

Scaffold	Proviral segment /IVSPER	Proviral/IVS PER sequence size (nt)	Proviral/IVSPER position in scaffold	Gene name	Gene position in scaffold	Introns in gene (yes/no)	Predicted protein size (aa)	NCBI accession	protein ID	Length (nt)	BlastP e-value	Identities (%)	Comments
Hyposoter didymator													
HdIV proviral segment													
scaffold49647	similar to Hd2	1537	1-1537 (partial)	Gly-Pro_P40-like_1	1-1235 - strand	yes	315	AAD40678.1	P40 protein [Hyposoter didymator ichnovirus]	397	2.00E-168	282/318(89%)	
scaffold184	Hd45.2	2051	3564791-3566841	U1_Hd45.2	3565610-3566474 - strand	yes	135	AIK25614.1	D8 [Hyposoter didymator ichnovirus]	138	4.00E-34	82/140(59%)	
scaffold128243	Hd44.1	3009	4203985-4206993	U1_Hd44.1	4205686-4205997 + strand	no	104	AIK25616.1	U2 [Hyposoter didymator ichnovirus]	104	1.00E-65	101/104(97%)	
scaffold64	Hd42	3157	2320523-2323679	Rep1_Hd42	2322099-2322881 - strand	no	261	AIK25619.1	Rep1 [Hyposoter didymator ichnovirus]	261	0.00E+00	248/261(95%)	
scaffold128213	Hd23.2	3362	248624-251985	Rep1_Hd23.2	249754-250470 - strand	no	238	AIK25664.1	Rep1 [Hyposoter didymator ichnovirus]	263	1.00E-124	180/239(75%)	
scaffold127348	Hd40	3494	926528-930021	U2_Hd40	926730-927180 - strand	no	148	AIK25622.1	U2 [Hyposoter didymator ichnovirus]	115	2.00E-69	101/104(97%)	pb (insertion) within CDS
scaffold127348	Hd40	3494	926528-930021	U1_Hd40	928473-928898 - strand	no	142	AIK25621.1	U1 [Hyposoter didymator ichnovirus]	143	5.00E-75	116/142(82%)	
scaffold175	Hd38	3664	3800393-3804056	U1_Hd38	3800677-3801003 - strand	no	108	AIK25624.1	U1 [Hyposoter didymator ichnovirus]	108	3.00E-69	105/108(97%)	insertion of a stop codon within CDS
scaffold175	Hd38	3664	3800393-3804056	Vinx1_Hd38	3801226-3802356 + strand	no	377	AIK25625.1	Vinx1 [Hyposoter didymator ichnovirus]	377	0.00E+00	362/377(96%)	
scaffold175	Hd38	3664	3800393-3804056	U2_Hd38	3802480-3802809 - strand	no	109	AIK25626.1	F1U2 [Hyposoter didymator ichnovirus]	107	5.00E-68	101/107(94%)	insertion of a stop codon within CDS
scaffold65	Hd37	3708	342293-346000	U1_Hd37	342555-342665 - strand	no	36	AIK25627.1	U1 [Hyposoter didymator ichnovirus]	143	2.00E-16	36/36(100%)	partial; corresponds to the N-term of the protein (aa 1-36)
scaffold65	Hd37	3708	342293-346000	Rep1_Hd37	343245-344048 + strand	no	268	AIK25629.1	Rep1 [Hyposoter didymator ichnovirus]	268	0.00E+00	262/268(98%)	
scaffold65	Hd37	3708	342293-346000	U2_Hd37	344748-344996 - strand	no	82	AIK25628.1	U2 [Hyposoter didymator ichnovirus]	146	1.00E-46	76/82(93%)	partial; corresponds to the C-term of the protein (aa 65-146) and one of the
scaffold116	Hd35	3710	473341-477050	Rep1_Hd35	475117-475821 + strand	no	235	AIK25632.1	Rep1 [Hyposoter didymator ichnovirus]	235	9.00E-177	234/235(99%)	
scaffold175	Hd36	3738	3796140-3799877	U1_Hd36	3797417-3797740 + strand	no	107	AIK25630.1	F1U1 [Hyposoter didymator ichnovirus]	107	2.00E-70	102/107(95%)	start codon modified (ATT instead of ATG in NCBI seq)
scaffold175	Hd36	3738	3796140-3799877	Vinx1_Hd36	3797918-3799006 - strand	no	363	AAO16963.1	viral innexin [Hyposoter didymator ichnovirus]	363	0.00E+00	335/363(92%)	
scaffold91	Hd33	3835	485063-488897	U1_Hd33	485760-486020 - strand	no	86		No significant similarity found				low transcription in parasitized lep larvae
scaffold91	Hd33	3835	485063-488897	U2_Hd33	487963-488427 - strand	no	154		No significant similarity found				
scaffold127548	Hd27	4002	13338255-13342256	U1_Hd27	13338842-13339126 + strand	no	94	AIK25654.1	U1 [Hyposoter didymator ichnovirus]	113	6.00E-62	92/93(99%)	modified start codon
scaffold127548	Hd27	4002	13338255-13342256	K19_Hd27	13340915-13341354 - strand	yes	106	AAF91314.1	P12 [Hyposoter didymator ichnovirus]	106	2.00E-71	105/106(99%)	
scaffold29771	Hd46	4109	19344-23452	Vank_Hd46	20304-20807 + strand	no	167	YP_00103123	vankyrin-b1 [Hyposoter fugitivus ichnovirus]	167	9.00E-86	127/165(77%)	
scaffold127549	Hd31-34	4119	144445-148563	U1_Hd31-34	145530-145901 + strand	no	124	AIK25633.1	F4U1 [Hyposoter didymator ichnovirus]	124	1.00E-71	121/124(98%)	
scaffold127549	Hd31-34	4119	144445-148563	U2_Hd31-34	146442-146729 - strand	no	95	AIK25634.1	F5U2 [Hyposoter didymator ichnovirus]	124	3.00E-64	94/95(99%)	shorter in C-term
scaffold22	Hd39	4122	1002620-1006741	Rep1_Hd39	1003991-1004692 - strand	no	234	AIK25623.1	Rep1 [Hyposoter didymator ichnovirus]	234	9.00E-170	227/234(97%)	
scaffold1868	Hd43	4159	193639-197797	U1_Hd43	194377-194676 - strand	no	100	AIK25617.1	U1 [Hyposoter didymator ichnovirus]	100	3.00E-67	97/100(97%)	
scaffold1868	Hd43	4159	193639-197797	Vank1_Hd43	196094-196618 - strand	no	175	AIK25618.1	Vank1 [Hyposoter didymator ichnovirus]	175	1.00E-125	171/175(98%)	
scaffold67	Hd30	4164	5867182-5871345	U1_Hd30	5867451-5867846 + strand	no	131	AIK25641.1	U1 [Hyposoter didymator ichnovirus]	104	3.00E-67	100/104(96%)	longer in C-term
scaffold67	Hd30	4164	5867182-5871345	U2_Hd30	5867871-5868734 - strand	no	288	AIK25642.1	U2 [Hyposoter didymator ichnovirus]	288	0.00E+00	284/288(99%)	
scaffold67	Hd30	4164	5867182-5871345	Vinx1_Hd30	5869217-5870347 - strand	no	376	AIK25643.1	Vinx1 [Hyposoter didymator ichnovirus]	376	0.00E+00	375/376(99%)	
scaffold67	Hd30	4164	5867182-5871345	U3_Hd30	5870662-5870985 + strand	no	107	AIK25644.1	U3 [Hyposoter didymator ichnovirus]	107	2.00E-68	105/107(98%)	
scaffold161	Hd25	4174	2449400-2453573	PRRP3_Hd25	2450118-2450525 + strand	no	136	AIK25660.1	PRRP2 [Hyposoter didymator ichnovirus]	136	1.00E-83	136/136(100%)	
scaffold161	Hd25	4174	2449400-2453573	PRRP2_Hd25	2451908-2452147 - strand	no	80	AIK25661.1	PRRP3 [Hyposoter didymator ichnovirus]	80	7.00E-46	75/80(94%)	
scaffold161	Hd25	4174	2449400-2453573	PRRP1_Hd25	2452642-2452827 - strand	no	61	AIK25659.1	PRRP1 [Hyposoter didymator ichnovirus]	61	4.00E-09	58/61(95%)	
scaffold28498	Hd45.1	NA	1-4214 (partial)	U1_Hd45.1	679-1541 - strand	yes	138	AAO33352.1	unknown [Hyposoter didymator ichnovirus]	138	3.00E-91	133/138(96%)	
scaffold28498	Hd45.1	NA	1-4214 (partial)	U2_Hd45.1	3317-4180 - strand	yes	135	AIK25614.1	D8 [Hyposoter didymator ichnovirus]	138	3.00E-33	82/140(59%)	
scaffold119	Hd22	4233	698410-702642	U1_Hd22	698775-699101 - strand	no	109	AIK25666.1	U1 [Hyposoter didymator ichnovirus]	109	2.00E-72	106/109(97%)	
scaffold119	Hd22	4233	698410-702642	Rep1_Hd22	700424-701035 - strand	no	204	AAR89180.1	repeat element protein 8 [Hyposoter didymator ichnovirus]	204	9.00E-150	204/204(100%)	
scaffold91	Hd29	4356	572514-576869	N1_Hd29	573680-574969 - strand	no	430	AIK25650.1	N-gene1 [Hyposoter didymator ichnovirus]	430	0.00E+00	427/430(99%)	
scaffold64	Hd21	4368	2353107-2357474	Rep1_Hd21	2353545-2354333 - strand	no	263	AIK25667.1	Rep1 [Hyposoter didymator ichnovirus]	263	0.00E+00	258/263(98%)	
scaffold64	Hd21	4368	2353107-2357474	Vinx1_Hd21	2355781-2356860 - strand	no	360	AIK25668.1	Vinx1 [Hyposoter didymator ichnovirus]	360	0.00E+00	356/360(99%)	
scaffold198	Hd19	4440	1265454-1269893	U1_Hd19	1266250-1268833 - strand	yes	618	AIK25671.1	U1 [Hyposoter didymator ichnovirus]	618	0.00E+00	606/618(98%)	
scaffold128213	Hd23.1	4457	208205-212661	Rep1_Hd23.1	209796-210587 - strand	no	263	AIK25664.1	Rep1 [Hyposoter didymator ichnovirus]	263	0.00E+00	262/263(99%)	
