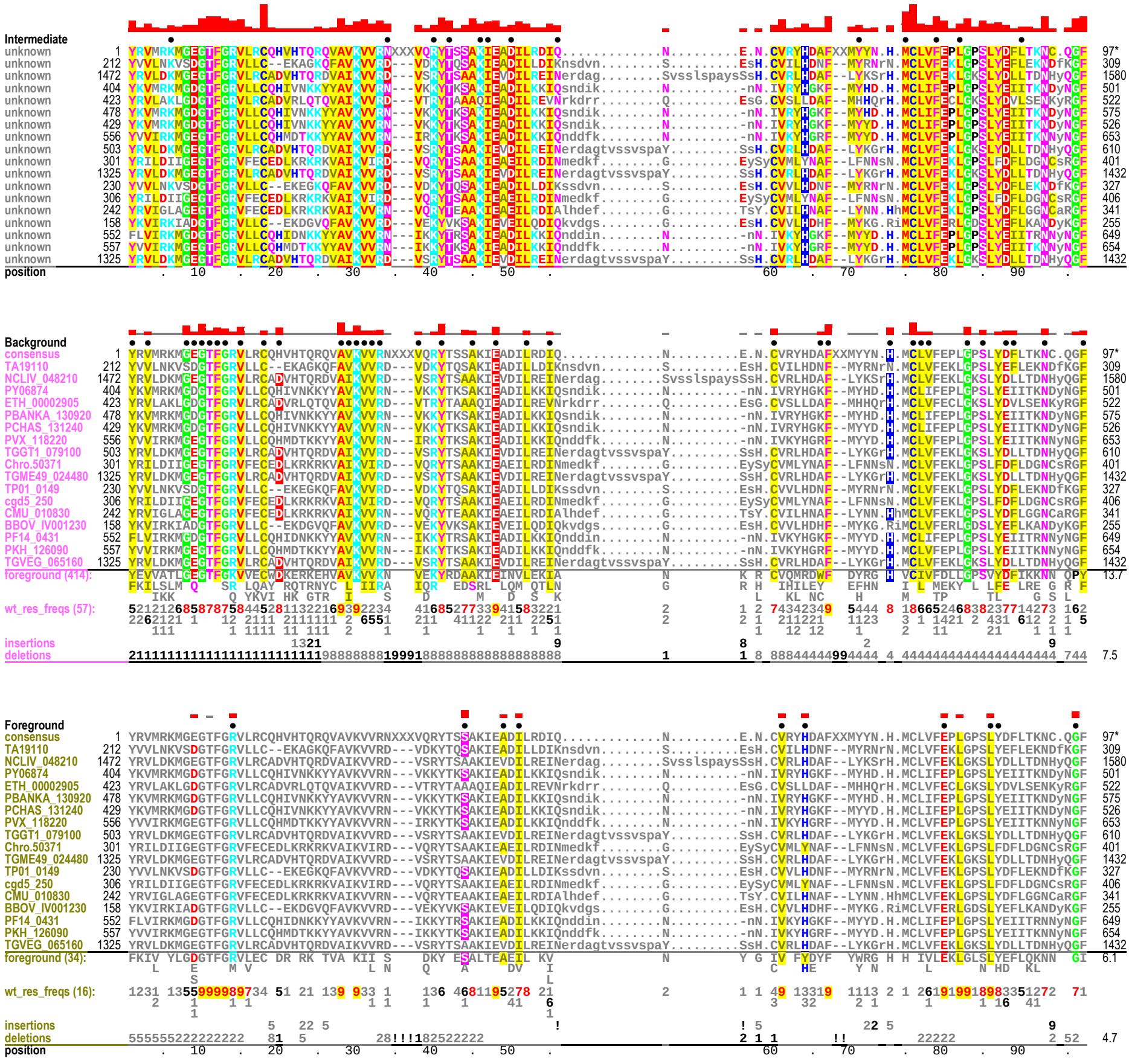
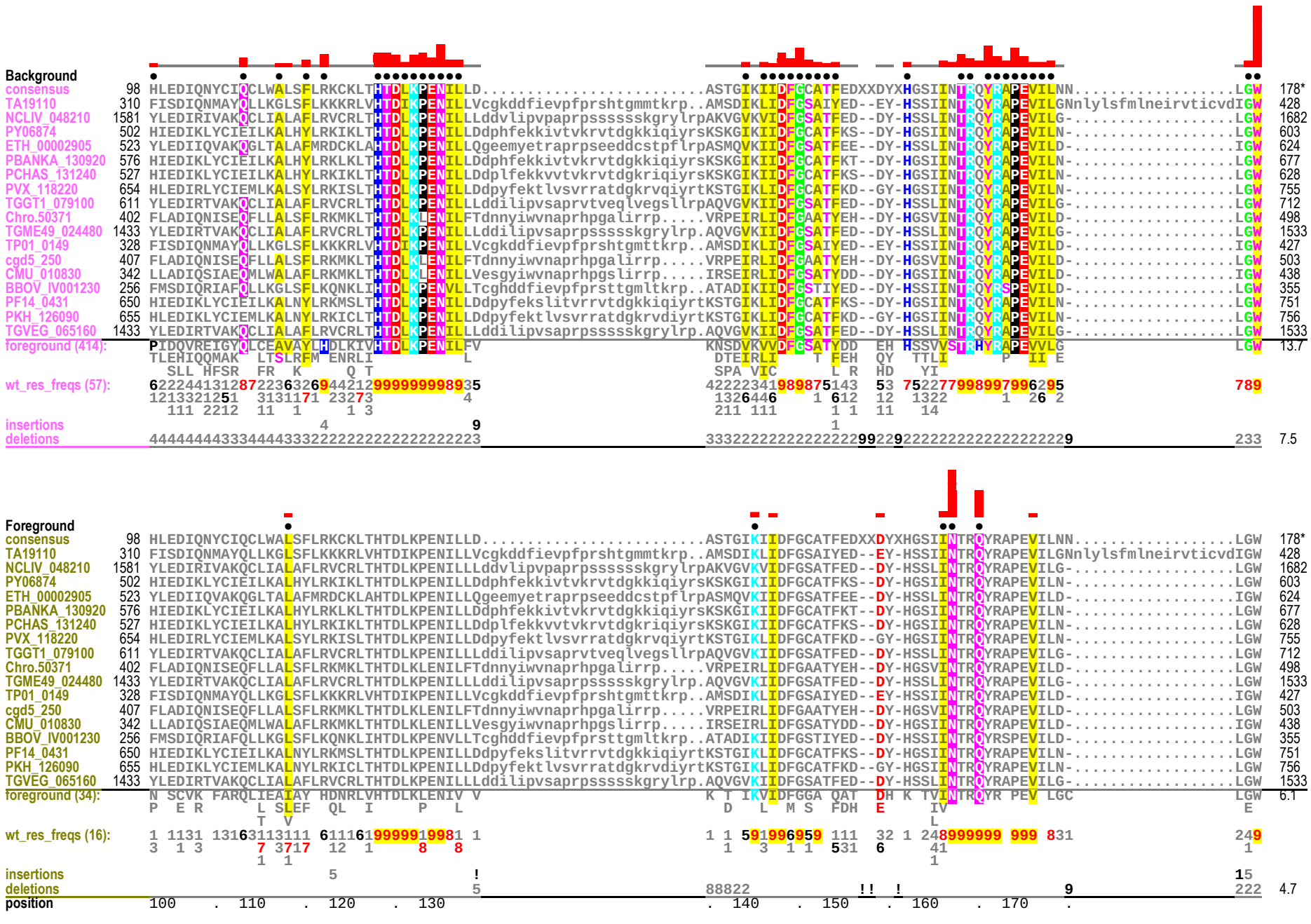
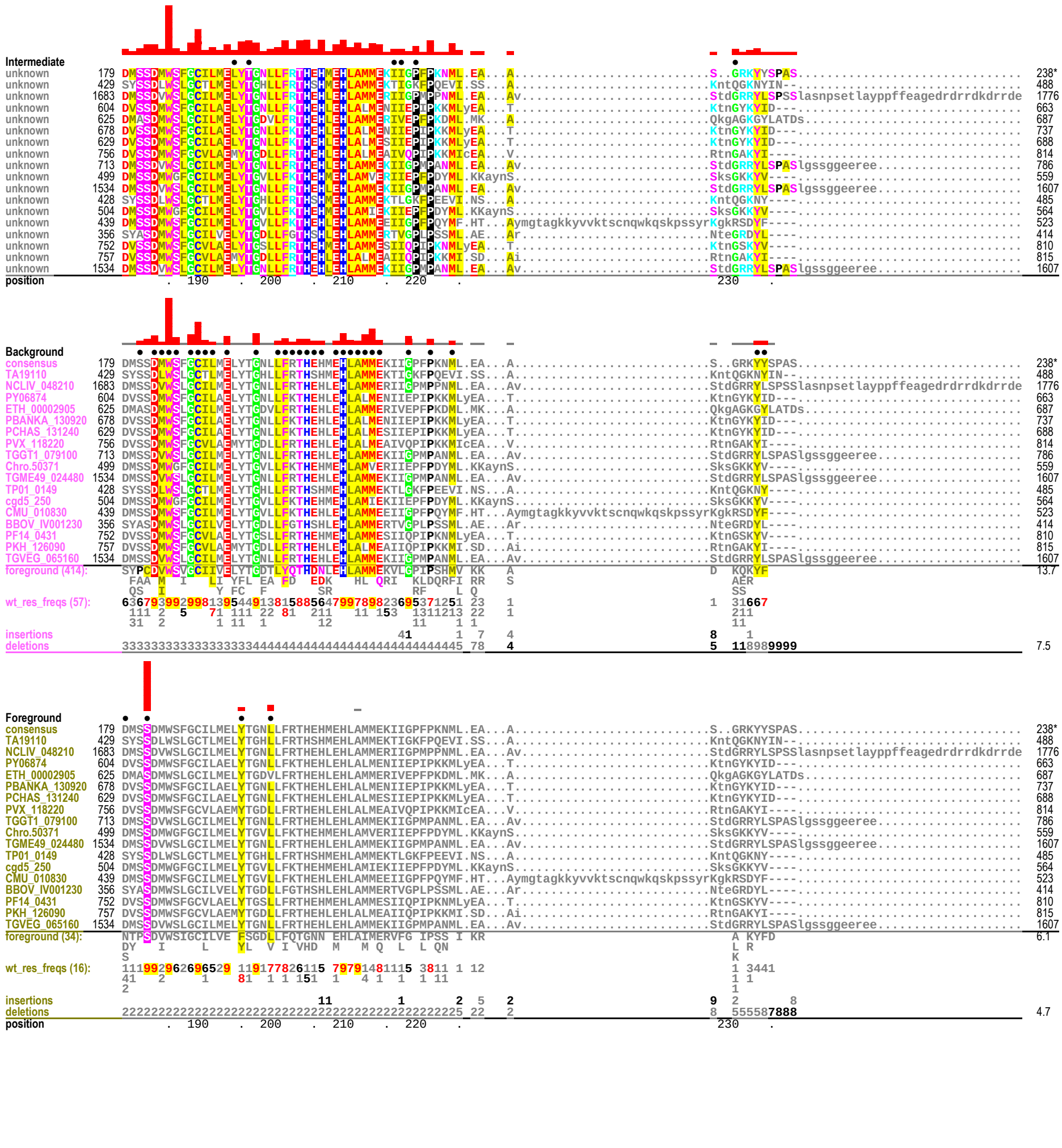
## Apicomplexan CLK vs. eukaryotic CLK



Intermediate
position
100 . 110 . 120 . 130 . 140 . 150 . 160 . 170 .


Background
consensus
TA19110
NCLIV_048210
PY06874
ETH_00002905
PBANKA_130920
PCHAS_131240
PVX_118220
TGGT1_079100
Chro.50371
TGME49_024480
TP01_0149
cgd5_250
CMU_010830
BBOV_IV001230
PF14_0431
PKH_126090
TGVEG_065160
foreground (414):
wt_res_freqs (57):
insertions
deletions
Foreground
foreground (34):
wt_res_freqs (16):
insertions
deletions
position
100 . 110 . 120 . 130 . 140 . 150 . 160 . 170 .


