

Figure S1A. Superfamily I ClustalX Alignment

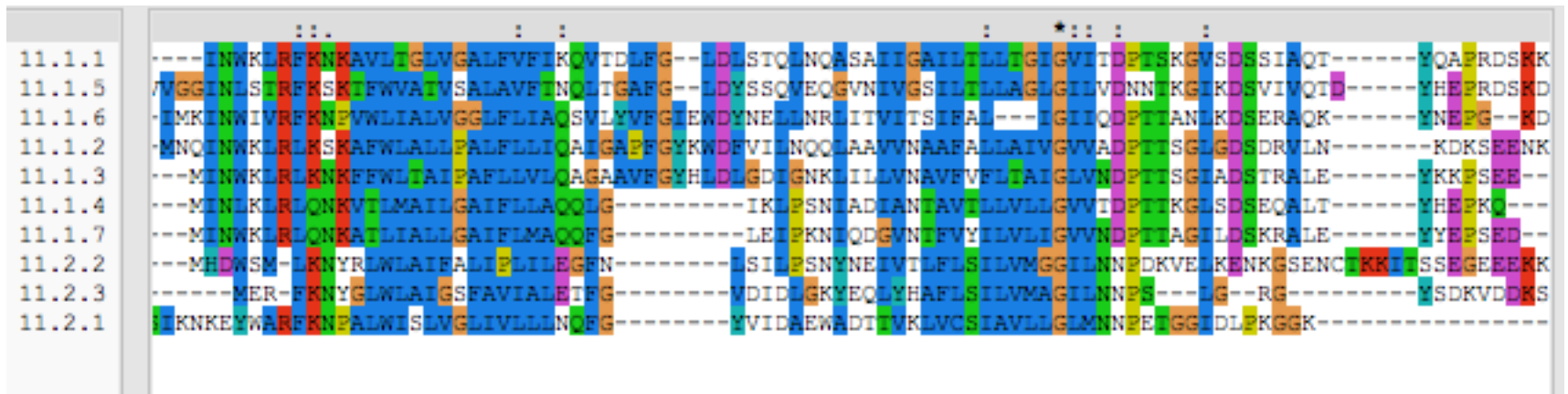


Figure S1B. Superfamily I
Motif Alignment

Name	Start	<i>p</i> -value	Sites <input type="checkbox"/>
11.1.7	1	7.45e-29	MINWKLRLQNKATLIALLGAIFLMAQQ FGLEIPKNIQ
11.1.2	3	6.68e-25	MN QINWKLRLKSKAFWLALLPALFLLIQA IGAPFGYKWD
11.1.1	2	1.56e-23	M DINWKLRFKNKAVLTGLVGALFVFIKQ VTDLEGLDLS
11.1.4	1	1.93e-23	MINLKLRLQNKVTLMAILGAIFLLAQQ LGIKLPSNIA
11.1.6	5	1.22e-21	MNIM KINWIVRFKNPVWLIALVGGFLIAQS VLYVFGIEWD
11.1.3	1	8.50e-21	MINWKLRLKKNKFFWLTAIPAFLLVLQA GAAVFGYHLD
11.1.5	13	3.35e-17	KKDKTPTVVG GINLSTRFKSKTFWVATVSALAVFTNQ LTGAFGLDYS
11.2.1	7	2.52e-16	MFNSIK NKEYWARFKNPALWISLVGLIVLLLNQ FGYVIDAEWA

Figure S1C. Superfamily I
Consensus Motif

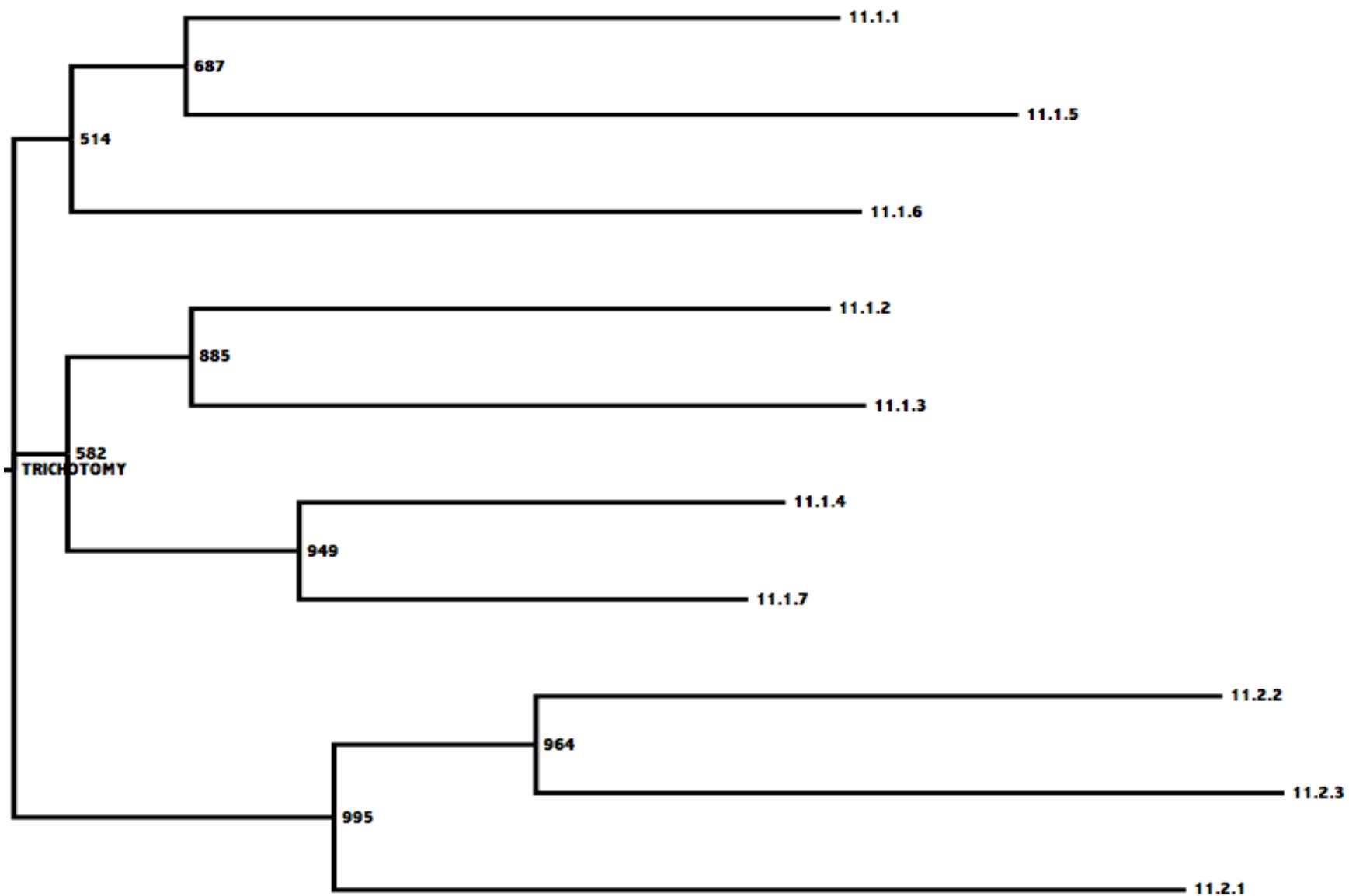
Figure S1D. Superfamily I
Bootstrap Values

Figure S2A. Superfamily II ClustalX Alignment

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25.1.2 -----MRNETIDT LAAVGGKASVIG-VGMTGVGWFLSNEFFGL---VGALVAIGGLVLAW---YYKREANRQLVEHE
25.1.4 -----MKTETLEAIGAAGNKATIIIG-GSAVAVAGKMSAADLAAY---VGAAVAVIGLLITW---YYKREANRQAKEYE
25.1.5 -----MKQEA YEALAAAVASKATYGGAGGSFAGFMLSNEFVAL---VGLLIALAGFLVNW---HYRAAQDRDQIEHE
1.1.1 -----MKSMDKLSTGIAYGTSAGSAGYWFLOWLDQVSPSQWAAIGVLGSLVLGFLTYYLTNL---YFKIREDRKAARG
1.1.2 -----MKSMDKLTTGVAYGTSAGNAGFWALQLLDKVTSPSQWAAIGVLGSLVFGLLTYLTNL---YFKIKEDRKAARG
1.1.3 -----MEKITTGVSYTTSAVGTGYWLLQLLDKVTSPSQWVAIGVLGSLLFGLLTYLTNL---YFKIREDRKAARG
1.1.4 -----MYRMDKLTGAAYGASAGSI---LNGMLNAYSPEQWNAIGVLVGIITAVMTYLTNL---YFKIREDNRSRSD
1.1.5 -----MSKLASGAAYGASAGTV---ANGLLTRLSPDEWSAVGVIAGIVVALLTFGINW---YFKRKTTLAQIQAYE
1.1.6 -----MNNIEKYTTGAYGASATTF---LCCGALS-LS---EWALV---LGIICSLLTVGLNW---YYRHK----EYRFRT
6.1.2 ---MS-LEVQFGDITVIRSVFVVGAAQVDV---VTRIF-GLT LSDWFYV---AAIGYTVVQAWAVL---YKTLK--R KEDK--
6.1.3 ---MAGLEIDFTNGVRAAPIAAGAGAEM---ASQVA-GMT LSDWFYA---AIIFYTIVQIVLV---FKITVMDEKRNKGD
6.1.1 ---MSLDFNNELIKAAPIVGTGADV---SARLFFGLSLNEWFYV---AAIAYTVVQIGAKV---VDKMIDWKANKE-
25.1.1 -----MSERAGMAVEVGVSVANKTTLAALAGALGWLAQINWVGL---IGVLVAVIGLLANI---YFVRRDRRESAESA
7.2.1 -----MAALFHCEGLMRASSEVASVYGVSVTAVASSLTLTDIGVI---VGIMTAIATFGLNF---FFMWRKDRREQRESI
25.1.3 -----MEPQPIVDKVAANVTYVG-SGWAVIFGLSANEFAAL---VGAAVAVVGLLVNL---WFKWQHLRIARTVAA
25.2.1 ---MPPALPRFKRSEHKAMEKITSFTIYAMALFLAWLGLKLSQDIAFL---VGAAVGIGTFLVNW---YYRKSLSQILKAIER
7.1.2 -----MRFNMLKNSEITGAYVGS---IAIYSGFTLADWAAI---FGILFGLFTMLINW---YYKNKEIKLKETALK
7.1.1 -----MNSKIDSAIFFIGS---LTALISGYSLHEWASL---FGILFGAVSVWIAYRKYKEDVQARDELAYK
6.2.4 -----MTKMTDFKIDAAVQASMNVPITIG-VAAATILGYTVSDWLVLG---AVLLTVLQLGYIVRKYWLLERGGKTD-----
6.2.1 -----MTTNDGATLADAAAYATRVAPPMAVIGASFLGLPLSEWVYI---VTIAYTLLQIAYFI---WKL VHNQLEKLRKD
6.2.2 ---RCCADFYFRSAFCCKTGVVVEAVKIAFVSVTAIFLGCQISDWSI---VTLTYTLGLLGHFI---WKL LVRPWRKRRLQ
6.2.3 -----MSNESKVQALIEAKAAFAV---AGAAASTMTLNHWVAIA---LGVYIVIQALYLLR---KWRBEERGKGGWLNEE

