Supplementary material

Cucumber metal transport protein MTP8 confers the increased tolerance to Mn when expressed in yeast and *Arabidopsis thaliana*.

Magdalena Migocka*[1], Anna Papierniak[1], Ewa Maciaszczyk-Dziubińska[2], Piotr Poździk[1], Ewelina Posyniak[1], Arnold Garbiec[3], Sophie Filleur[4,5]

Table S1

The accession numbers and nomenclature of MTP proteins from monocots and dicots used for the construction of phylogenetic tree. The number and symbols of proteins from *P. trichocarpa, O. sativa* and *Sorghum bicolor* were maintained according to previous annotations (Gustin *et al.*, 2011; Migeon *et al.*, 2010; Montanini *et al.*, 2007). The nomenclature for MTPs from *V. vinifera*, *B. diastychon* and *Z. mays* was assigned based on previously annotated *A. thaliana* MTPs.

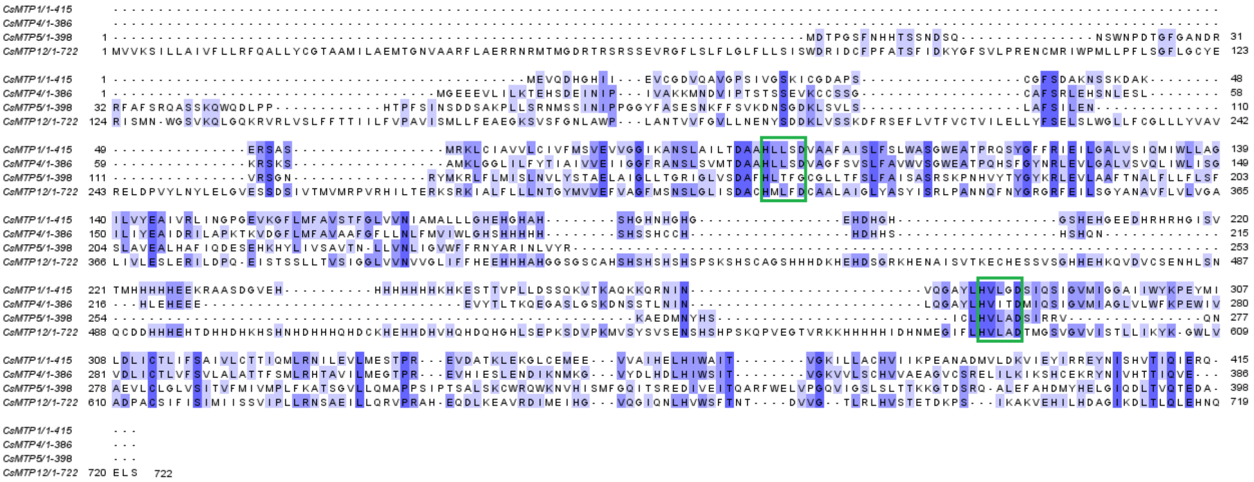
Table S1

Arabidopsis thaliana		*Populus trichocarpa*		*Vitis vinifera*		*Oryza sativa*		*Brachypodium diastychon*		*Sorghum bicolor*		*Zea mays*	
Symbol	TAIR	Symbol	GeneBank ID	Symbol	GeneBank ID	Symbol	RGAP ID	Symbol	GeneBank ID	Symbol	Phytozome v.8.0 ID	Symbol	Gramene-MaizeGDB ID
AtMTP1	At2g46800	PtrMTP1	POPTR_0014s10180.1	VvMTP1	XP_002266346.1	OsMTP1	LOC_Os05g03780.1	BdMTP1	XP_003569059.1	SbMTP1	Sb09g002460	ZmMTP1 ZmMTP1.1	ACL53182.1 ACR35635.1
AtMTP2	At3g61940	PtrMTP2	POPTR_0002s18080.1	N/A		N/A		N/A		N/A		N/A	
AtMTP3	At3g58810	PtrMTP3.1 PtrMTP3.2	POPTR_0001s45520.1 POPTR_0011s15370.1	VvMTP3	XP_002278303.1	N/A		N/A		N/A		N/A	
AtMTP4	At2g29410	PtrMTP4.1 PtrMTP4.2	POPTR_0001s25270.1 POPTR_2033s00200.1	VvMTP4	XM_002280347.2	N/A		N/A		N/A		N/A	
AtMTP5	At3g12100	PtrMTP5	POPTR_0016s04430.1	VvMTP5	XP_002279787.1	OsMTP5	LOC_Os02g58580.1	BdMTP5	XP_003570736.1	SbMTP5	Sb04g038530	N/A	
AtMTP6	At2g47830	PtrMTP6	POPTR_0002s20980.1	VvMTP6	XP_002269478.2	OsMTP6	LOC_Os03g22550.1	BdMTP6	XP_003557927.1	SbMTP6	Sb01g035530	ZmMTP6	ACF86507.1
AtMTP7	At1g51610	PtrMTP7	POPTR_0010s25780.1	VvMTP7	XP_002262765.1	OsMTP7	LOC_Os04g23180.1	BdMTP7	XP_003581101.1	SbMTP7	Sb06g007330	N/A	N/A
