

Genes in syntenic blocks Figure 6C, a

Hd scaffold	Position in scaffold	Hd gene ID	Orthogroup #	Best Blast hit	Expect	Cs gene	Orthogroup #	Position in scaffold
scaffold144	1380719..1397417	HD005010	OG0000722	gi 817190146 ref XP_012270430.1 uncharacterized protein LOC105694386 isoform X2 [Orussus abietir	Expect = 0.000e+0	gene.scaffold_16.g181.t1	OG0000722	2082674..2097848
scaffold144	1402033..1404758	HD005011	OG0008876	gi 1000730346 ref XP_015587582.1 dynein assembly factor 4, axonemal-like [Cephus cinctus]	Expect = 8.300e-150	gene.scaffold_16.g180.t1	OG0008876	2075777..2079078
scaffold144	1405145..1406140	HD005012	OG0008079	gi 340719499 ref XP_003398190.1 vascular endothelial growth factor A-A [Bombus terrestris]	Expect = 7.800e-47	gene.scaffold_16.g179.t1	OG0008079	2074775..2075425
scaffold144	1410042..1410578	HD005013	OG0009360	gi 987906890 ref XP_015428945.1 PREDICTED: uncharacterized protein LOC107185710 [Dufourea nov	Expect = 2.700e-41	gene.scaffold_16.g178.t1	OG0009360	2064292..2070214
scaffold144	1412742..1423051	HD005014	OG0007034	gi 755949684 ref XP_011301181.1 PREDICTED: nucleoprotein TPR [Fopius arisanus]	Expect = 0.000e+0	gene.scaffold_16.g177.t1	OG0007034	2058216..2067490
scaffold144	1423611..1429572	HD005015	OG0004177	gi 1000729872 ref XP_015587356.1 protein virilizer isoform X1 [Cephus cinctus]	Expect = 0.000e+0	NA		
scaffold144	1429964..1432653	HD005016	OG0007546	gi 1070214570 ref XP_018376608.1 PREDICTED: pentatricopeptide repeat-containing protein 1, mitochr	Expect = 7.200e-127	NA		
scaffold144	1434554..1435954	HD005017	OG0009748	gi 1070154465 ref XP_018340726.1 PREDICTED: RISC-loading complex subunit TARBP2-like [Trachymyr	Expect = 2.500e-30	NA		
scaffold144	1438643..1440697	HD005018	OG0003141	gi 645023101 ref XP_008202437.1 PREDICTED: neuralized-like protein 2 [Nasonia vitripennis]	Expect = 8.100e-114	gene.scaffold_16.g36.t1	OG0003141	254028..255633
scaffold144	1442194..1445201	HD005019	OG0003140	gi 1317987018 ref XP_023287837.1 neuronal acetylcholine receptor subunit alpha-5 isoform X1 [Orussu	Expect = 2.500e-59			
scaffold144	1446370..1448826	HD005020	OG0009176	gi 939631532 ref XP_008554100.2 PREDICTED: neuronal acetylcholine receptor subunit alpha-5-like [N	Expect = 7.200e-80	gene.scaffold_16.g37.t1	OG0009176	257530..261137
scaffold144	1450485..1451362	HD005021	OG0007822	Cys2_Hd20				
scaffold144	1454299..1455511	HD005022	OG0007822	Cys1_Hd20				
scaffold144	1457007..1457513	HD005023	OG0001009	gi 805787897 ref XP_012141035.1 PREDICTED: uncharacterized protein LOC100876911 isoform X2 [M	Expect = 2.000e-20	gene.scaffold_16.g38.t1	OG0001009	270567..274688
scaffold144	1464373..1467934	HD005024	OG0001009	gi 795056915 ref XP_011872016.1 PREDICTED: uncharacterized protein LOC105564328 isoform X1 [Vc	Expect = 2.100e-124			
scaffold144	1472127..1477975	HD005025	OG0006050	gi 1000745701 ref XP_015595595.1 cysteine and histidine-rich protein 1 homolog isoform X5 [Cephus c	Expect = 2.400e-190	gene.scaffold_16.g39.t1	OG0006050	278822..284602
scaffold144	1479354..1480103	HD005026	orphan	gi 759078894 ref XP_011349245.1 polyadenylate-binding protein 1 [Ooceraea biro]	Expect = 2.100e-23	gene.scaffold_16.g40.t1	orphan	287471..288253
scaffold144	1508038..1591917	HD005027	OG0001516	gi 755949182 ref XP_011301029.1 PREDICTED: regulating synaptic membrane exocytosis protein 1 iso	Expect = 0.000e+0	gene.scaffold_16.g42.t1	orphan	331489..359465
scaffold144	1601947..1606850	HD005028	orphan	gi 998501744 ref XP_015510887.1 PREDICTED: uncharacterized protein LOC107217756 [Neodiprion l	Expect = 2.200e-36	gene.scaffold_16.g43.t1	OG0001516	385633..394202
scaffold144						gene.scaffold_16.g44.t1	OG0001516	402325..405981
scaffold144	1607444..1607878	HD005029	OG0007431	gi 815909475 ref XP_003489119.2 chromosome transmission fidelity protein 8 homolog [Bombus imp	Expect = 9.300e-30	gene.scaffold_16.g45.t1	OG0001516	413940..415699
scaffold144	1609469..1618501	HD005030	OG0001137	gi 970888608 ref XP_015109471.1 PREDICTED: uncharacterized protein LOC107036203 [Diachasma all	Expect = 2.600e-122	gene.scaffold_16.g46.t1	OG0007431	427568..428032
						gene.scaffold_16.g47.t1	OG0001137	431251..442478

