

| Organism | Name | Sequence | pCR-Blunt | pnEA-vH | pnEA-vH | pGEX-NB | pDONR207 TM |
|-----------------------------|-----------------------------|---------------------------------|-----------|---------|---------|---------|------------------------|
| <i>Homo sapiens</i> | | | | | | | |
| | <i>HsPRMT7_5_NdeI</i> | GATCGACcatatgAAAATCTTCTGCAGTCGG | | X | X | X | X |
| | <i>HsPRMT7_3_BglII</i> | GAGCagatctGTCTGGGGTATCTGCATGCC | | X | X | X | |
| | <i>HsPRMT7_3_stop_BglII</i> | GAGCagatctTCAGTCTGGGGTATCTGCATG | | | | | X |
| <i>Mus musculus</i> | | | | | | | |
| | <i>MmPRMT7_5_NdeI</i> | catatgAAGGTCTTCTGTGGCCG | X | | | | |
| | <i>MmPRMT7_3_BglII</i> | agatctGCTCAAGGTGTCTGCAAG | X | | | | |
| | <i>MmPRMT7_3_stop_BglII</i> | agatctTCAGCTCAAGGTGTCTG | X | | | | |
| <i>Arabidopsis thaliana</i> | | | | | | | |
| | <i>AtPRMT7_5_NdeI</i> | GATCGATcatatgTCGCCTCTGTCTTCTC | | X | X | X | X |
| | <i>AtPRMT7_3_BamHI</i> | GGTCggatccAGAAATAGTATGAGTGACG | | X | X | X | |
| | <i>AtPRMT7_3_stop_BamHI</i> | GGTCggatccTCAAGAAATAGTATGAGTGAC | | | | | X |
| <i>Danio rerio</i> | | | | | | | |
| | <i>DrPRMT7_5_NdeI</i> | GATCGATcatatgAAGACGTTTTGCGGTC | | X | X | X | X |
| | <i>DrPRMT7_3_BamHI</i> | GAggatccAGATTCAGTGATGGAGAAGTC | | X | X | X | |
| | <i>DrPRMT7_3_stop_BamHI</i> | GAggatccTCAAGATTCAGTGATGGAGAAG | | | | | X |
| <i>Xenopus laevis</i> | | | | | | | |
| | <i>XlPRMT7_5_NdeI</i> | GAGCGATcatatgAAGGTATTTTGC GGTC | | X | X | X | X |
| | <i>XlPRMT7_3_BglII</i> | GAGCagatctAAAGTCTGGTTCAAAGCAC | | X | X | X | |
| | <i>XlPRMT7_3_stop_BglII</i> | GAGCagatctCTAAAAGTCTGGTTCAAAGC | | | | | X |

Supplementary Table S1 Pairs of oligonucleotides used for cloning PRMT7 genes in the different target vectors. The oligonucleotide names include the species with a two letters code, the extremity of the gene to which it is complementary (either 5' or 3' end), the presence of the stop codon and the restriction site used. In the sequence the nucleotides from the restriction site are lowercased.

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| HsPRMT7_dom1 | 1 | MKIFCSRANPTTGSVEWLEDEHY...DYHQEIARSSYADMLHDKDRNKYKYYQGITRAAVSRVKDRGQKALVLDIGTGTG |
| MmPRMT7_dom1 | 1 | MKVFCGRANPTTGSLEWLEDEHY...DYHQEIARSSYADMLHDKDRNKYKYYQGITRAAVSRVKDRGQKALVLDIGTGTG |
| XlPRMT7_dom1 | 1 | MKVFCGRANPTTGSLEWLEDEHY...DYHQEIARSSYADMLHDKDRNKYKYYQGITRAAVSRVKDRGQKALVLDIGTGTG |
| DrPRMT7_dom1 | 1 | MKTFCGRANPTTGSLEWLEDEHY...DYHQEIARSSYADMLHDKDRNKYKYYQGITRAAVSRVKDRGQKALVLDIGTGTG |
| AtPRMT7_dom1 | 1 | QRVFLRQDPLTGNSEWIVIEDNDQPGTSTDGLLATTSYLDMLNDSRRNIAYRLAIEKTI...TEPCHVLDIGAGTG |
| HsPRMT7_dom2 | 363 | ...PVCDCQAHLLWNRPR...FGEINDDQDRTRDRYVQALRTVLPD...SVCVLCVSDGS. |
| MmPRMT7_dom2 | 363 | ...PVCDCQAHLLWNRPR...FGEINDDQDRTRDRYVQALRTVLPD...SVCVLCVSDGS. |
| XlPRMT7_dom2 | 358 | ...PVCDCQAHLLWNRPR...FGEINDDQDRTRDRYVQALRTVLPD...SVCVLCVSDGS. |
| DrPRMT7_dom2 | 358 | ...PVCDCQAHLLWNRPR...FGEINDDQDRTRDRYVQALRTVLPD...SVCVLCVSDGS. |
| AtPRMT7_dom2 | 400 | ...PVCDCQAHLLWNRPR...FGEINDDQDRTRDRYVQALRTVLPD...SVCVLCVSDGS. |

