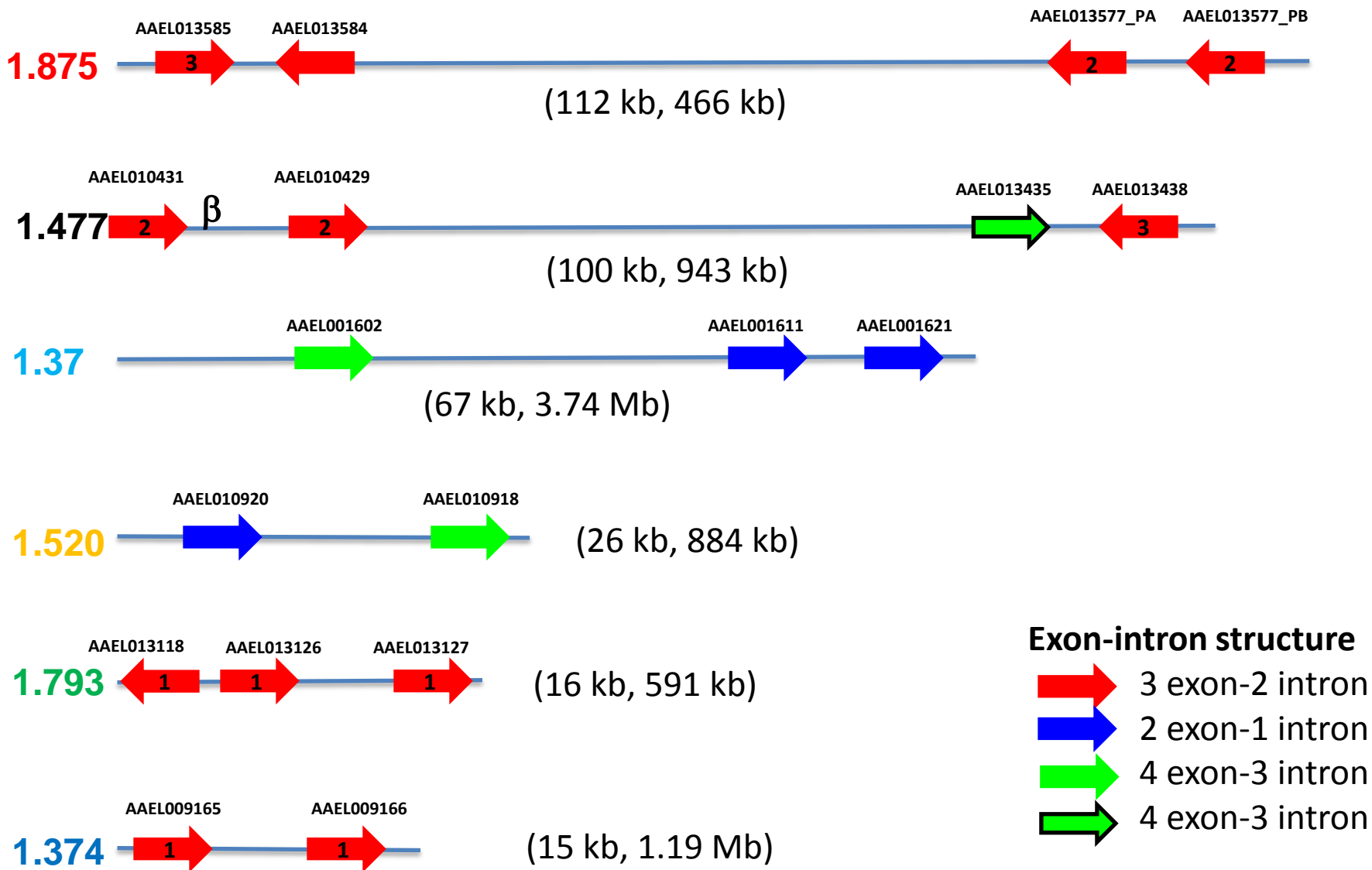
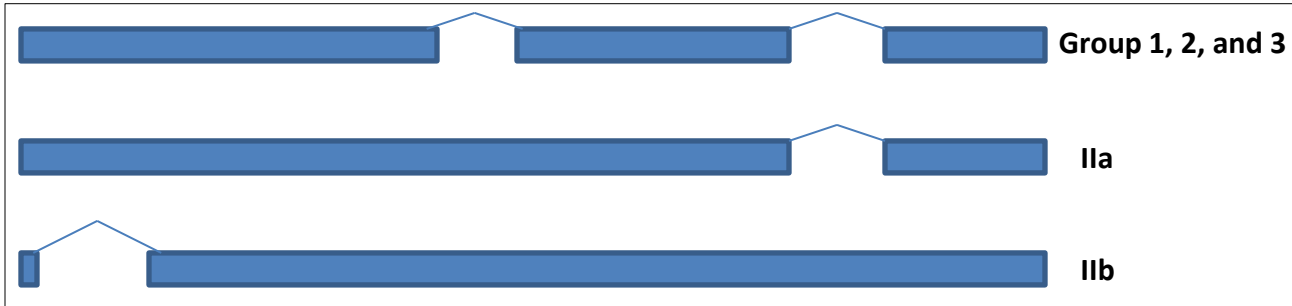


Supplemental Figure 1 Linkage of SDMA genes in *A. aegypti*
(SDMA cluster size, supercontig size)



Supplemental Figure 2 Conserved exon-intron junctions of multi exon SDMA genes

a conserved exon-intron structures in Dipterans



b 1st and 2nd exons in Dipterans

Group 1	122L-123K
AAEL009165	VKPTKGVKSLKAGGLSGFVD
AAEL009166	VKPVQGVKSLKAGGLSGFVD
AAEL013127	VKPTKGVKSLKAGGLSGFVD
AAEL013118	VKPVQDVKSLKTGGLSGFVD
AAEL013126-PA	VKPTKGVKSS--GGLSGFVD
120I-121K	
CPIJ012844-PA	VKPVRAVRSIKTGGLSGFLD
CPIJ012845-PA	VKPVRAVRSIKTGGLSGFLD
Group 2	117L-118R
AAEL010429	HHVKPTVHSLRTGGLTGFFD
AAEL010431	HHVKPTVHTLRTGGLTGFFD
AAEL013577-PB	HHVKPTVHTLRTGGLTGFFD
AAEL013577-PA	HHVKPTVHSLRTGGLTGFFD
Group 3	111F-112I
AAEL013585	FTGTNRVKRFIPKRQGGLSA
AAEL010438	FTGTNRVKRFIPKRQGGLSA

c 2nd and 3rd exons in Dipterans

Group 1	177Q-178N
AAEL009165	DFQKLVDFYQNSKEAQALVQ
AAEL009166	DFQKLVDFYQNSKEAQALVQ
AAEL013127	DFQKLVDFYQNSKEAQALVQ
AAEL013118	DFQKLVDFYQNS-EAQALVQ
AAEL013126-PA	DFQKLVDFYQNSKEAQALVQ
174/5N-175/6N	
CPIJ012844-PA	DFQKLVDFYNNNSKEVQSLFA
CPIJ012845-PA	DFQKLVDFYNNNSKEVQSLFA
CPIJ012846-PA	DFQELVELYKNSKEVQSLFN
AGAP006187-PA	DHKQLRALYESSTEVQNMIIH
Group 2	172N-173N
AAEL010429	DYQKFVDFHNNNSKEVQGYLQ
AAEL010431	DYQKFVDFHNNNSKEVQGFLQ
AAEL013577-PB	DYQKFVDFHNNNSKEVQGFLQ
AAEL013577-PA	DYQKFVDFHNNNSKEVQGFLQ
AAEL010436 (β)	DYQKFVDFHNNNSKEVQGFLQ
Group 3	169T-170E
AAEL013585	EFGQMMKEITEDPEVIEIQE
AAEL010438	EFGQMMKEITEDPEVIEIQE

d type IIa and IIb in Insecta

IIa	180D-181N
AAEL001621	DFQKLEFADNSTELKSLFQ
AAEL001611	DFQKLELADNSTELKSLFQ
AAEL010920	DFQKLEFADNSTELKSLFQ
IIb	
AAEL001418	MQKIFIVLAIF
AAEL005340	MKLLSLLVILG
CPIJ011431	MKLFLLLVILG
GB14426	MLKFTLAILGA
GB12716	MMKFLLAIV
TC002436	MLLFALILFAF

e Lepidopterans

	1 st -2 nd	2 nd -3 rd
HMEL005433-PB	EMEDLPEFKA-VVSFLEGHSI.....	FIDALNDIVGSIQRRGIRHS
EHJ70882	EMEDLPEFKA-EVVQFLEGHNI.....	FVNVINDLVDGIQRRSTRSV
BGIBMGA005025	EMEDLPEFKA-VVDFLENDNI.....	FIDIFNEMMETIGERVKRAR
BGIBMGA005024	EMEDLPEFKA-VVDFLENDNI.....	FIDIFNEMMETIGERVKRAR