Genes in syntenic blocks Figure 6C, b

Hd scaffold	Position in scaffold	Hd gene ID	Orthogroup #	Best Blast hit	Expect	Cs gene	Orthogroup #	Position in scaffold
scaffold351	2570811..2574280	HD010552	OG0006536	gi 970890219 ref XP_015110360.1 PREDICTED: GPI mannosyltransferase 4 [Diachasma alloemum]	Expect = 6.400e-248	gene.scaffold_16.g210.t1	OG0006536	2319748..2322545
scaffold351	2575688..2584750	HD010553	OG0000820	gi 1000729971 ref XP_015587409.1 histone deacetylase 6 isoform X3 [Cephus cinctus]	Expect = 0.000e+0	gene.scaffold_16.g211.t1	OG0000820	2323661..2331643
scaffold351	2585486..2590674	HD010554	OG0008529	gi 1000729989 ref XP_015587415.1 mitochondrial intermediate peptidase isoform X1 [Cephus cinctus]	Expect = 1.300e-309	gene.scaffold_16.g212.t1	OG0008529	2333001..2336567
scaffold351	2592030..2601204	HD010555	OG0005613	gi 755986949 ref XP_011311356.1 PREDICTED: cullin-4A [Fopius arisanus]	Expect = 0.000e+0	gene.scaffold_16.g213.t1	OG0005613	2338026..2342787
scaffold351	2603266..2606649	HD010556	OG0007486	gi 1000718247 ref XP_015598324.1 protein crooked neck [Cephus cinctus]	Expect = 1.700e-240	gene.scaffold_16.g214.t1	OG0007486	2344137..2346984
						gene.scaffold_16.g216.t1	orphan	2352827..2353396
scaffold351	2614497..2669283	HD010557	OG0000315	gi 1059231176 ref XP_017760895.1 PREDICTED: nuclear factor 1 X-type-like isoform X7 [Eufriesea mexi	Expect = 0.000e+0	gene.scaffold_16.g218.t1	OG0000315	2360992..2364340
						gene.scaffold_16.g219.t1	OG0000315	2373432..2374064
						gene.scaffold_16.g220.t1	OG0000315	2387249..2388404
scaffold351	2678768..2680678	HD010558	OG0007969	gi 755943768 ref XP_011299232.1 PREDICTED: actin-related protein 2/3 complex subunit 4 [Fopius ari	Expect = 5.700e-81	gene.scaffold_16.g221.t1	OG0007969	2416191..2419469
scaffold351	2683737..2685050	HD010559	orphan	N1_Hd18		gene.scaffold_16.g223.t1	OG0010684	2424942..2425688
						gene.scaffold_16.g564.t1	orphan	2426081..2426764
						gene.scaffold_16.g224.t1	orphan	2427951..2428691
scaffold351	2688803..2689573	HD010560	OG0005107	gi 972178531 ref XP_015191350.1 PREDICTED: transmembrane protein 45B-like [Polistes dominula]	Expect = 3.600e-95	gene.scaffold_16.g225.t1	OG0005107	2430738..2431508
scaffold351	2690793..2699707	HD010561	OG0003436	gi 820860113 ref XP_003697297.2 PREDICTED: LOW QUALITY PROTEIN: enhancer of mRNA-decapping	Expect = 0.000e+0	NA		
scaffold351	2700580..2701786	HD010562	OG0007575	gi 1227092722 gb OXU18804.1 hypothetical protein TSAR_005200 [Trichomalopsis sarcophagae]	Expect = 3.400e-82	NA		
scaffold351	2706953..2708212	HD010563	OG0009633	gi 1580172942 ref XP_028048451.1 uncharacterized protein LOC114255006 [Monomorium pharaonis]	Expect = 1.100e-29	NA		
scaffold351	2712014..2713607	HD010564	OG0000118	gi 795032310 ref XP_011863894.1 PREDICTED: speckle-type POZ protein A-like [Vollenhovia emeryi]	Expect = 6.600e-20	NA		
scaffold351	2714791..2716848	HD010565	OG0005178	gi 1000730046 ref XP_015587445.1 actin-related protein 10 [Cephus cinctus]	Expect = 2.800e-165	gene.scaffold_16.g124.t1	OG0005178	1439439..1441701
scaffold351	2717065..2719279	HD010566	OG0008078	gi 817195095 ref XP_012273078.1 eukaryotic translation initiation factor 3 subunit F [Orussus abietinu	Expect = 4.500e-139	gene.scaffold_16.g125.t1	OG0008078	1441946..1443651
scaffold351	2720235..2740116	HD010567	OG0000165	gi 915666462 gb KOC68367.1 Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha [Habropod	Expect = 0.000e+0	gene.scaffold_16.g126.t1	OG0000165	1444610..1449264
scaffold351	2744556..2745842	HD010568	OG0000280	gi 998499361 ref XP_015509568.1 PREDICTED: venom peptide isomerase heavy chain-like [Neodiprion	Expect = 5.200e-119	gene.scaffold_16.g129.t1	OG0000280	1468965..1476057
scaffold351	2746325..2748699	HD010569	OG0010371	no hit				
scaffold351	2749640..2750960	HD010570	OG0010371	no hit				
scaffold351	2754546..2756977	HD010571	OG0000280	gi 755977086 ref XP_011308165.1 PREDICTED: trypsin-like [Fopius arisanus]	Expect = 1.600e-80	gene.scaffold_16.g130.t1	OG0000280	1479694..1481353

scaffold351	2757727..2759955	HD010572	OG0000280	gi 755977086 ref XP_011308165.1 PREDICTED: trypsin-like [Fopius arisanus]	Expect = 2.500e-81	gene.scaffold_16.g131.t1	OG0000280	1482054..1483447
scaffold351	2760364..2762511	HD010573	OG0000280	gi 755977083 ref XP_011308164.1 PREDICTED: trypsin II-P29-like [Fopius arisanus]	Expect = 4.300e-75	gene.scaffold_16.g132.t1	OG0000280	1484135..1488423
scaffold351	2765019..2770447	HD010574	OG0008378	gi 755977080 ref XP_011308163.1 PREDICTED: carboxypeptidase B-like [Fopius arisanus]	Expect = 8.000e-215	gene.scaffold_16.g133.t1	OG0008378	1489809..1493726

