

**Supporting Figure 2. Motif Sequences Found By MEME Analysis For The 9 HCMP Groupings**

<b>MEME group</b>	<b>MEME motif ID</b>	<b>MEME motif length (aa)</b>	<b>MEME motif sequence</b>
<b>Group 1</b>	1	35	CTQCKDGYFLFMGGCYKIDRWPGNHVCKKAESGMC
<b>Group 1</b>	2	250	KFLFTNPDDSAAERCILCYDNVGFSGYKGVGDCRYCLPPLTGETSAECNWCQNEKYGPIDGVCKEPRHLCAD GACSNCYMTHIQHNGGCYTKTETVAQKICTTENQFQVINITACKKCAIKGEVPMDGRCIKGLLEPKCNYPNTDG SCTDCKKGGVNYDTFLFNEGCYNSDYIGSQICSKVNERAECELWNIGDYGVFKPPDDHMAHPCSDTSARGIQ GCSRCRYNNEEKKPCYDCEYDTLAFDRM
<b>Group 1</b>	3	34	LSAMAIIGIAIIVMVVVGALVGLVWVWFLFRRRR
<b>Group 1</b>	4	36	FLFMGGCYNINKYPGRFICKWAFDGGKCTECMEHYGY
<b>Group 1</b>	5	34	QMDRHHMKVMFVRGTEYCSQCRAHVPINGICV
<b>Group 1</b>	6	29	CRACHENCATCSGPQADQCLSCMPGKYWK
<b>Group 1</b>	7	28	QFEINGYHYCSKCKDQSEFPNGICKPH
<b>Group 2</b>	1	33	WMSMWMIVGISVFMIAIIVWIIWVFKRRK
<b>Group 2</b>	2	25	TCTRCAEGYFLWDGKCYPCCEMIPGK
<b>Group 2</b>	3	25	YEHEEYCLKCMPPGYMINGRCVHAN
<b>Group 2</b>	4	29	CKIRNCVKCHDDKQMCACKENFYLEKDG
<b>Group 2</b>	5	51	HRKRLFGRWLQQFQAKRADSQPANRRREDWEKELQGQQQYYREADIRVNNVR
<b>Group 2</b>	6	25	MCKECNTDNGQQCESCHEGYLDPT
<b>Group 2</b>	7	25	NCKQRDSATTCVECEPGYFLQPSRK
<b>Group 3</b>	1	220	GAKNVVCQKCEDGYLKEHDQNKVVCPEPPPPECTVELCAICVEDDPNRCEHCTAGAYLCPRTAACTKDCASCGG SMYPDEDLGECQPCDIANCRVCATGLKCESCAENAVPISPDVYHTACMGCSDTGGMDGWVGLAGCTTCELTDK GGGSVNCLDPGYRRRGGGLGGGAIAIIVVLLVLAVAGFLVWVVFRRRGRPRKRAKYTSLMRGESYDYRQSLI
<b>Group 3</b>	2	129	GNTCDKGVCTTCGNGYFFHYGSCYKFDGSPGSIVCPNQDTTGTVCGSCGSKFVKNPSSASSATSCLACYGLD GTLFCERCERMNVLTSADVKPTLCTQCKIGYVPVDGRCISNYSALAAALAGCSDPRGN
<b>Group 3</b>	3	137	EPPEDNACQALPPATPEGCAVQGCQACSKDSATTCDACFEPLIMKEDKTKCFGSCALGPGYYNNSGICAPCV ENLSCVDGTSCSQAEGYYLEVSGADSSTGACKPCAAGCSTCNDAGDSLCTCLFYGYIAFE
<b>Group 3</b>	4	49	CIRDFLFYRGGCYRTASLINAICKEKHIVEEGMYCGACAIEGDVPIDGV
<b>Group 3</b>	5	69	GLCEACSSGFMLFYGSCYSVDGPLAQAICKAEDQIYLNGRVFCRCAQPDHYPINGLCIAQKGDHTDEH
<b>Group 3</b>	6	69	MRVLILLLLHGFSECTQSDSCGGATGVCNVTIGGKKYCSKCDGARVPVNGDCRLLSLSRSICIVPTGS
