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Functional and evolutionary insights from the genomes of three parasitoid *Nasonia* species

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Table S50: Hymenoptera-specific orthologs. For each orthologous group (OG), the number of paralogs in the 2 hymenopterans *A. mellifera* (*A. mel.*) and *N. vitripennis* (*N. vit.*) is shown together with BLASTP E-values of the bee protein to *N. vit.*, *D. melanogaster* (*D. mel.*), and *T. castaneum* (*T. cas.*). Some bee proteins have a significant BLASTP hit with ESTs of a third hymenopteran species, *S. invicta* (fireant).

OG id	<i>A. mel.</i>	<i>N. vit.</i>	E-value <i>N. vit.</i>	E-value <i>D. mel.</i>	E-value <i>T. cas.</i>	Ratio min(<i>D. mel.</i> , <i>T. cas.</i>) / <i>N. vit.</i>	E-value	Fireant ESTs	<i>A. mel.</i> entries	<i>N. vit.</i> entries
1082	1	1	1.E-200	3.E-21	3.E-35	3.E+165	2.E-23	Sl.CL.27.cl.2789.Contig1	GB12664-PA	lcl hmm120804
2993	1	1	1.E-200	5.E-29	2.E-35	2.E+165	1.E-07	Sl.CL.08.cl.0815.Contig1	GB15657-PA	gij 156543612 ref XP_001604392.1
2854	1	1	1.E-200	1.E-30	3.E-37	3.E+163	9.E-23	SiJWG05BDU.scf	GB19102-PA	lcl hmm384594
844	1	1	1.E-200	7.E-33	5.E-39	5.E+161	8.E-58	SiJWA05ADJ.scf	GB15739-PA	lcl hmm114744
2140	1	1	1.E-200	3.E-34	5.E-41	5.E+159	9.E-19	SiJWG05BDU.scf	GB17048-PA	lcl hmm462894
3860	1	1	2.E-158	>0.1	>0.1	5.E+156	>0.1		GB14766-PA	gij 156554859 ref XP_001606677.1
1022	1	1	1.E-200	2.E-42	5.E-47	5.E+153	1.E-26	SiJWE09ADU.scf	GB14380-PA	lcl hmm408854
3947	1	1	2.E-157	2.E-25	3.E-24	1.E+132	7.E-62	SiJWG05ABY.scf	GB15091-PA	gij 156555372 ref XP_001605103.1
4517	1	1	9.E-133	3.E-05	1.E-04	3.E+127	>0.1		GB30327-PA	lcl hmm454314
5212	1	1	1.E-138	2.E-16	1.E-22	1.E+116	5.E-91	Sl.CL.33.cl.3325.Contig1	GB16855-PA	gij 156549800 ref XP_001606484.1
3595	1	1	1.E-155	6.E-43	4.E-44	4.E+111	7.E-25	SiJWE09ADU.scf	GB17527-PA	lcl hmm356784
2189	1	1	1.E-200	2.E-90	8.E-80	2.E+110	>0.1		GB16461-PA	gij 156542456 ref XP_001599154.1
1931	1	1	1.E-200	8.E-89	3.E-98	3.E+102	1.E-45	Sl.CL.25.cl.2532.Contig1	GB19100-PA	gij 156555634 ref XP_001603338.1
5690	1	1	4.E-106	5.E-13	1.E-12	1.E+93	1.E-03	Sl.CL.29.cl.2966.Contig1	GB18355-PA	lcl hmm658184
3082	2	1	1.E-162	5.E-72	3.E-66	5.E+90	4.E-13	gi_121964399-gb_EH413476.1	GB18547-PA GB16639-PA	gij 156554671 ref XP_001605677.1
2791	1	1	1.E-200	2.E-96	2.E-111	2.E+89	4.E-37	SiJWA04ACH.scf	GB18860-PA	gij 156538228 ref XP_001602112.1
6649	1	1	8.E-88	>0.1	>0.1	1.E+86	>0.1		GB16988-PA	gij 156550837 ref XP_001601166.1
6277	1	1	2.E-102	2.E-16	2.E-16	1.E+86	5.E-13	SiJWG05BDU.scf	GB17543-PA	lcl hmm478804
3147	1	1	1.E-200	1.E-99	2.E-115	2.E+85	4.E-04	Sl.CL.22.cl.2249.Contig1	GB19843-PA	gij 156547173 ref XP_001603910.1
4974	1	1	5.E-127	1.E-38	1.E-42	2.E+84	2.E-14	Sl.CL.43.cl.4316.Contig1	GB11845-PA	gij 156541698 ref XP_001603585.1
3970	1	1	5.E-161	>0.1	9.E-77	2.E+84	1.E-23	SiJWE10AAE_tag5_E10_10.scf	GB16528-PA	gij 156549762 ref XP_001606193.1
2528	1	1	1.E-200	2.E-87	2.E-119	2.E+81	1.E-79	SiJWC10BBX.scf	GB13613-PA	gij 156545565 ref XP_001607012.1

4617	1	1	8.E-137	1.E-54	1.E-55	1.E+81	3.E-22	SiJWH04ADF.scf	GB17068-PA	gij156545952 ref XP_001604771.1
6403	1	1	5.E-95	6.E-14	2.E-13	1.E+81	>0.1		GB30460-PA	lcl hmm505104
4395	1	1	9.E-141	5.E-23	3.E-60	3.E+80	3.E-72	Sl.CL.10.cl.1061.Contig1	GB12370-PA	lcl hmm500894
6100	1	1	1.E-99	1.E-17	3.E-19	3.E+80	2.E-94	Sl.CL.38.cl.3841.Contig1	GB17975-PA	gij156541974 ref XP_001599371.1
5306	1	1	6.E-121	3.E-43	4.E-39	5.E+77	2.E-51	SiJWD02BDG.scf	GB15539-PA	gij156546044 ref XP_001600286.1
6272	1	1	6.E-91	2.E-11	2.E-13	3.E+77	7.E-05	Sl.CL.22.cl.2245.Contig1	GB14844-PA	lcl hmm668384
5990	1	1	3.E-110	4.E-31	8.E-33	3.E+77	2.E-06	Sl.CL.08.cl.0815.Contig1	GB19743-PA	lcl hmm1630384
7052	1	1	5.E-76	>0.1	>0.1	2.E+74	3.E-40	Sl.CL.34.cl.3450.Contig1	GB18211-PA	lcl hmm470374