AtMTP8	At3g58060	PtMTP8.1 PtrMTP8.2 PtrMTP8.3 PtrMTP8.4	POPTR_0003s21540.1 POPTR_0001s04740.1 POPTR_0001s04750.1 POPTR_0001s04730.1	VvMTP8.1 VvMTP8.2	XP_002275885.1 XP_002285662.1	OsMTP8 OsMTP8.1	LOC_Os02g53490.1 LOC_Os03g12530.1	BdMTP8 BdMTP8.1	XP_003570531.1 XP_003558420.1	SbMTP8 SbMTP8.1	Sb04g034705 Sb01g041820	ZmMTP8 ZmMTP8.1	NP_001141097.1 NP_001167840.1
AtMTP9	At1g79520	PtrMTP9	POPTR_0008s08310.1	VvMTP9	XP_003634572.1	OsMTP9	LOC_Os01g03914.1	BdMTP9	XP_003565291.1	SbMTP9	Sb03g007250	ZmMTP9	ACN36717.1
AtMTP10	At1g16310	PtrMTP10.1 PtrMTP10.2 PtrMTP10.3 PtrMTP10.4	POPTR_0010s17950.1 POPTR_0010s17960.1 POPTR_0010s17980.1 POPTR_0010s18000.1	VvMTP10	XP_002263815.1	N/A		N/A		N/A		N/A	
AtMTP11	At2g39450	PtrMTP11.1 PtrMTP11.2	POPTR_0010s21810.1 POPTR_0008s04940.1	VvMTP11.1 VvMTP11.2	XP_002282508.1 XP_002282522.2	OsMTP11 OsMTP11.1	LOC_Os01g62070.1 LOC_Os05g38670.1	BdMTP11 BdMTP11.1	XP_003564566.1 XP_003568286.1	SbMTP11	Sb03g039220	N/A	
AtMTP12	At2g04620	PtrMTP12	POPTR_0005s11240.1	VvMTP12	XP_002280912.1	OsMTP12	LOC_Os08g32650.1	BdMTP12	XP_003572199.1	SbMTP12	Sb07g020630	ZmMTP12	NP_001167737.1

Figure S1

The conserved residues in TMDs II and V of Zn-CDF and Mn-CDF groups of cucumber MTP proteins. The alignment was performed using ClustalW. Zn-CDF group is represented by CsMTP1, CsMTP4, CsMTP5 and CsMTP12, whereas Mn-CDFs comprise CsMTP8, CsMTP9 and CsMTP11. Shading indicates identical (dark blue) or similar (light blue) amino acid residues. The green (ZnCDFs) or red (Mn-CDFs) boxes indicate the conserved sequences HxxxD and DxxxD in members of the Zn-CDF or Mn-CDF group, respectively (Montanini *et al.*, 2007).

Zn-CDF group



Mn-CDF group

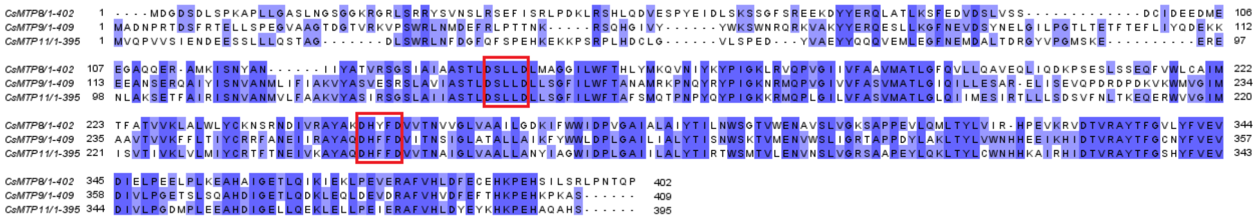


Figure S2

The characteristic motifs in cucumber MTP proteins. FGENESH algorithm was used to identify the full cDNA of *MTP* genes in the cucumber genome (Chinese long) and to translate the genes into amino acid sequences. Shading indicates the improved tentative signature sequence characteristic for all CDF proteins, according to Montanini et al. (2007), whereas the motifs characteristic for Zn-CDF, Mn-CDF or Zn/Fe-CDF subgroups of CDF family were marked in red.

