

Supplementary File 9: Sequence of Dnmt3bb.1, Dnmt3bb.2 and Dnmt3ba mutants. Catalytic site is underlined. TALEN target sequences are in green. Aminoacids coded on the wrong reading frame after the mutation site are italicized and red.

<u>DNMT3BB.1 E17 (Δ6)</u>			
	W G P F D M V I G G S P C N D L S I V N P A R		
Dnmt3bb.1	TGGGGGCCCTTTGACATGGTGATTGGTGGAAGTCCCTGTAAATGACCTTTCAATTGTCAACCCTGCTAGG	1940	
Dnmt3bb.1 (Δ6)	TGGGGGCCCTTTGACATGGTGATTGGTGGA-----TGTAATGACCTTTCAATTGTCAACCCTGCTAGG	1934	
	W G P F D M V I G G C N D L S I V N P A R		
Dnmt3bb.1	MRKEEIKKSSEIVMPSNKPSPAESDKMTATAAMNRDTSVGDGLSENDSGLEMTSENSPLT	60	
Dnmt3bb.1 (Δ6)	MRKEEIKKSSEIVMPSNKPSPAESDKMTATAAMNRDTSVGDGLSENDSGLEMTSENSPLT	60	
Dnmt3bb.1	PAEPPSPFCPKQNGGAASPAESVNSIRKRSRKRSDTEEDSAWSSNSEEKAEVSGSGCE	120	
Dnmt3bb.1 (Δ6)	PAEPPSPFCPKQNGGAASPAESVNSIRKRSRKRSDTEEDSAWSSNSEEKAEVSGSGCE	120	
Dnmt3bb.1	TGLRQRPRPRTIFQAGLTAHSPRSRERGHSHKEDHSDLVASVPEGPALELMEQDSKDSAQ	180	
Dnmt3bb.1 (Δ6)	TGLRQRPRPRTIFQAGLTAHSPRSRERGHSHKEDHSDLVASVPEGPALELMEQDSKDSAQ	180	
Dnmt3bb.1	SSTTSTSTTETASQPEYKDNKGFGIGELVWGKIKGFSWWPGMVVTWRATGRRQASHGMRW	240	
Dnmt3bb.1 (Δ6)	SSTTSTSTTETASQPEYKDNKGFGIGELVWGKIKGFSWWPGMVVTWRATGRRQASHGMRW	240	
Dnmt3bb.1	LQWFGDGKFSEVSADKLDSITAFPKFFNQSSYTKLASYRRAIFQALEVASLRAEKTFFPS	300	
Dnmt3bb.1 (Δ6)	LQWFGDGKFSEVSADKLDSITAFPKFFNQSSYTKLASYRRAIFQALEVASLRAEKTFFPS	300	
Dnmt3bb.1	EADSLQVQKPMLDWAHGGFLPKGQEGKPKENAEYCVFPLASESSTLLESSPPEFPPSA	360	
Dnmt3bb.1 (Δ6)	EADSLQVQKPMLDWAHGGFLPKGQEGKPKENAEYCVFPLASESSTLLESSPPEFPPSA	360	
Dnmt3bb.1	KRARLPLNKAAPGIEEVYSREQMVNEVLKNHRSIEEFCLSCGKTRVATFHPLFEGGLCLT	420	
Dnmt3bb.1 (Δ6)	KRARLPLNKAAPGIEEVYSREQMVNEVLKNHRSIEEFCLSCGKTRVATFHPLFEGGLCLT	420	
Dnmt3bb.1	CKDAYLENSYMYDDDGYSYCTVCCGGREMLLCGNANCCRCICVDCLDILVGAGAANSAR	480	
