

Additional file1: Figure S4. Results of a BLAST search of RhEcR and RhUSP sequences against genomic sequences of six tick species. The query was RhEcR and RhUSP gene nucleotide sequences in a search against genomic sequences of six tick (*I. persulcatus*, *H. longicornis*, *D. silvarum*, *H. asiaticum*, *R. sanguineus*, *R. microplus* and *I. scapularis*).

Query= *Rhipicephalus haemaphysaloides*-USP1
(435 letters)

Database: 207,181 sequences; 67,334,884 total letters

Sequences producing significant alignments:	Score (bits)	E Value
Rsan-GWHPAMMM003339 mRNA=GWHTAMMM003339 Gene=GWHGAMMM003339 Posi...	875	0.0
Rmic-GWHPAMMN003175 mRNA=GWHTAMMN003175 Gene=GWHGAMMN003175 Posi...	860	0.0
Hasi-GWHPAMMK005031 mRNA=GWHTAMMK005031 Gene=GWHGAMMK005031 Posi...	843	0.0
Hlon-GWHPAMMI005778 mRNA=GWHTAMMI005778 Gene=GWHGAMMI005778 Posi...	812	0.0
Dsyl-GWHPAMML001919 mRNA=GWHTAMML001919 Gene=GWHGAMML001919 Posi...	778	0.0

>Rsan-GWHPAMMM003339 mRNA=GWHTAMMM003339 Gene=GWHGAMMM003339
Position=GWHAMMM00001245: 195109842-195110092,
195116716-195117383,
Length = 433

Score = 875 bits (2262), Expect = 0.0
Identities = 432/435 (99%), Positives = 432/435 (99%), Gaps = 2/435 (0%)

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Query: 1 MYKKERPKLSVTALLYGSAGPAASWPTRPLQPPDVSPPGIRAAPGLNGGASNGVSSSLPP 60
MYKKERPKLSVTALLYGSAGPAASWPTRPLQPPDVSPPGIRAAPGLNGG SNGVSSSLPP
Sbjct: 1 MYKKERPKLSVTALLYGSAGPAASWPTRPLQPPDVSPPGIRAAPGLNGGPSNGVSSSLPP 60

Query: 61 QPSFLLSGYGAPSASRSPLDGRQLNNGPPAAPQQQQAATRYPPNHPLSGSKHLCSICGDR 120
QPSFLLSGYGAPSASRSPLDGRQLNNGPPAAPQQQQAATRYPPNHPLSGSKHLCSICGDR
Sbjct: 61 QPSFLLSGYGAPSASRSPLDGRQLNNGPPAAPQQQQAATRYPPNHPLSGSKHLCSICGDR 120

Query: 121 ASGKHYGVYSCEGCKGFFKRTVRKDLTYACREERNNCVIDKRQRNRCQYCRYQKCLSCGMK 180
ASGKHYGV CEGCKGFFKRTVRKDLTYACREERNNCVIDKRQRNRCQYCRYQKCLSCGMK
Sbjct: 121 ASGKHYGV--CEGCKGFFKRTVRKDLTYACREERNNCVIDKRQRNRCQYCRYQKCLSCGMK 178

Query: 181 REAVQEERQRTKDRADSEVESTSGGAPPEMPLERILEAELRVEPHTGTLSENAQQQDPVS 240
REAVQEERQRTKDRADSEVESTSGGAPPEMPLERILEAELRVEPHTGTLSENAQQQDPVS
Sbjct: 179 REAVQEERQRTKDRADSEVESTSGGAPPEMPLERILEAELRVEPHTGTLSENAQQQDPVS 238

Query: 241 SICQAADRQLHQLVQWAKHIPHFEELPIEDRMVLLKAGWNELLIAAFSHRSIDVRDGIVL 300
SICQAADRQLHQLVQWAKHIPHFEELPIEDRMVLLKAGWNELLIAAFSHRSIDVRDGIVL
Sbjct: 239 SICQAADRQLHQLVQWAKHIPHFEELPIEDRMVLLKAGWNELLIAAFSHRSIDVRDGIVL 298