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Figure S2B. Superfamily II
Motif Alignment

Name	Start	<i>p</i> -value	Sites ?
1.1.2	44	1.55e-19	SQWAAIGVLG SLVFGLLTYLTNLYFKIKEDR RKAARGE
1.1.3	41	2.09e-19	SQWVAIGVLG SLLFGLLTYLTNLYFKIREDR RKAVRGE
1.1.4	41	2.49e-18	EQWNAIGVLV GIIIAVMTYLTNLYFKIREDN RRSRSRDEPN
1.1.1	44	6.78e-18	SQWAAIGVLG SLVLGFLTLYLTNLYFKIREDR RKAARGE
7.1.2	36	2.77e-17	FTLADWAAIF GILFGLFTMLINWYYKNKEIK LKETALKQKI
1.1.6	35	1.57e-16	LSLSEWALVT GIICSLTGLNWWYRHKYR FRTRNPS
1.1.5	38	7.88e-16	DEWSAVGVIA GIVVALLTFGINWYYKRKTTL AQIQAYERWP
25.1.5	40	2.05e-15	MLSNEFVALV GLLIALAGFLVNWHYRAAQDR RDQIEHEARL
25.2.1	48	2.47e-15	LSPQDIAFLV GAAVGIGTFLVNWYYRRKSLQ ILKAIERNAT
7.2.1	42	1.24e-14	LTLTDIGVIV GIMTAIATFGLNFFFMWRKDR REQRESDMRI
25.1.1	43	1.36e-14	LAQINWVGLI GVLVAVIGLLANIYFQVRRDR RESAESAARI
25.1.3	37	1.62e-14	LSANEFAALV GAAVAVGLLVNLWFKWQHLR IARTVAATRK
25.1.4	39	2.94e-14	MSAADLAAYV GAAVAVIGLLITWYYKREANR RQAKEYERWE
25.1.2	39	7.17e-13	FLSNEFFGLV GALVAIGGLVLAWYYKREANR RQLVEHELRLV
6.2.2	40	2.06e-11	AQVIQVSHRL KAVFCFCRCCADFYFRSAPCK KTGVVVEAVK