Intermediate
Background
Foreground
consensus
TA19110
NCLIV_048210
PY06874
ETH_00002905
PBANKA_130920
PCHAS_131240
PVX_118220
TGGT1_079100
Chro.50371
TGME49_024480
TP01_0149
cgd5_250
CMU_010830
BBOV_IV001230
PF14_0431
PKH_126090
TGVEG_065160
foreground (414):
wt_res_freqs (57):
insertions
deletions
foreground (34):
wt_res_freqs (16):
position

```
Intermediate
unknown      239 ....N.............................SI.RVK..VPLQNLV...XXHHRLFCDFVYYILQIDPQARPTPEDALKHPFF  285*
unknown      489 ....Rdeprldwpegsksks..............SVhRVEecKTIMELVkp..--EHRLFGEFIRYILNLDSNKRPTPEEAMQHEFF  553
unknown     1777 reqtTsrlrlhwpegasstn..............SEeRVRncVPLHALVlp..--HHRAFADFVSSLLQIDPQARPTPGDALLHPFF  1845
unknown      664 ....Kknlrlawpenassid..............SIkHVKksLPLYNIIk..---HDLFCDFLYNILRIDPTRRASPIDLLKHEF-  725
unknown      688 ....Rggvhlkwpegaaslg...............SVnRVKncVPLEDLVlpq---DRILAEFVRYLLQVDPRKRPEPKEALRHPIF  752
unknown      738 ....Kndlklawpenassid...............SIkHVKksLPLYKIIk..---HDLFCDFLYTILRIDPTLRASPVDLLKHEF-  799
unknown      689 ....Kndlrlawpenassid...............SIkHVKrsLPLYKII...--RHDLFCDFLYTILRIDPTRRASPIDLLKHEF-  750
unknown      815 ....Nrdglrlawpenassfe..............SIkYVKrcLPLHKLI...--RNDLFCDFLYSILQIDPALRPAPAELLKHRF-  877
unknown      787 ....Ssrlrlnwpegssstn...............SEeRVRncVPLQALVlp..--HHRIFSDFVASLLQIDPQARPTPGDALMHPFF  851
unknown      560 ....NrlkisnninhhqneeykyvlnwpegsssntSIkRVNdcRPLENLVhk..--KHIMLAKFIRYILRPDPNLRPTPEMALRHEFF  639
unknown     1608 ....Ssrlrlnwpegssstn...............SEeRVRncVPLQALVlp..--HHRIFSDFVASLLQIDPQARPTPGDALMHPFF  1672
unknown      486 ....Ispneprlnwpegaksks.............SVhRVEecKTIMDLVkp..--EHRLFGEFIRYILNLDSNKRPTPEEAMQHEFF  552
unknown      565 ....NrlkisnnnnhhpseeykyilnwpegsssntSIkRVNdcRPLENLVhk..--KHIMLAKFIRYILRPDPNLRPTPEMALRHEFF  644
unknown      524 ....Kqstiptnytescdyeyqlyweeshinps..SFaRVQrcQPIEDYIhp..--KHKVFASFVRYILNLDPKLRPTPEMALKHEFF  601
unknown      415 ....Hptkdslnwpegaqsss..............SEeRVSccRSVMEIIrp..--EHRPFAEFIKYILNPDPSQRPTPEDAMEHEFF  480
unknown      811 ....Nkdelklawpenassin..............SIkHVKkcLPLYKIIk..---HELFCDFLYSILQIDPTLRPSPAELLKHKF-  873
unknown      816 ....Nrdhlrlawpenassfe..............SIkYVKrcLPLYKLI...--RNDLFCDFLYSVLQIDPALRSSPAELLKHRF-  878
unknown     1608 ....Ssrlrlnwpegssstn...............SEeRVRncVPLQALVlp..--HHRIFSDFVASLLQIDPQARPTPGDALMHPFF  1672
position                                         240       .  250       .  260     .  270     .  280     .

