRMT2B	2.11117794
ATAD2	1.69443586	MRPL51	4.77093	TTC28	1.61987678
ATG12	2.47868509	MRPL57	3.54151	TXNL4A	6.00147199
ATPAF2	3.85863233	MRPS14	4.07925	UACA	4.05988216
BAZ2A	2.46576708	MT-ATP6	5.13675	UNC79	3.55026257
BCKDHA	1.19230278	MTFR1L	1.32741	UQCC1	3.24961987
BPGM	4.39600753	MTG1	2.45602	YBEY	5.66401543
CAMK1	2.47360161	MTIF2	3.83324	ZBTB7A	3.64744044
CC2D1B	2.48701234	MT-ND4	2.34435	ZCCHC9	3.24670526
CCDC12	5.88046924	NBEAL2	1.15466	ZNF512	3.38993044
CDC23	2.03615016	NDUFAF6	3.45196	ZNG1F	2.11577998
CENPO	5.14091661	NDUFS7	5.18499		
CENPU	2.50717112	NEBL	4.40341		
CLCC1	6.14823119	NEMF	2.73708		
CLN5	3.50458307	NHERF2	2.95744		
COA3	5.642247	NME4	2.90275		
COL18A1	5.69017535	NNT	4.45715		
COMTD1	2.66436325	NOP10	4.43032		
COX6A1	3.96275427	NOTCH2	3.5928		
COX6C	1.54478862	NR3C1	4.62953		
CROT	2.78979802	NSMCE1	1.85243		
CSNK1G3	1.74890959	NT5DC3	4.37947		
CSPG4	2.39125932	NTHL1	2.53012		
CTSA	1.5319868	OSGEPL1	2.48379		
CYB561D2	1.4596457	OXNAD1	4.49696		
DACH1	3.61186517	OXSM	5.07642		
DBR1	2.50218178	P3H3	4.62992		
DES	5.51612288	PACSIN3	6.02634		
DHODH	6.12605364	PAK4	1.75839		
DMAC2L	1.64760908	PCYOX1L	4.62911		
DNAJB4	1.67004152	PFKFB2	3.14599		
DPCD	2.67179471	PGS1	1.63619		
DPP9	2.19141966	PIK3R2	2.92696		
DUS2	4.05070768	PIP4P1	1.09049		
EHBP1L1	2.50255223	PISD	5.31647		
EIF2AK4	1.16906094	POLG	2.08938		
ENPP7	4.49153498	PPP1R12C	1.30518		
EPHA2	1.14371158	PPP6R2	1.82203		
ERCC3	1.52315011	PRAF2	2.48638		
ERI3	4.59906514	PRKAA2	3.23091		
ERO1B	3.82760374	PRKCD	4.61064		
EXOC1	3.38308782	PTDSS1	3.34638		
F8A1	3.11387646	PTGR3	4.50574		
FASTKD2	4.92188523	PYGM	5.06577		
FASTKD5	4.76577281	R3HCC1	3.71893		
FBXL18	2.38584979	RAB34	3.61034		
FECH	4.92759028	RAB3D	2.74721		
GAMT	4.50194434	RAB8B	2.05056		
GHITM	1.93142723	RARS2	2.89749		
GLDC	5.89833719	RBM6	1.82996		
GLE1	3.0895287	RMND5A	4.73425		
GMPR	2.79976134	RREB1	1.3333		
GRPEL2	3.53568925	RSAD1	1.00651		
GTF2E1	4.22807181	SAR1B	1.72209		
H3C1	2.80677214	SEL1L	2.90183		
HAUS6	5.01495778	SELENOT	4.87032		
IFT70B	2.36881027	SLC12A7	2.50293		
IGF1R	1.35363961	SLC25A12	2.70947		
IKBIP	4.92548889	SLC4A7	3.16733		
IMP4	1.31215196	SLIT1	4.97154		
IST1	6.06454863	SMC5	1.54782		
KATNA1	3.11148346	SMC6	4.85952		
KXD1	2.79315238	SNCG	3.63078		
KYAT1	3.76570588	SNF8	1.79373		
LAMTOR2	2.58091912	SPOUT1	2.37465		
LBH	3.47462215	SRR	3.66231		
LDB1	4.12446135	STAT2	2.53868		
LGALS3BP	4.5702896	STK3	3.30788		