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>JYFJ01025622.1 Catajapyx aquilonaris Contig25622\_fixed, whole genome shotgun sequence//Chuvirus

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>QVQU01249695.1 Machilis hrabei contig\_249695, whole genome shotgun sequence//Mono-Chu clade

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>GASN02036638.1 TSA: Thermobia domestica C218246\_a\_5\_0\_l\_601 transcribed RNA sequence//partitivirus

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>QVQU01337473.1 Machilis hrabei contig\_337473, whole genome shotgun sequence//partitivirus

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Incomplete sequences and fragments of viral RdRPs in basal hexapods

Flavivirus NS5

>GATZ02003749.1 TSA: Sminthurus viridis C114795\_a\_4\_0\_l\_726 transcribed RNA sequence

Length=726

 Score = 231 bits (589), Expect = 2e-69, Method: Compositional matrix adjust.

 Identities = 126/247 (51%), Positives = 161/247 (65%), Gaps = 13/247 (5%)

 Frame = -3

Query 49 DTCPVEQTKYEERIFKIYKGLGMWFKGCGYKHRELTWEEVIMQANKVGAPGVIDHDVENV 108

 DT PVE + Y ++ ++Y+GL W G+ ++ EE++ QANK GAP +DH +NV

Sbjct 724 DTEPVENSPYHTKMREVYEGLADWMSSRGFCNQPFNDEEILRQANKQGAPTRLDH-WKNV 548

Query 109 GAFLRKPTAEAEVEAIRMSFLSGKPRGAIFNTMGKREKKESQSGQKGSRMVAFLPIGTRI 168

 G FL + E+ I +P AIF+TMGKREKK + G KGSRMVA+LPI TR+

Sbjct 547 GEFLADSEWKNELGKIEKGLTQNQPTRAIFSTMGKREKK--RGGDKGSRMVAYLPIPTRM 374

Query 169 LELKCLGMLINLTKPAINRFGVGGLGLHDLGMRLNQVWRGFGVSTDIAGFDTRVGLFIQS 228

 +ELK G LI TKPAINRFGVGG+GLHD+GMR ++++ + S DIAGFDTRVGL + S

Sbjct 373 VELKYFGRLIECTKPAINRFGVGGIGLHDMGMRAKEIFKTWACSDDIAGFDTRVGLHVLS 194

Query 229 CE--SWL-----VQYLGGNATCEALYRCYAYPHILIPMTGEHVRSELLKGRGQRMRGSNP 281

 E S++ QY + E LYR YAYPH+LIP RSEL+ GRGQRM G+ P

Sbjct 193 MEYHSFIKRLTPKQY---HPVIEGLYRIYAYPHLLIPTLSSFSRSELVAGRGQRMSGTAP 23

Query 282 TYAMNTI 288

 TY MNTI

Sbjct 22 TYTMNTI 2

>GATZ02000981.1 TSA: Sminthurus viridis C103834\_a\_5\_0\_l\_500 transcribed RNA sequence

Length=500

 Score = 126 bits (317), Expect = 4e-31, Method: Compositional matrix adjust.

 Identities = 65/140 (46%), Positives = 87/140 (62%), Gaps = 3/140 (2%)

 Frame = +3

Query 398 VERYMPTRSVAEILAKSCLRVGGPDQDLSNLAWISAQGNMLLTYYAHLRTVRLVGLCYKA 457

 VERY PTRS EI K + + G D LS AW SAQ N LL Y H+R R VGL ++

Sbjct 6 VERYQPTRSYGEIFGKLGIWIAGNDLQLSQDAWASAQANNLLVNYHHMRDCRRVGLMLRS 185

Query 458 LAPENLVMT-AKGGEFFPRPWMRPGDILEVMNAVLFGESTAYPVPDFALRSFRHVGYLKP 516

 + +N+++ + F PRPW++ GD L+++N LFG STAYPV +F +R +H+GYL

Sbjct 186 IVLDNIILLPMRKAGFLPRPWLQNGDTLDIINECLFGGSTAYPVQNFRVRQMQHLGYLMH 365

Query 517 QREQIYDPETFTMERVR-WR 535

 RE IY+P F E +R WR

Sbjct 366 GRELIYEPR-FESEAMRTWR 422

TSA: Sminthurus viridis C114795\_a\_4\_0\_l\_726 transcribed RNA sequence

Sequence ID: GATZ02003749.1Length: 726Number of Matches: 1

Related Information

Range 1: 2 to 724GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

231 bits(589) 6e-67 Compositional matrix adjust. 129/244(53%) 171/244(70%) 7/244(2%)

-3

Query 390 DTAPKENHKYEQHLVQIYEGLAHHFLKMGFSFRELDWTEVMHQANKQGAPGIIDTQFENV 449

 DT P EN Y + ++YEGLA GF + + E++ QANKQGAP +D ++NV

Sbjct 724 DTEPVENSPYHTKMREVYEGLADWMSSRGFCNQPFNDEEILRQANKQGAPTRLD-HWKNV 548

Query 450 GQFLSQPNWVKKVIYTRQALEKGRPVGGVFNTIGKREKKLSPHEMKGSRMVAYLPIATRl 509

 G+FL+ W ++ + L + +P +F+T+GKREKK KGSRMVAYLPI TR+

Sbjct 547 GEFLADSEWKNELGKIEKGLTQNQPTRAIFSTMGKREKKRGGD--KGSRMVAYLPIPTRM 374

Query 510 lelklfgkllelTKPAINHFGVGGLGLHDLGMRVEEIWQGHAVSDDIAGFDTRIGLFFLS 569

 +ELK FG+L+E TKPAIN FGVGG+GLHD+GMR +EI++ A SDDIAGFDTR+GL LS

Sbjct 373 VELKYFGRLIECTKPAINRFGVGGIGLHDMGMRAKEIFKTWACSDDIAGFDTRVGLHVLS 194

Query 570 LENH-FIRLLGGNETHTL---MYRLYAYPHILVPLASEFTRSQLLKGRGQRMSGTNVTYS 625

 +E H FI+ L + H + +YR+YAYPH+L+P S F+RS+L+ GRGQRMSGT TY+

Sbjct 193 MEYHSFIKRLTPKQYHPVIEGLYRIYAYPHLLIPTLSSFSRSELVAGRGQRMSGTAPTYT 14

Query 626 MNTI 629

 MNTI

Sbjct 13 MNTI 2

DownloadGenBankGraphics NextPreviousDescriptions

TSA: Sminthurus viridis C103834\_a\_5\_0\_l\_500 transcribed RNA sequence

Sequence ID: GATZ02000981.1Length: 500Number of Matches: 1

Related Information

Range 1: 3 to 428GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

124 bits(311) 8e-30 Compositional matrix adjust. 65/143(45%) 82/143(57%) 3/143(2%)

+3

Query 737 TTHRYMPTRDLTQIIAKSTIKIGGKDASLDDMAWLSAQGNNLLVNYAHLRTARAVGFGYK 796

 T RY PTR +I K I I G D L AW SAQ NNLLVNY H+R R VG +

Sbjct 3 TVERYQPTRSYGEIFGKLGIWIAGNDLQLSQDAWASAQANNLLVNYHHMRDCRRVGLMLR 182

Query 797 AIVNPNALLC--DTGGFLRPTPWMQPGDILNVTNKILFGESTHYPVEGFRVHSWKHVGFL 854

 +IV N +L GFL P PW+Q GD L++ N+ LFG ST YPV+ FRV +H+G+L

Sbjct 183 SIVLDNIILLPMRKAGFL-PRPWLQNGDTLDIINECLFGGSTAYPVQNFRVRQMQHLGYL 359

Query 855 KPKREMVYDQDTFSAGRAYWRSK 877

 RE++Y+ S WR+

Sbjct 360 MHGRELIYEPRFESEAMRTWRAN 428

DownloadGenBankGraphics NextPreviousDescriptions

TSA: Sminthurus viridis C109709\_a\_3\_0\_l\_603 transcribed RNA sequence

Sequence ID: GATZ02002474.1Length: 603Number of Matches: 1

Related Information

Range 1: 2 to 601GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

112 bits(280) 3e-25 Compositional matrix adjust. 73/201(36%) 104/201(51%) 7/201(3%)

+2

Query 125 THITSVTLGPGPGHEGHEAFTKIHFPGREKIRVLYGDARQFPI---ASHDTLLFDGGESH 181

 T++ VT G GHE FT F G+EK+ V+ D R+F D +LFDGGE

Sbjct 2 TNVWGVTFGKLQATPGHEDFTDRPFKGKEKVNVINMDVRKFVAEVDVEADWVLFDGGEQR 181

Query 182 SDADIEEARFYSLFYNVVMRQINSQTKHFVLKVLTPTSPRIQKLLEEIQRMTGRGAFYRS 241

 S+ D E ++F +L + I +TK F+ K+LTP I + LE IQ+MTG G F +

Sbjct 182 SNYDEEASKFRALVLPC-LEAIGPKTKGFIFKILTPFDDAIIRKLEHIQQMTGMGNFILN 358

Query 242 CHSRLSTMELYFVSTG-IAPVKGRAYSLLQSVMIQGRENKV--LKPRNYDLGFTFSREKI 298

 H+R S +ELYFVST + ++ A L++ + + L P R I

Sbjct 359 THTRQSNLELYFVSTKPVMNLRKSARQLIEYKLSRAEIESAHKLNPIRMANADYLGRTPI 538

Query 299 EPKTIPLLKPLDLTDSINELG 319

 +PLL P+D+ SI+ELG

Sbjct 539 NDPVVPLLMPVDMNRSISELG 601

Flavivirus NS3

TSA: Sminthurus viridis C106664\_a\_3\_0\_l\_547 transcribed RNA sequence

Sequence ID: GATZ02001699.1Length: 547Number of Matches: 1

Related Information

Range 1: 29 to 535GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

81.6 bits(200) 9e-15 Compositional matrix adjust. 55/173(32%) 86/173(49%) 12/173(6%)

+2

Query 207 GFAALGCVLIFVFFQTMLDHPSVYVASAASTPVRDGIYMVRTYWLGIPLSKGVGVATSGV 266

 GF + +Q M+D + +TP+++G Y++ G SK +GV+ +GV

Sbjct 29 GFVMFLSAVFIYTWQDMVD--KYQLMGTENTPIQEGSYLITRELFGHVFSKCMGVSYAGV 202

Query 267 LYIPYHVVTSMPVWIDNRCLLPSYVDVKRDLVTFGGTPSLVAPLDQEELVVS----LERD 322

 L+ PYH + I R + P +V V DL+T+GG PS + +VV+ +ER

Sbjct 203 LHAPYHGAHRNDIIIGGRLVKPYFVSVDCDLITWGGMPSFATLTADDRVVVNHEDEIERR 382

Query 323 DGRFCYRTVANVDEFGFTFVGKSSPGESGSPVYVLRGEKP----TLVGFCGRW 371

 Y+ +D F++ GKS PG+SGS V+ + E +LVG GRW

Sbjct 383 SMLVDYKYDDEIDS--FSWAGKSKPGQSGSGVWKVTEEGDIQIISLVGLVGRW 535

Gap 40 bp

TSA: Sminthurus viridis C120865\_a\_7\_0\_l\_931 transcribed RNA sequence

Sequence ID: GATZ02005284.1Length: 931Number of Matches: 1

Related Information

Range 1: 63 to 929GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

176 bits(447) 1e-46 Compositional matrix adjust. 116/300(39%) 176/300(58%) 12/300(4%)