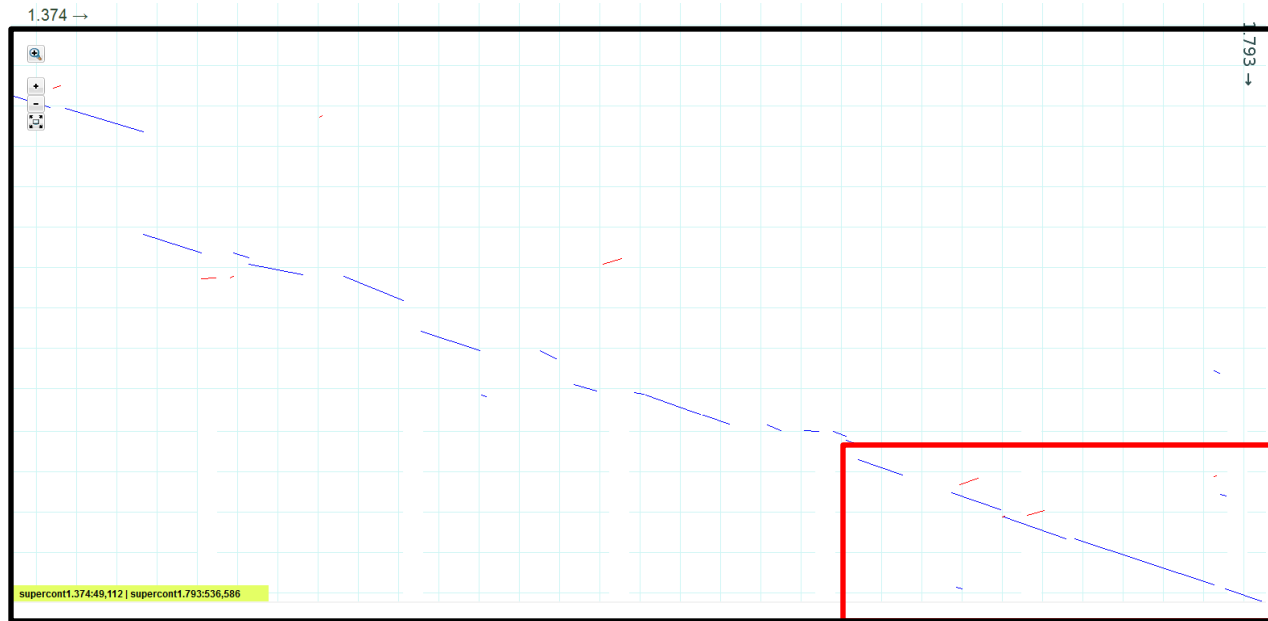
Supplemental Figure 4

AAEL001611-AAEL001621 alignment

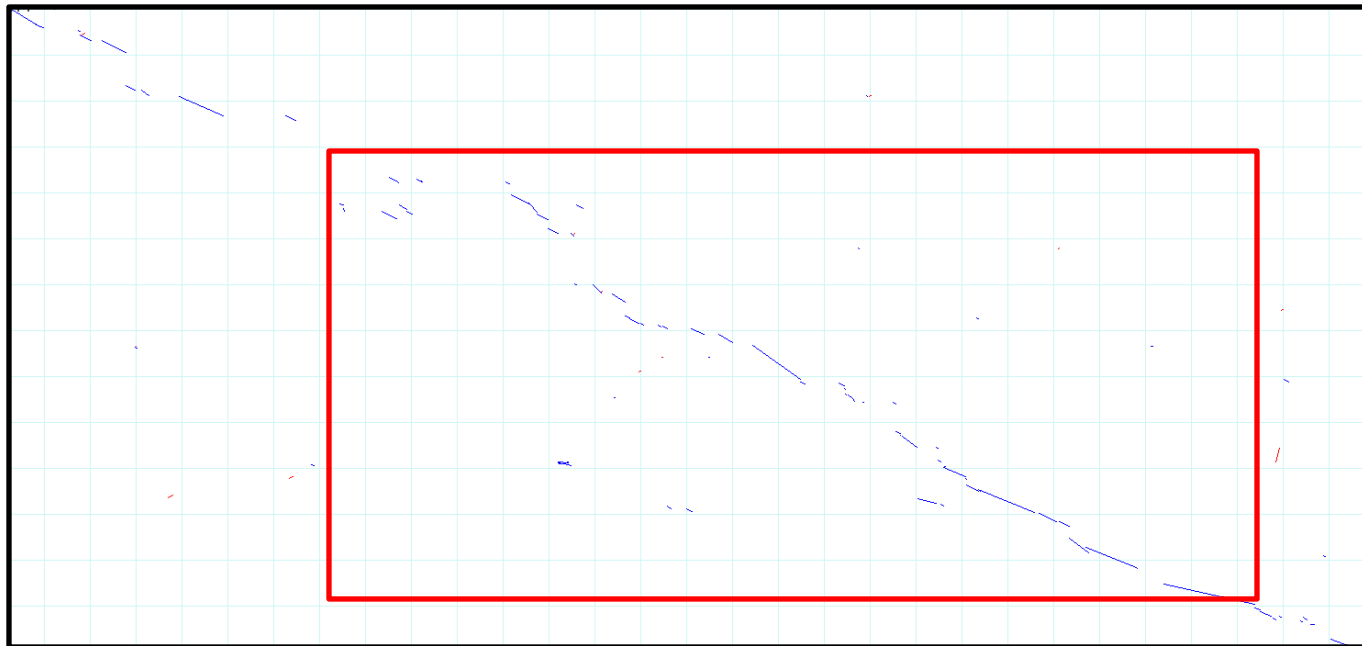
	1	85
AAEL001611	(1) TGCAGAGA-CCTTGAAATTGCAAAAACCGTTGCTAAGGGCAACCCAAAATCTACTGTAGAAAATGTCCTATTCCCGTCC	
AAEL001621	(1) AACATTTTGTATGGAAATTGAAAAA-----TGCACAAAAGTGTCCAAAATCTGT-----ATAATTGTAATTGTCCAGTCC	
AAEL001611	(85) ATTCCCCGCATTTCAAGCTTCATGCACTCACGTTGAGNAATATGCGCCCAACATAGGCTACTGTATGATGCGCTT	170
AAEL001621	(72) A-----AAAATTTGAAATA-----AAGACCTTAAACATGGAATATGATGAAATTT--GTCAATATATGAT	171
AAEL001611	(170) TTTGAACTACGTACTGGGAAGCCACGTTAATTCGGGAATTCAGCCTACTACTTTCCATCCAGCAATGATGAAACA	255
AAEL001621	(136) TTCAGCTATTTA--AAGGAGTTTGAGTTTGGCCGCAATTTGTTTGTAGATCGAACCTGTCGAGTTGCCACAGTGAAT	256
AAEL001611	(255) ICACATTTGTTTGGAAATGAGTTTTTTTTATAGGTG-ATCCCTTCCCAACATGTTGGGGCAE--GGTATTTCGCGC--	340
AAEL001621	(218) E--ATTGTTTGAACAAAGTTTCCACCACTGGAGCGGGATTCGAACCCCAATATGTCACAATCTCTATAAGGACTGAGCGT	341
AAEL001611	(336) ---AATTTTCAGTCCGTGATGCTCAAAATAGATACCAATCAGAAATCAAAATTAATGACGTGATAGTCCCTCAATTTGCAAT	425
AAEL001621	(300) CTAATAAGCGCAAAAATACTCAA--ATCAATATGAAATAAAT--AAATGCGATC--NACCCCAATATGTCGATGAT	426
AAEL001611	(418) CAC---AGGAAAAATTGAAATACATAATAACGTTAGTGTACATACAATGAAGTGAATAATGATTTTCTGTAATCCACT	510
AAEL001621	(379) TTAGTTGGAGCAATCTCCATGCTGTGGTTGATTAATCAATATACCT-----CAAGCTCAATTTTTCGCA-GGTAA	511
AAEL001611	(500) TCCCCACGTCCT---TATATCACTATGAGGTACTGTAAAACGGGGCATCTTTGATAATATGGGGTAATTTGAAAAAGGAACA	595
AAEL001621	(456) CATTATGSGCCCAACGATATATCACTATGAGGTACTGTAAAACGGGGTATCTTTGATAATATGGGGTAATTTGAAAAAGGAACA	596
AAEL001611	(582) TAATTCGTGTAATCAGTTAAGCAAAACGAAATGCAAAATATAAAACTATAAGTATGACCCCTTTATGTAAGAGCTATTTTCGAAGA	680
AAEL001621	(541) TAATTCGTGTAATCAGTTAAGCAAAACGAAATGCAAAATATAAAACTATAAGTATGACCCCTTTATGTAAGAGCTATTTTCGAAGA	681
AAEL001611	(667) AGAAGAAAGCTGTATTGACCAATCAATAGAAAACACATCATCTTACGGTTACGGTACTTCAGCAATCACTGTAATCAACTAA	765
AAEL001621	(626) AGAAGAAAG---CTGTATTGACCAATCAATAGAAAACACATCATCTTACGGTTACGGTACTTCAGCAATCACTGTAATCAACTAA	766
AAEL001611	(752) AATACAACAACACCACATCACTATCCATTCCGGTTCATATAAAATCCAATGCTCTCTAAGCTTAGATAGAGTATTTGTAATATG	850
AAEL001621	(708) AATACAACAACACCACATCACTATCCATTCCGGTTCATATAAAATCCAATGCTCTCTAAGCTTAGATAGAGTATTTGTAATATG	851
AAEL001611	(837) FACTGTAATACCTACCTCAATAGATGCTACATGGAATCACTACCCCTCCAACAGTATTCGTAACCAATACAGGAATGCACTCCGAC	935
AAEL001621	(793) FACTGTAATACCTACCAATAGATGCTACATGGAATCACTACCCCTCCAACAGTATTCGTAACCAATACAGGAATGCACTCCGAC	936
AAEL001611	(922) CTAGATGAAGAGATAATGATTAGCAGCGTGGCGCTATAAAATGTCGCCCTTCAGGTATTCGCTCATTCATATAATCTCCGTCAA	1020
AAEL001621	(878) CTAGATGAAGAGATAATGATTAGCAGCGTGGCGCTATAAAATGTCGCCCTTCAGGTATTCGCTCATTCATATAATCTCCGTCAA	1021