CsMTP1/ACHR01031515

MEVQDHGHIIEVCGDVQAVGPSIVGSKICGDAPSCGFSDAKNSSKDAKERSASMRKLCIAVVLCIVFMSVEVVGGIKAN**SLA**
ILTDAAHLLSDVAAFAISLFSLWASGWEATPRQSYGFFRIEILGALVSIQMIWLLAGILVYEAIVRLINGPGEVKGFLMFAV
STFGLVVNIAMALLLGHEHGHAHSHGHNHGHGEHDHGHGSHEHGEEDHRHRHGISVTMHHHHHEEKRAASDGVEHHHHHHHH
KHKESTTVPLLDSSQKVTKAQKKQRNINVQGAYL**HVLGD**SIQSIGVMIGGAIIWYKPEYMILDLICTLIFSAIVLCTTIQML
RNILEVLMESTPREVDATKLEKGLCEMEEVVAIHELHIWAITVGKILLACHVIIKPEANADMVLDKVIEYIRREYNISHVTI
QIERQ

CsMTP4/ACHR01049518

MGEEEVLILKTEHSDEINIPIVAKKMNDVIPTSTSSEVKCCSSGCAFSRLEHSNLESLKRSKSAMKLGGLILFYTIAIVVEI
IGGFRAN**SLSVMTDAAHLLSDVAGFSVSLFAVWVSGWEATPQHSFGYNRLE**VLGALVSVQLIWLISGILIYEAIDRILAPKT
KVDGFLMFAVAAFGFLLNLFMVIWLGHSHHHHHSHSSHCCHHDHHSHSHQNHLEHEEEEVYTLTKQEGASLGSKDNSSTLNI
NLQGAYL**HVITD**MIQSIGVMIAGLVLWFKPEWIVVDLICTLVFSVLALATTFSMLRHTAVILMEGTPREVHIESLENDIKNM
KGVYDLHDLHIWSITVGKVVLSCHVVAEAGVCSRELILKIKSHCEKRYNIVHTTIQVE

CsMTP5/ACHR01000847

MDTPGSFNHHTSSNDSQNSWNPDTGFGANDRRFAFSRQASSKQWQDLPPHTPFSINSDDSAKPLLSRNMSSINIPPGGYFAS
ESNKFFSVKDNSGDKLSVL**SLAFSILENVRSGNRYMKRLFLMISLNVLYSTAELAIGLLTGRIGLV**SDAF**HLTFG**CGLLTFS
LFAISASRSKPNHVYTYGYKRLEVLAAFTNALFLLFLSFSLAVEALHAFIQDESEHKHYLIVSAVTNLLVNLIGVWFFRNYA
RINLVYRKAEDMNYHSICL**HVLAD**SIRRVQNAEVLCLGLVSITVFMIVMPLFKATSGVLLQMAPPSIPTSALSKCWRQWKNV
HISMFGQITSREDIVEITQARFWELVPGQVIGSLSLTTKKGTDSRQALEFAHDMYHELGIQDLTVQTEDA

CsMTP6/ACHR01000689

MGYRFHRLNPILQSFYSRISPPTHKEFHSIPSFQSPSLHPQFTFLGIYDDPKSKICRRWHLGHSHRHDDDHRFGQEGENIFK
LGLGADIGLAVGKAVTGYLSG**STAIIADAAHSVSDVVLSGIALWSFKAGKAPKDKEHPYGHGKFE**TLGALGISSMLLATAGG
IAWHASELLLNLAIILSESQCFQGSRNLAWPSLFSCKQGLLSAAPEIVNQPFGHESLHNHSHSHGEHHHGIDMDHPILALNM
TIISICIKEGLYWITKRAGEKRGSGLMKANAW**HHRAD**AISSVVALIGVGGSILGVKFLDPLAGLVVSGMILKAGLQTGHQSI