DVGxGxG

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|--------------|-----|---|
| HsPRMT7_dom1 | 77 | LLSMMAVTAGA...DFCYAIEVFKPMA...DAAVKIVEKNGFS...DKIKVINKHSTEVTVGPEGDMPCRANILVTELFDT. |
| MmPRMT7_dom1 | 77 | LLSMMAVTAGA...DFCYAIEVFKPMA...EAAVKIVERNGFS...DKIKVINKHSTEVTVGPGDGLPCRANILITELFDT. |
| XlPRMT7_dom1 | 77 | LLSMMAVTAGA...DCCYAIEVFKPMS...DAAVQIVKANGFS...DKIKVINKHSTEVTVGPGDGMKTKANILITELFDT. |
| DrPRMT7_dom1 | 77 | LLSMMAVTAGA...DFCYAIEVFKPMA...QAASCIVERNGFS...DKIKVINKHSTEVTVGPGDGMQERANILVTELFDT. |
| AtPRMT7_dom1 | 75 | LLSMMAVRAMRGDSKGMVTAACESYLPV...KLMRKVMHKNGMT...KNINLINKRSD...ELKVGSE...DIASRADVLVSEILDS. |
| HsPRMT7_dom2 | 413 | LLSVLAHHLGV...EQVFTVESAAASH...KLLRKIFKANHLE...DKINIEKRP...ELLTNEEDLQGRKVSLLLEGPFFFTT. |
| MmPRMT7_dom2 | 413 | LLSVLAHHLGV...EQVFTVESAAASH...RMLRKIFKANHLE...DKISVINKRP...ELLTAADELGKVSLLLEGPFFFTT. |
| XlPRMT7_dom2 | 408 | LLSVLAHSLGA...KQYTLLESSIAQ...HLMKLLFQVNHLE...EKIQVLHKS...DSLITADFDKRISTLLEGPFFFTT. |
| DrPRMT7_dom2 | 408 | LLSVLAHSLGS...KKVFSLESSGMAK...QVIEQVLLHNSLK...DGVQLLGIRA...EQLSLADLDGNQISVLMGEPFFST. |
| AtPRMT7_dom2 | 452 | LLPMLALHISN...RSRVLISLSPGLOENAAARYF...EATADSNKGF...DRFEYF...RDGKTNLAKAYPG...KIDLLEGEPPYFST. |

SExMGxx

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|--------------|-----|---|
| HsPRMT7_dom1 | 149 | ELIGEG...ALPSYEAHHRHLVEENCEAVPHRATVYAQLVESGRMWSWNKLFPIHVQTSLGEQVIVPPVDVESCPCGAPSV |
| MmPRMT7_dom1 | 149 | ELIGEG...ALPSYEAHAKHLVQEDCEAVPHRATVYAQLVESRRMWSWNKLFPPVVRTSLGEQVIVPPSELERCPGAPSV |
| XlPRMT7_dom1 | 149 | ELIGEG...ALPSYEAHQHMLQETWEAVPHRATVYAQLVESTRLWSWNKLFPLNLET...GDIKPHPELETCPGAPSV |
| DrPRMT7_dom1 | 149 | ELIGEG...ALPSYEAHAKHLVQEDCEAVPHRATVYAQLVESTRLWSWNKLFPPVVRTSLGEQVIVPPSELERCPGAPSV |
| AtPRMT7_dom1 | 150 | ELIGEG...LIPSLQAHADMHLVNDPKTVPYRATVYAQLVESTFLCNLQDLRNNEAKTSDGVR...LV.PPGLESFGIKSQ |
| HsPRMT7_dom2 | 484 | SLLPWHNLYFWYVRTAVDQHLPGAMVMPQAASLHVVVEFRDLWRIRSP...CGDCEGFDVHIMDDMKRALDFRES |
| MmPRMT7_dom2 | 484 | SLLPWHNLYFWYVRTAVDQHLPGAMVMPQAASLHVVVEFRDLWRIRSP...CGDCEGFDVHIMDDMKRALDFRES |
| XlPRMT7_dom2 | 479 | NLLPWHNLYFWYVRTALSTNLAKDCVTLPLSASLHVVAVEFKDLWRIRSP...CGMCEGFDVSPMDKIKRSLNDFRES |
| DrPRMT7_dom2 | 479 | SLLPWHNLYFWYVRTAVDQHLPGAMVMPQAASLHVVVEFRDLWRIRSP...CGTCEGFDVSPMDKIKRSLNDFRES |
| AtPRMT7_dom2 | 526 | ENGLPWQNLRFWKDRTLVLDLSDVLEDAVVMFYKGYLRGCAMVLPDLWKSERC...LGSVEGFDHTLVNTLGGCGDLPSG |