Figure S2C. Superfamily II
Consensus Motif



Figure S2D. Superfamily II
Bootstrap Values

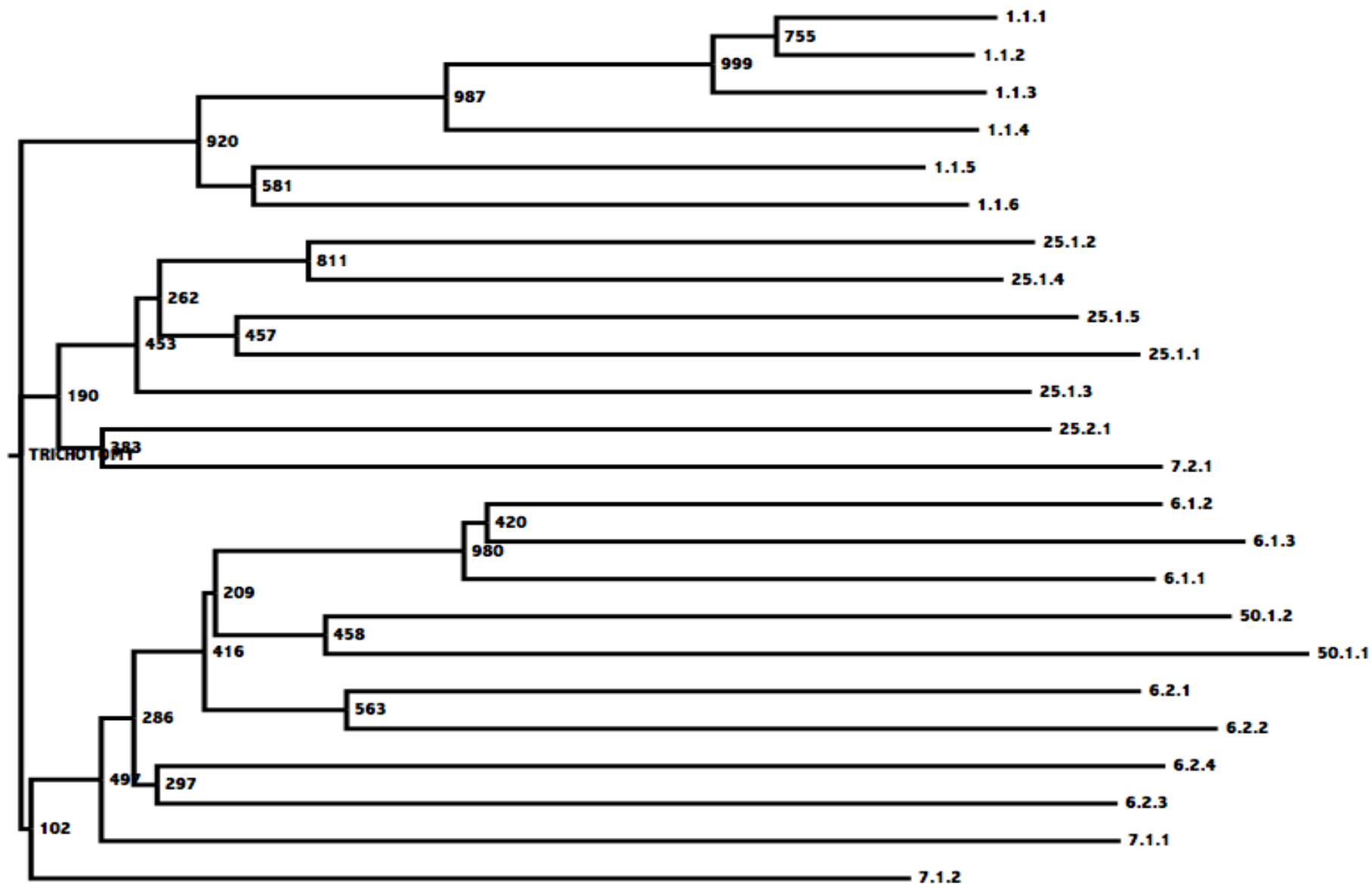


Figure S3A. Superfamily III ClustalX Alignment

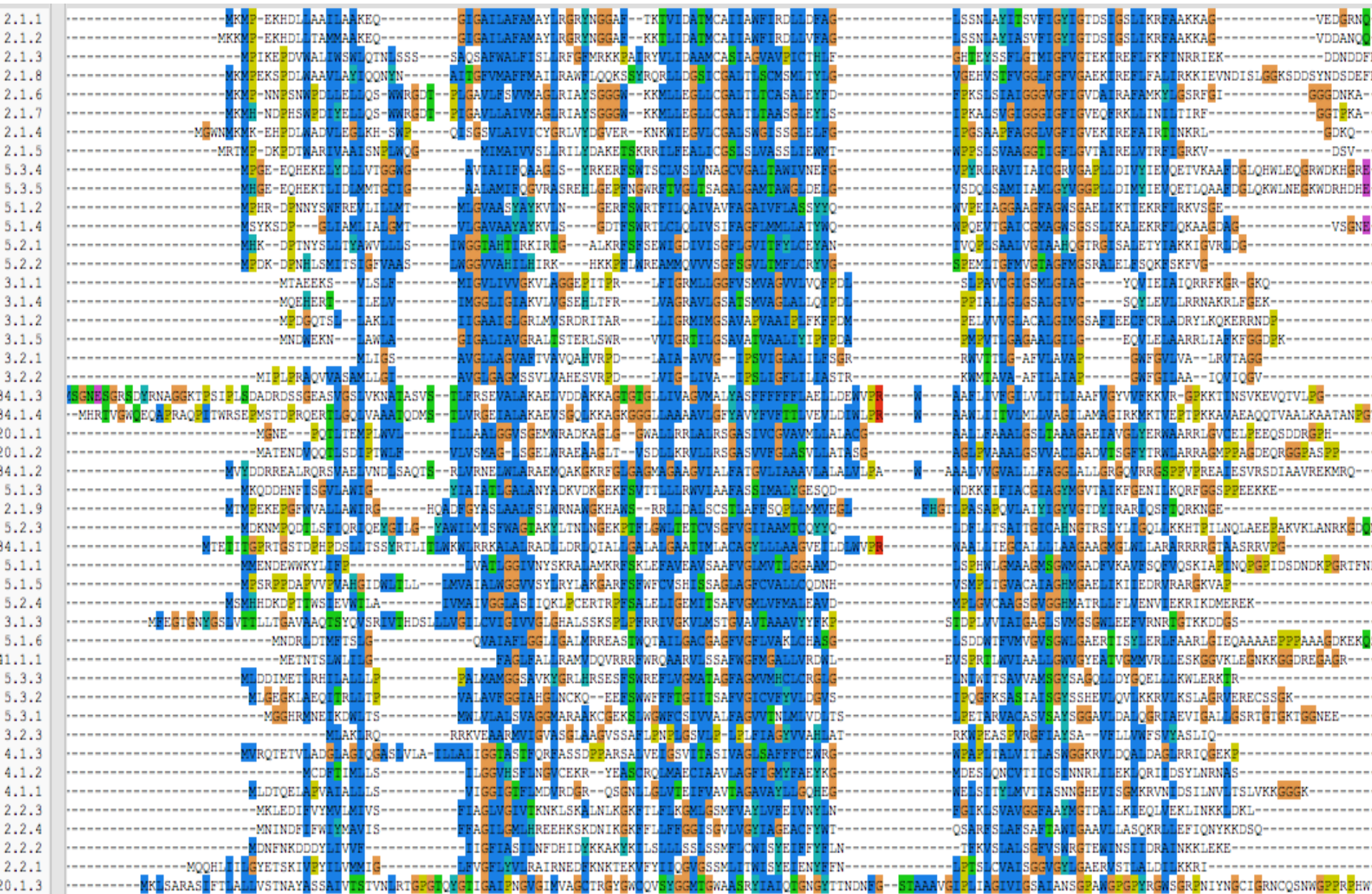


Figure S3B. Superfamily III Motif Alignment


Name	Start	p-value	Sites 		
5.1.5	82	6.96e-11	DNHVSMP	LTG VACAIAGHMGAELIK	IIEDRVRARG
2.1.3	81	6.96e-11	HLFGHTEYSS	FLGTMIGFVGT	EFLFKFINRR
5.1.3	75	9.43e-11	SQDWDKKFIF	IACGIAGYMGVTAIK	FGENILKQRF
5.1.4	72	5.16e-10	YWQWPQEV	TG AICGMAGWSGSSLIK	ALEKRFLQKA
2.1.4	82	5.16e-10	LFGIPGSAAP	FAGGLVGF	EF
5.1.2	74	5.90e-10	YYQWVPEIAG	GAAGFAGWSGAELIK	TIEKRFLRKV
2.1.8	81	8.72e-10	YLGVGEHVST	FVGGLFGFVGAEKIR	EFLFALIRKK
2.1.6	81	1.64e-09	YDFPKSLSI	AIGGGVGF	AFAMKYLGSR
2.1.9	85	2.09e-09	HGTLPASAPQ	VLAIYIGYVGT	ARIQSFTQRK
5.1.1	70	2.66e-09	AMDLSPHWL	G MAAGMSGWMA	AVFSQFVQSK
2.2.1	83	1.04e-08	FFNLPTSLCV	AISGGVGYLGAERVS	TLALDILKKR
2.1.5	79	1.60e-08	WMTWPPSLSV	AAGGTIGFLGVT	ELVTRFIGRK
2.2.3	73	2.18e-08	YLNFGIKLSV	AVGGFAAYMGT	KIEQLVEKLI
2.1.2	75	2.67e-08	FAGLSSNLAY	IASVFIGYIGT	SLIKRFAAKK
2.1.7	81	4.40e-08	YLSIPKALSV	GIGGGIGFIGVEQFR	KLLINILTIR
5.2.2	75	5.35e-08	YVGSPEMLTG	FMVGTAGFMGSR	LFSQKFSKFV
3.1.1	66	5.89e-08	FPDLSLP	AVC GIGSMLGIAGYQVIE	IAIQRRFKGR
2.1.1	74	1.04e-07	FAGLSSNLAY	ITSVFIGYIGT	SLIKRFAAKK
2.2.2	71	1.36e-07	YFLNTFKVSL	ALSGFVSWRGTEWIN	SIIDRAINKK
5.3.5	77	1.78e-07	ELGVSDQLSA	MIIAMLG	IMYIEVQETL
5.2.1	75	2.53e-07	YANIVQPLSA	ALVGIAAHQGT	ALETYIAKKI
5.2.3	83	3.57e-07	YYQLDFLLTS	AITGICAHNGTRS	LIGQLLKKHT
5.1.6	68	4.22e-07	ASGLSDDWTF	VMVGVSGWLGAERTI	SYLERLFAAR
5.3.3	75	7.49e-07	GLGLNIWITS	AVVAMSGYSAGQLLD	YGQELLLKWL
4.1.1	71	7.49e-07	HEGWELSITY	LMVTIASNNGHEVIS	GMKRVNIDSI
41.1.1	65	9.51e-07	WLEVSPRTLW	VIAALLGWVGYEATV	GMMVRLLESK
3.1.4	66	1.03e-06	IPDLPPIAL	L GLGSALGIVGSQYLE	VLLRRNAKRL
5.3.4	75	1.11e-06	EFGVPYRLRA	VIIAICGRVGA	IVYIEVQETV
2.2.4	17	1.40e-06	IFWIYMAVIS	FFAGILGMLHREEHK	SKDNIKGF
3.1.2	67	1.90e-06	FPDMP	ELVVV GLACALGIMGSAFIE	ECFCRLADRY
34.1.3	120	2.75e-06	IVFGILV	LIT LIAAFVGYVVF	GPKKTINSVK
5.3.2	72	2.75e-06	GVSIPQGF	KS ASIAISGYSSHEVLQ	VLKKRVLKSL
5.2.4	57	3.18e-06	LELIGEMITS	AFVGMLVFMAL	EAVD MPLGVCAAGS

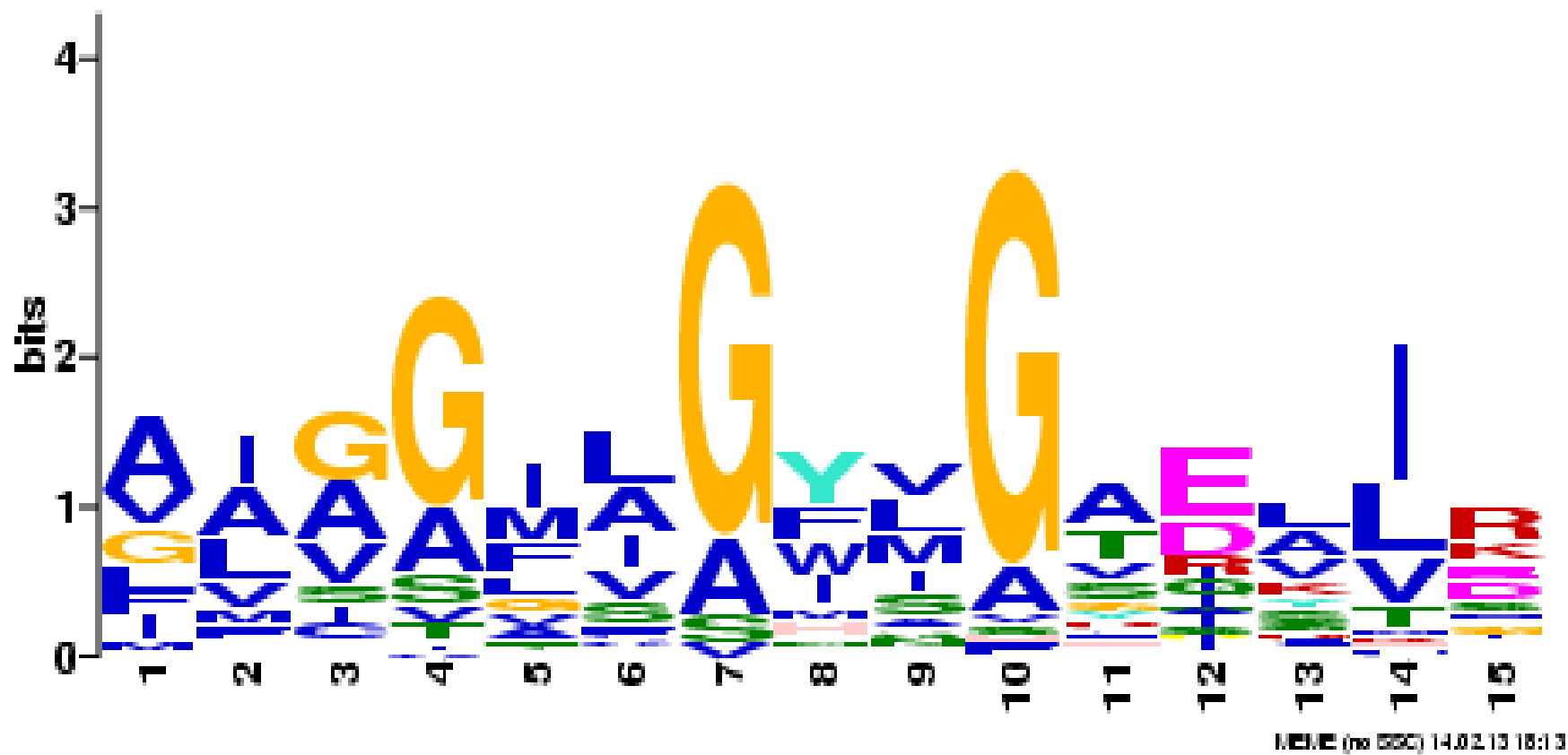
Figure S3C. Superfamily III
Consensus Motif