scaffold127548	Hd47	4503	12134587-12139089	Rep1_Hd47	12135113-12135841 - strand	no	242	YP_00103131	repeat element protein-d4.2 [Hyposoter fugitivus ichnovirus]	248	2.00E-122	166/238(70%)	
scaffold127548	Hd47	4503	12134587-12139089	Rep2_Hd47	12136931-12137599 - strand	no	222	YP_00103131	repeat element protein-d4.1 [Hyposoter fugitivus ichnovirus]	255	4.00E-116	154/220(70%)	
scaffold264	Hd28	4614	135485-140098	Vinx1_Hd28	136611-137621 + strand	no	336	AIK25662.1	Vinx1 [Hyposoter didymator ichnovirus]	357	0.00E+00	301/334(90%)	
scaffold264	Hd28	4614	135485-140098	Vank1_Hd28	138475-138984 + strand	no	170	AFH35114.1	vankyrin 1 [Hyposoter didymator ichnovirus]	170	2.00E-122	168/170(99%)	
scaffold82201	Hd51	4632	1077-5708	Rep1_Hd51	2537-3115 - strand	no	192	AIK25629.1	Rep1 [Hyposoter didymator ichnovirus]	268	2.00E-89	129/190(68%)	no reads RNAseq
scaffold351	Hd18	4696	2681961-2686656	N1_Hd18	2683737-2685050 + strand	no	438	AIK25675.1	N-gene1 [Hyposoter didymator ichnovirus]	438	0.00E+00	434/438(99%)	
scaffold91	Hd24	4697	535698-540394	Vank1_Hd24	536918-537427 - strand	no	170	AFH35112.1	vankyrin 1 [Hyposoter didymator ichnovirus]	170	1.00E-123	170/170(100%)	
scaffold91	Hd24	4697	535698-540394	Vinx1_Hd24	538200-539270 - strand	no	357	AIK25662.1	Vinx1 [Hyposoter didymator ichnovirus]	357	0.00E+00	351/357(98%)	
scaffold128243	Hd44.2	4831	4197203-4202033	Rep1_Hd44.2	4197838-4198440 - strand	no	200	YP_00103128	repeat element protein-c11.1 [Hyposoter fugitivus ichnovirus]	201	3.00E-58	106/186(57%)	
scaffold128243	Hd44.2	4831	4197203-4202033	U1_Hd44.2	4199950-4200297 + strand	no	115	AIG88525.1	hypothetical protein A7.1 [Diadegma fenestrale ichnovirus]	76	1.00E-20	56/76(74%)	strand may be incorrect
scaffold91	Hd15	4987	469105-474091	N1_Hd15	470135-471607 - strand	no	491	AIK25681.1	N-gene1 [Hyposoter didymator ichnovirus]	491	0.00E+00	478/491(97%)	
scaffold175	Hd26	5018	10942034-10947051	PRRP1_Hd26	10943182-10943589 + strand	no	136	AIK25646.1	PRRP1 [Hyposoter didymator ichnovirus]	136	2.00E-91	136/136(100%)	

scaffold175	Hd26	5018	10942034-10947051	PRRP2_Hd26	10945126-10945518 + strand	no	131	AIK25645.1	PRRP2 [Hyposoter didymator ichnovirus]	131	4,00E-83	130/131(99%)	
scaffold175	Hd26	5018	10942034-10947051	U1_Hd26	10946124-10946471 - strand	no	116	AIK25658.1	U1 [Hyposoter didymator ichnovirus]	116	2,00E-80	116/116(100%)	
scaffold64	Hd14	5196	36336-41531	Vinx1_Hd14	38977-39405 + strand	no	143	AIK25682.1	Vinx1 [Hyposoter didymator ichnovirus]	143	5,00E-101	143/143(100%)	
scaffold64	Hd14	5196	36336-41531	U1_Hd14	41196-41501 + strand	no	102	AIK25683.1	U1 [Hyposoter didymator ichnovirus]	102	8,00E-70	102/102(100%)	
scaffold128246	Hd49	5265	677866-683130	Rep1_Hd49	678304-679005 + strand	no	233	YP_001031325.1	repeat element protein-d7.2 [Hyposoter fugitivus ichnovirus]	242	1,00E-119	173/232(75%)	
scaffold128246	Hd49	5265	677866-683130	Rep2_Hd49	679573-680190 + strand	no	205	YP_001031326.1	repeat element protein-d7.3 [Hyposoter fugitivus ichnovirus]	240	3,00E-114	160/205(78%)	
scaffold128246	Hd49	5265	677866-683130	Rep3_Hd49	681373-682041 + strand	no	222	YP_001031323.1	repeat element protein-d7.1 [Hyposoter fugitivus ichnovirus]	255	5,00E-93	156/257(61%)	
scaffold128241	Hd13	5757	402487-408243	Cys2_Hd13	403839-404424 - strand	yes	157	AIK25685.1	Cys2 [Hyposoter didymator ichnovirus]	157	5,00E-94	133/157(85%)	
scaffold128241	Hd13	5757	402487-408243	Cys1_Hd13	406027-406868 - strand	yes	162	AIK25684.1	Cys1 [Hyposoter didymator ichnovirus]	162	1,00E-107	149/162(92%)	
scaffold357	Hd50	5787	2218373-2224159	Vinx1_Hd50	2219976-2221058 + strand	no	360	YP_001031328.1	innexin Vnx-d5.1 [Hyposoter fugitivus ichnovirus]	375	0,00E+00	280/357(78%)	
scaffold357	Hd50	5787	2218373-2224159	Vinx2_Hd50	2221574-2222647 + strand	no	357	YP_001031329.1	innexin Vnx-d5.2 [Hyposoter fugitivus ichnovirus]	378	7,00E-170	241/378(64%)	
scaffold59	Hd12	5902	674917-680818	U1_Hd12	675013-675345 + strand	no	111	AIK25686.1	U1 [Hyposoter didymator ichnovirus]	111	9,00E-77	110/111(99%)	
scaffold59	Hd12	5902	674917-680818	Rep1_Hd12	675996-676679 - strand	no	228	AIK25689.1	Rep1 [Hyposoter didymator ichnovirus]	228	1,00E-169	226/228(99%)	
scaffold59	Hd12	5902	674917-680818	U2_Hd12	678859-679170 - strand	no	104	AIK25687.1	U2 [Hyposoter didymator ichnovirus]	104	2,00E-67	103/104(99%)	
scaffold59	Hd12	5902	674917-680818	Rep2_Hd12	679544-680233 - strand	no	230	AIK25688.1	Rep2 [Hyposoter didymator ichnovirus]	230	1,00E-173	229/230(99%)	
scaffold59	Hd10	6507	2500377-2506883	Rep3_Hd10	2501422-2502045 - strand	no	208	AIK25696.1	Rep3 [Hyposoter didymator ichnovirus]	208	9,00E-154	207/208(99%)	
scaffold59	Hd10	6507	2500377-2506883	Rep2_Hd10	2502434-2503066 - strand	no	211	AIK25695.1	Rep2 [Hyposoter didymator ichnovirus]	211	3,00E-155	211/211(100%)	
scaffold59	Hd10	6507	2500377-2506883	Rep1_Hd10	2504201-2504872 - strand	no	224	AAR89179.1	repeat element protein 7 [Hyposoter didymator ichnovirus]	224	4,00E-167	224/224(100%)	
scaffold144	Hd20	6864	1449468-1456331	Cys2_Hd20	1450485-1451362 - strand	yes	145	AIK25636.1	Cys1 [Hyposoter didymator ichnovirus]	145	3,00E-104	144/145(99%)	
scaffold144	Hd20	6864	1449468-1456331	Cys1_Hd20	1454299-1455511 - strand	yes	254	AIK25669.1	Cys1 [Hyposoter didymator ichnovirus]	254	0,00E+00	252/254(99%)	
scaffold377	Hd8	7356	2186417-2193772	U5_Hd8	2186651-2186968 + strand	no	105	AIK25705.1	U4 [Hyposoter didymator ichnovirus]	105	2,00E-71	103/105(98%)	
scaffold377	Hd8	7356	2186417-2193772	U4_Hd8	2188345-2188632 - strand	no	95	YP_001031361.1	[Hyposoter fugitivus ichnovirus]	131	4,00E-07	46/131(35%)	
scaffold377	Hd8	7356	2186417-2193772	U3_Hd8	2190149-2190466 + strand	no	105	AIK25702.1	F6U1 [Hyposoter didymator ichnovirus]	105	5,00E-71	102/105(97%)	
scaffold377	Hd8	7356	2186417-2193772	U2_Hd8	2191793-2192095 - strand	no	100	AIK25703.1	U2 [Hyposoter didymator ichnovirus]	100	1,00E-64	98/100(98%)	
scaffold377	Hd8	7356	2186417-2193772	U1_Hd8	2192394-2192693 + strand	no	99	AIK25704.1	F6U3 [Hyposoter didymator ichnovirus]	106	6,00E-44	71/75(95%)	
scaffold59	Hd16	7704	690205-697908	Rep1_Hd16	690229-690951 - strand	no	241	AIK25680.1	Rep1 [Hyposoter didymator ichnovirus]	241	0,00E+00	241/241(100%)	
scaffold59	Hd16	7704	690205-697908	U2_Hd16	691425-691661 + strand	no	78		No significant similarity found				possibly not a CDS (low transcription in calyx)
scaffold59	Hd16	7704	690205-697908	U1_Hd16	693257-693817 + strand	no	187	AIK25679.1	U1 [Hyposoter didymator ichnovirus]	187	9,00E-122	186/187(99%)	
scaffold59	Hd16	7704	690205-697908	Rep2_Hd16	695154-695813 - strand	no	219	AAR89178.1	repeat element protein 6 [Hyposoter didymator ichnovirus]	219	1,00E-159	213/219(97%)	
scaffold59	Hd16	7704	690205-697908	Rep3_Hd16	696463-697149 - strand	no	228	AAR89177.1	repeat element protein 5 [Hyposoter didymator ichnovirus]	228	9,00E-170	228/228(100%)	
scaffold351	Hd17	7730	2329273-2337002	Rep5_Hd17	2329743-2330387 - strand	no	214	AHY22036.1	repeat element 36 [Diadegma semiclausum ichnovirus]	262	3,00E-124	174/214(81%)	
scaffold351	Hd17	7730	2329273-2337002	Rep4_Hd17	2330936-2331505 - strand	no	189	AIK25678.1	Rep1 [Hyposoter didymator ichnovirus]	230	1,00E-120	166/182(91%)	
scaffold351	Hd17	7730	2329273-2337002	Rep3_Hd17	2332279-2333010 - strand	no	244	AAO16957.1	repeat element protein [Hyposoter didymator ichnovirus]	244	0,00E+00	244/244(100%)	