LELVDAAIPADQIDPFKQTILQVEGVKGCHRLRGRRAGSSLYLDVHIEVDPFLSVSAAHSIGENVRHEIHTSHPEVSEVFIH
IDPSISHFPPKLSNQQAASAGTSNQSTDFPLTENIEATVSDIVQSKFPENMMVERITPHLLQGKILLQIEVSMPPDLLIRNA
MDVAKRAEMEILKADSNIVHVSIQLRLGQQIPQLSH

CsMTP7/ACHR01005111

MQISGPPSISPQKRFIVVLQVTRRLRPSSIECESVNRDKAKSSSCTIVLMRTSYLLQRFGFHHTHRSPQQQQQQQQQQQQHQ
PECDSYRIPLIGTYFQSRRLSSPSSCSRRSVLLGLISLDSNPPRPPLNHHYAFHRGFFTRAKPVQRIEFNDYHSQRAVTTAL
WCNFLVFSLKFGVWFATS**SHVMLAEVVHSVADFANQALLAYGLSSSRRAPDAIHPYGYSKER**FVWSLISAVGIFCLGSGATI
VNGIQNLWTSQPPANIHYAALVIGGSLIIEGASLVVAIQAVKKGAAAEGMKLRDYVWRGHDPTSVAVMTEVDGAAVTGLIIA
AASLVAVNTTGNAIYDPIGSIIVGNLLGMVAIFLIQRNRHALIGRAMDENDMQKVLQFLKNDPVVDALYDCKSEVIGPGFYR
FKAEIDFNGVMVVQNYLTRTGREEWAREFRQAAKSKDDSTLLKIMSNYGEEVVTALGSEVDRLEKEIQELVPGIRHVDIEAH
NPTGPTP

CsMTP8/ACHR01011125

MDGDSDLSPKAPLLGASLNGSGGKRGRLSRRYSVNSLRSEFISRLPDKLRSHLQDVESPYEIDLSKSSGFSREEKDYYERQL
ATLKSFEDVDSLVSSDCIDEEDMEEGAQQERAMKISNYANIIYATVRSG**SIAIAASTLDSLLDLMAGGILWFTHLYMKQVNI**
YKYPIGKLRVQPVGIIVFAAVMATLGFQVLLQAVEQLIQDKPSESLSSEQFVWLCAIMTFATVVKLALWLYCKNSRNDIVRA
YAK**DHYFD**VVTNVVGLVAAILGDKIFWWIDPVGAIALAIYTILNWSGTVWENAVSLVGKSAPPEVLQMLTYLVIRHPEVKRV
DTVRAYTFGVLYFVEVDIELPEELPLKEAHAIGETLQIKIEKLPEVERAFVHLDFECEHKPEHSILSRLPNTQP

CsMTP9/ACHR01003497

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EVDSYNELGILPGTLTETFTEFLIYQDEKKEEANSERQAIYISNVANMLIFIAKVYASVESR**SLAVIASTLDSLLDLLSGFI**
LWFTANAMRKPNQYRYPIGKNRMQPVGIVVFASVMATLGIQILLESARELISEVQPDRDPDKVKWMVGIMAAVTVVKFFLTI
YCRRFANEIIRAYAQ**DHFFD**VITNSIGLATALLAIKFYWWLDPLGAILIALYTISNWSKTVMENVWSLIGRTAPPDYLAKLT
YLVWNHHEEIKHIDTVRAYTFGCNYFVEVDIVLPGETSLSQAHDIGETLQDKLEQLDEVDRAFVHVDFEFTHKPEHKPKAS