Genes in synteny blocks Figure 6C, c

Hd scaffold	Position in scaffold	Hd gene ID	Orthogroup #	Best Blast hit		Cs gene	Orthogroup #	Position in scaffold
		NA				gene.scaffold_5890.g33.	OG0000028	162272..162676
		NA				gene.scaffold_5890.g32.	OG0000021	161726..162136
		NA				gene.scaffold_5890.g31.	OG0000024	156325..156699
		NA				gene.scaffold_5890.g30.	orphan	151548..155209
		NA				gene.scaffold_5890.g29.	OG0000024	151509..151883
		NA				gene.scaffold_5890.g28.	OG0002056	146321..147118
		NA				///		
		NA				gene.scaffold_5890.g59e	OG0002056	134843..135562
scaffold351	2270991..2271302	HD010503	OG0000028	gi 170058994 ref XP_001865168.1 histone 1 [Culex quinquefasciatus]	Expect = 3.900e-48			
scaffold351	2273424..2278678	HD010504	OG0003636	gi 1000742598 ref XP_015593950.1 equilibrative nucleoside transporter 4 [Cephus cinctus]	Expect = 1.500e-267	gene.scaffold_5890.g22.	OG0003636	128010..132737
scaffold351	2280628..2284708	HD010505	OG0001788	gi 954555894 ref XP_014601533.1 PREDICTED: serine/threonine-protein kinase ICK [Polistes canadensis]	Expect = 3.200e-256	gene.scaffold_5890.g20.	OG0001788	120284..125583
scaffold351	2288342..2289300	HD010506	orphan	no hit		gene.scaffold_5890.g18.	OG0000067	111355..111939
scaffold351	2292636..2299704	HD010507	OG0001161	gi 970889125 ref XP_015109758.1 PREDICTED: DENN domain-containing protein 1A-like isoform X1 [Drosophila melanogaster]	Expect = 0.000e+0	gene.scaffold_5890.g17.	OG0001161	101367..109432
scaffold351	2300822..2301232	HD010508	OG0000021	gi 170053440 ref XP_001862674.1 histone H3 type 2 [Culex quinquefasciatus]	Expect = 3.000e-64	gene.scaffold_5890.g16.	OG0000021	97954..100617
scaffold351	2302839..2303213	HD010509	OG0000024	gi 815814502 ref XP_012228276.1 PREDICTED: histone H2A-like [Linepithema humile]	Expect = 1.700e-58			
scaffold351	2304346..2305863	HD010510	OG0008873	gi 1000757495 ref XP_015601701.1 activator of basal transcription 1 isoform X2 [Cephus cinctus]	Expect = 1.900e-83			
scaffold351	2306413..2308908	HD010511	OG0004415	gi 307203421 gb EFN82496.1 mRNA-decapping enzyme 2 [Harpegnathos saltator]	Expect = 1.000e-159	gene.scaffold_5890.g15.	OG0004415	95411..97479
scaffold351	2310086..2311637	HD010512	OG0007967	gi 954580551 ref XP_014614868.1 PREDICTED: heme oxygenase 1 [Polistes canadensis]	Expect = 3.300e-93			
scaffold351	2312957..2318568	HD010513	OG0006585	gi 1000715934 ref XP_015586052.1 peroxisomal multifunctional enzyme type 2 isoform X1 [Cephus cinctus]	Expect = 2.200e-259	gene.scaffold_5890.g14.	OG0006585	86991..95435
scaffold351	2320285..2328116	HD010514	OG0002518	gi 1000757483 ref XP_015601693.1 hypoxia up-regulated protein 1 isoform X1 [Cephus cinctus]	Expect = 1.000e-304	gene.scaffold_5890.g13.	OG0002518	79568..85710
scaffold351	2329743..2330387	HD010515	orphan	Rep5_Hd17				
scaffold351	///							
scaffold351	2335459..2336166	HD010519	orphan	Rep1_Hd17				
scaffold351	2336786..2337193	HD010520	orphan	rep partial_Hd17				
scaffold351	2337418..2340007	HD010521	OG0002835	gi 808129402 ref XP_012167532.1 WW domain-binding protein 2 isoform X1 [Bombus terrestris]	Expect = 2.300e-101	gene.scaffold_5890.g12.	OG0002835	76069..78711
scaffold351	2345118..2346993	HD010522	OG0006513	gi 1227095170 gb OXU20342.1 hypothetical protein TSAR_005800 [Trichomalopsis sarcophagae]	Expect = 1.500e-104	gene.scaffold_5890.g11.	OG0006513	69897..70791
scaffold351	2349858..2352634	HD010523	OG0007554	gi 1059880711 ref XP_017795737.1 PREDICTED: ubiquitin domain-containing protein UBFD1-like [Habrobracon hebetor]	Expect = 2.500e-105	gene.scaffold_5890.g10.	OG0007554	63578..65852
scaffold351	2353611..2362101	HD010524	OG0003626	gi 970912543 ref XP_015122543.1 PREDICTED: polycomb protein suz12-B [Diachasma alloeum]	Expect = 0.000e+0	gene.scaffold_5890.g9.t1	OG0003626	55732..62546
scaffold351	2363619..2368282	HD010525	OG0004797	gi 1000730147 ref XP_015587495.1 methyltransferase-like protein 22 [Cephus cinctus]	Expect = 5.700e-92	gene.scaffold_5890.g8.t1	OG0004797	51570..54218
scaffold351	2368680..2372470	HD010526	OG0006517	gi 1476364581 gb AXY94695.1 disulfide-isomerase [Habrobracon hebetor]	Expect = 1.100e-196	gene.scaffold_5890.g7.t1	OG0006517	44960..49478