scaffold351	Hd17	7730	2329273-2337002	Rep2_Hd17	2334085-2334759 - strand	no	225	AAO16959.1	repeat element protein [Hyposoter didymator ichnovirus]	225	5,00E-166	221/225(98%)	
scaffold351	Hd17	7730	2329273-2337002	Rep1_Hd17	2335459-2336166 - strand	no	236	AIK25673.1	Rep1 [Hyposoter didymator ichnovirus]	236	4,00E-173	232/236(98%)	
scaffold64	Hd32	7916	88702-96617	U1.2_Hd32	88842-89159 - strand	no	105	AIK25638.1	U1 [Hyposoter didymator ichnovirus]	105	5,00E-65	96/105(91%)	
scaffold64	Hd32	7916	88702-96617	Vinx2_Hd32	90142-91254 - strand	no	370	AIK25637.1	Vinx1 [Hyposoter didymator ichnovirus]	366	0,00E+00	279/353(79%)	
scaffold64	Hd32	7916	88702-96617	U1.1_Hd32	93443-93757 - strand	no	105	AIK25638.1	U1 [Hyposoter didymator ichnovirus]	105	6,00E-72	105/105(100%)	
scaffold64	Hd32	7916	88702-96617	Vinx1_Hd32	94429-95526 - strand	no	366	AIK25637.1	Vinx1 [Hyposoter didymator ichnovirus]	366	0,00E+00	366/366(100%)	
scaffold184	Hd41	7953	3768924-3776876	U1_Hd41	3769919-3770824 + strand	yes	152	AIK25620.1	U1 [Hyposoter didymator ichnovirus]	197	9,00E-64	112/152(74%)	N-term shorter
scaffold184	Hd41	7953	3768924-3776876	U2_Hd41	3772675-3773716 + strand	yes	168	AIK25614.1	D8 [Hyposoter didymator ichnovirus]	138	3,00E-22	72/170(42%)	
scaffold184	Hd41	7953	3768924-3776876	U3_Hd41	3775212-3776089 + strand	yes	159	AIK25620.1	U1 [Hyposoter didymator ichnovirus]	197	2,00E-22	59/96(61%)	
scaffold127548	Hd7	8066	6062921-6070986	U1_Hd7	6065301-6068372 + strand	no	1024	AIK25706.1	U1 [Hyposoter didymator ichnovirus]	1080	0,00E+00	916/1080(85%)	repeated motif missing from the CDS
scaffold59	Hd11	9190	2183512-2192701	U1_Hd11	2184311-2184694 + strand	no	128	AIK25649.1	U1 [Hyposoter didymator ichnovirus]	128	8,00E-87	125/128(98%)	
scaffold59	Hd11	9190	2183512-2192701	Rep1_Hd11	2184915-2185607 + strand	no	231	AIK25648.1	Rep1 [Hyposoter didymator ichnovirus]	231	7,00E-172	229/231(99%)	
scaffold59	Hd11	9190	2183512-2192701	Vank1_Hd11	2186326-2186802 + strand	no	159	AFH35113.1	vankyrin 1 [Hyposoter didymator ichnovirus]	159	2,00E-113	159/159(100%)	
scaffold59	Hd11	9190	2183512-2192701	Vank5_Hd11	2187892-2188395 + strand	no	168	AFH35119.1	vankyrin 5 [Hyposoter didymator ichnovirus]	168	2,00E-123	168/168(100%)	
scaffold59	Hd11	9190	2183512-2192701	Vank4_Hd11	2188456-2189962 + strand	no	169	AFH35118.1	vankyrin 4 [Hyposoter didymator ichnovirus]	169	4,00E-123	168/169(99%)	
scaffold59	Hd11	9190	2183512-2192701	Vank3_Hd11	2190561-2191067 + strand	no	169	AFH35117.1	vankyrin 3 [Hyposoter didymator ichnovirus]	169	1,00E-121	168/169(99%)	
scaffold59	Hd11	9190	2183512-2192701	Vank2_Hd11	2191436-2191942 + strand	no	169	AFH35116.1	vankyrin 2 [Hyposoter didymator ichnovirus]	169	2,00E-116	163/169(96%)	
scaffold59	Hd11	9190	2183512-2192701	Vank1p_Hd11	2192415-2192701 + strand	no	95	AFH35113.1	vankyrin 1 [Hyposoter didymator ichnovirus]	159	2,00E-58	88/95(93%)	partial; corresponds to the N-term of the protein (aa 1-95)
scaffold429	Hd48	9673	531833-541505	Rep1_Hd48	533753-534487 - strand	no	244	AHY22018.1	repeat element 27 [Diadegma semiclausum ichnovirus]	246	3,00E-127	175/245(71%)	
scaffold429	Hd48	9673	531833-541505	Rep2_Hd48	538812-539549 - strand	no	245	YP_001031328.1	repeat element protein-c7.1 [Hyposoter fugitivus ichnovirus]	282	4,00E-133	179/244(73%)	

scaffold65	Hd3	10014	437082-447095	Cys1_Hd3	438828-439558 - strand	yes	181	AIK25727.1	Cys1 [Hyposoter didymator ichnovirus]	181	4,00E-136	181/181(100%)	
scaffold65	Hd3	10014	437082-447095	Cys2_Hd3	440422-441241 - strand	yes	200	AIK25728.1	Cys2 [Hyposoter didymator ichnovirus]	200	1,00E-147	200/200(100%)	
scaffold65	Hd3	10014	437082-447095	Cys3_Hd3	442538-443060 - strand	yes	147	AIK25729.1	Cys3 [Hyposoter didymator ichnovirus]	147	3,00E-105	144/147(98%)	
scaffold65	Hd3	10014	437082-447095	Cys4_Hd3	443574-444657 - strand	yes	267	AIK25730.1	Cys4 [Hyposoter didymator ichnovirus]	241	3,00E-168	232/267(87%)	
scaffold65	Hd3	10014	437082-447095	Cys5_Hd3	445264-445755 - strand	yes	125	AIK25731.1	Cys5 [Hyposoter didymator ichnovirus]	125	3,00E-83	117/125(94%)	
scaffold377	Hd4	10326	2459681-2470006	Rep1_Hd4	2461072-2461818 - strand	no	248	AIK25721.1	Rep1 [Hyposoter didymator ichnovirus]	248	0,00E+00	248/248(100%)	
scaffold377	Hd4	10326	2459681-2470006	Rep2_Hd4	2462404-2463012 + strand	no	202	AIK25722.1	Rep2 [Hyposoter didymator ichnovirus]	202	8,00E-144	197/202(98%)	
scaffold377	Hd4	10326	2459681-2470006	Rep3_Hd4	2463770-2464366 + strand	no	198	AIK25723.1	Rep3 [Hyposoter didymator ichnovirus]	198	2,00E-145	198/198(100%)	
scaffold377	Hd4	10326	2459681-2470006	Rep4_Hd4	2465099-2465706 + strand	no	202	AIK25724.1	Rep4 [Hyposoter didymator ichnovirus]	202	6,00E-150	202/202(100%)	
scaffold377	Hd4	10326	2459681-2470006	Rep5_Hd4	2466854-2467603 - strand	no	249	AIK25725.1	Rep5 [Hyposoter didymator ichnovirus]	249	0,00E+00	246/249(99%)	
scaffold377	Hd4	10326	2459681-2470006	Rep6_Hd4	2468587-2469195 + strand	no	202	AIK25726.1	Rep6 [Hyposoter didymator ichnovirus]	202	3,00E-149	200/202(99%)	
scaffold127548	Hd6	10461	5808388-5818848	Rep1_Hd6	5809242-5809907 + strand	no	221	AAO33572.1	rep protein [Hyposoter didymator ichnovirus]	221	1,00E-164	221/221(100%)	
scaffold127548	Hd6	10461	5808388-5818848	P30_Hd6	5810559-5811315 - strand	yes	159	AIK25713.1	P30 [Hyposoter didymator ichnovirus]	414	2,00E-64	121/131(92%)	repeated motifs missing from the CDS
scaffold127548	Hd6	10461	5808388-5818848	U1.1_Hd6	5814030-5814758 - strand	yes	151	AIK25712.1	U1 [Hyposoter didymator ichnovirus]	159	2,00E-94	151/159(95%)	
scaffold127548	Hd6	10461	5808388-5818848	U1.2_Hd6	5818232-5818829 - strand	yes	143	AIK25712.1	U1 [Hyposoter didymator ichnovirus]	159	7,00E-12	53/129(41%)	
scaffold127548	Hd5	10510	12941242-12951751	Vinx1_Hd5	12941923-12942945 - strand	no	340	AIK25715.1	Vinx1 [Hyposoter didymator ichnovirus]	340	0,00E+00	336/340(99%)	
scaffold127548	Hd5	10510	12941242-12951751	Vinx2_Hd5	12943091-12943896 - strand	no	267	AIK25716.1	Vinx2 [Hyposoter didymator ichnovirus]	180	1,00E-99	141/143(99%)	pb within CDS
scaffold127548	Hd5	10510	12941242-12951751	U1_Hd5	12944615-12944923 - strand	no	102	AIK25717.1	U1 [Hyposoter didymator ichnovirus]	102	1,00E-65	98/102(96%)	
scaffold127548	Hd5	10510	12941242-12951751	Vinx3_Hd5	12945139-12946200 - strand	no	353	AIK25718.1	Vinx3 [Hyposoter didymator ichnovirus]	353	0,00E+00	352/353(99%)	
scaffold127548	Hd5	10510	12941242-12951751	Vinx4_Hd5	12947754-12948800 - strand	no	348	AIK25719.1	Vinx4 [Hyposoter didymator ichnovirus]	348	0,00E+00	346/348(99%)	
scaffold127548	Hd5	10510	12941242-12951751	Vinx5_Hd5	12950651-12951697 - strand	no	348	AAR82838.1	innexin-like protein 2 [Hyposoter didymator ichnovirus]	348	0,00E+00	346/348(99%)	
scaffold127548	Hd5	10510	12941242-12951751	Vinx6_Hd5	12952927-12953967 - strand	no	346	AAR82840.1	innexin-like protein 4 [Hyposoter didymator ichnovirus]	393	0,00E+00	334/343(97%)	
scaffold127548	Hd2	13937	5940296-5954232	GlyPro1_Hd2	5941600-5943451 + strand	yes	452	AAF08193.1	glycine and proline-rich protein P45 precursor [Hyposoter didymator ichnovirus]	452	0,00E+00	451/452(99%)	
scaffold127548	Hd2	13937	5940296-5954232	U1_Hd2	5944265-5944609 - strand	no	115	AIK25733.1	F2U1 [Hyposoter didymator ichnovirus]	115	5,00E-77	115/115(100%)	
