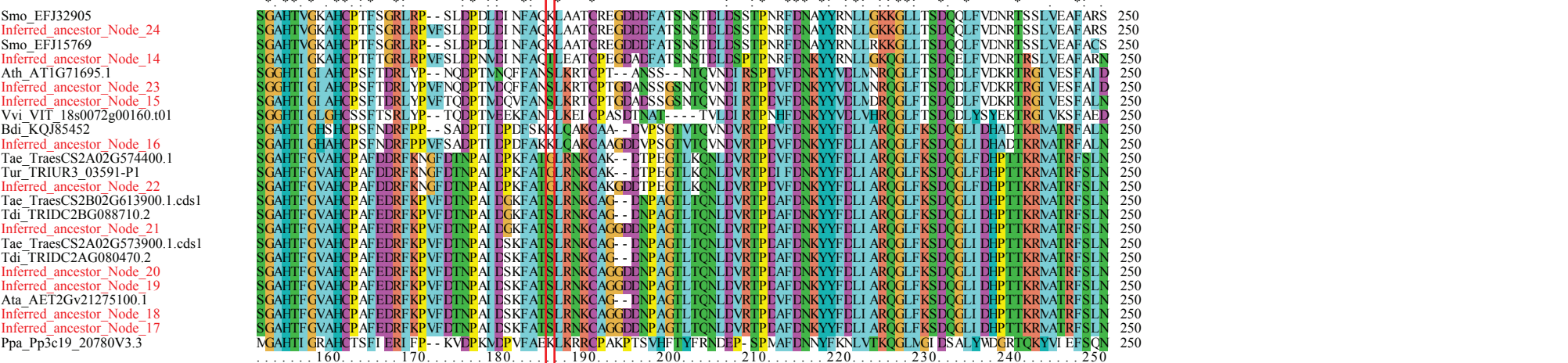
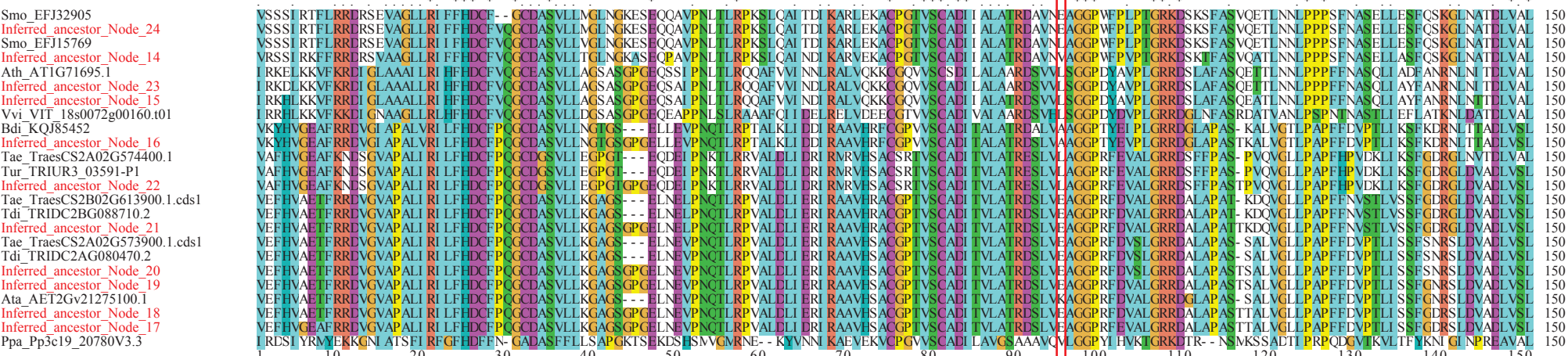
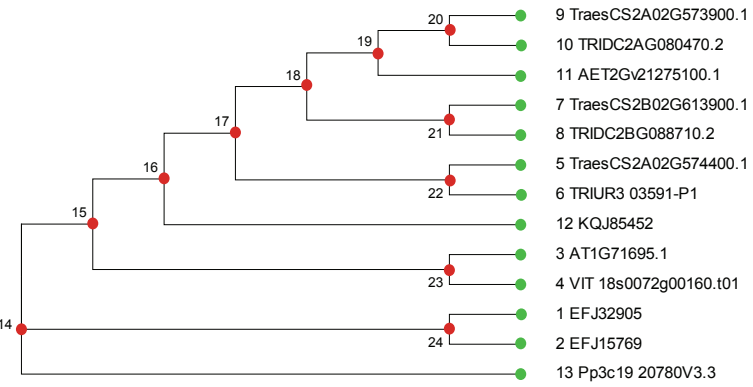


a

Positively selected sites and inferred ancestral sequences by M2a model of PAML

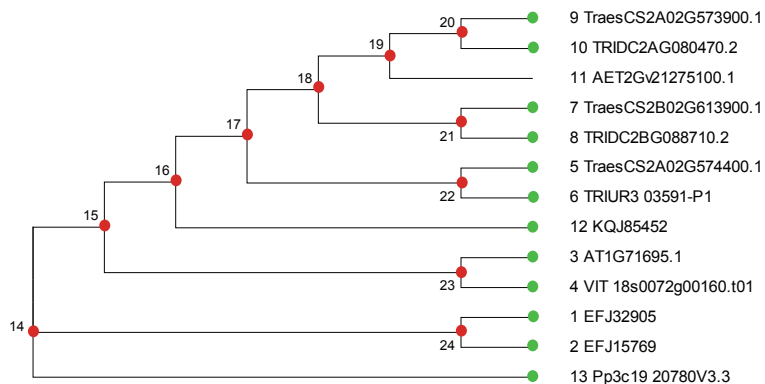
Naive Empirical Bayes (NEB) analysis
Bayes Empirical Bayes (BEB) analysis
Positively selected sites (*: P>95%; **: P>99%)
(amino acids refer to 1st sequence: EFJ32905)