Genes in synteny blocks Figure 7C, a

Hd scaffold	Position in scaffold	Hd gene ID	Orthogroup #	Best Blast hit		Cs gene	Orthogroup #	Position in scaffold
Scaffold 91	339180-342661	HD016092	OG0004987	gi 780657091 ref XP_011691874.1 PREDICTED: solute carrier organic anion transporter family member 5A1 isoform X1 [Fopius arisanus]	Expect = 1.400e-275	gene.scaffold_14.g96.t1	OG0004987	672138..680445
Scaffold 91	370839-379409	HD016093	OG0004824	gi 769843355 ref XP_011632893.1 solute carrier organic anion transporter family member 5A1 isoform X1 [Fopius arisanus]	Expect = 0.000e+0	gene.scaffold_14.g97.t1	OG0004824	687109..693641
Scaffold 91	386420-391295	HD016094	OG0004411	gi 755943227 ref XP_011299047.1 PREDICTED: G-protein coupled receptor Mth isoform X2 [Fopius arisanus]	Expect = 9.200e-139	gene.scaffold_14.g98.t1	orphan	691335..692107
Scaffold 91	392450-394130	HD016095	OG0001577	gi 1492480063 ref XP_026674315.1 probable RNA methyltransferase CG11342 isoform X1 [Ceratina californica]	Expect = 5.800e-72	gene.scaffold_14.g99.t1	OG0001577	701142..708415
Scaffold 91	396109-397563	HD016096	OG0001965	gi 749787677 ref XP_011147350.1 myosin-2 essential light chain isoform X2 [Harpegnathos saltator]	Expect = 3.300e-77	gene.scaffold_14.g100.t1	OG0001965	709518..710732
Scaffold 91	398929-404614	HD016097	OG0004676	gi 972210109 ref XP_015187432.1 PREDICTED: WDR repeat, SAM and U-box domain-containing protein [Habrobracon hebetor]	Expect = 2.500e-298	gene.scaffold_14.g101.t1	OG0004676	713039..718640
Scaffold 91	406627-407543	HD016098	OG0007680	gi 817183740 ref XP_012278017.1 GATA zinc finger domain-containing protein 1 isoform X2 [Orussus cinctus]	Expect = 1.600e-105	gene.scaffold_14.g102.t1	OG0007680	720734..721681
Scaffold 91	408455-411290	HD016099	OG0005425	gi 48142301 ref XP_397320.1 AP-3 complex subunit sigma-2 isoform X1 [Apis mellifera]	Expect = 8.100e-92	gene.scaffold_14.g103.t1	OG0005425	722419..724763
Scaffold 91	412851-415250	HD016100	OG0001553	gi 383857701 ref XP_003704342.1 PREDICTED: beta-1,3-galactosyltransferase 1-like isoform X2 [Megaselia scalaris]	Expect = 3.200e-143	NA		
Scaffold 91	418638-419902	HD016101	OG0008604	gi 345486223 ref XP_003425426.1 PREDICTED: G patch domain-containing protein 4-like [Nasonia vitriicola]	Expect = 1.400e-47	NA		
Scaffold 91	420807-422918	HD016102	OG0004778	gi 970907664 ref XP_015119881.1 PREDICTED: type 2 phosphatidylinositol 4,5-bisphosphate 4-phosphatase [Habrobracon hebetor]	Expect = 7.800e-127	NA		
Scaffold 91	425105..426659	HD016103	orphan	no hit		NA		
Scaffold 91	427639..428218	HD016104	orphan	no hit		NA		
Scaffold 91	429397..431144	HD016105	orphan	no hit		NA		

Scaffold 91	433475..434375	HD016106	orphan	no hit		NA
Scaffold 91	435700..436543	HD016107	orphan	no hit		NA
Scaffold 91	437892..438750	HD016108	orphan	no hit		NA
Scaffold 91	440012..441810	HD016109	orphan	no hit		NA
Scaffold 91	443803..449675	HD016110	orphan	no hit		NA
Scaffold 91	450623..452672	HD016111	OG0005467	gi 987911334 ref XP_015431390.1 PREDICTED: DNA repair protein XRCC1 [Dufourea novaengliae]	Expect = 5.400e-86	NA
Scaffold 91	453857..454591	HD016112	orphan	IVSP_U1		NA
Scaffold 91	///					NA
Scaffold 91	467172..467876	HD016611	orphan	IVSP_U25		NA
Scaffold 91	467893..468866	HD016610	OG0008504	no hit		NA
Scaffold 91	470135..471607	HD016121	orphan	N-gene1_Hd15		NA
Scaffold 91	474019..474459	HD016122	orphan	no hit		NA
Scaffold 91	475549..482783	HD016123	OG0008504	gi 1000724119 ref XP_015610535.1 uncharacterized protein LOC107275188 isoform X2 [Cephus cinctus]	Expect = 2.200e-140	gene.scaffold_50.g34.t1. OG0008504 228808..236437
Scaffold 91	485760..486020	HD016616	orphan	U1_Hd33		
Scaffold 91	487963..488427	HD016613	orphan	U2_Hd33		
Scaffold 91	487593..496279	HD016124	OG0008877	gi 1573754945 ref XP_028042060.1 inter-alpha-trypsin inhibitor heavy chain H4-like [Bombyx mandarin]	Expect = 1.400e-43	gene.scaffold_50.g35.t1 OG0008877 239447..245088
Scaffold 91	496775..497693	HD016125	OG0008877	gi 1185578680 ref XP_020720113.1 uncharacterized protein LOC100648520 [Bombus terrestris]	Expect = 2.200e-27	
Scaffold 91	498816..502616	HD016126	OG0007035	gi 817052951 ref XP_012259318.1 tetratricopeptide repeat protein 27 [Athalia rosae]	Expect = 4.100e-262	gene.scaffold_50.g36.t1 OG0007035 245526..250163
Scaffold 91	503255..504795	HD016127	orphan	no hit		gene.scaffold_50.g37.t1 orphan 250869..252609
Scaffold 91	506500..510737	HD016128	OG0008077	gi 970916129 ref XP_015124492.1 PREDICTED: uncharacterized protein LOC107046395 [Diachasma all	Expect = 3.700e-255	gene.scaffold_50.g38.t1 OG0008077 253612..257408
Scaffold 91	512122..516356	HD016129	OG0004493	gi 1061111877 ref XP_017881969.1 uridine-cytidine kinase-like 1 [Ceratina calcarata]	Expect = 1.600e-268	gene.scaffold_50.g39.t1 OG0004493 258014..261162
Scaffold 91	517628..518212	HD016130	OG0002787	gi 665791319 ref XP_008543211.1 PREDICTED: inosine triphosphate pyrophosphatase [Microplitis den	Expect = 2.700e-82	gene.scaffold_50.g40.t1 OG0002787 262054..262638
Scaffold 91	521509..534951	HD016131	OG0003558	gi 665791317 ref XP_008543209.1 PREDICTED: uncharacterized protein LOC103568231 [Microplitis de	Expect = 0.000e+0	NA
Scaffold 91	536918..537427	HD016132	OG0000328	Vank1_Hd24		NA
Scaffold 91	538200..539270	HD016133	OG0010755	Vinx1_Hd24		NA
Scaffold 91	541304..542734	HD016134	orphan	Ngene-4		NA
Scaffold 91	///					NA
Scaffold 91	567663..567944	HD016614	orphan	Ngene-3		NA
Scaffold 91	573680..574969	HD016150	orphan	N1_Hd29		NA
Scaffold 91	579785..581438	HD016151	OG0001925	gi 1000751647 ref XP_015598681.1 protein l(2)37Cc [Cephus cinctus]	>gi 1000751649 ref XP_015598681.1 Expect = 7.900e-133	NA
Scaffold 91	583666..596697	HD016152	OG0000557	gi 970889107 ref XP_015109747.1 PREDICTED: myosin-VIIa-like [Diachasma alloeuum]	Expect = 0.000e+0	NA
Scaffold 91	733490..737430	HD016153	OG0002720	gi 1061140064 ref XP_017893504.1 transcription factor Sox-2 isoform X1 [Ceratina calcarata]	Expect = 3.700e-147	NA

