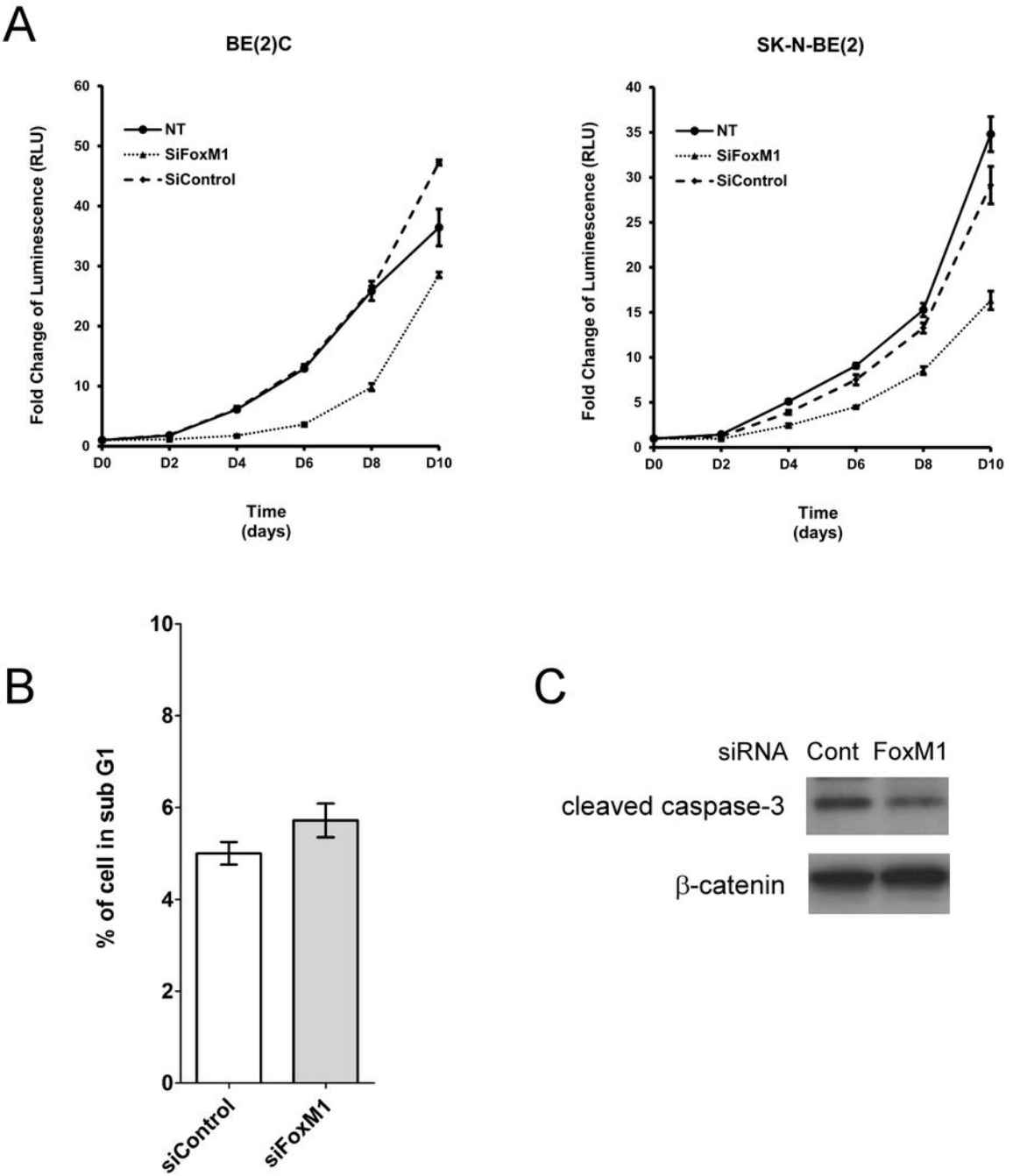
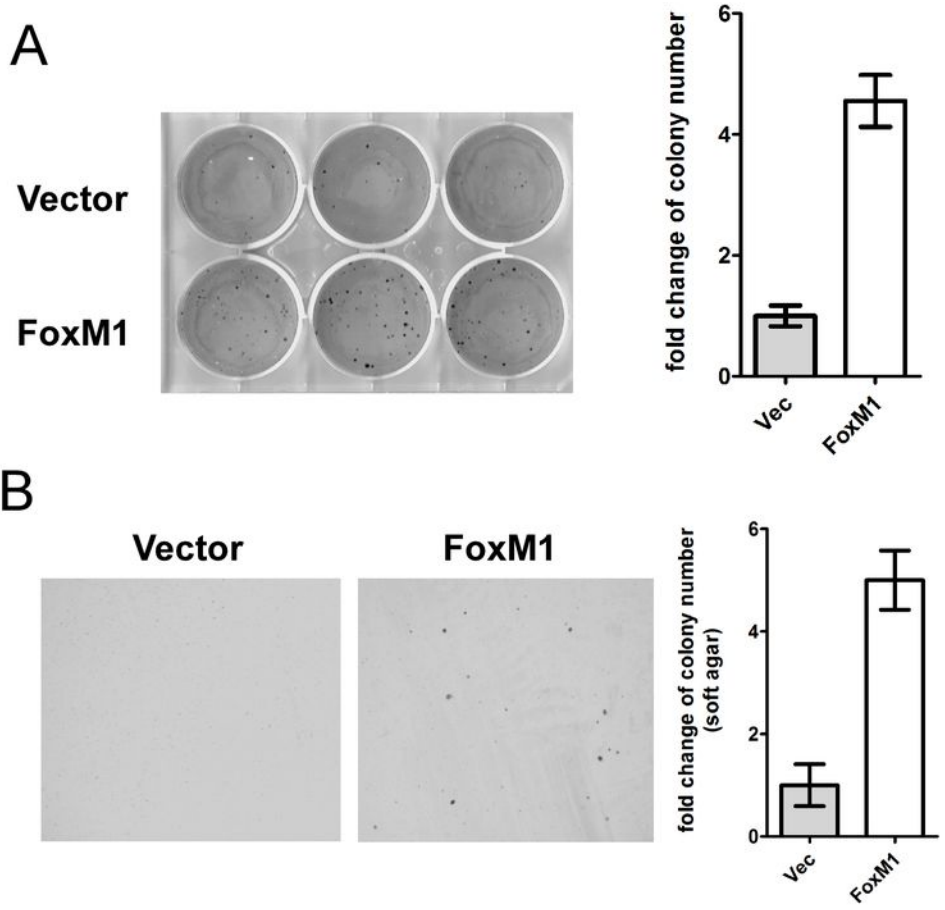