Dnmt3bb.1 (Δ6)	CKDAYLENSYMYDDDGYSYCTVCCGGREMLLCGNANCCRCICVDCLDILVGAGAANSAR	480	
Dnmt3bb.1	NLDPWRCYMCQPLQYQVGLKKRHDWSLKLQEFFFVNDSGQEFESPKIYPAPVPAEQRRPIRV	540	
Dnmt3bb.1 (Δ6)	NLDPWRCYMCQPLQYQVGLKKRHDWSLKLQEFFFVNDSGQEFESPKIYPAPVPAEQRRPIRV	540	
Dnmt3bb.1	LSLFDGIATGYLVLRDLGFKVDLYIASEVCEDSISVGAVRHEGKIQYVHDVNRNITRKNIA	600	
Dnmt3bb.1 (Δ6)	LSLFDGIATGYLVLRDLGFKVDLYIASEVCEDSISVGAVRHEGKIQYVHDVNRNITRKNIA	600	
Dnmt3bb.1	EWGPFDMVIGGSPCNDLSIVNPARKGLYEGTGRLFFEFYRLLSEAKPKEGEDRPFFWMFE	660	
Dnmt3bb.1 (Δ6)	EWGPFDMVIGG--CNDLSIVNPARKGLYEGTGRLFFEFYRLLSEAKPKEGEDRPFFWMFE	660	
Dnmt3bb.1	NVAVMSVNDKRDISRFLCNPVMIDAIEVSAHRARYFWGNLPGMKRPLCASGMDKLELQ	720	
Dnmt3bb.1 (Δ6)	NVAVMSVNDKRDISRFLCNPVMIDAIEVSAHRARYFWGNLPGMKRPLCASGMDKLELQ	720	
Dnmt3bb.1	DCLEHGRVAKFGKVRTITTRSNSIKQKQDQHFPVMMNGKEDILWCTELERIFGFPVHYTD	780	
Dnmt3bb.1 (Δ6)	DCLEHGRVAKFGKVRTITTRSNSIKQKQDQHFPVMMNGKEDILWCTELERIFGFPVHYTD	780	
Dnmt3bb.1	VSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE	816	
Dnmt3bb.1 (Δ6)	VSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE	816	

DNMT3BB.2 E20 (Δ5+13)

	W G P F D L L I G G	S P C N D L S I V N P A R	
Dnmt3bb.2	TGGGGTCCATTGATCTTCTCATTTGGTGGG-----AGTCCATGTAATGACTTGTCATAGTCAATCCTGCTCGG	3949	
Dnmt3bb.2 (Δ5+13)	TGGGGTCCATTGATCTTCTCATTTGGTGGGAGAAGATCAATGTAA-----TGTAATGACTTGTCATAGTCAATCCTGCTCGG	3957	
	W G P F D L L I G G E D Q C N	V M T C P *	

Dnmt3bb.2	MVADVKGIGDDKQSLCELLDWLNGLLQATFSQVEDTCSGA AFCQLMDIIQPGSIDVTKVNF	60
Dnmt3bb.2 (Δ5+13)	MVADVKGIGDDKQSLCELLDWLNGLLQATFSQVEDTCSGA AFCQLMDIIQPGSIDVTKVNF	60
Dnmt3bb.2	TAEENLDILNNYNLLQEA FSKAQIQKELELTLLVNGDIMTTCDLLTWFKDMYDHNFAKQK	120
Dnmt3bb.2 (Δ5+13)	TAEENLDILNNYNLLQEA FSKAQIQKELELTLLVNGDIMTTCDLLTWFKDMYDHNFAKQK	120
Dnmt3bb.2	CNPQVAFIKPEV VSLKSSREFETIEKENVSSLYNTEETSSNQKTQHVEKTSQESVSWSP	180
Dnmt3bb.2 (Δ5+13)	CNPQVAFIKPEV VSLKSSREFETIEKENVSSLYNTEETSSNQKTQHVEKTSQESVSWSP	180
