

Supplementary materials for the paper:

Duplication and concerted evolution in a master sex determiner under balancing selection

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Coding nucleotide sequences and protein sequences

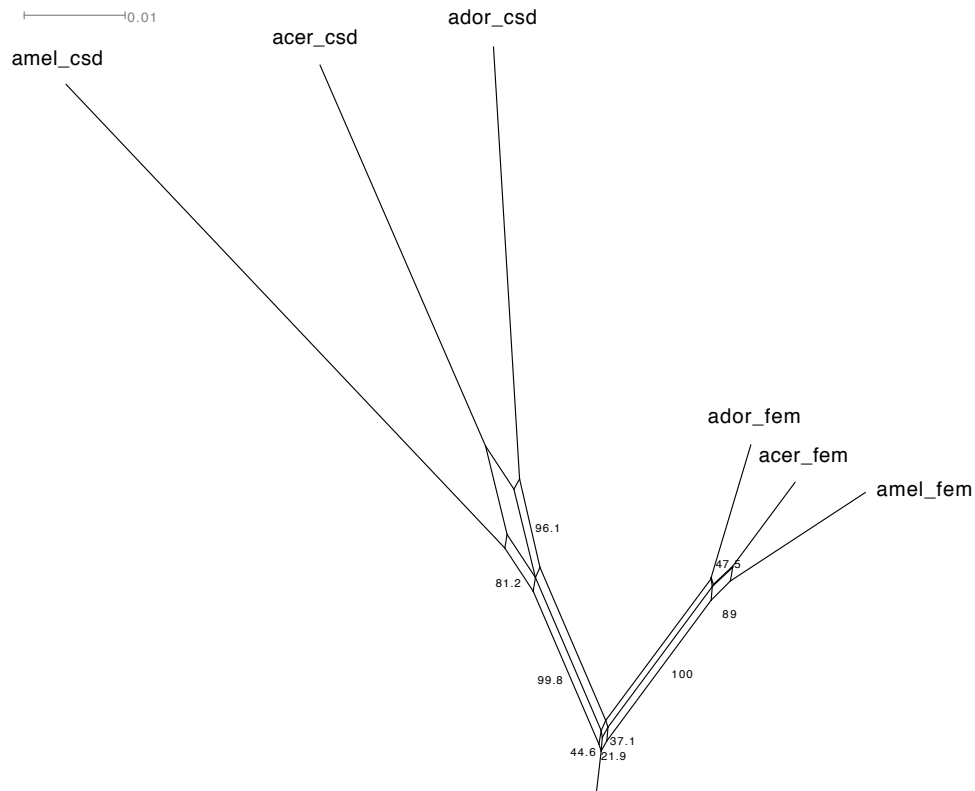


Figure S1. Phylogenetic splits networks constructed using SplitsTree for the honey bees. Parallelogram branches correspond to splits that represent putative recombination events. Bootstrap support for splits are indicated.