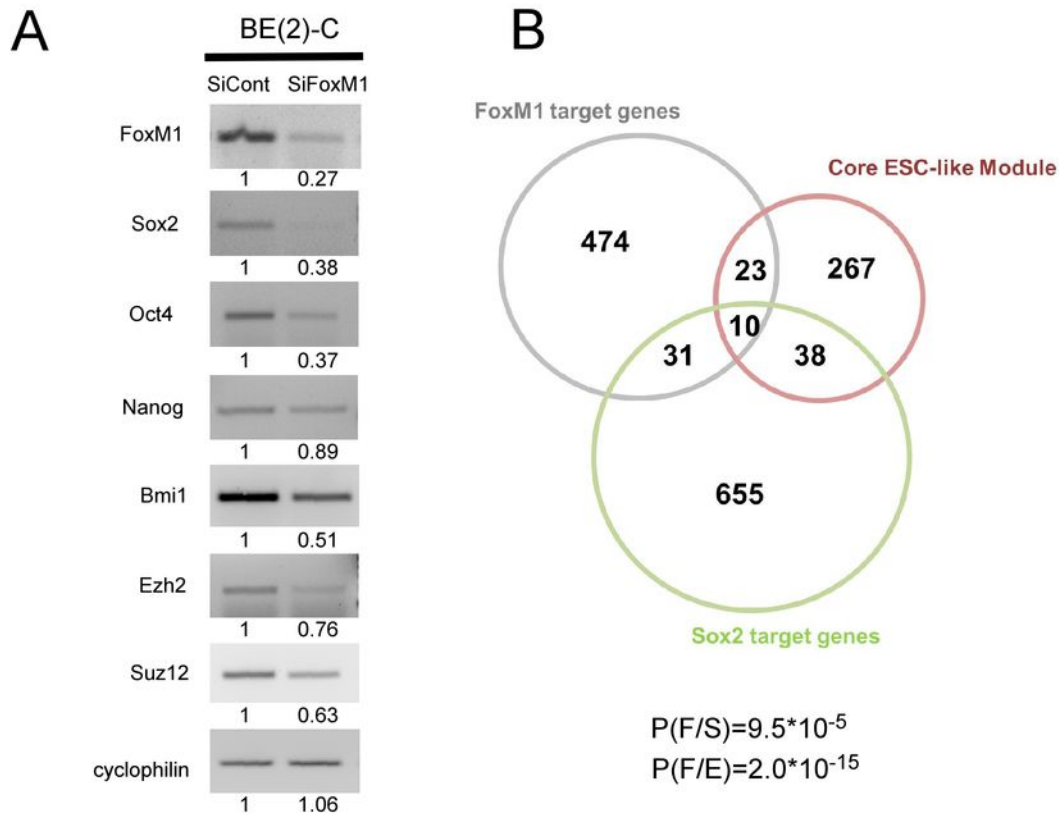
Supplement figure.1



