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3 **Supplementary Information for**

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5 **Inhibition of GCN2 sensitizes ASNS-low cancer cells to asparaginase by**
6 **disrupting the amino acid response**

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27

28 Supplementary text

29 Figs. S1 to S10

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31 References for SI reference citations

32 **Supporting Information Text**

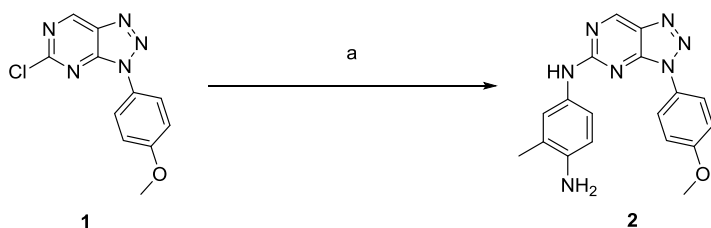
33

34 **Materials and Methods**

35

36 **Compound synthesis**

37 GCN2iA (**2**) was synthesized from compound **1** in a similar manner as that described in the patent (WO
38 2013110309A1).



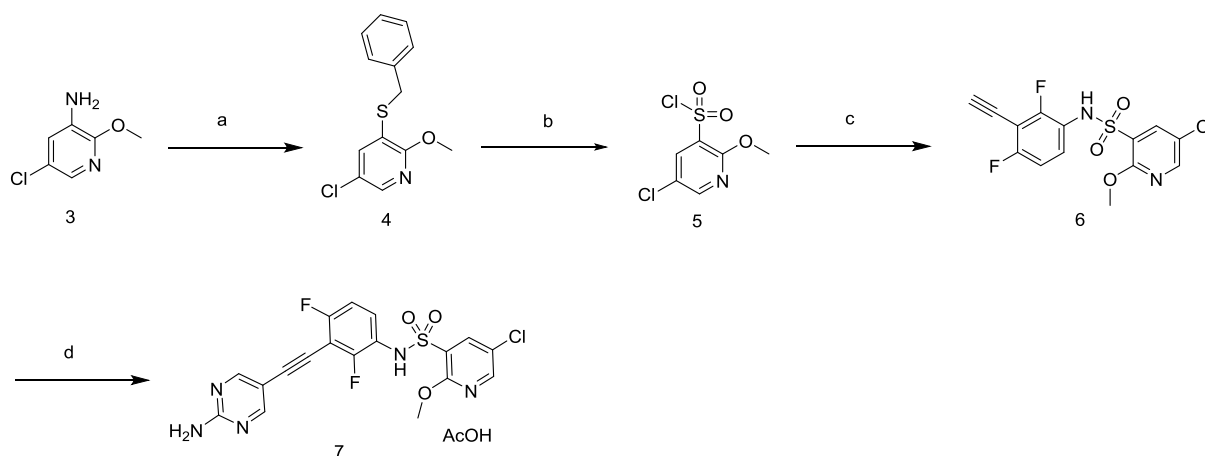
39 Reagents and conditions: (a) DIEA, 2-methylbenzene-1,4-diamine dihydrochloride, 74%.

40 *N*-4-(3-(4-methoxyphenyl)-3*H*-[1,2,3]triazolo[4,5-*d*]pyrimidin-5-yl)-2-methylbenzene-1,4-diamine
41 (**2**). To a mixture of 5-chloro-3-(4-methoxyphenyl)-3*H*-[1,2,3]triazolo[4,5-*d*]pyrimidine (50 mg, 0.19 mmol)
42 in dimethyl sulfoxide (DMSO; 1 mL), 2-methylbenzene-1,4-diamine dihydrochloride (74.6 mg, 0.38 mmol)
43 and diisopropylethylamine (DIEA; 0.167 mL, 0.96 mmol) were added at 25°C. The mixture was stirred at
44 90°C for 2 h, during which time its color gradually changed to dark brown. The mixture was then poured into
45 saturated NaHCO₃ (aq) (20 mL), extracted with ethyl acetate (20 mL), washed with brine, and dried over
46 MgSO₄. The filtrate was then concentrated *in vacuo*. The residue was purified by silica gel-column
47 chromatography (*n*-hexane-ethyl acetate = 70:30–0:100) and triturated with *i*Pr₂O. The precipitate was
48 collected by filtration to obtain compound **2** (49.2 mg; 74%) as a pale brown solid. ¹H NMR (300 MHz,
49 DMSO-*d*₆) δ 2.09 (3H, s), 3.86 (3H, s), 4.76 (2H, brs), 6.59 (1H, d, *J* = 8.5 Hz), 7.16–7.29 (3H, m), 7.54 (1H,
50 brs), 8.05 (2H, d, *J* = 8.9 Hz), 9.33 (1H, s), and 9.94 (1H, brs).

51

52 GCN2iB (**7**) was synthesized as shown in the following scheme:

53



54 Reagents and conditions: (a) dibenzyl disulfide, pentyl nitrite, MeCN; (b) *N*-chlorosuccinimide, AcOH, water, 53% (2 steps); (c) 3-ethynyl-2,4-difluoroaniline, pyridine; (d) 1) 2-amino-5-iodopyrimidine, Pd(PCy₃)₂Cl₂, Cs₂CO₃, DMSO, 2) recrystallization from DMSO-water-AcOH, 20% (2 steps).

55

56 3-(Benzylthio)-5-chloro-2-methoxypyridine (**4**). Pentyl nitrite (8.79 ml, 66.0 mmol) was added
57 dropwise over 20 min to a solution of 1,2-dibenzylsulfane (8.87 g, 36.0 mmol) and
58 5-chloro-2-methoxypyridin-3-amine (4.76 g, 30 mmol) in acetonitrile (63.1 mL) at 80°C. The mixture was
59 stirred at 80°C for 30 min and then concentrated *in vacuo*. The residue was purified by silica gel column
60 chromatography (n-hexane-ethyl acetate = 100 : 0-90 : 10) to obtain crude product **4** (5.40 g) as orange oil.
61 This material was used in the next reaction without further purification.

62 Next, 5-Chloro-2-methoxypyridine-3-sulfonyl chloride (**5**). N-chlorosuccinimide (16.3 g, 123
63 mmol) was added dropwise for over 10 min to a solution of **4** (5.40 g, 20.3 mmol) in acetic acid (34.9 mL)
64 and water (11.0 mL) at 25°C. The mixture was stirred at room temperature overnight. The mixture was
65 diluted with water, and extracted with EtOAc. The organic layer was washed with brine, dried over MgSO₄,
66 and concentrated *in vacuo*. The mixture was concentrated *in vacuo*. The residue was purified by silica gel
67 column chromatography (n-hexane-ethyl acetate = 100:0-80:20) to yield **5** (4.40 g, 53% for 2 steps) as orange
68 oil. ¹H NMR (300 MHz, DMSO-d₆) δ 3.86 (3H, s), 7.91 (1H, d, J = 2.6 Hz), 8.17 (1H, d, J = 2.6 Hz).

69 5-Chloro-N-(3-ethynyl-2,4-difluorophenyl)-2-methoxypyridine-3-sulfonamide (**6**). The mixture of
70 3-ethynyl-2,4-difluoroaniline (Ref; 1) (2.78 g, 18.18 mmol), **5** (4.40 g, 18.2 mmol) and pyridine (43.1 g, 545
71 mmol) was stirred at room temperature overnight. Then, MeOH (10 mL) was added to the mixture, and the
72 mixture was stirred at room temperature for 10 min. The mixture was concentrated *in vacuo*. The residue was
73 purified by silica gel column chromatography (n-hexane-ethyl acetate = 100:0-50:50) to give crude **6** (5.02 g)
74 as beige solid. This material was used in the next reaction without further purification.

75 N-(3-((2-aminopyrimidin-5-yl)ethynyl)-2,4-difluorophenyl)-5-chloro-2-methoxypyridine-3-sulfon
76 amide acetic acid salt (**7**). The mixture of **6** (1.24 g, 3.46 mmol), 5-iodopyrimidin-2-amine (1.15 g, 5.18
77 mmol), Pd(PCy₃)₂Cl₂ (170 mg, 0.24 mmol), cesium carbonate (4.51 g, 13.8 mmol) and DMSO (16.5 ml, 232
78 mmol) was stirred at 120°C for 3 h under N₂. The mixture was diluted with water and brine, and extracted
79 with EtOAc. The organic layer was collected, washed with brine, dried over MgSO₄, and concentrated *in*
80 *vacuo*. The residue was purified by silica gel column chromatography (n-hexane-ethyl acetate = 100 : 0-80 :
81 20) to yield crude product. The crude product was subjected to amino silica gel column chromatography and
82 eluted with (ethyl acetate-methanol = 100 : 0-50 : 50) to remove byproducts. The amino silica gel, including
83 the desired product, was subjected to water/EtOAc/AcOH (100 mL-100 mL-18 mL). The mixture was stirred
84 at room temperature for 10 min, the insoluble materials were filtered off, and further elution with
85 EtOAc-AcOH (30 mL-6 mL) was carried out 4 times. From the combined filtrate, the organic layer was
86 collected, washed with water and brine, dried over MgSO₄, and concentrated *in vacuo*. The residue was
87 dissolved with EtOAc/THF/saturated NaHCO₃aq. (120 ml-30 ml-30 ml). The organic layer was collected,
88 washed with saturated NaHCO₃aq, brine, dried over MgSO₄, and concentrated *in vacuo*. This solid was
89 triturated with EtOAc, and the precipitate was collected by filtration to yield crude product as a white solid
90 (872 mg). The obtained solid was purified by silica gel column chromatography (n-hexane-ethyl acetate =
91 100 : 0-0 : 100), and triturated with EtOAc. The precipitate was collected by filtration to yield free form of the
92 desired product (635 mg). Additional batches with 4.05 times scale and 4.12 times scale were carried out in a

93 similar manner to obtain free form of the desired product (4.83 g). All obtained free form of the desired
94 product were combined, and dissolved with AcOH (24.8 mL) and DMSO (66 mL) at 50°C. The solution was
95 filtered to remove small insoluble materials with washing with AcOH (24.8 mL). Water (50 mL) was added
96 dropwise to the filtrate at 50°C. The mixture was allowed to cool to 25°C for 30 min. The precipitate was
97 collected by filtration, washed with EtOH-water (1/10, 33 mL) 3 times and dried under vacuum at 50°C to
98 yield 7 (5.53 g, 20% for 2 steps) as a white solid. ¹H NMR (300 MHz, DMSO-d₆) δ 1.91 (3H, s), 3.94 (3H, s),
99 7.14-7.37 (4H, m), 8.07 (1H, d, J = 2.6 Hz), 8.43 (2H, s), 8.52 (1H, d, J = 2.6 Hz), 10.46 (1H, s), 11.94 (1H, s).
100 Anal. Calcd for C₂₀H₁₆ClF₂N₅O₅S: C, 46.93; H, 3.15; N, 13.68. Found: C, 46.85; H, 3.17; N, 13.64.