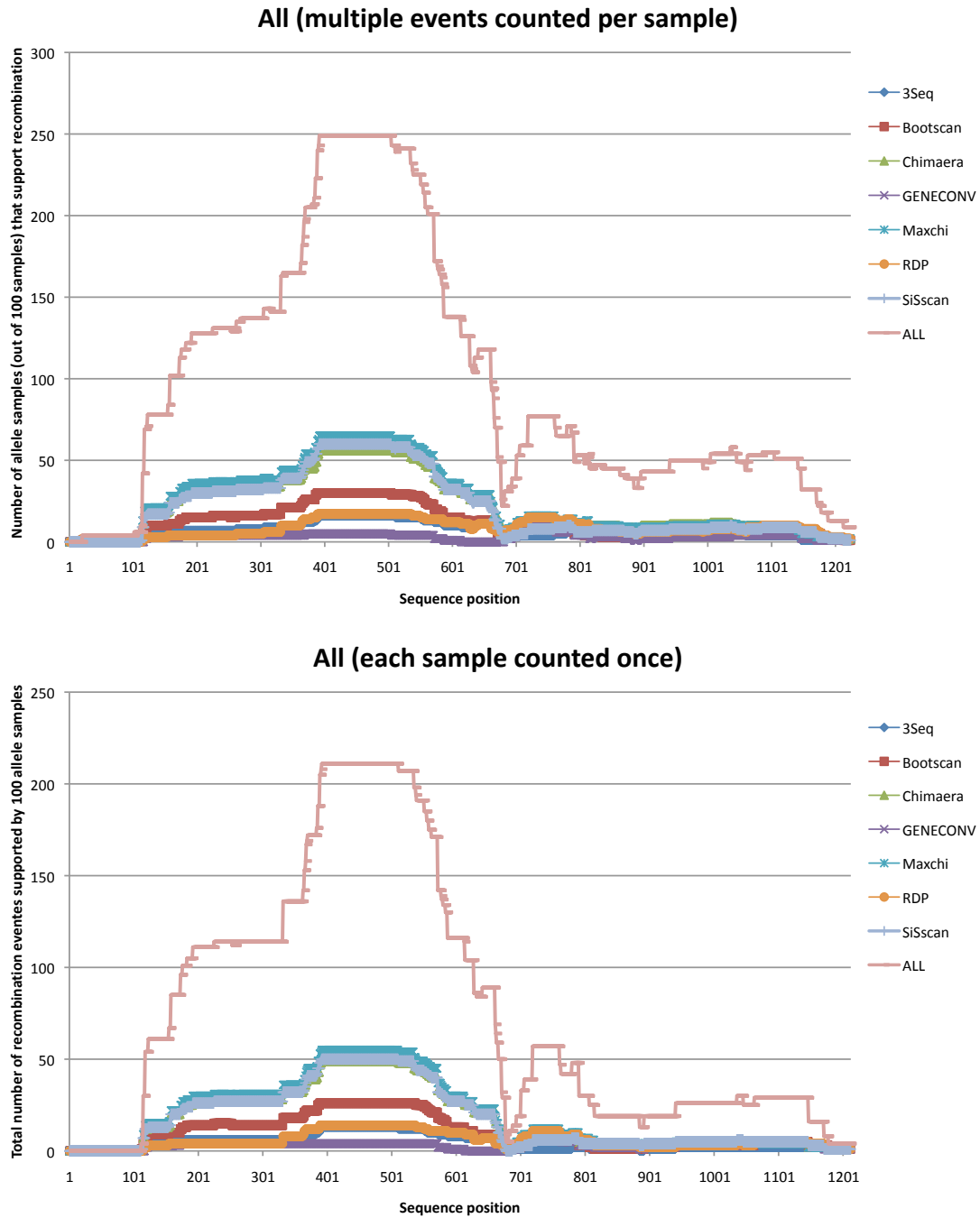


Figure S2. The number of instances of recombination event inference **(A)** or the number of allele samples **(B)** in which each sequence position of the *csd* coding sequence is within an inferred recombinant region. Summarized over 100 allele samples and all recombination test statistics.