Genes in synteny blocks Figure 7C, b

Hd scaffold	Position in scaffold	Hd gene ID	Orthogroup #	Best Blast hit	Expect	Cs gene	Orthogroup #	Position in scaffold
Scaffold 1275	5695132..5698339	HD001703	OG0002287	gi 1615708828 gb TGZ38293.1 Uncharacterized protein DBV15_00393, partial [Temnothorax longi]	Expect = 1.200e-89	gene.scaffold_134.g10.t1	OG0002287	124421..126230
Scaffold 1275	5698820..5699218	HD001704	OG0007747	gi 817198610 ref XP_012274957.1 proteasome assembly chaperone 4 isoform X1 [Orussus abietinus]	Expect = 8.200e-35	gene.scaffold_134.g11.t1	OG0007747	128625..129023
Scaffold 1275	5700119..5709232	HD001705	OG0007746	gi 1000763707 ref XP_015604930.1 midasin [Cephus cinctus]	Expect = 0.000e+0	gene.scaffold_134.g12.t1	OG0007746	129973..143060
Scaffold 1275	5715296..5722376	HD001706	OG0005758	gi 1000763721 ref XP_015604938.1 uncharacterized protein LOC107272369 isoform X1 [Cephus cinctus]	Expect = 6.200e-245	gene.scaffold_134.g13.t1	OG0005758	142507..148607
Scaffold 1275	5745780..5748027	HD001707	orphan	no hit		NA		
Scaffold 1275	5789342..5804341	HD001708	OG0010542	gi 1000763707 ref XP_015604930.1 midasin [Cephus cinctus]	Expect = 0.000e+0	gene.scaffold_6042.g1.t1	OG0010542	7898..20048
Scaffold 1275	5804928..5806155	HD001709	OG0008637	gi 817050671 ref XP_012269284.1 28S ribosomal protein S15, mitochondrial [Athalia rosae]	Expect = 3.900e-66	gene.scaffold_6042.g3.t1	OG0008637	20431..21692
Scaffold 1275	5806461..5808045	HD001710	OG0008638	gi 1000725354 ref XP_015585242.1 protein AATF [Cephus cinctus]	Expect = 1.900e-132	gene.scaffold_6042.g4.t1	OG0008638	22007..23884
Scaffold 1275	5809242..5809907	HD016565	orphan	Rep1_Hd6				
Scaffold 1275	///					gene.scaffold_6042.g5.t1	OG0000017	38407..41846
Scaffold 1275	5818232..5818829	HD016570	orphan	U1.2_Hd6				
Scaffold 1275	5853342..5855008	HD001713	OG0000907	gi 954550203 ref XP_014598460.1 PREDICTED: fibrillin-1-like [Polistes canadensis]	Expect = 2.700e-10			
Scaffold 1275	5859163..5862434	HD001714	OG0000759	gi 766921548 ref XP_011505297.1 PREDICTED: major royal jelly protein 1-like isoform X1 [Ceratosolen	Expect = 8.700e-75	gene.scaffold_6042.g6.t1	OG0000759	56163..59912
Scaffold 1275	5868688..5896004	HD001715	OG0000907	gi 1477752320 ref XP_006561358.2 fibrillin-2 isoform X1 [Apis mellifera]	Expect = 1.000e-135	gene.scaffold_6042.g7.t1	OG0000907	67573..82296
						gene.scaffold_6042.g8.t1	OG0000907	84612..89146
Scaffold 1275	5899594..5902437	HD001716	OG0008827	gi 925679321 gb KOX76257.1 hypothetical protein WN51_11586 [Melipona quadrifasciata]	Expect = 1.300e-41	gene.scaffold_6042.g9.t1	OG0008827	95154..98396
Scaffold 1275	5907509..5931751	HD001717	OG0000907	gi 951521230 ref XP_014484382.1 PREDICTED: uncharacterized protein LOC106749449 isoform X1 [Di	Expect = 1.400e-276	gene.scaffold_6042.g11.t1	OG0000907	102320..114213
Scaffold 1275	5934850..5939667	HD001718	OG0003835	gi 936686298 ref XP_014221120.1 protein henna isoform X1 [Trichogramma pretiosum]	Expect = 8.800e-249	gene.scaffold_6042.g12.t1	OG0003835	131205..134233