Dnmt3bb.2	TSFIRKYGSSTLTDDSEN NVNSKDCPGQKSFGDITPFWRQTPYCLYLLHGVELEDDKKAS	240
Dnmt3bb.2 (Δ5+13)	TSFIRKYGSSTLTDDSEN NVNSKDCPGQKSFGDITPFWRQTPYCLYLLHGVELEDDKKAS	240
Dnmt3bb.2	VLLLGFFDKETGENKIRLLDVVYPTKESTEDICNYILDTLRKIGIPLFNMAILYSDFPDH	300
Dnmt3bb.2 (Δ5+13)	VLLLGFFDKETGENKIRLLDVVYPTKESTEDICNYILDTLRKIGIPLFNMAILYSDFPDH	300
Dnmt3bb.2	EHLVAGLQLMKA EIVSLCGLTDLTGQVCHSGVEKIEFSDLILNLITEIYKHFPSPADLQ	360
Dnmt3bb.2 (Δ5+13)	EHLVAGLQLMKA EIVSLCGLTDLTGQVCHSGVEKIEFSDLILNLITEIYKHFPSPADLQ	360
Dnmt3bb.2	ALLEDVVGSDIDNLT SQCSLFWRI IKKIPLAWSHLENYFGSLGTEEEAVCLLLEDPKIKL	420
Dnmt3bb.2 (Δ5+13)	ALLEDVVGSDIDNLT SQCSLFWRI IKKIPLAWSHLENYFGSLGTEEEAVCLLLEDPKIKL	420
Dnmt3bb.2	NVLFLTHALQPLCDFQE I IDQGASVLQLLQDASKLLRLYTQSFLRPKAAEYFHRRGKTS	480
Dnmt3bb.2 (Δ5+13)	NVLFLTHALQPLCDFQE I IDQGASVLQLLQDASKLLRLYTQSFLRPKAAEYFHRRGKTS	480
Dnmt3bb.2	VQETVGHLPRGEVAVGEQAADFLQQHSEELSDYLETFHSSII SFYTTVTVNIVKRLPLPD	540
Dnmt3bb.2 (Δ5+13)	VQETVGHLPRGEVAVGEQAADFLQQHSEELSDYLETFHSSII SFYTTVTVNIVKRLPLPD	540
Dnmt3bb.2	STLRNLSLVLSPGKKLEVTGKMVQDLGVGFGVCIRPDNVSLLTDEFLEYQLIDGGDTGSV	600
Dnmt3bb.2 (Δ5+13)	STLRNLSLVLSPGKKLEVTGKMVQDLGVGFGVCIRPDNVSLLTDEFLEYQLIDGGDTGSV	600
Dnmt3bb.2	DQPTEKYWQTELRIMGNASNFGKLIVSLLALPKTLKKEI IFKQMFQQT DYLKMMRKEDCE	660
Dnmt3bb.2 (Δ5+13)	DQPTEKYWQTELRIMGNASNFGKLIVSLLALPKTLKKEI IFKQMFQQT DYLKMMRKEDCE	660
Dnmt3bb.2	EKDMMEDDVT DSSSYKSAPSHLSPETQGSSISDVIDLTEMDEIGPVEIEDIAPMDVDDIV	720
Dnmt3bb.2 (Δ5+13)	EKDMMEDDVT DSSSYKSAPSHLSPETQGSSISDVIDLTEMDEIGPVEIEDIAPMDVDDIV	720
Dnmt3bb.2	SISSDSETENQKVNVP HVSIVLDDDDDDDEMTDDDDY GCEAGEVMWKYSKNKGNTQNE	780
Dnmt3bb.2 (Δ5+13)	SISSDSETENQKVNVP HVSIVLDDDDDDDEMTDDDDY GCEAGEVMWKYSKNKGNTQNE	780
Dnmt3bb.2	MTDNTYQGGFSVGEMVLGP IEGFGLWPGLVQSWDSERPCGSMRKVIFFGNGMQTEVQADS	840
