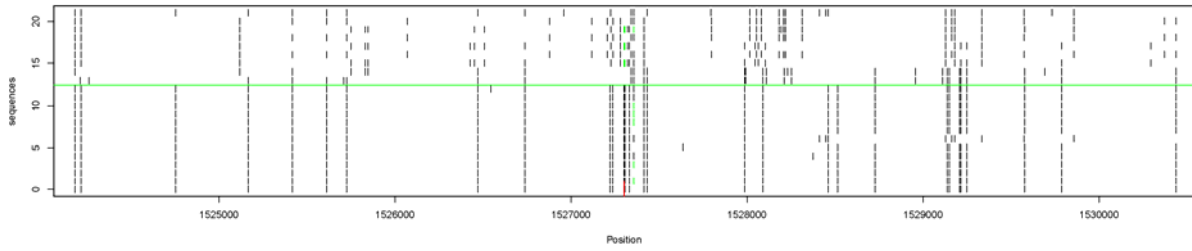


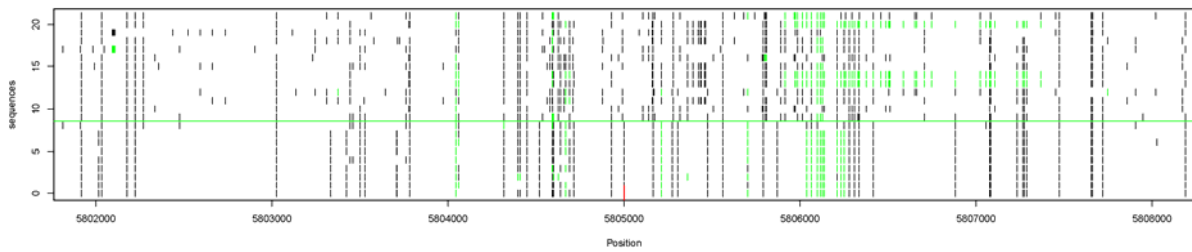
Figure S7

2L Patterns:

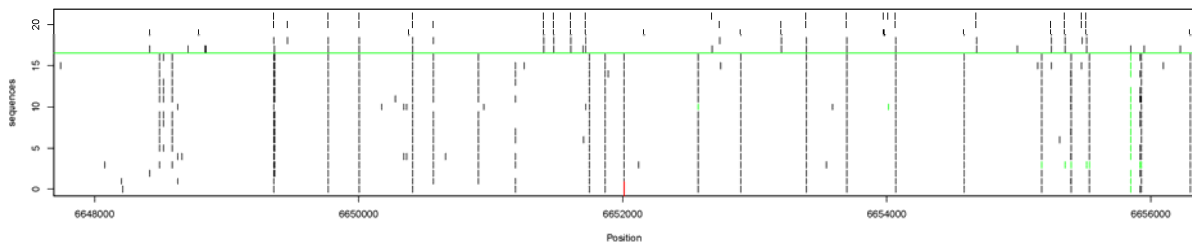
Putative site: 1527302*, closest gene: halo (1517533 – 1518148)



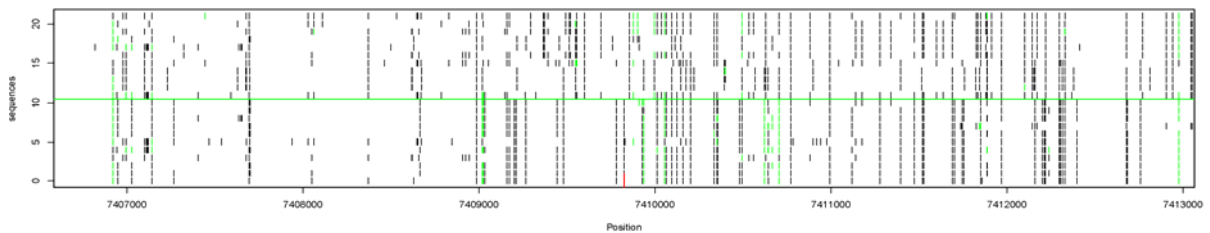
Putative site: 5805001*#\$, closest gene: CG11034 (5805395 – 5809063)



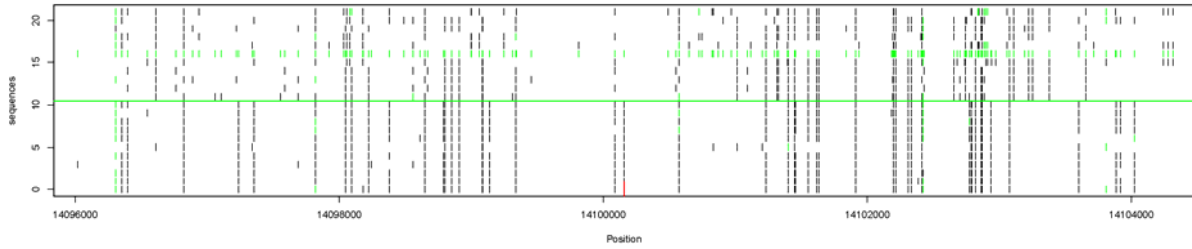
Putative site: 6652011*\$, closest gene: Tango1 (6649388 – 6654574)



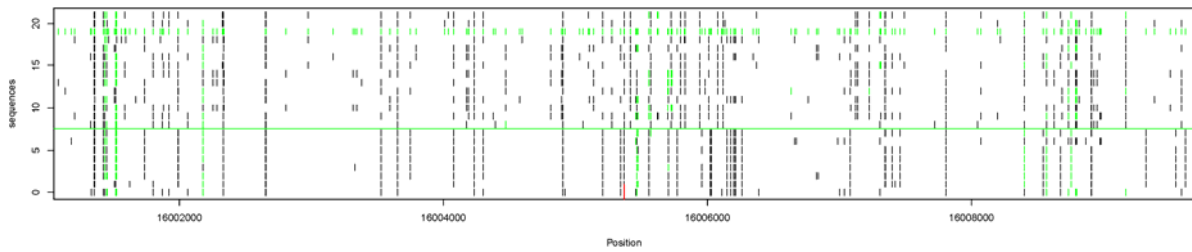
Putative site: 7409825, closest gene: CG5181 (7408533 – 7409809)