CsMTP11/ACHR01009952

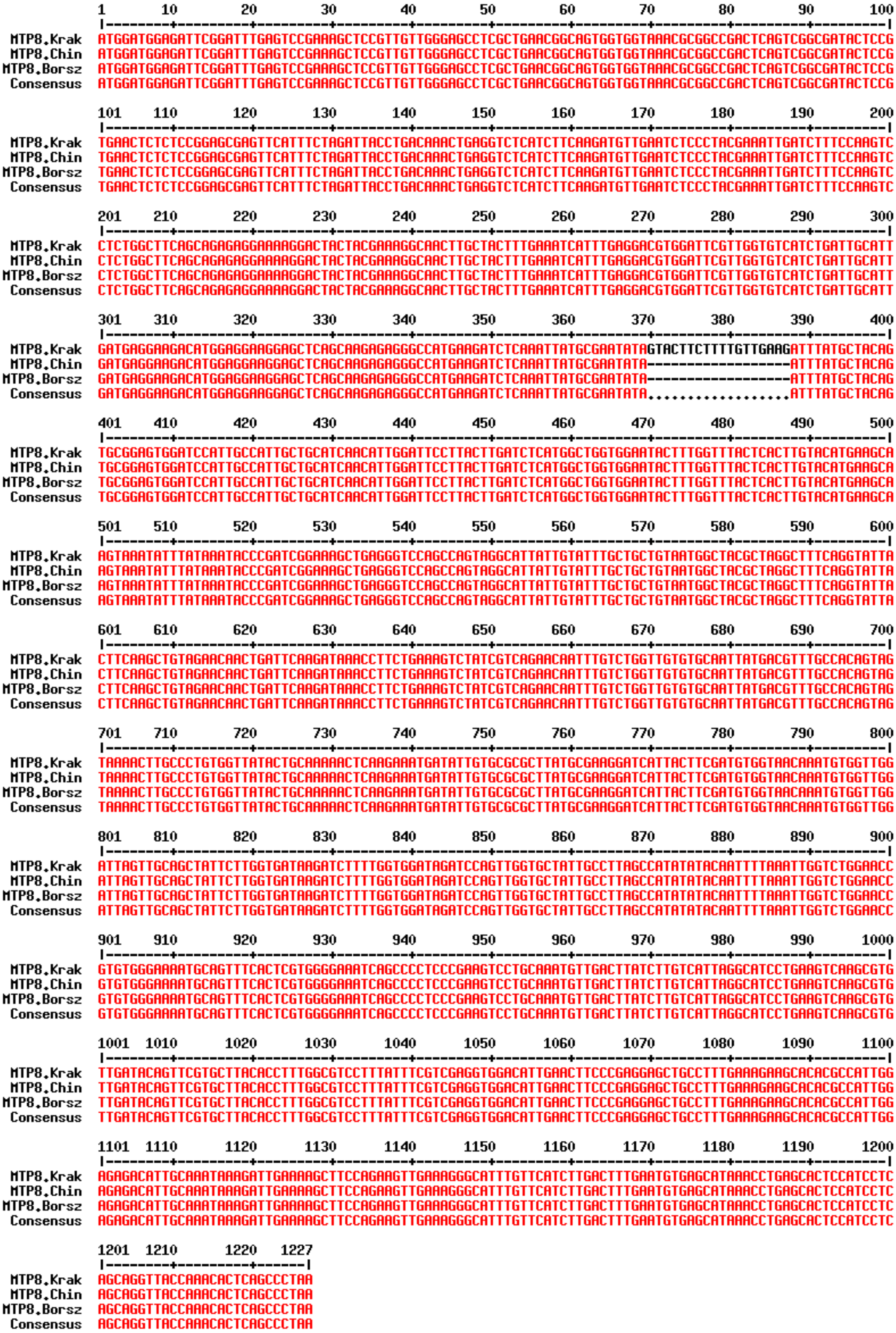
MVQPVVSIENDEESSLLLQSTAGDLSWRLNFDGFQFSPEHKEKKPSRPLHDCLGVLSPEDYVAEYYQQQVEMLEGFNEMDAL
TDRGYVPGMSKEERENLAKSETFAIRISNVANMVLFAAKVYASIRSG**SLAIIASTLDSLLDLLSGFILWFTAFSMQTPNPYQ**
YPIGKKRMQPLGILVFASVMATLGLQIIMESIRTLLLSDSVFNLTKEQERWVVGIMISVTIVKLVLMIYCRTFTNEIVKAYA
Q**DHFFD**VVTNAIGLVAALLANYIAGWIDPLGAIILALYTIRTWSMTVLENVNSLVGRSAAPEYLQKLTYLCWNHHKAIRHID
TVRAYTFGSHYFVEVDIVLPGDMPLEEAHDIGELLQEKLELLPEIERAFVHLDYEYKHKPEHAQAHS