101

102 **GCN2 kinase assay**

103 Recombinant GCN2 (1 nmol/L) protein (Carna Biosciences) was pre-incubated with GCN2 inhibitors for 60
104 min and then incubated with ATP (K_M value of GCN2 = 190 μmol/L) and the green fluorescent protein-eIF2α
105 substrate (130 nmol/L) at 25°C. The amount of phosphorylated substrate was determined using the
106 LanthaScreen Tb-anti-p-eIF2α (pSer52) antibody kit (Thermo Fisher Scientific). The IC₅₀ value of eIF2α
107 kinase was measured using the XLfit software (IDBS).

108

109 **Kinase panel**

110 Kinase selectivity of GCN2iA was evaluated at 1 μmol/L using a panel of 27 kinases that covers major kinase
111 families. Serine/threonine kinase assays were performed using [γ -³³P] ATP in 96-well plates. The reaction
112 conditions were optimized for each kinase: p38α (100 ng/well enzyme, 1 μg/well myelin basic protein
113 [MBP], 0.1 μCi/well [γ -³³P] ATP, 60-min reaction at 30°C); extracellular signal-regulated protein kinase 1
114 (ERK1; 100 ng/well enzyme, 2 μg/well MBP, 0.1 μCi/well [γ -³³P] ATP, 60-min reaction at 30°C); protein
115 kinase C ζ (PKCζ; 25 ng/well enzyme, 2 μg/well MBP, 0.1 μCi/well [γ -³³P] ATP, lipid activator [Millipore],
116 60-min reaction at 30°C); c-Jun N-terminal kinase 1 (JNK; 10 ng/well enzyme, 1 μg/well c-Jun, 0.1 μCi/well
117 [γ -³³P] ATP, 60-min reaction at 30°C); mitogen-activated protein kinase 1 (MEK1; 100 ng/well enzyme, 0.3
118 μg/well glutathione S-transferase-ERK1 [K71A], 0.2 μCi/well [γ -³³P] ATP, 20-min reaction at 25 °C);
119 Aurora-B (50 ng/well enzyme, 30 μmol/L Aurora-substrate peptide, 0.2 μCi/well [γ -³³P] ATP, 60-min
120 reaction at 25°C); protein kinase A (PKA; 3 nmol/L enzyme, 1 μmol/L PKA-substrate peptide [Millipore],
121 0.2 μCi/well [γ -³³P] ATP, 10-min reaction at 25°C); cyclin-dependent kinase 2 in complex with cyclin A
122 (CDK2/CycA; 1.8 mU/well enzyme, 1 μg/well histone H1, 0.2 μCi/well [γ -³³P]ATP, 20-min reaction at
123 25°C); casein kinase 1 δ (CK1δ; 120 ng/well enzyme, 2.4 μmol/L CK1tide [Millipore], 0.2 μCi/well [γ -³³P]
124 ATP, 20-min reaction at 25°C); checkpoint kinase 1 (CHK1; 30 ng/well enzyme, 25 μM CHKtide [Millipore],
125 0.2 μCi/well [γ -³³P] ATP, 10-min reaction at 25°C); GSK-3β (25 ng/well enzyme, 0.2 μg/well
126 GSK3-substrate peptide [Millipore], 0.1 μCi/well [γ -³³P] ATP, 30-min reaction at 25°C); Akt1 (120 ng/well
127 enzyme, 5 μmol/L Akt1-substrate [Millipore], 0.2 μCi/well [γ -³³P] ATP, 20-min reaction at 25°C); apoptosis
128 signal-regulating kinase 1 (ASK1; 25 ng/well enzyme, 2 μg/well MBP, 0.1 μCi/well [γ -³³P] ATP, 60-min
129 reaction at 25°C); mitogen-activated protein kinase-activated protein kinase 2 (MAPKAP2; 300 ng/well
130 enzyme, 0.5 μmol/L KKLNRTLSVA-NH₂, 0.1 μCi/well [γ -³³P] ATP, 10-min reaction at 25°C);

131 rho-associated, coiled-coil-containing protein kinase 1 (ROCK1; 164 ng/well enzyme, 0.5 μ mol/L long S6
132 peptide [Millipore], 0.2 μ Ci/well [γ -33P] ATP, 10-min reaction at 25°C); polo-like kinase 1 (PLK1; 25
133 ng/well enzyme, 3 μ g/well of casein [Sigma-Aldrich], 0.2 μ Ci/well [γ -33P] ATP, 60-min reaction at 25°C);
134 interleukin-1 receptor-associated kinase 4 (IRAK4; 27.7 ng/well enzyme, 0.5 μ mol/L MBP, 0.2 μ Ci/well of
135 [γ -33P] ATP, 60-min reaction at 25°C); and cell division cycle 7/activator of S-phase kinase (CDC7/Dbf4
136 complex; 3.1 ng/well enzyme, 500 ng/well His-tagged minichromosome maintenance complex component 2,
137 0.2 μ Ci/well [γ -33P] ATP, 60-min reaction at 25°C). Enzyme reactions were performed in 25 mmol/L HEPES
138 (pH 7.5) supplemented with 10 mmol/L magnesium acetate, 1 mmol/L dithiothreitol, and 500 nmol/l ATP,
139 and containing an optimized concentration of enzyme, substrate, and radiolabeled ATP, as described above,
140 in a total volume of 50 μ L. Prior to initiating the kinase reaction, the compound and enzyme were incubated
141 for 5 min at the reaction temperature described; the reaction was then initiated by adding ATP. After the
142 reaction periods mentioned, the reactions were terminated by adding 10% trichloroacetic acid. The
143 [γ -33P]-phosphorylated proteins were filtered into 96-well filter plates using a cell harvester (PerkinElmer),
144 and free [γ -33P] ATP was removed by washing with 3% phosphoric acid. The plates were dried, and 40 μ L
145 MicroScint0 (PerkinElmer) was added. Radioactivity was measured using a TopCount scintillation counter
146 (PerkinElmer).

147 Assays for tyrosine kinases were performed using the Alphascreen system (PerkinElmer) in
148 384-well plates at 25°C. The reaction conditions for these kinase assays were optimized for each kinase:
149 VEGF receptor 2 (VEGFR2; 19 ng/mL enzyme, 10 μ M ATP, 10-min reaction, PY-100-conjugated acceptor
150 beads [PY-100]); proto-oncogene tyrosine-protein kinase (SRC; 0.33 ng/mL enzyme, 2 μ mol/L ATP, 10-min
151 reaction, PY-100); IRK (100 ng/mL enzyme, 10 μ mol/L ATP, 60-min reaction, PT66); focal adhesion kinase
152 (FAK; 30 ng/mL enzyme, 2 μ mol/L ATP, 20-min reaction, PT66); ephrin receptor A5 (EphA5; 1 ng/mL
153 enzyme, 2 μ mol/L ATP, 10-min reaction, PY-100); Janus kinase 1 (JAK1; 100 ng/mL enzyme, 0.2 μ mol/L
154 ATP, 10-min reaction, PT66); and endothelial growth factor receptor (EGFR; 100 ng/mL enzyme, 1.0 μ mol/L
155 ATP, 10-min reaction, PT66). The enzyme reactions were performed in 50 mmol/L Tris-HCl (pH 7.5) with 5
156 mmol/L MnCl₂, 5 mmol/L MgCl₂, 0.01% Tween-20, 2 mmol/L dithiothreitol, 0.1 μ g/mL biotinylated
157 poly-GluTyr (4 : 1), and optimized concentrations of enzyme and ATP, as described. Prior to the initiation of
158 the kinase reaction, the compound and enzyme were incubated for 5 min at 25°C. The reaction was then
159 initiated by adding ATP. The reactions were stopped by the addition of 25 μ L of 100 mmol/L EDTA, 10
160 μ g/mL Alphascreen streptavidin donor beads (PerkinElmer), and 10 μ g/mL acceptor beads in 62.5 mmol/L
161 HEPES (pH 7.4), 250 mmol/L NaCl, and 0.1% bovine serum albumin. The plates were incubated in the dark
162 for > 12 h, followed by analysis using an EnVision plate reader (PerkinElmer).

163 Assays for phosphatidylinositol-4,5-bisphosphate 3-kinase α (PI3K α) were performed using a phospholipid
164 FlashPlate coated with 5 μ mol/L L- α -phosphatidyl-D-myo-inositol 4,5-diphosphate. The reaction conditions
165 were optimized for PI3K α (80 ng/well enzyme, 0.15 μ Ci/well of [γ -33P] ATP, 60-min reaction at 25°C), and
166 radioactivity was measured using a TopCount scintillation counter (PerkinElmer).

167 For kinome-wide profiling, kinase selectivity of GCN2iB was evaluated at 1 μ mol/L using a panel
168 of 468 kinases at DiscoverX (KINOMEScan). The platform employs an active site-directed competition

169 binding assay to quantitatively measure interactions between test compounds and kinases.

170

171 **Short interfering RNA**

172 ASNS or ATF4 siRNAs were purchased from GE Dharmacon (OnTARGETplus) or Thermo Fisher Scientific
173 (Silencer Select), respectively. Human Cell Death siRNA was purchased from Qiagen and used as a positive
174 control for transfection efficiency. The sequences of the sense siRNAs are shown below:

175 ASNS-1: 5'-GGG UAG AGA UAC AUA UGG A-3'; ASNS-2: 5'-UAU GUU GGA UGG UGU GUU U-3';

176 ASNS-3: 5'-GGU GAA AUC UAC AAC CAU A-3'; ATF4-1: 5'-GCC UAG GUC UCU UAG AUG A-3';

177 ATF4-2: 5'-CCC UGU UGG GUA UAG AUG A-3'; and ATF4-3: 5'-GUG AGA AAC UGG AUA AGA A-3'.

178

179 **Transfection and western blot analysis**

180 Adherent or floating cells were transfected with siRNAs using Lipofectamine RNAi MAX (Invitrogen) or
181 GenomeONE with inactivated Sendai virus envelope (Ishihara Sangyo), respectively. Western blot analysis
182 was performed as described in a previous study (Ref; 2).

183 The following antibodies were used for the western blot analysis: anti-phospho-Ser473-Akt (#4060,
184 1:1000), -ATF4 (#11815, 1:1000), -cleaved PARP (#5625, 1:1000), -eIF2 α (#5324, 1:2000),
185 -phospho-Ser51-eIF2 α (#3597, 1:1000), -phospho-Thr202/Tyr204-ERK (#4370, 1:1000), -GCN2 (#3302,
186 1:1000), -phospho-Thr183/Tyr185-JNK (#9251, 1:1000), -phospho-Thr180/Tyr182-p38 (#9211, 1:1000),
187 -PERK (#3192, 1:1000), -Sestrin2 (#8487, 1:1000), -S6K (#9202, 1:1000), and -phospho-Thr389-S6K
188 (#9234, 1:1000) (Cell Signaling Technology); anti-ASNS (#14681-1-AP, 1:2000) and -GADD34
189 (#10449-1-AP, 1:1000) (Proteintech); anti-HSP90 (#610419, 1:2000, BD Transduction Laboratories);
190 anti-phospho-Thr899-GCN2 (#ab75836, 1:1000, Abcam); and anti-puromycin (#MABE343, 1:1000,
191 Millipore). eIF2 α and HSP90 were used as loading controls.

