Supplementary Information

PHF20 Collaborates with PARP1 to Promote Stemness and Aggressiveness of Neuroblastoma Cells through Activation of *SOX2* and *OCT4*

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Supplementary Methods

Real-time PCR analysis

Complementary DNA was generated from total RNA of NB cells using SuperScript II Reverse Transcriptase (Invitrogen) with oligo (dT) primers. The primer sequences for the genes of interest were designed by using Primer BLAST software and are provided in **Supplementary Table S3**. Quantitative PCR was performed using QuantStudio 6 Flex Real-Time PCR System and Power SYBR Master Mix (Applied Biosystems, Foster City, CA) as per manufacturer's instructions. Relative mRNA expression level was calculated using the 2-ΔΔCt method; Ct values were normalized to GAPDH as an endogenous control.

ChIP-PCR

SH-EP cells were grown to 80-90% confluence and chemically cross-linked by the addition of fresh formaldehyde solution (37%) to a final concentration of 1% for 10 min at room temperature. Cells were rinsed twice with cold PBS, followed by the addition of 2 M glycine to stop crosslinking, and collected using a silicone scraper. Cells were lysed and sonicated to solubilize and shear cross-linked DNA with a minor modification. Briefly, we used a Misonix ultrasonic liquid processor and sonicated at an amplification of 4 for 12 sets of 10 s pulses, with 30 s pause between pulses, at 4 °C. The resulting whole cell extract was pre-cleared with 50 µl protein A/G agarose beads, 10 µl IgG, 10 µl 5% Bis(trimethylsilyl)acetamide (BSA), and 5 µg of sheared salmon sperm DNA for each sample. After centrifugation, 20% of the supernatant was incubated overnight at 4 °C with 30 µl of protein A/G agarose beads, 3 µg of the

appropriate antibodies, 1 µl BSA (5%), and 25 µg of sheared salmon sperm DNA. Beads were washed four times with ChIP buffer [0.1% SDS, 1% Triton X-100, 2 mM EDTA (pH 8.0), 150 mM NaCl, and 20 mM Tris-HCl (pH 8.0)], and once with Tris-EDTA (TE) containing 1 mM dithiothreitol (DTT). Bound complexes were eluted from the beads, and crosslinking was reversed by overnight incubation at 65 °C in reverse crosslink buffer solution (1% SDS, 100 mM NaHCO3, 1 µg/mL RNase A, and 500 mM NaCl). Whole cell extract DNA was also treated for reverse crosslinking. Immunoprecipitated DNA and whole cell extract DNA were purified using the Zymoclean PCR purification kit (Zymo Research, Irvine, CA). The ChIP DNA were used for qPCR analysis. As eukaryotic promoters are within 2 kb upstream of the transcription start site, we designed 4-6 primer pairs, generally 500 bp in length, to cover the key locus. These were labeled as #1, #2, #3, and so forth. After three rounds of screening, we found that only pairs #1 and #2 associated with critical regions associated with transcriptional regulation by PHF20; therefore, we focused our analysis these sets only. The primers sequences for the ChIP-qPCR are provided in **Supplementary Table S3**.

Western blot, immunoprecipitation (IP), and mass spectrometry

For Western blot analysis, cells were lysed in either low salt lysis buffer or RIPA buffer containing protease inhibitors. Equal amounts of protein samples were separated electrophoretically by SDS-PAGE, and then transferred onto PVDF membranes (Roche, Mannheim, Germany). The membranes were blocked for 1 h in Tris-buffered saline-Tween 20 (TBST) with 5% bovine serum albumin (BSA) or 5%

nonfat milk. Thereafter, Western blot analysis was performed using primary antibodies against PHF20, NANOG (1:1000; Cell Signaling Technology, Danvers, MA), SOX2 (1:1000; Millipore), OCT4, β-actin (1:1000; Abcam, Cambridge, MA), SSRP1 (1:1000; ThermoFisher Scientific, Sugarland, TX), and PARP1 (1:1000; Santa Cruz Biotechnology, Dallas, TX) in a blocking buffer containing either 5% BSA or 5% nonfat milk and 0.1% Tween 20 in TBS. The blots were then developed using Lumiglo substrate (KP Laboratories, Gaithersburg, MD) on BioMax LS film (Eastman Kodak, Rochester, NY).

For IP, cells were lysed in either low salt lysis buffer or RIPA buffer containing protease inhibitors. Samples were centrifuged at 10,000x g for 10 min. The supernatant was added to either a 10 l anti-Flag M2 affinity gel overnight at 4 °C or primary antibody at 4 °C for 2 h with rotation. After incubation with immobilized Protein A 16 (Replicen, Waltham, MA), samples were washed five time using low salt lysis buffer, and proteins were re-suspended in 4x SDS sample loading buffer and subjected to SDS/PAGE. The resolved proteins were either transferred to nitrocellulose membranes for immunoblotting or subjected to Coomassie Brilliant Blue staining and excised for matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) analysis.

The in vivo Tumor Formation Experiments

mice were divided into two groups of four mice each (one group for SH-EP cells and another group for SK-N-AS cells). Each mouse was injected subcutaneously in the right flank with 4 x 106 NB WT cells (with PHF20) diluted in 100 l of 50% Hank's

balanced salt / 50% Matrigel. In addition, each mouse was injected subcutaneously in the left flank with 4 x 106 NB KO cells (PHF20 depleted) diluted in 100 l of 50% Hank's balanced salt / 50% Matrigel. Every two days, tumor sizes were determined by measuring the length and width using calipers. Tumor volumes were calculated as per the formula: volume (mm3) = (length*width*width) / 2. Twenty-eight days after tumor cell injection, mice were sacrificed, tumor xenografts were removed, fixed in formalin, and stored at 4 °C.

Limit Dilution Experiments

mice were divided into three groups containing five mice each. Each group was injected subcutaneously in the right flank with either 1 x 106, 0.1 x 106, or 0.01 x 106 SH-EP WT cells (with PHF20) diluted in 100 L of 50% Hank's balanced salt / 50% Matrigel. Further, each group was injected subcutaneously in the left flank with either 1 x 106, 0.1 x 106, or 0.01x106 SH-EP KO cells (PHF20 depletion) diluted in 100 l of 50% Hank's balanced salt / 50% Matrigel. Tumor formation was determined 28 days after tumor cell injection.

Gene rescue experiment

For PHF20 gain-of-function experiments, human PHF20 (NM_016436.4) cDNA sequence was cloned into pLV-lentiviral vector. The PHF20-overexpressing lentiviral vector was co-transfected with the VSVG and PAX2 lentiviral packaging vectors into 293T cells. Supernatants containing lentiviruses were collected on day 3 and concentrated by ultra-centrifugation. The concentrated lentiviruses were re-suspended in 1 mL of PBS. PHF20 KO SH-EP cells were infected with lentivirus harboring

PHF20, which was expressed ectopically. Similarly, for SOX2 and OCT4 rescue, PHF20 KO SH-EP cells were infected with lentivirus harboring either SOX2 or OCT4 individually or in combination; we then induced ectopic expression. For negative and positive controls, we transfected PHF20 KO SH-EP cells with empty vector or MYCN, respectively.

Mice were divided into six groups of eight or nine mice per group. WT SH-EP cells with an empty vector and PHF20 KO NB cells with MYCN overexpression were used as positive controls; the negative control was PHF20 KO NB cells. The experimental groups consisted of PHF20 KO NB cells ectopically expressing SOX2, OCT4 alone, or both. Each group was implanted with 4 x 106 cells. Every two days, tumor sizes were determined by measuring the length and width using calipers. Tumor volumes were calculated as described above. Twenty-eight days after tumor cell injection, mice were sacrificed, tumor xenografts were removed, fixed in formalin, and stored at 4 °C.