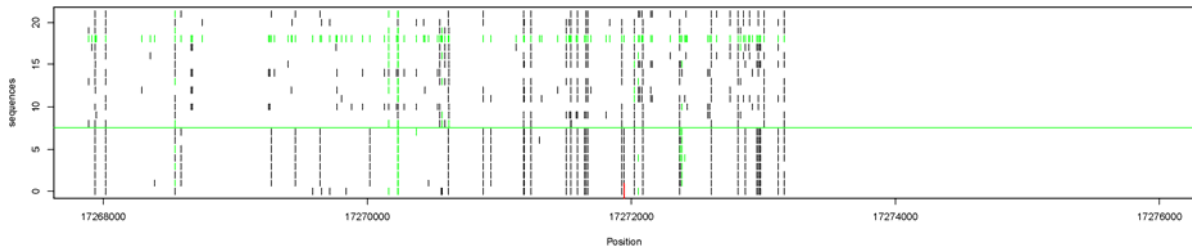
Putative site: 14100158*, closest gene: nAChRalpha5 (14040170 – 14094401)



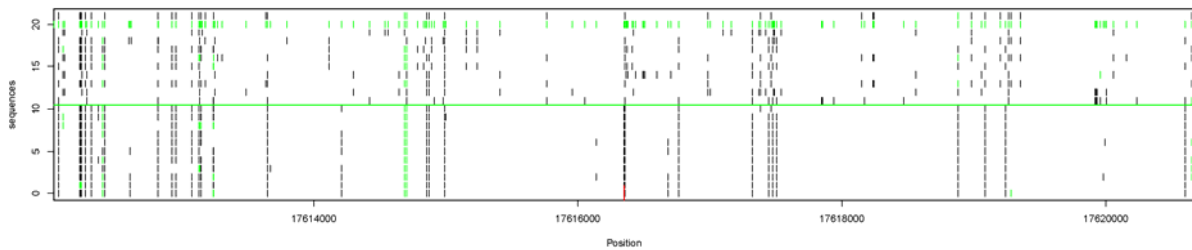
Putative site: 16005369#, closest gene: Beat-1c (16000291 – 16041703)



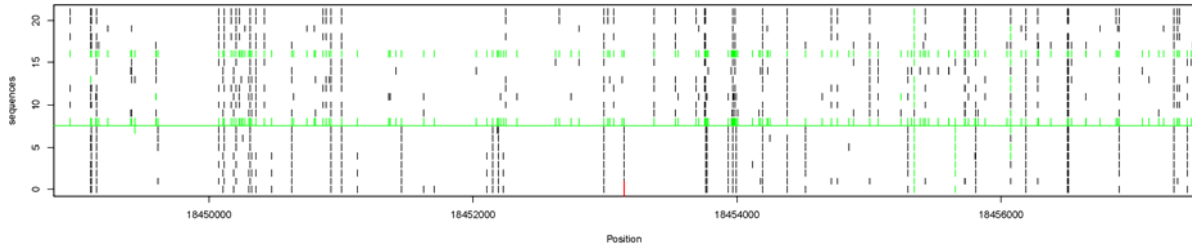
Putative site: 17271945#\$, closest gene: CG6380 (17291075 – 17292202)



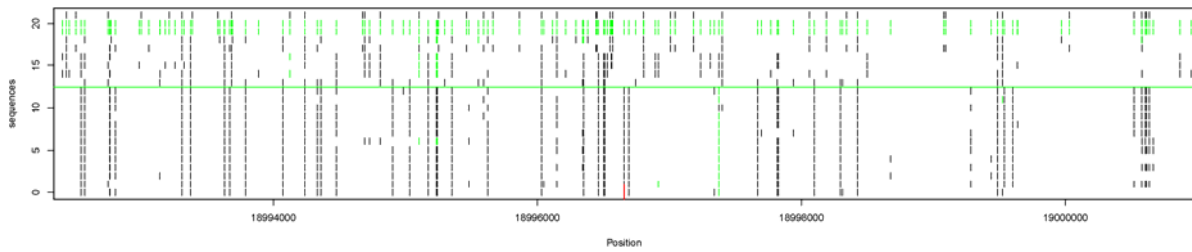
Putative site: 17616351#\$, closest gene: Sytalpha (17592260 – 17604387)



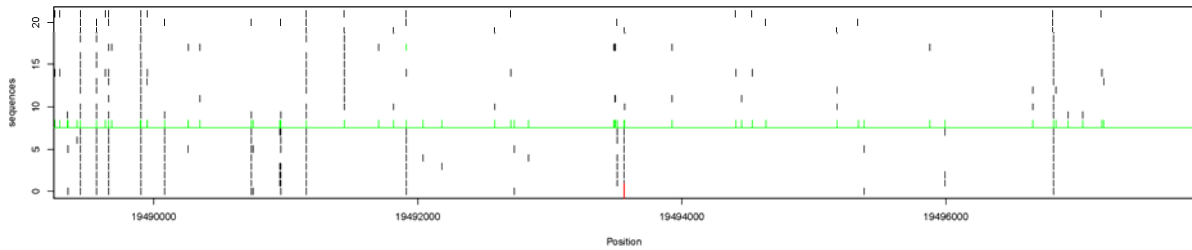
Putative site: 18453145, closest gene: bsf (18449517 – 18454587)