192

193 **Amino acid measurement**

194 Cells, culture medium, tissue, and plasma ($N = 3$) were homogenized in ice-cold methanol using a
195 ShakeMaster Auto (BioMedical Science) and centrifuged at $15,000 \times g$ for 5 min. The supernatant was dried
196 by nitrogen stream and derivatized using N-methyl-N-(tert-butyldimethylsilyl) trifluoroacetamide. The
197 reaction mixture was injected into an Agilent 7890A series GC system in the split injection mode (10/1 [v/v])
198 using a GC injector 80 autosampler (Agilent Technologies). GC separation was performed using an Agilent
199 J&W GC column HP-5 ms (30 m \times 0.25 mm i.d., $df = 0.25 \mu\text{m}$) and a temperature gradient (100°C for 4 min,
200 from 100°C to 285°C at 4 °C/min, from 285°C to 325°C at 4 °C/min, and 325°C for 2 min) with a constant
201 flow of helium gas at 1 mL/min. The eluate was ionized by electron-impact ionization (70 eV) at an
202 ion-source temperature of 230°C and introduced into an Agilent 7010B triple-quadrupole mass spectrometer
203 (Agilent Technologies). Each target molecule was detected by selected ion monitoring, the parameters for
204 which were optimized using standard reagents.

205 For quantitation of amino acids, a standard solution was prepared by mixing all amino acids at
206 concentrations of 0.2, 1, 2, 10, 20, 100, and 200 nmol/L. Internal standard solution 1 (IS1) was prepared by

207 diluting with (U-13C3, U-15N)-cell-free amino acid mix (20 AA; Cambridge Isotope Laboratories) until the
208 total amino acid concentration reached 2 mg/mL. Internal standard solution 2 (IS2) was diluted with
209 (U-13C3, U-15N)-cysteine (5 $\mu\text{mol/L}$). Each standard solution (25 μL) was mixed with 50 μL of methanol,
210 which was used as the blank control, and 10 μL of IS1 or IS2. The mixture was dried, derivatized, and
211 analyzed using GC-MS. Quantitative reliability was confirmed by the linearity of the calibration curve ($R^2 >$
212 0.99) and the accuracy ($< 20\%$) and precision ($< 20\%$; $N = 6$) of the spike-and-recovery test.

213

214 **Gene expression data for cancer cell lines**

215 Data were collected from public databases associated with the Cancer Cell Line Encyclopedia and
216 GlaxoSmithKline. All data were obtained as CEL files and signal values were extracted using the MAS5.0
217 algorithm.

218

219 **Microarray analysis**

220 Total RNA was extracted using the RNeasy Miniprep kit (Qiagen), according to the manufacturer's protocol.
221 Preparation of cRNA, hybridization, and microarray scanning were performed using MacroGen, according to
222 the manufacturer's protocol (Agilent Technologies). Labeled cRNA was hybridized to Agilent SurePrint G3
223 human GE 8X60K microarrays (Agilent Technologies), which were immediately scanned using an Agilent
224 microarray scanner D (Agilent Technologies). The results of the microarray were obtained using Agilent
225 Feature Extraction software (v.11.0; Agilent Technologies). Pathway and upstream analyses were performed
226 using Ingenuity Pathway Analysis (Qiagen).

227

228 **Cell viability assay**

229 Cell viability was assessed using the CellTiter-Glo luminescent cell viability assay (Promega), according to
230 the manufacturer's protocol. Sigmoidal dose-response (variable slope) curves were fitted using a nonlinear
231 regression analysis. The IC_{50} or IC_{70} values of the chemical compounds or enzymes were calculated using
232 GraphPad Prism software v.6.

233

234 **Caspase 3/7 assay**

235 Caspase 3/7 activity was assessed using the Caspase-Glo 3/7 assay (Promega), according to the
236 manufacturer's protocol.

237

238 **Animal study**

239 A suspension of CCRF-CEM, HPB-ALL, MV-4-11, or SU.86.86 cells (1×10^7 cells/site) was subcutaneously
240 injected into the right flanks of 6-week-old female SCID mice (C.B17/Icr-scid/scid Jcl; CLEA). Tumor
241 volume was calculated as $\text{volume} = L \times l^2 \times 1/2$, where L represents the longest diameter across the tumor and
242 l represents the corresponding perpendicular distance. Body weight was also measured. To assess the
243 anti-tumor activity, mice with tumor mass $\sim 200 \text{ mm}^3$ were sorted into treatment groups ($N = 5/\text{group}$) (to
244 ensure similarity in mean tumor volume among the groups). The tumors were monitored and mice were

245 euthanized when an endpoint (defined as tumor volume > 2,000 mm³, severe ataxia, and body weight loss >
246 20% compared with the body weight on the day of randomization) was reached, or at the end of the study,
247 whichever came first. From the next day of randomization, GCN2 inhibitors or ASNase dissolved in distilled
248 water containing 0.5% methylcellulose or 5% glucose was orally or intraperitoneally administered to mice
249 bearing the xenografts for 7 to 10 days, respectively. T/C (%), an index of anti-tumor activity, was calculated
250 by comparing the mean change in tumor volume during the treatment period in the control and treated
251 groups. For western blot analysis, tumors were homogenized with Lysing Matrix I (MP Biomedicals) in a
252 lysis buffer (10% glycerol, 1% sodium dodecyl sulfate, and 62.5 mmol/L Tris-HCl [pH 7.5] with protease and
253 phosphatase inhibitors, cOMplete Mini and PhosSTOP, respectively; Sigma-Aldrich).

254 For the disseminated leukemia model, suspension of MOLT-3 cells (1×10^7 cells/head) was
255 inoculated in to SCID mice via the tail vein. Fourteen days after inoculation, mice were assigned into
256 treatment groups ($N = 7$ /group) randomly based on body weight. From the next day of randomization, the
257 compounds were administered to mice for 28 days. The survival rate was determined by the Kaplan-Meier
258 analysis.

259 The mice were housed and maintained in accordance with the institutional guidelines established by
260 the Institutional Animal Care and Use Committee, in a facility accredited by the American Association for
261 Accreditation of Laboratory Animal Care. All animal experimental protocols were approved by the
262 Institutional Animal Care and Use Committee.

263

264 **Statistical analysis**

265 To assess the *in vitro* anti-proliferative effects of the GCN2 inhibitors in the presence or absence of ASNase
266 for the cell-panel study, a paired *t*-test comparison was performed using the GraphPad Prism software (v.6;
267 GraphPad Software). To assess the correlation between variables, linear regression analysis was performed,
268 and the correlation coefficient was determined by Pearson's correlation using the GraphPad Prism software.
269 To assess the *in vivo* antitumor effect of the treatment methods, Dunnett's multiple-comparison test was
270 performed, followed by one-way ANOVA with T/C (%) values. A two-way ANOVA was performed to
271 examine the primary effects of treatment with the GCN2 inhibitor or the ASNase, as well as the
272 combinatorial effect of treatments with T/C values. The combinatorial effect was assessed using the
273 following criteria: 1) synergistic effect, defined as the significant differences observed in the combined effect
274 of treatment with a GCN2 inhibitor and ASNase, along with the enhancements in effect caused by each
275 treatment; 2) additive effect, defined as significant differences observed in the primary effect of treatment
276 with a GCN2 inhibitor or ASNase, but not in their combined form; and 3) antagonistic effect, defined as the
277 significant differences observed in the combined effect of treatment with a GCN2 inhibitor and ASNase,
278 along with the reductions in effect caused by each treatment. To assess the effect of treatment on survival
279 curve in the disseminated model, log-rank test was performed between vehicle-treated group and treatment
280 groups. Cox regression analysis was performed to examine the main effect of a GCN2 inhibitor and ASNase,
281 and effect of interaction between the 2 treatments with survival curves using SAS version 9.1.3 (SAS
282 Institute Inc.). Other statistical analyses for *in vivo* studies were conducted using EXXSUS (Release 8.0; CAC

283 Croit Corporation). The different groups were compared using Bonferroni's multiple-comparison test, unless
 284 otherwise mentioned. Differences were considered significant when $P < 0.05$.

285

286 **Cell lines and culture**

287 Cell lines were cultured at 37°C with 5% CO₂ in the recommended medium supplemented with 10%–20%
 288 FBS. The cell lines for which the asparagine-free medium (e.g., Dulbecco's modified Eagle's medium) was
 289 recommended were maintained in RPMI1640 medium. We established two ASNase-resistant cell lines
 290 (MOLT-4-R1 and-R2; two replicates) by treating them with increasing concentrations of ASNase (0.00001–1
 291 U/mL) for 4 months. All cell lines were stocked after *Mycoplasma* testing (at the Central Institute for
 292 Experimental Animals) and used within 2 months of resuscitation. The authors did not perform any
 293 authentication. Detailed information on the cell lines is provided as follows.