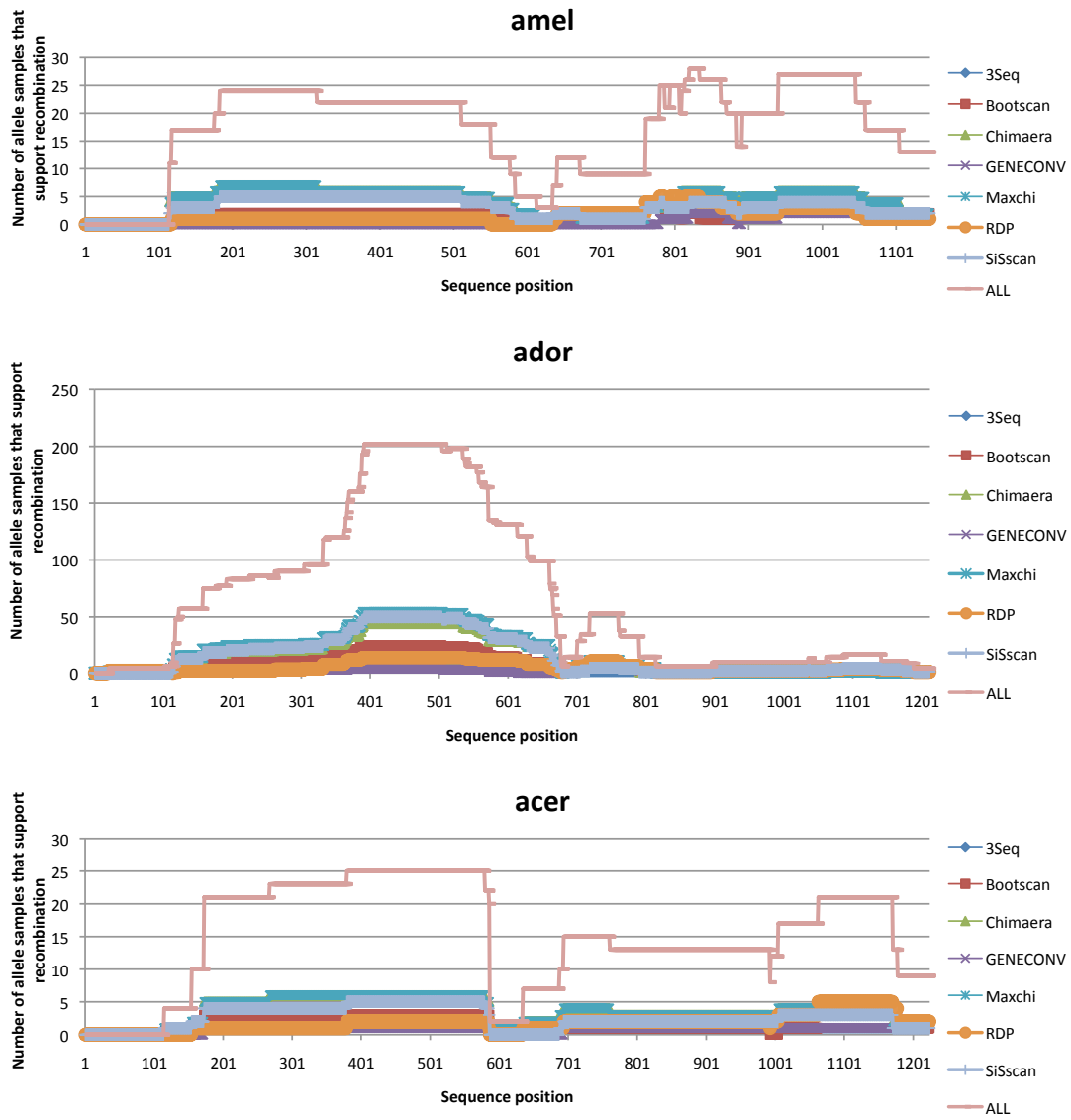


Figure S3. The number of allele samples in which each sequence position of the *csd* coding sequence is within an inferred recombinant region for each of *A. mellifera* (A), *A. dorsata* (B), and *A. cerana* (C). Summarized over 100 allele samples and all recombination test statistics.

Table S1. Conservation of synteny for pairs of neighboring loci across four ant genomes

Reference species	Conserved neighboring pairs	Total number of neighboring pairs	Proportion of conserved
<i>Camponotus floridanus</i>	150	13,106	1.13%
<i>Pogonomyrmex barbatus</i>	150	15,231	0.98%
<i>Solenopsis invicta</i>	150	11,838	1.25%
<i>Atta cephalotes</i>	150	15,981	0.93%

Table S2. Phylogenetic evidence for inter-locus recombination events in *Apis* allele samples from the “Approximately Unbiased” test (Shimodaira 2002) that attempts to reject the gene tree topology of the putative recombinant region in the non-recombinant region (“outSeq p-val) and vice versa (“inSeq p-val). P values were adjusted using the Benjamini-Hochberg (1995) FDR correction. P < 0.05 is in bold.

Sample No.	Out seq p-val	In seq p-val
32	1.89E-49	1
91	1.86E-06	1
93	5.49E-06	0.12
49	0.00018	1
16	0.000413	0.061
37	0.00058	1
33	0.00171	0.00124
14	0.00224	1
20	0.00495	1
27	0.00495	1
16	0.0053	0.12
2	0.0053	1
87	0.0102	1
54	0.02	1
47	0.0245	1
34	0.048	0.784
6	0.048	1
70	0.092	0.174
75	0.18	1
11	0.22	1
98	0.258	1
31	0.378	1
22	0.697	1
19	0.88	1