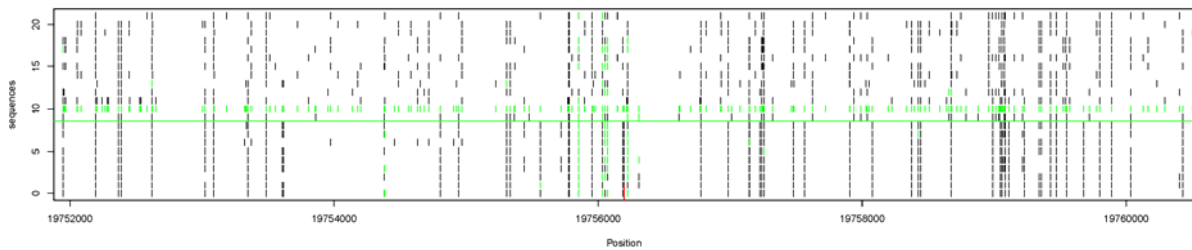
Putative site: 18996657, closest gene: CG10650 (18993360 – 18995934)



Putative site: 19493563, closest gene: swm (19493251 – 19497978)

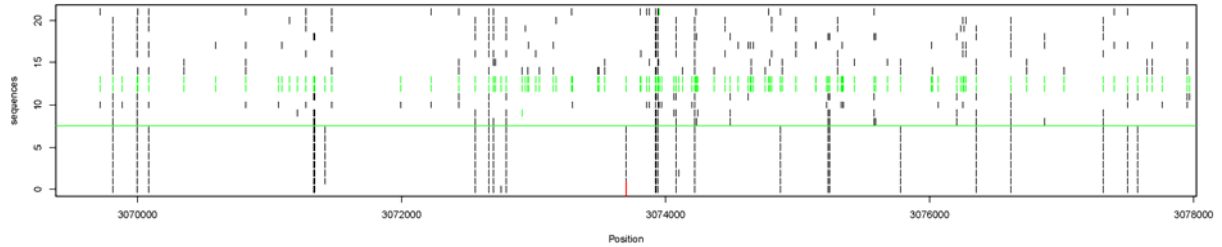


Putative site: 19756197^{#S}, closest gene: CG10631 (19742817 – 19756904)

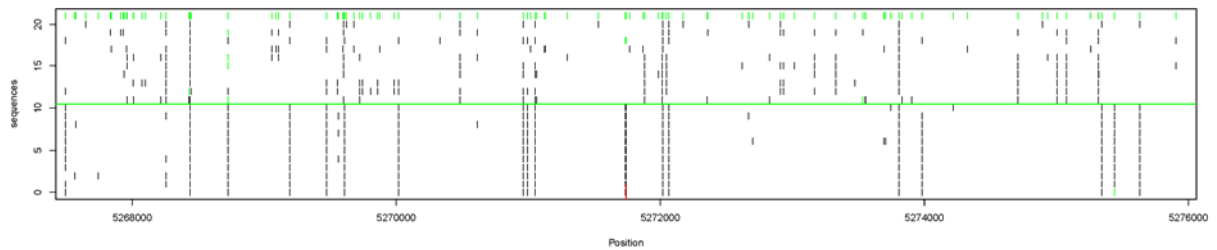


2R Patterns:

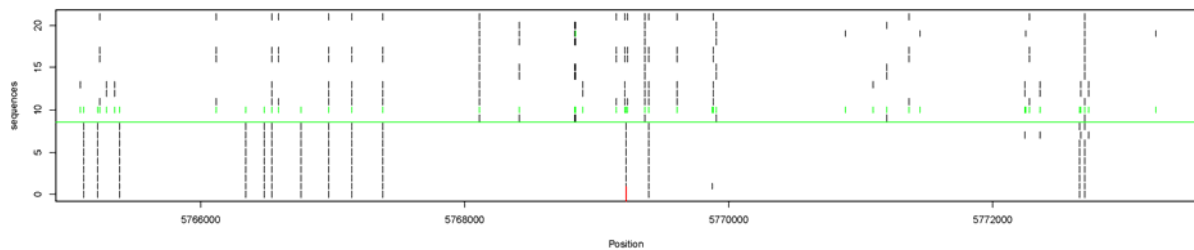
Putative site: 3073701, closest gene: *diddum* (3387652 – 3396130)



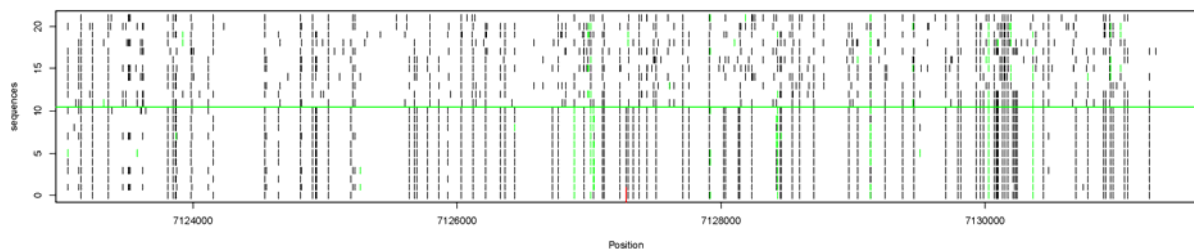
Putative site: 5271741^S, closest gene: *CG13954* (5196801 – 5276972)