Dnmt3bb.2 (Δ5+13)	MTDNTYQGGFSVGEMVLGP IEGFGLWPGLVQSWDSERPCGSMRKVIFFGNGMQTEVQADS	840
Dnmt3bb.2	LLPFSSSLAKCFCSNSFATVMAYKDAIFSS LQVASRRSRMFFSPESESKDELLRVMLN WAF	900
Dnmt3bb.2 (Δ5+13)	LLPFSSSLAKCFCSNSFATVMAYKDAIFSS LQVASRRSRMFFSPESESKDELLRVMLN WAF	900
Dnmt3bb.2	GGFEPLGADGLQPQA EYSVKVKKGKRKNPTGKLFNLTVPLNKI PESLDLNNGSVDLGTTD	960

Dnmt3bb.2 (Δ5+13)	 GGFEPLGADGLQPQAEYSVKVKKGKRKNPTGKLFNLTVPLNKIPESLDLNNGSVDLGTTD	960
Dnmt3bb.2	ADKKRLYSKWNGRSMQTVKIRRKYKQRNKNIIP TVQIESRQNSQKRHQM VHEFLKNKRKI	1020
Dnmt3bb.2 (Δ5+13)	ADKKRLYSKWNGRSMQTVKIRRKYKQRNKNIIP TVQIESRQNSQKRHQM VHEFLKNKRKI	1020
Dnmt3bb.2	EDFCLSCGSMVDIIHPLFEGKLCTNCKFNFTETLYRYDEDGYQSYCTVCCSGMEVILCG	1080
Dnmt3bb.2 (Δ5+13)	EDFCLSCGSMVDIIHPLFEGKLCTNCKFNFTETLYRYDEDGYQSYCTVCCSGMEVILCG	1080
Dnmt3bb.2	HDSCCRSFCVDCLDILVCQGTFDQLKNVDPWTCYLCAPETSSGALKPRHDWSIRVQEFFA	1140
Dnmt3bb.2 (Δ5+13)	HDSCCRSFCVDCLDILVCQGTFDQLKNVDPWTCYLCAPETSSGALKPRHDWSIRVQEFFA	1140
Dnmt3bb.2	NDTGMEFEPHRVYPSIPAIQRRPIRVLSLFDGIATGYLVLRDLGFKVEKYVASEIDEESI	1200
Dnmt3bb.2 (Δ5+13)	NDTGMEFEPHRVYPSIPAIQRRPIRVLSLFDGIATGYLVLRDLGFKVEKYVASEIDEESI	1200
Dnmt3bb.2	TISMVNHDGKITQVDDVKNITKKHIEQWGPFDLLIGGS PC NDLSIVNPARKGLYEGTGRL	1260
Dnmt3bb.2 (Δ5+13)	TISMVNHDGKITQVDDVKNITKKHIEQWGPFDLLIGGEDCNVMTCP	1246
Dnmt3bb.2	FFEYYRLNLVLPKEDDPQPF FFWLFENVTFMQTHVKADICRFLECNPVLVDAVKVSPAHR	1320
Dnmt3bb.2	ARYFWGNIPGMNRPIIASQNDKLCLQECLEPGRTAKYEKVRTITTRQNSLQGTND AHFP	1380
Dnmt3bb.2	VTMNGKDDHIWITELEKIFGF PKHYTDVKSMGRPQRQ RVLGKSWSVPVIRHLLAPLKDYF	1440
Dnmt3bb.2	ACDEFPVK 1448	

DNMT3Ba E20 (Δ5+6)

	G P F D L L I G G S P C N D L S M V N P A R K G	
Dnmt3ba	GGGCCATTTGACCTTCTGATTGGTGGGAAGTCCTTGTAATG-----ACTTGTCATGGTGAATCCAGCCAGAAAAGGT	3839
Dnmt3ba (Δ5+6)	GGGCCATTTGACCTTCTGATTGGTGGGAAGTCCTTGTAATGTCATGG-----TCCATGGTGAATCCAGCCAGAAAAGGT	3840
	G P F D L L I G G S P C N V M V H G E S S Q K R	