AAEL001611	(1007) TTGGCCGTCGGTTTCGAATCCAATAATAGCAATCAATATGAAAGTTCCTCGCGGTAATGCAATTTGCTGCTACTGCCGTAAACCT	1105
AAEL001621	(963) TTGGCCGTCGGTTTCGAATCCAATAATAGCAATCAATATGAAAGTTCCTCGCGGTAATGCAATTTGCTGCTACTGCCGTAAACCT	1106
AAEL001611	(1092) GATCTCGATAACATCCGGAGCCGACCAAGCCCCCTTCCCTGCAGGATGATTCAGTGAATTTGTCGAACTGCTCCGTTTGAT	1190
AAEL001621	(1048) GATCTCGAACACATCCGGAGCCGACCAAGCCCCCTTCCCTGCAGGATGATTCAGTGAATTTGTCGAACTGCTCCGTTTGAT	1191
AAEL001611	(1177) GAAATCGTGGATGTACCATACACTACTTCTGACCGGTAAGGACGCTCCAGCAGGCTCGCAATATCTCCTGGGACCCGAGTTTT	1275
AAEL001621	(1133) GAAATCGTGGATGTACCATACACTACTTCTGACCGGTAAGGACGCTCCAGCAGGCTCGCAATATCTCCTGGGACCCGAGTTTT	1276
AAEL001611	(1262) CAGCCATTTGGGATCAAGTGTTTGCCCTGAAGGAAGTGGCGGATGTGTTGGATTATTTGGAGGAGCCAGGAGTTGAAGCATACGC	1360
AAEL001621	(1218) CAGCCATTTGGGATCAAGTGTTTGCCCTGAAGGAAGTGGCGGATGTGTTGGATTATTTGGAGGAGCCAGGAGTTGAAGCATACGC	1361
AAEL001611	(1347) GTTCTTCAACGATATAGCTGCTCTGCTCGGATTGAGCCAAATCAAACCTGCGATGAAAAATGACCATCCGGTCACTACTCCGAGT	1445
AAEL001621	(1303) GTTCTTCAACGATATAGCTGCTTCTGCTCGGATTGAGCCAAATCAAACCTGCGATGAAAAATGACCATCCGGTCACTACTCCGAGT	1446
AAEL001611	(1432) TTGAGTGATTTTGTGATGCCATACTTGCCCTTACGCGGAGGAGGAAGTCTTTCGACTTTTTCGACCAAACTTGAACACAGTG	1530
AAEL001621	(1388) TTGAGTGATTTTGTGATGCCATACTTGCCCTTACGCGGAGGAGGAAGTCTTTCGACTTTTTCGACCAAACTTGAACACAGTG	1531
AAEL001611	(1517) CTGACTTCAAAGCATTCTTCGAAAAAGTGAAGGACCCGATTTCCAGAACTGTTGGAGTTGCTGTATGTAAGTTAGTGTGAAT	1615
AAEL001621	(1473) CTGACTTCAAAGCATTCTTCGAAAAAGTGAAGGACCCGATTTCCAGAACTGTTGGAGTTGCTGTATGTAAGTTAGTGTGAAT	1616
AAEL001611	(1602) TTCTGAAGATTTGCTTAAAGTATCTCTAATTTCTTTTCAAGATTCGACTGAGCTGAAGTATTGTTCCAGAAACTTCGGGATCAC	1700
AAEL001621	(1558) TTCTGAAGATTTGCTTAAAGTATCTCTAATTTCTTTTCAAGATTCGACTGAGCTGAAGTATTGTTCCAGAAACTTCGGGATCAC	1701
AAEL001611	(1687) GGGTGGATGCGCAAAATTTTCGAGCTTGTGAAGGATTTCTTTGGCTGGAATTTTAAACTTCTGTGTTAATGTTTCATAAA	1785
AAEL001621	(1643) GGGTGGATGCGCAAAATTTTCGAGCTTGTGAAGGATTTCTTTGGCTGGAATTTTAAACTTCTGTGTTAATGTTTCATAAA	1786
AAEL001611	(1772) AGGTTTTGGTAAAGTGAATATTTTTTGTAAACAATATACATAATGTTTTTAAACATCAGGCAGGGTTAAAGCTCTCTGTATAAT	1870
AAEL001621	(1728) ATAGTTTTGGTAAAGTGAATATTTTTTGTAAACAATATACATAATGTTTTTAAACATCAGGCAGGGTTAAAGCTCTCTGTATAAT	1871
AAEL001611	(1857) TTGTAAGTCTCTGTAATAATGTTTAAAGTTTAACTTTTGAATAATCAAAAAGTTGTTGATC-----	1955
AAEL001621	(1813) TTGTAAGTCTCTGTAATAATGTTTAAAGTTTAACTTTTGAATAATCAAAAAGTTGTTGATC-----ATATCTTTGGGATGTTTAAA	1956
AAEL001611	(1921) -----ATATCTTTGGGATTCAGCATGCCGCTCTGAGACCGCTTCCCCGCCATTTGTC	2040
AAEL001621	(1898) ACCTCTATAATGAACAAAACAAAAAATATATCTTTGGGATTCAGCATGCCGCTCTGAGACCGCTTCCCCGCCATTTGTC	2041
AAEL001611	(1977) CATGTGATATTTGAGCCATCTAATTTTCATCATCAATATCAGAAGTTT	2090
AAEL001621	(1983) CATGTGATATTTGAGCCATCTAATTTTCATCATCAATATCAGAAGTTT	

