

**Genes in syntenic blocks Figure 5C, a**

| Hd scaffold | Position in scaffold | Hd gene ID | Orthogroup # | Best Blast hit  | 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.t: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.t: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.t: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.t: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.t: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 [Trachymyrr 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 | 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.g44.t1 OG0001516 | 402325..405981   |                      |
| scaffold144 | 1609469..1618501     | HD005030   | OG0001137    | gi 970888608 ref XP_015109471.1 PREDICTED: uncharacterized protein LOC107036203 [Diachasma all Expect = 2.600e-122      | gene.scaffold_16.g45.t1 OG0001516 | 413940..415699   |                      |
|             |                      |            |              |   | gene.scaffold_16.g46.t1 OG0007431 | 427568..428032   |                      |
|             |                      |            |              |   | gene.scaffold_16.g47.t1 OG0001137 | 431251..442478   |                      |

**Genes in syntenic blocks Figure 5C, b**

| Hd scaffold | Position in scaffold | Hd gene ID | Orthogroup # | Best Blast hit   | Cs gene                           | Orthogroup #     | Position in scaffold |
|-------------|----------------------|------------|--------------|--|-----------------------------------|------------------|----------------------|
| scaffold351 | 2570811..2574280     | HD010552   | OG0006536    | gi 970890219 ref XP_015110360.1 PREDICTED: GPI mannosyltransferase 4 [Diachasma alloem] Expect = 6.400e-248                | gene.scaffold_16.g210.t: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.t: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.t: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.t: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.t:OG0007486 | 2344137..2346984 |                      |
| 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.g216.t:orphan    | 2352827..2353396 |                      |
| 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.g218.t:OG0000315 | 2360992..2364340 |                      |
| scaffold351 | 2683737..2685050     | HD010559   | orphan       | N1_Hd18  | gene.scaffold_16.g219.t:OG0000315 | 2373432..2374064 |                      |
| 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.g220.t:OG0000315 | 2387249..2388404 |                      |
| scaffold351 | 2690793..2699707     | HD010561   | OG0003436    | gi 820860113 ref XP_003697297.2 PREDICTED: LOW QUALITY PROTEIN: enhancer of mRNA-decapping Expect = 0.000e+0               | gene.scaffold_16.g221.t:OG0007969 | 2416191..2419469 |                      |
| scaffold351 | 2700580..2701786     | HD010562   | OG0007575    | gi 1227092722 gb OXU18804.1  hypothetical protein TSAR_005200 [Trichomalopsis sarcophagae] Expect = 3.400e-82              | gene.scaffold_16.g222.t:OG0010684 | 2424942..2425688 |                      |
| scaffold351 | 2706953..2708212     | HD010563   | OG0009633    | gi 1580172942 ref XP_028048451.1 uncharacterized protein LOC114255006 [Monomorium pharaonis] Expect = 1.100e-29            | gene.scaffold_16.g564.t:orphan    | 2426081..2426764 |                      |
| scaffold351 | 2712014..2713607     | HD010564   | OG0000118    | gi 795032310 ref XP_011863894.1 PREDICTED: speckle-type POZ protein A-like [Vollenhovia emeryi] Expect = 6.600e-20         | gene.scaffold_16.g224.t:orphan    | 2427951..2428691 |                      |
| scaffold351 | 2714791..2716848     | HD010565   | OG0005178    | gi 1000730046 ref XP_015587445.1 actin-related protein 10 [Cephus cinctus] Expect = 2.800e-165                             | gene.scaffold_16.g225.t:OG0005107 | 2430738..2431508 |                      |
| 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.g124.t:OG0005178 | 1439439..1441701 |                      |
| 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.g125.t:OG0008078 | 1441946..1443651 |                      |
| 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.g126.t:OG0000165 | 1444610..1449264 |                      |
| scaffold351 | 2746325..2748699     | HD010569   | OG0010371    | no hit   | gene.scaffold_16.g129.t:OG0000280 | 1468965..1476057 |                      |
| 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.t: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.t: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.t:OG0000280  | 1484135..1488423 |
| scaffold351 | 2765019..2770447 | HD010574 | OG00008378 | gi 755977080 ref XP_011308163.1 PREDICTED: carboxypeptidase B-like [Fopius arisanus] | Expect = 8.000e-215 | gene.scaffold_16.g133.t:OG00008378 | 1489809..1493726 |

**Genes in synteny blocks Figure 5C, 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.g59: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.t: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.t: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.t:OG0006517 |            | 44960..49478         |