4530	1	1	2.E-138	2.E-57	7.E-66	4.E+72	1.E-10	Sl.CL.01.cl.0132.Contig1	GB19132-PA	gij156550454 ref XP_001601022.1
7601	1	1	3.E-74	>0.1	>0.1	3.E+72	>0.1		GB13054-PA	lcl hmm71194
6553	1	1	3.E-101	3.E-29	2.E-24	1.E+72	1.E-09	SiJWB09BDF.scf	GB17795-PA	lcl hmm306774
5258	1	2	1.E-118	3.E-41	6.E-48	6.E+70	2.E-28	Sl.CL.47.cl.4714.Contig1	GB30584-PA	gij156541777 ref XP_001601388.1 lcl hmm181044
5558	1	1	7.E-113	>0.1	5.E-43	7.E+69	>0.1		GB15585-PA	lcl hmm237254
7865	2	1	2.E-71	>0.1	>0.1	5.E+69	>0.1		GB10620-PA GB15037-PA	lcl hmm502184
5393	1	1	8.E-117	2.E-31	4.E-47	5.E+69	1.E-41	Sl.CL.03.cl.0338.Contig1	GB14657-PA	gij156546768 ref XP_001607232.1
7204	1	1	1.E-93	9.E-20	4.E-24	4.E+69	>0.1		GB11695-PA	gij156537620 ref XP_001607769.1
7319	1	1	2.E-80	1.E-11	9.E-08	5.E+68	2.E-04	SiJWA12BDX.scf	GB30439-PA	lcl hmm344314
3831	1	1	1.E-126	1.E-49	4.E-58	4.E+68	2.E-25	SiJWE09ADU.scf	GB14692-PA	lcl hmm274144
2415	1	1	1.E-200	1.E-131	4.E-132	4.E+68	3.E-18	SiJWD10BAM.scf	GB16848-PA	gij156551744 ref XP_001602001.1
3380	1	2	5.E-168	7.E-45	1.E-99	2.E+68	2.E-135	Sl.CL.14.cl.1482.Contig1	GB14361-PA	gij156542452 ref XP_001599110.1 gij156542989 ref XP_001603025.1
5593	1	1	7.E-104	2.E-32	7.E-36	1.E+68	1.E-64	Sl.CL.40.cl.4055.Contig1	GB17170-PA	gij156555131 ref XP_001604908.1
4258	1	1	2.E-145	7.E-67	2.E-77	1.E+68	6.E-53	gi_62637997-gb_AY911645.1	GB16063-PA	gij156555119 ref XP_001604717.1
5450	1	1	5.E-126	4.E-58	3.E-57	8.E+67	>0.1		GB18225-PA	gij156550201 ref XP_001601020.1
7528	1	1	6.E-73	1.E-06	6.E-06	2.E+66	1.E-13	SiJWA12BDX.scf	GB11318-PA	lcl hmm598274
3508	1	1	3.E-99	5.E-29	1.E-35	3.E+63	8.E-19	SiJWE09ADU.scf	GB16901-PA	lcl hmm316244
3277	1	1	1.E-200	3.E-137	1.E-136	3.E+63	3.E-34	SiJWH10ADK.scf	GB11149-PA	gij156545370 ref XP_001606236.1
6888	1	1	2.E-69	>0.1	2.E-06	1.E+63	>0.1		GB14800-PA	lcl hmm252614
4182	1	1	2.E-152	1.E-68	9.E-90	5.E+62	>0.1		GB15594-PA	gij156555672 ref XP_001604104.1
7979	1	1	5.E-81	7.E-16	2.E-18	4.E+62	3.E-14	SiJWD02BDG.scf	GB12273-PA	gij156537055 ref XP_001601603.1
8111	1	1	5.E-64	>0.1	>0.1	2.E+62	>0.1		GB15756-PA	gij156539127 ref XP_001602547.1
7756	1	1	1.E-63	>0.1	>0.1	1.E+62	>0.1		GB13106-PA	lcl hmm667024
5856	1	1	2.E-134	6.E-66	1.E-73	5.E+60	2.E-45	gi_62637997-gb_AY911645.1	GB10764-PA	gij156548646 ref XP_001601813.1
8020	1	1	9.E-72	1.E-11	2.E-07	1.E+60	2.E-10	SiJWH09BDE2.scf	GB15456-PA	gij156553636 ref XP_001600312.1

8145	1	1	1.E-61	>0.1	>0.1	1.E+60	>0.1		GB15060-PA	gij156554166 ref XP_001599638.1
4352	1	1	2.E-159	4.E-101	2.E-99	2.E+58	2.E-10	SiJWG08BBI.scf	GB14047-PA	gij156554473 ref XP_001604452.1
6881	1	1	4.E-86	2.E-24	2.E-28	5.E+57	3.E-11	Sl.CL.39.cl.3946.Contig1	GB16963-PA	gij156541872 ref XP_001600432.1
6870	1	1	4.E-59	>0.1	>0.1	3.E+57	>0.1		GB16421-PA	lcl hmm244414
8486	1	1	6.E-59	>0.1	>0.1	2.E+57	4.E-13	SiJWG03AAF2.scf	GB15720-PA	gij156538208 ref XP_001601680.1
7814	1	1	1.E-63	4.E-07	6.E-07	4.E+56	>0.1		GB13537-PA	lcl hmm332624
8385	1	1	4.E-58	>0.1	>0.1	3.E+56	>0.1		GB17314-PA	lcl hmm12874
3517	1	1	3.E-178	9.E-85	1.E-122	3.E+55	5.E-21	Sl.CL.45.cl.4513.Contig1	GB11152-PA	lcl hmm474134
5765	1	1	1.E-103	3.E-48	1.E-46	3.E+55	3.E-22	Sl.CL.07.cl.0732.Contig1	GB13597-PA	gij156548112 ref XP_001606524.1
4990	1	1	9.E-126	2.E-66	2.E-70	2.E+55	5.E-32	Sl.CL.44.cl.4430.Contig1	GB30031-PA_2	gij156552969 ref XP_001603494.1
3088	1	1	1.E-200	8.E-146	1.E-143	8.E+54	1.E-22	SiJWD10BAM.scf	GB19418-PB	gij156555678 ref XP_001604417.1
8800	1	1	6.E-63	4.E-08	5.E-07	7.E+54	>0.1		GB13584-PA	lcl hmm78424
4495	1	1	1.E-142	2.E-67	5.E-88	5.E+54	2.E-36	Sl.CL.22.cl.2217.Contig1	GB15163-PA	gij156545201 ref XP_001603802.1
7647	1	1	3.E-64	3.E-08	1.E-09	3.E+54	>0.1		GB14610-PA	lcl hmm612374
8313	1	1	3.E-59	2.E-03	8.E-05	3.E+54	>0.1		GB13194-PA	lcl hmm366144
8196	1	1	2.E-64	>0.1	8.E-11	4.E+53	2.E-73	Sl.CL.19.cl.1963.Contig1	GB16051-PA	gij156548362 ref XP_001603752.1
