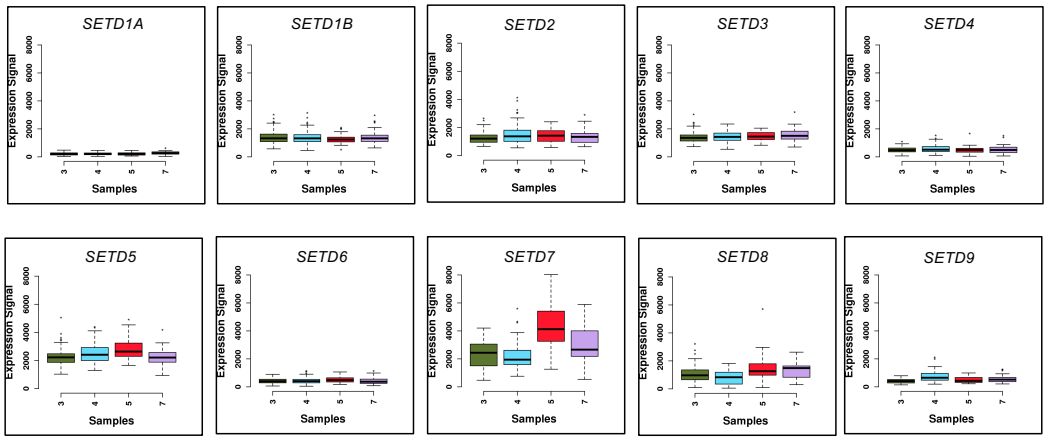
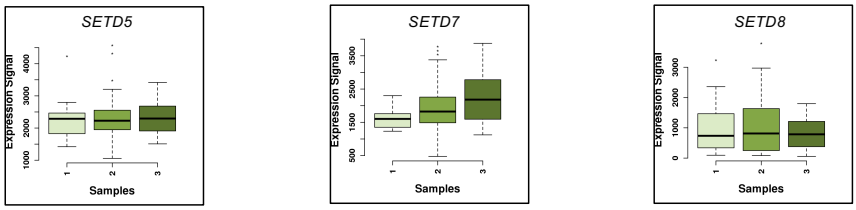
Figure S1

A



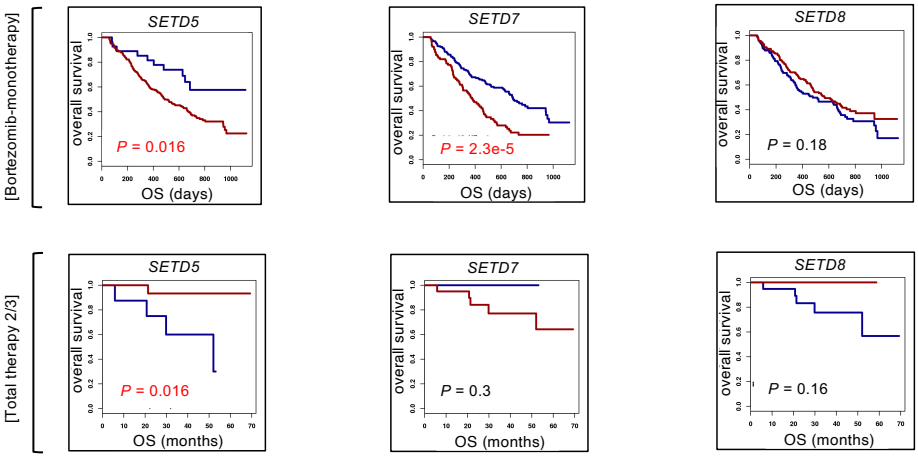
3 : t(4;14) 4: hyperdiploid 5: t(11:14) 7 : t(14:16)

B



1 : normal plasma cells 2: monoclonal gammopathy of undetermined significance (MGUS) 3: smoldering multiple myeloma (SMM)

C

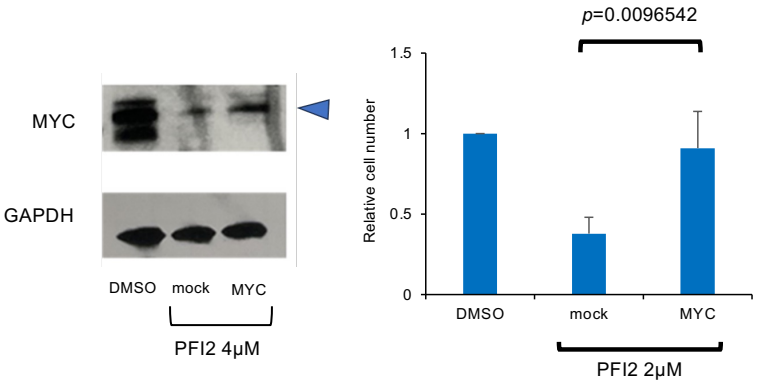


Supplemental Figure S1.

