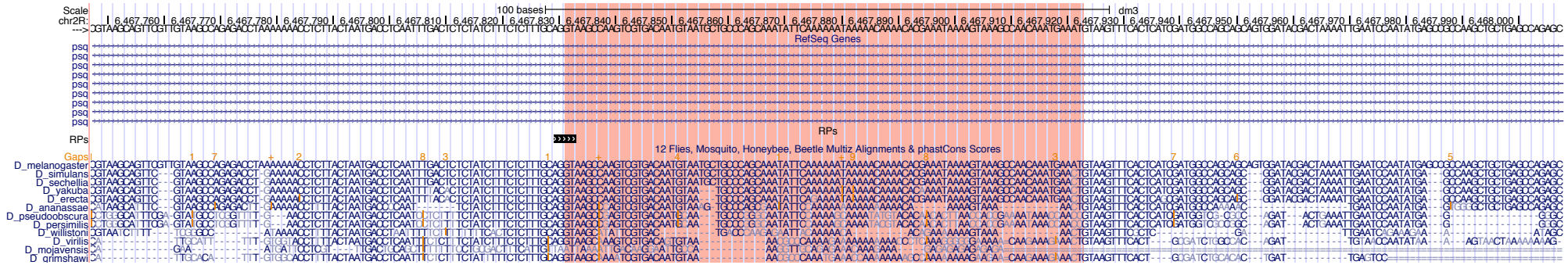
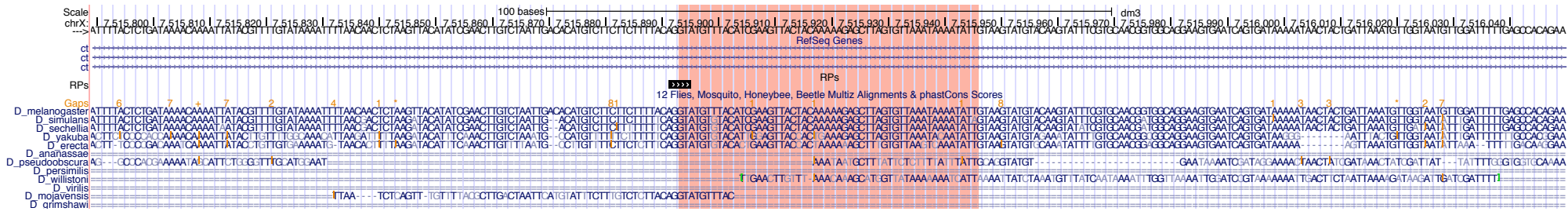
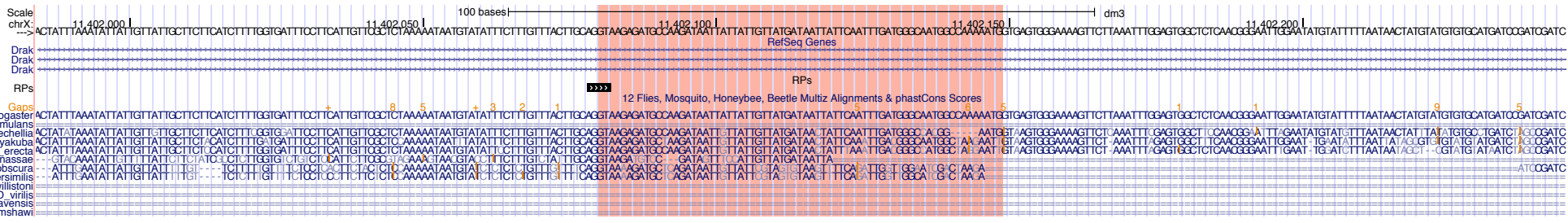


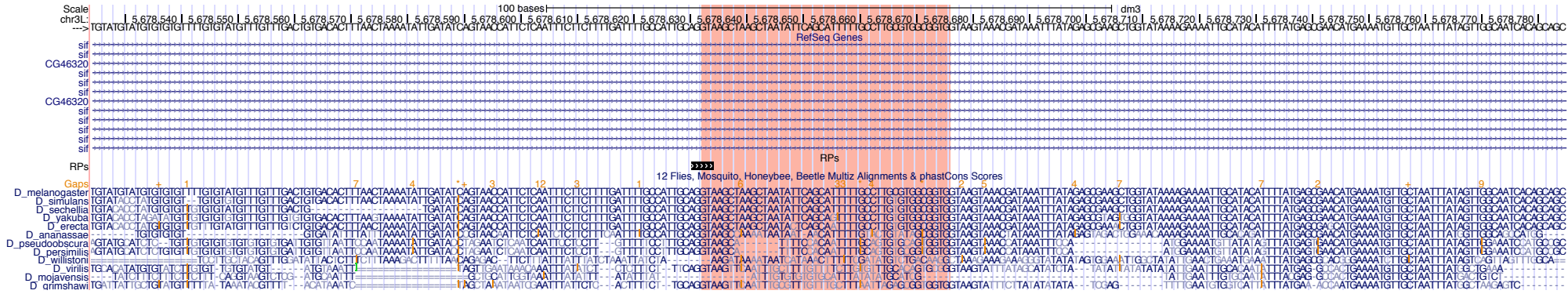
Supplementary Data Set 5. UCSC genome browser screenshots of intronic RPs and their associated cryptic exons. Shown are 50 examples of intronic RPs with high-scoring cryptic splice donors; the inferred cryptic exons are highlighted in red.