63	0.88	1
19	0.912	1
12	0.962	1
8	0.972	1
10	1	1
10	1	1
12	1	1
18	1	1
24	1	1
26	1	1
3	1	1
30	1	0.684
32	1	1
39	1	1
41	1	1
42	1	1
46	1	1
48	1	1.26E-34
50	1	1
51	1	1
52	1	1
56	1	1
69	1	1
69	1	1
7	1	1
71	1	1
74	1	1
78	1	1
79	1	1
81	1	1
82	1	1
83	1	1
84	1	1
86	1	1
89	1	1
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90	1	1
93	1	1
95	1	1

Sequence accession numbers for the *csd* alleles included in each allele sample:

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2 amel_csd41_AY352276.1_cdsid_AAQ67417.1
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6 acer_csd0_EU100916.1_cdsid_ABV58884.1
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8 ador_csd8_EU100919.1_cdsid_ABW36151.1
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Coding sequences for *tra* homologs annotated in the seven ant genomes

>aech_tra [organism=Acromyrmex echinatior] Transformer homolog
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GAACGACGCACAGTTGTAGCCATAGATAAAGAACAATCGGCCTTGACAAT
CAAGTCACGTTCTTTGAGGAAACGTTCTTTATCCTTGAGTCCTATTAGGA
ATCGTGTCTATTCTGGATATCCATCTTCTATCAATCCAGTCATCGCGTG
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TGGGAGAAGCGATTTAGAGAAACGCAGAGAATATAAAGAGAAATATACCG
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GGGAGAGAAACAGAGAAAGAGATAGGAATAGAGAGAGAACTAAAACCTAGA
GATAGGTCCAGGGAACGAAGAGATATAACGCCACGTTATATCGAATCGCC
AATACCTGTACCTATCTATTATGGTAGTTTTCTCCGAGACCTATCGTAG
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CATTTTGA

>acep_traA [organism=Atta cephalotes] Transformer homolog A
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TCCAGATATGTACAGATTGGGACATCCACCTCCAAATCCAAGTAAGTAA

>acep_traB [organism=Atta cephalotes] Transformer homolog B
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>Sinv_traA [organism=Solenopsis invicta] Transformer homolog A
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TCACCAATACCTGTGCCTATCTATTATGGCAGTTTTCTCCAAAGACCAAT
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>sinv_traB [organism=Solenopsis invicta] Transformer homolog B

ATGCGTACCATTGGGGCAATATTTGAAAATATTAAGAAAACGCAGATTAA
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CAACTAAGTCAACTACAGATGAAGAGGAGTTAGCCTTAAGCAATTCGGAA
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CTAAGGATAGGAATAGAGATTGGGATAAGGATGAAATTAGAGATAGGGAT
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TCCTTTAGGTCCGTTAAGAAGACCTATTCCCTCCTTTAGGTCCGTTAAGAG
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>pbar_traA [organism=Pogonomyrmex barbatus] Transformer homolog A

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>pbar_traB [organism=Pogonomyrmex barbatus] Transformer homolog B
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AATGCATAATGAAGATGATACTTATTCAATTTTTGAAAACCTGAAGAAGAGA
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>cflo_traA [organism=Camponotus floridanus] Transformer homolog A
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TCTTCGACAAGTGCTTCCAAATCTGGTACGCTGTTTAAAAAATTAGAGGG
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CGTACGGTTGTAGCTATAGATGGAGAGCAGCAGTCAGTTTCAACCAGTAA
ATCGCAGATTTCCAAGAAACGTTCTTTATCATTGAGTCCTACATTGTATG
ATTCTGAATATCTATCTTCTCACCAGTCTAGATACCGTACAGATACAAAA
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CTCCTATGGCAAGAGGCCGACATTCTGCTCTAATGGCACCGGTTAGACCA
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>cflo_traB [organism=Camponotus floridanus] Transformer homolog B

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TGCTCGTAATGAAGATTATGATTCTCATTCAAATCTACGTTCAAGAACCG
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TGGCAATGGAAACAAAACGGGAAAGGCAATATGAAAAATTGAAACAGCA
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TCACAAGACCAACATAAAGGAAGATCTATGACACGTGTTGCTCAATCTGA
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GCAACGAAATATAATTAATGCTGAAGATGTGATCCTCAAAGAAGAGAAG
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TGGCAAGAGGCCGACATTCTGCTCTAATGGCACCAGTTAGACCATTCCCT
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>lhum_traA [organism=Linepithema humile] Transformer homolog A