8609	1	1	2.E-54	>0.1	>0.1	5.E+52	>0.1		GB30490-PA	lcl hmm516624
2021	1	1	6.E-113	8.E-30	9.E-61	2.E+52	2.E-25	SiJWE09ADU.scf	GB19687-PA	lcl hmm390594
8614	1	1	7.E-58	5.E-07	9.E-05	7.E+50	>0.1		GB13079-PA	lcl hmm521024
8587	1	1	3.E-52	>0.1	>0.1	3.E+50	>0.1		GB19018-PA	lcl hmm945294
6373	1	1	2.E-93	3.E-37	4.E-43	2.E+50	9.E-42	Sl.CL.07.cl.0761.Contig1	GB11814-PA	gij156554465 ref XP_001604327.1
8465	1	2	5.E-55	4.E-05	7.E-05	8.E+49	>0.1		GB18865-PA	lcl hmm906384 lcl hmm1010384
6334	1	9	2.E-95	8.E-39	1.E-45	5.E+49	5.E-34	gi_62637997-gb_AY911645.1	GB15672-PA	gij156549648 ref XP_001604467.1 gij156549650 ref XP_001604493.1 gij156549652 ref XP_001604518.1 gij156550211 ref XP_001601403.1 gij156548240 ref XP_001607210.1 gij156548242 ref XP_001607216.1 gij156548244 ref XP_001607225.1 gij156548246 ref XP_001607233.1 gij156550313 ref XP_001603503.1
5903	1	1	1.E-106	1.E-54	5.E-57	5.E+49	>0.1		GB12998-PA	gij156549983 ref XP_001603860.1
9064	1	1	3.E-51	>0.1	>0.1	3.E+49	>0.1		GB15258-PA	lcl hmm298064
8147	1	1	1.E-56	1.E-03	3.E-07	3.E+49	3.E-11	SiJWG07AAC2.scf	GB19190-PA	lcl hmm218314
5194	1	1	2.E-63	3.E-10	3.E-14	2.E+49	8.E-10	SiJWB03ABW.scf	GB10271-PA	lcl hmm530794
8188	1	1	1.E-61	2.E-09	1.E-12	1.E+49	2.E-62	SiJWD07ABA.scf	GB16894-PA	gij156537419 ref XP_001606881.1

8809	1	1	2.E-49	>0.1	>0.1	5.E+47	>0.1		GB12923-PA	lcl hmm507174
8655	1	1	3.E-50	>0.1	1.E-02	3.E+47	>0.1		GB12066-PA	lcl hmm326224
7713	1	1	9.E-71	8.E-21	2.E-23	2.E+47	6.E-47	Sl.CL.12.cl.1295.Contig1	GB13705-PA	lcl hmm307164
8415	1	1	2.E-53	1.E-05	5.E-07	3.E+46	>0.1		GB14722-PA	lcl hmm174414
4474	1	1	1.E-140	4.E-92	4.E-95	4.E+45	2.E-55	Sl.CL.11.cl.1139.Contig3	GB19306-PA	gij 156545491 ref XP_001606990.1
7184	1	1	1.E-78	3.E-33	8.E-33	3.E+45	3.E-24	Sl.CL.02.cl.0298.Contig2	GB11297-PA	gij 156538303 ref XP_001603816.1
4579	1	1	4.E-138	3.E-93	3.E-87	8.E+44	2.E-09	gi_121964271-gb_EH413397.1	GB15561-PA	gij 156555298 ref XP_001603434.1
8953	1	1	7.E-50	>0.1	3.E-05	4.E+44	6.E-32	SiJWH08ADY.scf	GB16574-PA	lcl hmm94314
9067	1	1	4.E-46	>0.1	>0.1	3.E+44	1.E-24	Sl.CL.01.cl.0171.Contig1	GB10666-PA	lcl hmm655104
4651	1	1	1.E-135	1.E-86	2.E-91	2.E+44	5.E-84	Sl.CL.35.cl.3557.Contig1	GB18070-PA	gij 156549274 ref XP_001599877.1
9062	1	2	8.E-46	>0.1	>0.1	1.E+44	6.E-50	SiJWE02ADC.scf	GB18774-PA	gij 156547309 ref XP_001601644.1 lcl hmm574894
8027	1	1	1.E-61	2.E-16	1.E-17	1.E+44	3.E-13	SiJWH09BCL2.scf	GB10678-PA	lcl hmm608624
9258	1	1	1.E-45	>0.1	>0.1	1.E+44	>0.1		GB13908-PA	gij 156543697 ref XP_001605619.1
10054	1	1	3.E-45	>0.1	>0.1	3.E+43	>0.1		GB18783-PA	gij 156546286 ref XP_001605948.1
9172	1	1	3.E-46	>0.1	8.E-03	3.E+43	>0.1		GB18642-PA	lcl hmm124764
913	1	1	1.E-200	2.E-147	2.E-157	2.E+43	5.E-13	Sl.CL.08.cl.0860.Contig1	GB16385-PA	gij 156555205 ref XP_001604057.1
7029	1	1	4.E-57	2.E-09	4.E-14	1.E+43	1.E-12	SiJWB10ADI.scf	GB13523-PA	lcl hmm772624
7328	1	1	1.E-44	>0.1	9.E-02	9.E+42	>0.1		GB14290-PA	lcl hmm638054
8729	1	1	3.E-47	>0.1	5.E-05	2.E+42	5.E-19	SiJWE01BDM2.scf	GB30369-PA	lcl hmm238624
3545	1	1	3.E-165	2.E-123	9.E-116	7.E+41	8.E-108	Sl.CL.10.cl.1001.Contig1	GB12666-PA	gij 156552319 ref XP_001601288.1
4960	1	1	1.E-125	1.E-63	2.E-84	2.E+41	1.E-05	Sl.CL.26.cl.2671.Contig1	GB13086-PA	gij 156552347 ref XP_001601914.1
9771	1	1	6.E-43	>0.1	>0.1	2.E+41	>0.1		GB30054-PA	gij 156546110 ref XP_001601833.1
2558	1	1	1.E-200	4.E-151	3.E-160	3.E+40	4.E-42	SiJWD10BAM.scf	GB16967-PA	gij 156537624 ref XP_001607779.1
7234	1	1	1.E-79	3.E-39	5.E-18	3.E+40	9.E-19	Sl.CL.24.cl.2409.Contig1	GB18367-PA	gij 156547727 ref XP_001605392.1
3127	1	1	2.E-179	1.E-132	6.E-139	3.E+40	2.E-32	SiJWH10ADK.scf	GB10441-PA	gij 156545368 ref XP_001606222.1
5873	1	2	3.E-106	9.E-59	8.E-67	3.E+39	3.E-15	Sl.CL.43.cl.4393.Contig1	GB18224-PA	gij 156543565 ref XP_001603575.1 lcl hmm216664
8545	1	1	3.E-41	>0.1	7.E-02	2.E+39	2.E-07	SiJWF06ACP.scf	GB15941-PA	lcl hmm516374