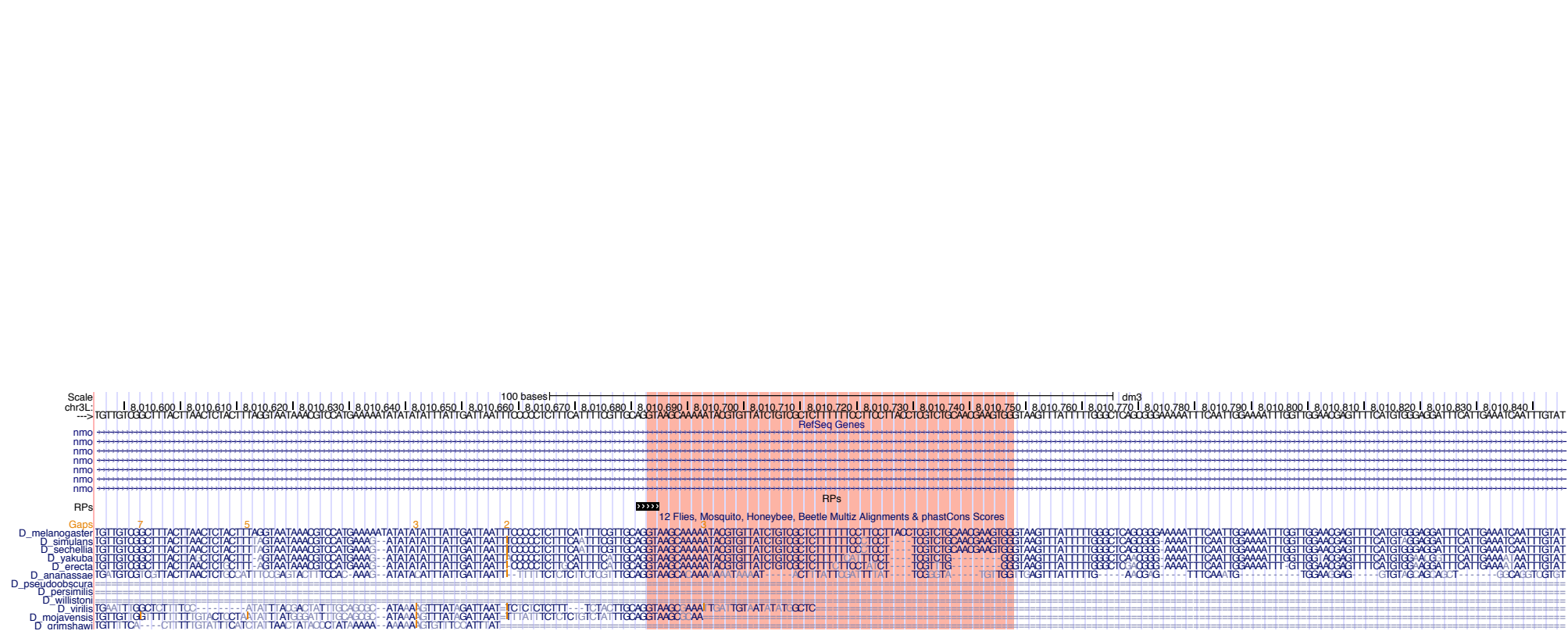


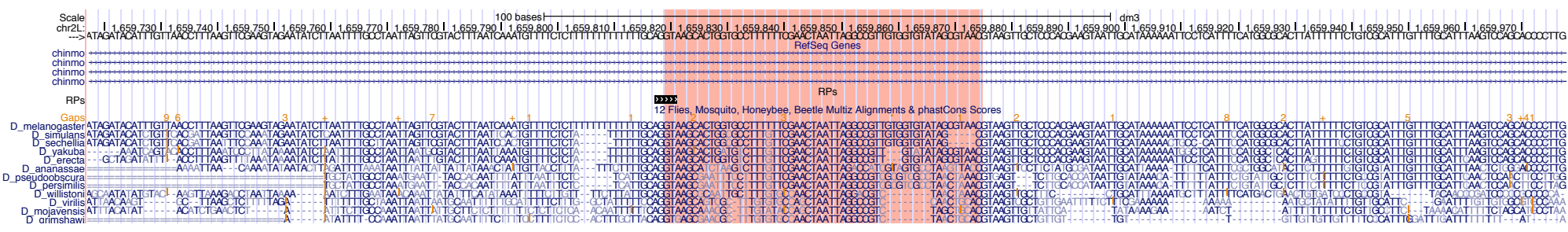


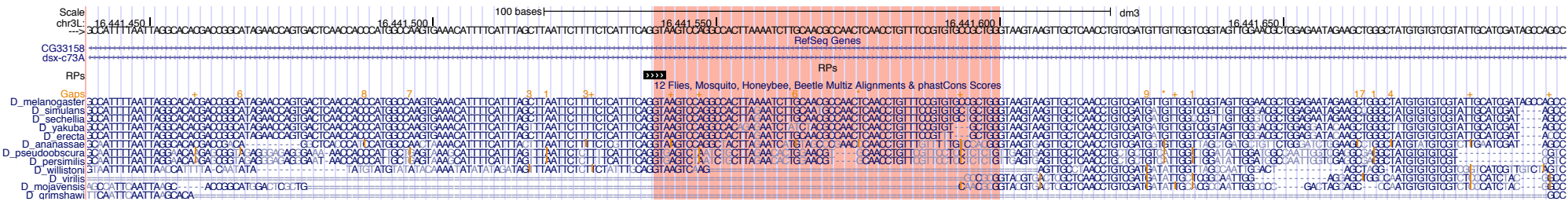


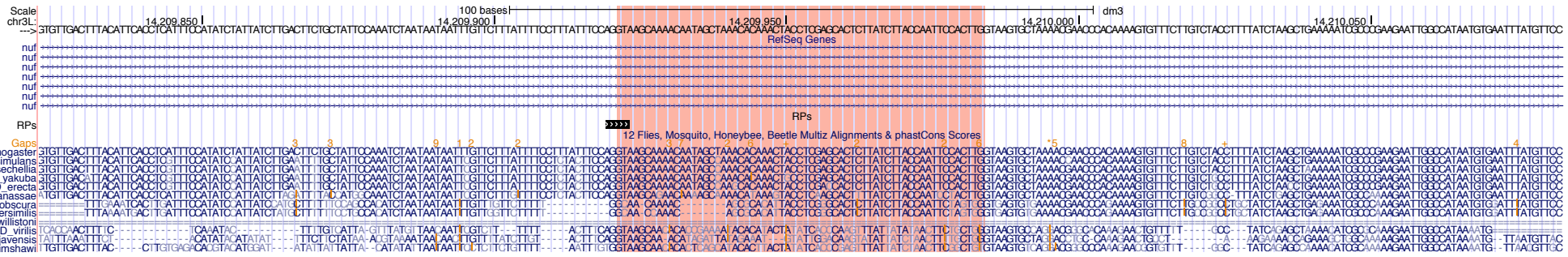


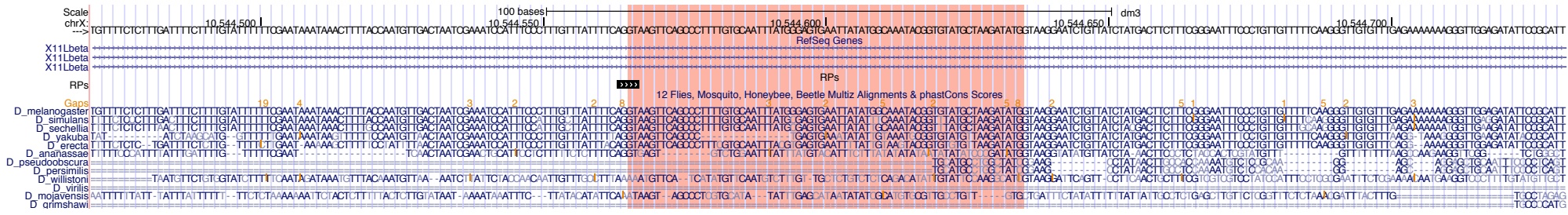




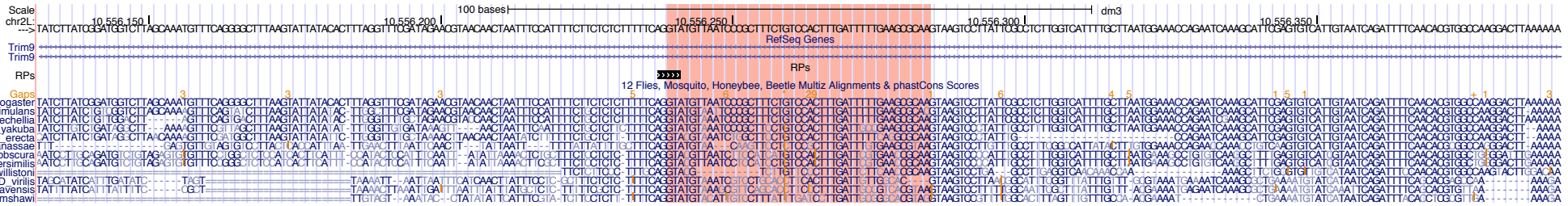








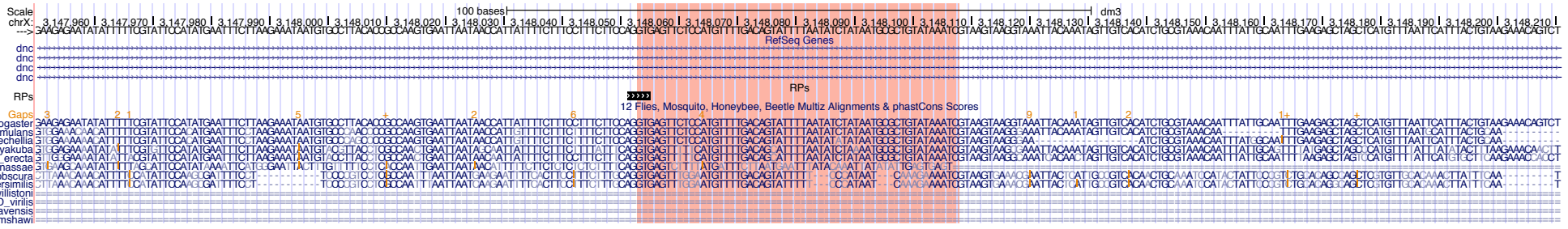


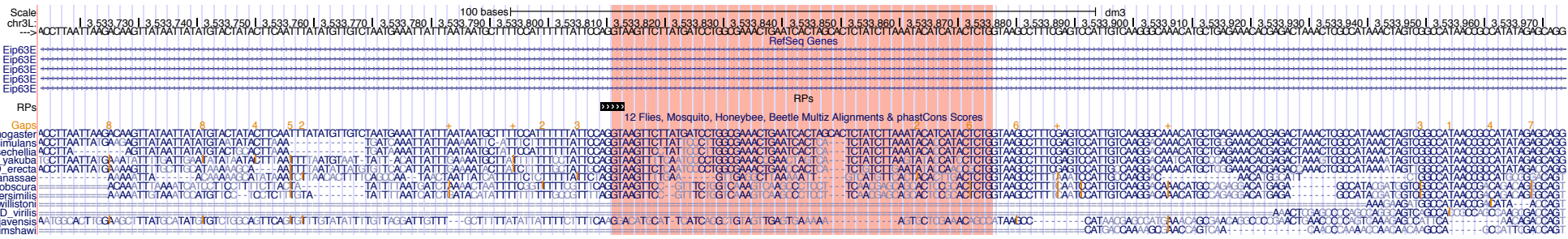


