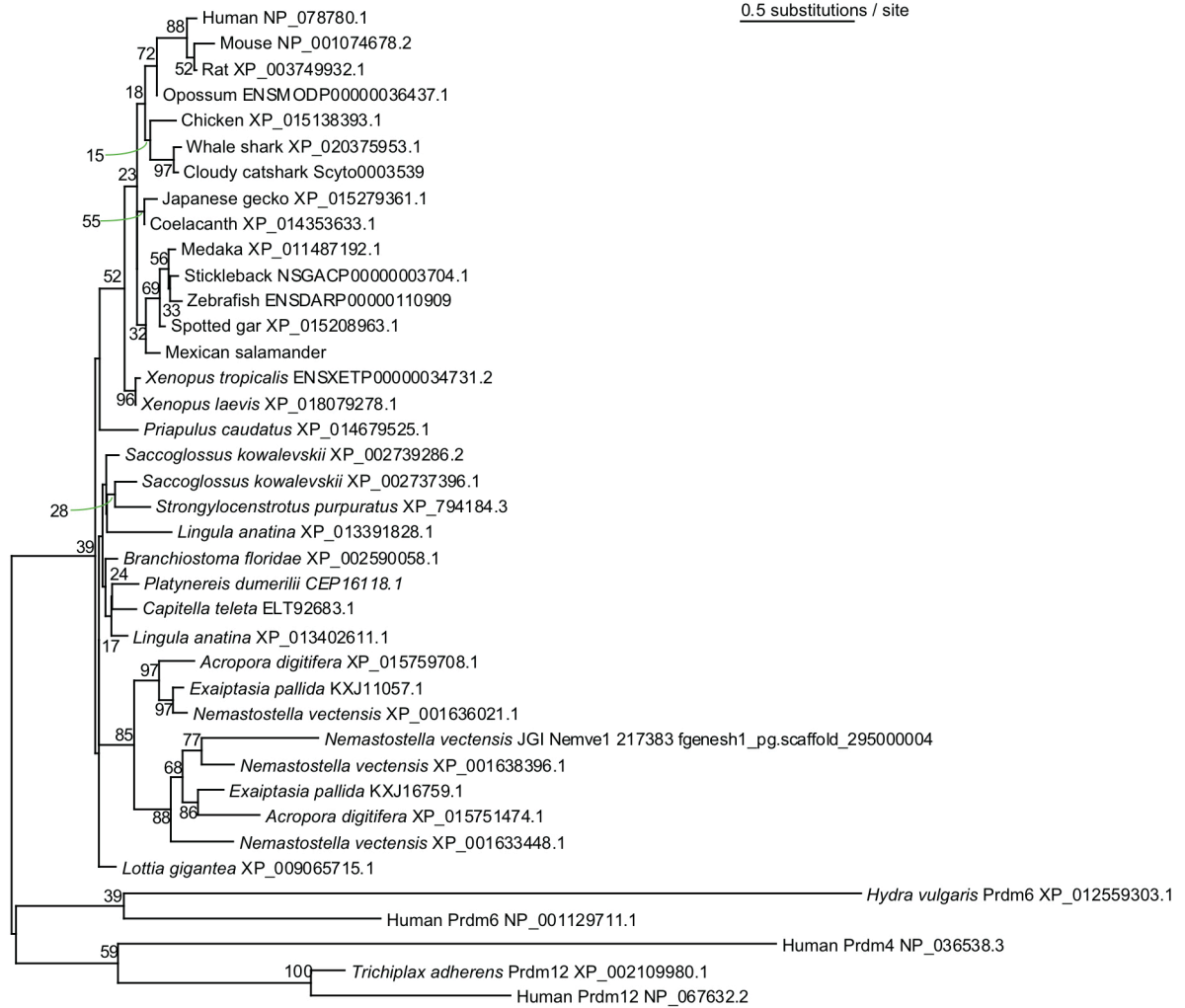


A



B



Fig. S1. Molecular phylogeny and sequence conservation for the metazoan PRDM14. (A) A maximum-likelihood tree was constructed using amino acid sequences of Prdm14 orthologues and human Prdm4/6/12, hydra Prdm6 and Trichoplax adherens Prdm12 as an outgroup. (B) Sequence alignment of PRDM14 orthologue proteins. The pink restriction box indicates the position of the PR domain and the green restriction box indicates the position of the zinc finger domain.

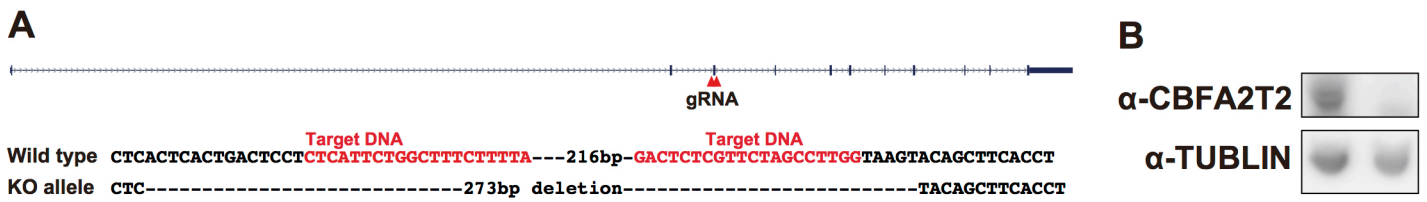


Fig. S2. Establishment of *mCbfa2t2* KO cell line using CRISPR/Cas9 system. (A) CRISPR design and the deletion sequence of *mCbfa2t2* KO cell line. (B) Western blot analysis of CBFA2T2.

