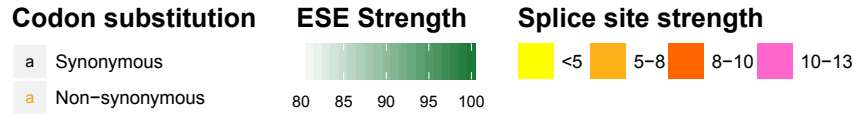
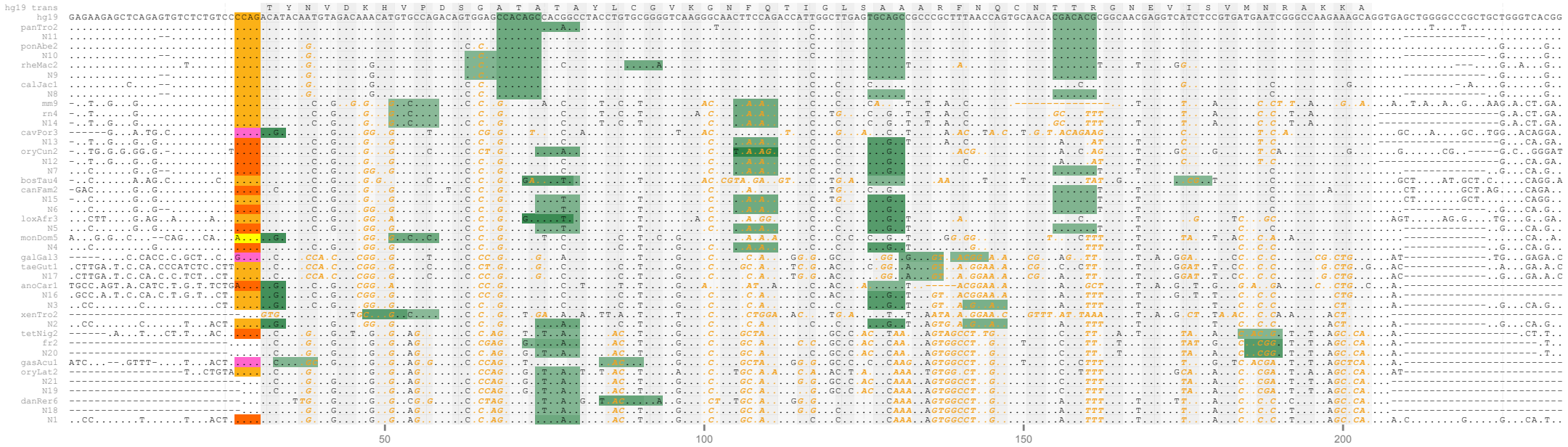
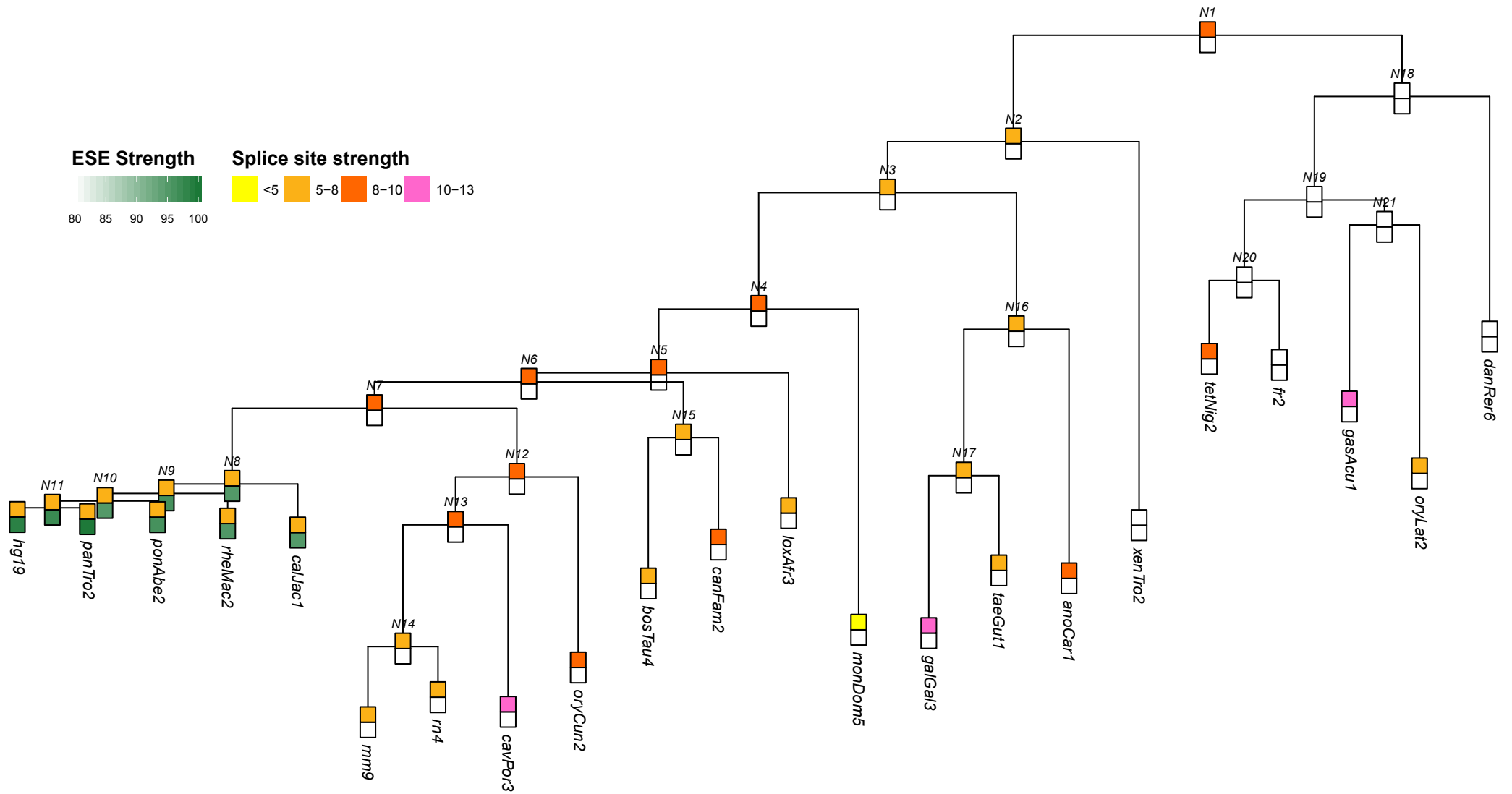


ALPP | SRPs



Supplementary figure 1

Comparative genomic alignment of ALPP orthologues along with reconstructed ancestral nodes (see Supplementary figure 2). 3' splice site strength is colour coded according to the splice site strength (the stronger the splice site the darker the colour). ESEfinder motif with more than 90% consensus are highlighted in green. The intensity of the shade of green reflects the strength of the score of the motifs. Reconstructed ancestral sequences (hypothetical taxonomy unit nodes) are named N1-N21 while the genomic sequence names follows the UCSC convention (<http://genome.ucsc.edu/FAQ/FAQreleases.html>).



Supplementary figure 2

Phylogenetic tree of the ALPP orthologues and reconstructed ancestral sequences. Boxes represent the presence/absence of an ESE in investigated positions relative to the strength of 3' splice site.