scaffold127548	Hd2	13937	5940296-5954232	U2_Hd2	5945077-5945436 + strand	no	120	AAO33351.1	unknown [Hyposoter didymator ichnovirus]	120	8,00E-79	120/120(100%)	
scaffold127548	Hd2	13937	5940296-5954232	GlyPro2_Hd2	5946971-5951238 + strand	yes	1357	AAF08192.1	glycine and proline-rich protein P69 precursor [Hyposoter didymator ichnovirus]	683	6,00E-157	417/786(53%)	differences in the repeated region
scaffold127548	Hd2	13937	5940296-5954232	SerThr1_Hd2	5952553-5953461 + strand	yes	216	AIK25709.1	SerThr [Hyposoter didymator ichnovirus]	216	2,00E-153	211/216(98%)	
scaffold90	Hd1	NA	1-14771 (partial)	U6_Hd1	3039-3506 + strand	no	156	AIK25750.1	F9U13 [Hyposoter didymator ichnovirus]	156	6,00E-109	153/156(98%)	
scaffold90	Hd1	NA	1-14771 (partial)	U5_Hd1	4779-5282 - strand	no	168	AIK25739.1	F8U2 [Hyposoter didymator ichnovirus]	168	9,00E-119	168/168(100%)	
scaffold90	Hd1	NA	1-14771 (partial)	U4_Hd1	6629-7054 + strand	no	142	AIK25738.1	F7U1 [Hyposoter didymator ichnovirus]	142	2,00E-99	142/142(100%)	
scaffold90	Hd1	NA	1-14771 (partial)	U3_Hd1	8197-8511 - strand	no	105	AIK25745.1	F11U8 [Hyposoter didymator ichnovirus]	106	2,00E-46	82/106(77%)	
scaffold90	Hd1	NA	1-14771 (partial)	U2_Hd1	8984-9325 - strand	no	114	AIK25746.1	U9 [Hyposoter didymator ichnovirus]	114	2,00E-79	114/114(100%)	
scaffold90	Hd1	NA	1-14771 (partial)	U1_Hd1	12650-12967 - strand	no	105	AIK25745.1	F11U8 [Hyposoter didymator ichnovirus]	106	2,00E-46	82/106(77%)	
scaffold128215	Hd9	17892	526917-544808	U1.3_Hd9	527725-528057 - strand	no	110	AIK25698.1	U1 [Hyposoter didymator ichnovirus]	111	3,00E-32	81/110(74%)	
scaffold128215	Hd9	17892	526917-544808	U5.2_Hd9	529943-530425 + strand	no	160		No significant similarity found				
scaffold128215	Hd9	17892	526917-544808	U4.2_Hd9	531702-532277 - strand	no	191	AIK25701.1	U4 [Hyposoter didymator ichnovirus]	116	1,00E-48	99/116(85%)	
scaffold128215	Hd9	17892	526917-544808	U3.2_Hd9	532913-533263 + strand	no	117	AIK25700.1	U3 [Hyposoter didymator ichnovirus]	117	9,00E-76	112/117(96%)	
scaffold128215	Hd9	17892	526917-544808	U6.2_Hd9	533349-533735 + strand	no	128	AIK25748.1	F7U11 [Hyposoter didymator ichnovirus]	111	6,00E-18	56/126(44%)	
scaffold128215	Hd9	17892	526917-544808	U1.2_Hd9	535076-535489 - strand	no	137	AIK25698.1	U1 [Hyposoter didymator ichnovirus]	111	2,00E-30	76/110(69%)	
scaffold128215	Hd9	17892	526917-544808	U5.1_Hd9	537399-537881 + strand	no	160		No significant similarity found				
scaffold128215	Hd9	17892	526917-544808	U4.1_Hd9	539200-539775 - strand	no	191	AIK25701.1	U4 [Hyposoter didymator ichnovirus]	116	5,00E-48	99/116(85%)	
scaffold128215	Hd9	17892	526917-544808	U3.1_Hd9	540411-540941 + strand	no	176	AIK25700.1	U3 [Hyposoter didymator ichnovirus]	117	2,00E-72	110/117(94%)	
scaffold128215	Hd9	17892	526917-544808	U6.1_Hd9	540847-541233 + strand	no	128	AIK25748.1	F7U11 [Hyposoter didymator ichnovirus]	111	8,00E-18	60/128(47%)	
scaffold128215	Hd9	17892	526917-544808	U2_Hd9	541468-541782 - strand	no	105	AIK25699.1	U2 [Hyposoter didymator ichnovirus]	104	3,00E-67	102/105(97%)	
scaffold128215	Hd9	17892	526917-544808	U1.1_Hd9	543144-543476 - strand	no	111	AIK25698.1	U1 [Hyposoter didymator ichnovirus]	111	3,00E-70	110/111(99%)	
H. didymator IVSPER													
scaffold127548	IVSPER-5	1629	10860001-10861630	U35	10860001-10860537 + strand	no	178	AKD28058.1	hypothetical protein [Glypta fumiferanae] gene="U26"	180	1,00E-29	60/150(40%)	transcribed in calyx
scaffold127548	IVSPER-5	1629	10860001-10861630	U36	10861166-10861630 - strand	no	154	AKD28080.1	hypothetical protein [Glypta fumiferanae] gene="U38"	175	3,00E-14	45/144(31%)	transcribed in calyx
scaffold29771	IVSP_U37	1839	16848-18686	single CDS: U37	16848-18686 + strand	no	612	AKD28048.1	helicase-primase domain [Glypta fumiferanae]	721	0,00E+00	340/625(54%)	
scaffold91	IVSPER-1	14020	453857-467876	U1	453857-454591 + strand	no	244	ADI40452.1	unknown [Hyposoter didymator]	244	0,00E+00	241/243(99%)	
scaffold91	IVSPER-1	14020	453857-467876	IVSP1-1	455614-456375 + strand	no	253	ADI40453.1	unknown [Hyposoter didymator]	253	0,00E+00	245/253(97%)	
scaffold91	IVSPER-1	14020	453857-467876	U2	456897-457582 - strand	no	228	ADI40454.1	unknown [Hyposoter didymator]	228	3,00E-171	228/228(100%)	
scaffold91	IVSPER-1	14020	453857-467876	U3	458215-458709 + strand	no	164	ADI40455.1	unknown [Hyposoter didymator]	162	2,00E-119	162/162(100%)	
scaffold91	IVSPER-1	14020	453857-467876	U4	459123-459518 + strand	no	131	ADI40456.1	unknown [Hyposoter didymator]	131	5,00E-91	130/131(99%)	
scaffold91	IVSPER-1	14020	453857-467876	p5-2	460033-461034 + strand	no	333	ADI40457.1	unknown [Hyposoter didymator]	333	0,00E+00	329/333(99%)	
scaffold91	IVSPER-1	14020	453857-467876	U5	461470-462000 + strand	no	176	ADI40458.1	unknown [Hyposoter didymator]	176	6,00E-129	175/176(99%)	
scaffold91	IVSPER-1	14020	453857-467876	IVSP2-1	462381-463910 + strand	no	509	ADI40459.1	unknown [Hyposoter didymator]	509	0,00E+00	508/509(99%)	
scaffold91	IVSPER-1	14020	453857-467876	N-1	464563-466050 + strand	no	495	ADI40460.1	unknown [Hyposoter didymator]	470	0,00E+00	467/470(99%)	N-term longer
scaffold91	IVSPER-1	14020	453857-467876	U25	467172-467876 - strand	no	234	AKD28083.1	ring finger domain [Glypta fumiferanae]	237	7,00E-14	37/118(31%)	putative IVSPER gene; may be wasp gene

scaffold127548	IVSPER-4	15811	6832835-6848646	U29	6832835-6833713 - strand	no	292		No significant similarity found					highly transcribed in calyx
scaffold127548	IVSPER-4	15811	6832835-6848646	U30	6834523-6838368 - strand	no	1281	AKD28060.1	hypothetical protein [Glypta fumiferanae] gene="U28"	1322	0,00E+00	616/1339(46%)		
scaffold127548	IVSPER-4	15811	6832835-6848646	U31	6839646-6840788 + strand	no	380	AKD28063.1	hypothetical protein [Glypta fumiferanae] gene="U31"	370	8,00E-27	93/323(29%)		transcribed in calyx
scaffold127548	IVSPER-4	15811	6832835-6848646	U32	6841304-6841912 + strand	no	202		No significant similarity found					transcribed in calyx
scaffold127548	IVSPER-4	15811	6832835-6848646	U33	6842790-6844940 - strand	no	716		No significant similarity found					transcribed in calyx
scaffold127548	IVSPER-4	15811	6832835-6848646	U34	6845548-6848646 - strand	no	1032	AKD28054.1	helicase domain [Glypta fumiferanae]	1012	0,00E+00	488/1040(47%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	U15	10761570-10762802 - strand	no	410	ADI40477.1	unknown [Hyposoter didymator]	410	0,00E+00	407/410(99%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	IVSP3-2	10763133-10765037 + strand	no	634	ADI40478.1	unknown [Hyposoter didymator]	527	0,00E+00	526/527(99%)		N-term 100aa longer in genomic seq
