

Additional file 3: Figure S1. Sequence alignment of dualCMDs in *T. vaginalis*.

a

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TvCMD1  MS-YKATEHDI EQNDPEYTAFFKRFELMVKNESKIDDKSRYLGILGALIGAKAIDYFPIILEMSLDNILTPNEVKEVLYEAAAYILGIANVFPFLKLTNDIFKAKNINLPLENQSKVAPGE
TvCMD2  MSNYKEVLDELEHNDPEYFEFFYRFEKLVQSETKIDEKNRYLGILGSLIGSKSIDYYPYII EQVLTKILTPOEIKEVLYEAAAYILGASTVYFPFLKVTNDIFKQHNINLPLENQCKVSPEE
TvCMD3  MS-NSLPSIDPRIPDAEFLNVFNEFENDVKNEIKVENEYRIPAILAILIGRSRIDYFPTFLDEAVSSGITITQIKEII YQGIMLIGMAHVYFPFLKIVNEHF---NISEPADHHSTVTKEN
** . : . *.*: .* .** *:.* *::: * .**.*:::***:* :: : . :* ::*:**.. **: *:*:***:.*: * **.* * :...*: :

TvCMD1  GLQKGIEKQAEAFPGMEKPFHTMGPMKWWVVSFMYGEFYTREVLTVKERELVLSCIFIGHGDAAPQFNQHIKANIHVGNKKFLIQMILSLVPYLYGYPRTFNALKVLND---AIPDE---
TvCMD2  ALKKGIEKQKESFGPGMEDFHTKGPMMKWVVTFMYGQLYTRVLTVKQREIVITCIFIYGDATPQFLQHVKALTNLGHGKWDLIQMILSLVPYIYGYPRTFNALRAINE---AVPDPLYM
TvCMD3  RKEKGIEKLNESFGFIMNGLPGLGPMSDWLMKYYGELYTRDILSMRQRELILLCFLSVHGDSYMALSAHVMSNINVGNDKEFLKNVYSLVPYMGSVKAYNAIKCIDDDWKSVPVHSD---
:***** *:* * : : *** .*:::: **::*:***:***:***:***: ** : *** : * : : **:* * : : ***** * :***:***: : : : . : .

TvCMD1  -----
TvCMD2  KVMKFAKGMYSIFG
TvCMD3  -----

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b

<p>TvCMD_1-110 Q88N35_P.putida Q8TJP3_M.acetivorans Q5ZYG6_L.pneumophila</p>	<p>MSYKATE-----HDIEQN---DPEYTAFFKR-FE MDEKQRYDAGMQRRAVLGDAHVDRLS-EKLNDF---NGEFQEMITRHAW MTEHEEILESMGEK-----GFTPQVL-ETLGDLD---DPEFLHKYRR-CD MSDKFSH-----ITKDITTLAKFRKEMPELMTGFSS-LA * : : : *</p>	<p>TvCMD1_111-233 Q88N35_P.putida Q8TJP3_M.acetivorans Q5ZYG6_L.pneumophila</p>	<p>NQSKVAPGEGLQKGIEKQAEAFG-PGM-EKFHTM-GPMKWWVVSF---MYG MDEKQRYDAGMQRRAVLGDAHVDRLS-EKLNDFNGEFQEMITRH---AWG MTEHEEILESMGEK-----MGFTPQVL-ETLGDLDPEFL---HKYRRCDH MSDKFSH-----ITKDITTLAKFRKEMPELMTGFSSLAQ . : : : *</p>
<p>TvCMD_1-110 Q88N35_P.putida Q8TJP3_M.acetivorans Q5ZYG6_L.pneumophila</p>	<p>LMVKNESKIDDKSRYLGILGALIGAKAIDYFPIILEMSLDNILTPNEVKE GDIWTRPGLPRHTRSLITIAMLIGMNRNDELKHLRAAANNGVTRDEIKE HKILTDGALPSKVKILMALAVVASKQCESCTVAQMKSALKNGATKEEIME QAATKDGDALDKKTKELIAMALAVAKQCPGCIGFHSQTLVKLQATREELLE . : : : * : * : * : *</p>	<p>TvCMD1_111-233 Q88N35_P.putida Q8TJP3_M.acetivorans Q5ZYG6_L.pneumophila</p>	<p>EFYTREVLTVKERELVLSCIFIGHGDAAPQFNQHIKANIHVGNKKFLIQ DIWTRPGLPRHTRSLITIAMLIGMNRNDELKHLRAAANNGVTRDEIKE KILTDGALPSKVKILMALAVVASKQ-CESCTVAQMKSALKNGATKEEIME AATKDGDALDKKTKELIAMALAVAKQ-CPGCIGFHSQTLVKLQATREELLE . * : : * : . : . : : : : . : . : .</p>
<p>TvCMD_1-110 Q88N35_P.putida Q8TJP3_M.acetivorans Q5ZYG6_L.pneumophila</p>	<p>VLYEAAAYILGIANVFPFLKLTNDIFKAKNINLPLE VLMQSAIYCGIPAAANATPHLAESVWDELGVESR-Q TMEVIFITSGAPAVAACRNALKM-LKD--M----- TLGMAVYMGGGPSLMYAAEALEA-FEFSK----- . : * . . : .</p>	<p>TvCMD1_111-233 Q88N35_P.putida Q8TJP3_M.acetivorans Q5ZYG6_L.pneumophila</p>	<p>MILSLVPYLYGYPRTFNALKVLNDAIPD-----E VLMQSAIYCGIPAA-NATPHLAESVWDELGVESRQ TMEVIFITSGAPAV-AACRNALKMLKDM----- TLGMAVYMGGGPSL-MYAAEALEAFEEF-SK---- : * * . . :</p>

a Protein sequence alignment of TvCMD1 (TVAG_256720), 2 (TVAG_107080) and 3 (TVAG_474690). Gray color indicates conserved CMD signatures in sequences. **b** CMD signature alignments against three bacterial CMDs. TvCMD1 was divided into 2 CMD signatures and aligned with the CMD of *Pseudomonas putida* (Q88N35), *Methanosarcina acetivorans* (Q8TJP3 or MA3736) and *Legionella pneumophila* (Q5ZYG6 or lpg0406). The blue box indicates the conserved thioredoxin-like domain (CXXC). The brown boxes indicate cysteine residues responsible for iron-sulfur cluster binding. Asterisks (*) indicates a fully conserved residue at the position; colon (:) indicates a residue with strong similarity; period (.) indicates a residue with weak similarity.