6270	1	1	7.E-89	6.E-38	1.E-49	1.E+39	2.E-09	Sl.CL.10.cl.1031.Contig1	GB10497-PA	lcl hmm136344
8681	1	1	9.E-55	2.E-13	4.E-16	4.E+38	3.E-07	Sl.CL.21.cl.2164.Contig1	GB13064-PA	lcl hmm658054
858	1	1	1.E-200	6.E-150	2.E-162	2.E+38	3.E-05	SiJWB11BDS2.scf	GB11737-PA	gij 156543396 ref XP_001600165.1
9634	1	1	1.E-39	>0.1	>0.1	1.E+38	>0.1		GB13107-PA	lcl hmm678624
9232	1	1	1.E-44	7.E-06	4.E-08	4.E+36	>0.1		GB17127-PA	lcl hmm186184
9234	1	1	3.E-38	>0.1	>0.1	3.E+36	2.E-11	SiJWD10BAH.scf	GB10261-PA	lcl hmm308054
9620	1	1	4.E-38	>0.1	>0.1	3.E+36	>0.1		GB19985-PA	lcl hmm244634

8366	1	1	2.E-64	6.E-12	5.E-29	3.E+35	>0.1		GB11811-PA	lcl hmm1300624
3942	1	1	7.E-155	3.E-115	1.E-119	1.E+35	5.E-44	Sl.CL.36.cl.3695.Contig1	GB14540-PA	gij 156551577 ref XP_001601942.1
9643	1	1	6.E-39	>0.1	4.E-04	7.E+34	3.E-32	Sl.CL.32.cl.3234.Contig1	GB18203-PA	gij 156548350 ref XP_001603528.1
9699	1	1	2.E-36	>0.1	>0.1	5.E+34	2.E-36	Sl.CL.13.cl.1359.Contig1	GB15144-PA	lcl hmm773234
7245	1	1	7.E-81	3.E-46	1.E-42	4.E+34	1.E-35	Sl.CL.00.cl.0015.Contig2	GB18530-PA	lcl hmm78444
10070	1	1	3.E-36	>0.1	>0.1	3.E+34	>0.1		GB11449-PA	lcl hmm1106384
8898	1	1	7.E-36	>0.1	>0.1	1.E+34	>0.1		GB16213-PA	gij 156553735 ref XP_001601033.1
7659	1	1	1.E-73	9.E-27	1.E-39	1.E+34	3.E-75	Sl.CL.07.cl.0740.Contig2	GB18695-PA	gij 156545414 ref XP_001606540.1
3540	1	1	1.E-172	3.E-130	3.E-139	3.E+33	3.E-51	SiJWD10BAM.scf	GB17446-PA	lcl hmm81154
9952	1	1	3.E-35	>0.1	8.E-02	3.E+33	7.E-44	gi_121963895-gb_EH413087.1	GB11111-PA	lcl hmm147234
7663	1	1	2.E-37	>0.1	3.E-04	2.E+33	4.E-07	SiJWG05ADK.scf	GB19287-PA	gij 156538667 ref XP_001607736.1
7427	1	1	9.E-61	4.E-19	1.E-27	1.E+33	1.E-19	Sl.CL.36.cl.3656.Contig1	GB14763-PA	gij 156538487 ref XP_001606915.1
9940	1	1	1.E-34	>0.1	>0.1	1.E+33	2.E-20	gi_62637997-gb_AY911645.1	GB16599-PA	lcl hmm111194
9723	1	1	1.E-34	>0.1	>0.1	1.E+33	2.E-13	Sl.CL.44.cl.4478.Contig1	GB19828-PA	lcl hmm160624
6533	1	1	3.E-95	2.E-33	3.E-62	1.E+33	>0.1		GB19393-PA	lcl hmm6834
9222	1	9	6.E-41	7.E-07	5.E-08	8.E+32	4.E-05	SiJWH09BDE2.scf	GB30136-PA	gij 156549839 ref XP_001606783.1 gij 156547319 ref XP_001601812.1 lcl hmm424134 lcl hmm234144 lcl hmm256144 lcl hmm396274 lcl hmm838274 lcl hmm544894 lcl hmm360944
8976	1	2	2.E-48	2.E-11	1.E-15	5.E+32	1.E-72	Sl.CL.30.cl.3076.Contig1	GB14761-PA	gij 156547739 ref XP_001605540.1 gij 156547741 ref XP_001605554.1
8708	1	1	4.E-54	2.E-20	2.E-21	5.E+32	>0.1		GB15251-PA	gij 156539579 ref XP_001599064.1
5516	1	1	1.E-90	1.E-48	3.E-58	3.E+32	7.E-10	SiJWA04ACH.scf	GB13558-PA	lcl hmm801024
5838	3	3	1.E-107	1.E-74	2.E-75	2.E+32	4.E-53	Sl.CL.36.cl.3637.Contig1	GB16342-PA GB14478-PA GB18657-PA	gij 156541136 ref XP_001601401.1 gij 156541789 ref XP_001602248.1 gij 156541793 ref XP_001602306.1
9958	1	1	6.E-34	>0.1	>0.1	2.E+32	3.E-15	SiJWB11ACG.scf	GB13354-PA	gij 156550472 ref XP_001601314.1
7268	1	1	3.E-48	5.E-16	1.E-15	2.E+32	3.E-10	SiJWG05BDU.scf	GB17567-PA	gij 156549018 ref XP_001607343.1
8787	1	1	2.E-42	5.E-04	2.E-10	1.E+32	>0.1		GB17575-PA	lcl hmm926624
9945	1	1	1.E-33	>0.1	>0.1	1.E+32	4.E-19	Sl.CL.02.cl.0264.Contig1	GB11948-PA	gij 156554988 ref XP_001602759.1
9941	1	1	1.E-33	>0.1	>0.1	1.E+32	3.E-13	SiJWC02ABB.scf	GB14511-PA	gij 156546128 ref XP_001602976.1
10181	1	1	5.E-33	>0.1	>0.1	2.E+31	>0.1		GB18304-PA	lcl hmm407174
7886	1	1	6.E-64	8.E-34	4.E-34	7.E+29	9.E-25	SiJWE09ADU.scf	GB19971-PA	lcl hmm510784
10089	1	1	2.E-31	>0.1	>0.1	5.E+29	>0.1		GB13342-PA	lcl hmm232624

7828	1	1	7.E-69	1.E-35	3.E-39	4.E+29	5.E-18	Sl.CL.42.cl.4270.Contig1	GB15650-PA	gij156539808 ref XP_001601067.1
7795	1	1	6.E-65	2.E-35	6.E-24	3.E+29	4.E-19	gi_121964271-gb_EH413397.1	GB17148-PA	gij156555300 ref XP_001603459.1
10339	1	1	3.E-31	>0.1	>0.1	3.E+29	>0.1		GB20061-PA	lcl hmm1020384
7875	1	1	9.E-73	5.E-42	2.E-43	2.E+29	1.E-69	gi_121964484-gb_EH413524.1	GB15963-PA	gij156547065 ref XP_001601749.1