Supplemental Figure 6 Dot plot of duplications

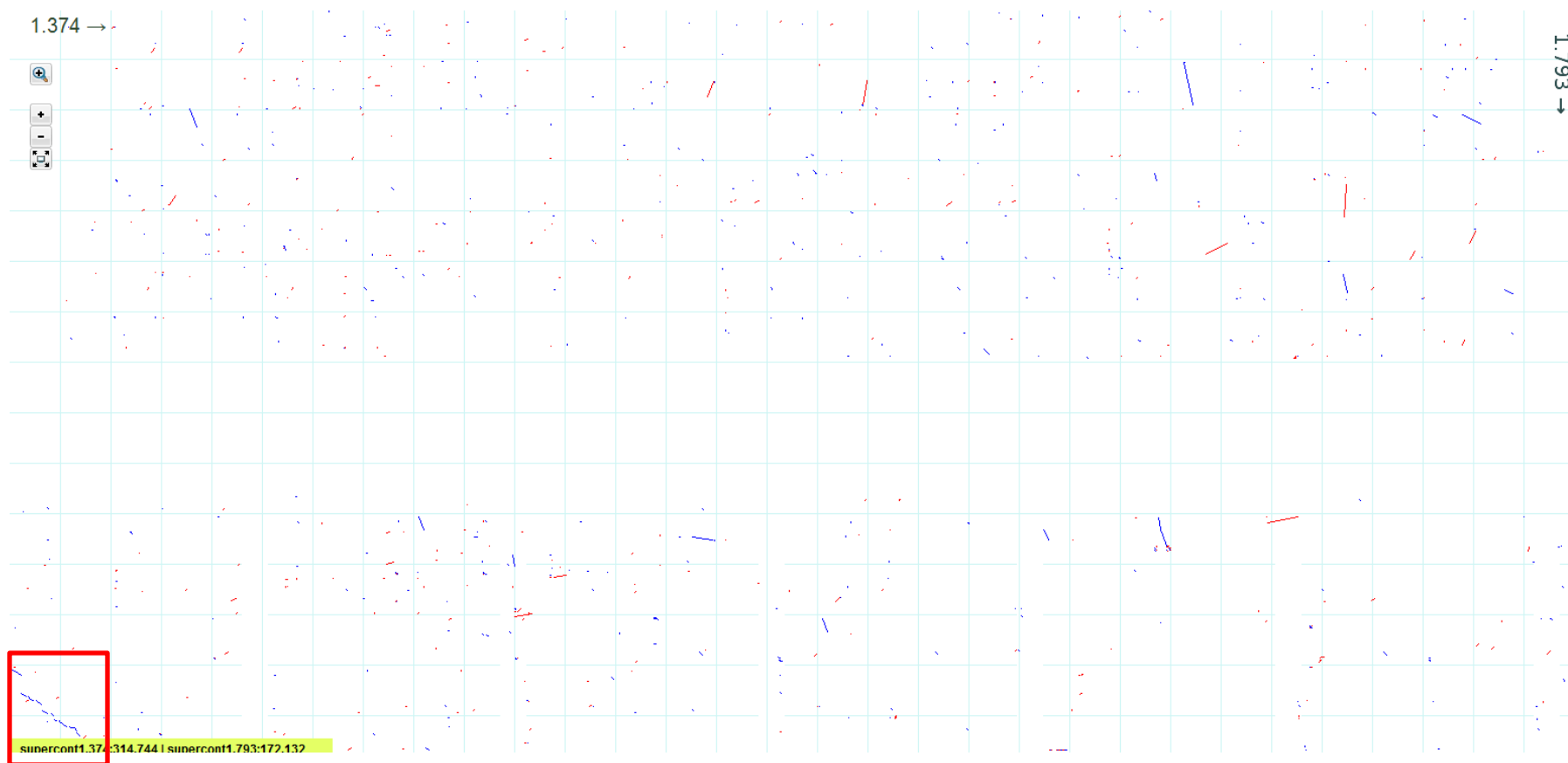
a
61 kb



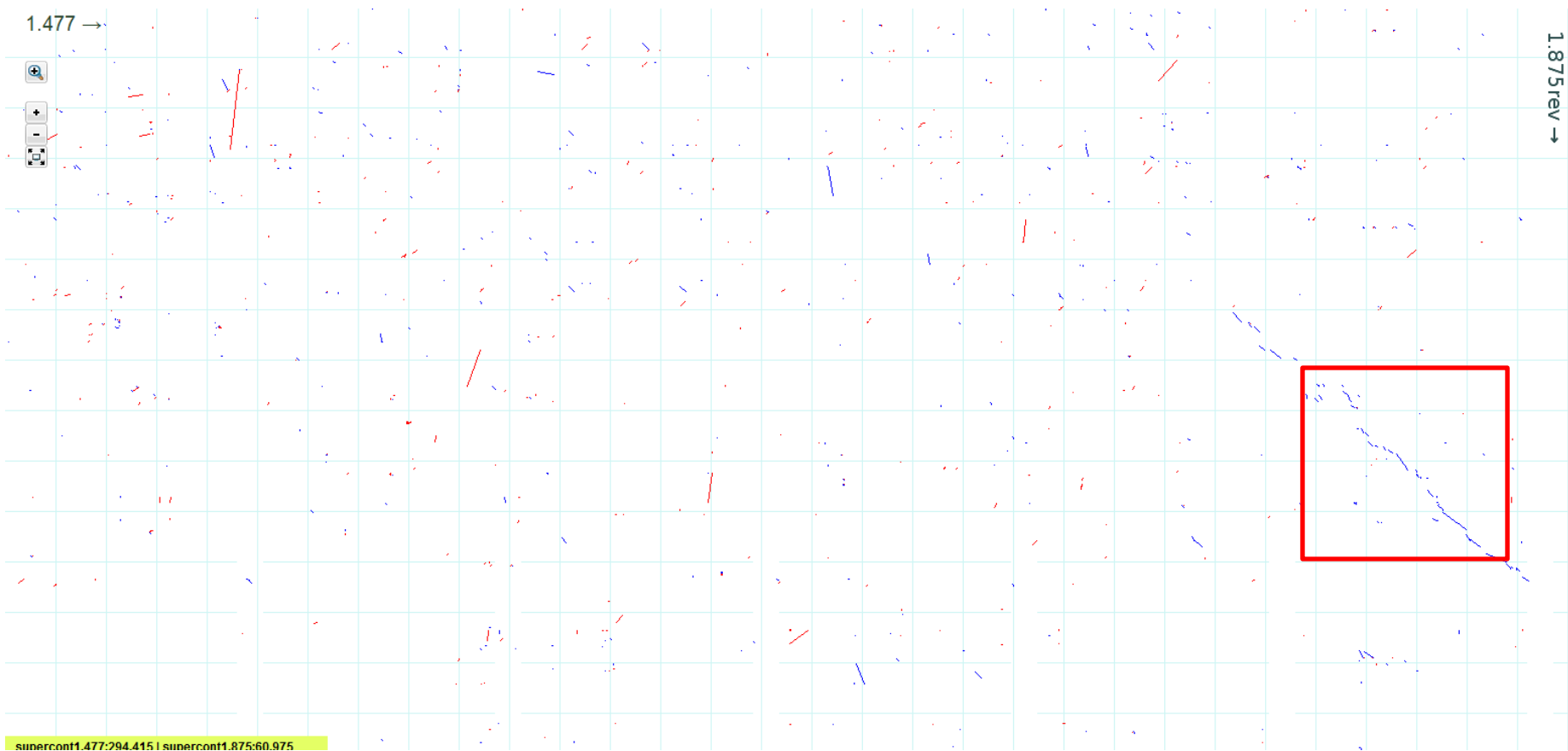
b
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Supplemental Figure 7 Full dot plot analysis of c1.374 and c1.793