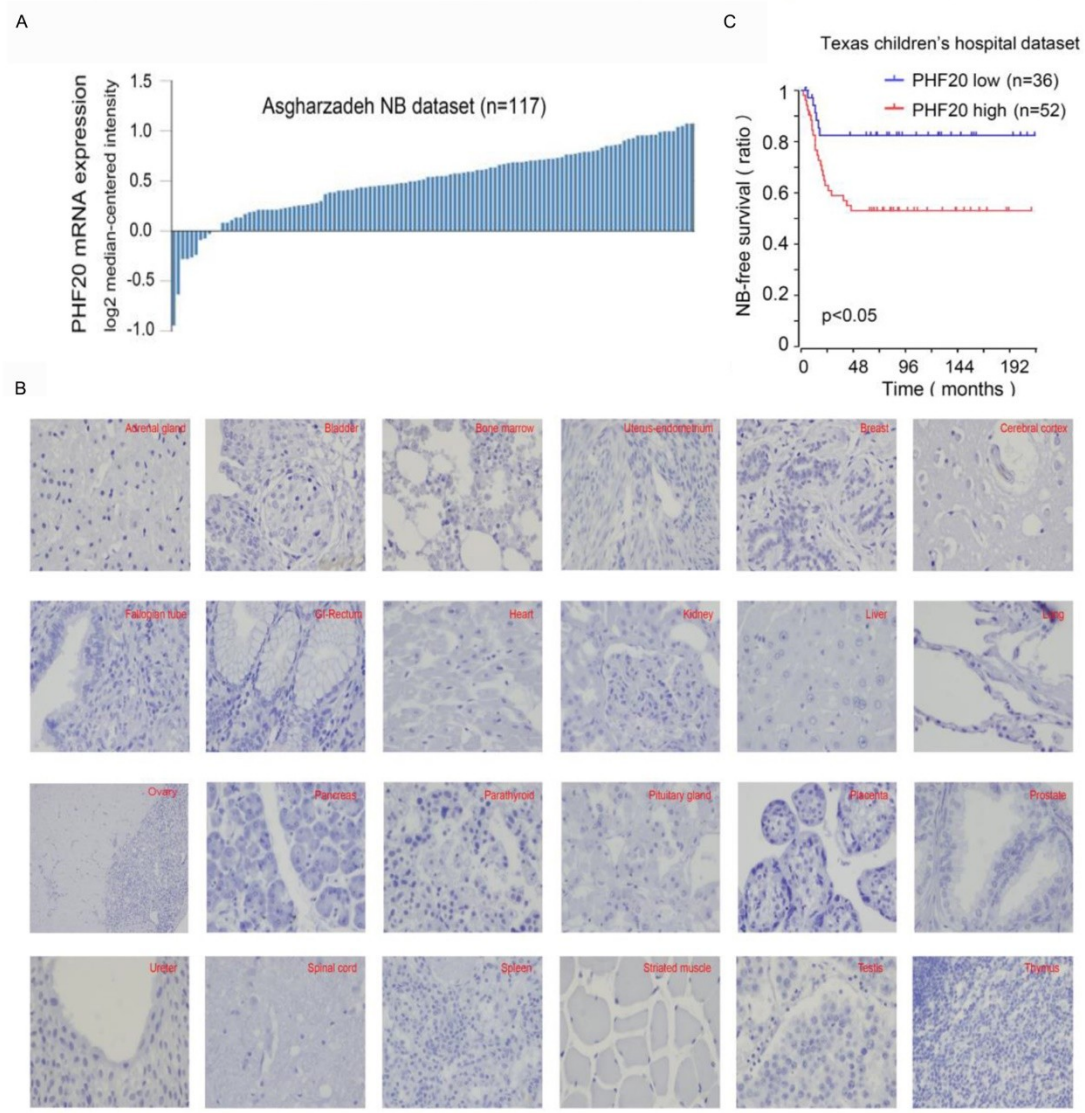
Supplemental Figure 1

Gene symbol	Differentiation degree
PHF20	3
FGFR2	3
MYD88	2
NOTCH1	2
TBL1XR1	2
TBX3	2
ING1	2
INPPL1	2
IDH2	2
ERCC2	2
PCBP1	2
CASP8	1
CHD4	1
CHD8	1
CHEK2	1
DNER	1
MET	1
MPO	1
NAV3	1
NCOR1	1
NFE2L3	1
ODAM	1
OMA1	1
PPP2R1A	1
PRDM1	1
RSBN1L	1
SF3B1	1
SLC4A5	1
TAF1	1
TNF	1
TP53	1
TP53BP1	1
TPX2	1
TSHZ3	1
U2AF1	1
XIRP2	1
ZNF471	1
MAP4K3	1
KEL	1

Supplementary Figure S1. A candidate gene list generated from sgRNA library screening of SH-SY5Y cell differentiation analysis. Differentiation degree 1: 10-30%

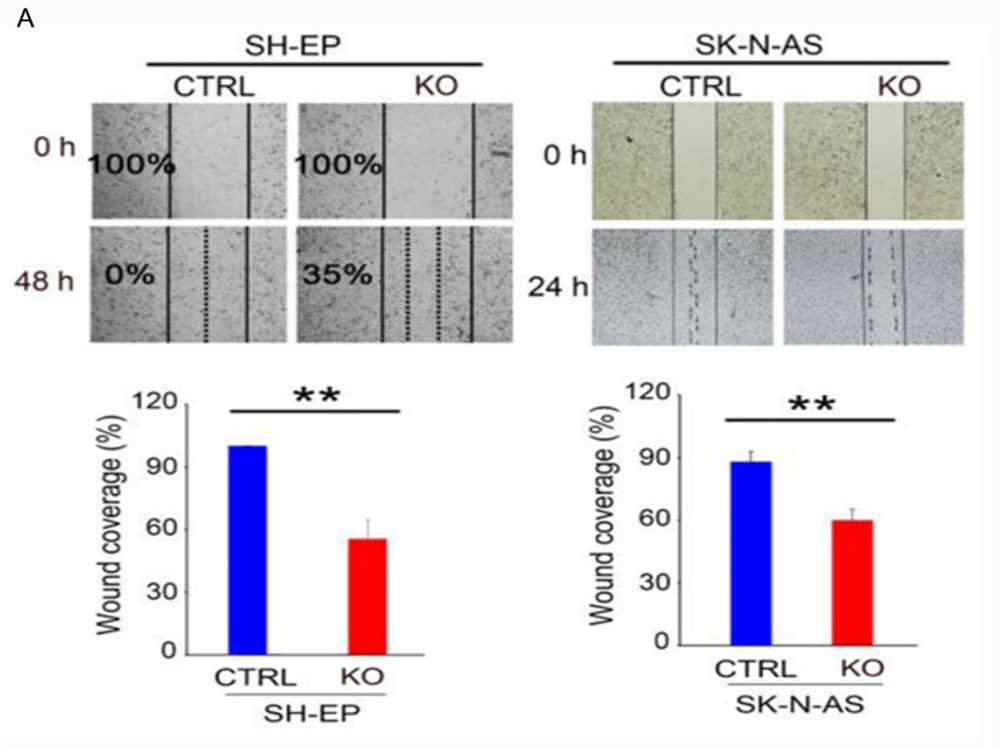
differentiated SH-SY5Y cells; differentiation degree 2: 30-60% differentiated SH-SY5Y cells; differentiation degree 3: 60-90% differentiated SH-SY5Y cells. **Related to Figure 1**.

Supplemental Figure 2



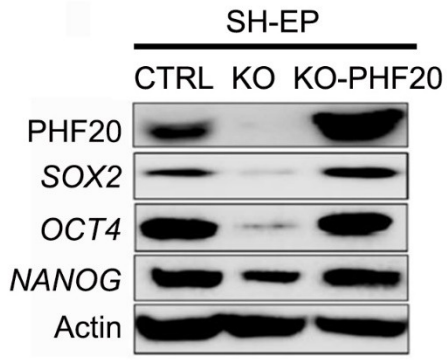
Supplementary Figure S2. PHF20 is highly expressed in NB and correlates with the poor outcome of NB patients. (**A**) The expression of PHF20 in 117 NB samples was analyzed on Affymetrix U133A microarrays. (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3446). (**B**) IHC staining of PHF20 in normal human tissues. (**C**) Using the Texas Children's Hospital (Houston, TX) dataset, the association between PHF20 expression in NB and tumor free survival time of selected patients was analyzed by Kaplan-Meier analysis. **Related to Figure 2**.