Background
consensus    239 ....N.............................SI.RVK..VPLQNLV...XXHHRLFCDFVYYILQIDPQARPTPEDALKHPFF  285*
TA19110      489 ....Rdeprldwpegsksks..............SVhRVEecKTIMELVkp..--EHRLFGEFIRYILNLDSNKRPTPEEAMQHEFF  553
NCLIV_048210 1777 reqtTsrlrlhwpegasstn..............SEeRVRncVPLHALVlp..--HHRAFADFVSSLLQIDPQARPTPGDALLHPFF  1845
PY06874      664 ....Kknlrlawpenassid..............SIkHVKksLPLYNIIk..---HDLFCDFLYNILRIDPTRRASPIDLLKHEF-  725
ETH_00002905 688 ....Rggvhlkwpegaaslg...............SVnRVKncVPLEDLVlpq---DRILAEFVRYLLQVDPRKRPEPKEALRHPIF  752
PBANKA_130920 738 ....Kndlklawpenassid..............SIkHVKksLPLYKIIk..---HDLFCDFLYTILRIDPTLRASPVDLLKHEF-  799
PCHAS_131240 689 ....Kndlrlawpenassid...............SIkHVKrsLPLYKII...--RHDLFCDFLYTILRIDPTRRASPIDLLKHEF-  750
PVX_118220   815 ....Nrdglrlawpenassfe..............SIkYVKrcLPLHKLI...--RNDLFCDFLYSILQIDPALRPAPAELLKHRF-  877
TGGT1_079100 787 ....Ssrlrlnwpegssstn...............SEeRVRncVPLQALVlp..--HHRIFSDFVASLLQIDPQARPTPGDALMHPFF  851
Chro.50371   560 ....NrlkisnninhhqneeykyvlnwpegsssntSIkRVNdcRPLENLVhk..--KHIMLAKFIRYILRPDPNLRPTPEMALRHEFF  639
TGME49_024480 1608 ....Ssrlrlnwpegssstn...............SEeRVRncVPLQALVlp..--HHRIFSDFVASLLQIDPQARPTPGDALMHPFF  1672
TP01_0149    486 ....Ispneprlnwpegaksks..............SVhRVEecKTIMDLVkp..--EHRLFGEFIRYILNLDSNKRPTPEEAMQHEFF  552
cgd5_250     565 ....NrlkisnnnnhhpseeykyilnwpegsssntSIkRVNdcRPLENLVhk..--KHIMLAKFIRYILRPDPNLRPTPEMALRHEFF  644
CMU_010830   524 ....Kqstiptnytescdyeyqlyweeshinps..SFaRVQrcQPIEDYIhp..--KHKVFASFVRYILNLDPKLRPTPEMALKHEFF  601
BBOV_IV001230 415 ....Hptkdslnwpegaqsss..............SEeRVSccRSVMEIIrp..--EHRPFAEFIKYILNPDPSQRPTPEDAMEHEFF  480
PF14_0431    811 ....Nkdelklawpenassin..............SIkHVKkcLPLYKIIk..---HELFCDFLYSILQIDPTLRPSPAELLKHKF-  873
PKH_126090   816 ....Nrdhlrlawpenassfe..............SIkYVKrcLPLYKLI...--RNDLFCDFLYSVLQIDPALRSSPAELLKHRF-  878
TGVEG_065160 1608 ....Ssrlrlnwpegssstn...............SEeRVRncVPLQALVlp..--HHRIFSDFVASLLQIDPQARPTPGDALMHPFF  1672
foreground (414):      Y                             SV AVK  KPLKDYI   DEDHGELFDLVQKMLEYDPAKRITAKEALQHPWF  13.7
                       R                             YI Y R  RR REFM   SHEDRQFL  LRRLFVFE SE L LRQ  R  F
                       N                                R E    QNVL     F  L I  IKG  R    Q     D  K  Y
wt_res_freqs (57):     1                             33 132  4472123   3113115368122473667239475257718617
                       2                             32 1 1  12 2212   11211131  42131111 11 2 211  1  5
                       1                                1 1     1111     1  1 1  312  1    1     1  1  1
insertions             9                              8  19        48   21 1
deletions              2                             88 549  8888888   11888888888888888888888888888891  7.5

Foreground