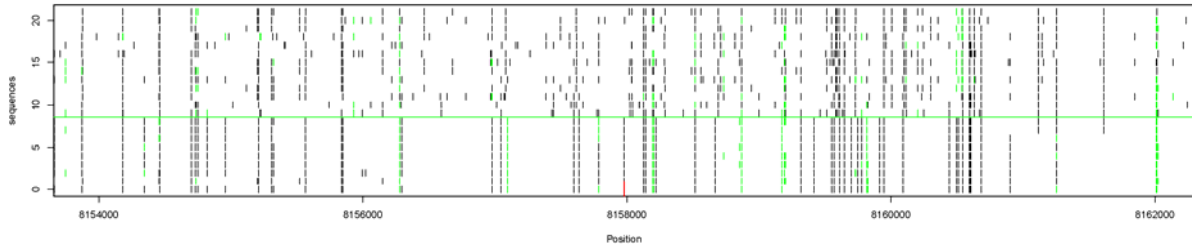
Putative site: 5769223, closest gene: *Sec24AB* (5763737 – 5769862)



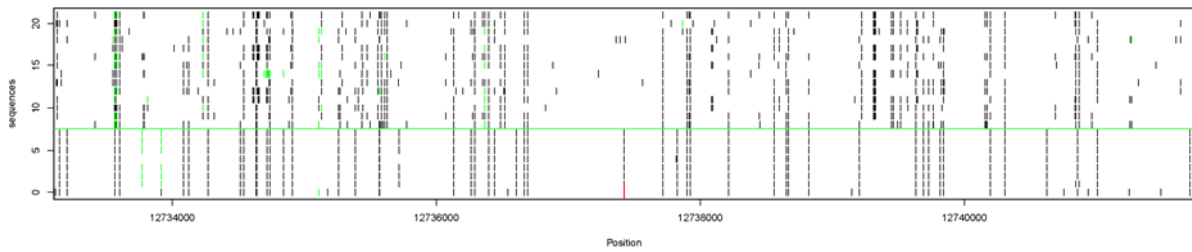
Putative site: 7127281^{#S}, closest gene: *CG13215* (7126999 – 7127619)



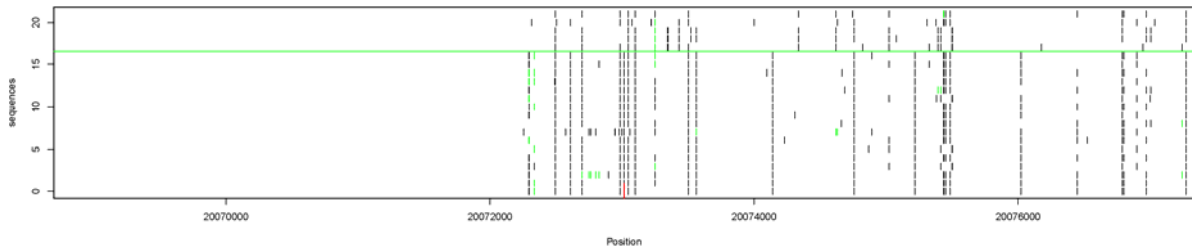
Putative site: 8157979[#]_{\$}, closest gene: otk (7888978 – 7907351)



Putative site: 12737423^{*#}_{\$}, closest gene: IntS8 (12737942 – 12741609)

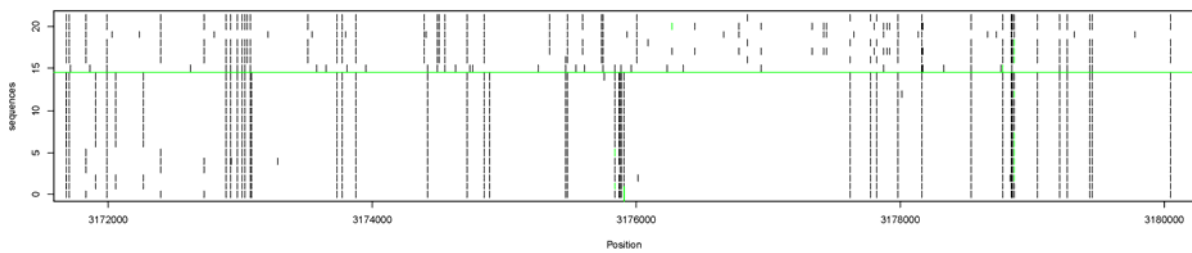


Putative site: 20073016^{*}, closest gene: Nop60B (20062400 – 20073866)

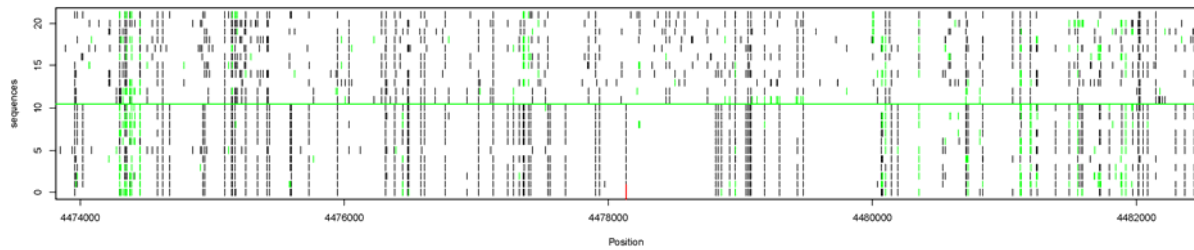


3L Patterns:

