Supplementary Table 7. Gene dependency results from DepMap Portal.
List of correlation coefficients and corresponding P values used in Extended Data Fig. 8a-c.
All correlation coefficients and P values were derived from Spearman's rank test and linear regression, respectively.

MLL1 dependency vs Borealin expression in different cancer types, related to Extended Data Fig. 8a

	correlation	p value
AML	0.269	0.225
Alveolar rhabdomyosarcoma	0.486	0.694
anaplastic thyroid cancer	0	0.734
Astrocytoma	0.064	0.462
atypical teratoid tumor	-0.233	0.383
B cell leukemia	0.706	0.0903
biliary tract	-0.164	0.399
bladder urothelial carcinoma	-0.409	0.0334
bone	-0.325	0.0916
bowel	-0.01	0.709
breast	0.105	0.485
burkitt lymphoma	0.1	0.419
cervix	0.348	0.159
CML	-0.6	0.301
colon	0.005	0.853
diffuse glioma	0.253	0.0596
DLBCL	-0.33	0.324
embryonal tumor	0.065	0.96
endometrial carcinoma	-0.184	0.283
esophageal squamous cell carcinoma	0.23	0.527
esophagogastric adenocarcinoma	0.017	0.949
ewing sarcoma	-0.434	0.254
gallbladder adenocarcinoma	0.6	0.329
glioblastoma	0.212	0.201
head and neck squamous cell carcinoma	0.202	0.278
high grade serous ovarian cancer	0.684	0.00706
intracholecystic papillary neoplasm	0.6	0.237
intraductal papillary neoplasm of bile duct	-0.308	0.125
intrahepatic cholangiocarcinoma	-0.224	0.343
renal cell carcinoma	0.238	0.192
large cell lung carcinoma	-0.233	0.999
lyposarcoma	0.048	0.801
HCC	-0.565	0.02
lung adenocarcinoma	-0.168	0.409
lung neuroendocrine tumor	0.194	0.0952
lung squamous cell carcinoma	-0.179	0.391
medulloblastoma	0.107	0.788
melanoma	0.134	0.192
myeloproliferative neoplasms	-0.503	0.402
neuroblastoma	0.088	0.904
non-hodgkin lymphoma	0.017	0.967
oral cavity squamous cell carcinoama	0.101	0.792
osteosarcoma	-0.225	0.329
ovarian epithelial tumor	0.289	0.134
ovary fallopian tube	0.286	0.13
pancreatic adenocarcinoma	0.218	0.972
peripheral nervous system	0.152	0.992
plasma cell myeloma	0.042	0.563
pleura mesothelioma	0.693	0.0288
primitive neuroectodermal tumor	0.7	0.35
prostate adenocarcinoma	-0.333	0.398
rectal adenocarcinoma	0.091	0.544

renal clear cell carcinoma	0.318	0.255
rhabdomyosarcoma	0.187	0.816
serious ovarian cancer	-0.147	0.668
small cell lung cancer	0.12	0.0655
soft tissue	0.17	0.832
staomach adenocarcinoma	-0.193	0.71
synovial sarcoma	0.429	0.201
T cell leukemia	0.8	0.33
thyroid	0.009	0.94
uterine carcinoma	-0.075	0.542

Dependency of epigenetic regulatory vs Borealin expression in HCC, related to Extended Data Fig. 8b

gene	correlation	P value
Gcn5	0.481	0.00634
Phf8	0.454	0.00913
Jmjd8	0.463	0.0123
Trim28	0.409	0.0135
MLL1	-0.565	0.02
Kdm3b	-0.49	0.0289
Ep300	0.379	0.0343
PRMT3	-0.595	0.0425
Brd9	0.298	0.065
Hdac3	-0.447	0.0678
Kdm8	-0.478	0.0747
Actr	0.457	0.0904
Smarcad1	0.402	0.0906
MLL3	0.394	0.108
Kdm5c	-0.278	0.12
Brpf3	-0.397	0.128
Hbo1	-0.248	0.134
Rad54l2	-0.365	0.142
Smyd2	0.164	0.152
Zmynd8	-0.305	0.161
Taf1	0.432	0.172
Chd5	-0.481	0.178
Brd4	0.317	0.179
Smyd5	0.359	0.183
Prdm2	0.405	0.186
Nat10	0.31	0.196
Jmjd4	-0.346	0.197
Kdm5a	-0.299	0.2
Chd7	0.352	0.206
Morf	-0.326	0.21
Jmjd1c	0.226	0.227
Rad54l	-0.295	0.228
Hdac1	0.226	0.239
Chd4	0.25	0.24
Atf2	0.259	0.244
Tet1	-0.236	0.26
Ehmt1	0.245	0.274
Ash1l	-0.263	0.283
Nsd1	-0.203	0.285
Smarca1	-0.044	0.309
MLL4	-0.257	0.312
Suv420h1	0.087	0.317
Brd8	-0.418	0.317