**Genes in synteny blocks Figure 6C, 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.t: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.t: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.t:orphan     |            | 691335..692107       |
| Scaffold 91 | 392450-394130        | HD016095   | OG0001577    | gi 1492480063 ref XP_026674315.1 probable RNA methyltransferase CG11342 isoform X1 [Ceratitis capitata]                            | Expect = 5.800e-72  | gene.scaffold_14.g99.t: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.t:OG0001965 |            | 709518..710732       |
| Scaffold 91 | 398929-404614        | HD016097   | OG0004676    | gi 972210109 ref XP_015187432.1 WD repeat, SAM and U-box domain-containing protein 4-like [Nasonia vitripennis]                    | Expect = 2.500e-298 | gene.scaffold_14.g101.t: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.t: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.t: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: WD repeat, SAM and U-box domain-containing protein 4-like [Nasonia vitripennis]         | 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 novaeangliae]          | 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 | OG0003588 | 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 I(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 alloeum]                      | 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 6C, b

| Hd scaffold  | Position in scaffold | Hd gene ID | Orthogroup # | Best Blast hit  | Cs gene                  | Orthogroup #             | Position in scaffold     |
|--------------|----------------------|------------|--------------|---|--------------------------|--------------------------|--------------------------|
| Scaffold 127 | 5695132..5698339     | HD001703   | OG0002287    | gi 1615708828 gb TGZ38293.1  Uncharacterized protein DBV15_00393, partial [Temnothorax longi]       | gene.scaffold_134.g10.t1 | OG0002287                | 124421..126230           |
| Scaffold 127 | 5698820..5699218     | HD001704   | OG0007747    | gi 817198610 ref XP_012274957.1 proteasome assembly chaperone 4 isoform X1 [Orussus abietinus]      | gene.scaffold_134.g11.t1 | OG0007747                | 128625..129023           |
| Scaffold 127 | 5700119..5709232     | HD001705   | OG0007746    | gi 1000763707 ref XP_015604930.1 midasin [Cephus cinctus]   | gene.scaffold_134.g12.t1 | OG0007746                | 129973..143060           |
| Scaffold 127 | 5715296..5722376     | HD001706   | OG0005758    | gi 1000763721 ref XP_015604938.1 uncharacterized protein LOC107272369 isoform X1 [Cephus cinctus]   | gene.scaffold_134.g13.t1 | OG0005758                | 142507..148607           |
| Scaffold 127 | 5745780..5748027     | HD001707   | orphan       | no hit  | NA                       |                          |                          |
| Scaffold 127 | 5789342..5804341     | HD001708   | OG0010542    | gi 1000763707 ref XP_015604930.1 midasin [Cephus cinctus]   | gene.scaffold_6042.g1.t1 | OG0010542                | 7898..20048              |
| Scaffold 127 | 5804928..5806155     | HD001709   | OG0008637    | gi 817050671 ref XP_012269284.1 28S ribosomal protein S15, mitochondrial [Athalia rosae]            | gene.scaffold_6042.g3.t1 | OG0008637                | 20431..21692             |
| Scaffold 127 | 5806461..5808045     | HD001710   | OG0008638    | gi 1000725354 ref XP_015585242.1 protein AATF [Cephus cinctus]                                      | gene.scaffold_6042.g4.t1 | OG0008638                | 22007..23884             |
| Scaffold 127 | 5809242..5809907     | HD016565   | orphan       | Rep1_Hd6  |                          |                          |                          |
| Scaffold 127 | ///                  |            |              |   | gene.scaffold_6042.g5.t1 | OG0000017                | 38407..41846             |
| Scaffold 127 | 5818232..5818829     | HD016570   | orphan       | U1.2_Hd6  |                          |                          |                          |
| Scaffold 127 | 5853342..5855008     | HD001713   | OG0000907    | gi 954550203 ref XP_014598460.1 PREDICTED: fibrillin-1-like [Polistes canadensis]                   | Expect = 2.700e-10       |                          |                          |
| Scaffold 127 | 5859163..5862434     | HD001714   | OG0000759    | gi 766921548 ref XP_011505297.1 PREDICTED: major royal jelly protein 1-like isoform X1 [Ceratosolen | gene.scaffold_6042.g6.t1 | OG0000759                | 56163..59912             |
| Scaffold 127 | 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 127 | 5899594..5902437     | HD001716   | OG0008827    | gi 925679321 gb K0X76257.1  hypothetical protein WNS1_11586 [Melipona quadrifasciata]               | Expect = 1.300e-41       | gene.scaffold_6042.g9.t1 | OG0008827 95154..98396   |
| Scaffold 127 | 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   | OG0000907 102320..114213 |
| Scaffold 127 | 5934850..5939667     | HD001718   | OG0003835    | gi 936686298 ref XP_014221120.1 protein henna isoform X1 [Trichogramma pretiosum]                   | Expect = 8.800e-249      | gene.scaffold_6042.g12   | OG0003835 131205..134233 |