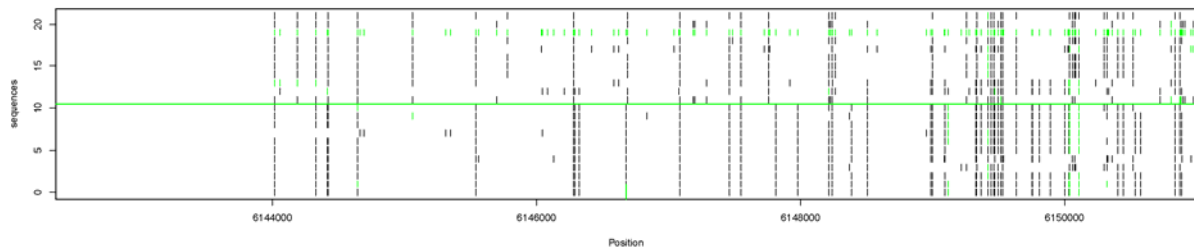
Putative site: 3175908^{*}, closest gene: Girdin (3178930 – 3185287)



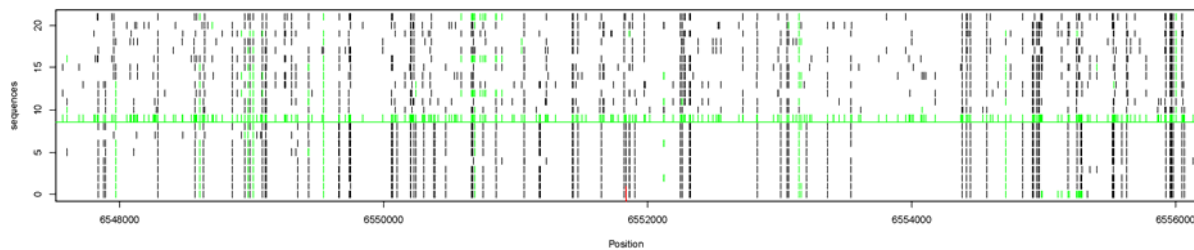
Putative site: 4478135*[#], closest gene: CG7465 (4480283 – 4481487)



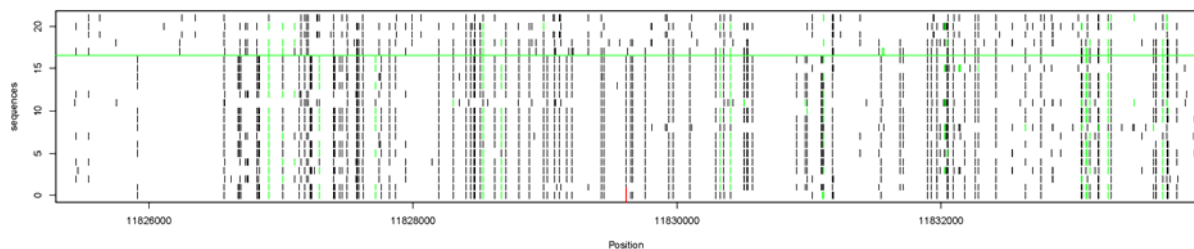
Putative site: 6146679*[#]\$, closest gene: Lcp65Ag2 (6126090 – 6126693)



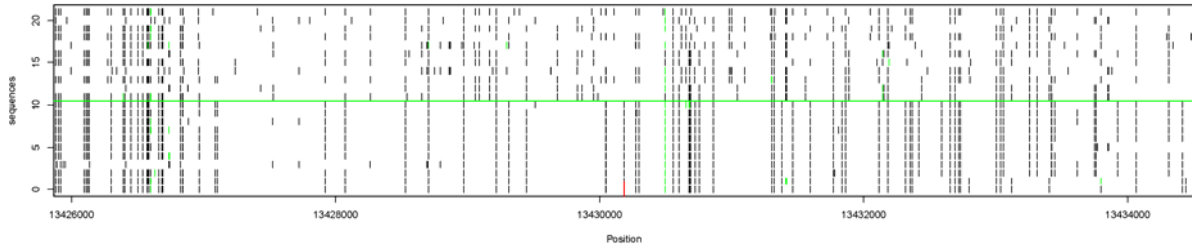
Putative site: 6551837*[#]\$, closest gene: CG18769 (6543838 – 6587040)



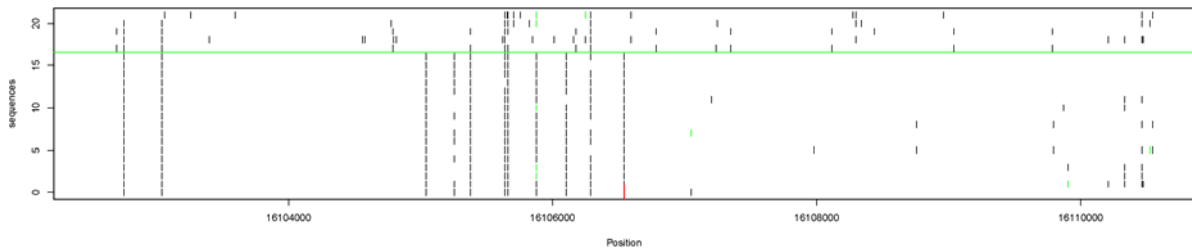
Putative site: 11829615*^{\$}, closest gene: CG43064 (11828293 – 11829821)



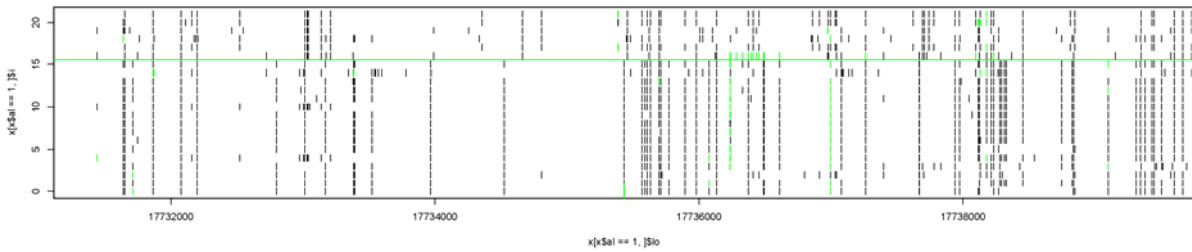
Putative site: 13430186*^S, closest gene: CG10713 (13421939 – 13428329)