Supplemental Figure 3



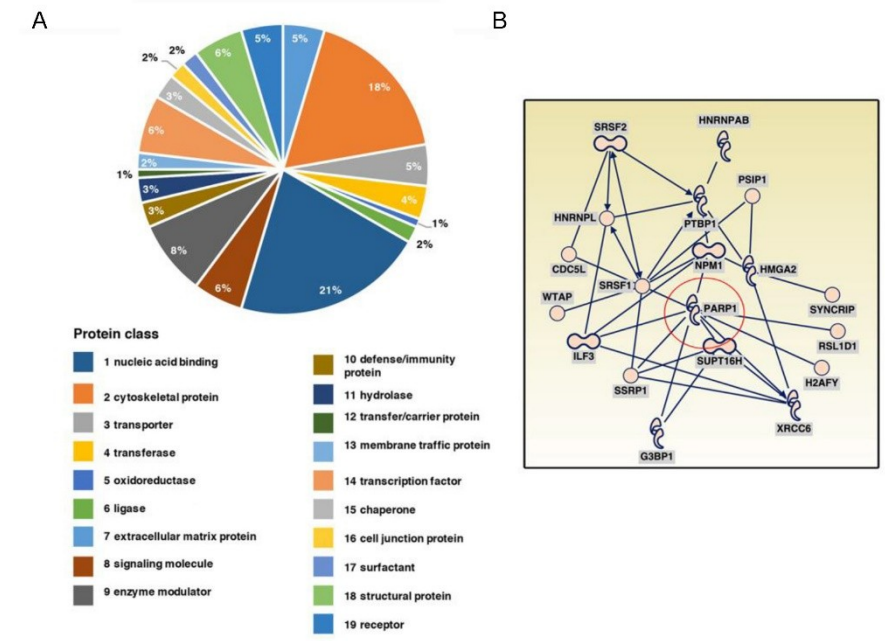
Supplementary Figure S3. PHF20 promotes migration of NB cells. Wound healing assay was conducted to evaluate the migration potential of NB cells after PHF20 depletion. The cell layers were wounded and monitored under a microscope every 24 h. Migration was determined by the rate at which the scratched area filled with cells (n = 3). **Related to Figure 4.**

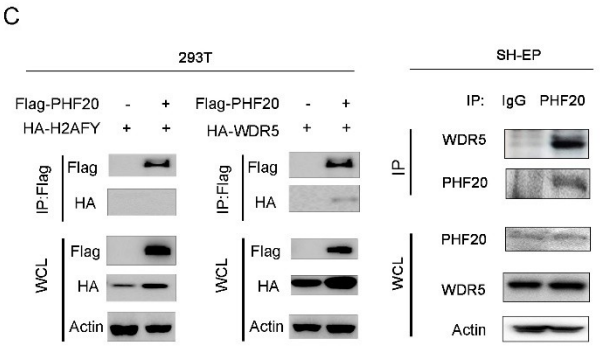
Supplemental Figure 4

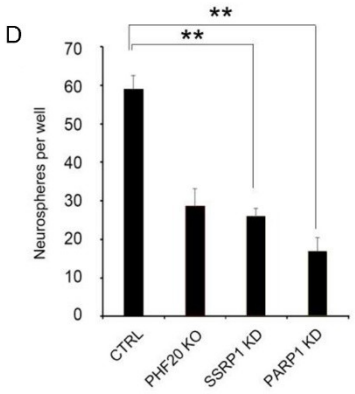


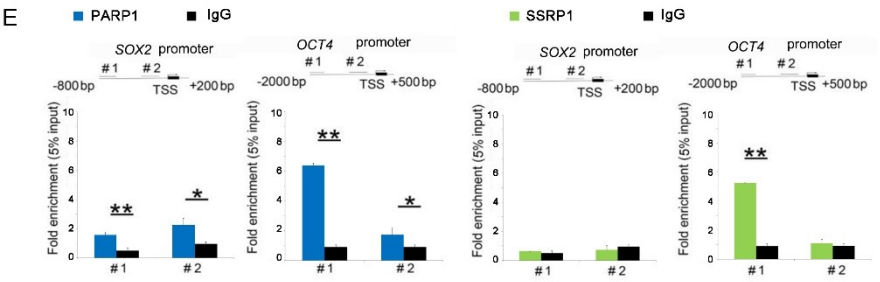
Supplementary Figure S4. PHF20 is required for upregulating stem cell core gene expression. Western blot analysis showed that ectopically expressing PHF20 in *PHF20* KO cells could rescue SOX2, OCT4, and NANOG expression. **Related to Figure 5.**

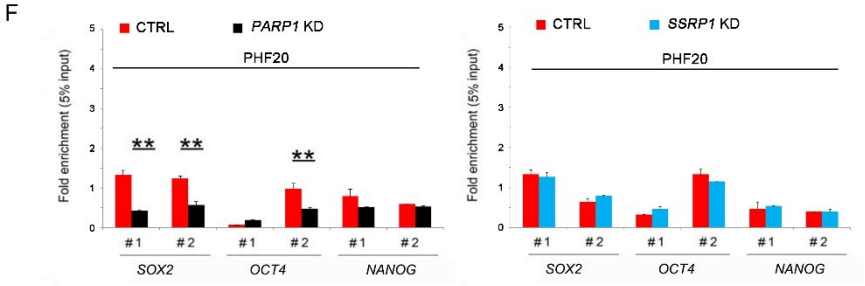
Supplemental Figure 5





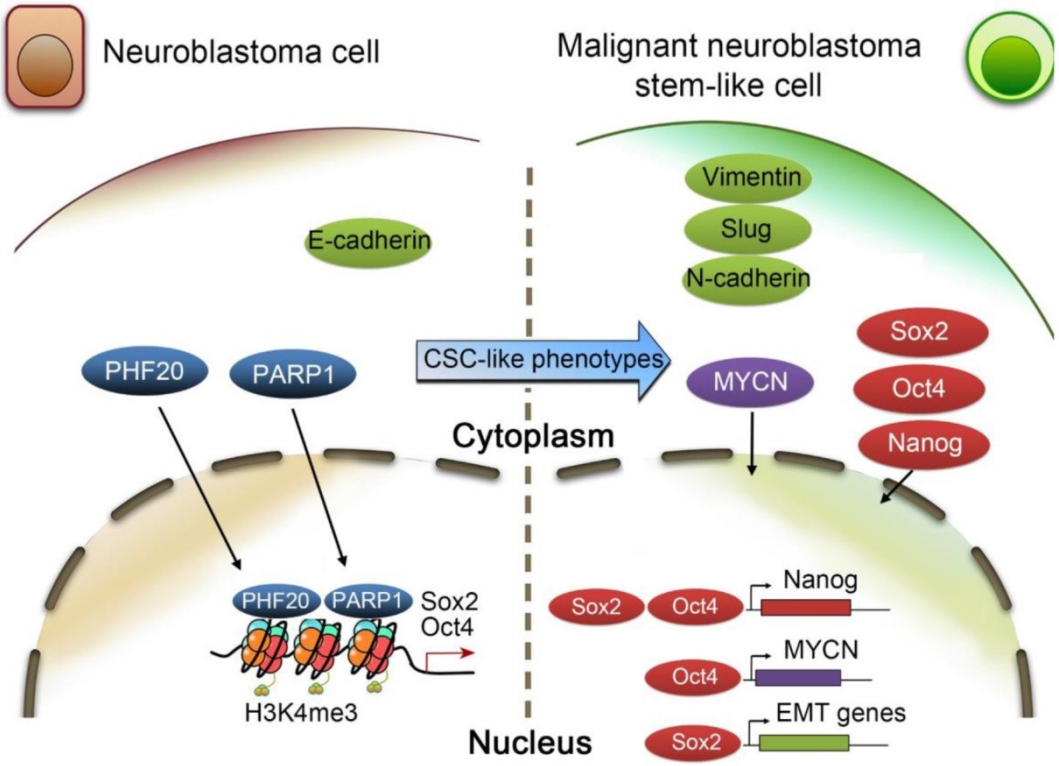






Supplementary Figure S5. PHF20 promotes emergence of stem cell-like behavior in NB by interacting with PARP1. (A) Gene ontology (GO) analysis of PHF20 binding proteins identified with mass spectrometry. The identified proteins were categorized into 19 classes by protein function. (**B**) An Ingenuity Pathway Analysis generated network of potential candidates identified through mass spectrometry. **(C)** Left, 293T cells were co-transfected with Flag-PHF20 and HA-H2AFY/HA-WDR5. Cell extracts were immunoprecipitated with anti-Flag beads, followed by immunoblotting with an anti-HA and anti-Flag antibody; Right, detection of endogenous interaction between PHF20 and WDR5 in SH-EP by IP with a PHF20 antibody, followed by IB with WDR5 antibodies. (**D**) The tumor sphere formation assay was used to assess the self-renewal capacity of control, SSRP1, and PARP1 KD SH-EP cells. SH-EP cells with non-specific sgRNA served as control. The sphere number was counted after 7 days. Five random wells were photographed. (**E**) Analysis of PARP1 and SSRP1 binding to the promoter regions of *SOX2* and *OCT4* in NB cells by ChIP-qPCR assay with PARP1 or SSRP1 specific antibody respectively. The data are presented as fold enrichment relative to input DNA. (**F**) ChIP-qPCR analysis of PHF20 binding to the *SOX2*, *OCT4*, and *NANOG* promoter in PARP1 KD or SSRP1 KD cells. **Related to Figure 6.**

Supplemental Figure 6



Supplementary Figure S6. Schematic illustration of the working model by which PHF20 interacts with PARP1 for the activation of SOX2 and OCT4, and confers stem cell-like traits in NB cells. The PHF20 and PARP1 trigger *SOX2* and *OCT4* expression, which in turn activates expression of *NANOG* and EMT-related genes (*Vimentin, Slug,* and *N-cadherin*). Activation of multiple signaling pathways may lead to rapid proliferation and malignant stem cell-like phenotypes in NB.