Figure S3D. Superfamily III

Bootstrap Values

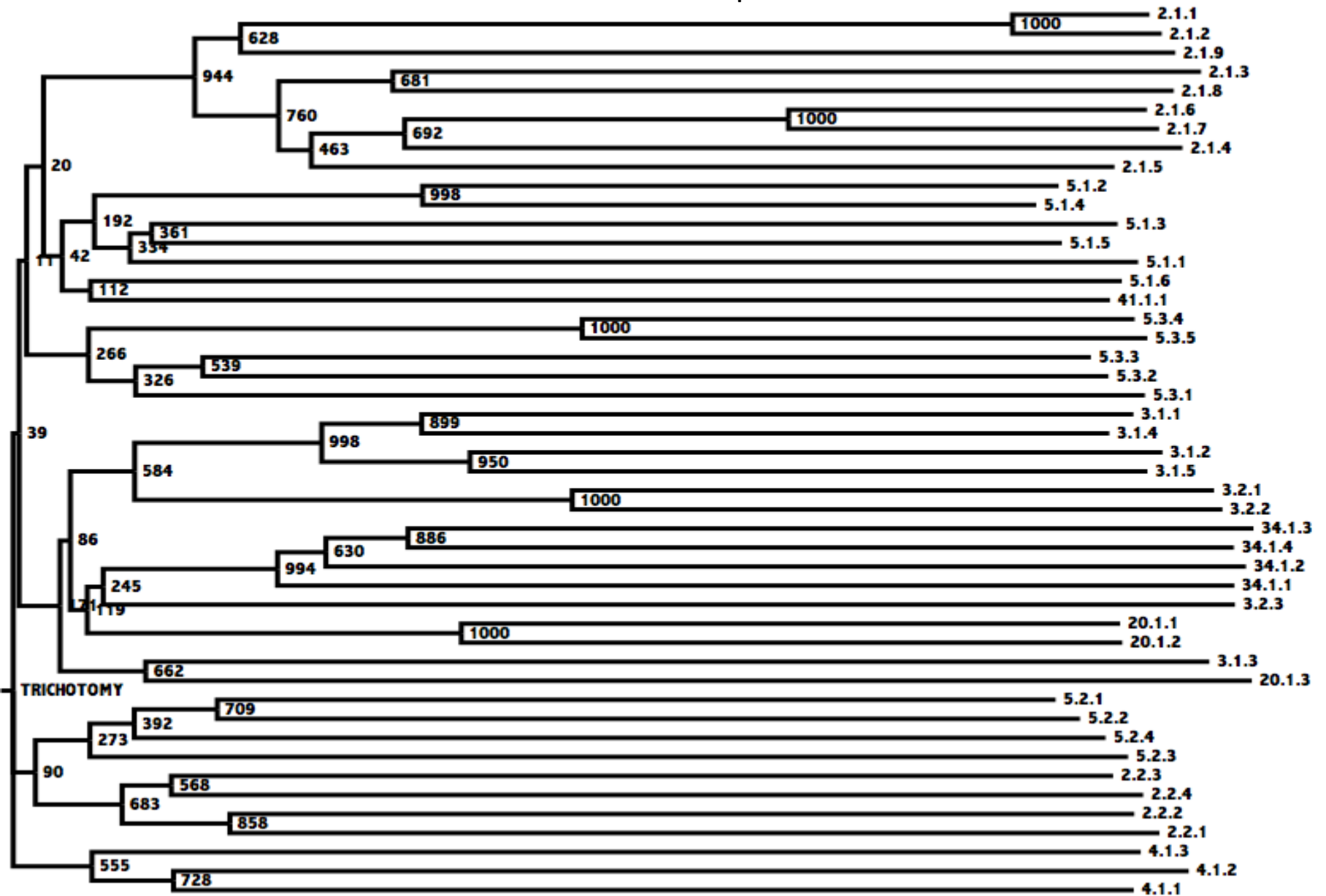


Figure S4A. Superfamily IV ClustalX Alignment

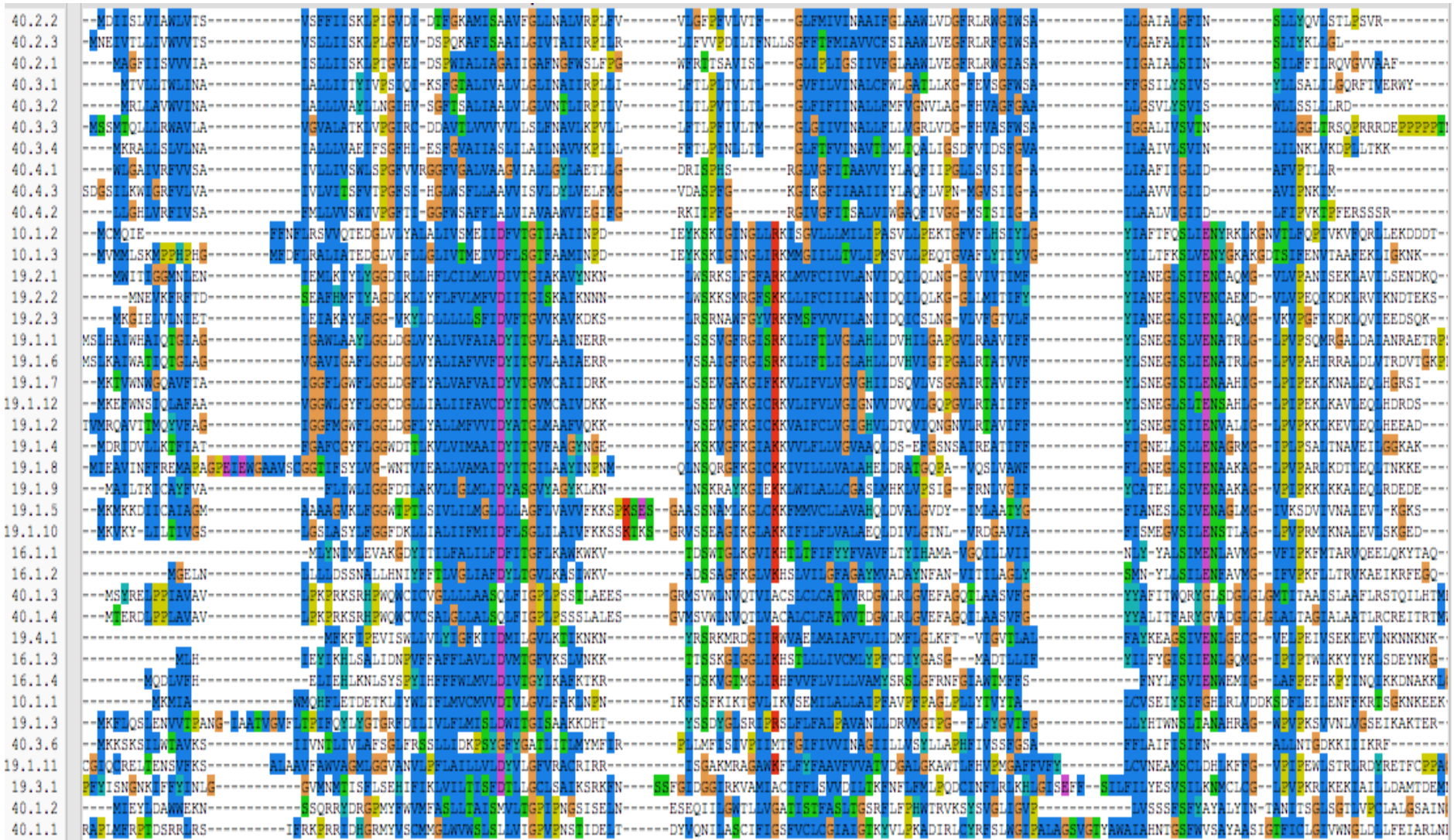


Figure S4B. Superfamily IV
Motif Alignment

Name	Start	p-value	Sites ?		
19.1.7	98	5.64e-28	GAIRTAVIFF	YLSNEGISILENAAHIGLPIPEKLNAL	QLHGRSIEED
19.2.3	94	2.71e-25	GVLVFGTVLF	YIANEGLSIIENLAQMGVKVPGFIKDKLQ	VIEEDSQKEK
19.1.2	141	2.71e-25	NVLRTAVIFF	YLSNEGISIIENVALIGLPVPKKLKEVLE	QLHEEADEKK
19.2.2	93	7.55e-25	GGLLMITIFY	YIANEGLSIVENCAEMDVLVPEQIKDKLR	VIKNDTEKSD
19.2.1	95	1.77e-24	GGLVIVTIMF	YIANEGLSIIENCAQMGVLV PANISEKLA	VILSENDKQS
19.1.8	110	1.77e-24	PAVQSLVAWF	FLGNEGLSIIENAAKAGLPV PARLKD TLE	QLTNKKEERK
19.1.11	98	3.07e-24	GVLRTAIIFF	YLSNEGSLTENS AHLGLPIPEK LKAVLE	QLHDRDSEEE
19.1.9	92	4.62e-24	IGFRNLVGIF	YCAT ELLSIVENAAKAGVPIPKKLK KALE	QLRDEDEK K
19.1.6	100	1.01e-22	GALRTATVVF	YLSNEGISLIENATRLGLPVP AHIRRALD	LVTRDVTGKP
19.1.1	108	1.85e-22	GVLRAAVIFF	YLSNEGISLVENATRLGLPVP SQMRGALD	AIANRAETRP
19.1.10	103	5.11e-21	NLVRDGAVIA	FISMEGVSILENSTLAGLPVPRMIK NAL	VLSKGEDK K
16.1.3	85	9.77e-21	SGMADTLLIF	YILFYGISIIENLGQMGIP IPTWLK KYIY	KLSDEYNKGD
19.1.4	97	1.21e-20	SAIREATIFF	FIGN ELLSLENAGR MGIP LPSALTNAVE	ILGGKAKQET
16.1.2	87	2.88e-19	ANVITILAGL	YSMNYLLSILENF AVMGIFVPK FLLTRVK	AEIKRFEGQL
19.3.1	122	1.01e-18	LGISEFFSIL	FILY ESVSILKNMCLCGLPVPKRLKEKIA	ILLDAMTDEM
19.1.5	104	1.22e-17	DYIMLAATYG	FIANESLSIVENAGLMGIVKSDVIVNAIE	VLKGSQKIE
16.1.1	81	3.51e-17	MAVGQILLVI	INLYYALSIMENLAVMGVFI PKFMTARVQ	EELQKYTAQL
19.4.1	80	1.17e-16	FTVIGVTLAL	FAYKEAGSIVENLGECGV ELPEIVSEKLE	VLNKNKNKE
19.5.1	116	1.78e-16	VPMGAFFV FY	LCVNEAMSCLDHLKFFGVPIPEWLSTR LR	DYRETFCPPA