-3

Query 405 TDEVIRVCKHPGYGKTRRIIPELIATHSTQVKNPKVIITGPTVVVCEELHKSLLANCALD 464

 +D + R+ HPG GKT ++IP ++ + ++ + KV+I GPT VVC+EL+ SL+

Sbjct 929 SDPLKRIIMHPGAGKTFKVIPSVVHKYLSEGRKGKVMIVGPTRVVCQELYNSLVRKFPC- 753

Query 465 VGLCVRDRKRYRVKRAPVQVMAHATLWRMIETDAFEVRNPTMLIIDEAHADMESTKVLLK 524

 VGL +++ RYR A +Q+ H T RMI+ + EV N +LI+DEAH + +T++ +K

Sbjct 752 VGLSMKNNTRYRKPTARIQITTHHTFLRMIQNASIEVANLGLLILDEAHVEGVATRLCVK 573

Query 525 YGEQLAKSGGKVVLLSATFSNDLYDDGSNYDIKDVDRVDDYVSNGITVLLEDLTHHVNLD 584

 Y E L+KSGG+ VLLSATF +D + +GSN+ I D ++++G + + + VN

Sbjct 572 YAENLSKSGGRAVLLSATF-DDTHSEGSNFTI-----TDKHINSGDEISI--VKSKVNDG 417

Query 585 QKVLVFCPGVMGSEGVNALRDKVKALHPEKRVLTLHRDVMAHRWNSLKTSNYDVILATNI 644

 ++VL F PG G G + D++ + + + + R + L + V++ATNI

Sbjct 416 KRVLWFVPGYHGKNGAKEMADRL--MRDGIQAIAVGRPSYTDYASRLNDTTVRVVVATNI 243

Query 645 AEMGMNIDVDVVLDLCKRFTYLG-DTYVVGSTLSINLssrvqrrgrvgrIKPGYYYYYGK 703

 AE GMNID DVV++ F Y D V G T +I SS +QRRGR GR K G +YY K

Sbjct 242 AECGMNIDCDVVVNTATEFDYFSFDNIVTGETRTIGHSSWIQRRGRCGRTKVGEHYYTAK 63

Partitivirus

>GASN02036638.1 TSA: Thermobia domestica C218246\_a\_5\_0\_l\_601 transcribed RNA

sequence

Length=601

Zygentoma

 Sort alignments for this subject sequence by:

 E value Score Percent identity

 Query start position Subject start position

 Score = 63.3 bits (138), Expect(2) = 1e-16, Method: Compositional matrix adjust.

 Identities = 33/67 (49%), Positives = 40/67 (60%), Gaps = 0/67 (0%)

 Frame = -3

Query 294 FINTPIQLSSGERFMKYGGVPSGSCFTNVVDGIVNALATRYLVYHMTGSLPLDDLYLGDD 353

 FI T +QLS+GERF K VPSGS +T +VD IV + TR V +T L LYLGDD

Sbjct 593 FIETVVQLSTGERFKKTRVVPSGSYYTSIVDSIVSMIVTRTCVLLITSRLTDAYLYLGDD 414

Query 354 SIVITDK 360

 +K

Sbjct 413 FCCCCNK 393

 Score = 51.7 bits (111), Expect(2) = 1e-16, Method: Compositional matrix adjust.

 Identities = 39/140 (28%), Positives = 63/140 (45%), Gaps = 10/140 (7%)

 Frame = -1

Query 355 IVITDKPLNMDVFSEKADEWFSLIYNVDKSYQTANPQNVHFLGYYNMTGVPFKPVDTTIA 414

 +V+T+KP + S+ A+ FS+I S T P V FLG++ G K + +

Sbjct 406 VVVTNKPYYIRKNSQIAESLFSMIMPDKMSVVTRRPNCVNFLGFHYRQGASWKNQASGVV 227

Query 415 SSVYPERMPRNK-FETAVRLVGQAYSCFEPTDAKNFFRAAKILVNEMEGANLDMIKEFTA 473

 S + PE R + A+ VGQ ++ +P A F + M NL+ + TA

Sbjct 226 SWIRPECESRTESTRMAICTVGQLFAFLDPGKAGVF-------MAYMARKNLEKVDVMTA 68

Query 474 DHPEF--FKYLQTIGVSTKE 491

 + YL+ IG+ +E

Sbjct 67 LRSNYDTLTYLREIGIDPRE 8

FIETVVQLSTGERFKKTRVVPSGSYYTSIVDSIVSMIVTRTCVLLITSRLTDAYLYLGDD

FVVVTNKPYYIRKNSQIAESLFSMIMPDKMSVVTRRPNCVNFLGFHYRQGASWKNQASGV

VSWIRPECESRTESTRMAICTVGQLFAFLDPGKAGVFMAYMARKNLEKVDVMTALRSNYD

TLTYLREIGIDPRE

nyamivirus

Catajapyx aquilonaris contig\_2370, whole genome shotgun sequence

Sequence ID: JYFJ02002370.1Length: 58159Number of Matches: 1

Range 1: 10635 to 10901GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

52.1 bits(112) 5e-06 Compositional matrix adjust. 29/89(33%) 48/89(53%) 6/89(6%)

-3

Query 141 MTGAGDNQVVSVKLVKTPAL------QSLvkkvkvkLAEGFAEVGLKVKLAETWHSSILL 194

 + G GDN+V+ + + A Q+ V LA+ + + +K E+W S+ILL

Sbjct 10901 IPGQGDNRVILLNIPDEIAPGPSEGNQAYVDGFLRSLAQWSKALKVPIKPEESWKSTILL 10722

Query 195 AYQRRYFLRGIPVPNAIKQGTRAFSGMSD 223

 Y RRY+L+G+ VPN +K+ +R + D

Sbjct 10721 EYARRYYLKGVEVPNDLKKASRLPAQAND 10635

KYVSKFQSMTLGESWLSKRLLKMTRTMISHVSLILAAAFDVGALISIPGQGDNRVILLNM

PDEIAPGPSEGNQAYVDGFLRSLAQWSKALKVPIKPEESWKSTILLEYASSYYLKGVEVP

NDLKKASSLPAQANDPFSWLLGDLYGIFTSGCTAAHEDLEEAKATMAFWL

chuvirus

Catajapyx aquilonaris contig\_6454, whole genome shotgun sequence

Sequence ID: JYFJ02006454.1Length: 19481Number of Matches: 1

Range 1: 1642 to 1947GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

76.3 bits(168) 2e-12 Composition-based stats. 36/104(35%) 55/104(52%) 4/104(3%)

-3

Query 550 NVDSSSWNNMFRHEALAPVIAATLDKYYNCSIFSKTQLAFQNTFIYLPDVEETYSWNGQK 609

 +D +WNN FR E PV D+ ++ F F + ++L D YSW+GQ+

Sbjct 1947 SIDIDAWNNCFRNELCEPVGRLIFDRIFDQ\*QFQHIMHVFNRSLVFLSDFSSMYSWDGQQ 1768

Query 610 GGIEGLNQ--YTWVTAYIHQMKVCMRNFAFPYHILCKGDDLRIC 651

 GGIEGLNQ +TW+ + + VC + + ++ GDDL+ C

Sbjct 1767 GGIEGLNQKFWTWIYESVARY-VCDQAGVTAF-LMANGDDLKTC 1642

partitivirus

Machilis hrabei contig\_337473, whole genome shotgun sequence

Sequence ID: QVQU01337473.1Length: 3397Number of Matches: 1

Related Information

Range 1: 720 to 1466GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

62.4 bits(150) 2e-08 Compositional matrix adjust. 70/276(25%) 111/276(40%) 61/276(22%)

-3

Query 162 DVAKQIHKE--LPKQNQLFAIP----YHRAQISGYVGKNGKLRPKATKHKDRLVWCVDAA 215

 D +IH E L + +P Y RAQI +K R W +

Sbjct 1466 DAVSEIHMEWALVGRGSRVQLPDAMVYFRAQIC-----------SPDTNKIRSTWGYPLS 1320

Query 216 TVLIESLYARPFID---------KVLTHIQNYAGGKDDNYISNLLI-AWNVDNWISIDYS 265

 +L E+ + P +D V I+ GG YI + A + ID+

Sbjct 1319 LILEEARFVYPHLDWIRHTNTSVPVAYGIEMANGGM--GYIDQMFQQAGPGAKCLMIDWR 1146

Query 266 KYDSTVQAWLIKDVFDIIRSFFSKRDV-----KVL---------QW--IENQFIHTRILD 309

 K+D ++ AWLI+D F I+ F +V KV +W + + FI+T

Sbjct 1145 KFDKSISAWLIRDAFGIMLESFKMNEVFDSEGKVWPVDPQKTGRRWRKLVSYFINTPFTL 966

Query 310 FDGNISTKHRGIPSGSYFTQIVGSLVNALVI--LTYEFARFRGNEAKVWEDMRYGDWLRF 367

 +G K G+ SGS FT I+ ++VN +V L Y+ + F +

Sbjct 965 PNGERFFKEGGVSSGSCFTNIIDTIVNCIVTRYLIYQTSGFLPEQD-------------- 828

Query 368 MTMGDDNIVFTRNKISLDDLASYVEHNFGLVINVEK 403

 M MGDD ++ ++L+D++ FG+ +N K

Sbjct 827 MYMGDDGLIICSGNLNLEDISRLAMRKFGMEVNEAK 720

Machilis hrabei contig\_73480, whole genome shotgun sequence

Sequence ID: QVQU01073480.1Length: 12352Number of Matches: 2

Related Information

Range 1: 287 to 1099GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

437 bits(1125) 4e-136 Compositional matrix adjust. 213/271(79%) 233/271(85%) 1/271(0%)

+2

Query 50 VSLDAIRNDVFDYDREYSPRVVDSIYSAVLESVRQDFSAKGSITPWTLGRVQNLPNLPTK 109

 VS +AIRNDVFDYDR+YSPRVVD++YSAVLE+VR+DFSA GSITPWTLGRV+N PNLPTK

Sbjct 287 VSHNAIRNDVFDYDRQYSPRVVDAVYSAVLETVRRDFSAHGSITPWTLGRVKNSPNLPTK 466

Query 110 KSPGMPWKERGYTTKKSVLEDHDAVSEIHMEWALVGRGSRVQLPDAMVYFRAQICSPDTN 169

 KSPGMPWKE+GY TK+SVLEDH AVSEIH EWALVG+G RVQL D+MVYFRAQICSPDTN

Sbjct 467 KSPGMPWKEKGYATKQSVLEDHTAVSEIHREWALVGKGLRVQLLDSMVYFRAQICSPDTN 646

Query 170 KIRSTWGYPLSLILEEARFVYPHLDWIRHTNTSVPVAYGIEMANGGMGYIDQMFQQAGPG 229

 K RSTWGYPL LILE+ARFVYP+LDWI HT TSVPVAYGI+MANGGMGYIDQMF+QAGP

Sbjct 647 KXRSTWGYPLGLILEKARFVYPYLDWIHHTQTSVPVAYGIQMANGGMGYIDQMFKQAGPE 826

Query 230 XKCLM-IDWRKFDKSISAWLIRDAFGIMLESFKMNEVFDSEGKVWPVDPQKTGRRWRKLV 288

 S+ LIRDAF IMLESFK+NEV+DSEGK WPVDPQKTGRRW+KLV

Sbjct 827 QNA\*W\*TGENLISLSLLG\*LIRDAFNIMLESFKLNEVYDSEGKTWPVDPQKTGRRWKKLV 1006

Query 289 SYFINTPFTLPNGERFFKEGGVSSGSCFTNI 319

 YFINTPF LPNGERF KEGGV SGSCF +

Sbjct 1007 QYFINTPFVLPNGERFLKEGGVPSGSCFQTL 1099

Range 2: 808 to 1458GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #2

Score Expect Method Identities Positives Gaps

Frame

235 bits(600) 5e-66 Compositional matrix adjust. 129/243(53%) 148/243(60%) 53/243(21%)