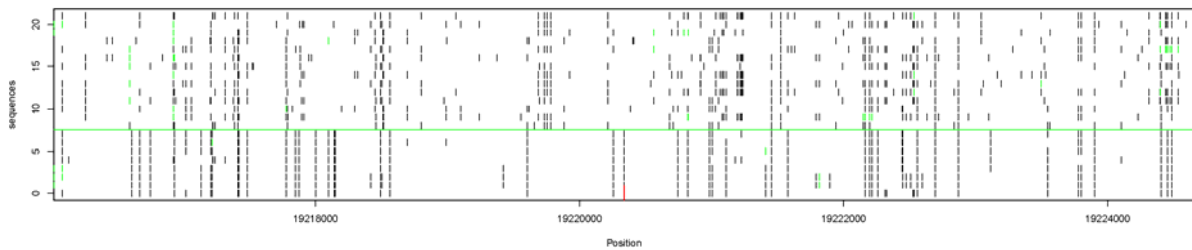
Putative site: 16106542*^S, closest gene: Taf4 (16106312 – 16114751)



Putative site: 17735433, closest gene: CG7460 (17733640 – 17735640)

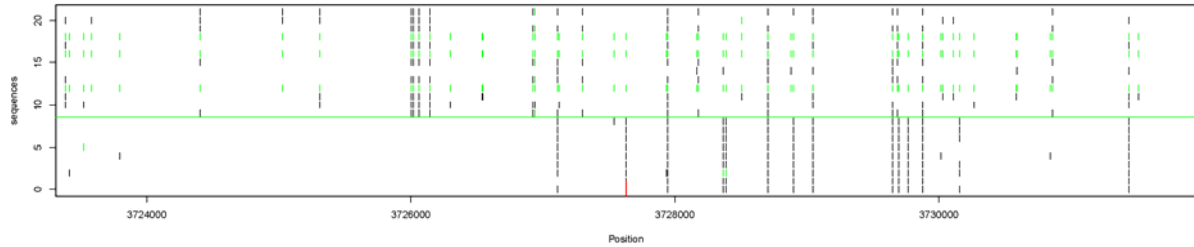


Putative site: 19220338*^S, closest gene: fz2 (19134075 – 19228473)

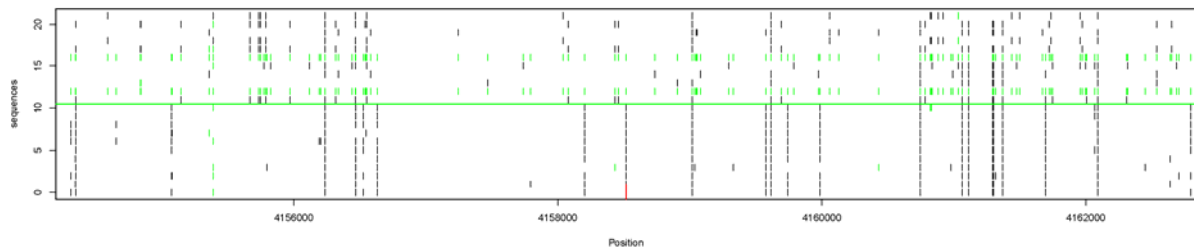


3R Patterns:

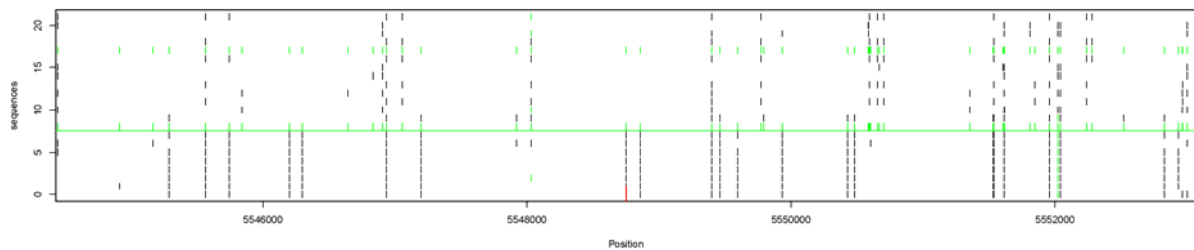
Putative site: 3727631, closest gene: mRpS9 (3714999 – 3728389)



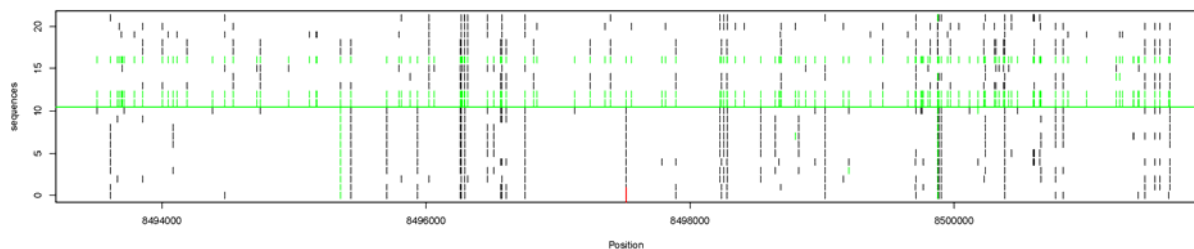
Putative gene: 4158518, closest gene: CG9601 (4167383 – 4169238)