Supplementary Table S1. Genes and sgRNA target sequences of a CRISPR/Cas9 library for SH-SY5Y cell differentiation screen.

sgRNA number	Gene symbol	sgRNA target sequence
1	ACO1	ATGACACGAGCAGGCTTAAA
2	ACO1	CGCACACCTTGCTGAGCCAT
3	ACVR1B	GAGCTGGTAGGCATCATCGC
4	ACVR1B	CCCCACATGGACGGGTGCTC
5	ACVR2A	ATCCCCGCAATTAACATAAG
6	ACVR2A	CGCTGTGTGACTTCCATCTC
7	ACVR2B	CGGCGCACAGCGATCCCCAG
8	ACVR2B	GTGTACTTCTGCTGCTGTGA
9	ADNP	TGCTCGTAAGTGCGCTTCAC
10	ADNP	TCCGGCTAAGCTGCCATGCA
11	AJUBA	TTTGAGGCGCCGCGCTACGA
12	AJUBA	GCCTTTGTTGCACTTGATAC
13	AKT1	GCGCCACAGAGAAGTTGTTG
14	AKT1	GCAGGATGTGGACCAACGTG
15	ALK	AATGGGACAGTCCTCCAGCT
16	ALK	TCAGGACCCTAAAGGATGCC
17	ALKBH6	ACAACCTGCTCCACTCTGAA
18	ALKBH6	AGCCCTGGAACCGTTCAGAG
19	ALPK2	GTGCTTCGCTGCATAATATC
20	ALPK2	AATAATGCCACTCCCATCGA
21	ANK3	GTCTCGGAGCGCGTTCTGCC
22	ANK3	TTATTCACGAAGCTCTAGAA
23	APC	GGATCTGTATCAAGCCGTTC
24	APC	GATTTATTAGAGCGTCTTAA
25	APOL2	GGGGCATACGCTCCTAACTG
26	APOL2	ACGAGCCCAAGCCCGCAACT

27	AR	CATTTCCGAAGACGACAAGA
28	AR	GGGTGGAAAGTAATAGTCAA
29	ARHGAP35	AAGGCATCTACCGGGTCAGC
30	ARHGAP35	CAGACTTGTTCCCGCTGACC
31	ARID1A	GCGGTACCCGATGACCATGC
32	ARID1A	GAGCTATCTCAAGATTCATT
33	ARID2	GAACTTTCTCGTACTTTTCT
34	ARID2	AGGTTTCTGAGAAGAATCAG
35	ARID5B	GCTATGCAAATCGGATCCTT
36	ARID5B	GAATGACCGTACCTTGGCAA
37	ASXL1	TGTCCGCCTCACCAGGCGCG
38	ASXL1	TCGCCATCCAGCTACAGTGG
39	ATM	TGATAGAGCTACAGAACGAA
40	ATM	ATCATTAAGTACTAGACTCA
41	ATP5B	AATGACCGCCACGATGCGCC
42	ATP5B	GCGGCGCCTGCTTTTGGCGA
43	ATR	GTATTTTAGTGCCACACCAG
44	ATR	GGATCATGGAAGCCAGCTCC
45	ATRX	TCGTGACGATCCTGAAGACT
46	ATRX	TTTTGATTCATTGCAAGTCG
47	AXIN2	ACCGTCTTGATCGCCCAATA
48	AXIN2	GCGTGGATACCTTAGACTTC
49	AZGP1	TGAAGACGTCCCCGCGTTTC
50	AZGP1	TTCAGGGTCTCACGTATTGC
51	B2M	ACCCAGACACATAGCAATTC
52	B2M	TCACGTCATCCAGCAGAGAA
53	BAP1	TACCGAAATCTTCCACGAGC
54	BAP1	CGACCTTCAGAGCAAATGTC
55	BCLAF1	TACCTGTTAGAATCATCAAG

56	BCLAF1	ATTCTAGAAAGAAGCGATAC
57	BCOR	TGTGTGGGGCGAGCGAAGAC
58	BCOR	TCTTACCACGTTGTGGTTCA
59	BHMT2	ATATCATGCATGTCTCCCTC
60	BHMT2	AAAAGAATCAGATAGACCCG
61	BRAF	GAGGCCCTATTGGACAAATT
62	BRAF	CTTACCTCCAGATATATTGA
63	BRCA1	TGCTAGTCTGGAGTTGATCA
64	BRCA1	AAATCTTAGAGTGTCCCATC
65	BRCA2	ATGTAGCACGCATTCACATA
66	BRCA2	CTGTCTACCTGACCAATCGA
67	BRE	ATTCGGTTCAAGGCCACTTC
68	BRE	CTCCCCTTTCATATCTAGCG
69	C3orf70	CAGATAGACAGCCCGTCGCA
70	C3orf70	CCCGACTTCCAGCCGTGCGA
71	CAP2	GGAACGAGCTGTCAGCCGCC
72	CAP2	GGGAACTGCGGGGAAGTCAA
73	CARD11	GCCCTACCTGCGTCAGTGTA
74	CARD11	CCATCCAAGATCAACCGAGC
75	CASP8	GGGTCGATCATCTATTAATA
76	CASP8	TCCTTTGCGGAATGTAGTCC
77	CBFB	GCCGACTTACGATTTCCGAG
78	CBFB	TTCCAGAACGCCTGCCGCGA
79	CCDC120	CCACCGACCTGGGGCATTGA
80	CCDC120	TCTCCTACCTTCAATGCCCC
81	CCDC6	GCTCTCCAGAAAATTGATGC
82	CCDC6	ATTTACCTGCATCAATTTTC
83	CCND1	GTTCGTGGCCTCTAAGATGA
84	CCND1	TTTTCACGGGCTCCAGCGAC

85	CD1D	CAGGCTTGGGGAAGCGCTGA
86	CD1D	CTTCAGCGCTTCCCCAAGCC
87	CD70	CAGCTACGTATCCATCGTGA
88	CD70	GAGCTGCAGCTGAATCACAC
89	CD79B	GCAGCAACGCCACCATCCAG
90	CD79B	CACAGGAGACAACGCCAGCC
91	CDC27	GCAGAACGCCTTTATGCAGA
92	CDC27	ATTTCAAACCTTCTGCATAA
93	CDH1	CGCCGAGAGCTACACGTTCA
94	CDH1	GAGTTTCCCTACGTATACCC
95	CDK12	GGCTCTATAACTCTGAAGAG
96	CDK12	GGGGGAGACAGATCTCCACC
97	CDK4	GTGCCACATCCCGAACTGAC
98	CDK4	CTTGCCAGCCGAAACGATCA
99	CDKN1A	CCGCGACTGTGATGCGCTAA
100	CDKN1A	AGATCAGCCGGCGTTTGGAG
101	CDKN1B	ATTGCTCCGCTAACCCCGTC
102	CDKN1B	TCAAACGTGCGAGTGTCTAA
103	CDKN2A	GGCCGCACGCGCGCCGAATC
104	CDKN2A	TCTTGGTGACCCTCCGGATT
105	CEBPA	TGACTACCCGGGCGCGCCCG
106	CEBPA	GAGCCCCTGTACGAGCGCGT
107	CEP76	ATCAAAGCCCTTAGACGTCG
108	CEP76	CAATGATTCCTCGACGTCTA
109	CHD4	TCGAACCCTCACCAACTACA
110	CHD4	GAGCGGAAGGGGATGGCGTC
111	CHD8	TGAATCGAAACGCATCACCC
112	CHD8	GGACATCGGCATGTTGTGCT
113	CHEK2	AAGAAGCCTTAAGACACCCG