+1

Query 224 QQAGPGXKCLMIDWRKFDKSISAWLIRDAFGIMLESFKMNEVFDSEGKVWPVDPQKTGRR 283

 Q +G KCLM+DWRKF D W +D ++

Sbjct 808 QTSGARAKCLMVDWRKF--------------------------DKSIPAWLID\*RRL\*HN 909

Query 284 WRKL--------------------------VSYFINTPFTLPNGERFFKEGGVSSG-SCF 316

 RKL VS + + R +GG S+

Sbjct 910 ARKL\*AKRSV\*F\*RQDMAR\*STEDWSQMEEVSTIFHKHTLCTS\*WRKILKGGRSTIWIML 1089

Query 317 TNIIDTIVNCIVTRYLIYQTSGFLPEQDMYMGDDGLIICSGNLNLEDISRLAMRKFGMEV 376

 NIIDTIVNCIVTRY++ QTSGF+PEQDMYMGDDGLII SG +NL DIS+LAM KFGMEV

Sbjct 1090 PNIIDTIVNCIVTRYVLLQTSGFIPEQDMYMGDDGLIIISGKINLSDISKLAMTKFGMEV 1269

Query 377 NEAKSYITTNPSNIYFLGFYNHHGFPVKEQDFLIASFMYPERYHQTFDPIFTAVRAAGQM 436

 NEAKSYIT+NP+NIYFLGFYNHHGFPV+EQDFLIASFMYPER+H+ FDPIFTAVRAAGQM

Sbjct 1270 NEAKSYITSNPTNIYFLGFYNHHGFPVREQDFLIASFMYPERFHKIFDPIFTAVRAAGQM 1449

Query 437 WST 439

 WST

Sbjct 1450 WST 1458

permutotetra

TSA: Megajapyx sp. UVienna-2012 DMPC16734223 mRNA sequence

Sequence ID: JT051866.1Length: 427Number of Matches: 1

Range 1: 4 to 390GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

158 bits(399) 7e-42 Compositional matrix adjust. 75/129(58%) 95/129(73%) 4/129(3%)

+1

Query 528 MYRGGPTRTEPVPYLPDDEWTNLIMVPRDDPENFRRGRPKDSQLTVSRRWYDRARGYMVT 587

 +Y GP + + VPYLP +EW +L++ PRDDPENFRRGRPK SQ+T++RRWYDR RGYM+T

Sbjct 4 IYEQGPNKIQLVPYLPYEEWVDLLLSPRDDPENFRRGRPKTSQVTIARRWYDRIRGYMIT 183

Query 588 GAFSNPLIRDWIHGFVNGLDPVSIVMNVQEGDGR----GAPPDSAFLEDFQYPDSAGFPT 643

 GAFSN IR W+ G VN +D V IVM+VQ G G+ G P E+F+YPDS+GFP+

Sbjct 184 GAFSNESIRLWLQGVVNDMDSVPIVMSVQAGGGKGEVPGIPGFFEEHEEFEYPDSSGFPS 363

Query 644 EEWCENLYF 652

 WC+NLY

Sbjct 364 VPWCQNLYL 390

The only case of HVT in basal hexapods

>Holacanthella duospinosa (GFPE01073448, 340 bp) Bromoviridae; Alfamovirus

ASFHFKEIDFSKFDKSQNELHHLIQERLLKYLGIPNEFLTLWFNAHRKSRISDSKNGVFF

NVDFQRRTGDALTYLGNTIVTLACLCHVYNLMDPNVKFVVASGDDSLIGTVEE

P2 protein [Alfalfa mosaic virus]

Sequence ID: ATS17298.1Length: 790Number of Matches: 1

Range 1: 522 to 634GenPeptGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

236 bits(603) 2e-71 Compositional matrix adjust. 112/113(99%) 112/113(99%) 0/113(0%)

Query 1 ASFHFKEIDFSKFDKSQNELHHLIQERLLKYLGIPNEFLTLWFNAHRKSRISDSKNGVFF 60

 AS HFKEIDFSKFDKSQNELHHLIQERLLKYLGIPNEFLTLWFNAHRKSRISDSKNGVFF

Sbjct 522 ASSHFKEIDFSKFDKSQNELHHLIQERLLKYLGIPNEFLTLWFNAHRKSRISDSKNGVFF 581

Query 61 NVDFQRRTGDALTYLGNTIVTLACLCHVYNLMDPNVKFVVASGDDSLIGTVEE 113

 NVDFQRRTGDALTYLGNTIVTLACLCHVYNLMDPNVKFVVASGDDSLIGTVEE

Sbjct 582 NVDFQRRTGDALTYLGNTIVTLACLCHVYNLMDPNVKFVVASGDDSLIGTVEE 634

Sobemo-like viruses

>Pogonognathellus sp. AD-2013 capsid of sobemovirus (GATD02018541, 390 bp) Collembola

RSNAALRKIVQDVTNNMSQMNLKTKSKKVKRKRKSGKKVEGSGAQQGSIRLRQSEIWTGV

TSTASKTQTTKTLPCVPGGSGIKYLDQMARLFDRFIFHSATVSWKPYCSASTNGGMLFGI

DWEVGSDIF



>GFPE01061060.1 TSA: Holacanthella duospinosa c72747\_g1\_i1 transcribed RNA sequence

Length=273

 Score = 55.1 bits (119), Expect = 5e-06, Method: Composition-based stats.

 Identities = 29/77 (38%), Positives = 47/77 (61%), Gaps = 3/77 (4%)

 Frame = -1

Query 175 AYYRFEQLYLKCVFITSGGHLLRQLRPGALKSGCVNTIADNSLMQYLLHLRVVFQLGYSP 234

 A +R+ LYL +F TS GH RQ+ PG +KSG + TI+DNS+ +L + + ++ P

Sbjct 270 AAWRYNCLYLNPLFQTSSGHQFRQMLPGIMKSGGLLTISDNSIGVAVLEV-LTSEMTSEP 94

Query 235 --GIIMSMGDDTLQQEP 249

 + +MGDD+ + +P

Sbjct 93 IDKSVKAMGDDSTRSKP 43

LAAWRYNCLYLNPLFQTSSGHQFRQMLPGIMKSGGLLTISDNSIGVAVLEVLTSEMTSEP

IDKSVKAMGDDSTRSKPMSPAKLVAQSKLGM



>Holacanthella duospinosa sobemo-like capsid (GFPE01060684, 469 bp)

VLRDMFQQLIDELGVRDPTPKYREFRDKFFSIPEAGLKEWTPDLLLVLTMMIPSVVFWLM

VMARFVGLLVALARWTFMIDGMKYIPEAIIEGSTFLAGEPPKFQARIRATELMGRLVGNA

VRMNNYLVVPTHVLQAASGASVTVEASKSKLILPKT

Endogenous qinvirus

>QVQU01284830.1 Machilis hrabei contig\_284830, whole genome shotgun sequence

Length=997

 Sort alignments for this subject sequence by:

 E value Score Percent identity

 Query start position Subject start position

 Score = 176 bits (400), Expect(2) = 8e-50, Method: Compositional matrix adjust.

 Identities = 105/300 (35%), Positives = 158/300 (53%), Gaps = 20/300 (7%)

 Frame = +1

Query 339 MKHGLAILQNNFHSHAEKLEMGLGNRNDMLWKEQKDIADLKIEWYSFLSDLDIPERDKVN 398

 MK +A+LQN+FH H+E LEMG R L + ++I + W+ + + +R +++

Sbjct 1 MK\*SVALLQNDFHEHSEVLEMGTKTRSTALKRIIREIHPMXTFWHEVVRANKLTDRARLD 180

Query 399 LAYLYHILPSPDAPPKEVYERVVTQLNDSNKEDVEEFATFLNYCKATDVSMFVTKSHGKV 458

 LA +Y+ L +PD + + R + + ++ C+ FV K

Sbjct 181 LANMYYGLTAPDDDEQNLRSRATEYMATAKRKT----------CR------FVRKFRRYP 312

Query 459 KLHCKDGYDPSVKKWYKSC--AQGKLMLPPKHEWGLCWIKNVVPVNLLIHTWYLNSADVT 516

 + ++GY+P W SC + +PP+ EWG CWI+ VP N W +++DVT

Sbjct 313 RYSIEEGYNPEGSAWADSCLSPEKLFKMPPEEEWGKCWIEGEVPYNDTTSQWPWDASDVT 492

Query 517 RVVPDISKYDSLVEKSSQVPMEV-NELLYTLMHAPDIEPGWSPELVLECVRNGSLNLPKI 575

 VV D Y S V K ++ V NELLY L+HAP + W P L+ C++ S ++

Sbjct 493 HVVADTKIY-SXVGKMNELKRYVHNELLYALVHAPYLSFKWDPSLLRFCMQCDSDIWDRL 669

Query 576 ADMSVKSENTKYGPKMRETWSADAITRELLTDYDHSLIGLSHMVDGVTSRKSNVHVDGIF 635

 A ++ KSENTK G K+RETWS D +TREL + YD S I L+ + GV RKS VD +F

Sbjct 670 ATIAAKSENTKPGMKVRETWSGDDVTRELTSAYDSSAIPLASLYSGVV\*RKSQGKVDEVF 849

 Score = 47.8 bits (102), Expect(2) = 8e-50, Method: Composition-based stats.

 Identities = 20/31 (65%), Positives = 23/31 (74%), Gaps = 1/31 (3%)

 Frame = +3

Query 649 IIISNDTSGWSPSAPREAWAQHHDYKVSLTS 679

 +II ND SGWSP R AWA+HHDY V+ TS

Sbjct 900 LIIFNDVSGWSPLGDRIAWAEHHDY-VARTS 989

>QVQU01284831.1 Machilis hrabei contig\_284831, whole genome shotgun sequence

Length=2829

 Score = 50.8 bits (109), Expect = 3e-04, Method: Compositional matrix adjust.

 Identities = 55/213 (26%), Positives = 85/213 (40%), Gaps = 53/213 (25%)

 Frame = +3

Query 794 LSESKTIYSSIKFIYLNRFFCEGSEVLVDMKTFSKVDRDYNRRLSTFFQASDTVMGGYRS 853

 L E KT+YSSIK ++LN CEGSE++ MK F++ D++ RR Y S

Sbjct 6 LDEVKTMYSSIKSLFLN\*MHCEGSELVFPMKVFARADKEKSRR--------------YAS 143

Query 854 SAMKGSDPMLCYYWYFFRSFDLMIQSNAIIKEIIPNLGYLVTAAFAPRSLNGLGMPHIVA 913

 +G DP++ Y + DL+ + K G+

Sbjct 144 E--RGDDPLVXYGTAIEKVCDLVWRPSGEXK------GF--------------------- 236

Query 914 FMTKEKVDALAMFFGVHVRLKNLISNVHIRNSLIYSFSAYVNQKLEPPTATVVFKDPMAV 973

 F+ ++ V L L+ L S R I S +NQ + K P ++

Sbjct 237 FLGQQDVCIL---------LETLASPGD-RELCINILSHTLNQTPAVVDIDALLKSPTSI 386

Query 974 YAADRISPDDNVYRTLKARMRLKCKSPAISEAF 1006

 A + PD V R +++ + KSP +AF

Sbjct 387 RAINIPDPDSAVMRRVRSALLKFAKSPVFLQAF 485

>QVQU01284830.1 Machilis hrabei contig\_284830, whole genome shotgun sequence

Length=997

 Sort alignments for this subject sequence by:

 E value Score Percent identity

 Query start position Subject start position

 Score = 255 bits (584), Expect(2) = 2e-78, Method: Compositional matrix adjust.