Query: 301 ATGLVVQRHSAHSAGVGAI FDRVLT ELVAKMREM KMDRTEL GCLRAVVL FNPEAKGLRST 360
ATGLVVQRHSAHSAGVGAI FDRVLT ELVAKMREM KMDRTEL GCLRAVVL FNPEAKGLRST
Sbjct: 299 ATGLVVQRHSAHSAGVGAI FDRVLT ELVAKMREM KMDRTEL GCLRAVVL FNPEAKGLRST 358

Query: 361 TQVEALREKVYAALEDHCRQQYPDQPGRFAKLLLRPALRSIGLKCLEHLFFFKLIGDTP 420
TQVEALREKVYAALEDHCRQQYPDQPGRFAKLLLRPALRSIGLKCLEHLFFFKLIGDTP
Sbjct: 359 TQVEALREKVYAALEDHCRQQYPDQPGRFAKLLLRPALRSIGLKCLEHLFFFKLIGDTP 418

Query: 421 IDNFLITMLETPSDA 435
IDNFLITMLETPSDA

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Sbjct: 419 IDNFLITMLETPSDA 433

>Rmic-GWHPAMMN003175 mRNA=GWHTAMMN003175 Gene=GWHGAMMN003175
Position=GWHAMMN00006827: 1460953-1460971,
1461723-1462224, 1467158-1467825,
Length = 479

Score = 860 bits (2221), Expect = 0.0
Identities = 426/435 (97%), Positives = 427/435 (98%), Gaps = 4/435 (0%)

Query: 1 MYKKERPKLSVTALLYGSAGPAASWPTRPLQPPDVSPPGIRAAPGLNGGASNGVSSSLPP 60
MYKKERPKLSVTALLYGSAGPAASWPTRPLQPPDVSPPGIR APGLNGG SNGVSSSLPP
Sbjct: 49 MYKKERPKLSVTALLYGSAGPAASWPTRPLQPPDVSPPGIRTAPGLNGGTSNGVSSSLPP 108

Query: 61 QPSFLLSGYGAPSASRSPLDGRQLNNGPPAAPQQQAATRYPPNHPLSGSKHLCSICGDR 120
QPSFLLSGYGAPSASRSPLDGRQLNNGPPAAPQQ AATRYPPNHPLSGSKHLCSICGDR
Sbjct: 109 QPSFLLSGYGAPSASRSPLDGRQLNNGPPAAPQQ - -AATRYPPNHPLSGSKHLCSICGDR 166

Query: 121 ASGKHYGVYSCEGCKGFFKRTVRKDLTYACREERNNCVIDKRQRNRCQYCRYQKCLSCGMK 180
ASGKHYGV CEGCKGFFKRTVRKDLTYACREERNNCVIDKRQRNRCQYCRYQKCLSCGMK
Sbjct: 167 ASGKHYGV - -CEGCKGFFKRTVRKDLTYACREERNNCVIDKRQRNRCQYCRYQKCLSCGMK 224

Query: 181 REAVQEERQRTKDRADSEVESTSGGAPPEMPLERILEAELRVEPHTGTLSENAQQQDPVS 240
REAVQEERQRTKDRADSEVESTSGGAPPEMPLERILEAELRVEPHTGTLSENAQQQDPVS
Sbjct: 225 REAVQEERQRTKDRADSEVESTSGGAPPEMPLERILEAELRVEPHTGTLSENAQQQDPVS 284

Query: 241 SICQAADRQLHQLVQWAKHIPHFEELPIEDRMVLLKAGWNELLIAAFSHRSIDVRDGIVL 300
SICQAADRQLHQLVQWAKHIPHFEELPIEDRMVLLKAGWNELLIAAFSHRSIDVRDGIVL
Sbjct: 285 SICQAADRQLHQLVQWAKHIPHFEELPIEDRMVLLKAGWNELLIAAFSHRSIDVRDGIVL 344

Query: 301 ATGLVVQRHSAHSAGVGAI FDRVLT ELVAKMREM KMDRTEL GCLRAV VLFNPEAKGLRST 360
ATGLVVQRHSAHSAGVGAI FDRVLT ELVAKMREM KMDRTEL GCLRAV VLFNPEAKGLRST
Sbjct: 345 ATGLVVQRHSAHSAGVGAI FDRVLT ELVAKMREM KMDRTEL GCLRAV VLFNPEAKGLRST 404