CsMTP12/ACHR01009785

MVVKSILLAIVFLLRFQALLYCGTAAMILAEMTGNVAARFLAERRNRMTMGDRTRSRSSEVRGFLSLFLGLFLLSISWDRID
CFPFATSFIDKYGFSVLPRENCMRIWPMLLPFLSGFLGCYERISMNWGSVKQLGQKRVRLVSLFFTTIILFVPAVISMLLFE
AEGKSVSFGNLAWPLANTVVFGVLLNENYSDDKLVSSKDFRSEFLVTFVCTVILELLYFSELSLWGLLFCGLLLYVAVRELD
PVYLNYLELGVESSDSIVTMVMRPVRHILTERKSRKIALFLLLNTGYMVVEFVAGFMSN**SLGLISDACHMLFDCAALAIGLY**
ASYISRLPANNQFNYGRGRFEILSGYANAVFLVLVGALIVLESLERILDPQEISTSSLLTVSIGGLVVNVVGLIFFHEEHHH
AHGGSGSCAHSHSHSHSHSPSKSHSCAGSHHHDKHEHDSGRKHENAISVTKECHESSVSGHHEHKQVDVCSENHLSNQCDDH
HHEHTDHHDHKHSHNHDHHHQHDCKHEHHDHVHQHDQHGHLSEPKSDVPKMVSYSVSENSHSHPSKQPVEGTVRKKHHHHHI
DHNMEGIFL**HVLAD**TMGSVGVVISTLLIKYKGWLVADPACSIFISIMIISSVIPLLRNSAEILLQRVPRAHEQDLKEAVRDI
MEIHGVQGIQNLHVWSFTNTDVVGTLRLHVSTETDKPSIKAKVEHILHDAGIKDLTLQLEHNQELS

Figure S3

Nucleic acid sequences of the *CsMTP8* from cucumbers Krak (1227 bp) and Chinese long (1209 bp). The alignment was performed using Multalin version 5.4.1(Corpet, 1988). The identical nucleotides are marked in red, whereas the additional 18 bp long sequence (370-387 bp) specific only for Krak cultivar was marked in black.



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           1       10        20        30        40        50        60        70        80        90       100
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
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 MTP8.Chin ATGGATGGAGATTCGGATTTGAGTCCGAAAGCTCCGTTGTTGGGAGCCTCGCTGAACGGCAGTGGTGGTAAACGCGGCCGACTCAGTCGGCGATACTCCG
MTP8.Borsz ATGGATGGAGATTCGGATTTGAGTCCGAAAGCTCCGTTGTTGGGAGCCTCGCTGAACGGCAGTGGTGGTAAACGCGGCCGACTCAGTCGGCGATACTCCG
 Consensus ATGGATGGAGATTCGGATTTGAGTCCGAAAGCTCCGTTGTTGGGAGCCTCGCTGAACGGCAGTGGTGGTAAACGCGGCCGACTCAGTCGGCGATACTCCG

           101    110       120       130       140       150       160       170       180       190       200
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
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 MTP8.Chin TGAACTCTCTCCGGAGCGAGTTCATTTCTAGATTACCTGACAAACTGAGGTCTCATCTTCAAGATGTTGAATCTCCCTACGAAATTGATCTTTCCAAGTC
MTP8.Borsz TGAACTCTCTCCGGAGCGAGTTCATTTCTAGATTACCTGACAAACTGAGGTCTCATCTTCAAGATGTTGAATCTCCCTACGAAATTGATCTTTCCAAGTC
 Consensus TGAACTCTCTCCGGAGCGAGTTCATTTCTAGATTACCTGACAAACTGAGGTCTCATCTTCAAGATGTTGAATCTCCCTACGAAATTGATCTTTCCAAGTC

           201    210       220       230       240       250       260       270       280       290       300
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
 MTP8.Krak CTCTGGCTTCAGCAGAGAGGAAAAGGACTACTACGAAAGGCAACTTGCTACTTTGAAATCATTTGAGGACGTGGATTCGTTGGTGTCATCTGATTGCATT
 MTP8.Chin CTCTGGCTTCAGCAGAGAGGAAAAGGACTACTACGAAAGGCAACTTGCTACTTTGAAATCATTTGAGGACGTGGATTCGTTGGTGTCATCTGATTGCATT
MTP8.Borsz CTCTGGCTTCAGCAGAGAGGAAAAGGACTACTACGAAAGGCAACTTGCTACTTTGAAATCATTTGAGGACGTGGATTCGTTGGTGTCATCTGATTGCATT
 Consensus CTCTGGCTTCAGCAGAGAGGAAAAGGACTACTACGAAAGGCAACTTGCTACTTTGAAATCATTTGAGGACGTGGATTCGTTGGTGTCATCTGATTGCATT