 Identities = 138/313 (44%), Positives = 182/313 (58%), Gaps = 22/313 (7%)

 Frame = +1

Query 333 MKQSVALMQNELHKHSEHLETNTEQKSANLREAIAGILPLDSYWHDHLSNAGISDRAKMD 392

 MK SVAL+QN+ H+HSE LE T+ +S L+ I I P+ ++WH+ + ++DRA++D

Sbjct 1 MK\*SVALLQNDFHEHSEVLEMGTKTRSTALKRIIREIHPMXTFWHEVVRANKLTDRARLD 180

Query 393 LANLYYNLPSPDADLESLWKKGAEIMCNASTADPEIWKLFMNYSKALDFCKLTAMIKEVP 452

 LAN+YY L +PD D + L + E M A C+ + P

Sbjct 181 LANMYYGLTAPDDDEQNLRSRATEYMATAKRKT----------------CRFVRKFRRYP 312

Query 453 KHRKKEGYEFEESQWFKSCLKGK--MRLPPDEEMGNVWIYHHFEFQNTLSEWYWEAGDVT 510

 ++ +EGY E S W SCL + ++PP+EE G WI + +T S+W W+A DVT

Sbjct 313 RYSIEEGYNPEGSAWADSCLSPEKLFKMPPEEEWGKCWIEGEVPYNDTTSQWPWDASDVT 492

Query 511 HVHADLANYTDQLKATSLTREDCNELLYAMDYAPLLSKKYSPSEVLDRVCT--GKKCWDS 568

 HV AD Y+ K L R NELLYA+ +AP LS K+ PS L R C WD

Sbjct 493 HVVADTKIYSXVGKMNELKRYVHNELLYALVHAPYLSFKWDPS--LLRFCMQCDSDIWDR 666

Query 569 IALMAAKSENTKPGAKVRETWSGDDVTRELTSCYDRQAIPLGSMYRGMVSRKPPVKVDAM 628

 +A +AAKSENTKPG KVRETWSGDDVTRELTS YD AIPL S+Y G+V RK KVD +

Sbjct 667 LATIAAKSENTKPGMKVRETWSGDDVTRELTSAYDSSAIPLASLYSGVV\*RKSQGKVDEV 846

Query 629 FDRIADLTTKPRE 641

 F I TT+ ++

Sbjct 847 FQLITSRTTQDKK 885

 Score = 64.2 bits (140), Expect(2) = 2e-78, Method: Composition-based stats.

 Identities = 24/31 (77%), Positives = 26/31 (84%), Gaps = 0/31 (0%)

 Frame = +3

Query 645 IIISNDVSGWSPQGDRKAWAEHHDYVVHTSD 675

 +II NDVSGWSP GDR AWAEHHDYV TS+

Sbjct 900 LIIFNDVSGWSPLGDRIAWAEHHDYVARTSN 992

>QVQU01284831.1 Machilis hrabei contig\_284831, whole genome shotgun sequence

Length=2829

 Score = 98.3 bits (219), Expect = 2e-18, Method: Compositional matrix adjust.

 Identities = 67/221 (30%), Positives = 101/221 (46%), Gaps = 59/221 (27%)

 Frame = +3

Query 789 EIDQVKTLYSSIKVIFLNRLYCEGAEVLTPMKVYARVDRELTRRFSTVYEQVDTILGGFR 848

 E+D+VKT+YSSIK +FLN ++CEG+E++ PMKV+AR D+E +RR+

Sbjct 3 ELDEVKTMYSSIKSLFLN\*MHCEGSELVFPMKVFARADKEKSRRY--------------- 137

Query 849 SASERGADPMVCYIMAIYRSLDLIIQSS---RGCIHGNLDVMEIVNAAFAPRGLGGWGLP 905

 ASERG DP+V Y AI + DL+ + S +G G DV ++ +P

Sbjct 138 -ASERGDDPLVXYGTAIEKVCDLVWRPSGEXKGFFLGQQDVCILLETLASP--------- 287

Query 906 HMTGWLTQESQDKLTAYLGVIFSLNEYMMESGTVTRLSSYIYKTLNQTLAEATVEGILDS 965

 G + TLNQT A ++ +L S

Sbjct 288 -------------------------------GDRELCINILSHTLNQTPAVVDIDALLKS 374

Query 966 PRDVRVGSLVGLSGAVLEKVKREMAQRAKSPIFRAALNSNS 1006

 P +R + AV+ +V+ + + AKSP+F A + S

Sbjct 375 PTSIRAINIPDPDSAVMRRVRSALLKFAKSPVFLQAFATTS 497

Endogenous tombus-like viruses

Machilis hrabei contig\_261130, whole genome shotgun sequence

Sequence ID: QVQU01261130.1Length: 2308Number of Matches: 5

Related Information

Range 1: 1722 to 2057GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

130 bits(327) 3e-36 Compositional matrix adjust. 64/113(57%) 82/113(72%) 2/113(1%)

+3

Query 658 RGT-RMSGDVDTSLGNSILNYAIIRQVLEMLGIQGDVIVNGDDSIIFTNVPIPIQQCERL 716

 RG+ RMS DV TS GNS++NYAII++ L + GI GDVIVNGDDSIIFTN P+P +

Sbjct 1722 RGSPRMSADVHTSFGNSLINYAIIKKALRIHGIDGDVIVNGDDSIIFTNEPLP-SSLQDT 1898

Query 717 MKMFNQESKLKPSTQNIHTVEYCRTKLIVTAEGETTLLFDPQRSVDMFGMTYQ 769

 ++FN E+KLKPS +NIH VE+CR K++V G+ L+ DP R +FGMTY

Sbjct 1899 FRVFNMEAKLKPSLRNIHQVEFCRCKVVVNTLGQWMLMMDPGRHERVFGMTYH 2057

Range 2: 1541 to 1726GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #2

Score Expect Method Identities Positives Gaps

Frame

47.4 bits(111) 3e-36 Compositional matrix adjust. 25/63(40%) 43/63(68%) 2/63(3%)

+2

Query 598 YRYFTELDHTSWDAHVTVEMLRVSHKFYQSCY-NHDRRLRTLSRKTIRNRCYLRDGGRHT 656

 ++Y++EL H++++ +VT EML ++HKFY++CY ++ L+ LS +TI NR R G

Sbjct 1541 WKYYSELXHSNFEKNVTEEMLLLTHKFYRACYPDNVEELKKLSARTI-NRFITRTG\*EME 1717

Query 657 IRG 659

 + G

Sbjct 1718 MEG 1726

Range 3: 1100 to 1405GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #3

Score Expect Method Identities Positives Gaps

Frame

90.1 bits(222) 7e-36 Compositional matrix adjust. 51/103(50%) 63/103(61%) 6/103(5%)

+2

Query 612 HVTVEMLR-----VSHKFYQSCYNHDRRLRTLSRKTIRNRCYLRDGGRHTIRGTRMSGDV 666

 H T+ ML+ + CY + LS +TI NRC R G + RG+RMS DV

Sbjct 1100 HSTLTMLKS\*RSCLRGLLTSVCYPDNVEELKLSVRTI-NRCITRTGEKWKWRGSRMSADV 1276

Query 667 DTSLGNSILNYAIIRQVLEMLGIQGDVIVNGDDSIIFTNVPIP 709

 DTS GNS++NYAII++ GI GDVIVNGDD IIFTN P+P

Sbjct 1277 DTSFGNSLINYAIIKKAYRXHGIDGDVIVNGDDCIIFTNEPLP 1405

Range 4: 864 to 1055GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #4

Score Expect Method Identities Positives Gaps

Frame

68.2 bits(165) 7e-36 Compositional matrix adjust. 31/65(48%) 46/65(70%) 1/65(1%)

+3

Query 547 IQARHPSFNIEYGRYLKPLEMLLFHSHREGYHFGKGTVDQVSANINKLRKKYRYFTELDH 606

 + ARHPSFNI YG+Y+KPLE + H + ++FGKG ++ I L KY+Y++ELDH

Sbjct 864 LDARHPSFNIAYGKYIKPLEYKVCHG-KHKHNFGKGNYLEMGERIRVLPMKYKYYSELDH 1040

Query 607 TSWDA 611

 +++DA

Sbjct 1041 SNFDA 1055

Range 5: 1413 to 1553GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #5

Score Expect Method Identities Positives Gaps

Frame

38.1 bits(87) 7e-36 Compositional matrix adjust. 19/48(40%) 30/48(62%) 1/48(2%)

+3

Query 714 ERLMKMFNQESKLKPSTQNIHTVEYCRTKLIVTAEGETTLLFDPQRSV 761

 R ++N E+KLKPS +NIH VE+ R ++V + TL+ DP ++

Sbjct 1413 SRTRSVYNTEAKLKPSLRNIHQVEFFRCTVVVNTLVQWTLM-DPGSTI 1553

DownloadGenBankGraphics Sort by: NextPreviousDescriptions

Machilis hrabei contig\_111567, whole genome shotgun sequence

Sequence ID: QVQU01111567.1Length: 6307Number of Matches: 2

Related Information

Range 1: 1982 to 2419GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

123 bits(308) 2e-28 Compositional matrix adjust. 63/147(43%) 88/147(59%) 1/147(0%)

-1

Query 445 YYYPSGTDTTIASYANRHEPVILPEYQPRLIPGIYRHIRRFLCHPRVWTRDEYCSSHTTS 504

 YYYP+ T +T+A A RH L EY P + +RH+R+F+ +T +Y S TS

Sbjct 2419 YYYPASTISTVAGVAKRHCVDPLLEYNPSSVRRCFRHLRKFITRYNSFTP\*QYVESMPTS 2240

Query 505 SKRQFYRDVLERMEETGKISSTIKPFTKLEKFNMSKYKAPRCIQARHPSFNIEYGRYLKP 564

 R YR VL+ + G + +++ PFTK EK + + YK PR IQARHPSFNI YGR++KP

Sbjct 2239 RARNHYRGVLDHLNNGGSVRTSVTPFTKFEKMSGTHYKPPRLIQARHPSFNIAYGRFIKP 2060

Query 565 LEMLLFHSHREGYHFGKGTVDQVSANI 591

 LE + H R ++FGKG ++ I

Sbjct 2059 LEHKVCHG-RYKFNFGKGNYLEMGTRI 1982

Range 2: 1918 to 1974GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #2

Score Expect Method Identities Positives Gaps

Frame

27.7 bits(60) 2e-28 Compositional matrix adjust. 10/19(53%) 17/19(89%) 0/19(0%)

-2

Query 594 LRKKYRYFTELDHTSWDAH 612

 L +KY+Y+TELDH++++ H

Sbjct 1974 LARKYKYYTELDHSNFE\*H 1918

DownloadGenBankGraphics Sort by: NextPreviousDescriptions

Machilis hrabei contig\_29330, whole genome shotgun sequence

Sequence ID: QVQU01029330.1Length: 6886Number of Matches: 2

Related Information

Range 1: 5680 to 5991GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

84.7 bits(208) 7e-15 Compositional matrix adjust. 46/104(44%) 62/104(59%) 0/104(0%)

-2

Query 444 HYYYPSGTDTTIASYANRHEPVILPEYQPRLIPGIYRHIRRFLCHPRVWTRDEYCSSHTT 503

 +YYP+ + +TIA+ A RH PEY RL +RH+RRF +TR+E S T

Sbjct 5991 QFYYPTCSASTIAAVARRHCIDNCPEYDKRLTRAAFRHLRRFXVRCTPFTREE\*FESMPT 5812

Query 504 SSKRQFYRDVLERMEETGKISSTIKPFTKLEKFNMSKYKAPRCI 547

 S R YR+VL +E G++ S ++PFTKLEKF+ YK PR I

Sbjct 5811 SRARSTYRNVLADLEVGGRVRSRVEPFTKLEKFSGRTYKPPRLI 5680

Range 2: 6372 to 6506GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #2

Score Expect Method Identities Positives Gaps

Frame

37.7 bits(86) 1.4 Compositional matrix adjust. 17/45(38%) 28/45(62%) 0/45(0%)

-3

Query 34 QREDAVAYLNVRCRGKRMDKNYVTYITTLFNEWCDAHAIRDYKIR 78

 Q++DA+A+L V G++MD+NY Y T + E+ A+ D I+

Sbjct 6506 QQQDALAWLRVTTAGRQMDRNYEAYCTAILREYFVDRAMVDANIQ 6372

DownloadGenBankGraphics NextPreviousDescriptions

Machilis hrabei contig\_29331, whole genome shotgun sequence

Sequence ID: QVQU01029331.1Length: 1282Number of Matches: 1

Related Information

Range 1: 868 to 1179GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

82.0 bits(201) 1e-14 Compositional matrix adjust. 44/104(42%) 61/104(58%) 0/104(0%)