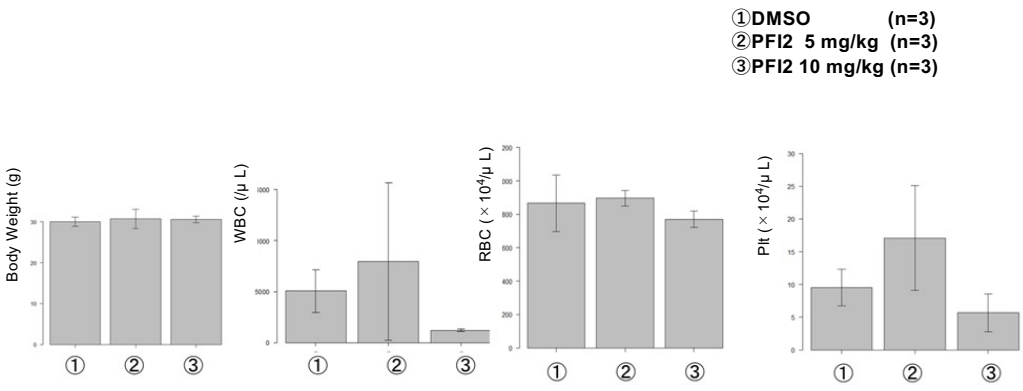
(A) Using the GenomicScape tool (www.genomicscape.com), we examined the gene expression of SET family HMTs in MM cells in the indicated groups. (B) We examined the gene expressions of SETD5, SETD7, and SETD8 in CD138-positive cells derived from normal healthy individuals (normal plasma cells), monoclonal gammopathy of undetermined significance (MGUS), and smoldering multiple myeloma (SMM) patients. (C) Kaplan–Meier curves of MM patients receiving bortezomib monotherapy (GEO accession number [GSE9782]) or total therapy 2/3 [GSE4581] in the indicated groups with high (red) or low (blue) expression. *P*-values were determined by log-rank test.

Figure S2

A


MYC
GAPDH
DMSO
mock
MYC
PFI2 4μM
p=0.0096542
Relative cell number
1.5
1
0.5
0
DMSO
mock
MYC
PFI2 2μM