Dnmt3ba	MATNVSLEPNNPDDKCSRYEVLGWINETLQTNFTQVEQCRSGACFCQLIDLFFPGTINLK	60
Dnmt3ba1	MATNVSLEPNNPDDKCSRYEVLGWINETLQTNFTQVEQCRSGACFCQLIDLFFPGTINLK	60
Dnmt3ba	KVKFESQKRSDFMQNYGLLQAAFRDLEVTEPVPVNELLSGKFRPNFTYLKWFKKFFYANV	120
Dnmt3ba	KVKFESQKRSDFMQNYGLLQAAFRDLEVTEPVPVNELLSGKFRPNFTYLKWFKKFFYANV	120
Dnmt3ba	KQERVYNAFEARDGQEIVPVDDVMKSPKALKSSYESGRAGEESDMEINGGRRSATYDPKW	180
Dnmt3ba	KQERVYNAFEARDGQEIVPVDDVMKSPKALKSSYESGRAGEESDMEINGGRRSATYDPKW	180
Dnmt3ba	QRNLKWIRASDMGDNYAYCTTCDYNIILLAGFHD LKRHQLTQN HMKHETGRTNLPGRKQI	240
Dnmt3ba	QRNLKWIRASDMGDNYAYCTTCDYNIILLAGFHD LKRHQLTQN HMKHETGRTNLPGRKQI	240
Dnmt3ba	EESISCS ETMLLF IQSHCLSSLPSRINRVSQRTAR CILGLKYPNDIVSACKLNPYCIYIY	300
Dnmt3ba	EESISCS ETMLLF IQSHCLSSLPSRINRVSQRTAR CILGLKYPNDIVSACKLNPYCIYIY	300
Dnmt3ba	GQVPLDVKTGDKTNCHVVLAGFFEEKQARYCIRFLDVFPEDSASSVSGGLFSILKKFEI	360
Dnmt3ba	GQVPLDVKTGDKTNCHVVLAGFFEEKQARYCIRFLDVFPEDSASSVSGGLFSILKKFEI	360
Dnmt3ba	PASN MVAVYINDHELTSES VVSQIRELNPQVIDLGGLYSIPDTACSAGLQTHSVQVQELI	420
Dnmt3ba	PASN MVAVYINDHELTSES VVSQIRELNPQVIDLGGLYSIPDTACSAGLQTHSVQVQELI	420
Dnmt3ba	ANIYRHFSTGSTSNDNLKMLFAGIDGLKVHSNPLSNSEEF CVLVKRIHEMWSDLVS YFSS	480
Dnmt3ba	ANIYRHFSTGSTSNDNLKMLFAGIDGLKVHSNPLSNSEEF CVLVKRIHEMWSDLVS YFSS	480
Dnmt3ba	CDENNDNVKQICSQLENPKIRLTLMFLDQALGPLRAFGQHLQQSKSSVRADLVEILREAS	540
Dnmt3ba	CDENNDNVKQICSQLENPKIRLTLMFLDQALGPLRAFGQHLQQSKSSVRADLVEILREAS	540
Dnmt3ba	GLLSYASSFLRPQAVIRYLKEQDPAILDNEAFCLPAAELSLGGVLEDFISAREEELADF	600
Dnmt3ba	GLLSYASSFLRPQAVIRYLKEQDPAILDNEAFCLPAAELSLGGVLEDFISAREEELADF	600
Dnmt3ba	LSTFYNECLA IYKTLTTSIAASLPLSDSVLRAISQLLSPAGRLKVTGKNIVDLAVRFGFC	660
Dnmt3ba	LSTFYNECLA IYKTLTTSIAASLPLSDSVLRAISQLLSPAGRLKVTGKNIVDLAVRFGFC	660
Dnmt3ba	SKPEDSAKL NDEFLEYQLAE EENLSSTHSIER YWCTVLKTFPPTSVFKRLVLCLLVLPSP	720
Dnmt3ba	SKPEDSAKL NDEFLEYQLAE EENLSSTHSIER YWCTVLKTFPPTSVFKRLVLCLLVLPSP	720