114	CHEK2	TGAATCCACAGCTCTACCCC
115	CNBD1	ACCTGTGTTGTCCTCTAATG
116	CNBD1	ATGTGAGACAAAATAGCTGC
117	CNKSR1	AAGCTGACGCCCTCCTCTTC
118	CNKSR1	GGACTATGCTCTGGAAGTCA
119	COL5A1	GCATGGACGTCCATACCCGC
120	COL5A1	GCGCCCTTACCTGCGCGGCT
121	COL5A3	ATTGGCTGGCTGTCCCCGCA
122	COL5A3	CCCCGCTTCATCAGCATAGC
123	CREBBP	AGCGGCTCTAGTATCAACCC
124	CREBBP	CCCGCGTGACCAGTCATTTG
125	CRIPAK	TCTGCACCTCGAGATAACGT
126	CRIPAK	AATATTCCTACGTTATCTCG
127	CTCF	CGATCCAAATTTGAACGCCG
128	CTCF	CGTCACATTCGCTCTCATAC
129	CTNNB1	GAAACAGCTCGTTGTACCGC
130	CTNNB1	AAAATGGCAGTGCGTTTAGC
131	CUL4B	CGGATGATGTCACAGTCATC
132	CUL4B	ATTCAATGCTACCCTCCATT
133	CUX1	AGAACTCGATGCCACCGCAA
134	CUX1	CCTTGGAAACTCTTCAGCAG
135	DDX3X	AACTCTTCAGATAATCAGAG
136	DDX3X	TCTGATTATCTGAAGAGTTC
137	DDX5	AGGTTTGGTGCACCTCGATT
138	DDX5	GCCCTACTTCCTCCAAATCG
139	DIAPH1	ATCTTGCAATGACTGTGCTG
140	DIAPH1	CCTTGGAGGTGTACAAGTAT
141	DIS3	TTAGACTTACAAGTGAAAGC
142	DIS3	TTATGAAGATAACTTGCAGC

143	DNAH12	CTTACAGTTTGAGGATAATC
144	DNAH12	ACCAGTGAAATGAAAAAAAA
145	DNER	GATCTCCGGCGCCAACTGCC
146	DNER	GTGCACCTCGCGCCCTGAGC
147	DNMT3A	CGATGACGAGCCAGAGTACG
148	DNMT3A	CCGCTCCGCAGCAGAGCTGC
149	EGFR	TGAGCTTGTTACTCGTGCCT
150	EGFR	ATCATAATTCCTCTGCACAT
151	EIF2S2	CGCAGCCATGTCTGGGGACG
152	EIF2S2	CCTCACCTCGTCCCCAGACA
153	EIF4A2	TCTTACCTCGATGACACCAT
154	EIF4A2	AGATTTGATCCTTAAAACCA
155	ELF3	CGAAGACGCAGGTTCTGGAC
156	ELF3	CCTGCGTCTTCGACCAGAAC
157	EP300	GAACCGTTCATGACTTGATT
158	EP300	TAGTTCCCCTAACCTCAATA
159	EPHA2	GAAGCGCGGCATGGAGCTCC
160	EPHA2	CGAAGCAGGCGCGGGCTGCC
161	EPHB6	GCTCTTCAATGTCGTGTGCA
162	EPHB6	TGCACACGACATTGAAGAGC
163	ERBB2	TTTCTGCCGGAGAGCTTTGA
164	ERBB2	CTTAGACAACTACCTTTCTA
165	ERBB3	CAGCATCGCCGGTCACACTC
166	ERBB3	CACTGTACAAGCTCTACGAG
167	ERBB4	GTTTTCATAGTACTTGCGCA
168	ERBB4	GCTTTACCCGCAGGAAGGAG
169	ERCC2	TTATCGGCAGGCATATCCGC
170	ERCC2	TCTTGAGCAGTAGATGAGTT
171	EZH1	ACAGGCTTCATTGACTGAAC

172	EZH1	GCTTTGCTAGGCTTTGTATG
173	EZH2	ACACGCTTCCGCCAACAAAC
174	EZH2	TGCGACTGAGACAGCTCAAG
175	EZR	CAATGTCCGAGTTACCACCA
176	EZR	GCAATCCAGCCAAATACAAC
177	FAM166A	TGTAGGGCTCCGTCAGGTCT
178	FAM166A	GAAACACGATCTCTTCACGC
179	FAM46C	TTTGCACGGACACTGACCGC
180	FAM46C	TTGTTCCGCCAGCACACGCA
181	FAT1	TGAGTACGTCACGTGTCCGT
182	FAT1	GTCTCATCACAACTACGTCA
183	FBXW7	CTGATGTATGCACTTTTCCA
184	FBXW7	AGCACAGAATTGATACTAAC
185	FGFBP1	CTAGTCAGCTCCACTCTATT
186	FGFBP1	ACGTGTCCTGCACTATGCTG
187	FGFR2	GTACCGTAACCATGGTCAGC
188	FGFR2	GCCCTCCTTCAGTTTAGTTG
189	FGFR3	GACGCGCTGCTCCGTCCCCA
190	FGFR3	GGGGACGGAGCAGCGCGTCG
191	FLG	CCAAAAGATGTCTACTCTCC
192	FLG	ATTGAGTAAAAAAGAGCTGA
193	FLT3	CCTTACCGAGCAGCGGCAGC
194	FLT3	TCCGGAGGCCATGCCGGCGT
195	FOXA1	CAGCTACTACGCAGACACGC
196	FOXA1	GTAGTAGCTGTTCCAGTCGC
197	FOXQ1	CCCGCGCCGTACGCGCAGAG
198	FOXQ1	TTCGTCCCTCGCGCGGCCCA
199	FRMD7	CCATCTAAATCTTGCTGAAA
200	FRMD7	CAGGTTAAACAATGCCTTCC

201	GATA3	GTACTGCGCCGCGTCCATGT
202	GATA3	TACGTGCCCGAGTACAGCTC
203	GNA13	CCAGTTGAAATTCTCGACGC
204	GNA13	AGATGATGTCGTTTGATACC
205	GNB1	TGAGTGAGCTTGACCAGTTA
206	GNB1	AATCTGGTTCTTAAGTTGCT
207	GNPTAB	GTAAACAACGTCAATCGGCA
208	GNPTAB	GTAGTTGAAGATGCCCACTC
209	GOT1	ACATTCGGTCCTATCGCTAC
210	GOT1	AGAAGATCGTGCGGATTACT
211	GPS2	GCTGCACCGGCACATTATGA
212	GPS2	CTTGGGGCGCTCCAGGAGTG
213	GUSB	GTGGTCATCGATGAGTGTCC
214	GUSB	GTGGCTGGTACGGAAAGCGT
215	H3F3C	GCGATGAGGCTTCACCCCGC
216	H3F3C	AAAAGCACCCCCTCTACCTG
217	HGF	TGTTCTTACCTGTGTTCGTG
218	HGF	CCCTTCAATAGCATGTCAAG
219	HIST1H1E	GGCCGCTCTCAAGAAAGCGC
220	HIST1H1E	ACCCGACGCGCCGGTGCCCT
221	HIST1H3B	CTCGTACTAAACAGACAGCT
222	HIST1H3B	AAAGCCTCACCGTTACCGCC
223	HIST1H4E	GTGTTGGTCATGTCTGGTCG
224	HLA-A	ACAGCGACGCCGCGAGCCAG
225	HLA-A	CCAGTCACAGACTGACCGAG
226	HLA-B	CGCTGTCGAACCTCACGAAC
227	HLA-B	GGTTCTATCTCCTGCTGGTC
228	HRAS	CATCCTGGATACCGCCGGCC
229	HRAS	TGATGGGGAGACGTGCCTGT

230	HSP90AB1	CTCACACCTTGACTGCCAAG
231	HSP90AB1	CATACTCACATAAAGGGTGA
232	IDH1	GCATGACGACCTATGATGAT
233	IDH1	GCCACCCAGAATATTTCGTA
234	IDH2	CCATAGGTTTGCCCAGATGC
235	IDH2	ACGTGTCCAGGCAAAGATGC
236	IL7R	ATTCTCATGCTATAGCCAGT
237	IL7R	AGATGTCAACATCACCAATC
238	ING1	GAGATCGACGCGAAATACCA
239	ING1	TATAAATCCGCGCCCGAAAG
240	INPPL1	TCCGCAGCCATCCACACGTA
241	INPPL1	ATGTACCTCAAAGGCCTGCA
242	INTS12	CAAGGTCCTCACAACTGAAA
243	INTS12	TATTTTGGGCTCTTGCTTAA
244	IPO7	CCTGATCGAGAAACAGCACC
245	IPO7	AATACATACCTGATGAGCTC
246	IRF4	CAAGCAGGACTACAACCGCG
247	IRF4	GGTACTTGCCGCTGTCGATC
248	IRF6	CTGGGTTAATGATCGAGCCC
249	IRF6	CCTTGGTGCCATCATACATC
250	ITGB7	AGCGGGTCCGGGTCACGCTG
251	ITGB7	TGAGCAGAACTTCACCGCGT
252	ITPKB	CCTTCAAGAAGAAGTACCCC
253	ITPKB	ATCCAGCTGGCAGGACACGC
254	KDM5C	GGGCTACCCGAGCCCACCGA
255	KDM5C	CAGCGCCTCAACTATCCACC
256	KDM6A	TTGGATAATCTTCCAATAAG
257	KDM6A	TTATTGGAAGATTATCCAAA
258	KEAP1	AGCCGCCCGCGGTGTAGATC