Query: 361 TQVEALREKVYAALEDHCRQQYPDQPGRFKLLLRLPALRSIGLKCLEHLFFFKLIGDTP 420
QVEALREKVYAALEDHCRQQYPDQPGRFKLLLRLPALRSIGLKCLEHLFFFKLIGDTP
Sbjct: 405 NQVEALREKVYAALEDHCRQQYPDQPGRFKLLLRLPALRSIGLKCLEHLFFFKLIGDTP 464

Query: 421 IDNFLITMLETPSDA 435
IDNFL+TMLET SDA
Sbjct: 465 IDNFLTMLETSSDA 479

Query= *Rhipicephalus haemaphysaloides-USP3*
(399 letters)

Sequences producing significant alignments:				Score	E
				(bits)	Value
Dsyl-GWHPAMML001919	mRNA=GWHTAMML001919	Gene=GWHGAMML001919	Posi...	790	0.0
Rsan-GWHPAMMM003339	mRNA=GWHTAMMM003339	Gene=GWHGAMMM003339	Posi...	789	0.0
Rmic-GWHPAMMN003175	mRNA=GWHTAMMN003175	Gene=GWHGAMMN003175	Posi...	775	0.0
Hasi-GWHPAMMK005031	mRNA=GWHTAMMK005031	Gene=GWHGAMMK005031	Posi...	763	0.0
Hlon-GWHPAMMI005778	mRNA=GWHTAMMI005778	Gene=GWHGAMMI005778	Posi...	733	0.0

>Dsyl-GWHPAMML001919 mRNA=GWHTAMML001919 Gene=GWHGAMML001919
Position=GWHAMML00001088: 95640361-95640379,
95641419-95641686, 95643882-95644549,
Length = 401

Score = 790 bits (2039), Expect = 0.0
Identities = 388/400 (97%), Positives = 393/400 (98%), Gaps = 2/400 (0%)

Query: 1 MATQERAPGLNGGASNGVSSSLPPQPSFLLSGYGAPSASRSPLDGRQLNNGPPAAPQQQQ 60
MATQERAPGLNGGASNGVSSSLPPQPSFLLSGYGAPSASRSPLDGRQLNNGPPA PQQQQ
Sbjct: 1 MATQERAPGLNGGASNGVSSSLPPQPSFLLSGYGAPSASRSPLDGRQLNNGPPATPQQQQ 60

Query: 61 A--ATRYPPNHPLSGSKHLCSICGDRASGKHYGVYSCEGCKGFFKRTVRKDLTYACREER 118
TRYPPNHPLSGSKHLCSICGDRASGKHYGVYSCEGCKGFFKRTVRKDLTYACREER
Sbjct: 61 QQQTTRYPPNHPLSGSKHLCSICGDRASGKHYGVYSCEGCKGFFKRTVRKDLTYACREER 120

Query: 119 NCVIDKRQRNRCQYCRYQKCLSCGMKREAVQEERQRTKDRADSEVESTSGGAPPEMPLE 178
NCVIDKRQRNRCQYCRYQKCLSCGMKREAVQEERQRTKDRADSEVESTSGGAPPEMPLE
Sbjct: 121 NCVIDKRQRNRCQYCRYQKCLSCGMKREAVQEERQRTKDRADSEVESTSGGAPPEMPLE 180

Query: 179 ILEAELRVEPHTGTLSENAQQQDPVSSICQAADRQLHQLVQWAKHIPHFEELPIEDRMVL 238
ILEAELRVEPHTGTLSE+AQQQDPVSSICQAADRQLHQLVQWAKHIPHFEELP+EDRMVL
Sbjct: 181 ILEAELRVEPHTGTLSESAQQQDPVSSICQAADRQLHQLVQWAKHIPHFEELPLEDRMVL 240

Query: 239 LKAGWNELLIAAFSHRSIDVRDGI VLATGLVVQRHSAHSAGVGAI FDRVL TELVAKMREM 298
LKAGWNELLIAAFSHRSIDVRDGI VLATGLVVQRHSAHSAGVGAI FDRVL TELVAKMREM
Sbjct: 241 LKAGWNELLIAAFSHRSIDVRDGI VLATGLVVQRHSAHSAGVGAI FDRVL TELVAKMREM 300