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CAGAAGAAGAAAAGCAGAGACGCAGACAAGAGTGGCTGCGACAGCAAGAA
CGTGAGAGACAACATGAAAAATTAAGCAGCAAAAAATTTTAGAGTATGA
GAGAAAACGTGCGCAATCTTTAAAACATGCGCAAACCTTTAAAGCATTCTG
AGCAAAAACCTTACGTCTATAGTCAAGTGAAGTGAAGTGAAGTGAAGTCTCC
TCCCTTACCAGGATAGAGGAAGATCTACATCAAATGTTTCAAATCTGG
CACTTTGTATGAAAAATTAGATGGGTCTTCAAGTGGGGCAGTACCCTTGT
TCAAAGGTGCTCAGGGCATAACAGATTAGTACTACAGAGCTACGTGCAATT
AAGGTTGATATTTCGAGAAATATTCTGCGAAAGGATCCATTTCTGAACT
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GTAAAATGCATTGGGAAGGATGTAAACCGATATTTCGACAGAGAAGAAAT
AAAACGGCGATAGTTAAACCTAACGAAGTGGAGGAGCGACGTACGGTTGT
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>lhum_traB [organism=Linepithema humile] Transformer homolog B

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AATTTTAGAGTATGAGAGAAAACGTGCGCAATCTTTAAAACATGCGCAAG
CTTTAAAGCTTGTGAGCAAAAATCTTCATATTATAGTCAAGTGAAGT
GACAGTAAGTCTCCCTCACTTACCAGCATAGAGGAAGATCTGCATCAAA
TGAGTCTAAATCAGGCACCTTTGTATGAAAAATTAGATGAGTCTTCAAGTG
TGGCGGTACCCTTGTGCAAAGGTCTTCAGGGCATAACAGATTAGTACTACA
GAGCTACGTCAAATTAAGGTTGATATAATTCGCAAAAATATTTCTGCGAA
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TCATCAAAGAAGAATGGGGGAAGGATGTAAACCGATATTTCGACAGAAAA
GAAATTAACAGCGATGGTCAAATCAATGAAGTGAAGGAGCAACATTC

GCTTGCAGTCGTAGATGGGGACCAACCAGGTTCCCTCGAGCAAATTACGAA
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>hsal_traA [organism=Harpegnathos saltator] Transformer homolog A
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AAAAGTCAAGGCGTAGACGAGAATGGAGGCATCAACAAGAATTGGAAAGA
CAACATGAAAAATTTAAAACGACAAATGATAATTAECTATGAGAAAAACG
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TCGGAAGCTCCCAAATCTAACACTATATTCAAAACAGATCGGTCCGCAAG
TGGGGCAGTACCTTTTATTCAAGGGTCTTGAGGGCACACAGATTAGTACTG
CAGAATTACGTCGTATTTAAAGTTGACATTCGTAGGAATATTCCTGCAAAA
GGACAAGTTACCGAACTACAACGGGATATACTTAATCCCAGGATGTGAT
CCTCAAGAGAAGAGAGGGTAAAACGTTATATTCTCCTTGGCATTCTTTTG
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GTACTCGTTCAAGTTCTAGAGAACGGGATACAAAACAATCCCATTCTAGC
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GAGGCCGATCCAGAGATAGGAGAGATCCAGCACACATTATGTTGAACAC
GTACCAGTGCCTATTTATTATGGTAATTTCCCTCCGAGACCATACATGGT
AAGTCCCATGGTCACAATTCCTAGGGGACAGGTTCCCTCCTTAGGAAGAG
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>hsal_traB [organism=Harpegnathos saltator] Transformer homolog B
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AGAGGACAGGTTCCCTTCTTTAGGAAGAAGTCGGCATCTTCCTTTAATGAG
ACCATTCTCACC GCGATTTGTTCCACCTGATATATATAGAATGGGACCTC
CAGCTCCAAATAGTGAAGTGGAGCAATGTCTTTATTCAAGAGTCTCTGAG
GGCACATAG