16.1.4	88	2.70e-16	RNFGIAWTMF	FSFN YLFSVIENWEMIGLAFPEFLKPYIN	QIKKDNAKKL
19.1.3	108	4.35e-14	GFLFYGVTFG	LLYHTWNSLTANAHRAGWPVPKSVVNLVG	SEIKAKTERA

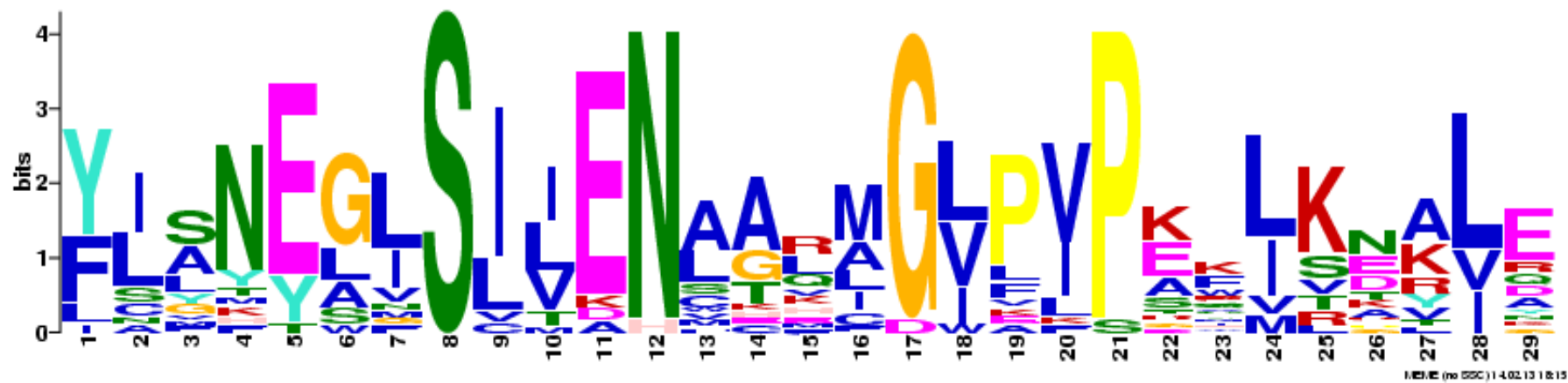
Figure S4C. Superfamily IV
Consensus Motif

Figure S4D. Superfamily IV

Bootstrap Values

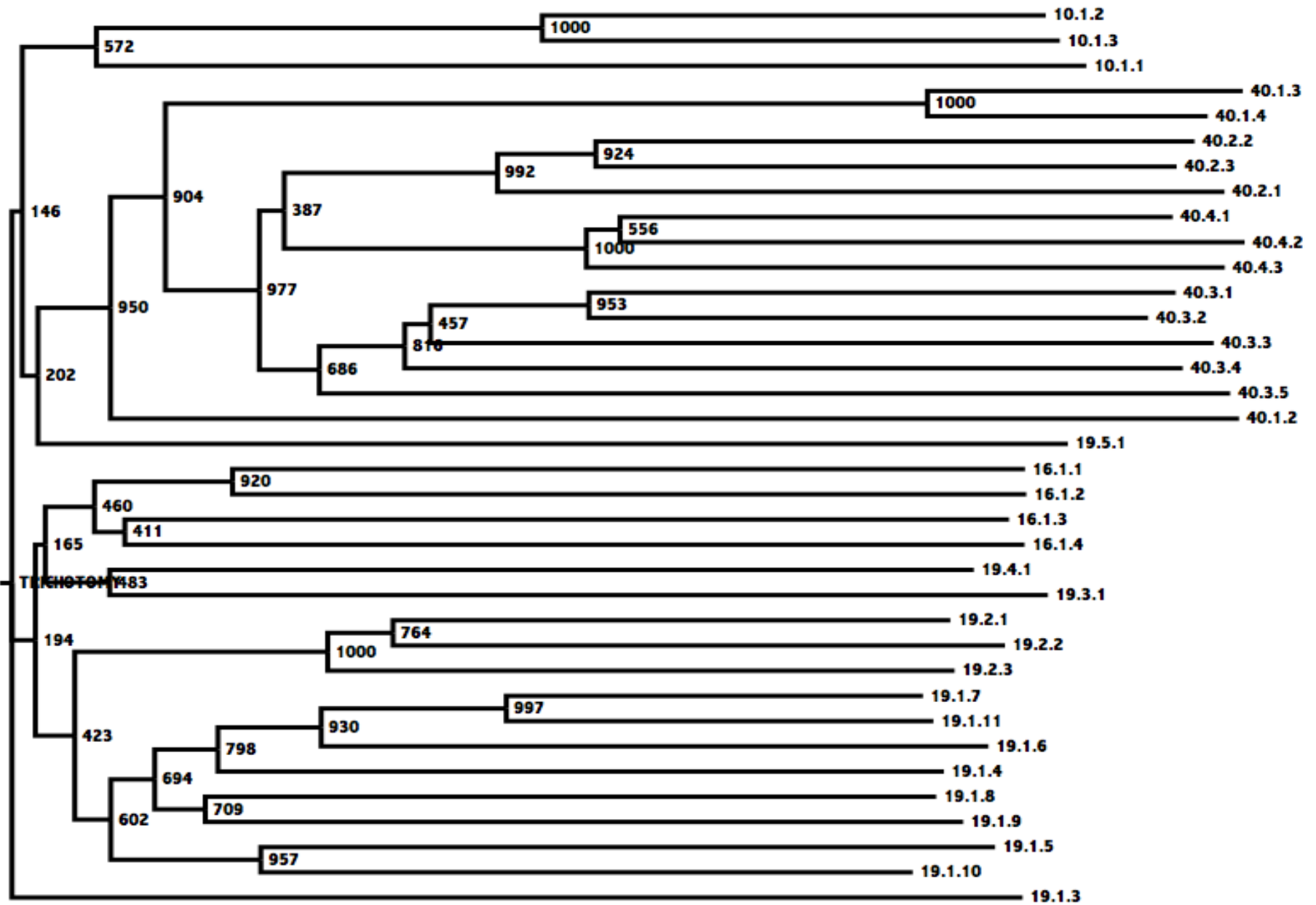


Figure S5A. Superfamily V ClustalX Alignment

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29.1.1  -----MDNLSIFIEQQLLILVAALSITIGKGCRRKYKQIDNKYIPWVLLILG--IGFSTWMLGLNFWA--VLOGVIC-WGVAIGINQYKQIK
29.1.2  -----MDNLSIFIEQQLLILVAALYVIGAGCRRKYKQIDNKYIPWVLLALG--IGFSTWMLGLNADS--VLOGVIC-WGVAIGINQYKQIK
29.2.3  ---MDLITFFNSITATVYGFILFVWVAQAIKQI-KIDNHWLPWSIVVGLVGFVAASYIYATDI--WLGAAFQ-FISGFAATGNEVIN
29.2.4  ---MDIITSNLTATAGELALISFFIGVIVQAIKKIGKVKNTYLPFISMGIGILAGLAAVVTKDITN--INGAVAG-LIVGAATSGLTDGLS'
21.1.3  -----MEIVISIAIVLGGVITAL---VNLVKSMEVWAKYLPVVALGIGWVFGVMSPLLG-VTI--YVGAISG-LVAGLSAMGFYELSK
21.1.1  ----MADSELVKSIVALGGVPLILGF-VQLFKRF-ISDIRYPLAVAMGLVINLWASWALGVSAISDWAVLFGIAGMAASGLYSTGS'
21.1.2  ---MEIKKIVEQSELIATILIPVSGFVQVFNILNQDRYVPLSLIVGATIAMTV-MLSAGQSL--NSAIVG-LISGLGACGLYDQKK
29.2.2  -----MTFNIDSNIAILLIHWLVQVLRPT-KINNHLPLVAVIIGALVAVALSLYTKDTKL--VQDWVLG-VWAGFASGLNETAT
29.2.1  -----MNLSDNDVIALIIIIAAVWFVQSSASIKLPSKFLPLWSIVVGIIVSLAYSYLSTKNIQ--LEQDLFFGLFAGFSASGLDDTIT
29.1.3  ----MMEFQLNGGTIAMIAIAIFVIVWVQI--PKNVVLSMIALGIGAVIGIAGFWLNGDIK--VWGLVDG-LVAGAVSVGGNEVFK
29.1.4  -----MDNDYLIPIIVVACLIVGVIR-VTALKIARDYIPLIACILGAILGAVIQDVT-----VEAIMG-AVSGLASGLNQVFR
21.2.1  ----MMEFQKELIVYMFVWVTPVFOAIKKELVPSKWLPLWSILIGAILGALATFLD-GSGS--LATMIWAGALAGAGGIGLFOFTI
21.2.2  ----MMEISTATALAIAIVALVAZLVQVCKY--LSEWVGSFAVAVAVLLGVIAIGATGGFDS--AAWVALAAVVGSNAAYQAVNR