259	KEAP1	AGCGTGCCCCGTAACCGCAT
260	KEL	GATAGCTGTCAGCACCCGCC
261	KEL	GCTTACGAGGGCCACAGTTC
262	KIT	ACCGCGATGAGAGGCGCTCG
263	KIT	CTTGTTGACCGCTCCTTGTA
264	KLHL8	AACAGATCCTCAATTAGTGA
265	KLHL8	ACTCTGTGATGTCACACTCA
266	KRAS	CAATGAGGGACCAGTACATG
267	KRAS	AACATCAGCAAAGACAAGAC
268	LCTL	GACCTTGTAGTAGCCGTCAC
269	LCTL	TAGCTCACCTCGGATGCCTG
270	LIFR	TATGTTTGAAACGACCATCC
271	LIFR	TAAATGTTGATAACAGCCAC
272	LRRK2	GAGAGTCGCGAGTGTGCAGC
273	LRRK2	CACACTCGCGACTCTCATAT
274	MAP2K1	CCATACTTACTCCGCAGAGC
275	MAP2K1	CCCGACGGCTCTGCAGTTAA
276	MAP2K4	ACAGCCAGCATCTCTTGTCT
277	MAP2K4	TTTGTAAAACTTATCAAACG
278	MAP3K1	CAAGATGGATGATCGTCCAG
279	MAP3K1	CCCGCATCACTTTGTTAACA
280	MAP4K3	CCAAATATTGTTGCTTATTT
281	MAP4K3	CCAAAATAAGCAACAATATT
282	MAPK8IP1	TTGCCCTTACCCGTAAGGAC
283	MAPK8IP1	ACTCATCAGTGATCTCCGAG
284	MBD1	AGCCAAGACTCGGAAACGTC
285	MBD1	GGCCCCGAGGGATGAGACCA
286	MECOM	TGGTACTAACCGTGGATATC
287	MECOM	CTCAAGTACATTAGATTCGC

288	MED12	CGTCAGCTTCAATCCTGCCA
289	MED12	AGGATTGAAGCTGACGTTCT
290	MED23	ACTGCAGAGCATTTTCGAAG
291	MED23	GAAAACGGAAGTTATAGAAG
292	MET	CACATGGCAGATCGATCCAT
293	MET	GGGTGTTTCCGCGGTGAAGT
294	MGA	CTATGCATCGTTACCTGCCG
295	MGA	CCCTCGATAACAATAGTATG
296	MICALCL	ACGGCTCGCCTCCGAAAGTT
297	MICALCL	GACCTCTCGAGACTTGCGAG
298	MLL	TCAGAGTGCGAAGTCCCACA
299	MLL	CGTACCTGAAGGAGACCTTG
300	MLL2	CAGAGAGCACAACGCCGCAC
301	MLL2	ACAGAGACCTCTCCCACATG
302	MLL3	TTTTCTGTAGACCTCGAAGT
303	MLL3	GGGGAAGCGCCATCTTTGCG
304	MLL4	CAACGGGGCCGAAAGAGTGC
305	MLL4	CAGAGCTACCCGCACTCTTT
306	MORC4	GCGACCCTTCAGTGCCATCG
307	MORC4	CTCACCTAGCAGCTCCGCGA
308	MPO	ACGAGGTGTCCACCTCCCCC
309	MPO	CCTACAAGGAGCGGCGGGAA
310	MTOR	AAGCACCTCTCGGAGTTCCA
311	MTOR	GCTCCAGCACTATGTCACCA
312	MUC17	GACGGTTCAAGACGTCCCCT
313	MUC17	TAACGTGCTGAGACAGCTGC
314	MXRA5	AAAGCTCCATCGGGGATGCT
315	MXRA5	GAGATCCCAAGCATCCCCGA
316	MYB	CAAGTCTGGAAAGCGTCACT

317	MYB	CAGCATATATAGCAGTGACG
318	MYCN	CGAGTGCGTGGATCCCGCCG
319	MYCN	GACCAGCGGCGGCGACCACA
320	MYD88	CACCACACTTGATGACCCCC
321	MYD88	TCTACAGCGGCCACCTGTAA
322	MYOCD	GAACTTGCTCCTAATCAGCA
323	MYOCD	GAAAAAATTGCTCTACGACC
324	NAV3	ATCGGAAGAGCAGTATGCAC
325	NAV3	GACCCAGTAGTGCCAAGATT
326	NCOR1	TCCCAACACCCGCCACCAGC
327	NCOR1	AATGTATACTGGACAGAGTG
328	NF1	GTTGTGCTCAGTACTGACTT
329	NF1	ACACTGGAAAAATGTCTTGC
330	NFE2L2	CCCGTTTGTAGATGACAATG
331	NFE2L2	ACAGCTCATCATGATGGACT
332	NFE2L3	ATTACCTCCAGTGAATTTTC
333	NFE2L3	GACCACTGAATCTAGAAATG
334	NOTCH1	CACGCAGGCCTCCGTGCCAT
335	NOTCH1	TCACCGGGCTGGGAGCATCG
336	NRAS	CTTCGCCTGTCCTCATGTAT
337	NRAS	CCATGAGAGACCAATACATG
338	NSD1	GATTCCAGTACCAGTACATT
339	NSD1	AAAGGGCTGTCCTTGTCTTC
340	NTN4	ACTAACTGCTCCGCTACATT
341	NTN4	TTAGTCGCAAAGTACTTATA
342	NUP210L	CTACCCTTCGGCCGAGAGCC
343	NUP210L	TCATCAAGACGCCGAGGCTT
344	ODAM	AGGCGGTGTTTGAAGCTGTA
345	ODAM	TTTACCTGTCCTTGCTCTTG

346	OMA1	CTGGAAGTAAGTCCAATCAC
347	OMA1	GGCACTTCCTCCTAACAAGA
348	OR4A16	CTGTACAGTCTACCAATCTG
349	OR4A16	CAATAGTAGTCACCCAAATG
350	OR52N1	GTACCTCATCTACTGTGATG
351	OR52N1	ATGACGTTGCCCTTGCAGTA
352	OTUD7A	CGACTATGAGCAGCTCCGCC
353	OTUD7A	AGACCTGAGCGTGTACAGCG
354	PAPD5	CCCGGTGCTGAGCGTGGACG
355	PAPD5	GCGCGCGCCTCAGAAGCTCC
356	PBRM1	TAATACCATCCGAGACTATA
357	PBRM1	CAATGCAAAGTCCTATTATA
358	PCBP1	GTCGGTTAAGAGGATCCGCG
359	PDAP1	CTGTTCTAGCAAAAGCGCAA
360	PDAP1	CAGCCGGGCCAGGTCAGCCT
361	PDCD2L	CATGGCGGCCGTTCTGAAGC
362	PDCD2L	CCTGTGGGGCTGCCGTGCAC
363	PDGFRA	AGCTATGGGGACTTCCCATC
364	PDGFRA	GTCTTAGGCTGTCTTCTCAC
365	PDSS2	GGGGGCTTGTACATGACAGC
366	PDSS2	ACATGAAGTGTTCACGCTGC
367	PHF6	GGCAGCGCACCATAAGTGCA
368	PHF6	CCTACAAGACAGCGCAAATG
369	PHF20	CAGCTGTCGACCTAGACCAT
370	PHF20	ACCCAGTGTGCTTCTTCCAC
371	PIK3CA	CTCACCTTATACTGACTCAG
372	PIK3CA	GCTTCAGCAATTACTTGTTC
373	PIK3CG	TTGGGTAAAGTCGTGCAGCA
374	PIK3CG	GCCAGATTTCTGCTGAAGCG