Protein sequences for *tra* homologs annotated in the seven ant genomes

>aech_tra [organism=Acromyrmex echinatio] Transformer homolog
MNPMSSTTFRSGEESRSTRNEDHNTLAILRSRTEEEKQRRRREWQRQERERQHEKLGKQK
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SGTVPLFRGPQNAQIDTSELRRKVDIHRNIPKGPVTELERDILNPEDVIVKRREGEGC
KPIFDREEFKKVINKTNEIEERTVVAIDKEQSALTIKSRSLRKRSLSLSPIRNRVYSGY
PSSYQSSHRVLDLKHQDKTEKCDTRKDDGRSDLEKRREYKEKYTERDGANKHDNNSRSRE
RNSHSRPFIEERSYRDRYRERSNERSYERRDRDRERNRERDRNRERTKTRDRSRERRDIT
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YRLGHPPPNNPRYGPF*

>acep_traA [organism=Atta cephalotes] Transformer homolog A
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ILEYERKRAQALKYAEEKSSRHSQSKSDSESPHVRVYRGRSTSTASKSGSLHEKLDDEST
SGTVPLFRGPQNAQIDTSELRRKVDIHRNIPAKGPVTELERAILNPEDVIVKRREGEGC
KPIFDREELKKVINKTNEIEERTVVAIDKEQSASTIKSRSLRKRSLSLSPIRNRVYSGY
PSSYQSSRRVLDLKHQDKTEKCDTRKDDGRSDLEKRREYKEKYTERDGANKHDNNSRSRE
RNSYSRPFIEERSYRDRYRERSNERSYERRDRDRERNRERDRNRDRTKTRDRSRERRDIA
PHYIESPIPVPIYYGSFPPRPIVVSMPVPLRGQIPPMGRGRHPTLMAQVRPFPFPPFPPDM
YRLGHPPPNNPSK*

>acep_traB [organism=Atta cephalotes] Transformer homolog B
MNPMLTTFRSEESRSTRNEDHNIFTVLLSRTEEEKQRRRREWQRQERERQHEKLGKQK
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GRSTSTASKSDNLHEKLDDESTSGTVPLFRGPQNAQIDTSELRRKVDIHRNIPAKGPVTE
LERAILNPEDVIVKRREGEGCKPIFDREELKKVINKTNEIEEQRTAVFINKEQSASTIKS
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GANKHDNNSRSRERNNSHSRPFIEERSYRDRYREKSNECSYERRDRERERNRERGRNRDR
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>sinv_traA [organism=Solenopsis invicta] Transformer homolog A
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SGSVPLFRGPENAIQINTMELRRKVDIHRNIPVKGVPVSELERDILNPEDVIVKRREGEGC
KPIFDREEIKRAVAKTNEVEERTVVAIDKEQSASVMKAYTSRKRSSSLSPSRNRIYNSG
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PRNSHSRPFIEERSYRDRYRERSNEYSYERRSDRDRDRDRDRDRDRDRDRDRDRDRDRDR
RDRDRDRDRNRDRDRDRDRERNRDRDRSRERRDIAPHYIESPIPVPIYYGSFPPRPIVVS
PMVPLRGQIPSMGRGRHPTLMAPIRPFPPFVPPDMYRLGHPPPNNPRYGPF*

>sinv_traB [organism=Solenopsis invicta] Transformer homolog B
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EYHSRHRMDIKYQDSKTKNYAFKNDERTHTEDYSKYKEKYIEKDTTKHDTIRLSREQHD
SHSRLFTDEKFYHRYRERSYKRSHERRESDRDRDRFRSRSRERKDEYFHESKAKDRNRD
WDKDEIRDRDKNREKEKDRDEGRNRSRERRDAPHI EPIIPAPTHHNNFPPRPIVNSML
VLREQIPPLGLRRPIPLGLRRPIPLGLRGIHIPPVPLRGIHIPPMPGRGRYLTPVWP
RFVQLDMCRPRHPSN*