Scaffold 1275 5941301..5941799	HD001719	orphan	no hit		NA
Scaffold 1275 5941600..5943451	HD001720	orphan	GlyPro1_Hd2		NA
Scaffold 1275 ///					NA
Scaffold 1275 5952553..5953461	HD016569	orphan	SerThr_Hd2		NA
Scaffold 1275 5954908..5957857	HD001723	OG0008292	gi 970914653 ref XP_015123688.1	PREDICTED: vacuolar fusion protein MON1 homolog A [Diachasma	Expect = 1.500e-249 NA
Scaffold 1275 5958966..5960611	HD001724	OG0008989	gi 1000737514 ref XP_015591270.1	pre-mRNA-splicing factor 38 isoform X1 [Cephus cinctus]	Expect = 7.300e-111 NA
Scaffold 1275 5963322..5967084	HD001725	OG0006130	gi 665789861 ref XP_008560590.1	PREDICTED: lipoma HMGIC fusion partner-like 3 protein [Microplitis	Expect = 1.500e-148 NA
Scaffold 1275 5970045..5989460	HD001726	OG0003941	gi 1000737447 ref XP_015591233.1	paired box pox-neuro protein isoform X2 [Cephus cinctus]	Expect = 3.600e-166 NA
Scaffold 1275 6031309..6031662	HD001727	orphan	no hit		NA
Scaffold 1275 6039464..6041203	HD001728	OG0008922	no hit		NA
Scaffold 1275 6047894..6053795	HD001729	OG0004544	gi 970914023 ref XP_015123344.1	PREDICTED: neither inactivation nor afterpotential protein G-like [D	Expect = 1.100e-201 NA
Scaffold 1275 6055912..6056223	HD001730	orphan	no hit		gene.scaffold_12.g37.t1 orphan 313226..314796
Scaffold 1275 6065301..6068372	HD001731	orphan	U1_Hd7		gene.scaffold_12.g36.t1 orphan 269465..272474
Scaffold 1275 6163755..6209923	HD001732	OG0001182	gi 665784719 ref XP_008543429.1	PREDICTED: zinc finger protein 608-like [Microplitis demolitor]	Expect = 8.000e-240 gene.scaffold_12.g35.t1 OG0001182 266509..281996
Scaffold 1275 6215883..6220739	HD001733	OG0009154	gi 665785226 ref XP_008546042.1	PREDICTED: focadhesin [Microplitis demolitor]	Expect = 3.500e-300 gene.scaffold_12.g34.t1 OG0009154 254503..262293
Scaffold 1275 6223570..6225534	HD001734	OG0005749	gi 759044886 ref XP_011331377.1	uncharacterized protein C1orf43 homolog [Ooceraea biroi]	Expect = 6.200e-121 gene.scaffold_12.g33.t1 OG0005749 246626..248241
Scaffold 1275 6233178..6236130	HD001735	orphan	gi 815899824 ref XP_012236112.1	RNA polymerase II elongation factor EII [Bombus impatiens]	Expect = 2.200e-20
Scaffold 1275 6237301..6258275	HD001736	OG0001096	gi 1000725348 ref XP_015585239.1	NGFI-A-binding protein homolog isoform X1 [Cephus cinctus]	Expect = 1.200e-181 gene.scaffold_12.g32.t1 OG0001096 233201..241710
Scaffold 1275 6262652..6270854	HD001737	OG0001213	gi 817221046 ref XP_012286061.1	girdin isoform X1 [Orussus abietinus]	Expect = 4.100e-256 gene.scaffold_12.g30.t1 OG0001213 210669..216809
Scaffold 1275 6273273..6277538	HD001738	OG0000750	gi 970914033 ref XP_015123349.1	PREDICTED: E3 ubiquitin-protein ligase RNF126 [Diachasma alloeu	Expect = 5.100e-91 NA
Scaffold 1275 6295663..6305891	HD001739	OG0001026	gi 805820120 ref XP_003707425.2	PREDICTED: monocarboxylate transporter 10-like isoform X2 [Mega	Expect = 4.400e-278 NA
Scaffold 1275 6326868..6327170	HD001740	orphan	no hit		NA
Scaffold 1275 6327762..6333610	HD001741	OG0001259	gi 755965602 ref XP_011305227.1	PREDICTED: uncharacterized protein LOC105267814 [Fopius arisan	Expect = 3.100e-204 NA
Scaffold 1275 6336069..6336941	HD001742	OG0008975	gi 826447337 ref XP_012531547.1	cytochrome c oxidase assembly factor 5 [Monomorium pharaonis]	Expect = 9.100e-32 NA
Scaffold 1275 6337655..6338948	HD001743	OG0007279	gi 970893534 ref XP_015112156.1	PREDICTED: lysM and putative peptidoglycan-binding domain-cont	Expect = 1.000e-66 NA
Scaffold 1275 ///					
Scaffold 1275 6498766..6500773	HD001752	OG0001027	gi 1059871709 ref XP_017790766.1	PREDICTED: uncharacterized protein LOC108572935 [Habropoda la	Expect = 1.300e-295 gene.scaffold_57.g37.t1 OG0001027 701460..703459
Scaffold 1275 6525619..6535728	HD001753	OG0008714	gi 1000769997 ref XP_015608184.1	zwei Ig domain protein zig-8 isoform X1 [Cephus cinctus]	Expect = 1.300e-115 gene.scaffold_57.g35.t1 OG0008714 673695..676530
Scaffold 1275 6576893..6577922	HD001754	orphan	no hit		gene.scaffold_57.g34.t1 OG0008714 667397..668577
Scaffold 1275 6589791..6590075	HD001755	orphan	no hit		
Scaffold 1275 6609826..6610452	HD001756	OG0010758	no hit		
Scaffold 1275 6654784..6656225	HD001757	OG0010662	no hit		
Scaffold 1275 6674792..6680997	HD001758	OG0010538	gi 817211154 ref XP_012281702.1	uncharacterized protein LOC105700447 [Orussus abietinus]	Expect = 4.400e-177 gene.scaffold_57.g33.t1 OG0010538 549863..558077
Scaffold 1275 6687225..6691596	HD001759	OG0000577	gi 665815849 ref XP_008556602.1	PREDICTED: acylcarnitine hydrolase-like [Microplitis demolitor]	Expect = 1.100e-123 gene.scaffold_57.g32.t1 OG0000577 527847..544092
Scaffold 1275 6694467..6698473	HD001760	OG0000577	gi 665815849 ref XP_008556602.1	PREDICTED: acylcarnitine hydrolase-like [Microplitis demolitor]	Expect = 2.300e-118
Scaffold 1275 6713912..6715341	HD001761	OG0010178	gi 954544039 ref XP_014610010.1	PREDICTED: UPF0602 protein C4orf47 homolog [Polistes canadensi	Expect = 2.700e-76 gene.scaffold_57.g31.t1 OG0010178 512556..513765
Scaffold 1275 6755517..6755963	HD001762	orphan	no hit		gene.scaffold_57.g29.t1 orphan 480378..482423
Scaffold 1275 6788558..6789189	HD001763	OG0000376	gi 998503073 ref XP_015511626.1	PREDICTED: uncharacterized protein LOC107218308 [Neodiprion le	Expect = 2.500e-25 gene.scaffold_57.g28.t1 OG0000376 445783..447418
Scaffold 127548					gene.scaffold_57.g27.t1 orphan 394294..400573
Scaffold 1275 6832835..6833713	HD001764	orphan	IVSP_U29		gene.scaffold_57.g26.t1. orphan 391820..393241
Scaffold 1275 ///					///
Scaffold 1275 6845548..6848464	HD001769	orphan	IVSP_U34		gene.scaffold_57.g24.t1. orphan 383305..386526
Scaffold 1275 6856068..6858621	HD001770	OG0000376	gi 755932577 ref XP_011314368.1	PREDICTED: lachesin-like [Fopius arisanus]	Expect = 2.700e-25 gene.scaffold_57.g22.t1 OG0000376 370164..371046
Scaffold 1275 6861330..6863003	HD001771	OG0001625	gi 1070588568 ref XP_018406776.1	PREDICTED: uncharacterized protein LOC108771307 [Cyphomyrme	Expect = 1.500e-186