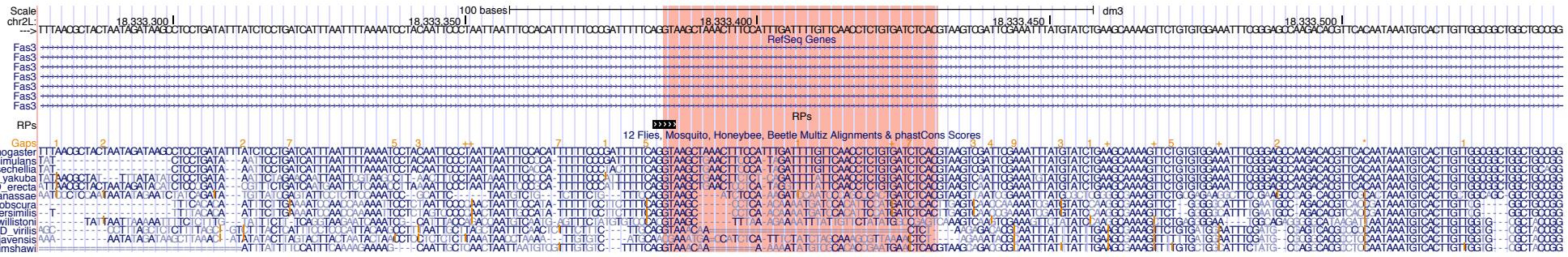
Scale chr3R: | 5,745,390 | 5,745,400 | 5,745,410 | 5,745,420 | 5,745,430 | 5,745,440 | 5,745,450 | 5,745,460 | 5,745,470 | 5,745,480 | 5,745,490 | 5,745,500 | 5,745,510 | 5,745,520 | 5,745,530 | 5,745,540 | 5,745,550 | 5,745,560 | 5,745,570 | 5,745,580 | 5,745,590 | 5,745,600 | 5,745,610 | 5,745,620 | 5,745,630 |