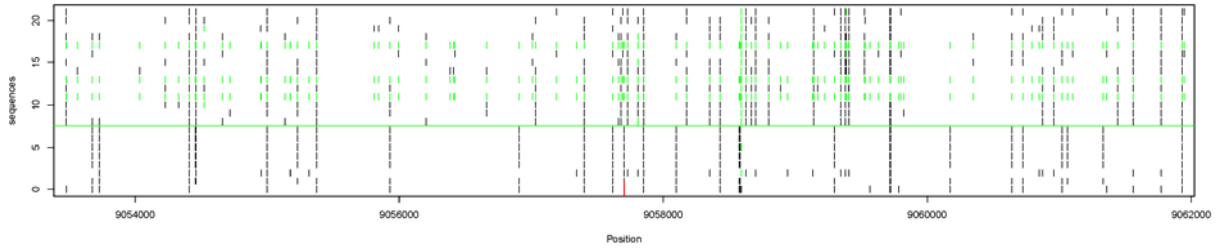
Putative site: 5548751, closest gene: CG8478 (5589372 – 5591857)



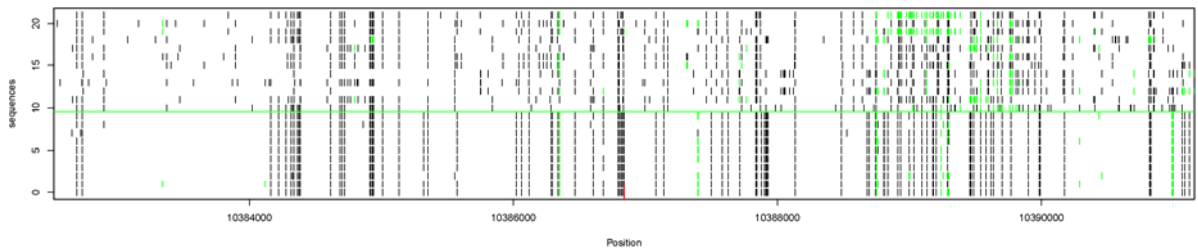
Putative site: 8497516, closest gene: CG14395 (8488553 – 8499681)



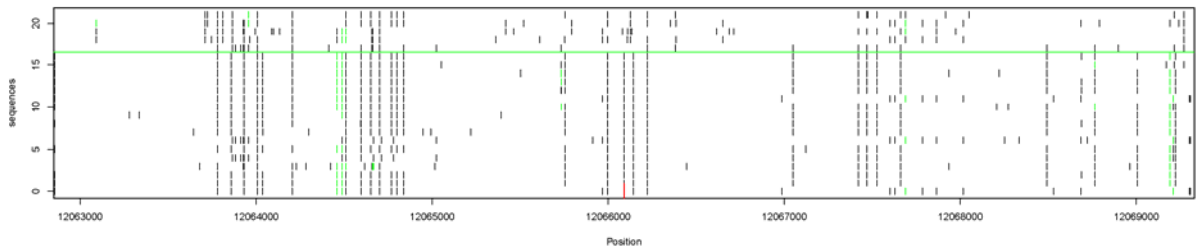
Putative site: 9057704[#], closest gene: Ace (9048673 – 9085239)



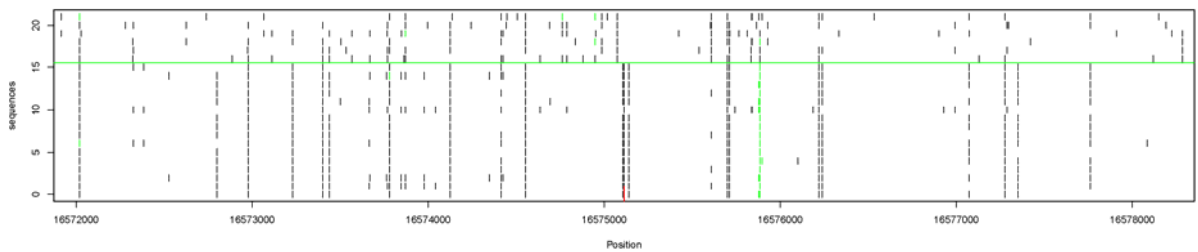
Putative site: 10386839[#]^S, closest gene: Pde6 (10339623 – 10384026)



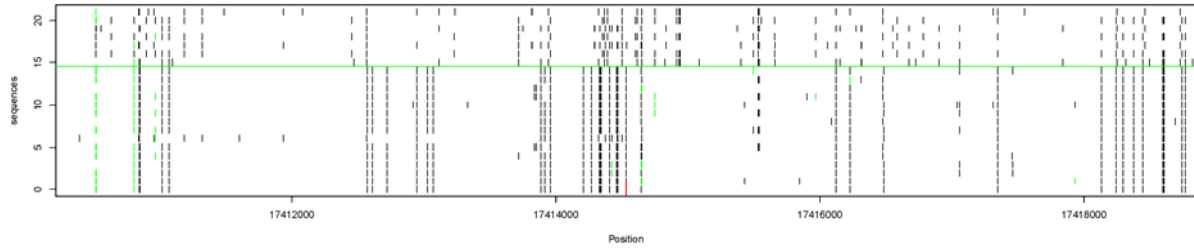
Putative site: 12066090[#]^S, closest gene: tara (12051373 – 12086051)



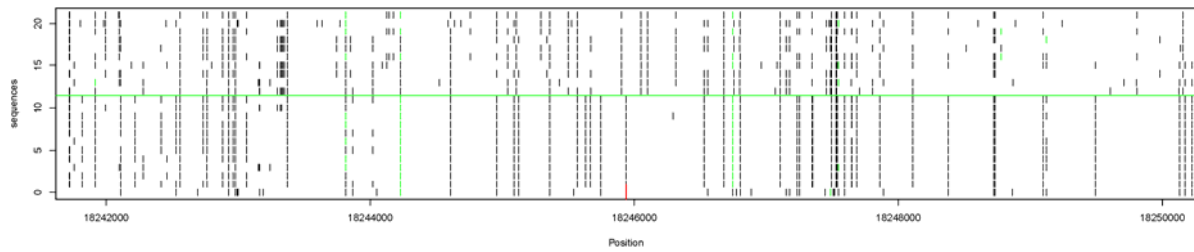
Putative site: 16575113[#]^S, closest gene: CG42322 (16565830 – 16582361)