           301    310       320       330       340       350       360       370       380       390       400
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
 MTP8.Krak GATGAGGAAGACATGGAGGAAGGAGCTCAGCAAGAGAGGGCCATGAAGATCTCAAATTATGCGAATATAGTACTTCTTTTGTTGAAGATTTATGCTACAG
 MTP8.Chin GATGAGGAAGACATGGAGGAAGGAGCTCAGCAAGAGAGGGCCATGAAGATCTCAAATTATGCGAATATA------------------ATTTATGCTACAG
MTP8.Borsz GATGAGGAAGACATGGAGGAAGGAGCTCAGCAAGAGAGGGCCATGAAGATCTCAAATTATGCGAATATA------------------ATTTATGCTACAG
 Consensus GATGAGGAAGACATGGAGGAAGGAGCTCAGCAAGAGAGGGCCATGAAGATCTCAAATTATGCGAATATA..................ATTTATGCTACAG

           401    410       420       430       440       450       460       470       480       490       500
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
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 MTP8.Chin TGCGGAGTGGATCCATTGCCATTGCTGCATCAACATTGGATTCCTTACTTGATCTCATGGCTGGTGGAATACTTTGGTTTACTCACTTGTACATGAAGCA
MTP8.Borsz TGCGGAGTGGATCCATTGCCATTGCTGCATCAACATTGGATTCCTTACTTGATCTCATGGCTGGTGGAATACTTTGGTTTACTCACTTGTACATGAAGCA
 Consensus TGCGGAGTGGATCCATTGCCATTGCTGCATCAACATTGGATTCCTTACTTGATCTCATGGCTGGTGGAATACTTTGGTTTACTCACTTGTACATGAAGCA

           501    510       520       530       540       550       560       570       580       590       600
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
 MTP8.Krak AGTAAATATTTATAAATACCCGATCGGAAAGCTGAGGGTCCAGCCAGTAGGCATTATTGTATTTGCTGCTGTAATGGCTACGCTAGGCTTTCAGGTATTA
 MTP8.Chin AGTAAATATTTATAAATACCCGATCGGAAAGCTGAGGGTCCAGCCAGTAGGCATTATTGTATTTGCTGCTGTAATGGCTACGCTAGGCTTTCAGGTATTA
MTP8.Borsz AGTAAATATTTATAAATACCCGATCGGAAAGCTGAGGGTCCAGCCAGTAGGCATTATTGTATTTGCTGCTGTAATGGCTACGCTAGGCTTTCAGGTATTA
 Consensus AGTAAATATTTATAAATACCCGATCGGAAAGCTGAGGGTCCAGCCAGTAGGCATTATTGTATTTGCTGCTGTAATGGCTACGCTAGGCTTTCAGGTATTA

           601    610       620       630       640       650       660       670       680       690       700
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
 MTP8.Krak CTTCAAGCTGTAGAACAACTGATTCAAGATAAACCTTCTGAAAGTCTATCGTCAGAACAATTTGTCTGGTTGTGTGCAATTATGACGTTTGCCACAGTAG
 MTP8.Chin CTTCAAGCTGTAGAACAACTGATTCAAGATAAACCTTCTGAAAGTCTATCGTCAGAACAATTTGTCTGGTTGTGTGCAATTATGACGTTTGCCACAGTAG
MTP8.Borsz CTTCAAGCTGTAGAACAACTGATTCAAGATAAACCTTCTGAAAGTCTATCGTCAGAACAATTTGTCTGGTTGTGTGCAATTATGACGTTTGCCACAGTAG
 Consensus CTTCAAGCTGTAGAACAACTGATTCAAGATAAACCTTCTGAAAGTCTATCGTCAGAACAATTTGTCTGGTTGTGTGCAATTATGACGTTTGCCACAGTAG

           701    710       720       730       740       750       760       770       780       790       800
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
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 MTP8.Chin TAAAACTTGCCCTGTGGTTATACTGCAAAAACTCAAGAAATGATATTGTGCGCGCTTATGCGAAGGATCATTACTTCGATGTGGTAACAAATGTGGTTGG
MTP8.Borsz TAAAACTTGCCCTGTGGTTATACTGCAAAAACTCAAGAAATGATATTGTGCGCGCTTATGCGAAGGATCATTACTTCGATGTGGTAACAAATGTGGTTGG
 Consensus TAAAACTTGCCCTGTGGTTATACTGCAAAAACTCAAGAAATGATATTGTGCGCGCTTATGCGAAGGATCATTACTTCGATGTGGTAACAAATGTGGTTGG