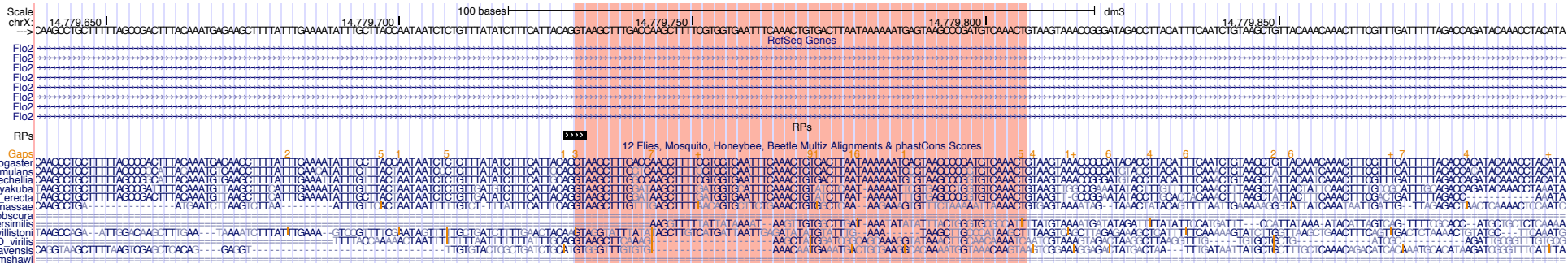
dm3
RelSeq Genes
Glut4EF
Glut4EF
Glut4EF
Glut4EF

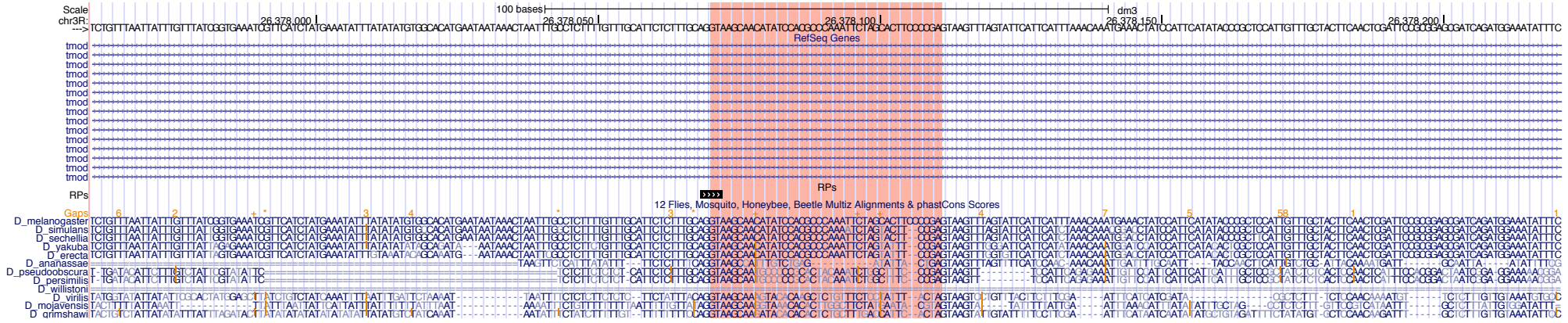
RP
12 Files, Mosquito, Honeybee, Beetle Multiz Alignments & phastCons Scores
D_melanogaster
D_simulians
D_sechellia
D_yakuba
D_erecia
D_ananassae
D_pseudoobscura
D_persimilis
D_willistoni
D_virilis
D_mojavensis
D_grimshawi