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Cell line	Cell type	Source	Year
CMK-11-5	Acute myelogenous leukemia	JCRB	2014
EOL-1	Acute myelogenous leukemia	DSMZ	2014
GF-D8	Acute myelogenous leukemia	DSMZ	2014
HEL.92.1.7	Acute myelogenous leukemia	ATCC	2014
HL-60	Acute myelogenous leukemia	ATCC	2014
HNT-34	Acute myelogenous leukemia	RIKEN	2015
Kasumi-1	Acute myelogenous leukemia	JCRB	2014
KG-1	Acute myelogenous leukemia	ATCC	2014
KG-1a	Acute myelogenous leukemia	RIKEN	2015
KO52	Acute myelogenous leukemia	JCRB	2014
M-07e	Acute myelogenous leukemia	DSMZ	2014
MKPL-1	Acute myelogenous leukemia	JCRB	2014
ML-1	Acute myelogenous leukemia	ECACC	2015
ML-2	Acute myelogenous leukemia	DSMZ	2014
MOLM-16	Acute myelogenous leukemia	DSMZ	2014
MV-4-11	Acute myelogenous leukemia	ATCC	2016
NKM-1	Acute myelogenous leukemia	JCRB	2014
NOMO-1	Acute myelogenous leukemia	JCRB	2014
OCI-AML3	Acute myelogenous leukemia	DSMZ	2014
OCI-M2	Acute myelogenous leukemia	DSMZ	2014
PL-21	Acute myelogenous leukemia	JCRB	2014
SKM-1	Acute myelogenous leukemia	JCRB	2014
SKNO-1	Acute myelogenous leukemia	JCRB	2015
TF-1	Acute myelogenous leukemia	ATCC	2014

TF-1a	Acute myelogenous leukemia	ATCC	2014
THP-1	Acute myelogenous leukemia	ATCC	2014
BALL-1	Acute lymphoblastic leukemia	JCRB	2015
CCRF-CEM	Acute lymphoblastic leukemia	ATCC	2014
CCRF-HSB-2	Acute lymphoblastic leukemia	JCRB	2015
CCRF-SB	Acute lymphoblastic leukemia	JCRB	2015
DND-41	Acute lymphoblastic leukemia	DSMZ	2014
HAL-01	Acute lymphoblastic leukemia	RIKEN	2014
HPB-ALL	Acute lymphoblastic leukemia	DSMZ	2014
Jurkat	Acute lymphoblastic leukemia	RIKEN	2014
Loucy	Acute lymphoblastic leukemia	ATCC	2015
MOLT-3	Acute lymphoblastic leukemia	ATCC	2014
MOLT-4	Acute lymphoblastic leukemia	ATCC	2014
NALM-6	Acute lymphoblastic leukemia	RIKEN	2014
PALL-2	Acute lymphoblastic leukemia	JCRB	2015
Peer	Acute lymphoblastic leukemia	JCRB	2015
Reh	Acute lymphoblastic leukemia	ATCC	2014
RS4;11	Acute lymphoblastic leukemia	ATCC	2015
SUP-B15	Acute lymphoblastic leukemia	ATCC	2015
TALL-1	Acute lymphoblastic leukemia	DSMZ	2014
Tanoue	Acute lymphoblastic leukemia	RIKEN	2015
TMD5	Acute lymphoblastic leukemia	JCRB	2015
AsPC-1	Pancreatic cancer	ATCC	2011
BxPC-3	Pancreatic cancer	ATCC	2013
Capan-1	Pancreatic cancer	ATCC	2011
Capan-2	Pancreatic cancer	ATCC	2011
CFPAC-1	Pancreatic cancer	ATCC	2011
DAN-G	Pancreatic cancer	DSMZ	2011
HPAC	Pancreatic cancer	ATCC	2011
HPAF-II	Pancreatic cancer	ATCC	2014
HuP-T3	Pancreatic cancer	ECACC	2011
HuP-T4	Pancreatic cancer	ECACC	2016
KP-4	Pancreatic cancer	JCRB	2011
Panc 02.03	Pancreatic cancer	ATCC	2011
Panc 04.03	Pancreatic cancer	ATCC	2011
Panc 05.04	Pancreatic cancer	ATCC	2011
PK-45H	Pancreatic cancer	RIKEN	2011

PK-59	Pancreatic cancer	RIKEN	2011
PL45	Pancreatic cancer	ATCC	2011
SU.86.86	Pancreatic cancer	ATCC	2011
SUIT2	Pancreatic cancer	JCRB	2011
TCC-PAN2	Pancreatic cancer	JCRB	2011
COLO-205	Colorectal cancer	ATCC	2014
HCT-116	Colorectal cancer	ATCC	2013
HCT-15	Colorectal cancer	ATCC	2012
HT-29	Colorectal cancer	ATCC	2013
SW1417	Colorectal cancer	ATCC	2014
SW48	Colorectal cancer	ATCC	2013
SW620	Colorectal cancer	ATCC	2014
SW948	Colorectal cancer	ATCC	2014
T84	Colorectal cancer	ATCC	2013
OCI-LY3	Diffuse large B-cell lymphoma	DSMZ	2015
Pfeiffer	Diffuse large B-cell lymphoma	ATCC	2012
SU-DHL-10	Diffuse large B-cell lymphoma	DSMZ	2012
SU-DHL-2	Diffuse large B-cell lymphoma	ATCC	2015
SU-DHL-4	Diffuse large B-cell lymphoma	DSMZ	2013
Toledo	Diffuse large B-cell lymphoma	ATCC	2012
WSU-DLCL2	Diffuse large B-cell lymphoma	DSMZ	2013
A549	Non-small cell lung cancer	ATCC	2013
NCI-H2228	Non-small cell lung cancer	ATCC	2013
NCI-H23	Non-small cell lung cancer	ATCC	2012
NCI-H460	Non-small cell lung cancer	ATCC	2013
NCI-H522	Non-small cell lung cancer	ATCC	2012
NCI-H661	Non-small cell lung cancer	ATCC	2014
SW1271	Non-small cell lung cancer	ATCC	2014
A2780	Ovarian cancer	ECACC	2014
Caov-3	Ovarian cancer	ATCC	2013
Caov-4	Ovarian cancer	ATCC	2015
OVCAR-3	Ovarian cancer	ATCC	2013
PA-1	Ovarian cancer	ATCC	2014
SKOV-3	Ovarian cancer	ATCC	2013
HepG2	Hepatocellular carcinoma	ATCC	2013
HLE	Hepatocellular carcinoma	JCRB	2016
Huh-7	Hepatocellular carcinoma	JCRB	2015

JHH-4	Hepatocellular carcinoma	JCRB	2016
Li-7	Hepatocellular carcinoma	RIKEN	2014
SK-HEP-1	Hepatocellular carcinoma	ATCC	2014
CAMA-1	Breast cancer	ATCC	2013
MCF7	Breast cancer	ATCC	2014
MDA-MB-361	Breast cancer	ATCC	2013
MDA-MB-468	Breast cancer	ATCC	2014
T47D	Breast cancer	ATCC	2014
SK-MEL-2	Melanoma	ATCC	2014
SK-MEL-24	Melanoma	ATCC	2013
SK-MEL-28	Melanoma	ATCC	2014
SK-MEL-5	Melanoma	ATCC	2014
NCI-H929	Multiple myeloma	ATCC	2012
RPMI-8226	Multiple myeloma	JCRB	2014
U266B1	Multiple myeloma	ATCC	2012
U-2-OS	Osteosarcoma	ATCC	2014

Abbreviations	Full name
ATCC	American Type Culture Collection
DSMZ	Deutsche Sammlung von Mikroorganismen und Zellkulturen
ECACC	The European Collection of Authenticated Cell Cultures
JCRB	Japanese Collection of Research Bioresources
RIKEN	RIKEN

296 **Supplementary Figures**

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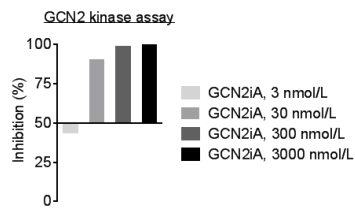
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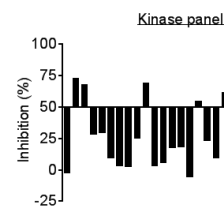
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Kinase	IC ₅₀ (nmol/L)	Inh. (%)	GCN2iA (nmol/L)
GCN2	4.0	44	3
		90	30
		98	300
		100	3,000

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Family	Kinase	Inh. @ 1 μmol/L (%)	Family	Kinase	Inh. @ 1 μmol/L (%)
TK	EGFR	-2	AGC	PKA	19
	VEGFR2	72		AKT1	-5
	cMET	67		Aurora B	54
	SRC	29		ROCK1	24
	FAK	30		PKCζ	10
	IRK	10	CAMK	CHK1	61
	EphA5	4		MAPKAP2	0
	JAK1	5	CMGC	ERK1	3
TKL	IRAK4	26		CDK2	61
	TrkA	68	STE	p38α	0
STE	MEK1	-2		GSK3β	95
	ASK1	-9	Others	CDC7	10
CK1	CK1δ	2		PLK1	63
			Lipid kinase	PI3Kα	18

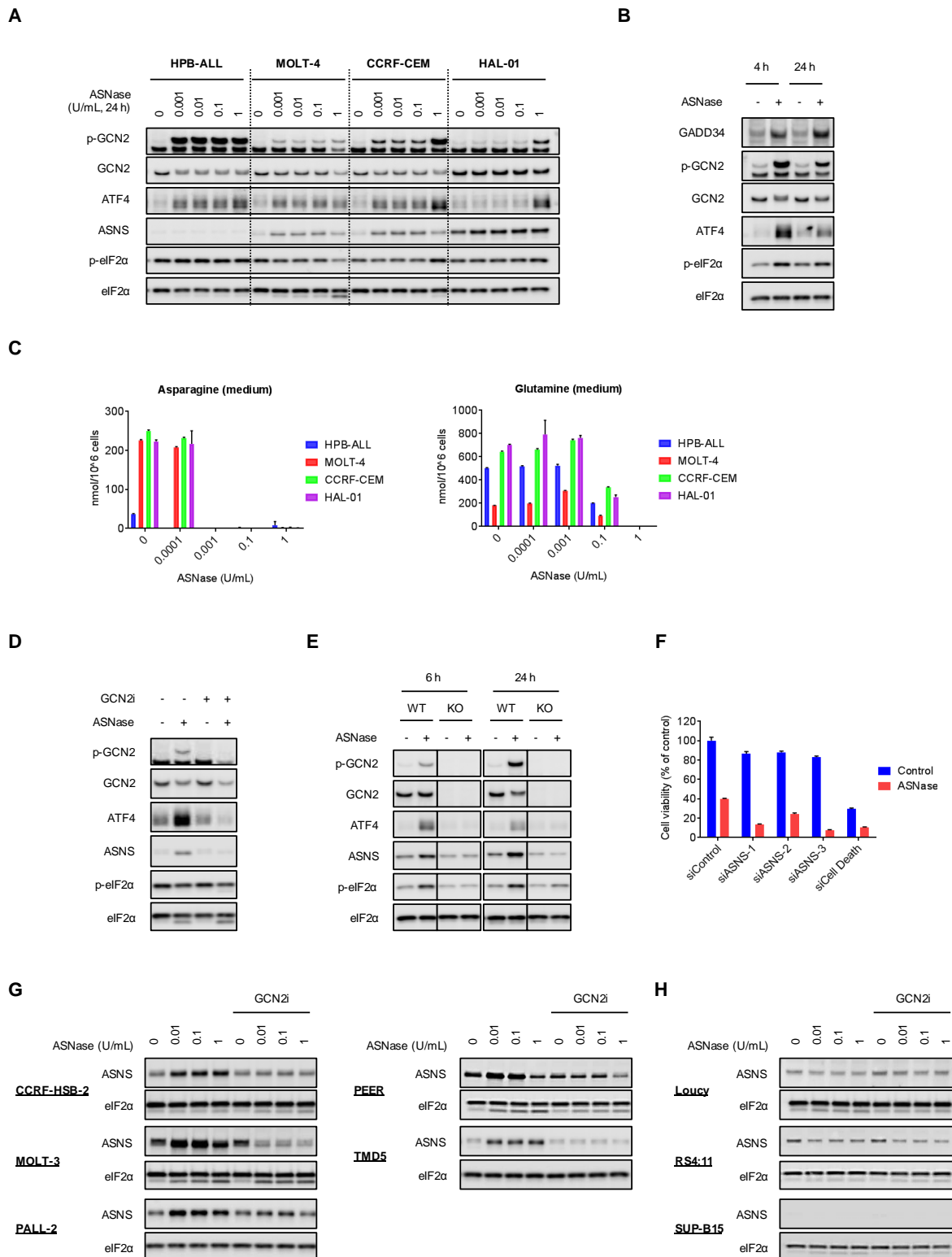
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308 **Fig. S1.** Potency and kinase selectivity of GCN2iA. (A) GCN2 kinase assay using GCN2iA. (B) Kinase
309 selectivity of GCN2iA in a focused kinase panel.