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Figure S5B. Superfamily V
Motif Alignment

Name	Start	p-value	Sites ?
29.2.3	30	3.17e-16	LFTWVAVQAI KQTKIDNHWLPLVSI VVGTLVGFVA
29.1.2	28	3.95e-13	ALYVIGAGCK KYKQLDNKYIPVLL ALGIGFSIWM
29.1.1	28	3.95e-13	ALSIIGKGCK KYKQLDNKYIPVLL ILGIGFSIWM
29.2.2	23	6.44e-13	IITWLVVQVL KPTKINNHLPLVAV IIGALVAVAL
29.1.3	28	1.07e-11	IATFVIVWGV KQTPLKNVYLP MIAL GIGAVIGIAF
29.2.4	31	8.72e-11	FIGVIVQAIK KTGKVKNTYLPFISM GIGILAGLAA
21.1.3	24	9.58e-11	VTTALVNLVK SMEVVAPKYLPLVAL GIGMVFGLVM
29.2.1	26	1.27e-10	AAVWFVVQSI SATKLPSKFLPLVSI VVGIIVSLAY
29.1.4	26	1.39e-10	LIVGYVIRVT PALKIARDYIPLIAC ILGAILGAVI
21.2.1	30	1.84e-10	VTPV FVQAIK KTELVP SKWLPTVSI LIGAILGALA
21.1.1	27	4.50e-10	PLILGFVQLF KPFISDIRYYPL LAV AMGLVINLVA
21.1.2	31	8.96e-10	IVSGFVQVFK NTLNLQDRYVPLLSL IVGATIAMTV
21.2.2	22	2.23e-09	ATAIVALVAP VLTQVCKKYIPSEWV GSEFAVAVAVL

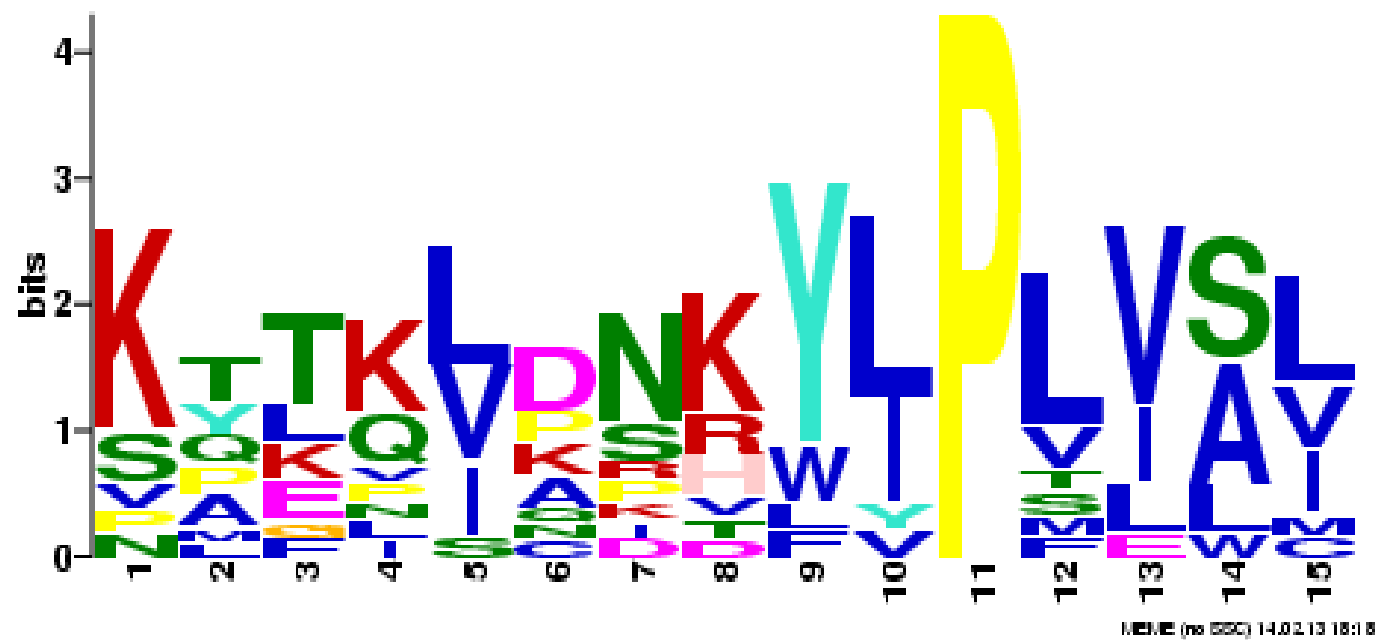
Figure S5C. Superfamily V
Consensus Motif

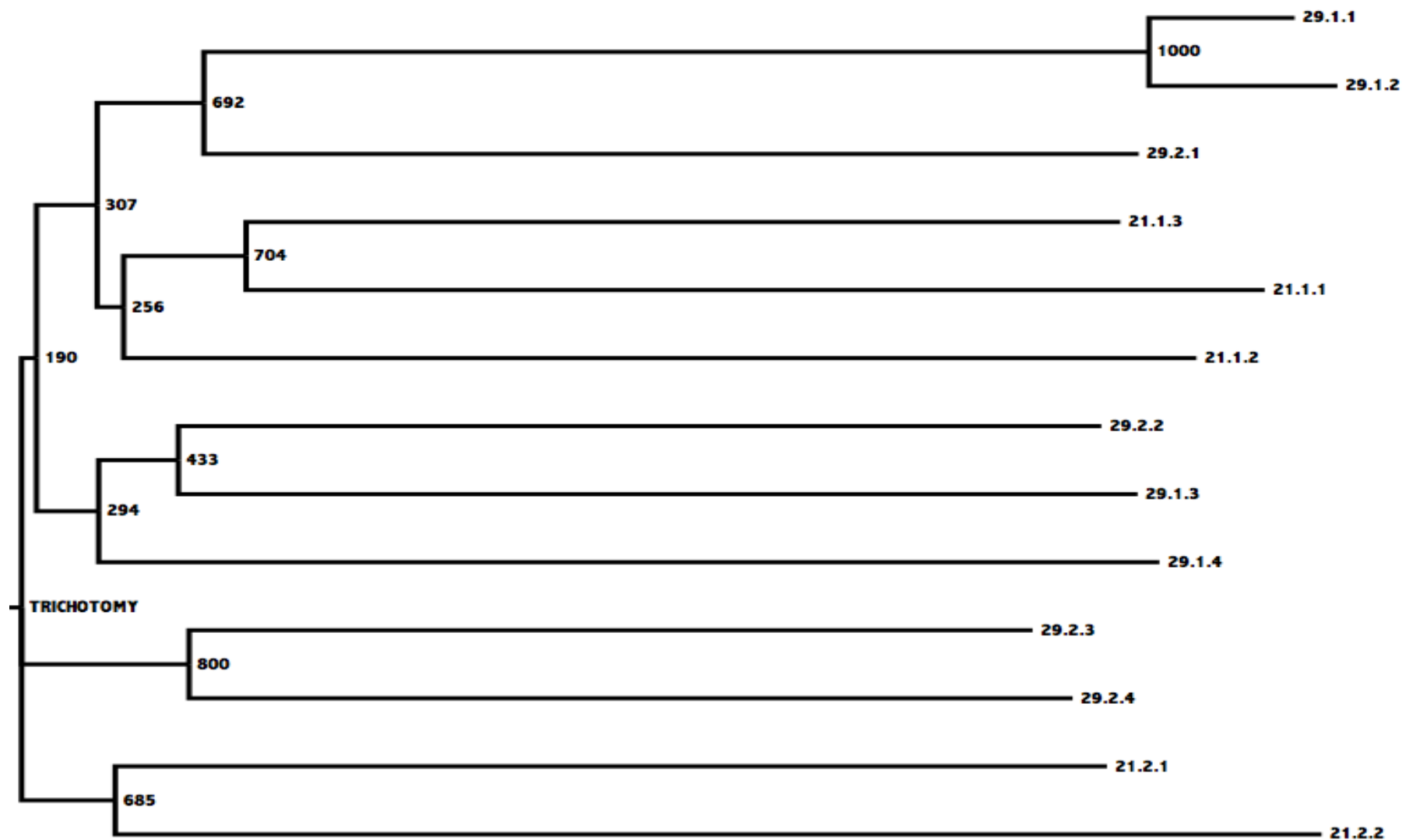
Figure S5D. Superfamily V
Bootstrap Values