-2

Query 444 HYYYPSGTDTTIASYANRHEPVILPEYQPRLIPGIYRHIRRFLCHPRVWTRDEYCSSHTT 503

 +YYP+ + +TIA+ + RH PEY RL + H+RRF+ +TR EY S T

Sbjct 1179 QFYYPTCSASTIAAVSRRHCIDNCPEYDKRLTRAAFXHLRRFIVRCTPFTRVEYVKSMPT 1000

Query 504 SSKRQFYRDVLERMEETGKISSTIKPFTKLEKFNMSKYKAPRCI 547

 S R YR+VL +E G++ S ++PFTKLEK + YK PR I

Sbjct 999 SRARSTYRNVLADLEVGGRVRSRVEPFTKLEKLSG\*TYKPPRLI 868

DownloadGenBankGraphics NextPreviousDescriptions

Machilis hrabei contig\_276258, whole genome shotgun sequence

Sequence ID: QVQU01276258.1Length: 4248Number of Matches: 1

Related Information

Range 1: 3518 to 3805GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

73.2 bits(178) 2e-11 Compositional matrix adjust. 36/96(38%) 60/96(62%) 0/96(0%)

-3

Query 33 NQREDAVAYLNVRCRGKRMDKNYVTYITTLFNEWCDAHAIRDYKIRYEMMNDVLLQHRNQ 92

 N+R+DA+A+L VR GK MD+NY +Y+ L E+ I +Y+++ E + ++ +H ++

Sbjct 3805 NERQDALAFLYVRTLGKVMDENYESYLRALMTEYFSHRKIVNYRVQREYLQKIIPEHISE 3626

Query 93 KLQEPDFWNEQIIRRAWEHNDANQGRDYTWQWWTPW 128

 KL EP + Q+IRRA ++N QG + WW P+

Sbjct 3625 KLTEPVIFTPQMIRRANDYNKELQGINTKSVWWWPF 3518

Endogenous totivirus

>QVQU01134226.1 Machilis hrabei contig\_134226, whole genome shotgun sequence

Length=4728

 Score = 58.2 bits (201), Expect = 8e-07, Method: Compositional matrix adjust.

 Identities = 96/388 (25%), Positives = 184/388 (47%), Gaps = 34/388 (9%)

 Frame = -1

Query 513 PNRGRWTRAQYLEDFDFALEQGYKQMFMKPKPVRVDSFVEFWKLRRQWVAKGSTVLNKIP 572

 P+R +W ++E++ L YKQ+ PK+ + + +F K R++WV+ GS +K+

Sbjct 1386 PSR-QWVVQTFFEELSAELKLIYKQLV--PKAPAIPNWADFIKRRQNWVSAGSGGGHKV- 1219

Query 573 PEMLTYVVQFGDKLSQQIQMRHNKKSLFESHQVIDLLNETAESWNTTKVVPKLNETGKKR 632

 + + +R +K LFE + +++ E + V + E GK R

Sbjct 1218 -------------MVEGESIRIKKPVLFEELETSEMVTWLDEEPKIIAVGSEKYEMGKGR 1078

Query 633 ELLPGTLMHYLVFSYVLYVAEKQ-APVGSTRLNVNDDDNI-KYYDRKMME---GIHHMLY 687

 + +Y + SYVLY E + V++ + D D++ R + I+ +

Sbjct 1077 SIYGTKPKDYTIMSYVLYAIEPHLNRVDGIESGLVDLDQVFSVLKRSRLARESRIEGTMI 898

Query 688 DWANFNAQHSTEDMAKVISYLA---RIPNTPADYGHFCMAIAESFSQMWVMDPAG-GKHK 743

 D A+FN QH+ E + V+ L + ++ AD + C A+++ + WV P + +

Sbjct 897 DYADFNYQHTLEAQSEVFIALRERLKTVSANADLIRACDWCAQALLNQWVHFPMEKSALR 718

Query 744 IEKGLFSGWRGTTWINTVLNYVYVSIGVECCKRIYN-DFQPTYFDHGGDDL---DAGFLM 799

 +G+FSG RGT INT+LN Y ++ + + + + Y H GDD+ +++ L

Sbjct 717 STQGMFSGVRGTNCINTLLNLAYFRVAERQVSKCFGLHARKLYHIHQGDDVWITNGSRLW 538

Query 800 PHDCYRLMEVMDKIGYEATAIKQMIGYD-AEFYRNTINERGVFASPSRALANFVSGNWES 858

 + Y M M G+ + KQM++ + + F R + G + RA++ + G+ +S

Sbjct 537 AITLYNTMIAM---GFVFQSSKQMFDTERGKFLRVNYDRSGCRGYLMRAVPTMIVGQMQS 367

Query 859 GGAKTLSEKTTSVLDQVSKLKRRGVKEV 886

 + + ++S+ Q++ L RRG+ +

Sbjct 366 VEEHSPAAMAASLNSQINLLHRRGMSTM 283

>QVQU01024963.1 Machilis hrabei contig\_24963, whole genome shotgun sequence

Length=11753

 Score = 55.3 bits (190), Expect = 7e-06, Method: Compositional matrix adjust.

 Identities = 99/405 (24%), Positives = 197/405 (49%), Gaps = 41/405 (10%)

 Frame = -1

Query 517 RWTRAQYLEDFDFALEQGYKQMFMKPKPVRVDSFVEFWKLRRQWVAKGSTVLNKIPPEML 576

 RW R +L + + ++ ++ + PK+ +V + +F K R++WV+ GS K+

Sbjct 4439 RWIR--FL\*GVE---GRAETHLQLVPKAPHVPTWPDFIKRRQNWVSAGSDGGLKV----- 4290

Query 577 TYVVQFGDKLSQQIQMRHNKKSLFESHQVIDLLNETAESWNTTKVVPKLNETGKKRELLP 636

 + + +R +K LFE + +++ + + V + E GK R

Sbjct 4289 ---------MVEGESIRIKKPVLFEELETKEMVTWIDDEPKIVAVGSEKYEMGKGRSTYG 4137

Query 637 GTLMHYLVFSYVLYVAEKQ----APVGSTRLNVNDDDNIKYYDRKMMEG-IHHMLYDWAN 691

 +Y + SYVLY E + + + S +++++ +I R E+ I+ + D A+

Sbjct 4136 TKPKDYTIMSYVLYAIEPHLYRMSGIESGLVDLDQVFSILKRSRLQKEARIEGTMIDYAD 3957

Query 692 FNAQHSTEDMAKVISYLA---RIPNTPADYGHFCMAIAESFSQMWVMDPAGGKH-KIEKG 747

 FN+ H+ + + V+ L R ++ D + C +A+++ + WV P + +G

Sbjct 3956 FNSPHTLQA\*SEVFIALRERLRTLSANVDLIRACDWFAQALLNQWVHFPMEKEALQSTQG 3777

Query 748 LFSGWRGTTWINTVLNYVYVSIGVECCKRIYNDFQPT--YFDHGGDDL---DAGFLMPHD 802

 +FSG RGT INT+LN Y ++ R + ++++T Y H GDD+ +++ L +

Sbjct 3776 MFSGVRGTNFINTILNLAYFRVAEKQVSRCF-GLHSTKLYHIHQGDDVWITNGSRLWAIT 3600

Query 803 CYRLMEVMDKIGYEATAIKQMIGYD-AEFYRNTINERGVFASPSRALANFVSGNWESGGA 861

 Y + M +G+ + KQM++ + +EF R ++ G + R L+ + G+ +S

Sbjct 3599 LY---NTMISMGFVFQGSKQMFDTERGEFLRVNYDHTGCRGYLMRVLPTMIVGQMQSIEE 3429

Query 862 KTLSEKTTSVLDQVSKLKRRGVKEVFCDKLIKMTLNHWLKIKIEE 906

 + ++S+ Q++ L RRG++ C L MT++H L+ I+

Sbjct 3428 HS---PAASLNSQINLLHRRGMNTRTCKSLWDMTVKHYLRSVIDG 3303

Machilis hrabei endogenised Tenuivirus/Phlebovirus nucleocapsid protein (Bunya) (QVQU01294448, 2913 bp) 20-30% id with phleboviruses

MCDYPQESPFELIDHLAGESXEDDVSECLXGLTNDVSNGDWYDSWXXHVFLPSHQ

GFDPFIIYNELSKKEPDEDVLQKDLLYLAFTYGVRGTNLIKMKKNSTPEFVSEIQRLALK

YSIEEITPSDDKTITMARIASTVPHLVCMCMKFFEDDALLVHPQQLPSNYPRVVMNAQFA

RLIPRNLPGITLNLVKAHLLYLIHLDQVVNKGKTIIRGMVEFQVSAMQWPMFSDDDRINF

CVQNGIIINTDAGLALNENLVTAATVINANNTTANILYKTLLYDLADDDDIDKVVRQQLE

ELVLDAGK\*



endogenised chuviruses

Machilis hrabei contig\_249695, whole genome shotgun sequence//

Sequence ID: QVQU01249695.1Length: 8568Number of Matches: 1

Range 1: 3042 to 4721GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

205 bits(522) 5e-51 Compositional matrix adjust. 159/578(28%) 268/578(46%) 26/578(4%)

+3

Query 405 NFYNKHKN-YPIFEHIPDDPALKHILFSPLAYKDHS-NYHIWKSISLKTWNQCEFGKNAE 462

 F+ KHK P+F P L + D S H ++S+S+ + +

Sbjct 3042 QFFIKHKV\*PPVFLDPGTSPGLTWCILHNKWISDRSYPIHKYESLSVINFETVSLQPCSH 3221

Query 463 FDFIDHGMLLLKDRAACRTRASFLAEIKGESRLAVEETKVLLQYLMSDDNSG-TREYIER 521

 FD++D MLLLKD A T S L + +R +++E + LL +LM+ + R Y+++

Sbjct 3222 FDYVDSQMLLLKDTALAFT-ISILENPELHARPSLKERRTLLFFLMTQNPPAEVRRYMDQ 3398

Query 522 YMEDDWGDEVLNYLVIKLTAKELEFKYKGRFFGASPIYERNRRIIQESNITRLMAHYIPD 581

 ++E D L+Y VIKLT K + K +G+ FG SP YER +R + E N++RLM Y

Sbjct 3399 FVEKD--PLALDYFVIKLTQKARDLKVEGKLFGQSPYYERAKRCVAEKNVSRLMKRYNSC 3572

Query 582 QLLTPPELSIIKKLMHYRTMRTLYPDSVVLNISFDFSSWNNRMRSGTVD-VAANVLDGWF 640

 Q +T EL KK+ + DS V++ S D +NN R + + D F

Sbjct 3573 QAMTLTELQKQKKMYIMSQLANKMKDSYVVHFSLDAEGFNNCFRRVLCEPIGREFFDRLF 3752

Query 641 GVKLYGKTMKAFQHALVIYKDGKFVRQWIGQEGGIEGLNQATWSWVFIGGMRHALEKTGF 700

 GV Y + M F +L D F W GQ+GGIEGL Q W+W++ TG

Sbjct 3753 GVNHYARVMDIF\*QSLFCC-DEFFRYNWTGQKGGIEGLAQKFWTWIYEAVASRIASLTGN 3929

Query 701 KYQITVKGDDVRAALVVPKNTLAIRSMDNIKSEIMSNIQELCAHVGWKLNPNECYISRTL 760

 K+ + V GDD+R L++PK T+++ + ++ +EI Q + + E Y S L

Sbjct 3930 KFFVMVNGDDLRVTLIIPKETVSLAQLSDLITEIAHAFQAEYESFVFNVKLEETYASSVL 4109

Query 761 MSTSKSYFVNDVHLPNATKKFMRSEGNTN----IPFPTLEDTVGTCFSIAHSVCYNSTSI 816

 + K YFVN V K + G N +P ++ + + V N I

Sbjct 4110 LGFGKVYFVNSVCSSTTLKMGCKMHGLANLIGDLPVEYIKGVMSETMATI-GVSSNHRFI 4286

Query 817 FPAYLGALLQATKAIHASYKNKPEFNSWKTSRCVVKDFLVVMLCWPQVIGGPGSLPLQTF 876

 + +L + + S K + KD +V+ML +P GG LP F

Sbjct 4287 YILWLVVVQFYLENSLGSLFQK-----------MSKDQMVLMLLFPSNFGGIPVLPYIRF 4433

Query 877 LVRGENDMLSVSVSLMRYILFRGSQNELQSVVRILNQKIDDRQNFDTMLLGDPYAIPLST 936

 L +G++D+ +V +SL ++I +V +++ + + L +P+++PLST

Sbjct 4434 LAKGDSDLETVWISLYKHIQ-TCDLPIFHRLVYLMSVCLKCSTQYQG-LASNPFSLPLST 4607

Query 937 PPRPQSLLKQMMRKAMRRITKQTDVKQLLDKSISVSEL 974

 P ++L+ ++ + + + + +++ + ++L

Sbjct 4608 PSDGIAVLEGAIKSVLPGLVENIEFAKIIHAANLCAQL 4721

Machilis hrabei contig\_249695, whole genome shotgun sequence

Sequence ID: QVQU01249695.1Length: 8568Number of Matches: 2

Range 1: 3042 to 4706GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

182 bits(463) 7e-54 Compositional matrix adjust. 137/579(24%) 263/579(45%) 43/579(7%)