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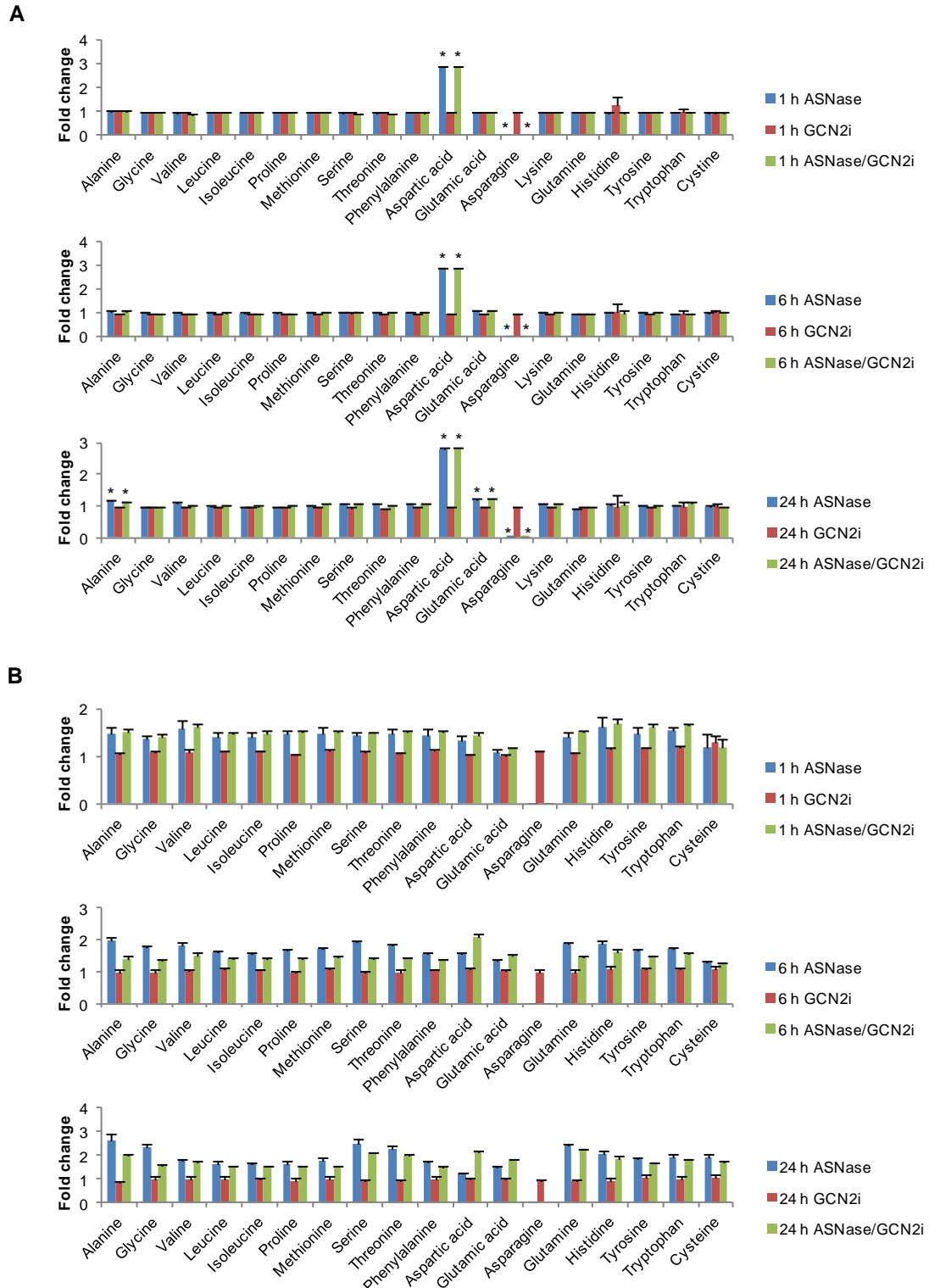
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Fig. S2. Characterization of ALL and MEF cells. (A) ALL cells were treated with ASNase at the indicated concentrations for 24 h. Cell lysates were analyzed by western blot. (B) CCRF-CEM cells were treated with 1 mU/mL ASNase as indicated. Cell lysates were analyzed by western blot. (C) ALL cells were treated with

316 ASNase at the indicated concentrations for 24 h and asparagine or glutamine levels in the culture medium
317 were measured by GC-MS (mean with SD; $N = 3$). (D) MOLT-4 cells were treated with 1 mU/mL ASNase
318 and/or 1 $\mu\text{mol/L}$ GCN2iA as indicated for 24 h. Cell lysates were analyzed by western blot. (E) MEF cells
319 (GCN2-WT or -KO) were treated with 1 mU/mL ASNase as indicated. Cell lysates were analyzed by western
320 blot. (F) CCRF-CEM cells were transfected with siRNA as indicated; 24 h after transfection, cells were
321 treated with 1 mU/mL ASNase for 72 h. Cell viability was measured (mean with SD; $N = 3$). (G) ALL cells
322 that were intermediately insensitive to ASNase were treated with ASNase and/or 1 $\mu\text{mol/L}$ GCN2iA as
323 indicated for 24 h. Cell lysates were analyzed by western blot. (H) ASNase-hypersensitive ALL cells were
324 treated with ASNase and/or 1 $\mu\text{mol/L}$ GCN2iA as indicated for 24 h. Cell lysates were analyzed by western
325 blot.
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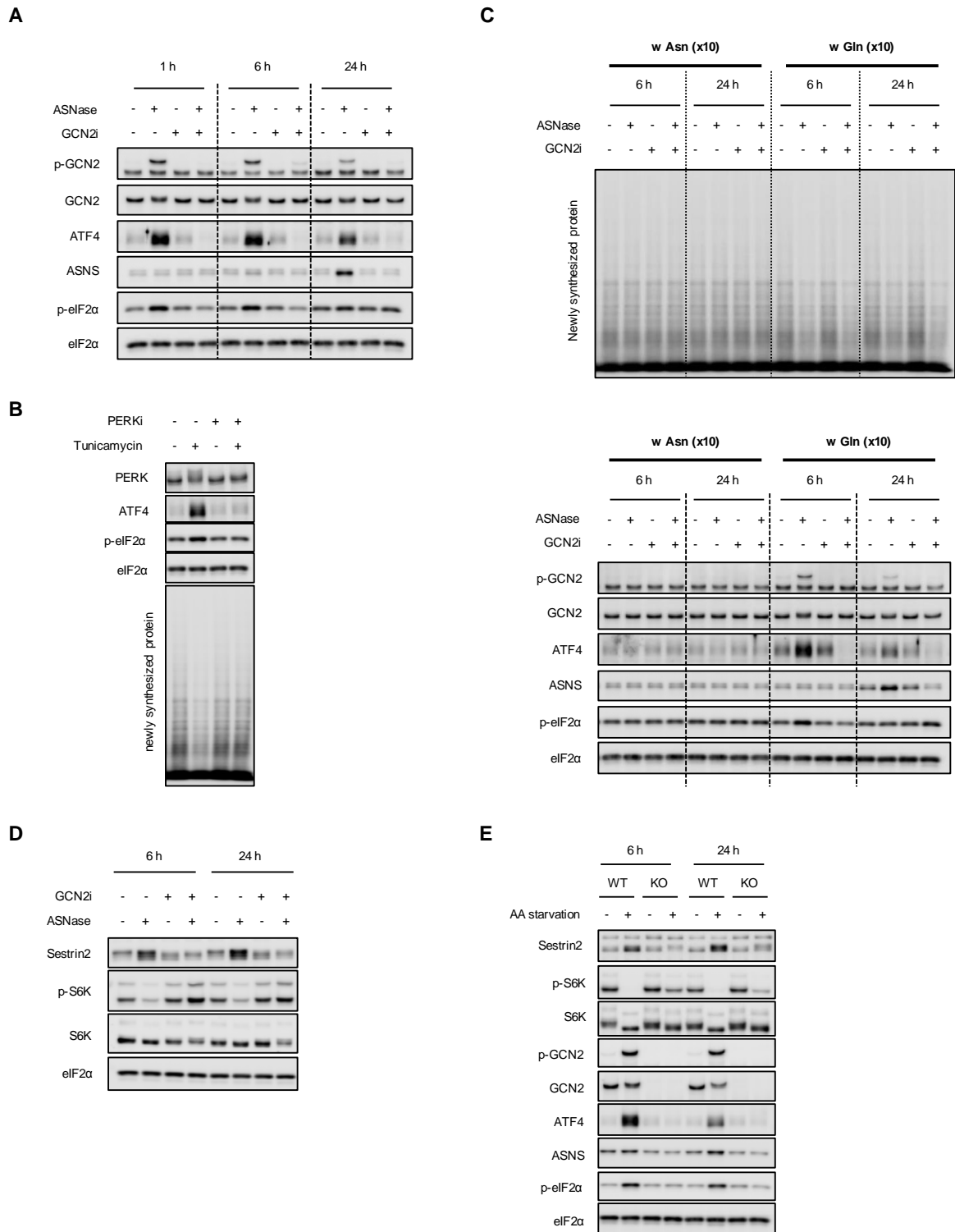
329 **Fig. S3.** Effects of GCN2 inhibition on extracellular/intracellular amino acid levels in the presence of
 330 ASNase. CCRF-CEM cells were treated with 1 μ M ASNase and/or 1 μ M GCN2iA as indicated.

331 Amino acid levels in the culture medium (A) or in the cells (B) were measured by GC-MS (mean with SD; N

332 = 3). * $P < 0.01$.