scaffold127548	IVSPER-3	25432	10761570-10787001	U16	10765894-10767732 - strand	no	612	ADI40479.1	unknown [Hyposoter didymator]	612	0,00E+00	612/612(100%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	U17	10768078-10768325 + strand	no	82	ADI40480.1	unknown [Hyposoter didymator]	82	1,00E-53	82/82(100%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	U18	10769122-10769379 + strand	no	85	ADI40481.1	unknown [Hyposoter didymator]	85	7,00E-53	84/85(99%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	p12-1	10770065-10770298 + strand	no	77	CAR31591.1	p12-like 1 protein [Hyposoter didymator]	77	6,00E-45	77/77(100%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	U19	10771340-10773322 + strand	no	660	ADI40483.1	unknown [Hyposoter didymator]	660	0,00E+00	658/660(99%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	IVSP4-2	10774112-10775407 - strand	no	431	ADI40484.1	unknown [Hyposoter didymator]	431	0,00E+00	430/431(99%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	U20	10776029-10776240 + strand	no	70	ADI40485.1	unknown [Hyposoter didymator]	70	6,00E-44	69/70(99%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	U21	10776822-10777061 + strand	no	79	ADI40486.1	unknown [Hyposoter didymator]	79	4,00E-47	77/79(97%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	U22	10777309-10778172 - strand	no	287	ADI40487.1	unknown [Hyposoter didymator]	257	0,00E+00	255/257(99%)		N-term longer in genomic seq
scaffold127548	IVSPER-3	25432	10761570-10787001	U28	10778369-10779088 + strand	no	239		No significant similarity found					newly identified, putative (no reads in calyx_1 transcriptome dataset)
scaffold127548	IVSPER-3	25432	10761570-10787001	U23	10779153-10780400 - strand	no	415	ADI40488.1	unknown [Hyposoter didymator]	415	0,00E+00	408/415(98%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	p53-1	10780635-10781822 + strand	no	395	CAR31590.1	p53-like 1 protein [Hyposoter didymator]	395	0,00E+00	391/395(99%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	U24	10782094-10783785 - strand	no	563	ADI40490.1	unknown [Hyposoter didymator]	563	0,00E+00	561/563(99%)		
scaffold127548	IVSPER-3	25432	10761570-10787001	N-2	10785523-10787001 + strand	no	492	ADI40491.1	unknown [Hyposoter didymator]	492	0,00E+00	490/492(99%)		
scaffold91	IVSPER-2	26611	541304-567914	N-4	541304-542734 - strand	no	476	ADI40491.1	unknown [Hyposoter didymator] gene="N-2"	492	0,00E+00	277/491(56%)		
scaffold91	IVSPER-2	26611	541304-567914	U26	542904-543740 - strand	no	278	AKD28081.1	hypothetical protein [Glypta fumiferanae] Gf_U39	298	9,00E-30	59/139(42%)		
scaffold91	IVSPER-2	26611	541304-567914	IVSP2-2	544341-545867 - strand	no	508	ADI40476.1	unknown, partial [Hyposoter didymator]	143	5,00E-96	143/143(100%)		completed IVSP2-2 sequence
scaffold91	IVSPER-2	26611	541304-567914	IVSP4-1	546767-548107 + strand	no	446	ADI40475.1	unknown [Hyposoter didymator]	446	0,00E+00	443/446(99%)		
scaffold91	IVSPER-2	26611	541304-567914	p12-2	548725-549038 - strand	no	104	ADI40474.1	unknown [Hyposoter didymator]	104	6,00E-69	103/104(99%)		
scaffold91	IVSPER-2	26611	541304-567914	U27	549438-549740 + strand	no	100		No significant similarity found					
scaffold91	IVSPER-2	26611	541304-567914	U14	549917-550078 - strand	no	53	ADI40473.1	unknown [Hyposoter didymator]	53	3,00E-29	53/53(100%)		
scaffold91	IVSPER-2	26611	541304-567914	p12-3	550341-550643 - strand	no	100	ADI40472.1	unknown [Hyposoter didymator]	100	8,00E-68	100/100(100%)		
scaffold91	IVSPER-2	26611	541304-567914	U13	551219-551677 - strand	no	152	ADI40471.1	unknown [Hyposoter didymator]	152	1,00E-107	152/152(100%)		
scaffold91	IVSPER-2	26611	541304-567914	U12	551947-552558 + strand	no	203	ADI40470.1	unknown [Hyposoter didymator]	203	1,00E-147	203/203(100%)		
scaffold91	IVSPER-2	26611	541304-567914	U11	553154-554104 - strand	no	316	ADI40469.1	unknown [Hyposoter didymator]	316	0,00E+00	312/316(99%)		
scaffold91	IVSPER-2	26611	541304-567914	U10	555456-559523 - strand	no	1355	ADI40468.1	unknown [Hyposoter didymator]	1355	0,00E+00	1352/1355(99%)		
scaffold91	IVSPER-2	26611	541304-567914	U9	559893-560717 + strand	no	274	ADI40467.1	unknown [Hyposoter didymator]	274	0,00E+00	274/274(100%)		
scaffold91	IVSPER-2	26611	541304-567914	U8	561319-561552 + strand	no	77	ADI40466.1	unknown [Hyposoter didymator]	77	3,00E-47	77/77(100%)		
scaffold91	IVSPER-2	26611	541304-567914	IVSP3-1	562225-564117 - strand	no	630	ADI40465.1	unknown [Hyposoter didymator]	630	0,00E+00	625/630(99%)		
scaffold91	IVSPER-2	26611	541304-567914	IVSP1-2	564643-565380 - strand	no	245	ADI40464.1	unknown [Hyposoter didymator]	196	5,00E-141	194/196(99%)		N-term longer
scaffold91	IVSPER-2	26611	541304-567914	U7	565507-566145 - strand	no	212	ADI40463.1	unknown [Hyposoter didymator]	212	4,00E-157	212/212(100%)		
scaffold91	IVSPER-2	26611	541304-567914	U6	566499-567548 - strand	no	349	ADI40462.1	unknown [Hyposoter didymator]	349	0,00E+00	348/349(99%)		
scaffold91	IVSPER-2	26611	541304-567914	N-3	567663-567944 - strand	no	93	ADI40461.1	unknown [Hyposoter didymator]	93	1,00E-60	90/93(97%)		

Campoletis sonorensis

CsIV proviral segment

scaffold_8749	rep gene	2269	na	rep gene 1	45-674 + strand	no	209	AHY22033.1	repeat element 33 [Diadegma semiclausum ic 243	3,00E-64	101/213(47%)		
scaffold_8748	rep gene	2287	na	rep gene 2	TO CREATE (2285,,1713)				there is no gene predicted in this scaffold; no possibility to click and drag feature				
scaffold_7280	CsV	2380	not applicable	cys_CsV, partial	1546-nn + strand	yes	NA	YP_589077.1	VHv1.4 protein [Campoletis sonorensis ichtnov 322				
scaffold_11	CsA	6368	861628-867995	HP_CsA	861717-862004 - strand	no	95		no significant similarity				
scaffold_11	CsA	6368	861628-867995	cys_CsA	864776-865537 - strand	yes	177	AAO43443.1	AHv0.8 cys-motif protein precursor [Campolet 177	8,00E-127	173/177(98%)		
scaffold_49	CsB	6626	22030-28655	rep_CsB	23475-24182 - strand	no	235	AAA42923.1	repeat element protein [Campoletis sonorensis: 235	2,00E-174	235/235(100%)		
scaffold_49	CsB	6626	22030-28655	HP_CsB	26564-27903 + strand	yes	220		no significant similarity				may not be a gene
scaffold_28	CsC	7350	25280-32629	overlap with Cs_IVSPER-2									
scaffold_17	CsE	7990	1330025-1338014	rep1_CsE	1331076-1331756 - strand	no	226	YP_00103133	repeat element protein-d11.1 [Hyposoter fugiti 199	4,00E-06	42/175(24%)		
scaffold_17	CsE	7990	1330025-1338014	rep2_CsE	1333207-1333722 - strand	no	171	YP_00103133	repeat element protein-d11.1 [Hyposoter fugiti 199	0.004	33/133(25%)		
scaffold_17	CsE	7990	1330025-1338014	rep3_CsE	1336256-1336924 - strand	no	222	AAA42923.1	repeat element protein [Campoletis sonorensis: 235	8,00E-53	87/197(44%)		
scaffold_131	CsF	8155	808380-816534	cys_CsF	812667-814550 - strand	yes	403	AY197491	FHV1.4 cys-motif protein precursor [Campoleti 403	0.0	403/403 (100%)		
scaffold_10	CsD	8168	961052-969219	vnX_CsD	963294-964382 - strand	no	362	AAO45828.1	inXen Vnx-d1 [Campoletis sonorensis ichtnov 362	0.0	361/362(99%)		
scaffold_10	CsD	8168	961052-969219	HP_CsD	964936-965238 - strand	no	100		no significant similarity				
scaffold_14	CsG2	8338	192247-200584	rep1_CsG2	192863-193606 + strand	no	247	BAF45598.1	c7-1.1 [Tranosema rostrale ichtnovirus]	248	5,00E-48	98/237(41%)	
scaffold_14	CsG2	8338	192247-200584	rep2_CsG2	194788-195492 + strand	no	234	BAF45598.1	c7-1.1 [Tranosema rostrale ichtnovirus]	248	2,00E-46	92/203(45%)	
scaffold_14	CsG2	8338	192247-200584	rep3_CsG2	196511-197119 + strand	no	202	BAF45598.1	c7-1.1 [Tranosema rostrale ichtnovirus]	248	1,00E-59	95/215(44%)	
scaffold_14	CsG2	8338	192247-200584	rep4_CsG2	198753-199601 + strand	no	282	BAF45598.1	c7-1.1 [Tranosema rostrale ichtnovirus]	248	1,00E-59	107/214(50%)	
scaffold_14	CsG	8656	76017-84672	vnX_CsG	80980-82059 - strand	no	359	AAO45829.1	inXen Vnx-g1 [Campoletis sonorensis ichtnov 359	0.0	359/359(100%)		