+3

Query 381 HYYKRHRKWPLCDMSPETPVRVARIILHN--LDPFSLETMRRYGGIPLEAYDYIQFRKLR 438

 ++ +H+ P + P T + ILHN + S + +Y + + ++ + +

Sbjct 3042 QFFIKHKV\*PPVFLDPGTSPGLTWCILHNKWISDRSYP-IHKYESLSVINFETVSLQPCS 3218

Query 439 EFEWLENFIPYIKDR----TISALRSDIMRVYFSETGETGRIPWQDTRLLLFYLMSPMSR 494

 F+++++ + +KD TIS L + + R ++ R LLF+LM+

Sbjct 3219 HFDYVDSQMLLLKDTALAFTISILENPELH---------ARPSLKERRTLLFFLMTQNPP 3371

Query 495 LNHVKYMHAYVAGQWEMIQDYLIIRIVPKEKEHKVEARGFGCKPYEDRARTIVQEYNTAG 554

 +YM +V + DY +I++ K ++ KVE + FG PY +RA+ V E N +

Sbjct 3372 AEVRRYMDQFVEKD-PLALDYFVIKLTQKARDLKVEGKLFGQSPYYERAKRCVAEKNVSR 3548

Query 555 ILHDYSSEHVMTLDELGLAKKLLAFRSMAKAYRGYRMLILSVDASAWNNAFRGEAIHPIM 614

 ++ Y+S MTL EL KK+ +A + ++ S+DA +NN FR PI

Sbjct 3549 LMKRYNSCQAMTLTELQKQKKMYIMSQLANKMKDSYVVHFSLDAEGFNNCFRRVLCEPIG 3728

Query 615 EETLDRFYDVDLWSKTQTAYERSFIYVPDVERMYSWDGQAGGIEGLNQ--YTWVYAYIHQ 672

 E DR + V+ +++ + +S + R Y+W GQ GGIEGL Q +TW+Y +

Sbjct 3729 REFFDRLFGVNHYARVMDIF\*QSLFCCDEFFR-YNWTGQKGGIEGLAQKFWTWIYEAVAS 3905

Query 673 MKVCLRDQPYPYYILCKGDDLRVAVLVAPDYLEAISIDALKVELLESVASIGRKFGHSIK 732

 L ++++ GDDLRV +++ + + + L E+ + + F ++K

Sbjct 3906 RIASLTGN--KFFVMVNGDDLRVTLIIPKETVSLAQLSDLITEIAHAFQAEYESFVFNVK 4079

Query 733 VEDSYASESYFAFSKDAYVEGAEQSQAMRKVQKCYGANNAFINILDEYVASAFSNAHSAS 792

 +E++YAS F K +V S ++ K +G N ++ EY+ S +

Sbjct 4080 LEETYASSVLLGFGKVYFVNSVCSSTTLKMGCKMHGLANLIGDLPVEYIKGVMSETMATI 4259

Query 793 KVAPSPVATYCVGVWWALVALLMDKR----YKELADWELVACMLVPNILGGFPIIYLHNM 848

 V+ + Y +W +V ++ +++++ ++V +L P+ GG P++

Sbjct 4260 GVSSNHRFIYI--LWLVVVQFYLENSLGSLFQKMSKDQMVLMLLFPSNFGGIPVLPYIRF 4433

Query 849 FTRAESDLLPPFLDLCRYAQ-------EHVPHLATILLRAWRQKLAPVHRCLSGLMMDIY 901

 + +SDL ++ L ++ Q + +L ++ L+ Q GL + +

Sbjct 4434 LAKGDSDLETVWISLYKHIQTCDLPIFHRLVYLMSVCLKCSTQ--------YQGLASNPF 4589

Query 902 SLPITKPSSATTILRREMSHMLQDRTQNEALQALFRAAS 940

 SLP++ PS +L + +L +N + AA+

Sbjct 4590 SLPLSTPSDGIAVLEGAIKSVLPGLVENIEFAKIIHAAN 4706

Range 2: 4724 to 5626GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #2

Score Expect Method Identities Positives Gaps

Frame

54.7 bits(130) 7e-54 Compositional matrix adjust. 75/328(23%) 133/328(40%) 50/328(15%)

+2

Query 947 LLLAYQEANVYNVKLMSALFDCLPEAIIRELVRKFESGKSIYLALH----RGRGFRRAQS 1002

 + A +++ K S LF+ P + EL KF +S++ L R RG R

Sbjct 4724 FIQALFSSHIIEAKAFSVLFETSPPGQVIELASKFTGTRSVFNLLQVKGRRHRGLR---- 4891

Query 1003 IVRQAYKADARMHQFRIELLT---RGVLKAVELLPADWAQRCPGEVCAEIRSQLWEKPII 1059

 ++++A K D + ++T R +++ ++ RCP + ++R LW+K +

Sbjct 4892 VLKRARKEDLAKLSYSARIITGELRNLVENRQITIILSRDRCPTLISEQLRDFLWQKRVK 5071

Query 1060 GVTQPPPQHQIYGGWVDSIEPTYYTLRNHFELWHTHPSGD------------RPHLLSVG 1107

 G T P ++D + RN ++ T SG +P +

Sbjct 5072 GFTYP--------CFLDQ-----FNFRNCRDMSFTGKSGGGFNHSTVLVAARKPGEIPCY 5212

Query 1108 EYTPF---VGSITGRGLSKPHVELKTQNIVSMKIHTLLDVYQWSRVCKSFEAHDMVGNLW 1164

 + PF GS T L K VE+ + ++ +L VY + F +V

Sbjct 5213 SHGPFPQYPGSHTDMKLIKSAVEIHGSSPGVGRVTKILQVYPF---MVRFGERALV---- 5371

Query 1165 QICESLIEDYTGRSIKA-FLPYAGDTFINKTIQHHLRAHNYRASIVPNTLMNIYTTMKGN 1223

 +ED TG IKA L A + ++ H + +++ + + PN L N T +K

Sbjct 5372 -YLNRSLEDITG--IKAELLTAASYRSSSGSVAHRVPLNHWSSMVGPNKLPNKTTYVKVI 5542

Query 1224 IYAHRIFKTSVDHYKMNYLQIMCHMISL 1251

 + R KT + Y +N+ I ++L

Sbjct 5543 MTTDRKLKTIIADYPLNFNYIKTLFMAL 5626

endogenous nyamivirus glycoproteins in Machilis

Machilis hrabei contig\_332204, whole genome shotgun sequence

Sequence ID: QVQU01332204.1Length: 9701Number of Matches: 4

Range 1: 2124 to 2891GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

124 bits(312) 9e-40 Compositional matrix adjust. 78/270(29%) 136/270(50%) 21/270(7%)

+3

Query 370 QSPGYTATVRGEVIHVGKCQPVHVNYTSSIDKCYNELPVTYDGNLAFMLPRTRILSKIGT 429

 ++PGYTA GEV+H+ KC P V + +CY+E+PV Y F+ P++R + K GT

Sbjct 2124 ETPGYTAITLGEVVHLAKCAPEEV-IMRNT\*QCYHEIPVLYQNQSVFLTPKSRPIQKHGT 2300

Query 430 EVDCSGLINIMYKLTDSWYSVSRDLIHTHK-PEIISITPNDI--WEFKMISGLAESGIYS 486

 ++DC L+N ++L WY++ H P I +TP+ + W+ + LA GIY+

Sbjct 2301 QIDCDNLVNAQFRLDGQWYAIGNS---KHPVPPPIELTPDPV\*HWKGYSFAELARYGIYT 2471

Query 487 QRDLDQVQKILMNPVEKEILSSRILRTLDGASSLPTGYSLYNTFTPQDLERLTKNTVSTF 546

 + +++++ +MNP E+ +++ + R + GA G SL + E + K+

Sbjct 2472 FDEPERLREWIMNPYERGAIANILTRGVTGAHV\*TQGISLSSLVD----EHMIKSMGERI 2639

Query 547 FMVFYGKMTTIGNFFSFLLALFMILRFIKFILNSIINWTYLYRTVGLSWKLIFCWWENLV 606

 + GN S + L+ ILR +KF+ +++ + +Y G S L+ W+ +

Sbjct 2640 M\*KIRSWTSVFGNISSGFIGLYFILRLVKFLXDTLFHCRAIYEVYGFSAALLGRAWDKVT 2819

Query 607 HHWVRDSKTQSTKQTD----QELVHIEVPI 632

 + QS K D +E +IE+PI

Sbjct 2820 ------TCIQSRKSRDCTPVKEKPYIELPI 2891

Range 2: 1864 to 2127GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #2

Score Expect Method Identities Positives Gaps

Frame

63.9 bits(154) 9e-40 Compositional matrix adjust. 34/90(38%) 53/90(58%) 2/90(2%)

+1

Query 281 TEHPKLSIIEEQQNLGFNLKPDKTLFNKEVNLMTYFNSKLLYIMKHTKDQVDSLYQKISH 340

 TEHPKL II + GF +L ++LM Y N+K +YI K +S+YQ+++

Sbjct 1864 TEHPKLVIIPDA-GTGFYFT-RHSLHPGTMDLMAYVNAKFVYIEKRRSRSAESMYQELAT 2037

Query 341 DRCNSETRIVNSMMTLALISPLEFAYEYFQ 370

 RC E R + +++++A +SP EFAY Y +

Sbjct 2038 QRCMIERRSLMNLLSMASVSPTEFAYIYMK 2127

Range 3: 3921 to 4724GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #3

Score Expect Method Identities Positives Gaps

Frame

152 bits(383) 2e-36 Compositional matrix adjust. 86/275(31%) 150/275(54%) 11/275(4%)