Putative site: 17414532*, closest gene: InR (17395970 – 17445043)

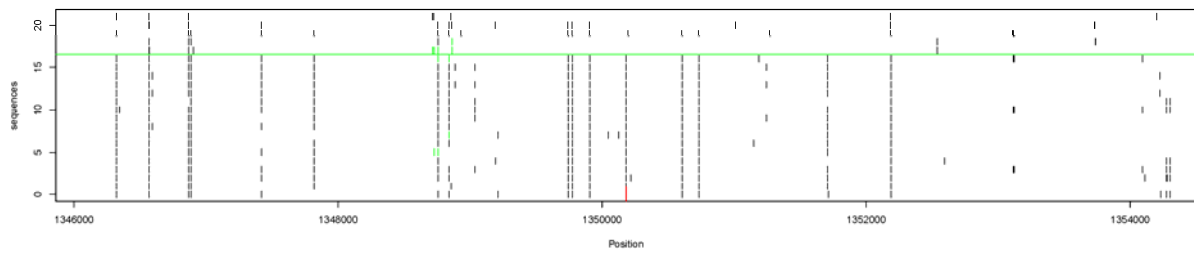


Putative site: 18245938*, closest gene: IqfR (18237023 – 18244773)

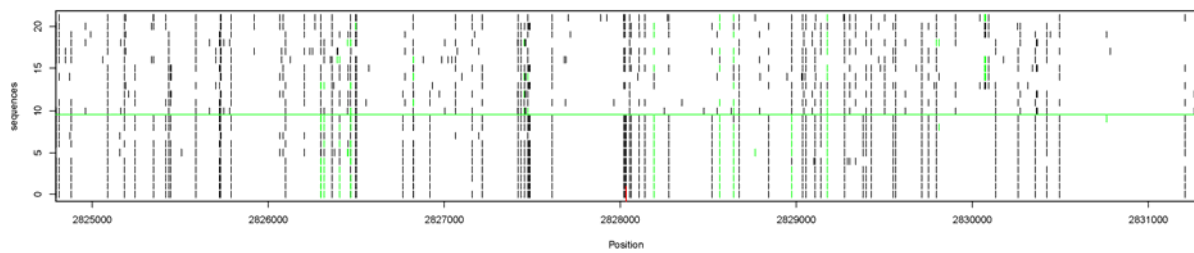


X Patterns:

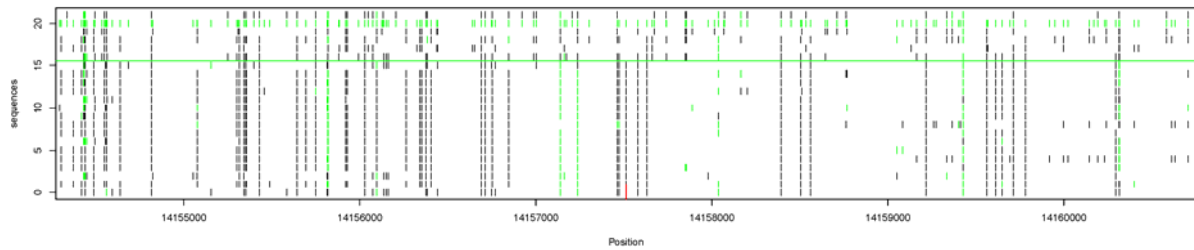
Putative site: 1350182[#], closest gene: MED18 (1759942 – 1760920)



Putative site: 2828033^{#S}, closest gene: kirre (2634417 – 3028565)



Putative site: 14157513*[§], closest gene: CG1461 (14155256 – 14159412)



Putative site: 15620351*, closest gene: CG8184 (15606661 – 15625968)

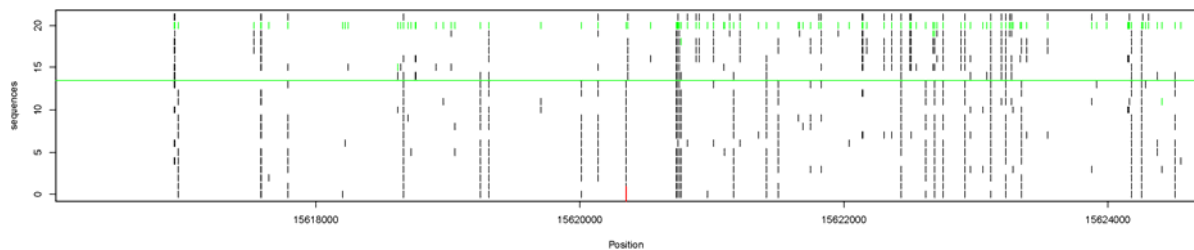


Figure S7 legend: Polymorphism pattern surrounding the site of strongest signal detected by CLR test within each cluster listed in Table 2. In each figure, 22 chromosomes are aligned (number from 0 to 21 vertically) and the putative site under selection (site with strongest signal) is located in the middle (red tick on horizontal axis). Chromosomes are arranged below or above a green line according to allele type (derived or ancestral, respectively) at the putative site. Derived alleles and missing base calls at polymorphic sites are represented by black and green bars, respectively. Whether each region overlaps with a candidate region of complete selective sweep, with a cluster detected by *iHS* test, and by nS_L test are indicated by *, #, and §, respectively.