scaffold_14	CsG	8656	76017-84672	HP_CsG	83584-83949 + strand	no	121		no significant similarity				
scaffold_22	CsI	8779	695663-704441	rep1_CsI	696515-697228 + strand	no	237	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	3,00E-54	91/197(46%)		
scaffold_22	CsI	8779	695663-704441	rep2_CsI	697713-698441 + strand	no	242	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	2,00E-62	98/199(49%)		
scaffold_22	CsI	8779	695663-704441	HP_CsI	700059-700382 - strand	no	107		no significant similarity				
scaffold_22	CsI	8779	695663-704441	rep3_CsI	700879-701784 + strand	no	301	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	3,00E-51	96/190(51%)		
scaffold_128	CsI2	9042	110016-119057	vank1_CsI2	110664-111179 - strand	no	171	AAX56959.1	vankyrin 3 [Campeletis sonorensi ichnovirus] 171	3,00E-125	171/171(100%)		
scaffold_128	CsI2	9042	110016-119057	rep_CsI2	112670-113302 - strand	no	210	BAF45598.1	c7-1.1 [Tranosema rostrale ichnovirus] 248	8,00E-61	98/187(52%)		
scaffold_128	CsI2	9042	110016-119057	vank2_CsI2	114140-114607 - strand	no	155	AAX56957.1	vankyrin 1 [Campeletis sonorensi ichnovirus] 155	2,00E-111	155/155(100%)		
scaffold_128	CsI2	9042	110016-119057	HP_CsI2	115736-116062 - strand	no	108		no significant similarity				
scaffold_128	CsI2	9042	110016-119057	vank3_CsI2	117111-117617 - strand	no	168	AAX56958.1	vankyrin 2 [Campeletis sonorensi ichnovirus] 168	8,00E-121	168/168(100%)		
scaffold_38	CsH	9050	1398066-1407115	HP_CsH	1400102-1400407 - strand	no	101		no significant similarity				
scaffold_38	CsH	9050	1398066-1407115	5rep_CsH	1402633-1405449 + strand	no	938	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	2,00E-41	89/215(41%)		
scaffold_16	CsX6	9213	504600-513812	2rep_CsX6	506770-507660 - strand	no	296	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	8,00E-45	84/175(48%)		
scaffold_16	CsX6	9213	504600-513812	rep_CsX6	512155-512874 - strand	no	239	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	8,00E-57	95/203(47%)		
scaffold_15	CsJ	9484	2621922-2631405	rep1_CsJ	2623490-2624194 + strand	no	234	BAF45598.1	c7-1.1 [Tranosema rostrale ichnovirus] 248	3,00E-59	98/216(45%)		
scaffold_15	CsJ	9484	2621922-2631405	rep2_CsJ	2625029-2625739 - strand	no	236	BAF45598.1	c7-1.1 [Tranosema rostrale ichnovirus] 248	6,00E-50	91/218(42%)		
scaffold_15	CsJ	9484	2621922-2631405	rep3_CsJ	2629669-2630322 + strand	no	217	BAF45598.1	c7-1.1 [Tranosema rostrale ichnovirus] 248	2,00E-37	80/187(43%)		
scaffold_35	CsX8	9999	164467-174465	HP1_CsX8	165205-165672 - strand	no	155		no significant similarity				
scaffold_35	CsX8	9999	164467-174465	cys_CsX8	168692-172561 - strand	yes	581	AAO43445.1	LHv2.8 cys-motif protein precursor [Campeletis 678	0.0	409/671(61%)		
scaffold_35	CsX8	9999	164467-174465	HP2_CsX8	172947-173360 - strand	no	137		no significant similarity				
scaffold_4391	CsL	10024	8079-18102	cys_CsL	10645-14521 - strand	yes	678	AAO43445.1	LHv2.8 cys-motif protein precursor [Campeletis 678	0.0	675/678(99%)	shorter	
scaffold_4391	CsL	10024	8079-18102	HP_CsL	16908-17306 + strand	no	132		no significant similarity				
scaffold_110	CsX2	10806	248068-258873	vank1_CsX2	249108-249605 + strand	no	165	ABH10021.1	vankyrin 2 [Campeletis chloridae ichnovirus] 168	2,00E-105	144/165(87%)		
scaffold_110	CsX2	10806	248068-258873	vank2_CsX2	251609-252118 + strand	no	169	AAX56956.1	vankyrin 4 [Campeletis sonorensi ichnovirus] 160	2,00E-65	100/151(66%)	short	
scaffold_110	CsX2	10806	248068-258873	vank3_CsX2	252614-253099 + strand	no	161	AAX56955.1	vankyrin 3 [Campeletis sonorensi ichnovirus] 161	9,00E-81	122/149(82%)		
scaffold_110	CsX2	10806	248068-258873	vank4_CsX2	254294-254672 + strand	no	125	AAX56955.1	vankyrin 3 [Campeletis sonorensi ichnovirus] 161	2,00E-23	62/147(42%)		
scaffold_110	CsX2	10806	248068-258873	rep_CsX2	256559-257191 + strand	no	210	BAF45598.1	c7-1.1 [Tranosema rostrale ichnovirus] 248	2,00E-60	94/189(50%)		
scaffold_5	CsN	10943	175169-186111	N1_CsN	177111-178547 - strand	no	478	AAS79017.1	NHv1.2 protein [Campeletis sonorensi ichnovirus] 400	0.0	305/404(75%)		
scaffold_5	CsN	10943	175169-186111	N2_CsN	180542-181744 - strand	no	400	AAS79017.1	NHv1.2 protein [Campeletis sonorensi ichnovirus] 400	0.0	400/400(100%)		
scaffold_5	CsN	10943	175169-186111	HP_CsN	185333-185656 + strand	no	107		no significant similarity				
scaffold_5218	CsP	12113	15720-27832	HP_CsP	19074-19379 - strand	no	101		no significant similarity				
scaffold_5218	CsP	12113	15720-27832	vank4_CsP	19628-20110 + strand	no	160	AAX56956.1	vankyrin 4 [Campeletis sonorensi ichnovirus] 160	3,00E-114	159/160(99%)		
scaffold_5218	CsP	12113	15720-27832	vank3_CsP	20609-21094 + strand	no	161	AAX56955.1	vankyrin 3 [Campeletis sonorensi ichnovirus] 161	4,00E-115	161/161(100%)		
scaffold_5218	CsP	12113	15720-27832	vank2_CsP	23733-24215 + strand	no	160	AAX56954.1	vankyrin 2 [Campeletis sonorensi ichnovirus] 160	1,00E-114	160/160(100%)		
scaffold_5218	CsP	12113	15720-27832	vank1_CsP	26747-27262 - strand	no	171	AAX56953.1	vankyrin 1 [Campeletis sonorensi ichnovirus] 171	3,00E-124	171/171(100%)		
scaffold_23	CsM	12197	1422227-1434423	HP1_CsM	1425348-1425740 - strand	no	130		no significant similarity				
scaffold_23	CsM	12197	1422227-1434423	N_CsM	1428224-1429615 + strand	no	463	AAS79017.1	NHv1.2 protein [Campeletis sonorensi ichnovirus] 400	3,00E-166	245/407(60%)		
scaffold_23	CsM	12197	1422227-1434423	HP2_CsM	1431734-1432099 - strand	no	121		no significant similarity				
scaffold_50	CsQ	12543	290527-303069	rep1_CsQ	291919-292629 - strand	no	236	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	2,00E-73	116/231(50%)		
scaffold_50	CsQ	12543	290527-303069	vinx1_CsQ	294036-295118 - strand	no	360	YP_589076.1	innexin-like protein 1 [Campeletis sonorensi i 369	0.0	323/328(98%)		
scaffold_50	CsQ	12543	290527-303069	vinx2_CsQ	296198-297295 + strand	no	365	YP_589075.1	innexin-like protein 2 [Campeletis sonorensi i 365	0.0	365/365(100%)		
scaffold_50	CsQ	12543	290527-303069	rep2_CsQ	299186-299929 - strand	no	247	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	9,00E-48	85/187(45%)		
scaffold_50	CsQ	12543	290527-303069	rep3_CsQ	300417-301001 - strand	no	194	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	6,00E-45	83/191(43%)		
scaffold_50	CsQ	12543	290527-303069	rep4_CsQ	301383-302144 - strand	no	253	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	2,00E-53	94/210(45%)		
scaffold_6070	CsO1	12746	168701-181446	4rep_CsO1	171805-173964 + strand	no	719	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	3,00E-43	83/184(45%)		
scaffold_6070	CsO1	12746	168701-181446	HP1_CsO1	174818-175135 + strand	no	105		no significant similarity				
scaffold_6070	CsO1	12746	168701-181446	HP2_CsO1	176713-177060 + strand	no	115		no significant similarity				
scaffold_6070	CsO1	12746	168701-181446	3rep_CsO1	177630-179456 + strand	no	608	AAA42923.1	repeat element protein [Campeletis sonorensi: 235	5,00E-33	81/223(36%)		
scaffold_149	CsU	15338	374074-389411	cys1_CsU	375123-375900 - strand	yes	180	AAO43446.1	UHV0.8a cys-motif protein precursor [Campeletis 180	8,00E-131	180/180(100%)	Number of Matches: 5	
scaffold_149	CsU	15338	374074-389411	cys2_CsU	377416-378140 - strand	yes	161	AAO43447.1	UHV0.8 cys-motif protein precursor [Campeletis 152	6,00E-54	91/151(60%)		