Figure S6A. Superfamily VI ClustalX Alignment

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12.2.1 ---MINIKNVTENLFWVSIVILFIAQKIASYDFAQKND-----FDIATKMKHIGLIAKWAVADQSRYADK-AGAAKFEDAVDKVKE-----GVSTTLAKGAVQASYSI--
12.2.2 ----MLKTISSDLEFWVAMVVMYVAGKIASYVEYSKKND-----FEVANKFKHVGELAKWAVADQSRYSK-AGSVKFFDAVKSITNQ-----GVDKSMACGAVQDAYLN-
12.1.1 ---MR--LDENLIWAIIVLLVAGMATAYS LNKGLEKLALH----FKLAKVLEIAGVLAKAIIYQASLDNK-EGSKKLYDATDEVFYQLOKLYENLIDRVTVRNIVQHEYEK--
12.1.2 ---MKEIVINLIWAVVLLVAMFIGAWYKDNQAVVEKIRLH----FEMGHVLDIVGMLAKASNYQETQDDK-NGDQKLDATDSAYNQIKALYPAISISKDTVRNVMVQFAYDT--
26.2.1 ----MEINSLADVITAVAAVSLPIIITYL SKNVKGNRTA-----ETIVSILLENLAKDAVVMQQLGVEKVI-KGEAKKSHAVQIVKQALANLG-FIMIDEATLQNAIHAARYAQ-
26.2.2 ----MNLVNSDLIIAIAVAVIPIVIGAYIVKILKAN-----KFWALLTFLAHDVVAVQKLGVVRYI-EGEAKKSKAVEIVVSALTKLG-FKKADLTTIENAVEDEYS--
12.2.3 -----MKINDYGLLIIVAVIIKSFFDYLKVHD-----FKMAEKFQIVDDIAEWA VSLQATKDIS--NAQKQVNAIQANVEQAKKVG--VETIEASAKGAVEKAVAE--
26.1.3 -----MQQITELITNGAISILVVLAVVVRVAVSEYLAKKVG----EKTIKIVELLAKNAVHAVEVQVAETGY-KGDEKLAQARAKVRAELTKYN--ISMTDKDLDTFVESAVKQ--
26.3.1 ----MDNNTIELQAVALLISTGAIALLTYEVKYG-----VNKVMRVLKIVKIGVKA VEQGLVNGW-DGKQKKAELDYITKTLNSKG--IKVKKADLDMIEHSVVAE--
26.1.5 ----MEEVLLKIVYVAVGVVYILVNSLLKSKKLES-----EVKTIKVIKHAVEVVEQVSKIEDL-HGNQKQYAKTVAKNMLKDLH--INVSDGIIIDTIEHSVVFY--
26.1.1 ----MNEILFSATQIIVVILGLVSRVYIENLVKLDL-----EKASQILAWIQAVTAABQIISGES--KGIEKKAFTVEYMNKLLKEKG--ISITEEQLNLLIHSAVKA--
26.1.2 --MSEFLNELLNLLRPTIMTEVTIILGFLGMKINYYNVKIS----EEQQKQIANIKAAMVEVQVA-GEHL-LSDDKLSMAKHRAKVTLNQVG--IDITDEELTWNIHAFVGG--
26.1.4 ----MREAVLQVEIYILQAVIVVLTFTIVAVVVKRLELLOQ----KIQERYLLVEVANNLVKAIEQTFGAGQEGELKRSEAIKFLMQN-----FKLIEDEAEKLVAAVFE--
26.4.1 ----MDQNMTEIFSGVLTLVGIVVSYFISQAASKHSN-----VKNIDALAKLANQEVTRAEKNFN--ENFEKLSEAINYVTEEAKRIK--IKTNPAQIEAQIETSLAQL-
26.1.6 ----MNTQLIDSLIINATDEVLI VGLLSPELLVQVLRFAKA----HTANKRQVLESYAERVLAVEQQRNL-LSDDKKLAVQRADYINRSKINDCVTDKQISDLIHSAVNS--
12.1.3 ----MFGYIIVNKEEMKEREEDVYHGYCGLCSKLKEHYKFGQIILSYDMVFLMTLISLYEPTIKSMKRQVTHLKHHEERVNNITDYVAHNNILLIYYKCKDDWDDRKLKK--

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Figure S6B. Superfamily VI
Motif Alignment

Name	Start	<i>p</i> -value	Sites ?
12.2.2	23	3.48e-40	AMVVMYVAGK IASYEYSKKNDPEVANKFKHVGE LAKWAVADQSRYS DKAG SVKFDDAVKS
12.2.1	25	1.07e-35	SIVILFIAQK IASYDFAQKNDPD IATKMKHIGLIAKWAVADQSR YADKAG AAKFEDAVDK
12.1.2	28	1.70e-31	AMFIGAWYKD NQAKVEKIRLTHPE MGHVLDIVGMLALKASNYQ ETQDDKNG DQKLDDATDS
12.2.3	17	4.57e-28	LGLLIIVAWI IKSFFDYLKVKDPK MAEKFQIVDDIAEWAVSLQ ATKDISNA QKQVNATQAV
12.1.1	26	2.11e-25	VAGMATAYSL NKQKLEKLAL THPKLAKVLETAGVLALKATIYQ ASLDNKEG SKKLYDATDE

Figure S6C. Superfamily VI
Consensus Motif

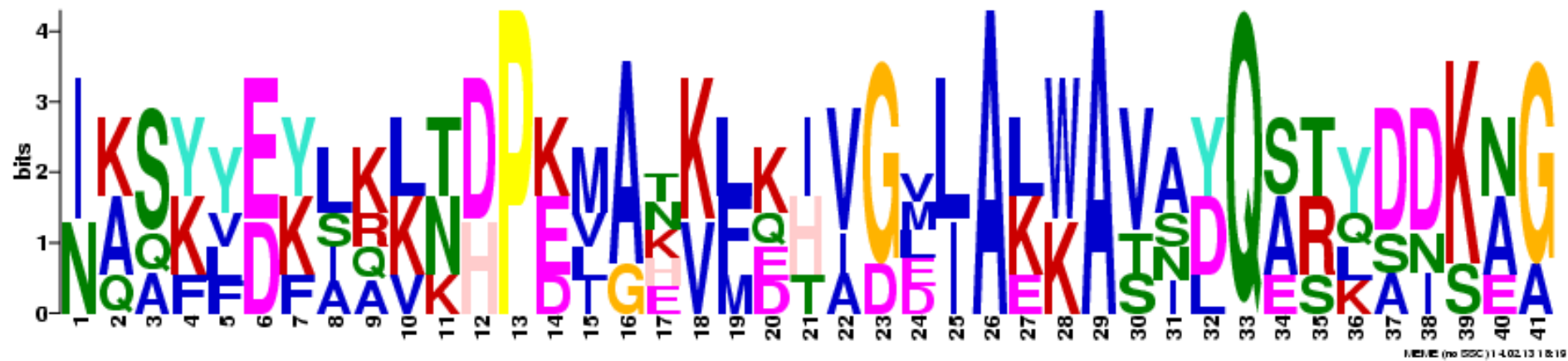


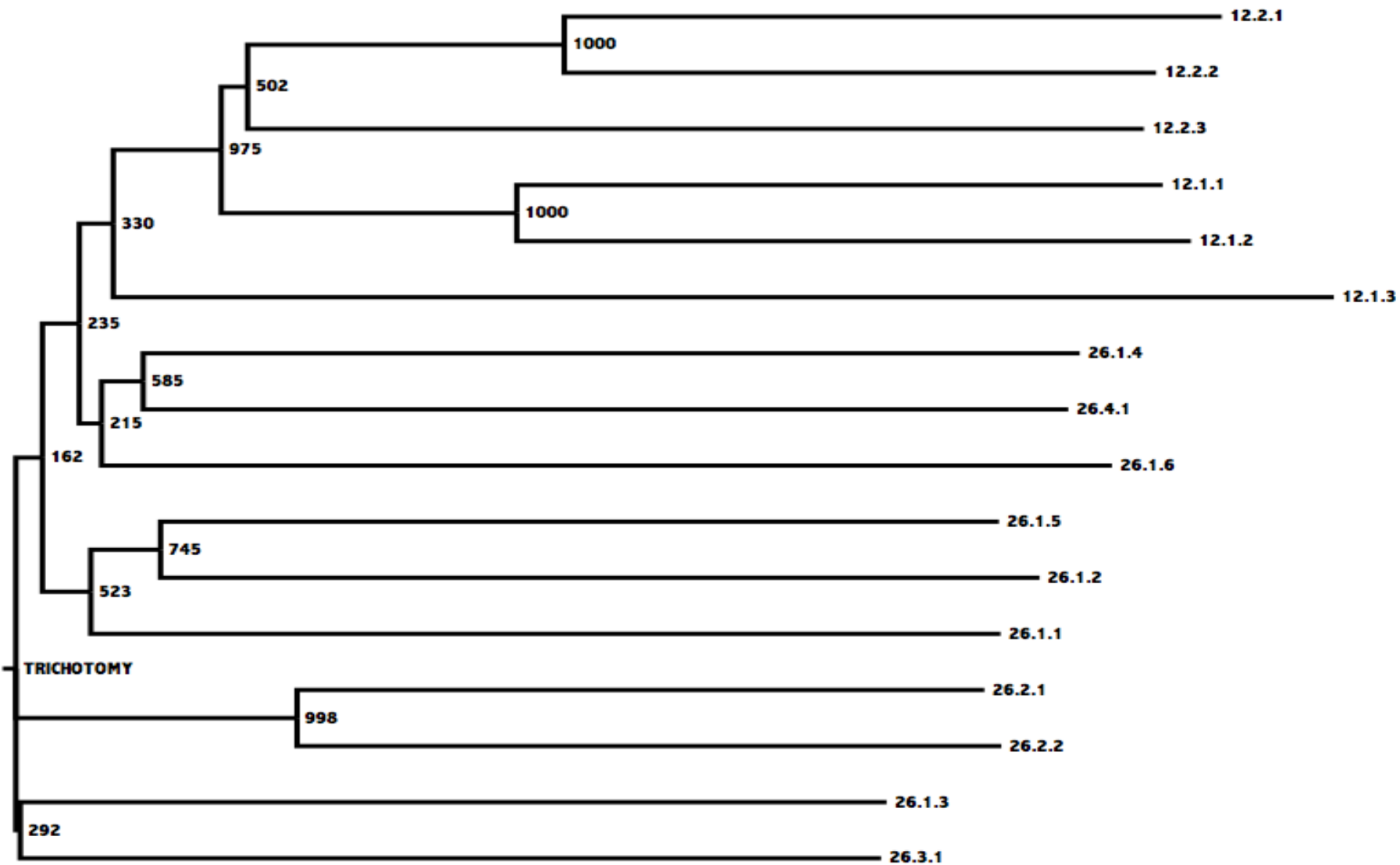
Figure S6D. Superfamily VI
Bootstrap Values

