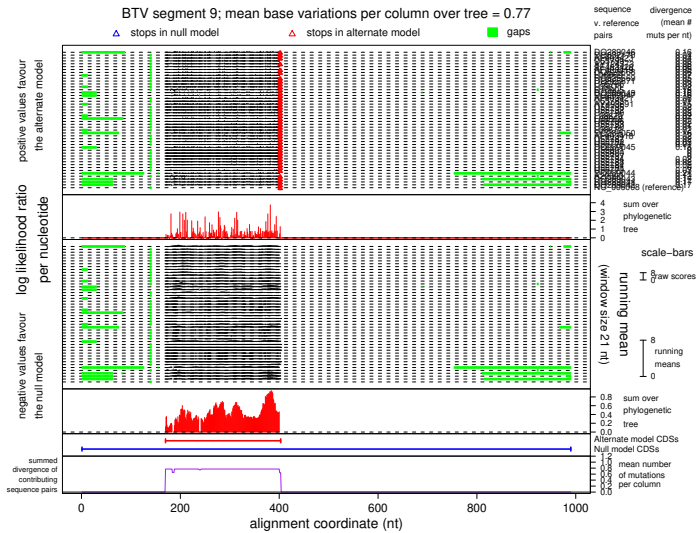
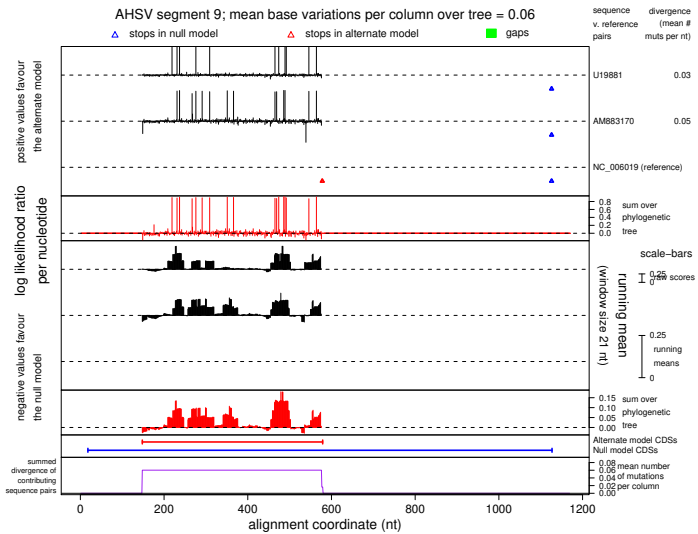
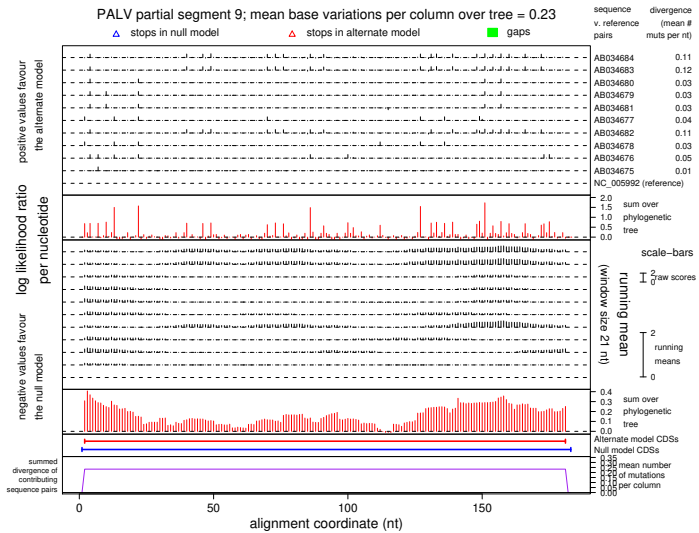
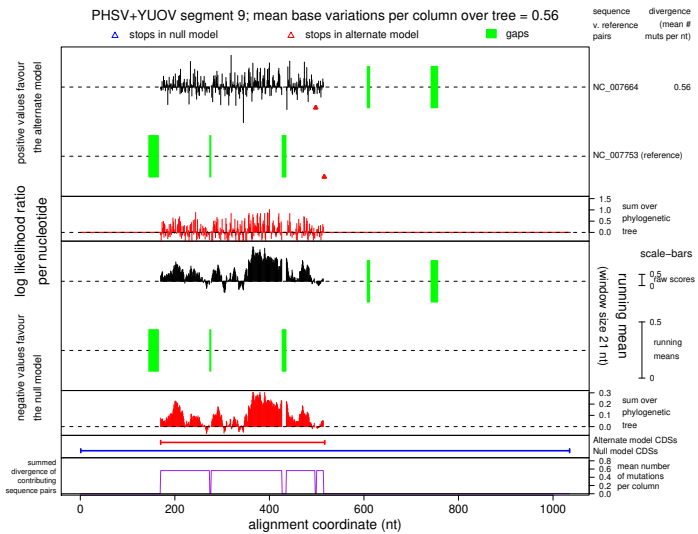

BTV segment 9; mean base variations per column over tree = 0.77
stops in null model
stops in alternate model
gaps
sequence v. reference pairs
divergence (mean # muts per nt)
positive values favour the alternate model
log likelihood ratio per nucleotide
negative values favour the null model
sum over phylogenetic tree
scale-bars
raw scores
running mean (window size 21 nt)
running means
Alternate model CDSs
Null model CDSs
summed divergence of contributing sequence pairs
mean number of mutations per column
alignment coordinate (nt)


AHSV segment 9; mean base variations per column over tree = 0.06
stops in null model
stops in alternate model
gaps
sequence v. reference pairs
divergence (mean # muts per nt)
U19881 0.03
AM883170 0.05
NC_006019 (reference)
positive values favour the alternate model
log likelihood ratio per nucleotide
negative values favour the null model
sum over phylogenetic tree
scale-bars
raw scores
running mean (window size 21 nt)
running means
Alternate model CDSs
Null model CDSs
summed divergence of contributing sequence pairs
mean number of mutations per column
alignment coordinate (nt)


PALV partial segment 9; mean base variations per column over tree = 0.23
stops in null model
stops in alternate model
gaps
sequence v. reference pairs
divergence (mean # muts per nt)
AB034684 0.11
AB034683 0.12
AB034680 0.03
AB034679 0.03
AB034681 0.03
AB034677 0.04
AB034682 0.11
AB034678 0.03
AB034676 0.05
AB034675 0.01
NC_005992 (reference)
positive values favour the alternate model
log likelihood ratio per nucleotide
negative values favour the null model
sum over phylogenetic tree
scale-bars
raw scores
running mean (window size 21 nt)
running means
Alternate model CDSs
Null model CDSs
summed divergence of contributing sequence pairs
mean number of mutations per column
alignment coordinate (nt)


PHSV+YUOV segment 9; mean base variations per column over tree = 0.56
stops in null model
stops in alternate model
gaps
sequence v. reference pairs
divergence (mean # muts per nt)
NC_007664 0.56
NC_007753 (reference)
positive values favour the alternate model
log likelihood ratio per nucleotide
negative values favour the null model
sum over phylogenetic tree
scale-bars
raw scores
running mean (window size 21 nt)
running means
Alternate model CDSs
Null model CDSs
summed divergence of contributing sequence pairs
mean number of mutations per column
alignment coordinate (nt)