scaffold_149	CsU	15338	374074-389411	cys3_CsU	383382-384157 - strand	yes	178	AAO43446.1	UHV0.8a cys-motif protein precursor [Campeletis 180	1,00E-62	96/164(59%)		
scaffold_149	CsU	15338	374074-389411	cys4_CsU	385182-385875 - strand	yes	152	AAO43447.1	UHV0.8 cys-motif protein precursor [Campeletis 152	2,00E-108	152/152(100%)		
scaffold_149	CsU	15338	374074-389411	cys5_CsU	387355-388121 - strand	yes	175	AAO43447.1	UHV0.8 cys-motif protein precursor [Campeletis 152	2,00E-66	104/152(68%)	NNN within the nt sequence	
scaffold_28	CsW	15807	614005-629811	cys1_CsW	615213-616060 + strand	yes	203	YP_589078.1	cysteine-rich protein [Campeletis sonorensi i 203	3,00E-140	192/203(95%)		
scaffold_28	CsW	15807	614005-629811	cys2_CsW	617470-618890 + strand	yes	261	YP_589079.1	cysteine-rich protein [Campeletis sonorensi i 198	8,00E-43	71/120(59%)		
scaffold_28	CsW	15807	614005-629811	rep1_CsW	619946-620629 - strand	no	227	BAF73402.1	f3.1 [Tranosema rostrale ichnovirus] 226	8,00E-73	107/222(48%)		
scaffold_28	CsW	15807	614005-629811	cys3_CsW	622282-623280 + strand	yes	198	YP_589079.1	cysteine-rich protein [Campeletis sonorensi i 198	2,00E-145	198/198(100%)		
scaffold_28	CsW	15807	614005-629811	rep2_CsW	624629-625342 - strand	no	237	YP_001031326	repeat element protein-b15.1 [Hyposoter fugiti 272	5,00E-80	122/237(51%)		
scaffold_28	CsW	15807	614005-629811	HP_CsW	627004-627324 - strand	no	106		no significant similarity				
scaffold_28	CsW	15807	614005-629811	rep3_CsW	628358-629077 - strand	no	239	YP_001031313	repeat element protein-d4.2 [Hyposoter fugiti 248	6,00E-98	132/226(58%)		
scaffold_5890	CsZ	15871	134147-150017	rep1_CsZ	134843-135562 + strand	no	239	AHY22033.1	repeat element 33 [Diadegma semiclausaum ic 243	5,00E-69	103/219(47%)		
scaffold_5890	CsZ	15871	134147-150017	rep2_CsZ	137736-138422 + strand	no	228	AIK25648.1	Rep1 [Hyposoter didymator ichnovirus] 231	9,00E-72	105/213(49%)		
scaffold_5890	CsZ	15871	134147-150017	rep3_CsZ	139610-140290 + strand	no	226	BAF45626.1	f3.2 [Tranosema rostrale ichnovirus] 237	3,00E-62	93/189(49%)		
scaffold_5890	CsZ	15871	134147-150017	rep4_CsZ	140771-141505 + strand	no	244	AHY21950.1	repeat element 11 [Diadegma semiclausaum ic 225	3,00E-55	87/202(43%)		
scaffold_5890	CsZ	15871	134147-150017	rep5_CsZ	142565-143128 - strand	no	187	YP_001031313	repeat element protein-d3.2 [Hyposoter fugiti 230	4,00E-51	87/178(49%)		
scaffold_5890	CsZ	15871	134147-150017	rep6_CsZ	144223-144912 + strand	no	229	BAF45611.1	d5.2 [Tranosema rostrale ichnovirus] 218	4,00E-72	107/206(52%)		

scaffold_5890	CsZ	15871	134147-150017	rep7_CsZ	146321-147118 + strand	no	265	BAF45598.1	c7-1.1 [Tranosema rostrale ichnovirus]	248	3,00E-106	153/249(61%)	
scaffold_5934	CsX1	17335	19391-36725	vank1_CsX1	20620-21141 + strand	no	173	AFH35119.1	vankyrin 5 [Hyposoter didymator ichnovirus]	168	7,00E-43	75/164(46%)	
scaffold_5934	CsX1	17335	19391-36725	vmx1_CsX1	22756-23850 + strand	no	364	AHY21960.1	viral innexin 3 [Diadegma semiclausaum ichnovirus]	357	7,00E-131	182/351(52%)	
scaffold_5934	CsX1	17335	19391-36725	rep1_CsX1	24562-25275 + strand	no	237	BAF45598.1	c7-1.1 [Tranosema rostrale ichnovirus]	248	6,00E-65	108/216(50%)	NNN within the nt sequence
scaffold_5934	CsX1	17335	19391-36725	vank2_CsX1	26300-26770 + strand	no	156	AFH35115.1	vankyrin 1 [Hyposoter didymator ichnovirus]	159	3,00E-52	82/152(54%)	Number of Matches: 4
scaffold_5934	CsX1	17335	19391-36725	vank3_CsX1	28742-29212 + strand	no	156	YP_00103123	vankyrin-b17 [Hyposoter fugitivus ichnovirus]	170	1,00E-46	78/156(50%)	Number of Matches: 3
scaffold_5934	CsX1	17335	19391-36725	vank4_CsX1	30120-30608 + strand	no	162	YP_00103123	vankyrin-b1 [Hyposoter fugitivus ichnovirus]	167	8,00E-55	88/162(54%)	
scaffold_5934	CsX1	17335	19391-36725	vmx2_CsX1	31535-32626 + strand	no	363	BAF45609.1	d4.1 [Tranosema rostrale ichnovirus]	376	3,00E-141	198/360(55%)	
scaffold_5934	CsX1	17335	19391-36725	rep2_CsX1	34635-35156 + strand	no	173	BAF45626.1	f3.2 [Tranosema rostrale ichnovirus]	237	3,00E-55	93/180(52%)	
scaffold_5934	CsX1	17335	19391-36725	vank5_CsX1	35714-36208 + strand	no	164	ABH10021.1	vankyrin 2 [Campoletis chloridae ichnovirus]	168	6,00E-50	80/163(49%)	
scaffold_116	CsT	23217	7789-31005	HP1_CsT	14790-15116 - strand	no	108		no significant similarity				
scaffold_116	CsT	23217	7789-31005	HP2_CsT	21883-22209 - strand	no	108		no significant similarity				
scaffold_116	CsT	23217	7789-31005	HP3_CsT	27023-27376 + strand	no	117		no significant similarity				
scaffold_116	CsT	23217	7789-31005	HP4_CsT	28660-29043 + strand	no	127		no significant similarity				
scaffold_8362	CsX5, partial	>5297	1-5297	rep1_CsX5	2289-3026 - strand	no	245	AAA42923.1	repeat element protein [Campoletis sonorensis]	235	3,00E-50	95/240(40%)	
scaffold_8362	CsX5, partial	>5297	1-5297	rep2_CsX5	3571-4296 + strand	no	241	AAA42923.1	repeat element protein [Campoletis sonorensis]	235	5,00E-57	104/233(45%)	
scaffold_6095	CsX7, partial	>6041	183042-189082	rep1_CsX7	183042-183731 - strand	no	229	BAF45626.1	f3.2 [Tranosema rostrale ichnovirus]	237	2,00E-76	112/202(55%)	
scaffold_6095	CsX7, partial	>6041	183042-189082	rep2_CsX7	185656-186273 - strand	no	235	BAF45626.1	f3.2 [Tranosema rostrale ichnovirus]	237	5,00E-72	106/201(53%)	
scaffold_6095	CsX7, partial	>6041	183042-189082	rep3_CsX7	188342-189082 - strand	no	246	BAF45626.1	f3.2 [Tranosema rostrale ichnovirus]	237	2,00E-74	112/201(56%)	
scaffold_60	CsX3, partial	>7876	304794-312669	rep1_CsX3	304794-305507 + strand	no	237	AHY22033.1	repeat element 33 [Diadegma semiclausaum ic	243	1,00E-77	115/225(51%)	
scaffold_60	CsX3, partial	>7876	304794-312669	rep2_CsX3	306761-307570 + strand	no	269	BAF45598.1	c7-1.1 [Tranosema rostrale ichnovirus]	248	2,00E-119	165/247(67%)	Number of Matches: 2, NNN in 5'region on gene (position 507,725)
scaffold_60	CsX3, partial	>7876	304794-312669	rep3_CsX3	309164-309979 + strand	no	271	BAF45598.1	c7-1.1 [Tranosema rostrale ichnovirus]	248	2,00E-115	162/247(66%)	
scaffold_60	CsX3, partial	>7876	304794-312669	rep4_CsX3	311747-312586 + strand	no	279	BAF45598.1	c7-1.1 [Tranosema rostrale ichnovirus]	248	8,00E-116	158/237(67%)	
scaffold_13	CsX4, partial	>9181	1407384-1416564	rep1_CsX4	1409287-1410012 - strand	no	241	AAA42923.1	repeat element protein [Campoletis sonorensis]	235	5,00E-57	104/233(45%)	
scaffold_13	CsX4, partial	>9181	1407384-1416564	rep2_CsX4	1410557-1411294 + strand	no	245	AAA42923.1	repeat element protein [Campoletis sonorensis]	235	3,00E-50	95/240(40%)	
scaffold_13	CsX4, partial	>9181	1407384-1416564	HP_CsX4	1411909-1412361 + strand	no	150		no significant similarity				
scaffold_13	CsX4, partial	>9181	1407384-1416564	rep3_CsX4	1415602-1416564 + strand	no	320	AAA42923.1	repeat element protein [Campoletis sonorensis]	235	6,00E-51	96/232(41%)	
C. sonorensis IVSPER													
scaffold_6122	IVSP_U36L	471	234803-235273	U36L	234803-235273 - strand	no	156	AKD28080.1	hypothetical protein [Glypta fumiferanae]	Gf_L 175	7,00E-15	49/146(34%)	
scaffold_12	IVSP_U37L	1863	104145-106007	U37L-2	104145-106007 - strand	no	620	AKD28048.1	helicase-primase domain [Glypta fumiferanae]	721	0.0	337/621(54%)	