Supplemental Figure 8 Full dot plot analysis of c1.477 and c1.875

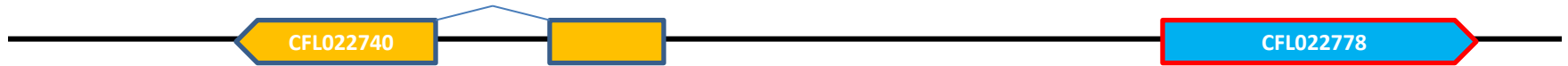


Supplemental Figure 9 Gene clusters in the Formicidae

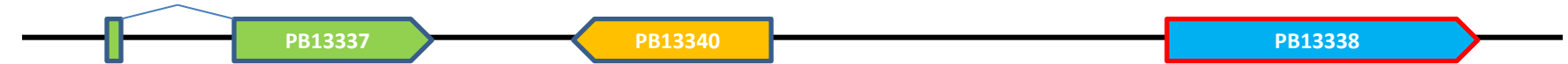
H. saltator < 10 kb



C. floridanus < 8 kb



P. barbata < 10 kb



S. invicta < 8.5 kb



L. humile < 9 kb



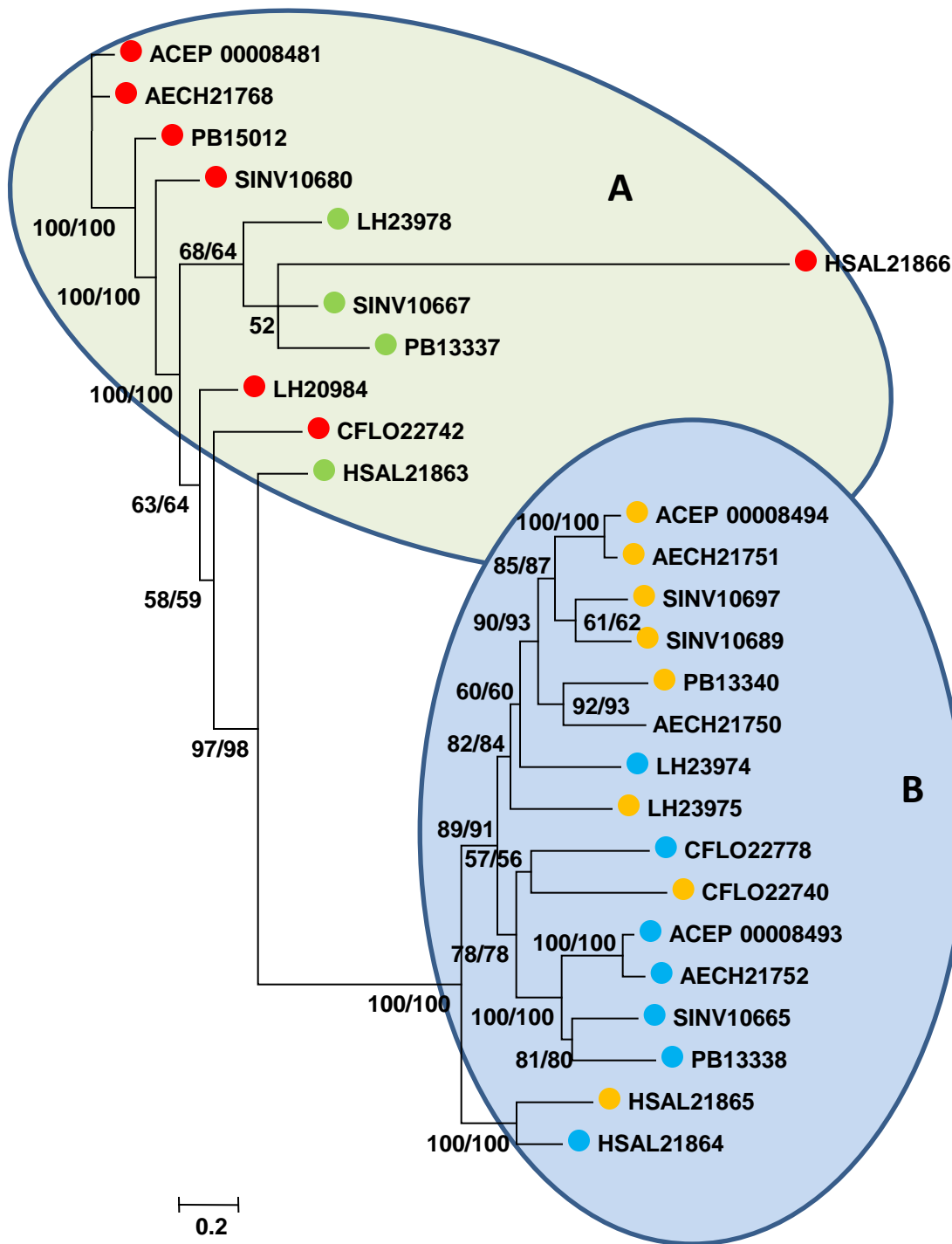
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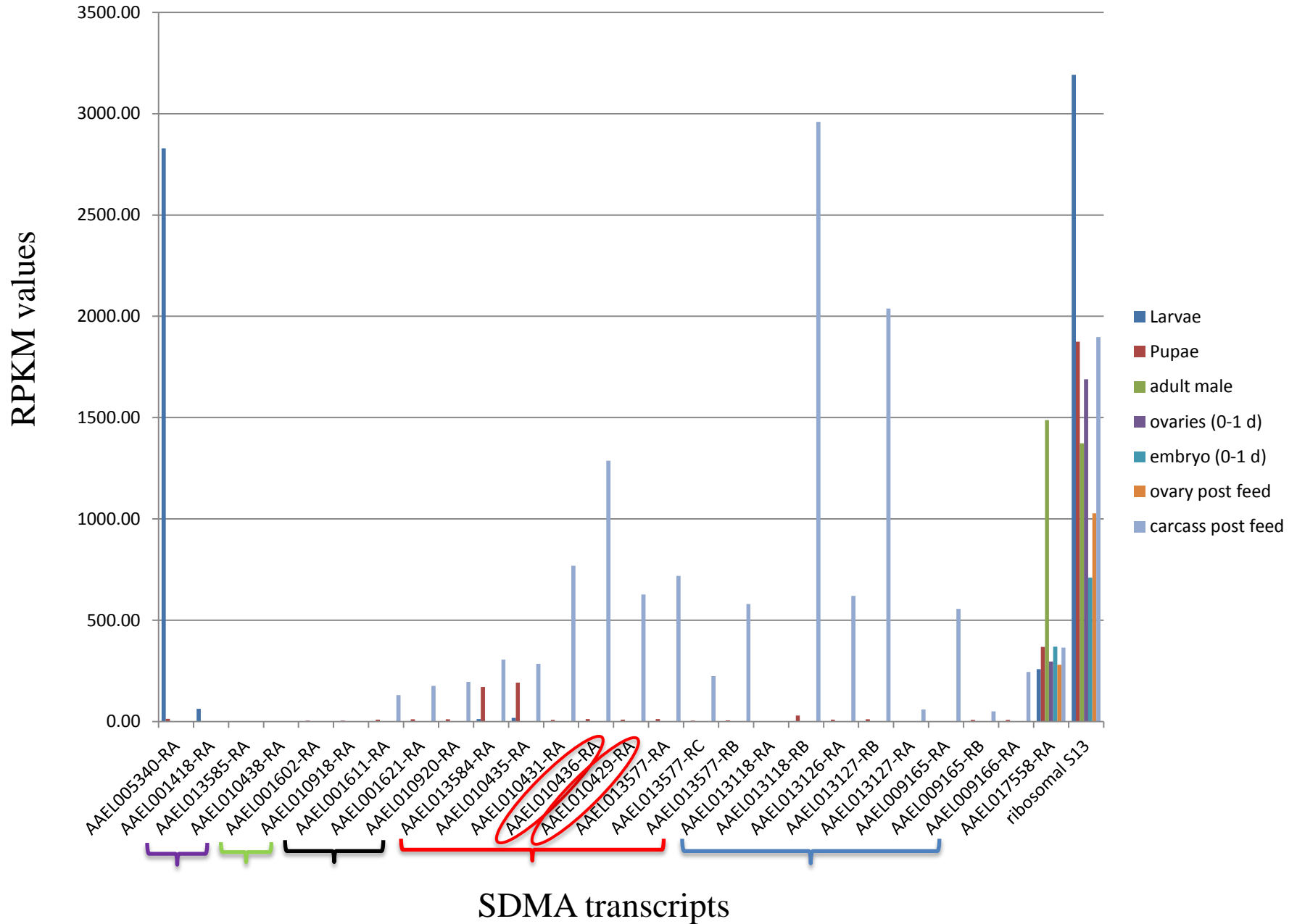