7755	1	1	5.E-49	3.E-12	6.E-20	1.E+29	5.E-12	Sl.CL.42.cl.4289.Contig1	GB17382-PA	gij156537692 ref XP_001608250.1
10098	1	1	9.E-31	>0.1	>0.1	1.E+29	2.E-30	SiJWC03ACC.scf	GB30487-PA	lcl hmm349294
6137	1	1	4.E-86	6.E-54	3.E-57	8.E+28	5.E-25	gi_121964097-gb_EH413264.1	GB14366-PA	gij156540996 ref XP_001600803.1
7996	2	1	1.E-38	>0.1	6.E-10	6.E+28	>0.1		GB16590-PA GB18040-PA	lcl hmm445234
9916	1	1	2.E-30	>0.1	>0.1	5.E+28	>0.1		GB13907-PA	lcl hmm607294
4350	1	1	2.E-145	1.E-115	5.E-117	3.E+28	2.E-77	Sl.CL.44.cl.4450.Contig1	GB18293-PA	gij156550009 ref XP_001604446.1
8603	1	1	5.E-30	>0.1	>0.1	2.E+28	>0.1		GB30597-PA	lcl hmm370574
6186	1	1	4.E-103	2.E-72	4.E-75	1.E+28	>0.1		GB11208-PA	gij156541122 ref XP_001601573.1
9336	1	1	6.E-44	3.E-13	3.E-16	5.E+27	1.E-14	Sl.CL.15.cl.1577.Contig1	GB30333-PA	gij156542506 ref XP_001601380.1
4692	1	1	3.E-133	3.E-41	7.E-106	2.E+27	>0.1		GB18264-PA	gij156542684 ref XP_001602998.1
2145	1	1	1.E-200	3.E-112	2.E-173	2.E+27	>0.1		GB16056-PA	gij156542149 ref XP_001601982.1
9138	1	1	3.E-30	5.E-03	5.E-02	2.E+27	>0.1		GB10449-PA	lcl hmm467174
10201	1	1	8.E-28	>0.1	>0.1	1.E+26	9.E-05	SiJWF10CAX.scf	GB16995-PA	lcl hmm392314
9803	1	1	8.E-40	4.E-13	3.E-14	4.E+25	5.E-06	Sl.CL.07.cl.0763.Contig1	GB19650-PA	lcl hmm198664
8736	1	1	2.E-52	7.E-27	4.E-26	4.E+25	>0.1		GB13590-PA	gij156550414 ref XP_001600106.1
9499	1	6	7.E-37	2.E-08	2.E-11	3.E+25	9.E-04	SiJWH07CAK2.scf	GB30121-PA	gij156553379 ref XP_001602050.1 gij156554940 ref XP_001601827.1 lcl hmm618344 lcl hmm1362624 lcl hmm606894 lcl hmm354924
6788	1	1	2.E-86	1.E-13	5.E-61	3.E+25	2.E-20	Sl.CL.24.cl.2443.Contig1	GB19755-PA	gij156552211 ref XP_001606251.1
10166	1	1	1.E-29	>0.1	2.E-04	2.E+25	5.E-05	Sl.CL.07.cl.0779.Contig1	GB18024-PA	lcl hmm116764
3767	2	1	6.E-107	3.E-55	1.E-81	2.E+25	8.E-25	SiJWG05BDU.scf	GB16690-PA GB18359-PA	gij156552043 ref XP_001604144.1
9136	1	1	8.E-43	1.E-17	3.E-17	1.E+25	3.E-13	SiJWH10ABH.scf	GB12524-PA	gij156554060 ref XP_001599440.1
10479	1	2	4.E-29	3.E-03	4.E-04	1.E+25	>0.1		GB17395-PA	gij156536848 ref XP_001600411.1 gij156536850 ref XP_001600382.1
9618	1	1	9.E-45	9.E-19	8.E-20	9.E+24	>0.1		GB14571-PA	gij156542841 ref XP_001599830.1

6769	1	6	9.E-73	3.E-37	5.E-48	6.E+24	1.E-15	Sl.CL.01.cl.0132.Contig1	GB11440- PAGB10622- PAGB16246- PAGB16324- PAGB16634- PA_2GB14888- PAGB11890- PAGB19216- PAGB16634- PAGB13789- PAGB11022- PAGB11768- PAGB14639- PAGB16459-PA	gij156555019 ref XP_001603306.1 gij156555021 ref XP_001603333.1 gij156555023 ref XP_001603369.1 gij156555025 ref XP_001603404.1 gij156541347 ref XP_001599090.1 gij156541349 ref XP_001599105.1
10224	1	1	6.E-26	>0.1	>0.1	2.E+24	>0.1		GB19040-PA	lc hmm406804
6152	1	4	1.E-97	3.E-71	9.E-74	9.E+23	1.E-72	Sl.CL.34.cl.3460.Contig1	GB13559-PA	gij156538781 ref XP_001607912.1 gij156538783 ref XP_001607913.1 gij156538785 ref XP_001607915.1 gij156538789 ref XP_001607922.1
11412	1	1	8.E-28	2.E-04	>0.1	3.E+23	>0.1		GB11478-PA	lc hmm330374
9007	1	1	3.E-46	9.E-15	7.E-23	2.E+23	1.E-14	SiJWB08AEA.scf	GB12006-PA	lc hmm36264
10319	1	1	2.E-27	>0.1	3.E-04	2.E+23	4.E-26	SiJWE06ADF.scf	GB13267-PA	lc hmm673234
6182	1	1	2.E-97	3.E-74	4.E-73	2.E+23	1.E-42	Sl.CL.42.cl.4235.Contig1	GB19317-PA	gij156545784 ref XP_001605710.1
8452	1	1	1.E-43	6.E-18	1.E-20	1.E+23	8.E-18	Sl.CL.35.cl.3524.Contig1	GB14408-PA	lc hmm1674384
10390	1	1	2.E-24	>0.1	>0.1	5.E+22	3.E-18	SiJWB05BCC_tag5_B05_03.scf	GB12143-PA	lc hmm632594
10441	1	1	2.E-24	>0.1	>0.1	5.E+22	>0.1		GB10818-PA	lc hmm360344
9026	1	1	2.E-51	3.E-28	4.E-29	2.E+22	3.E-24	Sl.CL.06.cl.0628.Contig1	GB11867-PA	gij156537749 ref XP_001607993.1
11245	1	1	9.E-24	>0.1	>0.1	1.E+22	>0.1		GB16339-PA	lc hmm490814
10470	1	1	2.E-23	>0.1	>0.1	5.E+21	>0.1		GB19632-PA	gij156544968 ref XP_001607781.1
1634	1	1	1.E-200	6.E-165	4.E-179	4.E+21	1.E-26	SiJWD10BAM.scf	GB13065-PA	gij156555676 ref XP_001604393.1