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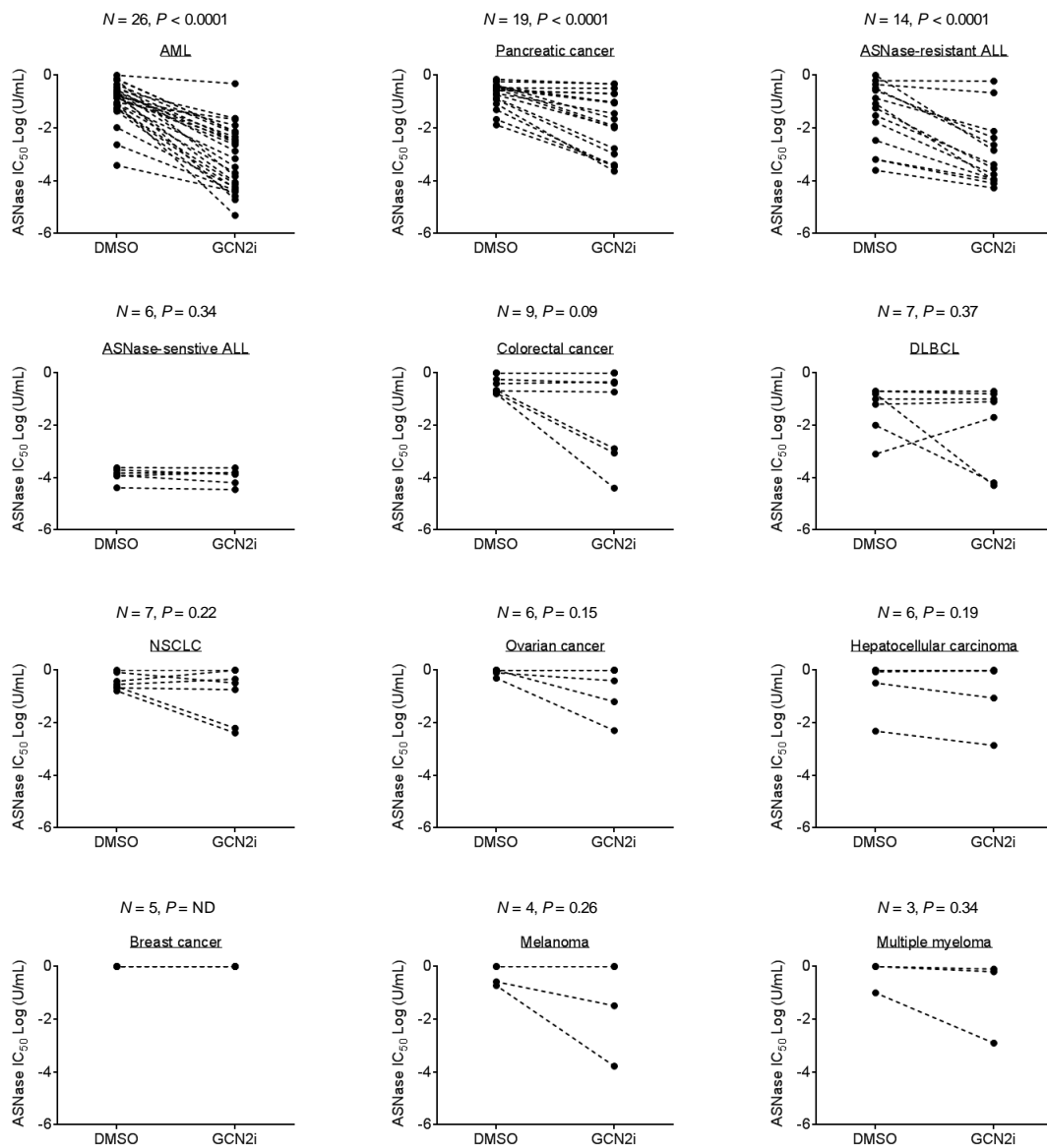
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338 **Fig. S4.** Suppression of protein translation by GCN2 inhibition in the presence of ASNase. (A) CCRF-CEM
 339 cells were treated with 1 mU/mL ASNase and/or 1 μmol/L GCN2iA as indicated. Cells were then treated with

340 10 $\mu\text{mol/L}$ puromycin for 10 min before harvesting. Cell lysates were analyzed by western blot. (B)
341 CCRF-CEM cells were treated with 5 $\mu\text{g/mL}$ tunicamycin and/or 1 $\mu\text{mol/L}$ PERK inhibitor as indicated for
342 1.5 h. Cells were then treated with 10 $\mu\text{mol/L}$ puromycin for 10 min before harvesting. Cell lysates were
343 analyzed by western blot. (C) CCRF-CEM cells were treated with 1 mU/mL ASNase and/or 1 $\mu\text{mol/L}$
344 GCN2iA, along with supraphysiological levels of asparagine (10 \times : 4.3 mmol/L) or glutamine (10 \times : 20
345 mmol/L) as indicated. Cells were then treated with 10 $\mu\text{mol/L}$ puromycin for 10 min before being harvested.
346 Cell lysates were analyzed by western blot using an anti-puromycin antibody to detect newly synthesized
347 proteins. (D) CCRF-CEM cells were treated with 1 mU/mL ASNase and/or 1 $\mu\text{mol/L}$ GCN2iA as indicated.
348 Cell lysates were analyzed by western blot. (E) MEF cells (GCN2-WT or -KO) were treated with amino
349 acid-free medium as indicated. Cell lysates were analyzed by western blot.



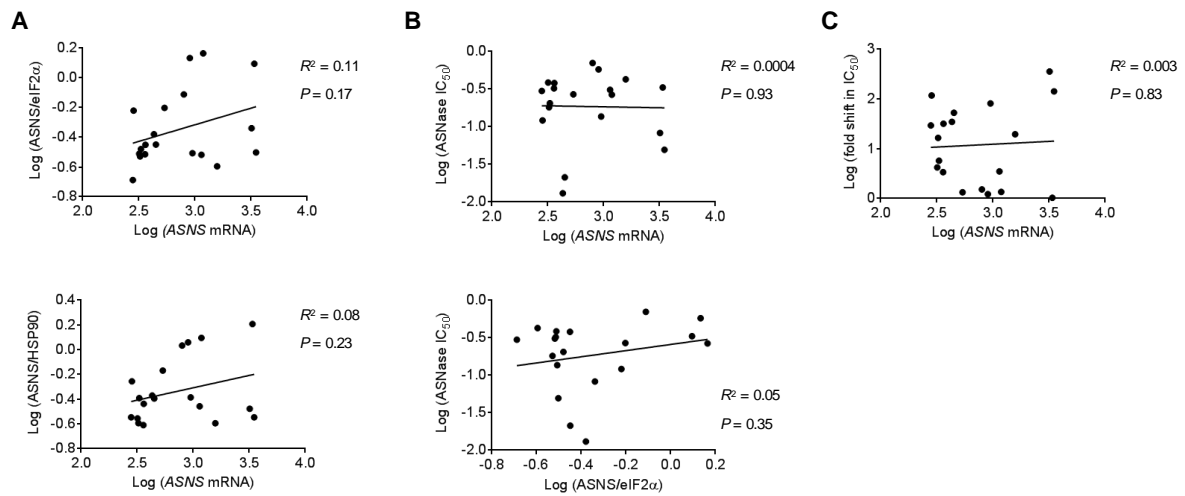
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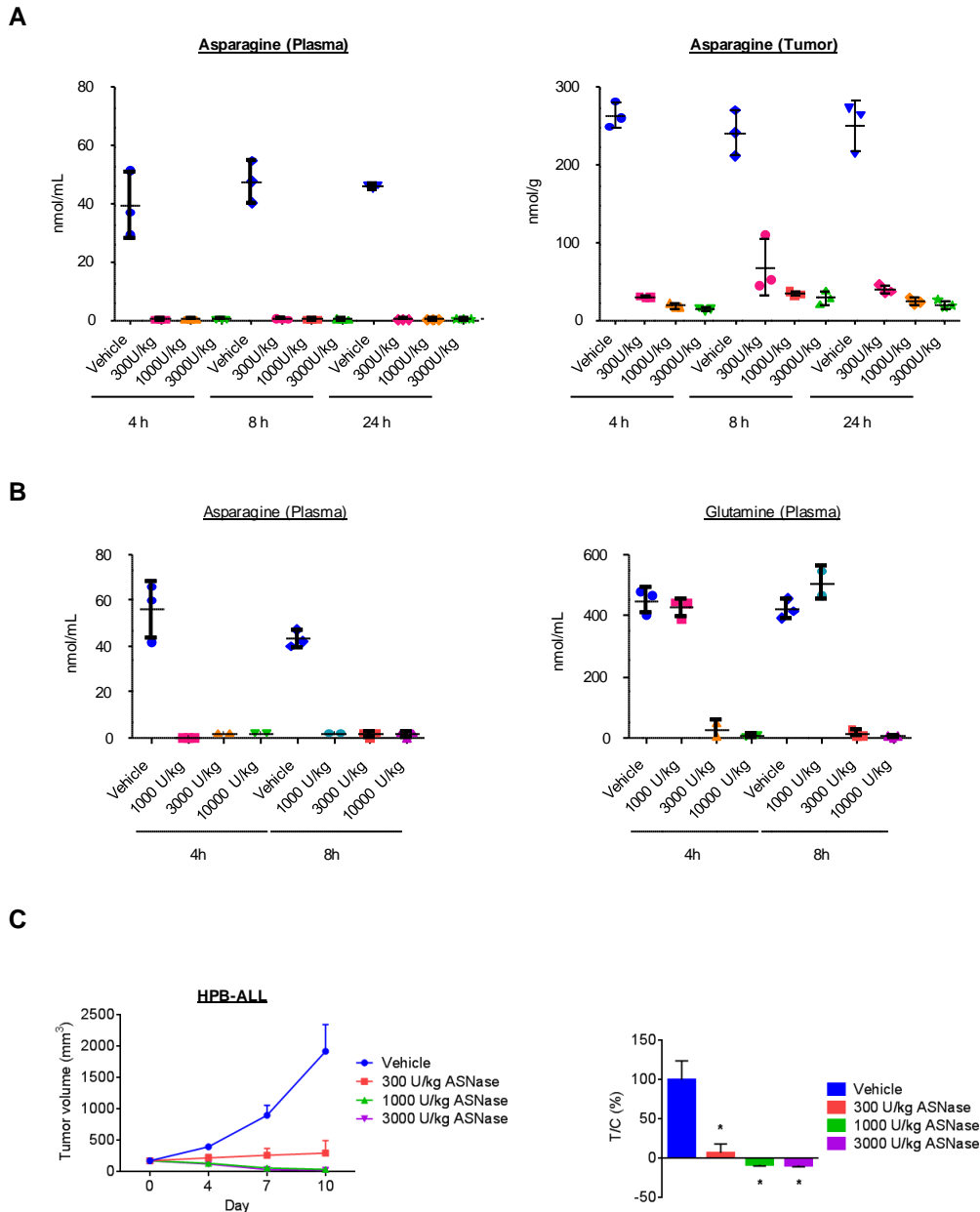
354 **Fig. S5.** *In vitro* antiproliferative effects of ASNase-GCN2iA combination treatment in various types of
 355 cancer cells. Cell lines of the indicated cancer types were treated with ASNase (0.000001–1 U/mL) and/or 1
 356 $\mu\text{mol/L}$ GCN2iA for 72 h. The cell viability was measured and the mean IC_{50} value of ASNase was calculated
 357 ($N = 3$). Plots for individual cell lines are connected by dotted lines. To assess the combined effects, a paired
 358 *t*-test was performed. DLBCL, diffuse large cell B-cell lymphoma; NSCLC, non-small cell lung cancer.