	Pr(w>1)	post mean +- SE for w
95 E	0.583	2.890 +- 2.403
185 K	0.558	2.760 +- 2.335



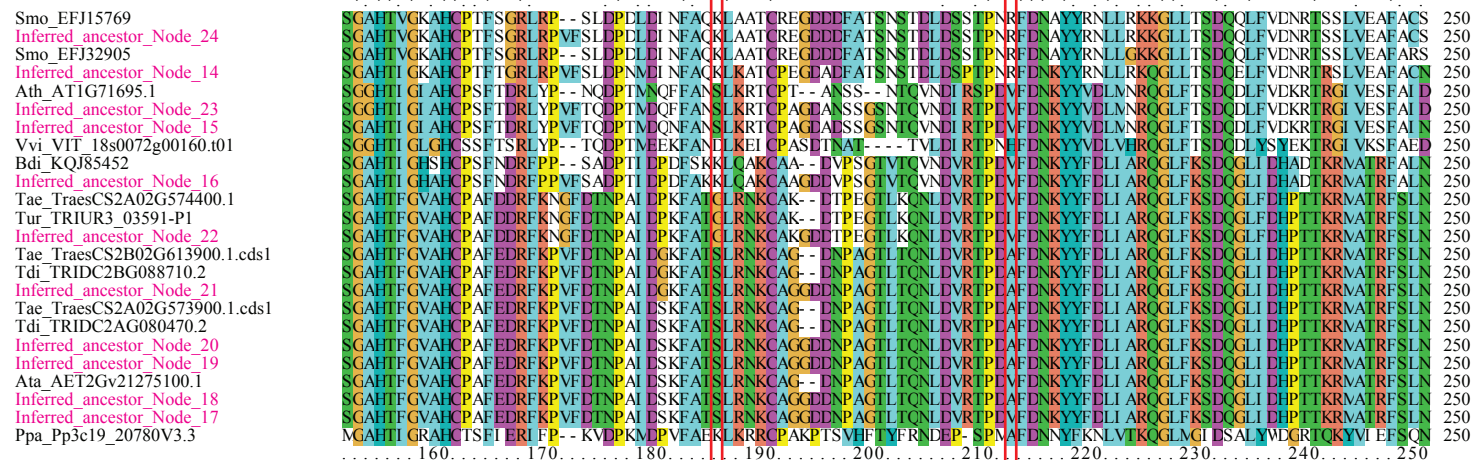
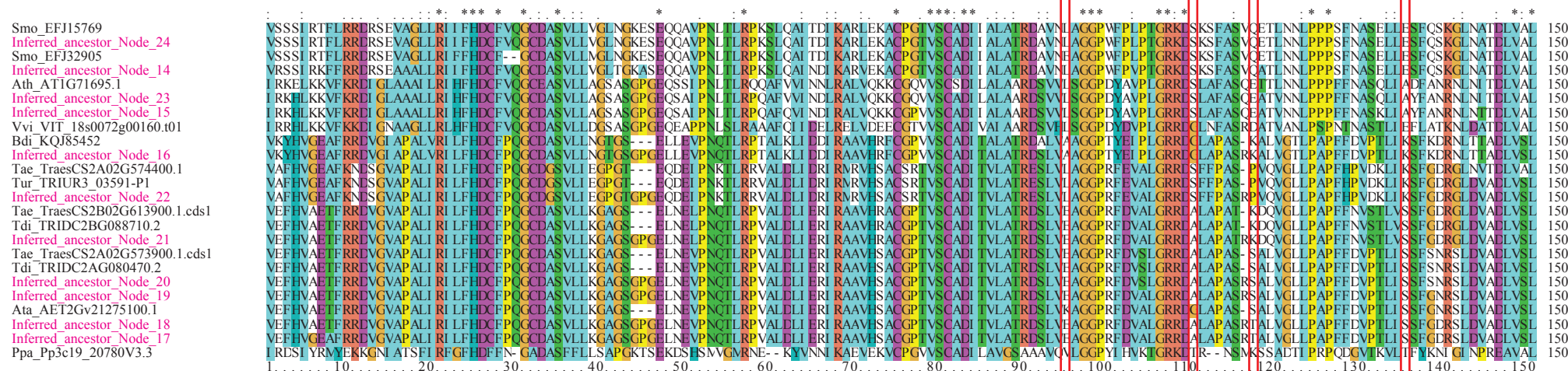
b

Positively selected sites and inferred ancestral sequences by M8 model of PAML



Naive Empirical Bayes (NEB) analysis
 Bayes Empirical Bayes (BEB) analysis
 Positively selected sites (*: P>95%; **: P>99%)
 (amino acids refer to 1st sequence: EFJ32905)

	Pr(w>1)	post mean +- SE for w
95 E	0.843	2.107 +- 1.258
110 S	0.531	1.427 +- 1.021
117 Q	0.665	1.798 +- 1.321
135 E	0.608	1.538 +- 1.007
185 K	0.867	2.131 +- 1.237
212 R	0.704	1.842 +- 1.248



C

Inferred ancestral sequences by MEGAX