<b>Group 3</b>	7	53	DTKQTADDTPEFFLFYNGCYDINHPIGKLICQEVSNACSTCNSNESSNIAN
<b>Group 4</b>	1	193	YPFNGVICPNTQRDAYCTSTANGACTTCSGAFLMNGGCYTTHEYPGSTICDKQSNKCTTTTKGYWISPDGKL LECDPTCLACTAPGPRCTRCPDCLKKRASGAATGSCVDPGACVDGYADGDACLPCATPGCKTCGHASFACT ECAGELFVSLDGGQSCLEECTGDKVVGEVPGGVRRCWCERGFPLALD
<b>Group 4</b>	2	97	ECPPDMPWCAACDESGRCLLCVTSGHNVQVDQRTCAEGCGARASSNQGVCMCELDAVLTKGICVPAKELARK RMAAIAGGTVAGVIVIGVLVGLFCW
<b>Group 4</b>	3	97	YTKQDRHFYPIDYQCQAKGLHNCVNGYCTSCYKTHLFYEGCYSRHSSTGFAICAEANQYELDNVTICKECVNT SHAPKNGACILIKENPSIMEFSD
<b>Group 4</b>	4	97	VEEGSESKEVSCRVCMPFTYNSSGTCTPCTDSCAVCKDGTPTGCQQCSPGKILNFSIVSSENADCVDQCSVG DECAECGITIDGSRYCTRCKDANM
<b>Group 4</b>	5	68	MLGLLPLLLLASFCKASRDVYVYKFGVECEQHQENCAQDRCIFMGWDQLCTQCVPGYVPINGKCKQYP
<b>Group 4</b>	6	69	FICSQASNGRCTECNVSTHEMYVFTNPDVSAAEKCILCSDTVGFNGYKASGCLDCLPPITDKIGIALC
<b>Group 4</b>	7	60	CTKDPSKGLCTACPASAKSFLFYGGCYDRDSHIGSRCLSRIGSGVCEQWNSQFDWIFSKN

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Group 5	1	185	STCQPCQQGCAFCMDGEHQFPYRCLSGGCAQGYFHPYAQVCMKCPEGCMDCYDEAHSIPVCERCTDSSQ LTVGPKIYGIWCSLDLPPKSCKEDEFQENGFICPCYLAIMGCIGCSDFRFRCTECQPGFYLDNICVRCDNCLACD GPGTNCKNCWDGFLVQNGTCVPGVEIPNCLHADNTTDP
Group 5	2	113	MNCPRDHYLLGNMVCEDDAMKWCLCERGPACTRCKAGYYLDHGKYCKPCDHTCERCNGPGKCLECSENHC RNQDGVCEPDGDDVYEGCIRCVDHTGKCMQCHEGYFHNGKGF
Group 5	3	110	GFYVADGACKKCVDNCLCKGPDISNMLGFEGYRYDSYKNQIEKCQDPNCERCAFTAKYCGTCKLGFYISPD QKCAKQVENCMVYVYGQSKCSECIHGYGFSEGGDP
Group 5	4	44	KLDLNFSGRPGVIAAIVLIIIGFIVAIPFIVKVLVRRGVR
Group 5	5	69	EGIKGEYFDDICEFVGVQVGFYFAYGDSKLEPPEGASMMKQFKNNVVRGRTRSGQVFAISLVMGYLLH
Group 5	6	46	CTKCKDNCYSCKNETECERPASGYVNPSTGEPAPCTDHNCIDACD
Group 5	7	25	RSRLMKIDRGSEDHNEFELEEDLL
Group 6	1	250	MICQDQYKIDVETGISVVPKGRWYMRIAHRKLWDSPKIHSDFCPKPDRCWACEDGYFLGWYGDKEAKILTGD YEGQDWKGVVCLKNTEESGKADTPATCTCEQEGYLLIPEDPKSEILPDGRIGPHFPMRCENKKDYPLEENAN GNRENRAYDDFHPNELGKAVLQKNSKGYNDEKLPKNKDISED SAPVYSYEDQILEPPAHKVKCDGYYKESNS IACYPGFDNRLSDGISANAVIQEGTRQY