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Fig. S6. Correlation between ASNS expression and the combined effects of ASNase treatment with GCN2 inhibition in pancreatic cancer cells. (A) Correlation between mRNA and protein levels of ASNS (normalized against eIF2 α or HSP90 levels) was analyzed. (B) Correlation between IC₅₀ value of ASNase and mRNA or protein levels of ASNS (normalized against eIF2 α levels) was analyzed. (C) Correlation between the combined effects of ASNase treatment with GCN2iA inhibition (fold-change in IC₅₀ value) and ASNS mRNA levels (normalized against eIF2 α level) was analyzed. Linear regression analysis was performed, and *R*- and *P*-values determined by Pearson's correlation are indicated. PL-45 cells were excluded from the analysis owing to their slow growth during the 72-h culture for the cell viability assay.



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383 **Fig. S7.** *In vivo* depletion of asparagine or glutamine in mice by ASNase administration. (A) Mice with

384 CCRF-CEM xenografts were treated with ASNase at the indicated doses for 4, 8, or 24 h. Asparagine levels

385 in plasma or tumors were measured by GC-MS. Plots represent values from three biological replicates with

386 SD. (B) Mice were treated once daily with ASNase at the indicated doses for 7 days. The asparagine and

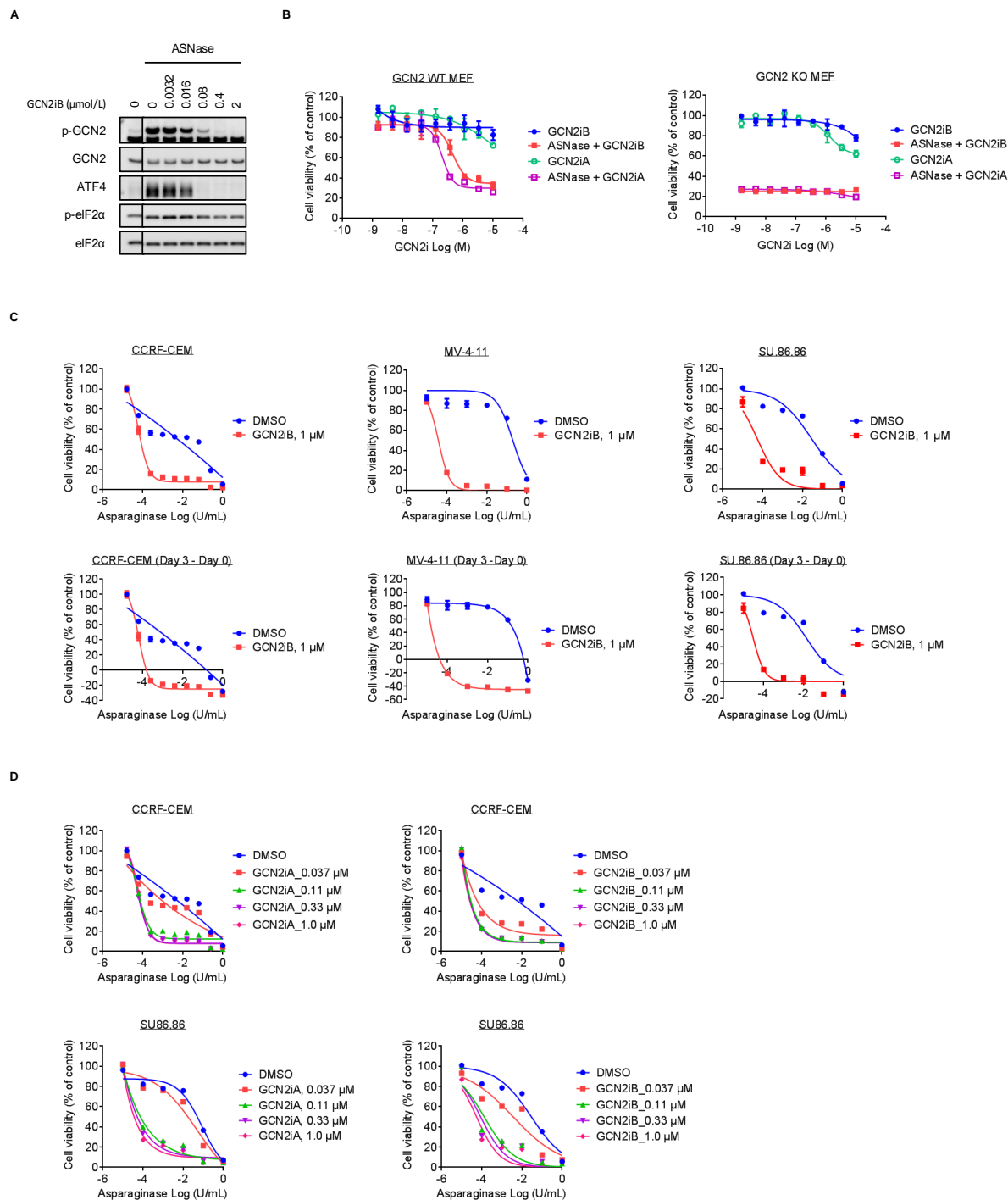
387 glutamine levels in plasma were measured with GC-MS 4 or 8 h after the final dose. Plots represent values of

388 two or three biological replicates with SD. (C) Mice bearing HPB-ALL xenografts were treated once daily

389 with ASNase at the indicated doses for 10 days. Left, Tumor growth curves; Right, T/C values on day 10.

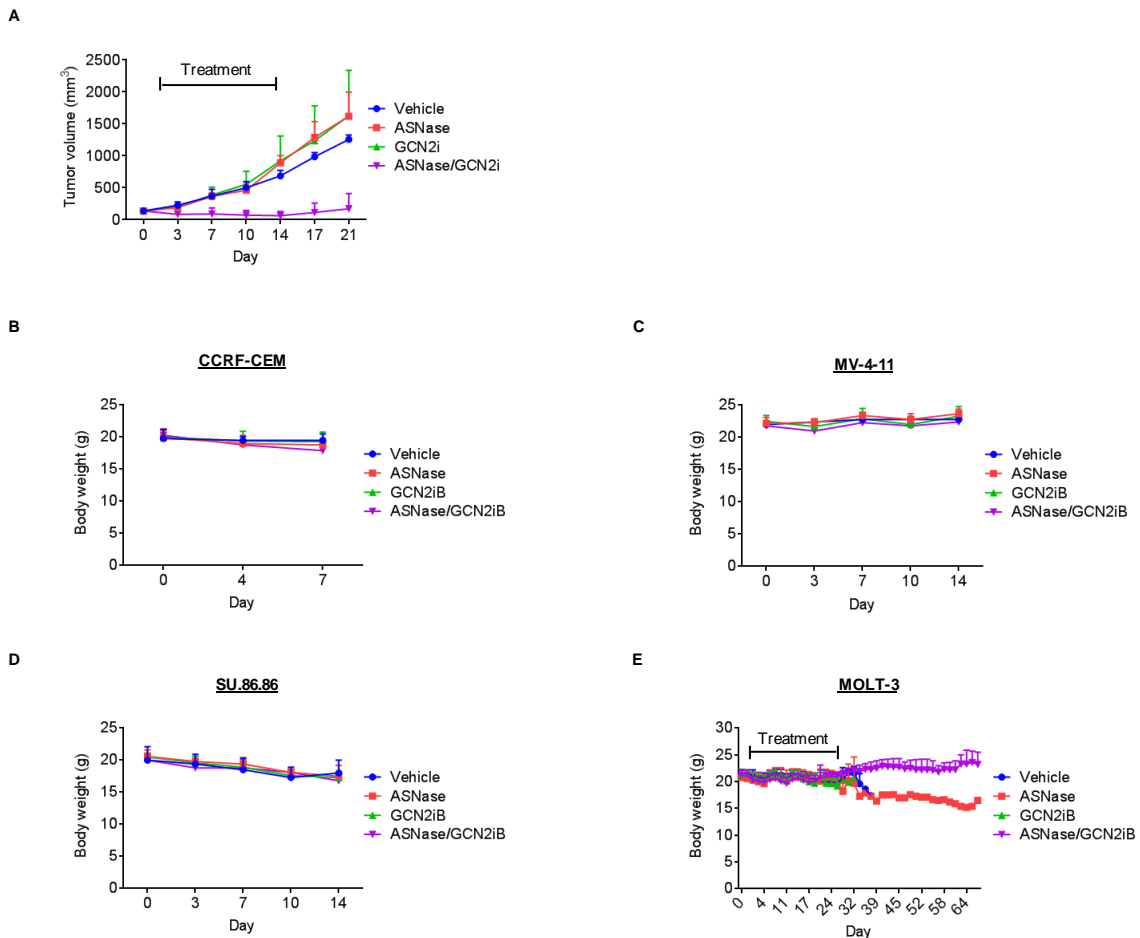
390 Day 1 indicates the beginning of treatment. Data show mean tumor volume or T/C values with SD ($N = 5$).

391 Dunnett's multiple-comparison test was performed; $*P < 0.0001$ (compared with vehicle-treated control).



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Fig. S8. *In vitro* characterization of GCN2iB. (A) CCRF-CEM cells were treated with 1 mU/mL ASNase and/or GCN2iB as indicated for 4 h. Cell lysates were analyzed by western blot. (B) MEF cells (GCN2-WT or -KO) were treated with 1 mU/mL ASNase and/or GCN2 inhibitors as indicated for 72 h. Cell viability was measured (mean with SD; $N = 3$). (C) CCRF-CEM, MV-4-11, and SU.86.86 cells were treated with ASNase and/or 1 μmol/L GCN2iB as indicated for 72 h. Cell viability was measured at day 0 and day 3 (mean with SD; $N = 3$). (D) CCRF-CEM and SU.86.86 cells were treated with ASNase and/or GCN2 inhibitors as indicated for 72 h. Cell viability was measured (mean with SD; $N = 3$).