Query: 299 KMDRTELGCLRAVVL FNPEAKGLRSTTQVEALREKVYAALEDHCRQQYPDQPGRFAKLLL 358
KMDRTELGCLRAVVL FNPEAKGLRST QVEALREKVYAALE+HCRQQYPDQPGRFAKLLL
Sbjct: 301 KMDRTELGCLRAVVL FNPEAKGLRSTAQVEALREKVYAALEEHCRQQYPDQPGRFAKLLL 360

Query: 359 RLPALRSIGLKCLEHLFFFKLIGDTPIDNFLITMLETPSD 398
RLPALRSIGLKCLEHLFFFKLIGDTPIDNFL++MLE PSD
Sbjct: 361 RLPALRSIGLKCLEHLFFFKLIGDTPIDNFLLSMLEAPSD 400

>Rsan-GWHPAMMM003339 mRNA=GWHTAMMM003339 Gene=GWHGAMMM003339
Position=GWHAMMM00001245: 195109842-195110092,
195116716-195117383,
Length = 433

Score = 789 bits (2038), Expect = 0.0
Identities = 390/393 (99%), Positives = 390/393 (99%), Gaps = 2/393 (0%)

Query: 7 APGLNGGASNGVSSSLPPQPSFLLSGYGAPSASRSPLDGRQLNNGPPAAPQQQQAATRY 66
APGLNGG SNGVSSSLPPQPSFLLSGYGAPSASRSPLDGRQLNNGPPAAPQQQQAATRY
Sbjct: 43 APGLNGGPSNGVSSSLPPQPSFLLSGYGAPSASRSPLDGRQLNNGPPAAPQQQQAATRY 102

Query: 67 PNHPLSGSKHLCSICGDRASGKHYGVYSCEGCKGFFKRTVRKDLTYACREERNVIDKRQ 126
PNHPLSGSKHLCSICGDRASGKHYGV CEGCKGFFKRTVRKDLTYACREERNVIDKRQ
Sbjct: 103 PNHPLSGSKHLCSICGDRASGKHYGV--CEGCKGFFKRTVRKDLTYACREERNVIDKRQ 160

Query: 127 RNRCQYCRYQKCLSCGMKREAVQEERQRTKDRADSEVESTSGGAPPEMPLEILEAELRV 186
RNRCQYCRYQKCLSCGMKREAVQEERQRTKDRADSEVESTSGGAPPEMPLEILEAELRV
Sbjct: 161 RNRCQYCRYQKCLSCGMKREAVQEERQRTKDRADSEVESTSGGAPPEMPLEILEAELRV 220

Query: 187 EPHTGTLSENAQQQDPVSSICQAADRQLHQLVQWAKHIPHFEELPIEDRMVLLKAGWNE 246

EPHTGTLSENAQQQDPVSSICQAADRQLHQLVQWAKHIPHFEELPIEDRMVLLKAGWNEL
 Sbjct: 221 EPHTGTLSENAQQQDPVSSICQAADRQLHQLVQWAKHIPHFEELPIEDRMVLLKAGWNEL 280
 Query: 247 LIAAFSHRSIDVRDGIVLATGLVVQRHSAHSAGVGAIIFDRVLTTELVAKMREMKMDRTELG 306
 LIAAFSHRSIDVRDGIVLATGLVVQRHSAHSAGVGAIIFDRVLTTELVAKMREMKMDRTELG
 Sbjct: 281 LIAAFSHRSIDVRDGIVLATGLVVQRHSAHSAGVGAIIFDRVLTTELVAKMREMKMDRTELG 340
 Query: 307 CLRAVVLNPEAKGLRSTTQVEALREKVYAALEDHCRQQYPDQPGRFAKLLLRPALRSI 366
 CLRAVVLNPEAKGLRSTTQVEALREKVYAALEDHCRQQYPDQPGRFAKLLLRPALRSI
 Sbjct: 341 CLRAVVLNPEAKGLRSTTQVEALREKVYAALEDHCRQQYPDQPGRFAKLLLRPALRSI 400
 Query: 367 GLKCLEHLFFFKLIGDTPIDNFLITMLETPSDA 399
 GLKCLEHLFFFKLIGDTPIDNFLITMLETPSDA
 Sbjct: 401 GLKCLEHLFFFKLIGDTPIDNFLITMLETPSDA 433

Query= *Rhipicephalus haemaphysaloides*-EcR1
 (559 letters)