Table S1. Primer lists for qRT-PCR, bisulfite sequencing and ChIP-qPCR.

qRT-PCR

Gene	Strand	Sequence(5'-3')
<i>Oct3/4</i>	Forward	CTCTCCCATGCATTCAAAGCTG
	Reverse	CCCCTGTTGTGCTTTTAATCC
<i>Nanog</i>	Forward	TTTGGAGGTGAATTTGGAAGC
	Reverse	TCACCTGGTGGAGTCACAGAG
<i>Esrrb</i>	Forward	CGTGTGACAAGGAGACAGGAG
	Reverse	TCCAGCCACAACGTCATTATC
<i>Tcl1</i>	Forward	TGGCCTCACTAGAACAAGAGG
	Reverse	CTCGGTCAAGGATGGAAGC
<i>Klf2</i>	Forward	CCCAGGAAAGAAGACAGGAG
	Reverse	AGGCATTTCTCACAAGGCATC
<i>Tcl1</i>	Forward	TGGCCTCACTAGAACAAGAGG
	Reverse	CTCGGTCAAGGATGGAAGC
<i>Tbx3</i>	Forward	TGATGTTTTAAGAGCCGATGC
	Reverse	AGGATAATGGGACTTCCGTTG
<i>Klf4</i>	Forward	GACCAGGATTCCCTTGAATTG
	Reverse	ACCAAGCACCATCATTTAGGC
<i>Klf5</i>	Forward	TGGAAGTCCCGATAGACAAGC
	Reverse	GTGGCAGGTAAATTTGGGTTG
<i>Dnmt3a2</i>	Forward	CAGACGGGCAGCTATTTACAG
	Reverse	TGTTTCTCTCCACAGCATTC
<i>Dnmt3b</i>	Forward	CTCGCAAGGTGTGGGCTTTTGTAAC
	Reverse	CTGGGCATCTGTCATCTTTGCACC
<i>Dnmt3l</i>	Forward	CTGGTGAAGAACTGCCTTCTC
	Reverse	AAACTGTGGAGGGAAGAGACC
<i>Prdm14 CDS</i>	Forward	TGTGGTACGGAAATGGCTATG
	Reverse	AAACACCTTTCCACAGCGTTC
<i>Prdm14 3'UTR</i>	Forward	GGAATCCATTCAGACCAGGAG
	Reverse	GCACATAGTCGCTGGCTACAG
<i>Gata6</i>	Forward	TTGCCTCCAAATCATGTGCTTC
	Reverse	GCCTCCAGGATAGACCAAATG
<i>Fgf5</i>	Forward	ATGAGTGCATCTGCTCTGCTC
	Reverse	CGTCTGTGGTTTCTGTTGAGG
<i>T</i>	Forward	AAGGACAGAGAGACGGCTGTG
	Reverse	AAAGTAGGACAGGGGGTGGAC
<i>Cdx2</i>	Forward	GTAATGCCAGAGCCAACCTG
	Reverse	GGCTTGTTTGGCTCGTTACAC
<i>Dazl</i>	Forward	GATGGACATGAGATCATTGGAC
	Reverse	ATACCAGGGAGCAATCCTGAC
<i>Sycp3</i>	Forward	CGAGCAGTTCATAAAGAGTTTG
	Reverse	TCTTGCTGCTGAGTTTCCATC

<i>Asz1</i>	Forward	GAGTGGGCTTCTCCCAGAAA
	Reverse	GGTCATTTTCCCGCTCATTC
<i>Gja1</i>	Forward	GTGCAAGTGTGTAAGCGTGTG
	Reverse	CACAAAGATCCATGAGGAAGG

Bisulfite sequencing

Gene	Strand	Sequence(5'-3')
<i>Tcl1</i>	Forward	GAAATAGGAGGGTTAGGGAGATTTTAGATG
	Reverse	TTTCTTTTAAACACCAACATTTAAACCCAT
<i>Dazl</i>	Forward	CCACTTCTCTTTTCTACACC
	Reverse	CCACTCTTATCCTCCAAACC
<i>Sycp3</i>	Forward	AAGGGTTAGGTTTTTTTAGA
	Reverse	AACTTCCTACCTAAATACCCAA
<i>Asz1</i>	Forward	TTGGAGAGAAAAAGATTTTT
	Reverse	TACCATAACTCCAAACTATTCT

ChIP-qPCR

Gene	Strand	Sequence(5'-3')
<i>Esrb</i>	Forward	GGTTGCTTTCTTTTGCTGGTG
	Reverse	TGATCCTTTGGAGTGGAGGAC
<i>Tfcp2l1</i>	Forward	TCATCCTTATCCTCCCAGCAG
	Reverse	GGGAAGAGGAAAGTGGATTC
<i>Fgfr1</i>	Forward	GCTTGGCCTTGGATGAATTGTTGGC
	Reverse	AGCCAGGTTGGCCTTTTGTCT
<i>Dnmt3b (-10.1 kb)</i>	Forward	CAGGAAATGCGTGCCTAGAGG
	Reverse	AGGCTTTTCACTTGAGGGCTG
<i>Dnmt3b (-6.3 kb)</i>	Forward	CTGCCACTACCACCAACAAAC
	Reverse	TTTCCACAGGAACACTCATGC