Supplementary figure.2



Supplement figure.3

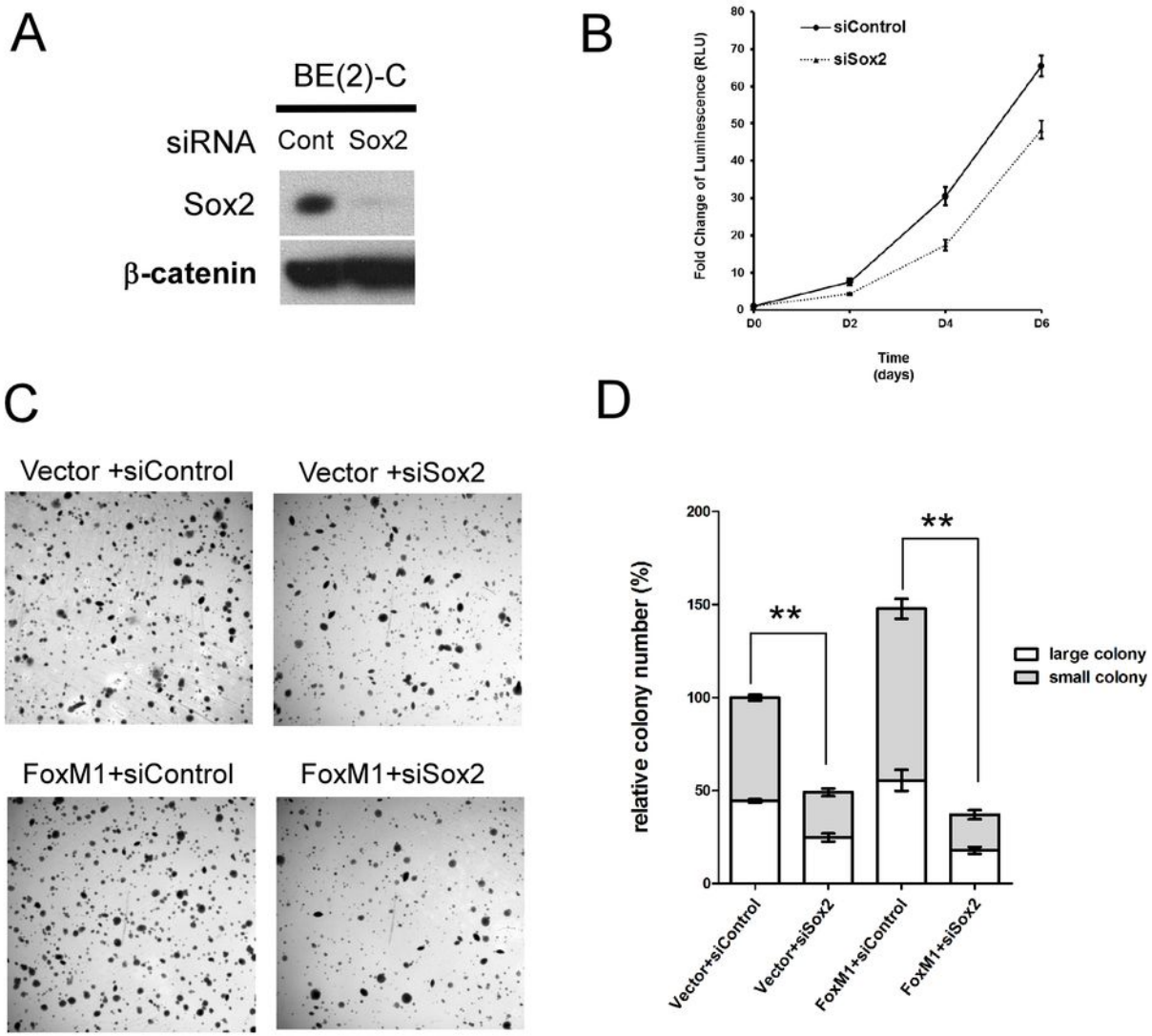


C

Overlapping gene list of FoxM1 targets and core ESC-like module

Human Entrez Gene ID	Name	Symbol
158	Adenylosuccinate lyase	ADSL
328	APEX nuclease (multifunctional DNA repair enzyme) 1	APEX1
332	Baculoviral IAP repeat-containing 5 (survivin)	BIRC5
595	Cyclin D1	CCND1
890	Cyclin A2	CCNA2
899	Cyclin F	CCNF
983	Cell division cycle 2, G1 to S and G2 to M	CDC2
997	Cell division cycle 34 homolog (S. cerevisiae)	CDC34
1033	Cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	CDKN3
3070	Helicase, lymphoid-specific	HELLS
4173	Minichromosome maintenance complex component 4	MCM4
4174	Minichromosome maintenance complex component 5	MCM5
4751	NIMA (never in mitosis gene a)-related kinase 2	NEK2
4841	Non-POU domain containing, octamer-binding	NONO
5347	Polo-like kinase 1 (Drosophila)	PLK1
6146	Ribosomal protein L22	RPL22
6566	Solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	SLC16A1
7050	TGFB-induced factor homeobox 1	TGIF1
7153	Topoisomerase (DNA) II alpha 170kDa	TOP2A
9133	Cyclin B2	CCNB2
9212	Aurora kinase B	AURKB
10007	Glucosamine-6-phosphate deaminase 1	GNPDA1
10112	Kinesin family member 20A	KIF20A
10434	Lysophospholipase I	LYPLA1
10961	Endoplasmic reticulum protein 29	ERP29
10963	Stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	STIP1
23658	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM5
25804	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM4
26354	Guanine nucleotide binding protein-like 3 (nucleolar)	GNL3
28973	Mitochondrial ribosomal protein S18B	MRPS18B
29088	Mitochondrial ribosomal protein L15	MRPL15
51203	Nucleolar and spindle associated protein 1	NUSAP1
79084	WD repeat domain 77	WDR77