xxLxxExM

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|--------------|-----|---|
| HsPRMT7_dom1 | 226 | CDIQLNQVSPADFT...VLSQVLPVMSIDF...SKQVSSAACHSRRFEP...LTSGRAQVLSWWDIEMDPEGKI...KCTMAPFWAH |
| MmPRMT7_dom1 | 226 | CDIQLNQVSPADFT...VLSQVLPVMSVDF...SKQVSSAACHSRQFVPLAS...GQAQVLSWWDIEMDPEGKI...KCTMAPFWAQ |
| XlPRMT7_dom1 | 222 | CDIQLSQLNPRDFK...ILSEVLCVFRVDF...SCQVSSAAPTSHPVHFTSLAS...GAAQVLSWWDIEMDPEGSI...TCTMQPSWMY |
| DrPRMT7_dom1 | 222 | CDIQLSQVPTDAFT...AISPVCMTMPSVDF...SKPVSAAQSYTVRFKSTG...GRAQVLSWWDIEMDPEGNI...VCTMAPSWY |
| AtPRMT7_dom1 | 225 | QYSMHVDAIEKEIK...LLSEPVKIFEFDFWKRPE...SNG.ELDVHIEAKT...GSVHAISWVWLQDLS...EGTIFYSTAPRID |
| HsPRMT7_dom2 | 559 | REAEPHPLWEYPCR...SLSEPWQILTFDF...QQPVP...LQPLCABGTVELRR...GQSHAAVLSWVWYHLLTPE...CTLSTGLLEPADP |
| MmPRMT7_dom2 | 559 | REAEPHPLWEYPCR...SLSKPQELTFDF...QQPVP...LQPLCABGTVELRR...GQSHAAVLSWVWYHLLTPE...CTLSTGLINPAD |
| XlPRMT7_dom2 | 554 | QEAEPHPLWEYPCR...ALSEPIQVMTFFNFTEPVTE...EIRASGSLNLVRS...GQCHGAVLSWVWYELTKEITVSTGLIGISEE |
| DrPRMT7_dom2 | 554 | WEAEPHPLWEYPCR...ALTKPCPVMTFFDF...TQCVP...EPISSDGAVPFTGR...GRCHGVALWVWYELTDDISVSMGLTKAVSQ |
| AtPRMT7_dom2 | 602 | KDSPLCLPFIFWQCGETK...LLSKEFTVMEFDF...SKPIT...GPCSGEVQIEFLRF...GVCHGVALWVWYELTDDIENSTVIS...TG |

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|--------------|-----|--|
| HsPRMT7_dom1 | 303 | SDP...EMQWRDHWMCVYFLPQEE...PVVQGSALYLV...AHDDYCVWYSLQRTSPEKNERVVRQMR. |
| MmPRMT7_dom1 | 303 | TDP...QELOWRDHWMCVYFLPQEE...PVVQGSALYLV...AHDDYCVWYSLQRTSPENDENSAYQVR. |
| XlPRMT7_dom1 | 299 | ETQ...QSVWRDHWMCVYFLPKKEC...SVTQGEVCLTAHQDDYCVWYSLNKSSA...ENDPVCRRER. |
| DrPRMT7_dom1 | 299 | ADP...HAYPWRDHWMCVYFLPAEE...NVSEGEELMLMVSHDDYS...LWYSLTHSEQ...NDVRVAPFR. |
| AtPRMT7_dom1 | 301 | SNSEIGVRDCHWMCVWVTFPGTGVSIKSGEKVHL...ASHTCTN...ILYLNKKTQSLTHER...THF. |
| HsPRMT7_dom2 | 636 | EGG...CCWNPCHKQAVYFFSPADPR...ALLGGPRTVS...YAVEFHPD...TGDIMEFFRHADTPD |
| MmPRMT7_dom2 | 636 | KGD...CCWNPCHKQAVYFFSTTLLDLR...VPLNGP...RVS...YVVEFHPD...TGDIMEFFRHADTPD |
| XlPRMT7_dom2 | 631 | MGE...CQWYPHRCKQGVYFFSSILNQTIPAQSP...SVS...YSVTFIPK...EGDIRMCFEPDF... |
| DrPRMT7_dom2 | 631 | EGA...CEWNPHRCKQGVYFFFRSAKET...SGDGR...EDLS...YSLTFEPH...SGDIKMFESITES... |
| AtPRMT7_dom2 | 676 | PDD...KYW...KQGVK...LGLKPV...VVRMEG...FS...S...IGIQAS...L...L...SSNS...ELIVTH...TI...S |

THWxQ

Supplementary Figure S1 Alignment of the cloned PRMT7 domains. Five PRMT7 domain sequences have been aligned with T-coffee (Notredame *et al.*, 2000). The full sequences were first aligned to delineate the catalytic cores. The four signature sequences are localized and the consensus written below. Abbreviations are as follow: Hs/*Homo sapiens*, Mm/*Mus musculus*, Xl/*Xenopus laevis*, Dr/*Danio rerio*, and At/*Arabidopsis thaliana*. The alignment was drawn with Esript (Gouet *et al.*, 1999).

Supplementary References

Gouet, P., Courcelle, E., Stuart, D. I. & Metoz, F. (1999). *Bioinformatics* **15**, 305-308.

Notredame, C., Higgins, D. G. & Heringa, J. (2000). *J Mol Biol* **302**, 205-217.