+3

Query 228 QEYTVLFEGACTKIIETKD-GFSITSYLMNIDDYDFQITRRDKQIRLCGQLGWATEHPKL 286

 +++ V +EG K ++ + S T Y+++ + F + R + C TEHPKL

Sbjct 3921 RKHLV\*YEGVAQKFLQLDEYNVSTTVYMVDSGERVFGL-RTTGYSKGCMFKALYTEHPKL 4097

Query 287 SIIEEQQNLGFNLKPDKTLFNKEVNLMTYFNSKLLYIMKHTKDQVDSLYQKISHDRCNSE 346

 II + + +L ++LM Y N+ +YI K +S+YQ+++ RC E

Sbjct 4098 VIIPNAGTXFYFTR--YSLHPGTMDLMAYVNATFVYIEKRRSRSAESMYQELATQRCMIE 4271

Query 347 TRIVNSMMTLALISPLEFAYEYFQSPGYTATVRGEVIHVGKCQPVHVNYTSSIDKCYNEL 406

 R + +++++A +SP EFAY Y +P YTA GEV+H+ KC PV V + ++CY+E+

Sbjct 4272 RRSLMNLLSMASVSPTEFAYTYMNAPAYTAITLGEVLHLAKCAPVDV-IMHNTEQCYHEI 4448

Query 407 PVTYDGNLAFMLPRTRILSKIGTEVDCSGLINIMYKLTDSWYSVSRDLIHTHK-PEIISI 465

 V Y F+ P++R++ K GT++DC L+N Y+L WY++ H P I +

Sbjct 4449 SVMYQNQPVFLTPKSRLIQKHGTQIDCDNLVNAQYRLDGQWYAIGNS---KHPVPPPIEL 4619

Query 466 TPNDI--WEFKMISGLAESGIYSQRDLDQVQKILM 498

 TP+ + W+ + LA SGIY+ + +++++ +M

Sbjct 4620 TPDPVRHWKGYSFAELARSGIYTFDETERLREQIM 4724

Range 4: 3310 to 3555GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #4

Score Expect Method Identities Positives Gaps

Frame

35.8 bits(81) 4.5 Compositional matrix adjust. 28/85(33%) 40/85(47%) 5/85(5%)

+1

Query 3 ILKLLFNYILFVHYSYALIAFDCESKISERRTFSLVETNPCIPIVHNITTSIEKIQVVQP 62

 +LK L I VH+ Y+L+ FDC + T +L + PC EK+Q+VQ

Sbjct 3310 MLKFLV-LICLVHHGYSLLGFDCFHPMVNVSTXALDKVPPCHVEDPMSQAKSEKVQLVQ- 3483

Query 63 RVFDK--LEYIQCMITISHQIFRCG 85

 + DK + QC IS + CG

Sbjct 3484 -LADKYPVHVYQCKTVISRIVTNCG 3555

DownloadGenBankGraphics Sort by: NextPreviousDescriptions

Machilis hrabei contig\_21209, whole genome shotgun sequence

Sequence ID: QVQU01021209.1Length: 2112Number of Matches: 2

Range 1: 34 to 1188GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

124 bits(310) 9e-28 Compositional matrix adjust. 113/411(27%) 179/411(43%) 40/411(9%)

-1

Query 11 ILFVHYSYALIAFDC------ESKISERRTFSLVETNPCIPIVHNITTSIEKIQVVQPRV 64

 I VHYS LI FDC S I+ R S +P P E+IQ+VQ

Sbjct 1188 IGLVHYSQCLIGFDCFHPMVNVSTIAHDRVPSCHLDDPPSP------AKCERIQLVQLAD 1027

Query 65 FDKLEYIQCMITISHQIFRCGKTIDTFQAGGIYSEVVE------VSRSQCEDLHKLRTFN 118

 + QC I +S + CG + ++ + VS E LH++

Sbjct 1026 NYPVHVYQCKIVVSRLVTHCGMHSHSSAVDWWVHDIYQAH\*QERVS\*YARETLHEI---- 859

Query 119 YFGVQIKLEKGNSVTKLSTETFGSIDSDGSCTPGNGQLHANN-RVYSRAVRTSNIEITLI 177

 G+ N+ + G+I G CT G +++ + V +I TL

Sbjct 858 LLGI-------NTSRSVPMTLGGNISISGGCT---GTSYSDVFGSWEYVVVQGSITKTLK 709

Query 178 KSLGTIDIDEKKFILEDTTKCRYEDFECFSVNNGYSYWEEANDKIHCPESQEYTVLFEGA 237

 D D L C +C Y+ WE +++ C +++++ VL+EG

Sbjct 708 DYTALADTDRDIINLXSGVTCPASRGDCMDTEVXYTMWE-SSEVTRC-DARKHVVLYEGV 535

Query 238 CTKIIETKD-GFSITSYLMNIDDYDFQITRRDKQIRLCGQLGWATEHPKLSIIEEQQNLG 296

 K + + S T Y+++ + F + R ++C TEHPKL II + G

Sbjct 534 SQKFNQLDEYNVSTTVYMVDSGERVFGL-RTTGYYKICMFKALHTEHPKLVIIPDA-GTG 361

Query 297 FNLKPDKTLFNKEVNLMTYFNSKLLYIMKHTKDQVDSLYQKISHDRCNSETRIVNSMMTL 356

 F +L + LM Y N+K +Y+ K +Y++++ RC E R + +++T+

Sbjct 360 FYFT-RHSLHPGTMXLMAYVNAKFVYVEKRRARTTKLMYRELATQRCMIERRSLMNLLTM 184

Query 357 ALISPLEFAYEYFQSPGYTATVRGEVIHVGKCQPVHVNYTSSIDKCYNELP 407

 A ISP EF Y Y +PGYTA GEV+++ KC V V S+ +CY+E+P

Sbjct 183 ASISPTEFPYTYMNAPGYTAVTLGEVVNLAKCTSVDVQ-VSNTGQCYHEIP 34

Range 2: 1671 to 1943GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #2

Score Expect Method Identities Positives Gaps

Frame

37.7 bits(86) 0.88 Compositional matrix adjust. 28/94(30%) 47/94(50%) 6/94(6%)

-2

Query 436 LINIMYKLTDSWYSVSRDLIHTHK-PEIISITPNDIWEFKMIS--GLAESGIYSQRDLDQ 492

 L+N ++L WY V H P I +TP+ + K S LA SGIY+ + ++

Sbjct 1943 LVNAQFRLEGQWYDVGXS---KHPVPAPIELTPDPVRV\*KGYSFAELARSGIYTFDETER 1773

Query 493 VQKILMNPVEKEILSSRILRTLDGASSLPTGYSL 526

 +++ MNP E+ +++ + R + A G SL

Sbjct 1772 LRERFMNPYERGTIANILTRGVT\*AHVQIPGISL 1671

DownloadGenBankGraphics Sort by: NextPreviousDescriptions

Machilis hrabei contig\_107066, whole genome shotgun sequence

Sequence ID: QVQU01107066.1Length: 2757Number of Matches: 2

Range 1: 1351 to 1941GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

93.6 bits(231) 5e-18 Compositional matrix adjust. 63/211(30%) 101/211(47%) 15/211(7%)

+1

Query 198 CRYEDFECFSVNNGYSYWEEANDKIHCPESQEYTVLFEGACTKIIET-KDGFSITSYLMN 256

 C +C GY+ WE + + C + +++ VL+EG + ++ S T Y+++

Sbjct 1351 CPASRGDCMDTEVGYTMWE-STEMTRC-DQRKHMVLYEGVAQMFAQLDENNVSSTVYMVD 1524

Query 257 IDDYDFQITRRDKQIRLCGQLGWATEHPKLSIIEEQQNLGFNLKPDKTLFNKEVNLMTYF 316

 ++ F + R + C W TEHPKL II + GF + +L LM Y

Sbjct 1525 SEEMVF\*L-RTTGYYKGCMFKAWHTEHPKLVIIPDA-GTGFYFR-RHSLHPGTXXLMAYV 1695

Query 317 NSKLLYIMKHTKDQVDSLYQKISHDRCNSETRIVNSMMTLALISPLEFAYEYFQSPGYTA 376

 N+K +Y+ K ++ + C E R + +++T+ ISP EFAY Y +PGYTA

Sbjct 1696 NAKFVYVEKRSR---------TTDLMCMIERRSLMNLLTMPSISPTEFAYMYMNAPGYTA 1848

Query 377 TVRGEVIHVGKCQPVHVNYTSSIDKCYNELP 407

 GE +H+ KC PV V + + Y P

Sbjct 1849 ITLGEGVHLAKCAPVVVQVNNQLYILYTGCP 1941

Range 2: 794 to 1075GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #2

Score Expect Method Identities Positives Gaps

Frame

35.4 bits(80) 5.0 Compositional matrix adjust. 27/99(27%) 45/99(45%) 11/99(11%)

+2

Query 14 VHYSYALIAFDCESKISERRTFSLVETNPCIPIVHNITTSI-----EKIQVVQPRVFDKL 68

 VHY++ LI FDC + T +L PC ++ I EKIQ+VQ +

Sbjct 794 VHYAHCLIGFDCFHPMVNVSTIALDRVPPC-----HVDEPIGPAKSEKIQLVQLADKYPV 958

Query 69 EYIQCMITISHQIFRCG-KTIDTFQAGGIYSEVVEVSRS 106

 QC +S + +CG + + GG + + +S++

Sbjct 959 HVYQCKFVVSRIVTQCGMHSHSSAVTGGYMTYIRPISKT 1075

endogenous mononegaviruses in Machilis

Machilis hrabei contig\_67087, whole genome shotgun sequence

Sequence ID: QVQU01067087.1Length: 8449Number of Matches: 1

Range 1: 2674 to 3882GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

159 bits(401) 6e-37 Compositional matrix adjust. 113/406(28%) 191/406(47%) 12/406(2%)

-2

Query 582 INLDLSKWNSSYRHALVTRFGKTLDQLFGLKNFYEYNHIWFLKANVFTNSRLHPPDYDIF 641

 IN+D KWN +R+ + LD LFG KN Y+ H NVF N + PP+ D

Sbjct 3882 INMDFKKWNMHFRNKACQPTFQCLDDLFGFKNVYQATHQLLTDCNVFLNCQTCPPETDRE 3703

Query 642 TKLPIPGDYYYNNHKGGMEGMRQKLWTIITIAIIKYSAETLNLRITVIGQGDNQVVLIKY 701

 P+ GDY++ N GG EG+R K W+++T I + L +++G GDNQVV ++

Sbjct 3702 GN-PLRGDYFHRNQLGGFEGLRHKGWSLVTTLTIMITLRQLCYLGSMMGAGDNQVVCLRI 3526

Query 702 ----REDQIDKKSELRN---RFLQLLKTNFLAVNLKLKLSETWISKNLFEYGKVRYYKGE 754

 + +KK +R+ +FL L+ +F + LK E+W S L Y K +

Sbjct 3525 PIPDGLSEEEKKQLVRDTVDKFLTKLQEDFRLMGHTLKTQESWASSCLIAYNKKFFLNAT 3346

Query 755 AISQTTKKISRLIPDINDGISSFMSSLSTINTITESAAKMDHCPDSCFLINSISILNYLM 814

 + K+ R+ PD+ND + + ++ + T E+ AK D S F + + ++NY

Sbjct 3345 PQCTSYKRACRISPDLNDSFPTVNAEITCVATAAEATAKEDFNQISAFSLFCLELVNYFF 3166

Query 815 RRKIIHQDTPSPVCFMYLC-YPSDFGGISLSHYFSHYVRGHEDKVTMWLAYYNHLRLYYP 873

 RR I + S LC + FGG+ ++ + +RGH D++T L H++ P

Sbjct 3165 RRDIFQIASRSEAEATALCLWNKTFGGLPITSLLNCTIRGHPDRLTQQLGLLFHIQRQDP 2986

Query 874 MNFEYLAHIINLIPSGKKNINRLIEDIYCLDVITLPSIEALFKEKALDYLKSDEVTNPE- 932

 F+ L + + + L++ + ++++ E+L +K + + +VT E

Sbjct 2985 EVFDILKRLCSYKTPRIPSYRALVQYPHSINIMVPRDPESLVNDKI--HERMIQVTKNEY 2812

Query 933 IKKLFDSNQCISQQELIDQLKTMKPMFLPLAHEILRHSNAGILIAF 978

 IK L S LI+ + +P + E+ SN GI + +

Sbjct 2811 IKTLIASASEQQVNTLIEDIIRTRPYHARMGCELFGLSNPGIFLEY 2674

DownloadGenBankGraphics Sort by: NextPreviousDescriptions

Machilis hrabei contig\_38110, whole genome shotgun sequence

Sequence ID: QVQU01038110.1Length: 10736Number of Matches: 2

Range 1: 3562 to 5118GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

140 bits(353) 3e-31 Compositional matrix adjust. 144/531(27%) 227/531(42%) 54/531(10%)