Group 6	2	192	QQLAIVDDSKFCGDDKAGYQPVDFMLDNKERVPVNGTPGPNVRSATVGERFEQSKRCQQGYYYPGNRLARS VGNKDTKSANIQAEDGYSLPADPDLNKPVDVDPQQISNCLPGYYNSRDKCVKCDAGYNWANEPNCVV AAPPSSNGQDSNQSVEGSGCGRGYGMRGGLSPPAIGDSVVVIFRVD
Group 6	3	69	YAGELPINGQCKQIVRMARRTIFCKKVNGLTVLVEDKVIERGLFFYFRKGGRYHVDNEPGQKLCIQEHE
Group 6	4	34	MLLTAF CIMASVLAATCTVEANTRDCAESKCEMV
Group 6	5	25	LCFDGYGPNETGSC TPCPDGKGGPN
Group 6	6	25	MLMSMFVIMLLVRAATCAVEDVDRD
TMK-like	1	250	RVICTRCKDKHPISEDSRCSQSCNDRSSESGNCKAGSCTAMGSLYCSRCALDDEWPINGACTGHDTDYVCEK GKGVCTGLRGYMLYMGCCYDPAIIPGSGICRELLTVGGRTYCKQCNLAGEFPINGLCTKDVPDGVSCSSGLCV ICPENYFFHEGGCYDITTTTPGSGICEVLGTGRDAGTCRRCRPGYRHNKELTCMCSAVSNCASCEIDVKYCTECI QPYTLTGVGAGAYCTKPKRVGQDACS
TMK-like	2	250	PPDRSSVSDSCVPTENS DTLKGIHPCKSCKVSNGLLVACEQFYRPMNGGTECVQTCVEAEADPKEHRCKR DKCDVLTGFYCSQCAADAEGPVNGVCASVAAGVCIQYKQANGTKYCTHGYIKYKGGCYEAGSFEAGDICDAQ DVVTSGAGSFCACKKQKDEVPVDGECKVSDCTVKGDGICRSCKQGVKSFQITKDGSPATVACFTKCPDGMYE SAEFCQMCDKSKCTCQD SAAKCTGCADGFYL
TMK-like	3	250	HCGDGMFLFEGACYTKGRAPGTSICGDDTESTSGCNACEAGFSKTDKGCVRCSDPNCGACVDDPNTCTACRA GYLLQSTSCIACHPACKTCDGMGADKCKEAEYFGTFATPLGLACLACSDTSGRDWSVWVSGCRLCEAPKVA GPALCKDCLPGYKALSTGTEVTCHAVCPMTYYEAADSCIPCAIDNCATCTSTRCTSCVPEHIWNGEECVPKICPP QCLCREQSIACIGCENAVEVRPTHSSASR
TMK-like	4	250	QDGYASGNSCVACTPGCKKCDSTGCKVCKDRFALRNNICIEECPVGLLSTSCAAGYCNVNGTLACSRCALLSS VIIDGKCKANDDACIRTPSSGTCAACKDTHLLYGGCYAKGAAAGTAICDSQHATLGPYTICKQCKRDGEVPID GSCVALANTRAIRSQVAATPSPTSCTRCGPRFFLHAGGCYEIGRSPGTVLCVAVDSAVAGVCTSCASGYST GLLDPTKESCILCNDTGATNGYTGVD
TMK-like	5	250	RLADRVGPVVCLACESGRKALTDGMLLCPDRDCTEGFWTSGRECIPCAPGCLRCTSAATCSACSQGYSTQS SVSAPSDCRPCDDVTSQNGFTGIPHCAVCAADRARAGVTCHACAEGYGLSGGSCSPCTAAGCARCDGGVCTS CKRGWHLGADRCLACPSPCAACSSAASCLACADGYFQATLLGGPRDVCPCDQTAPQGLQMAIGHGCLCQAQ AWSGAVLCLRCADGNLPLENYCGSSVKRRLGP
TMK-like	6	221	KVCEEIGIGPKCIYGGCTVRDNTFCSRCSEAEVPIIDGVCSLPRERARICLNMSGRCLRCAATHLLYGGCYKI TQPVIEICKQDHQIVEKFAYCKACNDAGEYVVDGSC TAE LDGNTCTSSKCTACGSGYFMHRGICMRQEFHSDI CARVGAGVCEECSYFKNPVASTAIDSCIHCSDTAGSNYTGIDHCDTCLPPKAAGPAHCTDCADRYILNE