Sequences producing significant alignments:	Score (bits)	E Value
Dsyl-GWHPAMML010889 mRNA=GWHTAMML010889 Gene=GWHGAMML010889 Posi...	1117	0.0
Hasi-GWHPAMMK012598 mRNA=GWHTAMMK012598 Gene=GWHGAMMK012598 Posi...	845	0.0
Hlon-GWHPAMMI014869 mRNA=GWHTAMMI014869 Gene=GWHGAMMI014869 Posi...	817	0.0
Rmic-GWHPAMMN007750 mRNA=GWHTAMMN007750 Gene=GWHGAMMN007750 Posi...	815	0.0
Ipers-GWHPAMMH024910.1 mRNA=GWHTAMMH024910.1 Gene=GWHGAMMH024910...	789	0.0

>Dsyl-GWHPAMML010889 mRNA=GWHTAMML010889 Gene=GWHGAMML010889
 Position=GWHAMML00001091: 197274423-197274459,
 197279342-197279580, 197280626-197280860,
 197336936-197337259, 197339173-197339498,
 197340861-197341016, 197341809-197342031,
 Length = 593

Score = 1117 bits (2890), Expect = 0.0
 Identities = 555/561 (98%), Positives = 556/561 (99%), Gaps = 3/561 (0%)

Query: 1 MLSELQLQLGRRSAAAAAAPSSDEVASMKPMMLQAAQGAGGLAAGSPPALSPNLPSVVK 60
 MLSELQLQLGRRSAAAAA PSSDEVASMKPMMLQAAQGAGGLAAGSPPALSPNLPSVVK
 Sbjct: 34 MLSELQLQLGRRSAAAAA-PSSDEVASMKPMMLQAAQGAGGLAAGSPPALSPNLPSVVK 92
 Query: 61 VEPRLPSPCVGGAASDG--VPQKRVRQDDAGAWISSPSSQMSVGSLSPPPPLLNGLANSS 118
 VEPRLPSPCVGGAASDG P KRVQRQDDAGAWISSPSSQMSVGSLSPPPPLLNGLANSS
 Sbjct: 93 VEPRLPSPCVGGAASDGGPAPSKRVRQDDAGAWISSPSSQMSVGSLSPPPPLLNGLANSS 152
 Query: 119 GLSPVSCSSYETYSRGPCKEEMSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQQEELCLV 178
 GLSPVSCSSYETYSRGPCKEEMSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQQEELCLV
 Sbjct: 153 GLSPVSCSSYETYSRGPCKEEMSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQQEELCLV 212
 Query: 179 CGDRASGYHYNALTCEGCKGFFRRSITKNAVYQCKYGNNCIDMYMRRKCQECRLKKCLS 238
 CGDRASGYHYNALTCEGCKGFFRRSITKNAVYQCKYGNNCIDMYMRRKCQECRLKKCLS
 Sbjct: 213 CGDRASGYHYNALTCEGCKGFFRRSITKNAVYQCKYGNNCIDMYMRRKCQECRLKKCLS 272
 Query: 239 VGMRPECVVPEYQCAIKRESKKHQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGG 298
 VGMRPECVVPEYQCAIKRESKKHQKDRPNSTTRESPSGLMAPSS+GGGVSPSSQPLGGGG
 Sbjct: 273 VGMRPECVVPEYQCAIKRESKKHQKDRPNSTTRESPSGLMAPSSVGGGVSPSSQPLGGGG 332

Query: 299 SSLGNSNSHEEDKKPLVLSPGVKPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTTFPLG 358
 SSLGNSNSHEEDKKPLVLSPGVKPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTTFPLG
 Sbjct: 333 SSLGNSNSHEEDKKPLVLSPGVKPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTTFPLG 392

Query: 359 DSEEDNQRRFQHTEITILTVQLIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGAR 418
 DSEEDNQRRFQHTEITILTVQLIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGAR
 Sbjct: 393 DSEEDNQRRFQHTEITILTVQLIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGAR 452

Query: 419 KYDVKTDSIVFANNQPYTRDNYRSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIF 478
 KYDVKTDSIVFANNQPYTRDNYRSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIF
 Sbjct: 453 KYDVKTDSIVFANNQPYTRDNYRSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIF 512

