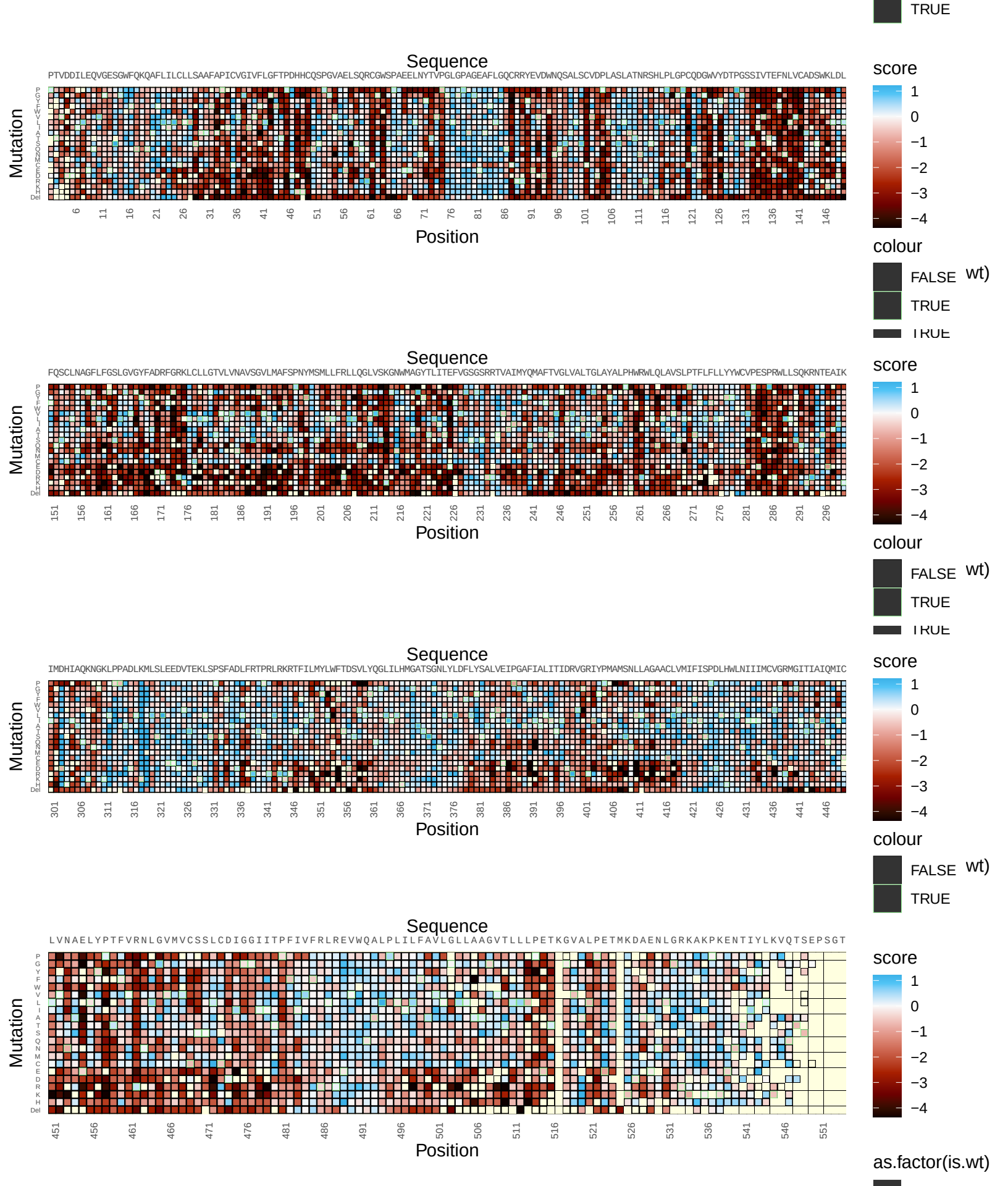
TRUE
Sequence
PTVDDILEQVGESGWFQKQAFLILCLLSAAFAPICVGIVFLGFTPDHHCQSPGVAELSQRCGWSPAEELNYTVPGLGPAGEAFLGQCRRYEVDWNQSALSCVDPLASLATNRSHLPLGPCQDGWVYDTPGSSIVTEFNLVCADSWKLDL
Mutation
P G Y F W V L I A T S Q N M C E D R K H Del
6 11 16 21 26 31 36 41 46 51 56 61 66 71 76 81 86 91 96 101 106 111 116 121 126 131 136 141 146
Position
score
1
0
−1
−2
−3
−4
colour
FALSE
TRUE
wt)
TRUE
Sequence
FQSCLNAGFLFGSLGVGYFADRFGRKLCLLGTVLVNAVSGVLMAFSPNYMSMLLFRLLQGLVSKGNWMAGYTLITEFVGSGSRRTVAIMYQMAFTVGLVALTGLAYALPHWRWLQLAVSLPTFLFLLYYWCVPESPRWLLSQKRNTEAIK
Mutation
P G Y F W V L I A T S Q N M C E D R K H Del
151 156 161 166 171 176 181 186 191 196 201 206 211 216 221 226 231 236 241 246 251 256 261 266 271 276 281 286 291 296
Position
score
1
0
−1
−2
−3
−4
colour
FALSE
TRUE
wt)
TRUE
Sequence
IMDHIAQKNGKLPPADLKMLSLEEDVTEKLSPSFADLFRTPRLRKRTFILMYLWFTDSVLYQGLILHMGATSGNLYLDFLYSALVEIPGAFIALITIDRVGRIYPMAMSNLLAGAACLVMIFISPDLHWLNIIIMCVGRMGITIAIQMIC
Mutation
P G Y F W V L I A T S Q N M C E D R K H Del
301 306 311 316 321 326 331 336 341 346 351 356 361 366 371 376 381 386 391 396 401 406 411 416 421 426 431 436 441 446
Position
score
1
0
−1
−2
−3
−4
colour
FALSE
TRUE
wt)
Sequence
LVNAELYPTFVRNLGVMVCSSLCDIGGIITPFIVFRLREVWQALPLILFAVLGLLAAGVTLLLPETKGVALPETMKDAENLGRKAKPKENTIYLKVQTSEPSGT
Mutation
P G Y F W V L I A T S Q N M C E D R K H Del
451 456 461 466 471 476 481 486 491 496 501 506 511 516 521 526 531 536 541 546 551
Position
score
1
0
−1
−2
−3
−4
as.factor(is.wt)