Figure S7A. Superfamily VII ClustalX Alignment

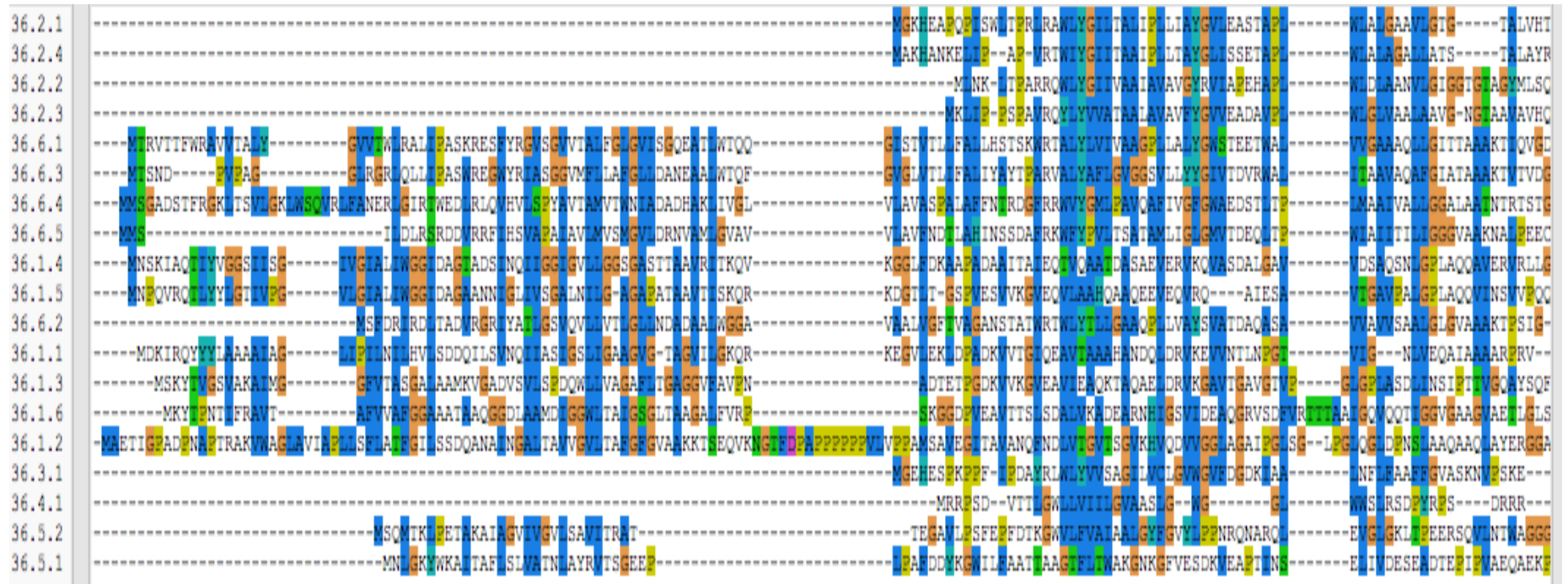


Figure S7B. Superfamily VII
Motif Alignment

Name	Start	<i>p</i> -value	Sites <input type="checkbox"/>
36.2.4	14	1.03e-17	HANKELIPAP VRTWYIGIITAAIPLLTAYGL ISSETAPLWL
36.2.1	17	1.03e-17	PQPISWLTPR LRAWLYGILTALIPLLIAYGV LEASTAPLWL
36.6.2	63	3.69e-17	TVAGANSTAT WRTWLYTLLGAAQPLLVAHSV ATDAQASAVV
36.2.2	9	3.58e-16	MLNKLTPA RRQWLYGIIVAAIAVAVGYRV IAPEHAPLWL
36.6.4	90	1.79e-15	ALAFFNTRDG FRRWVYGMLPAVQAFIVGFGW AEDSTLTPLM
36.6.5	63	2.64e-15	TLAHINSSDA FRKWFYVLTSAAMLIGLGM VTDEQLTPWI
36.2.3	10	4.95e-14	MKLIPPSPA VRQYLYVVATAALAVAVFYGV VEADAVPLWL
36.6.1	80	8.33e-14	LFALLHSTSK WRTALYLVIVAAGPLLALYGW STEETWALVV
36.3.1	16	4.07e-13	SPKPPFIPDA YRLWLYVVSAGILVCLGVWGV FDGDKIAALN

Figure S7C. Superfamily VII
Consensus Motif

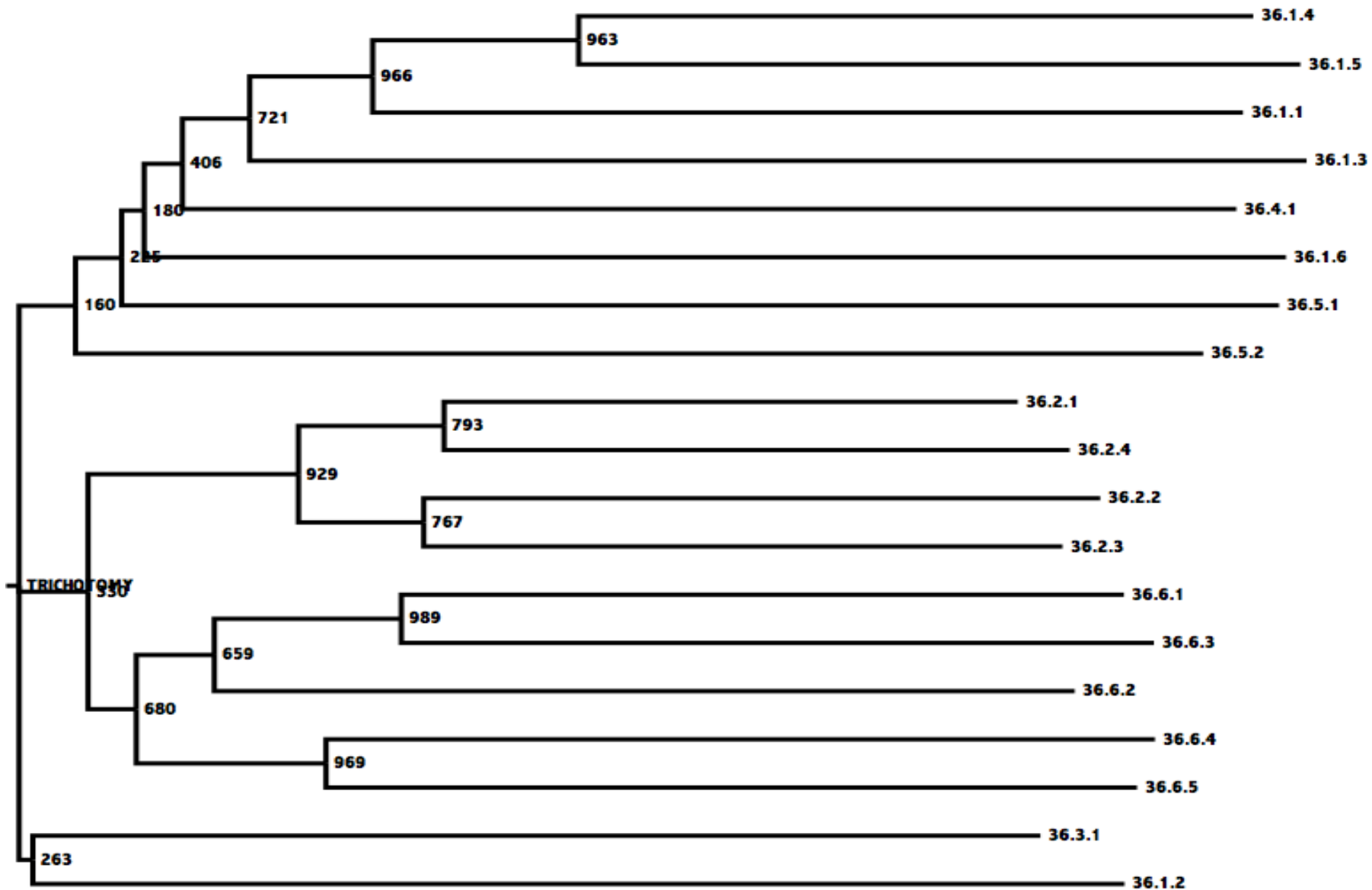
Figure S7D. Superfamily VII
Bootstrap Values

Figure S8: The Mapping of 267 TCDB Sequences to Pfam