Supplement figure.4



Supplementary figure 1

FoxM1 moderately affects the growth of neuroblastoma cells. A, Twenty-four hours after FoxM1 or control siRNA transfection, cells were trypsinized and seeded at a density of $2x10^3$ cells per 48-well plate for proliferation assay. Viable cell number was measured by using CellTiter-Glo luminescent cell viability assay kit (Promega) every two days. The fold change in cell count was presented by luminescence unit and was normalized by the value at day zero. B, Seventy-two hours after FoxM1 or control siRNA transfection, cells were fixed and stained with propidium iodide (PI) and analyzed by flow cytometry for sub-G1 population. C, Seventtwo hours after FoxM1 or control siRNA transfection, cell lysates were collected and assayed for cleaved caspase-3 by immunoblot. β-catenin was used as loading control.

Supplementary figure 2

FoxM1 promotes tumorigenicity in SK-N-AS cells. A, Colony formation is induced in cells stably expressing FoxM1. $2x10^3$ SK-N-AS cells stabling expressing empty vector or FoxM1 were plated per well in a six-well plate in triplicate. Colonies were stained and quantified after 2 weeks. B, Representative pictures and quantification of anchorage-independent growth of SK-N-AS cells stabling expressing empty vector or FoxM1. Cells were plated a density of $1.6x10^4$ cells per well in a six-well plate. Colonies were stained and counted after three weeks. C, Immunoblot showing expression of FoxM1 and Sox2 of SK-N-AS cells stabling expressing empty vector for FoxM1. α–tubulin was used as the loading control.

Supplementary figure 3

FoxM1 and ESC-like gene signature. A, Seventy-two hours after FoxM1 and control siRNA treatment, semiquantitative RT-PCR was performed to analyze the mRNA level of the pluripotency genes including Sox2, Oct4, Nanog, Bmi1, Ezh2, Suz12. Cyclophilin was used as a loading control. The intensity of the bands was determined by ImageJ software and the intensity of control samples were set at one. B, Venn diagram of overlapping genes in three groups: FoxM1 target genes, Sox2 target genes and core ESC-like module. FoxM1 target genes were summarized from 201 published FoxM1 related literature where FoxM1 regulated genes were reported and from differentially expressed genes from one publicly available FoxM1 array of breast carcinoma (NCBI GDS1477) (50). Sox2 target genes were reported from chip array study (49, 39, table S1)) and core ESC-like module was previously purposed (49(table S6)). P value for both FoxM1 with Sox2 targets overlap (F/S) and FoxM1 with core module overlap (F/E) were obtained using hypergeometric calculation. C, List of 33 overlapping genes of FoxM1 targets and core ESC-like module. Among them, genes that were also Sox2 targets were highlighted in red.

Supplementary figure 4

FoxM1 mediated anchorage-independent growth requires expression of Sox2. A, Immunoblot showing depletion of Sox2 by siRNA in BE(2)-C cells. Cell lysates were collected at four days after transfection. B, 24 hours after Sox2 or control siRNA transfection, cells were trypsinized and seeded at a density of $2x10^3$ cells per well in a 48-well plate for proliferation assay. Viable cell number was measured by using CellTiter-

Glo luminescent cell viability assay kit (Promega) every two days. The fold change in cell count was presented by luminescence unit and was normalized by day zero. C, BE(2)-C cells were first transfected with empty or pCMV-FoxM1 plasmid for 24 hours, and then transfected with either control siRNA or Sox2 siRNA for another 24 hours. Cells were plated at a density of $8x10^3$ cells per well in a six-well plate in soft agar plate. Colonies were stained and quantified after three weeks. D, Quantification of colonies numbers derived from C. Colony large than 100μm in diameter was defined as large colony and colony which has diameter between 25-100μm was defined as small colony.