Genes in synteny blocks Figure 7C, c

Hd scaffold	Position in scaffold	Hd gene ID	Orthogroup #	Best Blast hit	Cs gene	Orthogroup #	Position in scaffold
Scaffold 1275	10649612..1065171	HD002066	OG0004297	gi 815768838 ref XP_012233244.1	PREDICTED: caspase-3 isoform X1 [Linepithema humile]	Expect = 2.800e-70	gene.scaffold_12.g65.t1 OG0004297 668906..679965
Scaffold 1275	10653145..1065624	HD002067	OG0009466	gi 972201540 ref XP_015182858.1	PREDICTED: sodium channel protein Nach-like isoform X1 [Polistes	Expect = 6.900e-140	gene.scaffold_12.g66.t1 OG0009466 681861..685155
Scaffold 1275	10696314..1070282	HD002068	OG0002519	gi 1389785382 ref XP_024946756.1	uncharacterized protein LOC107273655 isoform X4 [Cephus cinctus	Expect = 1.000e-157	gene.scaffold_12.g67.t1 OG0002519 733521..738350
Scaffold 1275	10713573..1071834	HD002069	OG0002011	gi 817182955 ref XP_012273795.1	coiled-coil and C2 domain-containing protein 1-like isoform X2 [Oru	Expect = 2.300e-247	gene.scaffold_12.g68.t1 OG0002011 752453..758163
Scaffold 1275	10718988..1072124	HD002070	OG0008538	gi 817182522 ref XP_012271486.1	V-type proton ATPase subunit d [Orussus abietinus]	Expect = 3.600e-199	gene.scaffold_12.g70.t1 OG0008538 758815..760937
Scaffold 1275	10721836..1072315	HD002071	OG0004841	gi 817182518 ref XP_012271468.1	probable tRNA(His) guanylyltransferase isoform X1 [Orussus abietir	Expect = 2.500e-102	gene.scaffold_12.g71.t1 OG0004841 761672..762420