>pbar_traA [organism=Pogonomyrmex barbatus] Transformer homolog A
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TGYLSSYQSRHMDLKSQNNKTDNHGIHRNDRSSIEKRKYKEKYTERDVSKHITNRSRS
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>pbar_traB [organism=Pogonomyrmex barbatus] Transformer homolog B
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VPLFKDLQNTQINTELRRIKIDIHRNIPKVKGPVPELQDILNPDDIIIKRREGGCKPI
FDREEIKKVAIKTNEVEERRTVVAVDKQESASSRRLYTRKRSLSLSPIRNHEQTYSSGYL
SSYQSRHIDLKQDNKTDNRDIHRHDKRSSIEKHRDYKEYTEQDVSKHIANRSRSDRN
SYSRPFLEERSYRERYREESKERSLERRTRERDRNRDRDRDKDGDRAKDRERDRSR
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>cflo_traA [organism=Camponotus floridanus] Transformer homolog A
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GTIPLFKGPEGIQTISTTELRRIKVDIRRNIPVKGPIPDLQRSIVNAEDVILKRREGGCK
PIFDREEIKKATKINEIEERRTVVAIDGEOQSVSTSKSQISKRSLSLSPPLYDSEYLSS
HQSRYRTDTKHQDNRIEFRDHHKNNGRNSIEKHREYKEYTERDAHKYTNRSRSDRDRSR
KSAHTRPLIEERSYRDRYDRSSEHSRERRDRDKDRDRDRDRSRERRDVASHYIEPPIHV
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RYGPFF*

>cflo_traB [organism=Camponotus floridanus] Transformer homolog B
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LSFDQFSPKSHTRSLMEEKSYCDRYRDRSSEHSRKRKDRNRSDRSRKRDRDRDRDKS
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YRYINVI*

>lhum_traA [organism=Linepithema humile] Transformer homolog A
MDSTRATNFRRDEEPRSVRNEDHNSHSISRTTRTEEEKQRRRQEWLRQERERQHEKQKQ
QKILEYERKRAQSLKHAQTLKHSEQKPSRHSRSRSDSKSPSLHRHRGRSTSNVSKSGTLY
EKLDGSSSGAVPLFKGAQGIQISTTELRRIKVDIRRNIPAKGSISELERDILNPEDVVVK
RREGKMHWEKCKPIFDREEIKTAIVKPNEVEERRTVVAVDRDQPGIPTRNRGYSPPGYLSS
YQSKFV*

>lhum_traB [organism=Linepithema humile] Transformer homolog B
MDSTQAINFRRDEEPIASAYNEDFNHDLISLKTEEEKLRRRQEWLRRRQEWLRQERERQH
EKQKQKILEYERKRAQSLKHAQALKLAEQKSSYRSRSDSKSPSLHQHRGRSASNESK
SGTLYEKLDESSSVAVPLCKGLQGIQISTTELROIKVDIIRKNISAKESISELDRDIVNP
EDVVIKRRMGEGCKPIFDRKEIKTAMVKINEVKEQHSLAVVDGDQPGSSSKLRTSRKRFS
SLNTIRNRDYSPPGYRIDSKR*

>hsal_traA [organism=Harpegnathos saltator] Transformer homolog A
MNLTQSTNLRRDEESRSTRNEDDRLLMRLRSKEEKSRRRREWHRQOELERQHEKQKQMI
INYEKKRAEAMKFKQPSSHRSKSSSKSPSYHRHRERSPSEAPKSNTIFKTRDSAGAV
PLFKGPEGTQISTAEALRRIKVDIRRNIPAKGQVTELODILNPEDVILKRREGKTLTSPW
HSFVKDVSNDNGTPLSSREGSKPIFERDEIKVIGVEVEERRTVVAIDSEQSDSTRSSSR
ERDTNNSHSSRYRDRSDERSRERRDRDRDRDRDRDRDRDRDRDRDRDRDRDRDRDRDRDR
VPVPIYYGNFPPRYMVSMPVTIPRGQVPLGRGRHPPLMGVVRPFPFPRFVPPDIYRMGP
PAPNPRYGPMPFG*

>hsal_traB [organism=Harpegnathos saltator] Transformer homolog B
MWLKWEEAWEEEDKLRRRLEWIRQEFQIHIKQKQMIINYEKKRAEAMKQKPTSSHHSR

SKSRKSPSYRRHKEKSQDFAFKSDTIFKKLDGSASEAVPLFKGPEGTQINTTELRIKV
DIYRNIPTKRQVTDLQDILNPEDVILKRREGEKSKPIFERDEIKVIGEVEERTVVATD
GEQSDLPPGPIMVNPMTIPRGQVPSLGRSRHLPLMRPFSPRFVPPDIYRMGPPAPNSAS
GAMSLFKSPEGT*