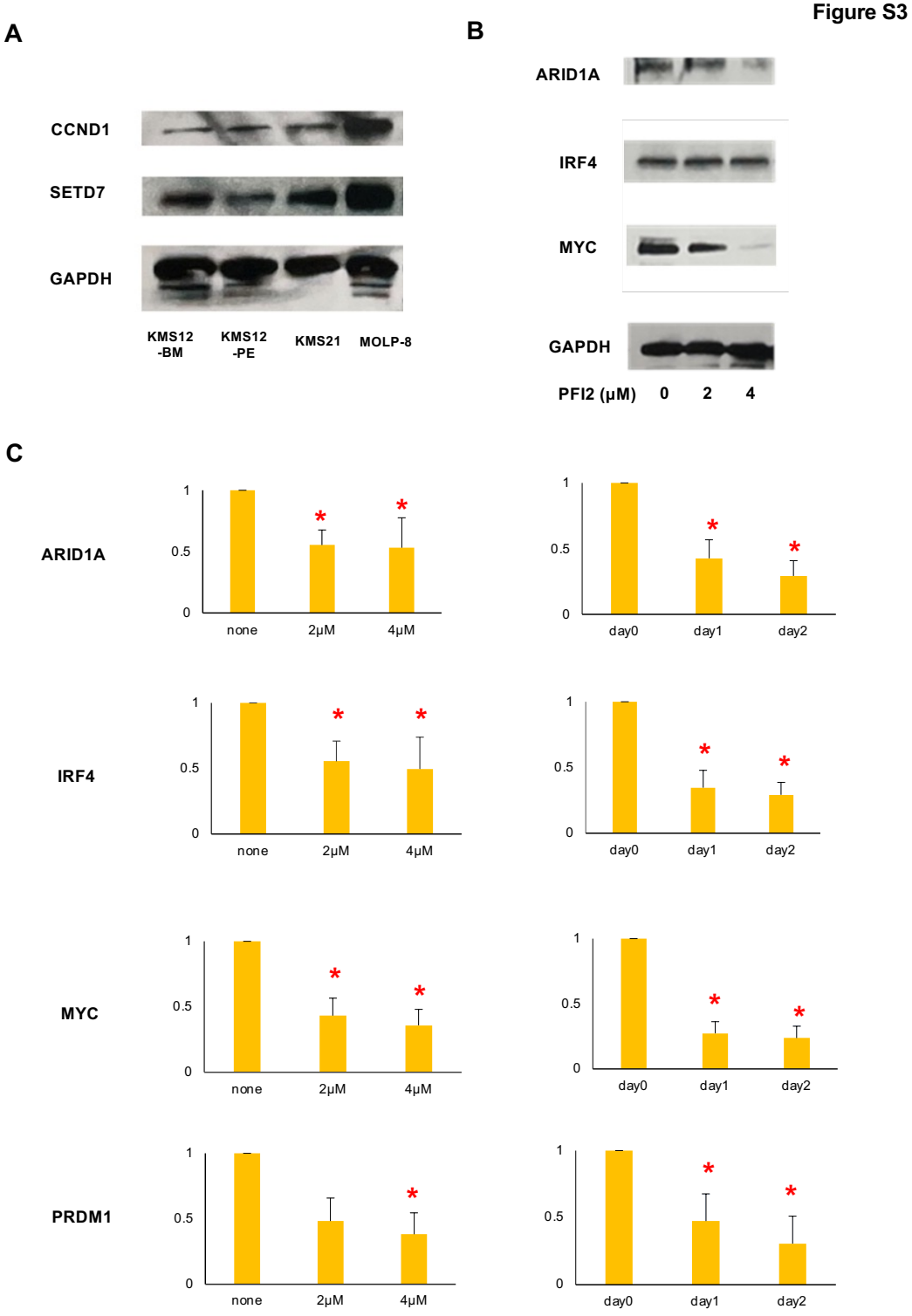
B


①DMSO (n=3)
②PFI2 5 mg/kg (n=3)
③PFI2 10 mg/kg (n=3)
Body Weight (g)
WBC (/μ L)
RBC (×10⁴/μ L)
Plt (×10⁴/μ L)
①
②
③

Supplemental Figure S2.

(A) KMS12-BM cells were transduced with an empty lentiviral vector (mock) or MYC-overexpressing vector (MYC) to establish stable transformants. Left panel: We cultured each transformant in the absence or presence of 4 μM PFI2 for 24 h. The expression level of MYC protein was determined by immunoblotting. An arrow head indicates transduced MYC protein. Right panel: The sublines were cultured in the presence or absence of 2 μM PFI2 for 72 h. Cell proliferation was assessed by MTT reduction assay and the data is shown relative to that of the corresponding untreated controls. Data are the means ± S.D. (bars) of multiple independent experiments (n = 3); *P*-values were determined by one-way ANOVA with a Tukey's multiple comparison test. (B) Balb/c mice (n=3) were administered DMSO vehicle control or PFI2 at the indicated dose twice a week for 3 weeks. We measured body weights, and counts of white blood cells (WBC), red blood cells (RBC), and platelets (PLT) in the peripheral blood of mice at day 21. The mean ± S.D. (bars) is shown. *P*-values were determined by one-way ANOVA with a Tukey's multiple comparison test.

Figure S3


A
CCND1
SETD7
GAPDH
KMS12 -BM
KMS12 -PE
KMS21
MOLP-8
B
ARID1A
IRF4
MYC
GAPDH
PFI2 (μM) 0 2 4
C
ARID1A
IRF4
MYC
PRDM1
1
0.5
0
none
2μM
4μM
day0
day1
day2
*

Supplemental Figure S3.

(A) Whole cell lysates were obtained from MM cell lines harboring t(11;14) including KMS12-PE and subjected to immunoblotting for SETD7, CCND1, and GAPDH proteins (loading control). (B) KMS12-PE cells were cultured with various concentrations of PFI2 for 24 h. Whole cell lysates were obtained and subjected to immunoblotting for ARID1A, IRF4, MYC, and GAPDH proteins (loading control). (C) KMS12-PE cells were cultured with various concentrations of PFI2 for 24 h or in the presence of 2μM PFI2 for the indicated periods. The expression levels of *ARID1A*, *IRF4*, *PRDM1*, and *MYC* along with GAPDH by QPCR are shown. Data were quantified by the $2^{-\Delta\Delta Ct}$ method using GAPDH as a reference and are shown as fold changes. The means ± SD (bars) of three independent experiments. **P* < 0.05 by one-way ANOVA with a Tukey's multiple comparison test.