           801    810       820       830       840       850       860       870       880       890       900
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
 MTP8.Krak ATTAGTTGCAGCTATTCTTGGTGATAAGATCTTTTGGTGGATAGATCCAGTTGGTGCTATTGCCTTAGCCATATATACAATTTTAAATTGGTCTGGAACC
 MTP8.Chin ATTAGTTGCAGCTATTCTTGGTGATAAGATCTTTTGGTGGATAGATCCAGTTGGTGCTATTGCCTTAGCCATATATACAATTTTAAATTGGTCTGGAACC
MTP8.Borsz ATTAGTTGCAGCTATTCTTGGTGATAAGATCTTTTGGTGGATAGATCCAGTTGGTGCTATTGCCTTAGCCATATATACAATTTTAAATTGGTCTGGAACC
 Consensus ATTAGTTGCAGCTATTCTTGGTGATAAGATCTTTTGGTGGATAGATCCAGTTGGTGCTATTGCCTTAGCCATATATACAATTTTAAATTGGTCTGGAACC

           901    910       920       930       940       950       960       970       980       990      1000
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
 MTP8.Krak GTGTGGGAAAATGCAGTTTCACTCGTGGGGAAATCAGCCCCTCCCGAAGTCCTGCAAATGTTGACTTATCTTGTCATTAGGCATCCTGAAGTCAAGCGTG
 MTP8.Chin GTGTGGGAAAATGCAGTTTCACTCGTGGGGAAATCAGCCCCTCCCGAAGTCCTGCAAATGTTGACTTATCTTGTCATTAGGCATCCTGAAGTCAAGCGTG
MTP8.Borsz GTGTGGGAAAATGCAGTTTCACTCGTGGGGAAATCAGCCCCTCCCGAAGTCCTGCAAATGTTGACTTATCTTGTCATTAGGCATCCTGAAGTCAAGCGTG
 Consensus GTGTGGGAAAATGCAGTTTCACTCGTGGGGAAATCAGCCCCTCCCGAAGTCCTGCAAATGTTGACTTATCTTGTCATTAGGCATCCTGAAGTCAAGCGTG

           1001  1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
 MTP8.Krak TTGATACAGTTCGTGCTTACACCTTTGGCGTCCTTTATTTCGTCGAGGTGGACATTGAACTTCCCGAGGAGCTGCCTTTGAAAGAAGCACACGCCATTGG
 MTP8.Chin TTGATACAGTTCGTGCTTACACCTTTGGCGTCCTTTATTTCGTCGAGGTGGACATTGAACTTCCCGAGGAGCTGCCTTTGAAAGAAGCACACGCCATTGG
MTP8.Borsz TTGATACAGTTCGTGCTTACACCTTTGGCGTCCTTTATTTCGTCGAGGTGGACATTGAACTTCCCGAGGAGCTGCCTTTGAAAGAAGCACACGCCATTGG
 Consensus TTGATACAGTTCGTGCTTACACCTTTGGCGTCCTTTATTTCGTCGAGGTGGACATTGAACTTCCCGAGGAGCTGCCTTTGAAAGAAGCACACGCCATTGG

           1101  1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
 MTP8.Krak AGAGACATTGCAAATAAAGATTGAAAAGCTTCCAGAAGTTGAAAGGGCATTTGTTCATCTTGACTTTGAATGTGAGCATAAACCTGAGCACTCCATCCTC
 MTP8.Chin AGAGACATTGCAAATAAAGATTGAAAAGCTTCCAGAAGTTGAAAGGGCATTTGTTCATCTTGACTTTGAATGTGAGCATAAACCTGAGCACTCCATCCTC
MTP8.Borsz AGAGACATTGCAAATAAAGATTGAAAAGCTTCCAGAAGTTGAAAGGGCATTTGTTCATCTTGACTTTGAATGTGAGCATAAACCTGAGCACTCCATCCTC
 Consensus AGAGACATTGCAAATAAAGATTGAAAAGCTTCCAGAAGTTGAAAGGGCATTTGTTCATCTTGACTTTGAATGTGAGCATAAACCTGAGCACTCCATCCTC

           1201  1210      1220   1227
           |--------+---------+------|
 MTP8.Krak AGCAGGTTACCAAACACTCAGCCCTAA
 MTP8.Chin AGCAGGTTACCAAACACTCAGCCCTAA
MTP8.Borsz AGCAGGTTACCAAACACTCAGCCCTAA
 Consensus AGCAGGTTACCAAACACTCAGCCCTAA
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