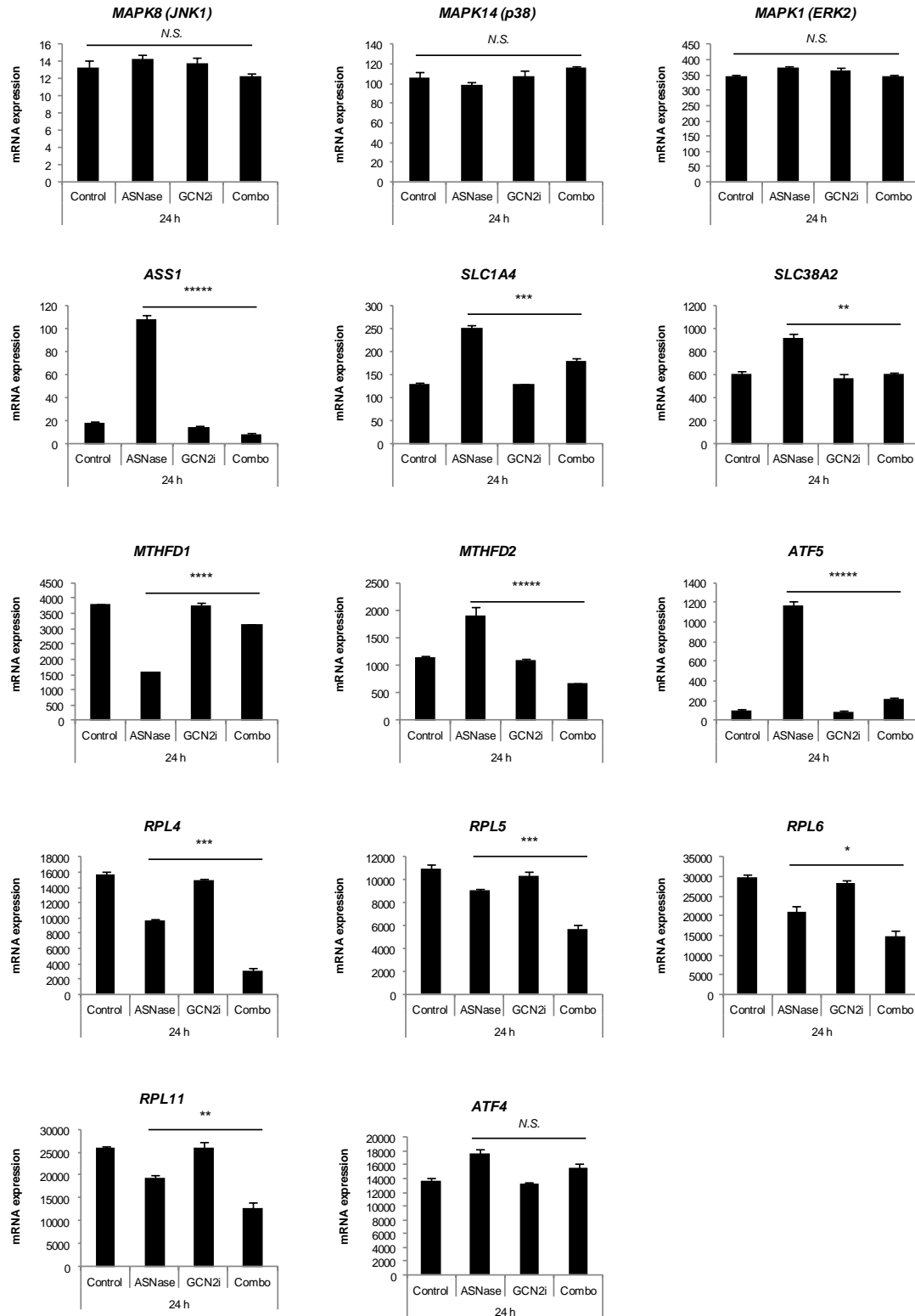


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403 **Fig. S9.** Changes in the body weight of mice. (A) Mice bearing MV-4-11 xenografts were treated first 3
 404 days a week with GCN2iB (10 mpk, twice a day) and/or ASNase (1,000 U/kg, once a day) as indicated for 14
 405 days. Data represent mean tumor volume with SD ($N = 5$). Tumor volume was measured until 1 week after
 406 drug cessation. (B) Mice bearing CCRF-CEM xenografts were treated daily with GCN2iB (10 mpk, twice a
 407 day) and/or ASNase (1,000 U/kg, once a day) as indicated for 7 days. (C) Mice bearing MV-4-11 xenografts
 408 were treated first 3 days a week with GCN2iB (10 mpk, twice a day) and/or ASNase (1,000 U/kg, once a day)
 409 as indicated for 14 days. (D) Mice bearing SU.86.86 xenografts were treated first 3 days a week with
 410 GCN2iB (10 mpk, twice a day) and/or ASNase (1,000 U/kg, once a day) as indicated for 14 days. Data
 411 represent mean body weight with SD ($N = 5$). (E) MOLT-3 cells were inoculated into SCID mice via the tail
 412 vein at 14 days before randomization. From the next day of randomization, mice were treated first 3 days a
 413 week with GCN2iB (10 mpk, twice a day) and/or ASNase (1,000 U/kg, once a day) as indicated for 28 days.
 414 Data represent mean body weight with SD ($N = 7$).

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 417 **Fig. S10.** Gene expression analysis of previously identified factors that determine ASNase sensitivity.
 418 CCRF-CEM cells were treated with 1 μM ASNase and/or 1 μM GCN2iA for 24 h, and gene
 419 expression levels were determined by microarray analysis (mean with SD; $N = 3$). * $P < 0.01$; ** $P < 0.001$;
 420 *** $P < 0.0001$; **** $P < 0.00001$; ***** $P < 0.000001$; and ***** $P < 0.0000001$. N.S., not significant ($P >$
 421 0.05).

422 **Supplementary Tables**423 **Table 1.** *In vitro* effects of combined treatment with ASNase and GCN2iA inhibition on the proliferation of

424 ALL cells.

ALL cell line	Log (ASNase IC ₅₀)			Log (ASNase IC ₇₀)			Log (ASNS mRNA)	Log (ASNS/eIF2α)	ASNase sensitivity
	DMSO	GCN2iA	Fold change	DMSO	GCN2iA	Fold change			
BALL-1	-0.35	-0.66	0.31	-0.23	-0.57	0.34	Not available	-0.29	Hyperinsensitive
CCRF-CEM	-1.78	-3.76	1.98	-1.06	-3.81	2.75	1.98	-0.92	Intermediately insensitive
CCRF-HSB-2	-3.19	-4.10	0.91	-2.26	-3.95	1.69	Not available	-0.77	Intermediately insensitive
DND-41	-3.71	-3.88	0.17	-3.68	-3.66	-0.02	1.66	-1.10	Hypersensitive
HAL-01	-0.87	-2.12	1.26	-0.30	-0.81	0.51	Not available	-0.10	Hyperinsensitive
HPB-ALL	-3.83	-3.81	-0.01	-3.72	-3.72	0.00	2.09	-1.28	Hypersensitive
Jurkat	-1.24	-3.54	2.30	-0.70	-2.76	2.06	3.06	-0.45	Intermediately insensitive
Loucy	-3.94	-3.80	-0.13	-3.76	-3.58	-0.18	1.43	-1.27	Hypersensitive
MOLT-3	-2.47	-3.95	1.48	-1.22	-3.84	2.62	Not available	-1.20	Intermediately insensitive
MOLT-4	-3.19	-3.97	0.78	-2.47	-3.79	1.33	2.10	-0.96	Intermediately insensitive
NALM-6	-0.57	-2.37	1.81	-0.10	-1.28	1.17	2.68	-0.27	Hyperinsensitive
PALL-2	-1.53	-3.39	1.86	-0.20	-2.49	2.29	Not available	-0.65	Intermediately insensitive
PEER	-3.60	-4.27	0.67	-2.72	-4.12	1.40	2.41	-0.99	Intermediately insensitive
Reh	-1.08	-3.98	2.90	-0.03	-2.68	2.65	2.63	-0.68	Intermediately insensitive
RS4;11	-3.91	-4.20	0.28	-3.76	-4.04	0.28	1.74	-1.49	Hypersensitive
SUP-B15	-4.39	-4.46	0.07	-4.29	-4.40	0.11	1.91	-1.40	Hypersensitive
SUP-T1	-0.49	-2.64	2.15	-0.02	-1.42	1.41	2.53	-0.46	Hyperinsensitive
TALL-1	-3.62	-3.63	0.00	-3.60	-3.60	0.00	2.12	-1.50	Hypersensitive
Tanoue	-0.20	-0.22	0.02	0.00	0.00	0.00	3.45	-0.09	Hyperinsensitive
TMD5	0.00	-2.85	2.85	0.00	-1.71	1.71	Not available	-1.28	Intermediately insensitive

425 NOTE: ALL cell lines were treated with ASNase (0.00001–1 U/mL) and/or GCN2iA (1 μmol/L). The IC₅₀426 or IC₇₀ value of ASNase, fold change in IC₅₀ or IC₇₀ value after GCN2iA treatment, ASNS mRNA427 expression, and ASNS protein expression are shown at log₁₀ scale. For ASNase sensitivity, cells are

428 categorized as follows.

429 Hypersensitive; both IC₅₀ and IC₇₀ < -3 on the log₁₀ scale

430 Intermediately insensitive; $-3 < IC_{50}$ or $IC_{70} < -1$ on the \log_{10} scale

431 Hyperinsensitive; both IC_{50} and $IC_{70} > -1$ on the \log_{10} scale

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433 **Table 2.** *In vitro* effects of combined treatment with ASNase and GCN2 inhibition on the proliferation of
 434 pancreatic cancer cells.

Pancreatic cancer cell line	Log (ASNase IC ₅₀)			Log (ASNS mRNA)	Log (ASNS/eIF2α)
	DMSO	GCN2iA	Fold change		
AsPC-1	-1.08	-3.64	-2.55	3.51	-0.34
BxPC-3	-0.49	-1.02	-0.53	2.56	-0.51
Capan-1	-0.57	-0.70	-0.13	3.07	0.17
Capan-2	-0.42	-1.92	-1.50	2.56	-0.45
CFPAC-1	-0.24	-0.32	-0.09	2.96	0.13
DAN-G	-0.57	-0.69	-0.12	2.73	-0.20
HPAC	-0.74	-1.96	-1.22	2.51	-0.53
HPAF-II	-0.15	-0.33	-0.18	2.90	-0.11
HuP-T3	-0.52	-1.99	-1.47	2.45	-0.69
HuP-T4	-0.86	-2.78	-1.91	2.98	-0.51
KP4	-0.48	-0.49	-0.01	3.53	0.10
Panc 02.03	-0.69	-1.45	-0.76	2.52	-0.48
Panc 04.03	-0.51	-1.05	-0.54	3.06	-0.52
Panc 05.04	-1.88	-3.43	-1.54	2.64	-0.38
PK-45H	-0.41	-1.04	-0.62	2.50	-0.51
PK-59	-0.37	-1.66	-1.29	3.20	-0.60
SU.86.86	-1.31	-3.46	-2.15	3.55	-0.50
SUIT2	-0.92	-2.99	-2.07	2.45	-0.22
TCC-PAN2	-1.67	-3.40	-1.72	2.65	-0.45

435 NOTE: Pancreatic cancer cell lines were treated with ASNase (0.00001–1 U/mL) and/or 1 μmol/L
 436 GCN2iA. The IC₅₀ value of ASNase, fold change in IC₅₀ value after GCN2iA treatment, and mRNA and
 437 protein levels of ASNA are shown at log₁₀ scale.

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439 **Supplementary References**

440

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