10719	1	1	6.E-31	2.E-09	4.E-09	3.E+21	2.E-03	SiJWA04ACG.scf	GB11418-PA	lc hmm259294
10981	1	1	3.E-23	>0.1	>0.1	3.E+21	>0.1		GB17509-PA	gij156551360 ref XP_001602694.1
9132	1	1	2.E-37	6.E-16	9.E-15	3.E+21	5.E-08	SiJWH10ABH.scf	GB30419-PA	lc hmm76684
10748	1	1	7.E-23	>0.1	>0.1	1.E+21	>0.1		GB15474-PA	lc hmm749294
10652	1	1	7.E-23	>0.1	>0.1	1.E+21	>0.1		GB19605-PA	lc hmm222844
10613	1	1	4.E-23	3.E-02	>0.1	8.E+20	>0.1		GB12075-PA	lc hmm762214

8199	1	1	8.E-61	3.E-31	2.E-40	3.E+20	2.E-67	Sl.CL.13.cl.1354.Contig1	GB14607-PA	gij156545754 ref XP_001605427.1
10550	1	1	8.E-22	>0.1	>0.1	1.E+20	>0.1		GB30039-PA	lcl hmm490054
11085	1	1	9.E-22	>0.1	>0.1	1.E+20	9.E-24	Sl.CL.24.cl.2437.SiJWD04BBN2.scf	GB19297-PA	gij156551015 ref XP_001600083.1
10539	1	1	2.E-25	2.E-05	5.E-05	1.E+20	>0.1		GB13909-PA	gij156555509 ref XP_001604456.1
8878	1	1	4.E-50	3.E-30	3.E-28	8.E+19	6.E-32	SiJWB08ADA.scf	GB18900-PA	gij156547195 ref XP_001604245.1
8684	1	1	8.E-57	7.E-35	6.E-37	8.E+19	1.E-58	SiJWC01CAX.scf	GB10937-PA	gij156553962 ref XP_001602782.1
10496	1	1	9.E-22	>0.1	3.E-02	3.E+19	>0.1		GB10356-PA	lcl hmm781174
10819	1	1	3.E-21	2.E-02	>0.1	8.E+18	>0.1		GB19449-PA	lcl hmm356444
10594	1	1	2.E-20	>0.1	>0.1	5.E+18	3.E-09	SiJWA07ACD.scf	GB17217-PA	lcl hmm347294
11225	1	1	3.E-20	>0.1	>0.1	3.E+18	>0.1		GB19851-PA	lcl hmm751234
11258	1	1	4.E-20	>0.1	>0.1	3.E+18	1.E-07	Sl.CL.07.cl.0774.Contig1	GB16927-PA	lcl hmm606184
10878	1	1	4.E-20	>0.1	>0.1	3.E+18	1.E-11	SiJWH11ADJ.scf	GB14633-PA	lcl hmm634624
10325	1	1	2.E-23	6.E-02	3.E-05	2.E+18	3.E-03	Sl.CL.03.cl.0349.Contig1	GB15403-PA	lcl hmm180414
10873	1	1	1.E-19	>0.1	>0.1	1.E+18	>0.1		GB19486-PA	gij156542875 ref XP_001600660.1
6041	1	1	1.E-118	1.E-100	4.E-95	1.E+18	1.E-17	SiJWG01CAC2.scf	GB15741-PA	gij156537036 ref XP_001601257.1
9845	1	1	1.E-32	5.E-15	4.E-14	5.E+17	1.E-16	SiJWH10ABH.scf	GB16121-PA	gij156554032 ref XP_001599487.1
10920	1	1	4.E-19	>0.1	>0.1	3.E+17	1.E-07	Sl.CL.46.cl.4672.Contig1	GB14078-PA	lcl hmm730924
10590	1	1	3.E-20	>0.1	5.E-03	2.E+17	>0.1		GB16868-PA	gij156545708 ref XP_001604794.1
10726	1	1	7.E-19	>0.1	>0.1	1.E+17	>0.1		GB30465-PA	lcl hmm694624
11276	1	1	8.E-19	>0.1	>0.1	1.E+17	>0.1		GB17713-PA	lcl hmm384924
11259	1	1	1.E-18	>0.1	>0.1	1.E+17	5.E-11	Sl.CL.32.cl.3243.Contig1	GB17538-PA	gij156545840 ref XP_001607881.1
9542	1	1	2.E-33	1.E-15	2.E-16	1.E+17	2.E-07	SiJWH04BDG.scf	GB12084-PA	lcl hmm716804
10015	1	1	8.E-34	7.E-08	6.E-17	8.E+16	7.E-07	Sl.CL.25.cl.2546.Contig1	GB12555-PA	lcl hmm360474
11083	1	1	2.E-18	>0.1	>0.1	5.E+16	2.E-07	Sl.CL.31.cl.3176.Contig1	GB11010-PA	lcl hmm1096274
11161	1	1	9.E-22	>0.1	9.E-06	1.E+16	>0.1		GB17904-PA	lcl hmm397104
10959	1	1	1.E-17	>0.1	>0.1	1.E+16	>0.1		GB16660-PA	lcl hmm560894
10720	1	1	6.E-22	6.E-04	3.E-06	5.E+15	6.E-05	Sl.CL.42.cl.4210.Contig1	GB16819-PA	lcl hmm162964
10516	1	1	4.E-25	>0.1	2.E-09	5.E+15	1.E-03	Sl.CL.03.cl.0338.Contig1	GB16314-PA	lcl hmm626384
10501	1	1	3.E-20	3.E-02	1.E-04	3.E+15	>0.1		GB18946-PA	lcl hmm474444
10968	1	1	9.E-18	>0.1	3.E-02	3.E+15	>0.1		GB17519-PA	lcl hmm124194
10813	1	1	3.E-18	8.E-03	>0.1	3.E+15	6.E-24	gi_121964375-gb_EH413461.1	GB14740-PA	gij156547788 ref XP_001606100.1
11094	1	1	4.E-17	>0.1	>0.1	3.E+15	3.E-21	Sl.CL.02.cl.0273.Contig1	GB13398-PA	lcl hmm189234
11586	1	1	3.E-17	3.E-02	>0.1	1.E+15	>0.1		GB14787-PA	lcl hmm270214
10744	1	1	1.E-16	>0.1	>0.1	1.E+15	>0.1		GB12424-PA	lcl hmm176744
11102	1	1	1.E-16	>0.1	9.E-02	9.E+14	>0.1		GB10824-PA	lcl hmm513104

7572	1	1	7.E-73	2.E-52	2.E-58	3.E+14	7.E-56	Sl.CL.21.cl.2169.Contig1	GB17154-PA	gij156541868 ref XP_001600249.1
9127	1	1	4.E-47	1.E-32	2.E-28	3.E+14	6.E-59	gi_121963929-gb_EH413108.1	GB13391-PA	lcl hmm444314
9316	1	1	1.E-41	2.E-27	7.E-09	2.E+14	5.E-02	SiJWH09BCL2.scf	GB12588-PA	lcl hmm281054
10866	1	1	9.E-16	>0.1	>0.1	1.E+14	>0.1		GB14587-PA	lcl hmm358134