TMK-like	7	250	DKKICTPFPDPNGMCSNCAKGHLLFQGGCYSVAEPLGQEVCAETSEVQERTVCVRCAPGFPVSVGVCLRYDA QEVAAVGCVTSRGSVPTDITTCASCGAKAFLYKGGCYSNETSPGNVICDELDTGGCKVCRNKYFRSGSTCA PCHQSCETCSSGAADSLCKKDVFFVFSGGRGMCKPCNDPVATITIVGVANCERCSPKPSGMTPICTKCTTG HVLKGNHCVQVCHEGAEGPGQCKTGHCNTI

<b>MEME group</b>	<b>MEME motif ID</b>	<b>MEME motif length (aa)</b>	<b>MEME motif sequence</b>
<b>VSP-like</b>	1	250	PAKRRLQYSDGAKGSCVPQCVDSSCAECGLTVGGTSSYCSRCVKSTEYPNNGACTSSSSRAAGIACANVAAGR CVACSSNSFSLNGGCYTSTLLPGKTVCTKASDGWCDSTVAGYGITYNGTLLTCTPTNCAMCSSGVCACNSGFYL EKGACKACSKGCATCPHGEACFDCLAGYFSESTCKACHKAISKSLCVVPEGAVKPCILEYDNTSKKSALSSG AISGIAIGVVLVGGVA AVLWVFFVFRKK
<b>VSP-like</b>	2	120	QIESQICQAMQNNVCTT CNSSTKEVFTKNNGCWRCGDSANGGIEGCQRCEMKD SGLQCLECRDLYLSLDRKRC LASC PKGQKGIQGSSSVHSCACDDGSYLKDGKCVGCAVENCAECDE
<b>VSP-like</b>	3	149	IMFFCTECEQDYQPIFPKNVKT VDEKARRAGCVKSPMGGWCTKCN DGYFLFYGGCYQLDQYWKRTICHRAERG ICQECAHGKMMYPIIFTNP NITSPERICHDGDIVGFGGYSGVYQQQKNQHRIPWNIIPDNPMSEHQMTPTYQ R
<b>EGF-like</b>	1	137	DYSGQEATKAPCNGRGRCLLKDPGLAGLSADDYACDCYPIYRGGLCQSCDDANAIAE SSSDALPTCNARAC QDSDGVVCSGGQGT CILDVGLDRESYHYRCKCNDGYTRVGHKCVRTECVATIDGSPV VCGGF GKC
<b>EGF-like</b>	2	232	FQNLPGQNGCVHSSCVSSDNKLC SFGACEKTGDTYGCLCASYYTLVDKDCIPTRCLKDGKVCN GGGTCSGEG SSATCSCSQGWTLHGTL CYPSACVSGGTLCGGNGDCQLSDGGSCSCRSGYETVSGGLCISSQCVQRGTDGTV TICGGNGRCVSENGVKPSCICDEGFSLTSD FVCGVPAPSNKSSAGTTAAIVVVLLVAVAGFLVWV FVIRPRK GGPLRERAPRKP
<b>EGF-like</b>	3	127	RRNAGYYCDDRGLATGDLLDTCTPEKSAIQIGDKCVPVGCLTSNNQESCKNGGT CVKSDGEYHCRCPDMLIAVH GECTSPACMDEELGKVC SGHGTCTDDPRNIQCTCEQDYTYIAPGRCILSSLVD
<b>EGF-like</b>	4	132	PDPQPLRMATAQDICNGTQGYTTFGDPSNPFITCVPKDASDGNVSAYNGTFSAKPGCVFISKIDKTRRFFCGFL ENVTENLPTNNLPTCAK PSEKPDLPETCTHCPTDFHLVHFGENNKTCMHKDCHDGQS
<b>EGF-like</b>	5	69	DNIRNPDINVHVC SGKGVCAYNQLTGRYGCECEDGLEAFGGYCTHPGCAGKVMHNGELKYVECKVYDGS
<b>EGF-like</b>	6	113	PDGYEELDGFCLPKACIFEITLDNQMQRTMCGGKQFGTCVLNATQQSKSYCKINRYDIIQITNGKCMKRTCLS DSLPGNPFQYVECSGHGKCKGDHIVGYSCNCDENYQTV
<b>EGF-like</b>	7	49	LAEACGTGPACVHGDCAYGDGAHFCQRRGWAGAACDAPRAGFRRVTT S