Query: 479 SERPALVDPCKVERIQEYYIETLRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCF 538
 SERPALVDPCKVERIQEYYIETLRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCF
 Sbjct: 513 SERPALVDPCKVERIQEYYIETLRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCF 572

Query: 539 SLKVQNKKLPPFLAEIWDIQE 559
 SLKVQNKKLPPFLAEIWDIQE
 Sbjct: 573 SLKVQNKKLPPFLAEIWDIQE 593

>Hasi-GWHPAMMK012598 mRNA=GWHTAMMK012598 Gene=GWHGAMMK012598
 Position=GWHAMMK00000151: 115710724-115710965,
 115712102-115712324, 115713112-115713267,
 115715373-115715698,
 Length = 419

Score = 845 bits (2182), Expect = 0.0
 Identities = 411/419 (98%), Positives = 416/419 (99%)

Query: 141 MSPSSGGGGMNGYFVDSFGDPKPKKKGAPRQQEELCLVCGDRASGYHYNALTCEGCKGFF 200
 MSPSSGGGGMNGYFVDSFGDPKPKKKGAPRQQEELCLVCGDRASGYHYNALTCEGCKGFF
 Sbjct: 1 MSPSSGGGGMNGYFVDSFGDPKPKKKGAPRQQEELCLVCGDRASGYHYNALTCEGCKGFF 60

Query: 201 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK 260
 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK
 Sbjct: 61 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK 120

Query: 261 HQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGNSNSHEEDKKPLVLSPGV 320
 HQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGS+SNHEEDKKPLV + +
 Sbjct: 121 HQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGSSSNHEEDKKPLVPNQNI 180

Query: 321 KPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTTFPLGDSEEDNQRRFQHTEITILTVQ 380
 KPL++SQEDLINKLVYYQQEFESPSEEDMKKTTTFPLGDSEEDNQRRFQHTEITILTVQ
 Sbjct: 181 KPLSTSQEDLINKLVYYQQEFESPSEEDMKKTTTFPLGDSEEDNQRRFQHTEITILTVQ 240

Query: 381 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY 440
 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY
 Sbjct: 241 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY 300

Query: 441 RSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIFSERPALVDPCKVERIQEYYIET 500
 RSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIFSERPALVDPCKVERIQEYYIET
 Sbjct: 301 RSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIFSERPALVDPCKVERIQEYYIET 360

Query: 501 LRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKKLPPFLAEIWDIQE 559
 LRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKKLPPFLAEIWDIQE
 Sbjct: 361 LRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKKLPPFLAEIWDIQE 419

Query= *Rhipicephalus haemaphysaloides*-EcR2
(453 letters)

Sequences producing significant alignments:				Score (bits)	E Value
Dsyl-GWHPAMML010889	mRNA=GWHTAMML010889	Gene=GWHGAMML010889	Posi...	863	0.0
Hasi-GWHPAMMK012598	mRNA=GWHTAMMK012598	Gene=GWHGAMMK012598	Posi...	845	0.0
Hlon-GWHPAMMI014869	mRNA=GWHTAMMI014869	Gene=GWHGAMMI014869	Posi...	817	0.0
Rmic-GWHPAMMN007750	mRNA=GWHTAMMN007750	Gene=GWHGAMMN007750	Posi...	815	0.0
Ipers-GWHPAMMH024910.1	mRNA=GWHTAMMH024910.1	Gene=GWHGAMMH024910...		782	0.0

>Dsyl-GWHPAMML010889 mRNA=GWHTAMML010889 Gene=GWHGAMML010889
Position=GWHAMML00001091: 197274423-197274459,
197279342-197279580, 197280626-197280860,
197336936-197337259, 197339173-197339498,
197340861-197341016, 197341809-197342031,
Length = 593

Score = 863 bits (2230), Expect = 0.0
Identities = 421/422 (99%), Positives = 422/422 (100%)

Query: 32 KEEMSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQQEELCLVCGDRASGYHYNALTCEGCK 91
KEEMSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQQEELCLVCGDRASGYHYNALTCEGCK
Sbjct: 172 KEEMSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQQEELCLVCGDRASGYHYNALTCEGCK 231

Query: 92 GFFRRSITKNAVYQCKYGNNCIDIMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRE 151
GFFRRSITKNAVYQCKYGNNCIDIMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRE
Sbjct: 232 GFFRRSITKNAVYQCKYGNNCIDIMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRE 291