|                               |          |           |  |                     |  |
|-------------------------------|----------|-----------|--|---------------------|--|
| Scaffold 127:5941301..5941799 | HD001719 | orphan    | no hit   |                     | NA   |
| Scaffold 127:5941600..5943451 | HD001720 | orphan    | GlyPro1_Hd2  |                     | NA   |
| Scaffold 127:5952553..5953461 | HD016569 | orphan    | SerThr_Hd2   |                     | NA   |
| Scaffold 127:5954908..5957857 | HD001723 | OG0008292 | gi 970914653 ref XP_015123688.1 PREDICTED: vacuolar fusion protein MON1 homolog A [Diachasma         | Expect = 1.500e-249 | NA   |
| Scaffold 127:5958966..5960611 | HD001724 | OG0008989 | gi 1000737514 ref XP_015591270.1 pre-mRNA-splicing factor 38 isoform X1 [Cephus cinctus]             | Expect = 7.300e-111 | NA   |
| Scaffold 127:5963322..5967084 | HD001725 | OG0006130 | gi 665789861 ref XP_008560590.1 PREDICTED: lipoma HMGIC fusion partner-like 3 protein [Microplitis   | Expect = 1.500e-148 | NA   |
| Scaffold 127:5970045..5989460 | HD001726 | OG0003941 | gi 1000737447 ref XP_015591233.1 paired box pox-neuro protein isoform X2 [Cephus cinctus]            | Expect = 3.600e-166 | NA   |
| Scaffold 127:6031309..6031662 | HD001727 | orphan    | no hit   |                     | NA   |
| Scaffold 127:6039464..6041203 | HD001728 | OG0008922 | no hit   |                     | NA   |
| Scaffold 127:6047894..6053795 | HD001729 | OG0004544 | gi 970914023 ref XP_015123344.1 PREDICTED: neither inactivation nor afterpotential protein G-like [D | Expect = 1.100e-201 | NA   |
| Scaffold 127:6055912..6056223 | HD001730 | orphan    | no hit   |                     | gene.scaffold_12.g37.t1 orphan 313226..314796    |
| Scaffold 127:6065301..6068372 | HD001731 | orphan    | U1_Hd7   |                     | gene.scaffold_12.g36.t1 orphan 269465..272474    |
| Scaffold 127:6163755..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 127:6215883..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 127:6223570..6225534 | HD001734 | OG0005749 | gi 759044886 ref XP_011331377.1 uncharacterized protein C1orf43 homolog [Ooceraea biro]              | Expect = 6.200e-121 | gene.scaffold_12.g33.t1 OG0005749 246626..248241 |
| Scaffold 127:6233178..6236130 | HD001735 | orphan    | gi 815899824 ref XP_012236112.1 RNA polymerase II elongation factor EII [Bombus impatiens]           | Expect = 2.200e-20  |  |
| Scaffold 127:6237301..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 127:6262652..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 127:6273273..6277538 | HD001738 | OG0000750 | gi 970914033 ref XP_015123349.1 PREDICTED: E3 ubiquitin-protein ligase RNF126 [Diachasma alloeu      | Expect = 5.100e-91  | NA   |
| Scaffold 127:6295663..6305891 | HD001739 | OG0001026 | gi 805820120 ref XP_003707425.2 PREDICTED: monocarboxylate transporter 10-like isoform X2 [Mega      | Expect = 4.400e-278 | NA   |
| Scaffold 127:6326868..6327170 | HD001740 | orphan    | no hit   |                     | NA   |
| Scaffold 127:6327762..6333610 | HD001741 | OG0001259 | gi 755965602 ref XP_011305227.1 PREDICTED: uncharacterized protein LOC105267814 [Fopius arisan       | Expect = 3.100e-204 | NA   |
| Scaffold 127:6336069..6336941 | HD001742 | OG0008975 | gi 826447337 ref XP_012531547.1 cytochrome c oxidase assembly factor 5 [Monomorium pharaonis]        | Expect = 9.100e-32  | NA   |
| Scaffold 127:6337655..6338948 | HD001743 | OG0007279 | gi 970893534 ref XP_015112156.1 PREDICTED: lysM and putative peptidoglycan-binding domain-cont       | Expect = 1.000e-66  | NA   |
| Scaffold 127:6498766..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 127:6525619..6535728 | HD001753 | OG0008714 | gi 1000769997 ref XP_015608184.1 zweiz lg domain protein zig-8 isoform X1 [Cephus cinctus]           | Expect = 1.300e-115 | gene.scaffold_57.g35.t1 OG0008714 673695..676530 |
| Scaffold 127:6576893..6577922 | HD001754 | orphan    | no hit   |                     | gene.scaffold_57.g34.t1 OG0008714 667397..668577 |
| Scaffold 127:6589791..6590075 | HD001755 | orphan    | no hit   |                     |  |
| Scaffold 127:6609826..6610452 | HD001756 | OG0010758 | no hit   |                     |  |
| Scaffold 127:6654784..6656225 | HD001757 | OG0010662 | no hit   |                     |  |
| Scaffold 127:6674792..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 127:6687225..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 127:6694467..6698473 | HD001760 | OG0000577 | gi 665815849 ref XP_008556602.1 PREDICTED: acylcarnitine hydrolase-like [Microplitis demolitor]      | Expect = 2.300e-118 |  |
| Scaffold 127:6713912..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 127:6755517..6755963 | HD001762 | orphan    | no hit   |                     | gene.scaffold_57.g29.t1 orphan 480378..482423    |
| Scaffold 127:6788558..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 127:6832835..6833713 | HD001764 | orphan    | IVSP_U29   |                     | gene.scaffold_57.g26.t1 orphan 391820..393241    |
| Scaffold 127:6845548..6848646 | HD001769 | orphan    | IVSP_U34   |                     | gene.scaffold_57.g24.t1 orphan 383305..386526    |
| Scaffold 127:6856068..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 127:6861330..6863003 | HD001771 | OG0001625 | gi 1070588568 ref XP_018406776.1 PREDICTED: uncharacterized protein LOC108771307 [Cyphomyrme         | Expect = 1.500e-186 |  |