375	PIK3R1	CGCTTTCAAACGCTATCTCC
376	PIK3R1	AATGATCGATGTGCACGTTT
377	PLCG2	TTTTGCTCGCTCGAAATCTT
378	PLCG2	TGGACGCATTCATCGCTTCC
379	POLE	CCGTCCACTGACTCCGTTCC
380	POLE	GATAAGATGGATTTGCGGTT
381	POLQ	AGCTTGTCTCTTTCGTAGTC
382	POLQ	CGAAAGAGACAAGCTACTAT
383	POU2AF1	ACTCTCACCGCCGTAGGTGC
384	POU2AF1	ATACCAGGGCGTCCGTGTGA
385	POU2F2	GACTCCCCATCAGAGCACAC
386	POU2F2	GGAGTCCAGACCTTGCTTCT
387	PPM1D	GCCCCGAATGATGACCACAC
388	PPM1D	GGAAGACCCGTCATAGTCTT
389	PPP2R1A	TGCCAATGTCCGCTTCAATG
390	PPP2R1A	CCCTATCTTCTGCAGAGACT
391	PPP6C	ATATCTCCACACACTGTTAC
392	PPP6C	TCAACACCAGTAACAGTGTG
393	PRDM1	AAAACGTGTGGGTACGACCT
394	PRDM1	TCAGATGTTGGATATTTGCT
395	PRX	TACGTTGATGCCGCTGACCC
396	PRX	GGGCACTCACCTCGGCACTC
397	PTEN	ACCGCCAAATTTAATTGCAG
398	PTEN	TTATCCAAACATTATTGCTA
399	PTPN11	GAGACTTCACACTTTCCGTT
400	PTPN11	GTTACTGACCTTTCAGAGGT
401	QKI	CTGTAAGTCCTCTAGGTCCA
402	QKI	TTCTCTTGTAACTGAACAAT
403	RAB40A	TGTAGTCGATCCCCCCGAGA

404	RAC1	ATTTGAAAATGTCCGTGCAA
405	RAD21	CTTCATTACAGTCTGCAAGA
406	RAD21	CATAGGTGAAAATGGCATTA
407	RASA1	CGATAGCAGAAGAACGCCTC
408	RASA1	ATCTTATAAGAGAGAGTGAT
409	RB1	ATATGGTTCTTTGAGCAACA
410	RB1	TTCAGGGGAAGTATTACAAA
411	RBM10	CGTTCATATCCTCGCGAGTA
412	RBM10	AGGACATGGAGTATGAAAGA
413	RHEB	CTTCAACTTGTAGACACAGC
414	RHEB	ACAATACTTACTGTTTTCTA
415	RHOA	ATCGACAGCCCTGATAGTTT
416	RHOA	GGCCACTCACCTAAACTATC
417	RIT1	GATTCTGGAACTCGCCCAGT
418	RIT1	GGAGTACAAACTAGTGATGC
419	RPL5	AAACAGAGATATCATTTGTC
420	RPS15	ACTAGGACATGTCCAGCAGC
421	RPS15	CTTCAACCAGGTGGAGATCA
422	RPS2	CGACGCGTACCTTAATAGGC
423	RPS2	GTACCTTGAACCTGGTGCGC
424	RSBN1L	CATATAGAGCACCAGCCTAA
425	RSBN1L	AATGAGATCAAGAAAGAGAA
426	RUNX1	TCACCTCTCATGAAGCACTG
427	RUNX1	TACCCACAGTGCTTCATGAG
428	RXRA	CGGGCCCATGCCGTTGATGG
429	RXRA	CTCGGTCATCAGCTCCCCCA
430	SACS	ACTCATTTACCTGTTCTCCT
431	SACS	AGAAGTGATCATGGAGACCA
432	SELP	CTAAGTCTGTGTAGCGATTC

433	SELP	GAATCGCTACACAGACTTAG
434	12-Sep	GAACAGCGTGTTCACCATCG
435	12-Sep	TCATAGCCTTGATCTTCAGC
436	SERPINB13	GACGAAGAGCTCAAGAATAA
437	SERPINB13	ATGAACTGAACATAACCAAC
438	SETBP1	CTTGCAGCCAGTGACCTCAA
439	SETBP1	CCTGTGGCTGAAATCCTTTG
440	SETD2	AACTTACGAAGGAAGGTCTT
441	SETD2	AGTTCTTCTCGGTGTCCAAA
442	SETDB1	AACTCTTTGATGATGCATCC
443	SETDB1	TGGATGCATCATCAAAGAGT
444	SF3B1	TCATCATCTACGAGTTTGCT
445	SF3B1	AAGATCGCCAAGACTCACGA
446	SGK1	GCACATTGCAGGTACGAAGG
447	SGK1	CACAAGGAAGACTCGAAGTC
448	SIN3A	AATTCCCGTAGCTGACTGCA
449	SIN3A	GGGCTGGATGAGCATGACTC
450	SIRT4	TCCCCGAAGAAAACGACATC
451	SIRT4	AACGCTCTTGCAGCACCCCC
452	SLC1A3	AGTGTTTACCTGTTTAAAGC
453	SLC1A3	GAACATGTTCCCTCCAAATC
454	SLC26A3	GGGATTGTGGCCGTACTACA
455	SLC26A3	CAGCATACCGGCTTAAAGAA
456	SLC44A3	GACGAAAGGATGGGATGATC
457	SLC44A3	GCAAAACGCACTGAAAGAAC
458	SLC4A5	GAATGCCCTCCTATCCACAT
459	SLC4A5	TAACCACAGGAGGAGATTTC
460	SMAD2	CTCCAGGTATCCCATCGAAA
461	SMAD2	CTAAATGTGTTACCATACCA

462	SMAD4	AATACACTTACCAGGATGAT
463	SMAD4	GGATTAACACTGCAGAGTAA
464	SMARCA4	GGATCCCTACCTTGTGCATC
465	SMARCA4	TTGTCCTGAGGGTACCCTCC
466	SMARCB1	AACTACCTCCGTATGTTCCG
467	SMARCB1	TGTGACCCTGTTAAAAGCCT
468	SMC1A	GTATCAGATTGCTGTAACCA
469	SMC1A	GAATCCACACCTTGTGGCGC
470	SMC1A	GGACTGTATTCAGTATATCA
471	SMC1A	GGCCTCCAAAGGCAATGCGG
472	SMC3	CTCTGTAACTTCGAAAACCC
473	SMC3	CACATTATGTTTTGAACTGA
474	SNX25	CACCTATGCCCCCTCTTACG
475	SNX25	ATGGATAAAGCTCTGAAAGA
476	SOS1	CCGAAGTGCTTCAGATGTAG
477	SOS1	CCTCTACATCTGAAGCACTT
478	SOX17	GCCGGCGAACAGCGGAGCAC
479	SOX17	GGCTCAGCGACTCGGCCCAG
480	SOX9	CGTGTTCTCGGTGTCCGAGC
481	SOX9	CGACTCACCCGAGTGCTCGC
482	SPEN	CGTTATGAGCGGAGACTTGA
483	SPEN	CCGTCACTTCATGCACGAGA
484	SPOP	CAAGCTTACCCTCTTCTGCG
485	SPOP	CCAGTAACAGGTAAAGTGAC
486	STAG2	CTTCAGTCGTAGAGATCCAG
487	STAG2	AGTCCCACATGCTATCCACA
488	STK11	TCTACCAGCCGCGCCGCAAG
489	STK11	CCACCGCATCGACTCCACCG
490	STK19	GTTCCCGGTACTTTGCCTTC

491	STK19	AGCTGGTGGCTAGCTGTGCC
492	STX2	CCGCTCACCGCCGTCAGGTC
493	STX2	TAGTGTAGGAAGAATGATGA
494	TAF1	CCGAAGATACCAGCAGACGA
495	TAF1	TTGCAGCCCCTTTGCCACTC
496	TAP1	GGTGCGAGGCCTATGTCTCT
497	TAP1	GCATGATCCCCAAGAGACAT
498	TBC1D12	TCAGTTGTCCATAGTGCTCC
499	TBC1D12	TTACCAAATAATTTCCAACC
500	TBL1XR1	ACCATCTTTAGTCCATATTC
501	TBL1XR1	GATATGGCTTTCTATACCAA
502	TBX3	CCGACCCCGAAATGCCAAAG
503	TBX3	CACAGCGATGAATTCAGTTT
504	TCEB1	CTTACCTGGGCCACTCAACA
505	TCEB1	AGGTCCTTCACAGCCACCAT
506	TCF7L2	TCTCGGAAACTTTCGGAGCG
507	TCF7L2	GCAAGCGAAATACTACGAGC
508	TCP11L2	TGAATCCAAGACGTCCCAGA
509	TCP11L2	CCCCCAGGTTACCTCTTTTC
510	TDRD10	CAACTCTCTGATAAACTGTT
511	TDRD10	CAAACAGTTTATCAGAGAGT
512	TET2	TACCGTTCAGAGCTGCCACC
513	TET2	GATTCCGCTTGGTGAAAACG
514	TGFBR2	CTCCATCTGTGAGAAGCCAC
515	TGFBR2	ATGATAGTCACTGACAACAA
516	TIMM17A	TCTTAGCCCATGGCGAATTG
517	TIMM17A	GGTATCTTTCAAGCAATCAA
518	TLR4	GATGATGTCTGCCTCGCGCC
519	TLR4	TATAGCTGCCTAAATGCCTC