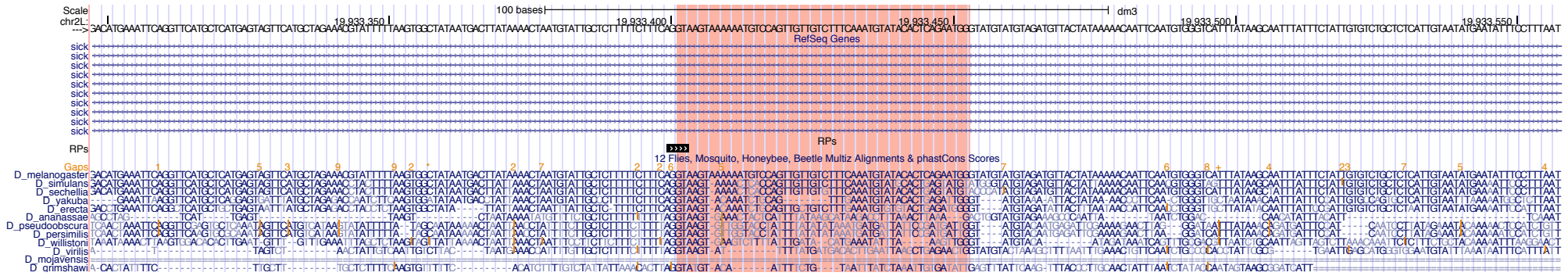


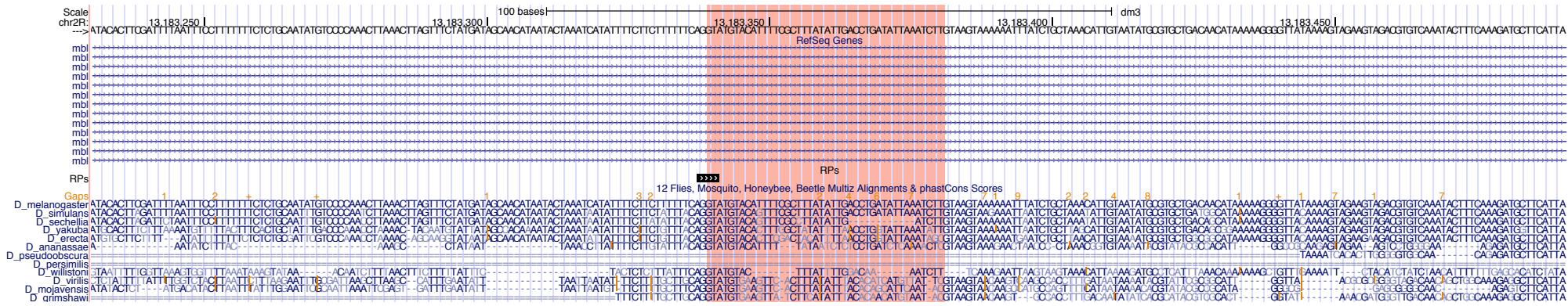


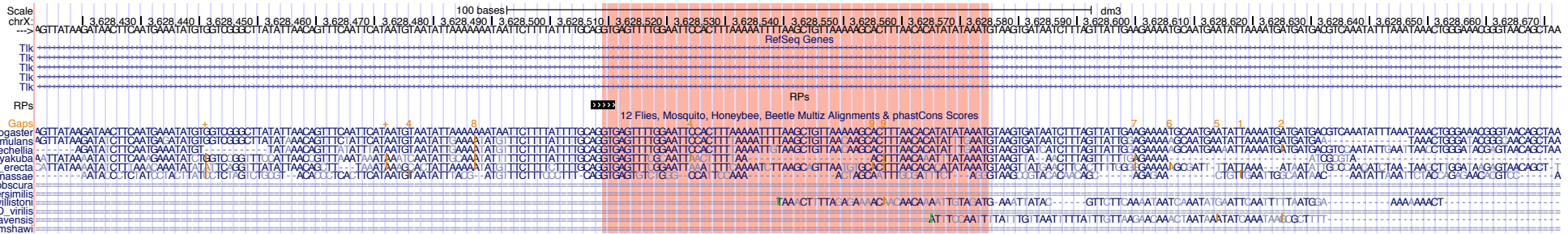


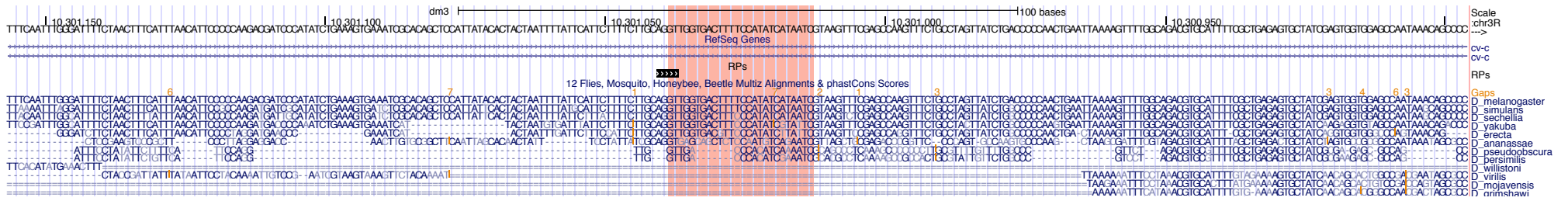


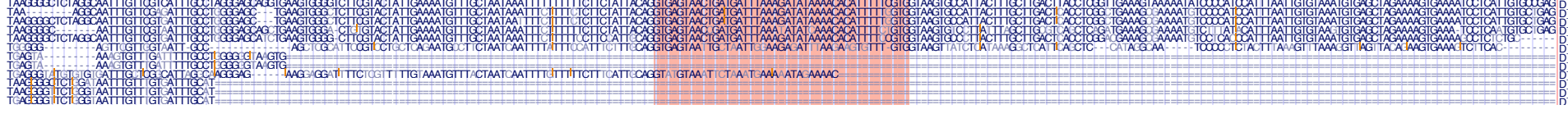
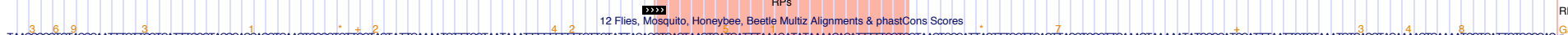
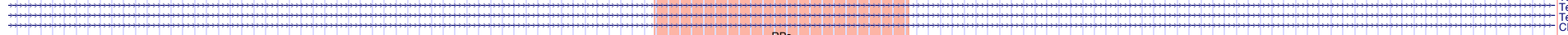
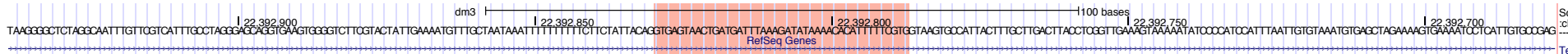


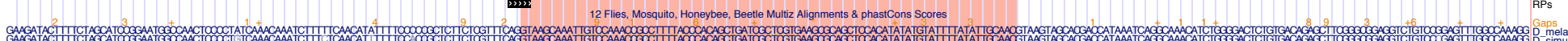
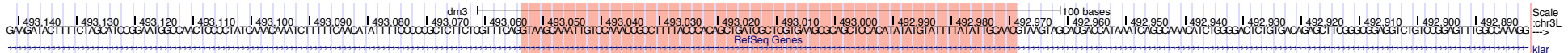