Query: 152 SKKHQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGSNSNHEEDKKPLVLS 211
SKKHQKDRPNSTTRESPSGLMAPSS+GGGVSPSSQPLGGGGSSLGSNSNHEEDKKPLVLS
Sbjct: 292 SKKHQKDRPNSTTRESPSGLMAPSSVGGGVSPSSQPLGGGGSSLGSNSNHEEDKKPLVLS 351

Query: 212 PGVKPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTPFPLGDSEEDNQRRFQHITEITIL 271
PGVKPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTPFPLGDSEEDNQRRFQHITEITIL
Sbjct: 352 PGVKPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTPFPLGDSEEDNQRRFQHITEITIL 411

Query: 272 TVQLLIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTR 331
TVQLLIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTR
Sbjct: 412 TVQLLIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTR 471

Query: 332 DNYRSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIFSERPALVDPCKVERIQEYY 391
DNYRSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIFSERPALVDPCKVERIQEYY
Sbjct: 472 DNYRSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIFSERPALVDPCKVERIQEYY 531

Query: 392 IETLRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKKLPPFLAEIWDI 451
IETLRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKKLPPFLAEIWDI
Sbjct: 532 IETLRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKKLPPFLAEIWDI 591

Query: 452 QE 453
QE
Sbjct: 592 QE 593

>Hasi-GWHPAMMK012598 mRNA=GWHTAMMK012598 Gene=GWHGAMMK012598
Position=GWHAMMK00000151: 115710724-115710965,
115712102-115712324, 115713112-115713267,
115715373-115715698,
Length = 419

Score = 845 bits (2182), Expect = 0.0
Identities = 411/419 (98%), Positives = 416/419 (99%)

Query: 35 MSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFF 94
MSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFF
Sbjct: 1 MSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFF 60

Query: 95 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK 154
RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK
Sbjct: 61 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK 120

Query: 155 HQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGSNSNHEEDKKPLVLSPGV 214
HQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGS+SNHEEDKKPLV + +
Sbjct: 121 HQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGSSSNHEEDKKPLVPNQNI 180

Query: 215 KPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTFPFLGDSEEDNQRRFQHTEITILTVQ 274
KPL++SQEDLINKLVYYQQEFESPSEEDMKKTTFPFLGDSEEDNQRRFQHTEITILTVQ
Sbjct: 181 KPLSTSQEDLINKLVYYQQEFESPSEEDMKKTTFPFLGDSEEDNQRRFQHTEITILTVQ 240

Query: 275 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY 334
LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY
Sbjct: 241 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY 300

Query: 335 RSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIFSERPALVDPCKVERIQEYYIET 394
RSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIFSERPALVDPCKVERIQEYYIET
Sbjct: 301 RSASVGDSADALFRFCRKMCQLRVDNAEYALLTAIVIFSERPALVDPCKVERIQEYYIET 360

Query: 395 LRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKLPFLAEIWDIQE 453
LRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKLPFLAEIWDIQE
Sbjct: 361 LRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKLPFLAEIWDIQE 419

Query= *Rhipicephalus haemaphysaloides*-Ecr3
(419 letters)

Sequences producing significant alignments:	Score (bits)	E Value
Dsyl-GWHPAMML010889 mRNA=GWHTAMML010889 Gene=GWHGAMML010889 Posi...	857	0.0
Hasi-GWHPAMMK012598 mRNA=GWHTAMMK012598 Gene=GWHGAMMK012598 Posi...	845	0.0
Hlon-GWHPAMMI014869 mRNA=GWHTAMMI014869 Gene=GWHGAMMI014869 Posi...	817	0.0
Rmic-GWHPAMMN007750 mRNA=GWHTAMMN007750 Gene=GWHGAMMN007750 Posi...	809	0.0
Ipers-GWHPAMMH024910.1 mRNA=GWHTAMMH024910.1 Gene=GWHGAMMH024910...	776	0.0

>Dsyl-GWHPAMML010889 mRNA=GWHTAMML010889 Gene=GWHGAMML010889
Position=GWHAMML00001091: 197274423-197274459,
197279342-197279580, 197280626-197280860,
197336936-197337259, 197339173-197339498,
197340861-197341016, 197341809-197342031,
Length = 593