Scaffold 1275 10723636..1072892:HD002072	OG0002227	gi 1000768710 ref XP_015607512.1 probable methyltransferase TARBP1 isoform X1 [Cephus cinctus]	Expect = 8.500e-229	gene.scaffold_6122.g8.t1	OG0002227	84619..90498
Scaffold 1275 10729352..1073001:HD002073	OG0006556	gi 970884085 ref XP_015126663.1 PREDICTED: ATP synthase subunit g, mitochondrial [Diachasma allo	Expect = 9.800e-33	gene.scaffold_6122.g9.t1	OG0006556	90282..90940
Scaffold 1275 10730306..1073170:HD002074	OG0008346	gi 817057993 ref XP_012269928.1 zinc finger protein 330 homolog [Athalia rosae]	Expect = 2.700e-140	gene.scaffold_6122.g10.t1	OG0008346	91228..92932
Scaffold 1275 10732736..1073820:HD002075	OG0006263	gi 665809833 ref XP_008553302.1 PREDICTED: arrestin domain-containing protein 2 [Microplitis demc	Expect = 3.600e-183	gene.scaffold_6122.g11.t1	OG0006263	93959..96475
Scaffold 1275 10740693..1074533:HD002076	OG0007281	gi 1389758539 ref XP_024943813.1 synaptotagmin-4 isoform X2 [Cephus cinctus]	Expect = 4.500e-179	gene.scaffold_6122.g12.t1	OG0007281	101239..105178
Scaffold 1275 10749875..1075318:HD002077	OG0007282	gi 970904570 ref XP_015118179.1 PREDICTED: dolichol kinase isoform X1 [Diachasma alloem]	Expect = 2.900e-175	gene.scaffold_6122.g14.t1	OG0007282	110423..112817
Scaffold 1275 10755559..1075930:HD002078	OG0005355	gi 936697175 ref XP_014226574.1 glucose-6-phosphate isomerase [Trichogramma pretiosum]	Expect = 5.700e-287	gene.scaffold_6122.g15.t1	OG0005355	116428..120182
Scaffold 1275 10761570..1076280:HD002079	orphan	IVSP_U15				
Scaffold 1275 ///						
Scaffold 1275 10785523..1078700:HD002089	orphan	IVSP_N-2				
Scaffold 1275 10788460..1079089:HD002090	OG0005583	gi 1000723328 ref XP_015610175.1 probable cysteine--tRNA ligase, mitochondrial [Cephus cinctus]	Expect = 7.000e-170	gene.scaffold_6122.g28.t1	OG0005583	158304..160353
Scaffold 1275 10790972..1079279:HD002091	OG0008727	gi 1000723356 ref XP_015610186.1 ribosome production factor 2 homolog [Cephus cinctus]	Expect = 5.600e-130	gene.scaffold_6122.g29.t1	OG0008727	160438..162016
Scaffold 1275 10794756..1080633:HD002092	OG0000882	gi 820843698 ref XP_012340057.1 PREDICTED: protein polybromo-1 isoform X4 [Apis florea]	Expect = 0.000e+0	gene.scaffold_6122.g30.t1	OG0000882	163578..176041
Scaffold 1275 10808631..1080918:HD002093	OG0004828	gi 795054949 ref XP_011871354.1 PREDICTED: succinate dehydrogenase assembly factor 4, mitochondr	Expect = 4.300e-21	gene.scaffold_6122.g31.t1	OG0004828	178896..179652
Scaffold 1275 10809957..1081106:HD002094	OG0006539	gi 925679306 gb K0X76242.1 GPI mannosyltransferase 2 [Melipona quadrifasciata]	Expect = 2.200e-60			
Scaffold 1275 10816751..1084960:HD002095	OG0003603	gi 1000760603 ref XP_015603308.1 angiopoietin-2 [Cephus cinctus] >gi 1389766659 ref XP_0249446C	Expect = 4.400e-295	gene.scaffold_6122.g32.t1	OG0003603	208607..221477
Scaffold 1275 10837195..1085690:HD002096	OG0009828	gi 1070171260 ref XP_018346064.1 PREDICTED: angiopoietin-4 isoform X2 [Trachymyrmex septentrion:	Expect = 3.600e-220	gene.scaffold_6122.g33.t1	OG0009828	227997..231684
Scaffold 1275 10859683..1086000:HD002097	orphan	no hit				
Scaffold 1275 10860001..1086053:HD002098	orphan	IVSP_U35		gene.scaffold_6122.g34.t1	orphan	234803..235273
Scaffold 1275 10861166..1086163:HD002099	orphan	IVSP_U36				
Scaffold 1275 10862390..1086479:HD002100	OG0006143	gi 107268279 ref XP_015596389.1 PREDICTED: serine/threonine-protein kinase rio2 [Cephus cinctus]		gene.scaffold_6122.g37.t1	OG0006143	241011..243008
Scaffold 1275 10866093..1087121:HD002101	OG0007135	gi 749759480 ref XP_011141208.1 sorbitol dehydrogenase [Harpegnathos saltator]	Expect = 5.900e-157	gene.scaffold_6122.g38.t1	OG0007135	243912..249324
Scaffold 1275 10872479..1087731:HD002102	OG0007814	gi 1569271860 gb Q8B02001.1 putative UPF0528 protein CG10038 [Cotesia chilonis]	Expect = 1.200e-113	gene.scaffold_6122.g39.t1	OG0007814	250807..256468
Scaffold 1275 10921663..1092207:HD002103	orphan	no hit				
Scaffold 1275 10970846..1103466:HD002104	OG0002894	gi 1494653095 gb RLU26944.1 hypothetical protein DMN91_000743 [Ooceraea biroii]	Expect = 1.500e-225	gene.scaffold_6122.g40.t1	OG0002894	361174..391485
Scaffold 1275 10983515..1098646:HD002105	orphan	no hit		NA		
Scaffold 1275 11051421..1105729:HD002106	OG0000642	gi 972199364 ref XP_015181683.1 PREDICTED: serine/threonine-protein kinase tricornet isoform X1 [F	Expect = 4.700e-266	gene.scaffold_6095.g2.t1	OG0000642	36848..43783
Scaffold 1275 11089871..1109165:HD002107	orphan	no hit		gene.scaffold_6095.g3.t1	orphan	79134..81658
Scaffold 1275 11110231..1111272:HD002108	OG0000107	gi 970917263 ref XP_015125099.1 PREDICTED: putative RNA-binding protein EEED8.10 [Diachasma all	Expect = 8.200e-156	gene.scaffold_6095.g5.t1	OG0000107	105829..109141
Scaffold 1275 11118585..1111968:HD002109	OG0001394	gi 1000769696 ref XP_015608031.1 dual specificity mitogen-activated protein kinase kinase dSOR1 isof	Expect = 1.300e-106	gene.scaffold_6095.g6.t1	OG0001394	113898..116393
Scaffold 1275 11120053..1112313:HD002110	OG0000139	gi 156547818 ref XP_001606363.1 PREDICTED: sodium/potassium-transporting ATPase subunit alpha-	Expect = 0.000e+0	gene.scaffold_6095.g7.t1	OG0000139	115279..118353
Scaffold 1275 11123403..1112437:HD002111	OG0001394	gi 571503163 ref XP_393416.2 dual specificity mitogen-activated protein kinase kinase dSOR1 [Api	Expect = 1.100e-91	gene.scaffold_6095.g8.t1	OG0001394	117396..119865