#### 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     |
|--------------------------------|----------------------|------------|--------------|---|---------------------|-------------------------|--------------------------|
| Scaffold 127:10649612..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 127:10653145..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 127:10696314..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 127:10713573..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 127:10718988..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 127:10721836..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 127:10723636..1072892:HD002072 | OG0002227 | gi 1000768710 ref XP_015607512.1 probable methyltransferase TARBP1 isoform X1 [Cephus cinctus]       | Expect = 8.500e-229 | gene.scaffold_6122.g8.t:OG0002227 | 84619..90498   |
| Scaffold 127:10729352..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.t:OG0006556 | 90282..90940   |
| Scaffold 127:10730306..1073170:HD002074 | OG0008346 | gi 817057993 ref XP_012269928.1 zinc finger protein 330 homolog [Athalia rosae]                      | Expect = 2.700e-140 | gene.scaffold_6122.g10:OG0008346  | 91228..92932   |
| Scaffold 127:10732736..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:OG0006263  | 93959..96475   |
| Scaffold 127:10740693..1074533:HD002076 | OG0007281 | gi 1389758539 ref XP_024943813.1 synaptotagmin-4 isoform X2 [Cephus cinctus]                         | Expect = 4.500e-179 | gene.scaffold_6122.g12:OG0007281  | 101239..105178 |
| Scaffold 127:10749875..1075318:HD002077 | OG0007282 | gi 970904570 ref XP_015118179.1 PREDICTED: dolichol kinase isoform X1 [Diachasma alloem]             | Expect = 2.900e-175 | gene.scaffold_6122.g14:OG0007282  | 110423..112817 |
| Scaffold 127:10755559..1075930:HD002078 | OG0005355 | gi 936697175 ref XP_014226574.1 glucose-6-phosphate isomerase [Trichogramma pretiosum]               | Expect = 5.700e-287 | gene.scaffold_6122.g15:OG0005355  | 116428..120182 |
| Scaffold 127:10761570..1076280:HD002079 | orphan    | IVSP_U15   |                     |                                   |                |
| Scaffold 127:10785523..1078700:HD002089 | orphan    | IVSP_N-2   |                     |                                   |                |
| Scaffold 127:10788460..1079089:HD002090 | OG0005583 | gi 1000723328 ref XP_015610175.1 probable cysteine--tRNA ligase, mitochondrial [Cephus cinctus]      | Expect = 7.000e-170 | gene.scaffold_6122.g28:OG0005583  | 158304..160353 |
| Scaffold 127:10790972..1079279:HD002091 | OG0008727 | gi 1000723356 ref XP_015610186.1 ribosome production factor 2 homolog [Cephus cinctus]               | Expect = 5.600e-130 | gene.scaffold_6122.g29:OG0008727  | 160438..162016 |
| Scaffold 127:10794756..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:OG0000882  | 163578..176041 |
| Scaffold 127:10808631..1080918:HD002093 | OG0004828 | gi 795054949 ref XP_011871354.1 PREDICTED: succinate dehydrogenase assembly factor 4, mitochondri    | Expect = 4.300e-21  | gene.scaffold_6122.g31:OG0004828  | 178896..179652 |