Score = 857 bits (2215), Expect = 0.0
Identities = 418/419 (99%), Positives = 419/419 (100%)

Query: 1 MSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFF 60
MSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFF
Sbjct: 175 MSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFF 234

Query: 61 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK 120
 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK
 Sbjct: 235 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK 294

Query: 121 HQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGSNSNHEEDKKPLVLSPGV 180
 HQKDRPNSTTRESPSGLMAPSS+GGGVSPSSQPLGGGGSSLGSNSNHEEDKKPLVLSPGV
 Sbjct: 295 HQKDRPNSTTRESPSGLMAPSSVGGGVSPSSQPLGGGGSSLGSNSNHEEDKKPLVLSPGV 354

Query: 181 KPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTFPPLGDSEEDNQRRFQHITEITILTVQ 240
 KPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTFPPLGDSEEDNQRRFQHITEITILTVQ
 Sbjct: 355 KPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTFPPLGDSEEDNQRRFQHITEITILTVQ 414

Query: 241 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY 300
 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY
 Sbjct: 415 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY 474

Query: 301 RSASVGDSADALFRFCRKMCLQVRDQAEYALLTAIVIFSERPALVDPCKVERIQEYYIET 360
 RSASVGDSADALFRFCRKMCLQVRDQAEYALLTAIVIFSERPALVDPCKVERIQEYYIET
 Sbjct: 475 RSASVGDSADALFRFCRKMCLQVRDQAEYALLTAIVIFSERPALVDPCKVERIQEYYIET 534

Query: 361 LRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKLPFLAEIWDIQE 419
 LRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKLPFLAEIWDIQE
 Sbjct: 535 LRMYSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKLPFLAEIWDIQE 593

>Hasi-GWHPAMMK012598 mRNA=GWHTAMMK012598 Gene=GWHGAMMK012598
 Position=GWHAMMK00000151: 115710724-115710965,
 115712102-115712324, 115713112-115713267,
 115715373-115715698,
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Score = 845 bits (2182), Expect = 0.0
 Identities = 411/419 (98%), Positives = 416/419 (99%)

Query: 1 MSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFF 60
 MSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFF
 Sbjct: 1 MSPSSGGGGMNGYFVDSFGDPKKKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFF 60

Query: 61 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK 120
 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK
 Sbjct: 61 RRSITKNAVYQCKYGNNCDIDMYMRRKCQECRLKKCLSVGMRPECVVPEYQCAIKRESKK 120

Query: 121 HQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGSNSNHEEDKKPLVLSPGV 180
 HQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGS+SNHEEDKKPLV + +
 Sbjct: 121 HQKDRPNSTTRESPSGLMAPSSMGGGVSPSSQPLGGGGSSLGSSSNHEEDKKPLVPNQNI 180

Query: 181 KPLTSSQEDLINKLVYYQQEFESPSEEDMKKTTFPPLGDSEEDNQRRFQHITEITILTVQ 240
 KPL++SQEDLINKLVYYQQEFESPSEEDMKKTTFPPLGDSEEDNQRRFQHITEITILTVQ
 Sbjct: 181 KPLSTSQEDLINKLVYYQQEFESPSEEDMKKTTFPPLGDSEEDNQRRFQHITEITILTVQ 240

Query: 241 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY 300
 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY
 Sbjct: 241 LIVEFSKRVPGFDTLAREDQITLLKACSSEVMMLRGARKYDVKTDSIVFANNQPYTRDNY 300

Query: 301 RSASVGDSADALFRFCRKMCLQVRDQAEYALLTAIVIFSERPALVDPCKVERIQEYYIET 360
 RSASVGDSADALFRFCRKMCLQVRDQAEYALLTAIVIFSERPALVDPCKVERIQEYYIET
 Sbjct: 301 RSASVGDSADALFRFCRKMCLQVRDQAEYALLTAIVIFSERPALVDPCKVERIQEYYIET 360

Query: 361 LRMYSSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKKLPPFLAEIWDIQE 419
LRMYSSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKKLPPFLAEIWDIQE
Sbjct: 361 LRMYSSENHRPPGKNYFARLLSILTELRTLGNMNAEMCFSLKVQNKKLPPFLAEIWDIQE 419