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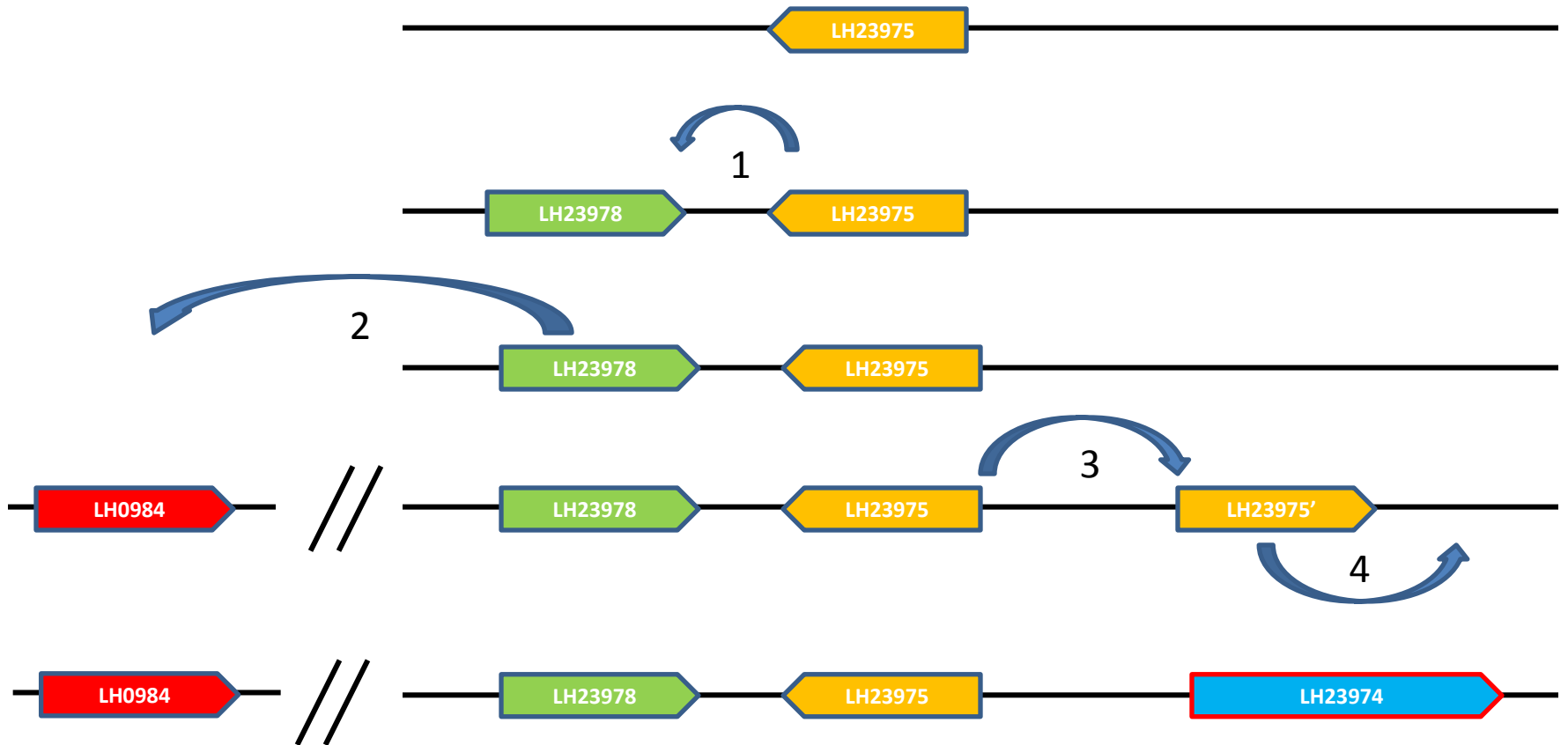
Supplemental Figure 10
Phylogenetic tree of
Hymenopteran
SDMA and 2DMA genes



Supplemental Figure 11 Expression of SDMA homologs in *A. aegypti* at various life stages



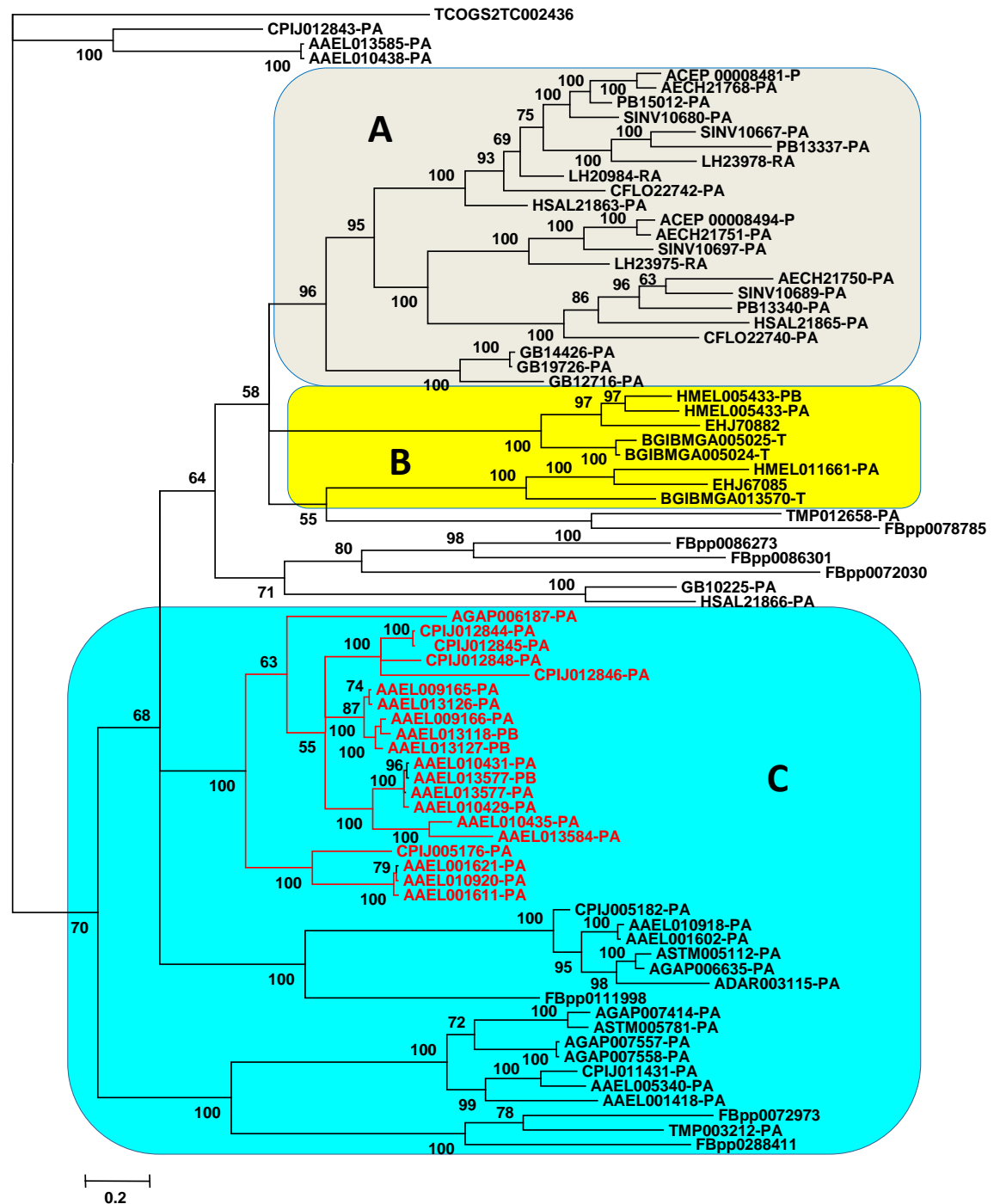
Supplemental Figure 12 A model for the generation of the conserved SDMA gene cluster in Formicidae