10995	1	1	2.E-18	>0.1	2.E-04	1.E+14	>0.1		GB14828-PA	lcl hmm241294
11172	1	1	1.E-15	>0.1	>0.1	1.E+14	>0.1		GB18873-PA	lcl hmm356804
10972	1	1	2.E-15	>0.1	>0.1	5.E+13	1.E-05	SiJWB02BAZ2.scf	GB11987-PA	lcl hmm766814
9766	1	2	2.E-30	8.E-16	1.E-16	5.E+13	2.E-06	Sl.CL.38.cl.3841.Contig1	GB15927-PA	gij156552317 ref XP_001601213.1 lcl hmm188614
10690	1	1	9.E-21	3.E-07	6.E-07	3.E+13	>0.1		GB12663-PA	lcl hmm818384
11491	1	1	5.E-15	>0.1	>0.1	2.E+13	>0.1		GB19202-PA	lcl hmm500184
11073	1	1	6.E-16	1.E-02	>0.1	2.E+13	>0.1		GB12444-PA	lcl hmm494924
10560	1	1	2.E-21	3.E-07	3.E-08	2.E+13	3.E-45	Sl.CL.25.cl.2589.Contig1	GB13052-PA	lcl hmm351104
11071	1	1	9.E-15	>0.1	>0.1	1.E+13	>0.1		GB11551-PA	lcl hmm265004
7738	1	5	1.E-68	1.E-42	1.E-55	1.E+13	7.E-61	Sl.CL.27.cl.2740.Contig1	GB19394-PA	gij156550995 ref XP_001604496.1 gij156545473 ref XP_001606910.1 gij156545475 ref XP_001606919.1 gij156550079 ref XP_001605515.1 gij156537596 ref XP_001607711.1
11155	1	1	4.E-15	>0.1	4.E-02	1.E+13	4.E-04	Sl.CL.25.cl.2557.Contig1	GB11550-PA	gij156555917 ref XP_001600757.1
5463	2	1	3.E-84	2.E-59	2.E-71	7.E+12	1.E-48	Sl.CL.36.cl.3637.Contig1	GB10854- PAGB15030-PA	gij156538002 ref XP_001608200.1
11184	1	1	2.E-14	>0.1	1.E-01	5.E+12	>0.1		GB10743-PA	lcl hmm653294
6784	1	2	9.E-92	5.E-70	4.E-79	4.E+12	1.E-51	gi_121963797-gb_EH413030.1	GB19797-PA	gij156548374 ref XP_001603966.1 gij156545517 ref XP_001607121.1
11204	1	1	5.E-14	>0.1	>0.1	2.E+12	>0.1		GB30410-PA	lcl hmm392244
10947	1	1	7.E-14	>0.1	>0.1	1.E+12	>0.1		GB11387-PA	lcl hmm530344
11438	1	1	8.E-14	>0.1	>0.1	1.E+12	>0.1		GB17952-PA	lcl hmm270084
11045	1	1	1.E-16	7.E-05	1.E-02	7.E+11	>0.1		GB15528-PA	lcl hmm231254
11747	1	1	2.E-13	>0.1	>0.1	5.E+11	>0.1		GB15596-PA	gij156546958 ref XP_001599398.1
7686	1	1	2.E-48	6.E-13	8.E-37	4.E+11	8.E-05	Sl.CL.35.cl.3584.Contig1	GB10551-PA	lcl hmm174174
11356	1	1	4.E-13	>0.1	>0.1	3.E+11	2.E-02	Sl.CL.46.cl.4605.Contig1	GB14087-PA	lcl hmm802924
11265	1	1	9.E-13	>0.1	>0.1	1.E+11	>0.1		GB12772-PA	lcl hmm267294
11439	1	1	3.E-17	2.E-06	3.E-05	7.E+10	1.E-05	Sl.CL.19.cl.1905.Contig1	GB19110-PA	lcl hmm1404384
10255	1	1	5.E-13	>0.1	3.E-02	6.E+10	>0.1		GB17276-PA	lcl hmm310664
11687	1	1	1.E-14	5.E-03	5.E-04	5.E+10	1.E-08	Sl.CL.11.cl.1160.Contig1	GB17322-PA	gij156554036 ref XP_001599904.1

11199	1	1	1.E-13	7.E-03	5.E-03	5.E+10	>0.1		GB16915-PA	lcl hmm196464
8139	1	2	8.E-59	2.E-37	4.E-48	5.E+10	4.E-32	Sl.CL.01.cl.0146.Contig1	GB14684-PA	gij 156545515 ref XP_001607111.1 gij 156555193 ref XP_001603768.1
11072	1	24	2.E-17	>0.1	1.E-06	5.E+10	>0.1		GB19307-PA	lcl hmm12144 lcl hmm214214 lcl hmm112404 lcl hmm104424 lcl hmm108424 lcl hmm264424 lcl hmm342424 lcl hmm28434 lcl hmm318464 lcl hmm62584 lcl hmm78614 lcl hmm232634 lcl hmm122654 lcl hmm44824 lcl hmm282834 lcl hmm162874 lcl hmm290934 lcl hmm68994 lcl hmm143164 lcl hmm199194 lcl hmm33204 lcl hmm179214 lcl hmm233244 lcl hmm229284
11049	1	4	2.E-12	>0.1	9.E-02	4.E+10	9.E-21	Sl.CL.06.cl.0696.Contig1	GB10048-PA	lcl hmm152534 lcl hmm154534 lcl hmm292804 lcl hmm294804
11341	1	1	3.E-12	>0.1	>0.1	3.E+10	>0.1		GB17807-PA	lcl hmm115054
9356	1	1	1.E-42	6.E-30	3.E-32	3.E+10	3.E-22	Sl.CL.45.cl.4506.Contig1	GB16352-PA	gij 156537317 ref XP_001606228.1
8089	1	1	2.E-63	1.E-53	5.E-47	5.E+09	3.E-61	Sl.CL.01.cl.0179.Contig1	GB16450-PA	gij 156550197 ref XP_001600810.1
11624	1	1	3.E-11	>0.1	>0.1	3.E+09	3.E-13	Sl.CL.06.cl.0651.Contig1	GB16334-PA	lcl hmm510144
9864	1	1	3.E-31	3.E-16	1.E-21	3.E+09	3.E-12	SiJWG03ADE.scf	GB11955-PA	gij 156538625 ref XP_001607611.1
11721	1	1	4.E-11	>0.1	>0.1	3.E+09	>0.1		GB19679-PA	lcl hmm90804
11456	1	1	4.E-11	>0.1	1.E-01	3.E+09	1.E-04	Sl.CL.06.cl.0638.Contig1	GB11961-PA	lcl hmm498594
10622	1	1	2.E-23	5.E-14	3.E-14	2.E+09	4.E-29	Sl.CL.29.cl.2918.Contig1	GB18566-PA	lcl hmm310274
10558	1	1	3.E-24	4.E-05	3.E-15	1.E+09	>0.1		GB10391-PA	lcl hmm416784
