

Supplementary Information S2 | **Biochemical Impact of Mutations in Dnmt3a found in Cancer Patients**

Residue (murine)	AA	Disease	Domain	Consequence	Ref
47 (44)	K		N-terminal	G9a/GLP methylation	1
308 (304)	Q	AML	PWWP	H3	2
333 (329)	D		PWWP	H3K36 (-)	3
337 (333)	S		PWWP	chromatin (-)	4
584 (580)	R		ADD	H3	2
640 (636)	F		Motif I	Cat	5
664 (660)	E	AML	Motif II	Cat	5
676 (672)	D		Motif III	AdoMet	5
710 (706)	C	sAML from MDS	Motif IV	Cat, DNA, AdoMet (-)	5
711 (707)	S		Motif V	Cat, AdoMet (-)	5
714 (710)	C	AML	Following motif IV	AdoMet	5
720 (716)	N	T-ALL	Following motif IV	Cat, DNA	5
721 (717)	R		Following motif IV	Cat	5
729 (725)	R	AML	Catalytic	DNA	6
733 (729)	E	AML, CMML	Catalytic	DNA	6
756 (752)	R		Motif VI	Cat (-),DNA (+)	5
757 (753)	K		Motif VI	Cat	5
771 (767)	R	AML, MDS, SM	Catalytic	DNA	6
792 (788)	R	T-ALL	Motif VIII	Cat, DNA (+)	5
826 (822)	K	MDS	Catalytic	DNAMult	7
831 (827)	R		Variable domain	DNA	5
836 (832)	R		Catalytic, Variable	DNAMult, DNA	7, 5
841 (837)	K	AML	Catalytic	DNAMult	7
844 (840)	K		Catalytic	Coop	7
845 (841)	D		Catalytic	DNA (+)	7
847 (843)	H		Catalytic	DNA (+)	7
855 (851)	K		Catalytic	Coop	7
856 (852)	E	T-ALL	Catalytic	DNA (+)	7
860 (856)	W	AML	Catalytic	Cat	8
873 (869)	H		Catalytic	Cat	8
876 (872)	D		Catalytic	Cat	8
879 (875)	N	AML	Catalytic	Cat	8
882 (878)	R	AML	In front of motif X	Cat, DNA	5

885 (881)	R	In front of motif X	Cat (-), AdoMet	⁵
887 (883)	R	Motif X	Cat, DNA	⁵

Analysis of amino acid residues tested for their DNA binding and/or catalytic activity. The human residue mutated in the indicated diseases, along with the mouse residue in which the functional consequences were tested, are indicated in the second column. A comprehensive summary of the role of additional residues is reported in Table S2. The indicated motifs are all part of the catalytic domain. Cat= reduced catalytic activity, Cat (-) = no catalytic activity; AdoMet= reduced AdoMet binding, AdoMet(-)=no AdoMet binding; DNA=reduced DNA binding; DNA(+)= enhanced DNA binding; DNAMulti= lose ability to multimerize on DNA; H3K36 (-)= lose H3K36 affinity; chromatin (-)= lose chromatin targeting; H3= insensitive to H3 peptide; Coop= lower cooperativity during multimerization; SM=systemic mastocytosis

REFERENCES

1. Chang, Y. et al. MPP8 mediates the interactions between DNA methyltransferase Dnmt3a and H3K9 methyltransferase GLP/G9a. *Nat Commun* **2**, 533 (2011).
2. Li, B.Z. et al. Histone tails regulate DNA methylation by allosterically activating de novo methyltransferase. *Cell Res* **21**, 1172-81 (2011).
3. Dhayalan, A. et al. The Dnmt3a PWWP domain reads histone 3 lysine 36 trimethylation and guides DNA methylation. *J Biol Chem* **285**, 26114-20 (2010).
4. Ge, Y.Z. et al. Chromatin targeting of de novo DNA methyltransferases by the PWWP domain. *J Biol Chem* **279**, 25447-54 (2004).
5. Gowher, H. et al. Mutational analysis of the catalytic domain of the murine Dnmt3a DNA-(cytosine C5)-methyltransferase. *J Mol Biol* **357**, 928-41 (2006).
6. Holz-Schietinger, C., Matje, D.M., Harrison, M.F. & Reich, N.O. Oligomerization of DNMT3A controls the mechanism of de novo DNA methylation. *J Biol Chem* **286**, 41479-88 (2011).
7. Rajavelu, A., Jurkowska, R.Z., Fritz, J. & Jeltsch, A. Function and disruption of DNA methyltransferase 3a cooperative DNA binding and nucleoprotein filament formation. *Nucleic Acids Res* **40**, 569-80 (2012).
8. Holz-Schietinger, C., Matje, D.M. & Reich, N.O. Mutations in DNA methyltransferase (DNMT3A) observed in acute myeloid leukemia patients disrupt processive methylation. *J Biol Chem* **287**, 30941-51 (2012).