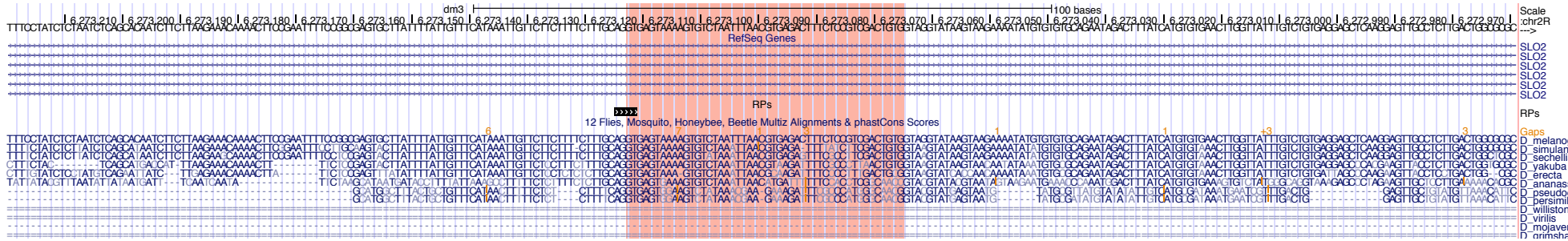


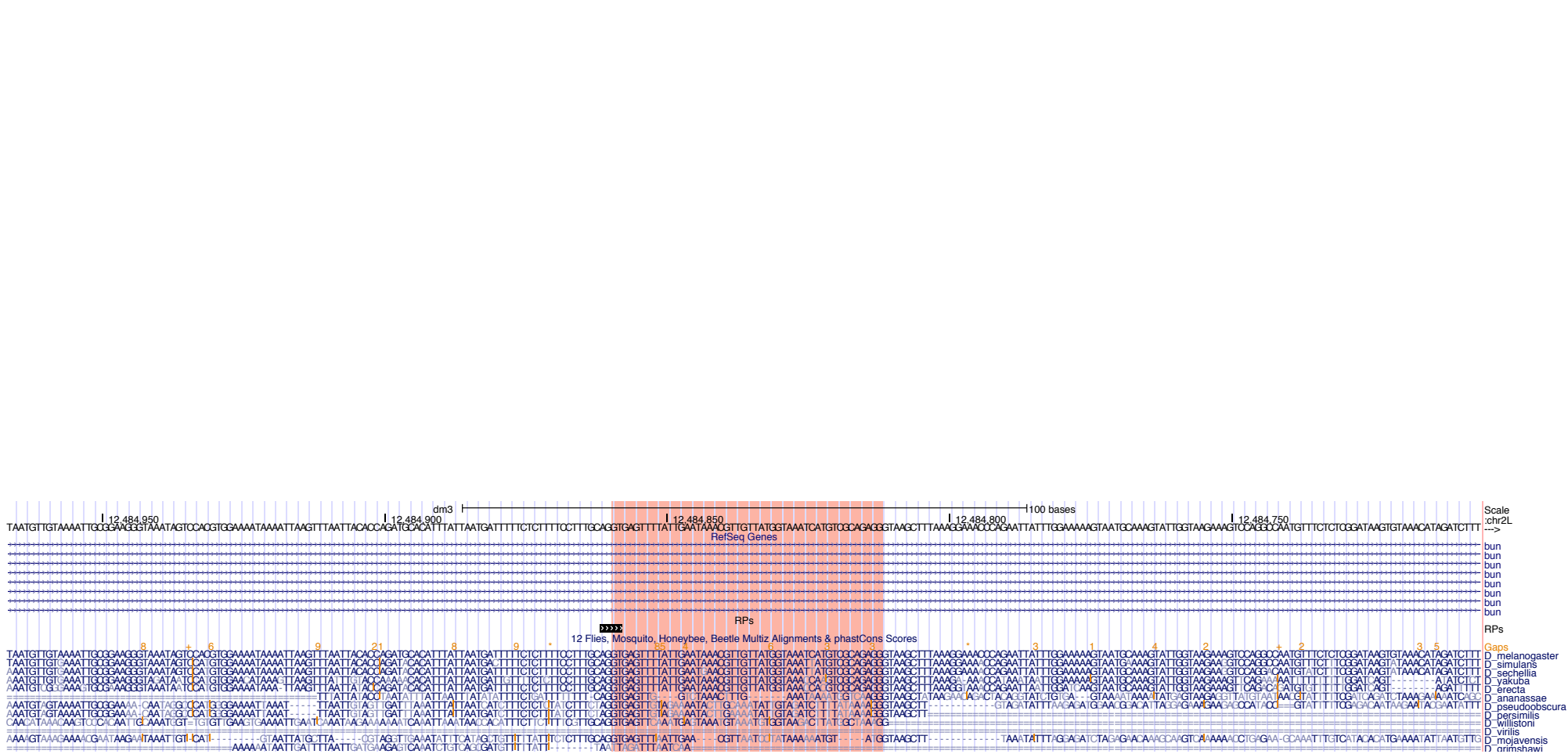


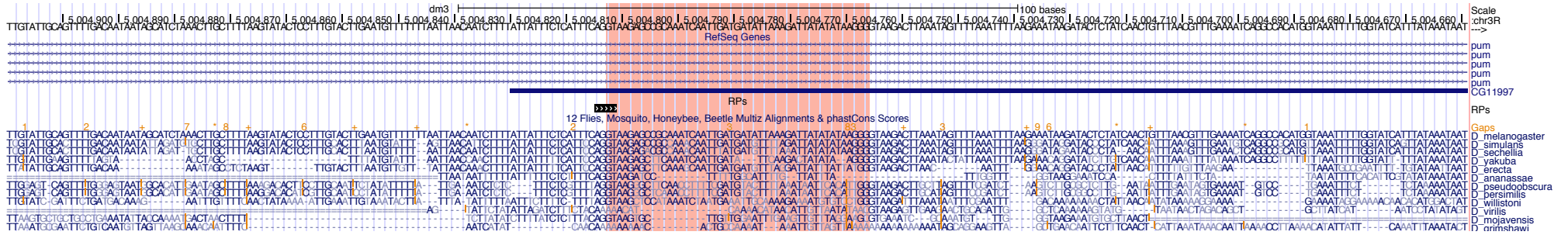


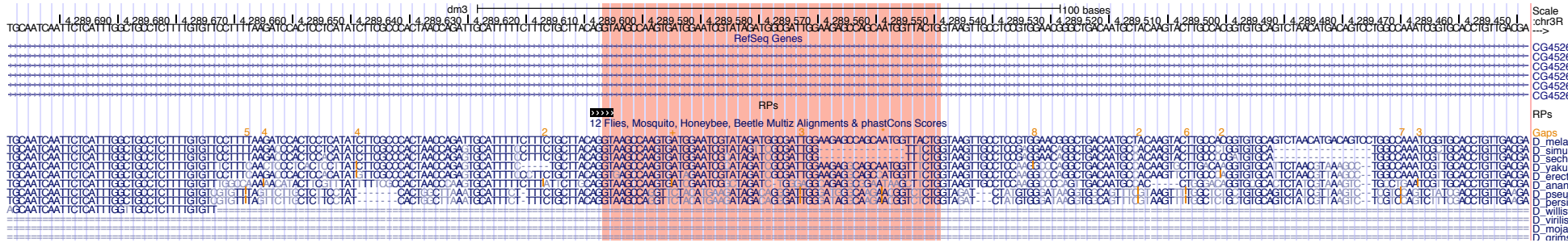


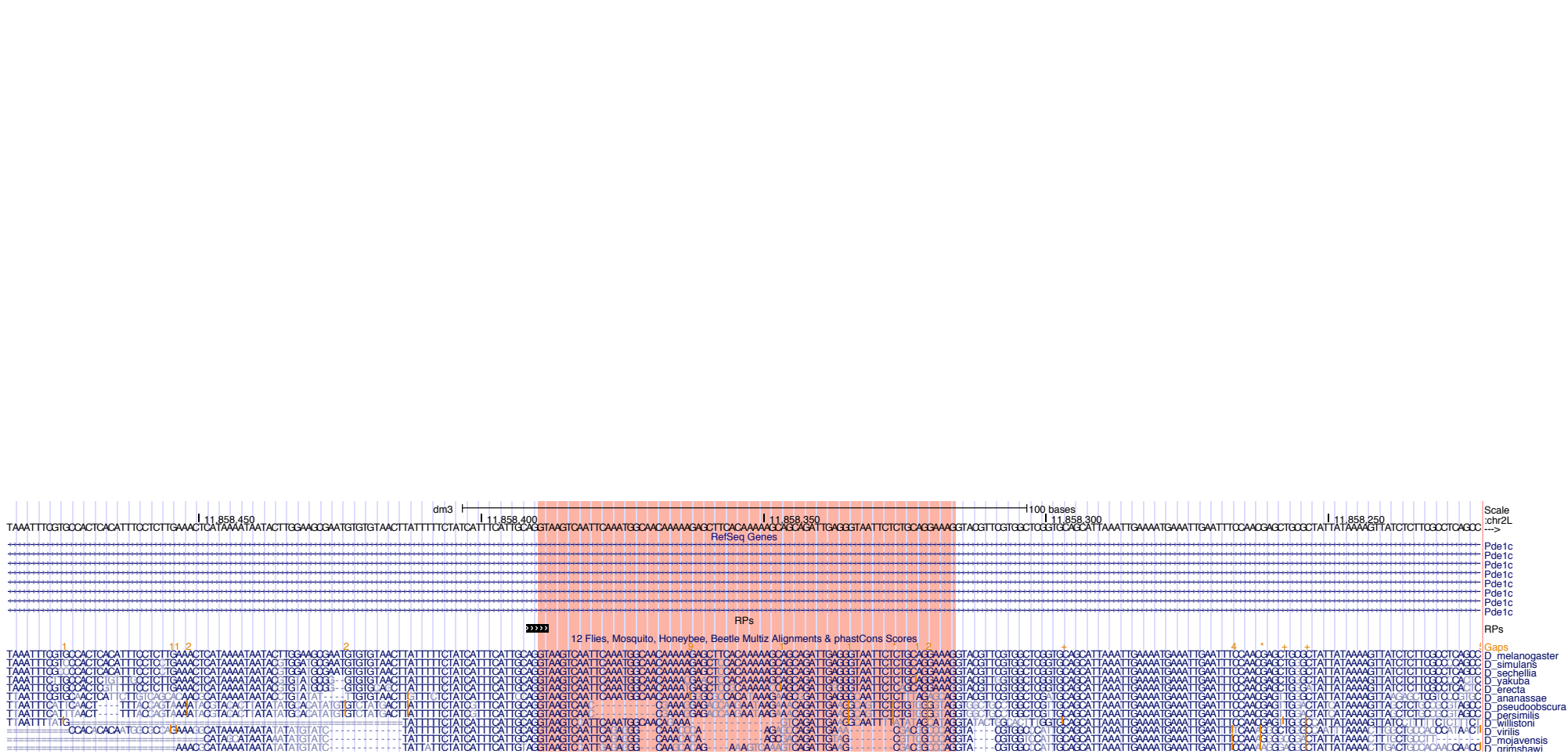
Species	Sequence
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D. simulans	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG
D. sechellia	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG
D. yakuba	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG
D. erecta	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG
D. ananassae	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG
D. pseudoobscura	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG
D. persimilis	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG
D. willistoni	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG
D. virilis	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG
D. mojavensis	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG
D. rimshawi	GAAGATACTTTTCTAGCATCGGAAATGGCCAACTGCCCATCAAAACAATCTTTTCAACATATTTTCCCGGCTCTCTCGTTCAGGTAAAGCAAAATGTCGAAACCGCCCTTTACCCACAGCTGATGCTCTGTAAGCGACCTCCACATATATGATTTTATATTCGAAAGTAAGTAGCAACCAATAAATCAGGCAAAACATCTGGGACTCTGTGACAGAGCTTGGCGGAGGTCTGTCCGAGTTTGGCAAAAGG

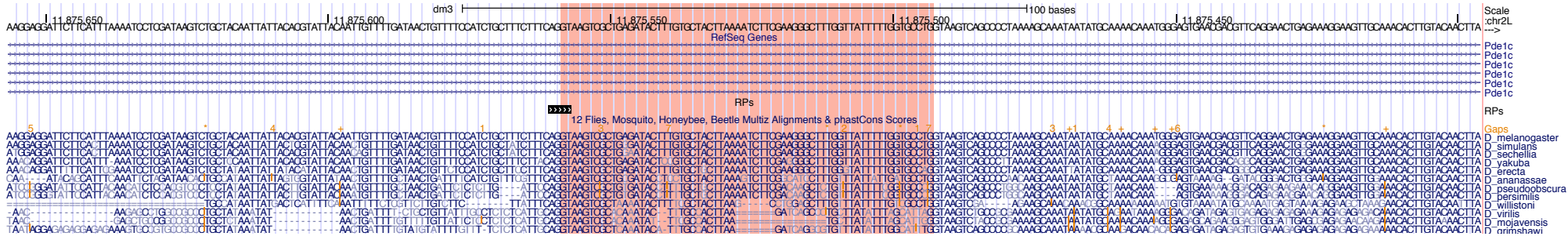












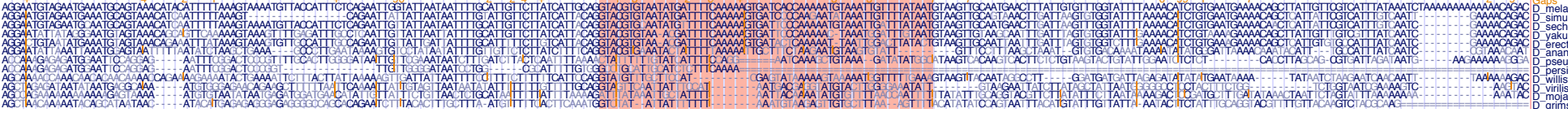
1 4,989,450 | 4,989,440 | 4,989,430 | 4,989,420 | 4,989,410 | 4,989,400 | 4,989,390 | 4,989,380 | 4,989,370 | 4,989,360 | 4,989,350 | 4,989,340 | 4,989,330 | 4,989,320 | 4,989,310 | 4,989,300 | 4,989,290 | 4,989,280 | 4,989,270 | 4,989,260 | 4,989,250 | 4,989,240 | 4,989,230 | 4,989,220 | 4,989,210 | Scale chr3R
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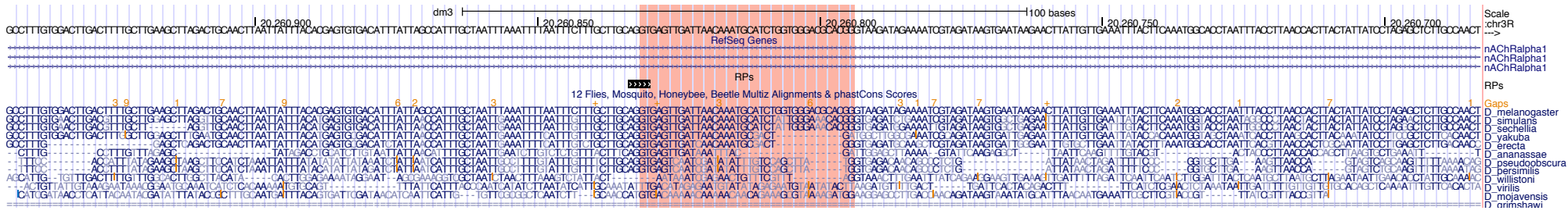
RelSeq Genes