consensus    239 ....N.............................SI.RVK..VPLQNLV...XXHHRLFCDFVYYILQIDPQARPTPEDALKHPFF  285*
TA19110      489 ....Rdeprldwpegsksks..............SVhRVEecKTIMELVkp..--EHRLFGEFIRYILNLDSNKRPTPEEAMQHEFF  553
NCLIV_048210 1777 reqtTsrlrlhwpegasstn..............SEeRVRncVPLHALVlp..--HHRAFADFVSSLLQIDPQARPTPGDALLHPFF  1845
PY06874      664 ....Kknlrlawpenassid..............SIkHVKksLPLYNIIk..---HDLFCDFLYNILRIDPTRRASPIDLLKHEF-  725
ETH_00002905 688 ....Rggvhlkwpegaaslg...............SVnRVKncVPLEDLVlpq---DRILAEFVRYLLQVDPRKRPEPKEALRHPIF  752
PBANKA_130920 738 ....Kndlklawpenassid..............SIkHVKksLPLYKIIk..---HDLFCDFLYTILRIDPTLRASPVDLLKHEF-  799
PCHAS_131240 689 ....Kndlrlawpenassid...............SIkHVKrsLPLYKII...--RHDLFCDFLYTILRIDPTRRASPIDLLKHEF-  750
PVX_118220   815 ....Nrdglrlawpenassfe..............SIkYVKrcLPLHKLI...--RNDLFCDFLYSILQIDPALRPAPAELLKHRF-  877
TGGT1_079100 787 ....Ssrlrlnwpegssstn...............SEeRVRncVPLQALVlp..--HHRIFSDFVASLLQIDPQARPTPGDALMHPFF  851
Chro.50371   560 ....NrlkisnninhhqneeykyvlnwpegsssntSIkRVNdcRPLENLVhk..--KHIMLAKFIRYILRPDPNLRPTPEMALRHEFF  639
TGME49_024480 1608 ....Ssrlrlnwpegssstn...............SEeRVRncVPLQALVlp..--HHRIFSDFVASLLQIDPQARPTPGDALMHPFF  1672
TP01_0149    486 ....Ispneprlnwpegaksks..............SVhRVEecKTIMDLVkp..--EHRLFGEFIRYILNLDSNKRPTPEEAMQHEFF  552
cgd5_250     565 ....NrlkisnnnnhhpseeykyilnwpegsssntSIkRVNdcRPLENLVhk..--KHIMLAKFIRYILRPDPNLRPTPEMALRHEFF  644
CMU_010830   524 ....Kqstiptnytescdyeyqlyweeshinps..SFaRVQrcQPIEDYIhp..--KHKVFASFVRYILNLDPKLRPTPEMALKHEFF  601
BBOV_IV001230 415 ....Hptkdslnwpegaqsss..............SEeRVSccRSVMEIIrp..--EHRPFAEFIKYILNPDPSQRPTPEDAMEHEFF  480
PF14_0431    811 ....Nkdelklawpenassin..............SIkHVKkcLPLYKIIk..---HELFCDFLYSILQIDPTLRPSPAELLKHKF-  873
PKH_126090   816 ....Nrdhlrlawpenassfe..............SIkYVKrcLPLYKLI...--RNDLFCDFLYSVLQIDPALRSSPAELLKHRF-  878
TGVEG_065160 1608 ....Ssrlrlnwpegssstn...............SEeRVRncVPLQALVlp..--HHRIFSDFVASLLQIDPQARPTPGDALMHPFF  1672
foreground (34):       D                              V Y     SLYKIV        DLIDLIQNLFELEH KRITAKEA DHPFF  6.1
                                                              P   LI                ML IDP       R I
                                                              Q   M
wt_res_freqs (16):     1                              1 1     161122        15166211211111 2934213 5 18197
                                                              4   56               47 778      1 1
                                                              1   1
insertions             9                              9   9       8
deletions              5                             22 222  2222222   993855222222222222222222222555 3  4.7
position                                         240       .  250       .  260     .  270     .  280     .
```