Smarcal1	-0.256	0.319
Hdac6	-0.141	0.328
Sirt3	0.215	0.336
Kdm4b	0.203	0.344
Tip60	-0.15	0.362
Jmjd6	-0.242	0.363
Ino80	-0.233	0.363
Smarca2	-0.104	0.363
Kdm2a	-0.281	0.375
Kdm4a	0.218	0.378
Kdm6b	0.203	0.381
Moz	-0.359	0.392
Hdac5	-0.278	0.397
Ep400	0.161	0.409
Setdb2	-0.192	0.416
Tet2	-0.182	0.42
Sirt2	0.116	0.424
Suv39h2	0.165	0.425
Pcaf	-0.189	0.425
Smarca4	0.086	0.43
Chd2	-0.251	0.439
Src1	0.296	0.442
Hdac10	-0.198	0.444
Chd1L	0.155	0.446
Trim33	0.128	0.448
Tet3	0.132	0.45
Phf2	-0.138	0.456
Atat	0.042	0.464
PRMT6	-0.227	0.473
Brpf1	-0.173	0.479
Chd1	-0.248	0.482
Smyd1	-0.161	0.491
Dot1L	-0.002	0.499
Kdm2b	0.186	0.505
MLL2	-0.214	0.513
Nds2	0.116	0.514
Setd1b	-0.036	0.518
Kdm1a	0.183	0.534
PRMT8	0.138	0.574
Sirt4	-0.162	0.577
Hat1	0.062	0.577
Chd6	0.054	0.58
Prdm9	0.114	0.583
Crebbp	-0.232	0.584
Kmd1b	-0.167	0.601
Bptf	-0.053	0.606
Hdac9	-0.28	0.607
Prdm8	-0.206	0.609
Acat1	0.057	0.609
Brd2	-0.128	0.622
Sirt1	0.146	0.623
Brd7	0.251	0.644
PRMT5	-0.003	0.648
Chd3	0.194	0.664
Ncoa2	0.077	0.665
Suv420h2	-0.011	0.668
Hdac8	0.155	0.678
Zmynd11	-0.126	0.679

Setd1a	0.206	0.68
Sirt6	-0.006	0.687
Kdm3a	0.182	0.708
Hdac4	0.107	0.724
Ehmt2	0.009	0.725
PRMT1	0.123	0.73
Kdm7a	-0.045	0.732
Brd1	0.086	0.734
Atrx	0.122	0.747
MLL5	-0.068	0.751
Ezh1	0.173	0.764
Brd3	0.203	0.775
Setd2	-0.03	0.786
Mof	-0.039	0.787
Setd6	0.164	0.791
Kdm6a	0.003	0.792
Smyd3	-0.027	0.794
Setd7	-0.003	0.808
Ezh2	0.006	0.809
Suv39h1	-0.03	0.818
Setd8	-0.078	0.836
Sirt5	0.132	0.837
Hdac7	0.119	0.854
Kdm4c	0.045	0.857
CARM1	0.092	0.858
Kdm5b	-0.029	0.859
Jmjd7	0.056	0.931
Trim24	0.12	0.933
Elp3	0.05	0.95
Sirt7	-0.03	0.963
PRMT2	-0.027	0.964
PRMT7	0.09	0.966
Kdm4d	-0.107	0.97
Ercc6	-0.026	0.972
Setdb1	-0.087	0.978
Nsd3	-0.108	0.989
Jarid2	-0.026	0.993
Hdac2	-0.08	0.994

MLL1 dependency vs expression of cell cycle regulator genes in HCC, related to Extended Data Fig. 8c

gene	correlation	p value
mad1	0.701	0.000916
cdk6	-0.436	0.022
survivin	-0.585	0.0225
borealin	-0.519	0.0347
ccnb1	-0.514	0.035
cdk7	-0.45	0.052
cdc25b	-0.432	0.061
ccnh	-0.451	0.062
cdc25c	-0.429	0.07
ccna2	-0.429	0.076
cdc20	-0.496	0.084
bub1	-0.417	0.088
cdk1	-0.453	0.1
bub3	-0.379	0.112
atr	-0.436	0.118

mps1	-0.302	0.119
ccne2	-0.478	0.134
chk2	0.338	0.165
c-myc	0.308	0.178
mad2	-0.383	0.211
cdc45	-0.386	0.211
atm	-0.433	0.245
chk1	-0.359	0.266
cdc6	-0.281	0.28
cdk2	-0.284	0.297
anapc1	0.226	0.314
rad21	-0.328	0.324
ccnd1	-0.289	0.325
cdc52a	0.183	0.376
cdc7	-0.254	0.4
smc1b	0.163	0.418
rb	-0.123	0.435
cdc14b	0.317	0.437
mad1l1	0.135	0.492
scf	-0.183	0.502
bubr1	-0.18	0.524
skp2	0.059	0.576
ccna1	-0.117	0.578
ccnd2	0.125	0.684
myt1	0.039	0.7
cdk4	-0.143	0.731
cdc14a	-0.118	0.737
ccne1	0.057	0.89
cdc14c	-0.027	0.899
wee1	-0.056	0.911
tp53	-0.056	0.968