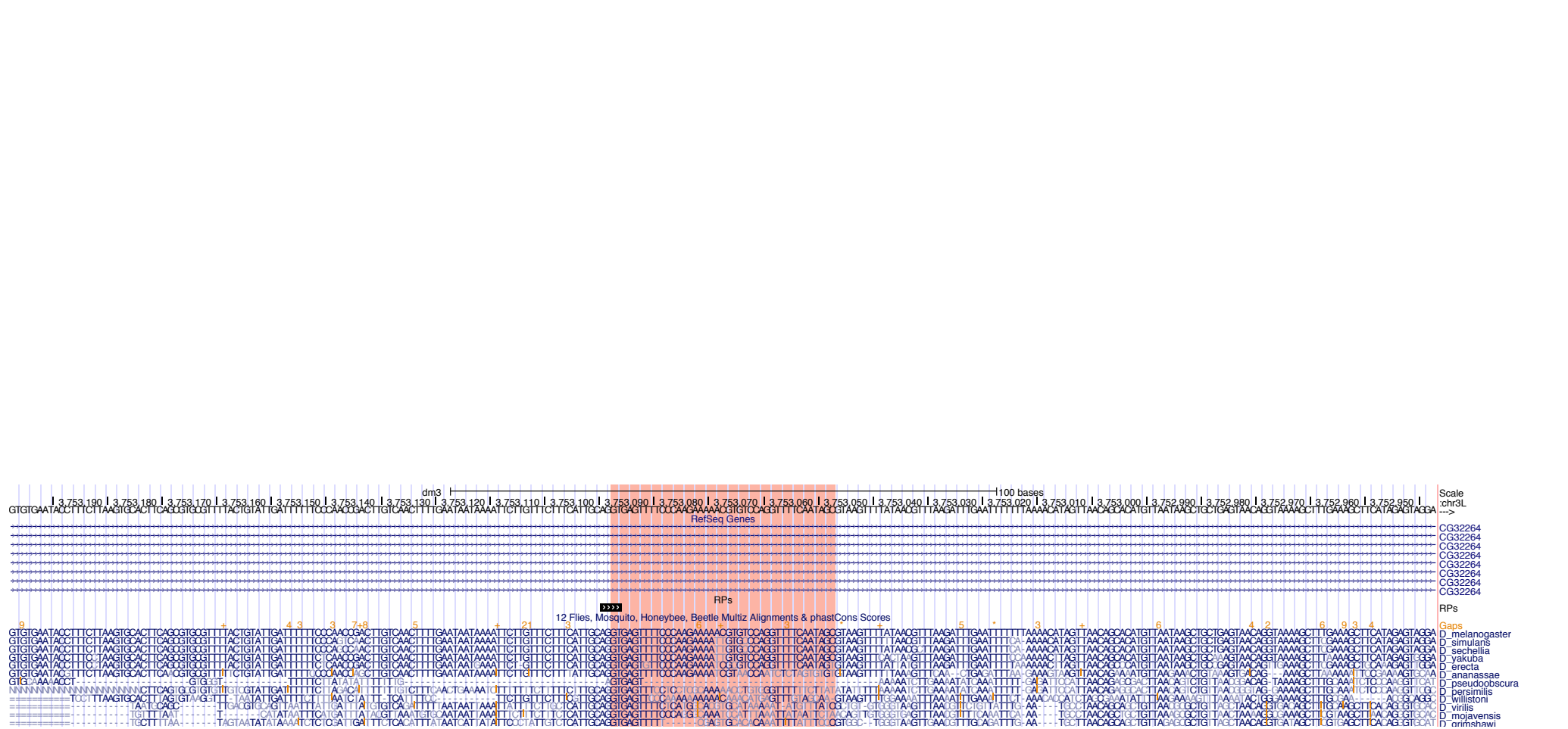


RP

12 Flies, Mosquito, Honeybee, Beetle Multiz Alignments & phastCons Scores







3,753,190 | 3,753,180 | 3,753,170 | 3,753,160 | 3,753,150 | 3,753,140 | 3,753,130 | 3,753,120 | 3,753,110 | 3,753,100 | 3,753,090 | 3,753,080 | 3,753,070 | 3,753,060 | 3,753,050 | 3,753,040 | 3,753,030 | 3,753,020 | 3,753,010 | 3,753,000 | 3,752,990 | 3,752,980 | 3,752,970 | 3,752,960 | 3,752,950 |

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CG32264
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CG32264

RPs
 12 Files, Mosquito, Honeybee, Beetle Multiz Alignments & phastCons Scores
 Gaps
 D. melanogaster
D. simulans
D. sechellia
D. yakuba
D. erecta
D. anansae
D. pseudoobscura
D. persimilis
D. willistoni
D. virilis
D. mjayensis
D. ornishawi

1 5 187 010 | 1 5 187 000 | 1 5 186 990 | 1 5 186 980 | 1 5 186 970 | 1 5 186 960 | 1 5 186 950 | 1 5 186 940 | 1 5 186 930 | 1 5 186 920 | 1 5 186 910 | 1 5 186 900 | 1 5 186 890 | 1 5 186 880 | 1 5 186 870 | 1 5 186 860 | 1 5 186 850 | 1 5 186 840 | 1 5 186 830 | 1 5 186 820 | 1 5 186 810 | 1 5 186 800 | 1 5 186 790 | 1 5 186 780 | 1 5 186 770 |

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RelSeq Genes

RPAs

12 Flies, Mosquito, Honeybee, Beetle Multiz Alignments & phasiCons Scores

Gaps

D melanogaster
D simulans
D sechellia
D yakuba
D erecta
D ananassae
D pseudoobscura
D persimilis
D willistoni
D virilis
D mojavensis
D orinshawii

