		10	20	30	40	50	60	70
		<u></u>	· · · · · · · · ·				<u></u> . <u> </u> <u> </u> .	<u>•••</u>
DNMT3A_CD	627	PAEKRKPIRVLSLFD(GIATGLLVLK <mark>D</mark>	LGIQVDRYI	ASEVCEDSI7	IVGMVRHQGKIN	1YVGDVRSVTQ	KHIQ
DNMT3A2_CD	404	PAEKRKPIRVLSLFD	GIATGLLVLKD	LGIQVDRYI	ASEVCEDSI	IVGMVRHQGKIN	4YVGDVRSVTQ	KHIQ
DNMT3B_CD	568	PAARRRPIRVLSLFD	GIATG <mark>YLVLK</mark> E	LGIKVGKYV	ASEVCE <mark>ESI</mark> Z	VGTVKHEGNIF	KYVNDVRNITK	KNIE
DNMT3B3_CLD	548	PAARRRPIRVLSLFD(GIATC <mark>YLVLK</mark> E	LGIKVGKYV	ASEVCE <mark>ESI</mark> Z	VGTVKHEGNIH	YVNDVRNITK	KNIE
DNMT3L_CLD	183	PVWRRQPVRVLSLFE	DIKKELTSIGF	LESGSD		P <mark>GQL</mark> I	HVVDVTDTVR	KDVE
Clustal Consen	sus	*. :*:*:*****:	.*. *	* .		*::	:* **:	*.::
		80	90	100	110	120	130	140
_			· · · · <mark>·</mark> · · · · ·			.	· · · · · · · · ·	
DNMT3A_CD	696	EWGPFDLVIGGSPCNI	DLSIVNPARKG	LYEGTCRIFI	DEPAY RUUHDA	ARPKEGDDRPFI	WLFENVVAMG	VSDK
DNMT3A2_CD	473	EWGPFDLVIGGSPCNI	DLSIVNPARKG	LYEGTGRLFI	EFYRLLHD	ARPKEGDDRPFI	WIIFENVVAMG	VSDK
DNMT3B_CD	637	EWGPFDLVIGGSPCNI	DLSNVNPARKG	LYEGTGRLFI	DEFYHIIINYS	RPKEGDDRPFI	WMFENVVAMK	VGDK
DNMT3B3_CLD	618	EWGPFDLVIGGSPCNI	DLSNVNPARKG	LYEGTGRLFI	FEFYHLLNYS	RPKEGDDRPF	WMFENVVAMK	VGDK
DNMT3L_CLD	234	EWGPFDLVYGATPPL	GHTCDRPP	SWYL	FQFHRLLQY/	ARPKPGSPGPF	WMITVDNLVLN	KEDL
Clustal Consen	sus	****** *.:*	. : .*.	. :'	*:*::**:	*** *. ***	*:* : :.:	*
		150	160	170	180	190	200	210
			.	••••	· <u>···</u>	<u></u>		<u></u>
DNMT3A_CD	766	RDISRFLESNPVMID	AKEVSAAHRAR	YFWGNLPGM	NRPLASTVNI	OKLELQECLEHO	RIAKFSKVRI	TINR
DNMT3A2_CD	543	RDISRFLESNPVMID	AKEVSAAHRAR	YFWGNLPGM	NRPLASTVNI	DKINEILÕE CIUEHO	CRITAKE SKVRU	III WR
DNMT3B_CD	707	RDISRFLECNPVMID	AIKVSAAHRAR	YFWGNLPGM	NRPVIASKNI	DKLELQDCLEYN	IRIAKIKKVQT	TITI
DNMT3B3_CLD	688	RDISRFLECNPVMID/	AIKVSAAHRAR	YFWGNLLPGMN	N			
DNMT3L_CLD	296	DVASRIDUPMEPVTUPI	DVHGGSLQNAV	RVWSNIPAI	3			
Clustal Consen	sus	***** :** *	: :.*	.*.*:*.:	•	0.00	0.5.0	
		220	230	240	250	260	270	280
	026							
DNMT3A_CD	830	SNSIKQGKDQHFPVH		EMERVEGEP	VHYIDVSNM		SWSVPVIRHLF	APLK
DNMT3A2_CD	613	SNSIKQGKDQHFPVH	MNEKEDI LWCT	EMERVFGPP	VHYTDVSNM		SWSVPVIRHLF	
DIMITSE_CD	777	SNSIKQGKNQIFPVVI		DIERIFGEP	VHITDVSNMO		WSVPVIRHLF	
DNMT3B3_CLD	224			CDWWAT			WSVPVIRHLF	
Clustel Concor	332					$\cdot \cdot \cdot +$		***
Ciustai Consen	sus	290		•	· · · · · ·	······	~ ~	~~.
						740 745 749	1	
	906					743 743		
DNMT3A2 CD	683	EYFACV						
DNMT3B CD	847	DYFACE						
DNMT3B3 CLD	765	DYFACE						
DNMT3L CLD	373	EYEKYESTELTSSL						
Clustal Consen	sus	:**						