| Scaffold 127:10809957..1081106:HD002094 | OG0006539 | gi 925679306 gb KOX76242.1  GPI mannosyltransferase 2 [Melipona quadrifasciata]                      | Expect = 2.200e-60  |                                   |                |
| Scaffold 127:10816751..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:OG0003603  | 208607..221477 |
| Scaffold 127:10837195..1085690:HD002096 | OG0009828 | gi 1070171260 ref XP_018346064.1 PREDICTED: angiopoietin-4 isoform X2 [Trachymyrmex septentrion      | Expect = 3.600e-220 | gene.scaffold_6122.g33:OG0009828  | 227997..231684 |
| Scaffold 127:10859683..1086000:HD002097 | orphan    | no hit   |                     |                                   |                |
| Scaffold 127:10860001..1086053:HD002098 | orphan    | IVSP_U35   |                     | gene.scaffold_6122.g34:orphan     | 234803..235273 |
| Scaffold 127:10861166..1086163:HD002099 | orphan    | IVSP_U36   |                     |                                   |                |
| Scaffold 127:10862390..1086479:HD002100 | OG0006143 | gi 107268279 ref XP_015596389.1 PREDICTED: serine/threonine-protein kinase rio2 [Cephus cinctus]     |                     | gene.scaffold_6122.g37:OG0006143  | 241011..243008 |
| Scaffold 127:10866093..1087121:HD002101 | OG0007135 | gi 749759480 ref XP_011141208.1 sorbitol dehydrogenase [Harpegnathos saltator]                       | Expect = 5.900e-157 | gene.scaffold_6122.g38:OG0007135  | 243912..249324 |
| Scaffold 127:10872479..1087731:HD002102 | OG0007814 | gi 1569271860 gb QBB02001.1  putative UPF0528 protein CG10038 [Cotesia chilonis]                     | Expect = 1.200e-113 | gene.scaffold_6122.g39:OG0007814  | 250807..256468 |
| Scaffold 127:10921663..1092207:HD002103 | orphan    | no hit   |                     |                                   |                |
| Scaffold 127:10970846..1103466:HD002104 | OG0002894 | gi 1494653095 gb RLU26944.1  hypothetical protein DMN91_000743 [Ooceraea biroij]                     | Expect = 1.500e-225 | gene.scaffold_6122.g40:OG0002894  | 361174..391485 |
| Scaffold 127:10983515..1098646:HD002105 | orphan    | no hit   |                     | NA                                |                |
| Scaffold 127:11051421..1105729:HD002106 | OG0000642 | gi 972199364 ref XP_015181683.1 PREDICTED: serine/threonine-protein kinase tricorner isoform X1 [F   | Expect = 4.700e-266 | gene.scaffold_6095.g2.t:OG0000642 | 36848..43783   |
| Scaffold 127:11089871..1109165:HD002107 | orphan    | no hit   |                     | gene.scaffold_6095.g3.t:orphan    | 79134..81658   |
| Scaffold 127:11110231..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.t:OG0000107 | 105829..109141 |
| Scaffold 127:11118585..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.t:OG0001394 | 113898..116393 |
| Scaffold 127:11120053..1112313:HD002110 | OG0000139 | gi 156547818 ref XP_001606363.1 PREDICTED: sodium/potassium-transporting ATPase subunit alpha-       | Expect = 0.000e+0   | gene.scaffold_6095.g7.t:OG0000139 | 115279..118353 |
| Scaffold 127:11123403..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.t:OG0001394 | 117396..119865 |