scaffold_16	Cs_IVSPER-5	3750	2424942-2428691	IVSP1L-3	2424942-2425688 + strand	no	248	ADI40453.1	unknown [Hyposoter didymator]	Hd_IVSP1-1	253	6,00E-57	104/257(40%)
scaffold_16	Cs_IVSPER-5	3750	2424942-2428691	U2L	2426081-2426764 + strand	no	227	ADI40454.1	unknown [Hyposoter didymator]	Hd_U2	228	3,00E-120	165/226(73%)
scaffold_16	Cs_IVSPER-5	3750	2424942-2428691	U1L	2427951-2428691 - strand	no	246	ADI40452.1	unknown [Hyposoter didymator]	Hd_U1	244	1,00E-65	101/245(41%)
scaffold_50	Cs_IVSPER-3	8610	218627-227236	IVSP4L-2	218627-219940 - strand	no	437	ADI40475.1	unknown [Hyposoter didymator]	Hd_IVSP4-1	446	7,00E-156	217/399(54%)
scaffold_50	Cs_IVSPER-3	8610	218627-227236	U4L	220560-221022 + strand	no	138	ADI40456.1	unknown [Hyposoter didymator]	Hd_U4	131	2,00E-29	52/118(44%)
scaffold_50	Cs_IVSPER-3	8610	218627-227236	p53L-3	221232-222284 + strand	no	350	CAR31590.1	p53-like1 protein [Hyposoter didymator]		395	6,00E-67	139/337(41%)
scaffold_50	Cs_IVSPER-3	8610	218627-227236	U5L	222667-223197 + strand	no	176	ADI40458.1	unknown [Hyposoter didymator]	Hd_U5	176	1,00E-74	105/174(60%)
scaffold_50	Cs_IVSPER-3	8610	218627-227236	IVSP2L-2	223589-224965 + strand	no	458	ADI40459.1	unknown [Hyposoter didymator]	Hd_IVSP2-1	509	0.0	303/459(66%)
scaffold_50	Cs_IVSPER-3	8610	218627-227236	CsN-3	225761-227236 + strand	no	491	ADI40491.1	unknown [Hyposoter didymator]	Hd_N-2	492	0.0	346/492(70%)
scaffold_57	Cs_IVSPER-4	9937	383305-393241	U30L	383305-386526 + strand	no	1073	AKD28060.1	hypothetical protein [Glypta fumiferanae]	Gf_L 1322	0.0	502/1044(48%)	
scaffold_57	Cs_IVSPER-4	9937	383305-393241	U34L	387873-390950 + strand	no	1025	AKD28054.1	helicase domain [Glypta fumiferanae]	Hd_U34 1012	0.0	486/1009(48%)	
scaffold_57	Cs_IVSPER-4	9937	383305-393241	IVSP4L-3	391820-393241 - strand	no	473	ADI40484.1	unknown [Hyposoter didymator]	Hd_IVSP4-2	431	2,00E-169	230/405(57%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	U15L	122689-123342 - strand	no	217	ADI40477.1	unknown [Hyposoter didymator]	Hd_U15	410	3,00E-97	130/212(61%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	IVSP1L-1	124770-125432 + strand	no	220	ADI40464.1	unknown [Hyposoter didymator]	Hd_IVSP1-2	196	6,00E-63	99/197(50%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	U37L-1	126353-128176 + strand	no	607	AKD28048.1	helicase-primase domain [Glypta fumiferanae]	721	0.0	338/624(54%)	
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	U31L-1	129117-130226 - strand	no	369	AKD28063.1	hypothetical protein [Glypta fumiferanae]	Gf_L 370	4,00E-32	95/341(28%)	
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	U35L	130724-131257 - strand	no	177	AKD28058.1	hypothetical protein [Glypta fumiferanae]	Gf_L 180	5,00E-37	70/156(45%)	
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	Gf_U27L	132692-134518 + strand	no	608	AKD28059.1	hypothetical protein [Glypta fumiferanae]	Gf_L 325	1,00E-31	97/312(31%)	
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	U17L	135604-135929 + strand	no	79	ADI40480.1	unknown [Hyposoter didymator]	Hd_U17	82	1,00E-14	31/66(47%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	p12L-1	137295-137555 + strand	no	86	AAD01200.1	p12 [Campoletis sonorensis ichnovirus]		92	8,00E-17	43/92(47%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	U19L	139263-141209 + strand	no	648	ADI40483.1	unknown [Hyposoter didymator]	Hd_U19	660	0.0	480/649(74%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	IVSP4L-1	141938-143242 - strand	no	434	ADI40484.1	unknown [Hyposoter didymator]	Hd_IVSP4-2	431	5,00E-175	232/434(53%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	U22L	143868-144761 - strand	no	297	ADI40487.1	unknown [Hyposoter didymator]	Hd_U22	257	4,00E-59	95/249(38%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	U23L	146427-147608 - strand	no	393	ADI40488.1	unknown [Hyposoter didymator]	Hd_U23	415	2,00E-170	245/389(63%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	p53L-1	148451-149548 + strand	no	365	AAD01199.1	p53 [Campoletis sonorensis ichnovirus]		364	0.0	306/365(84%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	U24L	150683-152365 + strand	no	560	ADI40490.1	unknown [Hyposoter didymator]	Hd_U24	563	0.0	387/558(69%)
scaffold_6122	Cs_IVSPER-1	31594	122689-154282	CsN-1	152861-154282 + strand	no	473	ADI40491.1	unknown [Hyposoter didymator]	Hd_N-2	492	0.0	307/491(63%)
scaffold_28	Cs_IVSPER-2	33269	7310-40578	U6L	10522-11574 + strand	no	350	ADI40462.1	unknown [Hyposoter didymator]	Hd_U6	349	0.0	297/350(85%)
scaffold_28	Cs_IVSPER-2	33269	7310-40578	U7L	13049-13684 + strand	no	211	ADI40463.1	unknown [Hyposoter didymator]	Hd_U7	212	5,00E-61	119/211(56%)
scaffold_28	Cs_IVSPER-2	33269	7310-40578	IVSP1L-2	13781-14701 - strand	no	306	ADI40464	unknown [Hyposoter didymator]	Hd_IVSP1-2	196	9,00E-58	93/195(48%)
scaffold_28	Cs_IVSPER-2	33269	7310-40578	IVSP3L	15113-17002 + strand	no	629	ADI40465.1	unknown [Hyposoter didymator]	Hd_IVSP3-1	630	0.0	423/628(67%)
scaffold_28	Cs_IVSPER-2	33269	7310-40578	U31L-2	17484-18179 - strand	no	231	AKD28063.1	hypothetical protein [Glypta fumiferanae]	Gf_L 370	0.029	40/136(29%)	
scaffold_28	Cs_IVSPER-2	33269	7310-40578	U8L	18541-18768 - strand	no	75	ADI40466.1	unknown [Hyposoter didymator]	Hd_U8	77	4,00E-14	36/75(48%)
scaffold_28	Cs_IVSPER-2	33269	7310-40578	U9L	19075-19890 - strand	no	271	ADI40467.1	unknown [Hyposoter didymator]	Hd_U9	274	2,00E-112	170/269(63%)
scaffold_28	Cs_IVSPER-2	33269	7310-40578	U16L	20258-22096 - strand	no	612	ADI40479.1	unknown [Hyposoter didymator]	Hd_U16	612	0.0	491/605(81%)
scaffold_28	Cs_IVSPER-2	33269	7310-40578	U10L	22789-27768 + strand	no	1344	ADI40468.1	unknown [Hyposoter didymator]	Hd_U10	1355	0.0	1035/1353(76%) partial?

scaffold_28	Cs_IVSPER-2 33269	7310-40578	U11L	27768-28709 + strand	no	313	ADI40469.1	unknown [Hyposoter didymator] Hd_U11	316	3,00E-180	244/317(77%)	
scaffold_28	Cs_IVSPER-2 33269	7310-40578	U12L	29360-29971 - strand	no	203	ADI40470.1	unknown [Hyposoter didymator] Hd_U12	203	1,00E-121	168/203(83%)	
scaffold_28	Cs_IVSPER-2 33269	7310-40578	U13L	30286-30768 + strand	no	160	ADI40471.1	unknown [Hyposoter didymator] Hd_U13	152	5,00E-29	66/160(41%)	
scaffold_28	Cs_IVSPER-2 33269	7310-40578	p12L-2	31075-31353 + strand	no	92	AA01200.1	p12 [Campoletis sonorensis ichnovirus]	92	5,00E-59	92/92(100%)	
scaffold_28	Cs_IVSPER-2 33269	7310-40578	U3L	32951-33436 + strand	no	161	ADI40455.1	unknown [Hyposoter didymator] Hd_U3	162	3,00E-67	93/155(60%)	frameshifts, partial?
scaffold_28	Cs_IVSPER-2 33269	7310-40578	IVSP2L-1	34504-36036 + strand	no	510	ADI40459.1	unknown [Hyposoter didymator] Hd_IVSP2	509	0.0	325/510(64%)	
scaffold_28	Cs_IVSPER-2 33269	7310-40578	U26L	36497-37327 + strand	no	276	AKD28081.1	hypothetical protein [Glypta fumiferanae] Gf_L_298	298	3,00E-29	66/165(40%)	
scaffold_28	Cs_IVSPER-2 33269	7310-40578	CsN-2	37470-38912 + strand	no	480	ADI40491.1	unknown [Hyposoter didymator] Hd_N-2	492	0.0	323/491(66%)	
scaffold_28	Cs_IVSPER-2 33269	7310-40578	U25L	39883-40578 - strand	no	231	AKD28083.1	ring finger domain [Glypta fumiferanae] Hd_U_237	237	2,00E-16	41/128(32%)	
scaffold_28	Cs_IVSPER-2 33269	7310-40578	p53L-2	7310-8944 + strand	no	544	CAR31590.1	p53-like 1 protein [Hyposoter didymator]	395	6,00E-57	155/247(62%)	

repeated motifs found within NCBI seq