+1

Query 371 RDFCQNYFKKHRRWP--NMKSYPAD--FGNFISKNLVMPKSFSN--RWNLWSKIKFDKCF 424

 R C Y K RWP + P + ++I + V ++ +W ++ IK K

Sbjct 3562 RILCLAYISKPGRWPPCDTSKMPDNSVLKSWIDHSNVNIDEYAEGYQWEDFAYIKHMKWL 3741

Query 425 EYDYSVDTTELLKDTASAPPFSEWFLAYDHCAFKHlhnknkpflpknkkptplRIIS--- 481

 E+D +VD TELL D ++ P S++ + YD + +P + L S

Sbjct 3742 EFDATVDYTELLNDKSATPTRSKFDVVYDSDLLGYQPTALRPSEDRRLLVNLLNRSSFNP 3921

Query 482 -RFLQGIPNEVEKKVFECTELYWHIDDSTAVVCLKEREIKND-GRLFVKQTYEQRLGQVS 539

 LQ I K ++C ++ KERE K + RLF T E +

Sbjct 3922 EETLQKIQTRQVPKEWKCVGVH-----------PKEREEKGEKPRLFALLTPEIQYYFCV 4068

Query 540 SEMNIANTIFRYIPDQTMTDSEVILAQKISSAVKNQNQDYE----LINLDLSKWNSSYRH 595

 +E NIA +F + QTMT SE L + + ++LD +WN ++

Sbjct 4069 TEKNIAQQLFE\*VEHQTMT\*SESSLLHRTLDTTQEHATPGAPIKIFVSLDFQRWNLTWDF 4248

Query 596 ALVTRFGKTLDQLFGLKNFYEYNHIWFLKANVFTNSRLHPPDYDIFTKL----PIPGDYY 651

 + + +D +FG Y Y H +F + + +SRL+PP L IPG +

Sbjct 4249 SGTFATFEMVDDIFGTPGLYTYTHEFFSECLCYLSSRLNPPPGLAKGHLGDPPEIPGYLW 4428

Query 652 YNNHKGGMEGMRQKLWTIITIAIIKYSAETLNLRITVIGQGDNQVVLI------KYREDQ 705

 YN+H GG EG QKLWT +T ++ A L LR + GDNQ+ I K R Q

Sbjct 4429 YNHH-GGFEGQHQKLWTFLTNGLVLSVAVELKLRCILNSCGDNQLAKILIPNSTKDRTPQ 4605

Query 706 ID------KKSELRNRFLQLLKTNFLAVNLKLKLSETWISKNLFEYGKVRYYKGEAISQT 759

 D K ++L R + LL+ + LK T++S ++ Y K +G T

Sbjct 4606 EDISCRREKINQLCKRIIHLLQERAAGIEQTLKAEATFLSDTVYIYEKEVVIRGAVAPST 4785

Query 760 TKKISRLIPDINDGISSFMSSLSTINTITESAAKMDHCPDSCFLINSISILNYL------ 813

 +K SR++ D + I SF + ++TI+T +AA + +L ++I L

Sbjct 4786 LRKASRIMEDTSGTIKSFDNIVATIHTGGHAAALKGNS\*VVAYLHSAIETFRTLYHDIMT 4965

Query 814 MRRKII-----HQDTPSPVCFMYLCYPSDFGGISLSHYFSHYVRGHEDKVT 859

 K+I +Q V + PS FGG+ + + RGH + +T

Sbjct 4966 THGKVIGLTLKNQQEVVDVVKILCLLPSCFGGVPSLPWTDYVFRGHPEPLT 5118

Range 2: 6045 to 6236GenBankGraphicsNext MatchPrevious MatchFirst Match

Alignment statistics for match #2

Score Expect Method Identities Positives Gaps

Frame

40.0 bits(92) 0.78 Compositional matrix adjust. 22/64(34%) 34/64(53%) 0/64(0%)

+3

Query 1184 GGNMVHRFRAAIERNSAVINSLPTTGSHFRQTTNMLSAITKGGRDWTIHFQLVFLFNVSV 1243

 GG+++HRF +SAVINS PT ++ T+ S ++ + IHFQ + L V

Sbjct 6045 GGSVLHRFMDVTTSHSAVINSNPTLHTNLNIHTDCFSPYSQSEVHYNIHFQGLVLQAAGV 6224

Query 1244 ISRL 1247

 + L

Sbjct 6225 VRAL 6236

DownloadGenBankGraphics NextPreviousDescriptions

Machilis hrabei contig\_83516, whole genome shotgun sequence

Sequence ID: QVQU01083516.1Length: 7956Number of Matches: 1

Range 1: 2211 to 4205GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

128 bits(322) 1e-27 Compositional matrix adjust. 165/701(24%) 288/701(41%) 78/701(11%)

+3

Query 619 HIWFLKANVFTNSRLHPP---DYDIFTKLP-IPGDYYYNNHKGGMEGMRQKLWTIITIAI 674

 H +F + +SRL+PP D P +PG +YN HKGG EG RQKLWT +T +

Sbjct 2211 HEFFAVCLCYLSSRLNPPPGLSKDHAGNPPDVPGHLWYN-HKGGFEGQRQKLWTFLTNGL 2387

Query 675 IKYSAETLNLRITVIGQGDNQVVLIKYREDQIDK--KSELRNR----------FLQLLKT 722

 + A L L+ + GDNQ+ I D+ + +L R +QLL+

Sbjct 2388 VLSVAIELKLKCLLNRCGDNQLATILIPNSTTDRTPQEDLSCRREEINLLCE\*IIQLLQE 2567

Query 723 NFLAVNLKLKLSETWISKNLFEYGKVRYYKGEAISQTTKKISRLIPDINDGISSFMSSLS 782

 LK ET++S ++ Y K +G T +K SR++ D + + SF + ++

Sbjct 2568 RAAGTGQTLKAEETFLSDTVYIYAKEVVIRGTVAPSTLRKASRIMEDTSGTVKSFDNIVA 2747

Query 783 TINTITESAAKMDHCPDSCFLINSISILNYLMRRKIIHQDTPSPVCFM------------ 830

 TI+T +AA H + + I R + H PS M

Sbjct 2748 TIHTGGHTAALKGHSWMVAYFHSVIETF-----RALYHDIMPSRGKVMGLTLKTQQEVLE 2912

Query 831 ---YLC-YPSDFGGISLSHYFSHYVRGHEDKVT---MWLAYYNHLRLYYPMNFEYLAHII 883

 LC PS FGG+ + + VRGH D +T + L +H +N+ Y +

Sbjct 2913 VVKILCQLPSCFGGLPSLPWTDYVVRGHPDPLTSGILALTLIDHRISRLILNYIYSLLLE 3092

Query 884 NLIPSGKKNINRLIEDIYCLDVITLPSIEALFKEKALDYLKSDEVTNPEIKKLFDSNQCI 943

 P +N L+ED LD+ ++ +++ +L S NP++K+LF S

Sbjct 3093 KRNPRSLP-LN-LVEDPASLDIPGKGKTASVVRQQLEKHLPS-YTRNPDLKQLFKSAP-- 3257

Query 944 SQQELIDQLKTMKPMFLPLAHEILRHSNAGILIAFRNKLSNIATINKIIQSSEENSYLEL 1003

 + + + KP L + + + S G F +N+ ++K++++ E +

Sbjct 3258 -----LSEDRQWKPRVL---NAMYKSSPHGARNNFVATFNNLNMVDKVMKTCEAGPIYSM 3413

Query 1004 MAVNNDAVREILISKARSRKRYSLRDSLIKENCPTQLAINIRNEHWNL--DLLGASKPVP 1061

 + + R ++ +R L C A+ +R L +LG + P P

Sbjct 3414 V---KEEERRRRVNLGVIVQRIFKAPKLPGHACGRIFAVGLRLHPSGLHEPILGVTVPHP 3584

Query 1062 HHQFTIKPLDECTQEEINMSILINTSREFAQSDLG---AYNQLGPFPIFHGAATKEKINK 1118

 + L E +L+ + +DL + GPF G+AT+EK +

Sbjct 3585 S-----EVLCRSDPEYFEFILLMCHGSQHKDTDLNIPLPFLNRGPFKPELGSATREKSSS 3749

Query 1119 PKMEMFTKSSYTKSLQQLFTIGTWIQKIQG--NNLMQLIENLILEKSSHIPEEFLDQELD 1176

 M +L I W+ N ++ ++ L+ S + L +++

Sbjct 3750 ELTNMEKGDRPLIEAFRLSKIKDWVSAPNSYVNKCIEYLQRLLTSADS-VVISLLAKKI- 3923

Query 1177 DWCVSTYGGNMVHRFRAAIERNSAVINSLPTTGSHFRQTTNMLSAITKGGRDWTIHFQLV 1236

 GG+++HRF +SAVINS P+ ++ T+ S ++ D+ IHFQ +

Sbjct 3924 ------VGGSVLHRFMDVTTSHSAVINSNPSLQTNLTIHTDCFSPYSQSEVDYNIHFQGL 4085

Query 1237 FLFNVSVISRLKRSIPLLYTQYAAYLSCNTCTQEVSNIVMD 1277

 L ++ R+ + +SC++C E+ + ++

Sbjct 4086 VLHAAGLV-RIMGLHGYDMSLNCFTISCSSCITELPEVKLN 4205

endogenous chuvirus glycoprotein

Catajapyx aquilonaris contig\_4110, whole genome shotgun sequence

Sequence ID: JYFJ02004110.1Length: 34860Number of Matches: 1

Range 1: 9458 to 10387GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Method Identities Positives Gaps

Frame

108 bits(269) 5e-23 Compositional matrix adjust. 90/321(28%) 151/321(47%) 15/321(4%)

-3

Query 102 EVSRSQCEDLHKLRTFNYFGVQIKLEKG-NSVTKLSTETFGSIDS-DGSCTPGNGQLHAN 159

 E +R +CE + + Y ++ N T S G DS G C+ G+ + +

Sbjct 10387 EHTRHECEMFTRTGVYRY\*TSLRPIDSPLNITTHASLVIVGHTDSASGECSGGDYNI--D 10214

Query 160 NRVYSRAVRTSNIEITLIKSLGTIDIDEKKFILEDTTKCRYEDFECFSVNNGYSYWEEAN 219

 VY V + I L TID + + +L +C Y+ C G ++W A

Sbjct 10213 GYVYKNVVVEVYLTIRLSDYWITIDRKKNEAVLPSGARCEYKKENCMDDFLG\*TFWT-AQ 10037

Query 220 DKIHCPESQEYTVLFEGACTKIIETKDGFSITSYLMNIDDYDFQITRRDKQIRLCGQLGW 279

 C + Q VL+EG ++I+ + G + + D F + D + +C Q +

Sbjct 10036 APTLC-DGQSIDVLYEGE-VRVIDPEKGRKVA--IGQDDGTAFAVEMGDGDV-MCNQHVF 9872

Query 280 ATEHPKLSIIEEQQNLGFNLKPDKTLFNKEVNLMTYF-NSKLLYIMKHTKDQVDSLYQKI 338

 EHP+L +I E N GF K +++ VN+ Y+ NSK +++ +H ++ +Y +

Sbjct 9871 RMEHPQLVLIPEGTN-GFIFK-KQSILTLNVNMAAYYYNSKFVFLEQHLGSEIGRMYGIM 9698

Query 339 SHDRCNSETRIVNSMMTLALISPLEFAYEYFQS-PGYTATVRGEVIHVGKCQPVHVNYTS 397

 +C + + ++ +LA I+P EFAY + PGYTA RGEV ++ KC+PV V+

Sbjct 9697 KKQQCQDRQQTLRTLQSLAYINPDEFAYALMSNEPGYTAFTRGEVCYIIKCKPVTVSLLK 9518

Query 398 SIDKCYNELPVTYDGNLAFML 418

 S + CY++L V N + L

Sbjct 9517 S-NSCYSDLQVRAADNSTWFL 9458