520	TNF	TGGTGGCGCCTGCCACGATC
521	TNF	CCAGAGGGCTGATTAGAGAG
522	TNFRSF14	TACTCGTCCTCCTTGCAGGA
523	TNFRSF14	GCACCTACCTGGACTGCACT
524	TP53	CTTACCAGAACGTTGTTTTC
525	TP53	ACTTCCTGAAAACAACGTTC
526	TP53BP1	GAACGAGGAGACGGTAATAG
527	TP53BP1	CAGAATCATCCTCTAGAACC
528	TPX2	TTATTCCTATGATGCCCCCT
529	TPX2	AGTATCTCCTTCATCATCCA
530	TRAF3	AGCCCGAAGCAGACCGAGTG
531	TRAF3	CCGCTTCTGCGAGAGCTGCA
532	TRIM23	GATCGACAAGTAACAGACCT
533	TRIM23	GTTCCCCGTCTTTTGCTTTG
534	TSC1	CGAGATAGACTTCCGCCACG
535	TSC1	ACCTTCGAGGGTCCAGTTCA
536	TSHZ2	GGTATTAGACCCGTTAGCAG
537	TSHZ2	GCTGCGTTGCTCCATTATAC
538	TSHZ3	CACGACTGTGTCGGATAGCC
539	TSHZ3	GGAGAAGCATCATGCCGAGG
540	TTLL9	CACCTAATGGCAGTTGTGCC
541	TTLL9	CGTCCATGAGTGTGTTCATG
542	TXNDC8	AACCACTGCGAGTTTGTGTC
543	TXNDC8	GTTGTACTCACATGGAAAAC
544	U2AF1	GTCTTTTCAGTTTCGCCGTG
545	U2AF1	GGTGGGGAACGTGTACGTCA
546	USP9X	AACTTTTAGGCCTCGATGGG
547	USP9X	AGTTGCCGGGGAATTTTCAT
548	VEZF1	AGAGCTTGTGTCGATTGAGA

549	VEZF1	TTCTTGACAGACTGGGTCAC
550	VHL	CGCGCGTCGTGCTGCCCGTA
551	VHL	TGTCCGTCAACATTGAGAGA
552	WASF3	TTGAGCCCCGGCACTTGTGC
553	WASF3	CTTCCACTGTTGAATCCAGC
554	WT1	TTCGACGGGACGCCCAGCTA
555	WT1	GTAGCTGGGCGTCCCGTCGA
556	XIRP2	GGAGCGGATGGCGAGGTACC
557	XIRP2	TTACATTAGCAGAGAAGCTG
558	XIRP2	ATCTGTTCTGATGTTGATAT
559	XPO1	GCTAACATTGTCATAATTGC
560	XPO1	ATTTTGACAGAGACTTTCGC
561	ZFHX3	CGTCGTGAACTTGTTGCAGA
562	ZFHX3	CGTCTGCAACAAGTTCACGA
563	ZNF180	TGTCCGATGCGCGCATGCGC
564	ZNF180	GACCCTGCGCATGCGCGCAT
565	ZNF471	AGTAGTAAAAGTCATGCCCC
566	ZNF471	ATCTCACTCGTCATCTCCCA
567	ZNF483	GTCTCAAAAAGCTCCCGACT
568	ZNF483	ACAGTAGAATCTTGAGAGAC
569	ZNF620	GGATAGCCCTATGCTTGGAC
570	ZNF620	GAATCTTCCACACCAGCTGA
571	ZNF750	TCTAACCTGCCGATTCCTTA
572	ZNF750	GAACTCGACGTGTTTTCTGT
573	ZRANB3	AGCTTTGCTCTTAGTCTGTC

Supplementary Table S2. Hits with the highest scores in mass spectrometry analyses of proteins from pull-down assay with PHF20 specific antibodies.

Gene	MW [kDa]	Score
PHF20	115.30	524.71
PARP1	113.00	466.65
H2AFY	39.60	396.46
NPM1	32.50	330.01
SSRP1	80.80	311.65
ILF3	95.30	225.72
PTBP1	57.20	182.45
HMGA2	11.80	119.59
PSIP1	59.70	100.79
HNRNPAB	36.20	94.43
RSL1D1	54.90	92.77
XRCC6	69.80	91.86
SYNCRIP	69.60	78.78
TOR1AIP1	66.20	72.52
CDC5L	92.20	70.83
RUVBL1	50.20	61.23
NOP2	89.20	60.62
SRSF2	25.50	54.86
SRSF1	27.70	54.13
RAI14	110.00	51.18
HNRNPL	64.10	50.58
PDCD11	208.60	49.72
HNRNPF	45.70	46.58
SURF6	41.40	43.01
SMU1	57.50	42.78
NAT10	115.30	40.60
ZHX3	103.70	40.49
RBM34	48.50	37.46
G3BP1	52.10	37.01
WTAP	44.20	29.62
NIFK	34.20	23.06
WDR5	36.60	21.98

Supplementary Table S3. Primers used for this study.

Real-time PCR primers

human PHF20-forward	ACCCGGCTCCCCAAAGGTGA
human PHF20-reverse	CTGCCACTGGTGCTGGGAGC
human Oct4-forward	GAAGCCTTTCCCCCTGTCTC
human Oct4-reverse	ATCCCAAAAACCCTGGCACA
human Sox2-forward	GCCCTGCAGTACAACTCCAT
human Sox2-reverse	GACTTGACCACCGAACCCAT
human Nanog-forward	CTGCAGAGAAGAGTGTCGCA
human Nanog-reverse	ATCTGCTGGAGGCTGAGGTA
human MYCN-forward	TCCCTACGTGGAGAGTGAGG
human MYCN-reverse	CTGAGCGTGAGAAAGCTGGA
human EGFR-forward	AAACCGGACTGAAGGAGCTG
human EGFR-reverse	CCCATTGGGACAGCTTGGAT
human Wnt3a-forward	TGCTGGACAAAGCTACCAGG
human Wnt3a-reverse	CGAGACACCATCCCACCAAA
human Bmi1-forward	TCTTGTTTGCCTAGCCCCAG
human Bmi1-reverse	GGCTGTTGCTGGTTCCATTC
human N-cadherin-forward	AGCAGTGAGCCTGCAGATTT
human N-cadherin-reverse	GCCACTTGCCACTTTTCCTG

human E-cadherin-forward	TGGATGTGAATGAAGCCCCC
human E-cadherin-reverse	TTAGGGCTGTGTACGTGCTG
human Vimentin-forward	GGACCAGCTAACCAACGACA
human Vimentin-reverse	AAGGTCAAGACGTGCCAGAG
human Slug-forward	CATCTTTGGGGCGAGTGAGT
human Slug-reverse	ATGGCATGGGGGTCTGAAAG
human GAPDH-forward	GTCAAGGCTGAGAACGGGAA
human GAPDH-reverse	AAATGAGCCCCAGCCTTCTC

ChIP qPCR primers

human Sox2-pro-1-F	GAGTTGGACAGGGAGATGGC
human Sox2-pro-1-R	CAACACTCTCTCACGCCCTT
human Sox2-pro-2-F	AAGGGCGTGAGAGAGTGTTG
human Sox2-pro-2-R	TTGTTCTCCCGCTCATCCAC
human Oct4-pro-1-F	TCAAGCACTAGACCAGCAGC
human Oct4-pro-1-R	GGCAGATTGAGGGATGTGCT
human Oct4-pro-2-F	GTGTGAGGGGATTGGGACTG
human Oct4-pro-2-R	CTCAACCCTTGAATGGGCCT
human Nanog-pro-1-F	TCAGGTTCTGTTGCTCGGTT
human Nanog-pro-1-R	TCCCGTCTACCAGTCTCACC
human Nanog-pro-2-F	GAGGGGTGGGTCTAAGGTGA
human Nanog-pro-2-R	ATGAGGCAACCAGCTCAGTC