10442	1	1	6.E-26	3.E-17	1.E-14	5.E+08	2.E-26	Sl.CL.14.cl.1429.Contig1	GB17875-PA	gij 156542279 ref XP_001601527.1
11511	1	1	3.E-10	>0.1	>0.1	3.E+08	>0.1		GB17362-PA	lcl hmm124894
11610	1	1	3.E-10	>0.1	>0.1	3.E+08	4.E-17	gi_121963721-gb_EH412983.1	GB16870-PA	lcl hmm60724
11674	1	1	4.E-10	>0.1	>0.1	3.E+08	2.E-11	Sl.CL.32.cl.3251.Contig1	GB15487-PA	gij 156538653 ref XP_001608217.1
11775	1	1	5.E-13	>0.1	1.E-04	2.E+08	2.E-04	SiJWA04BBD2.scf	GB15584-PA	gij 156554437 ref XP_001603903.1
11944	1	1	8.E-14	1.E-05	>0.1	1.E+08	>0.1		GB10615-PA	gij 156537858 ref XP_001608104.1
11388	1	1	3.E-14	3.E-06	2.E-02	1.E+08	>0.1		GB18597-PA	lcl hmm454054
6286	1	1	4.E-106	4.E-98	5.E-88	1.E+08	7.E-87	Sl.CL.28.cl.2860.Contig1	GB19374-PA	gij 156542297 ref XP_001604945.1
11475	1	1	3.E-12	2.E-02	2.E-04	7.E+07	>0.1		GB12073-PA	lcl hmm316144
11633	1	1	2.E-09	>0.1	>0.1	5.E+07	>0.1		GB14663-PA	gij 156549672 ref XP_001604827.1

11699	1	1	2.E-09	>0.1	>0.1	5.E+07	>0.1		GB19543-PA	lcl hmm328414
11554	1	1	2.E-09	>0.1	>0.1	5.E+07	>0.1		GB18976-PA	gij 156541781 ref XP_001601801.1
11649	1	1	3.E-09	>0.1	>0.1	3.E+07	>0.1		GB18177-PA	lcl hmm434514
9979	1	1	7.E-33	2.E-25	3.E-24	3.E+07	4.E-06	SiJWH10ABH.scf	GB16283-PA	gij 156551400 ref XP_001603623.1
11558	1	2	4.E-09	>0.1	>0.1	3.E+07	>0.1		GB15240-PA	lcl hmm1146384 lcl hmm1148384
11820	1	1	8.E-09	>0.1	>0.1	1.E+07	>0.1		GB13799-PA	lcl hmm163234
11543	1	1	8.E-09	>0.1	>0.1	1.E+07	4.E-11	Sl.CL.43.cl.4327.Contig1	GB13541-PA	gij 156548432 ref XP_001605415.1
11551	1	1	2.E-08	>0.1	>0.1	5.E+06	>0.1		GB11877-PA	lcl hmm413234
11179	1	1	1.E-18	8.E-06	4.E-12	4.E+06	>0.1		GB18461-PA	lcl hmm919024
11691	1	1	4.E-08	>0.1	>0.1	3.E+06	>0.1		GB16368-PA	lcl hmm304624
11833	1	1	4.E-08	>0.1	>0.1	3.E+06	2.E-09	gi_121964073-gb_EH413240.1	GB15046-PA	lcl hmm341034
11733	1	1	5.E-08	>0.1	>0.1	2.E+06	2.E-04	SiJWB01ABU.scf	GB12815-PA	lcl hmm154314
10118	1	1	5.E-67	8.E-61	4.E-38	2.E+06	8.E-29	Sl.CL.22.cl.2263.SiMN_AntpF-T7.ab1	GB13491-PA	gij 156551125 ref XP_001603700.1
10232	1	1	7.E-28	4.E-18	1.E-21	1.E+06	7.E-23	Sl.CL.14.cl.1472.Contig1	GB30336-PA	gij 156542508 ref XP_001600189.1
11709	1	1	1.E-09	1.E-03	9.E-02	1.E+06	>0.1		GB15713-PA	gij 156546580 ref XP_001601903.1
11933	1	1	1.E-07	>0.1	>0.1	1.E+06	>0.1		GB20100-PA	lcl hmm311004
9153	1	1	5.E-51	1.E-33	5.E-45	1.E+06	>0.1		GB18990-PA	lcl hmm206844
7464	1	1	1.E-77	4.E-67	1.E-71	1.E+06	2.E-42	Sl.CL.42.cl.4235.Contig1	GB10692-PA	gij 156549320 ref XP_001600923.1
10033	1	1	9.E-34	4.E-25	6.E-28	7.E+05	5.E-10	Sl.CL.14.cl.1487.Contig1	GB14777-PA	gij 156545651 ref XP_001603986.1
11827	1	1	2.E-07	>0.1	>0.1	5.E+05	4.E-05	SiJWA10ACN.scf	GB13672-PA	lcl hmm837174
11781	1	1	2.E-07	>0.1	>0.1	5.E+05	>0.1		GB20074-PA	lcl hmm266594
11690	1	1	4.E-07	>0.1	>0.1	3.E+05	>0.1		GB10072-PA	gij 156537382 ref XP_001606709.1
11603	1	1	5.E-08	>0.1	1.E-02	2.E+05	>0.1		GB18914-PA	lcl hmm812384
11598	1	1	8.E-07	>0.1	>0.1	1.E+05	>0.1		GB18835-PA	lcl hmm466344
11559	1	1	1.E-06	>0.1	>0.1	1.E+05	>0.1		GB16511-PA	lcl hmm295164
9849	1	1	2.E-35	2.E-30	6.E-30	1.E+05	1.E-30	Sl.CL.11.cl.1159.Contig2	GB19729-PA	gij 156542492 ref XP_001599932.1
11616	1	1	2.E-06	>0.1	>0.1	5.E+04	>0.1		GB19333-PA	lcl hmm380104
10380	1	1	2.E-30	1.E-23	1.E-25	5.E+04	6.E-22	Sl.CL.01.cl.0123.Contig1	GB19262-PA	gij 156555538 ref XP_001603745.1
8306	1	1	3.E-57	7.E-53	2.E-44	2.E+04	4.E-42	Sl.CL.25.cl.2512.Contig1	GB17012-PA	gij 156544442 ref XP_001607624.1
10585	1	1	5.E-23	2.E-14	7.E-19	1.E+04	9.E-22	SiJWF10BCS2.scf	GB13586-PA	lcl hmm158254
5193	1	1	3.E-83	4.E-79	5.E-79	1.E+04	1.E-43	SiJWD12CAP.scf	GB13568-PA	lcl hmm516594
9309	1	1	6.E-21	3.E-17	6.E-17	5.E+03	2.E-03	SiJWE01ADI.scf	GB10321-PA	lcl hmm118494
11857	2	1	1.E-07	3.E-04	3.E-02	3.E+03	>0.1		GB15810- PAGB13301-PA	lcl hmm332574
11994	1	1	1.E-04	>0.1	>0.1	1.E+03	>0.1		GB12792-PA	lcl hmm1410384