Supplementary Figure 13

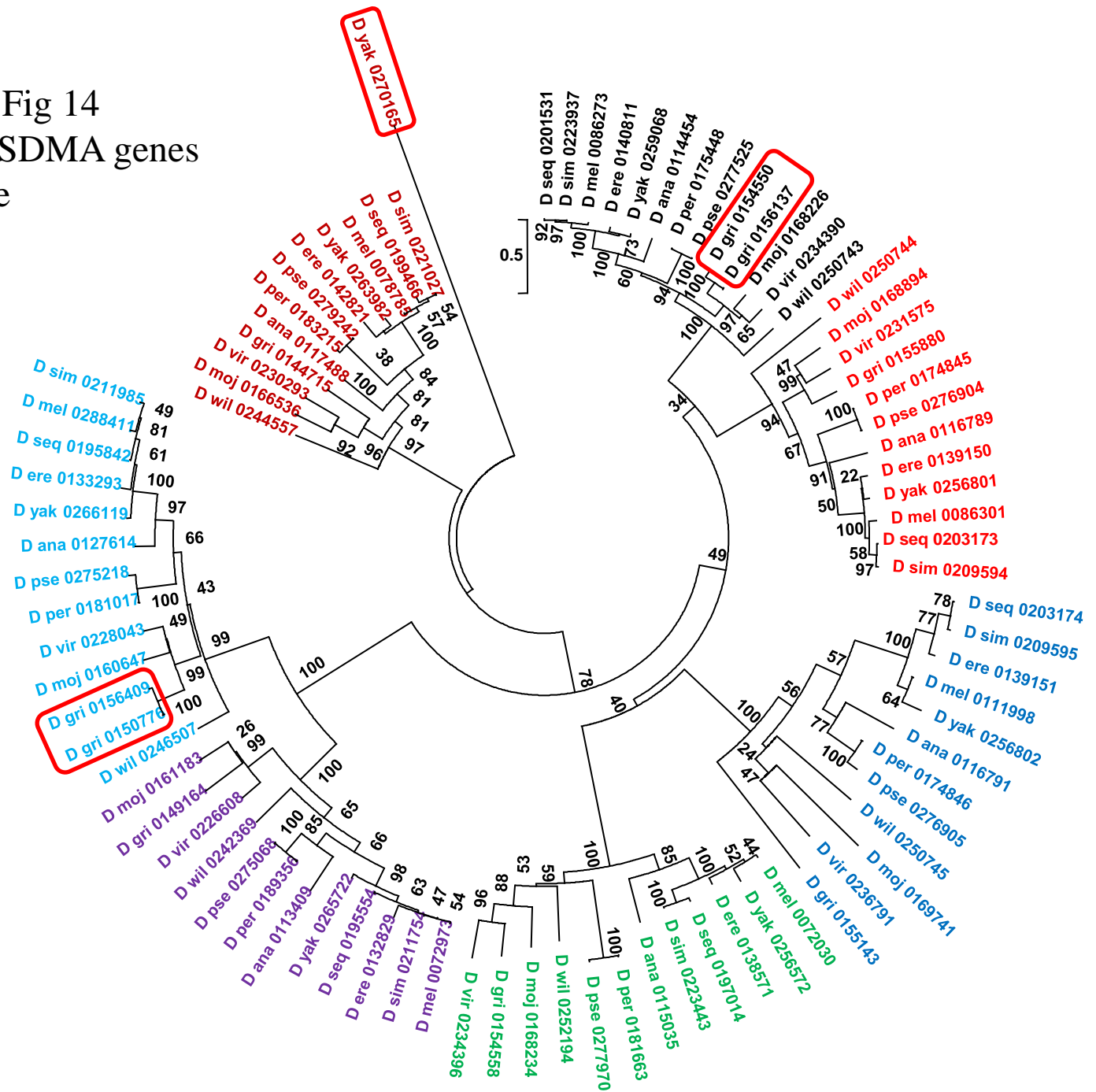
Phylogeny of SDMA genes

In Insects

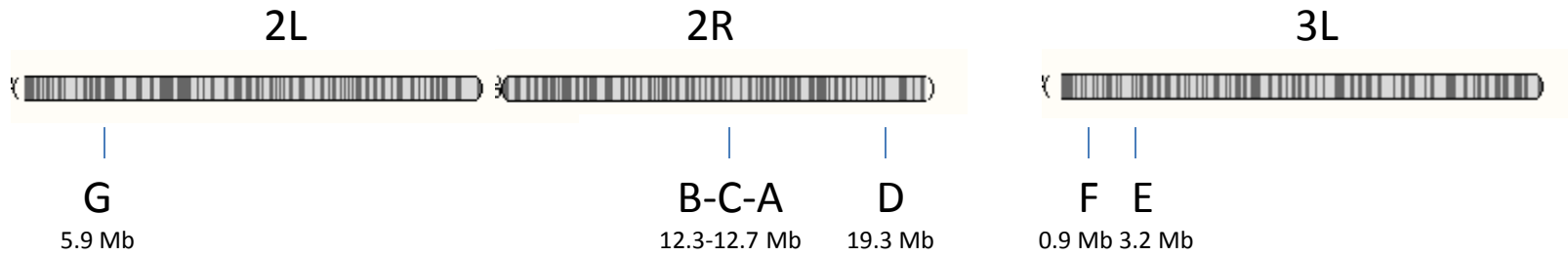


Supplemental Fig 14
 Phylogeny of SDMA genes
 In *Drosophilae*

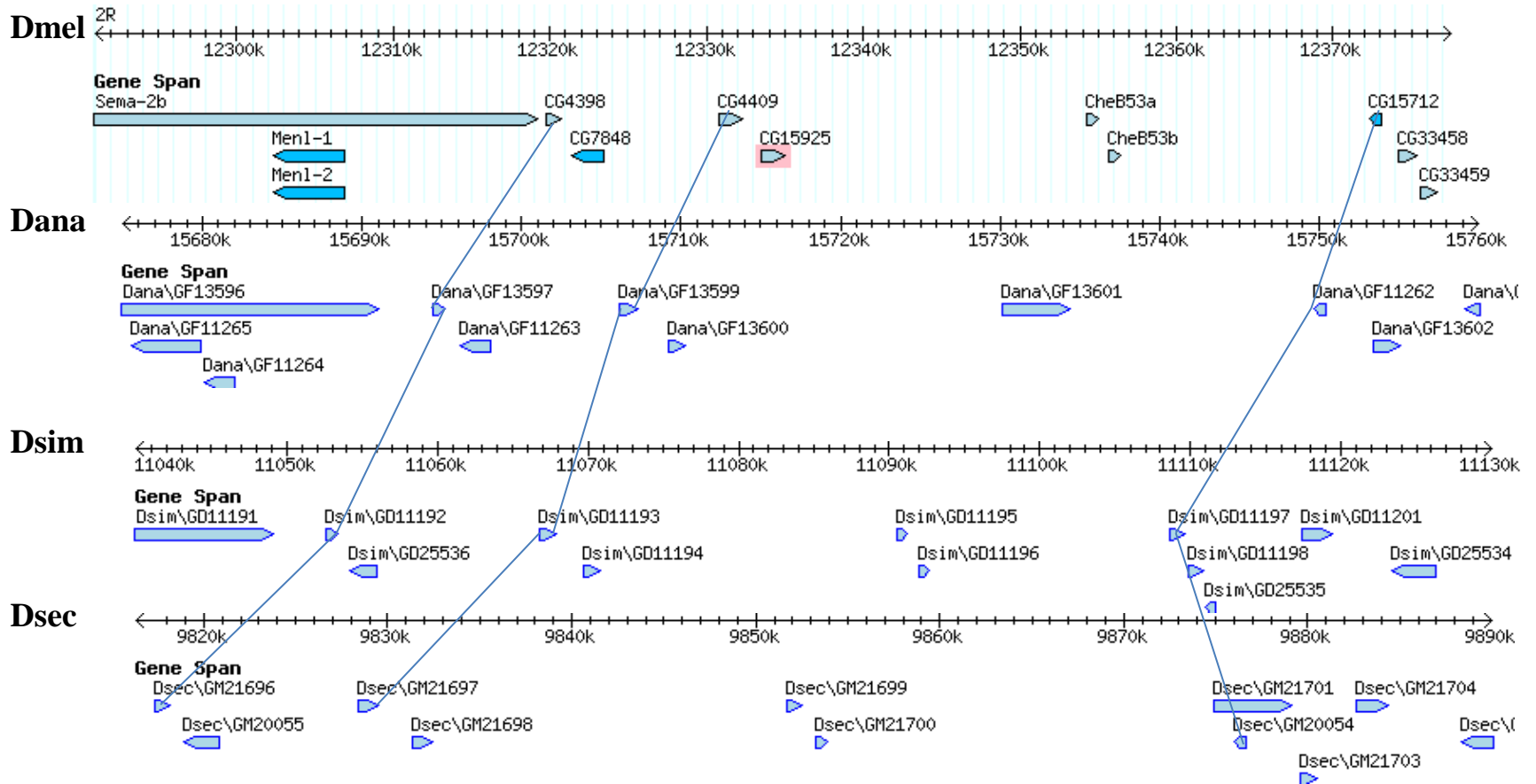
- Group A**, chr2R
- Group B**, chr2R
- Group C**, chr2R
- Group D**, chr2R
- Group E**, chr3L
- Group F**, chr3L
- Group G**, chr2L



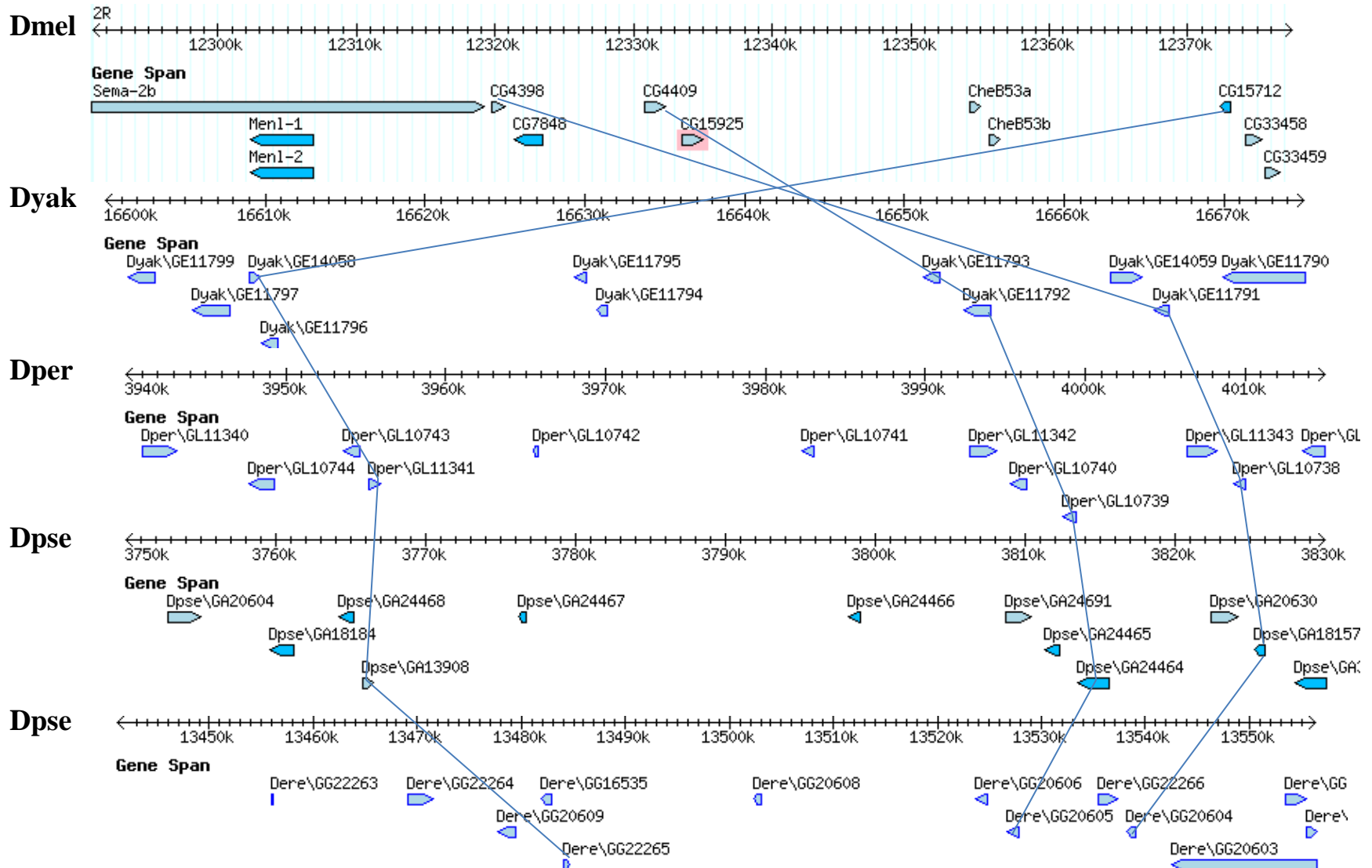
Supplemental Fig 15 Genome Level Organization of SDMA homologs in Drosophila



Supplemental Fig 16a chr2R synteny and clustering of group A,B, and C SDMA genes in *D. melanogaster*, *D. ananassae*, *D. simulans*, *D. sechellia*



Supplemental Fig 16b chr2R synteny and clustering of group A,B, and C SDMA genes in *D.melanogaster*, *D.yakuba*, *D.persimilis*, *D.pseudoobscura*, *D. erecta*



Supplemental Fig 16c chr2R synteny and clustering of group A,B, and C SDMA genes in *D. melanogaster*, *D. virilis*, *D. mojavensis*, *D. willistoni*, *D. grimshawi*