Dnmt3ba	SLDATKIFAQAIENG DADQLDDSSSES DTDMTKELDSNDDNSLDNSELQISPIKNGIMKK	780
Dnmt3ba	SLDATKIFAQAIENG DADQLDDSSSES DTDMTKELDSNDDNSLDNSELQISPIKNGIMKK	780
Dnmt3ba	SRRSTSETVQHSNAVKPCVVRLEKITSQREVNLKNDGAKNDGTLTSNTLKEVKNDLSNST	840
Dnmt3ba	SRRSTSETVQHSNAVKPCVVRLEKITSQREVNLKNDGAKNDGTLTSNTLKEVKNDLSNST	840

Dnmt3ba	PSPRRGKRDQAYNDGKGFAVGELVWGKVKDFSLWPGLVVPWKGRIVPVSMRRVEWFGDGM	900
Dnmt3ba		
Dnmt3ba	PSPRRGKRDQAYNDGKGFAVGELVWGKVKDFSLWPGLVVPWKGRIVPVSMRRVEWFGDGM	900
Dnmt3ba	FSEIHTDGLLPFGAFSKNFCSKSYEGLPTYKNAIYQILELAAERSGKLFPPSEKKGEEVK	960
Dnmt3ba		
Dnmt3ba	FSEIHTDGLLPFGAFSKNFCSKSYEGLPTYKNAIYQILELAAERSGKLFPPSEKKGEEVK	960
Dnmt3ba	AMMDWAFGGFQPMGADGFLPSADSSASNKTESDSSVSDYQPPAKRKYVFKNRPSTQECNR	1020
Dnmt3ba		
Dnmt3ba	AMMDWAFGGFQPMGADGFLPSADSSASNKTESDSSVSDYQPPAKRKYVFKNRPSTQECNR	1020
Dnmt3ba	DQMVQEVTSKGRKIEDFCLSCGSSNTEIFHPLFKGSLCIKCKENFTETLYRYDDDGYQSY	1080
Dnmt3ba		
Dnmt3ba	DQMVQEVTSKGRKIEDFCLSCGSSNTEIFHPLFKGSLCIKCKENFTETLYRYDDDGYQSY	1080
Dnmt3ba	CTVCCAGLEVILCGNASCCRCFCCKDCLNVLVGPFTDKLKEVDPWSCYVCLPSKCYGVLK	1140
Dnmt3ba		
Dnmt3ba	CTVCCAGLEVILCGNASCCRCFCCKDCLNVLVGPFTDKLKEVDPWSCYVCLPSKCYGVLK	1140
Dnmt3ba	LRTDWSVRVQEFFANNSAFEFEPHRVYPSIPAHKRRPIRVLSLFDGIATGYLVLKDLGFK	1200
Dnmt3ba		
Dnmt3ba	LRTDWSVRVQEFFANNSAFEFEPHRVYPSIPAHKRRPIRVLSLFDGIATGYLVLKDLGFK	1200
Dnmt3ba	LERYIASEICEDSIAVGMVKHEGKIEYVKDVRTITRKHLAEWGPFDLLIGGSPCNDLSMV	1260
Dnmt3ba		
Dnmt3ba	LERYIASEICEDSIAVGMVKHEGKIEYVKDVRTITRKHLAEWGPFDLLIGGSPC <i>NVMVHG</i>	1260
Dnmt3ba	NPARKGLFEGTGRLFFEYYRMLTMMRPKEDDDRPFWLFENVVAMSAHDKADICRFLECN	
Dnmt3ba	<i>ESSQKRSF</i> * 1268	
	EGTGRLFFEYYRMLTMMRPKEDDDRPFWLFENVVAMSAHDKADICRFLECNPVMIDAVK	
	VSPAVSPAHRARYFWGNLPGMNRPVATSLTDNVDLQDCLESGRTAMFSKVRTITTKSNSI	
	KQGKTGPLPVTMNGKEDYLWCTEMEKIFGFPKHYTDVNNMGRGQRQKVLGRSWSVPVIRH	
	LFAPLKDYFACE*	