Supplementary Figure S1. DNMT3 sequence alignment. Similar residues are shaded grey and identical residues are shaded black. The insertion domain is boxed, the acidic patch-interacting arginine finger residues (R740 and R743 in the context of full length DNMT3B3 and R823 and R826 in the context of full length DNMT3B1) are labeled with red arrows, and the control residues K745 and R749 are labeled with black arrows.

Fig. 4b



Supplementary Figure S2. Uncropped gel slices for Fig. 4b. Note that the gels were cut into 75 kD-top, 25-55 kd, and bottom-25 kd slices for separate probing with anti-Myc-tag(DNMT3B3) antibody, anti- β -actin/anti- β -tubulin antibody, and anti-histone H3 antibody, respectively. The boxed areas are the parts shown in Fig. 4b.

Extended Data Fig. 1a









Supplementary Figure S3. Uncropped gels for Extended Data Figs. 1a, 1c and 1e. The boxed areas are the parts shown in the respective panels.

Extended Data Fig. 2b



Supplementary Figure S4. Uncropped gels for Extended Data Fig. 2b. The boxed areas are the parts shown in Extended Data Fig. 2b.



Supplementary Figure S5. Uncropped gels for Extended Data Fig. 9a. The boxed areas are the parts shown in Extended Data Fig. 9a

Primers used for generate nucleosomal DNA template				
147F	ATCTGAGAATCCGGTGCCG			
147R	ATCGGATGTATATATCTGACACGTGC			
167F	ATCGGCCGCCCTGGAGAATC			
167R	ATCGGCCGCCACAGGATGTATATATC			
171extendF	ATCGGCCGCCtaCTGGAGAATCCCGGTGCCGAG			
171extendR	ATCGGCCGCCtgACAGGATGTATATATCTGACACGTGCCTGG			
171F	ATCGGCCGCCtaCTGGAG			
171R	ATCGGCCGCCtgACAGGATG			
5YX2F	ATCCATGCGTTCTAATTAGAACGCATGCTGGAGAATCCCGGTGCCGAGG			
5Yx2R	ATCCATGCGTTCTAATTAGAACGCATGACAGGATGTATATATCTGACACGTGCCTGG			
301extendF	GATAGACAGCTGCTGAACCAATGGGACCAAGCTTCACACCGAGTTCATCGCTTATGTG			
	ATCGACCATCGGCCGCCTACTGGAGAATC			
301extendR	GCCAGTTGGGCAGAAGCTTTCGGAACACTATCCGACTGGCACCGGCAAGGTCGCTG			
	TTCAATACAATCGGCCGCCTGACAGGATG			
301F	GATAGACAGCTGCTGAACCAATGGG			
301R	GCCAGTTGGGCAGAAGCTTTC			

The linker DNA sequences are underlined.